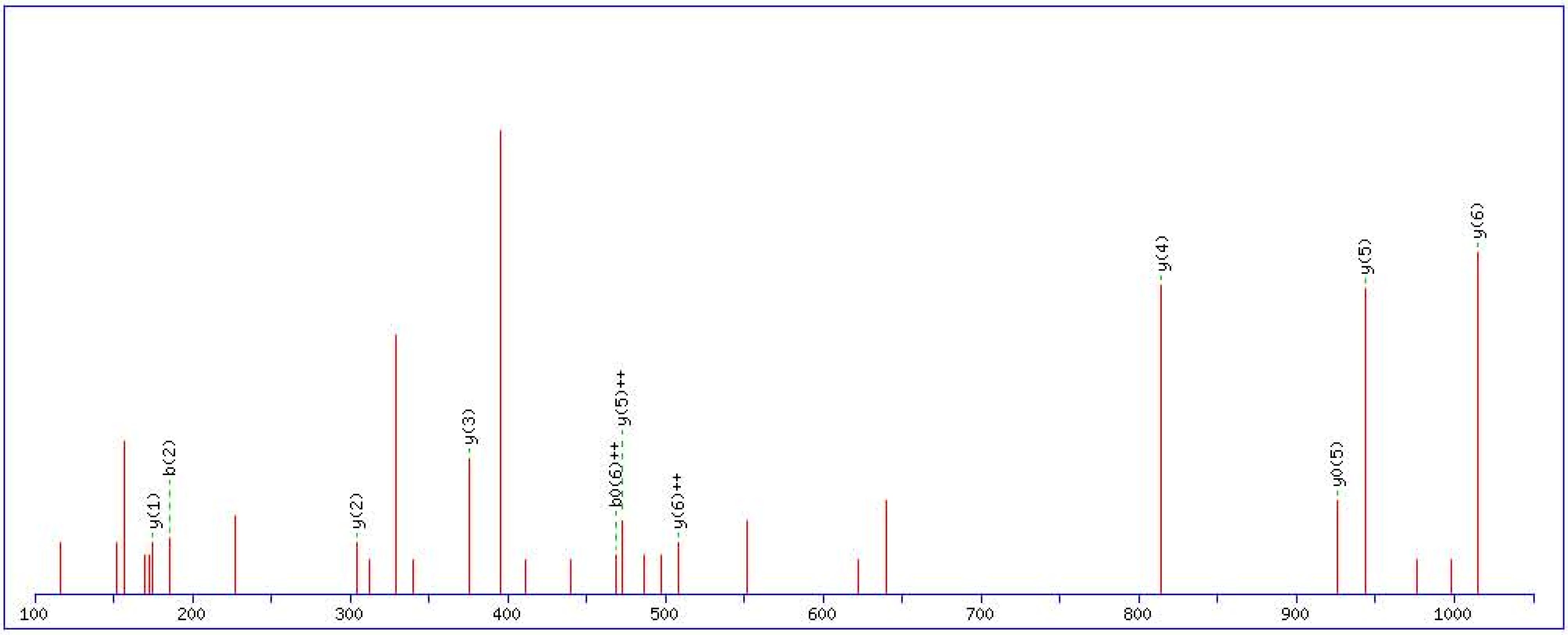
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAEQAER**
Found in **1433B_HUMAN**, 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3

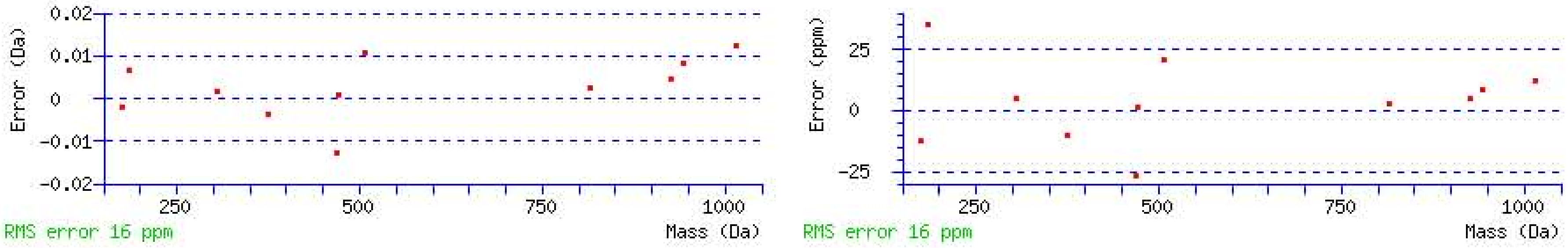
Match to Query 14957: 1126.580488 from(564.297520,2+) rtinseconds(1443) index(42521)
Title: Locus:1.1.1.3215.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1126.580444
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 25  Expect: 0.037
Matches : 11/60 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					**L**							7
2	185.128454	93.067865					**A**	***1014.503692***	507.755484	997.477143	499.242210	996.493127	498.750202	6
3	314.171047	157.589161			296.160482	148.583879	**E**	***943.466578***	472.236927	926.440029	463.723653	925.456013	463.231645	5
4	753.396373	377.201825	736.369824	368.688550	735.385808	368.196542	**Q**	***814.423985***	407.715631	797.397436	399.202356	796.413420	398.710348	4
5	824.433487	412.720382	807.406938	404.207107	806.422922	403.715099	**A**	***375.198659***	188.102968	358.172110	179.589693	357.188094	179.097685	3
6	953.476080	477.241678	936.449531	468.728404	935.465515	468.236396	**E**	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
7							**R**	***175.118952***	88.063114	158.092403	79.549840			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.3	1126.580444	0.000044	LAEQAER
9.5	1126.580444	0.000044	LAQAEER
0.6	1126.573074	0.007414	SPERPTGDLR

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

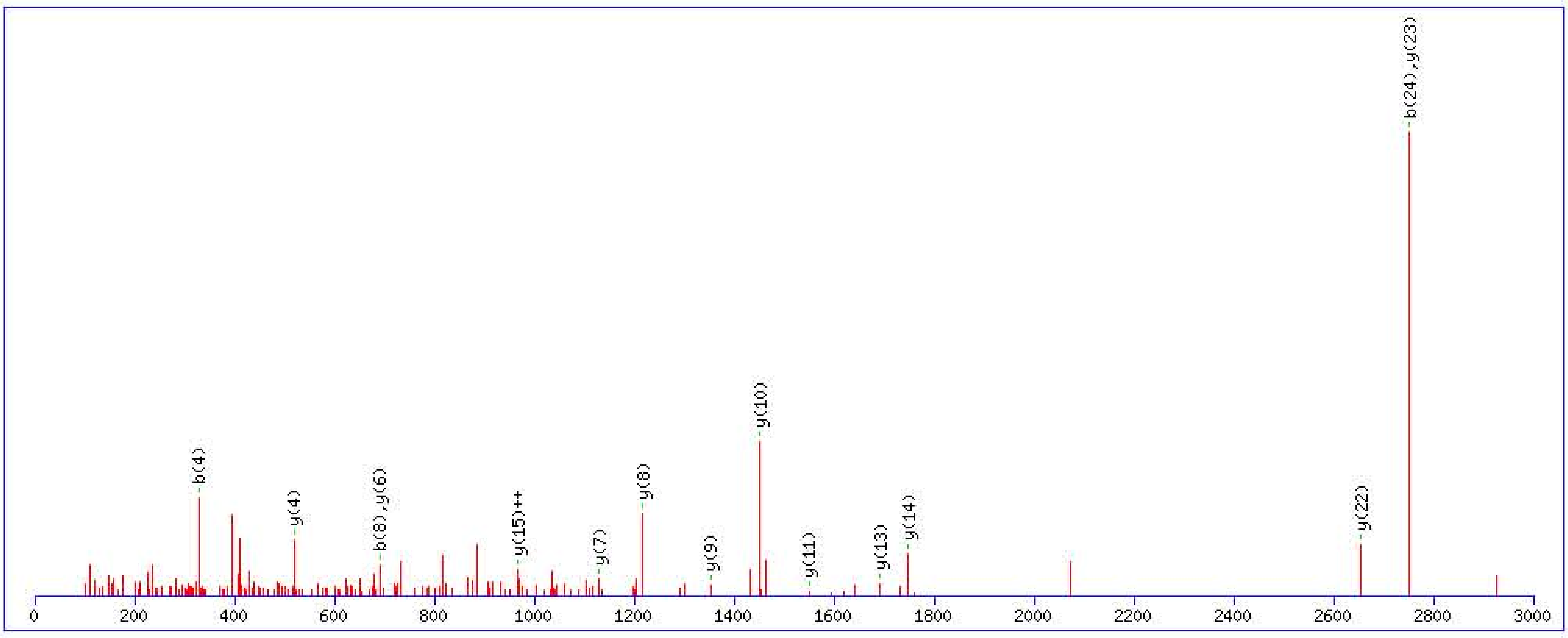
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSPGGASFYHWGAAVPHSQGDALCR**
Found in **ATS13_HUMAN**, A disintegrin and metalloproteinase with thrombospondin motifs 13 OS=Homo sapiens GN=ADAMTS13 PE=1 SV=1

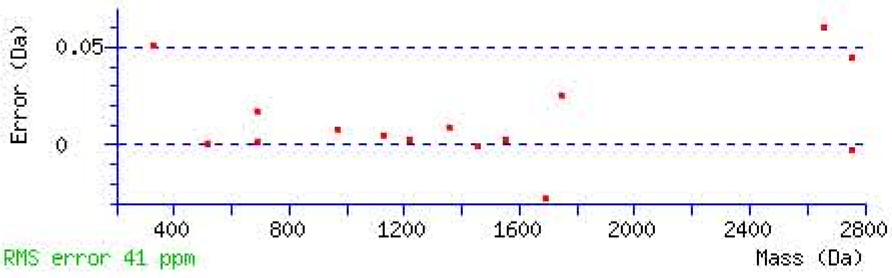
Match to Query 53296: 2925.342136 from(732.342810,4+) rtinseconds(2070) index(32283)
Title: Locus:1.1.1.3384.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

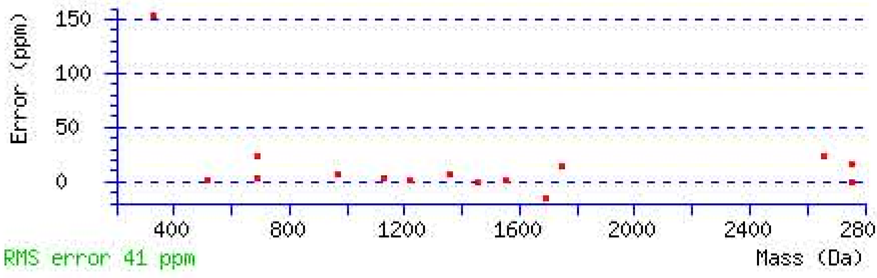
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2925.343918
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q19     : Biotin:Thermo-21345 (Q)
Ions Score: 71  Expect: 2.6e-007
Matches : 15/244 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	88.039304	44.523290			70.028739	35.518008	S							25
2	175.071332	88.039304			157.060767	79.034021	S	2839.319152	1420.163214	2822.292603	1411.649939	2821.308587	1411.157931	24
3	272.124096	136.565686			254.113531	127.560403	P	***2752.287124***	1376.647200	2735.260575	1368.133925	2734.276559	1367.641917	23
4	**329.145560**	165.076418			311.134995	156.071135	G	***2655.234360***	1328.120818	2638.207811	1319.607543	2637.223795	1319.115535	22
5	386.167024	193.587150			368.156459	184.581867	G	2598.212896	1299.610086	2581.186347	1291.096811	2580.202331	1290.604803	21
6	457.204138	229.105707			439.193573	220.100424	A	2541.191432	1271.099354	2524.164883	1262.586079	2523.180867	1262.094071	20
7	544.236166	272.621721			526.225601	263.616438	S	2470.154318	1235.580797	2453.127769	1227.067522	2452.143753	1226.575514	19
8	**691.304580**	346.155928			673.294015	337.150645	F	2383.122290	1192.064783	2366.095741	1183.551508	2365.111725	1183.059500	18
9	854.367909	427.687592			836.357344	418.682310	Y	2236.053876	1118.530576	2219.027327	1110.017301	2218.043311	1109.525293	17
10	991.426821	496.217048			973.416256	487.211766	H	2072.990547	1036.998911	2055.963998	1028.485637	2054.979982	1027.993629	16
11	1177.506134	589.256705			1159.495569	580.251422	W	1935.931635	968.469456	1918.905086	959.956181	1917.921070	959.464173	15
12	1234.527598	617.767437			1216.517033	608.762154	G	***1749.852322***	875.429799	1732.825773	866.916525	1731.841757	866.424517	14
13	1305.564712	653.285994			1287.554147	644.280711	A	***1692.830858***	846.919067	1675.804309	838.405793	1674.820293	837.913785	13
14	1376.601826	688.804551			1358.591261	679.799268	A	1621.793744	811.400510	1604.767195	802.887236	1603.783179	802.395228	12
15	1475.670240	738.338758			1457.659675	729.333475	V	***1550.756630***	775.881953	1533.730081	767.368679	1532.746065	766.876671	11
16	1572.723004	786.865140			1554.712439	777.859857	P	***1451.688216***	726.347746	1434.661667	717.834472	1433.677651	717.342464	10
17	1709.781916	855.394596			1691.771351	846.389313	H	***1354.635452***	677.821364	1337.608903	669.308090	1336.624887	668.816082	9
18	1796.813944	898.910610			1778.803379	889.905327	S	***1217.576540***	609.291908	1200.549991	600.778634	1199.565975	600.286626	8
19	2236.039270	1118.523273	2219.012721	1110.009998	2218.028705	1109.517990	Q	***1130.544512***	565.775894	1113.517963	557.262620	1112.533947	556.770612	7
20	2293.060734	1147.034005	2276.034185	1138.520730	2275.050169	1138.028722	G	***691.319186***	346.163231	674.292637	337.649956	673.308621	337.157948	6
21	2408.087677	1204.547476	2391.061128	1196.034202	2390.077112	1195.542194	D	634.297722	317.652499	617.271173	309.139225	616.287157	308.647217	5
22	2479.124791	1240.066033	2462.098242	1231.552759	2461.114226	1231.060751	A	***519.270779***	260.139028	502.244230	251.625753			4
23	2592.208855	1296.608065	2575.182306	1288.094791	2574.198290	1287.602783	L	448.233665	224.620470	431.207116	216.107196			3
24	**2752.239504**	1376.623390	2735.212955	1368.110115	2734.228939	1367.618107	C	335.149601	168.078438	318.123052	159.565164			2
25							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.8	2925.343918	-0.001782	SSPGGASFYHWGAAVPHSQGDALCR
0.5	2925.349747	-0.007611	GSYSNSPSNPVNSRANQDFSALMR
0.3	2925.312012	0.030124	MSASAPAAEGEGTPTQPASEKEPEMPGPR

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

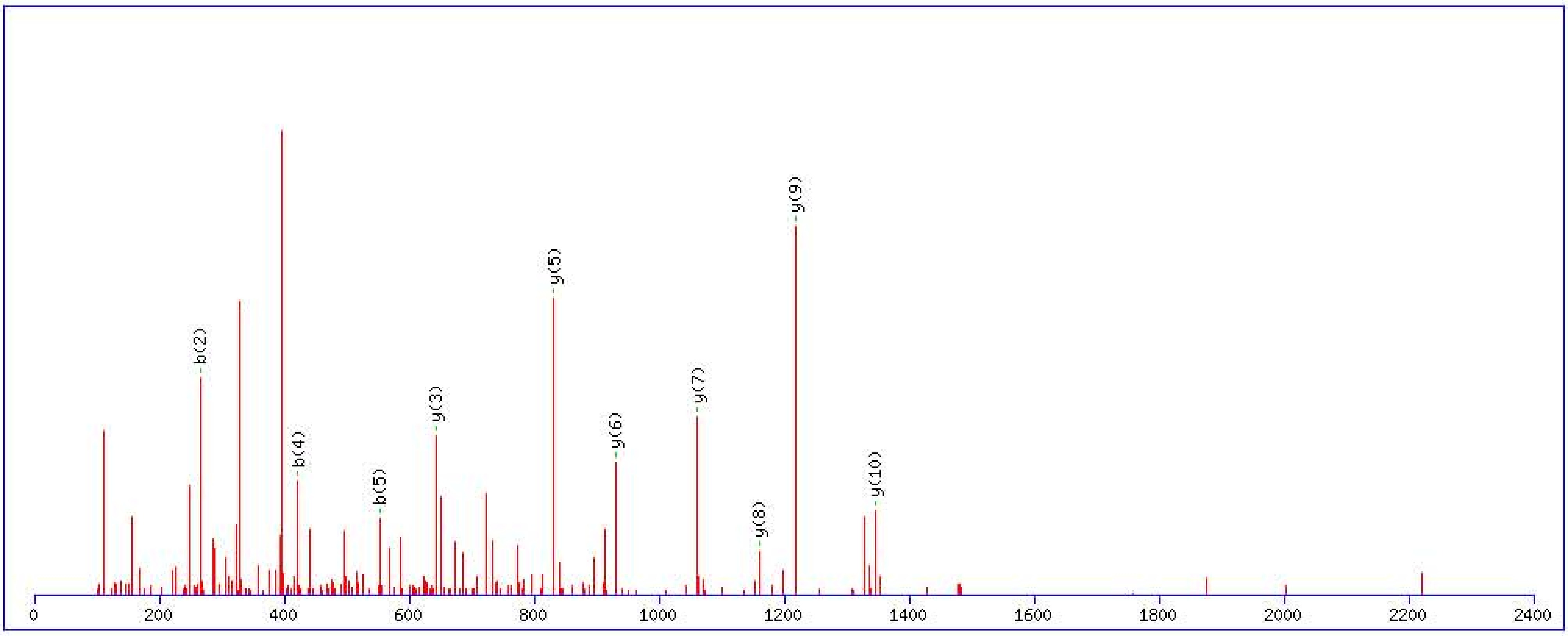
Mascot Search Results

Peptide View

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

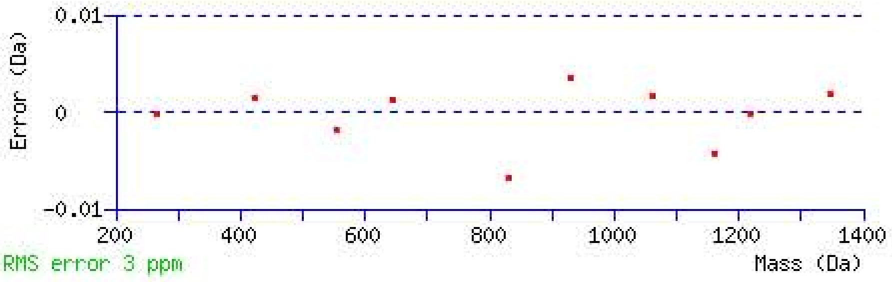
Match to Query 26756: 1481.718388 from(741.866470,2+) rtinseconds(1646) index(29758)
Title: Locus:1.1.1.3236.21 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

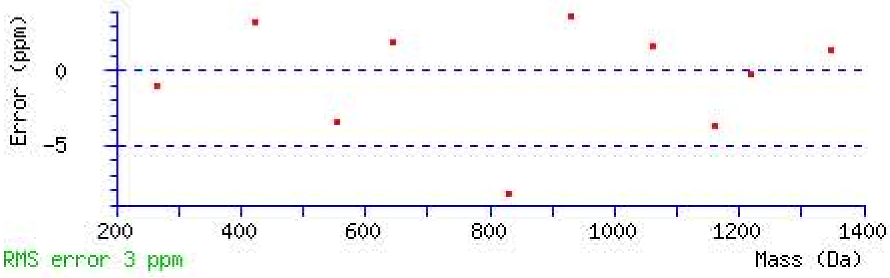
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1481.730545
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 0.0001
Matches : 10/78 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	138.066188	69.536732			H					11
2	**266.124766**	133.566021	249.098217	125.052746	Q	***1345.678898***	673.343087	1328.652349	664.829813	10
3	323.146230	162.076753	306.119681	153.563478	G	***1217.620320***	609.313798	1200.593771	600.800524	9
4	**422.214644**	211.610960	405.188095	203.097685	V	***1160.598856***	580.803066	1143.572307	572.289792	8
5	**553.255129**	277.131203	536.228580	268.617928	M	***1061.530442***	531.268859	1044.503893	522.755585	7
6	652.323543	326.665410	635.296994	318.152135	V	***930.489957***	465.748617	913.463408	457.235342	6
7	709.345007	355.176142	692.318458	346.662867	G	***831.421543***	416.214410	814.394994	407.701135	5
8	840.385492	420.696384	823.358943	412.183110	M	774.400079	387.703678	757.373530	379.190403	4
9	897.406956	449.207116	880.380407	440.693842	G	***643.359594***	322.183435	626.333045	313.670161	3
10	1336.632282	668.819779	1319.605733	660.306505	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 HQGVMVGMGQK
(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	1481.730545	-0.012157	HQGVMVGMGQK

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

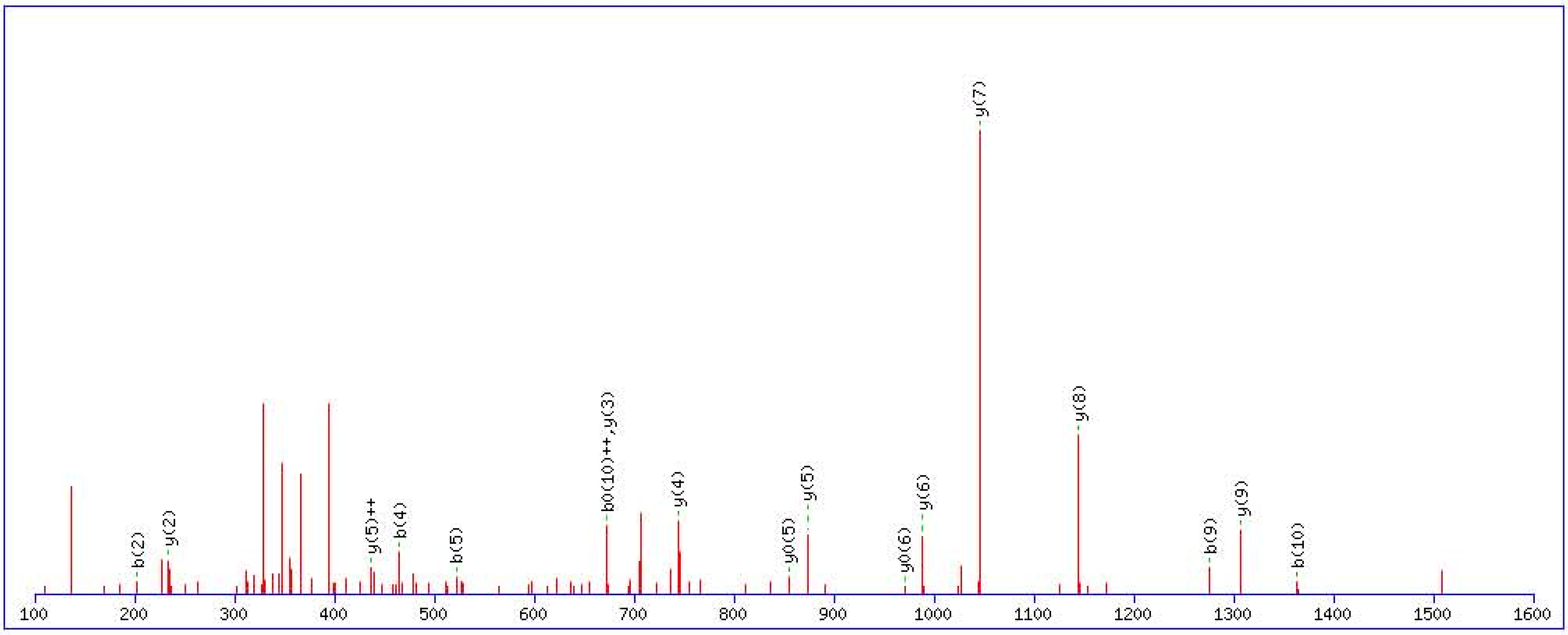
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

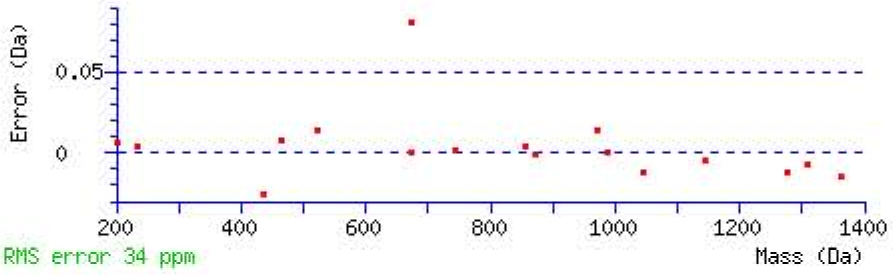
Match to Query 27447: 1508.675648 from(755.345100,2+) rtinseconds(1606) index(16558)
Title: Locus:1.1.1.3125.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

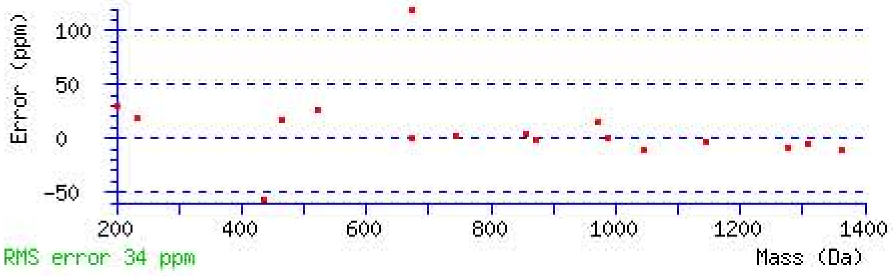
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1508.681702
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 5.9e-005
Matches : 17/102 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	**203.066247**	102.036761			185.055682	93.031479	S	1394.662043	697.834660	1377.635494	689.321385	1376.651478	688.829377	10
3	366.129576	183.568426			348.119011	174.563144	Y	***1307.630015***	654.318646	1290.603466	645.805371	1289.619450	645.313363	9
4	**465.197990**	233.102633			447.187425	224.097351	V	***1144.566686***	572.786981	1127.540137	564.273707	1126.556121	563.781699	8
5	**522.219454**	261.613365			504.208889	252.608083	G	***1045.498272***	523.252774	1028.471723	514.739500	1027.487707	514.247492	7
6	637.246397	319.126837			619.235832	310.121554	D	***988.476808***	494.742042	971.450259	486.228768	970.466243	485.736760	6
7	766.288990	383.648133			748.278425	374.642851	E	***873.449865***	437.228571	856.423316	428.715296	855.439300	428.223288	5
8	837.326104	419.166690			819.315539	410.161408	A	***744.407272***	372.707274	727.380723	364.194000	726.396707	363.701992	4
9	**1276.551430**	638.779353	1259.524881	630.266079	1258.540865	629.774070	Q	***673.370158***	337.188717	656.343609	328.675443	655.359593	328.183435	3
10	**1363.583458**	682.295367	1346.556909	673.782093	1345.572893	673.290085	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
11							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.5	1508.681702	-0.006054	DSYVGDEAQSK
7.9	1508.690277	-0.014629	GGRGGMGGSDRGGFNK

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

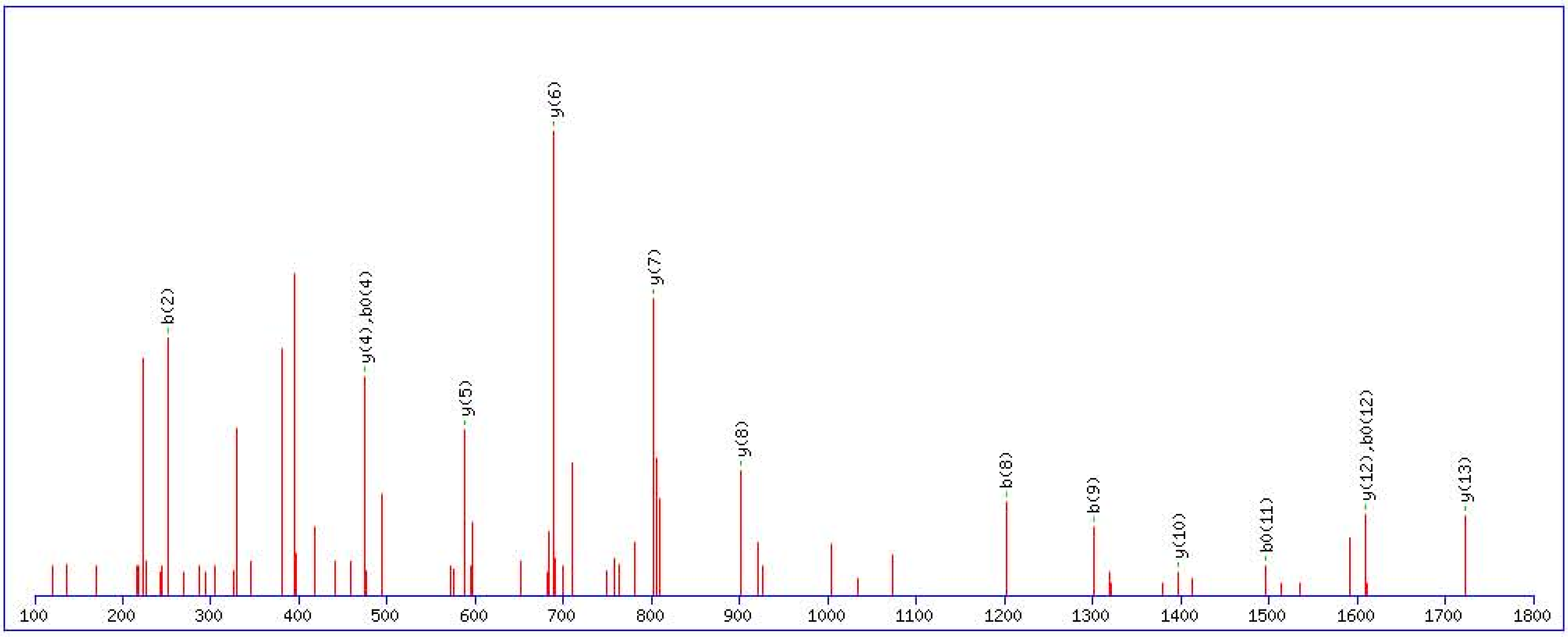
Mascot Search Results

Peptide View

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

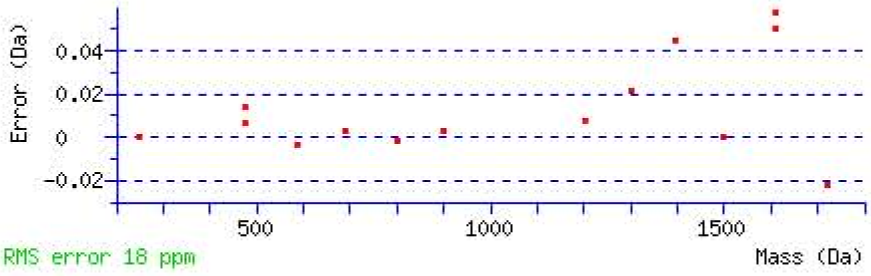
Match to Query 41632: 2101.048392 from(701.356740,3+) rtinseconds(2627) index(35424)
Title: Locus:1.1.1.3578.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

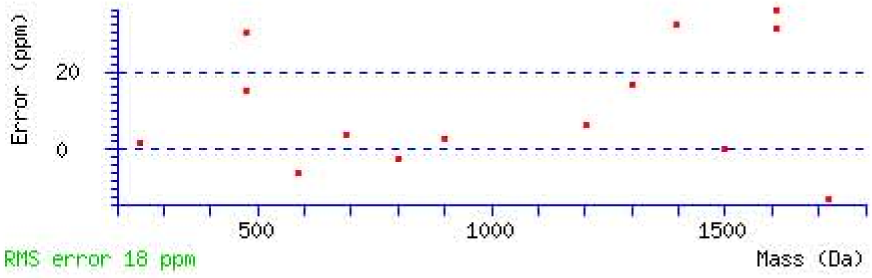
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2101.051376
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 59  Expect: 3.2e-006
Matches : 14/164 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	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
59.1	2101.051376	-0.002984	SYELPDGQVITIGNER
0.5	2101.022842	0.025550	SDGSKITYIDYYRQQHK

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

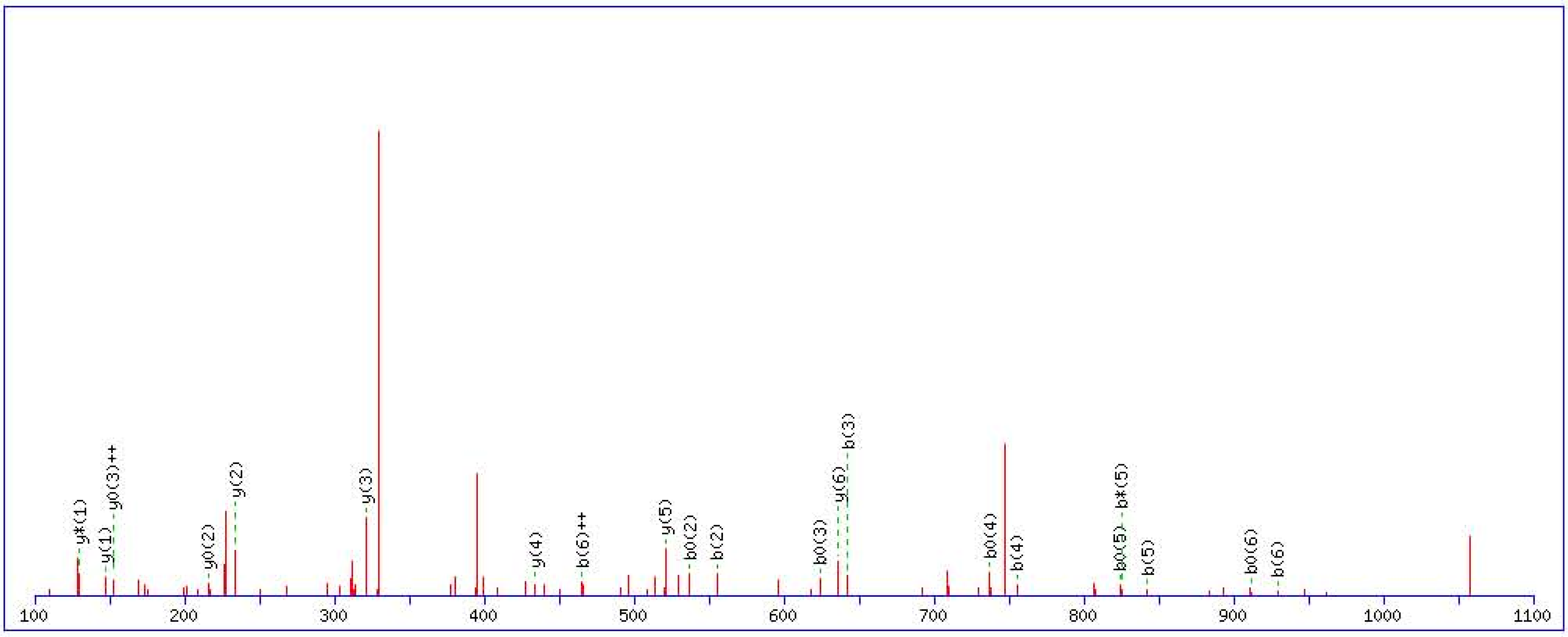
Mascot Search Results

Peptide View

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

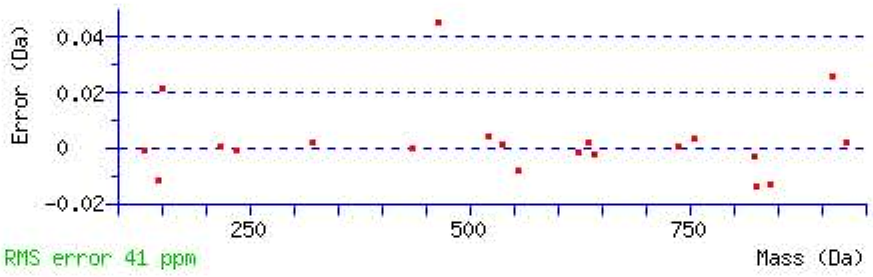
Match to Query 13386: 1074.538028 from(538.276290,2+) rtinseconds(1450) index(1658)
Title: Locus:1.1.1.3024.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

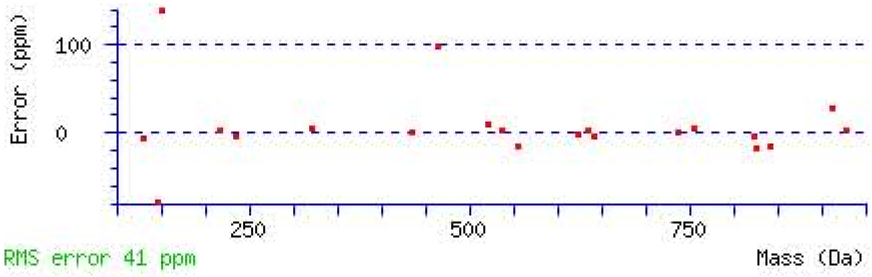
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1074.537933
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.01
Matches : 21/68 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	440.232602	220.619939	423.206053	212.106664			**Q**							7
2	**555.259545**	278.133411	538.232996	269.620136	537.248980	269.128128	**D**	***636.319895***	318.663586	619.293346	310.150311	618.309330	309.658303	6
3	**642.291573**	321.649425	625.265024	313.136150	624.281008	312.644142	**S**	***521.292952***	261.150114	504.266403	252.636840	503.282387	252.144832	5
4	**755.375637**	378.191457	738.349088	369.678182	737.365072	369.186174	**I**	***434.260924***	217.634100	417.234375	209.120826	416.250359	208.628818	4
5	**842.407665**	421.707471	825.381116	413.194196	824.397100	412.702188	**S**	***321.176860***	161.092068	304.150311	152.578794	303.166295	152.086786	3
6	**929.439693**	465.223484	912.413144	456.710210	911.429128	456.218202	**S**	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
7							**K**	***147.112804***	74.060040	130.086255	65.546766			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.9	1074.537933	0.000095	QDSISSK
11.3	1074.530548	0.007480	QVTEPTSSAR
7.4	1074.549164	-0.011136	NIRPVDMSK
6.0	1074.537933	0.000095	QDSSKSI
3.9	1074.531418	0.006610	LLACPSVCR
3.5	1074.553192	-0.015164	QPSFSAK
3.2	1074.537933	0.000095	SQEVSSK
2.4	1074.530518	0.007510	KPEDRSSEK
2.3	1074.549164	-0.011136	KSTLSMHQK
1.9	1074.537949	0.000079	ELVVNVCDK

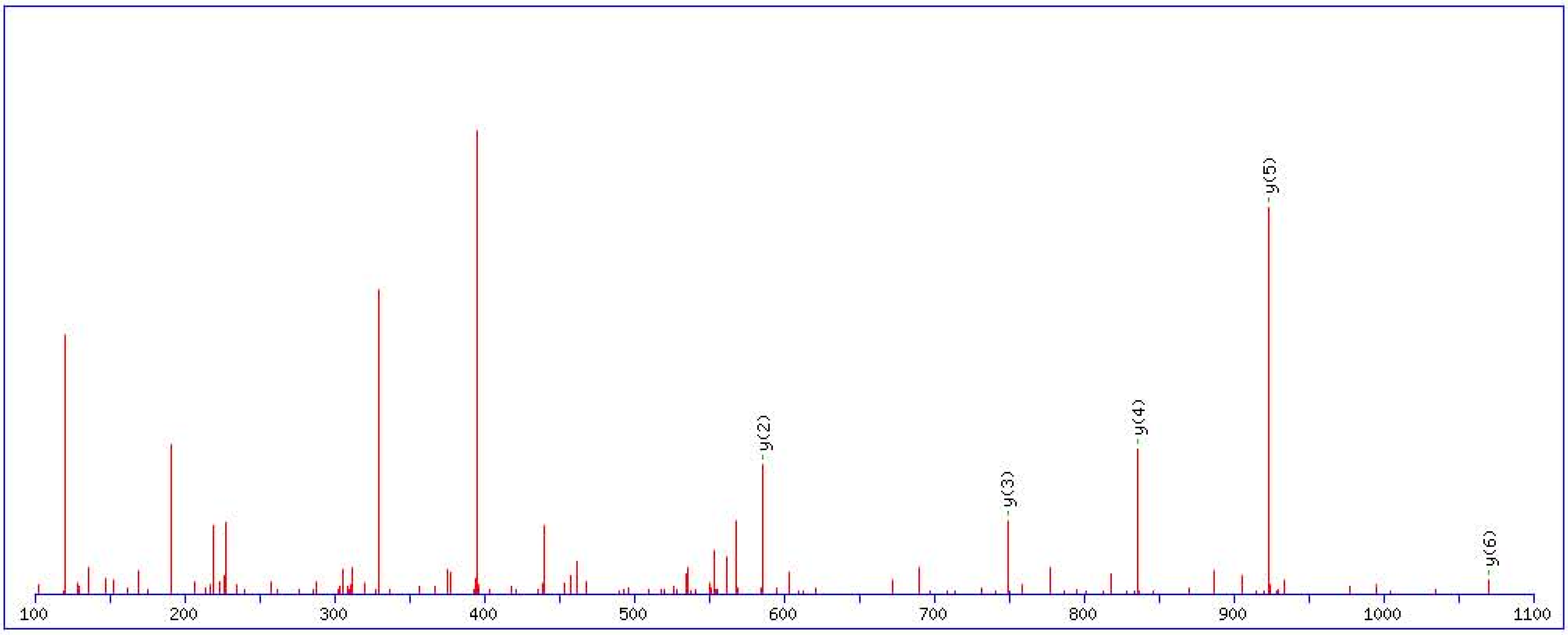
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

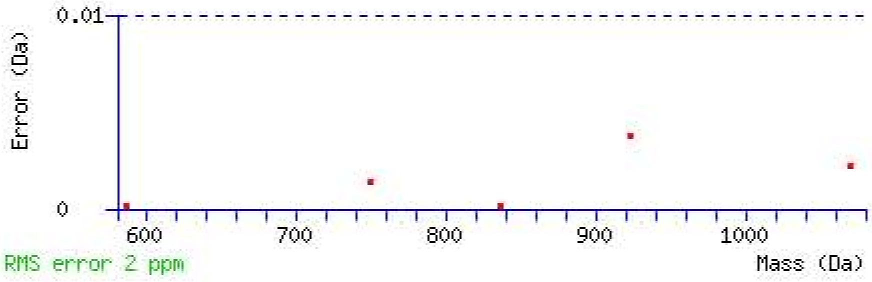
Match to Query 16020: 1140.562508 from(571.288530,2+) rtinseconds(1673) index(3088)
Title: Locus:1.1.1.3102.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

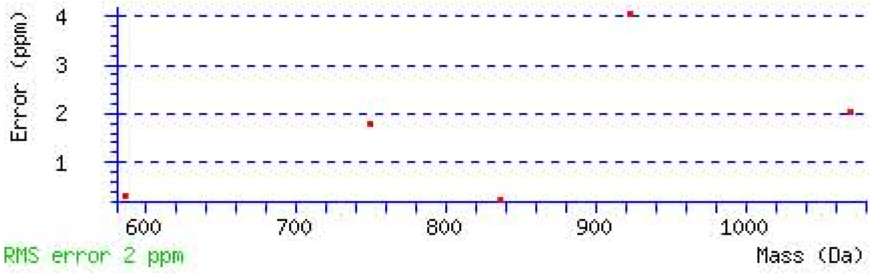
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1140.563751
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.0097
Matches : 5/52 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	72.044390	36.525833					A							7
2	219.112804	110.060040					F	*1070.533929*	535.770603	1053.507380	527.257328	1052.523364	526.765320	6
3	306.144832	153.576054			288.134267	144.570772	S	*923.465515*	462.236396	906.438966	453.723121	905.454950	453.231113	5
4	393.176860	197.092068			375.166295	188.086785	S	*836.433487*	418.720382	819.406938	410.207107	818.422922	409.715099	4
5	556.240189	278.623733			538.229624	269.618450	Y	*749.401459*	375.204368	732.374910	366.691093			3
6	995.465515	498.236396	978.438966	489.723121	977.454950	489.231113	Q	*586.338130*	293.672703	569.311581	285.159429			2
7							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of AFSSYQK
(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	1140.563751	-0.001243	AFSSYQK
6.1	1140.559723	0.002785	AFSRSSDLMK
1.6	1140.545792	0.016716	MAESAPARHR
0.9	1140.552322	0.010186	AHDEAVRSEK

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

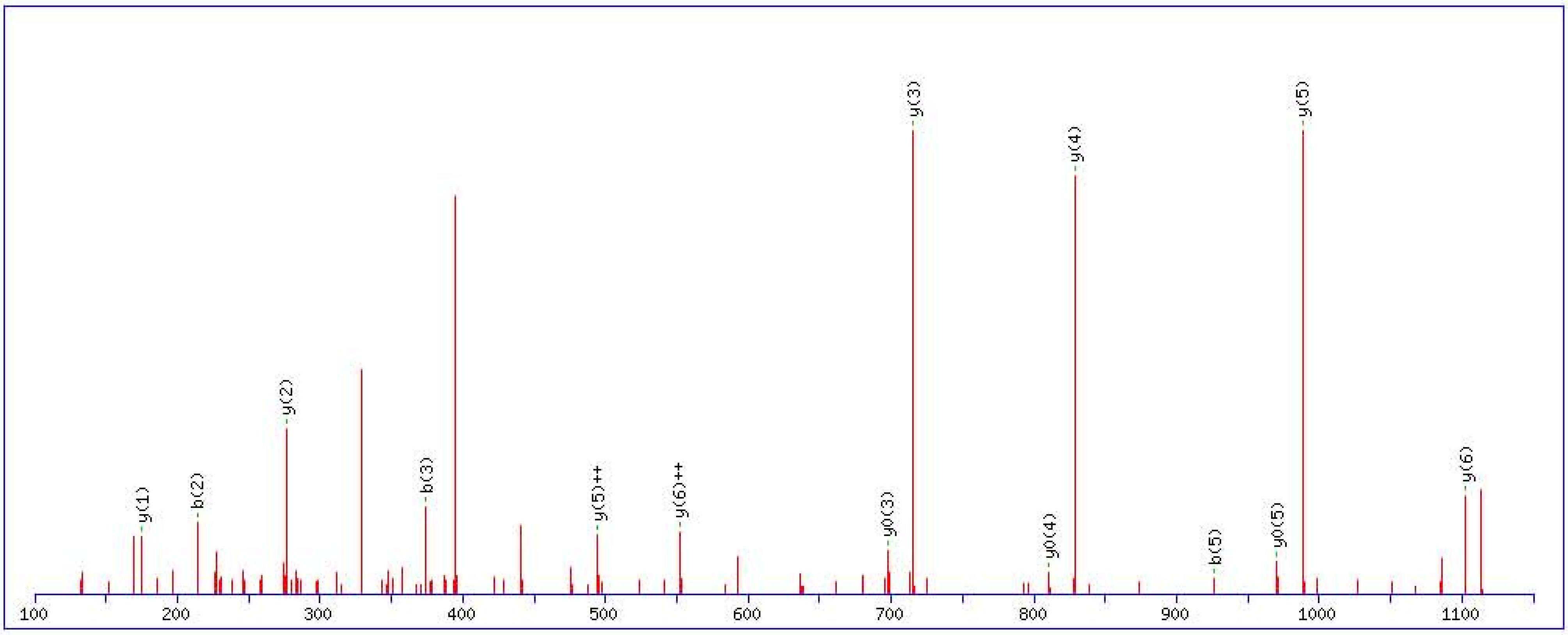
Mascot Search Results

Peptide View

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

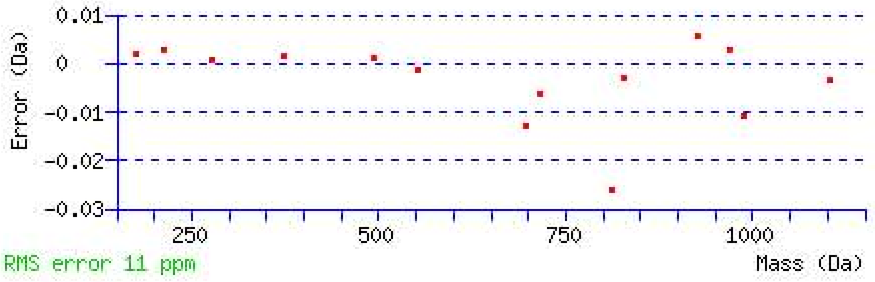
Match to Query 17758: 1200.601968 from(601.308260,2+) rtinseconds(1543) index(16135)
Title: Locus:1.1.1.3103.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

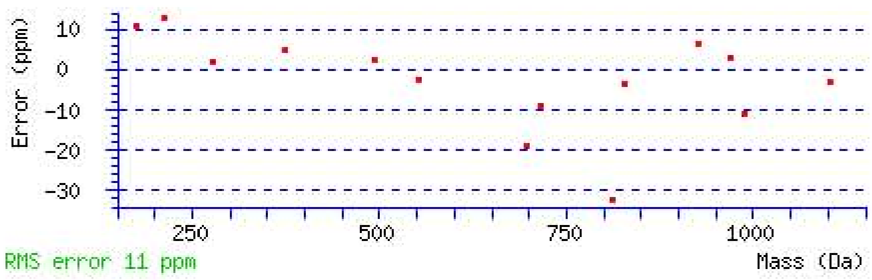
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 46  Expect: 0.00029
Matches : 14/58 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	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
46.2	1200.610733	-0.008765	VNCLQTR
7.9	1200.603333	-0.001365	VMSKSGHSNVR
6.1	1200.603333	-0.001365	GRIAEPSVCGR
4.2	1200.607361	-0.005393	RGDYVHVMPK
3.4	1200.617233	-0.015265	VMEETPNILR
1.0	1200.611191	-0.009223	HDSHLAKHTR
0.6	1200.592087	0.009881	SATEQQAR

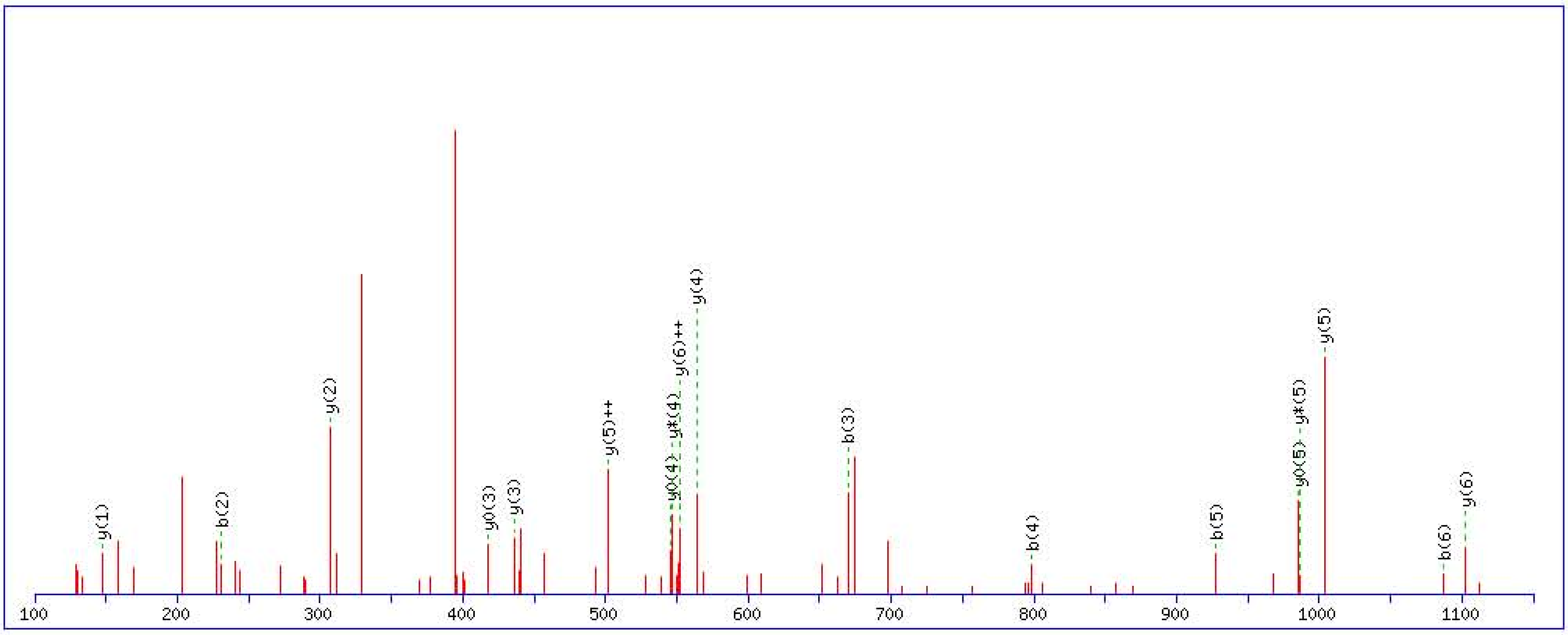
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

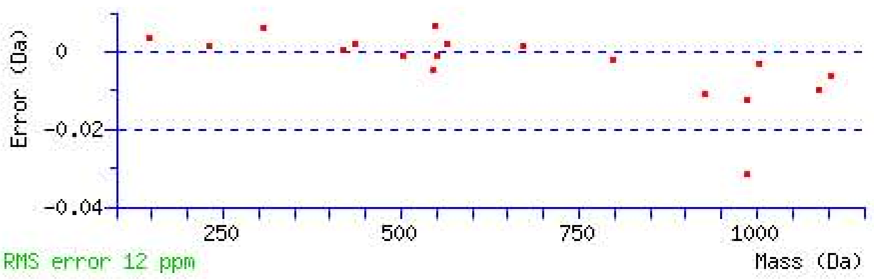
Match to Query 18474: 1232.568648 from(617.291600,2+) rtinseconds(1380) index(15088)
Title: Locus:1.1.1.3046.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

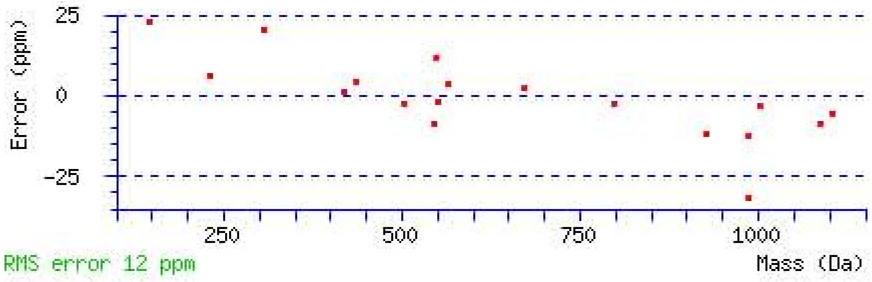
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1232.571564
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.012
Matches : 18/56 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	132.047761	66.527518					**M**							7
2	**231.116175**	116.061725					**V**	***1102.538364***	551.772820	1085.511815	543.259546	1084.527799	542.767538	6
3	**670.341501**	335.674389	653.314952	327.161114			**Q**	***1003.469950***	502.238613	986.443401	493.725339	985.459385	493.233331	5
4	**798.400079**	399.703678	781.373530	391.190403			**Q**	***564.244624***	282.625950	547.218075	274.112676	546.234059	273.620668	4
5	**927.442672**	464.224974	910.416123	455.711700	909.432107	455.219692	**E**	***436.186046***	218.596661	419.159497	210.083387	418.175481	209.591379	3
6	**1087.473321**	544.240299	1070.446772	535.727024	1069.462756	535.235016	**C**	***307.143453***	154.075365	290.116904	145.562090			2
7							**K**	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.6	1232.571564	-0.002916	MVQQECK
14.4	1232.571564	-0.002916	MVQQECK
5.0	1232.570694	-0.002046	QDDKSSDK
1.9	1232.570679	-0.002031	ENVPASSLCEK
1.8	1232.564163	0.004485	EPQRGMGSMPK
1.2	1232.556091	0.012557	ETPPSFPESDK
0.2	1232.564163	0.004485	EPQRGMGSMPK

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

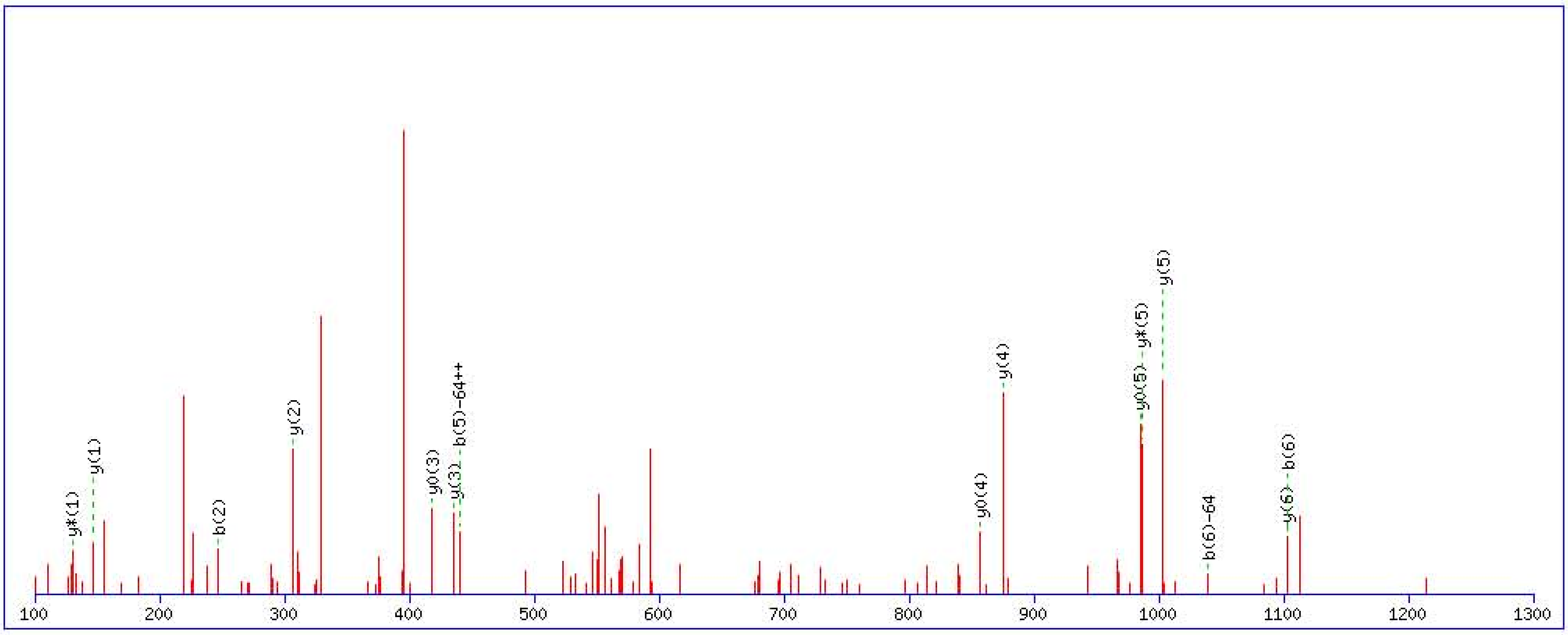
Mascot Search Results

Peptide View

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

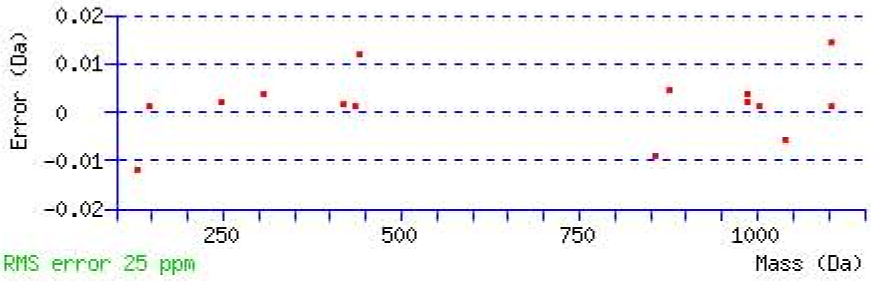
Match to Query 18927: 1248.568408 from(625.291480,2+) rtinseconds(1281) index(784)
Title: Locus:1.1.1.2965.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

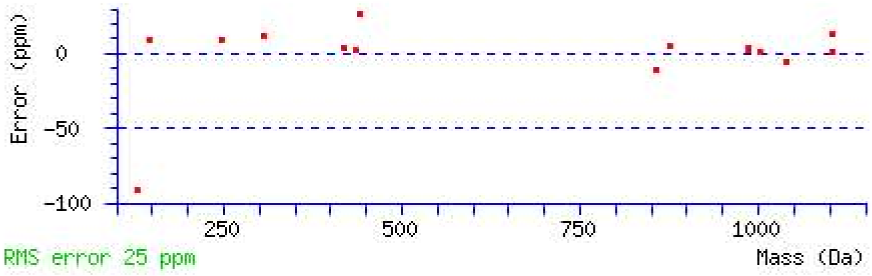
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1248.566483
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
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.0044
Matches : 15/80 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	148.042676	74.524976					M							7
2	247.111090	124.059183					V	*1102.538364*	551.772820	1085.511815	543.259546	1084.527799	542.767538	6
3	375.169668	188.088472	358.143119	179.575198			Q	*1003.469950*	502.238613	986.443401	493.725338	985.459385	493.233330	5
4	814.394994	407.701135	797.368445	399.187861			Q	*875.411372*	438.209324	858.384823	429.696050	857.400807	429.204042	4
5	943.437587	472.222432	926.411038	463.709157	925.427022	463.217149	E	*436.186046*	218.596661	419.159497	210.083386	418.175481	209.591378	3
6	**1103.468236**	552.237756	1086.441687	543.724482	1085.457671	543.232473	C	*307.143453*	154.075364	290.116904	145.562090			2
7							K	*147.112804*	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.5	1248.566483	0.001925	MVQQECK
18.5	1248.566483	0.001925	MVQQECK
4.2	1248.576813	-0.008405	KCESLEQEAR
1.8	1248.569611	-0.001203	MYEVYDAKSK
0.7	1248.584244	-0.015836	MHSMISSVDVK

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

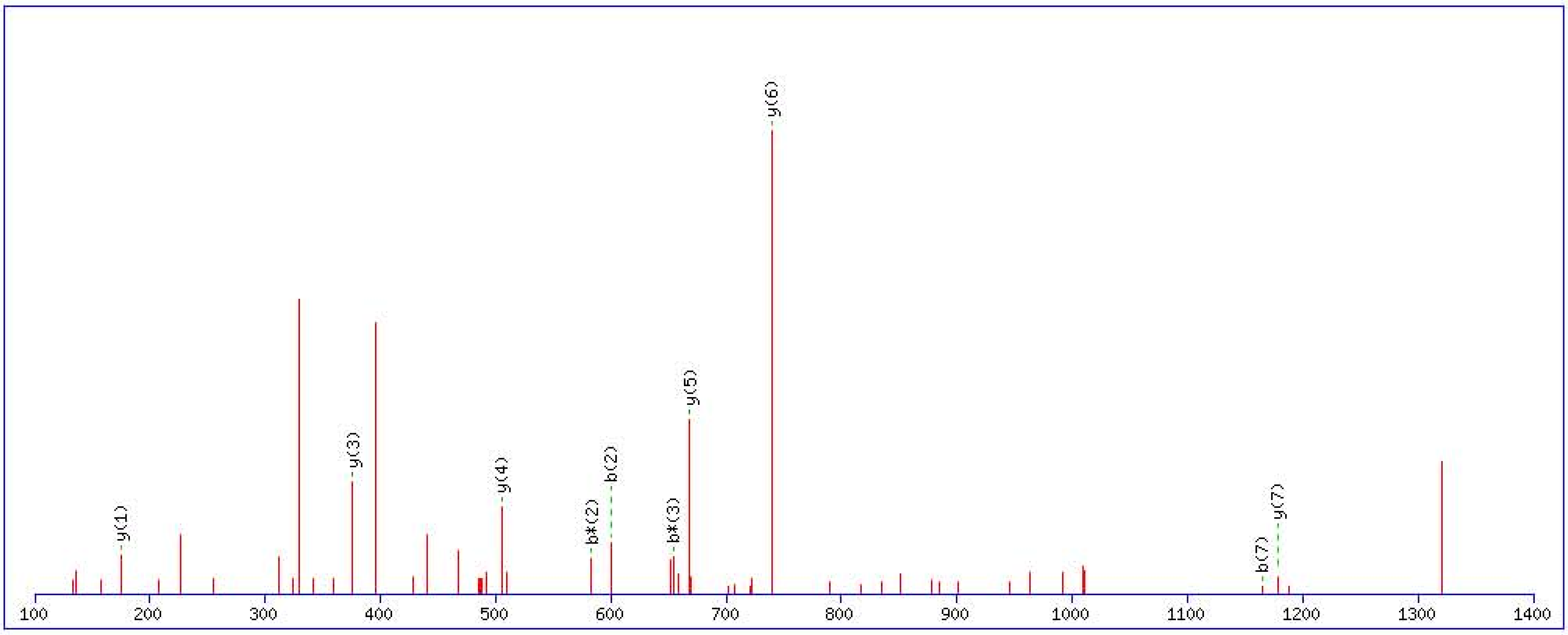
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

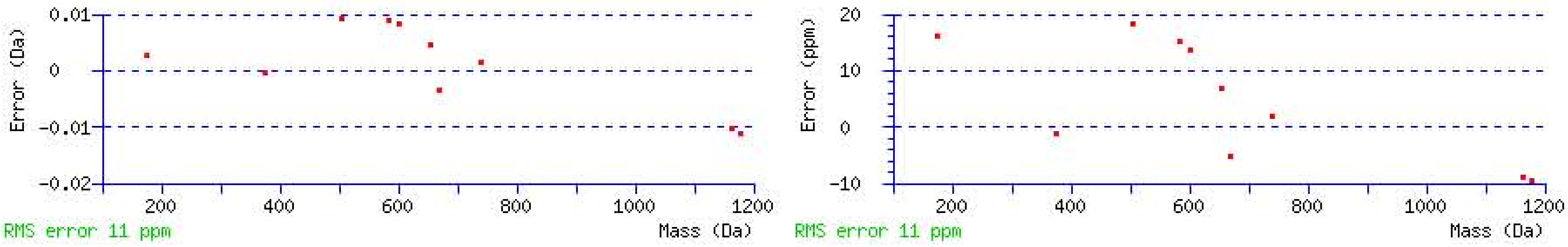
Match to Query 21073: 1337.586408 from(669.800480,2+) rtinseconds(1439) index(1573)
Title: Locus:1.1.1.3020.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 1337.585617
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 33 **Expect:** 0.0025
Matches : 10/70 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	161.037925	81.022600					C							8
2	**600.263251**	300.635264	583.236702	292.121989			Q	***1178.562269***	589.784773	1161.535720	581.271498	1160.551704	580.779490	7
3	671.300365	336.153821	654.273816	327.640546			A	***739.336943***	370.172110	722.310394	361.658835	721.326378	361.166827	6
4	834.363694	417.685485	817.337145	409.172211			Y	***668.299829***	334.653553	651.273280	326.140278	650.289264	325.648270	5
5	963.406287	482.206782	946.379738	473.693507	945.395722	473.201499	E	***505.236500***	253.121888	488.209951	244.608613	487.225935	244.116605	4
6	1050.438315	525.722796	1033.411766	517.209521	1032.427750	516.717513	S	***376.193907***	188.600591	359.167358	180.087317	358.183342	179.595309	3
7	**1164.481242**	582.744259	1147.454693	574.230985	1146.470677	573.738977	N	289.161879	145.084577	272.135330	136.571303			2
8							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.2	1337.585617	0.000791	CQAYESNR
12.2	1337.596848	-0.010440	CYEMASHLRR
0.5	1337.599365	-0.012957	SSGSSPAMETRGR

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

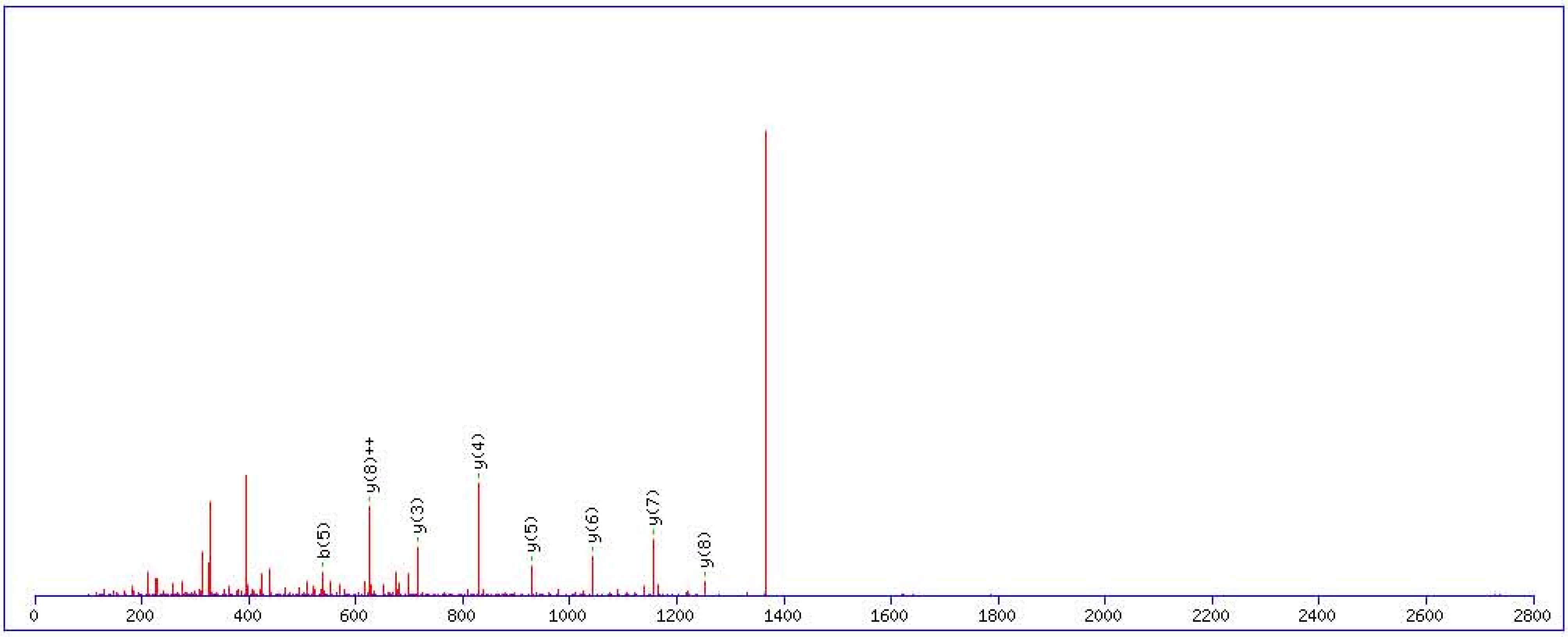
Mascot Search Results

Peptide View

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

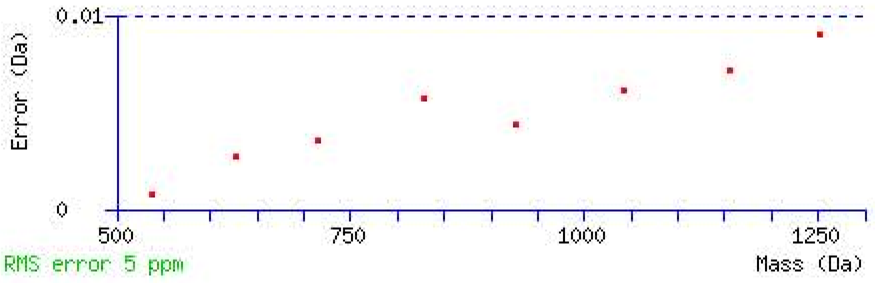
Match to Query 22507: 1364.756528 from(683.385540,2+) rtinseconds(1925) index(4356)
Title: Locus:1.1.1.3190.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

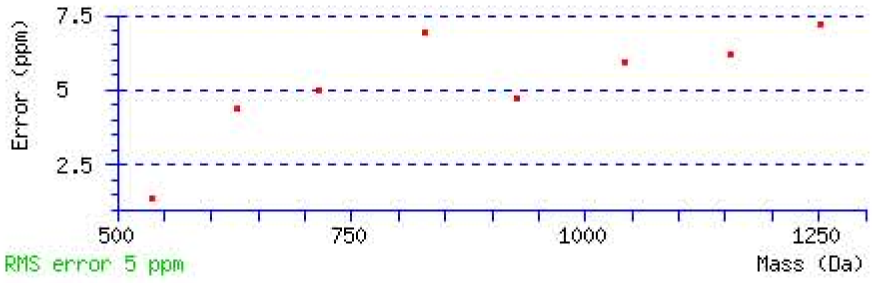
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1364.748581
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.00099
Matches : 8/76 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	211.144104	106.075690					P	*1252.671819*	626.839548	1235.645270	618.326273	1234.661254	617.834265	8
3	325.187031	163.097153	308.160482	154.583879			N	*1155.619055*	578.313166	1138.592506	569.799891	1137.608490	569.307883	7
4	439.229958	220.118617	422.203409	211.605343			N	*1041.576128*	521.291702	1024.549579	512.778428	1023.565563	512.286420	6
5	**538.298372**	269.652824	521.271823	261.139550			V	*927.533201*	464.270239	910.506652	455.756964	909.522636	455.264956	5
6	651.382436	326.194856	634.355887	317.681582			L	*828.464787*	414.736032	811.438238	406.222757	810.454222	405.730749	4
7	1090.607762	545.807519	1073.581213	537.294245			Q	*715.380723*	358.194000	698.354174	349.680725	697.370158	349.188717	3
8	1219.650355	610.328816	1202.623806	601.815541	1201.639790	601.323533	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 LPNNVLQEK
(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	1364.748581	0.007947	LPNNVLQEK
9.3	1364.745239	0.011289	KVVSWIDVYTR
7.0	1364.759827	-0.003299	QTSSLIIHR
4.4	1364.771240	-0.014712	IFQKLMFK
4.0	1364.752609	0.003919	KQFLDYLK
1.1	1364.742065	0.014463	LQMQLHLR

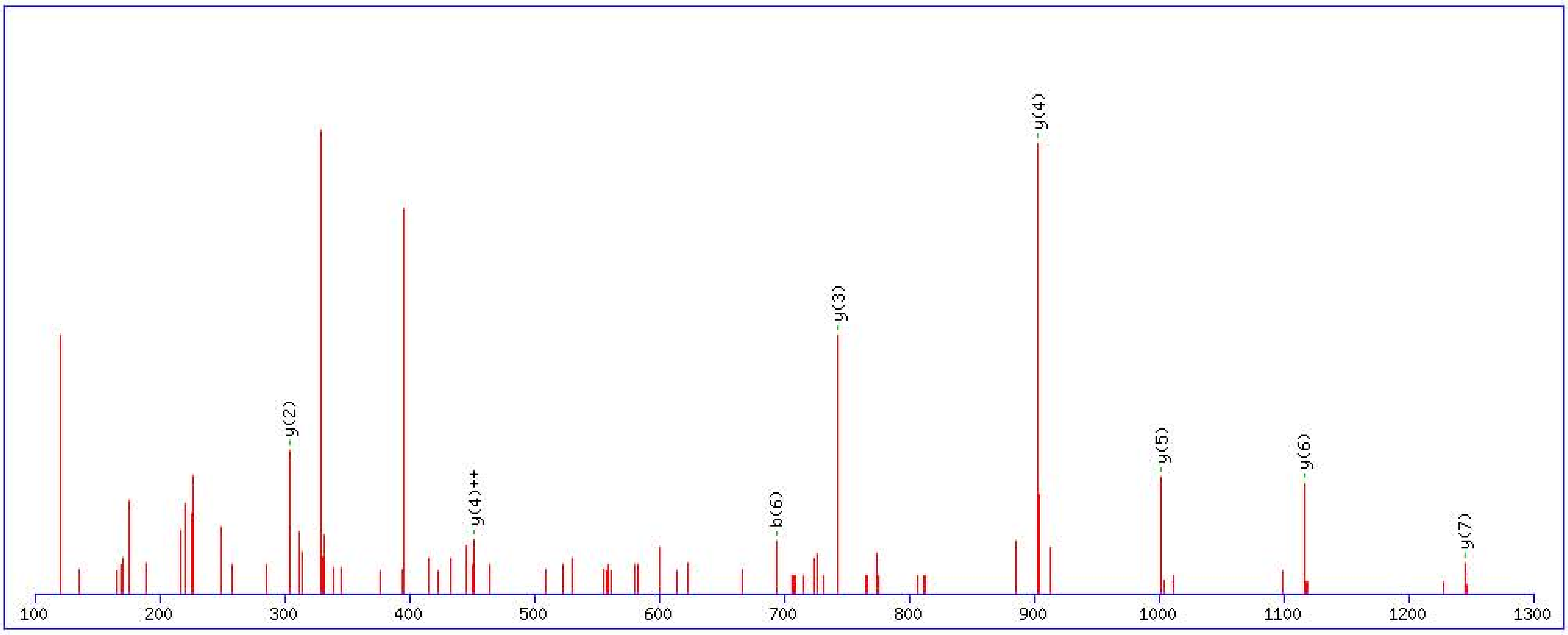
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

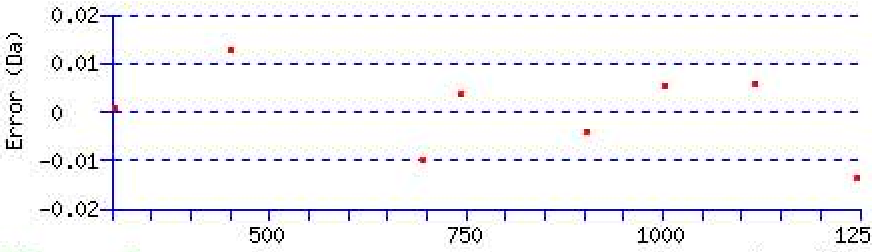
Match to Query 33535: 1694.738652 from(565.920160,3+) rtinseconds(1648) index(2918)
Title: Locus:1.1.1.3093.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

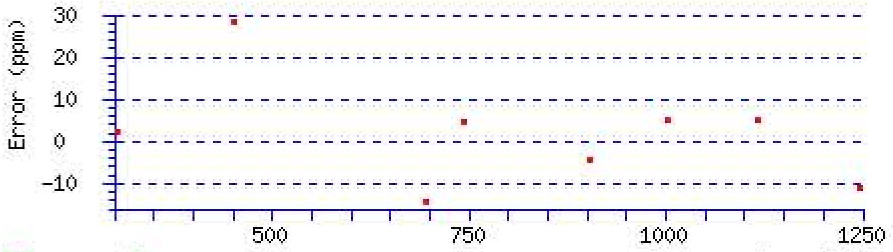


```
Monoisotopic mass of neutral peptide Mr(calc): 1694.739243
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.00038
Matches : 8/106 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.075690	74.541483					F							11
2	249.123369	125.065322			231.112804	116.060040	T	1548.678104	774.842690	1531.651555	766.329416	1530.667539	765.837408	10
3	364.150312	182.578794			346.139747	173.573512	D	1447.630425	724.318851	1430.603876	715.805576	1429.619860	715.313568	9
4	451.182340	226.094808			433.171775	217.089526	S	1332.603482	666.805379	1315.576933	658.292105	1314.592917	657.800097	8
5	580.224933	290.616105			562.214368	281.610822	E	***1245.571454***	623.289365	1228.544905	614.776091	1227.560889	614.284083	7
6	**694.267860**	347.637568	677.241311	339.124294	676.257295	338.632286	N	***1116.528861***	558.768069	1099.502312	550.254794	1098.518296	549.762786	6
7	793.336274	397.171775	776.309725	388.658501	775.325709	388.166493	V	***1002.485934***	501.746605	985.459385	493.233331	984.475369	492.741323	5
8	953.366923	477.187100	936.340374	468.673825	935.356358	468.181817	C	***903.417520***	452.212398	886.390971	443.699124	885.406955	443.207116	4
9	1392.592249	696.799763	1375.565700	688.286488	1374.581684	687.794480	Q	***743.386871***	372.197074	726.360322	363.683799	725.376306	363.191791	3
10	1521.634842	761.321059	1504.608293	752.807785	1503.624277	752.315777	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



RMS error 12 ppm



RMS error 12 ppm

NCBI **BLAST** search of FTDSENVCQER
(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	1694.739243	-0.000591	FTDSENVCQER

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

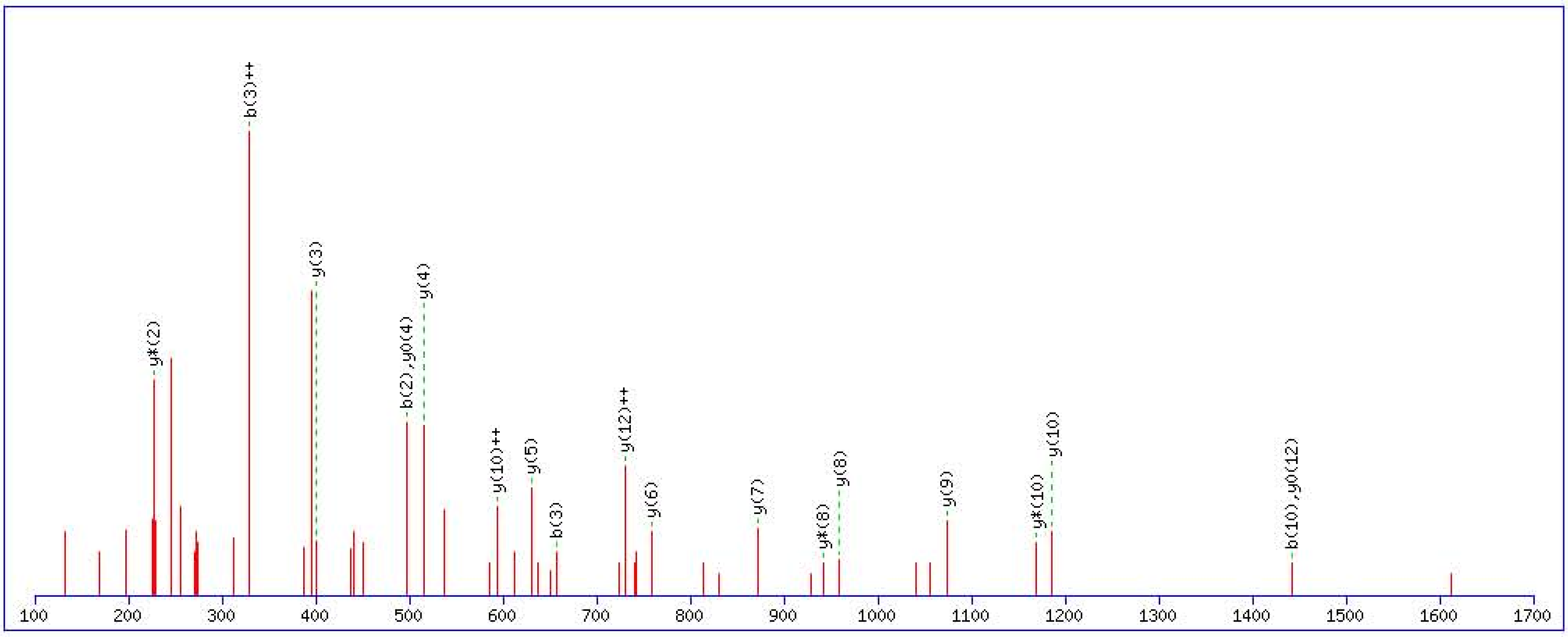
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

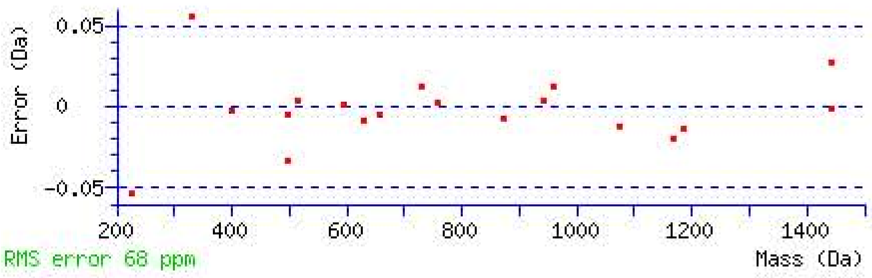
Match to Query 38433: 1954.967376 from(489.749120,4+) rtinseconds(1415) index(15311)
Title: Locus:1.1.1.3058.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

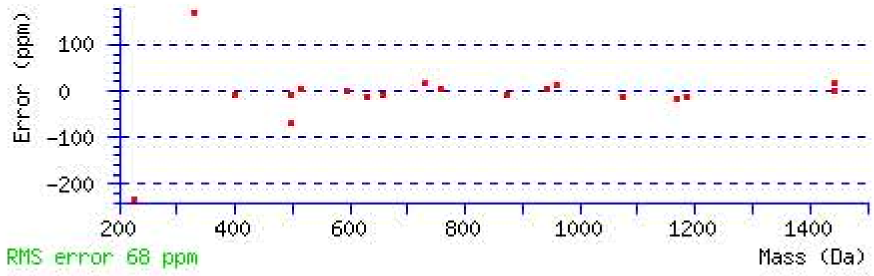
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1954.971680
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 0.00013
Matches : 19/136 fragment ions using 24 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
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
52.8	1954.971680	-0.004304	GQCIINSNKDDRPK

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

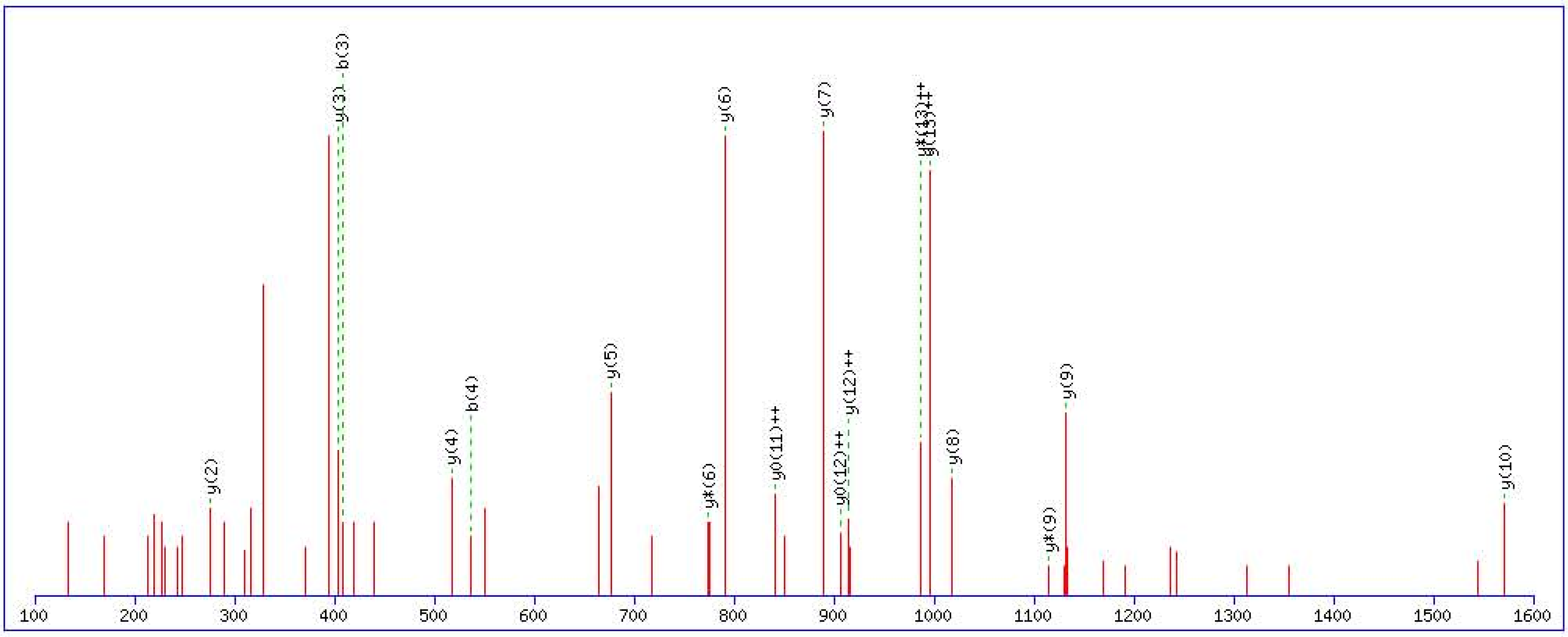
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

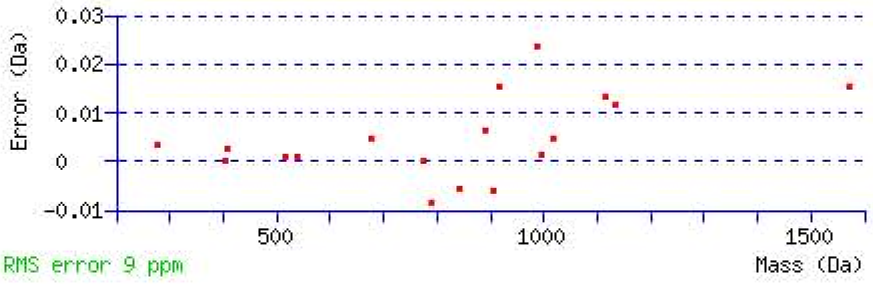
Match to Query 43880: 2235.983562 from(746.335130,3+) rtinseconds(1514) index(2053)
Title: Locus:1.1.1.3046.20 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

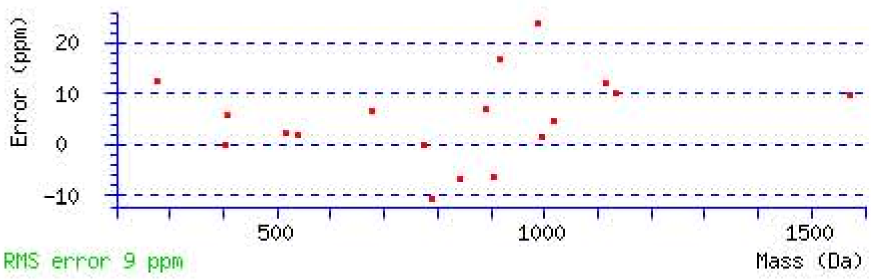
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2235.985703
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 37 **Expect:** 0.001
Matches : 18/156 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	88.039304	44.523290			70.028739	35.518008	S							15
2	248.069953	124.538614			230.059388	115.533332	C	2149.960963	1075.484119	2132.934414	1066.970845	2131.950398	1066.478837	14
3	**408.100602**	204.553939			390.090037	195.548657	C	1989.930314	995.468795	1972.903765	986.955521	1971.919749	986.463512	13
4	**537.143195**	269.075236			519.132630	260.069953	E	1829.899665	915.453470	1812.873116	906.940196	1811.889100	906.448188	12
5	666.185788	333.596532			648.175223	324.591250	E	1700.857072	850.932174	1683.830523	842.418899	1682.846507	841.926891	11
6	1105.411114	553.209195	1088.384565	544.695921	1087.400549	544.203913	Q	***1571.814479***	786.410877	1554.787930	777.897603	1553.803914	777.405595	10
7	1219.454041	610.230659	1202.427492	601.717384	1201.443476	601.225376	N	***1132.589153***	566.798214	1115.562604	558.284940	1114.578588	557.792932	9
8	1347.549004	674.278140	1330.522455	665.764866	1329.538439	665.272858	K	***1018.546226***	509.776751	1001.519677	501.263476	1000.535661	500.771468	8
9	1446.617418	723.812347	1429.590869	715.299073	1428.606853	714.807065	V	***890.451263***	445.729269	873.424714	437.215995	872.440698	436.723987	7
10	1560.660345	780.833811	1543.633796	772.320536	1542.649780	771.828528	N	***791.382849***	396.195062	774.356300	387.681788	773.372284	387.189780	6
11	1720.690994	860.849135	1703.664445	852.335861	1702.680429	851.843853	C	***677.339922***	339.173599	660.313373	330.660324	659.329357	330.168316	5
12	1833.775058	917.391167	1816.748509	908.877893	1815.764493	908.385885	L	***517.309273***	259.158274	500.282724	250.645000	499.298708	250.152992	4
13	1961.833636	981.420456	1944.807087	972.907182	1943.823071	972.415174	Q	***404.225209***	202.616242	387.198660	194.102968	386.214644	193.610960	3
14	2062.881315	1031.944295	2045.854766	1023.431021	2044.870750	1022.939013	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 SCCEEQNKVNCLQTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.2	2235.985703	-0.002141	SCCEEQNKVNCLQTR
0.4	2235.985703	-0.002141	SCCEEQNKVNCLQTR

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

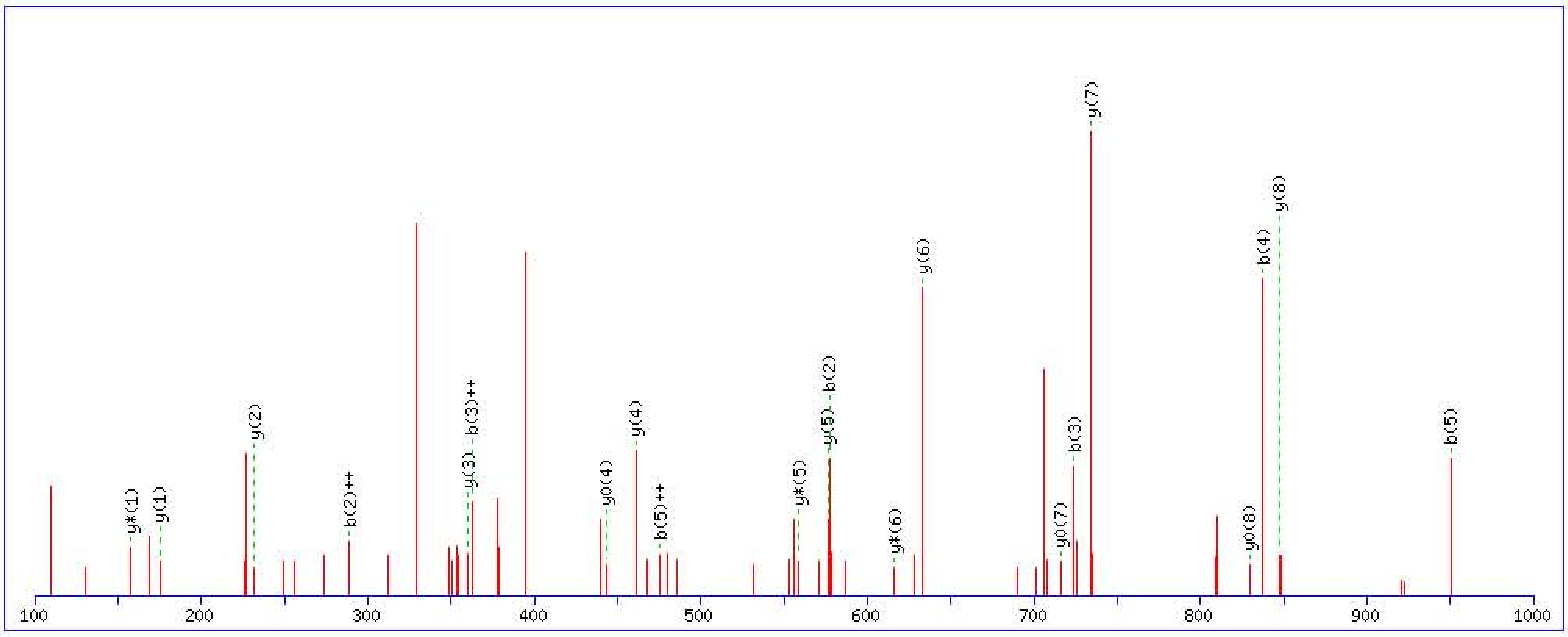
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQFLLTGDTQGR**
Found in **A1BG_HUMAN**, Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4

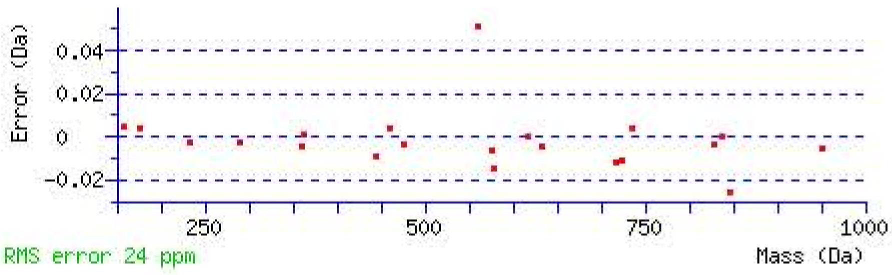
Match to Query 33363: 1682.851032 from(561.957620,3+) rtinseconds(1959) index(18828)
Title: Locus:1.1.1.3248.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

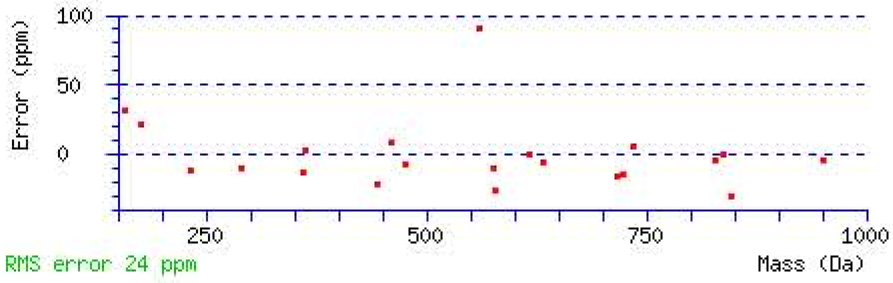
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1682.856277
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.0047
Matches : 21/114 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							12
2	**577.291514**	**289.149395**	560.264965	280.636121			Q	1546.804627	773.905951	1529.778078	765.392677	1528.794062	764.900669	11
3	**724.359928**	**362.683602**	707.333379	354.170327			F	1107.579301	554.293288	1090.552752	545.780014	1089.568736	545.288006	10
4	**837.443992**	419.225634	820.417443	410.712359			L	960.510887	480.759081	943.484338	472.245807	942.500322	471.753799	9
5	**950.528056**	**475.767666**	933.501507	467.254392			L	***847.426823***	424.217049	830.400274	415.703775	829.416258	415.211767	8
6	1051.575735	526.291505	1034.549186	517.778231	1033.565170	517.286223	T	***734.342759***	367.675017	717.316210	359.161743	716.332194	358.669735	7
7	1108.597199	554.802237	1091.570650	546.288963	1090.586634	545.796955	G	***633.295080***	317.151178	616.268531	308.637903	615.284515	308.145895	6
8	1223.624142	612.315709	1206.597593	603.802435	1205.613577	603.310426	D	***576.273616***	288.640446	559.247067	280.127171	558.263051	279.635163	5
9	1324.671821	662.839548	1307.645272	654.326274	1306.661256	653.834266	T	***461.246673***	231.126974	444.220124	222.613700	443.236108	222.121692	4
10	1452.730399	726.868837	1435.703850	718.355563	1434.719834	717.863555	Q	***360.198994***	180.603135	343.172445	172.089860			3
11	1509.751863	755.379569	1492.725314	746.866295	1491.741298	746.374287	G	***232.140416***	116.573846	215.113867	108.060571			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of HQFLLTGDTQGR
(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	1682.856277	-0.005245	HQFLLTGDTQGR
3.7	1682.845032	0.006000	APEHCELVVDLFVR
0.7	1682.845032	0.006000	QFHLTDDDLLR

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

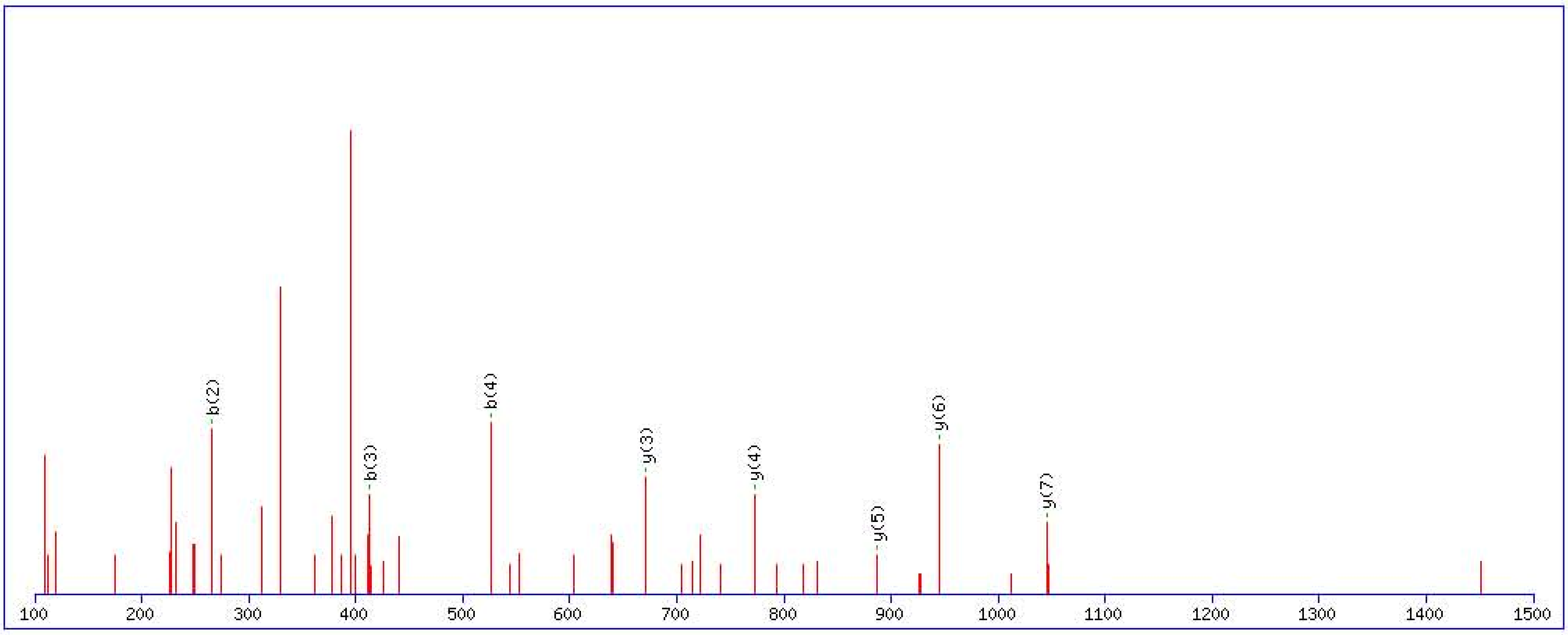
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQFLLTGDTQGR**
Found in **A1BG_HUMAN**, Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4

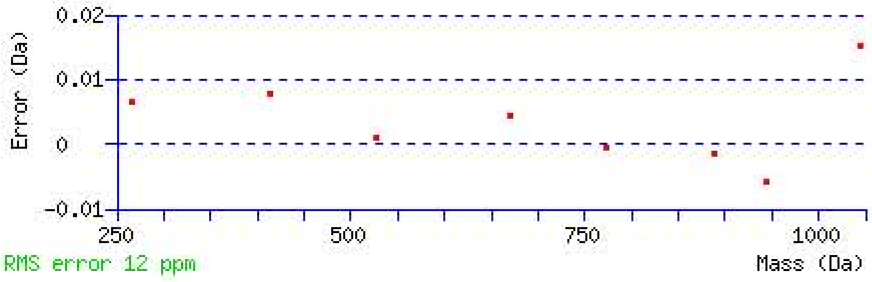
Match to Query 33366: 1682.861202 from(561.961010,3+) rtinseconds(1954) index(4497)
Title: Locus:1.1.1.3200.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

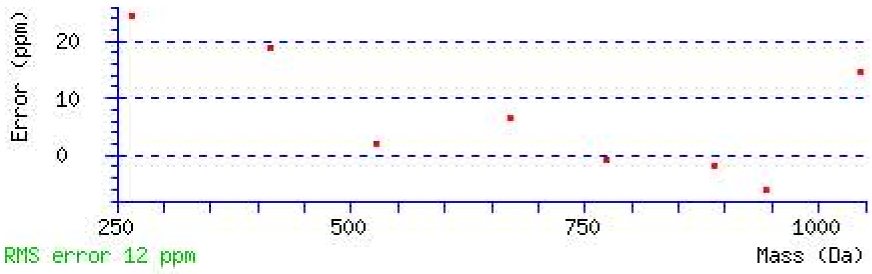
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1682.856277
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0047
Matches : 8/114 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	138.066188	69.536732					H							12
2	*266.124766*	133.566021	249.098217	125.052746			Q	1546.804627	773.905952	1529.778078	765.392677	1528.794062	764.900669	11
3	*413.193180*	207.100228	396.166631	198.586953			F	1418.746049	709.876663	1401.719500	701.363388	1400.735484	700.871380	10
4	*526.277244*	263.642260	509.250695	255.128986			L	1271.677635	636.342456	1254.651086	627.829181	1253.667070	627.337173	9
5	639.361308	320.184292	622.334759	311.671018			L	1158.593571	579.800424	1141.567022	571.287149	1140.583006	570.795141	8
6	740.408987	370.708132	723.382438	362.194857	722.398422	361.702849	T	*1045.509507*	523.258392	1028.482958	514.745117	1027.498942	514.253109	7
7	797.430451	399.218864	780.403902	390.705589	779.419886	390.213581	G	*944.461828*	472.734552	927.435279	464.221278	926.451263	463.729270	6
8	912.457394	456.732335	895.430845	448.219061	894.446829	447.727053	D	*887.440364*	444.223820	870.413815	435.710546	869.429799	435.218538	5
9	1013.505073	507.256175	996.478524	498.742900	995.494508	498.250892	T	*772.413421*	386.710349	755.386872	378.197074	754.402856	377.705066	4
10	1452.730399	726.868838	1435.703850	718.355563	1434.719834	717.863555	Q	*671.365742*	336.186509	654.339193	327.673235			3
11	1509.751863	755.379570	1492.725314	746.866295	1491.741298	746.374287	G	232.140416	116.573846	215.113867	108.060571			2
12							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of HQFLLTGDTQGR
(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	1682.856277	0.004925	HQFLLTGDTQGR

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

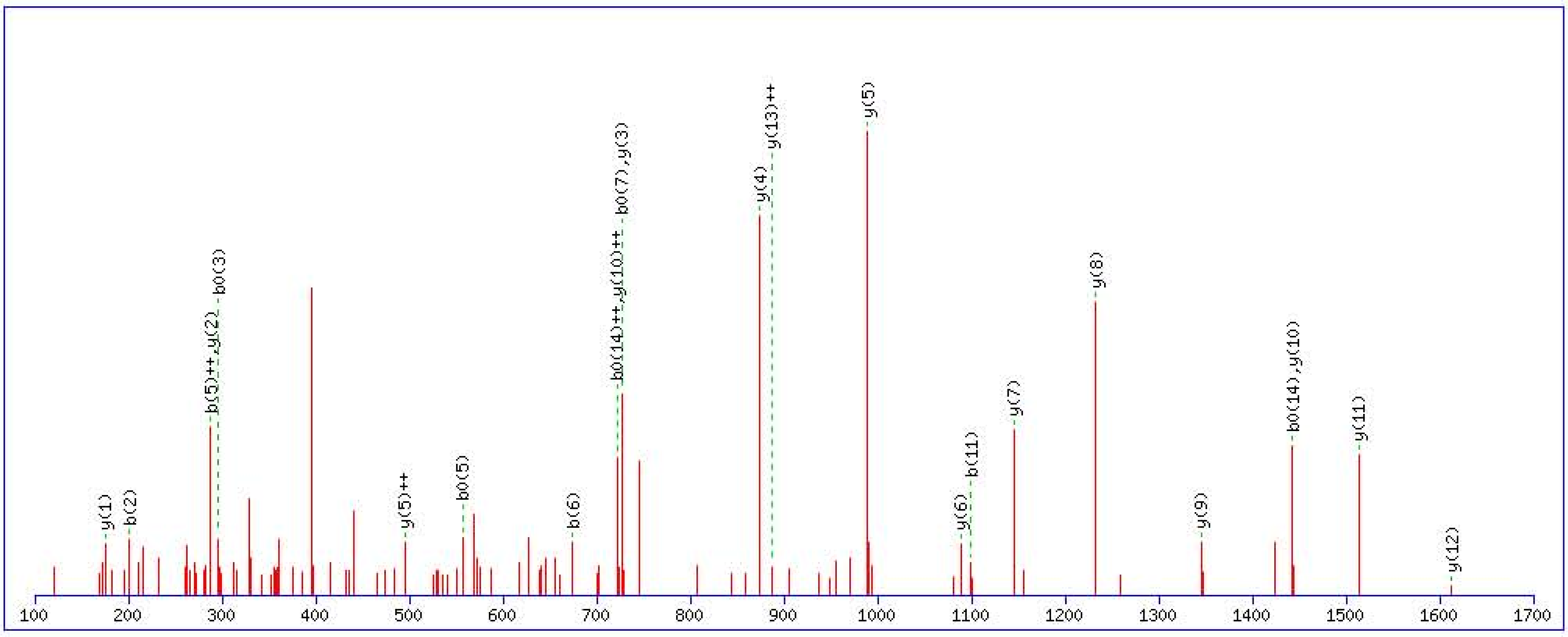
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTLTCVAPLSGVDFQLR**
Found in **A1BG_HUMAN**, Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4

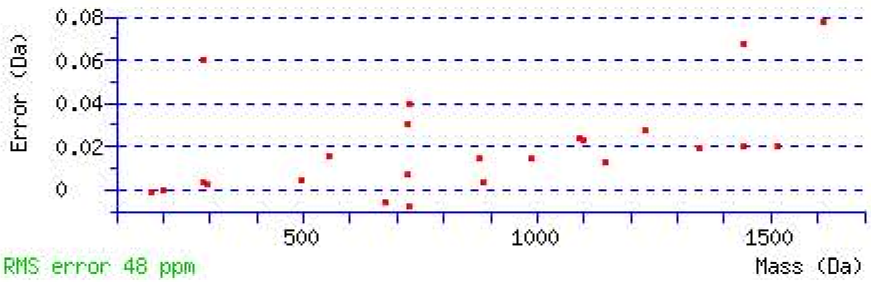
Match to Query 43049: 2186.176572 from(729.732800,3+) rtinseconds(2759) index(9051)
Title: Locus:1.1.1.3480.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

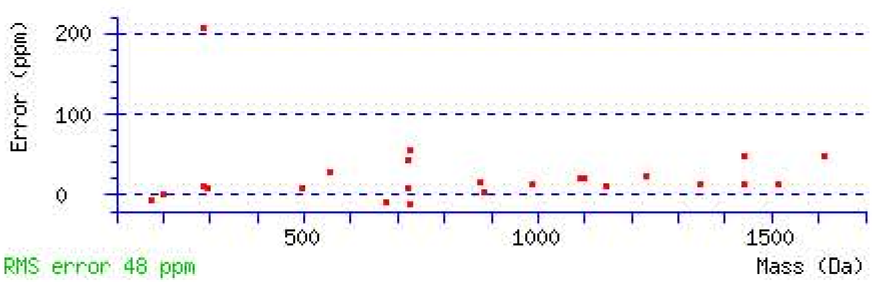
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2186.159195
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15 : Biotin:Thermo-21345 (Q)
Ions Score: 93 **Expect:** 7.1e-009
Matches : 24/154 fragment ions using 29 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	**201.123369**	101.065322			183.112804	92.060040	T	2088.098032	1044.552654	2071.071483	1036.039379	2070.087467	1035.547371	16
3	314.207433	157.607354			296.196868	148.602072	L	1987.050353	994.028815	1970.023804	985.515540	1969.039788	985.023532	15
4	415.255112	208.131194			397.244547	199.125912	T	1873.966289	937.486783	1856.939740	928.973508	1855.955724	928.481500	14
5	575.285761	288.146519			557.275196	279.141236	C	1772.918610	886.962943	1755.892061	878.449669	1754.908045	877.957661	13
6	**674.354175**	337.680726			656.343610	328.675443	V	***1612.887961***	806.947619	1595.861412	798.434344	1594.877396	797.942336	12
7	745.391289	373.199283			727.380724	364.194000	A	***1513.819547***	757.413412	1496.792998	748.900137	1495.808982	748.408129	11
8	842.444053	421.725665			824.433488	412.720382	P	***1442.782433***	721.894855	1425.755884	713.381580	1424.771868	712.889572	10
9	955.528117	478.267697			937.517552	469.262414	L	***1345.729669***	673.368473	1328.703120	664.855198	1327.719104	664.363190	9
10	1042.560145	521.783711			1024.549580	512.778428	S	***1232.645605***	616.826441	1215.619056	608.313166	1214.635040	607.821158	8
11	**1099.581609**	550.294443			1081.571044	541.289160	G	***1145.613577***	573.310427	1128.587028	564.797152	1127.603012	564.305144	7
12	1198.650023	599.828650			1180.639458	590.823367	V	***1088.592113***	544.799695	1071.565564	536.286420	1070.581548	535.794412	6
13	1313.676966	657.342121			1295.666401	648.336839	D	***989.523699***	495.265488	972.497150	486.752213	971.513134	486.260205	5
14	1460.745380	730.876328			1442.734815	721.871046	F	***874.496756***	437.752016	857.470207	429.238742			4
15	1899.970706	950.488991	1882.944157	941.975717	1881.960141	941.483709	Q	***727.428342***	364.217809	710.401793	355.704535			3
16	2013.054770	1007.031023	1996.028221	998.517749	1995.044205	998.025741	L	***288.203016***	144.605146	271.176467	136.091872			2
17							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
92.7	2186.159195	0.017377	VTLTCVAPLSGVDFQLR
5.5	2186.188126	-0.011554	KLTSHQMLSSTEILKWLR
2.2	2186.188995	-0.012423	QAVAYRQMSLLLR
0.7	2186.180267	-0.003695	RKGDLSPAELMMLTIGDVIK

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

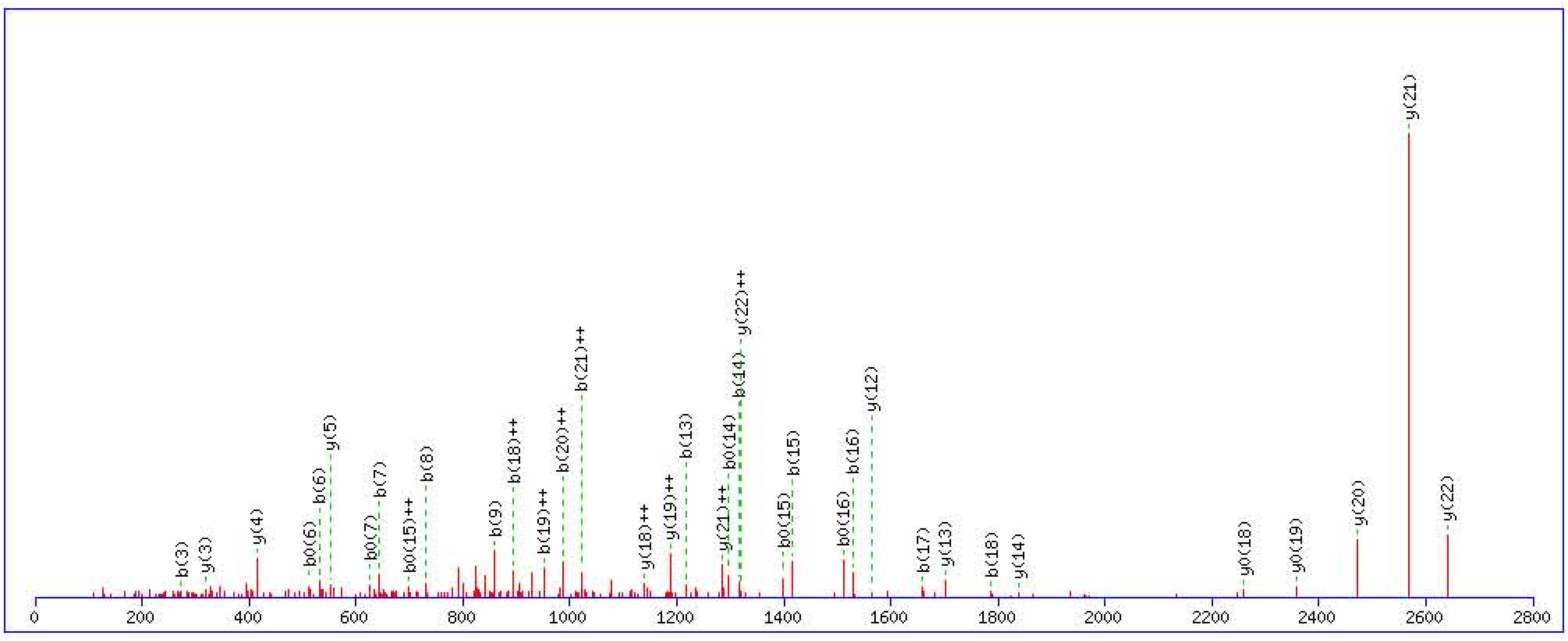
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TDGEGALSEPSATVTIEELAAPPPPVLMHHGESSQVLHPGNK**
Found in **A1BG_HUMAN**, Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4

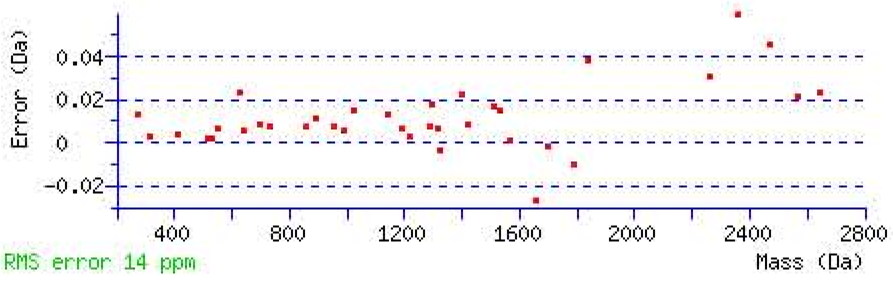
Match to Query 66293: 4610.333670 from(923.074010,5+) rtinseconds(2443) index(7316)
Title: Locus:1.1.1.3370.25 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

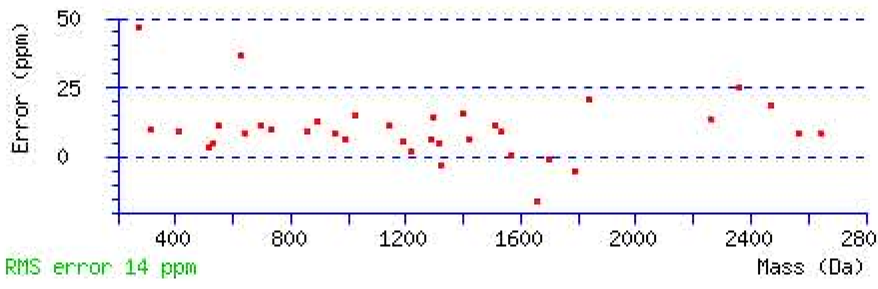
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 4610.278503
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q35 : Biotin:Thermo-21345 (Q)
Ions Score: 52 **Expect:** 1.5e-005
Matches : 36/408 fragment ions using 78 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							42
2	217.081898	109.044587			199.071333	100.039304	D	4510.238114	2255.622695	4493.211565	2247.109421	4492.227549	2246.617413	41
3	***274.103362***	137.555319			256.092797	128.550037	G	4395.211171	2198.109224	4378.184622	2189.595949	4377.200606	2189.103941	40
4	403.145955	202.076616			385.135390	193.071333	E	4338.189707	2169.598492	4321.163158	2161.085217	4320.179142	2160.593209	39
5	460.167419	230.587347			442.156854	221.582065	G	4209.147114	2105.077195	4192.120565	2096.563921	4191.136549	2096.071913	38
6	***531.204533***	266.105905			513.193968	257.100622	A	4152.125650	2076.566463	4135.099101	2068.053189	4134.115085	2067.561181	37
7	***644.288597***	322.647937			626.278032	313.642654	L	4081.088536	2041.047906	4064.061987	2032.534632	4063.077971	2032.042624	36
8	***731.320625***	366.163951			713.310060	357.158668	S	3968.004472	1984.505874	3950.977923	1975.992600	3949.993907	1975.500592	35
9	***860.363218***	430.685247			842.352653	421.679965	E	3880.972444	1940.989860	3863.945895	1932.476586	3862.961879	1931.984578	34
10	957.415982	479.211629			939.405417	470.206347	P	3751.929851	1876.468564	3734.903302	1867.955289	3733.919286	1867.463281	33
11	1044.448010	522.727643			1026.437445	513.722361	S	3654.877087	1827.942182	3637.850538	1819.428907	3636.866522	1818.936899	32
12	1115.485124	558.246200			1097.474559	549.240918	A	3567.845059	1784.426168	3550.818510	1775.912893	3549.834494	1775.420885	31
13	***1216.532803***	608.770040			1198.522238	599.764757	T	3496.807945	1748.907611	3479.781396	1740.394336	3478.797380	1739.902328	30
14	***1315.601217***	658.304247			1297.590652	649.298964	V	3395.760266	1698.383771	3378.733717	1689.870497	3377.749701	1689.378489	29
15	***1416.648896***	708.828086			1398.638331	699.822804	T	3296.691852	1648.849564	3279.665303	1640.336290	3278.681287	1639.844282	28
16	***1529.732960***	765.370118			1511.722395	756.364836	I	3195.644173	1598.325725	3178.617624	1589.812450	3177.633608	1589.320442	27
17	***1658.775553***	829.891415			1640.764988	820.886132	E	3082.560109	1541.783693	3065.533560	1533.270418	3064.549544	1532.778410	26
18	***1787.818146***	**894.412711**			1769.807581	885.407429	E	2953.517516	1477.262396	2936.490967	1468.749122	2935.506951	1468.257114	25
19	1900.902210	**950.954743**			1882.891645	941.949461	L	2824.474923	1412.741100	2807.448374	1404.227825	2806.464358	1403.735817	24
20	1971.939324	**986.473300**			1953.928759	977.468018	A	2711.390859	1356.199068	2694.364310	1347.685793	2693.380294	1347.193785	23
21	2042.976438	**1021.991857**			2024.965873	1012.986575	A	***2640.353745***	1320.680511	2623.327196	1312.167236	2622.343180	1311.675228	22
22	2140.029202	1070.518239			2122.018637	1061.512956	P	***2569.316631***	1285.161954	2552.290082	1276.648679	2551.306066	1276.156671	21
23	2237.081966	1119.044621			2219.071401	1110.039338	P	***2472.263867***	1236.635572	2455.237318	1228.122297	2454.253302	1227.630289	20
24	2334.134730	1167.571003			2316.124165	1158.565720	P	2375.211103	1188.109190	2358.184554	1179.595915	2357.200538	1179.103907	19
25	2431.187494	1216.097385			2413.176929	1207.092102	P	2278.158339	1139.582808	2261.131790	1131.069533	2260.147774	1130.577525	18
26	2530.255908	1265.631592			2512.245343	1256.626309	V	2181.105575	1091.056426	2164.079026	1082.543151	2163.095010	1082.051143	17
27	2643.339972	1322.173624			2625.329407	1313.168341	L	2082.037161	1041.522219	2065.010612	1033.008944	2064.026596	1032.516936	16
28	2774.380457	1387.693866			2756.369892	1378.688584	M	1968.953097	984.980187	1951.926548	976.466912	1950.942532	975.974904	15
29	2911.439369	1456.223322			2893.428804	1447.218040	H	***1837.912612***	919.459944	1820.886063	910.946670	1819.902047	910.454662	14
30	3048.498281	1524.752778			3030.487716	1515.747496	H	***1700.853700***	850.930488	1683.827151	842.417214	1682.843135	841.925206	13
31	3105.519745	1553.263510			3087.509180	1544.258228	G	***1563.794788***	782.401032	1546.768239	773.887758	1545.784223	773.395750	12
32	3234.562338	1617.784807			3216.551773	1608.779524	E	1506.773324	753.890300	1489.746775	745.377026	1488.762759	744.885018	11
33	3321.594366	1661.300821			3303.583801	1652.295538	S	1377.730731	689.369004	1360.704182	680.855729	1359.720166	680.363721	10
34	3408.626394	1704.816835			3390.615829	1695.811552	S	1290.698703	645.852990	1273.672154	637.339715	1272.688138	636.847707	9
35	3847.851720	1924.429498	3830.825171	1915.916223	3829.841155	1915.424215	Q	1203.666675	602.336976	1186.640126	593.823701			8
36	3946.920134	1973.963705	3929.893585	1965.450430	3928.909569	1964.958422	V	764.441349	382.724313	747.414800	374.211038			7
37	4060.004198	2030.505737	4042.977649	2021.992462	4041.993633	2021.500454	L	665.372935	333.190106	648.346386	324.676831			6
38	4197.063110	2099.035193	4180.036561	2090.521919	4179.052545	2090.029911	H	***552.288871***	276.648074	535.262322	268.134799			5
39	4294.115874	2147.561575	4277.089325	2139.048301	4276.105309	2138.556293	P	***415.229959***	208.118618	398.203410	199.605343			4
40	4351.137338	2176.072307	4334.110789	2167.559033	4333.126773	2167.067025	G	***318.177195***	159.592236	301.150646	151.078961			3
41	4465.180265	2233.093771	4448.153716	2224.580496	4447.169700	2224.088488	N	261.155731	131.081504	244.129182	122.568229			2
42							K	147.112804	74.060040	130.086255	65.546766			1





NCBI **BLAST** search of TDGEGALSEPSATVTIEELAAPPPPVLMHHGESSQVLHPGNK
(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	4610.278503	0.055167	TDGEGALSEPSATVTIEELAAPPPPVLMHHGESSQVLHPGNK
0.2	4610.344009	-0.010339	IEELARLNPQYPMFRAPPPLPPVYSMETETPTAEDIQLLK
0.0	4610.314880	0.018790	LRLEPLVLQMSSLESSGADPDWQELQIVGTCPDITKHYLR

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

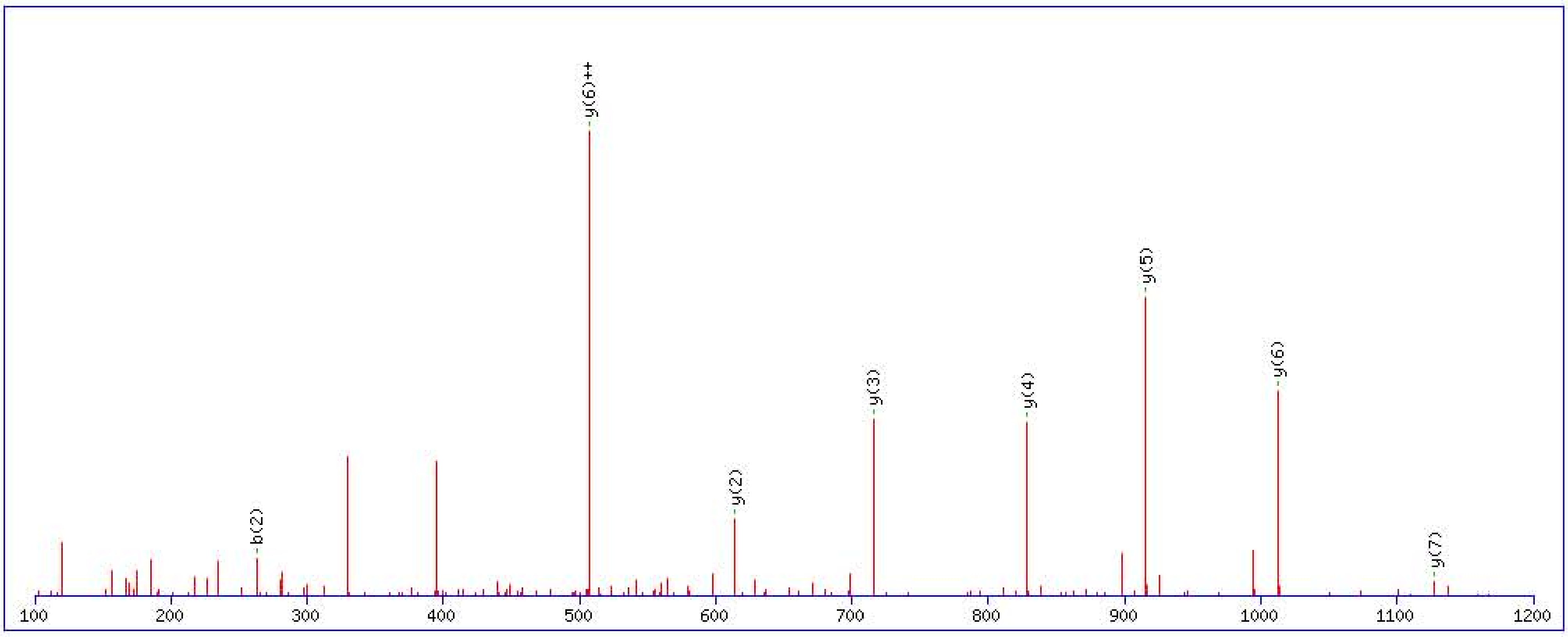
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

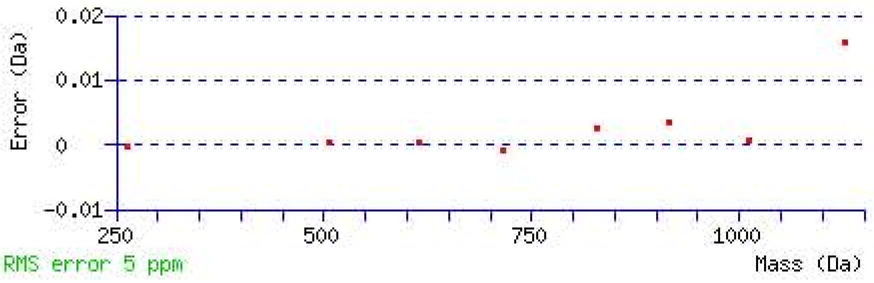
Match to Query 19637: 1273.651868 from(637.833210,2+) rtinseconds(1951) index(4478)
Title: Locus:1.1.1.3199.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

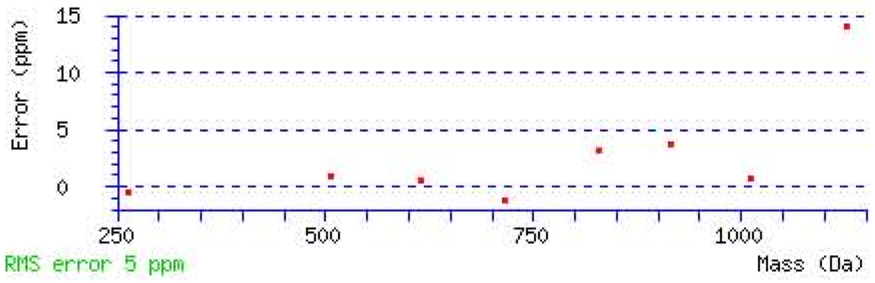
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1273.648895
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 48 **Expect:** 0.00042
Matches : 8/66 fragment ions using 11 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.075690	74.541483					F							8
2	**263.102633**	132.054954			245.092068	123.049672	D	***1127.587756***	564.297516	1110.561207	555.784242	1109.577191	555.292233	7
3	360.155397	180.581336			342.144832	171.576054	P	***1012.560813***	506.784045	995.534264	498.270770	994.550248	497.778762	6
4	447.187425	224.097350			429.176860	215.092068	S	***915.508049***	458.257663	898.481500	449.744388	897.497484	449.252380	5
5	560.271489	280.639383			542.260924	271.634100	L	***828.476021***	414.741649	811.449472	406.228374	810.465456	405.736366	4
6	661.319168	331.163222			643.308603	322.157940	T	***715.391957***	358.199617	698.365408	349.686342	697.381392	349.194334	3
7	1100.544494	550.775885	1083.517945	542.262611	1082.533929	541.770603	Q	***614.344278***	307.675777	597.317729	299.162503			2
8							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.2	1273.648895	0.002973	FDPSLTQR
21.2	1273.670654	-0.018786	FDIAIIYYTR
17.4	1273.633621	0.018247	ETESLTQR
5.7	1273.652695	-0.000827	EHQAHLEALAR
4.0	1273.670013	-0.018145	DLVTMVEQLAR
0.9	1273.670029	-0.018161	TDPSILGGMIVR
0.0	1273.648682	0.003186	SASSPSPRRSSR

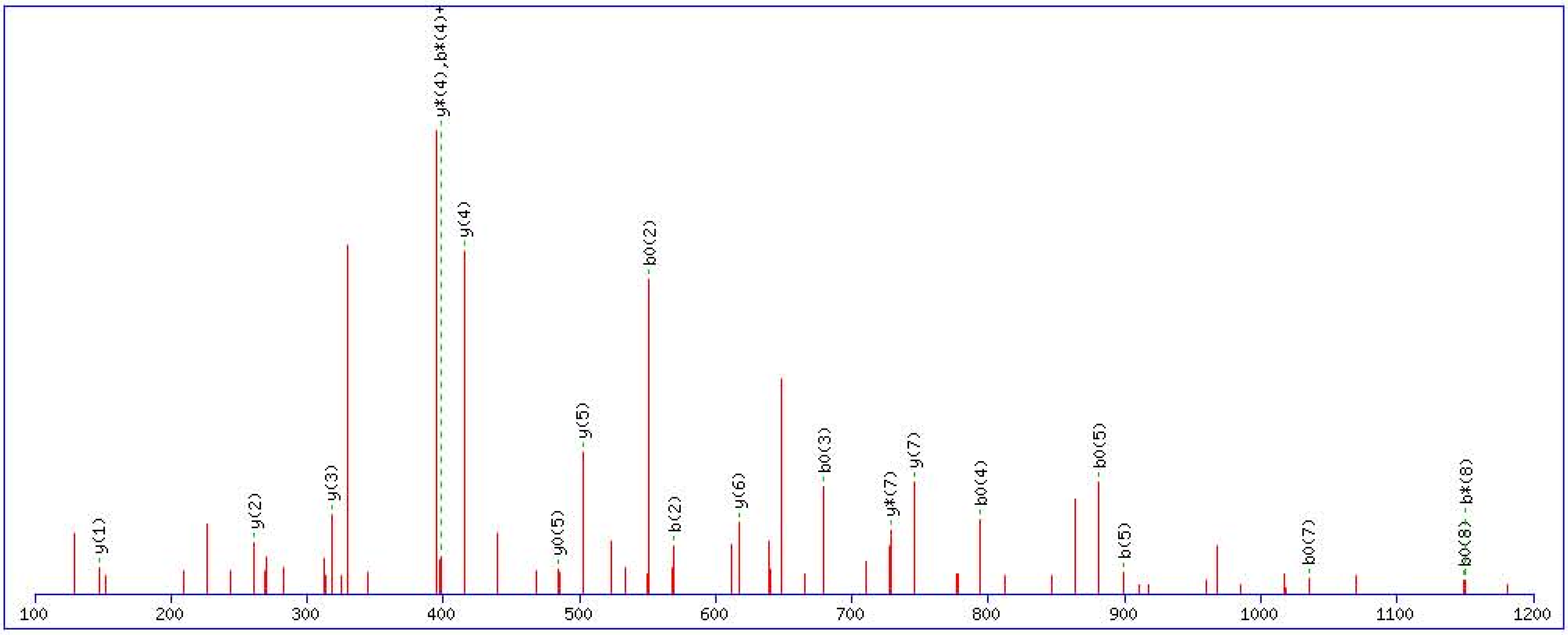
Mascot Search Results

Peptide View

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

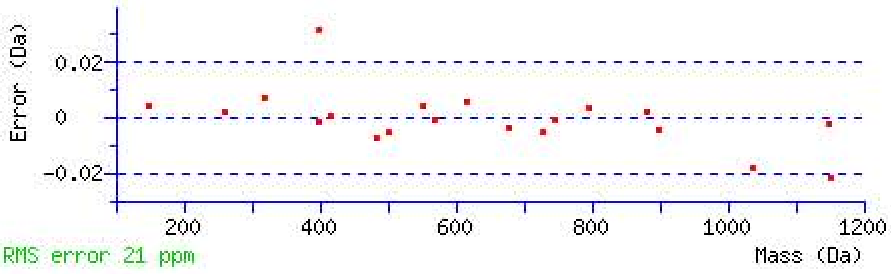
Match to Query 20555: 1312.592628 from(657.303590,2+) rtinseconds(1208) index(14391)
Title: Locus:1.1.1.2986.6 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

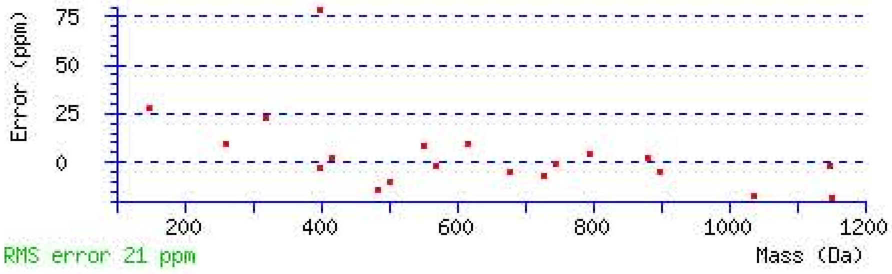
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1312.608139
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.00045
Matches : 20/86 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	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
36.8	1312.608139	-0.015511	EQQDSPGNK
18.7	1312.608139	-0.015511	EQQDSPGNK
1.1	1312.579178	0.013450	QDCETFGMVVK
0.2	1312.601624	-0.008996	CGECGKAFTRK

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

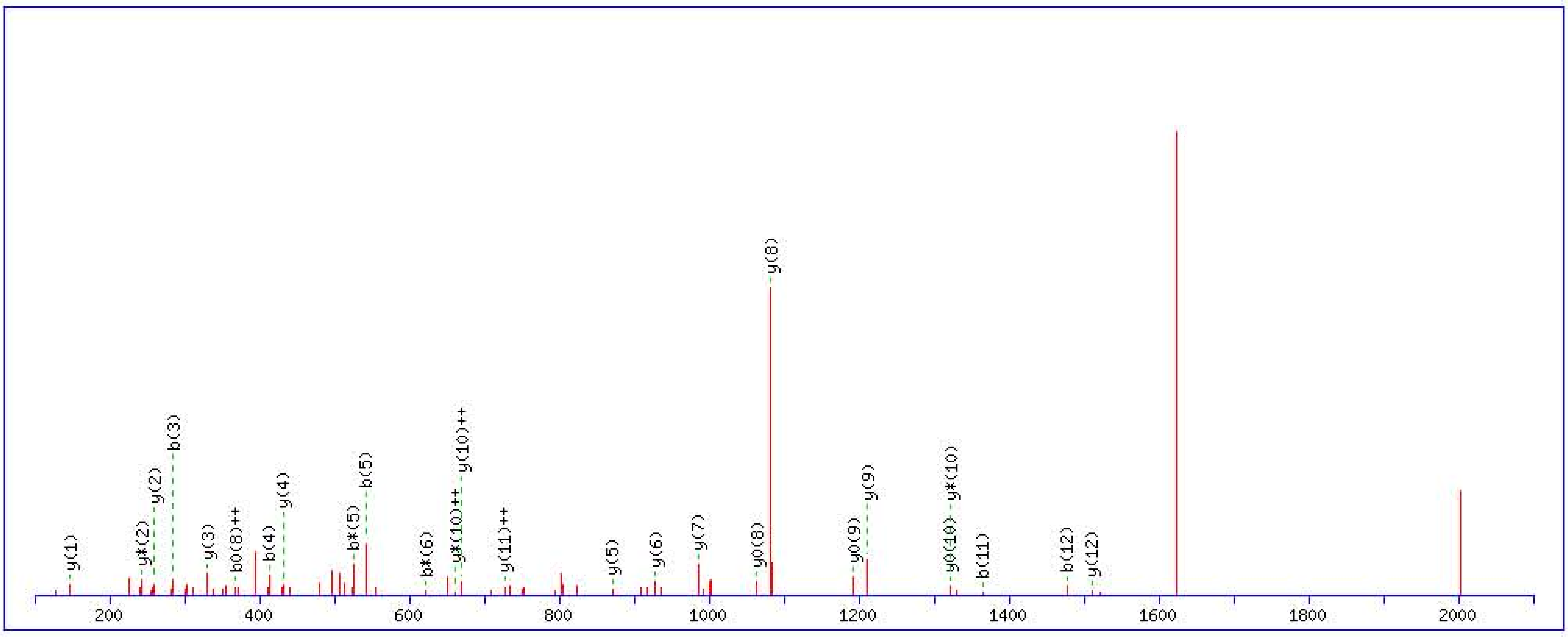
Mascot Search Results

Peptide View

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

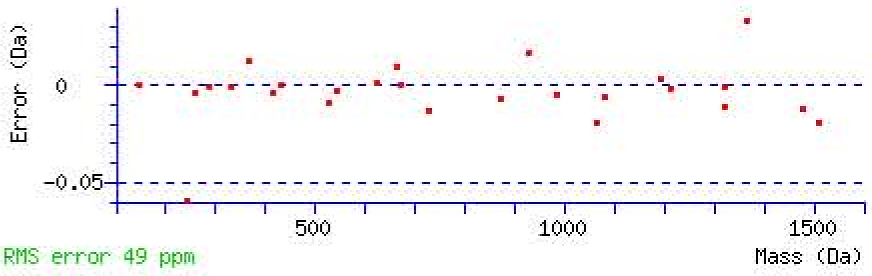
Match to Query 31532: 1622.840608 from(812.427580,2+) rtinseconds(1649) index(29781)
Title: Locus:1.1.1.3237.24 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

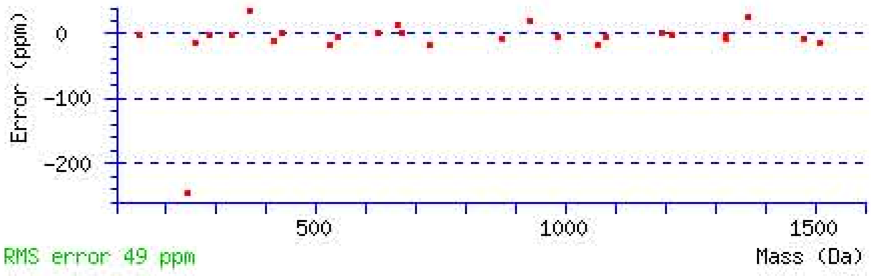


Monoisotopic mass of neutral peptide Mr(calc): 1622.845016
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 55 **Expect:** 4.6e-005
Matches : 26/126 fragment ions using 58 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	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



RMS error 49 ppm



RMS error 49 ppm

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
54.6	1622.845016	-0.004408	LGNQEPGGQTALK
10.8	1622.845016	-0.004408	LGNQEPGGQTALK
7.8	1622.858917	-0.018309	SVLLMELEVNYGLK
6.2	1622.820511	0.020097	FPPEASGYLHIGHAK
4.3	1622.833771	0.006837	LDLAGRDLTDYLMK
1.5	1622.849045	-0.008437	IPMPDFDLHLKGPK
0.9	1622.860260	-0.019652	EHSAFQAPAVKK
0.9	1622.819855	0.020753	NSSPRMPHLAVATDK
0.3	1622.864288	-0.023680	FPLPSMYRALVWK
0.0	1622.827713	0.012895	GLTPREFNSYGARR

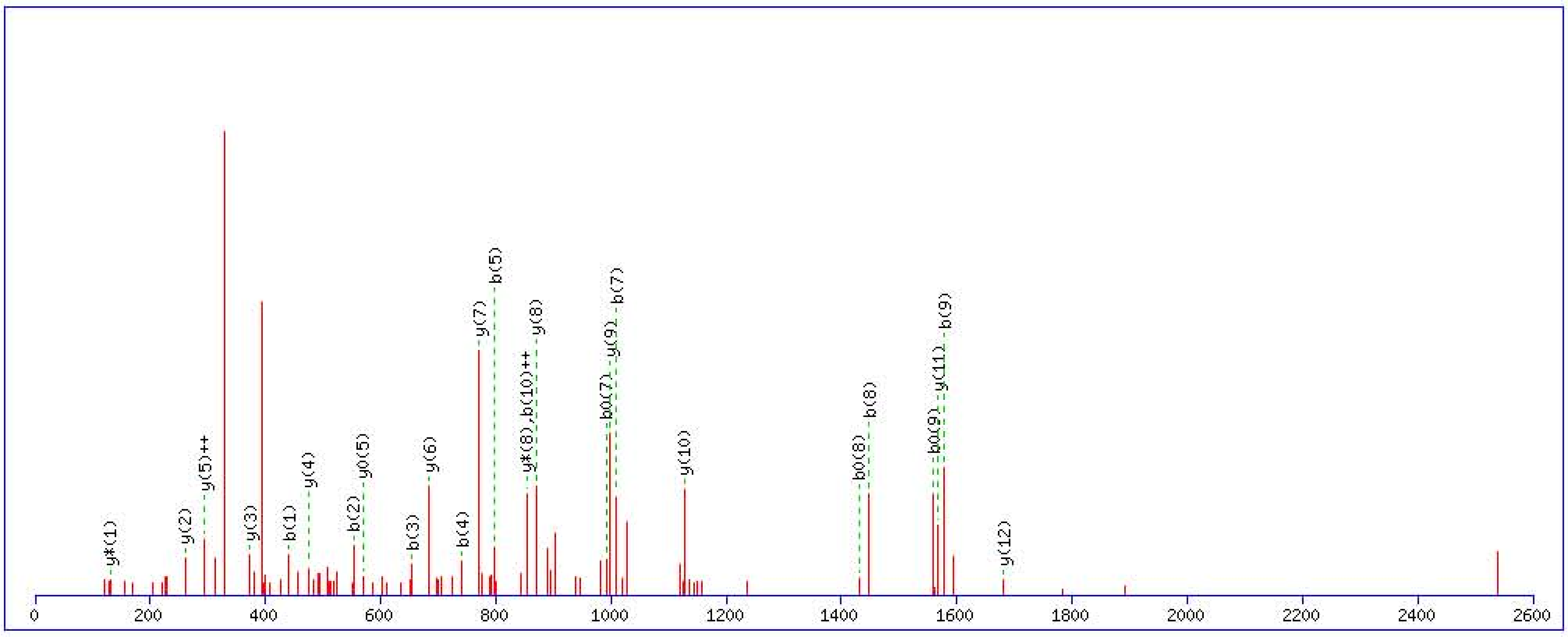
Mascot Search Results

Peptide View

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

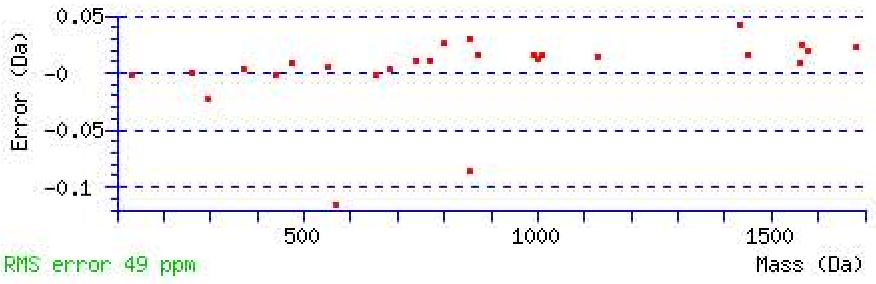
Match to Query 33964: 2574.425112 from(859.148980,3+) rtinseconds(2690) index(8646)
Title: Locus:1.1.1.3456.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

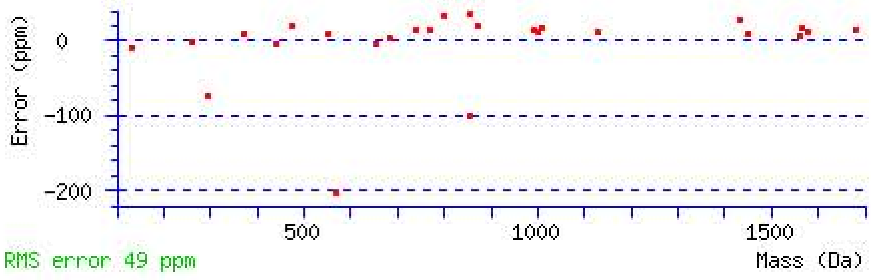


```
Monoisotopic mass of neutral peptide Mr(calc): 2574.391342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 68  Expect: 3e-006
Matches : 26/194 fragment ions using 42 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***440.232602***	220.619939	423.206053	212.106664			Q							18
2	***553.316666***	277.161971	536.290117	268.648697			L	2136.173304	1068.590290	2119.146755	1060.077015	2118.162739	1059.585007	17
3	***654.364345***	327.685811	637.337796	319.172536	636.353780	318.680528	T	2023.089240	1012.048258	2006.062691	1003.534984	2005.078675	1003.042976	16
4	***741.396373***	371.201825	724.369824	362.688550	723.385808	362.196542	S	1922.041561	961.524419	1905.015012	953.011144	1904.030996	952.519136	15
5	***798.417837***	399.712557	781.391288	391.199282	780.407272	390.707274	G	1835.009533	918.008405	1817.982984	909.495130	1816.998968	909.003122	14
6	895.470601	448.238939	878.444052	439.725664	877.460036	439.233656	P	1777.988069	889.497673	1760.961520	880.984398	1759.977504	880.492390	13
7	***1009.513528***	505.260402	992.486979	496.747128	991.502963	496.255120	N	***1680.935305***	840.971291	1663.908756	832.458016	1662.924740	831.966008	12
8	***1448.738854***	724.873065	1431.712305	716.359791	1430.728289	715.867782	Q	***1566.892378***	783.949827	1549.865829	775.436553	1548.881813	774.944545	11
9	***1577.781447***	789.394362	1560.754898	780.881087	1559.770882	780.389079	E	***1127.667052***	564.337164	1110.640503	555.823890	1109.656487	555.331882	10
10	1705.840025	853.423651	1688.813476	844.910376	1687.829460	844.418368	Q	***998.624459***	499.815868	981.597910	491.302593	980.613894	490.810585	9
11	1804.908439	902.957858	1787.881890	894.444583	1786.897874	893.952575	V	***870.565881***	435.786579	853.539332	427.273304	852.555316	426.781296	8
12	1891.940467	946.473872	1874.913918	937.960597	1873.929902	937.468589	S	***771.497467***	386.252372	754.470918	377.739097	753.486902	377.247089	7
13	1988.993231	995.000254	1971.966682	986.486979	1970.982666	985.994971	P	***684.465439***	342.736358	667.438890	334.223083	666.454874	333.731075	6
14	2102.077295	1051.542285	2085.050746	1043.029011	2084.066730	1042.537003	L	587.412675	294.209976	570.386126	285.696701	569.402110	285.204693	5
15	2203.124974	1102.066125	2186.098425	1093.552850	2185.114409	1093.060842	T	***474.328611***	237.667944	457.302062	229.154669	456.318046	228.662661	4
16	2316.209038	1158.608157	2299.182489	1150.094882	2298.198473	1149.602874	L	***373.280932***	187.144104	356.254383	178.630830			3
17	2429.293102	1215.150189	2412.266553	1206.636914	2411.282537	1206.144906	L	***260.196868***	130.602072	243.170319	122.088798			2
18							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 49 ppm



RMS error 49 ppm

NCBI **BLAST** search of QLTSGPNQEQVSPLTLLK
(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	2574.391342	0.033770	QLTSGPNQEQVSPLTLLK
40.6	2574.391342	0.033770	QLTSGPNQEQVSPLTLLK
5.2	2574.391342	0.033770	QLTSGPNQEQVSPLTLLK

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

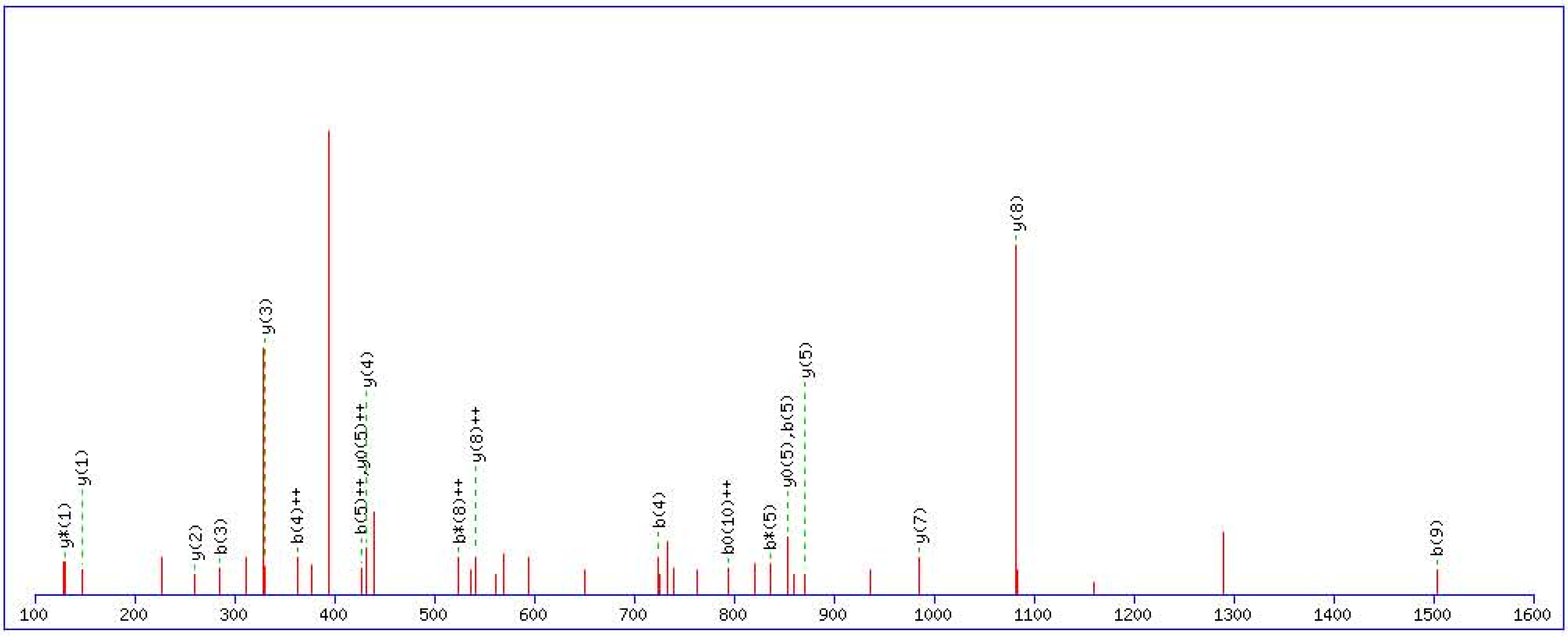
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

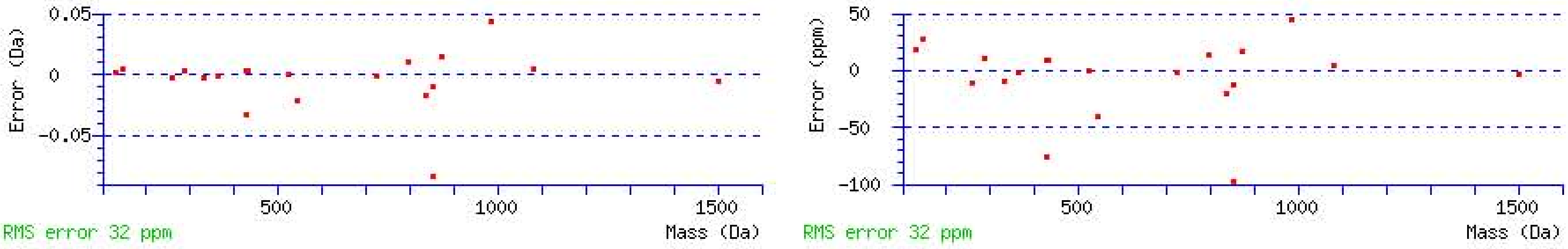
Match to Query 38078: 1934.009622 from(645.677150,3+) rtinseconds(2001) index(46077)
Title: Locus:1.1.1.3409.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 1934.011765
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.065
Matches : 20/126 fragment ions using 40 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	1821.934989	911.471133	1804.908440	902.957858	1803.924424	902.465850	12
3	***285.155731***	143.081504	268.129182	134.568229			N	1764.913525	882.960400	1747.886976	874.447126	1746.902960	873.955118	11
4	***724.381057***	**362.694167**	707.354508	354.180892			Q	1650.870598	825.938937	1633.844049	817.425663	1632.860033	816.933654	10
5	***853.423650***	**427.215463**	836.397101	418.702189	835.413085	418.210181	E	1211.645272	606.326274	1194.618723	597.813000	1193.634707	597.320991	9
6	950.476414	475.741845	933.449865	467.228571	932.465849	466.736563	P	***1082.602679***	541.804977	1065.576130	533.291703	1064.592114	532.799695	8
7	1007.497878	504.252577	990.471329	495.739303	989.487313	495.247295	G	***985.549915***	493.278595	968.523366	484.765321	967.539350	484.273313	7
8	1064.519342	532.763309	1047.492793	524.250035	1046.508777	523.758027	G	928.528451	464.767863	911.501902	456.254589	910.517886	455.762581	6
9	***1503.744668***	752.375972	1486.718119	743.862698	1485.734103	743.370690	Q	***871.506987***	436.257132	854.480438	427.743857	853.496422	427.251849	5
10	1604.792347	802.899812	1587.765798	794.386537	1586.781782	793.894529	T	***432.281661***	216.644468	415.255112	208.131194	414.271096	207.639186	4
11	1675.829461	838.418369	1658.802912	829.905094	1657.818896	829.413086	A	***331.233982***	166.120629	314.207433	157.607354			3
12	1788.913525	894.960400	1771.886976	886.447126	1770.902960	885.955118	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
25.7	1934.011765	-0.002143	LGNQEPGGQTALK
13.7	1934.032867	-0.023245	KSRPLTGLMDLAKEMTK
1.7	1933.982758	0.026864	TVSKLNQEIWMMK
1.3	1933.982758	0.026864	TVSKLNQEIWMMK

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

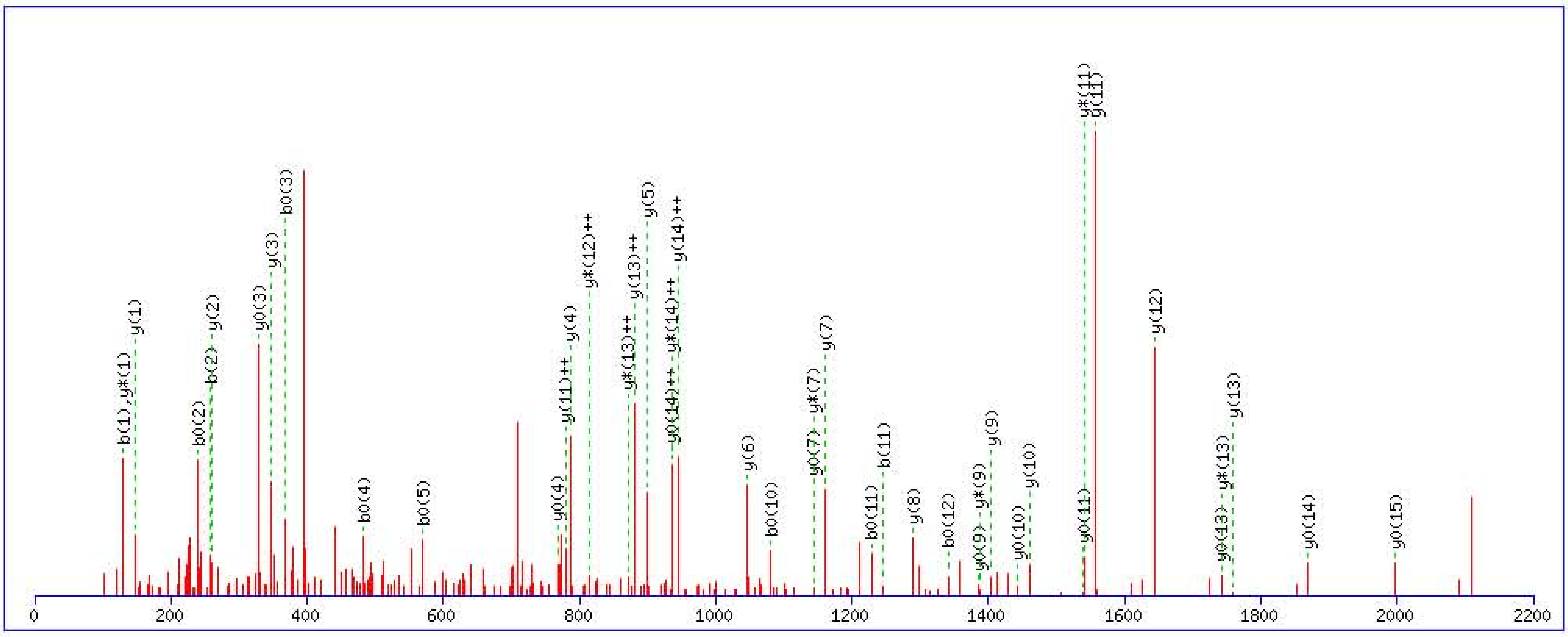
Mascot Search Results

Peptide View

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

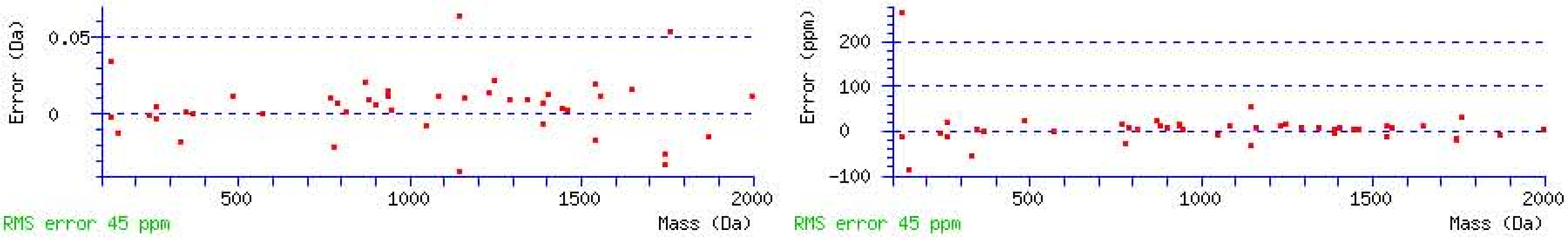
Match to Query 42233: 2144.069172 from(715.697000,3+) rtinseconds(2080) index(5364)
Title: Locus:1.1.1.3244.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 2144.057190
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 0.00018
Matches : 44/174 fragment ions using 114 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	**258.108447**	129.557862	241.081898	121.044587	240.097882	120.552579	Q	2016.021888	1008.514582	1998.995339	1000.001308	1998.011323	999.509300	15
3	386.167025	193.587151	369.140476	185.073876	368.156460	184.581868	Q	1887.963310	944.485293	1870.936761	935.972019	1869.952745	935.480011	14
4	501.193968	251.100622	484.167419	242.587348	483.183403	242.095340	D	***1759.904732***	880.456004	1742.878183	871.942730	1741.894167	871.450722	13
5	588.225996	294.616636	571.199447	286.103362	570.215431	285.611354	S	***1644.877789***	822.942533	1627.851240	814.429258	1626.867224	813.937250	12
6	685.278760	343.143018	668.252211	334.629744	667.268195	334.137736	P	***1557.845761***	779.426519	1540.819212	770.913244	1539.835196	770.421236	11
7	742.300224	371.653750	725.273675	363.140476	724.289659	362.648468	G	***1460.792997***	730.900137	1443.766448	722.386862	1442.782432	721.894854	10
8	856.343151	428.675214	839.316602	420.161939	838.332586	419.669931	N	***1403.771533***	702.389405	1386.744984	693.876130	1385.760968	693.384122	9
9	984.438114	492.722695	967.411565	484.209421	966.427549	483.717413	K	***1289.728606***	645.367941	1272.702057	636.854667	1271.718041	636.362659	8
10	1099.465057	550.236167	1082.438508	541.722892	1081.454492	541.230884	D	***1161.633643***	581.320460	1144.607094	572.807185	1143.623078	572.315177	7
11	**1246.533471**	623.770374	1229.506922	615.257099	1228.522906	614.765091	F	***1046.606700***	523.806988	1029.580151	515.293714	1028.596135	514.801706	6
12	1359.617535	680.312406	1342.590986	671.799131	1341.606970	671.307123	L	***899.538286***	450.272781	882.511737	441.759507	881.527721	441.267499	5
13	1798.842861	899.925069	1781.816312	891.411794	1780.832296	890.919786	Q	***786.454222***	393.730749	769.427673	385.217475	768.443657	384.725467	4
14	1885.874889	943.441083	1868.848340	934.927808	1867.864324	934.435800	S	***347.228896***	174.118086	330.202347	165.604812	329.218331	165.112804	3
15	1998.958953	999.983115	1981.932404	991.469840	1980.948388	990.977832	L	***260.196868***	130.602072	243.170319	122.088798			2
16							K	***147.112804***	74.060040	130.086255	65.546766			1



NCBI **BLAST** search of EQQDSPGNKDFLQSLK
(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	2144.057190	0.011982	EQQDSPGNKDFLQSLK

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

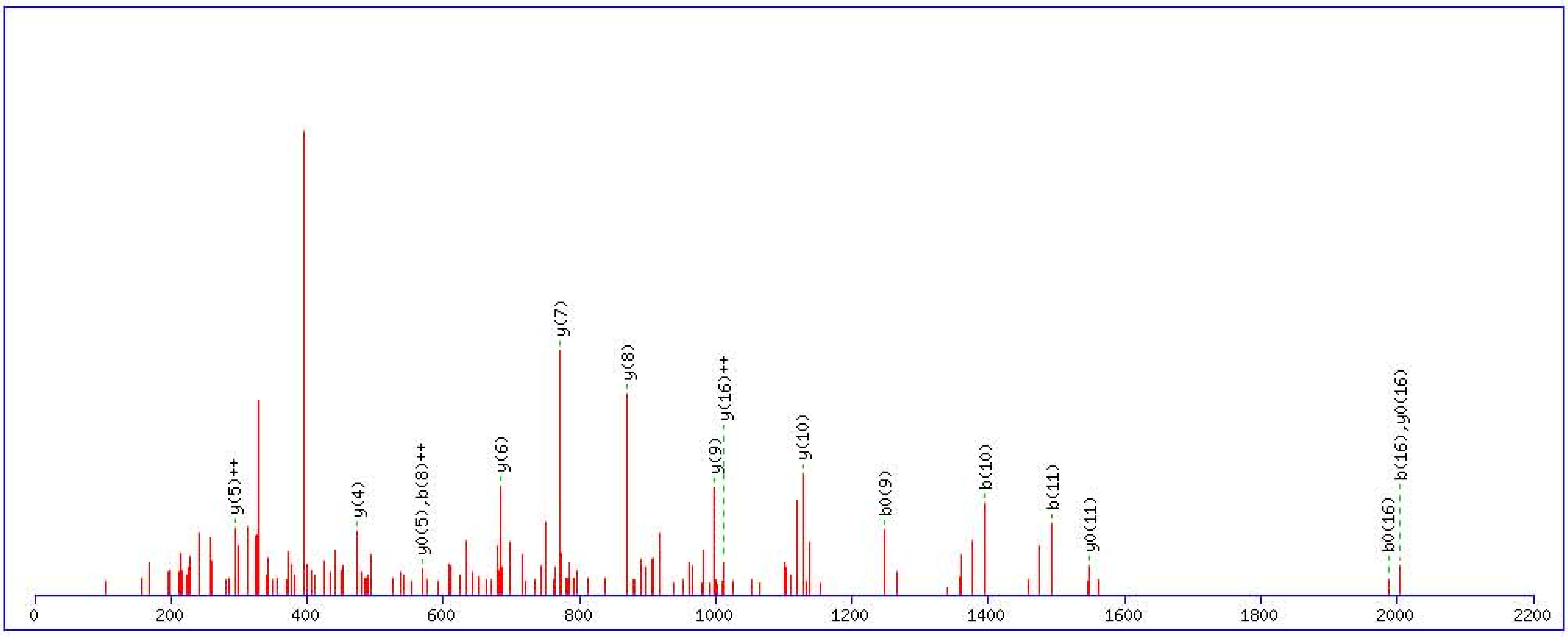
Mascot Search Results

Peptide View

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

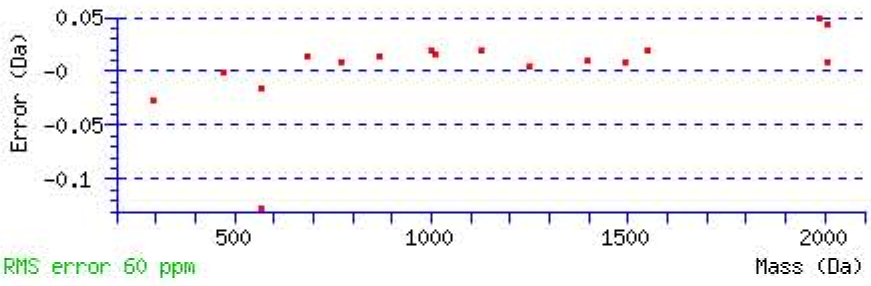
Match to Query 44416: 2263.244652 from(755.422160,3+) rtinseconds(2572) index(8046)
Title: Locus:1.1.1.3415.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

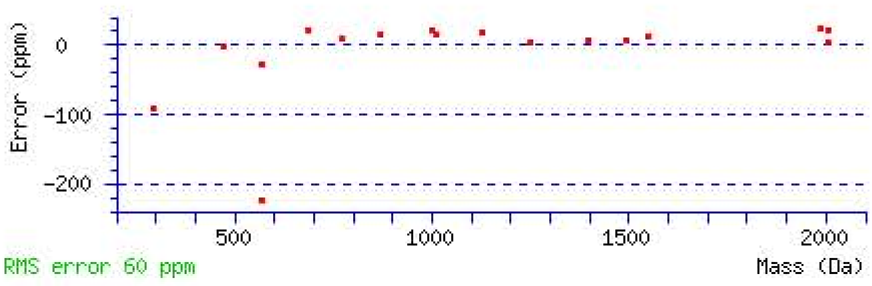
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2263.224594
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.00044
Matches : 17/194 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	129.065854	65.036565	112.039305	56.523291			Q							18
2	242.149918	121.578597	225.123369	113.065323			L	2136.173304	1068.590290	2119.146755	1060.077015	2118.162739	1059.585007	17
3	343.197597	172.102437	326.171048	163.589162	325.187032	163.097154	T	2023.089240	1012.048258	2006.062691	1003.534984	2005.078675	1003.042976	16
4	430.229625	215.618450	413.203076	207.105176	412.219060	206.613168	S	1922.041561	961.524419	1905.015012	953.011144	1904.030996	952.519136	15
5	487.251089	244.129182	470.224540	235.615908	469.240524	235.123900	G	1835.009533	918.008405	1817.982984	909.495130	1816.998968	909.003122	14
6	584.303853	292.655565	567.277304	284.142290	566.293288	283.650282	P	1777.988069	889.497673	1760.961520	880.984398	1759.977504	880.492390	13
7	698.346780	349.677028	681.320231	341.163753	680.336215	340.671745	N	1680.935305	840.971291	1663.908756	832.458016	1662.924740	831.966008	12
8	1137.572106	569.289691	1120.545557	560.776416	1119.561541	560.284408	Q	1566.892378	783.949827	1549.865829	775.436553	1548.881813	774.944545	11
9	1266.614699	633.810988	1249.588150	625.297713	1248.604134	624.805705	E	***1127.667052***	564.337164	1110.640503	555.823890	1109.656487	555.331882	10
10	**1394.673277**	697.840277	1377.646728	689.327002	1376.662712	688.834994	Q	***998.624459***	499.815868	981.597910	491.302593	980.613894	490.810585	9
11	**1493.741691**	747.374484	1476.715142	738.861209	1475.731126	738.369201	V	***870.565881***	435.786579	853.539332	427.273304	852.555316	426.781296	8
12	1580.773719	790.890498	1563.747170	782.377223	1562.763154	781.885215	S	***771.497467***	386.252372	754.470918	377.739097	753.486902	377.247089	7
13	1677.826483	839.416880	1660.799934	830.903605	1659.815918	830.411597	P	***684.465439***	342.736358	667.438890	334.223083	666.454874	333.731075	6
14	1790.910547	895.958912	1773.883998	887.445637	1772.899982	886.953629	L	587.412675	294.209976	570.386126	285.696701	569.402110	285.204693	5
15	1891.958226	946.482751	1874.931677	937.969477	1873.947661	937.477469	T	***474.328611***	237.667944	457.302062	229.154669	456.318046	228.662661	4
16	**2005.042290**	1003.024783	1988.015741	994.511509	1987.031725	994.019501	L	373.280932	187.144104	356.254383	178.630830			3
17	2118.126354	1059.566815	2101.099805	1051.053540	2100.115789	1050.561532	L	260.196868	130.602072	243.170319	122.088798			2
18							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.8	2263.224594	0.020058	QLTSGPNQEQVSPLTLLK
33.4	2263.224594	0.020058	QLTSGPNQEQVSPLTLLK
20.5	2263.224594	0.020058	QLTSGPNQEQVSPLTLLK
6.0	2263.224594	0.020058	GLALSSNKVKSVVMVVFDNEK

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

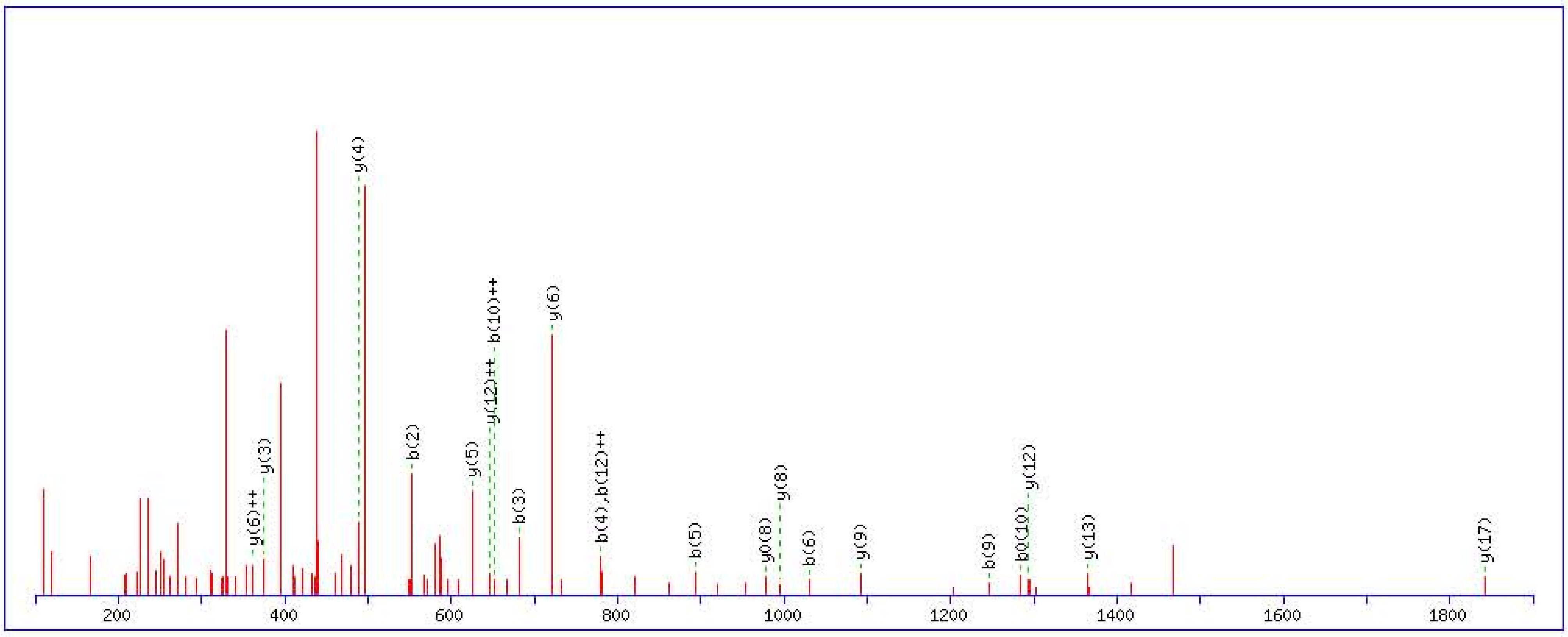
Mascot Search Results

Peptide View

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

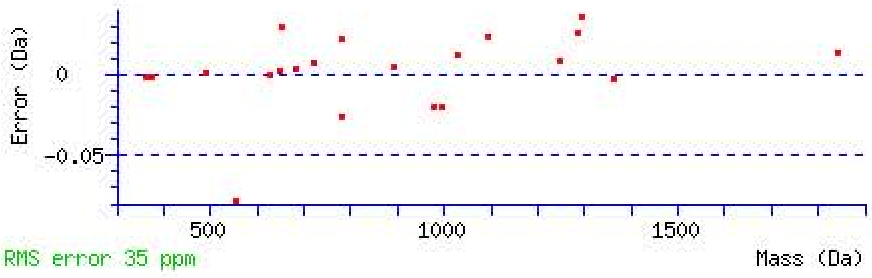
Match to Query 46272: 2393.284936 from(599.328510,4+) rtinseconds(2177) index(5868)
Title: Locus:1.1.1.3278.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

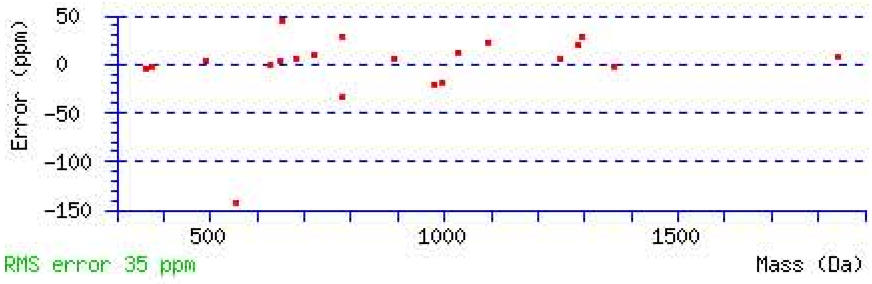
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2393.282410
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2     : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.0055
Matches : 21/196 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	114.091340	57.549308					L							19
2	***553.316666***	277.161971	536.290117	268.648697			Q	2281.205625	1141.106450	2264.179076	1132.593176	2263.195060	1132.101168	18
3	***681.375244***	341.191260	664.348695	332.677986			Q	***1841.980299***	921.493788	1824.953750	912.980513	1823.969734	912.488505	17
4	***780.443658***	390.725467	763.417109	382.212193			V	1713.921721	857.464498	1696.895172	848.951224	1695.911156	848.459216	16
5	***893.527722***	447.267499	876.501173	438.754225			L	1614.853307	807.930292	1597.826758	799.417017	1596.842742	798.925009	15
6	***1030.586634***	515.796955	1013.560085	507.283681			H	1501.769243	751.388260	1484.742694	742.874985	1483.758678	742.382977	14
7	1101.623748	551.315512	1084.597199	542.802238			A	***1364.710331***	682.858804	1347.683782	674.345529	1346.699766	673.853521	13
8	1158.645212	579.826244	1141.618663	571.312970			G	***1293.673217***	647.340247	1276.646668	638.826972	1275.662652	638.334964	12
9	***1245.677240***	623.342258	1228.650691	614.828984	1227.666675	614.336975	S	1236.651753	618.829515	1219.625204	610.316240	1218.641188	609.824232	11
10	1302.698704	**651.852990**	1285.672155	643.339716	1284.688139	642.847707	G	1149.619725	575.313501	1132.593176	566.800226	1131.609160	566.308218	10
11	1399.751468	700.379372	1382.724919	691.866098	1381.740903	691.374089	P	***1092.598261***	546.802769	1075.571712	538.289494	1074.587696	537.797486	9
12	1559.782117	**780.394697**	1542.755568	771.881422	1541.771552	771.389414	C	***995.545497***	498.276387	978.518948	489.763112	977.534932	489.271104	8
13	1672.866181	836.936728	1655.839632	828.423454	1654.855616	827.931446	L	835.514848	418.261062	818.488299	409.747788	817.504283	409.255780	7
14	1769.918945	885.463110	1752.892396	876.949836	1751.908380	876.457828	P	***722.430784***	361.719030	705.404235	353.205756	704.420219	352.713748	6
15	1906.977857	953.992566	1889.951308	945.479292	1888.967292	944.987284	H	***625.378020***	313.192648	608.351471	304.679374	607.367455	304.187366	5
16	2020.061921	1010.534598	2003.035372	1002.021324	2002.051356	1001.529316	L	***488.319108***	244.663192	471.292559	236.149918	470.308543	235.657910	4
17	2133.145985	1067.076630	2116.119436	1058.563356	2115.135420	1058.071348	L	***375.235044***	188.121160	358.208495	179.607886	357.224479	179.115878	3
18	2220.178013	1110.592644	2203.151464	1102.079370	2202.167448	1101.587362	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
19							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.8	2393.282410	0.002526	LQQVLHAGSGPCLPHLLSR
25.5	2393.282410	0.002526	LQQVLHAGSGPCLPHLLSR

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

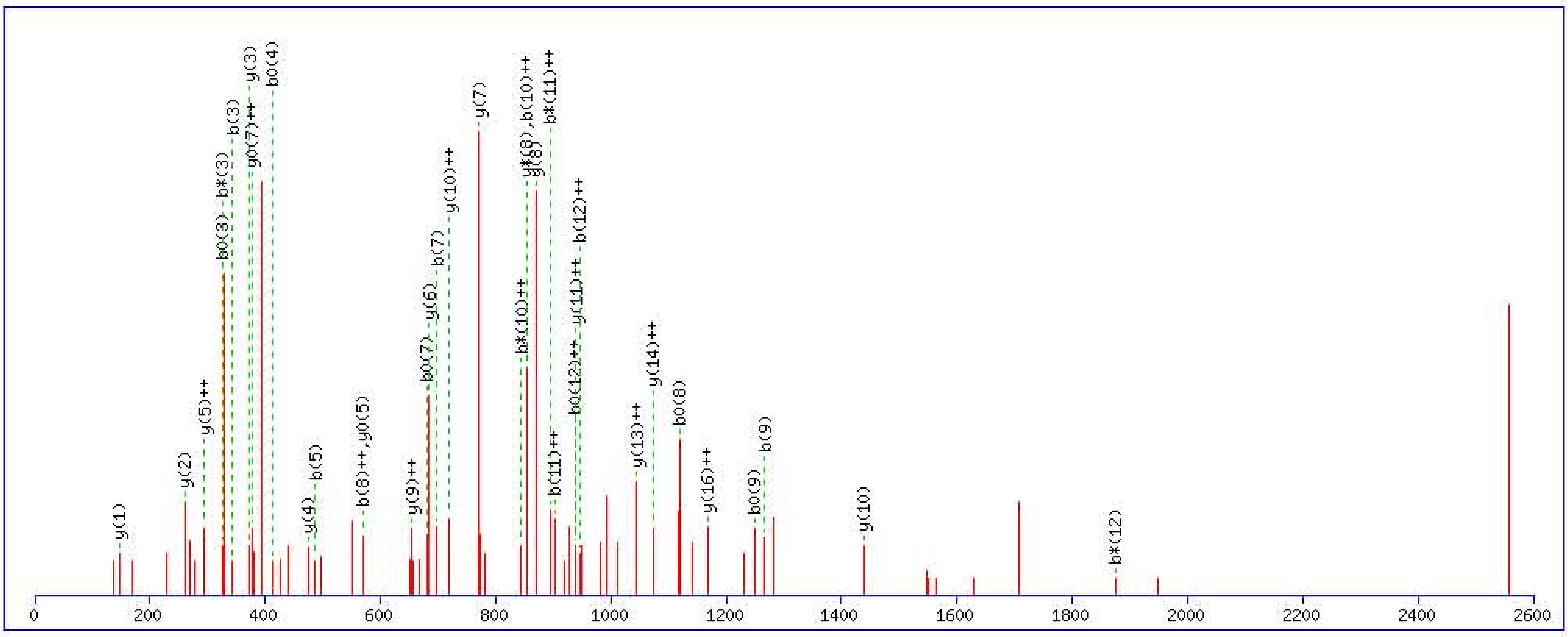
Mascot Search Results

Peptide View

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

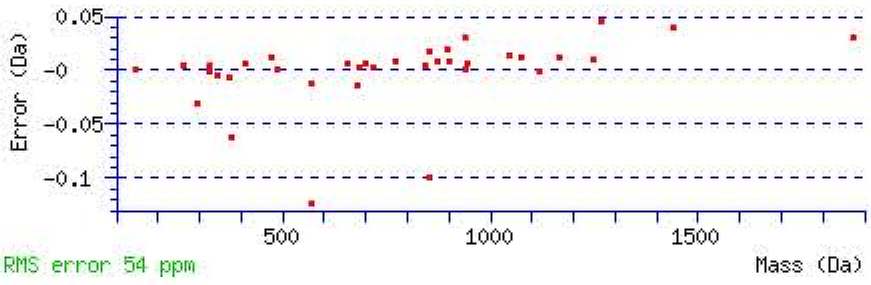
Match to Query 49282: 2574.416172 from(859.146000,3+) rtinseconds(2742) index(8961)
Title: Locus:1.1.1.3474.21 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

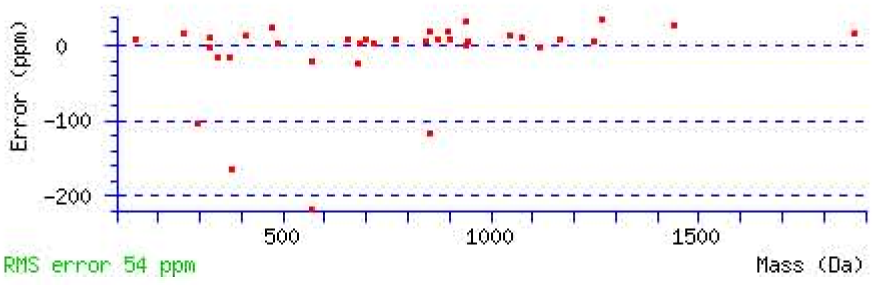
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2574.391342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 45 **Expect:** 8e-005
Matches : 36/194 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	129.065854	65.036565	112.039305	56.523291			Q							18
2	242.149918	121.578597	225.123369	113.065323			L	2447.340052	1224.173664	2430.313503	1215.660389	2429.329487	1215.168381	17
3	**343.197597**	172.102437	326.171048	163.589162	325.187032	163.097154	T	2334.255988	1167.631632	2317.229439	1159.118357	2316.245423	1158.626349	16
4	430.229625	215.618450	413.203076	207.105176	412.219060	206.613168	S	2233.208309	1117.107792	2216.181760	1108.594518	2215.197744	1108.102510	15
5	**487.251089**	244.129182	470.224540	235.615908	469.240524	235.123900	G	2146.176281	1073.591778	2129.149732	1065.078504	2128.165716	1064.586496	14
6	584.303853	292.655565	567.277304	284.142290	566.293288	283.650282	P	2089.154817	1045.081046	2072.128268	1036.567772	2071.144252	1036.075764	13
7	**698.346780**	349.677028	681.320231	341.163753	680.336215	340.671745	N	1992.102053	996.554665	1975.075504	988.041390	1974.091488	987.549382	12
8	1137.572106	**569.289691**	1120.545557	560.776416	1119.561541	560.284408	Q	1878.059126	939.533201	1861.032577	931.019927	1860.048561	930.527919	11
9	**1266.614699**	633.810988	1249.588150	625.297713	1248.604134	624.805705	E	***1438.833800***	719.920538	1421.807251	711.407264	1420.823235	710.915256	10
10	1705.840025	**853.423651**	1688.813476	844.910376	1687.829460	844.418368	Q	1309.791207	655.399242	1292.764658	646.885967	1291.780642	646.393959	9
11	1804.908439	**902.957858**	1787.881890	894.444583	1786.897874	893.952575	V	***870.565881***	435.786579	853.539332	427.273304	852.555316	426.781296	8
12	1891.940467	**946.473872**	1874.913918	937.960597	1873.929902	937.468589	S	***771.497467***	386.252372	754.470918	377.739097	753.486902	377.247089	7
13	1988.993231	995.000254	1971.966682	986.486979	1970.982666	985.994971	P	***684.465439***	342.736358	667.438890	334.223083	666.454874	333.731075	6
14	2102.077295	1051.542285	2085.050746	1043.029011	2084.066730	1042.537003	L	587.412675	294.209976	570.386126	285.696701	569.402110	285.204693	5
15	2203.124974	1102.066125	2186.098425	1093.552850	2185.114409	1093.060842	T	***474.328611***	237.667944	457.302062	229.154669	456.318046	228.662661	4
16	2316.209038	1158.608157	2299.182489	1150.094882	2298.198473	1149.602874	L	***373.280932***	187.144104	356.254383	178.630830			3
17	2429.293102	1215.150189	2412.266553	1206.636914	2411.282537	1206.144906	L	***260.196868***	130.602072	243.170319	122.088798			2
18							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.5	2574.391342	0.024830	QLTSGPNQEQVSPLTLLK
31.1	2574.391342	0.024830	QLTSGPNQEQVSPLTLLK
14.8	2574.391342	0.024830	QLTSGPNQEQVSPLTLLK
0.8	2574.383972	0.032200	QVGSYKKGTMTGHNVADLVVILK
0.3	2574.400543	0.015629	QRQSILPPPQGPAPIPFQHR

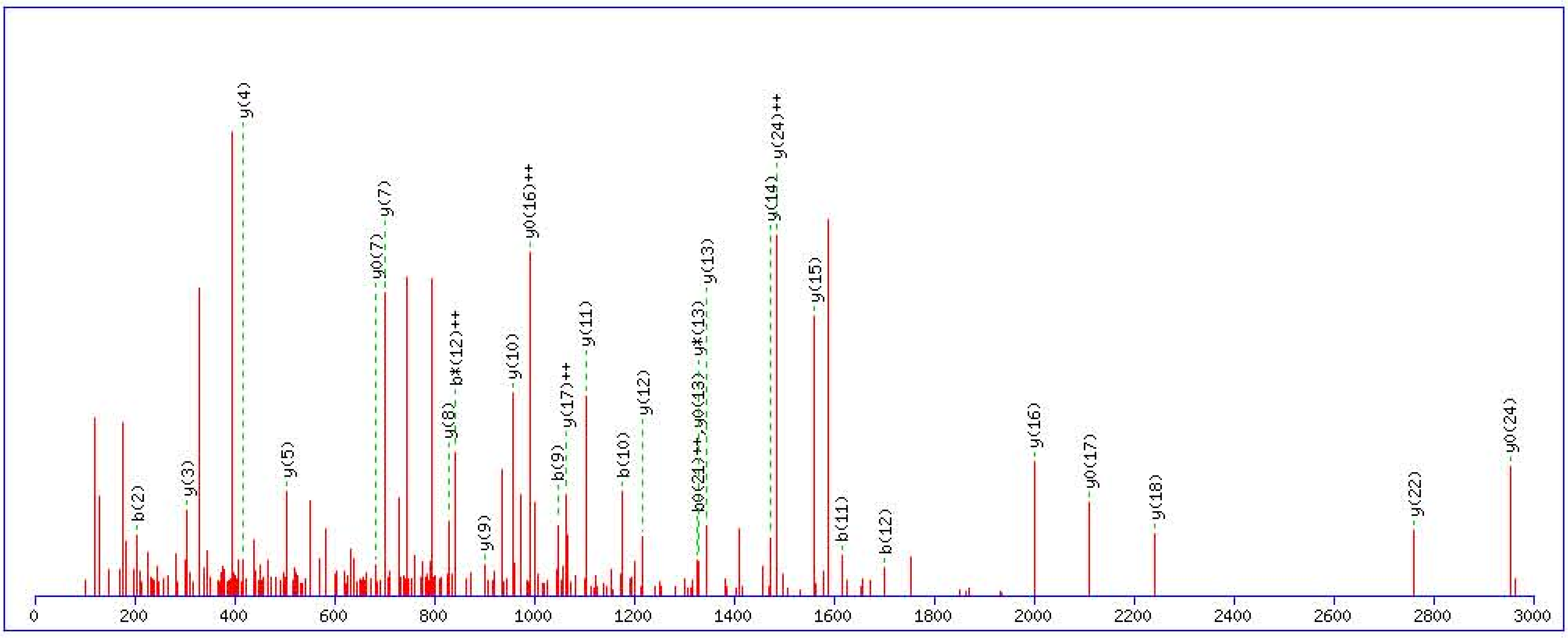
Mascot Search Results

Peptide View

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

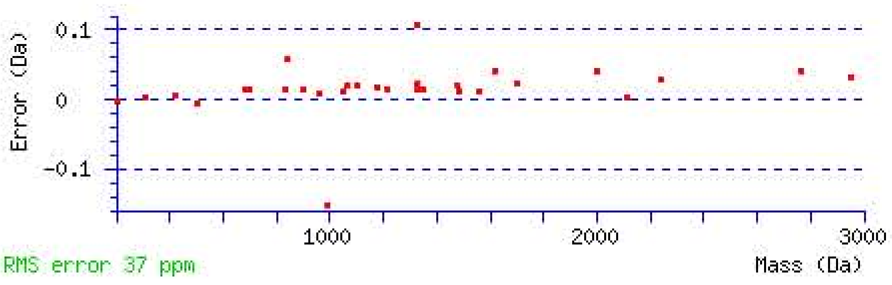
Match to Query 55345: 3175.692656 from(794.930440,4+) rtinseconds(2809) index(9332)
Title: Locus:1.1.1.3497.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

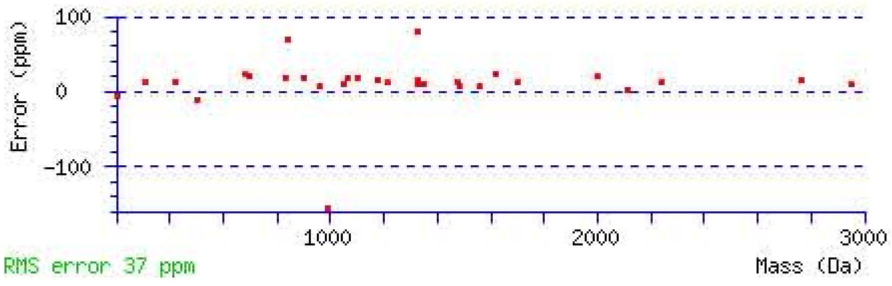
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3175.662750
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 78  Expect: 2.7e-007
Matches : 30/278 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	58.028740	29.518008					G							26
2	**205.097154**	103.052215					F	3119.648573	1560.327924	3102.622024	1551.814650	3101.638008	1551.322642	25
3	302.149918	151.578597					P	2972.580159	1486.793717	2955.553610	1478.280443	2954.569594	1477.788435	24
4	415.233982	208.120629					I	2875.527395	1438.267335	2858.500846	1429.754061	2857.516830	1429.262053	23
5	543.328945	272.168111	526.302396	263.654836			K	***2762.443331***	1381.725303	2745.416782	1373.212029	2744.432766	1372.720021	22
6	672.371538	336.689407	655.344989	328.176133	654.360973	327.684125	E	2634.348368	1317.677822	2617.321819	1309.164547	2616.337803	1308.672539	21
7	787.398481	394.202879	770.371932	385.689604	769.387916	385.197596	D	2505.305775	1253.156525	2488.279226	1244.643251	2487.295210	1244.151243	20
8	934.466895	467.737086	917.440346	459.223811	916.456330	458.731803	F	2390.278832	1195.643054	2373.252283	1187.129779	2372.268267	1186.637771	19
9	**1047.550959**	524.279117	1030.524410	515.765843	1029.540394	515.273835	L	***2243.210418***	1122.108847	2226.183869	1113.595572	2225.199853	1113.103564	18
10	**1176.593552**	588.800414	1159.567003	580.287140	1158.582987	579.795132	E	2130.126354	1065.566815	2113.099805	1057.053540	2112.115789	1056.561532	17
11	**1615.818878**	808.413077	1598.792329	799.899803	1597.808313	799.407795	Q	***2001.083761***	1001.045519	1984.057212	992.532244	1983.073196	992.040236	16
12	**1702.850906**	851.929091	1685.824357	843.415817	1684.840341	842.923809	S	***1561.858435***	781.432856	1544.831886	772.919581	1543.847870	772.427573	15
13	1831.893499	916.450388	1814.866950	907.937113	1813.882934	907.445105	E	***1474.826407***	737.916842	1457.799858	729.403567	1456.815842	728.911559	14
14	1959.952077	980.479677	1942.925528	971.966402	1941.941512	971.474394	Q	***1345.783814***	673.395545	1328.757265	664.882271	1327.773249	664.390263	13
15	2073.036141	1037.021709	2056.009592	1028.508434	2055.025576	1028.016426	L	***1217.725236***	609.366256	1200.698687	600.852982	1199.714671	600.360974	12
16	2220.104555	1110.555916	2203.078006	1102.042641	2202.093990	1101.550633	F	***1104.641172***	552.824224	1087.614623	544.310949	1086.630607	543.818941	11
17	2277.126019	1139.066648	2260.099470	1130.553373	2259.115454	1130.061365	G	***957.572758***	479.290017	940.546209	470.776743	939.562193	470.284735	10
18	2348.163133	1174.585205	2331.136584	1166.071930	2330.152568	1165.579922	A	***900.551294***	450.779285	883.524745	442.266011	882.540729	441.774003	9
19	2476.258096	1238.632686	2459.231547	1230.119412	2458.247531	1229.627404	K	***829.514180***	415.260728	812.487631	406.747453	811.503615	406.255445	8
20	2573.310860	1287.159068	2556.284311	1278.645794	2555.300295	1278.153786	P	***701.419217***	351.213246	684.392668	342.699972	683.408652	342.207964	7
21	2672.379274	1336.693275	2655.352725	1328.180001	2654.368709	1327.687993	V	604.366453	302.686864	587.339904	294.173590	586.355888	293.681582	6
22	2759.411302	1380.209289	2742.384753	1371.696015	2741.400737	1371.204007	S	***505.298039***	253.152657	488.271490	244.639383	487.287474	244.147375	5
23	2872.495366	1436.751321	2855.468817	1428.238047	2854.484801	1427.746039	L	***418.266011***	209.636643	401.239462	201.123369	400.255446	200.631361	4
24	2973.543045	1487.275161	2956.516496	1478.761886	2955.532480	1478.269878	T	***305.181947***	153.094611	288.155398	144.581337	287.171382	144.089329	3
25	3030.564509	1515.785893	3013.537960	1507.272618	3012.553944	1506.780610	G	204.134268	102.570772	187.107719	94.057497			2
26							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
78.4	3175.662750	0.029906	GFPIKEDFLEQSEQLFGAKPVSLTGK
44.0	3175.662750	0.029906	GFPIKEDFLEQSEQLFGAKPVSLTGK

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

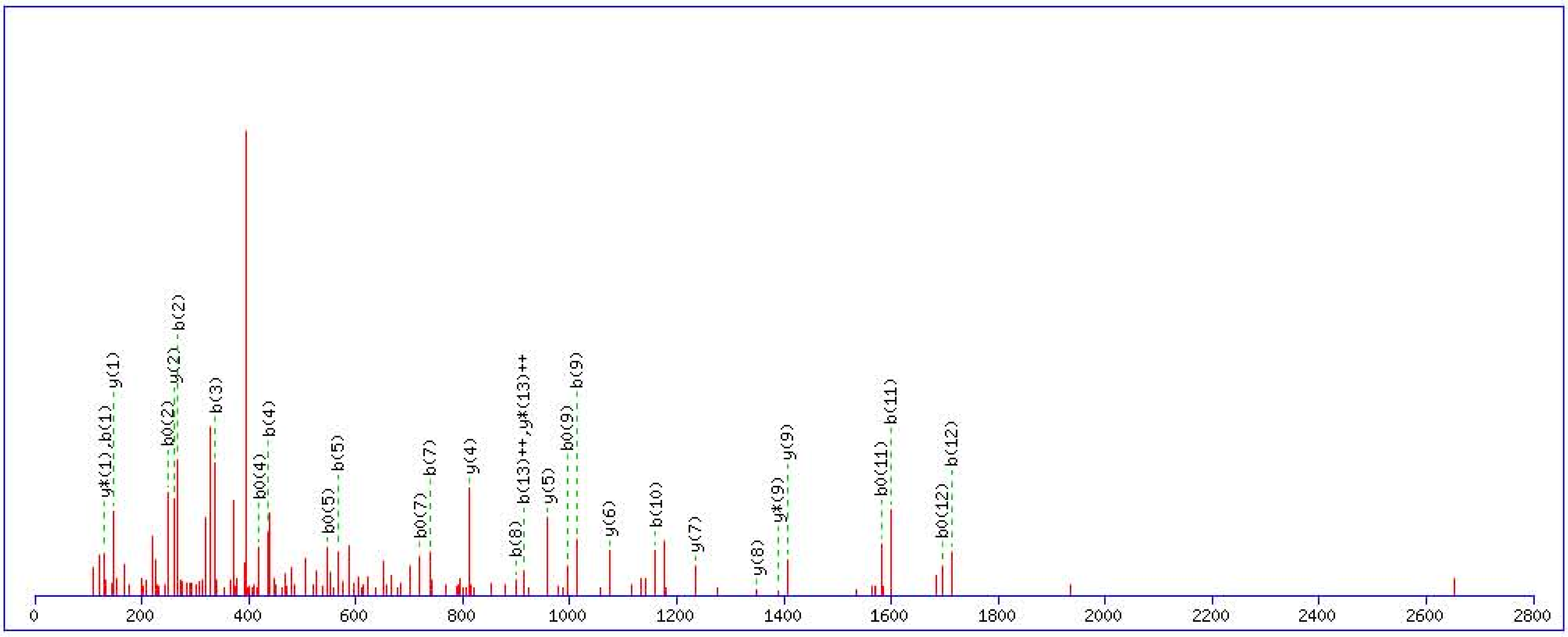
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

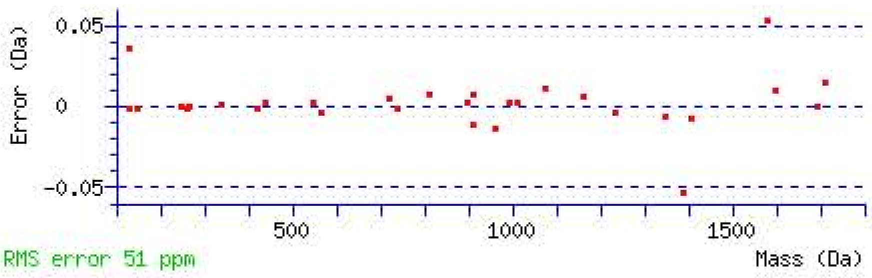
Match to Query 38806: 1970.922852 from(657.981560,3+) rtinseconds(2098) index(32441)
Title: Locus:1.1.1.3394.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

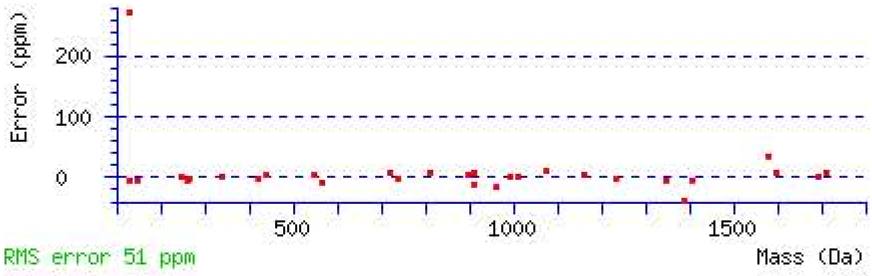
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1970.923019
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 74  Expect: 1.6e-007
Matches : 30/126 fragment ions using 45 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
73.6	1970.923019	-0.000167	EHAVEGDCDFQLLK
0.9	1970.905258	0.017594	LDFNMTTNHSFMCLIK

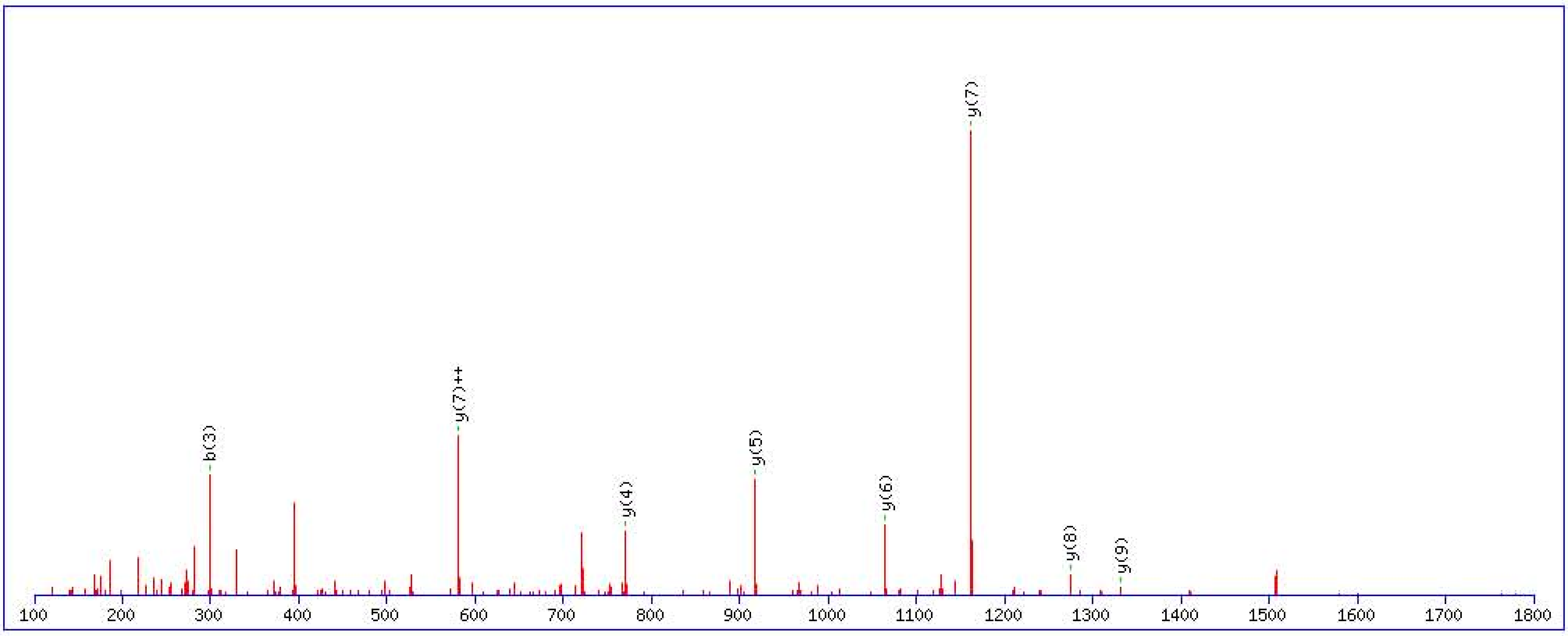
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

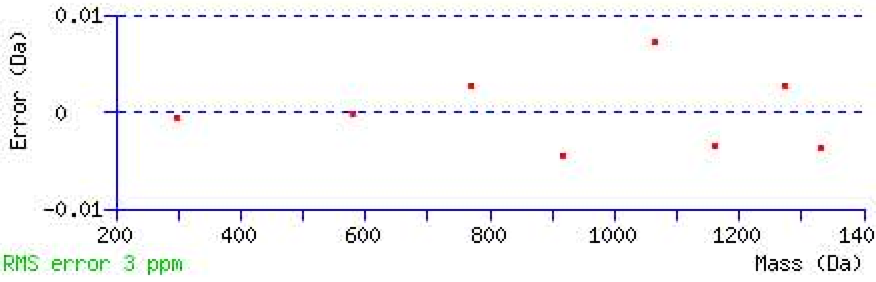
Match to Query 26133: 1458.778428 from(730.396490,2+) rtinseconds(2552) index(34922)
Title: Locus:1.1.1.3552.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

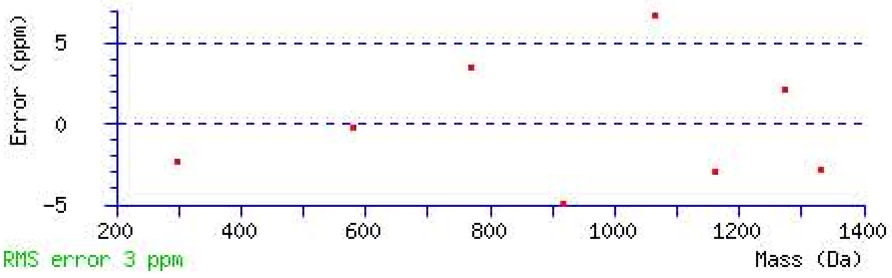
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1458.780594
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 40 **Expect:** 0.00029
Matches : 8/72 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	129.065854	65.036565	112.039305	56.523291	Q					10
2	186.087318	93.547297	169.060769	85.034023	G	*1331.729276*	666.368276	1314.702727	657.855002	9
3	299.171382	150.089329	282.144833	141.576055	I	*1274.707812*	637.857544	1257.681263	629.344270	8
4	396.224146	198.615711	379.197597	190.102436	P	*1161.623748*	581.315512	1144.597199	572.802238	7
5	543.292560	272.149918	526.266011	263.636643	F	*1064.570984*	532.789130	1047.544435	524.275856	6
6	690.360974	345.684125	673.334425	337.170850	F	*917.502570*	459.254923	900.476021	450.741649	5
7	747.382438	374.194857	730.355889	365.681582	G	*770.434156*	385.720716	753.407607	377.207442	4
8	1186.607764	593.807520	1169.581215	585.294246	Q	713.412692	357.209984	696.386143	348.696710	3
9	1285.676178	643.341727	1268.649629	634.828453	V	274.187366	137.597321	257.160817	129.084047	2
10					R	175.118952	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.9	1458.780594	-0.002166	QGIPFFGQVR
2.0	1458.786438	-0.008010	QVAASTAQLLVACK
0.8	1458.798340	-0.019912	KIGGIWTWVGTNK

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

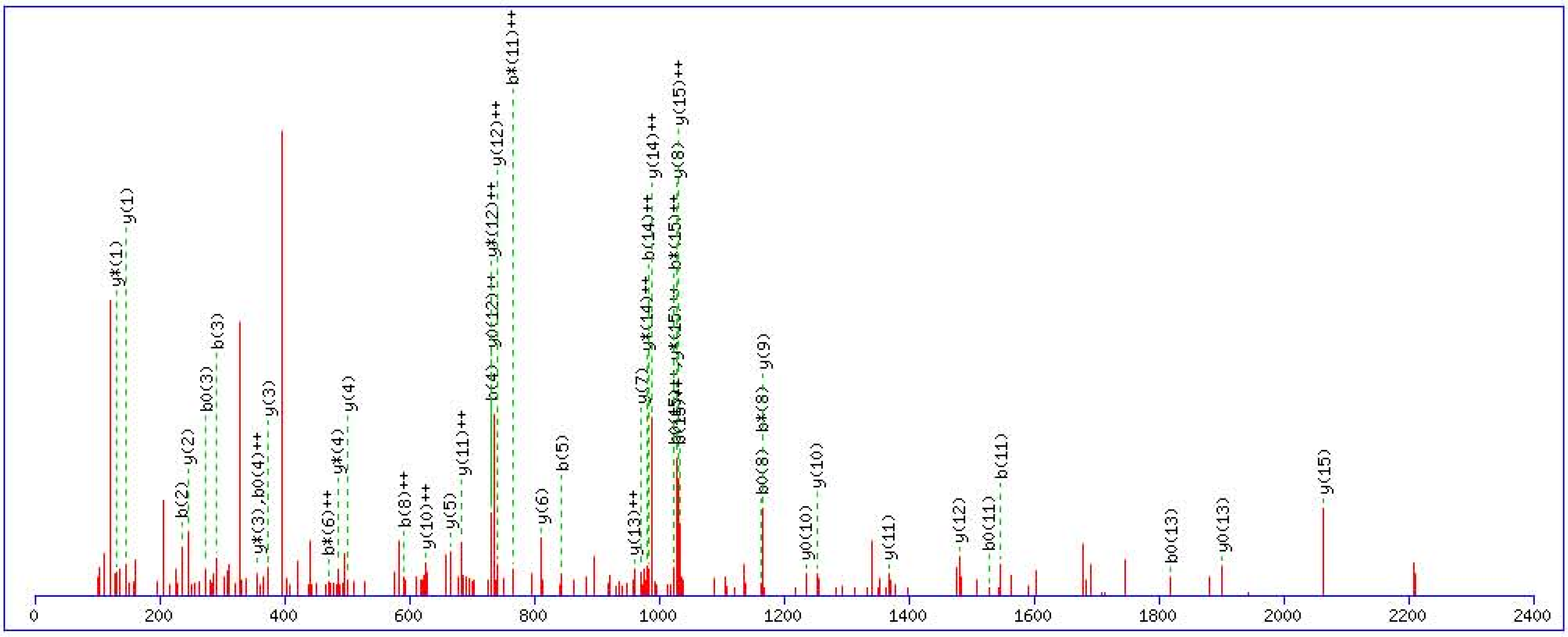
Mascot Search Results

Peptide View

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

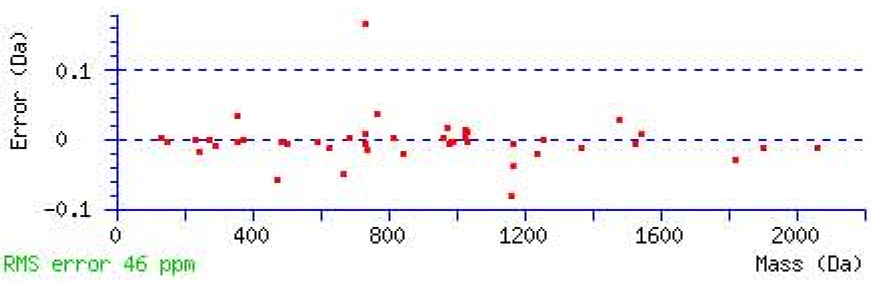
Match to Query 26481: 2210.036202 from(737.686010,3+) rtinseconds(1868) index(18091)
Title: Locus:1.1.1.3216.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

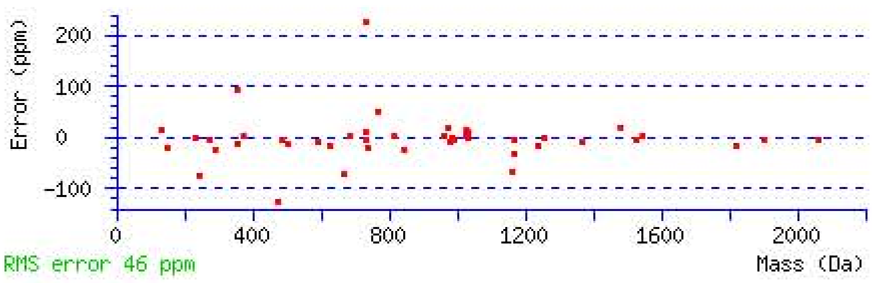
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2210.040131
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4     : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 0.00014
Matches : 46/154 fragment ions using 115 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	***2063.978979***	1032.493127	2046.952430	1023.979853	2045.968414	1023.487845	15
3	**292.129182**	146.568229			274.118617	137.562946	G	1976.946951	988.977114	1959.920402	980.463839	1958.936386	979.971831	14
4	**731.354508**	366.180892	714.327959	357.667618	713.343943	357.175610	Q	1919.925487	960.466382	1902.898938	951.953107	1901.914922	951.461099	13
5	**844.438572**	422.722924	827.412023	414.209650	826.428007	413.717642	L	***1480.700161***	740.853719	1463.673612	732.340444	1462.689596	731.848436	12
6	958.481499	479.744388	941.454950	471.231113	940.470934	470.739105	N	***1367.616097***	684.311687	1350.589548	675.798412	1349.605532	675.306404	11
7	1045.513527	523.260402	1028.486978	514.747127	1027.502962	514.255119	S	***1253.573170***	627.290223	1236.546621	618.776949	1235.562605	618.284941	10
8	1182.572439	**591.789858**	1165.545890	583.276583	1164.561874	582.784575	H	***1166.541142***	583.774209	1149.514593	575.260935			9
9	1239.593903	620.300590	1222.567354	611.787315	1221.583338	611.295307	G	***1029.482230***	515.244753	1012.455681	506.731479			8
10	1399.624552	700.315914	1382.598003	691.802640	1381.613987	691.310632	C	***972.460766***	486.734021	955.434217	478.220747			7
11	**1546.692966**	773.850121	1529.666417	765.336847	1528.682401	764.844839	F	***812.430117***	406.718697	795.403568	398.205422			6
12	1709.756295	855.381786	1692.729746	846.868511	1691.745730	846.376503	Y	***665.361703***	333.184490	648.335154	324.671215			5
13	1837.814873	919.411075	1820.788324	910.897800	1819.804308	910.405792	Q	***502.298374***	251.652825	485.271825	243.139550			4
14	1965.873451	**983.440364**	1948.846902	974.927089	1947.862886	974.435081	Q	***374.239796***	187.623536	357.213247	179.110261			3
15	2064.941865	**1032.974570**	2047.915316	1024.461296	2046.931300	1023.969288	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 FSGQLNSHGCFYQQVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.8	2210.040131	-0.003929	FSGQLNSHGCFYQQVK
15.1	2210.040131	-0.003929	FSGQLNSHGCFYQQVK
12.7	2210.040131	-0.003929	FSGQLNSHGCFYQQVK

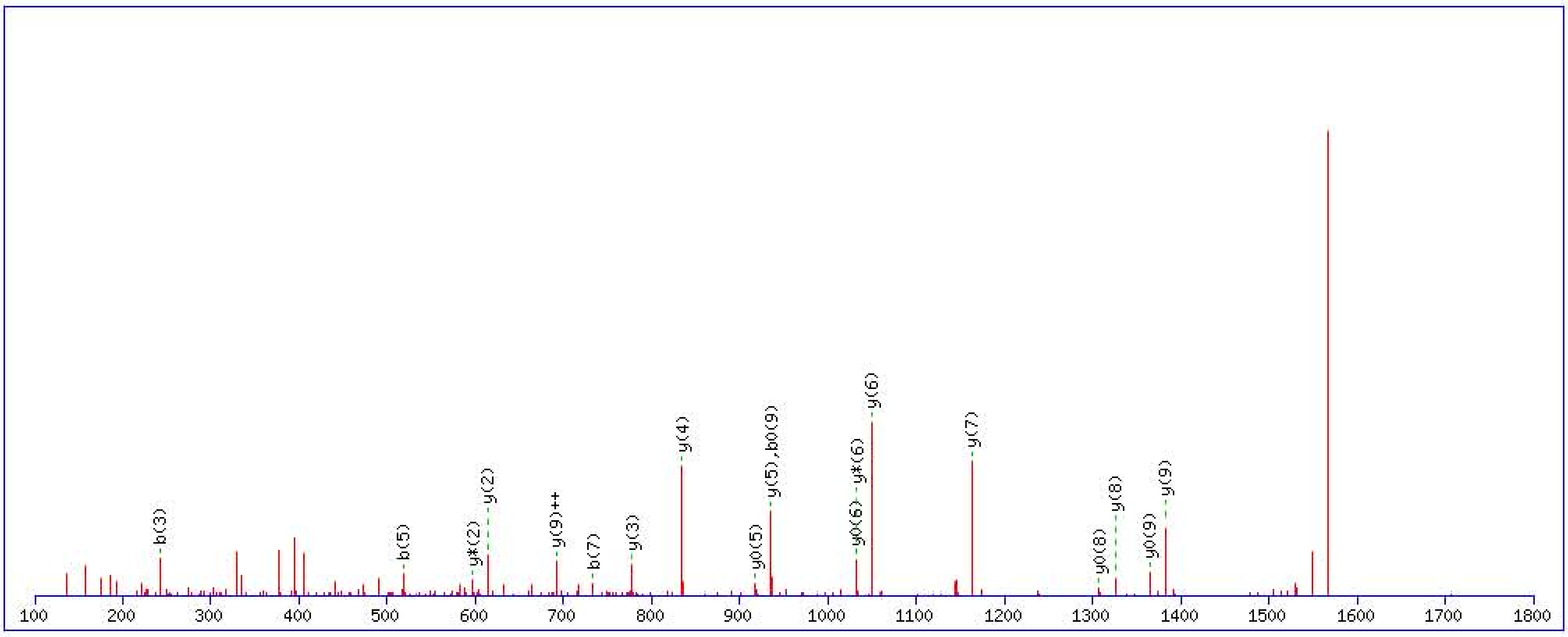
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

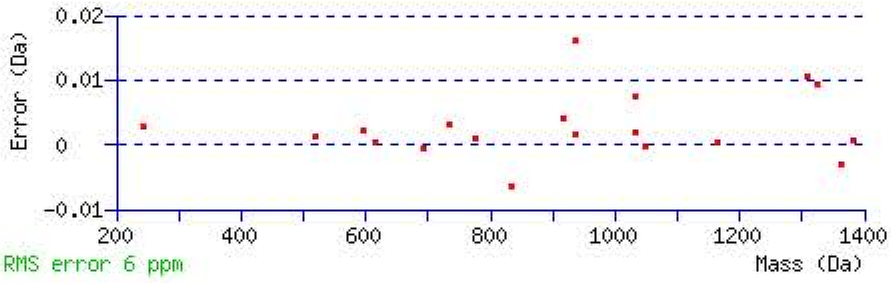
Match to Query 29064: 1565.797168 from(783.905860,2+) rtinseconds(2018) index(19167)
Title: Locus:1.1.1.3268.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

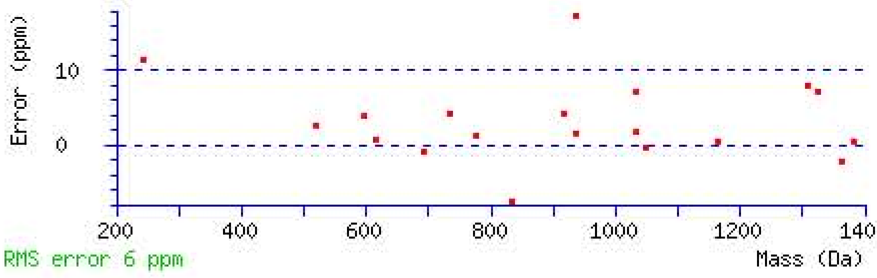
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1565.802414
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 8.8e-006
Matches : 19/90 fragment ions using 29 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	185.128454	93.067865					I	1495.772598	748.389937	1478.746049	739.876663	1477.762033	739.384655	10
3	**242.149918**	121.578597					G	***1382.688534***	691.847905	1365.661985	683.334631	1364.677969	682.842623	9
4	405.213247	203.110261					Y	***1325.667070***	663.337173	1308.640521	654.823899	1307.656505	654.331890	8
5	**518.297311**	259.652294					L	***1162.603741***	581.805509	1145.577192	573.292234	1144.593176	572.800226	7
6	632.340238	316.673757	615.313689	308.160483			N	***1049.519677***	525.263477	1032.493128	516.750202	1031.509112	516.258194	6
7	**733.387917**	367.197597	716.361368	358.684322	715.377352	358.192314	T	***935.476750***	468.242013	918.450201	459.728739	917.466185	459.236731	5
8	790.409381	395.708329	773.382832	387.195054	772.398816	386.703046	G	***834.429071***	417.718174	817.402522	409.204899			4
9	953.472710	477.239993	936.446161	468.726719	935.462145	468.234711	Y	***777.407607***	389.207442	760.381058	380.694167			3
10	1392.698036	696.852656	1375.671487	688.339382	1374.687471	687.847374	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 AIGYLNTGYQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.1	1565.802414	-0.005246	AIGYLNTGYQR
2.2	1565.806259	-0.009091	QIHKLQDWAGSRQ
2.0	1565.795013	0.002155	SSPASSPELPWRPR
1.7	1565.781296	0.015872	AGLFSWQYQR

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

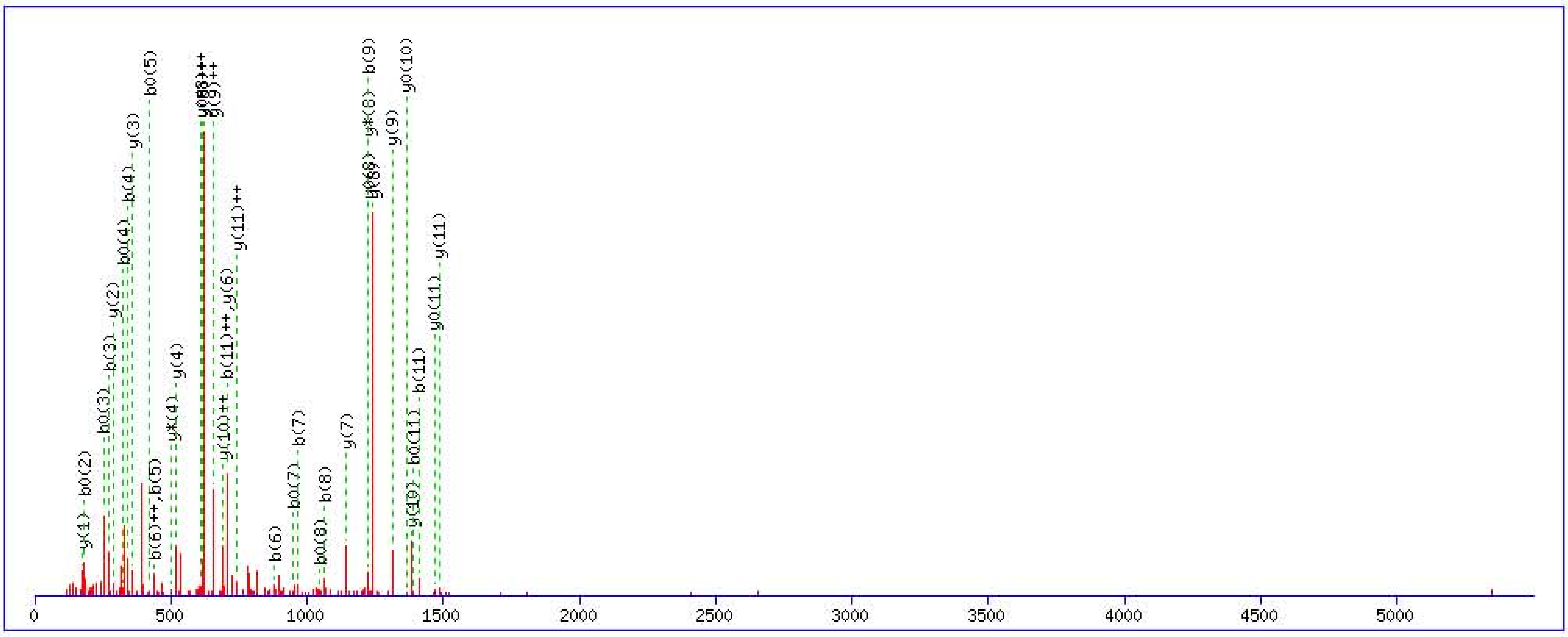
Mascot Search Results

Peptide View

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

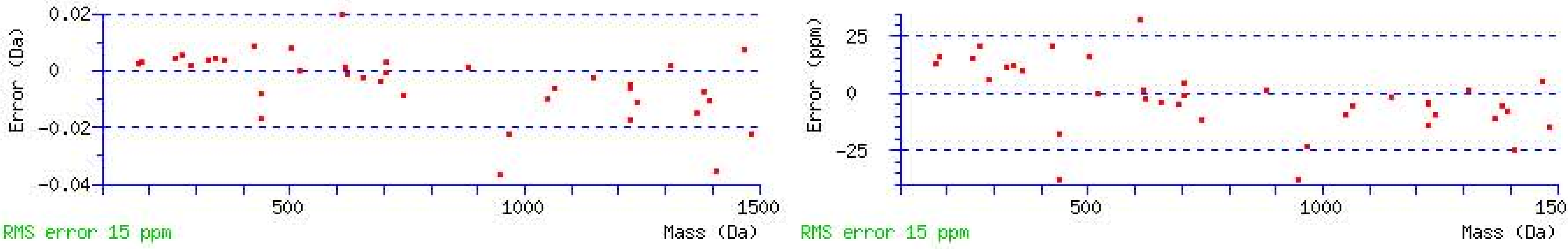
Match to Query 29726: 1582.827048 from(792.420800,2+) rtinseconds(1836) index(17930)
Title: Locus:1.1.1.3205.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 5500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1582.832352
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 1.9e-005
Matches : 38/110 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	100.075690	50.541483					V							12
2	201.123369	101.065322			183.112804	92.060040	T	***1484.771218***	742.889247	1467.744669	734.375972	1466.760653	733.883964	11
3	**272.160483**	136.583879			254.149918	127.578597	A	***1383.723539***	692.365407	1366.696990	683.852133	1365.712974	683.360125	10
4	**343.197597**	172.102437			325.187032	163.097154	A	***1312.686425***	656.846850	1295.659876	648.333576	1294.675860	647.841568	9
5	**440.250361**	220.628819			422.239796	211.623536	P	***1241.649311***	621.328293	1224.622762	612.815019	1223.638746	612.323011	8
6	**879.475687**	**440.241482**	862.449138	431.728207	861.465122	431.236199	Q	***1144.596547***	572.801911	1127.569998	564.288637	1126.585982	563.796629	7
7	**966.507715**	483.757496	949.481166	475.244221	948.497150	474.752213	S	***705.371221***	353.189248	688.344672	344.675974	687.360656	344.183966	6
8	**1065.576129**	533.291703	1048.549580	524.778428	1047.565564	524.286420	V	***618.339193***	309.673234	601.312644	301.159960			5
9	**1225.606778**	613.307027	1208.580229	604.793753	1207.596213	604.301745	C	***519.270779***	260.139028	502.244230	251.625753			4
10	1296.643892	648.825584	1279.617343	640.312310	1278.633327	639.820302	A	***359.240130***	180.123703	342.213581	171.610428			3
11	**1409.727956**	**705.367616**	1392.701407	696.854342	1391.717391	696.362333	L	***288.203016***	144.605146	271.176467	136.091871			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1



NCBI **BLAST** search of VTAAPQSVCALR
(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	1582.832352	-0.005304	VTAAPQSVCALR
5.8	1582.821564	0.005484	LSKAVATWHANTER
3.0	1582.821579	0.005469	IGGHGPTLKAYQEGR
1.1	1582.817535	0.009513	KTLSEETRQHQAR

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

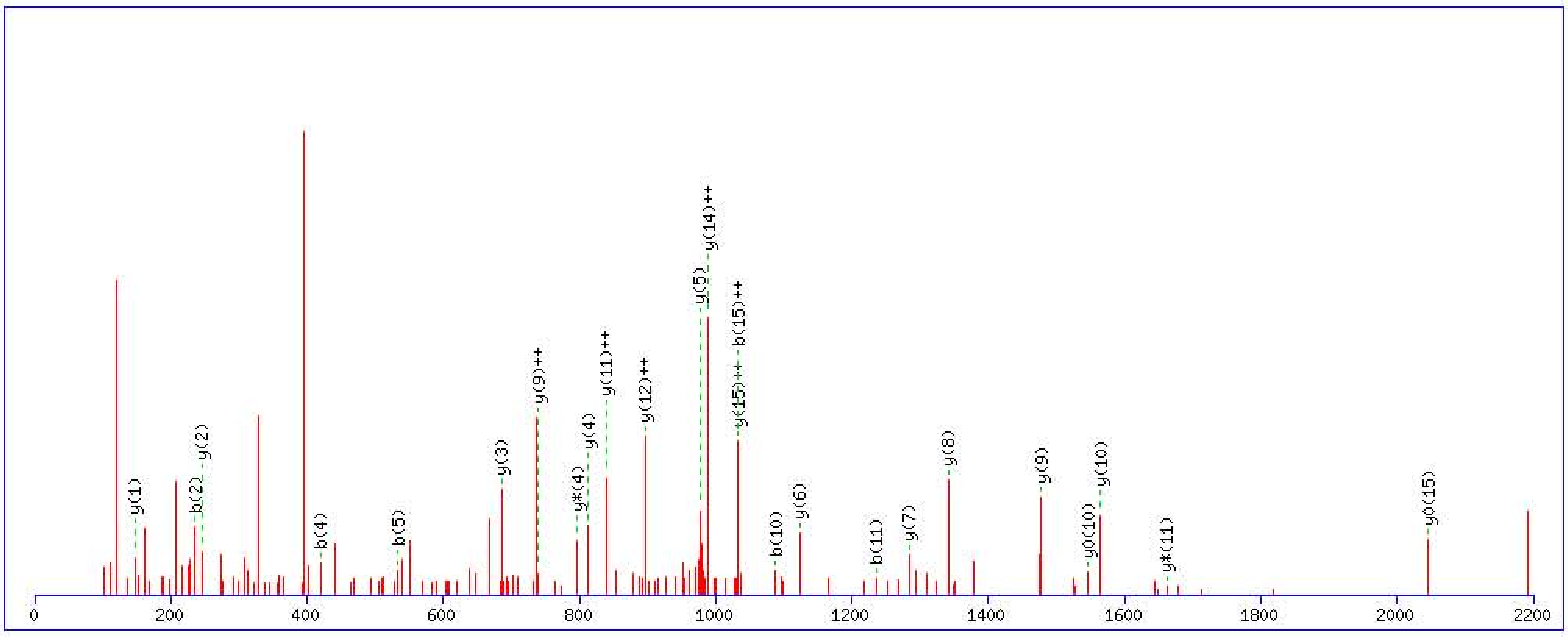
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

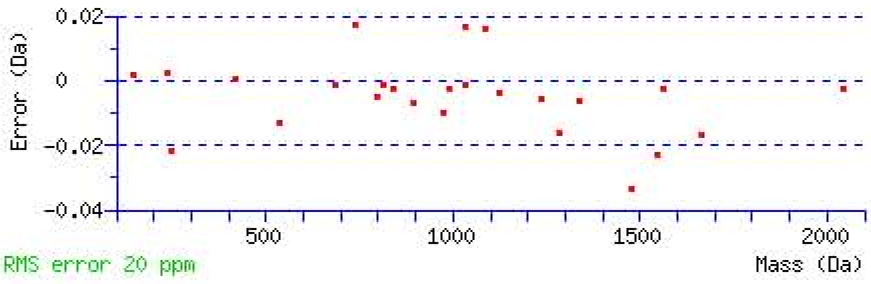
Match to Query 43341: 2210.032782 from(737.684870,3+) rtinseconds(1894) index(18269)
Title: Locus:1.1.1.3225.21 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

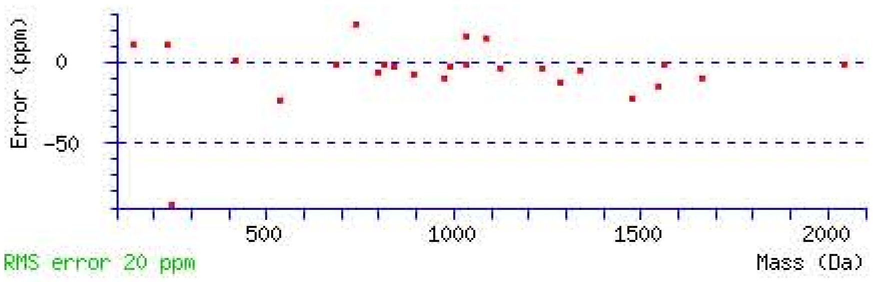
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2210.040131
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 4.8e-005
Matches : 25/154 fragment ions using 51 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	2063.978979	1032.493127	2046.952430	1023.979853	2045.968414	1023.487845	15
3	292.129182	146.568229			274.118617	137.562946	G	1976.946951	988.977114	1959.920402	980.463839	1958.936386	979.971831	14
4	**420.187760**	210.597518	403.161211	202.084243	402.177195	201.592235	Q	1919.925487	960.466382	1902.898938	951.953107	1901.914922	951.461099	13
5	**533.271824**	267.139550	516.245275	258.626276	515.261259	258.134268	L	1791.866909	896.437093	1774.840360	887.923818	1773.856344	887.431810	12
6	647.314751	324.161014	630.288202	315.647739	629.304186	315.155731	N	1678.782845	839.895061	1661.756296	831.381786	1660.772280	830.889778	11
7	734.346779	367.677028	717.320230	359.163753	716.336214	358.671745	S	***1564.739918***	782.873597	1547.713369	774.360323	1546.729353	773.868315	10
8	871.405691	436.206483	854.379142	427.693209	853.395126	427.201201	H	***1477.707890***	739.357583	1460.681341	730.844309			9
9	928.427155	464.717216	911.400606	456.203941	910.416590	455.711933	G	***1340.648978***	670.828127	1323.622429	662.314853			8
10	**1088.457804**	544.732540	1071.431255	536.219266	1070.447239	535.727257	C	***1283.627514***	642.317395	1266.600965	633.804121			7
11	**1235.526218**	618.266747	1218.499669	609.753473	1217.515653	609.261464	F	***1123.596865***	562.302071	1106.570316	553.788796			6
12	1398.589547	699.798412	1381.562998	691.285137	1380.578982	690.793129	Y	***976.528451***	488.767864	959.501902	480.254589			5
13	1526.648125	763.827700	1509.621576	755.314426	1508.637560	754.822418	Q	***813.465122***	407.236199	796.438573	398.722925			4
14	1965.873451	983.440364	1948.846902	974.927089	1947.862886	974.435081	Q	***685.406544***	343.206910	668.379995	334.693636			3
15	2064.941865	1032.974570	2047.915316	1024.461296	2046.931300	1023.969288	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 FSGQLNSHGCFYQQVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.9	2210.040131	-0.007349	FSGQLNSHGCFYQQVK
42.8	2210.040131	-0.007349	FSGQLNSHGCFYQQVK
4.7	2210.058075	-0.025293	FSHLSRNMTMQRTMK
4.6	2210.058075	-0.025293	FSHLSRNMTMQRTMK
1.6	2210.045486	-0.012704	MSMKEVDEQMLAIQSK

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

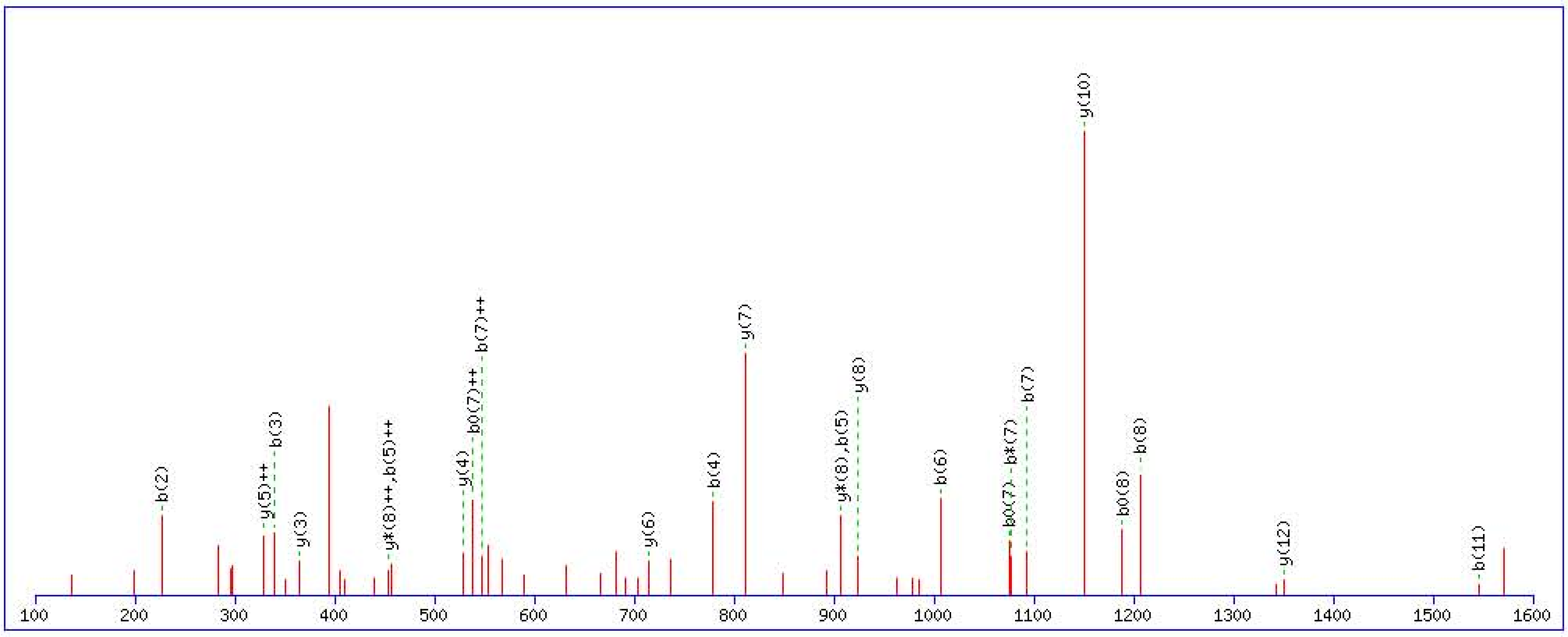
Mascot Search Results

Peptide View

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

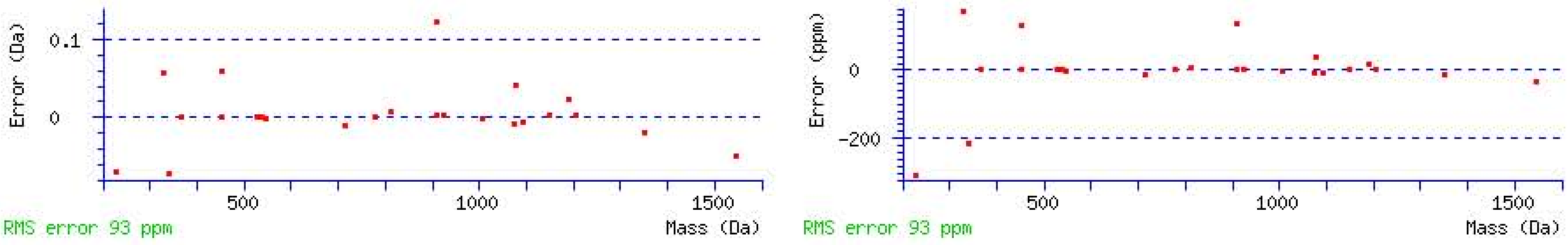
Match to Query 45898: 2355.254922 from(786.092250,3+) rtinseconds(2870) index(37114)
Title: Locus:1.1.1.3661.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 2355.258179
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 0.00021
Matches : 24/182 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	114.091340	57.549308					L							18
2	***227.175404***	114.091340					L	2243.181426	1122.094351	2226.154877	1113.581076	2225.170861	1113.089068	17
3	***340.259468***	170.633372					L	2130.097362	1065.552319	2113.070813	1057.039044	2112.086797	1056.547036	16
4	***779.484794***	390.246035	762.458245	381.732760			Q	2017.013298	1009.010287	1999.986749	1000.497013	1999.002733	1000.005005	15
5	***907.543372***	**454.275324**	890.516823	445.762049			Q	1577.787972	789.397624	1560.761423	780.884350	1559.777407	780.392342	14
6	***1006.611786***	503.809531	989.585237	495.296256			V	1449.729394	725.368335	1432.702845	716.855061	1431.718829	716.363053	13
7	***1093.643814***	**547.325545**	1076.617265	538.812271	1075.633249	538.320263	S	***1350.660980***	675.834128	1333.634431	667.320854	1332.650415	666.828846	12
8	***1206.727878***	603.867577	1189.701329	595.354303	1188.717313	594.862294	L	1263.628952	632.318114	1246.602403	623.804840	1245.618387	623.312832	11
9	1303.780642	652.393959	1286.754093	643.880685	1285.770077	643.388676	P	***1150.544888***	575.776082	1133.518339	567.262808	1132.534323	566.770800	10
10	1432.823235	716.915256	1415.796686	708.401981	1414.812670	707.909973	E	1053.492124	527.249700	1036.465575	518.736426	1035.481559	518.244418	9
11	***1545.907299***	773.457288	1528.880750	764.944013	1527.896734	764.452005	L	***924.449531***	462.728404	907.422982	454.215129	906.438966	453.723121	8
12	1642.960063	821.983670	1625.933514	813.470395	1624.949498	812.978387	P	***811.365467***	406.186372	794.338918	397.673097	793.354902	397.181089	7
13	1699.981527	850.494401	1682.954978	841.981127	1681.970962	841.489119	G	***714.312703***	357.659990	697.286154	349.146715	696.302138	348.654707	6
14	1829.024120	915.015698	1811.997571	906.502423	1811.013555	906.010415	E	657.291239	329.149258	640.264690	320.635983	639.280674	320.143975	5
15	1992.087449	996.547362	1975.060900	988.034088	1974.076884	987.542080	Y	***528.248646***	264.627961	511.222097	256.114687	510.238081	255.622679	4
16	2079.119477	1040.063376	2062.092928	1031.550102	2061.108912	1031.058094	S	***365.185317***	183.096297	348.158768	174.583022	347.174752	174.091014	3
17	2210.159962	1105.583619	2193.133413	1097.070344	2192.149397	1096.578336	M	278.153289	139.580282	261.126740	131.067008			2
18							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.9	2355.258179	-0.003257	LLLQQVSLPELPGEYSMK
43.0	2355.258179	-0.003257	LLLQQVSLPELPGEYSMK

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

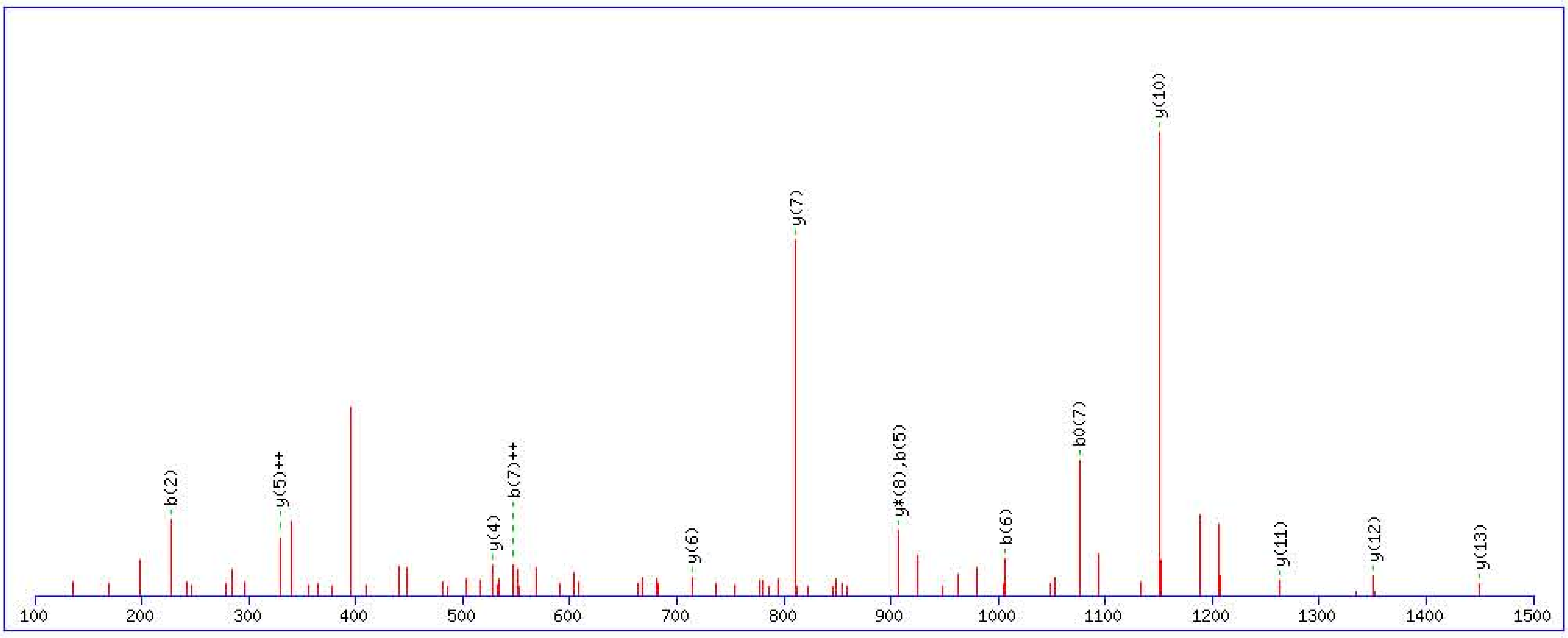
Mascot Search Results

Peptide View

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

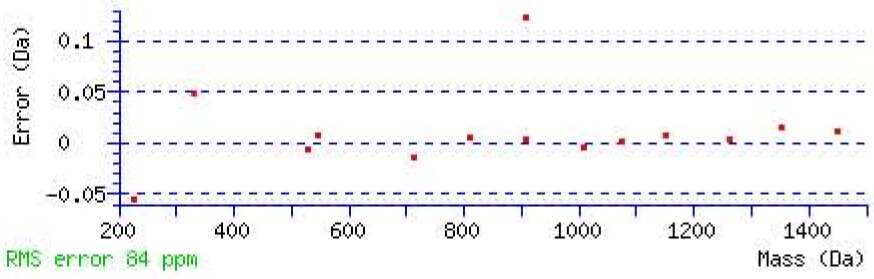
Match to Query 45904: 2355.265242 from(786.095690,3+) rtinseconds(2845) index(23998)
Title: Locus:1.1.1.3554.23 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

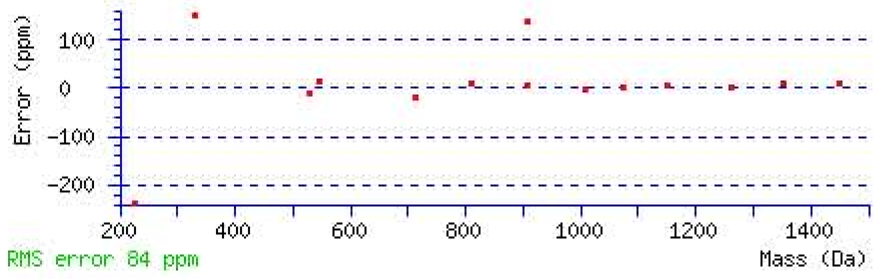
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2355.258179
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 58  Expect: 2.3e-005
Matches : 14/182 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	114.091340	57.549308					L							18
2	**227.175404**	114.091340					L	2243.181426	1122.094351	2226.154877	1113.581076	2225.170861	1113.089068	17
3	340.259468	170.633372					L	2130.097362	1065.552319	2113.070813	1057.039044	2112.086797	1056.547036	16
4	468.318046	234.662661	451.291497	226.149386			Q	2017.013298	1009.010287	1999.986749	1000.497013	1999.002733	1000.005005	15
5	**907.543372**	454.275324	890.516823	445.762049			Q	1888.954720	944.980998	1871.928171	936.467724	1870.944155	935.975715	14
6	**1006.611786**	503.809531	989.585237	495.296256			V	***1449.729394***	725.368335	1432.702845	716.855061	1431.718829	716.363053	13
7	1093.643814	**547.325545**	1076.617265	538.812271	1075.633249	538.320263	S	***1350.660980***	675.834128	1333.634431	667.320854	1332.650415	666.828846	12
8	1206.727878	603.867577	1189.701329	595.354303	1188.717313	594.862294	L	***1263.628952***	632.318114	1246.602403	623.804840	1245.618387	623.312832	11
9	1303.780642	652.393959	1286.754093	643.880685	1285.770077	643.388676	P	***1150.544888***	575.776082	1133.518339	567.262808	1132.534323	566.770800	10
10	1432.823235	716.915256	1415.796686	708.401981	1414.812670	707.909973	E	1053.492124	527.249700	1036.465575	518.736426	1035.481559	518.244418	9
11	1545.907299	773.457288	1528.880750	764.944013	1527.896734	764.452005	L	924.449531	462.728404	907.422982	454.215129	906.438966	453.723121	8
12	1642.960063	821.983670	1625.933514	813.470395	1624.949498	812.978387	P	***811.365467***	406.186372	794.338918	397.673097	793.354902	397.181089	7
13	1699.981527	850.494401	1682.954978	841.981127	1681.970962	841.489119	G	***714.312703***	357.659990	697.286154	349.146715	696.302138	348.654707	6
14	1829.024120	915.015698	1811.997571	906.502423	1811.013555	906.010415	E	657.291239	329.149258	640.264690	320.635983	639.280674	320.143975	5
15	1992.087449	996.547362	1975.060900	988.034088	1974.076884	987.542080	Y	***528.248646***	264.627961	511.222097	256.114687	510.238081	255.622679	4
16	2079.119477	1040.063376	2062.092928	1031.550102	2061.108912	1031.058094	S	365.185317	183.096297	348.158768	174.583022	347.174752	174.091014	3
17	2210.159962	1105.583619	2193.133413	1097.070344	2192.149397	1096.578336	M	278.153289	139.580282	261.126740	131.067008			2
18							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.1	2355.258179	0.007063	LLLQQVSLPELPGEYSMK
58.1	2355.258179	0.007063	LLLQQVSLPELPGEYSMK
8.1	2355.288498	-0.023256	LIQQERALLNFTEWKR
6.3	2355.288498	-0.023256	LIQQERALLNFTEWKR
1.0	2355.273926	-0.008684	LGLYTFVNLANFVKSWTNLR
0.4	2355.299271	-0.034029	KLLQMQPAQHGEIIK
0.3	2355.248795	0.016447	FYEQVVQAIQRHIHFDVVK

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

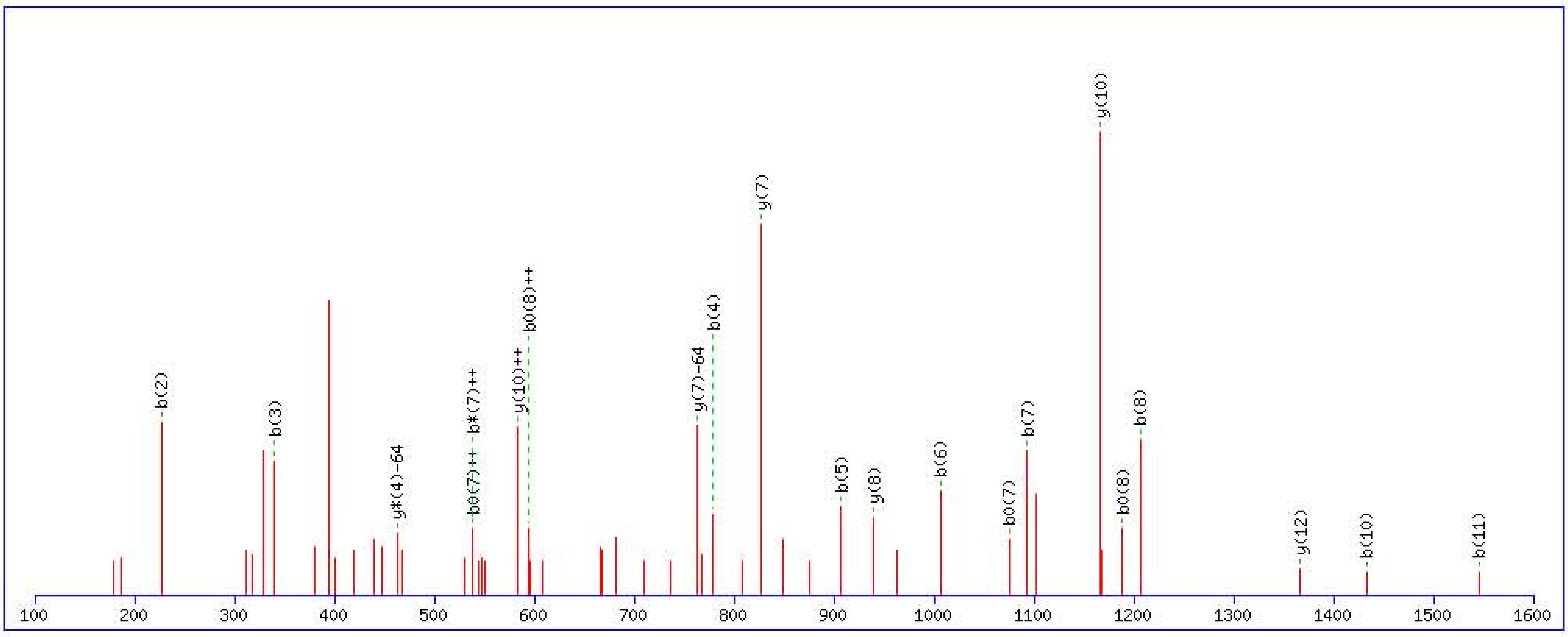
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

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

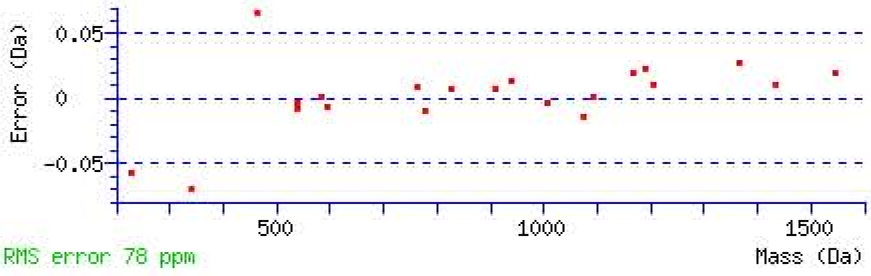
Match to Query 46029: 2371.261152 from(791.427660,3+) rtinseconds(2769) index(23560)
Title: Locus:1.1.1.3528.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

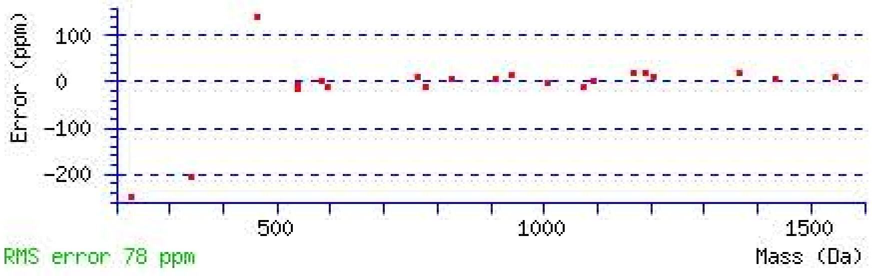
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2371.253098
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4     : Biotin:Thermo-21345 (Q)
M17    : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 65  Expect: 6.8e-006
Matches : 21/282 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							18
2	***227.175404***	114.091340					L	2259.176341	1130.091808	2242.149792	1121.578534	2241.165776	1121.086526	17
3	***340.259468***	170.633372					L	2146.092277	1073.549776	2129.065728	1065.036502	2128.081712	1064.544494	16
4	***779.484794***	390.246035	762.458245	381.732760			Q	2033.008213	1017.007745	2015.981664	1008.494470	2014.997648	1008.002462	15
5	***907.543372***	454.275324	890.516823	445.762049			Q	1593.782887	797.395082	1576.756338	788.881807	1575.772322	788.389799	14
6	***1006.611786***	503.809531	989.585237	495.296256			V	1465.724309	733.365793	1448.697760	724.852518	1447.713744	724.360510	13
7	***1093.643814***	547.325545	1076.617265	538.812271	1075.633249	538.320263	S	**1366.655895**	683.831586	1349.629346	675.318311	1348.645330	674.826303	12
8	***1206.727878***	603.867577	1189.701329	595.354303	1188.717313	594.862294	L	1279.623867	640.315572	1262.597318	631.802297	1261.613302	631.310289	11
9	1303.780642	652.393959	1286.754093	643.880685	1285.770077	643.388676	P	**1166.539803**	583.773540	1149.513254	575.260265	1148.529238	574.768257	10
10	***1432.823235***	716.915256	1415.796686	708.401981	1414.812670	707.909973	E	1069.487039	535.247158	1052.460490	526.733883	1051.476474	526.241875	9
11	***1545.907299***	773.457288	1528.880750	764.944013	1527.896734	764.452005	L	**940.444446**	470.725861	923.417897	462.212587	922.433881	461.720579	8
12	1642.960063	821.983670	1625.933514	813.470395	1624.949498	812.978387	P	**827.360382**	414.183829	810.333833	405.670555	809.349817	405.178547	7
13	1699.981527	850.494401	1682.954978	841.981127	1681.970962	841.489119	G	730.307618	365.657447	713.281069	357.144173	712.297053	356.652165	6
14	1829.024120	915.015698	1811.997571	906.502423	1811.013555	906.010415	E	673.286154	337.146715	656.259605	328.633441	655.275589	328.141433	5
15	1992.087449	996.547362	1975.060900	988.034088	1974.076884	987.542080	Y	544.243561	272.625419	527.217012	264.112144	526.232996	263.620136	4
16	2079.119477	1040.063376	2062.092928	1031.550102	2061.108912	1031.058094	S	381.180232	191.093754	364.153683	182.580480	363.169667	182.088472	3
17	2226.154877	1113.581076	2209.128328	1105.067802	2208.144312	1104.575794	M	294.148204	147.577740	277.121655	139.064466			2
18							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.0	2371.253098	0.008054	LLLQQVSLPELPGEYSMK
52.3	2371.253098	0.008054	LLLQQVSLPELPGEYSMK

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

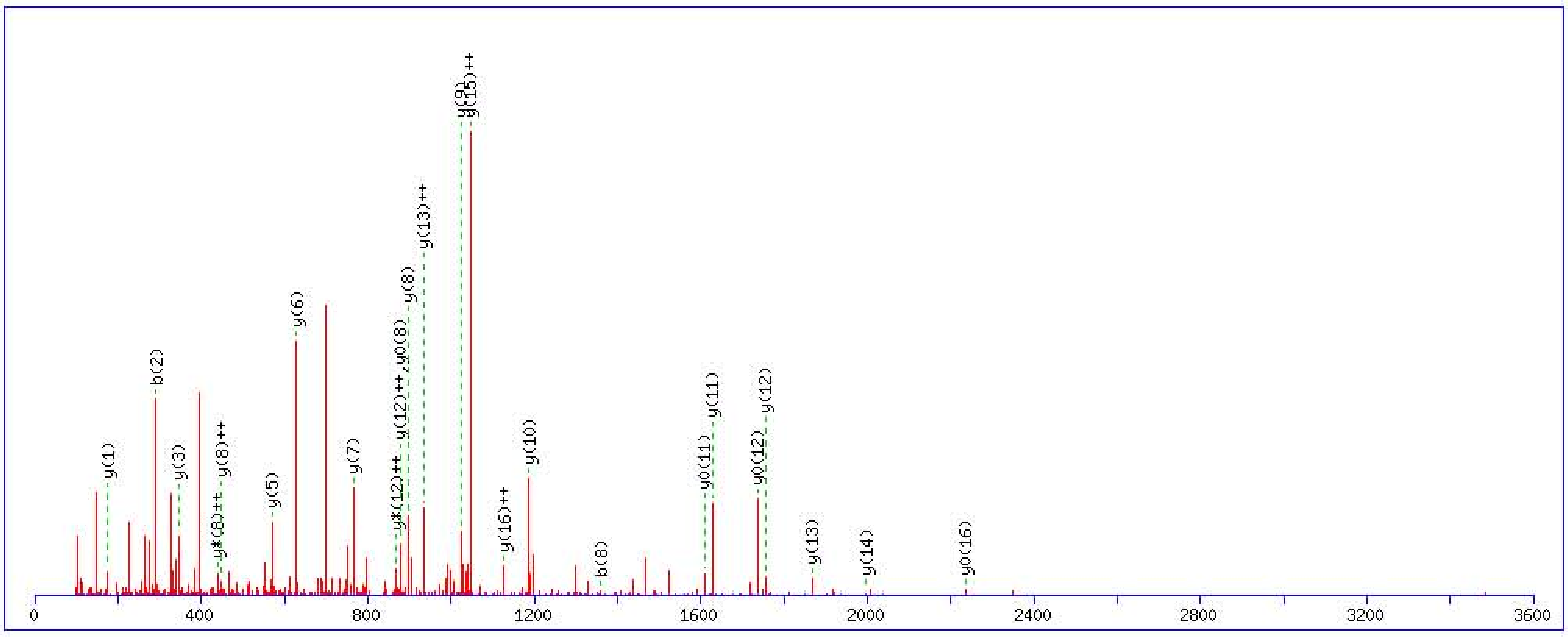
Mascot Search Results

Peptide View

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

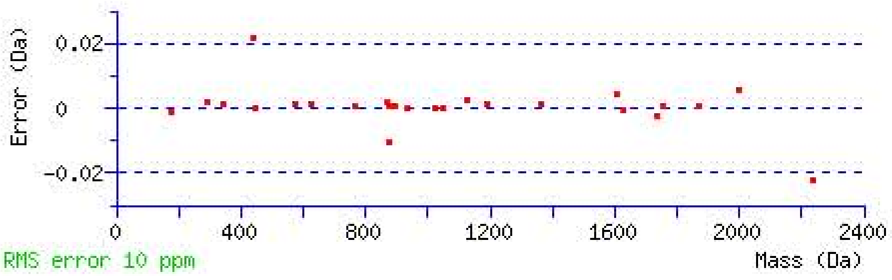
Match to Query 46163: 2384.083392 from(795.701740,3+) rtinseconds(2056) index(32200)
Title: Locus:1.1.1.3379.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

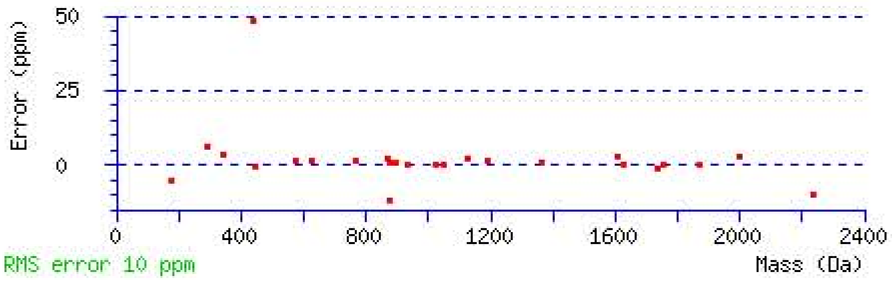
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 52 **Expect:** 5.7e-005
Matches : 25/164 fragment ions using 61 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
52.2	2384.089767	-0.006375	MCPQLQQYEMHGPEGLR
42.8	2384.089767	-0.006375	MCPQLQQYEMHGPEGLR
23.0	2384.089767	-0.006375	MCPQLQQYEMHGPEGLR

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

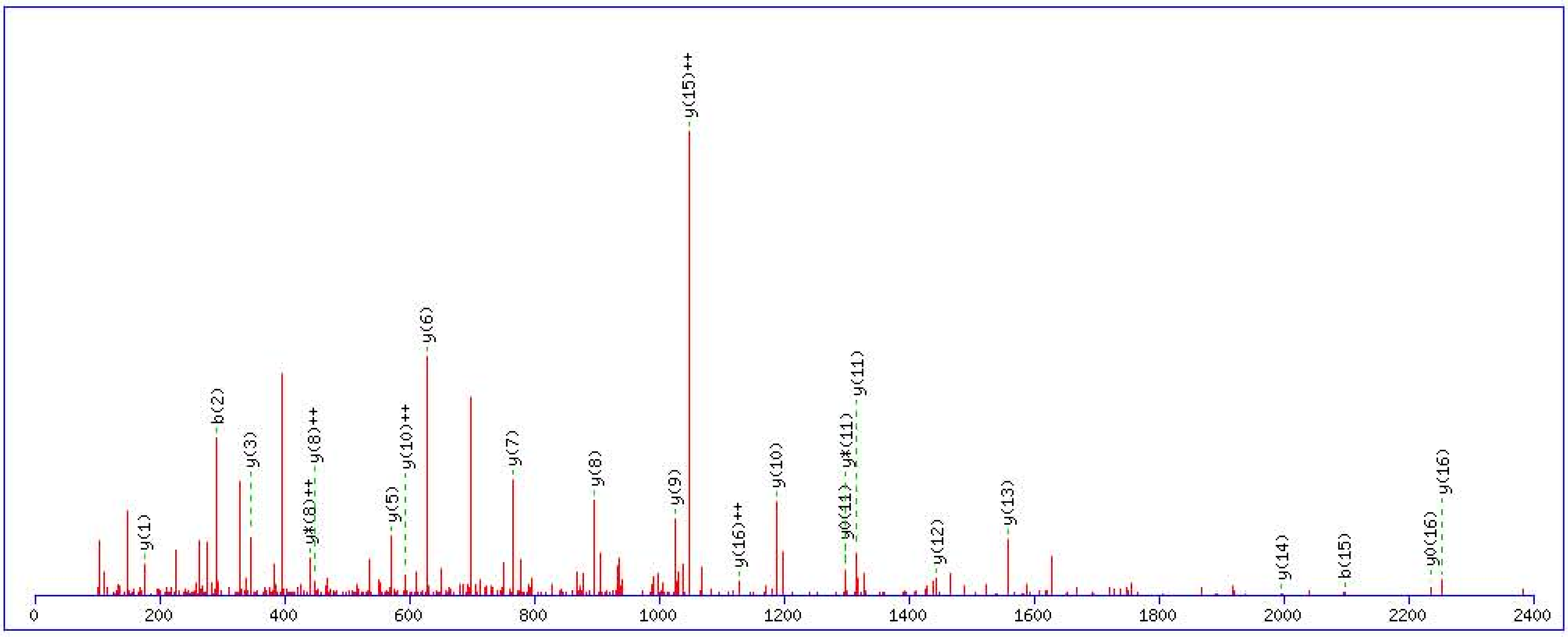
Mascot Search Results

Peptide View

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

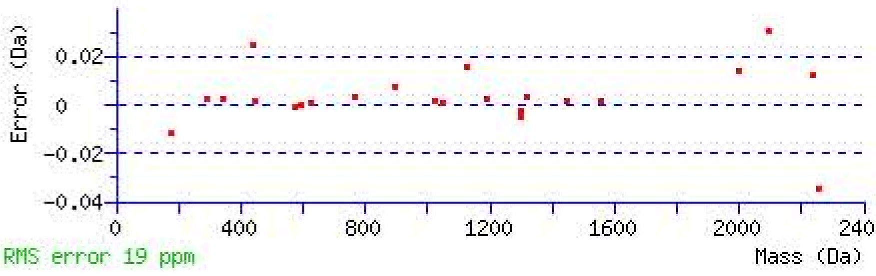
Match to Query 46165: 2384.084832 from(795.702220,3+) rtinseconds(2076) index(19457)
Title: Locus:1.1.1.3288.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

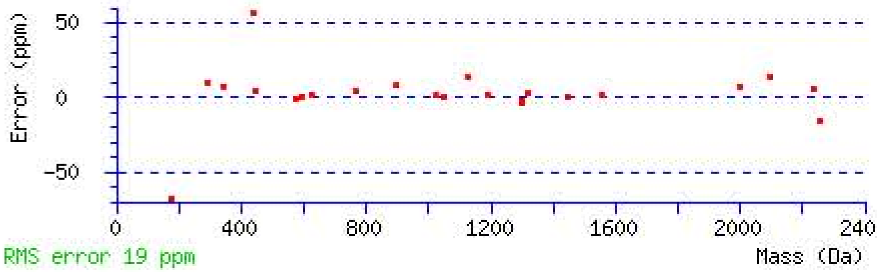
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2384.089767
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 56 **Expect:** 2.4e-005
Matches : 23/164 fragment ions using 62 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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	828.356500	414.681888	811.329951	406.168614			Q	***1996.973166***	998.990221	1979.946617	990.476947	1978.962601	989.984939	14
5	941.440564	471.223920	924.414015	462.710646			L	***1557.747840***	779.377558	1540.721291	770.864284	1539.737275	770.372276	13
6	1069.499142	535.253209	1052.472593	526.739935			Q	***1444.663776***	722.835526	1427.637227	714.322252	1426.653211	713.830244	12
7	1197.557720	599.282498	1180.531171	590.769224			Q	***1316.605198***	658.806237	1299.578649	650.292963	1298.594633	649.800955	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
56.1	2384.089767	-0.004935	MCPQLQQYEMHGPEGLR
49.4	2384.089767	-0.004935	MCPQLQQYEMHGPEGLR
47.9	2384.089767	-0.004935	MCPQLQQYEMHGPEGLR

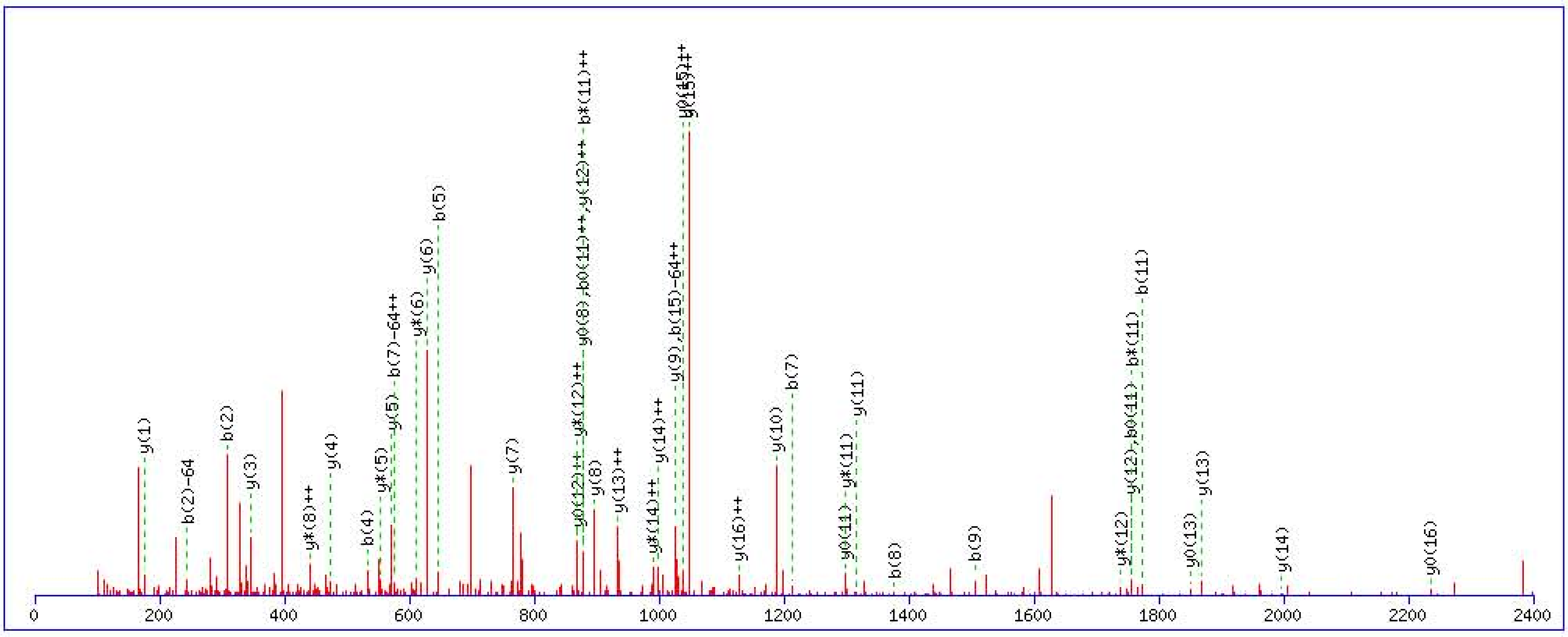
Mascot Search Results

Peptide View

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

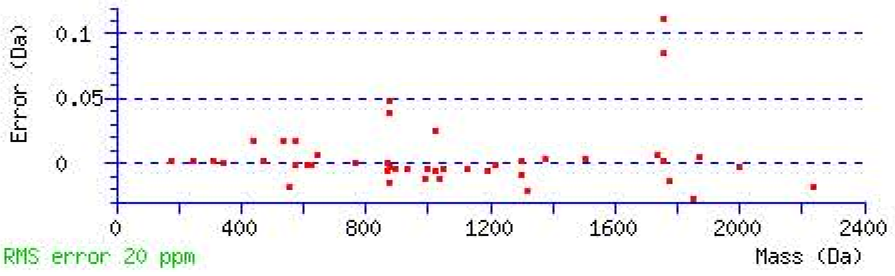
Match to Query 46425: 2400.075432 from(801.032420,3+) rtinseconds(1983) index(18992)
Title: Locus:1.1.1.3256.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

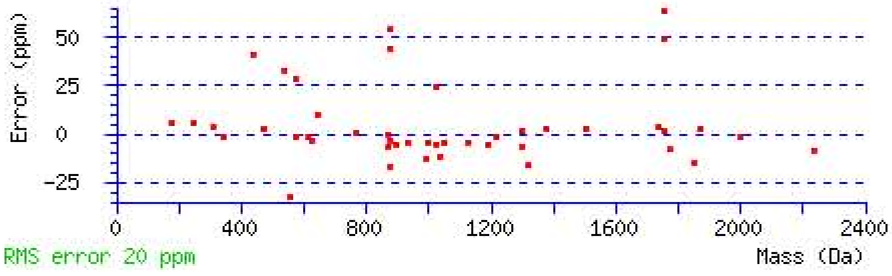
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 49  Expect: 8.6e-005
Matches : 45/238 fragment ions using 106 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
49.4	2400.084686	-0.009254	MCPQLQQYEMHGPEGLR
48.7	2400.084686	-0.009254	MCPQLQQYEMHGPEGLR
30.3	2400.084686	-0.009254	MCPQLQQYEMHGPEGLR

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

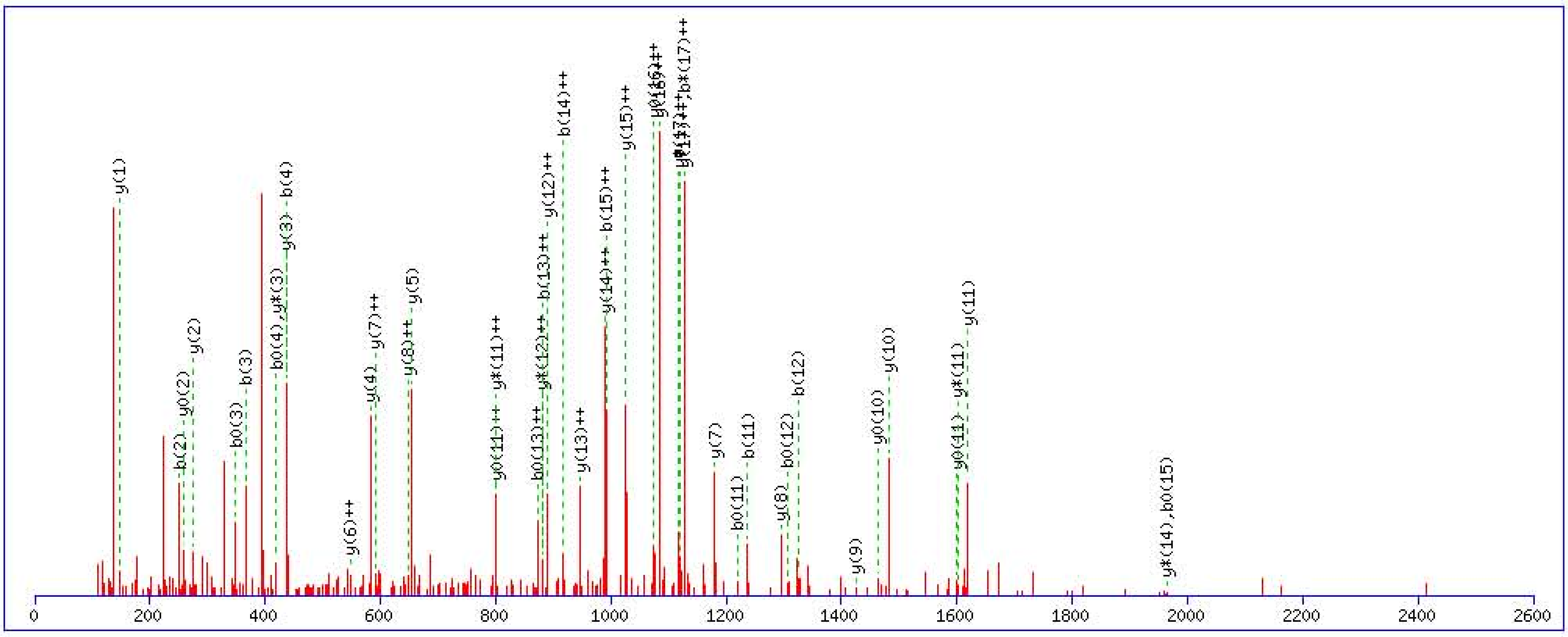
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

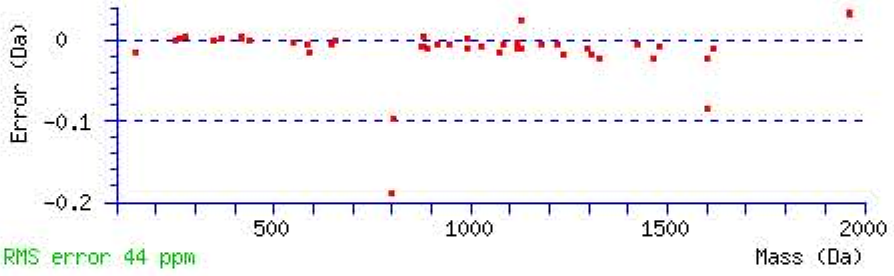
Match to Query 46696: 2415.923292 from(806.315040,3+) rtinseconds(1583) index(16396)
Title: Locus:1.1.1.3117.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

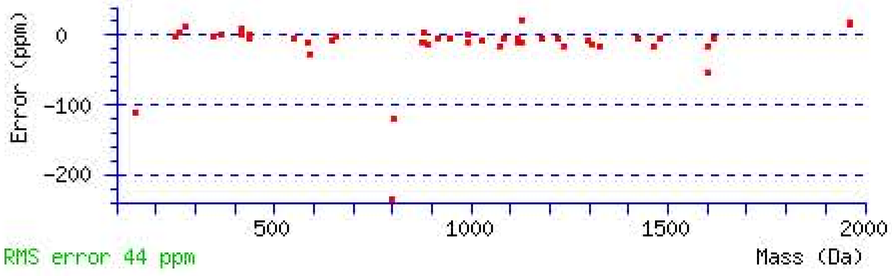
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2415.940598
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 1.3e-005
Matches : 46/176 fragment ions using 110 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	**251.102633**	126.054954			233.092068	117.049672	S	2253.884545	1127.445910	2236.857996	1118.932636	2235.873980	1118.440628	17
3	**366.129576**	183.568426			348.119011	174.563144	D	2166.852517	1083.929896	2149.825968	1075.416622	2148.841952	1074.924614	16
4	**437.166690**	219.086983			419.156125	210.081700	A	2051.825574	1026.416425	2034.799025	1017.903150	2033.815009	1017.411142	15
5	524.198718	262.602997			506.188153	253.597715	S	1980.788460	990.897868	1963.761911	982.384594	1962.777895	981.892586	14
6	639.225661	320.116469			621.215096	311.111186	D	1893.756432	947.381854	1876.729883	938.868580	1875.745867	938.376572	13
7	799.256310	400.131793			781.245745	391.126510	C	1778.729489	889.868383	1761.702940	881.355108	1760.718924	880.863100	12
8	936.315222	468.661249			918.304657	459.655966	H	***1618.698840***	809.853058	1601.672291	801.339784	1600.688275	800.847776	11
9	993.336686	497.171981			975.326121	488.166699	G	***1481.639928***	741.323602	1464.613379	732.810328	1463.629363	732.318320	10
10	1122.379279	561.693278			1104.368714	552.687995	E	***1424.618464***	712.812870	1407.591915	704.299596	1406.607899	703.807588	9
11	**1237.406222**	619.206749			1219.395657	610.201467	D	***1295.575871***	648.291574	1278.549322	639.778299	1277.565306	639.286291	8
12	**1324.438250**	662.722763			1306.427685	653.717481	S	***1180.548928***	590.778102	1163.522379	582.264828	1162.538363	581.772820	7
13	1763.663576	**882.335426**	1746.637027	873.822152	1745.653011	873.330144	Q	1093.516900	547.262088	1076.490351	538.748814	1075.506335	538.256806	6
14	1834.700690	**917.853983**	1817.674141	909.340709	1816.690125	908.848701	A	***654.291574***	327.649425	637.265025	319.136151	636.281009	318.644143	5
15	1981.769104	**991.388190**	1964.742555	982.874916	1963.758539	982.382908	F	***583.254460***	292.130868	566.227911	283.617594	565.243895	283.125586	4
16	2141.799753	1071.403514	2124.773204	1062.890240	2123.789188	1062.398232	C	***436.186046***	218.596661	419.159497	210.083386	418.175481	209.591378	3
17	2270.842346	1135.924811	2253.815797	1127.411536	2252.831781	1126.919528	E	***276.155397***	138.581337	259.128848	130.068062	258.144832	129.576054	2
18							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of YSDASDCHGEDSQAFCEK
(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	2415.940598	-0.017306	YSDASDCHGEDSQAFCEK

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

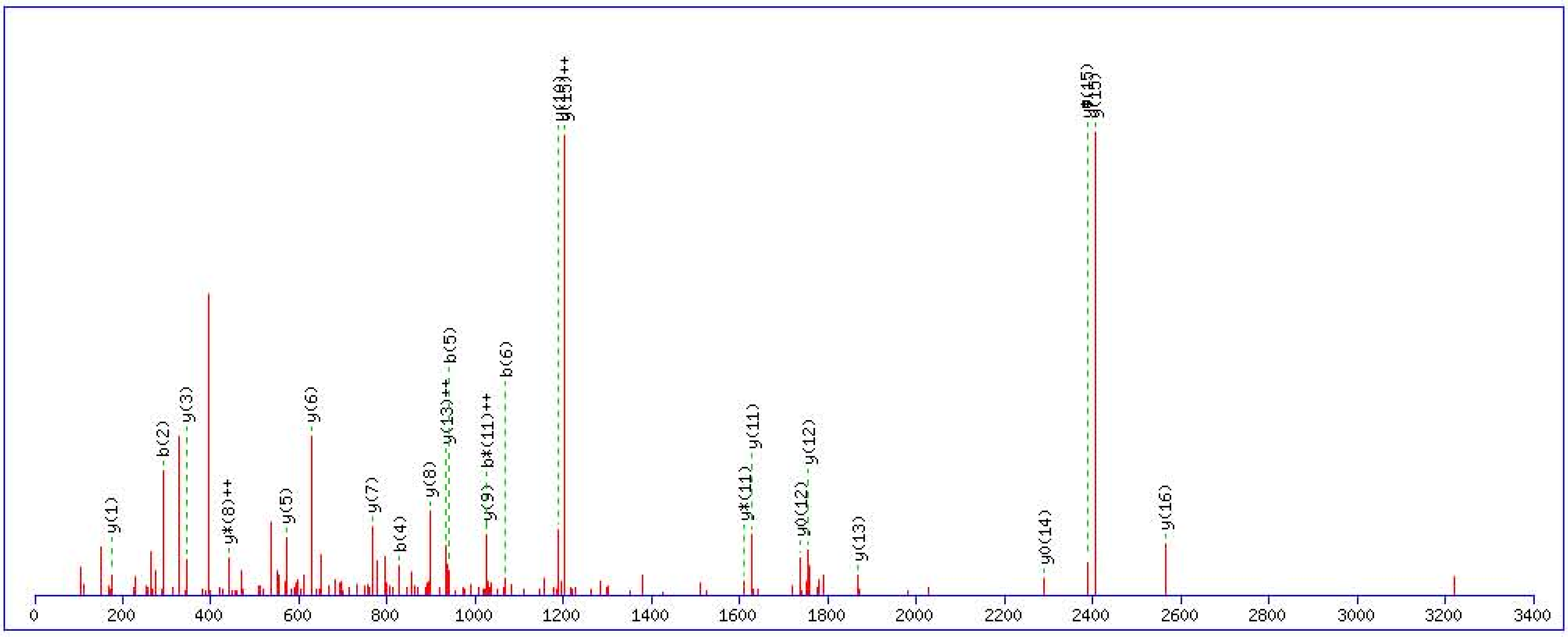
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

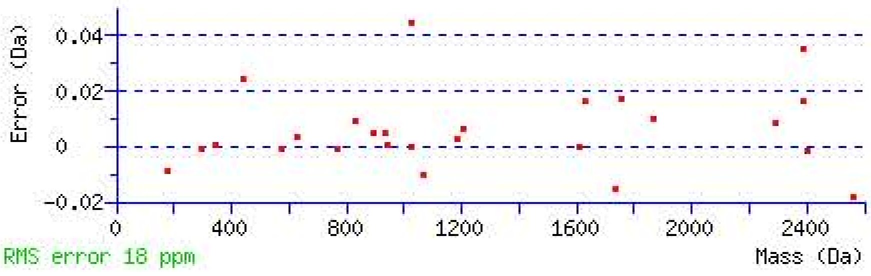
Match to Query 50318: 2695.252842 from(899.424890,3+) rtinseconds(2228) index(33221)
Title: Locus:1.1.1.3439.25 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

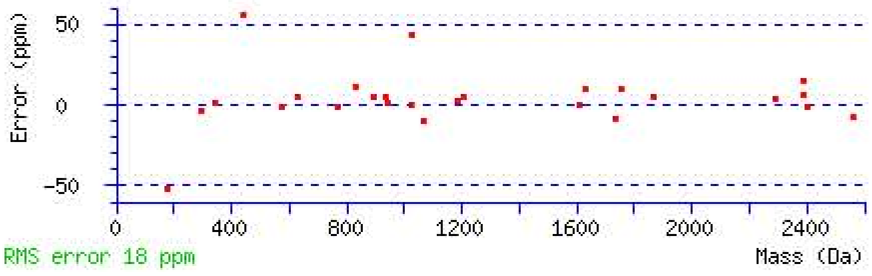
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2695.256516
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 1.3e-005
Matches : 26/164 fragment ions using 59 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	***2565.223327***	1283.115301	2548.196778	1274.602027	2547.212762	1274.110019	16
3	389.131174	195.069225					P	***2405.192678***	1203.099977	2388.166129	1194.586702	2387.182113	1194.094694	15
4	**828.356500**	414.681888	811.329951	406.168614			Q	2308.139914	1154.573595	2291.113365	1146.060320	2290.129349	1145.568312	14
5	**941.440564**	471.223920	924.414015	462.710646			L	***1868.914588***	934.960932	1851.888039	926.447658	1850.904023	925.955650	13
6	**1069.499142**	535.253209	1052.472593	526.739935			Q	***1755.830524***	878.418900	1738.803975	869.905626	1737.819959	869.413618	12
7	1508.724468	754.865872	1491.697919	746.352598			Q	***1627.771946***	814.389611	1610.745397	805.876337	1609.761381	805.384329	11
8	1671.787797	836.397537	1654.761248	827.884262			Y	***1188.546620***	594.776948	1171.520071	586.263674	1170.536055	585.771666	10
9	1800.830390	900.918833	1783.803841	892.405559	1782.819825	891.913551	E	***1025.483291***	513.245284	1008.456742	504.732009	1007.472726	504.240001	9
10	1931.870875	966.439076	1914.844326	957.925801	1913.860310	957.433793	M	***896.440698***	448.723987	879.414149	440.210713	878.430133	439.718705	8
11	2068.929787	1034.968531	2051.903238	1026.455257	2050.919222	1025.963249	H	***765.400213***	383.203745	748.373664	374.690470	747.389648	374.198462	7
12	2125.951251	1063.479263	2108.924702	1054.965989	2107.940686	1054.473981	G	***628.341301***	314.674289	611.314752	306.161014	610.330736	305.669006	6
13	2223.004015	1112.005645	2205.977466	1103.492371	2204.993450	1103.000363	P	***571.319837***	286.163557	554.293288	277.650282	553.309272	277.158274	5
14	2352.046608	1176.526942	2335.020059	1168.013667	2334.036043	1167.521659	E	474.267073	237.637175	457.240524	229.123900	456.256508	228.631892	4
15	2409.068072	1205.037674	2392.041523	1196.524399	2391.057507	1196.032391	G	***345.224480***	173.115878	328.197931	164.602603			3
16	2522.152136	1261.579706	2505.125587	1253.066431	2504.141571	1252.574424	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
60.5	2695.256516	-0.003674	MCPQLQQYEMHGPEGLR
50.8	2695.256516	-0.003674	MCPQLQQYEMHGPEGLR
34.9	2695.256516	-0.003674	MCPQLQQYEMHGPEGLR

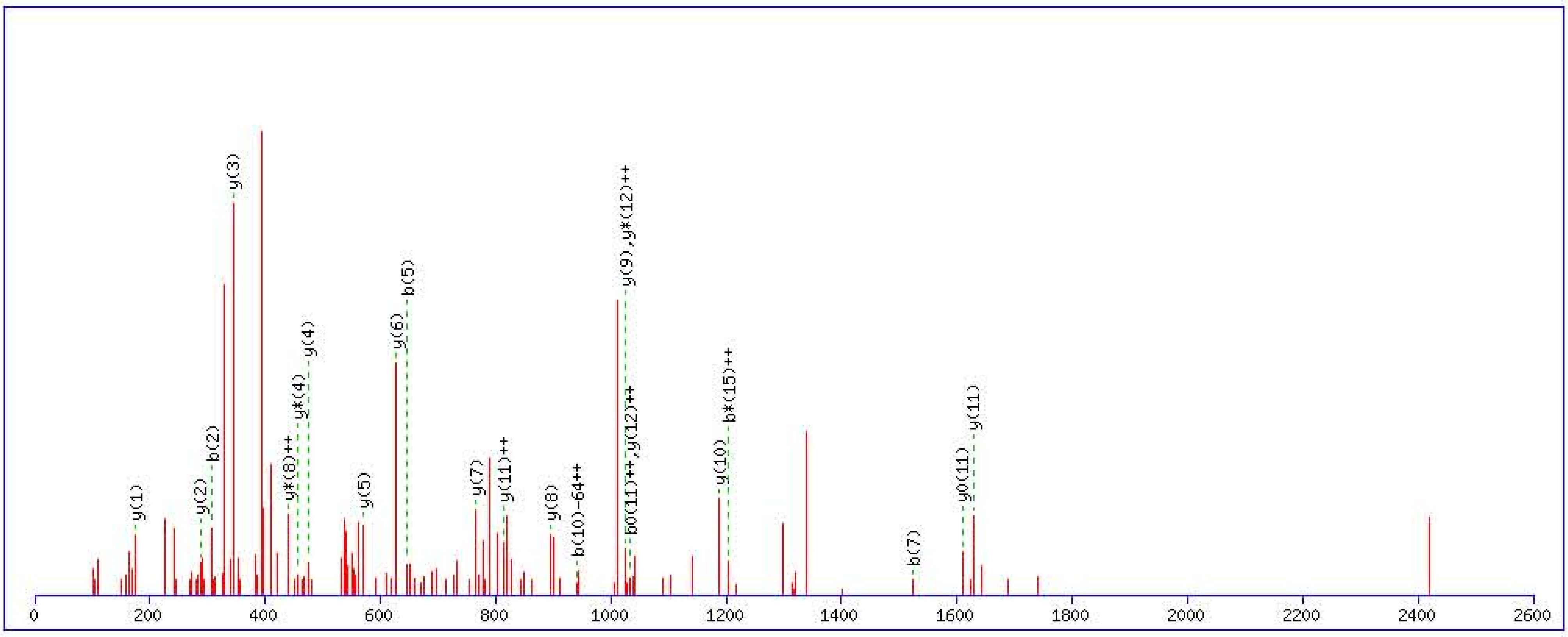
Mascot Search Results

Peptide View

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

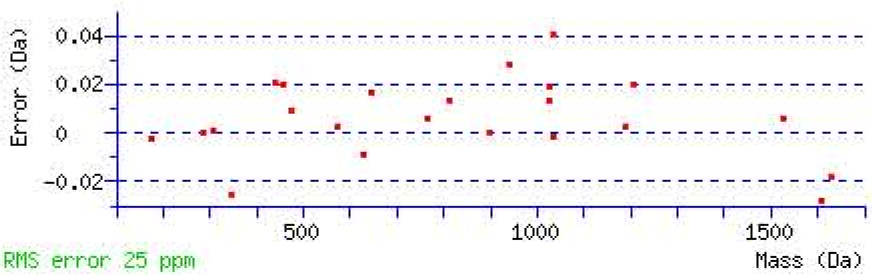
Match to Query 50481: 2711.245496 from(678.818650,4+) rtinseconds(2143) index(32702)
Title: Locus:1.1.1.3410.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

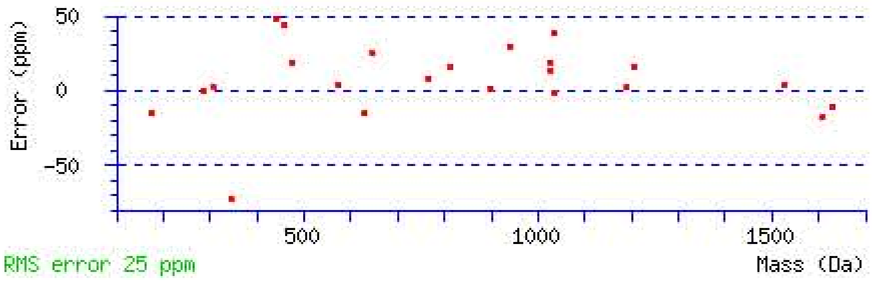
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2711.251434
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)
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.0095
Matches : 23/238 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	148.042676	74.524976					M							17
2	**308.073325**	154.540301					C	2565.223327	1283.115302	2548.196778	1274.602027	2547.212762	1274.110019	16
3	405.126089	203.066683					P	2405.192678	1203.099977	2388.166129	1194.586702	2387.182113	1194.094694	15
4	533.184667	267.095972	516.158118	258.582697			Q	2308.139914	1154.573595	2291.113365	1146.060320	2290.129349	1145.568312	14
5	**646.268731**	323.638004	629.242182	315.124729			L	2180.081336	1090.544306	2163.054787	1082.031031	2162.070771	1081.539023	13
6	1085.494057	543.250667	1068.467508	534.737392			Q	2066.997272	1034.002274	2049.970723	1025.488999	2048.986707	1024.996991	12
7	**1524.719383**	762.863330	1507.692834	754.350055			Q	***1627.771946***	814.389611	1610.745397	805.876337	1609.761381	805.384329	11
8	1687.782712	844.394994	1670.756163	835.881720			Y	***1188.546620***	594.776948	1171.520071	586.263674	1170.536055	585.771666	10
9	1816.825305	908.916291	1799.798756	900.403016	1798.814740	899.911008	E	***1025.483291***	513.245284	1008.456742	504.732009	1007.472726	504.240001	9
10	1947.865790	974.436533	1930.839241	965.923259	1929.855225	965.431251	M	***896.440698***	448.723987	879.414149	440.210713	878.430133	439.718705	8
11	2084.924702	1042.965989	2067.898153	1034.452715	2066.914137	1033.960707	H	***765.400213***	383.203745	748.373664	374.690470	747.389648	374.198462	7
12	2141.946166	1071.476721	2124.919617	1062.963446	2123.935601	1062.471439	G	***628.341301***	314.674289	611.314752	306.161014	610.330736	305.669006	6
13	2238.998930	1120.003103	2221.972381	1111.489828	2220.988365	1110.997821	P	***571.319837***	286.163557	554.293288	277.650282	553.309272	277.158274	5
14	2368.041523	1184.524400	2351.014974	1176.011125	2350.030958	1175.519117	E	***474.267073***	237.637175	457.240524	229.123900	456.256508	228.631892	4
15	2425.062987	1213.035132	2408.036438	1204.521857	2407.052422	1204.029849	G	***345.224480***	173.115878	328.197931	164.602603			3
16	2538.147051	1269.577164	2521.120502	1261.063889	2520.136486	1260.571881	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
31.6	2711.251434	-0.005938	MCPQLQQYEMHGPEGLR
31.4	2711.251434	-0.005938	MCPQLQQYEMHGPEGLR
30.4	2711.251434	-0.005938	MCPQLQQYEMHGPEGLR
27.3	2711.251434	-0.005938	MCPQLQQYEMHGPEGLR
20.7	2711.251434	-0.005938	MCPQLQQYEMHGPEGLR
17.8	2711.251434	-0.005938	MCPQLQQYEMHGPEGLR

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

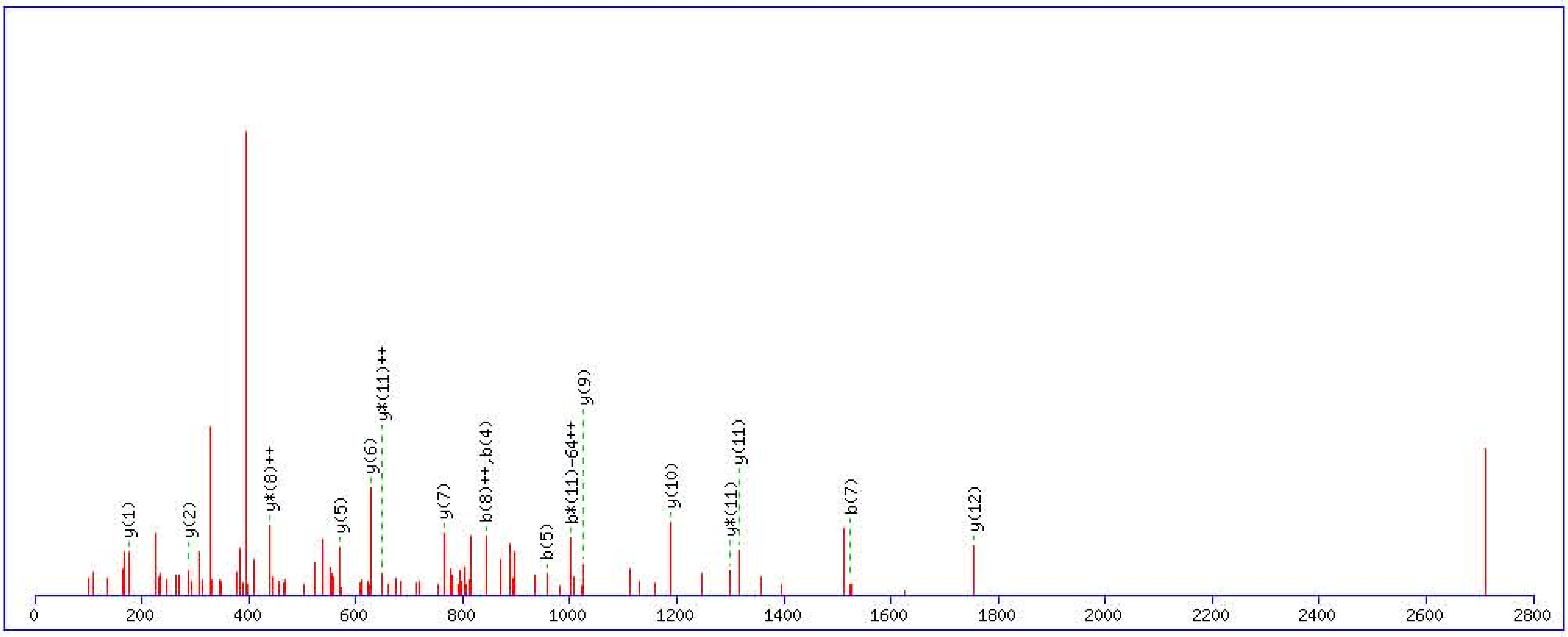
Mascot Search Results

Peptide View

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

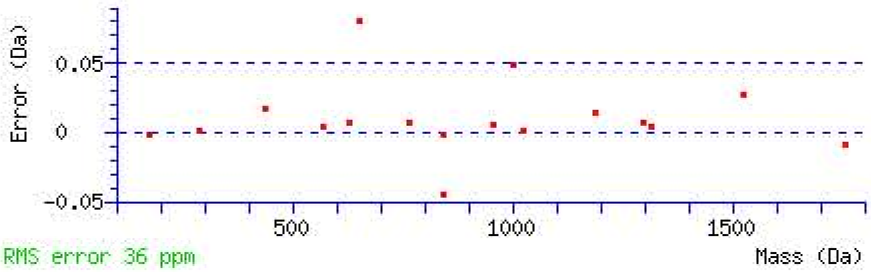
Match to Query 50512: 2711.273136 from(678.825560,4+) rtinseconds(2209) index(6031)
Title: Locus:1.1.1.3289.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

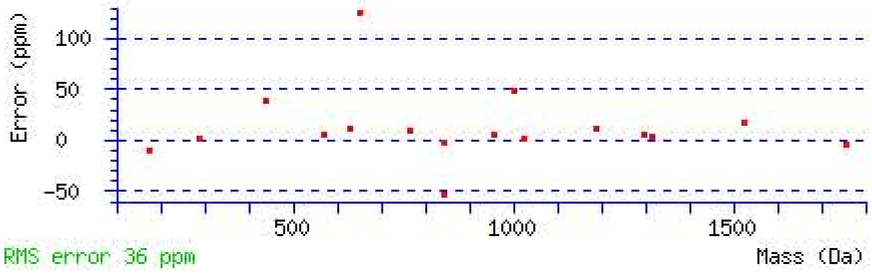
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2711.251434
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
Q4      : Biotin:Thermo-21345 (Q)
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.00017
Matches : 17/238 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	148.042676	74.524976					M							17
2	308.073325	154.540301					C	2565.223327	1283.115302	2548.196778	1274.602027	2547.212762	1274.110019	16
3	405.126089	203.066683					P	2405.192678	1203.099977	2388.166129	1194.586702	2387.182113	1194.094694	15
4	**844.351415**	422.679346	827.324866	414.166071			Q	2308.139914	1154.573595	2291.113365	1146.060320	2290.129349	1145.568312	14
5	**957.435479**	479.221378	940.408930	470.708103			L	1868.914588	934.960932	1851.888039	926.447658	1850.904023	925.955650	13
6	1396.660805	698.834041	1379.634256	690.320766			Q	***1755.830524***	878.418900	1738.803975	869.905626	1737.819959	869.413618	12
7	**1524.719383**	762.863330	1507.692834	754.350055			Q	***1316.605198***	658.806237	1299.578649	650.292963	1298.594633	649.800955	11
8	1687.782712	844.394994	1670.756163	835.881720			Y	***1188.546620***	594.776948	1171.520071	586.263674	1170.536055	585.771666	10
9	1816.825305	908.916291	1799.798756	900.403016	1798.814740	899.911008	E	***1025.483291***	513.245284	1008.456742	504.732009	1007.472726	504.240001	9
10	1947.865790	974.436533	1930.839241	965.923259	1929.855225	965.431251	M	896.440698	448.723987	879.414149	440.210713	878.430133	439.718705	8
11	2084.924702	1042.965989	2067.898153	1034.452715	2066.914137	1033.960707	H	***765.400213***	383.203745	748.373664	374.690470	747.389648	374.198462	7
12	2141.946166	1071.476721	2124.919617	1062.963446	2123.935601	1062.471439	G	***628.341301***	314.674289	611.314752	306.161014	610.330736	305.669006	6
13	2238.998930	1120.003103	2221.972381	1111.489828	2220.988365	1110.997821	P	***571.319837***	286.163557	554.293288	277.650282	553.309272	277.158274	5
14	2368.041523	1184.524400	2351.014974	1176.011125	2350.030958	1175.519117	E	474.267073	237.637175	457.240524	229.123900	456.256508	228.631892	4
15	2425.062987	1213.035132	2408.036438	1204.521857	2407.052422	1204.029849	G	345.224480	173.115878	328.197931	164.602603			3
16	2538.147051	1269.577164	2521.120502	1261.063889	2520.136486	1260.571881	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
40.4	2711.251434	0.021702	MCPQLQQYEMHGPEGLR
27.4	2711.251434	0.021702	MCPQLQQYEMHGPEGLR
15.2	2711.251434	0.021702	MCPQLQQYEMHGPEGLR
0.1	2711.300659	-0.027523	GEDQSEQEKQERLETQR

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

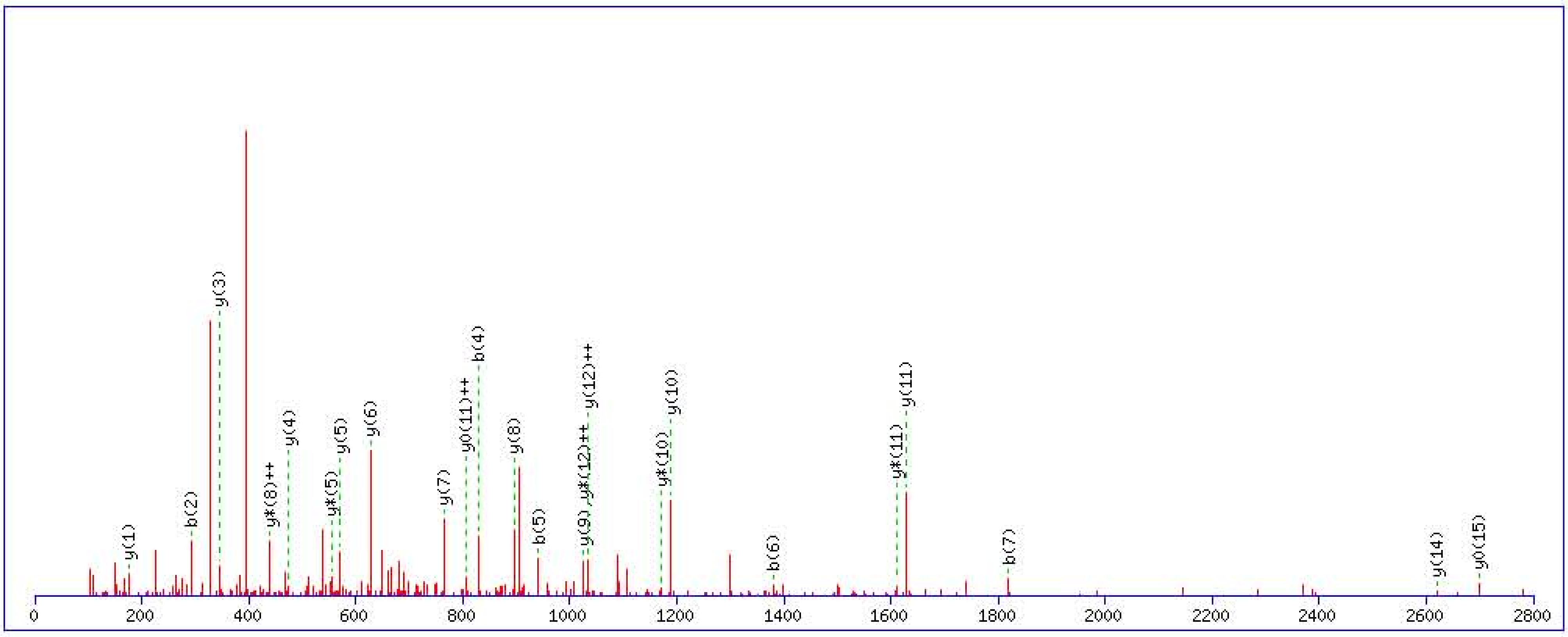
Mascot Search Results

Peptide View

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

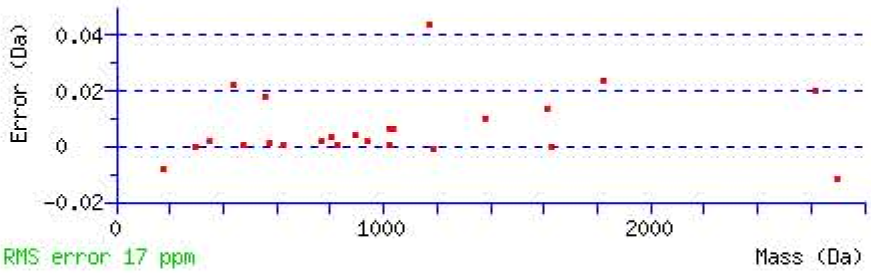
Match to Query 54074: 3006.423816 from(752.613230,4+) rtinseconds(2363) index(33885)
Title: Locus:1.1.1.3486.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

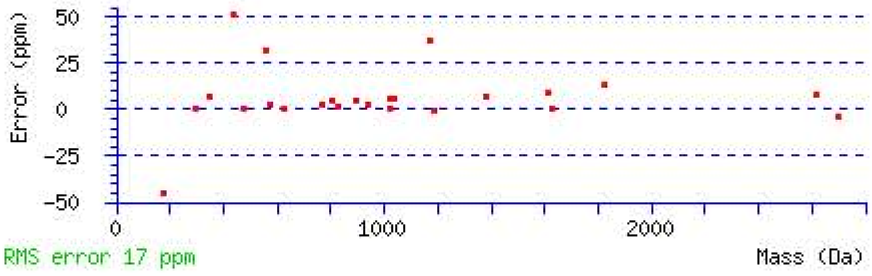
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3006.423264
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Q6 : Biotin:Thermo-21345 (Q)
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 30 **Expect:** 0.02
Matches : 24/164 fragment ions using 66 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	2876.390075	1438.698675	2859.363526	1430.185401	2858.379510	1429.693393	16
3	389.131174	195.069225					P	2716.359426	1358.683351	2699.332877	1350.170076	2698.348861	1349.678068	15
4	**828.356500**	414.681888	811.329951	406.168614			Q	***2619.306662***	1310.156969	2602.280113	1301.643694	2601.296097	1301.151686	14
5	**941.440564**	471.223920	924.414015	462.710646			L	2180.081336	1090.544306	2163.054787	1082.031031	2162.070771	1081.539023	13
6	**1380.665890**	690.836583	1363.639341	682.323309			Q	2066.997272	1034.002274	2049.970723	1025.488999	2048.986707	1024.996991	12
7	**1819.891216**	910.449246	1802.864667	901.935972			Q	***1627.771946***	814.389611	1610.745397	805.876337	1609.761381	805.384329	11
8	1982.954545	991.980911	1965.927996	983.467636			Y	***1188.546620***	594.776948	1171.520071	586.263674	1170.536055	585.771666	10
9	2111.997138	1056.502207	2094.970589	1047.988932	2093.986573	1047.496925	E	***1025.483291***	513.245284	1008.456742	504.732009	1007.472726	504.240001	9
10	2243.037623	1122.022450	2226.011074	1113.509175	2225.027058	1113.017167	M	***896.440698***	448.723987	879.414149	440.210713	878.430133	439.718705	8
11	2380.096535	1190.551906	2363.069986	1182.038631	2362.085970	1181.546623	H	***765.400213***	383.203745	748.373664	374.690470	747.389648	374.198462	7
12	2437.117999	1219.062637	2420.091450	1210.549363	2419.107434	1210.057355	G	***628.341301***	314.674289	611.314752	306.161014	610.330736	305.669006	6
13	2534.170763	1267.589019	2517.144214	1259.075745	2516.160198	1258.583737	P	***571.319837***	286.163557	554.293288	277.650282	553.309272	277.158274	5
14	2663.213356	1332.110316	2646.186807	1323.597041	2645.202791	1323.105034	E	***474.267073***	237.637175	457.240524	229.123900	456.256508	228.631892	4
15	2720.234820	1360.621048	2703.208271	1352.107773	2702.224255	1351.615766	G	***345.224480***	173.115878	328.197931	164.602603			3
16	2833.318884	1417.163080	2816.292335	1408.649806	2815.308319	1408.157798	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
30.2	3006.423264	0.000552	MCPQLQQYEMHGPEGLR

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

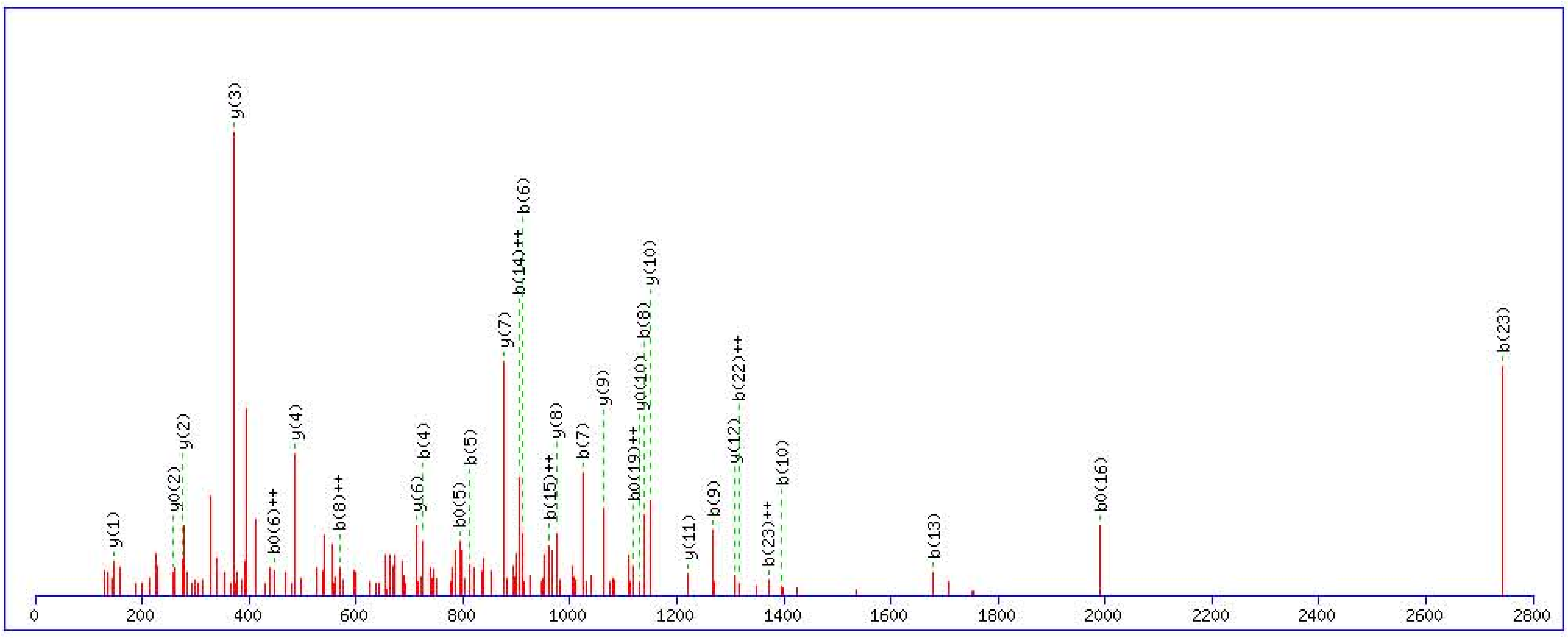
Mascot Search Results

Peptide View

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

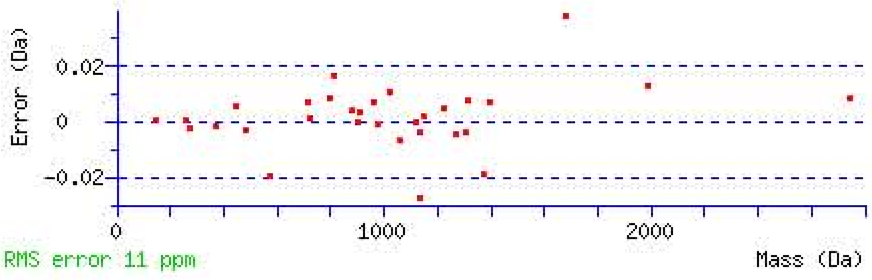
Match to Query 56579: 3227.682296 from(807.927850,4+) rtinseconds(2780) index(36508)
Title: Locus:1.1.1.3630.21 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

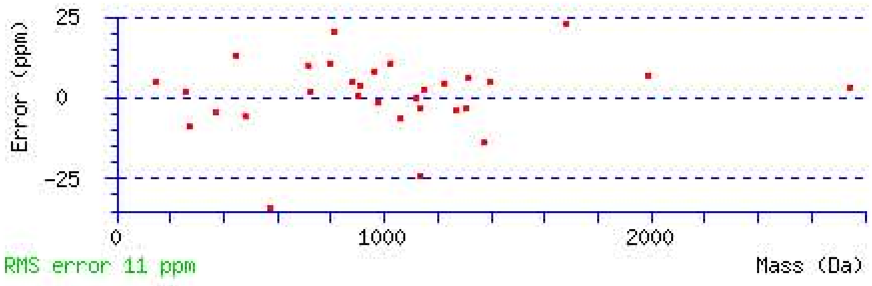


```
Monoisotopic mass of neutral peptide Mr(calc): 3227.682129
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4     : Biotin:Thermo-21345 (Q)
Ions Score: 70  Expect: 3.5e-007
Matches : 31/300 fragment ions using 59 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833					A							27
2	171.112804	86.060040					V	3157.652336	1579.329806	3140.625787	1570.816531	3139.641771	1570.324523	26
3	286.139747	143.573512			268.129182	134.568229	D	3058.583922	1529.795599	3041.557373	1521.282324	3040.573357	1520.790316	25
4	***725.365073***	363.186175	708.338524	354.672900	707.354508	354.180892	Q	2943.556979	1472.282127	2926.530430	1463.768853	2925.546414	1463.276845	24
5	***812.397101***	406.702189	795.370552	398.188914	794.386536	397.696906	S	2504.331653	1252.669464	2487.305104	1244.156190	2486.321088	1243.664182	23
6	***911.465515***	456.236396	894.438966	447.723121	893.454950	447.231113	V	2417.299625	1209.153451	2400.273076	1200.640176	2399.289060	1200.148168	22
7	***1024.549579***	512.778427	1007.523030	504.265153	1006.539014	503.773145	L	2318.231211	1159.619243	2301.204662	1151.105969	2300.220646	1150.613961	21
8	***1137.633643***	**569.320459**	1120.607094	560.807185	1119.623078	560.315177	L	2205.147147	1103.077212	2188.120598	1094.563937	2187.136582	1094.071929	20
9	***1268.674128***	634.840702	1251.647579	626.327428	1250.663563	625.835419	M	2092.063083	1046.535179	2075.036534	1038.021905	2074.052518	1037.529897	19
10	***1396.769091***	698.888183	1379.742542	690.374909	1378.758526	689.882901	K	1961.022598	981.014937	1943.996049	972.501663	1943.012033	972.009655	18
11	1493.821855	747.414565	1476.795306	738.901291	1475.811290	738.409283	P	1832.927635	916.967456	1815.901086	908.454181	1814.917070	907.962173	17
12	1608.848798	804.928037	1591.822249	796.414763	1590.838233	795.922755	D	1735.874871	868.441074	1718.848322	859.927799	1717.864306	859.435791	16
13	***1679.885912***	840.446594	1662.859363	831.933320	1661.875347	831.441311	A	1620.847928	810.927602	1603.821379	802.414328	1602.837363	801.922320	15
14	1808.928505	**904.967891**	1791.901956	896.454616	1790.917940	895.962608	E	1549.810814	775.409045	1532.784265	766.895771	1531.800249	766.403763	14
15	1922.012569	**961.509923**	1904.986020	952.996648	1904.002004	952.504640	L	1420.768221	710.887749	1403.741672	702.374474	1402.757656	701.882466	13
16	2009.044597	1005.025937	1992.018048	996.512662	1991.034032	996.020654	S	***1307.684157***	654.345717	1290.657608	645.832442	1289.673592	645.340434	12
17	2080.081711	1040.544493	2063.055162	1032.031219	2062.071146	1031.539211	A	***1220.652129***	610.829703	1203.625580	602.316428	1202.641564	601.824420	11
18	2167.113739	1084.060507	2150.087190	1075.547233	2149.103174	1075.055225	S	***1149.615015***	575.311146	1132.588466	566.797871	1131.604450	566.305863	10
19	2254.145767	1127.576521	2237.119218	1119.063247	2236.135202	1118.571239	S	***1062.582987***	531.795132	1045.556438	523.281857	1044.572422	522.789849	9
20	2353.214181	1177.110728	2336.187632	1168.597454	2335.203616	1168.105446	V	***975.550959***	488.279118	958.524410	479.765843	957.540394	479.273835	8
21	2516.277510	1258.642393	2499.250961	1250.129118	2498.266945	1249.637110	Y	***876.482545***	438.744911	859.455996	430.231636	858.471980	429.739628	7
22	2630.320437	**1315.663856**	2613.293888	1307.150582	2612.309872	1306.658574	N	***713.419216***	357.213246	696.392667	348.699972	695.408651	348.207964	6
23	***2743.404501***	**1372.205888**	2726.377952	1363.692614	2725.393936	1363.200606	L	599.376289	300.191783	582.349740	291.678508	581.365724	291.186500	5
24	2856.488565	1428.747921	2839.462016	1420.234646	2838.478000	1419.742638	L	***486.292225***	243.649751	469.265676	235.136476	468.281660	234.644468	4
25	2953.541329	1477.274303	2936.514780	1468.761028	2935.530764	1468.269020	P	***373.208161***	187.107719	356.181612	178.594444	355.197596	178.102436	3
26	3082.583922	1541.795599	3065.557373	1533.282325	3064.573357	1532.790317	E	***276.155397***	138.581337	259.128848	130.068062	258.144832	129.576054	2
27							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 11 ppm



RMS error 11 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.4	3227.682129	0.000167	AVDQSVLLMKPDAELSASSVYNLLPEK
1.5	3227.668900	0.013396	SQGRGKYDFYIGLGLAMSSSIFIGGSFILK
0.0	3227.669128	0.013168	QDSSPHLTSQRPVDMVQLLK

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

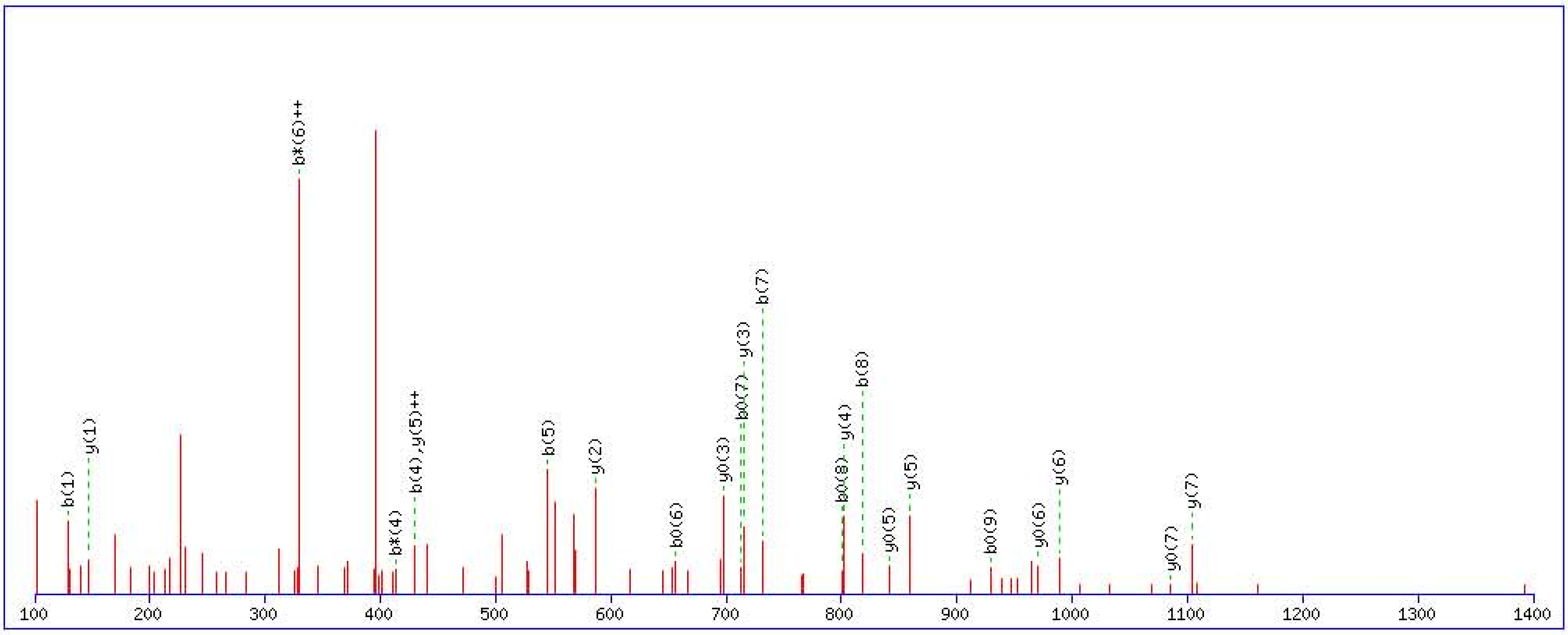
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

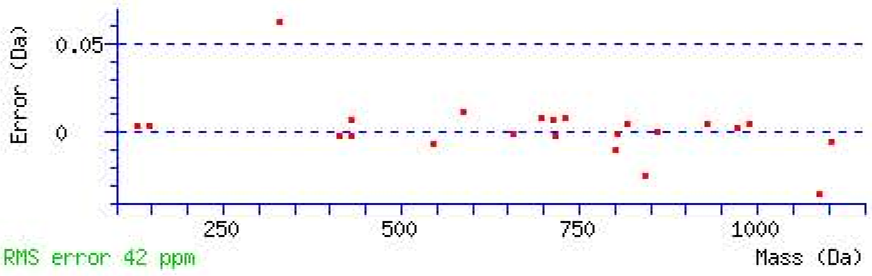
Match to Query 28106: 1531.716432 from(511.579420,3+) rtinseconds(1096) index(14060)
Title: Locus:1.1.1.2945.3 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

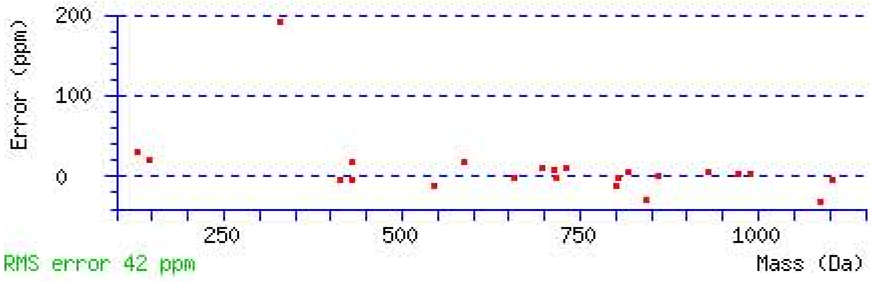
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1531.718796
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.0022
Matches : 23/112 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	**129.102239**	65.054757	112.075690	56.541483			K							11
2	200.139353	100.573315	183.112804	92.060040			A	1404.631137	702.819207	1387.604588	694.305932	1386.620572	693.813924	10
3	301.187032	151.097154	284.160483	142.583879	283.176467	142.091872	T	1333.594023	667.300650	1316.567474	658.787375	1315.583458	658.295367	9
4	**430.229625**	215.618450	413.203076	207.105176	412.219060	206.613168	E	1232.546344	616.776810	1215.519795	608.263536	1214.535779	607.771528	8
5	**545.256568**	273.131922	528.230019	264.618648	527.246003	264.126640	D	***1103.503751***	552.255514	1086.477202	543.742239	1085.493186	543.250231	7
6	674.299161	337.653219	657.272612	329.139944	656.288596	328.647936	E	***988.476808***	494.742042	971.450259	486.228768	970.466243	485.736760	6
7	**731.320625**	366.163951	714.294076	357.650676	713.310060	357.158668	G	***859.434215***	430.220746	842.407666	421.707471	841.423650	421.215463	5
8	**818.352653**	409.679965	801.326104	401.166690	800.342088	400.674682	S	***802.412751***	401.710014	785.386202	393.196739	784.402186	392.704731	4
9	947.395246	474.201261	930.368697	465.687987	929.384681	465.195979	E	***715.380723***	358.194000	698.354174	349.680725	697.370158	349.188717	3
10	1386.620572	693.813924	1369.594023	685.300650	1368.610007	684.808642	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 KATEDEGSEQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.0	1531.718796	-0.002364	KATEDEGSEQK
3.6	1531.715454	0.000978	EWNGVVSESDSPVK
2.5	1531.716309	0.000123	QVDSMWAEQK

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

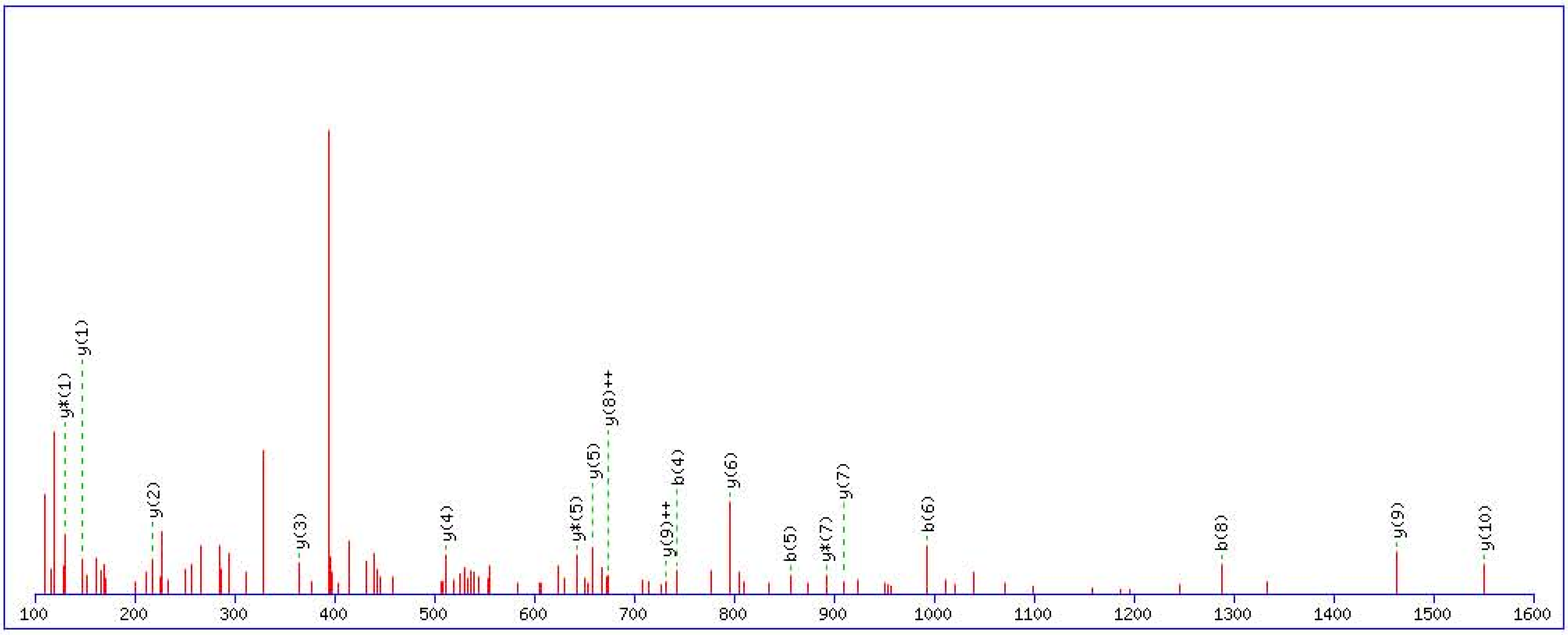
Mascot Search Results

Peptide View

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

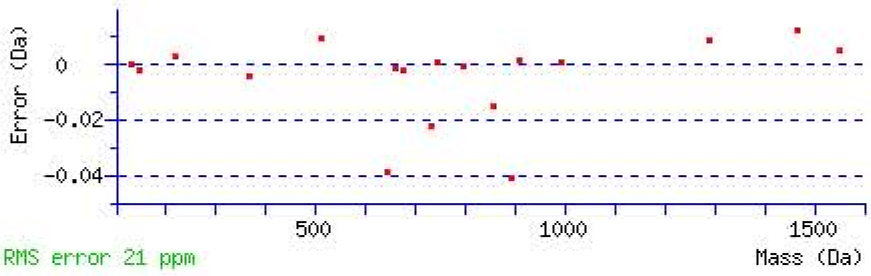
Match to Query 32717: 1650.828132 from(551.283320,3+) rtinseconds(2352) index(20990)
Title: Locus:1.1.1.3385.4 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

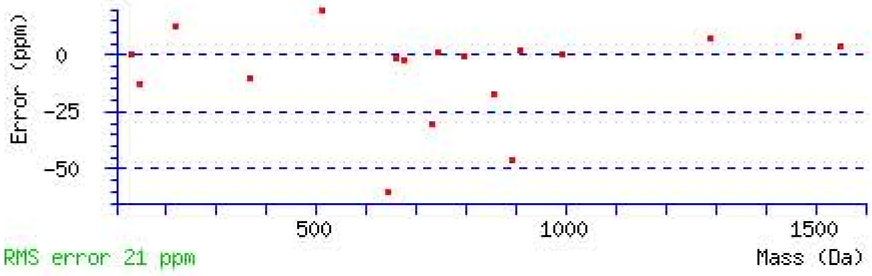
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1650.822845
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.029
Matches : 18/98 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	102.054955	51.531116			84.044390	42.525833	T							11
2	189.086983	95.047129			171.076418	86.041847	S	***1550.782433***	775.894855	1533.755884	767.381580	1532.771868	766.889572	10
3	304.113926	152.560601			286.103361	143.555319	D	***1463.750405***	732.378841	1446.723856	723.865566	1445.739840	723.373558	9
4	**743.339252**	372.173264	726.312703	363.659989	725.328687	363.167982	Q	1348.723462	674.865369	1331.696913	666.352095			8
5	**856.423316**	428.715296	839.396767	420.202022	838.412751	419.710014	I	***909.498136***	455.252706	892.471587	446.739432			7
6	**993.482228**	497.244752	976.455679	488.731477	975.471663	488.239469	H	***796.414072***	398.710674	779.387523	390.197400			6
7	1140.550642	570.778959	1123.524093	562.265685	1122.540077	561.773676	F	***659.355160***	330.181218	642.328611	321.667944			5
8	**1287.619056**	644.313166	1270.592507	635.799892	1269.608491	635.307884	F	***512.286746***	256.647011	495.260197	248.133737			4
9	1434.687470	717.847373	1417.660921	709.334099	1416.676905	708.842091	F	***365.218332***	183.112804	348.191783	174.599530			3
10	1505.724584	753.365930	1488.698035	744.852656	1487.714019	744.360648	A	***218.149918***	109.578597	201.123369	101.065322			2
11							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.3	1650.822845	0.005287	TSDQIHFFFAK

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

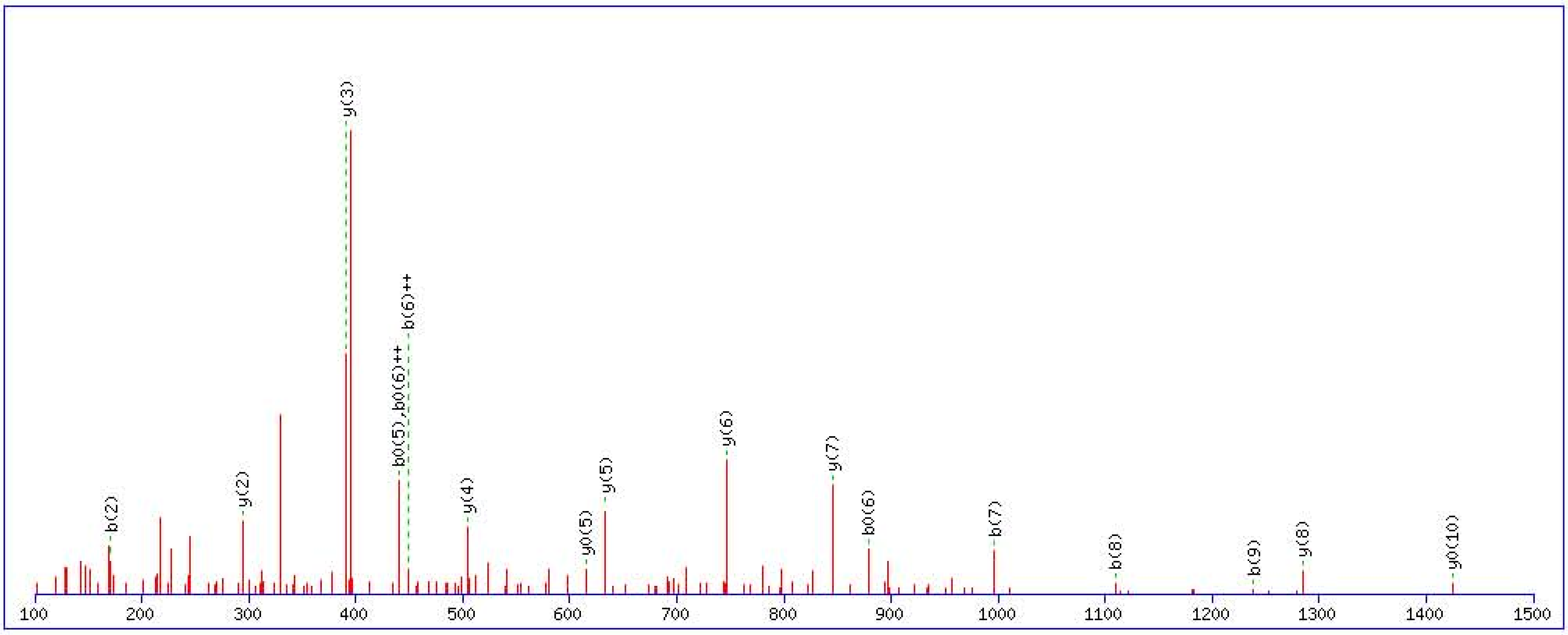
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

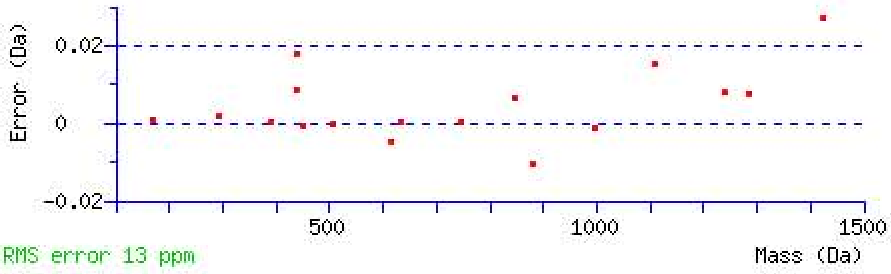
Match to Query 34393: 1740.945672 from(581.322500,3+) rtinseconds(2557) index(34934)
Title: Locus:1.1.1.3554.4 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

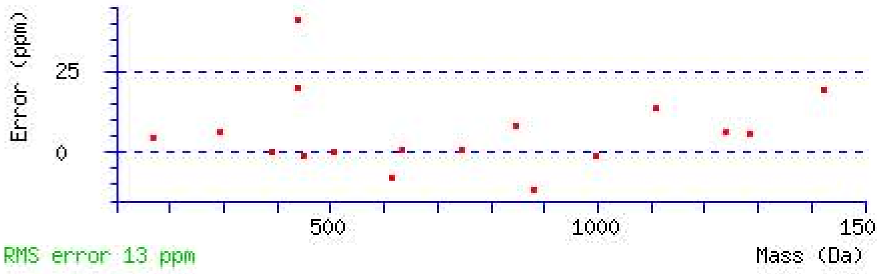
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1740.948425
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.0015
Matches : 17/122 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							13
2	**171.112804**	86.060040					A	1642.887293	821.947284	1625.860744	813.434010	1624.876728	812.942002	12
3	300.155397	150.581336			282.144832	141.576054	E	1571.850179	786.428727	1554.823630	777.915453	1553.839614	777.423445	11
4	357.176861	179.092068			339.166296	170.086786	G	1442.807586	721.907431	1425.781037	713.394157	1424.797021	712.902148	10
5	458.224540	229.615908			440.213975	220.610626	T	1385.786122	693.396699	1368.759573	684.883424	1367.775557	684.391416	9
6	897.449866	449.228571	880.423317	440.715297	879.439301	440.223289	Q	***1284.738443***	642.872860	1267.711894	634.359585	1266.727878	633.867577	8
7	**996.518280**	498.762778	979.491731	490.249504	978.507715	489.757496	V	***845.513117***	423.260196	828.486568	414.746922	827.502552	414.254914	7
8	**1109.602344**	555.304810	1092.575795	546.791536	1091.591779	546.299527	L	***746.444703***	373.725989	729.418154	365.212715	728.434138	364.720707	6
9	**1238.644937**	619.826106	1221.618388	611.312832	1220.634372	610.820824	E	***633.360639***	317.183958	616.334090	308.670683	615.350074	308.178675	5
10	1351.729001	676.368138	1334.702452	667.854864	1333.718436	667.362856	L	***504.318046***	252.662661	487.291497	244.149386			4
11	1448.781765	724.894520	1431.755216	716.381246	1430.771200	715.889238	P	***391.233982***	196.120629	374.207433	187.607355			3
12	1595.850179	798.428727	1578.823630	789.915453	1577.839614	789.423445	F	***294.181218***	147.594247	277.154669	139.080973			2
13							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.3	1740.948425	-0.002753	VAEGTQVLELPFK

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

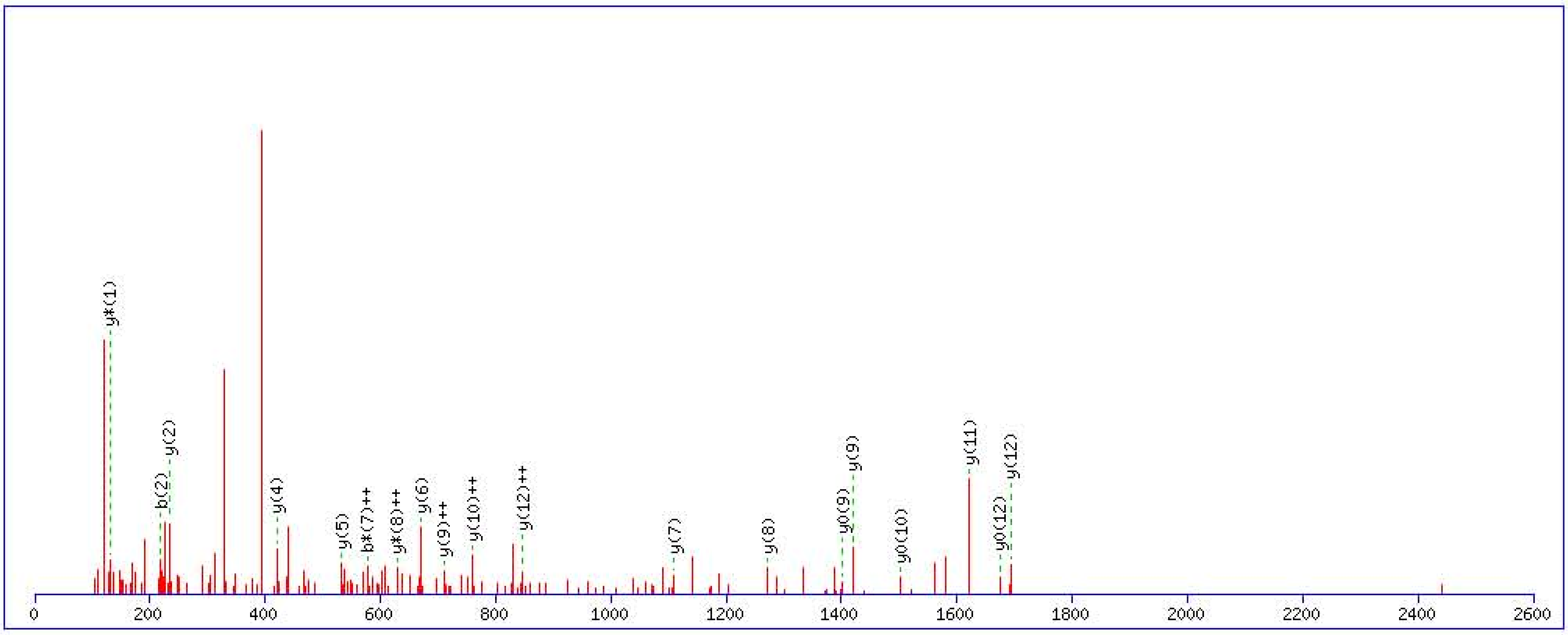
Mascot Search Results

Peptide View

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

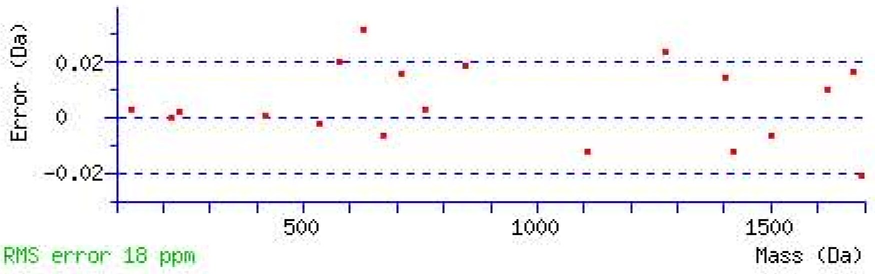
Match to Query 36427: 1838.906022 from(613.975950,3+) rtinseconds(2100) index(19609)
Title: Locus:1.1.1.3297.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

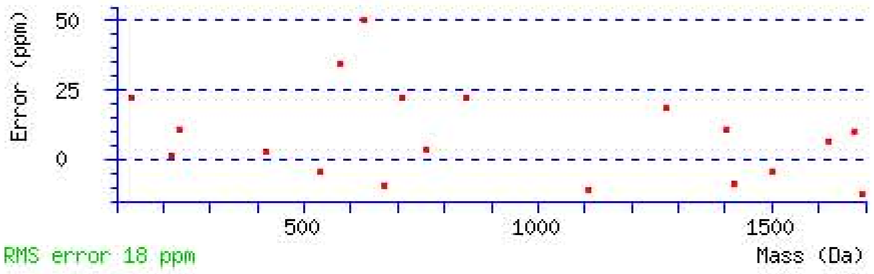
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1838.902542
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 32 **Expect:** 0.014
Matches : 19/126 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	148.075690	74.541483					F							13
2	219.112804	110.060040					A	***1692.841406***	846.924341	1675.814857	838.411067	1674.830841	837.919059	12
3	320.160483	160.583879			302.149918	151.578597	T	***1621.804292***	811.405784	1604.777743	802.892510	1603.793727	802.400502	11
4	421.208162	211.107719			403.197597	202.102437	T	1520.756613	760.881945	1503.730064	752.368670	1502.746048	751.876662	10
5	568.276576	284.641926			550.266011	275.636644	F	***1419.708934***	710.358105	1402.682385	701.844831	1401.698369	701.352823	9
6	731.339905	366.173591			713.329340	357.168308	Y	***1272.640520***	636.823898	1255.613971	628.310624	1254.629955	627.818616	8
7	1170.565231	585.786254	1153.538682	577.272979	1152.554666	576.780971	Q	***1109.577191***	555.292234	1092.550642	546.778959	1091.566626	546.286951	7
8	1307.624143	654.315710	1290.597594	645.802435	1289.613578	645.310427	H	***670.351865***	335.679571	653.325316	327.166296	652.341300	326.674288	6
9	1420.708207	710.857741	1403.681658	702.344467	1402.697642	701.852459	L	***533.292953***	267.150115	516.266404	258.636840	515.282388	258.144832	5
10	1491.745321	746.376298	1474.718772	737.863024	1473.734756	737.371016	A	***420.208889***	210.608083	403.182340	202.094808	402.198324	201.602800	4
11	1606.772264	803.889770	1589.745715	795.376496	1588.761699	794.884487	D	349.171775	175.089526	332.145226	166.576251	331.161210	166.084243	3
12	1693.804292	847.405784	1676.777743	838.892510	1675.793727	838.400502	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 FATTFYQHLADSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.0	1838.902542	0.003480	FATTFYQHLADSK

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

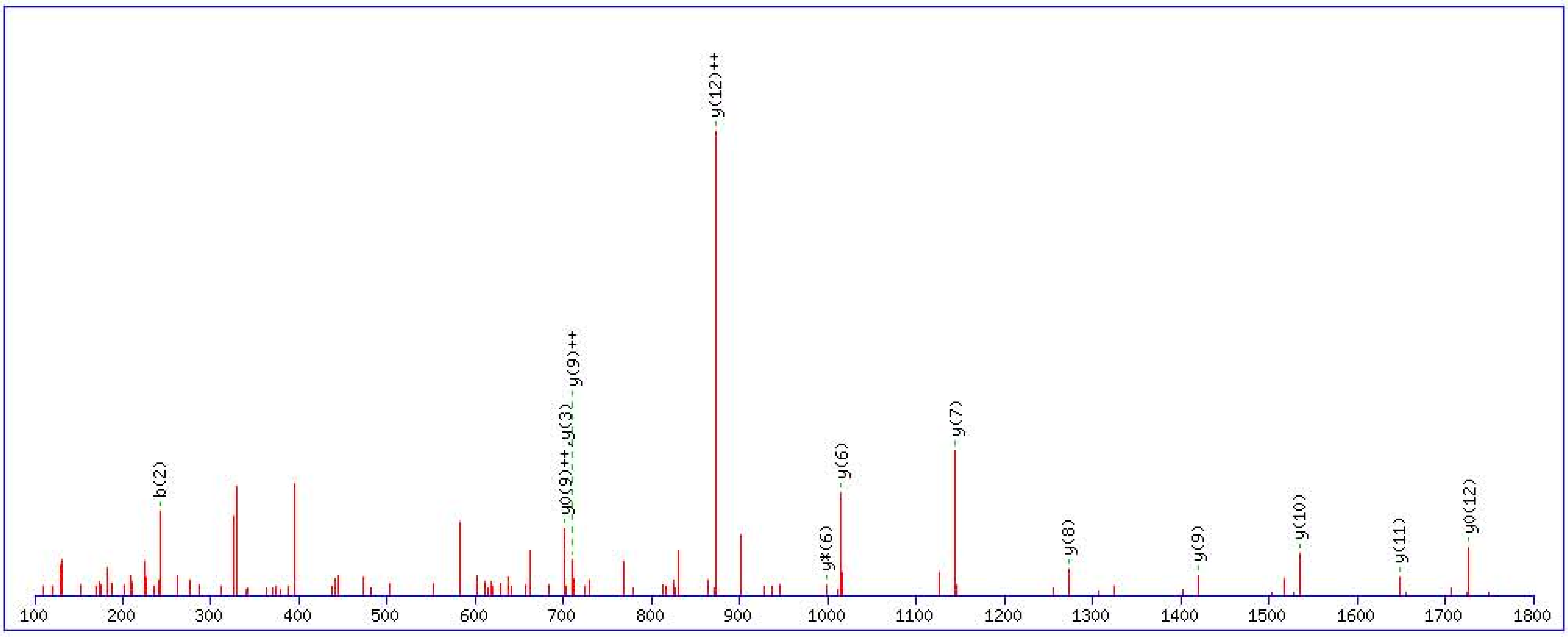
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

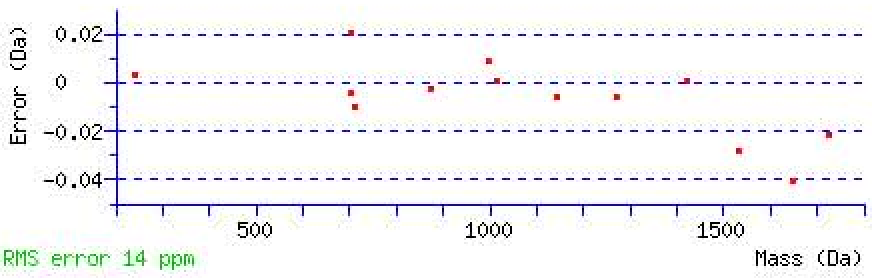
Match to Query 39045: 1985.000862 from(662.674230,3+) rtinseconds(1925) index(18535)
Title: Locus:1.1.1.3236.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

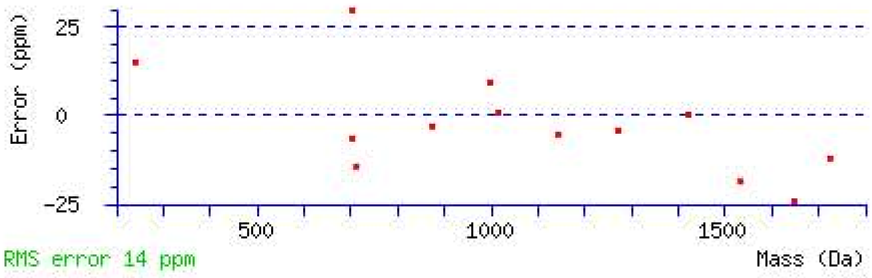
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1985.004013
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 44 **Expect:** 0.00099
Matches : 13/144 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	114.091340	57.549308					L							14
2	242.149918	121.578597	225.123369	113.065323			Q	1872.927259	936.967268	1855.900710	928.453993	1854.916694	927.961985	13
3	339.202682	170.104979	322.176133	161.591705			P	1744.868681	872.937979	1727.842132	864.424704	1726.858116	863.932696	12
4	452.286746	226.647011	435.260197	218.133737			L	***1647.815917***	824.411597	1630.789368	815.898322	1629.805352	815.406314	11
5	567.313689	284.160483	550.287140	275.647208	549.303124	275.155200	D	***1534.731853***	767.869565	1517.705304	759.356290	1516.721288	758.864282	10
6	714.382103	357.694690	697.355554	349.181415	696.371538	348.689407	F	***1419.704910***	710.356093	1402.678361	701.842819	1401.694345	701.350811	9
7	842.477066	421.742171	825.450517	413.228897	824.466501	412.736889	K	***1272.636496***	636.821886	1255.609947	628.308612	1254.625931	627.816604	8
8	971.519659	486.263468	954.493110	477.750193	953.509094	477.258185	E	***1144.541533***	572.774405	1127.514984	564.261130	1126.530968	563.769122	7
9	1085.562586	543.284931	1068.536037	534.771657	1067.552021	534.279649	N	***1015.498940***	508.253108	998.472391	499.739834	997.488375	499.247826	6
10	1156.599700	578.803488	1139.573151	570.290214	1138.589135	569.798205	A	901.456013	451.231645	884.429464	442.718370	883.445448	442.226362	5
11	1285.642293	643.324785	1268.615744	634.811510	1267.631728	634.319502	E	830.418899	415.713088	813.392350	407.199813	812.408334	406.707805	4
12	1724.867619	862.937448	1707.841070	854.424173	1706.857054	853.932165	Q	***701.376306***	351.191791	684.349757	342.678517	683.365741	342.186509	3
13	1811.899647	906.453462	1794.873098	897.940187	1793.889082	897.448179	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
14							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.2	1985.004013	-0.003151	LQPLDFKENAEQSR

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

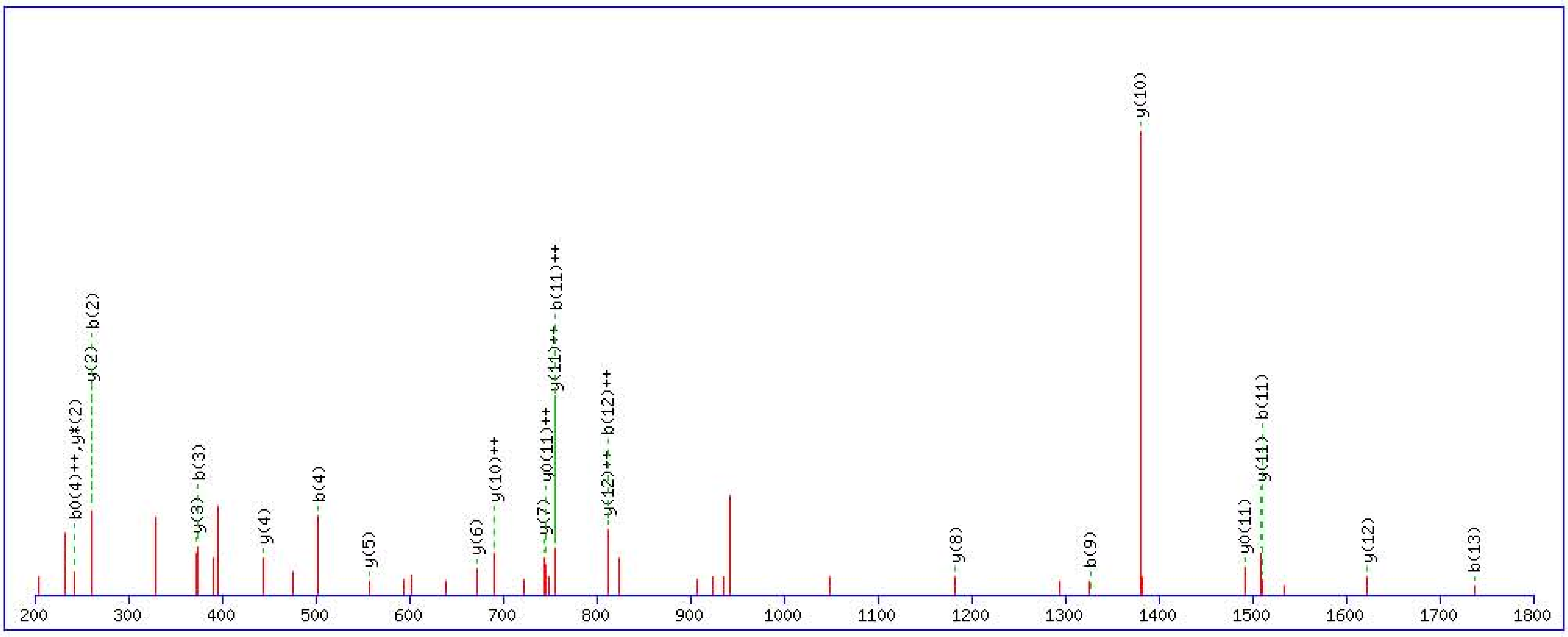
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFLEPTQADIALLK**
Found in **APOA_HUMAN**, Apolipoprotein(a) OS=Homo sapiens GN=LPA PE=1 SV=1

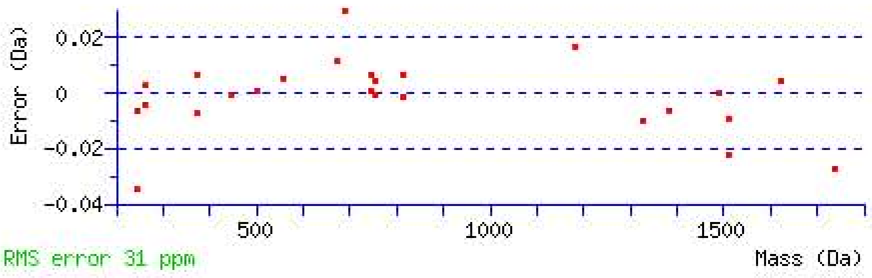
Match to Query 37211: 1882.065168 from(942.039860,2+) rtinseconds(2781) index(36509)
Title: Locus:1.1.1.3630.22 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

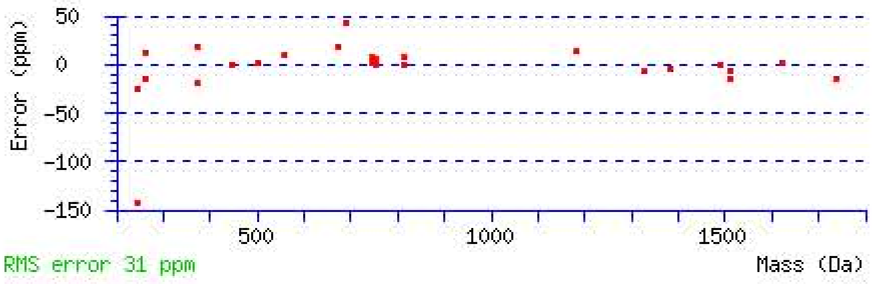
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1882.063766
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 7.4e-006
Matches : 25/128 fragment ions using 44 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							14
2	**261.159754**	131.083515					F	1769.987007	885.497142	1752.960458	876.983867	1751.976442	876.491859	13
3	**374.243818**	187.625547					L	*1622.918593*	811.962934	1605.892044	803.449660	1604.908028	802.957652	12
4	**503.286411**	252.146843			485.275846	243.141561	E	*1509.834529*	755.420903	1492.807980	746.907628	1491.823964	746.415620	11
5	600.339175	300.673226			582.328610	291.667943	P	*1380.791936*	690.899606	1363.765387	682.386331	1362.781371	681.894323	10
6	701.386854	351.197065			683.376289	342.191783	T	1283.739172	642.373224	1266.712623	633.859949	1265.728607	633.367941	9
7	1140.612180	570.809728	1123.585631	562.296454	1122.601615	561.804446	Q	*1182.691493*	591.849384	1165.664944	583.336110	1164.680928	582.844102	8
8	1211.649294	606.328285	1194.622745	597.815011	1193.638729	597.323003	A	*743.466167*	372.236721	726.439618	363.723447	725.455602	363.231439	7
9	**1326.676237**	663.841757	1309.649688	655.328482	1308.665672	654.836474	D	*672.429053*	336.718164	655.402504	328.204890	654.418488	327.712882	6
10	1439.760301	720.383789	1422.733752	711.870514	1421.749736	711.378506	I	*557.402110*	279.204693	540.375561	270.691418			5
11	**1510.797415**	**755.902346**	1493.770866	747.389071	1492.786850	746.897063	A	*444.318046*	222.662661	427.291497	214.149386			4
12	1623.881479	**812.444377**	1606.854930	803.931103	1605.870914	803.439095	L	*373.280932*	187.144104	356.254383	178.630829			3
13	**1736.965543**	868.986409	1719.938994	860.473135	1718.954978	859.981127	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 LFLEPTQADIALLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.5	1882.063766	0.001402	LFLEPTQADIALLK
6.4	1882.077469	-0.012301	NLQEVLGEEKLKEILK
5.8	1882.041122	0.024046	LLIIDSNLGVQDVENLK
1.6	1882.046021	0.019147	FLLLPDMMIKGLFGKK
1.2	1882.053238	0.011930	NQMITRVPLGSVIK
0.8	1882.045792	0.019376	EAIQSNKRLSALNK

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

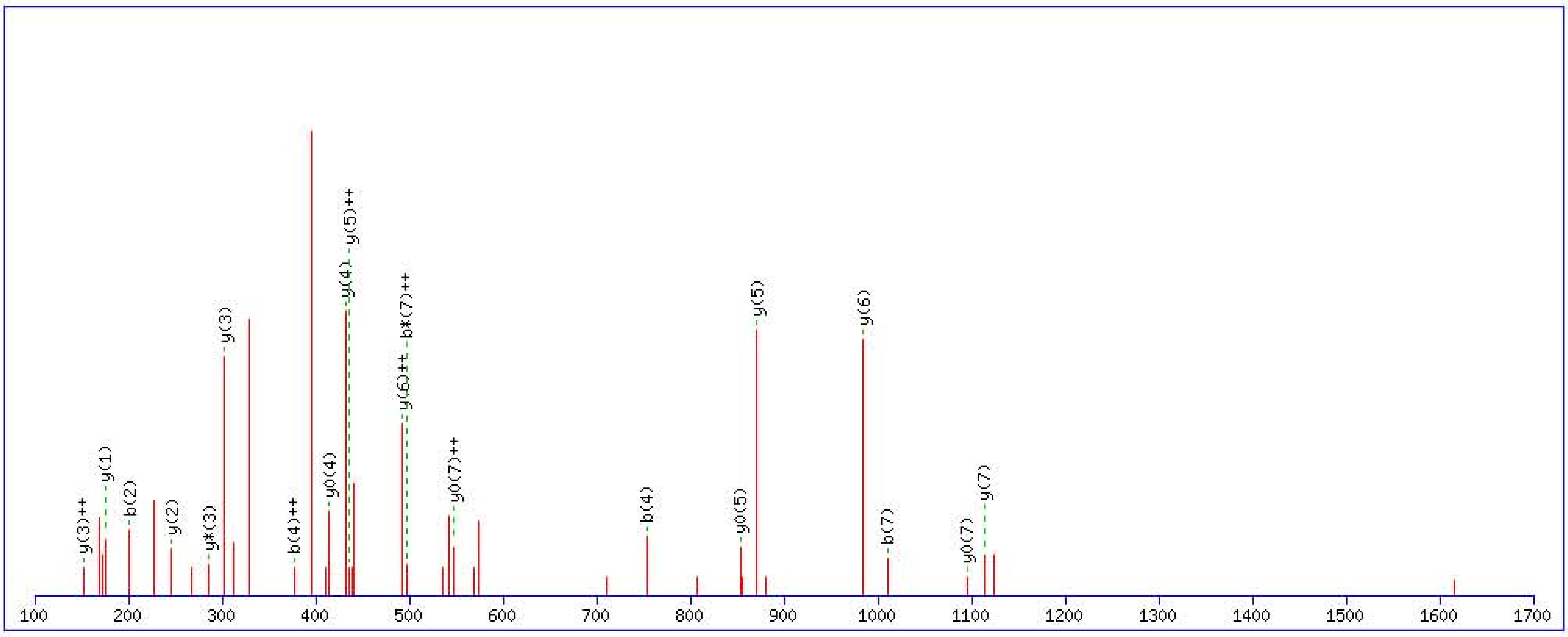
Mascot Search Results

Peptide View

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

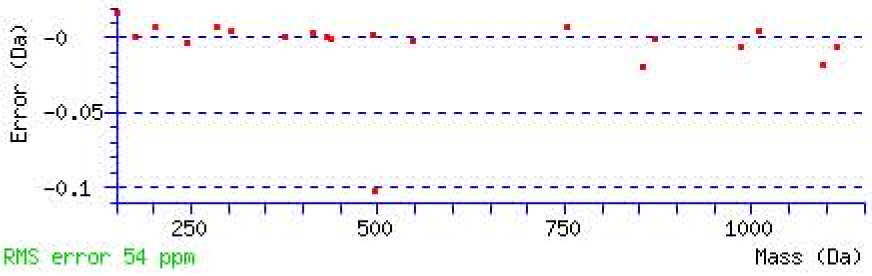
Match to Query 17361: 1183.598648 from(592.806600,2+) rtinseconds(1514) index(15939)
Title: Locus:1.1.1.3093.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

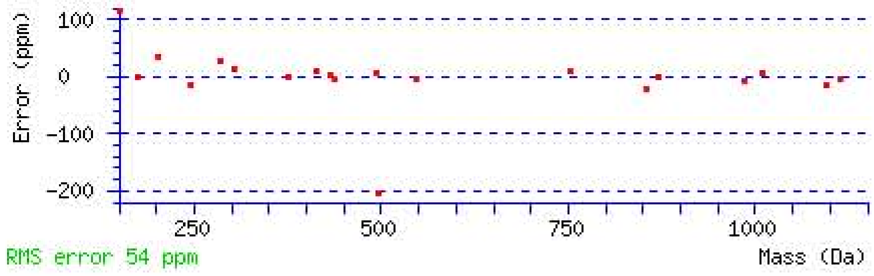
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1183.601913
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.0014
Matches : 20/70 fragment ions using 38 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833					A							8
2	**201.086983**	101.047130			183.076418	92.041847	E	***1113.572106***	557.289691	1096.545557	548.776417	1095.561541	548.284409	7
3	314.171047	157.589161			296.160482	148.583879	L	***984.529513***	492.768395	967.502964	484.255120	966.518948	483.763112	6
4	**753.396373**	377.201825	736.369824	368.688550	735.385808	368.196542	Q	***871.445449***	436.226363	854.418900	427.713088	853.434884	427.221080	5
5	882.438966	441.723121	865.412417	433.209847	864.428401	432.717839	E	***432.220123***	216.613699	415.193574	208.100425	414.209558	207.608417	4
6	939.460430	470.233853	922.433881	461.720579	921.449865	461.228571	G	***303.177530***	152.092403	286.150981	143.579128			3
7	**1010.497544**	505.752410	993.470995	497.239136	992.486979	496.747128	A	***246.156066***	123.581671	229.129517	115.068396			2
8							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.7	1183.601913	-0.003265	AELQEGAR
10.2	1183.601913	-0.003265	EALEQQR
9.4	1183.601913	-0.003265	QLAEQER
5.7	1183.613815	-0.015167	FHFEALPPAR
4.4	1183.587997	0.010651	EAKLDHCRR
3.7	1183.605743	-0.007095	APSERRSPER
3.6	1183.601913	-0.003265	AQEQELR
3.6	1183.583282	0.015366	EAASSPAGEPLR
3.3	1183.601913	-0.003265	ELQAEAGR
3.1	1183.607132	-0.008484	GGFRGGRGGAHR

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

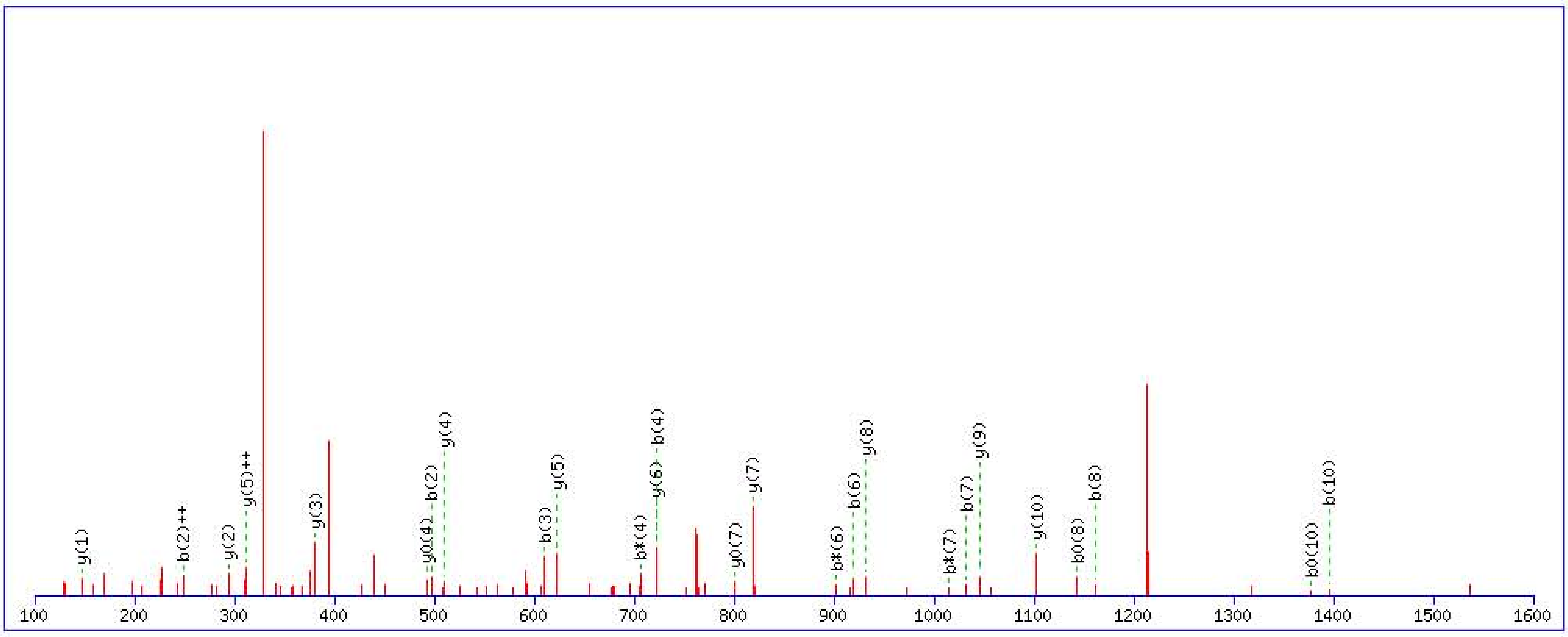
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

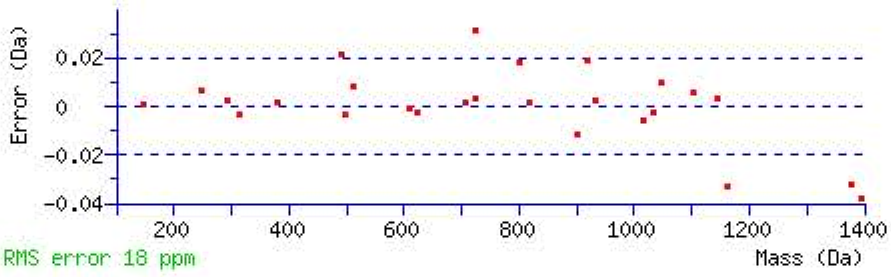
Match to Query 28320: 1540.867008 from(771.440780,2+) rtinseconds(2836) index(36948)
Title: Locus:1.1.1.3649.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

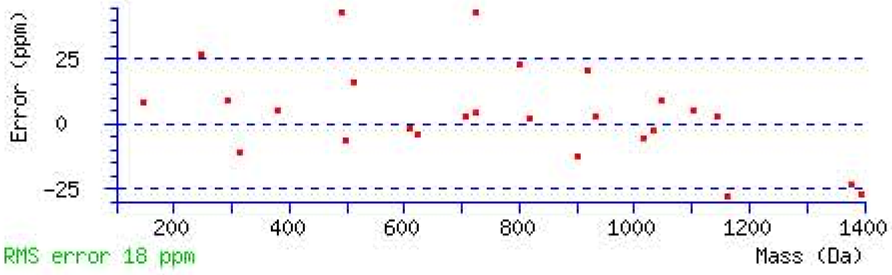
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 64 **Expect:** 3.4e-006
Matches : 26/102 fragment ions using 46 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							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
63.6	1540.868713	-0.001705	QGLLPVLESFK
4.9	1540.846054	0.020954	ISQDADLKTPTKPK
3.3	1540.872559	-0.005551	ELSRVLHTNVVFK
1.3	1540.872574	-0.005566	LPVGGQLGARFPTTK
0.8	1540.858154	0.008854	QGEVRLKCLK
0.3	1540.864700	0.002308	KVTVGKDDIQK
0.3	1540.858139	0.008869	LTNLRLQNMK

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

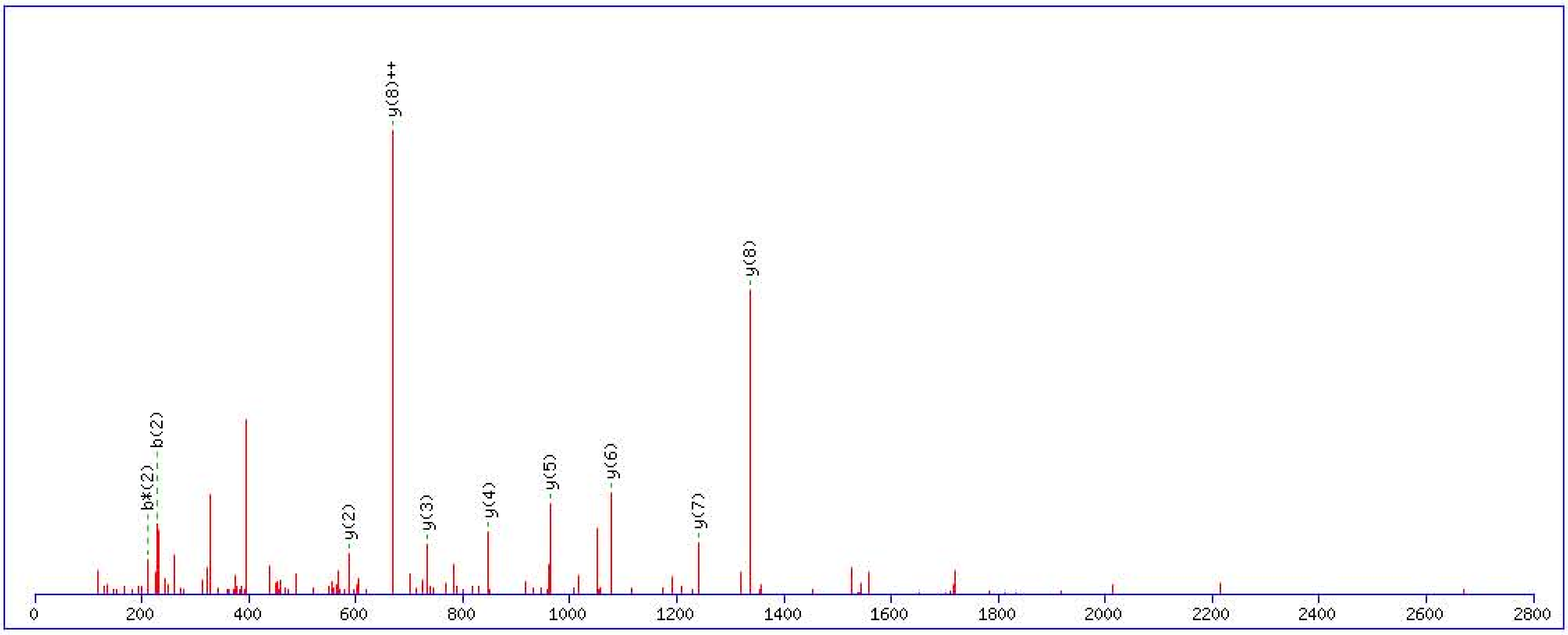
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

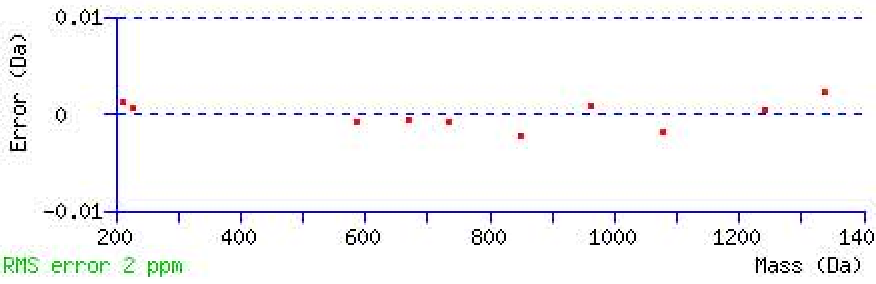
Match to Query 28902: 1562.776368 from(782.395460,2+) rtinseconds(2196) index(33006)
Title: Locus:1.1.1.3428.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

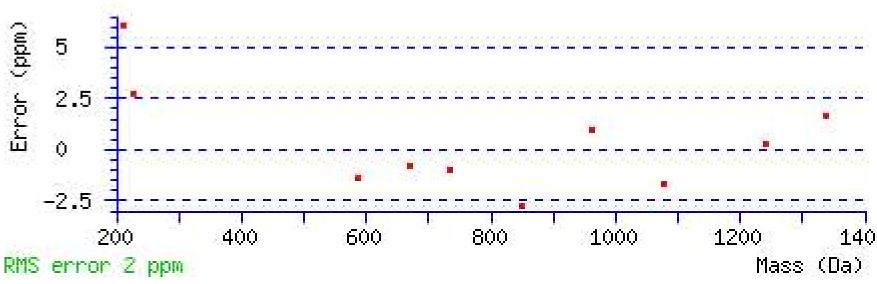
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1562.780304
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.00017
Matches : 10/90 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	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
40.9	1562.780304	-0.003936	VQPYLDDFQK
0.7	1562.787521	-0.011153	VQLVDNVYCIGQR
0.1	1562.768860	0.007508	LNFGASLQQTAEER

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

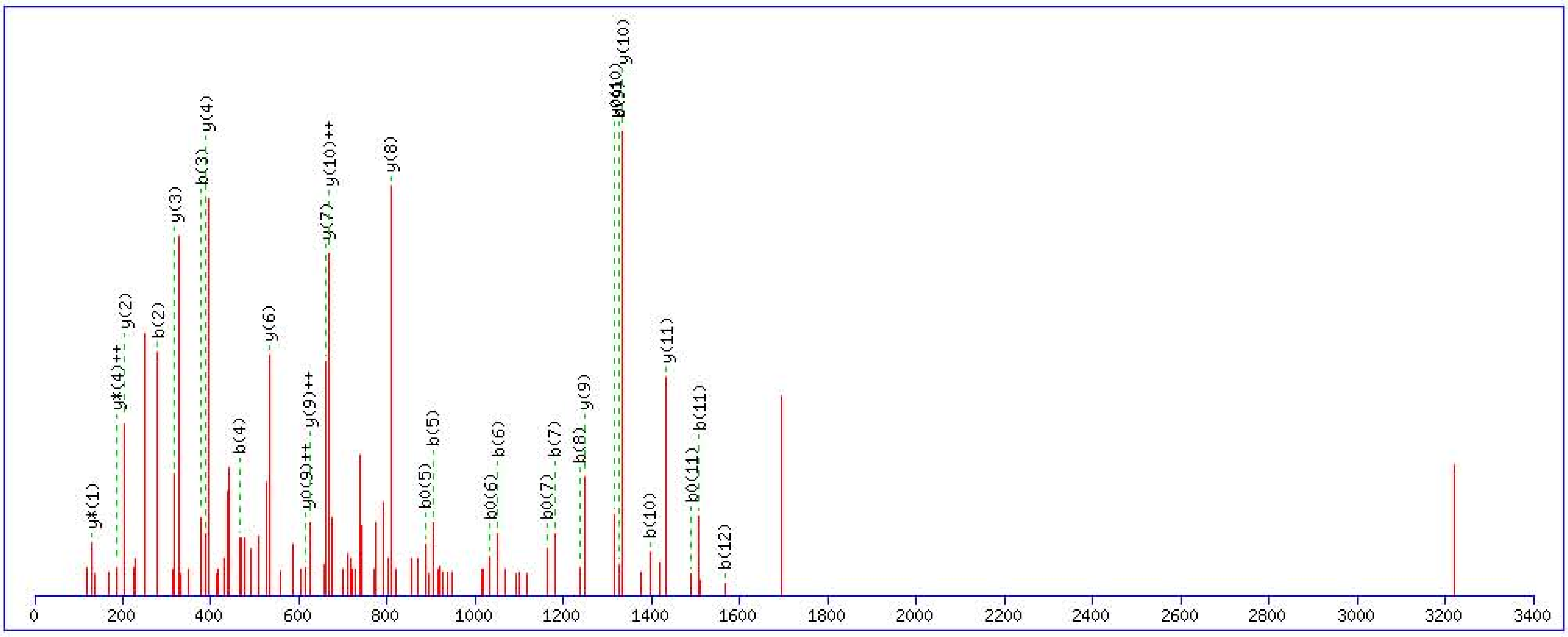
Mascot Search Results

Peptide View

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

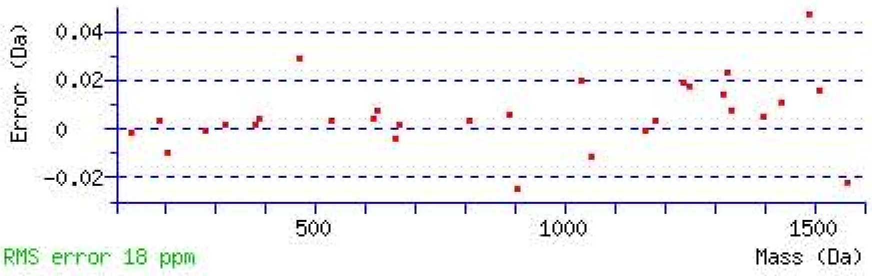
Match to Query 33854: 1710.833488 from(856.424020,2+) rtinseconds(2406) index(34128)
Title: Locus:1.1.1.3501.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

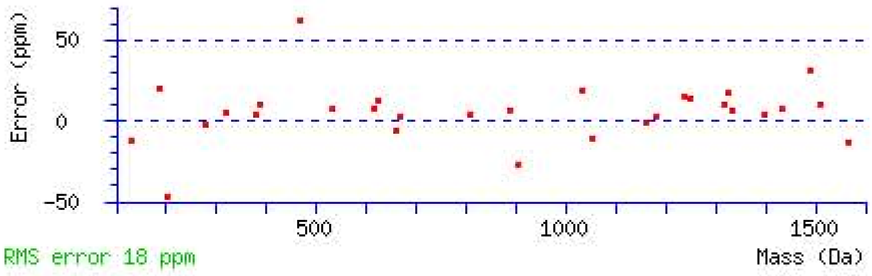
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1710.828705
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 69 **Expect:** 5.5e-007
Matches : 30/128 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	116.034219	58.520748			98.023654	49.515465	D							13
2	***279.097548***	140.052412			261.086983	131.047130	Y	1596.809042	798.908159	1579.782493	790.394884	1578.798477	789.902876	12
3	***378.165962***	189.586619			360.155397	180.581337	V	**1433.745713**	717.376495	1416.719164	708.863220	1415.735148	708.371212	11
4	***465.197990***	233.102633			447.187425	224.097351	S	**1334.677299**	667.842288	1317.650750	659.329013	1316.666734	658.837005	10
5	***904.423316***	452.715296	887.396767	444.202022	886.412751	443.710014	Q	**1247.645271**	624.326273	1230.618722	615.812999	1229.634706	615.320991	9
6	***1051.491730***	526.249503	1034.465181	517.736229	1033.481165	517.244221	F	**808.419945**	404.713610	791.393396	396.200336	790.409380	395.708328	8
7	***1180.534323***	590.770800	1163.507774	582.257525	1162.523758	581.765517	E	**661.351531**	331.179403	644.324982	322.666129	643.340966	322.174121	7
8	***1237.555787***	619.281532	1220.529238	610.768257	1219.545222	610.276249	G	**532.308938**	266.658107	515.282389	258.144832	514.298373	257.652824	6
9	***1324.587815***	662.797546	1307.561266	654.284271	1306.577250	653.792263	S	475.287474	238.147375	458.260925	229.634100	457.276909	229.142092	5
10	***1395.624929***	698.316103	1378.598380	689.802828	1377.614364	689.310820	A	**388.255446**	194.631361	371.228897	186.118086			4
11	***1508.708993***	754.858135	1491.682444	746.344860	1490.698428	745.852852	L	**317.218332**	159.112804	300.191783	150.599529			3
12	***1565.730457***	783.368866	1548.703908	774.855592	1547.719892	774.363584	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 DYVSQFEGSALGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.9	1710.828705	0.004783	DYVSQFEGSALGK
2.1	1710.835907	-0.002419	ASRKGSFGEMGEQTVK

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

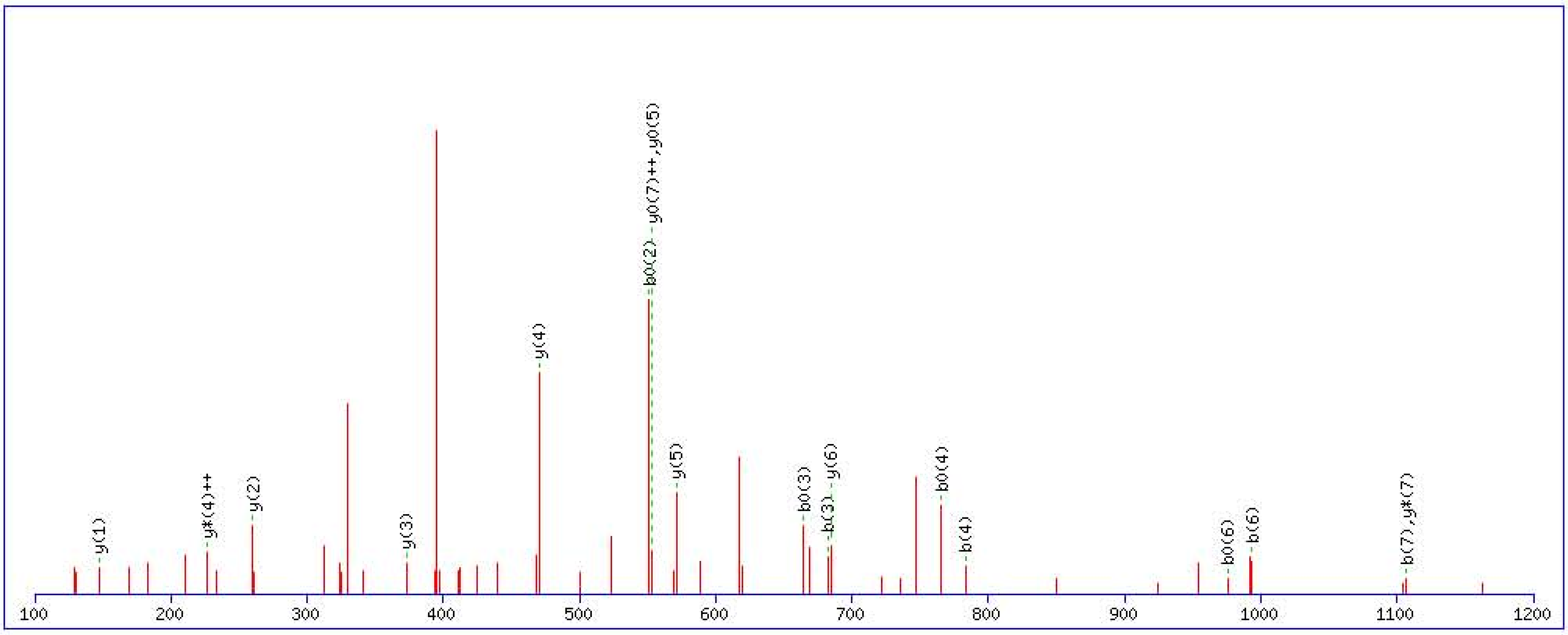
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

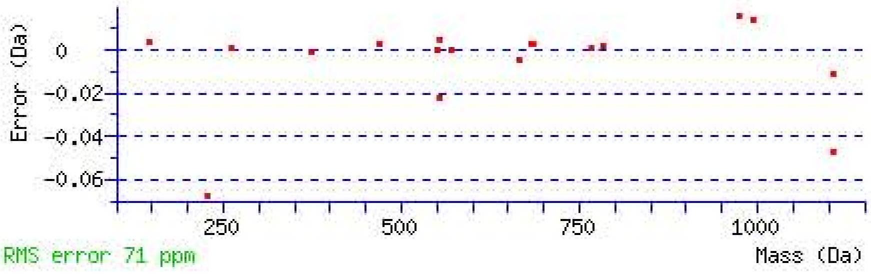
Match to Query 19084: 1251.728548 from(626.871550,2+) rtinseconds(2140) index(19848)
Title: Locus:1.1.1.3311.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

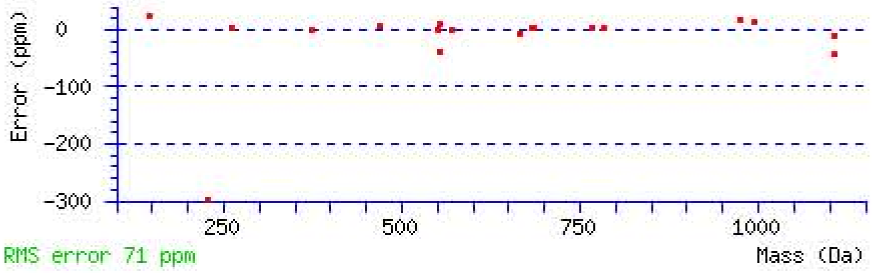
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1251.726059
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2     : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.013
Matches : 18/74 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	130.049869	65.528572			112.039304	56.523290	**E**							8
2	569.275195	285.141236	552.248646	276.627961	551.264630	276.135953	**Q**	1123.690765	562.349021	1106.664216	553.835746	1105.680200	553.343738	7
3	**682.359259**	341.683268	665.332710	333.169993	664.348694	332.677985	**L**	***684.465439***	342.736358	667.438890	334.223083	666.454874	333.731075	6
4	**783.406938**	392.207107	766.380389	383.693833	765.396373	383.201825	**T**	***571.381375***	286.194326	554.354826	277.681051	553.370810	277.189043	5
5	880.459702	440.733489	863.433153	432.220215	862.449137	431.728207	**P**	***470.333696***	235.670486	453.307147	227.157212			4
6	**993.543766**	497.275521	976.517217	488.762247	975.533201	488.270239	**L**	***373.280932***	187.144104	356.254383	178.630830			3
7	**1106.627830**	553.817553	1089.601281	545.304279	1088.617265	544.812271	**I**	***260.196868***	130.602072	243.170319	122.088798			2
8							**K**	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.4	1251.726059	0.002489	EQLTPLIK
6.2	1251.744690	-0.016142	QMLPIVLK
3.4	1251.722702	0.005846	FFKTLQDLLK
2.3	1251.722672	0.005876	NYIPYLTKLK
1.8	1251.733932	-0.005384	LPVIQLWDLR
1.6	1251.729874	-0.001326	RHKLESELIK

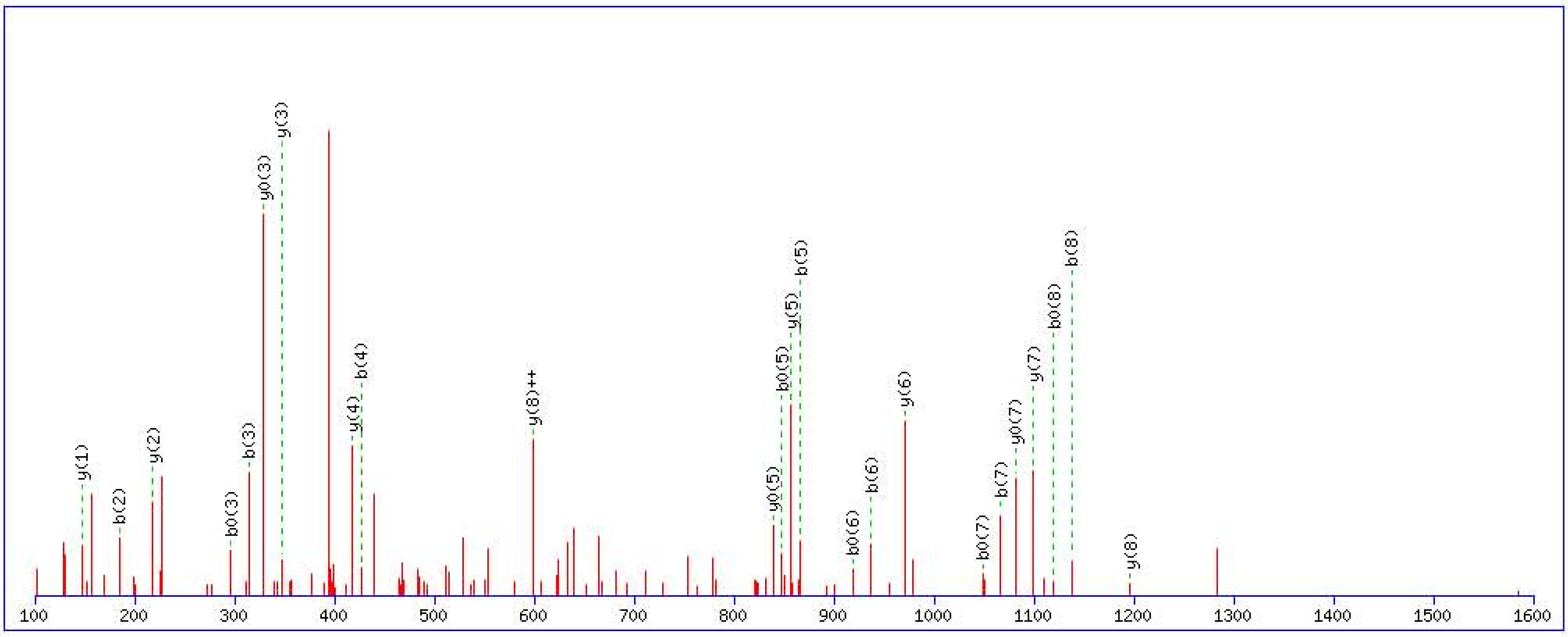
Mascot Search Results

Peptide View

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

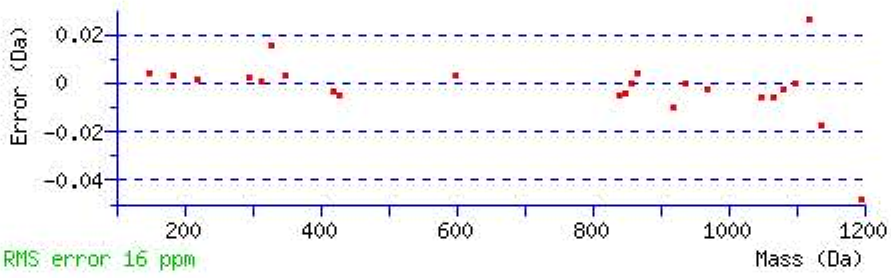
Match to Query 19976: 1282.654248 from(642.334400,2+) rtinseconds(1601) index(16515)
Title: Locus:1.1.1.3123.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

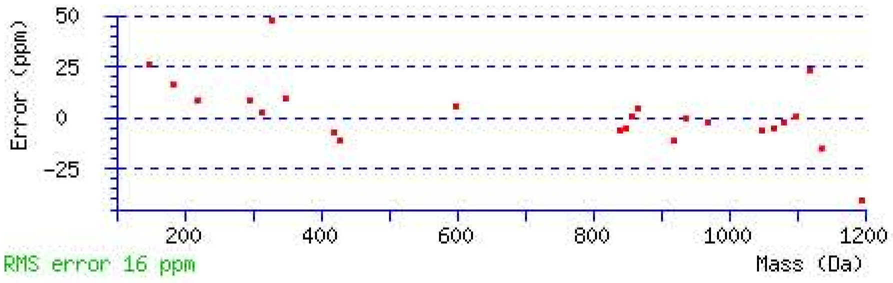
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1282.659088
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 49 **Expect:** 6.3e-005
Matches : 24/84 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	88.039304	44.523290			70.028739	35.518008	S							9
2	**185.092068**	93.049672			167.081503	84.044389	P	***1196.634372***	598.820824	1179.607823	590.307550	1178.623807	589.815541	8
3	**314.134661**	157.570968			296.124096	148.565686	E	***1099.581608***	550.294442	1082.555059	541.781168	1081.571043	541.289160	7
4	**427.218725**	214.113001			409.208160	205.107718	L	***970.539015***	485.773146	953.512466	477.259871	952.528450	476.767863	6
5	**866.444051**	433.725664	849.417502	425.212389	848.433486	424.720381	Q	***857.454951***	429.231114	840.428402	420.717839	839.444386	420.225831	5
6	**937.481165**	469.244221	920.454616	460.730946	919.470600	460.238938	A	***418.229625***	209.618450	401.203076	201.105176	400.219060	200.613168	4
7	**1066.523758**	533.765517	1049.497209	525.252243	1048.513193	524.760235	E	***347.192511***	174.099893	330.165962	165.586619	329.181946	165.094611	3
8	**1137.560872**	569.284074	1120.534323	560.770800	1119.550307	560.278792	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 SPELQAEAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.1	1282.659088	-0.004840	SPELQAEAK
4.1	1282.670334	-0.016086	EPIQASTAR
3.9	1282.637802	0.016446	KGHETLRDGDR
3.6	1282.641830	0.012418	SYPGHVQPATAR
3.4	1282.641815	0.012433	SEAFFRKADGR
2.9	1282.662949	-0.008701	DLSDTQRHLAK
2.7	1282.655716	-0.001468	ALEAEKYGFQK
1.5	1282.670334	-0.016086	QQQEQIAK
1.1	1282.652573	0.001675	KMRAISWTMK

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

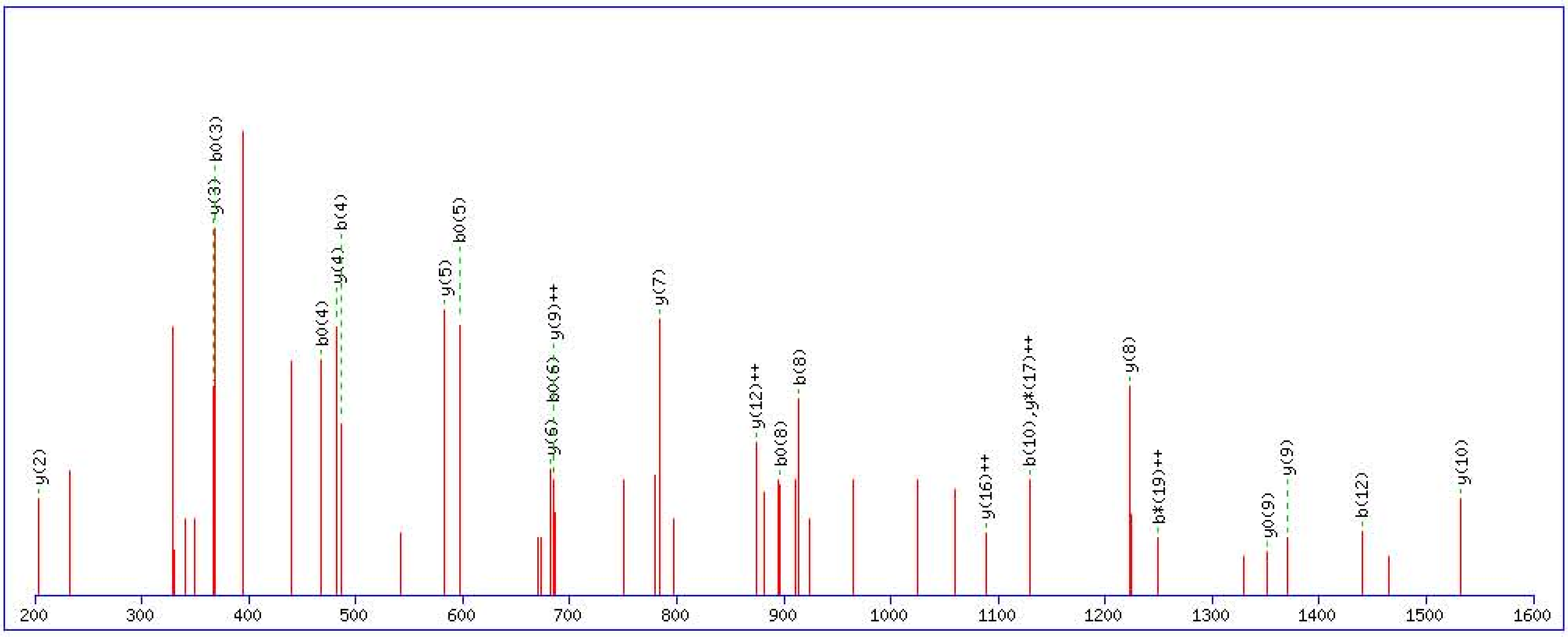
Mascot Search Results

Peptide View

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

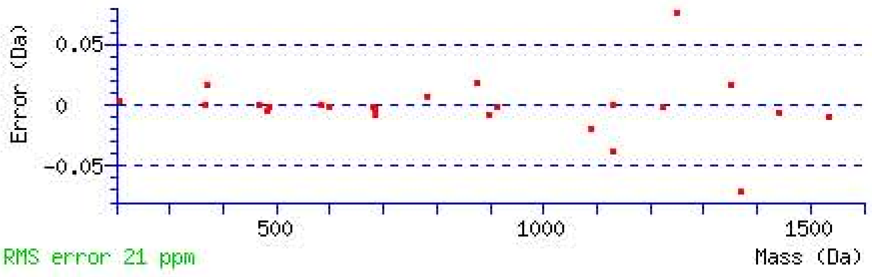
Match to Query 50012: 2660.247612 from(887.756480,3+) rtinseconds(3167) index(39146)
Title: Locus:1.1.1.3762.20 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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

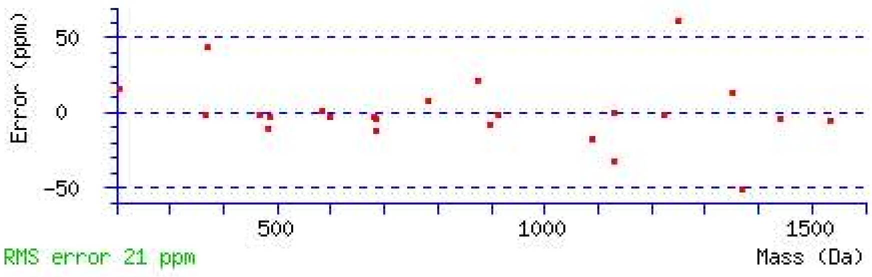


```
Monoisotopic mass of neutral peptide Mr(calc): 2660.250244
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.0021
Matches : 24/204 fragment ions using 45 most intense peaks   (help)
```

#	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



RMS error 21 ppm



RMS error 21 ppm

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
39.8	2660.250244	-0.002632	EPCVESLVSQYFQTVTDYGK
23.5	2660.250244	-0.002632	EPCVESLVSQYFQTVTDYGK

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

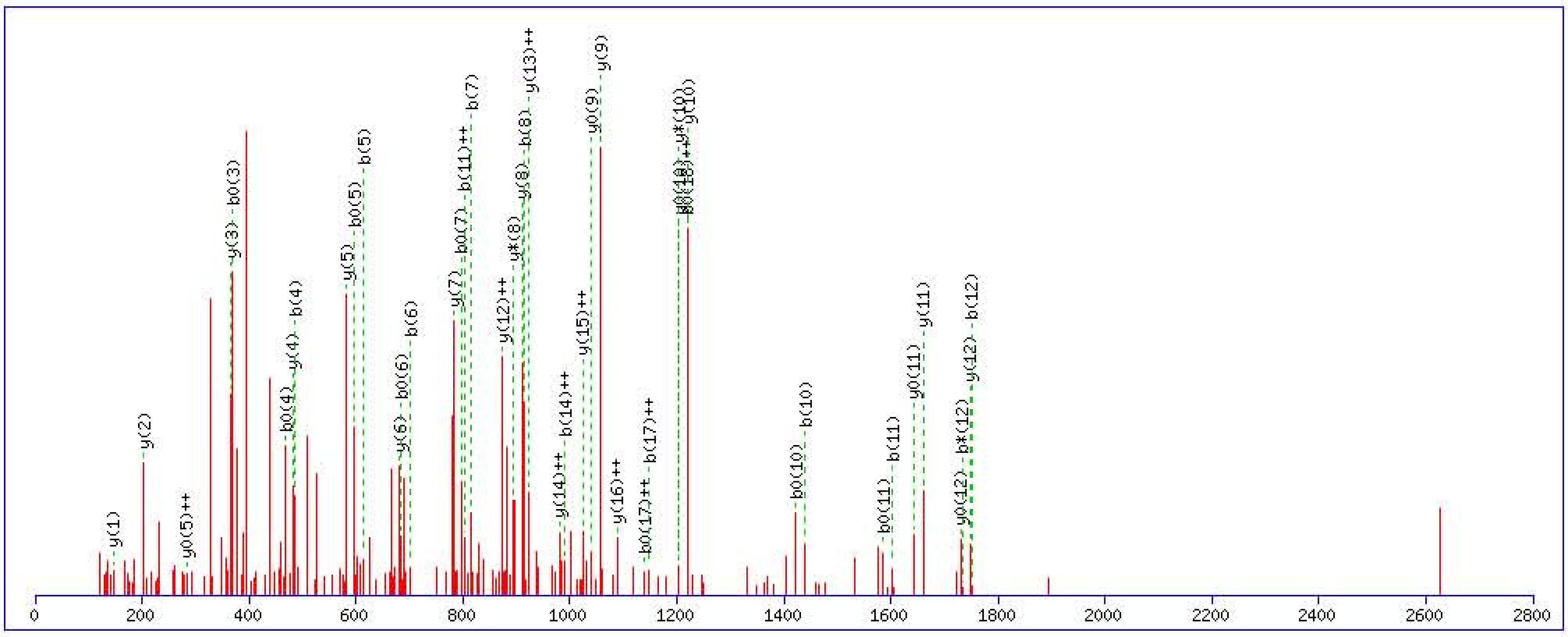
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

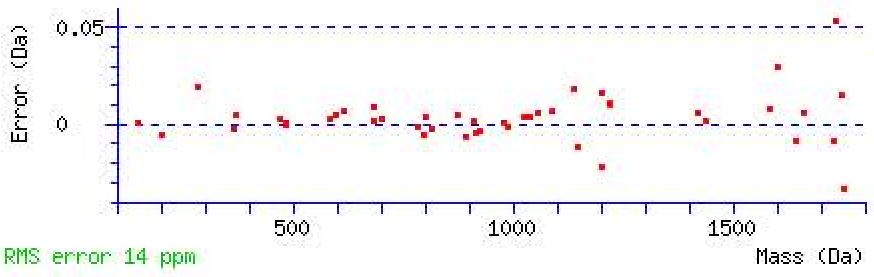
Match to Query 50013: 2660.247642 from(887.756490,3+) rtinseconds(3176) index(39179)
Title: Locus:1.1.1.3765.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

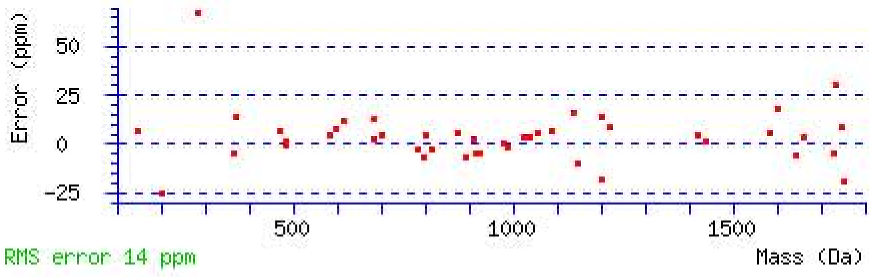
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2660.250244
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 0.00014
Matches : 45/204 fragment ions using 99 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	1024.013884	2029.993944	1015.500610	2029.009928	1015.008602	15
7	***815.360381***	408.183829			797.349816	399.178546	L	1959.988465	980.497870	1942.961916	971.984596	1941.977900	971.492588	14
8	***914.428795***	457.718036			896.418230	448.712753	V	1846.904401	923.955838	1829.877852	915.442564	1828.893836	914.950556	13
9	1001.460823	501.234050			983.450258	492.228767	S	***1747.835987***	874.421631	1730.809438	865.908357	1729.825422	865.416349	12
10	***1440.686149***	720.846712	1423.659600	712.333438	1422.675584	711.841430	Q	***1660.803959***	830.905617	1643.777410	822.392343	1642.793394	821.900335	11
11	***1603.749478***	**802.378377**	1586.722929	793.865103	1585.738913	793.373094	Y	***1221.578633***	611.292954	1204.552084	602.779680	1203.568068	602.287672	10
12	***1750.817892***	875.912584	1733.791343	867.399310	1732.807327	866.907302	F	***1058.515304***	529.761290	1041.488755	521.248015	1040.504739	520.756007	9
13	1878.876470	939.941873	1861.849921	931.428599	1860.865905	930.936590	Q	***911.446890***	456.227083	894.420341	447.713808	893.436325	447.221800	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	1039.999919	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
51.5	2660.250244	-0.002602	EPCVESLVSQYFQTVTDYGK
37.7	2660.250244	-0.002602	EPCVESLVSQYFQTVTDYGK

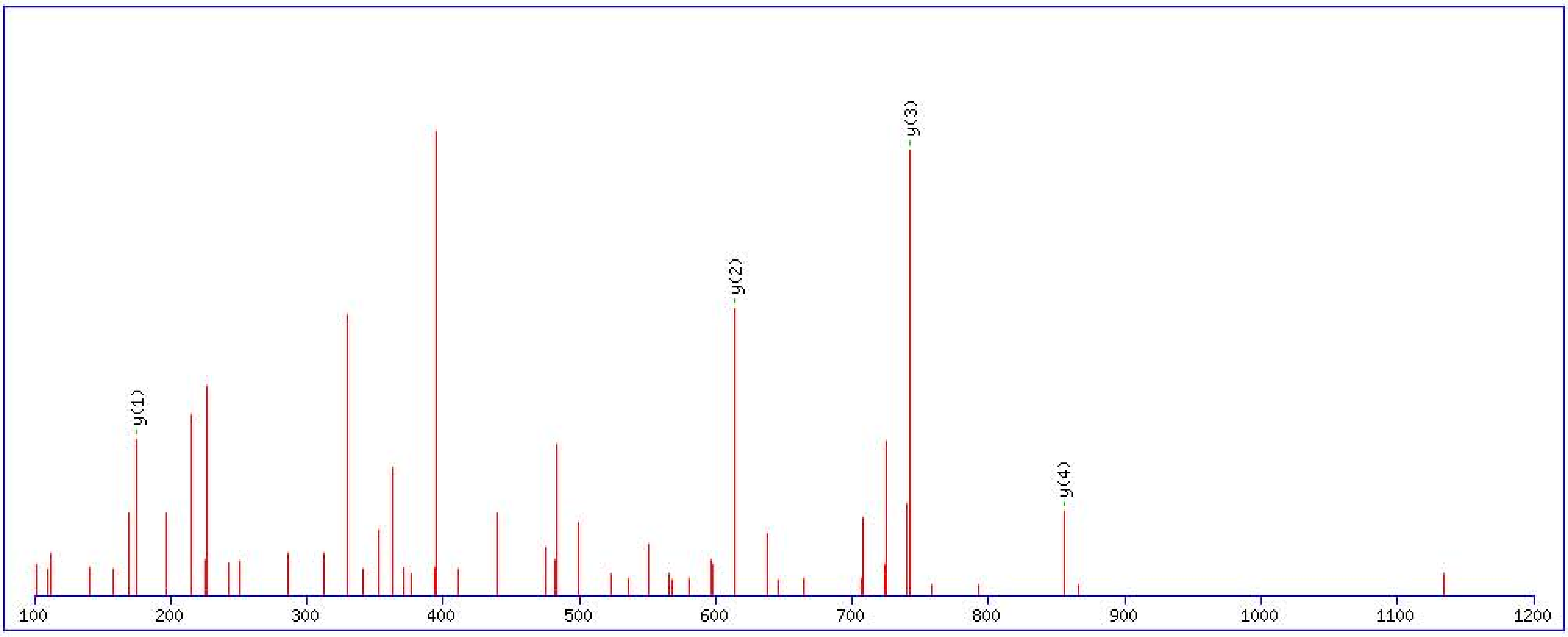
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EIQQR**
Found in **T161A_HUMAN**, Transmembrane protein 161A OS=Homo sapiens GN=TMEM161A PE=2 SV=1

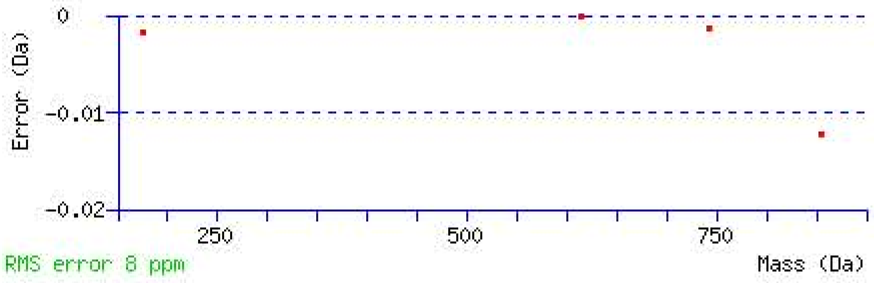
Match to Query 11195: 983.516348 from(492.765450,2+) rtinseconds(1418) index(28361)
Title: Locus:1.1.1.3157.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

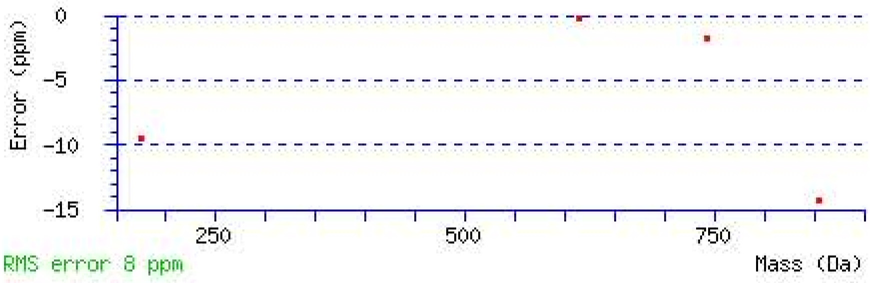
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 983.522217
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 25  Expect: 0.062
Matches : 4/36 fragment ions using 8 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	130.049869	65.528572			112.039304	56.523290	E					5
2	243.133933	122.070605			225.123368	113.065322	I	*855.486920*	428.247098	838.460371	419.733824	4
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	Q	*742.402856*	371.705066	725.376307	363.191792	3
4	810.417837	405.712557	793.391288	397.199282	792.407272	396.707274	Q	*614.344278*	307.675777	597.317729	299.162503	2
5							R	*175.118952*	88.063114	158.092403	79.549840	1





NCBI **BLAST** search of EIQQR
(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	983.522217	-0.005869	EIQQR
25.2	983.522217	-0.005869	ELQQR
25.2	983.503601	0.012747	ELQQVDPR
12.9	983.522217	-0.005869	IEQQR
12.9	983.507599	0.008749	LEKEFYR
12.9	983.522217	-0.005869	LEQQR
11.9	983.522217	-0.005869	EIQQR
11.9	983.503586	0.012762	EITSLHER
11.9	983.522217	-0.005869	ELQQR
11.0	983.522217	-0.005869	EAAVQR

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

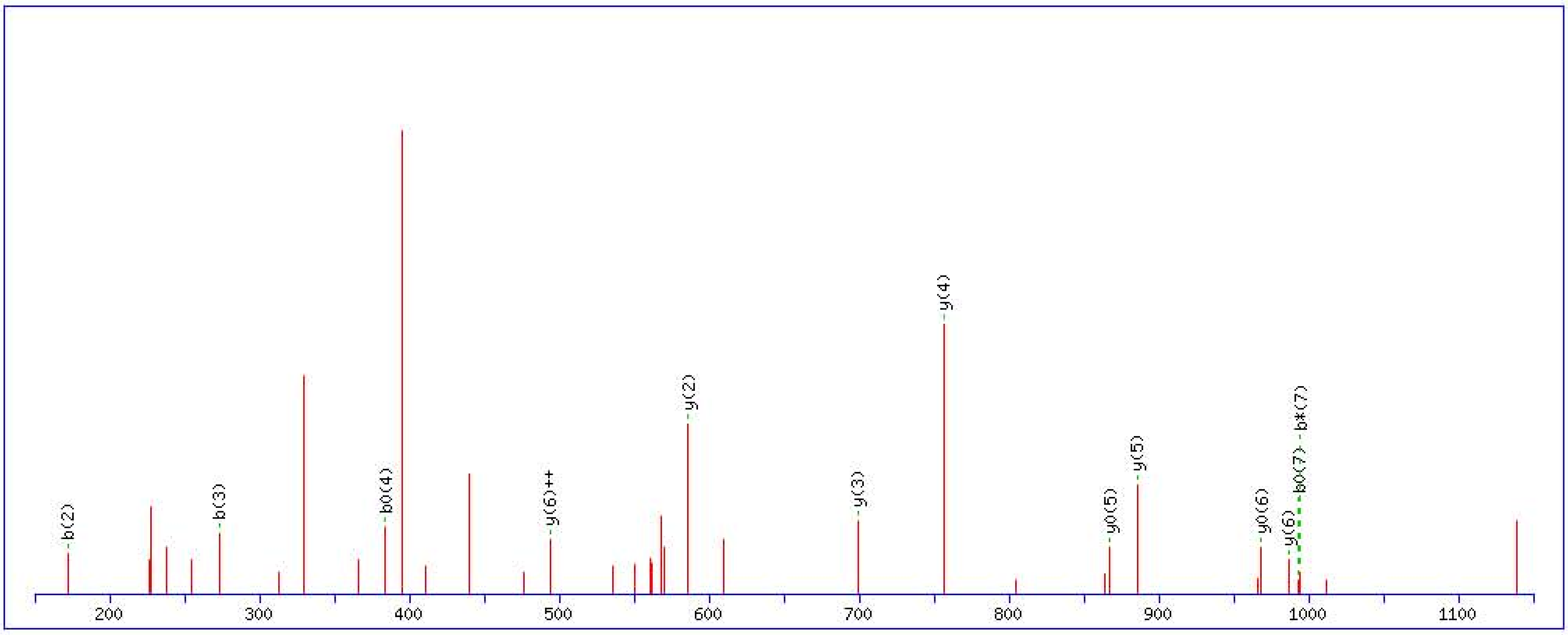
Mascot Search Results

Peptide View

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

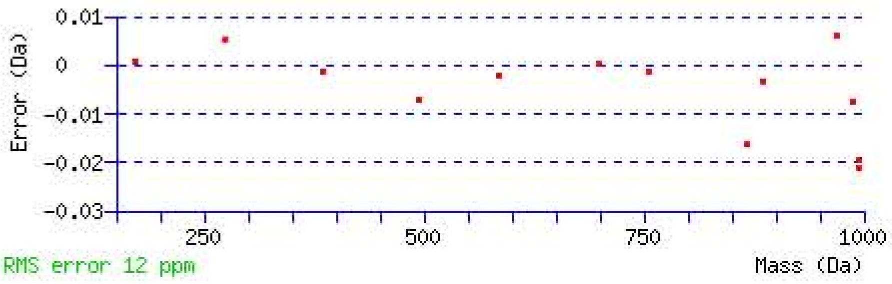
Match to Query 16414: 1156.587208 from(579.300880,2+) rtinseconds(1457) index(28526)
Title: Locus:1.1.1.3170.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

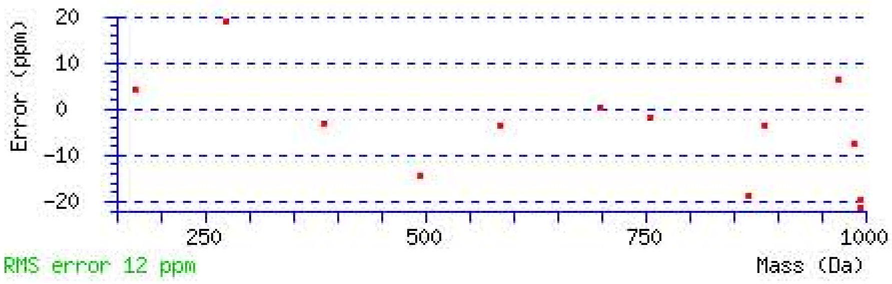
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 25  Expect: 0.013
Matches : 13/70 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							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
25.1	1156.591034	-0.003826	GNTEGLQK
4.7	1156.572418	0.014790	GPQTSTSPASPK
0.5	1156.598923	-0.011715	GDRGGPGIPGFK

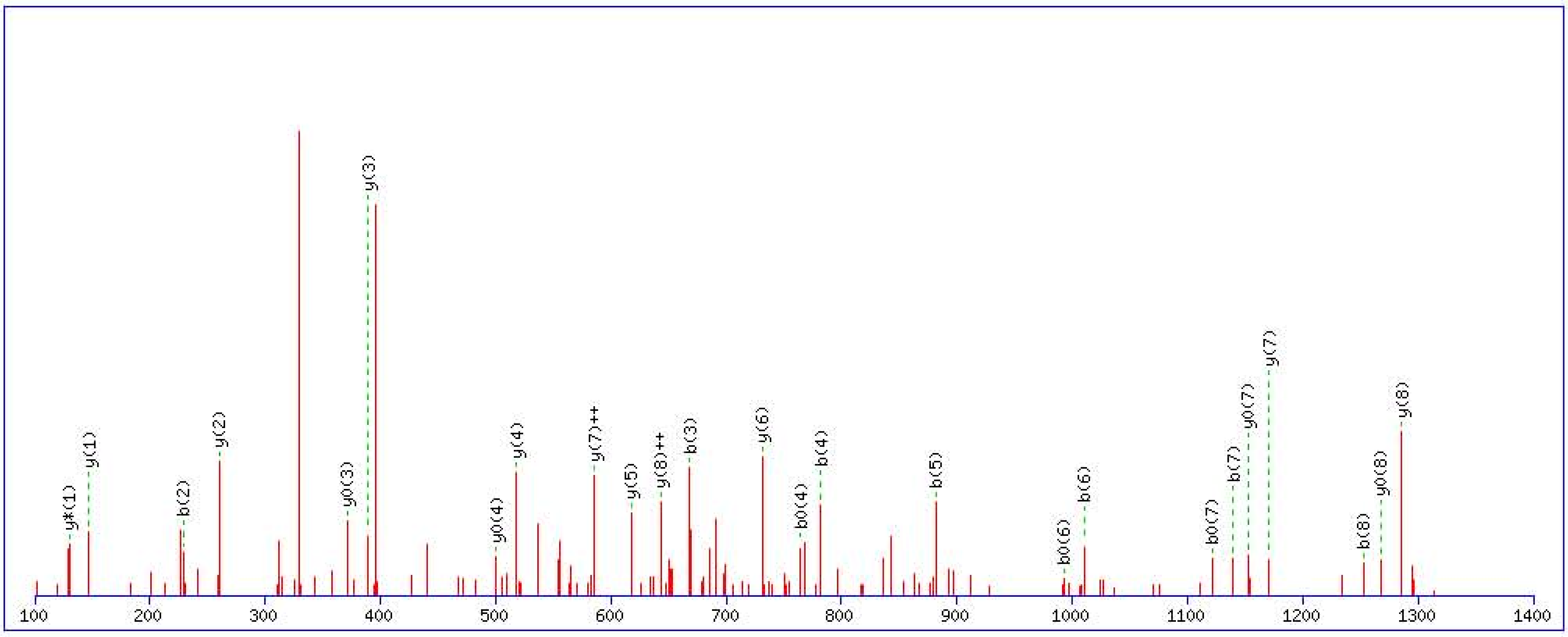
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

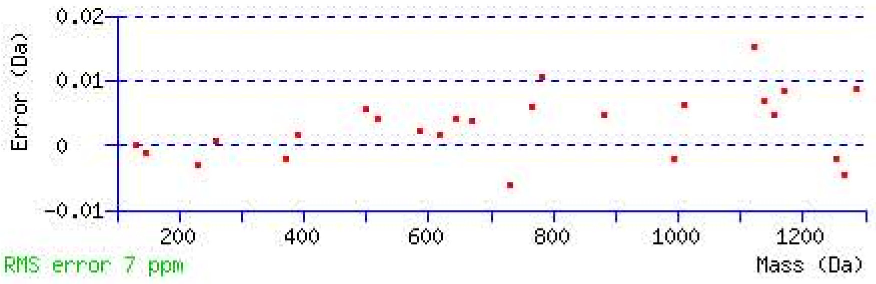
Match to Query 23553: 1397.716908 from(699.865730,2+) rtinseconds(1840) index(59630)
Title: Locus:1.1.1.1552.11 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

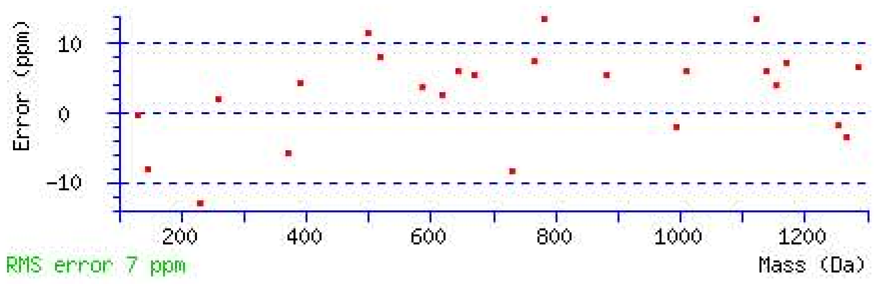
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1397.722427
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 43 **Expect:** 0.00037
Matches : 25/86 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					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
43.0	1397.722427	-0.005519	IDQNVEELK
6.0	1397.733688	-0.016780	LCDVTLKIGDHK
4.9	1397.737686	-0.020778	MYLNFLVSLGNK
4.7	1397.722412	-0.005504	QLEAQLEEK
4.5	1397.701309	0.015599	LLFNFVEQNMK
3.8	1397.737686	-0.020778	LKEFCGEFLKK
3.6	1397.715897	0.001011	IKSADKMPPMHK
3.6	1397.733658	-0.016750	QNITNQLEK
3.1	1397.715897	0.001011	IKSADKMPPMHK
3.0	1397.704651	0.012257	QLEKQMYSIMK

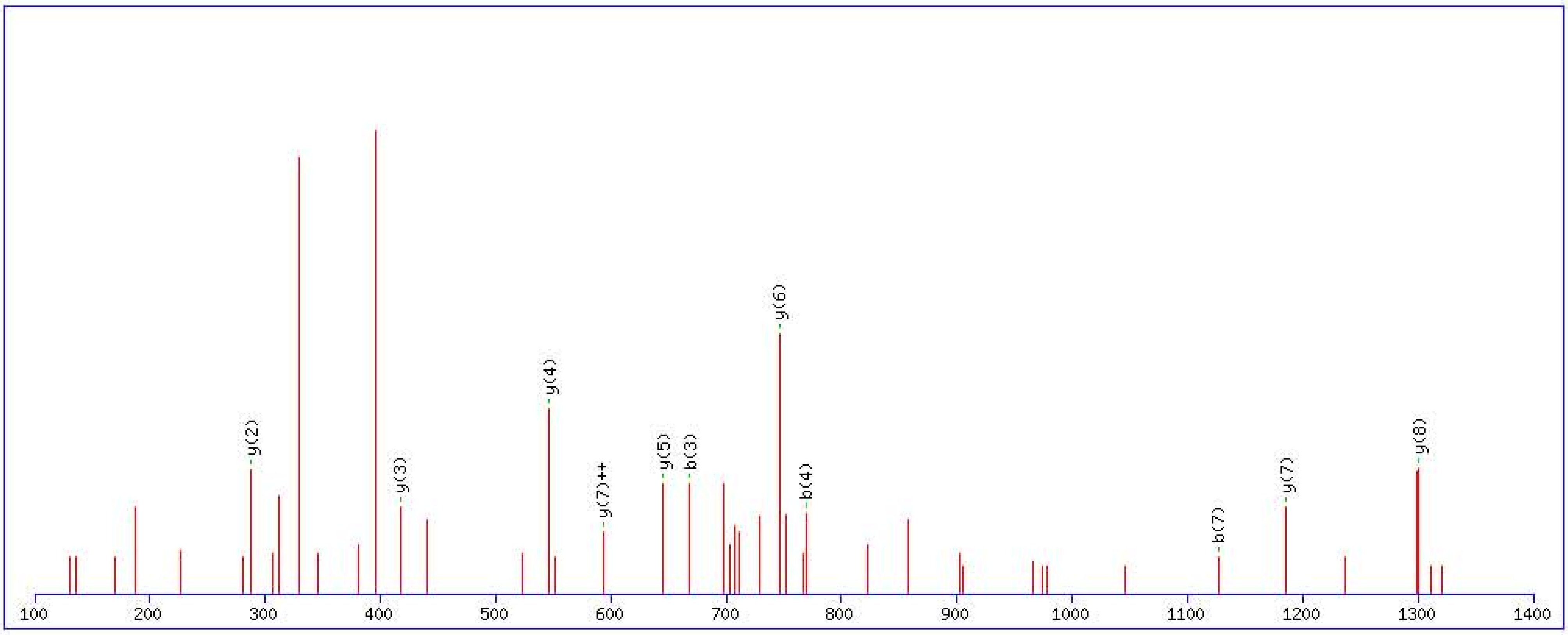
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

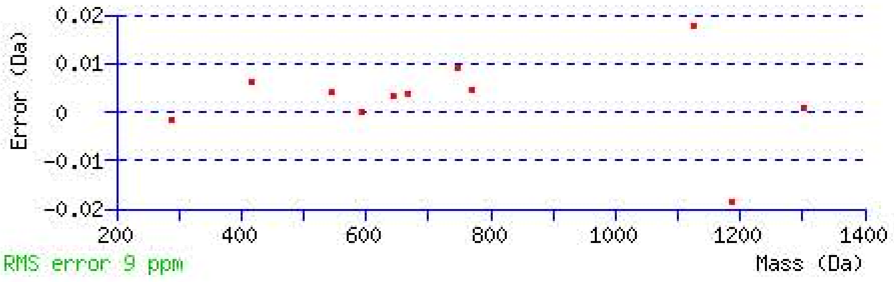
Match to Query 24506: 1412.724508 from(707.369530,2+) rtinseconds(1926) index(18540)
Title: Locus:1.1.1.3236.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

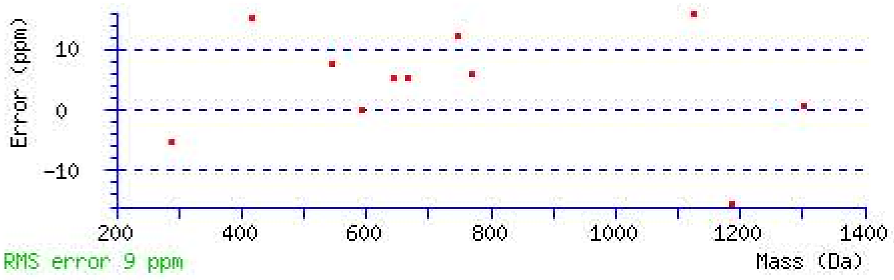
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1412.733337
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.00095
Matches : 11/86 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	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
35.9	1412.733337	-0.008829	IDQTVEELR
3.5	1412.744537	-0.020029	IPPEKMRELER
1.1	1412.708191	0.016317	LQESASGTGPR
1.1	1412.737167	-0.012659	HSESVKTERNVK

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

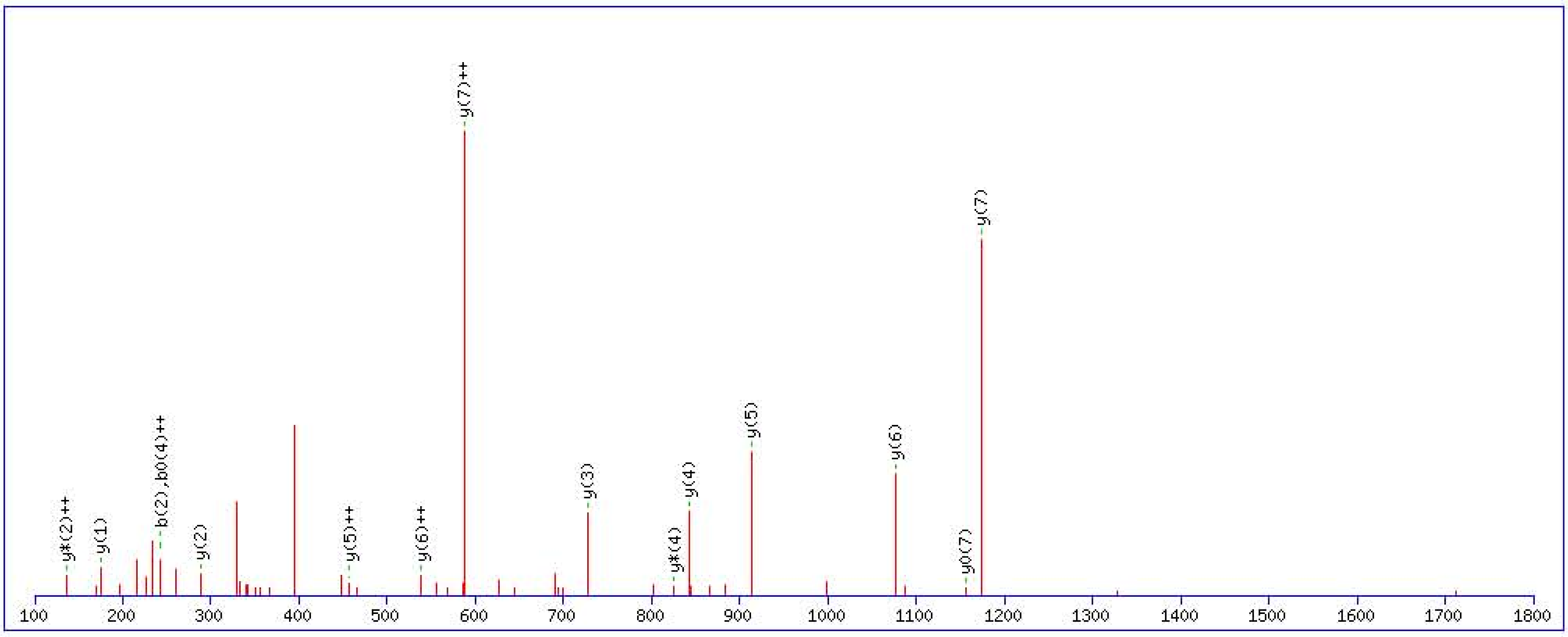
Mascot Search Results

Peptide View

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

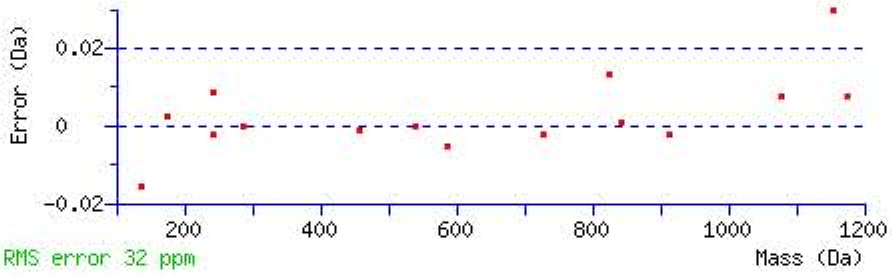
Match to Query 24541: 1414.720868 from(708.367710,2+) rtinseconds(2004) index(31924)
Title: Locus:1.1.1.3361.21 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

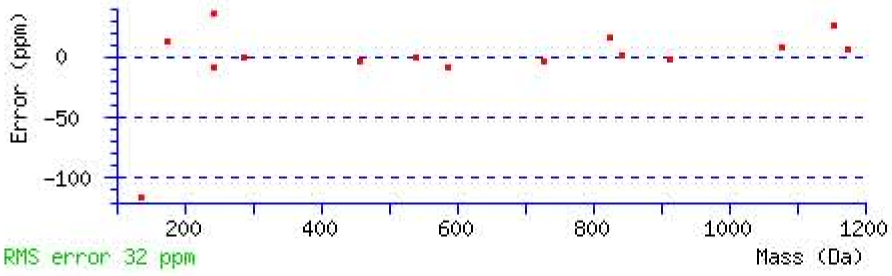
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1414.727844
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 32 **Expect:** 0.0032
Matches : 15/76 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	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
32.0	1414.727844	-0.006976	LEPYADQLR
5.1	1414.735931	-0.015063	LMRGLLHCMIR
3.0	1414.712585	0.008283	EISTEEQLR
1.3	1414.741547	-0.020679	EIEENQKRIEK
1.0	1414.741577	-0.020709	ELDVEVSRLEAR
0.7	1414.717789	0.003079	GKGAAGGSWQQRGR

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

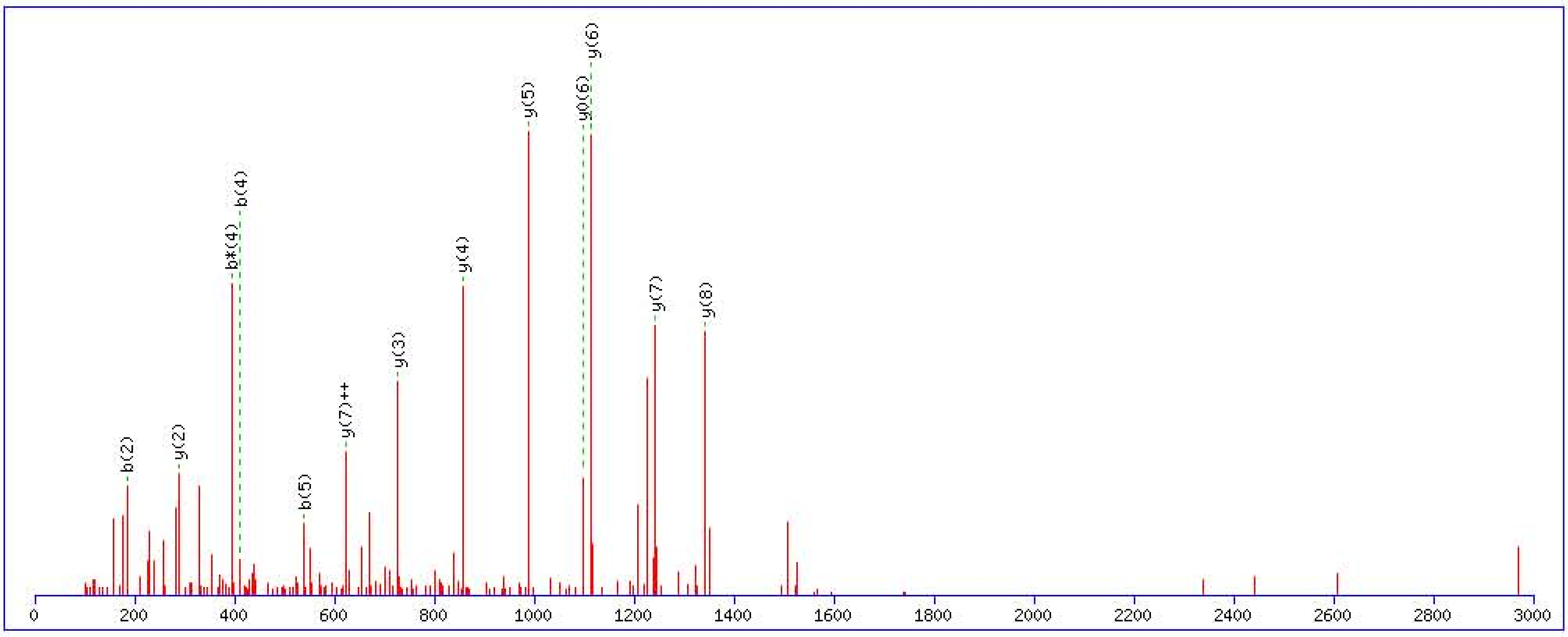
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

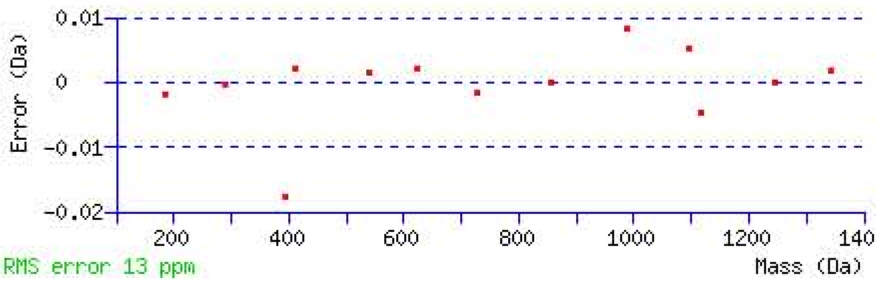
Match to Query 28010: 1525.807328 from(763.910940,2+) rtinseconds(2124) index(32592)
Title: Locus:1.1.1.3403.4 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

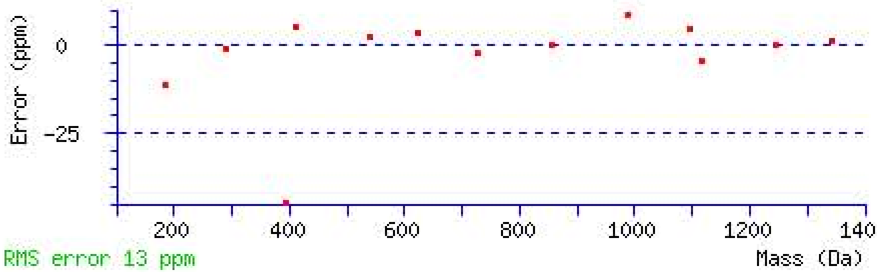
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1525.810867
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 62 **Expect:** 1.9e-005
Matches : 13/84 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							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
61.8	1525.810867	-0.003539	ALVQQMEQLR
19.9	1525.810867	-0.003539	ALVQQMEQLR
14.1	1525.792236	0.015092	ALTEQQEQLR
9.9	1525.798752	0.008576	SPVKEEEKPQEVK
7.2	1525.803467	0.003861	SPPSPRSSMAAVALR
6.9	1525.810867	-0.003539	ALVQQMEQLR
5.9	1525.784836	0.022492	LAQVATEEPERQR
5.4	1525.814697	-0.007369	ERQRTEQLR
5.0	1525.800064	0.007264	ARALQSYYEAKAR
4.0	1525.807495	-0.000167	WPPQQLMLSAALR

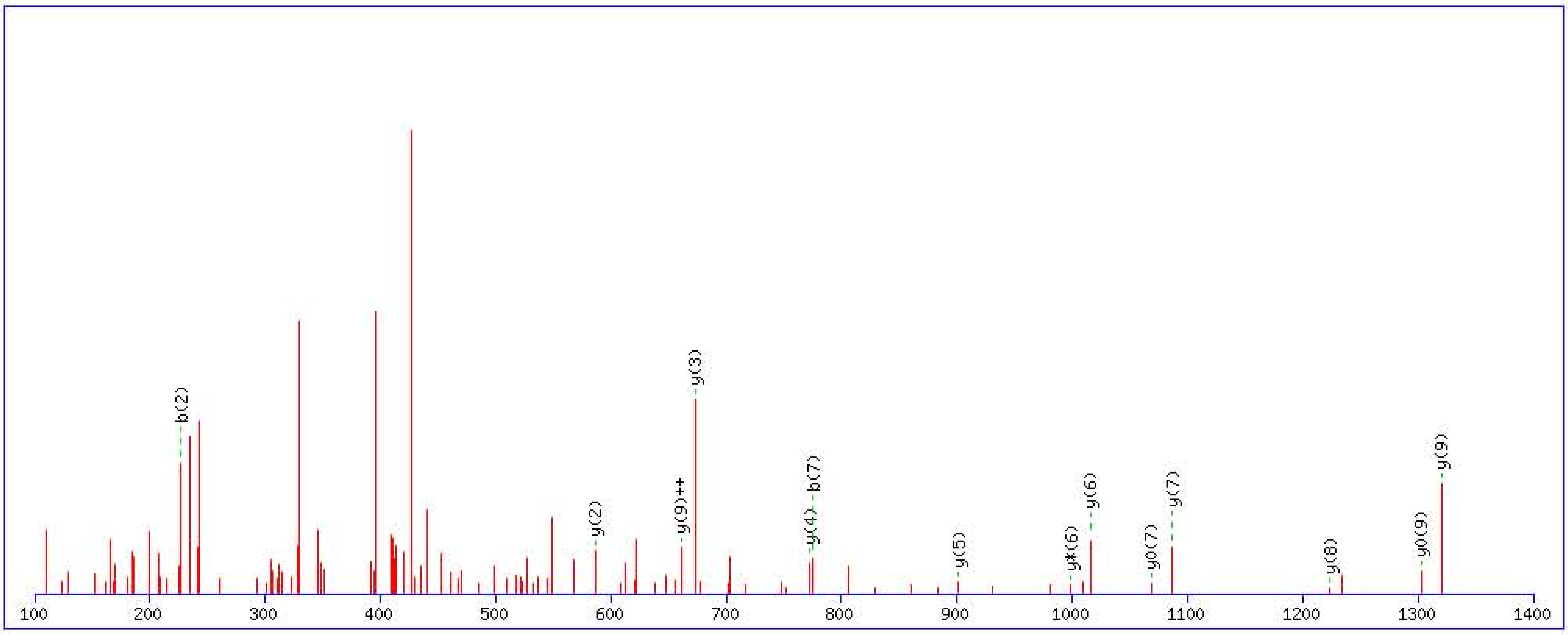
Mascot Search Results

Peptide View

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

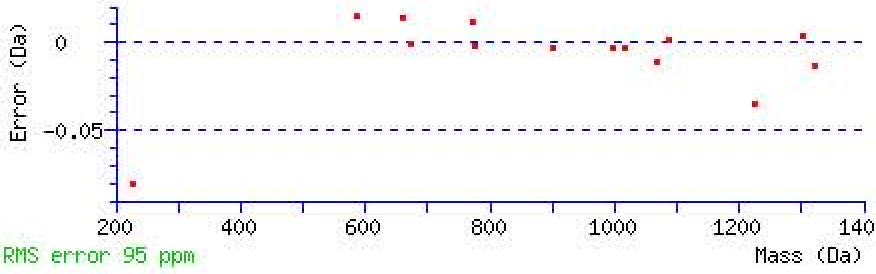
Match to Query 28428: 1545.828432 from(516.283420,3+) rtinseconds(1553) index(58246)
Title: Locus:1.1.1.1452.7 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

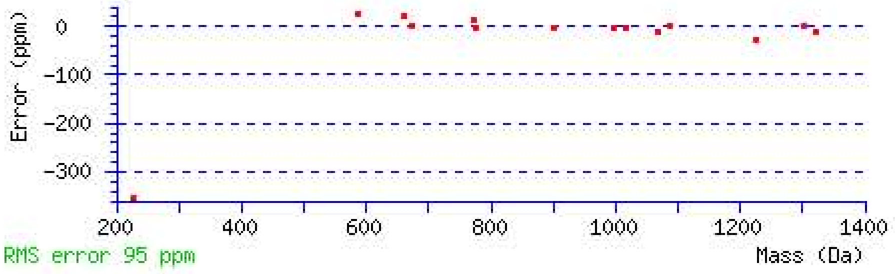
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1545.833710
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0092
Matches : 14/94 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					L							11
2	**227.175404**	114.091340					L	1433.756946	717.382111	1416.730397	708.868837	1415.746381	708.376828	10
3	324.228168	162.617722					P	***1320.672882***	660.840079	1303.646333	652.326804	1302.662317	651.834796	9
4	461.287080	231.147178					H	***1223.620118***	612.313697	1206.593569	603.800422	1205.609553	603.308414	8
5	532.324194	266.665735					A	***1086.561206***	543.784241	1069.534657	535.270966	1068.550641	534.778958	7
6	646.367121	323.687199	629.340572	315.173924			N	***1015.524092***	508.265684	998.497543	499.752409	997.513527	499.260401	6
7	**775.409714**	388.208495	758.383165	379.695221	757.399149	379.203213	E	***901.481165***	451.244220	884.454616	442.730946	883.470600	442.238938	5
8	874.478128	437.742702	857.451579	429.229427	856.467563	428.737419	V	***772.438572***	386.722924	755.412023	378.209649	754.428007	377.717641	4
9	961.510156	481.258716	944.483607	472.745441	943.499591	472.253433	S	***673.370158***	337.188717	656.343609	328.675442	655.359593	328.183434	3
10	1400.735482	700.871379	1383.708933	692.358104	1382.724917	691.866096	Q	***586.338130***	293.672703	569.311581	285.159428			2
11							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.7	1545.833710	-0.005278	LLPHANEVSQK

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

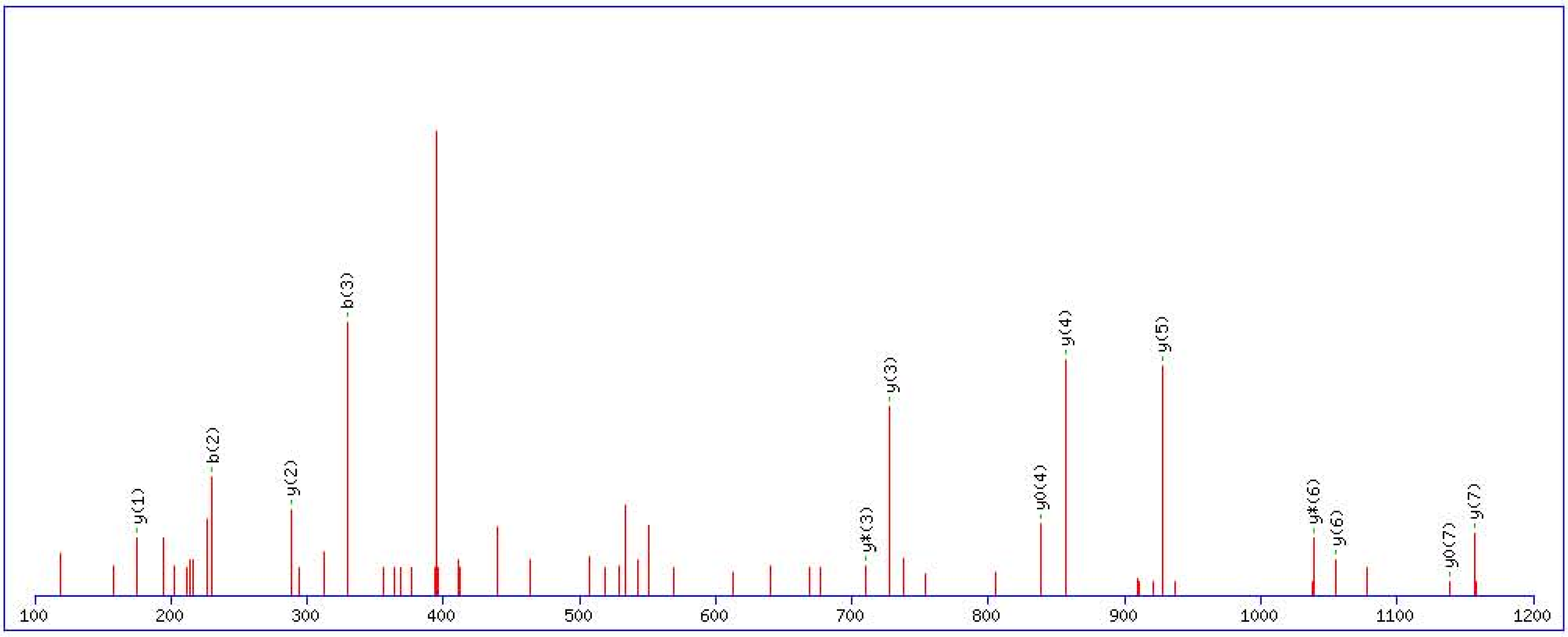
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

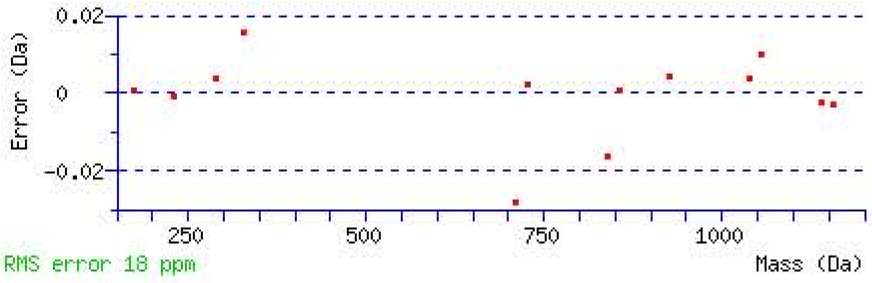
Match to Query 30518: 1597.815672 from(533.612500,3+) rtinseconds(1623) index(29572)
Title: Locus:1.1.1.3228.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

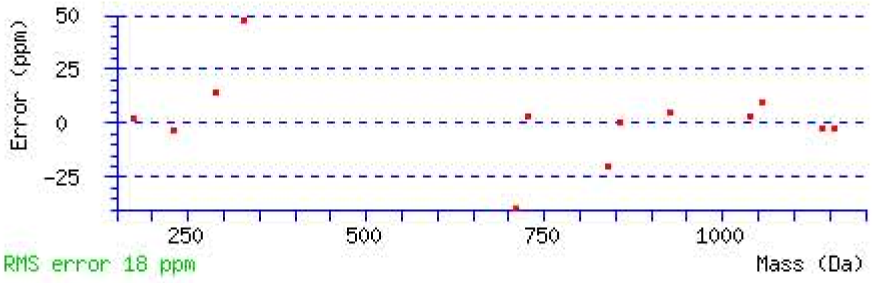
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1597.824615
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 43 **Expect:** 0.00045
Matches : 13/112 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	102.054955	51.531116			84.044390	42.525833	T							11
2	**230.113533**	115.560405	213.086984	107.047130	212.102968	106.555122	Q	1497.784225	749.395751	1480.757676	740.882476	1479.773660	740.390468	10
3	**329.181947**	165.094612	312.155398	156.581337	311.171382	156.089329	V	1369.725647	685.366462	1352.699098	676.853187	1351.715082	676.361179	9
4	443.224874	222.116075	426.198325	213.602801	425.214309	213.110793	N	1270.657233	635.832255	1253.630684	627.318980	1252.646668	626.826972	8
5	544.272553	272.639915	527.246004	264.126640	526.261988	263.634632	T	***1156.614306***	578.810791	1139.587757	570.297517	1138.603741	569.805509	7
6	672.331131	336.669204	655.304582	328.155929	654.320566	327.663921	Q	***1055.566627***	528.286951	1038.540078	519.773677	1037.556062	519.281669	6
7	743.368245	372.187761	726.341696	363.674486	725.357680	363.182478	A	***927.508049***	464.257663	910.481500	455.744388	909.497484	455.252380	5
8	872.410838	436.709057	855.384289	428.195783	854.400273	427.703775	E	***856.470935***	428.739106	839.444386	420.225831	838.460370	419.733823	4
9	1311.636164	656.321720	1294.609615	647.808446	1293.625599	647.316438	Q	***727.428342***	364.217809	710.401793	355.704535			3
10	1424.720228	712.863752	1407.693679	704.350478	1406.709663	703.858470	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
42.6	1597.824615	-0.008943	TQVNTQAEQLR
9.6	1597.824615	-0.008943	TQVNTQAEQLR
6.7	1597.835846	-0.020174	TKAAATAGGQGGAAR
6.3	1597.828629	-0.012957	AWDILSGEQLR
2.4	1597.797440	0.018232	RYSHGGTSWRVHR

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

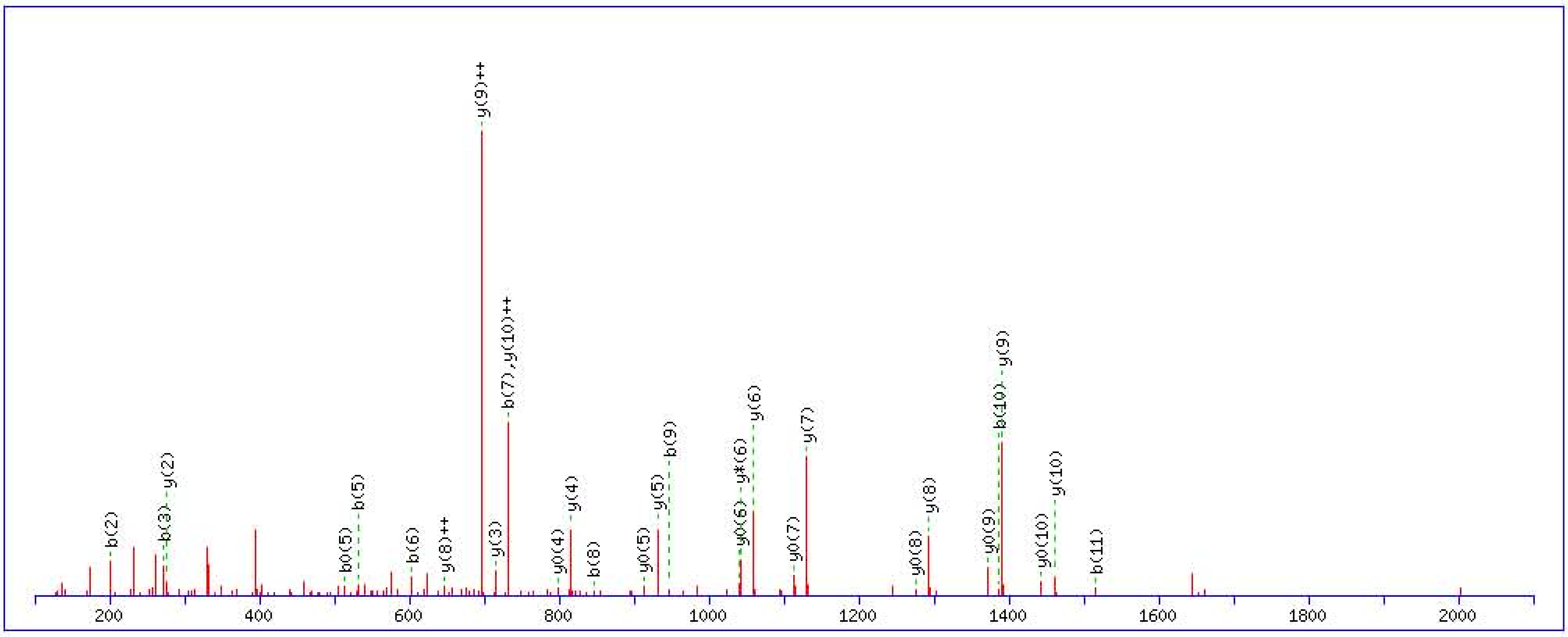
Mascot Search Results

Peptide View

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

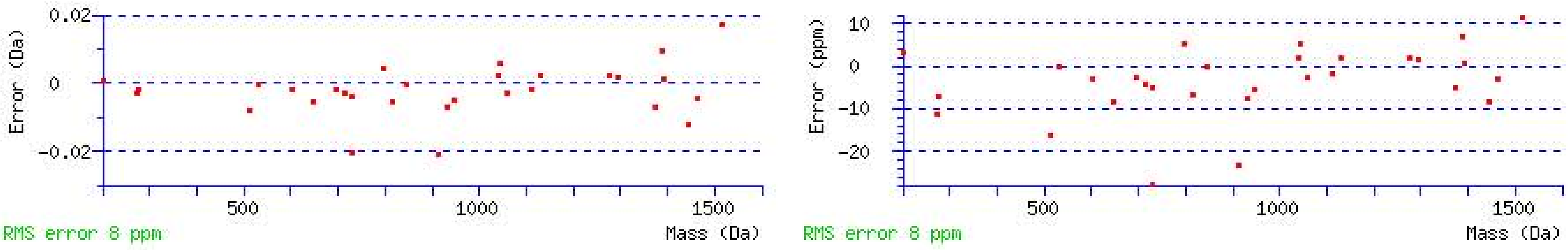
Match to Query 32905: 1660.811428 from(831.412990,2+) rtinseconds(1758) index(30321)
Title: Locus:1.1.1.3275.19 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 1660.813034
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 51   Expect: 8e-005
Matches : 30/118 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	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
51.2	1660.813034	-0.001606	SLAPYAQDTQEK
27.2	1660.813034	-0.001606	SLAPYAQDTQEK
7.3	1660.826782	-0.015354	EAATQAQQTLGSTIDK
7.1	1660.820908	-0.009480	SLARAGFYYTGVNDK
2.5	1660.813019	-0.001591	EAALMAEFDNPNIVK

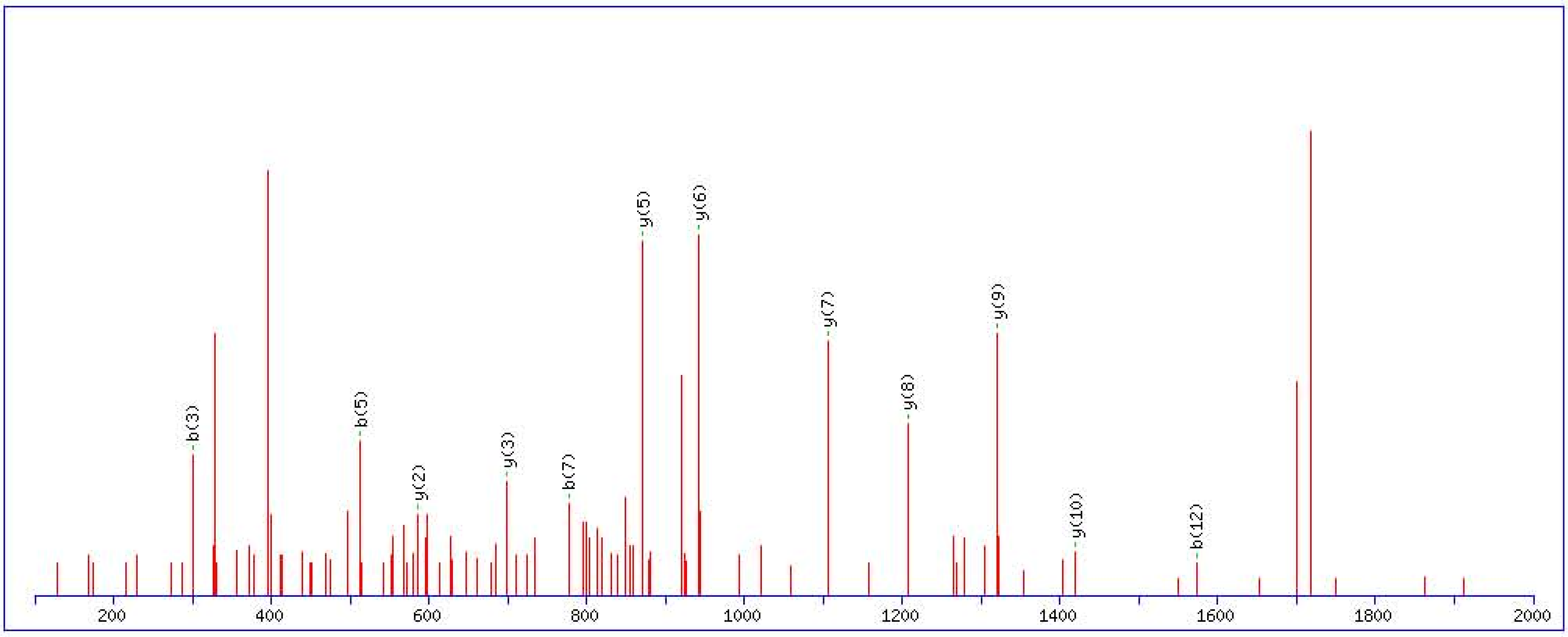
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

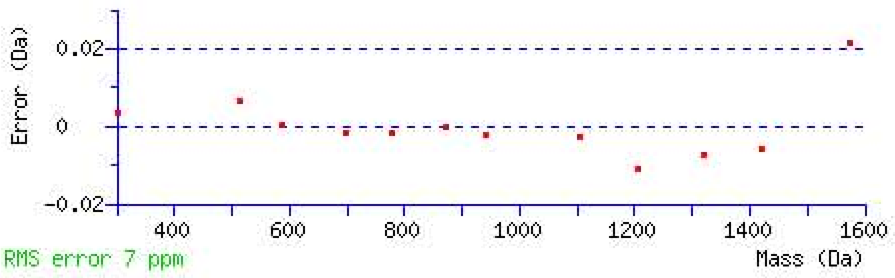
Match to Query 33995: 1717.866628 from(859.940590,2+) rtinseconds(2013) index(19147)
Title: Locus:1.1.1.3266.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

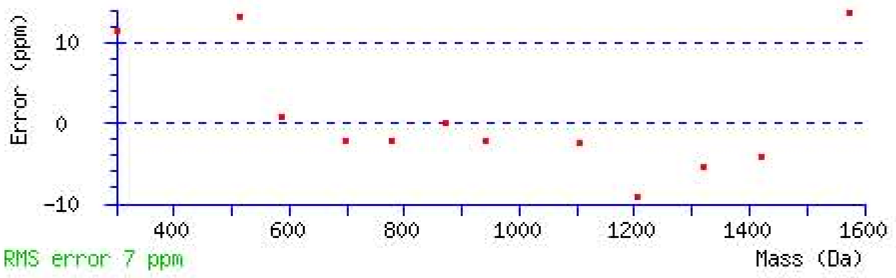


```
Monoisotopic mass of neutral peptide Mr(calc): 1717.870895
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12    : Biotin:Thermo-21345 (Q)
Ions Score: 69  Expect: 3e-006
Matches : 12/126 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	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



RMS error 7 ppm



RMS error 7 ppm

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
69.4	1717.870895	-0.004267	LGEVNTYAGDLQK
10.3	1717.866867	-0.000239	IDAVNAETIREVCTK
1.6	1717.878754	-0.012126	IDAVAWNTTPYQLAR

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

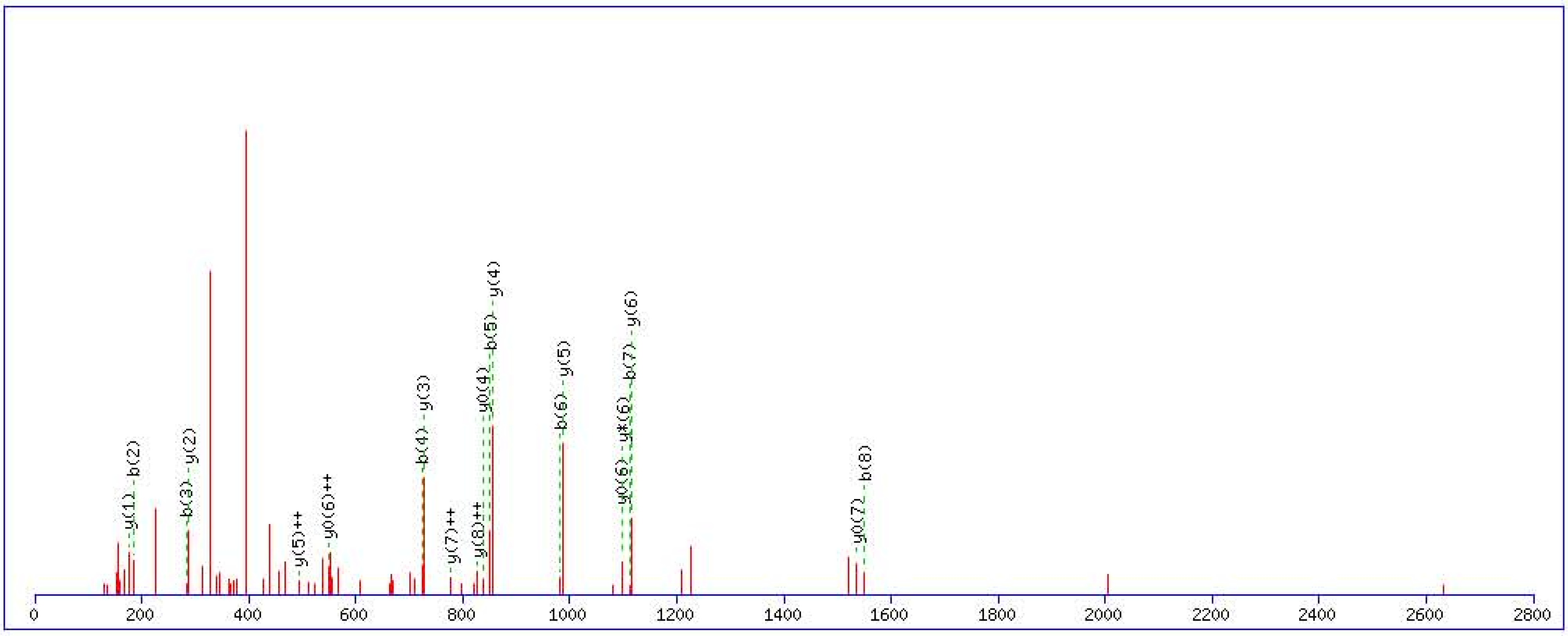
Mascot Search Results

Peptide View

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

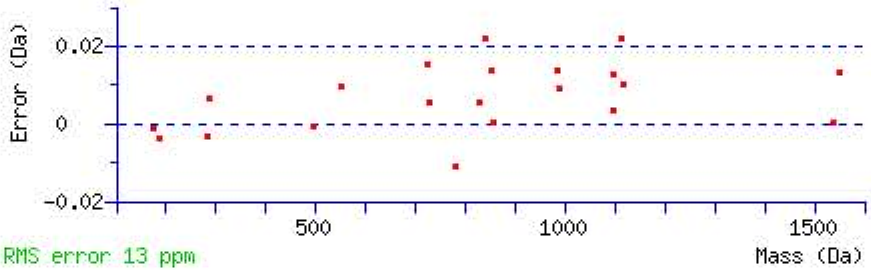
Match to Query 36409: 1836.980232 from(613.334020,3+) rtinseconds(2353) index(62445)
Title: Locus:1.1.1.1731.3 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

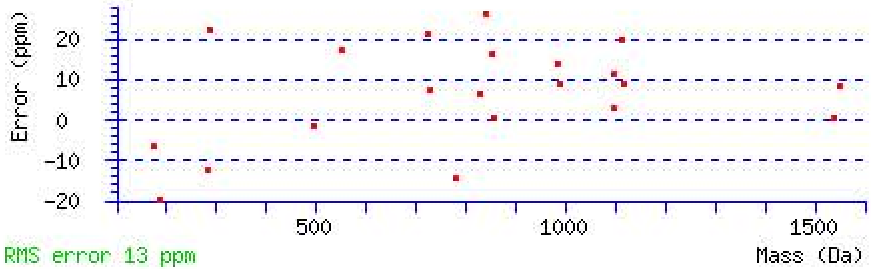
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1836.977615
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.019
Matches : 21/84 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							10
2	***185.128454***	93.067865					L	1766.947802	883.977539	1749.921253	875.464265	1748.937237	874.972256	9
3	***284.196868***	142.602072					V	1653.863738	827.435507	1636.837189	818.922232	1635.853173	818.430224	8
4	***723.422194***	362.214735	706.395645	353.701461			Q	1554.795324	777.901300	1537.768775	769.388026	1536.784759	768.896017	7
5	***851.480772***	426.244024	834.454223	417.730750			Q	***1115.569998***	558.288637	1098.543449	549.775363	1097.559433	549.283354	6
6	***982.521257***	491.764267	965.494708	483.250992			M	***987.511420***	494.259348	970.484871	485.746073	969.500855	485.254065	5
7	***1111.563850***	556.285563	1094.537301	547.772289	1093.553285	547.280281	E	***856.470935***	428.739105	839.444386	420.225831	838.460370	419.733823	4
8	***1550.789176***	775.898226	1533.762627	767.384952	1532.778611	766.892944	Q	***727.428342***	364.217809	710.401793	355.704534			3
9	1663.873240	832.440258	1646.846691	823.926984	1645.862675	823.434975	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
29.0	1836.977615	0.002617	ALVQQMEQLR
19.4	1836.977615	0.002617	ALVQQMEQLR
10.0	1836.999207	-0.018975	QQSLQRQLEQLR
5.8	1837.004578	-0.024346	RHSWRQQIFLR
2.2	1836.977615	0.002617	ALVQQMEQLR
0.1	1836.958984	0.021248	ALTEQQEQLR
0.1	1836.958984	0.021248	ALTEQQEQLR

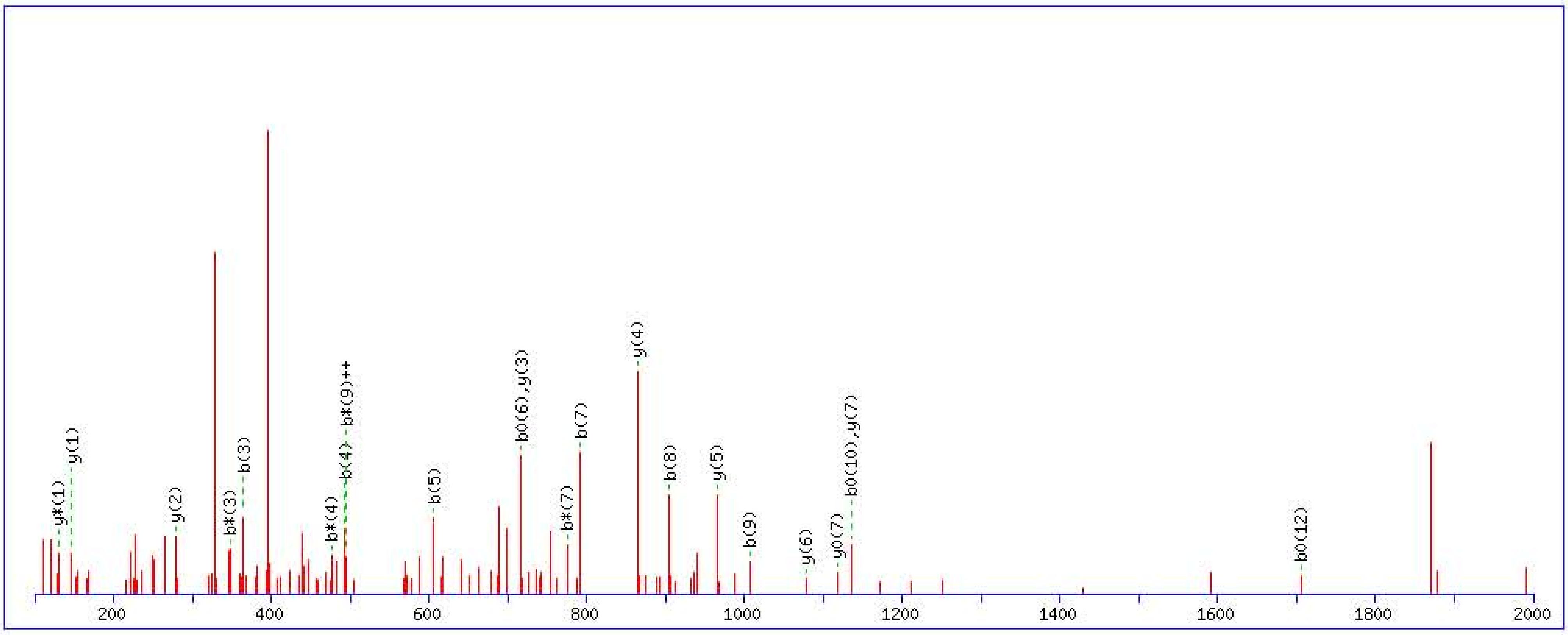
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

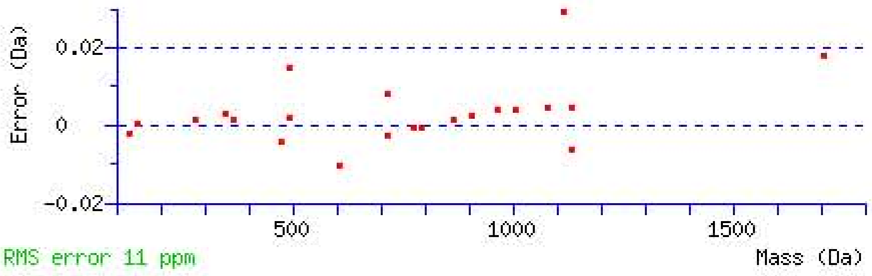
Match to Query 37009: 1868.960952 from(623.994260,3+) rtinseconds(2172) index(32869)
Title: Locus:1.1.1.3420.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

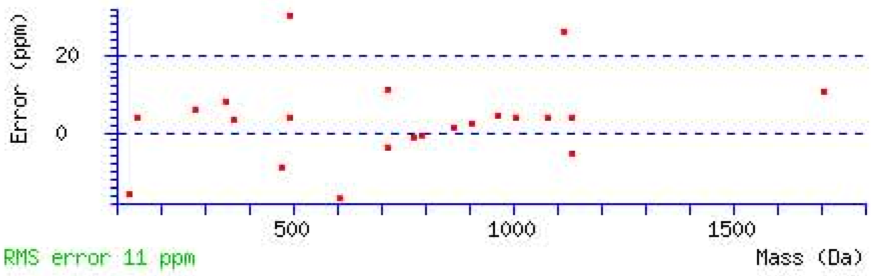
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1868.964081
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.015
Matches : 22/124 fragment ions using 45 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
32.4	1868.964081	-0.003129	LNHQLEGLTFQMK

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

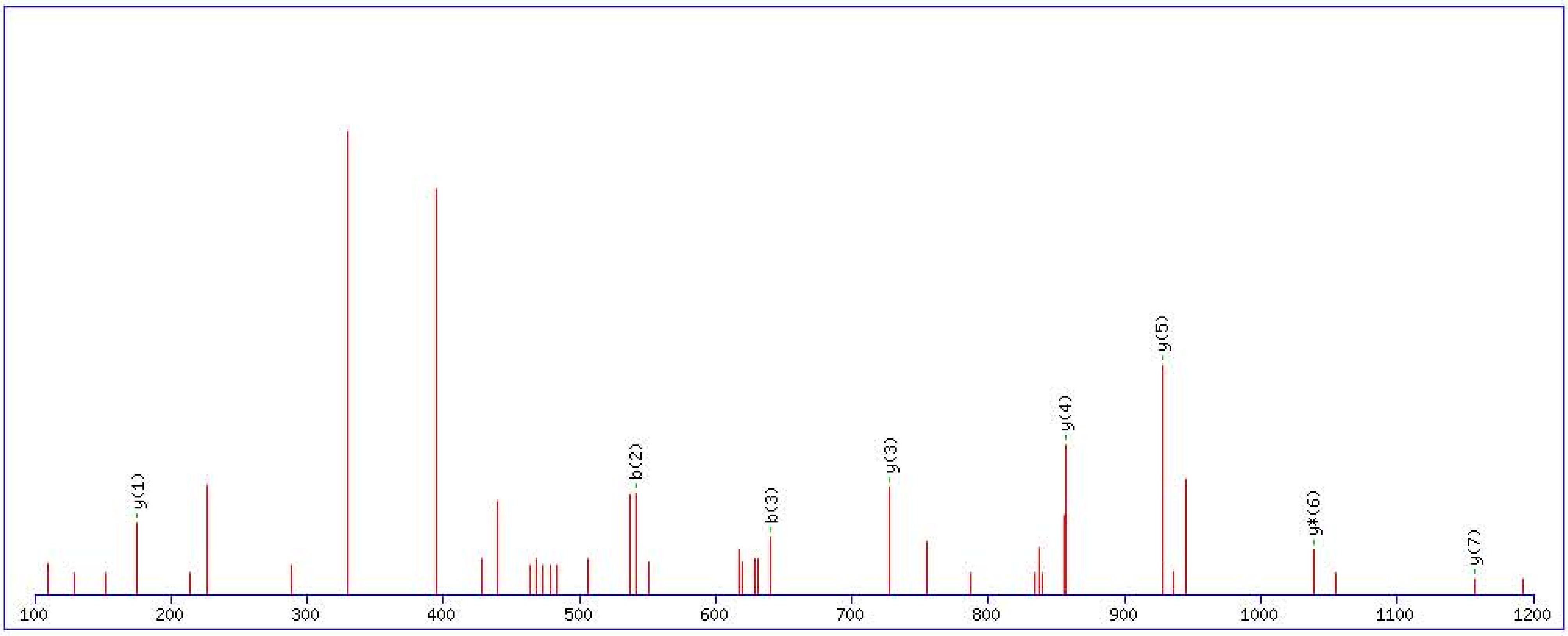
Mascot Search Results

Peptide View

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

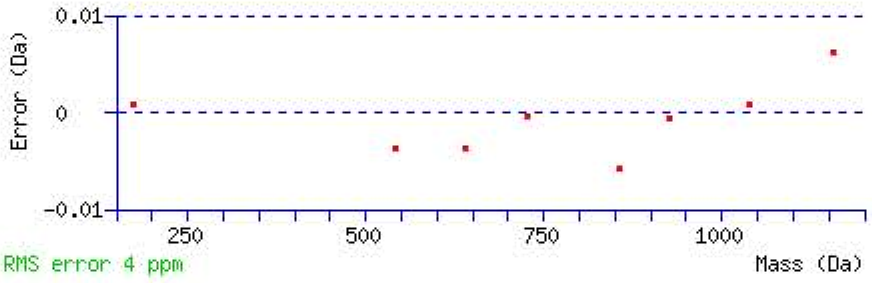
Match to Query 37579: 1908.985362 from(637.335730,3+) rtinseconds(1949) index(31461)
Title: Locus:1.1.1.3342.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

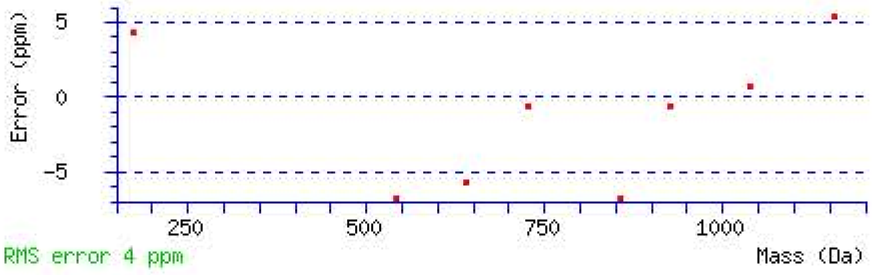
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 30  Expect: 0.0027
Matches : 8/112 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	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
29.7	1908.991364	-0.006002	TQVNTQAEQLR
15.7	1908.991364	-0.006002	TQVNTQAEQLR
8.3	1908.991364	-0.006002	TQVNTQAEQLR
2.3	1908.974045	0.011317	SAQWAINRVAMEIQHR

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

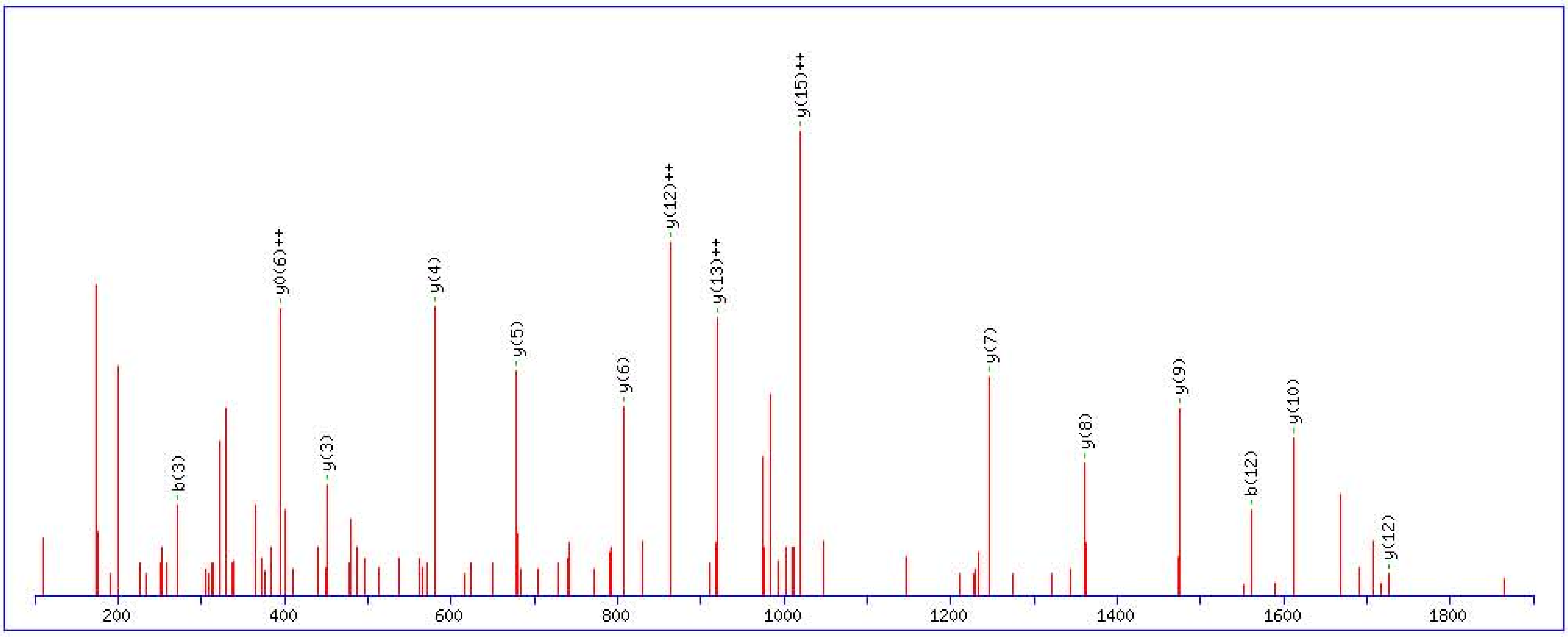
MATRIX SCIENCE Mascot Search Results

Peptide View

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

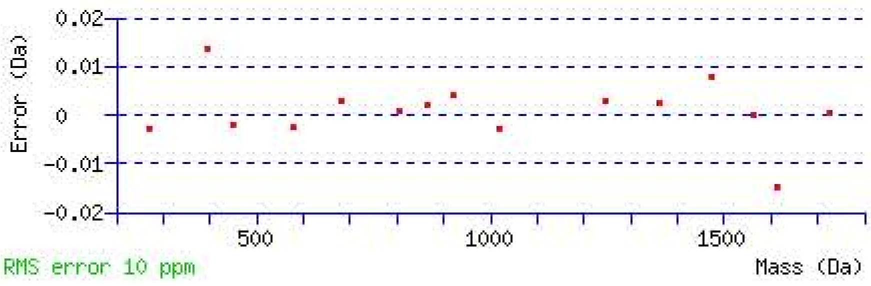
Match to Query 43906: 2238.107292 from(747.043040,3+) rtinseconds(2262) index(33454)
Title: Locus:1.1.1.3451.19 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

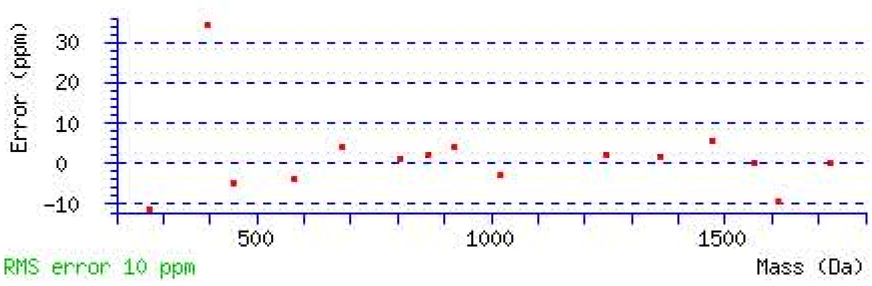
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2238.110291
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 72  Expect: 1.6e-006
Matches : 15/168 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							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
72.3	2238.110291	-0.002999	SLAELGGHLDQQVEEFR
54.5	2238.110291	-0.002999	SLAELGGHLDQQVEEFR

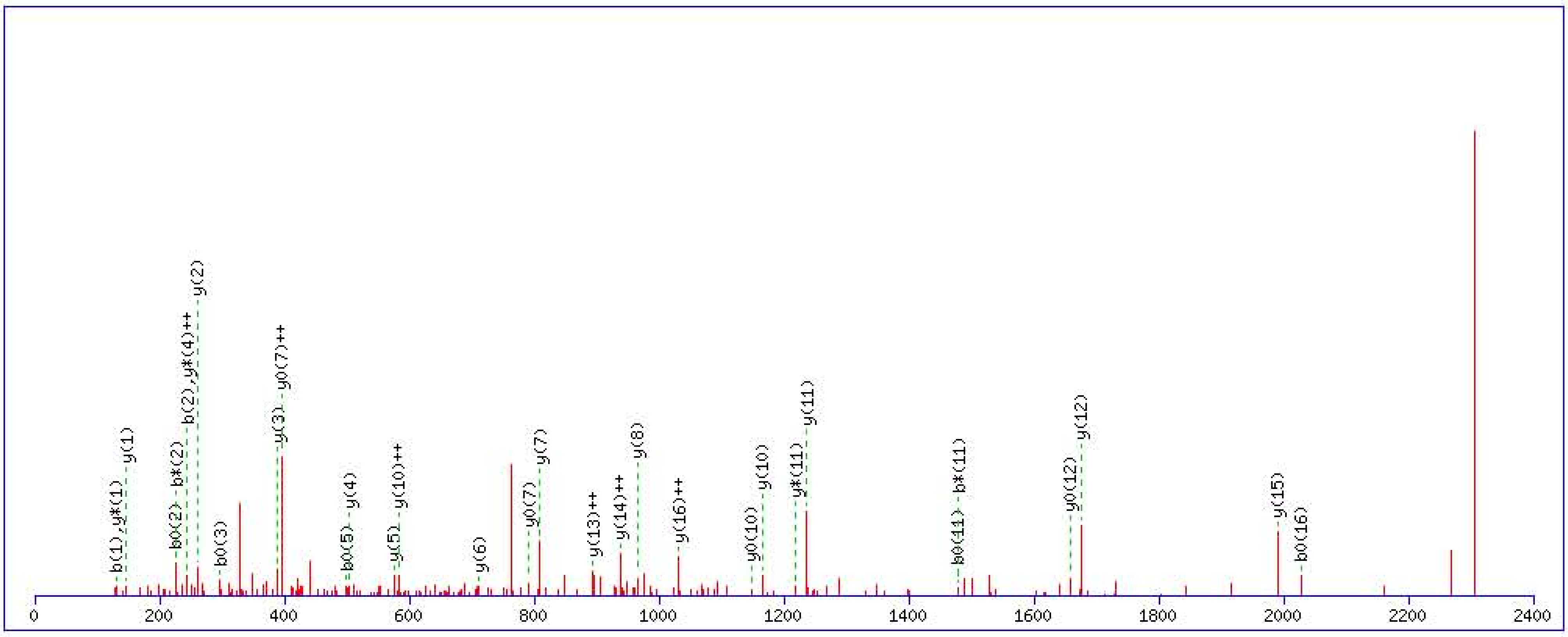
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

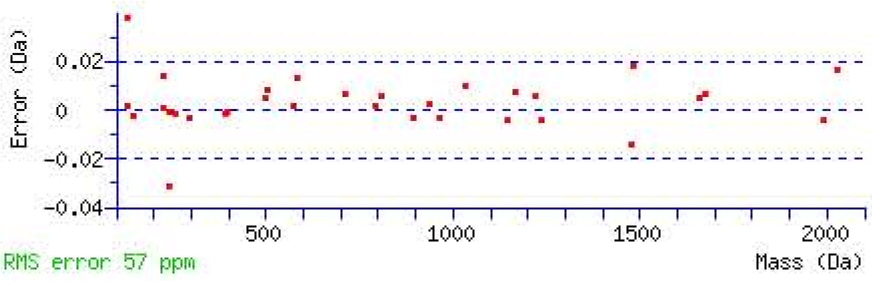
Match to Query 45156: 2304.165372 from(769.062400,3+) rtinseconds(1904) index(59894)
Title: Locus:1.1.1.1574.17 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

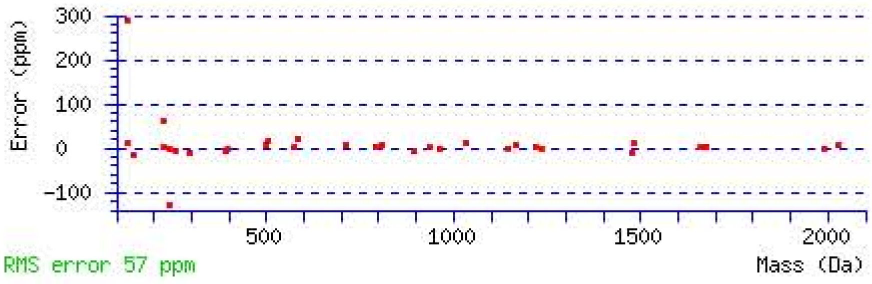
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2304.153183
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.0026
Matches : 32/198 fragment ions using 90 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							18
2	**244.092796**	122.550036	227.066247	114.036762	226.082231	113.544754	N	2176.117913	1088.562594	2159.091364	1080.049320	2158.107348	1079.557312	17
3	315.129910	158.068593	298.103361	149.555319	297.119345	149.063311	A	2062.074986	1031.541131	2045.048437	1023.027856	2044.064421	1022.535848	16
4	430.156853	215.582065	413.130304	207.068790	412.146288	206.576782	D	***1991.037872***	996.022574	1974.011323	987.509300	1973.027307	987.017292	15
5	517.188881	259.098079	500.162332	250.584804	499.178316	250.092796	S	1876.010929	938.509103	1858.984380	929.995828	1858.000364	929.503820	14
6	630.272945	315.640111	613.246396	307.126836	612.262380	306.634828	L	1788.978901	894.993089	1771.952352	886.479814	1770.968336	885.987806	13
7	1069.498271	535.252774	1052.471722	526.739499	1051.487706	526.247491	Q	***1675.894837***	838.451057	1658.868288	829.937782	1657.884272	829.445774	12
8	1140.535385	570.771331	1123.508836	562.258056	1122.524820	561.766048	A	***1236.669511***	618.838394	1219.642962	610.325119	1218.658946	609.833111	11
9	1227.567413	614.287345	1210.540864	605.774070	1209.556848	605.282062	S	***1165.632397***	583.319837	1148.605848	574.806562	1147.621832	574.314554	10
10	1340.651477	670.829377	1323.624928	662.316102	1322.640912	661.824094	L	1078.600369	539.803823	1061.573820	531.290548	1060.589804	530.798540	9
11	1496.752588	748.879932	1479.726039	740.366658	1478.742023	739.874650	R	***965.516305***	483.261791	948.489756	474.748516	947.505740	474.256508	8
12	1593.805352	797.406314	1576.778803	788.893040	1575.794787	788.401032	P	***809.415194***	405.211235	792.388645	396.697961	791.404629	396.205953	7
13	1730.864264	865.935770	1713.837715	857.422496	1712.853699	856.930488	H	***712.362430***	356.684853	695.335881	348.171579	694.351865	347.679571	6
14	1801.901378	901.454327	1784.874829	892.941053	1783.890813	892.449045	A	***575.303518***	288.155397	558.276969	279.642123	557.292953	279.150115	5
15	1916.928321	958.967799	1899.901772	950.454524	1898.917756	949.962516	D	***504.266404***	252.636840	487.239855	244.123566	486.255839	243.631558	4
16	2045.970914	1023.489095	2028.944365	1014.975821	2027.960349	1014.483813	E	***389.239461***	195.123369	372.212912	186.610094	371.228896	186.118086	3
17	2159.054978	1080.031127	2142.028429	1071.517852	2141.044413	1071.025844	L	***260.196868***	130.602072	243.170319	122.088798			2
18							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ENADSLQASLRPHADELK
(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	2304.153183	0.012189	ENADSLQASLRPHADELK

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

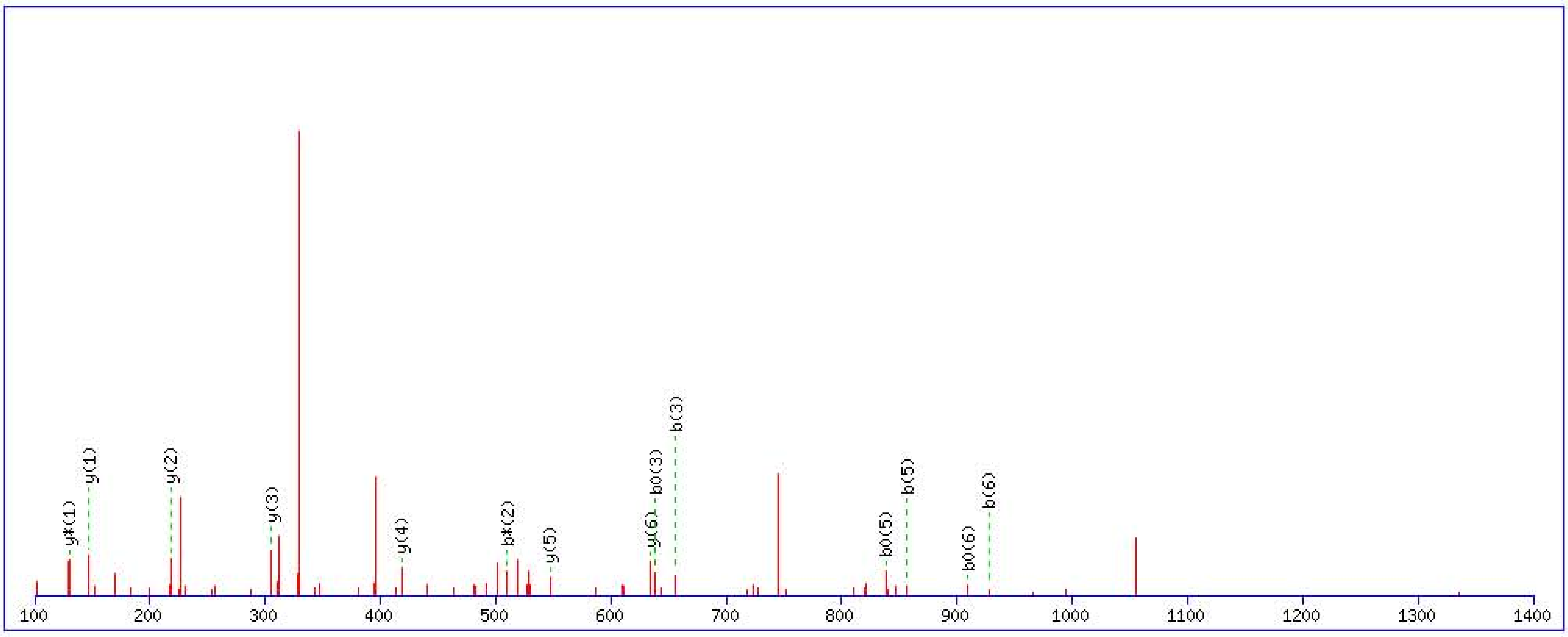
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QSELSAK**
Found in **APOC1_HUMAN**, Apolipoprotein C-I OS=Homo sapiens GN=APOC1 PE=1 SV=1

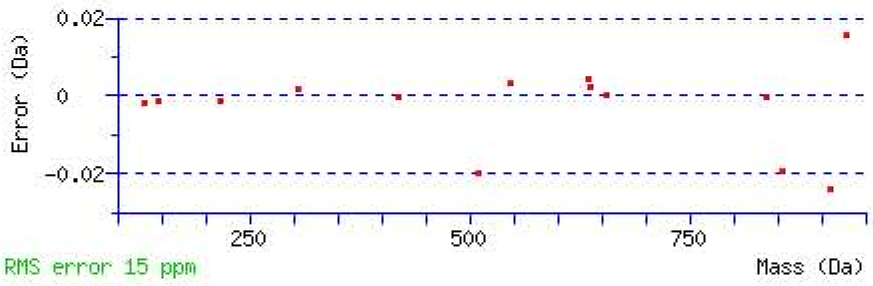
Match to Query 13355: 1072.552048 from(537.283300,2+) rtinseconds(1456) index(57702)
Title: Locus:1.1.1.1418.7 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

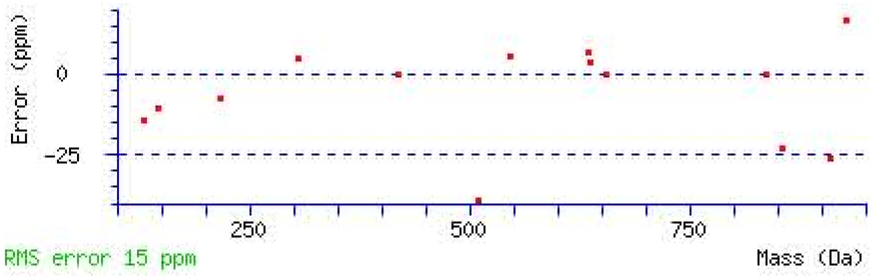
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1072.558655
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.05
Matches : 14/66 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	440.232602	220.619939	423.206053	212.106664			Q							7
2	527.264630	264.135953	510.238081	255.622679	509.254065	255.130671	S	***634.340631***	317.673954	617.314082	309.160679	616.330066	308.668671	6
3	**656.307223**	328.657250	639.280674	320.143975	638.296658	319.651967	E	***547.308603***	274.157940	530.282054	265.644665	529.298038	265.152657	5
4	769.391287	385.199282	752.364738	376.686007	751.380722	376.193999	L	***418.266010***	209.636643	401.239461	201.123368	400.255445	200.631360	4
5	**856.423315**	428.715296	839.396766	420.202021	838.412750	419.710013	S	***305.181946***	153.094611	288.155397	144.581336	287.171381	144.089328	3
6	**927.460429**	464.233853	910.433880	455.720578	909.449864	455.228570	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 QSELSAK
(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	1072.558655	-0.006607	QSELSAK
16.3	1072.562500	-0.010452	HSSTSSRIAK
12.9	1072.544739	0.007309	RPGQAAGMSAK
12.0	1072.551254	0.000794	KEAPRDETK
9.9	1072.551239	0.000809	ERQEALEAK
9.1	1072.551285	0.000763	TVQQVNQEK
8.2	1072.558655	-0.006607	QSLSAEK
7.3	1072.558670	-0.006622	QSEGLTK
6.1	1072.551239	0.000809	EAERELQAK
5.8	1072.540039	0.012009	VSQVESPEAK

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

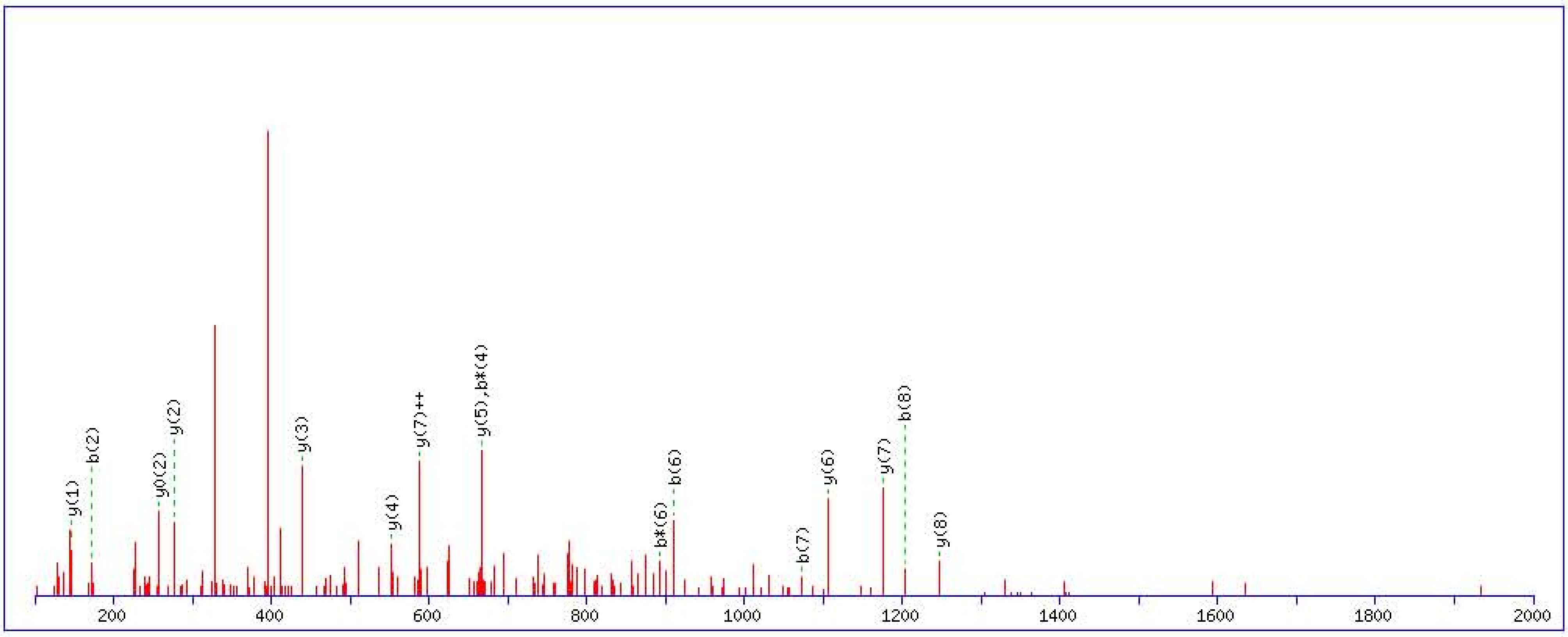
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

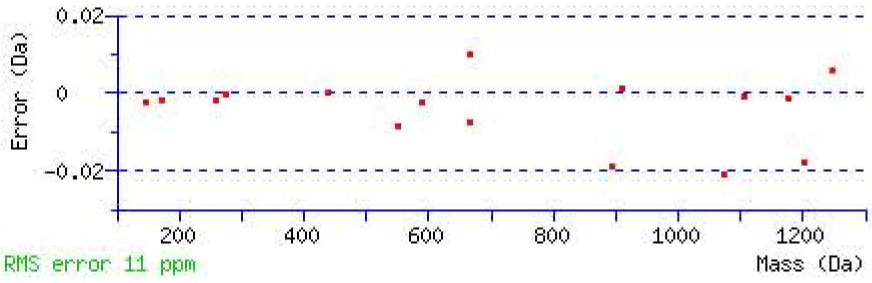
Match to Query 21287: 1347.675288 from(674.844920,2+) rtinseconds(1667) index(43965)
Title: Locus:1.1.1.3293.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

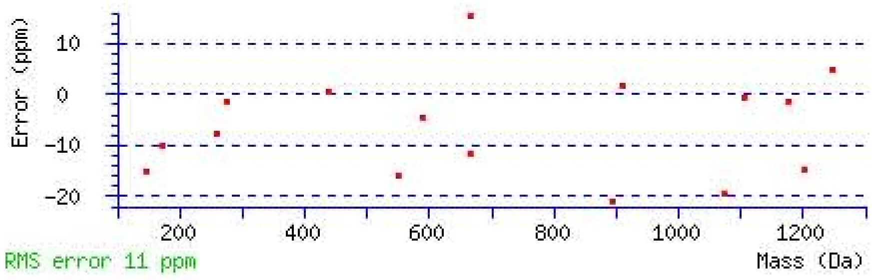
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1347.685638
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0011
Matches : 16/88 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	102.054955	51.531116			84.044390	42.525833	T							9
2	**173.092069**	87.049672			155.081504	78.044390	A	***1247.645271***	624.326273	1230.618722	615.812999	1229.634706	615.320991	8
3	244.129183	122.568229			226.118618	113.562947	A	***1176.608157***	588.807716	1159.581608	580.294442	1158.597592	579.802434	7
4	683.354509	342.180893	666.327960	333.667618	665.343944	333.175610	Q	***1105.571043***	553.289159	1088.544494	544.775885	1087.560478	544.283877	6
5	797.397436	399.202356	780.370887	390.689081	779.386871	390.197073	N	***666.345717***	333.676496	649.319168	325.163222	648.335152	324.671214	5
6	**910.481500**	455.744388	893.454951	447.231113	892.470935	446.739105	L	***552.302790***	276.655033	535.276241	268.141758	534.292225	267.649750	4
7	**1073.544829**	537.276052	1056.518280	528.762778	1055.534264	528.270770	Y	***439.218726***	220.113001	422.192177	211.599726	421.208161	211.107718	3
8	**1202.587422**	601.797349	1185.560873	593.284074	1184.576857	592.792066	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 TAAQNLYEK
(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	1347.685638	-0.010350	TAAQNLYEK
4.6	1347.682297	-0.007009	TAYFSLDTRFK
4.3	1347.681610	-0.006322	RSQISMEQLEK
2.4	1347.681641	-0.006353	QDMIVRTTQEK
2.4	1347.656464	0.018824	TALLNMDRENR
2.0	1347.660522	0.014766	GDILPNPCHTPK
1.5	1347.688156	-0.012868	LLSQDSVAASTEK
1.3	1347.667053	0.008235	EPEPPGVVGGPGEK
1.2	1347.664536	0.010752	QFWSNVEK
0.6	1347.682480	-0.007192	QSRMKMEK

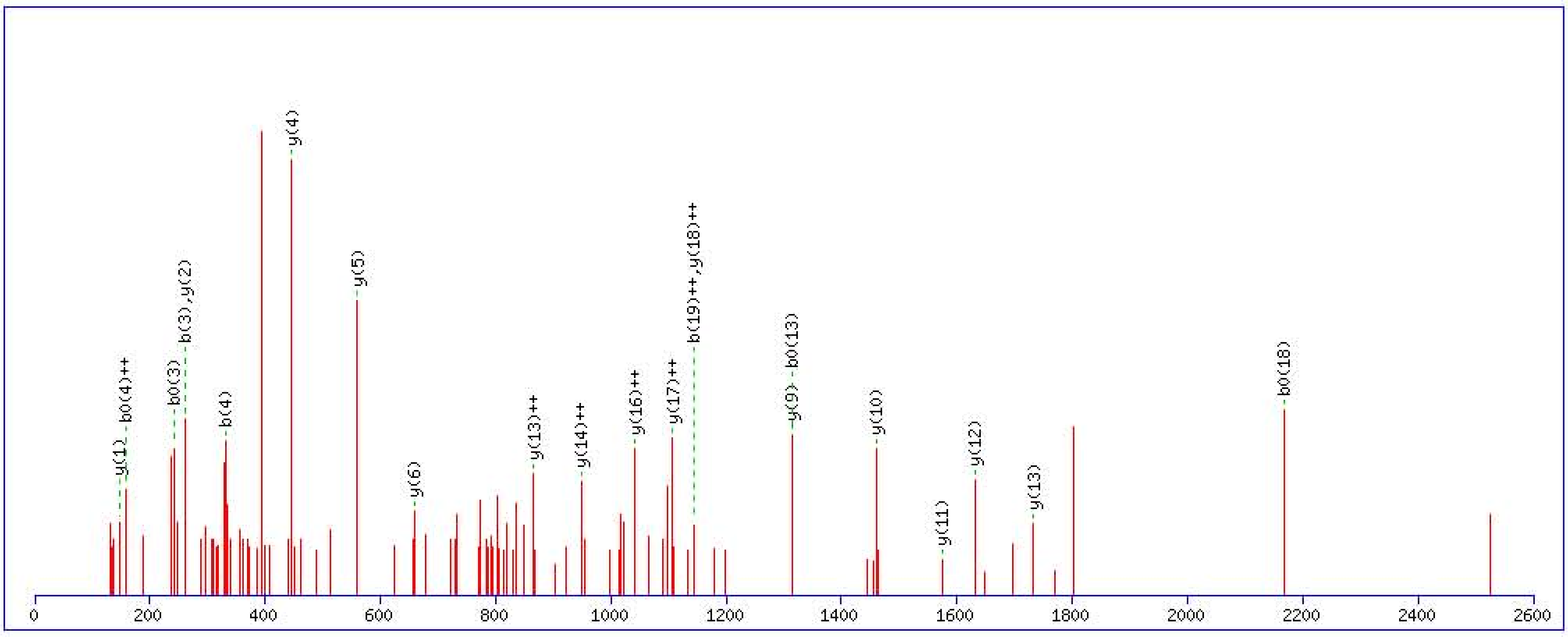
Mascot Search Results

Peptide View

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

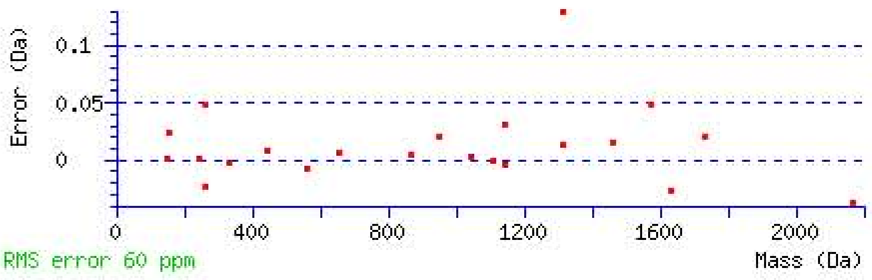
Match to Query 48992: 2543.300082 from(848.773970,3+) rtinseconds(3253) index(39529)
Title: Locus:1.1.1.3791.6 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

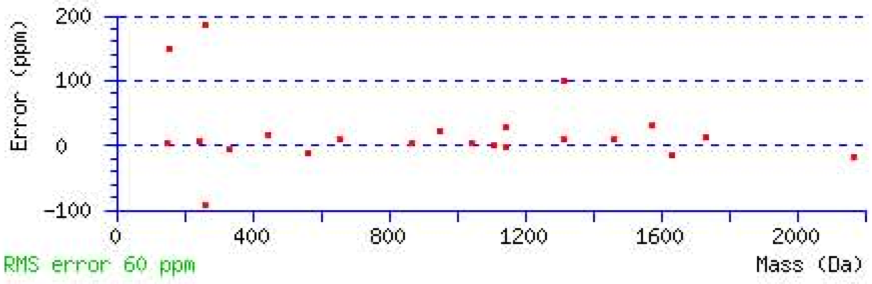
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2543.301544
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15     : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 2.8e-005
Matches : 22/206 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							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
60.4	2543.301544	-0.001462	STAAMSTYTGIFTDQVLSVLK

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

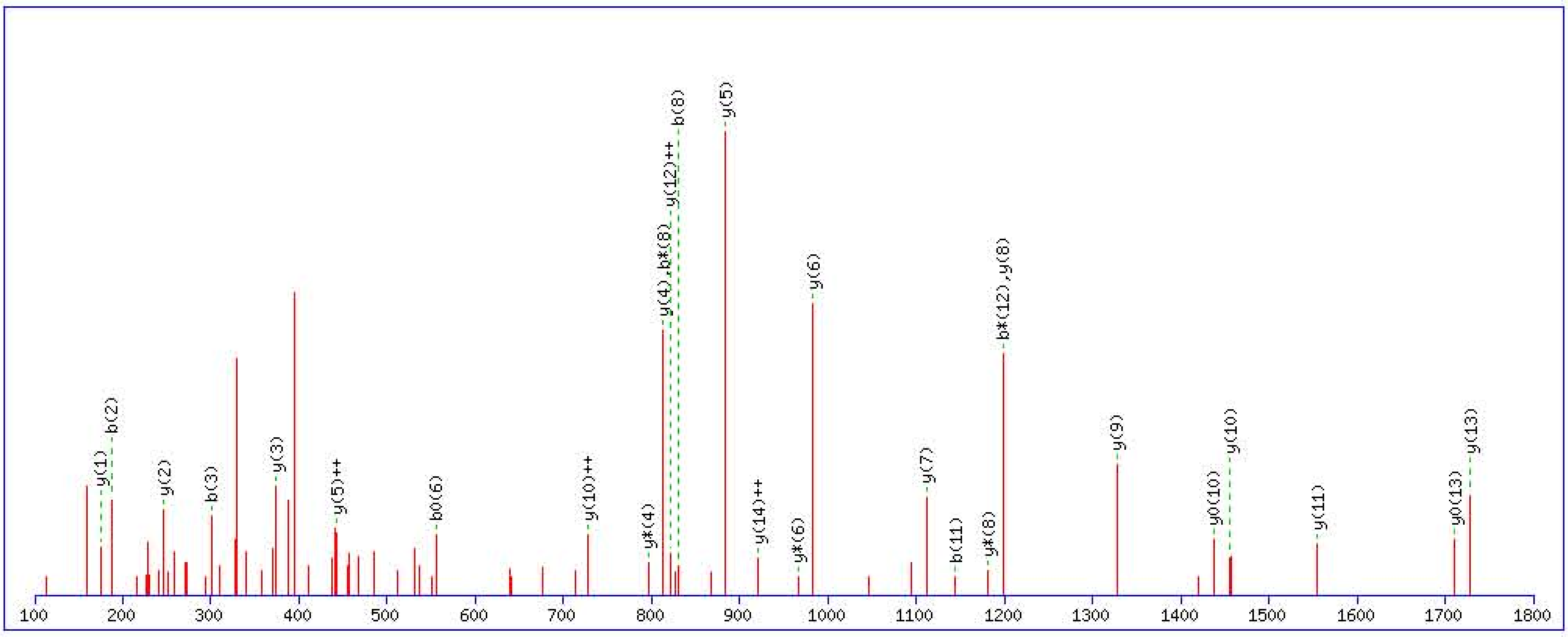
Mascot Search Results

Peptide View

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

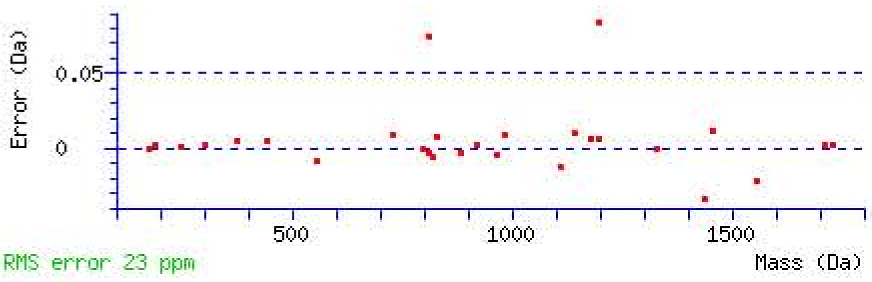
Match to Query 40302: 2027.001882 from(676.674570,3+) rtinseconds(1906) index(18367)
Title: Locus:1.1.1.3229.19 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

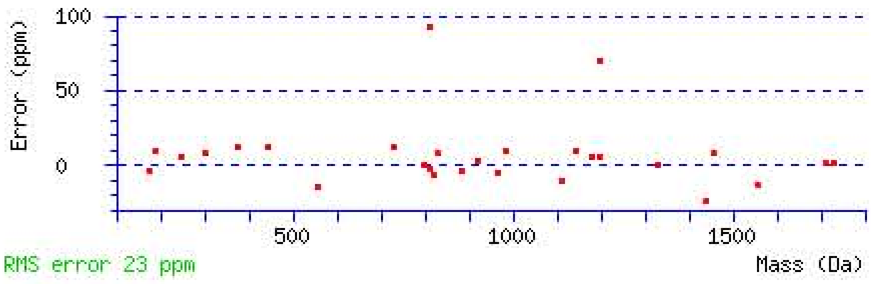
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2027.010574
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13 : Biotin:Thermo-21345 (Q)
Ions Score: 85 **Expect:** 1.4e-008
Matches : 28/154 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	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
84.9	2027.010574	-0.008692	DALSSVQESQVAQQAR
71.9	2027.010574	-0.008692	DALSSVQESQVAQQAR
44.4	2027.010574	-0.008692	DALSSVQESQVAQQAR
13.6	2027.010574	-0.008692	DALSSVQESQVAQQAR
1.1	2027.017960	-0.016078	MFELTLRGMSEALVDKR
0.7	2026.978012	0.023870	AEGAQNQGQKGEGAQNQGKK
0.1	2026.980667	0.021215	LEGAIAEAEQQGEAALNDAK

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

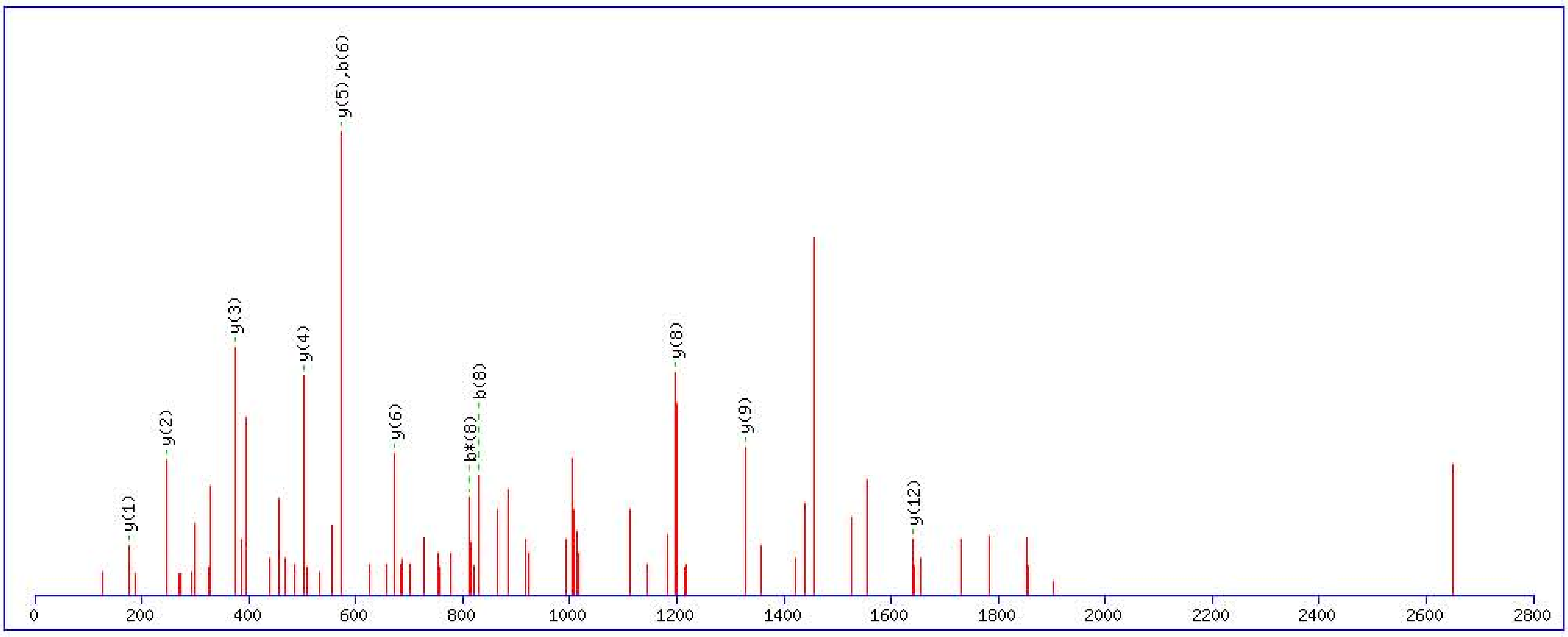
Mascot Search Results

Peptide View

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

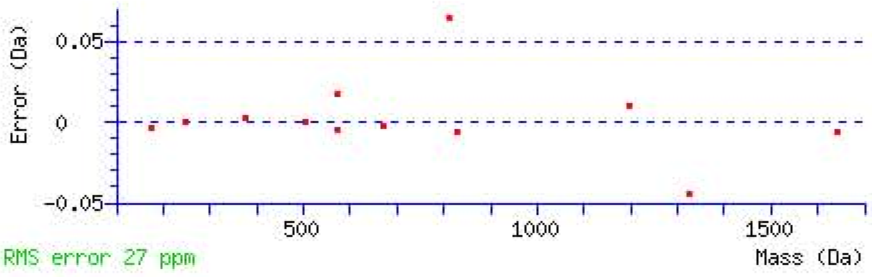
Match to Query 40303: 2027.003488 from(1014.509020,2+) rtinseconds(1961) index(18847)
Title: Locus:1.1.1.3248.24 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

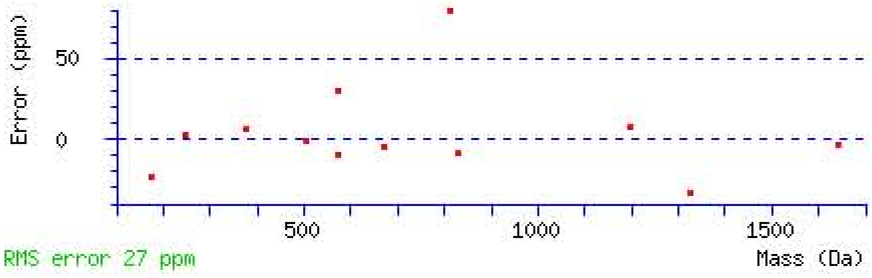
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2027.010574
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 66 **Expect:** 1e-006
Matches : 12/154 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	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
66.1	2027.010574	-0.007086	DALSSVQESQVAQQAR
53.1	2027.010574	-0.007086	DALSSVQESQVAQQAR
42.1	2027.010574	-0.007086	DALSSVQESQVAQQAR
33.3	2027.010574	-0.007086	DALSSVQESQVAQQAR
2.1	2026.994827	0.008661	GPHYWITRGFQMQGPPR
1.9	2026.977982	0.025506	QEEREQEQRQALEQAR

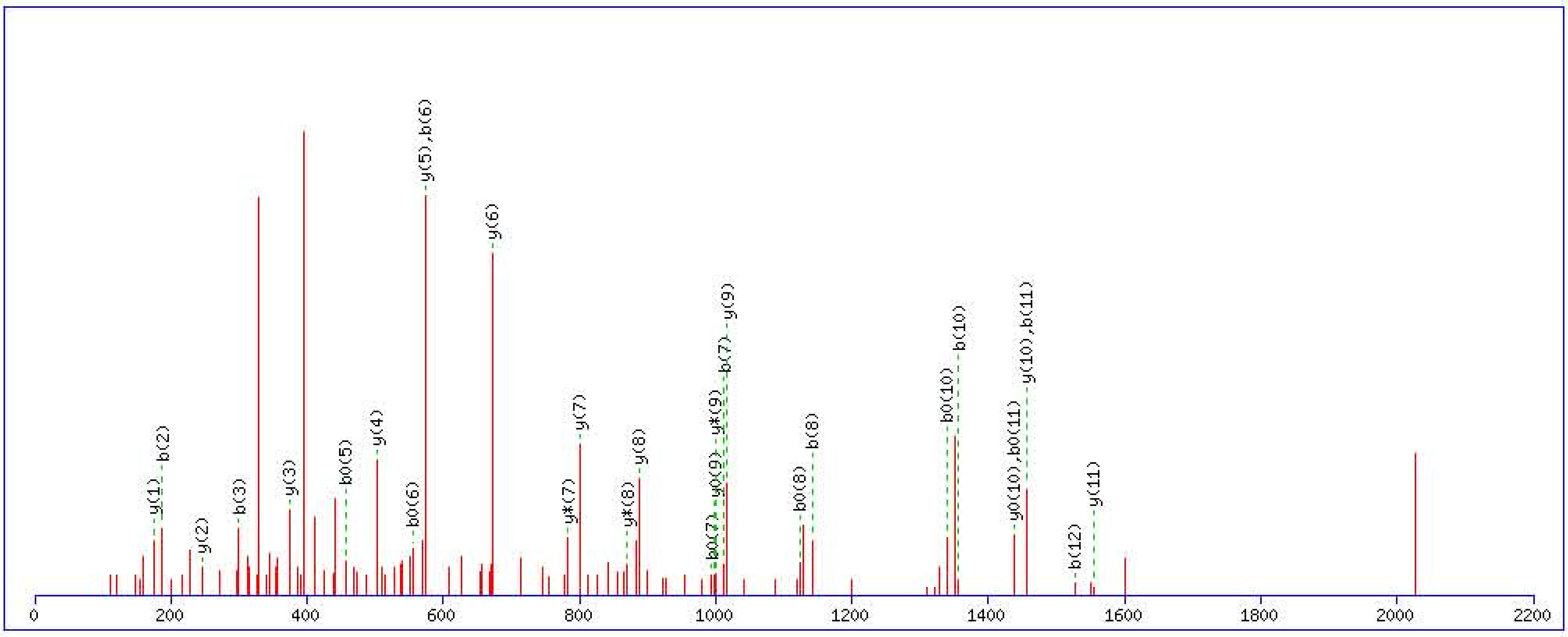
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

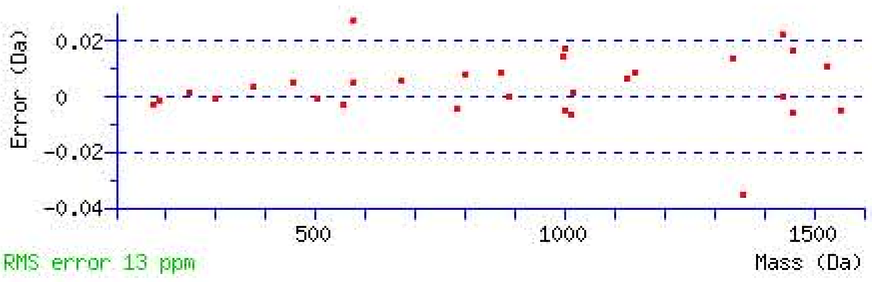
Match to Query 40305: 2027.003562 from(676.675130,3+) rtinseconds(1981) index(31718)
Title: Locus:1.1.1.3353.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

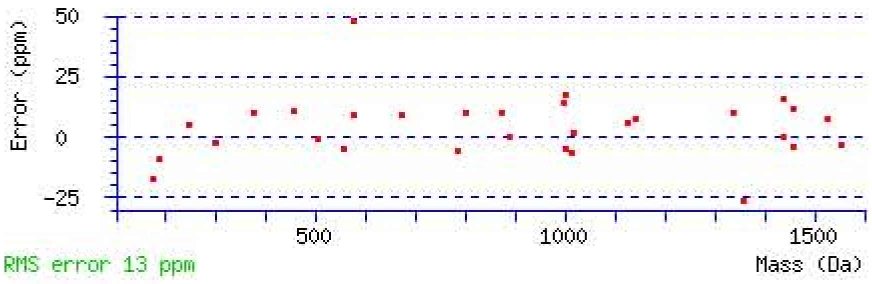
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2027.010574
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 2.2e-005
Matches : 30/154 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	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	**1012.513193**	506.760235	995.486644	498.246960	994.502628	497.754952	Q	***1455.737275***	728.372276	1438.710726	719.859001	1437.726710	719.366993	10
8	**1141.555786**	571.281531	1124.529237	562.768257	1123.545221	562.276249	E	***1016.511949***	508.759613	999.485400	500.246338	998.501384	499.754330	9
9	1228.587814	614.797545	1211.561265	606.284271	1210.577249	605.792263	S	***887.469356***	444.238316	870.442807	435.725042	869.458791	435.233034	8
10	**1356.646392**	678.826834	1339.619843	670.313560	1338.635827	669.821552	Q	***800.437328***	400.722302	783.410779	392.209028			7
11	**1455.714806**	728.361041	1438.688257	719.847767	1437.704241	719.355759	V	***672.378750***	336.693013	655.352201	328.179739			6
12	**1526.751920**	763.879598	1509.725371	755.366324	1508.741355	754.874316	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
56.8	2027.010574	-0.007012	DALSSVQESQVAQQAR
32.9	2027.010574	-0.007012	DALSSVQESQVAQQAR
23.2	2027.010574	-0.007012	DALSSVQESQVAQQAR
19.5	2027.010574	-0.007012	DALSSVQESQVAQQAR
6.7	2027.021805	-0.018243	VASVESQGQEISGNRR
3.3	2026.978012	0.025550	AEGAQNQGQKGEGAQNQGKK
0.5	2026.980667	0.022895	LEGAIAEAEQQGEAALNDAK

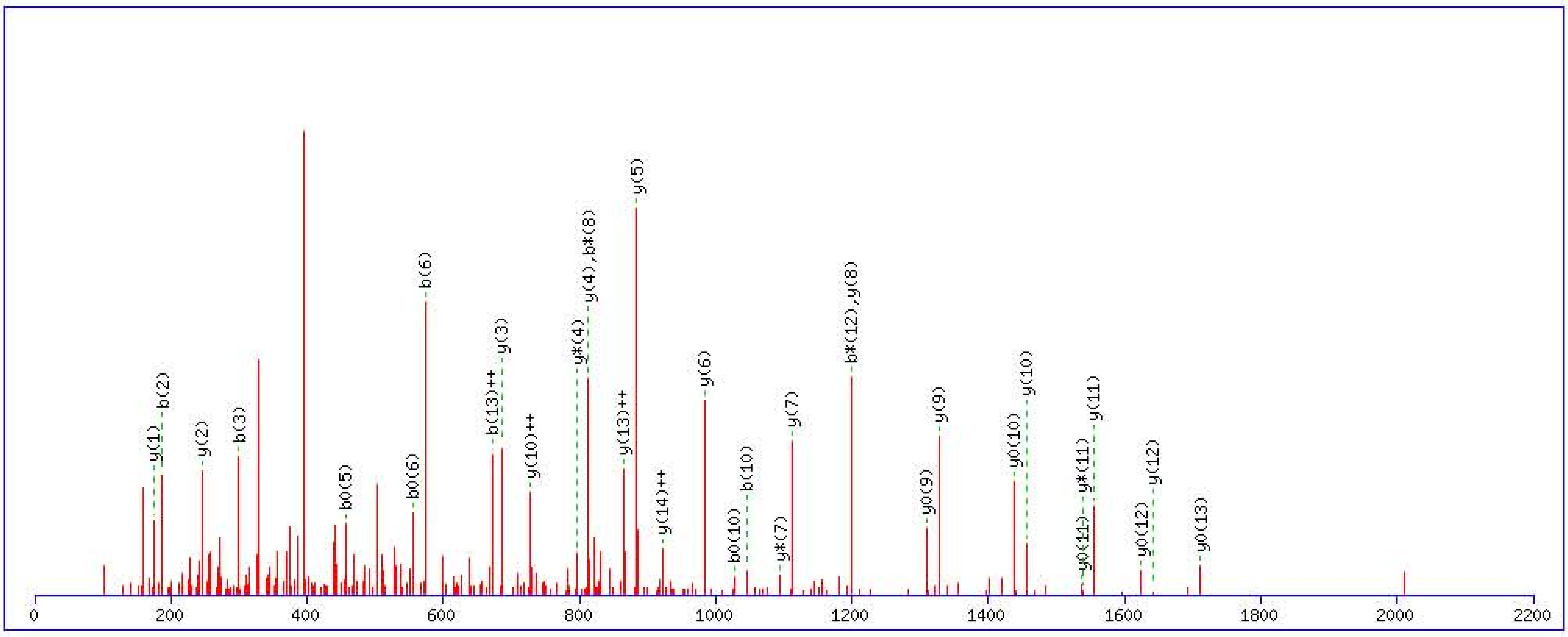
Mascot Search Results

Peptide View

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

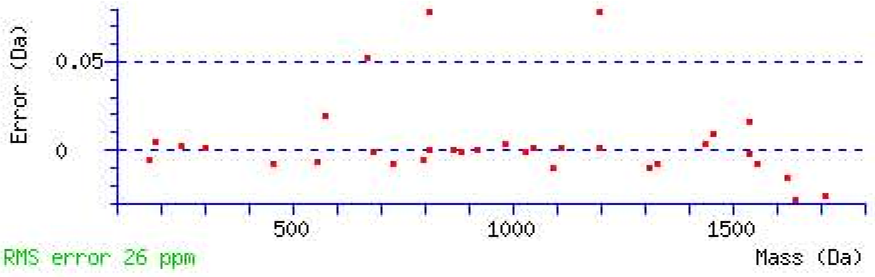
Match to Query 40311: 2027.005722 from(676.675850,3+) rtinseconds(1961) index(31562)
Title: Locus:1.1.1.3346.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

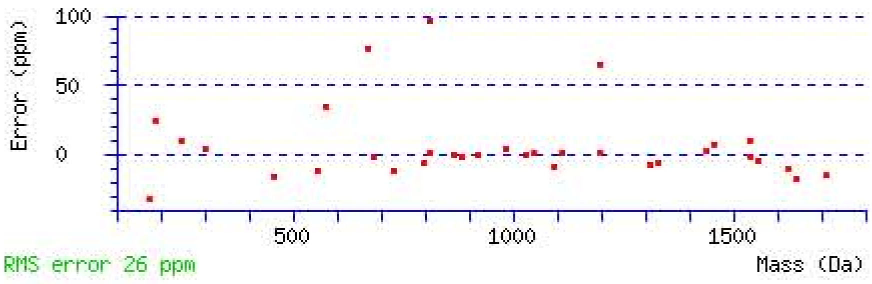
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 80  Expect: 5e-008
Matches : 33/154 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	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
79.7	2027.010574	-0.004852	DALSSVQESQVAQQAR
79.4	2027.010574	-0.004852	DALSSVQESQVAQQAR
73.7	2027.010574	-0.004852	DALSSVQESQVAQQAR
37.2	2027.010574	-0.004852	DALSSVQESQVAQQAR
1.8	2026.977982	0.027740	QEEREQEQRQALEQAR
1.2	2027.029633	-0.023911	QEESEHSHKHLIELRR

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

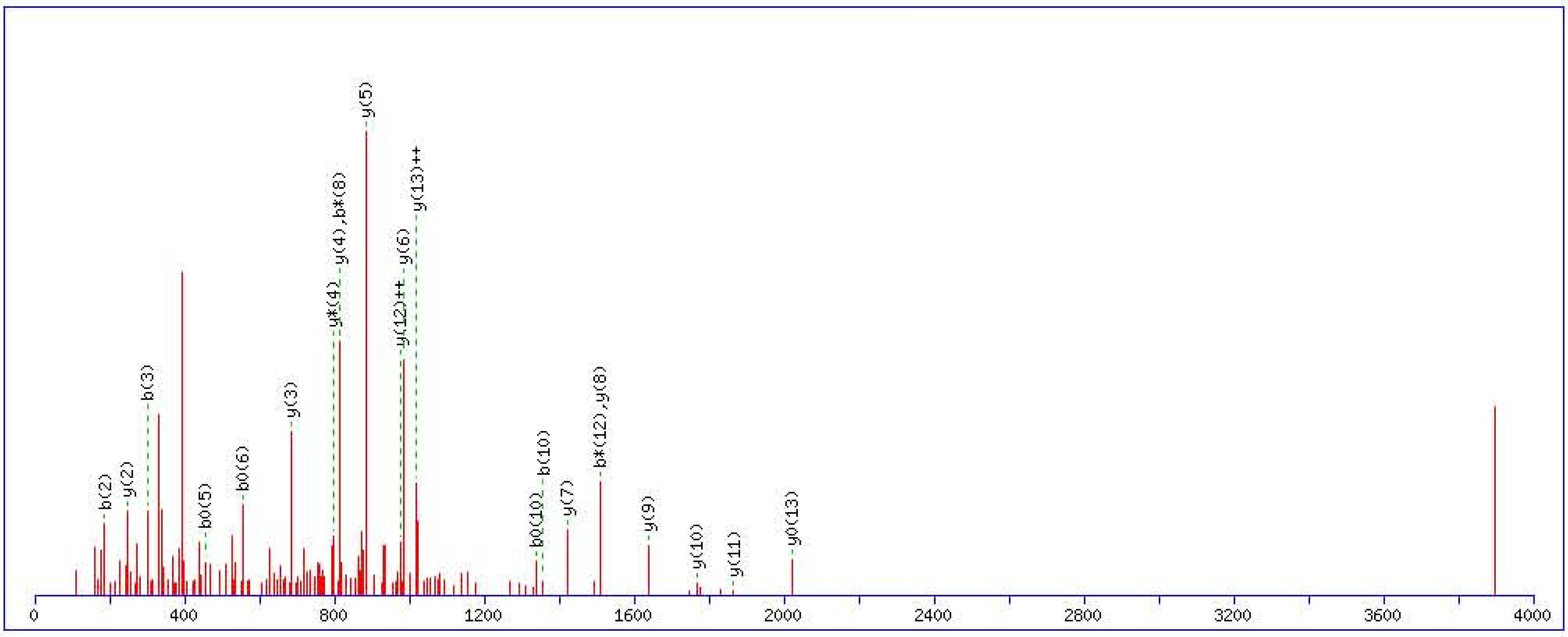
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

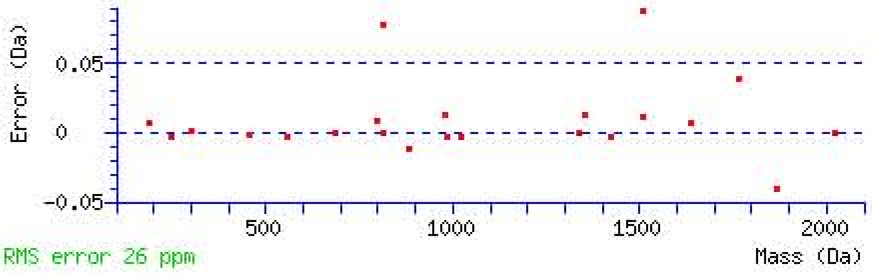
Match to Query 45727: 2338.177062 from(780.399630,3+) rtinseconds(2225) index(33193)
Title: Locus:1.1.1.3438.22 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

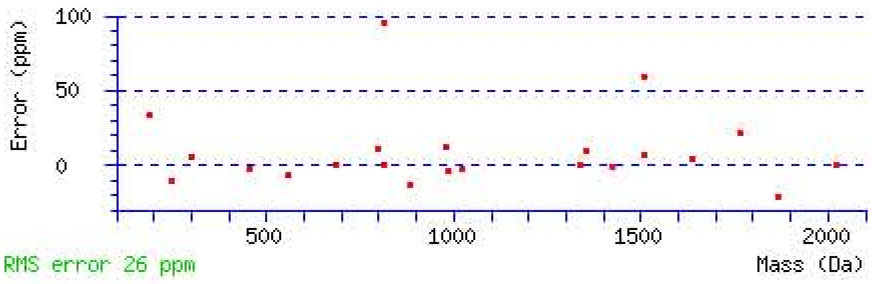
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2338.177322
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 58  Expect: 4.5e-005
Matches : 22/154 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	116.034219	58.520748			98.023654	49.515465	D							16
2	**187.071333**	94.039304			169.060768	85.034022	A	2224.157671	1112.582473	2207.131122	1104.069199	2206.147106	1103.577191	15
3	**300.155397**	150.581336			282.144832	141.576054	L	2153.120557	1077.063916	2136.094008	1068.550642	2135.109992	1068.058634	14
4	387.187425	194.097351			369.176860	185.092068	S	2040.036493	1020.521885	2023.009944	1012.008610	2022.025928	1011.516602	13
5	474.219453	237.613364			456.208888	228.608082	S	1953.004465	977.005871	1935.977916	968.492596	1934.993900	968.000588	12
6	573.287867	287.147572			555.277302	278.142289	V	***1865.972437***	933.489857	1848.945888	924.976582	1847.961872	924.484574	11
7	701.346445	351.176861	684.319896	342.663586	683.335880	342.171578	Q	***1766.904023***	883.955650	1749.877474	875.442375	1748.893458	874.950367	10
8	830.389038	415.698157	813.362489	407.184883	812.378473	406.692875	E	***1638.845445***	819.926361	1621.818896	811.413086	1620.834880	810.921078	9
9	917.421066	459.214171	900.394517	450.700897	899.410501	450.208889	S	***1509.802852***	755.405064	1492.776303	746.891790	1491.792287	746.399782	8
10	**1356.646392**	678.826834	1339.619843	670.313560	1338.635827	669.821551	Q	***1422.770824***	711.889050	1405.744275	703.375776			7
11	1455.714806	728.361041	1438.688257	719.847767	1437.704241	719.355758	V	***983.545498***	492.276387	966.518949	483.763113			6
12	1526.751920	763.879598	1509.725371	755.366324	1508.741355	754.874315	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	2094.035824	1047.521550	2077.009275	1039.008275	2076.025259	1038.516267	Q	***685.381392***	343.194334	668.354843	334.681060			3
15	2165.072938	1083.040107	2148.046389	1074.526833	2147.062373	1074.034825	A	***246.156066***	123.581671	229.129517	115.068397			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
57.9	2338.177322	-0.000260	DALSSVQESQVAQQAR
46.6	2338.177322	-0.000260	DALSSVQESQVAQQAR
29.1	2338.177322	-0.000260	DALSSVQESQVAQQAR
23.3	2338.177322	-0.000260	DALSSVQESQVAQQAR
20.6	2338.177322	-0.000260	DALSSVQESQVAQQAR
6.5	2338.177322	-0.000260	DALSSVQESQVAQQAR

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

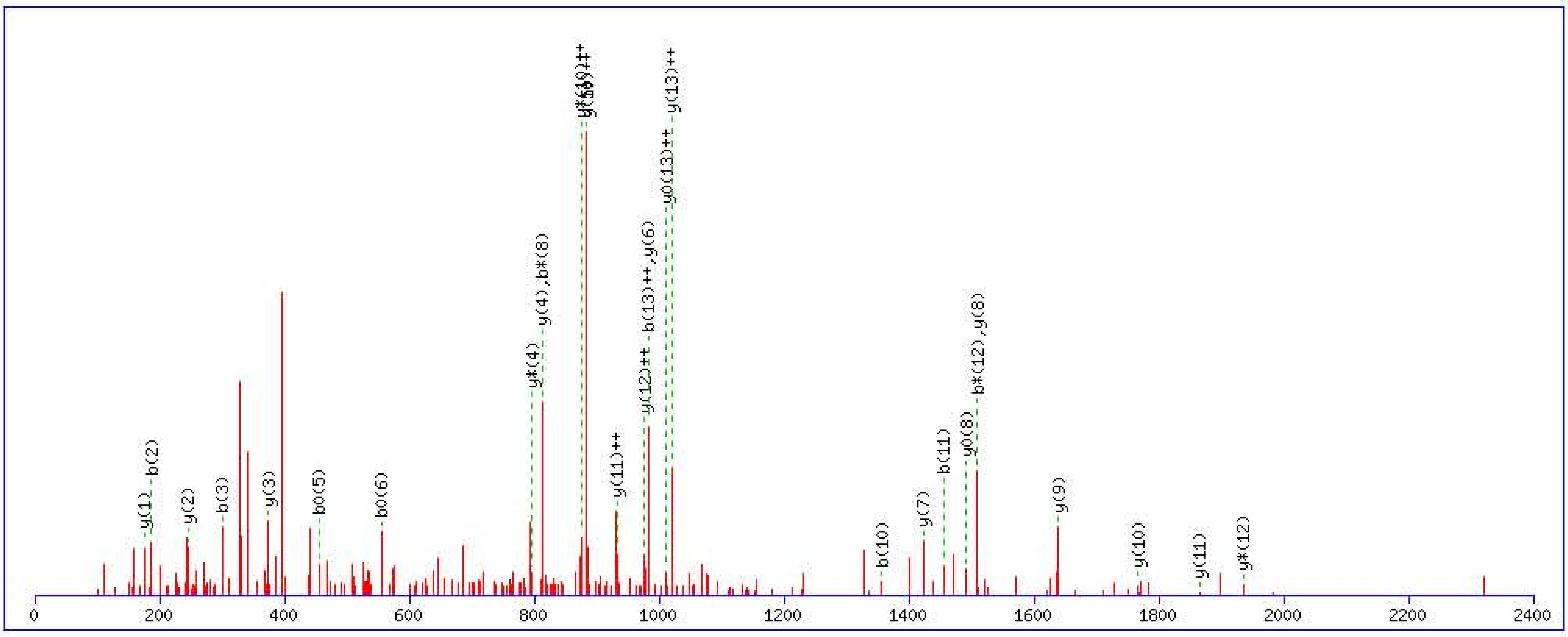
Mascot Search Results

Peptide View

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

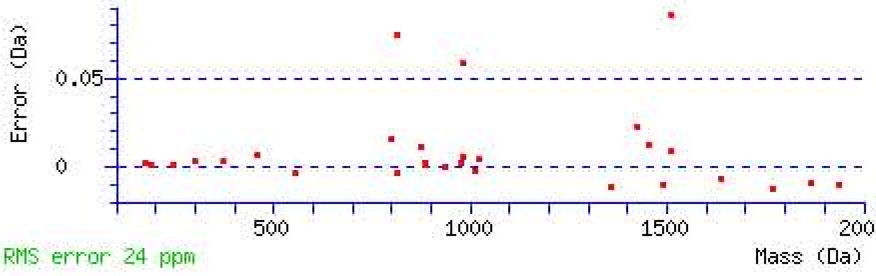
Match to Query 45728: 2338.178172 from(780.400000,3+) rtinseconds(2216) index(33119)
Title: Locus:1.1.1.3435.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

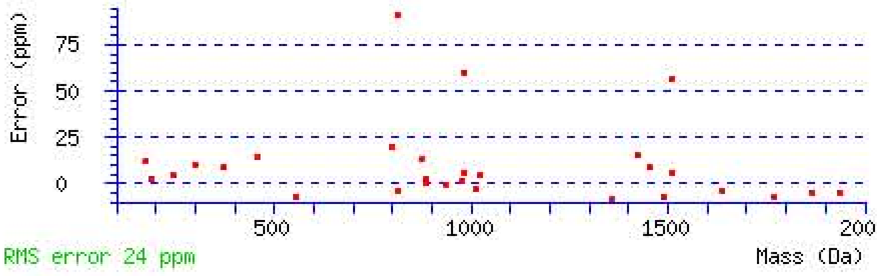
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2338.177322
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.0041
Matches : 29/154 fragment ions using 73 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	2224.157671	1112.582473	2207.131122	1104.069199	2206.147106	1103.577191	15
3	**300.155397**	150.581336			282.144832	141.576054	L	2153.120557	1077.063916	2136.094008	1068.550642	2135.109992	1068.058634	14
4	387.187425	194.097351			369.176860	185.092068	S	2040.036493	1020.521885	2023.009944	1012.008610	2022.025928	1011.516602	13
5	474.219453	237.613364			456.208888	228.608082	S	1953.004465	977.005871	1935.977916	968.492596	1934.993900	968.000588	12
6	573.287867	287.147572			555.277302	278.142289	V	***1865.972437***	933.489857	1848.945888	924.976582	1847.961872	924.484574	11
7	701.346445	351.176861	684.319896	342.663586	683.335880	342.171578	Q	***1766.904023***	883.955650	1749.877474	875.442375	1748.893458	874.950367	10
8	830.389038	415.698157	813.362489	407.184883	812.378473	406.692875	E	***1638.845445***	819.926361	1621.818896	811.413086	1620.834880	810.921078	9
9	917.421066	459.214171	900.394517	450.700897	899.410501	450.208889	S	***1509.802852***	755.405064	1492.776303	746.891790	1491.792287	746.399782	8
10	**1356.646392**	678.826834	1339.619843	670.313560	1338.635827	669.821551	Q	***1422.770824***	711.889050	1405.744275	703.375776			7
11	**1455.714806**	728.361041	1438.688257	719.847767	1437.704241	719.355758	V	***983.545498***	492.276387	966.518949	483.763113			6
12	1526.751920	763.879598	1509.725371	755.366324	1508.741355	754.874315	A	***884.477084***	442.742180	867.450535	434.228906			5
13	1965.977246	983.492261	1948.950697	974.978987	1947.966681	974.486979	Q	***813.439970***	407.223623	796.413421	398.710349			4
14	2094.035824	1047.521550	2077.009275	1039.008275	2076.025259	1038.516267	Q	***374.214644***	187.610960	357.188095	179.097686			3
15	2165.072938	1083.040107	2148.046389	1074.526833	2147.062373	1074.034825	A	***246.156066***	123.581671	229.129517	115.068397			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
38.2	2338.177322	0.000850	DALSSVQESQVAQQAR
38.2	2338.177322	0.000850	DALSSVQESQVAQQAR
22.9	2338.177322	0.000850	DALSSVQESQVAQQAR
22.9	2338.177322	0.000850	DALSSVQESQVAQQAR
15.3	2338.177322	0.000850	DALSSVQESQVAQQAR
7.4	2338.177322	0.000850	DALSSVQESQVAQQAR

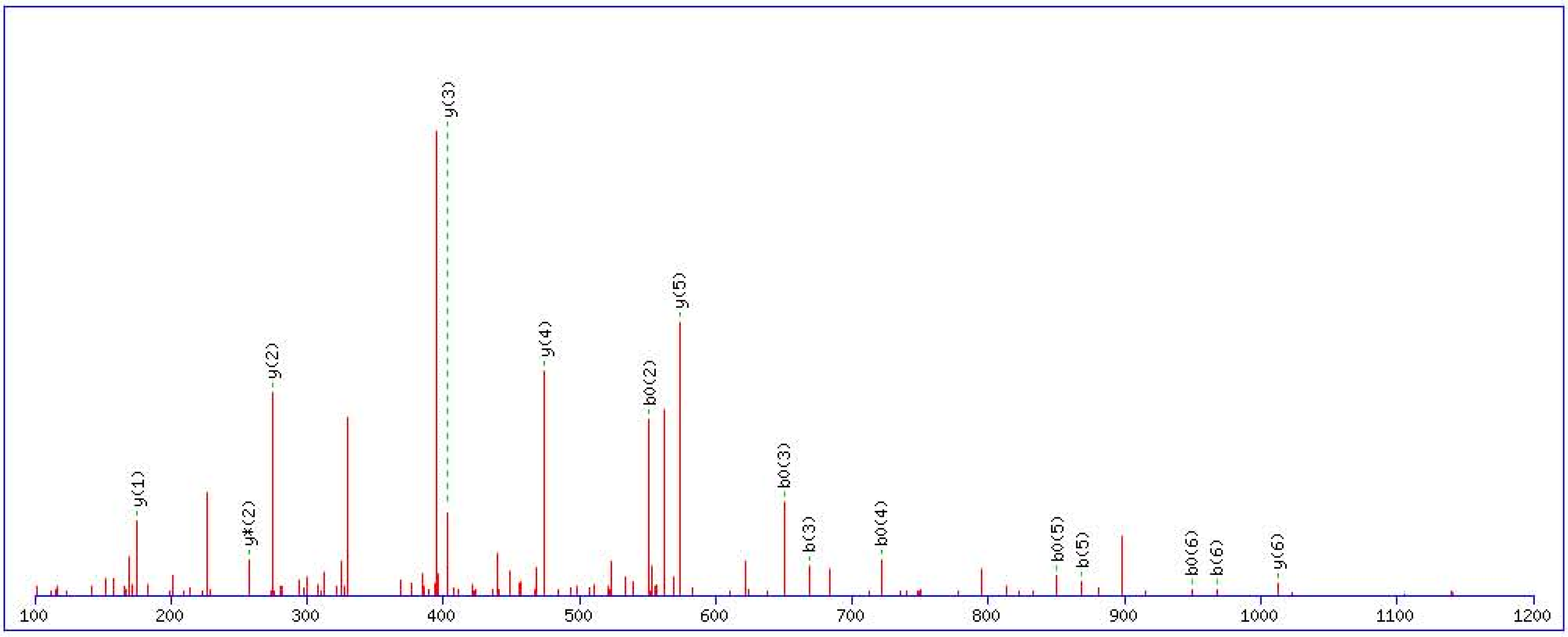
Mascot Search Results

Peptide View

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

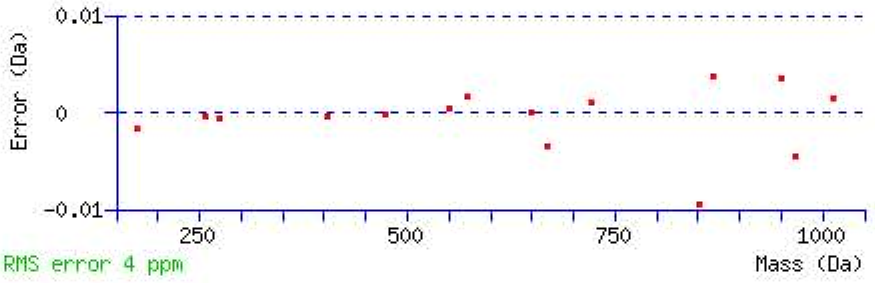
Match to Query 16026: 1140.592548 from(571.303550,2+) rtinseconds(1554) index(29119)
Title: Locus:1.1.1.3204.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

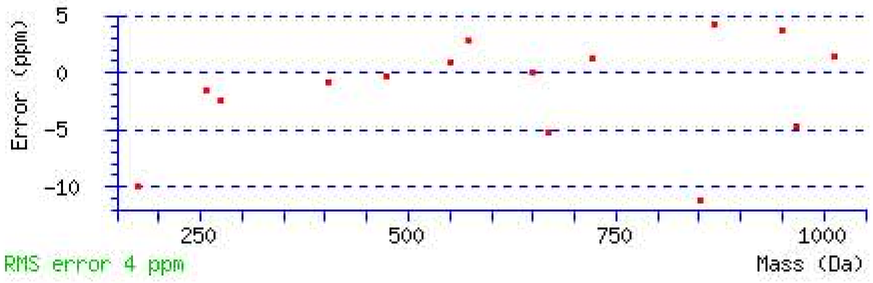
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1140.596115
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.011
Matches : 15/66 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	130.049869	65.528572			112.039304	56.523290	E							7
2	569.275195	285.141236	552.248646	276.627961	551.264630	276.135953	Q	***1012.560813***	506.784044	995.534264	498.270770	994.550248	497.778762	6
3	**668.343609**	334.675443	651.317060	326.162168	650.333044	325.670160	V	***573.335487***	287.171382	556.308938	278.658107	555.324922	278.166099	5
4	739.380723	370.194000	722.354174	361.680725	721.370158	361.188717	A	***474.267073***	237.637174	457.240524	229.123900	456.256508	228.631892	4
5	**868.423316**	434.715296	851.396767	426.202022	850.412751	425.710014	E	***403.229959***	202.118617	386.203410	193.605343	385.219394	193.113335	3
6	**967.491730**	484.249503	950.465181	475.736228	949.481165	475.244220	V	***274.187366***	137.597321	257.160817	129.084046			2
7							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.3	1140.596115	-0.003567	EQVAEVR
13.9	1140.596115	-0.003567	QEVADLR
13.7	1140.596115	-0.003567	EQALDVR
9.3	1140.599945	-0.007397	ERVALSHSSR
5.9	1140.588715	0.003833	RLAADDPEVR
5.5	1140.596115	-0.003567	QEGLDLR
4.2	1140.577484	0.015064	ADSVSELPAPR
4.0	1140.596115	-0.003567	EQSTLPR
3.8	1140.599945	-0.007397	SSSKLAQHQR
3.8	1140.596115	-0.003567	LQEGEVR

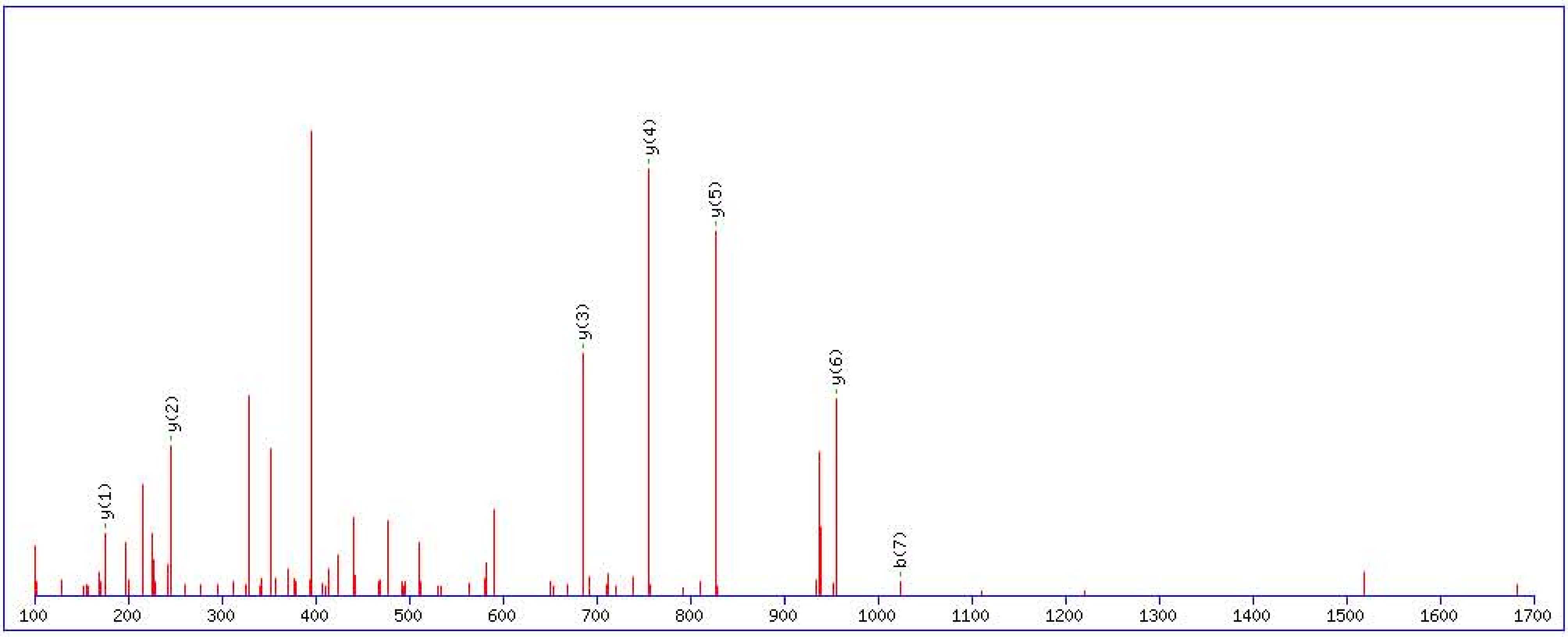
Mascot Search Results

Peptide View

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

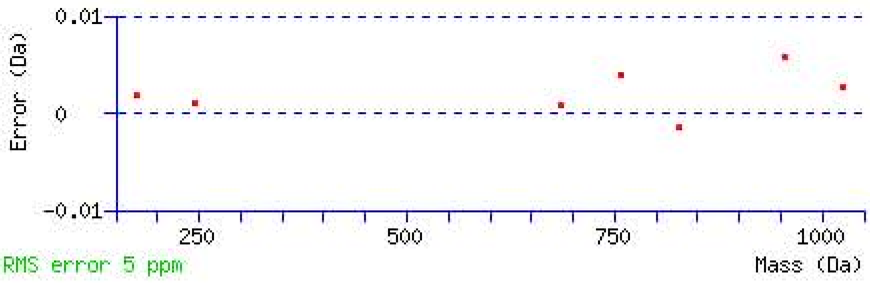
Match to Query 17681: 1196.625028 from(599.319790,2+) rtinseconds(1504) index(42949)
Title: Locus:1.1.1.3236.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

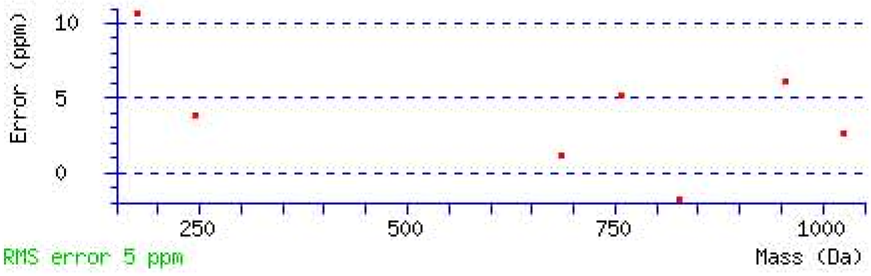
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1196.633545
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00024
Matches : 7/66 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	130.049869	65.528572			112.039304	56.523290	E					8
2	243.133933	122.070605			225.123368	113.065322	L	1068.598262	534.802769	1051.571713	526.289495	7
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	Q	***955.514198***	478.260737	938.487649	469.747463	6
4	442.229625	221.618450	425.203076	213.105176	424.219060	212.613168	A	***827.455620***	414.231448	810.429071	405.718174	5
5	513.266739	257.137008	496.240190	248.623733	495.256174	248.131725	A	***756.418506***	378.712891	739.391957	370.199617	4
6	952.492065	476.749671	935.465516	468.236396	934.481500	467.744388	Q	***685.381392***	343.194334	668.354843	334.681060	3
7	**1023.529179**	512.268227	1006.502630	503.754953	1005.518614	503.262945	A	***246.156066***	123.581671	229.129517	115.068397	2
8							R	***175.118952***	88.063114	158.092403	79.549840	1





NCBI **BLAST** search of ELQAAQAR
(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	1196.633545	-0.008517	ELQAAQAR
12.5	1196.641434	-0.016406	STRPQAWVPR
9.2	1196.627029	-0.002001	AGMPRQAR
8.6	1196.614914	0.010114	ELQQAELPNR
7.8	1196.633575	-0.008547	QASTQVPR
7.1	1196.633545	-0.008517	ELQAAQAR
6.6	1196.614929	0.010099	QITTELAEHR
6.0	1196.614944	0.010084	EAIGPGGEVVNR
2.7	1196.637390	-0.012362	TLRQAGAPNNR
1.9	1196.614929	0.010099	DAVPGEAALQAR

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

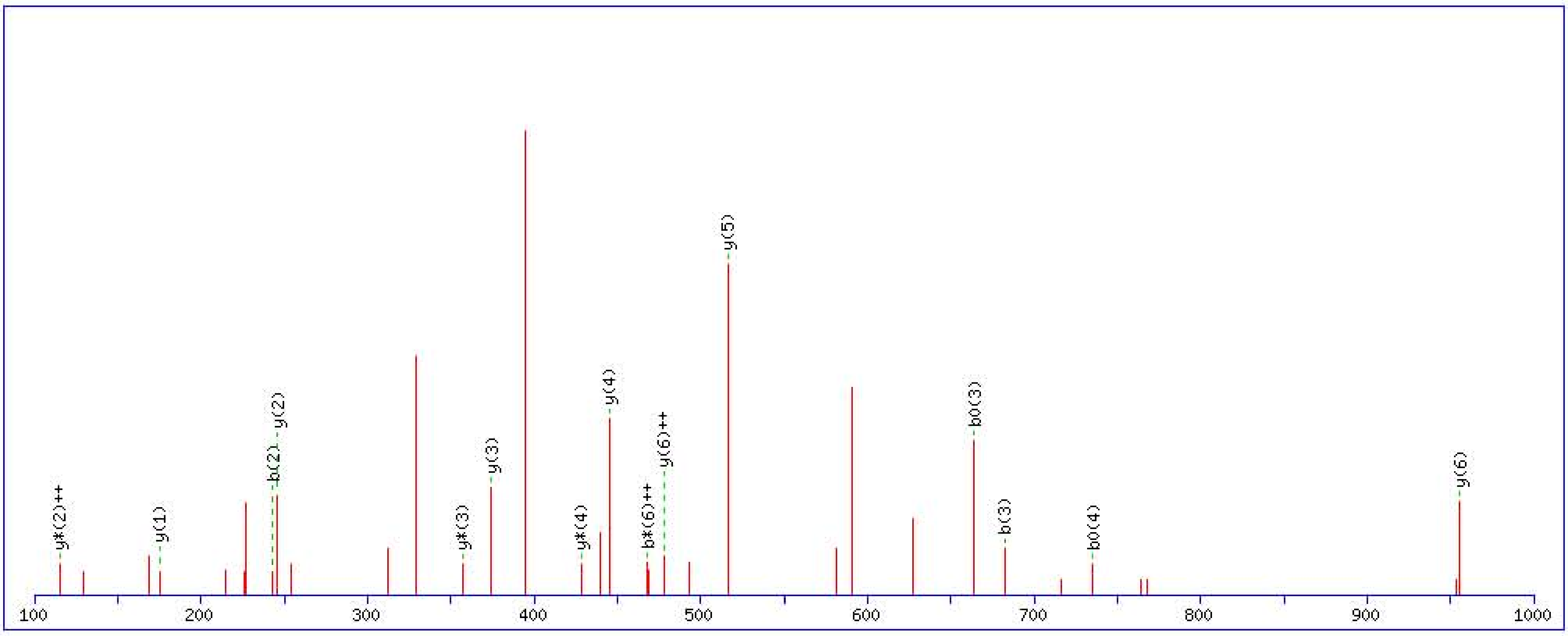
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

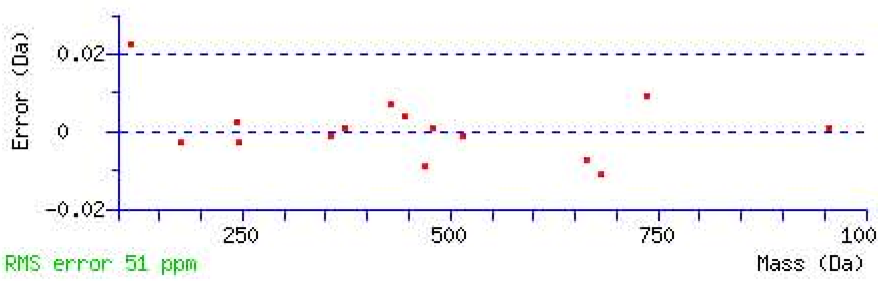
Match to Query 17686: 1196.631228 from(599.322890,2+) rtinseconds(1483) index(42777)
Title: Locus:1.1.1.3229.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

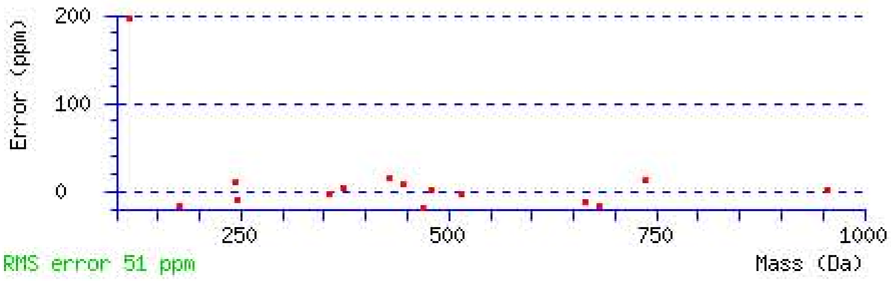
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1196.633545
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.012
Matches : 15/66 fragment ions using 32 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	130.049869	65.528572			112.039304	56.523290	E					8
2	**243.133933**	122.070605			225.123368	113.065322	L	1068.598262	534.802769	1051.571713	526.289495	7
3	**682.359259**	341.683268	665.332710	333.169993	664.348694	332.677985	Q	***955.514198***	478.260737	938.487649	469.747463	6
4	753.396373	377.201825	736.369824	368.688550	735.385808	368.196542	A	***516.288872***	258.648074	499.262323	250.134800	5
5	824.433487	412.720382	807.406938	404.207107	806.422922	403.715099	A	***445.251758***	223.129517	428.225209	214.616243	4
6	952.492065	476.749671	935.465516	468.236396	934.481500	467.744388	Q	***374.214644***	187.610960	357.188095	179.097686	3
7	1023.529179	512.268227	1006.502630	503.754953	1005.518614	503.262945	A	***246.156066***	123.581671	229.129517	115.068397	2
8							R	***175.118952***	88.063114	158.092403	79.549840	1





NCBI **BLAST** search of ELQAAQAR
(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	1196.633545	-0.002317	ELQAAQAR
10.8	1196.644775	-0.013547	LEQANRR
5.9	1196.641418	-0.010190	EAKKAGPGFHR
5.3	1196.633560	-0.002332	QNQDILR
0.4	1196.633575	-0.002347	MGITISPVSHR

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

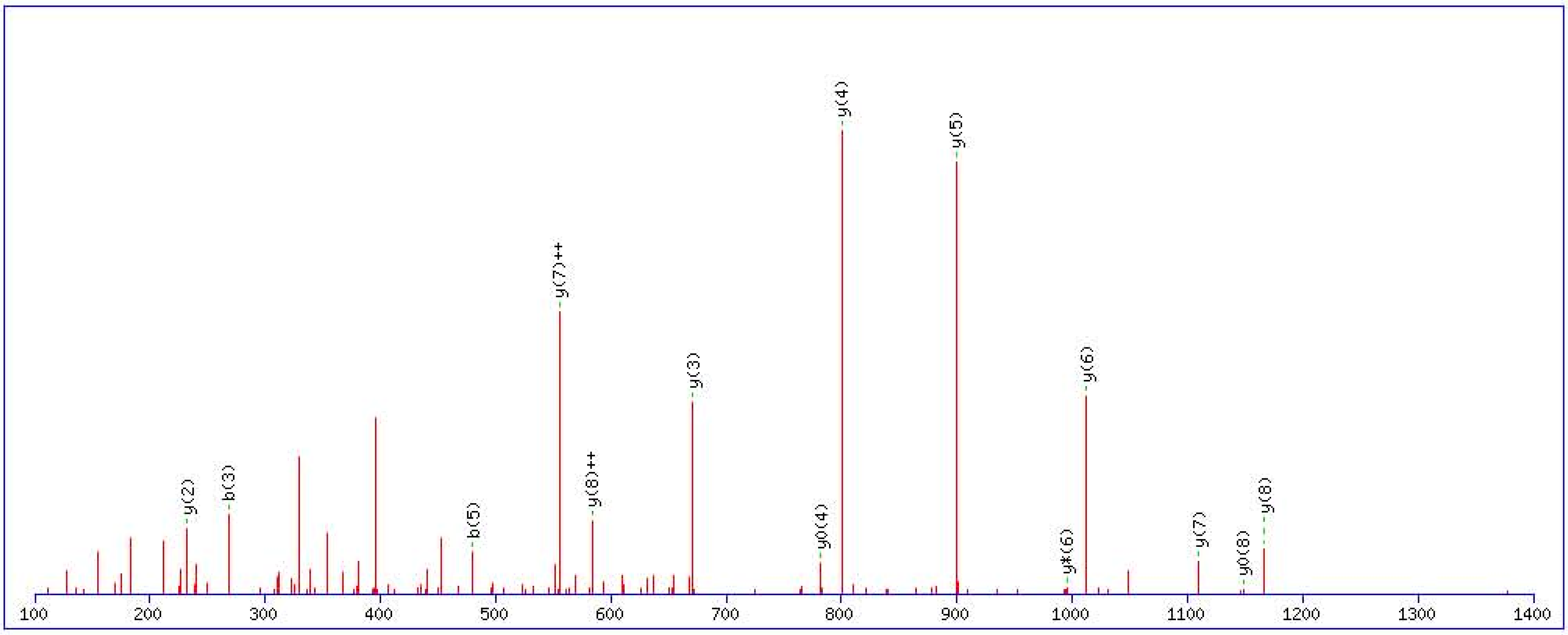
Mascot Search Results

Peptide View

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

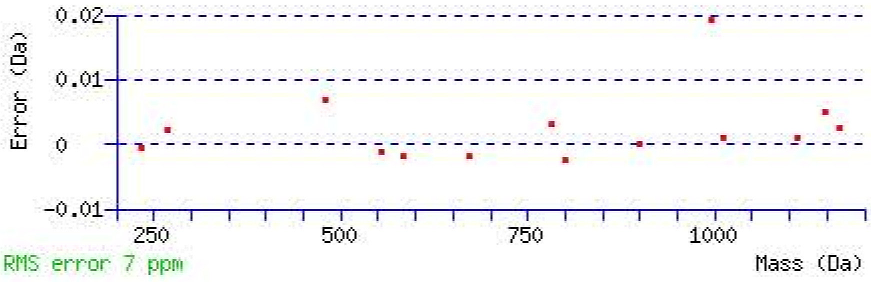
Match to Query 19745: 1278.708008 from(640.361280,2+) rtinseconds(1992) index(31814)
Title: Locus:1.1.1.3357.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

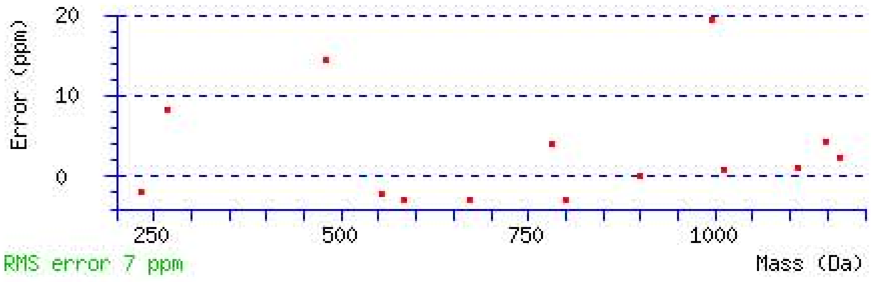
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1278.711823
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 50 **Expect:** 0.00014
Matches : 14/68 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					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
50.2	1278.711823	-0.003815	LGPLVEQGR

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

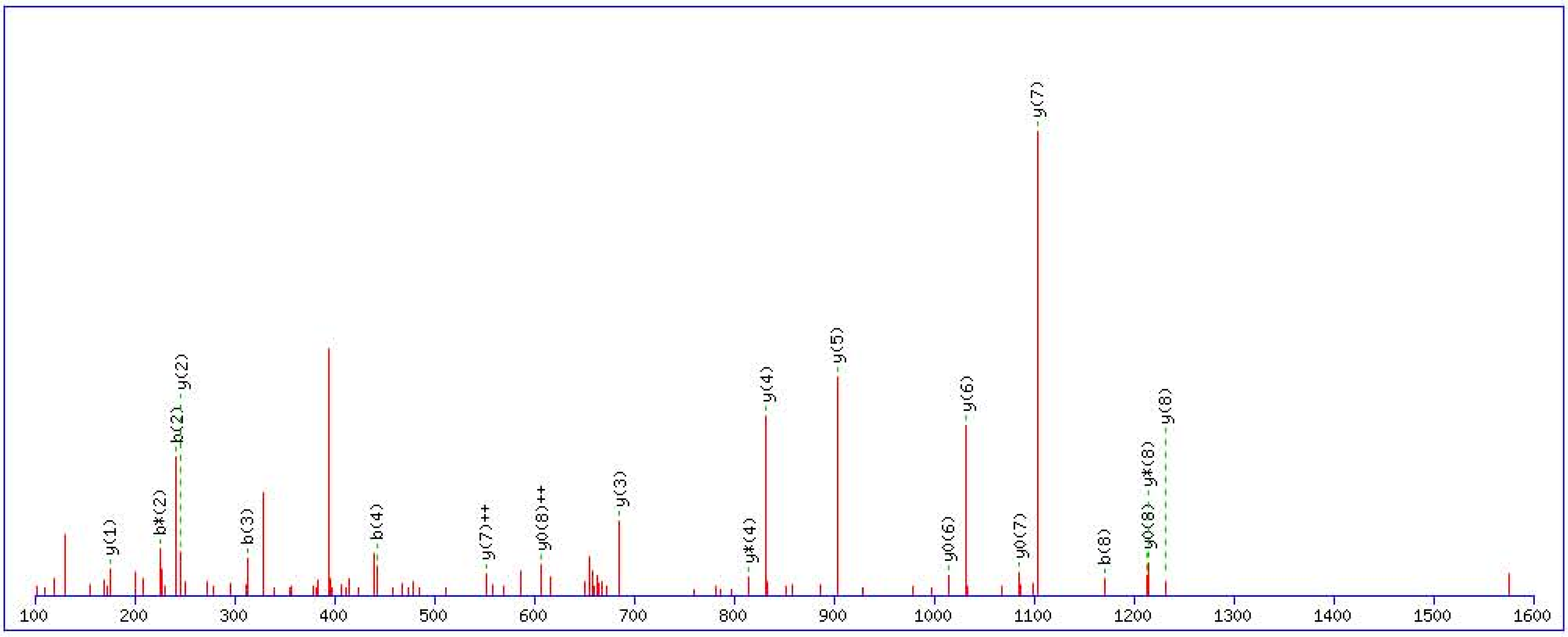
MATRIX SCIENCE Mascot Search Results

Peptide View

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

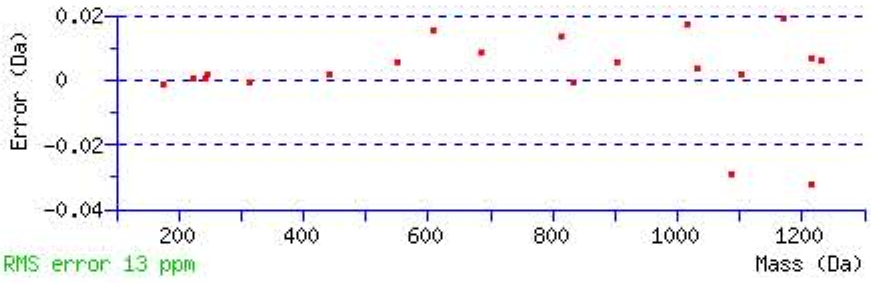
Match to Query 21214: 1343.701428 from(672.857990,2+) rtinseconds(1838) index(30812)
Title: Locus:1.1.1.3303.6 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

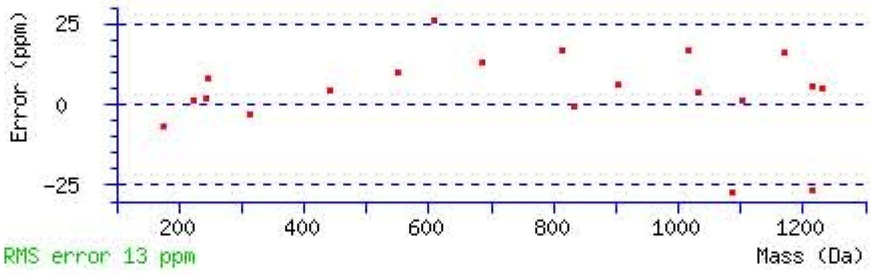
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1343.701965
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 49 **Expect:** 0.00023
Matches : 20/78 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					L							9
2	**242.149918**	121.578597	225.123369	113.065323			Q	***1231.625205***	616.316241	1214.598656	607.802966	1213.614640	607.310958	8
3	**313.187032**	157.097154	296.160483	148.583879			A	***1103.566627***	552.286951	1086.540078	543.773677	1085.556062	543.281669	7
4	**442.229625**	221.618450	425.203076	213.105176	424.219060	212.613168	E	***1032.529513***	516.768395	1015.502964	508.255120	1014.518948	507.763112	6
5	513.266739	257.137008	496.240190	248.623733	495.256174	248.131725	A	***903.486920***	452.247098	886.460371	443.733823			5
6	660.335153	330.671215	643.308604	322.157940	642.324588	321.665932	F	***832.449806***	416.728541	815.423257	408.215266			4
7	1099.560479	550.283878	1082.533930	541.770603	1081.549914	541.278595	Q	***685.381392***	343.194334	668.354843	334.681060			3
8	**1170.597593**	585.802435	1153.571044	577.289160	1152.587028	576.797152	A	***246.156066***	123.581671	229.129517	115.068396			2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.4	1343.701965	-0.000537	LQAEAFQAR
9.9	1343.694107	0.007321	IQAMSEVQK
7.8	1343.715683	-0.014255	LKDSEAELQRR
7.6	1343.704453	-0.003025	IQEKKDEDIAR
7.0	1343.683350	0.018078	GSPAAPEGALGYVR
5.6	1343.716583	-0.015155	LQQVMSRR
5.0	1343.704453	-0.003025	LQAANAEDIKSGK
5.0	1343.704453	-0.003025	IKGEELSEANVR
1.6	1343.694565	0.006863	QLAAFAPREEGR
1.5	1343.693207	0.008221	LAKDLEEELER

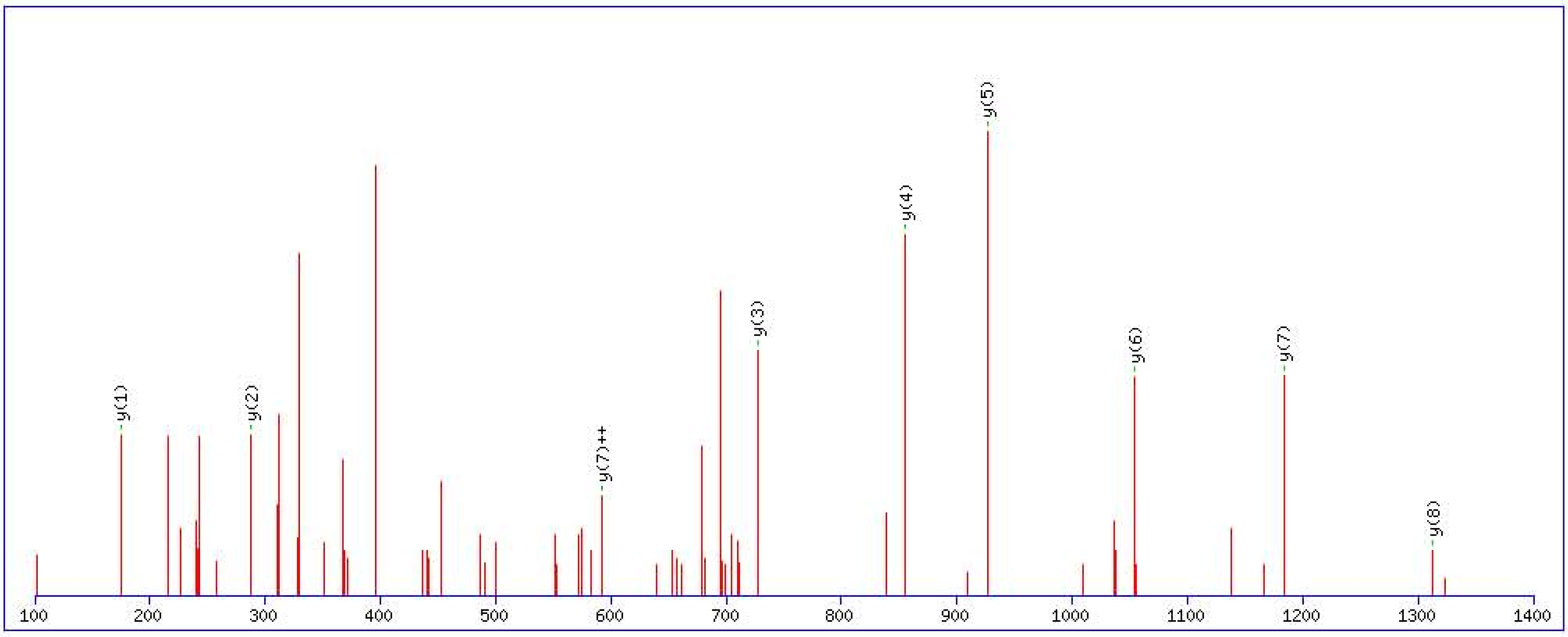
Mascot Search Results

Peptide View

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

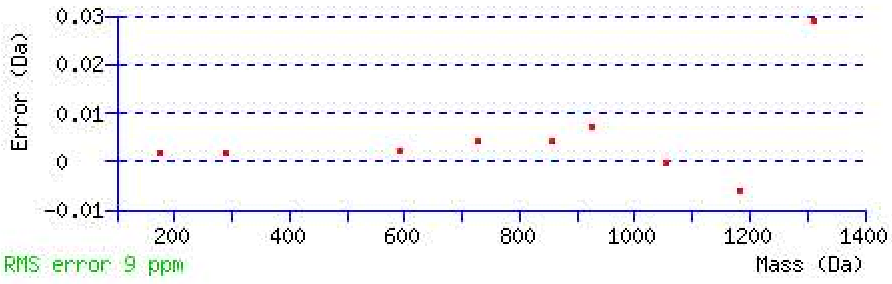
Match to Query 25099: 1424.732028 from(713.373290,2+) rtinseconds(1633) index(2797)
Title: Locus:1.1.1.3088.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

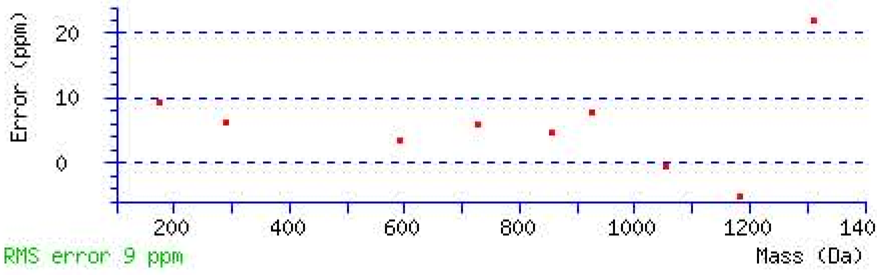
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1424.744553
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 69 **Expect:** 8.8e-006
Matches : 9/76 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					L							9
2	243.133933	122.070605			225.123368	113.065322	E	***1312.667798***	656.837537	1295.641249	648.324263	1294.657233	647.832255	8
3	372.176526	186.591901			354.165961	177.586619	E	***1183.625205***	592.316241	1166.598656	583.802966	1165.614640	583.310958	7
4	500.235104	250.621190	483.208555	242.107916	482.224539	241.615908	Q	***1054.582612***	527.794944	1037.556063	519.281670			6
5	571.272218	286.139747	554.245669	277.626473	553.261653	277.134465	A	***926.524034***	463.765655	909.497485	455.252381			5
6	699.330796	350.169036	682.304247	341.655762	681.320231	341.163754	Q	***855.486920***	428.247098	838.460371	419.733824			4
7	1138.556122	569.781699	1121.529573	561.268425	1120.545557	560.776417	Q	***727.428342***	364.217809	710.401793	355.704535			3
8	1251.640186	626.323731	1234.613637	617.810457	1233.629621	617.318449	I	***288.203016***	144.605146	271.176467	136.091871			2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.3	1424.744553	-0.012525	LEEQAQQIR
52.9	1424.744553	-0.012525	LEEQAQQIR
24.2	1424.744553	-0.012525	LEEQAQQIR
16.0	1424.733322	-0.001294	LEQETEPLR
15.2	1424.723465	0.008563	TWTVLPPMSTHR
10.7	1424.745438	-0.013410	QMQQIR
7.8	1424.734680	-0.002652	WVLTAAHCLAQR
4.7	1424.744583	-0.012555	QLSGDQPTIR
4.0	1424.726807	0.005221	QMNLQQQPK
2.9	1424.744583	-0.012555	QLSGDQPTIR

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

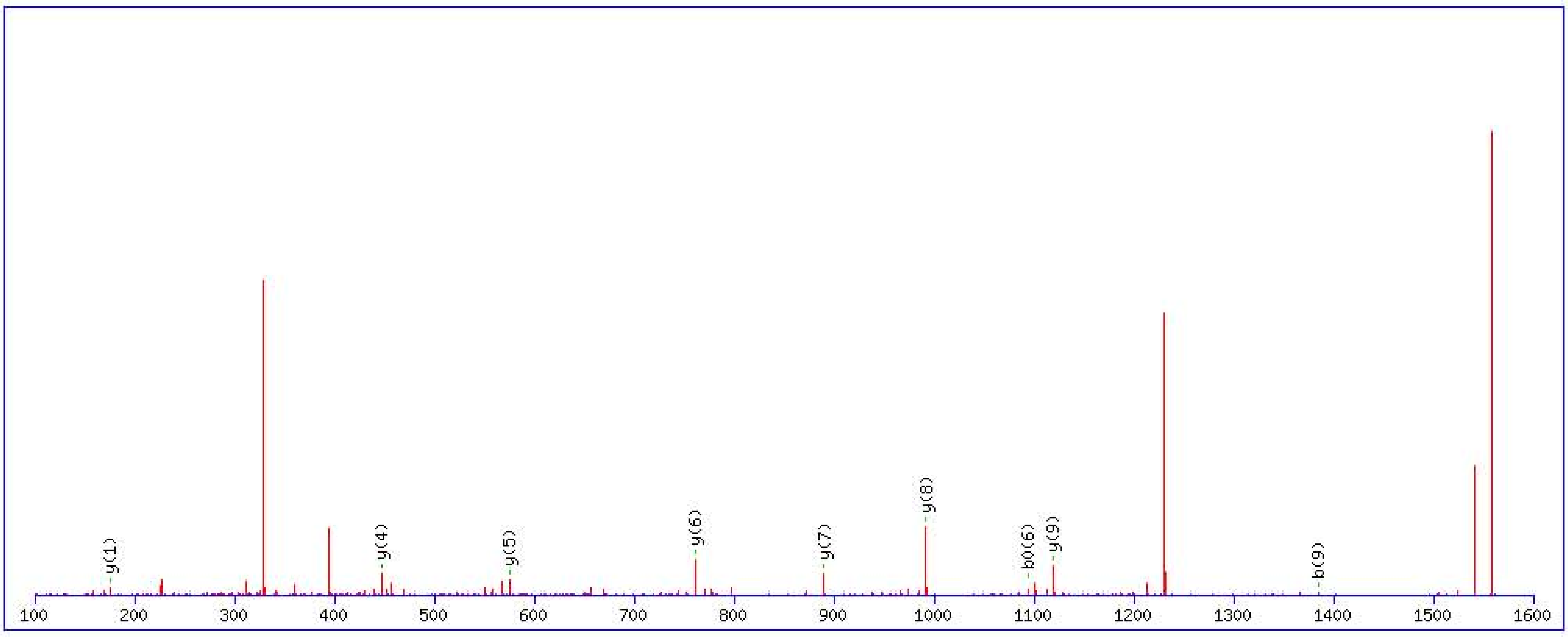
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

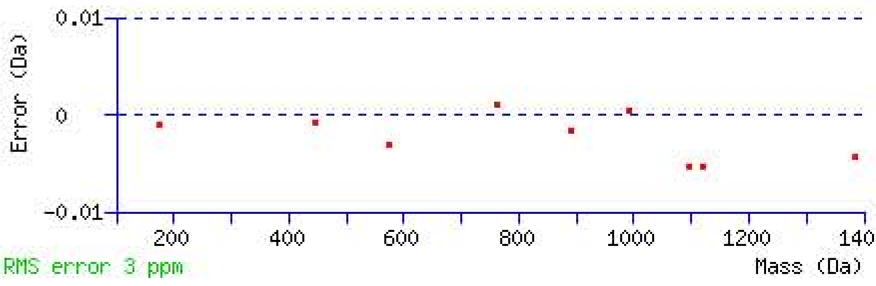
Match to Query 28648: 1557.731868 from(779.873210,2+) rtinseconds(1612) index(29499)
Title: Locus:1.1.1.3224.26 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

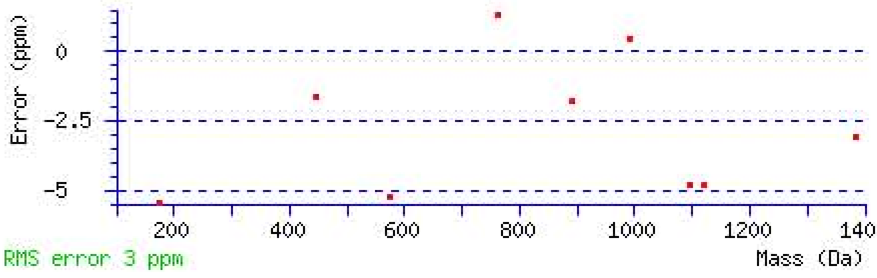
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1557.735809
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.0011
Matches : 9/98 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	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
41.1	1557.735809	-0.003941	QQTEWQSGQR
28.7	1557.735809	-0.003941	QQTEWQSGQR
9.5	1557.747040	-0.015172	AFSHCSSLTKHQR
9.0	1557.720566	0.011302	QEAATGVDTICTHR
7.0	1557.742340	-0.010472	TQSFEIPQPDSGPR
6.4	1557.710663	0.021205	ATQRPPYCDGTHR
6.1	1557.746567	-0.014699	QMSSPQSR
5.5	1557.735779	-0.003911	APPELPERNCGYR
4.2	1557.745697	-0.013829	GSSLFMDTEKSGKR
4.0	1557.720551	0.011317	LSQVSPEDDRPCR

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

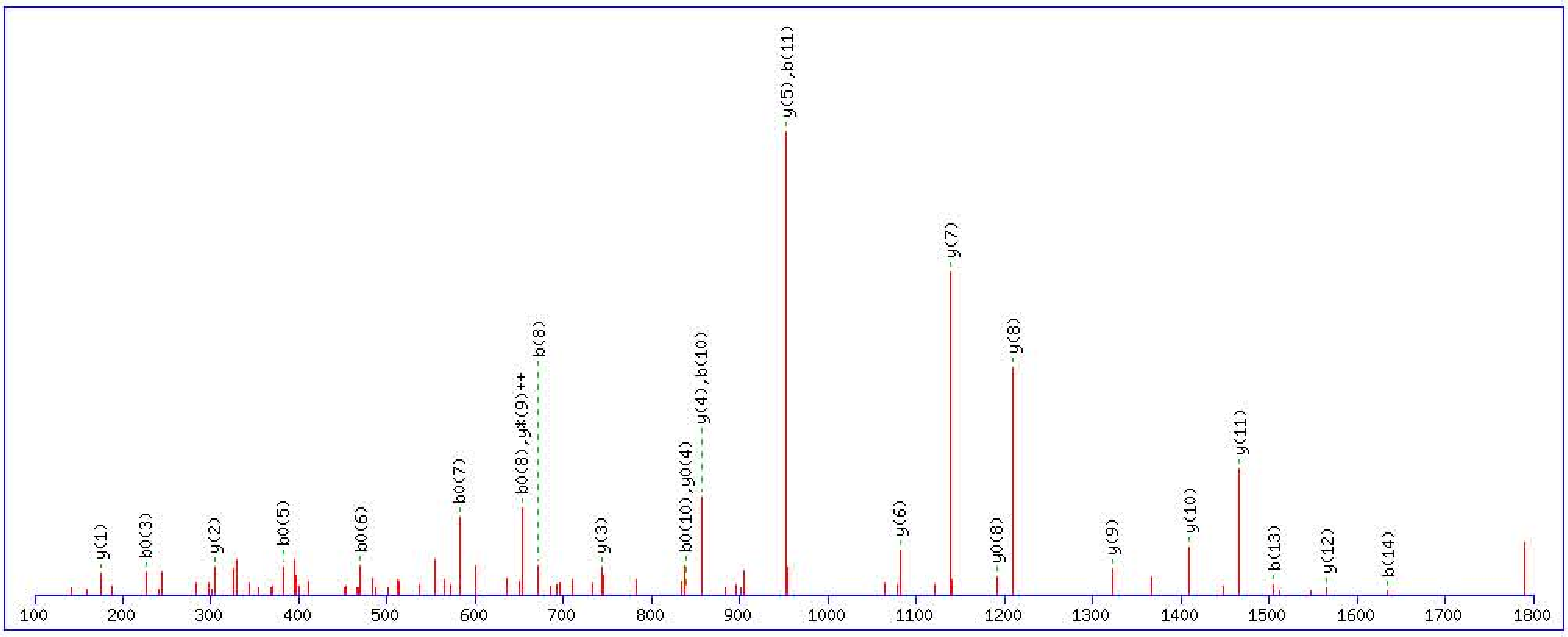
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

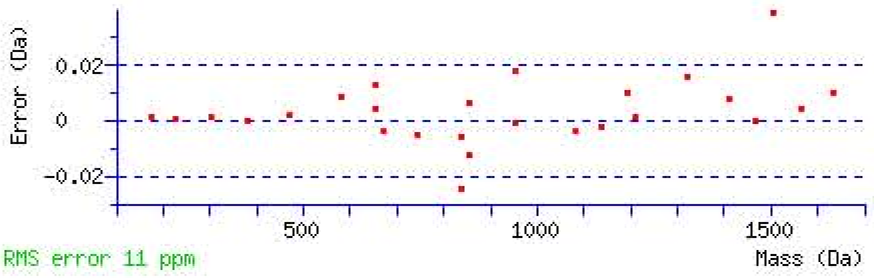
Match to Query 35862: 1807.972188 from(904.993370,2+) rtinseconds(2015) index(5022)
Title: Locus:1.1.1.3221.25 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

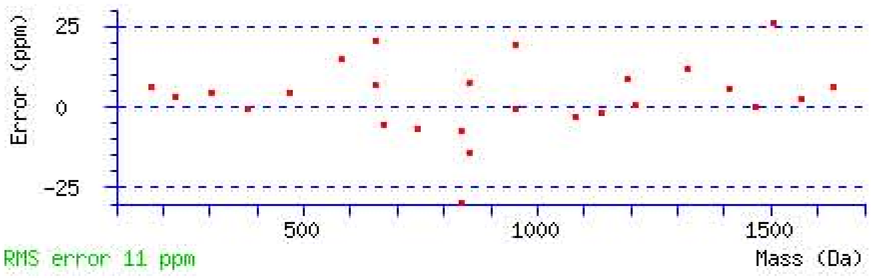
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1807.961441
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 107  Expect: 4.9e-010
Matches : 26/144 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	72.044390	36.525833					A							15
2	143.081504	72.044390					A	1737.931618	869.469447	1720.905069	860.956173	1719.921053	860.464165	14
3	244.129183	122.568230			226.118618	113.562947	T	1666.894504	833.950890	1649.867955	825.437616	1648.883939	824.945608	13
4	343.197597	172.102437			325.187032	163.097154	V	***1565.846825***	783.427051	1548.820276	774.913776	1547.836260	774.421768	12
5	400.219061	200.613169			382.208496	191.607886	G	***1466.778411***	733.892844	1449.751862	725.379569	1448.767846	724.887561	11
6	487.251089	244.129183			469.240524	235.123900	S	***1409.756947***	705.382112	1392.730398	696.868837	1391.746382	696.376829	10
7	600.335153	300.671215			582.324588	291.665932	L	***1322.724919***	661.866098	1305.698370	653.352823	1304.714354	652.860815	9
8	**671.372267**	336.189772			653.361702	327.184489	A	***1209.640855***	605.324066	1192.614306	596.810791	1191.630290	596.318783	8
9	728.393731	364.700504			710.383166	355.695221	G	***1138.603741***	569.805509	1121.577192	561.292234	1120.593176	560.800226	7
10	**856.452309**	428.729793	839.425760	420.216518	838.441744	419.724510	Q	***1081.582277***	541.294777	1064.555728	532.781502	1063.571712	532.289494	6
11	**953.505073**	477.256175	936.478524	468.742900	935.494508	468.250892	P	***953.523699***	477.265488	936.497150	468.752213	935.513134	468.260205	5
12	1066.589137	533.798207	1049.562588	525.284932	1048.578572	524.792924	L	***856.470935***	428.739106	839.444386	420.225831	838.460370	419.733823	4
13	**1505.814463**	753.410870	1488.787914	744.897595	1487.803898	744.405587	Q	***743.386871***	372.197074	726.360322	363.683799	725.376306	363.191791	3
14	**1634.857056**	817.932166	1617.830507	809.418892	1616.846491	808.926884	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
106.6	1807.961441	0.010747	AATVGSLAGQPLQER
59.4	1807.961441	0.010747	AATVGSLAGQPLQER
14.4	1807.947510	0.024678	VGLAQIAAMDISRGNHR
7.2	1807.961426	0.010762	DELEQVLAATRPR
3.3	1807.986542	-0.014354	QAALLEEAALLAER
1.8	1807.983887	-0.011699	KPVTAQERQRER
1.2	1807.954208	0.017980	INMLYNELFQSLVPK
0.9	1807.947464	0.024724	ENRLAERMAILHAER
0.5	1807.980042	-0.007854	TAAIKAMLQLHER

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

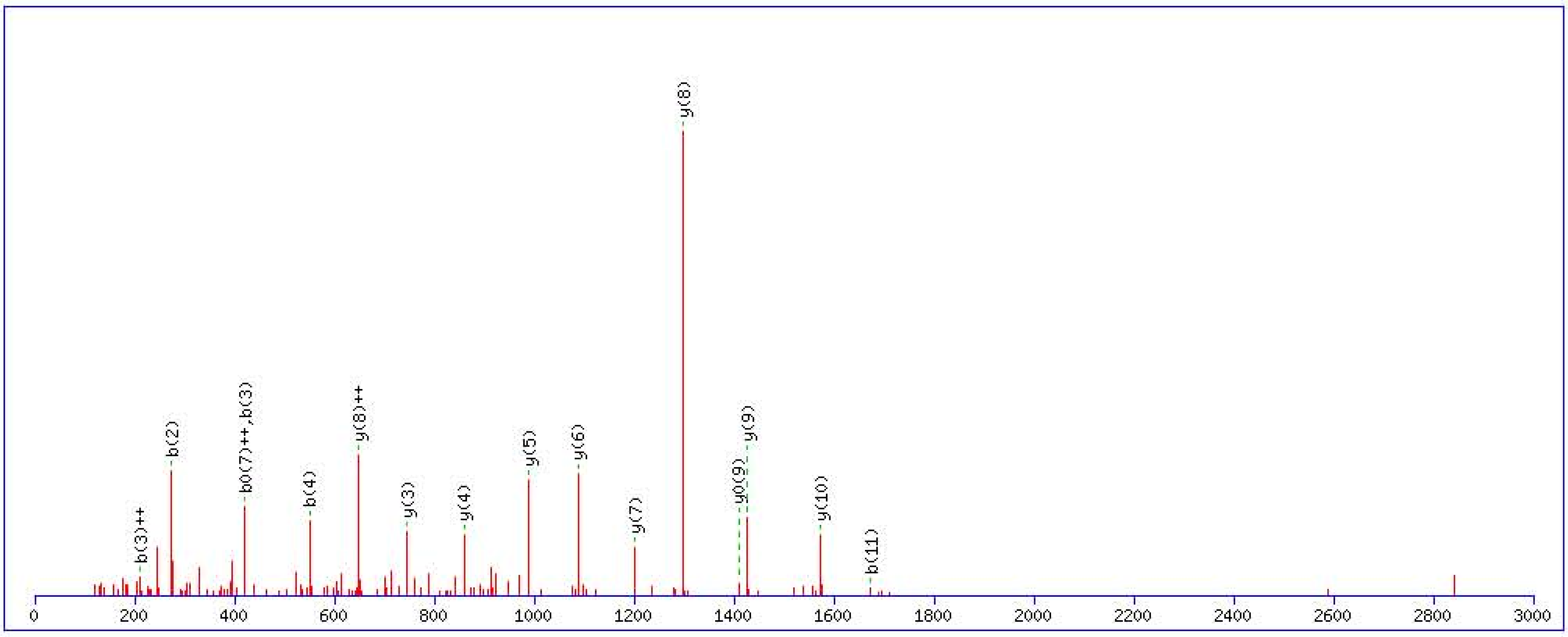
Mascot Search Results

Peptide View

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

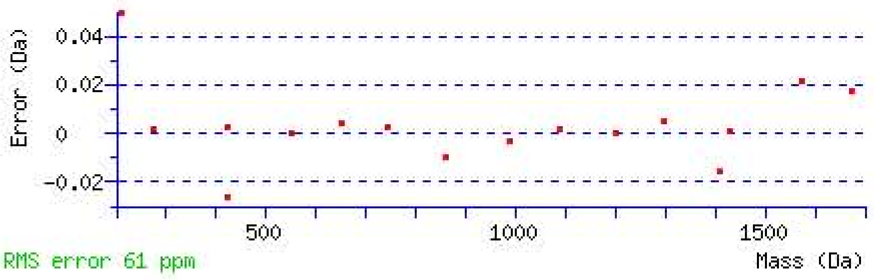
Match to Query 36556: 1846.872628 from(924.443590,2+) rtinseconds(2848) index(37023)
Title: Locus:1.1.1.3653.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

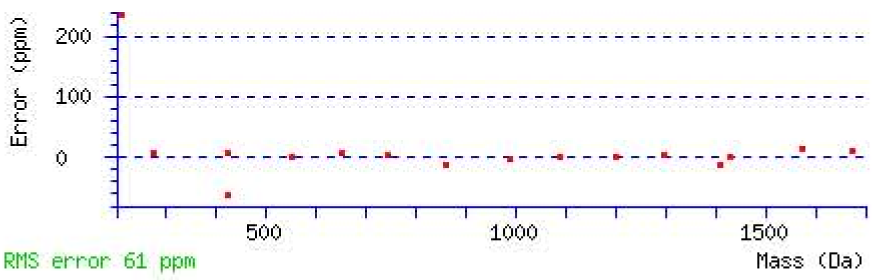
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1846.874603
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 67  Expect: 3.7e-006
Matches : 16/106 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	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
66.6	1846.874603	-0.001975	SWFEPLVEDMQR
17.1	1846.866562	0.006066	LCMAQPRTVQDVEER
15.5	1846.849426	0.023202	SFWENNCKMIYLAR
2.8	1846.895706	-0.023078	CFELQALLEEER
1.7	1846.870560	0.002068	IHIGEKPYECKECGK
0.7	1846.874603	-0.001975	MWTYMKSAEPSVFVR
0.7	1846.874603	-0.001975	MWTYMKSAEPSVFVR

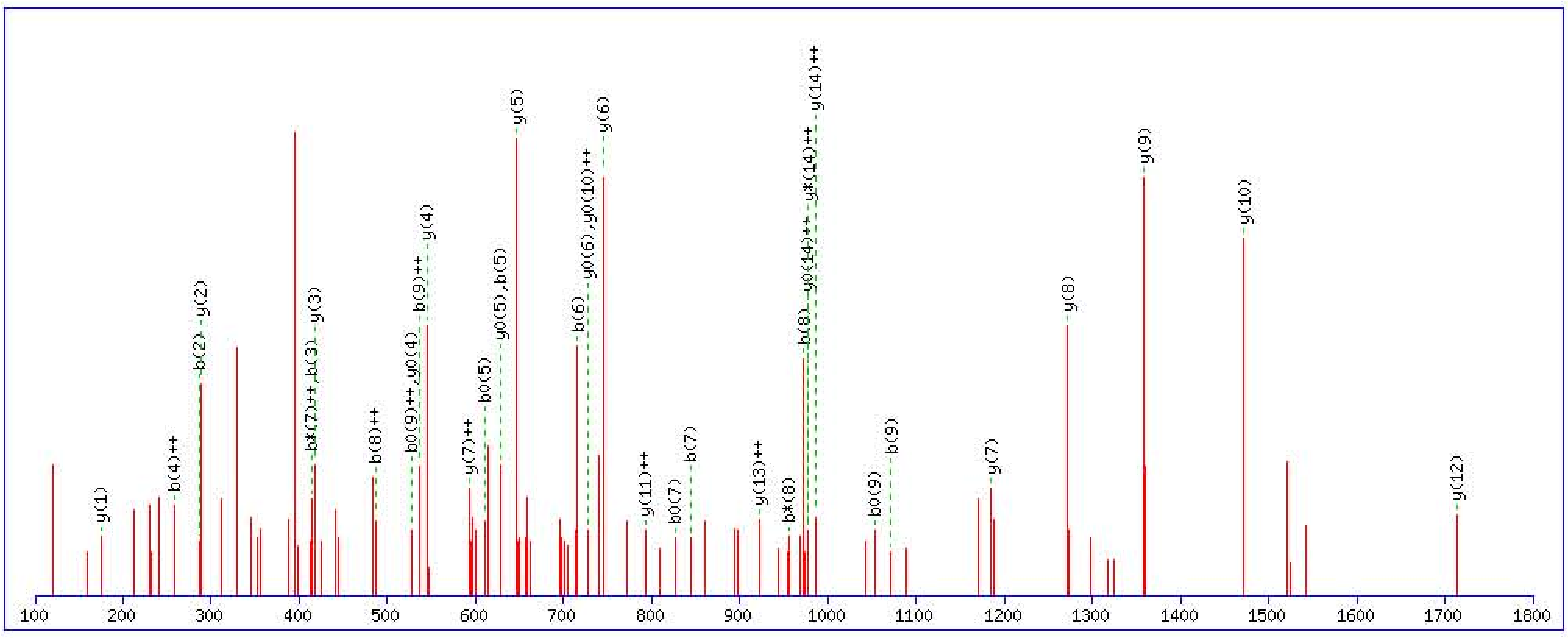
Mascot Search Results

Peptide View

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

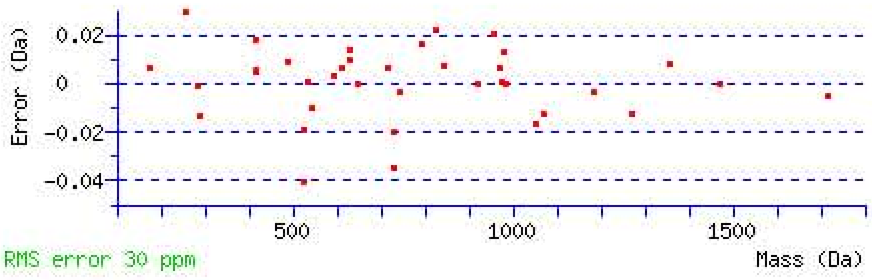
Match to Query 54322: 3040.554256 from(761.145840,4+) rtinseconds(2926) index(37549)
Title: Locus:1.1.1.3680.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

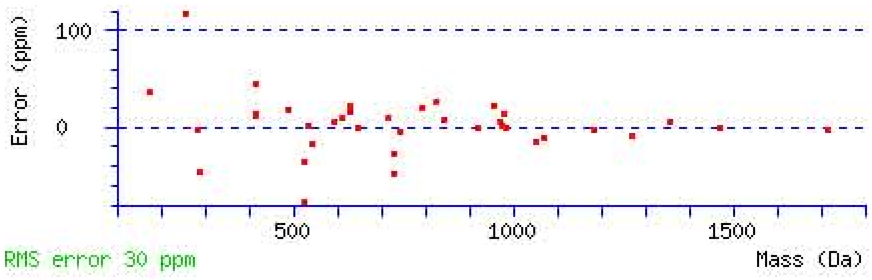
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3040.553925
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q17 : Biotin:Thermo-21345 (Q)
Ions Score: 54 **Expect:** 9.2e-006
Matches : 37/250 fragment ions using 75 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	187.086589	94.046932					W							23
2	***286.155003***	143.581140					V	2855.481902	1428.244589	2838.455353	1419.731314	2837.471337	1419.239306	22
3	***414.213581***	207.610429	397.187032	199.097154			Q	2756.413488	1378.710382	2739.386939	1370.197107	2738.402923	1369.705099	21
4	515.261260	**258.134268**	498.234711	249.620994	497.250695	249.128986	T	2628.354910	1314.681093	2611.328361	1306.167818	2610.344345	1305.675810	20
5	***628.345324***	314.676300	611.318775	306.163026	610.334759	305.671018	L	2527.307231	1264.157253	2510.280682	1255.643979	2509.296666	1255.151971	19
6	***715.377352***	358.192314	698.350803	349.679040	697.366787	349.187032	S	2414.223167	1207.615221	2397.196618	1199.101947	2396.212602	1198.609939	18
7	***844.419945***	422.713611	827.393396	414.200336	826.409380	413.708328	E	2327.191139	1164.099207	2310.164590	1155.585933	2309.180574	1155.093925	17
8	***972.478523***	**486.742900**	955.451974	478.229625	954.467958	477.737617	Q	2198.148546	1099.577911	2181.121997	1091.064636	2180.137981	1090.572628	16
9	***1071.546937***	**536.277107**	1054.520388	527.763832	1053.536372	527.271824	V	2070.089968	1035.548622	2053.063419	1027.035347	2052.079403	1026.543339	15
10	1199.605515	600.306396	1182.578966	591.793121	1181.594950	591.301113	Q	1971.021554	986.014415	1953.995005	977.501141	1953.010989	977.009133	14
11	1328.648108	664.827692	1311.621559	656.314418	1310.637543	655.822410	E	1842.962976	921.985126	1825.936427	913.471852	1824.952411	912.979844	13
12	1457.690701	729.348989	1440.664152	720.835714	1439.680136	720.343706	E	***1713.920383***	857.463830	1696.893834	848.950555	1695.909818	848.458547	12
13	1570.774765	785.891021	1553.748216	777.377746	1552.764200	776.885738	L	1584.877790	792.942533	1567.851241	784.429259	1566.867225	783.937251	11
14	1683.858829	842.433053	1666.832280	833.919778	1665.848264	833.427770	L	***1471.793726***	736.400501	1454.767177	727.887227	1453.783161	727.395219	10
15	1770.890857	885.949067	1753.864308	877.435792	1752.880292	876.943784	S	***1358.709662***	679.858469	1341.683113	671.345195	1340.699097	670.853187	9
16	1857.922885	929.465081	1840.896336	920.951806	1839.912320	920.459798	S	***1271.677634***	636.342455	1254.651085	627.829181	1253.667069	627.337173	8
17	2297.148211	1149.077744	2280.121662	1140.564469	2279.137646	1140.072461	Q	***1184.645606***	592.826441	1167.619057	584.313167	1166.635041	583.821159	7
18	2396.216625	1198.611950	2379.190076	1190.098676	2378.206060	1189.606668	V	***745.420280***	373.213778	728.393731	364.700504	727.409715	364.208496	6
19	2497.264304	1249.135790	2480.237755	1240.622515	2479.253739	1240.130507	T	***646.351866***	323.679571	629.325317	315.166297	628.341301	314.674289	5
20	2625.322882	1313.165079	2608.296333	1304.651804	2607.312317	1304.159796	Q	***545.304187***	273.155732	528.277638	264.642457	527.293622	264.150449	4
21	2754.365475	1377.686375	2737.338926	1369.173101	2736.354910	1368.681093	E	***417.245609***	209.126443	400.219060	200.613168	399.235044	200.121160	3
22	2867.449539	1434.228408	2850.422990	1425.715133	2849.438974	1425.223125	L	***288.203016***	144.605146	271.176467	136.091872			2
23							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of WVQTLSEQVQEELLSSQVTQELR
(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	3040.553925	0.000331	WVQTLSEQVQEELLSSQVTQELR
34.0	3040.553925	0.000331	WVQTLSEQVQEELLSSQVTQELR
19.4	3040.553925	0.000331	WVQTLSEQVQEELLSSQVTQELR
6.1	3040.553925	0.000331	WVQTLSEQVQEELLSSQVTQELR
2.6	3040.553925	0.000331	WVQTLSEQVQEELLSSQVTQELR
0.7	3040.532150	0.022106	ATLISLQVARDSGTGLMMSVNFSTQELR
0.7	3040.532150	0.022106	ATLISLQVARDSGTGLMMSVNFSTQELR

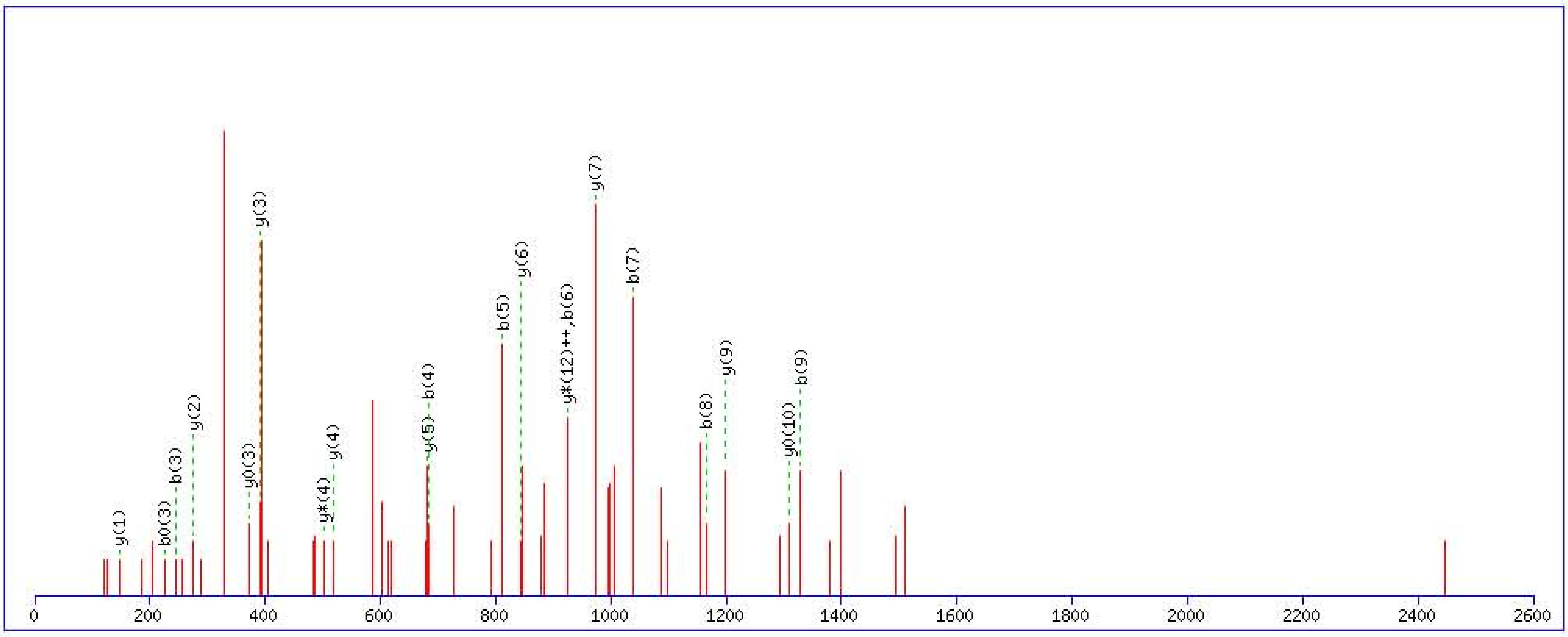
Mascot Search Results

Peptide View

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

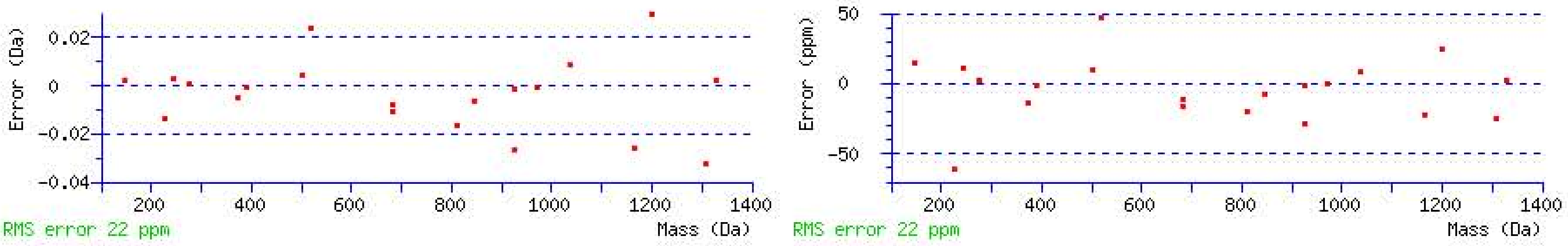
Match to Query 40026: 2008.009948 from(1005.012250,2+) rtinseconds(2507) index(34645)
Title: Locus:1.1.1.3536.24 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 2008.008789
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.0019
Matches : 20/146 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	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



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
33.2	2008.008789	0.001159	SGVQQLIQYYQDQK
30.4	2008.008789	0.001159	SGVQQLIQYYQDQK
14.5	2008.008789	0.001159	SGVQQLIQYYQDQK
4.6	2008.008789	0.001159	SGVQQLIQYYQDQK
4.1	2008.005630	0.004318	ITQRMVCAGYKEGGK

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

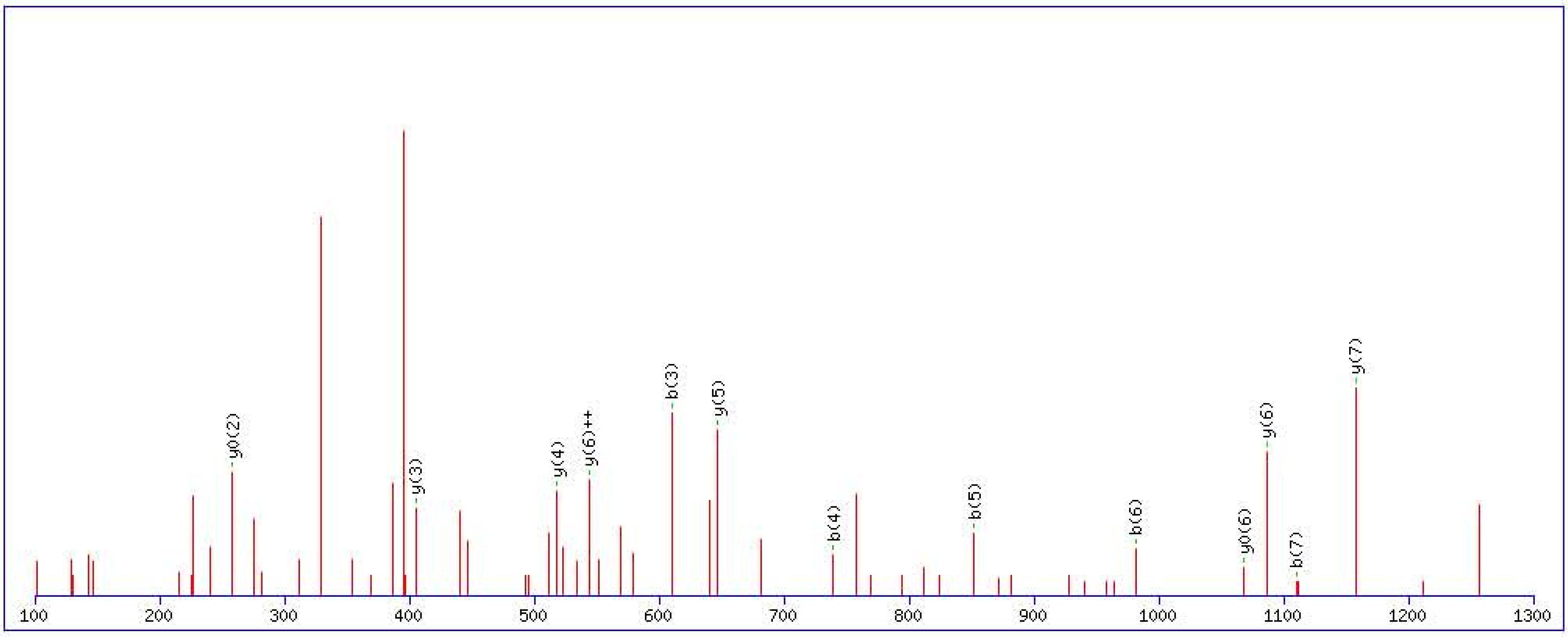
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VAQELEEK**
Found in **APOL1_HUMAN**, Apolipoprotein L1 OS=Homo sapiens GN=APOL1 PE=1 SV=5

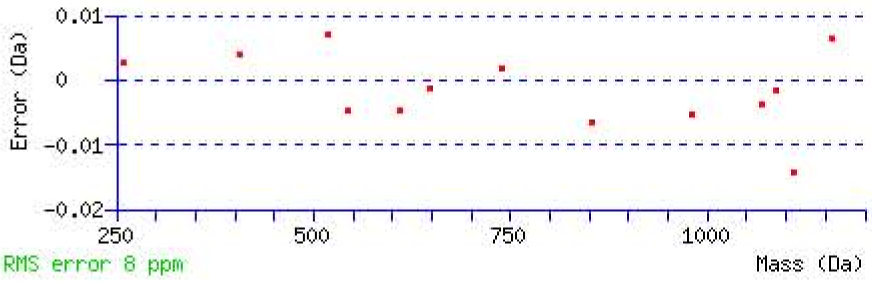
Match to Query 19148: 1255.643468 from(628.829010,2+) rtinseconds(1609) index(43556)
Title: Locus:1.1.1.3273.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

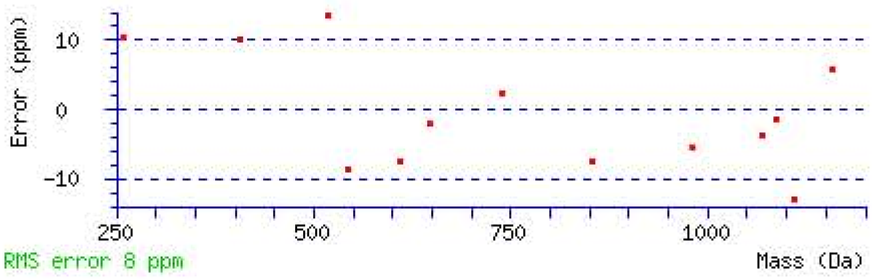
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1255.648193
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 31 **Expect:** 0.018
Matches : 13/72 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	100.075690	50.541483					V							8
2	171.112804	86.060040					A	***1157.587087***	579.297182	1140.560538	570.783907	1139.576522	570.291899	7
3	***610.338130***	305.672703	593.311581	297.159429			Q	***1086.549973***	543.778625	1069.523424	535.265350	1068.539408	534.773342	6
4	***739.380723***	370.194000	722.354174	361.680725	721.370158	361.188717	E	***647.324647***	324.165962	630.298098	315.652687	629.314082	315.160679	5
5	***852.464787***	426.736032	835.438238	418.222757	834.454222	417.730749	L	***518.282054***	259.644665	501.255505	251.131391	500.271489	250.639383	4
6	***981.507380***	491.257328	964.480831	482.744054	963.496815	482.252046	E	***405.197990***	203.102633	388.171441	194.589359	387.187425	194.097351	3
7	***1110.549973***	555.778625	1093.523424	547.265350	1092.539408	546.773342	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
8							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.9	1255.648193	-0.004725	VAQELEEK
15.3	1255.656067	-0.012599	ALPIQSFSHEK
14.4	1255.645508	-0.002040	TRMIEANIHR
10.9	1255.659424	-0.015956	QAEKNVEK
10.5	1255.659439	-0.015971	VALEQTER
9.2	1255.640793	0.002675	DTHKKLEEEK
4.6	1255.634262	0.009206	ADMKHLREEK
4.4	1255.659439	-0.015971	LLIENGVSMHK
3.7	1255.659439	-0.015971	GLQGEKGEK
3.2	1255.629547	0.013921	EKLESAEPPEK

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

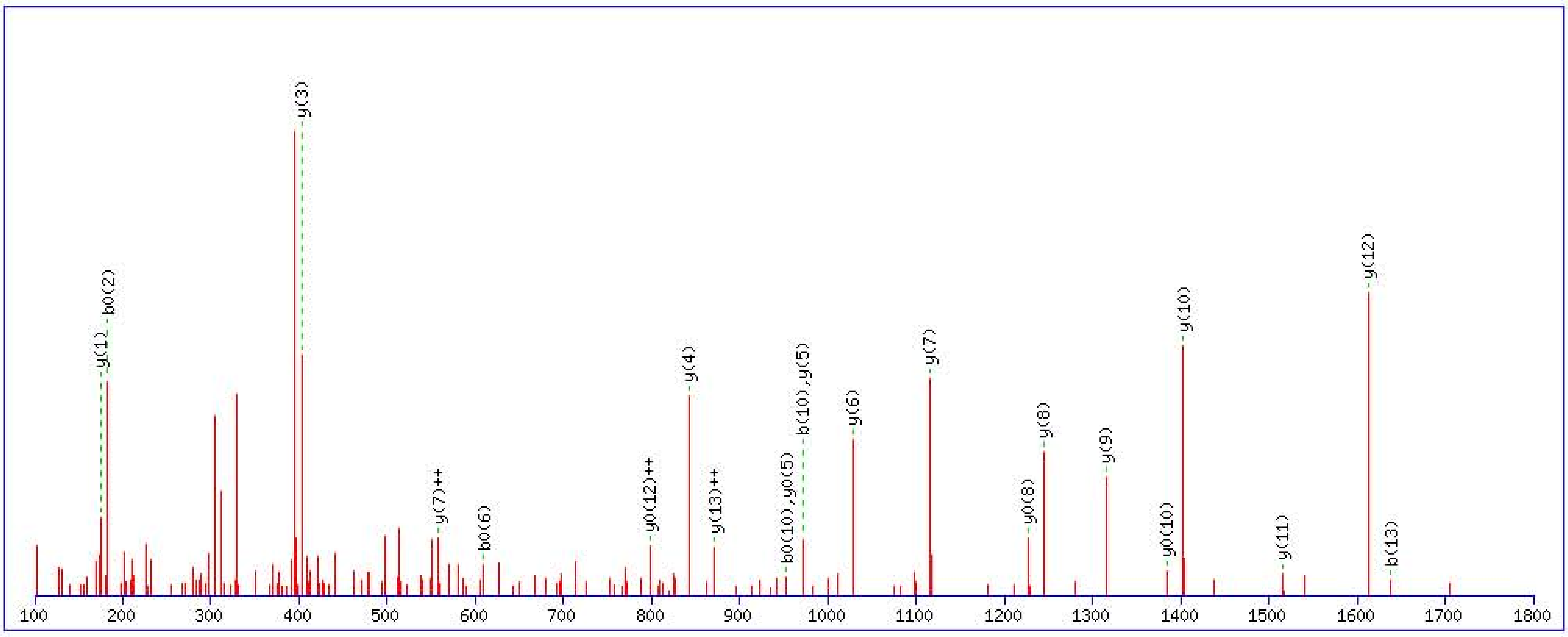
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTEPISAESGEQVER**
Found in **APOL1_HUMAN**, Apolipoprotein L1 OS=Homo sapiens GN=APOL1 PE=1 SV=5

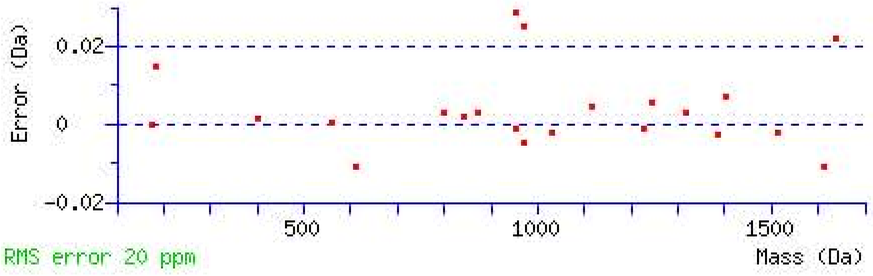
Match to Query 38179: 1940.944722 from(647.988850,3+) rtinseconds(1751) index(30277)
Title: Locus:1.1.1.3273.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

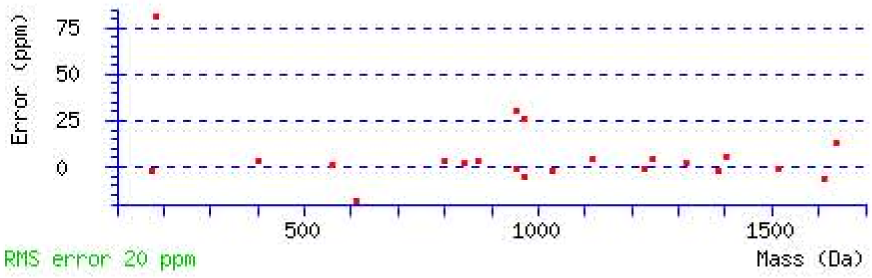
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1940.951324
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 76  Expect: 2.3e-007
Matches : 22/142 fragment ions using 33 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.075690	50.541483					V							15
2	201.123369	101.065322			183.112804	92.060040	T	1842.890205	921.948741	1825.863656	913.435466	1824.879640	912.943458	14
3	330.165962	165.586619			312.155397	156.581336	E	1741.842526	871.424901	1724.815977	862.911627	1723.831961	862.419619	13
4	427.218726	214.113001			409.208161	205.107719	P	***1612.799933***	806.903605	1595.773384	798.390330	1594.789368	797.898322	12
5	540.302790	270.655033			522.292225	261.649751	I	***1515.747169***	758.377223	1498.720620	749.863948	1497.736604	749.371940	11
6	627.334818	314.171047			609.324253	305.165765	S	***1402.663105***	701.835191	1385.636556	693.321916	1384.652540	692.829908	10
7	698.371932	349.689604			680.361367	340.684322	A	***1315.631077***	658.319177	1298.604528	649.805902	1297.620512	649.313894	9
8	827.414525	414.210901			809.403960	405.205618	E	***1244.593963***	622.800620	1227.567414	614.287345	1226.583398	613.795337	8
9	914.446553	457.726915			896.435988	448.721632	S	***1115.551370***	558.279323	1098.524821	549.766049	1097.540805	549.274041	7
10	**971.468017**	486.237647			953.457452	477.232364	G	***1028.519342***	514.763309	1011.492793	506.250035	1010.508777	505.758027	6
11	1100.510610	550.758943			1082.500045	541.753661	E	***971.497878***	486.252577	954.471329	477.739303	953.487313	477.247295	5
12	1539.735936	770.371606	1522.709387	761.858332	1521.725371	761.366324	Q	***842.455285***	421.731281	825.428736	413.218006	824.444720	412.725998	4
13	**1638.804350**	819.905813	1621.777801	811.392539	1620.793785	810.900531	V	***403.229959***	202.118617	386.203410	193.605343	385.219394	193.113335	3
14	1767.846943	884.427110	1750.820394	875.913835	1749.836378	875.421827	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
75.6	1940.951324	-0.006602	VTEPISAESGEQVER
4.8	1940.937378	0.007344	SNNLEREQEQLDR

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

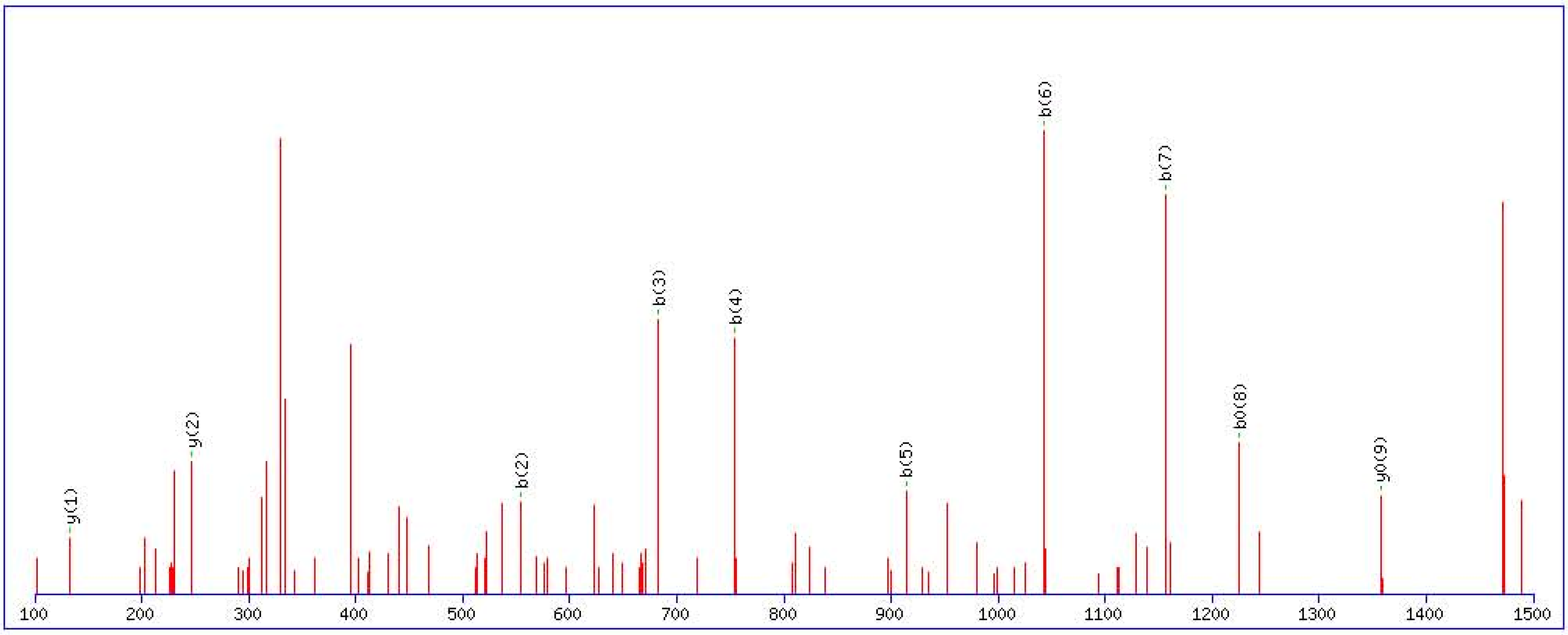
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NQEACELSNN**
Found in **APOM_HUMAN**, Apolipoprotein M OS=Homo sapiens GN=APOM PE=1 SV=2

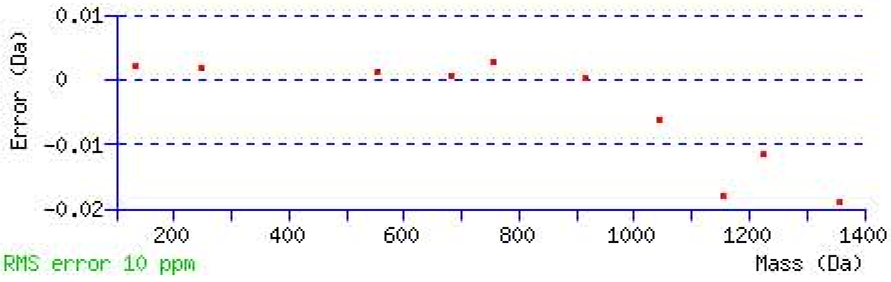
Match to Query 26844: 1488.625448 from(745.320000,2+) rtinseconds(1675) index(16971)
Title: Locus:1.1.1.3149.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

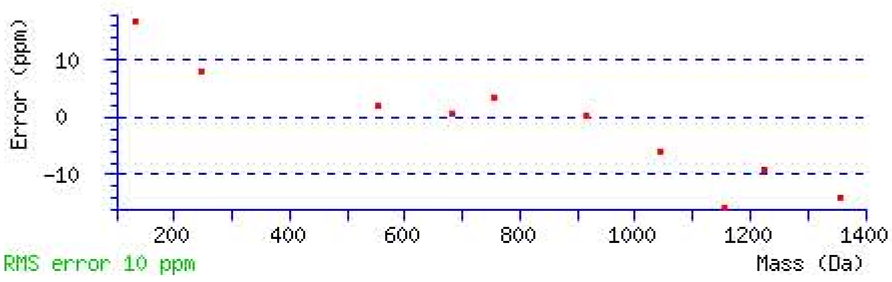
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1488.633682
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 6.6e-006
Matches : 11/100 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	115.050203	58.028740	98.023654	49.515465			N							10
2	***554.275529***	277.641403	537.248980	269.128128			Q	1375.598062	688.302669	1358.571513	679.789395	1357.587497	679.297387	9
3	***683.318122***	342.162699	666.291573	333.649425	665.307557	333.157417	E	936.372736	468.690006	919.346187	460.176732	918.362171	459.684724	8
4	***754.355236***	377.681256	737.328687	369.167982	736.344671	368.675974	A	807.330143	404.168710	790.303594	395.655435	789.319578	395.163427	7
5	***914.385885***	457.696581	897.359336	449.183306	896.375320	448.691298	C	736.293029	368.650153	719.266480	360.136878	718.282464	359.644870	6
6	***1043.428478***	522.217877	1026.401929	513.704603	1025.417913	513.212595	E	576.262380	288.634828	559.235831	280.121554	558.251815	279.629546	5
7	***1156.512542***	578.759909	1139.485993	570.246635	1138.501977	569.754626	L	447.219787	224.113531	430.193238	215.600257	429.209222	215.108249	4
8	1243.544570	622.275923	1226.518021	613.762649	1225.534005	613.270641	S	334.135723	167.571499	317.109174	159.058225	316.125158	158.566217	3
9	***1357.587497***	679.297387	1340.560948	670.784112	1339.576932	670.292104	N	**247.103695**	124.055485	230.077146	115.542211			2
10							N	**133.060768**	67.034022	116.034219	58.520747			1





NCBI **BLAST** search of NQEACELSNN
(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	1488.633682	-0.008234	NQEACELSNN

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

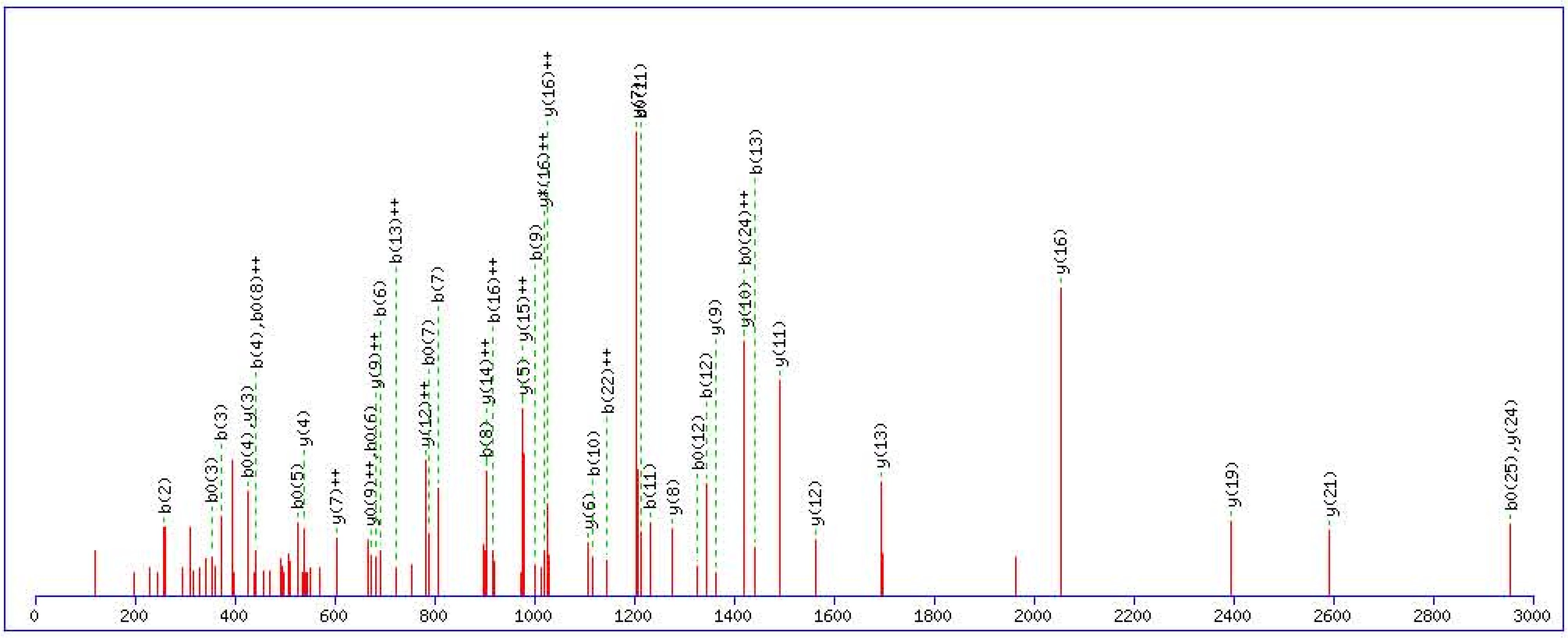
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EELATFDPVDNIVFNMAAGSAPMQLHLR**
Found in **APOM_HUMAN**, Apolipoprotein M OS=Homo sapiens GN=APOM PE=1 SV=2

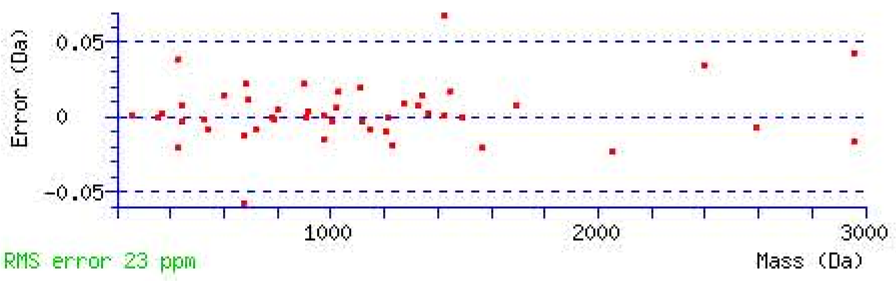
Match to Query 58765: 3396.661656 from(850.172690,4+) rtinseconds(3167) index(39142)
Title: Locus:1.1.1.3762.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

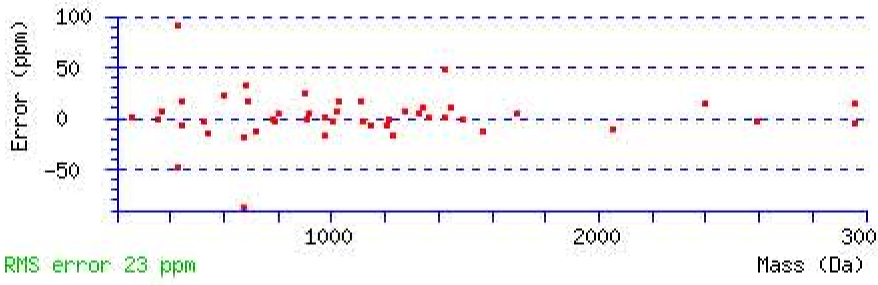
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3396.666855
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q24     : Biotin:Thermo-21345 (Q)
Ions Score: 95  Expect: 9.1e-009
Matches : 47/288 fragment ions using 79 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							28
2	***259.092462***	130.049869			241.081897	121.044587	E	3268.631560	1634.819418	3251.605011	1626.306143	3250.620995	1625.814135	27
3	***372.176526***	186.591901			354.165961	177.586619	L	3139.588967	1570.298122	3122.562418	1561.784847	3121.578402	1561.292839	26
4	***443.213640***	222.110458			425.203075	213.105176	A	3026.504903	1513.756089	3009.478354	1505.242815	3008.494338	1504.750807	25
5	544.261319	272.634298			526.250754	263.629015	T	***2955.467789***	1478.237532	2938.441240	1469.724258	2937.457224	1469.232250	24
6	***691.329733***	346.168505			673.319168	337.163222	F	2854.420110	1427.713693	2837.393561	1419.200418	2836.409545	1418.708410	23
7	***806.356676***	403.681976			788.346111	394.676694	D	2707.351696	1354.179486	2690.325147	1345.666211	2689.341131	1345.174204	22
8	***903.409440***	452.208358			885.398875	443.203076	P	***2592.324753***	1296.666014	2575.298204	1288.152740	2574.314188	1287.660732	21
9	***1002.477854***	501.742565			984.467289	492.737282	V	2495.271989	1248.139632	2478.245440	1239.626358	2477.261424	1239.134350	20
10	***1117.504797***	559.256037			1099.494232	550.250754	D	***2396.203575***	1198.605425	2379.177026	1190.092151	2378.193010	1189.600143	19
11	***1231.547724***	616.277500	1214.521175	607.764226	1213.537159	607.272218	N	2281.176632	1141.091954	2264.150083	1132.578679	2263.166067	1132.086672	18
12	***1344.631788***	672.819532	1327.605239	664.306258	1326.621223	663.814249	I	2167.133705	1084.070490	2150.107156	1075.557216	2149.123140	1075.065208	17
13	***1443.700202***	**722.353739**	1426.673653	713.840465	1425.689637	713.348457	V	***2054.049641***	1027.528458	2037.023092	1019.015184	2036.039076	1018.523176	16
14	1590.768616	795.887946	1573.742067	787.374672	1572.758051	786.882664	F	1954.981227	977.994252	1937.954678	969.480977	1936.970662	968.988969	15
15	1704.811543	852.909410	1687.784994	844.396135	1686.800978	843.904127	N	1807.912813	904.460045	1790.886264	895.946770	1789.902248	895.454762	14
16	1835.852028	**918.429652**	1818.825479	909.916378	1817.841463	909.424370	M	***1693.869886***	847.438581	1676.843337	838.925307	1675.859321	838.433299	13
17	1906.889142	953.948209	1889.862593	945.434935	1888.878577	944.942927	A	***1562.829401***	781.918339	1545.802852	773.405064	1544.818836	772.913056	12
18	1977.926256	989.466766	1960.899707	980.953492	1959.915691	980.461483	A	***1491.792287***	746.399782	1474.765738	737.886507	1473.781722	737.394499	11
19	2034.947720	1017.977498	2017.921171	1009.464224	2016.937155	1008.972215	G	***1420.755173***	710.881225	1403.728624	702.367950	1402.744608	701.875942	10
20	2121.979748	1061.493512	2104.953199	1052.980237	2103.969183	1052.488229	S	***1363.733709***	682.370493	1346.707160	673.857218	1345.723144	673.365210	9
21	2193.016862	1097.012069	2175.990313	1088.498794	2175.006297	1088.006786	A	***1276.701681***	638.854479	1259.675132	630.341204			8
22	2290.069626	**1145.538451**	2273.043077	1137.025176	2272.059061	1136.533168	P	***1205.664567***	603.335922	1188.638018	594.822647			7
23	2421.110111	1211.058693	2404.083562	1202.545419	2403.099546	1202.053411	M	***1108.611803***	554.809540	1091.585254	546.296265			6
24	2860.335437	1430.671357	2843.308888	1422.158082	2842.324872	1421.666074	Q	***977.571318***	489.289297	960.544769	480.776023			5
25	2973.419501	1487.213389	2956.392952	1478.700114	2955.408936	1478.208106	L	***538.345992***	269.676634	521.319443	261.163360			4
26	3110.478413	1555.742845	3093.451864	1547.229570	3092.467848	1546.737562	H	***425.261928***	213.134602	408.235379	204.621328			3
27	3223.562477	1612.284877	3206.535928	1603.771602	3205.551912	1603.279594	L	288.203016	144.605146	271.176467	136.091872			2
28							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
94.5	3396.666855	-0.005199	EELATFDPVDNIVFNMAAGSAPMQLHLR

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

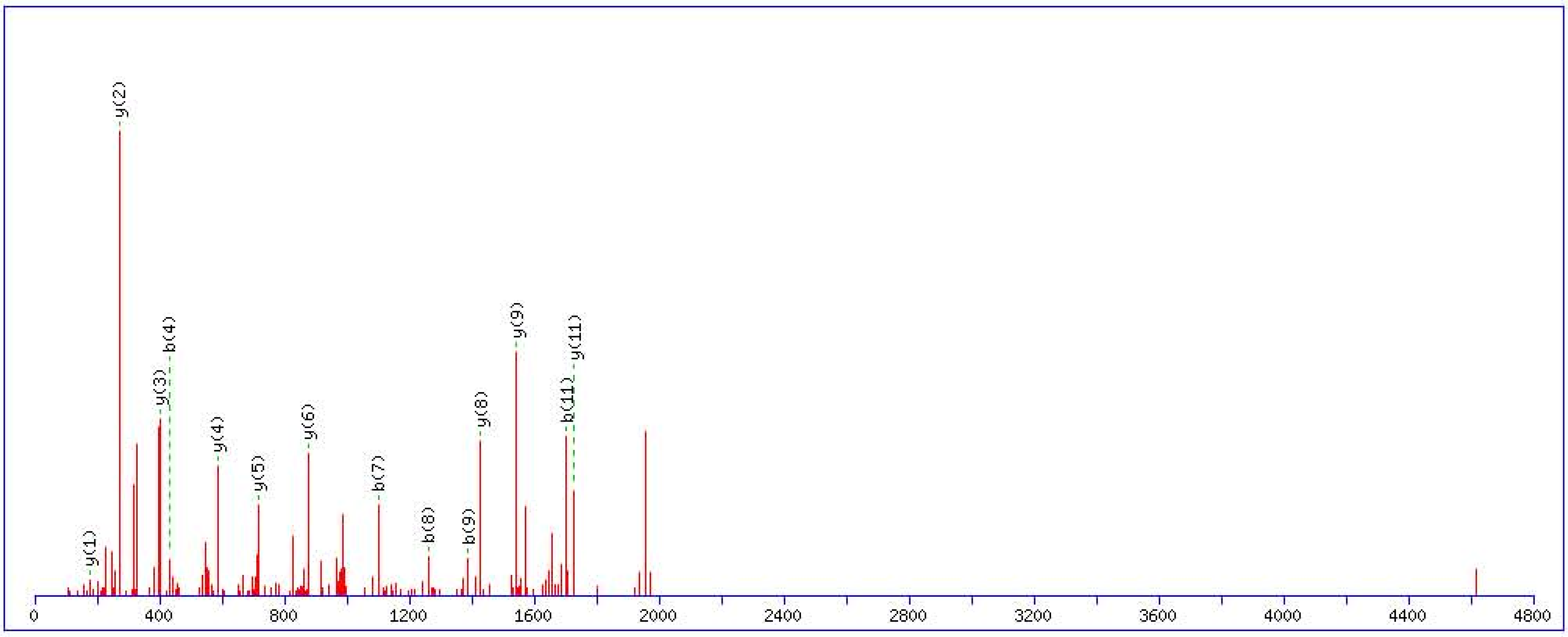
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SCALDQNCQWEPR**
Found in **ATRN_HUMAN**, Attractin OS=Homo sapiens GN=ATRN PE=1 SV=2

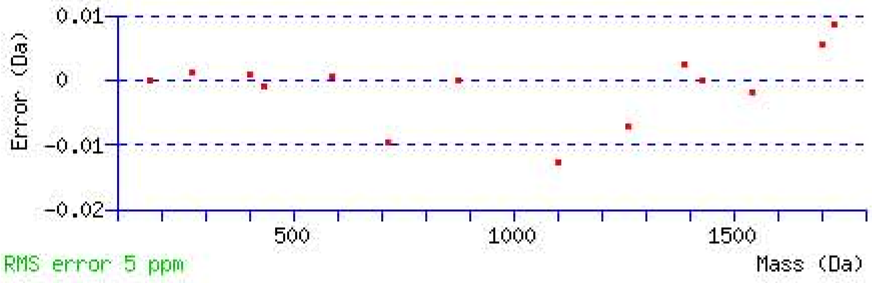
Match to Query 38850: 1973.852468 from(987.933510,2+) rtinseconds(1999) index(19073)
Title: Locus:1.1.1.3261.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

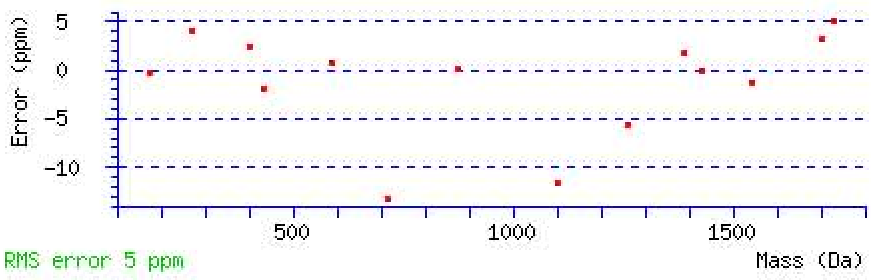
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1973.854614
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 76  Expect: 8.5e-008
Matches : 14/130 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**							**13**
2	248.069953	124.538614			230.059388	115.533332	**C**	1887.829872	944.418574	1870.803323	935.905300	1869.819307	935.413292	**12**
3	319.107067	160.057171			301.096502	151.051889	**A**	***1727.799223***	864.403250	1710.772674	855.889975	1709.788658	855.397967	**11**
4	**432.191131**	216.599203			414.180566	207.593921	**L**	1656.762109	828.884693	1639.735560	820.371418	1638.751544	819.879410	**10**
5	547.218074	274.112675			529.207509	265.107393	**D**	***1543.678045***	772.342661	1526.651496	763.829386	1525.667480	763.337378	**9**
6	986.443400	493.725338	969.416851	485.212064	968.432835	484.720056	**Q**	***1428.651102***	714.829189	1411.624553	706.315915	1410.640537	705.823907	**8**
7	**1100.486327**	550.746802	1083.459778	542.233527	1082.475762	541.741519	**N**	989.425776	495.216526	972.399227	486.703252	971.415211	486.211244	**7**
8	**1260.516976**	630.762126	1243.490427	622.248852	1242.506411	621.756844	**C**	***875.382849***	438.195063	858.356300	429.681788	857.372284	429.189780	**6**
9	**1388.575554**	694.791415	1371.549005	686.278141	1370.564989	685.786133	**Q**	***715.352200***	358.179738	698.325651	349.666464	697.341635	349.174456	**5**
10	1574.654867	787.831072	1557.628318	779.317797	1556.644302	778.825789	**W**	***587.293622***	294.150449	570.267073	285.637174	569.283057	285.145166	**4**
11	**1703.697460**	852.352368	1686.670911	843.839094	1685.686895	843.347086	**E**	***401.214309***	201.110792	384.187760	192.597518	383.203744	192.105510	**3**
12	1800.750224	900.878750	1783.723675	892.365476	1782.739659	891.873468	**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 SCALDQNCQWEPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
76.4	1973.854614	-0.002146	SCALDQNCQWEPR
41.9	1973.854614	-0.002146	SCALDQNCQWEPR
13.0	1973.853729	-0.001261	DSPETGEEMGRAEGAWPR
4.3	1973.831284	0.021184	CSDYESIEVPDSYTGPR

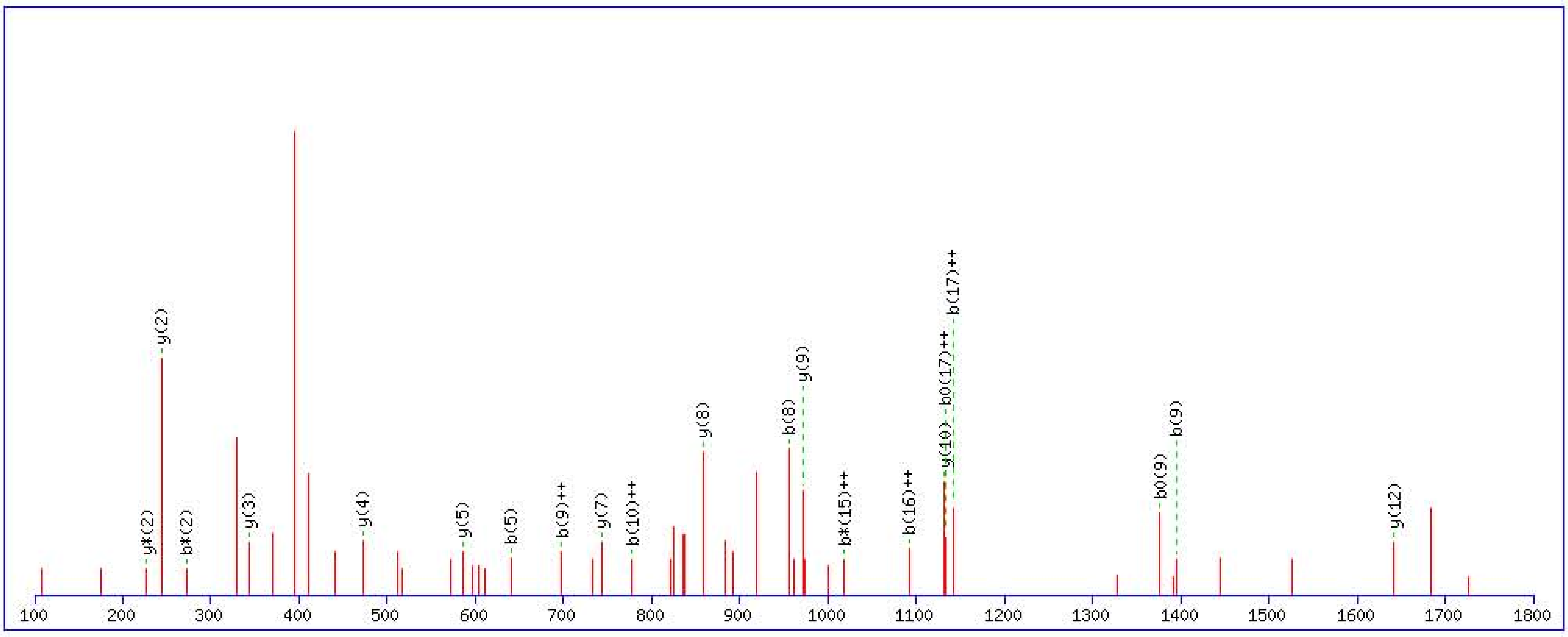
Mascot Search Results

Peptide View

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

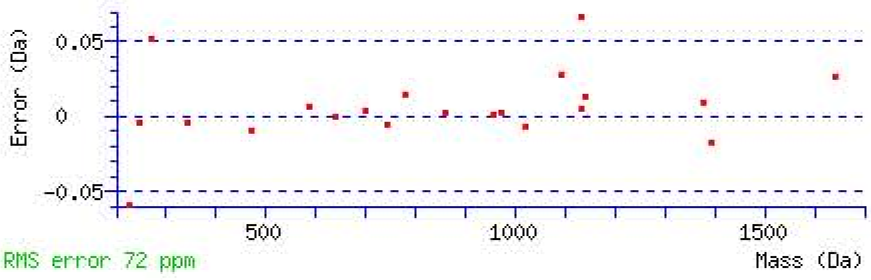
Match to Query 48817: 2524.177632 from(842.399820,3+) rtinseconds(2002) index(60663)
Title: Locus:1.1.1.1608.26 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

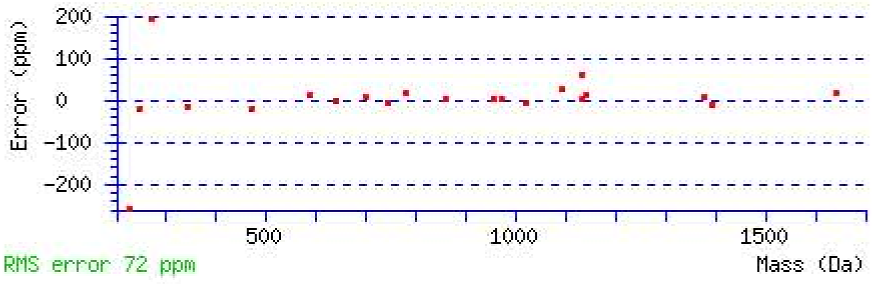
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2524.164780
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 36 **Expect:** 0.00055
Matches : 21/206 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	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
36.0	2524.164780	0.012852	KCSYTEDAQCIDGTIEVPK
1.2	2524.209503	-0.031871	EHIEGGGGPSDPSEFGTKFRAPPR

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

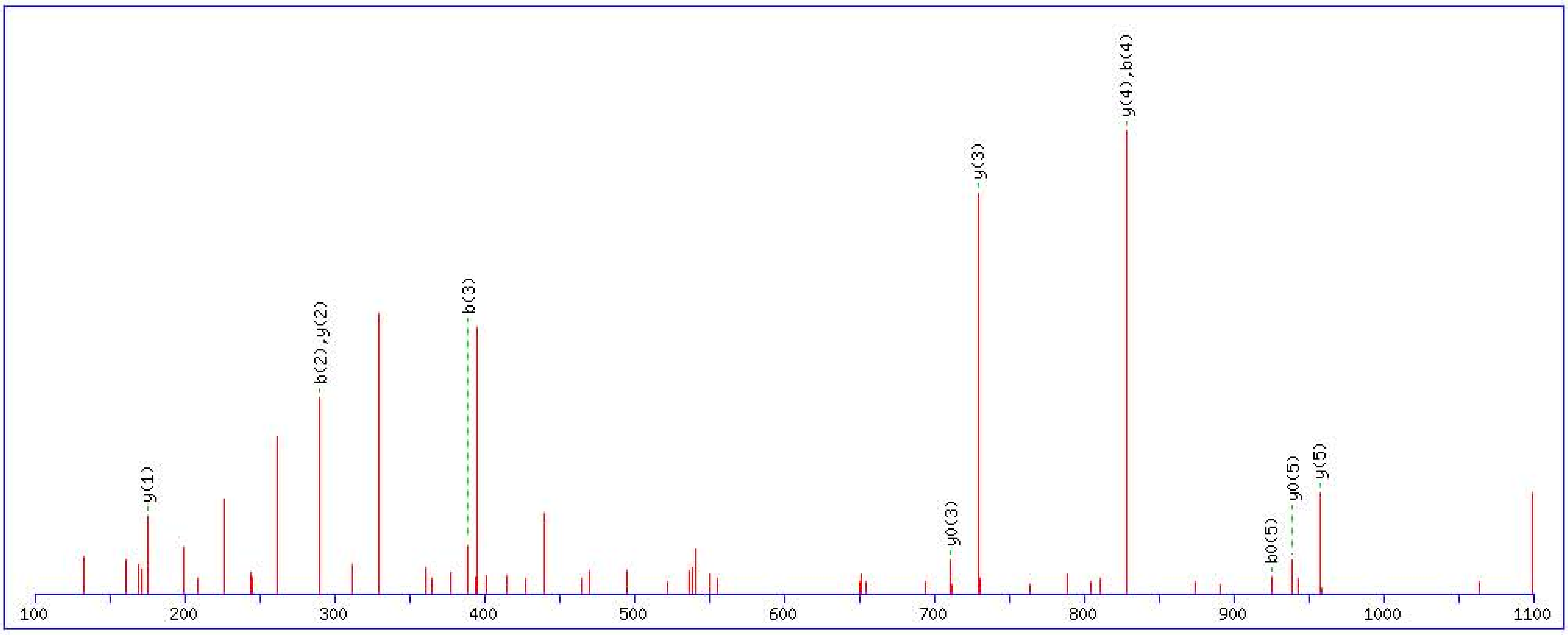
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

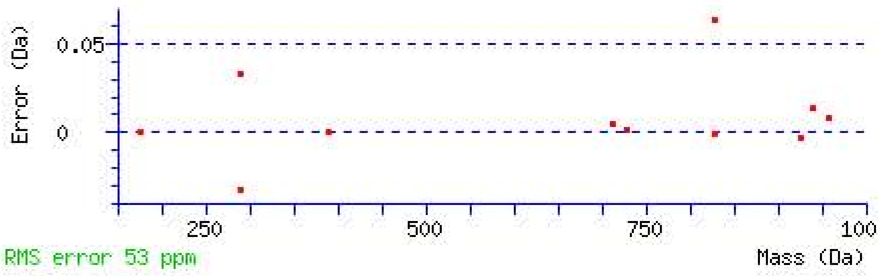
Match to Query 14674: 1116.503648 from(559.259100,2+) rtinseconds(1345) index(27956)
Title: Locus:1.1.1.3131.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

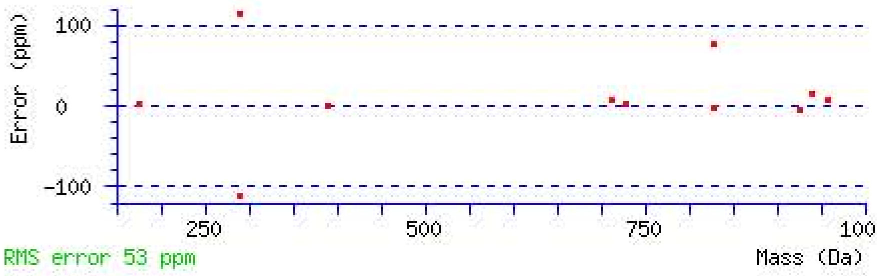
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1116.505600
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.01
Matches : 11/50 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	161.037925	81.022600					C							6
2	**290.080518**	145.543897			272.069953	136.538615	E	***957.482228***	479.244752	940.455679	470.731478	939.471663	470.239470	5
3	**389.148932**	195.078104			371.138367	186.072822	V	***828.439635***	414.723456	811.413086	406.210181	810.429070	405.718173	4
4	**828.374258**	414.690767	811.347709	406.177493	810.363693	405.685485	Q	***729.371221***	365.189249	712.344672	356.675974	711.360656	356.183966	3
5	943.401201	472.204239	926.374652	463.690964	925.390636	463.198956	D	***290.145895***	145.576585	273.119346	137.063311	272.135330	136.571303	2
6							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.8	1116.505600	-0.001952	CEVQDR
9.6	1116.505600	-0.001952	DICQDR
9.6	1116.486984	0.016664	DTDGQDR
9.6	1116.502228	0.001420	SWDQDR
5.8	1116.486969	0.016679	CETSPPSSPR
1.9	1116.502197	0.001451	NEYNFKMR
0.0	1116.504700	-0.001052	ELQAEQEDR

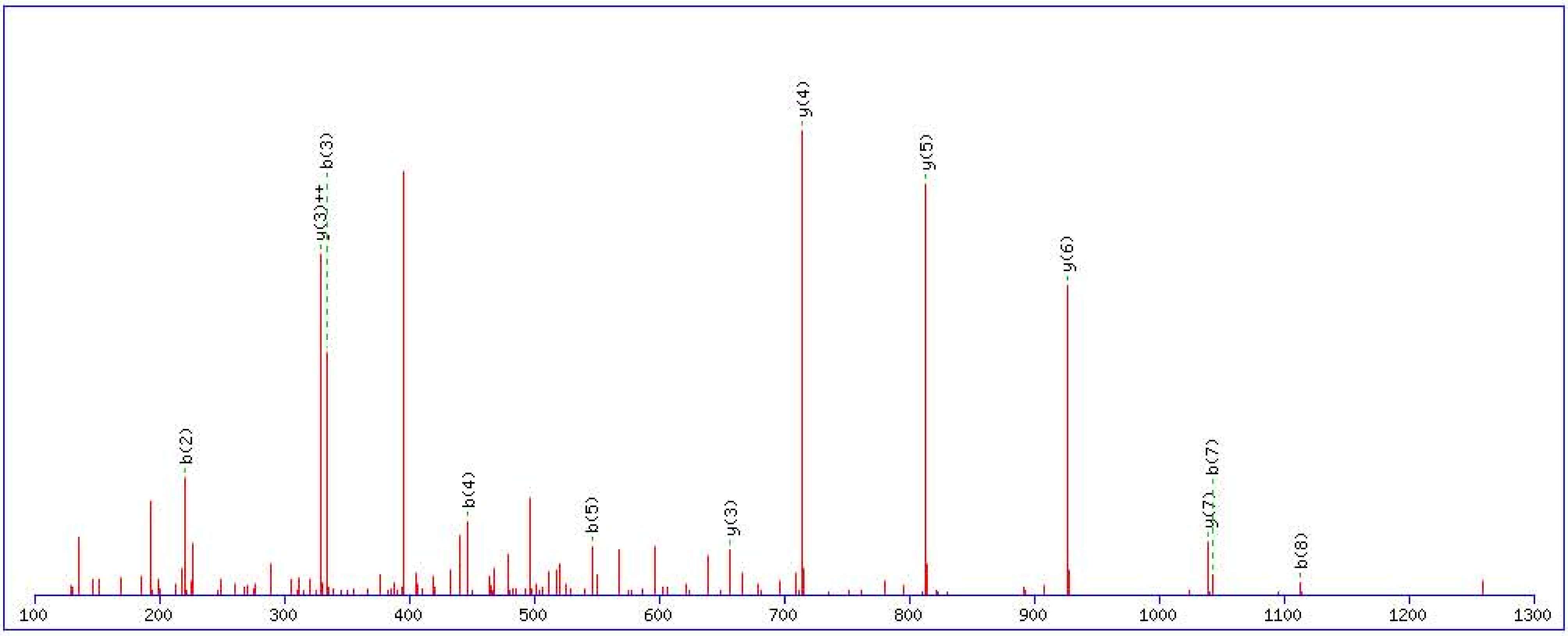
Mascot Search Results

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

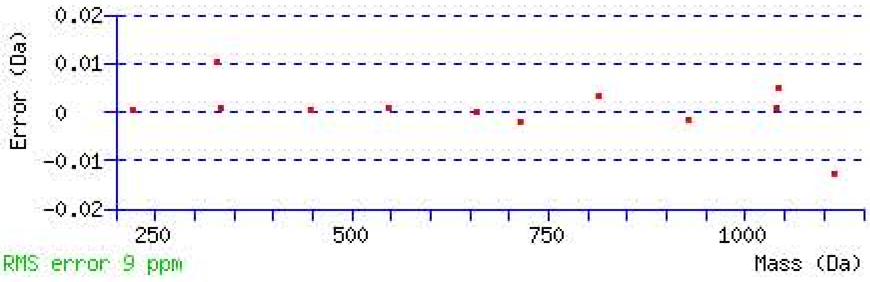
Match to Query 19185: 1258.708668 from(630.361610,2+) rtinseconds(2055) index(32194)
Title: Locus:1.1.1.3379.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

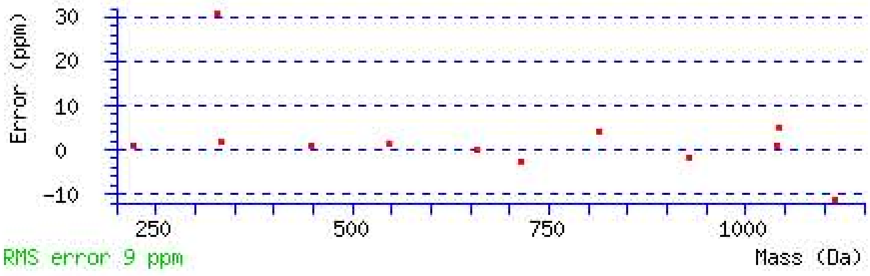
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 28 **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
28.4	1258.710754	-0.002086	GYILVGQAK
10.4	1258.717941	-0.009273	RILAKVQEMR
8.6	1258.721970	-0.013302	GYILQAKR

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

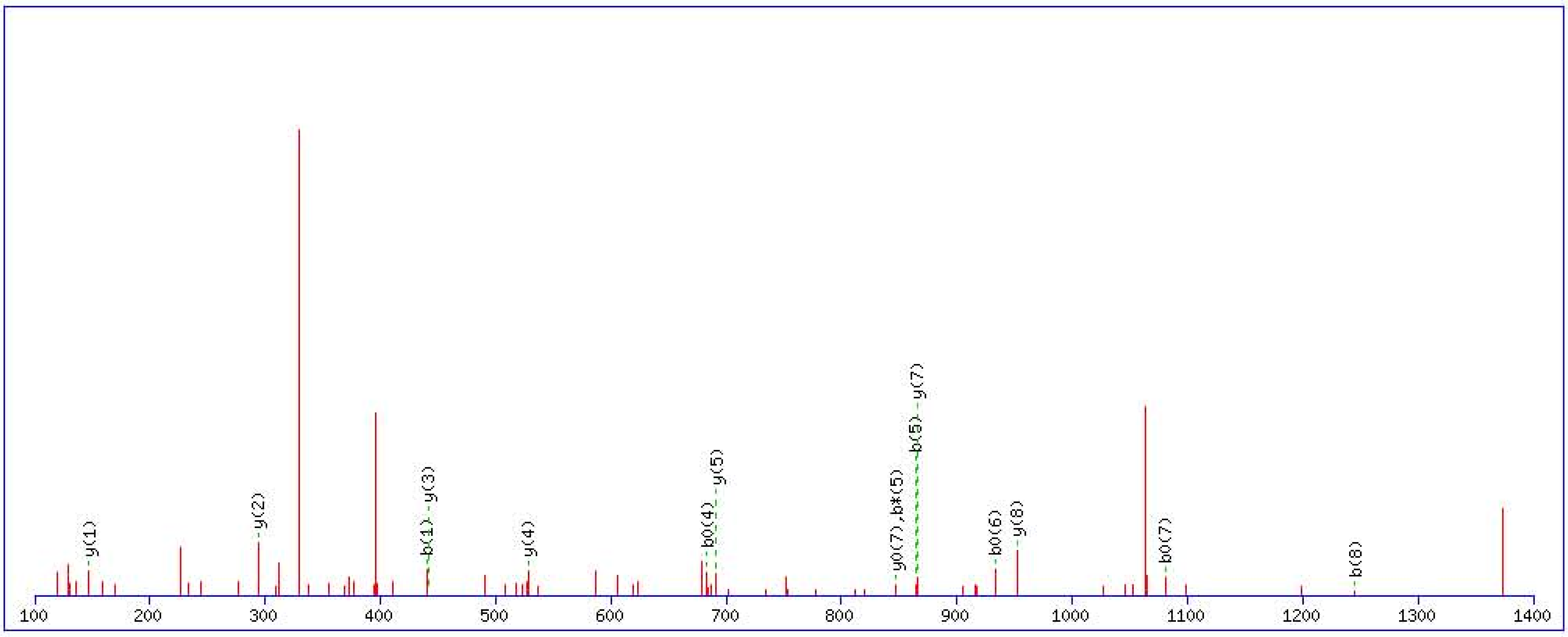
{MATRIX SCIENCE} Mascot Search Results

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

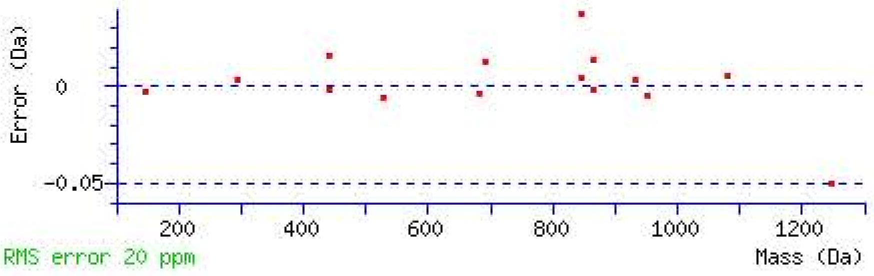
Match to Query 23270: 1390.657968 from(696.336260,2+) rtinseconds(2139) index(32674)
Title: Locus:1.1.1.3408.20 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

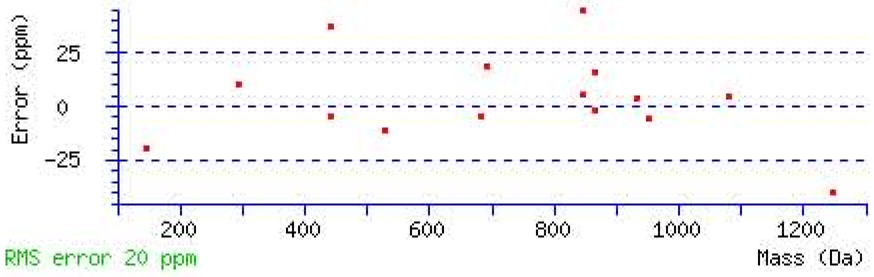
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1390.659119
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 : 15/88 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	**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
34.0	1390.659119	-0.001151	QSSSYSFFK
6.4	1390.676208	-0.018240	AEKSSSTDQK
5.9	1390.669678	-0.011710	CAPASIRLMDNK
4.7	1390.655075	0.002893	IHEQDQLYSMK
3.5	1390.676208	-0.018240	LTENNSQPLMTK
2.7	1390.676208	-0.018240	KMVNDAEPDTKK
2.2	1390.673721	-0.015753	QPNCSSLFK
1.6	1390.673706	-0.015738	TLNADLMMFAHK
1.5	1390.646317	0.011651	TNELEEELSAEK
0.9	1390.664963	-0.006995	EEGLEEGLLQMK

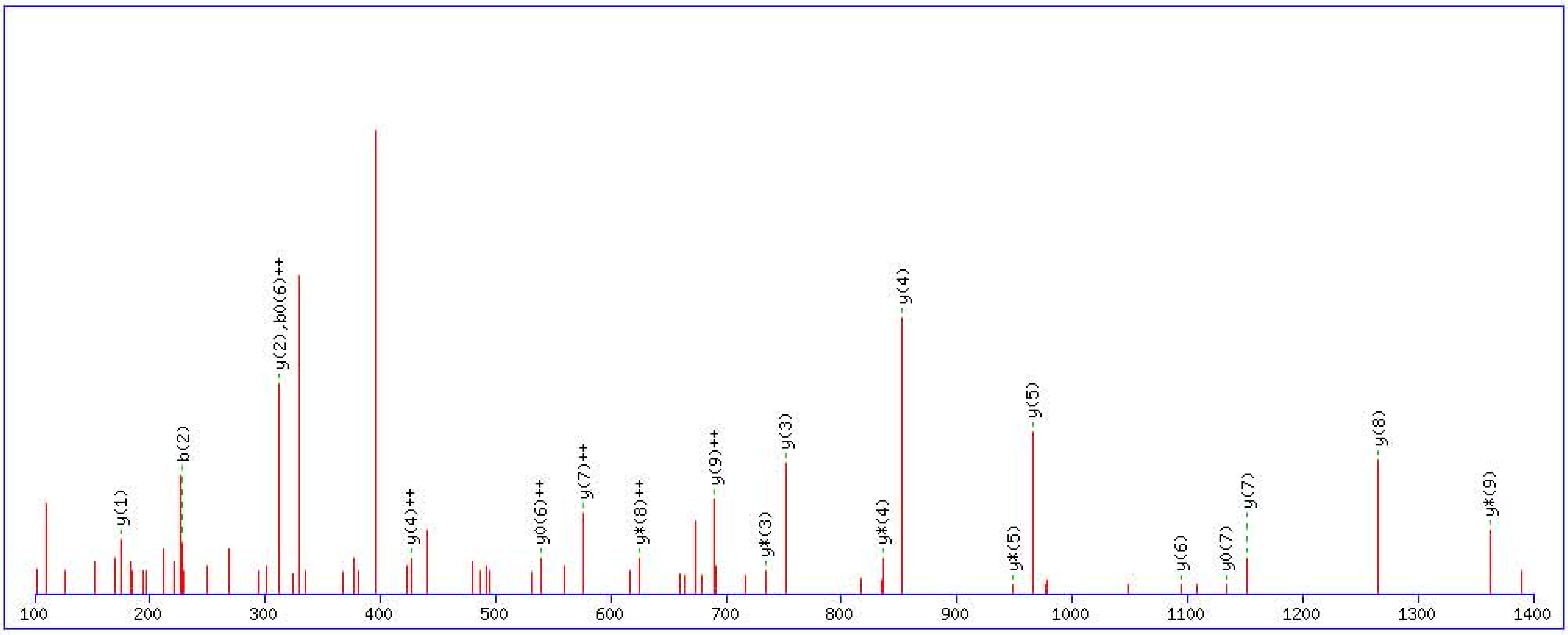
Mascot Search Results

Peptide View

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

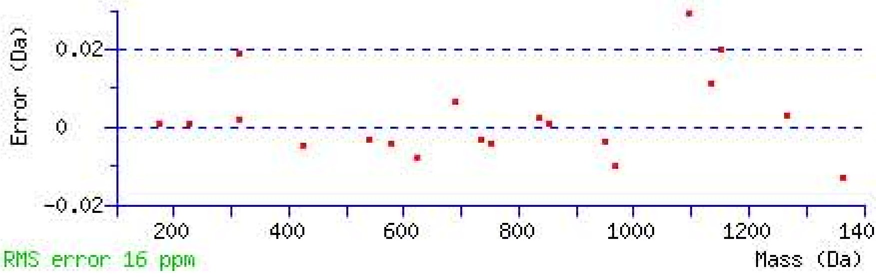
Match to Query 26949: 1491.761082 from(498.260970,3+) rtinseconds(1445) index(28470)
Title: Locus:1.1.1.3166.6 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

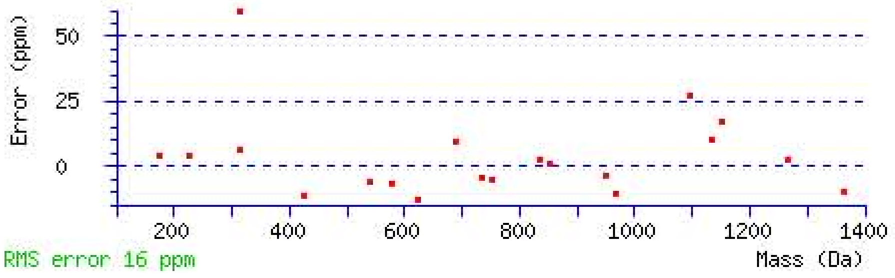
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1491.761612
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8     : Biotin:Thermo-21345 (Q)
Ions Score: 44  Expect: 0.00013
Matches : 20/92 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	114.091340	57.549308					L							10
2	228.134267	114.570771	211.107718	106.057497			N	1379.684844	690.346060	1362.658295	681.832786	1361.674279	681.340778	9
3	342.177194	171.592235	325.150645	163.078960			N	***1265.641917***	633.324596	1248.615368	624.811322	1247.631352	624.319314	8
4	399.198658	200.102967	382.172109	191.589692			G	***1151.598990***	576.303133	1134.572441	567.789859	1133.588425	567.297850	7
5	528.241251	264.624264	511.214702	256.110989	510.230686	255.618981	E	***1094.577526***	547.792401	1077.550977	539.279127	1076.566961	538.787119	6
6	641.325315	321.166296	624.298766	312.653021	623.314750	312.161013	I	***965.534933***	483.271105	948.508384	474.757830	947.524368	474.265822	5
7	742.372994	371.690135	725.346445	363.176861	724.362429	362.684853	T	***852.450869***	426.729073	835.424320	418.215798	834.440304	417.723790	4
8	1181.598320	591.302798	1164.571771	582.789524	1163.587755	582.297516	Q	***751.403190***	376.205233	734.376641	367.691959			3
9	1318.657232	659.832254	1301.630683	651.318980	1300.646667	650.826972	H	***312.177864***	156.592570	295.151315	148.079295			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.2	1491.761612	-0.000530	LNNGEITQHR
2.7	1491.756927	0.004155	IEEVIGTGSFGEVR

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

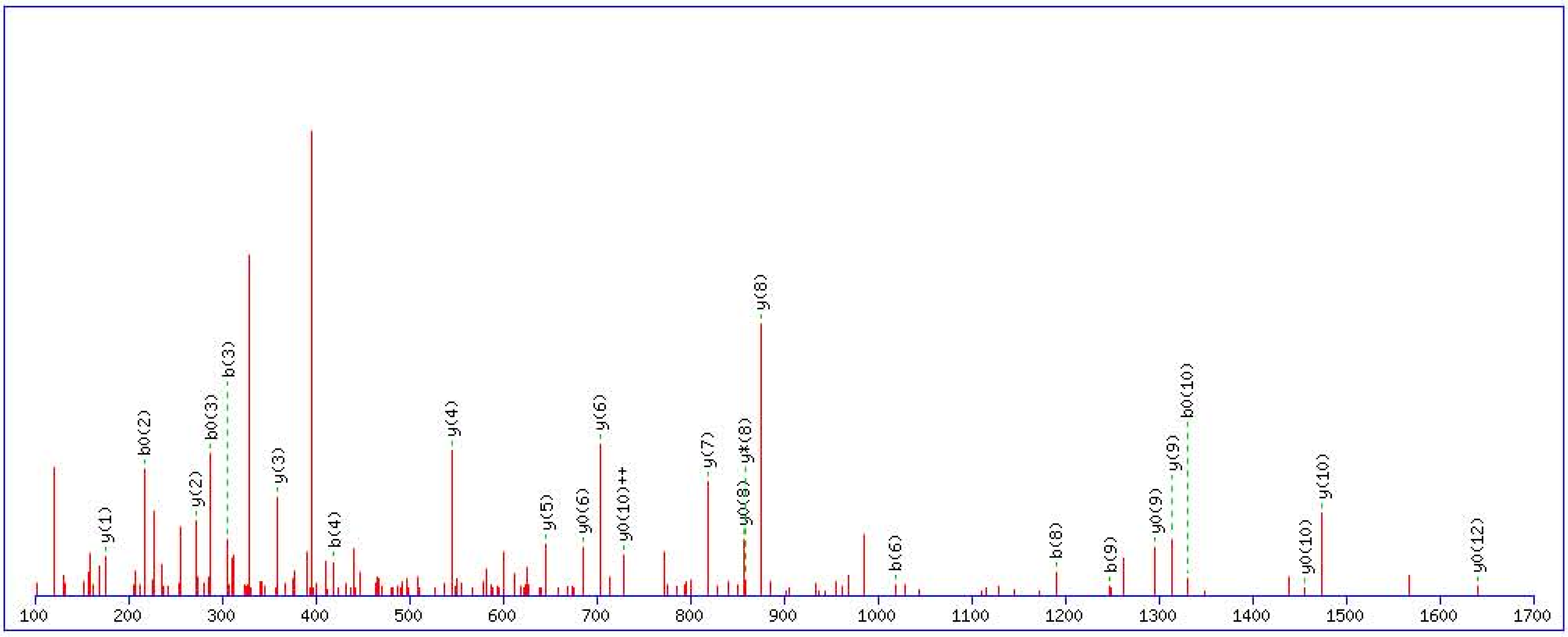
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

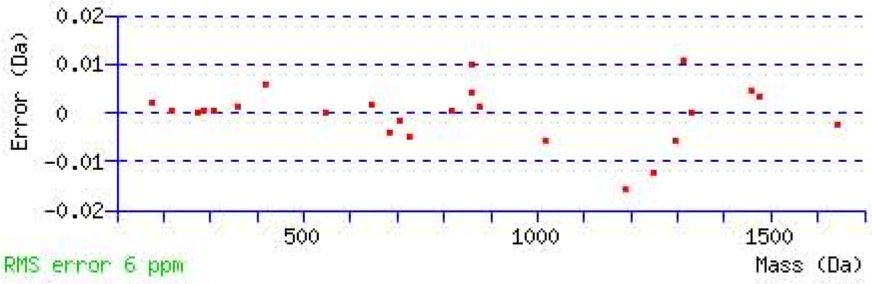
Match to Query 37298: 1891.870092 from(631.630640,3+) rtinseconds(2153) index(32753)
Title: Locus:1.1.1.3413.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

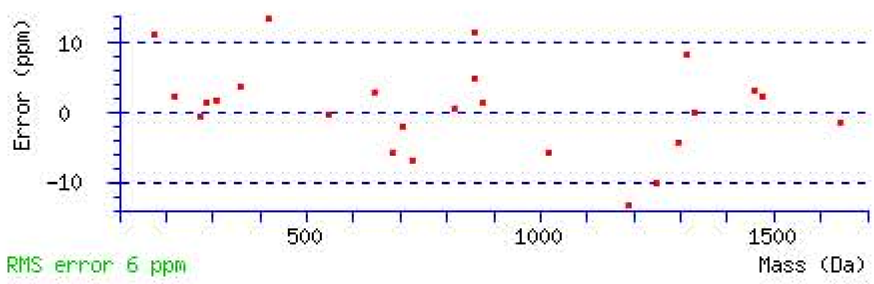
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1891.870941
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 46 **Expect:** 0.00035
Matches : 25/140 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	148.075690	74.541483					F							14
2	235.107718	118.057497			217.097153	109.052214	S	1745.809788	873.408532	1728.783239	864.895258	1727.799223	864.403250	13
3	**306.144832**	153.576054			288.134267	144.570772	A	1658.777760	829.892518	1641.751211	821.379244	1640.767195	820.887236	12
4	**419.228896**	210.118086			401.218331	201.112804	I	1587.740646	794.373961	1570.714097	785.860687	1569.730081	785.368678	11
5	579.259545	290.133411			561.248980	281.128128	C	***1474.656582***	737.831929	1457.630033	729.318655	1456.646017	728.826647	10
6	**1018.484871**	509.746074	1001.458322	501.232799	1000.474306	500.740791	Q	***1314.625933***	657.816605	1297.599384	649.303330	1296.615368	648.811322	9
7	1075.506335	538.256806	1058.479786	529.743531	1057.495770	529.251523	G	***875.400607***	438.203942	858.374058	429.690667	857.390042	429.198659	8
8	**1190.533278**	595.770277	1173.506729	587.257003	1172.522713	586.764995	D	***818.379143***	409.693210	801.352594	401.179935	800.368578	400.687927	7
9	**1247.554742**	624.281009	1230.528193	615.767735	1229.544177	615.275727	G	***703.352200***	352.179738	686.325651	343.666464	685.341635	343.174456	6
10	1348.602421	674.804849	1331.575872	666.291574	1330.591856	665.799566	T	***646.330736***	323.669006	629.304187	315.155732	628.320171	314.663724	5
11	1534.681734	767.844505	1517.655185	759.331231	1516.671169	758.839223	W	***545.283057***	273.145167	528.256508	264.631892	527.272492	264.139884	4
12	1621.713762	811.360519	1604.687213	802.847245	1603.703197	802.355237	S	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
13	1718.766526	859.886901	1701.739977	851.373627	1700.755961	850.881619	P	***272.171716***	136.589496	255.145167	128.076221			2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.6	1891.870941	-0.000849	FSAICQGDGTWSPR

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

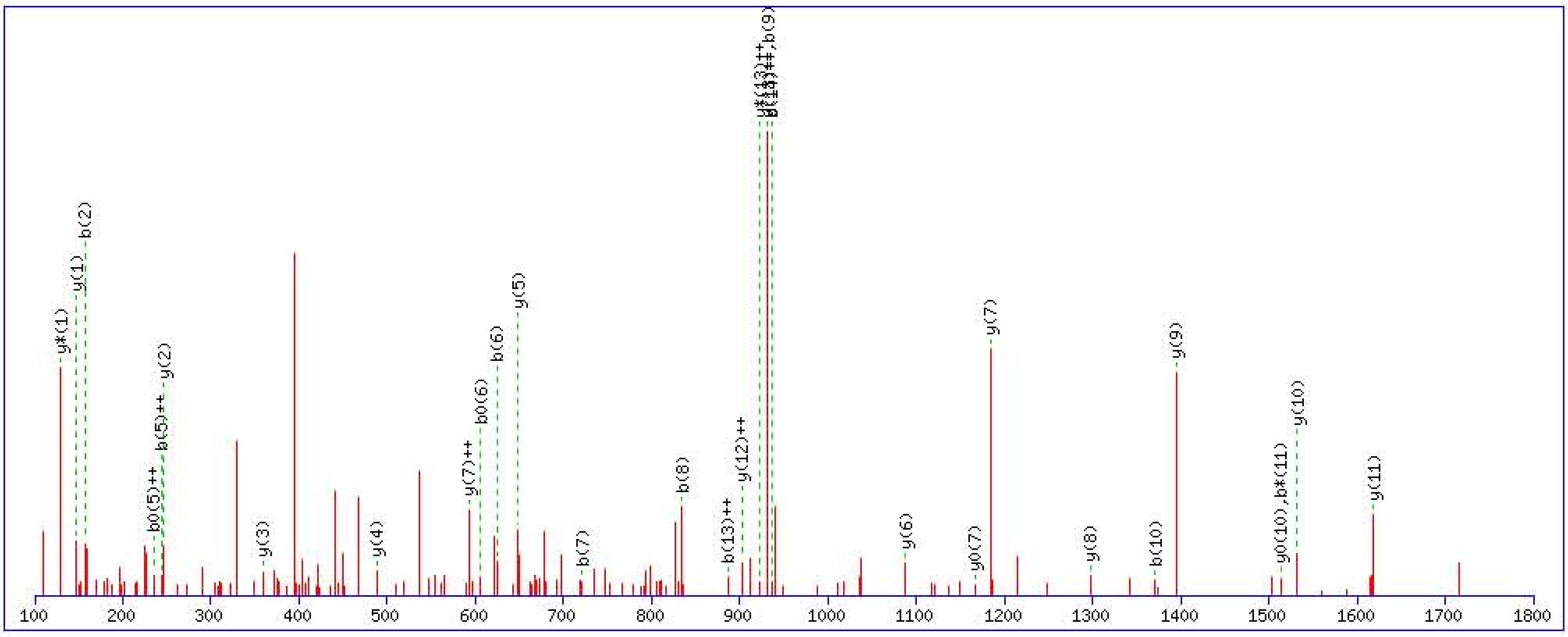
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

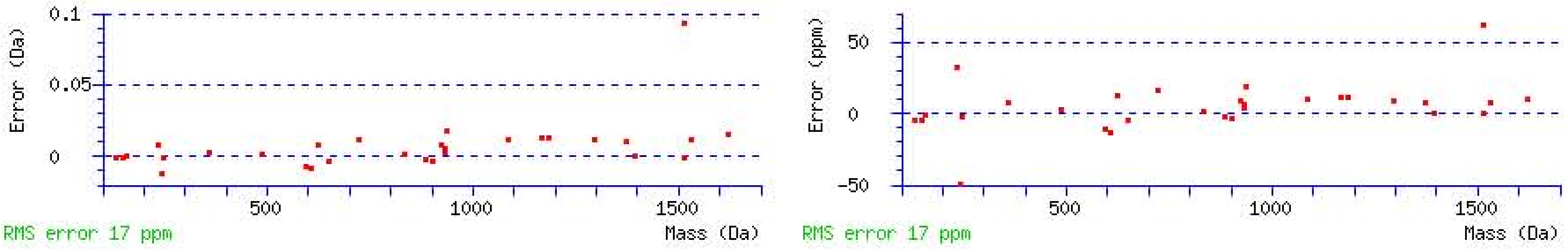
Match to Query 40161: 2017.025472 from(673.349100,3+) rtinseconds(2101) index(32458)
Title: Locus:1.1.1.3395.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 2017.027771
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0061
Matches : 30/136 fragment ions using 83 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							15
2	**157.097154**	79.052215					V	1961.013573	981.010425	1943.987024	972.497150	1943.003008	972.005142	14
3	214.118618	107.562947					G	1861.945159	931.476217	1844.918610	922.962943	1843.934594	922.470935	13
4	400.197931	200.602603					W	1804.923695	902.965486	1787.897146	894.452211	1786.913130	893.960203	12
5	487.229959	**244.118617**			469.219394	235.113335	S	***1618.844382***	809.925829	1601.817833	801.412555	1600.833817	800.920547	11
6	**624.288871**	312.648074			606.278306	303.642791	H	***1531.812354***	766.409815	1514.785805	757.896541	1513.801789	757.404532	10
7	**721.341635**	361.174456			703.331070	352.169173	P	***1394.753442***	697.880359	1377.726893	689.367085	1376.742877	688.875076	9
8	**834.425699**	417.716488			816.415134	408.711205	L	***1297.700678***	649.353977	1280.674129	640.840703	1279.690113	640.348694	8
9	**931.478463**	466.242870			913.467898	457.237587	P	***1184.616614***	592.811945	1167.590065	584.298670	1166.606049	583.806662	7
10	**1370.703789**	685.855532	1353.677240	677.342258	1352.693224	676.850250	Q	***1087.563850***	544.285563	1070.537301	535.772288	1069.553285	535.280280	6
11	1530.734438	765.870857	1513.707889	757.357583	1512.723873	756.865574	C	***648.338524***	324.672900	631.311975	316.159626	630.327959	315.667618	5
12	1659.777031	830.392153	1642.750482	821.878879	1641.766466	821.386871	E	***488.307875***	244.657575	471.281326	236.144301	470.297310	235.652293	4
13	1772.861095	**886.934185**	1755.834546	878.420911	1754.850530	877.928903	I	***359.265282***	180.136279	342.238733	171.623004			3
14	1871.929509	**936.468392**	1854.902960	927.955118	1853.918944	927.463110	V	***246.181218***	123.594247	229.154669	115.080973			2
15							K	***147.112804***	74.060040	130.086255	65.546765			1



NCBI **BLAST** search of GVGWSHPLPQCEIVK
(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	2017.027771	-0.002299	GVGWSHPLPQCEIVK

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

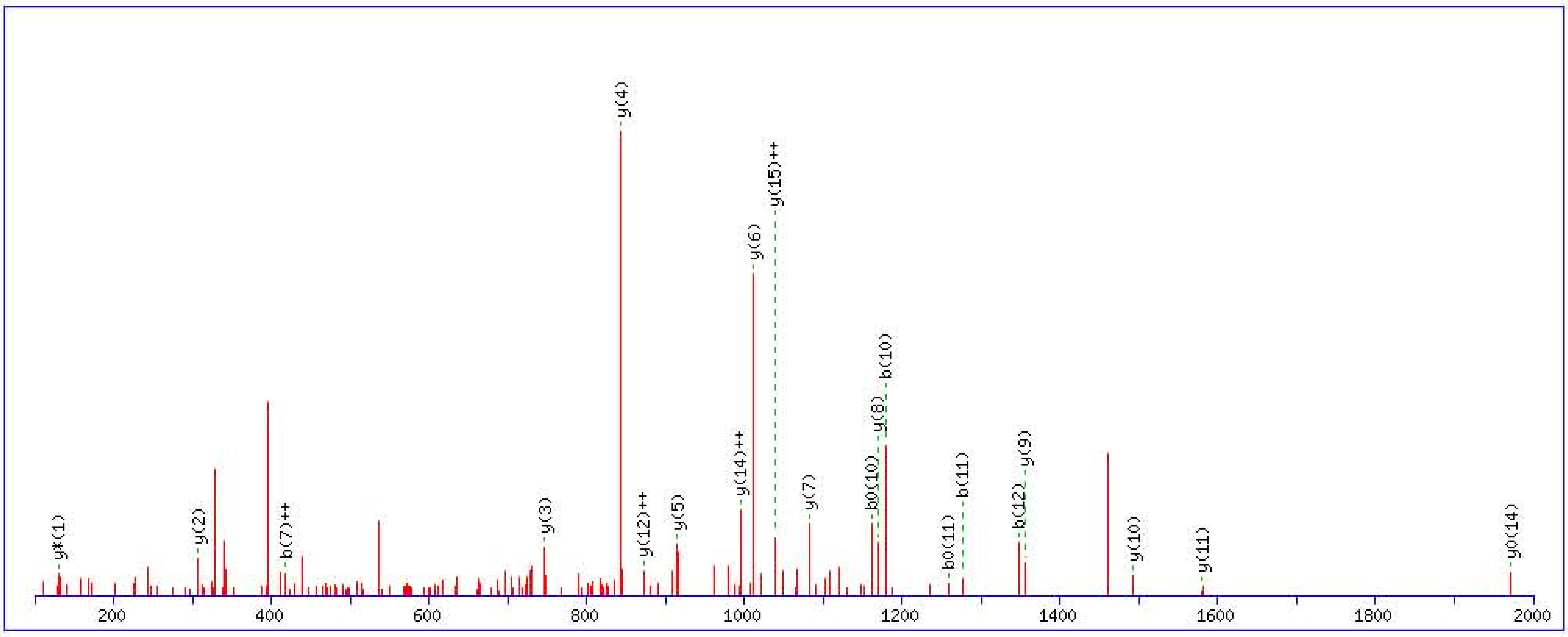
Mascot Search Results

Peptide View

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

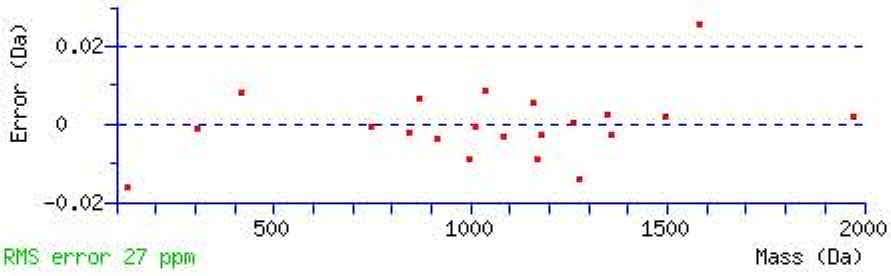
Match to Query 43071: 2188.980522 from(730.667450,3+) rtinseconds(1778) index(30448)
Title: Locus:1.1.1.3282.22 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

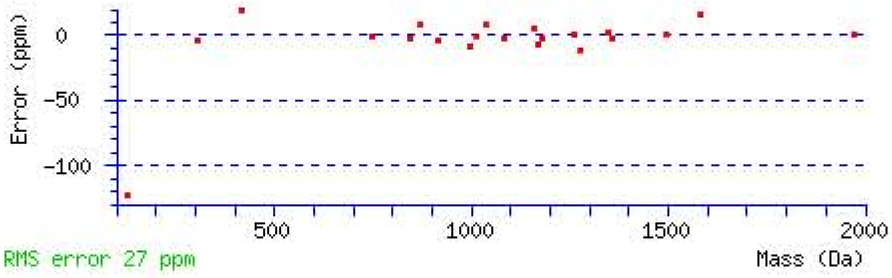
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2188.985626
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00016
Matches : 21/138 fragment ions using 44 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							16
2	201.123368	101.065322			183.112803	92.060039	S	2076.908850	1038.958063	2059.882301	1030.444788	2058.898285	1029.952780	15
3	361.154017	181.080647			343.143452	172.075364	C	1989.876822	995.442049	1972.850273	986.928775	1971.866257	986.436767	14
4	448.186045	224.596660			430.175480	215.591378	S	1829.846173	915.426725	1812.819624	906.913450	1811.835608	906.421442	13
5	611.249374	306.128325			593.238809	297.123043	Y	1742.814145	871.910711	1725.787596	863.397436	1724.803580	862.905428	12
6	698.281402	349.644339			680.270837	340.639056	S	***1579.750816***	790.379046	1562.724267	781.865772	1561.740251	781.373764	11
7	835.340314	418.173795			817.329749	409.168512	H	***1492.718788***	746.863032	1475.692239	738.349758	1474.708223	737.857750	10
8	1021.419627	511.213452			1003.409062	502.208169	W	***1355.659876***	678.333576	1338.633327	669.820302	1337.649311	669.328294	9
9	1108.451655	554.729466			1090.441090	545.724183	S	***1169.580563***	585.293920	1152.554014	576.780645	1151.569998	576.288637	8
10	**1179.488769**	590.248023			1161.478204	581.242740	A	***1082.548535***	541.777906	1065.521986	533.264631			7
11	**1276.541533**	638.774405			1258.530968	629.769122	P	***1011.511421***	506.259349	994.484872	497.746074			6
12	**1347.578647**	674.292962			1329.568082	665.287679	A	***914.458657***	457.732967	897.432108	449.219692			5
13	1444.631411	722.819344			1426.620846	713.814061	P	***843.421543***	422.214410	826.394994	413.701135			4
14	1883.856737	942.432007	1866.830188	933.918732	1865.846172	933.426724	Q	***746.368779***	373.688028	729.342230	365.174753			3
15	2043.887386	1022.447331	2026.860837	1013.934057	2025.876821	1013.442049	C	***307.143453***	154.075365	290.116904	145.562090			2
16							K	147.112804	74.060040	130.086255	65.546766			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.7	2188.985626	-0.005104	LSCSYSHWSAPAPQCK

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

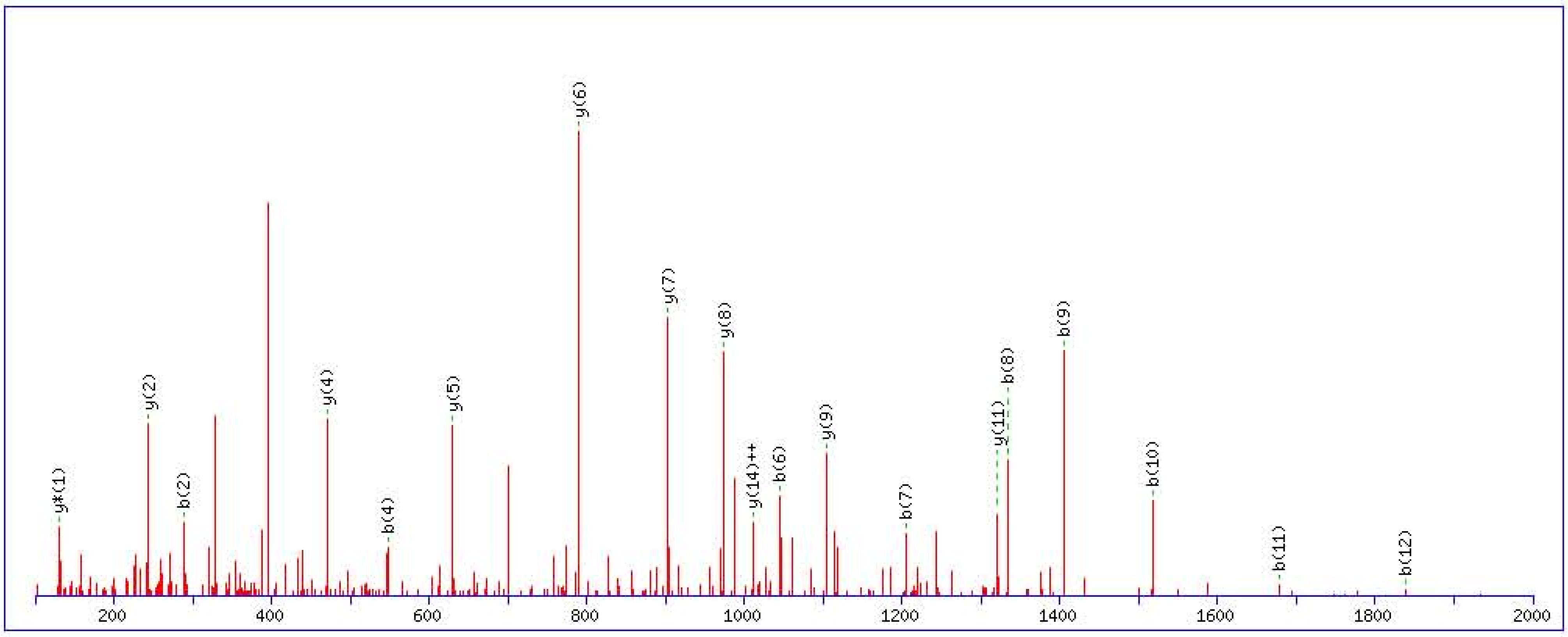
Mascot Search Results

Peptide View

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

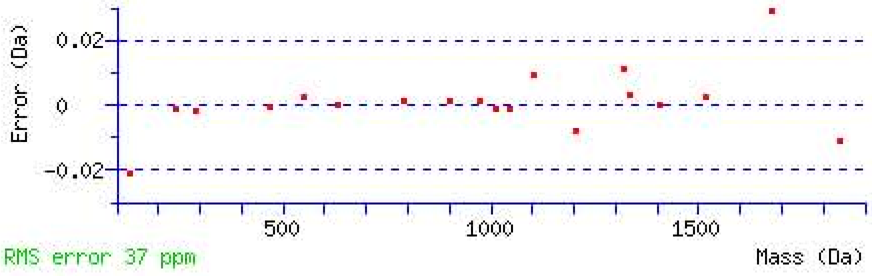
Match to Query 45205: 2305.997022 from(769.672950,3+) rtinseconds(2122) index(32586)
Title: Locus:1.1.1.3402.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

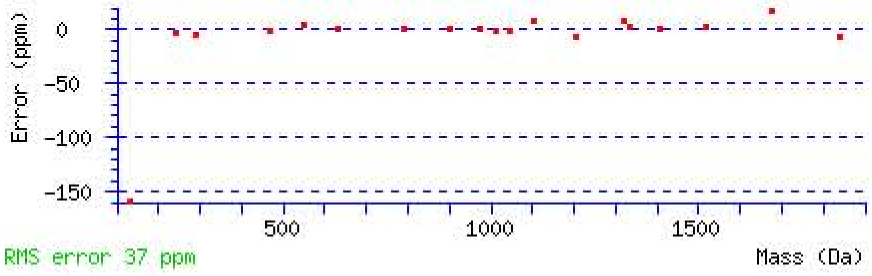
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2305.999237
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 48 **Expect:** 5.9e-005
Matches : 19/166 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	187.086589	94.046932					W							16
2	***288.134268***	144.570772			270.123703	135.565490	T	2120.927205	1060.967240	2103.900656	1052.453966	2102.916640	1051.961958	15
3	385.187032	193.097154			367.176467	184.091872	P	2019.879526	1010.443401	2002.852977	1001.930127	2001.868961	1001.438119	14
4	***548.250361***	274.628819			530.239796	265.623536	Y	1922.826762	961.917019	1905.800213	953.403745	1904.816197	952.911737	13
5	987.475687	494.241482	970.449138	485.728207	969.465122	485.236199	Q	1759.763433	880.385355	1742.736884	871.872080	1741.752868	871.380072	12
6	***1044.497151***	522.752214	1027.470602	514.238939	1026.486586	513.746931	G	***1320.538107***	660.772692	1303.511558	652.259417	1302.527542	651.767409	11
7	***1204.527800***	602.767538	1187.501251	594.254264	1186.517235	593.762256	C	1263.516643	632.261960	1246.490094	623.748685	1245.506078	623.256677	10
8	***1333.570393***	667.288835	1316.543844	658.775560	1315.559828	658.283552	E	***1103.485994***	552.246635	1086.459445	543.733361	1085.475429	543.241353	9
9	***1404.607507***	702.807392	1387.580958	694.294117	1386.596942	693.802109	A	***974.443401***	487.725339	957.416852	479.212064	956.432836	478.720056	8
10	***1517.691571***	759.349424	1500.665022	750.836149	1499.681006	750.344141	L	***903.406287***	452.206782	886.379738	443.693507	885.395722	443.201499	7
11	***1677.722220***	839.364748	1660.695671	830.851474	1659.711655	830.359466	C	***790.322223***	395.664750	773.295674	387.151475	772.311658	386.659467	6
12	***1837.752869***	919.380073	1820.726320	910.866798	1819.742304	910.374790	C	***630.291574***	315.649425	613.265025	307.136151	612.281009	306.644143	5
13	1934.805633	967.906455	1917.779084	959.393180	1916.795068	958.901172	P	***470.260925***	235.634101	453.234376	227.120826	452.250360	226.628818	4
14	2063.848226	1032.427751	2046.821677	1023.914477	2045.837661	1023.422469	E	373.208161	187.107719	356.181612	178.594444	355.197596	178.102436	3
15	2160.900990	1080.954133	2143.874441	1072.440858	2142.890425	1071.948850	P	***244.165568***	122.586422	227.139019	114.073148			2
16							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.3	2305.999237	-0.002215	WTPYQGCEALCCPEPK

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

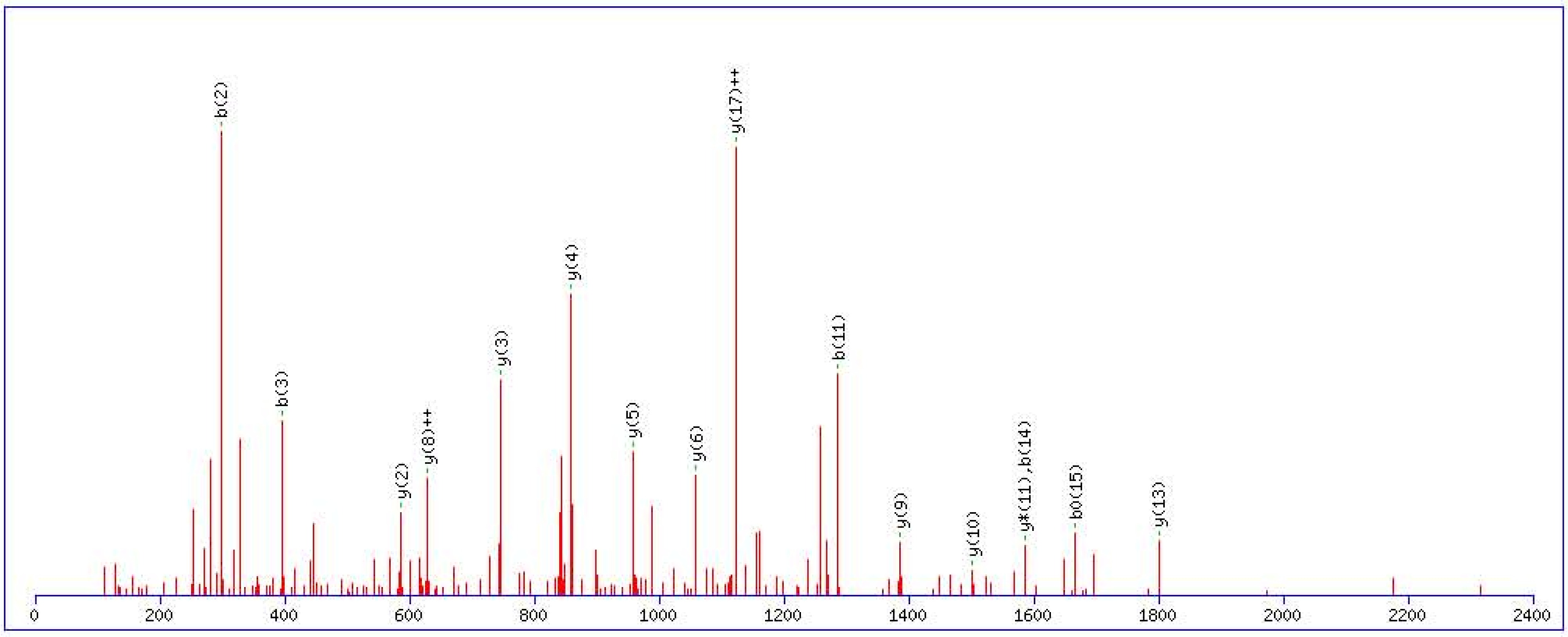
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

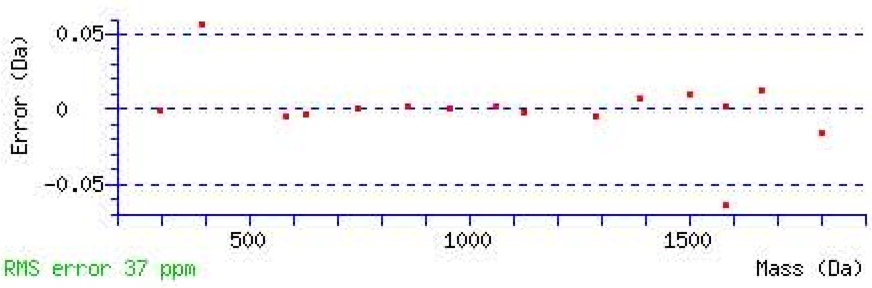
Match to Query 48975: 2542.189002 from(848.403610,3+) rtinseconds(1629) index(29620)
Title: Locus:1.1.1.3230.20 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

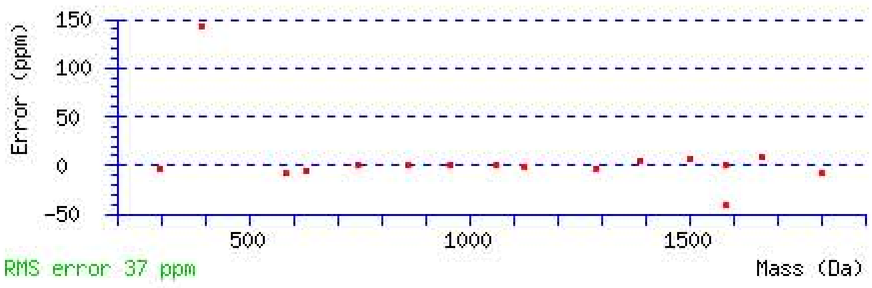
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2542.201859
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18     : Biotin:Thermo-21345 (Q)
Ions Score: 55  Expect: 4.8e-005
Matches : 16/182 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	161.037925	81.022600					C							19
2	***298.096837***	149.552056					H	2383.178469	1192.092872	2366.151920	1183.579598	2365.167904	1183.087590	18
3	***395.149601***	198.078439					P	2246.119557	1123.563416	2229.093008	1115.050142	2228.108992	1114.558134	17
4	452.171065	226.589170					G	2149.066793	1075.037034	2132.040244	1066.523760	2131.056228	1066.031752	16
5	615.234394	308.120835					Y	2092.045329	1046.526302	2075.018780	1038.013028	2074.034764	1037.521020	15
6	743.329357	372.168317	726.302808	363.655042			K	1928.982000	964.994638	1911.955451	956.481364	1910.971435	955.989356	14
7	840.382121	420.694699	823.355572	412.181424			P	***1800.887037***	900.947157	1783.860488	892.433882	1782.876472	891.941874	13
8	941.429800	471.218538	924.403251	462.705264	923.419235	462.213256	T	1703.834273	852.420775	1686.807724	843.907500	1685.823708	843.415492	12
9	1042.477479	521.742378	1025.450930	513.229103	1024.466914	512.737095	T	1602.786594	801.896935	1585.760045	793.383661	1584.776029	792.891653	11
10	1157.504422	579.255849	1140.477873	570.742575	1139.493857	570.250567	D	***1501.738915***	751.373096	1484.712366	742.859821	1483.728350	742.367813	10
11	***1286.547015***	643.777146	1269.520466	635.263871	1268.536450	634.771863	E	***1386.711972***	693.859624	1369.685423	685.346350	1368.701407	684.854342	9
12	1383.599779	692.303528	1366.573230	683.790253	1365.589214	683.298245	P	1257.669379	629.338328	1240.642830	620.825053	1239.658814	620.333045	8
13	1484.647458	742.827367	1467.620909	734.314093	1466.636893	733.822085	T	1160.616615	580.811946	1143.590066	572.298671	1142.606050	571.806663	7
14	***1585.695137***	793.351207	1568.668588	784.837932	1567.684572	784.345924	T	***1059.568936***	530.288106	1042.542387	521.774832	1041.558371	521.282824	6
15	1684.763551	842.885414	1667.737002	834.372139	1666.752986	833.880131	V	***958.521257***	479.764267	941.494708	471.250992			5
16	1797.847615	899.427446	1780.821066	890.914171	1779.837050	890.422163	I	***859.452843***	430.230060	842.426294	421.716785			4
17	1957.878264	979.442770	1940.851715	970.929496	1939.867699	970.437488	C	***746.368779***	373.688028	729.342230	365.174753			3
18	2397.103590	1199.055433	2380.077041	1190.542158	2379.093025	1190.050151	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 CHPGYKPTTDEPTTVICQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.4	2542.201859	-0.012857	CHPGYKPTTDEPTTVICQK

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

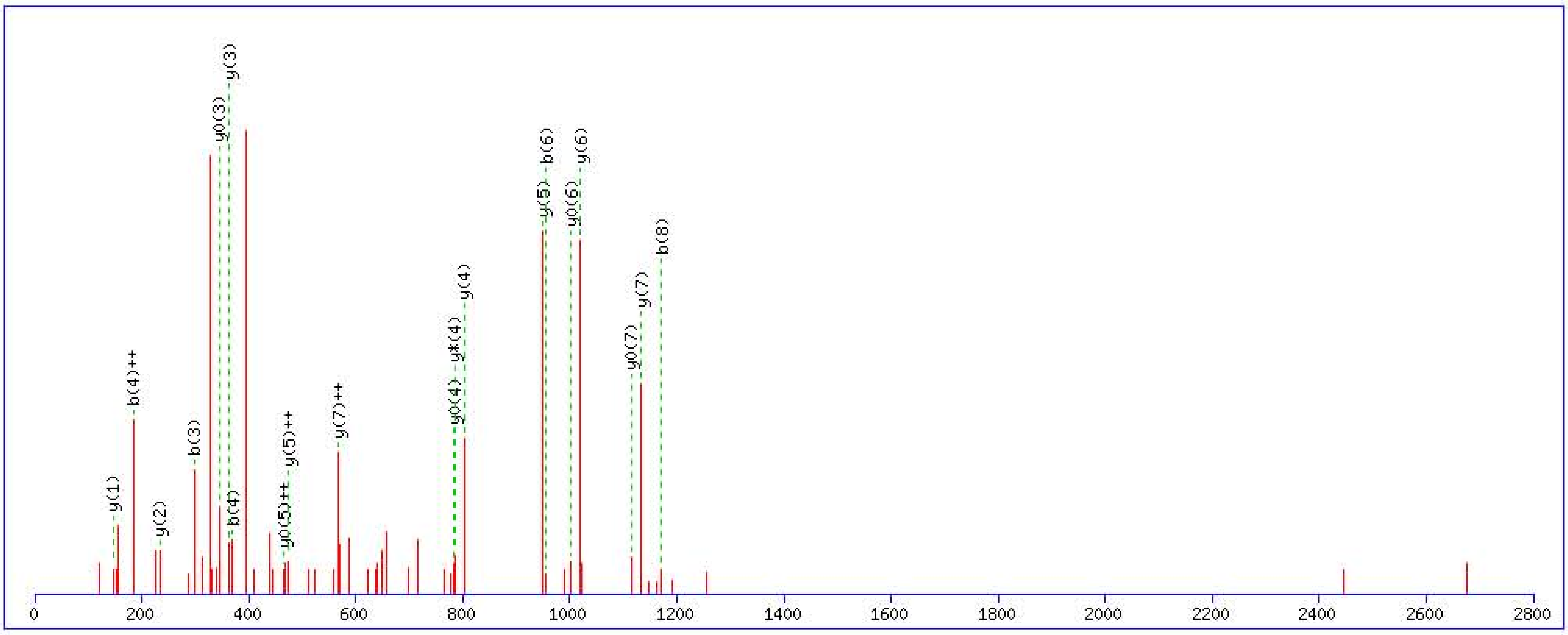
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALLAFQESK**
Found in **C4BPB_HUMAN**, C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=1 SV=1

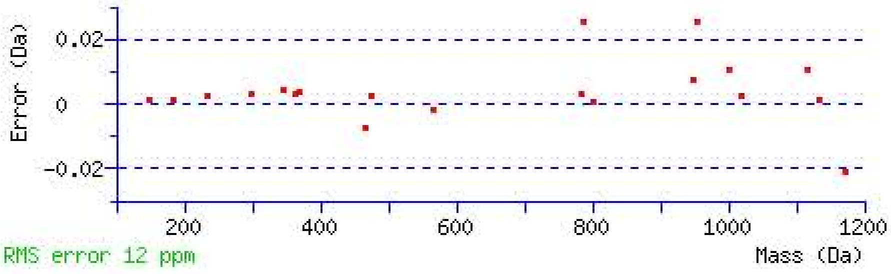
Match to Query 20631: 1316.719948 from(659.367250,2+) rtinseconds(2243) index(47506)
Title: Locus:1.1.1.3493.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

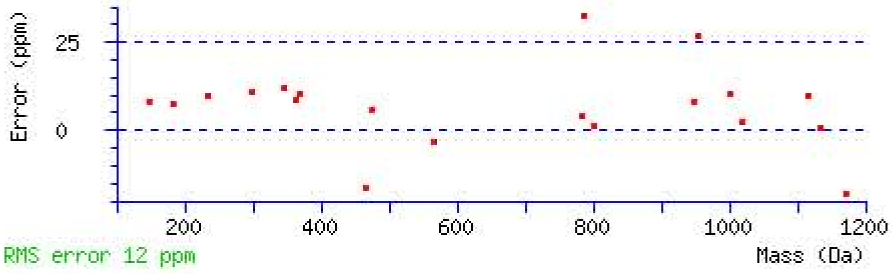
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1316.716217
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.0061
Matches : 21/72 fragment ions using 49 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	1246.686407	623.846842	1229.659858	615.333567	1228.675842	614.841559	8
3	**298.212518**	149.609897					L	***1133.602343***	567.304810	1116.575794	558.791535	1115.591778	558.299527	7
4	**369.249632**	185.128454					A	***1020.518279***	510.762778	1003.491730	502.249503	1002.507714	501.757495	6
5	516.318046	258.662661					F	***949.481165***	475.244221	932.454616	466.730946	931.470600	466.238938	5
6	**955.543372**	478.275324	938.516823	469.762049			Q	***802.412751***	401.710014	785.386202	393.196739	784.402186	392.704731	4
7	1084.585965	542.796621	1067.559416	534.283346	1066.575400	533.791338	E	***363.187425***	182.097351	346.160876	173.584076	345.176860	173.092068	3
8	**1171.617993**	586.312635	1154.591444	577.799360	1153.607428	577.307352	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 ALLAFQESK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.9	1316.716217	0.003731	ALLAFQESK
7.1	1316.731293	-0.011345	RVLAFISRNQN
5.5	1316.704788	0.015160	RATEEISKDLR
4.9	1316.733994	-0.014046	LALVINGDFLDK

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

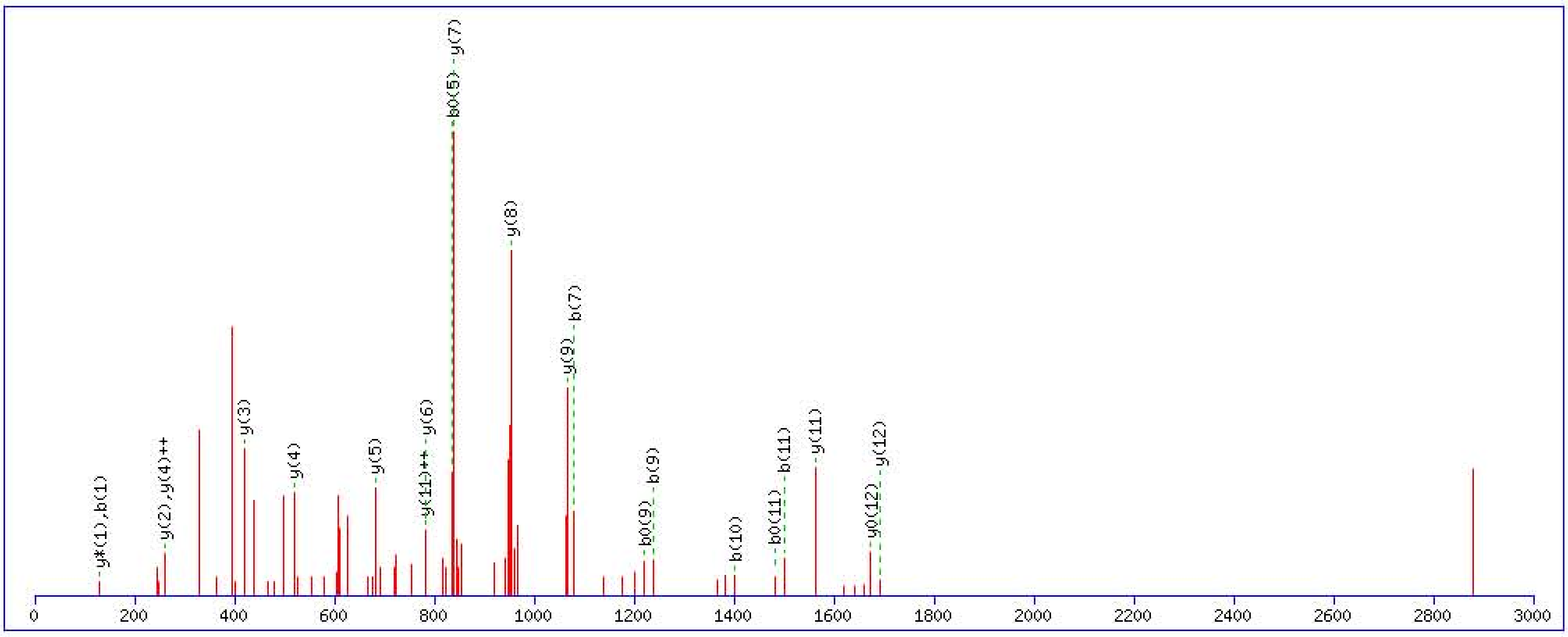
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVEGQILGTYVCIK**
Found in **C4BPB_HUMAN**, C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=1 SV=1

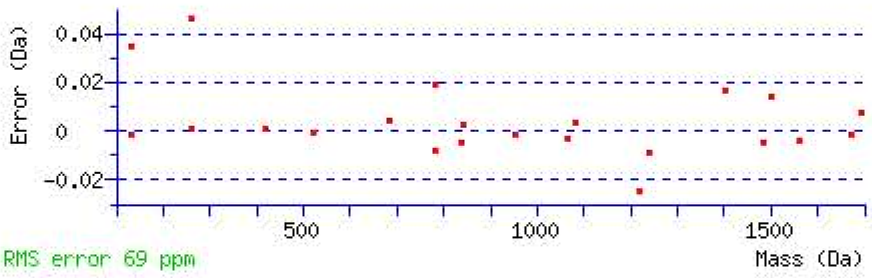
Match to Query 37773: 1918.990668 from(960.502610,2+) rtinseconds(2495) index(34546)
Title: Locus:1.1.1.3532.25 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

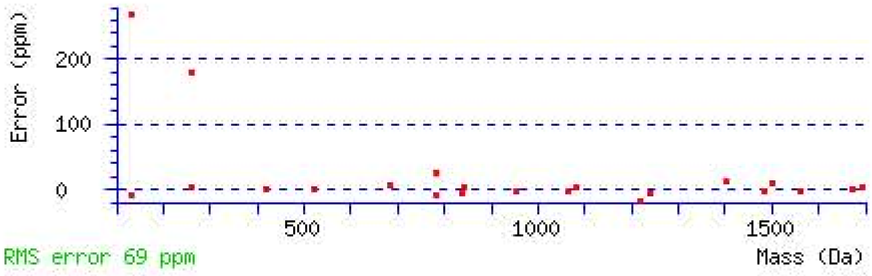
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1918.989639
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 74  Expect: 1.2e-006
Matches : 22/138 fragment ions using 30 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							14
2	229.118283	115.062780			211.107718	106.057497	V	1790.954328	895.980802	1773.927779	887.467528	1772.943763	886.975520	13
3	358.160876	179.584076			340.150311	170.578794	E	***1691.885914***	846.446595	1674.859365	837.933321	1673.875349	837.441313	12
4	415.182340	208.094808			397.171775	199.089526	G	***1562.843321***	781.925299	1545.816772	773.412024	1544.832756	772.920016	11
5	854.407666	427.707471	837.381117	419.194197	836.397101	418.702189	Q	1505.821857	753.414567	1488.795308	744.901292	1487.811292	744.409284	10
6	967.491730	484.249503	950.465181	475.736229	949.481165	475.244221	I	***1066.596531***	533.801904	1049.569982	525.288629	1048.585966	524.796621	9
7	**1080.575794**	540.791535	1063.549245	532.278261	1062.565229	531.786253	L	***953.512467***	477.259872	936.485918	468.746597	935.501902	468.254589	8
8	1137.597258	569.302267	1120.570709	560.788993	1119.586693	560.296985	G	***840.428403***	420.717840	823.401854	412.204565	822.417838	411.712557	7
9	**1238.644937**	619.826107	1221.618388	611.312832	1220.634372	610.820824	T	***783.406939***	392.207108	766.380390	383.693833	765.396374	383.201825	6
10	**1401.708266**	701.357771	1384.681717	692.844497	1383.697701	692.352489	Y	***682.359260***	341.683268	665.332711	333.169994			5
11	**1500.776680**	750.891978	1483.750131	742.378704	1482.766115	741.886696	V	***519.295931***	260.151604	502.269382	251.638329			4
12	1660.807329	830.907303	1643.780780	822.394028	1642.796764	821.902020	C	***420.227517***	210.617396	403.200968	202.104122			3
13	1773.891393	887.449335	1756.864844	878.936060	1755.880828	878.444052	I	***260.196868***	130.602072	243.170319	122.088797			2
14							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
73.7	1918.989639	0.001029	EVEGQILGTYVCIK

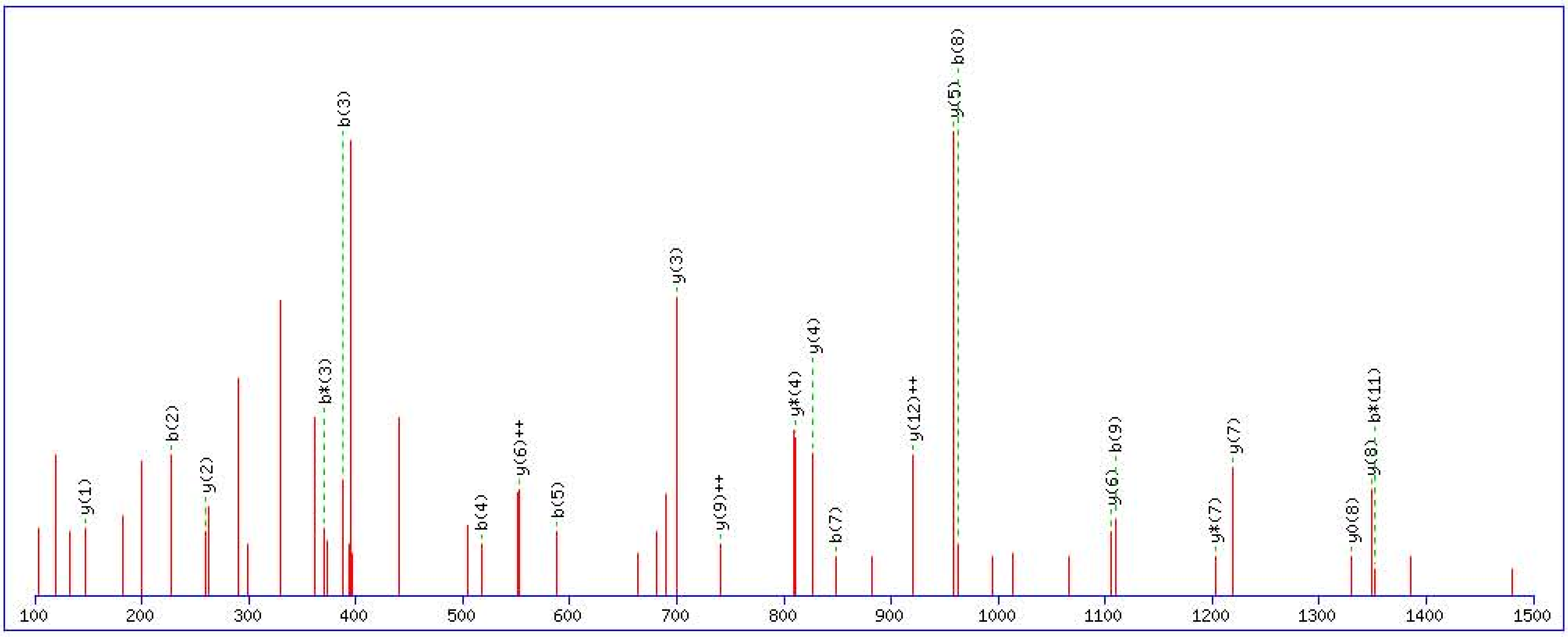
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLCEAMENFMQQLK**
Found in **C4BPB_HUMAN**, C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=1 SV=1

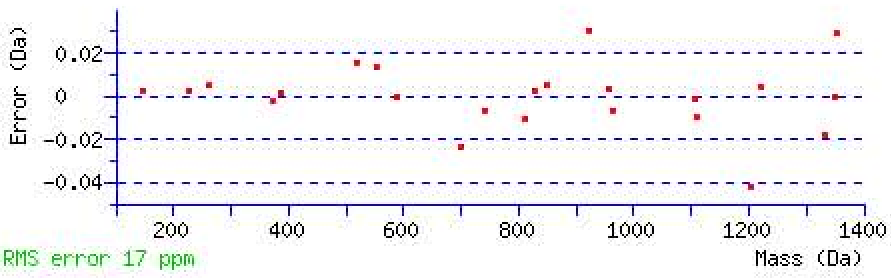
Match to Query 41126: 2065.940142 from(689.653990,3+) rtinseconds(3108) index(38767)
Title: Locus:1.1.1.3742.6 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

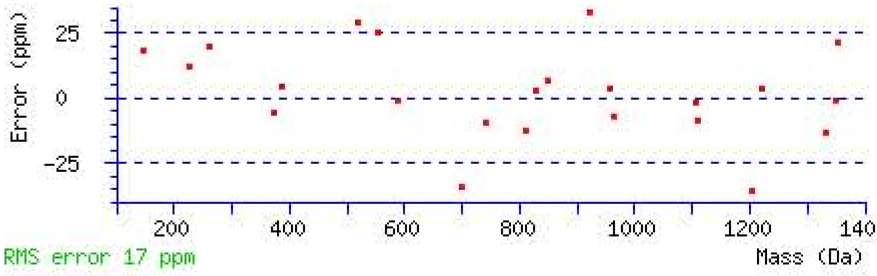
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2065.945709
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 45 **Expect:** 0.00032
Matches : 23/136 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	115.050203	58.028740	98.023654	49.515465			N							14
2	***228.134267***	114.570771	211.107718	106.057497			L	1952.910096	976.958686	1935.883547	968.445412	1934.899531	967.953404	13
3	***388.164916***	194.586096	371.138367	186.072822			C	1839.826032	920.416654	1822.799483	911.903380	1821.815467	911.411371	12
4	***517.207509***	259.107393	500.180960	250.594118	499.196944	250.102110	E	1679.795383	840.401329	1662.768834	831.888055	1661.784818	831.396047	11
5	***588.244623***	294.625950	571.218074	286.112675	570.234058	285.620667	A	1550.752790	775.880033	1533.726241	767.366759	1532.742225	766.874751	10
6	719.285108	360.146192	702.258559	351.632918	701.274543	351.140910	M	1479.715676	740.361476	1462.689127	731.848202	1461.705111	731.356194	9
7	***848.327701***	424.667489	831.301152	416.154214	830.317136	415.662206	E	***1348.675191***	674.841234	1331.648642	666.327959	1330.664626	665.835951	8
8	***962.370628***	481.688952	945.344079	473.175678	944.360063	472.683670	N	***1219.632598***	610.319937	1202.606049	601.806663			7
9	***1109.439042***	555.223159	1092.412493	546.709885	1091.428477	546.217876	F	***1105.589671***	553.298474	1088.563122	544.785199			6
10	1240.479527	620.743402	1223.452978	612.230127	1222.468962	611.738119	M	***958.521257***	479.764267	941.494708	471.250992			5
11	1368.538105	684.772690	1351.511556	676.259416	1350.527540	675.767408	Q	***827.480772***	414.244024	810.454223	405.730750			4
12	1807.763431	904.385354	1790.736882	895.872079	1789.752866	895.380071	Q	***699.422194***	350.214735	682.395645	341.701461			3
13	1920.847495	960.927386	1903.820946	952.414111	1902.836930	951.922103	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 NLCEAMENFMQQLK
(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	2065.945709	-0.005567	NLCEAMENFMQQLK
38.5	2065.945709	-0.005567	NLCEAMENFMQQLK

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

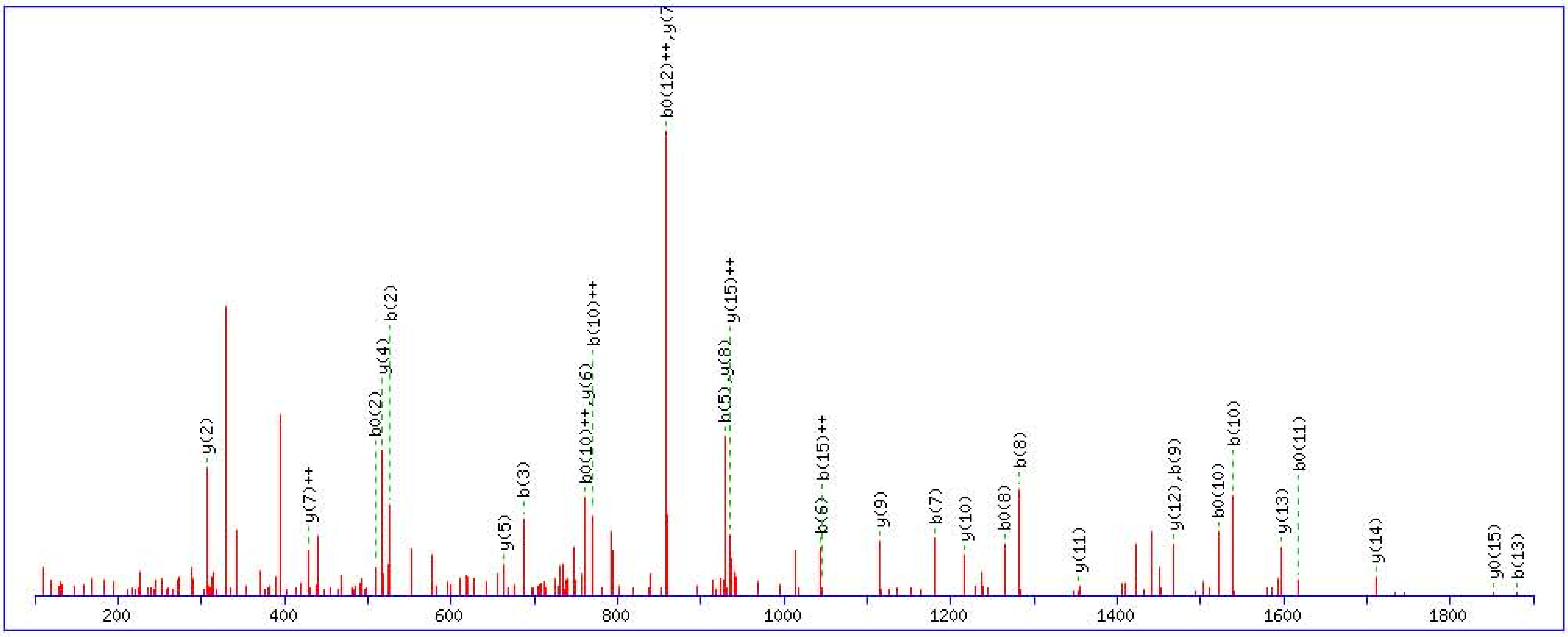
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SQCLEDHTWAPPFPICK**
Found in **C4BPB_HUMAN**, C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=1 SV=1

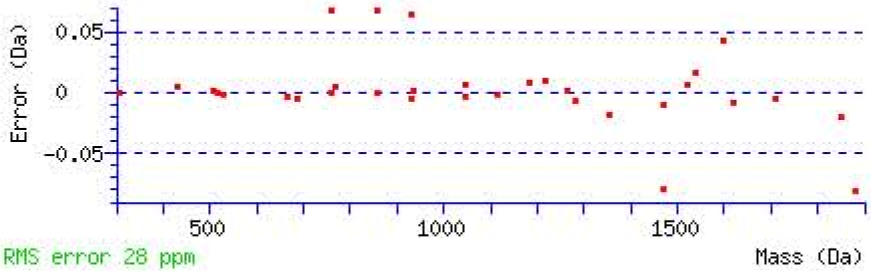
Match to Query 46302: 2396.108712 from(799.710180,3+) rtinseconds(2332) index(33750)
Title: Locus:1.1.1.3475.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

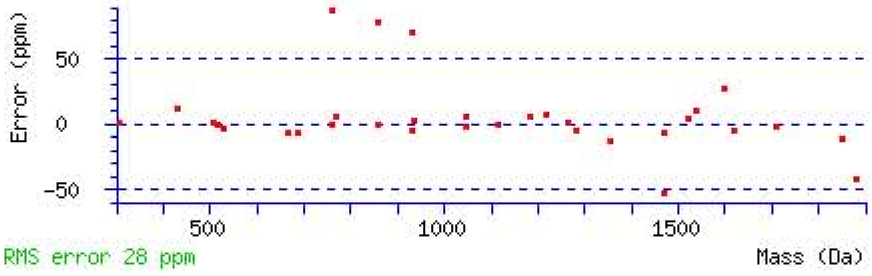


```
Monoisotopic mass of neutral peptide Mr(calc): 2396.111572
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2     : Biotin:Thermo-21345 (Q)
Ions Score: 68  Expect: 2.3e-006
Matches : 32/172 fragment ions using 51 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.039304	44.523290			70.028739	35.518008	S							17
2	**527.264630**	264.135953	510.238081	255.622679	509.254065	255.130671	Q	2310.086816	1155.547046	2293.060267	1147.033771	2292.076251	1146.541763	16
3	**687.295279**	344.151278	670.268730	335.638003	669.284714	335.145995	C	1870.861490	935.934383	1853.834941	927.421109	1852.850925	926.929101	15
4	800.379343	400.693310	783.352794	392.180035	782.368778	391.688027	L	***1710.830841***	855.919058	1693.804292	847.405784	1692.820276	846.913776	14
5	**929.421936**	465.214606	912.395387	456.701332	911.411371	456.209324	E	***1597.746777***	799.377026	1580.720228	790.863752	1579.736212	790.371744	13
6	**1044.448879**	522.728078	1027.422330	514.214803	1026.438314	513.722795	D	***1468.704184***	734.855730	1451.677635	726.342456	1450.693619	725.850447	12
7	**1181.507791**	591.257534	1164.481242	582.744259	1163.497226	582.252251	H	***1353.677241***	677.342258	1336.650692	668.828984	1335.666676	668.336976	11
8	**1282.555470**	641.781373	1265.528921	633.268099	1264.544905	632.776091	T	***1216.618329***	608.812802	1199.591780	600.299528	1198.607764	599.807520	10
9	**1468.634783**	734.821030	1451.608234	726.307755	1450.624218	725.815747	W	***1115.570650***	558.288963	1098.544101	549.775689			9
10	**1539.671897**	**770.339587**	1522.645348	761.826312	1521.661332	761.334304	A	***929.491337***	465.249306	912.464788	456.736032			8
11	1636.724661	818.865969	1619.698112	810.352694	1618.714096	809.860686	P	***858.454223***	429.730750	841.427674	421.217475			7
12	1733.777425	867.392351	1716.750876	858.879076	1715.766860	858.387068	P	***761.401459***	381.204367	744.374910	372.691093			6
13	**1880.845839**	940.926558	1863.819290	932.413283	1862.835274	931.921275	F	***664.348695***	332.677985	647.322146	324.164711			5
14	1977.898603	989.452940	1960.872054	980.939665	1959.888038	980.447657	P	***517.280281***	259.143778	500.253732	250.630504			4
15	2090.982667	**1045.994971**	2073.956118	1037.481697	2072.972102	1036.989689	I	420.227517	210.617396	403.200968	202.104122			3
16	2251.013316	1126.010296	2233.986767	1117.497021	2233.002751	1117.005013	C	***307.143453***	154.075364	290.116904	145.562090			2
17							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 28 ppm



RMS error 28 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.0	2396.111572	-0.002860	SQCLEDHTWAPPFPICK

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

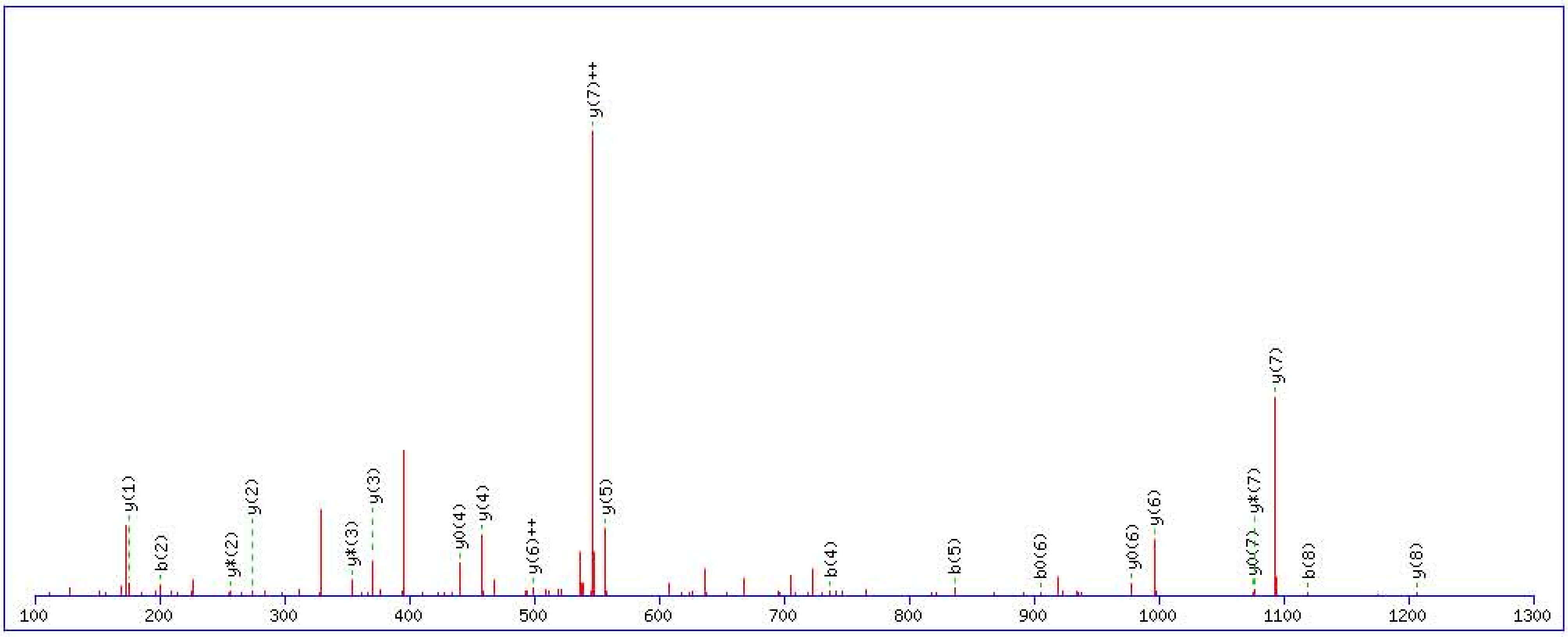
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SIPQVSPVR**
Found in **CBPN_HUMAN**, Carboxypeptidase N catalytic chain OS=Homo sapiens GN=CPN1 PE=1 SV=1

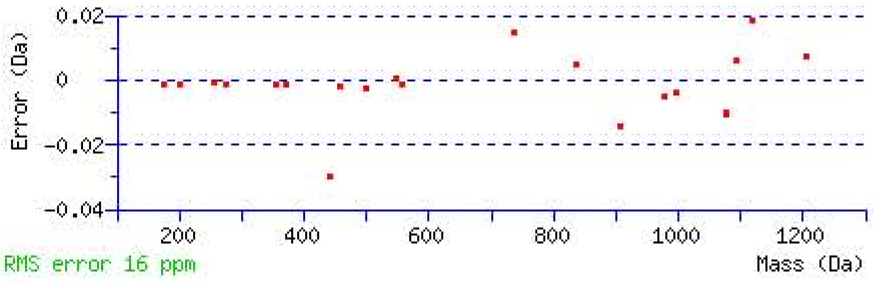
Match to Query 20236: 1292.723608 from(647.369080,2+) rtinseconds(1900) index(31110)
Title: Locus:1.1.1.3325.19 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

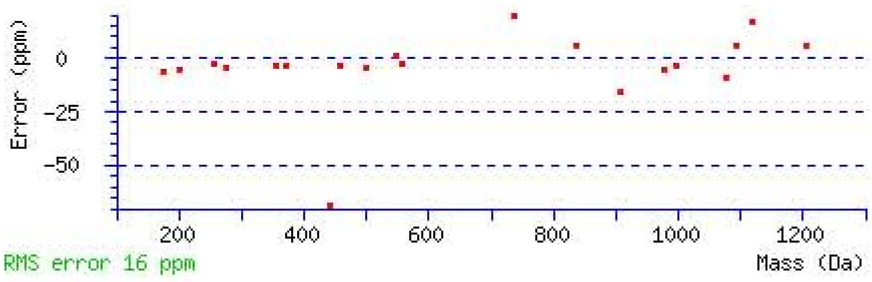
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1292.727478
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 45  Expect: 0.0002
Matches : 21/84 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	88.039304	44.523290			70.028739	35.518008	S							9
2	**201.123368**	101.065322			183.112803	92.060039	I	***1206.702726***	603.855001	1189.676177	595.341727	1188.692161	594.849718	8
3	298.176132	149.591704			280.165567	140.586422	P	***1093.618662***	547.312969	1076.592113	538.799695	1075.608097	538.307687	7
4	**737.401458**	369.204367	720.374909	360.691093	719.390893	360.199085	Q	***996.565898***	498.786587	979.539349	490.273313	978.555333	489.781305	6
5	**836.469872**	418.738574	819.443323	410.225300	818.459307	409.733292	V	***557.340572***	279.173924	540.314023	270.660650	539.330007	270.168642	5
6	923.501900	462.254588	906.475351	453.741313	905.491335	453.249305	S	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	4
7	1020.554664	510.780970	1003.528115	502.267696	1002.544099	501.775688	P	***371.240130***	186.123703	354.213581	177.610429			3
8	**1119.623078**	560.315177	1102.596529	551.801903	1101.612513	551.309895	V	***274.187366***	137.597321	257.160817	129.084047			2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.2	1292.727478	-0.003870	SIPQVSPVR
5.5	1292.708847	0.014761	VTQPELIQTHK
3.9	1292.731308	-0.007700	ASHVRDAVAVIR
1.4	1292.716202	0.007406	SLAMLQLYINK
1.4	1292.708801	0.014807	SLKRAEAEVYK
1.3	1292.708817	0.014791	AEVANHLAVLEK
1.3	1292.720078	0.003530	QNKSVLVPHGSK
0.8	1292.727448	-0.003840	LSKQHLEK

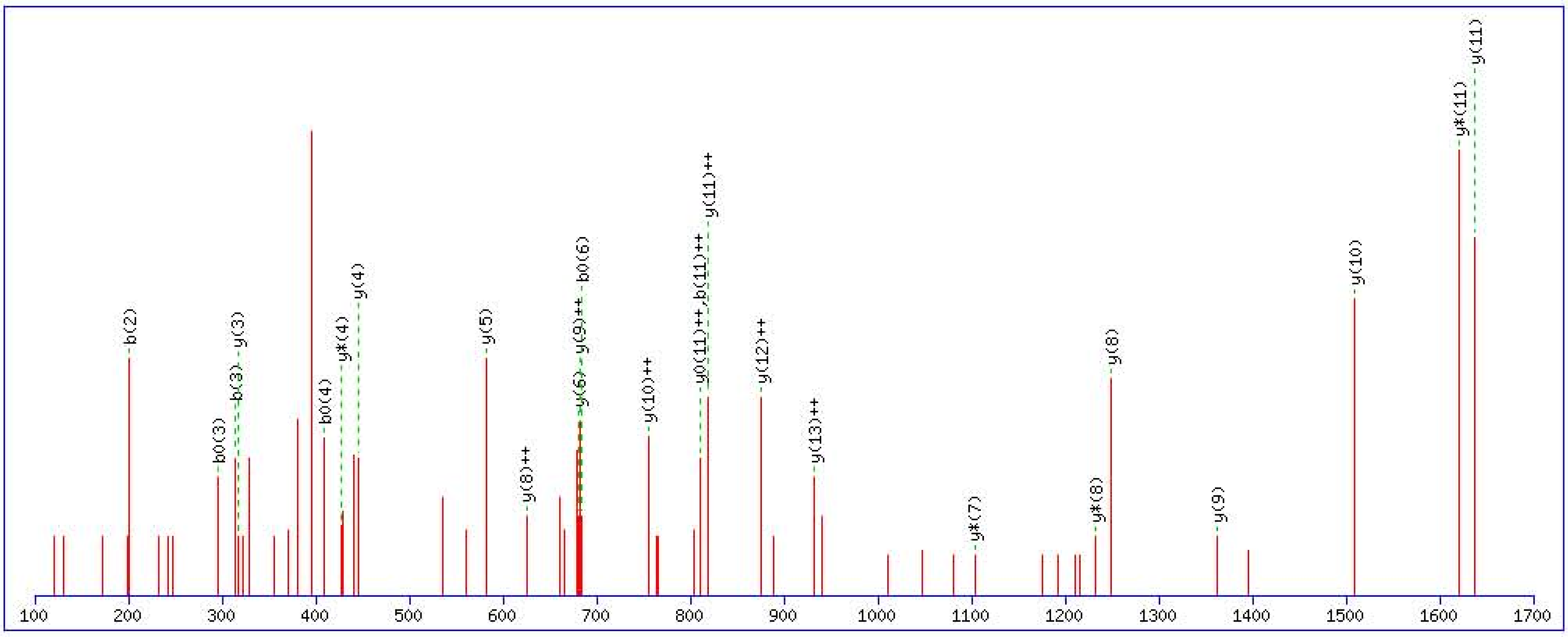
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EALIQFLEQVHQGIK**
Found in **CBPN_HUMAN**, Carboxypeptidase N catalytic chain OS=Homo sapiens GN=CPN1 PE=1 SV=1

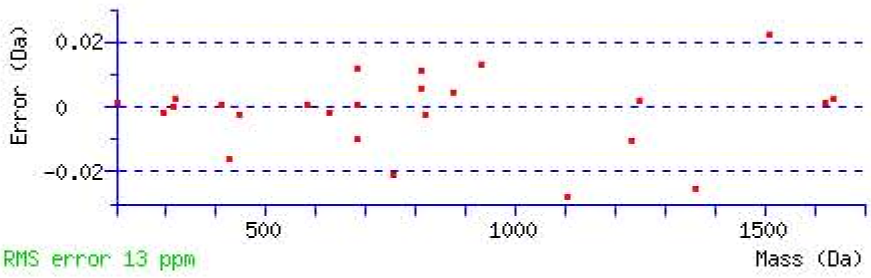
Match to Query 41101: 2063.121192 from(688.714340,3+) rtinseconds(2788) index(36569)
Title: Locus:1.1.1.3633.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

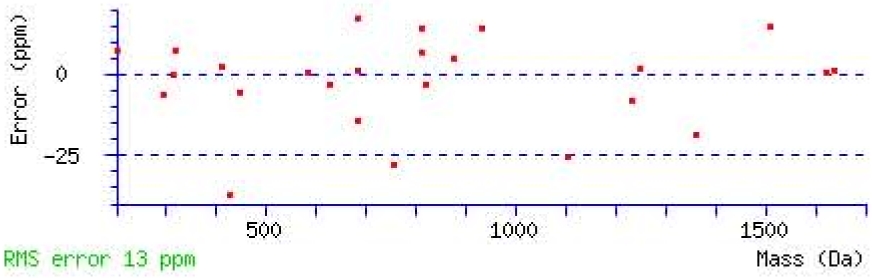
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2063.123749
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.027
Matches : 25/146 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	130.049869	65.528572			112.039304	56.523290	E							15
2	**201.086983**	101.047130			183.076418	92.041847	A	1935.088453	968.047865	1918.061904	959.534590	1917.077888	959.042582	14
3	**314.171047**	157.589161			296.160482	148.583879	L	1864.051339	932.529307	1847.024790	924.016033	1846.040774	923.524025	13
4	427.255111	214.131193			409.244546	205.125911	I	1750.967275	875.987276	1733.940726	867.474001	1732.956710	866.981993	12
5	555.313689	278.160483	538.287140	269.647208	537.303124	269.155200	Q	***1637.883211***	819.445244	1620.856662	810.931969	1619.872646	810.439961	11
6	702.382103	351.694690	685.355554	343.181415	684.371538	342.689407	F	***1509.824633***	755.415955	1492.798084	746.902680	1491.814068	746.410672	10
7	815.466167	408.236722	798.439618	399.723447	797.455602	399.231439	L	***1362.756219***	681.881748	1345.729670	673.368473	1344.745654	672.876465	9
8	944.508760	472.758018	927.482211	464.244744	926.498195	463.752736	E	***1249.672155***	625.339716	1232.645606	616.826441	1231.661590	616.334433	8
9	1383.734086	692.370681	1366.707537	683.857407	1365.723521	683.365399	Q	1120.629562	560.818419	1103.603013	552.305144			7
10	1482.802500	741.904888	1465.775951	733.391614	1464.791935	732.899606	V	***681.404236***	341.205756	664.377687	332.692481			6
11	1619.861412	810.434344	1602.834863	801.921070	1601.850847	801.429062	H	***582.335822***	291.671549	565.309273	283.158274			5
12	1747.919990	874.463633	1730.893441	865.950359	1729.909425	865.458351	Q	***445.276910***	223.142093	428.250361	214.628818			4
13	1804.941454	902.974365	1787.914905	894.461091	1786.930889	893.969083	G	***317.218332***	159.112804	300.191783	150.599529			3
14	1918.025518	959.516397	1900.998969	951.003123	1900.014953	950.511114	I	260.196868	130.602072	243.170319	122.088797			2
15							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of EALIQFLEQVHQGIK
(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	2063.123749	-0.002557	EALIQFLEQVHQGIK
16.8	2063.123749	-0.002557	EALIQFLEQVHQGIK
6.1	2063.123749	-0.002557	EALIQFLEQVHQGIK

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

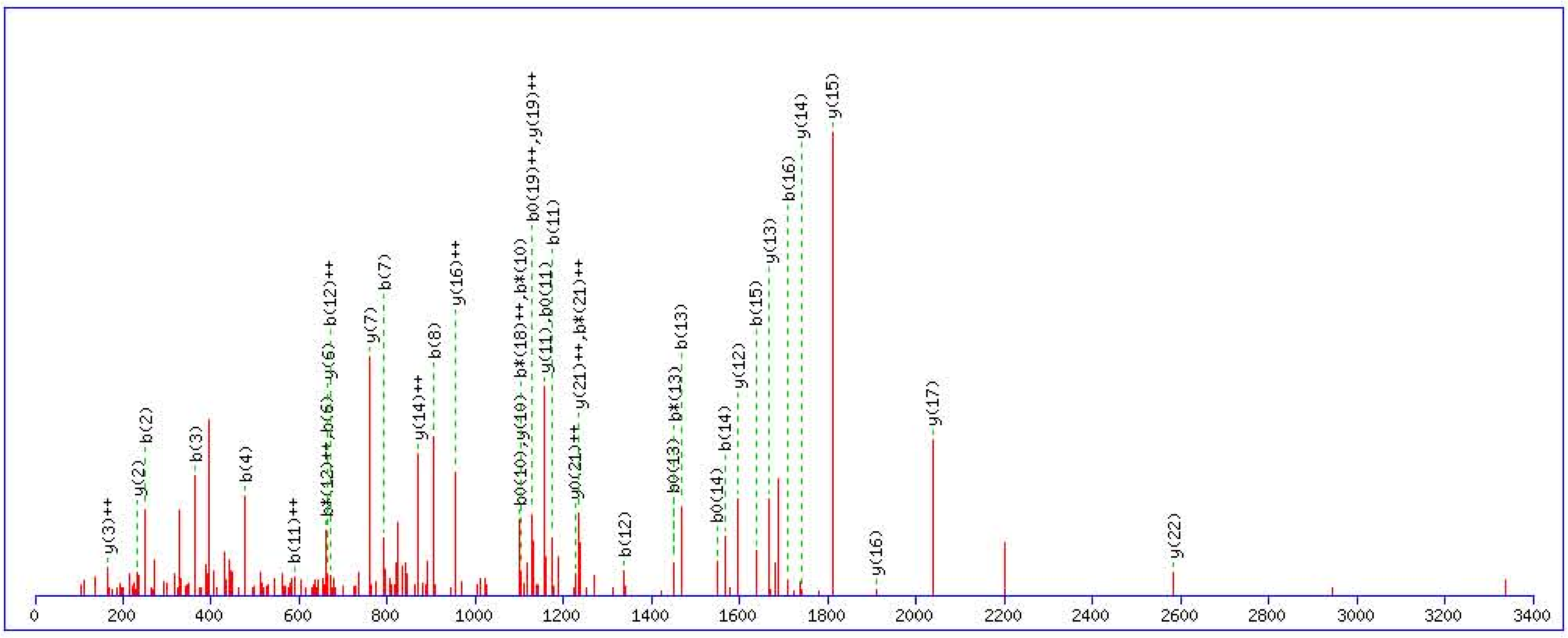
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IHILPSMNPDGYEVAAAQGPNKPGYLVGR**
Found in **CBPN_HUMAN**, Carboxypeptidase N catalytic chain OS=Homo sapiens GN=CPN1 PE=1 SV=1

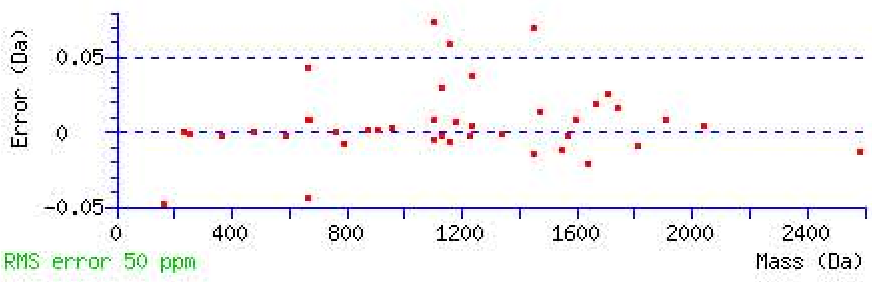
Match to Query 58492: 3374.723816 from(844.688230,4+) rtinseconds(2260) index(33435)
Title: Locus:1.1.1.3450.25 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

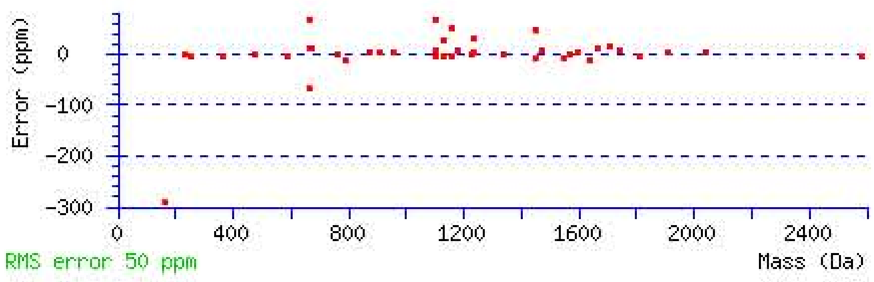
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3374.726746
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18     : Biotin:Thermo-21345 (Q)
Ions Score: 90  Expect: 9e-009
Matches : 42/280 fragment ions using 58 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					I							29
2	***251.150252***	126.078764					H	3262.649988	1631.828632	3245.623439	1623.315357	3244.639423	1622.823349	28
3	***364.234316***	182.620796					I	3125.591076	1563.299176	3108.564527	1554.785901	3107.580511	1554.293893	27
4	***477.318380***	239.162828					L	3012.507012	1506.757144	2995.480463	1498.243869	2994.496447	1497.751861	26
5	574.371144	287.689210					P	2899.422948	1450.215112	2882.396399	1441.701837	2881.412383	1441.209829	25
6	***661.403172***	331.205224			643.392607	322.199942	S	2802.370184	1401.688730	2785.343635	1393.175455	2784.359619	1392.683447	24
7	***792.443657***	396.725467			774.433092	387.720184	M	2715.338156	1358.172716	2698.311607	1349.659441	2697.327591	1349.167433	23
8	***906.486584***	453.746930	889.460035	445.233656	888.476019	444.741648	N	***2584.297671***	1292.652473	2567.271122	1284.139199	2566.287106	1283.647191	22
9	1003.539348	502.273312	986.512799	493.760038	985.528783	493.268030	P	2470.254744	1235.631010	2453.228195	1227.117735	2452.244179	1226.625727	21
10	1118.566291	559.786784	1101.539742	551.273509	1100.555726	550.781501	D	2373.201980	1187.104628	2356.175431	1178.591353	2355.191415	1178.099345	20
11	***1175.587755***	**588.297516**	1158.561206	579.784241	1157.577190	579.292233	G	2258.175037	1129.591156	2241.148488	1121.077882	2240.164472	1120.585874	19
12	***1338.651084***	**669.829180**	1321.624535	661.315906	1320.640519	660.823898	Y	2201.153573	1101.080424	2184.127024	1092.567150	2183.143008	1092.075142	18
13	***1467.693677***	734.350477	1450.667128	725.837202	1449.683112	725.345194	E	***2038.090244***	1019.548760	2021.063695	1011.035486	2020.079679	1010.543478	17
14	***1566.762091***	783.884684	1549.735542	775.371409	1548.751526	774.879401	V	***1909.047651***	955.027464	1892.021102	946.514189			16
15	***1637.799205***	819.403241	1620.772656	810.889966	1619.788640	810.397958	A	***1809.979237***	905.493257	1792.952688	896.979982			15
16	***1708.836319***	854.921798	1691.809770	846.408523	1690.825754	845.916515	A	***1738.942123***	869.974700	1721.915574	861.461425			14
17	1779.873433	890.440355	1762.846884	881.927080	1761.862868	881.435072	A	***1667.905009***	834.456143	1650.878460	825.942868			13
18	2219.098759	1110.053017	2202.072210	1101.539743	2201.088194	1101.047735	Q	***1596.867895***	798.937586	1579.841346	790.424311			12
19	2276.120223	1138.563749	2259.093674	1130.050475	2258.109658	1129.558467	G	***1157.642569***	579.324922	1140.616020	570.811648			11
20	2373.172987	1187.090131	2356.146438	1178.576857	2355.162422	1178.084849	P	***1100.621105***	550.814191	1083.594556	542.300916			10
21	2487.215914	1244.111595	2470.189365	1235.598320	2469.205349	1235.106312	N	1003.568341	502.287808	986.541792	493.774534			9
22	2615.310877	1308.159076	2598.284328	1299.645802	2597.300312	1299.153794	K	889.525414	445.266345	872.498865	436.753070			8
23	2712.363641	1356.685458	2695.337092	1348.172184	2694.353076	1347.680176	P	***761.430451***	381.218864	744.403902	372.705589			7
24	2769.385105	1385.196190	2752.358556	1376.682916	2751.374540	1376.190908	G	***664.377687***	332.692481	647.351138	324.179207			6
25	2932.448434	1466.727855	2915.421885	1458.214580	2914.437869	1457.722572	Y	607.356223	304.181750	590.329674	295.668475			5
26	3045.532498	1523.269887	3028.505949	1514.756612	3027.521933	1514.264604	L	444.292894	222.650085	427.266345	214.136810			4
27	3144.600912	1572.804094	3127.574363	1564.290819	3126.590347	1563.798811	V	331.208830	166.108053	314.182281	157.594778			3
28	3201.622376	1601.314826	3184.595827	1592.801551	3183.611811	1592.309543	G	***232.140416***	116.573846	215.113867	108.060571			2
29							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
89.7	3374.726746	-0.002930	IHILPSMNPDGYEVAAAQGPNKPGYLVGR
3.9	3374.698288	0.025528	HMVGPDWRQLFDVVIVQADKPSFFTDRR

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

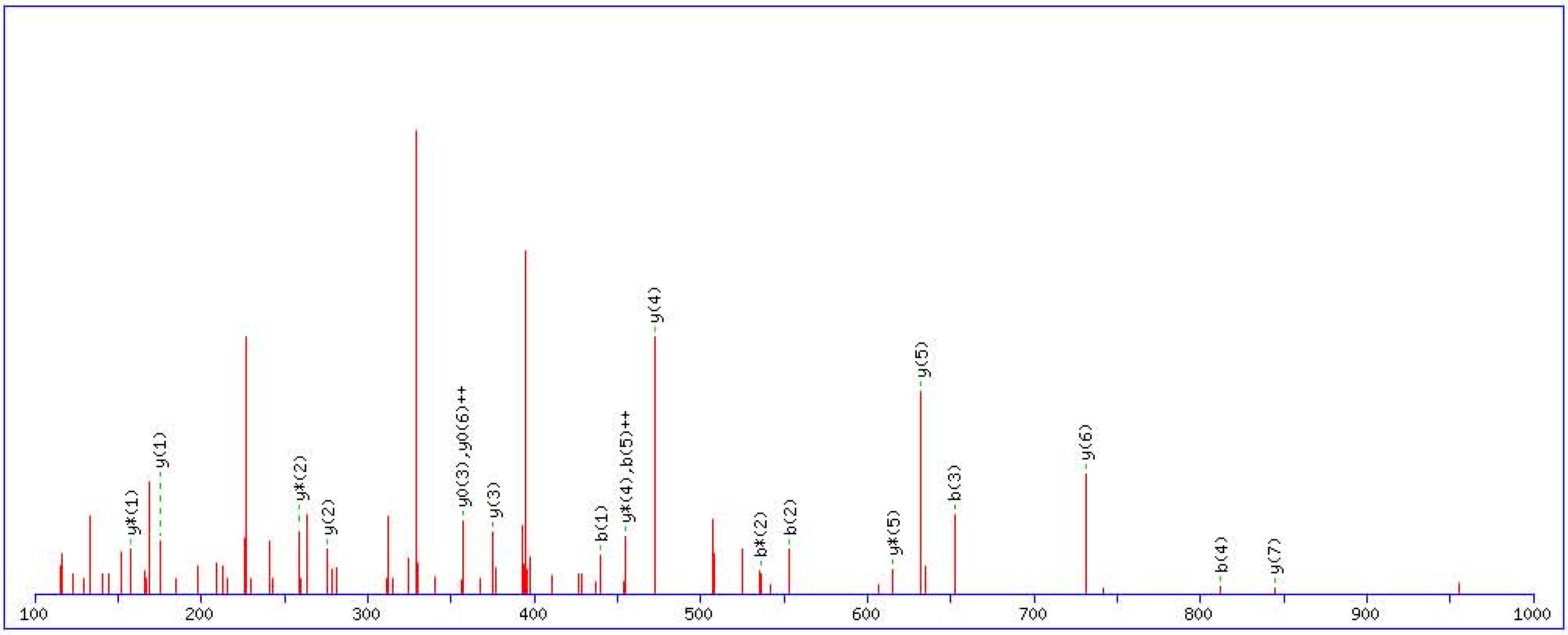
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLVCPVTR**
Found in **CPN2_HUMAN**, Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3

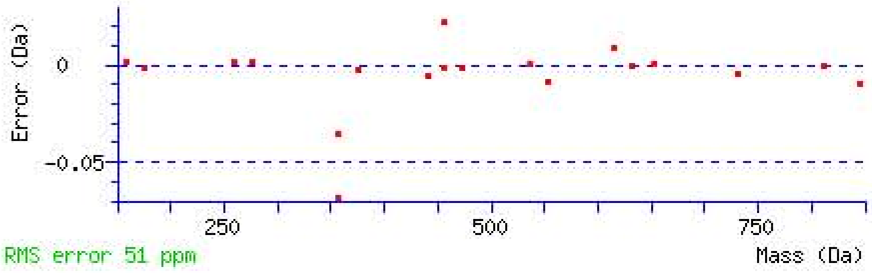
Match to Query 19991: 1282.684032 from(428.568620,3+) rtinseconds(1787) index(30516)
Title: Locus:1.1.1.3286.3 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

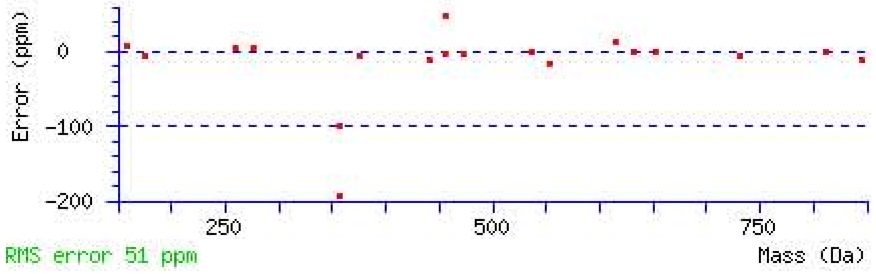
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1282.688995
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 29 **Expect:** 0.0027
Matches : 19/70 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	**440.232602**	220.619939	423.206053	212.106664			Q							8
2	**553.316666**	277.161971	536.290117	268.648697			L	***844.470936***	422.739106	827.444387	414.225831	826.460371	413.733823	7
3	**652.385080**	326.696178	635.358531	318.182904			V	***731.386872***	366.197074	714.360323	357.683799	713.376307	357.191791	6
4	**812.415729**	406.711503	795.389180	398.198228			C	***632.318458***	316.662867	615.291909	308.149592	614.307893	307.657584	5
5	909.468493	455.237885	892.441944	446.724610			P	***472.287809***	236.647542	455.261260	228.134268	454.277244	227.642260	4
6	1008.536907	504.772092	991.510358	496.258817			V	***375.235045***	188.121160	358.208496	179.607886	357.224480	179.115878	3
7	1109.584586	555.295931	1092.558037	546.782657	1091.574021	546.290648	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
8							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.9	1282.688995	-0.004963	QLVCPVTR
1.5	1282.688080	-0.004048	INEDPKDALLR
0.8	1282.681595	0.002437	KNMGGLGGLVHGK
0.5	1282.699341	-0.015309	LSAISLGQGQGPR

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

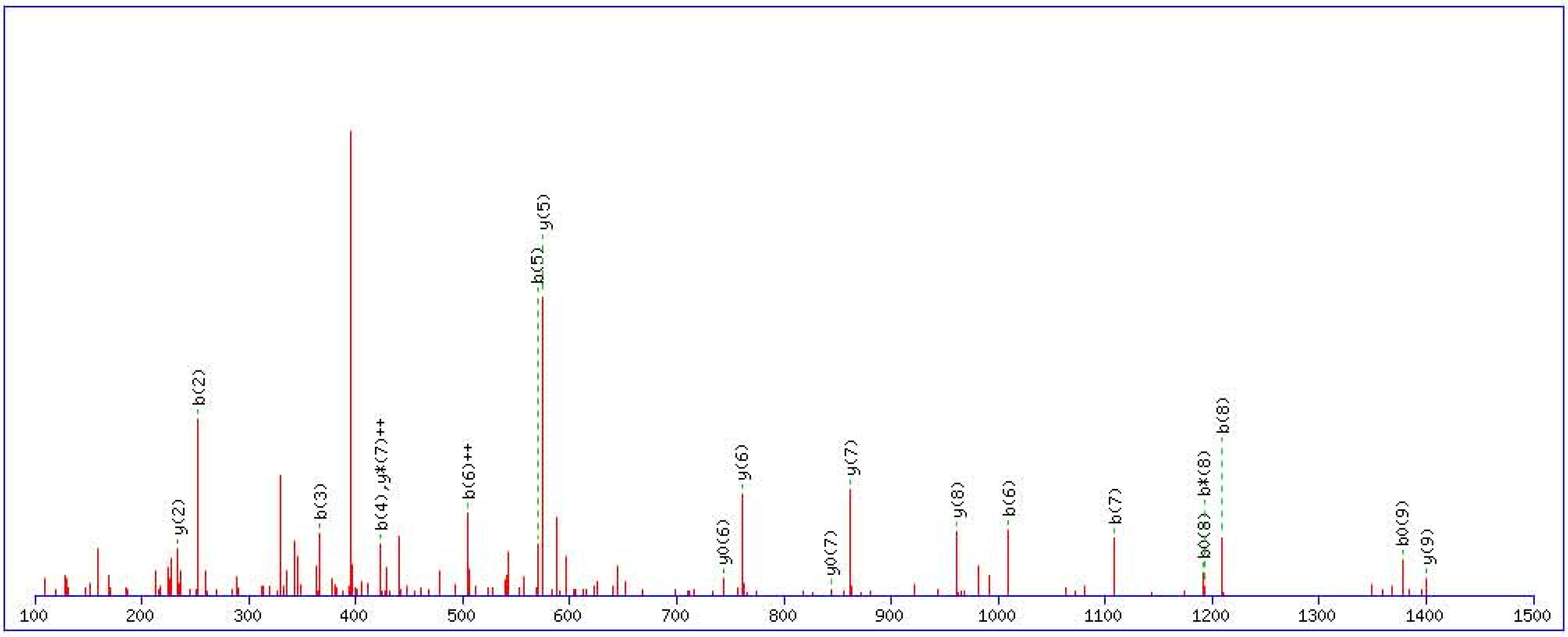
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DHLGFQVTWPDESK**
Found in **CPN2_HUMAN**, Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3

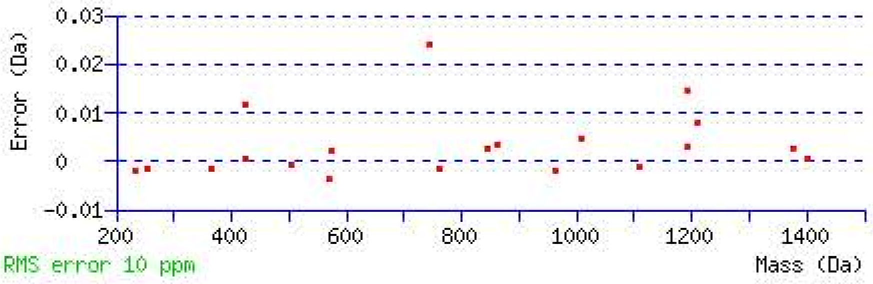
Match to Query 38780: 1968.935472 from(657.319100,3+) rtinseconds(2322) index(33711)
Title: Locus:1.1.1.3472.6 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

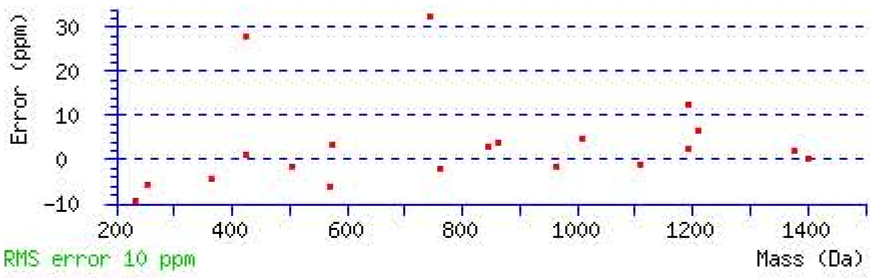
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1968.940399
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0029
Matches : 20/144 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	116.034219	58.520748			98.023654	49.515465	D							14
2	***253.093131***	127.050203			235.082566	118.044921	H	1854.920718	927.963997	1837.894169	919.450723	1836.910153	918.958715	13
3	***366.177195***	183.592235			348.166630	174.586953	L	1717.861806	859.434541	1700.835257	850.921267	1699.851241	850.429259	12
4	***423.198659***	212.102967			405.188094	203.097685	G	1604.777742	802.892509	1587.751193	794.379235	1586.767177	793.887227	11
5	***570.267073***	285.637175			552.256508	276.631892	F	1547.756278	774.381777	1530.729729	765.868503	1529.745713	765.376495	10
6	***1009.492399***	505.249838	992.465850	496.736563	991.481834	496.244555	Q	***1400.687864***	700.847570	1383.661315	692.334296	1382.677299	691.842288	9
7	***1108.560813***	554.784045	1091.534264	546.270770	1090.550248	545.778762	V	***961.462538***	481.234907	944.435989	472.721633	943.451973	472.229625	8
8	***1209.608492***	605.307884	1192.581943	596.794610	1191.597927	596.302602	T	***862.394124***	431.700700	845.367575	423.187426	844.383559	422.695418	7
9	1395.687805	698.347541	1378.661256	689.834266	1377.677240	689.342258	W	***761.346445***	381.176861	744.319896	372.663586	743.335880	372.171578	6
10	1492.740569	746.873923	1475.714020	738.360648	1474.730004	737.868640	P	***575.267132***	288.137204	558.240583	279.623930	557.256567	279.131922	5
11	1607.767512	804.387394	1590.740963	795.874120	1589.756947	795.382112	D	478.214368	239.610822	461.187819	231.097548	460.203803	230.605540	4
12	1736.810105	868.908691	1719.783556	860.395416	1718.799540	859.903408	E	363.187425	182.097351	346.160876	173.584076	345.176860	173.092068	3
13	1823.842133	912.424705	1806.815584	903.911430	1805.831568	903.419422	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
14							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.9	1968.940399	-0.004927	DHLGFQVTWPDESK
6.6	1968.949585	-0.014113	EGQMESVEAAMSSKTLKK
4.4	1968.921097	0.014375	EVDVNSEVHVQEMAEVR

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

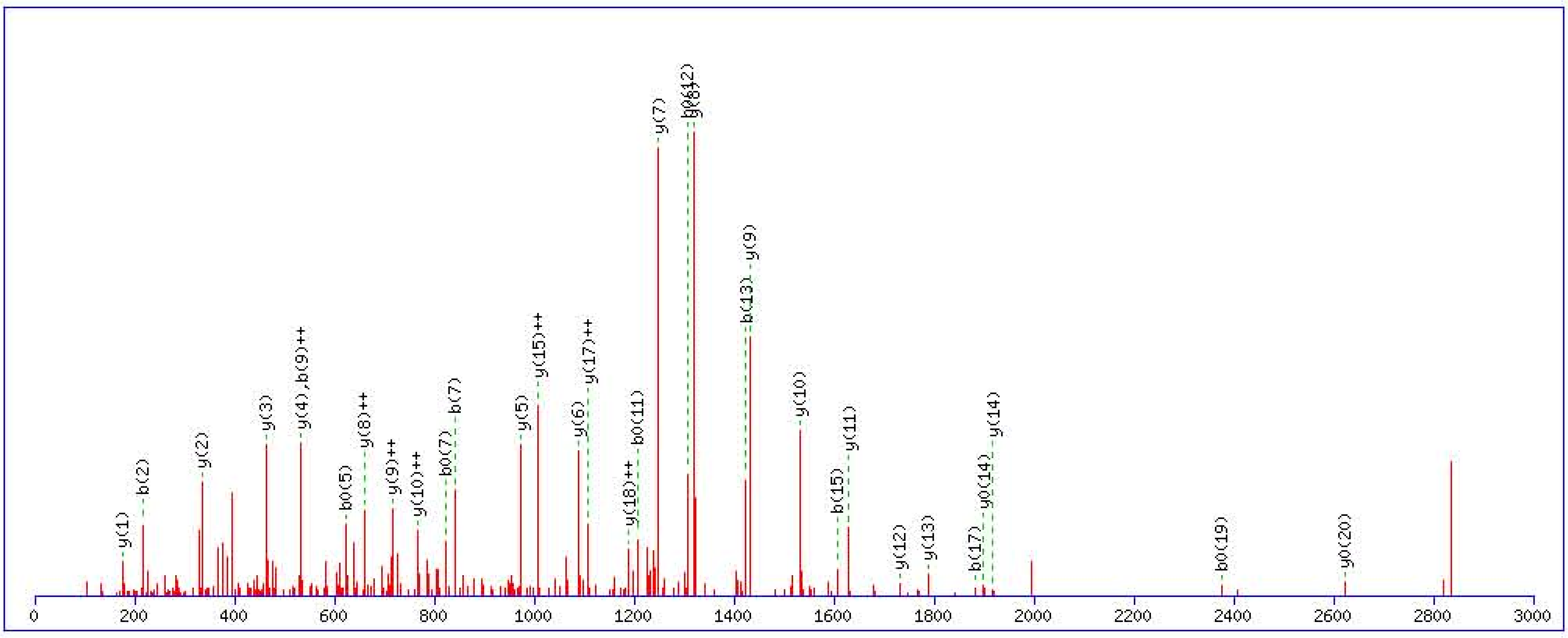
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SQCTYSNPEGTVVLACDQAQCR**
Found in **CPN2_HUMAN**, Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3

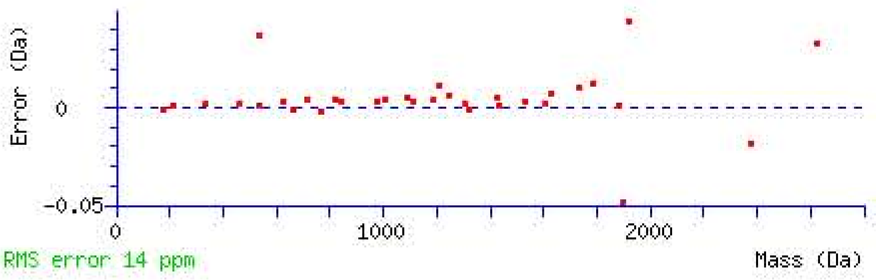
Match to Query 52407: 2854.252062 from(952.424630,3+) rtinseconds(2068) index(32273)
Title: Locus:1.1.1.3383.22 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

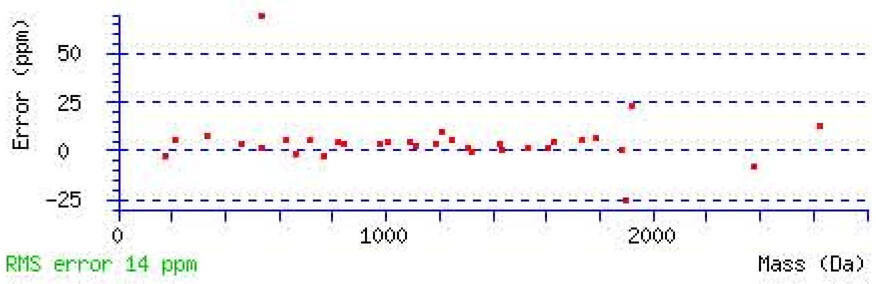
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2854.250671
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18 : Biotin:Thermo-21345 (Q)
Ions Score: 111 **Expect:** 4.3e-011
Matches : 33/240 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	88.039304	44.523290			70.028739	35.518008	S							22
2	**216.097882**	108.552579	199.071333	100.039305	198.087317	99.547296	Q	2768.225907	1384.616591	2751.199358	1376.103317	2750.215342	1375.611309	21
3	376.128531	188.567904	359.101982	180.054629	358.117966	179.562621	C	2640.167329	1320.587302	2623.140780	1312.074028	2622.156764	1311.582020	20
4	477.176210	239.091743	460.149661	230.578469	459.165645	230.086461	T	2480.136680	1240.571978	2463.110131	1232.058703	2462.126115	1231.566695	19
5	640.239539	320.623408	623.212990	312.110133	622.228974	311.618125	Y	2379.089001	1190.048138	2362.062452	1181.534864	2361.078436	1181.042856	18
6	727.271567	364.139422	710.245018	355.626147	709.261002	355.134139	S	2216.025672	1108.516474	2198.999123	1100.003199	2198.015107	1099.511191	17
7	**841.314494**	421.160885	824.287945	412.647611	823.303929	412.155603	N	2128.993644	1065.000460	2111.967095	1056.487185	2110.983079	1055.995177	16
8	938.367258	469.687267	921.340709	461.173993	920.356693	460.681985	P	2014.950717	1007.978997	1997.924168	999.465722	1996.940152	998.973714	15
9	1067.409851	534.208564	1050.383302	525.695289	1049.399286	525.203281	E	***1917.897953***	959.452615	1900.871404	950.939340	1899.887388	950.447332	14
10	1124.431315	562.719296	1107.404766	554.206021	1106.420750	553.714013	G	***1788.855360***	894.931318	1771.828811	886.418044	1770.844795	885.926036	13
11	1225.478994	613.243135	1208.452445	604.729861	1207.468429	604.237853	T	***1731.833896***	866.420586	1714.807347	857.907312	1713.823331	857.415304	12
12	1324.547408	662.777342	1307.520859	654.264068	1306.536843	653.772060	V	***1630.786217***	815.896747	1613.759668	807.383472	1612.775652	806.891464	11
13	**1423.615822**	712.311549	1406.589273	703.798275	1405.605257	703.306267	V	***1531.717803***	766.362540	1514.691254	757.849265	1513.707238	757.357257	10
14	1536.699886	768.853581	1519.673337	760.340307	1518.689321	759.848299	L	***1432.649389***	716.828333	1415.622840	708.315058	1414.638824	707.823050	9
15	**1607.737000**	804.372138	1590.710451	795.858864	1589.726435	795.366856	A	***1319.565325***	660.286301	1302.538776	651.773026	1301.554760	651.281018	8
16	1767.767649	884.387463	1750.741100	875.874188	1749.757084	875.382180	C	***1248.528211***	624.767744	1231.501662	616.254469	1230.517646	615.762461	7
17	**1882.794592**	941.900934	1865.768043	933.387660	1864.784027	932.895652	D	***1088.497562***	544.752419	1071.471013	536.239145	1070.486997	535.747137	6
18	2322.019918	1161.513597	2304.993369	1153.000322	2304.009353	1152.508314	Q	***973.470619***	487.238948	956.444070	478.725673			5
19	2393.057032	1197.032154	2376.030483	1188.518879	2375.046467	1188.026872	A	***534.245293***	267.626285	517.218744	259.113010			4
20	2521.115610	1261.061443	2504.089061	1252.548169	2503.105045	1252.056161	Q	***463.208179***	232.107727	446.181630	223.594453			3
21	2681.146259	1341.076768	2664.119710	1332.563493	2663.135694	1332.071485	C	***335.149601***	168.078438	318.123052	159.565164			2
22							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
110.6	2854.250671	0.001391	SQCTYSNPEGTVVLACDQAQCR
84.6	2854.250671	0.001391	SQCTYSNPEGTVVLACDQAQCR
5.0	2854.250671	0.001391	SQCTYSNPEGTVVLACDQAQCR

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

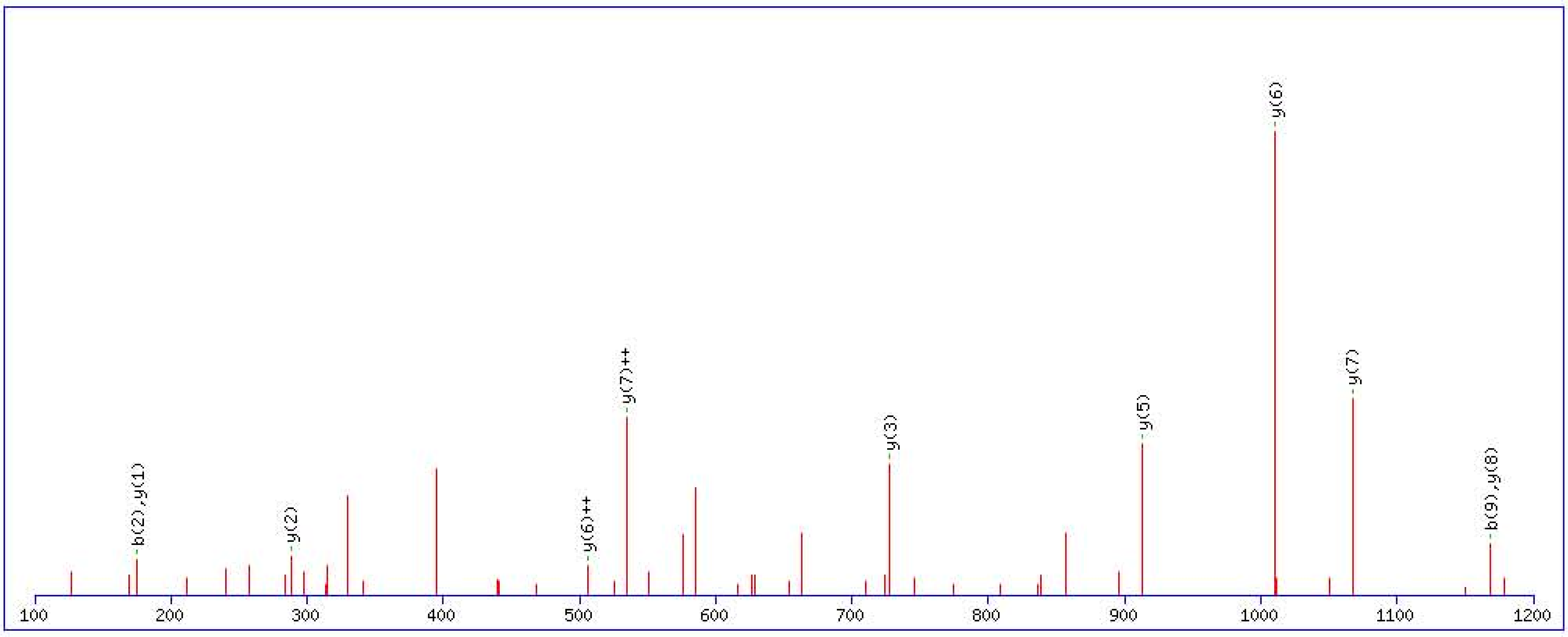
Mascot Search Results

Peptide View

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

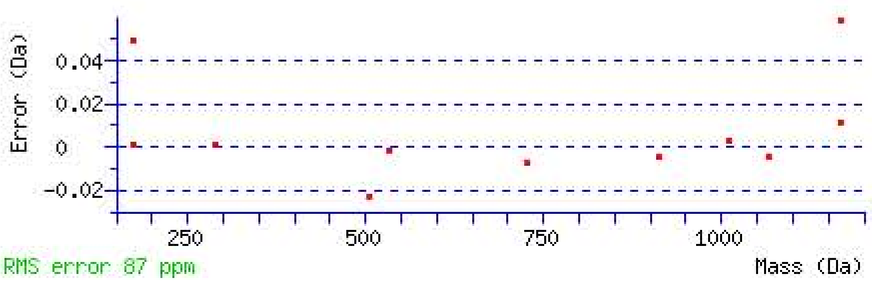
Match to Query 21168: 1341.669528 from(671.842040,2+) rtinseconds(1616) index(43609)
Title: Locus:1.1.1.3275.19 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

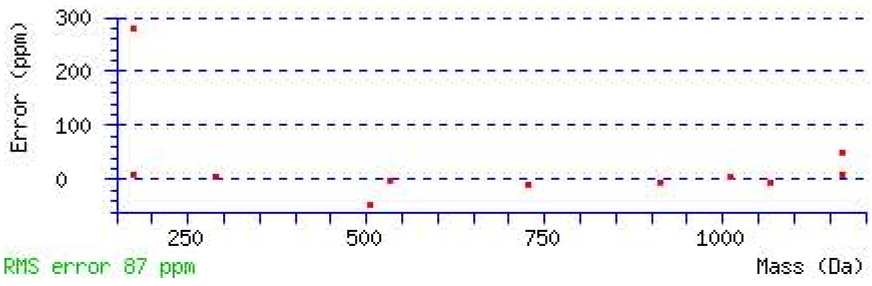
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1341.671082
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 67  Expect: 3.5e-006
Matches : 11/88 fragment ions using 11 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							10
2	**175.071332**	88.039304			157.060767	79.034021	S	1255.646334	628.326805	1238.619785	619.813530	1237.635769	619.321522	9
3	276.119011	138.563144			258.108446	129.557861	T	***1168.614306***	584.810791	1151.587757	576.297517	1150.603741	575.805508	8
4	333.140475	167.073875			315.129910	158.068593	G	***1067.566627***	534.286951	1050.540078	525.773677	1049.556062	525.281669	7
5	430.193239	215.600258			412.182674	206.594975	P	***1010.545163***	505.776219	993.518614	497.262945	992.534598	496.770937	6
6	487.214703	244.110989			469.204138	235.105707	G	***913.492399***	457.249837	896.465850	448.736563	895.481834	448.244555	5
7	616.257296	308.632286			598.246731	299.627004	E	856.470935	428.739105	839.444386	420.225831	838.460370	419.733823	4
8	1055.482622	528.244949	1038.456073	519.731675	1037.472057	519.239667	Q	***727.428342***	364.217809	710.401793	355.704534			3
9	**1168.566686**	584.786981	1151.540137	576.273707	1150.556121	575.781698	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 SSTGPGEQLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.3	1341.671082	-0.001554	SSTGPGEQLR
11.9	1341.674911	-0.005383	TSPERREPGTGR
11.3	1341.663651	0.005877	ESARDPKPEASR
7.3	1341.653793	0.015735	GFAEHGKQQQGR
6.8	1341.663681	0.005847	SSHKDSPRDVSK
6.8	1341.688828	-0.019300	DDAQLSGLPSALR
6.5	1341.682297	-0.012769	ASEQDVRAR
6.5	1341.653336	0.016192	STVQPPCSR
2.9	1341.680267	-0.010739	KFHEKHHSHR
2.7	1341.671051	-0.001523	ASQEEQIAR

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

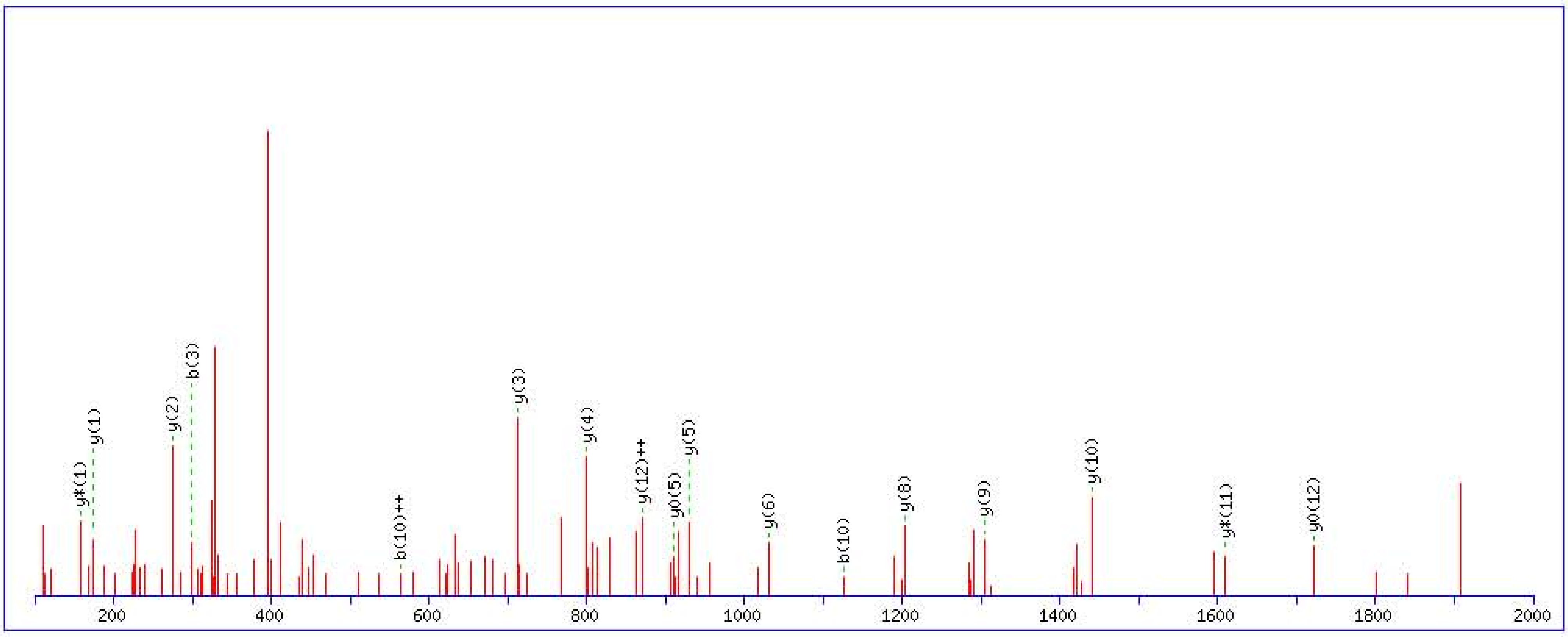
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

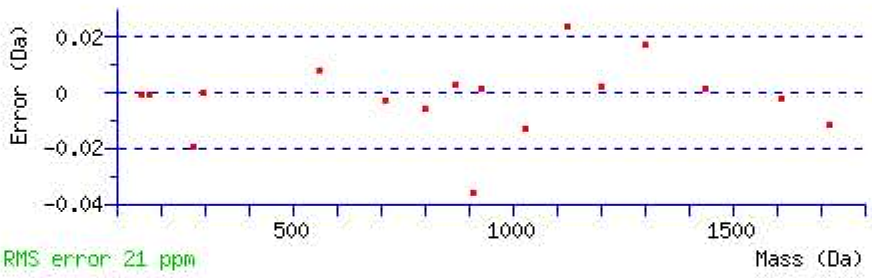
Match to Query 37864: 1923.922872 from(642.314900,3+) rtinseconds(1810) index(44827)
Title: Locus:1.1.1.3343.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

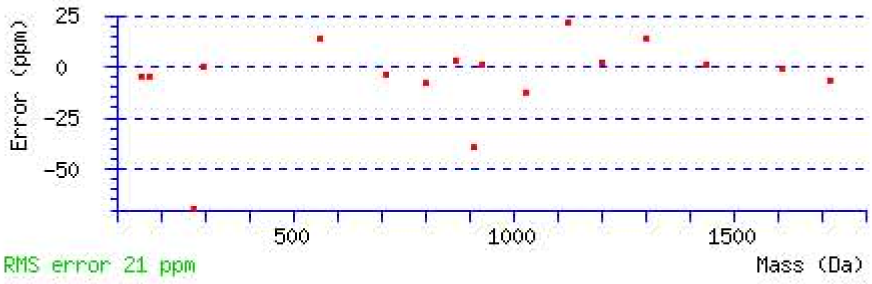
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 33  Expect: 0.0021
Matches : 17/140 fragment ions using 45 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
33.3	1923.926132	-0.003260	NALWHTGDTESQVR
4.8	1923.933533	-0.010661	ICGKGFDYPSSVQR

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

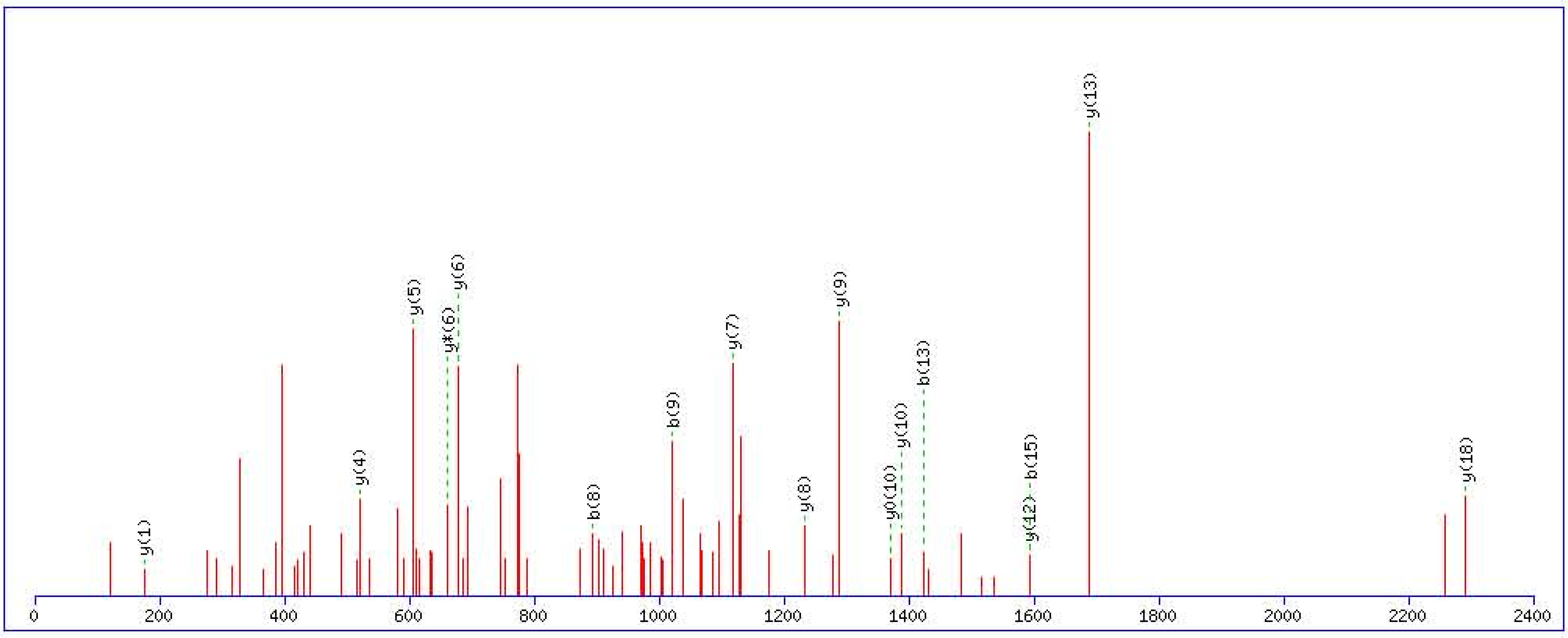
Mascot Search Results

Peptide View

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

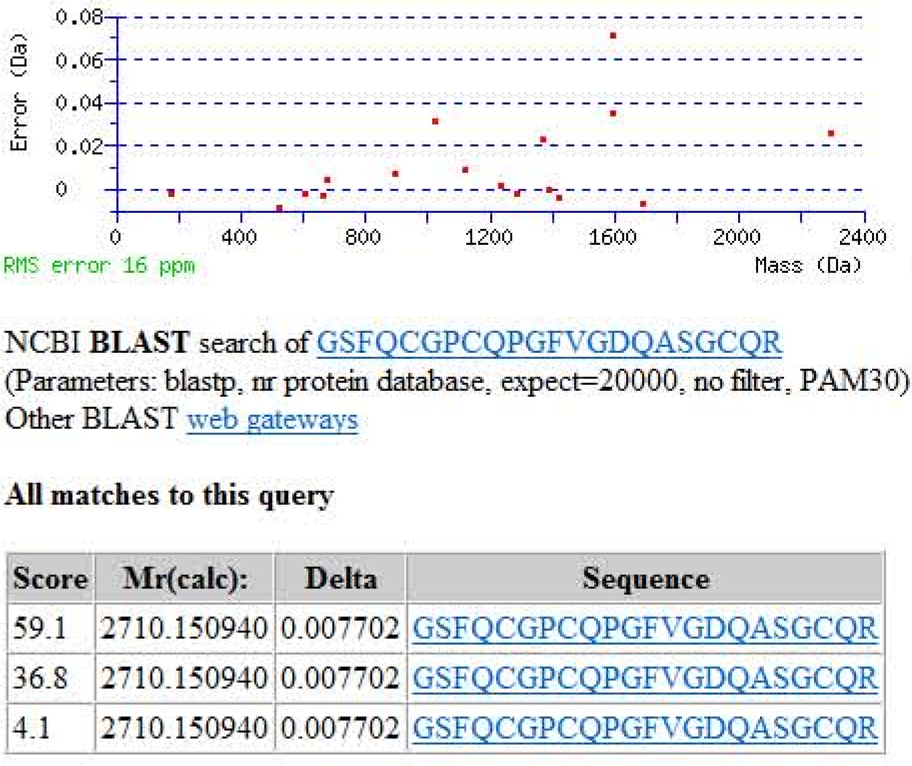
Match to Query 50464: 2710.158642 from(904.393490,3+) rtinseconds(1990) index(45989)
Title: Locus:1.1.1.3405.25 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

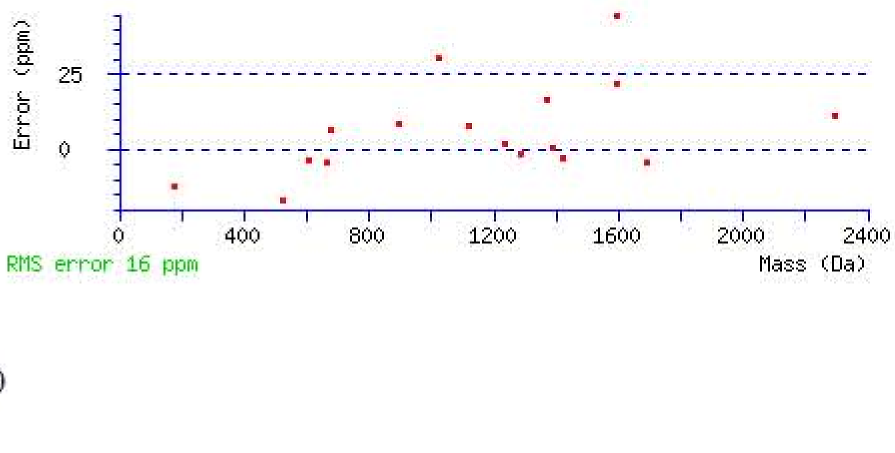
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2710.150940
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16     : Biotin:Thermo-21345 (Q)
Ions Score: 59  Expect: 3.9e-006
Matches : 17/236 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	58.028740	29.518008					G							22
2	145.060768	73.034022			127.050203	64.028740	S	2654.136698	1327.571987	2637.110149	1319.058712	2636.126133	1318.566704	21
3	292.129182	146.568229			274.118617	137.562946	F	2567.104670	1284.055973	2550.078121	1275.542698	2549.094105	1275.050690	20
4	420.187760	210.597518	403.161211	202.084243	402.177195	201.592235	Q	2420.036256	1210.521766	2403.009707	1202.008491	2402.025691	1201.516483	19
5	580.218409	290.612843	563.191860	282.099568	562.207844	281.607560	C	***2291.977678***	1146.492477	2274.951129	1137.979202	2273.967113	1137.487194	18
6	637.239873	319.123575	620.213324	310.610300	619.229308	310.118292	G	2131.947029	1066.477152	2114.920480	1057.963878	2113.936464	1057.471870	17
7	734.292637	367.649957	717.266088	359.136682	716.282072	358.644674	P	2074.925565	1037.966420	2057.899016	1029.453146	2056.915000	1028.961138	16
8	**894.323286**	447.665281	877.296737	439.152007	876.312721	438.659999	C	1977.872801	989.440039	1960.846252	980.926764	1959.862236	980.434756	15
9	**1022.381864**	511.694570	1005.355315	503.181296	1004.371299	502.689288	Q	1817.842152	909.424714	1800.815603	900.911440	1799.831587	900.419432	14
10	1119.434628	560.220952	1102.408079	551.707678	1101.424063	551.215670	P	***1689.783574***	845.395425	1672.757025	836.882151	1671.773009	836.390143	13
11	1176.456092	588.731684	1159.429543	580.218410	1158.445527	579.726402	G	***1592.730810***	796.869043	1575.704261	788.355769	1574.720245	787.863761	12
12	1323.524506	662.265891	1306.497957	653.752617	1305.513941	653.260609	F	1535.709346	768.358311	1518.682797	759.845037	1517.698781	759.353029	11
13	**1422.592920**	711.800098	1405.566371	703.286824	1404.582355	702.794816	V	***1388.640932***	694.824104	1371.614383	686.310830	1370.630367	685.818822	10
14	1479.614384	740.310830	1462.587835	731.797556	1461.603819	731.305548	G	***1289.572518***	645.289897	1272.545969	636.776623	1271.561953	636.284615	9
15	**1594.641327**	797.824302	1577.614778	789.311027	1576.630762	788.819019	D	***1232.551054***	616.779165	1215.524505	608.265891	1214.540489	607.773883	8
16	2033.866653	1017.436965	2016.840104	1008.923690	2015.856088	1008.431682	Q	***1117.524111***	559.265694	1100.497562	550.752419	1099.513546	550.260411	7
17	2104.903767	1052.955522	2087.877218	1044.442247	2086.893202	1043.950239	A	***678.298785***	339.653031	661.272236	331.139756	660.288220	330.647748	6
18	2191.935795	1096.471536	2174.909246	1087.958261	2173.925230	1087.466253	S	***607.261671***	304.134474	590.235122	295.621199	589.251106	295.129191	5
19	2248.957259	1124.982268	2231.930710	1116.468993	2230.946694	1115.976985	G	***520.229643***	260.618459	503.203094	252.105185			4
20	2408.987908	1204.997592	2391.961359	1196.484317	2390.977343	1195.992309	C	463.208179	232.107727	446.181630	223.594453			3
21	2537.046486	1269.026881	2520.019937	1260.513606	2519.035921	1260.021599	Q	303.177530	152.092403	286.150981	143.579129			2
22							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GSFQCGPCQPGFVGDQASGCQR
(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	2710.150940	0.007702	GSFQCGPCQPGFVGDQASGCQR
36.8	2710.150940	0.007702	GSFQCGPCQPGFVGDQASGCQR
4.1	2710.150940	0.007702	GSFQCGPCQPGFVGDQASGCQR

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

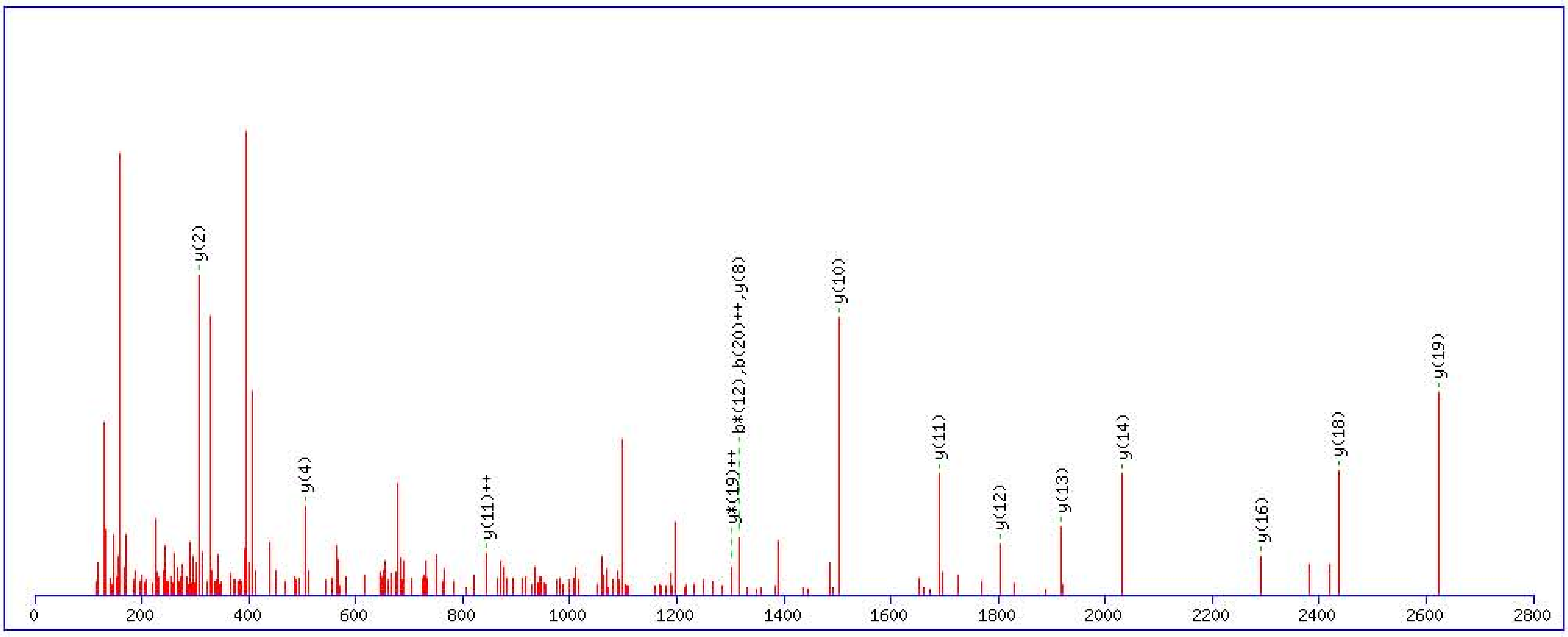
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVWGSVCDDNWGEKEDQVVCK**
Found in **CD5L_HUMAN**, CD5 antigen-like OS=Homo sapiens GN=CD5L PE=1 SV=1

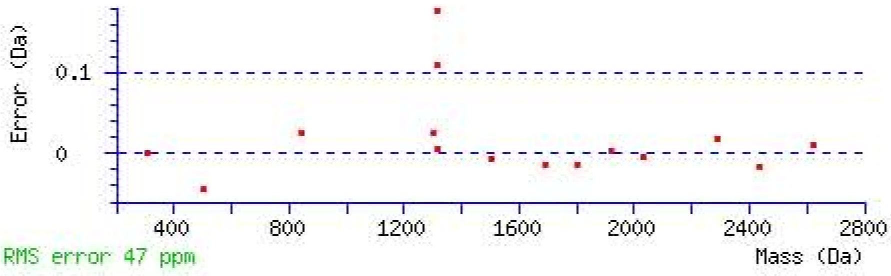
Match to Query 51240: 2777.224136 from(695.313310,4+) rtinseconds(2148) index(32726)
Title: Locus:1.1.1.3411.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

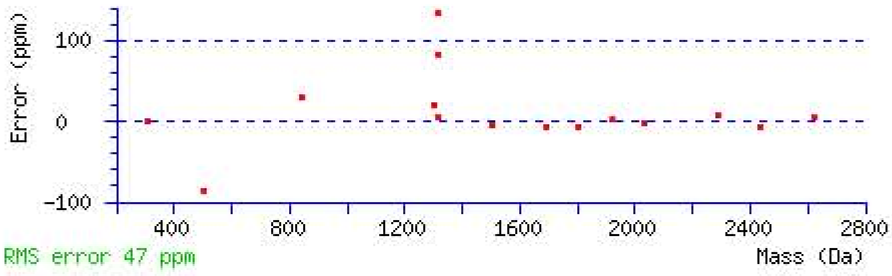
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2777.224792
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q17     : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 3.4e-006
Matches : 15/204 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							21
2	157.097154	79.052215					V	2721.210571	1361.108923	2704.184022	1352.595649	2703.200006	1352.103641	20
3	343.176467	172.091872					W	***2622.142157***	1311.574716	2605.115608	1303.061442	2604.131592	1302.569434	19
4	400.197931	200.602603					G	***2436.062844***	1218.535060	2419.036295	1210.021785	2418.052279	1209.529777	18
5	487.229959	244.118617			469.219394	235.113335	S	2379.041380	1190.024328	2362.014831	1181.511053	2361.030815	1181.019045	17
6	586.298373	293.652825			568.287808	284.647542	V	***2292.009352***	1146.508314	2274.982803	1137.995039	2273.998787	1137.503031	16
7	746.329022	373.668149			728.318457	364.662867	C	2192.940938	1096.974107	2175.914389	1088.460832	2174.930373	1087.968824	15
8	861.355965	431.181621			843.345400	422.176338	D	***2032.910289***	1016.958782	2015.883740	1008.445508	2014.899724	1007.953500	14
9	976.382908	488.695092			958.372343	479.689809	D	***1917.883346***	959.445311	1900.856797	950.932036	1899.872781	950.440028	13
10	1090.425835	545.716556	1073.399286	537.203281	1072.415270	536.711273	N	***1802.856403***	901.931840	1785.829854	893.418565	1784.845838	892.926557	12
11	1276.505148	638.756212	1259.478599	630.242938	1258.494583	629.750929	W	***1688.813476***	844.910376	1671.786927	836.397101	1670.802911	835.905093	11
12	1333.526612	667.266944	1316.500063	658.753670	1315.516047	658.261661	G	***1502.734163***	751.870719	1485.707614	743.357445	1484.723598	742.865437	10
13	1462.569205	731.788241	1445.542656	723.274966	1444.558640	722.782958	E	1445.712699	723.359987	1428.686150	714.846713	1427.702134	714.354705	9
14	1590.664168	795.835722	1573.637619	787.322448	1572.653603	786.830440	K	***1316.670106***	658.838691	1299.643557	650.325416	1298.659541	649.833408	8
15	1719.706761	860.357019	1702.680212	851.843744	1701.696196	851.351736	E	1188.575143	594.791209	1171.548594	586.277935	1170.564578	585.785927	7
16	1834.733704	917.870490	1817.707155	909.357216	1816.723139	908.865208	D	1059.532550	530.269913	1042.506001	521.756638	1041.521985	521.264630	6
17	2273.959030	1137.483153	2256.932481	1128.969878	2255.948465	1128.477870	Q	944.505607	472.756441	927.479058	464.243167			5
18	2373.027444	1187.017360	2356.000895	1178.504085	2355.016879	1178.012077	V	***505.280281***	253.143778	488.253732	244.630504			4
19	2472.095858	1236.551567	2455.069309	1228.038292	2454.085293	1227.546284	V	406.211867	203.609571	389.185318	195.096297			3
20	2632.126507	1316.566891	2615.099958	1308.053617	2614.115942	1307.561609	C	***307.143453***	154.075364	290.116904	145.562090			2
21							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.0	2777.224792	-0.000656	GVWGSVCDDNWGEKEDQVVCK

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

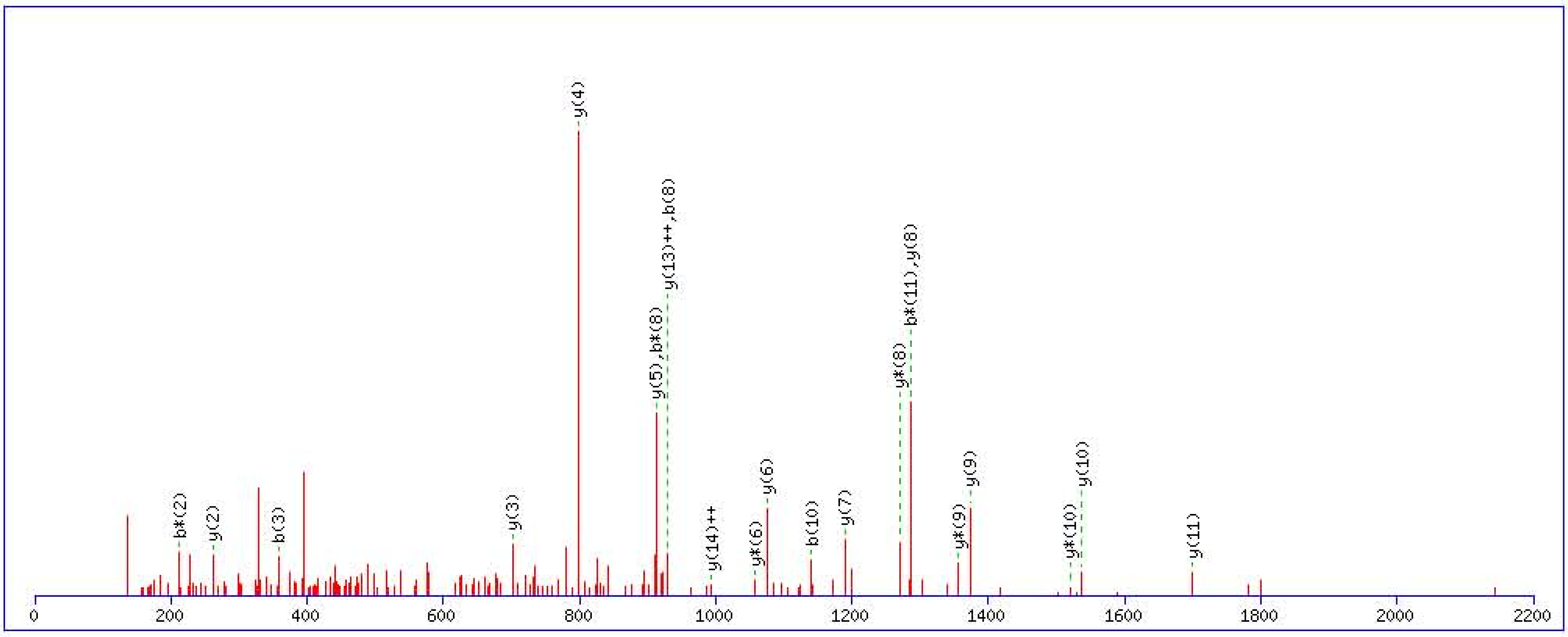
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NNEGTYYSPNYNPQSR**
Found in **CERU_HUMAN**, Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1

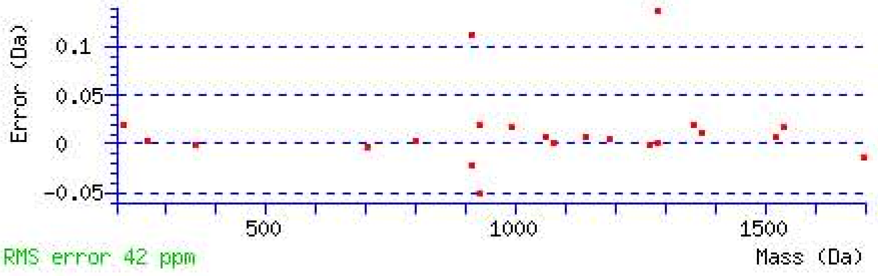
Match to Query 26525: 2213.985702 from(739.002510,3+) rtinseconds(1831) index(44931)
Title: Locus:1.1.1.3350.6 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

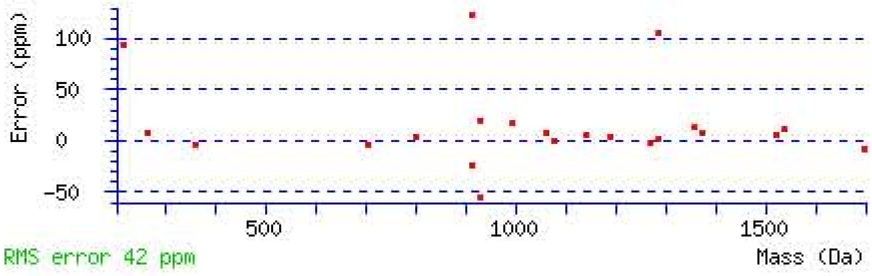
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2213.979980
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 59  Expect: 1e-005
Matches : 22/174 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							16
2	229.093130	115.050203	212.066581	106.536929			N	2100.944366	1050.975821	2083.917817	1042.462546	2082.933801	1041.970538	15
3	**358.135723**	179.571500	341.109174	171.058225	340.125158	170.566217	E	1986.901439	993.954358	1969.874890	985.441083	1968.890874	984.949075	14
4	415.157187	208.082232	398.130638	199.568957	397.146622	199.076949	G	1857.858846	929.433061	1840.832297	920.919787	1839.848281	920.427779	13
5	516.204866	258.606071	499.178317	250.092797	498.194301	249.600789	T	1800.837382	900.922329	1783.810833	892.409055	1782.826817	891.917047	12
6	679.268195	340.137736	662.241646	331.624461	661.257630	331.132453	Y	***1699.789703***	850.398490	1682.763154	841.885215	1681.779138	841.393207	11
7	842.331524	421.669400	825.304975	413.156126	824.320959	412.664118	Y	***1536.726374***	768.866825	1519.699825	760.353551	1518.715809	759.861543	10
8	**929.363552**	465.185414	912.337003	456.672140	911.352987	456.180132	S	***1373.663045***	687.335161	1356.636496	678.821886	1355.652480	678.329878	9
9	1026.416316	513.711796	1009.389767	505.198522	1008.405751	504.706514	P	***1286.631017***	643.819147	1269.604468	635.305872	1268.620452	634.813864	8
10	**1140.459243**	570.733260	1123.432694	562.219985	1122.448678	561.727977	N	***1189.578253***	595.292765	1172.551704	586.779490	1171.567688	586.287482	7
11	1303.522572	652.264924	1286.496023	643.751650	1285.512007	643.259642	Y	***1075.535326***	538.271301	1058.508777	529.758027	1057.524761	529.266019	6
12	1417.565499	709.286388	1400.538950	700.773113	1399.554934	700.281105	N	***912.471997***	456.739637	895.445448	448.226362	894.461432	447.734354	5
13	1514.618263	757.812770	1497.591714	749.299495	1496.607698	748.807487	P	***798.429070***	399.718173	781.402521	391.204899	780.418505	390.712891	4
14	1953.843589	977.425433	1936.817040	968.912158	1935.833024	968.420150	Q	***701.376306***	351.191791	684.349757	342.678517	683.365741	342.186509	3
15	2040.875617	1020.941447	2023.849068	1012.428172	2022.865052	1011.936164	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
16							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.6	2213.979980	0.005722	NNEGTYYSPNYNPQSR

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

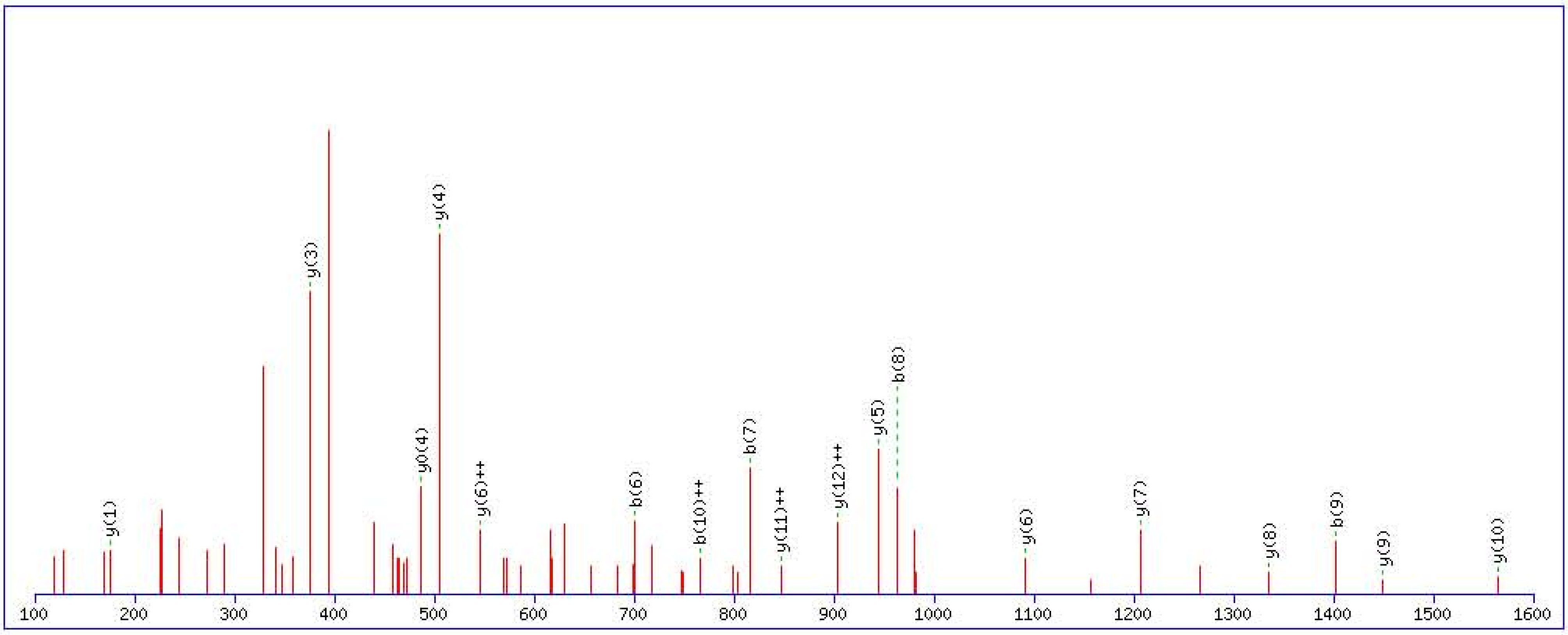
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VDKDNEDFQESNR**
Found in **CERU_HUMAN**, Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1

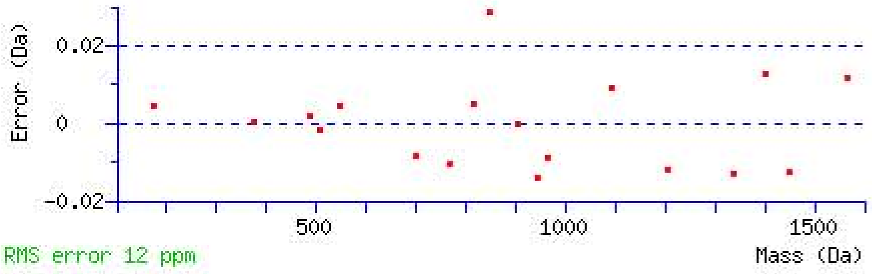
Match to Query 37483: 1905.845952 from(636.289260,3+) rtinseconds(1503) index(28860)
Title: Locus:1.1.1.3186.24 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

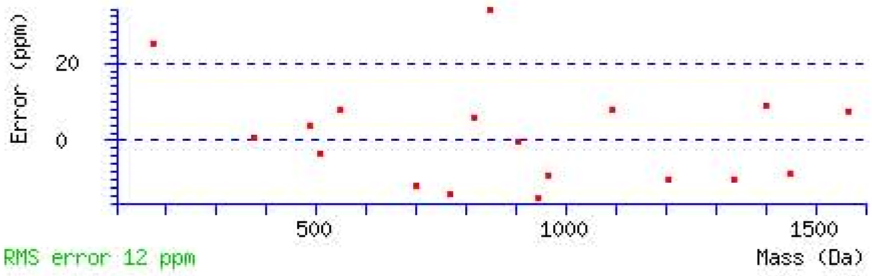
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1905.852676
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 7.6e-006
Matches : 18/134 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	100.075690	50.541483					V							13
2	215.102633	108.054954			197.092068	99.049672	D	1807.791552	904.399414	1790.765003	895.886140	1789.780987	895.394132	12
3	343.197596	172.102436	326.171047	163.589162	325.187031	163.097154	K	1692.764609	846.885943	1675.738060	838.372668	1674.754044	837.880660	11
4	458.224539	229.615908	441.197990	221.102633	440.213974	220.610625	D	***1564.669646***	782.838461	1547.643097	774.325187	1546.659081	773.833179	10
5	572.267466	286.637371	555.240917	278.124097	554.256901	277.632089	N	***1449.642703***	725.324990	1432.616154	716.811715	1431.632138	716.319707	9
6	**701.310059**	351.158668	684.283510	342.645393	683.299494	342.153385	E	***1335.599776***	668.303526	1318.573227	659.790252	1317.589211	659.298244	8
7	**816.337002**	408.672139	799.310453	400.158865	798.326437	399.666857	D	***1206.557183***	603.782230	1189.530634	595.268955	1188.546618	594.776947	7
8	**963.405416**	482.206346	946.378867	473.693072	945.394851	473.201064	F	***1091.530240***	546.268758	1074.503691	537.755484	1073.519675	537.263476	6
9	**1402.630742**	701.819009	1385.604193	693.305735	1384.620177	692.813727	Q	***944.461826***	472.734551	927.435277	464.221277	926.451261	463.729269	5
10	1531.673335	766.340306	1514.646786	757.827031	1513.662770	757.335023	E	***505.236500***	253.121888	488.209951	244.608614	487.225935	244.116606	4
11	1618.705363	809.856320	1601.678814	801.343045	1600.694798	800.851037	S	***376.193907***	188.600591	359.167358	180.087317	358.183342	179.595309	3
12	1732.748290	866.877783	1715.721741	858.364509	1714.737725	857.872501	N	289.161879	145.084577	272.135330	136.571303			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.8	1905.852676	-0.006724	VDKDNEDFQESNR

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

{MATRIX}{SCIENCE}

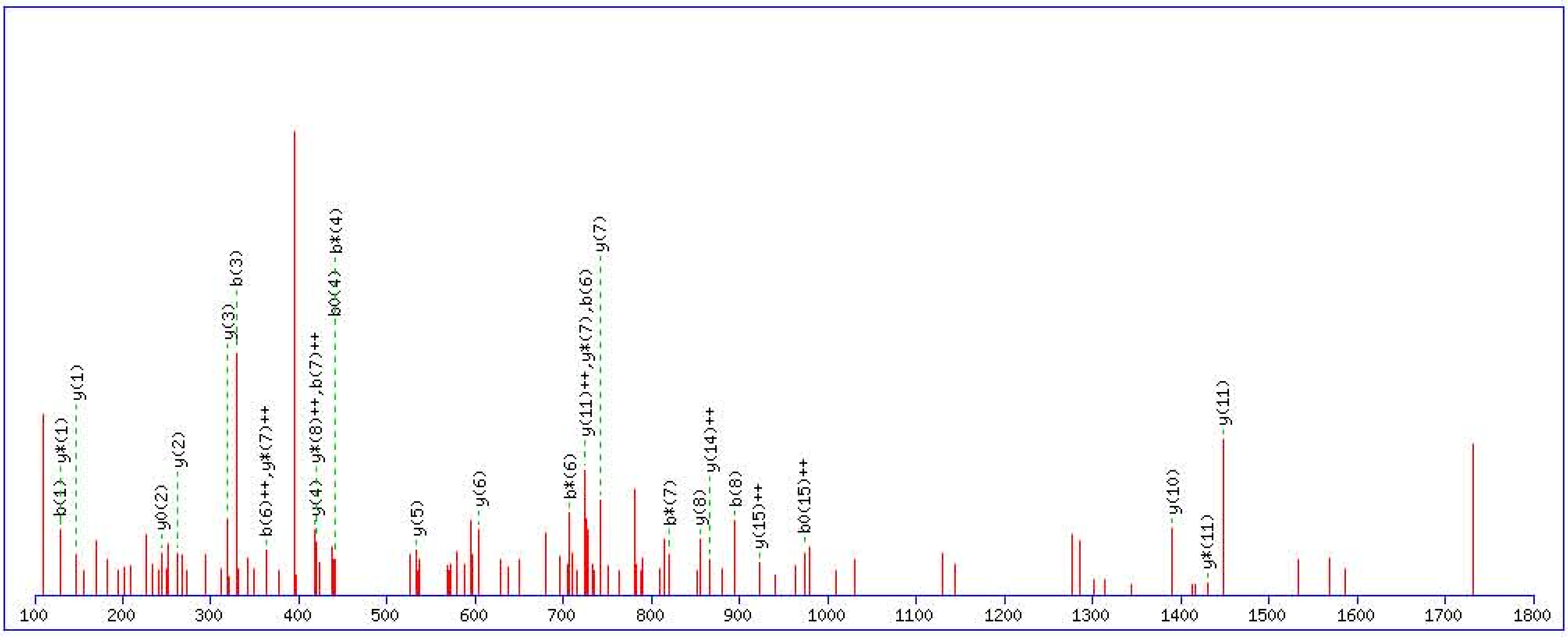
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KAEEEHLGILGPQLHADVGDK**
Found in **CERU_HUMAN**, Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1

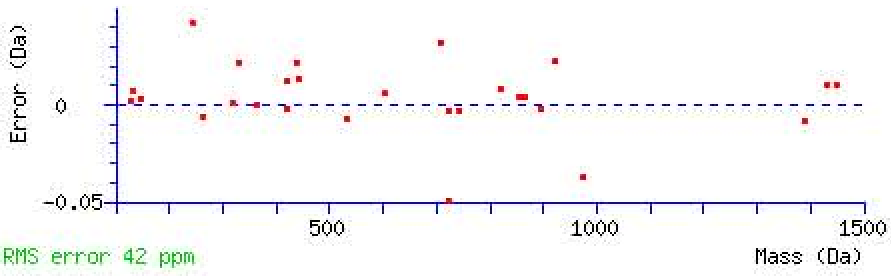
Match to Query 49145: 2566.313496 from(642.585650,4+) rtinseconds(1957) index(31531)
Title: Locus:1.1.1.3345.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

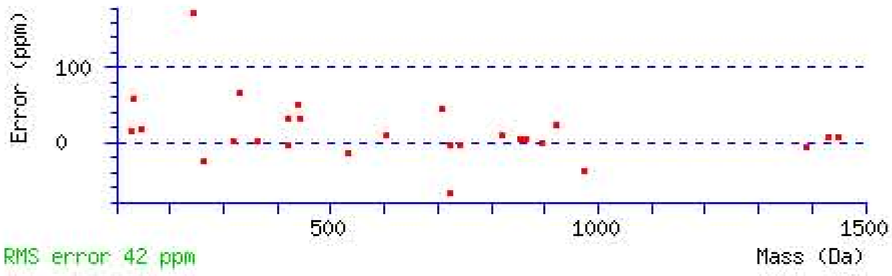
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2566.321335
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.00053
Matches : 30/234 fragment ions using 64 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	200.139353	100.573315	183.112804	92.060040			A	2439.233673	1220.120474	2422.207124	1211.607200	2421.223108	1211.115192	20
3	***329.181946***	165.094611	312.155397	156.581336	311.171381	156.089328	E	2368.196559	1184.601917	2351.170010	1176.088643	2350.185994	1175.596635	19
4	458.224539	229.615907	441.197990	221.102633	440.213974	220.610625	E	2239.153966	1120.080621	2222.127417	1111.567346	2221.143401	1111.075338	18
5	587.267132	294.137204	570.240583	285.623930	569.256567	285.131922	E	2110.111373	1055.559324	2093.084824	1047.046050	2092.100808	1046.554042	17
6	***724.326044***	**362.666660**	707.299495	354.153386	706.315479	353.661378	H	1981.068780	991.038028	1964.042231	982.524753	1963.058215	982.032745	16
7	837.410108	**419.208692**	820.383559	410.695418	819.399543	410.203410	L	1844.009868	922.508572	1826.983319	913.995297	1825.999303	913.503289	15
8	***894.431572***	447.719424	877.405023	439.206150	876.421007	438.714142	G	1730.925804	865.966540	1713.899255	857.453265	1712.915239	856.961257	14
9	1007.515636	504.261456	990.489087	495.748182	989.505071	495.256174	I	1673.904340	837.455808	1656.877791	828.942533	1655.893775	828.450525	13
10	1120.599700	560.803488	1103.573151	552.290214	1102.589135	551.798205	L	1560.820276	780.913776	1543.793727	772.400501	1542.809711	771.908493	12
11	1177.621164	589.314220	1160.594615	580.800946	1159.610599	580.308937	G	***1447.736212***	724.371744	1430.709663	715.858469	1429.725647	715.366461	11
12	1274.673928	637.840602	1257.647379	629.327328	1256.663363	628.835319	P	***1390.714748***	695.861012	1373.688199	687.347737	1372.704183	686.855729	10
13	1713.899254	857.453265	1696.872705	848.939991	1695.888689	848.447983	Q	1293.661984	647.334630	1276.635435	638.821355	1275.651419	638.329347	9
14	1826.983318	913.995297	1809.956769	905.482023	1808.972753	904.990015	L	***854.436658***	427.721967	837.410109	419.208692	836.426093	418.716684	8
15	1964.042230	982.524753	1947.015681	974.011479	1946.031665	973.519471	H	***741.352594***	371.179935	724.326045	362.666660	723.342029	362.174652	7
16	2035.079344	1018.043310	2018.052795	1009.530036	2017.068779	1009.038028	A	***604.293682***	302.650479	587.267133	294.137204	586.283117	293.645196	6
17	2150.106287	1075.556781	2133.079738	1067.043507	2132.095722	1066.551499	D	***533.256568***	267.131922	516.230019	258.618647	515.246003	258.126639	5
18	2249.174701	1125.090988	2232.148152	1116.577714	2231.164136	1116.085706	V	***418.229625***	209.618450	401.203076	201.105176	400.219060	200.613168	4
19	2306.196165	1153.601720	2289.169616	1145.088446	2288.185600	1144.596438	G	***319.161211***	160.084243	302.134662	151.570969	301.150646	151.078961	3
20	2421.223108	1211.115192	2404.196559	1202.601917	2403.212543	1202.109909	D	***262.139747***	131.573511	245.113198	123.060237	244.129182	122.568229	2
21							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.5	2566.321335	-0.007839	KAEEEHLGILGPQLHADVGDK
0.5	2566.329437	-0.015941	QMHGLRTLNIGQCVRITDK

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

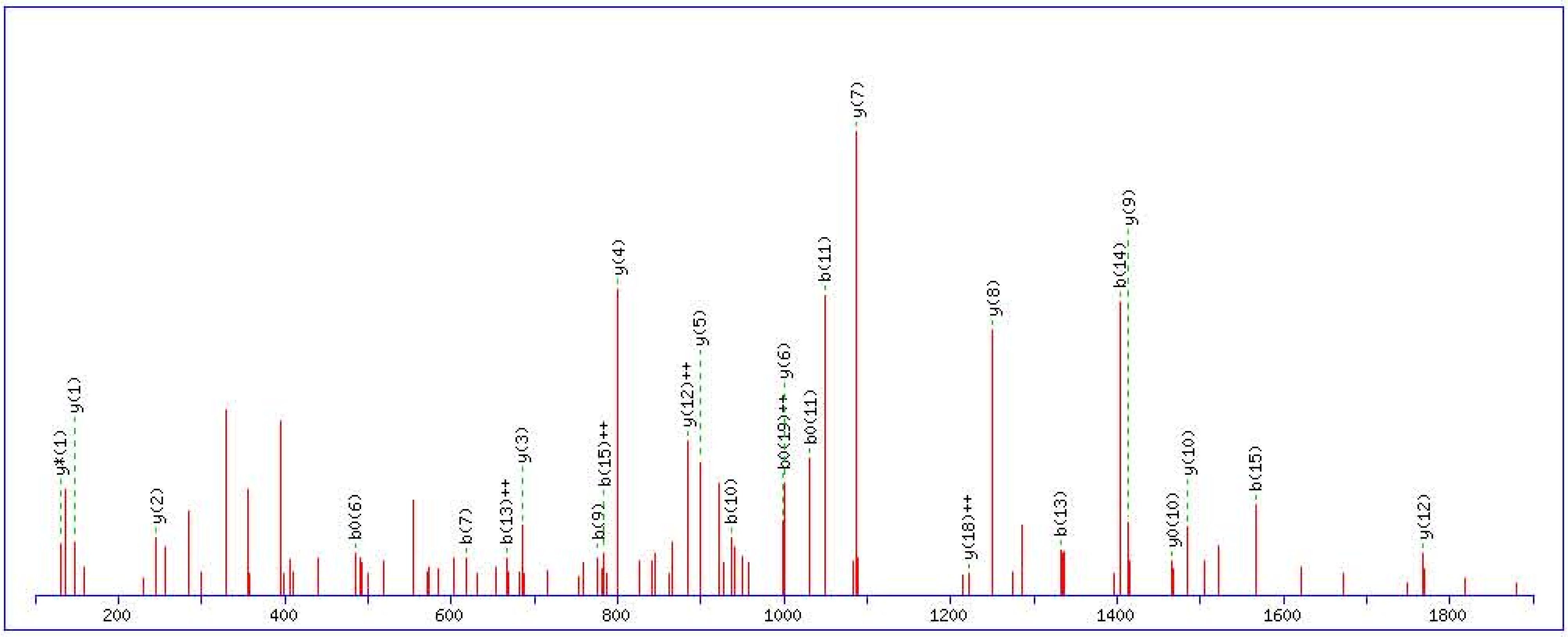
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGAGTEDSACIPWAYYSTVDQVK**
Found in **CERU_HUMAN**, Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1

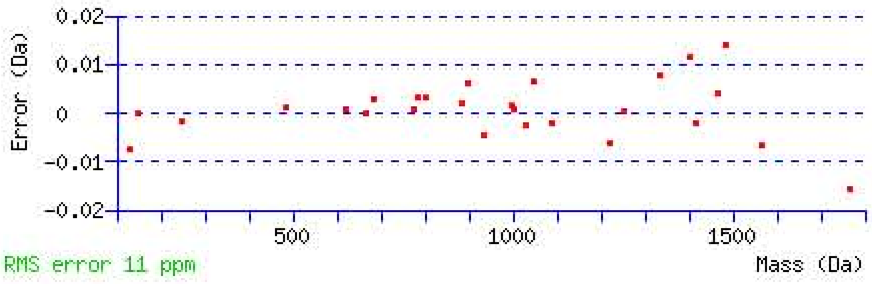
Match to Query 51748: 2815.280952 from(939.434260,3+) rtinseconds(2579) index(35018)
Title: Locus:1.1.1.3561.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

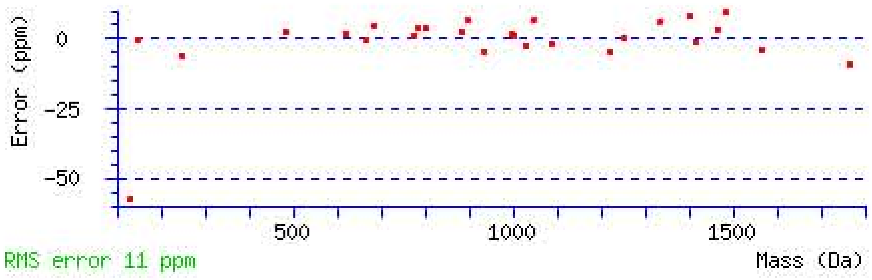


Monoisotopic mass of neutral peptide Mr(calc): 2815.283325
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q21 : Biotin:Thermo-21345 (Q)
Ions Score: 57 **Expect:** 1.9e-005
Matches : 27/218 fragment ions using 49 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							23
2	145.060768	73.034022			127.050203	64.028740	G	2729.258569	1365.132922	2712.232020	1356.619648	2711.248004	1356.127640	22
3	216.097882	108.552579			198.087317	99.547296	A	2672.237105	1336.622190	2655.210556	1328.108916	2654.226540	1327.616908	21
4	273.119346	137.063311			255.108781	128.058029	G	2601.199991	1301.103633	2584.173442	1292.590359	2583.189426	1292.098351	20
5	374.167025	187.587151			356.156460	178.581868	T	2544.178527	1272.592901	2527.151978	1264.079627	2526.167962	1263.587619	19
6	503.209618	252.108447			485.199053	243.103165	E	2443.130848	1222.069062	2426.104299	1213.555787	2425.120283	1213.063779	18
7	***618.236561***	309.621919			600.225996	300.616636	D	2314.088255	1157.547765	2297.061706	1149.034491	2296.077690	1148.542483	17
8	705.268589	353.137933			687.258024	344.132650	S	2199.061312	1100.034294	2182.034763	1091.521019	2181.050747	1091.029011	16
9	***776.305703***	388.656490			758.295138	379.651207	A	2112.029284	1056.518280	2095.002735	1048.005005	2094.018719	1047.512997	15
10	***936.336352***	468.671814			918.325787	459.666532	C	2040.992170	1020.999723	2023.965621	1012.486449	2022.981605	1011.994441	14
11	***1049.420416***	525.213846			1031.409851	516.208563	I	1880.961521	940.984399	1863.934972	932.471124	1862.950956	931.979116	13
12	1146.473180	573.740228			1128.462615	564.734945	P	***1767.877457***	884.442367	1750.850908	875.929092	1749.866892	875.437084	12
13	***1332.552493***	**666.779884**			1314.541928	657.774602	W	1670.824693	835.915985	1653.798144	827.402710	1652.814128	826.910702	11
14	***1403.589607***	702.298441			1385.579042	693.293159	A	***1484.745380***	742.876328	1467.718831	734.363054	1466.734815	733.871046	10
15	***1566.652936***	**783.830106**			1548.642371	774.824823	Y	***1413.708266***	707.357771	1396.681717	698.844497	1395.697701	698.352489	9
16	1729.716265	865.361771			1711.705700	856.356488	Y	***1250.644937***	625.826107	1233.618388	617.312832	1232.634372	616.820824	8
17	1816.748293	908.877785			1798.737728	899.872502	S	***1087.581608***	544.294442	1070.555059	535.781168	1069.571043	535.289160	7
18	1917.795972	959.401624			1899.785407	950.396342	T	***1000.549580***	500.778428	983.523031	492.265154	982.539015	491.773146	6
19	2016.864386	1008.935831			1998.853821	999.930549	V	***899.501901***	450.254589	882.475352	441.741314	881.491336	441.249306	5
20	2131.891329	1066.449302			2113.880764	1057.444020	D	***800.433487***	400.720382	783.406938	392.207107	782.422922	391.715099	4
21	2571.116655	1286.061966	2554.090106	1277.548691	2553.106090	1277.056683	Q	***685.406544***	343.206910	668.379995	334.693636			3
22	2670.185069	1335.596173	2653.158520	1327.082898	2652.174504	1326.590890	V	***246.181218***	123.594247	229.154669	115.080972			2
23							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 11 ppm



RMS error 11 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.2	2815.283325	-0.002373	SGAGTEDSACIPWAYYSTVDQVK

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

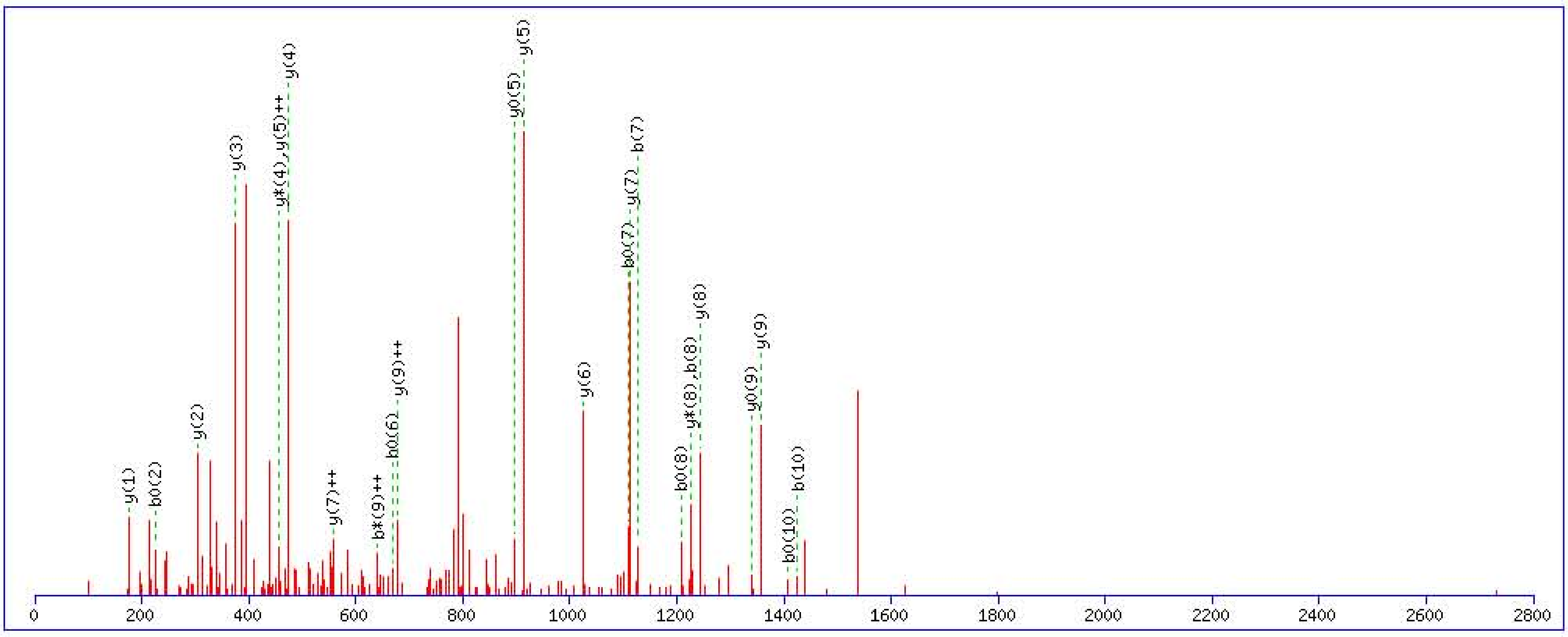
Mascot Search Results

Peptide View

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

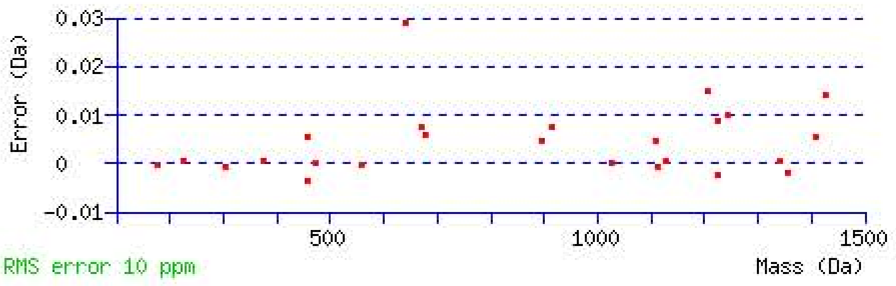
Match to Query 30550: 1598.798068 from(800.406310,2+) rtinseconds(1981) index(45911)
Title: Locus:1.1.1.3402.22 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

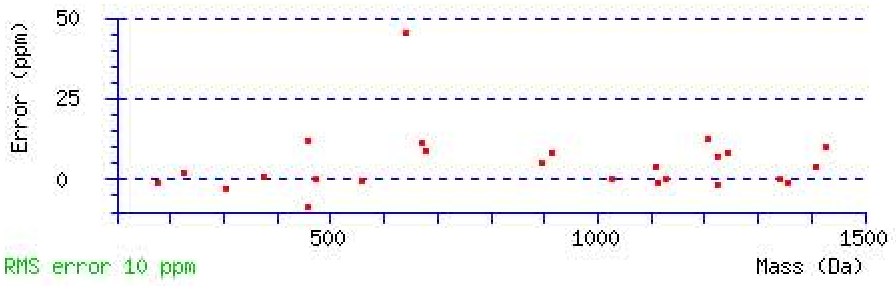
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1598.797379
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 55  Expect: 2.7e-005
Matches : 25/106 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	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
55.0	1598.797379	0.000689	ELDESLQVAER
5.9	1598.797379	0.000689	LEESDVLQEAR
3.4	1598.808624	-0.010556	SSSMVAAAPSLVNTHK
2.5	1598.802094	-0.004026	ELVSRCGEMLHIR
0.9	1598.817352	-0.019284	DRAALCQLWR
0.8	1598.789993	0.008075	AGATSGELPVVEAENR
0.8	1598.787506	0.010562	AGGSWDLAVQER
0.8	1598.797409	0.000659	EDVDDLVSQLR
0.1	1598.790024	0.008044	VTAEGDSHTEVVISR

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

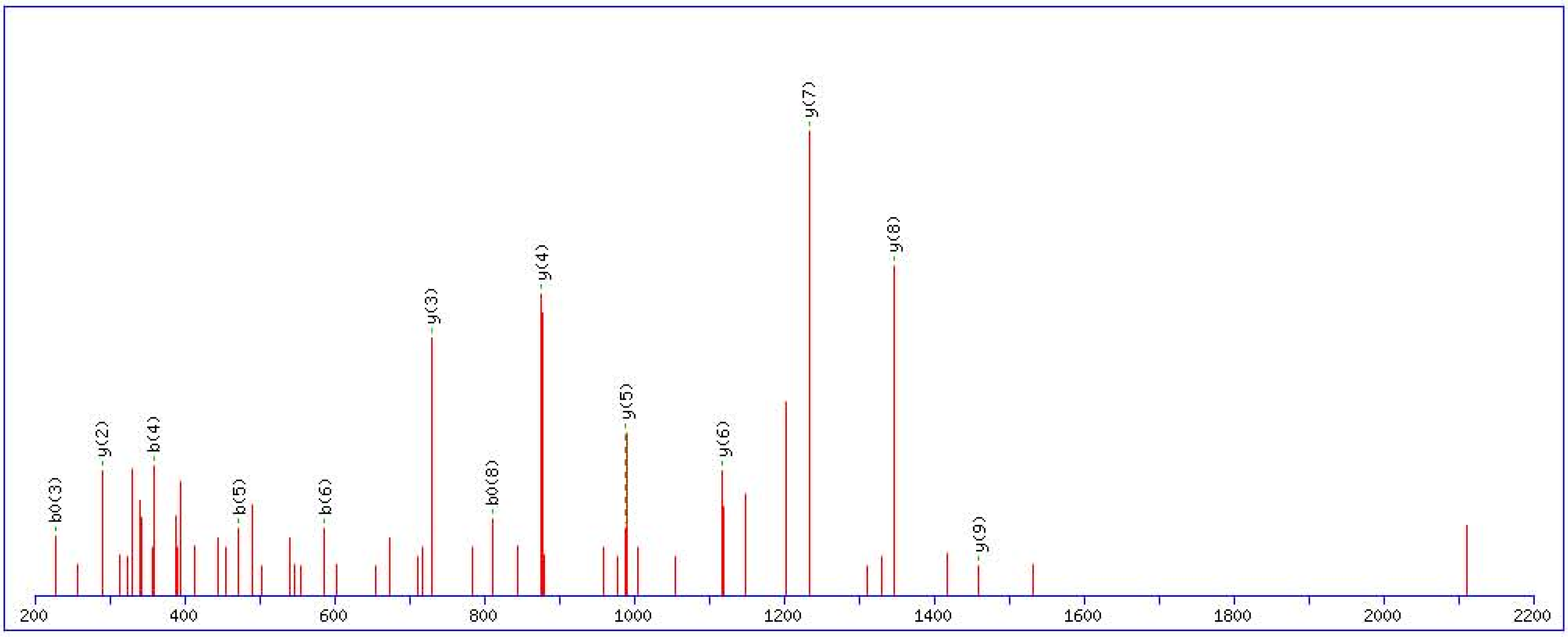
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

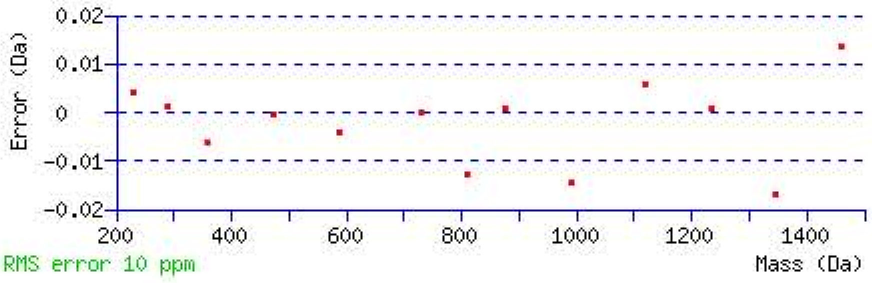
Match to Query 33724: 1703.855388 from(852.934970,2+) rtinseconds(2839) index(36978)
Title: Locus:1.1.1.3650.19 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

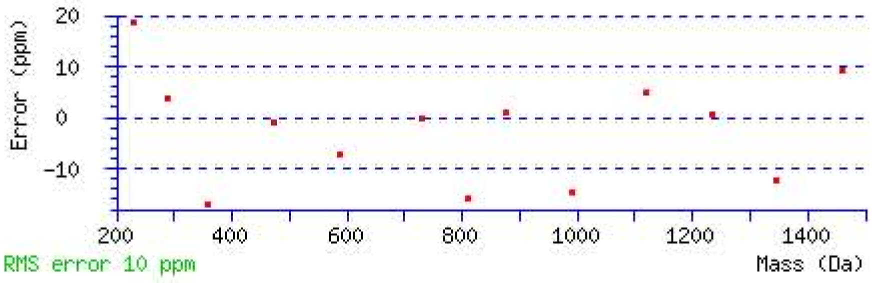
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 44 **Expect:** 0.00022
Matches : 13/110 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	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
43.6	1703.855240	0.000148	ASSIIDELFQDR
4.7	1703.870728	-0.015340	MQLVCCRAIVK
4.2	1703.859070	-0.003682	RWDELETTTQAKAR

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

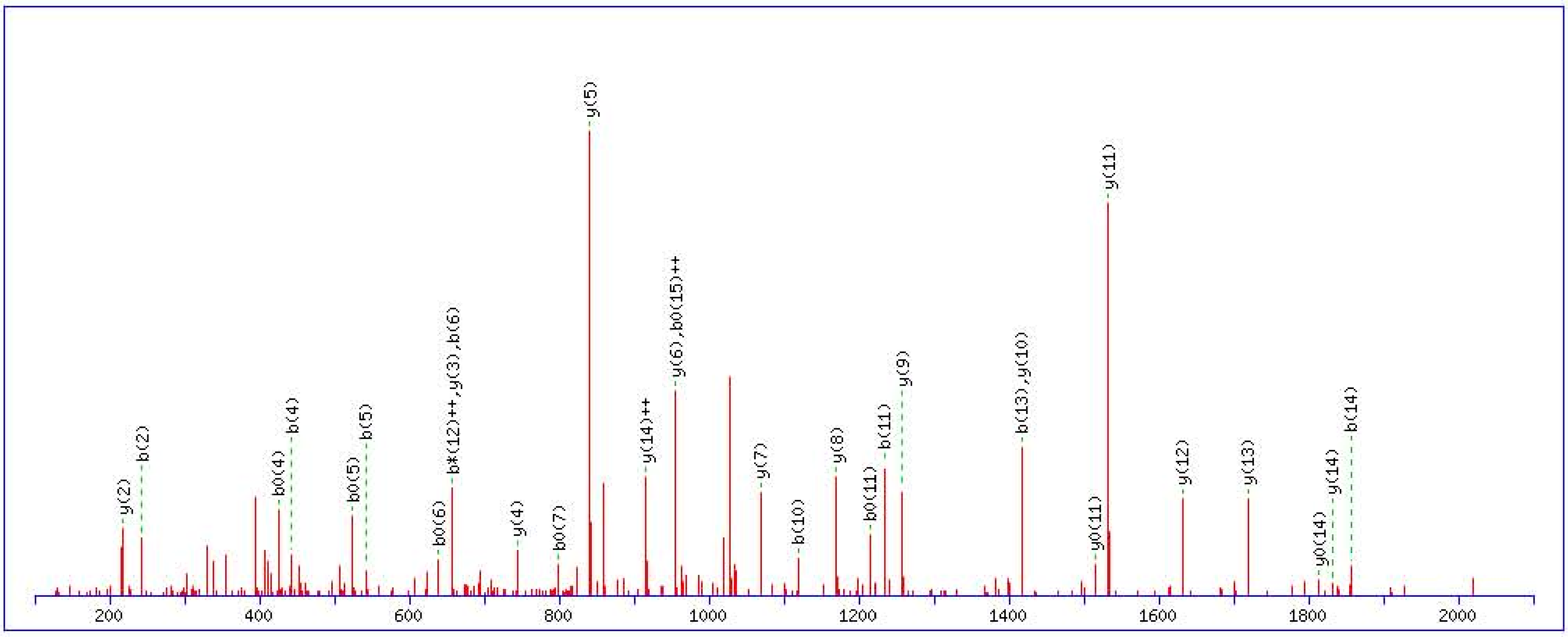
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

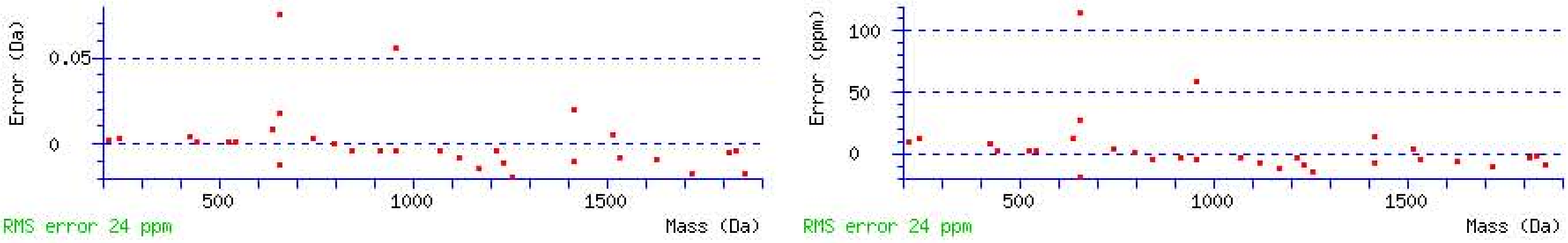
Match to Query 41212: 2072.976148 from(1037.495350,2+) rtinseconds(1817) index(17832)
Title: Locus:1.1.1.3198.21 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 2072.987061
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 107  Expect: 3.1e-010
Matches : 31/156 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	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
107.3	2072.987061	-0.010913	EILSVDCSTNNPSQAK

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

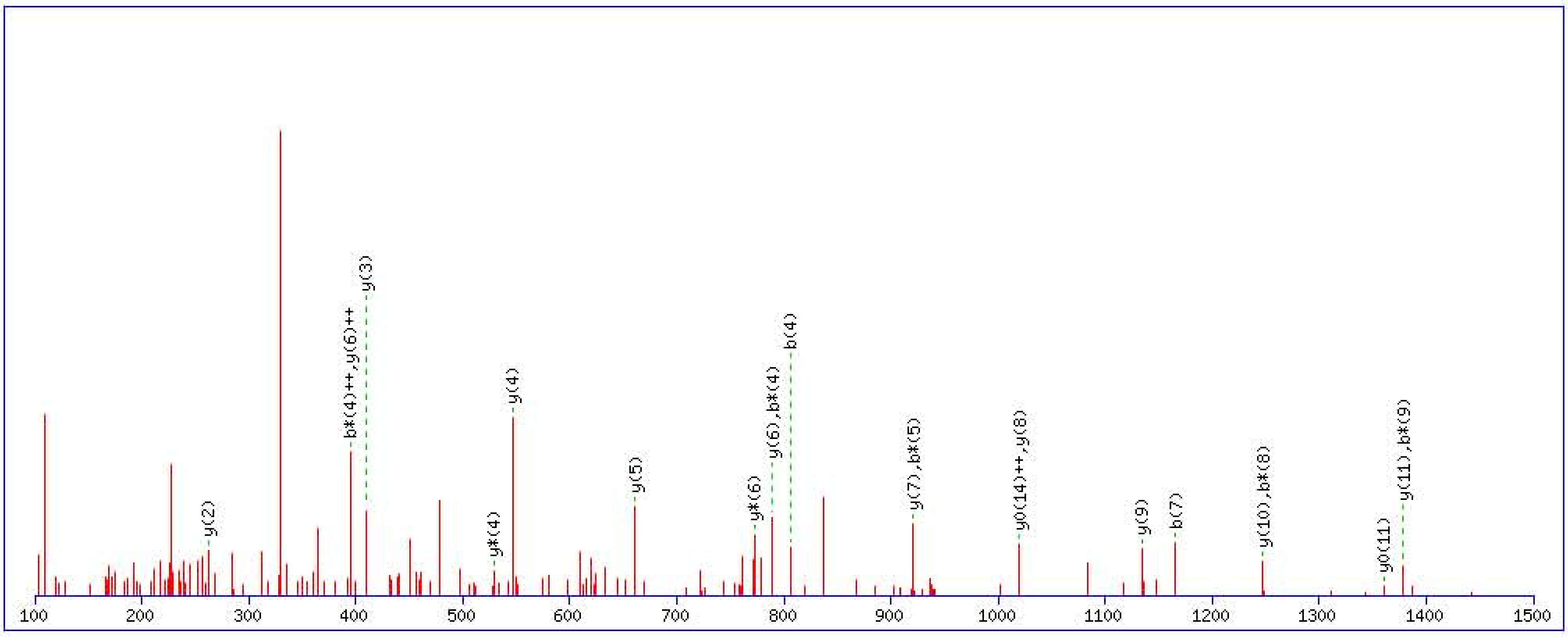
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

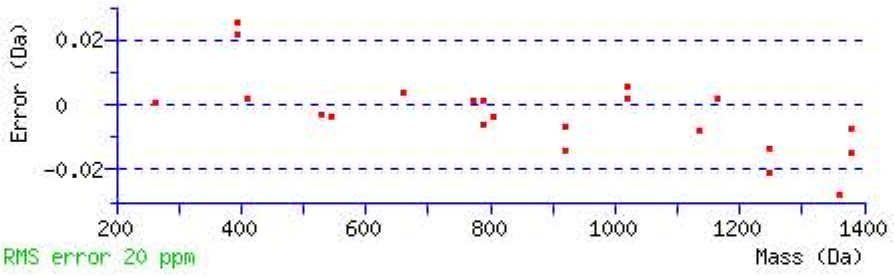
Match to Query 42940: 2183.002056 from(546.757790,4+) rtinseconds(2035) index(32089)
Title: Locus:1.1.1.3372.4 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

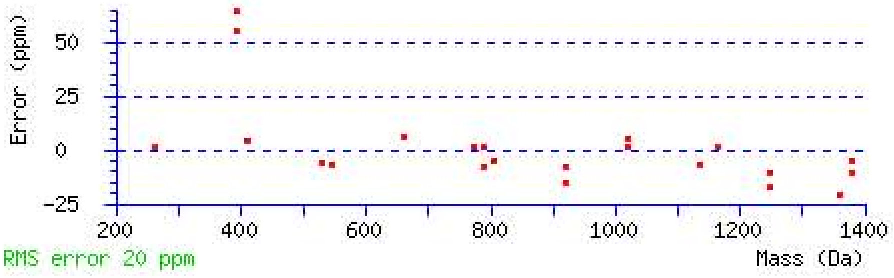
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2183.007446
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 65 **Expect:** 3.8e-006
Matches : 22/162 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	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
64.8	2183.007446	-0.005390	QQTHMLDVMQDHFSR
64.8	2183.007446	-0.005390	QQTHMLDVMQDHFSR

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

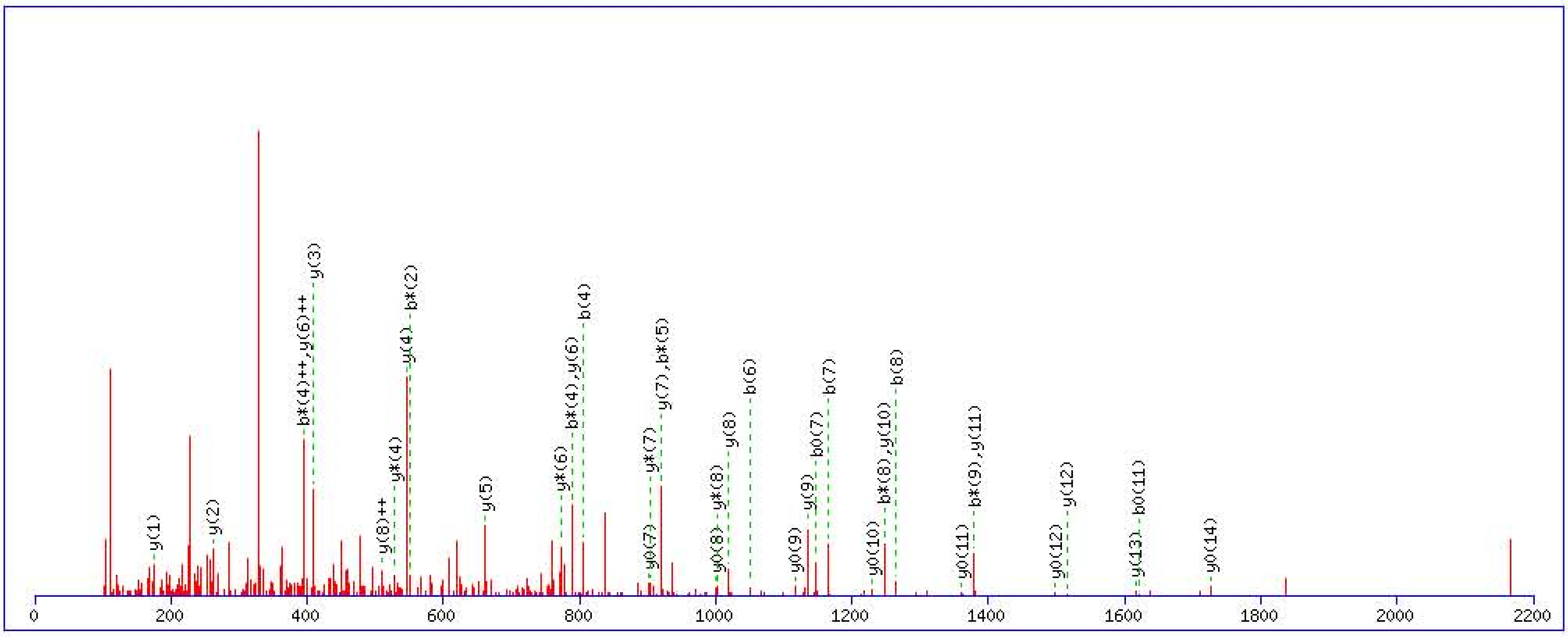
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

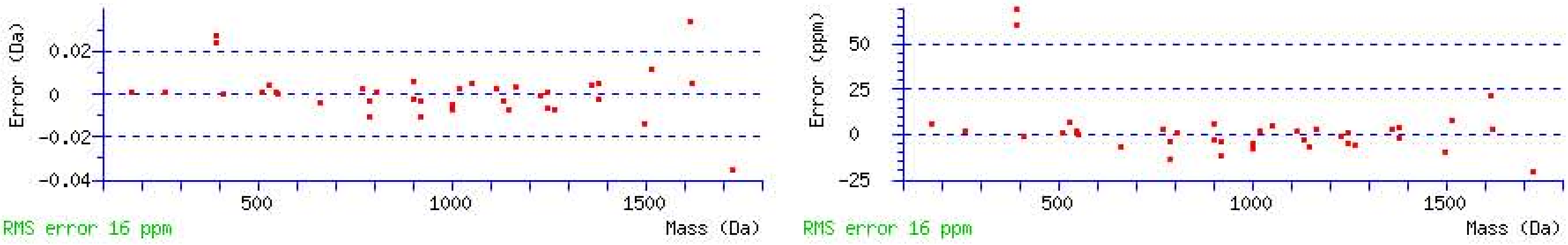
Match to Query 42943: 2183.004856 from(546.758490,4+) rtinseconds(2017) index(19164)
Title: Locus:1.1.1.3268.4 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 76  Expect: 2.8e-007
Matches : 38/162 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	440.232602	220.619939	423.206053	212.106664			Q							15
2	568.291180	284.649228	551.264631	276.135954			Q	1744.789387	872.898332	1727.762838	864.385057	1726.778822	863.893049	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
76.4	2183.007446	-0.002590	QQTHMLDVMQDHFSR
74.9	2183.007446	-0.002590	QQTHMLDVMQDHFSR

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

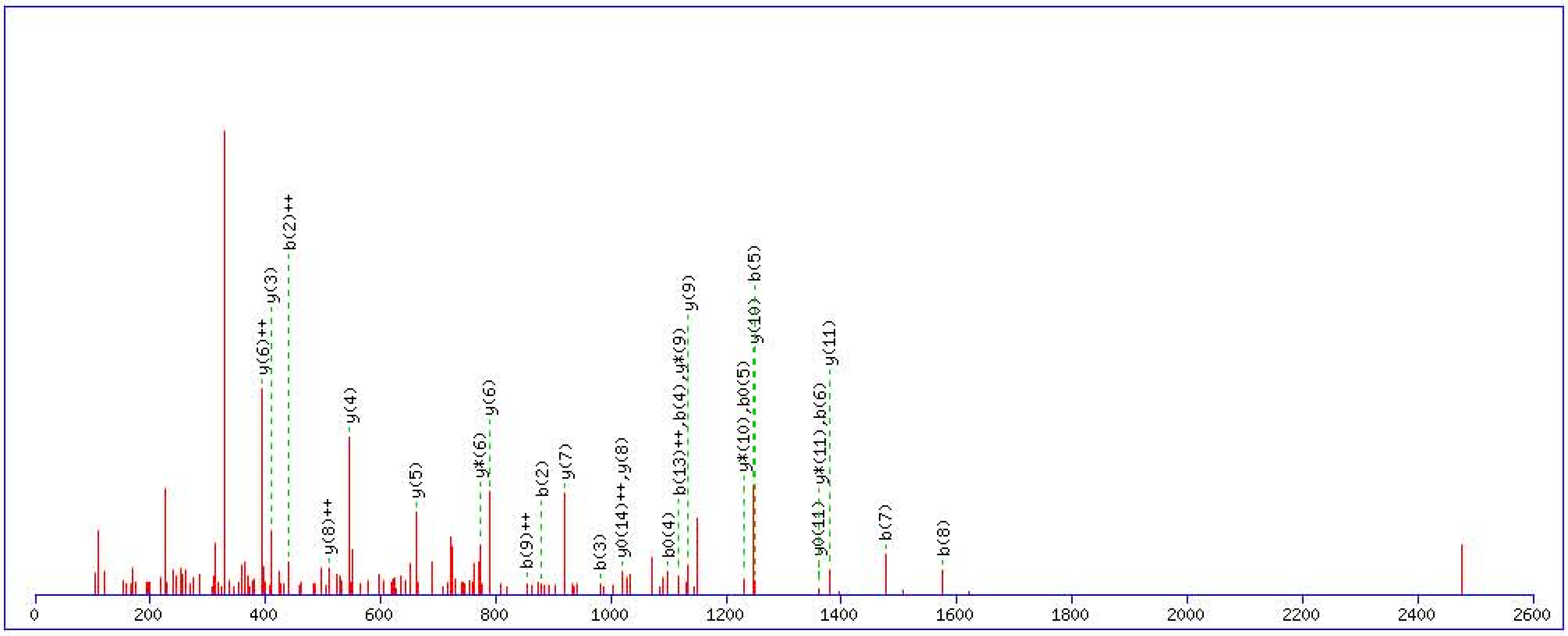
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

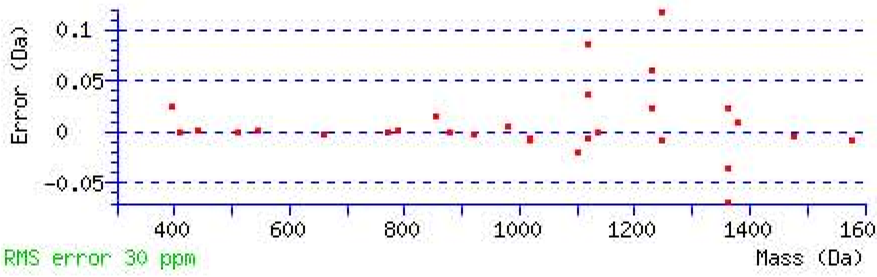
Match to Query 48384: 2494.190616 from(624.554930,4+) rtinseconds(2204) index(33052)
Title: Locus:1.1.1.3431.4 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

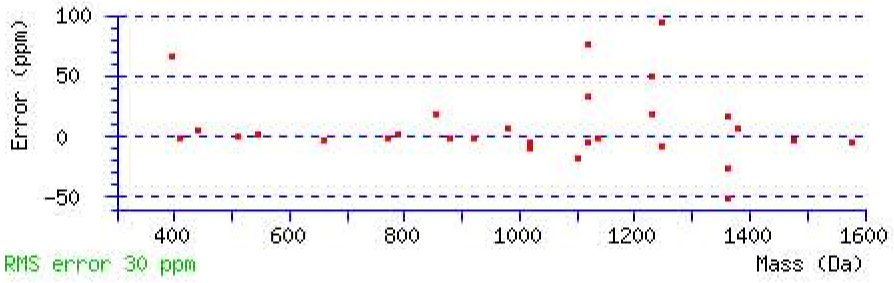
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2494.174194
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 0.00016
Matches : 30/162 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	***440.232602***	220.619939	423.206053	212.106664			Q							15
2	***879.457928***	**440.232602**	862.431379	431.719328			Q	2055.956135	1028.481705	2038.929586	1019.968431	2037.945570	1019.476423	14
3	***980.505607***	490.756442	963.479058	482.243167	962.495042	481.751159	T	1616.730809	808.869043	1599.704260	800.355768	1598.720244	799.863760	13
4	***1117.564519***	559.285898	1100.537970	550.772623	1099.553954	550.280615	H	1515.683130	758.345203	1498.656581	749.831929	1497.672565	749.339921	12
5	***1248.605004***	624.806140	1231.578455	616.292866	1230.594439	615.800858	M	***1378.624218***	689.815747	1361.597669	681.302473	1360.613653	680.810465	11
6	***1361.689068***	681.348172	1344.662519	672.834898	1343.678503	672.342889	L	***1247.583733***	624.295505	1230.557184	615.782230	1229.573168	615.290222	10
7	***1476.716011***	738.861644	1459.689462	730.348369	1458.705446	729.856361	D	***1134.499669***	567.753473	1117.473120	559.240198	1116.489104	558.748190	9
8	***1575.784425***	788.395851	1558.757876	779.882576	1557.773860	779.390568	V	***1019.472726***	510.240001	1002.446177	501.726727	1001.462161	501.234719	8
9	1706.824910	**853.916093**	1689.798361	845.402819	1688.814345	844.910811	M	***920.404312***	460.705794	903.377763	452.192520	902.393747	451.700512	7
10	1834.883488	917.945382	1817.856939	909.432108	1816.872923	908.940100	Q	***789.363827***	395.185552	772.337278	386.672277	771.353262	386.180269	6
11	1949.910431	975.458854	1932.883882	966.945579	1931.899866	966.453571	D	***661.305249***	331.156263	644.278700	322.642988	643.294684	322.150980	5
12	2086.969343	1043.988310	2069.942794	1035.475035	2068.958778	1034.983027	H	***546.278306***	273.642791	529.251757	265.129517	528.267741	264.637509	4
13	2234.037757	**1117.522516**	2217.011208	1109.009242	2216.027192	1108.517234	F	***409.219394***	205.113335	392.192845	196.600060	391.208829	196.108052	3
14	2321.069785	1161.038531	2304.043236	1152.525256	2303.059220	1152.033248	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
51.3	2494.174194	0.016422	QQTHMLDVMQDHFSR
5.6	2494.174194	0.016422	QQTHMLDVMQDHFSR

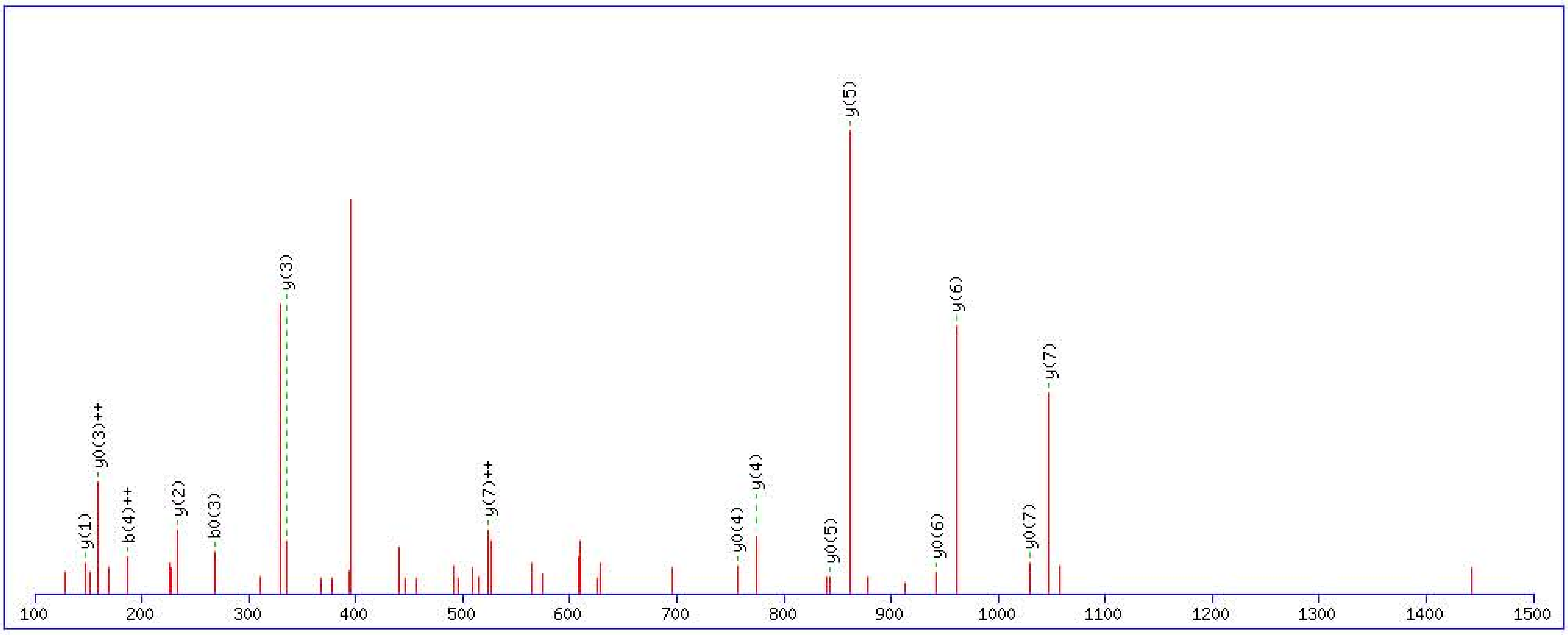
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

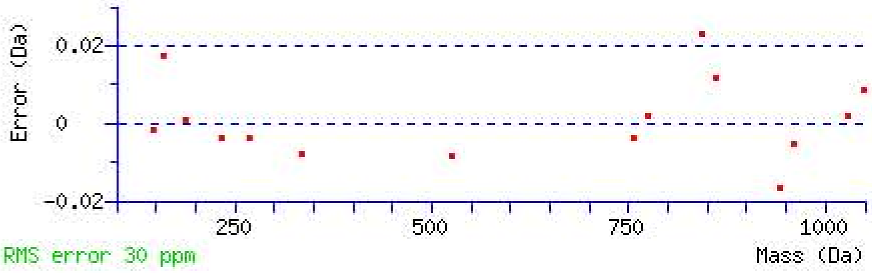
Match to Query 16126: 1145.608668 from(573.811610,2+) rtinseconds(1440) index(42497)
Title: Locus:1.1.1.3214.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

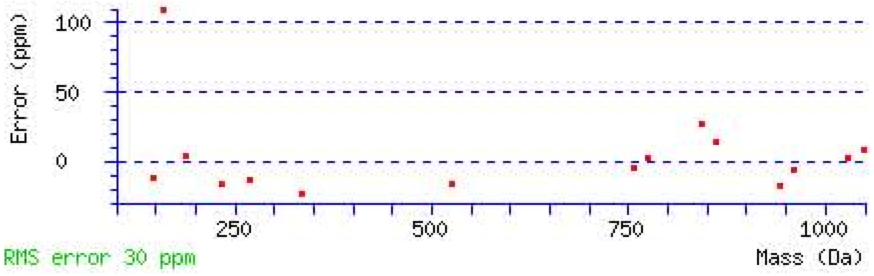
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1145.611450
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 43 **Expect:** 0.00055
Matches : 16/72 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	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
43.0	1145.611450	-0.002782	VSVSQTSK
7.8	1145.592819	0.015849	VSDGVTKSPEK
4.3	1145.622650	-0.013982	VDNAMSRLLK
0.5	1145.623337	-0.014669	WVDGGKPLFK

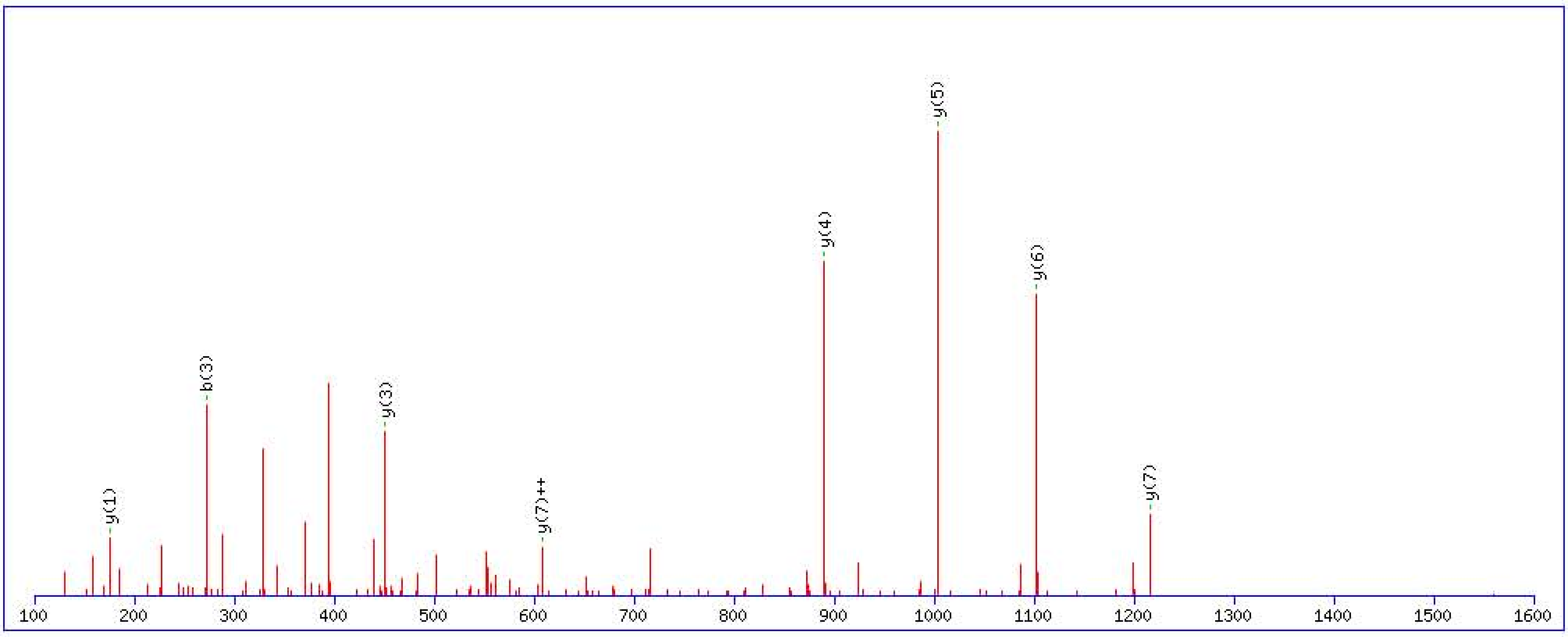
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

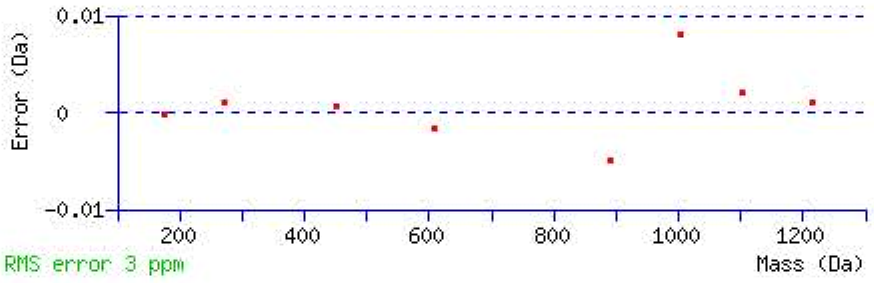
Match to Query 22753: 1372.796088 from(687.405320,2+) rtinseconds(2435) index(48511)
Title: Locus:1.1.1.3560.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

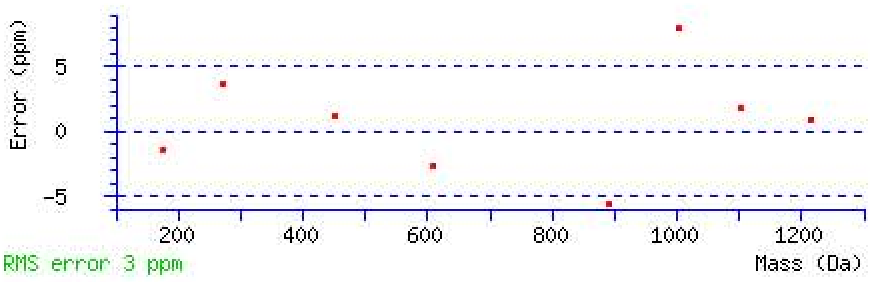
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1372.790054
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 7.8e-005
Matches : 8/70 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	88.039304	44.523290			70.028739	35.518008	S					9
2	159.076418	80.041847			141.065853	71.036564	A	1286.765327	643.886301	1269.738778	635.373027	8
3	**272.160482**	136.583879			254.149917	127.578597	L	*1215.728213*	608.367744	1198.701664	599.854470	7
4	371.228896	186.118086			353.218331	177.112804	V	*1102.644149*	551.825713	1085.617600	543.312438	6
5	484.312960	242.660118			466.302395	233.654836	L	*1003.575735*	502.291505	986.549186	493.778231	5
6	923.538286	462.272781	906.511737	453.759507	905.527721	453.267499	Q	*890.491671*	445.749473	873.465122	437.236199	4
7	1086.601615	543.804446	1069.575066	535.291171	1068.591050	534.799163	Y	*451.266345*	226.136810	434.239796	217.623536	3
8	1199.685679	600.346477	1182.659130	591.833203	1181.675114	591.341195	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 SALVLQYLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.5	1372.790054	0.006034	SALVLQYLR
2.6	1372.790039	0.006049	KELQILYR
1.6	1372.782669	0.013419	LSNKFNSVIPVR
1.6	1372.779999	0.016089	RTGHRIVAPPGGR
1.4	1372.790039	0.006049	IIEKYQLR
0.4	1372.778641	0.017447	EKISGTVNIRTR
0.3	1372.779984	0.016104	NIPRRHTLGGPR

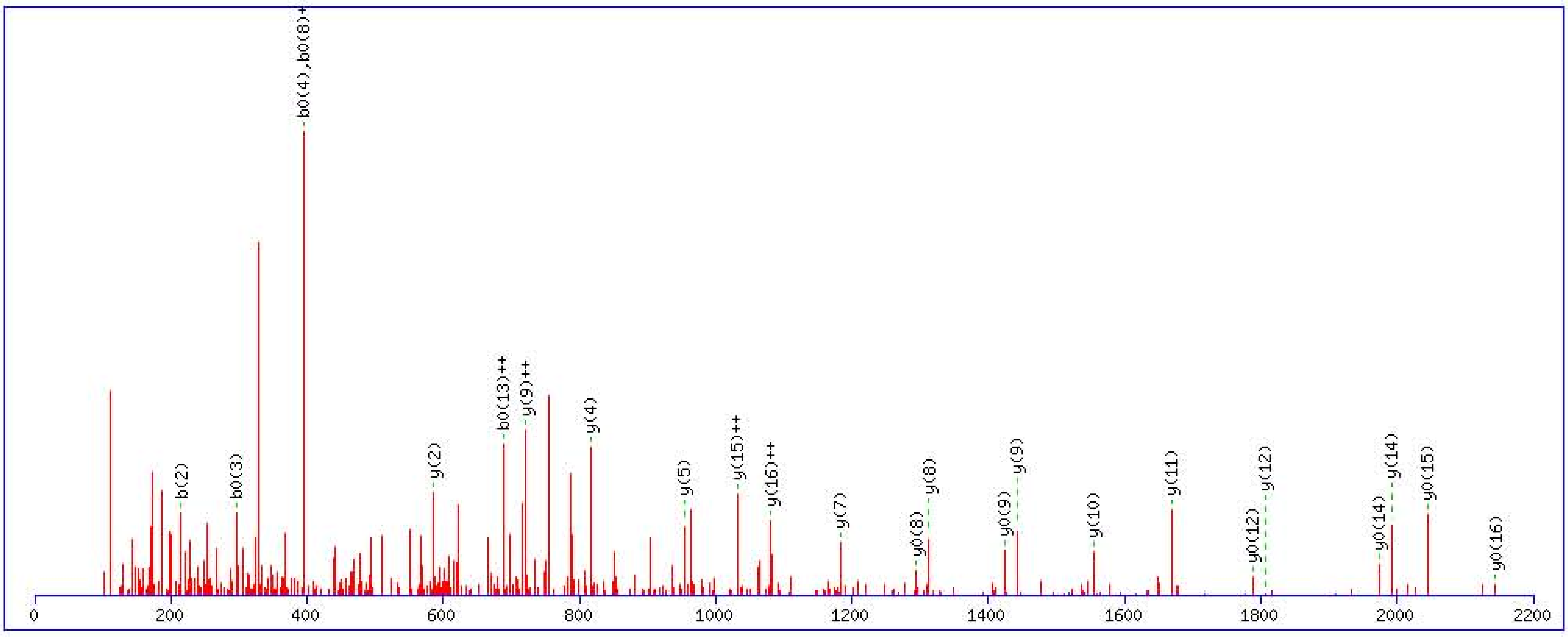
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

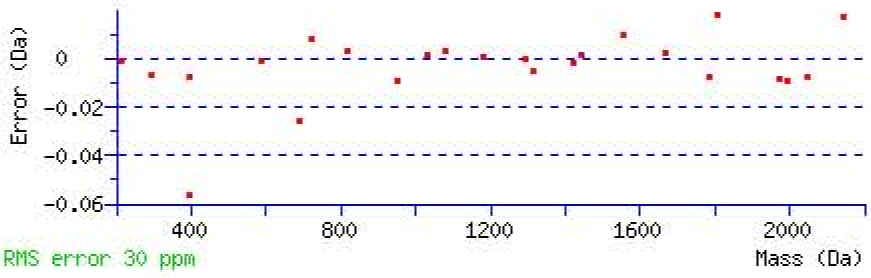
Match to Query 47811: 2474.206896 from(619.559000,4+) rtinseconds(1649) index(43863)
Title: Locus:1.1.1.3287.6 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

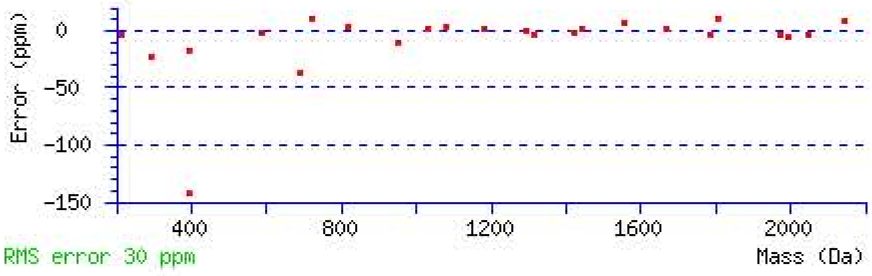
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2474.211121
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18     : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.0011
Matches : 24/194 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					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
43.3	2474.211121	-0.004225	ITVVAGEHNIEETEHTEQK

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

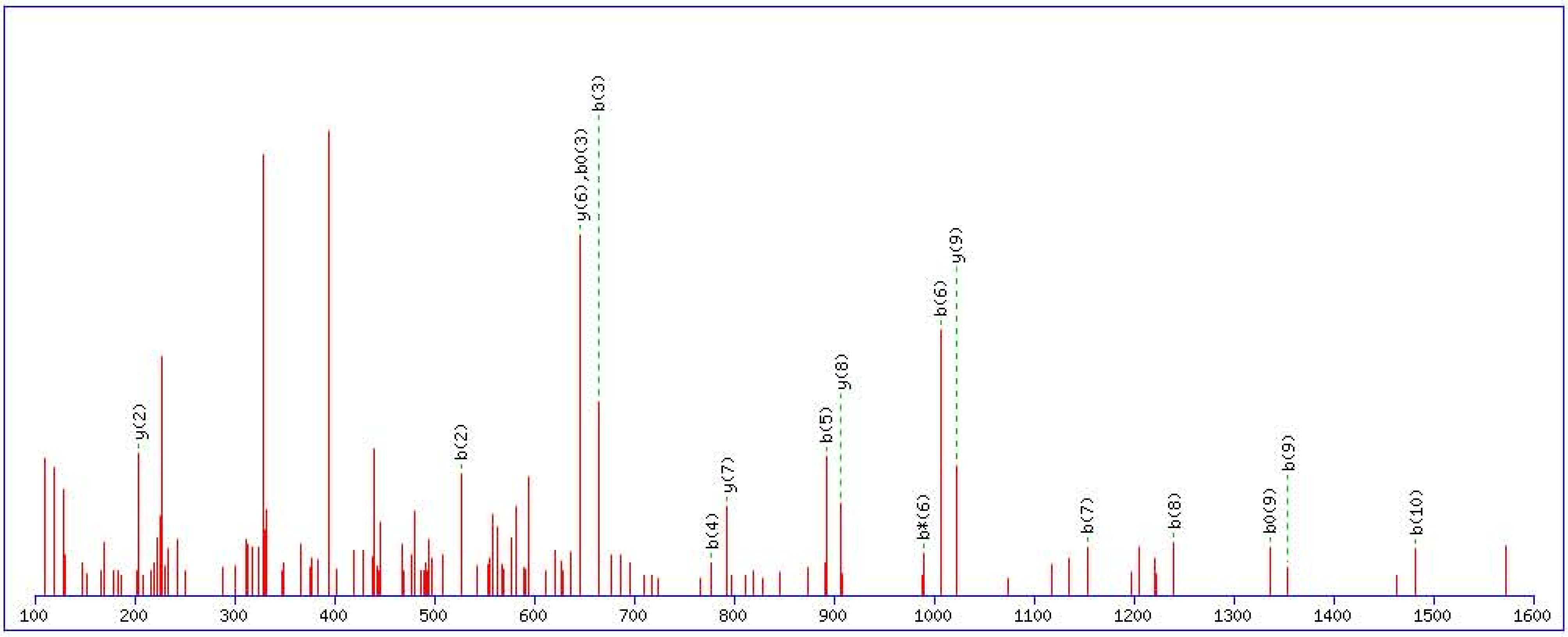
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

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

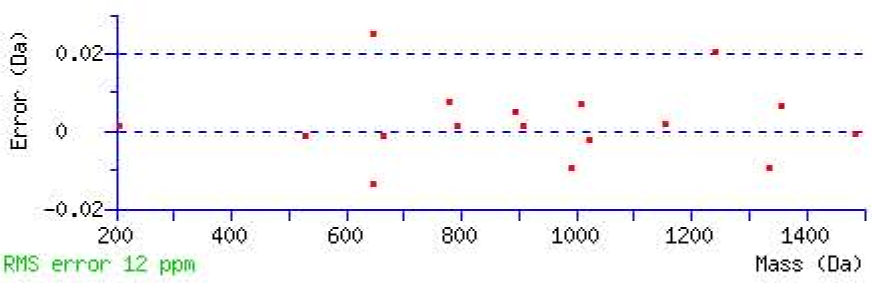
Match to Query 35667: 1797.879012 from(600.300280,3+) rtinseconds(1804) index(44780)
Title: Locus:1.1.1.3341.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

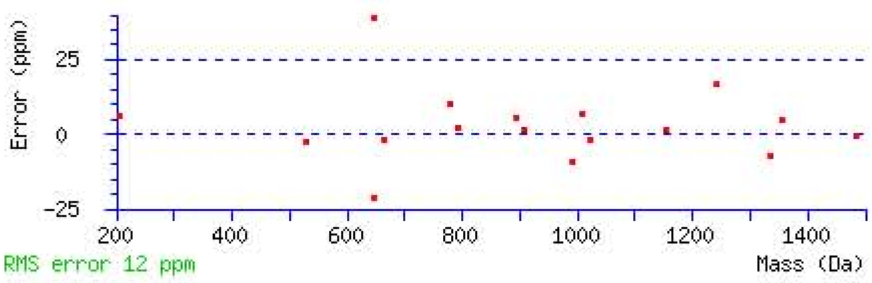
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1797.883194
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2     : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 3.5e-005
Matches : 17/132 fragment ions using 29 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
52.6	1797.883194	-0.004182	SQHLDNFSNQIGK
5.0	1797.872604	0.006408	KWDFSKYYVSNFSK

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

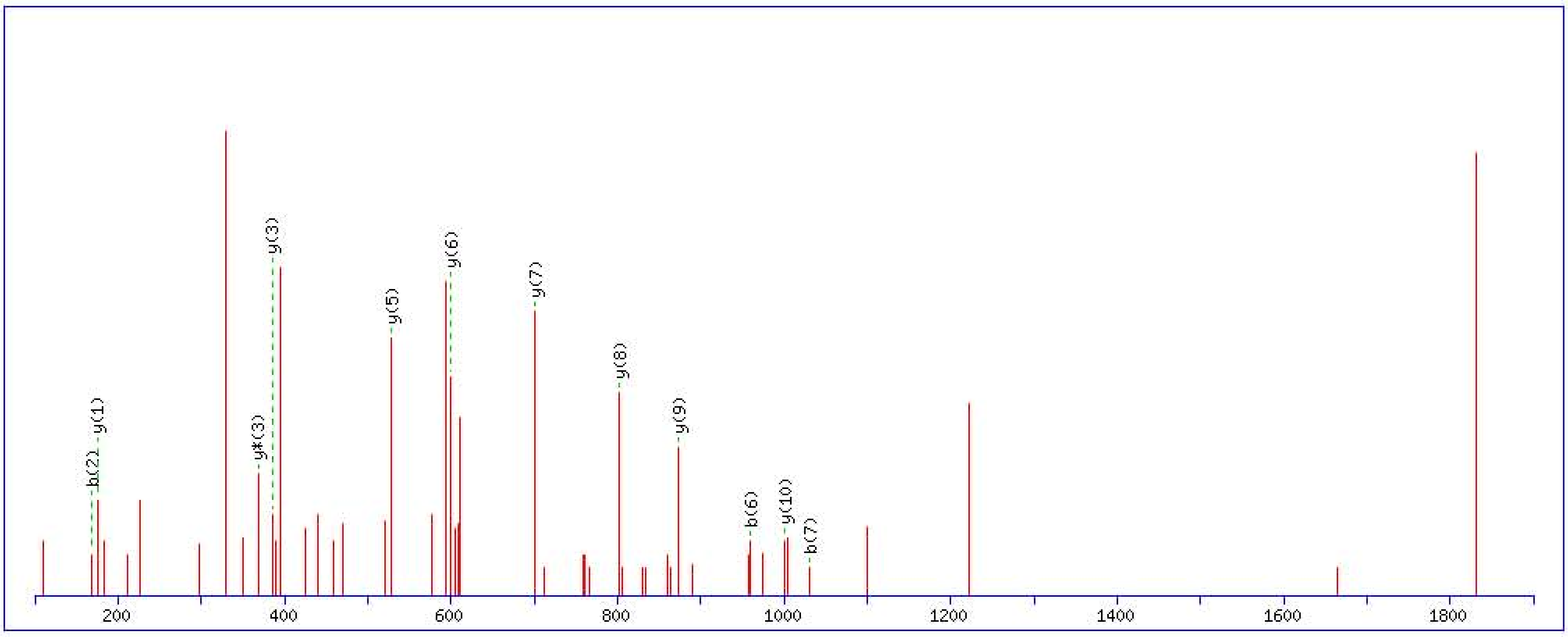
Mascot Search Results

Peptide View

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

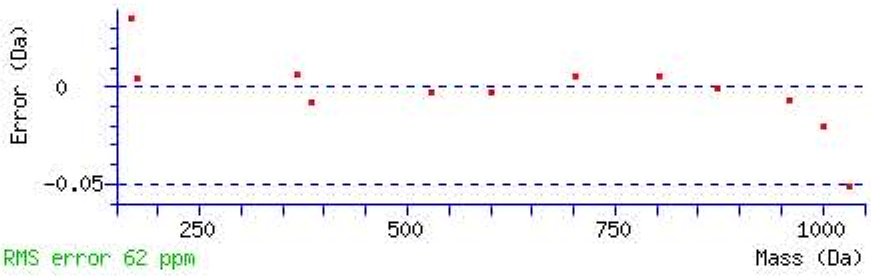
Match to Query 36345: 1831.933902 from(611.651910,3+) rtinseconds(1449) index(42567)
Title: Locus:1.1.1.3217.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

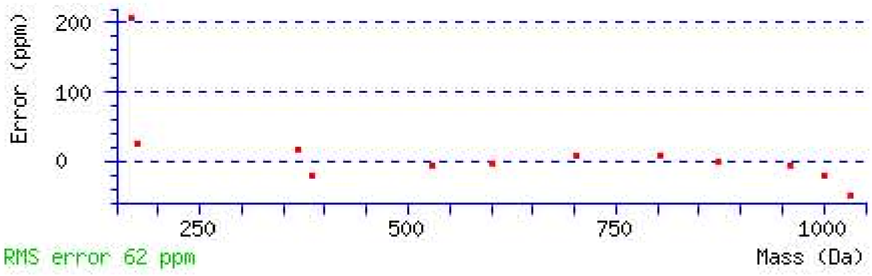
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 27  Expect: 0.0098
Matches : 12/150 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							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
27.0	1831.936295	-0.002393	APSHQQATTAGSPLR
19.2	1831.936295	-0.002393	APSHQQATTAGSPLR
5.5	1831.916336	0.017566	VQTTADSVSDEAELLVR
3.7	1831.954041	-0.020139	HSDLPPSKKGEQPGLSR

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

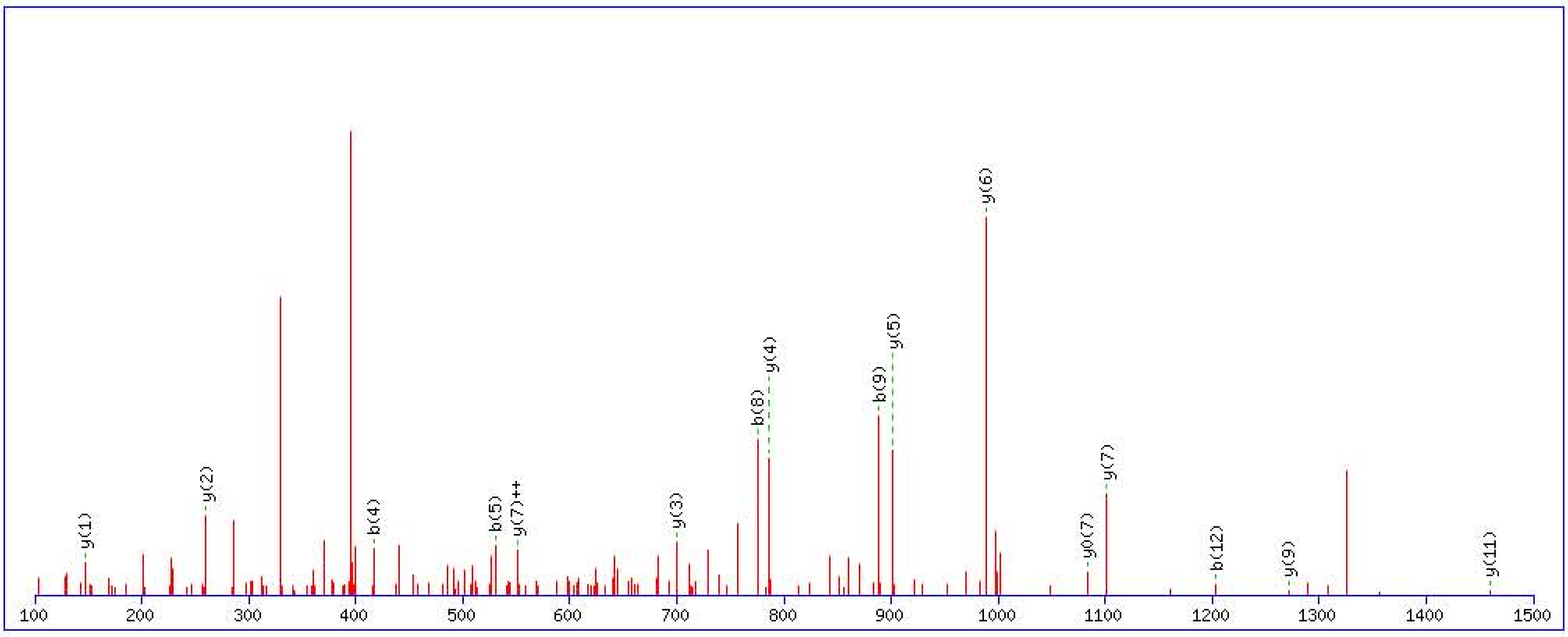
Mascot Search Results

Peptide View

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

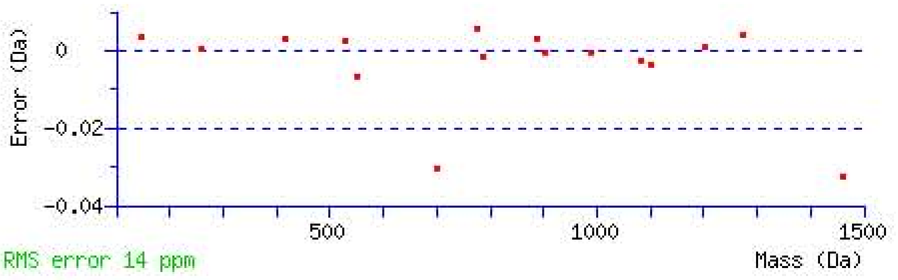
Match to Query 39074: 1988.018712 from(663.680180,3+) rtinseconds(2475) index(48662)
Title: Locus:1.1.1.3574.6 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

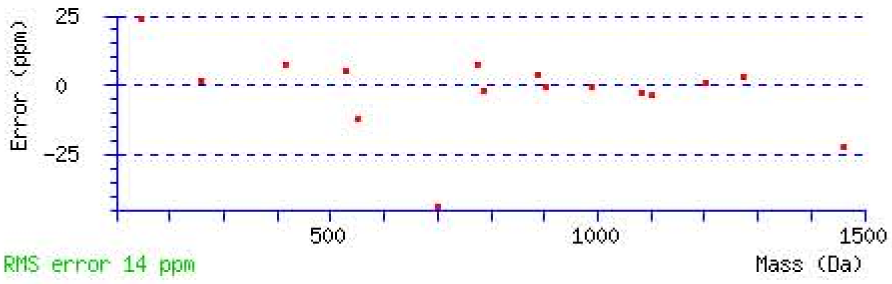
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1988.014465
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 1.8e-005
Matches : 16/138 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	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
53.3	1988.014465	0.004247	MPMGLSTGIISDSQIK
2.8	1988.000519	0.018193	QQMLENQMEVRKK
2.1	1988.011063	0.007649	EPLAAVYQEMLAQAK
0.2	1988.000519	0.018193	QQMLENQMEVRKK

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

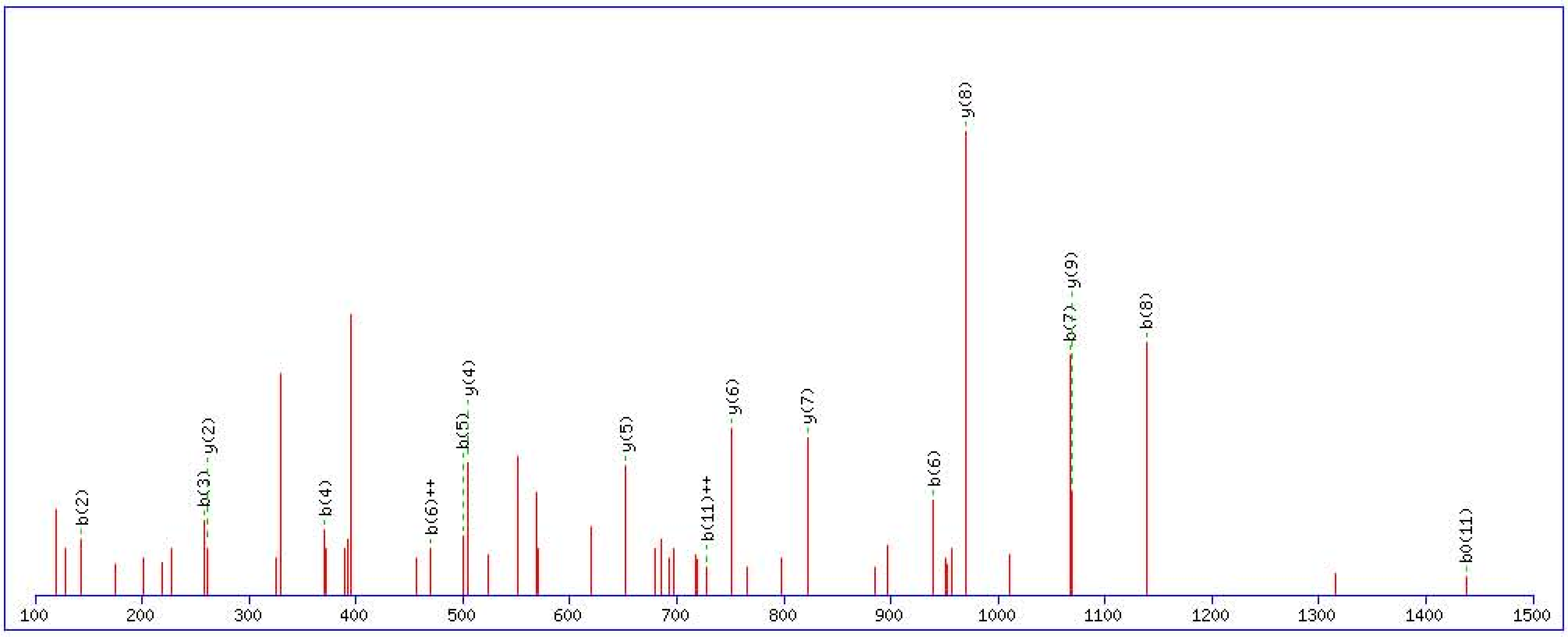
MATRIX SCIENCE Mascot Search Results

Peptide View

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

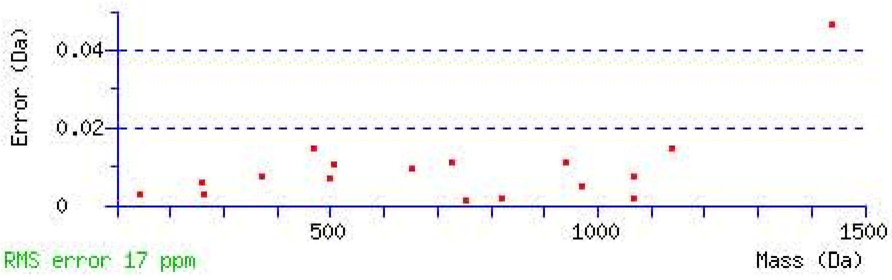
Match to Query 43279: 2205.087162 from(736.036330,3+) rtinseconds(2760) index(50452)
Title: Locus:1.1.1.3672.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

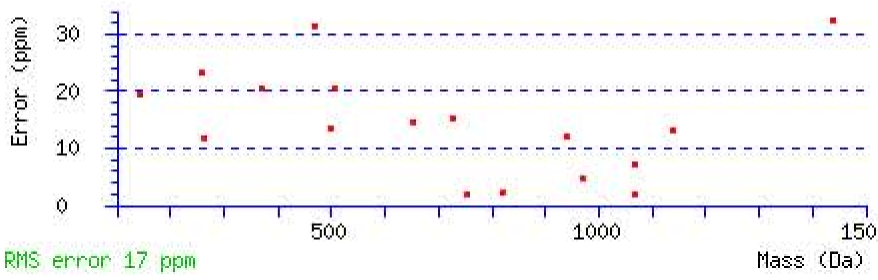
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 54  Expect: 2e-005
Matches : 17/174 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	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
54.2	2205.077591	0.009571	AADIEQQAVFAVFDENK
42.1	2205.077591	0.009571	AADIEQQAVFAVFDENK
3.8	2205.063492	0.023670	GERGEPGIRGEDGRPGQEGPR
0.2	2205.080063	0.007099	EKENDELDIQLKVFDENK

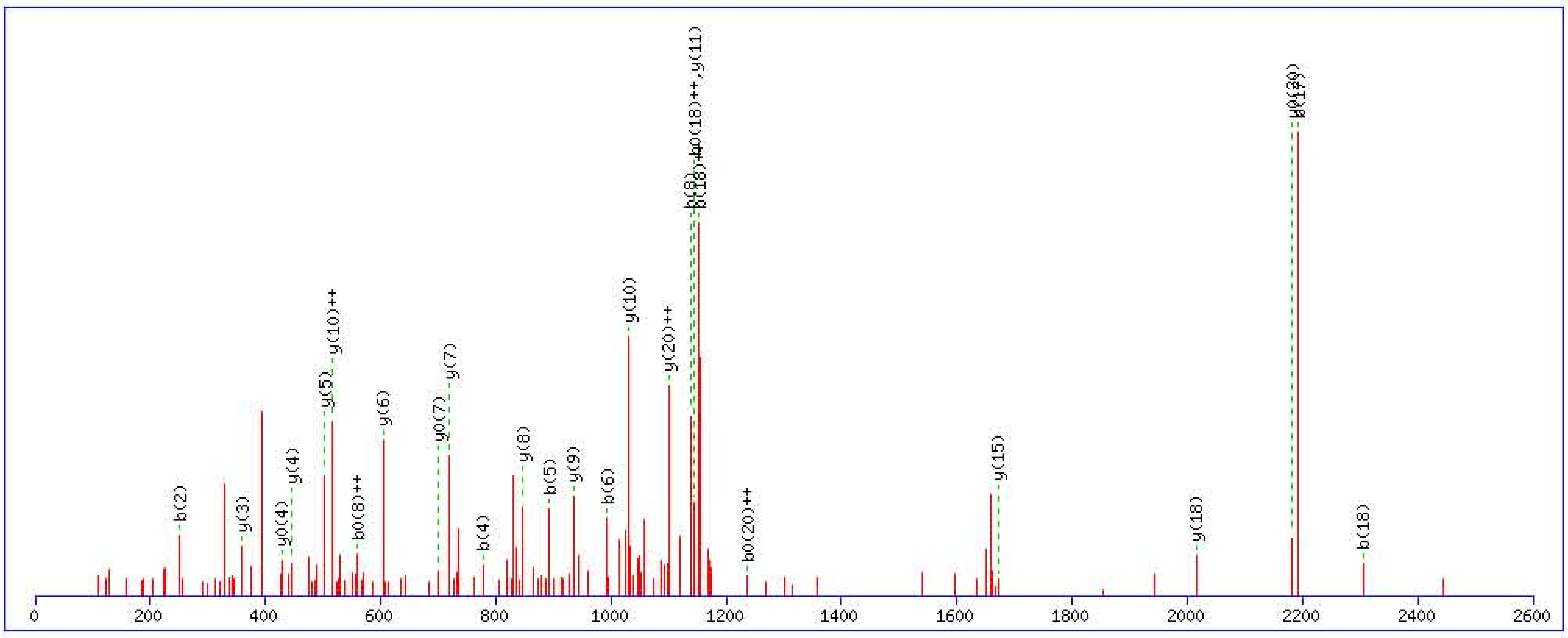
Mascot Search Results

Peptide View

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

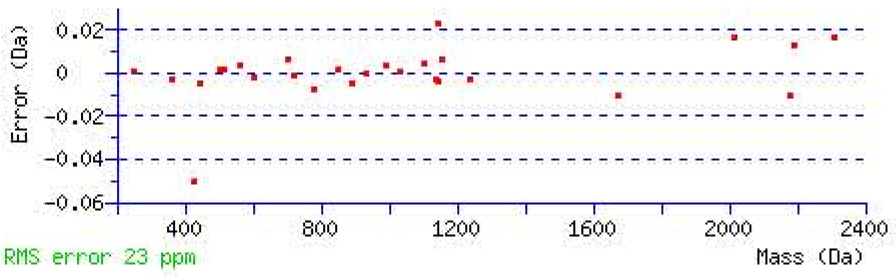
Match to Query 58324: 3335.547696 from(834.894200,4+) rtinseconds(1984) index(45935)
Title: Locus:1.1.1.3403.21 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

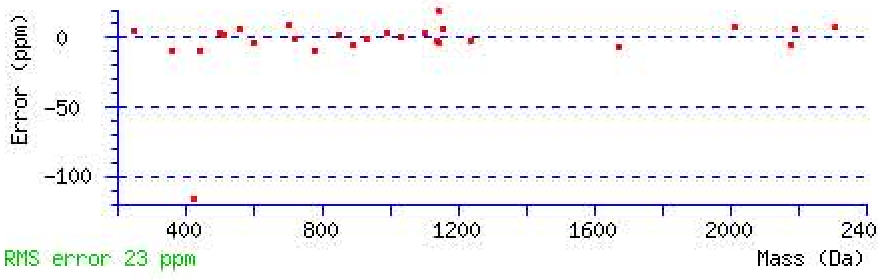
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3335.529938
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 0.00032
Matches : 27/312 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	138.066188	69.536732					H							28
2	***251.150252***	126.078764					L	3199.478289	1600.242782	3182.451740	1591.729508	3181.467724	1591.237500	27
3	338.182280	169.594778			320.171715	160.589495	S	3086.394225	1543.700750	3069.367676	1535.187476	3068.383660	1534.695468	26
4	***777.407606***	389.207441	760.381057	380.694166	759.397041	380.202159	Q	2999.362197	1500.184736	2982.335648	1491.671462	2981.351632	1491.179454	25
5	***892.434549***	446.720913	875.408000	438.207638	874.423984	437.715630	D	2560.136871	1280.572073	2543.110322	1272.058799	2542.126306	1271.566791	24
6	***993.482228***	497.244752	976.455679	488.731477	975.471663	488.239469	T	2445.109928	1223.058602	2428.083379	1214.545327	2427.099363	1214.053319	23
7	1050.503692	525.755484	1033.477143	517.242210	1032.493127	516.750202	G	2344.062249	1172.534762	2327.035700	1164.021488	2326.051684	1163.529480	22
8	***1137.535720***	569.271498	1120.509171	560.758224	1119.525155	560.266216	S	2287.040785	1144.024030	2270.014236	1135.510756	2269.030220	1135.018748	21
9	1234.588484	617.797880	1217.561935	609.284606	1216.577919	608.792598	P	2200.008757	1100.508016	2182.982208	1091.994742	2181.998192	1091.502734	20
10	1321.620512	661.313894	1304.593963	652.800620	1303.609947	652.308612	S	2102.955993	1051.981634	2085.929444	1043.468360	2084.945428	1042.976352	19
11	1378.641976	689.824626	1361.615427	681.311352	1360.631411	680.819344	G	***2015.923965***	1008.465620	1998.897416	999.952346	1997.913400	999.460338	18
12	1509.682461	755.344869	1492.655912	746.831594	1491.671896	746.339586	M	1958.902501	979.954888	1941.875952	971.441614	1940.891936	970.949606	17
13	1665.783572	833.395424	1648.757023	824.882150	1647.773007	824.390142	R	1827.862016	914.434646	1810.835467	905.921371	1809.851451	905.429363	16
14	1762.836336	881.921806	1745.809787	873.408532	1744.825771	872.916524	P	***1671.760905***	836.384090	1654.734356	827.870816	1653.750340	827.378808	15
15	1948.915649	974.961463	1931.889100	966.448188	1930.905084	965.956180	W	1574.708141	787.857708	1557.681592	779.344434	1556.697576	778.852426	14
16	2077.958242	1039.482759	2060.931693	1030.969484	2059.947677	1030.477476	E	1388.628828	694.818052	1371.602279	686.304778	1370.618263	685.812769	13
17	***2192.985185***	1096.996230	2175.958636	1088.482956	2174.974620	1087.990948	D	1259.586235	630.296756	1242.559686	621.783481	1241.575670	621.291473	12
18	***2306.069249***	1153.538262	2289.042700	1145.024988	2288.058684	1144.532980	L	***1144.559292***	572.783284	1127.532743	564.270010	1126.548727	563.778002	11
19	2403.122013	1202.064644	2386.095464	1193.551370	2385.111448	1193.059362	P	***1031.475228***	516.241252	1014.448679	507.727978	1013.464663	507.235970	10
20	2490.154041	1245.580658	2473.127492	1237.067384	2472.143476	1236.575376	S	***934.422464***	467.714870	917.395915	459.201596	916.411899	458.709588	9
21	2618.212619	1309.609947	2601.186070	1301.096673	2600.202054	1300.604665	Q	***847.390436***	424.198856	830.363887	415.685581	829.379871	415.193573	8
22	2733.239562	1367.123419	2716.213013	1358.610144	2715.228997	1358.118136	D	***719.331858***	360.169567	702.305309	351.656292	701.321293	351.164284	7
23	2834.287241	1417.647258	2817.260692	1409.133984	2816.276676	1408.641976	T	***604.304915***	302.656095	587.278366	294.142821	586.294350	293.650813	6
24	2891.308705	1446.157990	2874.282156	1437.644716	2873.298140	1437.152708	G	***503.257236***	252.132256	486.230687	243.618982	485.246671	243.126974	5
25	2978.340733	1489.674004	2961.314184	1481.160730	2960.330168	1480.668722	S	***446.235772***	223.621524	429.209223	215.108250	428.225207	214.616242	4
26	3075.393497	1538.200386	3058.366948	1529.687112	3057.382932	1529.195104	P	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
27	3162.425525	1581.716400	3145.398976	1573.203126	3144.414960	1572.711118	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
28							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.8	3335.529938	0.017758	HLSQDTGSPSGMRPWEDLPSQDTGSPSR

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

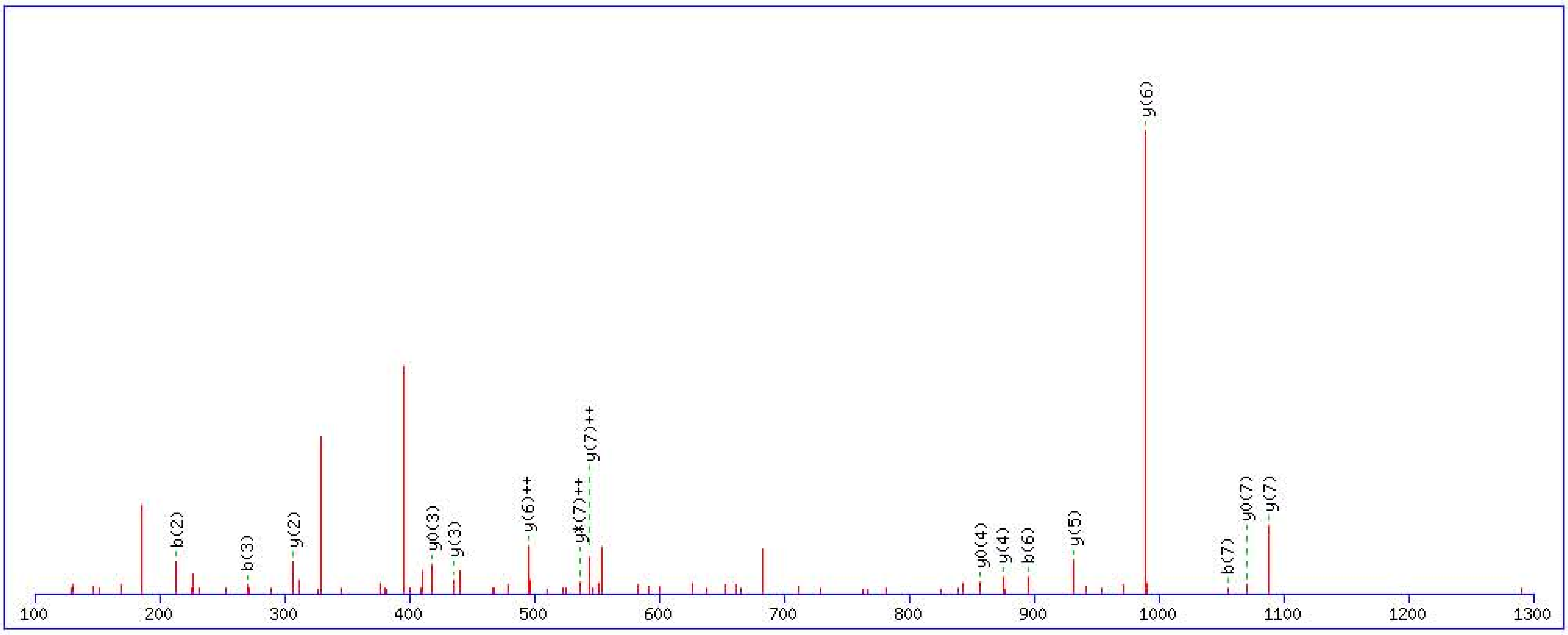
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

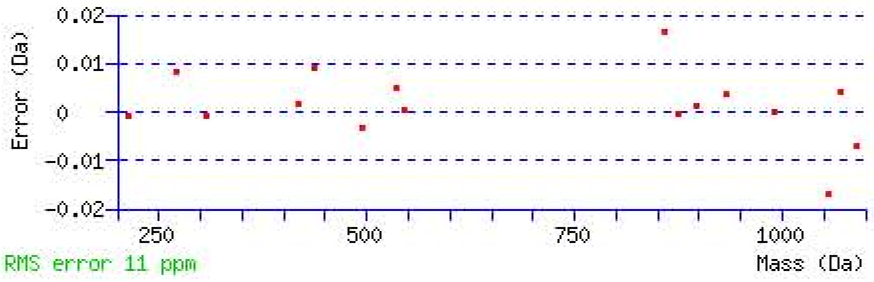
Match to Query 17754: 1200.596628 from(601.305590,2+) rtinseconds(1446) index(42544)
Title: Locus:1.1.1.3216.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

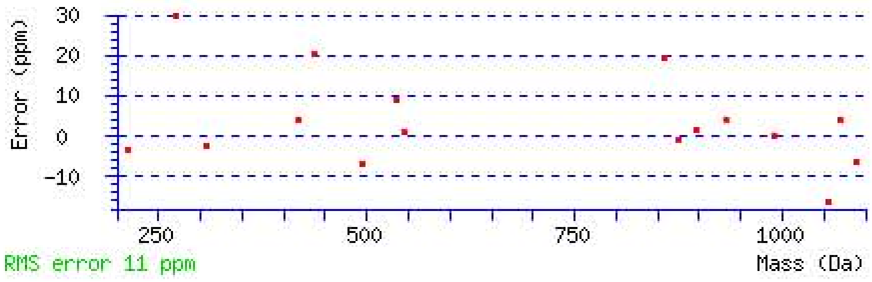
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1200.599503
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 33 **Expect:** 0.0022
Matches : 16/62 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	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
32.9	1200.599503	-0.002875	IVGGQECK
4.2	1200.599503	-0.002875	LIQGDGCK
1.1	1200.596100	0.000528	LVKYMYDNR
0.9	1200.607376	-0.010748	HTGVKPFQCK

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

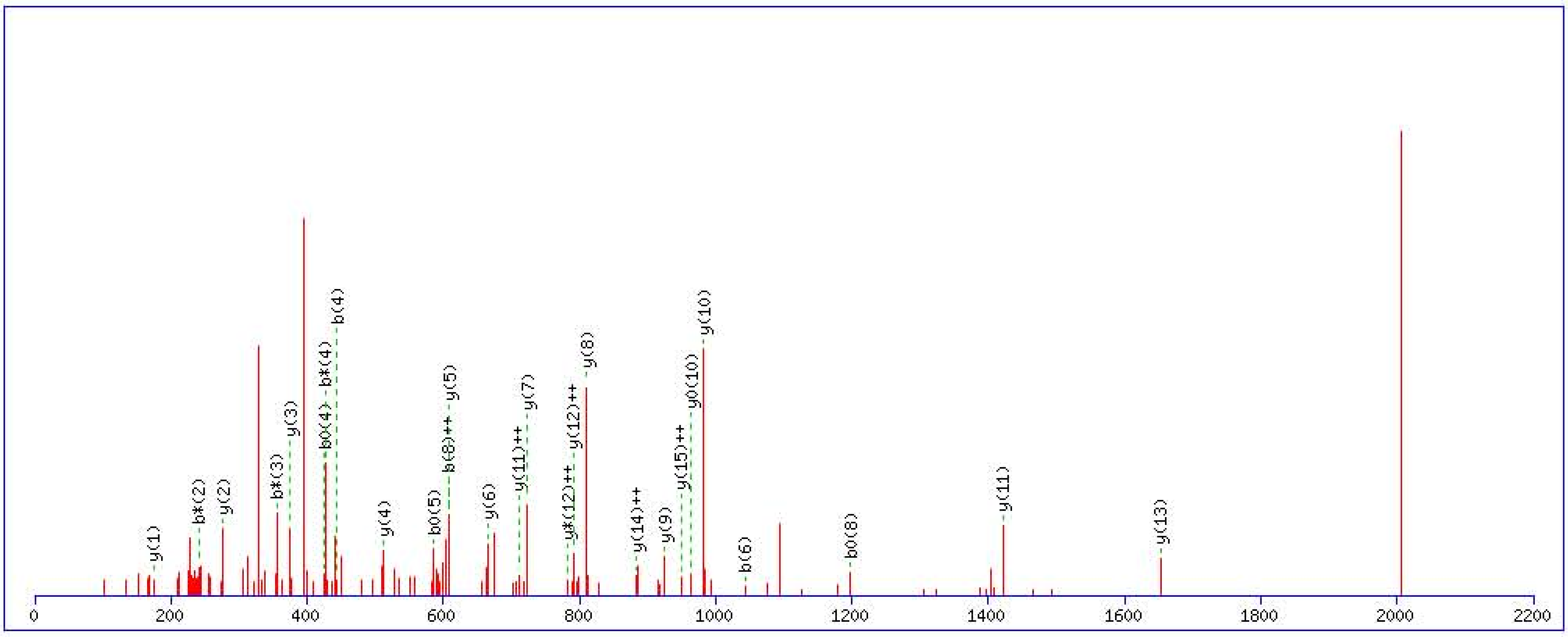
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

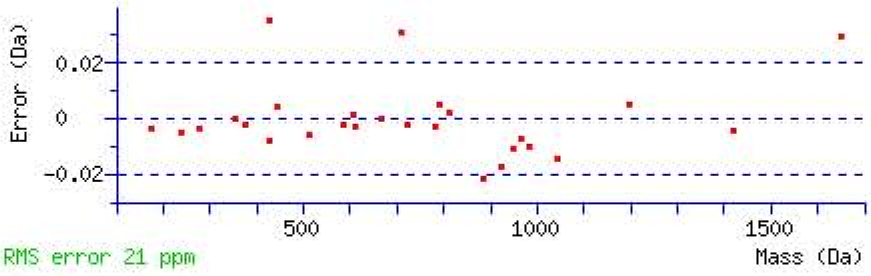
Match to Query 21304: 2023.877532 from(675.633120,3+) rtinseconds(1364) index(42140)
Title: Locus:1.1.1.3187.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

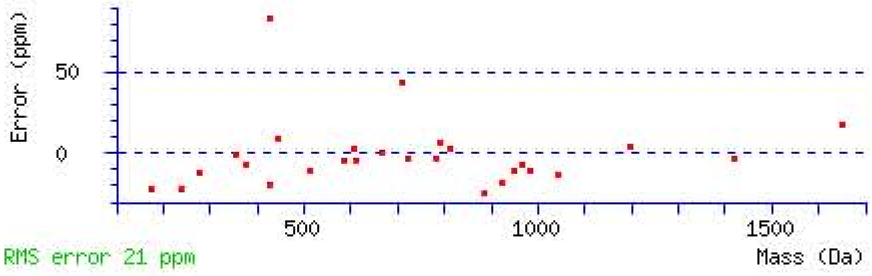


```
Monoisotopic mass of neutral peptide Mr(calc): 2023.884033
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 5.5e-005
Matches : 27/176 fragment ions using 70 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							16
2	258.108447	129.557862	241.081898	121.044587	240.097882	120.552579	E	1896.832709	948.919993	1879.806160	940.406718	1878.822144	939.914710	15
3	373.135390	187.071333	356.108841	178.558059	355.124825	178.066051	D	1767.790116	884.398696	1750.763567	875.885422	1749.779551	875.393414	14
4	**444.172504**	222.589890	427.145955	214.076616	426.161939	213.584608	A	***1652.763173***	826.885225	1635.736624	818.371950	1634.752608	817.879942	13
5	604.203153	302.605215	587.176604	294.091940	586.192588	293.599932	C	1581.726059	791.366668	1564.699510	782.853393	1563.715494	782.361385	12
6	**1043.428479**	522.217878	1026.401930	513.704603	1025.417914	513.212595	Q	***1421.695410***	711.351343	1404.668861	702.838069	1403.684845	702.346061	11
7	1100.449943	550.728610	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	599.236799	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	671.263545	G	***723.389649***	362.198463	706.363100	353.685188	705.379084	353.193180	7
11	1416.551842	708.779559	1399.525293	700.266285	1398.541277	699.774277	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	748.300659	P	***609.346721***	305.176999	592.320172	296.663724	591.336156	296.171716	5
13	1650.663518	825.835397	1633.636969	817.322123	1632.652953	816.830115	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	866.364322	V	***375.235045***	188.121161	358.208496	179.607886	357.224480	179.115878	3
15	1850.779611	925.893444	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



RMS error 21 ppm



RMS error 21 ppm

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
53.4	2023.884033	-0.006501	QEDACQGDSGGPHVTR
36.4	2023.884033	-0.006501	QEDACQGDSGGPHVTR

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

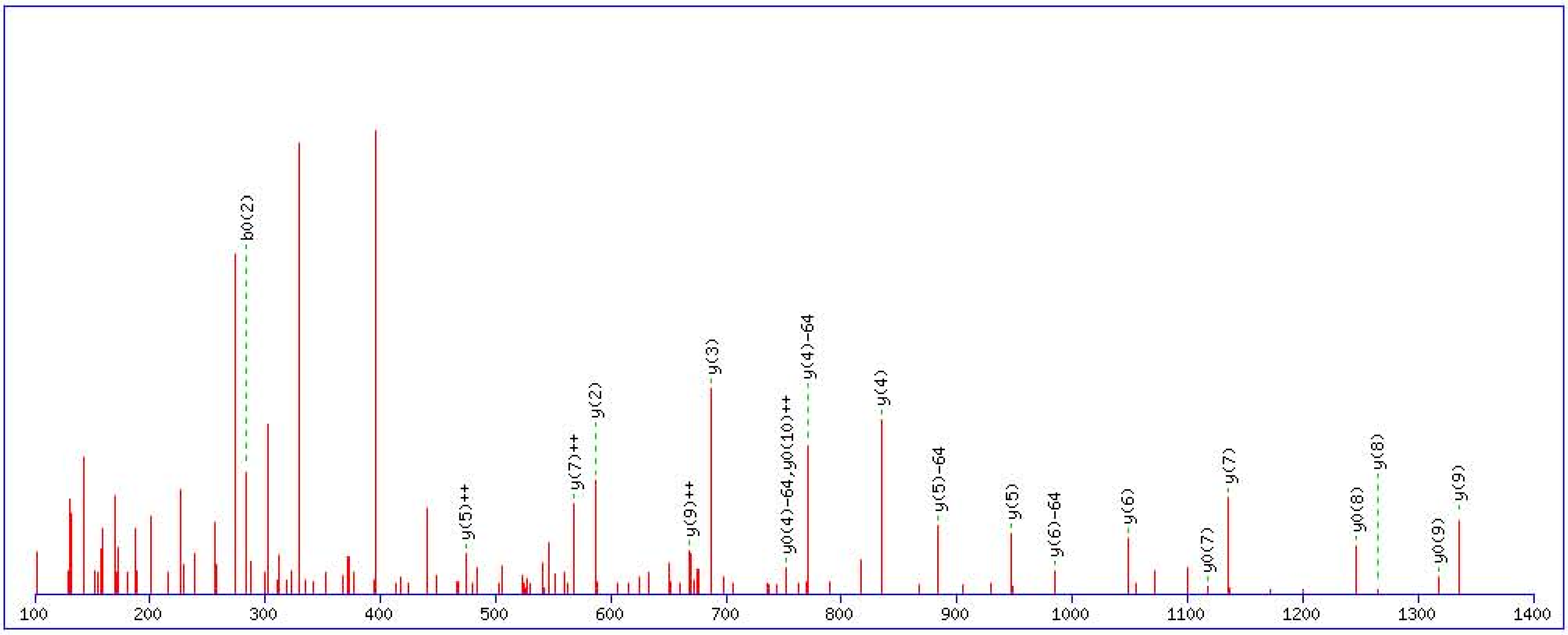
Mascot Search Results

Peptide View

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

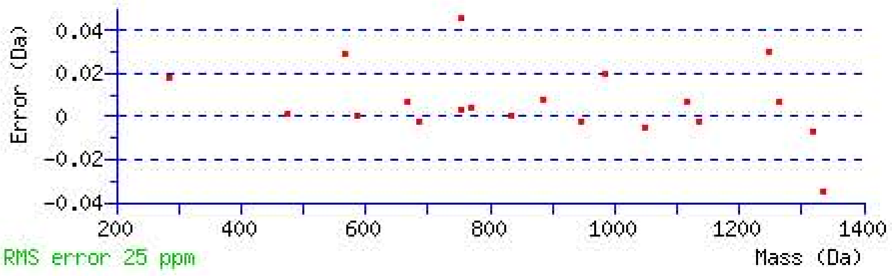
Match to Query 32364: 1635.767652 from(546.263160,3+) rtinseconds(2095) index(46551)
Title: Locus:1.1.1.3442.2 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

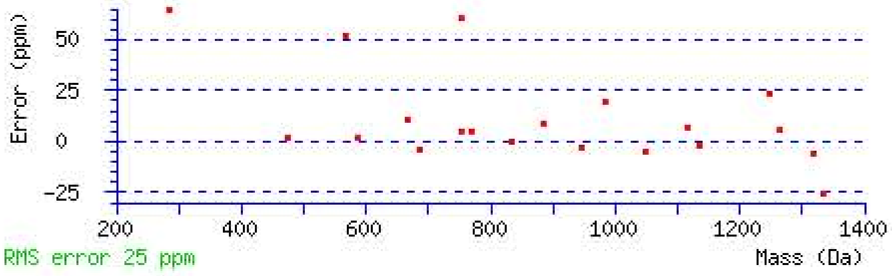
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1635.763657
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 55  Expect: 8.8e-006
Matches : 20/154 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	1521.744000	761.375638	1504.717451	752.862364	1503.733435	752.370356	10
3	373.150646	187.078961			355.140081	178.073679	A	***1335.664687***	668.335982	1318.638138	659.822707	1317.654122	659.330699	9
4	502.193239	251.600258			484.182674	242.594975	E	***1264.627573***	632.817425	1247.601024	624.304150	1246.617008	623.812142	8
5	589.225267	295.116272			571.214702	286.110989	S	***1135.584980***	568.296128	1118.558431	559.782854	1117.574415	559.290846	7
6	690.272946	345.640111			672.262381	336.634829	T	***1048.552952***	524.780114	1031.526403	516.266840	1030.542387	515.774832	6
7	803.357010	402.182143			785.346445	393.176861	L	***947.505273***	474.256275	930.478724	465.743000	929.494708	465.250992	5
8	950.392410	475.699843			932.381845	466.694561	M	***834.421209***	417.714243	817.394660	409.200968	816.410644	408.708960	4
9	1051.440089	526.223683			1033.429524	517.218400	T	***687.385809***	344.196543	670.359260	335.683268	669.375244	335.191260	3
10	1490.665415	745.836346	1473.638866	737.323071	1472.654850	736.831063	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
54.6	1635.763657	0.003995	DWAESTLMTQK
0.7	1635.789291	-0.021639	VSWTPPSDSVDRYK

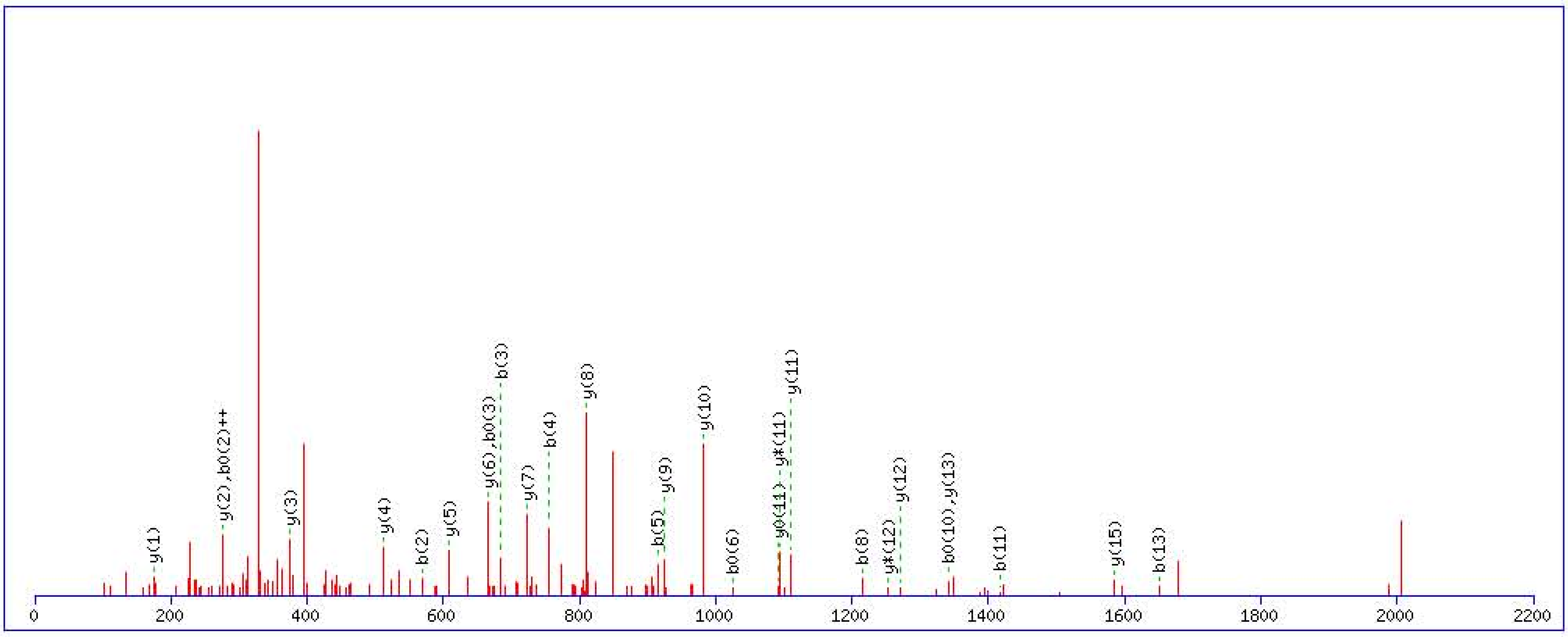
Mascot Search Results

Peptide View

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

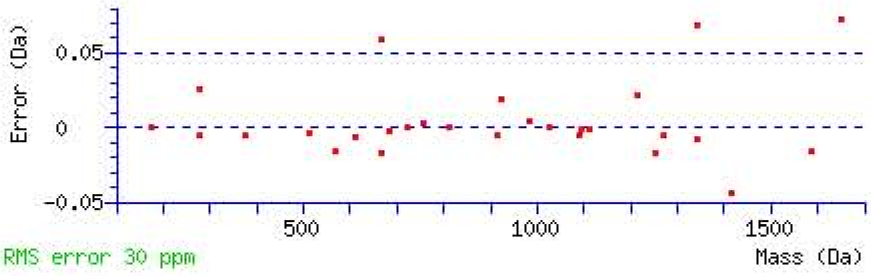
Match to Query 40264: 2023.876212 from(675.632680,3+) rtinseconds(1344) index(42018)
Title: Locus:1.1.1.3180.19 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

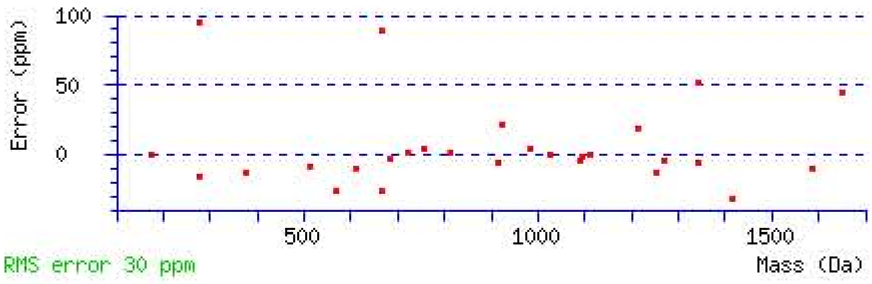
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2023.884033
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 98  Expect: 6.5e-010
Matches : 28/176 fragment ions using 47 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
98.2	2023.884033	-0.007821	QEDACQGDSGGPHVTR
57.7	2023.884033	-0.007821	QEDACQGDSGGPHVTR
2.2	2023.864899	0.011313	QEGETAICSEMTADR

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

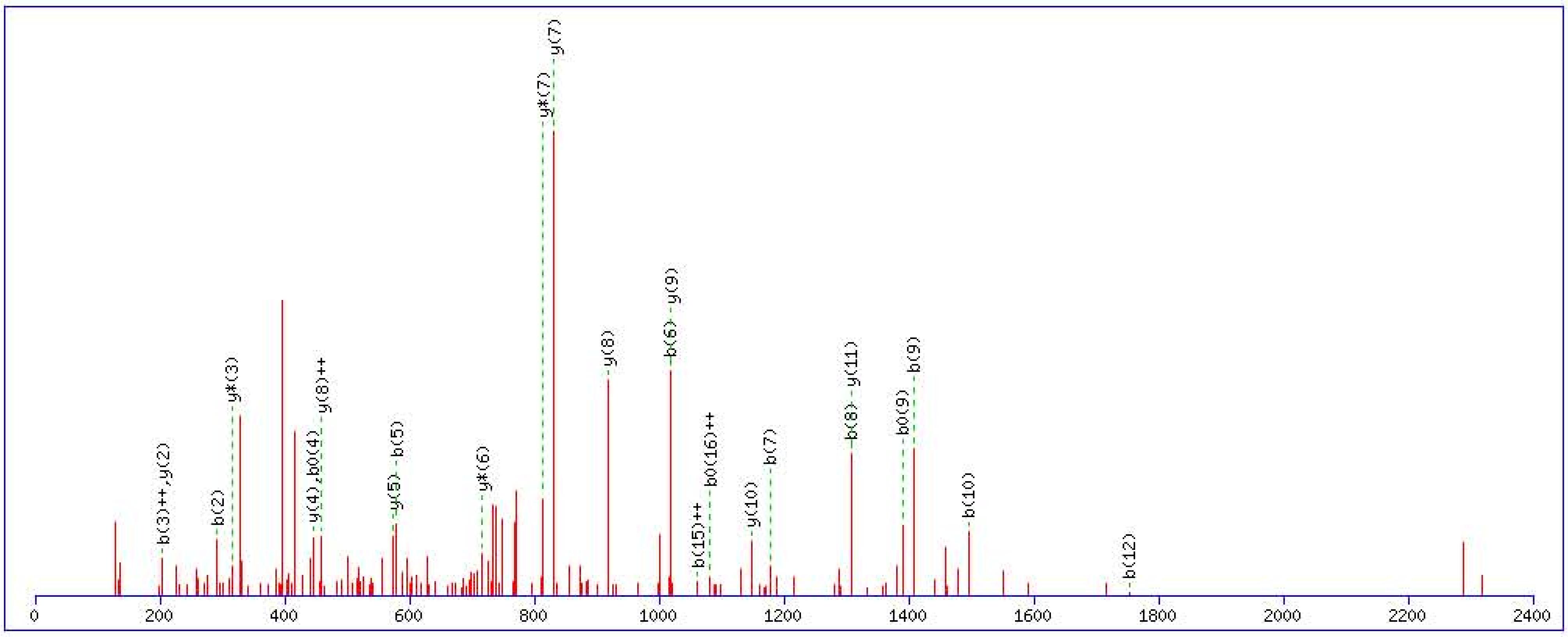
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

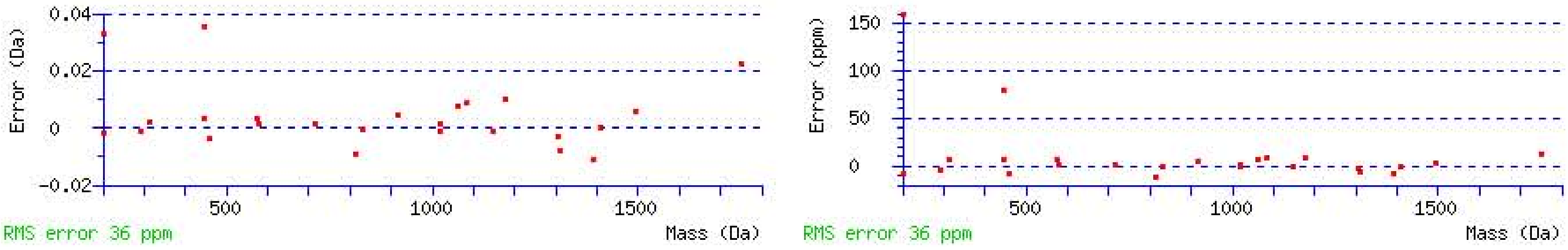
Match to Query 45534: 2324.978112 from(775.999980,3+) rtinseconds(1310) index(41872)
Title: Locus:1.1.1.3168.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 2324.982407
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 1.5e-005
Matches : 25/172 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	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
51.7	2324.982407	-0.004295	YKDGDQCETSPCQNQGK

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

{MATRIX SCIENCE}

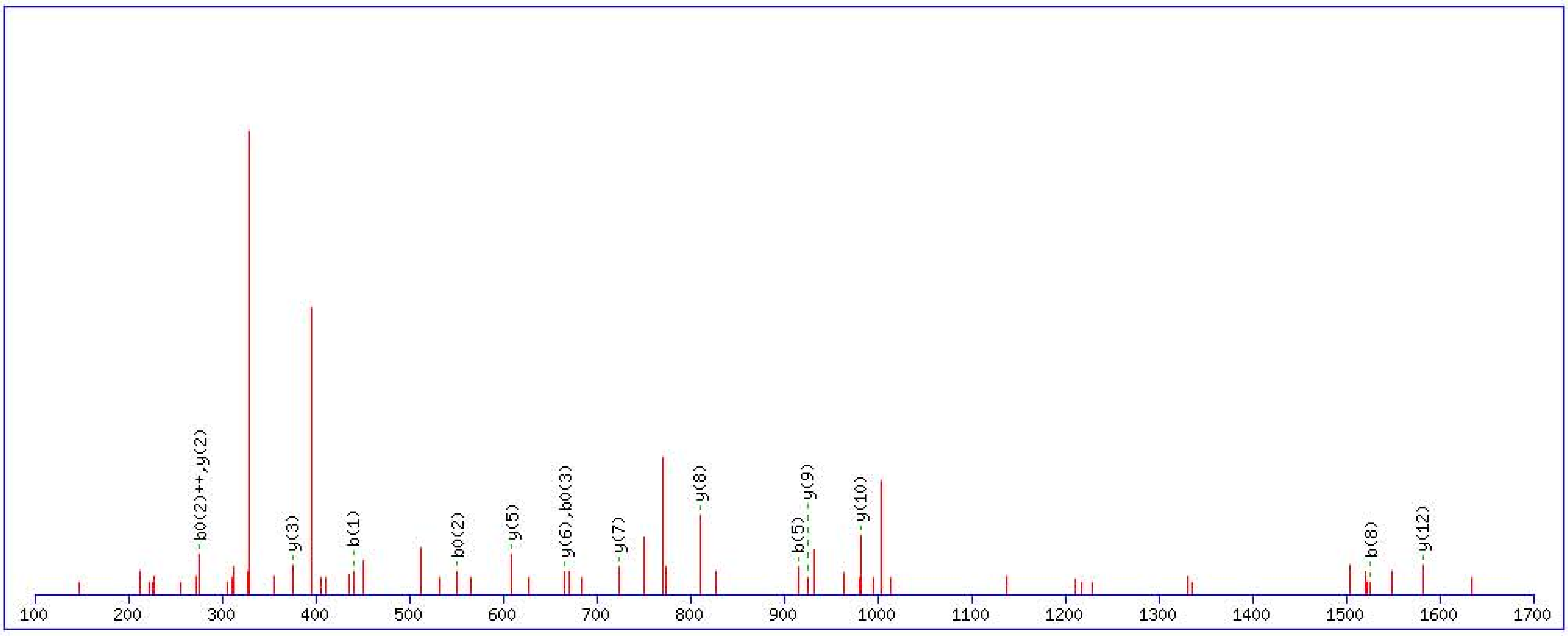
Mascot Search Results

Peptide View

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

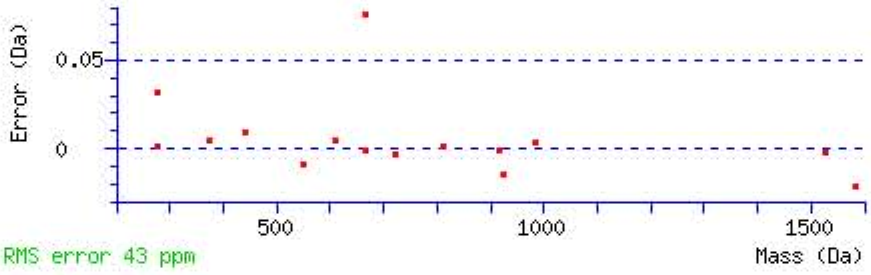
Match to Query 45672: 2335.040352 from(779.354060,3+) rtinseconds(1671) index(43989)
Title: Locus:1.1.1.3294.21 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

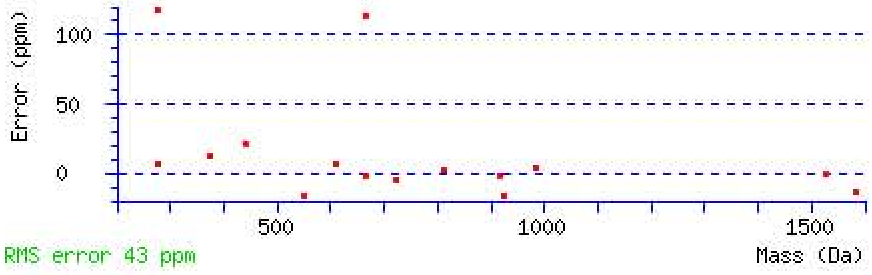
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2335.050781
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.0029
Matches : 15/176 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	**440.232602**	220.619939	423.206053	212.106664			Q							16
2	569.275195	285.141236	552.248646	276.627961	551.264630	276.135953	E	1896.832709	948.919992	1879.806160	940.406718	1878.822144	939.914710	15
3	684.302138	342.654707	667.275589	334.141433	666.291573	333.649425	D	1767.790116	884.398696	1750.763567	875.885422	1749.779551	875.393413	14
4	755.339252	378.173264	738.312703	369.659989	737.328687	369.167982	A	1652.763173	826.885224	1635.736624	818.371950	1634.752608	817.879942	13
5	**915.369901**	458.188589	898.343352	449.675314	897.359336	449.183306	C	***1581.726059***	791.366667	1564.699510	782.853393	1563.715494	782.361385	12
6	1354.595227	677.801252	1337.568678	669.287977	1336.584662	668.795969	Q	1421.695410	711.351343	1404.668861	702.838068	1403.684845	702.346060	11
7	1411.616691	706.311984	1394.590142	697.798709	1393.606126	697.306701	G	***982.470084***	491.738680	965.443535	483.225405	964.459519	482.733397	10
8	**1526.643634**	763.825455	1509.617085	755.312181	1508.633069	754.820173	D	***925.448620***	463.227948	908.422071	454.714673	907.438055	454.222665	9
9	1613.675662	807.341469	1596.649113	798.828195	1595.665097	798.336187	S	***810.421677***	405.714476	793.395128	397.201202	792.411112	396.709194	8
10	1670.697126	835.852201	1653.670577	827.338927	1652.686561	826.846919	G	***723.389649***	362.198462	706.363100	353.685188	705.379084	353.193180	7
11	1727.718590	864.362933	1710.692041	855.849659	1709.708025	855.357650	G	***666.368185***	333.687730	649.341636	325.174456	648.357620	324.682448	6
12	1824.771354	912.889315	1807.744805	904.376041	1806.760789	903.884032	P	***609.346721***	305.176998	592.320172	296.663724	591.336156	296.171716	5
13	1961.830266	981.418771	1944.803717	972.905497	1943.819701	972.413488	H	512.293957	256.650616	495.267408	248.137342	494.283392	247.645334	4
14	2060.898680	1030.952978	2043.872131	1022.439704	2042.888115	1021.947695	V	***375.235045***	188.121160	358.208496	179.607886	357.224480	179.115878	3
15	2161.946359	1081.476817	2144.919810	1072.963543	2143.935794	1072.471535	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
27.9	2335.050781	-0.010429	QEDACQGDSGGPHVTR
0.8	2335.030762	0.009590	NLTLETEMMSLHDELDQER

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

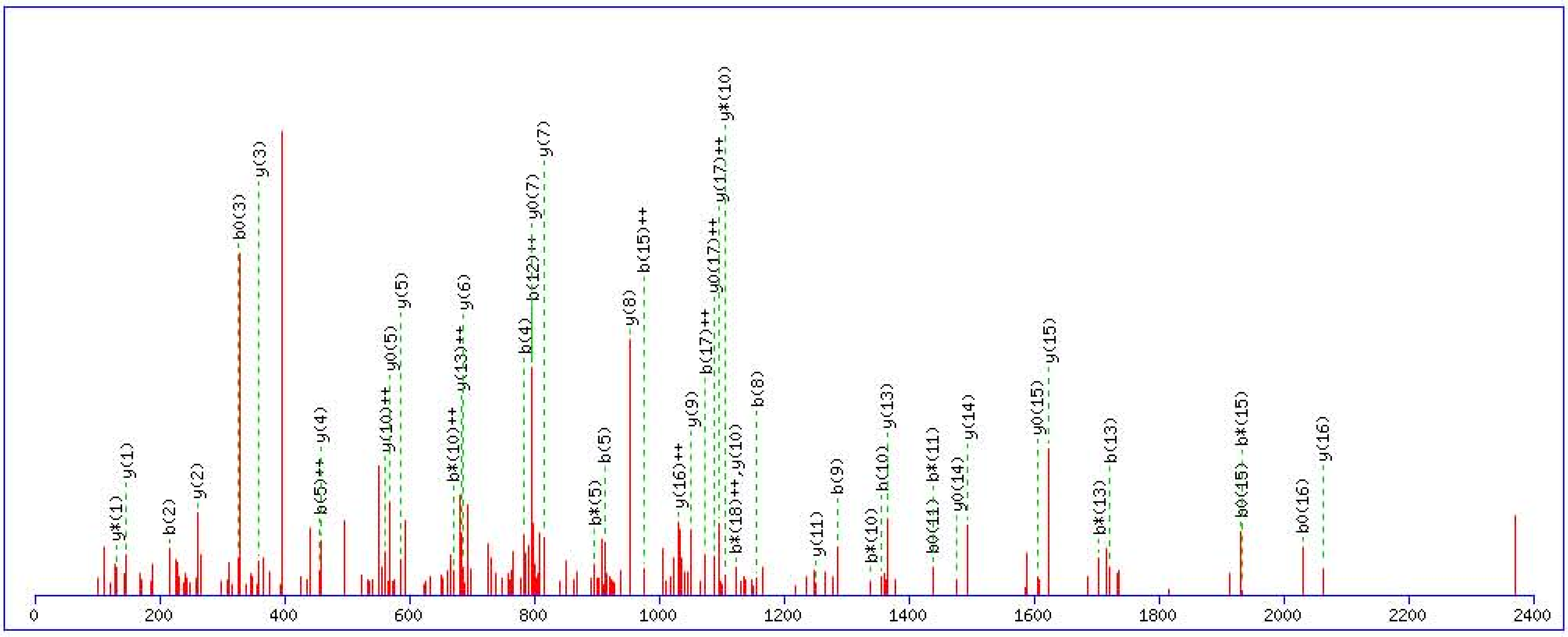
Mascot Search Results

Peptide View

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

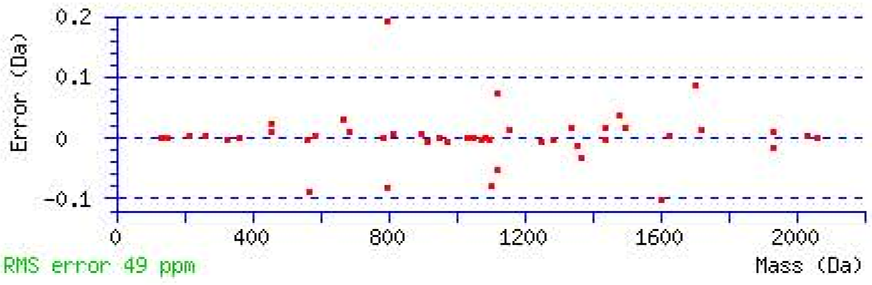
Match to Query 46533: 2406.175992 from(803.065940,3+) rtinseconds(2225) index(47362)
Title: Locus:1.1.1.3487.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

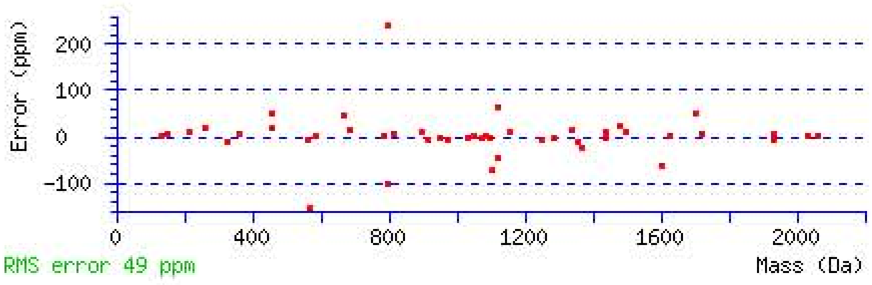
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2406.173676
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4     : Biotin:Thermo-21345 (Q)
Ions Score: 66  Expect: 6.8e-006
Matches : 48/206 fragment ions using 115 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	**216.097882**	108.552579	199.071333	100.039305	198.087317	99.547296	T	2293.138041	1147.072658	2276.111492	1138.559384	2275.127476	1138.067376	18
3	345.140475	173.073875	328.113926	164.560601	327.129910	164.068593	E	2192.090362	1096.548819	2175.063813	1088.035544	2174.079797	1087.543536	17
4	**784.365801**	392.686539	767.339252	384.173264	766.355236	383.681256	Q	***2063.047769***	1032.027522	2046.021220	1023.514248	2045.037204	1023.022240	16
5	**913.408394**	**457.207835**	896.381845	448.694561	895.397829	448.202553	E	***1623.822443***	812.414860	1606.795894	803.901585	1605.811878	803.409577	15
6	1042.450987	521.729131	1025.424438	513.215857	1024.440422	512.723849	E	***1494.779850***	747.893563	1477.753301	739.380289	1476.769285	738.888281	14
7	1099.472451	550.239863	1082.445902	541.726589	1081.461886	541.234581	G	***1365.737257***	683.372267	1348.710708	674.858992	1347.726692	674.366984	13
8	**1156.493915**	578.750595	1139.467366	570.237321	1138.483350	569.745313	G	1308.715793	654.861535	1291.689244	646.348260	1290.705228	645.856252	12
9	**1285.536508**	643.271892	1268.509959	634.758618	1267.525943	634.266609	E	***1251.694329***	626.350803	1234.667780	617.837528	1233.683764	617.345520	11
10	**1356.573622**	678.790449	1339.547073	670.277175	1338.563057	669.785166	A	***1122.651736***	561.829506	1105.625187	553.316232	1104.641171	552.824224	10
11	1455.642036	728.324656	1438.615487	719.811382	1437.631471	719.319373	V	***1051.614622***	526.310949	1034.588073	517.797675	1033.604057	517.305667	9
12	1592.700948	**796.854112**	1575.674399	788.340838	1574.690383	787.848829	H	***952.546208***	476.776742	935.519659	468.263468	934.535643	467.771460	8
13	**1721.743541**	861.375409	1704.716992	852.862134	1703.732976	852.370126	E	***815.487296***	408.247286	798.460747	399.734012	797.476731	399.242004	7
14	1820.811955	910.909616	1803.785406	902.396341	1802.801390	901.904333	V	***686.444703***	343.725990	669.418154	335.212715	668.434138	334.720707	6
15	1949.854548	**975.430912**	1932.827999	966.917638	1931.843983	966.425630	E	***587.376289***	294.191783	570.349740	285.678508	569.365724	285.186500	5
16	2048.922962	1024.965119	2031.896413	1016.451845	2030.912397	1015.959837	V	***458.333696***	229.670486	441.307147	221.157212			4
17	2147.991376	**1074.499326**	2130.964827	1065.986051	2129.980811	1065.494043	V	***359.265282***	180.136279	342.238733	171.623005			3
18	2261.075440	1131.041358	2244.048891	1122.528083	2243.064875	1122.036075	I	***260.196868***	130.602072	243.170319	122.088798			2
19							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.0	2406.173676	0.002316	NTEQEEGGEAVHEVEVVIK

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

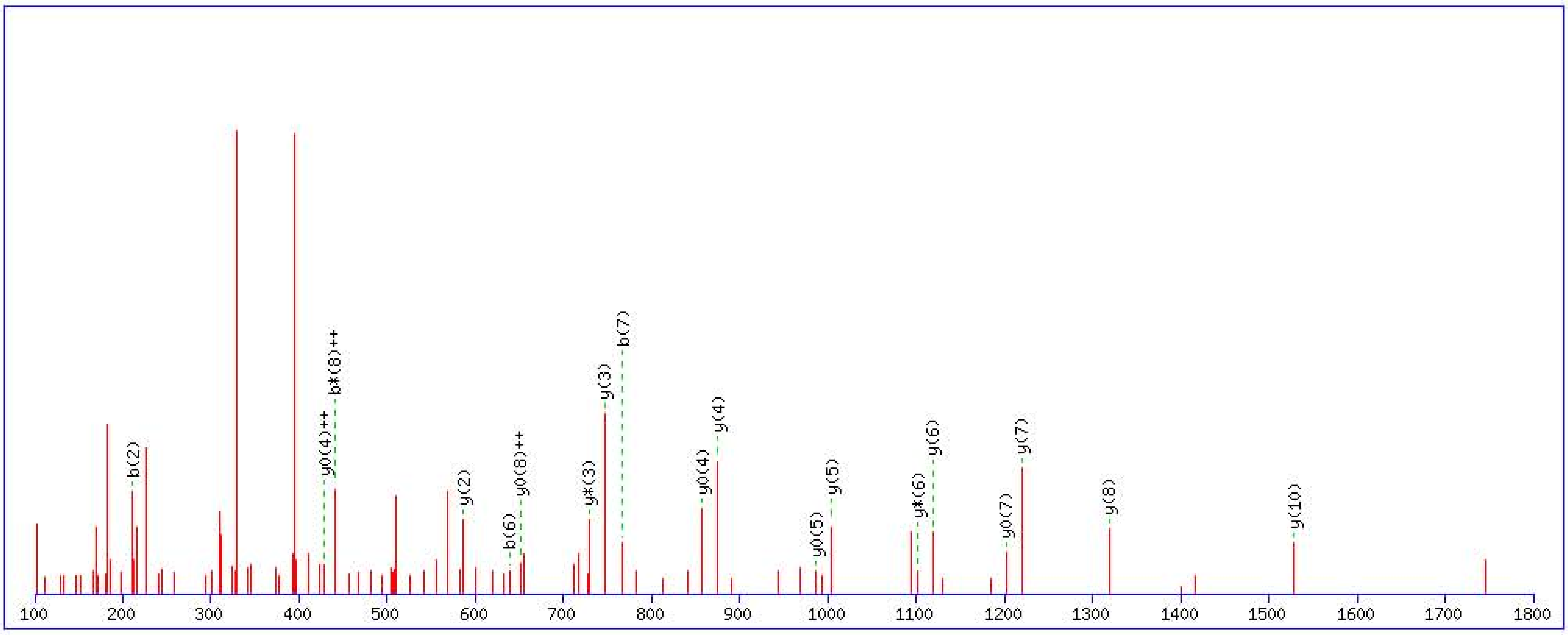
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPLVTNEECQK**
Found in **FA11_HUMAN**, Coagulation factor XI OS=Homo sapiens GN=F11 PE=1 SV=1

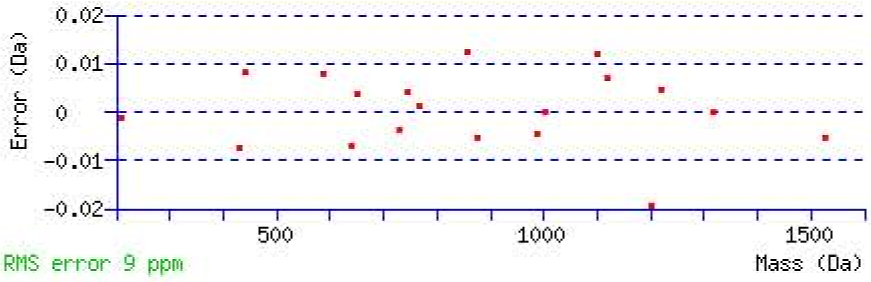
Match to Query 32542: 1640.822712 from(547.948180,3+) rtinseconds(1891) index(59834)
Title: Locus:1.1.1.1570.8 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

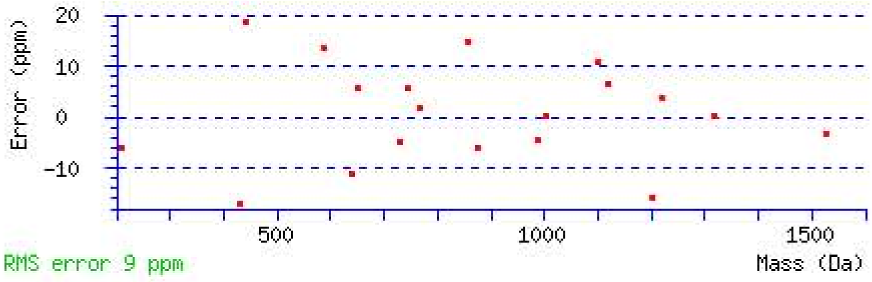
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1640.826584
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.00024
Matches : 19/96 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	114.091340	57.549308					I							11
2	**211.144104**	106.075690					P	***1528.749813***	764.878545	1511.723264	756.365270	1510.739248	755.873262	10
3	324.228168	162.617722					L	1431.697049	716.352163	1414.670500	707.838888	1413.686484	707.346880	9
4	423.296582	212.151929					V	***1318.612985***	659.810131	1301.586436	651.296856	1300.602420	650.804848	8
5	524.344261	262.675769			506.333696	253.670486	T	***1219.544571***	610.275924	1202.518022	601.762649	1201.534006	601.270641	7
6	**638.387188**	319.697232	621.360639	311.183958	620.376623	310.691950	N	***1118.496892***	559.752084	1101.470343	551.238810	1100.486327	550.746802	6
7	**767.429781**	384.218529	750.403232	375.705254	749.419216	375.213246	E	***1004.453965***	502.730621	987.427416	494.217346	986.443400	493.725338	5
8	896.472374	448.739825	879.445825	440.226551	878.461809	439.734543	E	***875.411372***	438.209324	858.384823	429.696050	857.400807	429.204042	4
9	1056.503023	528.755150	1039.476474	520.241875	1038.492458	519.749867	C	***746.368779***	373.688028	729.342230	365.174753			3
10	1495.728349	748.367813	1478.701800	739.854538	1477.717784	739.362530	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 IPLVTNEECQK
(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	1640.826584	-0.003872	IPLVTNEECQK
1.2	1640.842331	-0.019619	EGFFTVPPEHRLGR

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

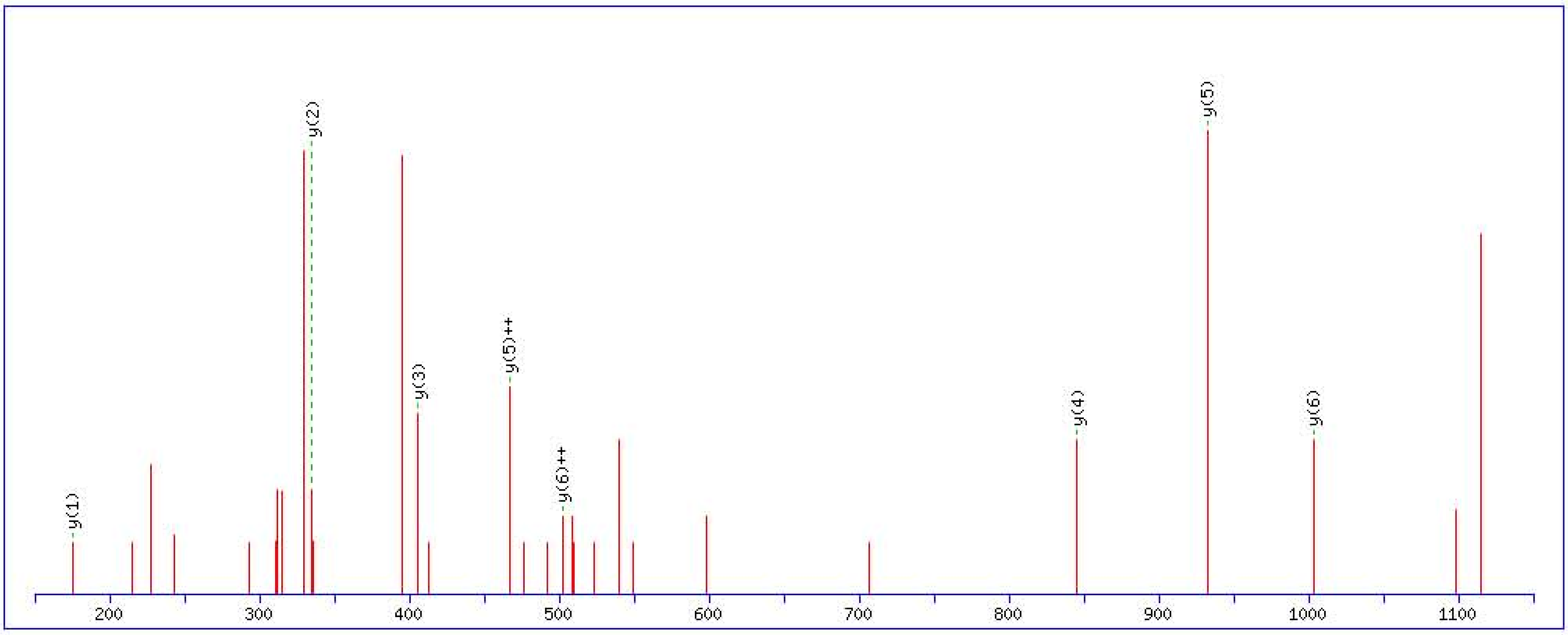
Mascot Search Results

Peptide View

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

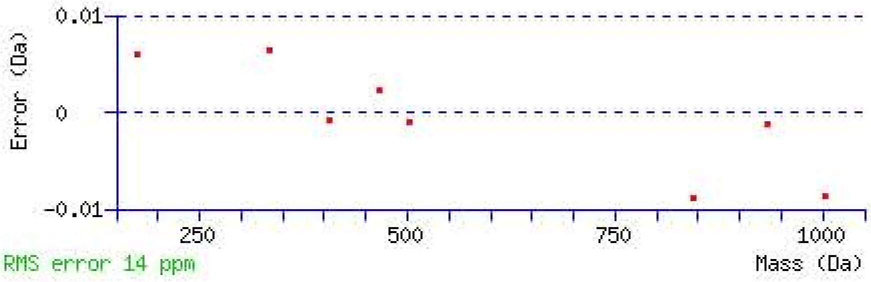
Match to Query 14650: 1115.553848 from(558.784200,2+) rtinseconds(1403) index(15231)
Title: Locus:1.1.1.3054.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

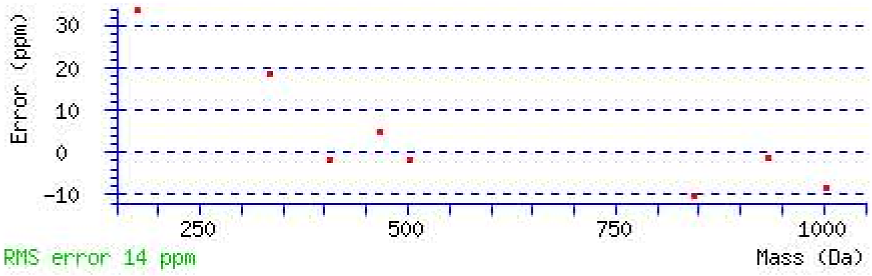
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1115.557953
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 35 **Expect:** 0.002
Matches : 8/54 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							7
2	185.128454	93.067865					A	***1003.481183***	502.244230	986.454634	493.730955	985.470618	493.238947	6
3	272.160482	136.583879			254.149917	127.578596	S	***932.444069***	466.725673	915.417520	458.212398	914.433504	457.720390	5
4	711.385808	356.196542	694.359259	347.683268	693.375243	347.191260	Q	***845.412041***	423.209659	828.385492	414.696384			4
5	782.422922	391.715099	765.396373	383.201824	764.412357	382.709816	A	***406.186715***	203.596995	389.160166	195.083721			3
6	942.453571	471.730424	925.427022	463.217149	924.443006	462.725141	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 LASQACR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.4	1115.557953	-0.004105	LASQACR
6.2	1115.550552	0.003296	LAAGSRCPER
3.9	1115.557098	-0.003250	LEQGGTADGLR
1.6	1115.564484	-0.010636	LVDPQEMLR
1.6	1115.543350	0.010498	LEYKFCTR
1.4	1115.546722	0.007126	LAQDACK

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

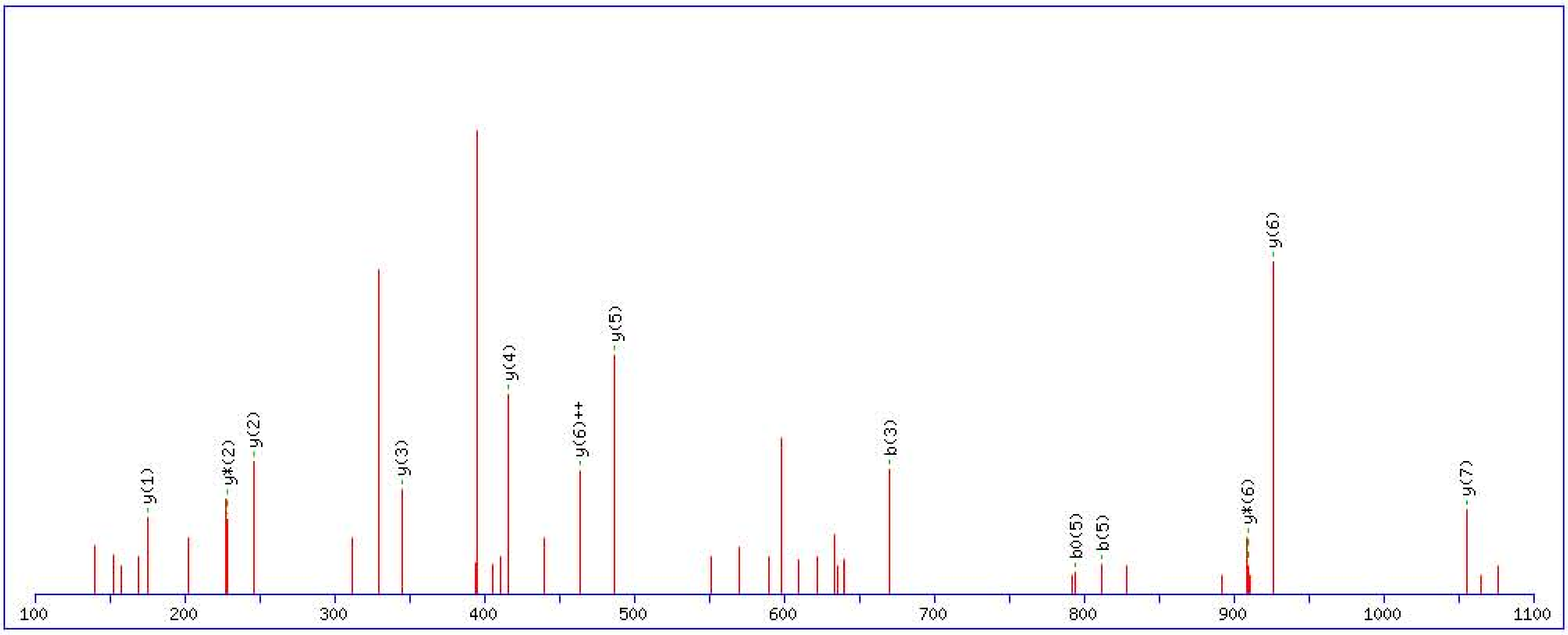
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

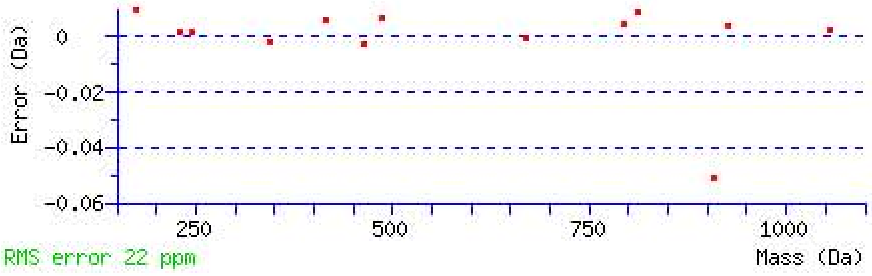
Match to Query 16393: 1155.603248 from(578.808900,2+) rtinseconds(1429) index(15438)
Title: Locus:1.1.1.3063.20 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

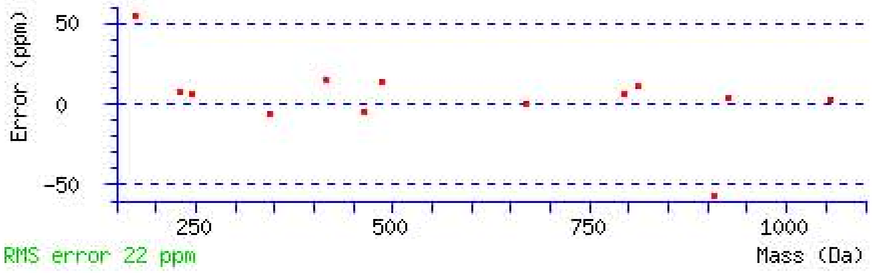
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1100] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1155.607010
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.0007
Matches : 13/68 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	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





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
42.4	1155.607010	-0.003762	TEQAAVAR
8.3	1155.588394	0.014854	VEQIEAGTPGR
6.1	1155.607025	-0.003777	VQDSAVAR
2.2	1155.614883	-0.011635	RSGDWLLPGR

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

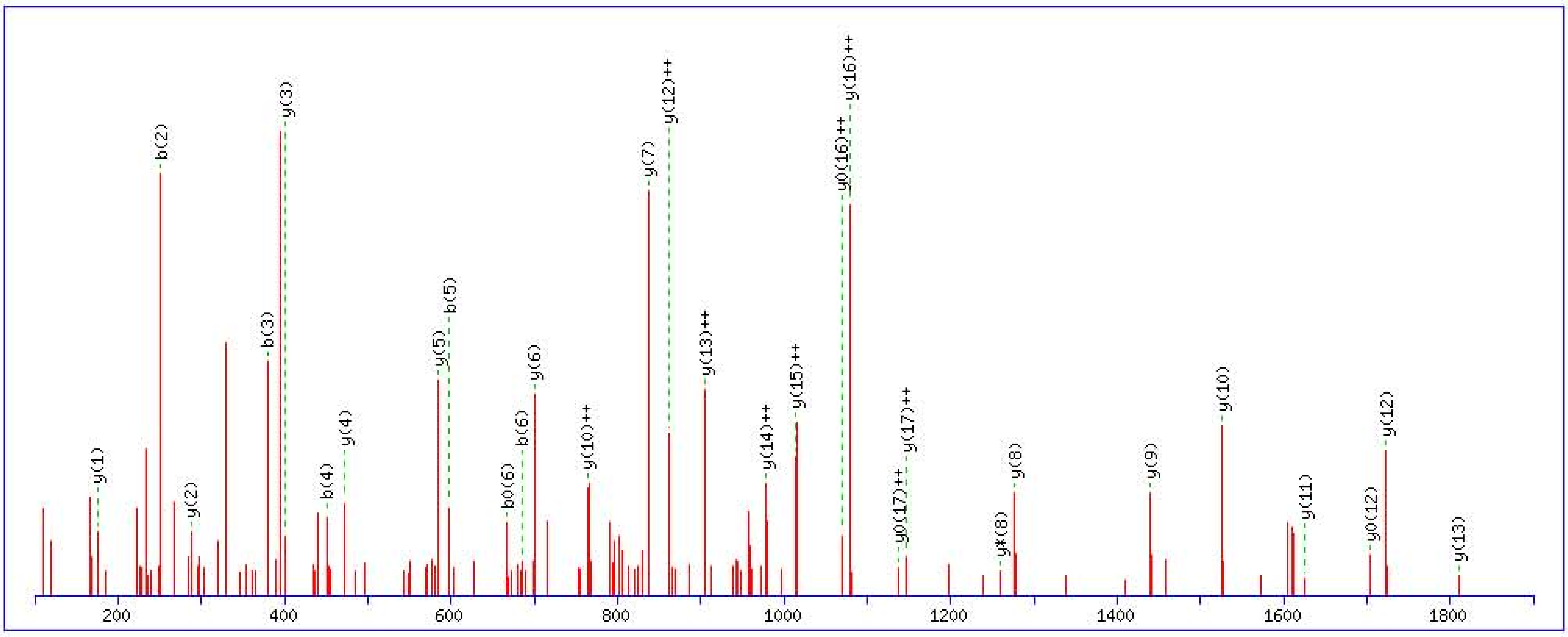
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

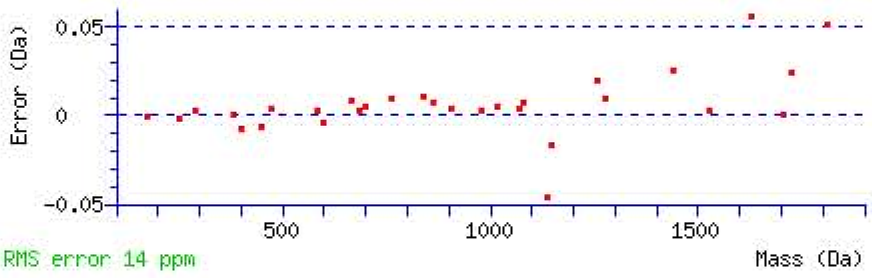
Match to Query 46538: 2406.278832 from(803.100220,3+) rtinseconds(2297) index(62227)
Title: Locus:1.1.1.1711.15 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

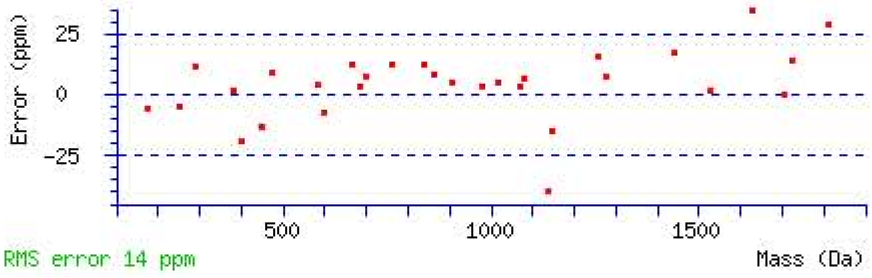
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1900] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2406.251801
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 2.2e-005
Matches : 30/170 fragment ions using 73 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							18
2	**251.150252**	126.078764					H	2294.175035	1147.591155	2277.148486	1139.077881	2276.164470	1138.585873	17
3	**380.192845**	190.600060			362.182280	181.594778	E	2157.116123	1079.061699	2140.089574	1070.548425	2139.105558	1070.056417	16
4	**451.229959**	226.118617			433.219394	217.113335	A	2028.073530	1014.540403	2011.046981	1006.027129	2010.062965	1005.535121	15
5	**598.298373**	299.652825			580.287808	290.647542	F	1957.036416	979.021846	1940.009867	970.508572	1939.025851	970.016564	14
6	**685.330401**	343.168838			667.319836	334.163556	S	***1809.968002***	905.487639	1792.941453	896.974365	1791.957437	896.482357	13
7	782.383165	391.695221			764.372600	382.689938	P	***1722.935974***	861.971625	1705.909425	853.458351	1704.925409	852.966343	12
8	881.451579	441.229427			863.441014	432.224145	V	***1625.883210***	813.445243	1608.856661	804.931969	1607.872645	804.439961	11
9	968.483607	484.745441			950.473042	475.740159	S	***1526.814796***	763.911036	1509.788247	755.397762	1508.804231	754.905754	10
10	1131.546936	566.277106			1113.536371	557.271823	Y	***1439.782768***	720.395022	1422.756219	711.881748	1421.772203	711.389740	9
11	1570.772262	785.889769	1553.745713	777.376495	1552.761697	776.884487	Q	***1276.719439***	638.863358	1259.692890	630.350083	1258.708874	629.858075	8
12	1707.831174	854.419225	1690.804625	845.905951	1689.820609	845.413943	H	***837.494113***	419.250695	820.467564	410.737420	819.483548	410.245412	7
13	1822.858117	911.932697	1805.831568	903.419422	1804.847552	902.927414	D	***700.435201***	350.721239	683.408652	342.207964	682.424636	341.715956	6
14	1935.942181	968.474729	1918.915632	959.961454	1917.931616	959.469446	L	***585.408258***	293.207767	568.381709	284.694492			5
15	2006.979295	1003.993286	1989.952746	995.480011	1988.968730	994.988003	A	***472.324194***	236.665735	455.297645	228.152460			4
16	2120.063359	1060.535317	2103.036810	1052.022043	2102.052794	1051.530035	L	***401.287080***	201.147178	384.260531	192.633903			3
17	2233.147423	1117.077349	2216.120874	1108.564075	2215.136858	1108.072067	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 LHEAFSPVSYQHDLALLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.0	2406.251801	0.027031	LHEAFSPVSYQHDLALLR

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

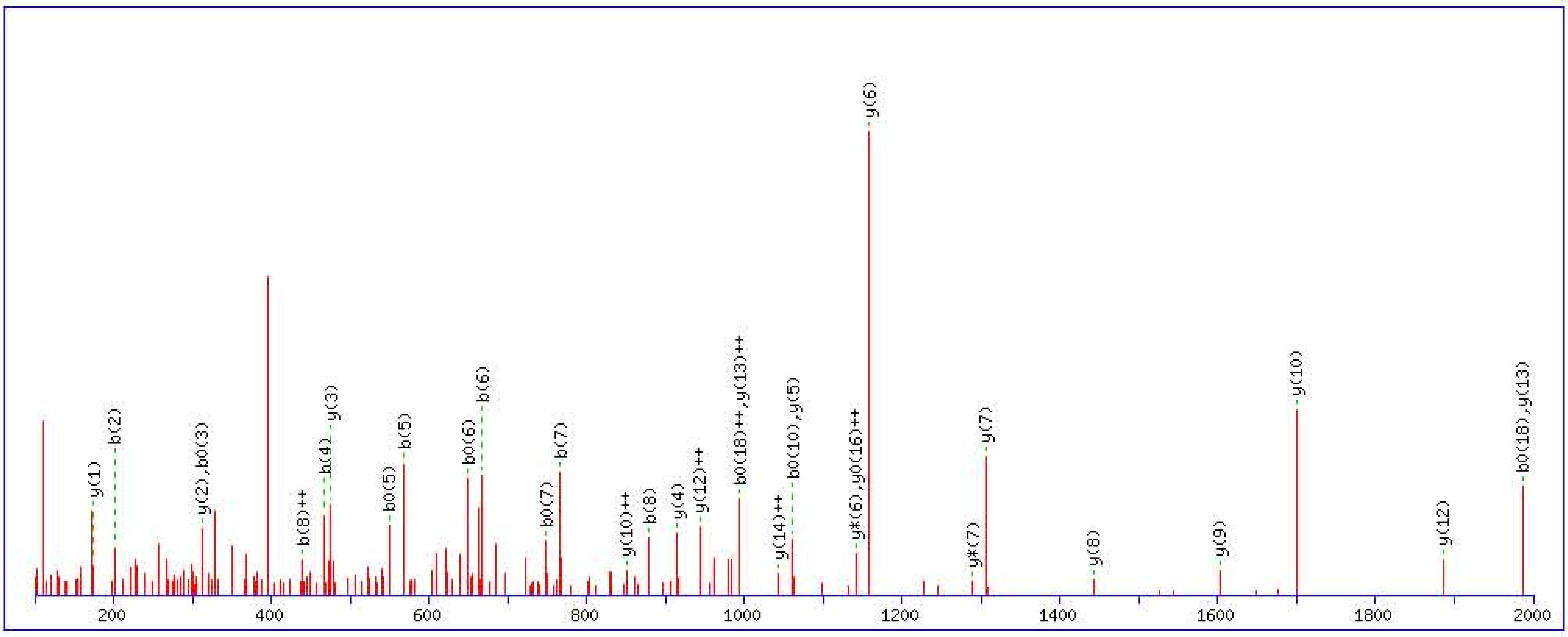
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

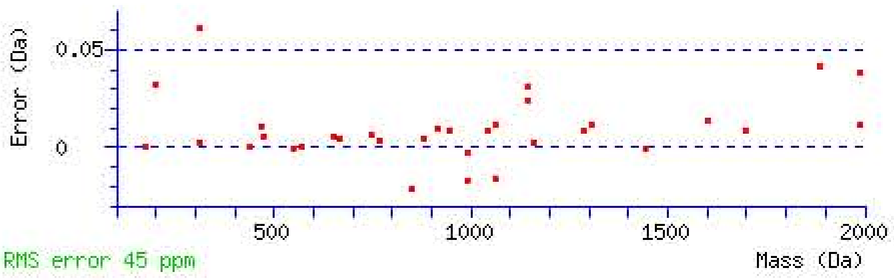
Match to Query 54457: 3064.479420 from(613.903160,5+) rtinseconds(2170) index(61492)
Title: Locus:1.1.1.1667.10 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

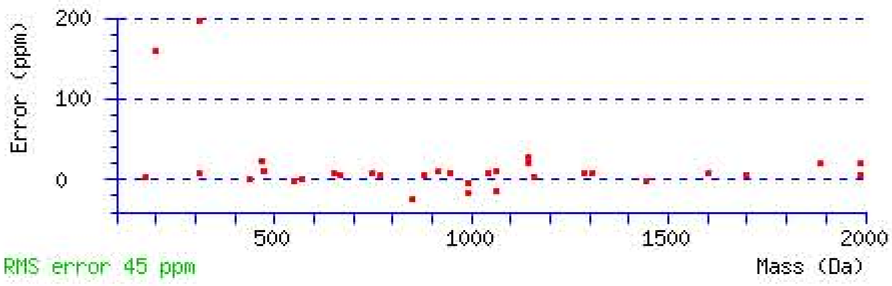


```
Monoisotopic mass of neutral peptide Mr(calc): 3064.468796
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20     : Biotin:Thermo-21345 (Q)
Ions Score: 72  Expect: 1.6e-006
Matches : 33/204 fragment ions using 48 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							23
2	***201.086983***	101.047130			183.076418	92.041847	E	2994.438934	1497.723105	2977.412385	1489.209830	2976.428369	1488.717822	22
3	330.129576	165.568426			312.119011	156.563144	E	2865.396341	1433.201808	2848.369792	1424.688534	2847.385776	1424.196526	21
4	***467.188488***	234.097882			449.177923	225.092599	H	2736.353748	1368.680512	2719.327199	1360.167237	2718.343183	1359.675229	20
5	***568.236167***	284.621722			550.225602	275.616439	T	2599.294836	1300.151056	2582.268287	1291.637781	2581.284271	1291.145773	19
6	***667.304581***	334.155929			649.294016	325.150646	V	2498.247157	1249.627216	2481.220608	1241.113942	2480.236592	1240.621934	18
7	***766.372995***	383.690136			748.362430	374.684853	V	2399.178743	1200.093009	2382.152194	1191.579735	2381.168178	1191.087727	17
8	***879.457059***	440.232168			861.446494	431.226885	L	2300.110329	1150.558802	2283.083780	1142.045528	2282.099764	1141.553520	16
9	980.504738	490.756007			962.494173	481.750724	T	2187.026265	1094.016770	2169.999716	1085.503496	2169.015700	1085.011488	15
10	1079.573152	540.290214			1061.562587	531.284931	V	2085.978586	1043.492931	2068.952037	1034.979656	2067.968021	1034.487648	14
11	1180.620831	590.814054			1162.610266	581.808771	T	***1986.910172***	993.958724	1969.883623	985.445450	1968.899607	984.953442	13
12	1237.642295	619.324785			1219.631730	610.319503	G	***1885.862493***	943.434885	1868.835944	934.921610	1867.851928	934.429602	12
13	1366.684888	683.846082			1348.674323	674.840800	E	1828.841029	914.924153	1811.814480	906.410878	1810.830464	905.918870	11
14	1463.737652	732.372464			1445.727087	723.367182	P	***1699.798436***	850.402856	1682.771887	841.889582			10
15	1623.768301	812.387789			1605.757736	803.382506	C	***1602.745672***	801.876474	1585.719123	793.363200			9
16	1760.827213	880.917245			1742.816648	871.911962	H	***1442.715023***	721.861150	1425.688474	713.347875			8
17	1907.895627	954.451452			1889.885062	945.446169	F	***1305.656111***	653.331694	1288.629562	644.818419			7
18	2004.948391	1002.977834			1986.937826	993.972551	P	***1158.587697***	579.797487	1141.561148	571.284212			6
19	2152.016805	1076.512040			2134.006240	1067.506758	F	***1061.534933***	531.271105	1044.508384	522.757830			5
20	2591.242131	1296.124703	2574.215582	1287.611429	2573.231566	1287.119421	Q	***914.466519***	457.736898	897.439970	449.223623			4
21	2754.305460	1377.656368	2737.278911	1369.143093	2736.294895	1368.651085	Y	***475.241193***	238.124234	458.214644	229.610960			3
22	2891.364372	1446.185824	2874.337823	1437.672549	2873.353807	1437.180541	H	***312.177864***	156.592570	295.151315	148.079295			2
23							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 45 ppm



RMS error 45 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.7	3064.468796	0.010624	AEEHTVVLTVTGEPCHFPFQYHR

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

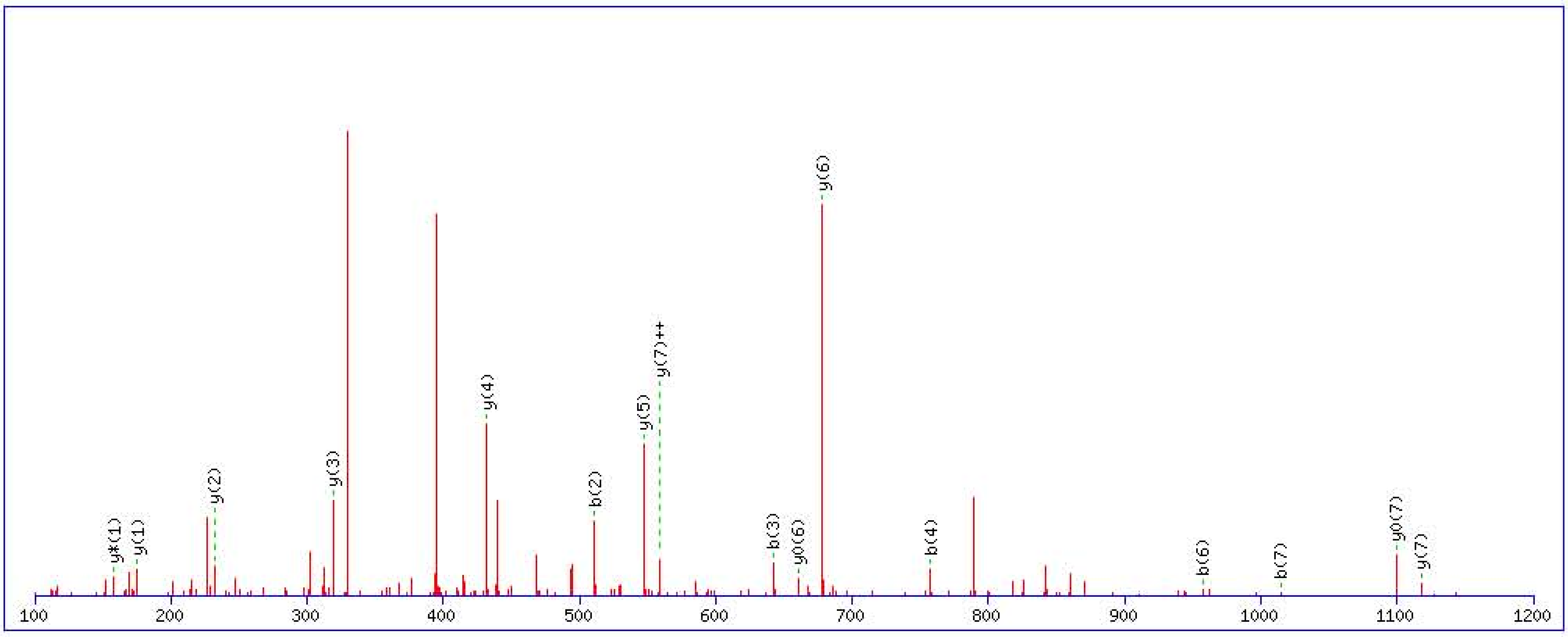
{MATRIX} {SCIENCE} Mascot Search Results

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

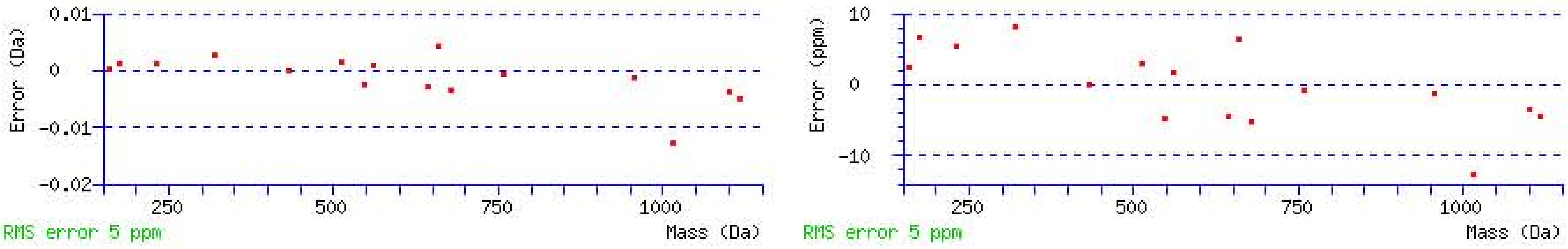
Match to Query 17453: 1187.574488 from(594.794520,2+) rtinseconds(1758) index(17490)
Title: Locus:1.1.1.3178.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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: 38 **Expect:** 0.0027
Matches : 16/72 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	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
37.8	1187.579086	-0.004598	AQMDLSGR
10.5	1187.578201	-0.003713	SSLENEPSLGR
9.0	1187.568344	0.006144	DHGFKVSADGR
7.5	1187.579086	-0.004598	QAAEVMGR
6.2	1187.590302	-0.015814	AQEAMRR
5.3	1187.568314	0.006174	QREDIWEGR
3.6	1187.557083	0.017405	EIGDVENWAR
3.1	1187.564255	0.010233	ARREEEENR
2.2	1187.575714	-0.001226	YQDAAGPR
1.8	1187.557968	0.016520	QPCPYGR

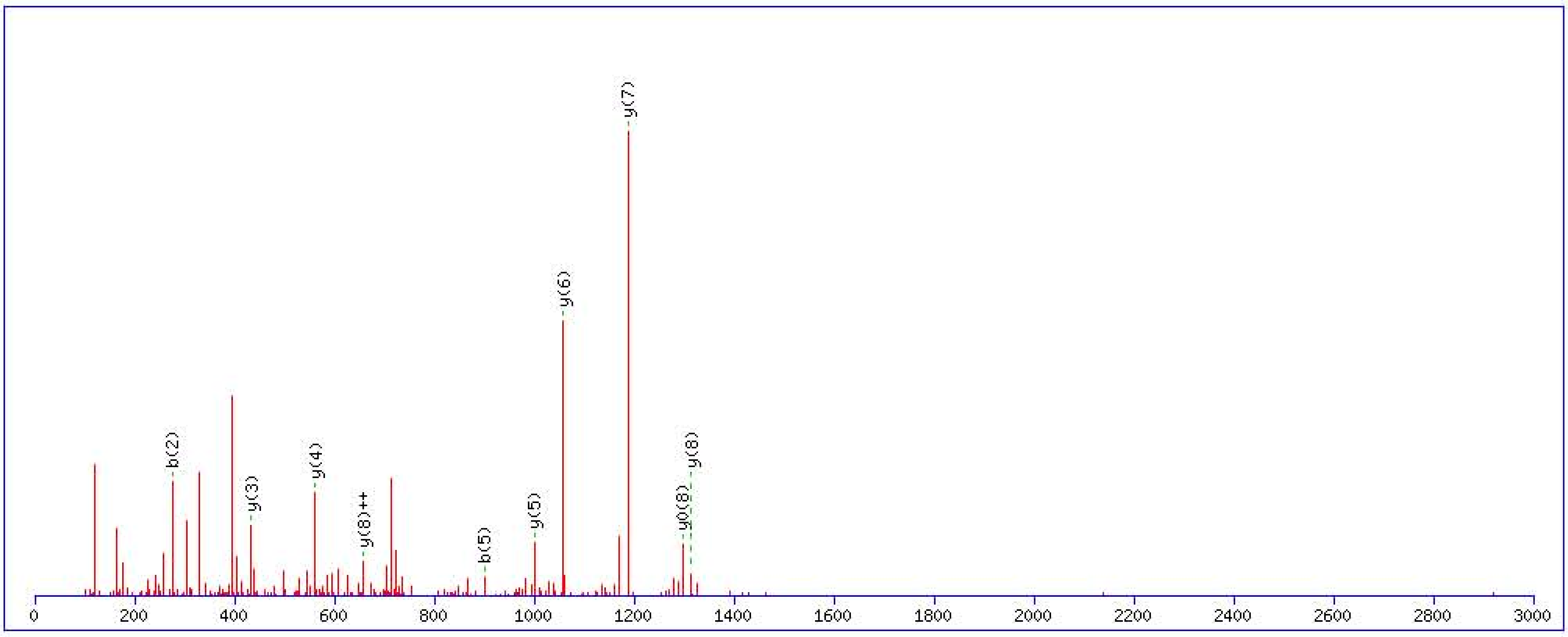
Mascot Search Results

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

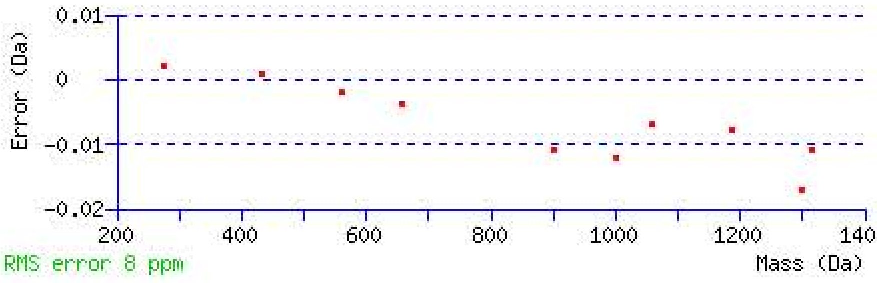
Match to Query 26184: 1461.647308 from(731.830930,2+) rtinseconds(1509) index(15903)
Title: Locus:1.1.1.3091.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

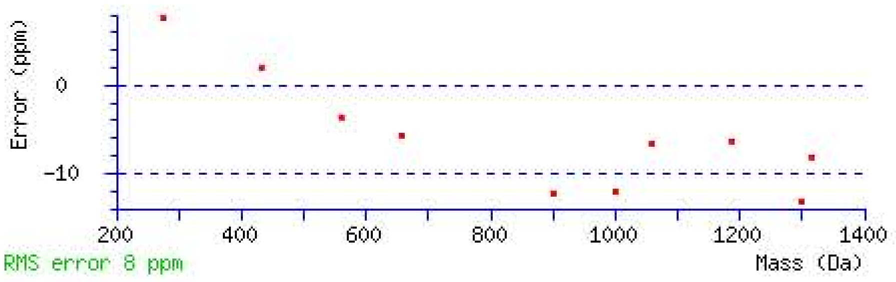
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1461.655807
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00016
Matches : 10/88 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	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
45.7	1461.655807	-0.008499	FQEGQEEER
11.0	1461.640564	0.006744	NSGTQSDGEEK
8.0	1461.648392	-0.001084	HREELSDYEER
8.0	1461.655807	-0.008499	FQEGQEEER
6.4	1461.640564	0.006744	VMTDVAGNPEEER
2.6	1461.637161	0.010147	ESELQWQEEER
1.6	1461.651794	-0.004486	ATSQHECSSSQLK

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

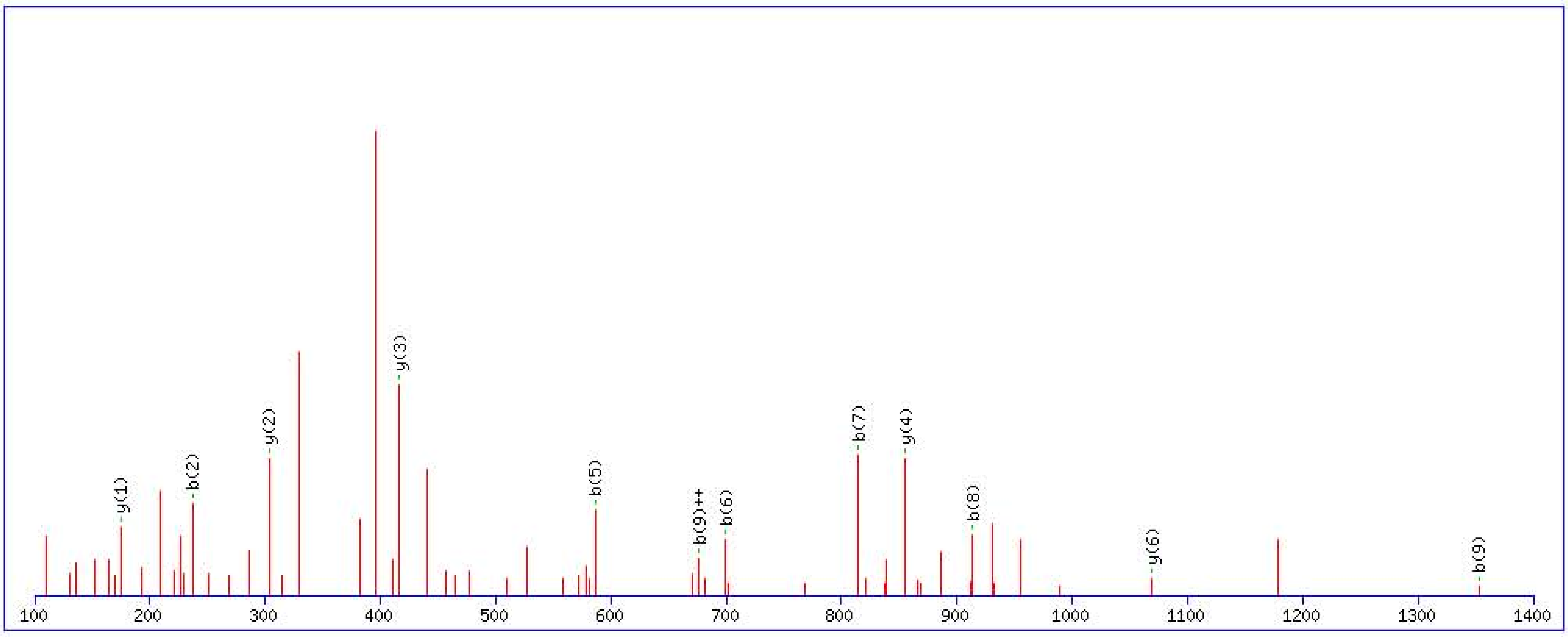
Mascot Search Results

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

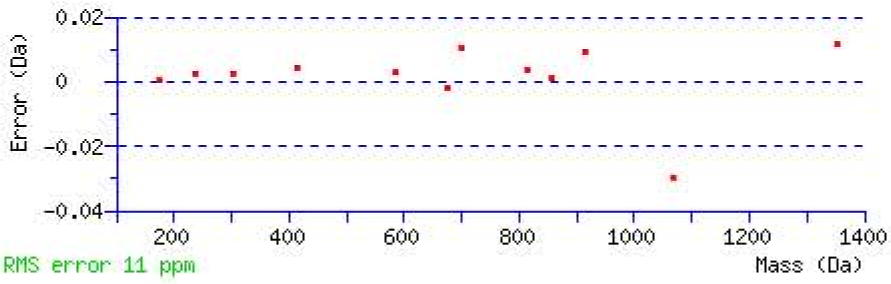
Match to Query 34995: 1766.909892 from(589.977240,3+) rtinseconds(1951) index(18755)
Title: Locus:1.1.1.3245.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

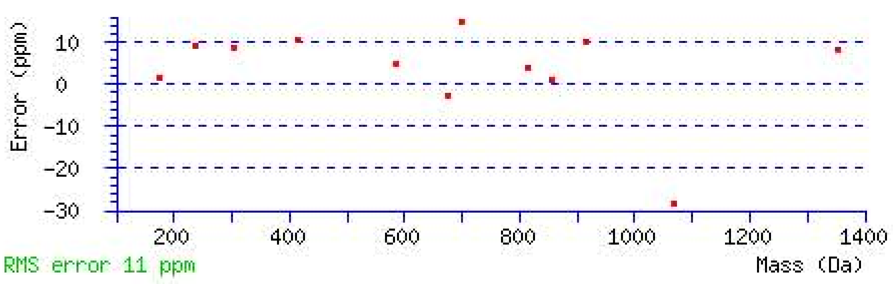
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1766.913773
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.0014
Matches : 12/98 fragment ions using 20 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
36.0	1766.913773	-0.003881	HVYGELDVQIQR
15.6	1766.913773	-0.003881	HVYGELDVQIQR
5.4	1766.888138	0.021754	IMQNGTILYTMR
4.9	1766.917130	-0.007238	KLSSQLVEHCQK
0.3	1766.924988	-0.015096	GNFPVEAVKMQHAIAR

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

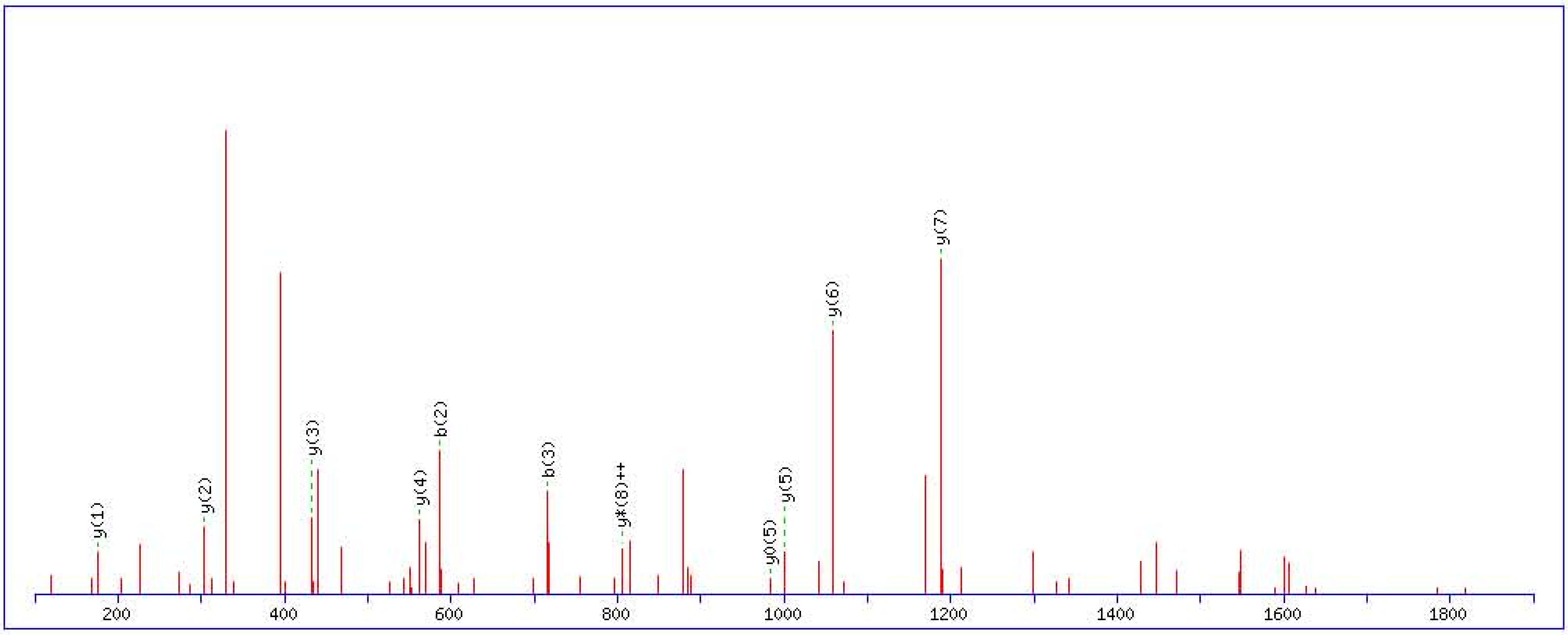
Mascot Search Results

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

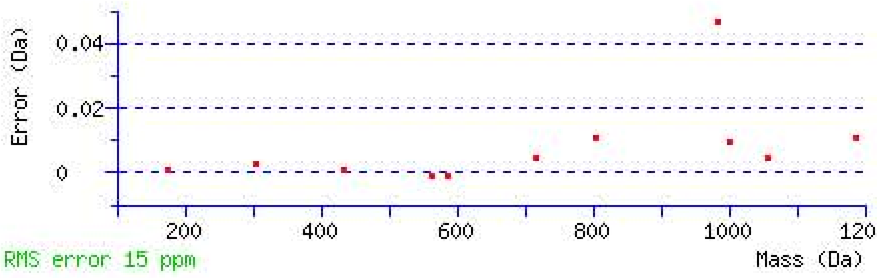
Match to Query 35192: 1772.832148 from(887.423350,2+) rtinseconds(1903) index(4260)
Title: Locus:1.1.1.3182.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

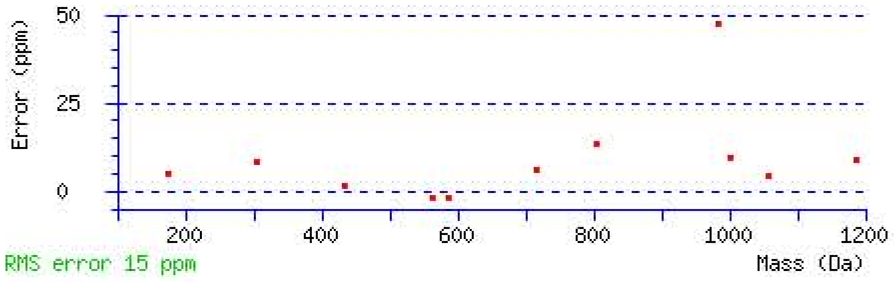
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 26  Expect: 0.034
Matches : 11/88 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	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
26.1	1772.822556	0.009592	FQEGQEEER
14.0	1772.828873	0.003275	QAEQEATVAREEQER
2.4	1772.836288	-0.004140	ADGSLTGGGLEAAAMAPER
0.7	1772.854904	-0.022756	AGNLMSAMLHVEALER
0.3	1772.851532	-0.019384	YEMFLNQARKNTDK

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

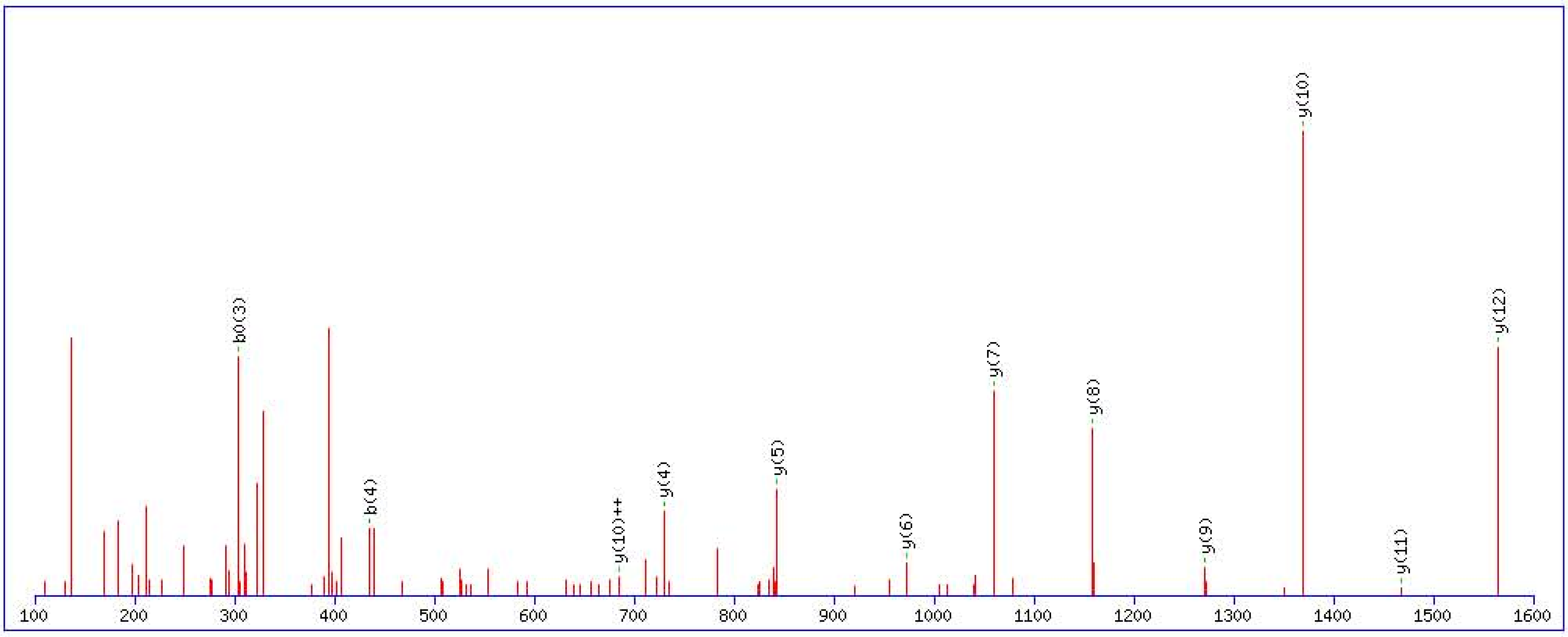
{MATRIX SCIENCE} Mascot Search Results

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

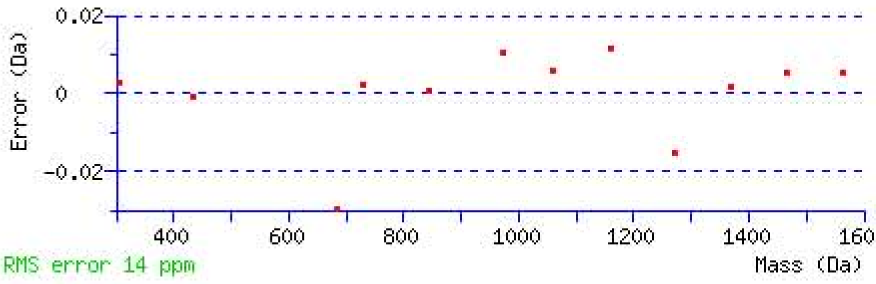
Match to Query 39257: 1998.085032 from(667.035620,3+) rtinseconds(2791) index(36596)
Title: Locus:1.1.1.3634.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

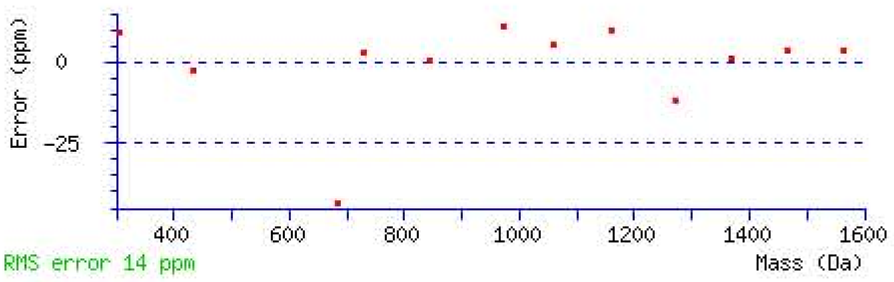
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1998.085983
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 63  Expect: 1.8e-006
Matches : 12/150 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	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
62.6	1998.085983	-0.000951	GTYIPVPIVSELQSGK
1.3	1998.099731	-0.014699	GDEVVVELVENGKKVTVGK

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

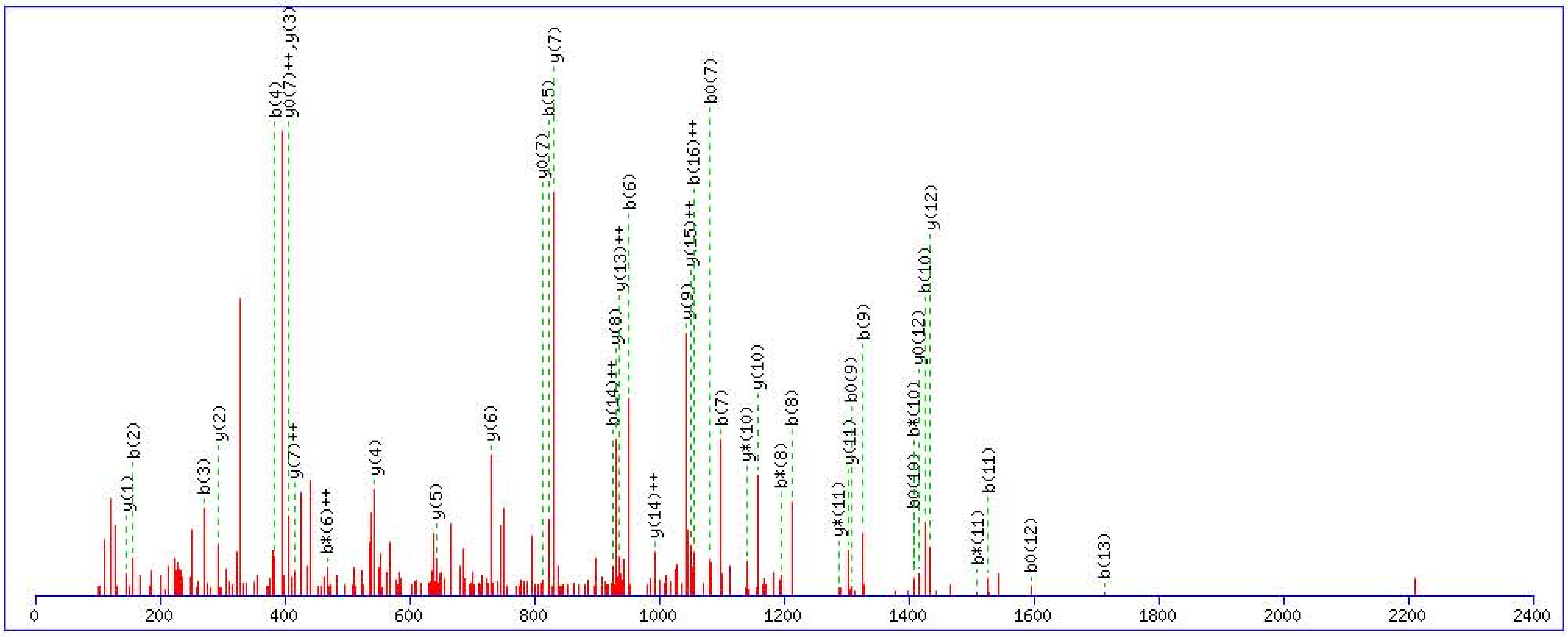
Mascot Search Results

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

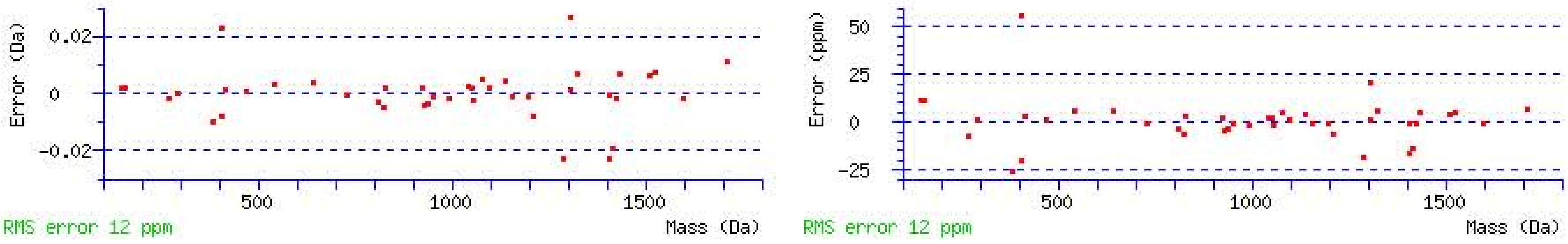
Match to Query 44156: 2255.211522 from(752.744450,3+) rtinseconds(3032) index(38251)
Title: Locus:1.1.1.3716.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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: 58  Expect: 3.4e-005
Matches : 42/168 fragment ions using 89 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
57.9	2255.213654	-0.002132	GVNLQEFLNVTSVHLFK

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

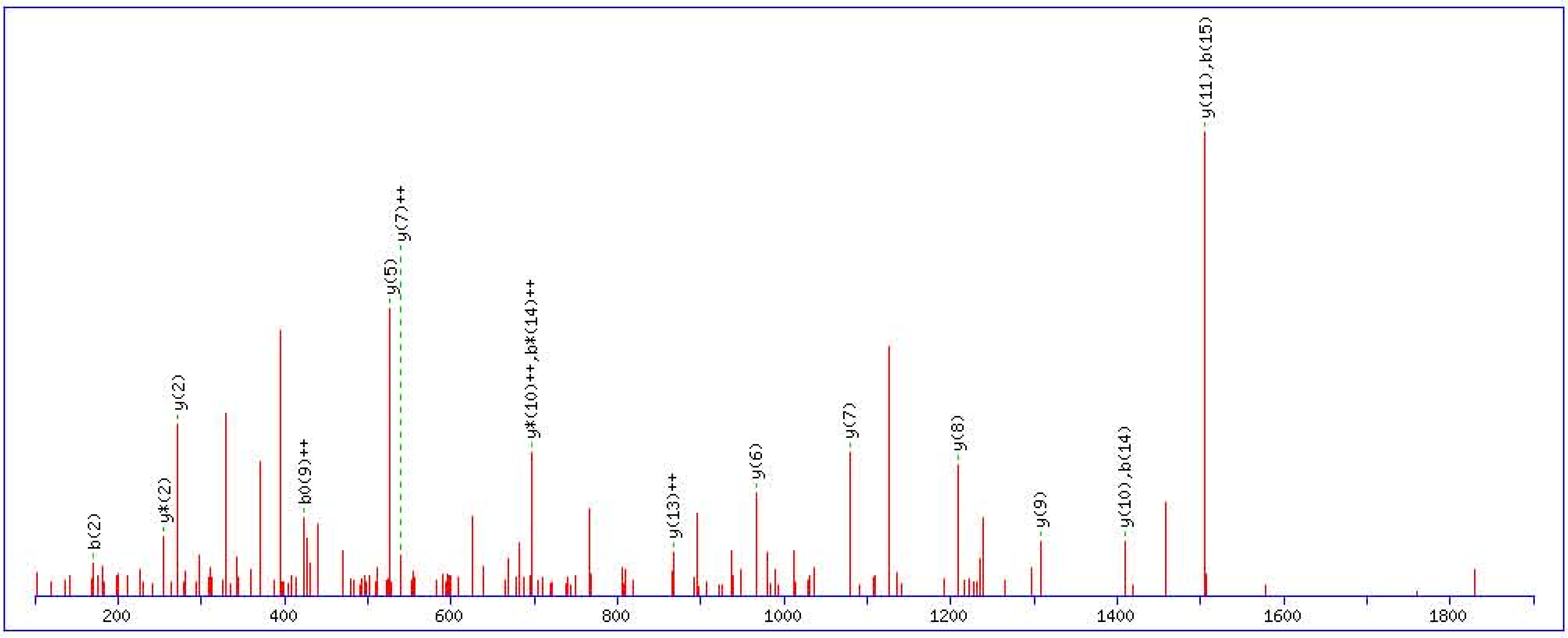
Mascot Search Results

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

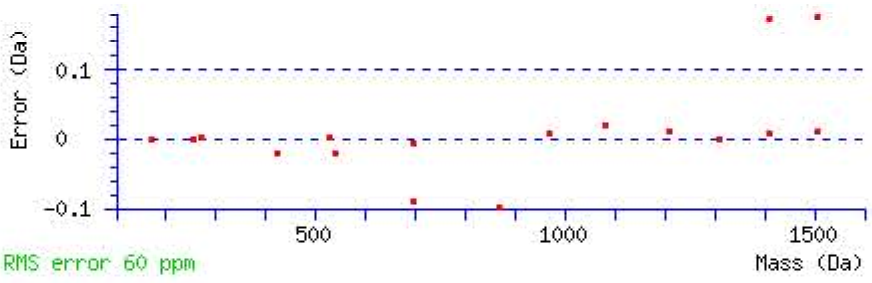
Match to Query 53101: 2912.458896 from(729.122000,4+) rtinseconds(2566) index(63593)
Title: Locus:1.1.1.1805.2 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

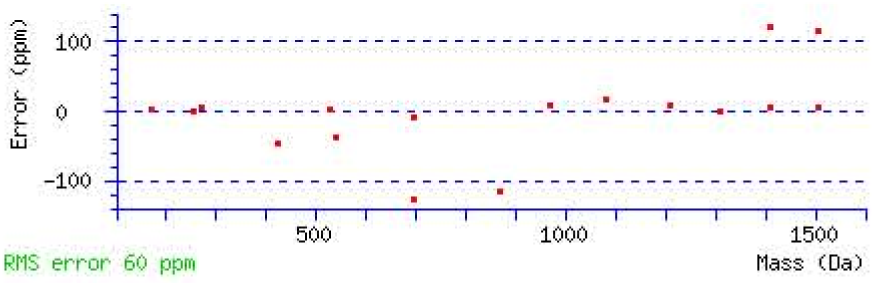
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2912.470200
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20     : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.037
Matches : 17/254 fragment ions using 32 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
29.2	2912.470200	-0.011304	AVPPNNSNAAEDDLPTVELQGVVPR

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

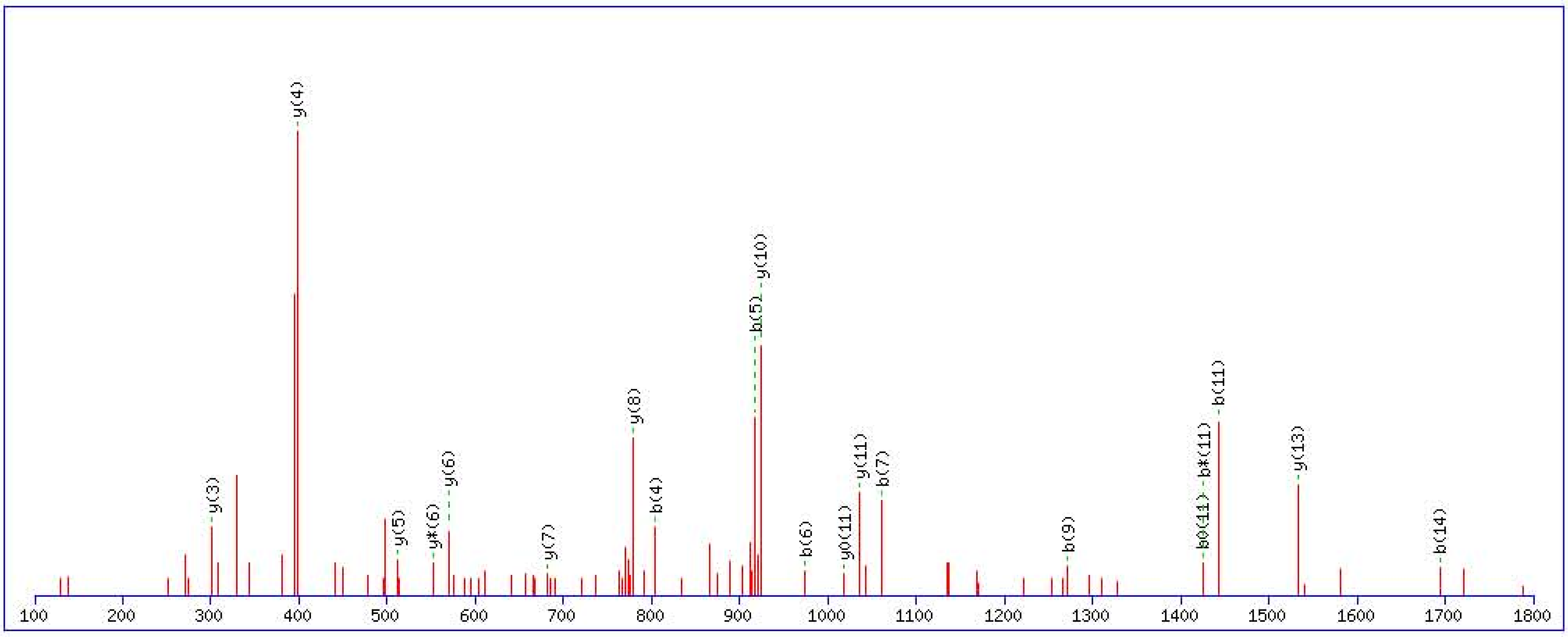
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FCGQLGSPLGNPPGK**
Found in **C1R_HUMAN**, Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2

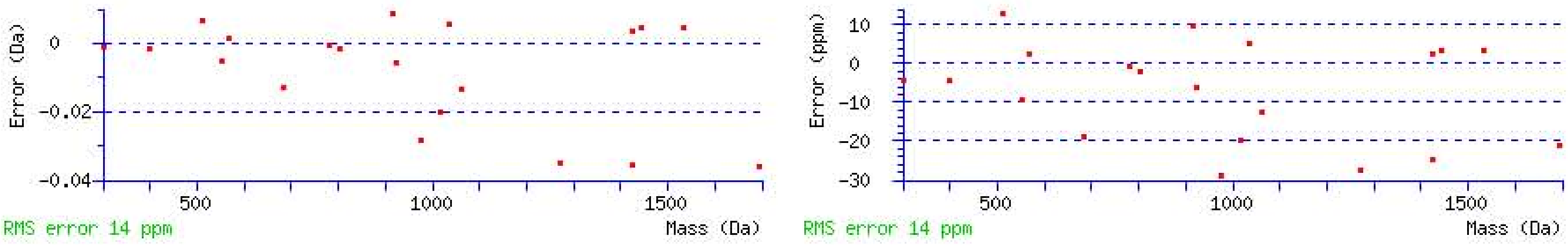
Match to Query 36428: 1838.907788 from(920.461170,2+) rtinseconds(2120) index(46717)
Title: Locus:1.1.1.3450.20 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 1838.917160
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 62 **Expect:** 2.2e-006
Matches : 20/134 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	148.075690	74.541483					F							15
2	308.106339	154.556807					C	1692.856010	846.931643	1675.829461	838.418369	1674.845445	837.926360	14
3	365.127803	183.067539					G	***1532.825361***	766.916318	1515.798812	758.403044	1514.814796	757.911036	13
4	***804.353129***	402.680203	787.326580	394.166928			Q	1475.803897	738.405587	1458.777348	729.892312	1457.793332	729.400304	12
5	***917.437193***	459.222235	900.410644	450.708960			L	***1036.578571***	518.792924	1019.552022	510.279649	1018.568006	509.787641	11
6	***974.458657***	487.732967	957.432108	479.219692			G	***923.494507***	462.250892	906.467958	453.737617	905.483942	453.245609	10
7	***1061.490685***	531.248981	1044.464136	522.735706	1043.480120	522.243698	S	866.473043	433.740160	849.446494	425.226885	848.462478	424.734877	9
8	1158.543449	579.775363	1141.516900	571.262088	1140.532884	570.770080	P	***779.441015***	390.224145	762.414466	381.710871			8
9	***1271.627513***	636.317395	1254.600964	627.804120	1253.616948	627.312112	L	***682.388251***	341.697763	665.361702	333.184489			7
10	1328.648977	664.828127	1311.622428	656.314852	1310.638412	655.822844	G	***569.304187***	285.155732	552.277638	276.642457			6
11	***1442.691904***	721.849590	1425.665355	713.336316	1424.681339	712.844308	N	***512.282723***	256.645000	495.256174	248.131725			5
12	1539.744668	770.375972	1522.718119	761.862698	1521.734103	761.370690	P	***398.239796***	199.623536	381.213247	191.110261			4
13	1636.797432	818.902354	1619.770883	810.389080	1618.786867	809.897072	P	***301.187032***	151.097154	284.160483	142.583879			3
14	***1693.818896***	847.413086	1676.792347	838.899812	1675.808331	838.407804	G	204.134268	102.570772	187.107719	94.057497			2
15							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.5	1838.917160	-0.009372	FCGQLGSPLGNPPGK
1.2	1838.905029	0.002759	EEFIERIQGLDFDTK

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

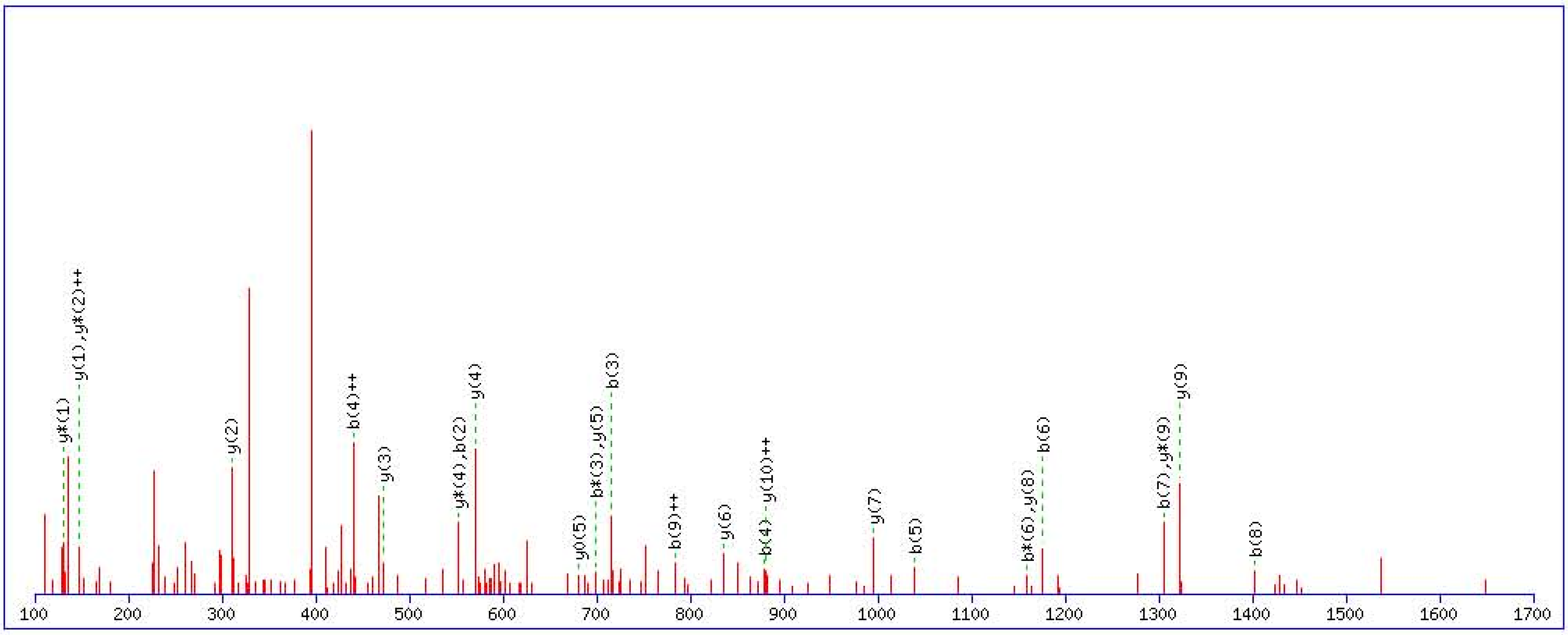
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQYYCHEPYYK**
Found in **C1R_HUMAN**, Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2

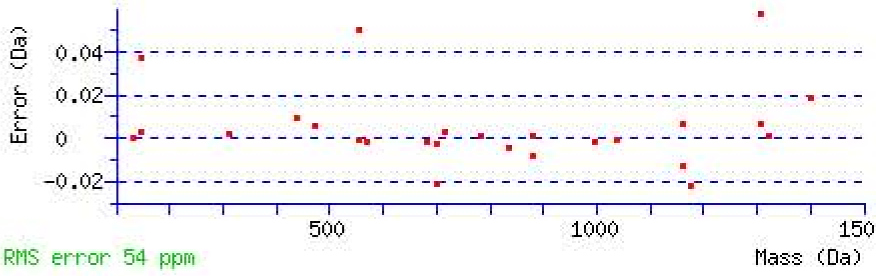
Match to Query 37105: 1873.850382 from(625.624070,3+) rtinseconds(1725) index(30111)
Title: Locus:1.1.1.3264.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

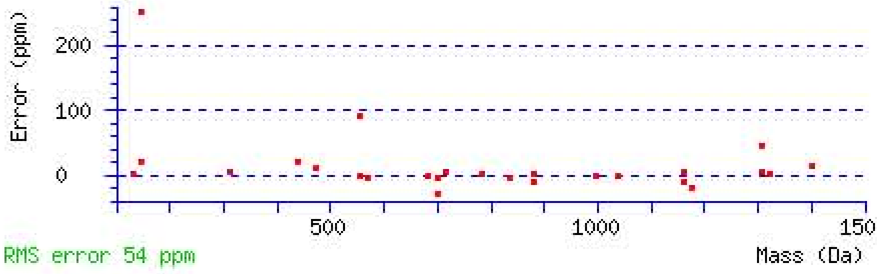
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1873.853119
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.029
Matches : 26/98 fragment ions using 66 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	**553.316666**	277.161971	536.290117	268.648697			**Q**	1761.776364	881.391820	1744.749815	872.878546	1743.765799	872.386538	**10**
3	**716.379995**	358.693636	699.353446	350.180361			**Y**	***1322.551038***	661.779157	1305.524489	653.265883	1304.540473	652.773875	**9**
4	**879.443324**	**440.225300**	862.416775	431.712026			**Y**	***1159.487709***	580.247493	1142.461160	571.734218	1141.477144	571.242210	**8**
5	**1039.473973**	520.240625	1022.447424	511.727350			**C**	***996.424380***	498.715828	979.397831	490.202554	978.413815	489.710546	**7**
6	**1176.532885**	588.770081	1159.506336	580.256806			**H**	***836.393731***	418.700504	819.367182	410.187229	818.383166	409.695221	**6**
7	**1305.575478**	653.291377	1288.548929	644.778103	1287.564913	644.286094	**E**	***699.334819***	350.171048	682.308270	341.657773	681.324254	341.165765	**5**
8	**1402.628242**	701.817759	1385.601693	693.304485	1384.617677	692.812477	**P**	***570.292226***	285.649751	553.265677	277.136477			**4**
9	1565.691571	**783.349424**	1548.665022	774.836149	1547.681006	774.344141	**Y**	***473.239462***	237.123369	456.212913	228.610095			**3**
10	1728.754900	864.881088	1711.728351	856.367814	1710.744335	855.875806	**Y**	***310.176133***	155.591705	293.149584	147.078430			**2**
11							**K**	***147.112804***	74.060040	130.086255	65.546765			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.7	1873.853119	-0.002737	IQYYCHEPYYK

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

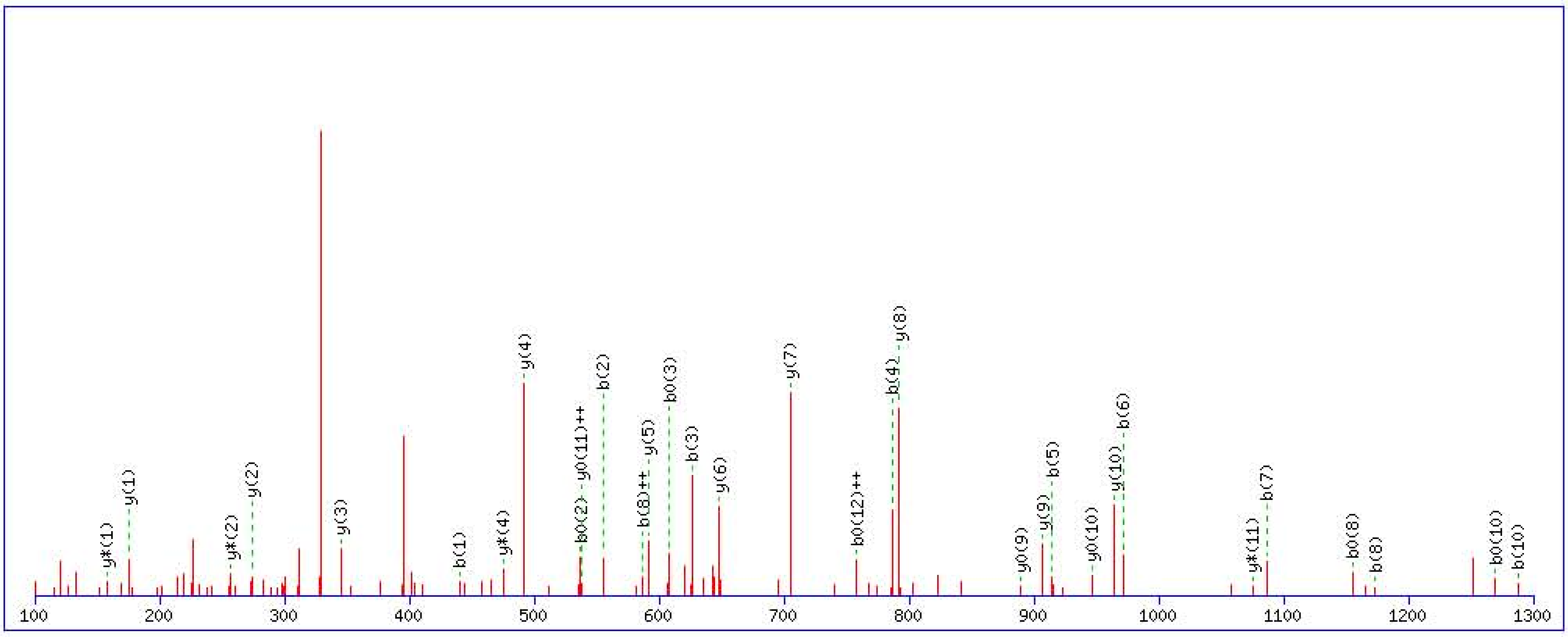
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QDACQGDSGGVFAVR**
Found in **C1R_HUMAN**, Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2

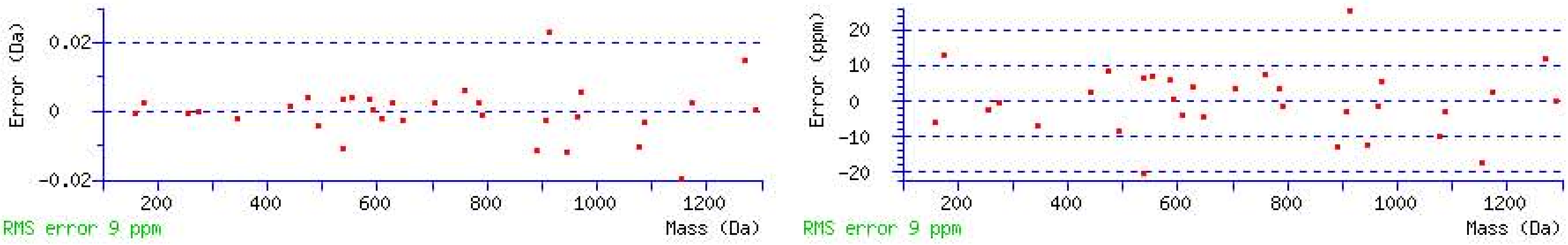
Match to Query 37141: 1876.849182 from(626.623670,3+) rtinseconds(1969) index(31619)
Title: Locus:1.1.1.3349.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 1876.856033
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 73  Expect: 4.4e-007
Matches : 32/152 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	***440.232602***	220.619939	423.206053	212.106664			Q							15
2	***555.259545***	278.133411	538.232996	269.620136	537.248980	269.128128	D	1438.637955	719.822616	1421.611406	711.309341	1420.627390	710.817333	14
3	***626.296659***	313.651968	609.270110	305.138693	608.286094	304.646685	A	1323.611012	662.309144	1306.584463	653.795870	1305.600447	653.303862	13
4	***786.327308***	393.667292	769.300759	385.154018	768.316743	384.662010	C	1252.573898	626.790587	1235.547349	618.277313	1234.563333	617.785305	12
5	***914.385886***	457.696581	897.359337	449.183307	896.375321	448.691299	Q	1092.543249	546.775263	1075.516700	538.261988	1074.532684	537.769980	11
6	***971.407350***	486.207313	954.380801	477.694039	953.396785	477.202031	G	***964.484671***	482.745974	947.458122	474.232699	946.474106	473.740691	10
7	***1086.434293***	543.720785	1069.407744	535.207510	1068.423728	534.715502	D	***907.463207***	454.235242	890.436658	445.721967	889.452642	445.229959	9
8	***1173.466321***	587.236799	1156.439772	578.723524	1155.455756	578.231516	S	***792.436264***	396.721770	775.409715	388.208496	774.425699	387.716488	8
9	1230.487785	615.747531	1213.461236	607.234256	1212.477220	606.742248	G	***705.404236***	353.205756	688.377687	344.692482			7
10	***1287.509249***	644.258263	1270.482700	635.744988	1269.498684	635.252980	G	***648.382772***	324.695024	631.356223	316.181750			6
11	1386.577663	693.792470	1369.551114	685.279195	1368.567098	684.787187	V	***591.361308***	296.184292	574.334759	287.671018			5
12	1533.646077	767.326677	1516.619528	758.813402	1515.635512	758.321394	F	***492.292894***	246.650085	475.266345	238.136811			4
13	1604.683191	802.845234	1587.656642	794.331959	1586.672626	793.839951	A	***345.224480***	173.115878	328.197931	164.602603			3
14	1703.751605	852.379441	1686.725056	843.866166	1685.741040	843.374158	V	***274.187366***	137.597321	257.160817	129.084047			2
15							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
73.2	1876.856033	-0.006851	QDACQGDSGGVFAVR
50.0	1876.856033	-0.006851	QDACQGDSGGVFAVR

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

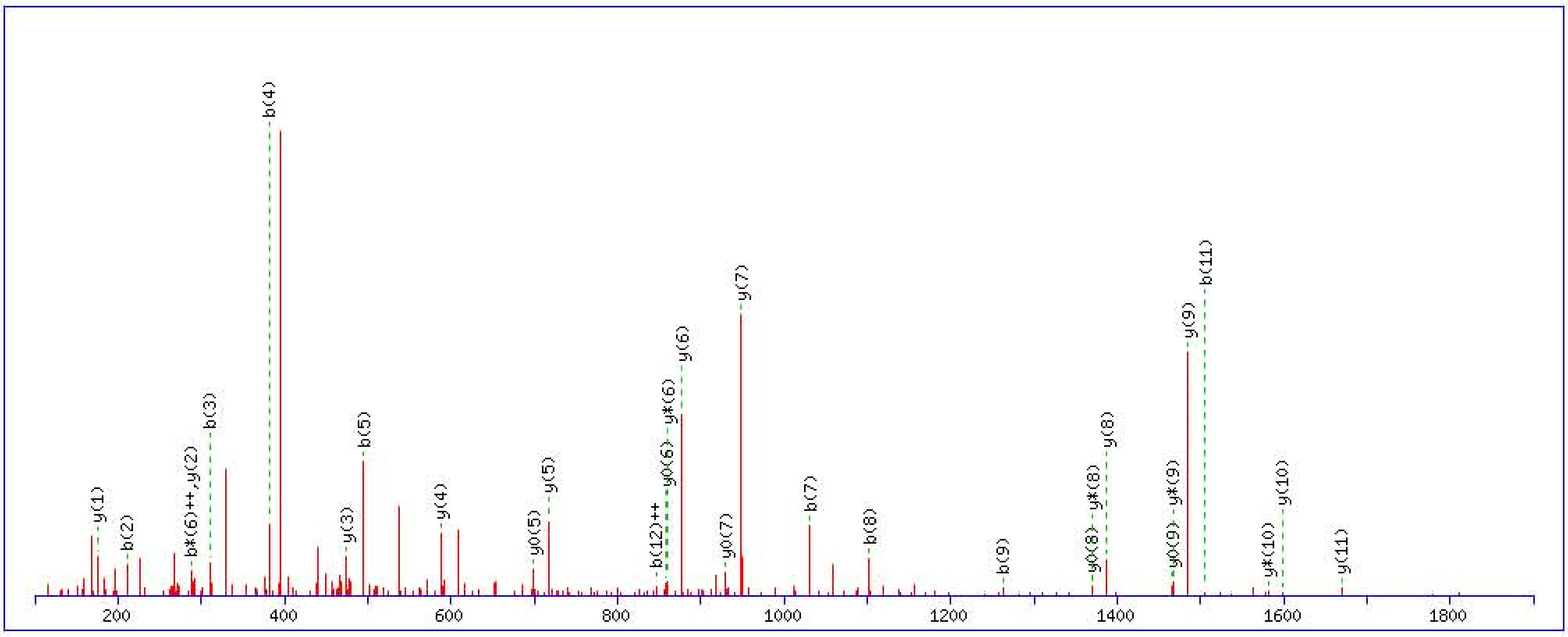
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPVANPQACENWLR**
Found in **C1R_HUMAN**, Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2

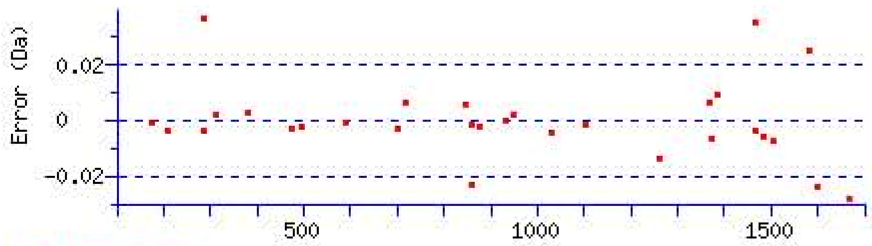
Match to Query 38926: 1977.986112 from(660.335980,3+) rtinseconds(2299) index(33607)
Title: Locus:1.1.1.3464.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

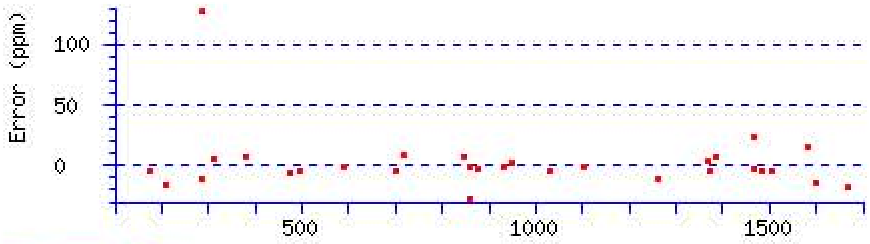


```
Monoisotopic mass of neutral peptide Mr(calc): 1977.991684
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 0.0001
Matches : 30/122 fragment ions using 63 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							14
2	**211.144104**	106.075690					P	1865.914921	933.461099	1848.888372	924.947824	1847.904356	924.455816	13
3	**310.212518**	155.609897					V	1768.862157	884.934717	1751.835608	876.421442	1750.851592	875.929434	12
4	**381.249632**	191.128454					A	***1669.793743***	835.400510	1652.767194	826.887235	1651.783178	826.395227	11
5	**495.292559**	248.149917	478.266010	239.636643			N	***1598.756629***	799.881953	1581.730080	791.368678	1580.746064	790.876670	10
6	592.345323	296.676300	575.318774	288.163025			P	***1484.713702***	742.860489	1467.687153	734.347215	1466.703137	733.855207	9
7	**1031.570649**	516.288963	1014.544100	507.775688			Q	***1387.660938***	694.334107	1370.634389	685.820833	1369.650373	685.328825	8
8	**1102.607763**	551.807520	1085.581214	543.294245			A	***948.435612***	474.721444	931.409063	466.208170	930.425047	465.716162	7
9	**1262.638412**	631.822844	1245.611863	623.309570			C	***877.398498***	439.202887	860.371949	430.689613	859.387933	430.197605	6
10	1391.681005	696.344141	1374.654456	687.830866	1373.670440	687.338858	E	***717.367849***	359.187563	700.341300	350.674288	699.357284	350.182280	5
11	**1505.723932**	753.365604	1488.697383	744.852330	1487.713367	744.360322	N	***588.325256***	294.666266	571.298707	286.152991			4
12	1691.803245	846.405261	1674.776696	837.891986	1673.792680	837.399978	W	***474.282329***	237.644802	457.255780	229.131528			3
13	1804.887309	902.947293	1787.860760	894.434018	1786.876744	893.942010	L	***288.203016***	144.605146	271.176467	136.091871			2
14							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 25 ppm



RMS error 25 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.7	1977.991684	-0.005572	LPVANPQACENWLR
10.0	1977.983856	0.002256	VLGKGGFGEVSACQMK

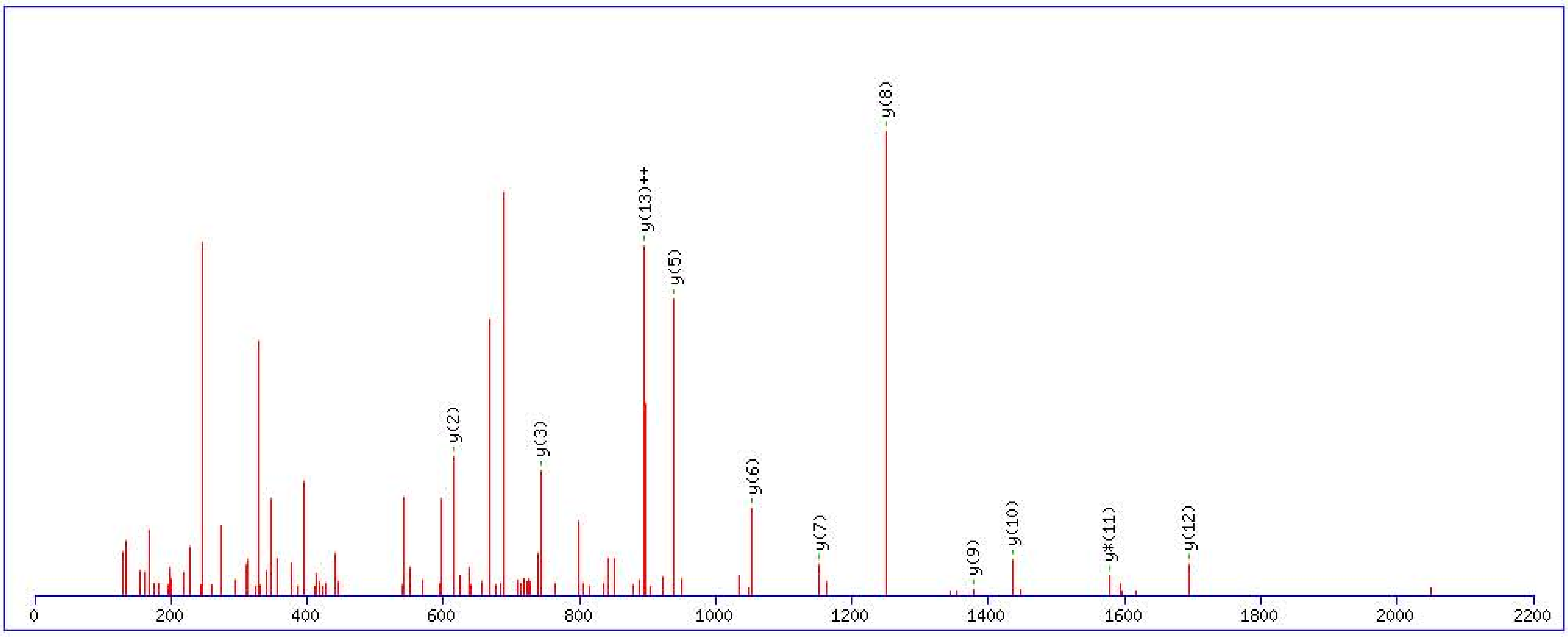
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CLPVCGKPVNPVEQR**
Found in **C1R_HUMAN**, Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2

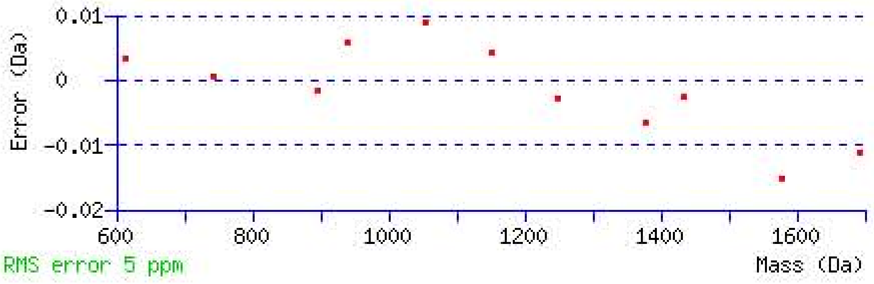
Match to Query 41099: 2063.047032 from(688.689620,3+) rtinseconds(1805) index(44784)
Title: Locus:1.1.1.3341.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

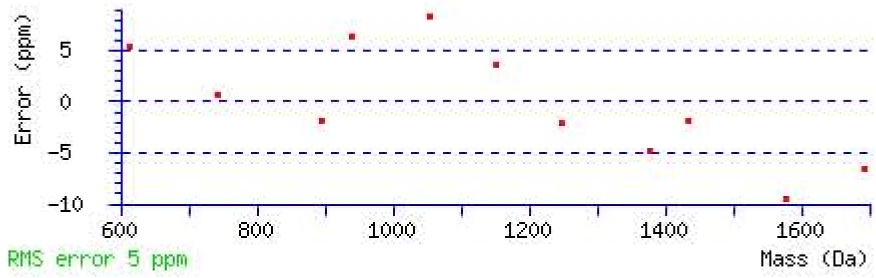
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2063.047852
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Biotin:Thermo-21345 (Q)
Ions Score: 59 **Expect:** 4.4e-006
Matches : 11/128 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	161.037925	81.022600					C							15
2	274.121989	137.564632					L	1904.024472	952.515874	1886.997923	944.002600	1886.013907	943.510592	14
3	371.174753	186.091014					P	1790.940408	895.973842	1773.913859	887.460568	1772.929843	886.968560	13
4	470.243167	235.625221					V	***1693.887644***	847.447460	1676.861095	838.934186	1675.877079	838.442178	12
5	630.273816	315.640546					C	1594.819230	797.913253	1577.792681	789.399979	1576.808665	788.907971	11
6	687.295280	344.151278					G	***1434.788581***	717.897929	1417.762032	709.384654	1416.778016	708.892646	10
7	815.390243	408.198760	798.363694	399.685485			K	***1377.767117***	689.387197	1360.740568	680.873922	1359.756552	680.381914	9
8	912.443007	456.725142	895.416458	448.211867			P	***1249.672154***	625.339715	1232.645605	616.826441	1231.661589	616.334433	8
9	1011.511421	506.259349	994.484872	497.746074			V	***1152.619390***	576.813333	1135.592841	568.300059	1134.608825	567.808051	7
10	1125.554348	563.280812	1108.527799	554.767538			N	***1053.550976***	527.279126	1036.524427	518.765852	1035.540411	518.273844	6
11	1222.607112	611.807194	1205.580563	603.293920			P	***939.508049***	470.257663	922.481500	461.744388	921.497484	461.252380	5
12	1321.675526	661.341401	1304.648977	652.828127			V	842.455285	421.731281	825.428736	413.218006	824.444720	412.725998	4
13	1450.718119	725.862698	1433.691570	717.349423	1432.707554	716.857415	E	***743.386871***	372.197074	726.360322	363.683799	725.376306	363.191791	3
14	1889.943445	945.475361	1872.916896	936.962086	1871.932880	936.470078	Q	***614.344278***	307.675777	597.317729	299.162503			2
15							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.2	2063.047852	-0.000820	CLPVCGKPVNPVEQR
2.0	2063.029678	0.017354	SYSFVLTNRGNSAGGLQHR
1.0	2063.077286	-0.030254	SLQQVDEHSKPPHLRHR

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

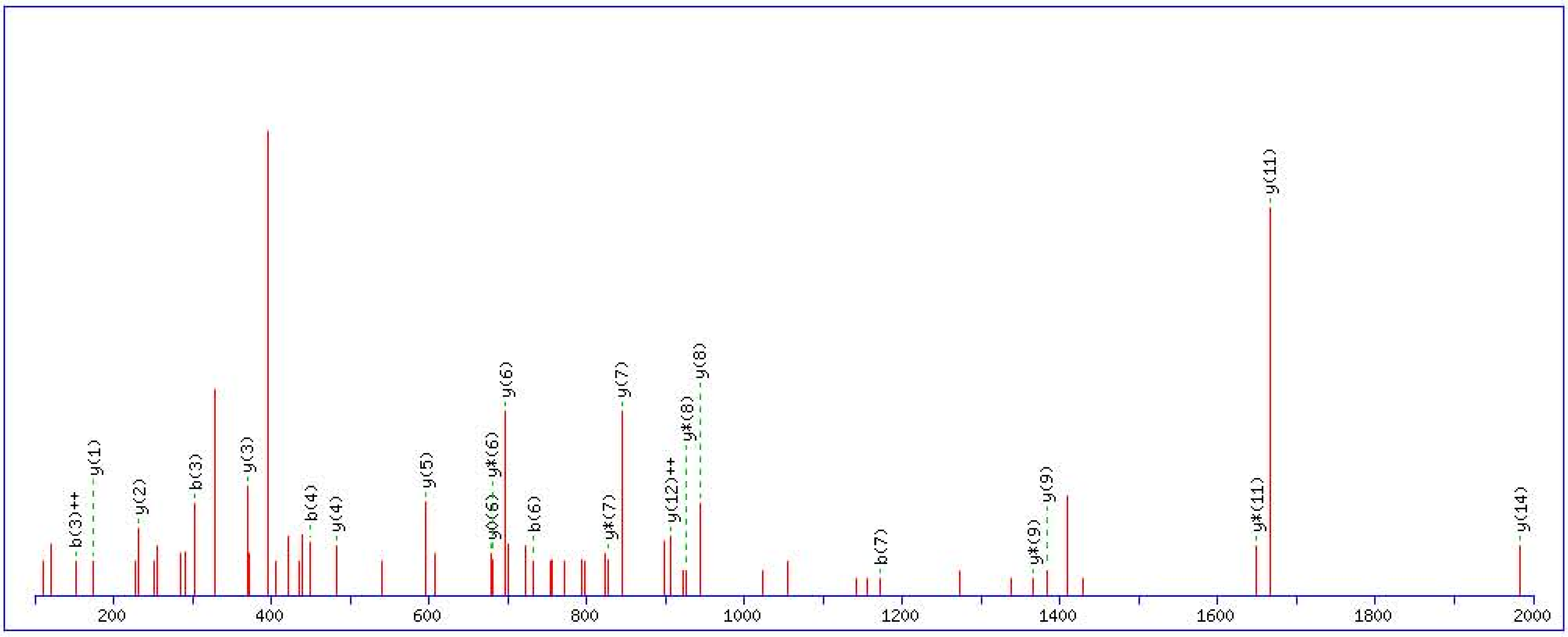
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MGNFPWQVFTNIHGR**
Found in **C1R_HUMAN**, Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2

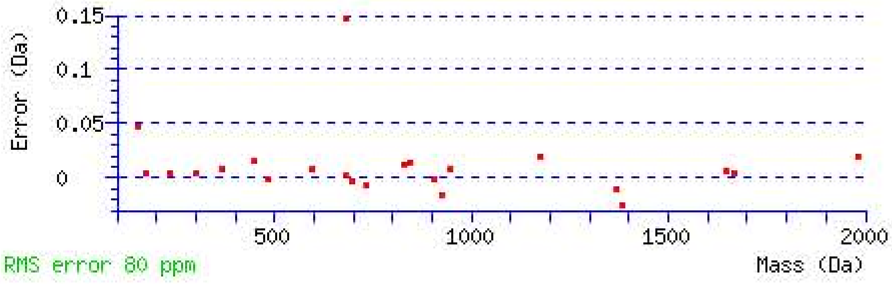
Match to Query 41797: 2114.043912 from(705.688580,3+) rtinseconds(2684) index(49929)
Title: Locus:1.1.1.3646.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

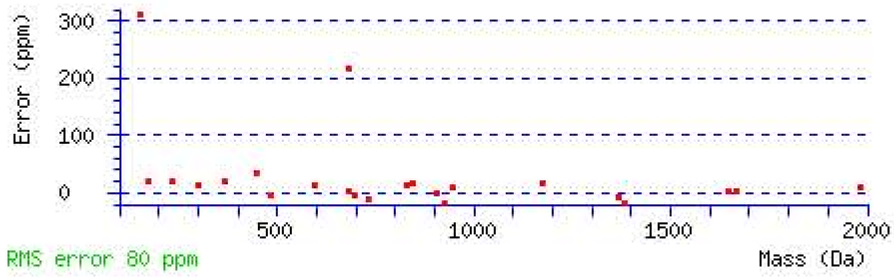
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2114.034256
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00063
Matches : 23/136 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	132.047761	66.527518					M							15
2	189.069225	95.038250					G	***1984.001034***	992.504155	1966.974485	983.990881	1965.990469	983.498873	14
3	**303.112152**	152.059714	286.085603	143.546439			N	1926.979570	963.993423	1909.953021	955.480149	1908.969005	954.988141	13
4	**450.180566**	225.593921	433.154017	217.080646			F	1812.936643	906.971960	1795.910094	898.458685	1794.926078	897.966677	12
5	547.233330	274.120303	530.206781	265.607029			P	***1665.868229***	833.437753	1648.841680	824.924478	1647.857664	824.432470	11
6	**733.312643**	367.159960	716.286094	358.646685			W	1568.815465	784.911371	1551.788916	776.398096	1550.804900	775.906088	10
7	**1172.537969**	586.772623	1155.511420	578.259348			Q	***1382.736152***	691.871714	1365.709603	683.358440	1364.725587	682.866432	9
8	1271.606383	636.306830	1254.579834	627.793555			V	***943.510826***	472.259051	926.484277	463.745777	925.500261	463.253769	8
9	1418.674797	709.841037	1401.648248	701.327762			F	***844.442412***	422.724844	827.415863	414.211570	826.431847	413.719562	7
10	1519.722476	760.364876	1502.695927	751.851602	1501.711911	751.359594	T	***697.373998***	349.190637	680.347449	340.677363	679.363433	340.185355	6
11	1633.765403	817.386340	1616.738854	808.873065	1615.754838	808.381057	N	***596.326319***	298.666798	579.299770	290.153523			5
12	1746.849467	873.928372	1729.822918	865.415097	1728.838902	864.923089	I	***482.283392***	241.645334	465.256843	233.132059			4
13	1883.908379	942.457828	1866.881830	933.944553	1865.897814	933.452545	H	***369.199328***	185.103302	352.172779	176.590028			3
14	1940.929843	970.968559	1923.903294	962.455285	1922.919278	961.963277	G	***232.140416***	116.573846	215.113867	108.060572			2
15							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.1	2114.034256	0.009656	MGNFPWQVFTNIHGR

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

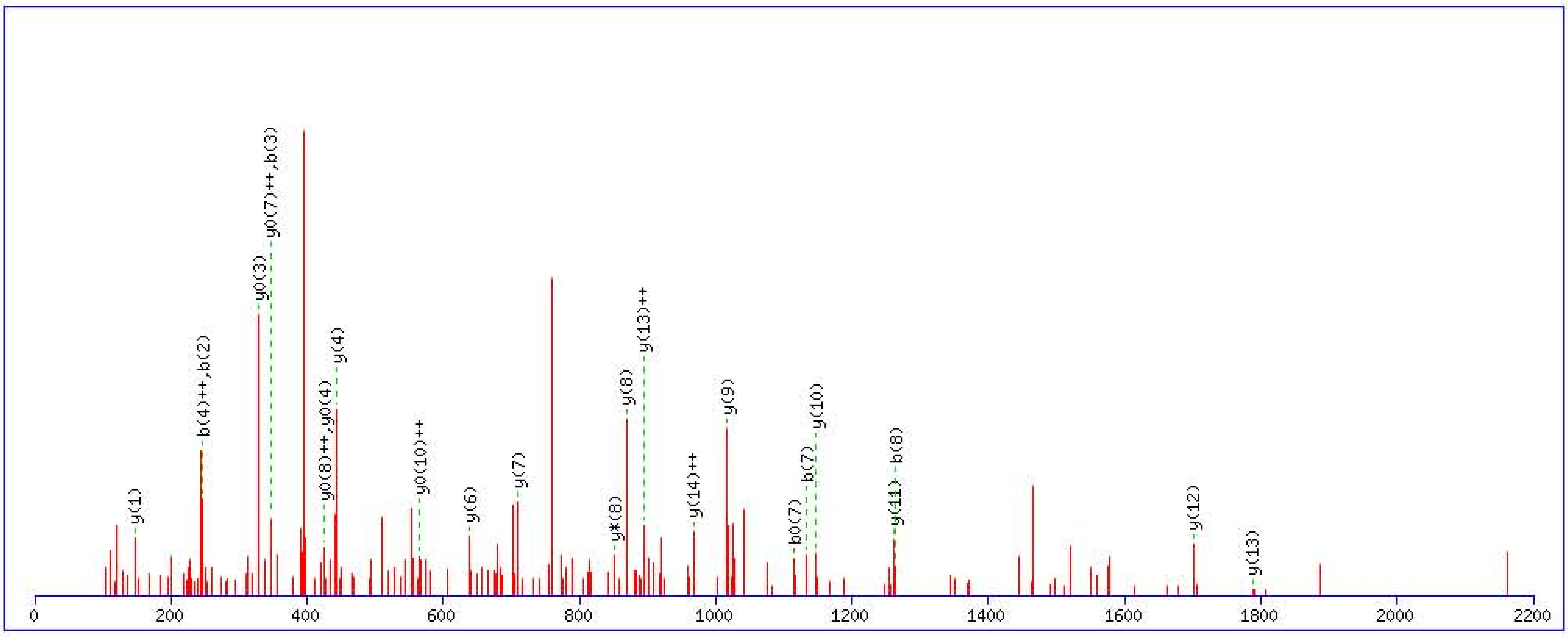
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MDVFSQNMFCAGHPSLK**
Found in **C1R_HUMAN**, Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2

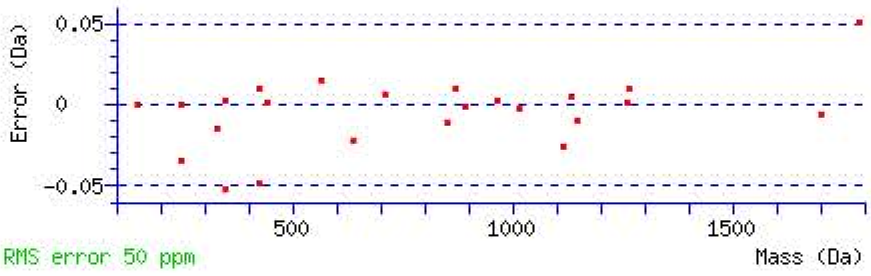
Match to Query 44709: 2279.034012 from(760.685280,3+) rtinseconds(2379) index(33962)
Title: Locus:1.1.1.3492.6 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

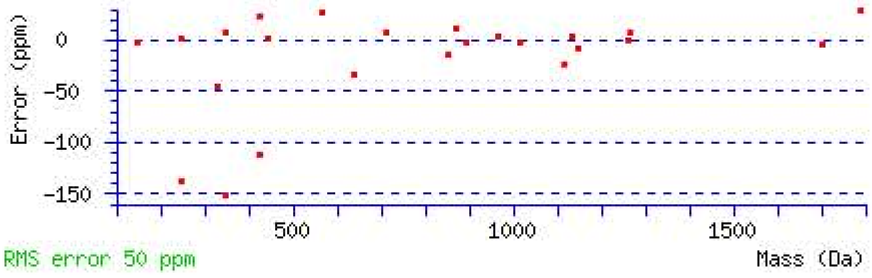
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2279.035965
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0006
Matches : 24/176 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	**247.074704**	124.040990			229.064139	115.035708	D	2149.002750	1075.005013	2131.976201	1066.491738	2130.992185	1065.999730	16
3	**346.143118**	173.575197			328.132553	164.569915	V	2033.975807	1017.491542	2016.949258	1008.978267	2015.965242	1008.486259	15
4	493.211532	247.109404			475.200967	238.104121	F	1934.907393	967.957335	1917.880844	959.444060	1916.896828	958.952052	14
5	580.243560	290.625418			562.232995	281.620136	S	***1787.838979***	894.423128	1770.812430	885.909853	1769.828414	885.417845	13
6	1019.468886	510.238081	1002.442337	501.724807	1001.458321	501.232799	Q	***1700.806951***	850.907114	1683.780402	842.393839	1682.796386	841.901831	12
7	**1133.511813**	567.259545	1116.485264	558.746270	1115.501248	558.254262	N	***1261.581625***	631.294451	1244.555076	622.781176	1243.571060	622.289168	11
8	**1264.552298**	632.779787	1247.525749	624.266513	1246.541733	623.774505	M	***1147.538698***	574.272987	1130.512149	565.759713	1129.528133	565.267705	10
9	1411.620712	706.313994	1394.594163	697.800720	1393.610147	697.308712	F	***1016.498213***	508.752745	999.471664	500.239470	998.487648	499.747462	9
10	1571.651361	786.329319	1554.624812	777.816044	1553.640796	777.324036	C	***869.429799***	435.218538	852.403250	426.705263	851.419234	426.213255	8
11	1642.688475	821.847876	1625.661926	813.334601	1624.677910	812.842593	A	***709.399150***	355.203213	692.372601	346.689939	691.388585	346.197931	7
12	1699.709939	850.358608	1682.683390	841.845333	1681.699374	841.353325	G	***638.362036***	319.684656	621.335487	311.171382	620.351471	310.679374	6
13	1836.768851	918.888064	1819.742302	910.374789	1818.758286	909.882781	H	581.340572	291.173924	564.314023	282.660650	563.330007	282.168642	5
14	1933.821615	967.414446	1916.795066	958.901171	1915.811050	958.409163	P	***444.281660***	222.644468	427.255111	214.131194	426.271095	213.639186	4
15	2020.853643	1010.930460	2003.827094	1002.417185	2002.843078	1001.925177	S	347.228896	174.118086	330.202347	165.604812	329.218331	165.112804	3
16	2133.937707	1067.472491	2116.911158	1058.959217	2115.927142	1058.467209	L	260.196868	130.602072	243.170319	122.088798			2
17							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.7	2279.035965	-0.001953	MDVFSQNMFCAGHPSLK
2.3	2279.029694	0.004318	DMLMEGTEEVEAELPDSRTK

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

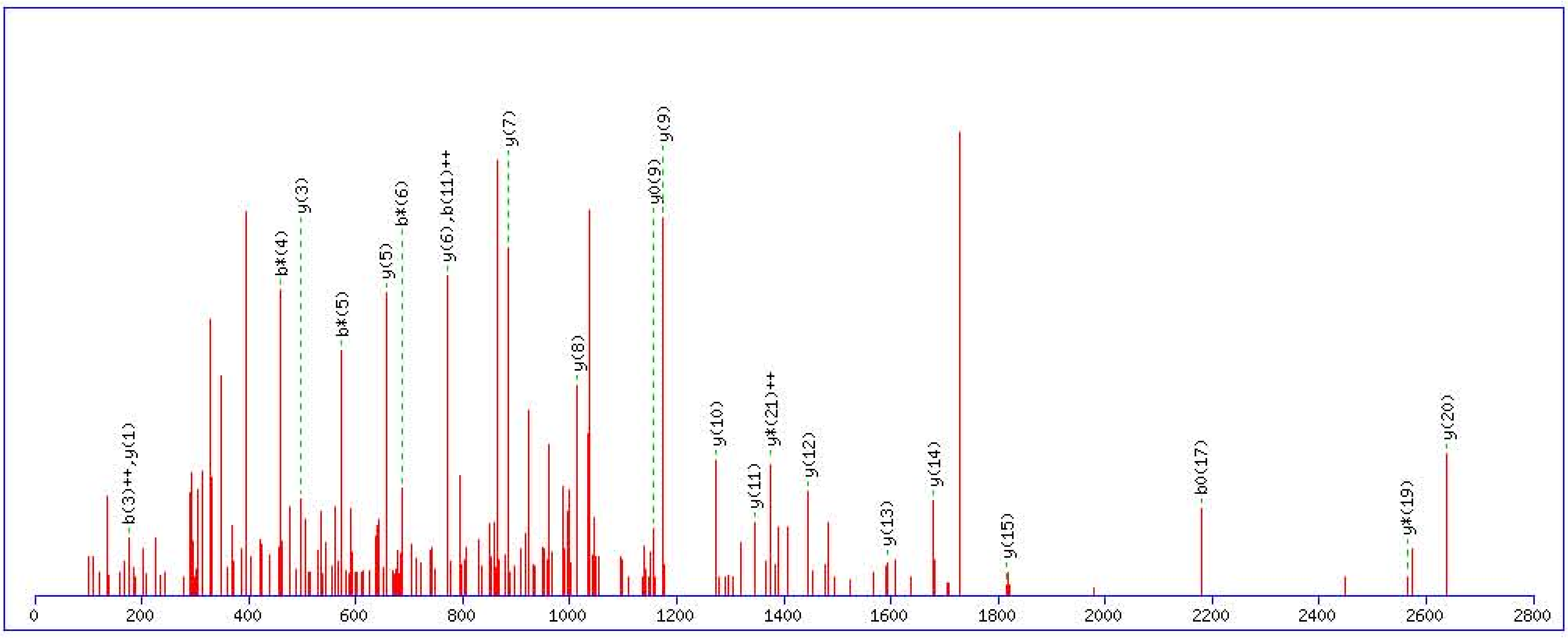
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QGYQLIEGNQVLHSFTAVCQDDGTWHR**
Found in **C1R_HUMAN**, Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2

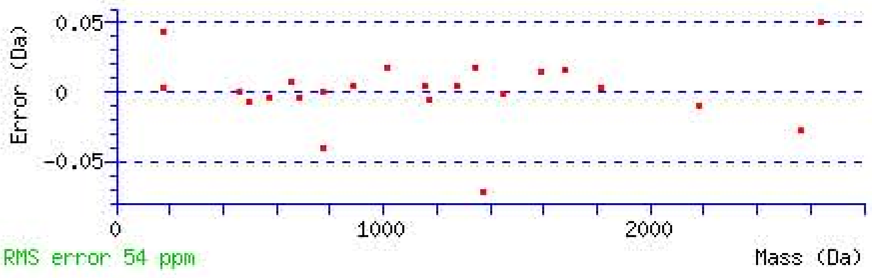
Match to Query 59289: 3469.626256 from(868.413840,4+) rtinseconds(2472) index(34385)
Title: Locus:1.1.1.3524.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

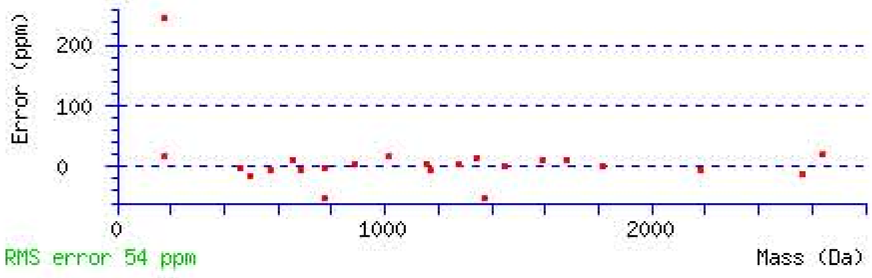
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3469.629608
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 4.8e-006
Matches : 23/294 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	129.065854	65.036565	112.039305	56.523291			Q							27
2	186.087318	93.547297	169.060769	85.034023			G	3342.578281	1671.792778	3325.551732	1663.279504	3324.567716	1662.787496	26
3	349.150647	**175.078961**	332.124098	166.565687			Y	3285.556817	1643.282046	3268.530268	1634.768772	3267.546252	1634.276764	25
4	477.209225	239.108251	460.182676	230.594976			Q	3122.493488	1561.750382	3105.466939	1553.237107	3104.482923	1552.745099	24
5	590.293289	295.650283	573.266740	287.137008			L	2994.434910	1497.721093	2977.408361	1489.207818	2976.424345	1488.715810	23
6	703.377353	352.192315	686.350804	343.679040			I	2881.350846	1441.179061	2864.324297	1432.665786	2863.340281	1432.173778	22
7	832.419946	416.713611	815.393397	408.200337	814.409381	407.708329	E	2768.266782	1384.637029	2751.240233	1376.123754	2750.256217	1375.631746	21
8	889.441410	445.224343	872.414861	436.711069	871.430845	436.219061	G	***2639.224189***	1320.115732	2622.197640	1311.602458	2621.213624	1311.110450	20
9	1003.484337	502.245807	986.457788	493.732532	985.473772	493.240524	N	2582.202725	1291.605000	2565.176176	1283.091726	2564.192160	1282.599718	19
10	1442.709663	721.858470	1425.683114	713.345195	1424.699098	712.853187	Q	2468.159798	1234.583537	2451.133249	1226.070262	2450.149233	1225.578254	18
11	1541.778077	**771.392677**	1524.751528	762.879402	1523.767512	762.387394	V	2028.934472	1014.970874	2011.907923	1006.457599	2010.923907	1005.965591	17
12	1654.862141	827.934709	1637.835592	819.421434	1636.851576	818.929426	L	1929.866058	965.436667	1912.839509	956.923392	1911.855493	956.431384	16
13	1791.921053	896.464165	1774.894504	887.950890	1773.910488	887.458882	H	***1816.781994***	908.894635	1799.755445	900.381360	1798.771429	899.889352	15
14	1878.953081	939.980179	1861.926532	931.466904	1860.942516	930.974896	S	***1679.723082***	840.365179	1662.696533	831.851904	1661.712517	831.359896	14
15	2026.021495	1013.514386	2008.994946	1005.001111	2008.010930	1004.509103	F	***1592.691054***	796.849165	1575.664505	788.335890	1574.680489	787.843882	13
16	2127.069174	1064.038225	2110.042625	1055.524950	2109.058609	1055.032943	T	***1445.622640***	723.314958	1428.596091	714.801683	1427.612075	714.309675	12
17	2198.106288	1099.556782	2181.079739	1091.043508	2180.095723	1090.551500	A	***1344.574961***	672.791118	1327.548412	664.277844	1326.564396	663.785836	11
18	2297.174702	1149.090989	2280.148153	1140.577715	2279.164137	1140.085707	V	***1273.537847***	637.272561	1256.511298	628.759287	1255.527282	628.267279	10
19	2457.205351	1229.106313	2440.178802	1220.593039	2439.194786	1220.101031	C	***1174.469433***	587.738354	1157.442884	579.225080	1156.458868	578.733072	9
20	2585.263929	1293.135603	2568.237380	1284.622328	2567.253364	1284.130320	Q	***1014.438784***	507.723030	997.412235	499.209755	996.428219	498.717747	8
21	2700.290872	1350.649074	2683.264323	1342.135799	2682.280307	1341.643791	D	***886.380206***	443.693741	869.353657	435.180466	868.369641	434.688458	7
22	2815.317815	1408.162545	2798.291266	1399.649271	2797.307250	1399.157263	D	***771.353263***	386.180269	754.326714	377.666995	753.342698	377.174987	6
23	2872.339279	1436.673277	2855.312730	1428.160003	2854.328714	1427.667995	G	***656.326320***	328.666798	639.299771	320.153523	638.315755	319.661515	5
24	2973.386958	1487.197117	2956.360409	1478.683842	2955.376393	1478.191834	T	599.304856	300.156066	582.278307	291.642791	581.294291	291.150783	4
25	3159.466271	1580.236773	3142.439722	1571.723499	3141.455706	1571.231491	W	***498.257177***	249.632227	481.230628	241.118952			3
26	3296.525183	1648.766229	3279.498634	1640.252955	3278.514618	1639.760947	H	312.177864	156.592570	295.151315	148.079295			2
27							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.4	3469.629608	-0.003352	QGYQLIEGNQVLHSFTAVCQDDGTWHR
49.7	3469.629608	-0.003352	QGYQLIEGNQVLHSFTAVCQDDGTWHR
49.6	3469.629608	-0.003352	QGYQLIEGNQVLHSFTAVCQDDGTWHR
8.7	3469.629608	-0.003352	QGYQLIEGNQVLHSFTAVCQDDGTWHR

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

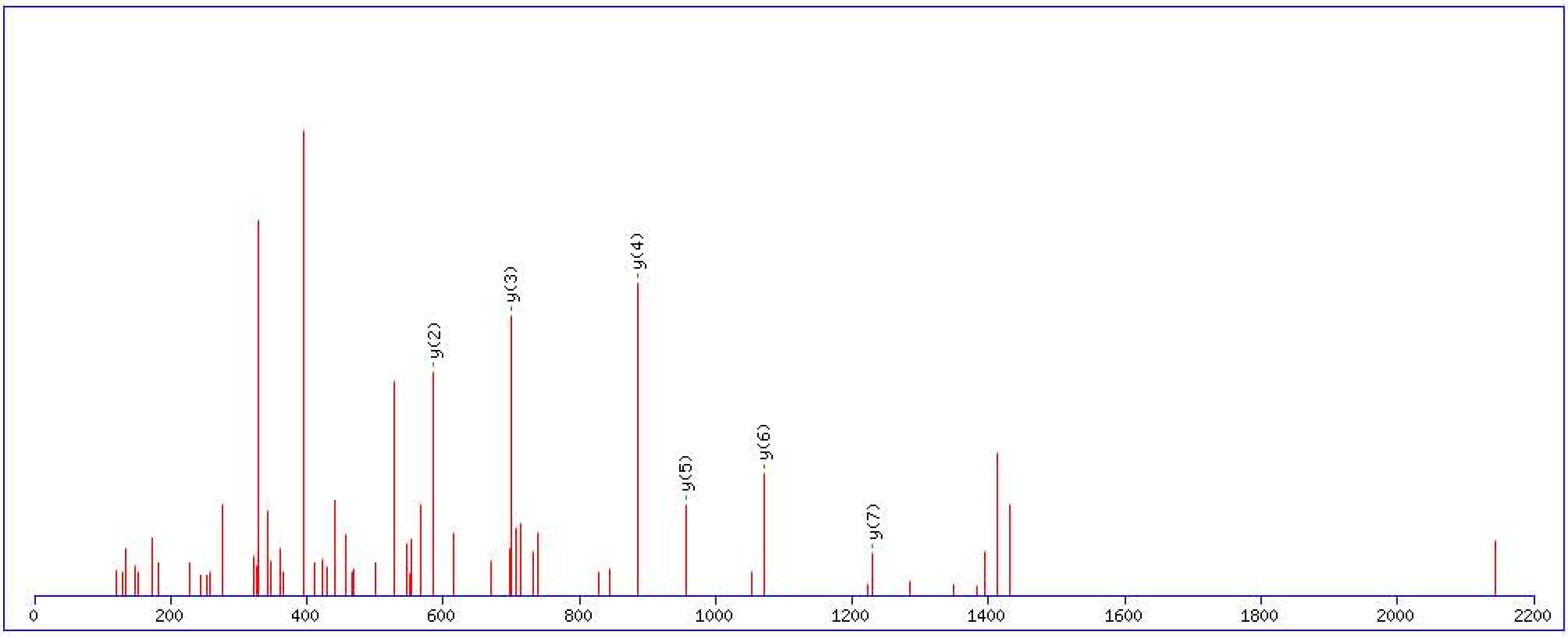
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EACNAWLQK**
Found in **C1RL_HUMAN**, Complement C1r subcomponent-like protein OS=Homo sapiens GN=C1RL PE=1 SV=2

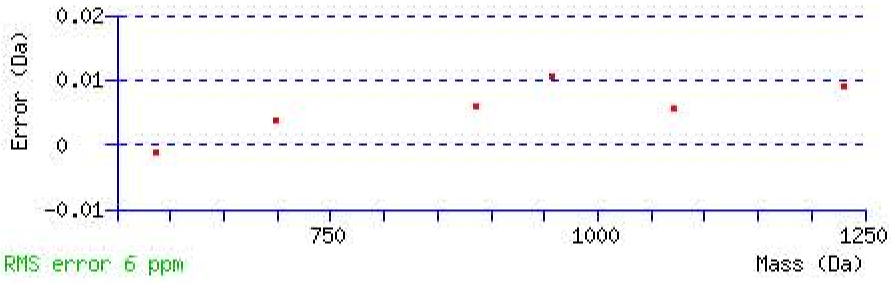
Match to Query 25283: 1429.684808 from(715.849680,2+) rtinseconds(1973) index(60451)
Title: Locus:1.1.1.1598.21 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

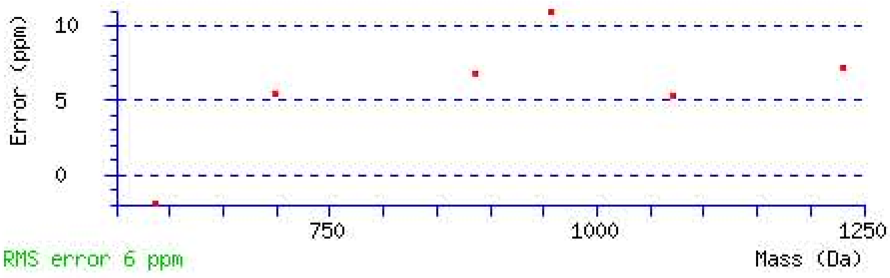
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1429.684601
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.003
Matches : 6/74 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	130.049869	65.528572			112.039304	56.523290	E					9
2	201.086983	101.047130			183.076418	92.041847	A	1301.649311	651.328293	1284.622762	642.815019	8
3	361.117632	181.062454			343.107067	172.057172	C	***1230.612197***	615.809736	1213.585648	607.296462	7
4	475.160559	238.083918	458.134010	229.570643	457.149994	229.078635	N	***1070.581548***	535.794412	1053.554999	527.281138	6
5	546.197673	273.602475	529.171124	265.089200	528.187108	264.597192	A	***956.538621***	478.772948	939.512072	470.259674	5
6	732.276986	366.642131	715.250437	358.128857	714.266421	357.636849	W	***885.501507***	443.254392	868.474958	434.741117	4
7	845.361050	423.184163	828.334501	414.670889	827.350485	414.178881	L	***699.422194***	350.214735	682.395645	341.701461	3
8	1284.586376	642.796826	1267.559827	634.283552	1266.575811	633.791543	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 EACNAWLQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.0	1429.684601	0.000207	EACNAWLQK
14.6	1429.680588	0.004220	MRIHCLENVDK
13.6	1429.687988	-0.003180	CNTPAMGLQK
9.4	1429.679886	0.004922	MDDKELIEYFK
8.5	1429.666016	0.018792	NHGGYVDVMPVDK
7.9	1429.702362	-0.017554	LSNWESQQK
7.6	1429.687103	-0.002295	QSEADNNTLK
6.8	1429.687119	-0.002311	EQHQTMDISLTK
6.5	1429.705734	-0.020926	QEMNTLQQK
6.5	1429.705719	-0.020911	EANALAMQQK

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

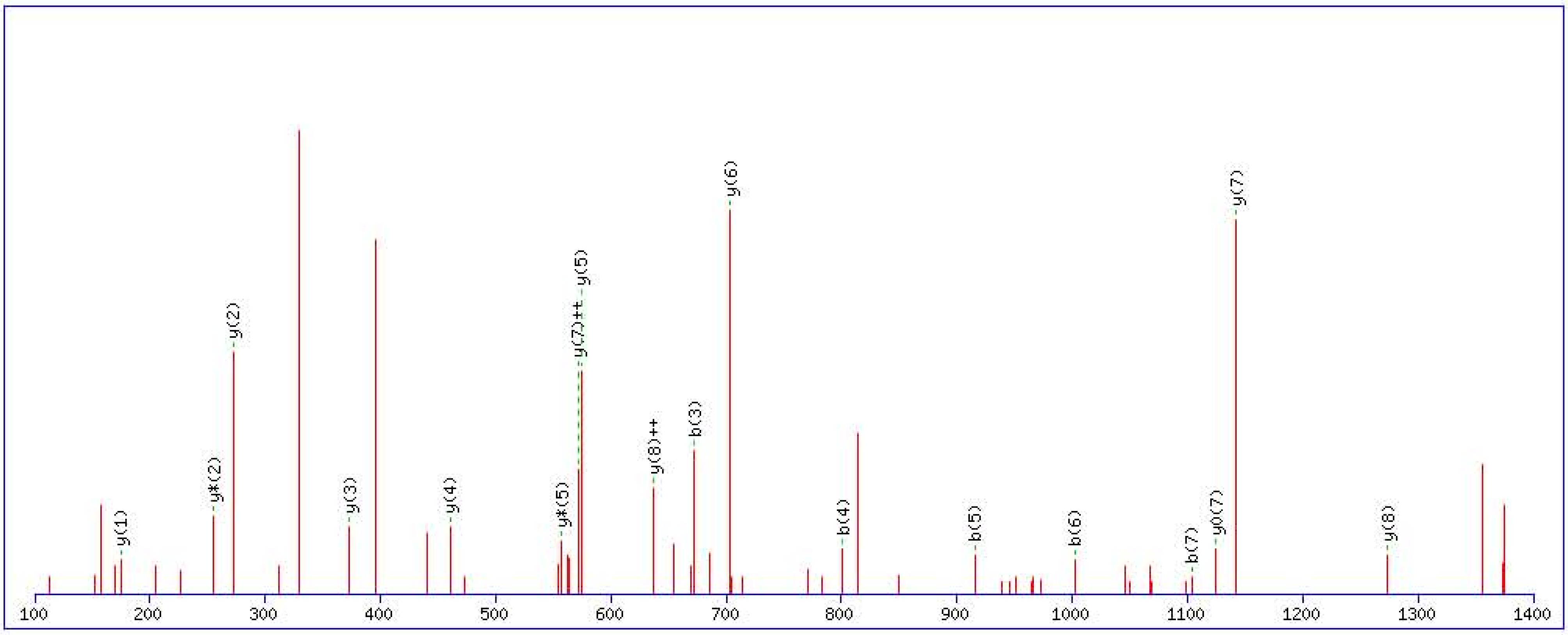
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TMQENSTPR**
Found in **C1S_HUMAN**, Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1

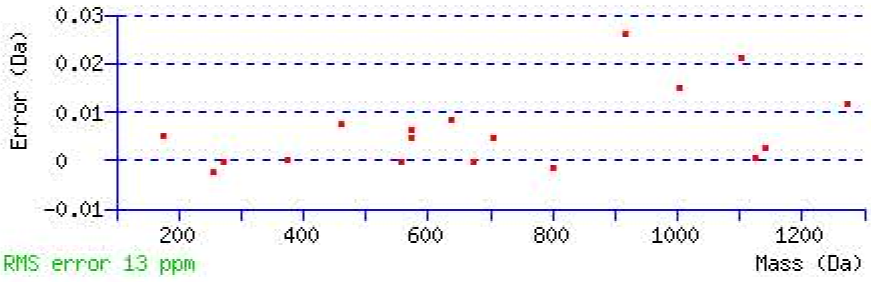
Match to Query 22757: 1373.637288 from(687.825920,2+) rtinseconds(1403) index(28254)
Title: Locus:1.1.1.3151.24 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

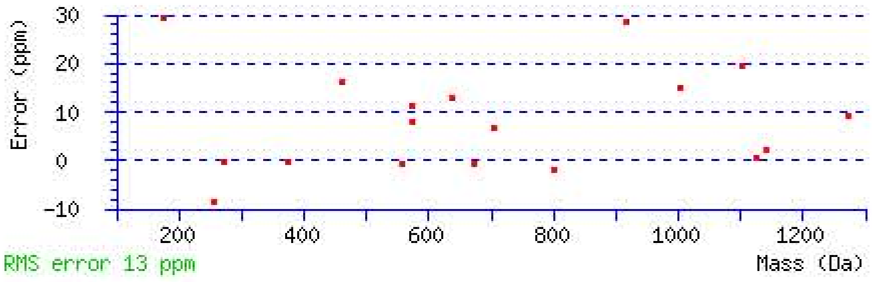
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1373.643143
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 7.8e-005
Matches : 18/88 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	102.054955	51.531116			84.044390	42.525833	T							9
2	233.095440	117.051358			215.084875	108.046076	M	***1273.602754***	637.305015	1256.576205	628.791741	1255.592189	628.299733	8
3	**672.320766**	336.664021	655.294217	328.150747	654.310201	327.658739	Q	***1142.562269***	571.784773	1125.535720	563.271498	1124.551704	562.779490	7
4	**801.363359**	401.185318	784.336810	392.672043	783.352794	392.180035	E	***703.336943***	352.172110	686.310394	343.658835	685.326378	343.166827	6
5	**915.406286**	458.206781	898.379737	449.693507	897.395721	449.201499	N	***574.294350***	287.650813	557.267801	279.137539	556.283785	278.645531	5
6	**1002.438314**	501.722795	985.411765	493.209521	984.427749	492.717513	S	***460.251423***	230.629349	443.224874	222.116075	442.240858	221.624067	4
7	**1103.485993**	552.246635	1086.459444	543.733360	1085.475428	543.241352	T	***373.219395***	187.113335	356.192846	178.600061	355.208830	178.108053	3
8	1200.538757	600.773017	1183.512208	592.259742	1182.528192	591.767734	P	***272.171716***	136.589496	255.145167	128.076221			2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TMQENSTPR
(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	1373.643143	-0.005855	TMQENSTPR
11.8	1373.635742	0.001546	DRGMPSDSPEKR

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

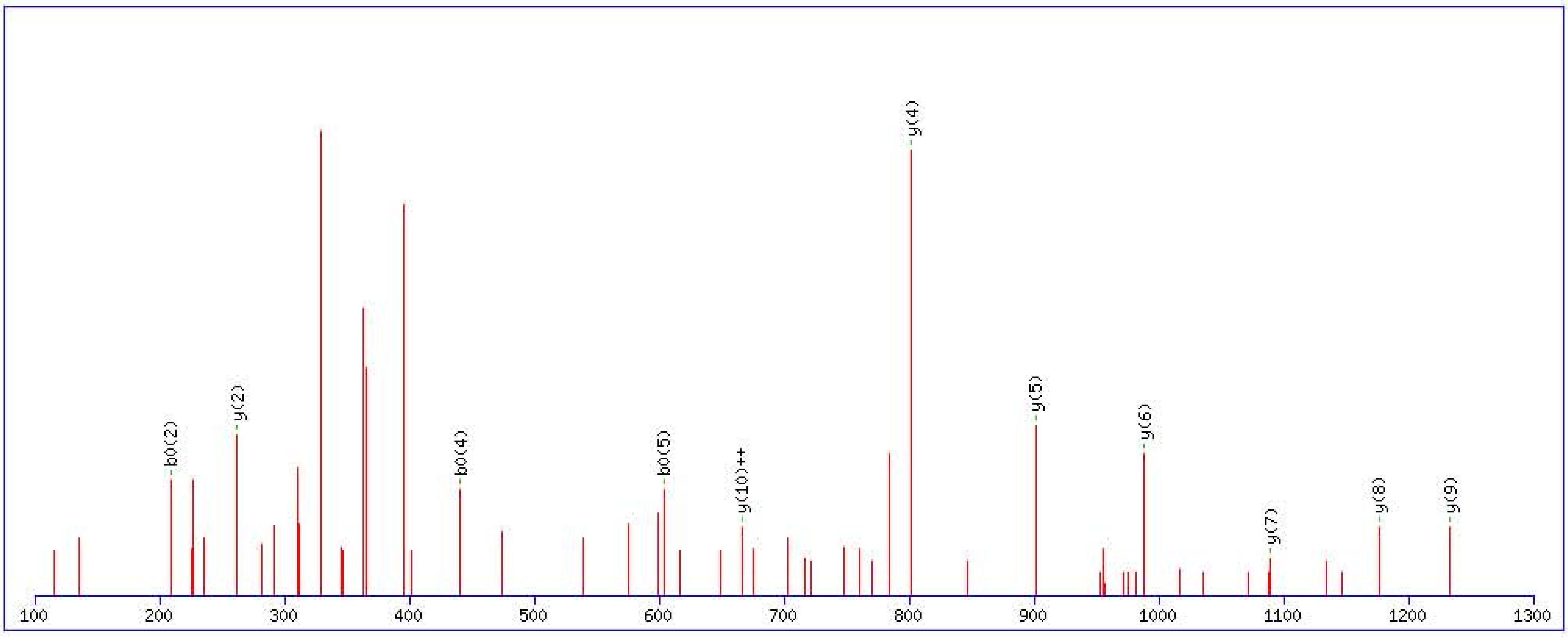
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPTMYVGSTSVQTSR**
Found in **C1S_HUMAN**, Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1

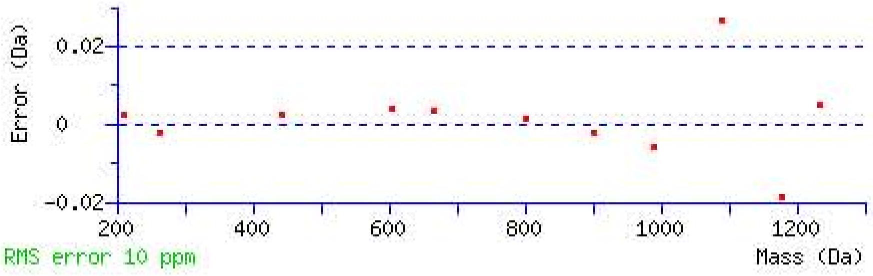
Match to Query 38390: 1952.927052 from(651.982960,3+) rtinseconds(1913) index(45339)
Title: Locus:1.1.1.3379.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

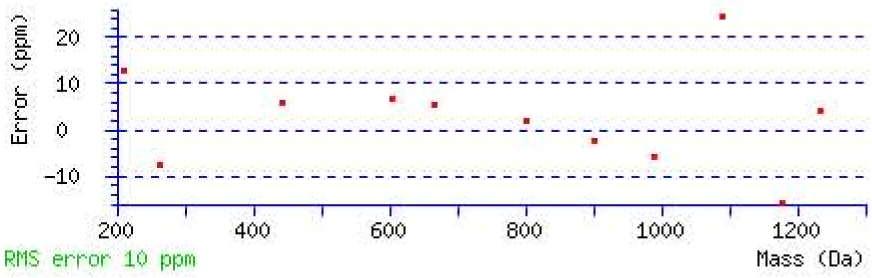
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1952.933594
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12    : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 0.00023
Matches : 11/144 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	130.049869	65.528572			112.039304	56.523290	E							15
2	227.102633	114.054954			209.092068	105.049672	P	1824.898269	912.952773	1807.871720	904.439498	1806.887704	903.947490	14
3	328.150312	164.578794			310.139747	155.573512	T	1727.845505	864.426391	1710.818956	855.913116	1709.834940	855.421108	13
4	459.190797	230.099036			441.180232	221.093754	M	1626.797826	813.902551	1609.771277	805.389277	1608.787261	804.897269	12
5	622.254126	311.630701			604.243561	302.625419	Y	1495.757341	748.382309	1478.730792	739.869034	1477.746776	739.377026	11
6	721.322540	361.164908			703.311975	352.159626	V	1332.694012	666.850644	1315.667463	658.337370	1314.683447	657.845362	10
7	778.344004	389.675640			760.333439	380.670358	G	***1233.625598***	617.316437	1216.599049	608.803163	1215.615033	608.311155	9
8	865.376032	433.191654			847.365467	424.186372	S	***1176.604134***	588.805705	1159.577585	580.292431	1158.593569	579.800423	8
9	966.423711	483.715494			948.413146	474.710211	T	***1089.572106***	545.289691	1072.545557	536.776417	1071.561541	536.284409	7
10	1053.455739	527.231508			1035.445174	518.226225	S	***988.524427***	494.765852	971.497878	486.252577	970.513862	485.760569	6
11	1152.524153	576.765715			1134.513588	567.760432	V	***901.492399***	451.249838	884.465850	442.736563	883.481834	442.244555	5
12	1591.749479	796.378378	1574.722930	787.865103	1573.738914	787.373095	Q	***802.423985***	401.715631	785.397436	393.202356	784.413420	392.710348	4
13	1692.797158	846.902217	1675.770609	838.388943	1674.786593	837.896935	T	363.198659	182.102968	346.172110	173.589693	345.188094	173.097685	3
14	1779.829186	890.418231	1762.802637	881.904957	1761.818621	881.412949	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 EPTMYVGSTSVQTSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.9	1952.933594	-0.006542	EPTMYVGSTSVQTSR
8.0	1952.944794	-0.017742	MNQVTSKYANQSAGK

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

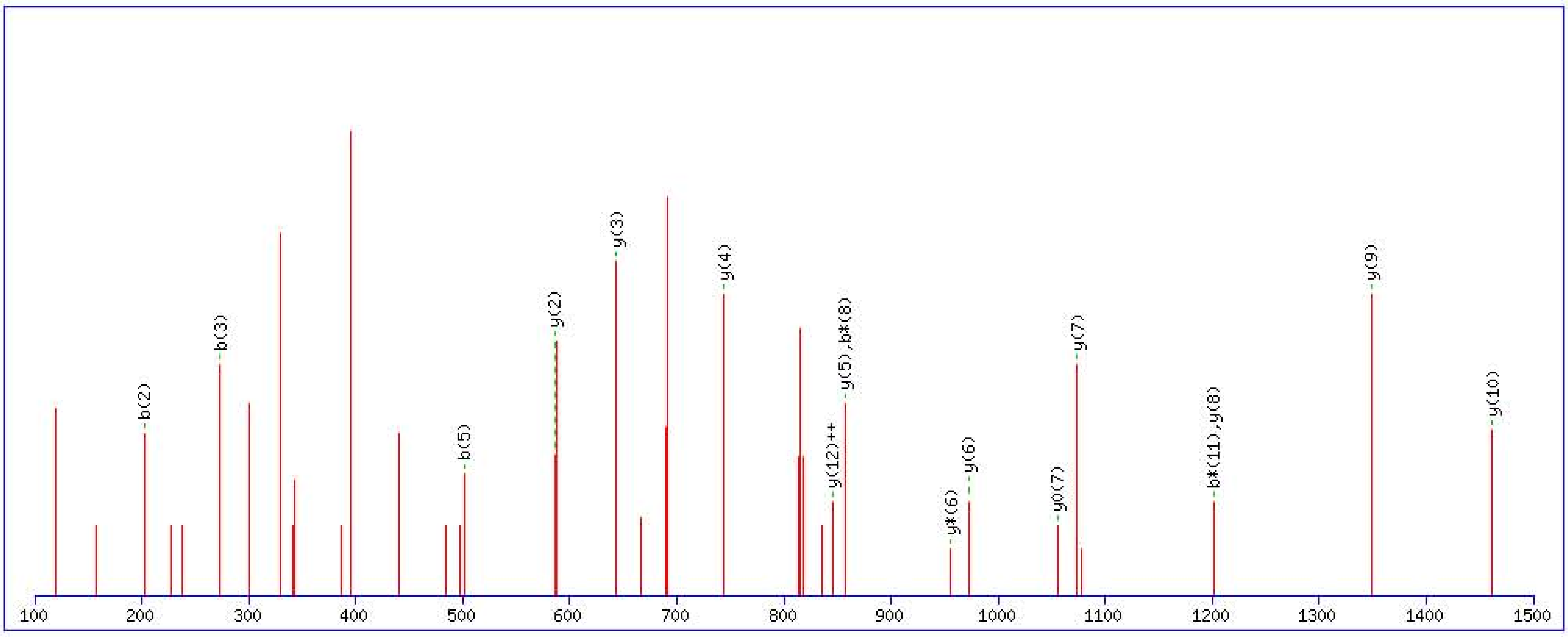
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SNALDIIFQTDLTGQK**
Found in **C1S_HUMAN**, Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1

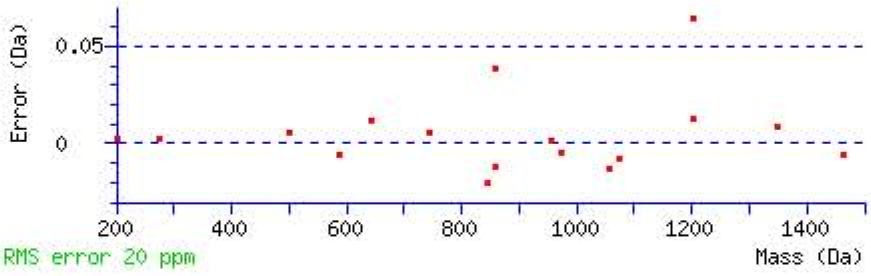
Match to Query 41241: 2074.072122 from(692.364650,3+) rtinseconds(2875) index(37159)
Title: Locus:1.1.1.3663.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

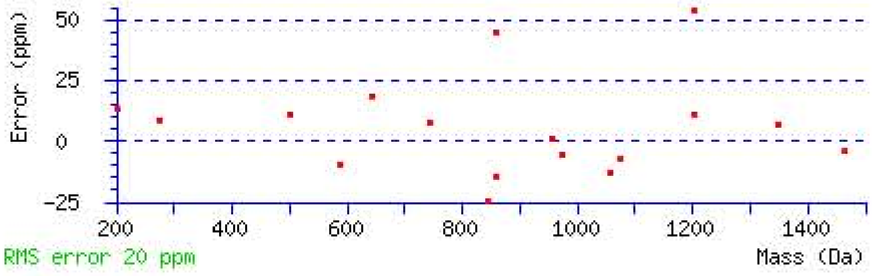
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2074.076874
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15     : Biotin:Thermo-21345 (Q)
Ions Score: 58  Expect: 4.2e-005
Matches : 17/172 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	88.039304	44.523290			70.028739	35.518008	S							16
2	**202.082231**	101.544753	185.055682	93.031479	184.071666	92.539471	N	1988.052127	994.529702	1971.025578	986.016427	1970.041562	985.524419	15
3	**273.119345**	137.063311	256.092796	128.550036	255.108780	128.058028	A	1874.009200	937.508238	1856.982651	928.994964	1855.998635	928.502956	14
4	386.203409	193.605343	369.176860	185.092068	368.192844	184.600060	L	1802.972086	901.989681	1785.945537	893.476407	1784.961521	892.984399	13
5	**501.230352**	251.118814	484.203803	242.605540	483.219787	242.113532	D	1689.888022	845.447649	1672.861473	836.934375	1671.877457	836.442367	12
6	614.314416	307.660846	597.287867	299.147572	596.303851	298.655564	I	1574.861079	787.934178	1557.834530	779.420903	1556.850514	778.928895	11
7	727.398480	364.202878	710.371931	355.689604	709.387915	355.197596	I	***1461.777015***	731.392146	1444.750466	722.878871	1443.766450	722.386863	10
8	874.466894	437.737085	857.440345	429.223811	856.456329	428.731803	F	***1348.692951***	674.850114	1331.666402	666.336839	1330.682386	665.844831	9
9	1002.525472	501.766374	985.498923	493.253100	984.514907	492.761092	Q	***1201.624537***	601.315907	1184.597988	592.802632	1183.613972	592.310624	8
10	1103.573151	552.290214	1086.546602	543.776939	1085.562586	543.284931	T	***1073.565959***	537.286618	1056.539410	528.773343	1055.555394	528.281335	7
11	1218.600094	609.803685	1201.573545	601.290411	1200.589529	600.798403	D	***972.518280***	486.762778	955.491731	478.249504	954.507715	477.757496	6
12	1331.684158	666.345717	1314.657609	657.832443	1313.673593	657.340435	L	***857.491337***	429.249307	840.464788	420.736032	839.480772	420.244024	5
13	1432.731837	716.869557	1415.705288	708.356282	1414.721272	707.864274	T	***744.407273***	372.707275	727.380724	364.194000	726.396708	363.701992	4
14	1489.753301	745.380289	1472.726752	736.867014	1471.742736	736.375006	G	***643.359594***	322.183435	626.333045	313.670161			3
15	1928.978627	964.992952	1911.952078	956.479677	1910.968062	955.987669	Q	***586.338130***	293.672703	569.311581	285.159429			2
16							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.1	2074.076874	-0.004752	SNALDIIFQTDLTGQK
10.0	2074.076874	-0.004752	SNALDIIFQTDLTGQK

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

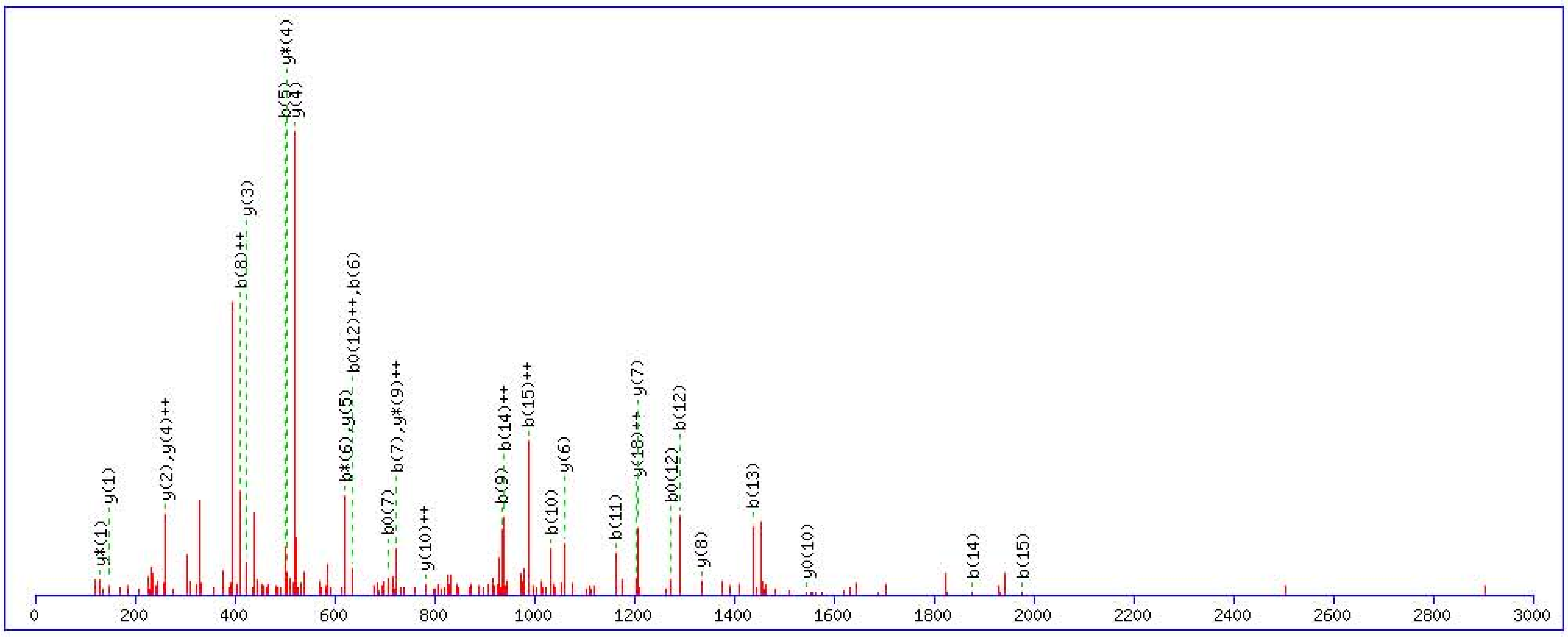
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSNNPHSPIVEEFQVPYNK**
Found in **C1S_HUMAN**, Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1

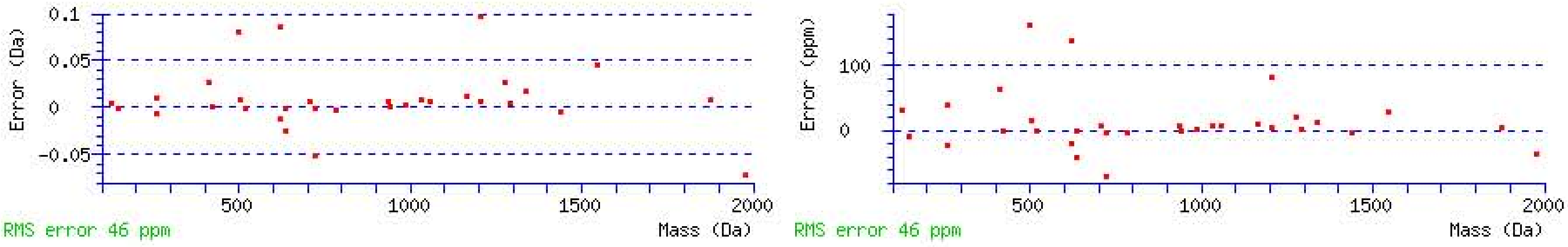
Match to Query 48467: 2496.209532 from(833.077120,3+) rtinseconds(2136) index(32653)
Title: Locus:1.1.1.3407.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 2496.210724
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Biotin:Thermo-21345 (Q)
Ions Score: 36 **Expect:** 0.00048
Matches : 32/198 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	88.039304	44.523290			70.028739	35.518008	S							19
2	175.071332	88.039304			157.060767	79.034021	S	2410.185992	1205.596634	2393.159443	1197.083359	2392.175427	1196.591351	18
3	289.114259	145.060768	272.087710	136.547493	271.103694	136.055485	N	2323.153964	1162.080620	2306.127415	1153.567345	2305.143399	1153.075337	17
4	403.157186	202.082231	386.130637	193.568957	385.146621	193.076949	N	2209.111037	1105.059156	2192.084488	1096.545882	2191.100472	1096.053874	16
5	***500.209950***	250.608613	483.183401	242.095339	482.199385	241.603331	P	2095.068110	1048.037693	2078.041561	1039.524418	2077.057545	1039.032410	15
6	***637.268862***	319.138069	620.242313	310.624795	619.258297	310.132787	H	1998.015346	999.511311	1980.988797	990.998037	1980.004781	990.506028	14
7	***724.300890***	362.654083	707.274341	354.140808	706.290325	353.648800	S	1860.956434	930.981855	1843.929885	922.468581	1842.945869	921.976572	13
8	821.353654	**411.180465**	804.327105	402.667191	803.343089	402.175183	P	1773.924406	887.465841	1756.897857	878.952567	1755.913841	878.460559	12
9	***934.437718***	467.722497	917.411169	459.209223	916.427153	458.717215	I	1676.871642	838.939459	1659.845093	830.426185	1658.861077	829.934177	11
10	***1033.506132***	517.256704	1016.479583	508.743429	1015.495567	508.251421	V	1563.787578	782.397427	1546.761029	773.884153	1545.777013	773.392145	10
11	***1162.548725***	581.778000	1145.522176	573.264726	1144.538160	572.772718	E	1464.719164	732.863220	1447.692615	724.349946	1446.708599	723.857938	9
12	***1291.591318***	646.299297	1274.564769	637.786023	1273.580753	637.294015	E	***1335.676571***	668.341924	1318.650022	659.828649	1317.666006	659.336641	8
13	***1438.659732***	719.833504	1421.633183	711.320230	1420.649167	710.828222	F	***1206.633978***	603.820627	1189.607429	595.307353			7
14	***1877.885058***	**939.446167**	1860.858509	930.932893	1859.874493	930.440885	Q	***1059.565564***	530.286420	1042.539015	521.773146			6
15	***1976.953472***	**988.980374**	1959.926923	980.467100	1958.942907	979.975092	V	***620.340238***	310.673757	603.313689	302.160483			5
16	2074.006236	1037.506756	2056.979687	1028.993481	2055.995671	1028.501473	P	***521.271824***	261.139550	504.245275	252.626275			4
17	2237.069565	1119.038420	2220.043016	1110.525146	2219.059000	1110.033138	Y	***424.219060***	212.613168	407.192511	204.099894			3
18	2351.112492	1176.059884	2334.085943	1167.546609	2333.101927	1167.054601	N	***261.155731***	131.081503	244.129182	122.568229			2
19							K	***147.112804***	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.5	2496.210724	-0.001192	SSNNPHSPIVEEFQVPYNK
0.1	2496.236603	-0.027071	RPVFSHCQVPETQKTDTR

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

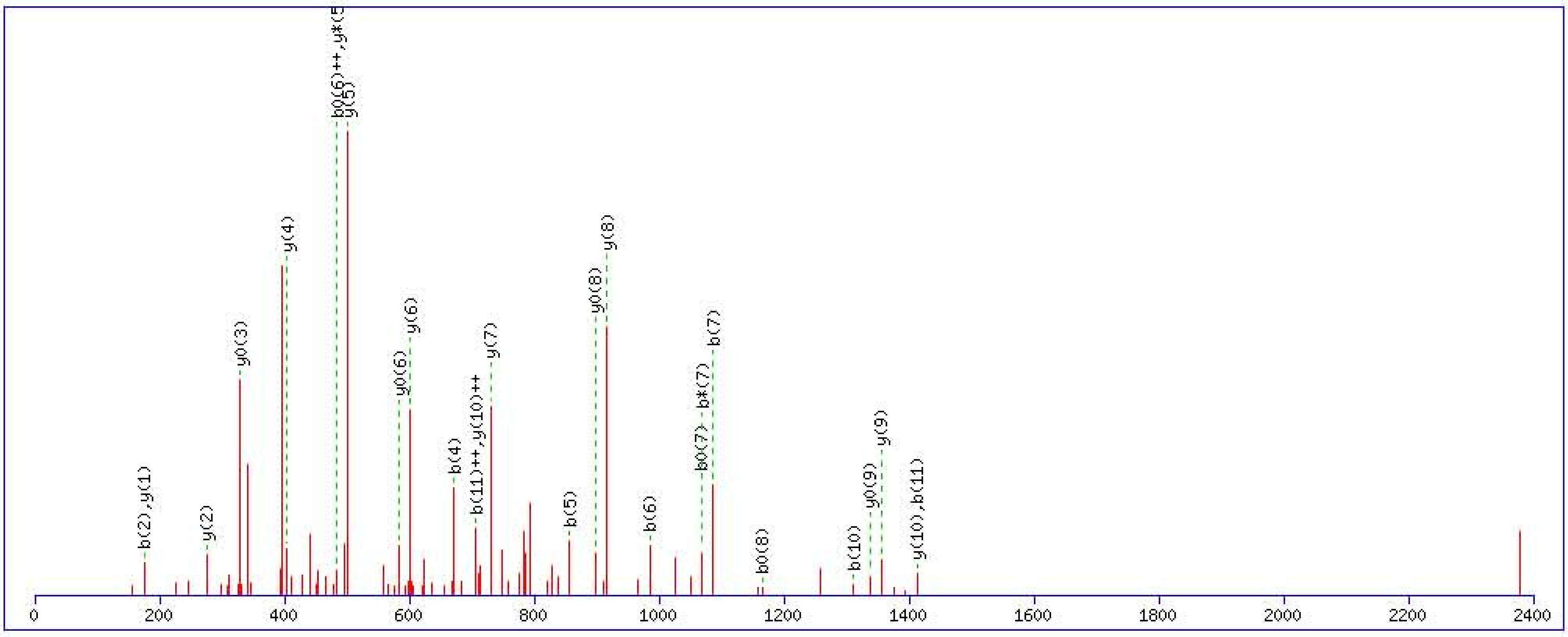
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSGQWQTPGATR**
Found in **CO2_HUMAN**, Complement C2 OS=Homo sapiens GN=C2 PE=1 SV=2

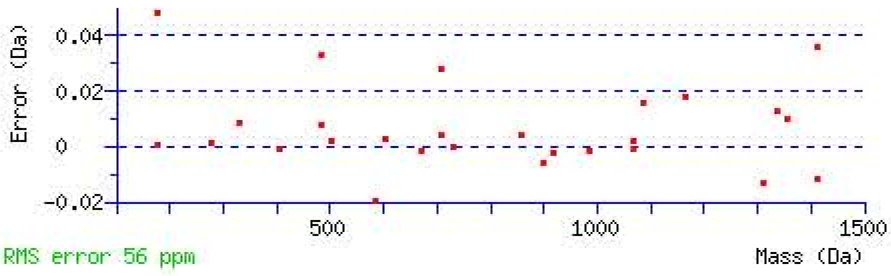
Match to Query 29966: 1585.771128 from(793.892840,2+) rtinseconds(1731) index(59086)
Title: Locus:1.1.1.1514.11 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

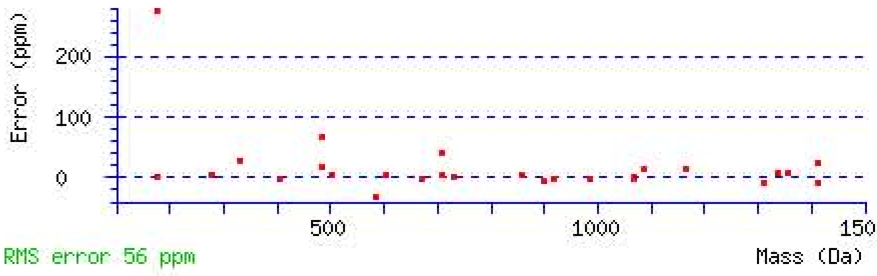
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1585.767120
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 1e-005
Matches : 27/124 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	88.039304	44.523290			70.028739	35.518008	S							12
2	**175.071332**	88.039304			157.060767	79.034021	S	1499.742361	750.374818	1482.715812	741.861544	1481.731796	741.369536	11
3	232.092796	116.550036			214.082231	107.544753	G	***1412.710333***	706.858805	1395.683784	698.345530	1394.699768	697.853522	10
4	**671.318122**	336.162699	654.291573	327.649425	653.307557	327.157417	Q	***1355.688869***	678.348072	1338.662320	669.834798	1337.678304	669.342790	9
5	**857.397435**	429.202356	840.370886	420.689081	839.386870	420.197073	W	***916.463543***	458.735410	899.436994	450.222135	898.452978	449.730127	8
6	**985.456013**	493.231645	968.429464	484.718370	967.445448	484.226362	Q	***730.384230***	365.695753	713.357681	357.182478	712.373665	356.690470	7
7	**1086.503692**	543.755484	1069.477143	535.242210	1068.493127	534.750202	T	***602.325652***	301.666464	585.299103	293.153189	584.315087	292.661181	6
8	1183.556456	592.281866	1166.529907	583.768592	1165.545891	583.276584	P	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.137342	5
9	1240.577920	620.792598	1223.551371	612.279324	1222.567355	611.787315	G	***404.225209***	202.616242	387.198660	194.102968	386.214644	193.610960	4
10	**1311.615034**	656.311155	1294.588485	647.797881	1293.604469	647.305872	A	347.203745	174.105510	330.177196	165.592236	329.193180	165.100228	3
11	**1412.662713**	706.834994	1395.636164	698.321720	1394.652148	697.829712	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 SSGQWQTPGATR
(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	1585.767120	0.004008	SSGQWQTPGATR
32.5	1585.767120	0.004008	SSGQWQTPGATR
6.6	1585.751846	0.019282	LMDEPALRSPGGGDR
4.5	1585.766922	0.004206	RTSNERPGSGQGQGR
4.3	1585.781006	-0.009878	AYHLVCLDPELEK
3.6	1585.769592	0.001536	ETDHKSLSSSPDKR
3.6	1585.769653	0.001475	GDVGTAGSVGGTGEPGLR
2.9	1585.765717	0.005411	DLEEALPALEEAMR
2.6	1585.767075	0.004053	AWENLGEQMGKAPR
1.1	1585.794785	-0.023657	VVDDDGETIAVLGAGR

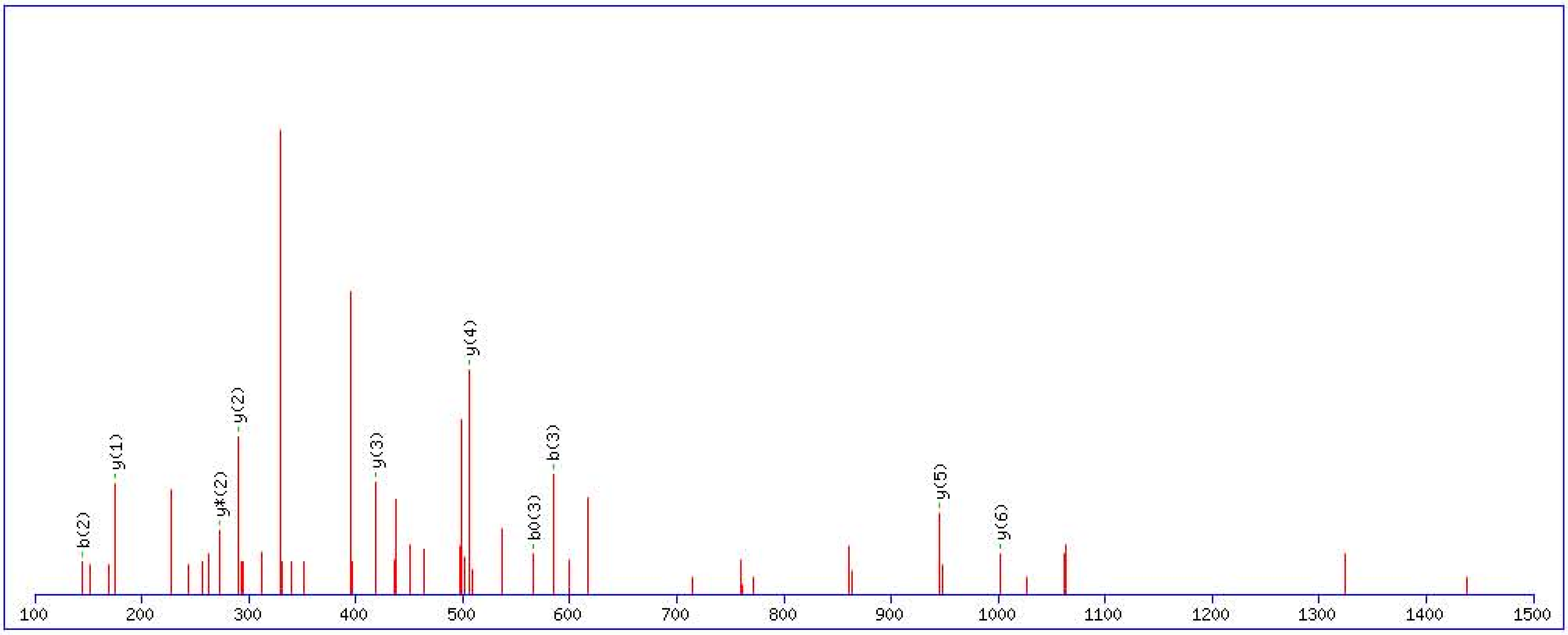
Mascot Search Results

Peptide View

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

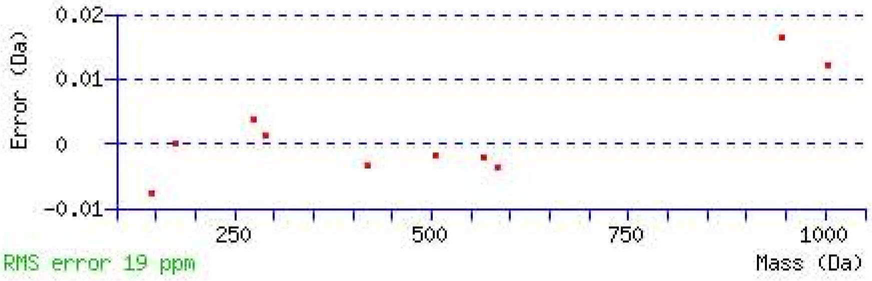
Match to Query 13625: 1088.492168 from(545.253360,2+) rtinseconds(1164) index(27387)
Title: Locus:1.1.1.3068.6 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

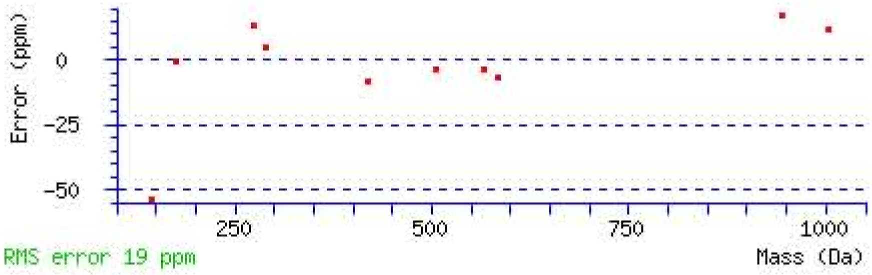
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1088.492050
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.0023
Matches : 10/66 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	88.039304	44.523290			70.028739	35.518008	S							7
2	**145.060768**	73.034022			127.050203	64.028740	G	***1002.467306***	501.737291	985.440757	493.224017	984.456741	492.732009	6
3	**584.286094**	292.646685	567.259545	284.133411	566.275529	283.641403	Q	***945.445842***	473.226559	928.419293	464.713285	927.435277	464.221277	5
4	671.318122	336.162699	654.291573	327.649425	653.307557	327.157417	S	***506.220516***	253.613896	489.193967	245.100621	488.209951	244.608613	4
5	800.360715	400.683996	783.334166	392.170721	782.350150	391.678713	E	***419.188488***	210.097882	402.161939	201.584608	401.177923	201.092600	3
6	915.387658	458.197467	898.361109	449.684192	897.377093	449.192185	D	***290.145895***	145.576585	273.119346	137.063311	272.135330	136.571303	2
7							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of SGQSEDR
(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	1088.492050	0.000118	SGQSEDR
0.1	1088.478134	0.014034	SQGCPNRDR

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

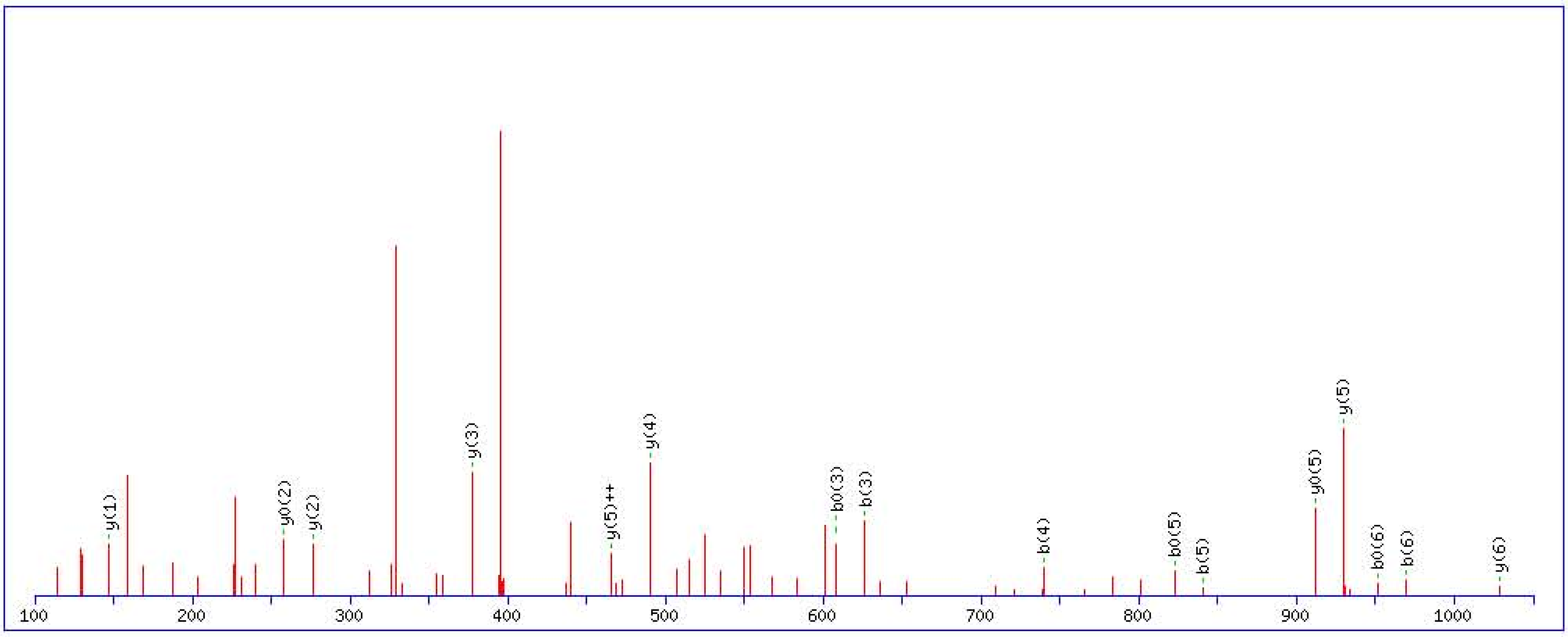
Mascot Search Results

Peptide View

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

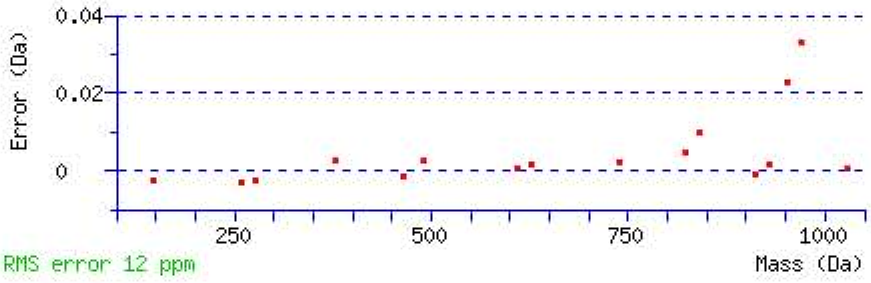
Match to Query 14637: 1114.601068 from(558.307810,2+) rtinseconds(1572) index(43315)
Title: Locus:1.1.1.3260.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

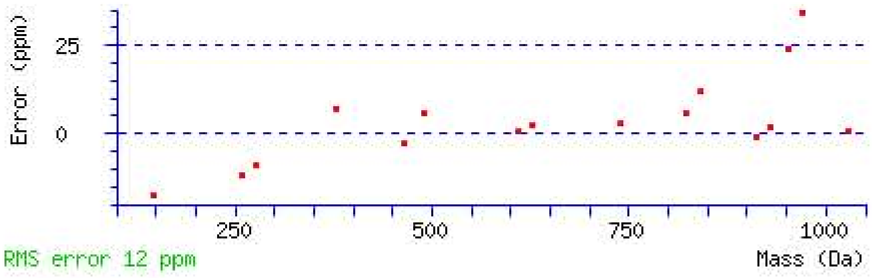
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1114.605621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.013
Matches : 16/66 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	88.039304	44.523290			70.028739	35.518008	S							7
2	187.107718	94.057497			169.097153	85.052214	V	***1028.580880***	514.794078	1011.554331	506.280804	1010.570315	505.788796	6
3	**626.333044**	313.670160	609.306495	305.156885	608.322479	304.664877	Q	***929.512466***	465.259871	912.485917	456.746597	911.501901	456.254589	5
4	**739.417108**	370.212192	722.390559	361.698917	721.406543	361.206909	L	***490.287140***	245.647208	473.260591	237.133934	472.276575	236.641926	4
5	**840.464787**	420.736032	823.438238	412.222757	822.454222	411.730749	T	***377.203076***	189.105176	360.176527	180.591902	359.192511	180.099894	3
6	**969.507380**	485.257328	952.480831	476.744054	951.496815	476.252046	E	***276.155397***	138.581336	259.128848	130.068062	258.144832	129.576054	2
7							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SVQLTEK
(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	1114.605621	-0.004553	SVQLTEK
11.0	1114.613480	-0.012412	SVFAKHGLEK
7.5	1114.591690	0.009378	ASVHSMISRK
4.5	1114.609436	-0.008368	EGIKRQQEK
3.7	1114.584503	0.016565	DAQVFPK
3.0	1114.588318	0.012750	RHTGEKPYK
2.4	1114.613480	-0.012412	NKEIVHTFK
2.2	1114.598190	0.002878	QEQEAAKLAK
2.1	1114.609451	-0.008383	SVARLSPETR
2.0	1114.598236	0.002832	SAVITSLDPGR

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

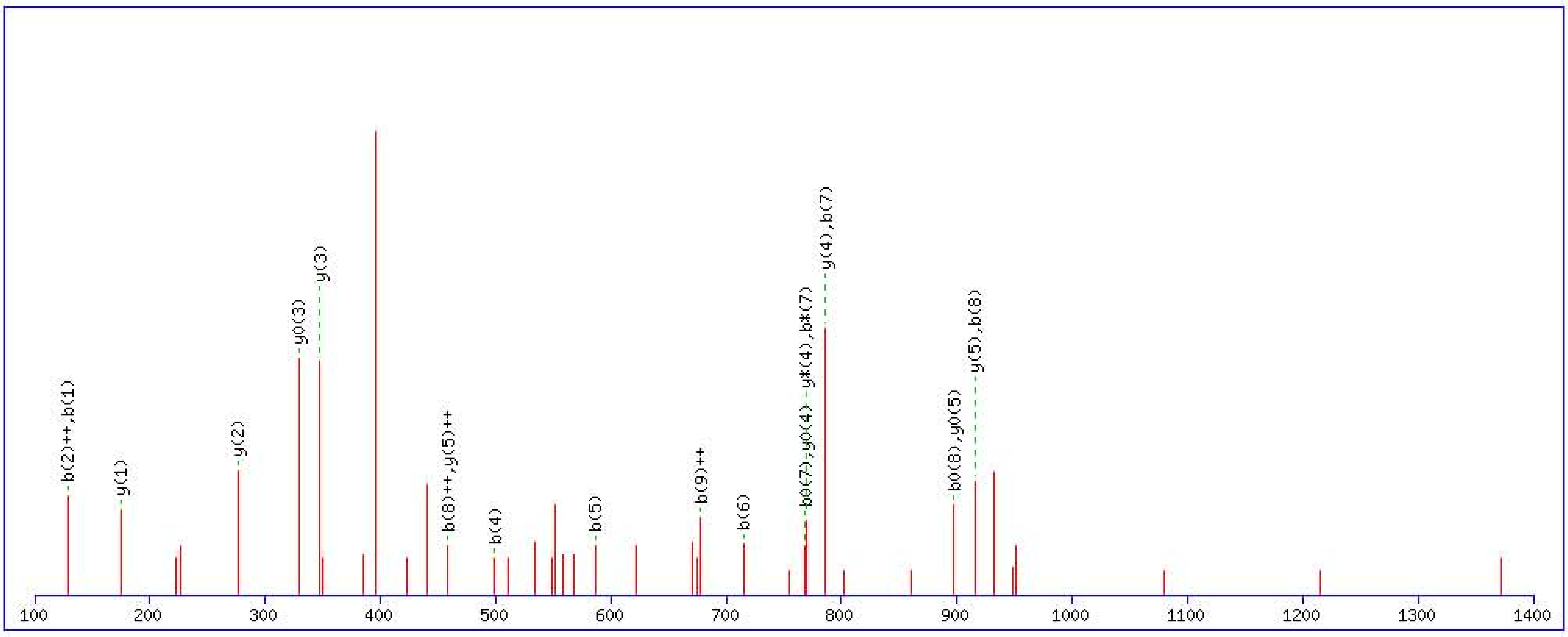
Mascot Search Results

Peptide View

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

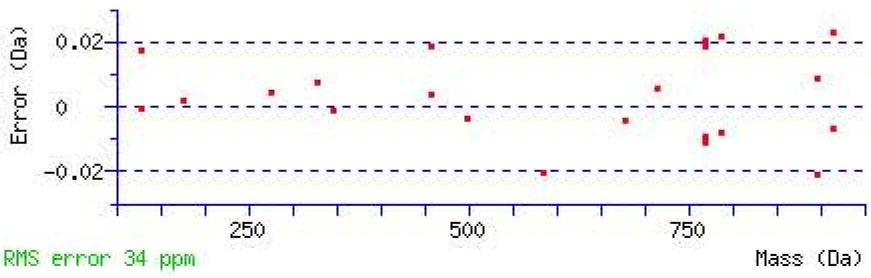
Match to Query 15525: 1699.847862 from(567.623230,3+) rtinseconds(1435) index(42461)
Title: Locus:1.1.1.3212.21 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

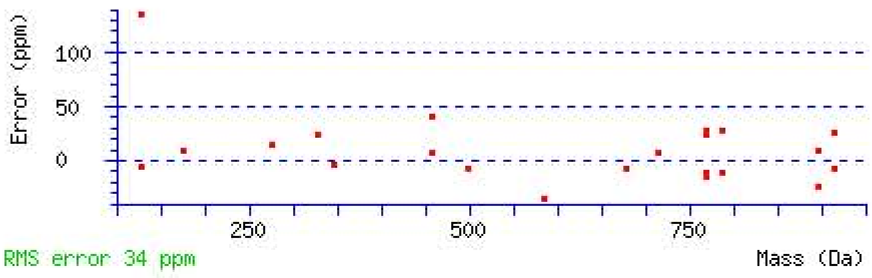
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1699.856277
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.014
Matches : 22/126 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	***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
30.6	1699.856277	-0.008415	KQELSEAEQATR
10.4	1699.856277	-0.008415	KQELSEAEQATR
10.1	1699.845932	0.001930	QAMQEQLSK
9.5	1699.846405	0.001457	HQEVKMQAPAFRDK
9.4	1699.845932	0.001930	QAMQEQLSK
7.5	1699.843063	0.004799	GKVSEGIDFVHHYGR
5.3	1699.849091	-0.001229	KIFETSIICGEEK
0.6	1699.838562	0.009300	EAPTQGLACVSTR

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

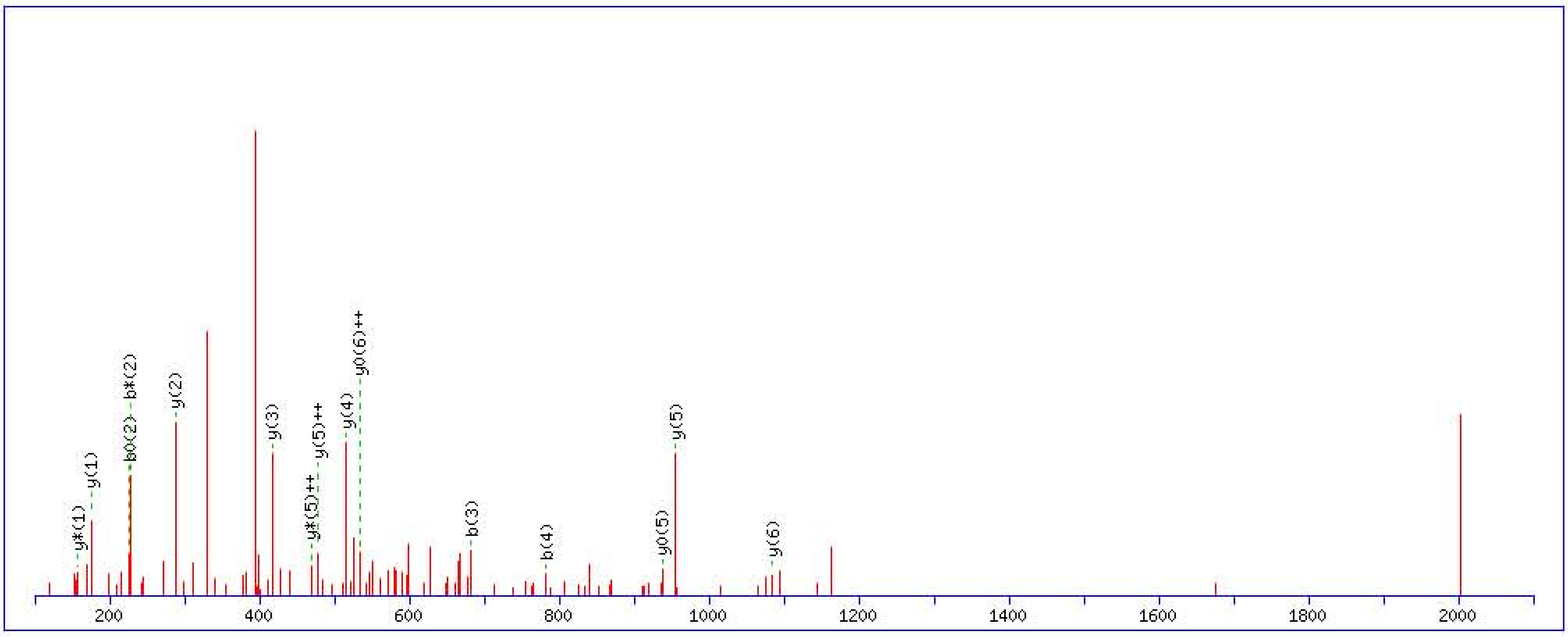
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

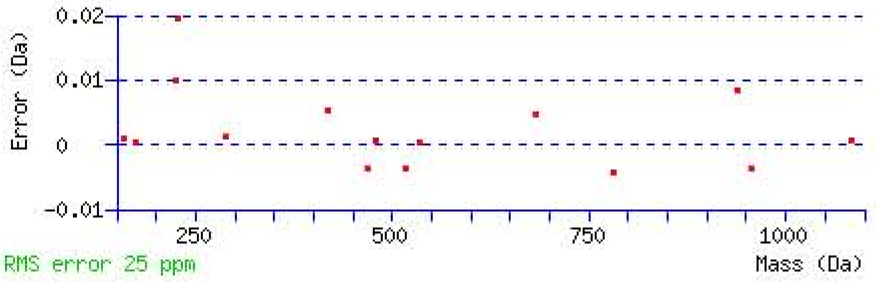
Match to Query 17699: 1197.604068 from(599.809310,2+) rtinseconds(1684) index(44070)
Title: Locus:1.1.1.3299.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

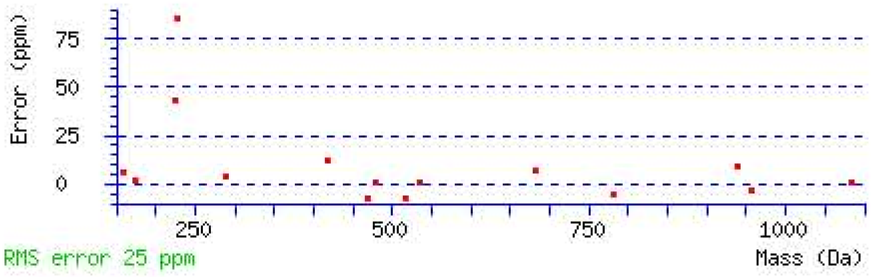
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1197.617569
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.014
Matches : 15/66 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	115.050203	58.028740	98.023654	49.515465			N							7
2	244.092796	122.550036	227.066247	114.036762	226.082231	113.544754	E	***1084.581942***	542.794609	1067.555393	534.281335	1066.571377	533.789327	6
3	**683.318122**	342.162699	666.291573	333.649425	665.307557	333.157417	Q	***955.539349***	478.273313	938.512800	469.760038	937.528784	469.268030	5
4	**782.386536**	391.696906	765.359987	383.183632	764.375971	382.691624	V	***516.314023***	258.660650	499.287474	250.147375	498.303458	249.655367	4
5	911.429129	456.218203	894.402580	447.704928	893.418564	447.212920	E	***417.245609***	209.126443	400.219060	200.613168	399.235044	200.121160	3
6	1024.513193	512.760235	1007.486644	504.246960	1006.502628	503.754952	I	***288.203016***	144.605146	271.176467	136.091872			2
7							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of NEQVEIR
(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	1197.617569	-0.013501	NEQVEIR
8.3	1197.598953	0.005115	EISPGSGPGEIR
6.5	1197.598938	0.005130	AAQEGDLPELR
6.3	1197.617569	-0.013501	NQEDLLR
4.0	1197.588593	0.015475	TMLAVVDYMR
3.7	1197.617569	-0.013501	QEVNELR
3.7	1197.598953	0.005115	VDNQPEELVR
1.2	1197.589050	0.015018	DKSGLAEHWR
0.7	1197.617584	-0.013516	QDLDQLR
0.5	1197.598953	0.005115	QDNLPDIEVR

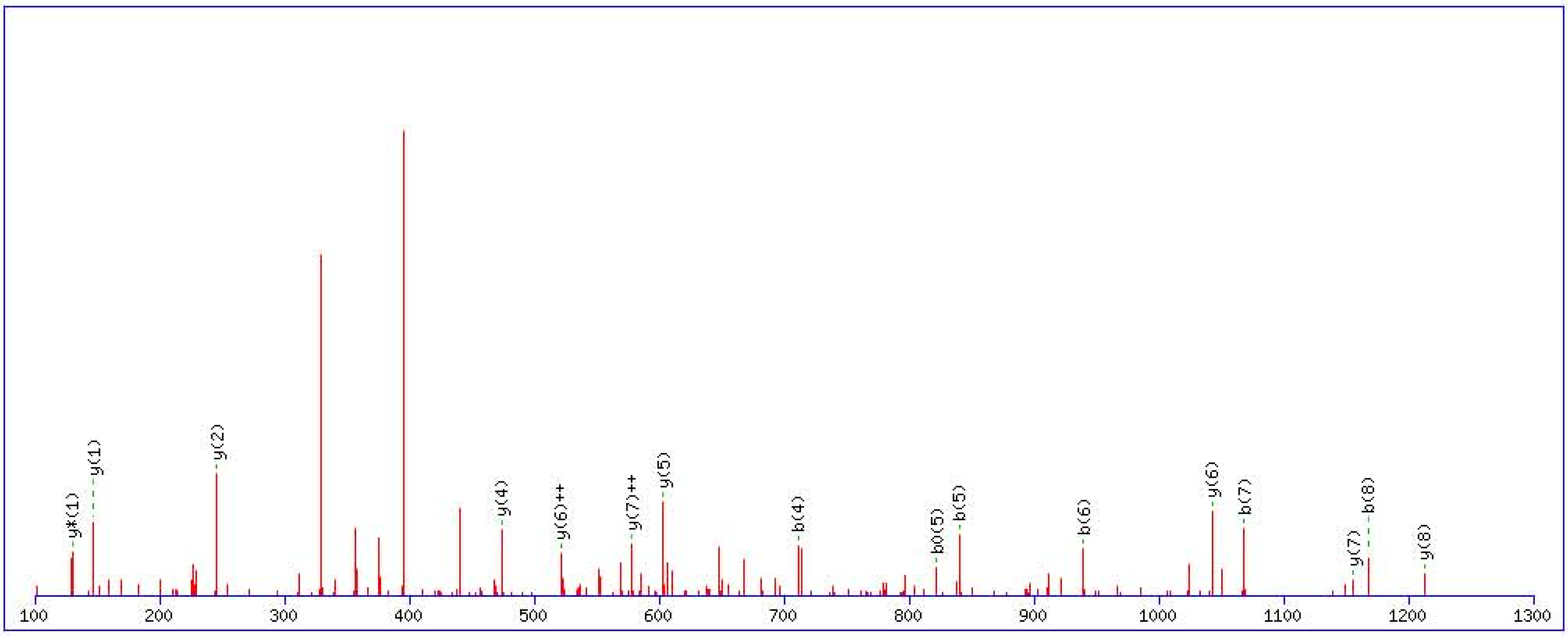
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

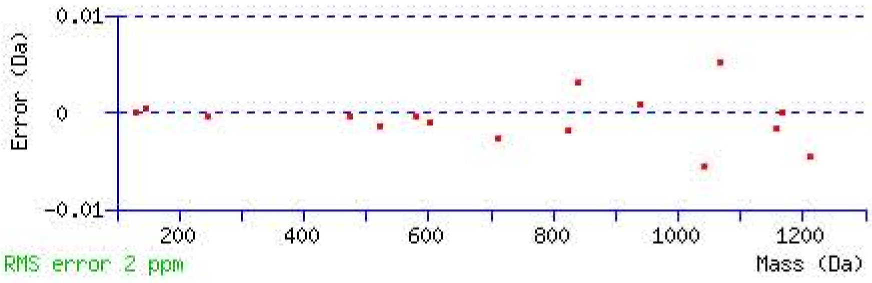
Match to Query 20565: 1312.702108 from(657.358330,2+) rtinseconds(1823) index(30753)
Title: Locus:1.1.1.3298.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

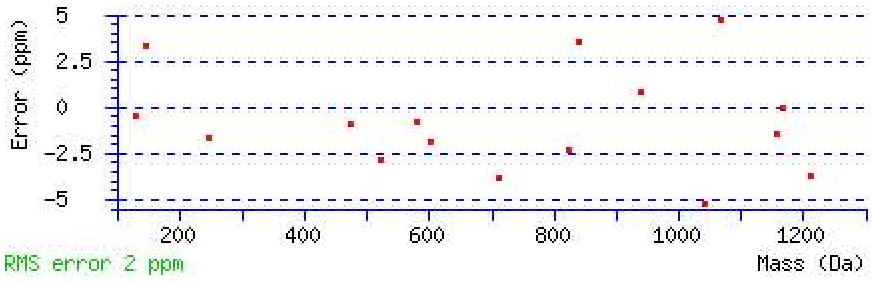
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1312.706070
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 52 **Expect:** 0.00015
Matches : 16/86 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	102.054955	51.531116			84.044390	42.525833	T							9
2	159.076419	80.041847			141.065854	71.036565	G	***1212.665672***	606.836474	1195.639123	598.323200	1194.655107	597.831192	8
3	272.160483	136.583879			254.149918	127.578597	L	***1155.644208***	578.325742	1138.617659	569.812468	1137.633643	569.320460	7
4	**711.385809**	356.196543	694.359260	347.683268	693.375244	347.191260	Q	***1042.560144***	521.783710	1025.533595	513.270436	1024.549579	512.778428	6
5	**840.428402**	420.717839	823.401853	412.204565	822.417837	411.712557	E	***603.334818***	302.171047	586.308269	293.657773	585.324253	293.165765	5
6	**939.496816**	470.252046	922.470267	461.738772	921.486251	461.246764	V	***474.292225***	237.649751	457.265676	229.136476	456.281660	228.644468	4
7	**1068.539409**	534.773343	1051.512860	526.260068	1050.528844	525.768060	E	375.223811	188.115544	358.197262	179.602269	357.213246	179.110261	3
8	**1167.607823**	584.307550	1150.581274	575.794275	1149.597258	575.302267	V	***246.181218***	123.594247	229.154669	115.080973			2
9							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TGLQEVEVK
(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	1312.706070	-0.003962	TGLQEVEVK
12.2	1312.699524	0.002584	TIMHLMINNVK
11.4	1312.713913	-0.011805	KVFEKYTTAAR
7.1	1312.709869	-0.007761	QAEEAVAKLQAR
6.5	1312.717300	-0.015192	ASLQTVDIR
5.0	1312.692139	0.009969	DRQSQIQK
3.5	1312.721130	-0.019022	QVEVLTNQRAR
2.9	1312.709915	-0.007807	VKDATQITQGPR
2.8	1312.721115	-0.019007	KKPQRDSQAQK
2.6	1312.703384	-0.001276	RGGSLGQTAR

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

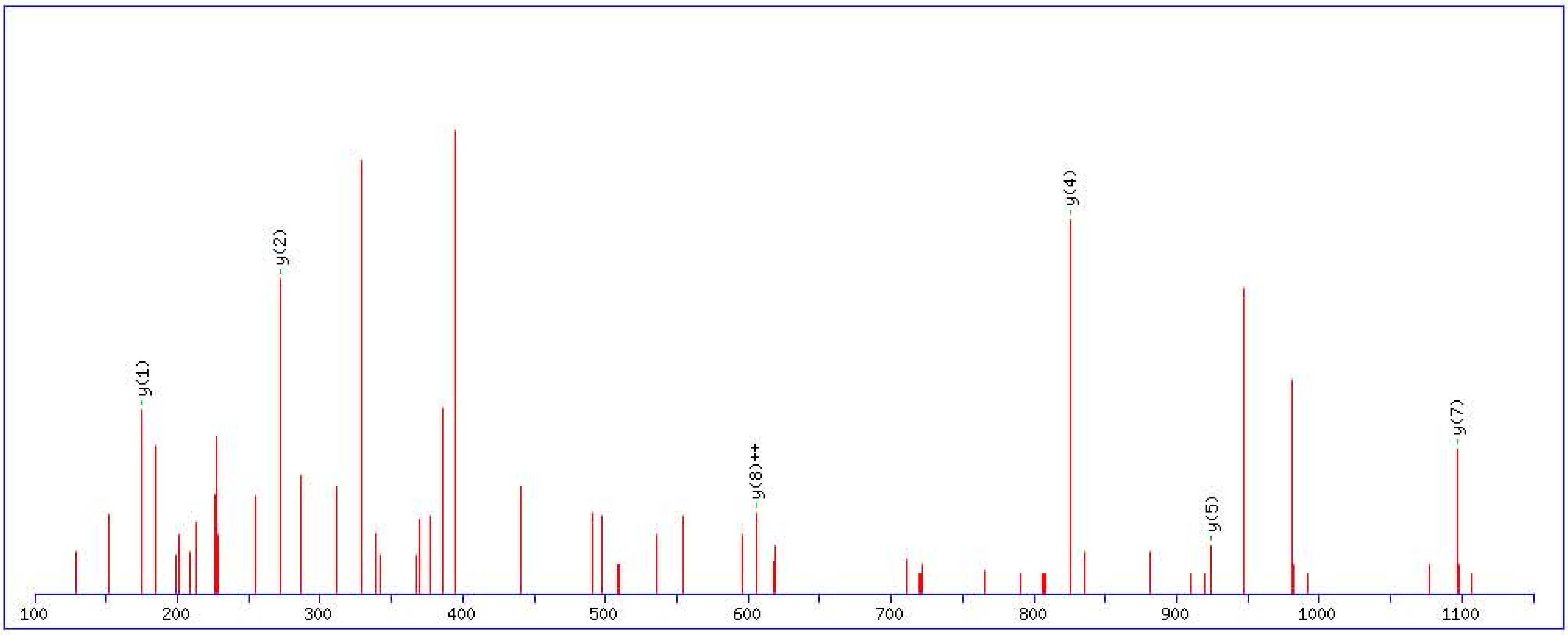
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

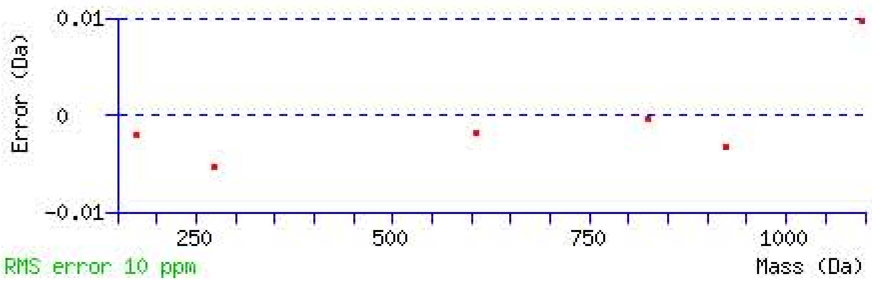
Match to Query 24704: 1420.782012 from(474.601280,3+) rtinseconds(2004) index(31916)
Title: Locus:1.1.1.3361.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

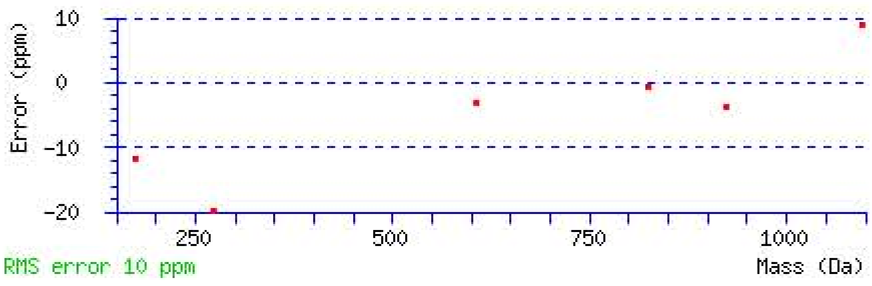
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1420.786057
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 29 **Expect:** 0.0022
Matches : 6/78 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							10
2	213.159754	107.083515					L	1322.724918	661.866097	1305.698369	653.352823	1304.714353	652.860814	9
3	326.243818	163.625547					L	1209.640854	605.324065	1192.614305	596.810791	1191.630289	596.318783	8
4	441.270761	221.139018			423.260196	212.133736	D	***1096.556790***	548.782033	1079.530241	540.268758	1078.546225	539.776750	7
5	498.292225	249.649750			480.281660	240.644468	G	981.529847	491.268562	964.503298	482.755287			6
6	597.360639	299.183958			579.350074	290.178675	V	***924.508383***	462.757830	907.481834	454.244555			5
7	1036.585965	518.796621	1019.559416	510.283346	1018.575400	509.791338	Q	***825.439969***	413.223623	808.413420	404.710348			4
8	1150.628892	575.818084	1133.602343	567.304810	1132.618327	566.812801	N	386.214643	193.610959	369.188094	185.097685			3
9	1247.681656	624.344466	1230.655107	615.831192	1229.671091	615.339183	P	***272.171716***	136.589496	255.145167	128.076221			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.8	1420.786057	-0.004045	VLLDGVQNPR
0.6	1420.793915	-0.011903	TVTPLRWQPAPR

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

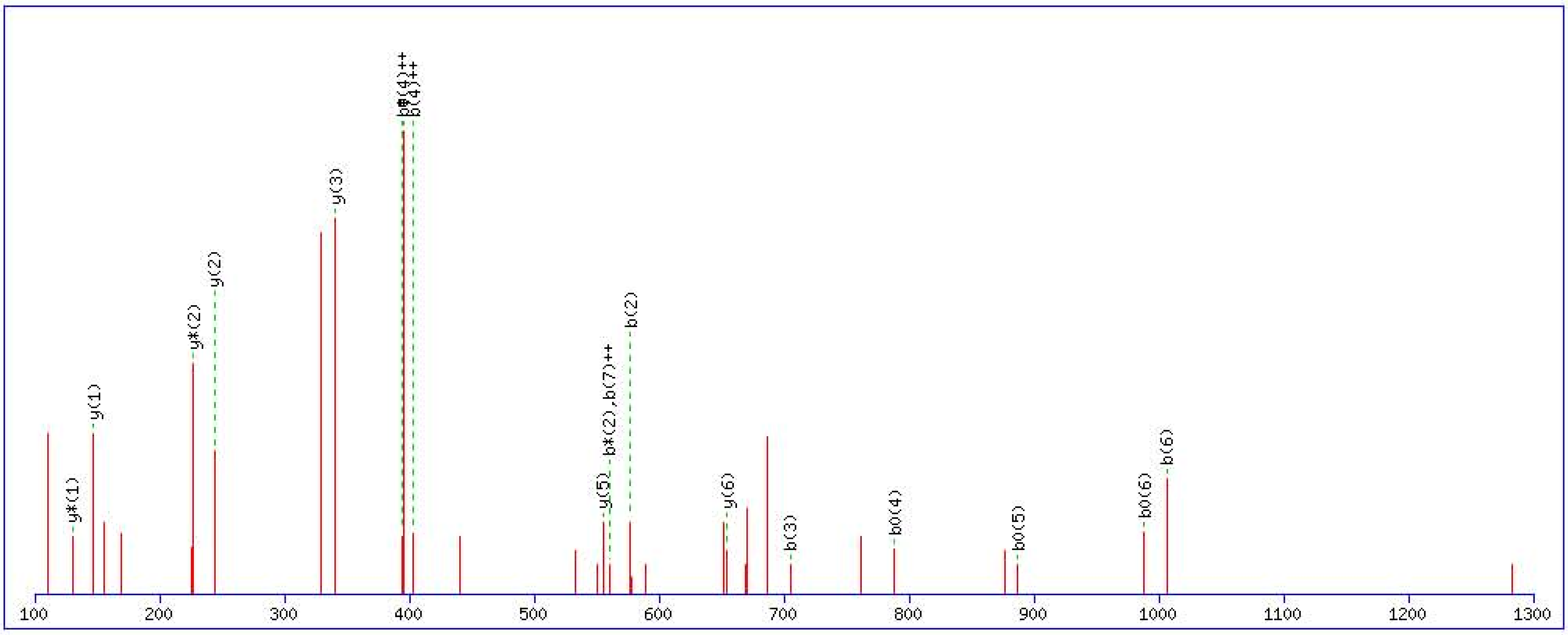
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

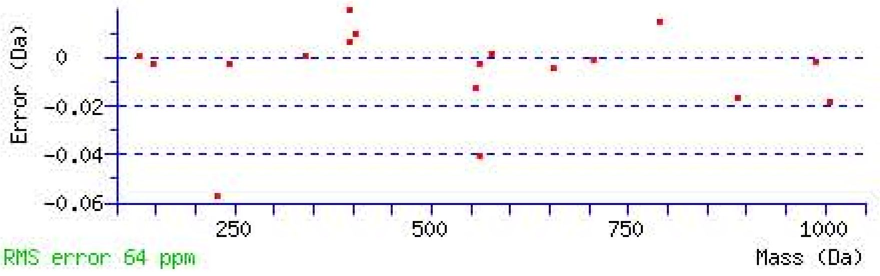
Match to Query 26138: 1458.794322 from(487.272050,3+) rtinseconds(1636) index(29679)
Title: Locus:1.1.1.3233.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

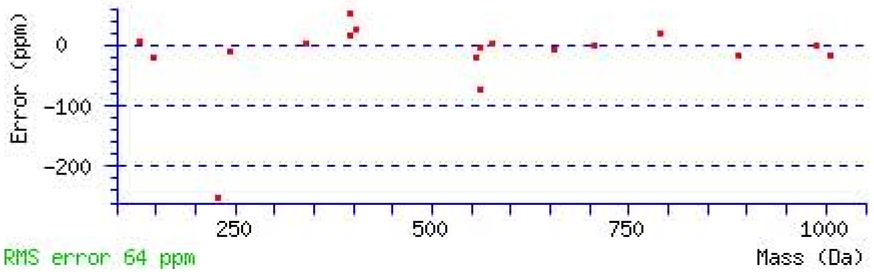
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1458.801712
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.0053
Matches : 18/92 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	138.066188	69.536732					H							10
2	***577.291514***	289.149395	560.264965	280.636121			Q	1322.750072	661.878674	1305.723523	653.365400	1304.739507	652.873392	9
3	***705.350092***	353.178684	688.323543	344.665410			Q	883.524746	442.266011	866.498197	433.752737	865.514181	433.260729	8
4	806.397771	**403.702524**	789.371222	395.189249	788.387206	394.697241	T	755.466168	378.236722	738.439619	369.723448	737.455603	369.231440	7
5	905.466185	453.236731	888.439636	444.723456	887.455620	444.231448	V	***654.418489***	327.712883	637.391940	319.199608	636.407924	318.707600	6
6	***1006.513864***	503.760570	989.487315	495.247296	988.503299	494.755288	T	***555.350075***	278.178676	538.323526	269.665401	537.339510	269.173393	5
7	1119.597928	**560.302602**	1102.571379	551.789328	1101.587363	551.297319	I	454.302396	227.654836	437.275847	219.141561			4
8	1216.650692	608.828984	1199.624143	600.315710	1198.640127	599.823701	P	***341.218332***	171.112804	324.191783	162.599530			3
9	1313.703456	657.355366	1296.676907	648.842092	1295.692891	648.350083	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 HQQTVTIPPK
(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	1458.801712	-0.007390	HQQTVTIPPK
21.6	1458.801712	-0.007390	HQQTVTIPPK
2.5	1458.809555	-0.015233	VIQVWFQNARAK
2.5	1458.809555	-0.015233	VLQVWFQNARAK

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

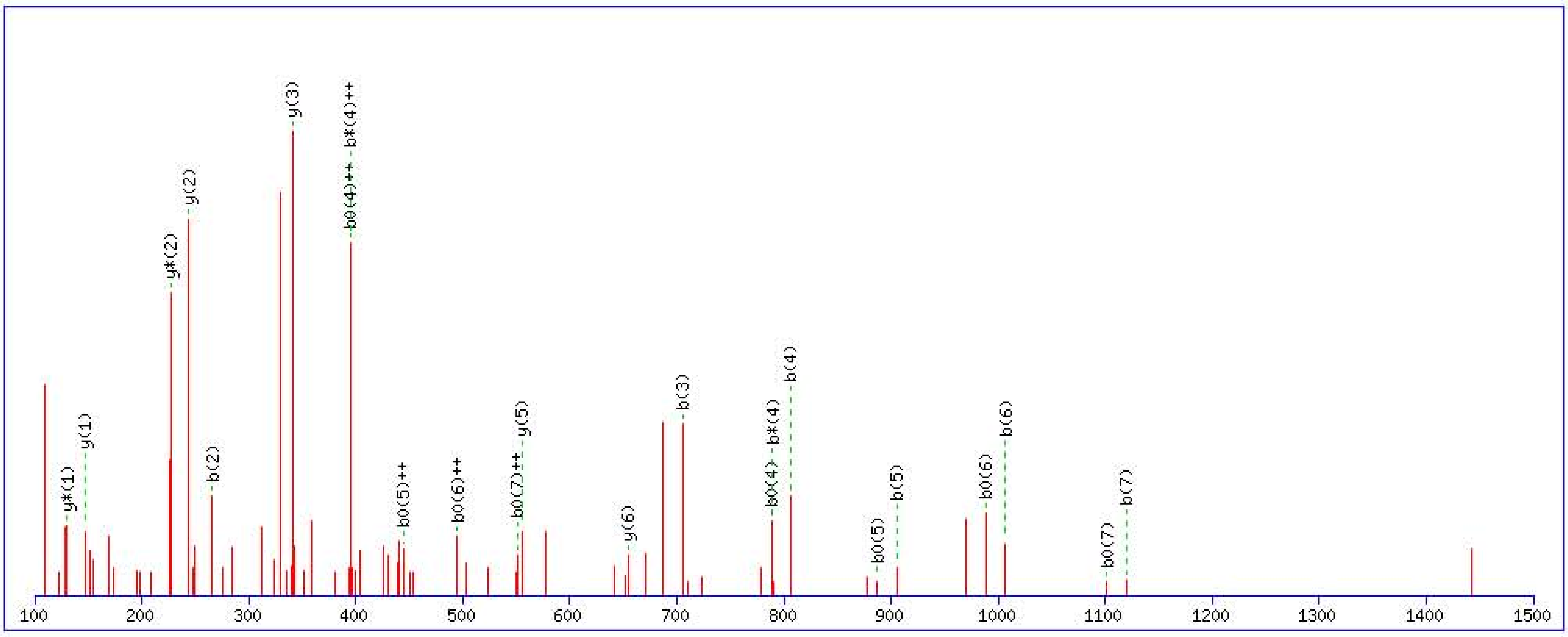
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

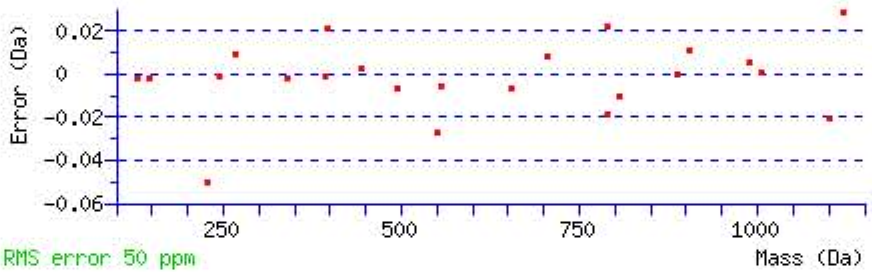
Match to Query 26140: 1458.794412 from(487.272080,3+) rtinseconds(1596) index(29373)
Title: Locus:1.1.1.3219.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

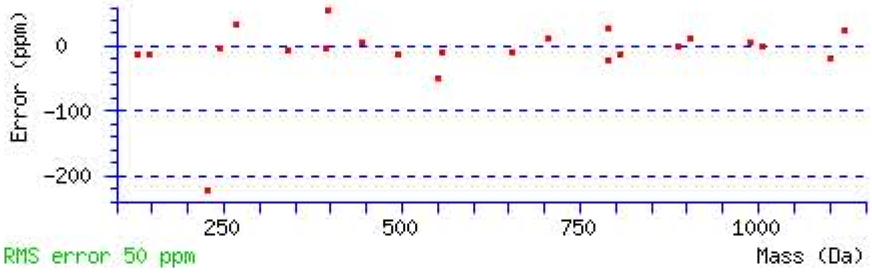
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1458.801712
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.0015
Matches : 23/92 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	138.066188	69.536732					H							10
2	***266.124766***	133.566021	249.098217	125.052746			Q	1322.750072	661.878674	1305.723523	653.365400	1304.739507	652.873392	9
3	***705.350092***	353.178684	688.323543	344.665410			Q	1194.691494	597.849385	1177.664945	589.336111	1176.680929	588.844102	8
4	***806.397771***	403.702524	789.371222	395.189249	788.387206	394.697241	T	755.466168	378.236722	738.439619	369.723448	737.455603	369.231440	7
5	***905.466185***	453.236731	888.439636	444.723456	887.455620	444.231448	V	***654.418489***	327.712883	637.391940	319.199608	636.407924	318.707600	6
6	***1006.513864***	503.760570	989.487315	495.247296	988.503299	494.755288	T	***555.350075***	278.178676	538.323526	269.665401	537.339510	269.173393	5
7	***1119.597928***	560.302602	1102.571379	551.789328	1101.587363	551.297319	I	454.302396	227.654836	437.275847	219.141561			4
8	1216.650692	608.828984	1199.624143	600.315710	1198.640127	599.823701	P	***341.218332***	171.112804	324.191783	162.599530			3
9	1313.703456	657.355366	1296.676907	648.842092	1295.692891	648.350083	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 HQQTVTIPPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.8	1458.801712	-0.007300	HQQTVTIPPK
37.8	1458.801712	-0.007300	HQQTVTIPPK
7.2	1458.776535	0.017877	QHPADKLPSR
3.3	1458.786392	0.008020	EALRIAKECIEK
0.9	1458.794281	0.000131	EYDIPGLVRKNR

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

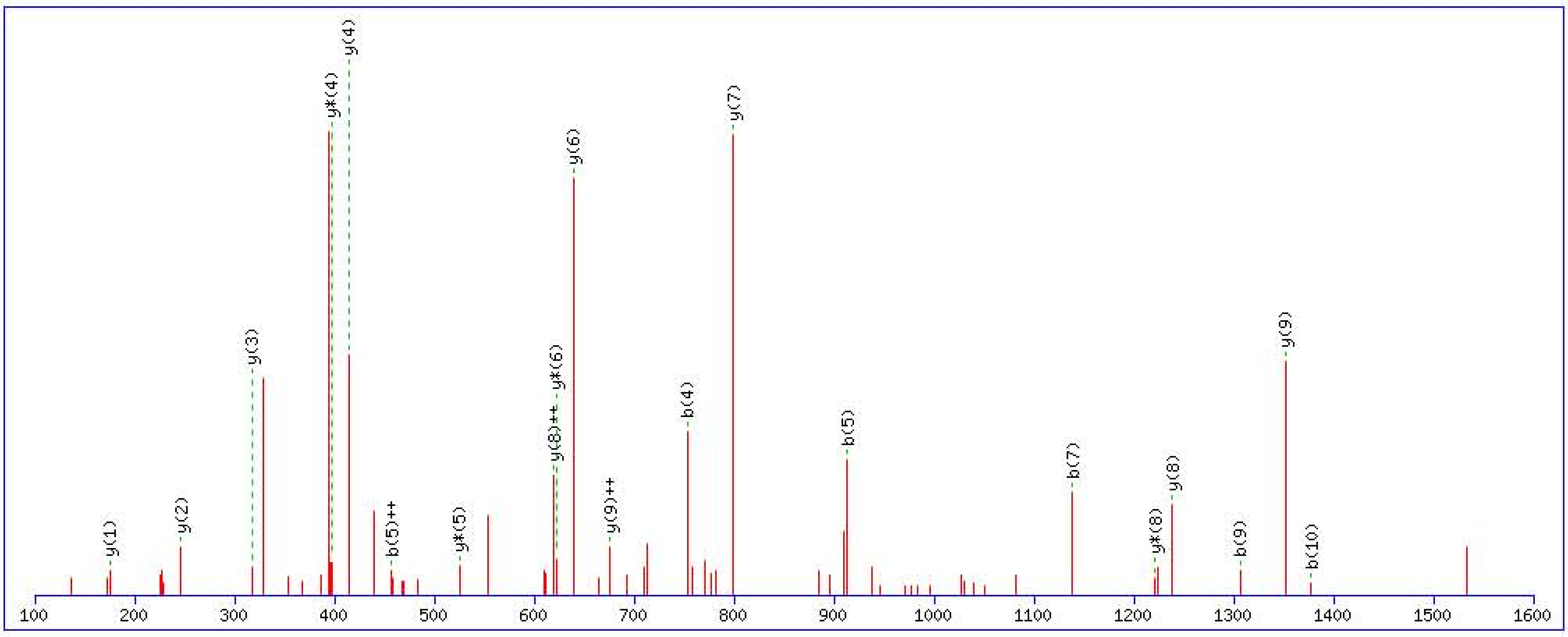
Mascot Search Results

Peptide View

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

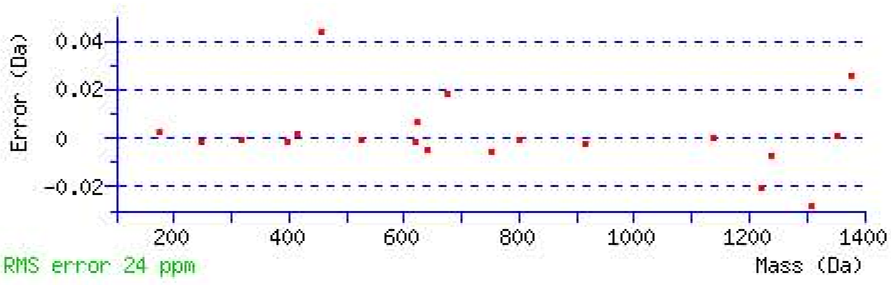
Match to Query 28517: 1550.761368 from(776.387960,2+) rtinseconds(1600) index(29396)
Title: Locus:1.1.1.3220.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

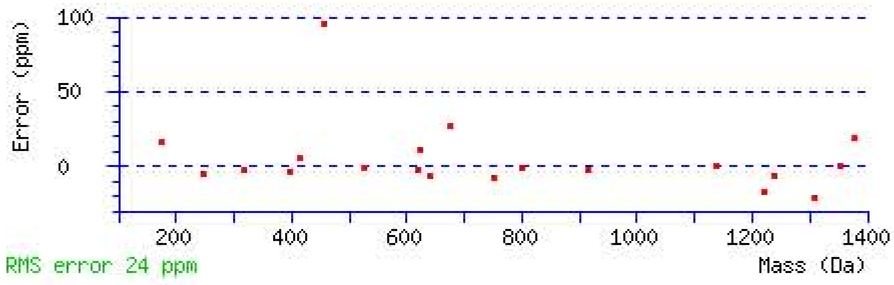
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1550.769730
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 44  Expect: 0.00076
Matches : 20/94 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	72.044390	36.525833					A							11
2	201.086983	101.047130			183.076418	92.041847	E	1480.739918	740.873597	1463.713369	732.360323	1462.729353	731.868315	10
3	314.171047	157.589161			296.160482	148.583879	L	***1351.697325***	676.352301	1334.670776	667.839026			9
4	**753.396373**	377.201825	736.369824	368.688550	735.385808	368.196542	Q	***1238.613261***	619.810269	1221.586712	611.296994			8
5	**913.427022**	457.217149	896.400473	448.703875	895.416457	448.211867	C	***799.387935***	400.197606	782.361386	391.684331			7
6	1010.479786	505.743531	993.453237	497.230257	992.469221	496.738249	P	***639.357286***	320.182281	622.330737	311.669007			6
7	**1138.538364**	569.772820	1121.511815	561.259546	1120.527799	560.767538	Q	542.304522	271.655899	525.277973	263.142625			5
8	1235.591128	618.299202	1218.564579	609.785928	1217.580563	609.293920	P	***414.245944***	207.626610	397.219395	199.113335			4
9	**1306.628242**	653.817759	1289.601693	645.304485	1288.617677	644.812477	A	***317.193180***	159.100228	300.166631	150.586953			3
10	**1377.665356**	689.336316	1360.638807	680.823042	1359.654791	680.331034	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 AELQCPQPAAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.4	1550.769730	-0.008362	AELQCPQPAAR
17.5	1550.769730	-0.008362	AELQCPQPAAR
15.4	1550.780945	-0.019577	EAIREHQMAR
13.3	1550.741196	0.020172	LWNMPENNGLHAR
9.4	1550.761856	-0.000488	MCSLMLSKELPAR
7.7	1550.780121	-0.018753	GSSPGPRPVEGTPASR
6.6	1550.743912	0.017456	ISGLVEGTMYYFR
6.3	1550.780975	-0.019607	AANGQGQQR
4.7	1550.761856	-0.000488	MCSLMLSKELPAR
4.5	1550.768845	-0.007477	SLGKRDLYDEAER

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

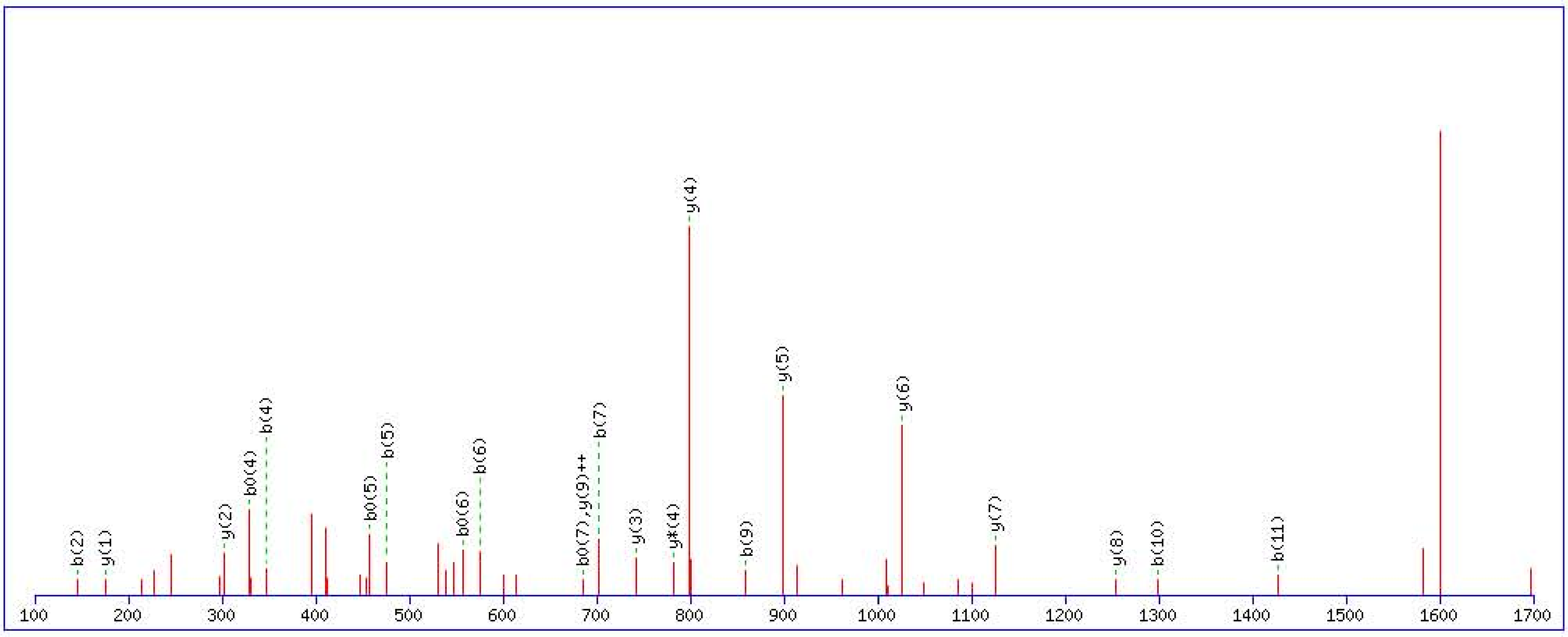
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

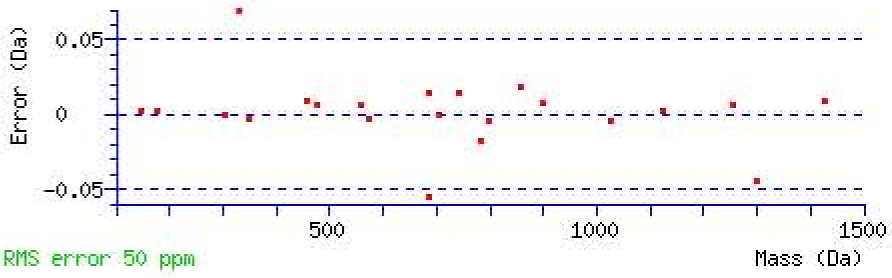
Match to Query 30567: 1599.764408 from(800.889480,2+) rtinseconds(1594) index(29363)
Title: Locus:1.1.1.3218.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

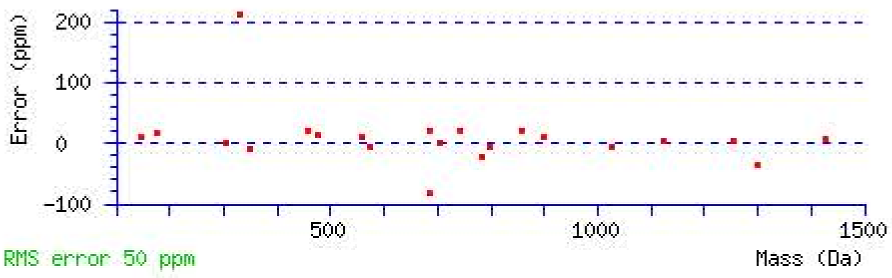
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1599.767517
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 2.7e-005
Matches : 22/106 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	88.039304	44.523290			70.028739	35.518008	S							12
2	***145.060768***	73.034022			127.050203	64.028740	G	1513.742754	757.375015	1496.716205	748.861741	1495.732189	748.369733	11
3	232.092796	116.550036			214.082231	107.544753	S	1456.721290	728.864283	1439.694741	720.351009	1438.710725	719.859001	10
4	***347.119739***	174.063507			329.109174	165.058225	D	1369.689262	685.348269	1352.662713	676.834995	1351.678697	676.342987	9
5	***476.162332***	238.584804			458.151767	229.579522	E	***1254.662319***	627.834798	1237.635770	619.321523	1236.651754	618.829515	8
6	***575.230746***	288.119011			557.220181	279.113729	V	***1125.619726***	563.313501	1108.593177	554.800227			7
7	***703.289324***	352.148300	686.262775	343.635026	685.278759	343.143018	Q	***1026.551312***	513.779294	1009.524763	505.266020			6
8	802.357738	401.682507	785.331189	393.169233	784.347173	392.677225	V	***898.492734***	449.750005	881.466185	441.236731			5
9	***859.379202***	430.193239	842.352653	421.679965	841.368637	421.187957	G	***799.424320***	400.215798	782.397771	391.702524			4
10	***1298.604528***	649.805902	1281.577979	641.292628	1280.593963	640.800620	Q	***742.402856***	371.705066	725.376307	363.191792			3
11	***1426.663106***	713.835191	1409.636557	705.321917	1408.652541	704.829909	Q	***303.177530***	152.092403	286.150981	143.579129			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1

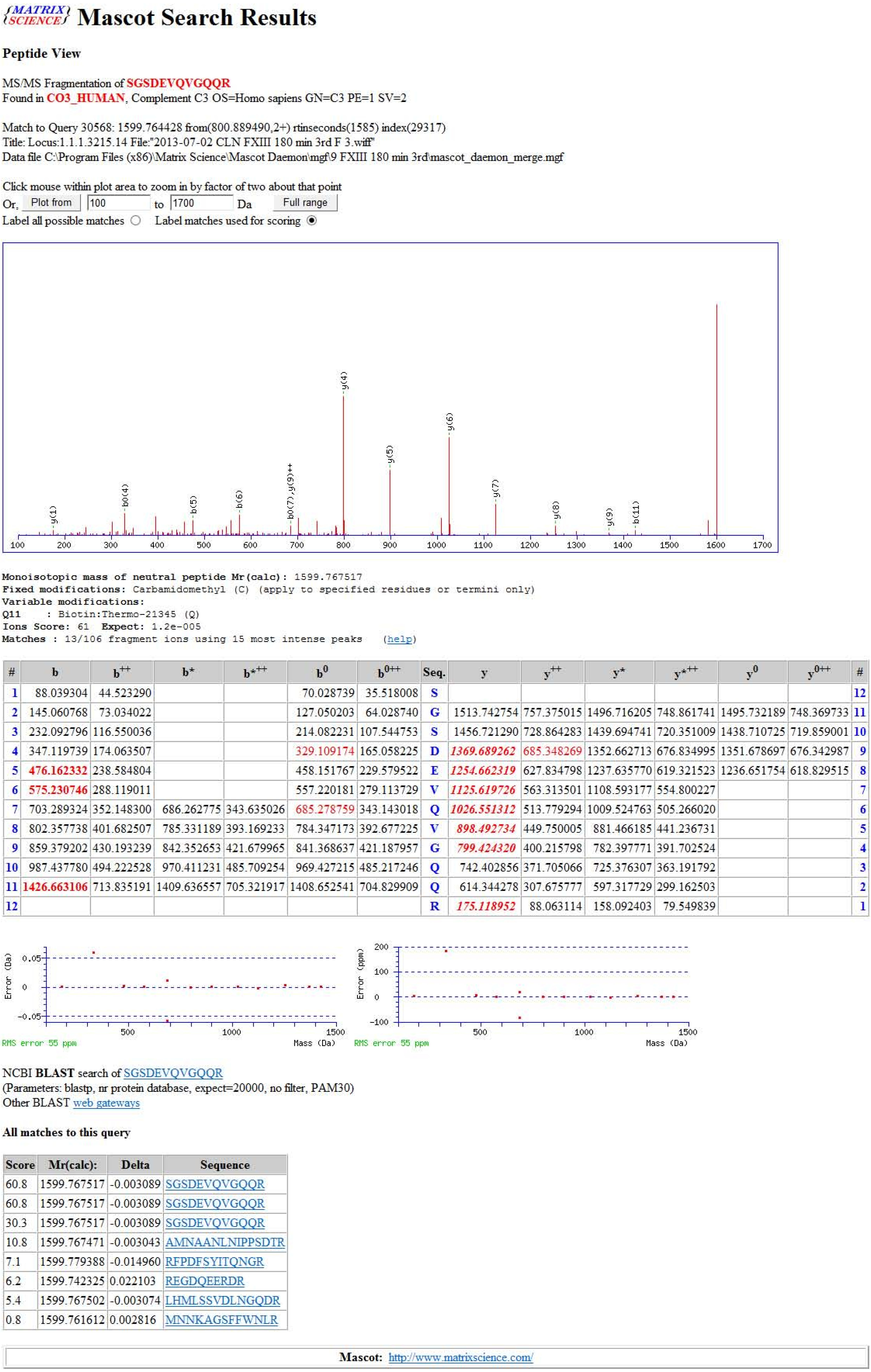




NCBI **BLAST** search of SGSDEVQVGQQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.2	1599.767517	-0.003109	SGSDEVQVGQQR
43.9	1599.767517	-0.003109	SGSDEVQVGQQR
22.4	1599.767517	-0.003109	SGSDEVQVGQQR
8.3	1599.785217	-0.020809	AQDLEAAQALAQSER
5.3	1599.774872	-0.010464	MAKEAIFQDTMRK
1.8	1599.742325	0.022083	REGDQEERDR
1.1	1599.767471	-0.003063	AMNAANLNIPPSDTR
0.0	1599.785217	-0.020809	SELNIQNAVNENQK



Mascot Search Results

Peptide View

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

Match to Query 30568: 1599.764428 from(800.889490,2+) rtinseconds(1585) index(29317)
Title: Locus:1.1.1.3215.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\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): 1599.767517
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 1.2e-005
Matches : 13/106 fragment ions using 15 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	145.060768	73.034022			127.050203	64.028740	G	1513.742754	757.375015	1496.716205	748.861741	1495.732189	748.369733	11
3	232.092796	116.550036			214.082231	107.544753	S	1456.721290	728.864283	1439.694741	720.351009	1438.710725	719.859001	10
4	347.119739	174.063507			329.109174	165.058225	D	***1369.689262***	685.348269	1352.662713	676.834995	1351.678697	676.342987	9
5	**476.162332**	238.584804			458.151767	229.579522	E	***1254.662319***	627.834798	1237.635770	619.321523	1236.651754	618.829515	8
6	**575.230746**	288.119011			557.220181	279.113729	V	***1125.619726***	563.313501	1108.593177	554.800227			7
7	703.289324	352.148300	686.262775	343.635026	685.278759	343.143018	Q	***1026.551312***	513.779294	1009.524763	505.266020			6
8	802.357738	401.682507	785.331189	393.169233	784.347173	392.677225	V	***898.492734***	449.750005	881.466185	441.236731			5
9	859.379202	430.193239	842.352653	421.679965	841.368637	421.187957	G	***799.424320***	400.215798	782.397771	391.702524			4
10	987.437780	494.222528	970.411231	485.709254	969.427215	485.217246	Q	742.402856	371.705066	725.376307	363.191792			3
11	**1426.663106**	713.835191	1409.636557	705.321917	1408.652541	704.829909	Q	614.344278	307.675777	597.317729	299.162503			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1

RMS error 55 ppm

RMS error 55 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.8	1599.767517	-0.003089	SGSDEVQVGQQR
60.8	1599.767517	-0.003089	SGSDEVQVGQQR
30.3	1599.767517	-0.003089	SGSDEVQVGQQR
10.8	1599.767471	-0.003043	AMNAANLNIPPSDTR
7.1	1599.779388	-0.014960	RFPDFSYITQNGR
6.2	1599.742325	0.022103	REGDQEERDR
5.4	1599.767502	-0.003074	LHMLSSVDLNGQDR
0.8	1599.761612	0.002816	MNNKAGSFFWNLR

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

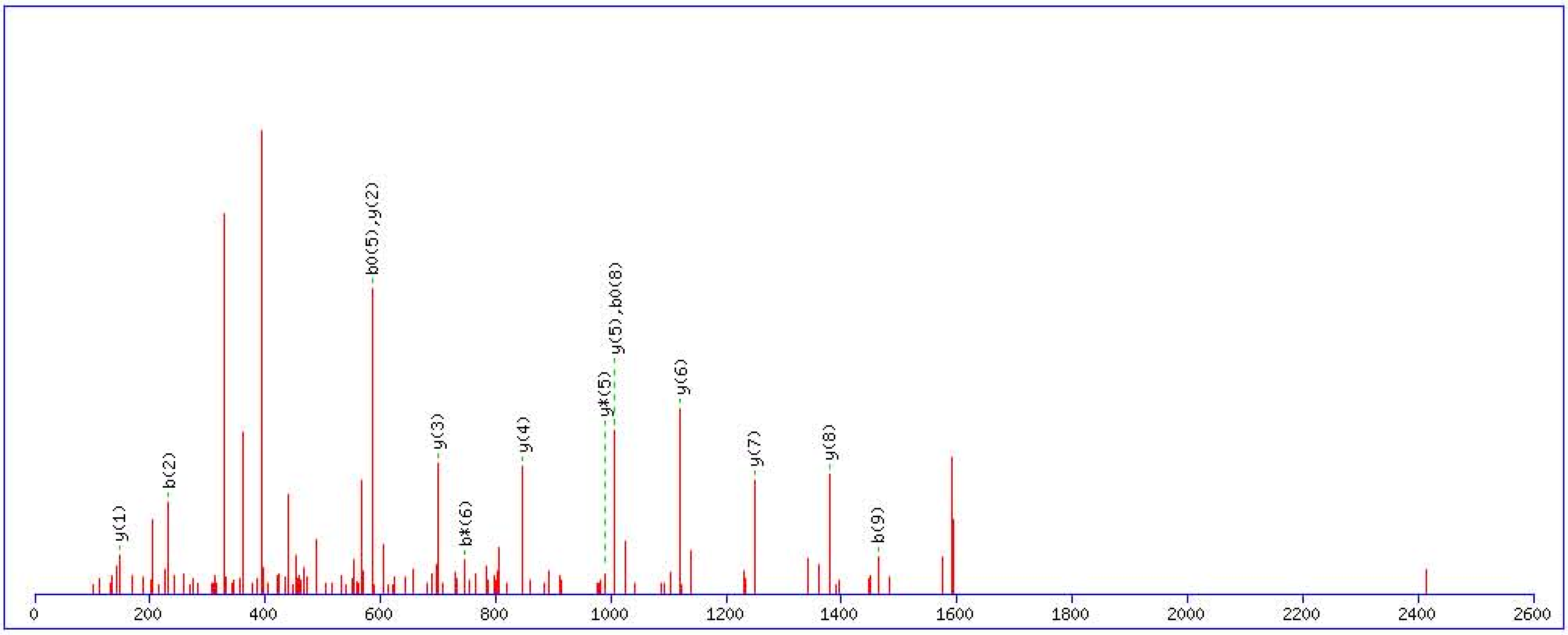
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

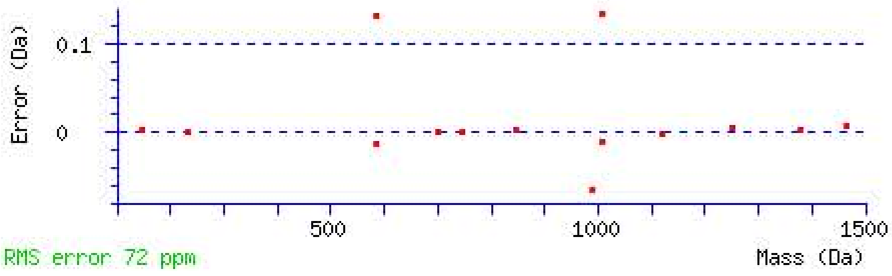
Match to Query 30816: 1608.706268 from(805.360410,2+) rtinseconds(1811) index(30678)
Title: Locus:1.1.1.3294.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

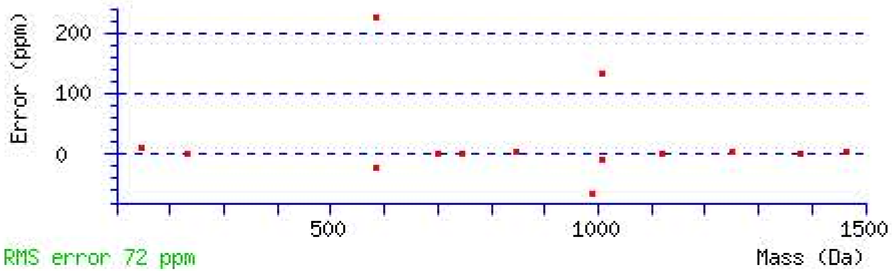
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1608.709839
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 70 **Expect:** 5.3e-007
Matches : 14/84 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	161.037925	81.022600					C							10
2	**232.075039**	116.541158					A	1449.686484	725.346880	1432.659935	716.833606	1431.675919	716.341598	9
3	361.117632	181.062454			343.107067	172.057172	E	***1378.649370***	689.828323	1361.622821	681.315049	1360.638805	680.823041	8
4	490.160225	245.583751			472.149660	236.578468	E	***1249.606777***	625.307027	1232.580228	616.793752	1231.596212	616.301744	7
5	604.203152	302.605214	587.176603	294.091940	586.192587	293.599932	N	***1120.564184***	560.785730	1103.537635	552.272456			6
6	764.233801	382.620539	747.207252	374.107264	746.223236	373.615256	C	***1006.521257***	503.764267	989.494708	495.250992			5
7	911.302215	456.154746	894.275666	447.641471	893.291650	447.149463	F	***846.490608***	423.748942	829.464059	415.235668			4
8	1024.386279	512.696777	1007.359730	504.183503	1006.375714	503.691495	I	***699.422194***	350.214735	682.395645	341.701461			3
9	**1463.611605**	732.309441	1446.585056	723.796166	1445.601040	723.304158	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 CAEENCFIQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.4	1608.709839	-0.003571	CAEENCFIQK
9.2	1608.721085	-0.014817	CNECGKGFAQK
3.7	1608.704941	0.001327	MAEAASGAGGTSLEGER
3.5	1608.723602	-0.017334	CAQAQTGIDLSGCTK

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

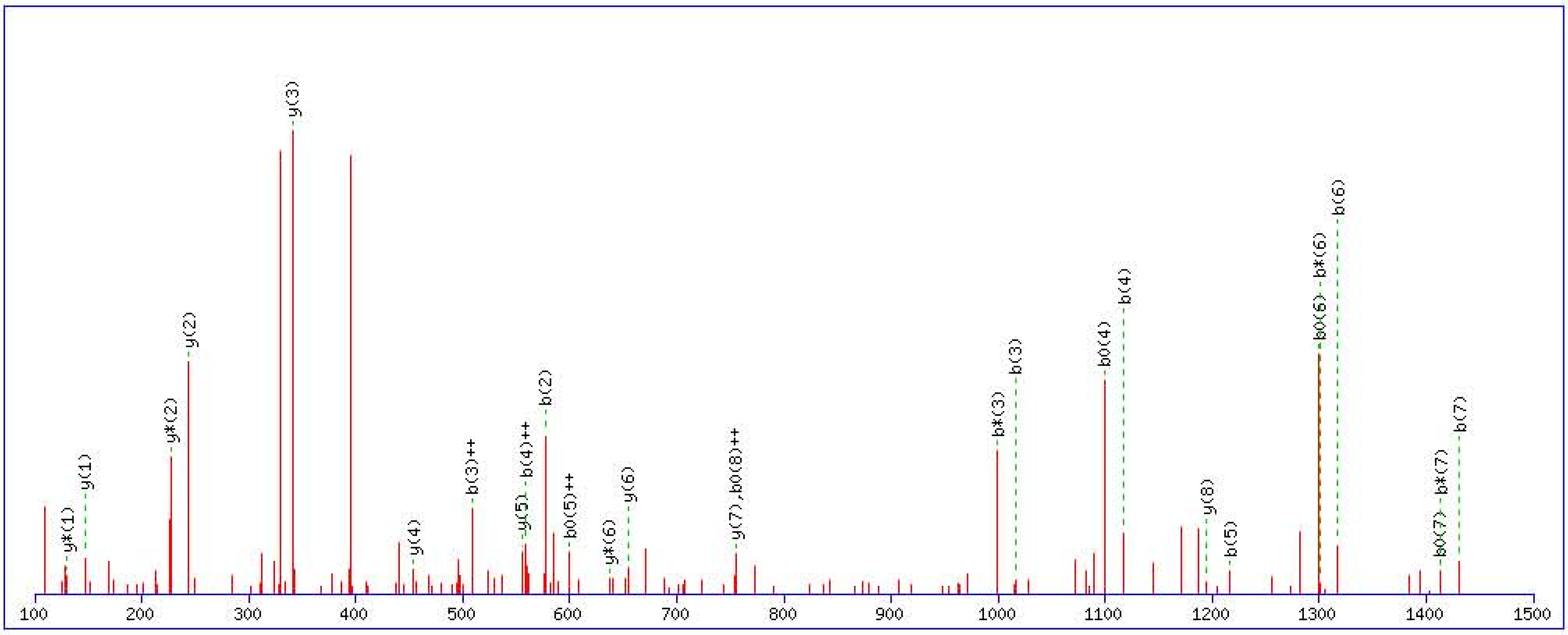
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

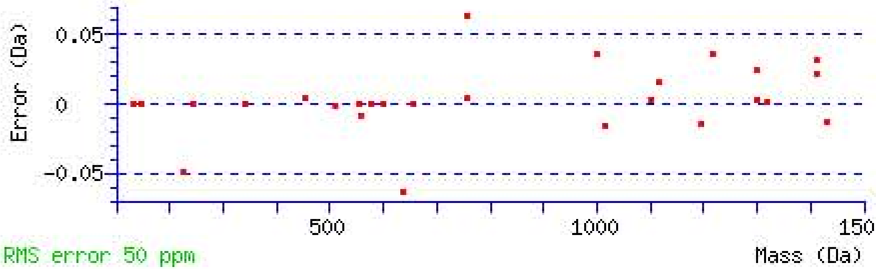
Match to Query 35116: 1769.961462 from(590.994430,3+) rtinseconds(1951) index(31478)
Title: Locus:1.1.1.3343.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

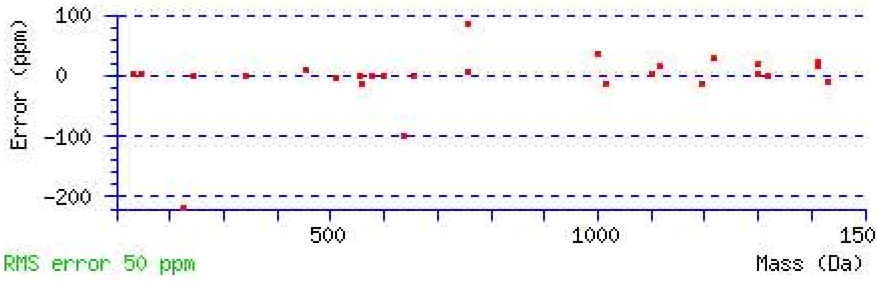
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1769.968460
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: 27  Expect: 0.0031
Matches : 27/92 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	138.066188	69.536732					H							10
2	**577.291514**	289.149395	560.264965	280.636121			Q	1633.916820	817.462048	1616.890271	808.948774	1615.906255	808.456766	9
3	**1016.516840**	**508.762058**	999.490291	500.248784			Q	***1194.691494***	597.849385	1177.664945	589.336111	1176.680929	588.844103	8
4	**1117.564519**	**559.285898**	1100.537970	550.772623	1099.553954	550.280615	T	***755.466168***	378.236722	738.439619	369.723448	737.455603	369.231440	7
5	**1216.632933**	608.820105	1199.606384	600.306830	1198.622368	599.814822	V	***654.418489***	327.712883	637.391940	319.199608	636.407924	318.707600	6
6	**1317.680612**	659.343944	1300.654063	650.830670	1299.670047	650.338662	T	***555.350075***	278.178676	538.323526	269.665401	537.339510	269.173393	5
7	**1430.764676**	715.885976	1413.738127	707.372702	1412.754111	706.880694	I	***454.302396***	227.654836	437.275847	219.141561			4
8	1527.817440	764.412358	1510.790891	755.899084	1509.806875	755.407076	P	***341.218332***	171.112804	324.191783	162.599530			3
9	1624.870204	812.938740	1607.843655	804.425466	1606.859639	803.933458	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 HQQTVTIPPK
(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	1769.968460	-0.006998	HQQTVTIPPK
0.4	1769.961029	0.000433	WMLSRDRASTLPLPK

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

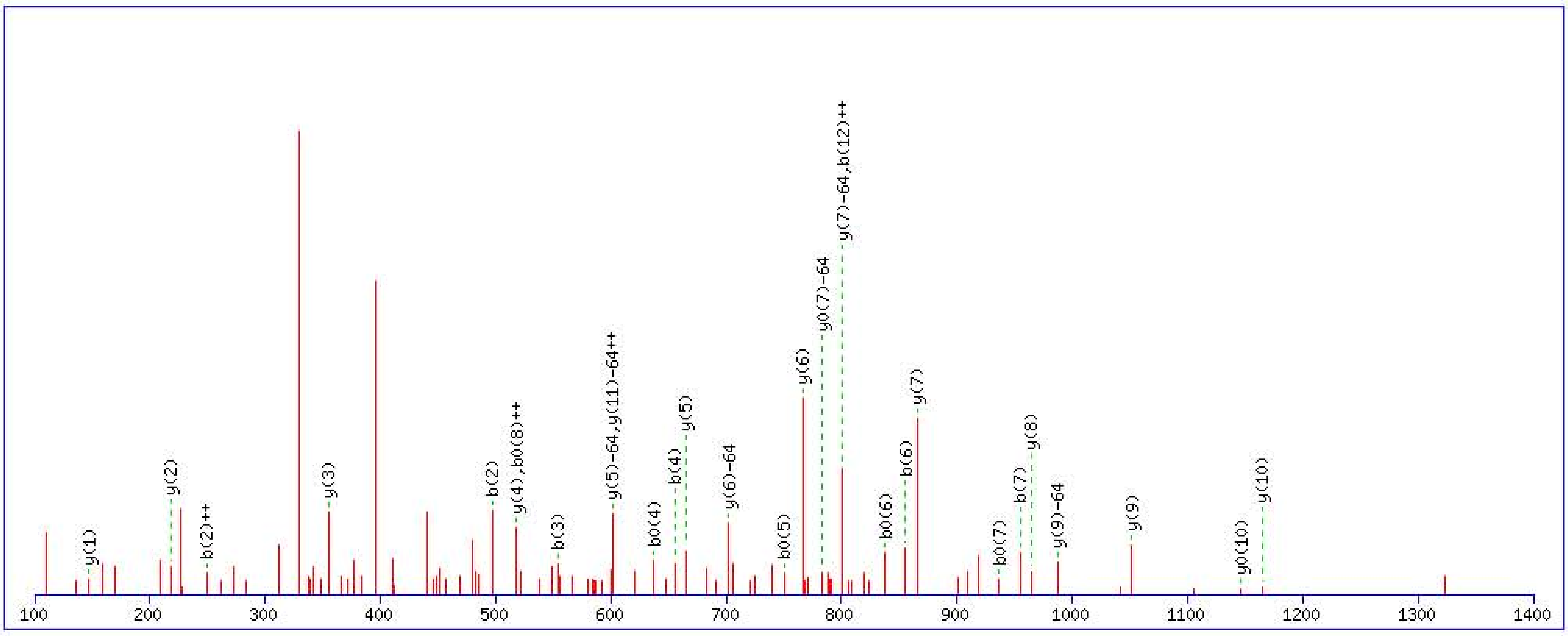
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

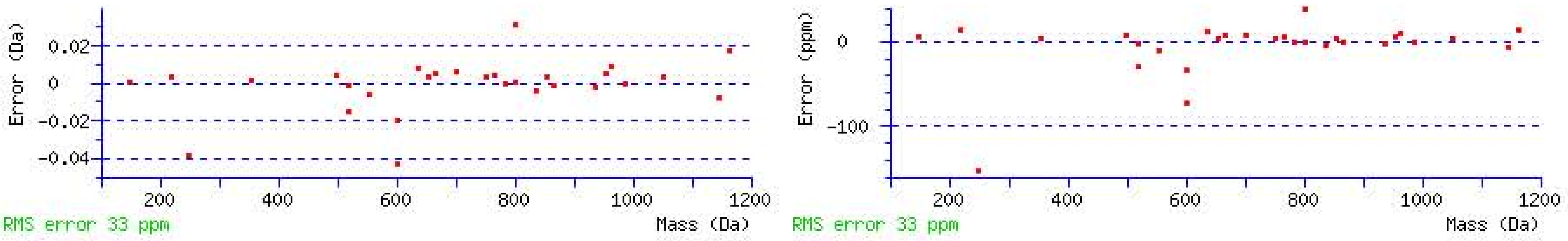
Match to Query 36116: 1817.910462 from(606.977430,3+) rtinseconds(1857) index(30889)
Title: Locus:1.1.1.3310.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 1817.916824
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
M10     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 51  Expect: 0.00018
Matches : 29/214 fragment ions using 51 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	1761.902627	881.454952	1744.876078	872.941677	1743.892062	872.449669	13
3	**554.275530**	277.641403	537.248981	269.128129			G	1322.677301	661.842289	1305.650752	653.329014	1304.666736	652.837006	12
4	**655.323209**	328.165243	638.296660	319.651968	637.312644	319.159960	T	1265.655837	633.331557	1248.629288	624.818282	1247.645272	624.326274	11
5	768.407273	384.707275	751.380724	376.194000	750.396708	375.701992	L	***1164.608158***	582.807717	1147.581609	574.294443	1146.597593	573.802435	10
6	**855.439301**	428.223289	838.412752	419.710014	837.428736	419.218006	S	***1051.524094***	526.265685	1034.497545	517.752411	1033.513529	517.260403	9
7	**954.507715**	477.757496	937.481166	469.244221	936.497150	468.752213	V	***964.492066***	482.749671	947.465517	474.236397	946.481501	473.744389	8
8	1053.576129	527.291703	1036.549580	518.778428	1035.565564	518.286420	V	***865.423652***	433.215464	848.397103	424.702190	847.413087	424.210182	7
9	1154.623808	577.815542	1137.597259	569.302268	1136.613243	568.810260	T	***766.355238***	383.681257	749.328689	375.167983	748.344673	374.675975	6
10	1301.659208	651.333242	1284.632659	642.819968	1283.648643	642.327960	M	***665.307559***	333.157418	648.281010	324.644143			5
11	1464.722537	732.864907	1447.695988	724.351632	1446.711972	723.859624	Y	***518.272159***	259.639718	501.245610	251.126443			4
12	1601.781449	**801.394363**	1584.754900	792.881088	1583.770884	792.389080	H	***355.208830***	178.108053	338.182281	169.594778			3
13	1672.818563	836.912920	1655.792014	828.399645	1654.807998	827.907637	A	***218.149918***	109.578597	201.123369	101.065322			2
14							K	***147.112804***	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.5	1817.916824	-0.006362	GQGTLSVVTMYHAK

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

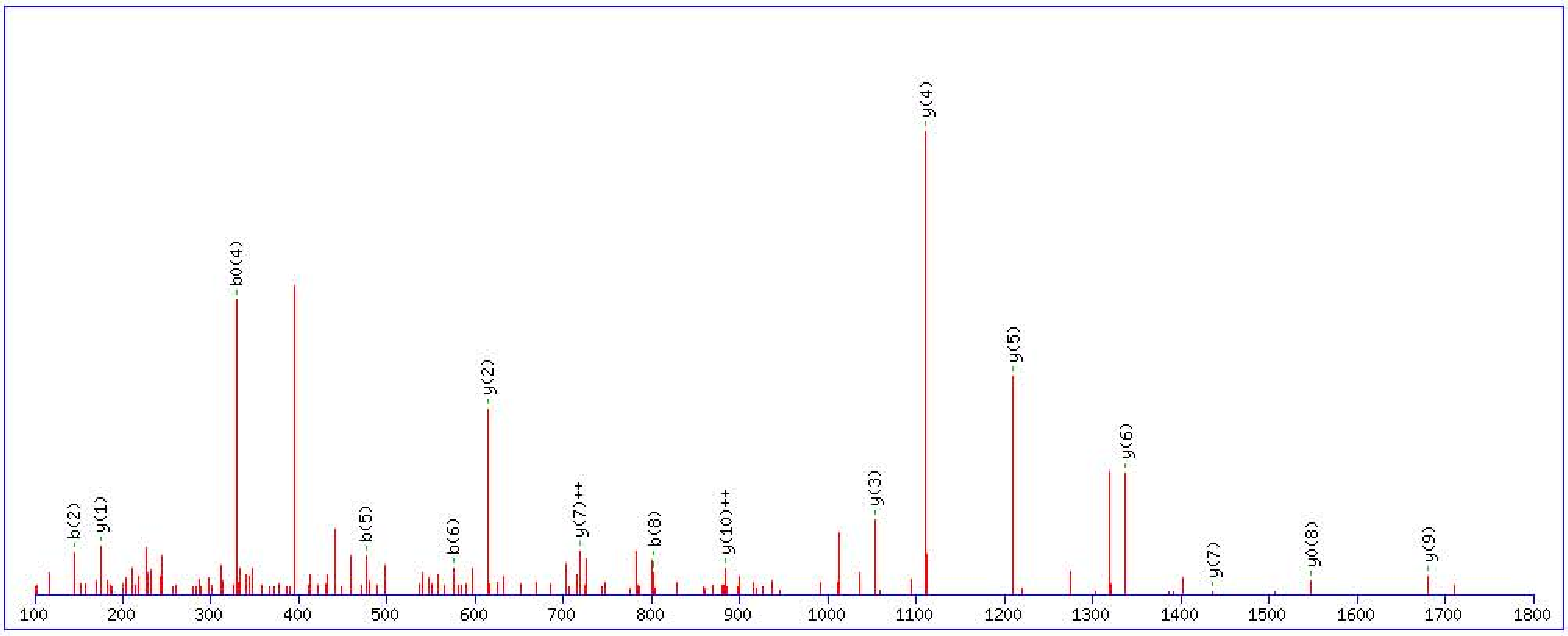
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

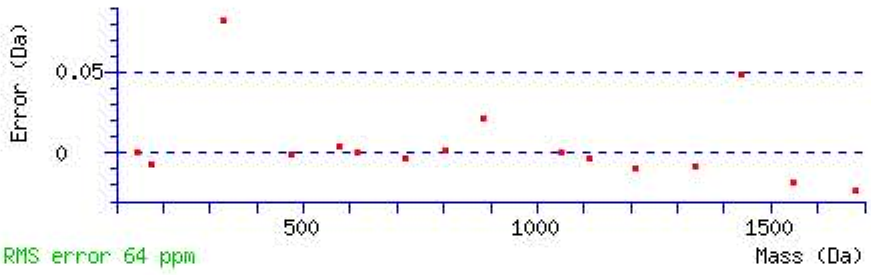
Match to Query 37639: 1910.930052 from(637.983960,3+) rtinseconds(1923) index(31254)
Title: Locus:1.1.1.3333.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

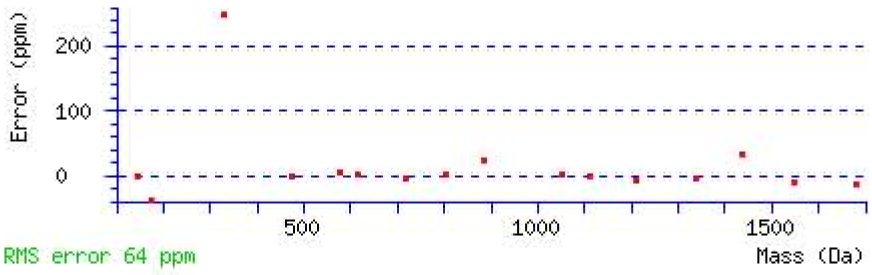
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1910.934265
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 40 **Expect:** 0.00083
Matches : 16/106 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	88.039304	44.523290			70.028739	35.518008	S							12
2	**145.060768**	73.034022			127.050203	64.028740	G	1824.909502	912.958389	1807.882953	904.445115	1806.898937	903.953107	11
3	232.092796	116.550036			214.082231	107.544753	S	1767.888038	884.447657	1750.861489	875.934383	1749.877473	875.442375	10
4	347.119739	174.063507			329.109174	165.058225	D	***1680.856010***	840.931643	1663.829461	832.418369	1662.845445	831.926361	9
5	**476.162332**	238.584804			458.151767	229.579522	E	1565.829067	783.418172	1548.802518	774.904897	1547.818502	774.412889	8
6	**575.230746**	288.119011			557.220181	279.113729	V	***1436.786474***	718.896875	1419.759925	710.383601			7
7	703.289324	352.148300	686.262775	343.635026	685.278759	343.143018	Q	***1337.718060***	669.362668	1320.691511	660.849394			6
8	**802.357738**	401.682507	785.331189	393.169233	784.347173	392.677225	V	***1209.659482***	605.333379	1192.632933	596.820105			5
9	859.379202	430.193239	842.352653	421.679965	841.368637	421.187957	G	***1110.591068***	555.799172	1093.564519	547.285898			4
10	1298.604528	649.805902	1281.577979	641.292628	1280.593963	640.800620	Q	***1053.569604***	527.288440	1036.543055	518.775166			3
11	1737.829854	869.418565	1720.803305	860.905291	1719.819289	860.413283	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 SGSDEVQVGQQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.1	1910.934265	-0.004213	SGSDEVQVGQQR
12.3	1910.934265	-0.004213	SGSDEVQVGQQR
6.8	1910.958542	-0.028490	TDDYGRDLSSVQTLLTK
6.2	1910.934265	-0.004213	SGSDEVQVGQQR
1.9	1910.915619	0.014433	EDSGSGMKAELPPGPGAVGR
0.0	1910.949310	-0.019258	GILSQMGRHSQSRSHSK

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

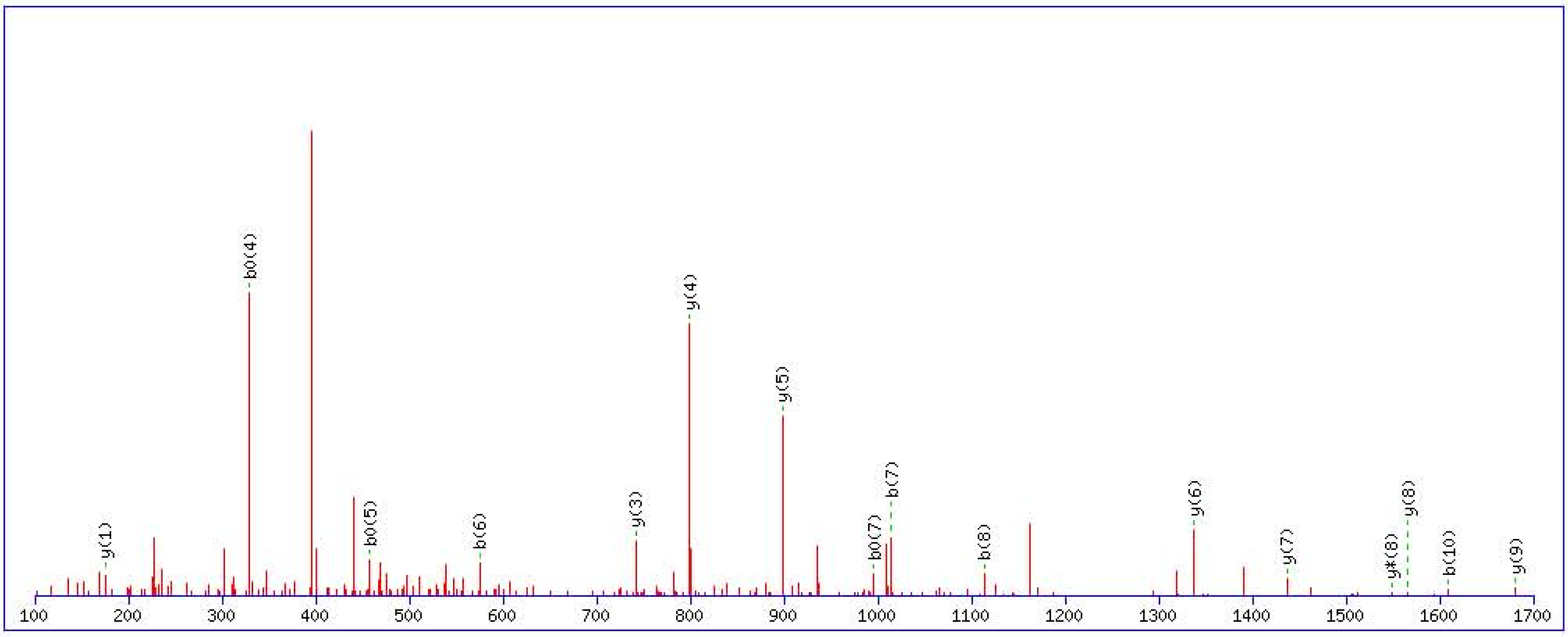
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

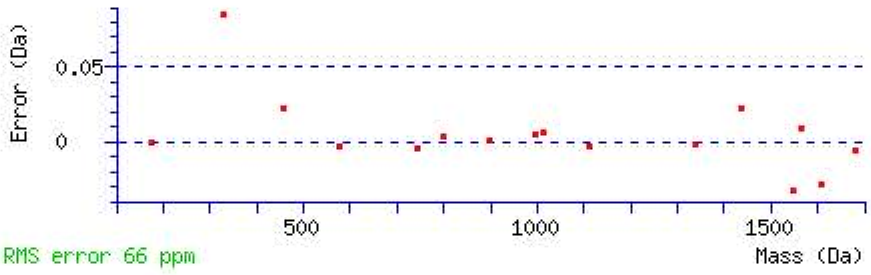
Match to Query 37642: 1910.930802 from(637.984210,3+) rtinseconds(1891) index(31052)
Title: Locus:1.1.1.3322.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

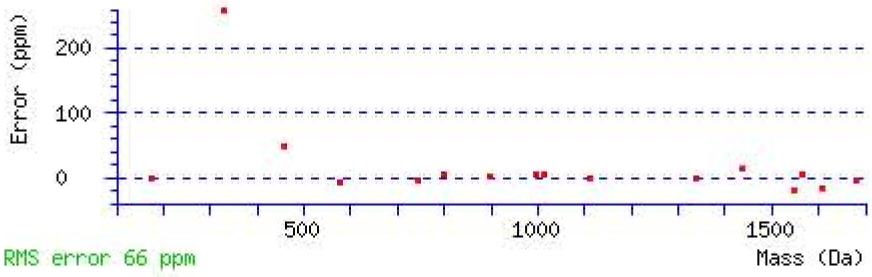
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1910.934265
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Q10    : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.0021
Matches : 16/106 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							12
2	145.060768	73.034022			127.050203	64.028740	G	1824.909502	912.958389	1807.882953	904.445115	1806.898937	903.953107	11
3	232.092796	116.550036			214.082231	107.544753	S	1767.888038	884.447657	1750.861489	875.934383	1749.877473	875.442375	10
4	347.119739	174.063507			329.109174	165.058225	D	***1680.856010***	840.931643	1663.829461	832.418369	1662.845445	831.926361	9
5	476.162332	238.584804			458.151767	229.579522	E	***1565.829067***	783.418172	1548.802518	774.904897	1547.818502	774.412889	8
6	**575.230746**	288.119011			557.220181	279.113729	V	***1436.786474***	718.896875	1419.759925	710.383601			7
7	**1014.456072**	507.731674	997.429523	499.218400	996.445507	498.726392	Q	***1337.718060***	669.362668	1320.691511	660.849394			6
8	**1113.524486**	557.265881	1096.497937	548.752607	1095.513921	548.260599	V	***898.492734***	449.750005	881.466185	441.236731			5
9	1170.545950	585.776613	1153.519401	577.263339	1152.535385	576.771330	G	***799.424320***	400.215798	782.397771	391.702524			4
10	**1609.771276**	805.389276	1592.744727	796.876002	1591.760711	796.383994	Q	***742.402856***	371.705066	725.376307	363.191792			3
11	1737.829854	869.418565	1720.803305	860.905291	1719.819289	860.413283	Q	303.177530	152.092403	286.150981	143.579129			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SGSDEVQVGQQR
(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	1910.934265	-0.003463	SGSDEVQVGQQR
38.6	1910.934265	-0.003463	SGSDEVQVGQQR
32.7	1910.938263	-0.007461	YVTSAPMPEPQAPGR
1.6	1910.934265	-0.003463	SGSDEVQVGQQR

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

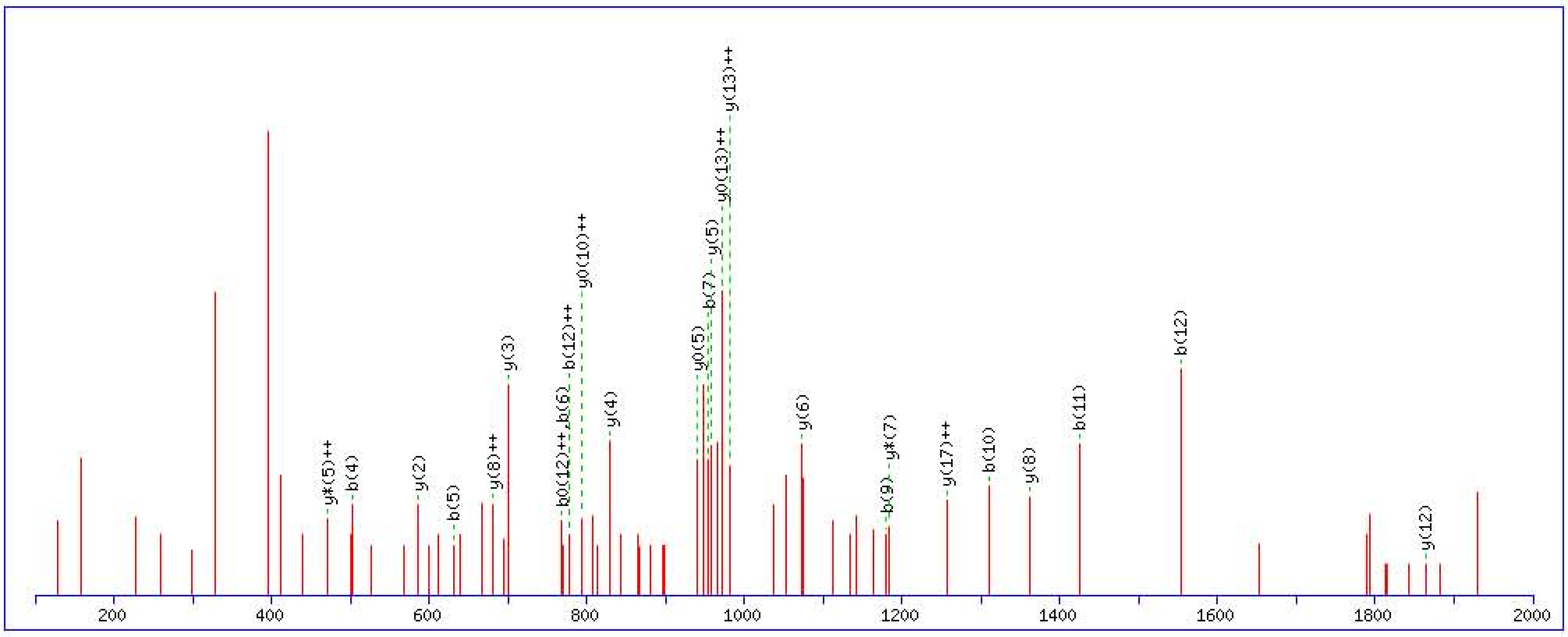
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

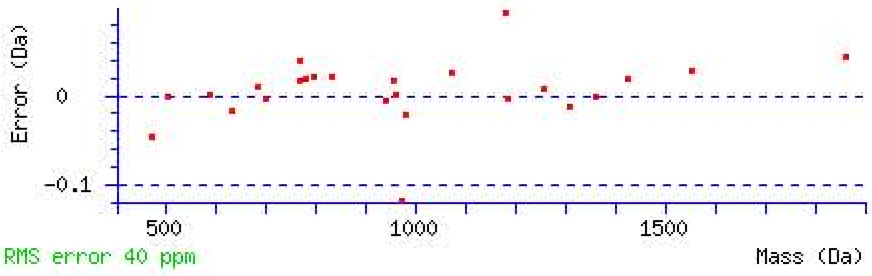
Match to Query 38202: 2913.174372 from(972.065400,3+) rtinseconds(2137) index(46828)
Title: Locus:1.1.1.3456.24 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

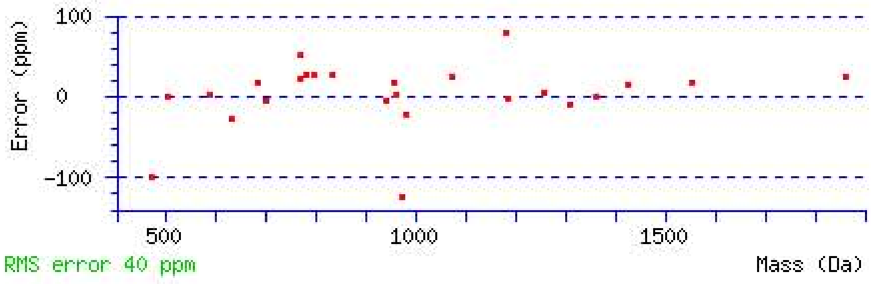


Monoisotopic mass of neutral peptide Mr(calc): 2913.185776
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q19 : Biotin:Thermo-21345 (Q)
Ions Score: 28 **Expect:** 0.012
Matches : 25/196 fragment ions using 68 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							20
2	217.081898	109.044587			199.071333	100.039304	T	2799.166123	1400.086699	2782.139574	1391.573425	2781.155558	1391.081417	19
3	403.161211	202.084244			385.150646	193.078961	W	2698.118444	1349.562860	2681.091895	1341.049585	2680.107879	1340.557577	18
4	***502.229625***	251.618451			484.219060	242.613168	V	2512.039131	1256.523203	2495.012582	1248.009929	2494.028566	1247.517921	17
5	***631.272218***	316.139747			613.261653	307.134465	E	2412.970717	1206.988996	2395.944168	1198.475722	2394.960152	1197.983714	16
6	***768.331130***	384.669203			750.320565	375.663921	H	2283.928124	1142.467700	2266.901575	1133.954425	2265.917559	1133.462417	15
7	***954.410443***	477.708860			936.399878	468.703577	W	2146.869212	1073.938244	2129.842663	1065.424969	2128.858647	1064.932961	14
8	1051.463207	526.235242			1033.452642	517.229959	P	1960.789899	980.898588	1943.763350	972.385313	1942.779334	971.893305	13
9	***1180.505800***	590.756538			1162.495235	581.751256	E	***1863.737135***	932.372206	1846.710586	923.858931	1845.726570	923.366923	12
10	***1309.548393***	655.277835			1291.537828	646.272552	E	1734.694542	867.850909	1717.667993	859.337635	1716.683977	858.845627	11
11	***1424.575336***	712.791306			1406.564771	703.786024	D	1605.651949	803.329613	1588.625400	794.816338	1587.641384	794.324330	10
12	***1553.617929***	777.312603			1535.607364	768.307320	E	1490.625006	745.816141	1473.598457	737.302867	1472.614441	736.810859	9
13	1713.648578	857.327927			1695.638013	848.322645	C	***1361.582413***	681.294845	1344.555864	672.781570	1343.571848	672.289562	8
14	1841.707156	921.357216	1824.680607	912.843942	1823.696591	912.351934	Q	1201.551764	601.279520	1184.525215	592.766246	1183.541199	592.274238	7
15	1956.734099	978.870688	1939.707550	970.357413	1938.723534	969.865405	D	***1073.493186***	537.250231	1056.466637	528.736957	1055.482621	528.244949	6
16	2085.776692	1043.391984	2068.750143	1034.878709	2067.766127	1034.386701	E	***958.466243***	479.736760	941.439694	471.223485	940.455678	470.731477	5
17	2214.819285	1107.913280	2197.792736	1099.400006	2196.808720	1098.907998	E	***829.423650***	415.215463	812.397101	406.702189	811.413085	406.210181	4
18	2328.862212	1164.934744	2311.835663	1156.421469	2310.851647	1155.929461	N	***700.381057***	350.694167	683.354508	342.180892			3
19	2768.087538	1384.547407	2751.060989	1376.034132	2750.076973	1375.542125	Q	***586.338130***	293.672703	569.311581	285.159429			2
20							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 40 ppm



RMS error 40 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.4	2913.185776	-0.011404	DTWVEHWPEEDECQDEENQK
12.3	2913.185776	-0.011404	DTWVEHWPEEDECQDEENQK

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

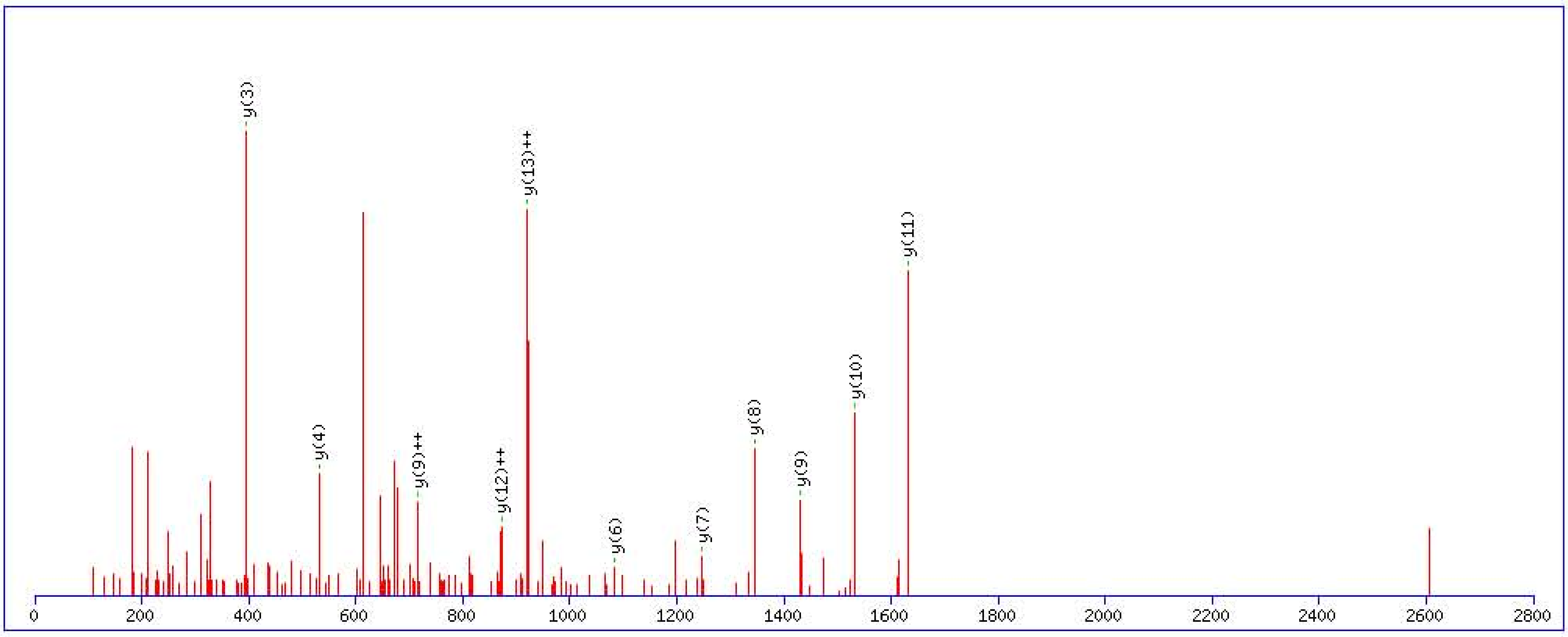
Mascot Search Results

Peptide View

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

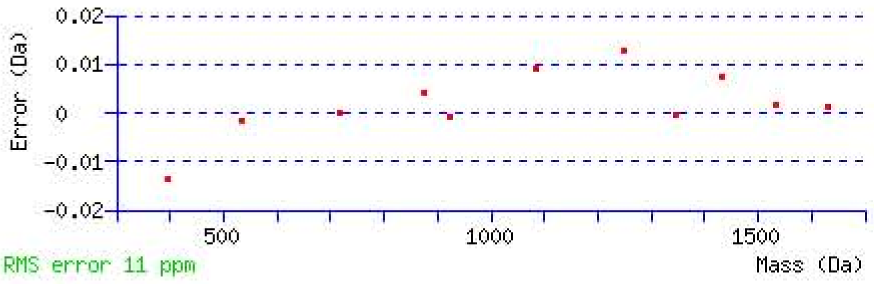
Match to Query 41576: 2098.126542 from(700.382790,3+) rtinseconds(2330) index(33743)
Title: Locus:1.1.1.3475.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

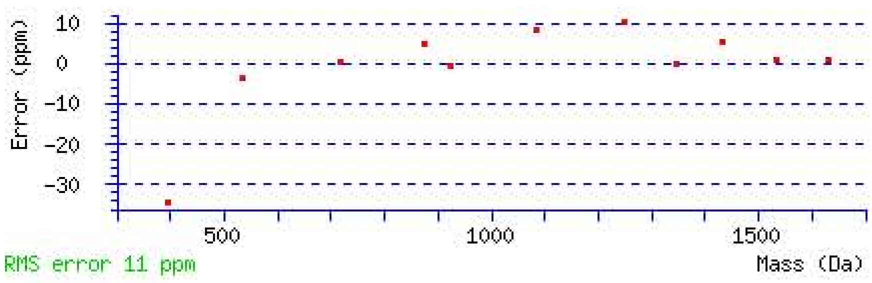
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2098.128525
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 55  Expect: 6.7e-006
Matches : 11/158 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	88.039304	44.523290			70.028739	35.518008	S							16
2	145.060768	73.034022			127.050203	64.028740	G	2012.103769	1006.555523	1995.077220	998.042248	1994.093204	997.550240	15
3	258.144832	129.576054			240.134267	120.570772	I	1955.082305	978.044791	1938.055756	969.531516	1937.071740	969.039508	14
4	355.197596	178.102436			337.187031	169.097154	P	1841.998241	921.502759	1824.971692	912.989484	1823.987676	912.497476	13
5	468.281660	234.644468			450.271095	225.639186	I	1744.945477	872.976377	1727.918928	864.463102	1726.934912	863.971094	12
6	567.350074	284.178675			549.339509	275.173393	V	***1631.861413***	816.434345	1614.834864	807.921070	1613.850848	807.429062	11
7	668.397753	334.702515			650.387188	325.697232	T	***1532.792999***	766.900138	1515.766450	758.386863	1514.782434	757.894855	10
8	755.429781	378.218529			737.419216	369.213246	S	***1431.745320***	716.376298	1414.718771	707.863024	1413.734755	707.371016	9
9	852.482545	426.744911			834.471980	417.739628	P	***1344.713292***	672.860284	1327.686743	664.347010	1326.702727	663.855002	8
10	1015.545874	508.276575			997.535309	499.271293	Y	***1247.660528***	624.333902	1230.633979	615.820628	1229.649963	615.328620	7
11	1454.771200	727.889238	1437.744651	719.375964	1436.760635	718.883956	Q	***1084.597199***	542.802238	1067.570650	534.288963	1066.586634	533.796955	6
12	1567.855264	784.431270	1550.828715	775.917996	1549.844699	775.425988	I	645.371873	323.189574	628.345324	314.676300	627.361308	314.184292	5
13	1704.914176	852.960726	1687.887627	844.447452	1686.903611	843.955444	H	***532.287809***	266.647542	515.261260	258.134268	514.277244	257.642260	4
14	1851.982590	926.494933	1834.956041	917.981659	1833.972025	917.489651	F	***395.228897***	198.118086	378.202348	189.604812	377.218332	189.112804	3
15	1953.030269	977.018773	1936.003720	968.505498	1935.019704	968.013490	T	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	2
16							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SGIPIVTSPYQIHFTK
(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	2098.128525	-0.001983	SGIPIVTSPYQIHFTK
0.0	2098.157700	-0.031158	QRMKMVIGQLEGILR

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

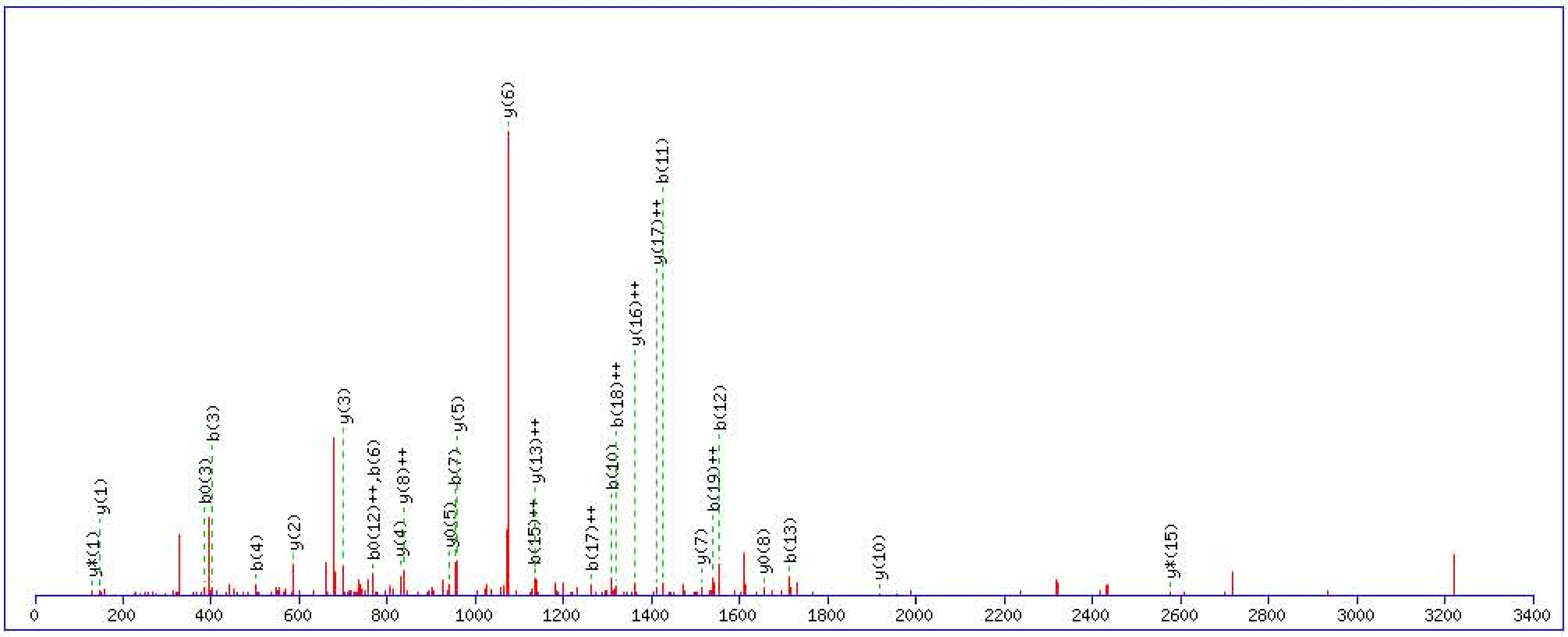
Mascot Search Results

Peptide View

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

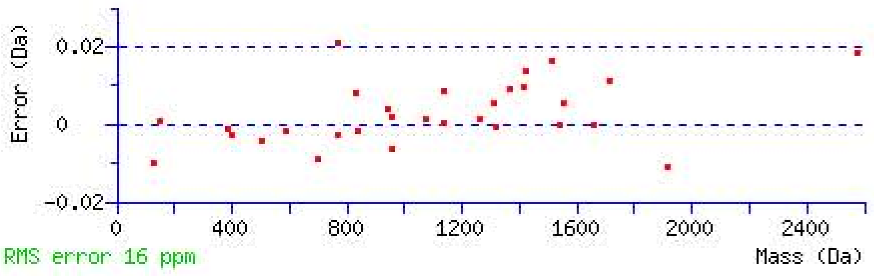
Match to Query 42326: 3224.325432 from(1075.782420,3+) rtinseconds(2286) index(33562)
Title: Locus:1.1.1.3459.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

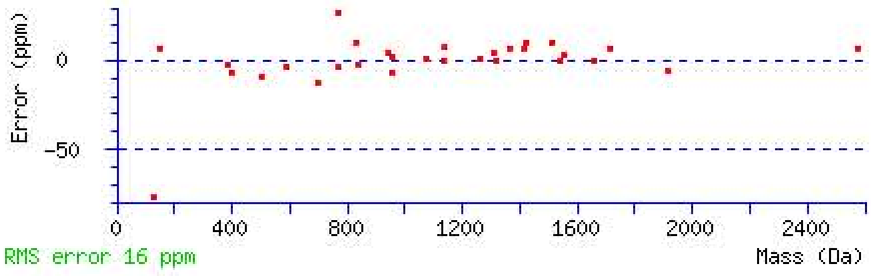
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3224.352524
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14    : Biotin:Thermo-21345 (Q)
Q19    : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.00083
Matches : 30/196 fragment ions using 65 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							20
2	217.081898	109.044587			199.071333	100.039304	T	3110.332871	1555.670073	3093.306322	1547.156799	3092.322306	1546.664791	19
3	***403.161211***	202.084244			385.150646	193.078961	W	3009.285192	1505.146234	2992.258643	1496.632959	2991.274627	1496.140951	18
4	***502.229625***	251.618451			484.219060	242.613168	V	2823.205879	1412.106577	2806.179330	1403.593303	2805.195314	1403.101295	17
5	631.272218	316.139747			613.261653	307.134465	E	2724.137465	1362.572370	2707.110916	1354.059096	2706.126900	1353.567088	16
6	***768.331130***	384.669203			750.320565	375.663921	H	2595.094872	1298.051074	2578.068323	1289.537799	2577.084307	1289.045792	15
7	***954.410443***	477.708860			936.399878	468.703577	W	2458.035960	1229.521618	2441.009411	1221.008343	2440.025395	1220.516335	14
8	1051.463207	526.235242			1033.452642	517.229959	P	2271.956647	1136.481961	2254.930098	1127.968687	2253.946082	1127.476679	13
9	1180.505800	590.756538			1162.495235	581.751256	E	2174.903883	1087.955579	2157.877334	1079.442305	2156.893318	1078.950297	12
10	***1309.548393***	655.277835			1291.537828	646.272552	E	2045.861290	1023.434283	2028.834741	1014.921009	2027.850725	1014.429001	11
11	***1424.575336***	712.791306			1406.564771	703.786024	D	***1916.818697***	958.912987	1899.792148	950.399712	1898.808132	949.907704	10
12	***1553.617929***	777.312603			1535.607364	768.307320	E	1801.791754	901.399515	1784.765205	892.886241	1783.781189	892.394233	9
13	***1713.648578***	857.327927			1695.638013	848.322645	C	1672.749161	836.878219	1655.722612	828.364944	1654.738596	827.872936	8
14	2152.873904	1076.940590	2135.847355	1068.427315	2134.863339	1067.935307	Q	***1512.718512***	756.862894	1495.691963	748.349620	1494.707947	747.857612	7
15	2267.900847	**1134.454061**	2250.874298	1125.940787	2249.890282	1125.448779	D	***1073.493186***	537.250231	1056.466637	528.736957	1055.482621	528.244949	6
16	2396.943440	1198.975358	2379.916891	1190.462083	2378.932875	1189.970075	E	***958.466243***	479.736760	941.439694	471.223485	940.455678	470.731477	5
17	2525.986033	**1263.496655**	2508.959484	1254.983380	2507.975468	1254.491372	E	***829.423650***	415.215463	812.397101	406.702189	811.413085	406.210181	4
18	2640.028960	**1320.518118**	2623.002411	1312.004843	2622.018395	1311.512835	N	***700.381057***	350.694167	683.354508	342.180892			3
19	3079.254286	**1540.130781**	3062.227737	1531.617507	3061.243721	1531.125499	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 DTWVEHWPEEDECQDEENQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.9	3224.352524	-0.027092	DTWVEHWPEEDECQDEENQK

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

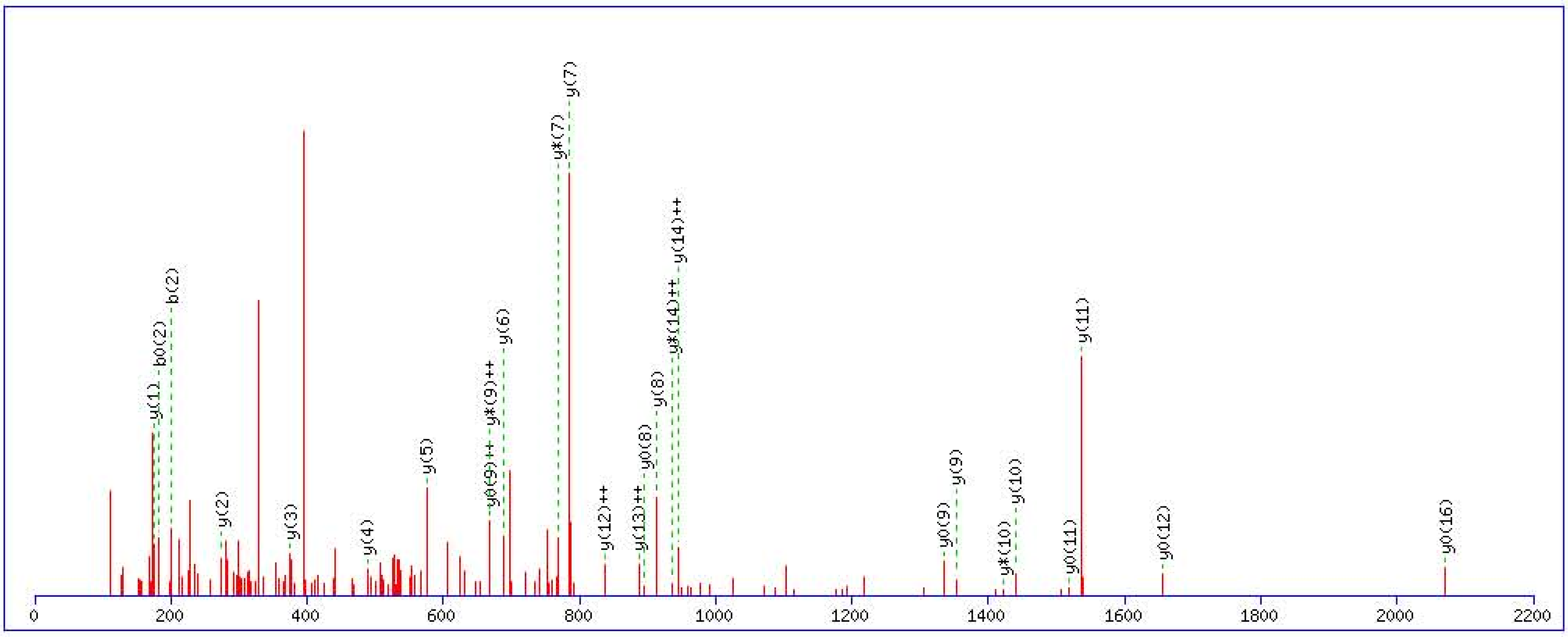
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

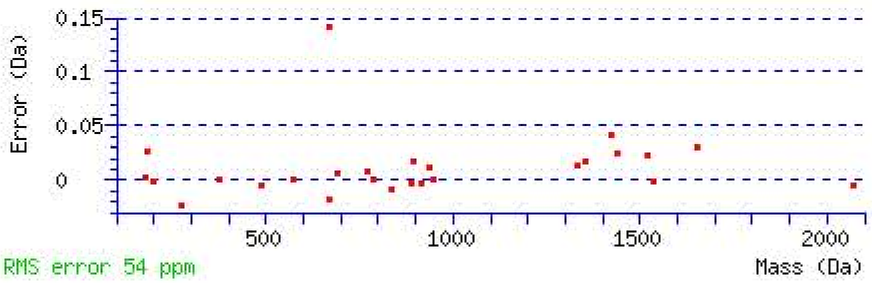
Match to Query 43234: 2201.229016 from(551.314530,4+) rtinseconds(1902) index(31125)
Title: Locus:1.1.1.3326.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

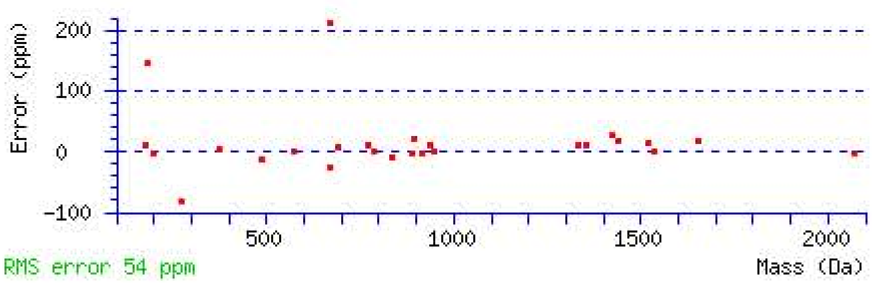
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 41  Expect: 0.00083
Matches : 26/180 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	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
40.5	2201.235428	-0.006412	LSINTHPSQKPLSITVR

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

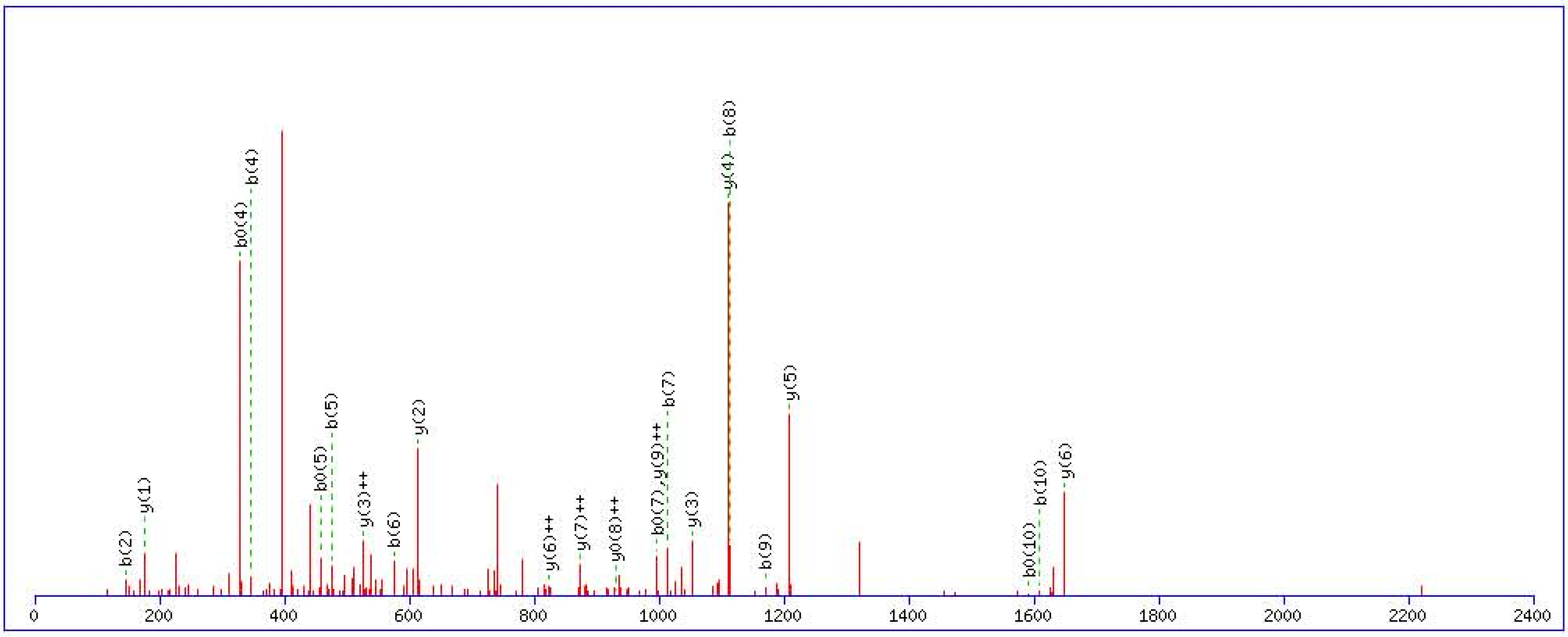
Mascot Search Results

Peptide View

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

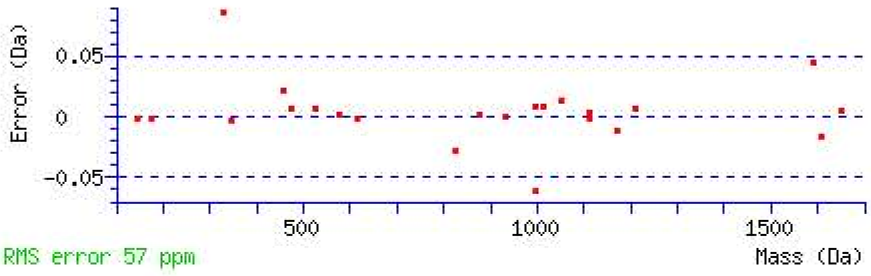
Match to Query 43653: 2222.094192 from(741.705340,3+) rtinseconds(2150) index(32738)
Title: Locus:1.1.1.3412.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

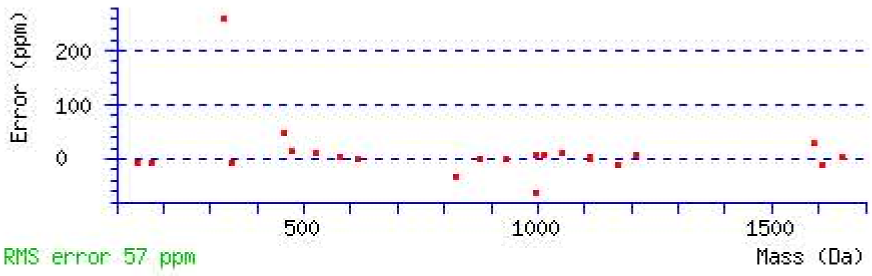
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2222.101013
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Q10 : Biotin:Thermo-21345 (Q)
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 25 **Expect:** 0.0052
Matches : 23/106 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	88.039304	44.523290			70.028739	35.518008	S							12
2	***145.060768***	73.034022			127.050203	64.028740	G	2136.076250	1068.541763	2119.049701	1060.028488	2118.065685	1059.536480	11
3	232.092796	116.550036			214.082231	107.544753	S	2079.054786	1040.031031	2062.028237	1031.517756	2061.044221	1031.025748	10
4	***347.119739***	174.063507			329.109174	165.058225	D	1992.022758	996.515017	1974.996209	988.001743	1974.012193	987.509735	9
5	***476.162332***	238.584804			458.151767	229.579522	E	1876.995815	939.001546	1859.969266	930.488271	1858.985250	929.996263	8
6	***575.230746***	288.119011			557.220181	279.113729	V	1747.953222	874.480249	1730.926673	865.966975			7
7	***1014.456072***	507.731674	997.429523	499.218400	996.445507	498.726392	Q	**1648.884808**	824.946042	1631.858259	816.432768			6
8	***1113.524486***	557.265881	1096.497937	548.752607	1095.513921	548.260599	V	**1209.659482**	605.333379	1192.632933	596.820105			5
9	***1170.545950***	585.776613	1153.519401	577.263339	1152.535385	576.771330	G	**1110.591068**	555.799172	1093.564519	547.285898			4
10	***1609.771276***	805.389276	1592.744727	796.876002	1591.760711	796.383994	Q	**1053.569604**	527.288440	1036.543055	518.775166			3
11	2048.996602	1025.001939	2031.970053	1016.488665	2030.986037	1015.996657	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 SGSDEVQVGQQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.3	2222.101013	-0.006821	SGSDEVQVGQQR
0.9	2222.116058	-0.021866	GILSQMGRHSQSRSHSK
0.5	2222.125290	-0.031098	TDDYGRDLSSVQTLLTK

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

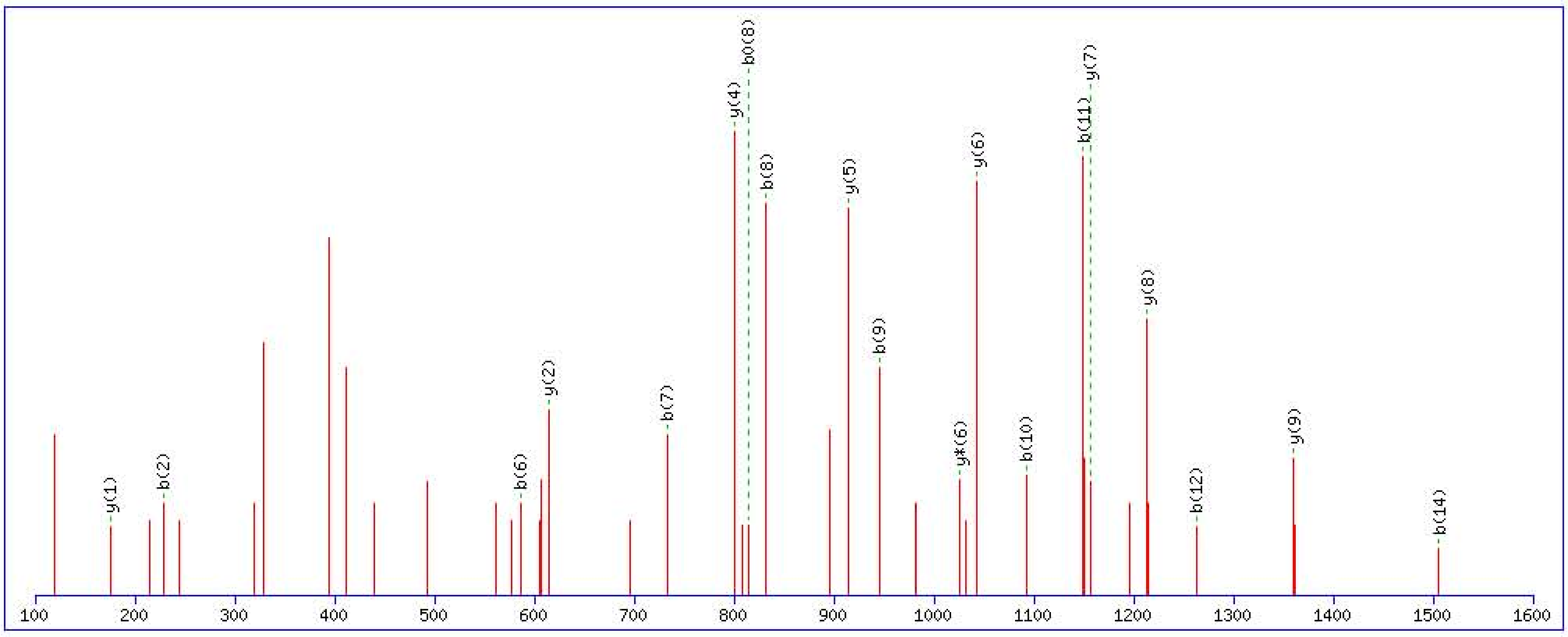
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

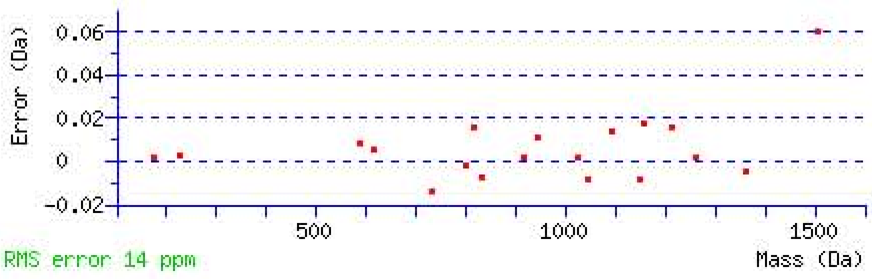
Match to Query 45160: 2304.192192 from(769.071340,3+) rtinseconds(2500) index(34589)
Title: Locus:1.1.1.3534.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

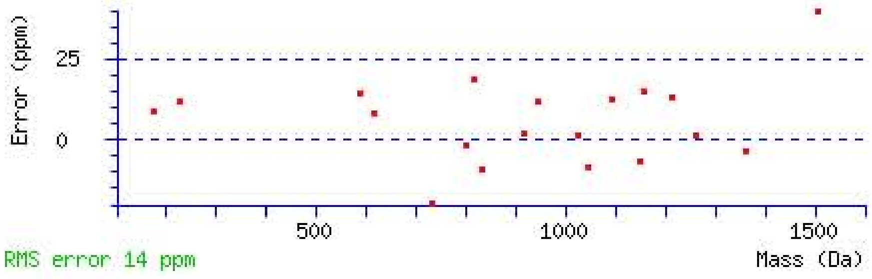
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2304.193649
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q17    : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 1.9e-005
Matches : 19/196 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	129.102239	65.054757	112.075690	56.541483			K							18
2	***228.170653***	114.588965	211.144104	106.075690			V	2177.105954	1089.056615	2160.079405	1080.543340	2159.095389	1080.051332	17
3	357.213246	179.110261	340.186697	170.596987	339.202681	170.104979	E	2078.037540	1039.522408	2061.010991	1031.009133	2060.026975	1030.517125	16
4	414.234710	207.620993	397.208161	199.107719	396.224145	198.615711	G	1948.994947	975.001111	1931.968398	966.487837	1930.984382	965.995829	15
5	515.282389	258.144833	498.255840	249.631558	497.271824	249.139550	T	1891.973483	946.490380	1874.946934	937.977105	1873.962918	937.485097	14
6	***586.319503***	293.663390	569.292954	285.150115	568.308938	284.658107	A	1790.925804	895.966540	1773.899255	887.453265	1772.915239	886.961257	13
7	***733.387917***	367.197597	716.361368	358.684322	715.377352	358.192314	F	1719.888690	860.447983	1702.862141	851.934709	1701.878125	851.442701	12
8	***832.456331***	416.731804	815.429782	408.218529	814.445766	407.726521	V	1572.820276	786.913776	1555.793727	778.400502	1554.809711	777.908493	11
9	***945.540395***	473.273836	928.513846	464.760561	927.529830	464.268553	I	1473.751862	737.379569	1456.725313	728.866294	1455.741297	728.374286	10
10	***1092.608809***	546.808043	1075.582260	538.294768	1074.598244	537.802760	F	***1360.667798***	680.837537	1343.641249	672.324263	1342.657233	671.832254	9
11	***1149.630273***	575.318775	1132.603724	566.805500	1131.619708	566.313492	G	***1213.599384***	607.303330	1196.572835	598.790055	1195.588819	598.298047	8
12	***1262.714337***	631.860806	1245.687788	623.347532	1244.703772	622.855524	I	***1156.577920***	578.792598	1139.551371	570.279324	1138.567355	569.787315	7
13	1390.772915	695.890095	1373.746366	687.376821	1372.762350	686.884813	Q	***1043.493856***	522.250566	1026.467307	513.737292	1025.483291	513.245284	6
14	***1505.799858***	753.403567	1488.773309	744.890292	1487.789293	744.398284	D	***915.435278***	458.221277	898.408729	449.708003	897.424713	449.215995	5
15	1562.821322	781.914299	1545.794773	773.401024	1544.810757	772.909016	G	***800.408335***	400.707806	783.381786	392.194531	782.397770	391.702523	4
16	1691.863915	846.435595	1674.837366	837.922321	1673.853350	837.430313	E	743.386871	372.197074	726.360322	363.683799	725.376306	363.191791	3
17	2131.089241	1066.048258	2114.062692	1057.534984	2113.078676	1057.042976	Q	***614.344278***	307.675777	597.317729	299.162503			2
18							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.6	2304.193649	-0.001457	KVEGTAFVIFGIQDGEQR
29.1	2304.193649	-0.001457	KVEGTAFVIFGIQDGEQR
0.3	2304.160568	0.031624	LILCADNRKEMEDWIAALK

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

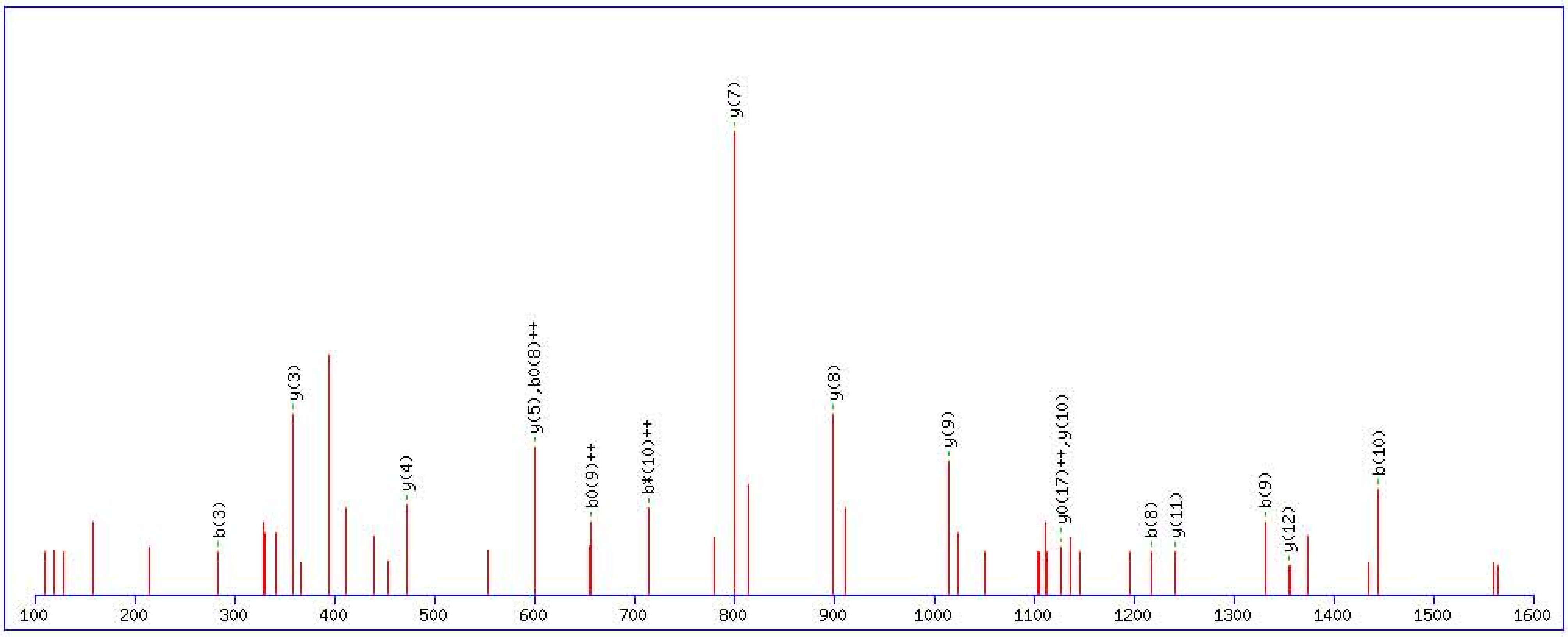
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

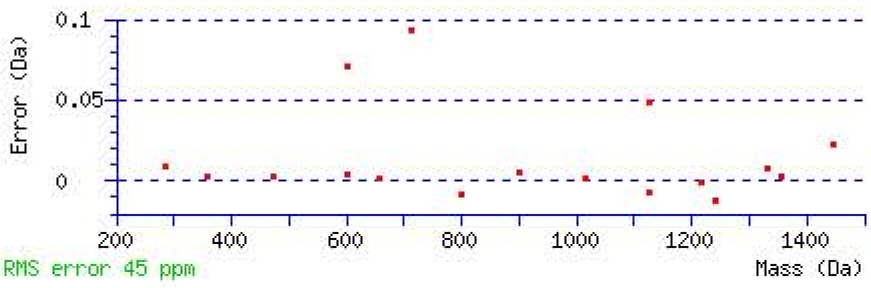
Match to Query 47406: 2457.230982 from(820.084270,3+) rtinseconds(2610) index(35280)
Title: Locus:1.1.1.3572.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

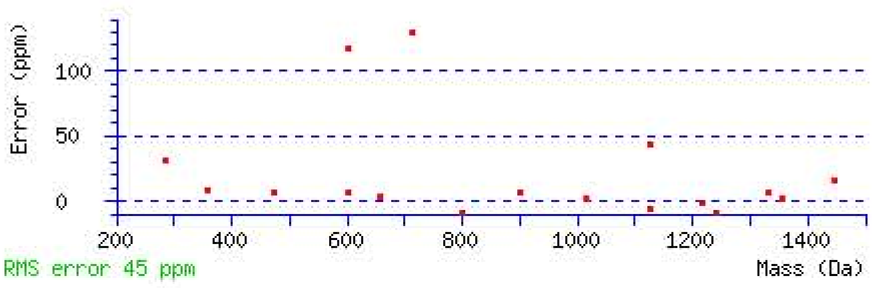
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2457.232193
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0033
Matches : 17/204 fragment ions using 36 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**							**19**
2	187.071333	94.039304			169.060768	85.034022	**A**	2343.212542	1172.109909	2326.185993	1163.596634	2325.201977	1163.104626	**18**
3	**284.124097**	142.565686			266.113532	133.560404	**P**	2272.175428	1136.591352	2255.148879	1128.078077	2254.164863	1127.586069	**17**
4	399.151040	200.079158			381.140475	191.073875	**D**	2175.122664	1088.064970	2158.096115	1079.551695	2157.112099	1079.059687	**16**
5	536.209952	268.608614			518.199387	259.603332	**H**	2060.095721	1030.551498	2043.069172	1022.038224	2042.085156	1021.546216	**15**
6	975.435278	488.221277	958.408729	479.708003	957.424713	479.215995	**Q**	1923.036809	962.022043	1906.010260	953.508768	1905.026244	953.016760	**14**
7	1104.477871	552.742574	1087.451322	544.229299	1086.467306	543.737291	**E**	1483.811483	742.409380	1466.784934	733.896105	1465.800918	733.404097	**13**
8	**1217.561935**	609.284606	1200.535386	600.771331	1199.551370	600.279323	**L**	***1354.768890***	677.888083	1337.742341	669.374809	1336.758325	668.882801	**12**
9	**1331.604862**	666.306069	1314.578313	657.792795	1313.594297	657.300786	**N**	***1241.684826***	621.346051	1224.658277	612.832777	1223.674261	612.340769	**11**
10	**1444.688926**	722.848101	1427.662377	714.334826	1426.678361	713.842818	**L**	***1127.641899***	564.324588	1110.615350	555.811313	1109.631334	555.319305	**10**
11	1559.715869	780.361572	1542.689320	771.848298	1541.705304	771.356290	**D**	***1014.557835***	507.782556	997.531286	499.269281	996.547270	498.777273	**9**
12	1658.784283	829.895780	1641.757734	821.382505	1640.773718	820.890497	**V**	***899.530892***	450.269084	882.504343	441.755810	881.520327	441.263802	**8**
13	1745.816311	873.411794	1728.789762	864.898519	1727.805746	864.406511	**S**	***800.462478***	400.734877	783.435929	392.221603	782.451913	391.729595	**7**
14	1858.900375	929.953825	1841.873826	921.440551	1840.889810	920.948543	**L**	713.430450	357.218863	696.403901	348.705589	695.419885	348.213581	**6**
15	1986.958953	993.983115	1969.932404	985.469840	1968.948388	984.977832	**Q**	***600.346386***	300.676831	583.319837	292.163557	582.335821	291.671549	**5**
16	2100.043017	1050.525146	2083.016468	1042.011872	2082.032452	1041.519864	**L**	***472.287808***	236.647542	455.261259	228.134268	454.277243	227.642260	**4**
17	2197.095781	1099.051528	2180.069232	1090.538254	2179.085216	1090.046246	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
18	2284.127809	1142.567542	2267.101260	1134.054268	2266.117244	1133.562260	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
19							**R**	175.118952	88.063114	158.092403	79.549839			**1**





NCBI **BLAST** search of DAPDHQELNLDVSLQLPSR
(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	2457.232193	-0.001211	DAPDHQELNLDVSLQLPSR
10.8	2457.243423	-0.012441	TGLSDAFMILNPSPDVPESRRR
2.1	2457.232193	-0.001211	DAPDHQELNLDVSLQLPSR

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

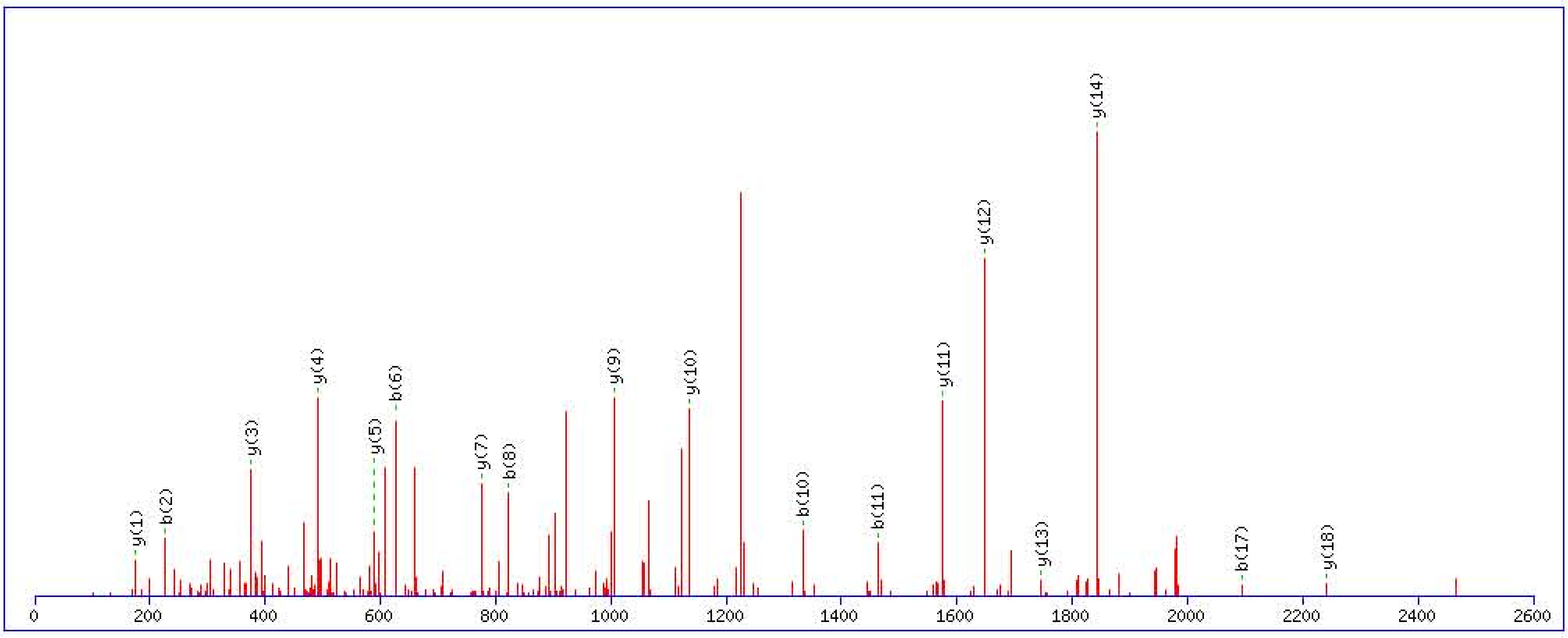
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

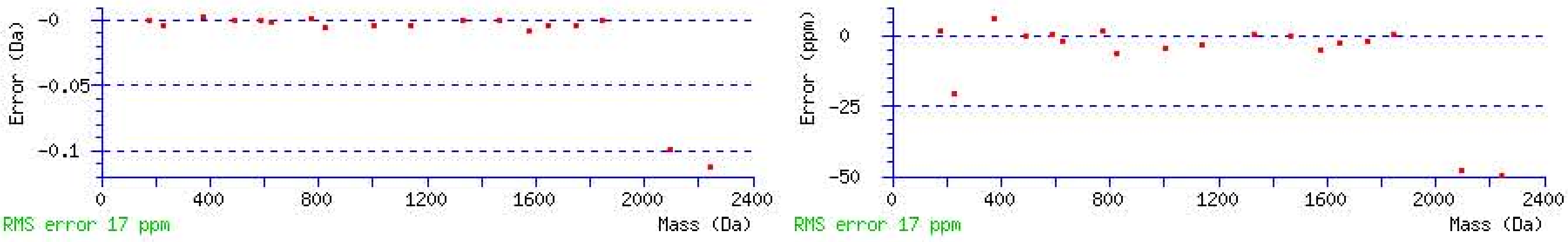
Match to Query 47630: 2467.245828 from(1234.630190,2+) rtinseconds(2669) index(35642)
Title: Locus:1.1.1.3592.26 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 2467.245071
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 106  Expect: 2.1e-010
Matches : 18/210 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							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
106.1	2467.245071	0.000757	ILLQGTPVAQMTEDAVDAER
41.8	2467.245071	0.000757	ILLQGTPVAQMTEDAVDAER
2.8	2467.257614	-0.011786	DQAIATREELHAQHAR
1.1	2467.252884	-0.007056	KLGLTMQYPEGYLEALANRER
0.1	2467.252914	-0.007086	LLHSFHSELPVLSDSERDMKK

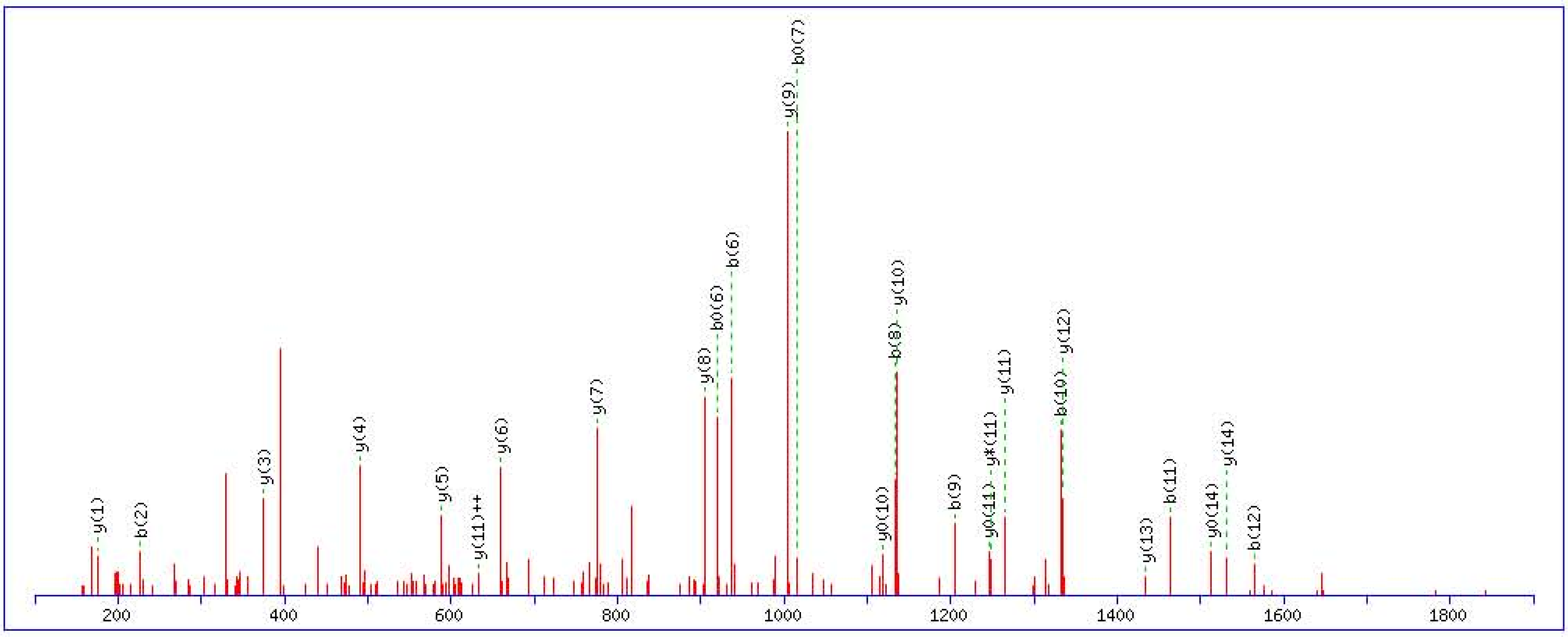
Mascot Search Results

Peptide View

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

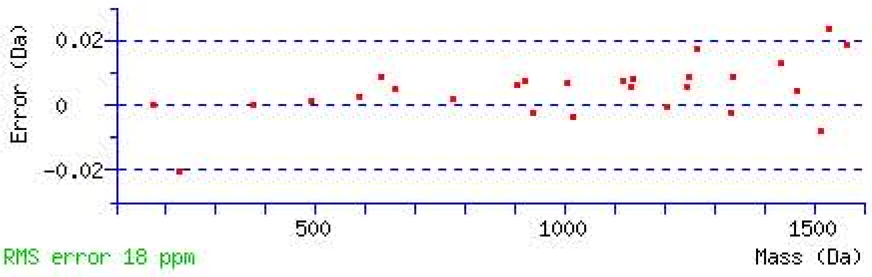
Match to Query 47631: 2467.246122 from(823.422650,3+) rtinseconds(2688) index(35730)
Title: Locus:1.1.1.3599.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

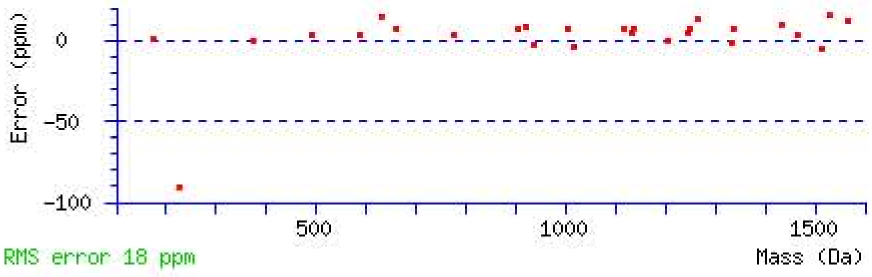
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2467.245071
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 82  Expect: 1.9e-007
Matches : 27/210 fragment ions using 45 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	779.484794	390.246035	762.458245	381.732760			Q	2129.000169	1065.003722	2111.973620	1056.490448	2110.989604	1055.998440	17
5	836.506258	418.756767	819.479709	410.243493			G	1689.774843	845.391060	1672.748294	836.877785	1671.764278	836.385777	16
6	**937.553937**	469.280607	920.527388	460.767332	919.543372	460.275324	T	1632.753379	816.880328	1615.726830	808.367053	1614.742814	807.875045	15
7	1034.606701	517.806988	1017.580152	509.293714	1016.596136	508.801706	P	***1531.705700***	766.356488	1514.679151	757.843214	1513.695135	757.351206	14
8	**1133.675115**	567.341196	1116.648566	558.827921	1115.664550	558.335913	V	***1434.652936***	717.830106	1417.626387	709.316832	1416.642371	708.824824	13
9	**1204.712229**	602.859753	1187.685680	594.346478	1186.701664	593.854470	A	***1335.584522***	668.295899	1318.557973	659.782625	1317.573957	659.290617	12
10	**1332.770807**	666.889042	1315.744258	658.375767	1314.760242	657.883759	Q	***1264.547408***	632.777342	1247.520859	624.264068	1246.536843	623.772060	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
82.2	2467.245071	0.001051	ILLQGTPVAQMTEDAVDAER
53.6	2467.245071	0.001051	ILLQGTPVAQMTEDAVDAER

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

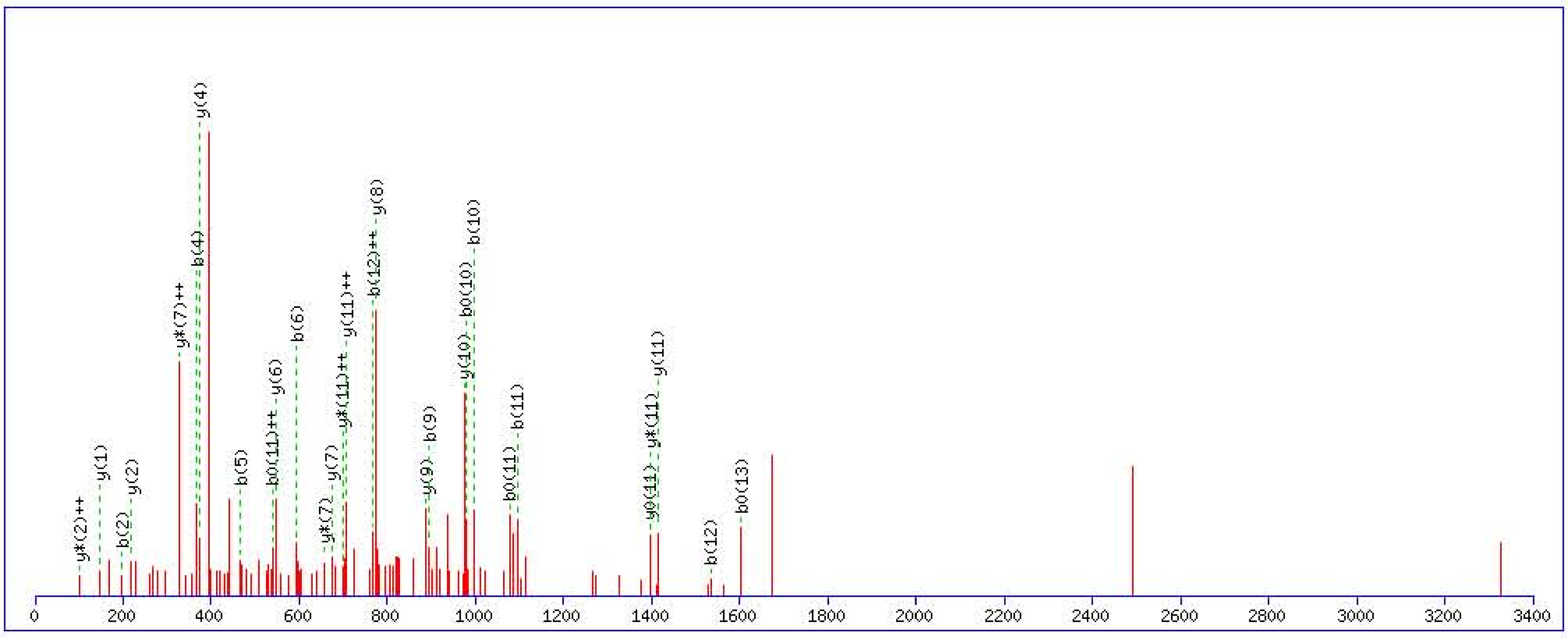
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

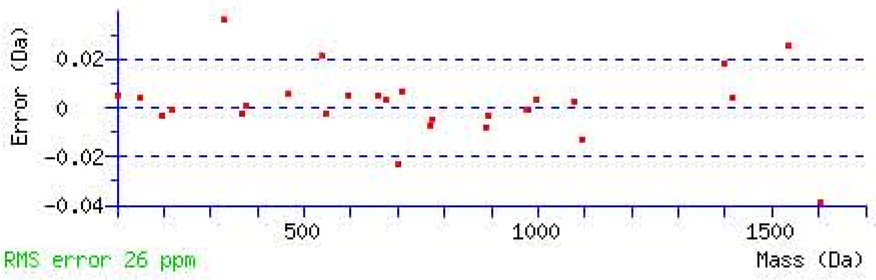
Match to Query 48626: 2508.279582 from(837.100470,3+) rtinseconds(2255) index(47589)
Title: Locus:1.1.1.3497.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

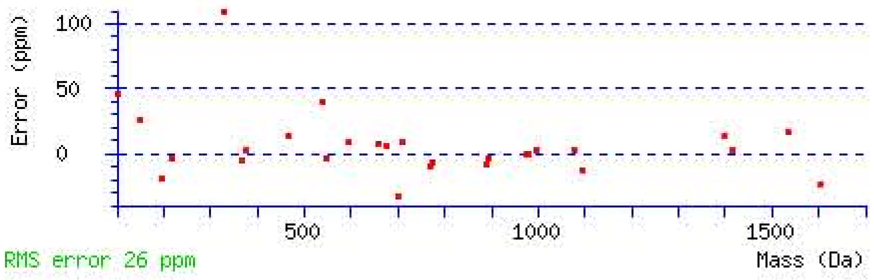
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2508.289429
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 0.00018
Matches : 29/220 fragment ions using 59 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	***197.128454***	99.067865					P	2410.228255	1205.617765	2393.201706	1197.104491	2392.217690	1196.612483	21
3	296.196868	148.602072					V	2313.175491	1157.091383	2296.148942	1148.578109	2295.164926	1148.086101	20
4	***367.233982***	184.120629					A	2214.107077	1107.557176	2197.080528	1099.043902	2196.096512	1098.551894	19
5	***466.302396***	233.654836					V	2143.069963	1072.038619	2126.043414	1063.525345	2125.059398	1063.033337	18
6	***594.360974***	297.684125	577.334425	289.170851			Q	2044.001549	1022.504413	2026.975000	1013.991138	2025.990984	1013.499130	17
7	651.382438	326.194857	634.355889	317.681583			G	1915.942971	958.475124	1898.916422	949.961849	1897.932406	949.469841	16
8	780.425031	390.716154	763.398482	382.202879	762.414466	381.710871	E	1858.921507	929.964391	1841.894958	921.451117	1840.910942	920.959109	15
9	***895.451974***	448.229625	878.425425	439.716351	877.441409	439.224343	D	1729.878914	865.443095	1712.852365	856.929821	1711.868349	856.437812	14
10	***996.499653***	498.753465	979.473104	490.240190	978.489088	489.748182	T	1614.851971	807.929623	1597.825422	799.416349	1596.841406	798.924341	13
11	***1095.568067***	548.287672	1078.541518	539.774397	1077.557502	539.282389	V	1513.804292	757.405784	1496.777743	748.892510	1495.793727	748.400502	12
12	***1534.793393***	767.900335	1517.766844	759.387060	1516.782828	758.895052	Q	***1414.735878***	707.871577	1397.709329	699.358303	1396.725313	698.866294	11
13	1621.825421	811.416349	1604.798872	802.903074	1603.814856	802.411066	S	***975.510552***	488.258914	958.484003	479.745639	957.499987	479.253631	10
14	1734.909485	867.958381	1717.882936	859.445106	1716.898920	858.953098	L	***888.478524***	444.742900	871.451975	436.229625	870.467959	435.737617	9
15	1835.957164	918.482220	1818.930615	909.968946	1817.946599	909.476938	T	***775.394460***	388.200868	758.367911	379.687593	757.383895	379.195585	8
16	1964.015742	982.511509	1946.989193	973.998235	1946.005177	973.506227	Q	***674.346781***	337.677029	657.320232	329.163754	656.336216	328.671746	7
17	2021.037206	1011.022241	2004.010657	1002.508967	2003.026641	1002.016959	G	***546.288203***	273.647739	529.261654	265.134465	528.277638	264.642457	6
18	2136.064149	1068.535712	2119.037600	1060.022438	2118.053584	1059.530430	D	489.266739	245.137007	472.240190	236.623733	471.256174	236.131725	5
19	2193.085613	1097.046444	2176.059064	1088.533170	2175.075048	1088.041162	G	***374.239796***	187.623536	357.213247	179.110261			4
20	2292.154027	1146.580651	2275.127478	1138.067377	2274.143462	1137.575369	V	317.218332	159.112804	300.191783	150.599530			3
21	2363.191141	1182.099208	2346.164592	1173.585934	2345.180576	1173.093926	A	***218.149918***	109.578597	201.123369	101.065323			2
22							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VPVAVQGEDTVQSLTQGDGVAK
(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	2508.289429	-0.009847	VPVAVQGEDTVQSLTQGDGVAK
25.2	2508.289429	-0.009847	VPVAVQGEDTVQSLTQGDGVAK
24.7	2508.289429	-0.009847	VPVAVQGEDTVQSLTQGDGVAK

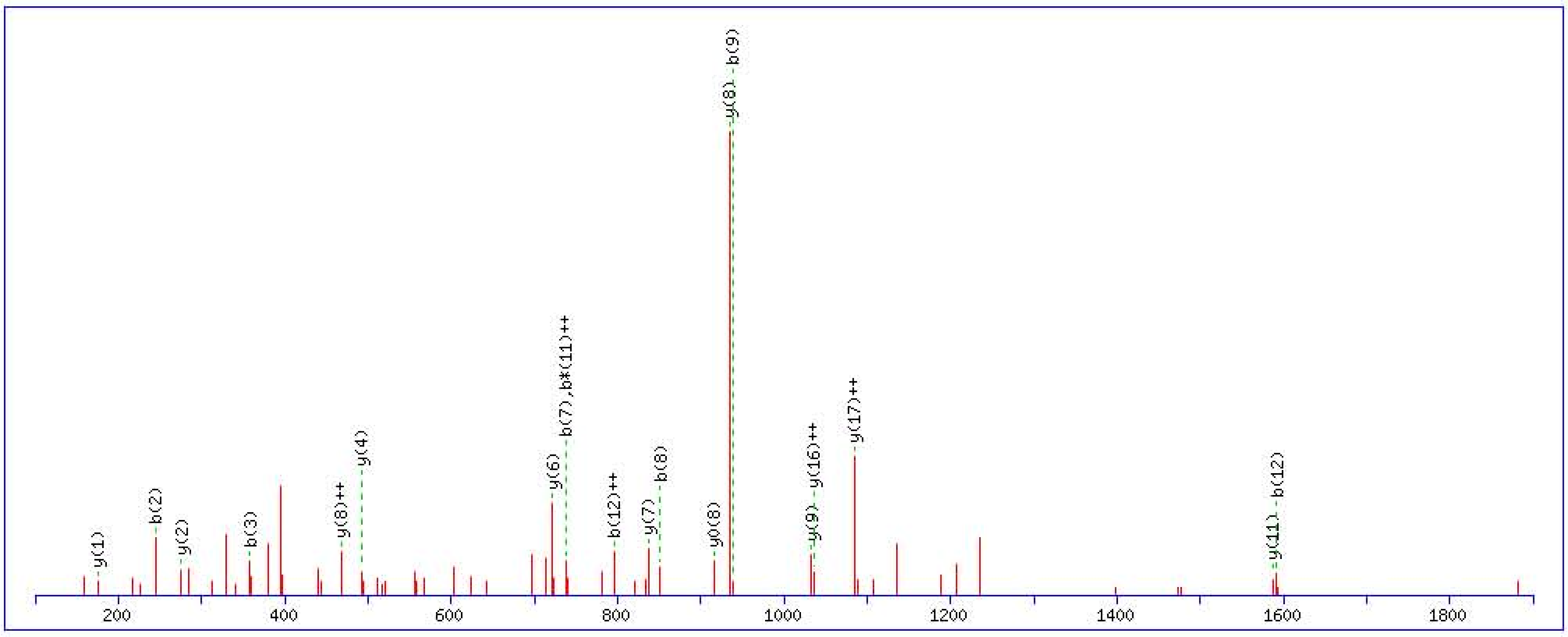
Mascot Search Results

Peptide View

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

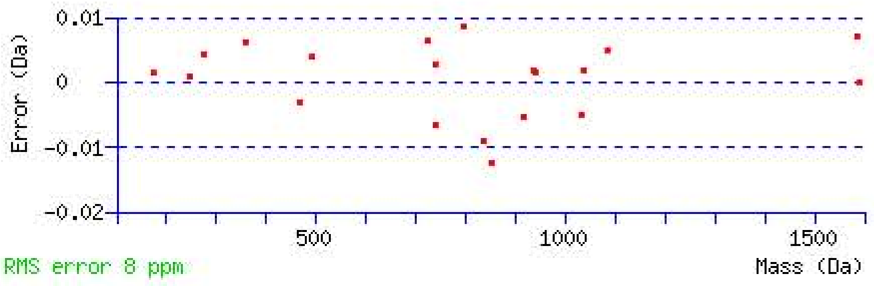
Match to Query 48808: 2524.161852 from(842.394560,3+) rtinseconds(2222) index(33168)
Title: Locus:1.1.1.3437.22 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

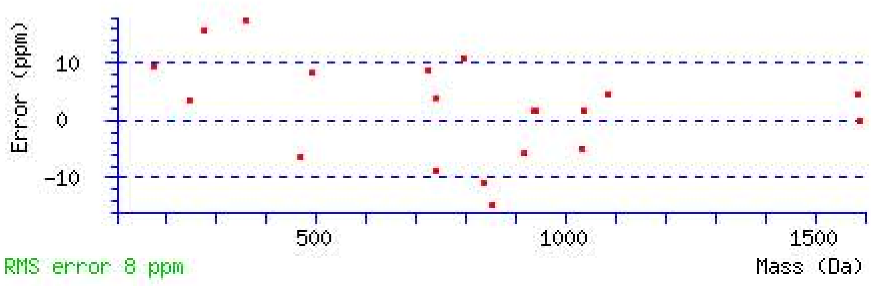
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2524.163910
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 32 **Expect:** 0.0071
Matches : 20/206 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	130.049869	65.528572			112.039304	56.523290	E							20
2	***245.076812***	123.042044			227.066247	114.036762	D	2396.128598	1198.567937	2379.102049	1190.054662	2378.118033	1189.562654	19
3	***358.160876***	179.584076			340.150311	170.578794	I	2281.101655	1141.054465	2264.075106	1132.541191	2263.091090	1132.049183	18
4	455.213640	228.110458			437.203075	219.105176	P	2168.017591	1084.512433	2150.991042	1075.999159	2150.007026	1075.507151	17
5	552.266404	276.636840			534.255839	267.631558	P	2070.964827	1035.986051	2053.938278	1027.472777	2052.954262	1026.980769	16
6	623.303518	312.155397			605.292953	303.150115	A	1973.912063	987.459670	1956.885514	978.946395	1955.901498	978.454387	15
7	***738.330461***	369.668869			720.319896	360.663586	D	1902.874949	951.941113	1885.848400	943.427838	1884.864384	942.935830	14
8	***851.414525***	426.210901			833.403960	417.205618	L	1787.848006	894.427641	1770.821457	885.914367	1769.837441	885.422359	13
9	***938.446553***	469.726915			920.435988	460.721632	S	1674.763942	837.885609	1657.737393	829.372335	1656.753377	828.880327	12
10	1053.473496	527.240386			1035.462931	518.235104	D	***1587.731914***	794.369595	1570.705365	785.856321	1569.721349	785.364313	11
11	1492.698822	746.853049	1475.672273	738.339775	1474.688257	737.847767	Q	1472.704971	736.856124	1455.678422	728.342849	1454.694406	727.850841	10
12	***1591.767236***	796.387256	1574.740687	787.873982	1573.756671	787.381974	V	***1033.479645***	517.243461	1016.453096	508.730186	1015.469080	508.238178	9
13	1688.820000	844.913638	1671.793451	836.400364	1670.809435	835.908356	P	***934.411231***	467.709254	917.384682	459.195979	916.400666	458.703971	8
14	1803.846943	902.427110	1786.820394	893.913835	1785.836378	893.421827	D	***837.358467***	419.182872	820.331918	410.669597	819.347902	410.177589	7
15	1904.894622	952.950949	1887.868073	944.437675	1886.884057	943.945667	T	***722.331524***	361.669400	705.304975	353.156125	704.320959	352.664117	6
16	2033.937215	1017.472246	2016.910666	1008.958971	2015.926650	1008.466963	E	621.283845	311.145560	604.257296	302.632286	603.273280	302.140278	5
17	2120.969243	1060.988259	2103.942694	1052.474985	2102.958678	1051.982977	S	***492.241252***	246.624264	475.214703	238.110989	474.230687	237.618981	4
18	2250.011836	1125.509556	2232.985287	1116.996281	2232.001271	1116.504274	E	405.209224	203.108250	388.182675	194.594975	387.198659	194.102967	3
19	2351.059515	1176.033395	2334.032966	1167.520121	2333.048950	1167.028113	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
20							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EDIPPADLSDQVPDTESETR
(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	2524.163910	-0.002058	EDIPPADLSDQVPDTESETR

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

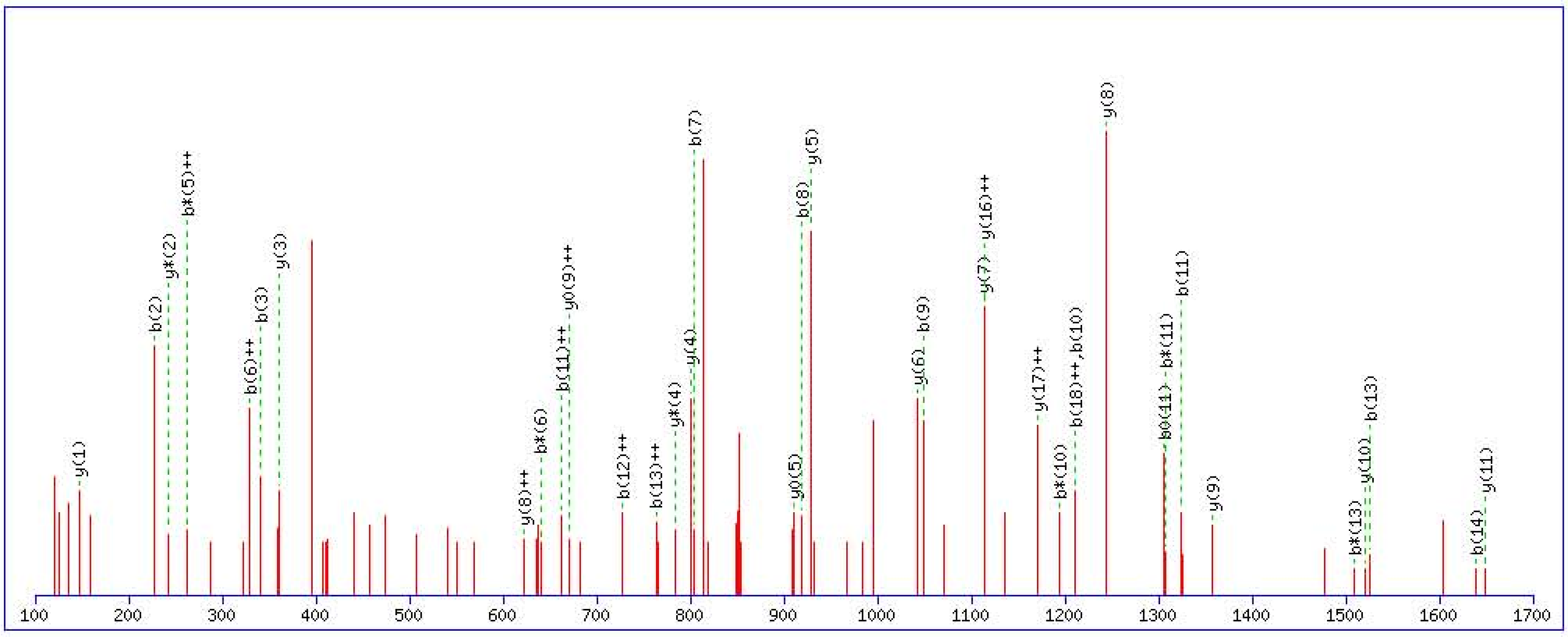
Mascot Search Results

Peptide View

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

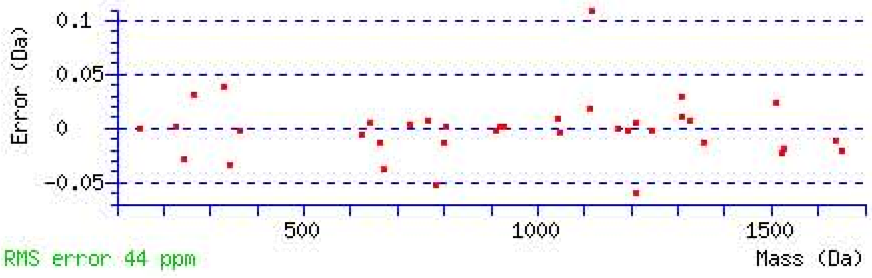
Match to Query 49151: 2567.260932 from(856.760920,3+) rtinseconds(3286) index(39655)
Title: Locus:1.1.1.3802.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

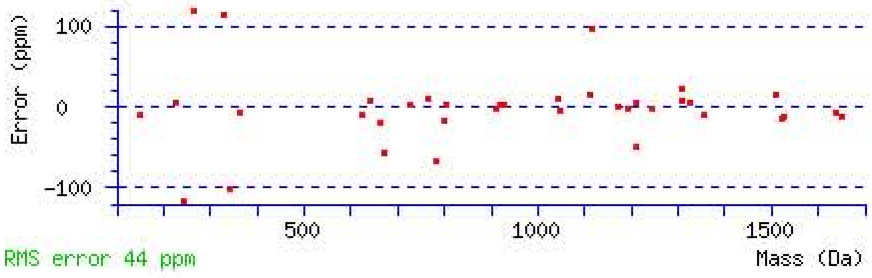
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2567.265121
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16 : Biotin:Thermo-21345 (Q)
Ions Score: 49 **Expect:** 2.8e-005
Matches : 37/204 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	100.075690	50.541483					V							19
2	***228.134268***	114.570772	211.107719	106.057498			Q	2469.204012	1235.105644	2452.177463	1226.592369	2451.193447	1226.100361	18
3	***341.218332***	171.112804	324.191783	162.599530			L	2341.145434	1171.076355	2324.118885	1162.563080	2323.134869	1162.071072	17
4	428.250360	214.628818	411.223811	206.115544	410.239795	205.623536	S	2228.061370	1114.534323	2211.034821	1106.021048	2210.050805	1105.529040	16
5	542.293287	271.650282	525.266738	263.137007	524.282722	262.644999	N	2141.029342	1071.018309	2124.002793	1062.505034	2123.018777	1062.013026	15
6	657.320230	**329.163753**	640.293681	320.650479	639.309665	320.158471	D	2026.986415	1013.996845	2009.959866	1005.483571	2008.975850	1004.991563	14
7	***804.388644***	402.697960	787.362095	394.184686	786.378079	393.692678	F	1911.959472	956.483374	1894.932923	947.970099	1893.948907	947.478091	13
8	***919.415587***	460.211432	902.389038	451.698157	901.405022	451.206149	D	1764.891058	882.949167	1747.864509	874.435893	1746.880493	873.943884	12
9	***1048.458180***	524.732728	1031.431631	516.219453	1030.447615	515.727445	E	***1649.864115***	825.435695	1632.837566	816.922421	1631.853550	816.430413	11
10	***1211.521509***	606.264392	1194.494960	597.751118	1193.510944	597.259110	Y	***1520.821522***	760.914399	1503.794973	752.401125	1502.810957	751.909116	10
11	***1324.605573***	**662.806424**	1307.579024	654.293150	1306.595008	653.801142	I	***1357.758193***	679.382734	1340.731644	670.869460	1339.747628	670.377452	9
12	1455.646058	**728.326667**	1438.619509	719.813392	1437.635493	719.321384	M	***1244.674129***	622.840703	1227.647580	614.327428	1226.663564	613.835420	8
13	***1526.683172***	**763.845224**	1509.656623	755.331949	1508.672607	754.839941	A	***1113.633644***	557.320460	1096.607095	548.807186	1095.623079	548.315178	7
14	***1639.767236***	820.387256	1622.740687	811.873981	1621.756671	811.381973	I	***1042.596530***	521.801903	1025.569981	513.288629	1024.585965	512.796621	6
15	1768.809829	884.908552	1751.783280	876.395278	1750.799264	875.903270	E	***929.512466***	465.259871	912.485917	456.746597	911.501901	456.254589	5
16	2208.035155	1104.521215	2191.008606	1096.007941	2190.024590	1095.515933	Q	***800.469873***	400.738575	783.443324	392.225300	782.459308	391.733292	4
17	2309.082834	1155.045055	2292.056285	1146.531780	2291.072269	1146.039772	T	***361.244547***	181.125911	344.217998	172.612637	343.233982	172.120629	3
18	2422.166898	**1211.587087**	2405.140349	1203.073812	2404.156333	1202.581804	I	260.196868	130.602072	243.170319	122.088798			2
19							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.2	2567.265121	-0.004189	VQLSNDFDEYIMAIEQTIK
0.7	2567.264923	-0.003991	IQSDLTSHEISLEEMKKHNQGK

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

{MATRIX} {SCIENCE}

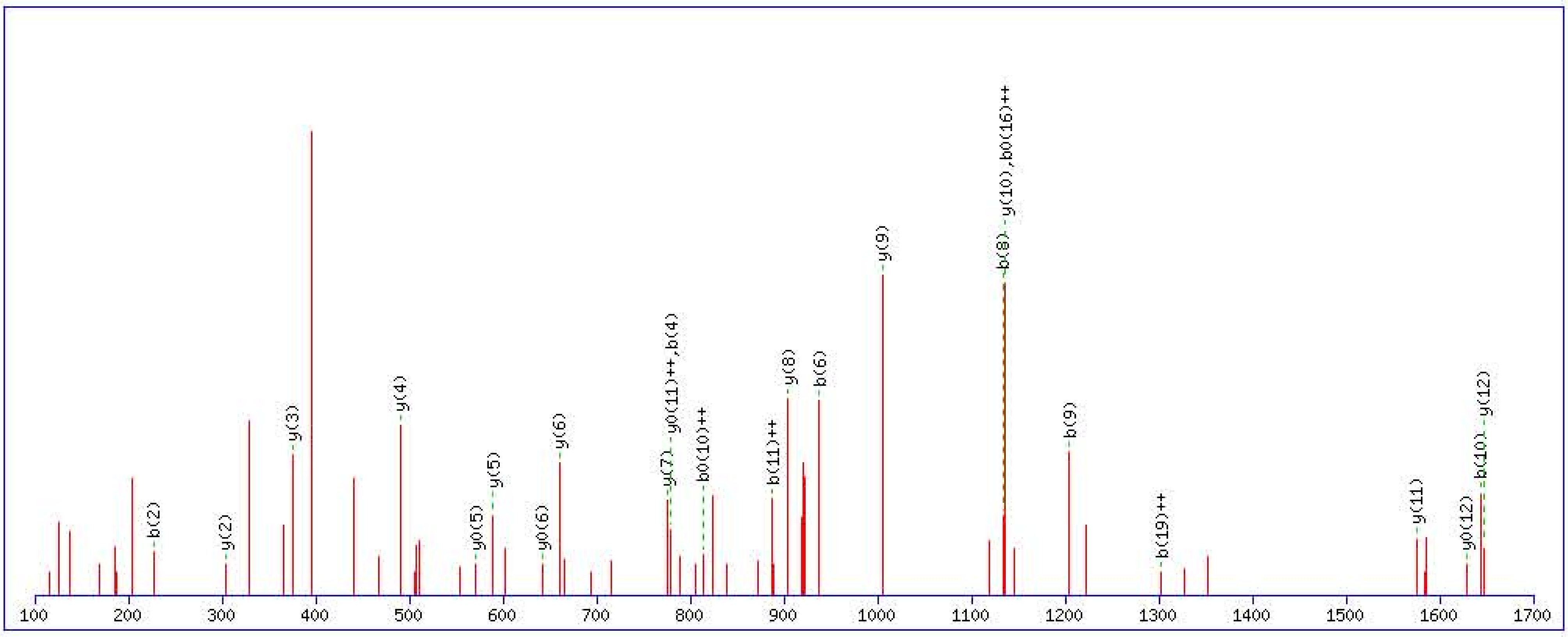
Mascot Search Results

Peptide View

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

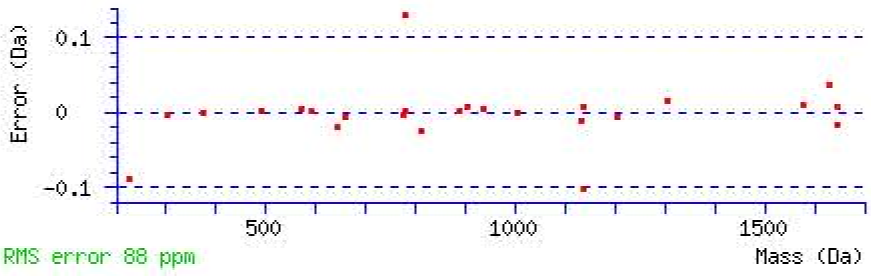
Match to Query 51256: 2778.409872 from(927.143900,3+) rtinseconds(2802) index(36685)
Title: Locus:1.1.1.3637.26 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

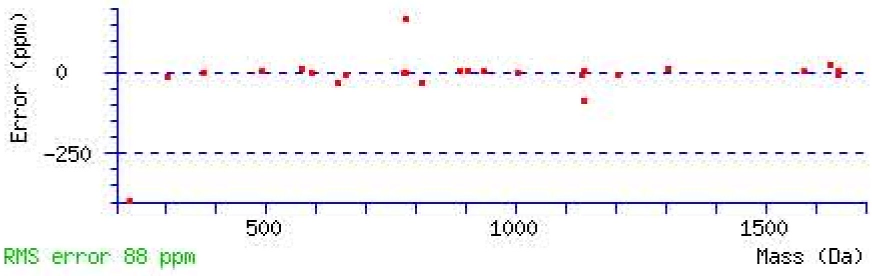
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2778.411819
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4     : Biotin:Thermo-21345 (Q)
Q10    : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 2.5e-006
Matches : 25/210 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	114.091340	57.549308					I							20
2	**227.175404**	114.091340					L	2666.335045	1333.671160	2649.308496	1325.157886	2648.324480	1324.665878	19
3	340.259468	170.633372					L	2553.250981	1277.129128	2536.224432	1268.615854	2535.240416	1268.123846	18
4	**779.484794**	390.246035	762.458245	381.732760			Q	2440.166917	1220.587096	2423.140368	1212.073822	2422.156352	1211.581814	17
5	836.506258	418.756767	819.479709	410.243493			G	2000.941591	1000.974434	1983.915042	992.461159	1982.931026	991.969151	16
6	**937.553937**	469.280607	920.527388	460.767332	919.543372	460.275324	T	1943.920127	972.463702	1926.893578	963.950427	1925.909562	963.458419	15
7	1034.606701	517.806988	1017.580152	509.293714	1016.596136	508.801706	P	1842.872448	921.939862	1825.845899	913.426588	1824.861883	912.934580	14
8	**1133.675115**	567.341196	1116.648566	558.827921	1115.664550	558.335913	V	1745.819684	873.413480	1728.793135	864.900206	1727.809119	864.408198	13
9	**1204.712229**	602.859753	1187.685680	594.346478	1186.701664	593.854470	A	***1646.751270***	823.879273	1629.724721	815.365999	1628.740705	814.873991	12
10	**1643.937555**	822.472416	1626.911006	813.959141	1625.926990	813.467133	Q	***1575.714156***	788.360716	1558.687607	779.847442	1557.703591	779.355434	11
11	1774.978040	**887.992658**	1757.951491	879.479384	1756.967475	878.987376	M	***1136.488830***	568.748053	1119.462281	560.234779	1118.478265	559.742771	10
12	1876.025719	938.516498	1858.999170	930.003223	1858.015154	929.511215	T	***1005.448345***	503.227811	988.421796	494.714536	987.437780	494.222528	9
13	2005.068312	1003.037794	1988.041763	994.524520	1987.057747	994.032512	E	***904.400666***	452.703971	887.374117	444.190697	886.390101	443.698689	8
14	2120.095255	1060.551265	2103.068706	1052.037991	2102.084690	1051.545983	D	***775.358073***	388.182675	758.331524	379.669400	757.347508	379.177392	7
15	2191.132369	1096.069822	2174.105820	1087.556548	2173.121804	1087.064540	A	***660.331130***	330.669203	643.304581	322.155929	642.320565	321.663921	6
16	2290.200783	1145.604029	2273.174234	1137.090755	2272.190218	1136.598747	V	***589.294016***	295.150646	572.267467	286.637372	571.283451	286.145364	5
17	2405.227726	1203.117501	2388.201177	1194.604226	2387.217161	1194.112218	D	***490.225602***	245.616439	473.199053	237.103165	472.215037	236.611157	4
18	2476.264840	1238.636058	2459.238291	1230.122783	2458.254275	1229.630775	A	***375.198659***	188.102968	358.172110	179.589693	357.188094	179.097685	3
19	2605.307433	**1303.157354**	2588.280884	1294.644080	2587.296868	1294.152072	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
61.8	2778.411819	-0.001947	ILLQGTPVAQMTEDAVDAER
2.0	2778.403030	0.006842	RKAVVPGPAEHPLQYNYTFWYSR

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

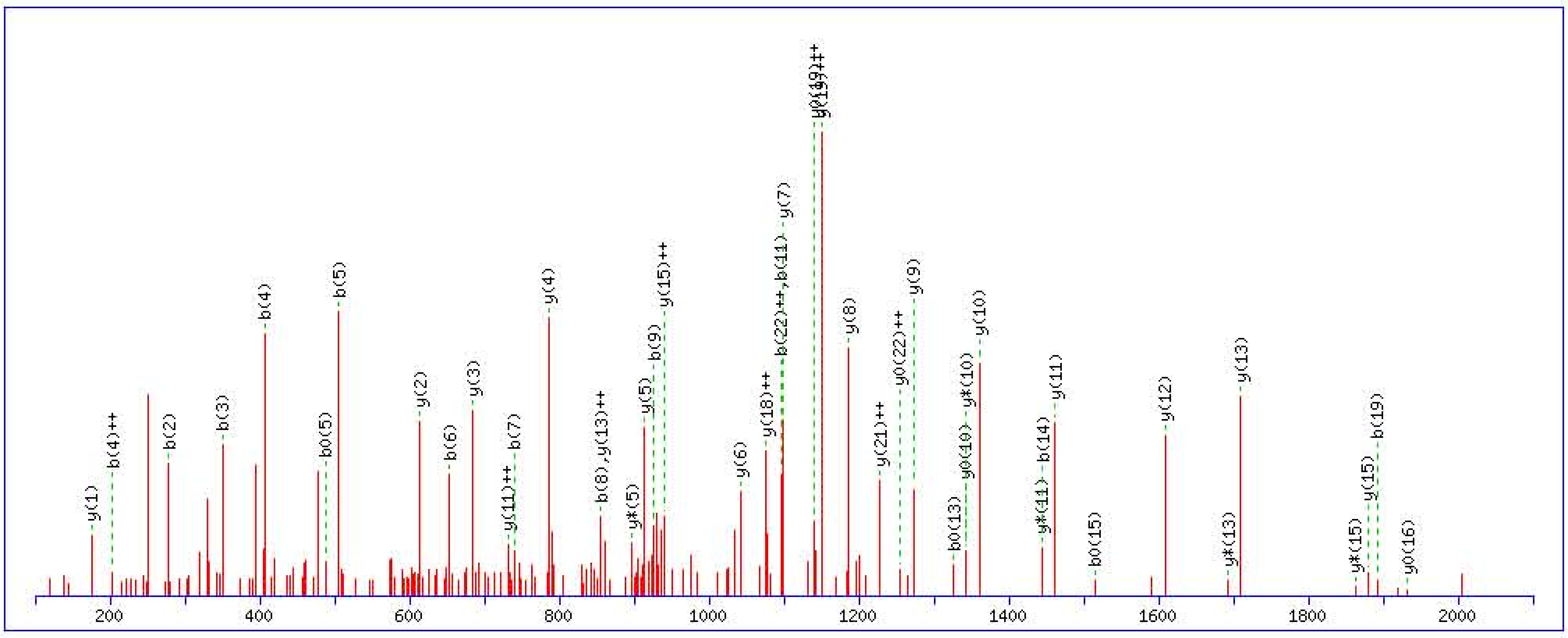
Mascot Search Results

Peptide View

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

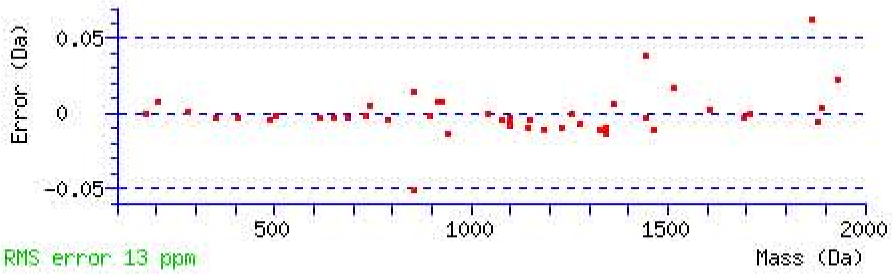
Match to Query 51586: 2804.307132 from(935.776320,3+) rtinseconds(2570) index(34987)
Title: Locus:1.1.1.3558.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

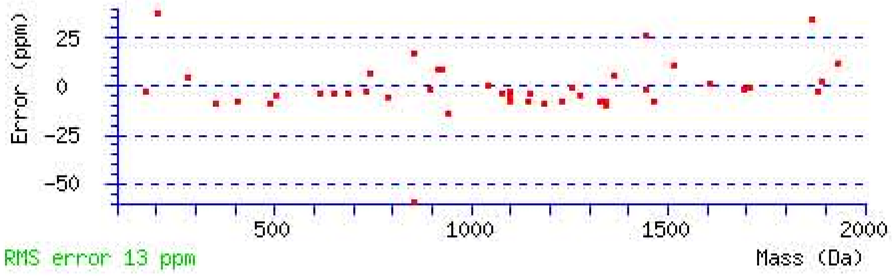
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2804.307587
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q23     : Biotin:Thermo-21345 (Q)
Ions Score: 104  Expect: 5.8e-010
Matches : 45/234 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	116.034219	58.520748			98.023654	49.515465	**D**							**24**
2	***279.097548***	140.052412			261.086983	131.047130	**Y**	2690.287895	1345.647585	2673.261346	1337.134311	2672.277330	1336.642303	**23**
3	***350.134662***	175.570969			332.124097	166.565687	**A**	2527.224566	1264.115921	2510.198017	1255.602646	2509.214001	1255.110638	**22**
4	***407.156126***	**204.081701**			389.145561	195.076418	**G**	2456.187452	1228.597364	2439.160903	1220.084089	2438.176887	1219.592081	**21**
5	***506.224540***	253.615908			488.213975	244.610626	**V**	2399.165988	1200.086632	2382.139439	1191.573357	2381.155423	1191.081349	**20**
6	***653.292954***	327.150115			635.282389	318.144833	**F**	2300.097574	1150.552425	2283.071025	1142.039150	2282.087009	1141.547142	**19**
7	***740.324982***	370.666129			722.314417	361.660846	**S**	2153.029160	1077.018218	2136.002611	1068.504943	2135.018595	1068.012935	**18**
8	***855.351925***	428.179600			837.341360	419.174318	**D**	2065.997132	1033.502204	2048.970583	1024.988929	2047.986567	1024.496921	**17**
9	***926.389039***	463.698157			908.378474	454.692875	**A**	1950.970189	975.988733	1933.943640	967.475458	1932.959624	966.983450	**16**
10	983.410503	492.208890			965.399938	483.203607	**G**	***1879.933075***	940.470176	1862.906526	931.956901	1861.922510	931.464893	**15**
11	***1096.494567***	548.750922			1078.484002	539.745639	**L**	1822.911611	911.959444	1805.885062	903.446169	1804.901046	902.954161	**14**
12	1197.542246	599.274761			1179.531681	590.269478	**T**	***1709.827547***	855.417412	1692.800998	846.904137	1691.816982	846.412129	**13**
13	1344.610660	672.808968			1326.600095	663.803686	**F**	***1608.779868***	804.893572	1591.753319	796.380298	1590.769303	795.888290	**12**
14	***1445.658339***	723.332808			1427.647774	714.327525	**T**	***1461.711454***	731.359365	1444.684905	722.846091	1443.700889	722.354083	**11**
15	1532.690367	766.848822			1514.679802	757.843539	**S**	***1360.663775***	680.835526	1343.637226	672.322251	1342.653210	671.830243	**10**
16	1619.722395	810.364836			1601.711830	801.359553	**S**	***1273.631747***	637.319512	1256.605198	628.806237	1255.621182	628.314229	**9**
17	1706.754423	853.880850			1688.743858	844.875567	**S**	***1186.599719***	593.803498	1169.573170	585.290223	1168.589154	584.798215	**8**
18	1763.775887	882.391582			1745.765322	873.386299	**G**	***1099.567691***	550.287484	1082.541142	541.774209	1081.557126	541.282201	**7**
19	***1891.834465***	946.420871	1874.807916	937.907596	1873.823900	937.415588	**Q**	***1042.546227***	521.776752	1025.519678	513.263477	1024.535662	512.771469	**6**
20	2019.893043	1010.450160	2002.866494	1001.936885	2001.882478	1001.444877	**Q**	***914.487649***	457.747463	897.461100	449.234188	896.477084	448.742180	**5**
21	2120.940722	1060.973999	2103.914173	1052.460724	2102.930157	1051.968716	**T**	***786.429071***	393.718174	769.402522	385.204899	768.418506	384.712891	**4**
22	2191.977836	**1096.492556**	2174.951287	1087.979281	2173.967271	1087.487273	**A**	***685.381392***	343.194334	668.354843	334.681060			**3**
23	2631.203162	1316.105219	2614.176613	1307.591945	2613.192597	1307.099937	**Q**	***614.344278***	307.675777	597.317729	299.162503			**2**
24							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
104.2	2804.307587	-0.000455	DYAGVFSDAGLTFTSSSGQQTAQR
79.3	2804.307587	-0.000455	DYAGVFSDAGLTFTSSSGQQTAQR
73.8	2804.307587	-0.000455	DYAGVFSDAGLTFTSSSGQQTAQR

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

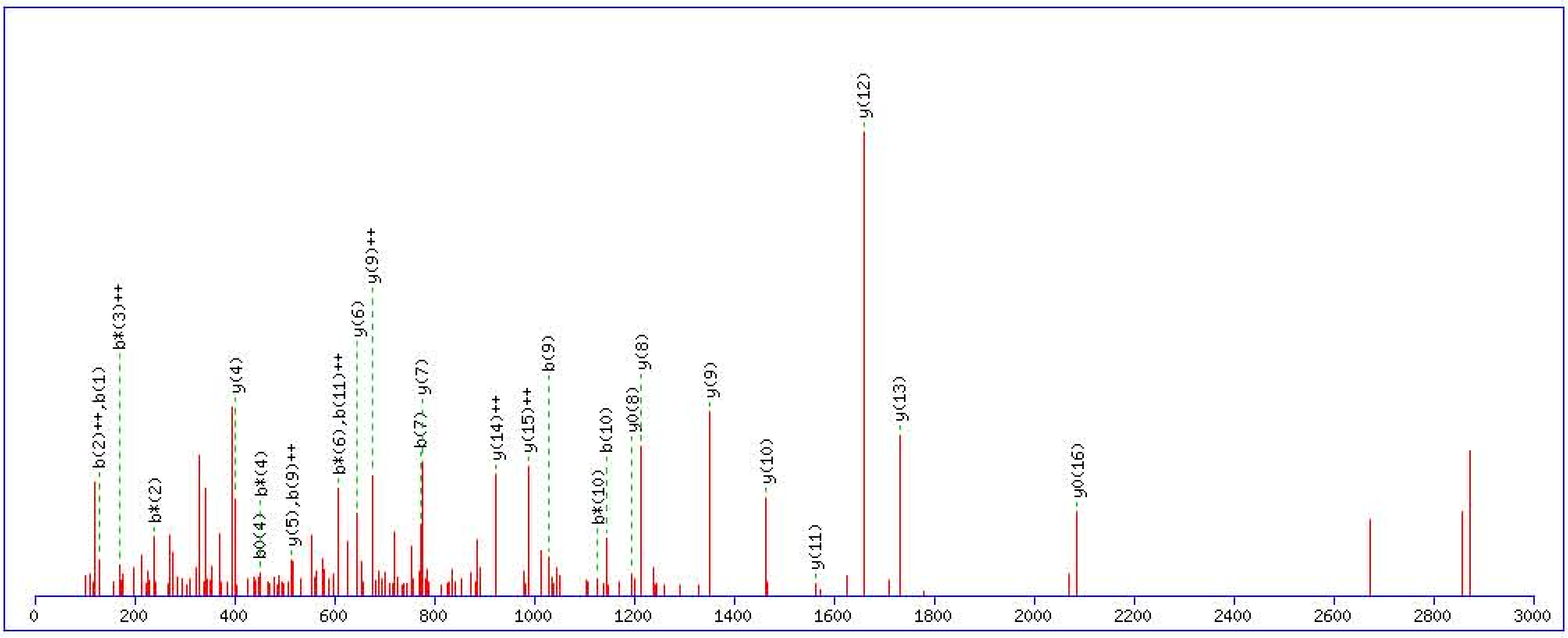
Mascot Search Results

Peptide View

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

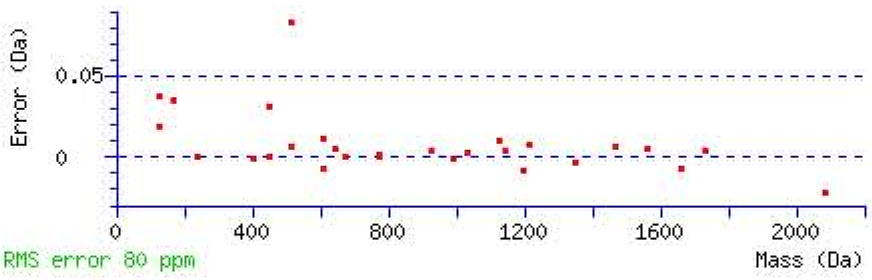
Match to Query 52772: 2874.446696 from(719.618950,4+) rtinseconds(2248) index(33349)
Title: Locus:1.1.1.3446.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

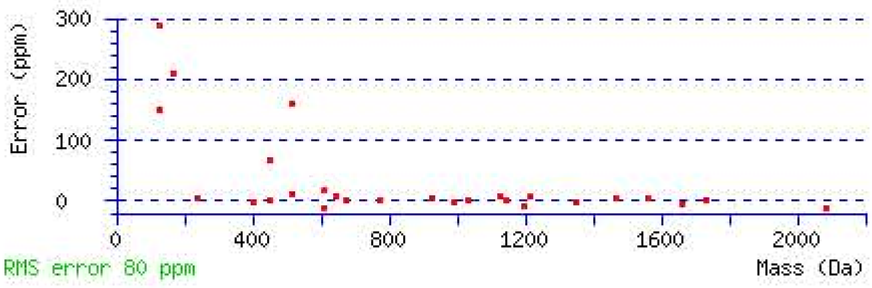
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2874.452057
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16     : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.0014
Matches : 28/246 fragment ions using 51 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							23
2	257.160817	**129.084047**	240.134268	120.570772			K	2747.400756	1374.204016	2730.374207	1365.690741	2729.390191	1365.198733	22
3	354.213581	177.610429	337.187032	169.097154			P	2619.305793	1310.156534	2602.279244	1301.643260	2601.295228	1301.151252	21
4	469.240524	235.123900	452.213975	226.610626	451.229959	226.118618	D	2522.253029	1261.630152	2505.226480	1253.116878	2504.242464	1252.624870	20
5	526.261988	263.634632	509.235439	255.121358	508.251423	254.629350	G	2407.226086	1204.116681	2390.199537	1195.603406	2389.215521	1195.111398	19
6	625.330402	313.168839	608.303853	304.655565	607.319837	304.163557	V	2350.204622	1175.605949	2333.178073	1167.092674	2332.194057	1166.600666	18
7	**772.398816**	386.703046	755.372267	378.189772	754.388251	377.697764	F	2251.136208	1126.071742	2234.109659	1117.558467	2233.125643	1117.066459	17
8	900.457394	450.732335	883.430845	442.219061	882.446829	441.727053	Q	2104.067794	1052.537535	2087.041245	1044.024260	2086.057229	1043.532252	16
9	**1029.499987**	**515.253631**	1012.473438	506.740357	1011.489422	506.248349	E	1976.009216	988.508246	1958.982667	979.994972	1957.998651	979.502964	15
10	**1144.526930**	572.767103	1127.500381	564.253829	1126.516365	563.761821	D	1846.966623	923.986950	1829.940074	915.473675	1828.956058	914.981667	14
11	1215.564044	**608.285660**	1198.537495	599.772386	1197.553479	599.280377	A	***1731.939680***	866.473478	1714.913131	857.960204	1713.929115	857.468196	13
12	1312.616808	656.812042	1295.590259	648.298768	1294.606243	647.806760	P	***1660.902566***	830.954921	1643.876017	822.441647	1642.892001	821.949639	12
13	1411.685222	706.346249	1394.658673	697.832975	1393.674657	697.340967	V	***1563.849802***	782.428539	1546.823253	773.915265	1545.839237	773.423257	11
14	1524.769286	762.888281	1507.742737	754.375007	1506.758721	753.882998	I	***1464.781388***	732.894332	1447.754839	724.381058	1446.770823	723.889050	10
15	1661.828198	831.417737	1644.801649	822.904463	1643.817633	822.412454	H	***1351.697324***	676.352300	1334.670775	667.839026	1333.686759	667.347018	9
16	2101.053524	1051.030400	2084.026975	1042.517125	2083.042959	1042.025117	Q	***1214.638412***	607.822844	1197.611863	599.309570	1196.627847	598.817562	8
17	2230.096117	1115.551696	2213.069568	1107.038422	2212.085552	1106.546414	E	***775.413086***	388.210181	758.386537	379.696907	757.402521	379.204899	7
18	2361.136602	1181.071939	2344.110053	1172.558664	2343.126037	1172.066656	M	***646.370493***	323.688885	629.343944	315.175610			6
19	2474.220666	1237.613971	2457.194117	1229.100696	2456.210101	1228.608689	I	***515.330008***	258.168642	498.303459	249.655368			5
20	2531.242130	1266.124703	2514.215581	1257.611428	2513.231565	1257.119420	G	***402.245944***	201.626610	385.219395	193.113335			4
21	2588.263594	1294.635435	2571.237045	1286.122160	2570.253029	1285.630152	G	345.224480	173.115878	328.197931	164.602603			3
22	2701.347658	1351.177467	2684.321109	1342.664192	2683.337093	1342.172185	L	288.203016	144.605146	271.176467	136.091872			2
23							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.3	2874.452057	-0.005361	QKPDGVFQEDAPVIHQEMIGGLR
3.0	2874.452057	-0.005361	QKPDGVFQEDAPVIHQEMIGGLR

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

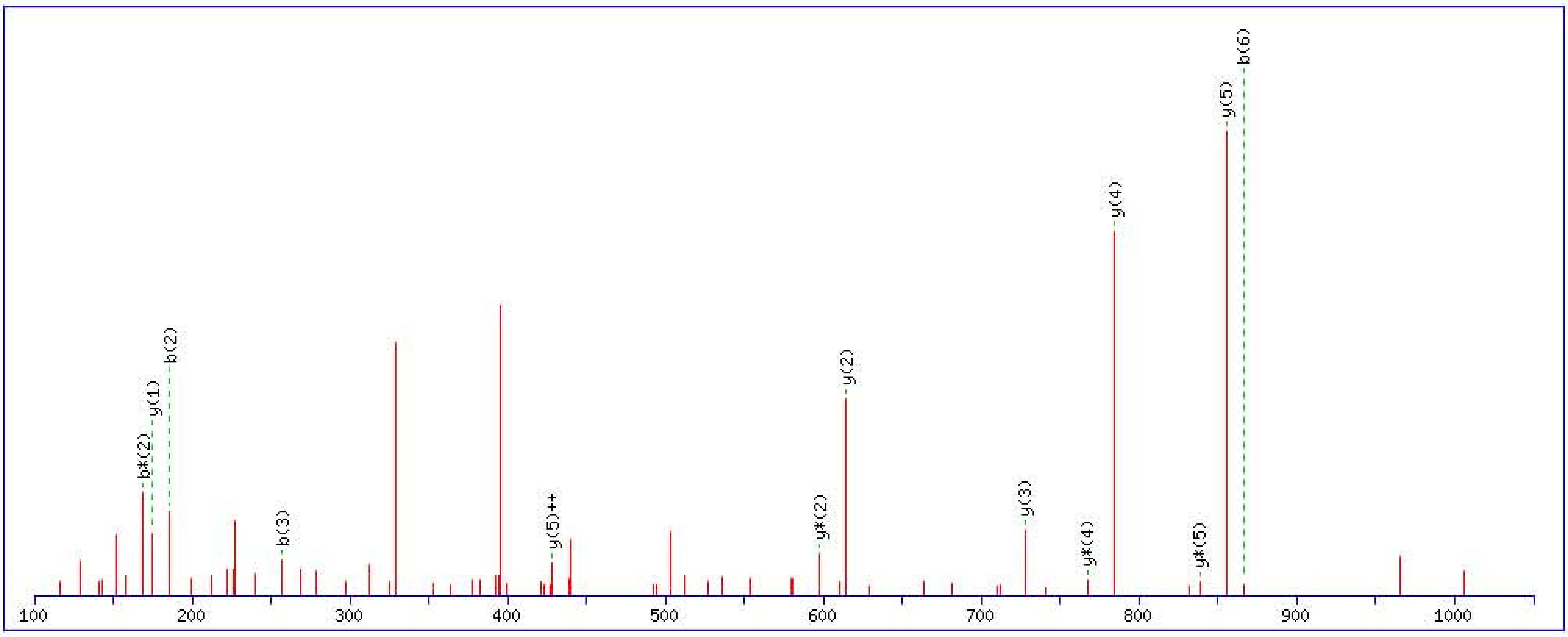
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

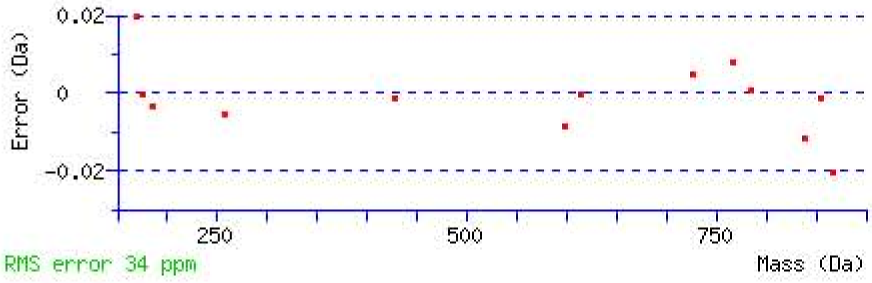
Match to Query 12627: 1039.550328 from(520.782440,2+) rtinseconds(1460) index(42646)
Title: Locus:1.1.1.3221.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

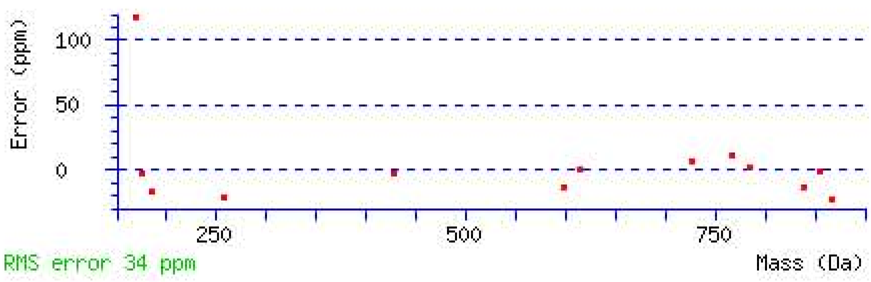
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1039.559677
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.028
Matches : 13/46 fragment ions using 26 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	Seq.	y	y^{++}	y^*	y^{*++}	#
1	58.028740	29.518008			G					7
2	**186.087318**	93.547297	169.060769	85.034023	Q	983.545498	492.276387	966.518949	483.763113	6
3	**257.124432**	129.065854	240.097883	120.552580	A	***855.486920***	428.247098	838.460371	419.733824	5
4	314.145896	157.576586	297.119347	149.063312	G	***784.449806***	392.728541	767.423257	384.215267	4
5	427.229960	214.118618	410.203411	205.605344	L	***727.428342***	364.217809	710.401793	355.704535	3
6	**866.455286**	433.731281	849.428737	425.218007	Q	***614.344278***	307.675777	597.317729	299.162503	2
7					R	***175.118952***	88.063114	158.092403	79.549840	1





NCBI **BLAST** search of GQAGLQR
(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	1039.559677	-0.009349	GQAGLQR
14.2	1039.559677	-0.009349	GQQIQR
10.9	1039.541061	0.009267	GQGDLLQPGR
7.0	1039.559677	-0.009349	KGGPSQR
6.8	1039.541046	0.009282	NATTAPNPVR
5.3	1039.552277	-0.001949	GQPQELGRR
4.3	1039.552277	-0.001949	QRAALDGGPR
1.8	1039.563492	-0.013164	AEGARARGPR
1.8	1039.563492	-0.013164	SSHLRERR
1.5	1039.541061	0.009267	AGVTTPAPGNR

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

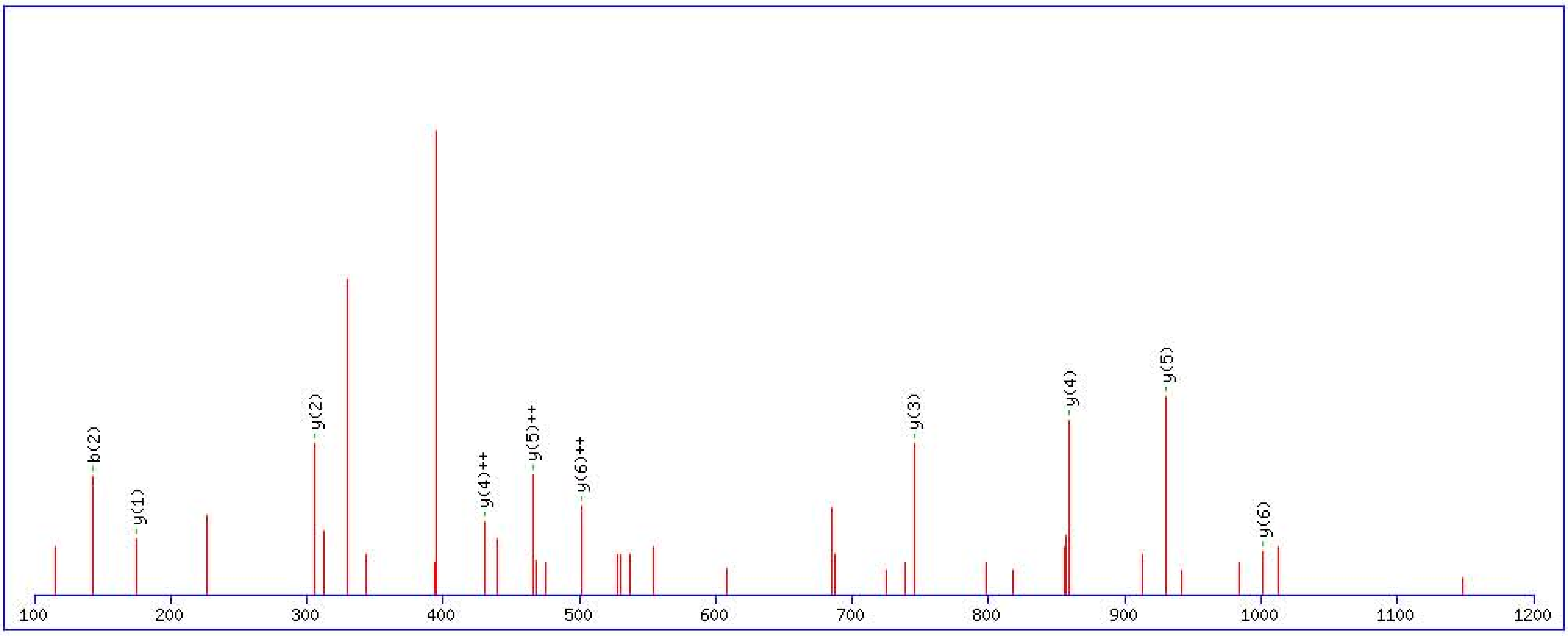
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

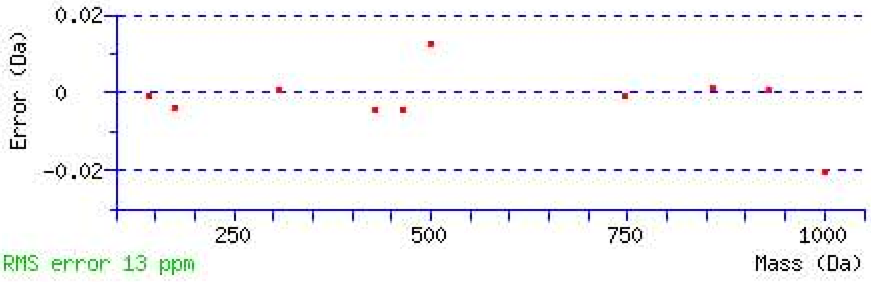
Match to Query 13331: 1071.528988 from(536.771770,2+) rtinseconds(1406) index(42337)
Title: Locus:1.1.1.3202.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

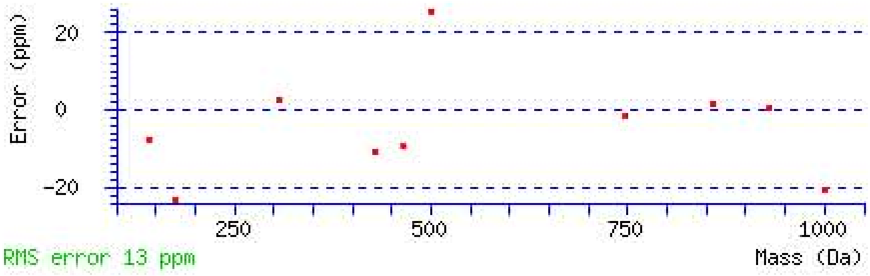
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1071.531723
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.024
Matches : 10/42 fragment ions using 26 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.044390	36.525833			A					7
2	143.081504	72.044390			A	***1001.501918***	501.254597	984.475369	492.741323	6
3	214.118618	107.562947			A	***930.464804***	465.736040	913.438255	457.222766	5
4	328.161545	164.584410	311.134996	156.071136	N	***859.427690***	430.217483	842.401141	421.704209	4
5	767.386871	384.197074	750.360322	375.683799	Q	***745.384763***	373.196020	728.358214	364.682745	3
6	898.427356	449.717316	881.400807	441.204042	M	***306.159437***	153.583357	289.132888	145.070082	2
7					R	***175.118952***	88.063114	158.092403	79.549840	1





NCBI **BLAST** search of AAANQMR
(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	1071.531723	-0.002735	AAANQMR
15.9	1071.530853	-0.001865	AAEESGAKGPR
5.4	1071.519608	0.009380	AAESAEIEPR
5.4	1071.539597	-0.010609	HHLIEHMR

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

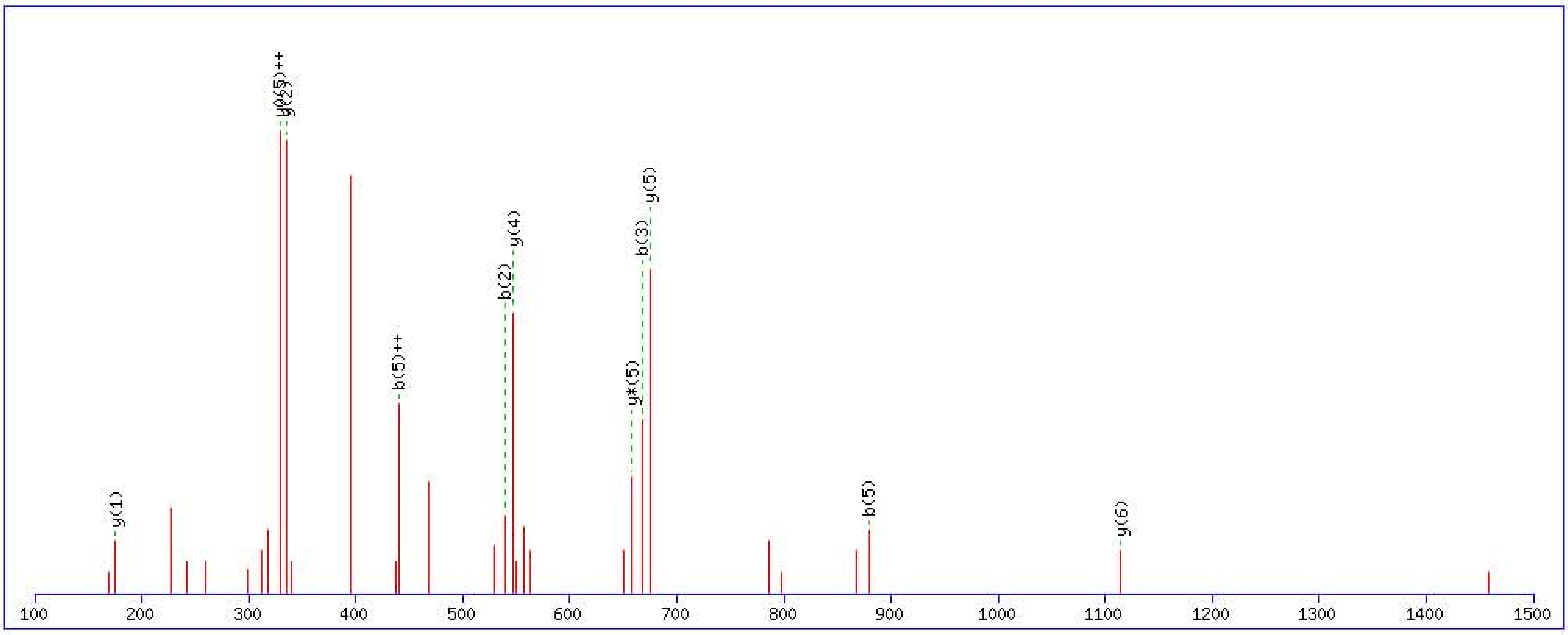
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

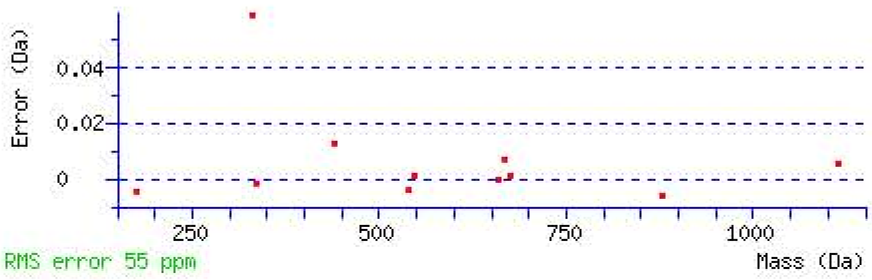
Match to Query 17990: 1212.569008 from(607.291780,2+) rtinseconds(1327) index(41941)
Title: Locus:1.1.1.3174.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

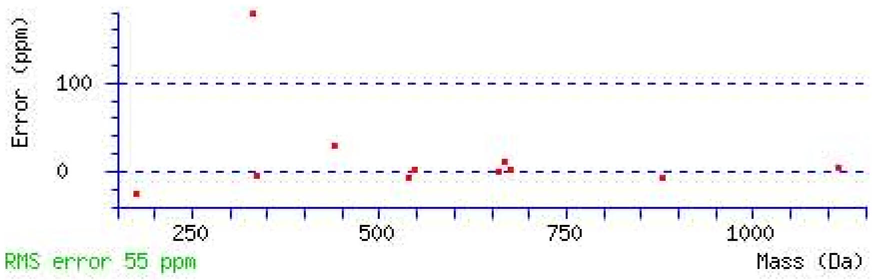
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1212.574356
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 35 **Expect:** 0.00063
Matches : 11/58 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	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
34.8	1212.574356	-0.005348	VQQPDCR
15.7	1212.574356	-0.005348	VQQPDCR
0.7	1212.582199	-0.013191	GRMPPSEFHR

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

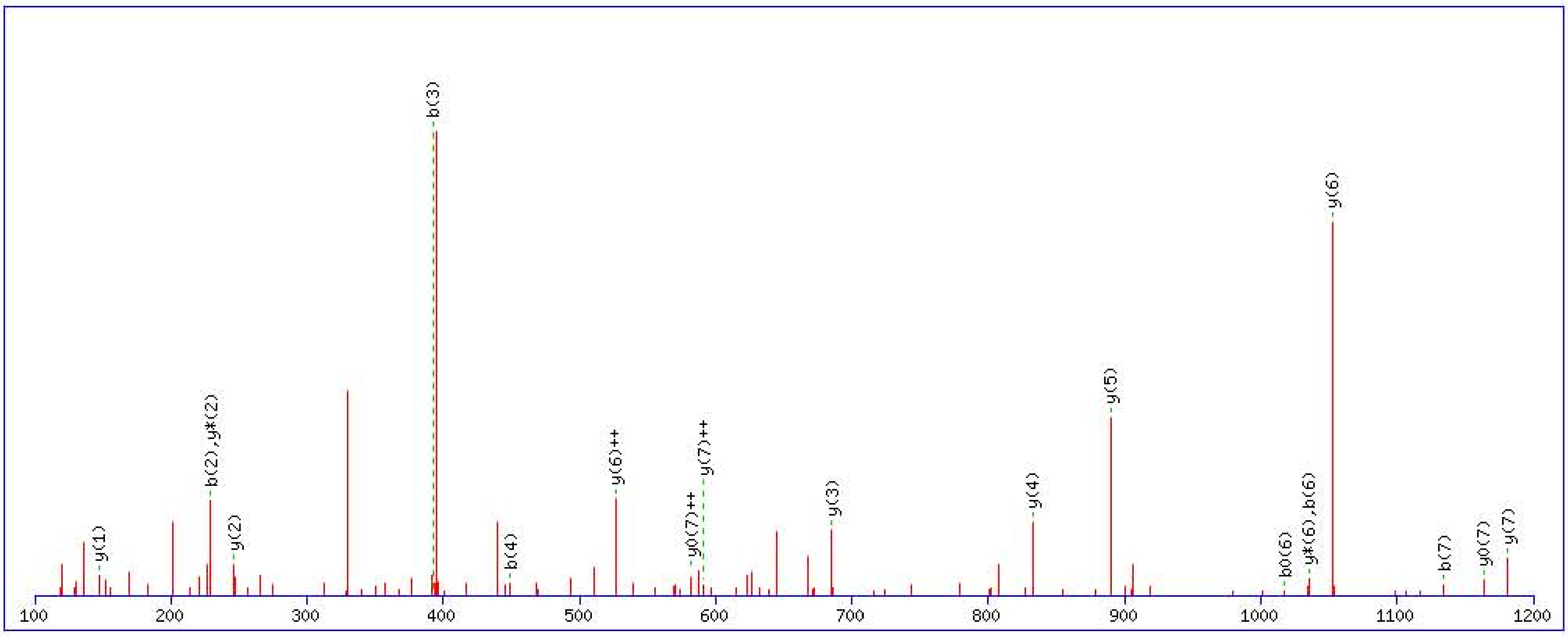
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

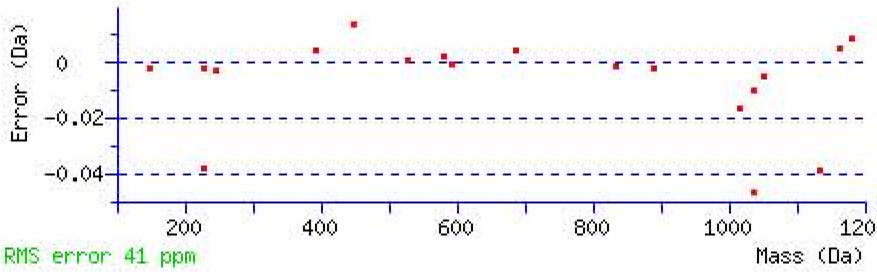
Match to Query 19793: 1279.659568 from(640.837060,2+) rtinseconds(2000) index(31887)
Title: Locus:1.1.1.3360.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

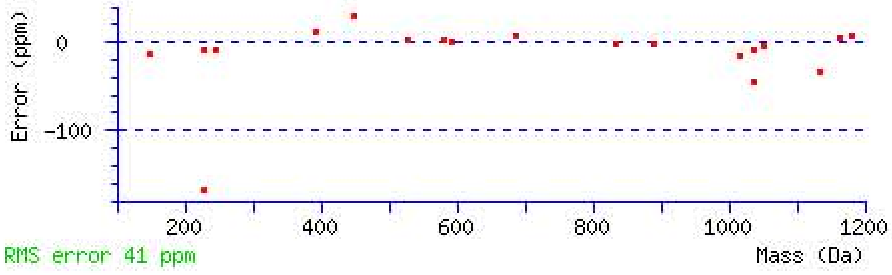
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1279.663483
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 26 **Expect:** 0.01
Matches : 19/60 fragment ions using 51 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
25.6	1279.663483	-0.003915	VEYGFQVK
4.1	1279.663483	-0.003915	QFVGYLDK
2.1	1279.677216	-0.017648	VFKTEDTQGKK
0.5	1279.659470	0.000098	VCSFGKQVVEK
0.4	1279.652039	0.007529	VERAITEASPAH
0.3	1279.652054	0.007514	DAHDPQDKKVK
0.1	1279.677200	-0.017632	EYVGKTSLVER

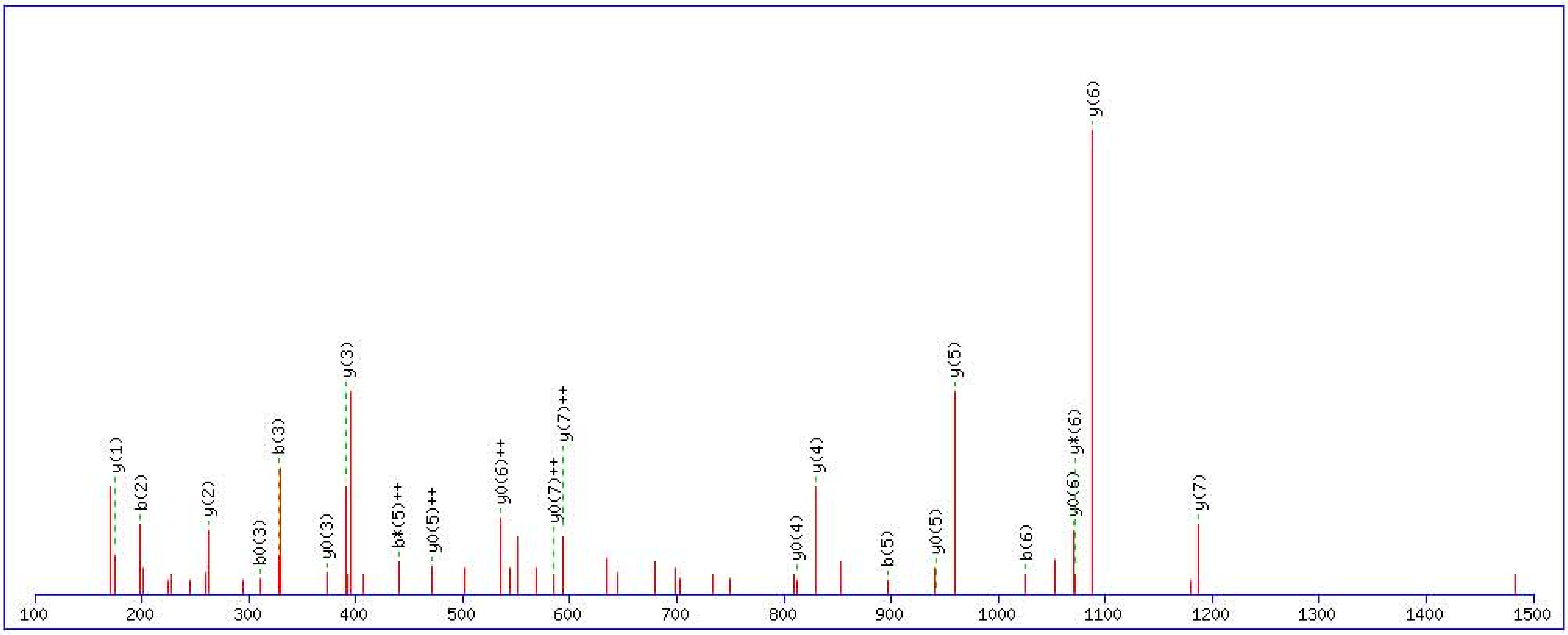
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

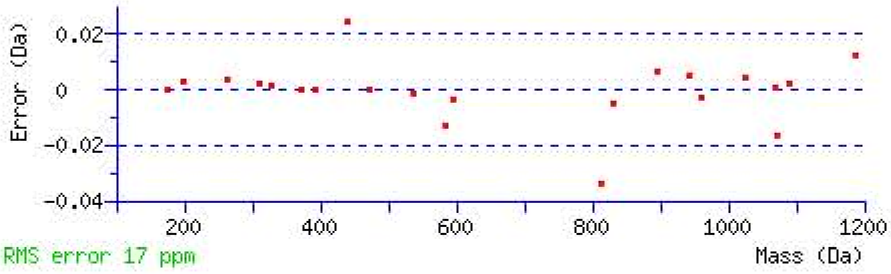
Match to Query 20080: 1285.627528 from(643.821040,2+) rtinseconds(1386) index(28142)
Title: Locus:1.1.1.3145.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

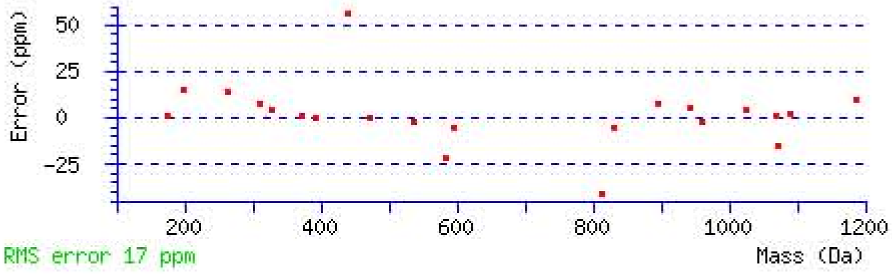
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1285.633621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.0012
Matches : 22/70 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	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
42.0	1285.633621	-0.006093	VVEEQESR

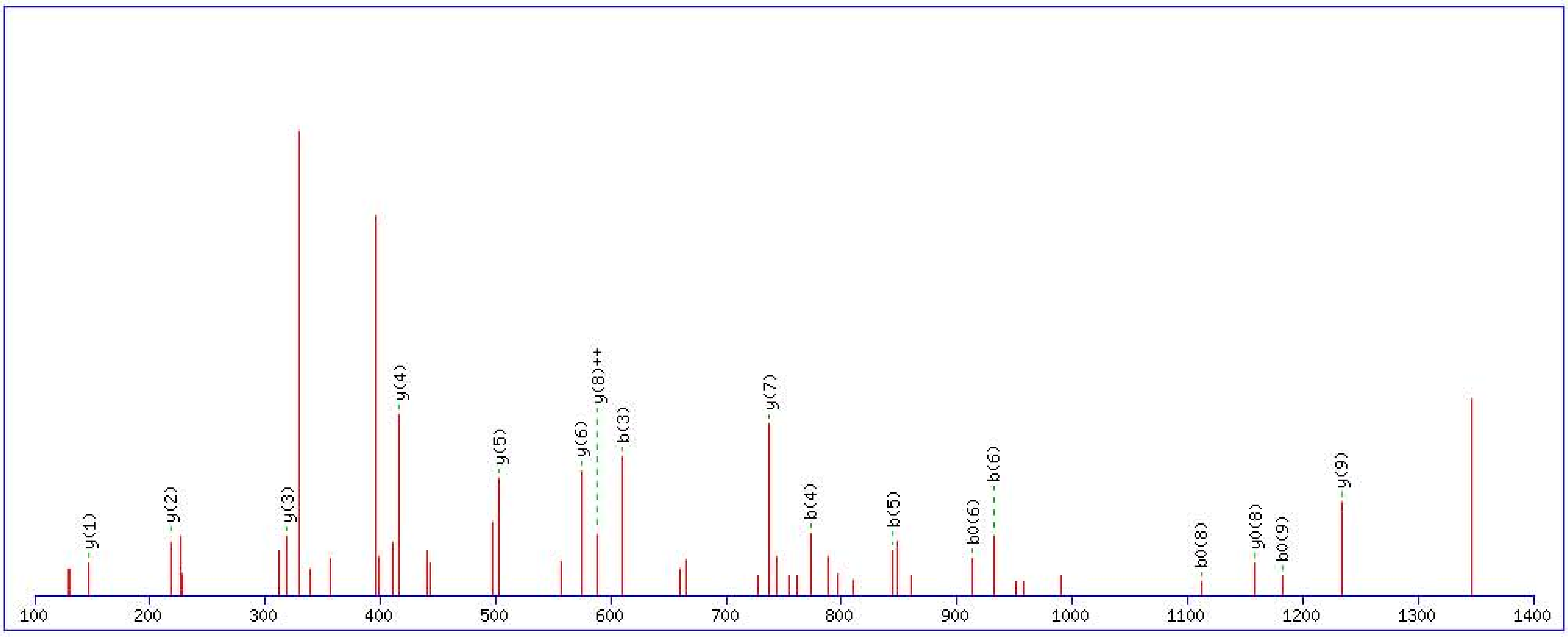
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

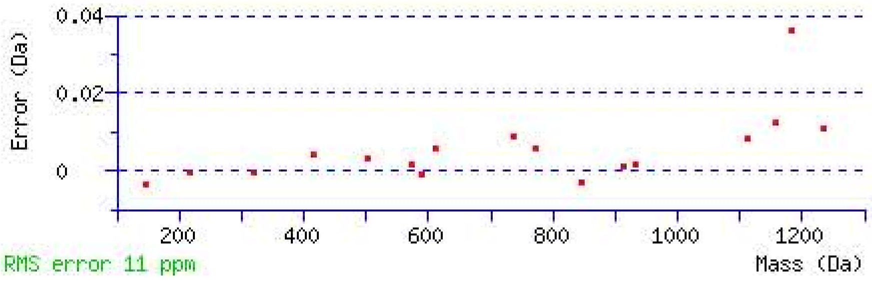
Match to Query 21270: 1345.697228 from(673.855890,2+) rtinseconds(1635) index(29667)
Title: Locus:1.1.1.3232.22 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

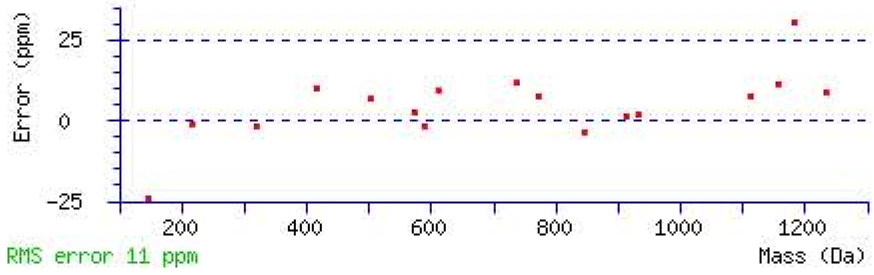
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 51  Expect: 8.5e-005
Matches : 17/90 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	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
50.9	1345.706390	-0.009162	LGQYASPTAK
7.1	1345.706406	-0.009178	QGLYTPQTK
6.7	1345.706390	-0.009162	LGQYDQALK
6.2	1345.692474	0.004754	VASCRYPALGPR
2.6	1345.681213	0.016015	ENKMTWAPKNK
1.0	1345.692505	0.004723	DHTVFGRVMLR

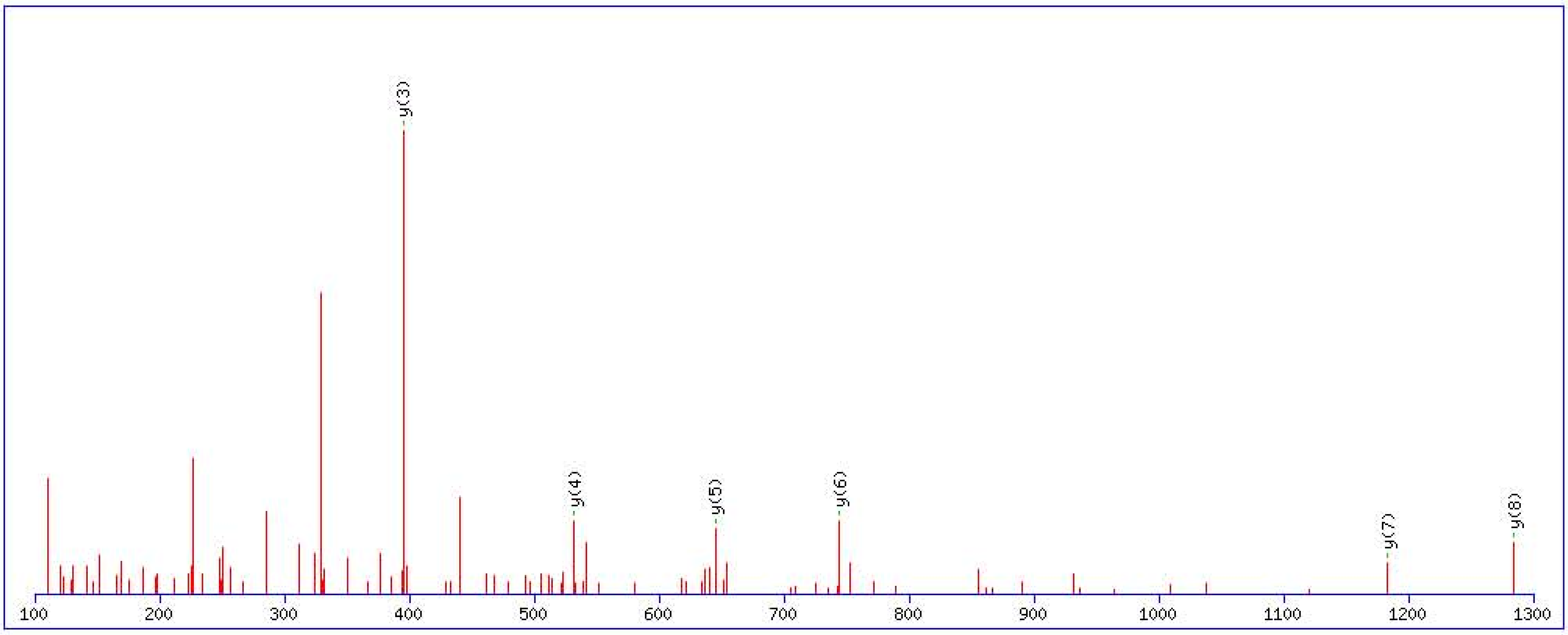
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

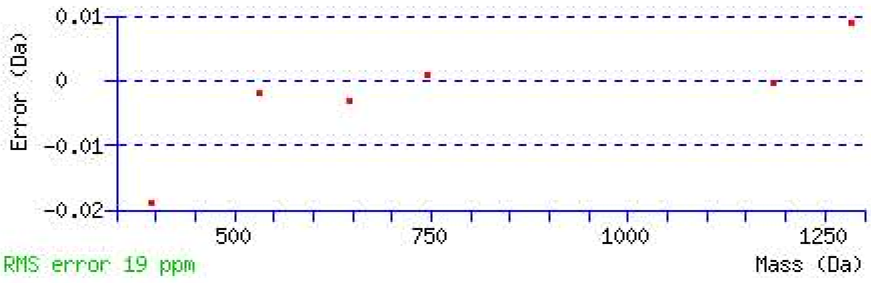
Match to Query 23538: 1396.788582 from(466.603470,3+) rtinseconds(1965) index(45767)
Title: Locus:1.1.1.3397.3 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

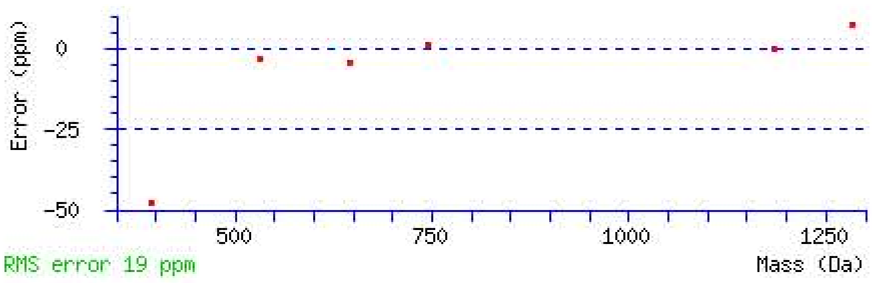
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1396.790085
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 35 **Expect:** 0.00061
Matches : 6/88 fragment ions using 12 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	215.139019	108.073147			197.128454	99.067865	T	*1284.713292*	642.860284	1267.686743	634.347010	1266.702727	633.855002	8
3	654.364345	327.685811	637.337796	319.172536	636.353780	318.680528	Q	*1183.665613*	592.336445	1166.639064	583.823170	1165.655048	583.331162	7
4	753.432759	377.220018	736.406210	368.706743	735.422194	368.214735	V	*744.440287*	372.723782	727.413738	364.210507	726.429722	363.718499	6
5	866.516823	433.762050	849.490274	425.248775	848.506258	424.756767	L	*645.371873*	323.189575	628.345324	314.676300	627.361308	314.184292	5
6	1003.575735	502.291506	986.549186	493.778231	985.565170	493.286223	H	*532.287809*	266.647543	515.261260	258.134268	514.277244	257.642260	4
7	1150.644149	575.825713	1133.617600	567.312438	1132.633584	566.820430	F	*395.228897*	198.118086	378.202348	189.604812	377.218332	189.112804	3
8	1251.691828	626.349552	1234.665279	617.836278	1233.681263	617.344270	T	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	2
9							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.6	1396.790085	-0.001503	ITQVLHFTK
0.3	1396.792557	-0.003975	LLGELQEQIVQK

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

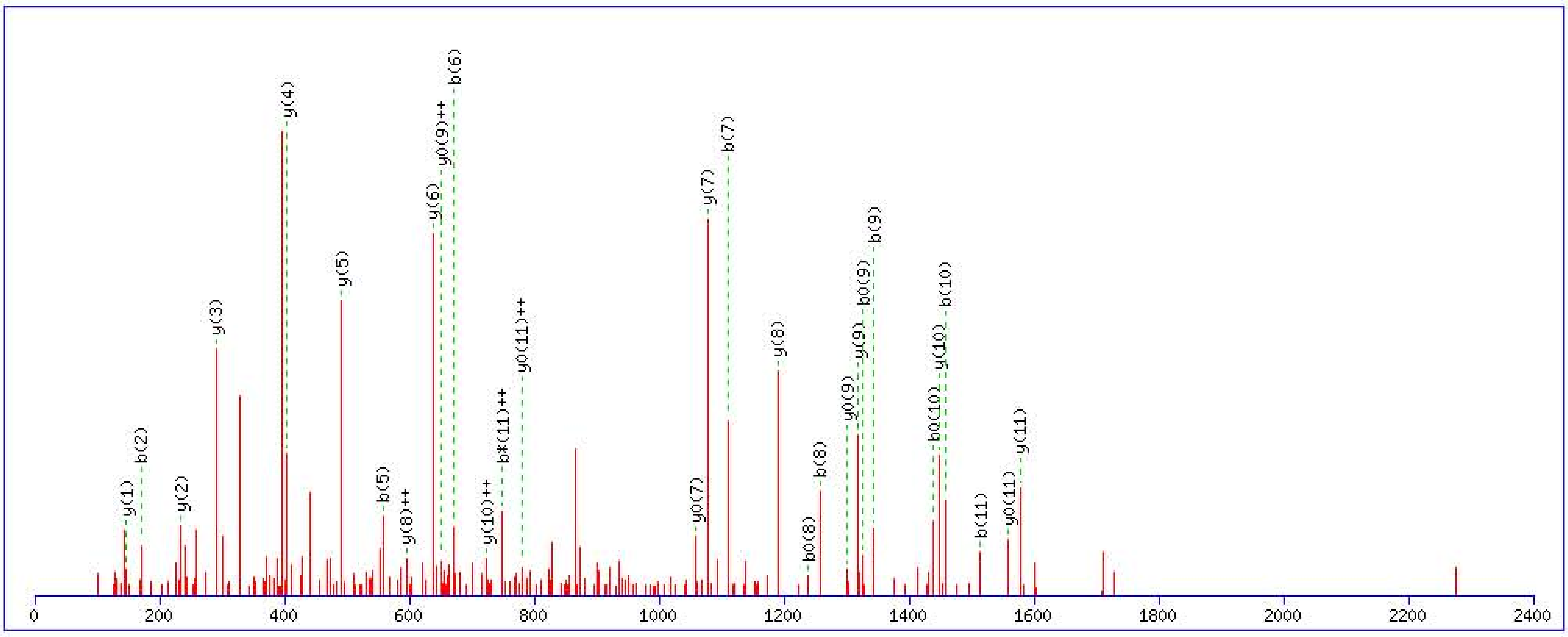
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

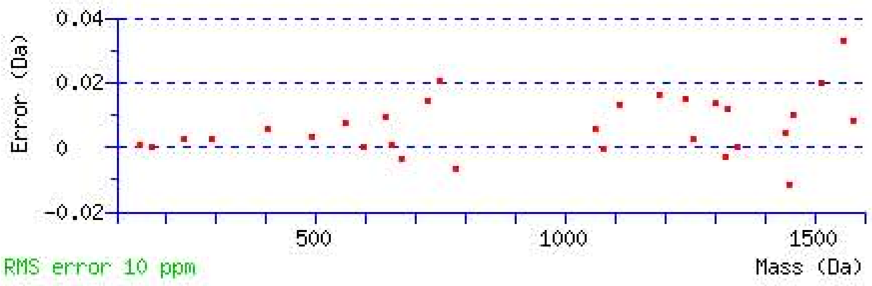
Match to Query 34611: 1746.895648 from(874.455100,2+) rtinseconds(2556) index(49068)
Title: Locus:1.1.1.3602.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

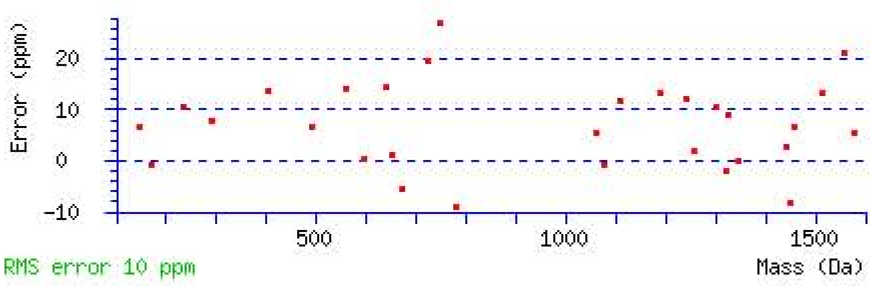
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1746.886200
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 80  Expect: 6.9e-008
Matches : 30/126 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	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
79.6	1746.886200	0.009448	GLEEELQFSLGSK
3.2	1746.887558	0.008090	AVQSKAFCAGGLAPGWK

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

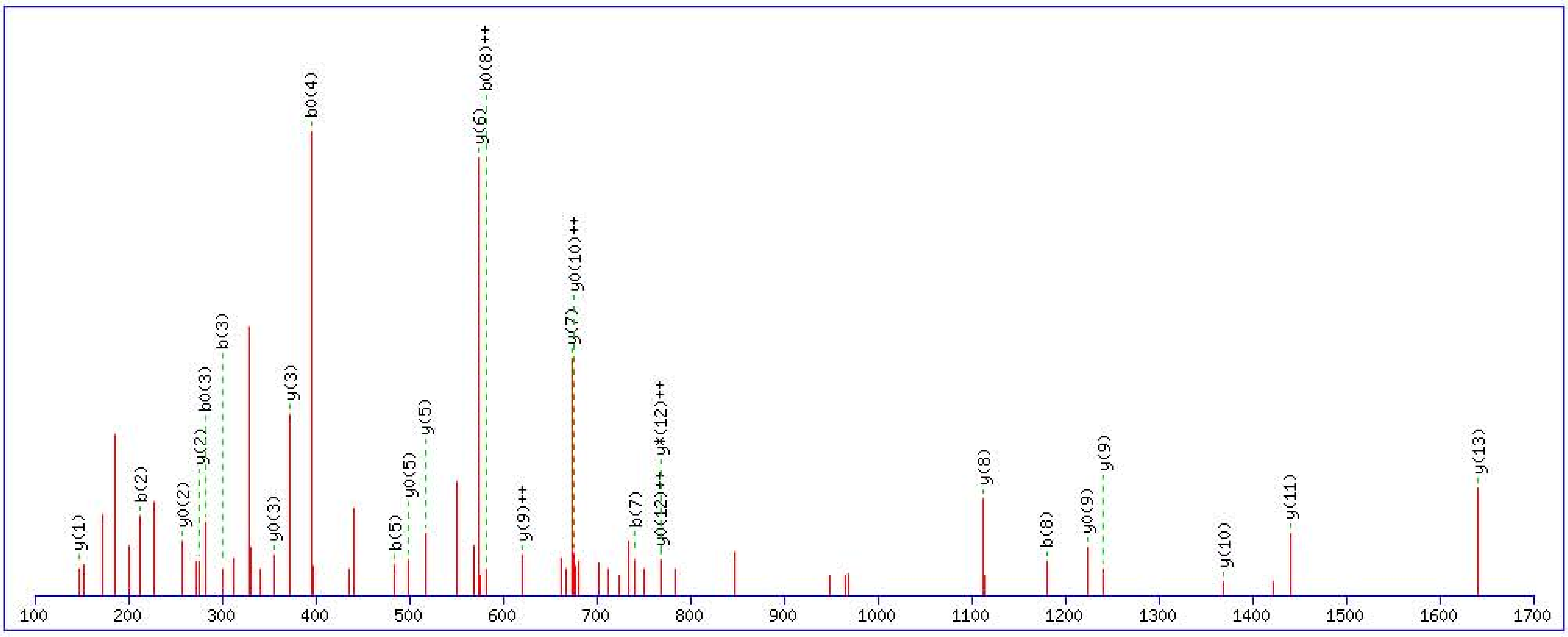
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

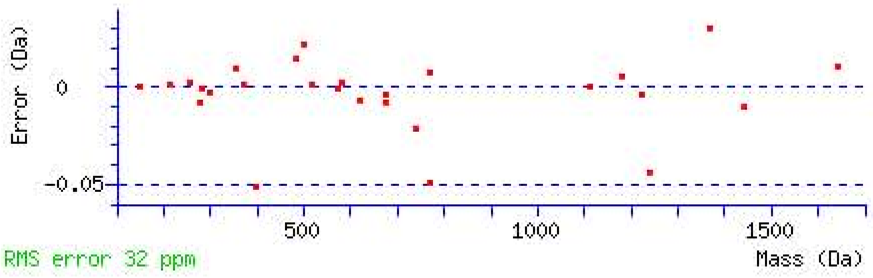
Match to Query 36652: 1851.976662 from(618.332830,3+) rtinseconds(2001) index(46074)
Title: Locus:1.1.1.3409.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

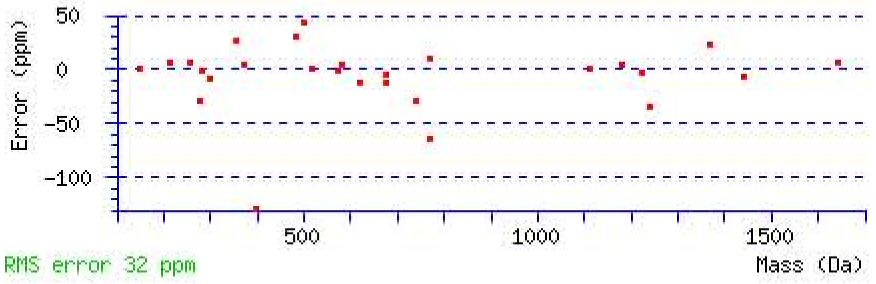
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1851.976425
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 58 **Expect:** 3.7e-005
Matches : 27/152 fragment ions using 57 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							15
2	**213.159754**	107.083515					L	1753.915298	877.461287	1736.888749	868.948013	1735.904733	868.456004	14
3	**300.191782**	150.599529			282.181217	141.594247	S	***1640.831234***	820.919255	1623.804685	812.405981	1622.820669	811.913973	13
4	413.275846	207.141561			395.265281	198.136279	L	1553.799206	777.403241	1536.772657	768.889967	1535.788641	768.397958	12
5	**484.312960**	242.660118			466.302395	233.654836	A	***1440.715142***	720.861209	1423.688593	712.347935	1422.704577	711.855927	11
6	612.371538	306.689407	595.344989	298.176133	594.360973	297.684125	Q	***1369.678028***	685.342652	1352.651479	676.829378	1351.667463	676.337370	10
7	**741.414131**	371.210704	724.387582	362.697429	723.403566	362.205421	E	***1241.619450***	621.313363	1224.592901	612.800089	1223.608885	612.308080	9
8	**1180.639457**	590.823367	1163.612908	582.310092	1162.628892	581.818084	Q	***1112.576857***	556.792066	1095.550308	548.278792	1094.566292	547.786784	8
9	1279.707871	640.357574	1262.681322	631.844299	1261.697306	631.352291	V	***673.351531***	337.179404	656.324982	328.666129	655.340966	328.174121	7
10	1336.729335	668.868306	1319.702786	660.355031	1318.718770	659.863023	G	***574.283117***	287.645197	557.256568	279.131922	556.272552	278.639914	6
11	1393.750799	697.379037	1376.724250	688.865763	1375.740234	688.373755	G	***517.261653***	259.134465	500.235104	250.621190	499.251088	250.129182	5
12	1480.782827	740.895052	1463.756278	732.381777	1462.772262	731.889769	S	460.240189	230.623732	443.213640	222.110458	442.229624	221.618450	4
13	1577.835591	789.421434	1560.809042	780.908159	1559.825026	780.416151	P	***373.208161***	187.107718	356.181612	178.594444	355.197596	178.102436	3
14	1706.878184	853.942730	1689.851635	845.429456	1688.867619	844.937447	E	***276.155397***	138.581336	259.128848	130.068062	258.144832	129.576054	2
15							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.3	1851.976425	0.000237	VLSLAQEQVGGSPEK
37.0	1851.976425	0.000237	VLSLAQEQVGGSPEK

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

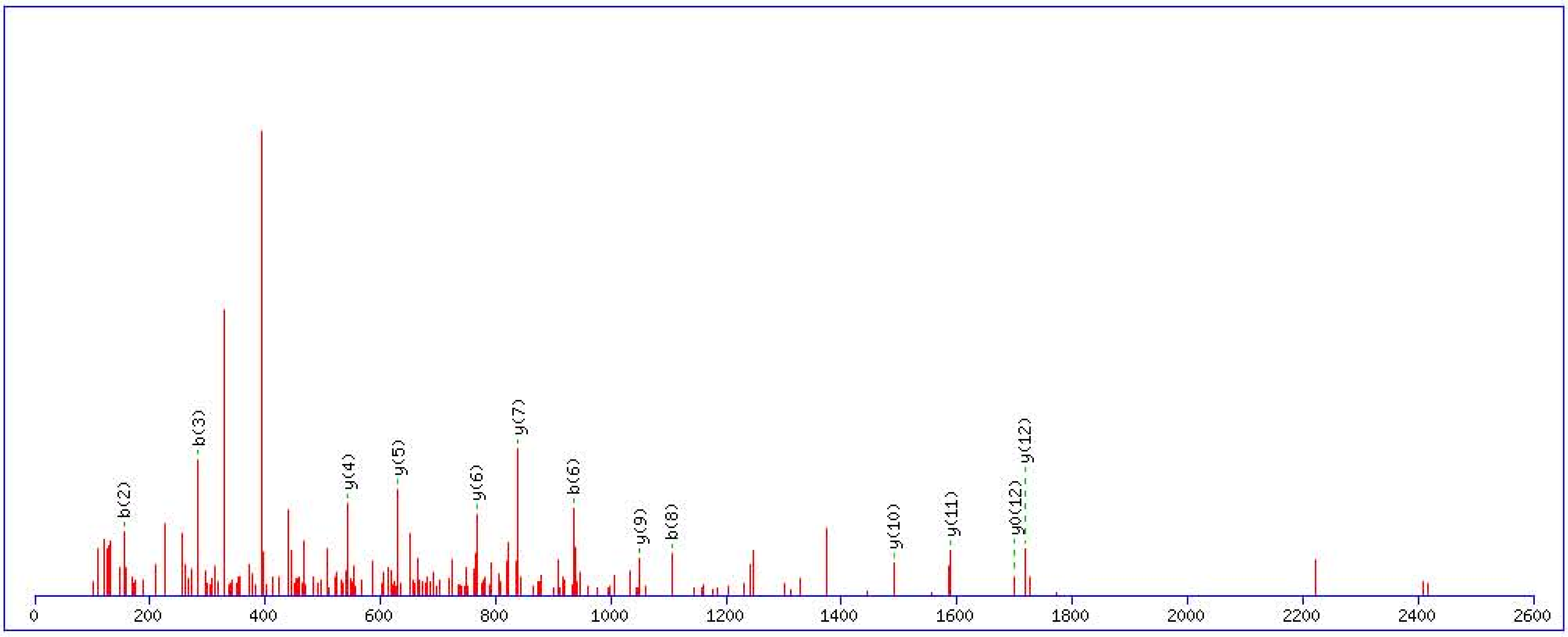
Mascot Search Results

Peptide View

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

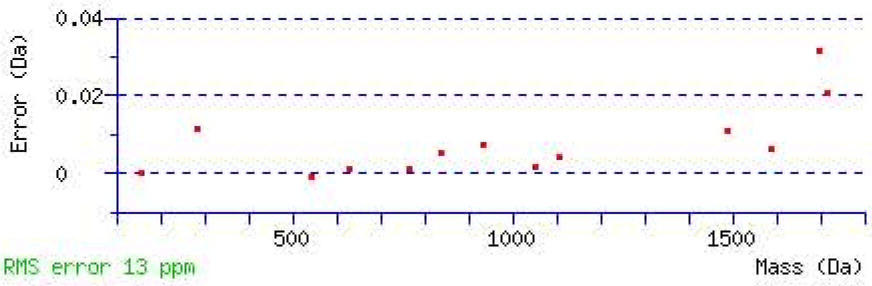
Match to Query 37065: 1871.013762 from(624.678530,3+) rtinseconds(2248) index(47552)
Title: Locus:1.1.1.3495.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

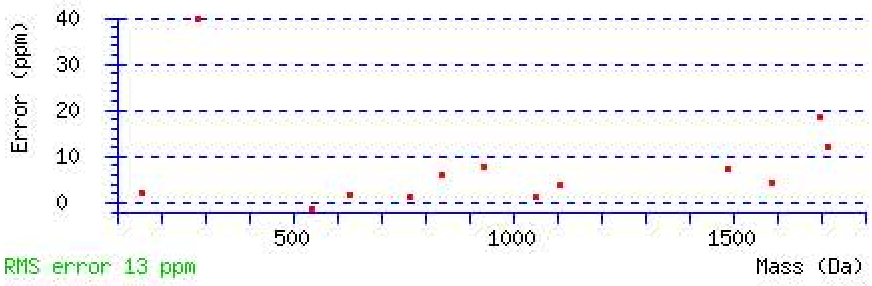
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1871.012756
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 59  Expect: 7.5e-006
Matches : 13/136 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	58.028740	29.518008					G							14
2	**155.081504**	78.044390					P	1814.998574	908.002925	1797.972025	899.489651	1796.988009	898.997643	13
3	**284.124097**	142.565687			266.113532	133.560404	E	***1717.945810***	859.476543	1700.919261	850.963269	1699.935245	850.471261	12
4	383.192511	192.099894			365.181946	183.094611	V	***1588.903217***	794.955247	1571.876668	786.441972	1570.892652	785.949964	11
5	822.417837	411.712557	805.391288	403.199282	804.407272	402.707274	Q	***1489.834803***	745.421040	1472.808254	736.907765	1471.824238	736.415757	10
6	**935.501901**	468.254589	918.475352	459.741314	917.491336	459.249306	L	***1050.609477***	525.808377	1033.582928	517.295102	1032.598912	516.803094	9
7	1034.570315	517.788796	1017.543766	509.275521	1016.559750	508.783513	V	937.525413	469.266345	920.498864	460.753070	919.514848	460.261062	8
8	**1105.607429**	553.307353	1088.580880	544.794078	1087.596864	544.302070	A	***838.456999***	419.732138	821.430450	411.218863	820.446434	410.726855	7
9	1242.666341	621.836809	1225.639792	613.323534	1224.655776	612.831526	H	***767.419885***	384.213581	750.393336	375.700306	749.409320	375.208298	6
10	1329.698369	665.352823	1312.671820	656.839548	1311.687804	656.347540	S	***630.360973***	315.684125	613.334424	307.170850	612.350408	306.678842	5
11	1426.751133	713.879205	1409.724584	705.365930	1408.740568	704.873922	P	***543.328945***	272.168111	526.302396	263.654836			4
12	1612.830446	806.918861	1595.803897	798.405587	1594.819881	797.913579	W	446.276181	223.641728	429.249632	215.128454			3
13	1725.914510	863.460893	1708.887961	854.947619	1707.903945	854.455611	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 GPEVQLVAHSPWLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.0	1871.012756	0.001006	GPEVQLVAHSPWLK
4.4	1870.994781	0.018981	NVNQAKLSEHRHK

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

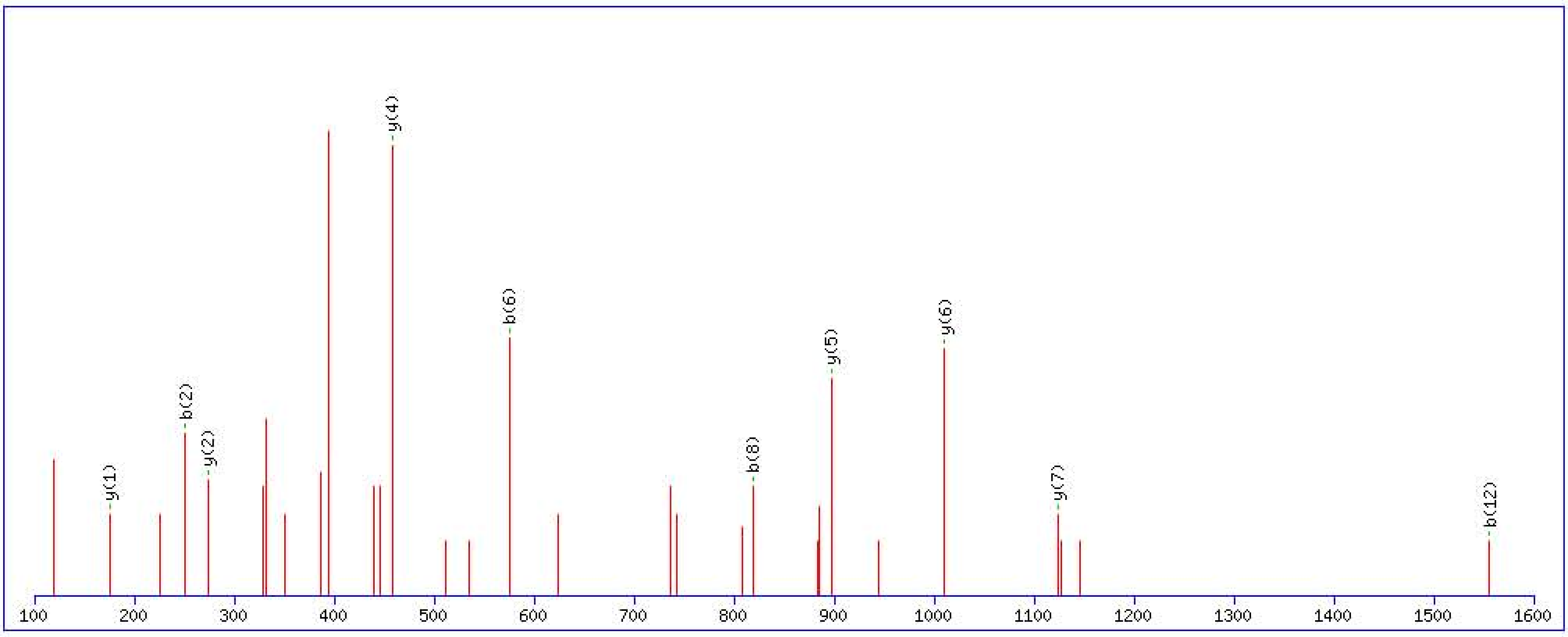
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

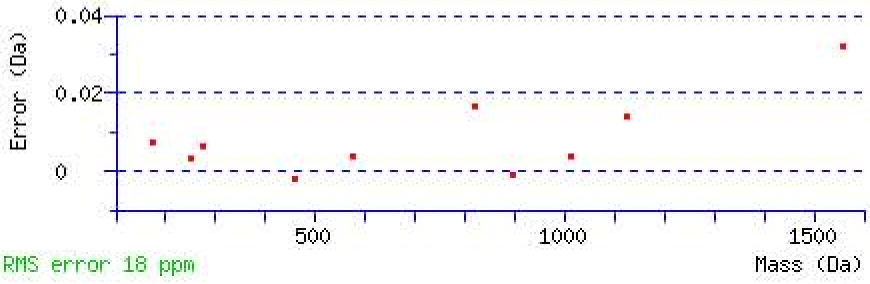
Match to Query 38193: 1941.148422 from(648.056750,3+) rtinseconds(2881) index(51423)
Title: Locus:1.1.1.3713.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

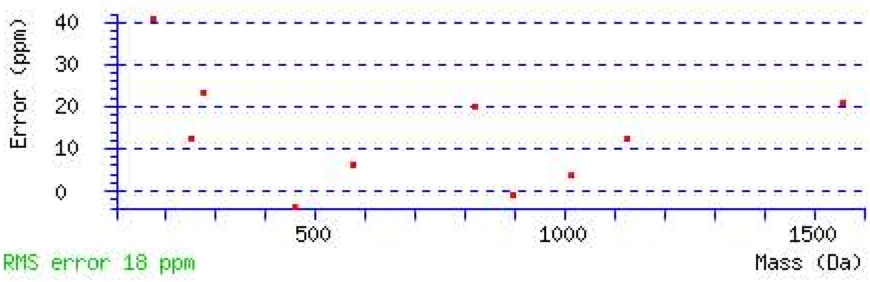
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1941.138626
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.00084
Matches : 10/92 fragment ions using 20 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	138.066188	69.536732			H					15
2	***251.150252***	126.078764			L	1805.086996	903.047136	1788.060447	894.533862	14
3	350.218666	175.612971			V	1692.002932	846.505104	1674.976383	837.991830	13
4	447.271430	224.139353			P	1592.934518	796.970897	1575.907969	788.457623	12
5	504.292894	252.650085			G	1495.881754	748.444515	1478.855205	739.931241	11
6	***575.330008***	288.168642			A	1438.860290	719.933783	1421.833741	711.420509	10
7	672.382772	336.695024			P	1367.823176	684.415226	1350.796627	675.901952	9
8	***819.451186***	410.229231			F	1270.770412	635.888844	1253.743863	627.375570	8
9	932.535250	466.771263			L	***1123.701998***	562.354637	1106.675449	553.841363	7
10	1045.619314	523.313295			L	***1010.617934***	505.812605	993.591385	497.299331	6
11	1484.844640	742.925958	1467.818091	734.412684	Q	***897.533870***	449.270573	880.507321	440.757298	5
12	***1555.881754***	778.444515	1538.855205	769.931241	A	***458.308544***	229.657910	441.281995	221.144635	4
13	1668.965818	834.986547	1651.939269	826.473273	L	387.271430	194.139353	370.244881	185.626078	3
14	1768.034232	884.520754	1751.007683	876.007480	V	***274.187366***	137.597321	257.160817	129.084047	2
15					R	***175.118952***	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.0	1941.138626	0.009796	HLVPGAPFLLQALVR

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

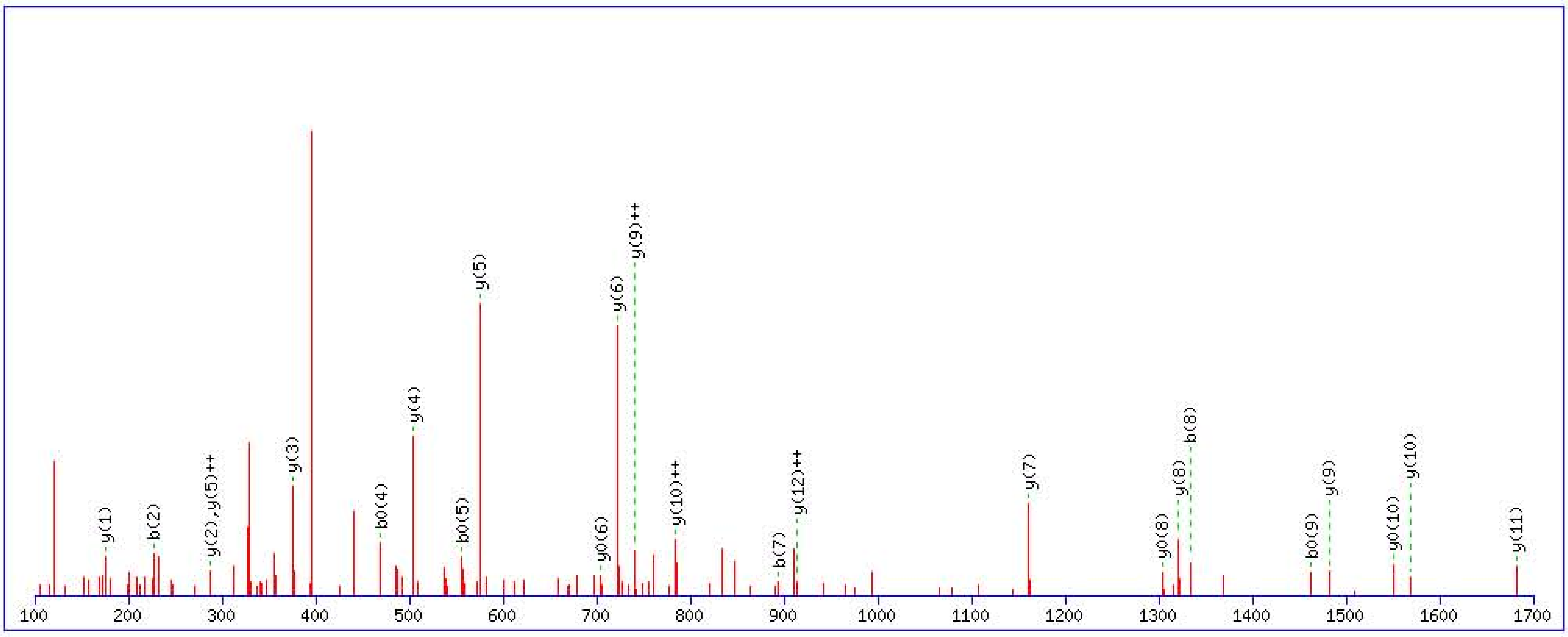
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

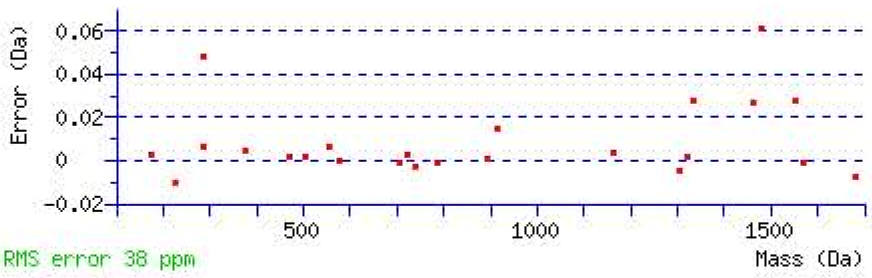
Match to Query 40920: 2053.946352 from(685.656060,3+) rtinseconds(2498) index(48782)
Title: Locus:1.1.1.3582.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

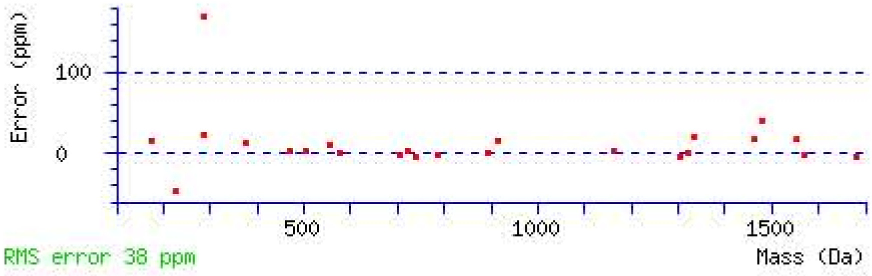
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2053.942368
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 65 **Expect:** 1.4e-006
Matches : 24/138 fragment ions using 42 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							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
65.3	2053.942368	0.003984	EPFLSCCQFAESLR
3.1	2053.948227	-0.001875	EKSTCSMGSELLPMISPR

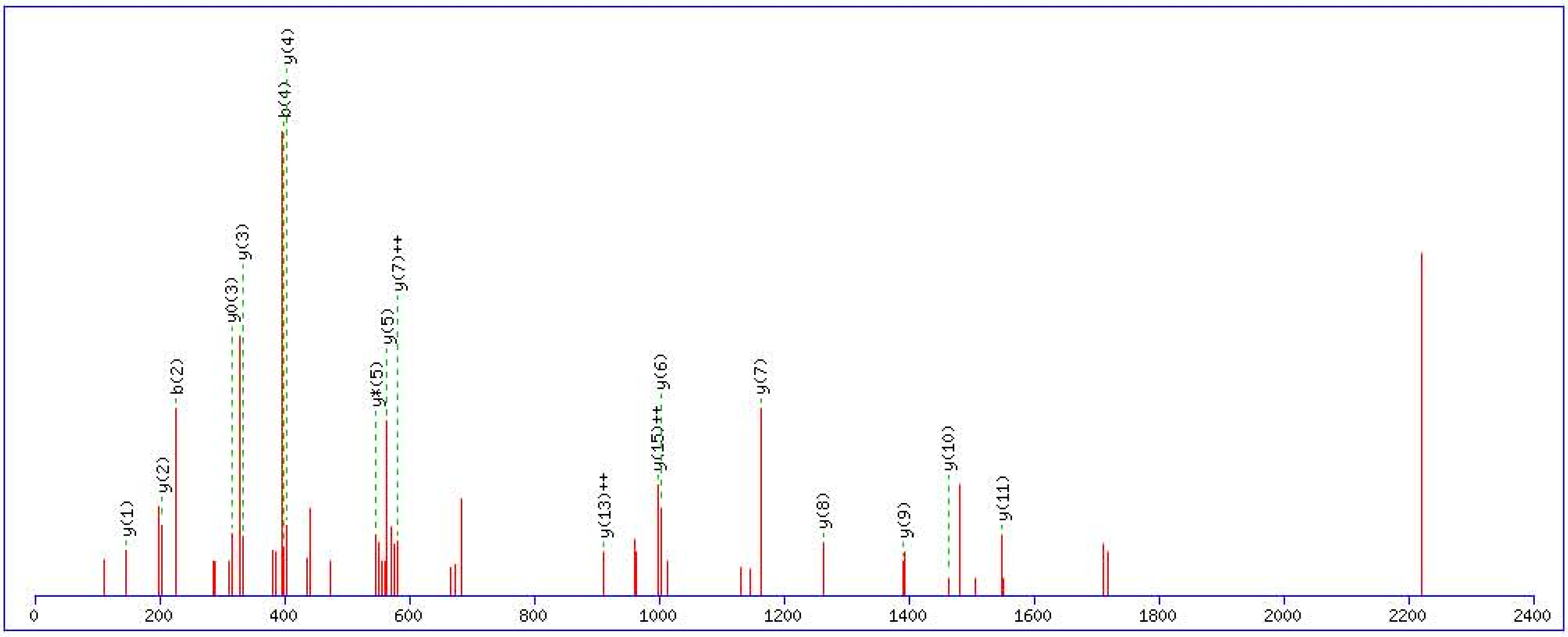
MATRIX SCIENCE Mascot Search Results

Peptide View

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

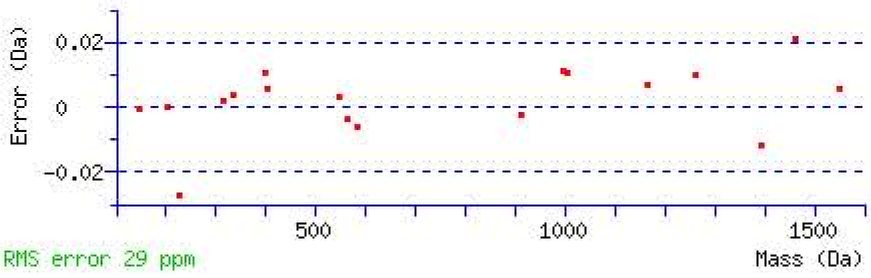
Match to Query 43621: 2220.038922 from(741.020250,3+) rtinseconds(2229) index(47386)
Title: Locus:1.1.1.3488.20 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

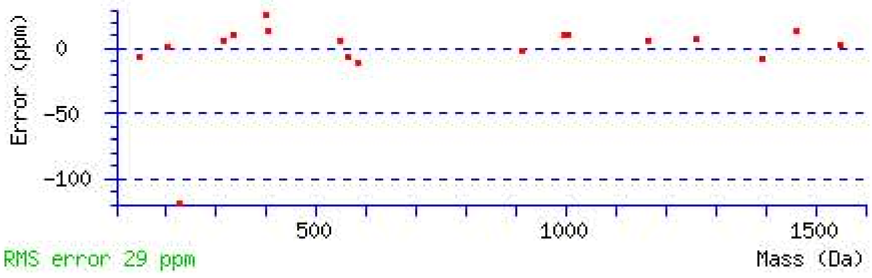
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2220.041092
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 50  Expect: 0.00017
Matches : 18/160 fragment ions using 45 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
49.7	2220.041092	-0.002170	LLATLCSAEVCQCAEGK

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

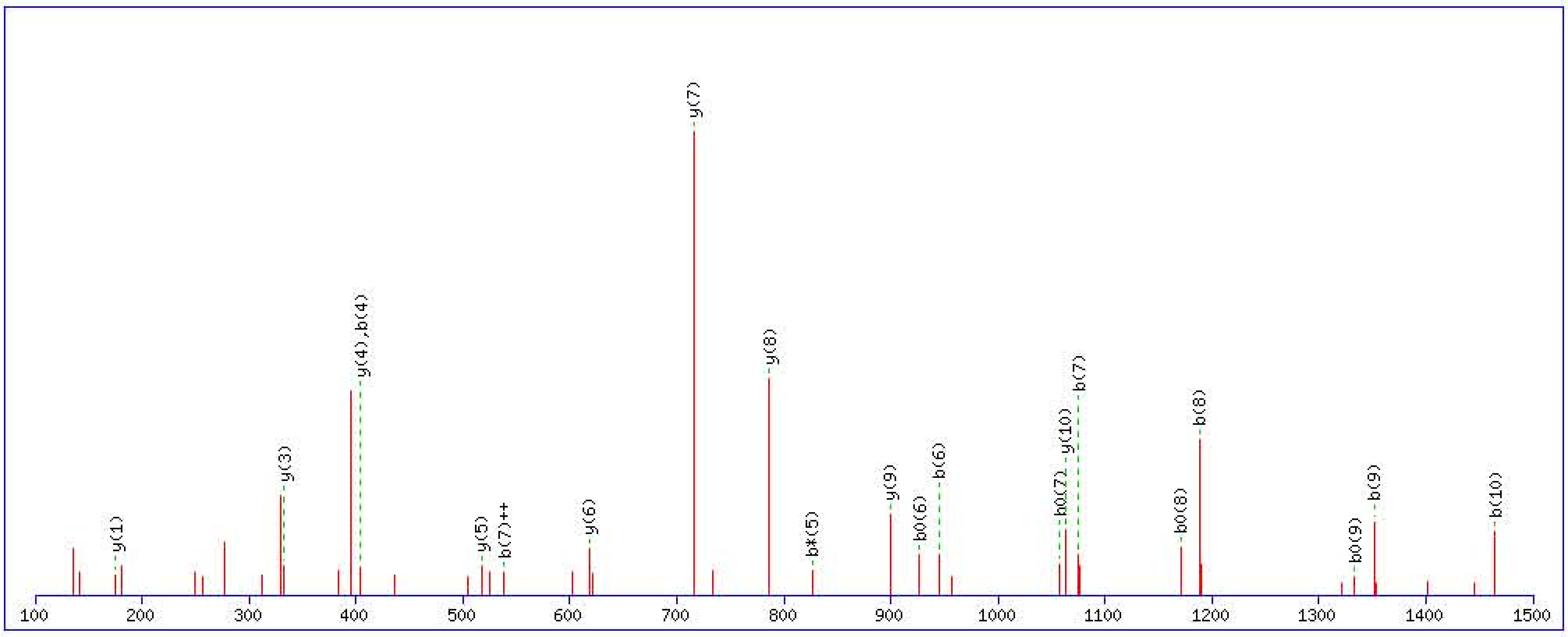
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

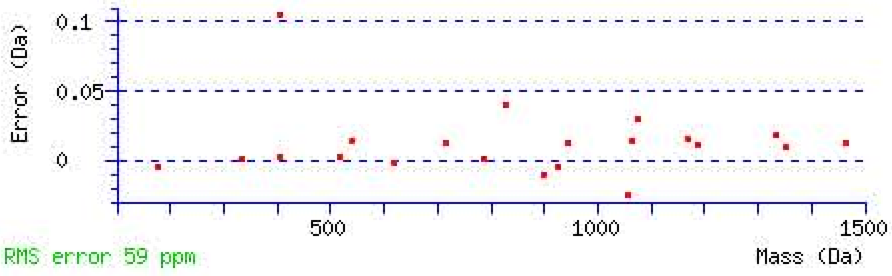
Match to Query 44062: 2249.109492 from(750.710440,3+) rtinseconds(2515) index(48930)
Title: Locus:1.1.1.3588.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

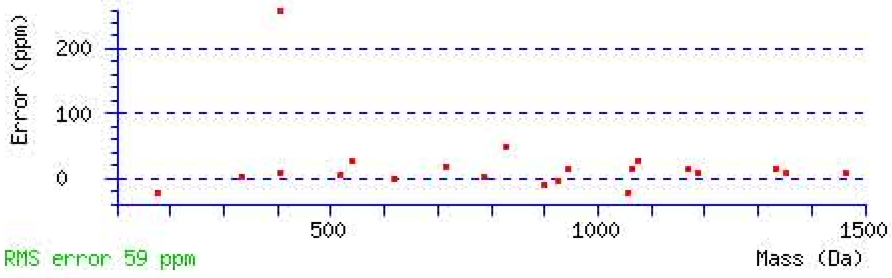
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2249.100647
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.0011
Matches : 21/188 fragment ions using 45 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							18
2	218.059389	109.533333					C	2193.086482	1097.046879	2176.059933	1088.533604	2175.075917	1088.041596	17
3	275.080853	138.044064					G	2033.055833	1017.031555	2016.029284	1008.518280	2015.045268	1008.026272	16
4	***404.123446***	202.565361			386.112881	193.560079	E	1976.034369	988.520822	1959.007820	980.007548	1958.023804	979.515540	15
5	843.348772	422.178024	826.322223	413.664750	825.338207	413.172742	Q	1846.991776	923.999526	1829.965227	915.486251	1828.981211	914.994243	14
6	***944.396451***	472.701864	927.369902	464.188589	926.385886	463.696581	T	1407.766450	704.386863	1390.739901	695.873588	1389.755885	695.381580	13
7	***1075.436936***	538.222106	1058.410387	529.708832	1057.426371	529.216824	M	1306.718771	653.863023	1289.692222	645.349749	1288.708206	644.857741	12
8	***1188.521000***	594.764138	1171.494451	586.250864	1170.510435	585.758855	I	1175.678286	588.342781	1158.651737	579.829506	1157.667721	579.337498	11
9	***1351.584329***	676.295803	1334.557780	667.782528	1333.573764	667.290520	Y	***1062.594222***	531.800749	1045.567673	523.287475	1044.583657	522.795466	10
10	***1464.668393***	732.837834	1447.641844	724.324560	1446.657828	723.832552	L	***899.530893***	450.269084	882.504344	441.755810	881.520328	441.263802	9
11	1535.705507	768.356391	1518.678958	759.843117	1517.694942	759.351109	A	***786.446829***	393.727053	769.420280	385.213778	768.436264	384.721770	8
12	1632.758271	816.882773	1615.731722	808.369499	1614.747706	807.877491	P	***715.409715***	358.208496	698.383166	349.695221	697.399150	349.203213	7
13	1733.805950	867.406613	1716.779401	858.893339	1715.795385	858.401330	T	***618.356951***	309.682114	601.330402	301.168839	600.346386	300.676831	6
14	1846.890014	923.948645	1829.863465	915.435370	1828.879449	914.943362	L	***517.309272***	259.158274	500.282723	250.644999	499.298707	250.152991	5
15	1917.927128	959.467202	1900.900579	950.953927	1899.916563	950.461919	A	***404.225208***	202.616242	387.198659	194.102967	386.214643	193.610959	4
16	1988.964242	994.985759	1971.937693	986.472484	1970.953677	985.980476	A	***333.188094***	167.097685	316.161545	158.584410	315.177529	158.092402	3
17	2075.996270	1038.501773	2058.969721	1029.988498	2057.985705	1029.496490	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
18							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.9	2249.100647	0.008845	GCGEQTMIYLAPTLAASR
6.2	2249.115051	-0.005559	YSTSLYASPSMVHEGVAVVPR
3.2	2249.137527	-0.028035	QKFERPICVSWSTDVKGGR
1.9	2249.096420	0.013072	SDNTVTWLAAWTESVQNSIK
0.3	2249.078659	0.030833	FENGVAEGMVDPSLNPISAFR

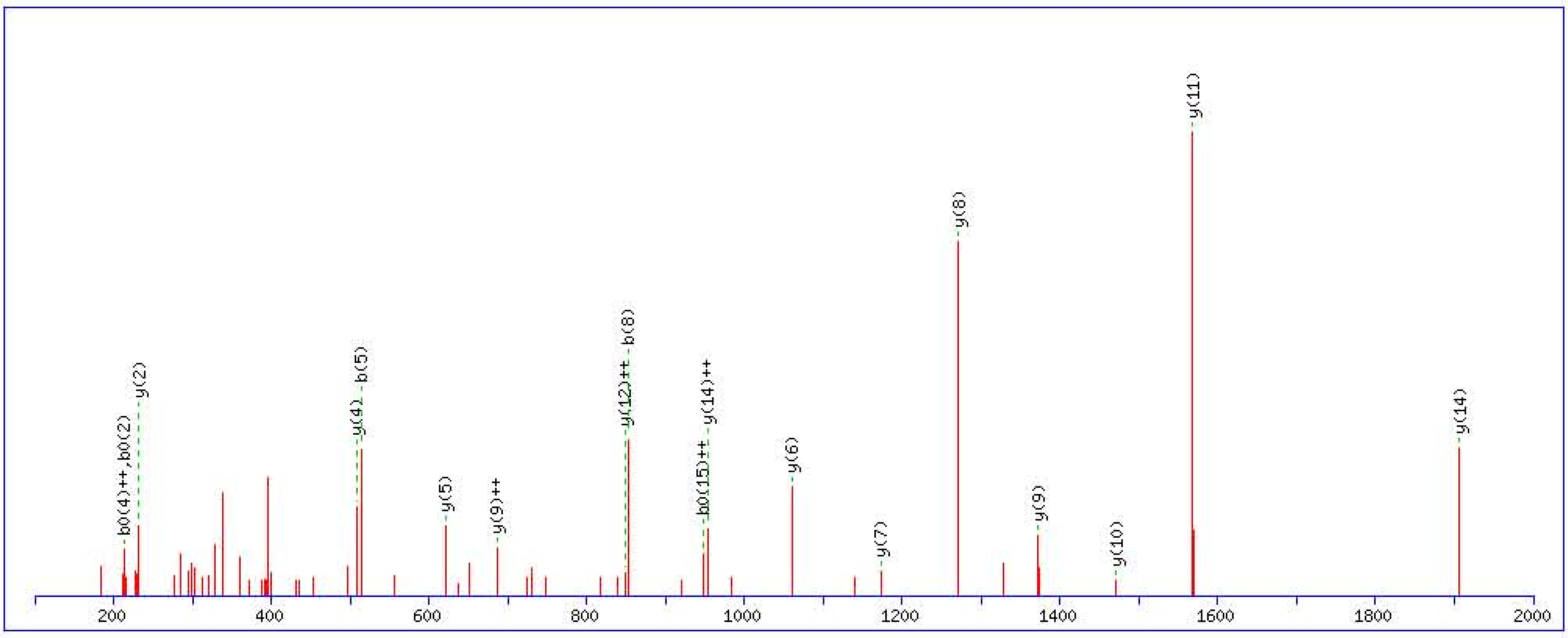
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

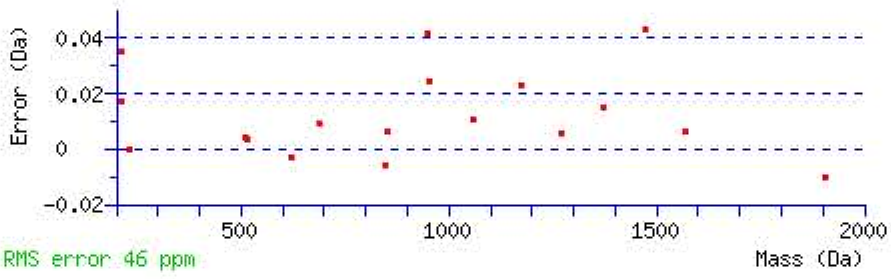
Match to Query 46770: 2418.237822 from(807.086550,3+) rtinseconds(3010) index(52389)
Title: Locus:1.1.1.3756.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

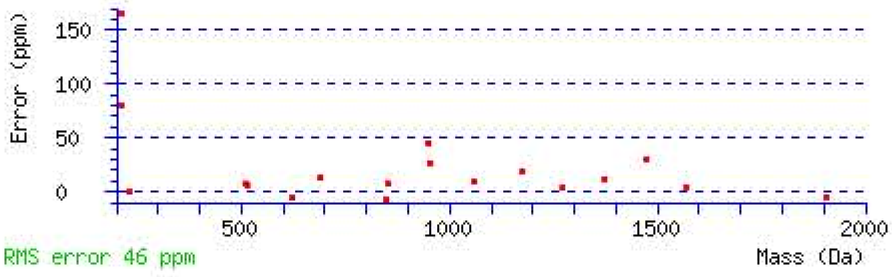
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2418.225342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Biotin:Thermo-21345 (Q)
Ions Score: 66 **Expect:** 8.1e-007
Matches : 18/198 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	116.034219	58.520748			98.023654	49.515465	D							19
2	231.061162	116.034219			213.050597	107.028936	D	2304.205668	1152.606472	2287.179119	1144.093197	2286.195103	1143.601189	18
3	328.113926	164.560601			310.103361	155.555319	P	2189.178725	1095.093000	2172.152176	1086.579726	2171.168160	1086.087718	17
4	443.140869	222.074073			425.130304	213.068790	D	2092.125961	1046.566618	2075.099412	1038.053344	2074.115396	1037.561336	16
5	**514.177983**	257.592630			496.167418	248.587347	A	1977.099018	989.053147	1960.072469	980.539873	1959.088453	980.047865	15
6	611.230747	306.119012			593.220182	297.113729	P	***1906.061904***	953.534590	1889.035355	945.021316	1888.051339	944.529308	14
7	724.314811	362.661044			706.304246	353.655761	L	1809.009140	905.008208	1791.982591	896.494934	1790.998575	896.002926	13
8	**852.373389**	426.690333	835.346840	418.177058	834.362824	417.685050	Q	1695.925076	848.466176	1678.898527	839.952902	1677.914511	839.460894	12
9	949.426153	475.216715	932.399604	466.703440	931.415588	466.211432	P	***1567.866498***	784.436887	1550.839949	775.923613	1549.855933	775.431605	11
10	1048.494567	524.750922	1031.468018	516.237647	1030.484002	515.745639	V	***1470.813734***	735.910505	1453.787185	727.397231	1452.803169	726.905223	10
11	1149.542246	575.274761	1132.515697	566.761487	1131.531681	566.269479	T	***1371.745320***	686.376298	1354.718771	677.863024	1353.734755	677.371016	9
12	1246.595010	623.801143	1229.568461	615.287869	1228.584445	614.795861	P	***1270.697641***	635.852459	1253.671092	627.339184	1252.687076	626.847176	8
13	1359.679074	680.343175	1342.652525	671.829901	1341.668509	671.337893	L	***1173.644877***	587.326077	1156.618328	578.812802	1155.634312	578.320794	7
14	1798.904400	899.955838	1781.877851	891.442564	1780.893835	890.950556	Q	***1060.560813***	530.784045	1043.534264	522.270770	1042.550248	521.778762	6
15	1911.988464	956.497870	1894.961915	947.984596	1893.977899	947.492588	L	***621.335487***	311.171382	604.308938	302.658107	603.324922	302.166099	5
16	2059.056878	1030.032077	2042.030329	1021.518803	2041.046313	1021.026794	F	***508.251423***	254.629350	491.224874	246.116075	490.240858	245.624067	4
17	2188.099471	1094.553373	2171.072922	1086.040099	2170.088906	1085.548091	E	361.183009	181.095142	344.156460	172.581868	343.172444	172.089860	3
18	2245.120935	1123.064105	2228.094386	1114.550831	2227.110370	1114.058823	G	***232.140416***	116.573846	215.113867	108.060571			2
19							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.7	2418.225342	0.012480	DDPDAPLQPVTPLQLFEGR
12.7	2418.225342	0.012480	DDPDAPLQPVTPLQLFEGR
0.7	2418.247803	-0.009981	GQTLNVNRLLHIVGYGDFQMK
0.2	2418.259033	-0.021211	QQQRALLGPWLSGPQGTDR
0.2	2418.259033	-0.021211	QQQRALLGPWLSGPQGTDR
0.2	2418.259033	-0.021211	QQQRALLGPWLSGPQGTDR

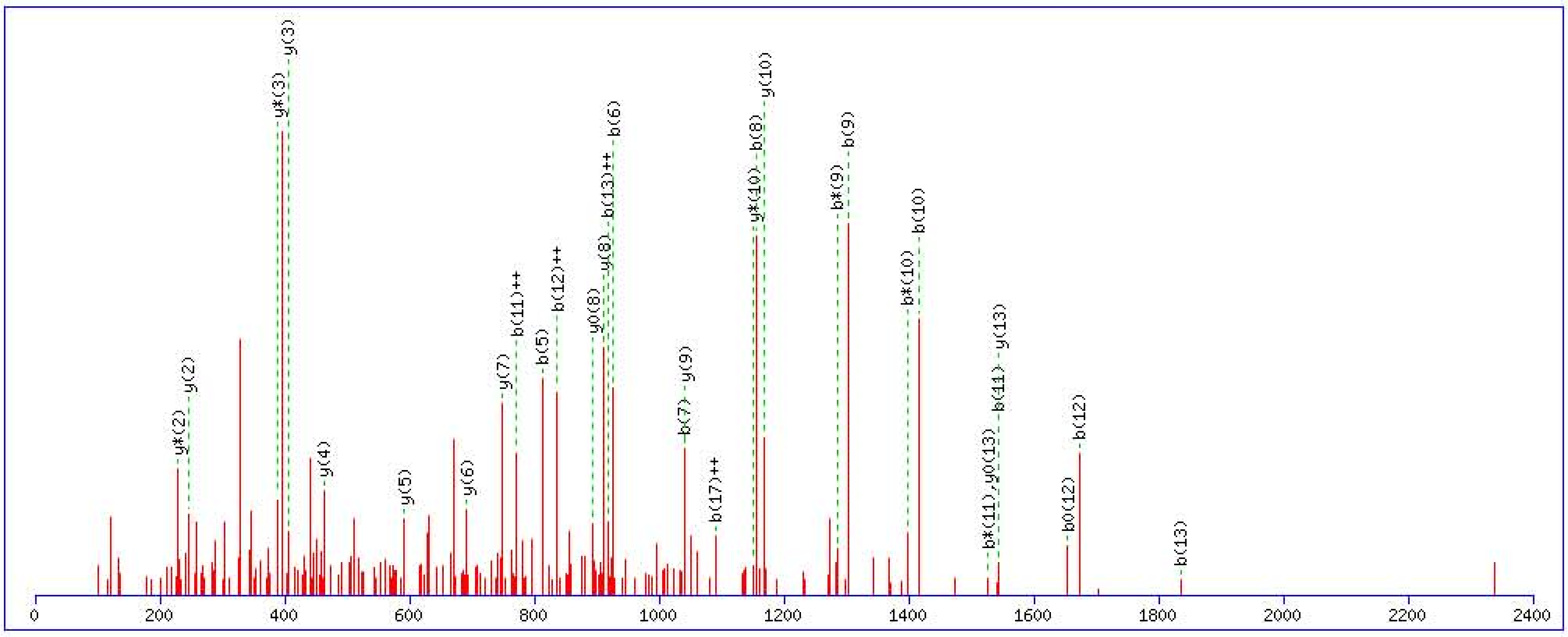
Mascot Search Results

Peptide View

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

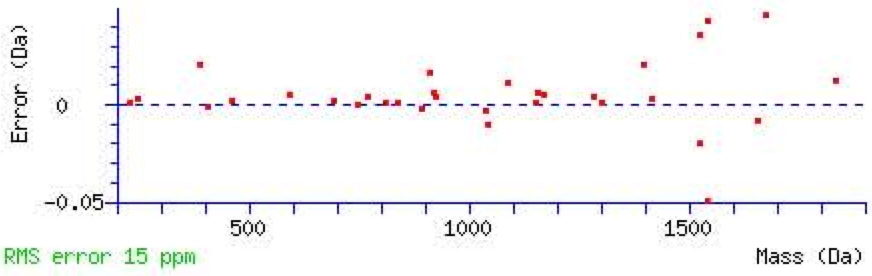
Match to Query 49357: 2583.165192 from(862.062340,3+) rtinseconds(2731) index(50237)
Title: Locus:1.1.1.3662.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

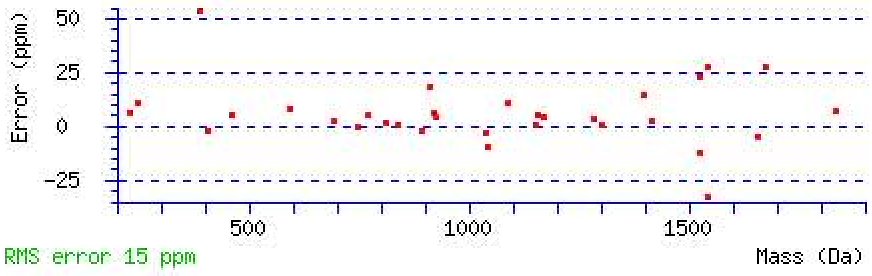
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 65  Expect: 3e-006
Matches : 32/194 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	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
64.7	2583.155624	0.009568	AACAQLNDFLQEYGTQGCQV
21.7	2583.155624	0.009568	AACAQLNDFLQEYGTQGCQV

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

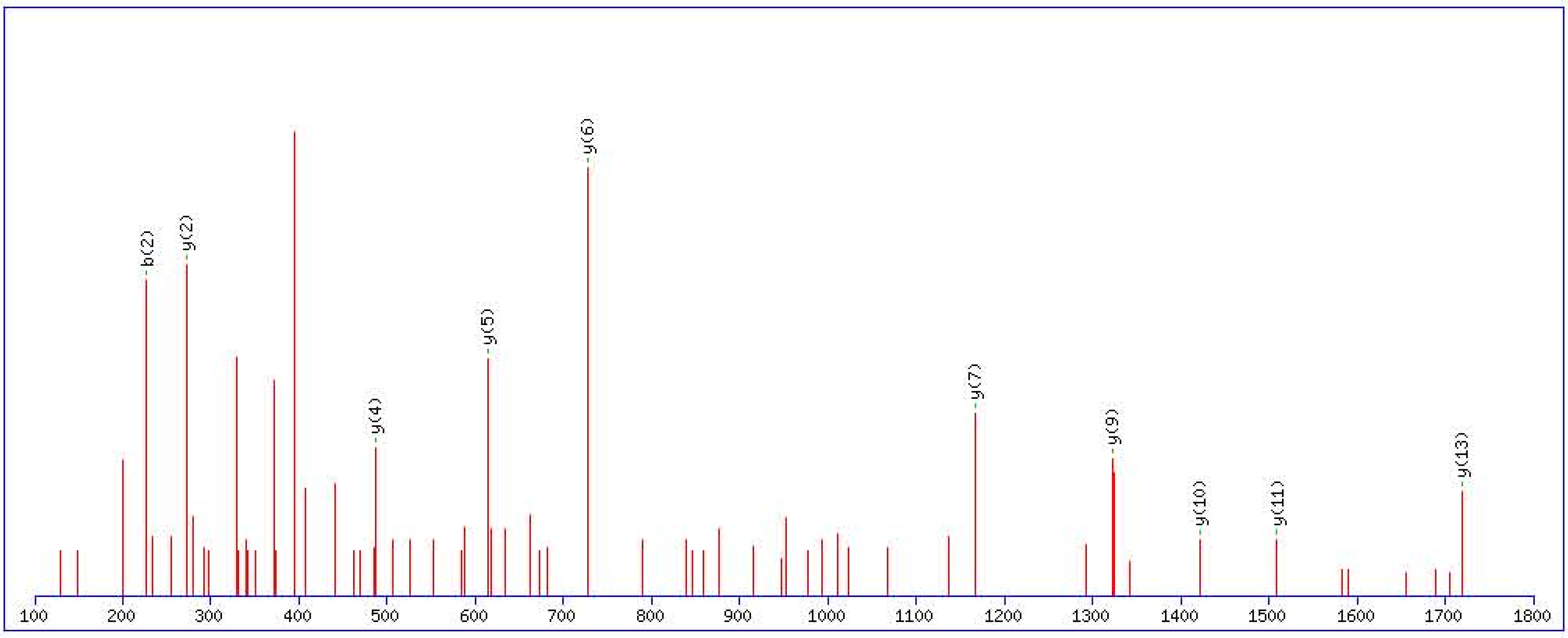
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

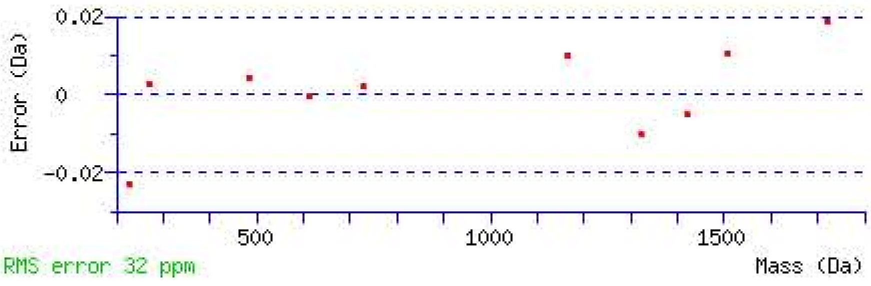
Match to Query 54597: 3079.780496 from(770.952400,4+) rtinseconds(3070) index(52599)
Title: Locus:1.1.1.3778.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

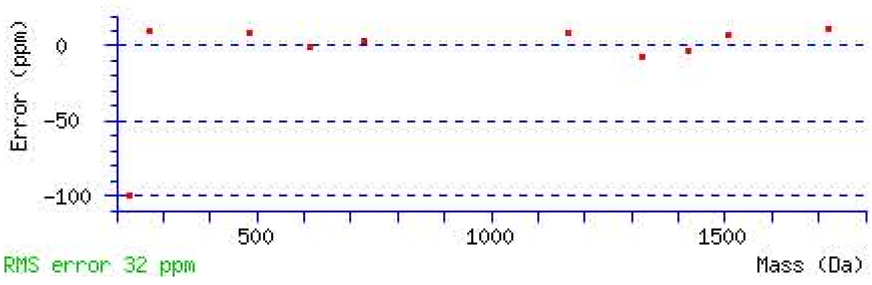
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3079.762054
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20 : Biotin:Thermo-21345 (Q)
Ions Score: 51 **Expect:** 1.6e-005
Matches : 10/248 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							26
2	227.175404	114.091340					L	2967.685233	1484.346254	2950.658684	1475.832980	2949.674668	1475.340972	25
3	340.259468	170.633372					L	2854.601169	1427.804222	2837.574620	1419.290948	2836.590604	1418.798940	24
4	487.327882	244.167579					F	2741.517105	1371.262190	2724.490556	1362.748916	2723.506540	1362.256908	23
5	574.359910	287.683593			556.349345	278.678311	S	2594.448691	1297.727983	2577.422142	1289.214709	2576.438126	1288.722701	22
6	671.412674	336.209975			653.402109	327.204693	P	2507.416663	1254.211969	2490.390114	1245.698695	2489.406098	1245.206687	21
7	758.444702	379.725989			740.434137	370.720707	S	2410.363899	1205.685587	2393.337350	1197.172313	2392.353334	1196.680305	20
8	857.513116	429.260196			839.502551	420.254913	V	2323.331871	1162.169573	2306.305322	1153.656299	2305.321306	1153.164291	19
9	956.581530	478.794403			938.570965	469.789120	V	2224.263457	1112.635366	2207.236908	1104.122092	2206.252892	1103.630084	18
10	1093.640442	547.323859			1075.629877	538.318576	H	2125.195043	1063.101159	2108.168494	1054.587885	2107.184478	1054.095877	17
11	1206.724506	603.865891			1188.713941	594.860608	L	1988.136131	994.571704	1971.109582	986.058429	1970.125566	985.566421	16
12	1263.745970	632.376623			1245.735405	623.371340	G	1875.052067	938.029672	1858.025518	929.516397	1857.041502	929.024389	15
13	1362.814384	681.910830			1344.803819	672.905547	V	1818.030603	909.518940	1801.004054	901.005665	1800.020038	900.513657	14
14	1459.867148	730.437212			1441.856583	721.431929	P	*1718.962189*	859.984733	1701.935640	851.471458	1700.951624	850.979450	13
15	1572.951212	786.979244			1554.940647	777.973961	L	1621.909425	811.458351	1604.882876	802.945076	1603.898860	802.453068	12
16	1659.983240	830.495258			1641.972675	821.489975	S	*1508.825361*	754.916319	1491.798812	746.403044	1490.814796	745.911036	11
17	1759.051654	880.029465			1741.041089	871.024182	V	*1421.793333*	711.400305	1404.766784	702.887030	1403.782768	702.395022	10
18	1816.073118	908.540197			1798.062553	899.534914	G	*1322.724919*	661.866098	1305.698370	653.352823	1304.714354	652.860815	9
19	1915.141532	958.074404			1897.130967	949.069121	V	1265.703455	633.355366	1248.676906	624.842091	1247.692890	624.350083	8
20	2354.366858	1177.687067	2337.340309	1169.173792	2336.356293	1168.681784	Q	*1166.635041*	583.821159	1149.608492	575.307884	1148.624476	574.815876	7
21	2467.450922	1234.229099	2450.424373	1225.715824	2449.440357	1225.223816	L	*727.409715*	364.208496	710.383166	355.695221	709.399150	355.203213	6
22	2595.509500	1298.258388	2578.482951	1289.745113	2577.498935	1289.253105	Q	*614.325651*	307.666463	597.299102	299.153189	596.315086	298.661181	5
23	2710.536443	1355.771859	2693.509894	1347.258585	2692.525878	1346.766577	D	*486.267073*	243.637174	469.240524	235.123900	468.256508	234.631892	4
24	2809.604857	1405.306066	2792.578308	1396.792792	2791.594292	1396.300784	V	371.240130	186.123703	354.213581	177.610428			3
25	2906.657621	1453.832448	2889.631072	1445.319174	2888.647056	1444.827166	P	*272.171716*	136.589496	255.145167	128.076221			2
26							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLLFSPSVVHLGVPLSVGVQLQDVPR
(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	3079.762054	0.018442	LLLFSPSVVHLGVPLSVGVQLQDVPR
27.9	3079.762054	0.018442	LLLFSPSVVHLGVPLSVGVQLQDVPR

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

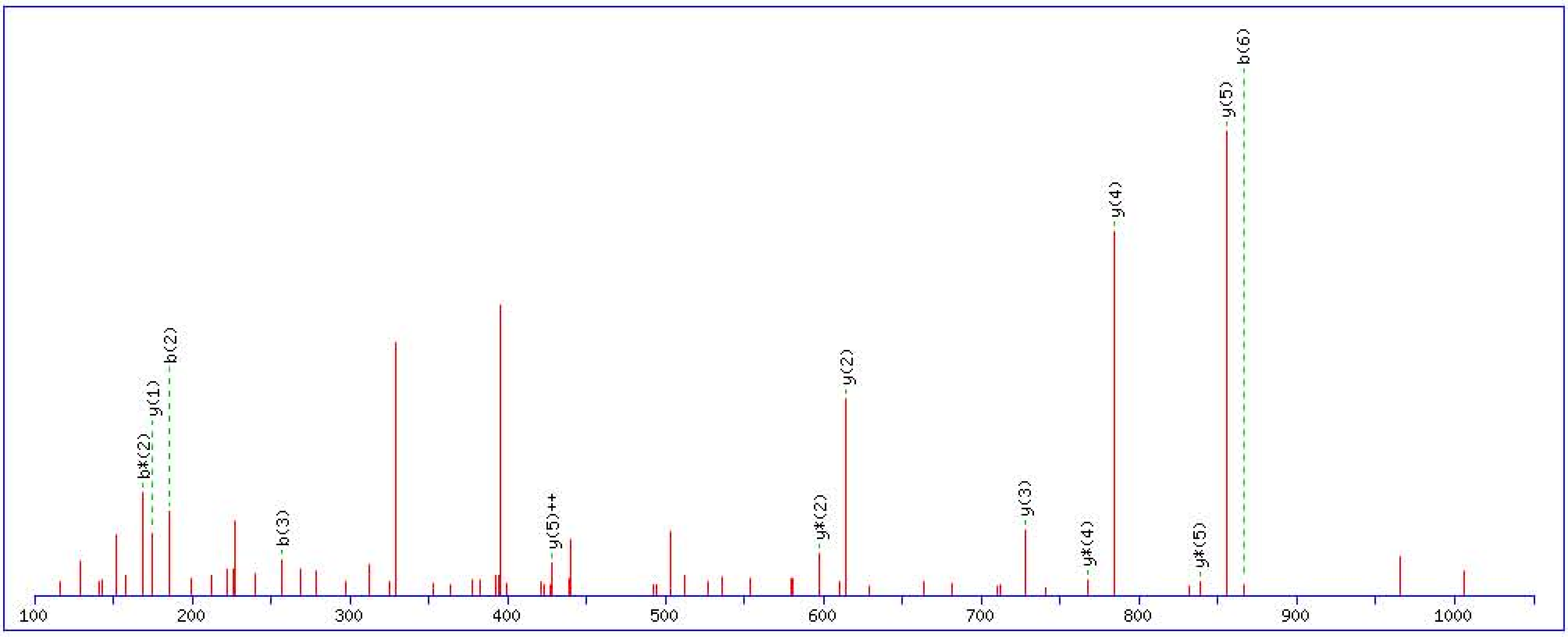
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

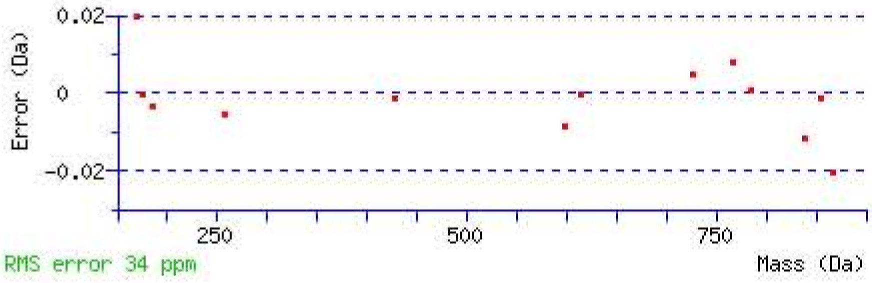
Match to Query 12627: 1039.550328 from(520.782440,2+) rtinseconds(1460) index(42646)
Title: Locus:1.1.1.3221.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

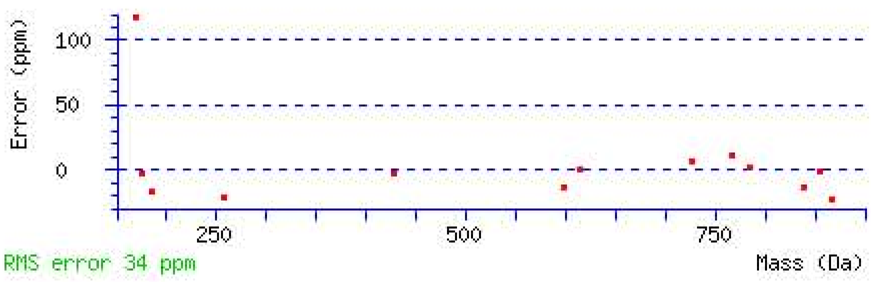
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1039.559677
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.028
Matches : 13/46 fragment ions using 26 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	58.028740	29.518008			G					7
2	**186.087318**	93.547297	169.060769	85.034023	Q	983.545498	492.276387	966.518949	483.763113	6
3	**257.124432**	129.065854	240.097883	120.552580	A	***855.486920***	428.247098	838.460371	419.733824	5
4	314.145896	157.576586	297.119347	149.063312	G	***784.449806***	392.728541	767.423257	384.215267	4
5	427.229960	214.118618	410.203411	205.605344	L	***727.428342***	364.217809	710.401793	355.704535	3
6	**866.455286**	433.731281	849.428737	425.218007	Q	***614.344278***	307.675777	597.317729	299.162503	2
7					R	***175.118952***	88.063114	158.092403	79.549840	1





NCBI **BLAST** search of GQAGLQR
(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	1039.559677	-0.009349	GQAGLQR
14.2	1039.559677	-0.009349	GQQIQR
10.9	1039.541061	0.009267	GQGDLLQPGR
7.0	1039.559677	-0.009349	KGGPSQR
6.8	1039.541046	0.009282	NATTAPNPVR
5.3	1039.552277	-0.001949	GQPQELGRR
4.3	1039.552277	-0.001949	QRAALDGGPR
1.8	1039.563492	-0.013164	AEGARARGPR
1.8	1039.563492	-0.013164	SSHLRERR
1.5	1039.541061	0.009267	AGVTTPAPGNR

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

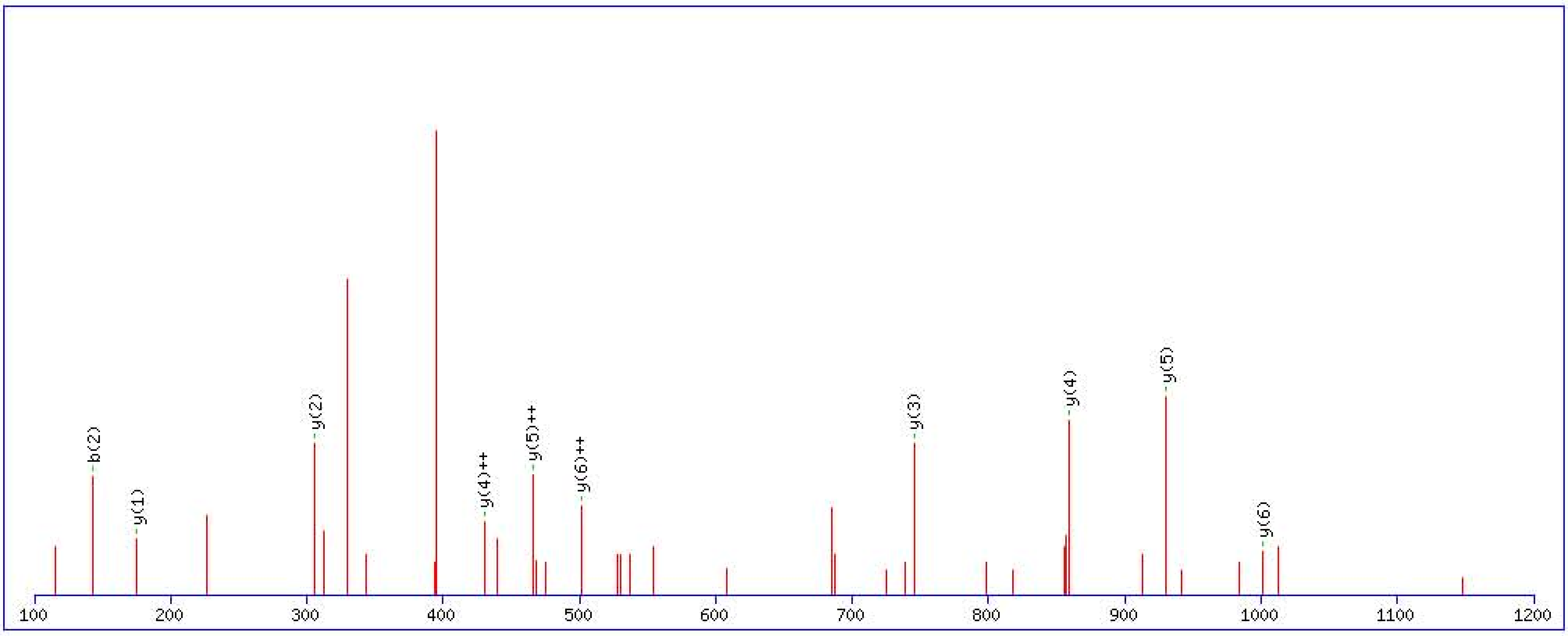
Mascot Search Results

Peptide View

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

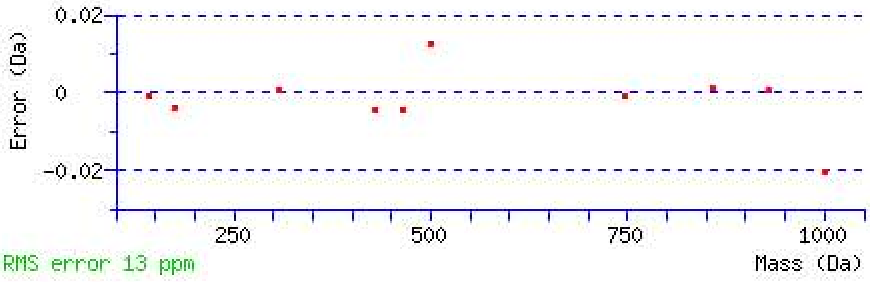
Match to Query 13331: 1071.528988 from(536.771770,2+) rtinseconds(1406) index(42337)
Title: Locus:1.1.1.3202.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

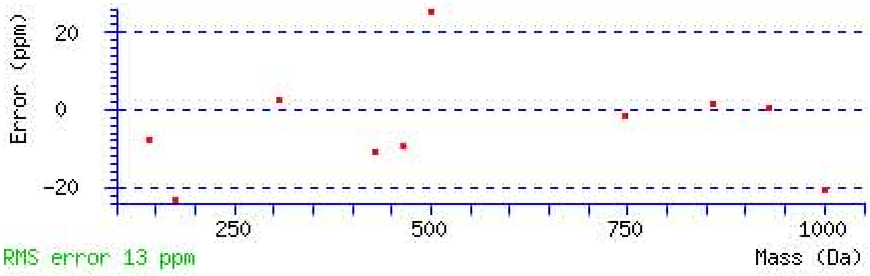
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1071.531723
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.024
Matches : 10/42 fragment ions using 26 most intense peaks   (help)
```

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	72.044390	36.525833			A					7
2	143.081504	72.044390			A	1001.501918	501.254597	984.475369	492.741323	6
3	214.118618	107.562947			A	930.464804	465.736040	913.438255	457.222766	5
4	328.161545	164.584410	311.134996	156.071136	N	859.427690	430.217483	842.401141	421.704209	4
5	767.386871	384.197074	750.360322	375.683799	Q	745.384763	373.196020	728.358214	364.682745	3
6	898.427356	449.717316	881.400807	441.204042	M	306.159437	153.583357	289.132888	145.070082	2
7					R	175.118952	88.063114	158.092403	79.549840	1





NCBI **BLAST** search of AAANQMR
(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	1071.531723	-0.002735	AAANQMR
15.9	1071.530853	-0.001865	AAEESGAKGPR
5.4	1071.519608	0.009380	AAESAEIEPR
5.4	1071.539597	-0.010609	HHLIEHMR

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

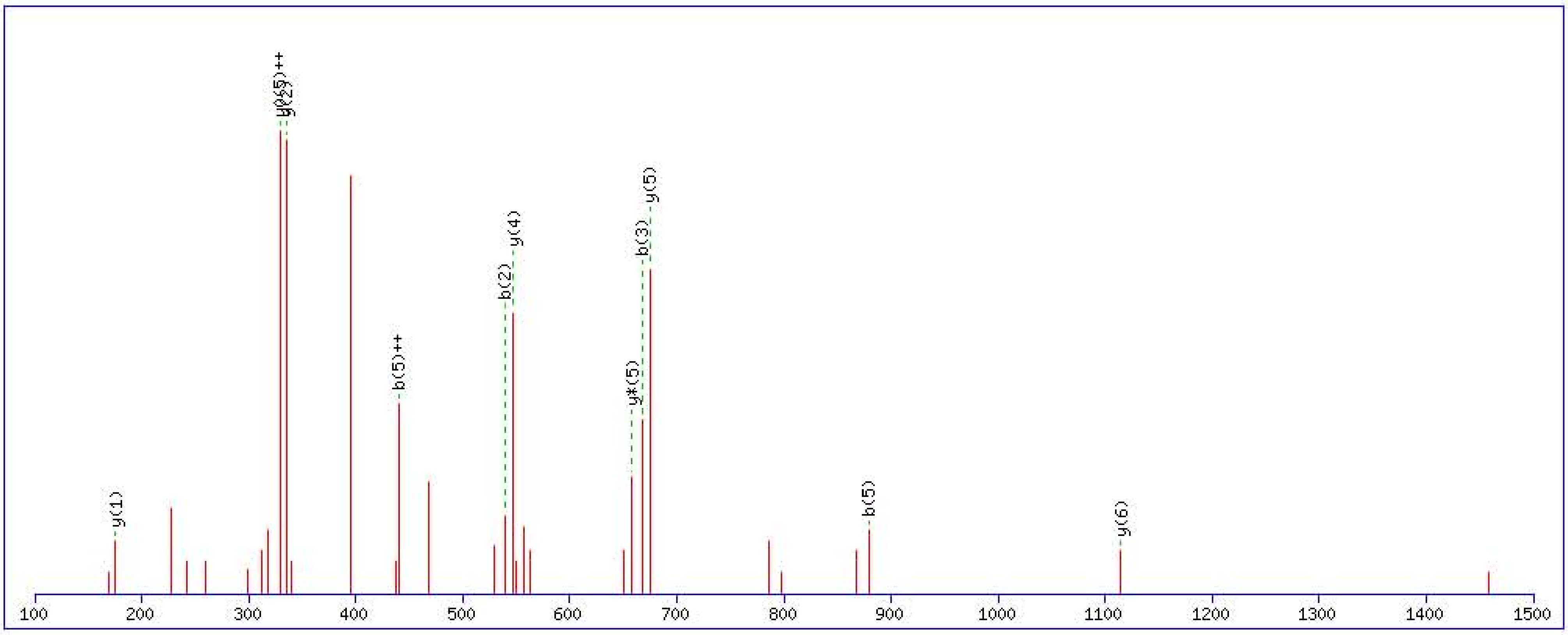
Mascot Search Results

Peptide View

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

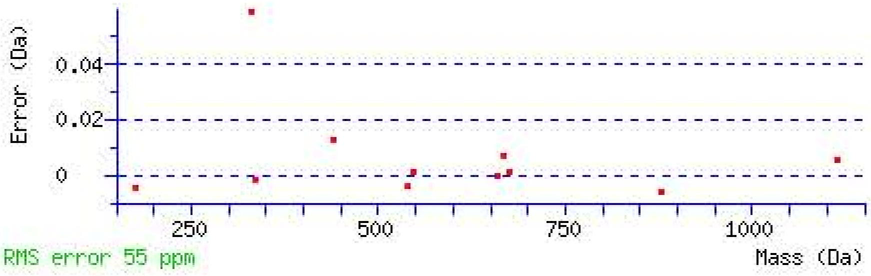
Match to Query 17990: 1212.569008 from(607.291780,2+) rtinseconds(1327) index(41941)
Title: Locus:1.1.1.3174.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

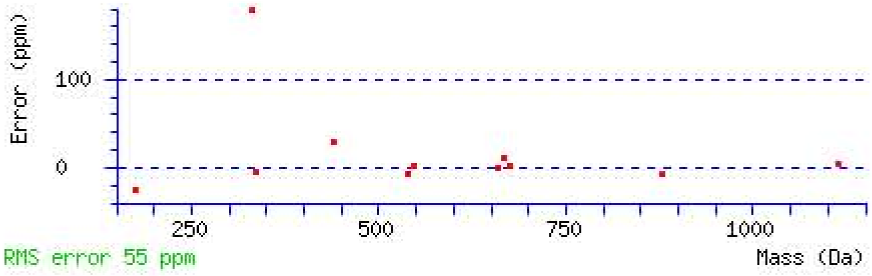
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1212.574356
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2     : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.00063
Matches : 11/58 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	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
34.8	1212.574356	-0.005348	VQQPDCR
15.7	1212.574356	-0.005348	VQQPDCR
0.7	1212.582199	-0.013191	GRMPPSEFHR

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

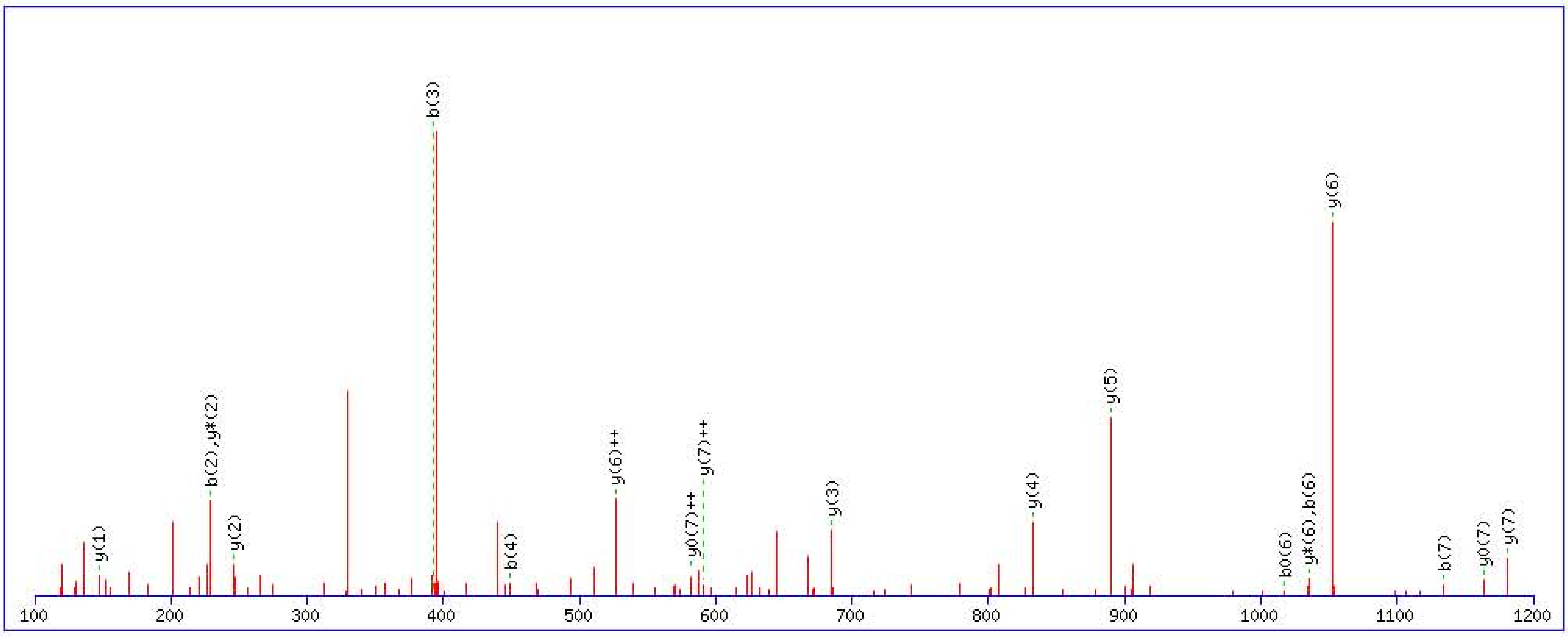
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

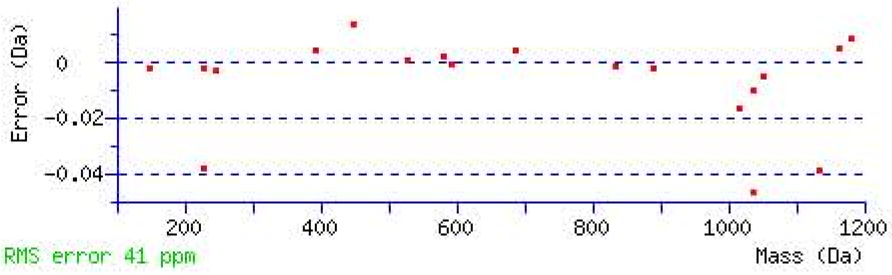
Match to Query 19793: 1279.659568 from(640.837060,2+) rtinseconds(2000) index(31887)
Title: Locus:1.1.1.3360.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

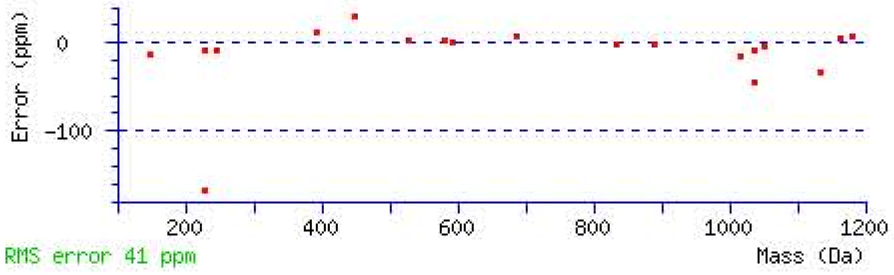
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1279.663483
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 26 **Expect:** 0.01
Matches : 19/60 fragment ions using 51 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
25.6	1279.663483	-0.003915	VEYGFQVK
4.1	1279.663483	-0.003915	QFVGYLDK
2.1	1279.677216	-0.017648	VFKTEDTQGKK
0.5	1279.659470	0.000098	VCSFGKQVVEK
0.4	1279.652039	0.007529	VERAITEASPAH
0.3	1279.652054	0.007514	DAHDPQDKKVK
0.1	1279.677200	-0.017632	EYVGKTSLVER

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

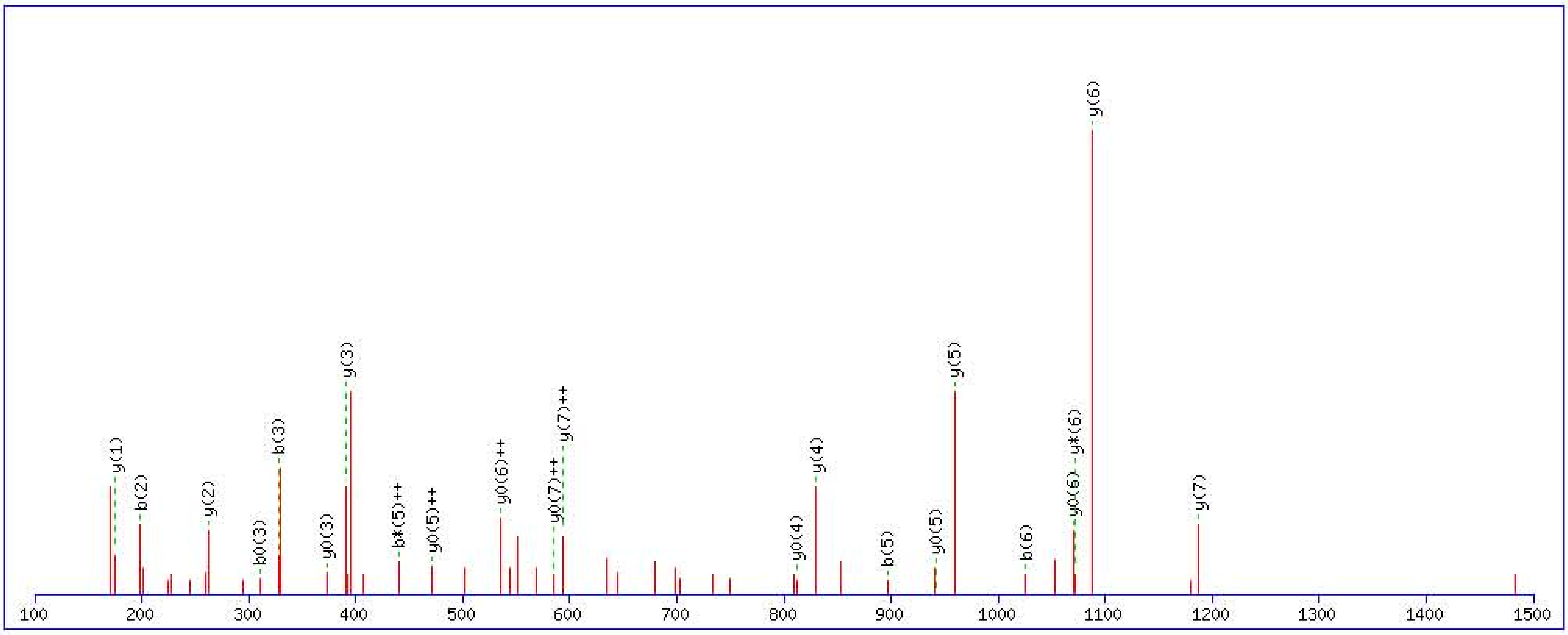
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

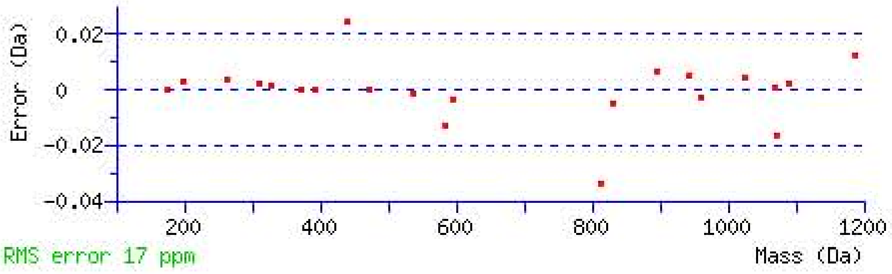
Match to Query 20080: 1285.627528 from(643.821040,2+) rtinseconds(1386) index(28142)
Title: Locus:1.1.1.3145.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

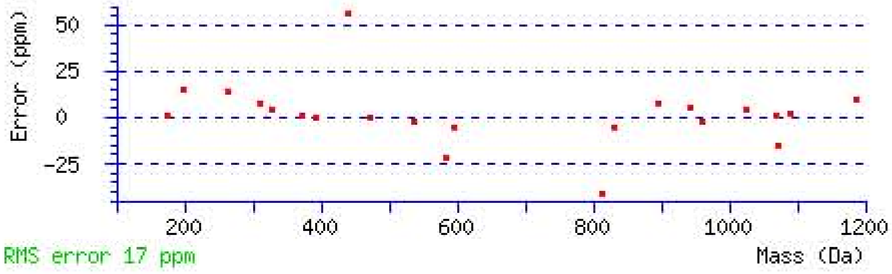
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1285.633621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.0012
Matches : 22/70 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	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
42.0	1285.633621	-0.006093	VVEEQESR

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

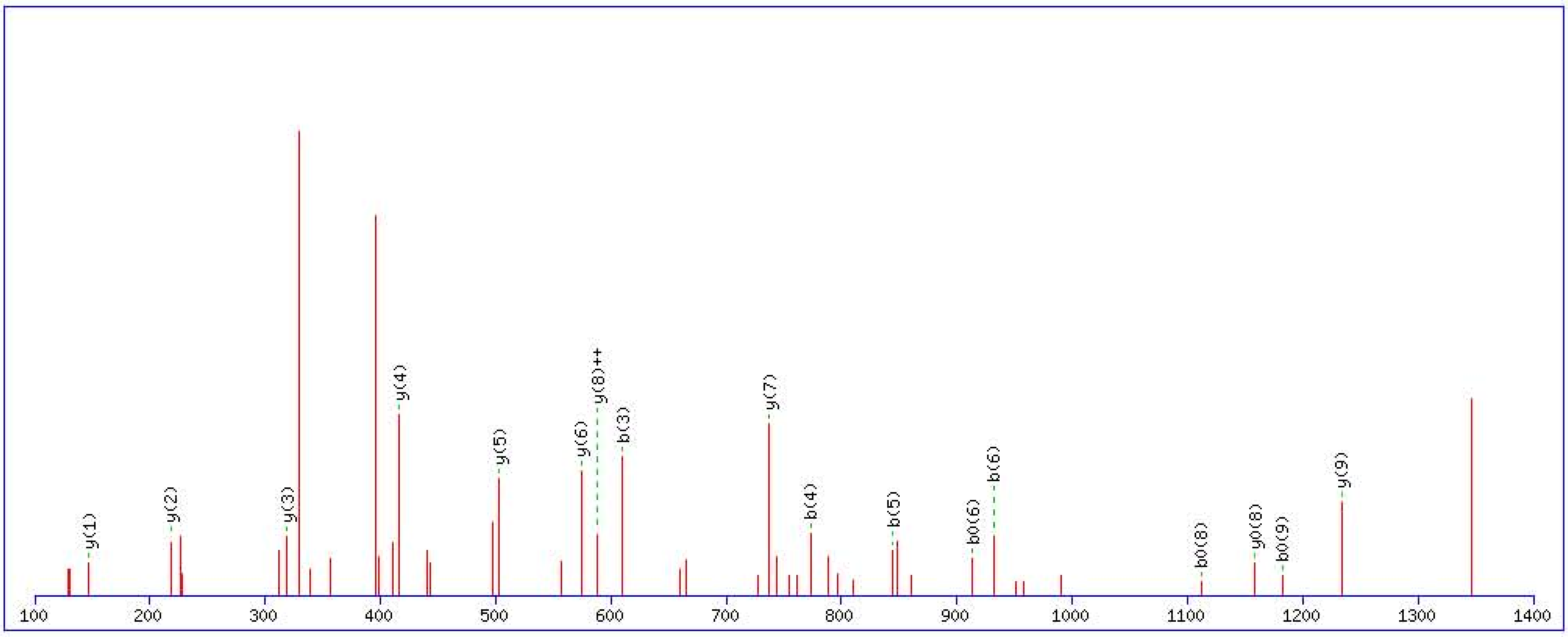
Mascot Search Results

Peptide View

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

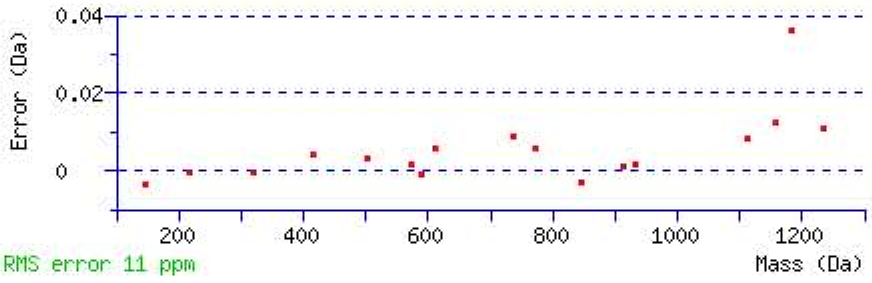
Match to Query 21270: 1345.697228 from(673.855890,2+) rtinseconds(1635) index(29667)
Title: Locus:1.1.1.3232.22 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

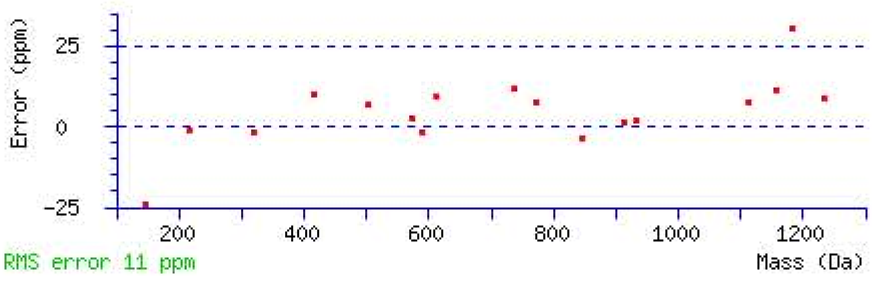
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 51 **Expect:** 8.5e-005
Matches : 17/90 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	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
50.9	1345.706390	-0.009162	LGQYASPTAK
7.1	1345.706406	-0.009178	QGLYTPQTK
6.7	1345.706390	-0.009162	LGQYDQALK
6.2	1345.692474	0.004754	VASCRYPALGPR
2.6	1345.681213	0.016015	ENKMTWAPKNK
1.0	1345.692505	0.004723	DHTVFGRVMLR

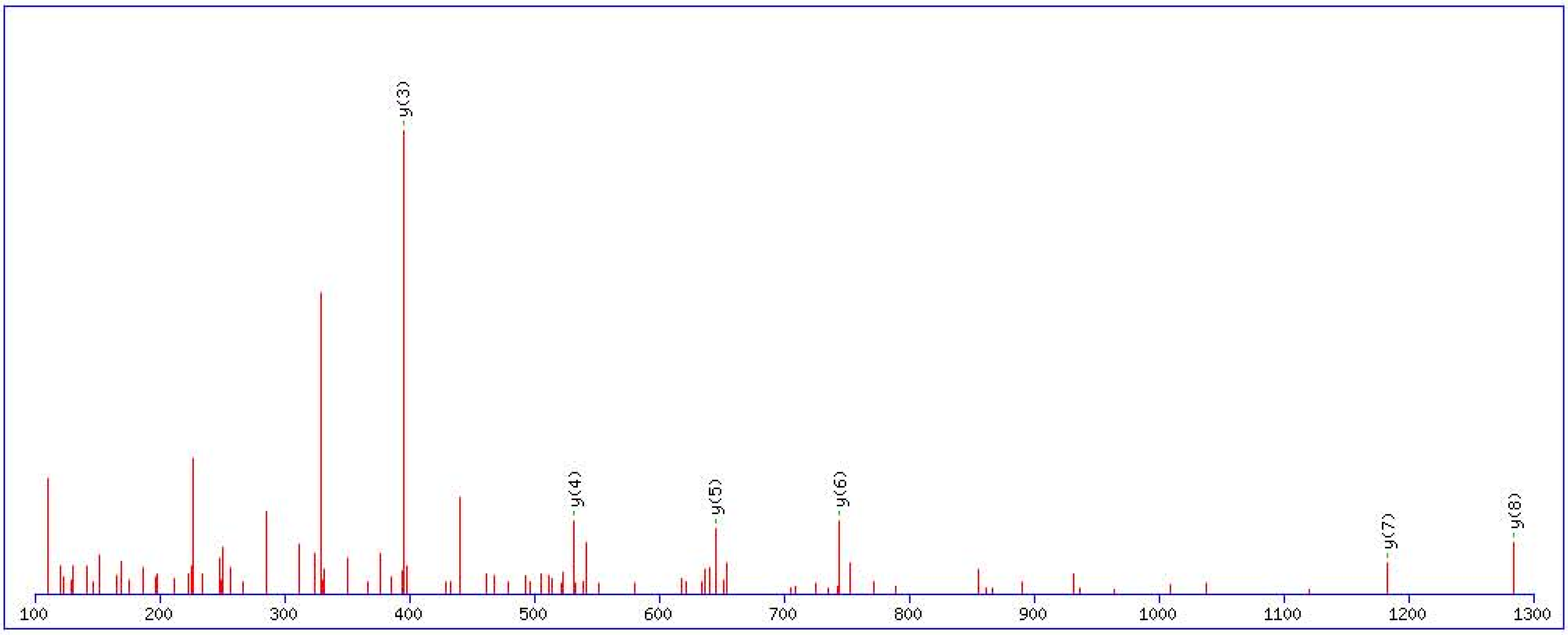
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

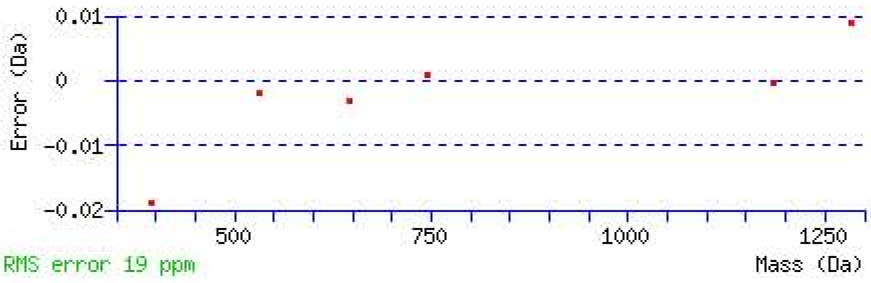
Match to Query 23538: 1396.788582 from(466.603470,3+) rtinseconds(1965) index(45767)
Title: Locus:1.1.1.3397.3 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

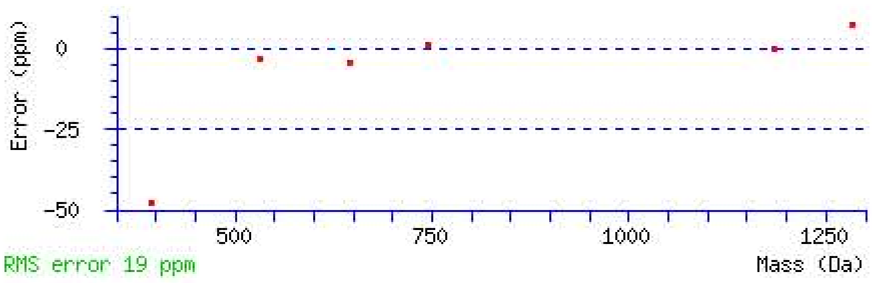
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1396.790085
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.00061
Matches : 6/88 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	215.139019	108.073147			197.128454	99.067865	T	***1284.713292***	642.860284	1267.686743	634.347010	1266.702727	633.855002	8
3	654.364345	327.685811	637.337796	319.172536	636.353780	318.680528	Q	***1183.665613***	592.336445	1166.639064	583.823170	1165.655048	583.331162	7
4	753.432759	377.220018	736.406210	368.706743	735.422194	368.214735	V	***744.440287***	372.723782	727.413738	364.210507	726.429722	363.718499	6
5	866.516823	433.762050	849.490274	425.248775	848.506258	424.756767	L	***645.371873***	323.189575	628.345324	314.676300	627.361308	314.184292	5
6	1003.575735	502.291506	986.549186	493.778231	985.565170	493.286223	H	***532.287809***	266.647543	515.261260	258.134268	514.277244	257.642260	4
7	1150.644149	575.825713	1133.617600	567.312438	1132.633584	566.820430	F	***395.228897***	198.118086	378.202348	189.604812	377.218332	189.112804	3
8	1251.691828	626.349552	1234.665279	617.836278	1233.681263	617.344270	T	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	2
9							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.6	1396.790085	-0.001503	ITQVLHFTK
0.3	1396.792557	-0.003975	LLGELQEQIVQK

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

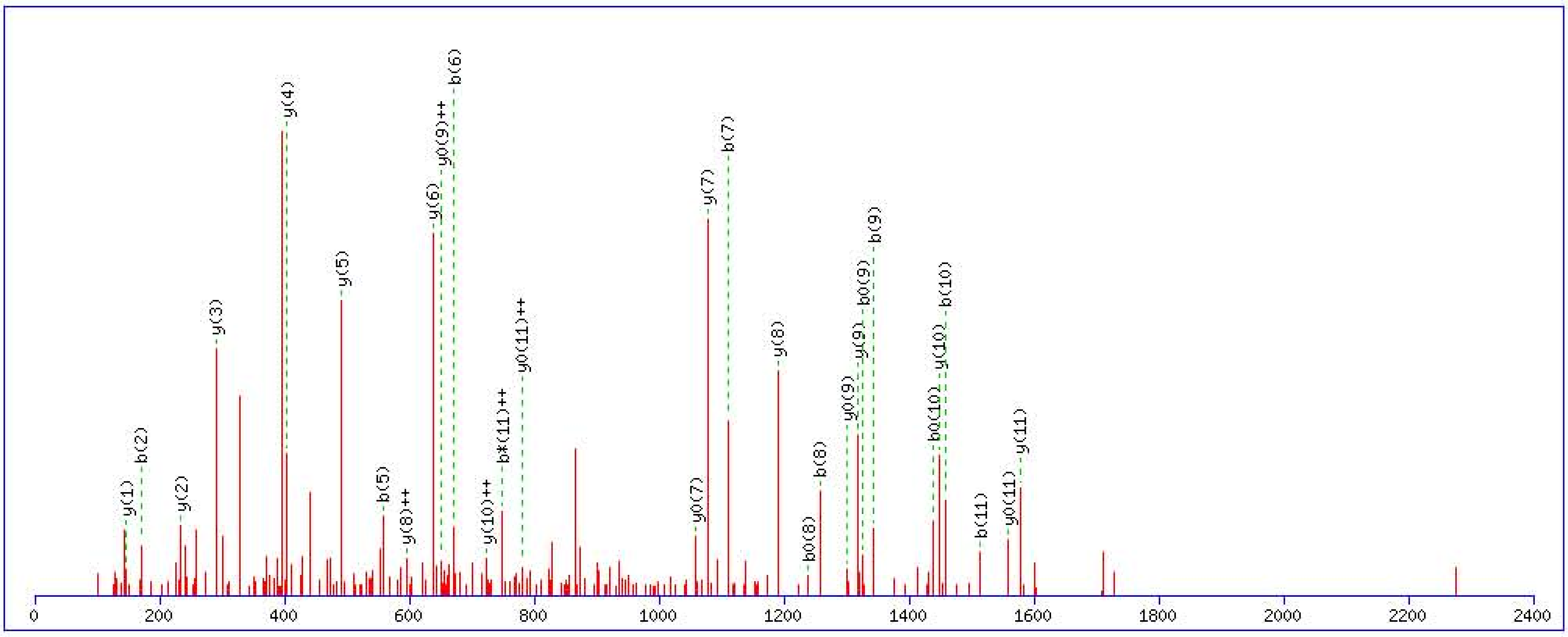
MATRIX SCIENCE Mascot Search Results

Peptide View

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

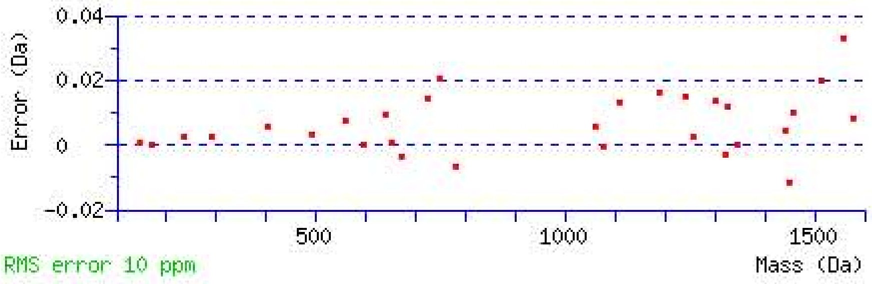
Match to Query 34611: 1746.895648 from(874.455100,2+) rtinseconds(2556) index(49068)
Title: Locus:1.1.1.3602.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

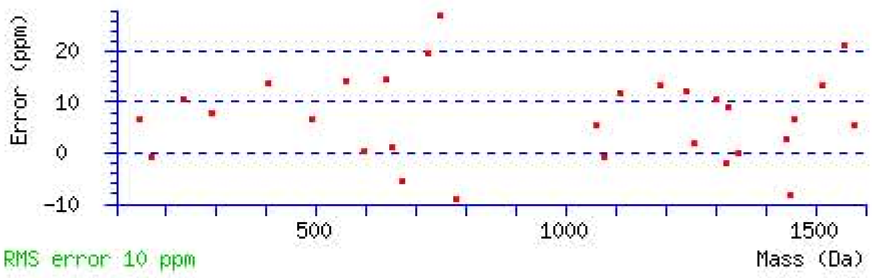
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1746.886200
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 80  Expect: 6.9e-008
Matches : 30/126 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	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
79.6	1746.886200	0.009448	GLEEELQFSLGSK
3.2	1746.887558	0.008090	AVQSKAFCAGGLAPGWK

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

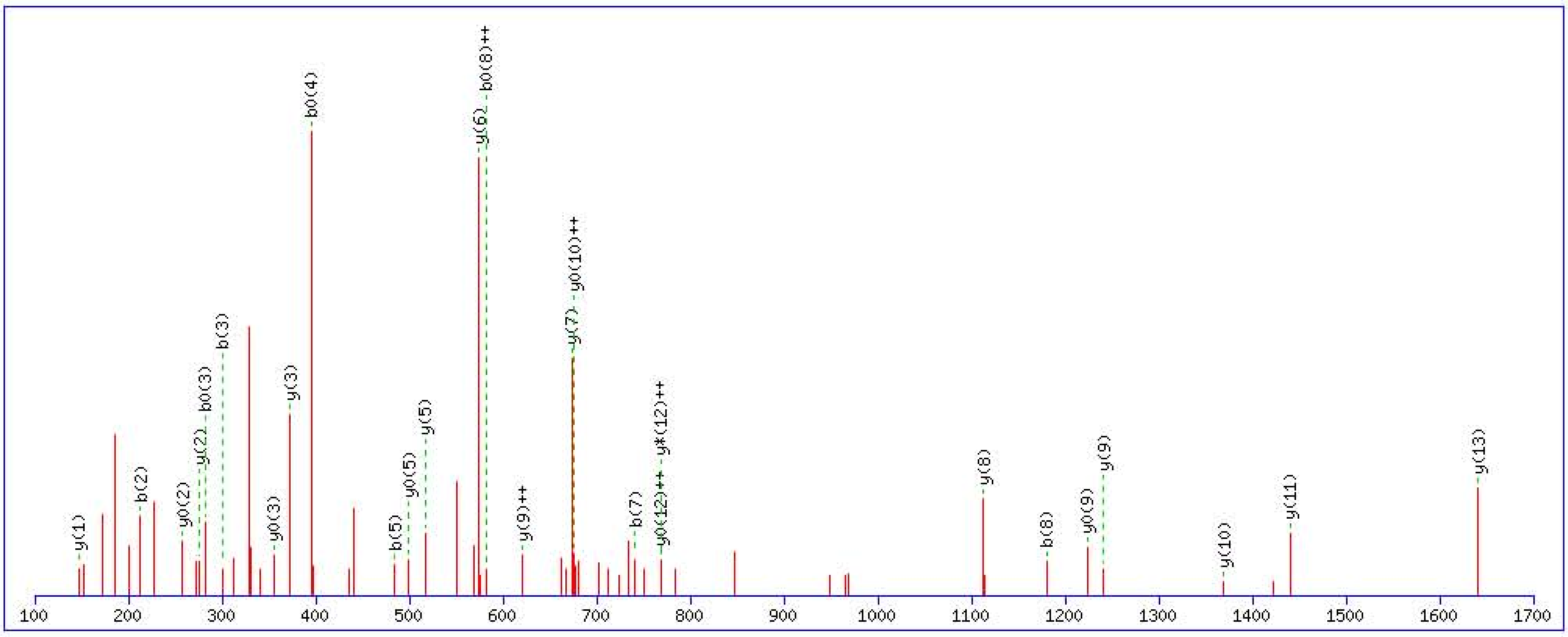
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

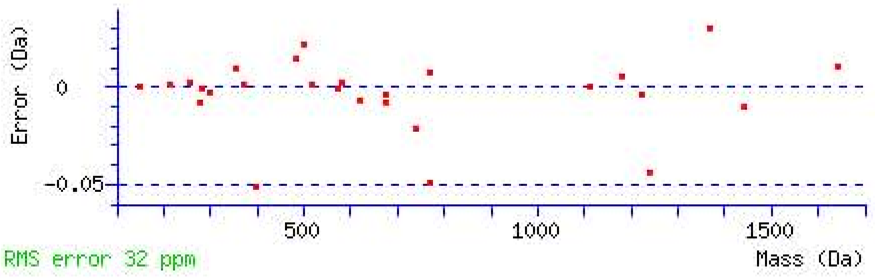
Match to Query 36652: 1851.976662 from(618.332830,3+) rtinseconds(2001) index(46074)
Title: Locus:1.1.1.3409.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

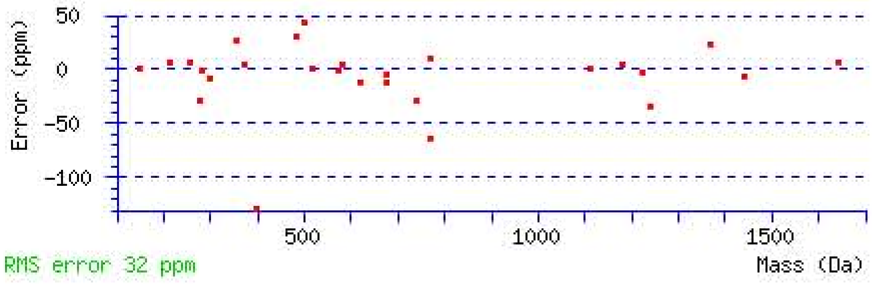
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1851.976425
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 58 **Expect:** 3.7e-005
Matches : 27/152 fragment ions using 57 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							15
2	**213.159754**	107.083515					L	1753.915298	877.461287	1736.888749	868.948013	1735.904733	868.456004	14
3	**300.191782**	150.599529			282.181217	141.594247	S	***1640.831234***	820.919255	1623.804685	812.405981	1622.820669	811.913973	13
4	413.275846	207.141561			395.265281	198.136279	L	1553.799206	777.403241	1536.772657	768.889967	1535.788641	768.397958	12
5	**484.312960**	242.660118			466.302395	233.654836	A	***1440.715142***	720.861209	1423.688593	712.347935	1422.704577	711.855927	11
6	612.371538	306.689407	595.344989	298.176133	594.360973	297.684125	Q	***1369.678028***	685.342652	1352.651479	676.829378	1351.667463	676.337370	10
7	**741.414131**	371.210704	724.387582	362.697429	723.403566	362.205421	E	***1241.619450***	621.313363	1224.592901	612.800089	1223.608885	612.308080	9
8	**1180.639457**	590.823367	1163.612908	582.310092	1162.628892	581.818084	Q	***1112.576857***	556.792066	1095.550308	548.278792	1094.566292	547.786784	8
9	1279.707871	640.357574	1262.681322	631.844299	1261.697306	631.352291	V	***673.351531***	337.179404	656.324982	328.666129	655.340966	328.174121	7
10	1336.729335	668.868306	1319.702786	660.355031	1318.718770	659.863023	G	***574.283117***	287.645197	557.256568	279.131922	556.272552	278.639914	6
11	1393.750799	697.379037	1376.724250	688.865763	1375.740234	688.373755	G	***517.261653***	259.134465	500.235104	250.621190	499.251088	250.129182	5
12	1480.782827	740.895052	1463.756278	732.381777	1462.772262	731.889769	S	460.240189	230.623732	443.213640	222.110458	442.229624	221.618450	4
13	1577.835591	789.421434	1560.809042	780.908159	1559.825026	780.416151	P	***373.208161***	187.107718	356.181612	178.594444	355.197596	178.102436	3
14	1706.878184	853.942730	1689.851635	845.429456	1688.867619	844.937447	E	***276.155397***	138.581336	259.128848	130.068062	258.144832	129.576054	2
15							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.3	1851.976425	0.000237	VLSLAQEQVGGSPEK
37.0	1851.976425	0.000237	VLSLAQEQVGGSPEK

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

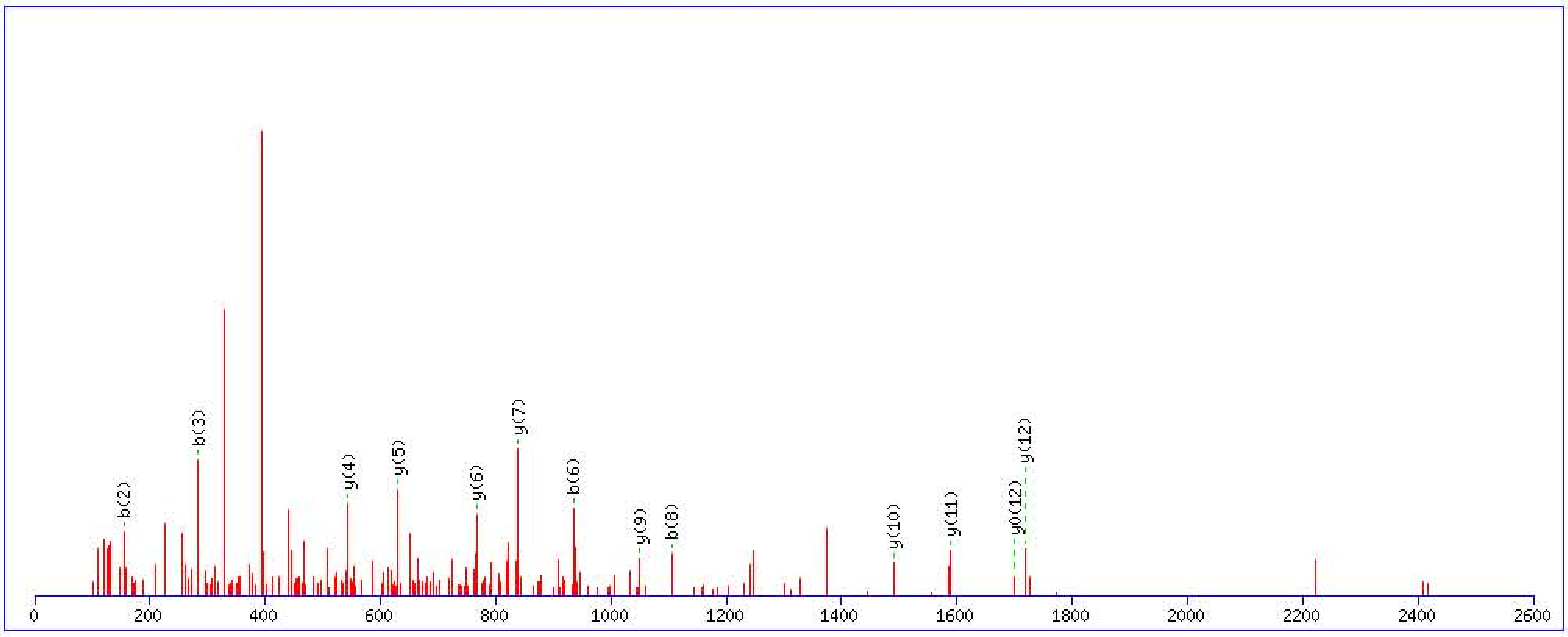
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

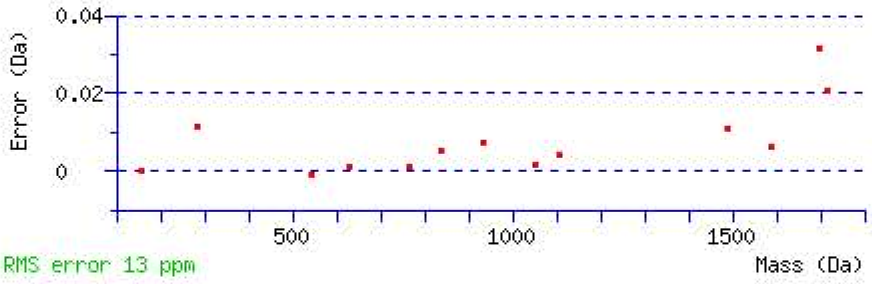
Match to Query 37065: 1871.013762 from(624.678530,3+) rtinseconds(2248) index(47552)
Title: Locus:1.1.1.3495.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

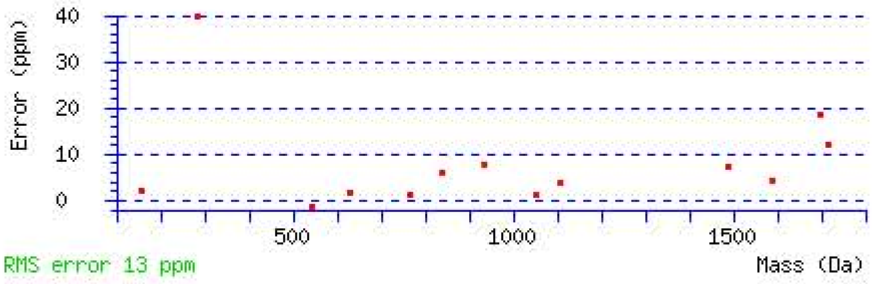
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1871.012756
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 59 **Expect:** 7.5e-006
Matches : 13/136 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	58.028740	29.518008					G							14
2	**155.081504**	78.044390					P	1814.998574	908.002925	1797.972025	899.489651	1796.988009	898.997643	13
3	**284.124097**	142.565687			266.113532	133.560404	E	***1717.945810***	859.476543	1700.919261	850.963269	1699.935245	850.471261	12
4	383.192511	192.099894			365.181946	183.094611	V	***1588.903217***	794.955247	1571.876668	786.441972	1570.892652	785.949964	11
5	822.417837	411.712557	805.391288	403.199282	804.407272	402.707274	Q	***1489.834803***	745.421040	1472.808254	736.907765	1471.824238	736.415757	10
6	**935.501901**	468.254589	918.475352	459.741314	917.491336	459.249306	L	***1050.609477***	525.808377	1033.582928	517.295102	1032.598912	516.803094	9
7	1034.570315	517.788796	1017.543766	509.275521	1016.559750	508.783513	V	937.525413	469.266345	920.498864	460.753070	919.514848	460.261062	8
8	**1105.607429**	553.307353	1088.580880	544.794078	1087.596864	544.302070	A	***838.456999***	419.732138	821.430450	411.218863	820.446434	410.726855	7
9	1242.666341	621.836809	1225.639792	613.323534	1224.655776	612.831526	H	***767.419885***	384.213581	750.393336	375.700306	749.409320	375.208298	6
10	1329.698369	665.352823	1312.671820	656.839548	1311.687804	656.347540	S	***630.360973***	315.684125	613.334424	307.170850	612.350408	306.678842	5
11	1426.751133	713.879205	1409.724584	705.365930	1408.740568	704.873922	P	***543.328945***	272.168111	526.302396	263.654836			4
12	1612.830446	806.918861	1595.803897	798.405587	1594.819881	797.913579	W	446.276181	223.641728	429.249632	215.128454			3
13	1725.914510	863.460893	1708.887961	854.947619	1707.903945	854.455611	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 GPEVQLVAHSPWLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.0	1871.012756	0.001006	GPEVQLVAHSPWLK
4.4	1870.994781	0.018981	NVNQAKLSEHRHK

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

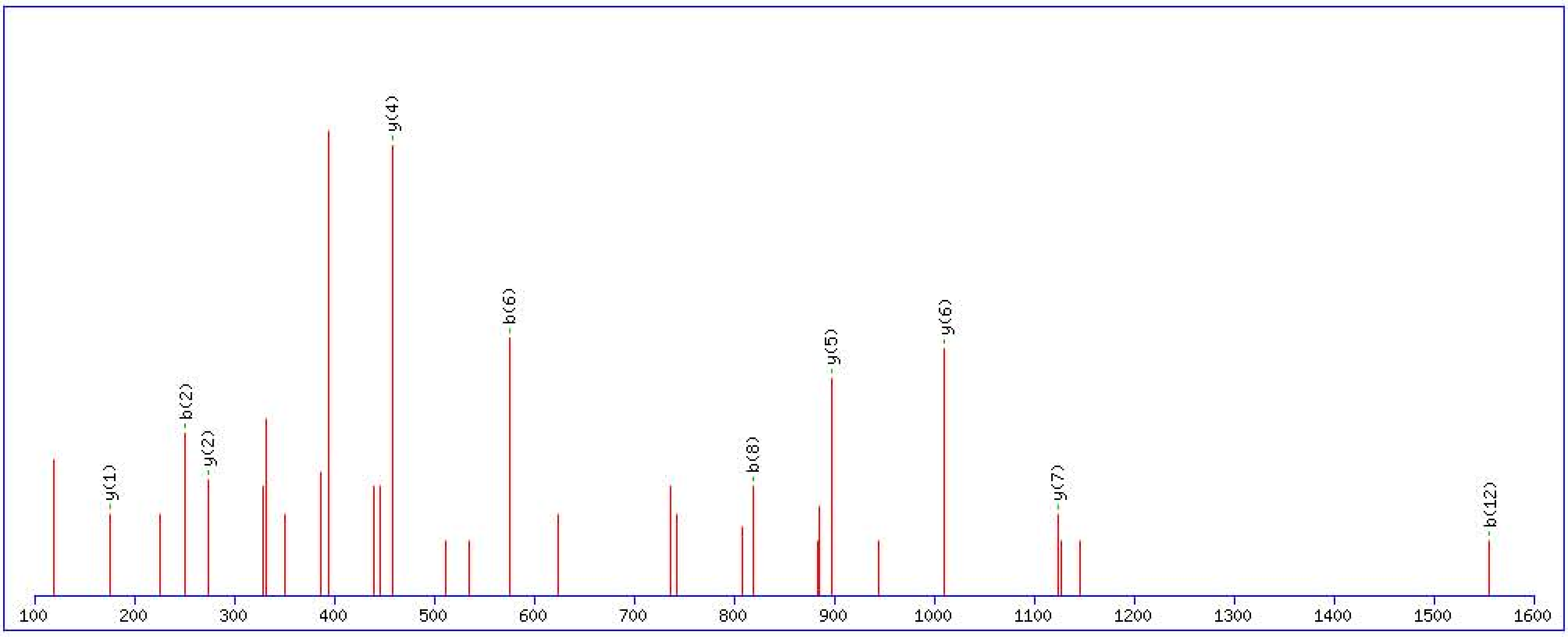
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

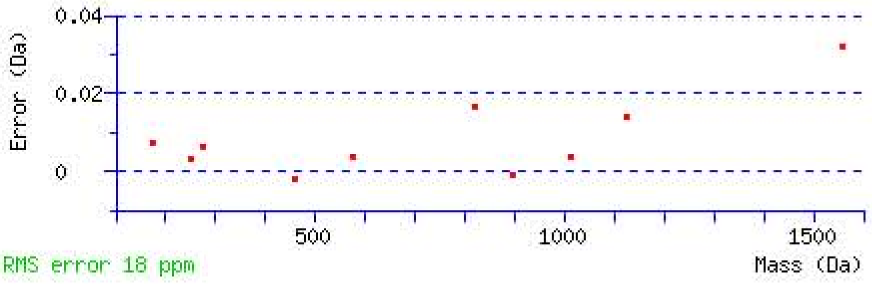
Match to Query 38193: 1941.148422 from(648.056750,3+) rtinseconds(2881) index(51423)
Title: Locus:1.1.1.3713.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

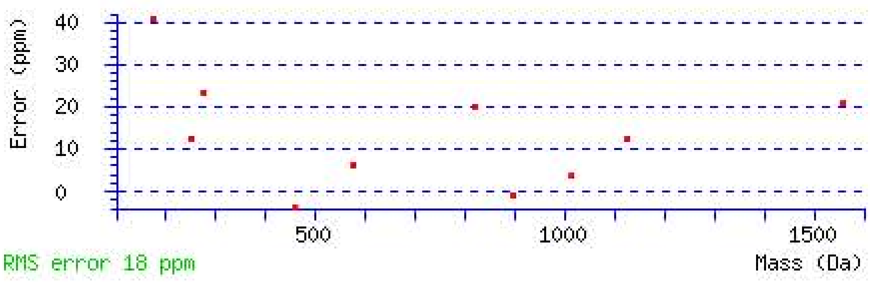
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1941.138626
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.00084
Matches : 10/92 fragment ions using 20 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	138.066188	69.536732			H					15
2	*251.150252*	126.078764			L	1805.086996	903.047136	1788.060447	894.533862	14
3	350.218666	175.612971			V	1692.002932	846.505104	1674.976383	837.991830	13
4	447.271430	224.139353			P	1592.934518	796.970897	1575.907969	788.457623	12
5	504.292894	252.650085			G	1495.881754	748.444515	1478.855205	739.931241	11
6	*575.330008*	288.168642			A	1438.860290	719.933783	1421.833741	711.420509	10
7	672.382772	336.695024			P	1367.823176	684.415226	1350.796627	675.901952	9
8	*819.451186*	410.229231			F	1270.770412	635.888844	1253.743863	627.375570	8
9	932.535250	466.771263			L	*1123.701998*	562.354637	1106.675449	553.841363	7
10	1045.619314	523.313295			L	*1010.617934*	505.812605	993.591385	497.299331	6
11	1484.844640	742.925958	1467.818091	734.412684	Q	*897.533870*	449.270573	880.507321	440.757298	5
12	*1555.881754*	778.444515	1538.855205	769.931241	A	*458.308544*	229.657910	441.281995	221.144635	4
13	1668.965818	834.986547	1651.939269	826.473273	L	387.271430	194.139353	370.244881	185.626078	3
14	1768.034232	884.520754	1751.007683	876.007480	V	*274.187366*	137.597321	257.160817	129.084047	2
15					R	*175.118952*	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.0	1941.138626	0.009796	HLVPGAPFLLQALVR

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

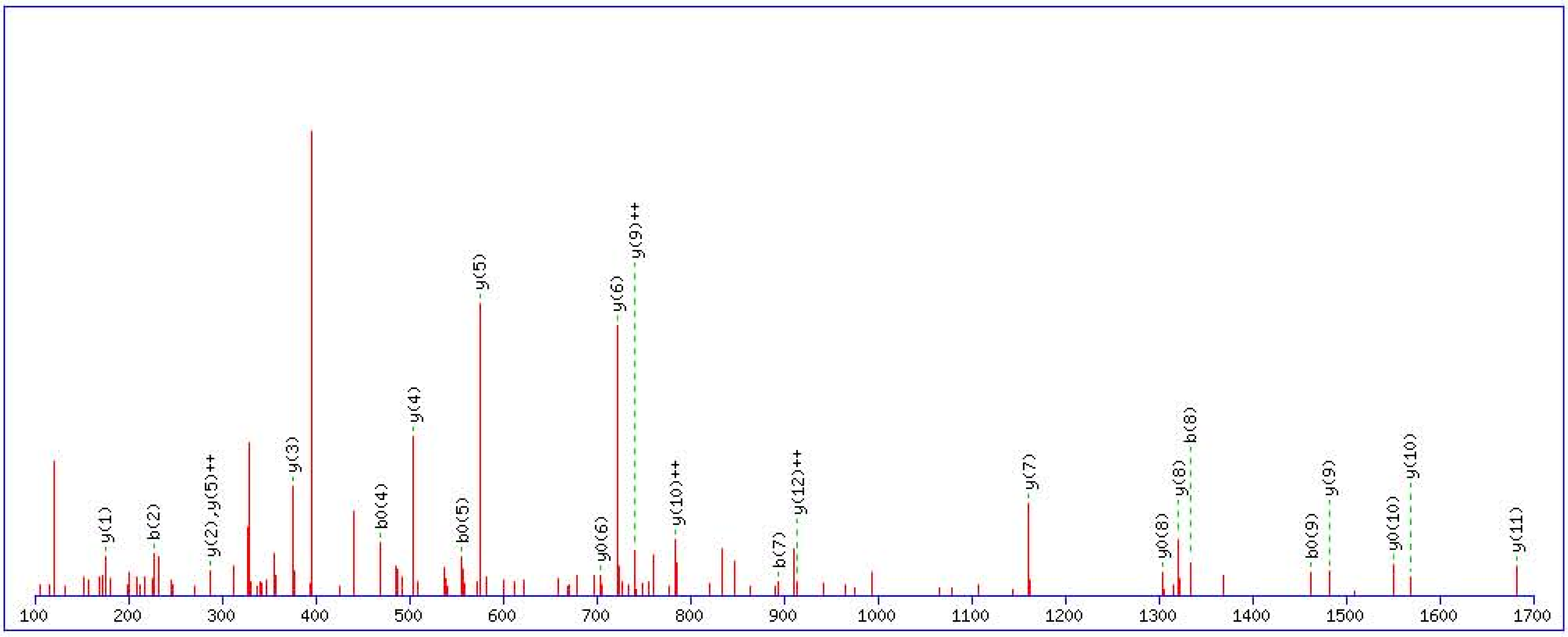
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

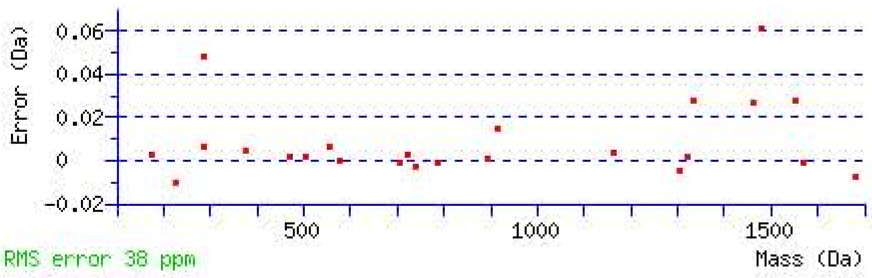
Match to Query 40920: 2053.946352 from(685.656060,3+) rtinseconds(2498) index(48782)
Title: Locus:1.1.1.3582.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

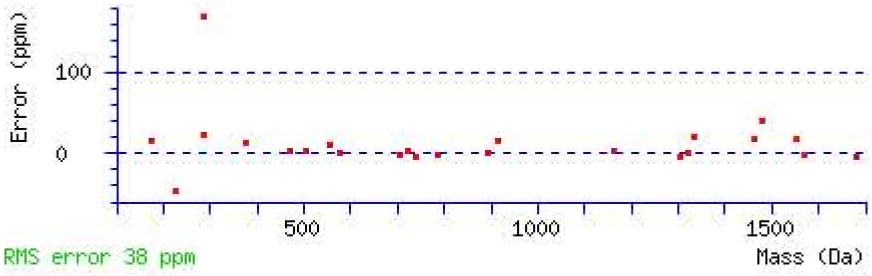
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2053.942368
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 65 **Expect:** 1.4e-006
Matches : 24/138 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	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
65.3	2053.942368	0.003984	EPFLSCCQFAESLR
3.1	2053.948227	-0.001875	EKSTCSMGSELLPMISPR

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

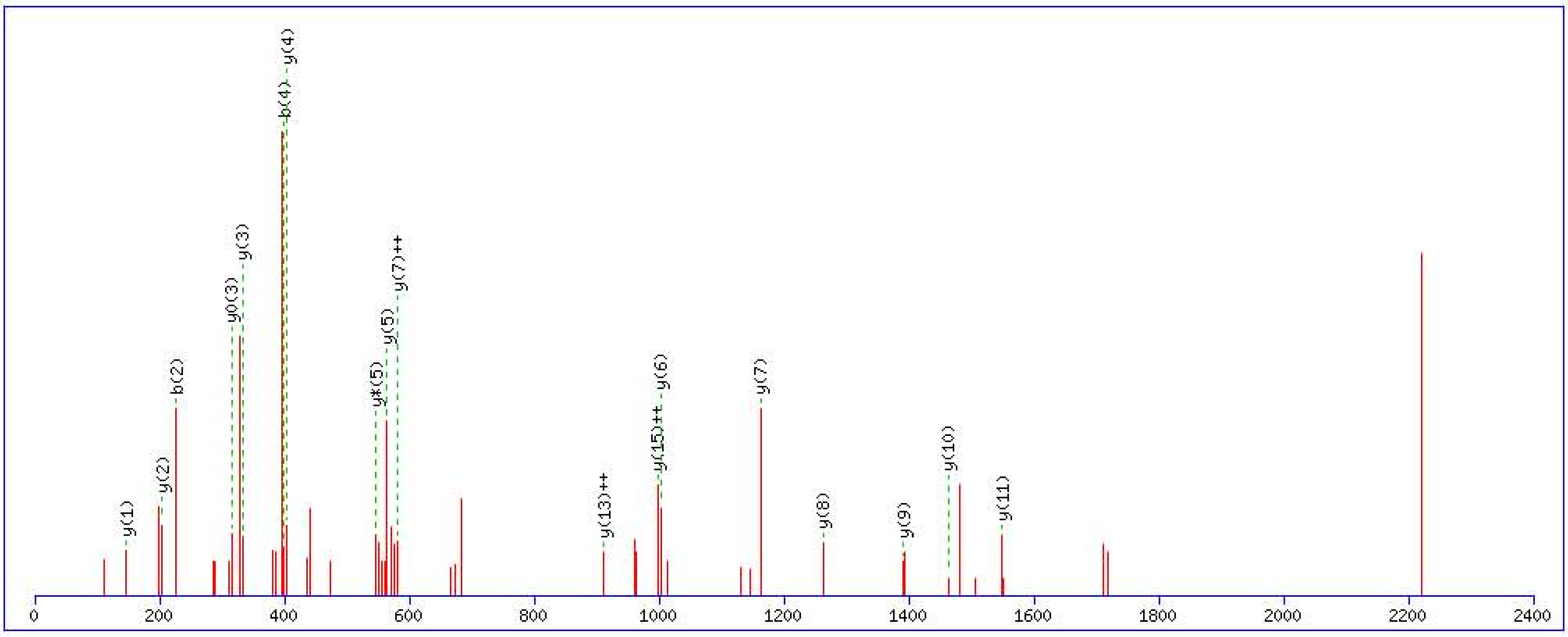
Mascot Search Results

Peptide View

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

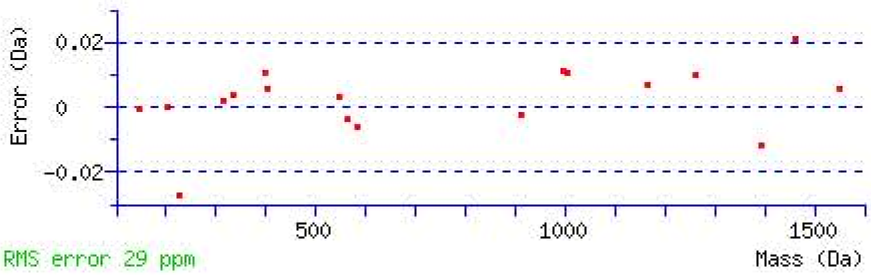
Match to Query 43621: 2220.038922 from(741.020250,3+) rtinseconds(2229) index(47386)
Title: Locus:1.1.1.3488.20 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

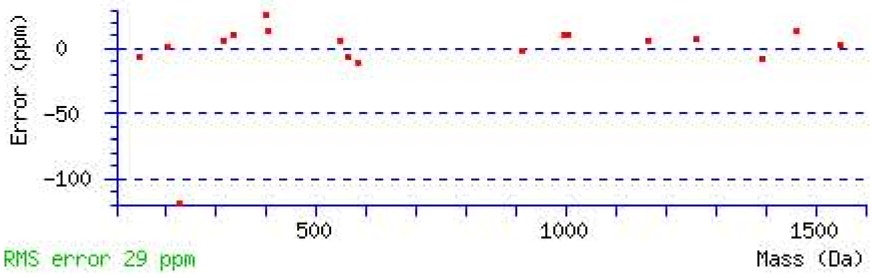
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2220.041092
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 50  Expect: 0.00017
Matches : 18/160 fragment ions using 45 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
49.7	2220.041092	-0.002170	LLATLCSAEVCQCAEGK

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

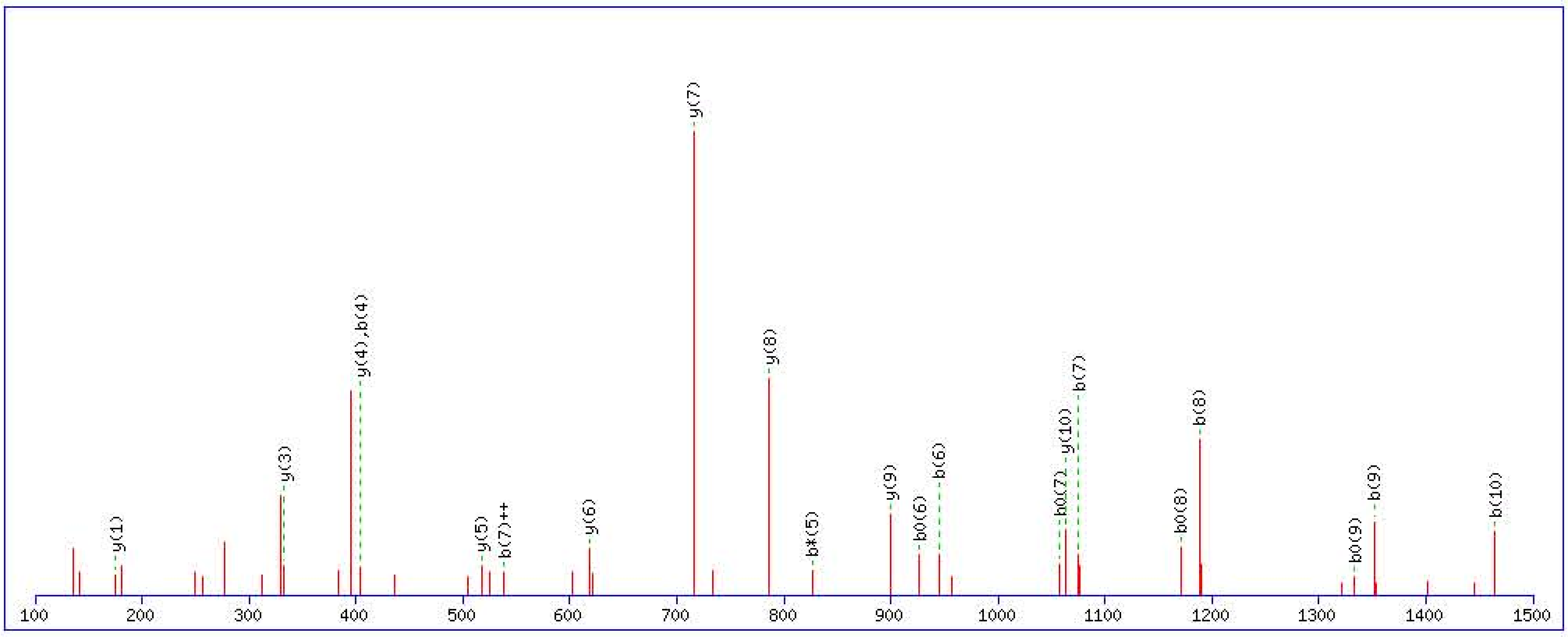
Mascot Search Results

Peptide View

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

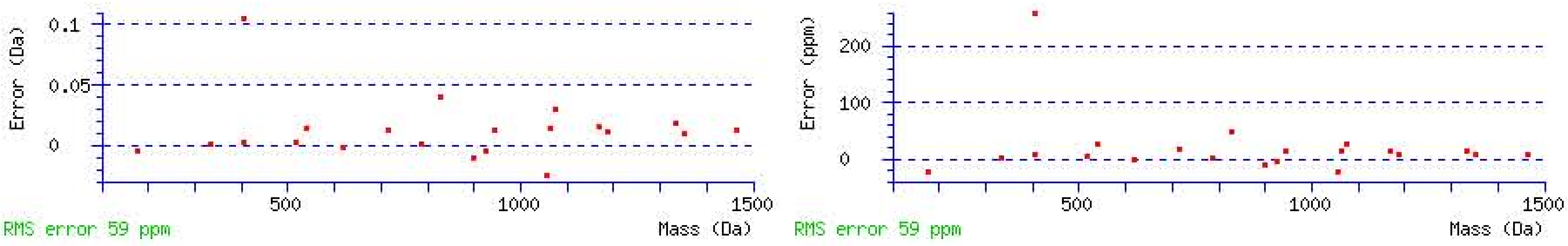
Match to Query 44062: 2249.109492 from(750.710440,3+) rtinseconds(2515) index(48930)
Title: Locus:1.1.1.3588.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 2249.100647
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.0011
Matches : 21/188 fragment ions using 45 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	58.028740	29.518008					G							18
2	218.059389	109.533333					C	2193.086482	1097.046879	2176.059933	1088.533604	2175.075917	1088.041596	17
3	275.080853	138.044064					G	2033.055833	1017.031555	2016.029284	1008.518280	2015.045268	1008.026272	16
4	***404.123446***	202.565361			386.112881	193.560079	E	1976.034369	988.520822	1959.007820	980.007548	1958.023804	979.515540	15
5	843.348772	422.178024	826.322223	413.664750	825.338207	413.172742	Q	1846.991776	923.999526	1829.965227	915.486251	1828.981211	914.994243	14
6	***944.396451***	472.701864	927.369902	464.188589	926.385886	463.696581	T	1407.766450	704.386863	1390.739901	695.873588	1389.755885	695.381580	13
7	***1075.436936***	538.222106	1058.410387	529.708832	1057.426371	529.216824	M	1306.718771	653.863023	1289.692222	645.349749	1288.708206	644.857741	12
8	***1188.521000***	594.764138	1171.494451	586.250864	1170.510435	585.758855	I	1175.678286	588.342781	1158.651737	579.829506	1157.667721	579.337498	11
9	***1351.584329***	676.295803	1334.557780	667.782528	1333.573764	667.290520	Y	***1062.594222***	531.800749	1045.567673	523.287475	1044.583657	522.795466	10
10	***1464.668393***	732.837834	1447.641844	724.324560	1446.657828	723.832552	L	***899.530893***	450.269084	882.504344	441.755810	881.520328	441.263802	9
11	1535.705507	768.356391	1518.678958	759.843117	1517.694942	759.351109	A	***786.446829***	393.727053	769.420280	385.213778	768.436264	384.721770	8
12	1632.758271	816.882773	1615.731722	808.369499	1614.747706	807.877491	P	***715.409715***	358.208496	698.383166	349.695221	697.399150	349.203213	7
13	1733.805950	867.406613	1716.779401	858.893339	1715.795385	858.401330	T	***618.356951***	309.682114	601.330402	301.168839	600.346386	300.676831	6
14	1846.890014	923.948645	1829.863465	915.435370	1828.879449	914.943362	L	***517.309272***	259.158274	500.282723	250.644999	499.298707	250.152991	5
15	1917.927128	959.467202	1900.900579	950.953927	1899.916563	950.461919	A	***404.225208***	202.616242	387.198659	194.102967	386.214643	193.610959	4
16	1988.964242	994.985759	1971.937693	986.472484	1970.953677	985.980476	A	***333.188094***	167.097685	316.161545	158.584410	315.177529	158.092402	3
17	2075.996270	1038.501773	2058.969721	1029.988498	2057.985705	1029.496490	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
18							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.9	2249.100647	0.008845	GCGEQTMIYLAPTLAASR
6.2	2249.115051	-0.005559	YSTSLYASPSMVHEGVAVVPR
3.2	2249.137527	-0.028035	QKFERPICVSWSTDVKGGR
1.9	2249.096420	0.013072	SDNTVTWLAAWTESVQNSIK
0.3	2249.078659	0.030833	FENGVAEGMVDPSLNPISAFR

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

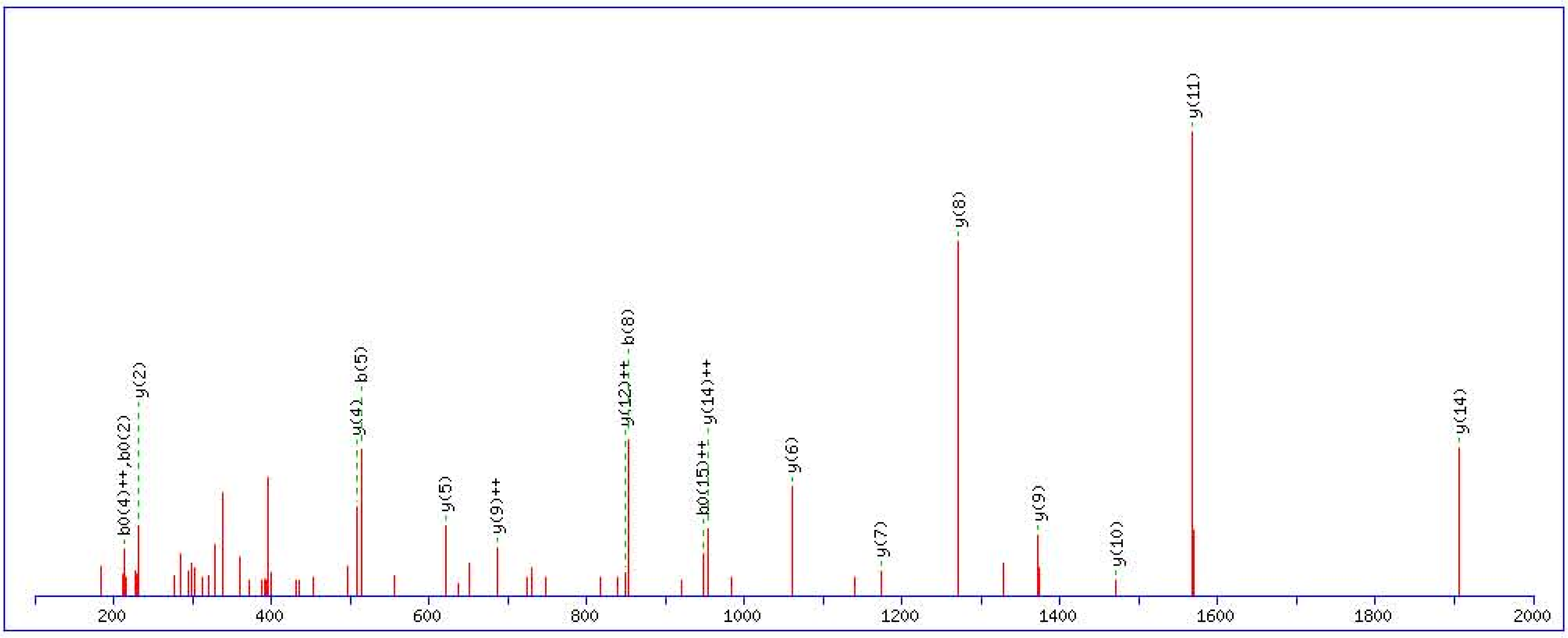
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

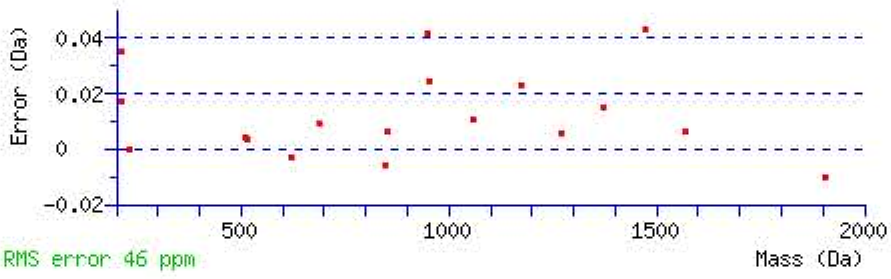
Match to Query 46770: 2418.237822 from(807.086550,3+) rtinseconds(3010) index(52389)
Title: Locus:1.1.1.3756.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

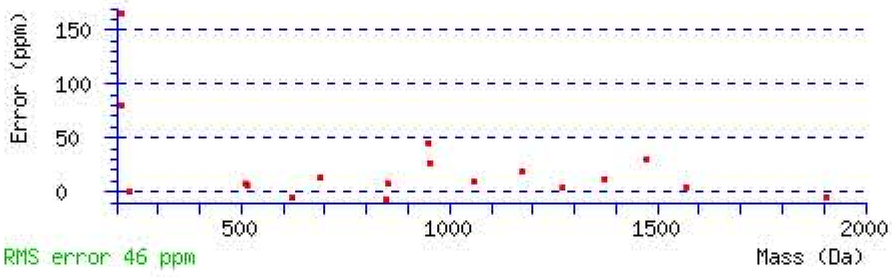
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2418.225342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 66  Expect: 8.1e-007
Matches : 18/198 fragment ions using 27 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							19
2	231.061162	116.034219			213.050597	107.028936	D	2304.205668	1152.606472	2287.179119	1144.093197	2286.195103	1143.601189	18
3	328.113926	164.560601			310.103361	155.555319	P	2189.178725	1095.093000	2172.152176	1086.579726	2171.168160	1086.087718	17
4	443.140869	222.074073			425.130304	213.068790	D	2092.125961	1046.566618	2075.099412	1038.053344	2074.115396	1037.561336	16
5	**514.177983**	257.592630			496.167418	248.587347	A	1977.099018	989.053147	1960.072469	980.539873	1959.088453	980.047865	15
6	611.230747	306.119012			593.220182	297.113729	P	***1906.061904***	953.534590	1889.035355	945.021316	1888.051339	944.529308	14
7	724.314811	362.661044			706.304246	353.655761	L	1809.009140	905.008208	1791.982591	896.494934	1790.998575	896.002926	13
8	**852.373389**	426.690333	835.346840	418.177058	834.362824	417.685050	Q	1695.925076	848.466176	1678.898527	839.952902	1677.914511	839.460894	12
9	949.426153	475.216715	932.399604	466.703440	931.415588	466.211432	P	***1567.866498***	784.436887	1550.839949	775.923613	1549.855933	775.431605	11
10	1048.494567	524.750922	1031.468018	516.237647	1030.484002	515.745639	V	***1470.813734***	735.910505	1453.787185	727.397231	1452.803169	726.905223	10
11	1149.542246	575.274761	1132.515697	566.761487	1131.531681	566.269479	T	***1371.745320***	686.376298	1354.718771	677.863024	1353.734755	677.371016	9
12	1246.595010	623.801143	1229.568461	615.287869	1228.584445	614.795861	P	***1270.697641***	635.852459	1253.671092	627.339184	1252.687076	626.847176	8
13	1359.679074	680.343175	1342.652525	671.829901	1341.668509	671.337893	L	***1173.644877***	587.326077	1156.618328	578.812802	1155.634312	578.320794	7
14	1798.904400	899.955838	1781.877851	891.442564	1780.893835	890.950556	Q	***1060.560813***	530.784045	1043.534264	522.270770	1042.550248	521.778762	6
15	1911.988464	956.497870	1894.961915	947.984596	1893.977899	947.492588	L	***621.335487***	311.171382	604.308938	302.658107	603.324922	302.166099	5
16	2059.056878	1030.032077	2042.030329	1021.518803	2041.046313	1021.026794	F	***508.251423***	254.629350	491.224874	246.116075	490.240858	245.624067	4
17	2188.099471	1094.553373	2171.072922	1086.040099	2170.088906	1085.548091	E	361.183009	181.095142	344.156460	172.581868	343.172444	172.089860	3
18	2245.120935	1123.064105	2228.094386	1114.550831	2227.110370	1114.058823	G	***232.140416***	116.573846	215.113867	108.060571			2
19							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.7	2418.225342	0.012480	DDPDAPLQPVTPLQLFEGR
12.7	2418.225342	0.012480	DDPDAPLQPVTPLQLFEGR
0.7	2418.247803	-0.009981	GQTLNVNRLLHIVGYGDFQMK
0.2	2418.259033	-0.021211	QQQRALLGPWLSGPQGTDR
0.2	2418.259033	-0.021211	QQQRALLGPWLSGPQGTDR
0.2	2418.259033	-0.021211	QQQRALLGPWLSGPQGTDR

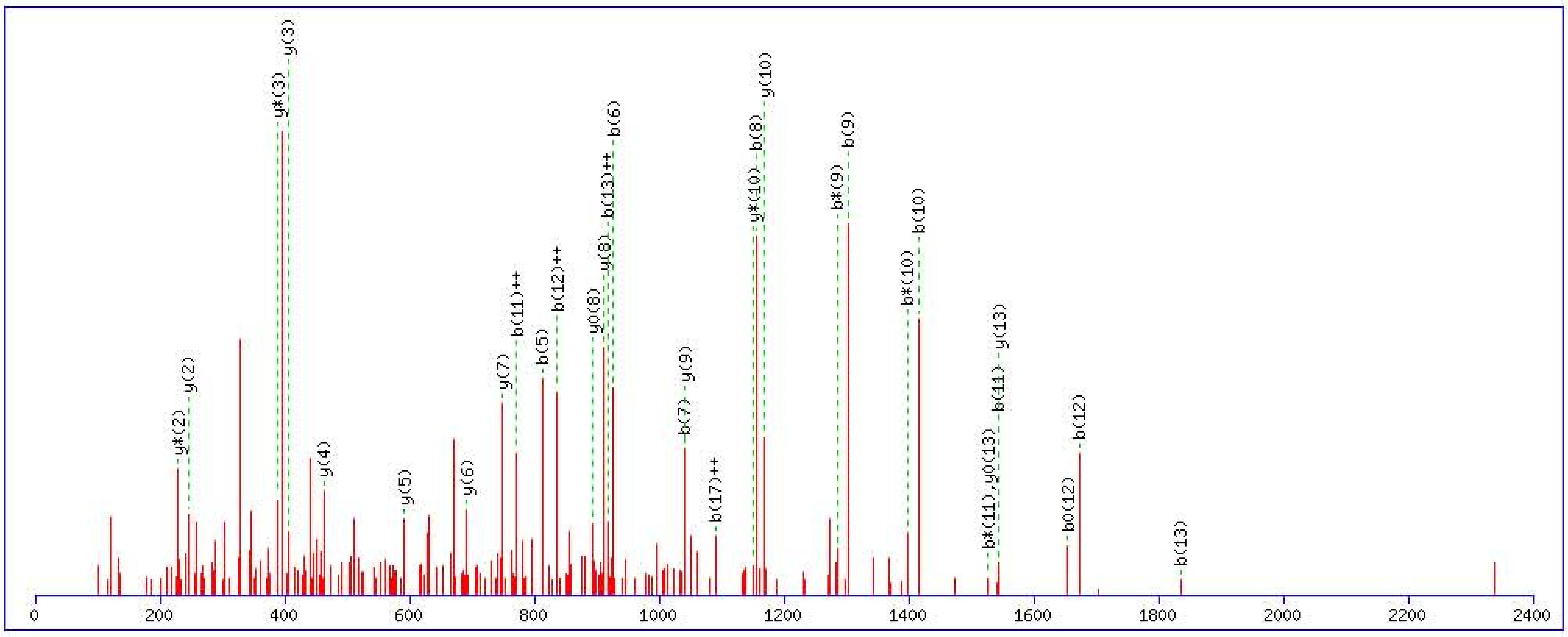
Mascot Search Results

Peptide View

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

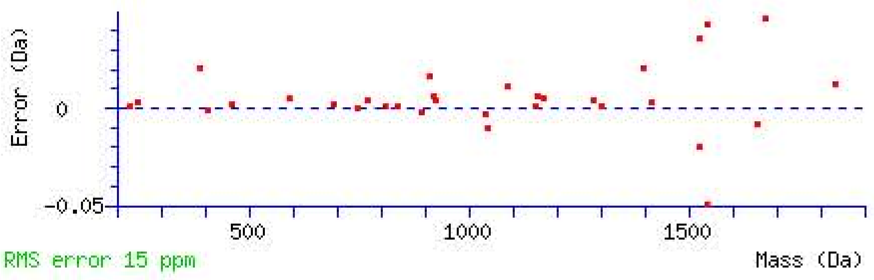
Match to Query 49357: 2583.165192 from(862.062340,3+) rtinseconds(2731) index(50237)
Title: Locus:1.1.1.3662.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

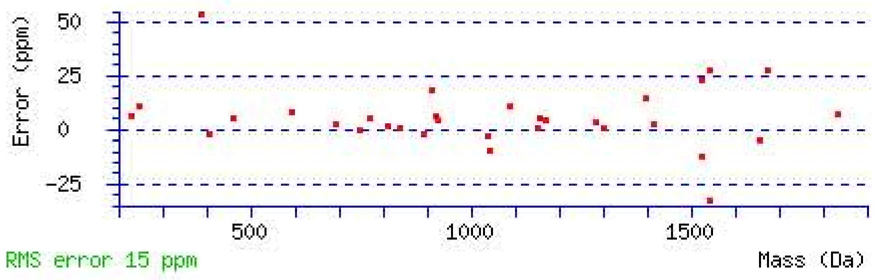
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 65  Expect: 3e-006
Matches : 32/194 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	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
64.7	2583.155624	0.009568	AACAQLNDFLQEYGTQGCQV
21.7	2583.155624	0.009568	AACAQLNDFLQEYGTQGCQV

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

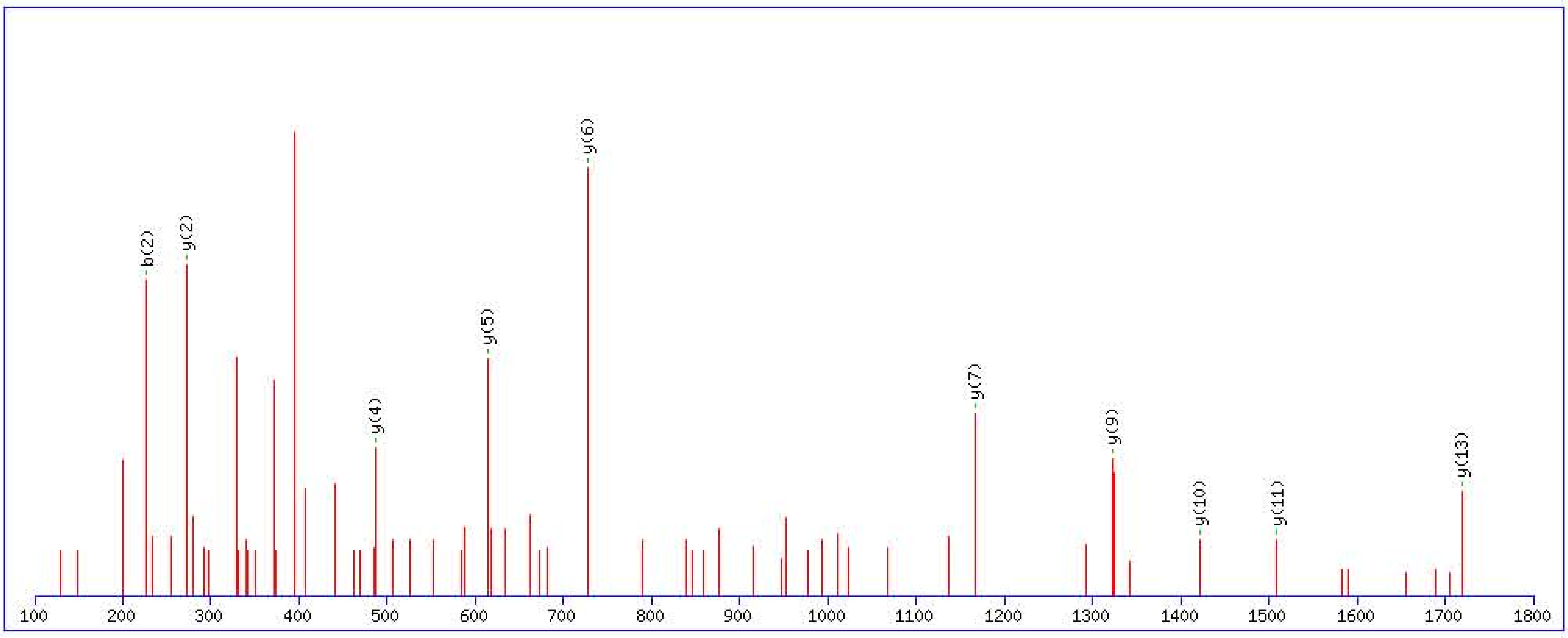
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

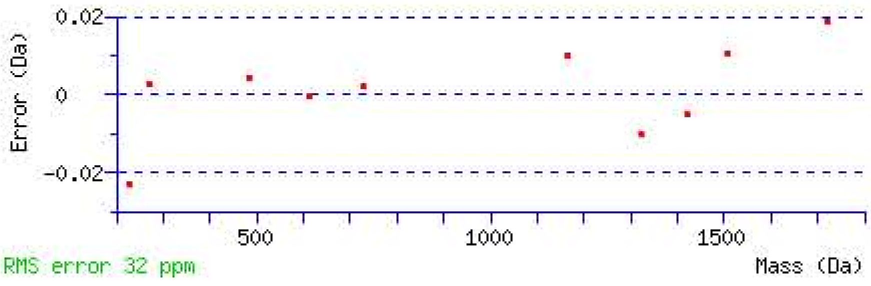
Match to Query 54597: 3079.780496 from(770.952400,4+) rtinseconds(3070) index(52599)
Title: Locus:1.1.1.3778.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

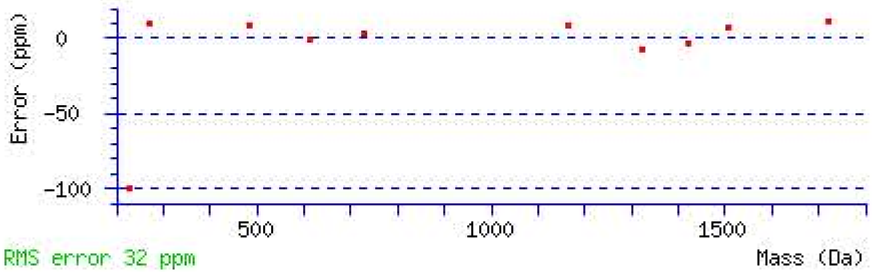


Monoisotopic mass of neutral peptide Mr(calc): 3079.762054
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20 : Biotin:Thermo-21345 (Q)
Ions Score: 51 **Expect:** 1.6e-005
Matches : 10/248 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							26
2	227.175404	114.091340					L	2967.685233	1484.346254	2950.658684	1475.832980	2949.674668	1475.340972	25
3	340.259468	170.633372					L	2854.601169	1427.804222	2837.574620	1419.290948	2836.590604	1418.798940	24
4	487.327882	244.167579					F	2741.517105	1371.262190	2724.490556	1362.748916	2723.506540	1362.256908	23
5	574.359910	287.683593			556.349345	278.678311	S	2594.448691	1297.727983	2577.422142	1289.214709	2576.438126	1288.722701	22
6	671.412674	336.209975			653.402109	327.204693	P	2507.416663	1254.211969	2490.390114	1245.698695	2489.406098	1245.206687	21
7	758.444702	379.725989			740.434137	370.720707	S	2410.363899	1205.685587	2393.337350	1197.172313	2392.353334	1196.680305	20
8	857.513116	429.260196			839.502551	420.254913	V	2323.331871	1162.169573	2306.305322	1153.656299	2305.321306	1153.164291	19
9	956.581530	478.794403			938.570965	469.789120	V	2224.263457	1112.635366	2207.236908	1104.122092	2206.252892	1103.630084	18
10	1093.640442	547.323859			1075.629877	538.318576	H	2125.195043	1063.101159	2108.168494	1054.587885	2107.184478	1054.095877	17
11	1206.724506	603.865891			1188.713941	594.860608	L	1988.136131	994.571704	1971.109582	986.058429	1970.125566	985.566421	16
12	1263.745970	632.376623			1245.735405	623.371340	G	1875.052067	938.029672	1858.025518	929.516397	1857.041502	929.024389	15
13	1362.814384	681.910830			1344.803819	672.905547	V	1818.030603	909.518940	1801.004054	901.005665	1800.020038	900.513657	14
14	1459.867148	730.437212			1441.856583	721.431929	P	***1718.962189***	859.984733	1701.935640	851.471458	1700.951624	850.979450	13
15	1572.951212	786.979244			1554.940647	777.973961	L	1621.909425	811.458351	1604.882876	802.945076	1603.898860	802.453068	12
16	1659.983240	830.495258			1641.972675	821.489975	S	***1508.825361***	754.916319	1491.798812	746.403044	1490.814796	745.911036	11
17	1759.051654	880.029465			1741.041089	871.024182	V	***1421.793333***	711.400305	1404.766784	702.887030	1403.782768	702.395022	10
18	1816.073118	908.540197			1798.062553	899.534914	G	***1322.724919***	661.866098	1305.698370	653.352823	1304.714354	652.860815	9
19	1915.141532	958.074404			1897.130967	949.069121	V	1265.703455	633.355366	1248.676906	624.842091	1247.692890	624.350083	8
20	2354.366858	1177.687067	2337.340309	1169.173792	2336.356293	1168.681784	Q	***1166.635041***	583.821159	1149.608492	575.307884	1148.624476	574.815876	7
21	2467.450922	1234.229099	2450.424373	1225.715824	2449.440357	1225.223816	L	***727.409715***	364.208496	710.383166	355.695221	709.399150	355.203213	6
22	2595.509500	1298.258388	2578.482951	1289.745113	2577.498935	1289.253105	Q	***614.325651***	307.666463	597.299102	299.153189	596.315086	298.661181	5
23	2710.536443	1355.771859	2693.509894	1347.258585	2692.525878	1346.766577	D	***486.267073***	243.637174	469.240524	235.123900	468.256508	234.631892	4
24	2809.604857	1405.306066	2792.578308	1396.792792	2791.594292	1396.300784	V	371.240130	186.123703	354.213581	177.610428			3
25	2906.657621	1453.832448	2889.631072	1445.319174	2888.647056	1444.827166	P	***272.171716***	136.589496	255.145167	128.076221			2
26							R	175.118952	88.063114	158.092403	79.549839			1



RMS error 32 ppm



RMS error 32 ppm

NCBI **BLAST** search of LLLFSPSVVHLGVPLSVGVQLQDVPR
(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	3079.762054	0.018442	LLLFSPSVVHLGVPLSVGVQLQDVPR
27.9	3079.762054	0.018442	LLLFSPSVVHLGVPLSVGVQLQDVPR

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

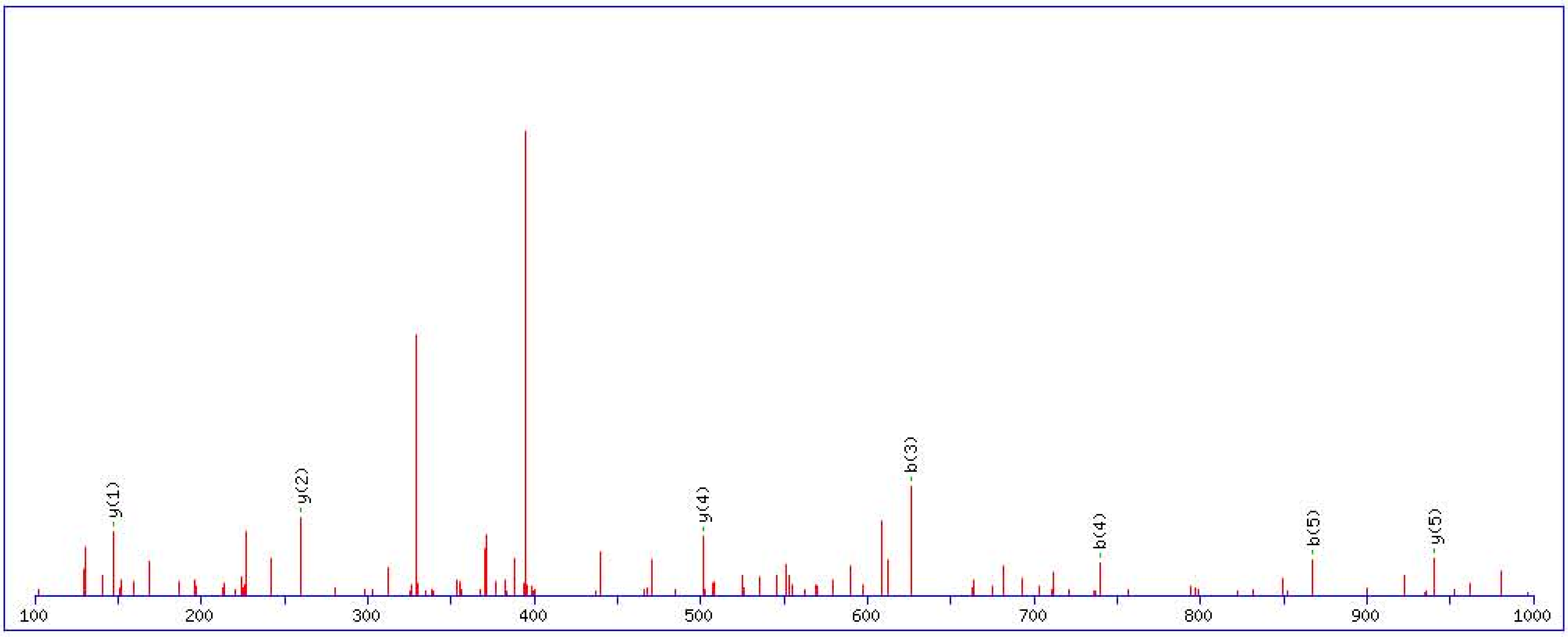
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GEQIQLK**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

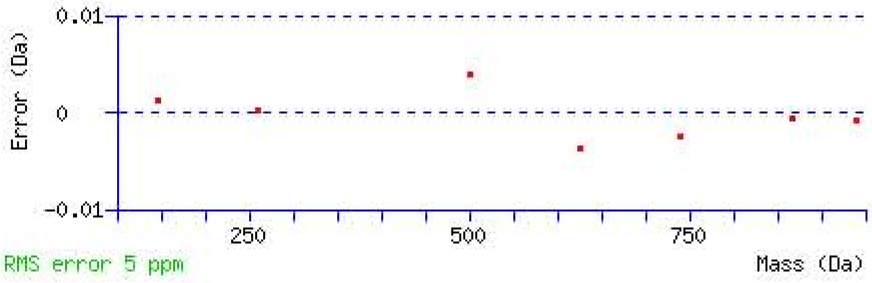
Match to Query 14948: 1125.619048 from(563.816800,2+) rtinseconds(1768) index(30383)
Title: Locus:1.1.1.3279.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

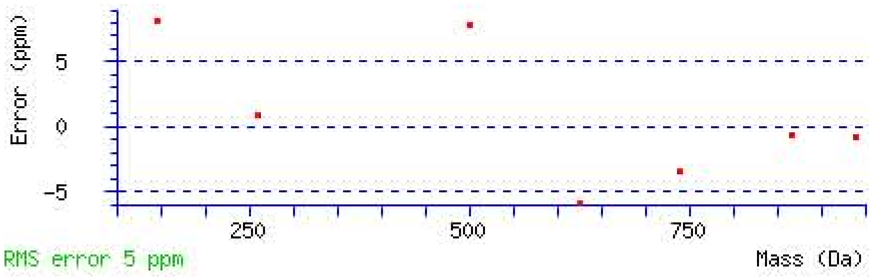
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1125.621597
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.04
Matches : 7/56 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	58.028740	29.518008					G							7
2	187.071333	94.039305			169.060768	85.034022	E	1069.607429	535.307353	1052.580880	526.794078	1051.596864	526.302070	6
3	***626.296659***	313.651968	609.270110	305.138693	608.286094	304.646685	Q	***940.564836***	470.786056	923.538287	462.272782			5
4	***739.380723***	370.194000	722.354174	361.680725	721.370158	361.188717	I	***501.339510***	251.173393	484.312961	242.660119			4
5	***867.439301***	434.223289	850.412752	425.710014	849.428736	425.218006	Q	388.255446	194.631361	371.228897	186.118087			3
6	980.523365	490.765321	963.496816	482.252046	962.512800	481.760038	L	***260.196868***	130.602072	243.170319	122.088798			2
7							K	***147.112804***	74.060040	130.086255	65.546766			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.3	1125.621597	-0.002549	GEQIQLK
11.7	1125.621597	-0.002549	EQVAQLK
11.6	1125.632813	-0.013764	EQAARLK
10.3	1125.632828	-0.013780	KLCLSHLQK
10.0	1125.607666	0.011382	QMDRHAKIK
7.6	1125.602966	0.016082	VSISKSTYNK
7.2	1125.606979	0.012069	LKEAFDYIK
7.1	1125.629486	-0.010438	RVDGWPVGLK
6.1	1125.621597	-0.002549	GEQIQLK
6.1	1125.633499	-0.014451	VSHFLPWIK

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

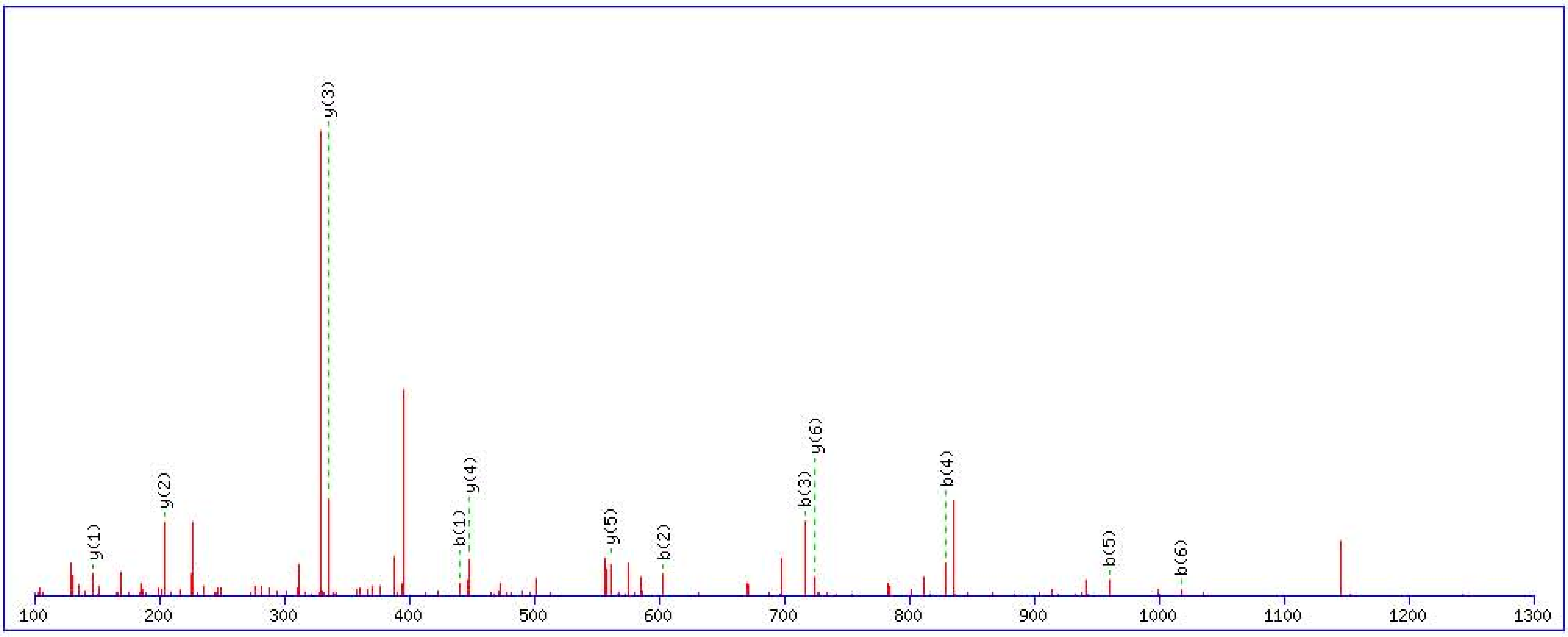
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QYLIMGK**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

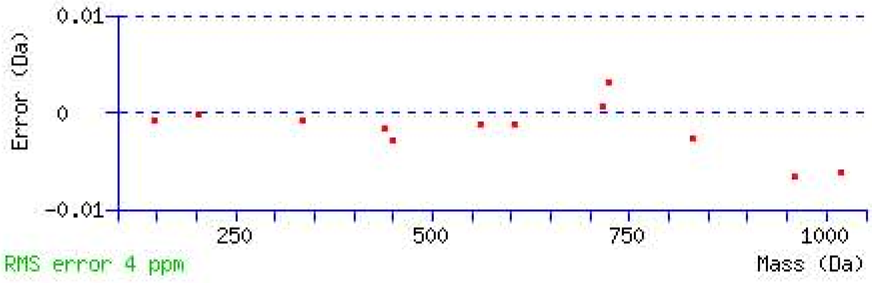
Match to Query 16610: 1162.621308 from(582.317930,2+) rtinseconds(2121) index(32577)
Title: Locus:1.1.1.3402.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

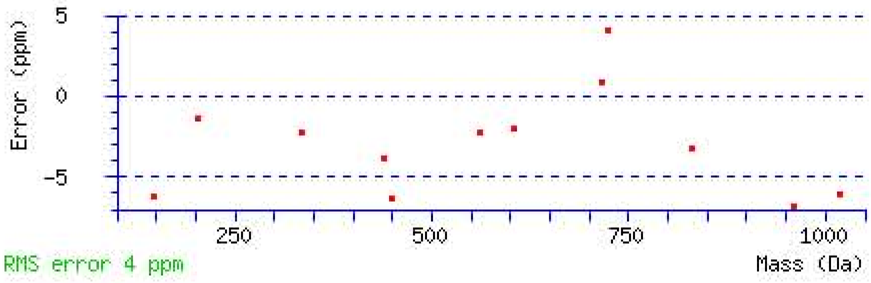
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1162.624237
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 25 **Expect:** 0.018
Matches : 12/48 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	Seq.	y	y^{++}	y^*	y^{*++}	#
1	*440.232602*	220.619939	423.206053	212.106664	Q					7
2	*603.295931*	302.151604	586.269382	293.638329	Y	**724.406210**	362.706743	707.379661	354.193469	6
3	*716.379995*	358.693636	699.353446	350.180361	L	**561.342881**	281.175079	544.316332	272.661804	5
4	*829.464059*	415.235668	812.437510	406.722393	I	**448.258817**	224.633046	431.232268	216.119772	4
5	*960.504544*	480.755910	943.477995	472.242636	M	**335.174753**	168.091014	318.148204	159.577740	3
6	*1017.526008*	509.266642	1000.499459	500.753368	G	**204.134268**	102.570772	187.107719	94.057497	2
7					K	**147.112804**	74.060040	130.086255	65.546765	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.0	1162.624237	-0.002929	QYLIMGK
6.0	1162.624069	-0.002761	VGRCRSLSTK
5.5	1162.626724	-0.005416	KVEIAEMSLK
4.0	1162.626740	-0.005432	EVLKMDTSIK
3.5	1162.609451	0.011857	QNTNKFNGIK
1.6	1162.612823	0.008485	KTVAMSNLQR
1.6	1162.620697	0.000611	QLSGQRFTAR
1.1	1162.628098	-0.006790	AGLGPQGPR
1.0	1162.635956	-0.014648	WGGFLGRRSK
0.5	1162.637955	-0.016647	KLEMATNKTK

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

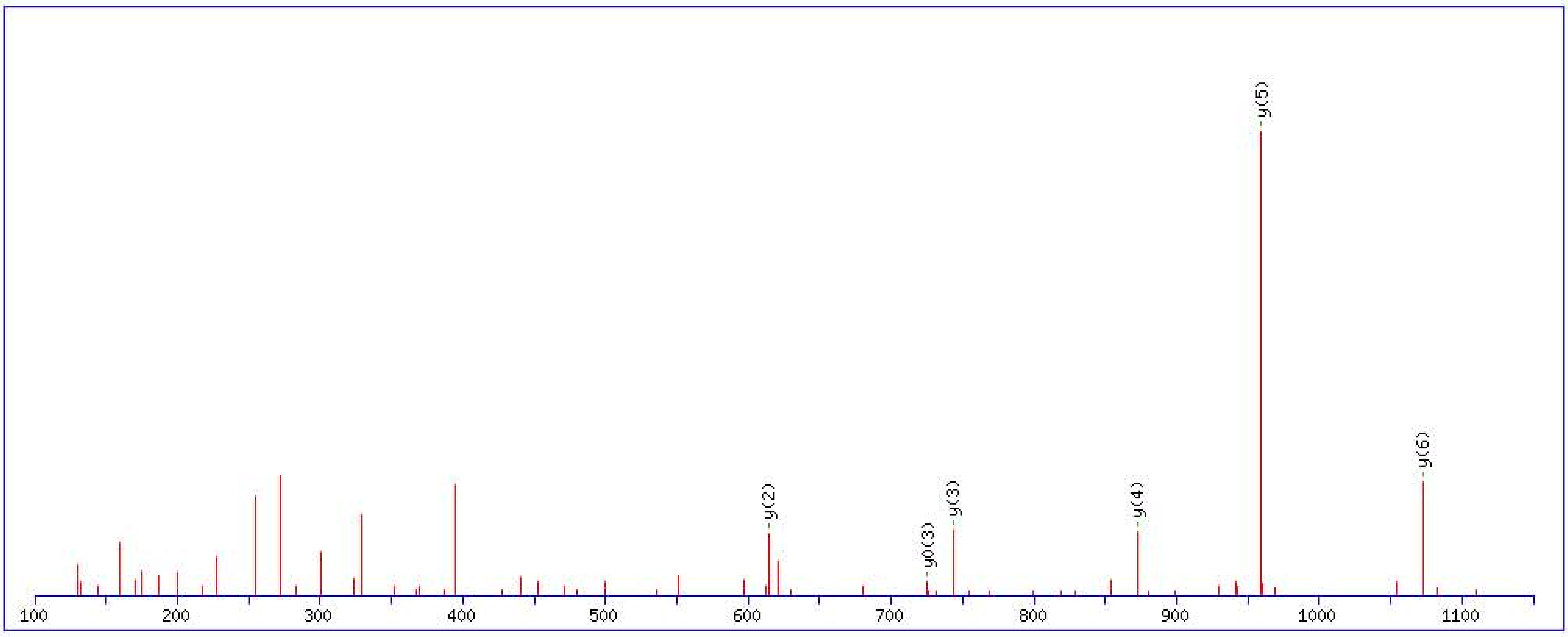
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WLSEEQR**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

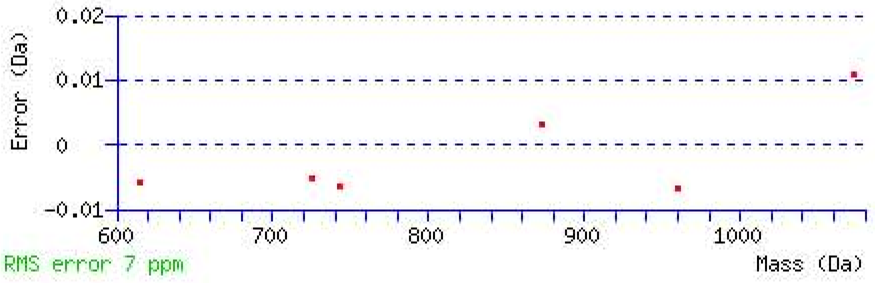
Match to Query 19174: 1257.615708 from(629.815130,2+) rtinseconds(1848) index(30858)
Title: Locus:1.1.1.3307.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

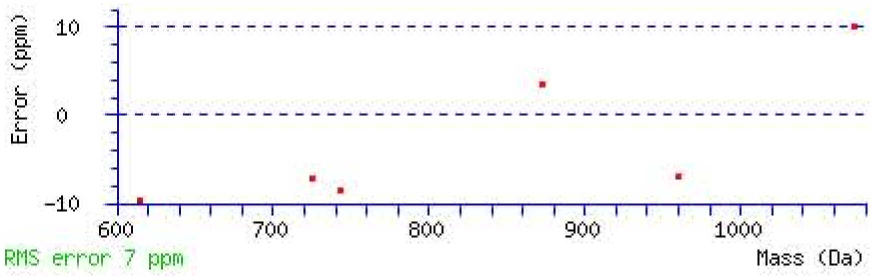
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1257.617569
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 33 **Expect:** 0.0097
Matches : 6/54 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	187.086589	94.046932					W							7
2	300.170653	150.588965					L	***1072.545556***	536.776416	1055.519007	528.263142	1054.534991	527.771134	6
3	387.202681	194.104979			369.192116	185.099696	S	***959.461492***	480.234384	942.434943	471.721109	941.450927	471.229101	5
4	516.245274	258.626275			498.234709	249.620993	E	***872.429464***	436.718370	855.402915	428.205095	854.418899	427.713087	4
5	645.287867	323.147572			627.277302	314.142289	E	***743.386871***	372.197073	726.360322	363.683799	725.376306	363.191791	3
6	1084.513193	542.760235	1067.486644	534.246960	1066.502628	533.754952	Q	***614.344278***	307.675777	597.317729	299.162502			2
7							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of WLSEEQR
(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	1257.617569	-0.001861	WLSEEQR
11.2	1257.621414	-0.005706	ASSNRSWTPPR
5.4	1257.602295	0.013413	EKEEEQR
3.5	1257.621445	-0.005737	GFRGETGPQGPR
3.0	1257.631287	-0.015579	ADAEEALKQQR
2.7	1257.606155	0.009553	DASSRANGIPDR
2.2	1257.617599	-0.001891	QADVFPDR
2.1	1257.607040	0.008668	RGVCAGAMAPPR
0.6	1257.620071	-0.004363	EGLEEGDQILR

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

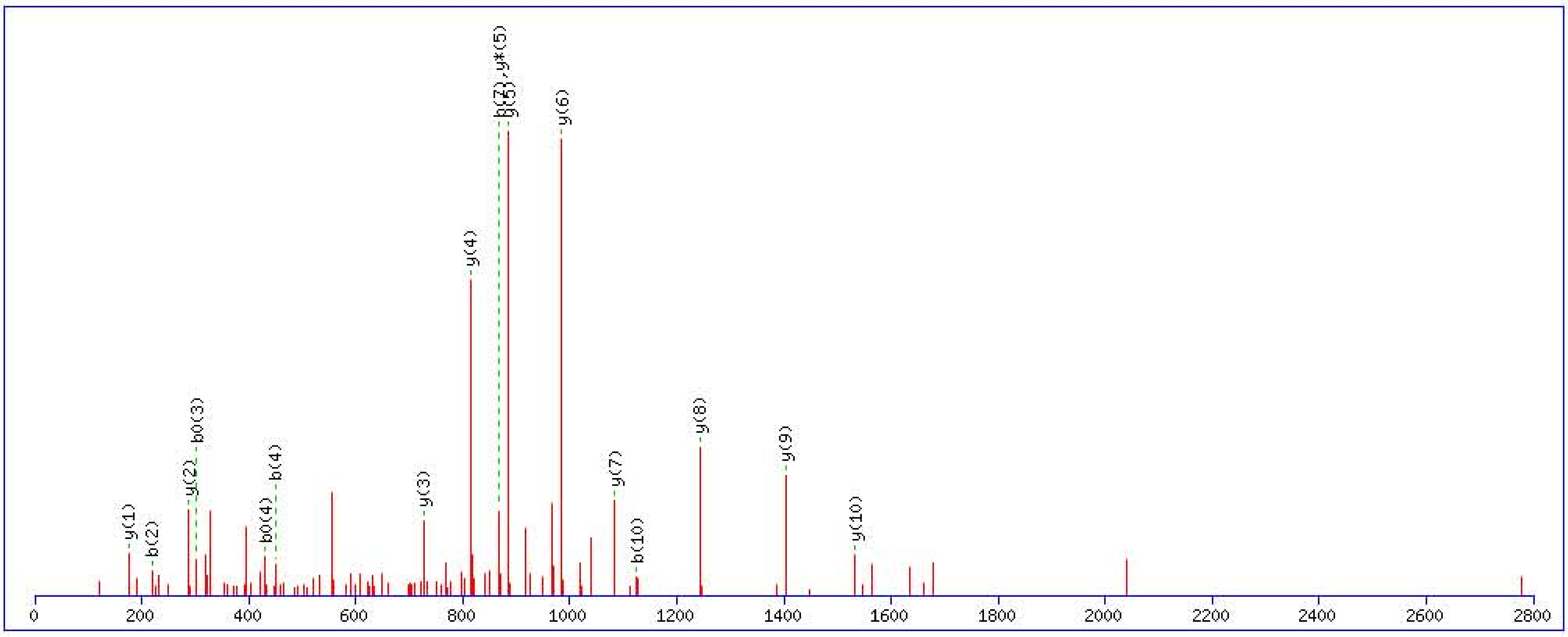
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFTECCVVASQLR**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

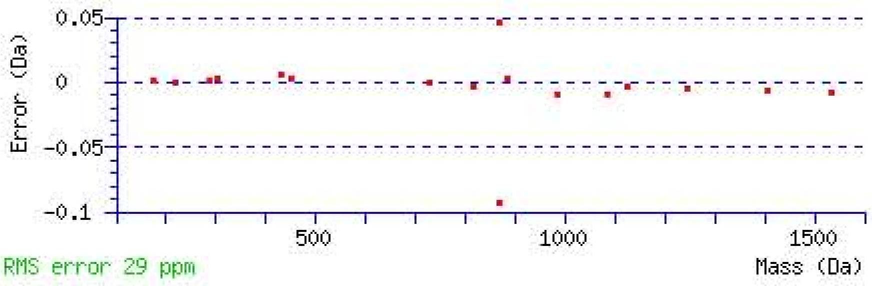
Match to Query 36629: 1850.881628 from(926.448090,2+) rtinseconds(2194) index(32995)
Title: Locus:1.1.1.3427.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

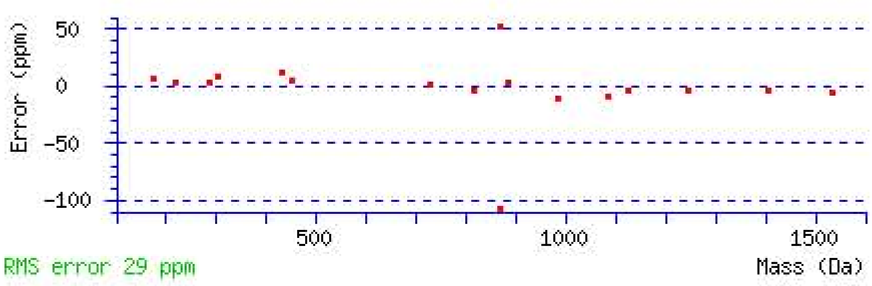
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1850.884140
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 7.7e-006
Matches : 17/114 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	72.044390	36.525833					A							13
2	**219.112804**	110.060040					F	1780.854296	890.930786	1763.827747	882.417512	1762.843731	881.925504	12
3	320.160483	160.583879			302.149918	151.578597	T	1633.785882	817.396579	1616.759333	808.883305	1615.775317	808.391297	11
4	**449.203076**	225.105176			431.192511	216.099894	E	***1532.738203***	766.872740	1515.711654	758.359465	1514.727638	757.867457	10
5	609.233725	305.120501			591.223160	296.115218	C	***1403.695610***	702.351443	1386.669061	693.838169	1385.685045	693.346161	9
6	769.264374	385.135825			751.253809	376.130543	C	***1243.664961***	622.336119	1226.638412	613.822844	1225.654396	613.330836	8
7	**868.332788**	434.670032			850.322223	425.664750	V	***1083.634312***	542.320794	1066.607763	533.807520	1065.623747	533.315512	7
8	967.401202	484.204239			949.390637	475.198957	V	***984.565898***	492.786587	967.539349	484.273313	966.555333	483.781305	6
9	1038.438316	519.722796			1020.427751	510.717514	A	***885.497484***	443.252380	868.470935	434.739106	867.486919	434.247098	5
10	**1125.470344**	563.238810			1107.459779	554.233528	S	***814.460370***	407.733823	797.433821	399.220549	796.449805	398.728541	4
11	1564.695670	782.851473	1547.669121	774.338199	1546.685105	773.846191	Q	***727.428342***	364.217809	710.401793	355.704535			3
12	1677.779734	839.393505	1660.753185	830.880231	1659.769169	830.388223	L	***288.203016***	144.605146	271.176467	136.091871			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.5	1850.884140	-0.002512	AFTECCVVASQLR
6.5	1850.898499	-0.016871	EDGMPVPELYNRIFR
0.2	1850.893127	-0.011499	AMESTATAAVAAELVSADK

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

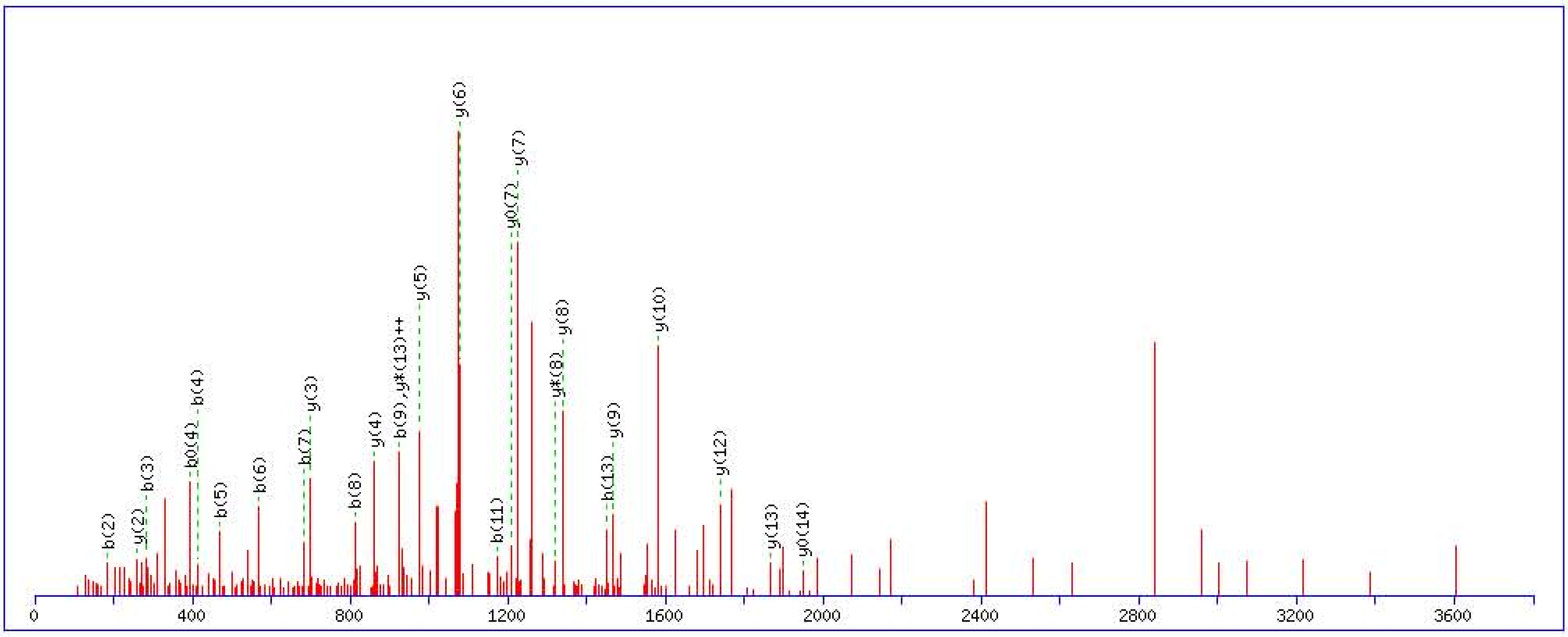
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALVEGVDQLFTDYQIK**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

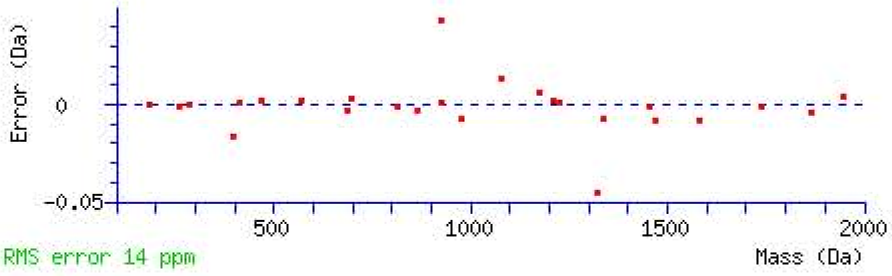
Match to Query 42317: 2149.131308 from(1075.572930,2+) rtinseconds(2848) index(37024)
Title: Locus:1.1.1.3653.6 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

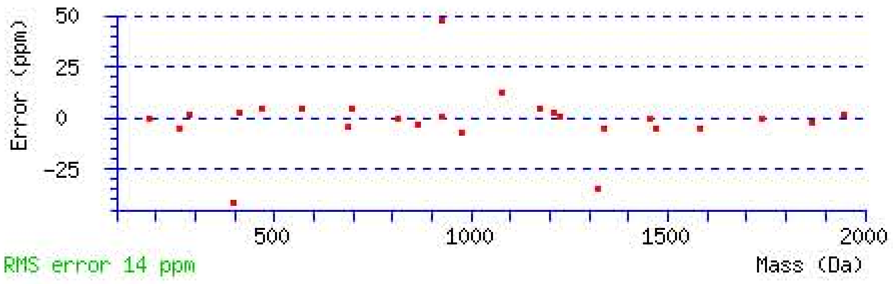
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2149.112930
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 76  Expect: 7.9e-008
Matches : 26/152 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	72.044390	36.525833					A							16
2	***185.128454***	93.067865					L	2079.083093	1040.045184	2062.056544	1031.531910	2061.072528	1031.039902	15
3	***284.196868***	142.602072					V	1965.999029	983.503153	1948.972480	974.989878	1947.988464	974.497870	14
4	***413.239461***	207.123369			395.228896	198.118086	E	***1866.930615***	933.968946	1849.904066	925.455671	1848.920050	924.963663	13
5	***470.260925***	235.634100			452.250360	226.628818	G	***1737.888022***	869.447649	1720.861473	860.934375	1719.877457	860.442367	12
6	***569.329339***	285.168308			551.318774	276.163025	V	1680.866558	840.936917	1663.840009	832.423643	1662.855993	831.931635	11
7	***684.356282***	342.681779			666.345717	333.676496	D	***1581.798144***	791.402710	1564.771595	782.889436	1563.787579	782.397428	10
8	***812.414860***	406.711068	795.388311	398.197793	794.404295	397.705785	Q	***1466.771201***	733.889239	1449.744652	725.375964	1448.760636	724.883956	9
9	***925.498924***	463.253100	908.472375	454.739825	907.488359	454.247818	L	***1338.712623***	669.859950	1321.686074	661.346675	1320.702058	660.854667	8
10	1072.567338	536.787307	1055.540789	528.274033	1054.556773	527.782025	F	***1225.628559***	613.317918	1208.602010	604.804643	1207.617994	604.312635	7
11	***1173.615017***	587.311147	1156.588468	578.797872	1155.604452	578.305864	T	***1078.560145***	539.783711	1061.533596	531.270436	1060.549580	530.778428	6
12	1288.641960	644.824618	1271.615411	636.311344	1270.631395	635.819336	D	***977.512466***	489.259871	960.485917	480.746597	959.501901	480.254589	5
13	***1451.705289***	726.356283	1434.678740	717.843008	1433.694724	717.351000	Y	***862.485523***	431.746400	845.458974	423.233125			4
14	1890.930615	945.968946	1873.904066	937.455671	1872.920050	936.963663	Q	***699.422194***	350.214735	682.395645	341.701461			3
15	2004.014679	1002.510978	1986.988130	993.997703	1986.004114	993.505695	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 ALVEGVDQLFTDYQIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
76.2	2149.112930	0.018378	ALVEGVDQLFTDYQIK
13.6	2149.112930	0.018378	ALVEGVDQLFTDYQIK
0.5	2149.116257	0.015051	QDEQLAMKLLTYELK

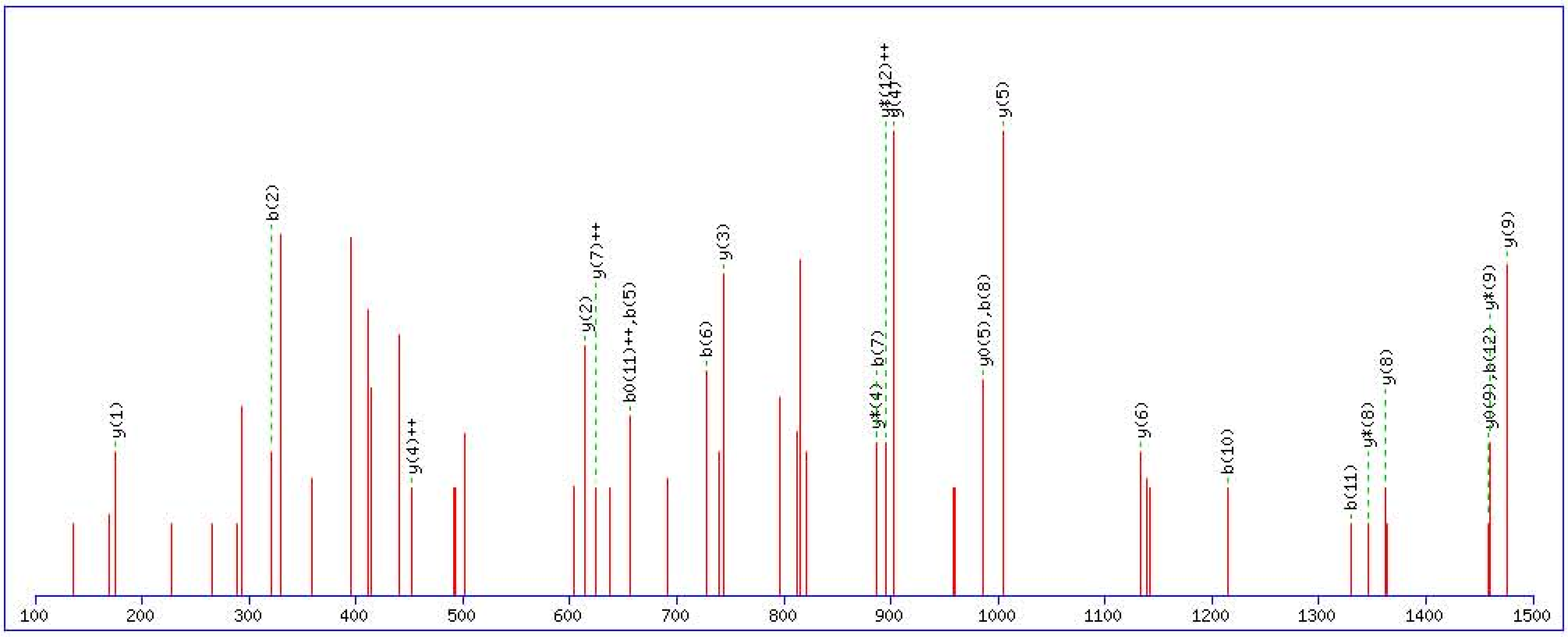
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CCYDGACVNNDETCEQR**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

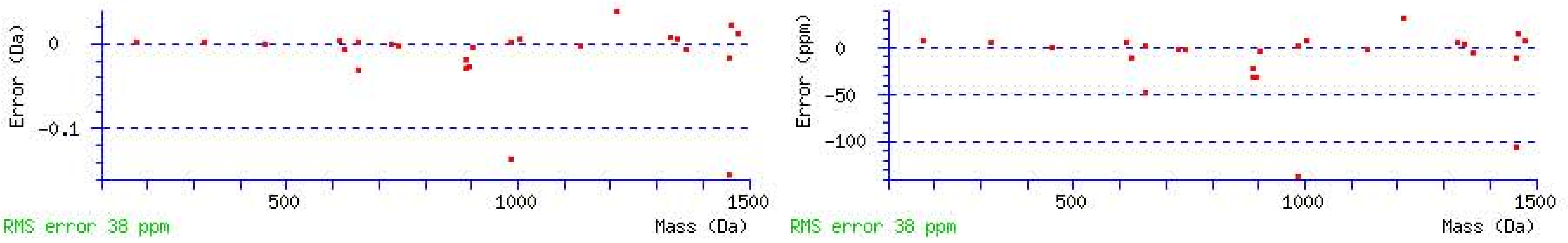
Match to Query 47462: 2460.930432 from(821.317420,3+) rtinseconds(1600) index(29397)
Title: Locus:1.1.1.3220.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 2460.922531
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16     : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 2.3e-005
Matches : 25/166 fragment ions using 46 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	161.037925	81.022600					C							17
2	***321.068574***	161.037925					C	2301.899151	1151.453213	2284.872602	1142.939939	2283.888586	1142.447931	16
3	484.131903	242.569590					Y	2141.868502	1071.437889	2124.841953	1062.924614	2123.857937	1062.432606	15
4	599.158846	300.083061			581.148281	291.077779	D	1978.805173	989.906225	1961.778624	981.392950	1960.794608	980.900942	14
5	***656.180310***	328.593793			638.169745	319.588511	G	1863.778230	932.392753	1846.751681	923.879479	1845.767665	923.387471	13
6	***727.217424***	364.112350			709.206859	355.107068	A	1806.756766	903.882021	1789.730217	895.368747	1788.746201	894.876739	12
7	***887.248073***	444.127675			869.237508	435.122392	C	1735.719652	868.363464	1718.693103	859.850190	1717.709087	859.358182	11
8	***986.316487***	493.661882			968.305922	484.656599	V	1575.689003	788.348140	1558.662454	779.834865	1557.678438	779.342857	10
9	1100.359414	550.683345	1083.332865	542.170071	1082.348849	541.678063	N	***1476.620589***	738.813933	1459.594040	730.300658	1458.610024	729.808650	9
10	***1214.402341***	607.704809	1197.375792	599.191534	1196.391776	598.699526	N	***1362.577662***	681.792469	1345.551113	673.279195	1344.567097	672.787187	8
11	***1329.429284***	665.218280	1312.402735	656.705006	1311.418719	656.212998	D	1248.534735	624.771006	1231.508186	616.257731	1230.524170	615.765723	7
12	***1458.471877***	729.739577	1441.445328	721.226302	1440.461312	720.734294	E	***1133.507792***	567.257534	1116.481243	558.744260	1115.497227	558.252252	6
13	1559.519556	780.263416	1542.493007	771.750142	1541.508991	771.258134	T	***1004.465199***	502.736238	987.438650	494.222963	986.454634	493.730955	5
14	1719.550205	860.278741	1702.523656	851.765466	1701.539640	851.273458	C	***903.417520***	452.212398	886.390971	443.699124	885.406955	443.207116	4
15	1848.592798	924.800037	1831.566249	916.286763	1830.582233	915.794755	E	***743.386871***	372.197074	726.360322	363.683799	725.376306	363.191791	3
16	2287.818124	1144.412700	2270.791575	1135.899426	2269.807559	1135.407418	Q	***614.344278***	307.675777	597.317729	299.162503			2
17							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.5	2460.922531	0.007901	CCYDGACVNNDETCEQR

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

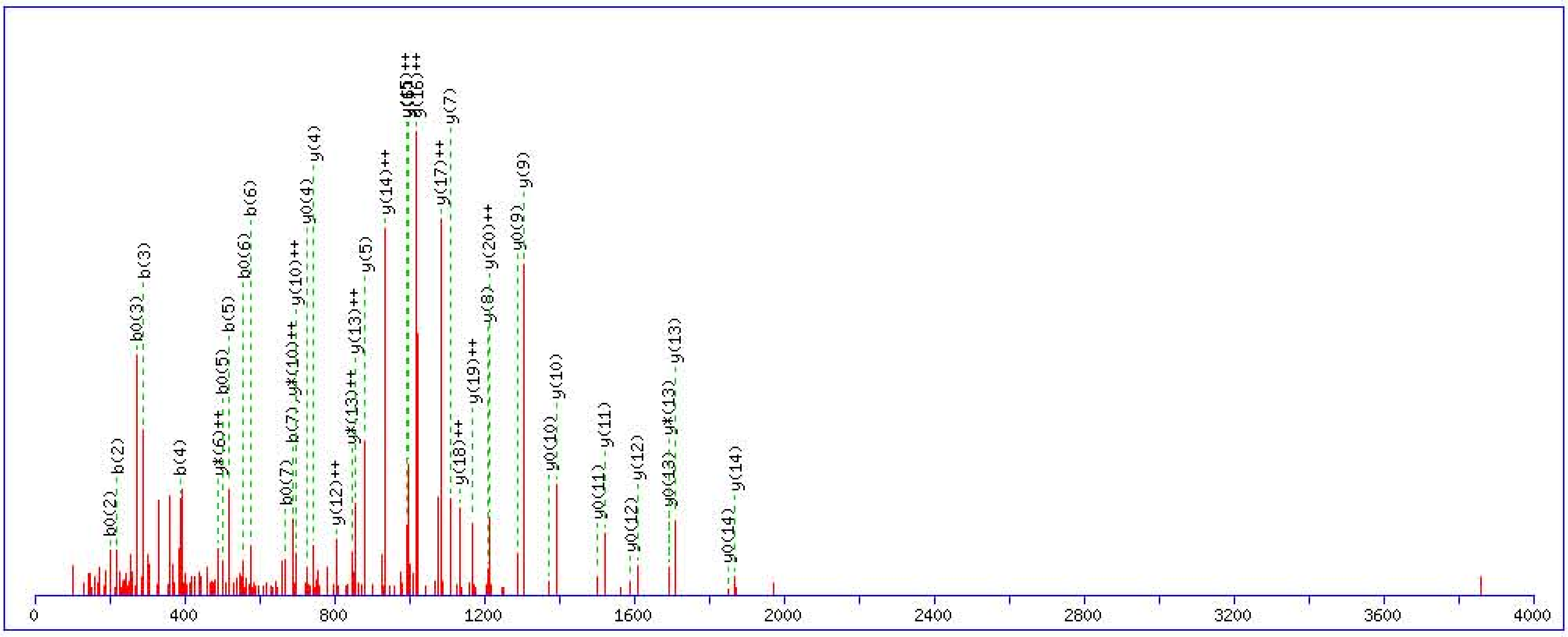
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MSAVEGICTSESPVIDHQGTK**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

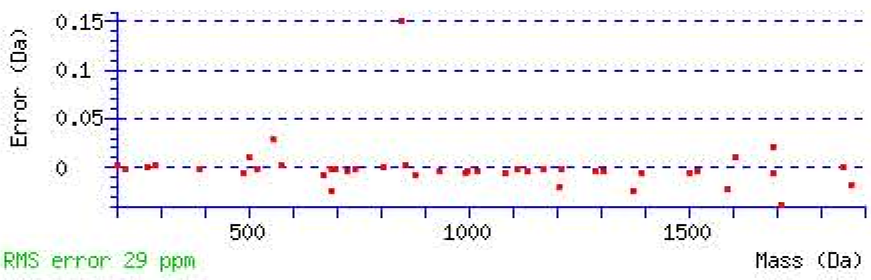
Match to Query 49061: 2556.195702 from(853.072510,3+) rtinseconds(1964) index(31596)
Title: Locus:1.1.1.3347.26 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

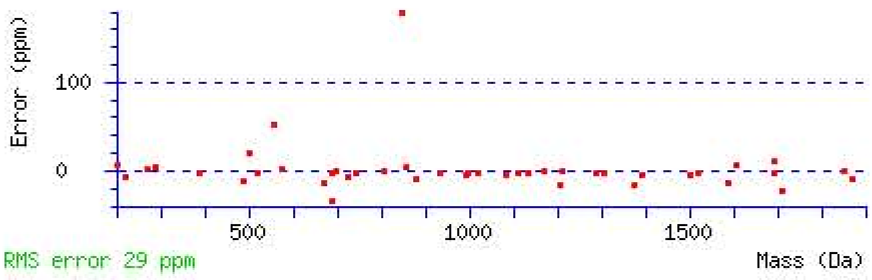


```
Monoisotopic mass of neutral peptide Mr(calc): 2556.202240
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18    : Biotin:Thermo-21345 (Q)
Ions Score: 83  Expect: 2.2e-008
Matches : 43/202 fragment ions using 65 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	132.047761	66.527518					M							21
2	**219.079789**	110.043532			201.069224	101.038250	S	2426.169024	1213.588150	2409.142475	1205.074875	2408.158459	1204.582867	20
3	**290.116903**	145.562089			272.106338	136.556807	A	2339.136996	1170.072136	2322.110447	1161.558861	2321.126431	1161.066853	19
4	**389.185317**	195.096296			371.174752	186.091014	V	2268.099882	1134.553579	2251.073333	1126.040304	2250.089317	1125.548296	18
5	**518.227910**	259.617593			500.217345	250.612311	E	2169.031468	1085.019372	2152.004919	1076.506097	2151.020903	1076.014089	17
6	**575.249374**	288.128325			557.238809	279.123043	G	2039.988875	1020.498076	2022.962326	1011.984801	2021.978310	1011.492793	16
7	**688.333438**	344.670357			670.322873	335.665075	I	1982.967411	991.987343	1965.940862	983.474069	1964.956846	982.982061	15
8	848.364087	424.685682			830.353522	415.680399	C	***1869.883347***	935.445312	1852.856798	926.932037	1851.872782	926.440029	14
9	949.411766	475.209521			931.401201	466.204239	T	***1709.852698***	855.429987	1692.826149	846.916713	1691.842133	846.424704	13
10	1036.443794	518.725535			1018.433229	509.720253	S	***1608.805019***	804.906147	1591.778470	796.392873	1590.794454	795.900865	12
11	1165.486387	583.246832			1147.475822	574.241549	E	***1521.772991***	761.390133	1504.746442	752.876859	1503.762426	752.384851	11
12	1252.518415	626.762846			1234.507850	617.757563	S	***1392.730398***	696.868837	1375.703849	688.355563	1374.719833	687.863554	10
13	1349.571179	675.289228			1331.560614	666.283945	P	***1305.698370***	653.352823	1288.671821	644.839548	1287.687805	644.347540	9
14	1448.639593	724.823435			1430.629028	715.818152	V	***1208.645606***	604.826441	1191.619057	596.313166	1190.635041	595.821158	8
15	1561.723657	781.365467			1543.713092	772.360184	I	***1109.577192***	555.292234	1092.550643	546.778959	1091.566627	546.286951	7
16	1676.750600	838.878938			1658.740035	829.873656	D	***996.493128***	498.750202	979.466579	490.236927	978.482563	489.744919	6
17	1813.809512	907.408394			1795.798947	898.403112	H	***881.466185***	441.236730	864.439636	432.723456	863.455620	432.231448	5
18	2253.034838	1127.021057	2236.008289	1118.507782	2235.024273	1118.015774	Q	***744.407273***	372.707274	727.380724	364.194000	726.396708	363.701992	4
19	2310.056302	1155.531789	2293.029753	1147.018514	2292.045737	1146.526506	G	305.181947	153.094611	288.155398	144.581337	287.171382	144.089329	3
20	2411.103981	1206.055628	2394.077432	1197.542354	2393.093416	1197.050346	T	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	2
21							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 29 ppm



RMS error 29 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
82.6	2556.202240	-0.006538	MSAVEGICTSESPVIDHQGTK
1.0	2556.161118	0.034584	EAADMILVDDDFQTIMSAIEEGK

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

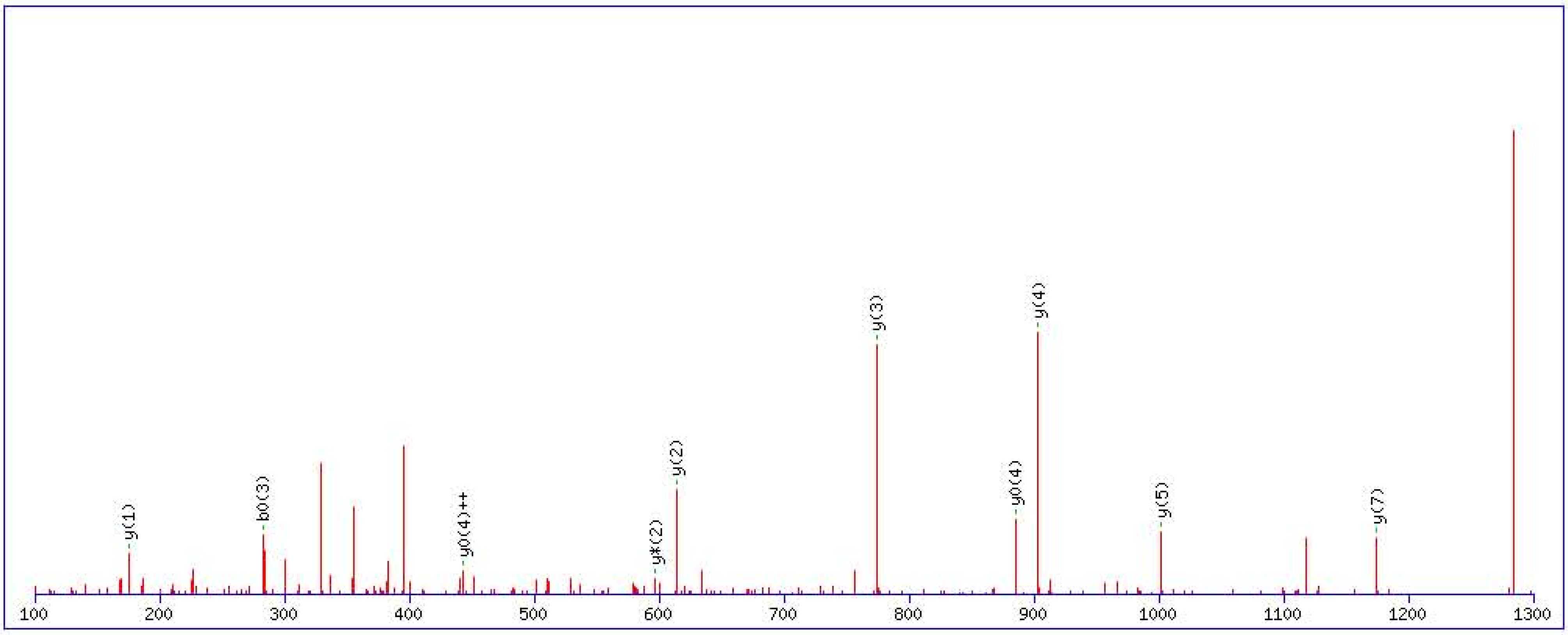
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QGDVECQR**
Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

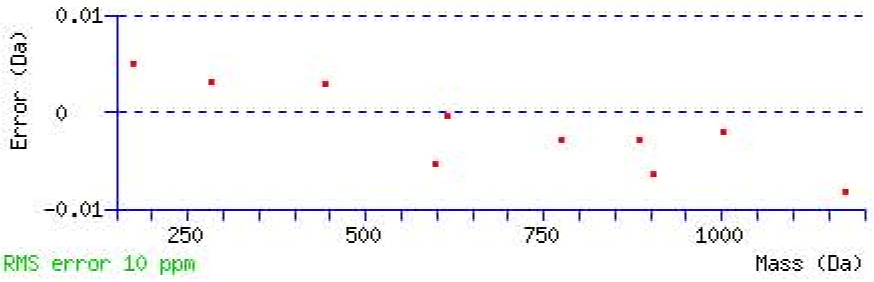
Match to Query 20386: 1301.579668 from(651.797110,2+) rtinseconds(1375) index(15070)
Title: Locus:1.1.1.3044.6 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

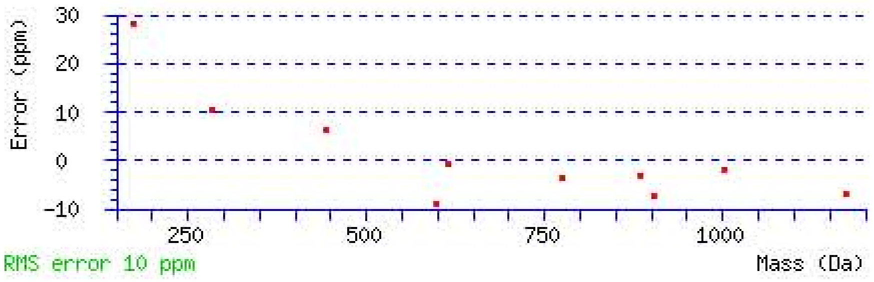
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1301.585648
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 52 **Expect:** 2.7e-005
Matches : 10/74 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	129.065854	65.036565	112.039305	56.523291			Q							8
2	186.087318	93.547297	169.060769	85.034023			G	***1174.534341***	587.770809	1157.507792	579.257534	1156.523776	578.765526	7
3	301.114261	151.060768	284.087712	142.547494	283.103696	142.055486	D	1117.512877	559.260077	1100.486328	550.746802	1099.502312	550.254794	6
4	400.182675	200.594976	383.156126	192.081701	382.172110	191.589693	V	***1002.485934***	501.746605	985.459385	493.233331	984.475369	492.741323	5
5	529.225268	265.116272	512.198719	256.602998	511.214703	256.110990	E	***903.417520***	452.212398	886.390971	443.699124	885.406955	443.207116	4
6	689.255917	345.131597	672.229368	336.618322	671.245352	336.126314	C	***774.374927***	387.691102	757.348378	379.177827			3
7	1128.481243	564.744260	1111.454694	556.230985	1110.470678	555.738977	Q	***614.344278***	307.675777	597.317729	299.162503			2
8							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of QGDVECQR
(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	1301.585648	-0.005980	QGDVECQR
8.1	1301.584747	-0.005079	QESPSQENIDR
7.1	1301.584763	-0.005095	KATEDAEGGDGPR
4.5	1301.560471	0.019197	QEPRCEAPCR
2.1	1301.567001	0.012667	RDQCEAPSDPK

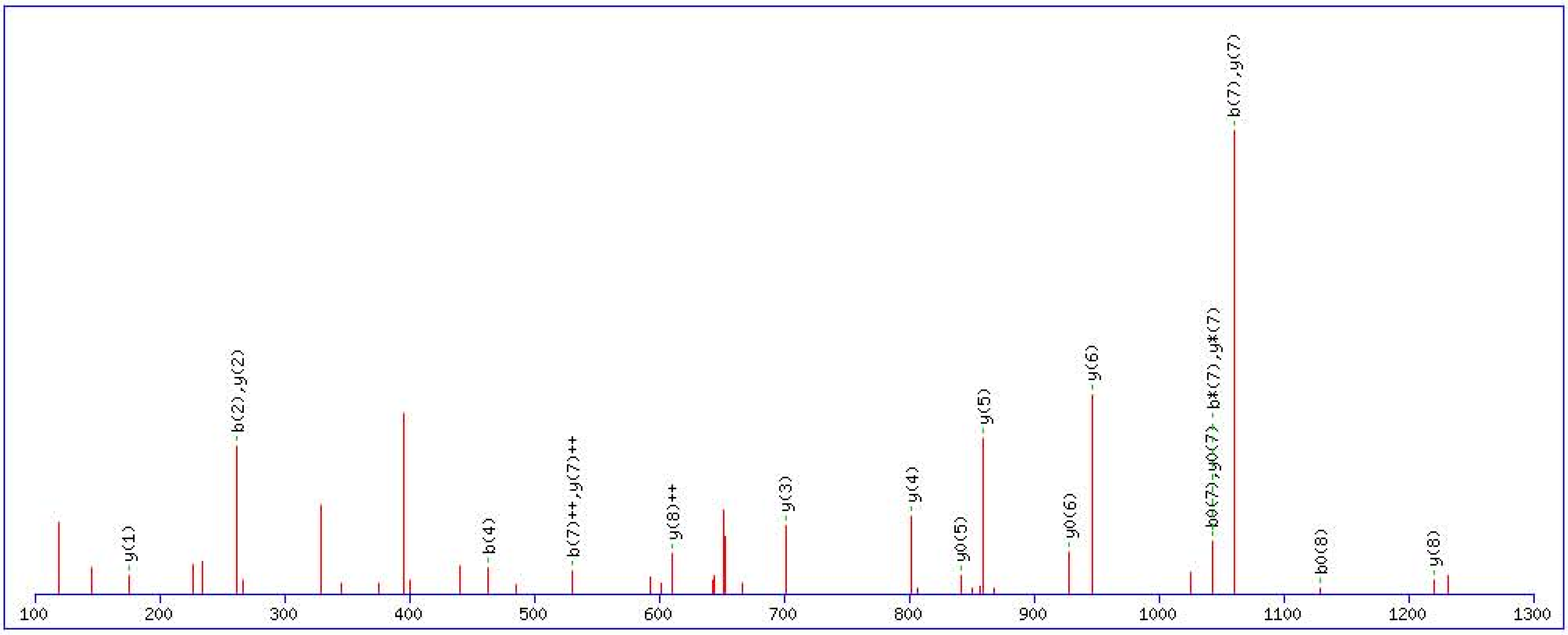
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TCNSGTQSR**
Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

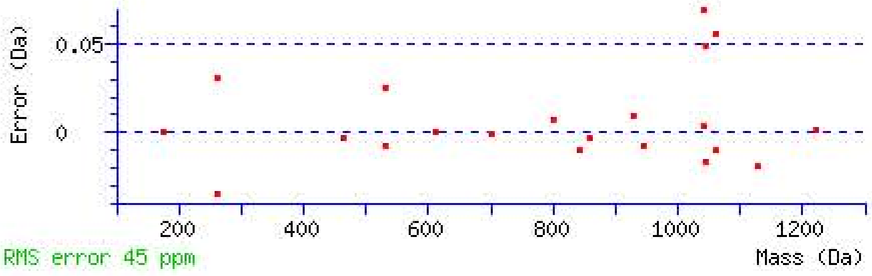
Match to Query 20677: 1320.585268 from(661.299910,2+) rtinseconds(1132) index(14125)
Title: Locus:1.1.1.2959.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

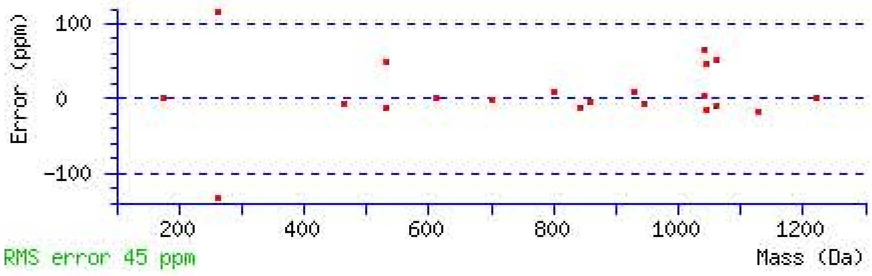
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1320.591461
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 55 **Expect:** 1.8e-005
Matches : 21/90 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	102.054955	51.531116			84.044390	42.525833	T							9
2	**262.085604**	131.546440			244.075039	122.541158	C	***1220.551053***	610.779165	1203.524504	602.265890	1202.540488	601.773882	8
3	376.128531	188.567904	359.101982	180.054629	358.117966	179.562621	N	***1060.520404***	530.763840	1043.493855	522.250566	1042.509839	521.758558	7
4	**463.160559**	232.083917	446.134010	223.570643	445.149994	223.078635	S	***946.477477***	473.742377	929.450928	465.229102	928.466912	464.737094	6
5	520.182023	260.594650	503.155474	252.081375	502.171458	251.589367	G	***859.445449***	430.226363	842.418900	421.713088	841.434884	421.221080	5
6	621.229702	311.118489	604.203153	302.605215	603.219137	302.113207	T	***802.423985***	401.715631	785.397436	393.202356	784.413420	392.710348	4
7	**1060.455028**	530.731152	1043.428479	522.217878	1042.444463	521.725870	Q	***701.376306***	351.191791	684.349757	342.678517	683.365741	342.186509	3
8	1147.487056	574.247166	1130.460507	565.733892	1129.476491	565.241884	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TCNSGTQSR
(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	1320.591461	-0.006193	TCNSGTQSR
11.9	1320.599289	-0.014021	NELPMHHNSSR
4.2	1320.584045	0.001223	SQGCSREASPSR
3.0	1320.597946	-0.012678	LMNTNDLEESR
2.1	1320.570984	0.014284	MNWFGSNFFR

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

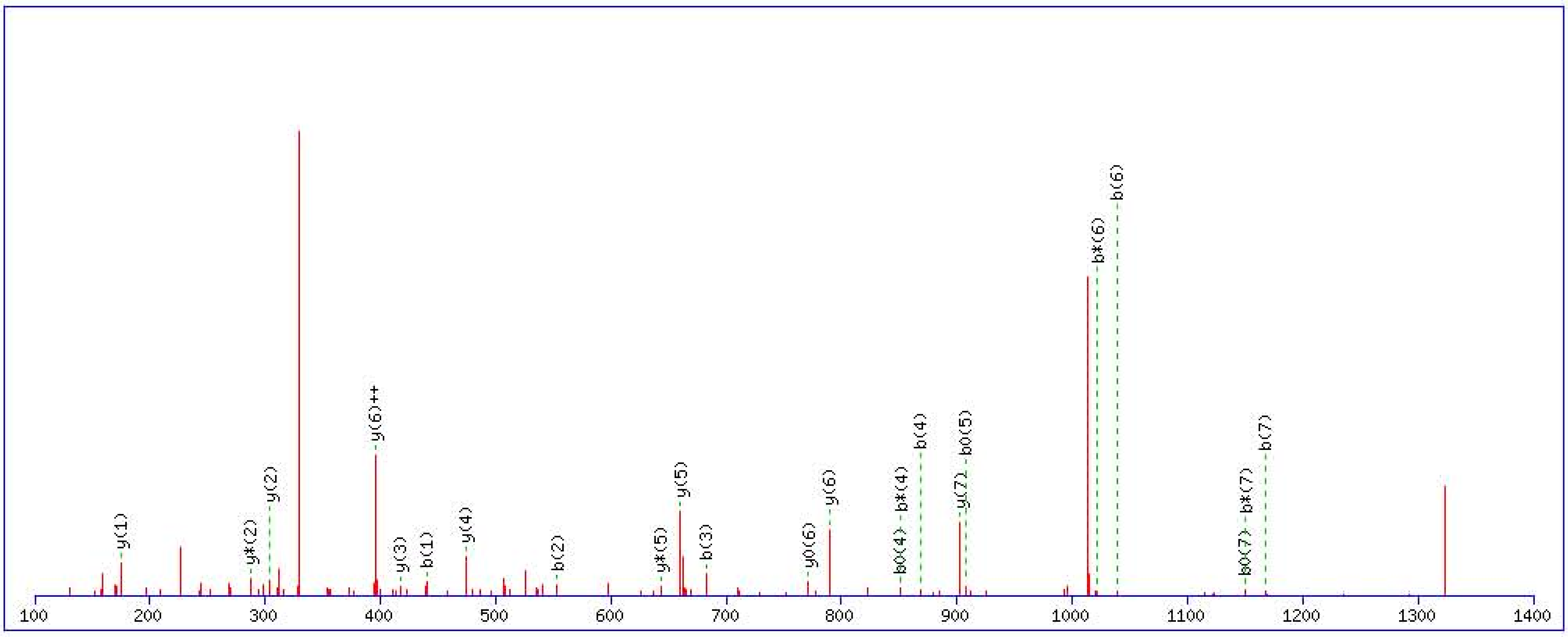
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLEWGLER**
Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

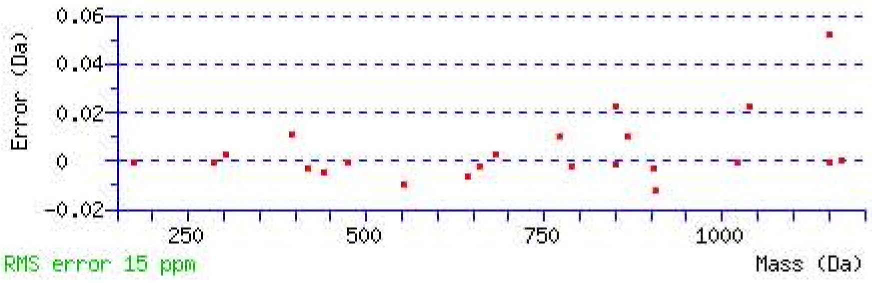
Match to Query 21145: 1340.687588 from(671.351070,2+) rtinseconds(2257) index(33403)
Title: Locus:1.1.1.3449.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

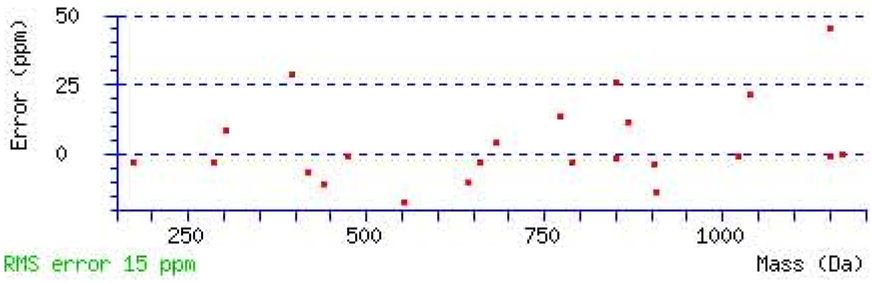
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1340.691071
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 27   Expect: 0.032
Matches : 23/78 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	**440.232602**	220.619939	423.206053	212.106664			**Q**							8
2	**553.316666**	277.161971	536.290117	268.648697			**L**	***902.473043***	451.740160	885.446494	443.226885	884.462478	442.734877	7
3	**682.359259**	341.683268	665.332710	333.169993	664.348694	332.677985	**E**	***789.388979***	395.198128	772.362430	386.684853	771.378414	386.192845	6
4	**868.438572**	434.722924	851.412023	426.209650	850.428007	425.717642	**W**	***660.346386***	330.676831	643.319837	322.163556	642.335821	321.671548	5
5	925.460036	463.233656	908.433487	454.720382	907.449471	454.228374	**G**	***474.267073***	237.637174	457.240524	229.123900	456.256508	228.631892	4
6	**1038.544100**	519.775688	1021.517551	511.262414	1020.533535	510.770406	**L**	***417.245609***	209.126442	400.219060	200.613168	399.235044	200.121160	3
7	**1167.586693**	584.296985	1150.560144	575.783710	1149.576128	575.291702	**E**	***304.161545***	152.584410	287.134996	144.071136	286.150980	143.579128	2
8							**R**	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of QLEWGLER
(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	1340.691071	-0.003483	QLEWGLER
10.2	1340.668427	0.019161	SELGGTDLEKHR
9.5	1340.675812	0.011776	QLQDELER
7.9	1340.675812	0.011776	LQEGEEGIR
4.9	1340.687027	0.000561	QLREEAER
3.9	1340.704834	-0.017246	LTLNDSSVTVHR
3.1	1340.694916	-0.007328	RNGLEPVTYHR
3.1	1340.675812	0.011776	QVELQEER
2.8	1340.687042	0.000546	QINDSANLR
2.4	1340.687042	0.000546	ALGSAAADAQR

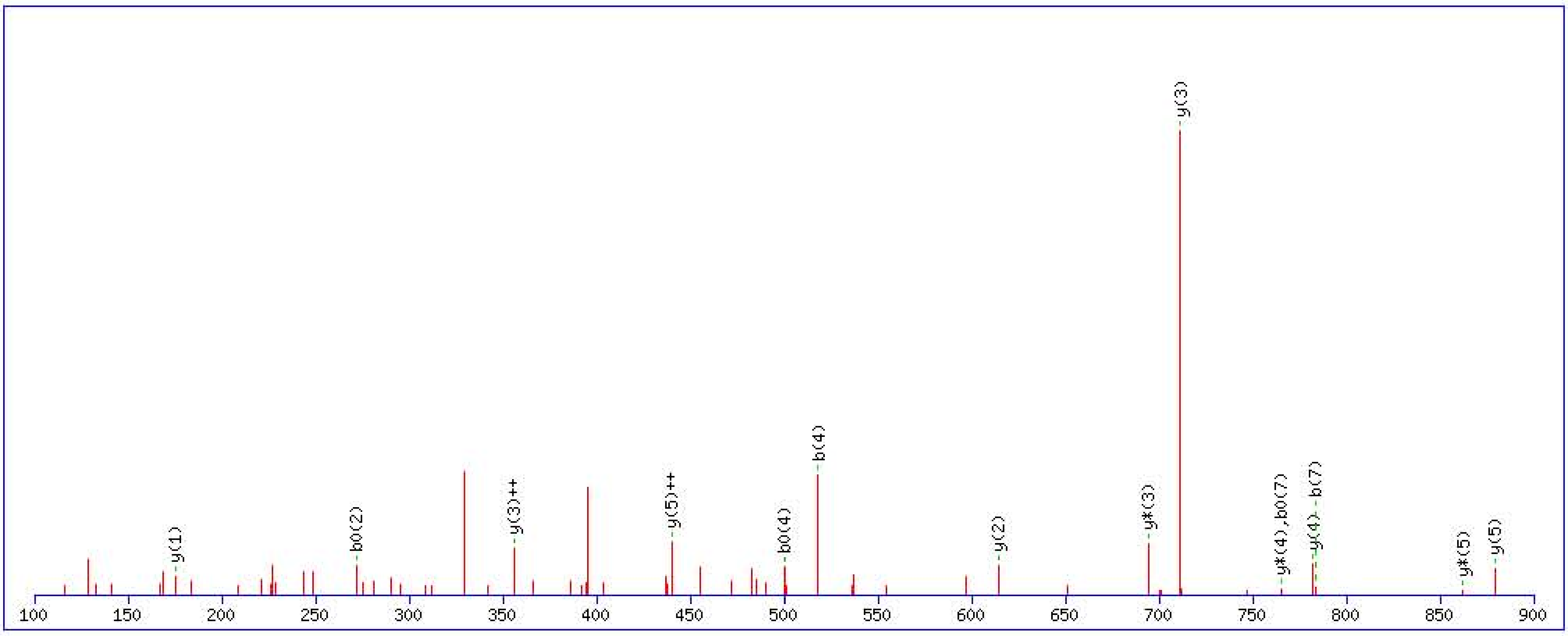
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of ECNNPAPQR
Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

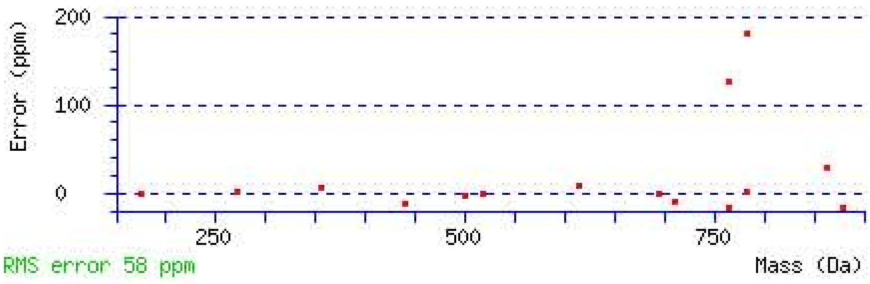
Match to Query 23508: 1395.637422 from(466.219750,3+) rtinseconds(1333) index(14883)
Title: Locus:1.1.1.3030.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1395.638718
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.0043
Matches : 15/76 fragment ions using 23 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	130.049869	65.528572			112.039304	56.523290	E					9
2	290.080518	145.543897			272.069953	136.538615	C	1267.603423	634.305350	1250.576874	625.792075	8
3	404.123445	202.565361	387.096896	194.052086	386.112880	193.560078	N	1107.572774	554.290025	1090.546225	545.776751	7
4	**518.166372**	259.586824	501.139823	251.073550	500.155807	250.581542	N	993.529847	497.268562	976.503298	488.755287	6
5	615.219136	308.113206	598.192587	299.599932	597.208571	299.107924	P	***879.486920***	440.247098	862.460371	431.733824	5
6	686.256250	343.631763	669.229701	335.118489	668.245685	334.626481	A	***782.434156***	391.720716	765.407607	383.207442	4
7	**783.309014**	392.158145	766.282465	383.644871	765.298449	383.152863	P	***711.397042***	356.202159	694.370493	347.688885	3
8	1222.534340	611.770808	1205.507791	603.257534	1204.523775	602.765526	Q	***614.344278***	307.675777	597.317729	299.162503	2
9							R	***175.118952***	88.063114	158.092403	79.549839	1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.4	1395.638718	-0.001296	ECNNPAPQR
2.0	1395.631332	0.006090	HLQENTQSHMR
1.2	1395.627502	0.009920	QHAGMFSISQMK
1.0	1395.645264	-0.007842	LNKDFTCDVER
0.0	1395.645264	-0.007842	VTEQCFNTLER

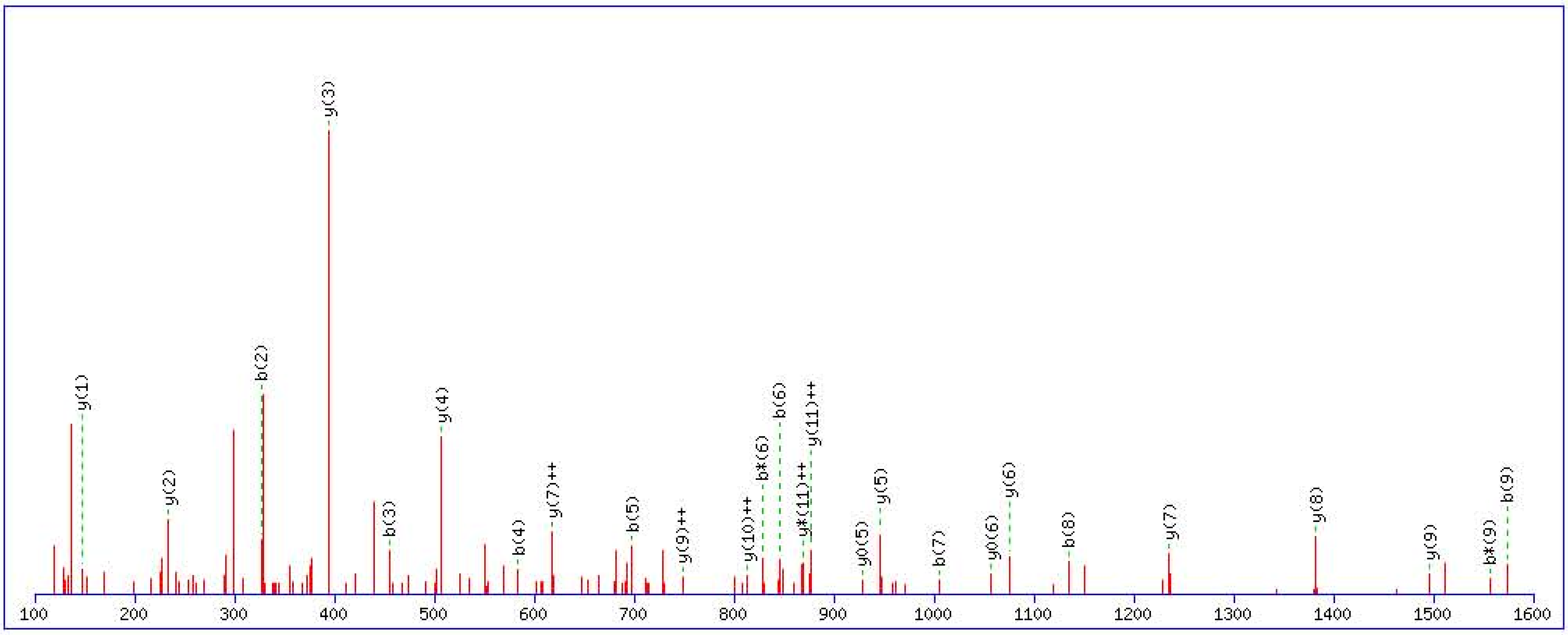
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YYQENFCEQICSK**
Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

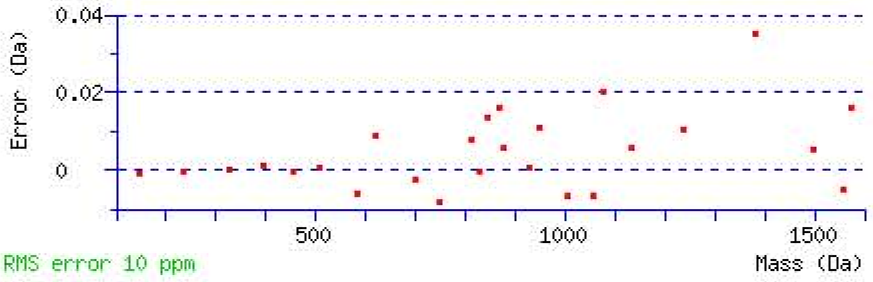
Match to Query 41286: 2078.885772 from(693.969200,3+) rtinseconds(2067) index(32264)
Title: Locus:1.1.1.3383.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

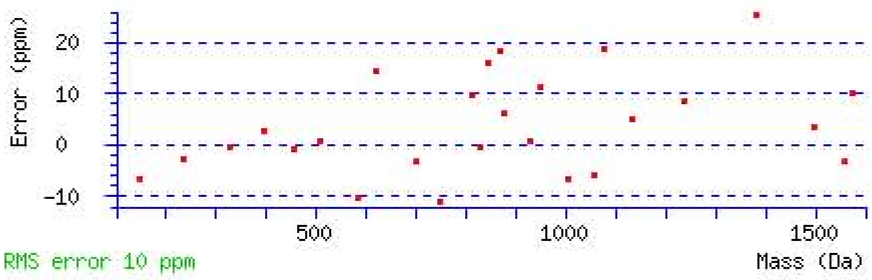
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2078.889984
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.00014
Matches : 26/132 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	164.070605	82.538940					Y							13
2	***327.133934***	164.070605					Y	1916.833954	958.920615	1899.807405	950.407341	1898.823389	949.915333	12
3	***455.192512***	228.099894	438.165963	219.586620			Q	1753.770625	877.388951	1736.744076	868.875676	1735.760060	868.383668	11
4	***584.235105***	292.621191	567.208556	284.107916	566.224540	283.615908	E	1625.712047	813.359662	1608.685498	804.846387	1607.701482	804.354379	10
5	***698.278032***	349.642654	681.251483	341.129380	680.267467	340.637372	N	***1496.669454***	748.838365	1479.642905	740.325091	1478.658889	739.833083	9
6	***845.346446***	423.176861	828.319897	414.663587	827.335881	414.171579	F	***1382.626527***	691.816902	1365.599978	683.303627	1364.615962	682.811619	8
7	***1005.377095***	503.192186	988.350546	494.678911	987.366530	494.186903	C	***1235.558113***	618.282695	1218.531564	609.769420	1217.547548	609.277412	7
8	***1134.419688***	567.713482	1117.393139	559.200208	1116.409123	558.708200	E	***1075.527464***	538.267370	1058.500915	529.754096	1057.516899	529.262088	6
9	***1573.645014***	787.326145	1556.618465	778.812871	1555.634449	778.320863	Q	***946.484871***	473.746074	929.458322	465.232799	928.474306	464.740791	5
10	1686.729078	843.868177	1669.702529	835.354903	1668.718513	834.862895	I	***507.259545***	254.133411	490.232996	245.620136	489.248980	245.128128	4
11	1846.759727	923.883502	1829.733178	915.370227	1828.749162	914.878219	C	***394.175481***	197.591379	377.148932	189.078104	376.164916	188.586096	3
12	1933.791755	967.399516	1916.765206	958.886241	1915.781190	958.394233	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 YYQENFCEQICSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.2	2078.889984	-0.004212	YYQENFCEQICSK

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

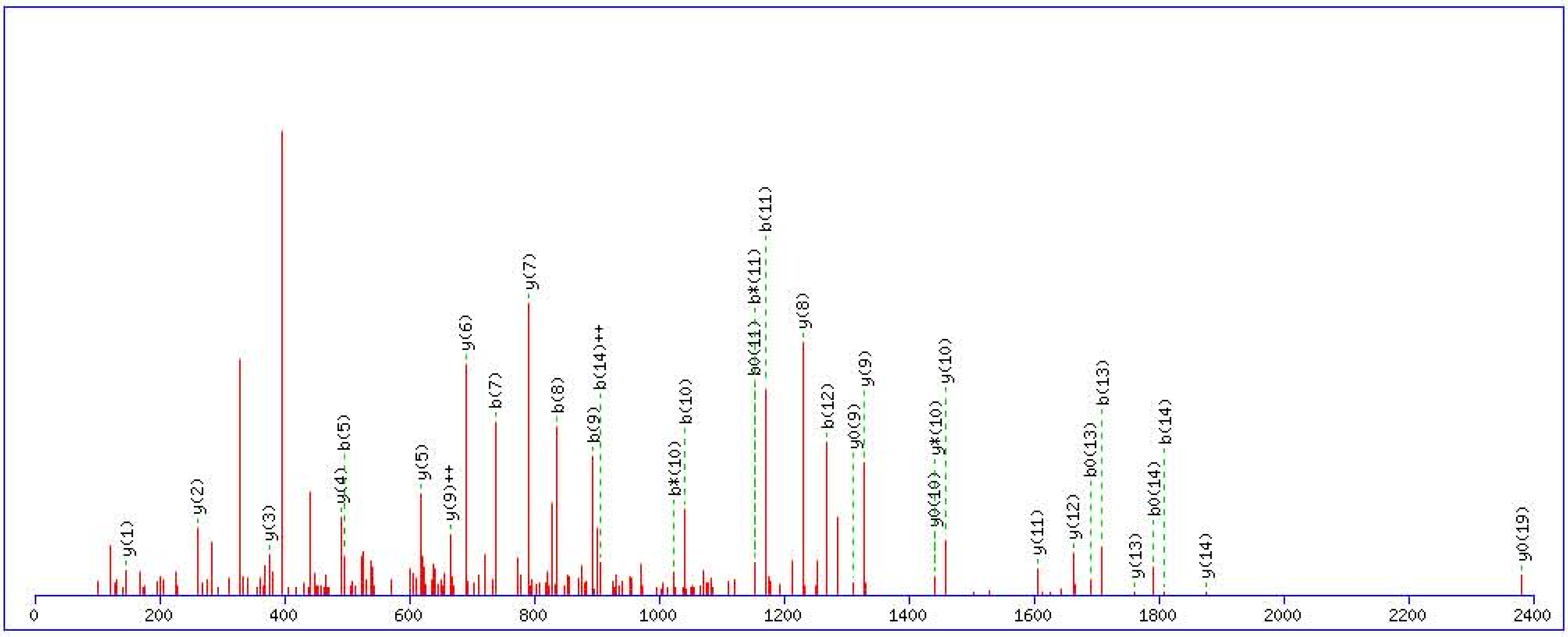
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPANLENVGFEVQTAEDDLK**
Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

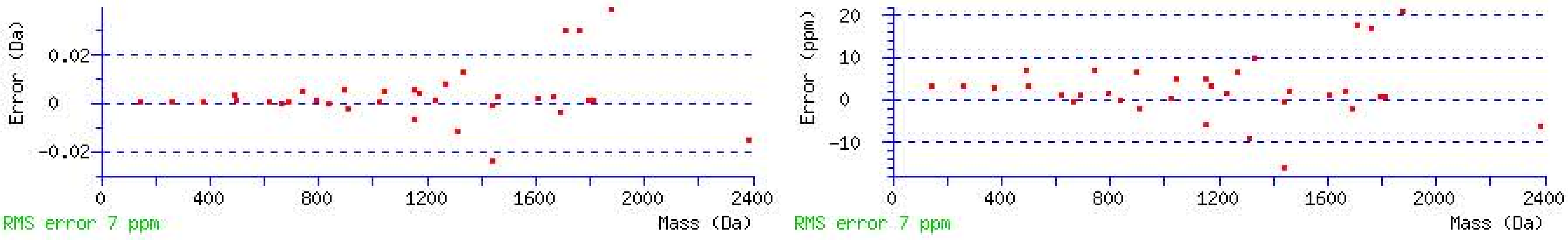
Match to Query 48501: 2498.246292 from(833.756040,3+) rtinseconds(2666) index(22707)
Title: Locus:1.1.1.3493.23 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 2498.236282
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 91  Expect: 2.3e-008
Matches : 34/208 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	100.075690	50.541483					V							20
2	197.128454	99.067865					P	2400.175154	1200.591215	2383.148605	1192.077940	2382.164589	1191.585932	19
3	268.165568	134.586422					A	2303.122390	1152.064833	2286.095841	1143.551558	2285.111825	1143.059550	18
4	382.208495	191.607885	365.181946	183.094611			N	2232.085276	1116.546276	2215.058727	1108.033001	2214.074711	1107.540993	17
5	**495.292559**	248.149917	478.266010	239.636643			L	2118.042349	1059.524812	2101.015800	1051.011538	2100.031784	1050.519530	16
6	624.335152	312.671214	607.308603	304.157940	606.324587	303.665932	E	2004.958285	1002.982781	1987.931736	994.469506	1986.947720	993.977498	15
7	**738.378079**	369.692678	721.351530	361.179403	720.367514	360.687395	N	***1875.915692***	938.461484	1858.889143	929.948210	1857.905127	929.456202	14
8	**837.446493**	419.226885	820.419944	410.713610	819.435928	410.221602	V	***1761.872765***	881.440021	1744.846216	872.926746	1743.862200	872.434738	13
9	**894.467957**	447.737617	877.441408	439.224342	876.457392	438.732334	G	***1662.804351***	831.905814	1645.777802	823.392539	1644.793786	822.900531	12
10	**1041.536371**	521.271824	1024.509822	512.758549	1023.525806	512.266541	F	***1605.782887***	803.395082	1588.756338	794.881807	1587.772322	794.389799	11
11	**1170.578964**	585.793120	1153.552415	577.279846	1152.568399	576.787838	E	***1458.714473***	729.860875	1441.687924	721.347600	1440.703908	720.855592	10
12	**1269.647378**	635.327327	1252.620829	626.814053	1251.636813	626.322045	V	***1329.671880***	665.339578	1312.645331	656.826304	1311.661315	656.334296	9
13	**1708.872704**	854.939990	1691.846155	846.426716	1690.862139	845.934708	Q	***1230.603466***	615.805371	1213.576917	607.292097	1212.592901	606.800089	8
14	**1809.920383**	905.463830	1792.893834	896.950555	1791.909818	896.458547	T	***791.378140***	396.192708	774.351591	387.679434	773.367575	387.187426	7
15	1880.957497	940.982387	1863.930948	932.469112	1862.946932	931.977104	A	***690.330461***	345.668869	673.303912	337.155594	672.319896	336.663586	6
16	2010.000090	1005.503683	1992.973541	996.990409	1991.989525	996.498401	E	***619.293347***	310.150312	602.266798	301.637037	601.282782	301.145029	5
17	2125.027033	1063.017154	2108.000484	1054.503880	2107.016468	1054.011872	D	***490.250754***	245.629015	473.224205	237.115740	472.240189	236.623732	4
18	2240.053976	1120.530626	2223.027427	1112.017351	2222.043411	1111.525343	D	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	3
19	2353.138040	1177.072658	2336.111491	1168.559383	2335.127475	1168.067375	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 VPANLENVGFEVQTAEDDLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
91.1	2498.236282	0.010010	VPANLENVGFEVQTAEDDLK

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

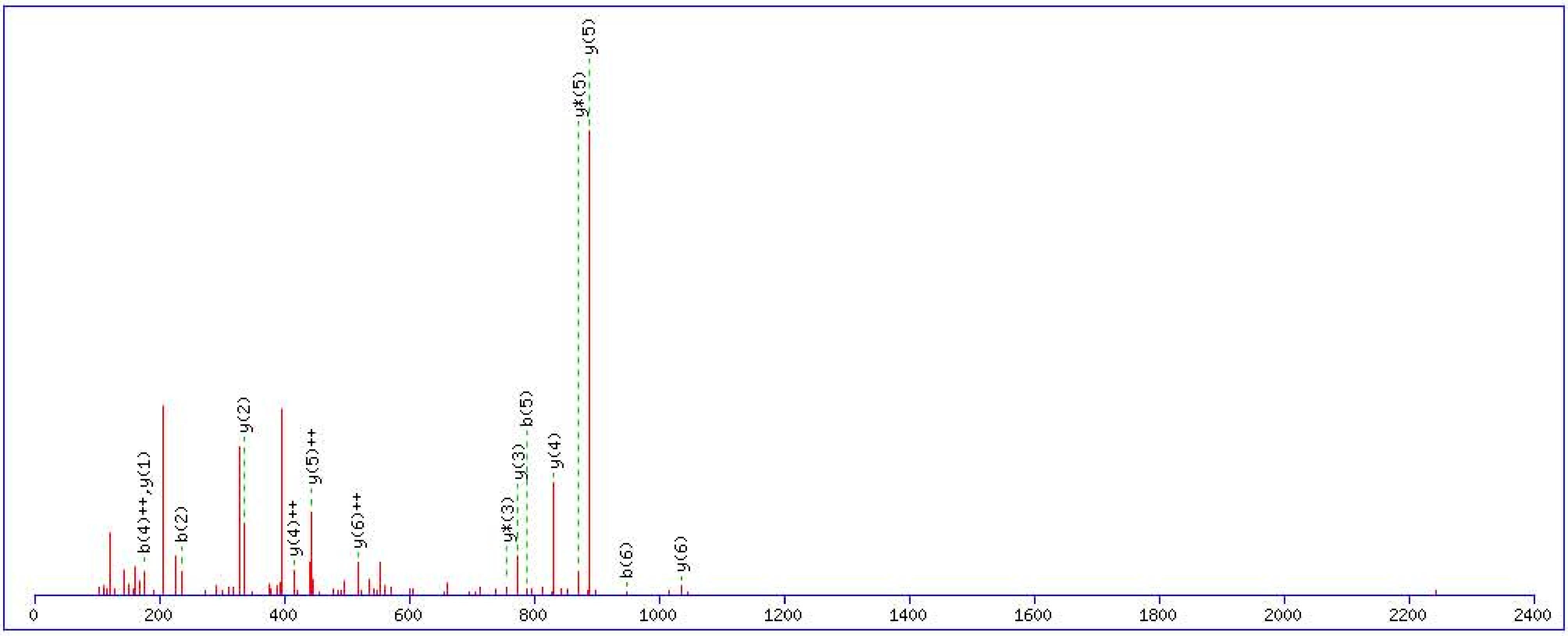
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

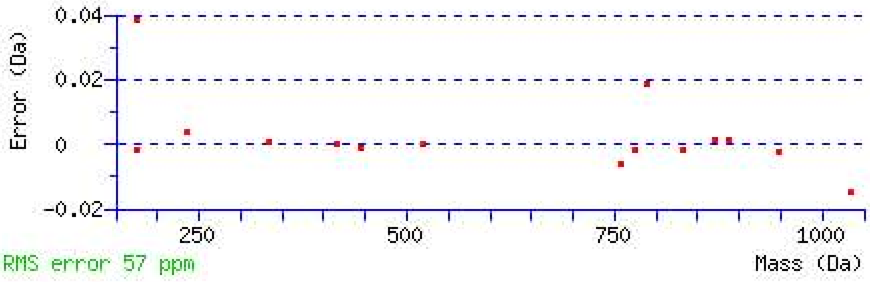
Match to Query 14863: 1121.508988 from(561.761770,2+) rtinseconds(1587) index(2517)
Title: Locus:1.1.1.3072.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

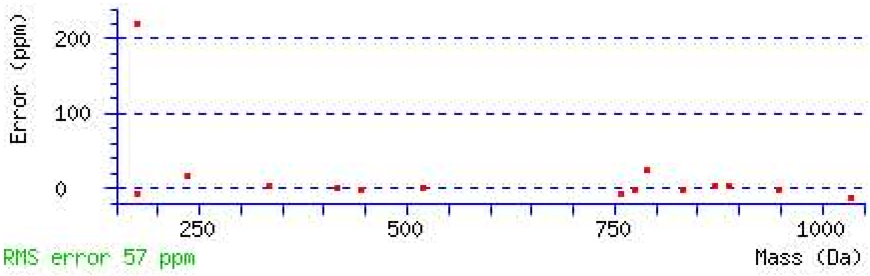
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1121.511032
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 25  Expect: 0.0071
Matches : 15/52 fragment ions using 36 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	88.039304	44.523290			70.028739	35.518008	S					7
2	**235.107718**	118.057497			217.097153	109.052214	F	***1035.486269***	518.246773	1018.459720	509.733498	6
3	292.129182	146.568229			274.118617	137.562946	G	***888.417855***	444.712566	871.391306	436.199291	5
4	349.150646	175.078961			331.140081	166.073678	G	***831.396391***	416.201834	814.369842	407.688559	4
5	**788.375972**	394.691624	771.349423	386.178350	770.365407	385.686342	Q	***774.374927***	387.691102	757.348378	379.177827	3
6	**948.406621**	474.706949	931.380072	466.193674	930.396056	465.701666	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 SFGGQCR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.0	1121.511032	-0.002044	SFGGQCR
2.1	1121.502274	0.006714	MSVEEQIDR
2.0	1121.494873	0.014115	SANTSPESSSR
1.1	1121.500259	0.008729	HPGFHQEDR

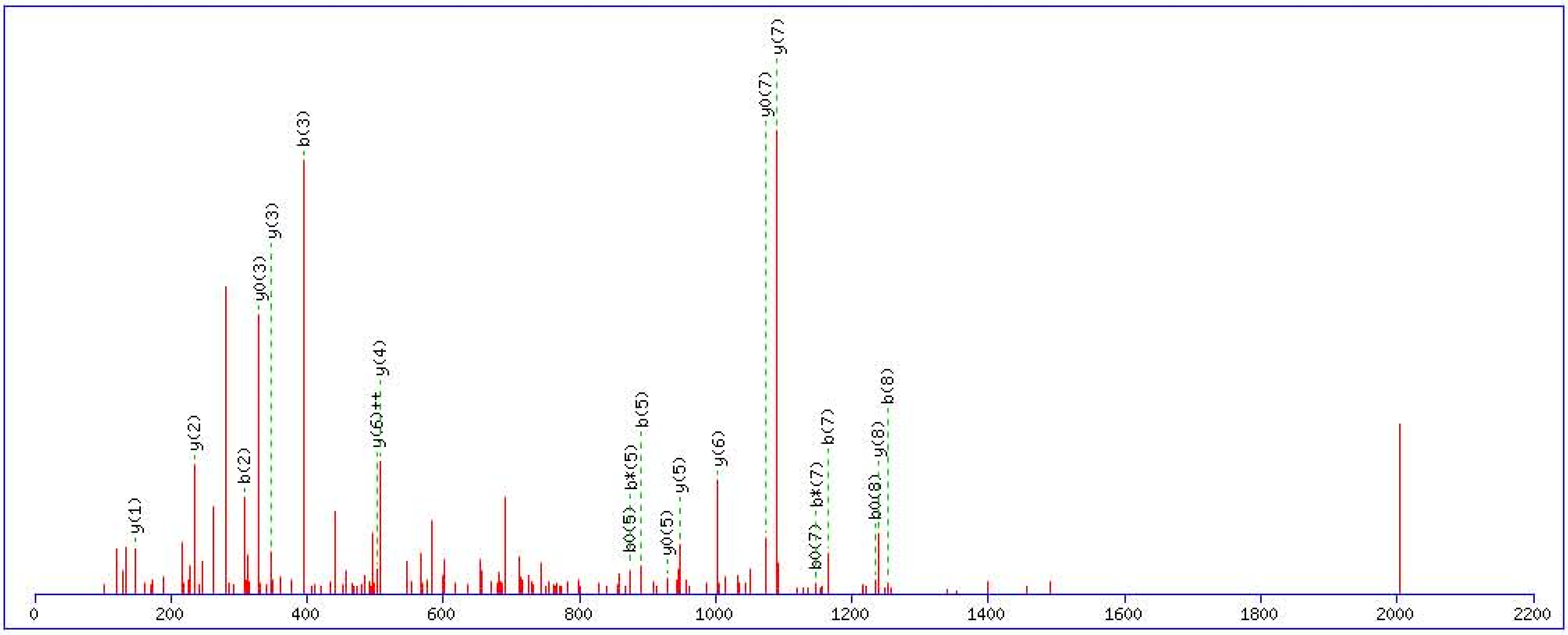
Mascot Search Results

Peptide View

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

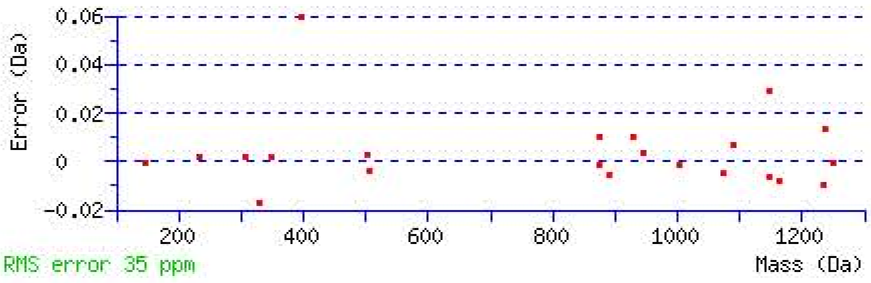
Match to Query 23527: 1396.630768 from(699.322660,2+) rtinseconds(1705) index(3239)
Title: Locus:1.1.1.3113.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

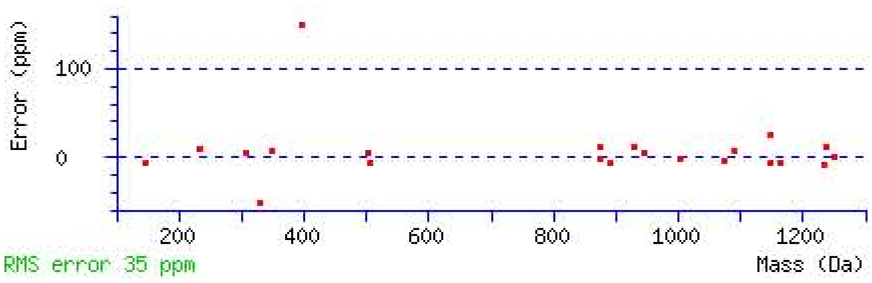
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1396.630157
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 40 **Expect:** 0.00096
Matches : 22/82 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	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
39.6	1396.630157	0.000611	CFSGQCISK
23.7	1396.629272	0.001496	QLSQAEATDFCK

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

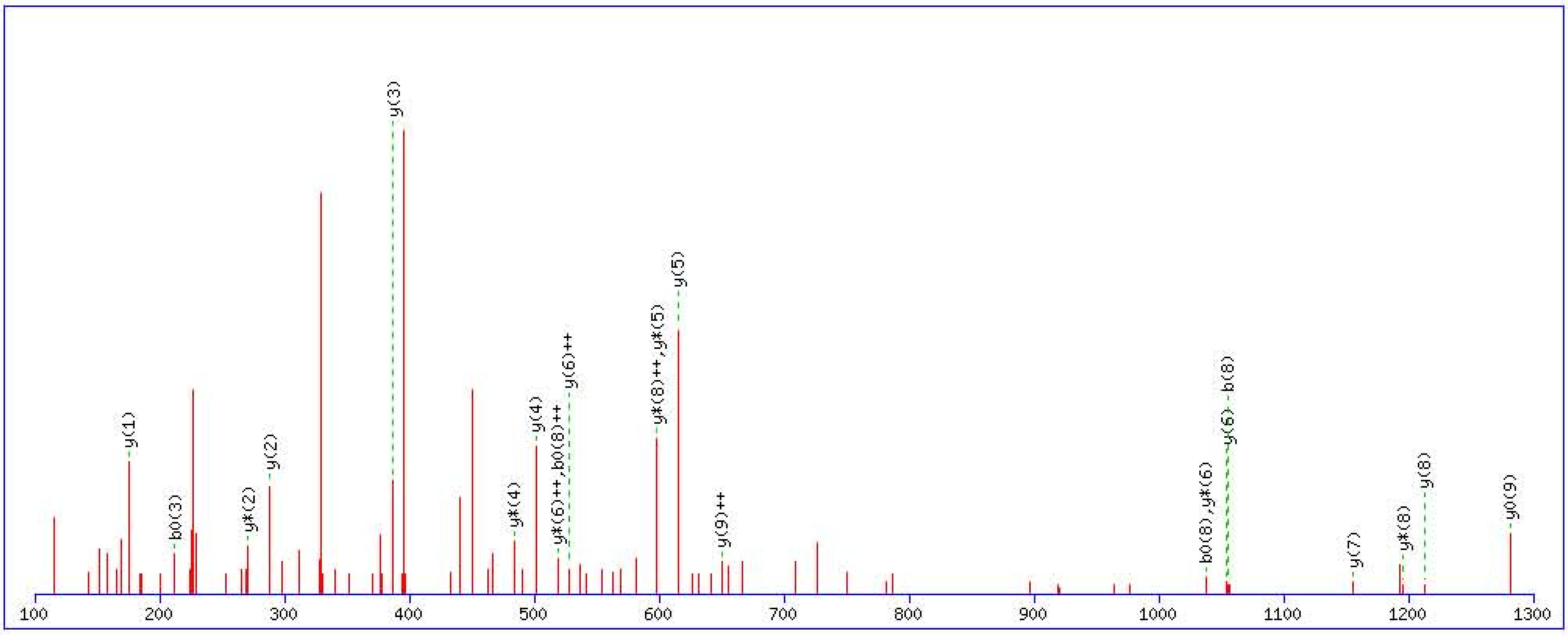
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

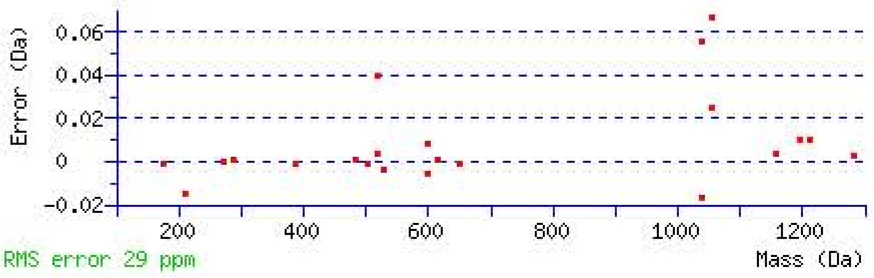
Match to Query 25637: 1440.747522 from(481.256450,3+) rtinseconds(1644) index(2889)
Title: Locus:1.1.1.3092.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

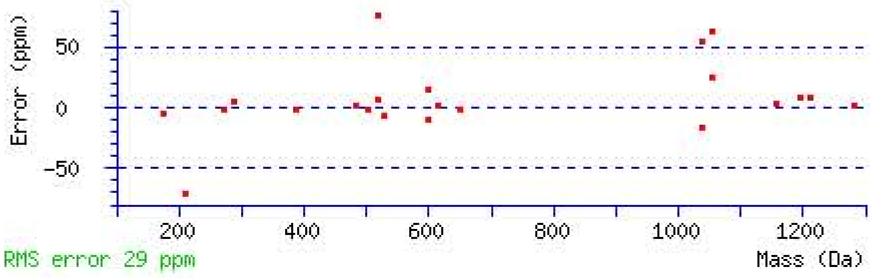
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1440.750717
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 32 **Expect:** 0.002
Matches : 22/94 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	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
31.6	1440.750717	-0.003195	AASGTQNNVLR
2.7	1440.750717	-0.003195	LDQLDASRGR
2.0	1440.754745	-0.007223	WEATQQVLR

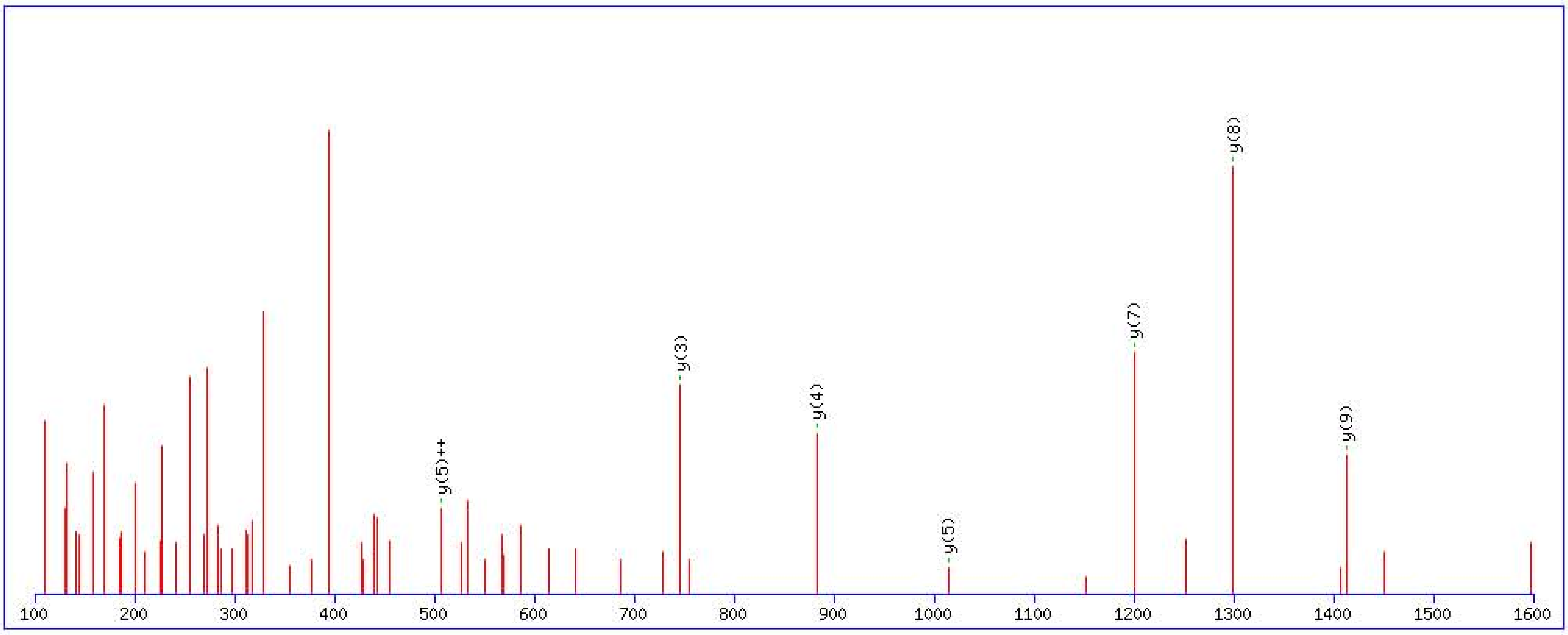
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

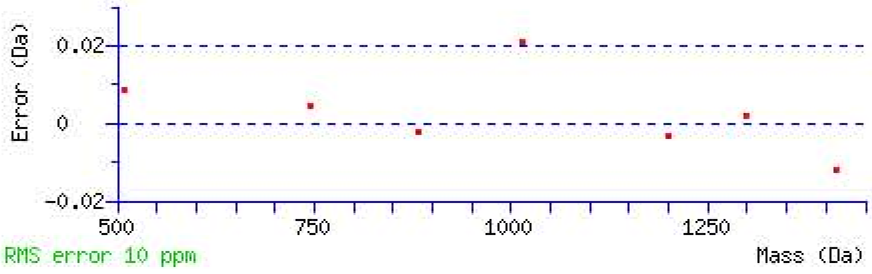
Match to Query 30508: 1597.751052 from(533.590960,3+) rtinseconds(1901) index(18330)
Title: Locus:1.1.1.3228.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

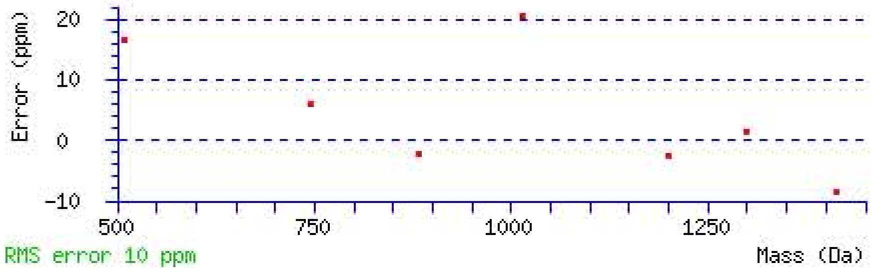
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 33  Expect: 0.0076
Matches : 7/74 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	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
33.0	1597.756744	-0.005692	WLVGEMHCQK

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

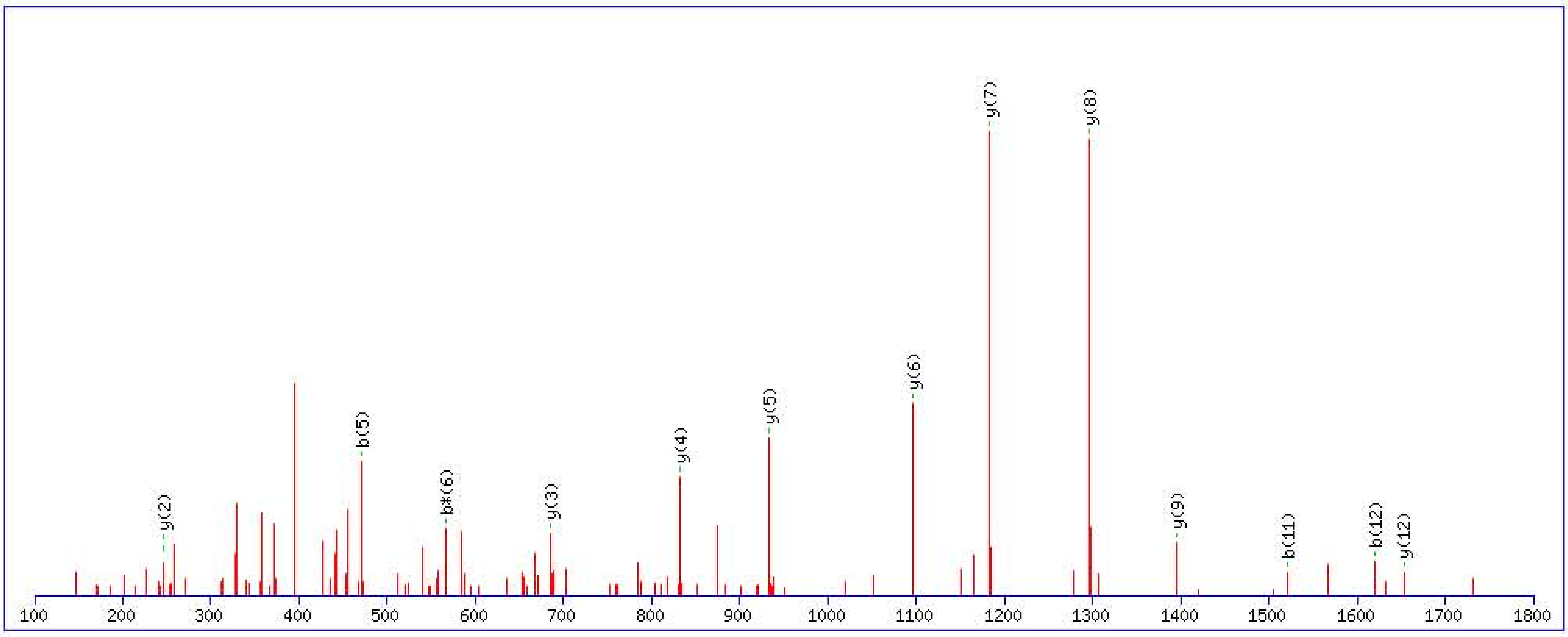
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

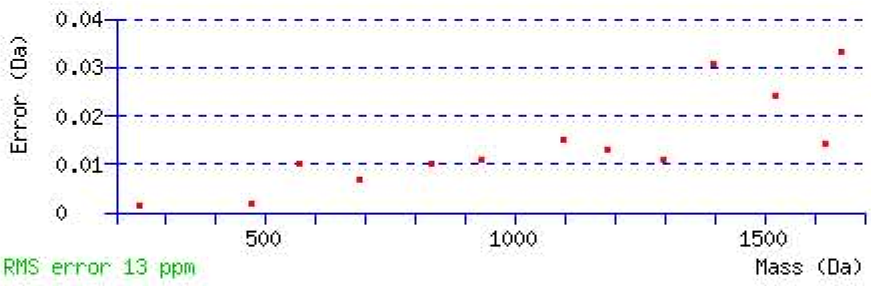
Match to Query 34973: 1765.964068 from(883.989310,2+) rtinseconds(2523) index(7677)
Title: Locus:1.1.1.3398.20 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

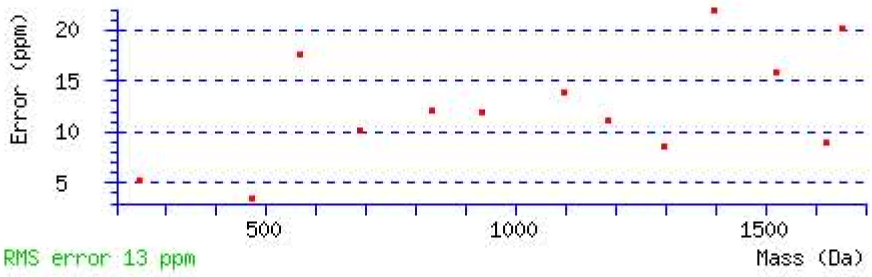
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1765.943680
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 79 **Expect:** 2.7e-007
Matches : 13/128 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	201.123368	101.065322			183.112803	92.060039	S	*1653.866891*	827.437084	1636.840342	818.923809	1635.856326	818.431801	12
3	258.144832	129.576054			240.134267	120.570771	G	1566.834863	783.921070	1549.808314	775.407795	1548.824298	774.915787	11
4	372.187759	186.597517	355.161210	178.084243	354.177194	177.592235	N	1509.813399	755.410338	1492.786850	746.897063	1491.802834	746.405055	10
5	**471.256173**	236.131724	454.229624	227.618450	453.245608	227.126442	V	*1395.770472*	698.388874	1378.743923	689.875600	1377.759907	689.383592	9
6	584.340237	292.673757	567.313688	284.160482	566.329672	283.668474	L	*1296.702058*	648.854667	1279.675509	640.341393	1278.691493	639.849385	8
7	671.372265	336.189771	654.345716	327.676496	653.361700	327.184488	S	*1183.617994*	592.312635	1166.591445	583.799361	1165.607429	583.307353	7
8	834.435594	417.721435	817.409045	409.208161	816.425029	408.716153	Y	*1096.585966*	548.796621	1079.559417	540.283347	1078.575401	539.791339	6
9	935.483273	468.245275	918.456724	459.732000	917.472708	459.239992	T	*933.522637*	467.264957	916.496088	458.751682	915.512072	458.259674	5
10	1082.551687	541.779482	1065.525138	533.266207	1064.541122	532.774199	F	*832.474958*	416.741117	815.448409	408.227843			4
11	**1521.777013**	761.392145	1504.750464	752.878870	1503.766448	752.386862	Q	*685.406544*	343.206910	668.379995	334.693636			3
12	**1620.845427**	810.926352	1603.818878	802.413077	1602.834862	801.921069	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 LSGNVLSYTFQVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
78.7	1765.943680	0.020388	LSGNVLSYTFQVK
8.3	1765.982544	-0.018476	SLQLDIIPASIPGSEVK
5.8	1765.950882	0.013186	VTGNVSKKTNYLVMGR
5.0	1765.973328	-0.009260	GKRPSQGCPSKIARPK
2.3	1765.987244	-0.023176	GNVDVALNMLRNILPK
1.7	1765.964767	-0.000699	IKEVEEKQPEVK

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

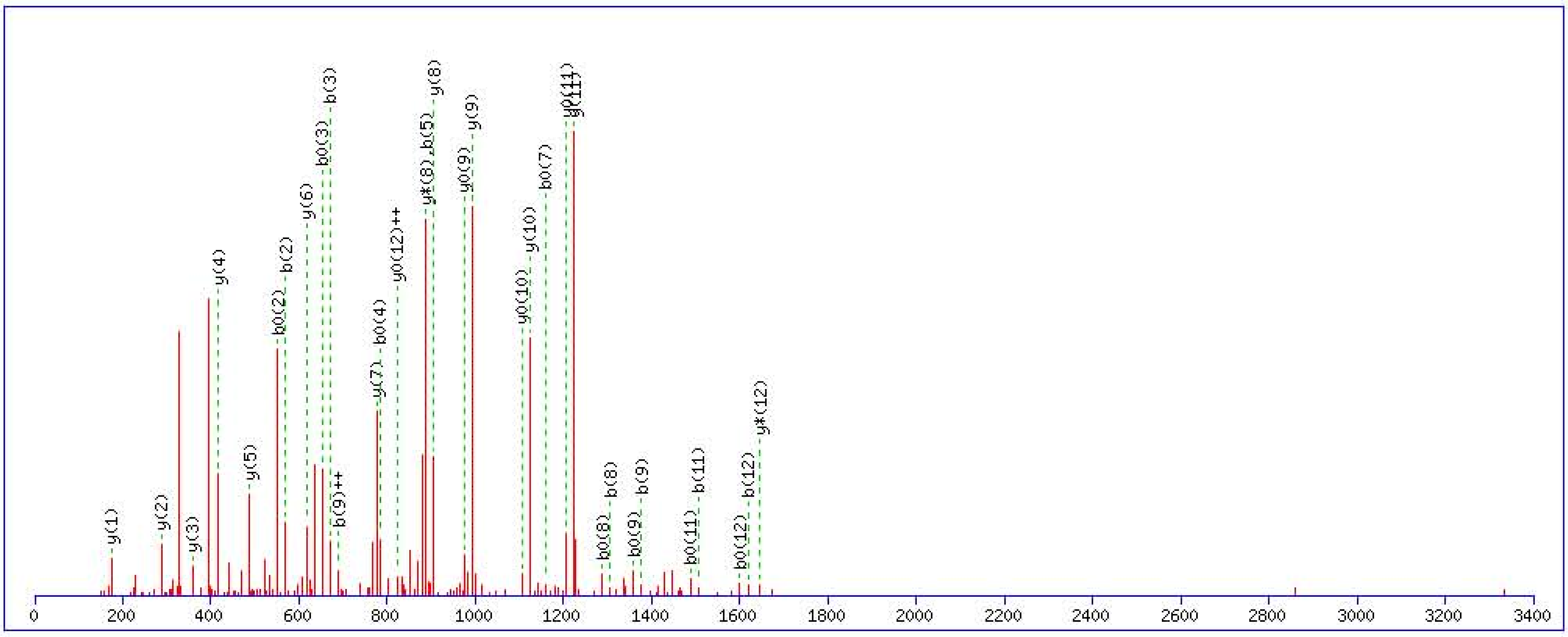
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

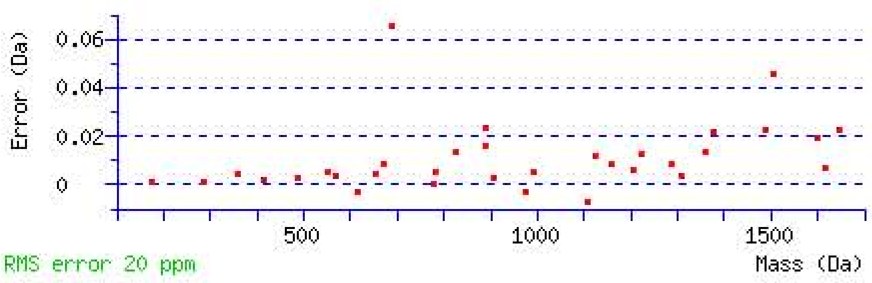
Match to Query 35550: 1791.807768 from(896.911160,2+) rtinseconds(1814) index(3825)
Title: Locus:1.1.1.3151.19 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

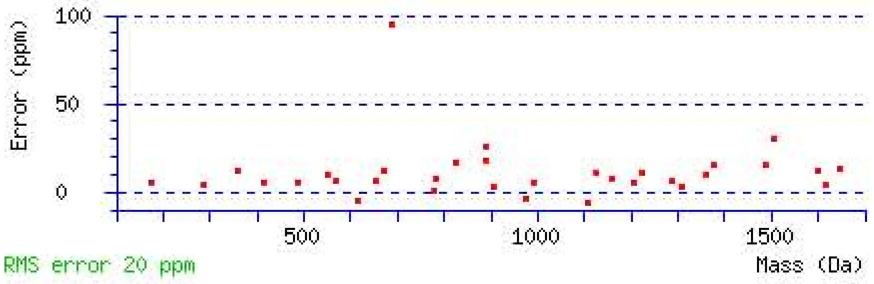
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1791.795349
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 64  Expect: 2.3e-006
Matches : 33/132 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	130.049869	65.528572			112.039304	56.523290	E							13
2	**569.275195**	285.141236	552.248646	276.627961	551.264630	276.135953	Q	1663.760061	832.383668	1646.733512	823.870394	1645.749496	823.378386	12
3	**670.322874**	335.665075	653.296325	327.151801	652.312309	326.659793	T	***1224.534735***	612.771005	1207.508186	604.257731	1206.524170	603.765723	11
4	801.363359	401.185318	784.336810	392.672043	783.352794	392.180035	M	***1123.487056***	562.247166	1106.460507	553.733891	1105.476491	553.241883	10
5	**888.395387**	444.701332	871.368838	436.188057	870.384822	435.696049	S	***992.446571***	496.726923	975.420022	488.213649	974.436006	487.721641	9
6	1017.437980	509.222628	1000.411431	500.709354	999.427415	500.217346	E	***905.414543***	453.210909	888.387994	444.697635	887.403978	444.205627	8
7	1177.468629	589.237953	1160.442080	580.724678	1159.458064	580.232670	C	***776.371950***	388.689613	759.345401	380.176338	758.361385	379.684330	7
8	**1306.511222**	653.759249	1289.484673	645.245974	1288.500657	644.753966	E	***616.341301***	308.674288	599.314752	300.161014	598.330736	299.669006	6
9	**1377.548336**	689.277806	1360.521787	680.764531	1359.537771	680.272523	A	***487.298708***	244.152992	470.272159	235.639717			5
10	1434.569800	717.788538	1417.543251	709.275263	1416.559235	708.783255	G	***416.261594***	208.634435	399.235045	200.121160			4
11	**1505.606914**	753.307095	1488.580365	744.793820	1487.596349	744.301812	A	***359.240130***	180.123703	342.213581	171.610428			3
12	**1618.690978**	809.849127	1601.664429	801.335852	1600.680413	800.843844	L	***288.203016***	144.605146	271.176467	136.091871			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EQTMSECEAGALR
(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	1791.795349	0.012419	EQTMSECEAGALR
4.0	1791.821854	-0.014086	YNVSCIMIMPQHQR

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

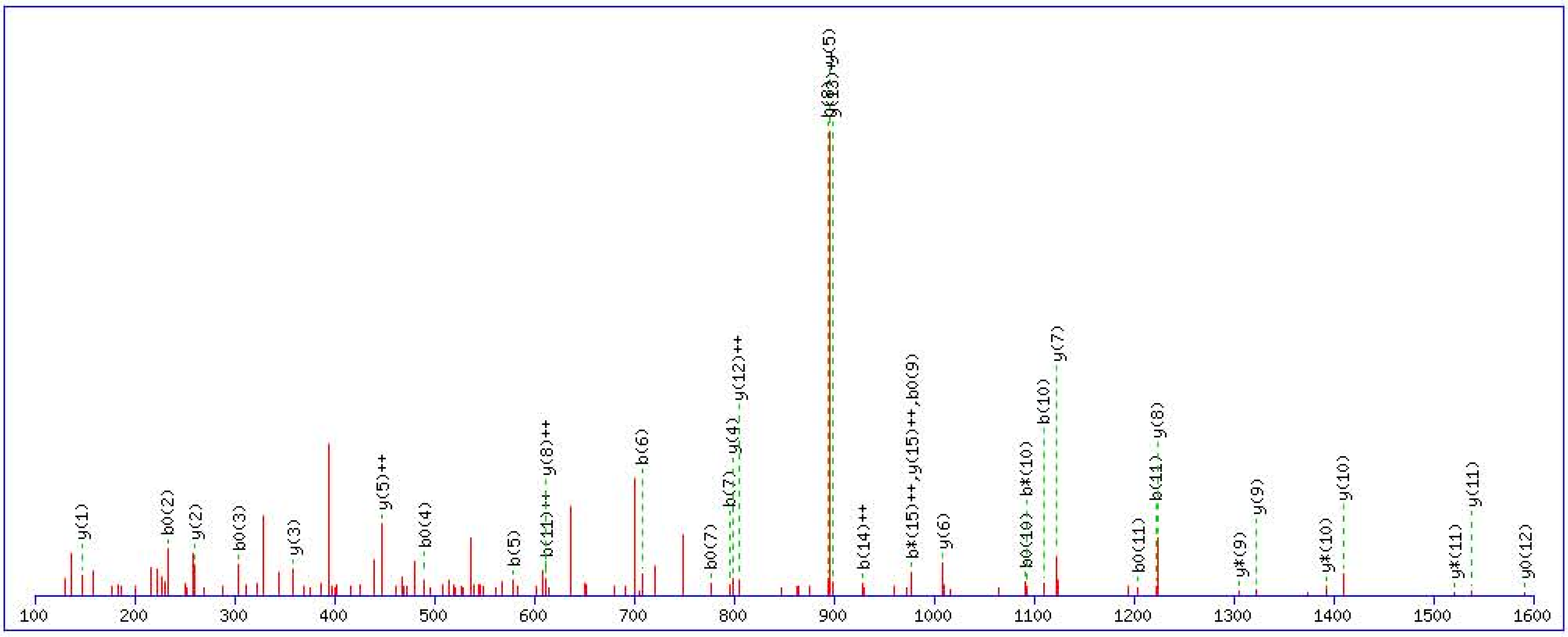
Mascot Search Results

Peptide View

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

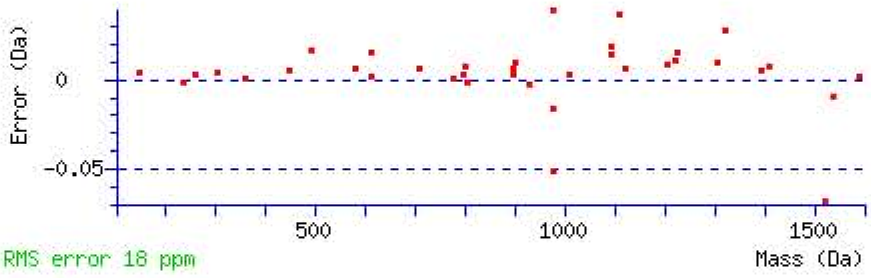
Match to Query 41821: 2116.119372 from(706.380400,3+) rtinseconds(2643) index(8431)
Title: Locus:1.1.1.3440.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

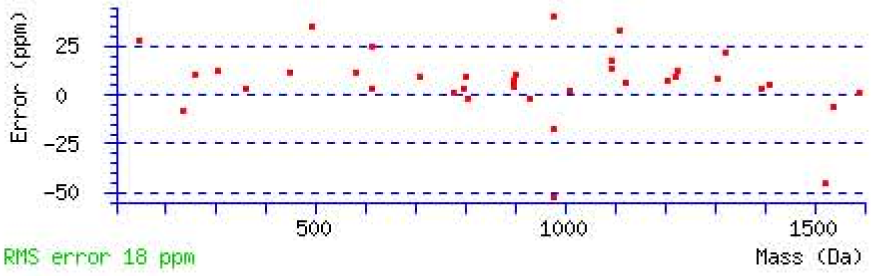
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2116.102676
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 4.8e-005
Matches : 37/146 fragment ions using 64 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							16
2	251.102633	126.054954			233.092068	117.049672	S	1954.046646	977.526961	1937.020097	969.013687	1936.036081	968.521679	15
3	322.139747	161.573512			304.129182	152.568229	A	1867.014618	934.010947	1849.988069	925.497673	1849.004053	925.005665	14
4	508.219060	254.613168			490.208495	245.607886	W	1795.977504	898.492390	1778.950955	889.979116	1777.966939	889.487108	13
5	**579.256174**	290.131725			561.245609	281.126443	A	1609.898191	805.452734	1592.871642	796.939459	1591.887626	796.447451	12
6	**708.298767**	354.653022			690.288202	345.647739	E	***1538.861077***	769.934177	1521.834528	761.420902	1520.850512	760.928894	11
7	**795.330795**	398.169036			777.320230	389.163753	S	***1409.818484***	705.412880	1392.791935	696.899606	1391.807919	696.407598	10
8	**894.399209**	447.703243			876.388644	438.697960	V	***1322.786456***	661.896866	1305.759907	653.383592	1304.775891	652.891584	9
9	995.446888	498.227082			977.436323	489.221800	T	***1223.718042***	612.362659	1206.691493	603.849385	1205.707477	603.357377	8
10	**1109.489815**	555.248546	1092.463266	546.735271	1091.479250	546.243263	N	***1122.670363***	561.838820	1105.643814	553.325545			7
11	**1222.573879**	**611.790578**	1205.547330	603.277303	1204.563314	602.785295	L	***1008.627436***	504.817356	991.600887	496.304082			6
12	1319.626643	660.316960	1302.600094	651.803685	1301.616078	651.311677	P	***895.543372***	448.275324	878.516823	439.762050			5
13	1758.851969	879.929623	1741.825420	871.416348	1740.841404	870.924340	Q	***798.490608***	399.748942	781.464059	391.235668			4
14	1857.920383	**929.463830**	1840.893834	920.950555	1839.909818	920.458547	V	***359.265282***	180.136279	342.238733	171.623004			3
15	1971.004447	986.005862	1953.977898	977.492587	1952.993882	977.000579	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 YSAWAESVTNLPQVIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.3	2116.102676	0.016696	YSAWAESVTNLPQVIK

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

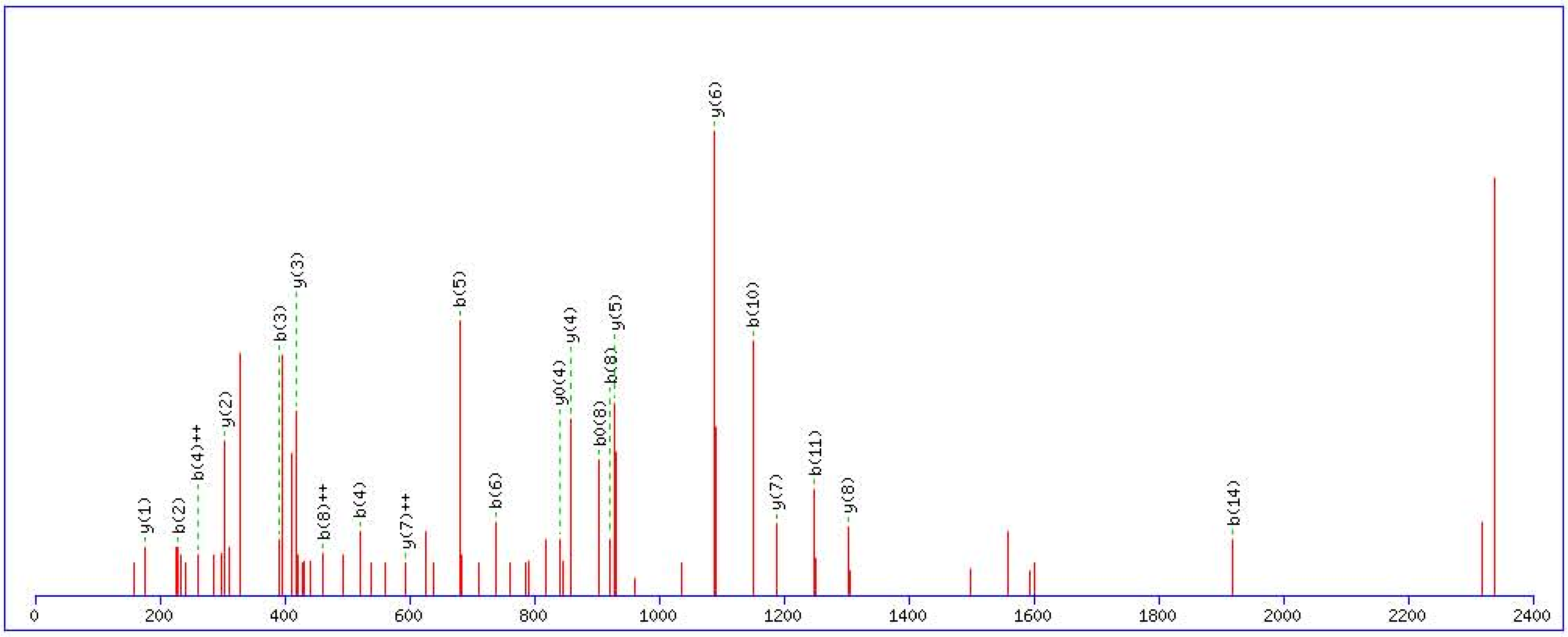
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

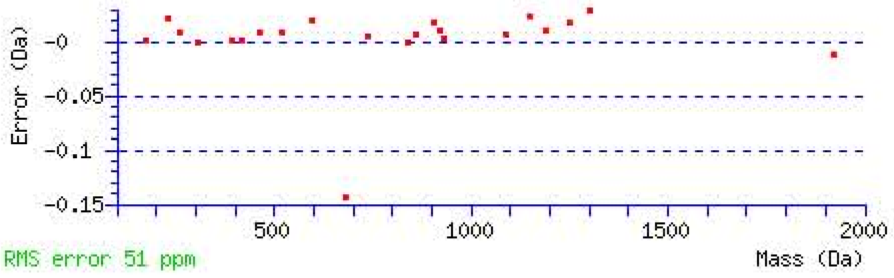
Match to Query 45706: 2337.003942 from(780.008590,3+) rtinseconds(2175) index(5857)
Title: Locus:1.1.1.3277.22 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

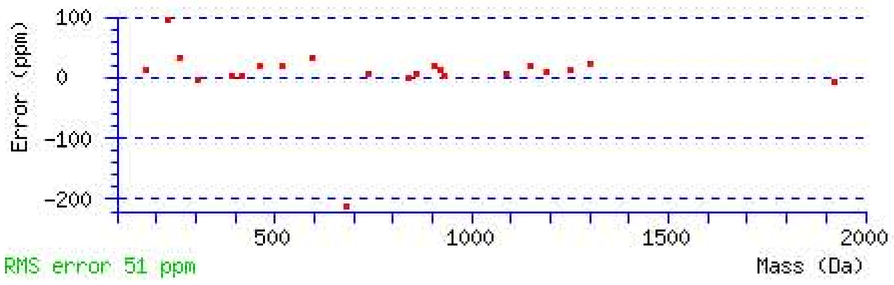
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2336.989792
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Biotin:Thermo-21345 (Q)
Ions Score: 45 **Expect:** 0.00011
Matches : 22/158 fragment ions using 57 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	132.047761	66.527518					M							17
2	***229.100525***	115.053900					P	2206.956589	1103.981932	2189.930040	1095.468658	2188.946024	1094.976650	16
3	***392.163854***	196.585565					Y	2109.903825	1055.455550	2092.877276	1046.942276	2091.893260	1046.450268	15
4	***521.206447***	**261.106862**			503.195882	252.101579	E	1946.840496	973.923886	1929.813947	965.410612	1928.829931	964.918604	14
5	***681.237096***	341.122186			663.226531	332.116904	C	1817.797903	909.402590	1800.771354	900.889315	1799.787338	900.397307	13
6	***738.258560***	369.632918			720.247995	360.627636	G	1657.767254	829.387265	1640.740705	820.873991	1639.756689	820.381983	12
7	835.311324	418.159300			817.300759	409.154018	P	1600.745790	800.876533	1583.719241	792.363259	1582.735225	791.871251	11
8	***922.343352***	**461.675314**			904.332787	452.670032	S	1503.693026	752.350151	1486.666477	743.836877	1485.682461	743.344869	10
9	1035.427416	518.217346			1017.416851	509.212064	L	1416.660998	708.834137	1399.634449	700.320863	1398.650433	699.828855	9
10	***1150.454359***	575.730818			1132.443794	566.725535	D	***1303.576934***	652.292105	1286.550385	643.778831	1285.566369	643.286823	8
11	***1249.522773***	625.265025			1231.512208	616.259742	V	***1188.549991***	594.778634	1171.523442	586.265359	1170.539426	585.773351	7
12	1409.553422	705.280349			1391.542857	696.275067	C	***1089.481577***	545.244427	1072.455028	536.731152	1071.471012	536.239144	6
13	1480.590536	740.798906			1462.579971	731.793624	A	***929.450928***	465.229102	912.424379	456.715827	911.440363	456.223819	5
14	***1919.815862***	960.411569	1902.789313	951.898295	1901.805297	951.406287	Q	***858.413814***	429.710545	841.387265	421.197271	840.403249	420.705263	4
15	2034.842805	1017.925041	2017.816256	1009.411766	2016.832240	1008.919758	D	***419.188488***	210.097882	402.161939	201.584607	401.177923	201.092599	3
16	2163.885398	1082.446337	2146.858849	1073.933062	2145.874833	1073.441054	E	***304.161545***	152.584410	287.134996	144.071136	286.150980	143.579128	2
17							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.2	2336.989792	0.014150	MPYECGPSLDVCAQDER

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

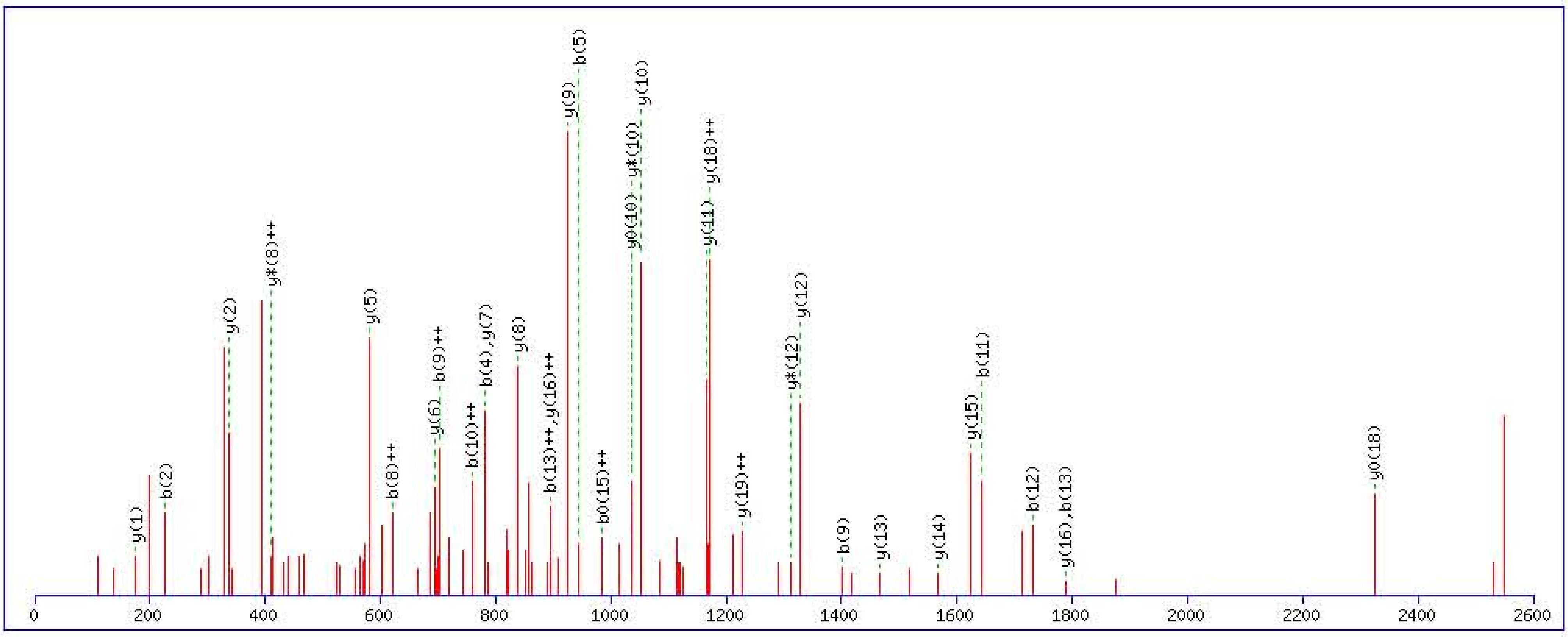
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

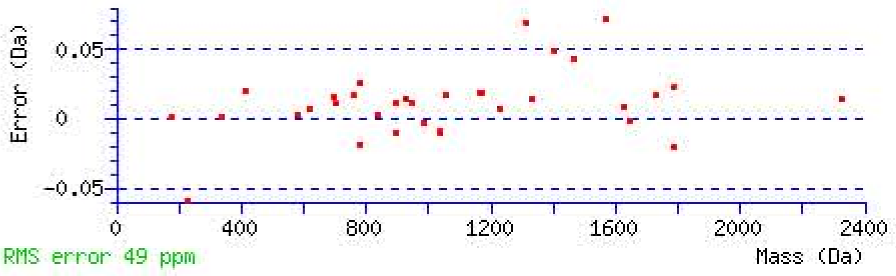
Match to Query 49158: 2567.271522 from(856.764450,3+) rtinseconds(2187) index(5917)
Title: Locus:1.1.1.3281.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

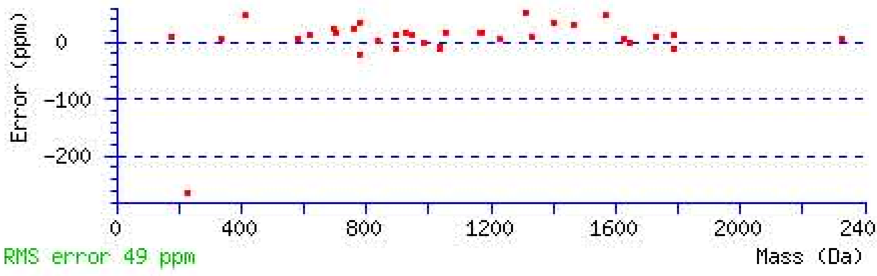
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2567.247849
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 92 **Expect:** 4.9e-009
Matches : 34/214 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	114.091340	57.549308					L							20
2	**227.175404**	114.091340					I	2455.171074	1228.089175	2438.144525	1219.575900	2437.160509	1219.083892	19
3	342.202347	171.604811			324.191782	162.599529	D	2342.087010	1171.547143	2325.060461	1163.033868	2324.076445	1162.541860	18
4	**781.427673**	391.217475	764.401124	382.704200	763.417108	382.212192	Q	2227.060067	1114.033671	2210.033518	1105.520397	2209.049502	1105.028389	17
5	**944.491002**	472.749139	927.464453	464.235864	926.480437	463.743856	Y	***1787.834741***	894.421009	1770.808192	885.907734	1769.824176	885.415726	16
6	1001.512466	501.259871	984.485917	492.746597	983.501901	492.254589	G	***1624.771412***	812.889344	1607.744863	804.376070	1606.760847	803.884062	15
7	1102.560145	551.783710	1085.533596	543.270436	1084.549580	542.778428	T	***1567.749948***	784.378612	1550.723399	775.865338	1549.739383	775.373330	14
8	1239.619057	**620.313166**	1222.592508	611.799892	1221.608492	611.307884	H	***1466.702269***	733.854773	1449.675720	725.341498	1448.691704	724.849490	13
9	**1402.682386**	**701.844831**	1385.655837	693.331557	1384.671821	692.839548	Y	***1329.643357***	665.325317	1312.616808	656.812042	1311.632792	656.320034	12
10	1515.766450	**758.386863**	1498.739901	749.873588	1497.755885	749.381580	L	***1166.580028***	583.793652	1149.553479	575.280378	1148.569463	574.788370	11
11	**1643.825028**	822.416152	1626.798479	813.902878	1625.814463	813.410869	Q	***1053.495964***	527.251620	1036.469415	518.738346	1035.485399	518.246338	10
12	**1730.857056**	865.932166	1713.830507	857.418892	1712.846491	856.926884	S	***925.437386***	463.222331	908.410837	454.709057	907.426821	454.217049	9
13	**1787.878520**	**894.442898**	1770.851971	885.929624	1769.867955	885.437615	G	***838.405358***	419.706317	821.378809	411.193043	820.394793	410.701035	8
14	1874.910548	937.958912	1857.883999	929.445638	1856.899983	928.953630	S	***781.383894***	391.195585	764.357345	382.682311	763.373329	382.190303	7
15	1987.994612	994.500944	1970.968063	985.987670	1969.984047	985.495661	L	***694.351866***	347.679571	677.325317	339.166297	676.341301	338.674289	6
16	2045.016076	1023.011676	2027.989527	1014.498402	2027.005511	1014.006393	G	***581.267802***	291.137539	564.241253	282.624265	563.257237	282.132257	5
17	2102.037540	1051.522408	2085.010991	1043.009133	2084.026975	1042.517125	G	524.246338	262.626807	507.219789	254.113533	506.235773	253.621525	4
18	2231.080133	1116.043704	2214.053584	1107.530430	2213.069568	1107.038422	E	467.224874	234.116075	450.198325	225.602801	449.214309	225.110793	3
19	2394.143462	1197.575369	2377.116913	1189.062094	2376.132897	1188.570086	Y	***338.182281***	169.594778	321.155732	161.081504			2
20							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
91.8	2567.247849	0.023673	LIDQYGTHYLQSGSLGGEYR
14.8	2567.247849	0.023673	LIDQYGTHYLQSGSLGGEYR
3.2	2567.294800	-0.023278	LLSDGQQHLTESLREKCSR

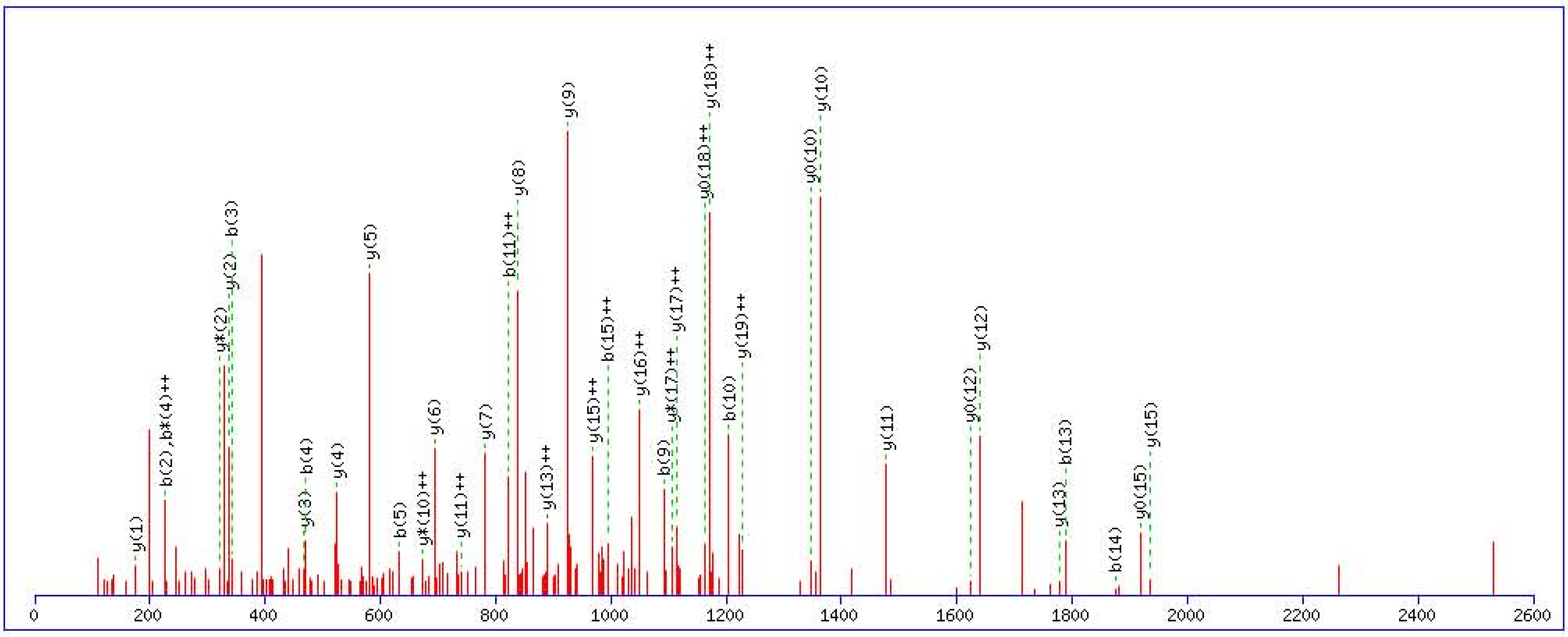
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

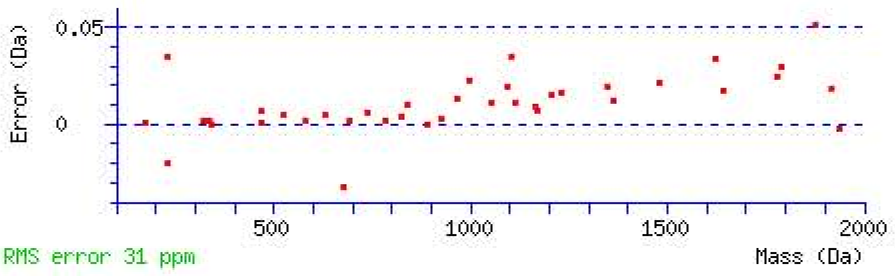
Match to Query 49160: 2567.278482 from(856.766770,3+) rtinseconds(2167) index(5807)
Title: Locus:1.1.1.3274.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

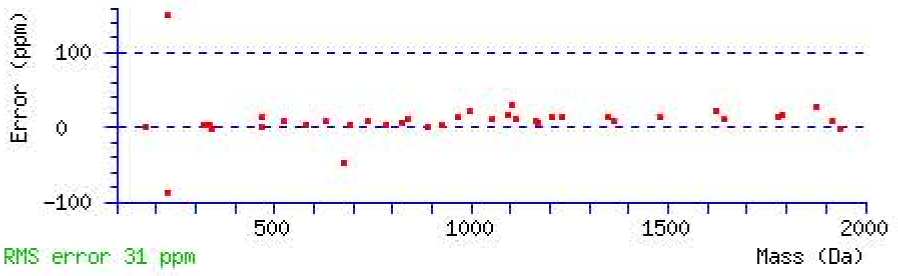


```
Monoisotopic mass of neutral peptide Mr(calc): 2567.247849
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 70  Expect: 3.1e-006
Matches : 39/214 fragment ions using 80 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							20
2	**227.175404**	114.091340					I	2455.171074	1228.089175	2438.144525	1219.575900	2437.160509	1219.083892	19
3	**342.202347**	171.604811			324.191782	162.599529	D	2342.087010	1171.547143	2325.060461	1163.033868	2324.076445	1162.541860	18
4	**470.260925**	235.634100	453.234376	227.120826	452.250360	226.628818	Q	2227.060067	1114.033671	2210.033518	1105.520397	2209.049502	1105.028389	17
5	**633.324254**	317.165765	616.297705	308.652491	615.313689	308.160483	Y	2099.001489	1050.004382	2081.974940	1041.491108	2080.990924	1040.999100	16
6	690.345718	345.676497	673.319169	337.163223	672.335153	336.671215	G	***1935.938160***	968.472718	1918.911611	959.959444	1917.927595	959.467436	15
7	791.393397	396.200337	774.366848	387.687062	773.382832	387.195054	T	1878.916696	939.961986	1861.890147	931.448712	1860.906131	930.956704	14
8	928.452309	464.729793	911.425760	456.216518	910.441744	455.724510	H	***1777.869017***	889.438147	1760.842468	880.924872	1759.858452	880.432864	13
9	**1091.515638**	546.261457	1074.489089	537.748183	1073.505073	537.256175	Y	***1640.810105***	820.908691	1623.783556	812.395416	1622.799540	811.903408	12
10	**1204.599702**	602.803489	1187.573153	594.290215	1186.589137	593.798206	L	***1477.746776***	739.377026	1460.720227	730.863752	1459.736211	730.371744	11
11	1643.825028	**822.416152**	1626.798479	813.902878	1625.814463	813.410869	Q	***1364.662712***	682.834994	1347.636163	674.321720	1346.652147	673.829712	10
12	1730.857056	865.932166	1713.830507	857.418892	1712.846491	856.926884	S	***925.437386***	463.222331	908.410837	454.709057	907.426821	454.217049	9
13	**1787.878520**	894.442898	1770.851971	885.929624	1769.867955	885.437615	G	***838.405358***	419.706317	821.378809	411.193043	820.394793	410.701035	8
14	**1874.910548**	937.958912	1857.883999	929.445638	1856.899983	928.953630	S	***781.383894***	391.195585	764.357345	382.682311	763.373329	382.190303	7
15	1987.994612	**994.500944**	1970.968063	985.987670	1969.984047	985.495661	L	***694.351866***	347.679571	677.325317	339.166297	676.341301	338.674289	6
16	2045.016076	1023.011676	2027.989527	1014.498402	2027.005511	1014.006393	G	***581.267802***	291.137539	564.241253	282.624265	563.257237	282.132257	5
17	2102.037540	1051.522408	2085.010991	1043.009133	2084.026975	1042.517125	G	***524.246338***	262.626807	507.219789	254.113533	506.235773	253.621525	4
18	2231.080133	1116.043704	2214.053584	1107.530430	2213.069568	1107.038422	E	***467.224874***	234.116075	450.198325	225.602801	449.214309	225.110793	3
19	2394.143462	1197.575369	2377.116913	1189.062094	2376.132897	1188.570086	Y	***338.182281***	169.594778	321.155732	161.081504			2
20							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 31 ppm



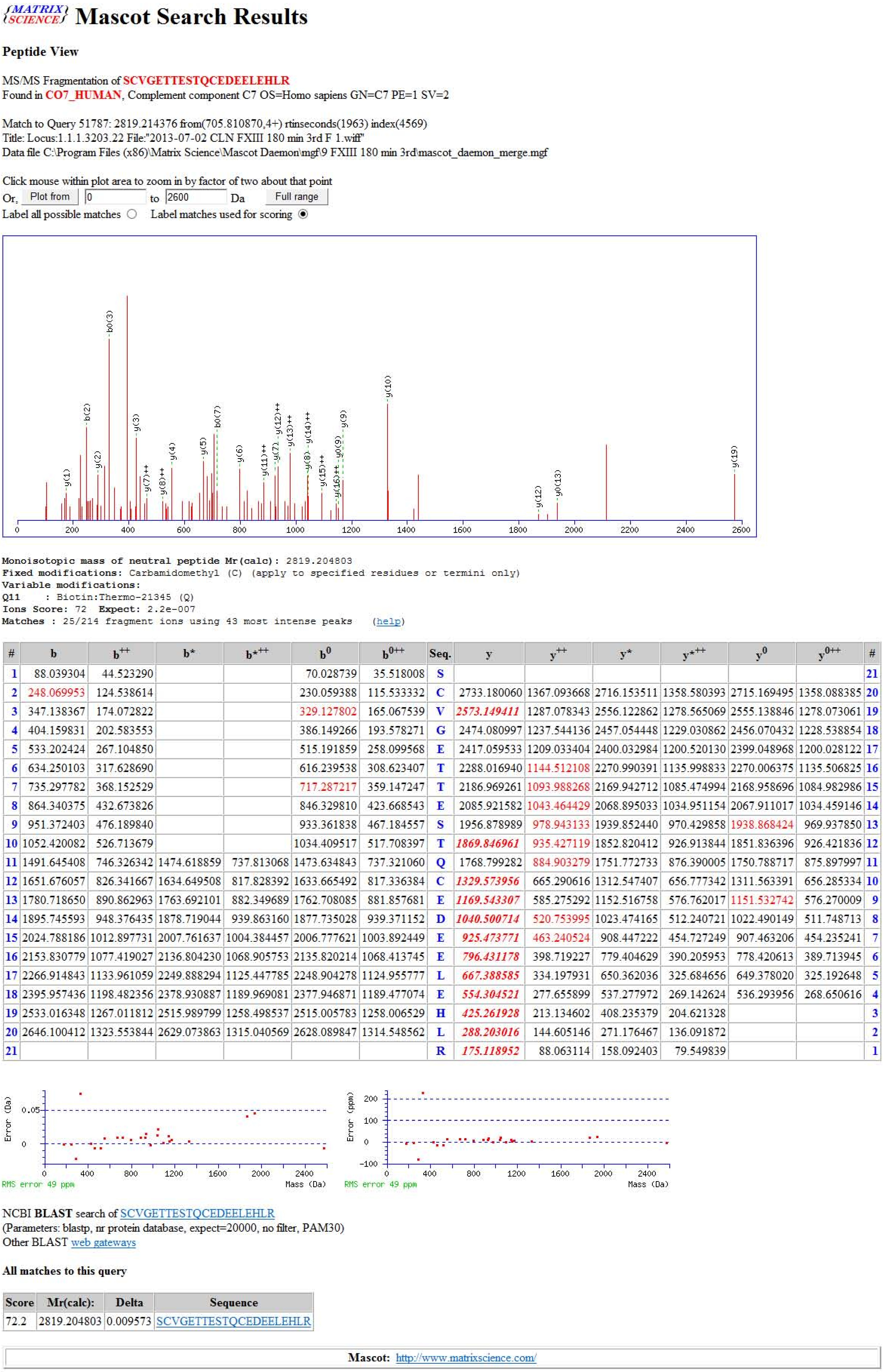
RMS error 31 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.6	2567.247849	0.030633	LIDQYGTHYLQSGSLGGEYR
27.5	2567.247849	0.030633	LIDQYGTHYLQSGSLGGEYR

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



Mascot Search Results

Peptide View

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

Match to Query 51787: 2819.214376 from(705.810870,4+) rtinseconds(1963) index(4569)
Title: Locus:1.1.1.3203.22 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\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): 2819.204803
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 72  Expect: 2.2e-007
Matches : 25/214 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	88.039304	44.523290			70.028739	35.518008	S							21
2	248.069953	124.538614			230.059388	115.533332	C	2733.180060	1367.093668	2716.153511	1358.580393	2715.169495	1358.088385	20
3	347.138367	174.072822			329.127802	165.067539	V	***2573.149411***	1287.078343	2556.122862	1278.565069	2555.138846	1278.073061	19
4	404.159831	202.583553			386.149266	193.578271	G	2474.080997	1237.544136	2457.054448	1229.030862	2456.070432	1228.538854	18
5	533.202424	267.104850			515.191859	258.099568	E	2417.059533	1209.033404	2400.032984	1200.520130	2399.048968	1200.028122	17
6	634.250103	317.628690			616.239538	308.623407	T	2288.016940	1144.512108	2270.990391	1135.998833	2270.006375	1135.506825	16
7	735.297782	368.152529			717.287217	359.147247	T	2186.969261	1093.988268	2169.942712	1085.474994	2168.958696	1084.982986	15
8	864.340375	432.673826			846.329810	423.668543	E	2085.921582	1043.464429	2068.895033	1034.951154	2067.911017	1034.459146	14
9	951.372403	476.189840			933.361838	467.184557	S	1956.878989	978.943133	1939.852440	970.429858	1938.868424	969.937850	13
10	1052.420082	526.713679			1034.409517	517.708397	T	***1869.846961***	935.427119	1852.820412	926.913844	1851.836396	926.421836	12
11	1491.645408	746.326342	1474.618859	737.813068	1473.634843	737.321060	Q	1768.799282	884.903279	1751.772733	876.390005	1750.788717	875.897997	11
12	1651.676057	826.341667	1634.649508	817.828392	1633.665492	817.336384	C	***1329.573956***	665.290616	1312.547407	656.777342	1311.563391	656.285334	10
13	1780.718650	890.862963	1763.692101	882.349689	1762.708085	881.857681	E	***1169.543307***	585.275292	1152.516758	576.762017	1151.532742	576.270009	9
14	1895.745593	948.376435	1878.719044	939.863160	1877.735028	939.371152	D	***1040.500714***	520.753995	1023.474165	512.240721	1022.490149	511.748713	8
15	2024.788186	1012.897731	2007.761637	1004.384457	2006.777621	1003.892449	E	***925.473771***	463.240524	908.447222	454.727249	907.463206	454.235241	7
16	2153.830779	1077.419027	2136.804230	1068.905753	2135.820214	1068.413745	E	***796.431178***	398.719227	779.404629	390.205953	778.420613	389.713945	6
17	2266.914843	1133.961059	2249.888294	1125.447785	2248.904278	1124.955777	L	***667.388585***	334.197931	650.362036	325.684656	649.378020	325.192648	5
18	2395.957436	1198.482356	2378.930887	1189.969081	2377.946871	1189.477074	E	***554.304521***	277.655899	537.277972	269.142624	536.293956	268.650616	4
19	2533.016348	1267.011812	2515.989799	1258.498537	2515.005783	1258.006529	H	***425.261928***	213.134602	408.235379	204.621328			3
20	2646.100412	1323.553844	2629.073863	1315.040569	2628.089847	1314.548562	L	***288.203016***	144.605146	271.176467	136.091872			2
21							R	***175.118952***	88.063114	158.092403	79.549839			1

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
72.2	2819.204803	0.009573	SCVGETTESTQCEDEELEHLR

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

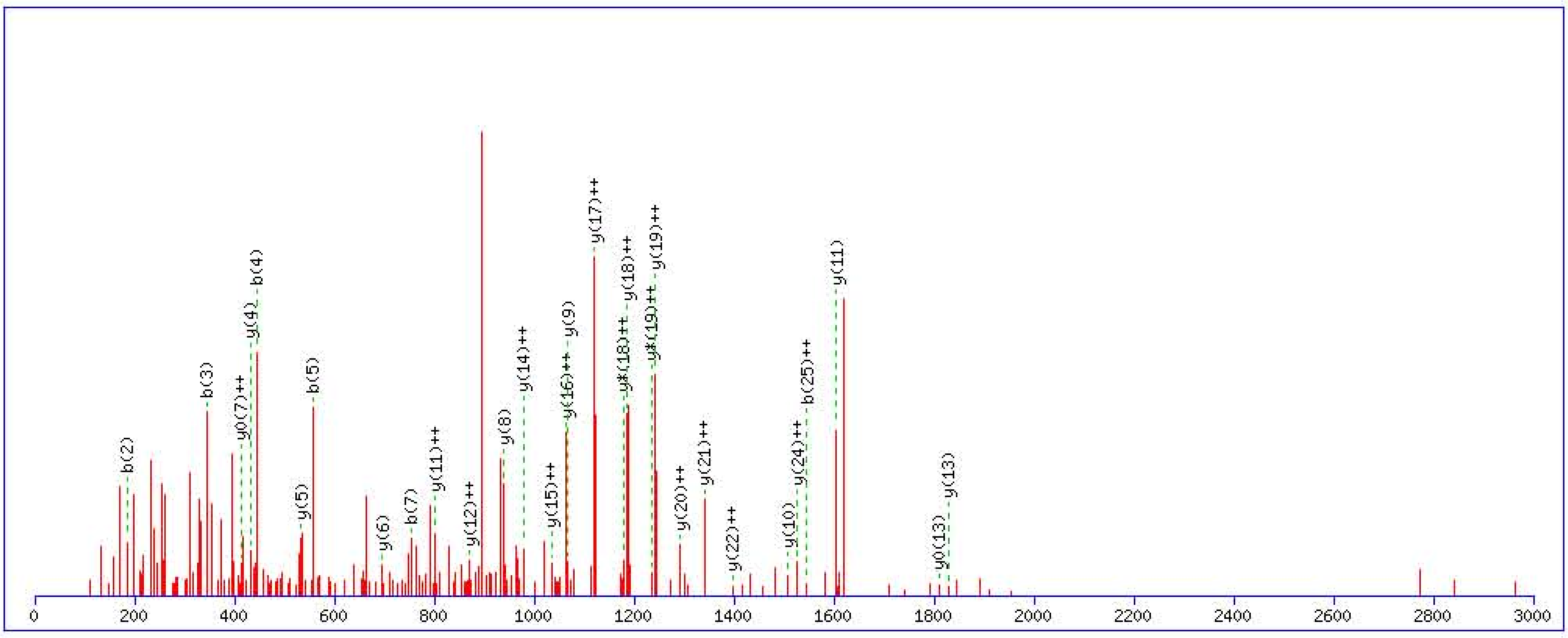
Mascot Search Results

Peptide View

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

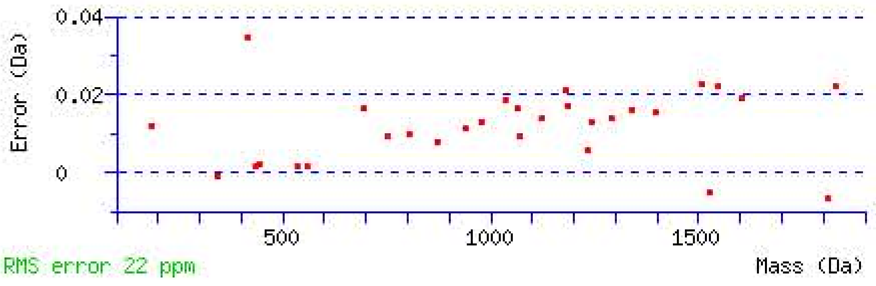
Match to Query 56896: 3237.709936 from(810.434760,4+) rtinseconds(2522) index(7675)
Title: Locus:1.1.1.3398.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

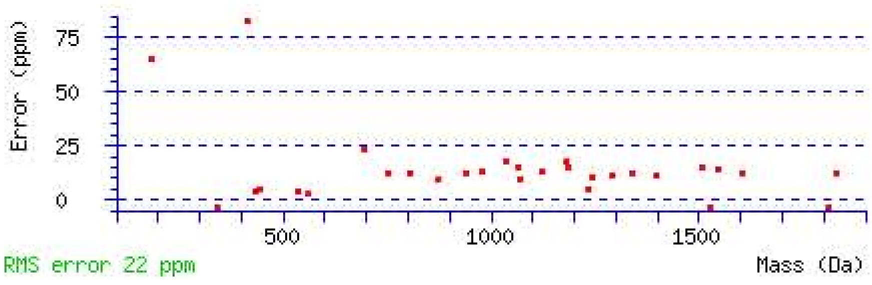
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3237.675262
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q17 : Biotin:Thermo-21345 (Q)
Ions Score: 44 **Expect:** 0.00081
Matches : 30/256 fragment ions using 88 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							26
2	**185.128454**	93.067865					A	3125.598471	1563.302873	3108.571922	1554.789599	3107.587906	1554.297591	25
3	**345.159103**	173.083190					C	3054.561357	1527.784316	3037.534808	1519.271042	3036.550792	1518.779034	24
4	**444.227517**	222.617397					V	2894.530708	1447.768992	2877.504159	1439.255717	2876.520143	1438.763709	23
5	**557.311581**	279.159429					L	2795.462294	1398.234785	2778.435745	1389.721510	2777.451729	1389.229502	22
6	654.364345	327.685811					P	2682.378230	1341.692753	2665.351681	1333.179478	2664.367665	1332.687470	21
7	**753.432759**	377.220018					V	2585.325466	1293.166371	2568.298917	1284.653096	2567.314901	1284.161088	20
8	866.516823	433.762050					L	2486.257052	1243.632164	2469.230503	1235.118889	2468.246487	1234.626881	19
9	997.557308	499.282292					M	2373.172988	1187.090132	2356.146439	1178.576857	2355.162423	1178.084849	18
10	1112.584251	556.795764			1094.573686	547.790481	D	2242.132503	1121.569889	2225.105954	1113.056615	2224.121938	1112.564607	17
11	1169.605715	585.306495			1151.595150	576.301213	G	2127.105560	1064.056418	2110.079011	1055.543143	2109.094995	1055.051135	16
12	1282.689779	641.848527			1264.679214	632.843245	I	2070.084096	1035.545686	2053.057547	1027.032411	2052.073531	1026.540403	15
13	1410.748357	705.877816	1393.721808	697.364542	1392.737792	696.872534	Q	1957.000032	979.003654	1939.973483	970.490380	1938.989467	969.998371	14
14	1497.780385	749.393830	1480.753836	740.880556	1479.769820	740.388548	S	***1828.941454***	914.974365	1811.914905	906.461091	1810.930889	905.969083	13
15	1634.839297	817.923286	1617.812748	809.410012	1616.828732	808.918004	H	1741.909426	871.458351	1724.882877	862.945077	1723.898861	862.453068	12
16	1731.892061	866.449668	1714.865512	857.936394	1713.881496	857.444386	P	***1604.850514***	802.928895	1587.823965	794.415621	1586.839949	793.923612	11
17	2171.117387	1086.062331	2154.090838	1077.549057	2153.106822	1077.057049	Q	***1507.797750***	754.402513	1490.771201	745.889239	1489.787185	745.397230	10
18	2299.212350	1150.109813	2282.185801	1141.596538	2281.201785	1141.104530	K	***1068.572424***	534.789850	1051.545875	526.276575	1050.561859	525.784567	9
19	2396.265114	1198.636195	2379.238565	1190.122920	2378.254549	1189.630912	P	***940.477461***	470.742368	923.450912	462.229094	922.466896	461.737086	8
20	2543.333528	1272.170402	2526.306979	1263.657127	2525.322963	1263.165119	F	843.424697	422.215986	826.398148	413.702712	825.414132	413.210704	7
21	2706.396857	1353.702066	2689.370308	1345.188792	2688.386292	1344.696784	Y	***696.356283***	348.681779	679.329734	340.168505	678.345718	339.676497	6
22	2807.444536	1404.225906	2790.417987	1395.712631	2789.433971	1395.220623	T	***533.292954***	267.150115	516.266405	258.636840	515.282389	258.144832	5
23	2906.512950	1453.760113	2889.486401	1445.246838	2888.502385	1444.754830	V	***432.245275***	216.626275	415.218726	208.113001	414.234710	207.620993	4
24	2963.534414	1482.270845	2946.507865	1473.757570	2945.523849	1473.265562	G	333.176861	167.092069	316.150312	158.578794	315.166296	158.086786	3
25	3092.577007	1546.792141	3075.550458	1538.278867	3074.566442	1537.786859	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
26							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of IACVLPVLMDGIQSHPQKPFYTVGEK
(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	3237.675262	0.034674	IACVLPVLMDGIQSHPQKPFYTVGEK
26.2	3237.675262	0.034674	IACVLPVLMDGIQSHPQKPFYTVGEK

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

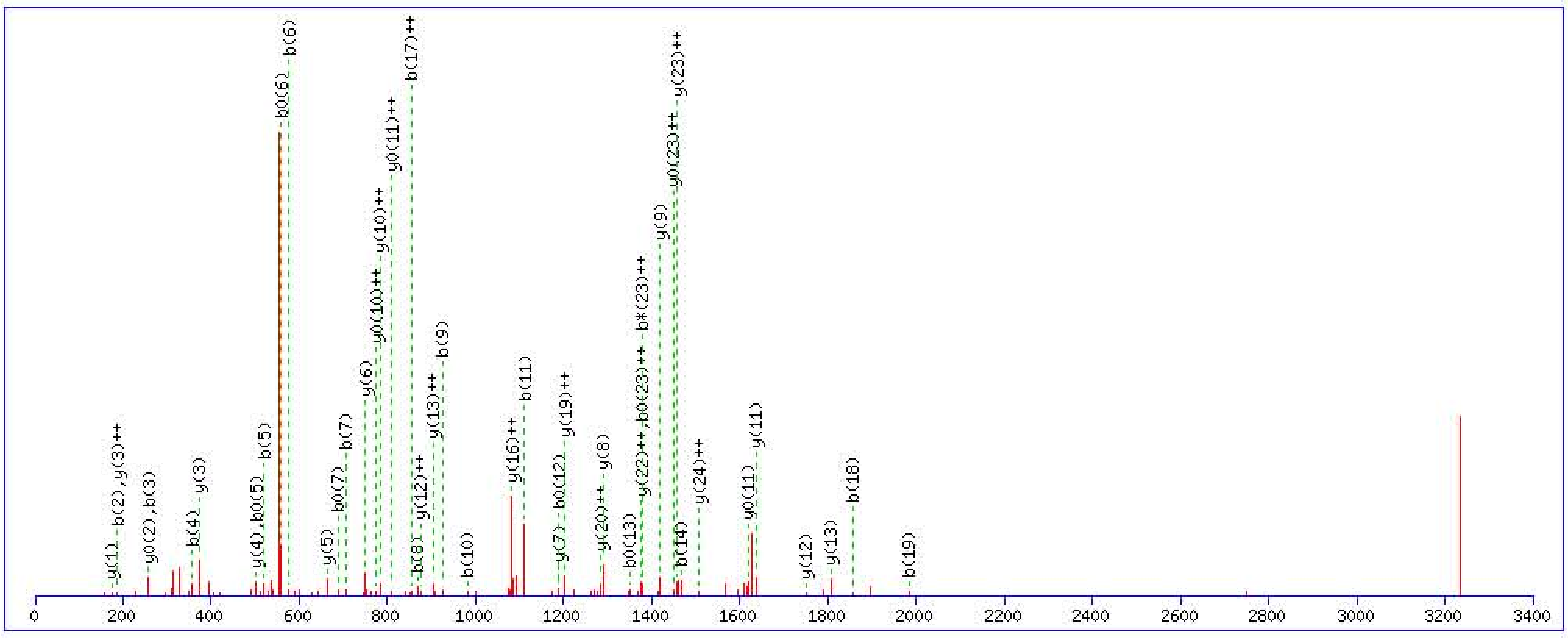
Mascot Search Results

Peptide View

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

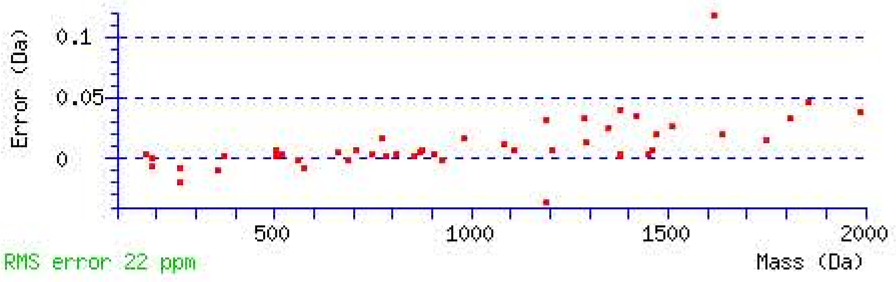
Match to Query 57885: 3272.503122 from(1091.841650,3+) rtinseconds(2219) index(6098)
Title: Locus:1.1.1.3292.25 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

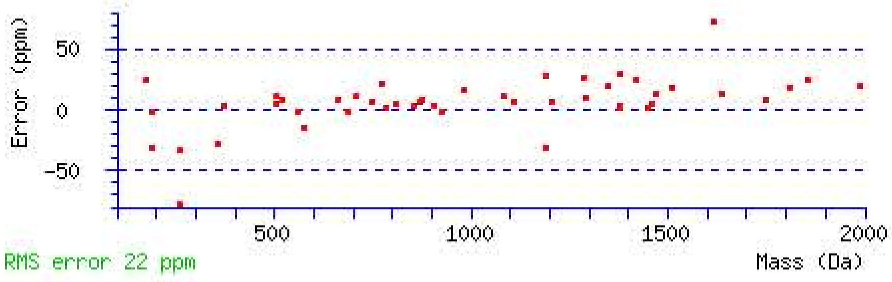
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3272.468933
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q21     : Biotin:Thermo-21345 (Q)
Ions Score: 68  Expect: 2e-006
Matches : 47/298 fragment ions using 95 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
67.9	3272.468933	0.034189	SVAVYGQYGGQPCVGNAFETQSCEPTR
11.2	3272.468933	0.034189	SVAVYGQYGGQPCVGNAFETQSCEPTR

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

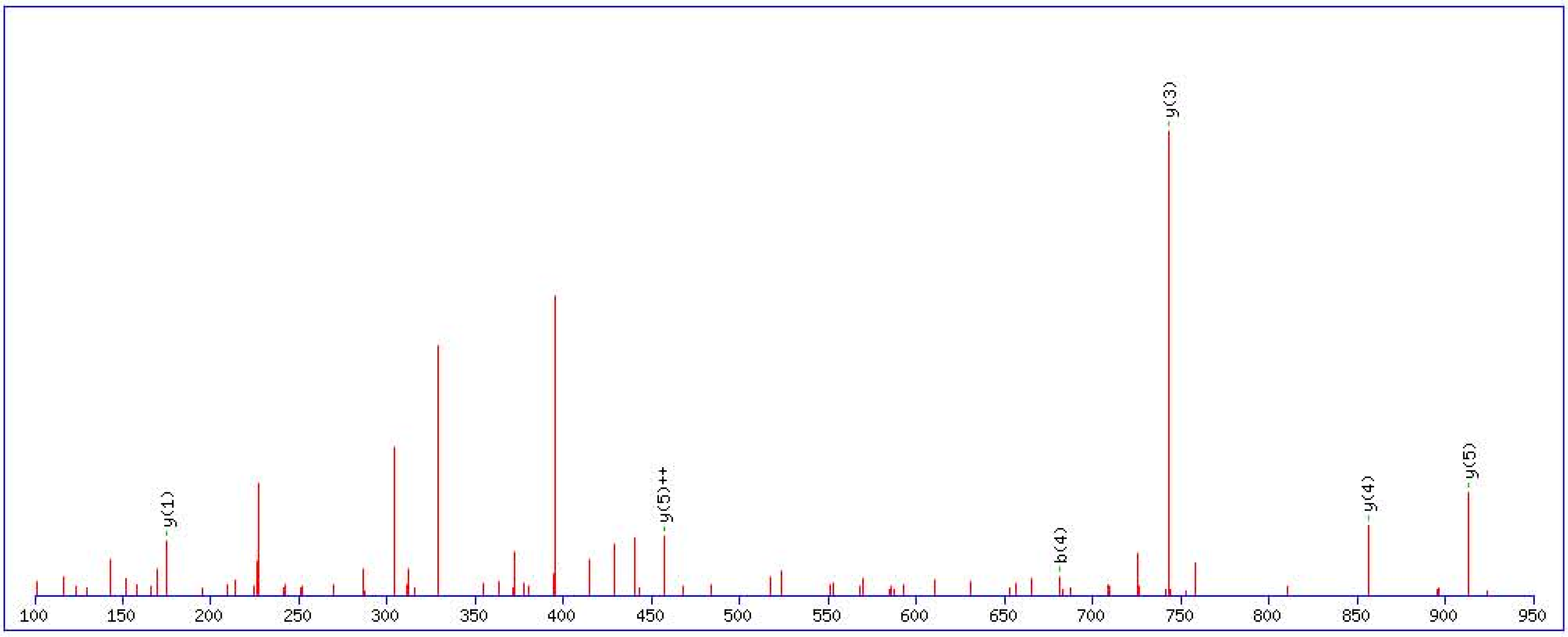
Mascot Search Results

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

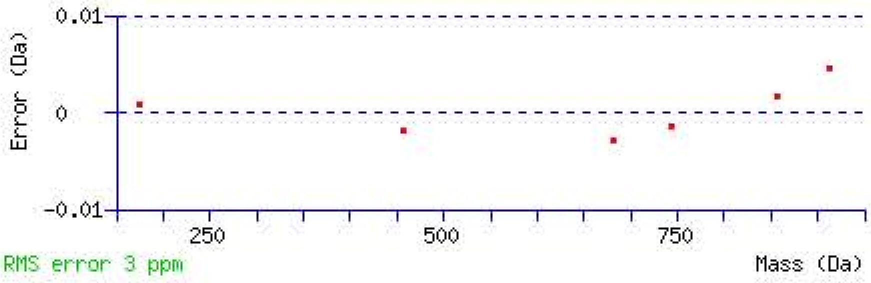
Match to Query 11197: 983.518528 from(492.766540,2+) rtinseconds(1430) index(28415)
Title: Locus:1.1.1.3161.6 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

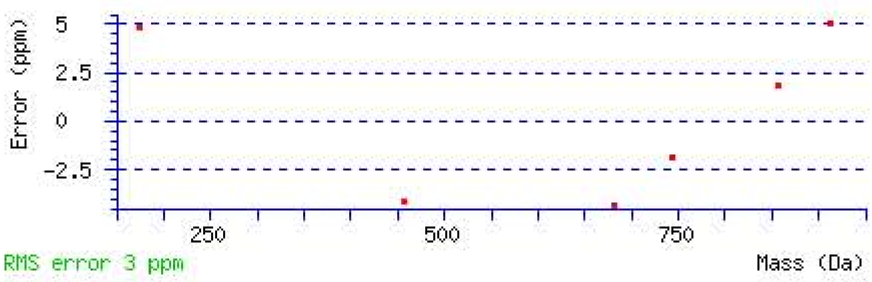
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 983.522217
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 26 **Expect:** 0.044
Matches : 6/44 fragment ions using 9 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
26.3	983.522217	-0.003689	AGIQER
23.4	983.522217	-0.003689	AGLEQR
11.4	983.522217	-0.003689	QIQER
11.4	983.522217	-0.003689	QLQER
9.2	983.514816	0.003712	QPVREAER
9.1	983.522202	-0.003674	KLMENPPR
9.1	983.522217	-0.003689	QLEQR
9.1	983.530090	-0.011562	QLLNHFGR
8.1	983.522217	-0.003689	AGQELR
5.3	983.522217	-0.003689	AAQVER

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

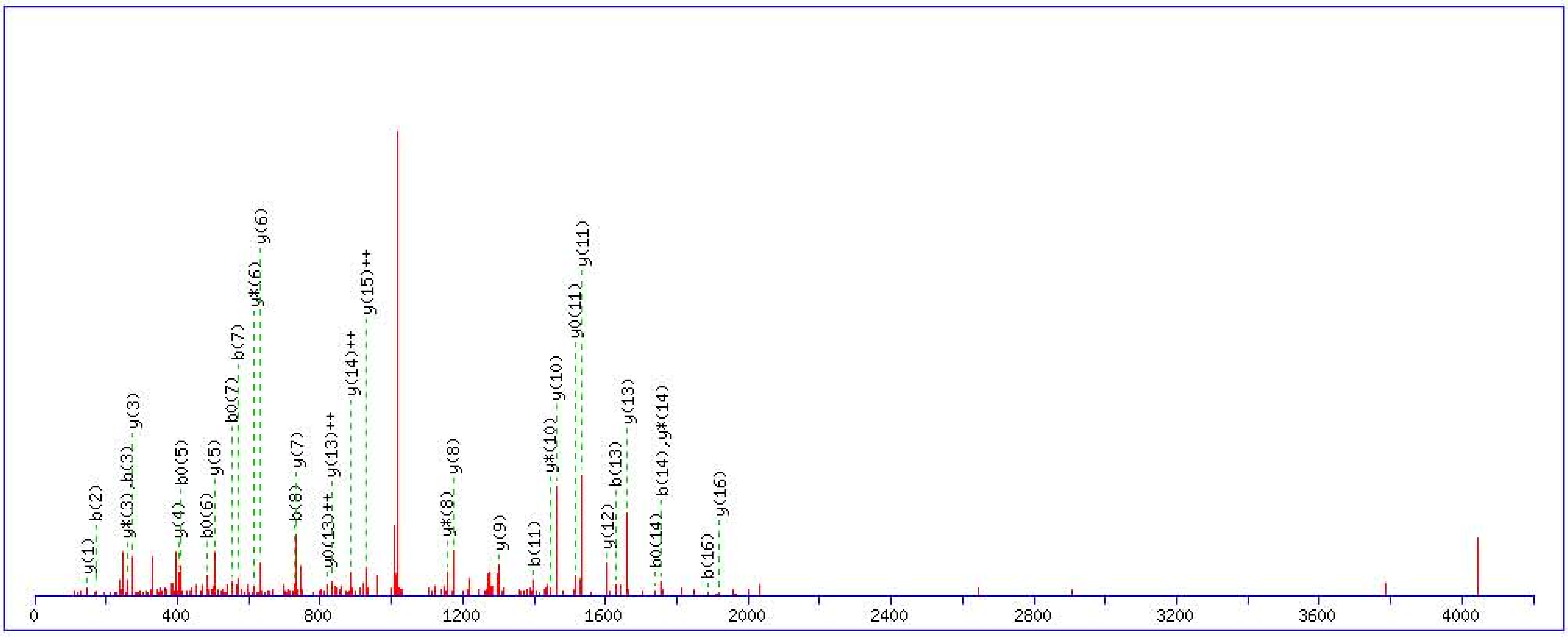
{MATRIX SCIENCE} Mascot Search Results

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

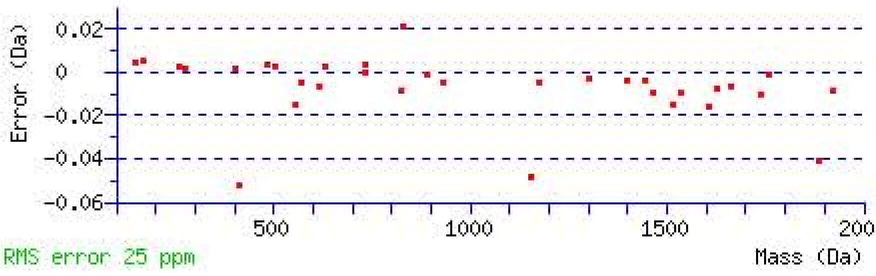
Match to Query 40408: 2030.961488 from(1016.488020,2+) rtinseconds(1734) index(17331)
Title: Locus:1.1.1.3169.23 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

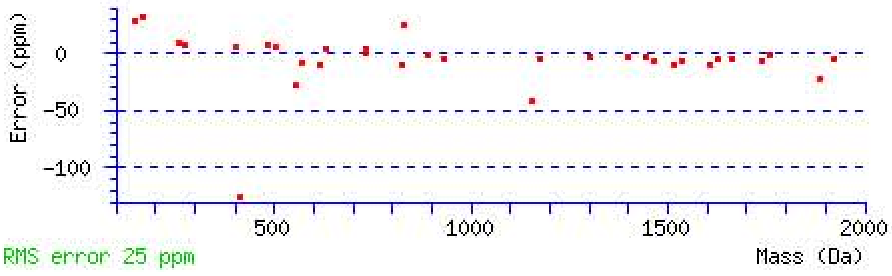
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2030.976501
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10    : Biotin:Thermo-21345 (Q)
Ions Score: 85  Expect: 6e-008
Matches : 35/164 fragment ions using 57 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
84.6	2030.976501	-0.015013	LGSLGAACEQTQTEGAK
57.5	2030.976501	-0.015013	LGSLGAACEQTQTEGAK

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

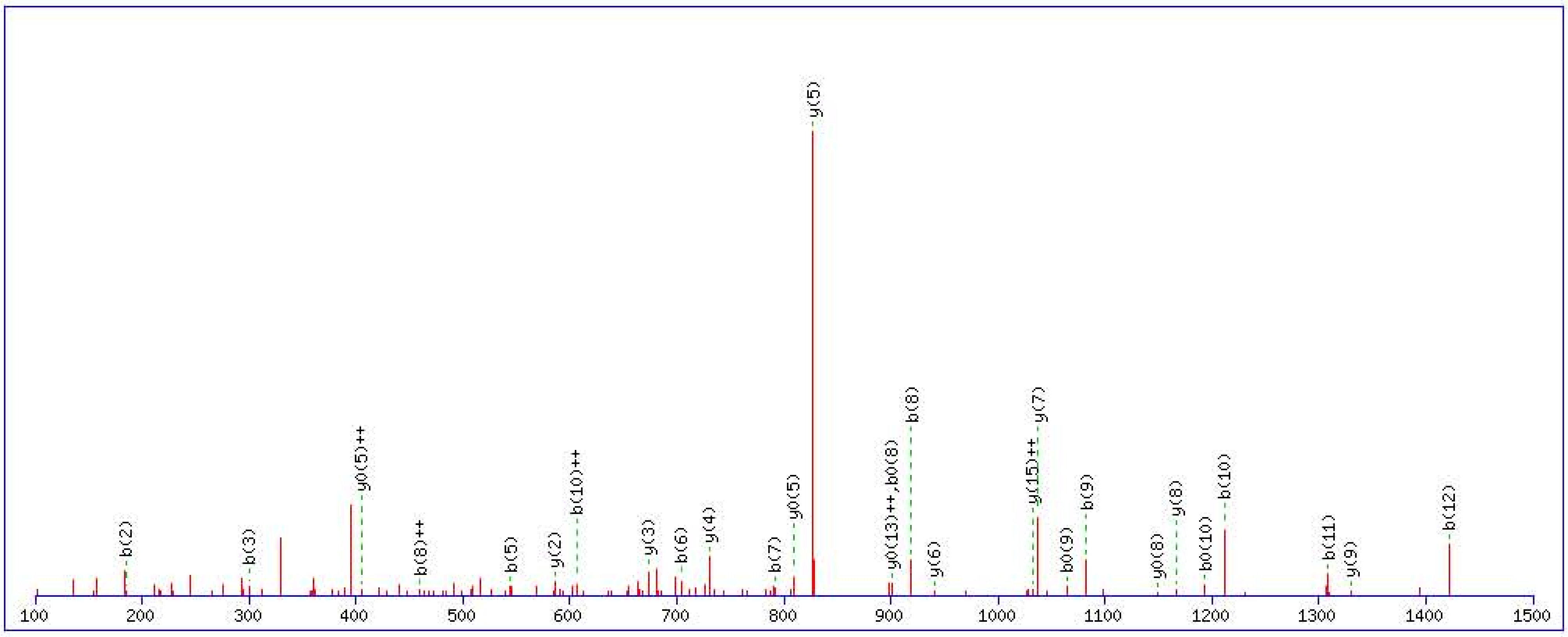
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

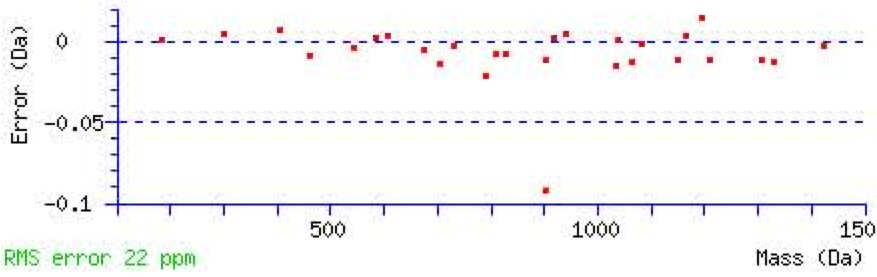
Match to Query 44029: 2247.011712 from(750.011180,3+) rtinseconds(1924) index(31261)
Title: Locus:1.1.1.3333.22 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

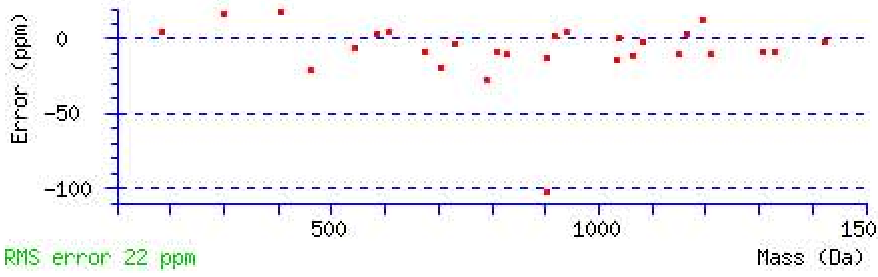
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2247.018753
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16     : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.00098
Matches : 28/170 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	72.044390	36.525833					A							17
2	***185.128454***	93.067865					I	2176.988934	1088.998105	2159.962385	1080.484830	2158.978369	1079.992822	16
3	***300.155397***	150.581336			282.144832	141.576054	D	2063.904870	1032.456073	2046.878321	1023.942798	2045.894305	1023.450790	15
4	429.197990	215.102633			411.187425	206.097351	E	1948.877927	974.942602	1931.851378	966.429327	1930.867362	965.937319	14
5	***544.224933***	272.616105			526.214368	263.610822	D	1819.835334	910.421305	1802.808785	901.908031	1801.824769	901.416022	13
6	***704.255582***	352.631429			686.245017	343.626147	C	1704.808391	852.907833	1687.781842	844.394559	1686.797826	843.902551	12
7	***791.287610***	396.147443			773.277045	387.142161	S	1544.777742	772.892509	1527.751193	764.379235	1526.767177	763.887227	11
8	***919.346188***	**460.176732**	902.319639	451.663458	901.335623	451.171450	Q	1457.745714	729.376495	1440.719165	720.863221	1439.735149	720.371212	10
9	***1082.409517***	541.708397	1065.382968	533.195122	1064.398952	532.703114	Y	***1329.687136***	665.347206	1312.660587	656.833931	1311.676571	656.341923	9
10	***1211.452110***	**606.229693**	1194.425561	597.716419	1193.441545	597.224410	E	***1166.623807***	583.815541	1149.597258	575.302267	1148.613242	574.810259	8
11	***1308.504874***	654.756075	1291.478325	646.242801	1290.494309	645.750792	P	***1037.581214***	519.294245	1020.554665	510.780971	1019.570649	510.288963	7
12	***1421.588938***	711.298107	1404.562389	702.784832	1403.578373	702.292824	I	***940.528450***	470.767863	923.501901	462.254589	922.517885	461.762581	6
13	1518.641702	759.824489	1501.615153	751.311215	1500.631137	750.819206	P	***827.444386***	414.225831	810.417837	405.712557	809.433821	405.220549	5
14	1575.663166	788.335221	1558.636617	779.821946	1557.652601	779.329938	G	***730.391622***	365.699449	713.365073	357.186175	712.381057	356.694167	4
15	1662.695194	831.851235	1645.668645	823.337961	1644.684629	822.845952	S	***673.370158***	337.188717	656.343609	328.675443	655.359593	328.183435	3
16	2101.920520	1051.463898	2084.893971	1042.950623	2083.909955	1042.458615	Q	***586.338130***	293.672703	569.311581	285.159429			2
17							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of AIDEDCSQYEPIPGSQK
(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	2247.018753	-0.007041	AIDEDCSQYEPIPGSQK

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

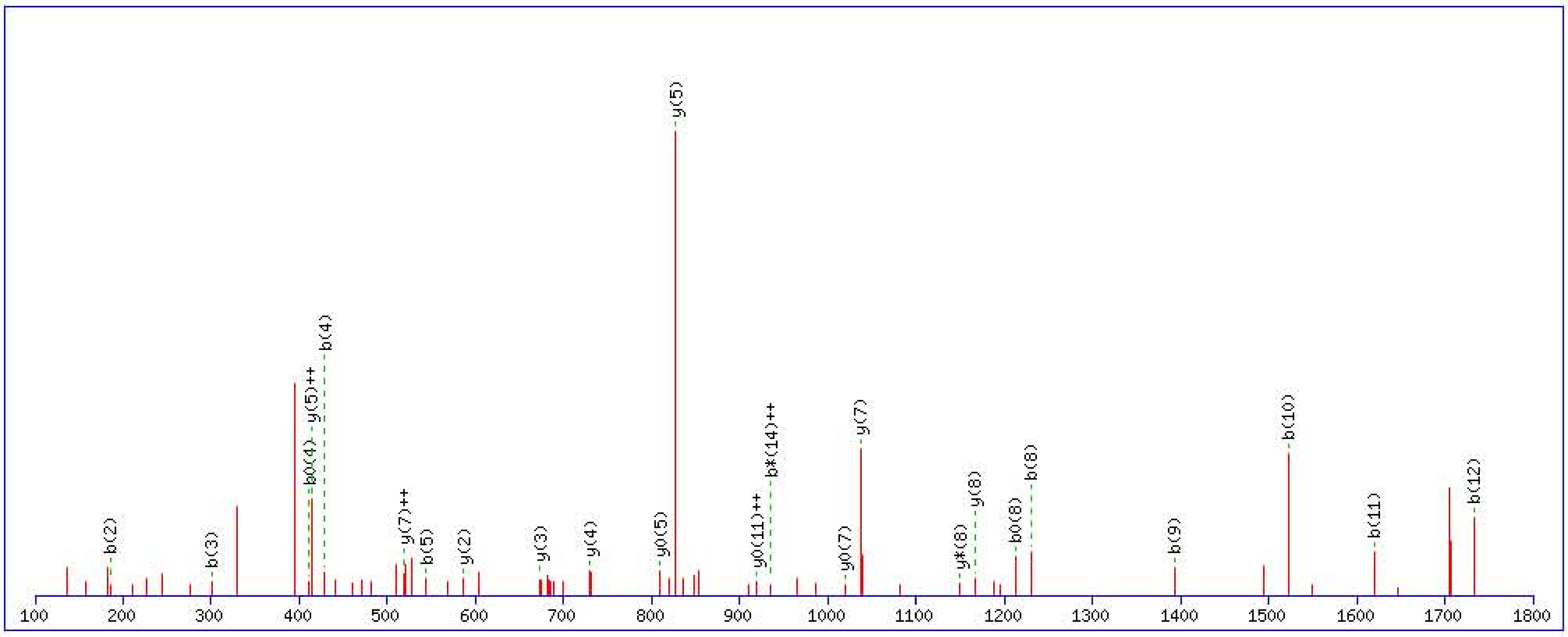
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

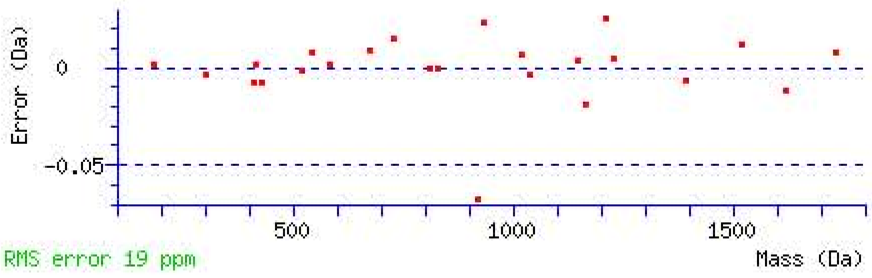
Match to Query 49088: 2558.183262 from(853.735030,3+) rtinseconds(2171) index(32859)
Title: Locus:1.1.1.3419.25 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

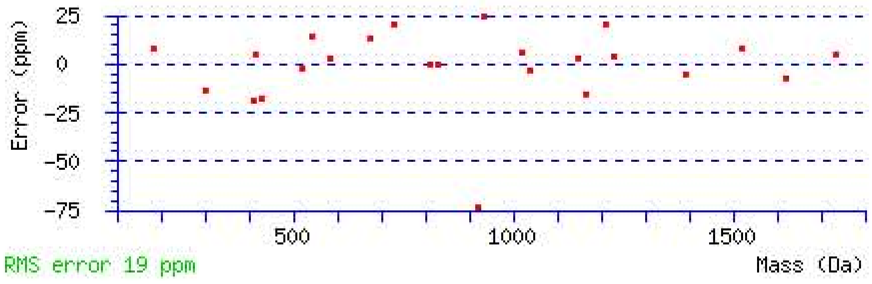
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2558.185501
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8     : Biotin:Thermo-21345 (Q)
Q16    : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.0015
Matches : 24/170 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	72.044390	36.525833					A							17
2	***185.128454***	93.067865					I	2488.155682	1244.581479	2471.129133	1236.068204	2470.145117	1235.576196	16
3	***300.155397***	150.581336			282.144832	141.576054	D	2375.071618	1188.039447	2358.045069	1179.526172	2357.061053	1179.034164	15
4	***429.197990***	215.102633			411.187425	206.097351	E	2260.044675	1130.525975	2243.018126	1122.012701	2242.034110	1121.520693	14
5	***544.224933***	272.616105			526.214368	263.610822	D	2131.002082	1066.004679	2113.975533	1057.491404	2112.991517	1056.999396	13
6	704.255582	352.631429			686.245017	343.626147	C	2015.975139	1008.491208	1998.948590	999.977933	1997.964574	999.485925	12
7	791.287610	396.147443			773.277045	387.142161	S	1855.944490	928.475883	1838.917941	919.962609	1837.933925	919.470601	11
8	***1230.512936***	615.760106	1213.486387	607.246832	1212.502371	606.754824	Q	1768.912462	884.959869	1751.885913	876.446595	1750.901897	875.954587	10
9	***1393.576265***	697.291771	1376.549716	688.778496	1375.565700	688.286488	Y	1329.687136	665.347206	1312.660587	656.833932	1311.676571	656.341924	9
10	***1522.618858***	761.813067	1505.592309	753.299793	1504.608293	752.807785	E	***1166.623807***	583.815541	1149.597258	575.302267	1148.613242	574.810259	8
11	***1619.671622***	810.339449	1602.645073	801.826175	1601.661057	801.334167	P	***1037.581214***	519.294245	1020.554665	510.780971	1019.570649	510.288963	7
12	***1732.755686***	866.881481	1715.729137	858.368207	1714.745121	857.876198	I	940.528450	470.767863	923.501901	462.254589	922.517885	461.762581	6
13	1829.808450	915.407863	1812.781901	906.894589	1811.797885	906.402581	P	***827.444386***	414.225831	810.417837	405.712557	809.433821	405.220549	5
14	1886.829914	943.918595	1869.803365	935.405321	1868.819349	934.913312	G	***730.391622***	365.699449	713.365073	357.186175	712.381057	356.694167	4
15	1973.861942	987.434609	1956.835393	978.921335	1955.851377	978.429327	S	***673.370158***	337.188717	656.343609	328.675443	655.359593	328.183435	3
16	2413.087268	1207.047272	2396.060719	1198.533997	2395.076703	1198.041989	Q	***586.338130***	293.672703	569.311581	285.159429			2
17							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of AIDEDCSQYEPIPGSQK
(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	2558.185501	-0.002239	AIDEDCSQYEPIPGSQK
1.1	2558.171906	0.011356	QGSGSGQSPGHGQRGSGSRQSPSYGR

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

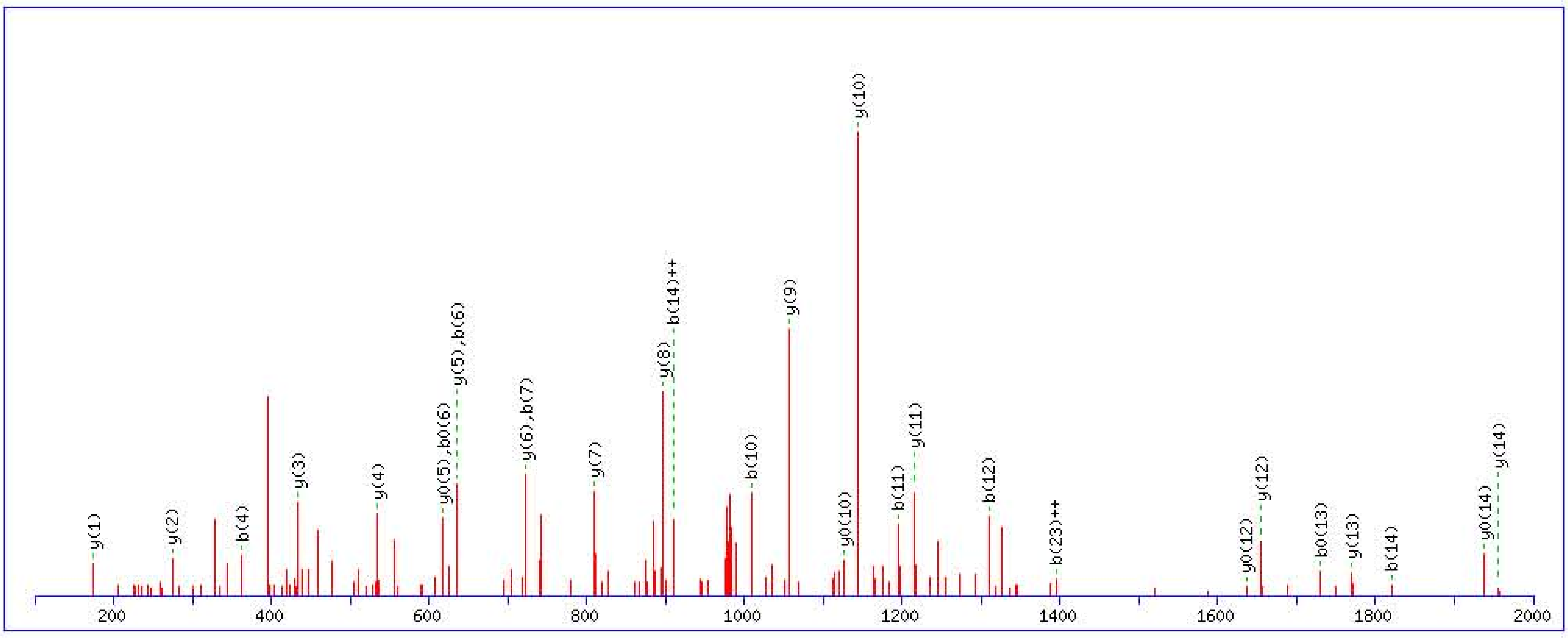
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

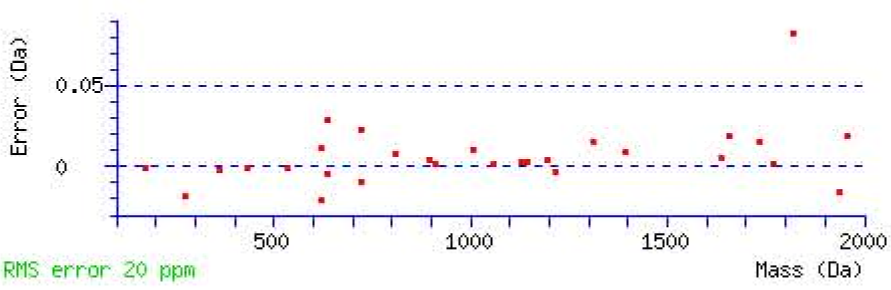
Match to Query 53707: 2962.273242 from(988.431690,3+) rtinseconds(2392) index(34047)
Title: Locus:1.1.1.3496.25 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

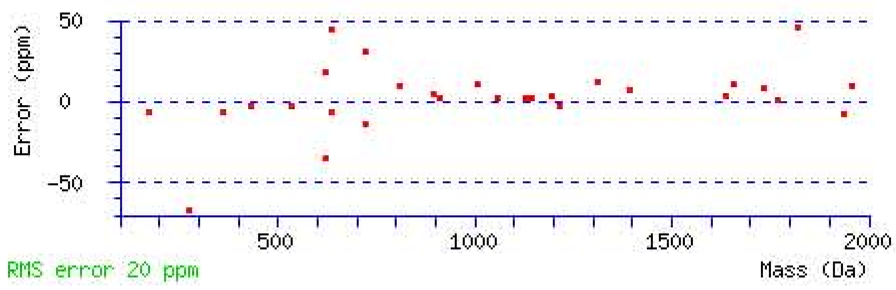
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2962.271835
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 109  Expect: 4.2e-011
Matches : 29/240 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	148.075690	74.541483					F							24
2	205.097154	103.052215					G	2816.210649	1408.608962	2799.184100	1400.095688	2798.200084	1399.603680	23
3	262.118618	131.562947					G	2759.189185	1380.098230	2742.162636	1371.584956	2741.178620	1371.092948	22
4	**363.166297**	182.086786			345.155732	173.081504	T	2702.167721	1351.587498	2685.141172	1343.074224	2684.157156	1342.582216	21
5	476.250361	238.628818			458.239796	229.623536	I	2601.120042	1301.063659	2584.093493	1292.550384	2583.109477	1292.058376	20
6	**636.281010**	318.644143			618.270445	309.638861	C	2488.035978	1244.521627	2471.009429	1236.008352	2470.025413	1235.516344	19
7	**723.313038**	362.160157			705.302473	353.154875	S	2328.005329	1164.506302	2310.978780	1155.993028	2309.994764	1155.501020	18
8	780.334502	390.670889			762.323937	381.665607	G	2240.973301	1120.990288	2223.946752	1112.477014	2222.962736	1111.985006	17
9	895.361445	448.184361			877.350880	439.179078	D	2183.951837	1092.479556	2166.925288	1083.966282	2165.941272	1083.474274	16
10	**1008.445509**	504.726393			990.434944	495.721110	I	2068.924894	1034.966085	2051.898345	1026.452810	2050.914329	1025.960802	15
11	**1194.524822**	597.766049			1176.514257	588.760767	W	***1955.840830***	978.424053	1938.814281	969.910778	1937.830265	969.418770	14
12	**1309.551765**	655.279521			1291.541200	646.274238	D	***1769.761517***	885.384396	1752.734968	876.871122	1751.750952	876.379114	13
13	1748.777091	874.892184	1731.750542	866.378909	1730.766526	865.886901	Q	***1654.734574***	827.870925	1637.708025	819.357650	1636.724009	818.865642	12
14	**1819.814205**	**910.410741**	1802.787656	901.897466	1801.803640	901.405458	A	***1215.509248***	608.258262	1198.482699	599.744987	1197.498683	599.252979	11
15	1906.846233	953.926755	1889.819684	945.413480	1888.835668	944.921472	S	***1144.472134***	572.739705	1127.445585	564.226430	1126.461569	563.734422	10
16	2066.876882	1033.942079	2049.850333	1025.428804	2048.866317	1024.936796	C	***1057.440106***	529.223691	1040.413557	520.710416	1039.429541	520.218408	9
17	2153.908910	1077.458093	2136.882361	1068.944818	2135.898345	1068.452810	S	***897.409457***	449.208366	880.382908	440.695092	879.398892	440.203084	8
18	2240.940938	1120.974107	2223.914389	1112.460832	2222.930373	1111.968825	S	***810.377429***	405.692352	793.350880	397.179078	792.366864	396.687070	7
19	2327.972966	1164.490121	2310.946417	1155.976847	2309.962401	1155.484839	S	***723.345401***	362.176338	706.318852	353.663064	705.334836	353.171056	6
20	2429.020645	1215.013960	2411.994096	1206.500686	2411.010080	1206.008678	T	***636.313373***	318.660324	619.286824	310.147050	618.302808	309.655042	5
21	2530.068324	1265.537800	2513.041775	1257.024525	2512.057759	1256.532517	T	***535.265694***	268.136485	518.239145	259.623210	517.255129	259.131202	4
22	2690.098973	1345.553124	2673.072424	1337.039850	2672.088408	1336.547842	C	***434.218015***	217.612645	417.191466	209.099371			3
23	2789.167387	**1395.087331**	2772.140838	1386.574057	2771.156822	1386.082049	V	***274.187366***	137.597321	257.160817	129.084046			2
24							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
109.4	2962.271835	0.001407	FGGTICSGDIWDQASCSSSTTCVR

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

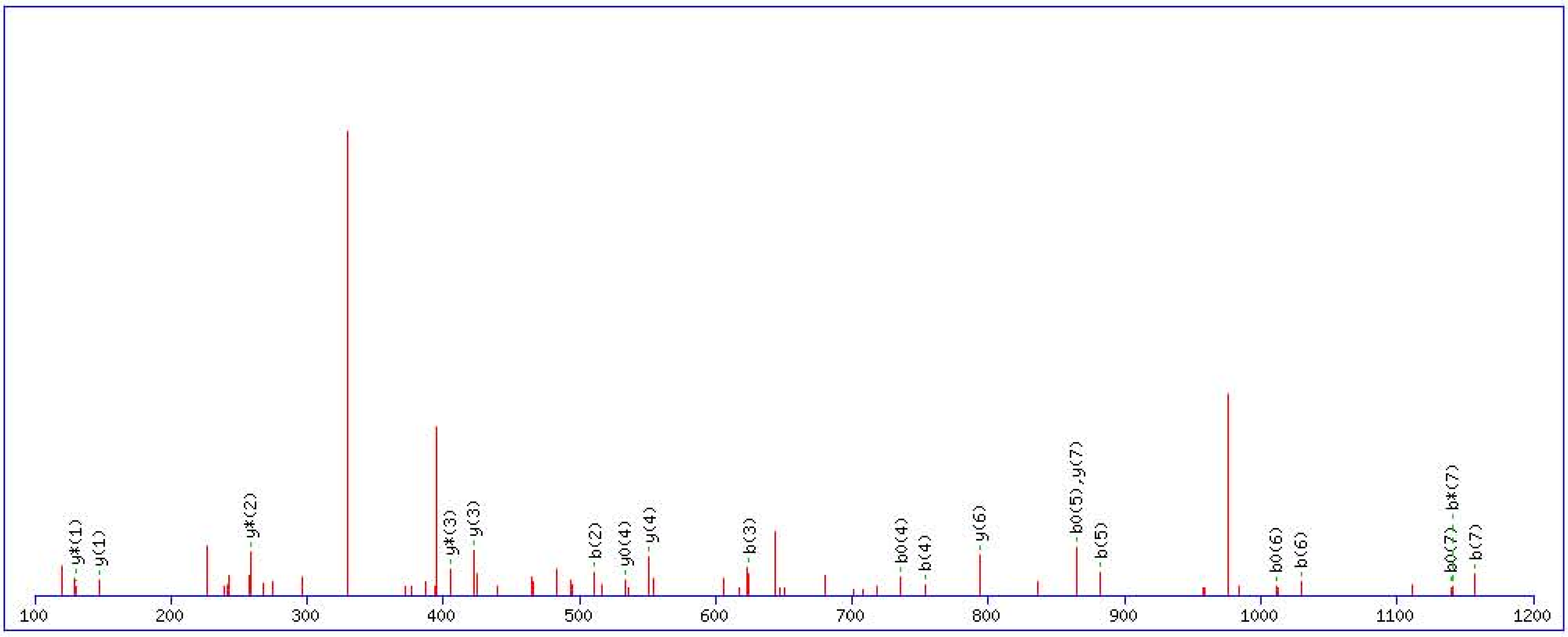
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QALEEFQK**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

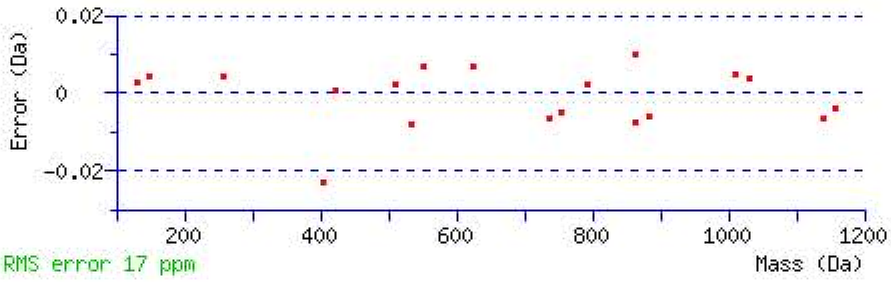
Match to Query 20406: 1302.661688 from(652.338120,2+) rtinseconds(1896) index(18288)
Title: Locus:1.1.1.3226.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

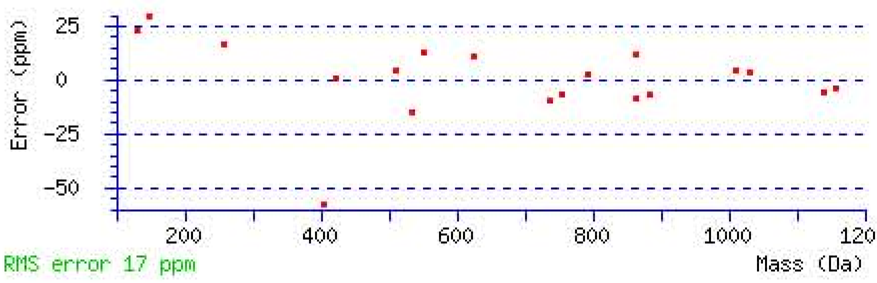
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1302.664185
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.047
Matches : 20/72 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	440.232602	220.619939	423.206053	212.106664			Q							8
2	***511.269716***	256.138496	494.243167	247.625221			A	***864.446160***	432.726718	847.419611	424.213443	846.435595	423.721435	7
3	***624.353780***	312.680528	607.327231	304.167254			L	***793.409046***	397.208161	776.382497	388.694887	775.398481	388.202879	6
4	***753.396373***	377.201825	736.369824	368.688550	735.385808	368.196542	E	680.324982	340.666129	663.298433	332.152854	662.314417	331.660846	5
5	***882.438966***	441.723121	865.412417	433.209847	864.428401	432.717839	E	***551.282389***	276.144833	534.255840	267.631558	533.271824	267.139550	4
6	***1029.507380***	515.257328	1012.480831	506.744054	1011.496815	506.252046	F	***422.239796***	211.623536	405.213247	203.110261			3
7	***1157.565958***	579.286617	1140.539409	570.773343	1139.555393	570.281334	Q	275.171382	138.089329	258.144833	129.576054			2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.4	1302.664185	-0.002497	QALEEFQK
18.3	1302.650269	0.011419	YLKQQCHAQK
12.9	1302.667542	-0.005854	KEALMQEK
7.7	1302.660141	0.001547	EAEGKLAAQMQK
7.4	1302.660187	0.001501	QPPVTMETTKR
7.4	1302.643097	0.018591	CQLGFFGFSIK
7.3	1302.668030	-0.006342	YLKQQQDAPGR
7.1	1302.649582	0.012106	FYSLLDPSYAK
6.7	1302.668045	-0.006357	QPAGPASATPPGPR
5.3	1302.667542	-0.005854	EAKEMLQK

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

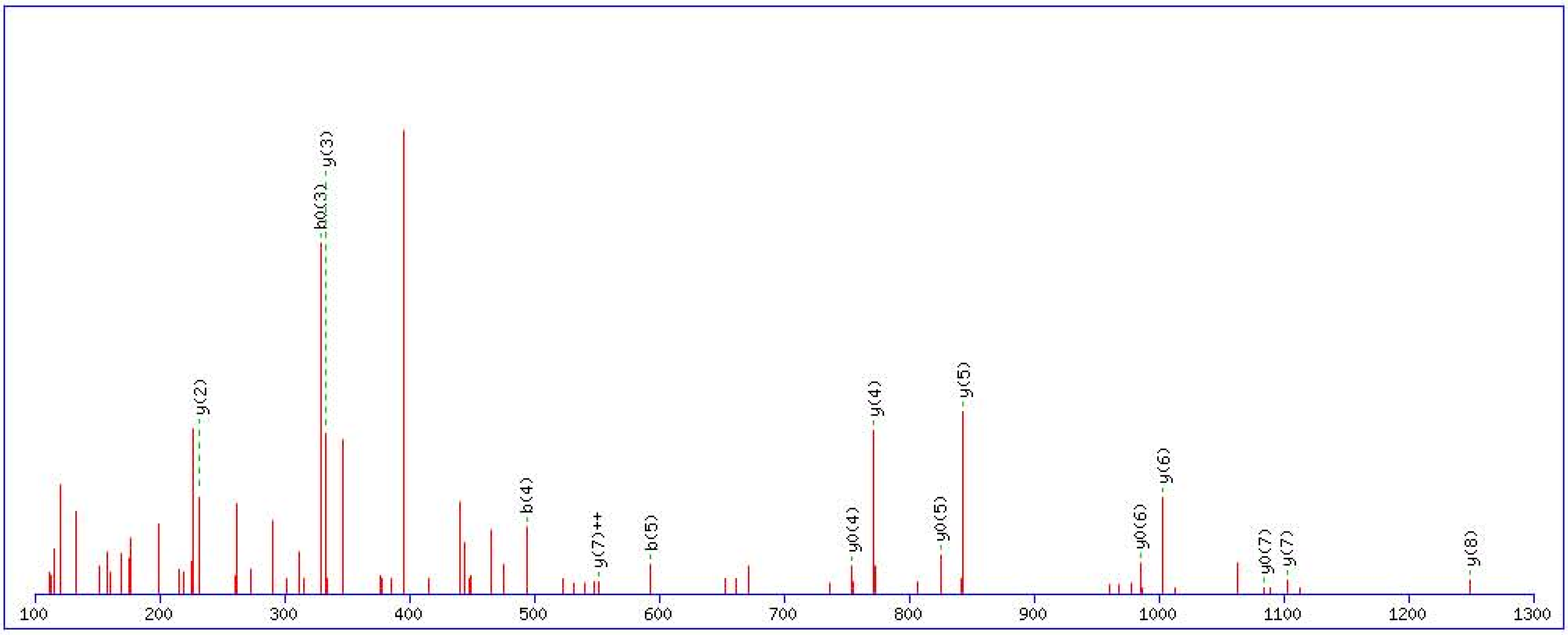
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **CEGFVCAQTGR**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

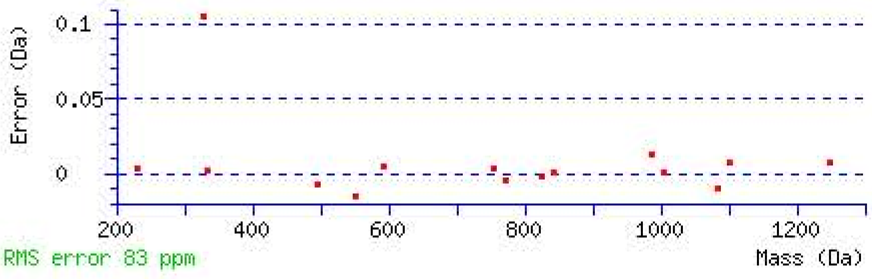
Match to Query 30279: 1594.702002 from(532.574610,3+) rtinseconds(1801) index(17738)
Title: Locus:1.1.1.3193.6 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

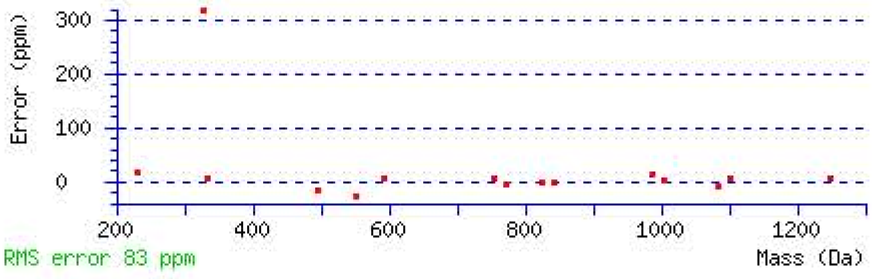
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1594.705460
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.0048
Matches : 15/100 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	161.037925	81.022600					C							11
2	290.080518	145.543897			272.069953	136.538615	E	1435.682069	718.344673	1418.655520	709.831398	1417.671504	709.339390	10
3	347.101982	174.054629			329.091417	165.049347	G	1306.639476	653.823376	1289.612927	645.310102	1288.628911	644.818094	9
4	**494.170396**	247.588836			476.159831	238.583554	F	***1249.618012***	625.312644	1232.591463	616.799370	1231.607447	616.307361	8
5	**593.238810**	297.123043			575.228245	288.117761	V	***1102.549598***	551.778437	1085.523049	543.265162	1084.539033	542.773154	7
6	753.269459	377.138368			735.258894	368.133085	C	***1003.481184***	502.244230	986.454635	493.730955	985.470619	493.238947	6
7	824.306573	412.656925			806.296008	403.651642	A	***843.450535***	422.228906	826.423986	413.715631	825.439970	413.223623	5
8	1263.531899	632.269588	1246.505350	623.756313	1245.521334	623.264305	Q	***772.413421***	386.710349	755.386872	378.197074	754.402856	377.705066	4
9	1364.579578	682.793427	1347.553029	674.280153	1346.569013	673.788145	T	***333.188095***	167.097685	316.161546	158.584411	315.177530	158.092403	3
10	1421.601042	711.304159	1404.574493	702.790885	1403.590477	702.298877	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 CEGFVCAQTGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.7	1594.705460	-0.003458	CEGFVCAQTGR

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

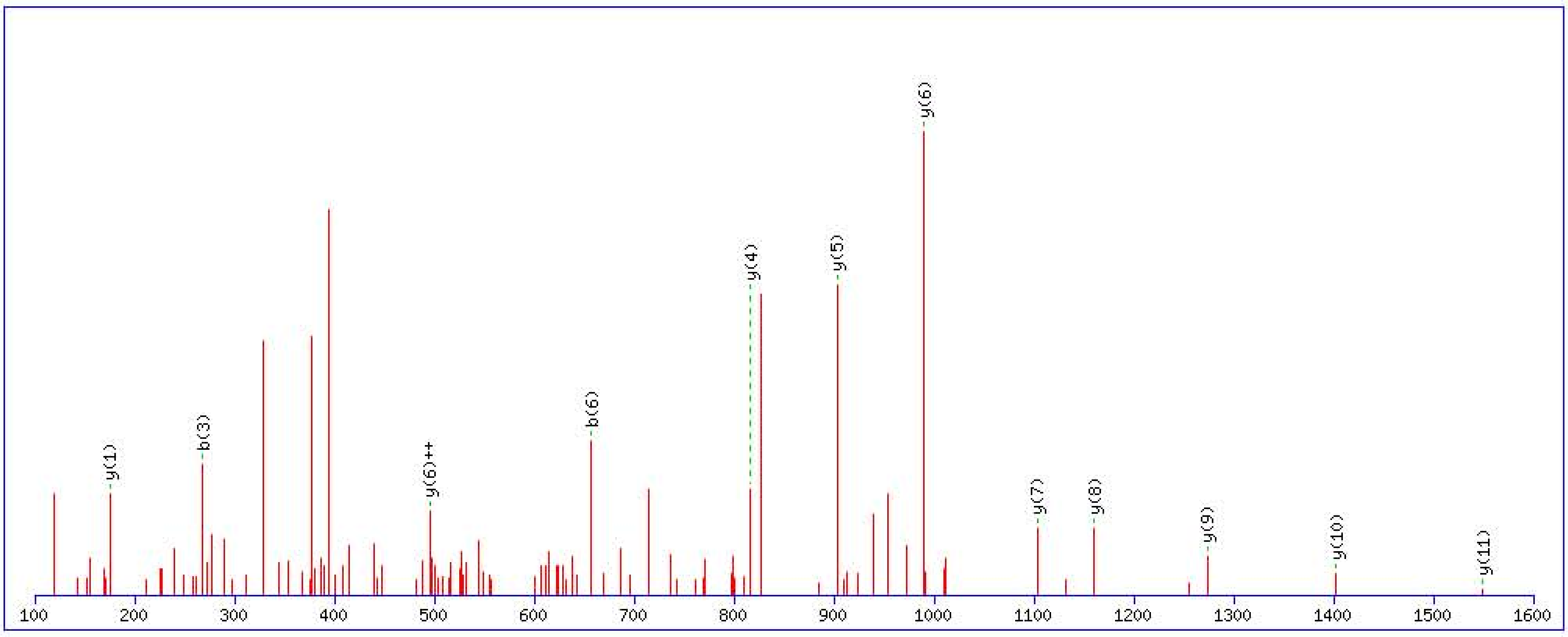
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPGIFELGISSQSDR**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

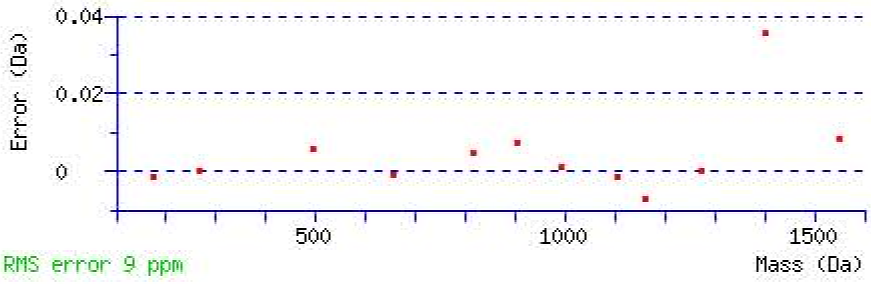
Match to Query 37963: 1929.009162 from(644.010330,3+) rtinseconds(2703) index(23017)
Title: Locus:1.1.1.3506.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

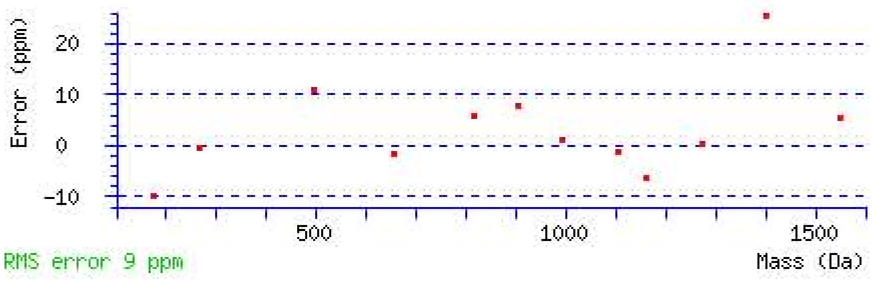
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1929.002975
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 78  Expect: 1.7e-007
Matches : 12/134 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	114.091340	57.549308					I							15
2	211.144104	106.075690					P	1816.926196	908.966736	1799.899647	900.453462	1798.915631	899.961454	14
3	**268.165568**	134.586422					G	1719.873432	860.440354	1702.846883	851.927080	1701.862867	851.435072	13
4	381.249632	191.128454					I	1662.851968	831.929622	1645.825419	823.416348	1644.841403	822.924340	12
5	528.318046	264.662661					F	***1549.767904***	775.387590	1532.741355	766.874316	1531.757339	766.382308	11
6	**657.360639**	329.183958			639.350074	320.178675	E	***1402.699490***	701.853383	1385.672941	693.340109	1384.688925	692.848101	10
7	770.444703	385.725990			752.434138	376.720707	L	***1273.656897***	637.332087	1256.630348	628.818812	1255.646332	628.326804	9
8	827.466167	414.236722			809.455602	405.231439	G	***1160.572833***	580.790055	1143.546284	572.276780	1142.562268	571.784772	8
9	940.550231	470.778754			922.539666	461.773471	I	***1103.551369***	552.279323	1086.524820	543.766048	1085.540804	543.274040	7
10	1027.582259	514.294768			1009.571694	505.289485	S	***990.467305***	495.737291	973.440756	487.224016	972.456740	486.732008	6
11	1114.614287	557.810782			1096.603722	548.805499	S	***903.435277***	452.221277	886.408728	443.708002	885.424712	443.215994	5
12	1553.839613	777.423445	1536.813064	768.910170	1535.829048	768.418162	Q	***816.403249***	408.705263	799.376700	400.191988	798.392684	399.699980	4
13	1640.871641	820.939459	1623.845092	812.426184	1622.861076	811.934176	S	377.177923	189.092600	360.151374	180.579325	359.167358	180.087317	3
14	1755.898584	878.452930	1738.872035	869.939656	1737.888019	869.447648	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 IPGIFELGISSQSDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
78.1	1929.002975	0.006187	IPGIFELGISSQSDR
5.6	1928.996445	0.012717	QCQVILNFLAAEGR
1.8	1929.020721	-0.011559	RELEELSVGSDGVLIWK
1.7	1929.018219	-0.009057	LPEFLVQLYSYMRVR
0.1	1929.012833	-0.003671	EMEERTITIEIPEVLK

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

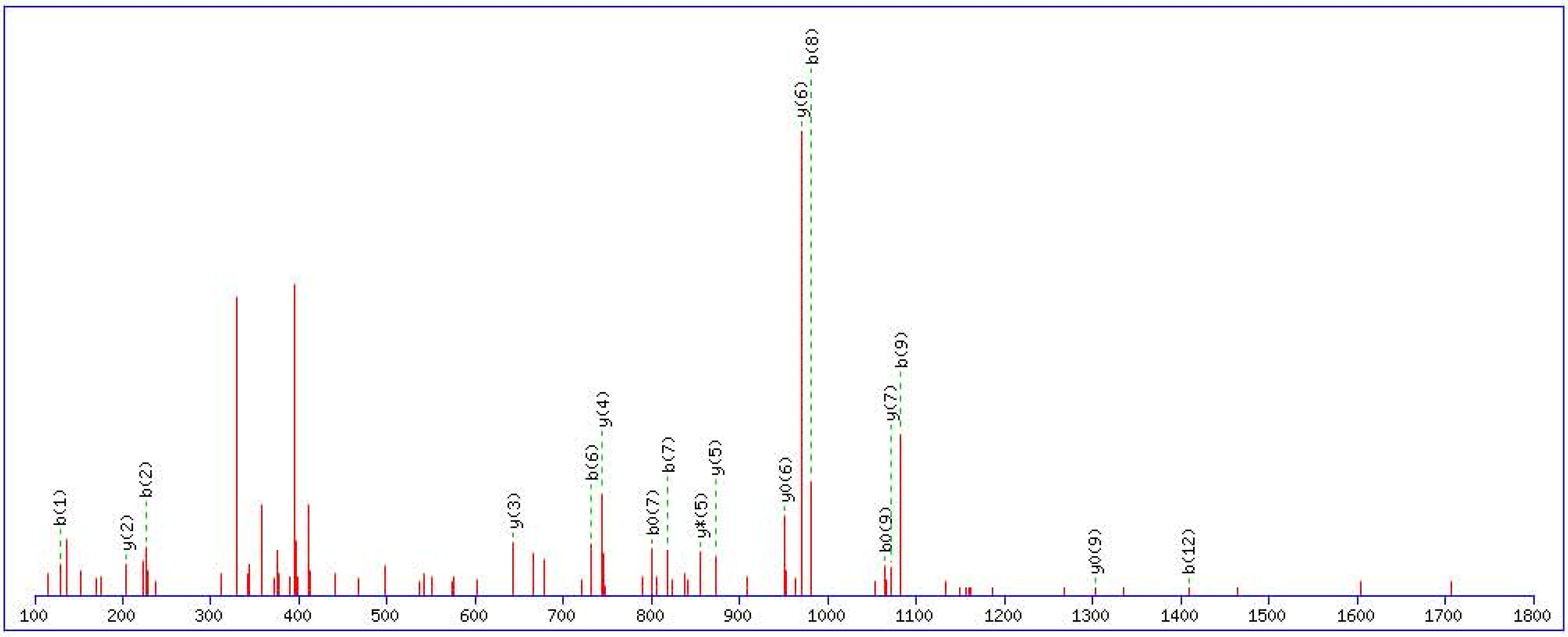
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPYNVESYTPQTQGK**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

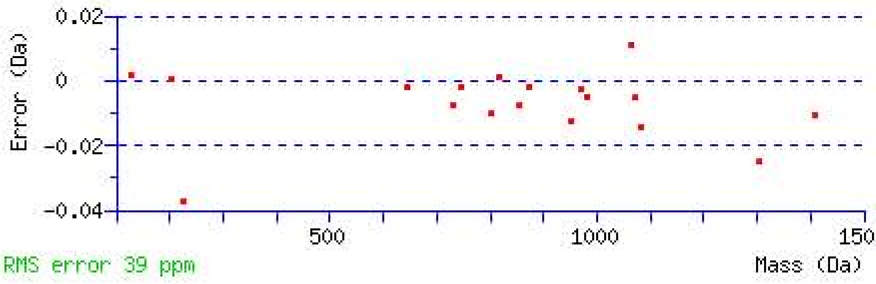
Match to Query 40856: 2050.007952 from(684.343260,3+) rtinseconds(1636) index(16749)
Title: Locus:1.1.1.3135.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

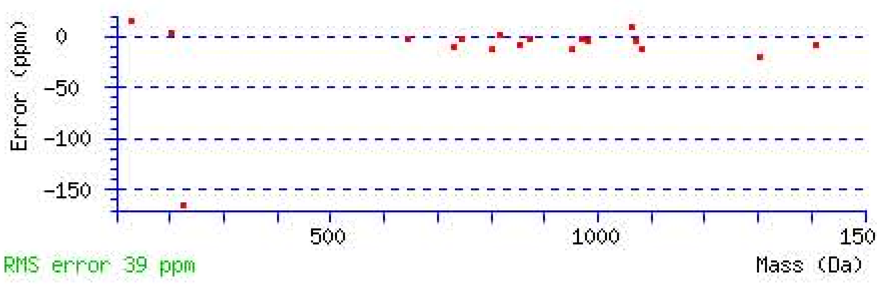


```
Monoisotopic mass of neutral peptide Mr(calc): 2050.019348
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.001
Matches : 18/152 fragment ions using 40 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	***129.102239***	65.054757	112.075690	56.541483			K							15
2	***226.155003***	113.581139	209.128454	105.067865			P	1922.931678	961.969477	1905.905129	953.456203	1904.921113	952.964195	14
3	389.218332	195.112804	372.191783	186.599529			Y	1825.878914	913.443095	1808.852365	904.929821	1807.868349	904.437813	13
4	503.261259	252.134267	486.234710	243.620993			N	1662.815585	831.911431	1645.789036	823.398156	1644.805020	822.906148	12
5	602.329673	301.668475	585.303124	293.155200			V	1548.772658	774.889967	1531.746109	766.376693	1530.762093	765.884685	11
6	***731.372266***	366.189771	714.345717	357.676497	713.361701	357.184489	E	1449.704244	725.355760	1432.677695	716.842486	1431.693679	716.350478	10
7	***818.404294***	409.705785	801.377745	401.192511	800.393729	400.700503	S	1320.661651	660.834464	1303.635102	652.321189	1302.651086	651.829181	9
8	***981.467623***	491.237450	964.441074	482.724175	963.457058	482.232167	Y	1233.629623	617.318450	1216.603074	608.805175	1215.619058	608.313167	8
9	***1082.515302***	541.761289	1065.488753	533.248015	1064.504737	532.756007	T	***1070.566294***	535.786785	1053.539745	527.273511	1052.555729	526.781503	7
10	1179.568066	590.287671	1162.541517	581.774397	1161.557501	581.282389	P	***969.518615***	485.262946	952.492066	476.749671	951.508050	476.257663	6
11	1307.626644	654.316960	1290.600095	645.803686	1289.616079	645.311678	Q	***872.465851***	436.736564	855.439302	428.223289	854.455286	427.731281	5
12	***1408.674323***	704.840800	1391.647774	696.327525	1390.663758	695.835517	T	***744.407273***	372.707275	727.380724	364.194000	726.396708	363.701992	4
13	1847.899649	924.453463	1830.873100	915.940188	1829.889084	915.448180	Q	***643.359594***	322.183435	626.333045	313.670161			3
14	1904.921113	952.964195	1887.894564	944.450920	1886.910548	943.958912	G	***204.134268***	102.570772	187.107719	94.057497			2
15							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 39 ppm



RMS error 39 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.1	2050.019348	-0.011396	KPYNVESYTPQTQGK
17.6	2050.019348	-0.011396	KPYNVESYTPQTQGK
1.3	2050.026566	-0.018614	LFVGMLNKQQSEDDVRR
1.1	2050.033966	-0.026014	QTVMFTATMPPAVERLAR

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

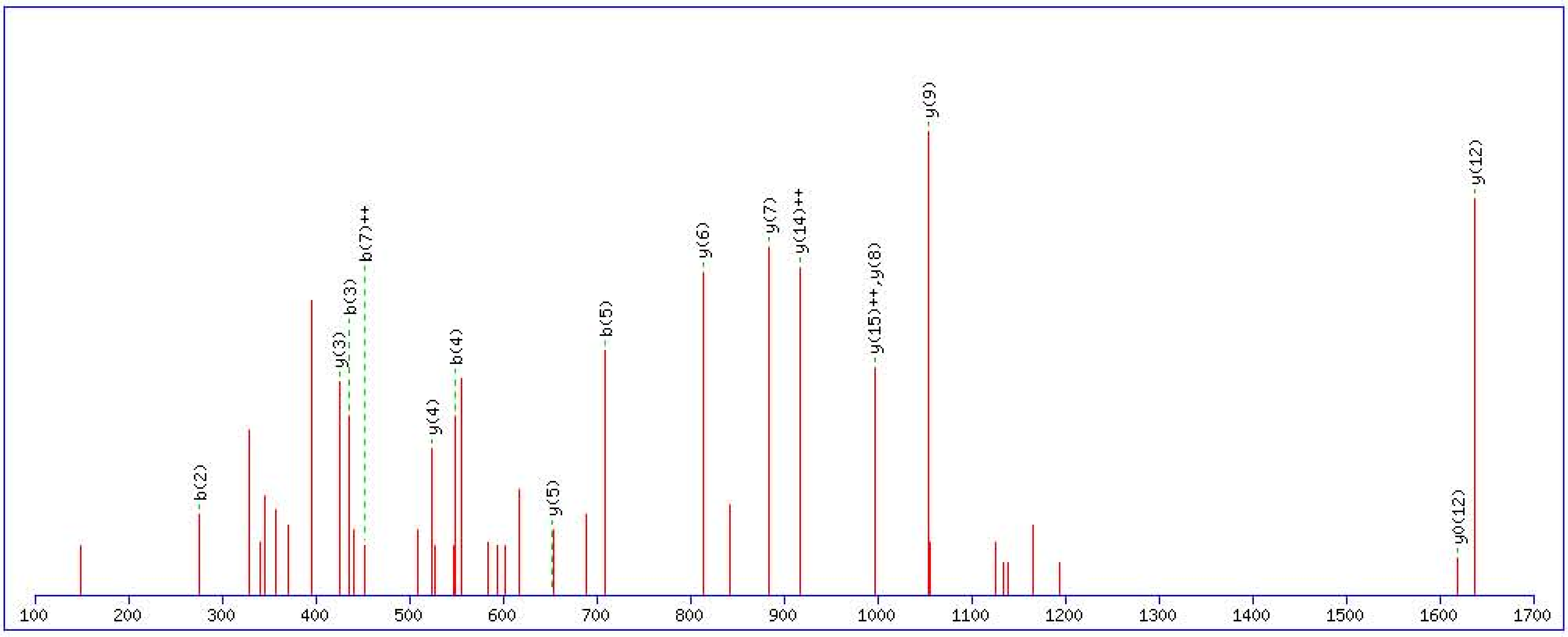
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CDCICPVGSQGLACEVSYR**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

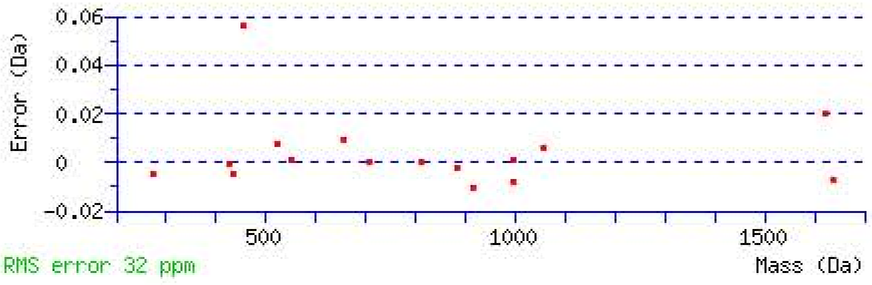
Match to Query 48965: 2541.097872 from(848.039900,3+) rtinseconds(2185) index(20159)
Title: Locus:1.1.1.3326.24 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

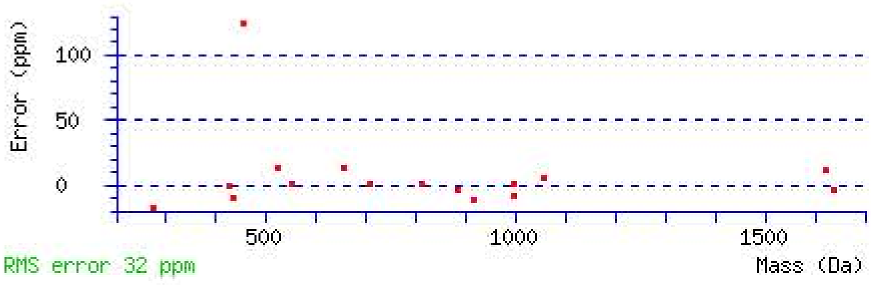
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2541.094299
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 37 **Expect:** 0.00075
Matches : 16/192 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	161.037925	81.022600					C							19
2	***276.064868***	138.536072			258.054303	129.530790	D	2382.070908	1191.539092	2365.044359	1183.025817	2364.060343	1182.533809	18
3	***436.095517***	218.551397			418.084952	209.546114	C	2267.043965	1134.025620	2250.017416	1125.512346	2249.033400	1125.020338	17
4	***549.179581***	275.093429			531.169016	266.088146	I	2107.013316	1054.010296	2089.986767	1045.497021	2089.002751	1045.005013	16
5	***709.210230***	355.108753			691.199665	346.103471	C	1993.929252	997.468264	1976.902703	988.954990	1975.918687	988.462982	15
6	806.262994	403.635135			788.252429	394.629853	P	1833.898603	917.452940	1816.872054	908.939665	1815.888038	908.447657	14
7	905.331408	453.169342			887.320843	444.164060	V	1736.845839	868.926558	1719.819290	860.413283	1718.835274	859.921275	13
8	962.352872	481.680074			944.342307	472.674792	G	***1637.777425***	819.392351	1620.750876	810.879076	1619.766860	810.387068	12
9	1049.384900	525.196088			1031.374335	516.190806	S	1580.755961	790.881619	1563.729412	782.368344	1562.745396	781.876336	11
10	1488.610226	744.808751	1471.583677	736.295477	1470.599661	735.803469	Q	1493.723933	747.365605	1476.697384	738.852330	1475.713368	738.360322	10
11	1545.631690	773.319483	1528.605141	764.806209	1527.621125	764.314201	G	***1054.498607***	527.752941	1037.472058	519.239667	1036.488042	518.747659	9
12	1658.715754	829.861515	1641.689205	821.348241	1640.705189	820.856233	L	***997.477143***	499.242209	980.450594	490.728935	979.466578	490.236927	8
13	1729.752868	865.380072	1712.726319	856.866798	1711.742303	856.374790	A	***884.393079***	442.700178	867.366530	434.186903	866.382514	433.694895	7
14	1889.783517	945.395397	1872.756968	936.882122	1871.772952	936.390114	C	***813.355965***	407.181621	796.329416	398.668346	795.345400	398.176338	6
15	2018.826110	1009.916693	2001.799561	1001.403419	2000.815545	1000.911411	E	***653.325316***	327.166296	636.298767	318.653021	635.314751	318.161013	5
16	2117.894524	1059.450900	2100.867975	1050.937625	2099.883959	1050.445617	V	***524.282723***	262.645000	507.256174	254.131725	506.272158	253.639717	4
17	2204.926552	1102.966914	2187.900003	1094.453639	2186.915987	1093.961631	S	***425.214309***	213.110793	408.187760	204.597518	407.203744	204.105510	3
18	2367.989881	1184.498578	2350.963332	1175.985304	2349.979316	1175.493296	Y	338.182281	169.594778	321.155732	161.081504			2
19							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.2	2541.094299	0.003573	CDCICPVGSQGLACEVSYR

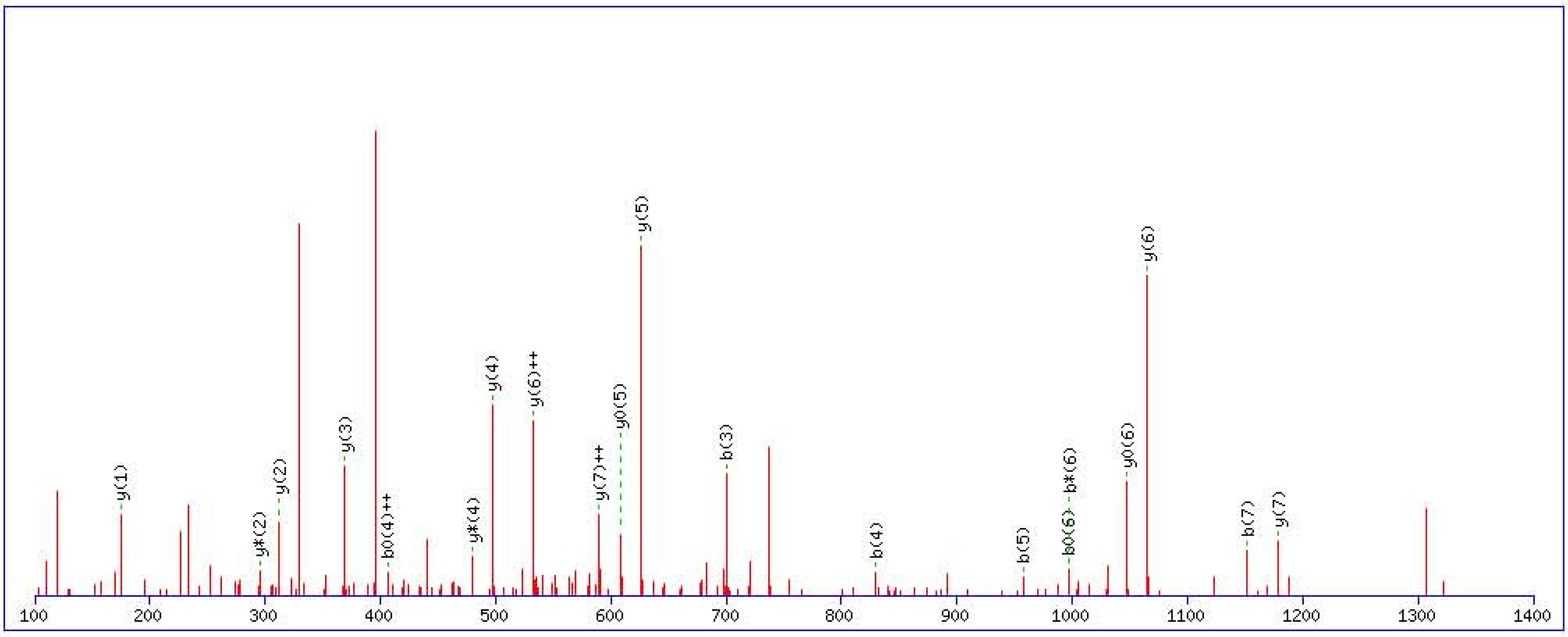
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLQEQGHR**
Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

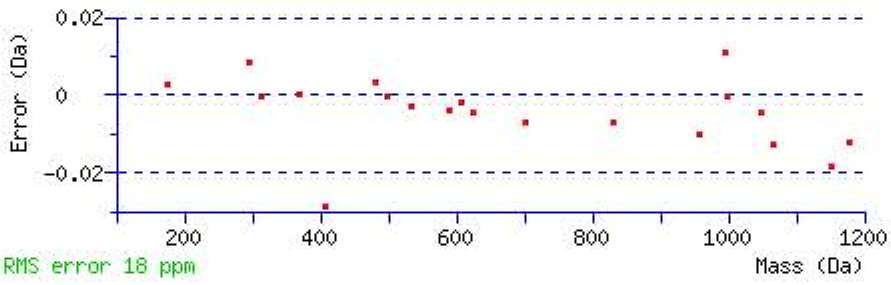
Match to Query 20787: 1324.666948 from(663.340750,2+) rtinseconds(1541) index(16123)
Title: Locus:1.1.1.3102.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

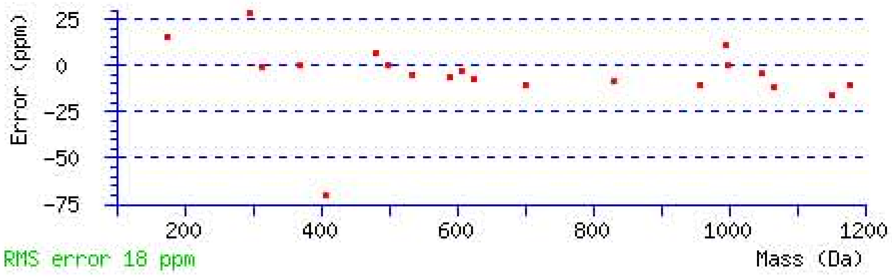
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1324.671021
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.0063
Matches : 20/66 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	148.075690	74.541483					F							8
2	261.159754	131.083515					L	*1178.609889*	589.808583	1161.583340	581.295308	1160.599324	580.803300	7
3	**700.385080**	350.696178	683.358531	342.182904			Q	*1065.525825*	533.266551	1048.499276	524.753276	1047.515260	524.261268	6
4	**829.427673**	415.217475	812.401124	406.704200	811.417108	406.212192	E	*626.300499*	313.653888	609.273950	305.140613	608.289934	304.648605	5
5	**957.486251**	479.246764	940.459702	470.733489	939.475686	470.241481	Q	*497.257906*	249.132591	480.231357	240.619317			4
6	1014.507715	507.757496	997.481166	499.244221	996.497150	498.752213	G	*369.199328*	185.103302	352.172779	176.590028			3
7	**1151.566627**	576.286952	1134.540078	567.773677	1133.556062	567.281669	H	*312.177864*	156.592570	295.151315	148.079296			2
8							R	*175.118952*	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.7	1324.671021	-0.004073	FLQEQGHR
10.2	1324.671021	-0.004073	FLQEQGHR
8.7	1324.669647	-0.002699	MKEIAEAYLGGK
8.1	1324.663605	0.003343	RLDWEGKEHR
3.4	1324.663620	0.003328	SKSHEFQLGHR
2.6	1324.647888	0.019060	LMKSAIGEGMTR
1.5	1324.684753	-0.017805	VLVGDRNDNAPR
0.9	1324.680908	-0.013960	FIASTGMDRSLK

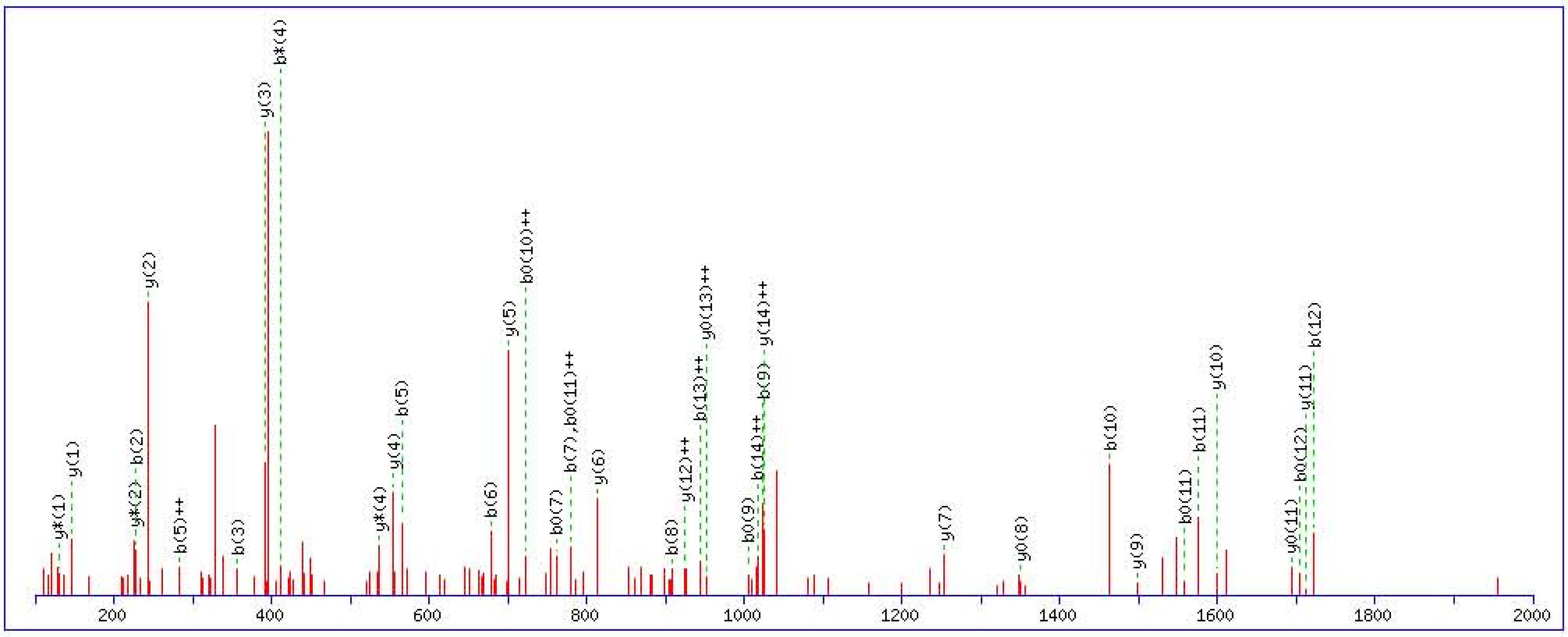
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQEAHLTEDQIFYFPK**
Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

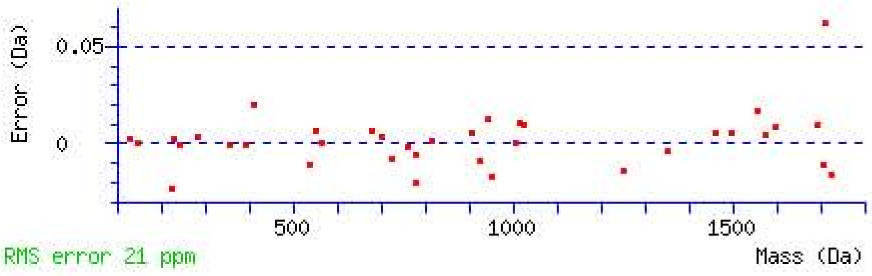
Match to Query 27818: 2275.127052 from(759.382960,3+) rtinseconds(2374) index(33934)
Title: Locus:1.1.1.3490.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

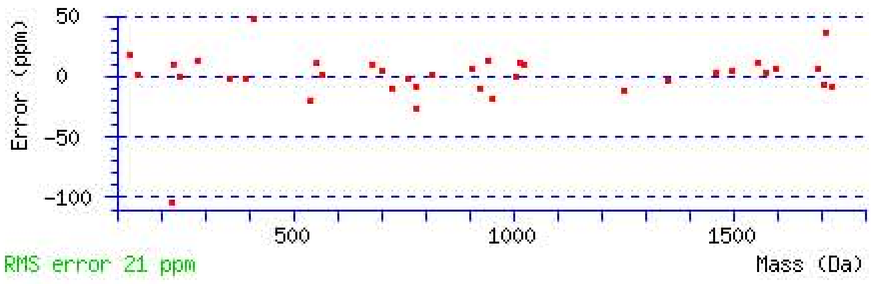
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2275.134720
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.00016
Matches : 38/160 fragment ions using 86 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							16
2	***228.134268***	114.570772	211.107719	106.057498			Q	2177.073591	1089.040433	2160.047042	1080.527159	2159.063026	1080.035151	15
3	***357.176861***	179.092069	340.150312	170.578794	339.166296	170.086786	E	2049.015013	1025.011144	2031.988464	1016.497870	2031.004448	1016.005862	14
4	428.213975	214.610626	411.187426	206.097351	410.203410	205.605343	A	1919.972420	960.489848	1902.945871	951.976573	1901.961855	951.484565	13
5	***565.272887***	**283.140082**	548.246338	274.626807	547.262322	274.134799	H	1848.935306	924.971291	1831.908757	916.458016	1830.924741	915.966008	12
6	***678.356951***	339.682114	661.330402	331.168839	660.346386	330.676831	L	***1711.876394***	856.441835	1694.849845	847.928561	1693.865829	847.436552	11
7	***779.404630***	390.205953	762.378081	381.692679	761.394065	381.200671	T	***1598.792330***	799.899803	1581.765781	791.386529	1580.781765	790.894521	10
8	***908.447223***	454.727250	891.420674	446.213975	890.436658	445.721967	E	***1497.744651***	749.375963	1480.718102	740.862689	1479.734086	740.370681	9
9	***1023.474166***	512.240721	1006.447617	503.727447	1005.463601	503.235439	D	1368.702058	684.854667	1351.675509	676.341392	1350.691493	675.849384	8
10	***1462.699492***	731.853384	1445.672943	723.340110	1444.688927	722.848101	Q	***1253.675115***	627.341195	1236.648566	618.827921			7
11	***1575.783556***	788.395416	1558.757007	779.882141	1557.772991	779.390133	I	***814.449789***	407.728533	797.423240	399.215258			6
12	***1722.851970***	861.929623	1705.825421	853.416349	1704.841405	852.924340	F	***701.365725***	351.186501	684.339176	342.673226			5
13	1885.915299	**943.461288**	1868.888750	934.948013	1867.904734	934.456005	Y	***554.297311***	277.652294	537.270762	269.139019			4
14	2032.983713	**1016.995495**	2015.957164	1008.482220	2014.973148	1007.990212	F	***391.233982***	196.120629	374.207433	187.607354			3
15	2130.036477	1065.521876	2113.009928	1057.008602	2112.025912	1056.516594	P	***244.165568***	122.586422	227.139019	114.073147			2
16							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.7	2275.134720	-0.007668	VQEAHLTEDQIFYFPK
19.9	2275.134720	-0.007668	VQEAHLTEDQIFYFPK
2.1	2275.116302	0.010750	HTEQQESLDQK
2.0	2275.160538	-0.033486	VLPYCWKGMTPEQQAAIRK

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

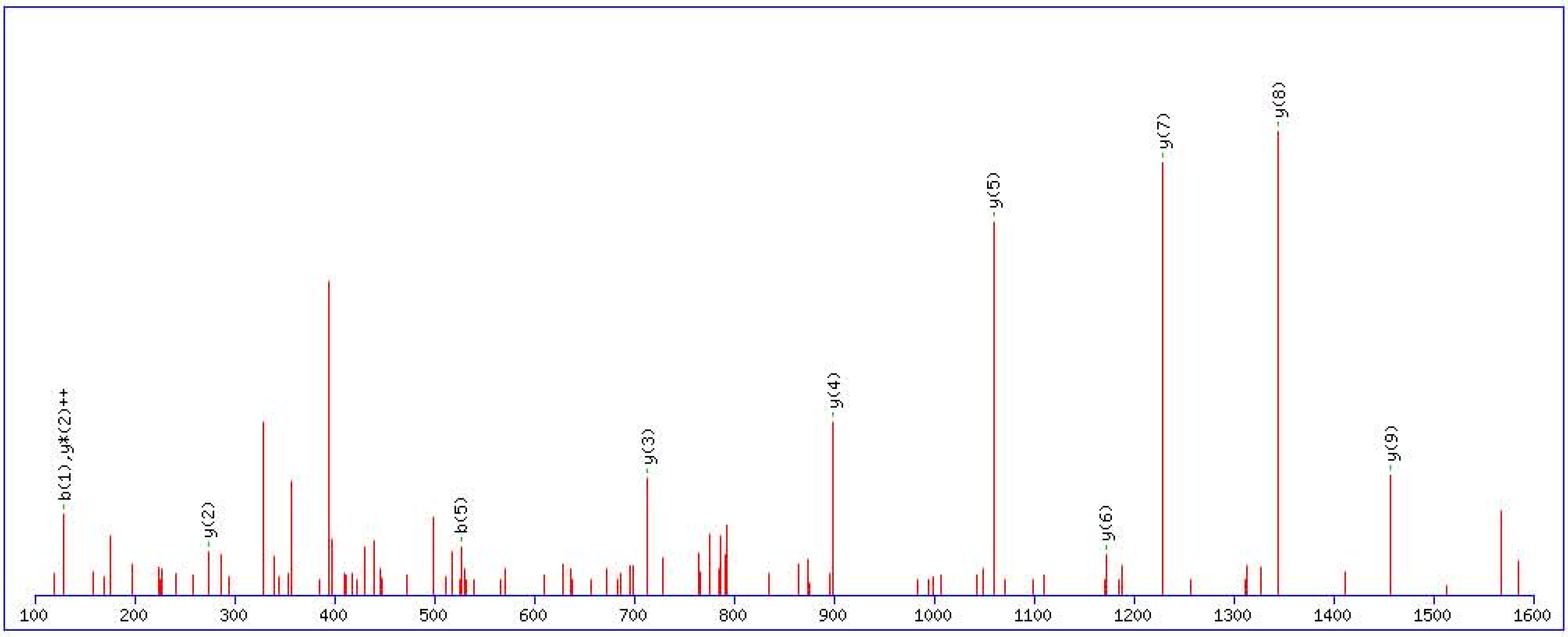
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLDGICWQVR**
Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

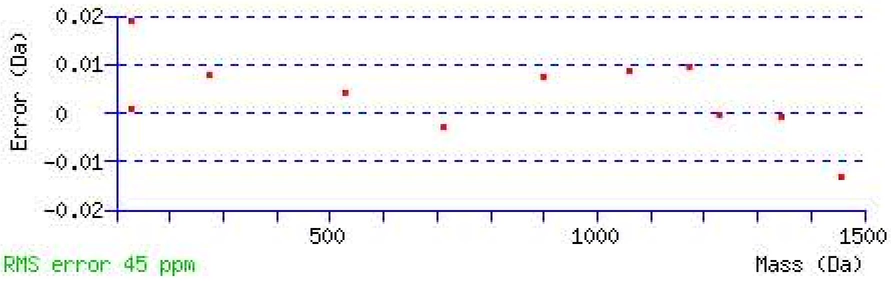
Match to Query 29936: 1584.826188 from(793.420370,2+) rtinseconds(2075) index(19456)
Title: Locus:1.1.1.3288.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

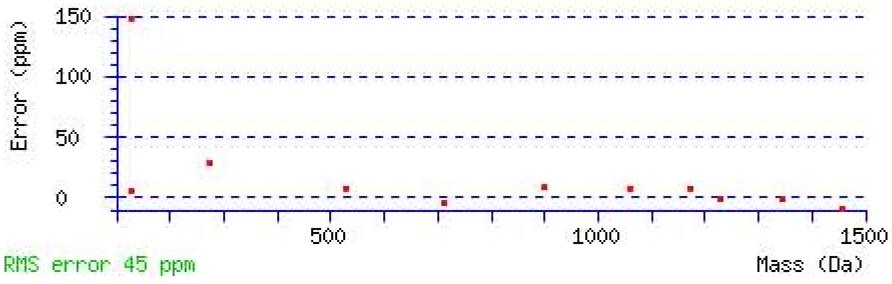
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1584.826874
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 64  Expect: 3.9e-006
Matches : 11/90 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	**129.102239**	65.054757	112.075690	56.541483			**K**							10
2	242.186303	121.596790	225.159754	113.083515			**L**	***1457.739189***	729.373233	1440.712640	720.859958	1439.728624	720.367950	9
3	357.213246	179.110261	340.186697	170.596987	339.202681	170.104979	**D**	***1344.655125***	672.831201	1327.628576	664.317926	1326.644560	663.825918	8
4	414.234710	207.620993	397.208161	199.107719	396.224145	198.615711	**G**	***1229.628182***	615.317729	1212.601633	606.804455			7
5	**527.318774**	264.163025	510.292225	255.649751	509.308209	255.157743	**I**	***1172.606718***	586.806997	1155.580169	578.293723			6
6	687.349423	344.178350	670.322874	335.665075	669.338858	335.173067	**C**	***1059.522654***	530.264965	1042.496105	521.751691			5
7	873.428736	437.218006	856.402187	428.704732	855.418171	428.212724	**W**	***899.492005***	450.249641	882.465456	441.736366			4
8	1312.654062	656.830669	1295.627513	648.317395	1294.643497	647.825387	**Q**	***713.412692***	357.209984	696.386143	348.696710			3
9	1411.722476	706.364876	1394.695927	697.851602	1393.711911	697.359594	**V**	***274.187366***	137.597321	257.160817	129.084047			2
10							**R**	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.9	1584.826874	-0.000686	KLDGICWQVR
5.9	1584.829346	-0.003158	GAEATETQAKLR
4.1	1584.844620	-0.018432	KAQPKEVMFPPGTR
3.7	1584.822845	0.003343	SQMSPQGLRVR
2.9	1584.844620	-0.018432	LQSSGIQPAAFR
2.7	1584.810730	0.015458	KVSPDPQKSSEDIR
2.0	1584.822830	0.003358	QLDQKCKQAR
2.0	1584.822830	0.003358	QLDQKCKQAR
1.9	1584.829346	-0.003158	QAESQINKQTK
1.8	1584.841278	-0.015090	QLAWVGDGVWVSIR

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

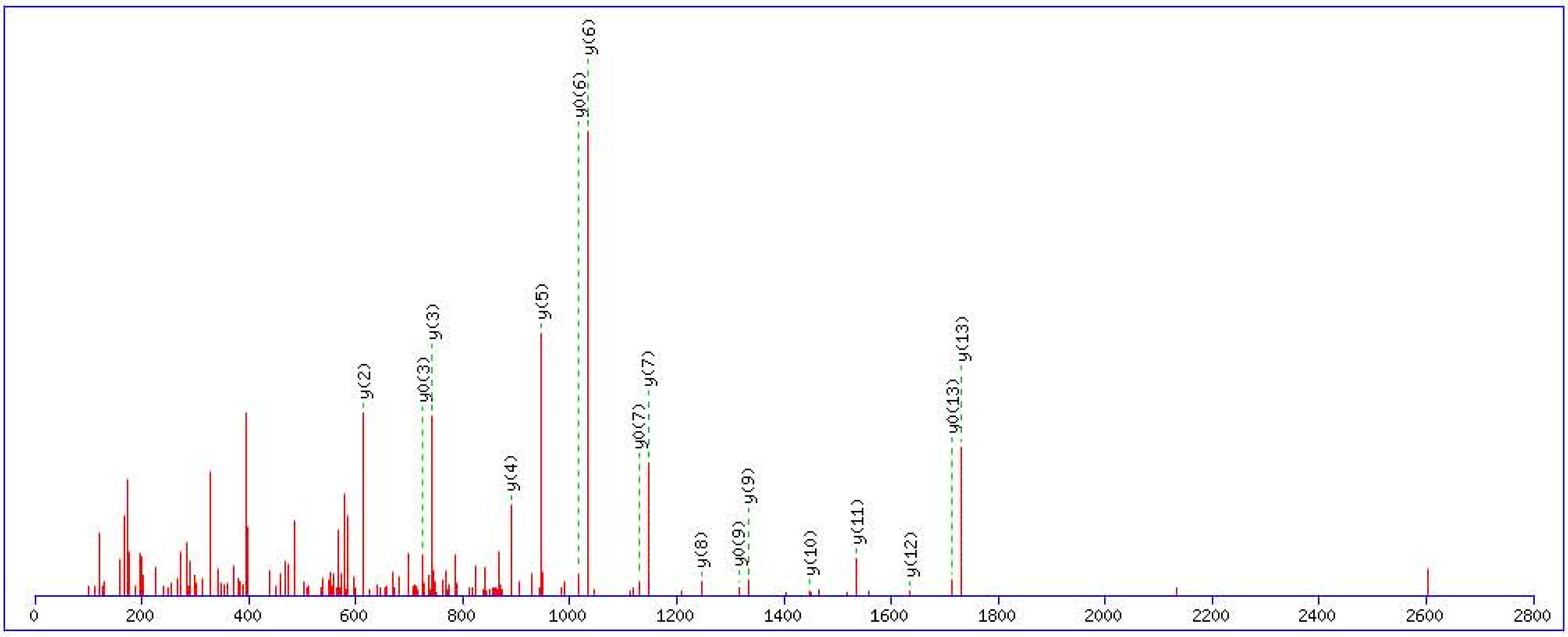
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLPVSDSVLSGFEQR**
Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

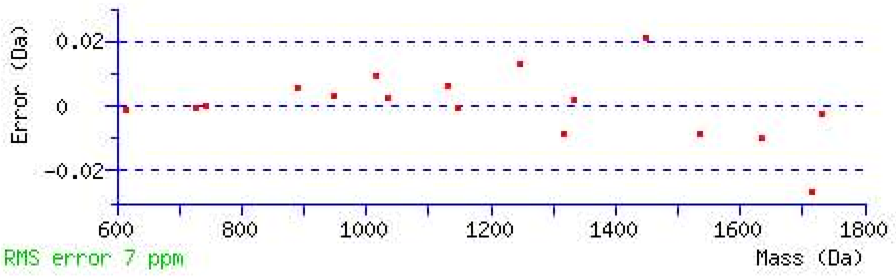
Match to Query 37977: 1930.982322 from(644.668050,3+) rtinseconds(2529) index(34830)
Title: Locus:1.1.1.3544.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

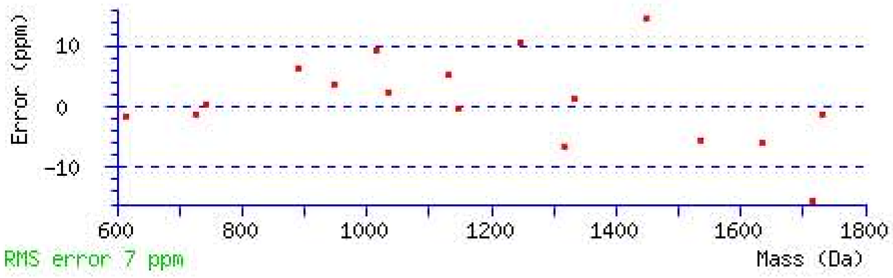
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1930.982254
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 77  Expect: 5.9e-008
Matches : 17/138 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	88.039304	44.523290			70.028739	35.518008	S							15
2	201.123368	101.065322			183.112803	92.060039	L	1844.957496	922.982386	1827.930947	914.469112	1826.946931	913.977104	14
3	298.176132	149.591704			280.165567	140.586422	P	***1731.873432***	866.440354	1714.846883	857.927080	1713.862867	857.435072	13
4	397.244546	199.125911			379.233981	190.120629	V	***1634.820668***	817.913972	1617.794119	809.400698	1616.810103	808.908690	12
5	484.276574	242.641925			466.266009	233.636643	S	***1535.752254***	768.379765	1518.725705	759.866491	1517.741689	759.374483	11
6	599.303517	300.155397			581.292952	291.150114	D	***1448.720226***	724.863751	1431.693677	716.350477	1430.709661	715.858469	10
7	686.335545	343.671411			668.324980	334.666128	S	***1333.693283***	667.350280	1316.666734	658.837005	1315.682718	658.344997	9
8	785.403959	393.205618			767.393394	384.200335	V	***1246.661255***	623.834266	1229.634706	615.320991	1228.650690	614.828983	8
9	898.488023	449.747650			880.477458	440.742367	L	***1147.592841***	574.300059	1130.566292	565.786784	1129.582276	565.294776	7
10	985.520051	493.263664			967.509486	484.258381	S	***1034.508777***	517.758027	1017.482228	509.244752	1016.498212	508.752744	6
11	1042.541515	521.774395			1024.530950	512.769113	G	***947.476749***	474.242013	930.450200	465.728738	929.466184	465.236730	5
12	1189.609929	595.308603			1171.599364	586.303320	F	***890.455285***	445.731281	873.428736	437.218006	872.444720	436.725998	4
13	1318.652522	659.829899			1300.641957	650.824617	E	***743.386871***	372.197074	726.360322	363.683799	725.376306	363.191791	3
14	1757.877848	879.442562	1740.851299	870.929288	1739.867283	870.437280	Q	***614.344278***	307.675777	597.317729	299.162503			2
15							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SLPVSDSVLSGFEQR
(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	1930.982254	0.000068	SLPVSDSVLSGFEQR
0.2	1930.989410	-0.007088	EAQSQLIKSDEMQRLR

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

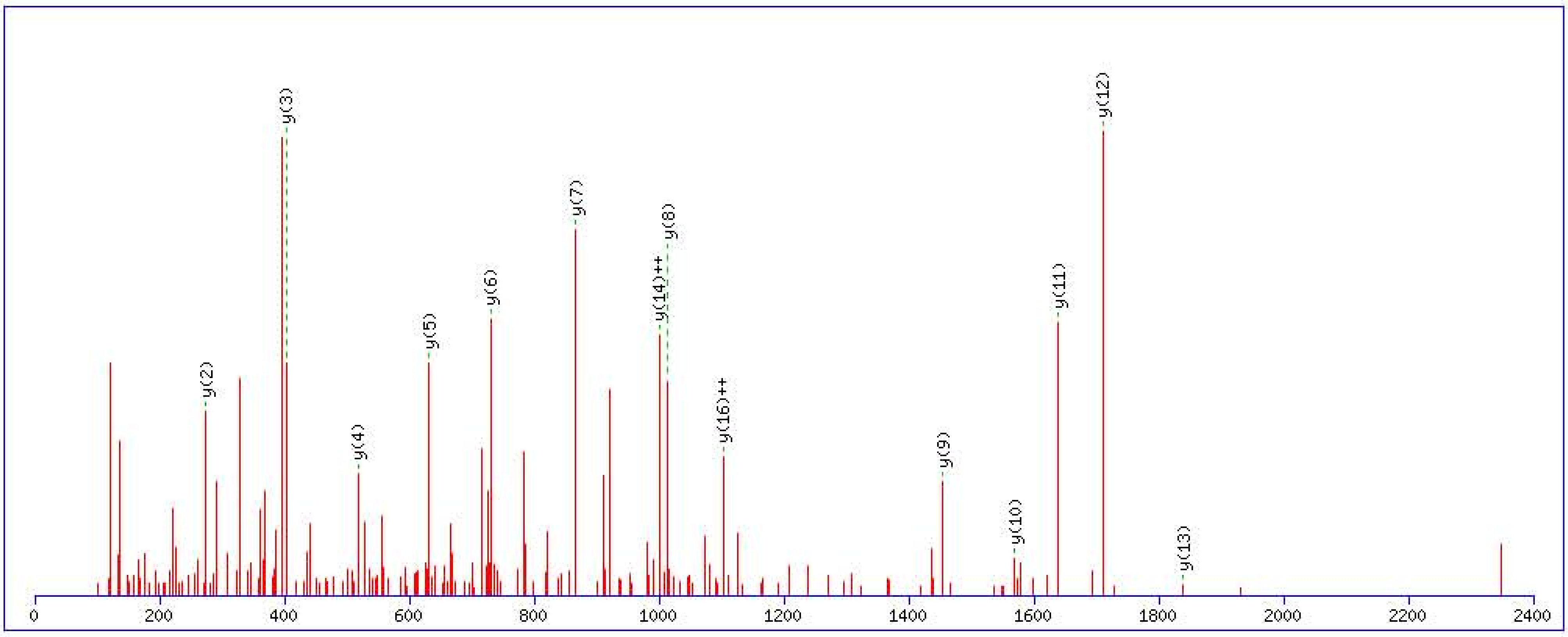
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGFCEAADQFHVLDEVR**
Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

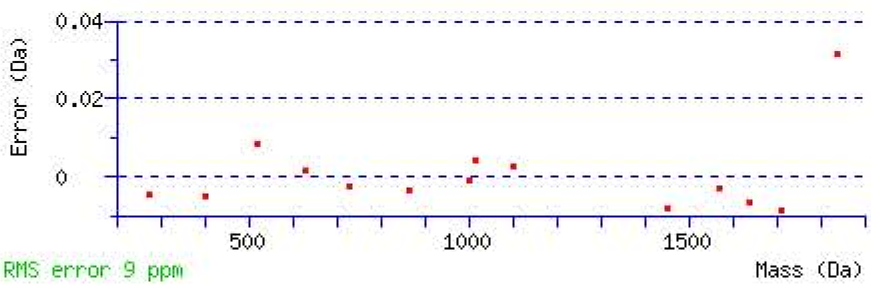
Match to Query 45992: 2366.080182 from(789.700670,3+) rtinseconds(2578) index(35013)
Title: Locus:1.1.1.3561.6 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

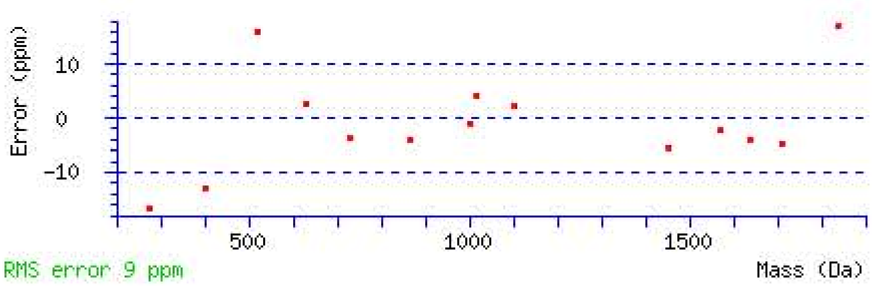
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2366.082382
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 98  Expect: 1.8e-009
Matches : 14/164 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	164.070605	82.538940					Y							17
2	221.092069	111.049673					G	2204.026323	1102.516799	2186.999774	1094.003525	2186.015758	1093.511517	16
3	368.160483	184.583879					F	2147.004859	1074.006067	2129.978310	1065.492793	2128.994294	1065.000785	15
4	528.191132	264.599204					C	1999.936445	1000.471860	1982.909896	991.958586	1981.925880	991.466578	14
5	657.233725	329.120501			639.223160	320.115218	E	***1839.905796***	920.456536	1822.879247	911.943261	1821.895231	911.451253	13
6	728.270839	364.639058			710.260274	355.633775	A	***1710.863203***	855.935239	1693.836654	847.421965	1692.852638	846.929957	12
7	799.307953	400.157615			781.297388	391.152332	A	***1639.826089***	820.416682	1622.799540	811.903408	1621.815524	811.411400	11
8	914.334896	457.671086			896.324331	448.665803	D	***1568.788975***	784.898125	1551.762426	776.384851	1550.778410	775.892843	10
9	1353.560222	677.283749	1336.533673	668.770474	1335.549657	668.278466	Q	***1453.762032***	727.384654	1436.735483	718.871379	1435.751467	718.379371	9
10	1500.628636	750.817956	1483.602087	742.304682	1482.618071	741.812673	F	***1014.536706***	507.771991	997.510157	499.258717	996.526141	498.766709	8
11	1637.687548	819.347412	1620.660999	810.834138	1619.676983	810.342129	H	***867.468292***	434.237784	850.441743	425.724510	849.457727	425.232502	7
12	1736.755962	868.881619	1719.729413	860.368345	1718.745397	859.876336	V	***730.409380***	365.708328	713.382831	357.195054	712.398815	356.703046	6
13	1849.840026	925.423651	1832.813477	916.910376	1831.829461	916.418368	L	***631.340966***	316.174121	614.314417	307.660846	613.330401	307.168838	5
14	1964.866969	982.937122	1947.840420	974.423848	1946.856404	973.931840	D	***518.256902***	259.632089	501.230353	251.118815	500.246337	250.626807	4
15	2093.909562	1047.458419	2076.883013	1038.945144	2075.898997	1038.453136	E	***403.229959***	202.118617	386.203410	193.605343	385.219394	193.113335	3
16	2192.977976	1096.992626	2175.951427	1088.479351	2174.967411	1087.987343	V	***274.187366***	137.597321	257.160817	129.084046			2
17							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
98.0	2366.082382	-0.002200	YGFCEAADQFHVLDEVR

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

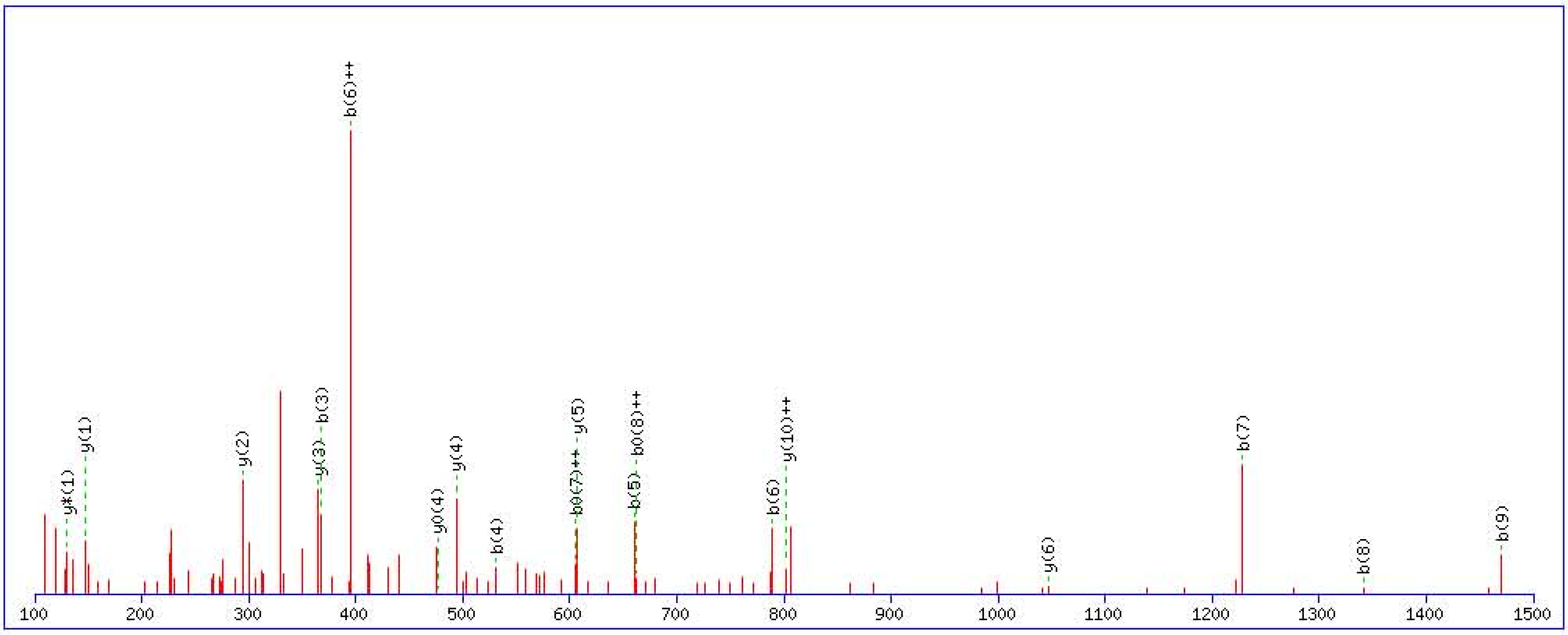
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEHYEEQIEAFK**
Found in **CO9_HUMAN**, Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2

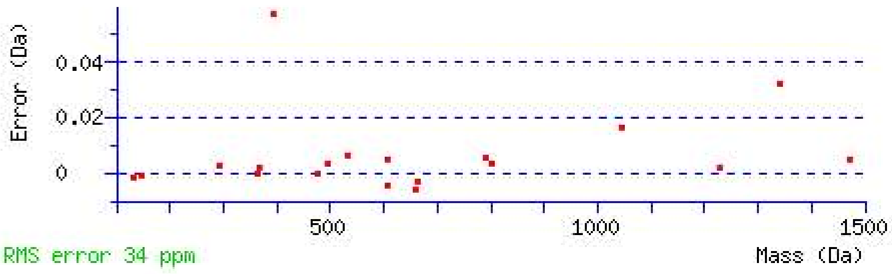
Match to Query 36368: 1833.857502 from(612.293110,3+) rtinseconds(1998) index(31866)
Title: Locus:1.1.1.3359.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

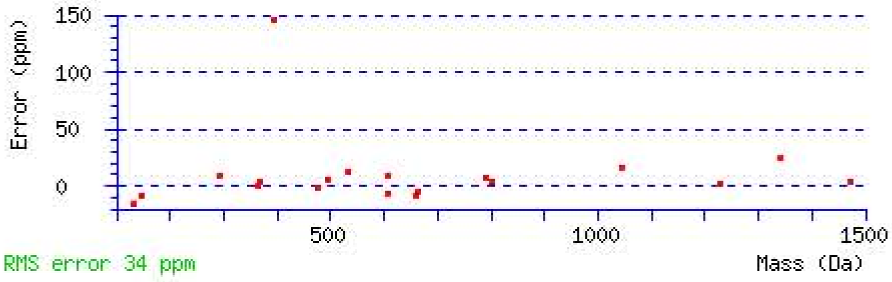


```
Monoisotopic mass of neutral peptide Mr(calc): 1833.860703
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.018
Matches : 19/114 fragment ions using 42 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							12
2	231.097548	116.052412			213.086983	107.047130	E	1733.820335	867.413805	1716.793786	858.900531	1715.809770	858.408523	11
3	***368.156460***	184.581868			350.145895	175.576585	H	1604.777742	802.892509	1587.751193	794.379235	1586.767177	793.887227	10
4	***531.219789***	266.113533			513.209224	257.108250	Y	1467.718830	734.363053	1450.692281	725.849779	1449.708265	725.357771	9
5	***660.262382***	330.634829			642.251817	321.629547	E	1304.655501	652.831389	1287.628952	644.318114	1286.644936	643.826106	8
6	***789.304975***	395.156126			771.294410	386.150843	E	1175.612908	588.310092	1158.586359	579.796817	1157.602343	579.304809	7
7	***1228.530301***	614.768789	1211.503752	606.255514	1210.519736	605.763506	Q	***1046.570315***	523.788795	1029.543766	515.275521	1028.559750	514.783513	6
8	***1341.614365***	671.310820	1324.587816	662.797546	1323.603800	662.305538	I	***607.344989***	304.176132	590.318440	295.662858	589.334424	295.170850	5
9	***1470.656958***	735.832117	1453.630409	727.318842	1452.646393	726.826834	E	***494.260925***	247.634100	477.234376	239.120826	476.250360	238.628818	4
10	1541.694072	771.350674	1524.667523	762.837399	1523.683507	762.345391	A	***365.218332***	183.112804	348.191783	174.599530			3
11	1688.762486	844.884881	1671.735937	836.371606	1670.751921	835.879598	F	***294.181218***	147.594247	277.154669	139.080973			2
12							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 34 ppm



RMS error 34 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.8	1833.860703	-0.003201	TEHYEEQIEAFK

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

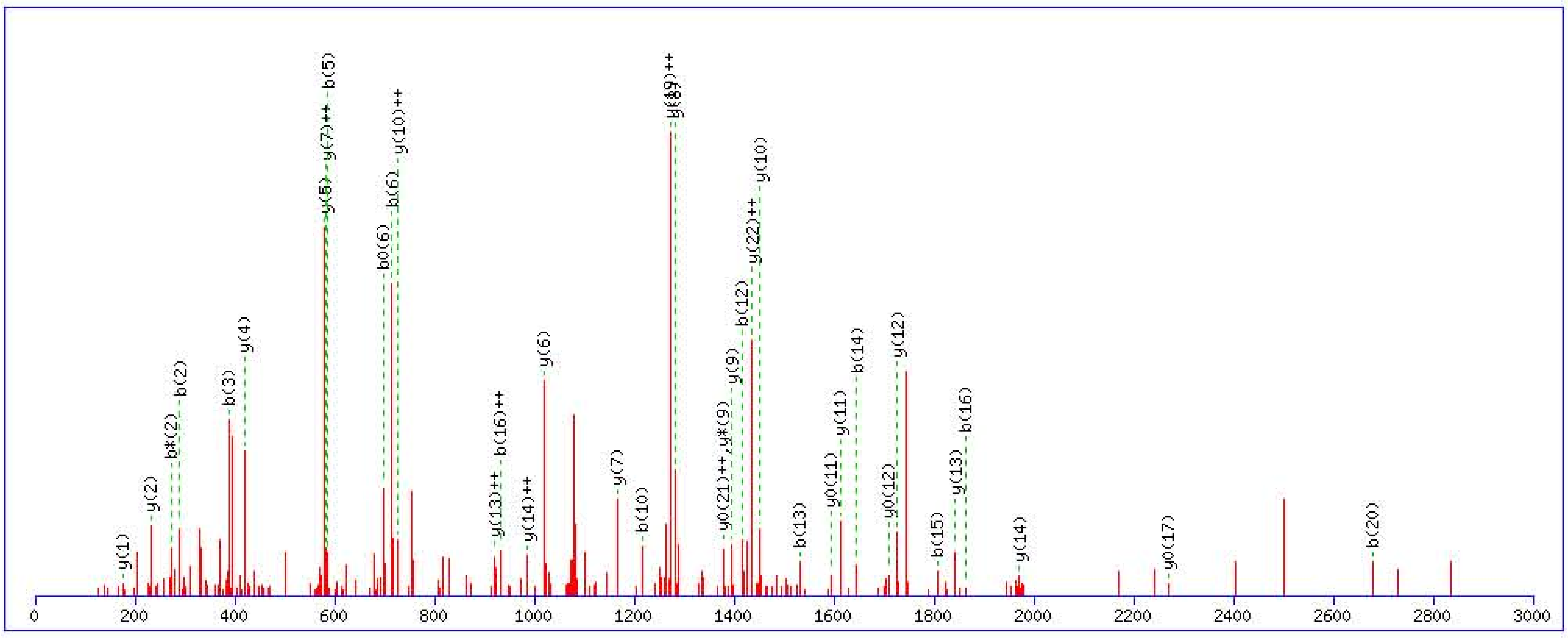
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QCVPTEPCEDAEDDCGNDFQCSTGR**
Found in **CO9_HUMAN**, Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2

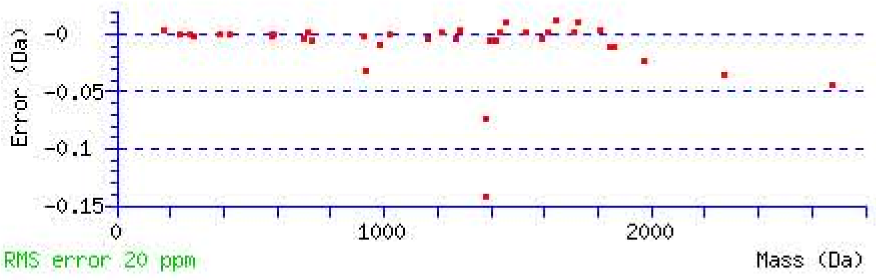
Match to Query 42742: 3257.230272 from(1086.750700,3+) rtinseconds(1887) index(31032)
Title: Locus:1.1.1.3320.25 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

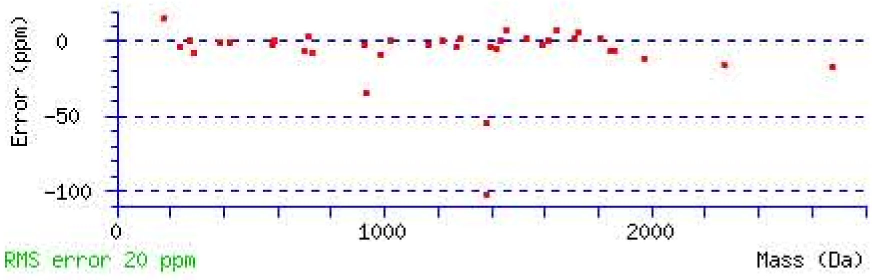
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3257.246475
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20     : Biotin:Thermo-21345 (Q)
Ions Score: 77  Expect: 2e-007
Matches : 38/276 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	129.065854	65.036565	112.039305	56.523291			Q							25
2	***289.096503***	145.051890	272.069954	136.538615			C	3130.195136	1565.601206	3113.168587	1557.087931	3112.184571	1556.595923	24
3	***388.164917***	194.586097	371.138368	186.072822			V	2970.164487	1485.585881	2953.137938	1477.072607	2952.153922	1476.580599	23
4	485.217681	243.112479	468.191132	234.599204			P	2871.096073	1436.051674	2854.069524	1427.538400	2853.085508	1427.046392	22
5	***586.265360***	293.636318	569.238811	285.123044	568.254795	284.631036	T	2774.043309	1387.525292	2757.016760	1379.012018	2756.032744	1378.520010	21
6	***715.307953***	358.157615	698.281404	349.644340	697.297388	349.152332	E	2672.995630	1337.001453	2655.969081	1328.488178	2654.985065	1327.996170	20
7	812.360717	406.683997	795.334168	398.170722	794.350152	397.678714	P	2543.953037	1272.480156	2526.926488	1263.966882	2525.942472	1263.474874	19
8	972.391366	486.699321	955.364817	478.186047	954.380801	477.694039	C	2446.900273	1223.953774	2429.873724	1215.440500	2428.889708	1214.948492	18
9	1101.433959	551.220618	1084.407410	542.707343	1083.423394	542.215335	E	2286.869624	1143.938450	2269.843075	1135.425175	2268.859059	1134.933167	17
10	***1216.460902***	608.734089	1199.434353	600.220815	1198.450337	599.728807	D	2157.827031	1079.417153	2140.800482	1070.903879	2139.816466	1070.411871	16
11	1287.498016	644.252646	1270.471467	635.739372	1269.487451	635.247364	A	2042.800088	1021.903682	2025.773539	1013.390408	2024.789523	1012.898400	15
12	***1416.540609***	708.773943	1399.514060	700.260668	1398.530044	699.768660	E	***1971.762974***	986.385125	1954.736425	977.871851	1953.752409	977.379843	14
13	***1531.567552***	766.287414	1514.541003	757.774140	1513.556987	757.282132	D	***1842.720381***	921.863828	1825.693832	913.350554	1824.709816	912.858546	13
14	***1646.594495***	823.800886	1629.567946	815.287611	1628.583930	814.795603	D	***1727.693438***	864.350357	1710.666889	855.837082	1709.682873	855.345074	12
15	***1806.625144***	903.816210	1789.598595	895.302936	1788.614579	894.810928	C	***1612.666495***	806.836885	1595.639946	798.323611	1594.655930	797.831603	11
16	***1863.646608***	932.326942	1846.620059	923.813668	1845.636043	923.321660	G	***1452.635846***	726.821561	1435.609297	718.308286	1434.625281	717.816278	10
17	1977.689535	989.348406	1960.662986	980.835131	1959.678970	980.343123	N	***1395.614382***	698.310829	1378.587833	689.797554	1377.603817	689.305546	9
18	2092.716478	1046.861877	2075.689929	1038.348603	2074.705913	1037.856595	D	***1281.571455***	641.289365	1264.544906	632.776091	1263.560890	632.284083	8
19	2239.784892	1120.396084	2222.758343	1111.882809	2221.774327	1111.390802	F	***1166.544512***	583.775894	1149.517963	575.262619	1148.533947	574.770611	7
20	***2679.010218***	1340.008747	2661.983669	1331.495473	2660.999653	1331.003465	Q	***1019.476098***	510.241687	1002.449549	501.728412	1001.465533	501.236404	6
21	2839.040867	1420.024072	2822.014318	1411.510797	2821.030302	1411.018789	C	***580.250772***	290.629024	563.224223	282.115749	562.240207	281.623741	5
22	2926.072895	1463.540086	2909.046346	1455.026811	2908.062330	1454.534803	S	***420.220123***	210.613699	403.193574	202.100425	402.209558	201.608417	4
23	3027.120574	1514.063925	3010.094025	1505.550650	3009.110009	1505.058642	T	333.188095	167.097685	316.161546	158.584411	315.177530	158.092403	3
24	3084.142038	1542.574657	3067.115489	1534.061382	3066.131473	1533.569374	G	***232.140416***	116.573846	215.113867	108.060571			2
25							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
76.7	3257.246475	-0.016203	QCVPTEPCEDAEDDCGNDFQCSTGR

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

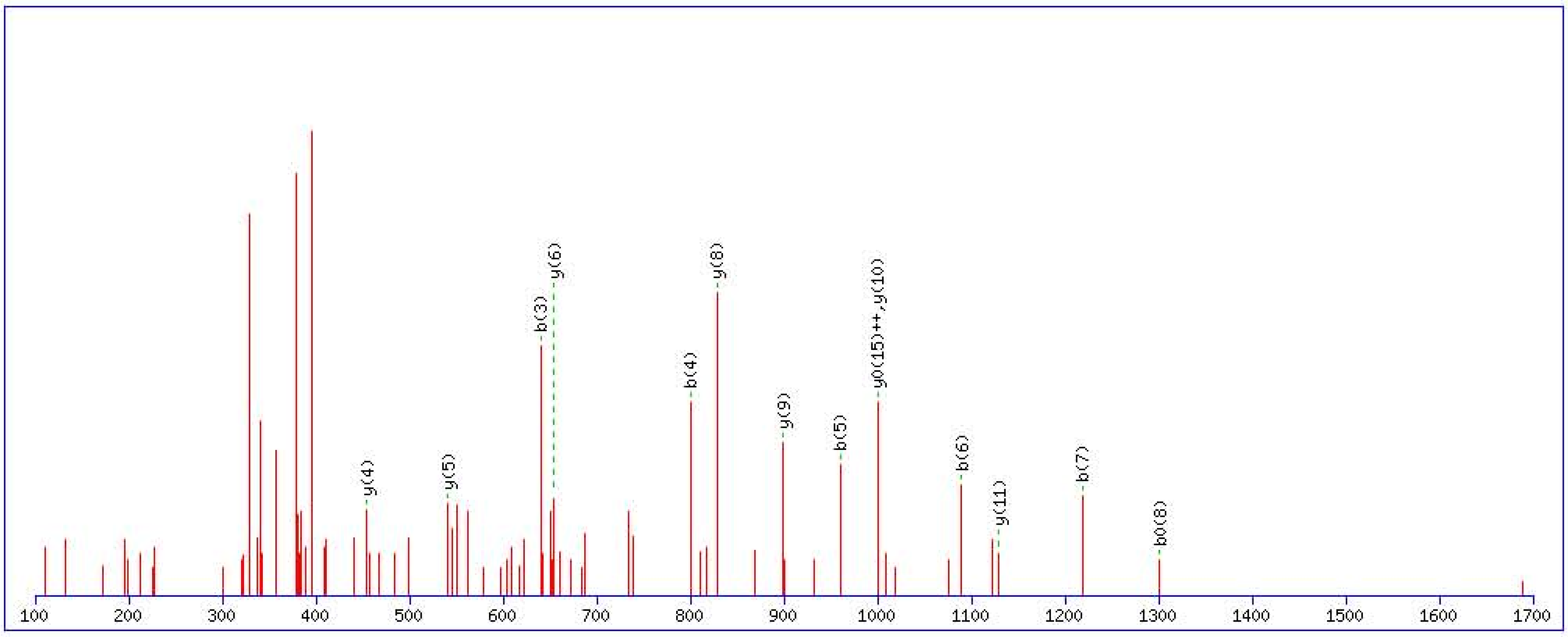
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEQCCEETASSISLHGK**
Found in **CO9_HUMAN**, Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2

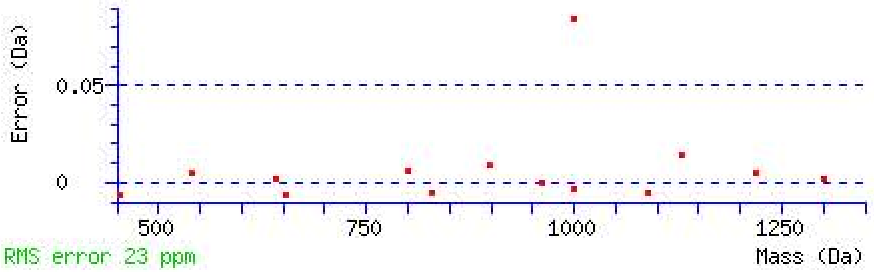
Match to Query 43540: 2216.978622 from(740.000150,3+) rtinseconds(1626) index(29598)
Title: Locus:1.1.1.3229.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

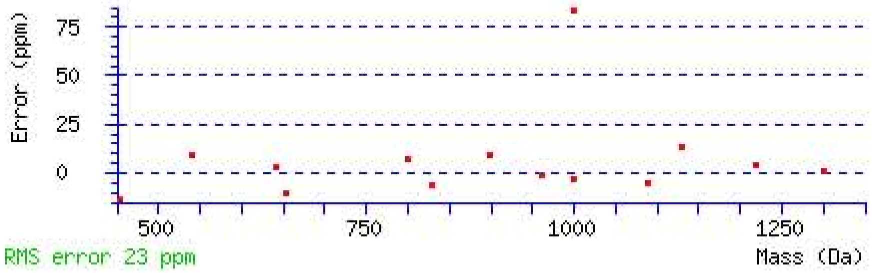
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2216.986404
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.0011
Matches : 14/178 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	201.086983	101.047130			183.076418	92.041847	E	2146.956588	1073.981932	2129.930039	1065.468657	2128.946023	1064.976649	16
3	***640.312309***	320.659793	623.285760	312.146518	622.301744	311.654510	Q	2017.913995	1009.460636	2000.887446	1000.947361	1999.903430	1000.455353	15
4	***800.342958***	400.675117	783.316409	392.161843	782.332393	391.669835	C	1578.688669	789.847972	1561.662120	781.334698	1560.678104	780.842690	14
5	***960.373607***	480.690442	943.347058	472.177167	942.363042	471.685159	C	1418.658020	709.832648	1401.631471	701.319374	1400.647455	700.827366	13
6	***1089.416200***	545.211738	1072.389651	536.698464	1071.405635	536.206456	E	1258.627371	629.817323	1241.600822	621.304049	1240.616806	620.812041	12
7	***1218.458793***	609.733035	1201.432244	601.219760	1200.448228	600.727752	E	***1129.584778***	565.296027	1112.558229	556.782753	1111.574213	556.290744	11
8	1319.506472	660.256874	1302.479923	651.743600	1301.495907	651.251592	T	***1000.542185***	500.774731	983.515636	492.261456	982.531620	491.769448	10
9	1390.543586	695.775431	1373.517037	687.262157	1372.533021	686.770149	A	***899.494506***	450.250891	882.467957	441.737617	881.483941	441.245609	9
10	1477.575614	739.291445	1460.549065	730.778171	1459.565049	730.286163	S	***828.457392***	414.732334	811.430843	406.219060	810.446827	405.727052	8
11	1564.607642	782.807459	1547.581093	774.294185	1546.597077	773.802177	S	741.425364	371.216320	724.398815	362.703045	723.414799	362.211037	7
12	1677.691706	839.349491	1660.665157	830.836217	1659.681141	830.344209	I	***654.393336***	327.700306	637.366787	319.187031	636.382771	318.695023	6
13	1764.723734	882.865505	1747.697185	874.352231	1746.713169	873.860223	S	***541.309272***	271.158274	524.282723	262.644999	523.298707	262.152991	5
14	1877.807798	939.407537	1860.781249	930.894263	1859.797233	930.402255	L	***454.277244***	227.642260	437.250695	219.128985			4
15	2014.866710	1007.936993	1997.840161	999.423719	1996.856145	998.931711	H	341.193180	171.100228	324.166631	162.586953			3
16	2071.888174	1036.447725	2054.861625	1027.934450	2053.877609	1027.442442	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 AEQCCEETASSISLHGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.1	2216.986404	-0.007782	AEQCCEETASSISLHGK

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

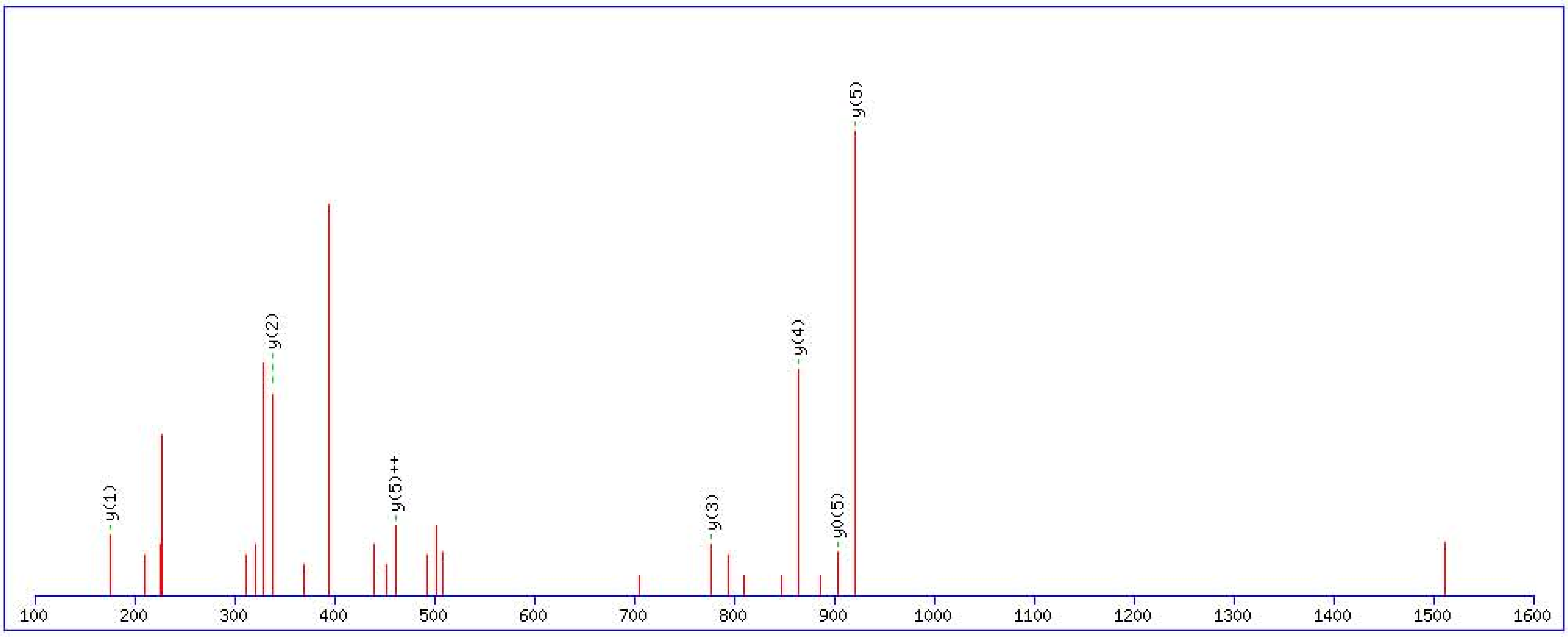
Mascot Search Results

Peptide View

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

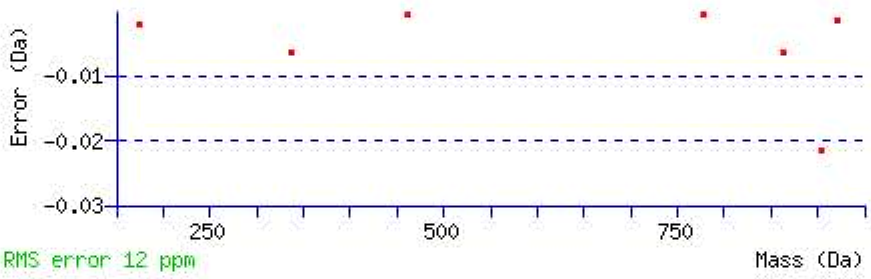
Match to Query 12096: 1019.517328 from(510.765940,2+) rtinseconds(1437) index(42473)
Title: Locus:1.1.1.3213.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

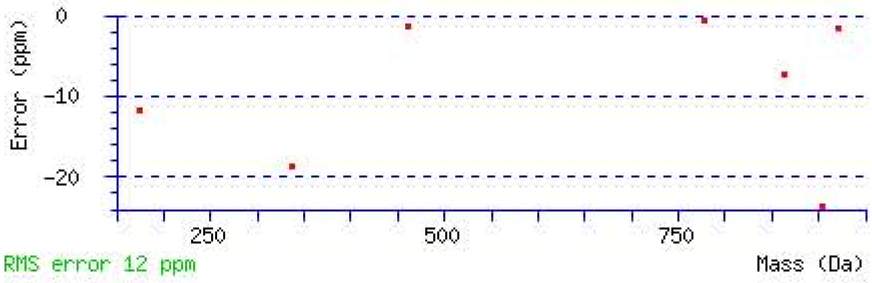
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1019.522232
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 34 **Expect:** 0.0051
Matches : 7/44 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							6
2	157.097154	79.052215					G	***921.461099***	461.234188	904.434550	452.720913	903.450534	452.228905	5
3	244.129182	122.568229			226.118617	113.562946	S	***864.439635***	432.723456	847.413086	424.210181	846.429070	423.718173	4
4	683.354508	342.180892	666.327959	333.667618	665.343943	333.175610	Q	***777.407607***	389.207442	760.381058	380.694167			3
5	846.417837	423.712557	829.391288	415.199282	828.407272	414.707274	Y	***338.182281***	169.594778	321.155732	161.081504			2
6							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.0	1019.522232	-0.004904	VGSQYR
9.0	1019.510818	0.006510	RSSVSSGGAGR
5.1	1019.512146	0.005182	RSRGHHDR
4.8	1019.526047	-0.008719	SRERGPYR
0.9	1019.526077	-0.008749	VPQAGGQHAR
0.8	1019.529419	-0.012091	RGEISRMR
0.2	1019.506973	0.010355	VMDVINSAR
0.2	1019.525589	-0.008261	VMMEVQKR
0.2	1019.525604	-0.008276	VQLTMCLR
0.2	1019.518204	-0.000876	VRSCETLR

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

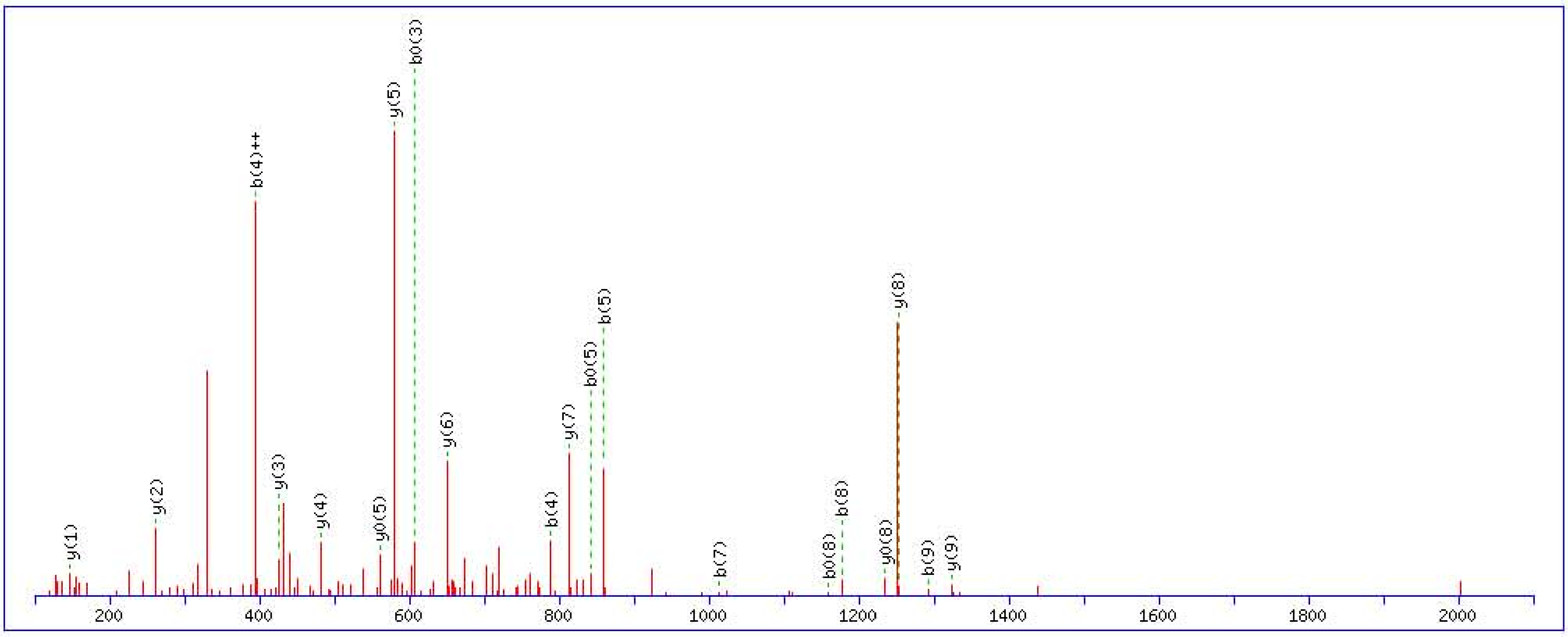
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

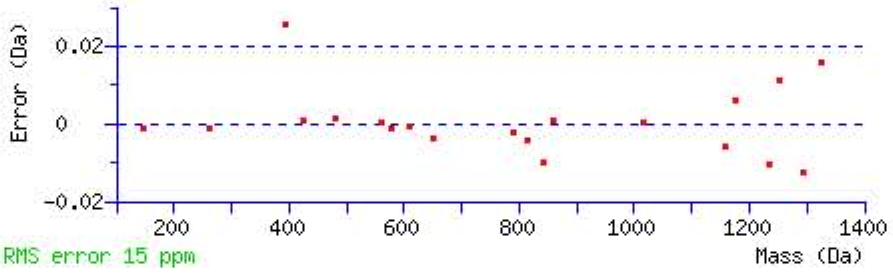
Match to Query 25535: 1437.662568 from(719.838560,2+) rtinseconds(1663) index(58798)
Title: Locus:1.1.1.1490.12 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

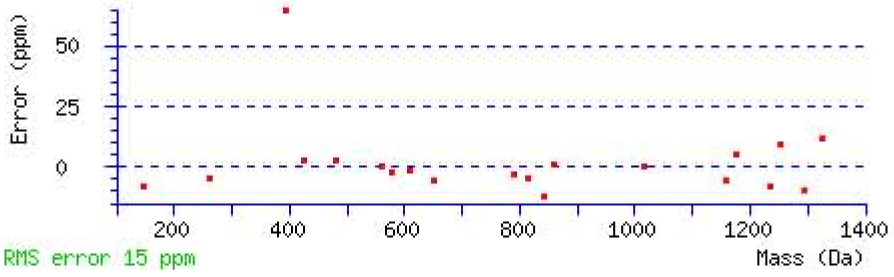
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1437.659836
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 0.00022
Matches : 20/102 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	116.034219	58.520748			98.023654	49.515465	D							10
2	187.071333	94.039304			169.060768	85.034022	A	***1323.640187***	662.323732	1306.613638	653.810457	1305.629622	653.318449	9
3	626.296659	313.651968	609.270110	305.138693	608.286094	304.646685	Q	***1252.603073***	626.805175	1235.576524	618.291900	1234.592508	617.799892	8
4	**789.359988**	395.183632	772.333439	386.670358	771.349423	386.178350	Y	***813.377747***	407.192512	796.351198	398.679237	795.367182	398.187229	7
5	**860.397102**	430.702189	843.370553	422.188915	842.386537	421.696907	A	***650.314418***	325.660847	633.287869	317.147573	632.303853	316.655565	6
6	957.449866	479.228571	940.423317	470.715297	939.439301	470.223289	P	***579.277304***	290.142290	562.250755	281.629016	561.266739	281.137008	5
7	**1014.471330**	507.739303	997.444781	499.226029	996.460765	498.734021	G	***482.224540***	241.615908	465.197991	233.102634	464.213975	232.610626	4
8	**1177.534659**	589.270968	1160.508110	580.757693	1159.524094	580.265685	Y	***425.203076***	213.105176	408.176527	204.591902	407.192511	204.099894	3
9	**1292.561602**	646.784439	1275.535053	638.271165	1274.551037	637.779157	D	***262.139747***	131.573512	245.113198	123.060237	244.129182	122.568229	2
10							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of DAQYAPGYDK
(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	1437.659836	0.002732	DAQYAPGYDK
19.6	1437.647064	0.015504	ASSDLSIASSEEDK
10.4	1437.659164	0.003404	LAEAEQMALMGSR
4.9	1437.680969	-0.018401	EGFLKGEDGEMVK
0.6	1437.644577	0.017991	EDLGAGNLEDFMK
0.6	1437.645264	0.017304	SDASCMSQRRPK

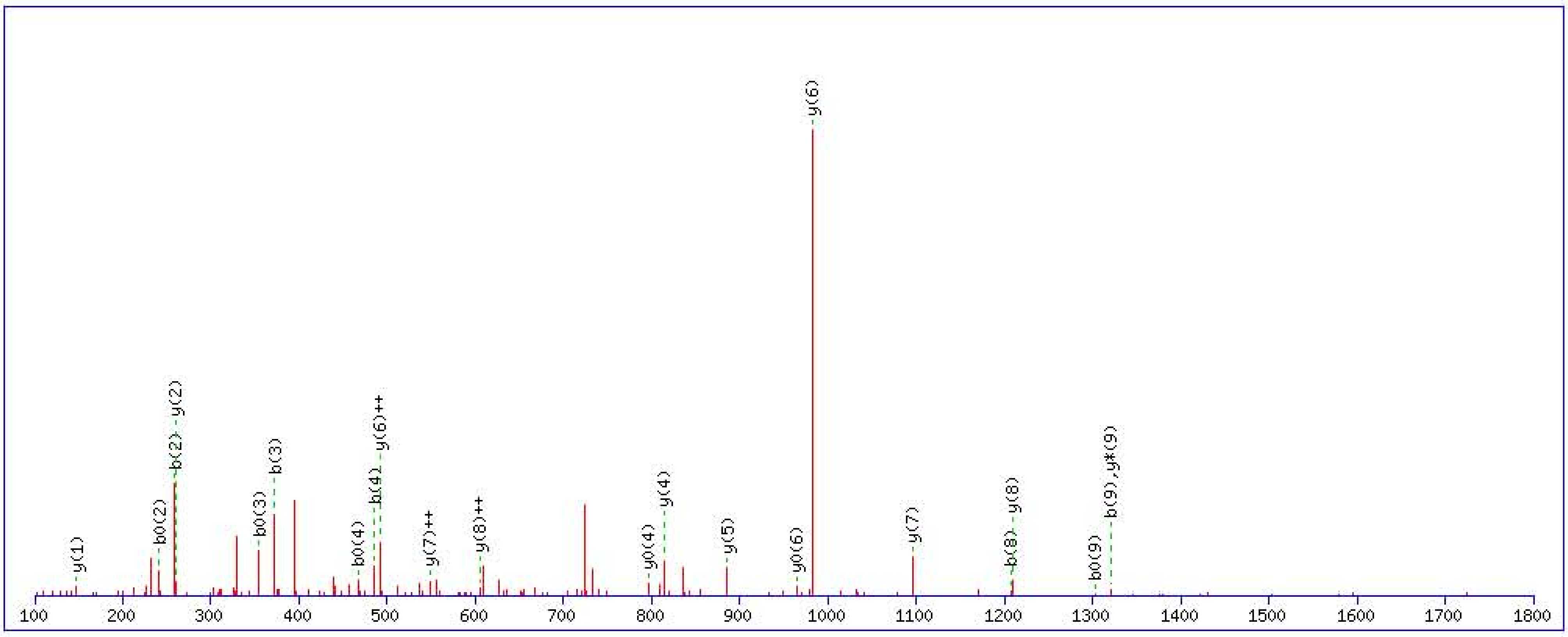
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

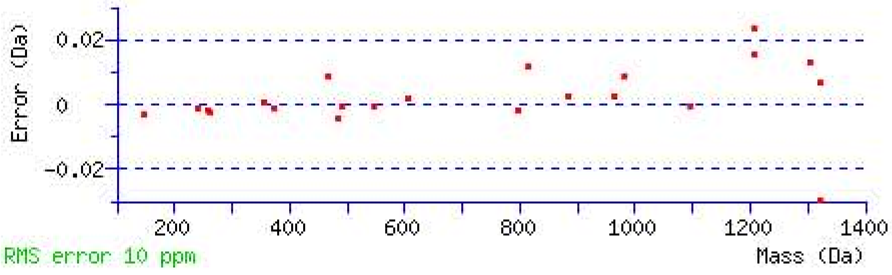
Match to Query 26317: 1465.793588 from(733.904070,2+) rtinseconds(2156) index(61413)
Title: Locus:1.1.1.1662.11 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

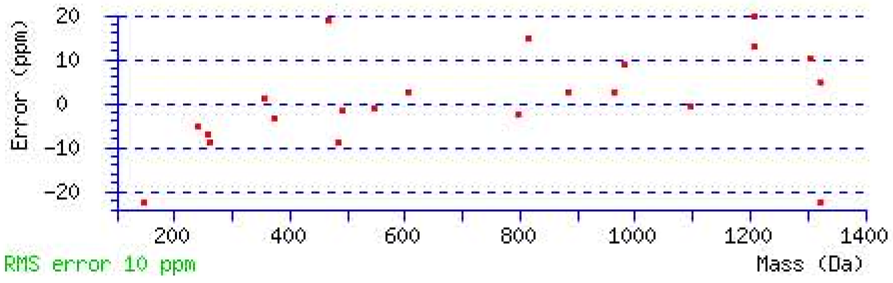
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1465.785019
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.016
Matches : 22/92 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	130.049869	65.528572			112.039304	56.523290	E							10
2	**259.092462**	130.049869			241.081897	121.044587	E	1337.749736	669.378506	1320.723187	660.865232	1319.739171	660.373223	9
3	**372.176526**	186.591901			354.165961	177.586619	L	***1208.707143***	604.857210	1191.680594	596.343935	1190.696578	595.851927	8
4	**485.260590**	243.133933			467.250025	234.128651	L	***1095.623079***	548.315178	1078.596530	539.801903	1077.612514	539.309895	7
5	582.313354	291.660315			564.302789	282.655033	P	***982.539015***	491.773146	965.512466	483.259871	964.528450	482.767863	6
6	653.350468	327.178872			635.339903	318.173590	A	***885.486251***	443.246764	868.459702	434.733489	867.475686	434.241481	5
7	1092.575794	546.791535	1075.549245	538.278261	1074.565229	537.786253	Q	***814.449137***	407.728207	797.422588	399.214932	796.438572	398.722924	4
8	**1207.602737**	604.305007	1190.576188	595.791732	1189.592172	595.299724	D	375.223811	188.115543	358.197262	179.602269	357.213246	179.110261	3
9	**1320.686801**	660.847039	1303.660252	652.333764	1302.676236	651.841756	I	***260.196868***	130.602072	243.170319	122.088797			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.9	1465.785019	0.008569	EELLPAQDIK
12.4	1465.813995	-0.020407	SQLKHEILELEK
4.5	1465.788849	0.004739	SKHLQEQLNELK
0.5	1465.794235	-0.000647	KWGIGYHLSLHR
0.0	1465.788849	0.004739	KQVEHQLEEAKK
0.0	1465.800125	-0.006537	LAQDGAHVVVSSRK
0.0	1465.789734	0.003854	TAAALGMHQKK

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

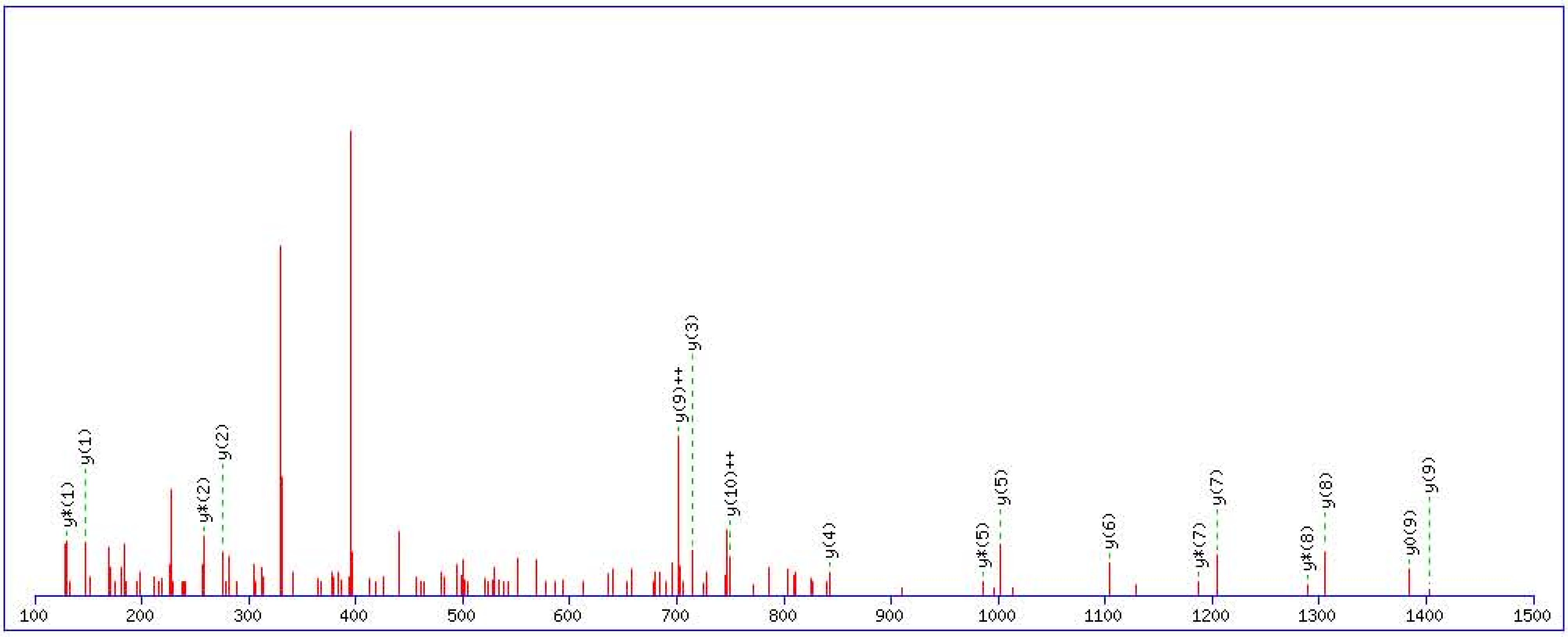
Mascot Search Results

Peptide View

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

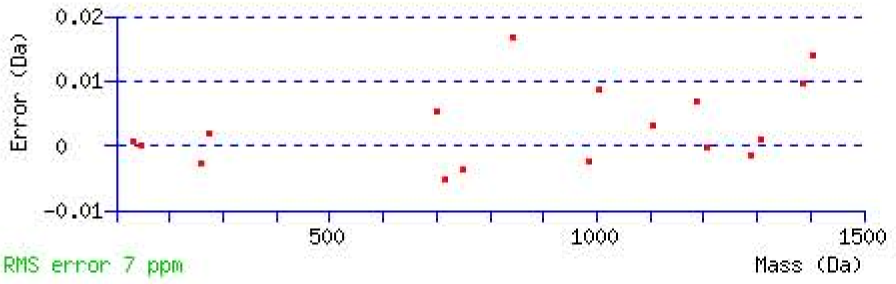
Match to Query 31048: 1611.811032 from(538.277620,3+) rtinseconds(1504) index(1979)
Title: Locus:1.1.1.3043.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

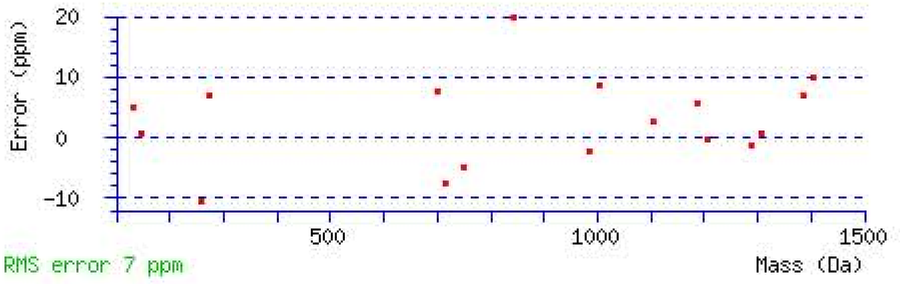
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1611.811295
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00012
Matches : 17/90 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	114.091340	57.549308					L							11
2	211.144104	106.075690					P	1499.734500	750.370888	1482.707951	741.857614	1481.723935	741.365606	10
3	308.196868	154.602072					P	***1402.681736***	701.844506	1385.655187	693.331232	1384.671171	692.839224	9
4	409.244547	205.125911			391.233982	196.120629	T	***1305.628972***	653.318124	1288.602423	644.804850	1287.618407	644.312842	8
5	510.292226	255.649751			492.281661	246.644468	T	***1204.581293***	602.794285	1187.554744	594.281010	1186.570728	593.789002	7
6	611.339905	306.173591			593.329340	297.168308	T	***1103.533614***	552.270445	1086.507065	543.757171	1085.523049	543.265163	6
7	771.370554	386.188915			753.359989	377.183633	C	***1002.485935***	501.746606	985.459386	493.233331			5
8	899.429132	450.218204	882.402583	441.704930	881.418567	441.212922	Q	***842.455286***	421.731281	825.428737	413.218007			4
9	1338.654458	669.830867	1321.627909	661.317593	1320.643893	660.825585	Q	***714.396708***	357.701992	697.370159	349.188718			3
10	1466.713036	733.860156	1449.686487	725.346882	1448.702471	724.854874	Q	***275.171382***	138.089329	258.144833	129.576055			2
11							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.7	1611.811295	-0.000263	LPPTTTCQQQK
36.4	1611.811295	-0.000263	LPPTTTCQQQK
34.4	1611.811295	-0.000263	LPPTTTCQQQK
5.6	1611.803406	0.007626	TPIKMGISASTMTMK
4.8	1611.829010	-0.017978	EDNSTYIMRVLKK
2.3	1611.817780	-0.006748	KMAKSFTAEEDIVK
1.8	1611.803406	0.007626	TPIKMGISASTMTMK

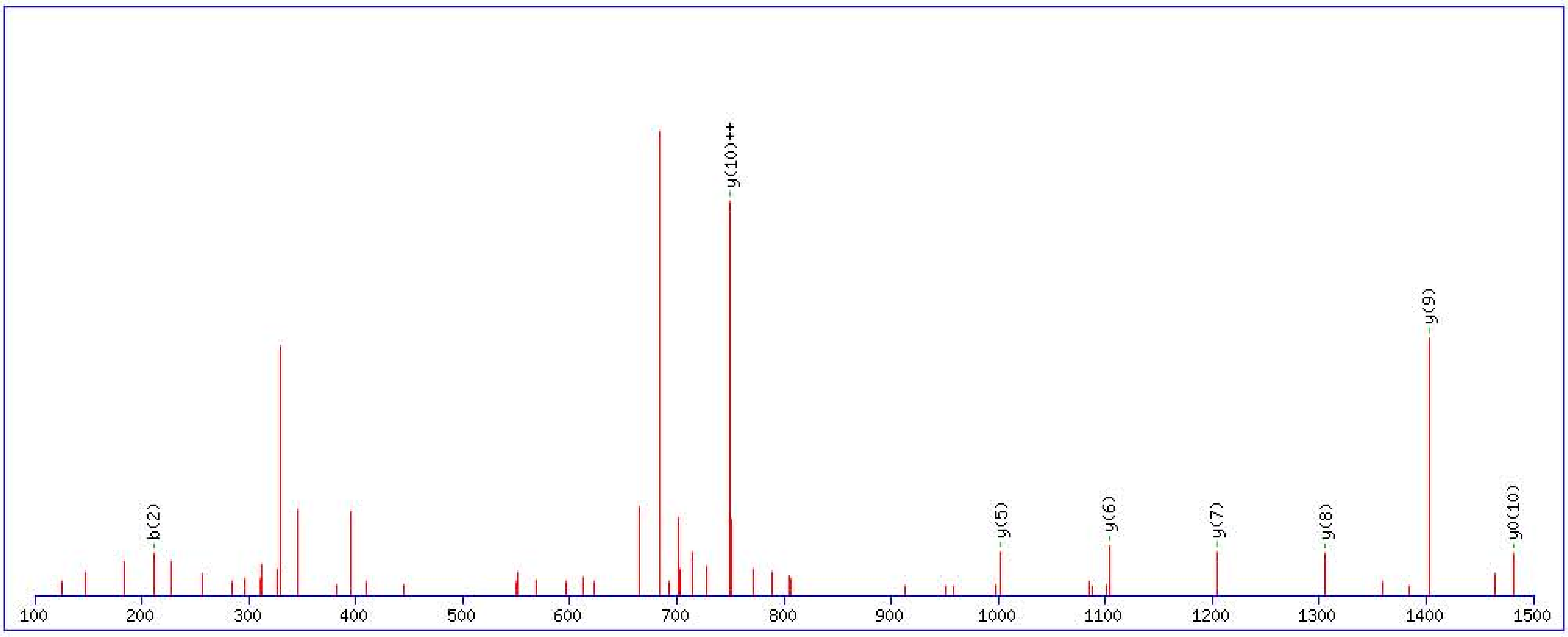
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

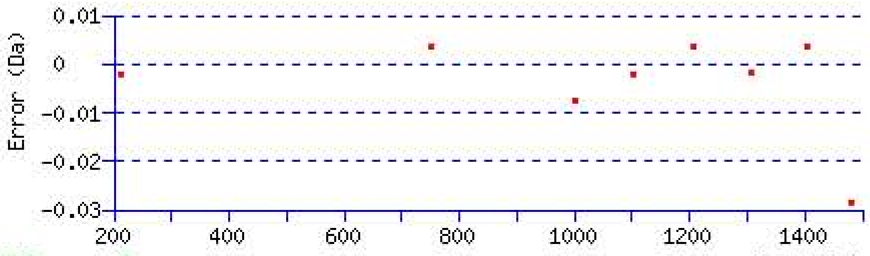
Match to Query 31052: 1611.814968 from(806.914760,2+) rtinseconds(1485) index(1852)
Title: Locus:1.1.1.3036.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

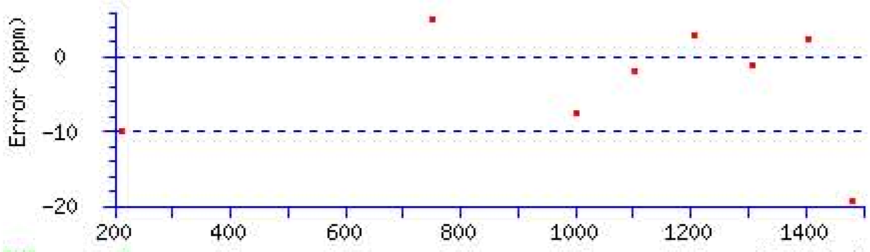
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1611.811295
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 26 **Expect:** 0.0064
Matches : 8/90 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	114.091340	57.549308					L							11
2	**211.144104**	106.075690					P	1499.734500	750.370888	1482.707951	741.857614	1481.723935	741.365606	10
3	308.196868	154.602072					P	***1402.681736***	701.844506	1385.655187	693.331232	1384.671171	692.839224	9
4	409.244547	205.125911			391.233982	196.120629	T	***1305.628972***	653.318124	1288.602423	644.804850	1287.618407	644.312842	8
5	510.292226	255.649751			492.281661	246.644468	T	***1204.581293***	602.794285	1187.554744	594.281010	1186.570728	593.789002	7
6	611.339905	306.173591			593.329340	297.168308	T	***1103.533614***	552.270445	1086.507065	543.757171	1085.523049	543.265163	6
7	771.370554	386.188915			753.359989	377.183633	C	***1002.485935***	501.746606	985.459386	493.233331			5
8	899.429132	450.218204	882.402583	441.704930	881.418567	441.212922	Q	842.455286	421.731281	825.428737	413.218007			4
9	1027.487710	514.247493	1010.461161	505.734219	1009.477145	505.242211	Q	714.396708	357.701992	697.370159	349.188718			3
10	1466.713036	733.860156	1449.686487	725.346882	1448.702471	724.854874	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 LPPTTTCQQQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.1	1611.811295	0.003673	LPPTTTCQQQK
26.1	1611.811295	0.003673	LPPTTTCQQQK
26.1	1611.811295	0.003673	LPPTTTCQQQK
0.6	1611.826324	-0.011356	LQSHMDALRKQNR

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

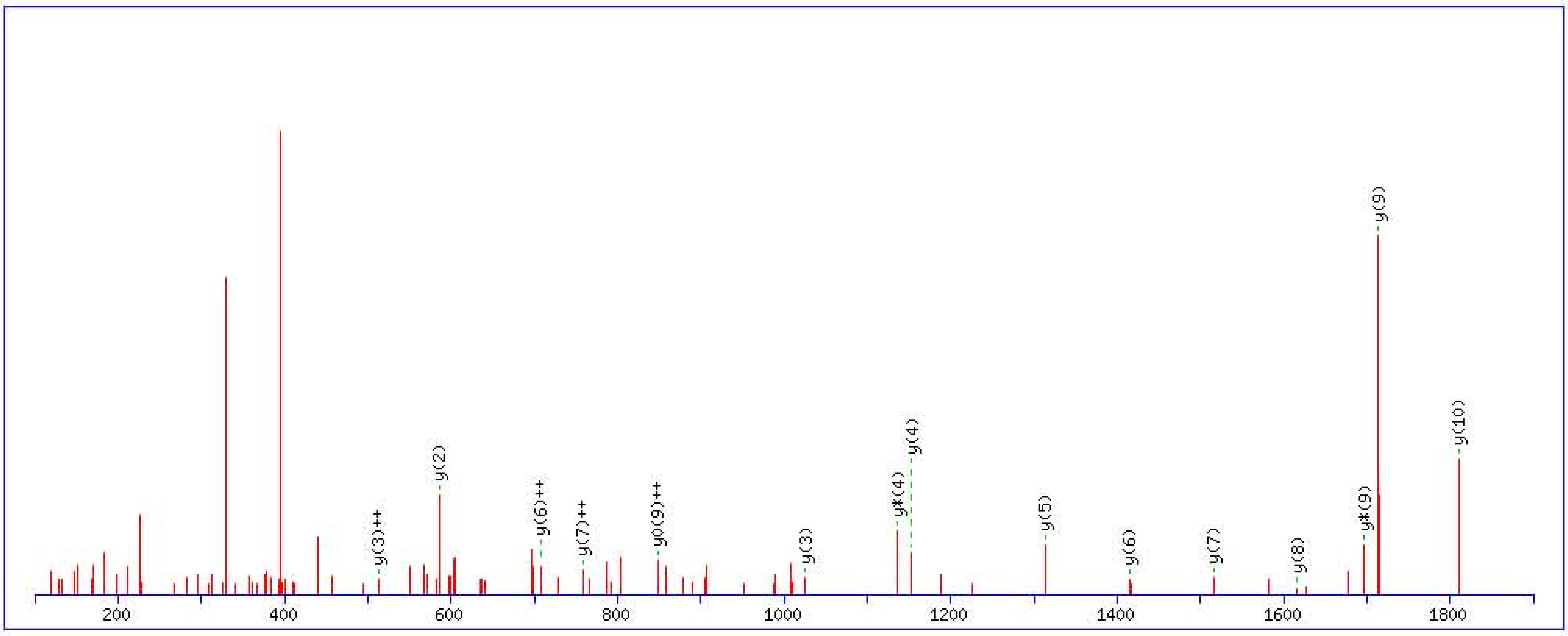
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

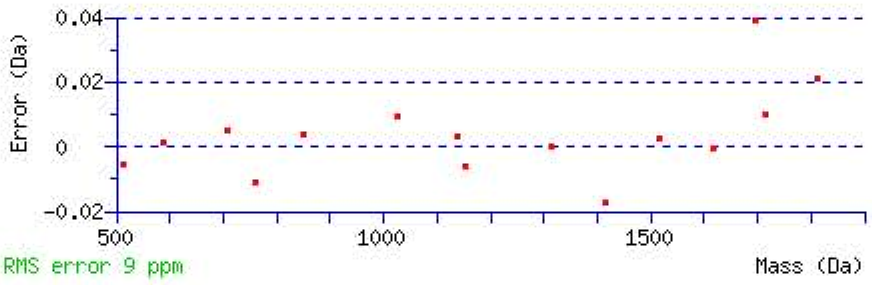
Match to Query 37853: 1922.984952 from(642.002260,3+) rtinseconds(1831) index(3922)
Title: Locus:1.1.1.3157.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

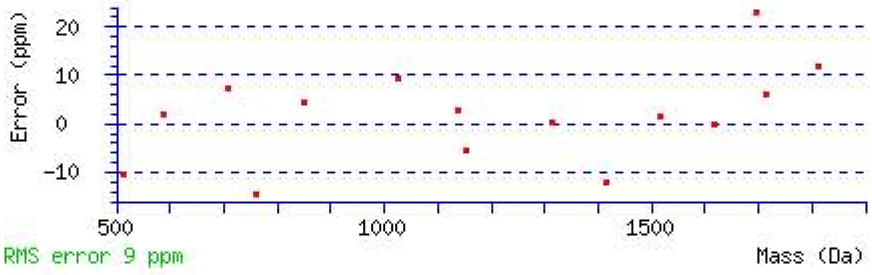
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1922.978043
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9     : Biotin:Thermo-21345 (Q)
Q10    : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.0012
Matches : 15/90 fragment ions using 45 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	211.144104	106.075690					P	***1810.901248***	905.954262	1793.874699	897.440988	1792.890683	896.948980	10
3	308.196868	154.602072					P	***1713.848484***	857.427880	1696.821935	848.914606	1695.837919	848.422598	9
4	409.244547	205.125911			391.233982	196.120629	T	***1616.795720***	808.901498	1599.769171	800.388224	1598.785155	799.896216	8
5	510.292226	255.649751			492.281661	246.644468	T	***1515.748041***	758.377659	1498.721492	749.864384	1497.737476	749.372376	7
6	611.339905	306.173591			593.329340	297.168308	T	***1414.700362***	707.853819	1397.673813	699.340545	1396.689797	698.848537	6
7	771.370554	386.188915			753.359989	377.183633	C	***1313.652683***	657.329980	1296.626134	648.816705			5
8	899.429132	450.218204	882.402583	441.704930	881.418567	441.212922	Q	***1153.622034***	577.314655	1136.595485	568.801381			4
9	1338.654458	669.830867	1321.627909	661.317593	1320.643893	660.825585	Q	***1025.563456***	513.285366	1008.536907	504.772092			3
10	1777.879784	889.443530	1760.853235	880.930256	1759.869219	880.438248	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 LPPTTTCQQQK
(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	1922.978043	0.006909	LPPTTTCQQQK
23.2	1922.978043	0.006909	LPPTTTCQQQK
15.7	1922.978043	0.006909	LPPTTTCQQQK
0.2	1923.003632	-0.018680	AKELHVQNVHMYLPTK

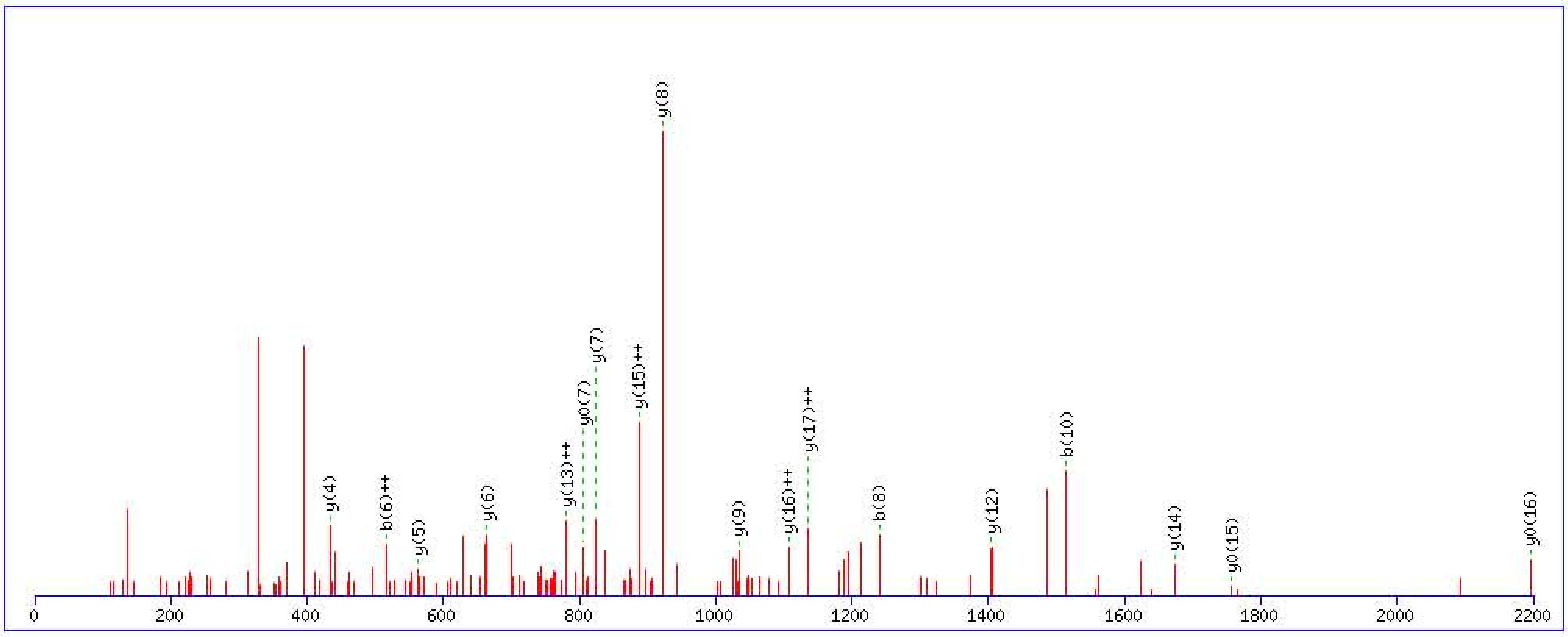
Mascot Search Results

Peptide View

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

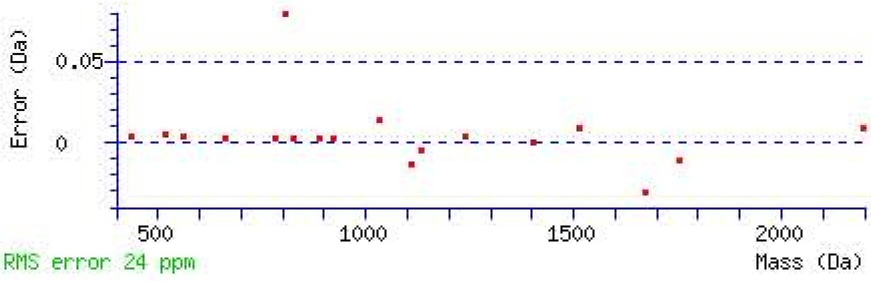
Match to Query 47029: 2433.198042 from(812.073290,3+) rtinseconds(2076) index(19458)
Title: Locus:1.1.1.3288.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

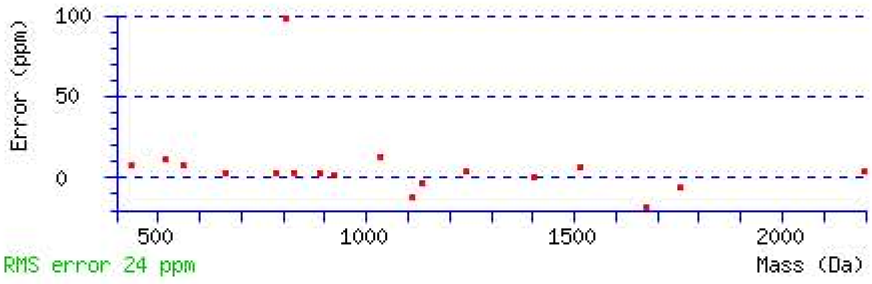
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2433.196701
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 38 **Expect:** 0.0039
Matches : 18/192 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							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





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
38.3	2433.196701	0.001341	YGQTIRPICLPCTEGTTR

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

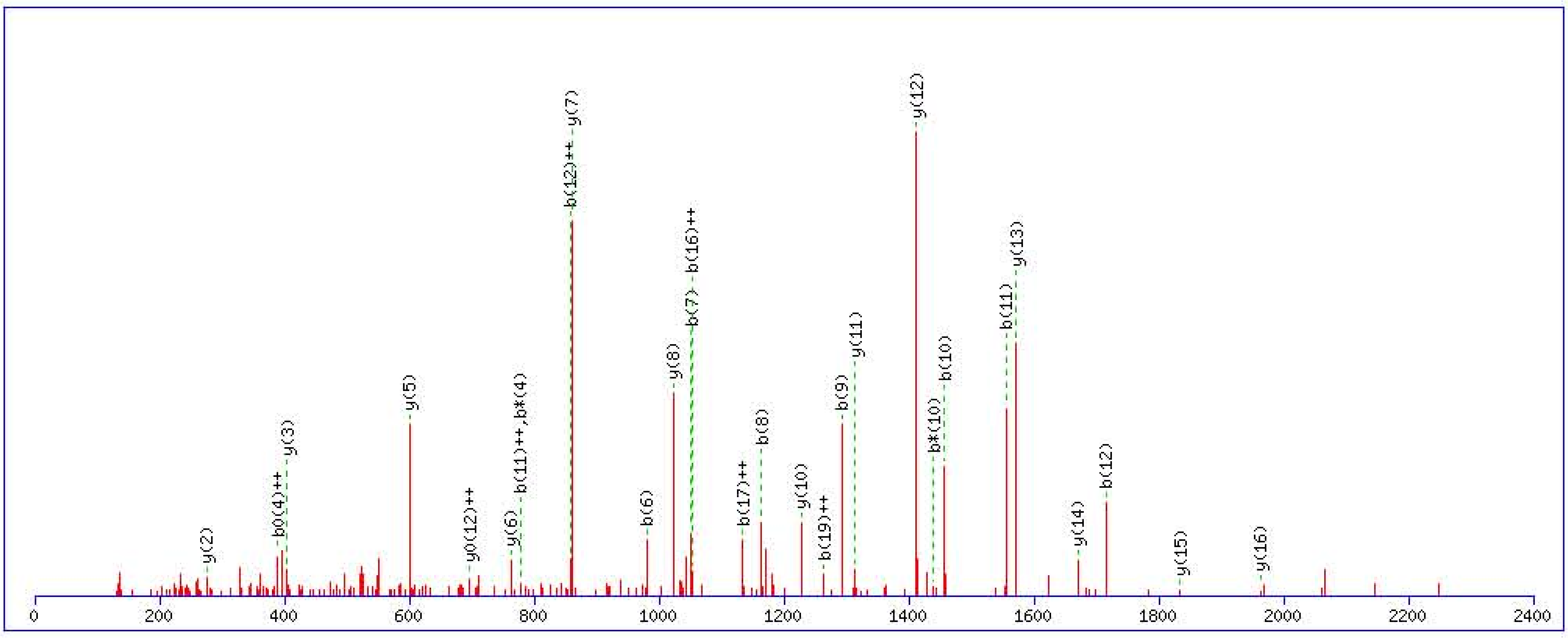
Mascot Search Results

Peptide View

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

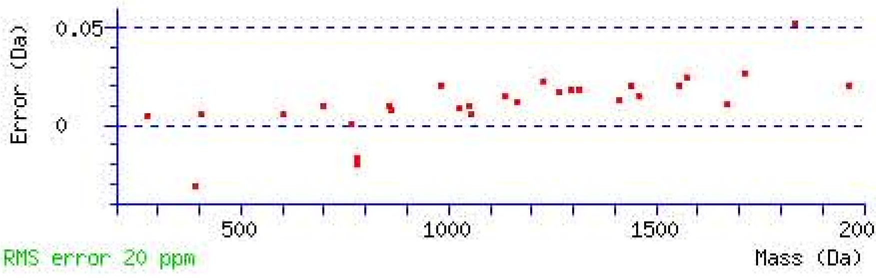
Match to Query 54869: 3125.572602 from(1042.864810,3+) rtinseconds(2705) index(8692)
Title: Locus:1.1.1.3461.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

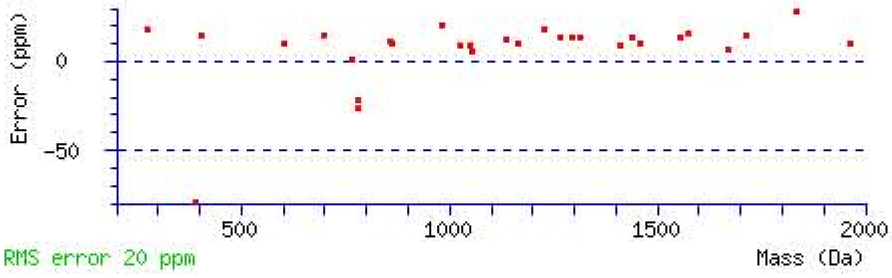
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3125.535446
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 62 **Expect:** 2e-005
Matches : 29/264 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	114.091340	57.549308					L							24
2	227.175404	114.091340					L	3013.458667	1507.232971	2996.432118	1498.719697	2995.448102	1498.227689	23
3	666.400730	333.704003	649.374181	325.190729			Q	2900.374603	1450.690939	2883.348054	1442.177665	2882.364038	1441.685657	22
4	795.443323	398.225300	778.416774	389.712025	777.432758	389.220017	E	2461.149277	1231.078276	2444.122728	1222.565002	2443.138712	1222.072994	21
5	852.464787	426.736032	835.438238	418.222757	834.454222	417.730749	G	2332.106684	1166.556980	2315.080135	1158.043705	2314.096119	1157.551697	20
6	**980.523365**	490.765321	963.496816	482.252046	962.512800	481.760038	Q	2275.085220	1138.046248	2258.058671	1129.532973	2257.074655	1129.040965	19
7	**1051.560479**	526.283878	1034.533930	517.770603	1033.549914	517.278595	A	2147.026642	1074.016959	2130.000093	1065.503684	2129.016077	1065.011676	18
8	**1164.644543**	582.825910	1147.617994	574.312635	1146.633978	573.820627	L	2075.989528	1038.498402	2058.962979	1029.985127	2057.978963	1029.493119	17
9	**1293.687136**	647.347206	1276.660587	638.833932	1275.676571	638.341924	E	***1962.905464***	981.956370	1945.878915	973.443096	1944.894899	972.951088	16
10	**1456.750465**	728.878871	1439.723916	720.365596	1438.739900	719.873588	Y	***1833.862871***	917.435074	1816.836322	908.921799	1815.852306	908.429791	15
11	**1555.818879**	**778.413078**	1538.792330	769.899803	1537.808314	769.407795	V	***1670.799542***	835.903409	1653.772993	827.390135	1652.788977	826.898126	14
12	**1715.849528**	**858.428402**	1698.822979	849.915128	1697.838963	849.423120	C	***1571.731128***	786.369202	1554.704579	777.855928	1553.720563	777.363919	13
13	1812.902292	906.954784	1795.875743	898.441510	1794.891727	897.949502	P	***1411.700479***	706.353877	1394.673930	697.840603	1393.689914	697.348595	12
14	1899.934320	950.470798	1882.907771	941.957524	1881.923755	941.465516	S	***1314.647715***	657.827495	1297.621166	649.314221	1296.637150	648.822213	11
15	1956.955784	978.981530	1939.929235	970.468256	1938.945219	969.976248	G	***1227.615687***	614.311481	1210.589138	605.798207	1209.605122	605.306199	10
16	2104.024198	**1052.515737**	2086.997649	1044.002462	2086.013633	1043.510454	F	1170.594223	585.800749	1153.567674	577.287475	1152.583658	576.795467	9
17	2267.087527	**1134.047402**	2250.060978	1125.534127	2249.076962	1125.042119	Y	***1023.525809***	512.266543	1006.499260	503.753268	1005.515244	503.261260	8
18	2364.140291	1182.573784	2347.113742	1174.060509	2346.129726	1173.568501	P	***860.462480***	430.734878	843.435931	422.221603	842.451915	421.729595	7
19	2527.203620	**1264.105448**	2510.177071	1255.592173	2509.193055	1255.100166	Y	***763.409716***	382.208496	746.383167	373.695221	745.399151	373.203213	6
20	2624.256384	1312.631830	2607.229835	1304.118556	2606.245819	1303.626548	P	***600.346387***	300.676831	583.319838	292.163557	582.335822	291.671549	5
21	2723.324798	1362.166037	2706.298249	1353.652762	2705.314233	1353.160754	V	503.293623	252.150449	486.267074	243.637175	485.283058	243.145167	4
22	2851.383376	1426.195326	2834.356827	1417.682051	2833.372811	1417.190044	Q	***404.225209***	202.616242	387.198660	194.102968	386.214644	193.610960	3
23	2952.431055	1476.719165	2935.404506	1468.205891	2934.420490	1467.713883	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
24							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.6	3125.535446	0.037156	LLQEGQALEYVCPSGFYPYPVQTR
61.6	3125.535446	0.037156	LLQEGQALEYVCPSGFYPYPVQTR

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

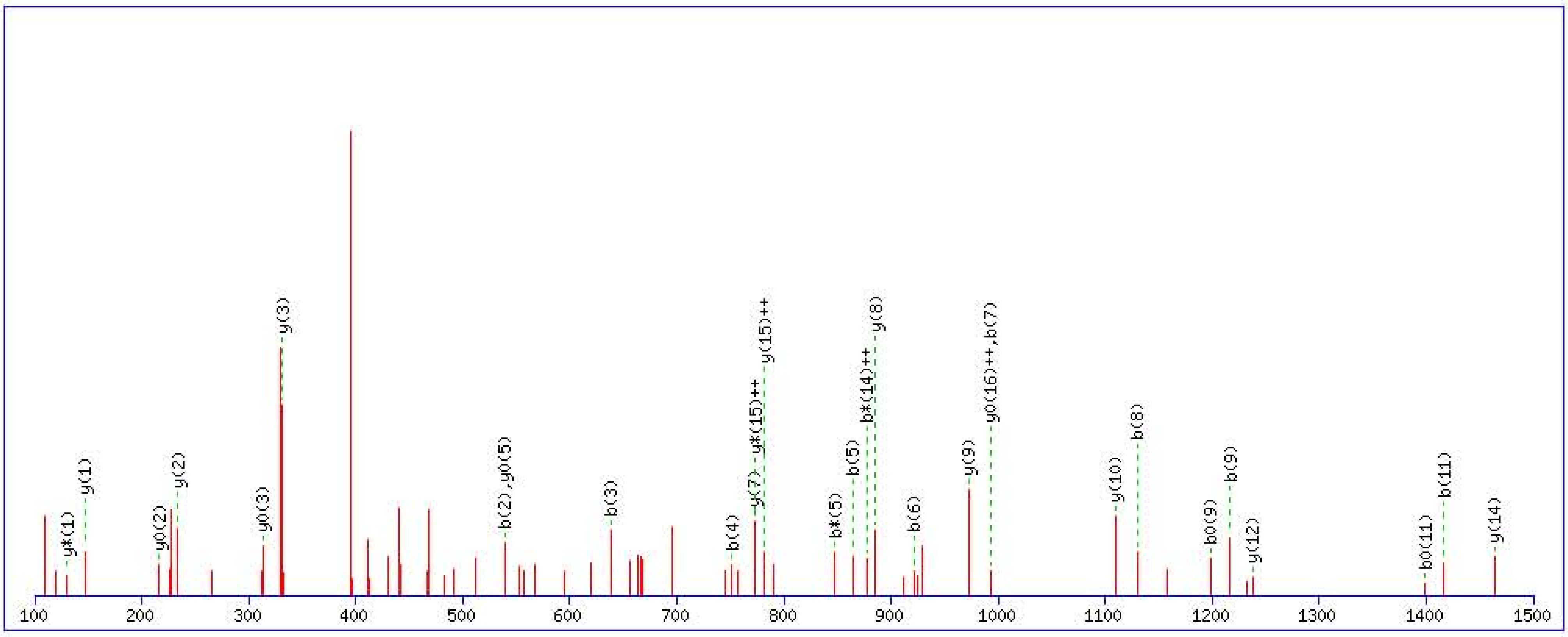
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQVLLGAHSLSQPEPSK**
Found in **CFAD_HUMAN**, Complement factor D OS=Homo sapiens GN=CFD PE=1 SV=5

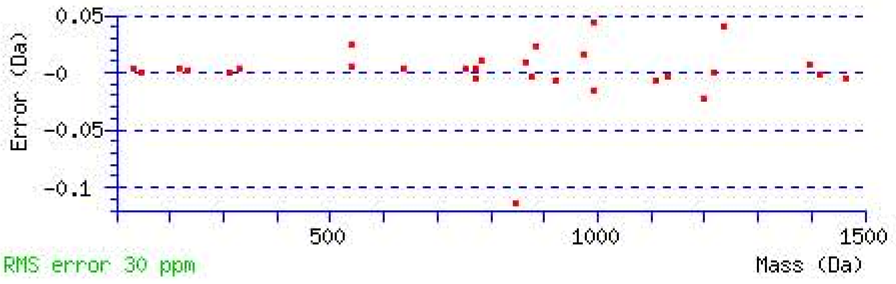
Match to Query 41616: 2100.138852 from(701.053560,3+) rtinseconds(2001) index(31891)
Title: Locus:1.1.1.3360.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

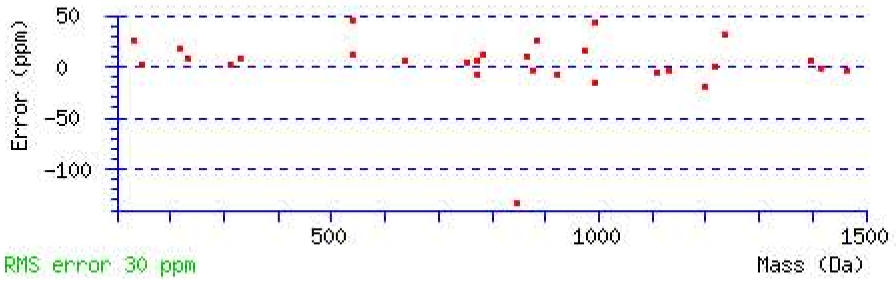
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2100.140137
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 62 **Expect:** 1.3e-005
Matches : 29/172 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	100.075690	50.541483					V							17
2	***539.301016***	270.154146	522.274467	261.640872			Q	2002.079009	1001.543143	1985.052460	993.029868	1984.068444	992.537860	16
3	***638.369430***	319.688353	621.342881	311.175079			V	1562.853683	781.930480	1545.827134	773.417205	1544.843118	772.925197	15
4	***751.453494***	376.230385	734.426945	367.717111			L	***1463.785269***	732.396273	1446.758720	723.882998	1445.774704	723.390990	14
5	***864.537558***	432.772417	847.511009	424.259143			L	1350.701205	675.854241	1333.674656	667.340966	1332.690640	666.848958	13
6	***921.559022***	461.283149	904.532473	452.769875			G	***1237.617141***	619.312209	1220.590592	610.798934	1219.606576	610.306926	12
7	***992.596136***	496.801706	975.569587	488.288432			A	1180.595677	590.801477	1163.569128	582.288202	1162.585112	581.796194	11
8	***1129.655048***	565.331162	1112.628499	556.817888			H	***1109.558563***	555.282920	1092.532014	546.769645	1091.547998	546.277637	10
9	***1216.687076***	608.847176	1199.660527	600.333902	1198.676511	599.841894	S	***972.499651***	486.753464	955.473102	478.240189	954.489086	477.748181	9
10	1329.771140	665.389208	1312.744591	656.875934	1311.760575	656.383926	L	***885.467623***	443.237450	868.441074	434.724175	867.457058	434.232167	8
11	***1416.803168***	708.905222	1399.776619	700.391948	1398.792603	699.899940	S	***772.383559***	386.695418	755.357010	378.182143	754.372994	377.690135	7
12	1544.861746	772.934511	1527.835197	764.421237	1526.851181	763.929229	Q	685.351531	343.179404	668.324982	334.666129	667.340966	334.174121	6
13	1641.914510	821.460893	1624.887961	812.947619	1623.903945	812.455611	P	557.292953	279.150115	540.266404	270.636840	539.282388	270.144832	5
14	1770.957103	885.982190	1753.930554	877.468915	1752.946538	876.976907	E	460.240189	230.623733	443.213640	222.110458	442.229624	221.618450	4
15	1868.009867	934.508572	1850.983318	925.995297	1849.999302	925.503289	P	***331.197596***	166.102436	314.171047	157.589162	313.187031	157.097154	3
16	1955.041895	978.024586	1938.015346	969.511311	1937.031330	969.019303	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
17							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.9	2100.140137	-0.001285	VQVLLGAHSLSQPEPSK

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

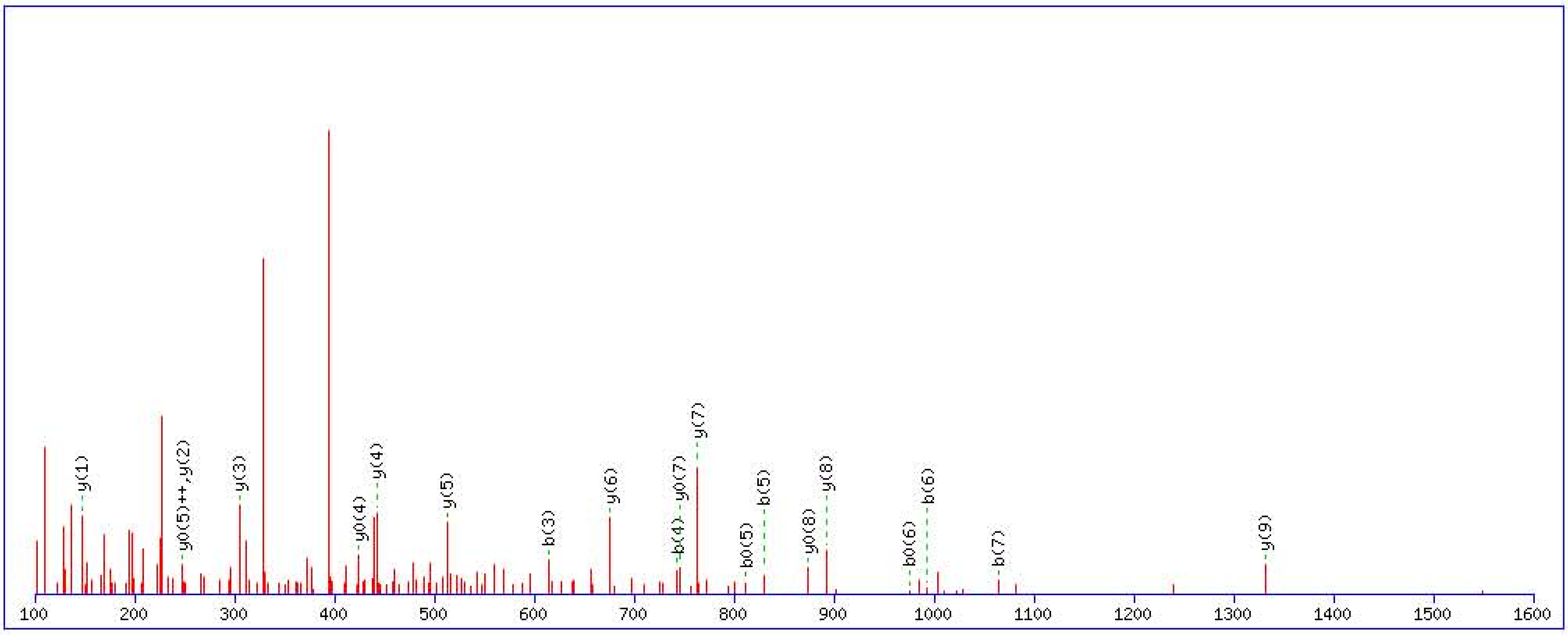
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSQESYAHGTK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

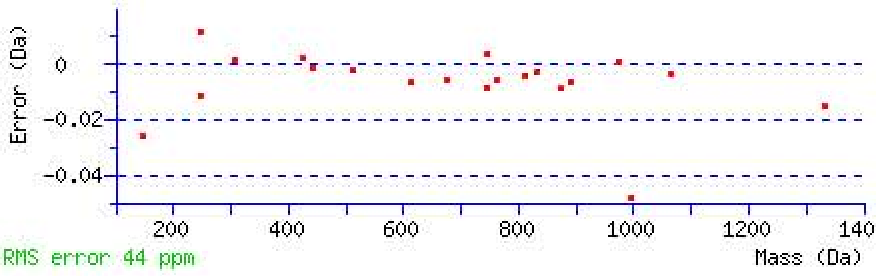
Match to Query 27267: 1504.695012 from(502.572280,3+) rtinseconds(1248) index(14533)
Title: Locus:1.1.1.3000.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

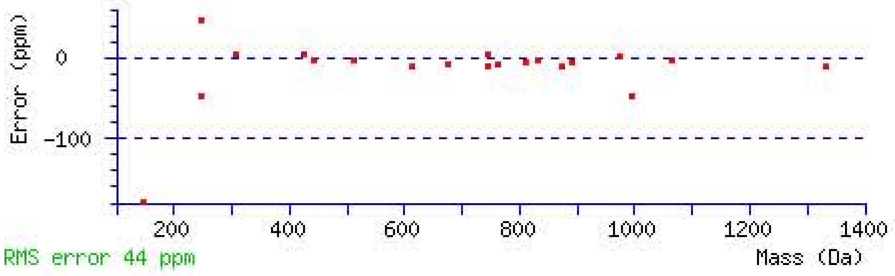
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1504.698013
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 45  Expect: 0.00035
Matches : 20/114 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	88.039304	44.523290			70.028739	35.518008	S							11
2	175.071332	88.039304			157.060767	79.034021	S	1418.673277	709.840276	1401.646728	701.327002	1400.662712	700.834994	10
3	**614.296658**	307.651967	597.270109	299.138692	596.286093	298.646684	Q	***1331.641249***	666.324263	1314.614700	657.810988	1313.630684	657.318980	9
4	**743.339251**	372.173264	726.312702	363.659989	725.328686	363.167981	E	***892.415923***	446.711600	875.389374	438.198325	874.405358	437.706317	8
5	**830.371279**	415.689278	813.344730	407.176003	812.360714	406.683995	S	***763.373330***	382.190303	746.346781	373.677029	745.362765	373.185021	7
6	**993.434608**	497.220942	976.408059	488.707668	975.424043	488.215660	Y	***676.341302***	338.674289	659.314753	330.161015	658.330737	329.669007	6
7	**1064.471722**	532.739499	1047.445173	524.226225	1046.461157	523.734217	A	***513.277973***	257.142625	496.251424	248.629350	495.267408	248.137342	5
8	1201.530634	601.268955	1184.504085	592.755681	1183.520069	592.263672	H	***442.240859***	221.624067	425.214310	213.110793	424.230294	212.618785	4
9	1258.552098	629.779687	1241.525549	621.266413	1240.541533	620.774404	G	***305.181947***	153.094611	288.155398	144.581337	287.171382	144.089329	3
10	1359.599777	680.303526	1342.573228	671.790252	1341.589212	671.298244	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
11							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SSQESYAHGTK
(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	1504.698013	-0.003001	SSQESYAHGTK

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

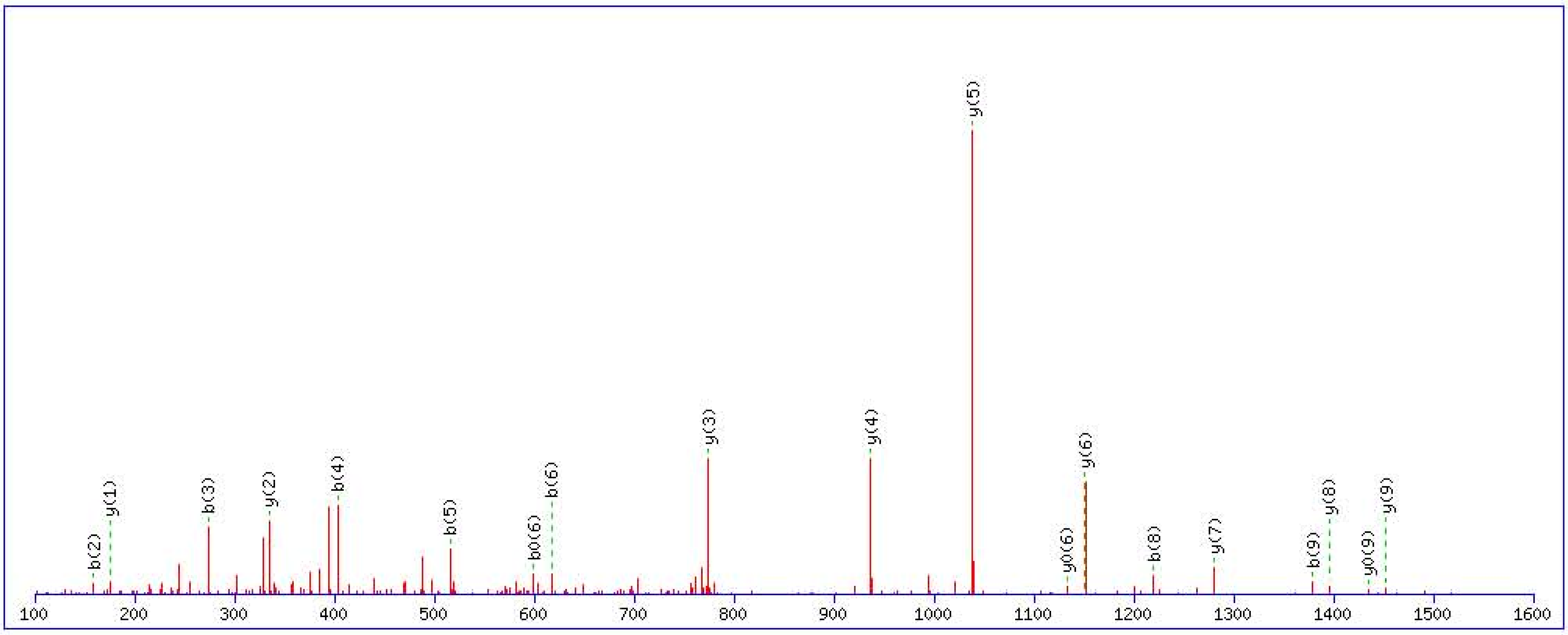
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TGDEITYQCR**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

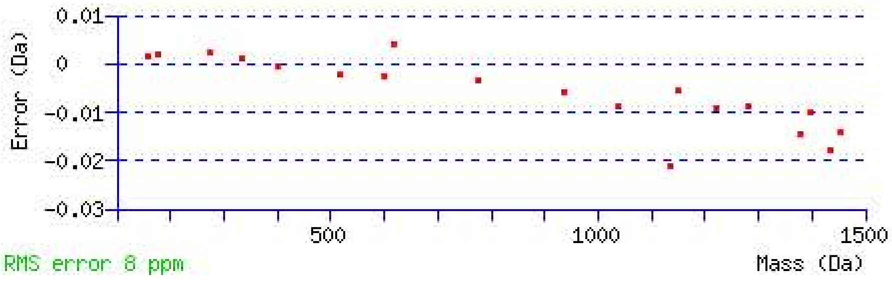
Match to Query 28538: 1552.691508 from(777.353030,2+) rtinseconds(1715) index(17210)
Title: Locus:1.1.1.3163.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

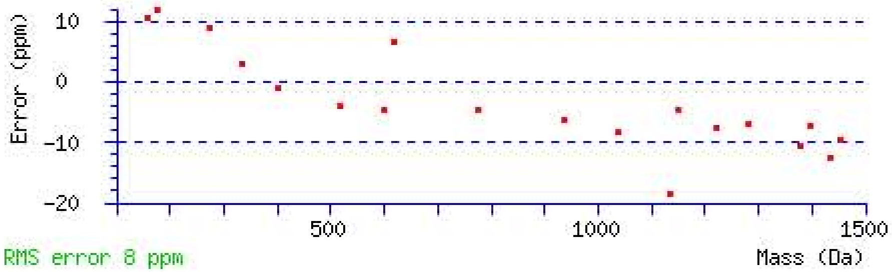
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1552.701401
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 72  Expect: 4.7e-007
Matches : 19/86 fragment ions using 29 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							10
2	**159.076419**	80.041847			141.065854	71.036565	G	***1452.660999***	726.834138	1435.634450	718.320863	1434.650434	717.828855	9
3	**274.103362**	137.555319			256.092797	128.550037	D	***1395.639535***	698.323406	1378.612986	689.810131	1377.628970	689.318123	8
4	**403.145955**	202.076616			385.135390	193.071333	E	***1280.612592***	640.809934	1263.586043	632.296660	1262.602027	631.804652	7
5	**516.230019**	258.618648			498.219454	249.613365	I	***1151.569999***	576.288638	1134.543450	567.775363	1133.559434	567.283355	6
6	**617.277698**	309.142487			599.267133	300.137205	T	***1038.485935***	519.746606	1021.459386	511.233331	1020.475370	510.741323	5
7	780.341027	390.674152			762.330462	381.668869	Y	***937.438256***	469.222766	920.411707	460.709492			4
8	**1219.566353**	610.286815	1202.539804	601.773540	1201.555788	601.281532	Q	***774.374927***	387.691102	757.348378	379.177827			3
9	**1379.597002**	690.302139	1362.570453	681.788865	1361.586437	681.296857	C	***335.149601***	168.078438	318.123052	159.565164			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.8	1552.701401	-0.009893	TGDEITYQCR
6.0	1552.712616	-0.021108	NVGMPVAHMESPER
2.1	1552.678772	0.012736	DGTQCLSGSSDGTIR
0.8	1552.686142	0.005366	VMDAVMSDGNLETR

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

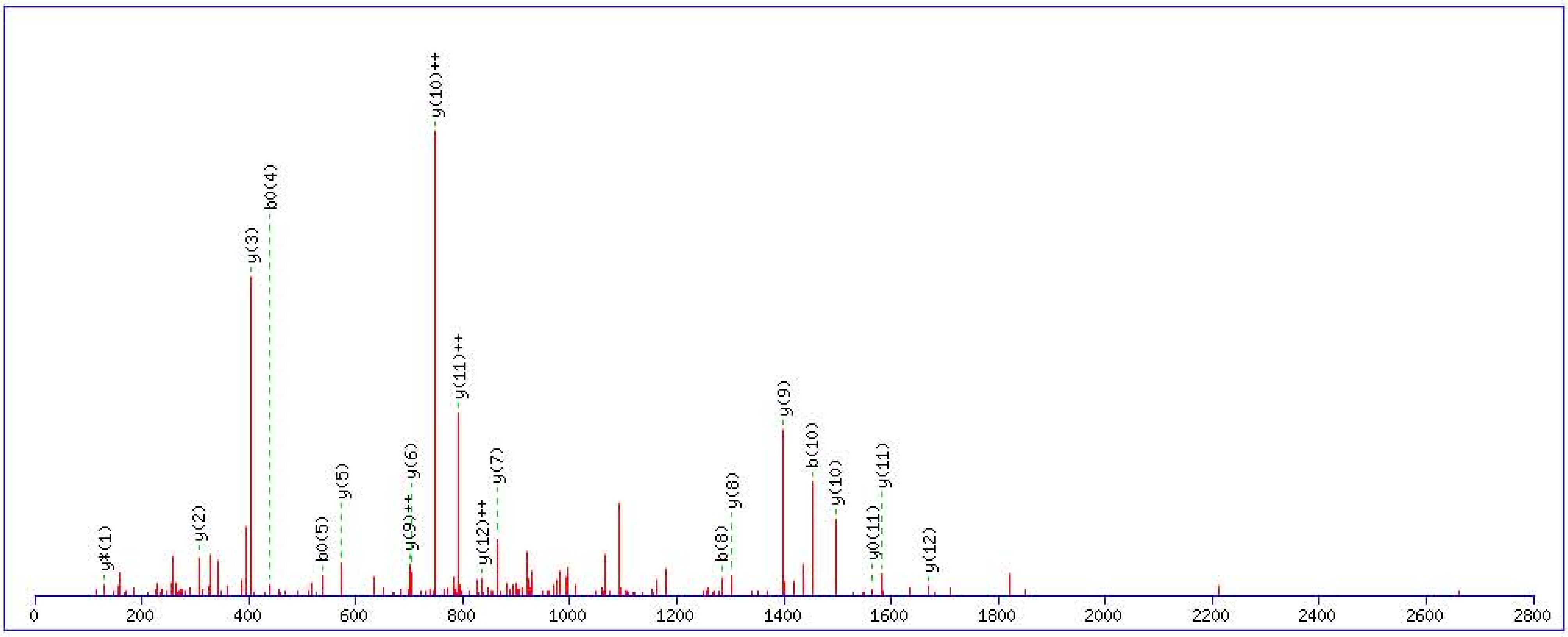
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WSSPPQCEGLPCK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

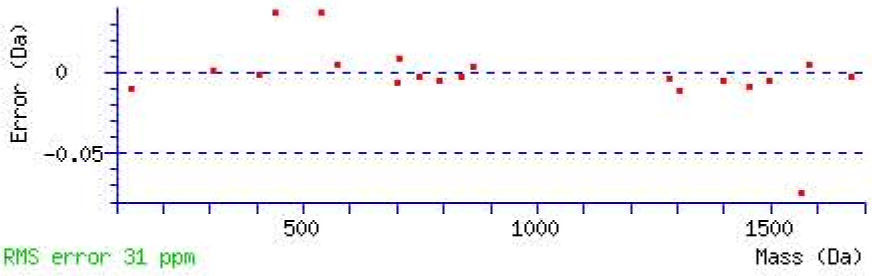
Match to Query 36842: 1855.836888 from(928.925720,2+) rtinseconds(1938) index(18648)
Title: Locus:1.1.1.3240.25 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

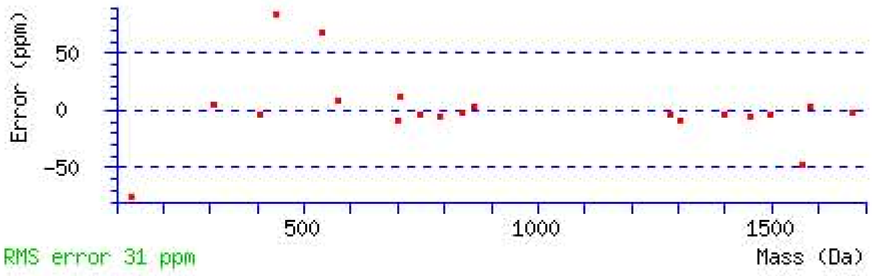
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1855.841934
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 70  Expect: 4.1e-007
Matches : 20/122 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	187.086589	94.046932					W							13
2	274.118617	137.562947			256.108052	128.557664	S	***1670.769897***	835.888587	1653.743348	827.375312	1652.759332	826.883304	12
3	361.150645	181.078960			343.140080	172.073678	S	***1583.737869***	792.372573	1566.711320	783.859298	1565.727304	783.367290	11
4	458.203409	229.605343			440.192844	220.600060	P	***1496.705841***	748.856559	1479.679292	740.343284	1478.695276	739.851276	10
5	555.256173	278.131725			537.245608	269.126442	P	***1399.653077***	700.330177	1382.626528	691.816902	1381.642512	691.324894	9
6	994.481499	497.744388	977.454950	489.231113	976.470934	488.739105	Q	***1302.600313***	651.803795	1285.573764	643.290520	1284.589748	642.798512	8
7	1154.512148	577.759712	1137.485599	569.246438	1136.501583	568.754430	C	***863.374987***	432.191132	846.348438	423.677857	845.364422	423.185849	7
8	**1283.554741**	642.281009	1266.528192	633.767734	1265.544176	633.275726	E	***703.344338***	352.175807	686.317789	343.662533	685.333773	343.170525	6
9	1340.576205	670.791741	1323.549656	662.278466	1322.565640	661.786458	G	***574.301745***	287.654511	557.275196	279.141236			5
10	**1453.660269**	727.333773	1436.633720	718.820498	1435.649704	718.328490	L	517.280281	259.143779	500.253732	250.630504			4
11	1550.713033	775.860155	1533.686484	767.346880	1532.702468	766.854872	P	***404.196217***	202.601747	387.169668	194.088472			3
12	1710.743682	855.875479	1693.717133	847.362205	1692.733117	846.870197	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 WSSPPQCEGLPCK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.2	1855.841934	-0.005046	WSSPPQCEGLPCK
2.1	1855.848465	-0.011577	FGGQDIFMTEEQK

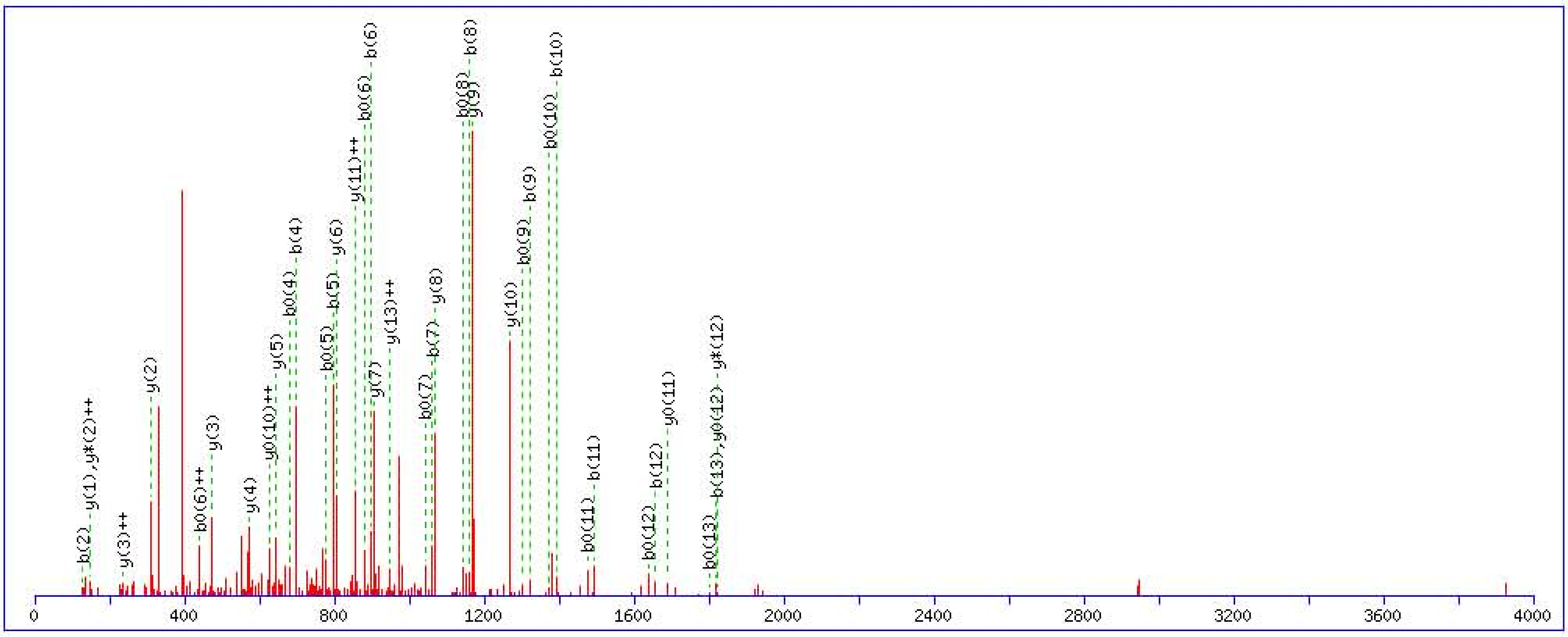
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGEQVTYTCATYYK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

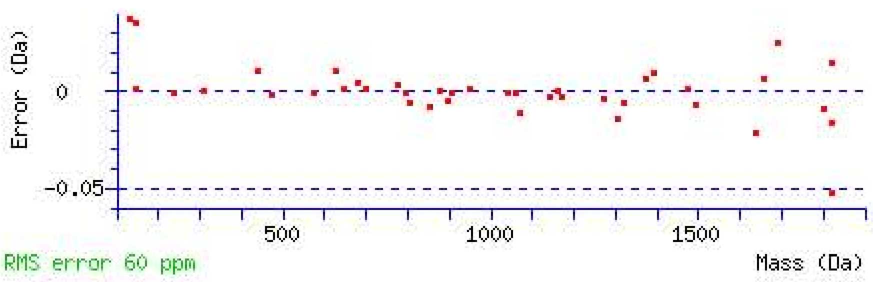
Match to Query 38680: 1964.892648 from(983.453600,2+) rtinseconds(1883) index(18173)
Title: Locus:1.1.1.3221.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

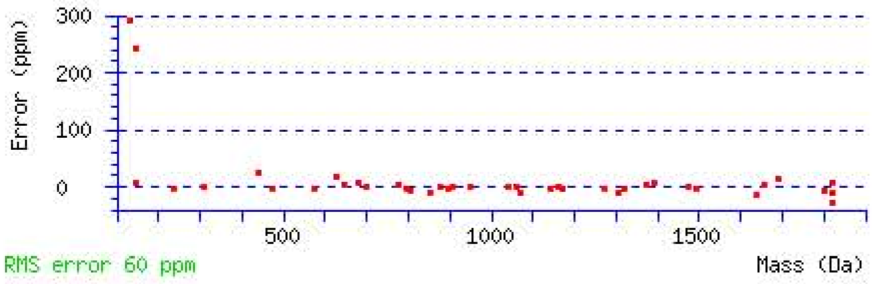
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1964.901215
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 63  Expect: 1.4e-006
Matches : 40/140 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	72.044390	36.525833					A							14
2	***129.065854***	65.036565					G	1894.871388	947.939332	1877.844839	939.426058	1876.860823	938.934050	13
3	258.108447	129.557862			240.097882	120.552579	E	1837.849924	919.428600	1820.823375	910.915326	1819.839359	910.423318	12
4	***697.333773***	349.170525	680.307224	340.657250	679.323208	340.165242	Q	1708.807331	854.907304	1691.780782	846.394029	1690.796766	845.902021	11
5	***796.402187***	398.704732	779.375638	390.191457	778.391622	389.699449	V	**1269.582005**	635.294641	1252.555456	626.781366	1251.571440	626.289358	10
6	***897.449866***	449.228571	880.423317	440.715297	879.439301	440.223289	T	**1170.513591**	585.760434	1153.487042	577.247159	1152.503026	576.755151	9
7	***1060.513195***	530.760236	1043.486646	522.246961	1042.502630	521.754953	Y	**1069.465912**	535.236594	1052.439363	526.723320	1051.455347	526.231312	8
8	***1161.560874***	581.284075	1144.534325	572.770801	1143.550309	572.278793	T	**906.402583**	453.704930	889.376034	445.191655	888.392018	444.699647	7
9	***1321.591523***	661.299400	1304.564974	652.786125	1303.580958	652.294117	C	**805.354904**	403.181090	788.328355	394.667816	787.344339	394.175808	6
10	***1392.628637***	696.817957	1375.602088	688.304682	1374.618072	687.812674	A	**645.324255**	323.165766	628.297706	314.652491	627.313690	314.160483	5
11	***1493.676316***	747.341796	1476.649767	738.828522	1475.665751	738.336514	T	**574.287141**	287.647209	557.260592	279.133934	556.276576	278.641926	4
12	***1656.739645***	828.873461	1639.713096	820.360186	1638.729080	819.868178	Y	**473.239462**	237.123369	456.212913	228.610095			3
13	***1819.802974***	910.405125	1802.776425	901.891851	1801.792409	901.399843	Y	**310.176133**	155.591705	293.149584	147.078430			2
14							K	**147.112804**	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.2	1964.901215	-0.008567	AGEQVTYTCATYYK
0.8	1964.883255	0.009393	RTHSGEKPYECKECGK
0.1	1964.900574	-0.007926	YCSTSLVKCASGTMGSIK

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

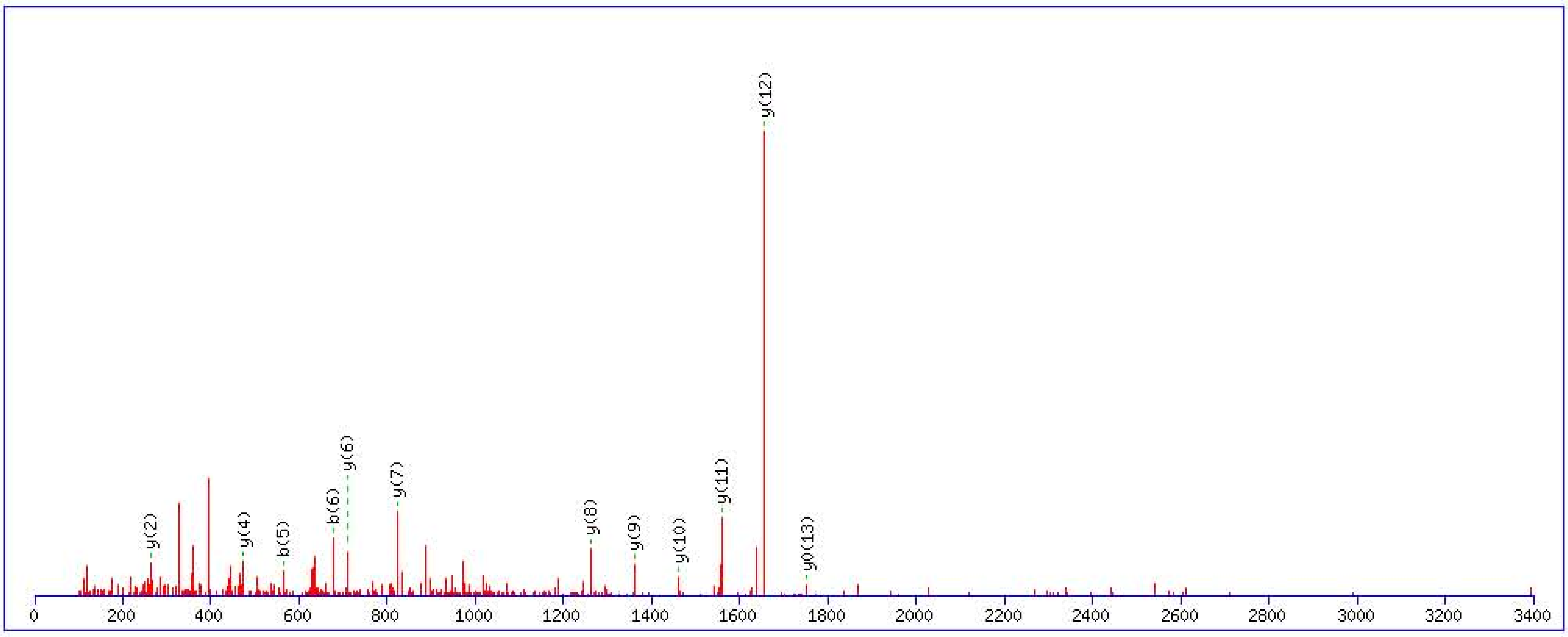
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTSCVNPPTVQNAYIVSR**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

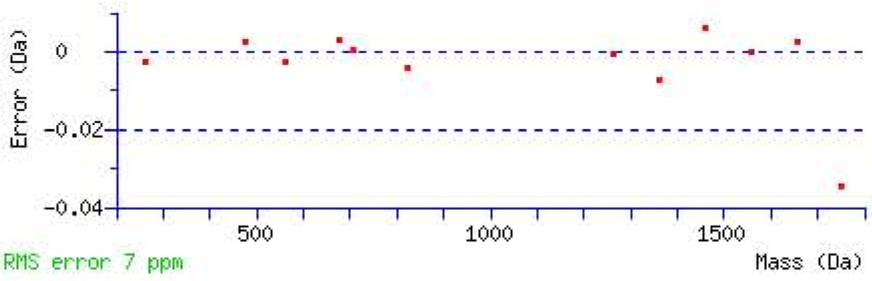
Match to Query 45637: 2331.139992 from(778.053940,3+) rtinseconds(2131) index(19801)
Title: Locus:1.1.1.3307.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

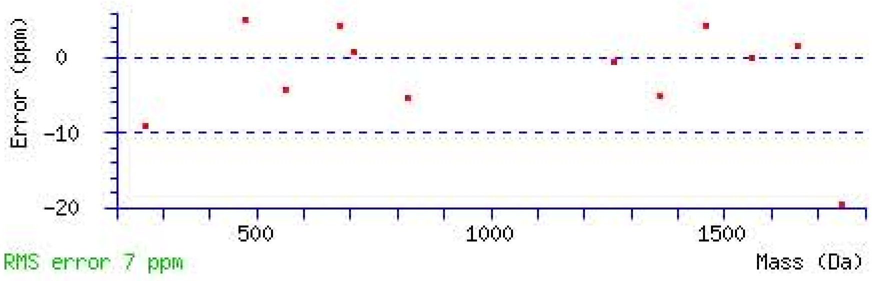
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2331.135147
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.00029
Matches : 12/192 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	116.034219	58.520748			98.023654	49.515465	D							18
2	217.081898	109.044587			199.071333	100.039304	T	2217.115472	1109.061374	2200.088923	1100.548099	2199.104907	1100.056091	17
3	304.113926	152.560601			286.103361	143.555319	S	2116.067793	1058.537534	2099.041244	1050.024260	2098.057228	1049.532252	16
4	464.144575	232.575925			446.134010	223.570643	C	2029.035765	1015.021521	2012.009216	1006.508246	2011.025200	1006.016238	15
5	**563.212989**	282.110133			545.202424	273.104850	V	1869.005116	935.006196	1851.978567	926.492922	1850.994551	926.000914	14
6	**677.255916**	339.131596	660.229367	330.618321	659.245351	330.126313	N	1769.936702	885.471989	1752.910153	876.958715	1751.926137	876.466707	13
7	774.308680	387.657978	757.282131	379.144703	756.298115	378.652695	P	***1655.893775***	828.450526	1638.867226	819.937251	1637.883210	819.445243	12
8	871.361444	436.184360	854.334895	427.671086	853.350879	427.179078	P	***1558.841011***	779.924144	1541.814462	771.410869	1540.830446	770.918861	11
9	972.409123	486.708200	955.382574	478.194925	954.398558	477.702917	T	***1461.788247***	731.397762	1444.761698	722.884487	1443.777682	722.392479	10
10	1071.477537	536.242407	1054.450988	527.729132	1053.466972	527.237124	V	***1360.740568***	680.873922	1343.714019	672.360648	1342.730003	671.868639	9
11	1510.702863	755.855070	1493.676314	747.341795	1492.692298	746.849787	Q	***1261.672154***	631.339715	1244.645605	622.826441	1243.661589	622.334433	8
12	1624.745790	812.876533	1607.719241	804.363259	1606.735225	803.871251	N	***822.446828***	411.727052	805.420279	403.213777	804.436263	402.721769	7
13	1695.782904	848.395090	1678.756355	839.881816	1677.772339	839.389808	A	***708.403901***	354.705588	691.377352	346.192314	690.393336	345.700306	6
14	1858.846233	929.926755	1841.819684	921.413480	1840.835668	920.921472	Y	637.366787	319.187031	620.340238	310.673757	619.356222	310.181749	5
15	1971.930297	986.468787	1954.903748	977.955512	1953.919732	977.463504	I	***474.303458***	237.655367	457.276909	229.142092	456.292893	228.650084	4
16	2070.998711	1036.002993	2053.972162	1027.489719	2052.988146	1026.997711	V	361.219394	181.113335	344.192845	172.600060	343.208829	172.108052	3
17	2158.030739	1079.519007	2141.004190	1071.005733	2140.020174	1070.513725	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
18							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.2	2331.135147	0.004845	DTSCVNPPTVQNAYIVSR

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

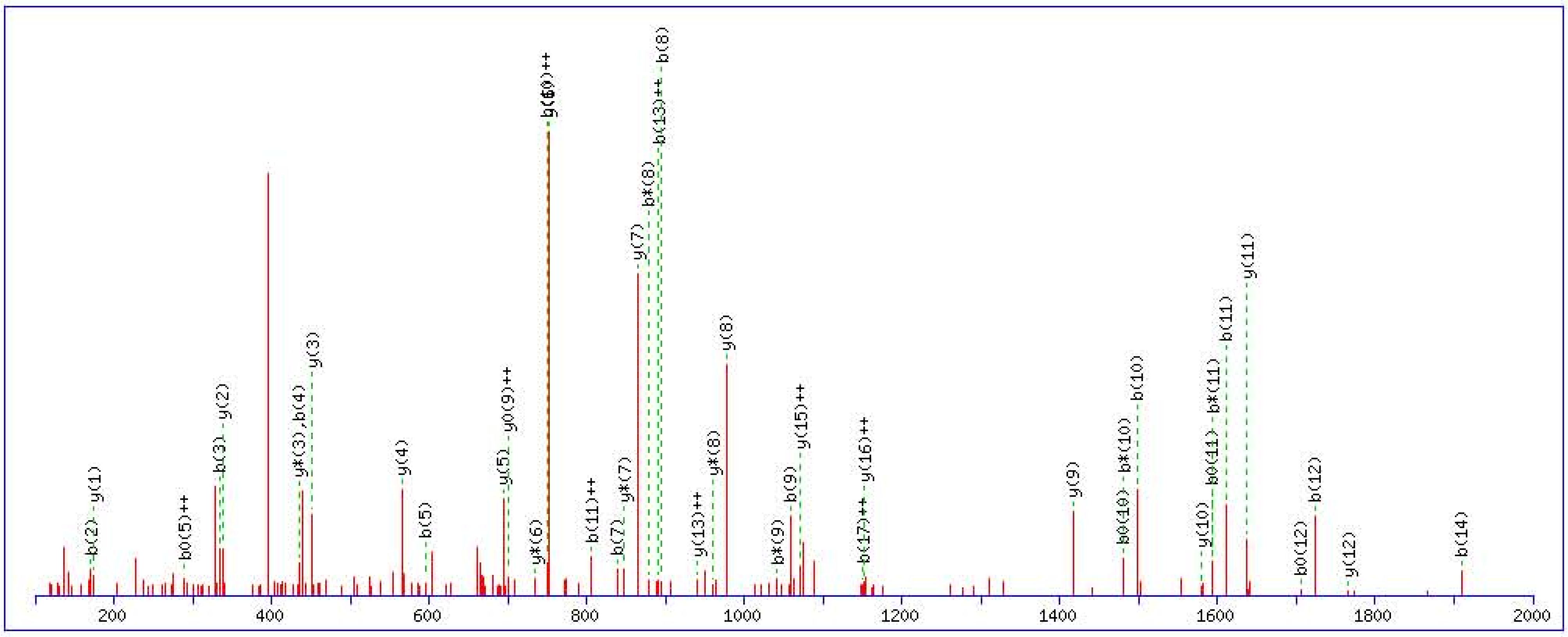
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVYTCNEGYQLLGEINYR**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

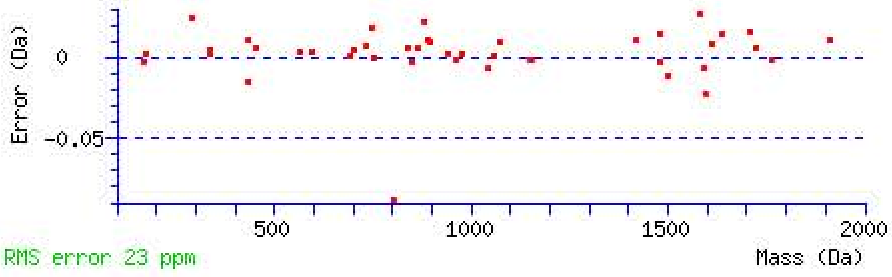
Match to Query 47783: 2473.193352 from(825.405060,3+) rtinseconds(2558) index(22076)
Title: Locus:1.1.1.3456.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

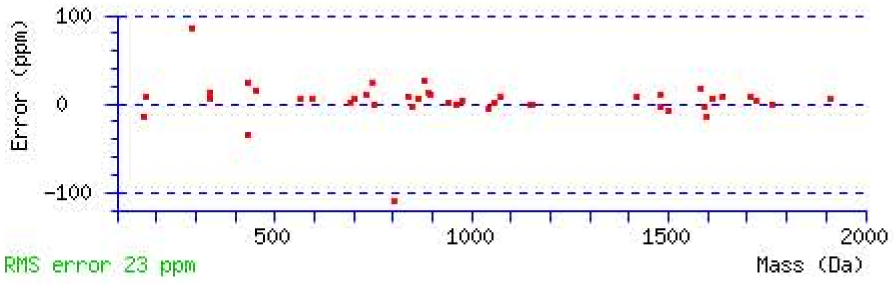
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2473.176971
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 0.00017
Matches : 43/180 fragment ions using 104 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							18
2	***171.112804***	86.060040					V	2403.147167	1202.077221	2386.120618	1193.563947	2385.136602	1193.071939	17
3	***334.176133***	167.591704					Y	2304.078753	1152.543014	2287.052204	1144.029740	2286.068188	1143.537732	16
4	***435.223812***	218.115544			417.213247	209.110262	T	2141.015424	1071.011350	2123.988875	1062.498075	2123.004859	1062.006067	15
5	***595.254461***	298.130869			577.243896	289.125586	C	2039.967745	1020.487511	2022.941196	1011.974236	2021.957180	1011.482228	14
6	709.297388	355.152332	692.270839	346.639058	691.286823	346.147050	N	1879.937096	940.472186	1862.910547	931.958912	1861.926531	931.466903	13
7	***838.339981***	419.673629	821.313432	411.160354	820.329416	410.668346	E	***1765.894169***	883.450722	1748.867620	874.937448	1747.883604	874.445440	12
8	***895.361445***	448.184361	878.334896	439.671086	877.350880	439.179078	G	***1636.851576***	818.929426	1619.825027	810.416152	1618.841011	809.924144	11
9	***1058.424774***	529.716025	1041.398225	521.202751	1040.414209	520.710743	Y	***1579.830112***	790.418694	1562.803563	781.905419	1561.819547	781.413411	10
10	***1497.650100***	**749.328688**	1480.623551	740.815414	1479.639535	740.323406	Q	***1416.766783***	708.887030	1399.740234	700.373755	1398.756218	699.881747	9
11	***1610.734164***	**805.870720**	1593.707615	797.357446	1592.723599	796.865437	L	***977.541457***	489.274367	960.514908	480.761092	959.530892	480.269084	8
12	***1723.818228***	862.412752	1706.791679	853.899477	1705.807663	853.407469	L	***864.457393***	432.732335	847.430844	424.219060	846.446828	423.727052	7
13	1780.839692	**890.923484**	1763.813143	882.410209	1762.829127	881.918201	G	***751.373329***	376.190303	734.346780	367.677028	733.362764	367.185020	6
14	***1909.882285***	955.444780	1892.855736	946.931506	1891.871720	946.439498	E	***694.351865***	347.679571	677.325316	339.166296	676.341300	338.674288	5
15	2022.966349	1011.986812	2005.939800	1003.473538	2004.955784	1002.981530	I	***565.309272***	283.158274	548.282723	274.645000			4
16	2137.009276	1069.008276	2119.982727	1060.495001	2118.998711	1060.002993	N	***452.225208***	226.616242	435.198659	218.102968			3
17	2300.072605	**1150.539940**	2283.046056	1142.026666	2282.062040	1141.534658	Y	***338.182281***	169.594778	321.155732	161.081504			2
18							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of AVYTCNEGYQLLGEINYR
(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	2473.176971	0.016381	AVYTCNEGYQLLGEINYR

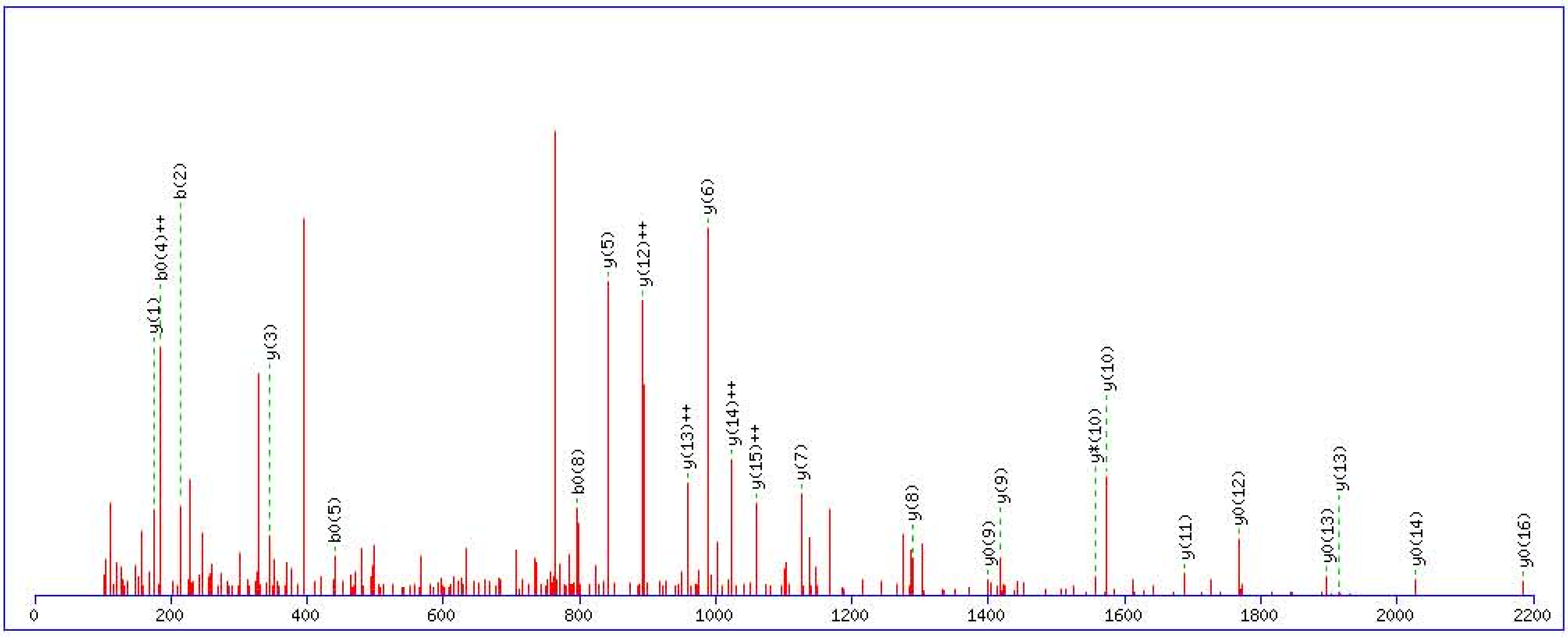
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVSSAMEPDREYHFGQAVR**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

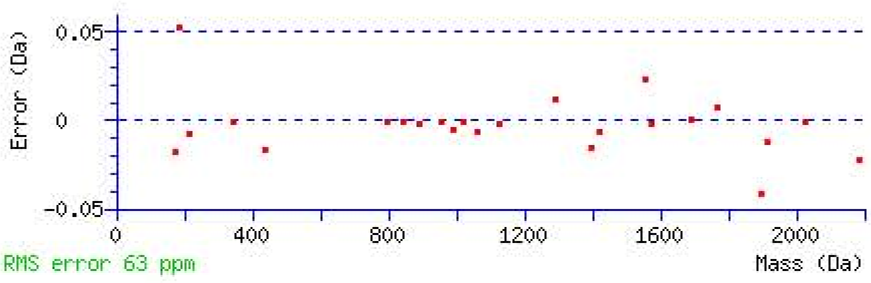
Match to Query 48527: 2502.207656 from(626.559190,4+) rtinseconds(1864) index(18070)
Title: Locus:1.1.1.3215.4 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

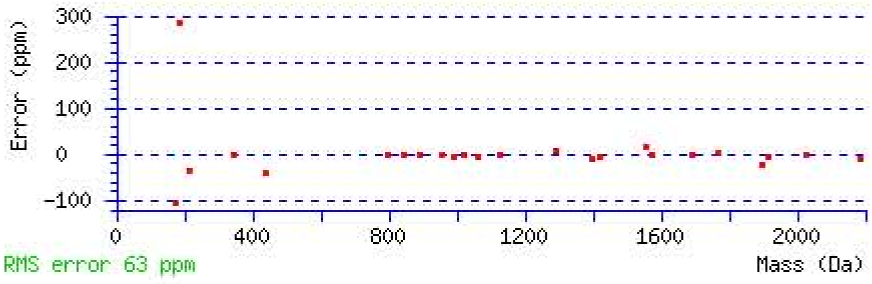
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2502.214767
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16    : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.021
Matches : 24/178 fragment ions using 59 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	213.159754	107.083515					V	2390.137998	1195.572637	2373.111449	1187.059362	2372.127433	1186.567354	18
3	300.191782	150.599529			282.181217	141.594247	S	2291.069584	1146.038430	2274.043035	1137.525155	2273.059019	1137.033147	17
4	387.223810	194.115543			369.213245	185.110261	S	2204.037556	1102.522416	2187.011007	1094.009141	2186.026991	1093.517133	16
5	458.260924	229.634100			440.250359	220.628818	A	2117.005528	1059.006402	2099.978979	1050.493127	2098.994963	1050.001119	15
6	589.301409	295.154343			571.290844	286.149060	M	2045.968414	1023.487845	2028.941865	1014.974571	2027.957849	1014.482563	14
7	718.344002	359.675639			700.333437	350.670357	E	***1914.927929***	957.967603	1897.901380	949.454328	1896.917364	948.962320	13
8	815.396766	408.202021			797.386201	399.196739	P	1785.885336	893.446306	1768.858787	884.933032	1767.874771	884.441024	12
9	930.423709	465.715493			912.413144	456.710210	D	***1688.832572***	844.919924	1671.806023	836.406650	1670.822007	835.914642	11
10	1086.524820	543.766048	1069.498271	535.252774	1068.514255	534.760766	R	***1573.805629***	787.406453	1556.779080	778.893178	1555.795064	778.401170	10
11	1215.567413	608.287345	1198.540864	599.774070	1197.556848	599.282062	E	***1417.704518***	709.355897	1400.677969	700.842623	1399.693953	700.350615	9
12	1378.630742	689.819009	1361.604193	681.305735	1360.620177	680.813727	Y	***1288.661925***	644.834601	1271.635376	636.321326			8
13	1515.689654	758.348465	1498.663105	749.835191	1497.679089	749.343183	H	***1125.598596***	563.302936	1108.572047	554.789662			7
14	1662.758068	831.882672	1645.731519	823.369398	1644.747503	822.877390	F	***988.539684***	494.773480	971.513135	486.260206			6
15	1719.779532	860.393404	1702.752983	851.880130	1701.768967	851.388122	G	***841.471270***	421.239273	824.444721	412.725999			5
16	2159.004858	1080.006067	2141.978309	1071.492792	2140.994293	1071.000784	Q	784.449806	392.728541	767.423257	384.215267			4
17	2230.041972	1115.524624	2213.015423	1107.011349	2212.031407	1106.519341	A	***345.224480***	173.115878	328.197931	164.602603			3
18	2329.110386	1165.058831	2312.083837	1156.545556	2311.099821	1156.053548	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 IVSSAMEPDREYHFGQAVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.1	2502.214767	-0.007111	IVSSAMEPDREYHFGQAVR

Mascot: http://www.matrixscience.com/

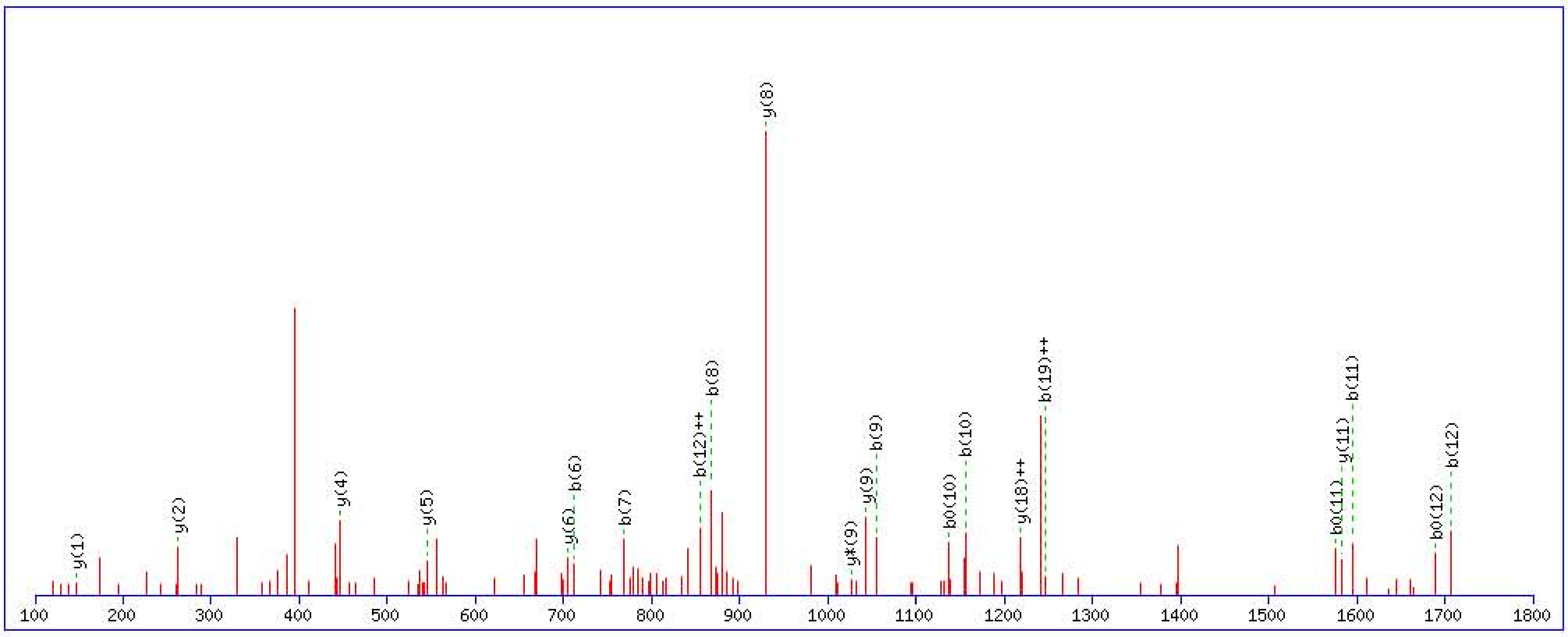
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SITCIHGVWTQLPQCVAIDK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

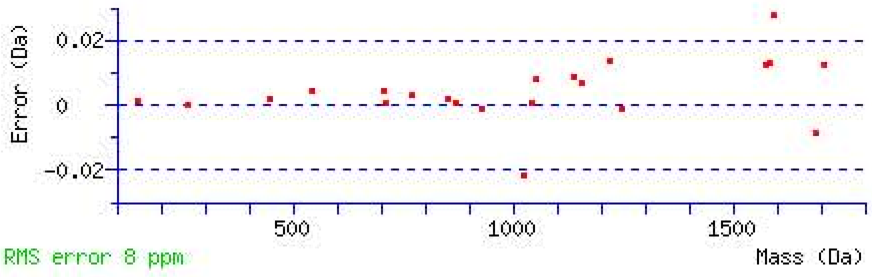
Match to Query 49829: 2636.335062 from(879.785630,3+) rtinseconds(2386) index(21131)
Title: Locus:1.1.1.3396.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

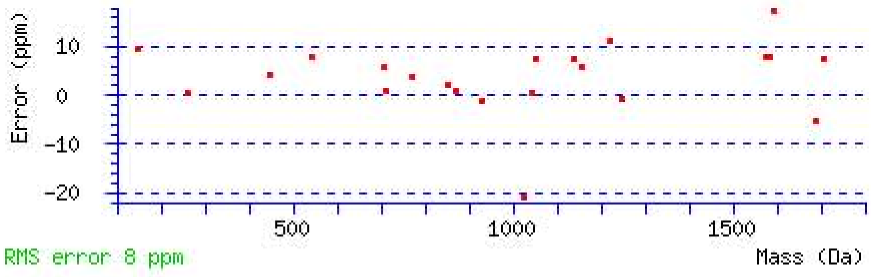


Monoisotopic mass of neutral peptide Mr(calc): 2636.327728
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 38 **Expect:** 0.0042
Matches : 22/206 fragment ions using 46 most intense peaks (help)

#	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							20
2	201.123368	101.065322			183.112803	92.060039	I	2550.302958	1275.655117	2533.276409	1267.141842	2532.292393	1266.649834	19
3	302.171047	151.589161			284.160482	142.583879	T	2437.218894	1219.113085	2420.192345	1210.599810	2419.208329	1210.107802	18
4	462.201696	231.604486			444.191131	222.599204	C	2336.171215	1168.589245	2319.144666	1160.075971	2318.160650	1159.583963	17
5	575.285760	288.146518			557.275195	279.141236	I	2176.140566	1088.573921	2159.114017	1080.060646	2158.130001	1079.568638	16
6	***712.344672***	356.675974			694.334107	347.670692	H	2063.056502	1032.031889	2046.029953	1023.518614	2045.045937	1023.026606	15
7	***769.366136***	385.186706			751.355571	376.181424	G	1925.997590	963.502433	1908.971041	954.989159	1907.987025	954.497151	14
8	***868.434550***	434.720913			850.423985	425.715631	V	1868.976126	934.991701	1851.949577	926.478427	1850.965561	925.986419	13
9	***1054.513863***	527.760570			1036.503298	518.755287	W	1769.907712	885.457494	1752.881163	876.944220	1751.897147	876.452211	12
10	***1155.561542***	578.284409			1137.550977	569.279127	T	***1583.828399***	792.417838	1566.801850	783.904563	1565.817834	783.412555	11
11	***1594.786868***	797.897072	1577.760319	789.383798	1576.776303	788.891790	Q	1482.780720	741.893998	1465.754171	733.380724	1464.770155	732.888715	10
12	***1707.870932***	**854.439104**	1690.844383	845.925830	1689.860367	845.433822	L	***1043.555394***	522.281335	1026.528845	513.768060	1025.544829	513.276052	9
13	1804.923696	902.965486	1787.897147	894.452212	1786.913131	893.960204	P	***930.471330***	465.739303	913.444781	457.226028	912.460765	456.734020	8
14	1932.982274	966.994775	1915.955725	958.481501	1914.971709	957.989493	Q	833.418566	417.212921	816.392017	408.699646	815.408001	408.207638	7
15	2093.012923	1047.010099	2075.986374	1038.496825	2075.002358	1038.004817	C	***705.359988***	353.183632	688.333439	344.670357	687.349423	344.178349	6
16	2192.081337	1096.544306	2175.054788	1088.031032	2174.070772	1087.539024	V	***545.329339***	273.168308	528.302790	264.655033	527.318774	264.163025	5
17	2263.118451	1132.062863	2246.091902	1123.549589	2245.107886	1123.057581	A	***446.260925***	223.634101	429.234376	215.120826	428.250360	214.628818	4
18	2376.202515	1188.604895	2359.175966	1180.091621	2358.191950	1179.599613	I	375.223811	188.115543	358.197262	179.602269	357.213246	179.110261	3
19	2491.229458	**1246.118367**	2474.202909	1237.605092	2473.218893	1237.113084	D	***262.139747***	131.573511	245.113198	123.060237	244.129182	122.568229	2
20							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 8 ppm



RMS error 8 ppm

NCBI **BLAST** search of SITCIHGVWTQLPQCVAIDK
(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	2636.327728	0.007334	SITCIHGVWTQLPQCVAIDK
31.5	2636.327728	0.007334	SITCIHGVWTQLPQCVAIDK

Mascot: http://www.matrixscience.com/

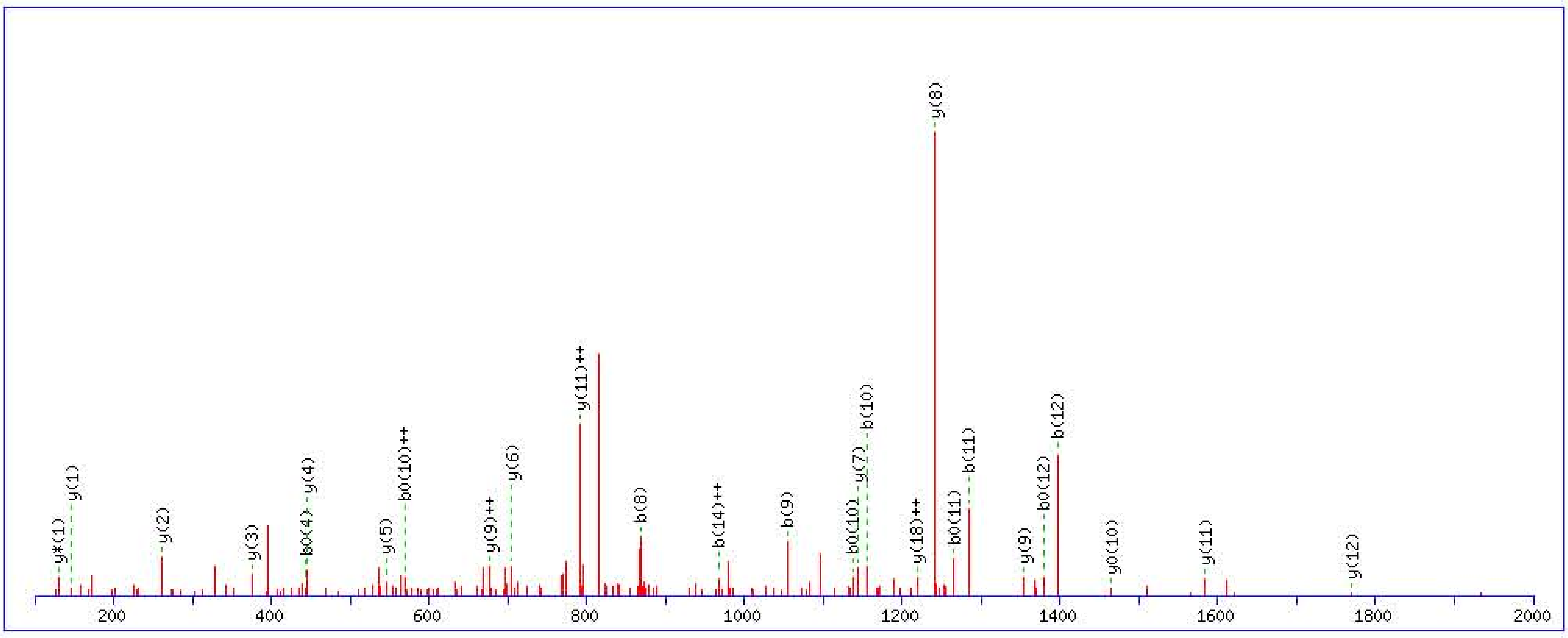
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SITCIHGVWTQLPQCVAIDK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

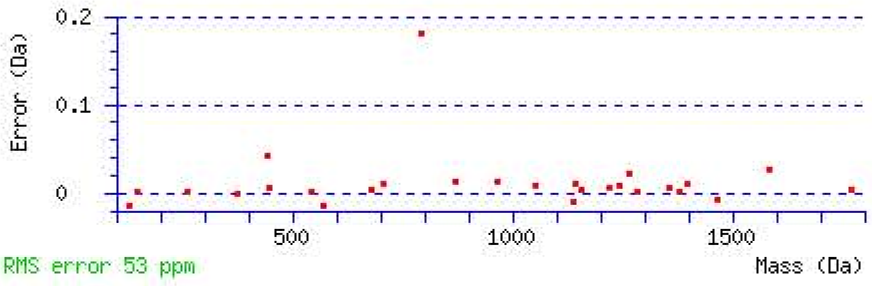
Match to Query 49832: 2636.337342 from(879.786390,3+) rtinseconds(2411) index(21306)
Title: Locus:1.1.1.3405.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

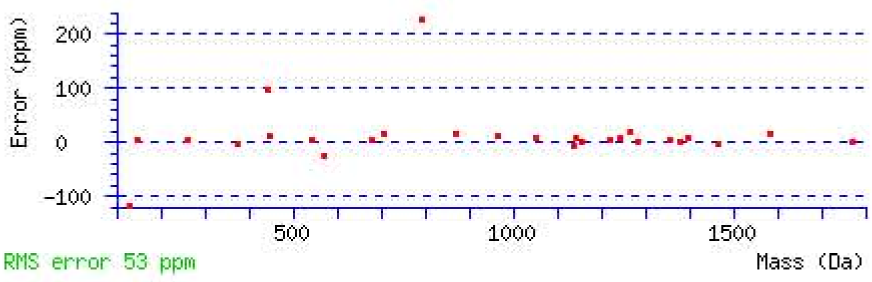


```
Monoisotopic mass of neutral peptide Mr(calc): 2636.327728
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 44  Expect: 9e-005
Matches : 27/206 fragment ions using 61 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							20
2	201.123368	101.065322			183.112803	92.060039	I	2550.302958	1275.655117	2533.276409	1267.141842	2532.292393	1266.649834	19
3	302.171047	151.589161			284.160482	142.583879	T	2437.218894	1219.113085	2420.192345	1210.599810	2419.208329	1210.107802	18
4	462.201696	231.604486			444.191131	222.599204	C	2336.171215	1168.589245	2319.144666	1160.075971	2318.160650	1159.583963	17
5	575.285760	288.146518			557.275195	279.141236	I	2176.140566	1088.573921	2159.114017	1080.060646	2158.130001	1079.568638	16
6	712.344672	356.675974			694.334107	347.670692	H	2063.056502	1032.031889	2046.029953	1023.518614	2045.045937	1023.026606	15
7	769.366136	385.186706			751.355571	376.181424	G	1925.997590	963.502433	1908.971041	954.989159	1907.987025	954.497151	14
8	**868.434550**	434.720913			850.423985	425.715631	V	1868.976126	934.991701	1851.949577	926.478427	1850.965561	925.986419	13
9	**1054.513863**	527.760570			1036.503298	518.755287	W	***1769.907712***	885.457494	1752.881163	876.944220	1751.897147	876.452211	12
10	**1155.561542**	578.284409			1137.550977	569.279127	T	***1583.828399***	792.417838	1566.801850	783.904563	1565.817834	783.412555	11
11	**1283.620120**	642.313698	1266.593571	633.800424	1265.609555	633.308416	Q	1482.780720	741.893998	1465.754171	733.380724	1464.770155	732.888715	10
12	**1396.704184**	698.855730	1379.677635	690.342456	1378.693619	689.850448	L	***1354.722142***	677.864709	1337.695593	669.351434	1336.711577	668.859426	9
13	1493.756948	747.382112	1476.730399	738.868838	1475.746383	738.376830	P	***1241.638078***	621.322677	1224.611529	612.809403	1223.627513	612.317394	8
14	1932.982274	966.994775	1915.955725	958.481501	1914.971709	957.989493	Q	***1144.585314***	572.796295	1127.558765	564.283021	1126.574749	563.791012	7
15	2093.012923	1047.010099	2075.986374	1038.496825	2075.002358	1038.004817	C	***705.359988***	353.183632	688.333439	344.670357	687.349423	344.178349	6
16	2192.081337	1096.544306	2175.054788	1088.031032	2174.070772	1087.539024	V	***545.329339***	273.168308	528.302790	264.655033	527.318774	264.163025	5
17	2263.118451	1132.062863	2246.091902	1123.549589	2245.107886	1123.057581	A	***446.260925***	223.634101	429.234376	215.120826	428.250360	214.628818	4
18	2376.202515	1188.604895	2359.175966	1180.091621	2358.191950	1179.599613	I	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	3
19	2491.229458	1246.118367	2474.202909	1237.605092	2473.218893	1237.113084	D	***262.139747***	131.573511	245.113198	123.060237	244.129182	122.568229	2
20							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 53 ppm



RMS error 53 ppm

NCBI **BLAST** search of SITCIHGVWTQLPQCVAIDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.5	2636.327728	0.009614	SITCIHGVWTQLPQCVAIDK
23.9	2636.327728	0.009614	SITCIHGVWTQLPQCVAIDK
1.3	2636.357361	-0.020019	RWWTLAGQEITVTFNQFTK
1.0	2636.301682	0.035660	TPDVLESSGPAVRSGLNATFMAFNR
0.2	2636.366592	-0.029250	ASKTTDLRIPASVCTMFNVLVDAK

Mascot: http://www.matrixscience.com/

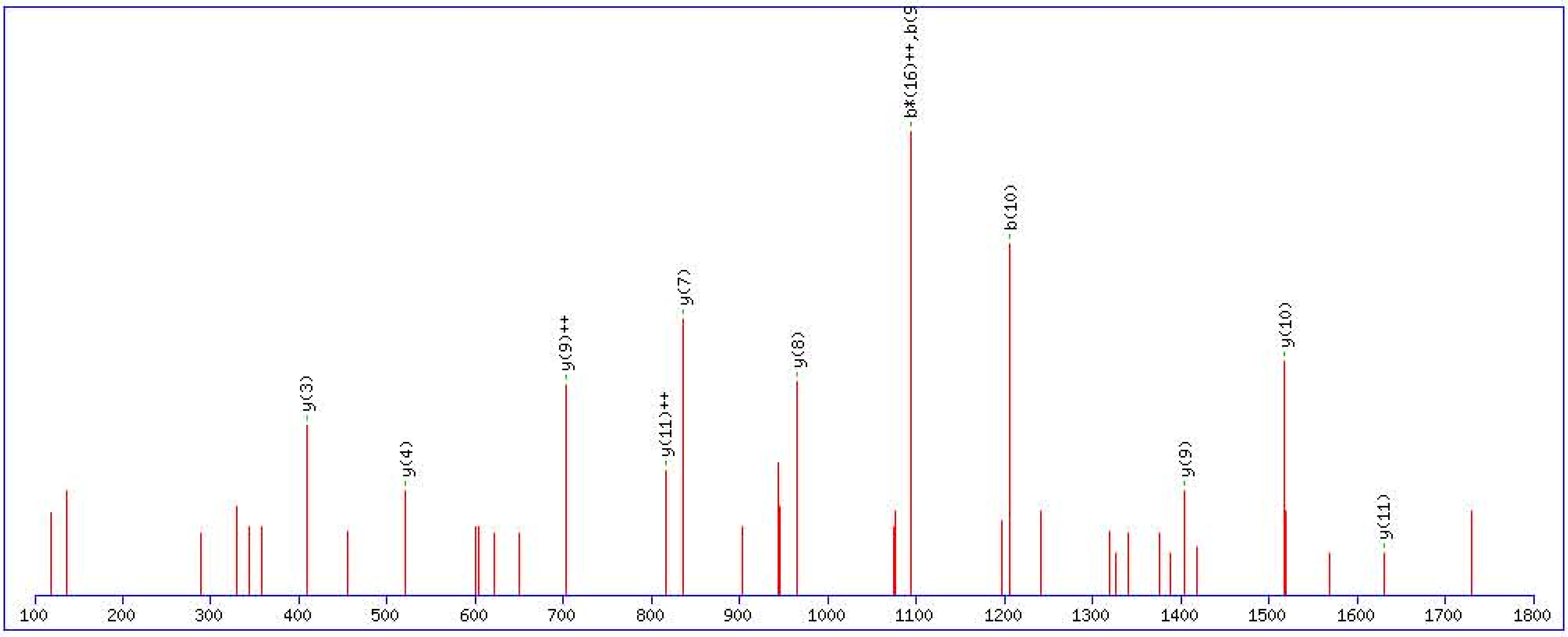
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSVLCQENYLIQEGEEITCK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

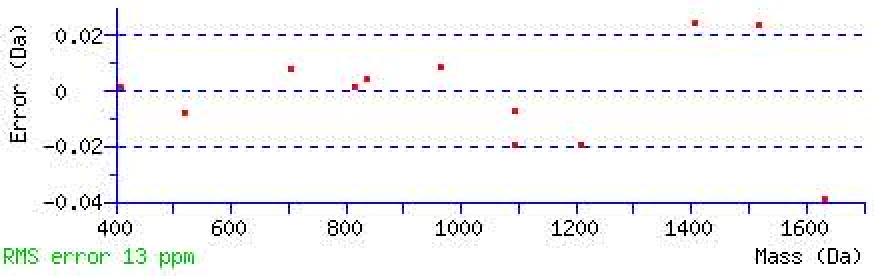
Match to Query 50605: 2722.300362 from(908.440730,3+) rtinseconds(2775) index(36460)
Title: Locus:1.1.1.3628.23 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

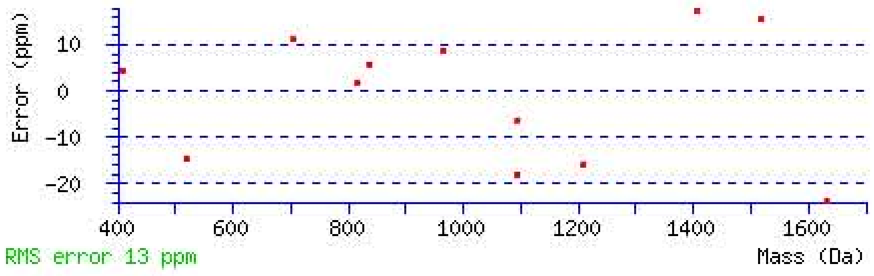
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2722.301590
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12    : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.0014
Matches : 12/212 fragment ions using 17 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.075690	50.541483					V							20
2	187.107718	94.057497			169.097153	85.052214	S	2624.240475	1312.623875	2607.213926	1304.110601	2606.229910	1303.618593	19
3	286.176132	143.591704			268.165567	134.586422	V	2537.208447	1269.107861	2520.181898	1260.594587	2519.197882	1260.102579	18
4	399.260196	200.133736			381.249631	191.128454	L	2438.140033	1219.573654	2421.113484	1211.060380	2420.129468	1210.568372	17
5	559.290845	280.149061			541.280280	271.143778	C	2325.055969	1163.031622	2308.029420	1154.518348	2307.045404	1154.026340	16
6	687.349423	344.178350	670.322874	335.665075	669.338858	335.173067	Q	2165.025320	1083.016298	2147.998771	1074.503023	2147.014755	1074.011015	15
7	816.392016	408.699646	799.365467	400.186372	798.381451	399.694364	E	2036.966742	1018.987009	2019.940193	1010.473735	2018.956177	1009.981727	14
8	930.434943	465.721110	913.408394	457.207835	912.424378	456.715827	N	1907.924149	954.465713	1890.897600	945.952438	1889.913584	945.460430	13
9	**1093.498272**	547.252774	1076.471723	538.739500	1075.487707	538.247492	Y	1793.881222	897.444249	1776.854673	888.930975	1775.870657	888.438967	12
10	**1206.582336**	603.794806	1189.555787	595.281532	1188.571771	594.789523	L	***1630.817893***	815.912585	1613.791344	807.399310	1612.807328	806.907302	11
11	1319.666400	660.336838	1302.639851	651.823563	1301.655835	651.331555	I	***1517.733829***	759.370553	1500.707280	750.857278	1499.723264	750.365270	10
12	1758.891726	879.949501	1741.865177	871.436227	1740.881161	870.944219	Q	***1404.649765***	702.828521	1387.623216	694.315246	1386.639200	693.823238	9
13	1887.934319	944.470798	1870.907770	935.957523	1869.923754	935.465515	E	***965.424439***	483.215858	948.397890	474.702583	947.413874	474.210575	8
14	1944.955783	972.981530	1927.929234	964.468255	1926.945218	963.976247	G	***836.381846***	418.694561	819.355297	410.181287	818.371281	409.689279	7
15	2073.998376	1037.502826	2056.971827	1028.989551	2055.987811	1028.497543	E	779.360382	390.183829	762.333833	381.670555	761.349817	381.178547	6
16	2203.040969	1102.024123	2186.014420	1093.510848	2185.030404	1093.018840	E	650.317789	325.662533	633.291240	317.149258	632.307224	316.657250	5
17	2316.125033	1158.566155	2299.098484	1150.052880	2298.114468	1149.560872	I	***521.275196***	261.141236	504.248647	252.627961	503.264631	252.135953	4
18	2417.172712	1209.089994	2400.146163	1200.576719	2399.162147	1200.084711	T	***408.191132***	204.599204	391.164583	196.085929	390.180567	195.593921	3
19	2577.203361	1289.105318	2560.176812	1280.592044	2559.192796	1280.100036	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 VSVLCQENYLIQEGEEITCK
(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	2722.301590	-0.001228	VSVLCQENYLIQEGEEITCK
37.9	2722.301590	-0.001228	VSVLCQENYLIQEGEEITCK
10.5	2722.339783	-0.039421	QDREHLWKLIEGGAHIYVCGDAR

Mascot: http://www.matrixscience.com/

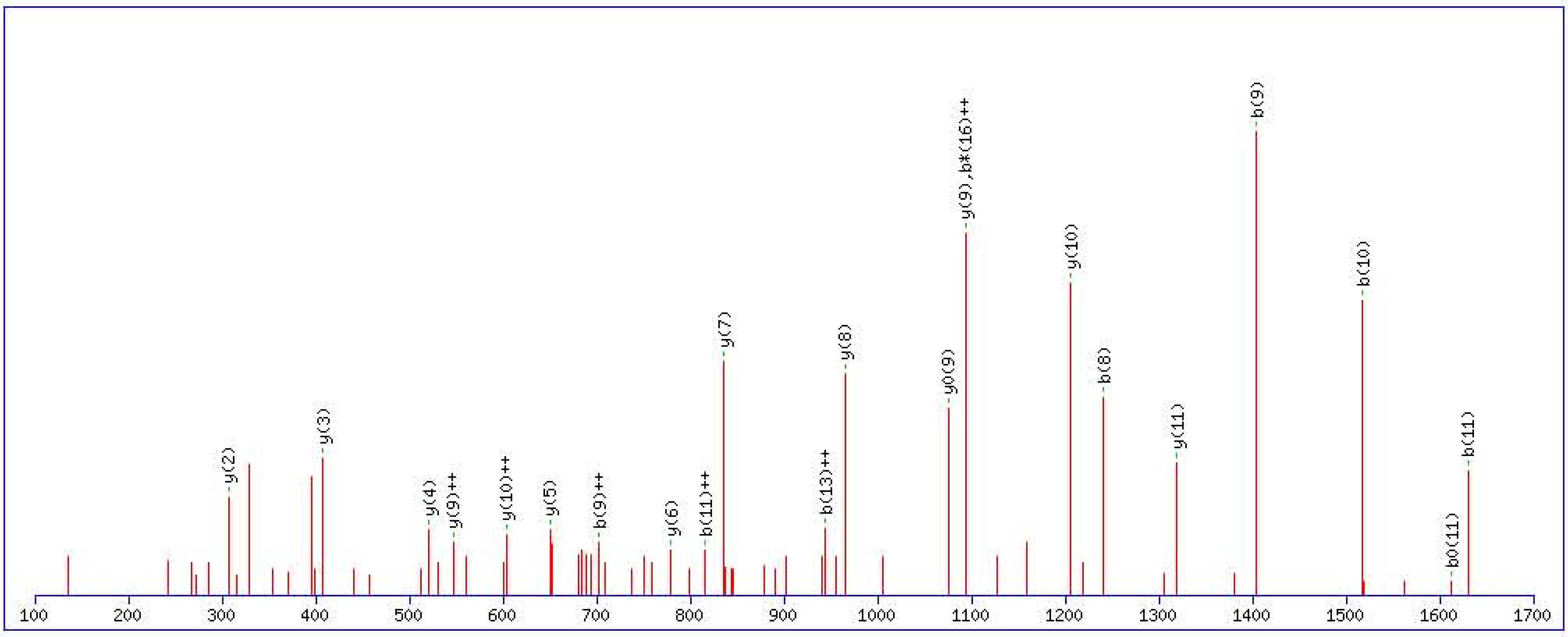
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSVLCQENYLIQEGEEITCK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

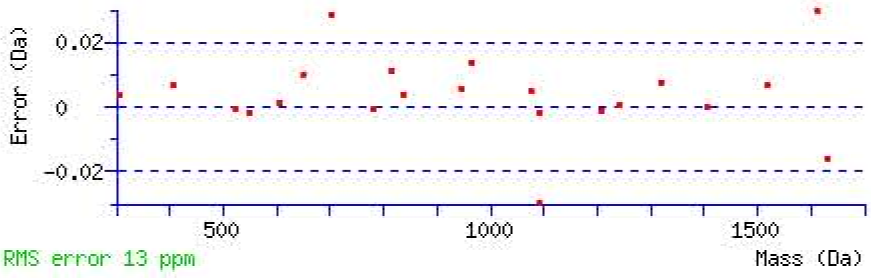
Match to Query 50606: 2722.300362 from(908.440730,3+) rtinseconds(2766) index(36384)
Title: Locus:1.1.1.3625.22 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

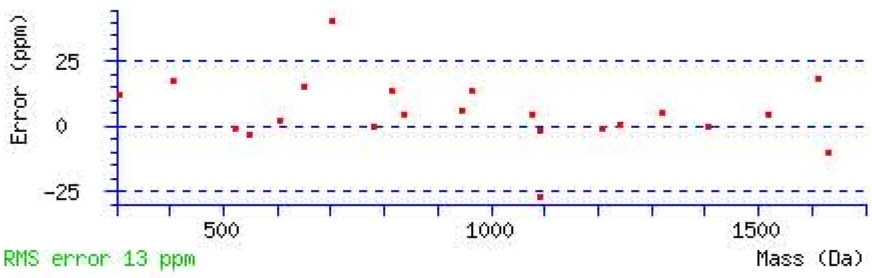
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2722.301590
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 69  Expect: 2.8e-006
Matches : 22/212 fragment ions using 29 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							20
2	187.107718	94.057497			169.097153	85.052214	S	2624.240475	1312.623875	2607.213926	1304.110601	2606.229910	1303.618593	19
3	286.176132	143.591704			268.165567	134.586422	V	2537.208447	1269.107861	2520.181898	1260.594587	2519.197882	1260.102579	18
4	399.260196	200.133736			381.249631	191.128454	L	2438.140033	1219.573654	2421.113484	1211.060380	2420.129468	1210.568372	17
5	559.290845	280.149061			541.280280	271.143778	C	2325.055969	1163.031622	2308.029420	1154.518348	2307.045404	1154.026340	16
6	998.516171	499.761724	981.489622	491.248449	980.505606	490.756441	Q	2165.025320	1083.016298	2147.998771	1074.503023	2147.014755	1074.011015	15
7	1127.558764	564.283020	1110.532215	555.769746	1109.548199	555.277738	E	1725.799994	863.403635	1708.773445	854.890361	1707.789429	854.398353	14
8	**1241.601691**	621.304484	1224.575142	612.791209	1223.591126	612.299201	N	1596.757401	798.882339	1579.730852	790.369064	1578.746836	789.877056	13
9	**1404.665020**	**702.836148**	1387.638471	694.322874	1386.654455	693.830866	Y	1482.714474	741.860875	1465.687925	733.347601	1464.703909	732.855593	12
10	**1517.749084**	759.378180	1500.722535	750.864906	1499.738519	750.372898	L	***1319.651145***	660.329211	1302.624596	651.815936	1301.640580	651.323928	11
11	**1630.833148**	**815.920212**	1613.806599	807.406938	1612.822583	806.914929	I	***1206.567081***	603.787179	1189.540532	595.273904	1188.556516	594.781896	10
12	1758.891726	879.949501	1741.865177	871.436227	1740.881161	870.944219	Q	***1093.483017***	547.245147	1076.456468	538.731872	1075.472452	538.239864	9
13	1887.934319	**944.470798**	1870.907770	935.957523	1869.923754	935.465515	E	***965.424439***	483.215858	948.397890	474.702583	947.413874	474.210575	8
14	1944.955783	972.981530	1927.929234	964.468255	1926.945218	963.976247	G	***836.381846***	418.694561	819.355297	410.181287	818.371281	409.689279	7
15	2073.998376	1037.502826	2056.971827	1028.989551	2055.987811	1028.497543	E	***779.360382***	390.183829	762.333833	381.670555	761.349817	381.178547	6
16	2203.040969	1102.024123	2186.014420	1093.510848	2185.030404	1093.018840	E	***650.317789***	325.662533	633.291240	317.149258	632.307224	316.657250	5
17	2316.125033	1158.566155	2299.098484	1150.052880	2298.114468	1149.560872	I	***521.275196***	261.141236	504.248647	252.627961	503.264631	252.135953	4
18	2417.172712	1209.089994	2400.146163	1200.576719	2399.162147	1200.084711	T	***408.191132***	204.599204	391.164583	196.085929	390.180567	195.593921	3
19	2577.203361	1289.105318	2560.176812	1280.592044	2559.192796	1280.100036	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 VSVLCQENYLIQEGEEITCK
(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	2722.301590	-0.001228	VSVLCQENYLIQEGEEITCK
65.8	2722.301590	-0.001228	VSVLCQENYLIQEGEEITCK
19.1	2722.339783	-0.039421	QDREHLWKLIEGGAHIYVCGDAR

Mascot: http://www.matrixscience.com/

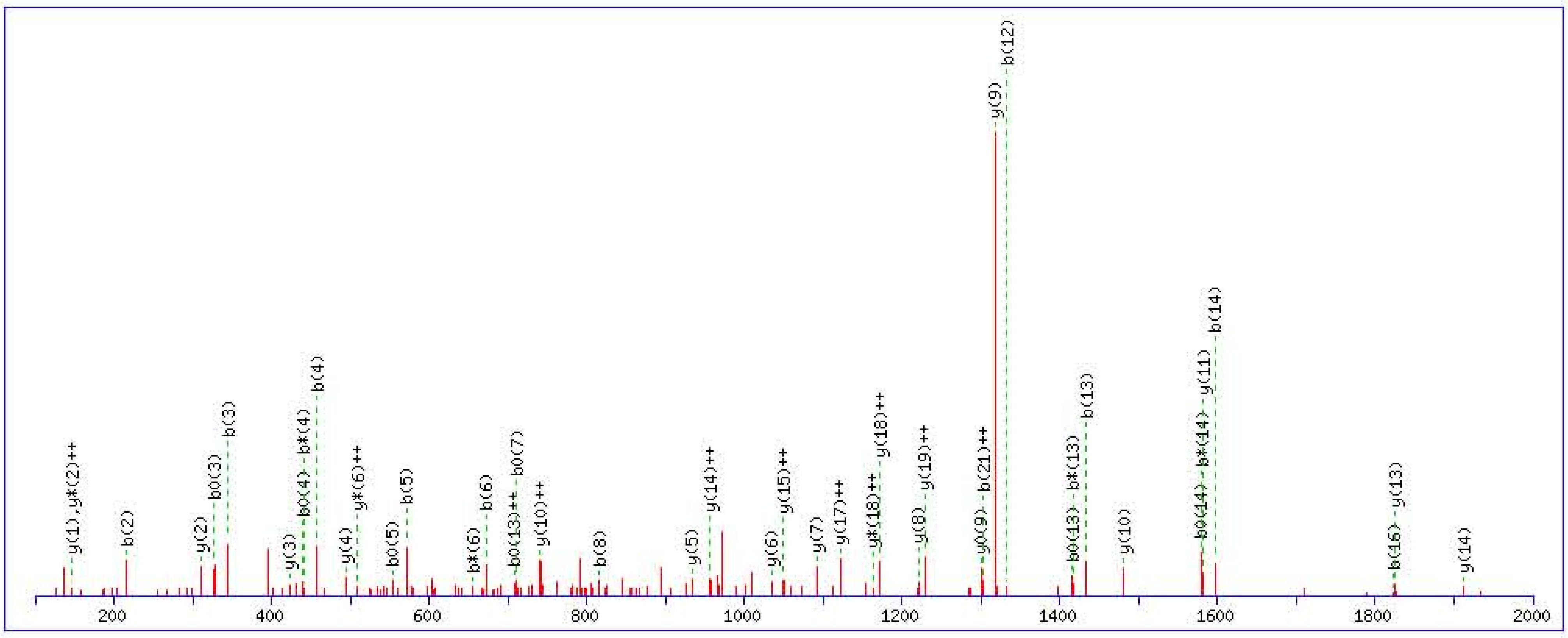
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NTEILTGSWSDQTYPEGTQAIYK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

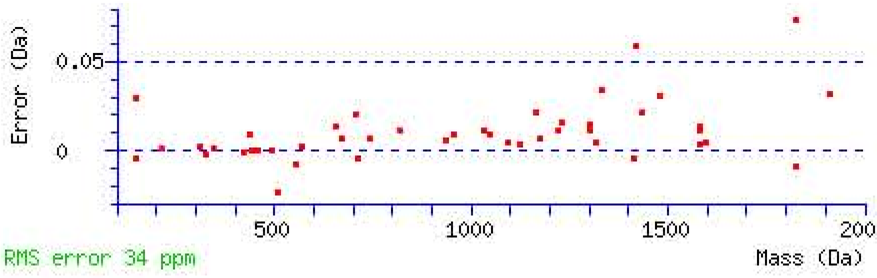
Match to Query 53096: 2912.404242 from(971.808690,3+) rtinseconds(2412) index(21309)
Title: Locus:1.1.1.3405.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

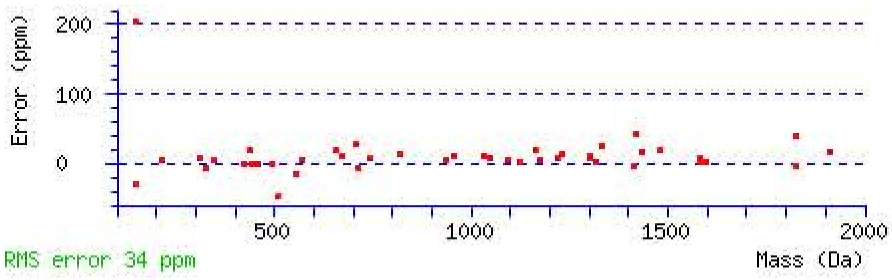


Monoisotopic mass of neutral peptide Mr(calc): 2912.390213
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q19 : Biotin:Thermo-21345 (Q)
Ions Score: 69 **Expect:** 3e-006
Matches : 45/252 fragment ions using 89 most intense peaks (help)

#	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							23
2	***216.097882***	108.552579	199.071333	100.039305	198.087317	99.547296	T	2799.354578	1400.180927	2782.328029	1391.667652	2781.344013	1391.175644	22
3	***345.140475***	173.073875	328.113926	164.560601	327.129910	164.068593	E	2698.306899	1349.657087	2681.280350	1341.143813	2680.296334	1340.651805	21
4	***458.224539***	229.615907	441.197990	221.102633	440.213974	220.610625	I	2569.264306	1285.135791	2552.237757	1276.622516	2551.253741	1276.130508	20
5	***571.308603***	286.157940	554.282054	277.644665	553.298038	277.152657	L	2456.180242	1228.593759	2439.153693	1220.080484	2438.169677	1219.588476	19
6	***672.356282***	336.681779	655.329733	328.168505	654.345717	327.676497	T	2343.096178	1172.051727	2326.069629	1163.538452	2325.085613	1163.046444	18
7	729.377746	365.192511	712.351197	356.679237	711.367181	356.187229	G	2242.048499	1121.527887	2225.021950	1113.014613	2224.037934	1112.522605	17
8	***816.409774***	408.708525	799.383225	400.195251	798.399209	399.703243	S	2185.027035	1093.017155	2168.000486	1084.503881	2167.016470	1084.011873	16
9	1002.489087	501.748182	985.462538	493.234907	984.478522	492.742899	W	2097.995007	1049.501141	2080.968458	1040.987867	2079.984442	1040.495859	15
10	1089.521115	545.264196	1072.494566	536.750921	1071.510550	536.258913	S	***1911.915694***	956.461485	1894.889145	947.948211	1893.905129	947.456203	14
11	1204.548058	602.777667	1187.521509	594.264393	1186.537493	593.772385	D	***1824.883666***	912.945471	1807.857117	904.432197	1806.873101	903.940189	13
12	***1332.606636***	666.806956	1315.580087	658.293682	1314.596071	657.801674	Q	1709.856723	855.432000	1692.830174	846.918725	1691.846158	846.426717	12
13	***1433.654315***	717.330796	1416.627766	708.817521	1415.643750	708.325513	T	***1581.798145***	791.402711	1564.771596	782.889436	1563.787580	782.397428	11
14	***1596.717644***	798.862460	1579.691095	790.349186	1578.707079	789.857178	Y	***1480.750466***	740.878871	1463.723917	732.365597	1462.739901	731.873589	10
15	1693.770408	847.388842	1676.743859	838.875568	1675.759843	838.383560	P	***1317.687137***	659.347207	1300.660588	650.833932	1299.676572	650.341924	9
16	***1822.813001***	911.910139	1805.786452	903.396864	1804.802436	902.904856	E	***1220.634373***	610.820825	1203.607824	602.307550	1202.623808	601.815542	8
17	1879.834465	940.420871	1862.807916	931.907596	1861.823900	931.415588	G	***1091.591780***	546.299528	1074.565231	537.786254	1073.581215	537.294246	7
18	1980.882144	990.944710	1963.855595	982.431436	1962.871579	981.939428	T	***1034.570316***	517.788796	1017.543767	509.275522	1016.559751	508.783514	6
19	2420.107470	1210.557373	2403.080921	1202.044098	2402.096905	1201.552090	Q	***933.522637***	467.264957	916.496088	458.751682			5
20	2491.144584	1246.075930	2474.118035	1237.562655	2473.134019	1237.070648	A	***494.297311***	247.652294	477.270762	239.139019			4
21	2604.228648	1302.617962	2587.202099	1294.104688	2586.218083	1293.612680	I	***423.260197***	212.133737	406.233648	203.620462			3
22	2767.291977	1384.149627	2750.265428	1375.636352	2749.281412	1375.144344	Y	***310.176133***	155.591705	293.149584	147.078430			2
23							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 34 ppm



RMS error 34 ppm

NCBI **BLAST** search of NTEILTGSWSDQTYPEGTQAIYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.2	2912.390213	0.014029	NTEILTGSWSDQTYPEGTQAIYK
17.3	2912.390213	0.014029	NTEILTGSWSDQTYPEGTQAIYK

Mascot: http://www.matrixscience.com/

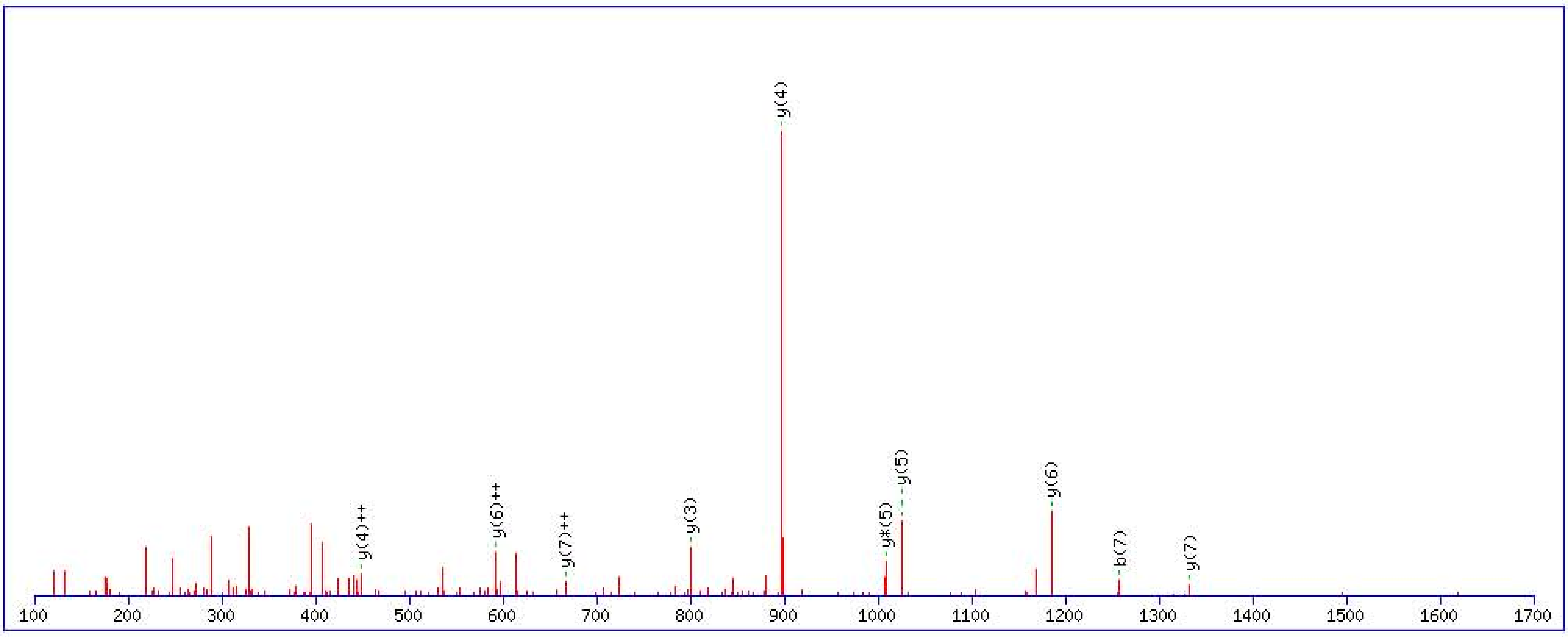
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VFCQPWQR**
Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

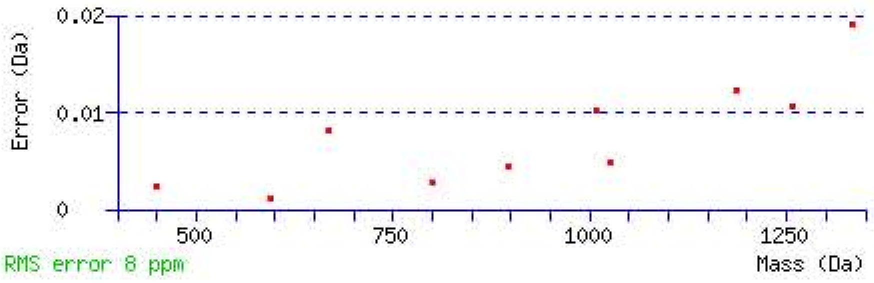
Match to Query 25327: 1430.700788 from(716.357670,2+) rtinseconds(2043) index(60838)
Title: Locus:1.1.1.1623.5 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

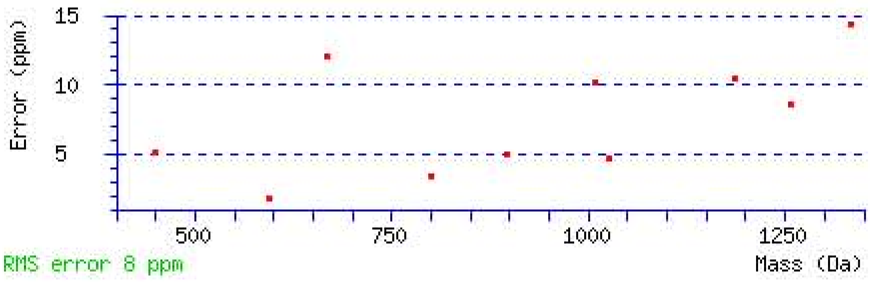
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1430.695145
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 36 **Expect:** 0.00057
Matches : 10/50 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	100.075690	50.541483			V					8
2	247.144104	124.075690			F	***1332.633996***	666.820636	1315.607447	658.307362	7
3	407.174753	204.091014			C	***1185.565582***	593.286429	1168.539033	584.773155	6
4	535.233331	268.120304	518.206782	259.607029	Q	***1025.534933***	513.271105	1008.508384	504.757830	5
5	632.286095	316.646686	615.259546	308.133411	P	***897.476355***	449.241816	880.449806	440.728541	4
6	818.365408	409.686342	801.338859	401.173068	W	***800.423591***	400.715434	783.397042	392.202159	3
7	**1257.590734**	629.299005	1240.564185	620.785731	Q	614.344278	307.675777	597.317729	299.162503	2
8					R	175.118952	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of VFCQPWQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.8	1430.695145	0.005643	VFCQPWQR
7.5	1430.695145	0.005643	VFCQPWQR
1.1	1430.693619	0.007169	QLQTLSMPGGGGNR
1.1	1430.697144	0.003644	EATMKMAVMIFK
1.1	1430.697144	0.003644	EATMKMAVMIFK
0.9	1430.711319	-0.010531	RAKAEDENETLR
0.8	1430.700989	-0.000201	DMGLMNAIGLQPR
0.3	1430.700989	-0.000201	NMPQADAMVLVAR

Mascot: http://www.matrixscience.com/

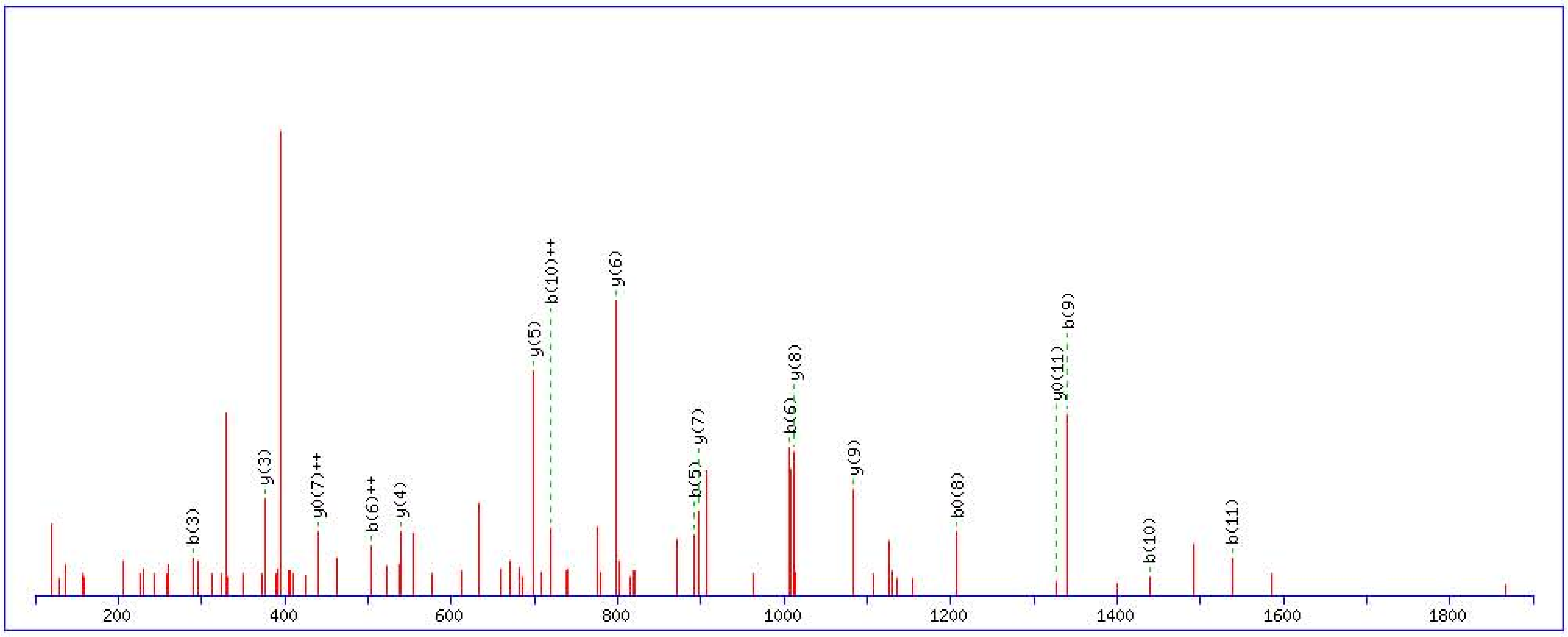
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TMGYQDFADVVCYTQK**
Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

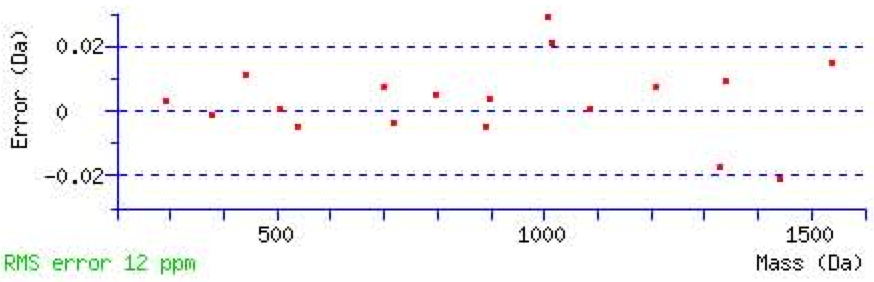
Match to Query 26881: 2236.026252 from(746.349360,3+) rtinseconds(2518) index(63365)
Title: Locus:1.1.1.1788.19 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

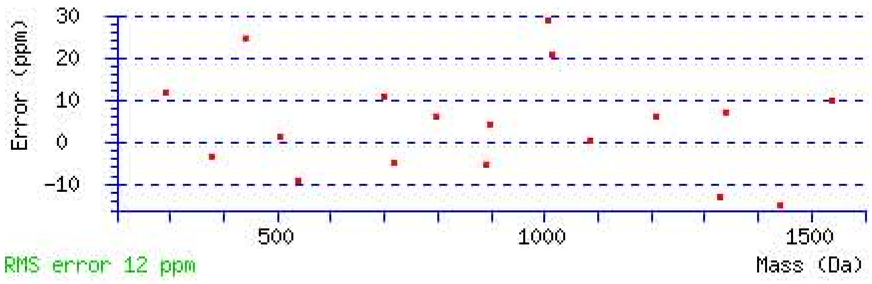
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2236.000305
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.0031
Matches : 18/168 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							16
2	233.095440	117.051358			215.084875	108.046076	M	2135.959885	1068.483580	2118.933336	1059.970306	2117.949320	1059.478298	15
3	***290.116904***	145.562090			272.106339	136.556807	G	2004.919400	1002.963338	1987.892851	994.450064	1986.908835	993.958056	14
4	453.180233	227.093754			435.169668	218.088472	Y	1947.897936	974.452606	1930.871387	965.939332	1929.887371	965.447324	13
5	***892.405559***	446.706418	875.379010	438.193143	874.394994	437.701135	Q	1784.834607	892.920942	1767.808058	884.407667	1766.824042	883.915659	12
6	***1007.432502***	**504.219889**	990.405953	495.706615	989.421937	495.214607	D	1345.609281	673.308279	1328.582732	664.795004	1327.598716	664.302996	11
7	1154.500916	577.754096	1137.474367	569.240822	1136.490351	568.748813	F	1230.582338	615.794807	1213.555789	607.281533	1212.571773	606.789525	10
8	1225.538030	613.272653	1208.511481	604.759379	1207.527465	604.267370	A	***1083.513924***	542.260600	1066.487375	533.747326	1065.503359	533.255318	9
9	***1340.564973***	670.786125	1323.538424	662.272850	1322.554408	661.780842	D	***1012.476810***	506.742043	995.450261	498.228769	994.466245	497.736761	8
10	***1439.633387***	**720.320332**	1422.606838	711.807057	1421.622822	711.315049	V	***897.449867***	449.228572	880.423318	440.715297	879.439302	440.223289	7
11	***1538.701801***	769.854539	1521.675252	761.341264	1520.691236	760.849256	V	***798.381453***	399.694365	781.354904	391.181090	780.370888	390.689082	6
12	1698.732450	849.869863	1681.705901	841.356589	1680.721885	840.864581	C	***699.313039***	350.160158	682.286490	341.646883	681.302474	341.154875	5
13	1861.795779	931.401528	1844.769230	922.888253	1843.785214	922.396245	Y	***539.282390***	270.144833	522.255841	261.631559	521.271825	261.139551	4
14	1962.843458	981.925367	1945.816909	973.412093	1944.832893	972.920085	T	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.607886	3
15	2090.902036	1045.954656	2073.875487	1037.441381	2072.891471	1036.949373	Q	275.171382	138.089329	258.144833	129.576054			2
16							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TMGYQDFADVVCYTQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.7	2236.000305	0.025947	TMGYQDFADVVCYTQK
4.8	2236.057587	-0.031335	RVLGESGEMDALRIQMEDR

Mascot: http://www.matrixscience.com/

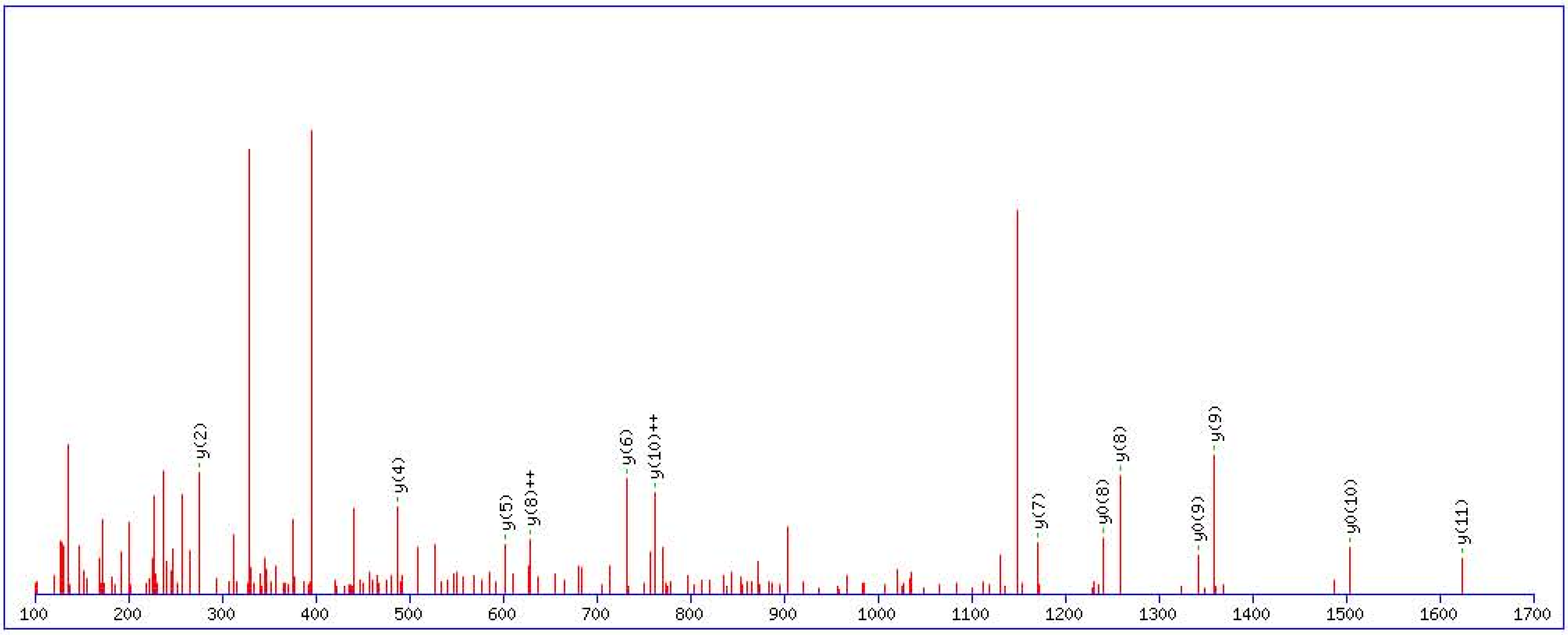
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTYTSQEDLVEK**
Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

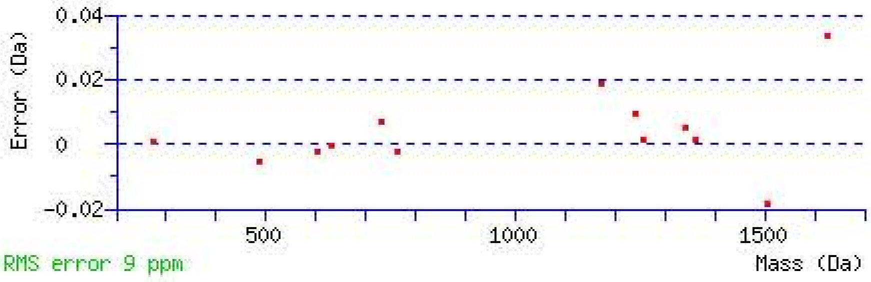
Match to Query 34094: 1721.855622 from(574.959150,3+) rtinseconds(1897) index(59866)
Title: Locus:1.1.1.1572.9 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

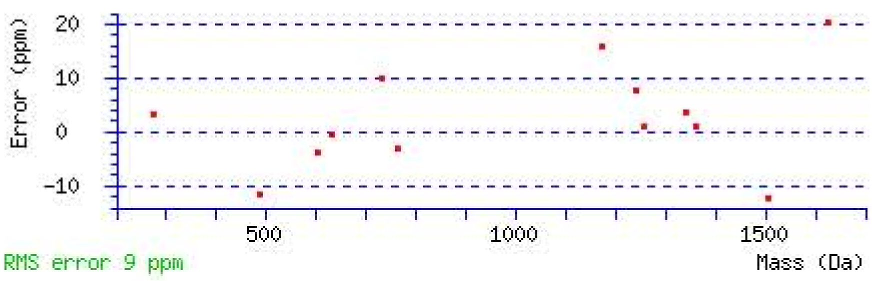
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1721.854584
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0047
Matches : 13/118 fragment ions using 29 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							12
2	201.123369	101.065322			183.112804	92.060040	T	***1623.793452***	812.400364	1606.766903	803.887090	1605.782887	803.395081	11
3	364.186698	182.596987			346.176133	173.591705	Y	1522.745773	761.876524	1505.719224	753.363250	1504.735208	752.871242	10
4	465.234377	233.120827			447.223812	224.115544	T	***1359.682444***	680.344860	1342.655895	671.831585	1341.671879	671.339577	9
5	552.266405	276.636841			534.255840	267.631558	S	***1258.634765***	629.821021	1241.608216	621.307746	1240.624200	620.815738	8
6	991.491731	496.249504	974.465182	487.736229	973.481166	487.244221	Q	***1171.602737***	586.305006	1154.576188	577.791732	1153.592172	577.299724	7
7	1120.534324	560.770800	1103.507775	552.257526	1102.523759	551.765517	E	***732.377411***	366.692343	715.350862	358.179069	714.366846	357.687061	6
8	1235.561267	618.284272	1218.534718	609.770997	1217.550702	609.278989	D	***603.334818***	302.171047	586.308269	293.657773	585.324253	293.165765	5
9	1348.645331	674.826303	1331.618782	666.313029	1330.634766	665.821021	L	***488.307875***	244.657575	471.281326	236.144301	470.297310	235.652293	4
10	1447.713745	724.360511	1430.687196	715.847236	1429.703180	715.355228	V	375.223811	188.115543	358.197262	179.602269	357.213246	179.110261	3
11	1576.756338	788.881807	1559.729789	780.368533	1558.745773	779.876524	E	***276.155397***	138.581336	259.128848	130.068062	258.144832	129.576054	2
12							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VTYTSQEDLVEK
(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	1721.854584	0.001038	VTYTSQEDLVEK

Mascot: http://www.matrixscience.com/

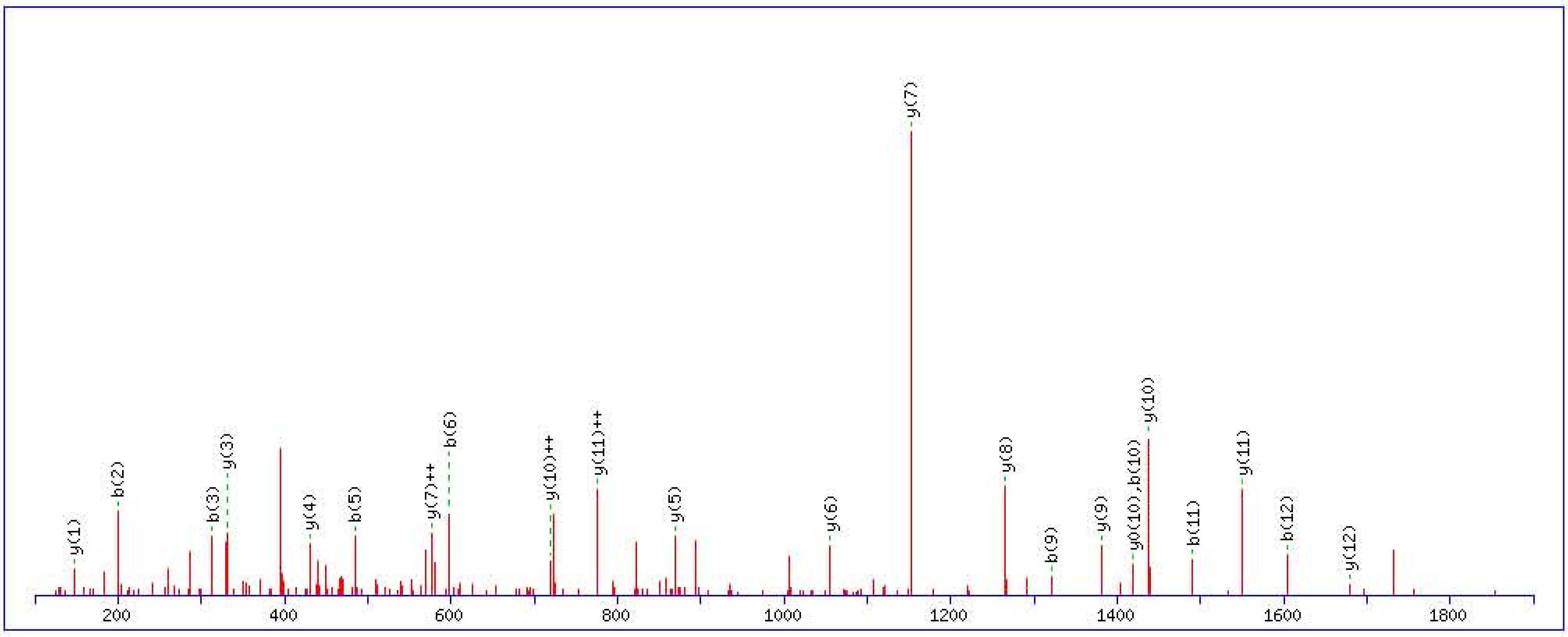
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AQLGDLPWQVAIK**
Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

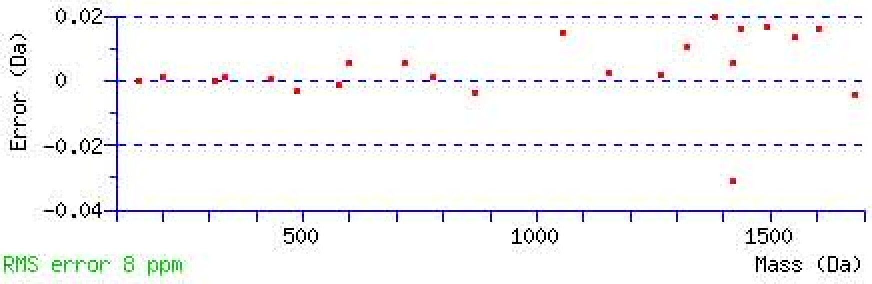
Match to Query 34653: 1748.979588 from(875.497070,2+) rtinseconds(2664) index(64236)
Title: Locus:1.1.1.1838.10 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

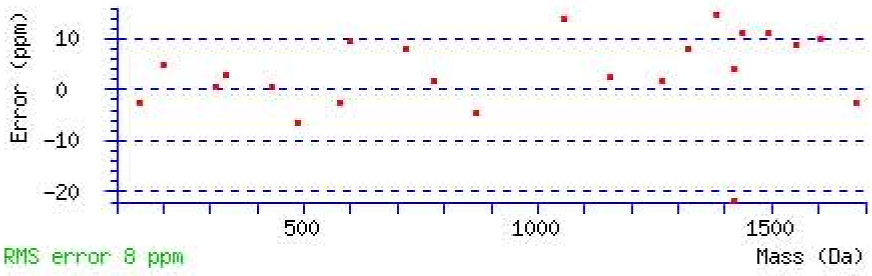
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1748.964737
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9     : Biotin:Thermo-21345 (Q)
Ions Score: 88  Expect: 1.5e-008
Matches : 23/118 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							13
2	**200.102968**	100.555122	183.076419	92.041848			Q	***1678.934912***	839.971094	1661.908363	831.457820	1660.924347	830.965812	12
3	**313.187032**	157.097154	296.160483	148.583879			L	***1550.876334***	775.941805	1533.849785	767.428531	1532.865769	766.936523	11
4	370.208496	185.607886	353.181947	177.094611			G	***1437.792270***	719.399773	1420.765721	710.886499	1419.781705	710.394491	10
5	**485.235439**	243.121357	468.208890	234.608083	467.224874	234.116075	D	***1380.770806***	690.889041	1363.744257	682.375767	1362.760241	681.883759	9
6	**598.319503**	299.663390	581.292954	291.150115	580.308938	290.658107	L	***1265.743863***	633.375570	1248.717314	624.862295			8
7	695.372267	348.189772	678.345718	339.676497	677.361702	339.184489	P	***1152.659799***	576.833538	1135.633250	568.320263			7
8	881.451580	441.229428	864.425031	432.716154	863.441015	432.224146	W	***1055.607035***	528.307156	1038.580486	519.793881			6
9	**1320.676906**	660.842091	1303.650357	652.328817	1302.666341	651.836809	Q	***869.527722***	435.267499	852.501173	426.754225			5
10	**1419.745320**	710.376298	1402.718771	701.863024	1401.734755	701.371016	V	***430.302396***	215.654836	413.275847	207.141561			4
11	**1490.782434**	745.894855	1473.755885	737.381581	1472.771869	736.889573	A	***331.233982***	166.120629	314.207433	157.607354			3
12	**1603.866498**	802.436887	1586.839949	793.923613	1585.855933	793.431605	I	260.196868	130.602072	243.170319	122.088797			2
13							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of AQLGDLPWQVAIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
88.0	1748.964737	0.014851	AQLGDLPWQVAIK
7.7	1748.964737	0.014851	AQLGDLPWQVAIK
4.3	1748.978439	0.001149	YARKISGTTALQEALK
3.2	1748.985840	-0.006252	LPLGSLMKSPHLESLK
2.1	1748.964523	0.015065	AAAALSLAHRLLDGAGSR
2.1	1748.958649	0.020939	AYIRRQINHIFYR
1.8	1748.987183	-0.007595	QPARSRLWLPSK
0.3	1748.989685	-0.010097	KALSEHNVLVVEGARK
0.1	1748.957336	0.022252	LTYQFDSALLPAVRR

Mascot: http://www.matrixscience.com/

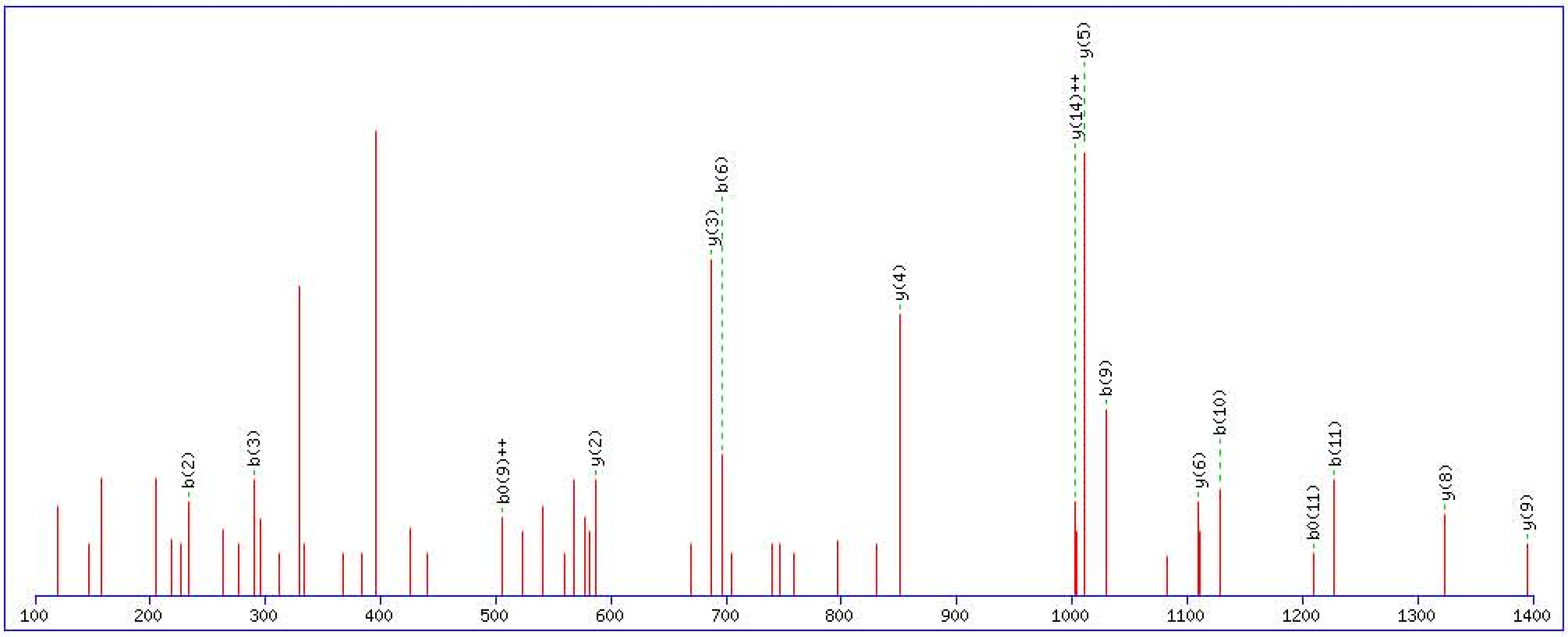
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TMGYQDFADVVCYTQK**
Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

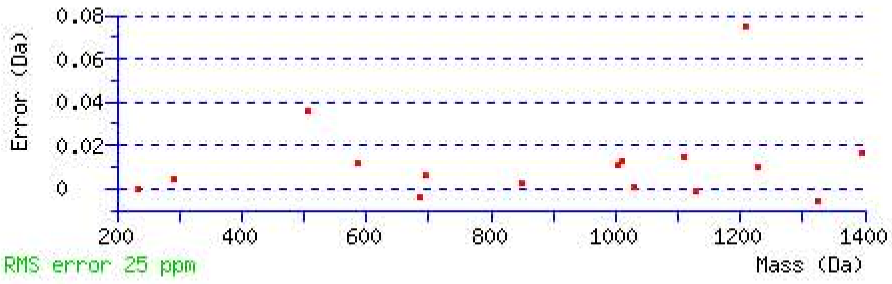
Match to Query 43883: 2236.018692 from(746.346840,3+) rtinseconds(2590) index(63761)
Title: Locus:1.1.1.1813.12 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

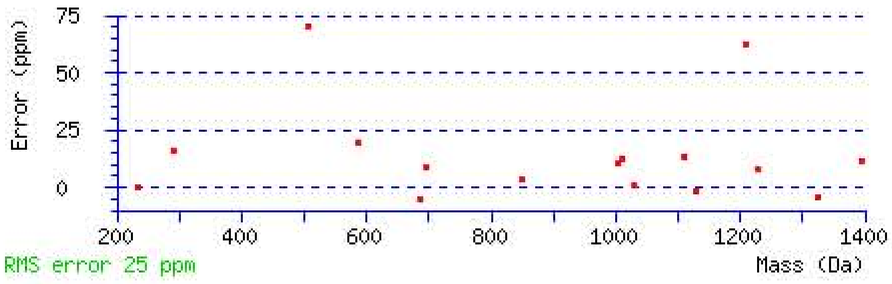
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2236.000305
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15    : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.00013
Matches : 16/168 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	102.054955	51.531116			84.044390	42.525833	T							16
2	***233.095440***	117.051358			215.084875	108.046076	M	2135.959885	1068.483580	2118.933336	1059.970306	2117.949320	1059.478298	15
3	***290.116904***	145.562090			272.106339	136.556807	G	2004.919400	1002.963338	1987.892851	994.450064	1986.908835	993.958056	14
4	453.180233	227.093754			435.169668	218.088472	Y	1947.897936	974.452606	1930.871387	965.939332	1929.887371	965.447324	13
5	581.238811	291.123044	564.212262	282.609769	563.228246	282.117761	Q	1784.834607	892.920942	1767.808058	884.407667	1766.824042	883.915659	12
6	***696.265754***	348.636515	679.239205	340.123241	678.255189	339.631233	D	1656.776029	828.891653	1639.749480	820.378378	1638.765464	819.886370	11
7	843.334168	422.170722	826.307619	413.657447	825.323603	413.165439	F	1541.749086	771.378181	1524.722537	762.864907	1523.738521	762.372899	10
8	914.371282	457.689279	897.344733	449.176004	896.360717	448.683996	A	***1394.680672***	697.843974	1377.654123	689.330700	1376.670107	688.838692	9
9	***1029.398225***	515.202750	1012.371676	506.689476	1011.387660	506.197468	D	***1323.643558***	662.325417	1306.617009	653.812143	1305.632993	653.320135	8
10	***1128.466639***	564.736958	1111.440090	556.223683	1110.456074	555.731675	V	1208.616615	604.811946	1191.590066	596.298671	1190.606050	595.806663	7
11	***1227.535053***	614.271165	1210.508504	605.757890	1209.524488	605.265882	V	***1109.548201***	555.277739	1092.521652	546.764464	1091.537636	546.272456	6
12	1387.565702	694.286489	1370.539153	685.773215	1369.555137	685.281207	C	***1010.479787***	505.743532	993.453238	497.230257	992.469222	496.738249	5
13	1550.629031	775.818154	1533.602482	767.304879	1532.618466	766.812871	Y	***850.449138***	425.728207	833.422589	417.214933	832.438573	416.722925	4
14	1651.676710	826.341993	1634.650161	817.828719	1633.666145	817.336711	T	***687.385809***	344.196543	670.359260	335.683268	669.375244	335.191260	3
15	2090.902036	1045.954656	2073.875487	1037.441381	2072.891471	1036.949373	Q	***586.338130***	293.672703	569.311581	285.159429			2
16							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TMGYQDFADVVCYTQK
(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	2236.000305	0.018387	TMGYQDFADVVCYTQK

Mascot: http://www.matrixscience.com/

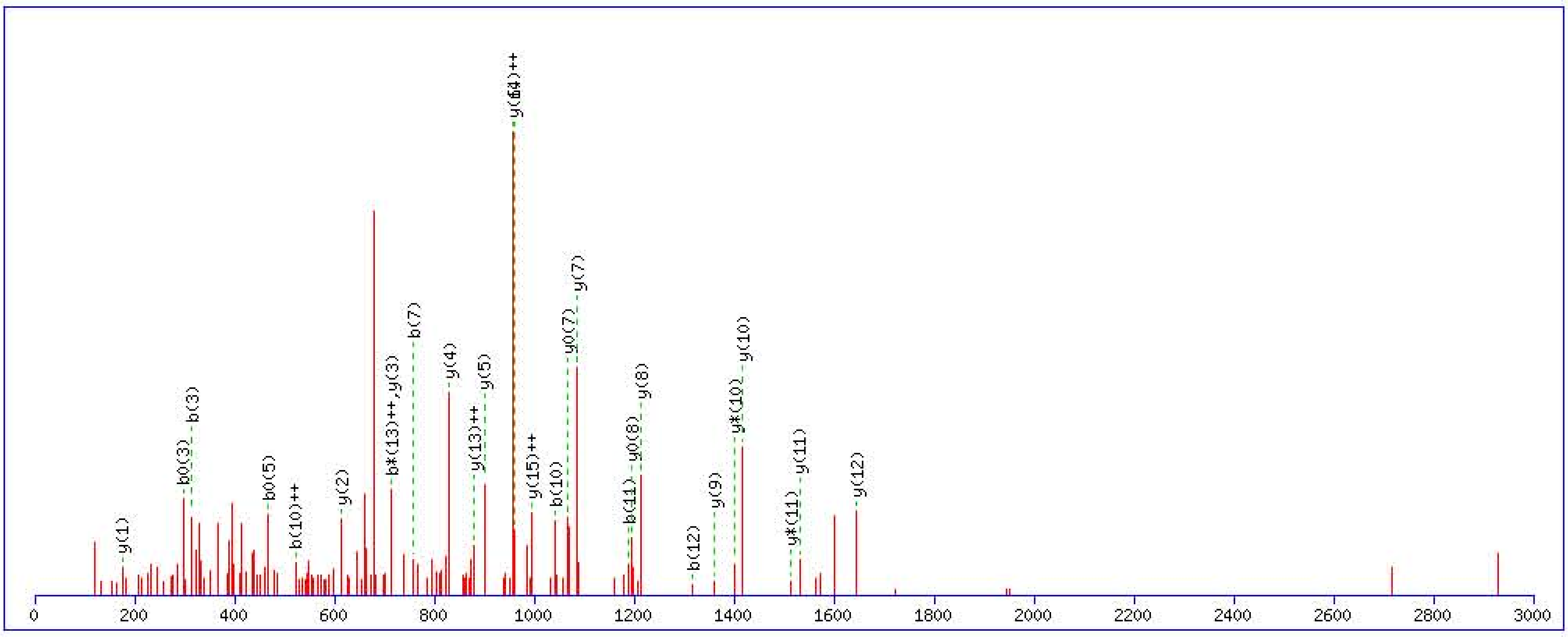
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EANVACLDLGFQQGADTQR**
Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

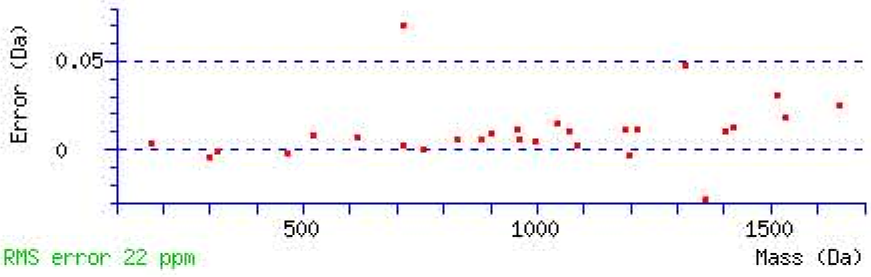
Match to Query 46509: 2403.142032 from(802.054620,3+) rtinseconds(2285) index(62174)
Title: Locus:1.1.1.1707.10 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

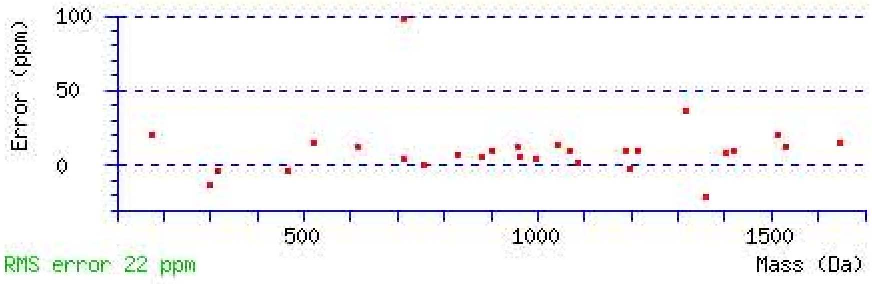
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from [0] to [3000] Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2403.131119
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18     : Biotin:Thermo-21345 (Q)
Ions Score: 72  Expect: 2.8e-007
Matches : 28/208 fragment ions using 45 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	201.086983	101.047130			183.076418	92.041847	A	2275.095801	1138.051538	2258.069252	1129.538264	2257.085236	1129.046256	18
3	**315.129910**	158.068593	298.103361	149.555319	297.119345	149.063311	N	2204.058687	1102.532981	2187.032138	1094.019707	2186.048122	1093.527699	17
4	414.198324	207.602800	397.171775	199.089526	396.187759	198.597518	V	2090.015760	1045.511518	2072.989211	1036.998243	2072.005195	1036.506235	16
5	485.235438	243.121357	468.208889	234.608082	467.224873	234.116075	A	1990.947346	995.977311	1973.920797	987.464037	1972.936781	986.972029	15
6	645.266087	323.136682	628.239538	314.623407	627.255522	314.131399	C	1919.910232	960.458754	1902.883683	951.945480	1901.899667	951.453472	14
7	**758.350151**	379.678714	741.323602	371.165439	740.339586	370.673431	L	1759.879583	880.443430	1742.853034	871.930155	1741.869018	871.438147	13
8	873.377094	437.192185	856.350545	428.678911	855.366529	428.186903	D	***1646.795519***	823.901398	1629.768970	815.388123	1628.784954	814.896115	12
9	986.461158	493.734217	969.434609	485.220943	968.450593	484.728935	L	***1531.768576***	766.387926	1514.742027	757.874652	1513.758011	757.382644	11
10	**1043.482622**	522.244949	1026.456073	513.731675	1025.472057	513.239667	G	***1418.684512***	709.845894	1401.657963	701.332620	1400.673947	700.840612	10
11	**1190.551036**	595.779156	1173.524487	587.265882	1172.540471	586.773874	F	***1361.663048***	681.335162	1344.636499	672.821888	1343.652483	672.329880	9
12	**1318.609614**	659.808445	1301.583065	651.295171	1300.599049	650.803163	Q	***1214.594634***	607.800955	1197.568085	599.287681	1196.584069	598.795673	8
13	1446.668192	723.837734	1429.641643	715.324460	1428.657627	714.832452	Q	***1086.536056***	543.771666	1069.509507	535.258392	1068.525491	534.766384	7
14	1503.689656	752.348466	1486.663107	743.835192	1485.679091	743.343184	G	***958.477478***	479.742377	941.450929	471.229103	940.466913	470.737095	6
15	1574.726770	787.867023	1557.700221	779.353749	1556.716205	778.861741	A	***901.456014***	451.231645	884.429465	442.718371	883.445449	442.226363	5
16	1689.753713	845.380495	1672.727164	836.867220	1671.743148	836.375212	D	***830.418900***	415.713088	813.392351	407.199814	812.408335	406.707806	4
17	1790.801392	895.904334	1773.774843	887.391060	1772.790827	886.899052	T	***715.391957***	358.199617	698.365408	349.686342	697.381392	349.194334	3
18	2230.026718	1115.516997	2213.000169	1107.003722	2212.016153	1106.511714	Q	***614.344278***	307.675777	597.317729	299.162503			2
19							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EANVACLDLGFQQGADTQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
72.4	2403.131119	0.010913	EANVACLDLGFQQGADTQR
26.8	2403.131119	0.010913	EANVACLDLGFQQGADTQR
17.6	2403.131119	0.010913	EANVACLDLGFQQGADTQR
2.5	2403.157135	-0.015103	QAMMKTDFPGDLGSQR

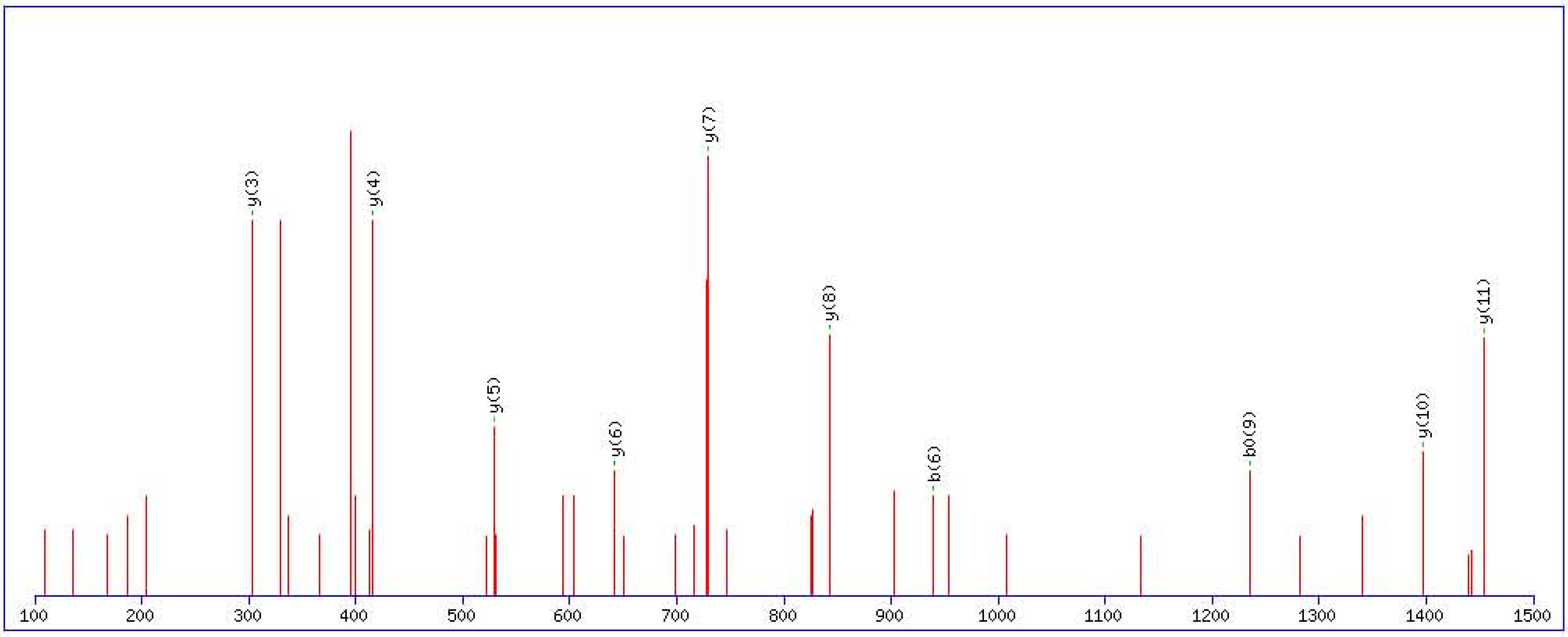
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLGDQLSLLLGAR**
Found in **MRC2_HUMAN**, C-type mannose receptor 2 OS=Homo sapiens GN=MRC2 PE=1 SV=2

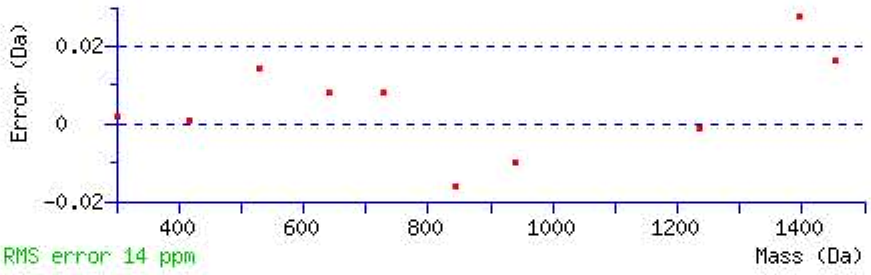
Match to Query 33008: 1666.944188 from(834.479370,2+) rtinseconds(3000) index(38081)
Title: Locus:1.1.1.3705.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

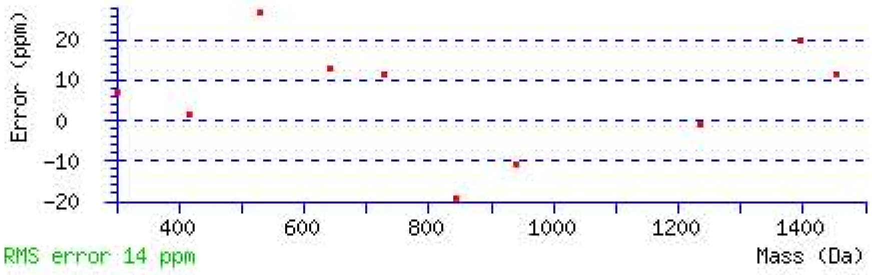
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1666.944000
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 66 **Expect:** 3.6e-006
Matches : 10/124 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	102.054955	51.531116			84.044390	42.525833	T							13
2	215.139019	108.073147			197.128454	99.067865	L	1566.903611	783.955443	1549.877062	775.442169	1548.893046	774.950161	12
3	272.160483	136.583879			254.149918	127.578597	G	***1453.819547***	727.413411	1436.792998	718.900137	1435.808982	718.408129	11
4	387.187426	194.097351			369.176861	185.092069	D	***1396.798083***	698.902679	1379.771534	690.389405	1378.787518	689.897397	10
5	826.412752	413.710014	809.386203	405.196740	808.402187	404.704732	Q	1281.771140	641.389208	1264.744591	632.875933	1263.760575	632.383925	9
6	**939.496816**	470.252046	922.470267	461.738772	921.486251	461.246764	L	***842.545814***	421.776545	825.519265	413.263270	824.535249	412.771262	8
7	1026.528844	513.768060	1009.502295	505.254786	1008.518279	504.762778	S	***729.461750***	365.234513	712.435201	356.721238	711.451185	356.229230	7
8	1139.612908	570.310092	1122.586359	561.796818	1121.602343	561.304810	L	***642.429722***	321.718499	625.403173	313.205224			6
9	1252.696972	626.852124	1235.670423	618.338850	1234.686407	617.846841	L	***529.345658***	265.176467	512.319109	256.663192			5
10	1365.781036	683.394156	1348.754487	674.880881	1347.770471	674.388873	L	***416.261594***	208.634435	399.235045	200.121160			4
11	1422.802500	711.904888	1405.775951	703.391613	1404.791935	702.899605	G	***303.177530***	152.092403	286.150981	143.579128			3
12	1493.839614	747.423445	1476.813065	738.910170	1475.829049	738.418162	A	246.156066	123.581671	229.129517	115.068396			2
13							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TLGDQLSLLLGAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.6	1666.944000	0.000188	TLGDQLSLLLGAR
14.7	1666.926697	0.017491	HSELVHVHAELLRK
2.1	1666.955231	-0.011043	RLGIPECILLVTQR
1.6	1666.944016	0.000172	LTNSPTVIVMVGLPAR
0.5	1666.955215	-0.011027	DLESVQRLLRK
0.2	1666.925354	0.018834	KAEPLASGKGEPVSLGK

Mascot: http://www.matrixscience.com/

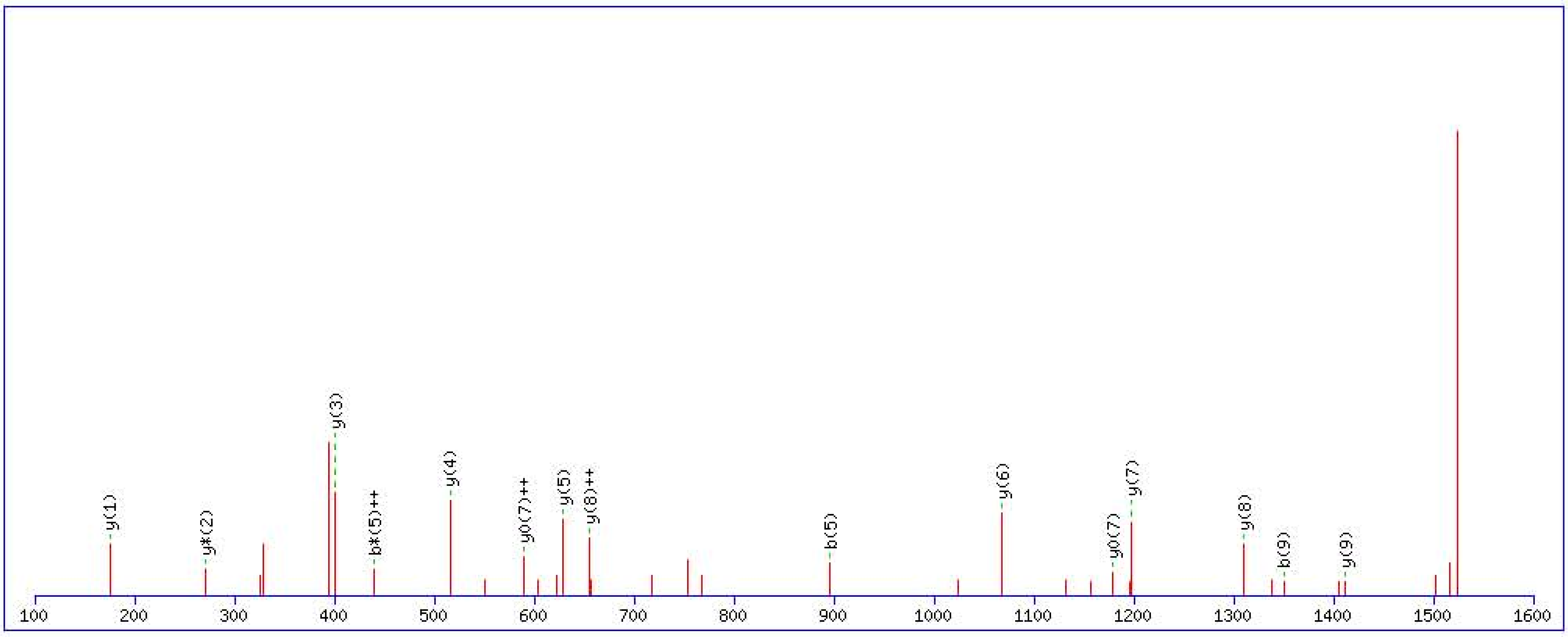
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTLEQIDLIR**
Found in **DPEP2_HUMAN**, Dipeptidase 2 OS=Homo sapiens GN=DPEP2 PE=1 SV=2

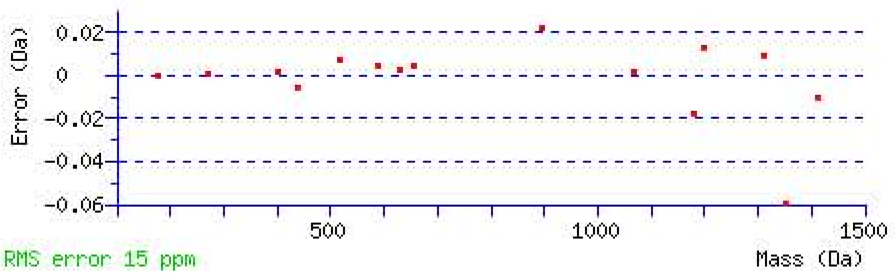
Match to Query 27987: 1523.871668 from(762.943110,2+) rtinseconds(2601) index(35204)
Title: Locus:1.1.1.3569.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

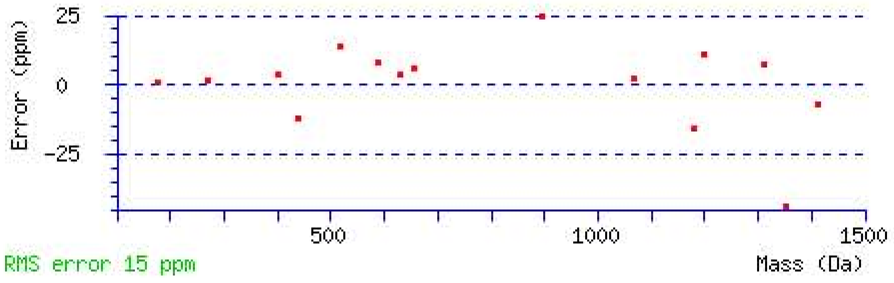
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1523.874512
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 49 **Expect:** 0.00016
Matches : 15/92 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	114.091340	57.549308					L							10
2	215.139019	108.073147			197.128454	99.067865	T	***1411.797749***	706.402513	1394.771200	697.889238	1393.787184	697.397230	9
3	328.223083	164.615179			310.212518	155.609897	L	***1310.750070***	655.878673	1293.723521	647.365399	1292.739505	646.873391	8
4	457.265676	229.136476			439.255111	220.131193	E	***1197.666006***	599.336641	1180.639457	590.823367	1179.655441	590.331358	7
5	**896.491002**	448.749139	879.464453	440.235865	878.480437	439.743857	Q	***1068.623413***	534.815345	1051.596864	526.302070	1050.612848	525.810062	6
6	1009.575066	505.291171	992.548517	496.777897	991.564501	496.285889	I	***629.398087***	315.202681	612.371538	306.689407	611.387522	306.197399	5
7	1124.602009	562.804643	1107.575460	554.291368	1106.591444	553.799360	D	***516.314023***	258.660649	499.287474	250.147375	498.303458	249.655367	4
8	1237.686073	619.346675	1220.659524	610.833400	1219.675508	610.341392	L	***401.287080***	201.147178	384.260531	192.633903			3
9	**1350.770137**	675.888707	1333.743588	667.375432	1332.759572	666.883424	I	288.203016	144.605146	271.176467	136.091871			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LTLEQIDLIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.1	1523.874512	-0.002844	LTLEQIDLIR
12.8	1523.867111	0.004557	TLIEAGLPQKVAER
12.3	1523.878357	-0.006689	TLLADKGEIRVGPR
8.1	1523.878357	-0.006689	LVDLVNQRDALIR
1.8	1523.849365	0.022303	TLLQQNQQLK
1.8	1523.849365	0.022303	TLLQQNQQLK
1.0	1523.857224	0.014444	TLIRPTYRVSYR

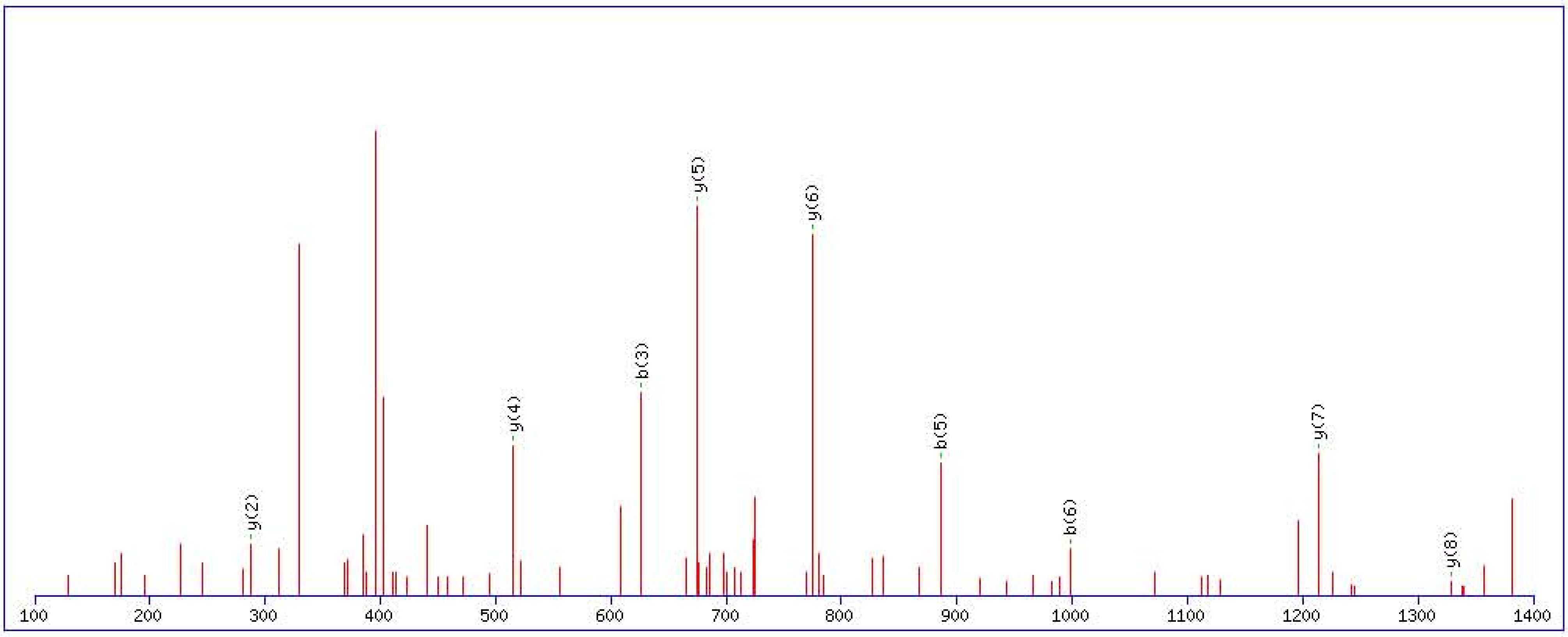
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADQVCINLR**
Found in **FBLN3_HUMAN**, EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2

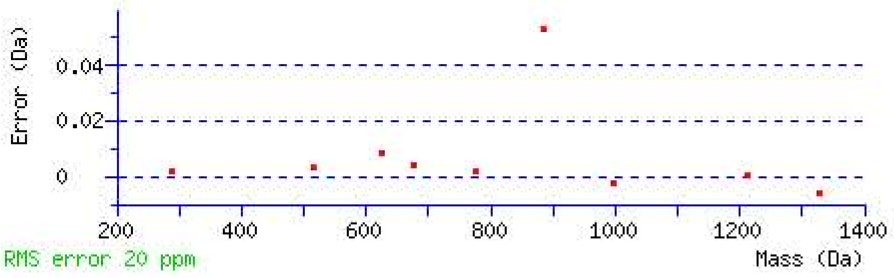
Match to Query 23581: 1398.701568 from(700.358060,2+) rtinseconds(2038) index(32107)
Title: Locus:1.1.1.3373.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

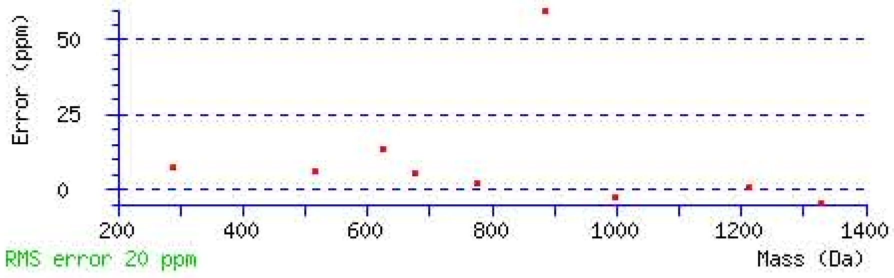
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1398.711166
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00018
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	72.044390	36.525833					A							9
2	187.071333	94.039304			169.060768	85.034022	D	***1328.681339***	664.844308	1311.654790	656.331033	1310.670774	655.839025	8
3	**626.296659**	313.651968	609.270110	305.138693	608.286094	304.646685	Q	***1213.654396***	607.330836	1196.627847	598.817562			7
4	725.365073	363.186175	708.338524	354.672900	707.354508	354.180892	V	***774.429070***	387.718173	757.402521	379.204898			6
5	**885.395722**	443.201499	868.369173	434.688225	867.385157	434.196217	C	***675.360656***	338.183966	658.334107	329.670691			5
6	**998.479786**	499.743531	981.453237	491.230257	980.469221	490.738249	I	***515.330007***	258.168641	498.303458	249.655367			4
7	1112.522713	556.764995	1095.496164	548.251720	1094.512148	547.759712	N	402.245943	201.626609	385.219394	193.113335			3
8	1225.606777	613.307027	1208.580228	604.793752	1207.596212	604.301744	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 ADQVCINLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.8	1398.711166	-0.009598	ADQVCINLR
5.5	1398.703766	-0.002198	GERMADGAPLAGVR
4.2	1398.696396	0.005172	RDGGKVDTSATHR
3.6	1398.721527	-0.019959	AATASAGAGGIDGKPR
3.5	1398.703766	-0.002198	DQAIQSRDR
1.8	1398.689163	0.012405	APSTYTYTSRPR
0.7	1398.703781	-0.002213	AVVHMNGKEVSGR
0.2	1398.704422	-0.002854	LWATDHYQPLR

Mascot: http://www.matrixscience.com/

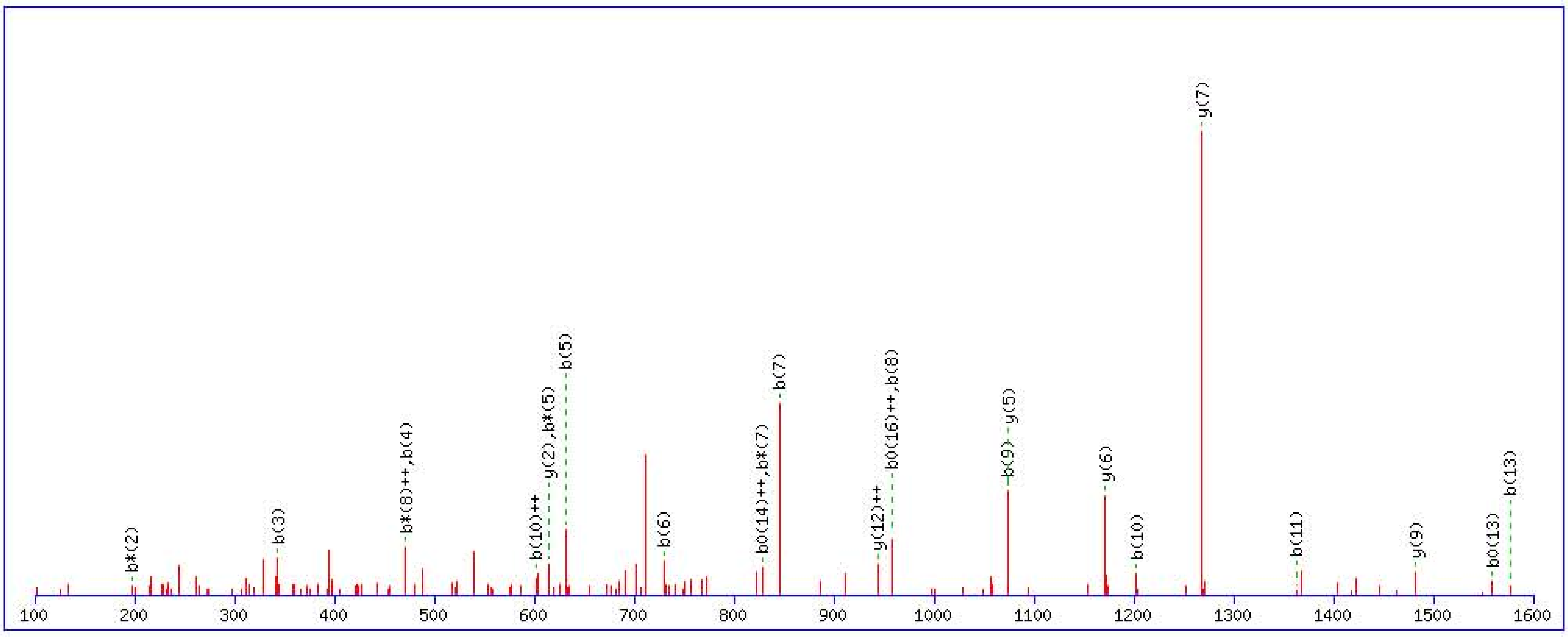
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RGEQCVDIDECTIPPYCHQR**
Found in **FBLN3_HUMAN**, EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2

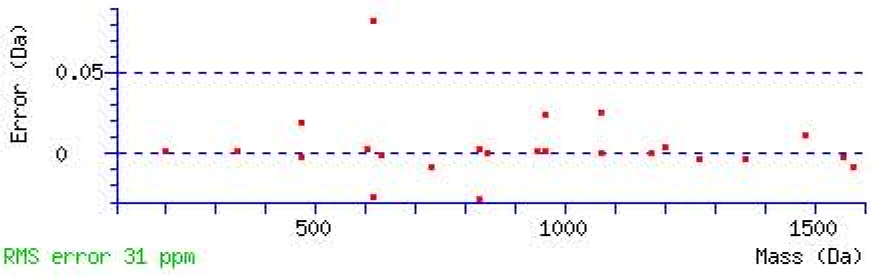
Match to Query 52112: 2843.260496 from(711.822400,4+) rtinseconds(1794) index(30569)
Title: Locus:1.1.1.3288.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

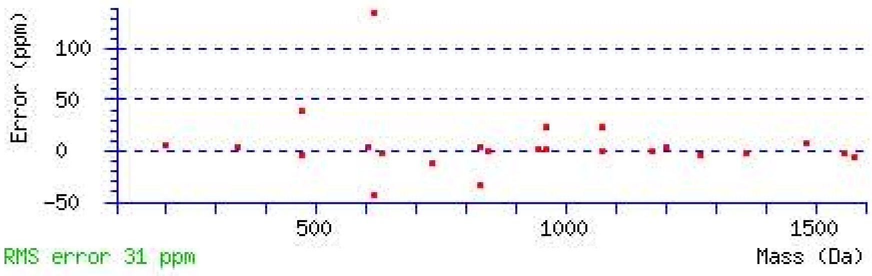
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2843.261169
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q19     : Biotin:Thermo-21345 (Q)
Ions Score: 58  Expect: 1e-005
Matches : 24/208 fragment ions using 30 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	157.108387	79.057831	140.081838	70.544557			R							20
2	214.129851	107.568564	197.103302	99.055289			G	2688.167329	1344.587302	2671.140780	1336.074028	2670.156764	1335.582020	19
3	***343.172444***	172.089860	326.145895	163.576585	325.161879	163.084577	E	2631.145865	1316.076570	2614.119316	1307.563296	2613.135300	1307.071288	18
4	***471.231022***	236.119149	454.204473	227.605875	453.220457	227.113867	Q	2502.103272	1251.555274	2485.076723	1243.041999	2484.092707	1242.549991	17
5	***631.261671***	316.134474	614.235122	307.621199	613.251106	307.129191	C	2374.044694	1187.525985	2357.018145	1179.012710	2356.034129	1178.520702	16
6	***730.330085***	365.668681	713.303536	357.155406	712.319520	356.663398	V	2214.014045	1107.510660	2196.987496	1098.997386	2196.003480	1098.505378	15
7	***845.357028***	423.182152	828.330479	414.668878	827.346463	414.176870	D	2114.945631	1057.976453	2097.919082	1049.463179	2096.935066	1048.971171	14
8	***958.441092***	479.724184	941.414543	471.210910	940.430527	470.718902	I	1999.918688	1000.462982	1982.892139	991.949708	1981.908123	991.457700	13
9	***1073.468035***	537.237656	1056.441486	528.724381	1055.457470	528.232373	D	1886.834624	943.920950	1869.808075	935.407676	1868.824059	934.915668	12
10	***1202.510628***	601.758952	1185.484079	593.245678	1184.500063	592.753670	E	1771.807681	886.407479	1754.781132	877.894204	1753.797116	877.402196	11
11	***1362.541277***	681.774277	1345.514728	673.261002	1344.530712	672.768994	C	1642.765088	821.886182	1625.738539	813.372908	1624.754523	812.880900	10
12	1463.588956	732.298116	1446.562407	723.784842	1445.578391	723.292834	T	**1482.734439**	741.870858	1465.707890	733.357583	1464.723874	732.865575	9
13	***1576.673020***	788.840148	1559.646471	780.326874	1558.662455	779.834866	I	1381.686760	691.347018	1364.660211	682.833744			8
14	1673.725784	837.366530	1656.699235	828.853256	1655.715219	828.361248	P	**1268.602696**	634.804986	1251.576147	626.291712			7
15	1770.778548	885.892912	1753.751999	877.379638	1752.767983	876.887630	P	**1171.549932**	586.278604	1154.523383	577.765330			6
16	1933.841877	967.424577	1916.815328	958.911302	1915.831312	958.419294	Y	**1074.497168**	537.752222	1057.470619	529.238948			5
17	2093.872526	1047.439901	2076.845977	1038.926626	2075.861961	1038.434618	C	911.433839	456.220558	894.407290	447.707283			4
18	2230.931438	1115.969357	2213.904889	1107.456082	2212.920873	1106.964074	H	751.403190	376.205233	734.376641	367.691959			3
19	2670.156764	1335.582020	2653.130215	1327.068746	2652.146199	1326.576738	Q	**614.344278**	307.675777	597.317729	299.162503			2
20							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of RGEQCVDIDECTIPPYCHQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.7	2843.261169	-0.000673	RGEQCVDIDECTIPPYCHQR

Mascot: http://www.matrixscience.com/

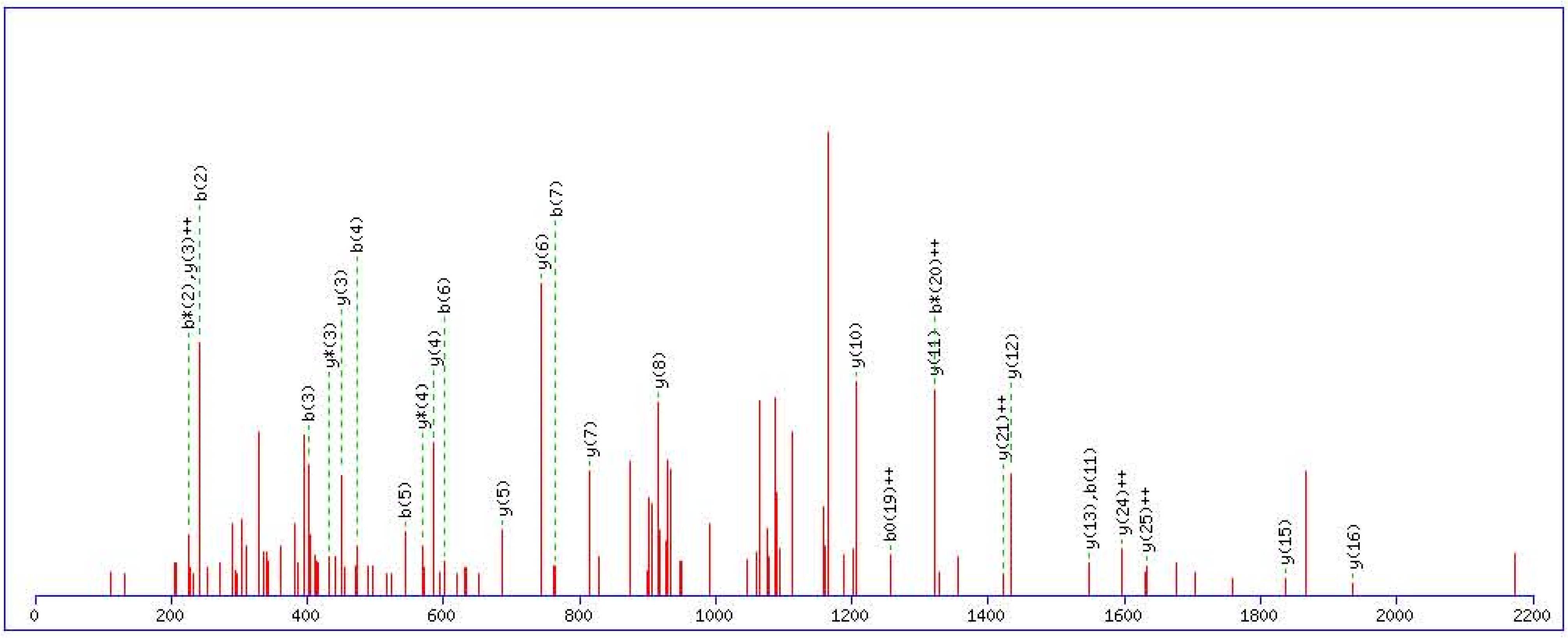
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQCAAGYEQSEHNVCQDIDECTAGTHNCR**
Found in **FBLN3_HUMAN**, EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2

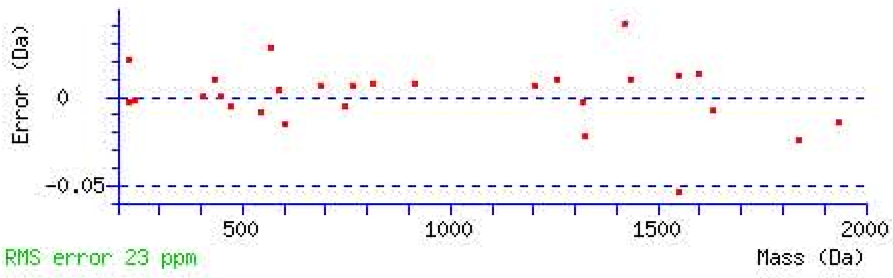
Match to Query 61095: 3733.534576 from(934.390920,4+) rtinseconds(1769) index(30392)
Title: Locus:1.1.1.3279.23 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

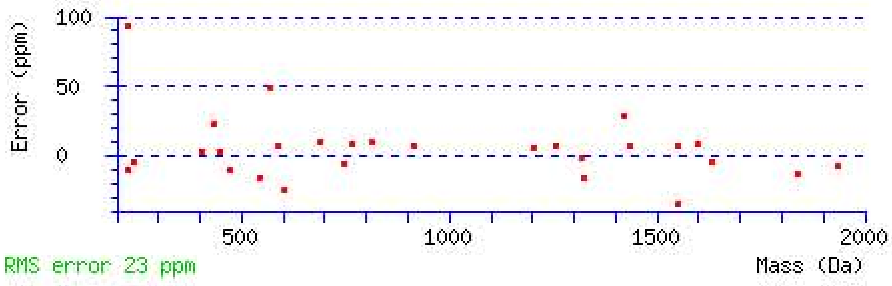
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3733.543625
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9     : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 1.7e-005
Matches : 28/312 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					I							29
2	***242.149918***	121.578597	225.123369	113.065323			Q	3621.466836	1811.237056	3604.440287	1802.723781	3603.456271	1802.231773	28
3	***402.180567***	201.593922	385.154018	193.080647			C	3493.408258	1747.207767	3476.381709	1738.694492	3475.397693	1738.202484	27
4	***473.217681***	237.112479	456.191132	228.599204			A	3333.377609	1667.192442	3316.351060	1658.679168	3315.367044	1658.187160	26
5	***544.254795***	272.631036	527.228246	264.117761			A	3262.340495	1631.673885	3245.313946	1623.160611	3244.329930	1622.668603	25
6	***601.276259***	301.141768	584.249710	292.628493			G	3191.303381	1596.155328	3174.276832	1587.642054	3173.292816	1587.150046	24
7	***764.339588***	382.673432	747.313039	374.160158			Y	3134.281917	1567.644596	3117.255368	1559.131322	3116.271352	1558.639314	23
8	893.382181	447.194729	876.355632	438.681454	875.371616	438.189446	E	2971.218588	1486.112932	2954.192039	1477.599657	2953.208023	1477.107649	22
9	1332.607507	666.807391	1315.580958	658.294117	1314.596942	657.802109	Q	2842.175995	1421.591635	2825.149446	1413.078361	2824.165430	1412.586353	21
10	1419.639535	710.323406	1402.612986	701.810131	1401.628970	701.318123	S	2402.950669	1201.978972	2385.924120	1193.465698	2384.940104	1192.973690	20
11	***1548.682128***	774.844702	1531.655579	766.331428	1530.671563	765.839420	E	2315.918641	1158.462958	2298.892092	1149.949684	2297.908076	1149.457676	19
12	1685.741040	843.374158	1668.714491	834.860884	1667.730475	834.368876	H	2186.876048	1093.941662	2169.849499	1085.428387	2168.865483	1084.936379	18
13	1799.783967	900.395622	1782.757418	891.882347	1781.773402	891.390339	N	2049.817136	1025.412206	2032.790587	1016.898931	2031.806571	1016.406923	17
14	1898.852381	949.929829	1881.825832	941.416554	1880.841816	940.924546	V	***1935.774209***	968.390742	1918.747660	959.877468	1917.763644	959.385460	16
15	2058.883030	1029.945153	2041.856481	1021.431879	2040.872465	1020.939871	C	***1836.705795***	918.856535	1819.679246	910.343261	1818.695230	909.851253	15
16	2186.941608	1093.974442	2169.915059	1085.461167	2168.931043	1084.969159	Q	1676.675146	838.841211	1659.648597	830.327936	1658.664581	829.835928	14
17	2301.968551	1151.487913	2284.942002	1142.974639	2283.957986	1142.482631	D	***1548.616568***	774.811922	1531.590019	766.298647	1530.606003	765.806639	13
18	2415.052615	1208.029945	2398.026066	1199.516671	2397.042050	1199.024663	I	***1433.589625***	717.298450	1416.563076	708.785176	1415.579060	708.293168	12
19	2530.079558	1265.543417	2513.053009	1257.030142	2512.068993	1256.538134	D	***1320.505561***	660.756418	1303.479012	652.243144	1302.494996	651.751136	11
20	2659.122151	1330.064713	2642.095602	1321.551439	2641.111586	1321.059431	E	***1205.478618***	603.242947	1188.452069	594.729672	1187.468053	594.237664	10
21	2819.152800	1410.080038	2802.126251	1401.566763	2801.142235	1401.074755	C	1076.436025	538.721650	1059.409476	530.208376	1058.425460	529.716368	9
22	2920.200479	1460.603877	2903.173930	1452.090603	2902.189914	1451.598595	T	***916.405376***	458.706326	899.378827	450.193051	898.394811	449.701043	8
23	2991.237593	1496.122434	2974.211044	1487.609160	2973.227028	1487.117152	A	***815.357697***	408.182486	798.331148	399.669212	797.347132	399.177204	7
24	3048.259057	1524.633166	3031.232508	1516.119892	3030.248492	1515.627884	G	***744.320583***	372.663929	727.294034	364.150655	726.310018	363.658647	6
25	3149.306736	1575.157006	3132.280187	1566.643731	3131.296171	1566.151723	T	***687.299119***	344.153197	670.272570	335.639923	669.288554	335.147915	5
26	3286.365648	1643.686462	3269.339099	1635.173187	3268.355083	1634.681179	H	***586.251440***	293.629358	569.224891	285.116083			4
27	3400.408575	1700.707925	3383.382026	1692.194651	3382.398010	1691.702643	N	***449.192528***	225.099902	432.165979	216.586627			3
28	3560.439224	1780.723250	3543.412675	1772.209975	3542.428659	1771.717967	C	335.149601	168.078438	318.123052	159.565164			2
29							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IQCAAGYEQSEHNVCQDIDECTAGTHNCR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.6	3733.543625	-0.009049	IQCAAGYEQSEHNVCQDIDECTAGTHNCR
33.5	3733.543625	-0.009049	IQCAAGYEQSEHNVCQDIDECTAGTHNCR
27.0	3733.543625	-0.009049	IQCAAGYEQSEHNVCQDIDECTAGTHNCR

Mascot: http://www.matrixscience.com/

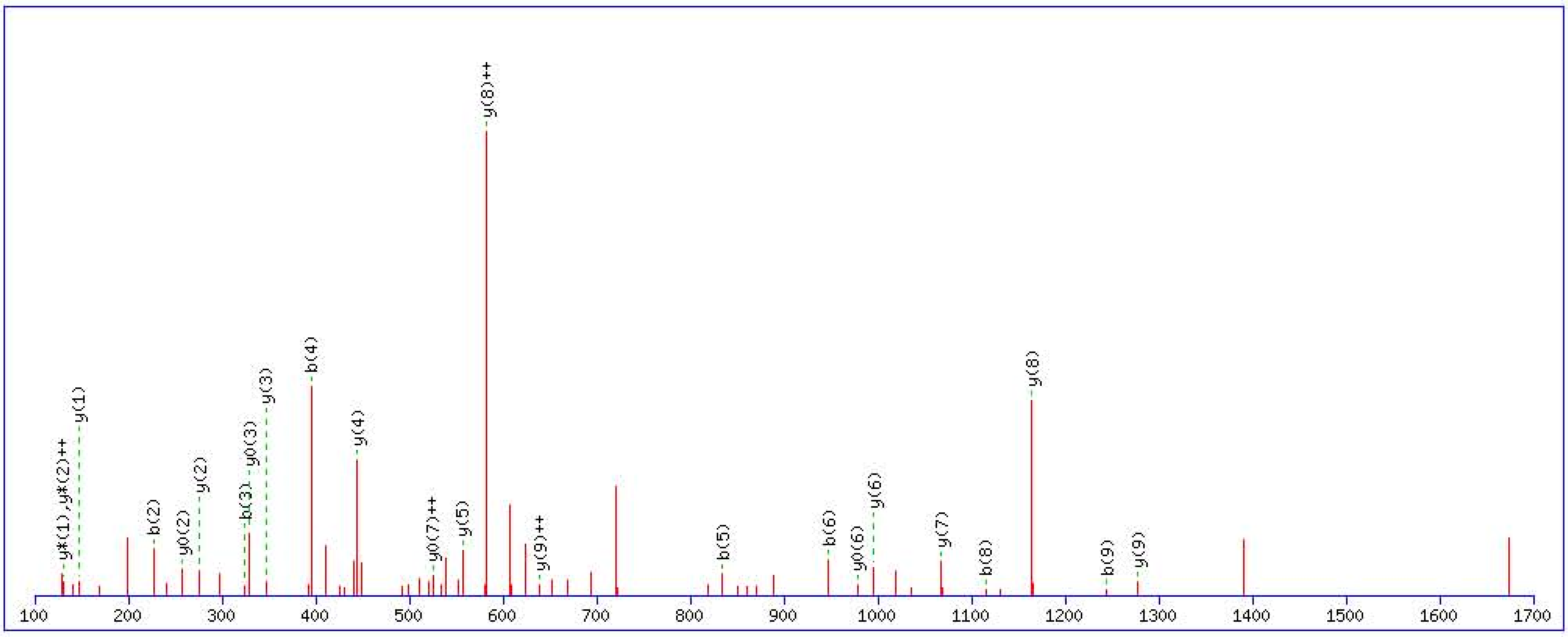
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLPAQLPAEK**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

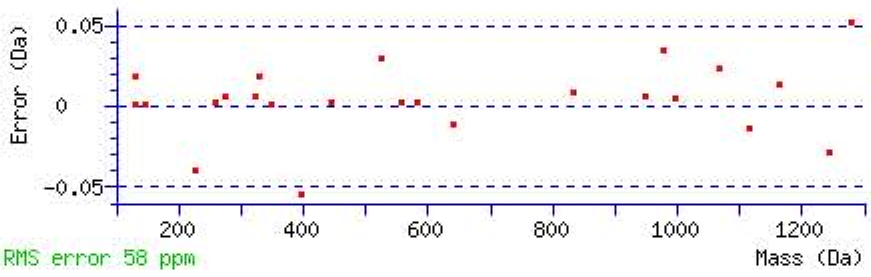
Match to Query 23261: 1389.811308 from(695.912930,2+) rtinseconds(2065) index(5290)
Title: Locus:1.1.1.3239.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

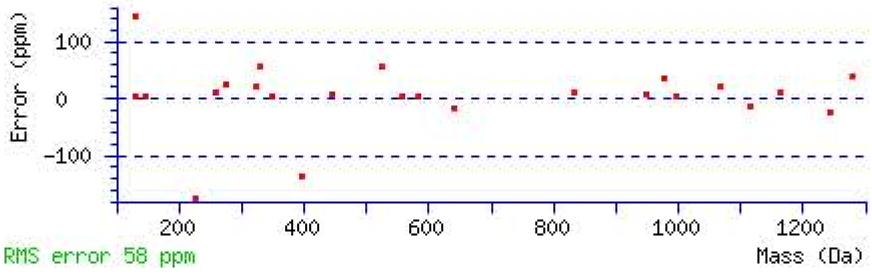
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1389.805359
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 50  Expect: 6e-005
Matches : 24/82 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							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
50.5	1389.805359	0.005949	LLPAQLPAEK
9.6	1389.809189	0.002119	LIKRLDLSYNR
3.2	1389.809204	0.002104	IARVPRLPPDEK
1.1	1389.813232	-0.001924	LIQAPSKFAFLR
1.0	1389.797989	0.013319	LLNLQSLFVTSR
0.9	1389.823135	-0.011827	ILIVITDGQKYK
0.6	1389.816605	-0.005297	ILGPLPKHMIQK
0.4	1389.805359	0.005949	LLSSYLQKK

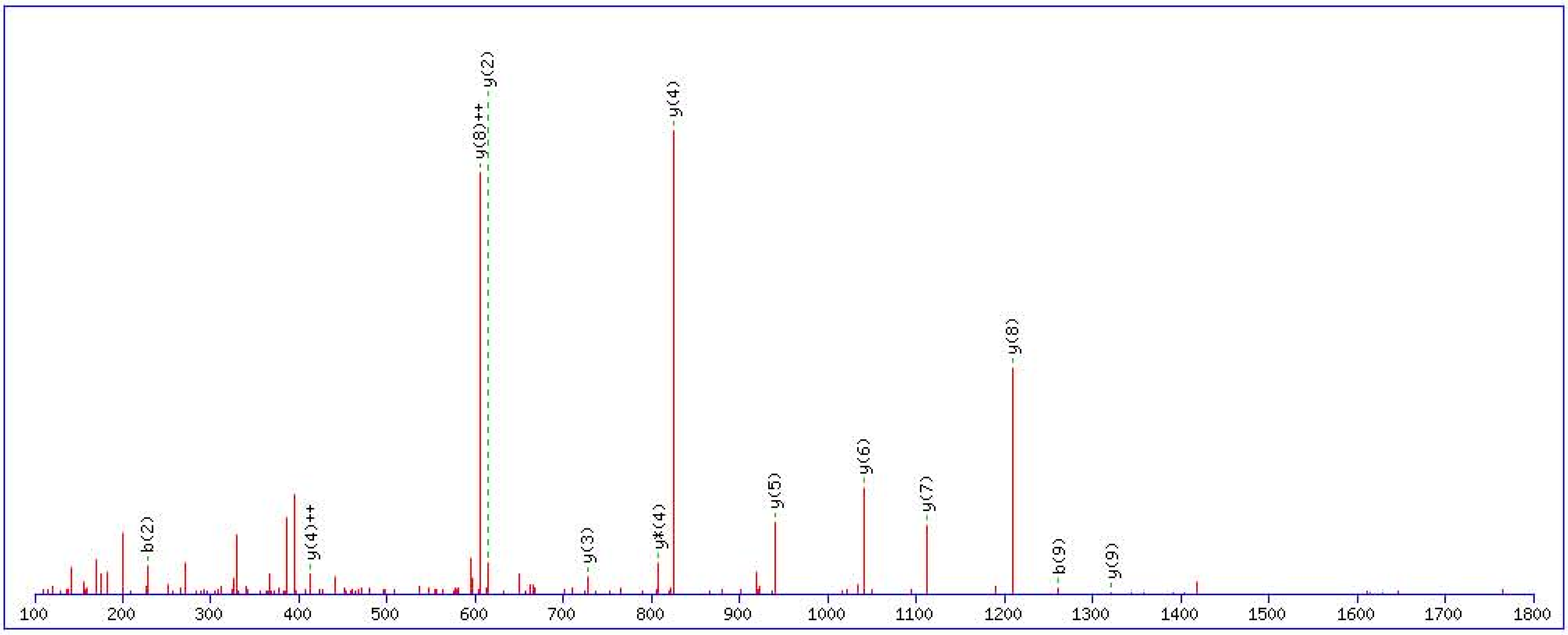
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLPATDPLQR**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

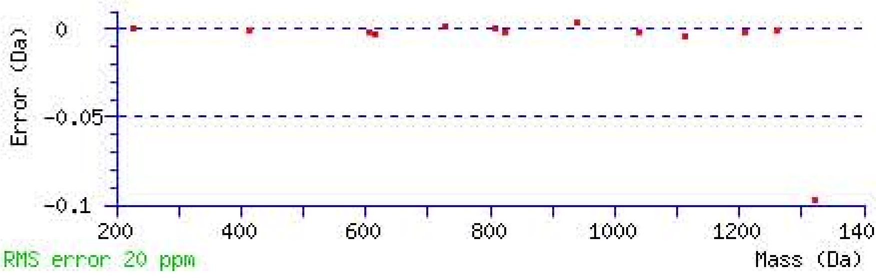
Match to Query 25500: 1434.761708 from(718.388130,2+) rtinseconds(1997) index(19068)
Title: Locus:1.1.1.3261.4 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

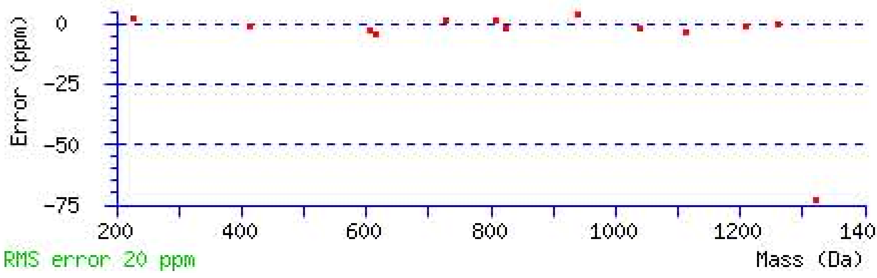
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1434.765305
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 7.5e-005
Matches : 13/92 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	115.050203	58.028740	98.023654	49.515465			N							10
2	**228.134267**	114.570771	211.107718	106.057497			L	***1321.729670***	661.368473	1304.703121	652.855199	1303.719105	652.363190	9
3	325.187031	163.097153	308.160482	154.583879			P	***1208.645606***	604.826441	1191.619057	596.313166	1190.635041	595.821158	8
4	396.224145	198.615710	379.197596	190.102436			A	***1111.592842***	556.300059	1094.566293	547.786784	1093.582277	547.294776	7
5	497.271824	249.139550	480.245275	240.626275	479.261259	240.134267	T	***1040.555728***	520.781502	1023.529179	512.268227	1022.545163	511.776220	6
6	612.298767	306.653022	595.272218	298.139747	594.288202	297.647739	D	***939.508049***	470.257662	922.481500	461.744388	921.497484	461.252380	5
7	709.351531	355.179404	692.324982	346.666129	691.340966	346.174121	P	***824.481106***	412.744191	807.454557	404.230916			4
8	822.435595	411.721436	805.409046	403.208161	804.425030	402.716153	L	***727.428342***	364.217809	710.401793	355.704534			3
9	**1261.660921**	631.334098	1244.634372	622.820824	1243.650356	622.328816	Q	***614.344278***	307.675777	597.317729	299.162502			2
10							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of NLPATDPLQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.4	1434.765305	-0.003597	NLPATDPLQR
7.9	1434.757889	0.003819	NLIRQISSGEYR
3.4	1434.783066	-0.021358	VKDQKLFVSESR
0.7	1434.761932	-0.000224	NIFPSNLVSAAFR

Mascot: http://www.matrixscience.com/

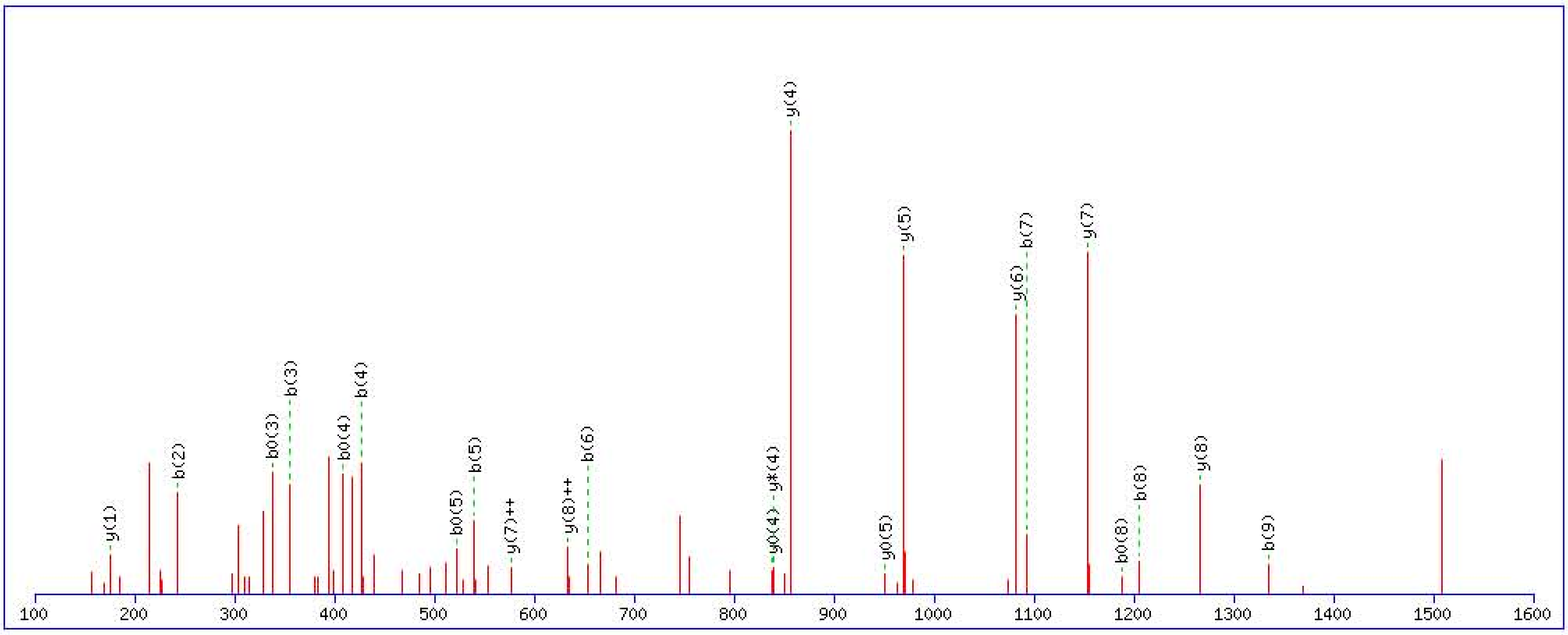
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELLALIQLER**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

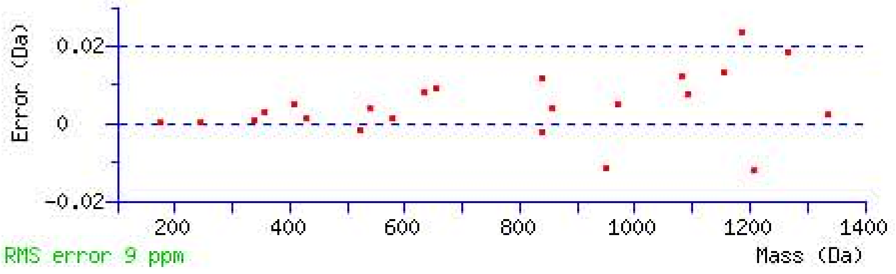
Match to Query 27421: 1507.887508 from(754.951030,2+) rtinseconds(2769) index(23558)
Title: Locus:1.1.1.3528.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

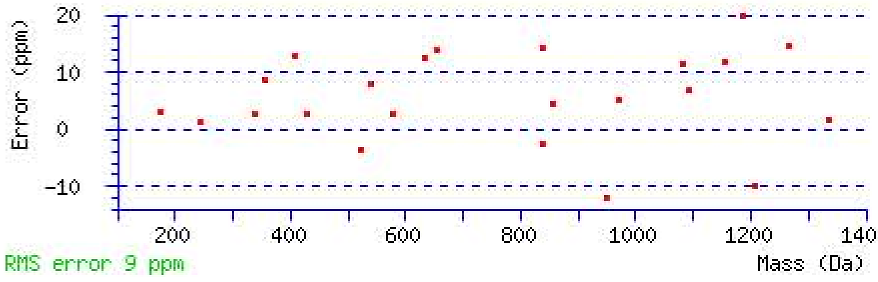
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1507.879578
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 : 23/94 fragment ions using 35 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							10
2	***243.133933***	122.070605			225.123368	113.065322	L	1379.844305	690.425790	1362.817756	681.912516	1361.833740	681.420508	9
3	***356.217997***	178.612637			338.207432	169.607354	L	**1266.760241**	633.883759	1249.733692	625.370484	1248.749676	624.878476	8
4	***427.255111***	214.131193			409.244546	205.125911	A	**1153.676177**	577.341727	1136.649628	568.828452	1135.665612	568.336444	7
5	***540.339175***	270.673226			522.328610	261.667943	L	**1082.639063**	541.823169	1065.612514	533.309895	1064.628498	532.817887	6
6	***653.423239***	327.215258			635.412674	318.209975	I	**969.554999**	485.281138	952.528450	476.767863	951.544434	476.275855	5
7	***1092.648565***	546.827921	1075.622016	538.314646	1074.638000	537.822638	Q	**856.470935**	428.739105	839.444386	420.225831	838.460370	419.733823	4
8	***1205.732629***	603.369953	1188.706080	594.856678	1187.722064	594.364670	L	417.245609	209.126442	400.219060	200.613168	399.235044	200.121160	3
9	***1334.775222***	667.891249	1317.748673	659.377975	1316.764657	658.885966	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
10							R	**175.118952**	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ELLALIQLER
(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	1507.879578	0.007930	ELLALIQLER

Mascot: http://www.matrixscience.com/

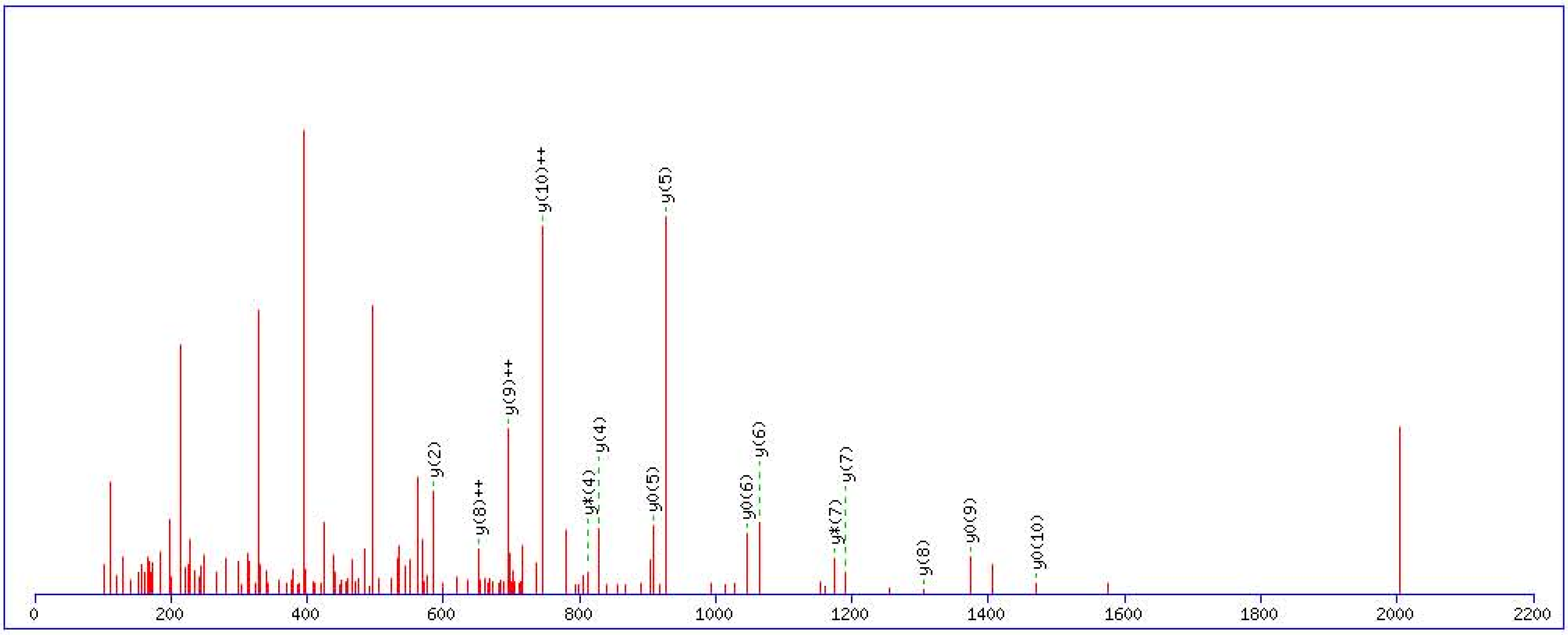
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELPSLQHPNEQK**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

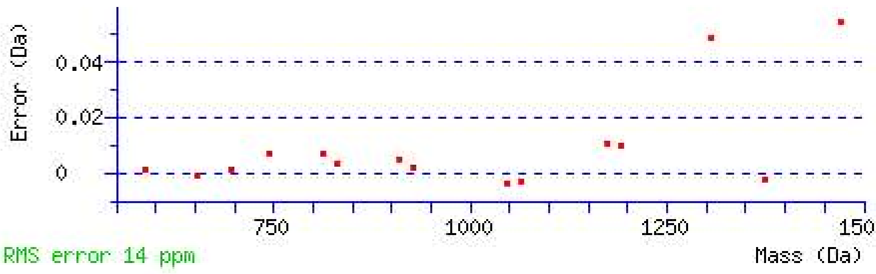
Match to Query 34222: 1729.884012 from(577.635280,3+) rtinseconds(1690) index(3180)
Title: Locus:1.1.1.3108.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

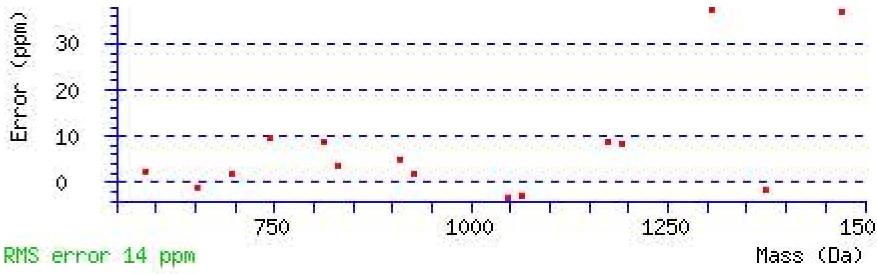
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1729.882111
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 26 **Expect:** 0.063
Matches : 15/118 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	130.049869	65.528572			112.039304	56.523290	E							12
2	243.133933	122.070605			225.123368	113.065322	L	1601.846824	801.427050	1584.820275	792.913776	1583.836259	792.421767	11
3	340.186697	170.596987			322.176132	161.591704	P	1488.762760	744.885018	1471.736211	736.371744	1470.752195	735.879736	10
4	427.218725	214.113001			409.208160	205.107718	S	1391.709996	696.358636	1374.683447	687.845362	1373.699431	687.353354	9
5	540.302789	270.655033			522.292224	261.649750	L	***1304.677968***	652.842622	1287.651419	644.329348	1286.667403	643.837340	8
6	668.361367	334.684322	651.334818	326.171047	650.350802	325.679039	Q	***1191.593904***	596.300590	1174.567355	587.787316	1173.583339	587.295308	7
7	805.420279	403.213778	788.393730	394.700503	787.409714	394.208495	H	***1063.535326***	532.271301	1046.508777	523.758027	1045.524761	523.266018	6
8	902.473043	451.740160	885.446494	443.226885	884.462478	442.734877	P	***926.476414***	463.741845	909.449865	455.228571	908.465849	454.736563	5
9	1016.515970	508.761623	999.489421	500.248349	998.505405	499.756341	N	***829.423650***	415.215463	812.397101	406.702189	811.413085	406.210181	4
10	1145.558563	573.282920	1128.532014	564.769645	1127.547998	564.277637	E	715.380723	358.194000	698.354174	349.680725	697.370158	349.188717	3
11	1584.783889	792.895583	1567.757340	784.382308	1566.773324	783.890300	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 ELPSLQHPNEQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.4	1729.882111	0.001901	ELPSLQHPNEQK

Mascot: http://www.matrixscience.com/

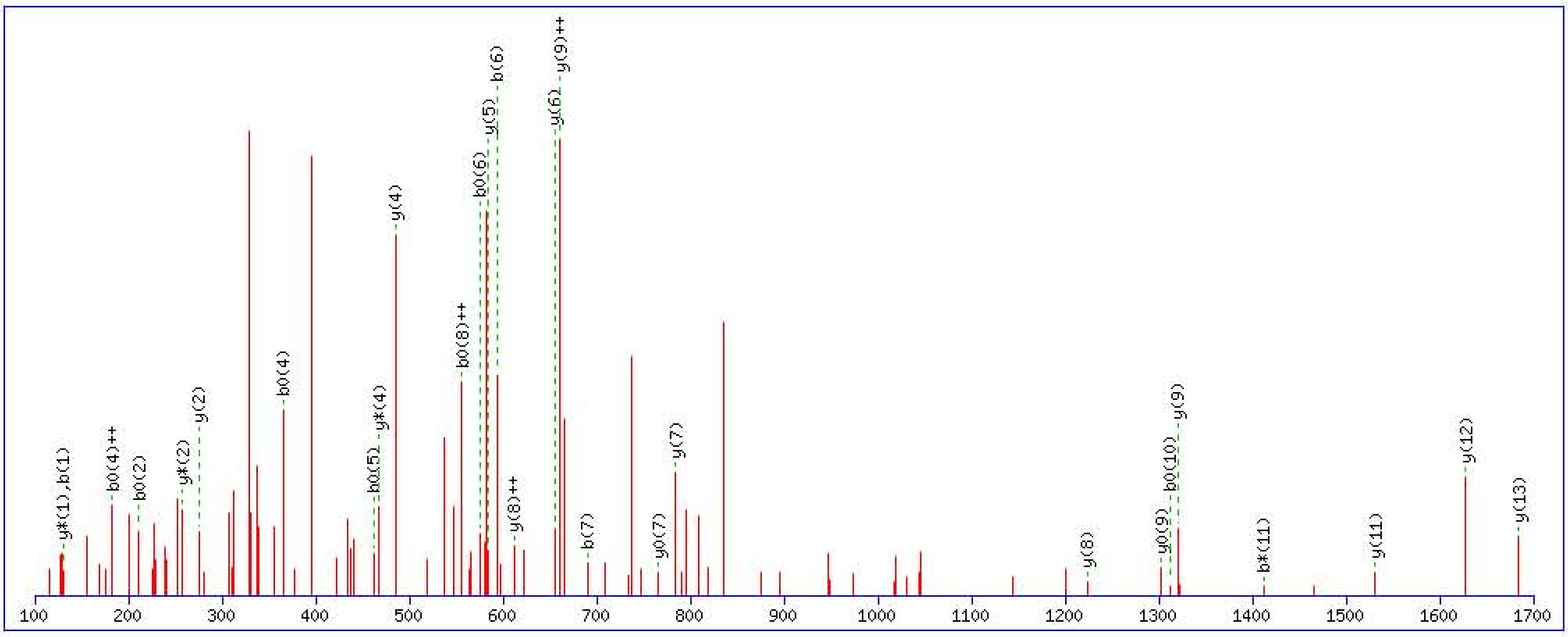
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVGPPLPQEAVPLQK**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

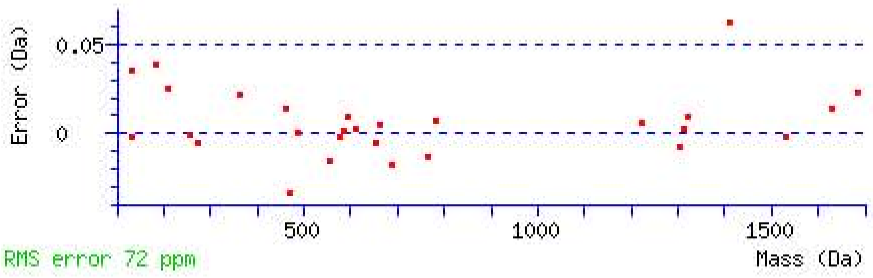
Match to Query 37690: 1912.059222 from(638.360350,3+) rtinseconds(2266) index(6337)
Title: Locus:1.1.1.3309.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

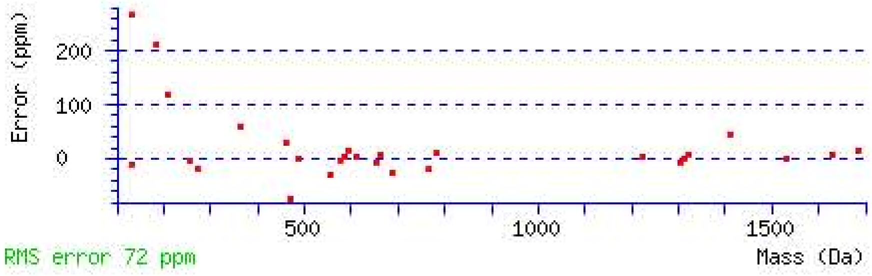
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1912.049194
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.023
Matches : 28/142 fragment ions using 90 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							15
2	229.118283	115.062780			211.107718	106.057497	V	1784.013891	892.510583	1766.987342	883.997309	1766.003326	883.505301	14
3	286.139747	143.573512			268.129182	134.568229	G	***1684.945477***	842.976377	1667.918928	834.463102	1666.934912	833.971094	13
4	383.192511	192.099894			365.181946	183.094611	P	***1627.924013***	814.465645	1610.897464	805.952370	1609.913448	805.460362	12
5	480.245275	240.626276			462.234710	231.620993	P	***1530.871249***	765.939263	1513.844700	757.425988	1512.860684	756.933980	11
6	**593.329339**	297.168308			575.318774	288.163025	L	1433.818485	717.412881	1416.791936	708.899606	1415.807920	708.407598	10
7	**690.382103**	345.694690			672.371538	336.689407	P	***1320.734421***	660.870848	1303.707872	652.357574	1302.723856	651.865566	9
8	1129.607429	565.307353	1112.580880	556.794078	1111.596864	556.302070	Q	***1223.681657***	612.344466	1206.655108	603.831192	1205.671092	603.339184	8
9	1258.650022	629.828649	1241.623473	621.315375	1240.639457	620.823367	E	***784.456331***	392.731803	767.429782	384.218529	766.445766	383.726521	7
10	1329.687136	665.347206	1312.660587	656.833932	1311.676571	656.341924	A	***655.413738***	328.210507	638.387189	319.697232			6
11	1428.755550	714.881413	1411.729001	706.368139	1410.744985	705.876131	V	***584.376624***	292.691950	567.350075	284.178676			5
12	1525.808314	763.407795	1508.781765	754.894521	1507.797749	754.402513	P	***485.308210***	243.157743	468.281661	234.644468			4
13	1638.892378	819.949827	1621.865829	811.436553	1620.881813	810.944545	L	388.255446	194.631361	371.228897	186.118086			3
14	1766.950956	883.979116	1749.924407	875.465842	1748.940391	874.973833	Q	***275.171382***	138.089329	258.144833	129.576054			2
15							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of EVGPPLPQEAVPLQK
(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	1912.049194	0.010028	EVGPPLPQEAVPLQK
19.8	1912.049194	0.010028	EVGPPLPQEAVPLQK

Mascot: http://www.matrixscience.com/

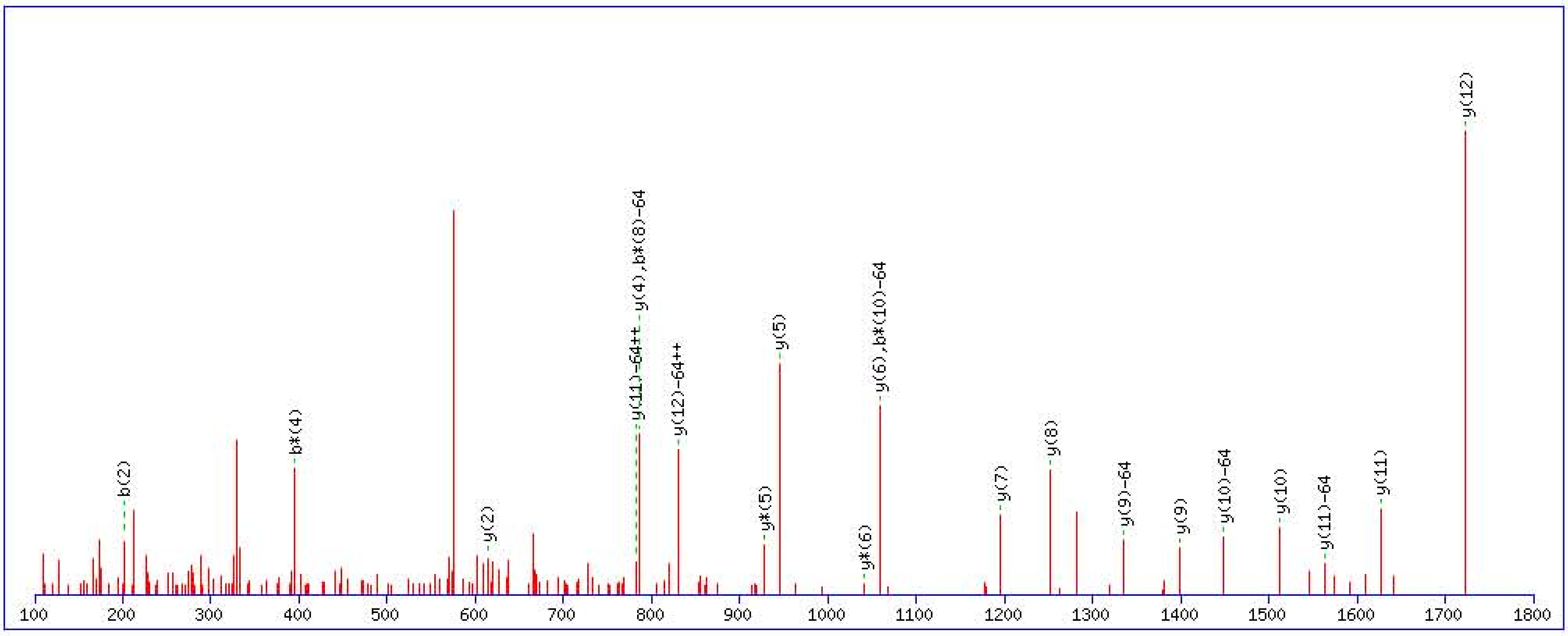
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTPNLMGHLCGNQR**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

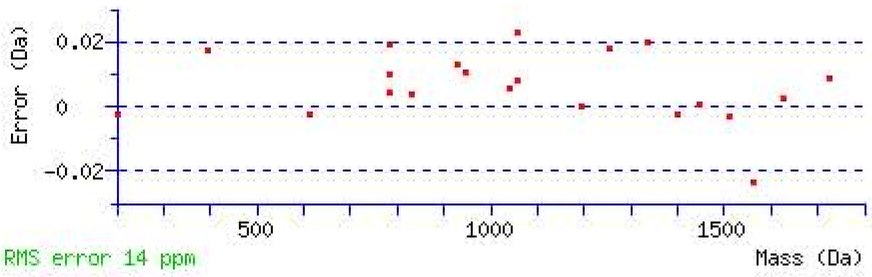
Match to Query 37841: 1922.931072 from(641.984300,3+) rtinseconds(1674) index(3091)
Title: Locus:1.1.1.3102.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

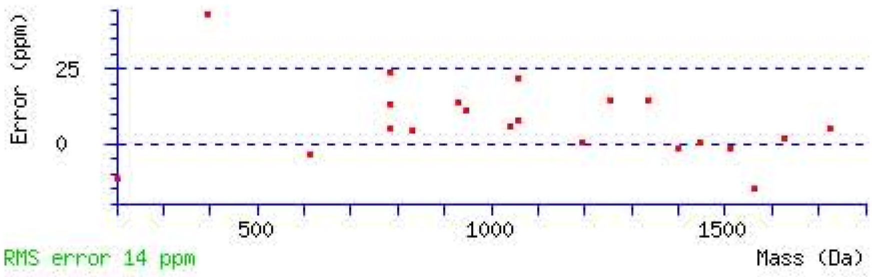
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1922.927734
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M6     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 1.9e-005
Matches : 21/194 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	1824.866592	912.936934	1807.840043	904.423659	1806.856027	903.931651	13
3	298.176133	149.591704			280.165568	140.586422	P	*1723.818913*	862.413094	1706.792364	853.899820			12
4	412.219060	206.613168	395.192511	198.099894	394.208495	197.607886	N	*1626.766149*	813.886712	1609.739600	805.373438			11
5	525.303124	263.155200	508.276575	254.641926	507.292559	254.149918	L	*1512.723222*	756.865249	1495.696673	748.351974			10
6	672.338524	336.672900	655.311975	328.159626	654.327959	327.667618	M	*1399.639158*	700.323217	1382.612609	691.809943			9
7	729.359988	365.183632	712.333439	356.670358	711.349423	356.178350	G	*1252.603758*	626.805517	1235.577209	618.292243			8
8	866.418900	433.713088	849.392351	425.199814	848.408335	424.707806	H	*1195.582294*	598.294785	1178.555745	589.781511			7
9	979.502964	490.255120	962.476415	481.741846	961.492399	481.249838	L	*1058.523382*	529.765329	1041.496833	521.252055			6
10	1139.533613	570.270445	1122.507064	561.757170	1121.523048	561.265162	C	*945.439318*	473.223297	928.412769	464.710022			5
11	1196.555077	598.781177	1179.528528	590.267902	1178.544512	589.775894	G	*785.408669*	393.207972	768.382120	384.694698			4
12	1310.598004	655.802640	1293.571455	647.289366	1292.587439	646.797357	N	728.387205	364.697241	711.360656	356.183966			3
13	1749.823330	875.415303	1732.796781	866.902029	1731.812765	866.410020	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
60.4	1922.927734	0.003338	VTPNLMGHLCGNQR

Mascot: http://www.matrixscience.com/

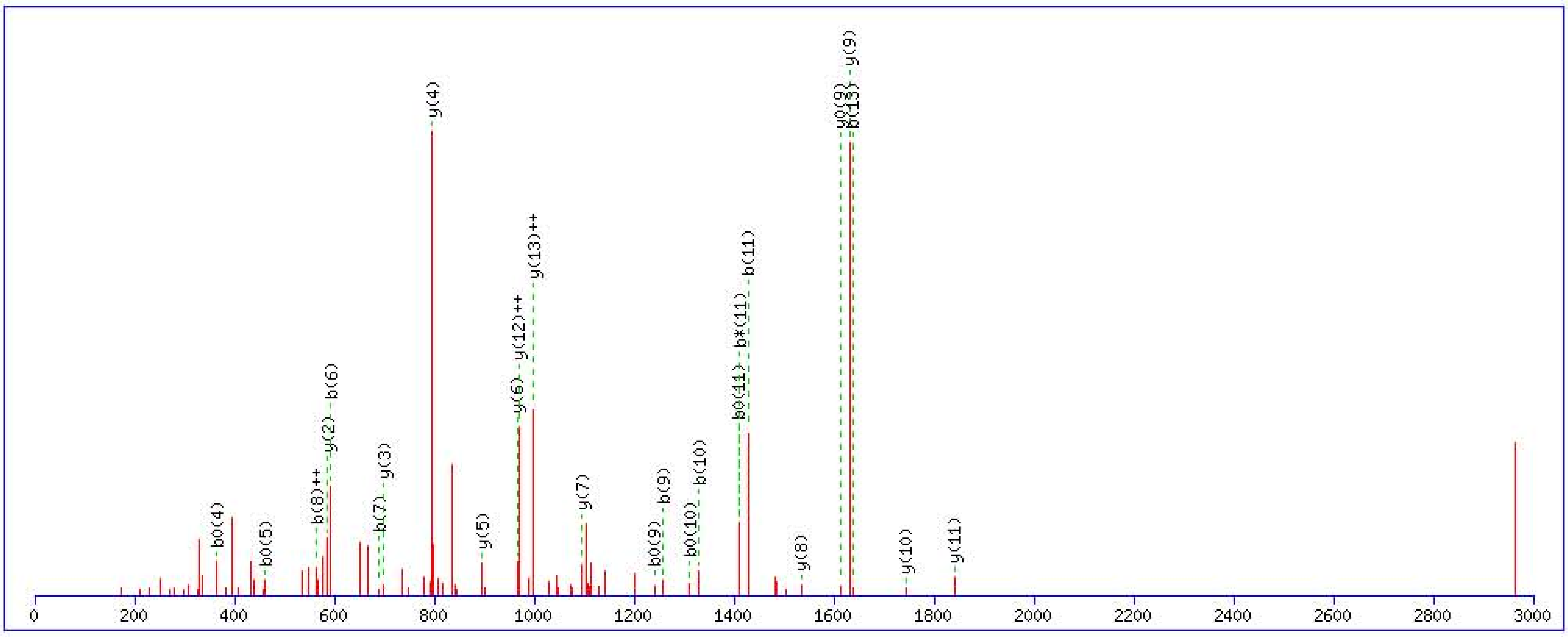
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVGPPLPQEAVPLQK**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

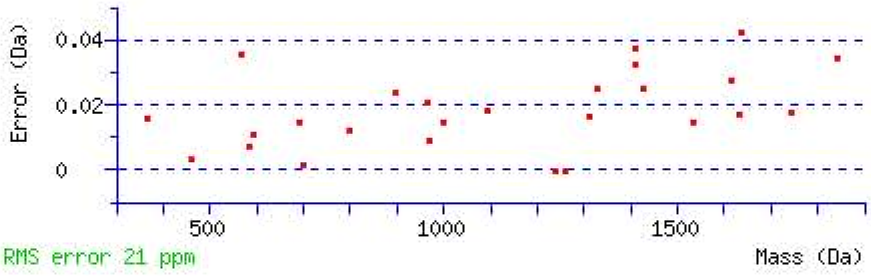
Match to Query 43674: 2223.248428 from(1112.631490,2+) rtinseconds(2503) index(7561)
Title: Locus:1.1.1.3391.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

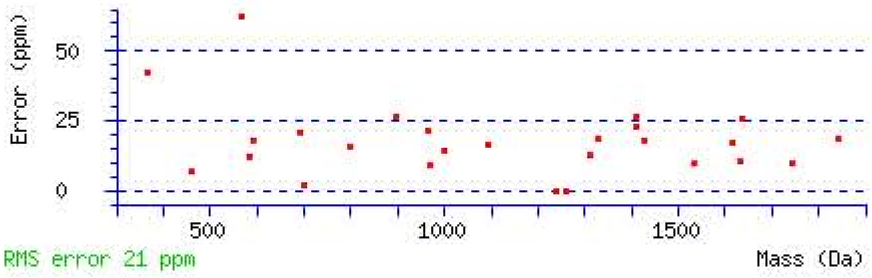
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2223.215942
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Q14 : Biotin:Thermo-21345 (Q)
Ions Score: 45 **Expect:** 0.00034
Matches : 26/142 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	130.049869	65.528572			112.039304	56.523290	E							15
2	229.118283	115.062780			211.107718	106.057497	V	2095.180639	1048.093957	2078.154090	1039.580683	2077.170074	1039.088675	14
3	286.139747	143.573512			268.129182	134.568229	G	1996.112225	998.559751	1979.085676	990.046476	1978.101660	989.554468	13
4	383.192511	192.099894			365.181946	183.094611	P	1939.090761	970.049019	1922.064212	961.535744	1921.080196	961.043736	12
5	480.245275	240.626276			462.234710	231.620993	P	***1842.037997***	921.522637	1825.011448	913.009362	1824.027432	912.517354	11
6	**593.329339**	297.168308			575.318774	288.163025	L	***1744.985233***	872.996255	1727.958684	864.482980	1726.974668	863.990972	10
7	**690.382103**	345.694690			672.371538	336.689407	P	***1631.901169***	816.454223	1614.874620	807.940948	1613.890604	807.448940	9
8	1129.607429	565.307353	1112.580880	556.794078	1111.596864	556.302070	Q	***1534.848405***	767.927841	1517.821856	759.414566	1516.837840	758.922558	8
9	**1258.650022**	629.828649	1241.623473	621.315375	1240.639457	620.823367	E	***1095.623079***	548.315178	1078.596530	539.801903	1077.612514	539.309895	7
10	**1329.687136**	665.347206	1312.660587	656.833932	1311.676571	656.341924	A	***966.580486***	483.793881	949.553937	475.280607			6
11	**1428.755550**	714.881413	1411.729001	706.368139	1410.744985	705.876131	V	***895.543372***	448.275324	878.516823	439.762050			5
12	1525.808314	763.407795	1508.781765	754.894521	1507.797749	754.402513	P	***796.474958***	398.741117	779.448409	390.227843			4
13	**1638.892378**	819.949827	1621.865829	811.436553	1620.881813	810.944545	L	***699.422194***	350.214735	682.395645	341.701461			3
14	2078.117704	1039.562490	2061.091155	1031.049215	2060.107139	1030.557207	Q	***586.338130***	293.672703	569.311581	285.159429			2
15							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of EVGPPLPQEAVPLQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.5	2223.215942	0.032486	EVGPPLPQEAVPLQK

Mascot: http://www.matrixscience.com/

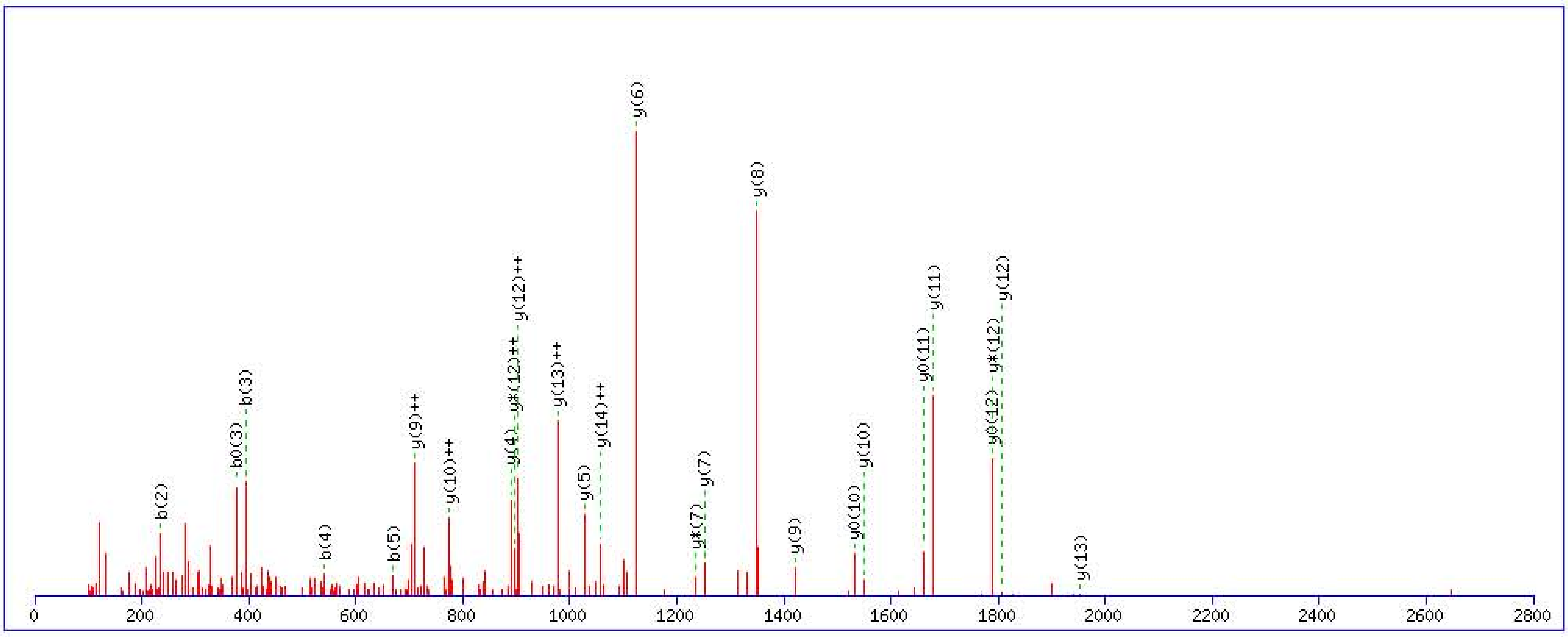
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSCFQEEAPQPHYQLR**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

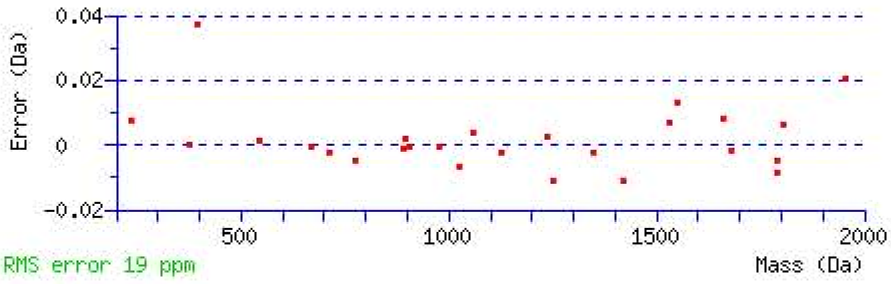
Match to Query 45810: 2347.080942 from(783.367590,3+) rtinseconds(1955) index(18794)
Title: Locus:1.1.1.3246.21 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

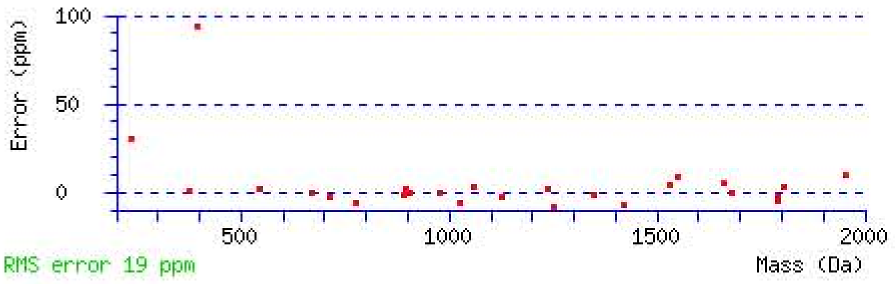
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2347.087784
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Biotin:Thermo-21345 (Q)
Ions Score: 64 **Expect:** 5e-006
Matches : 26/152 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
64.5	2347.087784	-0.006842	FSCFQEEAPQPHYQLR
31.7	2347.087784	-0.006842	FSCFQEEAPQPHYQLR
1.1	2347.087784	-0.006842	FSCFQEEAPQPHYQLR

Mascot: http://www.matrixscience.com/

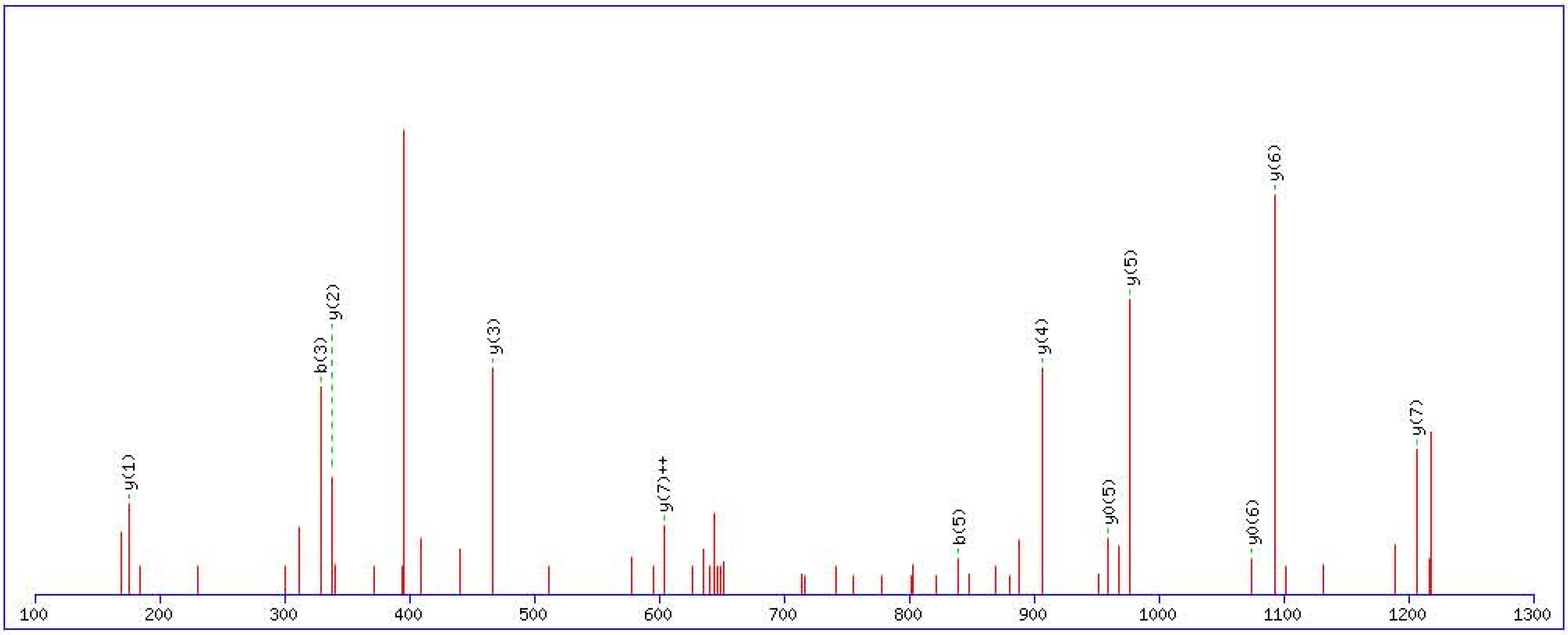
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNDAQEYR**
Found in **FETUB_HUMAN**, Fetuin-B OS=Homo sapiens GN=FETUB PE=1 SV=2

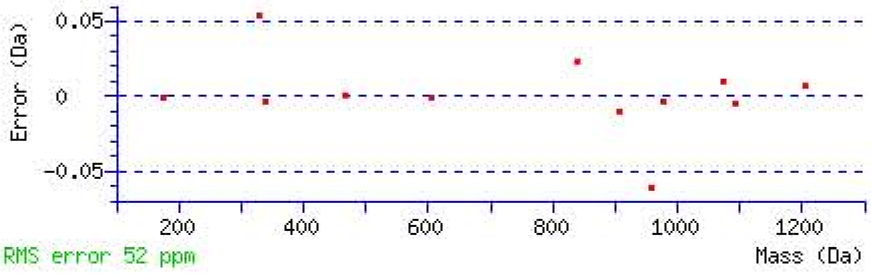
Match to Query 20430: 1304.618008 from(653.316280,2+) rtinseconds(1497) index(57981)
Title: Locus:1.1.1.1432.21 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

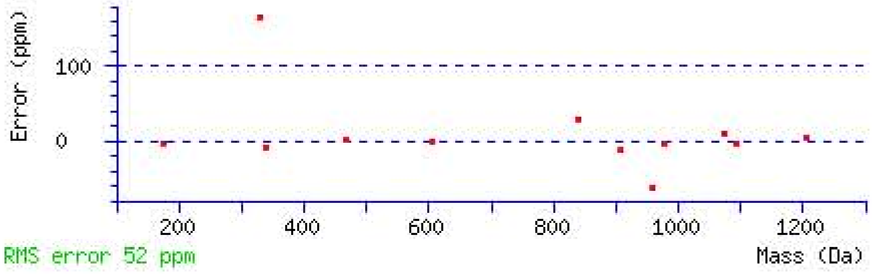
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1304.618301
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 49 **Expect:** 0.00019
Matches : 12/74 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	100.075690	50.541483					V							8
2	214.118617	107.562947	197.092068	99.049672			N	***1206.557184***	603.782230	1189.530635	595.268956	1188.546619	594.776948	7
3	**329.145560**	165.076418	312.119011	156.563144	311.134995	156.071136	D	***1092.514257***	546.760767	1075.487708	538.247492	1074.503692	537.755484	6
4	400.182674	200.594975	383.156125	192.081700	382.172109	191.589692	A	***977.487314***	489.247295	960.460765	480.734021	959.476749	480.242013	5
5	**839.408000**	420.207638	822.381451	411.694364	821.397435	411.202356	Q	***906.450200***	453.728738	889.423651	445.215464	888.439635	444.723456	4
6	968.450593	484.728935	951.424044	476.215660	950.440028	475.723652	E	***467.224874***	234.116075	450.198325	225.602801	449.214309	225.110793	3
7	1131.513922	566.260599	1114.487373	557.747325	1113.503357	557.255317	Y	***338.182281***	169.594778	321.155732	161.081504			2
8							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VNDAQEYR
(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	1304.618301	-0.000293	VNDAQEYR

Mascot: http://www.matrixscience.com/

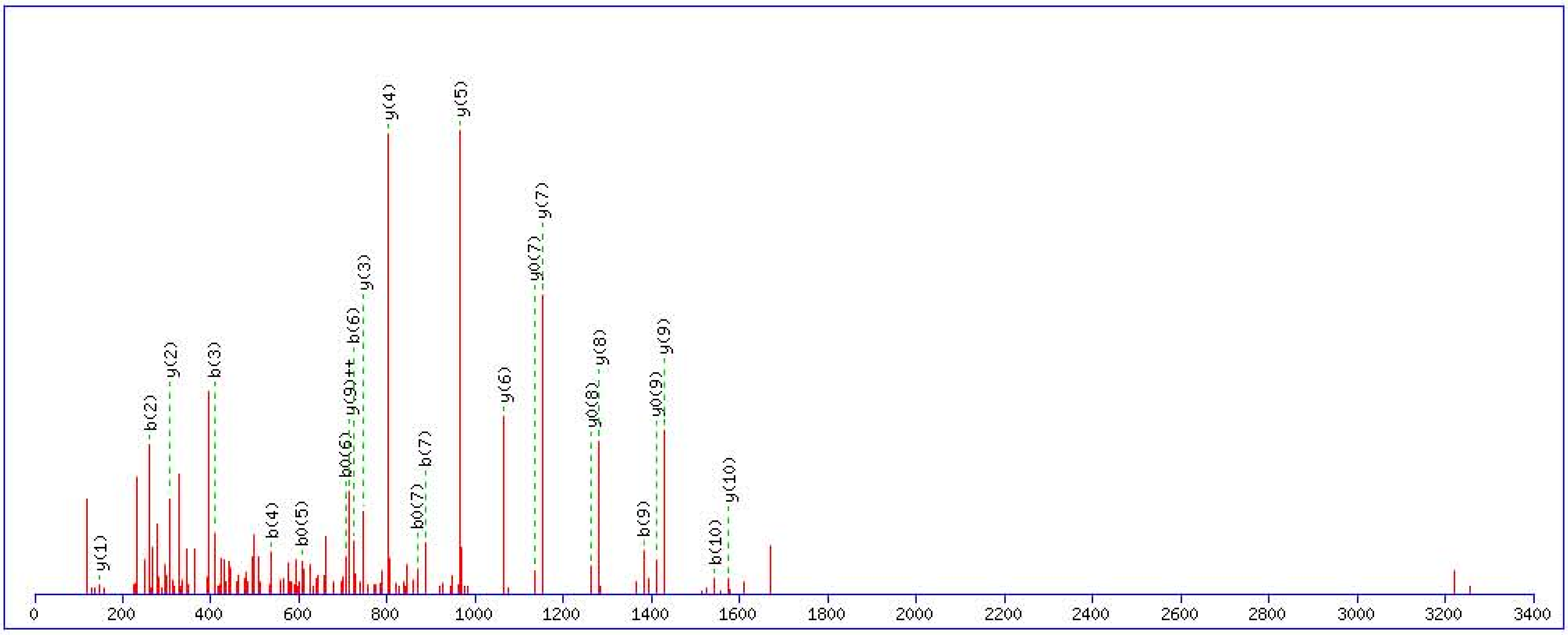
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IFFESVYGQCK**
Found in **FETUB_HUMAN**, Fetuin-B OS=Homo sapiens GN=FETUB PE=1 SV=2

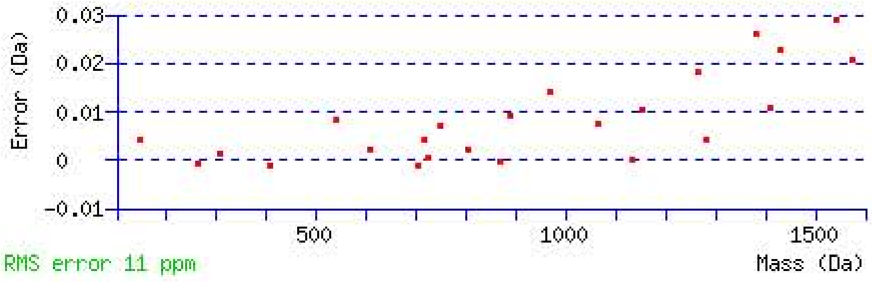
Match to Query 33451: 1687.821308 from(844.917930,2+) rtinseconds(2340) index(62390)
Title: Locus:1.1.1.1726.12 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

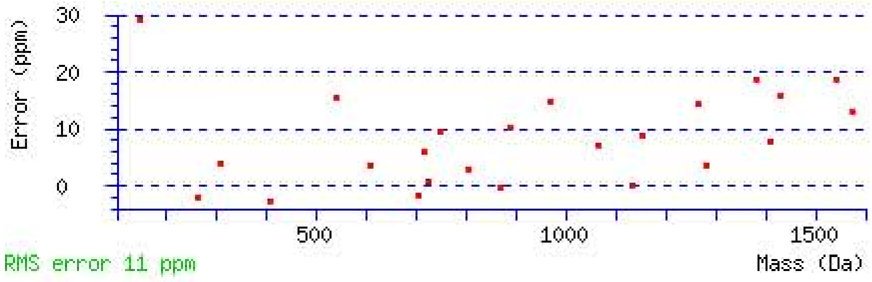
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1687.810226
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 61 **Expect:** 6.3e-006
Matches : 24/86 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					I							11
2	**261.159754**	131.083515					F	***1575.733435***	788.370356	1558.706886	779.857081	1557.722870	779.365073	10
3	**408.228168**	204.617722					F	***1428.665021***	714.836149	1411.638472	706.322874	1410.654456	705.830866	9
4	**537.270761**	269.139019			519.260196	260.133736	E	***1281.596607***	641.301942	1264.570058	632.788667	1263.586042	632.296659	8
5	624.302789	312.655033			606.292224	303.649750	S	***1152.554014***	576.780645	1135.527465	568.267371	1134.543449	567.775363	7
6	**723.371203**	362.189239			705.360638	353.183957	V	***1065.521986***	533.264631	1048.495437	524.751357			6
7	**886.434532**	443.720904			868.423967	434.715622	Y	***966.453572***	483.730424	949.427023	475.217150			5
8	943.455996	472.231636			925.445431	463.226354	G	***803.390243***	402.198760	786.363694	393.685485			4
9	**1382.681322**	691.844299	1365.654773	683.331025	1364.670757	682.839017	Q	***746.368779***	373.688028	729.342230	365.174753			3
10	**1542.711971**	771.859624	1525.685422	763.346349	1524.701406	762.854341	C	***307.143453***	154.075365	290.116904	145.562090			2
11							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of IFFESVYGQCK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.0	1687.810226	0.011082	IFFESVYGQCK
5.5	1687.831345	-0.010037	MIFSSPACLTASFLK

Mascot: http://www.matrixscience.com/

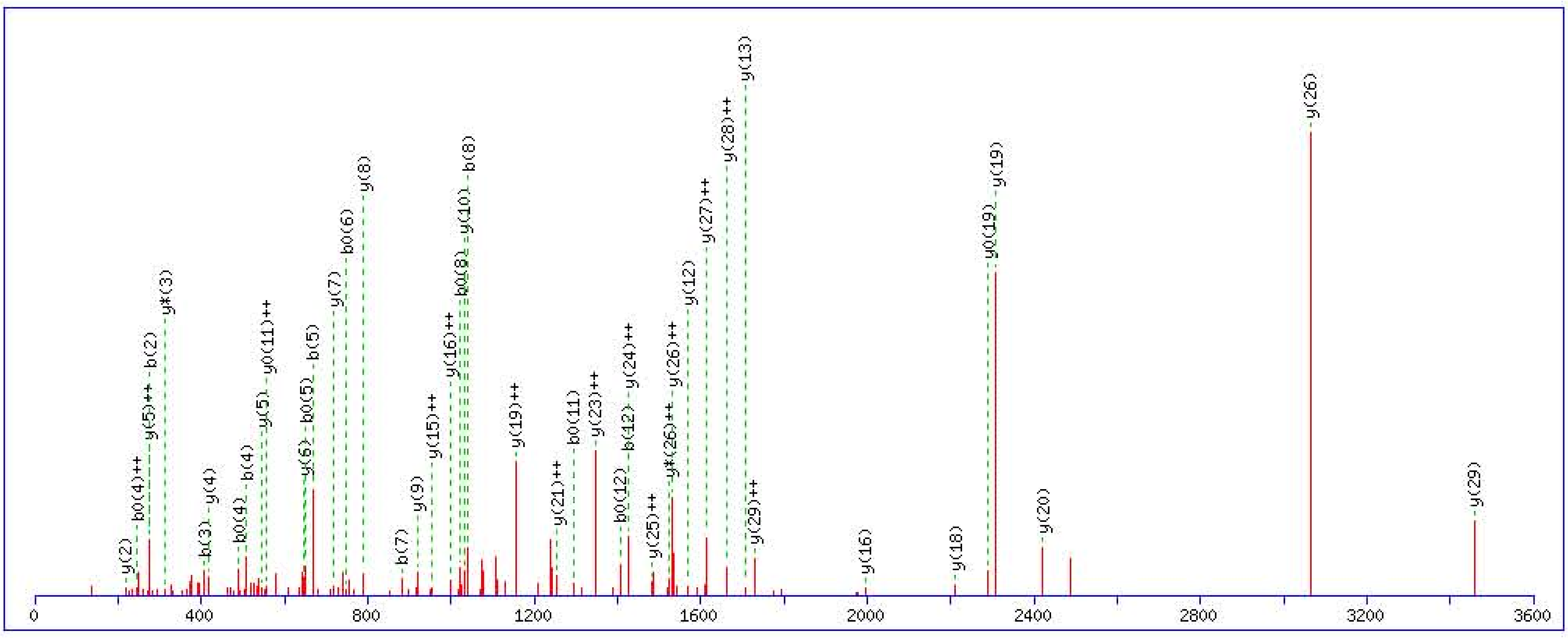
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IYMTCPDCPSSIPTDSSNHQVLEAATESLAK**
Found in **FETUB_HUMAN**, Fetuin-B OS=Homo sapiens GN=FETUB PE=1 SV=2

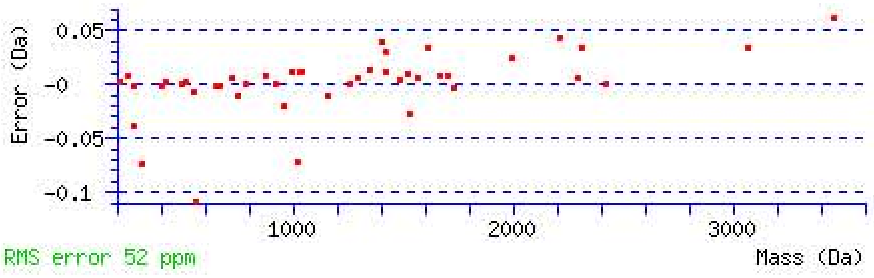
Match to Query 61081: 3732.757482 from(1245.259770,3+) rtinseconds(2329) index(62341)
Title: Locus:1.1.1.1722.11 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

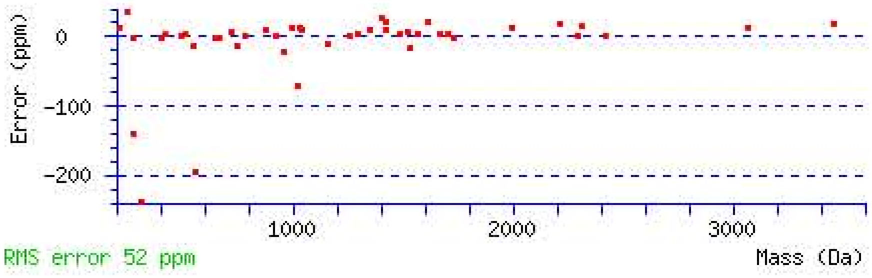
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3732.714340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20    : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 1.2e-005
Matches : 46/314 fragment ions using 128 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					I							31
2	**277.154669**	139.080973					Y	3620.637570	1810.822423	3603.611021	1802.309149	3602.627005	1801.817141	30
3	**408.195154**	204.601215					M	***3457.574241***	1729.290759	3440.547692	1720.777484	3439.563676	1720.285476	29
4	**509.242833**	255.125055			491.232268	246.119772	T	3326.533756	1663.770516	3309.507207	1655.257242	3308.523191	1654.765234	28
5	**669.273482**	335.140379			651.262917	326.135097	C	3225.486077	1613.246677	3208.459528	1604.733402	3207.475512	1604.241394	27
6	766.326246	383.666761			748.315681	374.661479	P	***3065.455428***	1533.231352	3048.428879	1524.718078	3047.444863	1524.226070	26
7	**881.353189**	441.180233			863.342624	432.174950	D	2968.402664	1484.704970	2951.376115	1476.191696	2950.392099	1475.699688	25
8	**1041.383838**	521.195557			1023.373273	512.190274	C	2853.375721	1427.191499	2836.349172	1418.678224	2835.365156	1418.186216	24
9	1138.436602	569.721939			1120.426037	560.716657	P	2693.345072	1347.176174	2676.318523	1338.662900	2675.334507	1338.170892	23
10	1225.468630	613.237953			1207.458065	604.232671	S	2596.292308	1298.649792	2579.265759	1290.136518	2578.281743	1289.644510	22
11	1312.500658	656.753967			1294.490093	647.748685	S	2509.260280	1255.133778	2492.233731	1246.620504	2491.249715	1246.128496	21
12	**1425.584722**	713.295999			1407.574157	704.290717	I	***2422.228252***	1211.617764	2405.201703	1203.104490	2404.217687	1202.612482	20
13	1522.637486	761.822381			1504.626921	752.817099	P	***2309.144188***	1155.075732	2292.117639	1146.562458	2291.133623	1146.070450	19
14	1623.685165	812.346221			1605.674600	803.340938	T	***2212.091424***	1106.549350	2195.064875	1098.036076	2194.080859	1097.544068	18
15	1738.712108	869.859692			1720.701543	860.854410	D	2111.043745	1056.025511	2094.017196	1047.512236	2093.033180	1047.020228	17
16	1825.744136	913.375706			1807.733571	904.370424	S	***1996.016802***	998.512039	1978.990253	989.998765	1978.006237	989.506757	16
17	1912.776164	956.891720			1894.765599	947.886438	S	1908.984774	954.996025	1891.958225	946.482751	1890.974209	945.990743	15
18	2026.819091	1013.913184	2009.792542	1005.399909	2008.808526	1004.907901	N	1821.952746	911.480011	1804.926197	902.966737	1803.942181	902.474729	14
19	2163.878003	1082.442640	2146.851454	1073.929365	2145.867438	1073.437357	H	***1707.909819***	854.458548	1690.883270	845.945273	1689.899254	845.453265	13
20	2603.103329	1302.055303	2586.076780	1293.542028	2585.092764	1293.050020	Q	***1570.850907***	785.929092	1553.824358	777.415817	1552.840342	776.923809	12
21	2702.171743	1351.589510	2685.145194	1343.076235	2684.161178	1342.584227	V	1131.625581	566.316429	1114.599032	557.803154	1113.615016	557.311146	11
22	2815.255807	1408.131542	2798.229258	1399.618267	2797.245242	1399.126259	L	***1032.557167***	516.782222	1015.530618	508.268947	1014.546602	507.776939	10
23	2944.298400	1472.652838	2927.271851	1464.139564	2926.287835	1463.647556	E	***919.473103***	460.240190	902.446554	451.726915	901.462538	451.234907	9
24	3015.335514	1508.171395	2998.308965	1499.658121	2997.324949	1499.166113	A	***790.430510***	395.718893	773.403961	387.205619	772.419945	386.713611	8
25	3086.372628	1543.689952	3069.346079	1535.176678	3068.362063	1534.684670	A	***719.393396***	360.200336	702.366847	351.687062	701.382831	351.195054	7
26	3187.420307	1594.213792	3170.393758	1585.700517	3169.409742	1585.208509	T	***648.356282***	324.681779	631.329733	316.168505	630.345717	315.676497	6
27	3316.462900	1658.735088	3299.436351	1650.221814	3298.452335	1649.729806	E	***547.308603***	274.157940	530.282054	265.644665	529.298038	265.152657	5
28	3403.494928	1702.251102	3386.468379	1693.737828	3385.484363	1693.245820	S	***418.266010***	209.636643	401.239461	201.123369	400.255445	200.631361	4
29	3516.578992	1758.793134	3499.552443	1750.279860	3498.568427	1749.787852	L	331.233982	166.120629	314.207433	157.607355			3
30	3587.616106	1794.311691	3570.589557	1785.798417	3569.605541	1785.306409	A	***218.149918***	109.578597	201.123369	101.065323			2
31							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of IYMTCPDCPSSIPTDSSNHQVLEAATESLAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.8	3732.714340	0.043142	IYMTCPDCPSSIPTDSSNHQVLEAATESLAK

Mascot: http://www.matrixscience.com/

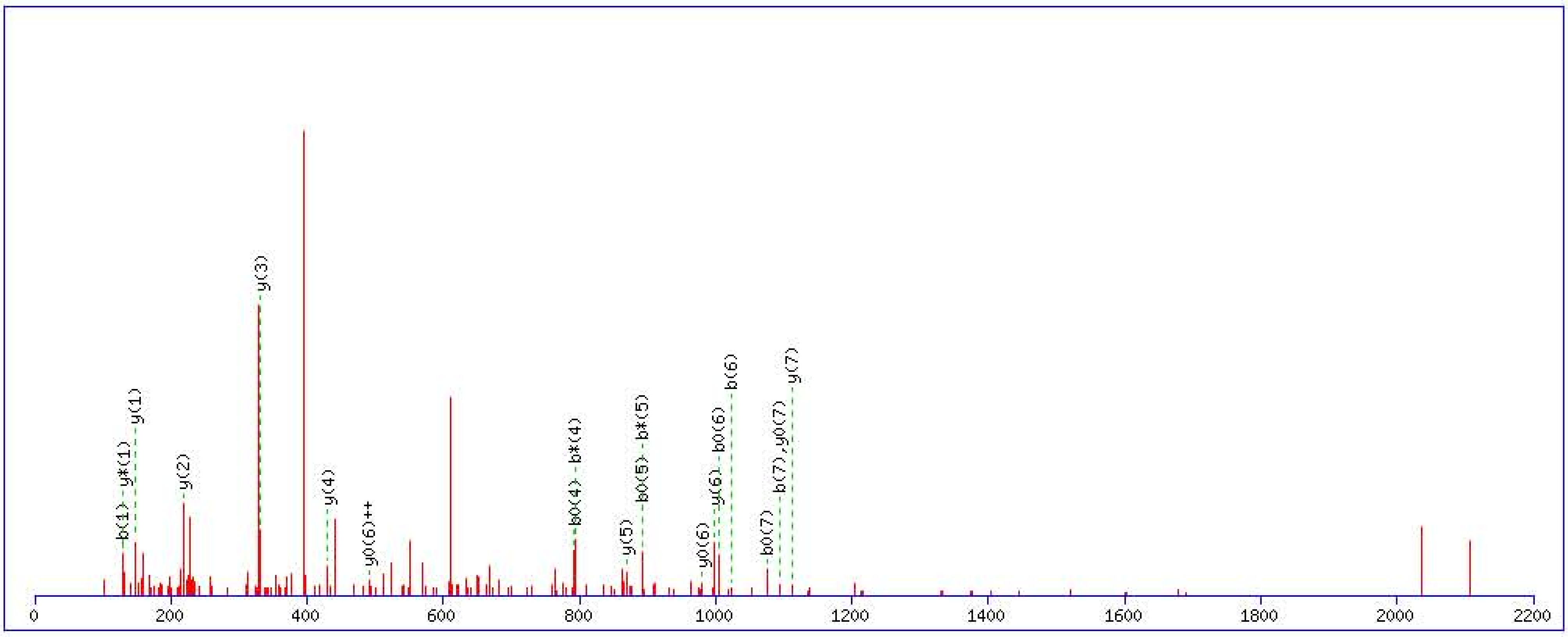
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLEQVIAK**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

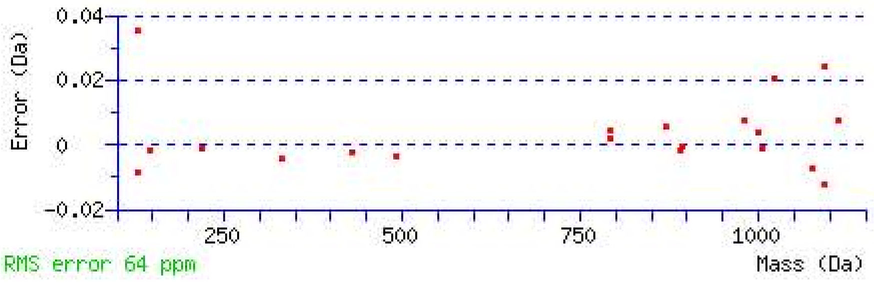
Match to Query 18647: 1238.703848 from(620.359200,2+) rtinseconds(1818) index(44868)
Title: Locus:1.1.1.3346.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

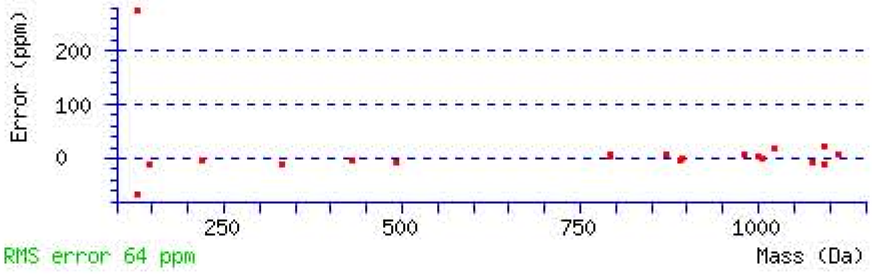
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 31  Expect: 0.013
Matches : 20/70 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	**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
30.9	1238.705658	-0.001810	QLEQVIAK
10.6	1238.687027	0.016821	KEETQPPVALK
10.5	1238.705658	-0.001810	QLEQVIAK
6.1	1238.698273	0.005575	GHVTQLKESLK
6.1	1238.698257	0.005591	IHADASSKVLAK
5.7	1238.716904	-0.013056	DRVQVAIK
4.8	1238.702301	0.001547	DVFKKGFSIAK
3.4	1238.705658	-0.001810	QIAQEIVK
1.8	1238.691040	0.012808	LYKEFIDLAK
1.7	1238.716888	-0.013040	KRILCPLDPK

Mascot: http://www.matrixscience.com/

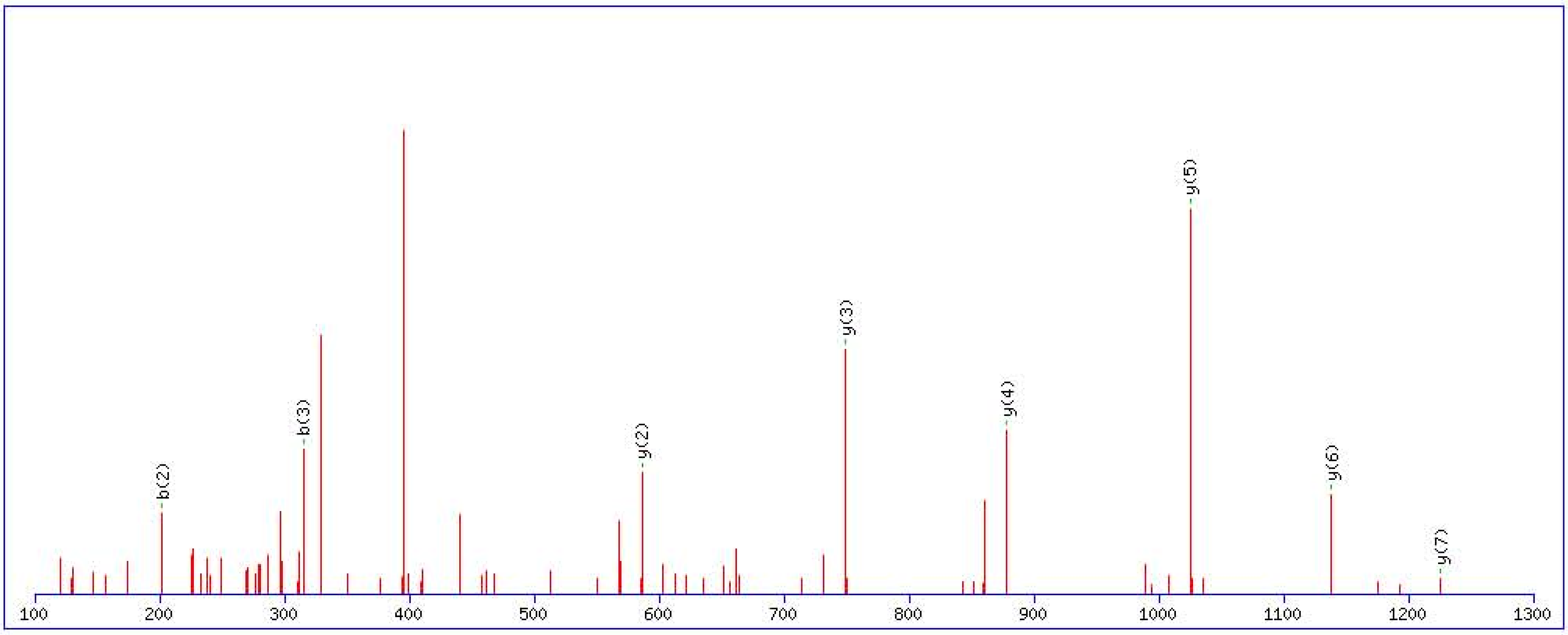
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NSLFEYQK**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

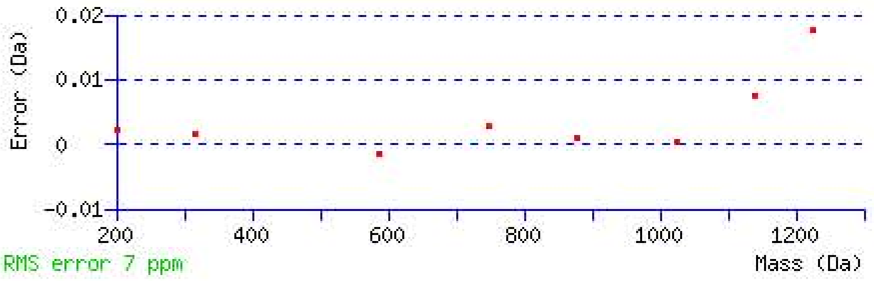
Match to Query 21083: 1338.664988 from(670.339770,2+) rtinseconds(2075) index(19449)
Title: Locus:1.1.1.3288.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

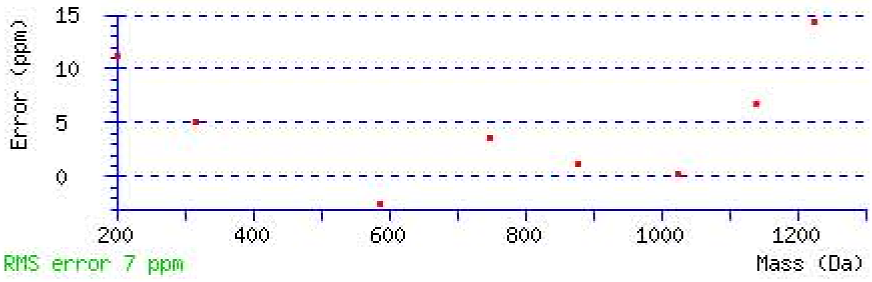
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1338.664185
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00046
Matches : 8/76 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	115.050203	58.028740	98.023654	49.515465			N							8
2	**202.082231**	101.544753	185.055682	93.031479	184.071666	92.539471	S	***1225.628558***	613.317917	1208.602009	604.804643	1207.617993	604.312635	7
3	**315.166295**	158.086785	298.139746	149.573511	297.155730	149.081503	L	***1138.596530***	569.801903	1121.569981	561.288629	1120.585965	560.796621	6
4	462.234709	231.620993	445.208160	223.107718	444.224144	222.615710	F	***1025.512466***	513.259871	1008.485917	504.746597	1007.501901	504.254589	5
5	591.277302	296.142289	574.250753	287.629015	573.266737	287.137007	E	***878.444052***	439.725664	861.417503	431.212390	860.433487	430.720382	4
6	754.340631	377.673954	737.314082	369.160679	736.330066	368.668671	Y	***749.401459***	375.204368	732.374910	366.691093			3
7	1193.565957	597.286617	1176.539408	588.773342	1175.555392	588.281334	Q	***586.338130***	293.672703	569.311581	285.159429			2
8							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of NSLFEYQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.6	1338.664185	0.000803	NSLFEYQK
14.8	1338.660172	0.004816	NSMFTAGKGVAEK
8.0	1338.660172	0.004816	BTVYLQMBSLR
3.4	1338.682632	-0.017644	NLSRMQSRFGK
3.1	1338.666672	-0.001684	ESIKDLADYASK
1.9	1338.644913	0.020075	NSVMSPSSSKSTK

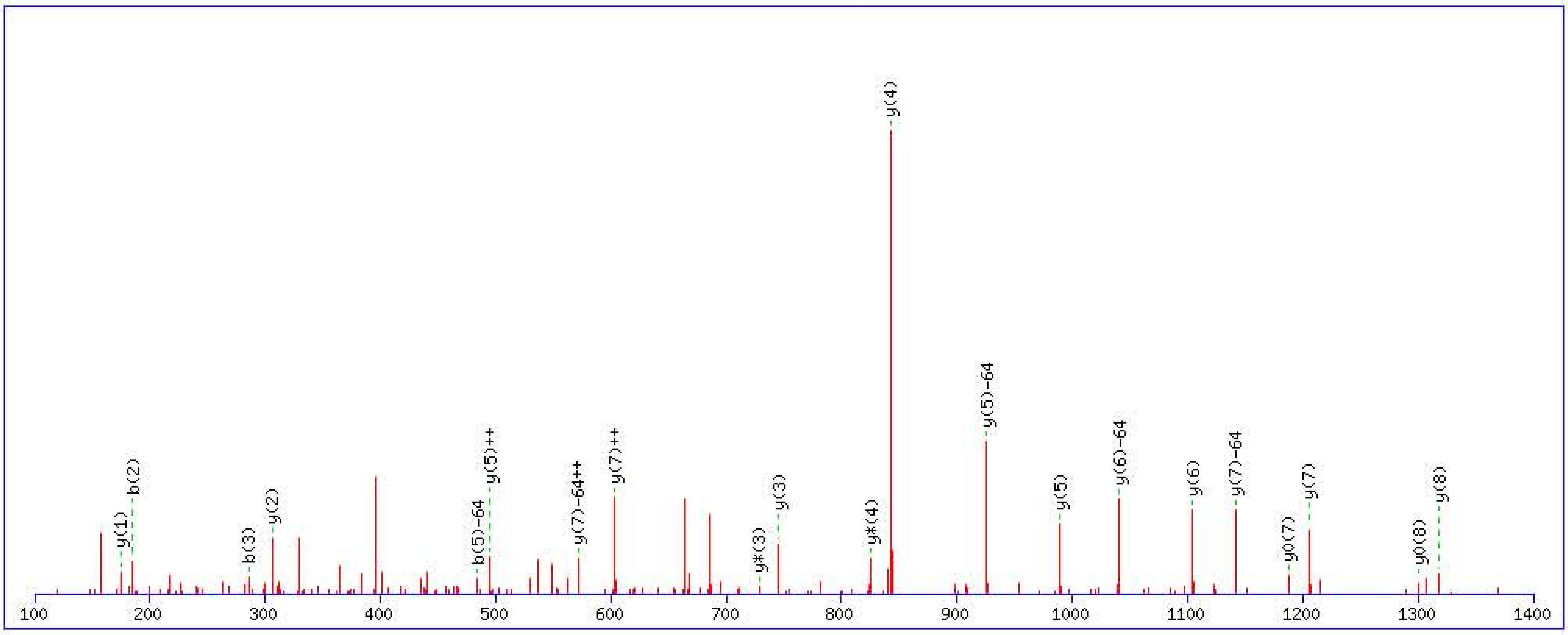
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALTDMPQMR**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

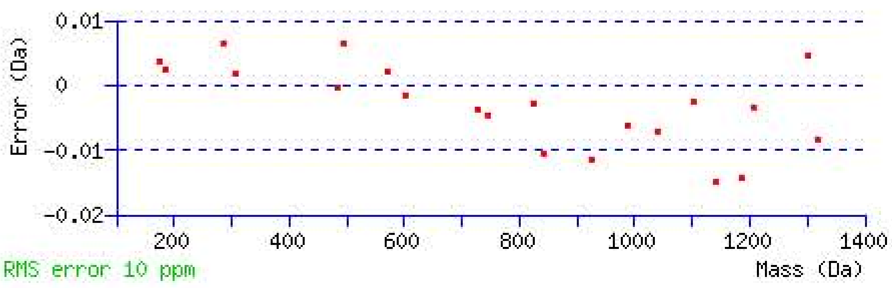
Match to Query 23135: 1388.651948 from(695.333250,2+) rtinseconds(1692) index(17044)
Title: Locus:1.1.1.3155.6 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

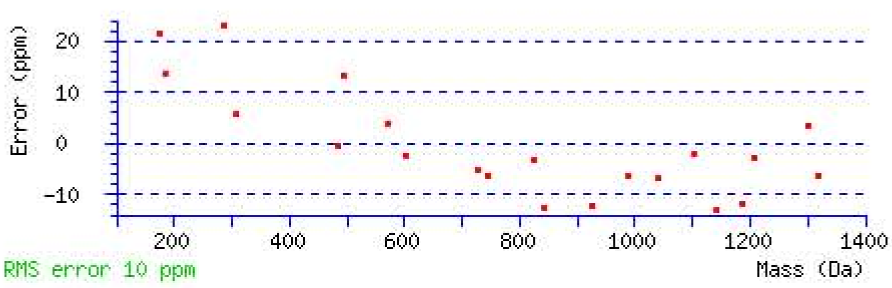
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 53 **Expect:** 2.3e-005
Matches : 21/112 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							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
53.3	1388.661438	-0.009490	ALTDMPQMR
18.8	1388.661438	-0.009490	ALTDMPQMR
3.8	1388.660568	-0.008620	SEMTASPLVGPER

Mascot: http://www.matrixscience.com/

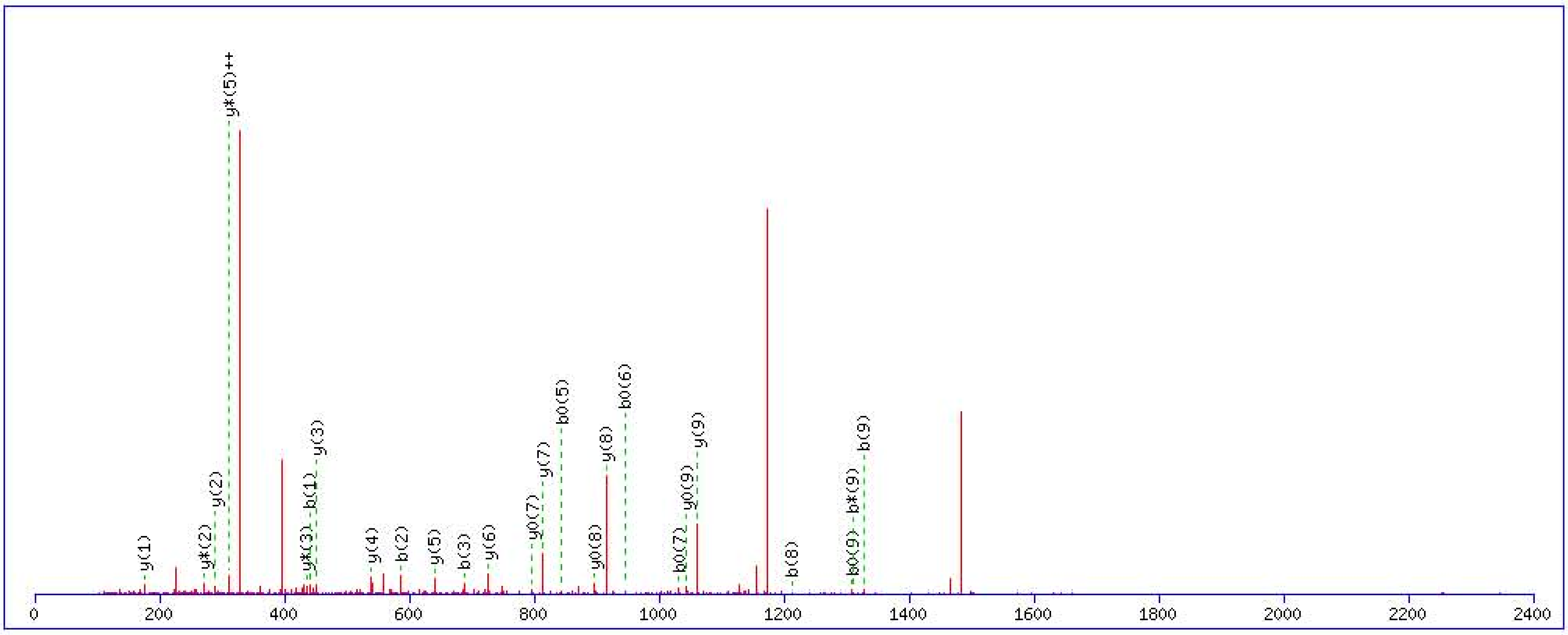
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QFTSSTSYNR**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

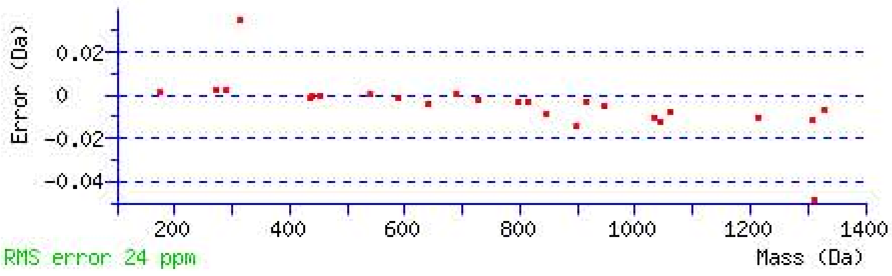
Match to Query 27122: 1500.695728 from(751.355140,2+) rtinseconds(1615) index(16623)
Title: Locus:1.1.1.3128.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

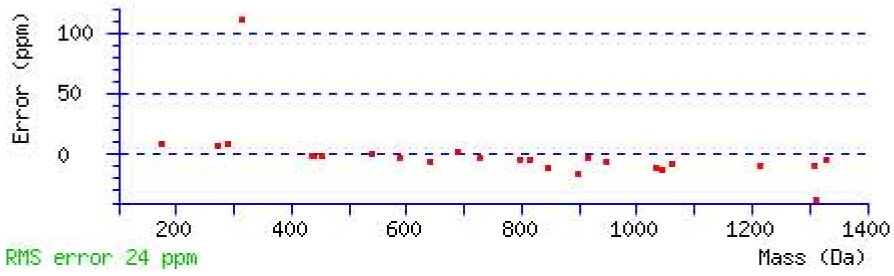
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1500.703110
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 45  Expect: 0.00015
Matches : 25/98 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	**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
44.6	1500.703110	-0.007382	QFTSSTSYNR
3.5	1500.699768	-0.004040	AEAGSGGPGFTFTFR
1.6	1500.703110	-0.007382	DAEGWETVQR
0.1	1500.714340	-0.018612	QCGKAFNLSSSFR

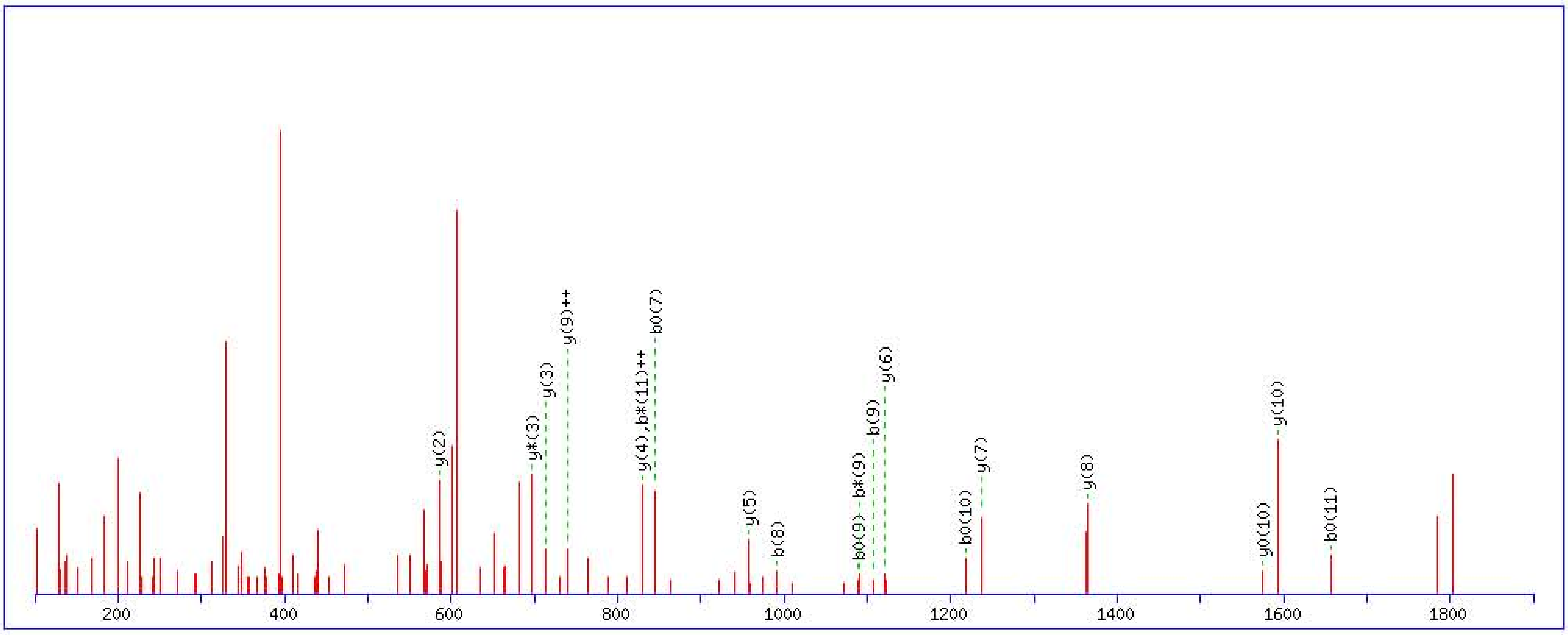
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVDLKDYEDQQK**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

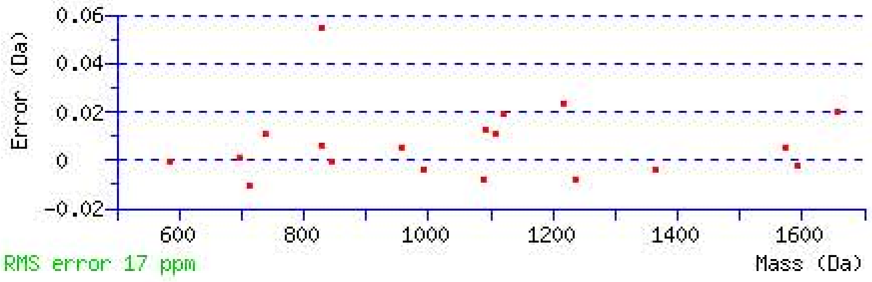
Match to Query 36166: 1819.868112 from(607.629980,3+) rtinseconds(1807) index(44805)
Title: Locus:1.1.1.3342.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

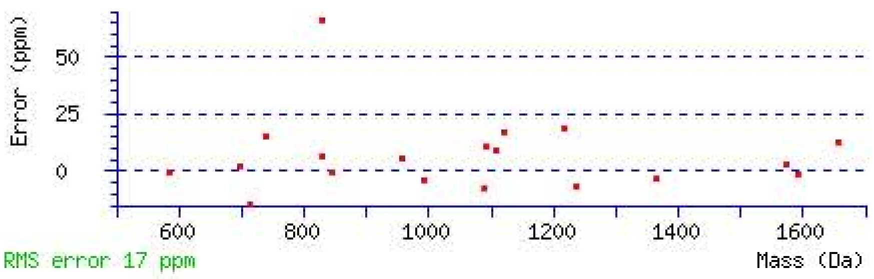
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1819.866196
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 45 **Expect:** 0.00054
Matches : 19/118 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	130.049869	65.528572			112.039304	56.523290	E							12
2	229.118283	115.062780			211.107718	106.057497	V	1691.830900	846.419088	1674.804351	837.905814	1673.820335	837.413806	11
3	344.145226	172.576251			326.134661	163.570969	D	***1592.762486***	796.884881	1575.735937	788.371607	1574.751921	787.879599	10
4	457.229290	229.118283			439.218725	220.113001	L	1477.735543	739.371410	1460.708994	730.858135	1459.724978	730.366127	9
5	585.324253	293.165765	568.297704	284.652490	567.313688	284.160482	K	***1364.651479***	682.829378	1347.624930	674.316103	1346.640914	673.824095	8
6	700.351196	350.679236	683.324647	342.165962	682.340631	341.673954	D	***1236.556516***	618.781896	1219.529967	610.268622	1218.545951	609.776614	7
7	863.414525	432.210901	846.387976	423.697626	845.403960	423.205618	Y	***1121.529573***	561.268425	1104.503024	552.755150	1103.519008	552.263142	6
8	**992.457118**	496.732197	975.430569	488.218923	974.446553	487.726915	E	***958.466244***	479.736760	941.439695	471.223486	940.455679	470.731478	5
9	**1107.484061**	554.245669	1090.457512	545.732394	1089.473496	545.240386	D	***829.423651***	415.215464	812.397102	406.702189	811.413086	406.210181	4
10	1235.542639	618.274958	1218.516090	609.761683	1217.532074	609.269675	Q	***714.396708***	357.701992	697.370159	349.188718			3
11	1674.767965	837.887621	1657.741416	829.374346	1656.757400	828.882338	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 EVDLKDYEDQQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.4	1819.866196	0.001916	EVDLKDYEDQQK
32.5	1819.866196	0.001916	EVDLKDYEDQQK

Mascot: http://www.matrixscience.com/

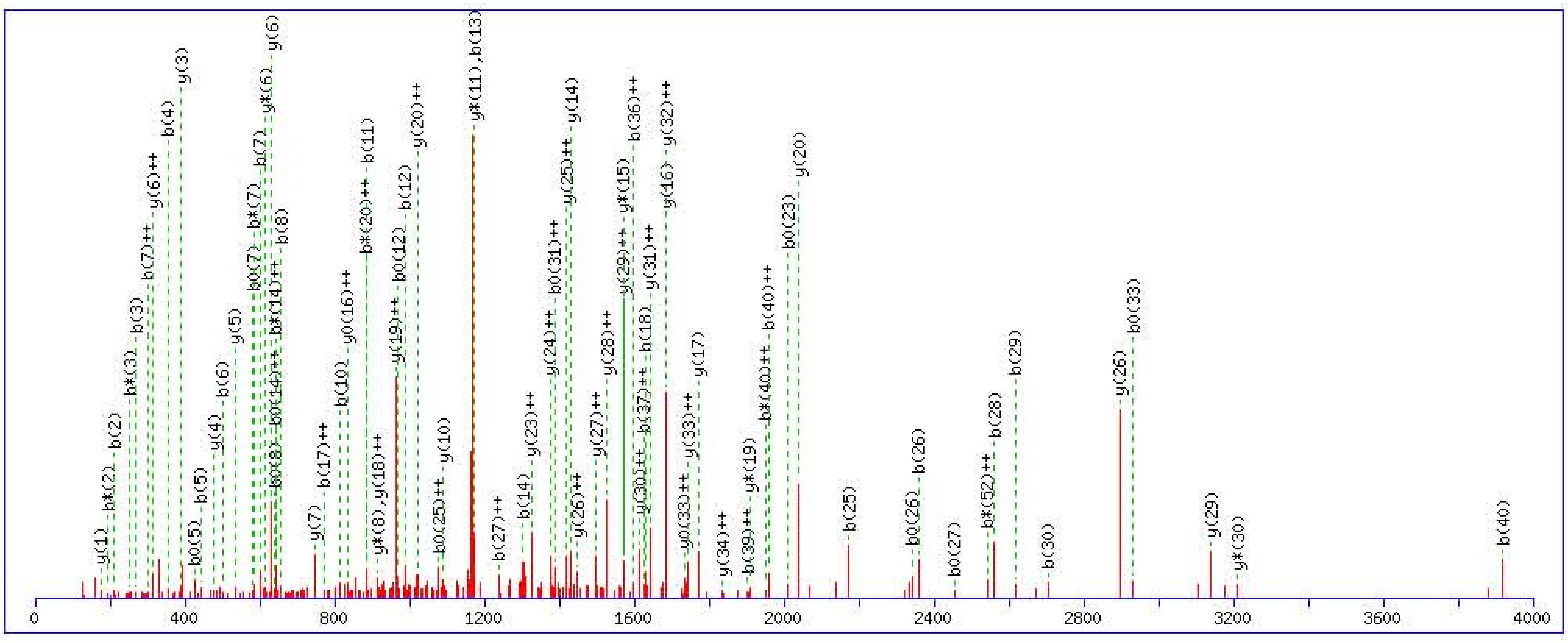
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPGSSGTGGTATWKPGSSGPGSTGSWNSGSSGTGSTGNQNPGSPRPGSTGTWNPGSSER**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

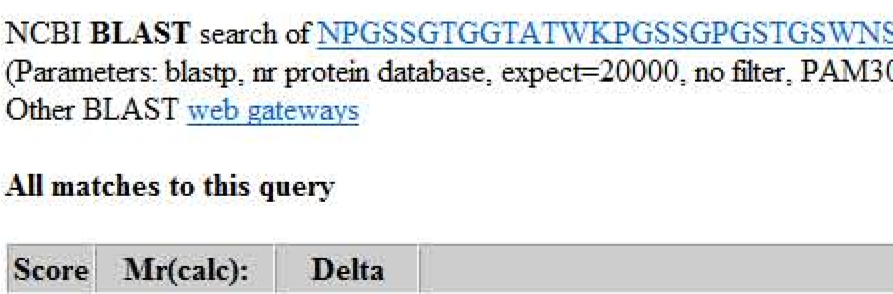
Match to Query 68465: 5844.571520 from(1169.921580,5+) rtinseconds(1797) index(17724)
Title: Locus:1.1.1.3191.22 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4000 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: 108 **Expect:** 4.3e-011
Matches : 81/688 fragment ions using 137 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
108.1	5844.608032	-0.036512	NPGSSGTGGTATWKPGSSGPGSTGSWNSGSSGTGSTGNQNPGSPRPGSTGTWNPGSSER

Mascot: http://www.matrixscience.com/

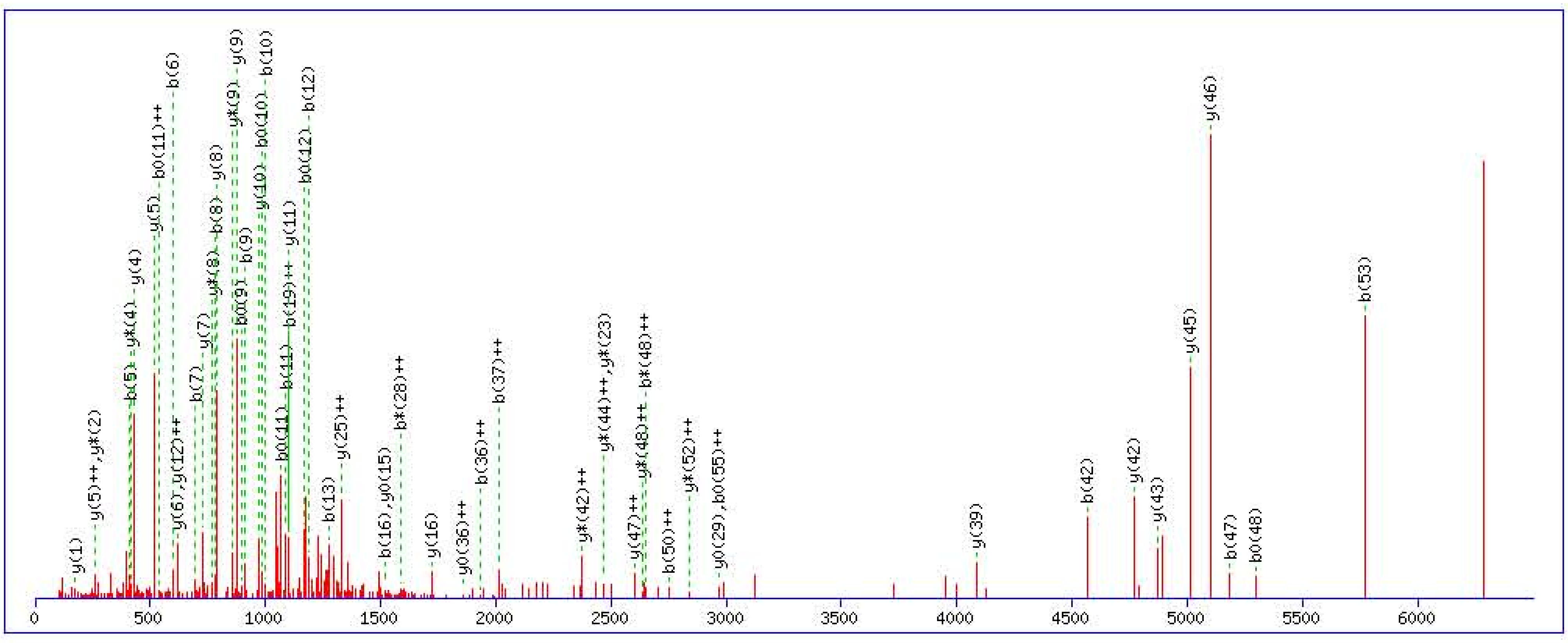
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSAGHWTSESSVSGSTGQWHSESGSFRPDSPGSGNARPNNPDWGTFEEVSGNVSPGTR**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

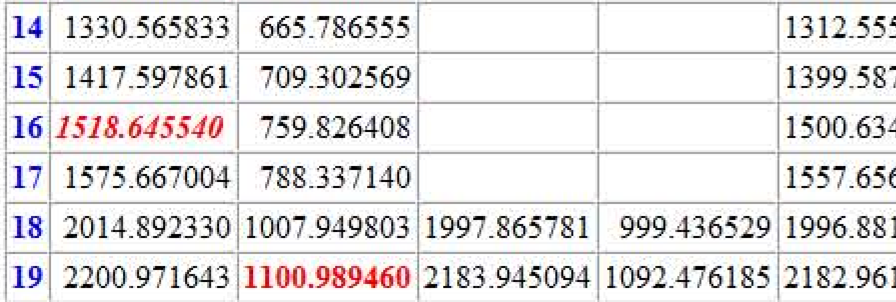
Match to Query 68664: 6284.791884 from(1048.472590,6+) rtinseconds(2071) index(32286)
Title: Locus:1.1.1.3384.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●



```
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: 49  Expect: 5e-005
Matches : 57/646 fragment ions using 117 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							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
49.0	6284.792847	-0.000963	GSAGHWTSESSVSGSTGQWHSESGSFRPDSPGSGNARPNNPDWGTFEEVSGNVSPGTR

Mascot: http://www.matrixscience.com/

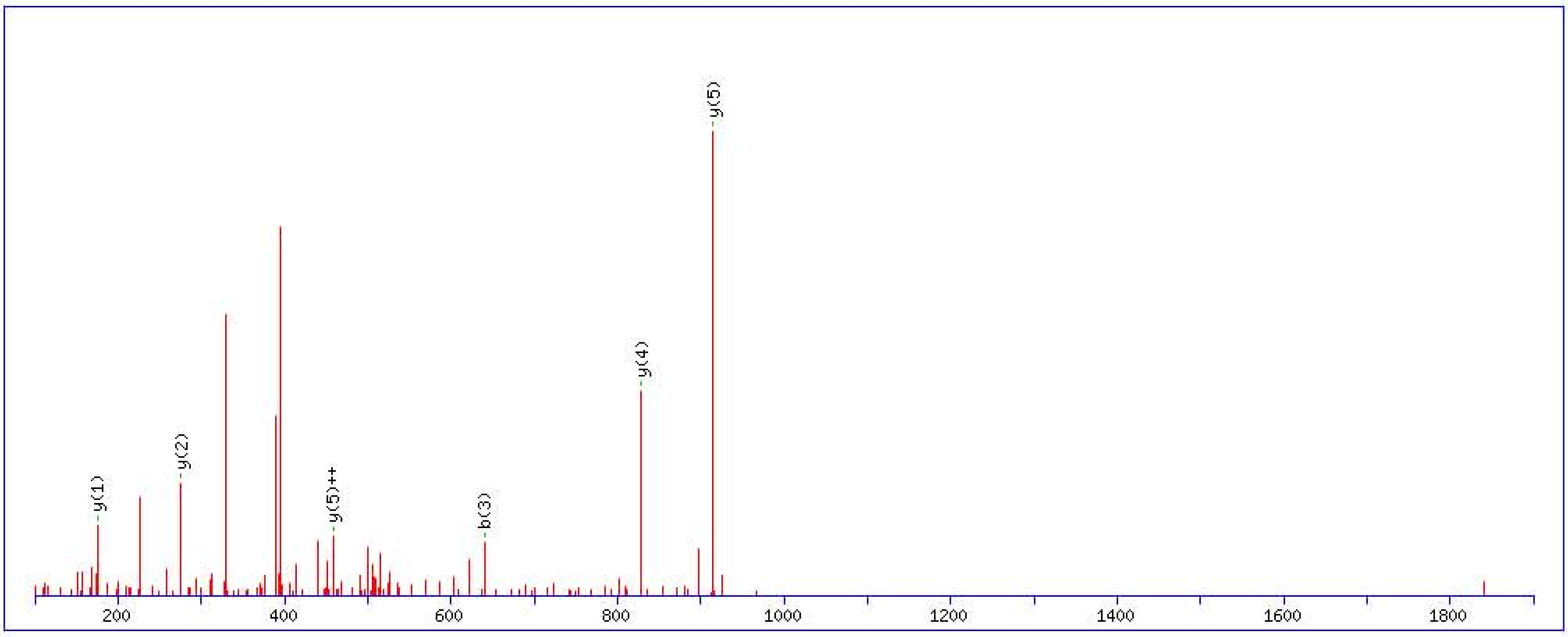
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISQLTR**
Found in **FIBB_HUMAN**, Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2

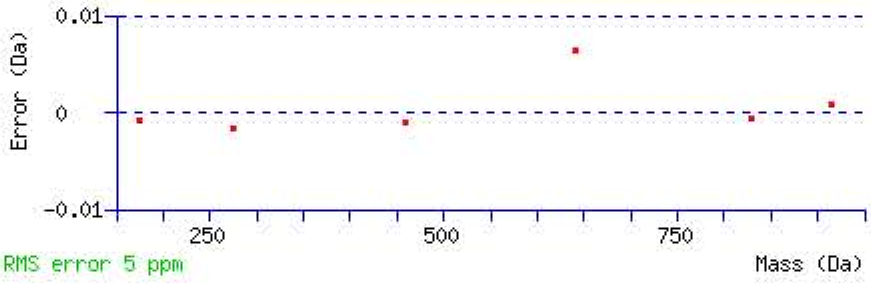
Match to Query 12329: 1027.581788 from(514.798170,2+) rtinseconds(1646) index(43843)
Title: Locus:1.1.1.3286.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

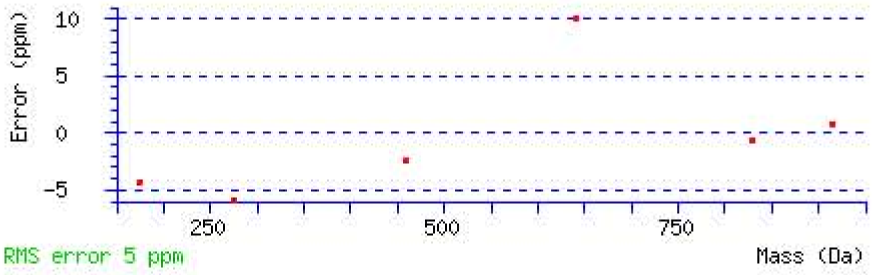
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1027.584824
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 26 **Expect:** 0.057
Matches : 6/52 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	114.091340	57.549308					I							6
2	201.123368	101.065322			183.112803	92.060039	S	***915.508049***	458.257663	898.481500	449.744388	897.497484	449.252380	5
3	**640.348694**	320.677985	623.322145	312.164711	622.338129	311.672703	Q	***828.476021***	414.741649	811.449472	406.228374	810.465456	405.736366	4
4	753.432758	377.220017	736.406209	368.706743	735.422193	368.214735	L	389.250695	195.128986	372.224146	186.615711	371.240130	186.123703	3
5	854.480437	427.743857	837.453888	419.230582	836.469872	418.738574	T	***276.166631***	138.586954	259.140082	130.073679	258.156066	129.581671	2
6							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of ISQLTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.6	1027.584824	-0.003036	ISQLTR
13.7	1027.573578	0.008210	ISQLEK
12.1	1027.584824	-0.003036	ILSQTR
10.7	1027.584839	-0.003051	LQTVTR
10.7	1027.592682	-0.010894	LRLSWPTR
9.2	1027.592667	-0.010879	IIYQAHKR
9.1	1027.584839	-0.003051	VTQLTR
8.9	1027.573578	0.008210	ILQVPAMEK
7.2	1027.584839	-0.003051	VTQTLR
6.1	1027.584839	-0.003051	TVLQTR

Mascot: http://www.matrixscience.com/

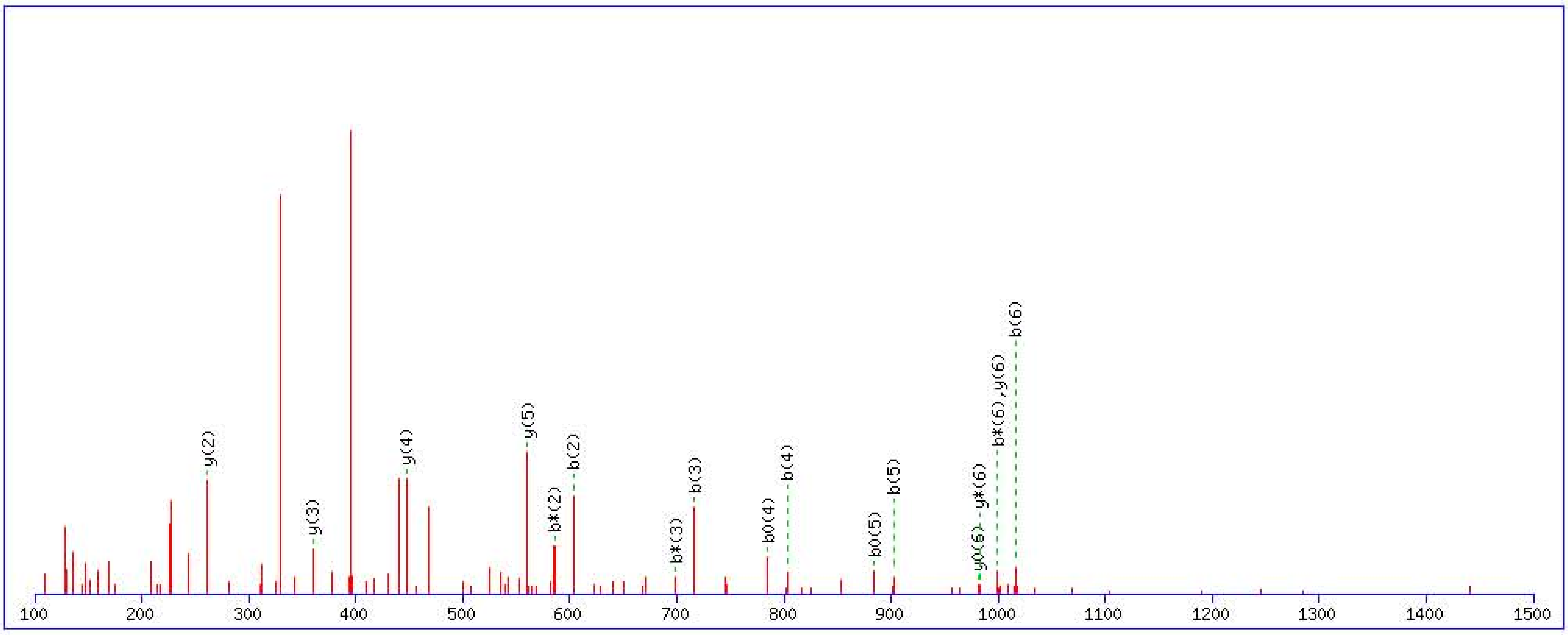
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YQISVNK**
Found in **FIBB_HUMAN**, Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2

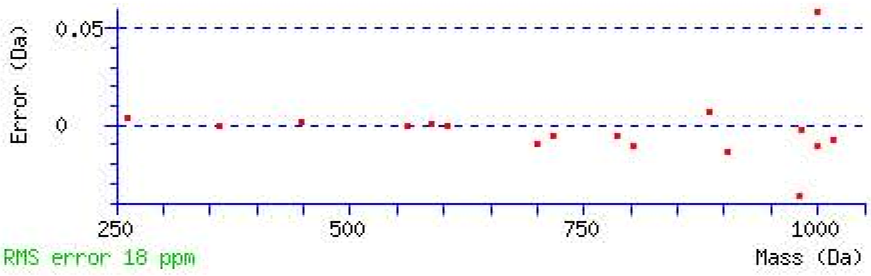
Match to Query 16590: 1161.617408 from(581.815980,2+) rtinseconds(1709) index(17168)
Title: Locus:1.1.1.3161.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

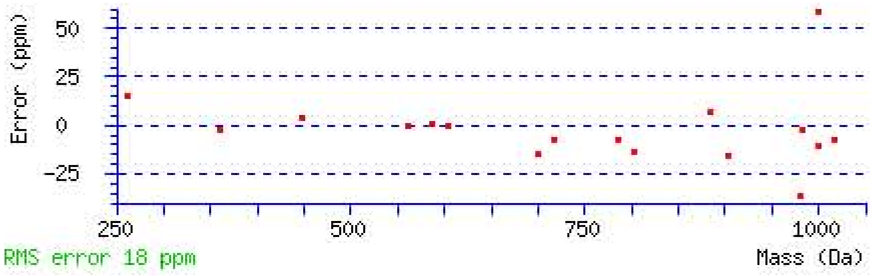
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1161.621597
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 25  Expect: 0.059
Matches : 17/58 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	164.070605	82.538940					Y							7
2	***603.295931***	302.151604	586.269382	293.638329			Q	***999.565563***	500.286419	982.539014	491.773145	981.554998	491.281137	6
3	***716.379995***	358.693636	699.353446	350.180361			I	***560.340237***	280.673756	543.313688	272.160482	542.329672	271.668474	5
4	***803.412023***	402.209650	786.385474	393.696375	785.401458	393.204367	S	***447.256173***	224.131724	430.229624	215.618450	429.245608	215.126442	4
5	***902.480437***	451.743857	885.453888	443.230582	884.469872	442.738574	V	***360.224145***	180.615710	343.197596	172.102436			3
6	***1016.523364***	508.765320	999.496815	500.252046	998.512799	499.760038	N	***261.155731***	131.081503	244.129182	122.568229			2
7							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of YQISVNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.1	1161.621597	-0.004189	YQISVNK
22.7	1161.629456	-0.012048	DFALRLWNK
3.8	1161.611694	0.005714	WMIRNWIK
2.4	1161.606323	0.011085	EQAIAMLKDK
2.0	1161.628128	-0.010720	LESLDIPFTK
0.9	1161.602982	0.014426	KNSVDPDFLK
0.4	1161.614197	0.003211	YDISVKPANR

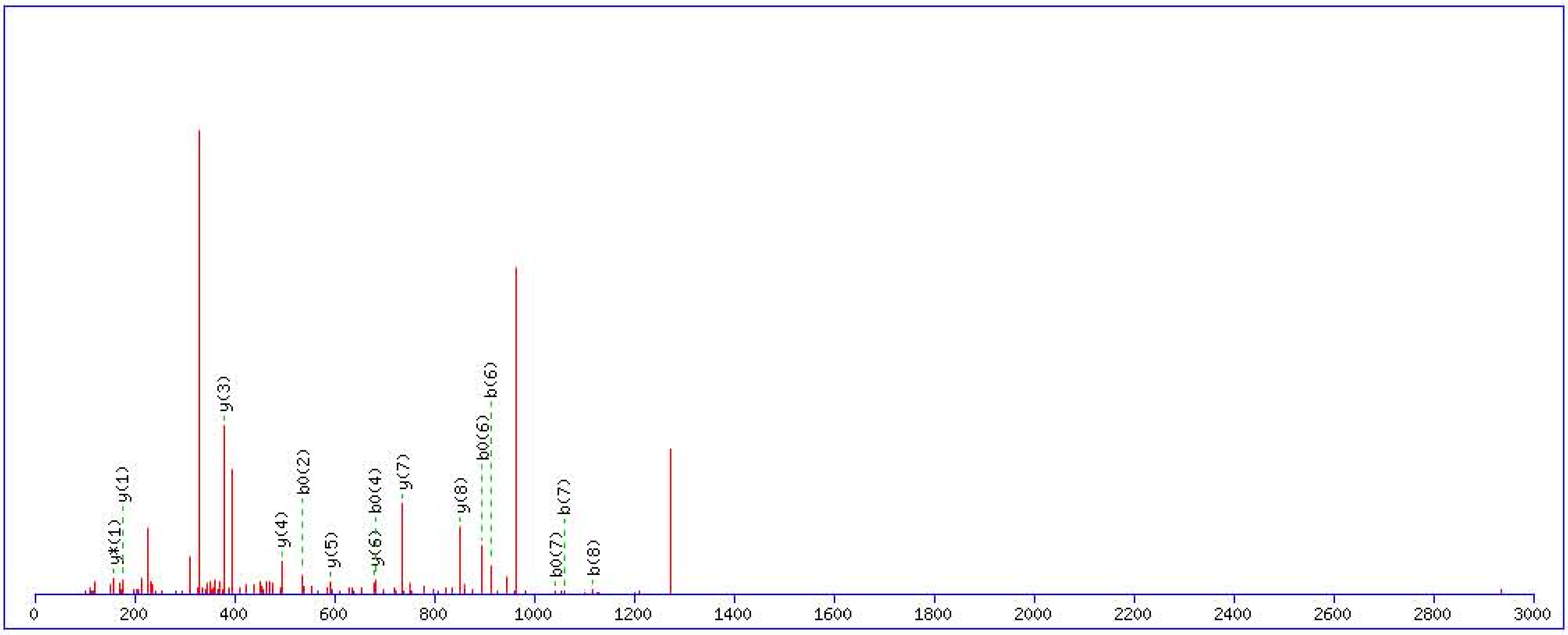
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QDGSVDFGR**
Found in **FIBB_HUMAN**, Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2

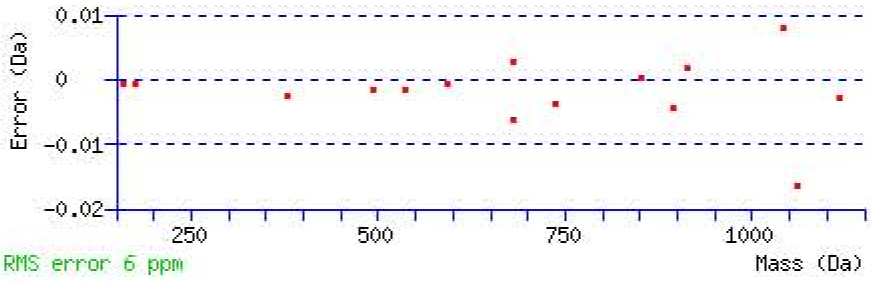
Match to Query 20193: 1290.607388 from(646.310970,2+) rtinseconds(1811) index(44828)
Title: Locus:1.1.1.3343.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

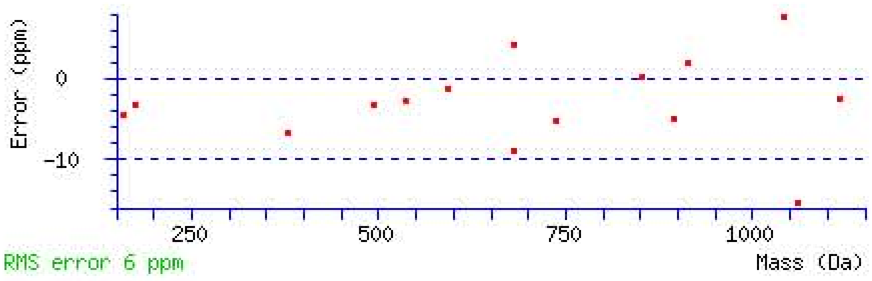
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1290.602692
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 48 **Expect:** 0.00022
Matches : 15/88 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	440.232602	220.619939	423.206053	212.106664			**Q**							9
2	555.259545	278.133411	538.232996	269.620136	537.248980	269.128128	**D**	***852.384622***	426.695949	835.358073	418.182674	834.374057	417.690666	8
3	612.281009	306.644143	595.254460	298.130868	594.270444	297.638860	**G**	***737.357679***	369.182477	720.331130	360.669203	719.347114	360.177195	7
4	699.313037	350.160157	682.286488	341.646882	681.302472	341.154874	**S**	***680.336215***	340.671745	663.309666	332.158471	662.325650	331.666463	6
5	798.381451	399.694364	781.354902	391.181089	780.370886	390.689081	**V**	***593.304187***	297.155731	576.277638	288.642457	575.293622	288.150449	5
6	**913.408394**	457.207835	896.381845	448.694560	895.397829	448.202552	**D**	***494.235773***	247.621524	477.209224	239.108250	476.225208	238.616242	4
7	**1060.476808**	530.742042	1043.450259	522.228768	1042.466243	521.736759	**F**	***379.208830***	190.108053	362.182281	181.594778			3
8	**1117.498272**	559.252774	1100.471723	550.739499	1099.487707	550.247491	**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 QDGSVDFGR
(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	1290.602692	0.004696	QDGSVDFGR

Mascot: http://www.matrixscience.com/

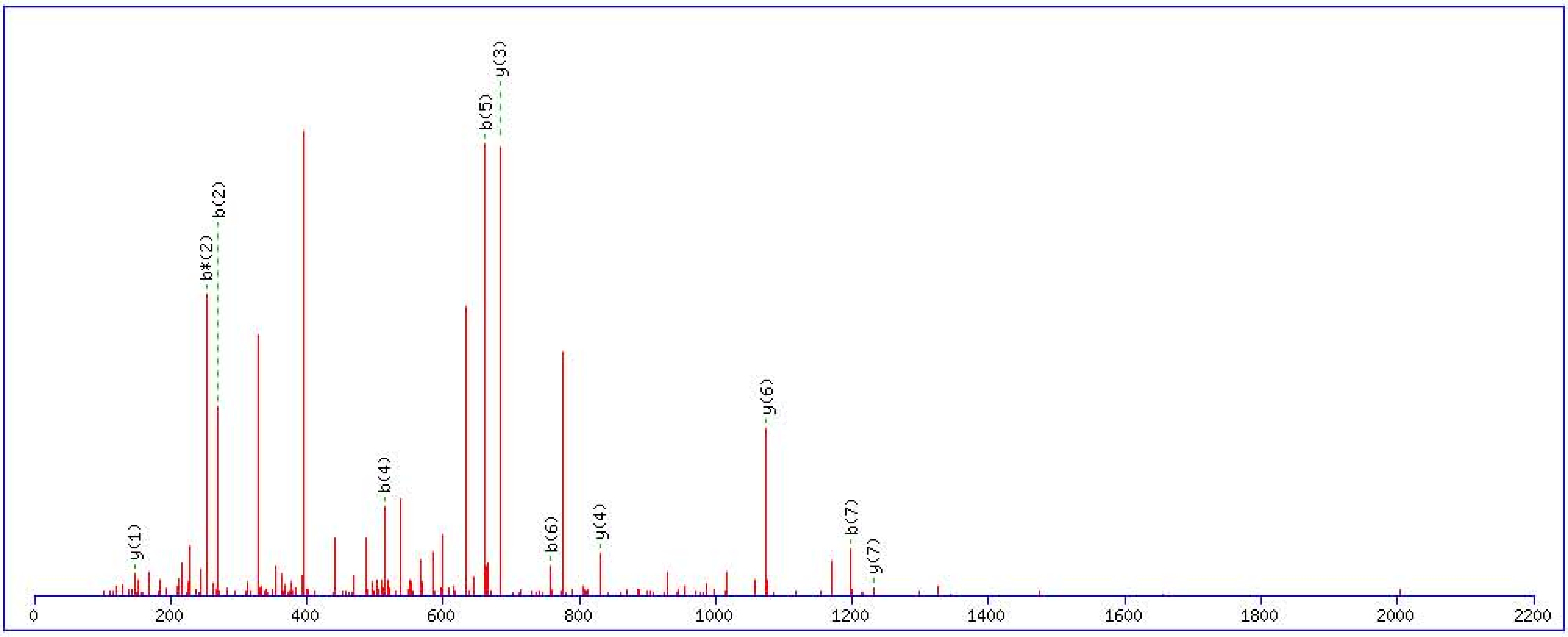
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IRPFFPQQ**
Found in **FIBB_HUMAN**, Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2

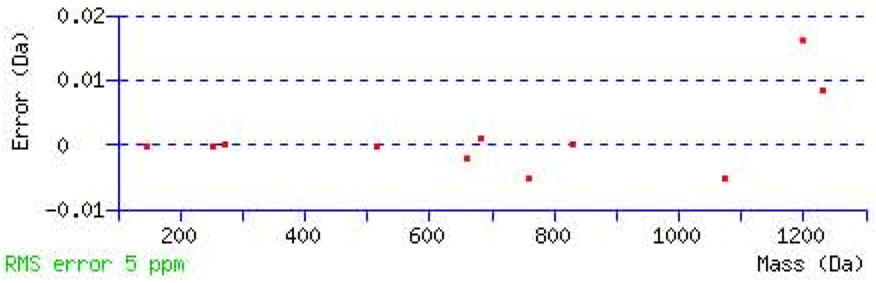
Match to Query 21183: 1342.721888 from(672.368220,2+) rtinseconds(2303) index(47856)
Title: Locus:1.1.1.3514.6 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

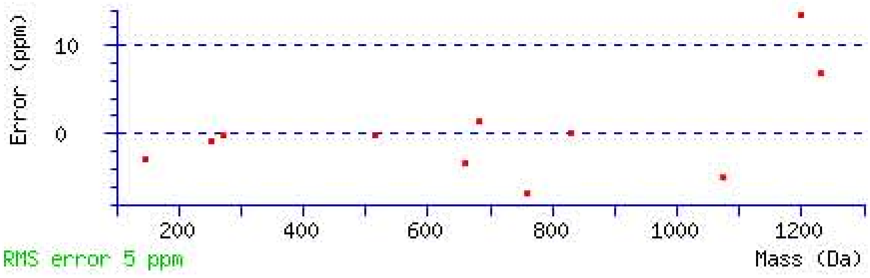
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1342.722000
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 25 **Expect:** 0.033
Matches : 11/54 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	114.091340	57.549308			I					8
2	*270.192451*	135.599864	253.165902	127.086589	R	*1230.645212*	615.826244	1213.618663	607.312970	7
3	367.245215	184.126245	350.218666	175.612971	P	*1074.544101*	537.775689	1057.517552	529.262414	6
4	*514.313629*	257.660453	497.287080	249.147178	F	977.491337	489.249307	960.464788	480.736032	5
5	*661.382043*	331.194660	644.355494	322.681385	F	*830.422923*	415.715100	813.396374	407.201825	4
6	*758.434807*	379.721042	741.408258	371.207767	P	*683.354509*	342.180893	666.327960	333.667618	3
7	*1197.660133*	599.333705	1180.633584	590.820430	Q	586.301745	293.654511	569.275196	285.141236	2
8					Q	*147.076419*	74.041848	130.049870	65.528573	1





NCBI **BLAST** search of IRPFFPQQ
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.1	1342.722000	-0.000112	IRPFFPQQ
15.2	1342.722000	-0.000112	IRPFFPQQ
8.9	1342.716629	0.005259	LLSVTEDQK
4.4	1342.710098	0.011790	VPMMSDPKAVLR
4.1	1342.727844	-0.005956	LALEQQQLICK
3.5	1342.727859	-0.005971	ATPTSTAKQK
1.9	1342.729187	-0.007299	QPHRPIER

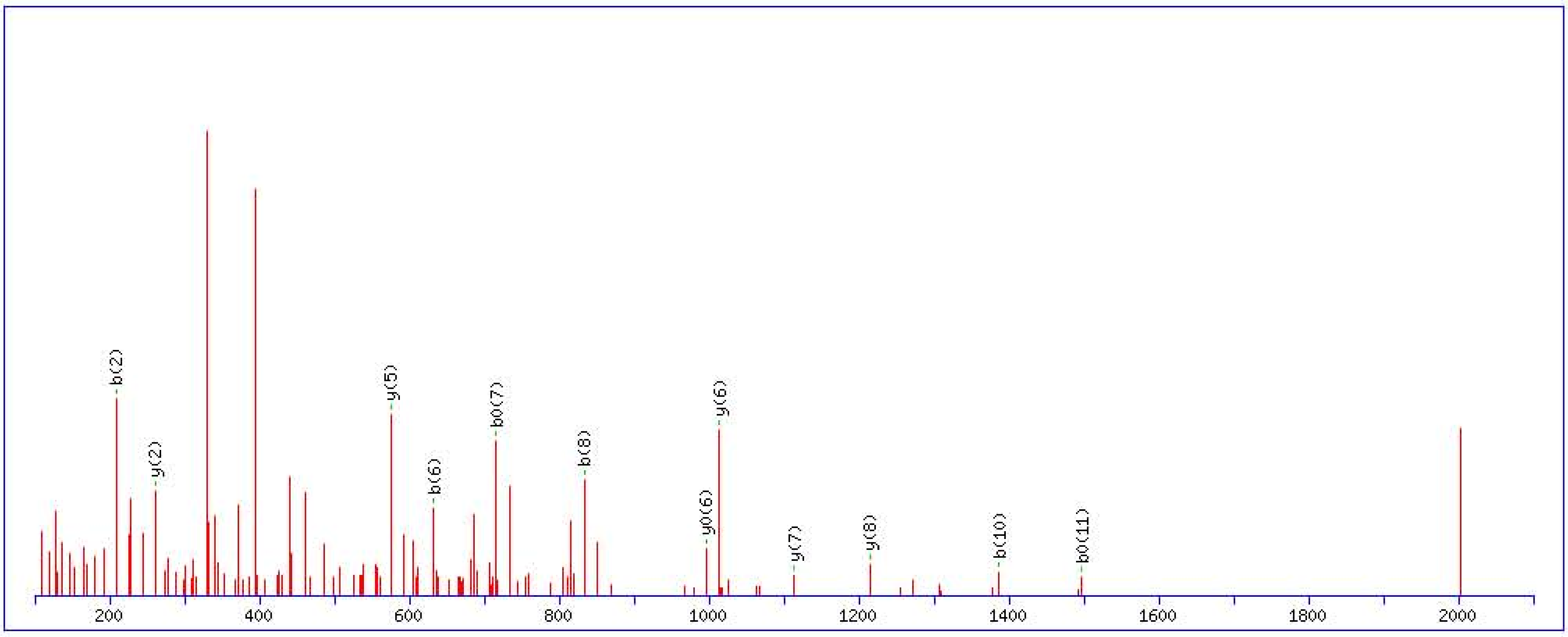
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AHYGGFTVQNEANK**
Found in **FIBB_HUMAN**, Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2

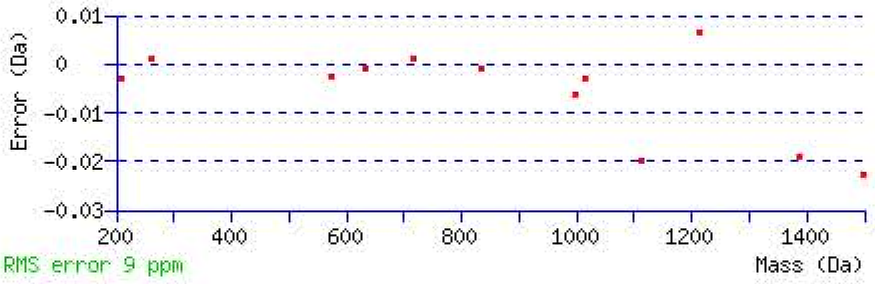
Match to Query 36541: 1845.880782 from(616.300870,3+) rtinseconds(1712) index(44196)
Title: Locus:1.1.1.3309.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

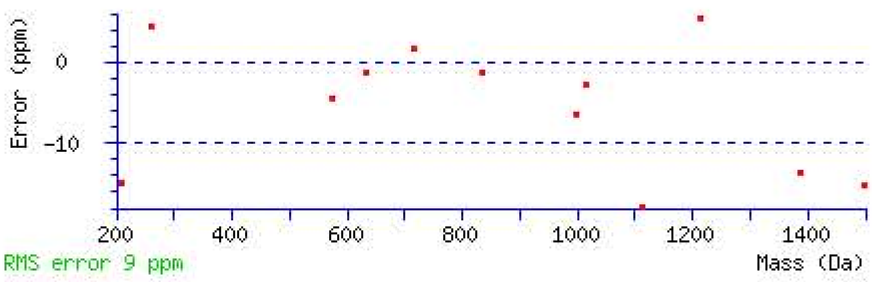
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1845.883194
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 40 **Expect:** 0.0019
Matches : 12/122 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	72.044390	36.525833					A							14
2	***209.103302***	105.055289					H	1775.853367	888.430321	1758.826818	879.917047	1757.842802	879.425039	13
3	372.166631	186.586953					Y	1638.794455	819.900866	1621.767906	811.387591	1620.783890	810.895583	12
4	429.188095	215.097685					G	1475.731126	738.369201	1458.704577	729.855927	1457.720561	729.363918	11
5	486.209559	243.608417					G	1418.709662	709.858469	1401.683113	701.345195	1400.699097	700.853186	10
6	***633.277973***	317.142625					F	1361.688198	681.347737	1344.661649	672.834463	1343.677633	672.342455	9
7	734.325652	367.666464			716.315087	358.661182	T	***1214.619784***	607.813530	1197.593235	599.300256	1196.609219	598.808247	8
8	***833.394066***	417.200671			815.383501	408.195388	V	***1113.572105***	557.289691	1096.545556	548.776416	1095.561540	548.284408	7
9	1272.619392	636.813334	1255.592843	628.300059	1254.608827	627.808051	Q	***1014.503691***	507.755484	997.477142	499.242209	996.493126	498.750201	6
10	***1386.662319***	693.834797	1369.635770	685.321523	1368.651754	684.829515	N	***575.278365***	288.142821	558.251816	279.629546	557.267800	279.137538	5
11	1515.704912	758.356094	1498.678363	749.842820	1497.694347	749.350811	E	461.235438	231.121357	444.208889	222.608083	443.224873	222.116075	4
12	1586.742026	793.874651	1569.715477	785.361377	1568.731461	784.869368	A	332.192845	166.600060	315.166296	158.086786			3
13	1700.784953	850.896114	1683.758404	842.382840	1682.774388	841.890832	N	***261.155731***	131.081503	244.129182	122.568229			2
14							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of AHYGGFTVQNEANK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.1	1845.883194	-0.002412	AHYGGFTVQNEANK

Mascot: http://www.matrixscience.com/

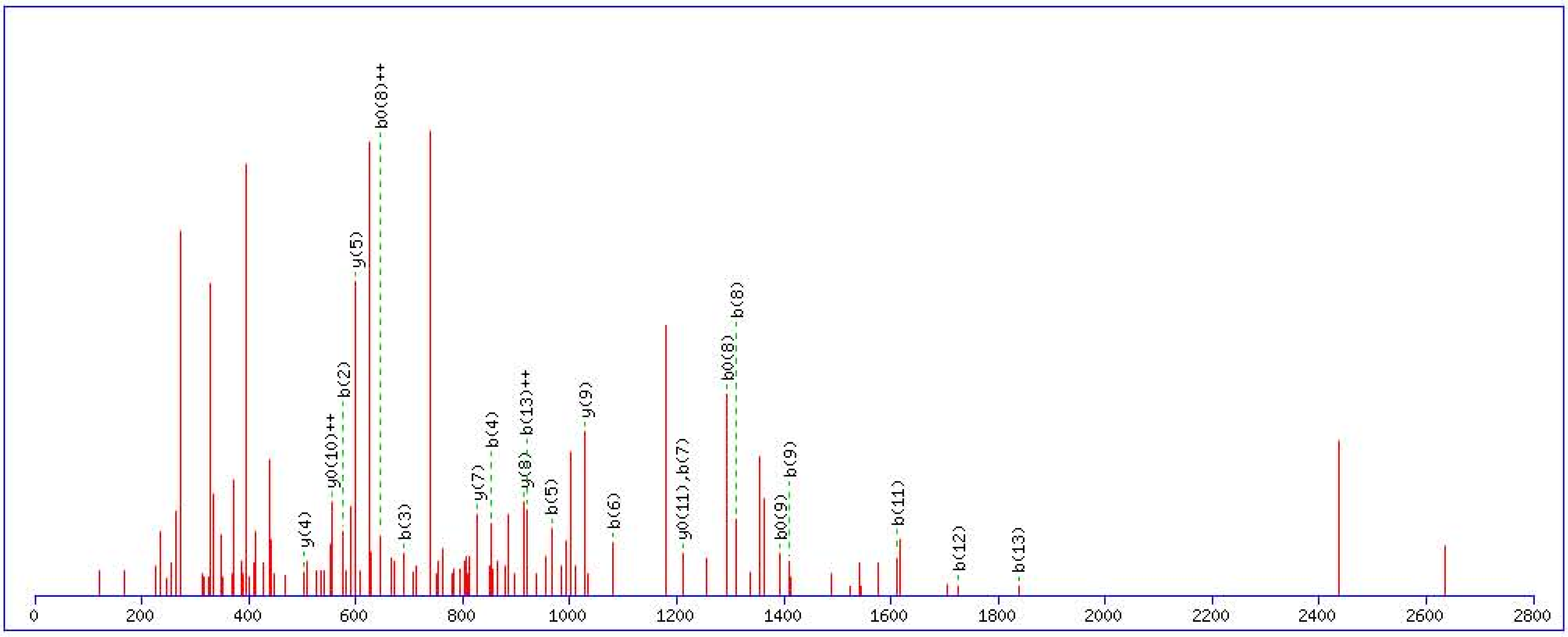
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQLYIDETVNSNIPTNLR**
Found in **FIBB_HUMAN**, Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2

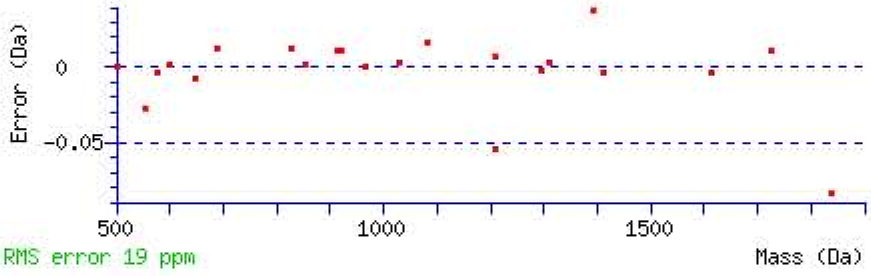
Match to Query 47071: 2437.244052 from(813.421960,3+) rtinseconds(2189) index(47197)
Title: Locus:1.1.1.3474.21 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

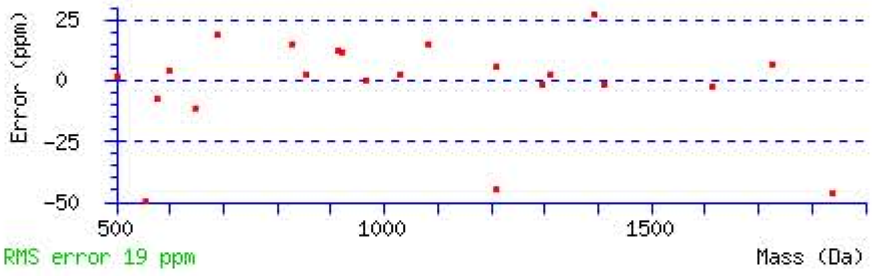
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2437.242355
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 32 **Expect:** 0.02
Matches : 22/186 fragment ions using 66 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
31.5	2437.242355	0.001697	HQLYIDETVNSNIPTNLR

Mascot: http://www.matrixscience.com/

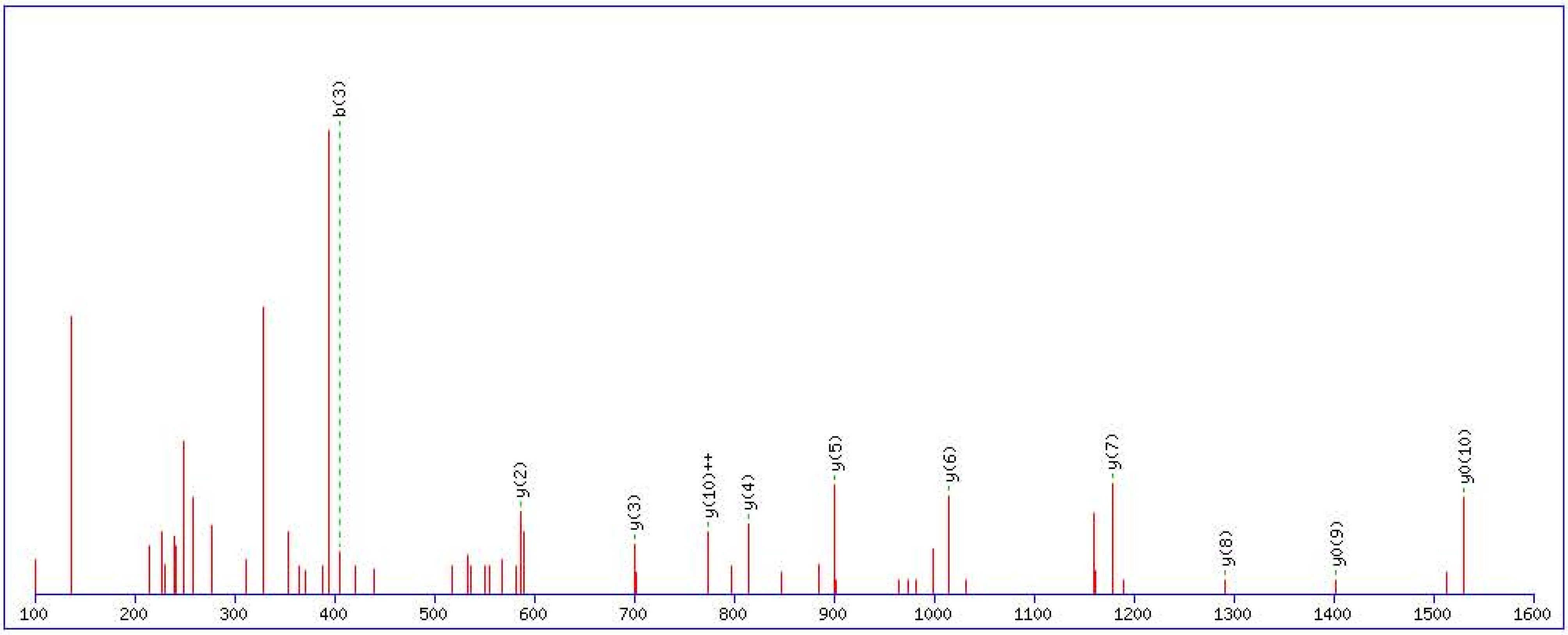
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLQEIYNSNNQK**
Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

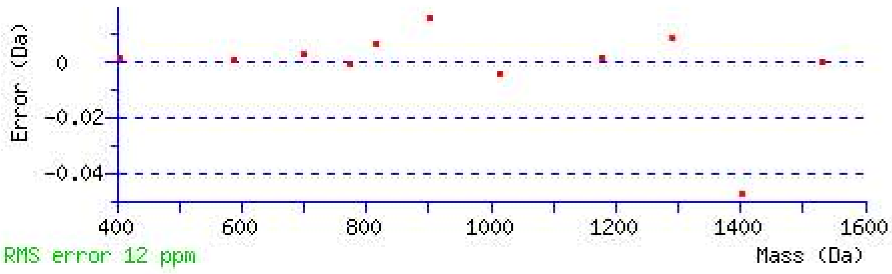
Match to Query 36218: 1823.890962 from(608.970930,3+) rtinseconds(1875) index(45163)
Title: Locus:1.1.1.3366.6 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

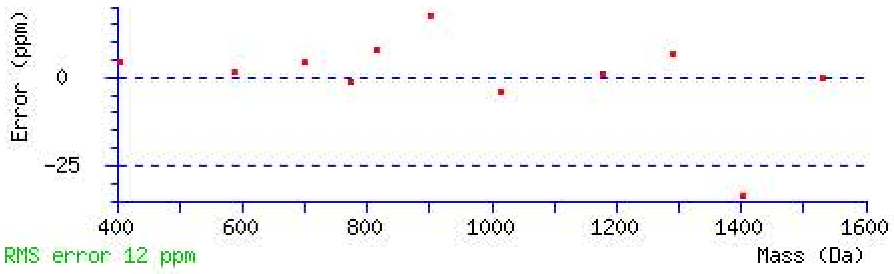
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 51 **Expect:** 0.00018
Matches : 11/114 fragment ions using 14 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
50.8	1823.887573	0.003389	YLQEIYNSNNQK

Mascot: http://www.matrixscience.com/

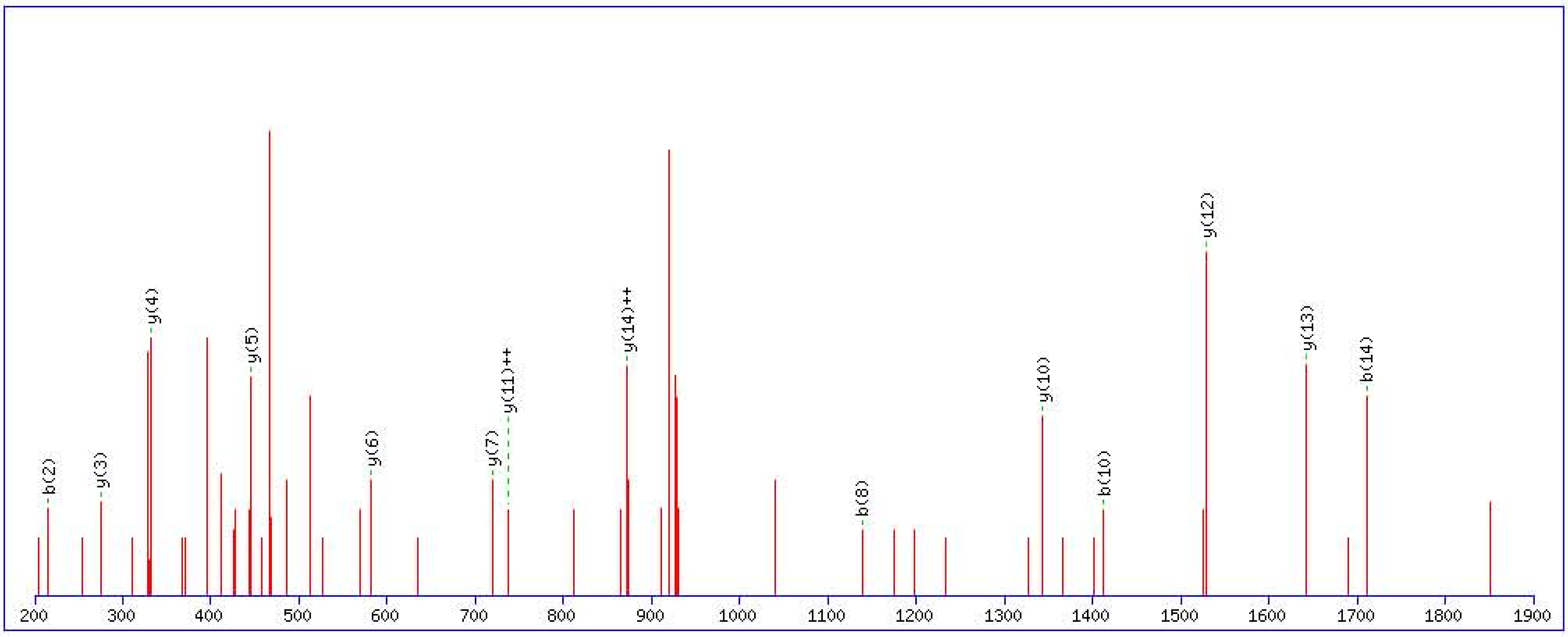
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTIGEGQQHHLGGAK**
Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

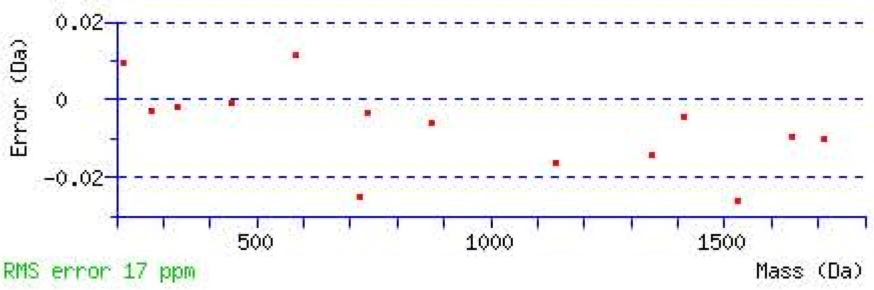
Match to Query 36849: 1855.960428 from(928.987490,2+) rtinseconds(1562) index(16251)
Title: Locus:1.1.1.3109.24 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

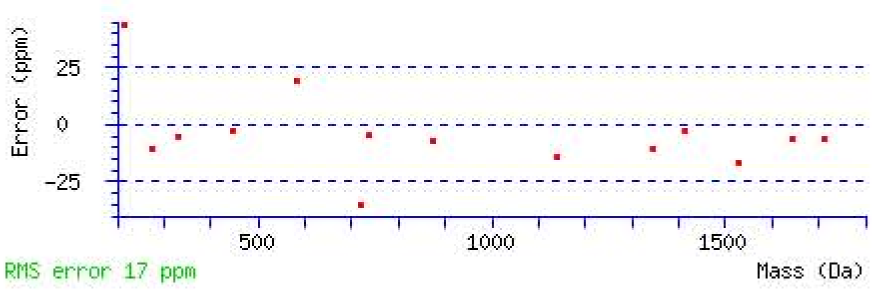
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 44  Expect: 0.00011
Matches : 14/134 fragment ions using 28 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	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
43.8	1855.972687	-0.012259	LTIGEGQQHHLGGAK
43.8	1855.972687	-0.012259	LTIGEGQQHHLGGAK
1.4	1855.935806	0.024622	DSEIMQQKQK

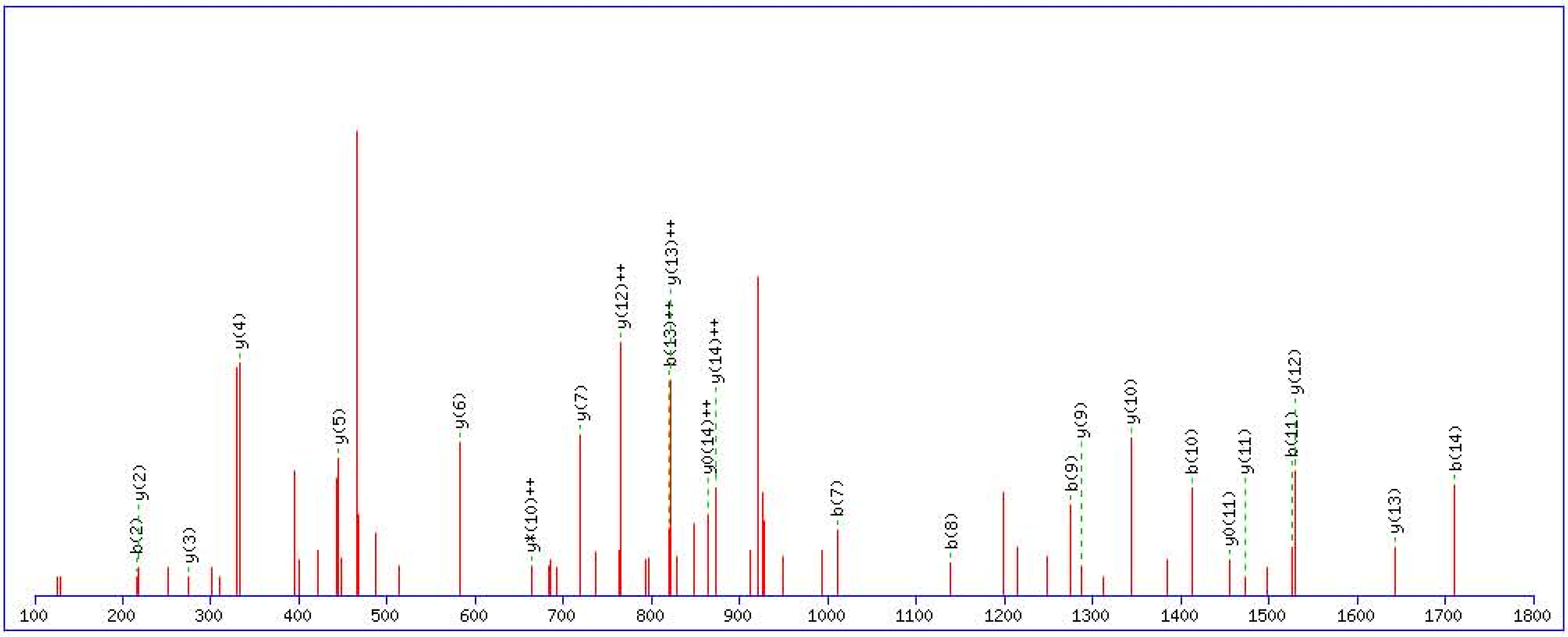
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTIGEGQQHHLGGAK**
Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

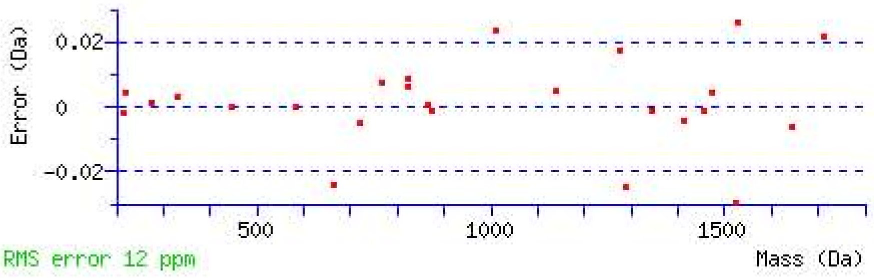
Match to Query 36854: 1855.966708 from(928.990630,2+) rtinseconds(1588) index(2526)
Title: Locus:1.1.1.3072.21 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

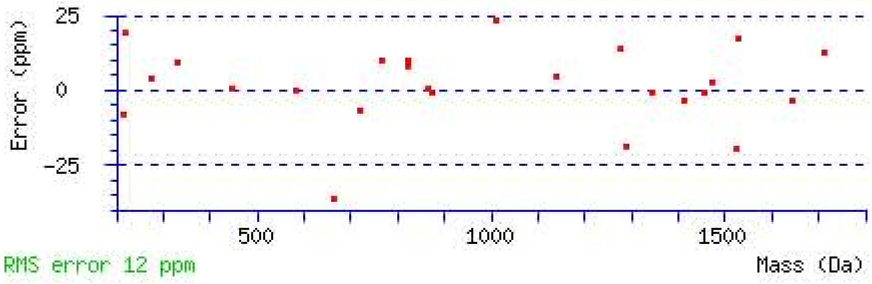
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1855.972687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 75  Expect: 2e-007
Matches : 25/134 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					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
75.1	1855.972687	-0.005979	LTIGEGQQHHLGGAK
73.1	1855.972687	-0.005979	LTIGEGQQHHLGGAK
3.7	1855.989944	-0.023236	MLSITPSQLENGKK

Mascot: http://www.matrixscience.com/

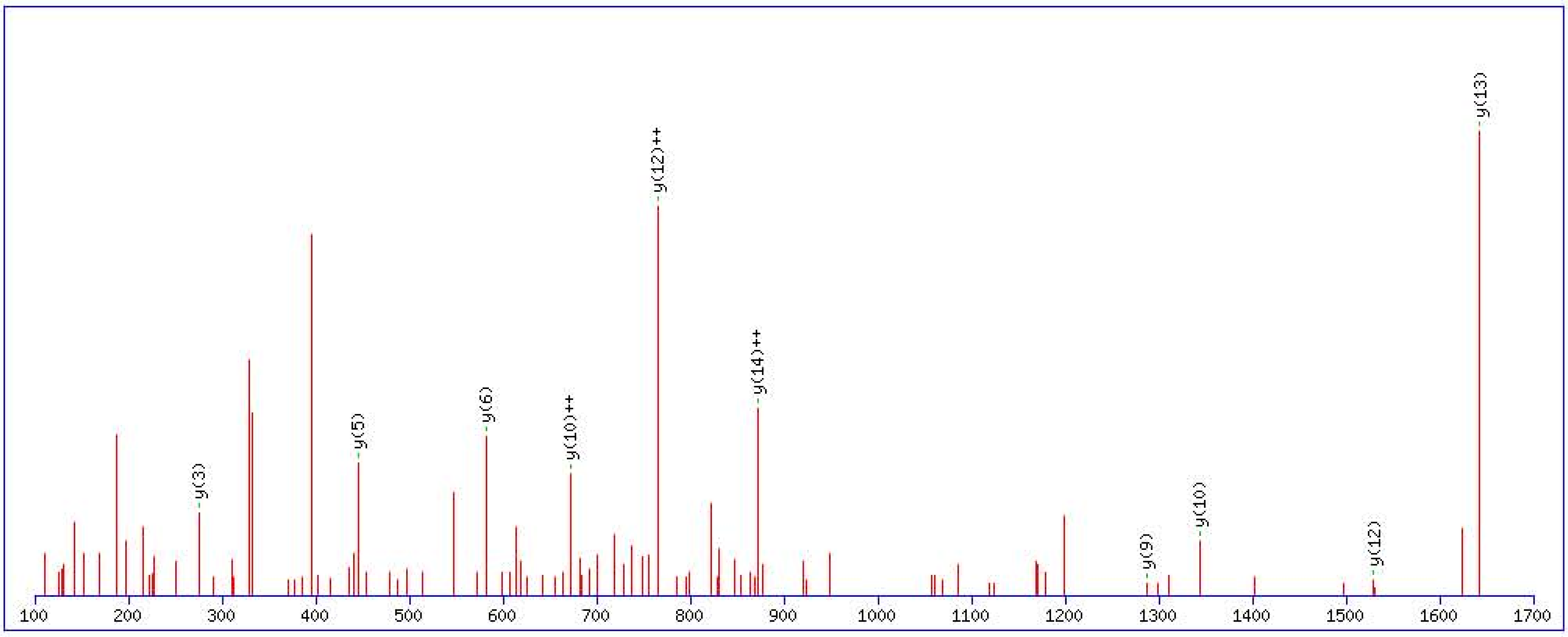
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTIGEGQQHHLGGAK**
Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

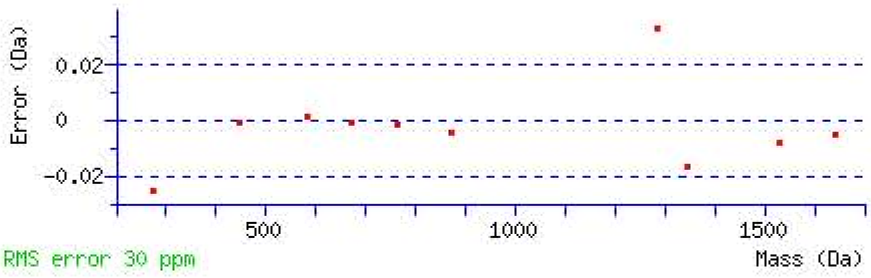
Match to Query 36855: 1855.967502 from(619.663110,3+) rtinseconds(1569) index(43298)
Title: Locus:1.1.1.3259.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

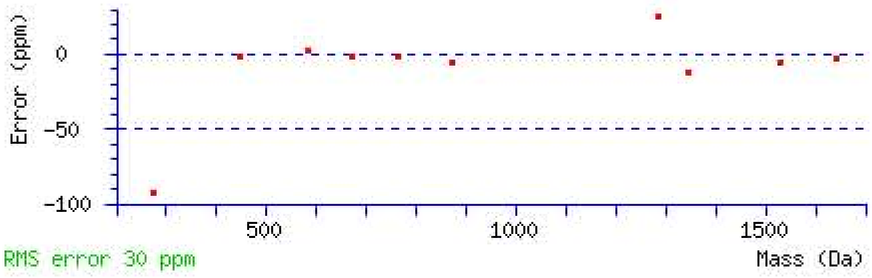
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 44  Expect: 0.00029
Matches : 10/134 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							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
43.6	1855.972687	-0.005185	LTIGEGQQHHLGGAK
43.6	1855.972687	-0.005185	LTIGEGQQHHLGGAK
5.9	1855.979202	-0.011700	ITIVENVGSVEGLAYHR

Mascot: http://www.matrixscience.com/

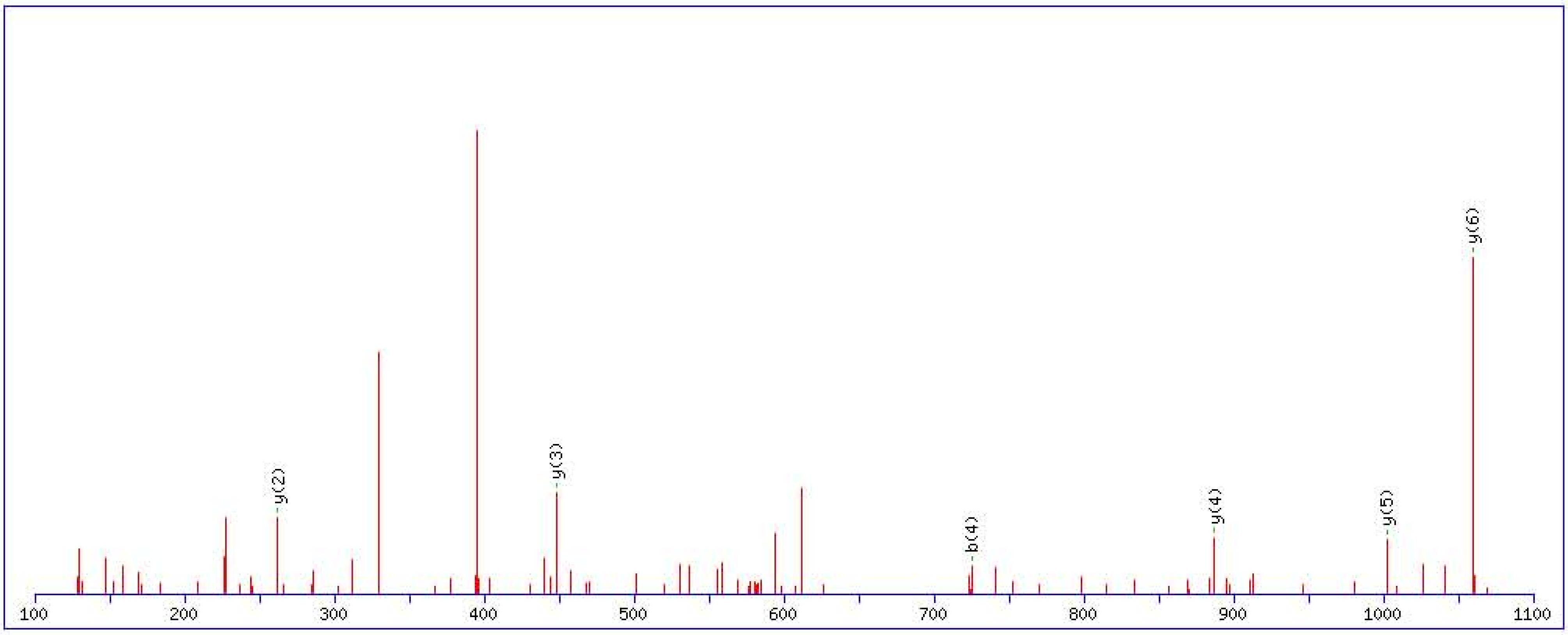
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGDQWDK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

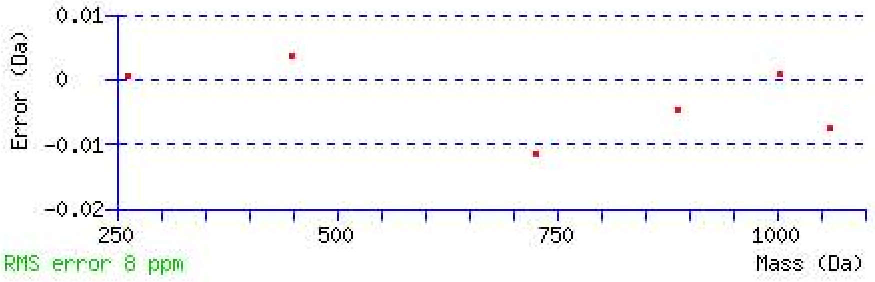
Match to Query 16908: 1171.565488 from(586.790020,2+) rtinseconds(1839) index(30820)
Title: Locus:1.1.1.3304.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

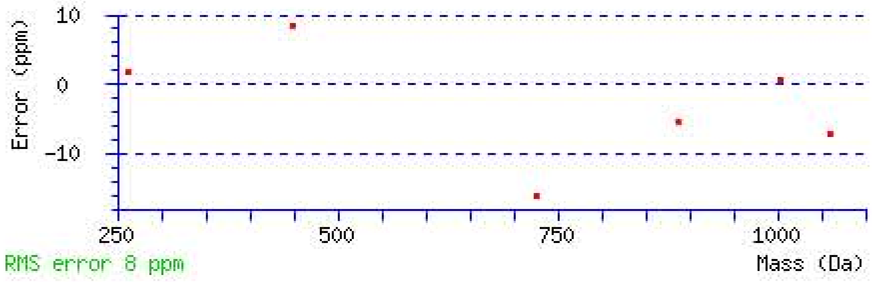
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1171.569580
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.0045
Matches : 6/60 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	114.091340	57.549308					I							7
2	171.112804	86.060040					G	***1059.492793***	530.250035	1042.466244	521.736760	1041.482228	521.244752	6
3	286.139747	143.573512			268.129182	134.568229	D	***1002.471329***	501.739303	985.444780	493.226028	984.460764	492.734020	5
4	**725.365073**	363.186175	708.338524	354.672900	707.354508	354.180892	Q	***887.444386***	444.225831	870.417837	435.712557	869.433821	435.220549	4
5	911.444386	456.225831	894.417837	447.712557	893.433821	447.220549	W	***448.219060***	224.613168	431.192511	216.099894	430.208495	215.607886	3
6	1026.471329	513.739303	1009.444780	505.226028	1008.460764	504.734020	D	***262.139747***	131.573512	245.113198	123.060237	244.129182	122.568229	2
7							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of IGDQWDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.2	1171.569580	-0.004092	IGDQWDK
5.8	1171.569565	-0.004077	LGPEWSQPMK
5.1	1171.572067	-0.006579	LGSGPDGAEEIK
3.5	1171.576096	-0.010608	LYFSDATLDK
2.9	1171.572037	-0.006549	ENPEVKAEEK
1.9	1171.554337	0.011151	ALCDTPGVDPK
0.1	1171.565536	-0.000048	MGSGEPNPAGKK

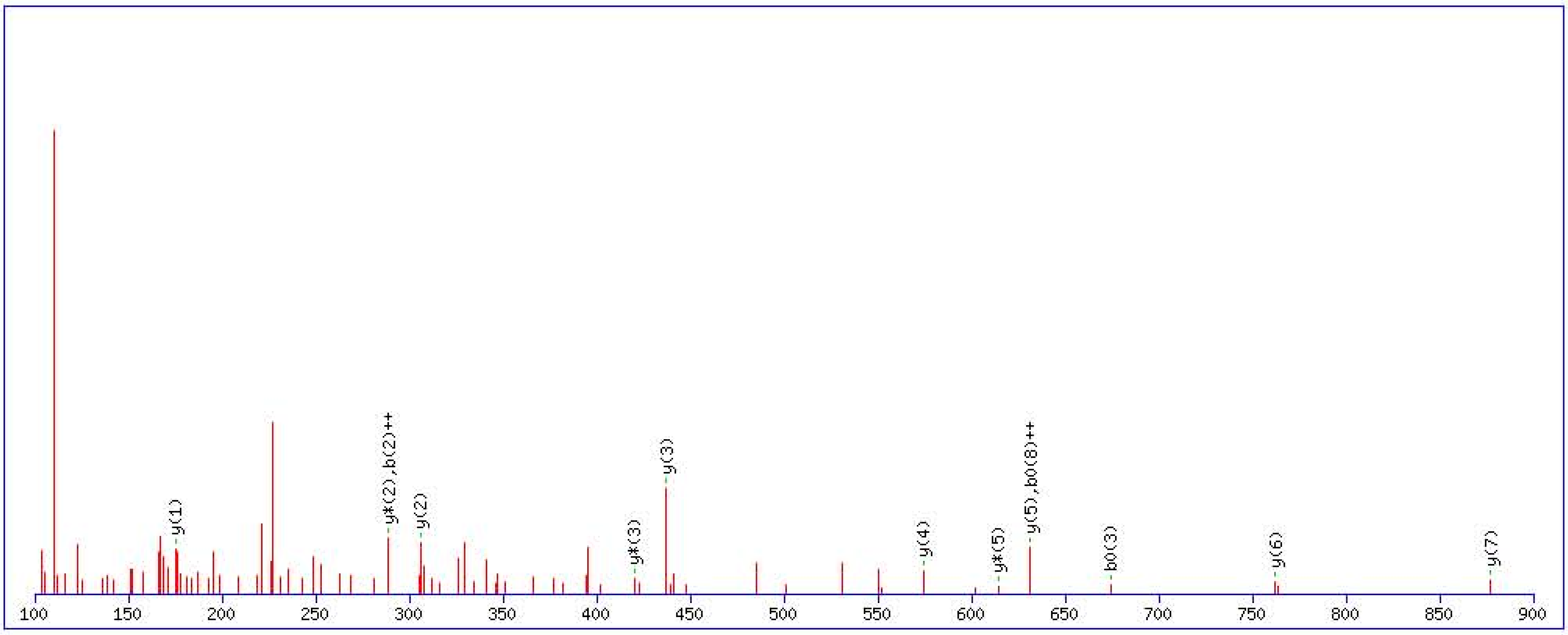
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QHDMGHMMR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

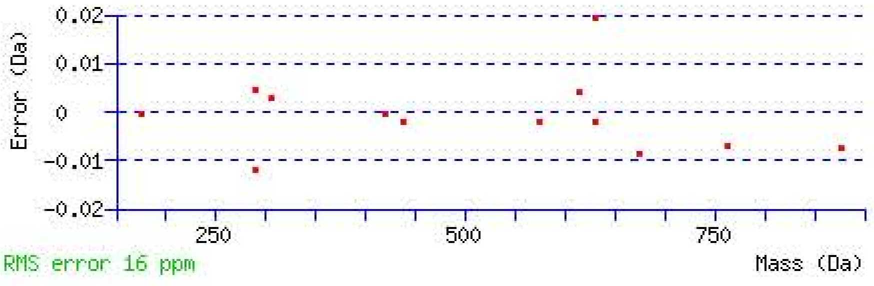
Match to Query 25904: 1452.619736 from(364.162210,4+) rtinseconds(1444) index(28466)
Title: Locus:1.1.1.3166.2 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

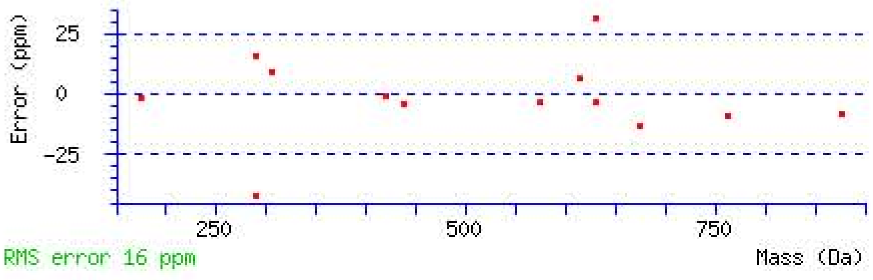
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1452.624680
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 28 **Expect:** 0.0059
Matches : 13/80 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							9
2	577.291514	289.149395	560.264965	280.636121			H	1014.406638	507.706957	997.380089	499.193682	996.396073	498.701674	8
3	692.318457	346.662867	675.291908	338.149592	674.307892	337.657584	D	***877.347726***	439.177501	860.321177	430.664226	859.337161	430.172218	7
4	823.358942	412.183109	806.332393	403.669834	805.348377	403.177826	M	***762.320783***	381.664030	745.294234	373.150755			6
5	880.380406	440.693841	863.353857	432.180567	862.369841	431.688559	G	***631.280298***	316.143787	614.253749	307.630513			5
6	1017.439318	509.223297	1000.412769	500.710022	999.428753	500.218014	H	***574.258834***	287.633055	557.232285	279.119780			4
7	1148.479803	574.743540	1131.453254	566.230265	1130.469238	565.738257	M	***437.199922***	219.103599	420.173373	210.590324			3
8	1279.520288	640.263782	1262.493739	631.750508	1261.509723	631.258499	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 QHDMGHMMR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.4	1452.624680	-0.004944	QHDMGHMMR
1.4	1452.638382	-0.018646	MAMEAGRRDNMR

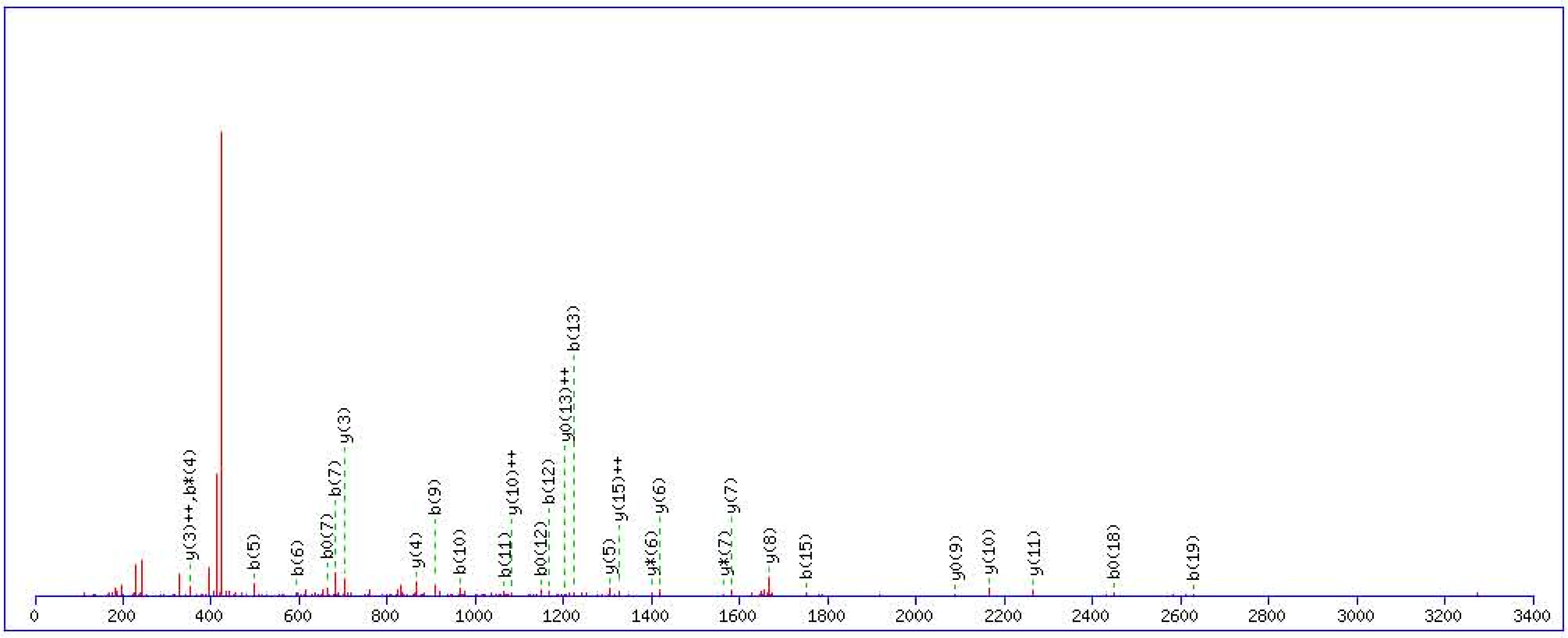
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPGGEPSPEGTTGQSYNQYSQR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

Match to Query 32963: 3328.570736 from(833.149960,4+) rtinseconds(2038) index(32110)
Title: Locus:1.1.1.3373.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\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 ●



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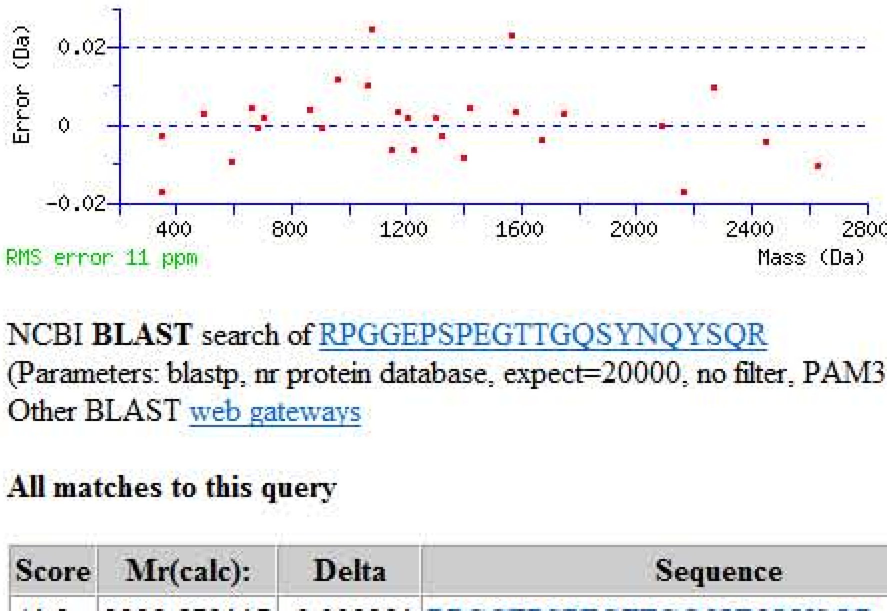
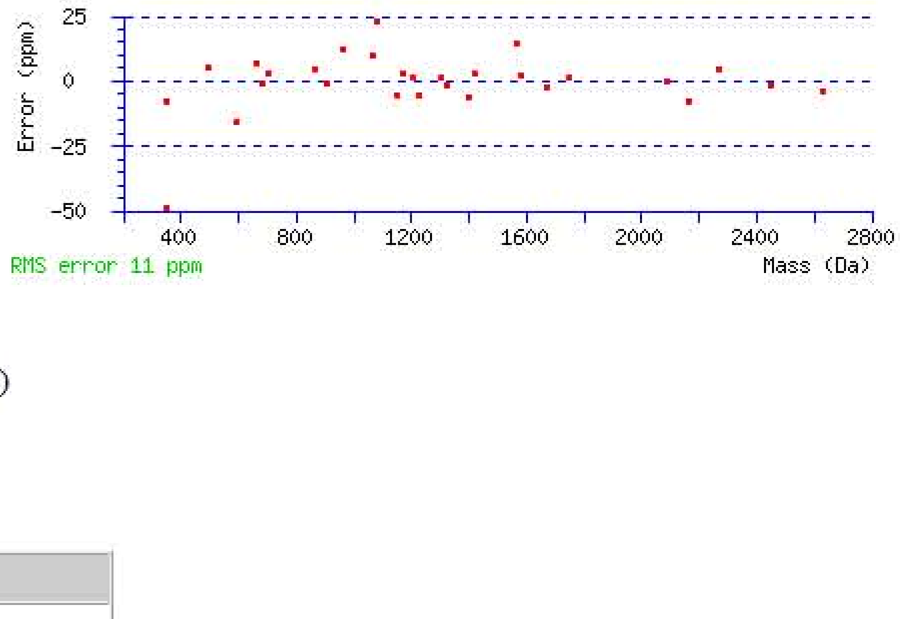
Monoisotopic mass of neutral peptide Mr(calc): 3328.579117
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Q18     : Biotin:Thermo-21345 (Q)
Q21     : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.00019
Matches : 29/240 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	157.108387	79.057831	140.081838	70.544557			R							22
2	254.161151	127.584213	237.134602	119.070939			P	3173.485291	1587.246283	3156.458742	1578.733009	3155.474726	1578.241001	21
3	311.182615	156.094945	294.156066	147.581671			G	3076.432527	1538.719901	3059.405978	1530.206627	3058.421962	1529.714619	20
4	368.204079	184.605677	351.177530	176.092403			G	3019.411063	1510.209169	3002.384514	1501.695895	3001.400498	1501.203887	19
5	***497.246672***	249.126974	480.220123	240.613700	479.236107	240.121692	E	2962.389599	1481.698438	2945.363050	1473.185163	2944.379034	1472.693155	18
6	***594.299436***	297.653356	577.272887	289.140082	576.288871	288.648074	P	2833.347006	1417.177141	2816.320457	1408.663866	2815.336441	1408.171858	17
7	***681.331464***	341.169370	664.304915	332.656095	663.320899	332.164087	S	2736.294242	1368.650759	2719.267693	1360.137484	2718.283677	1359.645476	16
8	778.384228	389.695752	761.357679	381.182478	760.373663	380.690470	P	2649.262214	1325.134745	2632.235665	1316.621470	2631.251649	1316.129462	15
9	***907.426821***	454.217049	890.400272	445.703774	889.416256	445.211766	E	2552.209450	1276.608363	2535.182901	1268.095088	2534.198885	1267.603080	14
10	***964.448285***	482.727781	947.421736	474.214506	946.437720	473.722498	G	2423.166857	1212.087066	2406.140308	1203.573792	2405.156292	1203.081784	13
11	***1065.495964***	533.251620	1048.469415	524.738346	1047.485399	524.246337	T	2366.145393	1183.576334	2349.118844	1175.063060	2348.134828	1174.571052	12
12	***1166.543643***	583.775460	1149.517094	575.262185	1148.533078	574.770177	T	***2265.097714***	1133.052495	2248.071165	1124.539220	2247.087149	1124.047212	11
13	***1223.565107***	612.286191	1206.538558	603.772917	1205.554542	603.280909	G	***2164.050035***	1082.528655	2147.023486	1074.015381	2146.039470	1073.523373	10
14	1662.790433	831.898854	1645.763884	823.385580	1644.779868	822.893572	Q	2107.028571	1054.017924	2090.002022	1045.504649	2089.018006	1045.012641	9
15	***1749.822461***	875.414869	1732.795912	866.901594	1731.811896	866.409586	S	***1667.803245***	834.405261	1650.776696	825.891986	1649.792680	825.399978	8
16	1912.885790	956.946533	1895.859241	948.433259	1894.875225	947.941251	Y	***1580.771217***	790.889247	1563.744668	782.375972	1562.760652	781.883964	7
17	2026.928717	1013.967997	2009.902168	1005.454722	2008.918152	1004.962714	N	***1417.707888***	709.357582	1400.681339	700.844308	1399.697323	700.352300	6
18	2466.154043	1233.580659	2449.127494	1225.067385	2448.143478	1224.575377	Q	***1303.664961***	652.336119	1286.638412	643.822844	1285.654396	643.330836	5
19	***2629.217372***	1315.112324	2612.190823	1306.599049	2611.206807	1306.107041	Y	***864.439635***	432.723456	847.413086	424.210181	846.429070	423.718173	4
20	2716.249400	1358.628338	2699.222851	1350.115063	2698.238835	1349.623056	S	***701.376306***	351.191791	684.349757	342.678517	683.365741	342.186509	3
21	3155.474726	1578.241001	3138.448177	1569.727727	3137.464161	1569.235719	Q	614.344278	307.675777	597.317729	299.162503			2
22							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of RPGGEPSPEGTTGQSYNQYSQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.3	3328.579117	-0.008381	RPGGEPSPEGTTGQSYNQYSQR
1.7	3328.600220	-0.029484	VPPEWKALTDMPQMRMELERPGGNEITR

Mascot: http://www.matrixscience.com/

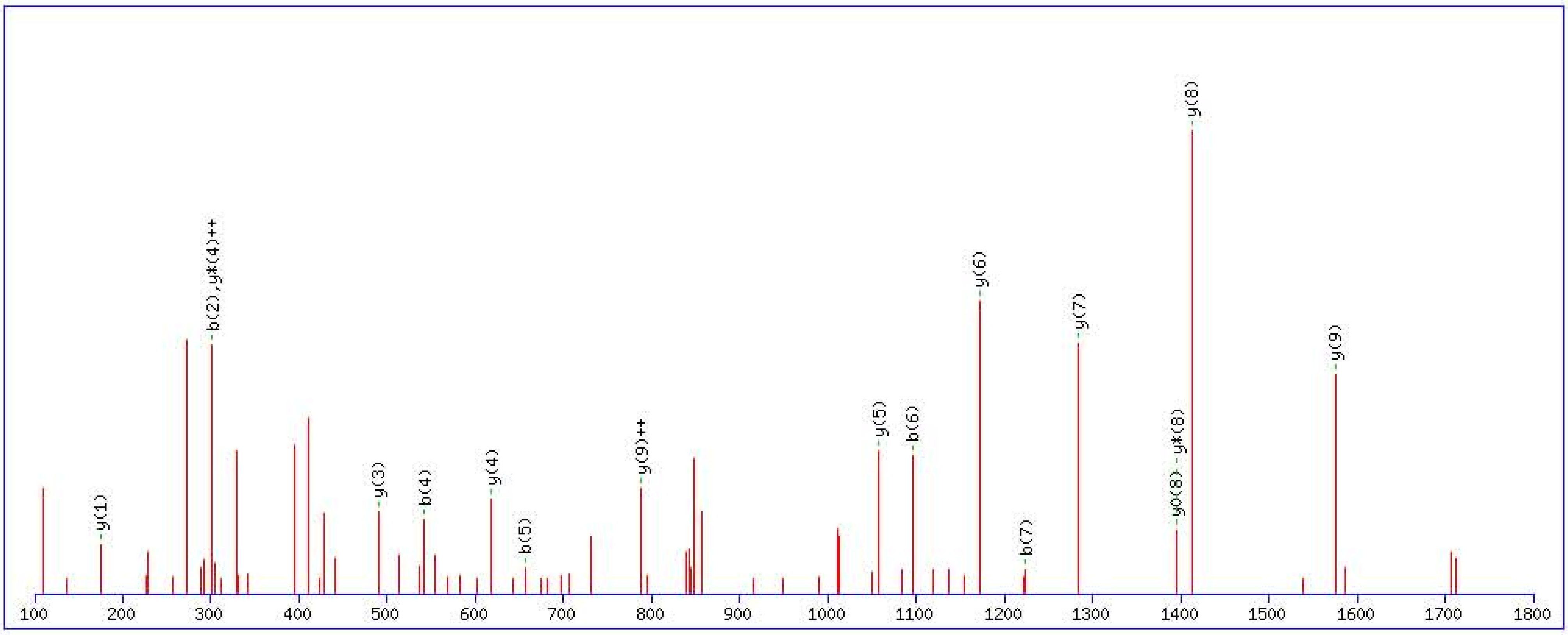
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HYQINQQWER**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

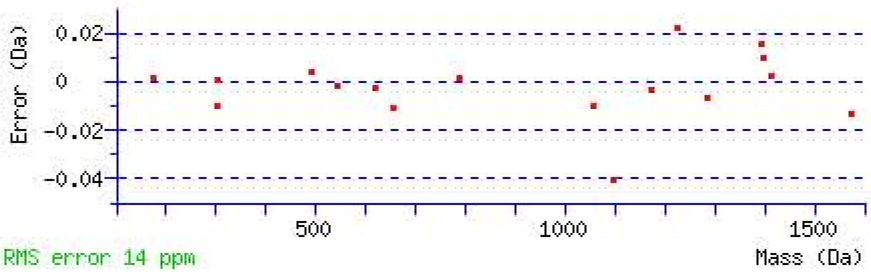
Match to Query 33872: 1711.831708 from(856.923130,2+) rtinseconds(1795) index(30573)
Title: Locus:1.1.1.3288.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

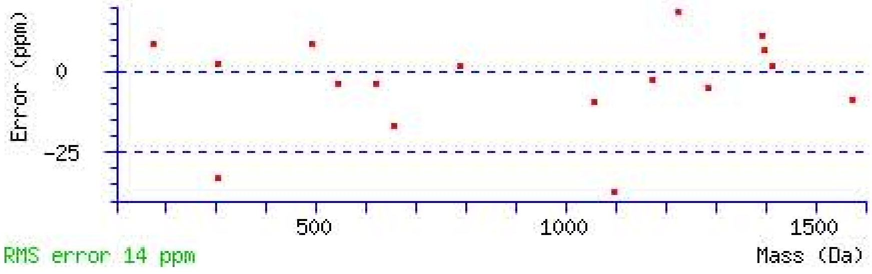


Monoisotopic mass of neutral peptide Mr(calc): 1711.825272
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 44 **Expect:** 0.00086
Matches : 17/86 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	138.066188	69.536732					H							10
2	**301.129517**	151.068397					Y	***1575.773660***	788.390468	1558.747111	779.877194	1557.763095	779.385186	9
3	429.188095	215.097686	412.161546	206.584411			Q	***1412.710331***	706.858804	1395.683782	698.345529	1394.699766	697.853521	8
4	**542.272159**	271.639718	525.245610	263.126443			I	***1284.651753***	642.829514	1267.625204	634.316240	1266.641188	633.824232	7
5	**656.315086**	328.661181	639.288537	320.147907			N	***1171.567689***	586.287483	1154.541140	577.774208	1153.557124	577.282200	6
6	**1095.540412**	548.273844	1078.513863	539.760570			Q	***1057.524762***	529.266019	1040.498213	520.752745	1039.514197	520.260737	5
7	**1223.598990**	612.303133	1206.572441	603.789859			Q	***618.299436***	309.653356	601.272887	301.140082	600.288871	300.648074	4
8	1409.678303	705.342790	1392.651754	696.829515			W	***490.240858***	245.624067	473.214309	237.110792	472.230293	236.618784	3
9	1538.720896	769.864086	1521.694347	761.350812	1520.710331	760.858804	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
10							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 14 ppm



RMS error 14 ppm

NCBI **BLAST** search of HYQINQQWER
(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	1711.825272	0.006436	HYQINQQWER
31.7	1711.825272	0.006436	HYQINQQWER
13.1	1711.825272	0.006436	HYQINQQWER

Mascot: http://www.matrixscience.com/

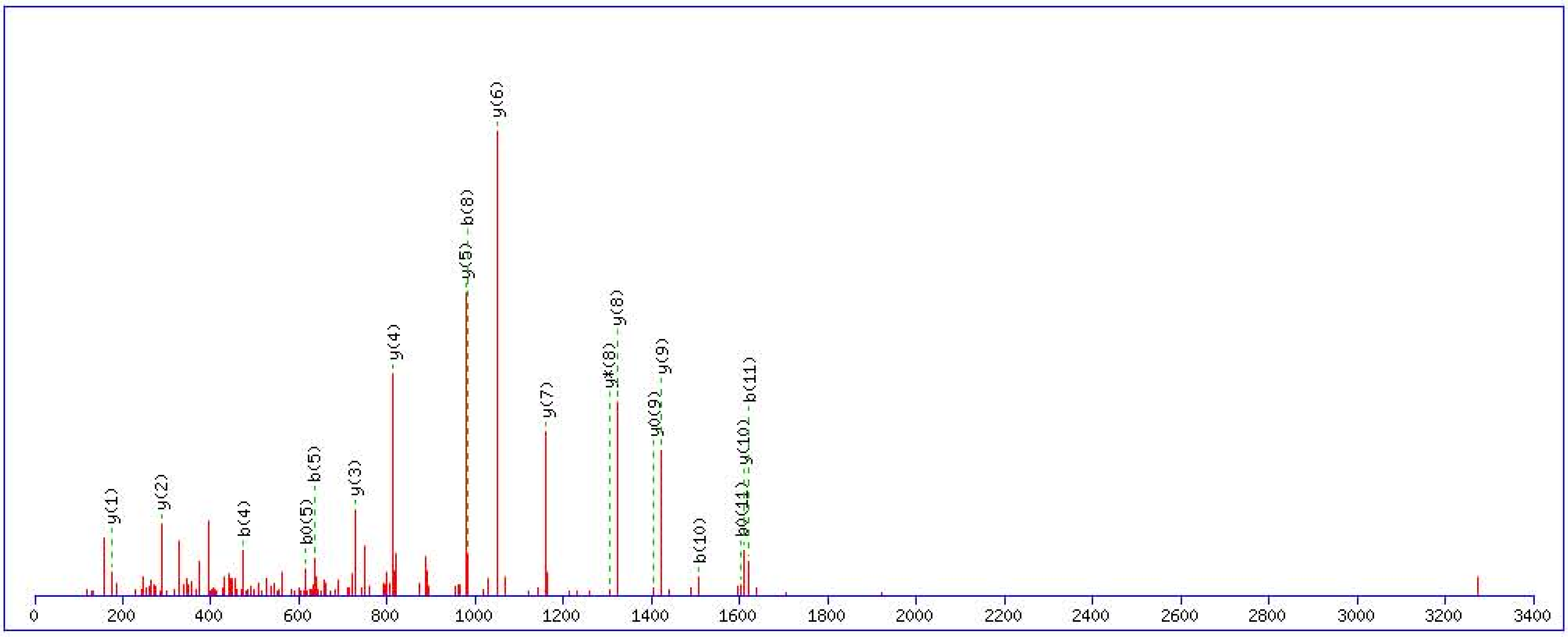
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GEWTCIAYSQLR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

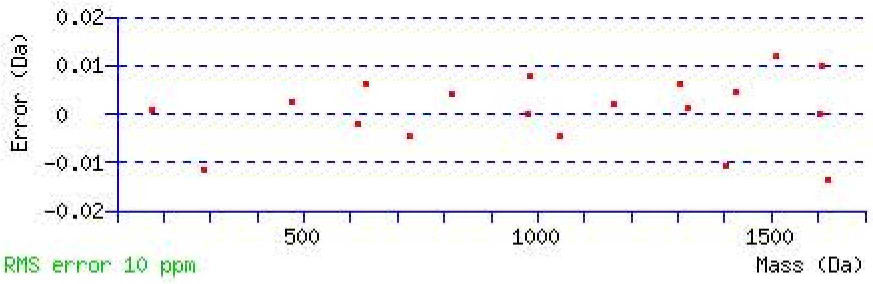
Match to Query 35590: 1793.862048 from(897.938300,2+) rtinseconds(2380) index(33969)
Title: Locus:1.1.1.3492.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

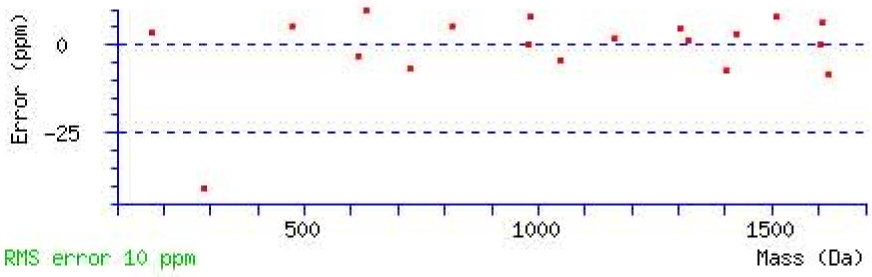
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1793.859283
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 72  Expect: 1.2e-006
Matches : 19/106 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							12
2	187.071333	94.039305			169.060768	85.034022	E	1737.845111	869.426194	1720.818562	860.912919	1719.834546	860.420911	11
3	373.150646	187.078961			355.140081	178.073679	W	***1608.802518***	804.904897	1591.775969	796.391623	1590.791953	795.899614	10
4	**474.198325**	237.602801			456.187760	228.597518	T	***1422.723205***	711.865241	1405.696656	703.351966	1404.712640	702.859958	9
5	**634.228974**	317.618125			616.218409	308.612843	C	***1321.675526***	661.341401	1304.648977	652.828127	1303.664961	652.336119	8
6	747.313038	374.160157			729.302473	365.154875	I	***1161.644877***	581.326077	1144.618328	572.812802	1143.634312	572.320794	7
7	818.350152	409.678714			800.339587	400.673432	A	***1048.560813***	524.784044	1031.534264	516.270770	1030.550248	515.778762	6
8	**981.413481**	491.210379			963.402916	482.205096	Y	***977.523699***	489.265488	960.497150	480.752213	959.513134	480.260205	5
9	1068.445509	534.726393			1050.434944	525.721110	S	***814.460370***	407.733823	797.433821	399.220549	796.449805	398.728541	4
10	**1507.670835**	754.339056	1490.644286	745.825781	1489.660270	745.333773	Q	***727.428342***	364.217809	710.401793	355.704534			3
11	**1620.754899**	810.881088	1603.728350	802.367813	1602.744334	801.875805	L	***288.203016***	144.605146	271.176467	136.091871			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GEWTCIAYSQLR
(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	1793.859283	0.002765	GEWTCIAYSQLR
18.7	1793.865158	-0.003110	ACLECELTSKDVTLR
6.2	1793.888275	-0.026227	QYVVEPNFANKAVCR
1.9	1793.873016	-0.010968	DQKLFVSESRMPDSR
1.9	1793.870529	-0.008481	MAPGCWFLISSRPTR

Mascot: http://www.matrixscience.com/

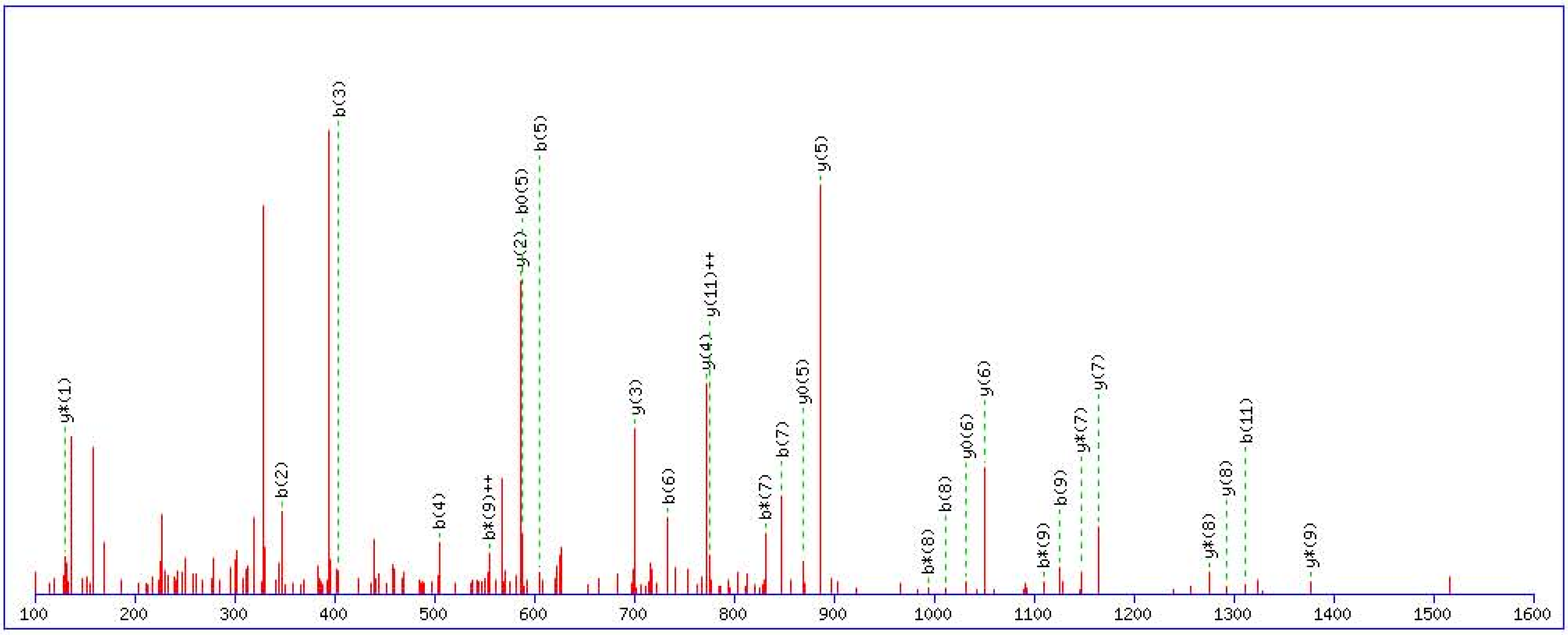
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WCGTTQNYDADQK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

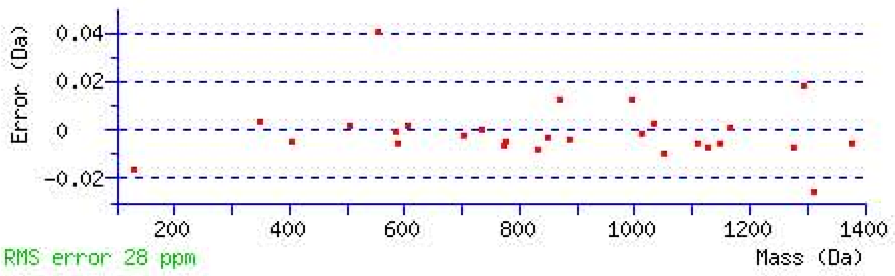
Match to Query 37359: 1896.804942 from(633.275590,3+) rtinseconds(1688) index(29940)
Title: Locus:1.1.1.3251.6 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

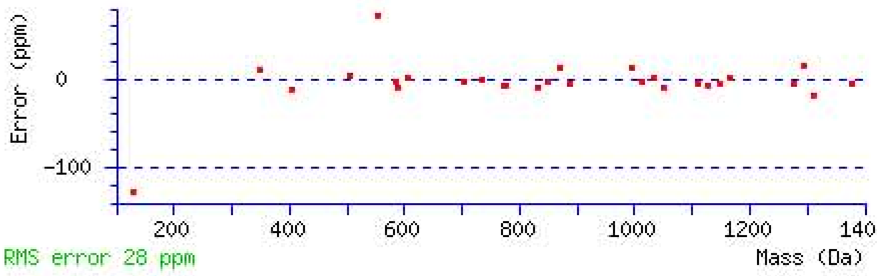
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1896.813477
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 34 **Expect:** 0.0012
Matches : 28/124 fragment ions using 64 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							13
2	***347.117238***	174.062257					C	1711.741435	856.374356	1694.714886	847.861081	1693.730870	847.369073	12
3	***404.138702***	202.572989					G	1551.710786	776.359031	1534.684237	767.845757	1533.700221	767.353749	11
4	***505.186381***	253.096828			487.175816	244.091546	T	1494.689322	747.848299	1477.662773	739.335025	1476.678757	738.843017	10
5	***606.234060***	303.620668			588.223495	294.615386	T	1393.641643	697.324460	1376.615094	688.811185	1375.631078	688.319177	9
6	***734.292638***	367.649957	717.266089	359.136683	716.282073	358.644675	Q	**1292.593964**	646.800620	1275.567415	638.287346	1274.583399	637.795338	8
7	***848.335565***	424.671421	831.309016	416.158146	830.325000	415.666138	N	**1164.535386**	582.771331	1147.508837	574.258057	1146.524821	573.766049	7
8	***1011.398894***	506.203085	994.372345	497.689810	993.388329	497.197802	Y	**1050.492459**	525.749868	1033.465910	517.236593	1032.481894	516.744585	6
9	***1126.425837***	563.716557	1109.399288	555.203282	1108.415272	554.711274	D	**887.429130**	444.218203	870.402581	435.704929	869.418565	435.212921	5
10	1197.462951	599.235114	1180.436402	590.721839	1179.452386	590.229831	A	**772.402187**	386.704732	755.375638	378.191457	754.391622	377.699449	4
11	***1312.489894***	656.748585	1295.463345	648.235311	1294.479329	647.743303	D	**701.365073**	351.186175	684.338524	342.672900	683.354508	342.180892	3
12	1751.715220	876.361248	1734.688671	867.847974	1733.704655	867.355966	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 WCGTTQNYDADQK
(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	1896.813477	-0.008535	WCGTTQNYDADQK

Mascot: http://www.matrixscience.com/

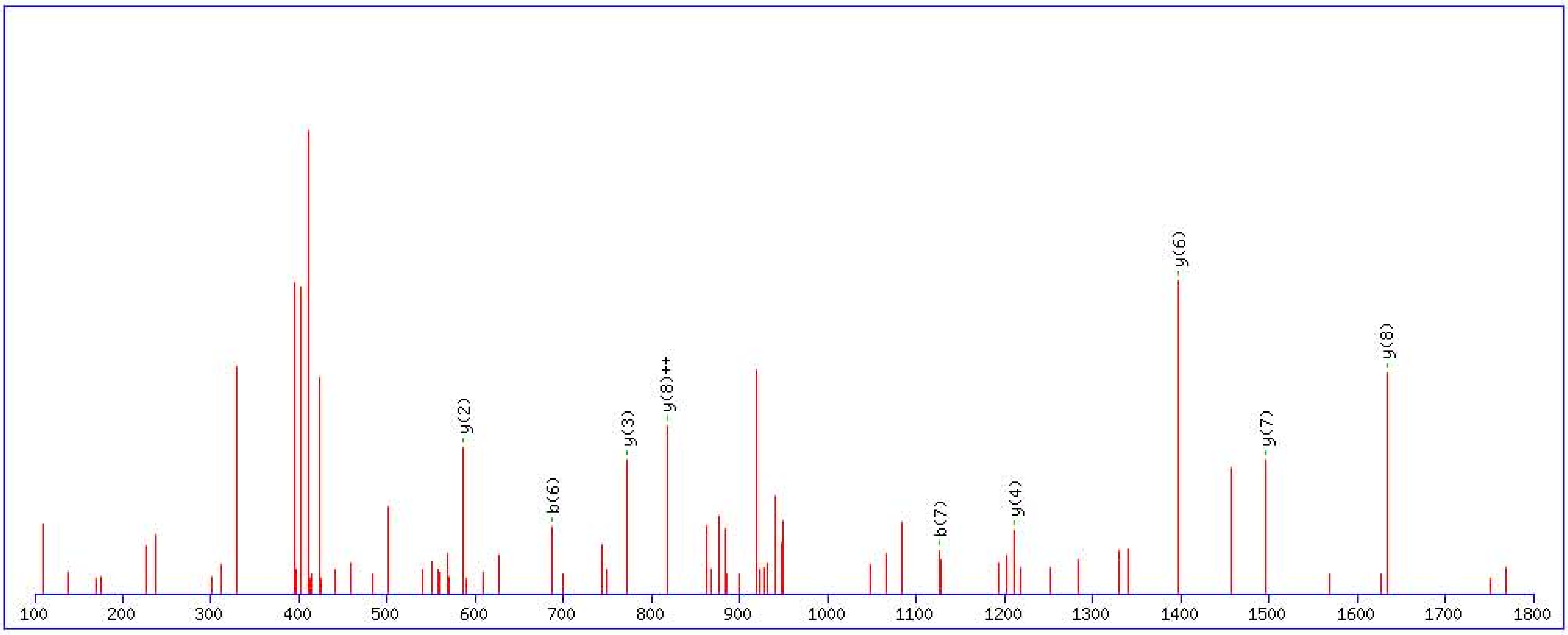
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TYHVGEQWQK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

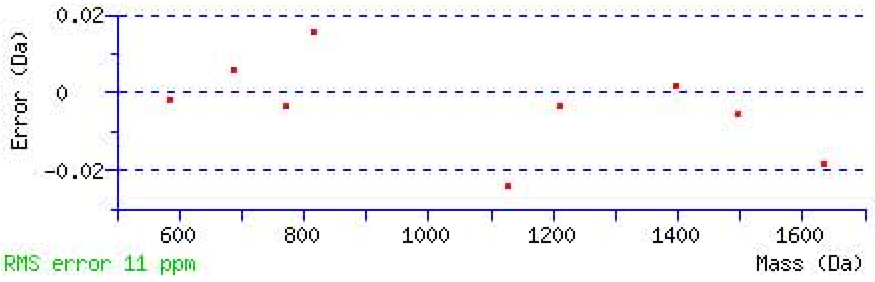
Match to Query 37366: 1896.938908 from(949.476730,2+) rtinseconds(2039) index(32114)
Title: Locus:1.1.1.3373.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

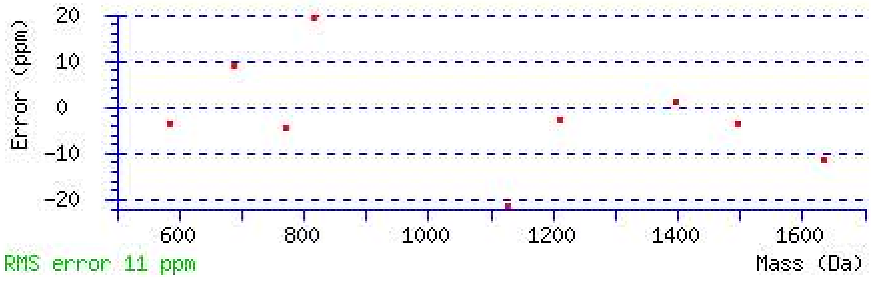
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1896.937881
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.0055
Matches : 9/88 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	102.054955	51.531116			84.044390	42.525833	T							10
2	265.118284	133.062780			247.107719	124.057498	Y	1796.897481	898.952379	1779.870932	890.439104	1778.886916	889.947096	9
3	402.177196	201.592236			384.166631	192.586954	H	***1633.834152***	817.420714	1616.807603	808.907440	1615.823587	808.415431	8
4	501.245610	251.126443			483.235045	242.121161	V	***1496.775240***	748.891258	1479.748691	740.377984	1478.764675	739.885975	7
5	558.267074	279.637175			540.256509	270.631893	G	***1397.706826***	699.357051	1380.680277	690.843776	1379.696261	690.351768	6
6	**687.309667**	344.158472			669.299102	335.153189	E	1340.685362	670.846319	1323.658813	662.333045	1322.674797	661.841036	5
7	**1126.534993**	563.771135	1109.508444	555.257860	1108.524428	554.765852	Q	***1211.642769***	606.325022	1194.616220	597.811748			4
8	1312.614306	656.810791	1295.587757	648.297517	1294.603741	647.805508	W	***772.417443***	386.712360	755.390894	378.199085			3
9	1751.839632	876.423454	1734.813083	867.910180	1733.829067	867.418171	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 TYHVGEQWQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.1	1896.937881	0.001027	TYHVGEQWQK
1.9	1896.947586	-0.008678	GATGDSHLLCTRKPEQK
0.8	1896.933640	0.005268	QQGESNQERGARAR

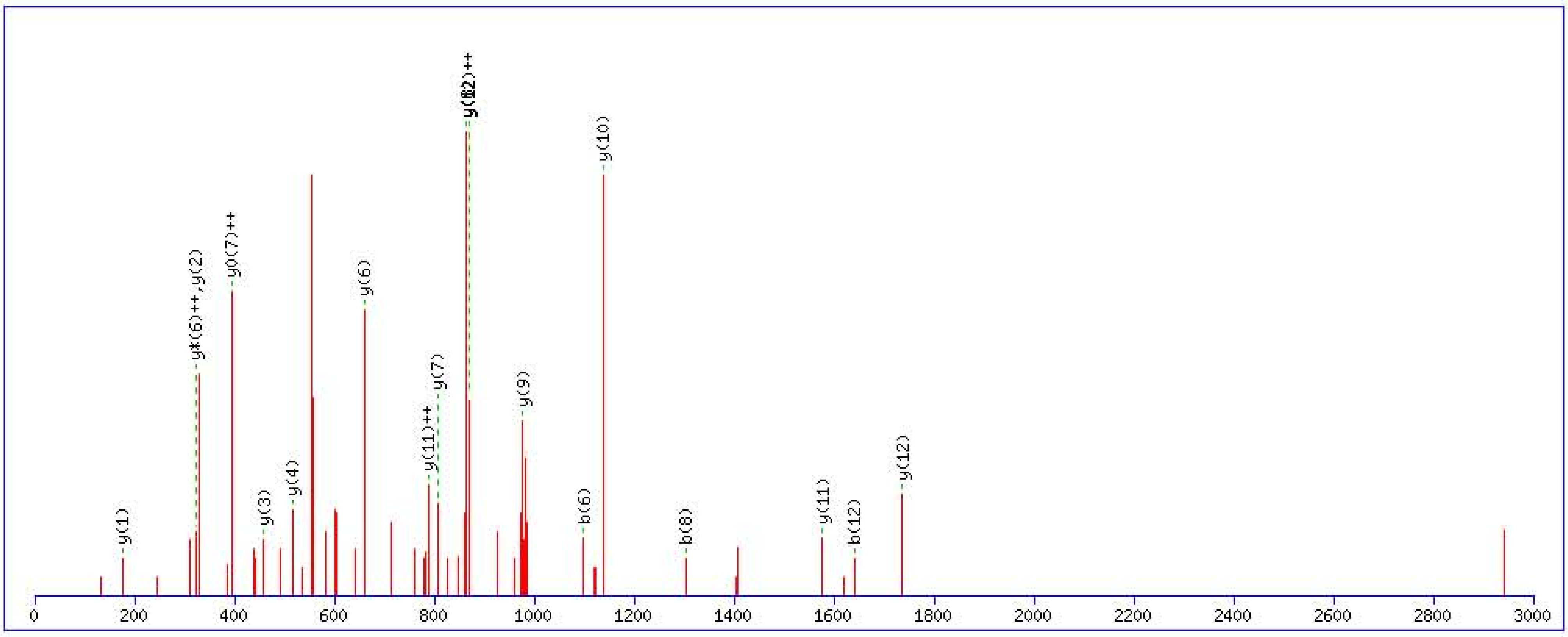
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLCQCLGFGSGHFR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

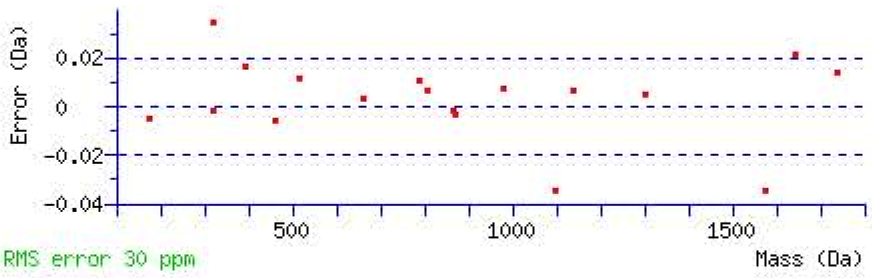
Match to Query 38589: 1961.929708 from(981.972130,2+) rtinseconds(2194) index(32996)
Title: Locus:1.1.1.3427.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

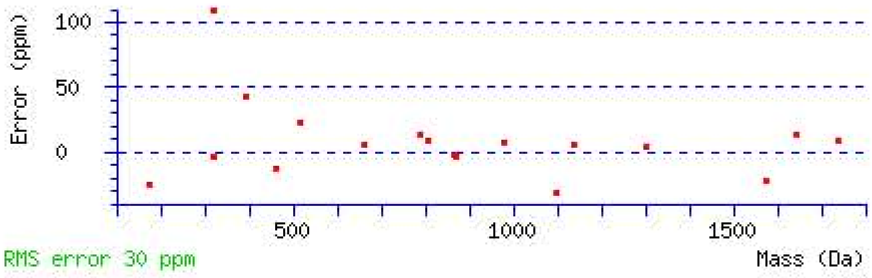
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1961.942673
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 77  Expect: 1.1e-007
Matches : 18/124 fragment ions using 29 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							14
2	227.175404	114.091340					L	1849.865864	925.436570	1832.839315	916.923296	1831.855299	916.431288	13
3	387.206053	194.106664					C	***1736.781800***	868.894538	1719.755251	860.381264	1718.771235	859.889255	12
4	826.431379	413.719328	809.404830	405.206053			Q	***1576.751151***	788.879213	1559.724602	780.365939	1558.740586	779.873931	11
5	986.462028	493.734652	969.435479	485.221378			C	***1137.525825***	569.266550	1120.499276	560.753276	1119.515260	560.261268	10
6	**1099.546092**	550.276684	1082.519543	541.763410			L	***977.495176***	489.251226	960.468627	480.737952	959.484611	480.245944	9
7	1156.567556	578.787416	1139.541007	570.274142			G	***864.411112***	432.709194	847.384563	424.195920	846.400547	423.703912	8
8	**1303.635970**	652.321623	1286.609421	643.808349			F	***807.389648***	404.198462	790.363099	395.685188	789.379083	395.193180	7
9	1360.657434	680.832355	1343.630885	672.319081			G	***660.321234***	330.664255	643.294685	322.150981	642.310669	321.658973	6
10	1447.689462	724.348369	1430.662913	715.835095	1429.678897	715.343087	S	603.299770	302.153523	586.273221	293.640249	585.289205	293.148241	5
11	1504.710926	752.859101	1487.684377	744.345827	1486.700361	743.853818	G	***516.267742***	258.637509	499.241193	250.124235			4
12	**1641.769838**	821.388557	1624.743289	812.875283	1623.759273	812.383274	H	***459.246278***	230.126777	442.219729	221.613502			3
13	1788.838252	894.922764	1771.811703	886.409490	1770.827687	885.917482	F	***322.187366***	161.597321	305.160817	153.084047			2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLCQCLGFGSGHFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
76.6	1961.942673	-0.012965	LLCQCLGFGSGHFR
2.3	1961.938614	-0.008906	HECMAPLTALVKHMHR

Mascot: http://www.matrixscience.com/

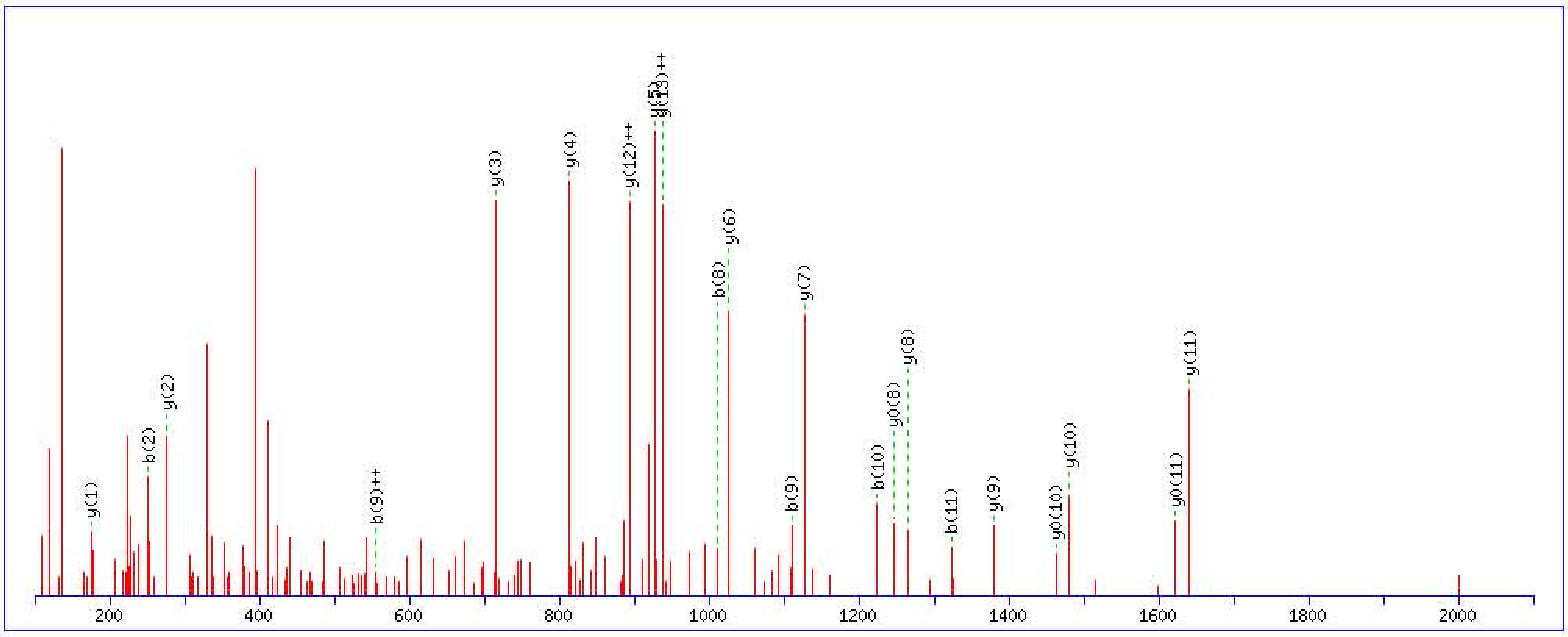
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YSFCTDHTVLVQTR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

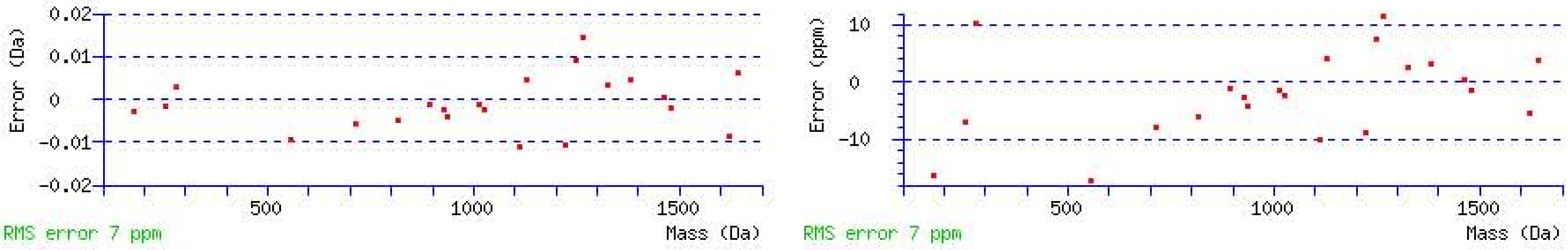
Match to Query 40520: 2036.975682 from(679.999170,3+) rtinseconds(2029) index(32064)
Title: Locus:1.1.1.3370.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 2036.981232
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 59  Expect: 2.7e-005
Matches : 22/130 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	164.070605	82.538940					Y							14
2	**251.102633**	126.054954			233.092068	117.049672	S	1874.925153	937.966215	1857.898604	929.452940	1856.914588	928.960932	13
3	398.171047	199.589161			380.160482	190.583879	F	1787.893125	894.450201	1770.866576	885.936926	1769.882560	885.444918	12
4	558.201696	279.604486			540.191131	270.599204	C	***1640.824711***	820.915994	1623.798162	812.402719	1622.814146	811.910711	11
5	659.249375	330.128326			641.238810	321.123043	T	***1480.794062***	740.900669	1463.767513	732.387395	1462.783497	731.895387	10
6	774.276318	387.641797			756.265753	378.636515	D	***1379.746383***	690.376830	1362.719834	681.863555	1361.735818	681.371547	9
7	911.335230	456.171253			893.324665	447.165971	H	***1264.719440***	632.863358	1247.692891	624.350084	1246.708875	623.858076	8
8	**1012.382909**	506.695093			994.372344	497.689810	T	***1127.660528***	564.333902	1110.633979	555.820628	1109.649963	555.328620	7
9	**1111.451323**	556.229300			1093.440758	547.224017	V	***1026.612849***	513.810063	1009.586300	505.296788	1008.602284	504.804780	6
10	**1224.535387**	612.771331			1206.524822	603.766049	L	***927.544435***	464.275856	910.517886	455.762581	909.533870	455.270573	5
11	**1323.603801**	662.305539			1305.593236	653.300256	V	***814.460371***	407.733824	797.433822	399.220549	796.449806	398.728541	4
12	1762.829127	881.918202	1745.802578	873.404927	1744.818562	872.912919	Q	***715.391957***	358.199617	698.365408	349.686342	697.381392	349.194334	3
13	1863.876806	932.442041	1846.850257	923.928767	1845.866241	923.436759	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
14							R	***175.118952***	88.063114	158.092403	79.549839			1



NCBI **BLAST** search of YSFCTDHTVLVQTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.9	2036.981232	-0.005550	YSFCTDHTVLVQTR

Mascot: http://www.matrixscience.com/

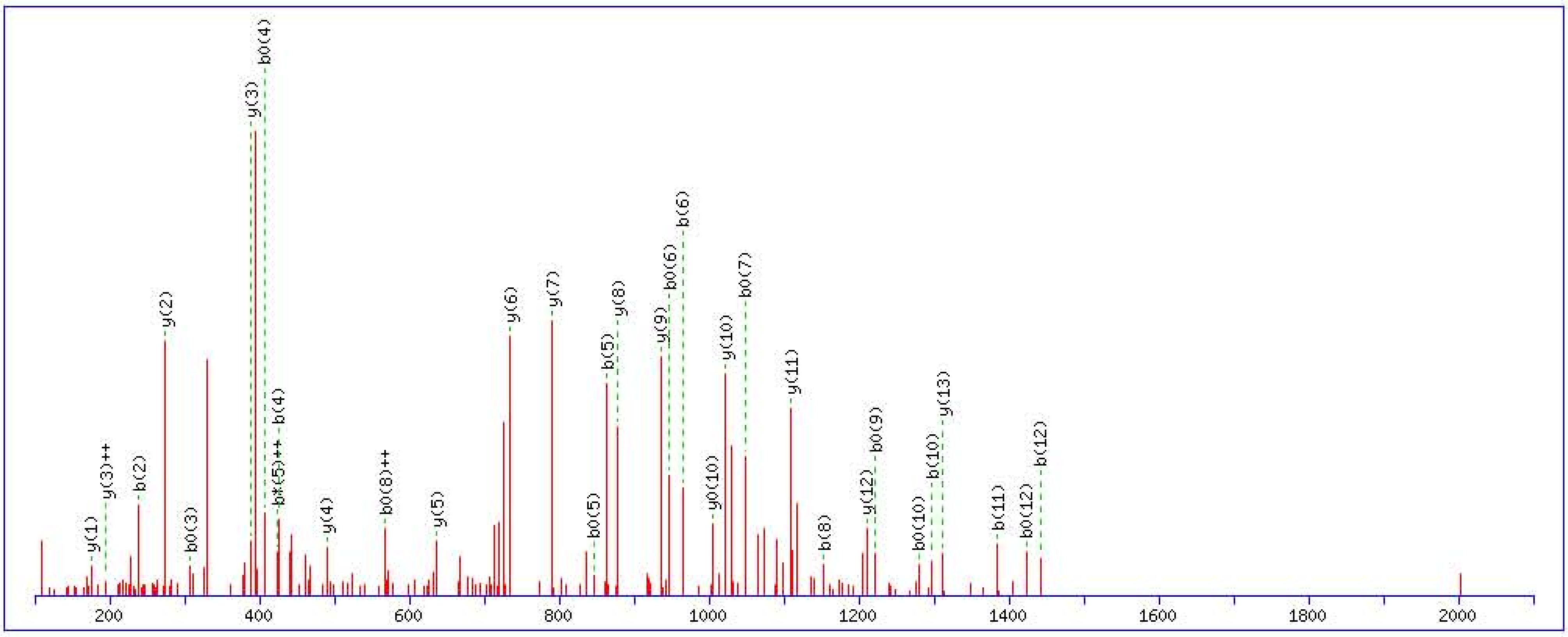
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HTSVQTTSSGSGPFTDVR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

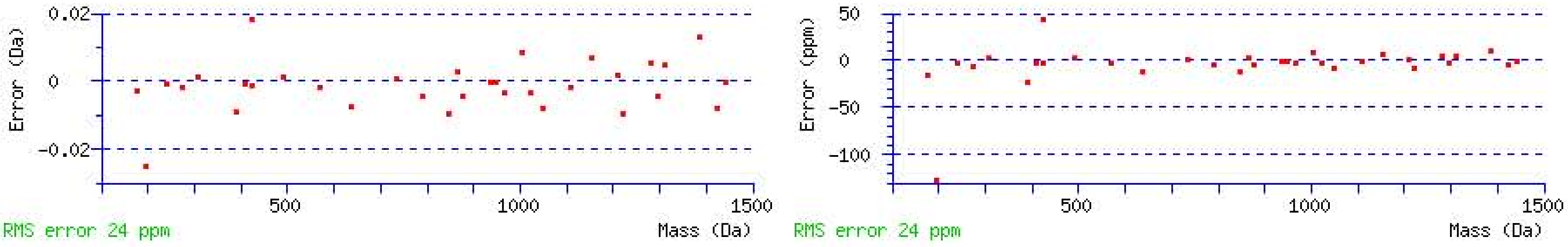
Match to Query 42784: 2174.033832 from(725.685220,3+) rtinseconds(1691) index(29953)
Title: Locus:1.1.1.3252.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 2174.042664
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 82  Expect: 1.1e-007
Matches : 33/190 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							18
2	**239.113867**	120.060571			221.103302	111.055289	T	2037.990983	1019.499130	2020.964434	1010.985855	2019.980418	1010.493847	17
3	326.145895	163.576585			308.135330	154.571303	S	1936.943304	968.975290	1919.916755	960.462016	1918.932739	959.970008	16
4	**425.214309**	213.110792			407.203744	204.105510	V	1849.911276	925.459276	1832.884727	916.946002	1831.900711	916.453994	15
5	**864.439635**	432.723456	847.413086	424.210181	846.429070	423.718173	Q	1750.842862	875.925069	1733.816313	867.411795	1732.832297	866.919787	14
6	**965.487314**	483.247295	948.460765	474.734021	947.476749	474.242013	T	***1311.617536***	656.312406	1294.590987	647.799132	1293.606971	647.307124	13
7	1066.534993	533.771135	1049.508444	525.257860	1048.524428	524.765852	T	***1210.569857***	605.788567	1193.543308	597.275292	1192.559292	596.783284	12
8	**1153.567021**	577.287149	1136.540472	568.773874	1135.556456	568.281866	S	***1109.522178***	555.264727	1092.495629	546.751453	1091.511613	546.259445	11
9	1240.599049	620.803163	1223.572500	612.289888	1222.588484	611.797880	S	***1022.490150***	511.748713	1005.463601	503.235439	1004.479585	502.743431	10
10	**1297.620513**	649.313895	1280.593964	640.800620	1279.609948	640.308612	G	***935.458122***	468.232699	918.431573	459.719425	917.447557	459.227417	9
11	**1384.652541**	692.829909	1367.625992	684.316634	1366.641976	683.824626	S	***878.436658***	439.721967	861.410109	431.208693	860.426093	430.716685	8
12	**1441.674005**	721.340641	1424.647456	712.827366	1423.663440	712.335358	G	***791.404630***	396.205953	774.378081	387.692679	773.394065	387.200671	7
13	1538.726769	769.867023	1521.700220	761.353748	1520.716204	760.861740	P	***734.383166***	367.695221	717.356617	359.181947	716.372601	358.689939	6
14	1685.795183	843.401230	1668.768634	834.887955	1667.784618	834.395947	F	***637.330402***	319.168839	620.303853	310.655565	619.319837	310.163557	5
15	1786.842862	893.925069	1769.816313	885.411795	1768.832297	884.919787	T	***490.261988***	245.634632	473.235439	237.121358	472.251423	236.629350	4
16	1901.869805	951.438541	1884.843256	942.925266	1883.859240	942.433258	D	***389.214309***	195.110793	372.187760	186.597518	371.203744	186.105510	3
17	2000.938219	1000.972748	1983.911670	992.459473	1982.927654	991.967465	V	***274.187366***	137.597321	257.160817	129.084047			2
18							R	***175.118952***	88.063114	158.092403	79.549839			1



NCBI **BLAST** search of HTSVQTTSSGSGPFTDVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
82.2	2174.042664	-0.008832	HTSVQTTSSGSGPFTDVR

Mascot: http://www.matrixscience.com/

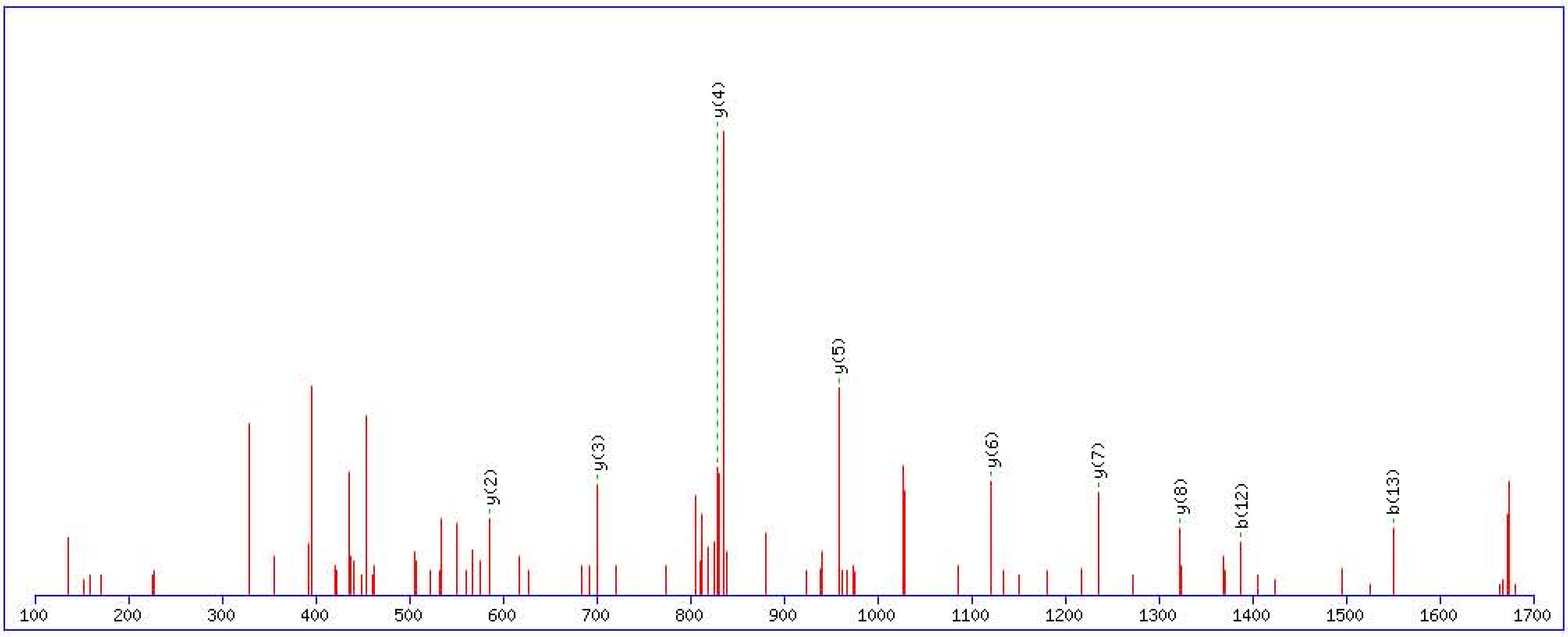
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QDGHLWCSTTSNYEQDQK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

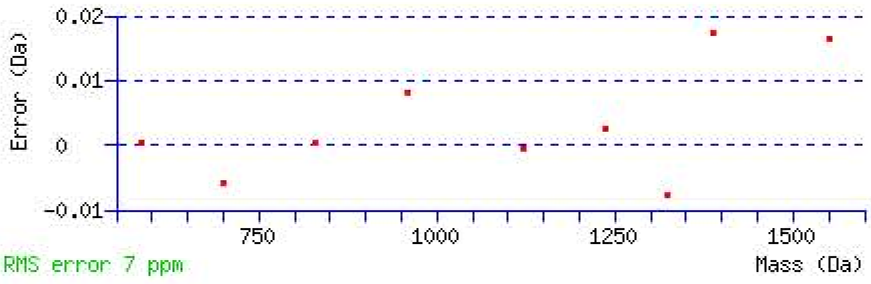
Match to Query 48602: 2507.077272 from(836.699700,3+) rtinseconds(1804) index(30627)
Title: Locus:1.1.1.3291.22 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

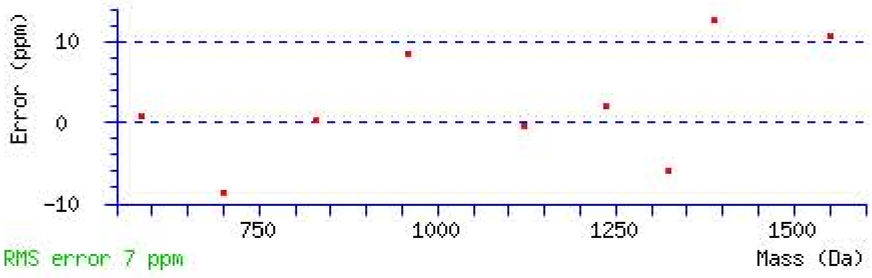
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2507.084564
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q17 : Biotin:Thermo-21345 (Q)
Ions Score: 34 **Expect:** 0.0014
Matches : 9/198 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	129.065854	65.036565	112.039305	56.523291			Q							18
2	244.092797	122.550037	227.066248	114.036762	226.082232	113.544754	D	2380.033259	1190.520267	2363.006710	1182.006993	2362.022694	1181.514985	17
3	301.114261	151.060768	284.087712	142.547494	283.103696	142.055486	G	2265.006316	1133.006796	2247.979767	1124.493521	2246.995751	1124.001513	16
4	438.173173	219.590224	421.146624	211.076950	420.162608	210.584942	H	2207.984852	1104.496064	2190.958303	1095.982789	2189.974287	1095.490781	15
5	551.257237	276.132257	534.230688	267.618982	533.246672	267.126974	L	2070.925940	1035.966608	2053.899391	1027.453333	2052.915375	1026.961325	14
6	737.336550	369.171913	720.310001	360.658639	719.325985	360.166631	W	1957.841876	979.424576	1940.815327	970.911302	1939.831311	970.419294	13
7	897.367199	449.187238	880.340650	440.673963	879.356634	440.181955	C	1771.762563	886.384920	1754.736014	877.871645	1753.751998	877.379637	12
8	984.399227	492.703252	967.372678	484.189977	966.388662	483.697969	S	1611.731914	806.369595	1594.705365	797.856321	1593.721349	797.364313	11
9	1085.446906	543.227091	1068.420357	534.713817	1067.436341	534.221808	T	1524.699886	762.853581	1507.673337	754.340307	1506.689321	753.848299	10
10	1186.494585	593.750930	1169.468036	585.237656	1168.484020	584.745648	T	1423.652207	712.329742	1406.625658	703.816467	1405.641642	703.324459	9
11	1273.526613	637.266945	1256.500064	628.753670	1255.516048	628.261662	S	***1322.604528***	661.805902	1305.577979	653.292628	1304.593963	652.800620	8
12	**1387.569540**	694.288408	1370.542991	685.775134	1369.558975	685.283125	N	***1235.572500***	618.289888	1218.545951	609.776614	1217.561935	609.284606	7
13	**1550.632869**	775.820073	1533.606320	767.306798	1532.622304	766.814790	Y	***1121.529573***	561.268425	1104.503024	552.755150	1103.519008	552.263142	6
14	1679.675462	840.341369	1662.648913	831.828095	1661.664897	831.336086	E	***958.466244***	479.736760	941.439695	471.223486	940.455679	470.731478	5
15	1807.734040	904.370658	1790.707491	895.857384	1789.723475	895.365376	Q	***829.423651***	415.215464	812.397102	406.702189	811.413086	406.210181	4
16	1922.760983	961.884130	1905.734434	953.370855	1904.750418	952.878847	D	***701.365073***	351.186175	684.338524	342.672900	683.354508	342.180892	3
17	2361.986309	1181.496792	2344.959760	1172.983518	2343.975744	1172.491510	Q	***586.338130***	293.672703	569.311581	285.159429			2
18							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of QDGHLWCSTTSNYEQDQK
(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	2507.084564	-0.007292	QDGHLWCSTTSNYEQDQK
16.7	2507.084564	-0.007292	QDGHLWCSTTSNYEQDQK

Mascot: http://www.matrixscience.com/

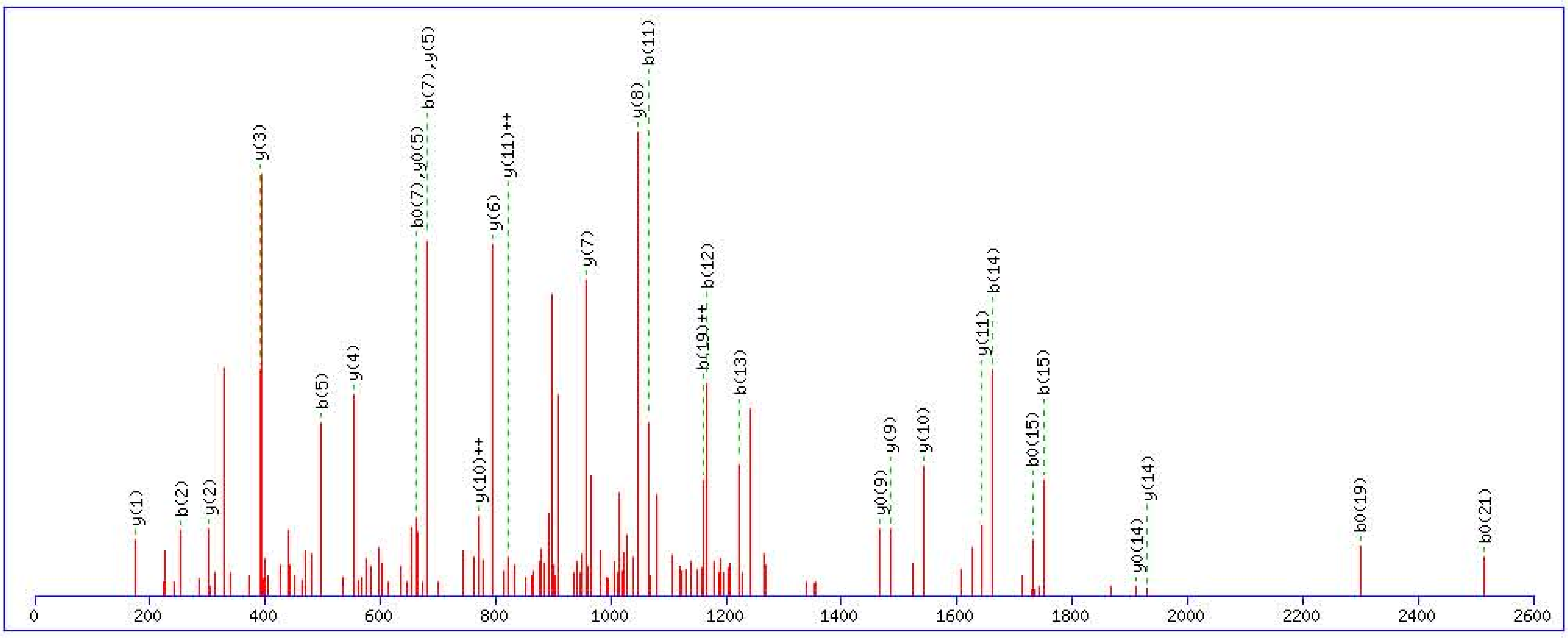
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPGGEPSPEGTTGQSYNQYSQR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

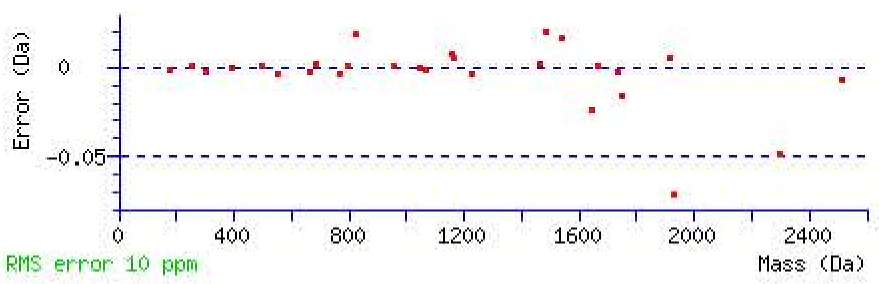
Match to Query 50403: 2706.237522 from(903.086450,3+) rtinseconds(1560) index(29154)
Title: Locus:1.1.1.3206.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

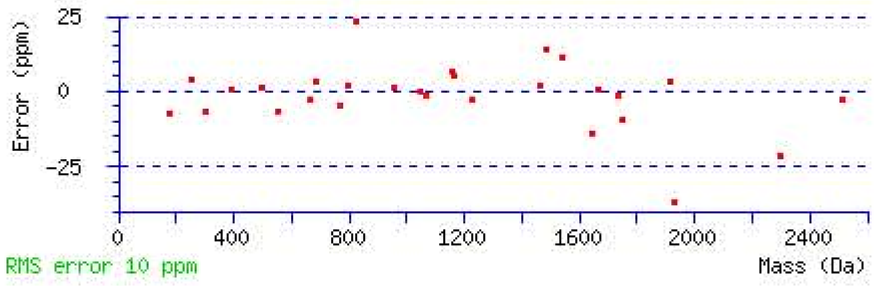
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2706.245621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 87   Expect: 2.3e-008
Matches : 30/240 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	157.108387	79.057831	140.081838	70.544557			R							22
2	**254.161151**	127.584213	237.134602	119.070939			P	2551.151795	1276.079535	2534.125246	1267.566261	2533.141230	1267.074253	21
3	311.182615	156.094945	294.156066	147.581671			G	2454.099031	1227.553153	2437.072482	1219.039879	2436.088466	1218.547871	20
4	368.204079	184.605677	351.177530	176.092403			G	2397.077567	1199.042421	2380.051018	1190.529147	2379.067002	1190.037139	19
5	**497.246672**	249.126974	480.220123	240.613700	479.236107	240.121692	E	2340.056103	1170.531689	2323.029554	1162.018415	2322.045538	1161.526407	18
6	594.299436	297.653356	577.272887	289.140082	576.288871	288.648074	P	2211.013510	1106.010393	2193.986961	1097.497118	2193.002945	1097.005110	17
7	**681.331464**	341.169370	664.304915	332.656095	663.320899	332.164087	S	2113.960746	1057.484011	2096.934197	1048.970736	2095.950181	1048.478728	16
8	778.384228	389.695752	761.357679	381.182478	760.373663	380.690470	P	2026.928718	1013.967997	2009.902169	1005.454723	2008.918153	1004.962715	15
9	907.426821	454.217049	890.400272	445.703774	889.416256	445.211766	E	***1929.875954***	965.441615	1912.849405	956.928341	1911.865389	956.436333	14
10	964.448285	482.727781	947.421736	474.214506	946.437720	473.722498	G	1800.833361	900.920319	1783.806812	892.407044	1782.822796	891.915036	13
11	**1065.495964**	533.251620	1048.469415	524.738346	1047.485399	524.246337	T	1743.811897	872.409587	1726.785348	863.896312	1725.801332	863.404304	12
12	**1166.543643**	583.775460	1149.517094	575.262185	1148.533078	574.770177	T	***1642.764218***	821.885747	1625.737669	813.372473	1624.753653	812.880465	11
13	**1223.565107**	612.286191	1206.538558	603.772917	1205.554542	603.280909	G	***1541.716539***	771.361908	1524.689990	762.848633	1523.705974	762.356625	10
14	**1662.790433**	831.898854	1645.763884	823.385580	1644.779868	822.893572	Q	***1484.695075***	742.851176	1467.668526	734.337901	1466.684510	733.845893	9
15	**1749.822461**	875.414869	1732.795912	866.901594	1731.811896	866.409586	S	***1045.469749***	523.238513	1028.443200	514.725238	1027.459184	514.233230	8
16	1912.885790	956.946533	1895.859241	948.433259	1894.875225	947.941251	Y	***958.437721***	479.722499	941.411172	471.209224	940.427156	470.717216	7
17	2026.928717	1013.967997	2009.902168	1005.454722	2008.918152	1004.962714	N	***795.374392***	398.190834	778.347843	389.677560	777.363827	389.185552	6
18	2154.987295	1077.997285	2137.960746	1069.484011	2136.976730	1068.992003	Q	***681.331465***	341.169371	664.304916	332.656096	663.320900	332.164088	5
19	2318.050624	1159.528950	2301.024075	1151.015675	2300.040059	1150.523667	Y	***553.272887***	277.140082	536.246338	268.626807	535.262322	268.134799	4
20	2405.082652	1203.044964	2388.056103	1194.531689	2387.072087	1194.039681	S	***390.209558***	195.608417	373.183009	187.095143	372.198993	186.603135	3
21	2533.141230	1267.074253	2516.114681	1258.560978	2515.130665	1258.068971	Q	***303.177530***	152.092403	286.150981	143.579129			2
22							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of RPGGEPSPEGTTGQSYNQYSQR
(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	2706.245621	-0.008099	RPGGEPSPEGTTGQSYNQYSQR
58.5	2706.245621	-0.008099	RPGGEPSPEGTTGQSYNQYSQR
38.3	2706.245621	-0.008099	RPGGEPSPEGTTGQSYNQYSQR

Mascot: http://www.matrixscience.com/

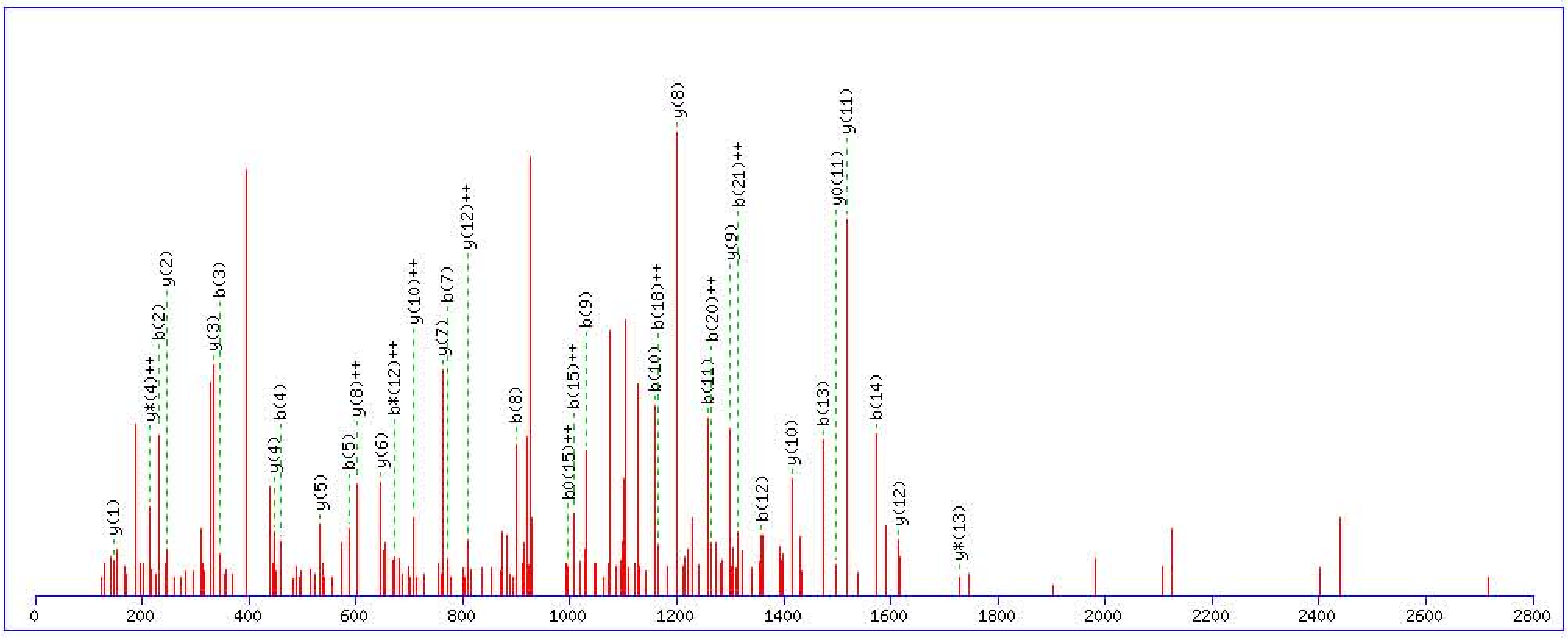
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEIDKPSQMQVTDVQDNSISVK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

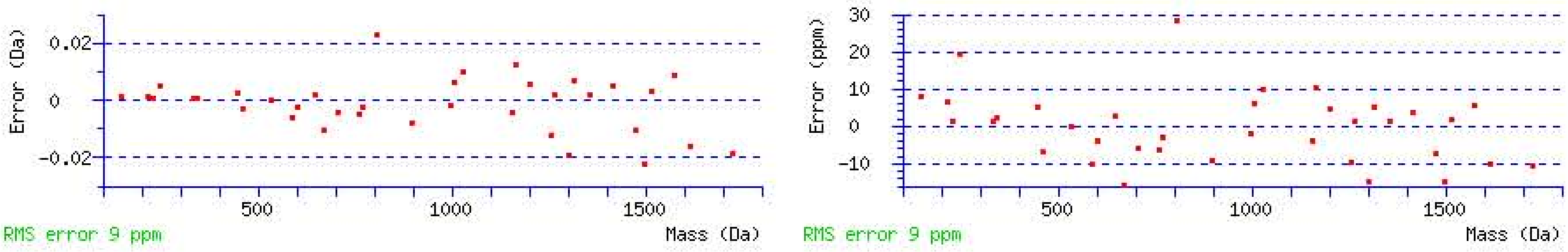
Match to Query 51217: 2772.363312 from(925.128380,3+) rtinseconds(1982) index(31727)
Title: Locus:1.1.1.3353.24 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 2772.367386
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15     : Biotin:Thermo-21345 (Q)
Ions Score: 69  Expect: 3.7e-006
Matches : 36/240 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	102.054955	51.531116			84.044390	42.525833	T							22
2	***231.097548***	116.052412			213.086983	107.047130	E	2672.326980	1336.667128	2655.300431	1328.153854	2654.316415	1327.661846	21
3	***344.181612***	172.594444			326.171047	163.589162	I	2543.284387	1272.145832	2526.257838	1263.632557	2525.273822	1263.140549	20
4	***459.208555***	230.107916			441.197990	221.102633	D	2430.200323	1215.603799	2413.173774	1207.090525	2412.189758	1206.598517	19
5	***587.303518***	294.155397	570.276969	285.642123	569.292953	285.150115	K	2315.173380	1158.090328	2298.146831	1149.577053	2297.162815	1149.085046	18
6	684.356282	342.681779	667.329733	334.168505	666.345717	333.676497	P	2187.078417	1094.042847	2170.051868	1085.529572	2169.067852	1085.037564	17
7	***771.388310***	386.197793	754.361761	377.684519	753.377745	377.192511	S	2090.025653	1045.516465	2072.999104	1037.003190	2072.015088	1036.511182	16
8	***899.446888***	450.227082	882.420339	441.713808	881.436323	441.221800	Q	2002.993625	1002.000451	1985.967076	993.487176	1984.983060	992.995168	15
9	***1030.487373***	515.747325	1013.460824	507.234050	1012.476808	506.742042	M	1874.935047	937.971162	1857.908498	929.457887	1856.924482	928.965879	14
10	***1158.545951***	579.776614	1141.519402	571.263339	1140.535386	570.771331	Q	1743.894562	872.450919	1726.868013	863.937645	1725.883997	863.445637	13
11	***1257.614365***	629.310821	1240.587816	620.797546	1239.603800	620.305538	V	***1615.835984***	808.421630	1598.809435	799.908356	1597.825419	799.416348	12
12	***1358.662044***	679.834660	1341.635495	671.321386	1340.651479	670.829378	T	***1516.767570***	758.887423	1499.741021	750.374149	1498.757005	749.882141	11
13	***1473.688987***	737.348132	1456.662438	728.834857	1455.678422	728.342849	D	***1415.719891***	708.363584	1398.693342	699.850309	1397.709326	699.358301	10
14	***1572.757401***	786.882339	1555.730852	778.369064	1554.746836	777.877056	V	***1300.692948***	650.850112	1283.666399	642.336838	1282.682383	641.844830	9
15	2011.982727	**1006.495002**	1994.956178	997.981727	1993.972162	997.489719	Q	***1201.624534***	601.315905	1184.597985	592.802631	1183.613969	592.310623	8
16	2127.009670	1064.008473	2109.983121	1055.495199	2108.999105	1055.003191	D	***762.399208***	381.703242	745.372659	373.189968	744.388643	372.697960	7
17	2241.052597	1121.029937	2224.026048	1112.516662	2223.042032	1112.024654	N	***647.372265***	324.189771	630.345716	315.676496	629.361700	315.184488	6
18	2328.084625	**1164.545951**	2311.058076	1156.032676	2310.074060	1155.540668	S	***533.329338***	267.168307	516.302789	258.655033	515.318773	258.163025	5
19	2441.168689	1221.087983	2424.142140	1212.574708	2423.158124	1212.082700	I	***446.297310***	223.652293	429.270761	215.139019	428.286745	214.647011	4
20	2528.200717	**1264.603997**	2511.174168	1256.090722	2510.190152	1255.598714	S	***333.213246***	167.110261	316.186697	158.596986	315.202681	158.104978	3
21	2627.269131	**1314.138204**	2610.242582	1305.624929	2609.258566	1305.132921	V	***246.181218***	123.594247	229.154669	115.080972			2
22							K	***147.112804***	74.060040	130.086255	65.546765			1



NCBI **BLAST** search of TEIDKPSQMQVTDVQDNSISVK
(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	2772.367386	-0.004074	TEIDKPSQMQVTDVQDNSISVK
17.0	2772.367386	-0.004074	TEIDKPSQMQVTDVQDNSISVK
10.6	2772.367386	-0.004074	TEIDKPSQMQVTDVQDNSISVK

Mascot: http://www.matrixscience.com/

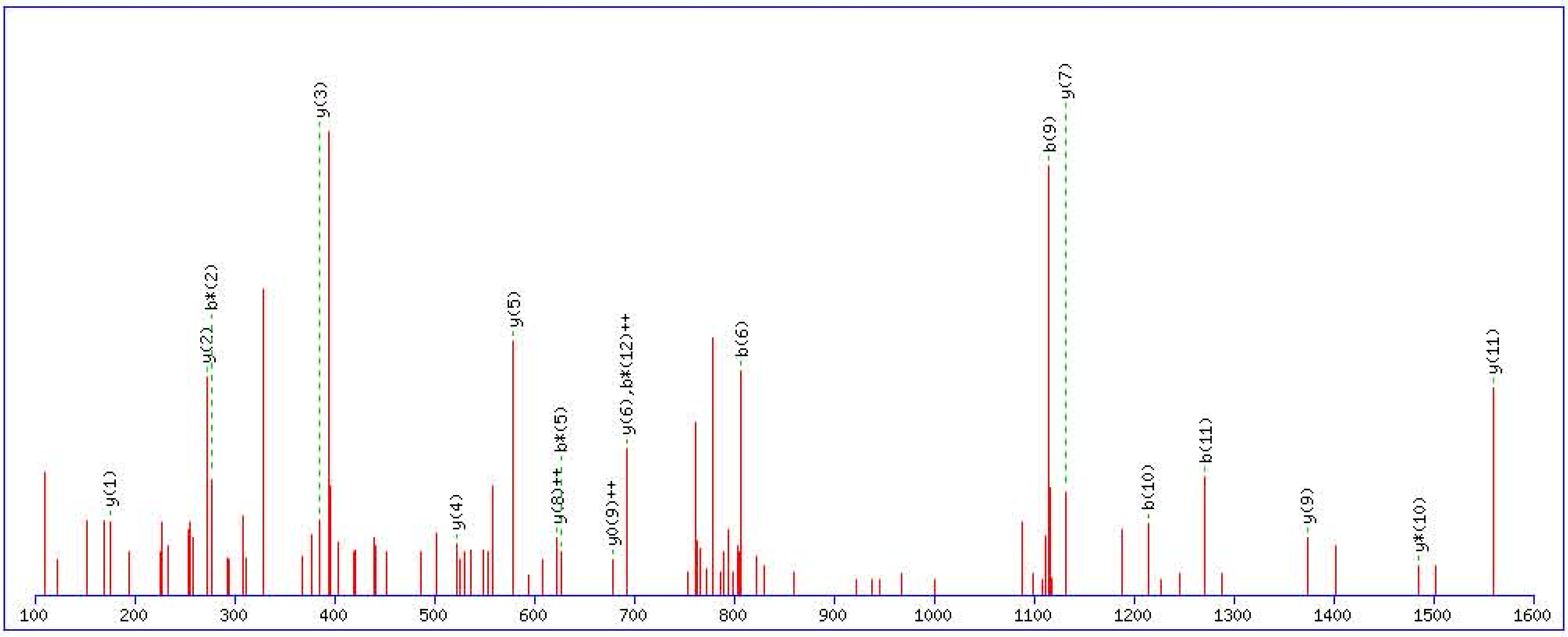
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HRPRPYPPNVGEEIQIGHIPR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

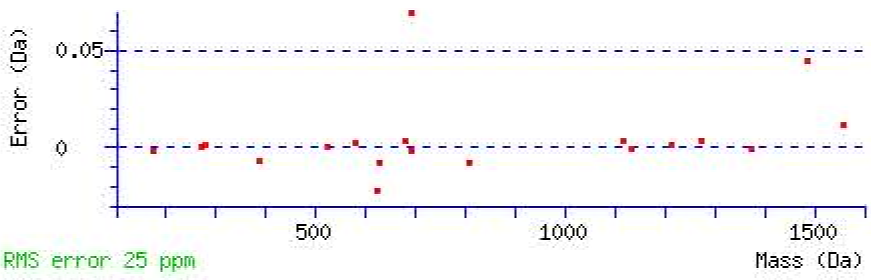
Match to Query 51224: 2772.466770 from(555.500630,5+) rtinseconds(1788) index(30523)
Title: Locus:1.1.1.3286.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

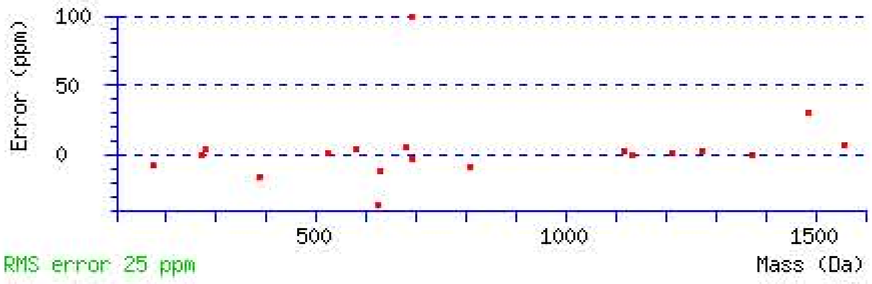
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2772.475815
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15 : Biotin:Thermo-21345 (Q)
Ions Score: 25 **Expect:** 0.0051
Matches : 19/200 fragment ions using 51 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							21
2	294.167299	147.587288	277.140750	139.074013			R	2636.424208	1318.715742	2619.397659	1310.202467	2618.413643	1309.710459	20
3	391.220063	196.113670	374.193514	187.600395			P	2480.323097	1240.665186	2463.296548	1232.151912	2462.312532	1231.659904	19
4	547.321174	274.164225	530.294625	265.650951			R	2383.270333	1192.138804	2366.243784	1183.625530	2365.259768	1183.133522	18
5	644.373938	322.690607	627.347389	314.177333			P	2227.169222	1114.088249	2210.142673	1105.574974	2209.158657	1105.082966	17
6	**807.437267**	404.222272	790.410718	395.708997			Y	2130.116458	1065.561867	2113.089909	1057.048592	2112.105893	1056.556584	16
7	904.490031	452.748654	887.463482	444.235379			P	1967.053129	984.030203	1950.026580	975.516928	1949.042564	975.024920	15
8	1001.542795	501.275036	984.516246	492.761761			P	1870.000365	935.503821	1852.973816	926.990546	1851.989800	926.498538	14
9	**1115.585722**	558.296499	1098.559173	549.783225			N	1772.947601	886.977439	1755.921052	878.464164	1754.937036	877.972156	13
10	**1214.654136**	607.830706	1197.627587	599.317432			V	1658.904674	829.955975	1641.878125	821.442701	1640.894109	820.950693	12
11	**1271.675600**	636.341438	1254.649051	627.828164			G	***1559.836260***	780.421768	1542.809711	771.908494	1541.825695	771.416486	11
12	1400.718193	700.862735	1383.691644	692.349460	1382.707628	691.857452	E	1502.814796	751.911036	1485.788247	743.397762	1484.804231	742.905754	10
13	1529.760786	765.384031	1512.734237	756.870757	1511.750221	756.378749	E	***1373.772203***	687.389740	1356.745654	678.876465	1355.761638	678.384457	9
14	1642.844850	821.926063	1625.818301	813.412789	1624.834285	812.920781	I	1244.729610	622.868443	1227.703061	614.355169			8
15	2082.070176	1041.538726	2065.043627	1033.025451	2064.059611	1032.533444	Q	***1131.645546***	566.326411	1114.618997	557.813137			7
16	2195.154240	1098.080758	2178.127691	1089.567484	2177.143675	1089.075476	I	***692.420220***	346.713748	675.393671	338.200474			6
17	2252.175704	1126.591490	2235.149155	1118.078215	2234.165139	1117.586208	G	***579.336156***	290.171716	562.309607	281.658442			5
18	2389.234616	1195.120946	2372.208067	1186.607671	2371.224051	1186.115664	H	***522.314692***	261.660984	505.288143	253.147710			4
19	2502.318680	1251.662978	2485.292131	1243.149704	2484.308115	1242.657696	I	***385.255780***	193.131528	368.229231	184.618254			3
20	2599.371444	1300.189360	2582.344895	1291.676086	2581.360879	1291.184078	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 HRPRPYPPNVGEEIQIGHIPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.3	2772.475815	-0.009045	HRPRPYPPNVGEEIQIGHIPR
0.8	2772.429306	0.037464	EKHLAILKENNISEEVEAPEVEPR

Mascot: http://www.matrixscience.com/

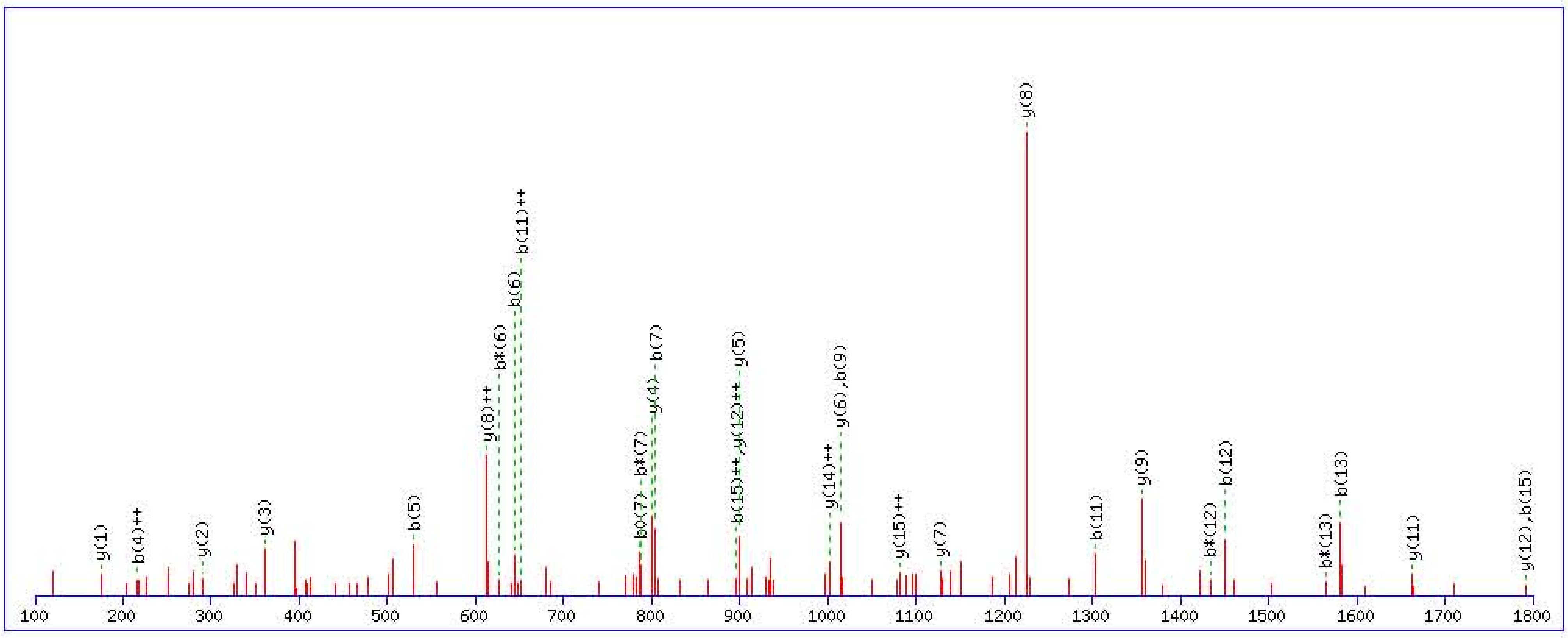
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TNTNVNCPIECFMPLDVQADR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

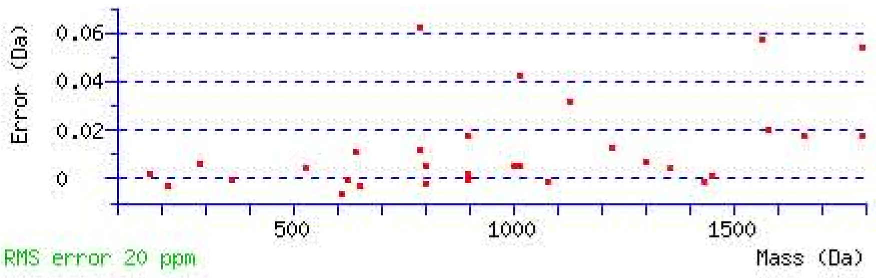
Match to Query 51583: 2804.287332 from(935.769720,3+) rtinseconds(2704) index(35859)
Title: Locus:1.1.1.3604.22 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

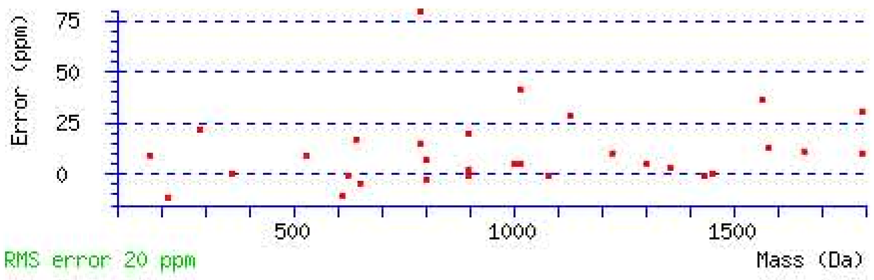
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2804.275421
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18    : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 3.2e-005
Matches : 32/236 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	102.054955	51.531116			84.044390	42.525833	T							21
2	***216.097882***	108.552579	199.071333	100.039305	198.087317	99.547296	N	2704.235012	1352.621144	2687.208463	1344.107869	2686.224447	1343.615861	20
3	317.145561	159.076418	300.119012	150.563144	299.134996	150.071136	T	2590.192085	1295.599680	2573.165536	1287.086406	2572.181520	1286.594398	19
4	431.188488	**216.097882**	414.161939	207.584608	413.177923	207.092600	N	2489.144406	1245.075841	2472.117857	1236.562566	2471.133841	1236.070558	18
5	***530.256902***	265.632089	513.230353	257.118815	512.246337	256.626807	V	2375.101479	1188.054377	2358.074930	1179.541103	2357.090914	1179.049095	17
6	***644.299829***	322.653553	627.273280	314.140278	626.289264	313.648270	N	2276.033065	1138.520170	2259.006516	1130.006896	2258.022500	1129.514888	16
7	***804.330478***	402.668877	787.303929	394.155603	786.319913	393.663595	C	2161.990138	1081.498707	2144.963589	1072.985432	2143.979573	1072.493424	15
8	901.383242	451.195259	884.356693	442.681985	883.372677	442.189977	P	2001.959489	1001.483383	1984.932940	992.970108	1983.948924	992.478100	14
9	***1014.467306***	507.737291	997.440757	499.224017	996.456741	498.732009	I	1904.906725	952.957001	1887.880176	944.443726	1886.896160	943.951718	13
10	1143.509899	572.258588	1126.483350	563.745313	1125.499334	563.253305	E	***1791.822661***	896.414969	1774.796112	887.901694	1773.812096	887.409686	12
11	***1303.540548***	**652.273912**	1286.513999	643.760638	1285.529983	643.268630	C	***1662.780068***	831.893672	1645.753519	823.380398	1644.769503	822.888390	11
12	***1450.608962***	725.808119	1433.582413	717.294845	1432.598397	716.802837	F	1502.749419	751.878348	1485.722870	743.365073	1484.738854	742.873065	10
13	***1581.649447***	791.328362	1564.622898	782.815087	1563.638882	782.323079	M	***1355.681005***	678.344141	1338.654456	669.830866	1337.670440	669.338858	9
14	1678.702211	839.854744	1661.675662	831.341469	1660.691646	830.849461	P	***1224.640520***	612.823898	1207.613971	604.310624	1206.629955	603.818616	8
15	***1791.786275***	**896.396776**	1774.759726	887.883501	1773.775710	887.391493	L	***1127.587756***	564.297516	1110.561207	555.784242	1109.577191	555.292234	7
16	1906.813218	953.910247	1889.786669	945.396973	1888.802653	944.904965	D	***1014.503692***	507.755484	997.477143	499.242210	996.493127	498.750202	6
17	2005.881632	1003.444454	1988.855083	994.931180	1987.871067	994.439172	V	***899.476749***	450.242013	882.450200	441.728738	881.466184	441.236730	5
18	2445.106958	1223.057117	2428.080409	1214.543843	2427.096393	1214.051835	Q	***800.408335***	400.707806	783.381786	392.194531	782.397770	391.702523	4
19	2516.144072	1258.575674	2499.117523	1250.062400	2498.133507	1249.570392	A	***361.183009***	181.095142	344.156460	172.581868	343.172444	172.089860	3
20	2631.171015	1316.089146	2614.144466	1307.575871	2613.160450	1307.083863	D	***290.145895***	145.576585	273.119346	137.063311	272.135330	136.571303	2
21							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TNTNVNCPIECFMPLDVQADR
(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	2804.275421	0.011911	TNTNVNCPIECFMPLDVQADR
24.3	2804.307587	-0.020255	DYAGVFSDAGLTFTSSSGQQTAQR
10.0	2804.307587	-0.020255	DYAGVFSDAGLTFTSSSGQQTAQR
5.3	2804.307587	-0.020255	DYAGVFSDAGLTFTSSSGQQTAQR

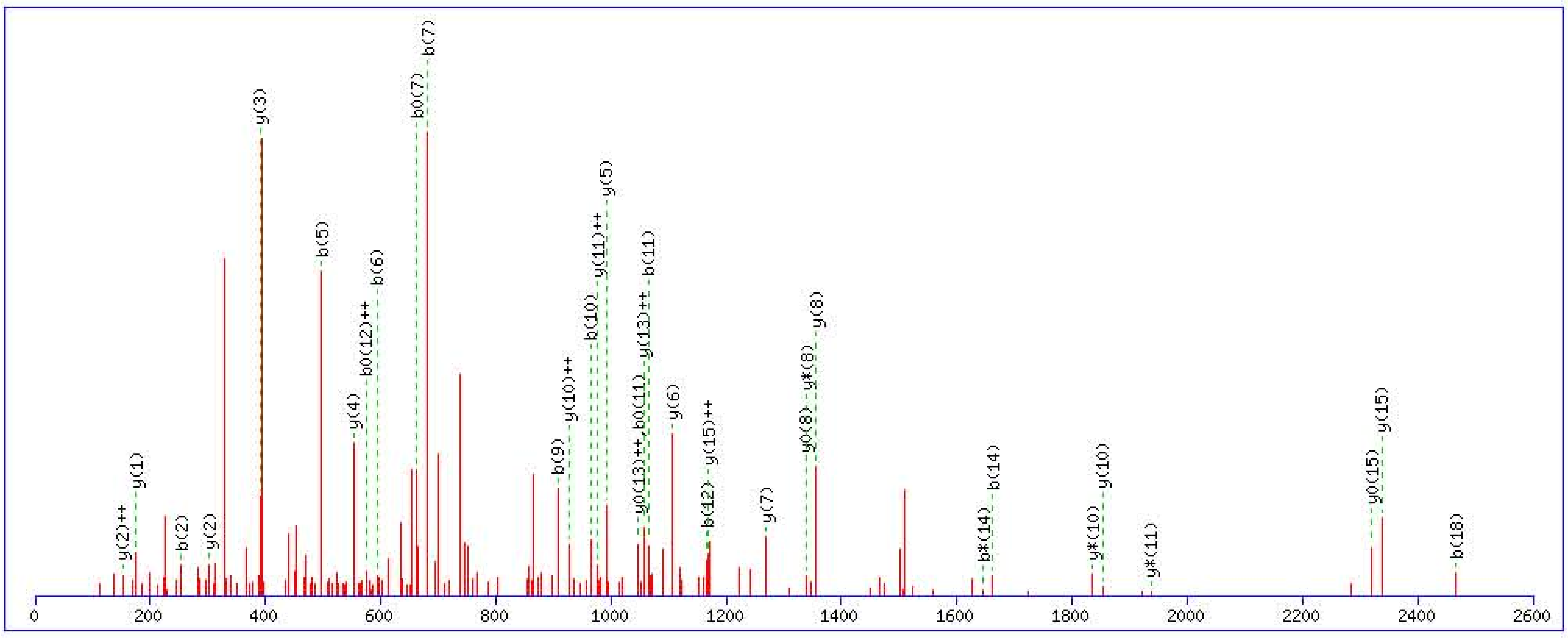
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPGGEPSPEGTTGQSYNQYSQR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

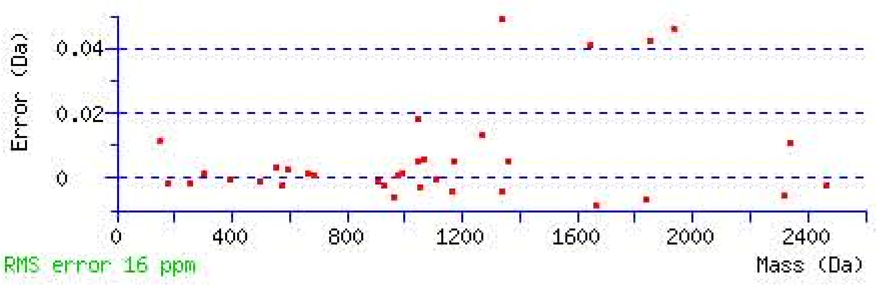
Match to Query 54131: 3017.406816 from(755.358980,4+) rtinseconds(1814) index(30696)
Title: Locus:1.1.1.3295.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

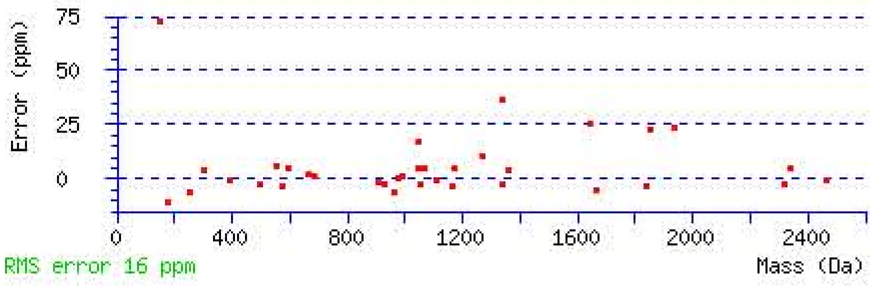
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3017.412369
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Biotin:Thermo-21345 (Q)
Q18 : Biotin:Thermo-21345 (Q)
Ions Score: 55 **Expect:** 4.9e-005
Matches : 35/240 fragment ions using 71 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	157.108387	79.057831	140.081838	70.544557			R							22
2	***254.161151***	127.584213	237.134602	119.070939			P	2862.318543	1431.662909	2845.291994	1423.149635	2844.307978	1422.657627	21
3	311.182615	156.094945	294.156066	147.581671			G	2765.265779	1383.136527	2748.239230	1374.623253	2747.255214	1374.131245	20
4	368.204079	184.605677	351.177530	176.092403			G	2708.244315	1354.625795	2691.217766	1346.112521	2690.233750	1345.620513	19
5	***497.246672***	249.126974	480.220123	240.613700	479.236107	240.121692	E	2651.222851	1326.115063	2634.196302	1317.601789	2633.212286	1317.109781	18
6	***594.299436***	297.653356	577.272887	289.140082	576.288871	288.648074	P	2522.180258	1261.593767	2505.153709	1253.080492	2504.169693	1252.588484	17
7	***681.331464***	341.169370	664.304915	332.656095	663.320899	332.164087	S	2425.127494	1213.067385	2408.100945	1204.554110	2407.116929	1204.062102	16
8	778.384228	389.695752	761.357679	381.182478	760.373663	380.690470	P	***2338.095466***	1169.551371	2321.068917	1161.038096	2320.084901	1160.546088	15
9	***907.426821***	454.217049	890.400272	445.703774	889.416256	445.211766	E	2241.042702	1121.024989	2224.016153	1112.511714	2223.032137	1112.019706	14
10	***964.448285***	482.727781	947.421736	474.214506	946.437720	473.722498	G	2112.000109	1056.503692	2094.973560	1047.990418	2093.989544	1047.498410	13
11	***1065.495964***	533.251620	1048.469415	524.738346	1047.485399	524.246337	T	2054.978645	1027.992960	2037.952096	1019.479686	2036.968080	1018.987678	12
12	***1166.543643***	583.775460	1149.517094	575.262185	1148.533078	574.770177	T	1953.930966	977.469121	1936.904417	968.955847	1935.920401	968.463839	11
13	1223.565107	612.286191	1206.538558	603.772917	1205.554542	603.280909	G	***1852.883287***	926.945282	1835.856738	918.432007	1834.872722	917.939999	10
14	***1662.790433***	831.898854	1645.763884	823.385580	1644.779868	822.893572	Q	1795.861823	898.434550	1778.835274	889.921275	1777.851258	889.429267	9
15	1749.822461	875.414869	1732.795912	866.901594	1731.811896	866.409586	S	***1356.636497***	678.821887	1339.609948	670.308612	1338.625932	669.816604	8
16	1912.885790	956.946533	1895.859241	948.433259	1894.875225	947.941251	Y	***1269.604469***	635.305873	1252.577920	626.792598	1251.593904	626.300590	7
17	2026.928717	1013.967997	2009.902168	1005.454722	2008.918152	1004.962714	N	***1106.541140***	553.774208	1089.514591	545.260934	1088.530575	544.768926	6
18	***2466.154043***	1233.580659	2449.127494	1225.067385	2448.143478	1224.575377	Q	***992.498213***	496.752745	975.471664	488.239470	974.487648	487.747462	5
19	2629.217372	1315.112324	2612.190823	1306.599049	2611.206807	1306.107041	Y	***553.272887***	277.140082	536.246338	268.626807	535.262322	268.134799	4
20	2716.249400	1358.628338	2699.222851	1350.115063	2698.238835	1349.623056	S	***390.209558***	195.608417	373.183009	187.095143	372.198993	186.603135	3
21	2844.307978	1422.657627	2827.281429	1414.144353	2826.297413	1413.652345	Q	***303.177530***	152.092403	286.150981	143.579129			2
22							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of RPGGEPSPEGTTGQSYNQYSQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.3	3017.412369	-0.005553	RPGGEPSPEGTTGQSYNQYSQR
47.7	3017.412369	-0.005553	RPGGEPSPEGTTGQSYNQYSQR
18.6	3017.412369	-0.005553	RPGGEPSPEGTTGQSYNQYSQR

Mascot: http://www.matrixscience.com/

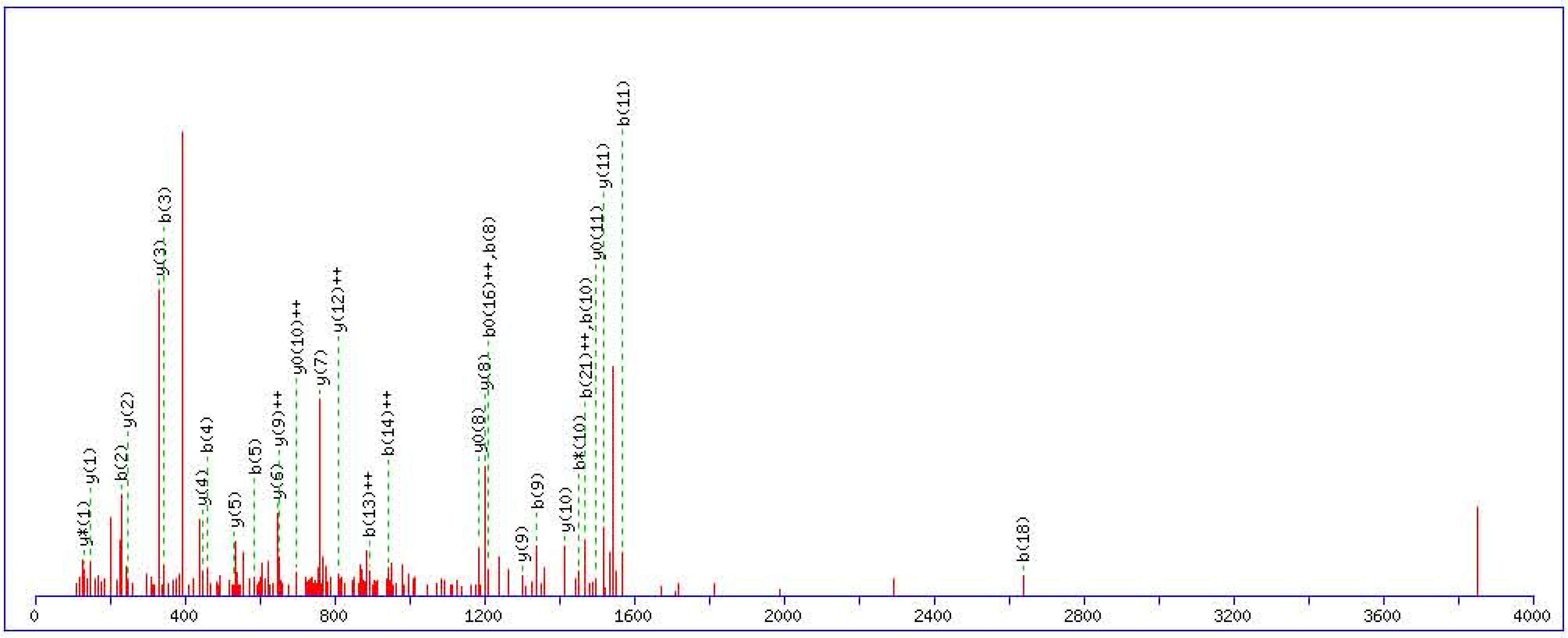
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEIDKPSQMQVTDVQDNSISVK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

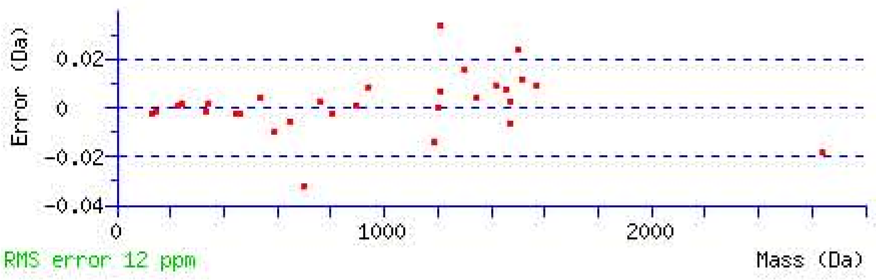
Match to Query 54629: 3083.527736 from(771.889210,4+) rtinseconds(2173) index(32873)
Title: Locus:1.1.1.3420.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

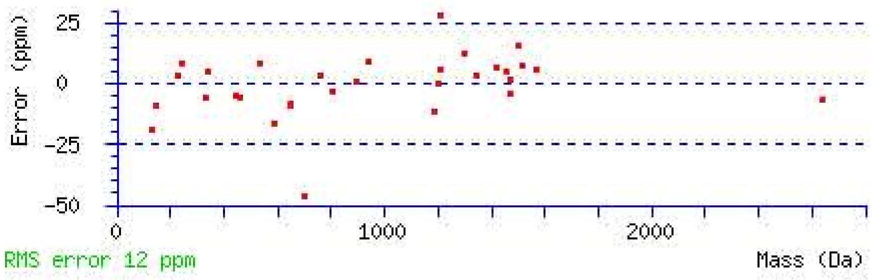
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3083.534134
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Q15 : Biotin:Thermo-21345 (Q)
Ions Score: 40 **Expect:** 0.0027
Matches : 31/240 fragment ions using 95 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							22
2	***231.097548***	116.052412			213.086983	107.047130	E	2983.493728	1492.250502	2966.467179	1483.737228	2965.483163	1483.245220	21
3	***344.181612***	172.594444			326.171047	163.589162	I	2854.451135	1427.729206	2837.424586	1419.215931	2836.440570	1418.723923	20
4	***459.208555***	230.107916			441.197990	221.102633	D	2741.367071	1371.187174	2724.340522	1362.673899	2723.356506	1362.181891	19
5	***587.303518***	294.155397	570.276969	285.642123	569.292953	285.150115	K	2626.340128	1313.673702	2609.313579	1305.160428	2608.329563	1304.668420	18
6	684.356282	342.681779	667.329733	334.168505	666.345717	333.676497	P	2498.245165	1249.626220	2481.218616	1241.112946	2480.234600	1240.620938	17
7	771.388310	386.197793	754.361761	377.684519	753.377745	377.192511	S	2401.192401	1201.099838	2384.165852	1192.586564	2383.181836	1192.094556	16
8	***1210.613636***	605.810456	1193.587087	597.297182	1192.603071	596.805174	Q	2314.160373	1157.583825	2297.133824	1149.070550	2296.149808	1148.578542	15
9	***1341.654121***	671.330699	1324.627572	662.817424	1323.643556	662.325416	M	1874.935047	937.971162	1857.908498	929.457887	1856.924482	928.965879	14
10	***1469.712699***	735.359988	1452.686150	726.846713	1451.702134	726.354705	Q	1743.894562	872.450919	1726.868013	863.937645	1725.883997	863.445637	13
11	***1568.781113***	784.894195	1551.754564	776.380920	1550.770548	775.888912	V	1615.835984	808.421630	1598.809435	799.908356	1597.825419	799.416348	12
12	1669.828792	835.418034	1652.802243	826.904760	1651.818227	826.412752	T	***1516.767570***	758.887423	1499.741021	750.374149	1498.757005	749.882141	11
13	1784.855735	**892.931506**	1767.829186	884.418231	1766.845170	883.926223	D	***1415.719891***	708.363584	1398.693342	699.850309	1397.709326	699.358301	10
14	1883.924149	**942.465713**	1866.897600	933.952438	1865.913584	933.460430	V	***1300.692948***	650.850112	1283.666399	642.336838	1282.682383	641.844830	9
15	2323.149475	1162.078376	2306.122926	1153.565101	2305.138910	1153.073093	Q	***1201.624534***	601.315905	1184.597985	592.802631	1183.613969	592.310623	8
16	2438.176418	1219.591847	2421.149869	1211.078573	2420.165853	1210.586565	D	***762.399208***	381.703242	745.372659	373.189968	744.388643	372.697960	7
17	2552.219345	1276.613311	2535.192796	1268.100036	2534.208780	1267.608028	N	***647.372265***	324.189771	630.345716	315.676496	629.361700	315.184488	6
18	***2639.251373***	1320.129325	2622.224824	1311.616050	2621.240808	1311.124042	S	***533.329338***	267.168307	516.302789	258.655033	515.318773	258.163025	5
19	2752.335437	1376.671357	2735.308888	1368.158082	2734.324872	1367.666074	I	***446.297310***	223.652293	429.270761	215.139019	428.286745	214.647011	4
20	2839.367465	1420.187371	2822.340916	1411.674096	2821.356900	1411.182088	S	***333.213246***	167.110261	316.186697	158.596986	315.202681	158.104978	3
21	2938.435879	**1469.721578**	2921.409330	1461.208303	2920.425314	1460.716295	V	***246.181218***	123.594247	229.154669	115.080972			2
22							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TEIDKPSQMQVTDVQDNSISVK
(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	3083.534134	-0.006398	TEIDKPSQMQVTDVQDNSISVK
30.8	3083.534134	-0.006398	TEIDKPSQMQVTDVQDNSISVK
10.4	3083.534134	-0.006398	TEIDKPSQMQVTDVQDNSISVK

Mascot: http://www.matrixscience.com/

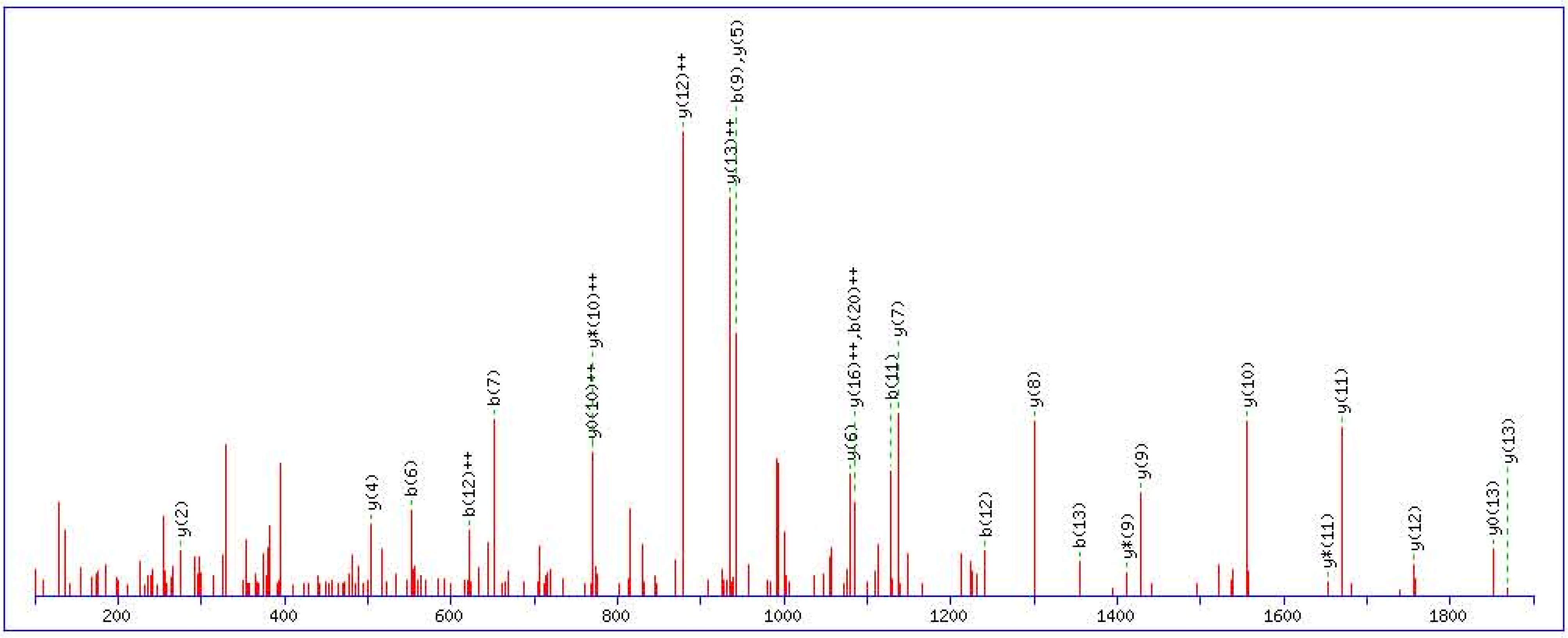
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLKPGVVYEGQLISIQQYGHQEVTR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

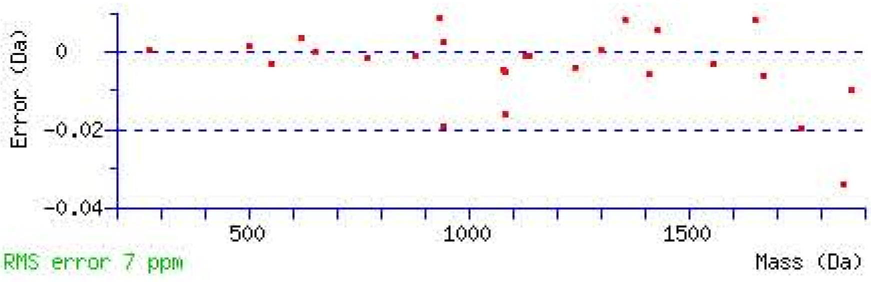
Match to Query 54768: 3109.637496 from(778.416650,4+) rtinseconds(2210) index(33085)
Title: Locus:1.1.1.3433.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

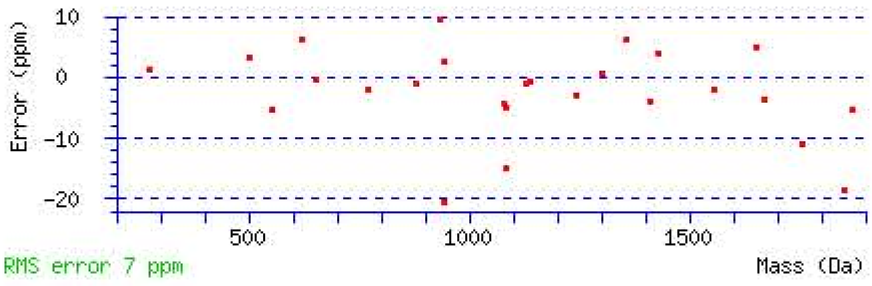
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3109.638275
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q21     : Biotin:Thermo-21345 (Q)
Ions Score: 68  Expect: 3.4e-006
Matches : 27/266 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	58.028740	29.518008					G							25
2	171.112804	86.060040					L	3053.624092	1527.315684	3036.597543	1518.802409	3035.613527	1518.310401	24
3	299.207767	150.107521	282.181218	141.594247			K	2940.540028	1470.773652	2923.513479	1462.260377	2922.529463	1461.768369	23
4	396.260531	198.633903	379.233982	190.120629			P	2812.445065	1406.726170	2795.418516	1398.212896	2794.434500	1397.720888	22
5	453.281995	227.144635	436.255446	218.631361			G	2715.392301	1358.199788	2698.365752	1349.686514	2697.381736	1349.194506	21
6	**552.350409**	276.678843	535.323860	268.165568			V	2658.370837	1329.689056	2641.344288	1321.175782	2640.360272	1320.683774	20
7	**651.418823**	326.213050	634.392274	317.699775			V	2559.302423	1280.154849	2542.275874	1271.641575	2541.291858	1271.149567	19
8	814.482152	407.744714	797.455603	399.231440			Y	2460.234009	1230.620642	2443.207460	1222.107368	2442.223444	1221.615360	18
9	**943.524745**	472.266011	926.498196	463.752736	925.514180	463.260728	E	2297.170680	1149.088978	2280.144131	1140.575703	2279.160115	1140.083695	17
10	1000.546209	500.776743	983.519660	492.263468	982.535644	491.771460	G	2168.128087	1084.567681	2151.101538	1076.054407	2150.117522	1075.562399	16
11	**1128.604787**	564.806032	1111.578238	556.292757	1110.594222	555.800749	Q	2111.106623	1056.056949	2094.080074	1047.543675	2093.096058	1047.051667	15
12	**1241.688851**	**621.348063**	1224.662302	612.834789	1223.678286	612.342781	L	1983.048045	992.027660	1966.021496	983.514386	1965.037480	983.022378	14
13	**1354.772915**	677.890095	1337.746366	669.376821	1336.762350	668.884813	I	***1869.963981***	935.485628	1852.937432	926.972354	1851.953416	926.480346	13
14	1441.804943	721.406109	1424.778394	712.892835	1423.794378	712.400827	S	***1756.879917***	878.943597	1739.853368	870.430322	1738.869352	869.938314	12
15	1554.889007	777.948141	1537.862458	769.434867	1536.878442	768.942859	I	***1669.847889***	835.427582	1652.821340	826.914308	1651.837324	826.422300	11
16	1682.947585	841.977430	1665.921036	833.464156	1664.937020	832.972148	Q	***1556.763825***	778.885551	1539.737276	770.372276	1538.753260	769.880268	10
17	1811.006163	906.006719	1793.979614	897.493445	1792.995598	897.001437	Q	***1428.705247***	714.856262	1411.678698	706.342987	1410.694682	705.850979	9
18	1974.069492	987.538384	1957.042943	979.025109	1956.058927	978.533101	Y	***1300.646669***	650.826973	1283.620120	642.313698	1282.636104	641.821690	8
19	2031.090956	1016.049116	2014.064407	1007.535841	2013.080391	1007.043833	G	***1137.583340***	569.295308	1120.556791	560.782034	1119.572775	560.290025	7
20	2168.149868	**1084.578572**	2151.123319	1076.065297	2150.139303	1075.573289	H	***1080.561876***	540.784576	1063.535327	532.271302	1062.551311	531.779293	6
21	2607.375194	1304.191235	2590.348645	1295.677960	2589.364629	1295.185952	Q	***943.502964***	472.255120	926.476415	463.741846	925.492399	463.249838	5
22	2736.417787	1368.712531	2719.391238	1360.199257	2718.407222	1359.707249	E	***504.277638***	252.642457	487.251089	244.129182	486.267073	243.637174	4
23	2835.486201	1418.246738	2818.459652	1409.733464	2817.475636	1409.241456	V	375.235045	188.121160	358.208496	179.607886	357.224480	179.115878	3
24	2936.533880	1468.770578	2919.507331	1460.257303	2918.523315	1459.765295	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
25							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GLKPGVVYEGQLISIQQYGHQEVTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.0	3109.638275	-0.000779	GLKPGVVYEGQLISIQQYGHQEVTR
37.4	3109.638275	-0.000779	GLKPGVVYEGQLISIQQYGHQEVTR
29.2	3109.638275	-0.000779	GLKPGVVYEGQLISIQQYGHQEVTR

Mascot: http://www.matrixscience.com/

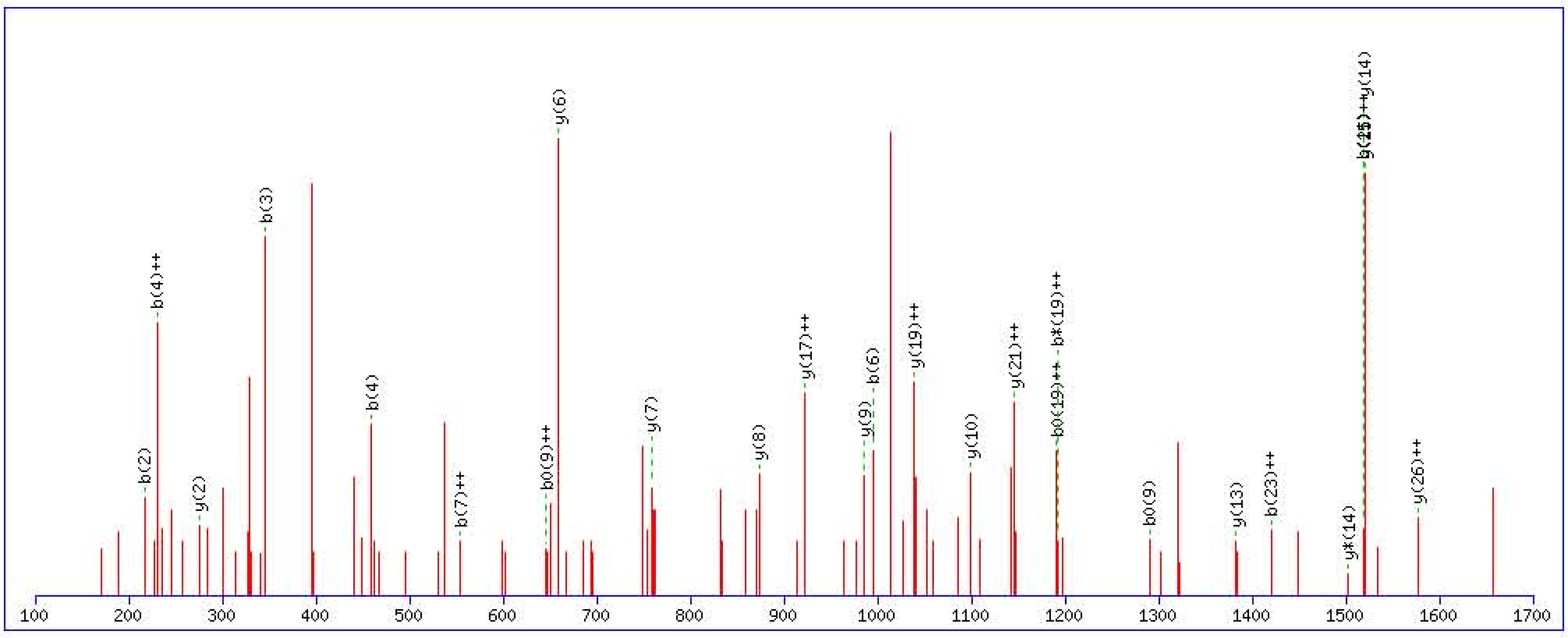
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TDELPQLVTLPHPNLHGPEILDVPSTVQK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

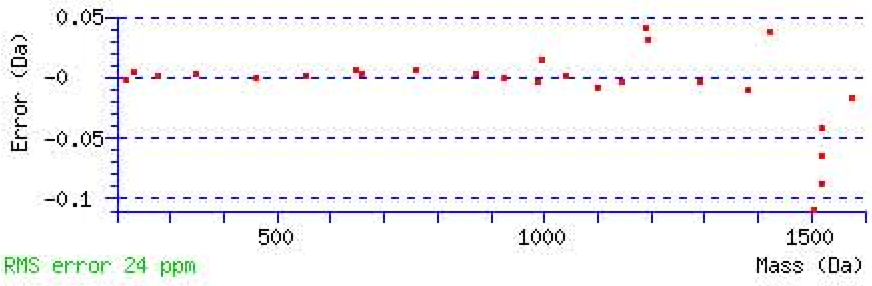
Match to Query 59572: 3497.861696 from(875.472700,4+) rtinseconds(2605) index(35237)
Title: Locus:1.1.1.3570.24 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

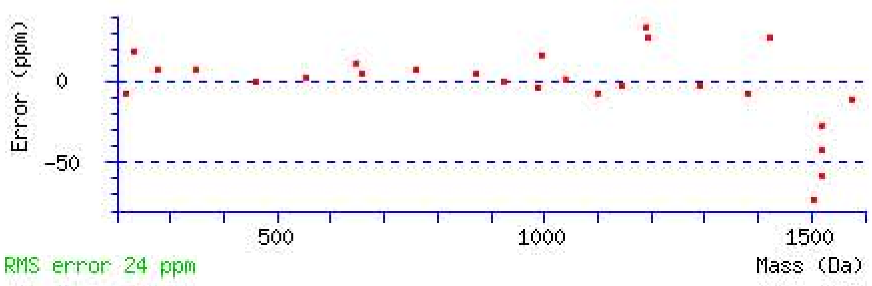
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3497.859238
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.042
Matches : 26/320 fragment ions using 65 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							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
26.1	3497.859238	0.002458	TDELPQLVTLPHPNLHGPEILDVPSTVQK

Mascot: http://www.matrixscience.com/

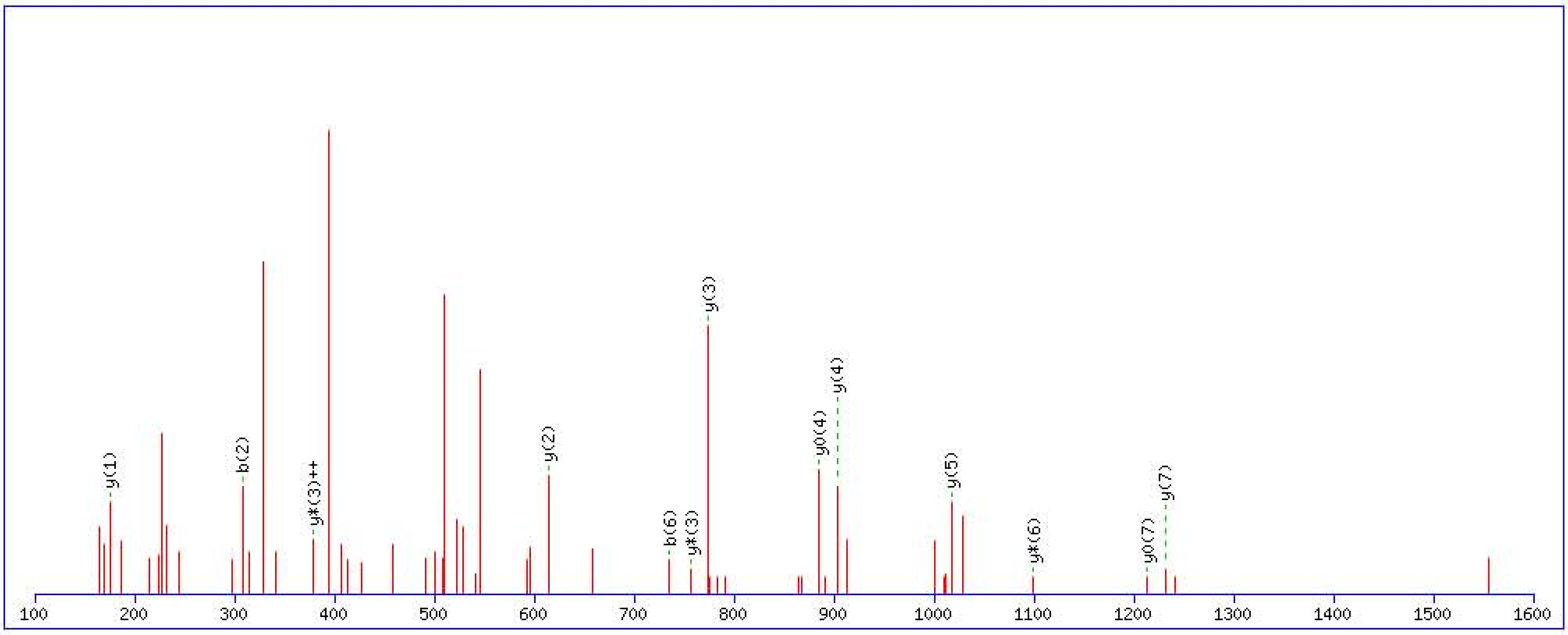
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MCVDVNECQR**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

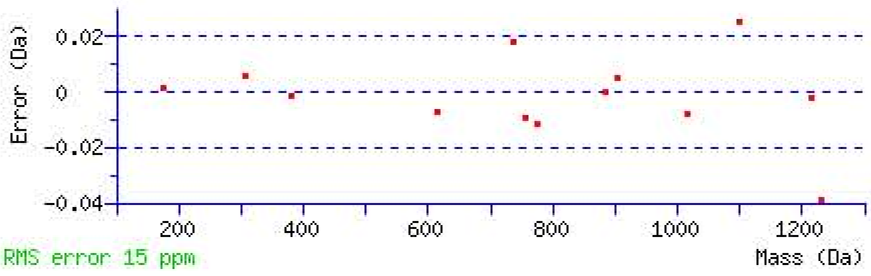
Match to Query 13702: 1636.683672 from(546.568500,3+) rtinseconds(1542) index(29057)
Title: Locus:1.1.1.3200.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

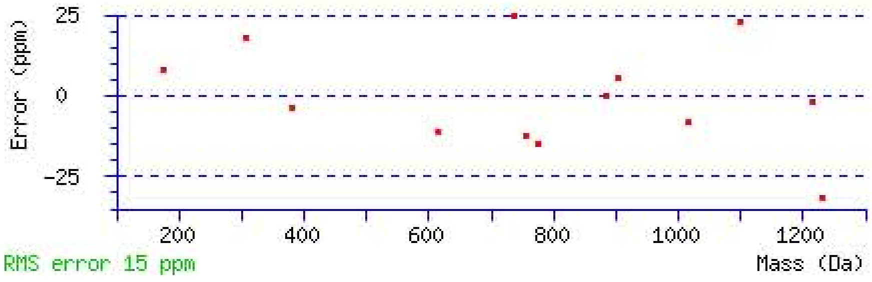
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1636.682999
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
Q9     : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.0042
Matches : 13/124 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	148.042676	74.524976					M							10
2	**308.073325**	154.540301					C	1490.654867	745.831072	1473.628318	737.317797	1472.644302	736.825789	9
3	407.141739	204.074508					V	1330.624218	665.815747	1313.597669	657.302473	1312.613653	656.810465	8
4	522.168682	261.587979			504.158117	252.582697	D	***1231.555804***	616.281540	1214.529255	607.768266	1213.545239	607.276258	7
5	621.237096	311.122186			603.226531	302.116904	V	1116.528861	558.768069	1099.502312	550.254794	1098.518296	549.762786	6
6	**735.280023**	368.143650	718.253474	359.630375	717.269458	359.138367	N	***1017.460447***	509.233862	1000.433898	500.720587	999.449882	500.228579	5
7	864.322616	432.664946	847.296067	424.151672	846.312051	423.659664	E	***903.417520***	452.212398	886.390971	443.699124	885.406955	443.207116	4
8	1024.353265	512.680271	1007.326716	504.166996	1006.342700	503.674988	C	***774.374927***	387.691102	757.348378	379.177827			3
9	1463.578591	732.292934	1446.552042	723.779659	1445.568026	723.287651	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 MCVDVNECQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.1	1636.682999	0.000673	MCVDVNECQR

Mascot: http://www.matrixscience.com/

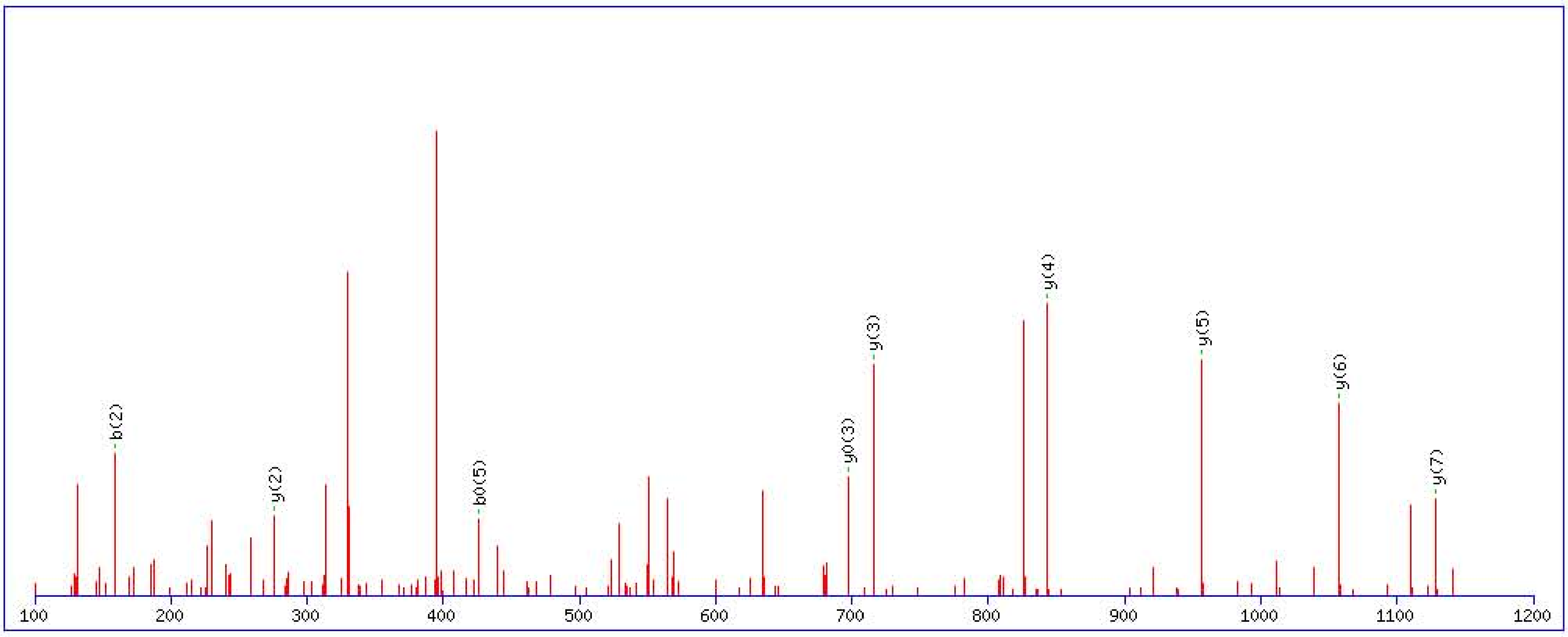
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SAATLQQEK**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

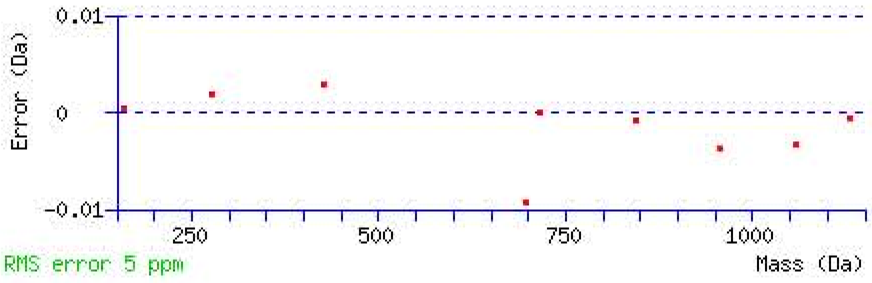
Match to Query 20085: 1285.665028 from(643.839790,2+) rtinseconds(1521) index(43021)
Title: Locus:1.1.1.3242.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

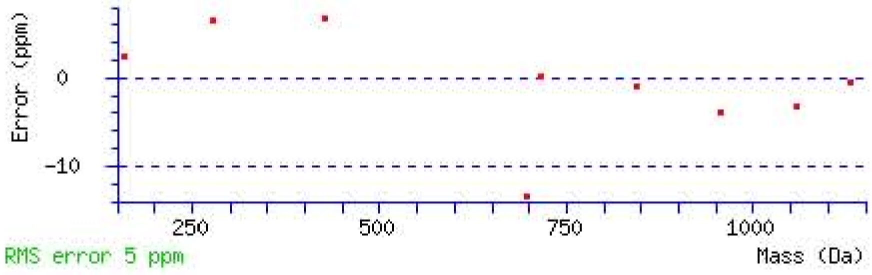
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1285.669998
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.00016
Matches : 9/84 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	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
49.0	1285.669998	-0.004970	SAATLQQEK
30.2	1285.669998	-0.004970	SAATLQQEK
7.9	1285.651367	0.013661	LLQAVENGDAEK
6.3	1285.652237	0.012791	AMQIQEQK
5.7	1285.669998	-0.004970	ASLDQGKEK
4.0	1285.649582	0.015446	SVPCPRCVRR
2.5	1285.662598	0.002430	EARSDQVKPEK
2.0	1285.669998	-0.004970	KQEESVQK
1.8	1285.651382	0.013646	ALEPTGQSGEAVK
1.5	1285.655380	0.009648	KYEFEKDLSK

Mascot: http://www.matrixscience.com/

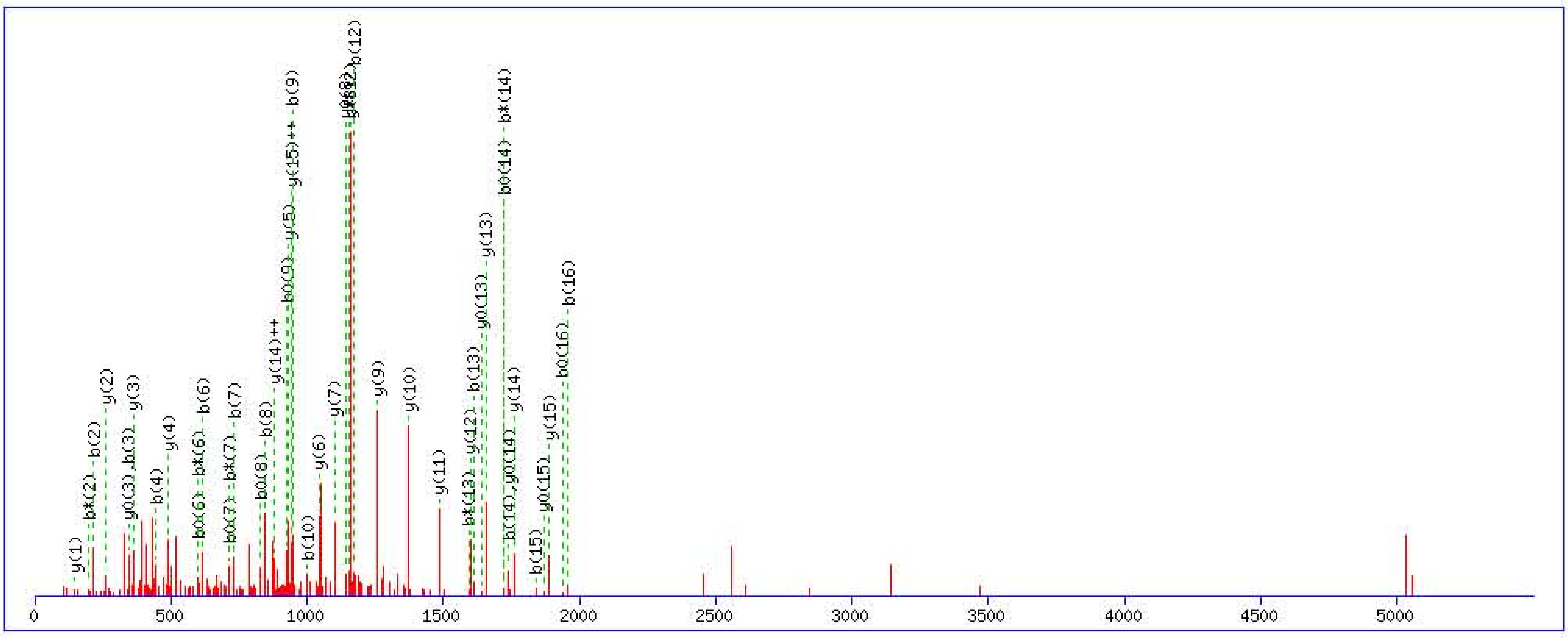
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SQETGDLDVGGLQETDK**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

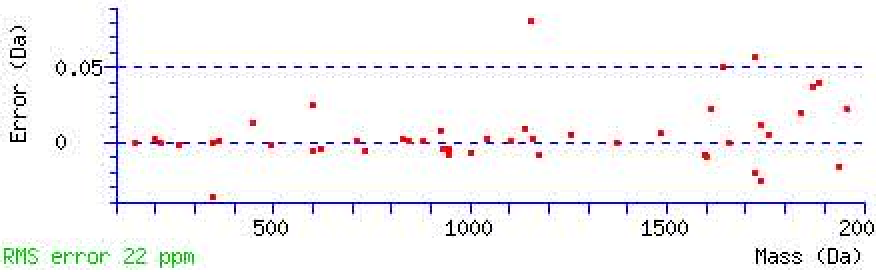
Match to Query 41643: 2101.975648 from(1051.995100,2+) rtinseconds(2045) index(32136)
Title: Locus:1.1.1.3375.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

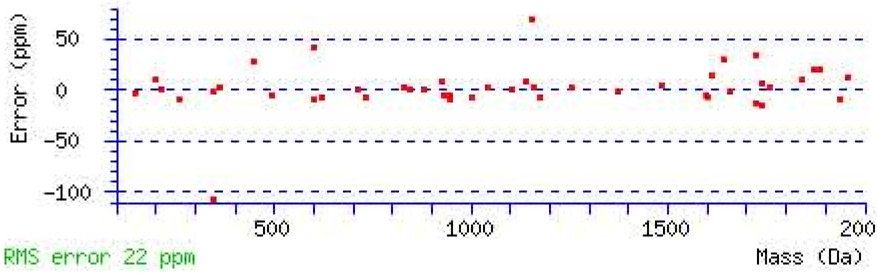
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 5500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2101.983780
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 92  Expect: 8.3e-009
Matches : 47/188 fragment ions using 90 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	**216.097882**	108.552579	199.071333	100.039305	198.087317	99.547296	Q	2015.959015	1008.483146	1998.932466	999.969871	1997.948450	999.477863	16
3	**345.140475**	173.073875	328.113926	164.560601	327.129910	164.068593	E	***1887.900437***	944.453857	1870.873888	935.940582	1869.889872	935.448574	15
4	**446.188154**	223.597715	429.161605	215.084441	428.177589	214.592433	T	***1758.857844***	879.932560	1741.831295	871.419286	1740.847279	870.927278	14
5	503.209618	252.108447	486.183069	243.595172	485.199053	243.103164	G	***1657.810165***	829.408721	1640.783616	820.895446	1639.799600	820.403438	13
6	**618.236561**	309.621919	601.210012	301.108644	600.225996	300.616636	D	***1600.788701***	800.897989	1583.762152	792.384714	1582.778136	791.892706	12
7	**731.320625**	366.163951	714.294076	357.650676	713.310060	357.158668	L	***1485.761758***	743.384517	1468.735209	734.871243	1467.751193	734.379235	11
8	**846.347568**	423.677422	829.321019	415.164148	828.337003	414.672140	D	***1372.677694***	686.842485	1355.651145	678.329211	1354.667129	677.837203	10
9	**945.415982**	473.211629	928.389433	464.698354	927.405417	464.206347	V	***1257.650751***	629.329014	1240.624202	620.815739	1239.640186	620.323731	9
10	**1002.437446**	501.722361	985.410897	493.209087	984.426881	492.717079	G	***1158.582337***	579.794807	1141.555788	571.281532	1140.571772	570.789524	8
11	1059.458910	530.233093	1042.432361	521.719819	1041.448345	521.227811	G	***1101.560873***	551.284075	1084.534324	542.770800	1083.550308	542.278792	7
12	**1172.542974**	586.775125	1155.516425	578.261851	1154.532409	577.769842	L	***1044.539409***	522.773343	1027.512860	514.260068	1026.528844	513.768060	6
13	**1611.768300**	806.387788	1594.741751	797.874514	1593.757735	797.382505	Q	***931.455345***	466.231311	914.428796	457.718036	913.444780	457.226028	5
14	**1740.810893**	870.909085	1723.784344	862.395810	1722.800328	861.903802	E	***492.230019***	246.618648	475.203470	238.105373	474.219454	237.613365	4
15	**1841.858572**	921.432924	1824.832023	912.919650	1823.848007	912.427642	T	***363.187426***	182.097351	346.160877	173.584077	345.176861	173.092069	3
16	**1956.885515**	978.946396	1939.858966	970.433121	1938.874950	969.941113	D	***262.139747***	131.573512	245.113198	123.060237	244.129182	122.568229	2
17							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SQETGDLDVGGLQETDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
91.8	2101.983780	-0.008132	SQETGDLDVGGLQETDK
5.4	2101.988480	-0.012832	MQQVGGNSQTESSLPGR
4.2	2101.978729	-0.003081	KSFMMIKYMHDHYLDK
4.2	2101.978729	-0.003081	KSFMMLKYMHDHYLDK
4.0	2101.978729	-0.003081	KSFMMIKYMHDHYLDK
4.0	2101.978729	-0.003081	KSFMMLKYMHDHYLDK
3.6	2101.959503	0.016145	GNCQTQGDSILDCVPK
3.6	2101.959503	0.016145	GNCQTQGDSILDCVPK
3.1	2101.978729	-0.003081	KSFMMIKYMHDHYLDK
3.1	2101.978729	-0.003081	KSFMMLKYMHDHYLDK

Mascot: http://www.matrixscience.com/

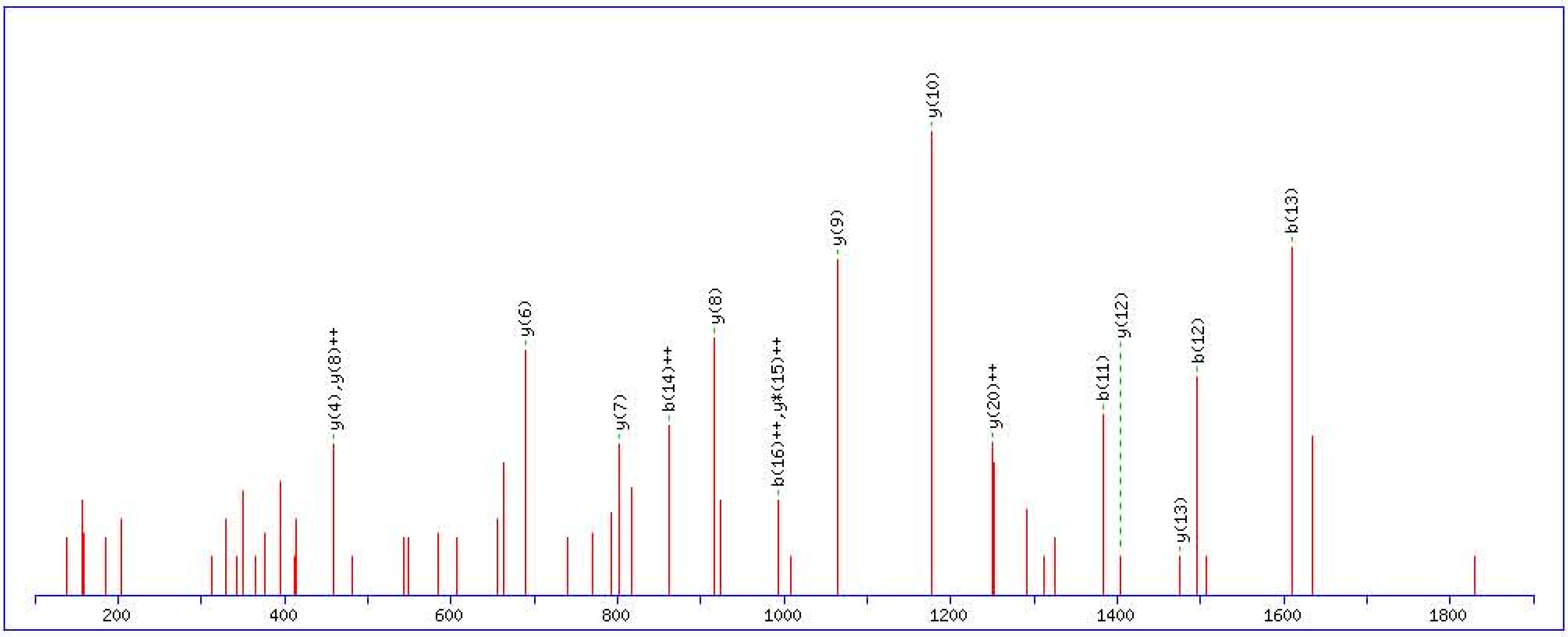
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AITPPHPASQANIIFDITEGNLR**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

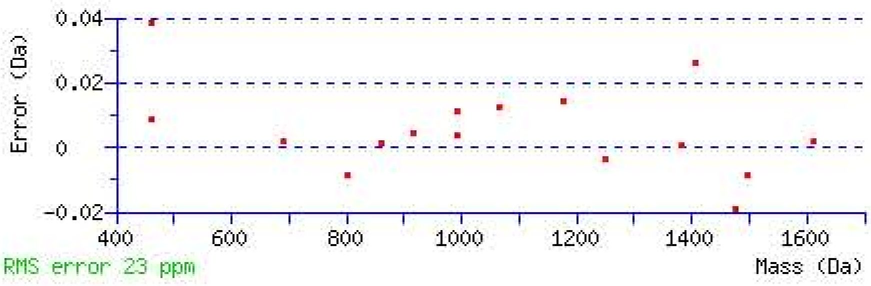
Match to Query 51337: 2785.457232 from(929.493020,3+) rtinseconds(2721) index(36004)
Title: Locus:1.1.1.3610.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

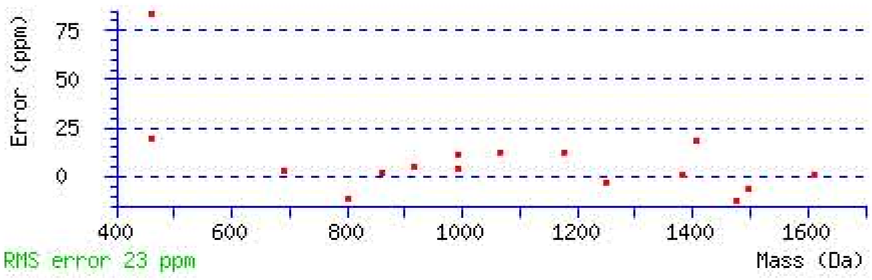
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2785.458496
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0076
Matches : 16/234 fragment ions using 29 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833					A							23
2	185.128454	93.067865					I	2715.428684	1358.217980	2698.402135	1349.704705	2697.418119	1349.212697	22
3	286.176133	143.591704			268.165568	134.586422	T	2602.344620	1301.675948	2585.318071	1293.162673	2584.334055	1292.670665	21
4	383.228897	192.118087			365.218332	183.112804	P	2501.296941	1251.152108	2484.270392	1242.638834	2483.286376	1242.146826	20
5	480.281661	240.644469			462.271096	231.639186	P	2404.244177	1202.625726	2387.217628	1194.112452	2386.233612	1193.620444	19
6	617.340573	309.173925			599.330008	300.168642	H	2307.191413	1154.099344	2290.164864	1145.586070	2289.180848	1145.094062	18
7	714.393337	357.700307			696.382772	348.695024	P	2170.132501	1085.569888	2153.105952	1077.056614	2152.121936	1076.564606	17
8	785.430451	393.218864			767.419886	384.213581	A	2073.079737	1037.043506	2056.053188	1028.530232	2055.069172	1028.038224	16
9	872.462479	436.734878			854.451914	427.729595	S	2002.042623	1001.524950	1985.016074	993.011675	1984.032058	992.519667	15
10	1311.687805	656.347541	1294.661256	647.834266	1293.677240	647.342258	Q	1915.010595	958.008936	1897.984046	949.495661	1897.000030	949.003653	14
11	**1382.724919**	691.866098	1365.698370	683.352823	1364.714354	682.860815	A	***1475.785269***	738.396273	1458.758720	729.882998	1457.774704	729.390990	13
12	**1496.767846**	748.887561	1479.741297	740.374287	1478.757281	739.882278	N	***1404.748155***	702.877716	1387.721606	694.364441	1386.737590	693.872433	12
13	**1609.851910**	805.429593	1592.825361	796.916318	1591.841345	796.424310	I	1290.705228	645.856252	1273.678679	637.342978	1272.694663	636.850970	11
14	1722.935974	**861.971625**	1705.909425	853.458350	1704.925409	852.966342	I	***1177.621164***	589.314220	1160.594615	580.800946	1159.610599	580.308938	10
15	1870.004388	935.505832	1852.977839	926.992557	1851.993823	926.500549	F	***1064.537100***	532.772188	1047.510551	524.258914	1046.526535	523.766906	9
16	1985.031331	**993.019303**	1968.004782	984.506029	1967.020766	984.014021	D	***917.468686***	459.237981	900.442137	450.724707	899.458121	450.232699	8
17	2098.115395	1049.561335	2081.088846	1041.048061	2080.104830	1040.556053	I	***802.441743***	401.724510	785.415194	393.211235	784.431178	392.719227	7
18	2199.163074	1100.085175	2182.136525	1091.571900	2181.152509	1091.079892	T	***689.357679***	345.182478	672.331130	336.669203	671.347114	336.177195	6
19	2328.205667	1164.606471	2311.179118	1156.093197	2310.195102	1155.601189	E	588.310000	294.658638	571.283451	286.145364	570.299435	285.653356	5
20	2385.227131	1193.117203	2368.200582	1184.603929	2367.216566	1184.111921	G	***459.267407***	230.137341	442.240858	221.624067			4
21	2499.270058	1250.138667	2482.243509	1241.625392	2481.259493	1241.133384	N	402.245943	201.626610	385.219394	193.113335			3
22	2612.354122	1306.680699	2595.327573	1298.167424	2594.343557	1297.675416	L	288.203016	144.605146	271.176467	136.091872			2
23							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of AITPPHPASQANIIFDITEGNLR
(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	2785.458496	-0.001264	AITPPHPASQANIIFDITEGNLR

Mascot: http://www.matrixscience.com/

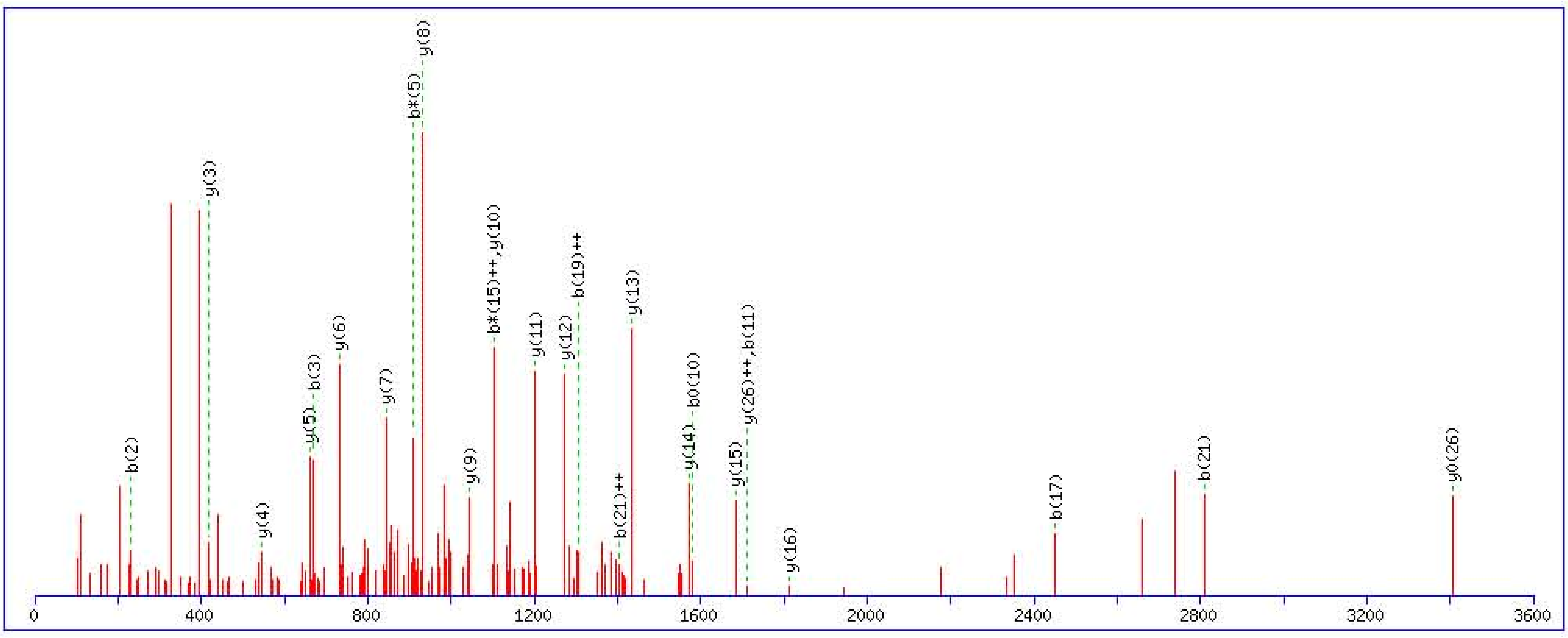
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVQEQCCHSQLEELHCATGISLANEQDR**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

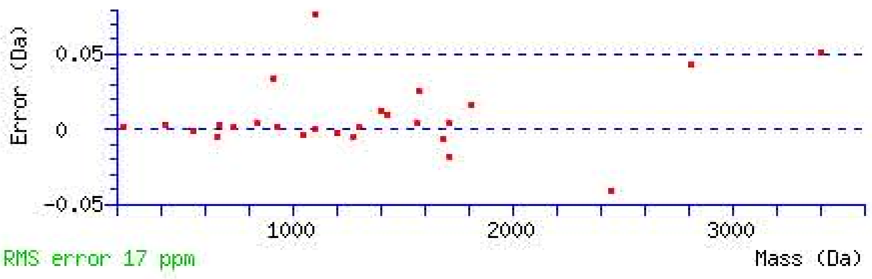
Match to Query 60712: 3653.611256 from(914.410090,4+) rtinseconds(2002) index(31903)
Title: Locus:1.1.1.3360.25 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

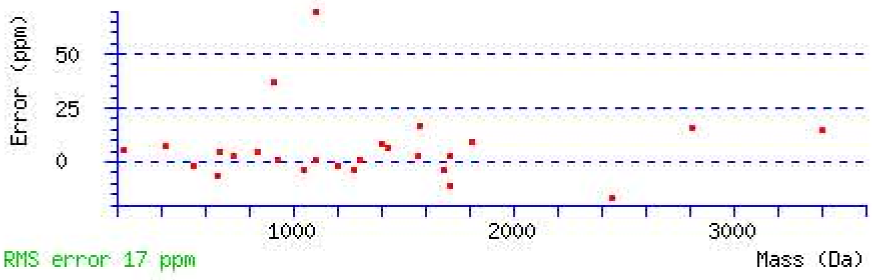
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 79  Expect: 8.2e-008
Matches : 26/312 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	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
78.9	3653.615311	-0.004055	MVQEQCCHSQLEELHCATGISLANEQDR
76.5	3653.615311	-0.004055	MVQEQCCHSQLEELHCATGISLANEQDR
76.4	3653.615311	-0.004055	MVQEQCCHSQLEELHCATGISLANEQDR

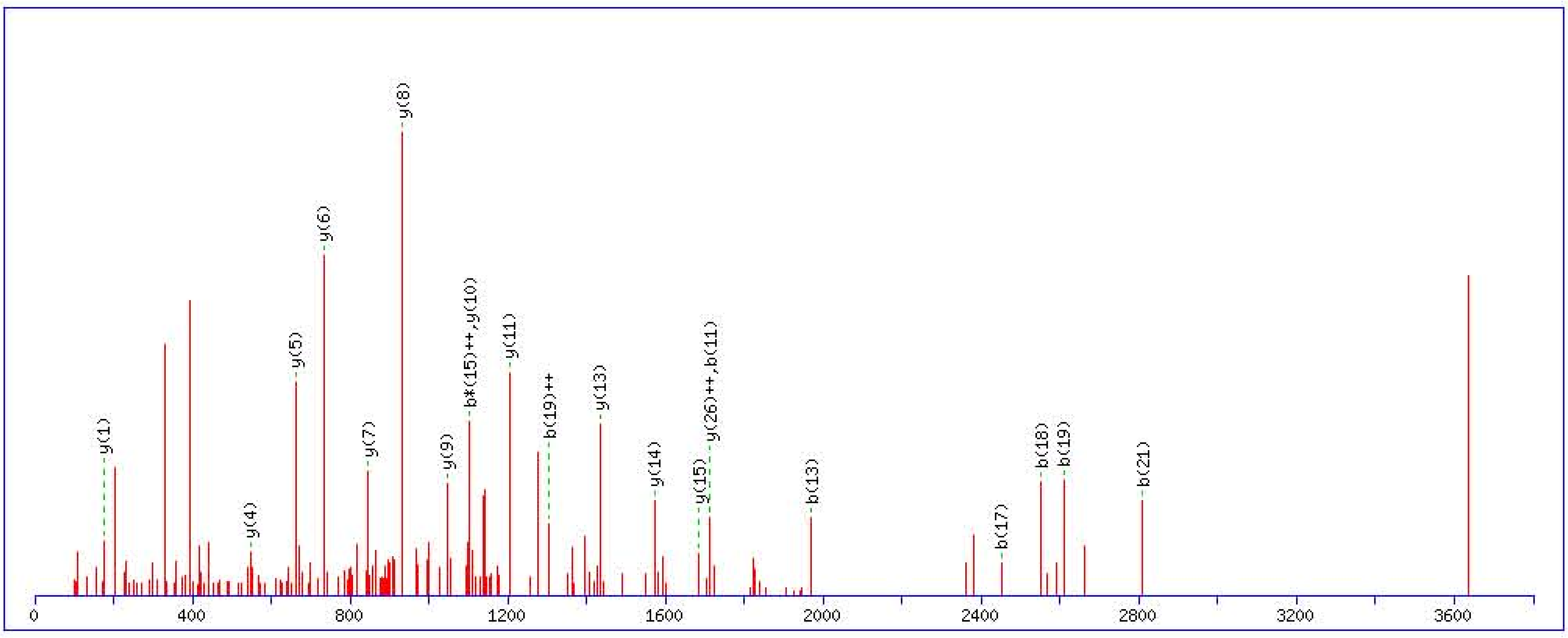
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVQEQCCHSQLEELHCATGISLANEQDR**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

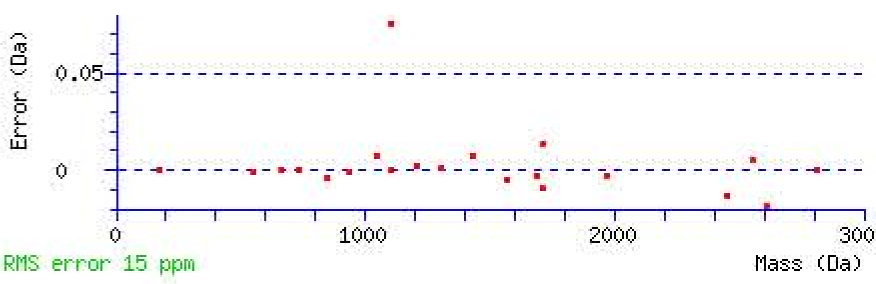
Match to Query 60713: 3653.611256 from(914.410090,4+) rtinseconds(1993) index(31828)
Title: Locus:1.1.1.3357.25 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

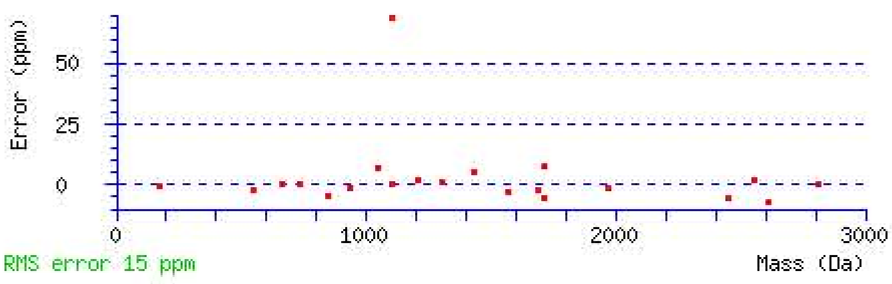
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3653.615311
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 85  Expect: 2.2e-008
Matches : 21/312 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	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	359.174753	180.091015	342.148204	171.577740			Q	3424.513708	1712.760492	3407.487159	1704.247217	3406.503143	1703.755209	26
4	488.217346	244.612311	471.190797	236.099037	470.206781	235.607029	E	3296.455130	1648.731203	3279.428581	1640.217928	3278.444565	1639.725920	25
5	616.275924	308.641600	599.249375	300.128326	598.265359	299.636318	Q	3167.412537	1584.209906	3150.385988	1575.696632	3149.401972	1575.204624	24
6	776.306573	388.656925	759.280024	380.143650	758.296008	379.651642	C	3039.353959	1520.180617	3022.327410	1511.667343	3021.343394	1511.175335	23
7	936.337222	468.672249	919.310673	460.158975	918.326657	459.666967	C	2879.323310	1440.165293	2862.296761	1431.652018	2861.312745	1431.160010	22
8	1073.396134	537.201705	1056.369585	528.688431	1055.385569	528.196423	H	2719.292661	1360.149968	2702.266112	1351.636694	2701.282096	1351.144686	21
9	1160.428162	580.717719	1143.401613	572.204445	1142.417597	571.712437	S	2582.233749	1291.620512	2565.207200	1283.107238	2564.223184	1282.615230	20
10	1599.653488	800.330382	1582.626939	791.817108	1581.642923	791.325100	Q	2495.201721	1248.104498	2478.175172	1239.591224	2477.191156	1239.099216	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
84.5	3653.615311	-0.004055	MVQEQCCHSQLEELHCATGISLANEQDR
84.5	3653.615311	-0.004055	MVQEQCCHSQLEELHCATGISLANEQDR
84.5	3653.615311	-0.004055	MVQEQCCHSQLEELHCATGISLANEQDR

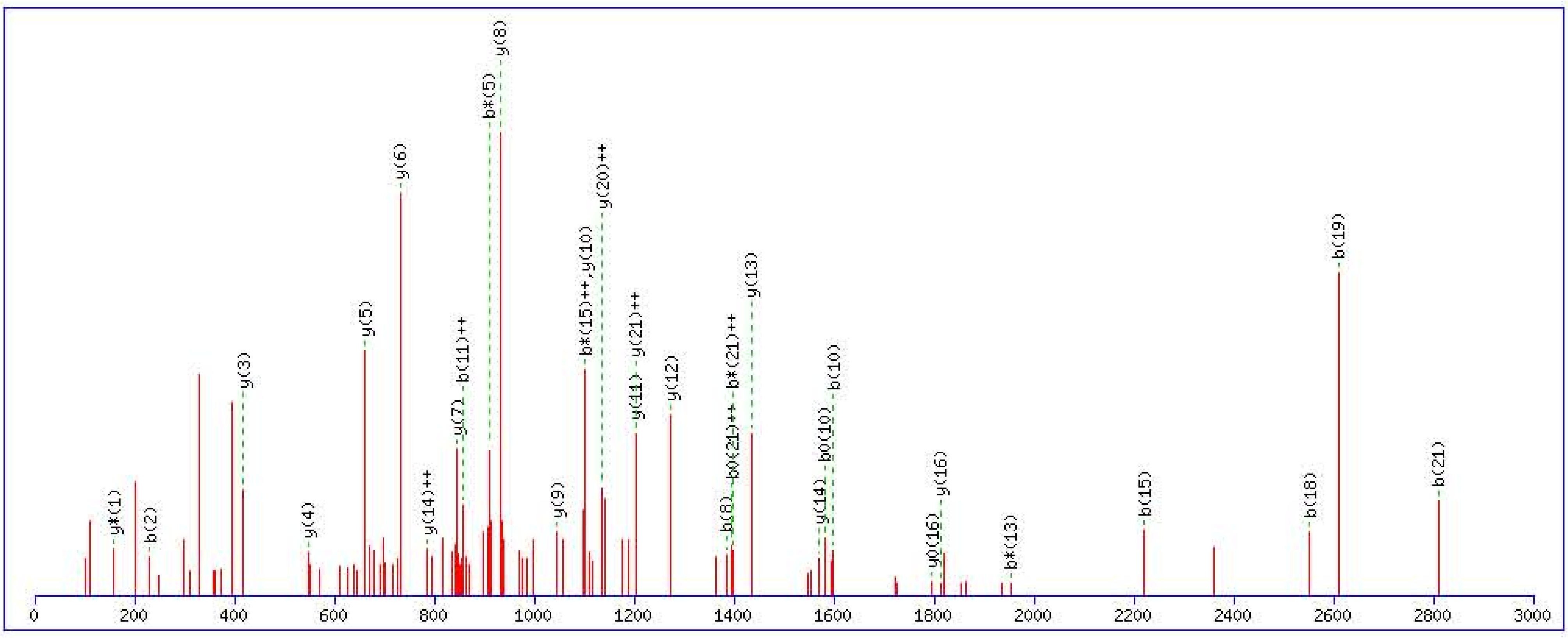
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVQEQCCHSQLEELHCATGISLANEQDR**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

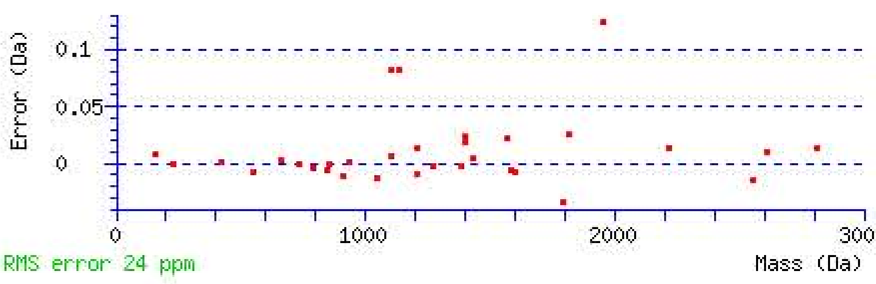
Match to Query 60714: 3653.621256 from(914.412590,4+) rtinseconds(2002) index(46087)
Title: Locus:1.1.1.3409.23 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

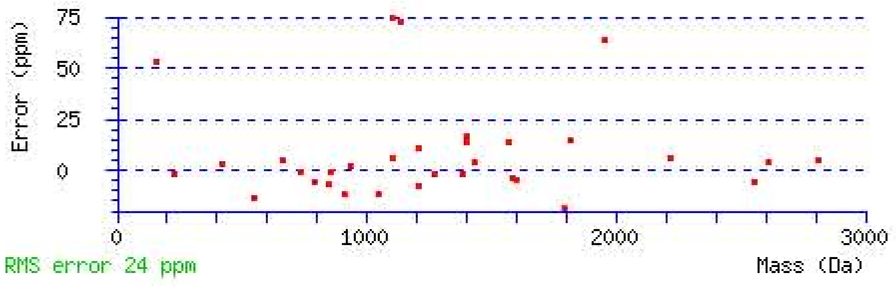
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3653.615311
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 2.5e-006
Matches : 32/312 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							28
2	**231.116175**	116.061725					V	3523.582122	1762.294699	3506.555573	1753.781424	3505.571557	1753.289416	27
3	359.174753	180.091015	342.148204	171.577740			Q	3424.513708	1712.760492	3407.487159	1704.247217	3406.503143	1703.755209	26
4	488.217346	244.612311	471.190797	236.099037	470.206781	235.607029	E	3296.455130	1648.731203	3279.428581	1640.217928	3278.444565	1639.725920	25
5	927.442672	464.224974	910.416123	455.711700	909.432107	455.219692	Q	3167.412537	1584.209906	3150.385988	1575.696632	3149.401972	1575.204624	24
6	1087.473321	544.240298	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	615.250340	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	683.779796	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
64.7	3653.615311	0.005945	MVQEQCCHSQLEELHCATGISLANEQDR
64.7	3653.615311	0.005945	MVQEQCCHSQLEELHCATGISLANEQDR
56.2	3653.615311	0.005945	MVQEQCCHSQLEELHCATGISLANEQDR

Mascot: http://www.matrixscience.com/

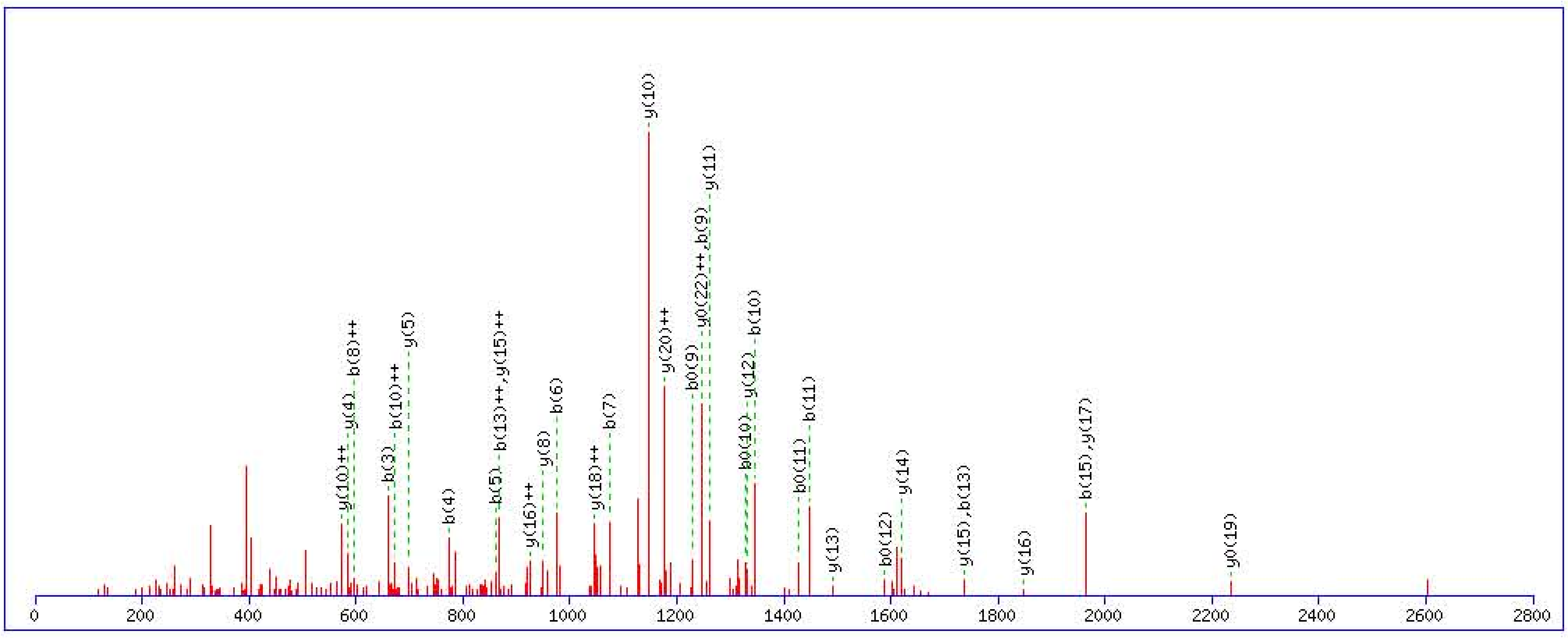
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GYQLSDVDGVTCEDIDECALPTGGHICSYR**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

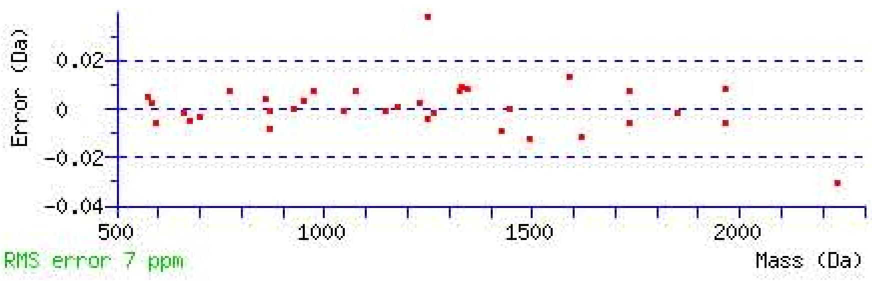
Match to Query 60925: 3697.607656 from(925.409190,4+) rtinseconds(2306) index(33637)
Title: Locus:1.1.1.3466.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

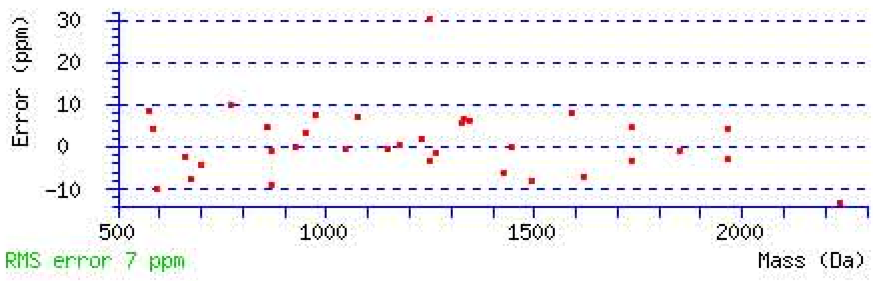
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3697.615738
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 75 **Expect:** 1.2e-007
Matches : 35/332 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	58.028740	29.518008					G							30
2	221.092069	111.049673					Y	3641.601521	1821.304398	3624.574972	1812.791124	3623.590956	1812.299116	29
3	***660.317395***	330.662336	643.290846	322.149061			Q	3478.538192	1739.772734	3461.511643	1731.259459	3460.527627	1730.767451	28
4	***773.401459***	387.204368	756.374910	378.691093			L	3039.312866	1520.160071	3022.286317	1511.646796	3021.302301	1511.154788	27
5	***860.433487***	430.720382	843.406938	422.207107	842.422922	421.715099	S	2926.228802	1463.618039	2909.202253	1455.104764	2908.218237	1454.612756	26
6	***975.460430***	488.233853	958.433881	479.720578	957.449865	479.228570	D	2839.196774	1420.102025	2822.170225	1411.588750	2821.186209	1411.096742	25
7	***1074.528844***	537.768060	1057.502295	529.254786	1056.518279	528.762777	V	2724.169831	1362.588553	2707.143282	1354.075279	2706.159266	1353.583271	24
8	1189.555787	**595.281532**	1172.529238	586.768257	1171.545222	586.276249	D	2625.101417	1313.054346	2608.074868	1304.541072	2607.090852	1304.049064	23
9	***1246.577251***	623.792263	1229.550702	615.278989	1228.566686	614.786981	G	2510.074474	1255.540875	2493.047925	1247.027600	2492.063909	1246.535592	22
10	***1345.645665***	**673.326471**	1328.619116	664.813196	1327.635100	664.321188	V	2453.053010	1227.030143	2436.026461	1218.516868	2435.042445	1218.024860	21
11	***1446.693344***	723.850310	1429.666795	715.337036	1428.682779	714.845028	T	2353.984596	1177.495936	2336.958047	1168.982661	2335.974031	1168.490653	20
12	1606.723993	803.865635	1589.697444	795.352360	1588.713428	794.860352	C	2252.936917	1126.972096	2235.910368	1118.458822	2234.926352	1117.966814	19
13	***1735.766586***	**868.386931**	1718.740037	859.873657	1717.756021	859.381648	E	2092.906268	1046.956772	2075.879719	1038.443497	2074.895703	1037.951489	18
14	1850.793529	925.900403	1833.766980	917.387128	1832.782964	916.895120	D	***1963.863675***	982.435475	1946.837126	973.922201	1945.853110	973.430193	17
15	***1963.877593***	982.442434	1946.851044	973.929160	1945.867028	973.437152	I	***1848.836732***	924.922004	1831.810183	916.408729	1830.826167	915.916721	16
16	2078.904536	1039.955906	2061.877987	1031.442631	2060.893971	1030.950623	D	***1735.752668***	868.379972	1718.726119	859.866697	1717.742103	859.374689	15
17	2207.947129	1104.477202	2190.920580	1095.963928	2189.936564	1095.471920	E	***1620.725725***	810.866501	1603.699176	802.353226	1602.715160	801.861218	14
18	2367.977778	1184.492527	2350.951229	1175.979252	2349.967213	1175.487244	C	***1491.683132***	746.345204	1474.656583	737.831930	1473.672567	737.339921	13
19	2439.014892	1220.011084	2421.988343	1211.497809	2421.004327	1211.005801	A	***1331.652483***	666.329880	1314.625934	657.816605	1313.641918	657.324597	12
20	2552.098956	1276.553116	2535.072407	1268.039841	2534.088391	1267.547833	L	***1260.615369***	630.811322	1243.588820	622.298048	1242.604804	621.806040	11
21	2649.151720	1325.079498	2632.125171	1316.566223	2631.141155	1316.074215	P	***1147.531305***	574.269290	1130.504756	565.756016	1129.520740	565.264008	10
22	2750.199399	1375.603337	2733.172850	1367.090063	2732.188834	1366.598055	T	1050.478541	525.742908	1033.451992	517.229634	1032.467976	516.737626	9
23	2807.220863	1404.114069	2790.194314	1395.600795	2789.210298	1395.108787	G	***949.430862***	475.219069	932.404313	466.705794	931.420297	466.213786	8
24	2864.242327	1432.624801	2847.215778	1424.111527	2846.231762	1423.619519	G	892.409398	446.708337	875.382849	438.195063	874.398833	437.703055	7
25	3001.301239	1501.154257	2984.274690	1492.640983	2983.290674	1492.148975	H	835.387934	418.197605	818.361385	409.684331	817.377369	409.192323	6
26	3114.385303	1557.696289	3097.358754	1549.183015	3096.374738	1548.691007	I	***698.329022***	349.668149	681.302473	341.154875	680.318457	340.662867	5
27	3274.415952	1637.711614	3257.389403	1629.198339	3256.405387	1628.706331	C	***585.244958***	293.126117	568.218409	284.612843	567.234393	284.120835	4
28	3361.447980	1681.227628	3344.421431	1672.714353	3343.437415	1672.222345	S	425.214309	213.110793	408.187760	204.597518	407.203744	204.105510	3
29	3524.511309	1762.759292	3507.484760	1754.246018	3506.500744	1753.754010	Y	338.182281	169.594778	321.155732	161.081504			2
30							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GYQLSDVDGVTCEDIDECALPTGGHICSYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
74.9	3697.615738	-0.008082	GYQLSDVDGVTCEDIDECALPTGGHICSYR

Mascot: http://www.matrixscience.com/

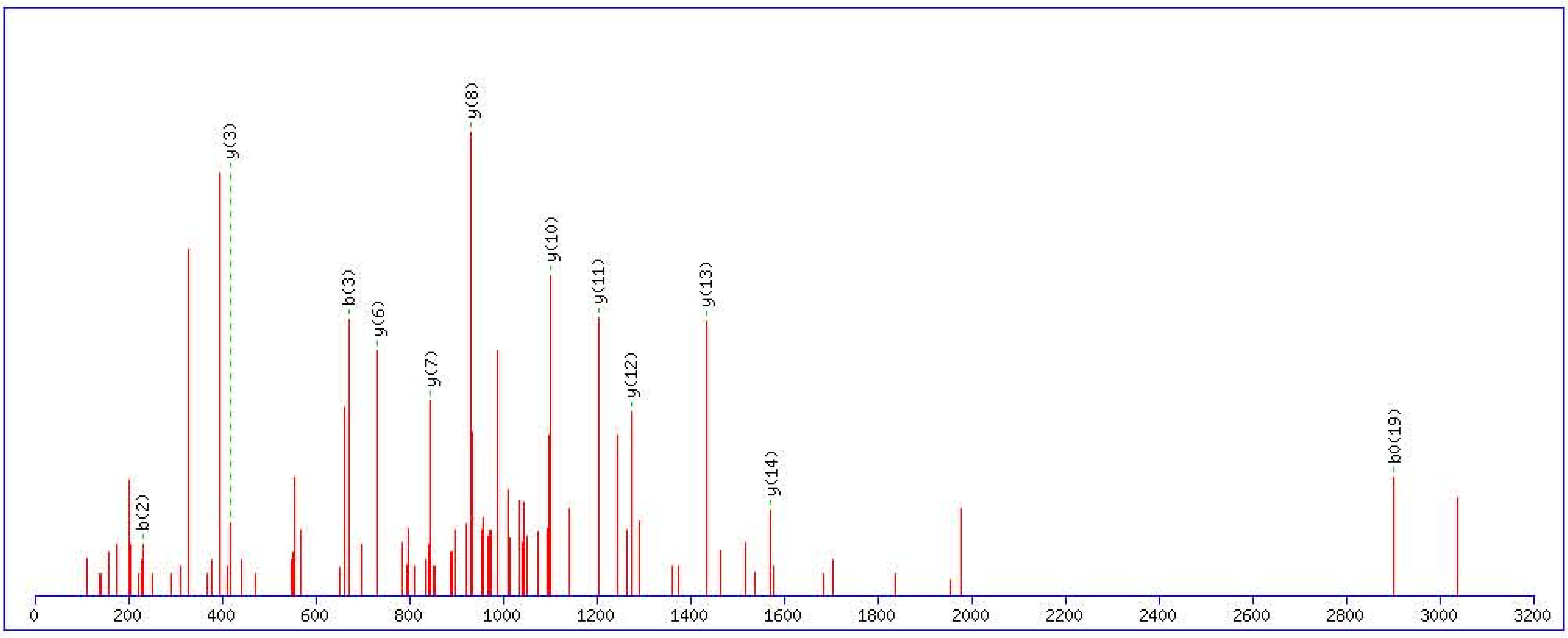
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVQEQCCHSQLEELHCATGISLANEQDR**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

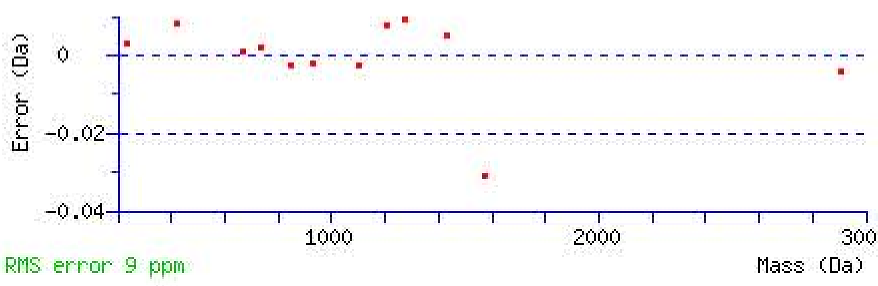
Match to Query 62116: 3964.776416 from(992.201380,4+) rtinseconds(2223) index(33171)
Title: Locus:1.1.1.3437.25 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

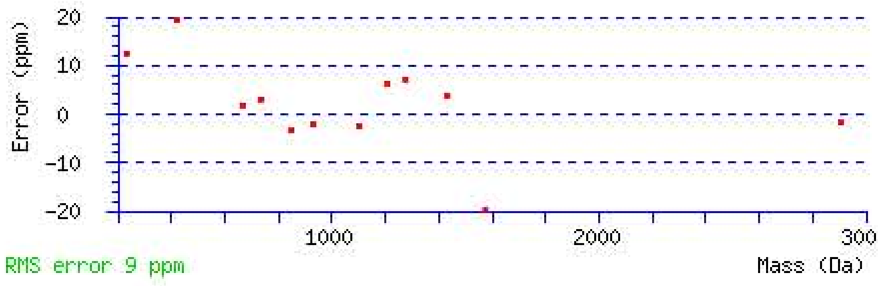
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3964.782059
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Q10    : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 5e-005
Matches : 12/312 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	132.047761	66.527518					M							28
2	**231.116175**	116.061725					V	3834.748870	1917.878073	3817.722321	1909.364798	3816.738305	1908.872790	27
3	**670.341501**	335.674389	653.314952	327.161114			Q	3735.680456	1868.343866	3718.653907	1859.830591	3717.669891	1859.338583	26
4	799.384094	400.195685	782.357545	391.682411	781.373529	391.190403	E	3296.455130	1648.731203	3279.428581	1640.217928	3278.444565	1639.725920	25
5	927.442672	464.224974	910.416123	455.711700	909.432107	455.219692	Q	3167.412537	1584.209906	3150.385988	1575.696632	3149.401972	1575.204624	24
6	1087.473321	544.240299	1070.446772	535.727024	1069.462756	535.235016	C	3039.353959	1520.180617	3022.327410	1511.667343	3021.343394	1511.175335	23
7	1247.503970	624.255623	1230.477421	615.742349	1229.493405	615.250341	C	2879.323310	1440.165293	2862.296761	1431.652018	2861.312745	1431.160010	22
8	1384.562882	692.785079	1367.536333	684.271805	1366.552317	683.779797	H	2719.292661	1360.149968	2702.266112	1351.636694	2701.282096	1351.144686	21
9	1471.594910	736.301093	1454.568361	727.787819	1453.584345	727.295811	S	2582.233749	1291.620512	2565.207200	1283.107238	2564.223184	1282.615230	20
10	1910.820236	955.913756	1893.793687	947.400482	1892.809671	946.908474	Q	2495.201721	1248.104498	2478.175172	1239.591224	2477.191156	1239.099216	19
11	2023.904300	1012.455788	2006.877751	1003.942514	2005.893735	1003.450506	L	2055.976395	1028.491835	2038.949846	1019.978561	2037.965830	1019.486553	18
12	2152.946893	1076.977084	2135.920344	1068.463810	2134.936328	1067.971802	E	1942.892331	971.949804	1925.865782	963.436529	1924.881766	962.944521	17
13	2281.989486	1141.498381	2264.962937	1132.985106	2263.978921	1132.493098	E	1813.849738	907.428507	1796.823189	898.915233	1795.839173	898.423225	16
14	2395.073550	1198.040413	2378.047001	1189.527138	2377.062985	1189.035130	L	1684.807145	842.907211	1667.780596	834.393936	1666.796580	833.901928	15
15	2532.132462	1266.569869	2515.105913	1258.056594	2514.121897	1257.564586	H	***1571.723081***	786.365179	1554.696532	777.851904	1553.712516	777.359896	14
16	2692.163111	1346.585193	2675.136562	1338.071919	2674.152546	1337.579911	C	***1434.664169***	717.835723	1417.637620	709.322448	1416.653604	708.830440	13
17	2763.200225	1382.103750	2746.173676	1373.590476	2745.189660	1373.098468	A	***1274.633520***	637.820398	1257.606971	629.307124	1256.622955	628.815116	12
18	2864.247904	1432.627590	2847.221355	1424.114315	2846.237339	1423.622307	T	***1203.596406***	602.301841	1186.569857	593.788567	1185.585841	593.296559	11
19	2921.269368	1461.138322	2904.242819	1452.625047	2903.258803	1452.133039	G	***1102.548727***	551.778002	1085.522178	543.264727	1084.538162	542.772719	10
20	3034.353432	1517.680354	3017.326883	1509.167079	3016.342867	1508.675071	I	1045.527263	523.267270	1028.500714	514.753995	1027.516698	514.261987	9
21	3121.385460	1561.196368	3104.358911	1552.683093	3103.374895	1552.191085	S	***932.443199***	466.725238	915.416650	458.211963	914.432634	457.719955	8
22	3234.469524	1617.738400	3217.442975	1609.225125	3216.458959	1608.733117	L	***845.411171***	423.209224	828.384622	414.695949	827.400606	414.203941	7
23	3305.506638	1653.256957	3288.480089	1644.743683	3287.496073	1644.251675	A	***732.327107***	366.667192	715.300558	358.153917	714.316542	357.661909	6
24	3419.549565	1710.278421	3402.523016	1701.765146	3401.539000	1701.273138	N	661.289993	331.148635	644.263444	322.635360	643.279428	322.143352	5
25	3548.592158	1774.799717	3531.565609	1766.286443	3530.581593	1765.794435	E	547.247066	274.127171	530.220517	265.613897	529.236501	265.121889	4
26	3676.650736	1838.829006	3659.624187	1830.315732	3658.640171	1829.823724	Q	***418.204473***	209.605874	401.177924	201.092600	400.193908	200.600592	3
27	3791.677679	1896.342478	3774.651130	1887.829203	3773.667114	1887.337195	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
46.2	3964.782059	-0.005643	MVQEQCCHSQLEELHCATGISLANEQDR
46.2	3964.782059	-0.005643	MVQEQCCHSQLEELHCATGISLANEQDR
37.8	3964.782059	-0.005643	MVQEQCCHSQLEELHCATGISLANEQDR
0.4	3964.786865	-0.010449	SSSDSSYMSGSPGGSPGSGSAEKPSSDVDISTHSPSLPLAR

Mascot: http://www.matrixscience.com/

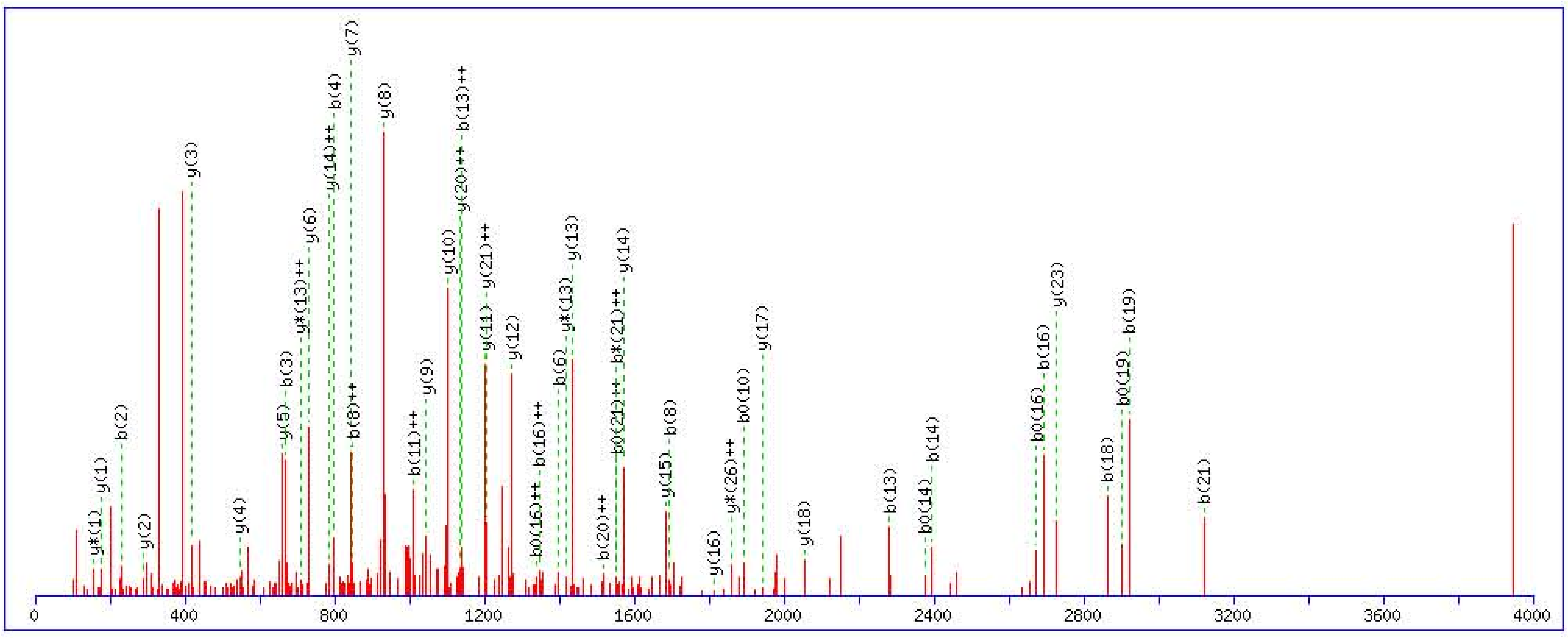
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVQEQCCHSQLEELHCATGISLANEQDR**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

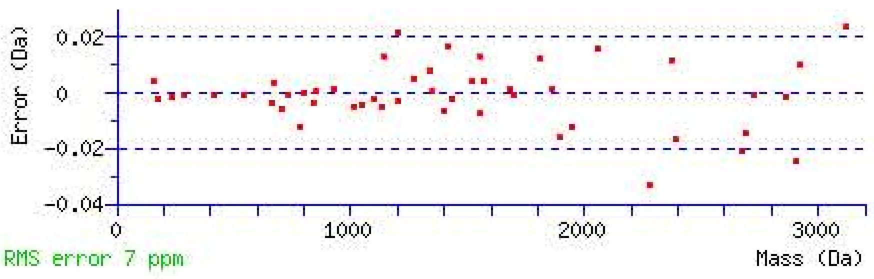
Match to Query 62118: 3964.781976 from(992.202770,4+) rtinseconds(2151) index(32746)
Title: Locus:1.1.1.3412.19 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

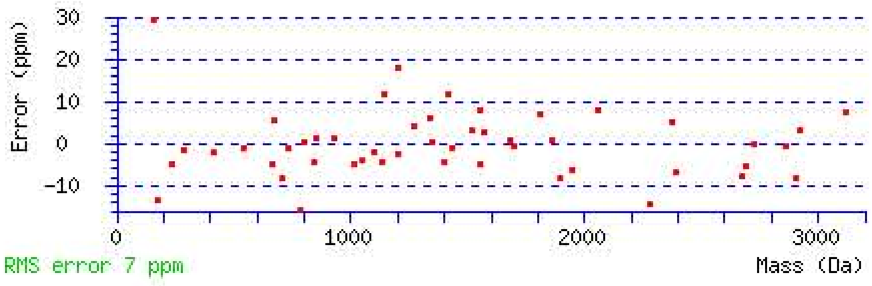
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3964.782059
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 81 **Expect:** 7.6e-008
Matches : 49/312 fragment ions using 115 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	3834.748870	1917.878073	3817.722321	1909.364798	3816.738305	1908.872790	27
3	***670.341501***	335.674389	653.314952	327.161114			Q	3735.680456	1868.343866	3718.653907	1859.830591	3717.669891	1859.338583	26
4	***799.384094***	400.195685	782.357545	391.682411	781.373529	391.190403	E	3296.455130	1648.731203	3279.428581	1640.217928	3278.444565	1639.725920	25
5	1238.609420	619.808348	1221.582871	611.295074	1220.598855	610.803066	Q	3167.412537	1584.209906	3150.385988	1575.696632	3149.401972	1575.204624	24
6	***1398.640069***	699.823673	1381.613520	691.310398	1380.629504	690.818390	C	***2728.187211***	1364.597243	2711.160662	1356.083969	2710.176646	1355.591961	23
7	1558.670718	779.838997	1541.644169	771.325723	1540.660153	770.833715	C	2568.156562	1284.581919	2551.130013	1276.068644	2550.145997	1275.576636	22
8	***1695.729630***	**848.368453**	1678.703081	839.855179	1677.719065	839.363171	H	2408.125913	1204.566594	2391.099364	1196.053320	2390.115348	1195.561312	21
9	1782.761658	891.884467	1765.735109	883.371193	1764.751093	882.879185	S	2271.067001	1136.037138	2254.040452	1127.523864	2253.056436	1127.031856	20
10	1910.820236	955.913756	1893.793687	947.400482	1892.809671	946.908474	Q	2184.034973	1092.521124	2167.008424	1084.007850	2166.024408	1083.515842	19
11	2023.904300	**1012.455788**	2006.877751	1003.942514	2005.893735	1003.450506	L	***2055.976395***	1028.491835	2038.949846	1019.978561	2037.965830	1019.486553	18
12	2152.946893	1076.977084	2135.920344	1068.463810	2134.936328	1067.971802	E	***1942.892331***	971.949804	1925.865782	963.436529	1924.881766	962.944521	17
13	***2281.989486***	**1141.498381**	2264.962937	1132.985106	2263.978921	1132.493098	E	***1813.849738***	907.428507	1796.823189	898.915233	1795.839173	898.423225	16
14	***2395.073550***	1198.040413	2378.047001	1189.527138	2377.062985	1189.035130	L	***1684.807145***	842.907211	1667.780596	834.393936	1666.796580	833.901928	15
15	2532.132462	1266.569869	2515.105913	1258.056594	2514.121897	1257.564586	H	***1571.723081***	786.365179	1554.696532	777.851904	1553.712516	777.359896	14
16	***2692.163111***	**1346.585193**	2675.136562	1338.071919	2674.152546	1337.579911	C	***1434.664169***	717.835723	1417.637620	709.322448	1416.653604	708.830440	13
17	2763.200225	1382.103750	2746.173676	1373.590476	2745.189660	1373.098468	A	***1274.633520***	637.820398	1257.606971	629.307124	1256.622955	628.815116	12
18	***2864.247904***	1432.627590	2847.221355	1424.114315	2846.237339	1423.622307	T	***1203.596406***	602.301841	1186.569857	593.788567	1185.585841	593.296559	11
19	***2921.269368***	1461.138322	2904.242819	1452.625047	2903.258803	1452.133039	G	***1102.548727***	551.778002	1085.522178	543.264727	1084.538162	542.772719	10
20	3034.353432	**1517.680354**	3017.326883	1509.167079	3016.342867	1508.675071	I	***1045.527263***	523.267270	1028.500714	514.753995	1027.516698	514.261987	9
21	***3121.385460***	1561.196368	3104.358911	1552.683093	3103.374895	1552.191085	S	***932.443199***	466.725238	915.416650	458.211963	914.432634	457.719955	8
22	3234.469524	1617.738400	3217.442975	1609.225125	3216.458959	1608.733117	L	***845.411171***	423.209224	828.384622	414.695949	827.400606	414.203941	7
23	3305.506638	1653.256957	3288.480089	1644.743683	3287.496073	1644.251675	A	***732.327107***	366.667192	715.300558	358.153917	714.316542	357.661909	6
24	3419.549565	1710.278421	3402.523016	1701.765146	3401.539000	1701.273138	N	***661.289993***	331.148635	644.263444	322.635360	643.279428	322.143352	5
25	3548.592158	1774.799717	3531.565609	1766.286443	3530.581593	1765.794435	E	***547.247066***	274.127171	530.220517	265.613897	529.236501	265.121889	4
26	3676.650736	1838.829006	3659.624187	1830.315732	3658.640171	1829.823724	Q	***418.204473***	209.605874	401.177924	201.092600	400.193908	200.600592	3
27	3791.677679	1896.342478	3774.651130	1887.829203	3773.667114	1887.337195	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
80.5	3964.782059	-0.000083	MVQEQCCHSQLEELHCATGISLANEQDR
63.4	3964.782059	-0.000083	MVQEQCCHSQLEELHCATGISLANEQDR
60.9	3964.782059	-0.000083	MVQEQCCHSQLEELHCATGISLANEQDR

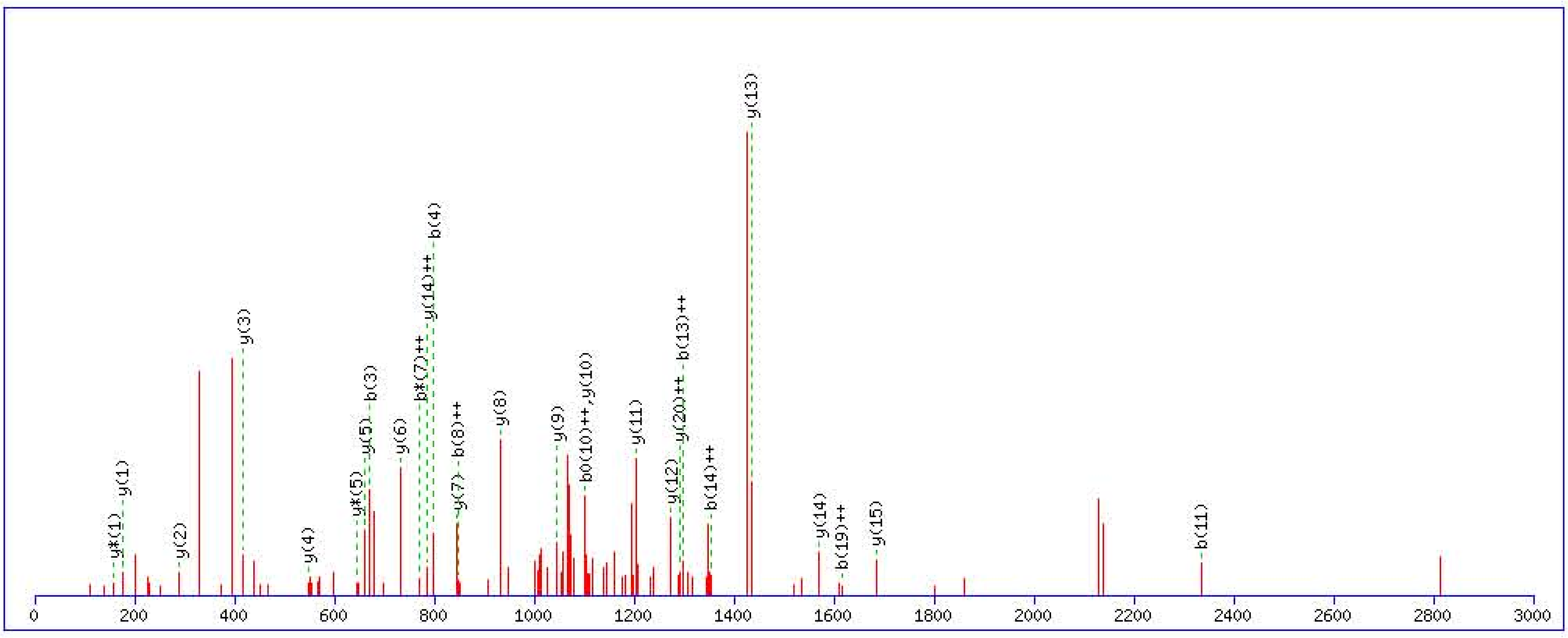
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVQEQCCHSQLEELHCATGISLANEQDR**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

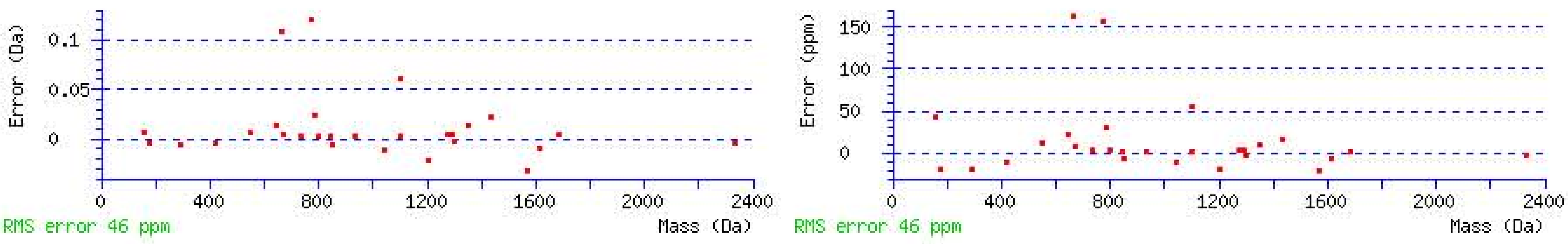
Match to Query 64806: 4275.950016 from(1069.994780,4+) rtinseconds(2326) index(33730)
Title: Locus:1.1.1.3473.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 4275.948807
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Q5     : Biotin:Thermo-21345 (Q)
Q10    : Biotin:Thermo-21345 (Q)
Ions Score: 45  Expect: 0.0003
Matches : 28/312 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	132.047761	66.527518					M							28
2	231.116175	116.061725					V	4145.915618	2073.461447	4128.889069	2064.948173	4127.905053	2064.456165	27
3	**670.341501**	335.674389	653.314952	327.161114			Q	4046.847204	2023.927240	4029.820655	2015.413966	4028.836639	2014.921958	26
4	**799.384094**	400.195685	782.357545	391.682411	781.373529	391.190403	E	3607.621878	1804.314577	3590.595329	1795.801303	3589.611313	1795.309295	25
5	1238.609420	619.808348	1221.582871	611.295074	1220.598855	610.803066	Q	3478.579285	1739.793281	3461.552736	1731.280006	3460.568720	1730.787998	24
6	1398.640069	699.823673	1381.613520	691.310398	1380.629504	690.818390	C	3039.353959	1520.180618	3022.327410	1511.667343	3021.343394	1511.175335	23
7	1558.670718	779.838997	1541.644169	771.325723	1540.660153	770.833715	C	2879.323310	1440.165293	2862.296761	1431.652019	2861.312745	1431.160011	22
8	1695.729630	**848.368453**	1678.703081	839.855179	1677.719065	839.363171	H	2719.292661	1360.149969	2702.266112	1351.636694	2701.282096	1351.144686	21
9	1782.761658	891.884467	1765.735109	883.371193	1764.751093	882.879185	S	2582.233749	1291.620513	2565.207200	1283.107238	2564.223184	1282.615230	20
10	2221.986984	1111.497130	2204.960435	1102.983855	2203.976419	1102.491847	Q	2495.201721	1248.104499	2478.175172	1239.591224	2477.191156	1239.099216	19
11	**2335.071048**	1168.039162	2318.044499	1159.525888	2317.060483	1159.033880	L	2055.976395	1028.491836	2038.949846	1019.978561	2037.965830	1019.486553	18
12	2464.113641	1232.560459	2447.087092	1224.047184	2446.103076	1223.555176	E	1942.892331	971.949804	1925.865782	963.436529	1924.881766	962.944521	17
13	2593.156234	**1297.081755**	2576.129685	1288.568481	2575.145669	1288.076473	E	1813.849738	907.428507	1796.823189	898.915233	1795.839173	898.423225	16
14	2706.240298	**1353.623787**	2689.213749	1345.110513	2688.229733	1344.618505	L	***1684.807145***	842.907211	1667.780596	834.393936	1666.796580	833.901928	15
15	2843.299210	1422.153243	2826.272661	1413.639969	2825.288645	1413.147961	H	***1571.723081***	786.365179	1554.696532	777.851904	1553.712516	777.359896	14
16	3003.329859	1502.168568	2986.303310	1493.655293	2985.319294	1493.163285	C	***1434.664169***	717.835723	1417.637620	709.322448	1416.653604	708.830440	13
17	3074.366973	1537.687125	3057.340424	1529.173850	3056.356408	1528.681842	A	***1274.633520***	637.820398	1257.606971	629.307124	1256.622955	628.815116	12
18	3175.414652	1588.210964	3158.388103	1579.697690	3157.404087	1579.205682	T	***1203.596406***	602.301841	1186.569857	593.788567	1185.585841	593.296559	11
19	3232.436116	**1616.721696**	3215.409567	1608.208422	3214.425551	1607.716414	G	***1102.548727***	551.778002	1085.522178	543.264727	1084.538162	542.772719	10
20	3345.520180	1673.263728	3328.493631	1664.750454	3327.509615	1664.258446	I	***1045.527263***	523.267270	1028.500714	514.753995	1027.516698	514.261987	9
21	3432.552208	1716.779742	3415.525659	1708.266468	3414.541643	1707.774460	S	***932.443199***	466.725238	915.416650	458.211963	914.432634	457.719955	8
22	3545.636272	1773.321774	3528.609723	1764.808500	3527.625707	1764.316492	L	***845.411171***	423.209224	828.384622	414.695949	827.400606	414.203941	7
23	3616.673386	1808.840331	3599.646837	1800.327057	3598.662821	1799.835049	A	***732.327107***	366.667192	715.300558	358.153917	714.316542	357.661909	6
24	3730.716313	1865.861795	3713.689764	1857.348520	3712.705748	1856.856512	N	***661.289993***	331.148635	644.263444	322.635360	643.279428	322.143352	5
25	3859.758906	1930.383091	3842.732357	1921.869817	3841.748341	1921.377809	E	***547.247066***	274.127171	530.220517	265.613897	529.236501	265.121889	4
26	3987.817484	1994.412380	3970.790935	1985.899106	3969.806919	1985.407098	Q	***418.204473***	209.605875	401.177924	201.092600	400.193908	200.600592	3
27	4102.844427	2051.925852	4085.817878	2043.412577	4084.833862	2042.920569	D	***290.145895***	145.576586	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
45.4	4275.948807	0.001209	MVQEQCCHSQLEELHCATGISLANEQDR

Mascot: http://www.matrixscience.com/

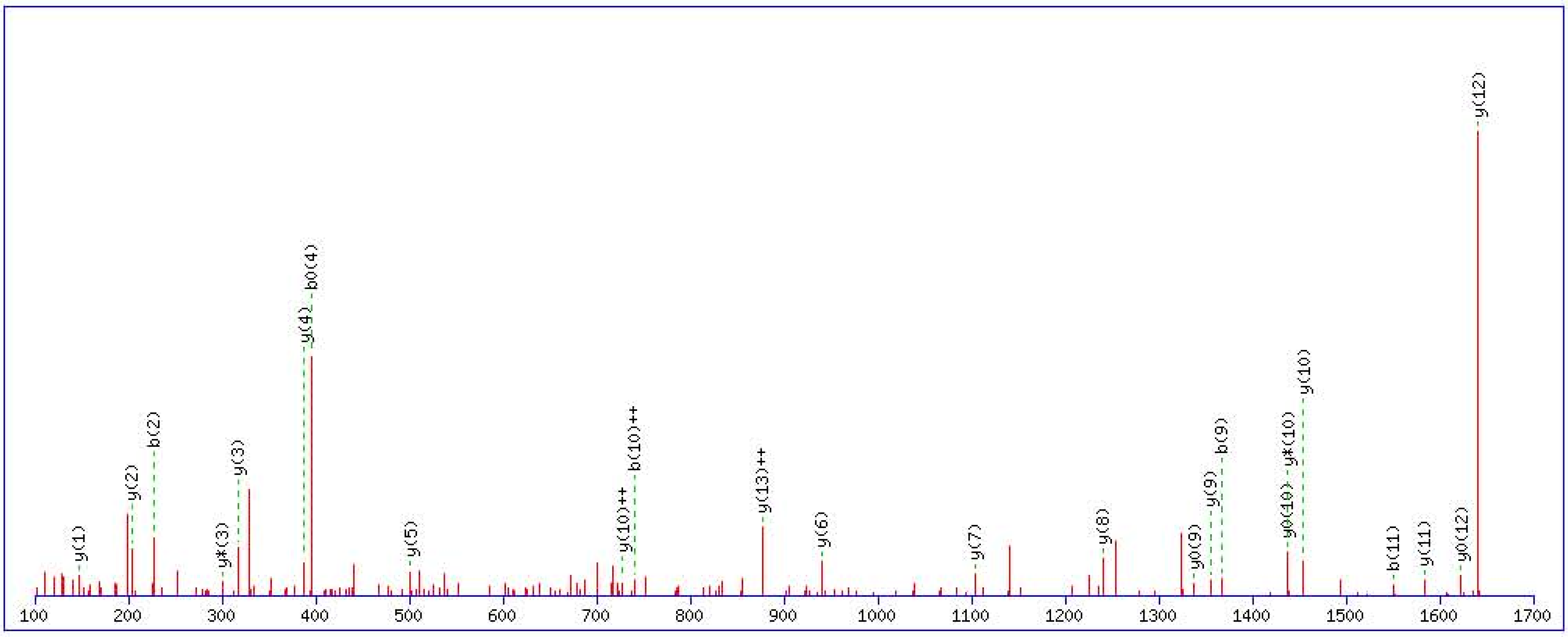
{MATRIX SCIENCE}
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLGEVDHYQLALGK**
Found in **FCN3_HUMAN**, Ficolin-3 OS=Homo sapiens GN=FCN3 PE=1 SV=2

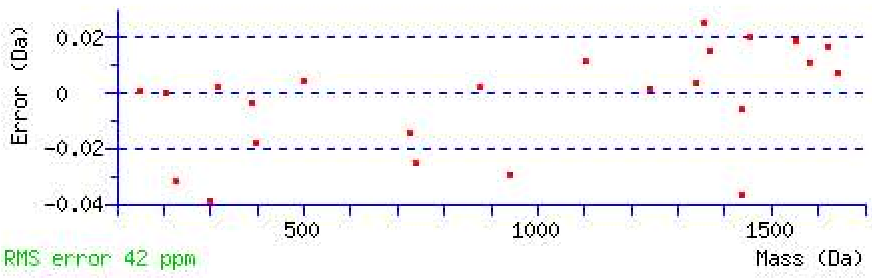
Match to Query 36975: 1866.005862 from(623.009230,3+) rtinseconds(2227) index(20351)
Title: Locus:1.1.1.3341.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

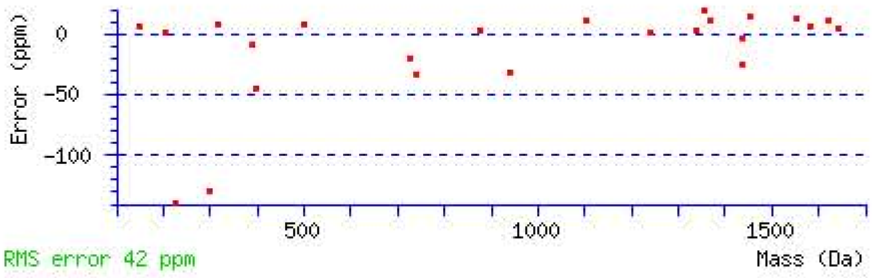
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1866.007324
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9     : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 4.9e-005
Matches : 24/118 fragment ions using 64 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							14
2	**227.175404**	114.091340					L	1753.930555	877.468916	1736.904006	868.955641	1735.919990	868.463633	13
3	284.196868	142.602072					G	***1640.846491***	820.926884	1623.819942	812.413609	1622.835926	811.921601	12
4	413.239461	207.123369			395.228896	198.118086	E	***1583.825027***	792.416152	1566.798478	783.902877	1565.814462	783.410869	11
5	512.307875	256.657576			494.297310	247.652293	V	***1454.782434***	727.894855	1437.755885	719.381581	1436.771869	718.889572	10
6	627.334818	314.171047			609.324253	305.165765	D	***1355.714020***	678.360648	1338.687471	669.847374	1337.703455	669.355366	9
7	764.393730	382.700503			746.383165	373.695221	H	***1240.687077***	620.847177	1223.660528	612.333902			8
8	927.457059	464.232168			909.446494	455.226885	Y	***1103.628165***	552.317721	1086.601616	543.804446			7
9	**1366.682385**	683.844831	1349.655836	675.331556	1348.671820	674.839548	Q	***940.564836***	470.786056	923.538287	462.272782			6
10	1479.766449	740.386863	1462.739900	731.873588	1461.755884	731.381580	L	***501.339510***	251.173393	484.312961	242.660118			5
11	**1550.803563**	775.905420	1533.777014	767.392145	1532.792998	766.900137	A	***388.255446***	194.631361	371.228897	186.118086			4
12	1663.887627	832.447452	1646.861078	823.934177	1645.877062	823.442169	L	***317.218332***	159.112804	300.191783	150.599529			3
13	1720.909091	860.958184	1703.882542	852.444909	1702.898526	851.952901	G	***204.134268***	102.570772	187.107719	94.057497			2
14							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LLGEVDHYQLALGK
(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	1866.007324	-0.001462	LLGEVDHYQLALGK

Mascot: http://www.matrixscience.com/

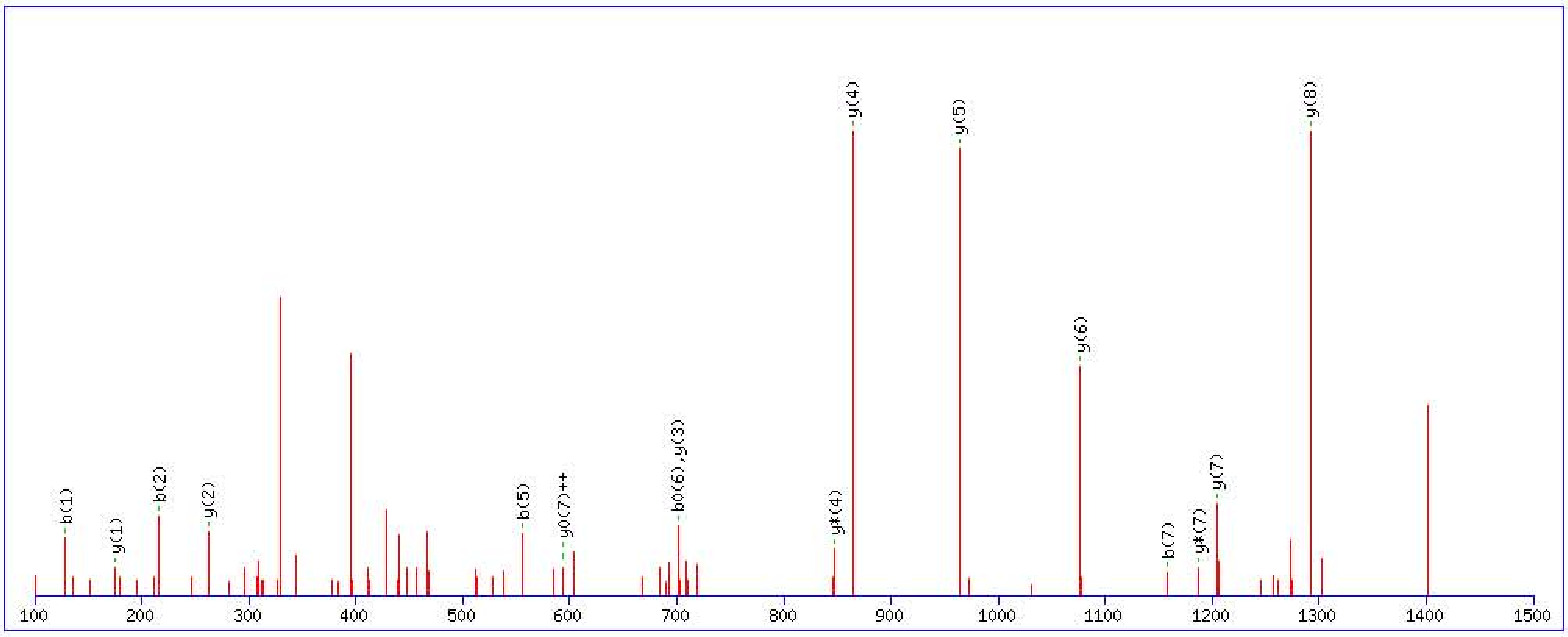
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KSQLVYQSR**
Found in **LG3BP_HUMAN**, Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1

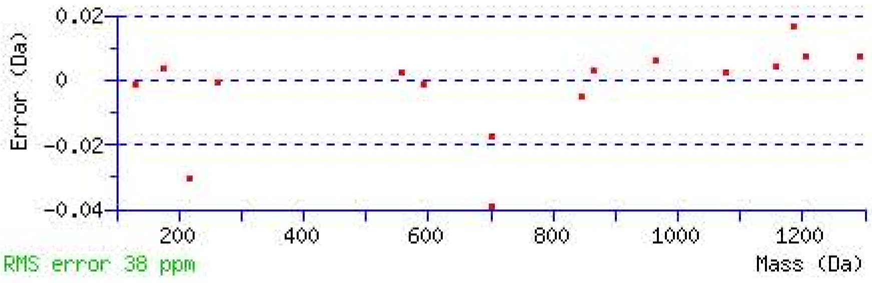
Match to Query 24663: 1418.772768 from(710.393660,2+) rtinseconds(1546) index(43177)
Title: Locus:1.1.1.3251.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

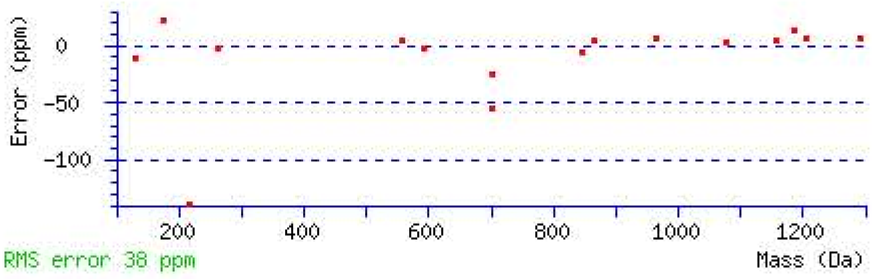
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1418.770386
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 59  Expect: 2e-005
Matches : 16/92 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	**129.102239**	65.054757	112.075690	56.541483			K							9
2	**216.134267**	108.570771	199.107718	100.057497	198.123702	99.565489	S	***1291.682719***	646.344998	1274.656170	637.831723	1273.672154	637.339715	8
3	344.192845	172.600060	327.166296	164.086786	326.182280	163.594778	Q	***1204.650691***	602.828984	1187.624142	594.315709	1186.640126	593.823701	7
4	457.276909	229.142092	440.250360	220.628818	439.266344	220.136810	L	***1076.592113***	538.799695	1059.565564	530.286420	1058.581548	529.794412	6
5	**556.345323**	278.676300	539.318774	270.163025	538.334758	269.671017	V	***963.508049***	482.257663	946.481500	473.744388	945.497484	473.252380	5
6	719.408652	360.207964	702.382103	351.694690	701.398087	351.202682	Y	***864.439635***	432.723456	847.413086	424.210181	846.429070	423.718173	4
7	**1158.633978**	579.820627	1141.607429	571.307353	1140.623413	570.815345	Q	***701.376306***	351.191791	684.349757	342.678517	683.365741	342.186509	3
8	1245.666006	623.336641	1228.639457	614.823367	1227.655441	614.331359	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of KSQLVYQSR
(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	1418.770386	0.002382	KSQLVYQSR
11.7	1418.770386	0.002382	KSQLVYQSR
7.9	1418.788147	-0.015379	QSQVDRLYVALK
5.6	1418.780273	-0.007505	TNQLMETLKTIK
3.8	1418.778259	-0.005491	RVSLPQWPPPSR
0.3	1418.787659	-0.014891	KEILLAMLMVDK

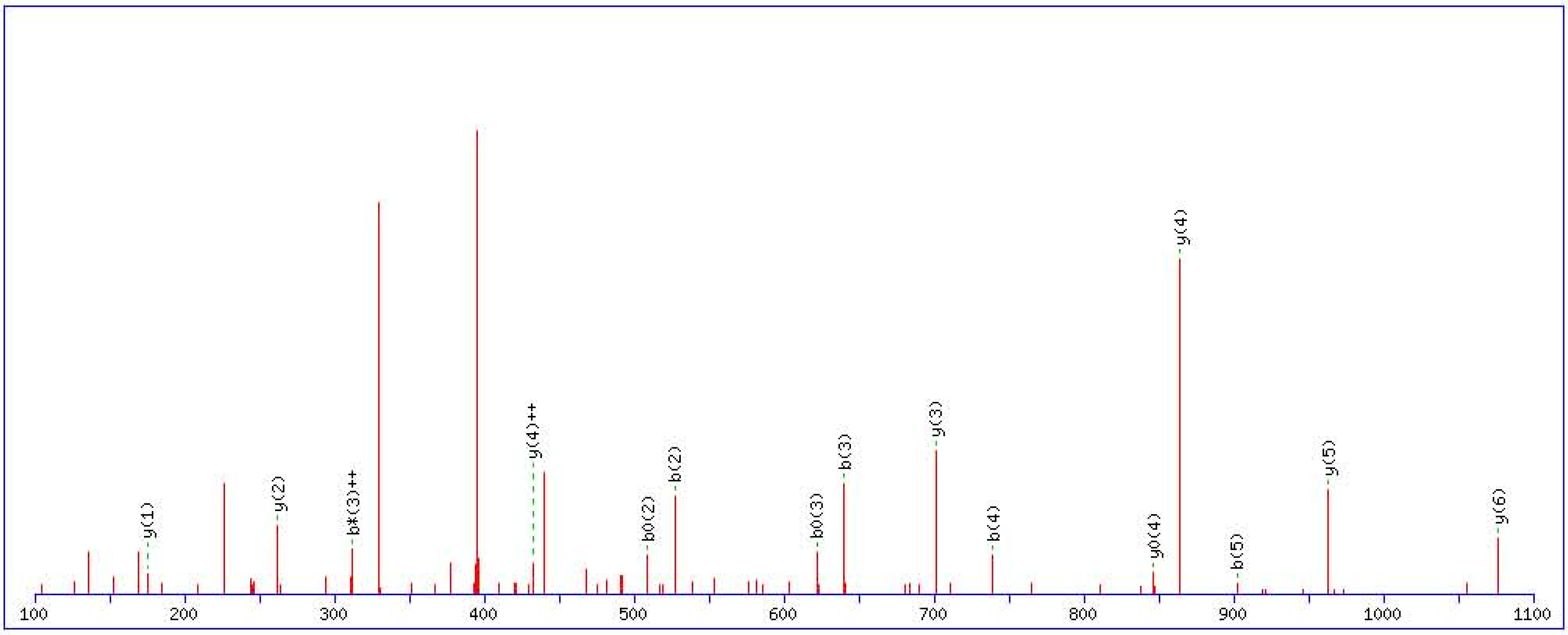
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SQLVYQSR**
Found in **LG3BP_HUMAN**, Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1

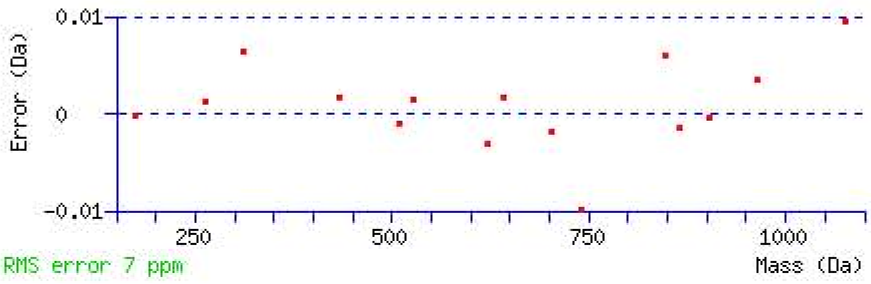
Match to Query 30624: 1601.839452 from(534.953760,3+) rtinseconds(2092) index(46537)
Title: Locus:1.1.1.3441.4 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

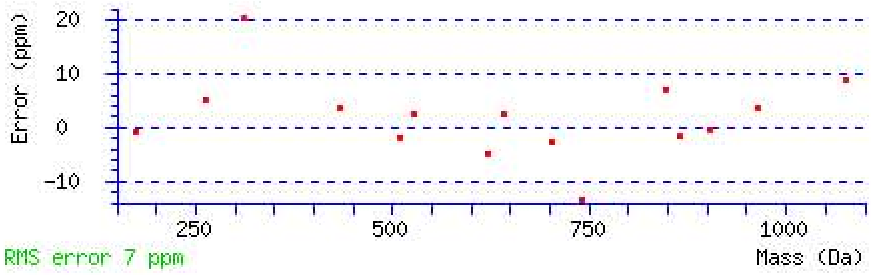
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 26  Expect: 0.012
Matches : 15/80 fragment ions using 29 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							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
26.1	1601.842178	-0.002726	SQLVYQSR
5.8	1601.846024	-0.006572	RFVLSCSLLSHQR

Mascot: http://www.matrixscience.com/

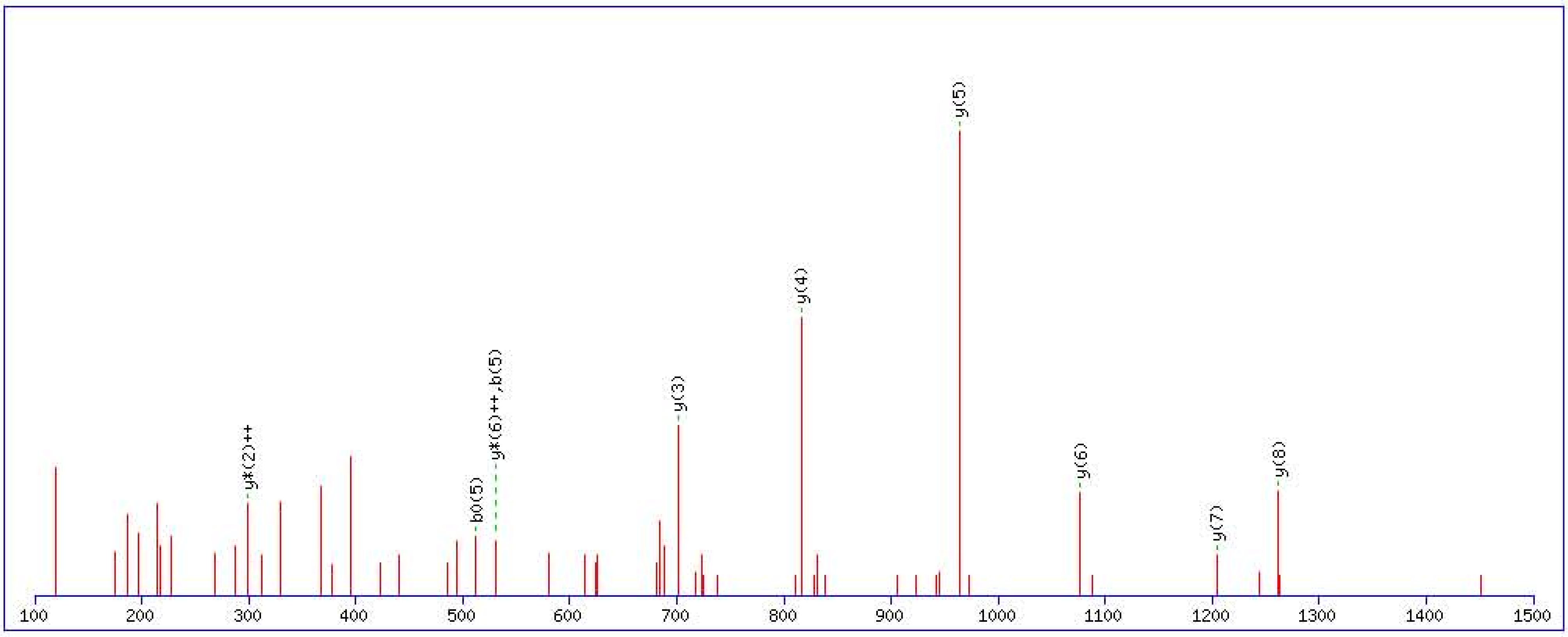
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELSEALGQIFDSQR**
Found in **LG3BP_HUMAN**, Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1

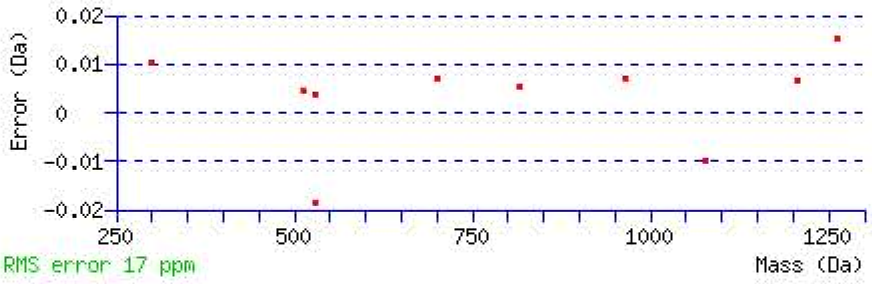
Match to Query 37448: 1902.955872 from(635.325900,3+) rtinseconds(2701) index(50077)
Title: Locus:1.1.1.3652.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

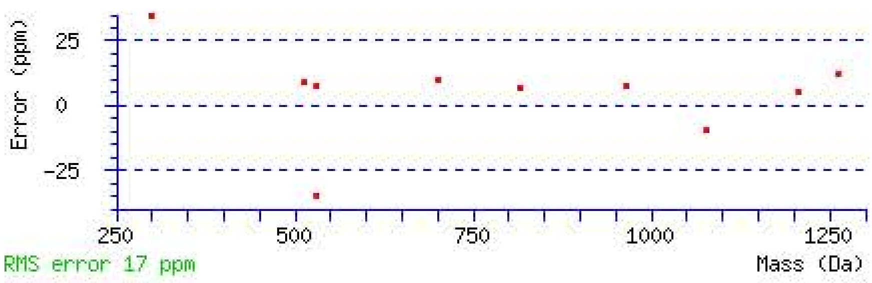
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1902.950928
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.00024
Matches : 10/138 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	130.049869	65.528572			112.039304	56.523290	E							14
2	243.133933	122.070605			225.123368	113.065322	L	1774.915632	887.961454	1757.889083	879.448180	1756.905067	878.956172	13
3	330.165961	165.586618			312.155396	156.581336	S	1661.831568	831.419422	1644.805019	822.906148	1643.821003	822.414140	12
4	459.208554	230.107915			441.197989	221.102633	E	1574.799540	787.903408	1557.772991	779.390134	1556.788975	778.898126	11
5	**530.245668**	265.626472			512.235103	256.621190	A	1445.756947	723.382112	1428.730398	714.868837	1427.746382	714.376829	10
6	643.329732	322.168504			625.319167	313.163222	L	1374.719833	687.863555	1357.693284	679.350280	1356.709268	678.858272	9
7	700.351196	350.679236			682.340631	341.673954	G	***1261.635769***	631.321523	1244.609220	622.808248	1243.625204	622.316240	8
8	828.409774	414.708525	811.383225	406.195251	810.399209	405.703243	Q	***1204.614305***	602.810791	1187.587756	594.297516	1186.603740	593.805508	7
9	941.493838	471.250557	924.467289	462.737283	923.483273	462.245275	I	***1076.555727***	538.781502	1059.529178	530.268227	1058.545162	529.776219	6
10	1088.562252	544.784764	1071.535703	536.271490	1070.551687	535.779482	F	***963.471663***	482.239470	946.445114	473.726195	945.461098	473.234187	5
11	1203.589195	602.298236	1186.562646	593.784961	1185.578630	593.292953	D	***816.403249***	408.705263	799.376700	400.191988	798.392684	399.699980	4
12	1290.621223	645.814250	1273.594674	637.300975	1272.610658	636.808967	S	***701.376306***	351.191791	684.349757	342.678517	683.365741	342.186509	3
13	1729.846549	865.426913	1712.820000	856.913638	1711.835984	856.421630	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 ELSEALGQIFDSQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.8	1902.950928	0.004944	ELSEALGQIFDSQR
0.3	1902.947739	0.008133	MKEQLREMENLR

Mascot: http://www.matrixscience.com/

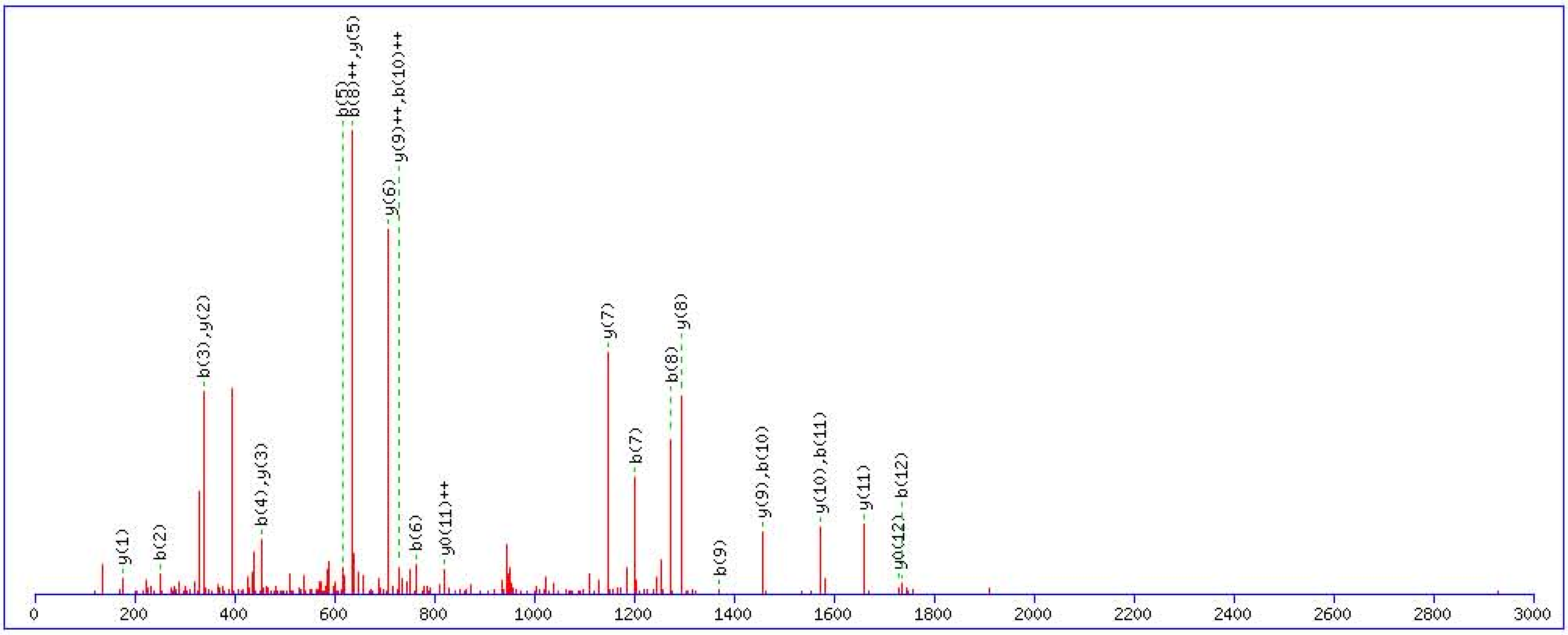
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YSSDYFQAPSDYR**
Found in **LG3BP_HUMAN**, Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1

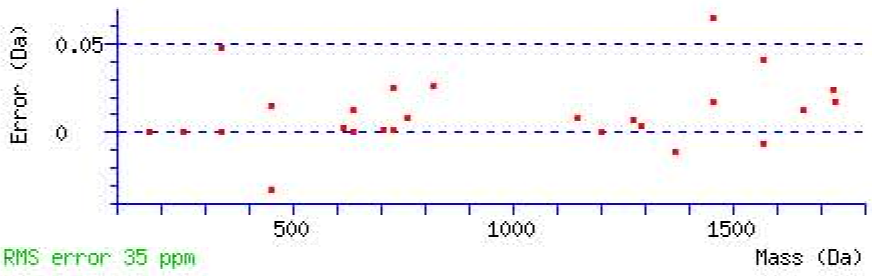
Match to Query 37575: 1908.840388 from(955.427470,2+) rtinseconds(2111) index(46665)
Title: Locus:1.1.1.3447.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

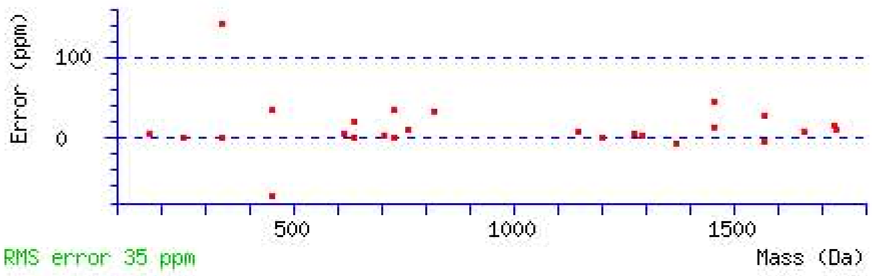
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1908.835236
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 77  Expect: 1.1e-007
Matches : 26/126 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	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
77.4	1908.835236	0.005152	YSSDYFQAPSDYR

Mascot: http://www.matrixscience.com/

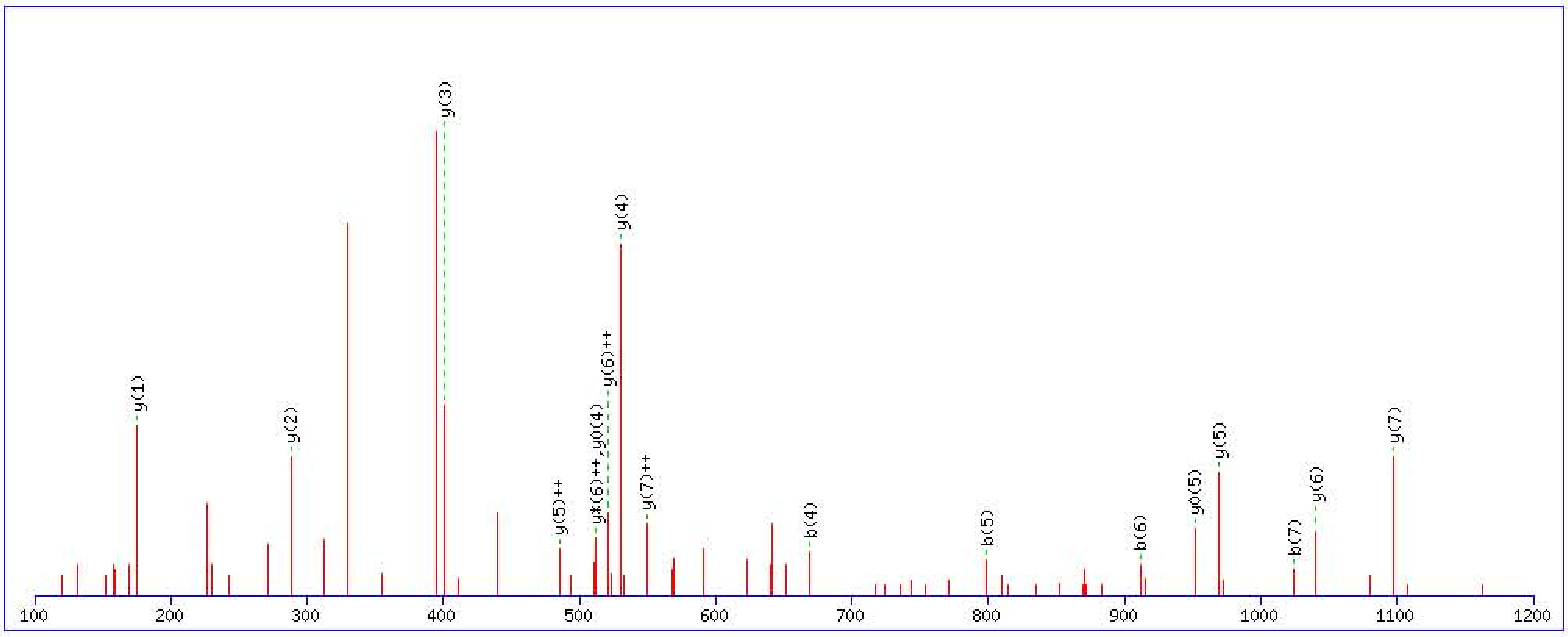
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TGAQELLR**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

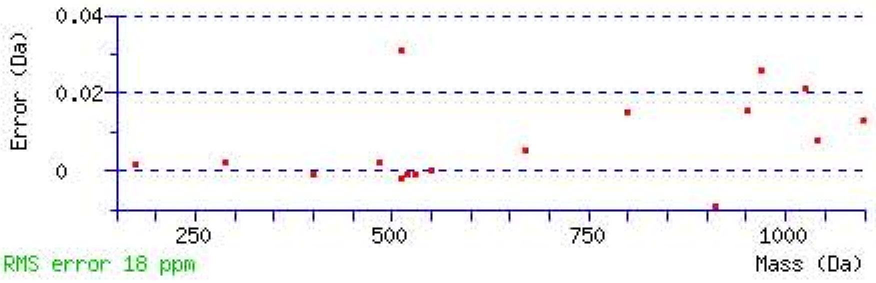
Match to Query 17703: 1197.659108 from(599.836830,2+) rtinseconds(1960) index(4539)
Title: Locus:1.1.1.3202.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

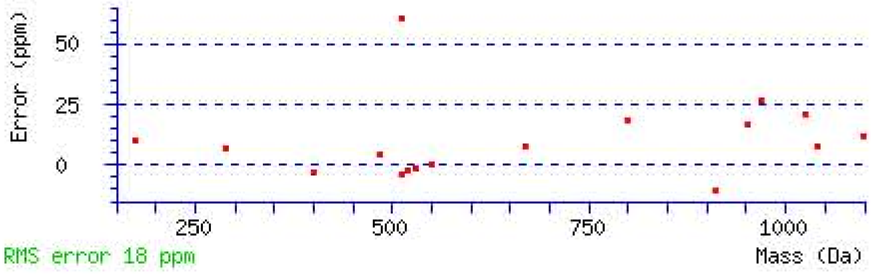
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1197.653961
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 43 **Expect:** 0.0013
Matches : 17/72 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	102.054955	51.531116			84.044390	42.525833	T							8
2	159.076419	80.041847			141.065854	71.036565	G	***1097.613577***	549.310427	1080.587028	540.797152	1079.603012	540.305144	7
3	230.113533	115.560404			212.102968	106.555122	A	***1040.592113***	520.799695	1023.565564	512.286420	1022.581548	511.794412	6
4	**669.338859**	335.173068	652.312310	326.659793	651.328294	326.167785	Q	***969.554999***	485.281138	952.528450	476.767863	951.544434	476.275855	5
5	**798.381452**	399.694364	781.354903	391.181090	780.370887	390.689082	E	***530.329673***	265.668475	513.303124	257.155200	512.319108	256.663192	4
6	**911.465516**	456.236396	894.438967	447.723122	893.454951	447.231114	L	***401.287080***	201.147178	384.260531	192.633903			3
7	**1024.549580**	512.778428	1007.523031	504.265153	1006.539015	503.773145	L	***288.203016***	144.605146	271.176467	136.091871			2
8							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TGAQELLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.8	1197.653961	0.005147	TGAQELLR
22.7	1197.653961	0.005147	QTQEILR
21.6	1197.653961	0.005147	QTQEILR
17.2	1197.669220	-0.010112	TLWAQLR
14.4	1197.653961	0.005147	TQQLLER
13.6	1197.669220	-0.010112	WTLQAIR
12.0	1197.653961	0.005147	QTEQLLR
11.6	1197.646545	0.012563	RSPQEAEILR
10.0	1197.653961	0.005147	QTEQLLR
9.6	1197.669220	-0.010112	QWTALIR

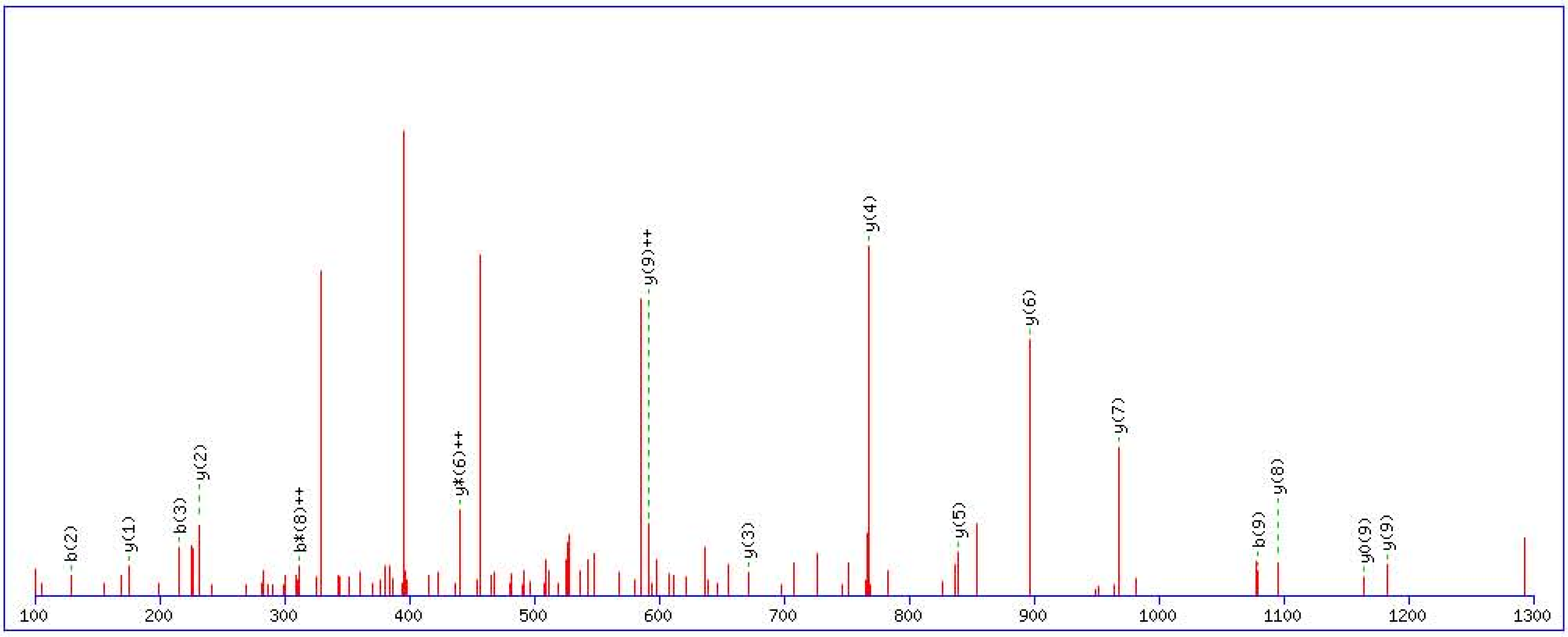
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GASQAGAPQGR**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

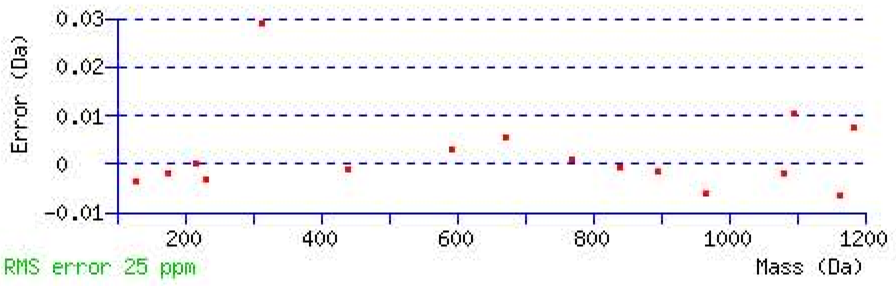
Match to Query 20511: 1309.657408 from(655.835980,2+) rtinseconds(1304) index(855)
Title: Locus:1.1.1.2973.19 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

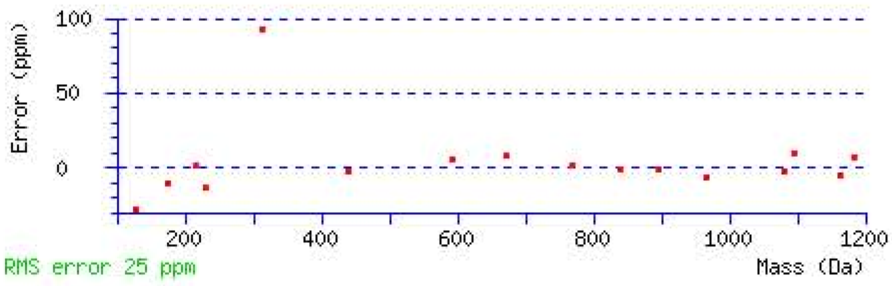
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1309.656097
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 56 **Expect:** 1.4e-005
Matches : 16/94 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	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
56.2	1309.656097	0.001311	GASQAGAPQGR
39.9	1309.656097	0.001311	GASQAGAPQGR
4.1	1309.648682	0.008726	SLQAQEDARHR
3.5	1309.660110	-0.002702	TVQQRYWAMK
2.7	1309.669998	-0.012590	LIETQMERFK
0.3	1309.647354	0.010054	KSESSNTTSLTR

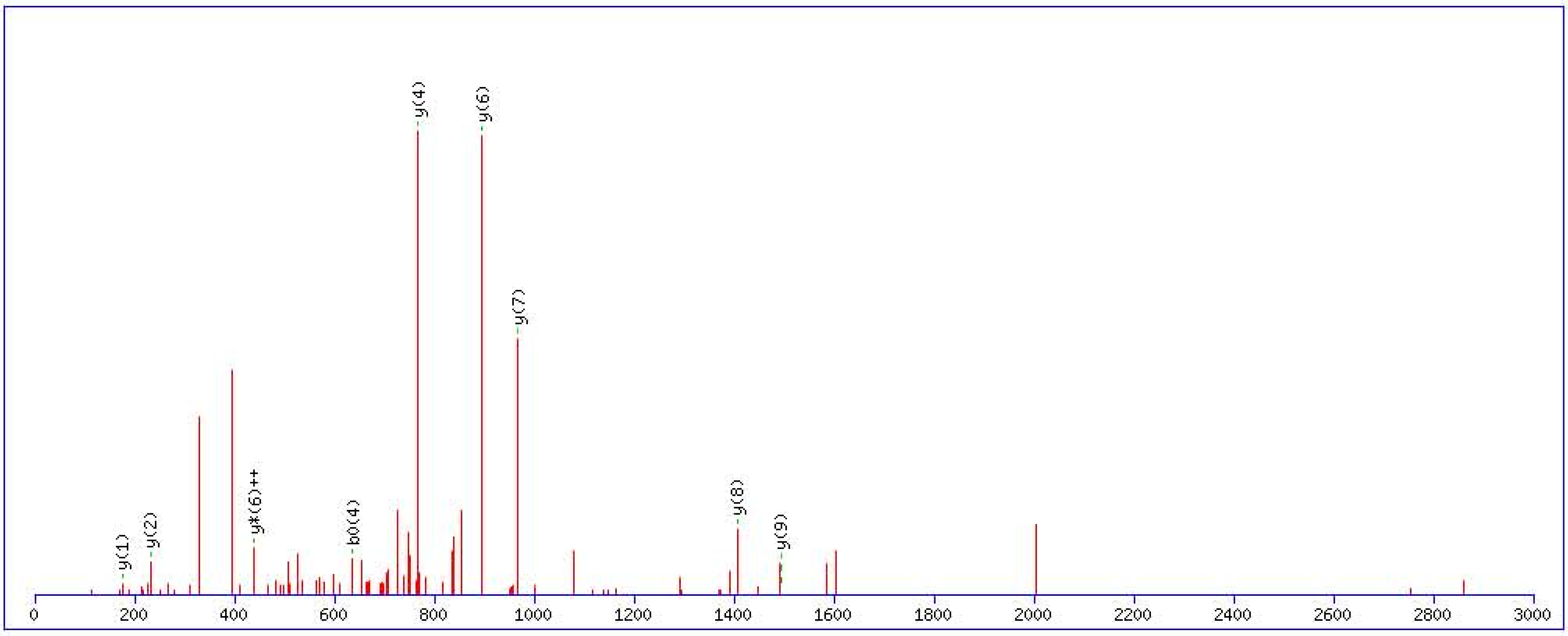
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GASQAGAPQGR**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

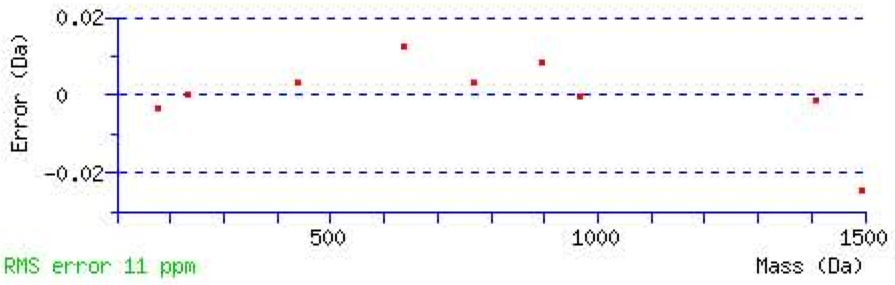
Match to Query 31395: 1620.833288 from(811.423920,2+) rtinseconds(1742) index(3412)
Title: Locus:1.1.1.3126.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

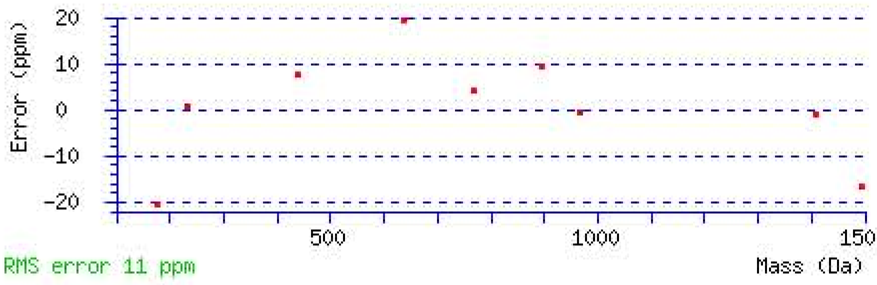


```
Monoisotopic mass of neutral peptide Mr(calc): 1620.822845
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 0.0002
Matches : 9/94 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							11
2	129.065854	65.036565					A	1564.808666	782.907971	1547.782117	774.394697	1546.798101	773.902689	10
3	216.097882	108.552579			198.087317	99.547296	S	***1493.771552***	747.389414	1476.745003	738.876140	1475.760987	738.384131	9
4	655.323208	328.165242	638.296659	319.651968	637.312643	319.159960	Q	***1406.739524***	703.873400	1389.712975	695.360126			8
5	726.360322	363.683799	709.333773	355.170525	708.349757	354.678517	A	***967.514198***	484.260737	950.487649	475.747463			7
6	783.381786	392.194531	766.355237	383.681257	765.371221	383.189249	G	***896.477084***	448.742180	879.450535	440.228906			6
7	854.418900	427.713088	837.392351	419.199814	836.408335	418.707806	A	839.455620	420.231448	822.429071	411.718174			5
8	951.471664	476.239470	934.445115	467.726196	933.461099	467.234188	P	***768.418506***	384.712891	751.391957	376.199617			4
9	1390.696990	695.852133	1373.670441	687.338859	1372.686425	686.846851	Q	671.365742	336.186509	654.339193	327.673235			3
10	1447.718454	724.362865	1430.691905	715.849591	1429.707889	715.357583	G	***232.140416***	116.573846	215.113867	108.060571			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 11 ppm



RMS error 11 ppm

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
47.1	1620.822845	0.010443	GASQAGAPQGR
7.4	1620.815430	0.017858	AGSLASVERYCPRR
4.8	1620.841248	-0.007960	SRVTNPINPWYFK
3.6	1620.838562	-0.005274	FHFIRHEKNHTR

Mascot: http://www.matrixscience.com/

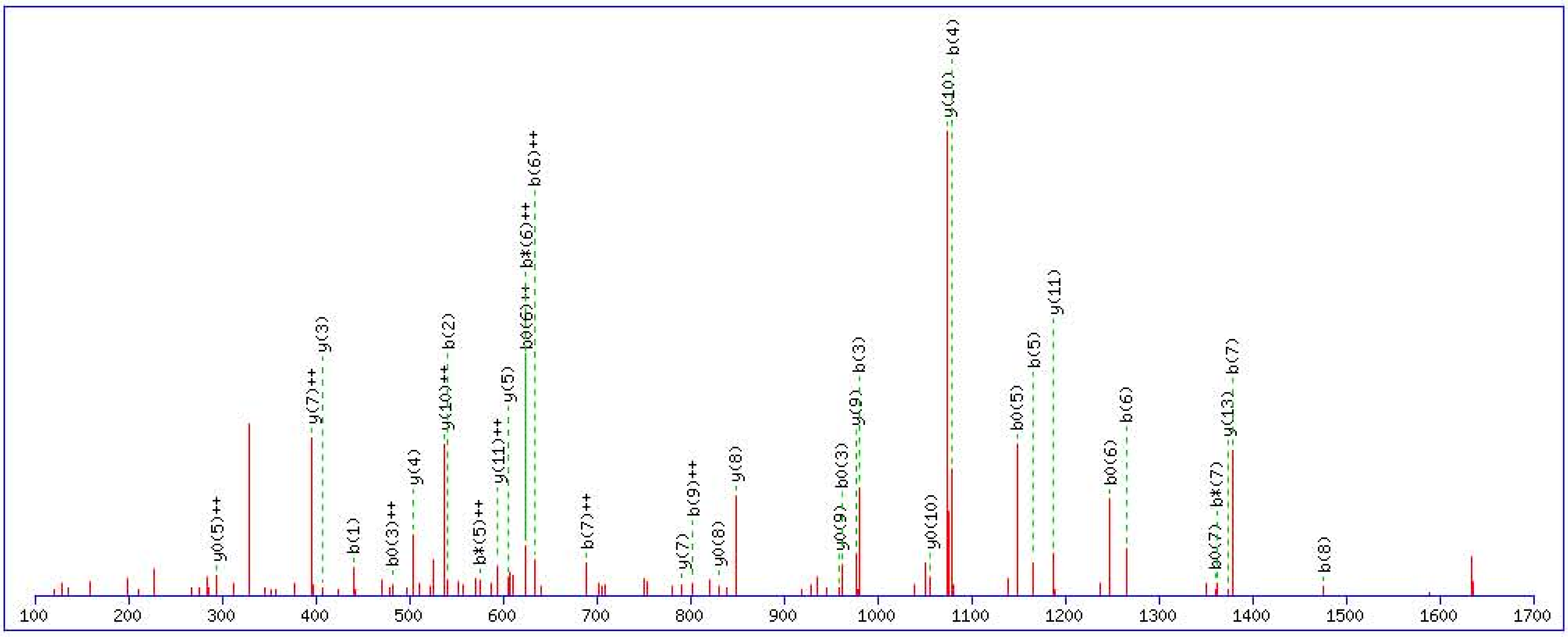
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QTQVSVLPEGGETPLFK**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

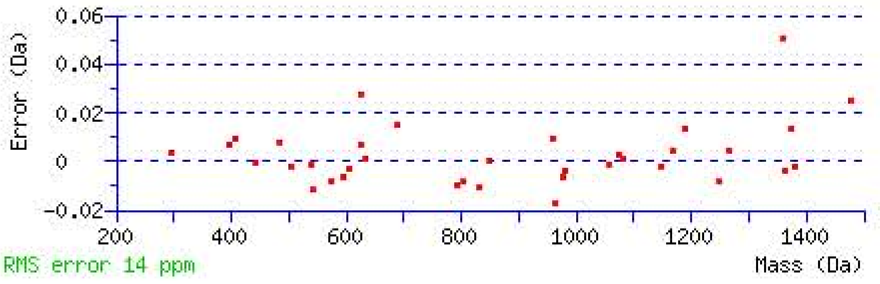
Match to Query 47285: 2451.287712 from(818.103180,3+) rtinseconds(2619) index(35355)
Title: Locus:1.1.1.3575.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

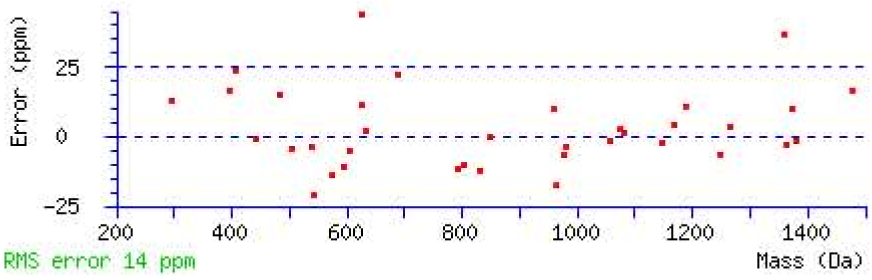
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 36  Expect: 0.00064
Matches : 37/182 fragment ions using 97 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





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
35.8	2451.290588	-0.002876	QTQVSVLPEGGETPLFK
1.8	2451.277130	0.010582	GFPSDTQLLDLRRNHFPSVPR

Mascot: http://www.matrixscience.com/

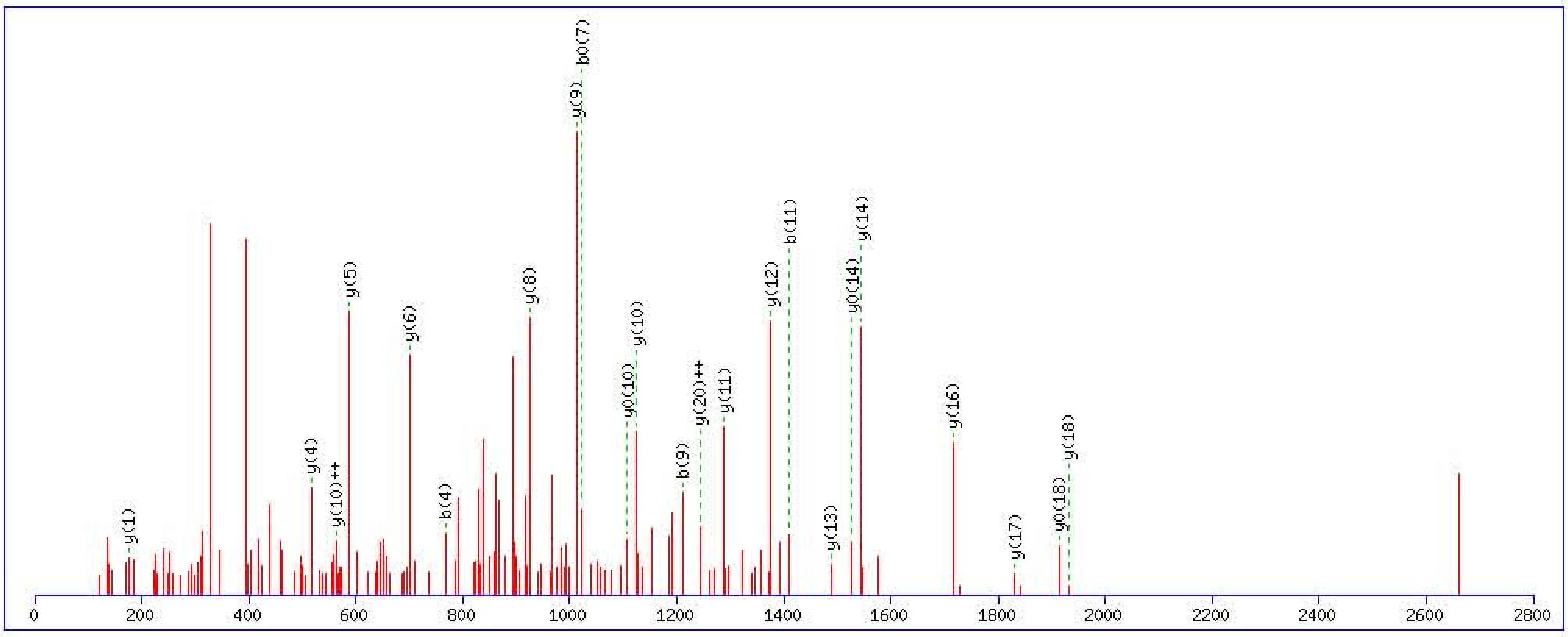
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DPDQTDGLGLSYLSSHIANVER**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

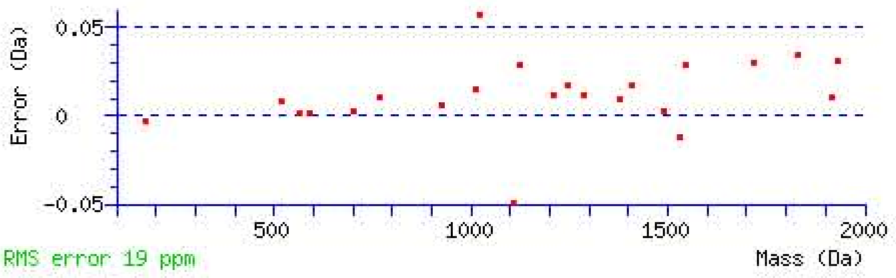
Match to Query 50349: 2697.338442 from(900.120090,3+) rtinseconds(2604) index(8137)
Title: Locus:1.1.1.3426.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

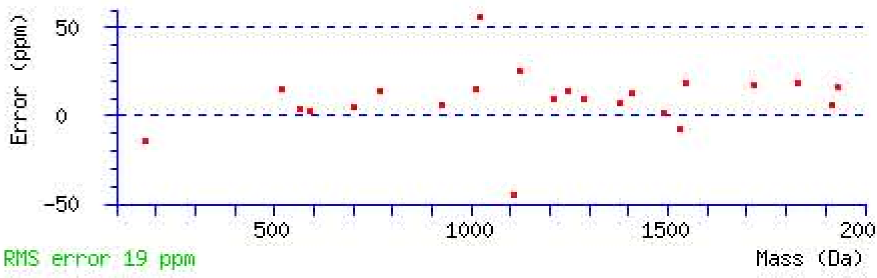
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2697.306824
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4     : Biotin:Thermo-21345 (Q)
Ions Score: 103  Expect: 1.5e-009
Matches : 23/244 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	116.034219	58.520748			98.023654	49.515465	D							22
2	213.086983	107.047129			195.076418	98.041847	P	2583.287164	1292.147220	2566.260615	1283.633945	2565.276599	1283.141937	21
3	328.113926	164.560601			310.103361	155.555319	D	2486.234400	1243.620838	2469.207851	1235.107563	2468.223835	1234.615555	20
4	**767.339252**	384.173264	750.312703	375.659989	749.328687	375.167982	Q	2371.207457	1186.107366	2354.180908	1177.594092	2353.196892	1177.102084	19
5	868.386931	434.697104	851.360382	426.183829	850.376366	425.691821	T	***1931.982131***	966.494704	1914.955582	957.981429	1913.971566	957.489421	18
6	983.413874	492.210575	966.387325	483.697300	965.403309	483.205292	D	***1830.934452***	915.970864	1813.907903	907.457590	1812.923887	906.965581	17
7	1040.435338	520.721307	1023.408789	512.208032	1022.424773	511.716025	G	***1715.907509***	858.457392	1698.880960	849.944118	1697.896944	849.452110	16
8	1153.519402	577.263339	1136.492853	568.750065	1135.508837	568.258056	L	1658.886045	829.946661	1641.859496	821.433386	1640.875480	820.941378	15
9	**1210.540866**	605.774071	1193.514317	597.260796	1192.530301	596.768788	G	***1545.801981***	773.404629	1528.775432	764.891354	1527.791416	764.399346	14
10	1323.624930	662.316103	1306.598381	653.802828	1305.614365	653.310820	L	***1488.780517***	744.893897	1471.753968	736.380622	1470.769952	735.888614	13
11	**1410.656958**	705.832117	1393.630409	697.318842	1392.646393	696.826834	S	***1375.696453***	688.351865	1358.669904	679.838590	1357.685888	679.346582	12
12	1573.720287	787.363781	1556.693738	778.850507	1555.709722	778.358499	Y	***1288.664425***	644.835851	1271.637876	636.322576	1270.653860	635.830568	11
13	1686.804351	843.905813	1669.777802	835.392539	1668.793786	834.900531	L	***1125.601096***	563.304186	1108.574547	554.790912	1107.590531	554.298904	10
14	1773.836379	887.421827	1756.809830	878.908553	1755.825814	878.416545	S	***1012.517032***	506.762154	995.490483	498.248880	994.506467	497.756872	9
15	1860.868407	930.937841	1843.841858	922.424567	1842.857842	921.932559	S	***925.485004***	463.246140	908.458455	454.732866	907.474439	454.240858	8
16	1997.927319	999.467297	1980.900770	990.954023	1979.916754	990.462015	H	838.452976	419.730126	821.426427	411.216852	820.442411	410.724844	7
17	2111.011383	1056.009329	2093.984834	1047.496055	2093.000818	1047.004047	I	***701.394064***	351.200670	684.367515	342.687396	683.383499	342.195388	6
18	2182.048497	1091.527886	2165.021948	1083.014612	2164.037932	1082.522604	A	***588.310000***	294.658638	571.283451	286.145364	570.299435	285.653356	5
19	2296.091424	1148.549350	2279.064875	1140.036075	2278.080859	1139.544067	N	***517.272886***	259.140081	500.246337	250.626806	499.262321	250.134798	4
20	2395.159838	1198.083557	2378.133289	1189.570282	2377.149273	1189.078274	V	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	3
21	2524.202431	1262.604853	2507.175882	1254.091579	2506.191866	1253.599571	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
22							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of DPDQTDGLGLSYLSSHIANVER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
102.8	2697.306824	0.031618	DPDQTDGLGLSYLSSHIANVER

Mascot: http://www.matrixscience.com/

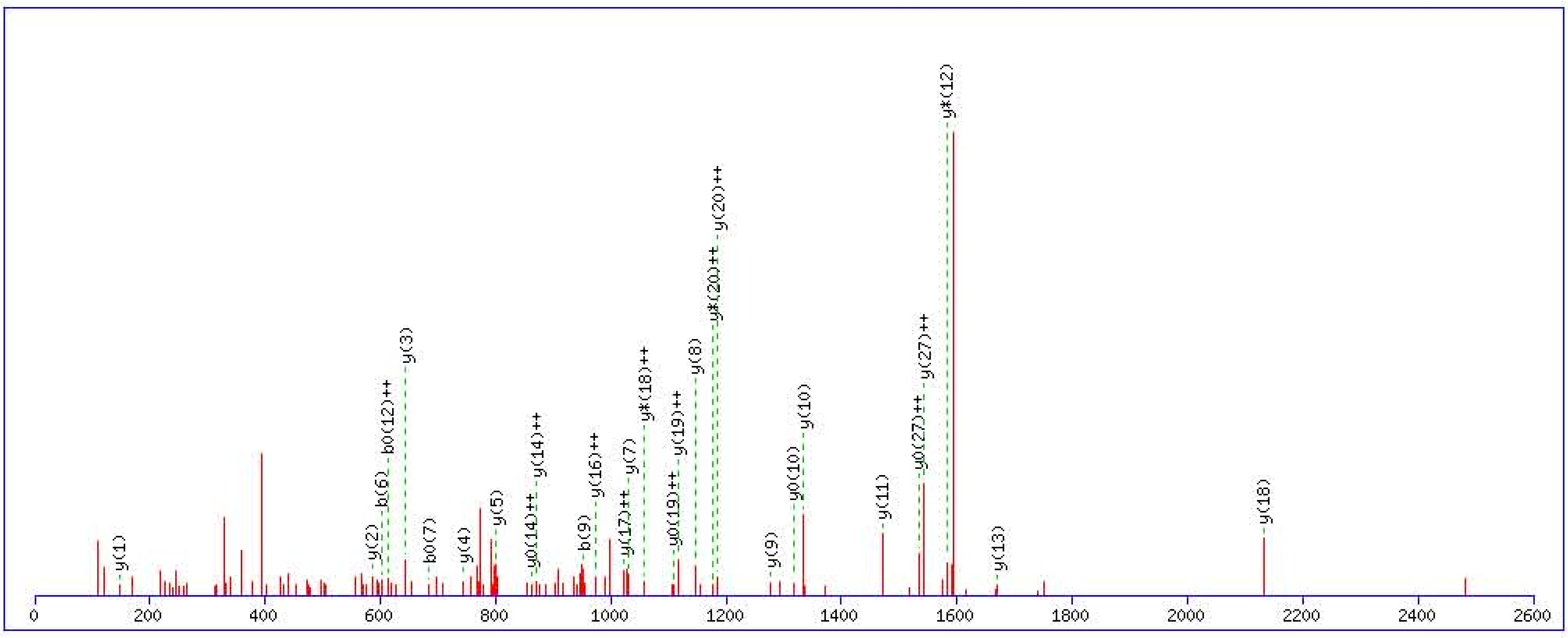
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPFDAATLHTSTAMAAQHGMDDDGTGQK**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

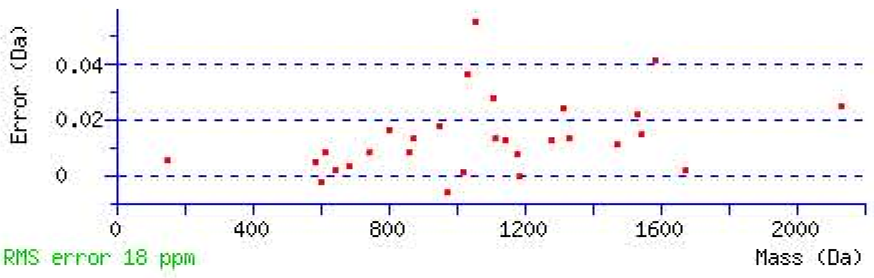
Match to Query 55377: 3183.462856 from(796.872990,4+) rtinseconds(2018) index(5045)
Title: Locus:1.1.1.3222.23 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

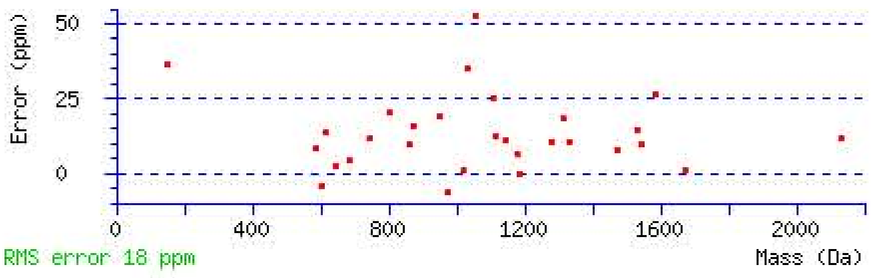
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 35  Expect: 0.0044
Matches : 29/280 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	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
34.7	3183.442383	0.020473	VPFDAATLHTSTAMAAQHGMDDDGTGQK
6.8	3183.442383	0.020473	VPFDAATLHTSTAMAAQHGMDDDGTGQK

Mascot: http://www.matrixscience.com/

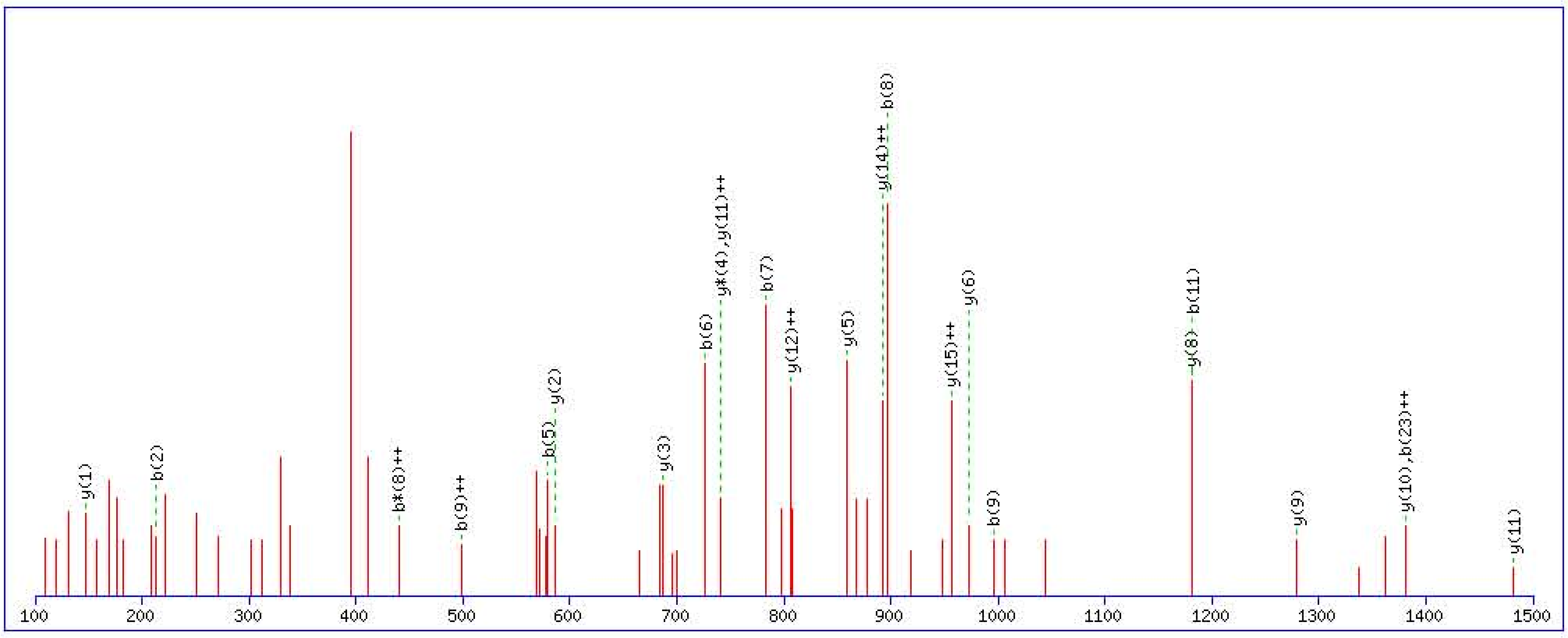
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VIHDNFGIVEGLMTTVHAITATQK**
Found in **G3P_HUMAN**, Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3

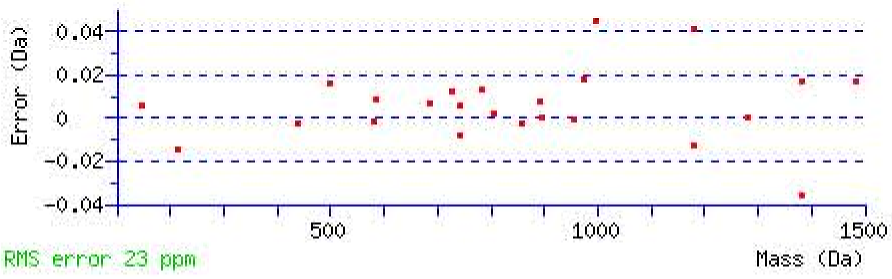
Match to Query 53060: 2905.532696 from(727.390450,4+) rtinseconds(3130) index(53064)
Title: Locus:1.1.1.3798.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

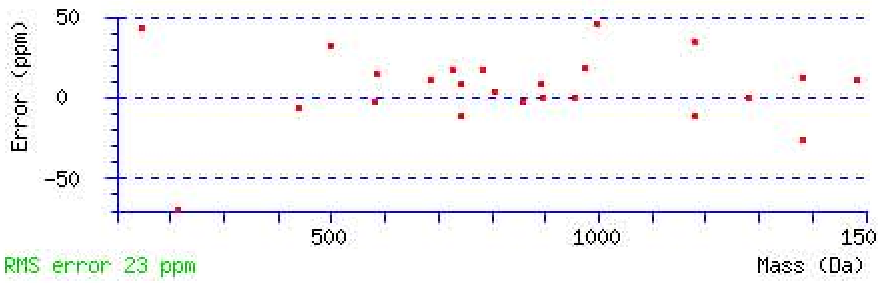
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2905.519424
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q23 : Biotin:Thermo-21345 (Q)
Ions Score: 52 **Expect:** 0.00013
Matches : 24/258 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	100.075690	50.541483					V							24
2	***213.159754***	107.083515					I	2807.458272	1404.232774	2790.431723	1395.719499	2789.447707	1395.227491	23
3	350.218666	175.612971					H	2694.374208	1347.690742	2677.347659	1339.177467	2676.363643	1338.685459	22
4	465.245609	233.126443			447.235044	224.121160	D	2557.315296	1279.161286	2540.288747	1270.648011	2539.304731	1270.156003	21
5	***579.288536***	290.147906	562.261987	281.634632	561.277971	281.142624	N	2442.288353	1221.647814	2425.261804	1213.134540	2424.277788	1212.642532	20
6	***726.356950***	363.682113	709.330401	355.168838	708.346385	354.676830	F	2328.245426	1164.626351	2311.218877	1156.113076	2310.234861	1155.621068	19
7	***783.378414***	392.192845	766.351865	383.679571	765.367849	383.187563	G	2181.177012	1091.092144	2164.150463	1082.578869	2163.166447	1082.086861	18
8	***896.462478***	448.734877	879.435929	440.221603	878.451913	439.729595	I	2124.155548	1062.581412	2107.128999	1054.068137	2106.144983	1053.576129	17
9	***995.530892***	**498.269084**	978.504343	489.755810	977.520327	489.263802	V	2011.071484	1006.039380	1994.044935	997.526105	1993.060919	997.034097	16
10	1124.573485	562.790381	1107.546936	554.277106	1106.562920	553.785098	E	1912.003070	956.505173	1894.976521	947.991899	1893.992505	947.499890	15
11	***1181.594949***	591.301113	1164.568400	582.787838	1163.584384	582.295830	G	1782.960477	891.983876	1765.933928	883.470602	1764.949912	882.978594	14
12	1294.679013	647.843144	1277.652464	639.329870	1276.668448	638.837862	L	1725.939013	863.473144	1708.912464	854.959870	1707.928448	854.467862	13
13	1425.719498	713.363387	1408.692949	704.850113	1407.708933	704.358104	M	1612.854949	806.931113	1595.828400	798.417838	1594.844384	797.925830	12
14	1526.767177	763.887227	1509.740628	755.373952	1508.756612	754.881944	T	***1481.814464***	741.410870	1464.787915	732.897596	1463.803899	732.405588	11
15	1627.814856	814.411066	1610.788307	805.897792	1609.804291	805.405783	T	***1380.766785***	690.887031	1363.740236	682.373756	1362.756220	681.881748	10
16	1726.883270	863.945273	1709.856721	855.431999	1708.872705	854.939991	V	***1279.719106***	640.363191	1262.692557	631.849917	1261.708541	631.357909	9
17	1863.942182	932.474729	1846.915633	923.961455	1845.931617	923.469447	H	***1180.650692***	590.828984	1163.624143	582.315710	1162.640127	581.823701	8
18	1934.979296	967.993286	1917.952747	959.480012	1916.968731	958.988003	A	1043.591780	522.299528	1026.565231	513.786254	1025.581215	513.294245	7
19	2048.063360	1024.535318	2031.036811	1016.022044	2030.052795	1015.530036	I	***972.554666***	486.780971	955.528117	478.267697	954.544101	477.775689	6
20	2149.111039	1075.059157	2132.084490	1066.545883	2131.100474	1066.053875	T	***859.470602***	430.238939	842.444053	421.725665	841.460037	421.233657	5
21	2220.148153	1110.577714	2203.121604	1102.064440	2202.137588	1101.572432	A	758.422923	379.715100	741.396374	371.201825	740.412358	370.709817	4
22	2321.195832	1161.101554	2304.169283	1152.588279	2303.185267	1152.096271	T	***687.385809***	344.196543	670.359260	335.683268	669.375244	335.191260	3
23	2760.421158	**1380.714217**	2743.394609	1372.200942	2742.410593	1371.708934	Q	***586.338130***	293.672703	569.311581	285.159429			2
24							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VIHDNFGIVEGLMTTVHAITATQK
(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	2905.519424	0.013272	VIHDNFGIVEGLMTTVHAITATQK

Mascot: http://www.matrixscience.com/

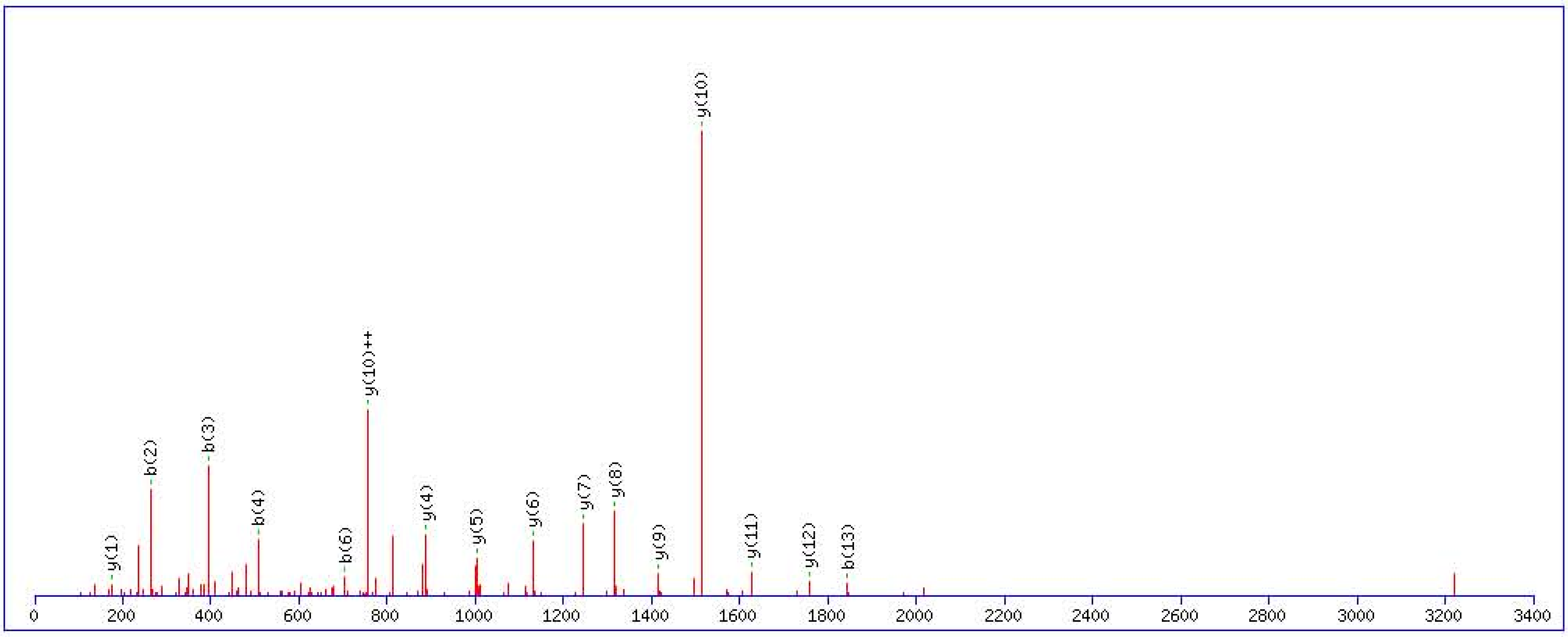
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YVMLPVADQDQCIR**
Found in **HPT_HUMAN**, Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1

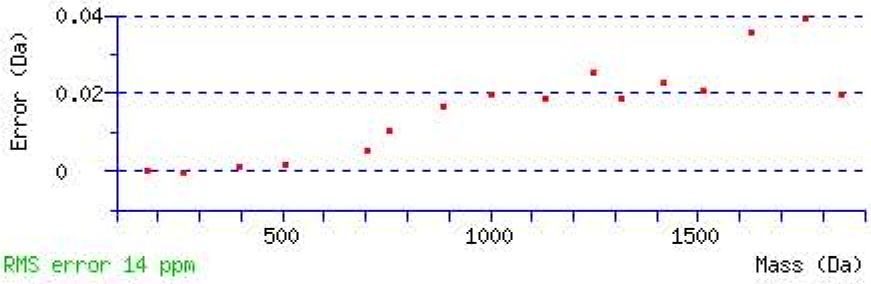
Match to Query 40169: 2018.005028 from(1010.009790,2+) rtinseconds(2336) index(6725)
Title: Locus:1.1.1.3333.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

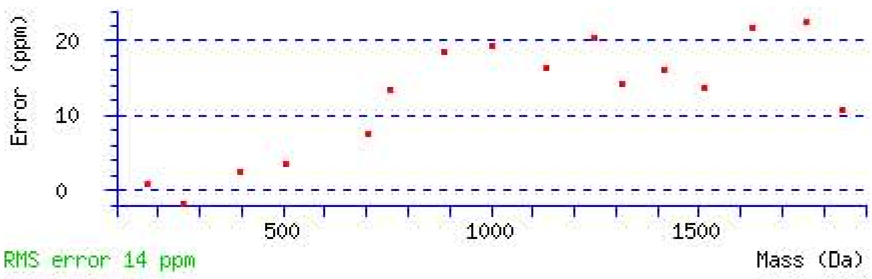
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2017.978760
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 85  Expect: 1.3e-008
Matches : 16/118 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	164.070605	82.538940					Y							14
2	**263.139019**	132.073148					V	1855.922710	928.464993	1838.896161	919.951719	1837.912145	919.459711	13
3	**394.179504**	197.593390					M	***1756.854296***	878.930786	1739.827747	870.417512	1738.843731	869.925504	12
4	**507.263568**	254.135422					L	***1625.813811***	813.410544	1608.787262	804.897269	1607.803246	804.405261	11
5	604.316332	302.661804					P	***1512.729747***	756.868512	1495.703198	748.355237	1494.719182	747.863229	10
6	**703.384746**	352.196011					V	***1415.676983***	708.342130	1398.650434	699.828855	1397.666418	699.336847	9
7	774.421860	387.714568					A	***1316.608569***	658.807923	1299.582020	650.294648	1298.598004	649.802640	8
8	889.448803	445.228040			871.438238	436.222757	D	***1245.571455***	623.289366	1228.544906	614.776091	1227.560890	614.284083	7
9	1017.507381	509.257329	1000.480832	500.744054	999.496816	500.252046	Q	***1130.544512***	565.775894	1113.517963	557.262620	1112.533947	556.770612	6
10	1132.534324	566.770800	1115.507775	558.257526	1114.523759	557.765517	D	***1002.485934***	501.746605	985.459385	493.233331	984.475369	492.741323	5
11	1571.759650	786.383463	1554.733101	777.870189	1553.749085	777.378181	Q	***887.458991***	444.233134	870.432442	435.719859			4
12	1731.790299	866.398788	1714.763750	857.885513	1713.779734	857.393505	C	448.233665	224.620470	431.207116	216.107196			3
13	**1844.874363**	922.940820	1827.847814	914.427545	1826.863798	913.935537	I	288.203016	144.605146	271.176467	136.091871			2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of YVMLPVADQDQCIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
84.6	2017.978760	0.026268	YVMLPVADQDQCIR
55.6	2017.978760	0.026268	YVMLPVADQDQCIR
0.5	2017.977875	0.027153	ITLTDLFENAYGSSMKGR

Mascot: http://www.matrixscience.com/

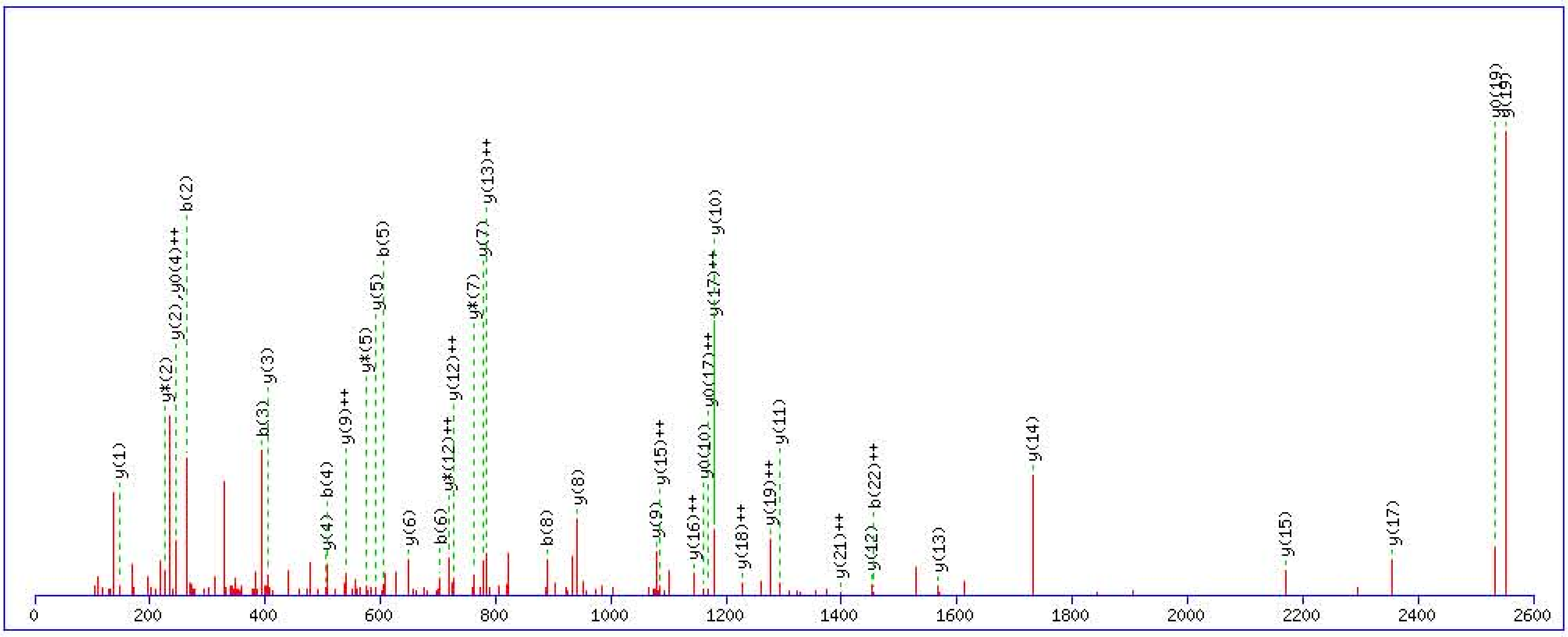
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YVMLPVADQYDCITHYEGSTCPK**
Found in **HPTR_HUMAN**, Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=1 SV=2

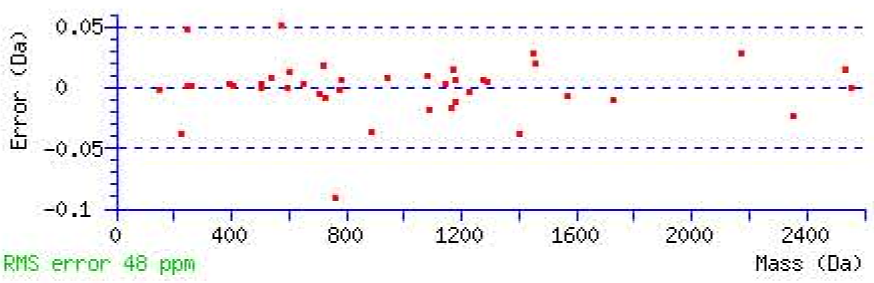
Match to Query 54426: 3057.368096 from(765.349300,4+) rtinseconds(2469) index(34376)
Title: Locus:1.1.1.3523.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

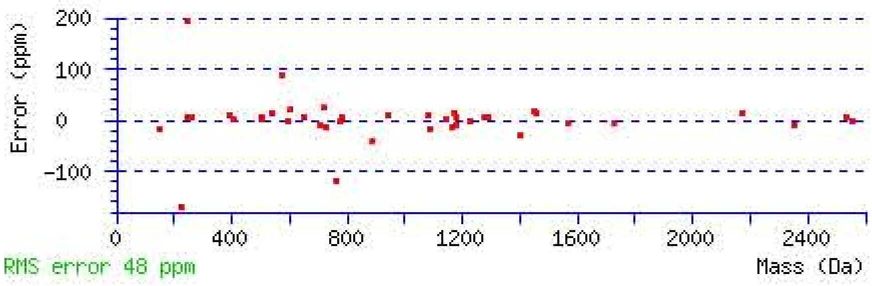
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3057.374466
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 71  Expect: 5.7e-007
Matches : 41/228 fragment ions using 104 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	164.070605	82.538940					Y							23
2	**263.139019**	132.073148					V	2895.318410	1448.162843	2878.291861	1439.649568	2877.307845	1439.157560	22
3	**394.179504**	197.593390					M	2796.249996	1398.628636	2779.223447	1390.115361	2778.239431	1389.623353	21
4	**507.263568**	254.135422					L	2665.209511	1333.108393	2648.182962	1324.595119	2647.198946	1324.103111	20
5	**604.316332**	302.661804					P	***2552.125447***	1276.566361	2535.098898	1268.053087	2534.114882	1267.561079	19
6	**703.384746**	352.196011					V	2455.072683	1228.039979	2438.046134	1219.526705	2437.062118	1219.034697	18
7	774.421860	387.714568					A	***2356.004269***	1178.505772	2338.977720	1169.992498	2337.993704	1169.500490	17
8	**889.448803**	445.228040			871.438238	436.222757	D	2284.967155	1142.987215	2267.940606	1134.473941	2266.956590	1133.981933	16
9	1328.674129	664.840703	1311.647580	656.327428	1310.663564	655.835420	Q	***2169.940212***	1085.473744	2152.913663	1076.960469	2151.929647	1076.468461	15
10	1491.737458	746.372367	1474.710909	737.859093	1473.726893	737.367085	Y	***1730.714886***	865.861081	1713.688337	857.347807	1712.704321	856.855799	14
11	1606.764401	803.885839	1589.737852	795.372564	1588.753836	794.880556	D	***1567.651557***	784.329417	1550.625008	775.816142	1549.640992	775.324134	13
12	1766.795050	883.901163	1749.768501	875.387889	1748.784485	874.895881	C	***1452.624614***	726.815945	1435.598065	718.302671	1434.614049	717.810663	12
13	1879.879114	940.443195	1862.852565	931.929921	1861.868549	931.437913	I	***1292.593965***	646.800621	1275.567416	638.287346	1274.583400	637.795338	11
14	1980.926793	990.967035	1963.900244	982.453760	1962.916228	981.961752	T	***1179.509901***	590.258589	1162.483352	581.745314	1161.499336	581.253306	10
15	2117.985705	1059.496490	2100.959156	1050.983216	2099.975140	1050.491208	H	***1078.462222***	539.734749	1061.435673	531.221475	1060.451657	530.729467	9
16	2281.049034	1141.028155	2264.022485	1132.514880	2263.038469	1132.022872	Y	***941.403310***	471.205293	924.376761	462.692018	923.392745	462.200010	8
17	2410.091627	1205.549452	2393.065078	1197.036177	2392.081062	1196.544169	E	***778.339981***	389.673628	761.313432	381.160354	760.329416	380.668346	7
18	2467.113091	1234.060184	2450.086542	1225.546909	2449.102526	1225.054901	G	***649.297388***	325.152332	632.270839	316.639057	631.286823	316.147049	6
19	2554.145119	1277.576198	2537.118570	1269.062923	2536.134554	1268.570915	S	***592.275924***	296.641600	575.249375	288.128325	574.265359	287.636317	5
20	2655.192798	1328.100037	2638.166249	1319.586762	2637.182233	1319.094754	T	***505.243896***	253.125586	488.217347	244.612311	487.233331	244.120303	4
21	2815.223447	1408.115361	2798.196898	1399.602087	2797.212882	1399.110079	C	***404.196217***	202.601746	387.169668	194.088472			3
22	2912.276211	1456.641743	2895.249662	1448.128469	2894.265646	1447.636461	P	***244.165568***	122.586422	227.139019	114.073148			2
23							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of YVMLPVADQYDCITHYEGSTCPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.1	3057.374466	-0.006370	YVMLPVADQYDCITHYEGSTCPK

Mascot: http://www.matrixscience.com/

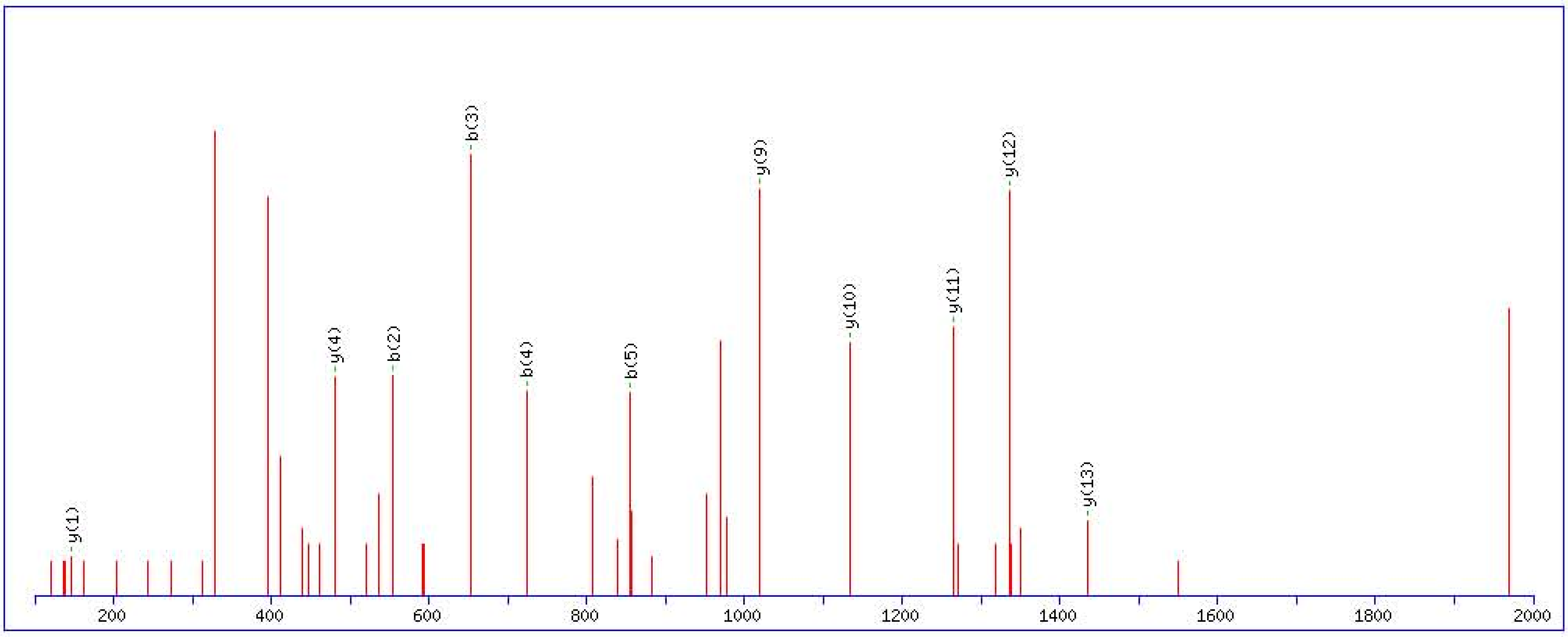
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NQVAMNPQNTVFDAK**
Found in **HS71L_HUMAN**, Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2

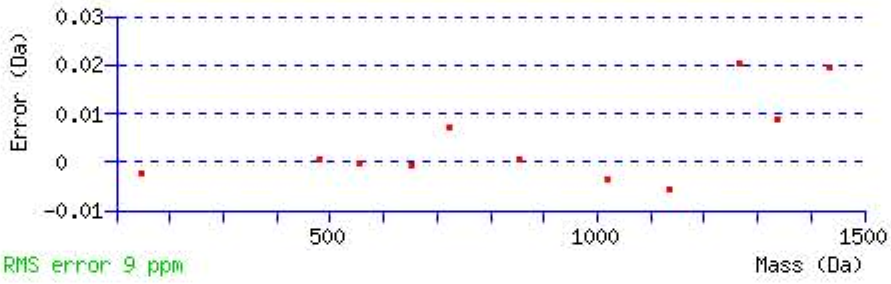
Match to Query 39065: 1986.965208 from(994.489880,2+) rtinseconds(2174) index(20059)
Title: Locus:1.1.1.3322.24 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

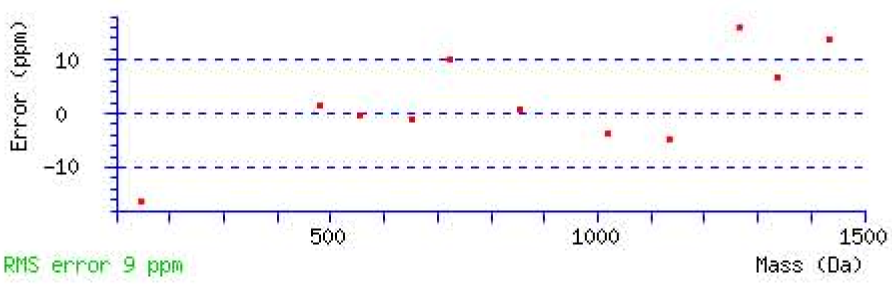
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1986.965546
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 2.1e-005
Matches : 11/146 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	115.050203	58.028740	98.023654	49.515465			N							15
2	**554.275529**	277.641403	537.248980	269.128128			Q	1873.929903	937.468590	1856.903354	928.955315	1855.919338	928.463307	14
3	**653.343943**	327.175610	636.317394	318.662335			V	***1434.704577***	717.855927	1417.678028	709.342652	1416.694012	708.850644	13
4	**724.381057**	362.694166	707.354508	354.180892			A	***1335.636163***	668.321720	1318.609614	659.808445	1317.625598	659.316437	12
5	**855.421542**	428.214409	838.394993	419.701134			M	***1264.599049***	632.803163	1247.572500	624.289888	1246.588484	623.797880	11
6	969.464469	485.235872	952.437920	476.722598			N	***1133.558564***	567.282920	1116.532015	558.769646	1115.547999	558.277638	10
7	1066.517233	533.762254	1049.490684	525.248980			P	***1019.515637***	510.261457	1002.489088	501.748182	1001.505072	501.256174	9
8	1194.575811	597.791543	1177.549262	589.278269			Q	922.462873	461.735075	905.436324	453.221800	904.452308	452.729792	8
9	1308.618738	654.813007	1291.592189	646.299733			N	794.404295	397.705786	777.377746	389.192511	776.393730	388.700503	7
10	1409.666417	705.336846	1392.639868	696.823572	1391.655852	696.331564	T	680.361368	340.684322	663.334819	332.171048	662.350803	331.679040	6
11	1508.734831	754.871054	1491.708282	746.357779	1490.724266	745.865771	V	579.313689	290.160483	562.287140	281.647208	561.303124	281.155200	5
12	1655.803245	828.405261	1638.776696	819.891986	1637.792680	819.399978	F	***480.245275***	240.626276	463.218726	232.113001	462.234710	231.620993	4
13	1770.830188	885.918732	1753.803639	877.405458	1752.819623	876.913450	D	333.176861	167.092069	316.150312	158.578794	315.166296	158.086786	3
14	1841.867302	921.437289	1824.840753	912.924015	1823.856737	912.432007	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 NQVAMNPQNTVFDAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.8	1986.965546	-0.000338	NQVAMNPQNTVFDAK
3.5	1986.961700	0.003508	DFQYVLKMETQMK
3.5	1986.961700	0.003508	DFQYVLKMETQMK
0.1	1986.987152	-0.021944	QHSSGQENTVKNPTHVPK

Mascot: http://www.matrixscience.com/

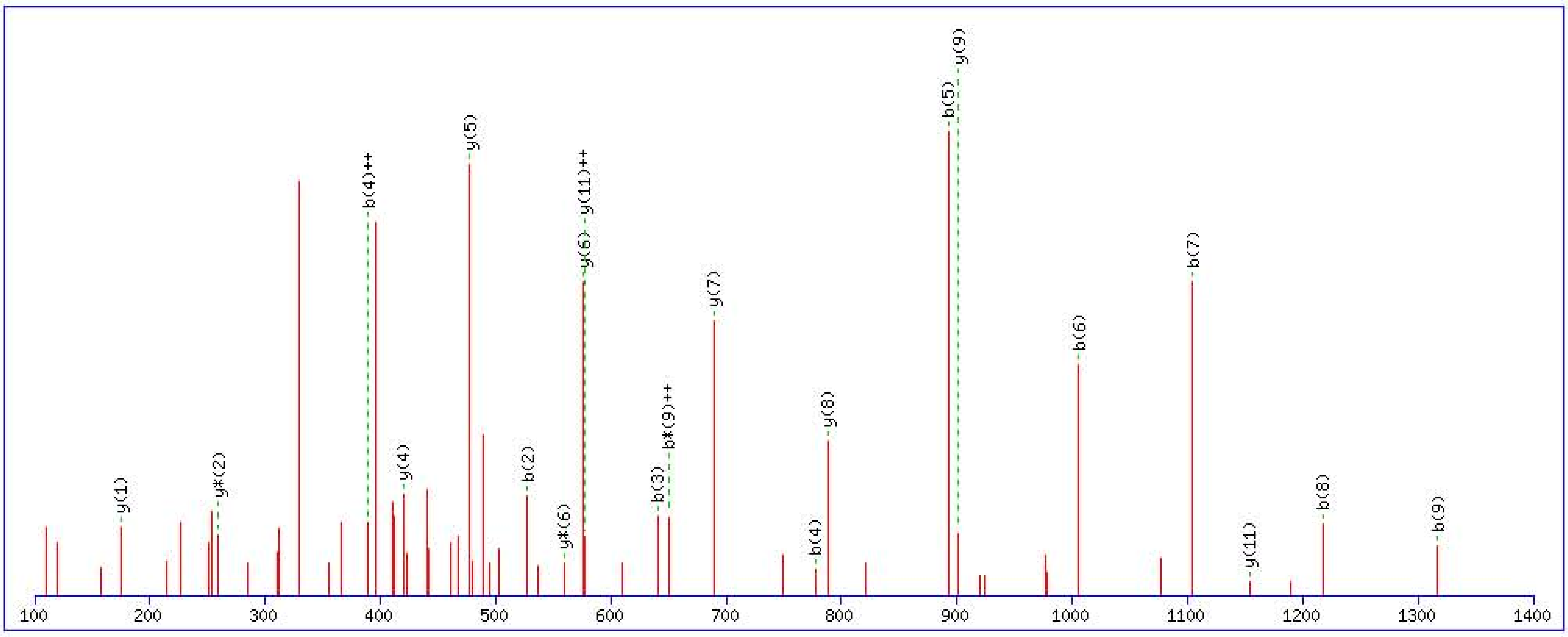
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SQIHDIVLVGGSTR**
Found in **HSP7C_HUMAN**, Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1

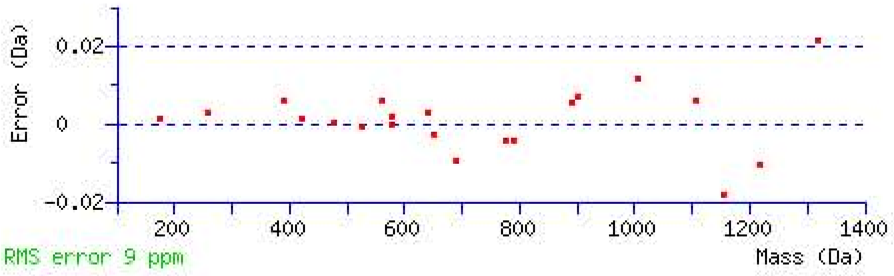
Match to Query 35560: 1791.968952 from(598.330260,3+) rtinseconds(2011) index(19137)
Title: Locus:1.1.1.3266.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

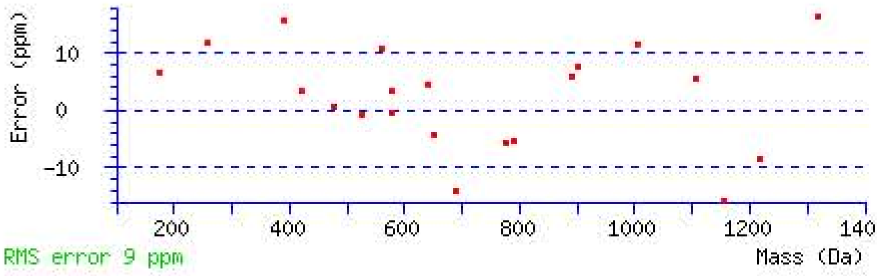
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1791.966553
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 7.3e-005
Matches : 21/152 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							14
2	***527.264630***	264.135953	510.238081	255.622679	509.254065	255.130671	Q	1705.941788	853.474532	1688.915239	844.961257	1687.931223	844.469249	13
3	***640.348694***	320.677985	623.322145	312.164711	622.338129	311.672703	I	1266.716462	633.861869	1249.689913	625.348595	1248.705897	624.856587	12
4	***777.407606***	389.207441	760.381057	380.694166	759.397041	380.202159	H	***1153.632398***	577.319837	1136.605849	568.806563	1135.621833	568.314554	11
5	***892.434549***	446.720913	875.408000	438.207638	874.423984	437.715630	D	1016.573486	508.790381	999.546937	500.277107	998.562921	499.785099	10
6	***1005.518613***	503.262945	988.492064	494.749670	987.508048	494.257662	I	***901.546543***	451.276910	884.519994	442.763635	883.535978	442.271627	9
7	***1104.587027***	552.797152	1087.560478	544.283877	1086.576462	543.791869	V	***788.462479***	394.734878	771.435930	386.221603	770.451914	385.729595	8
8	***1217.671091***	609.339183	1200.644542	600.825909	1199.660526	600.333901	L	***689.394065***	345.200671	672.367516	336.687396	671.383500	336.195388	7
9	***1316.739505***	658.873391	1299.712956	650.360116	1298.728940	649.868108	V	***576.310001***	288.658639	559.283452	280.145364	558.299436	279.653356	6
10	1373.760969	687.384122	1356.734420	678.870848	1355.750404	678.378840	G	***477.241587***	239.124431	460.215038	230.611157	459.231022	230.119149	5
11	1430.782433	715.894854	1413.755884	707.381580	1412.771868	706.889572	G	***420.220123***	210.613699	403.193574	202.100425	402.209558	201.608417	4
12	1517.814461	759.410868	1500.787912	750.897594	1499.803896	750.405586	S	363.198659	182.102968	346.172110	173.589693	345.188094	173.097685	3
13	1618.862140	809.934708	1601.835591	801.421434	1600.851575	800.929425	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SQIHDIVLVGGSTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.2	1791.966553	0.002399	SQIHDIVLVGGSTR
2.1	1791.947891	0.021061	LGYKNSDVINTVLSNR

Mascot: http://www.matrixscience.com/

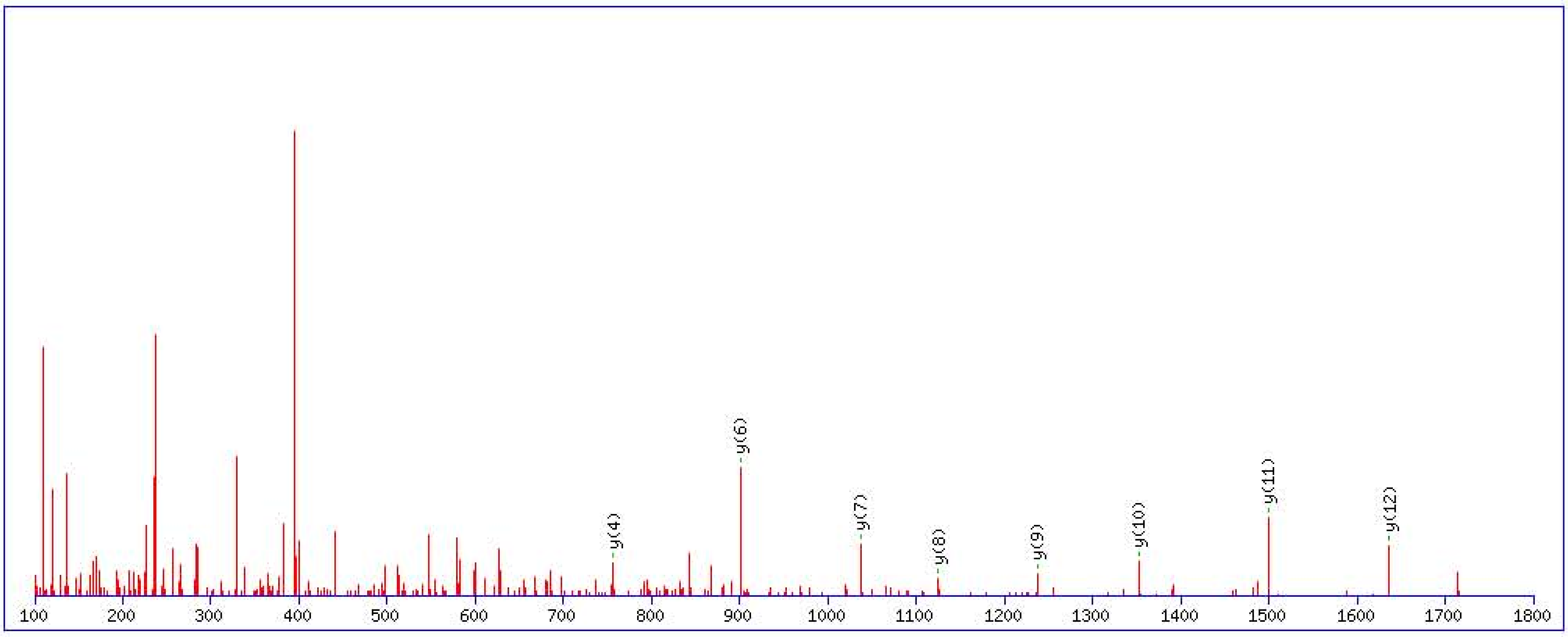
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TYFPHFDLSHGSAQVK**
Found in **HBA_HUMAN**, Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2

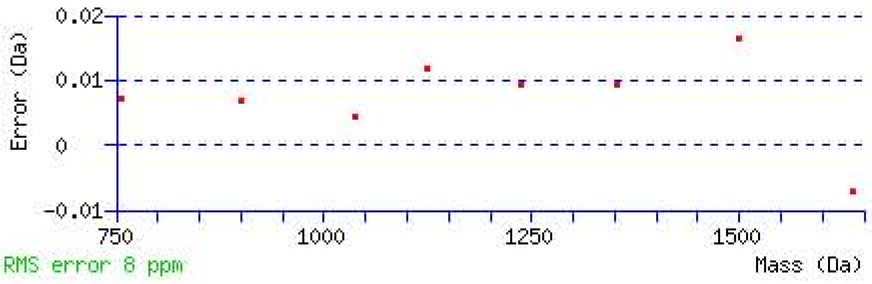
Match to Query 42230: 2144.054976 from(537.021020,4+) rtinseconds(2146) index(5700)
Title: Locus:1.1.1.3267.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

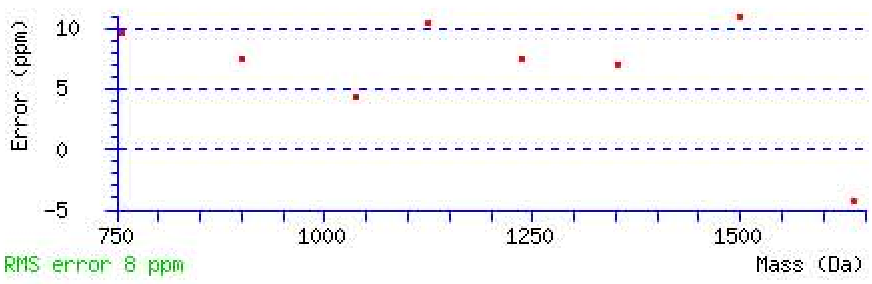
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2144.051346
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14    : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.0042
Matches : 8/146 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	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
37.8	2144.051346	0.003630	TYFPHFDLSHGSAQVK

Mascot: http://www.matrixscience.com/

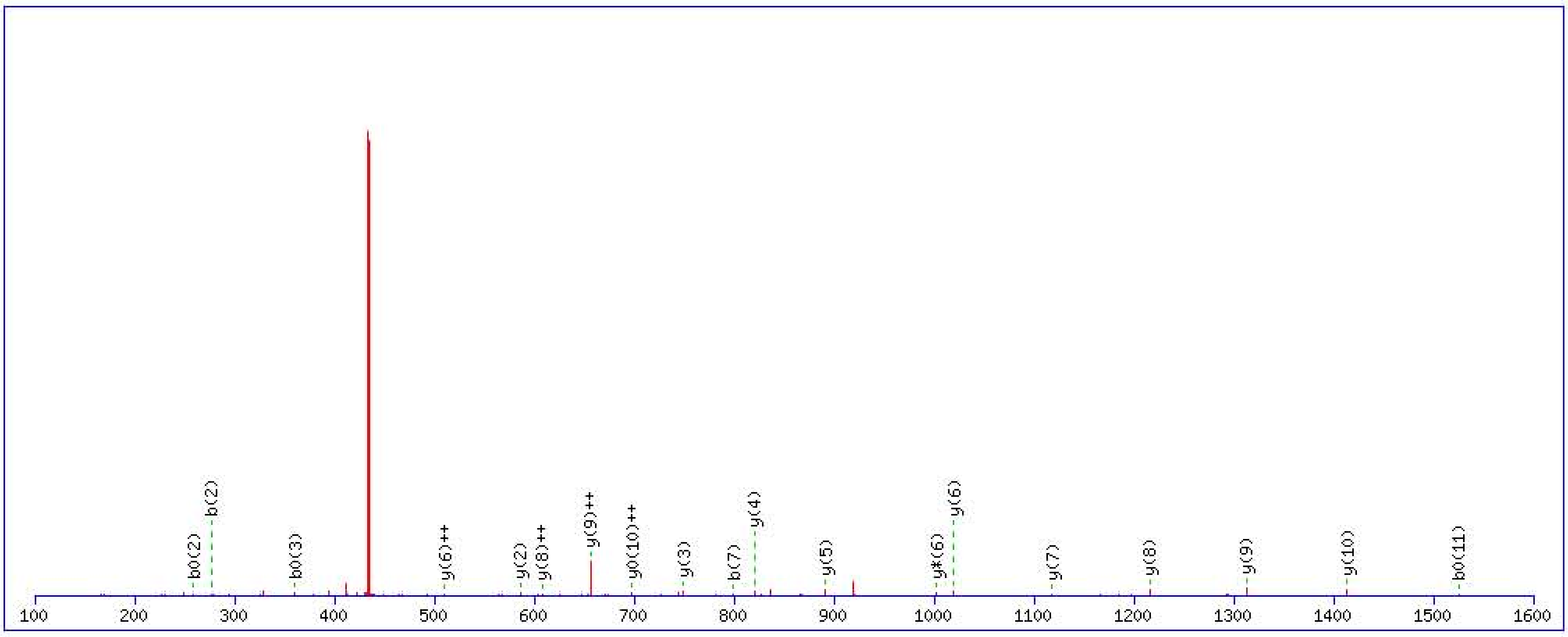
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EFTPPVQAAYQK**
Found in **HBB_HUMAN**, Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2

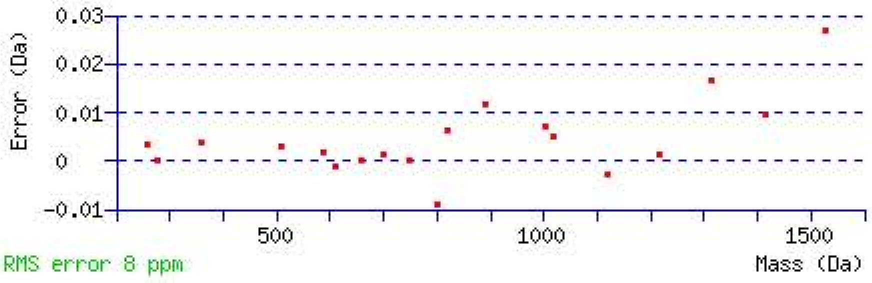
Match to Query 33465: 1688.876348 from(845.445450,2+) rtinseconds(2057) index(5252)
Title: Locus:1.1.1.3236.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

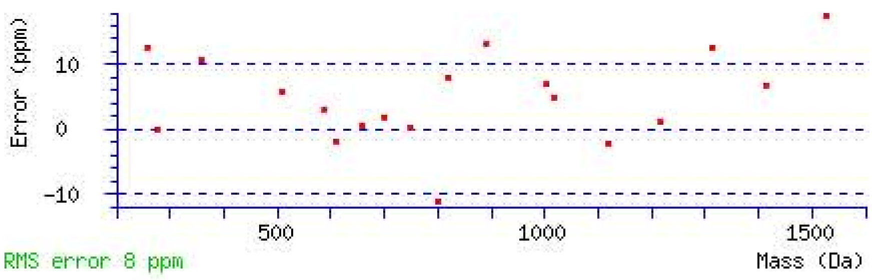
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1688.859604
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.00084
Matches : 19/102 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	130.049869	65.528572			112.039304	56.523290	E							12
2	**277.118283**	139.062779			259.107718	130.057497	F	1560.824300	780.915788	1543.797751	772.402514	1542.813735	771.910506	11
3	378.165962	189.586619			360.155397	180.581336	T	***1413.755886***	707.381581	1396.729337	698.868307	1395.745321	698.376299	10
4	475.218726	238.113001			457.208161	229.107719	P	***1312.708207***	656.857742	1295.681658	648.344467			9
5	572.271490	286.639383			554.260925	277.634101	P	***1215.655443***	608.331360	1198.628894	599.818085			8
6	671.339904	336.173590			653.329339	327.168308	V	***1118.602679***	559.804978	1101.576130	551.291703			7
7	**799.398482**	400.202879	782.371933	391.689605	781.387917	391.197597	Q	***1019.534265***	510.270771	1002.507716	501.757496			6
8	870.435596	435.721436	853.409047	427.208162	852.425031	426.716154	A	***891.475687***	446.241482	874.449138	437.728207			5
9	941.472710	471.239993	924.446161	462.726719	923.462145	462.234711	A	***820.438573***	410.722925	803.412024	402.209650			4
10	1104.536039	552.771658	1087.509490	544.258383	1086.525474	543.766375	Y	***749.401459***	375.204368	732.374910	366.691093			3
11	1543.761365	772.384321	1526.734816	763.871046	1525.750800	763.379038	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 EFTPPVQAAYQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.2	1688.859604	0.016744	EFTPPVQAAYQK
14.6	1688.859604	0.016744	EFTPPVQAAYQK
0.4	1688.874008	0.002340	MSSQKGNVARSRPQK
0.0	1688.877563	-0.001215	TEMAMLVTQARK

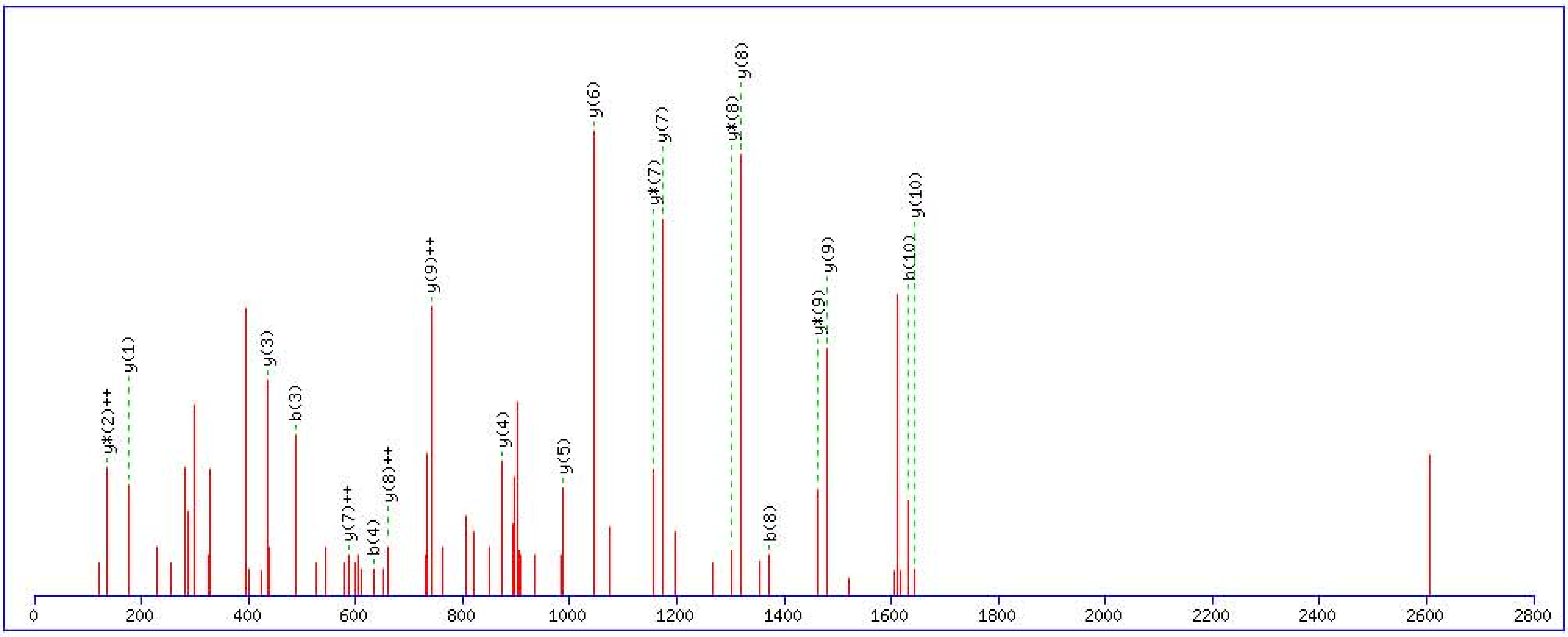
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YYCFQGNQFLR**
Found in **HEMO_HUMAN**, Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

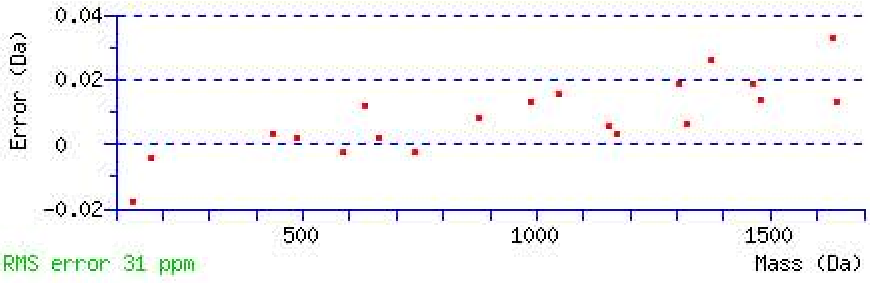
Match to Query 35819: 1805.852468 from(903.933510,2+) rtinseconds(2314) index(62292)
Title: Locus:1.1.1.1717.12 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

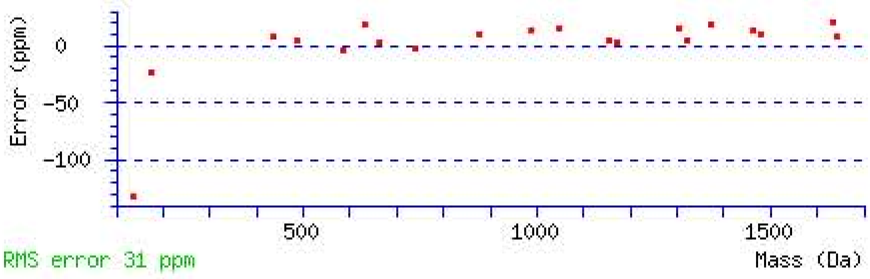
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1805.838165
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8     : Biotin:Thermo-21345 (Q)
Ions Score: 58  Expect: 8.2e-006
Matches : 20/72 fragment ions using 32 most intense peaks   (help)
```

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	164.070605	82.538940			Y					11
2	327.133934	164.070605			Y	***1643.782117***	822.394697	1626.755568	813.881422	10
3	**487.164583**	244.085930			C	***1480.718788***	740.863032	1463.692239	732.349758	9
4	**634.232997**	317.620137			F	***1320.688139***	660.847708	1303.661590	652.334433	8
5	762.291575	381.649426	745.265026	373.136151	Q	***1173.619725***	587.313501	1156.593176	578.800226	7
6	819.313039	410.160158	802.286490	401.646883	G	***1045.561147***	523.284212	1028.534598	514.770937	6
7	933.355966	467.181621	916.329417	458.668347	N	***988.539683***	494.773480	971.513134	486.260205	5
8	**1372.581292**	686.794284	1355.554743	678.281010	Q	***874.496756***	437.752016	857.470207	429.238742	4
9	1519.649706	760.328491	1502.623157	751.815217	F	***435.271430***	218.139353	418.244881	209.626078	3
10	**1632.733770**	816.870523	1615.707221	808.357249	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 YYCFQGNQFLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.1	1805.838165	0.014303	YYCFQGNQFLR
35.0	1805.838165	0.014303	YYCFQGNQFLR
3.7	1805.873886	-0.021418	QMFQERSSR
2.3	1805.873032	-0.020564	VSTGDNWNGIMKDTLR

Mascot: http://www.matrixscience.com/

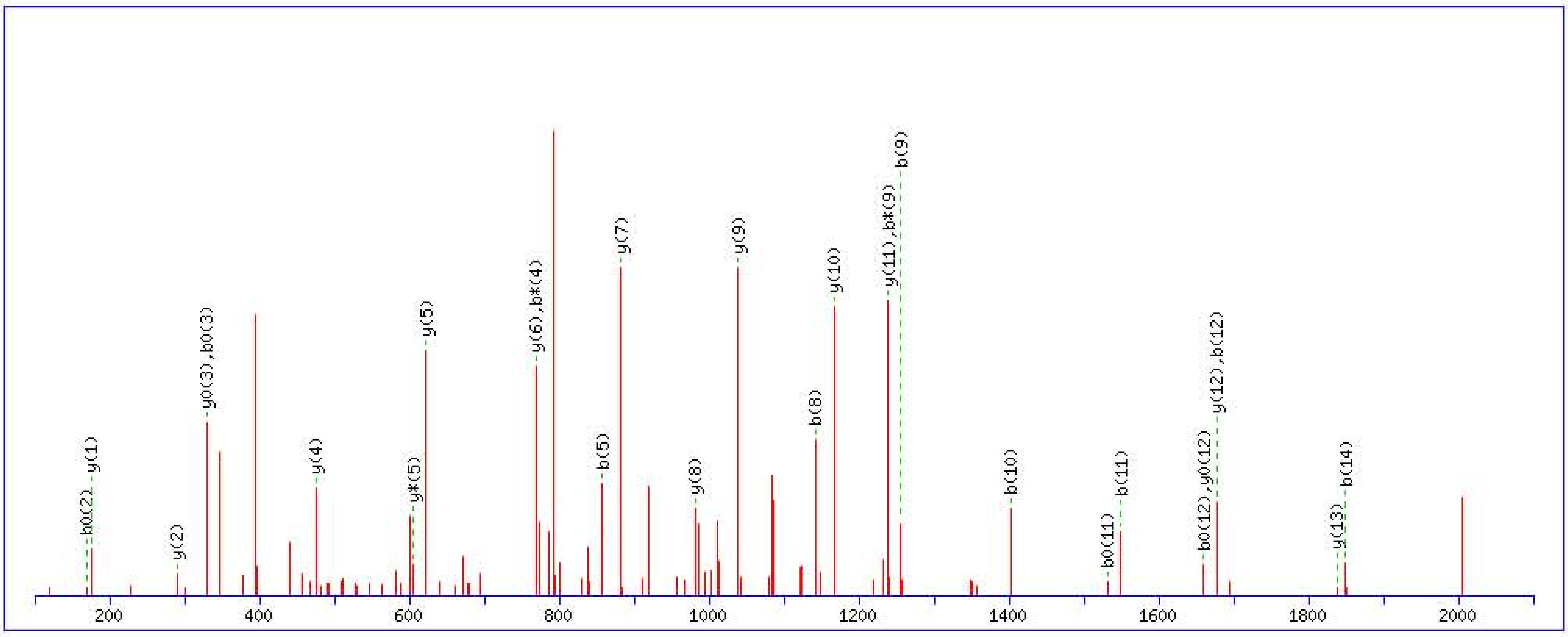
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GECQAEGVLFFQGDR**
Found in **HEMO_HUMAN**, Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

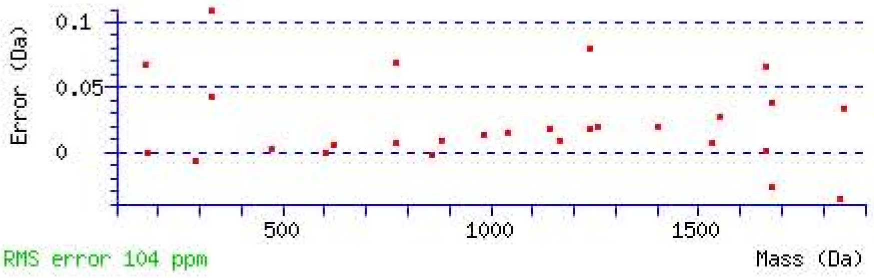
Match to Query 40252: 2022.937528 from(1012.476040,2+) rtinseconds(2426) index(62845)
Title: Locus:1.1.1.1756.12 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

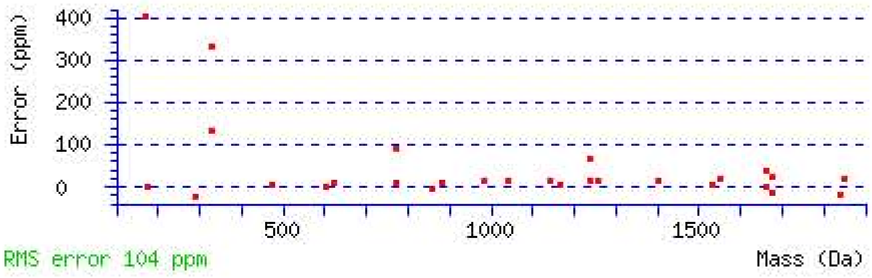
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2022.929184
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 96 **Expect:** 1.9e-009
Matches : 28/158 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	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
95.9	2022.929184	0.008344	GECQAEGVLFFQGDR
20.4	2022.929184	0.008344	GECQAEGVLFFQGDR
2.8	2022.950317	-0.012789	NMSFVNDLTVTQDGR

Mascot: http://www.matrixscience.com/

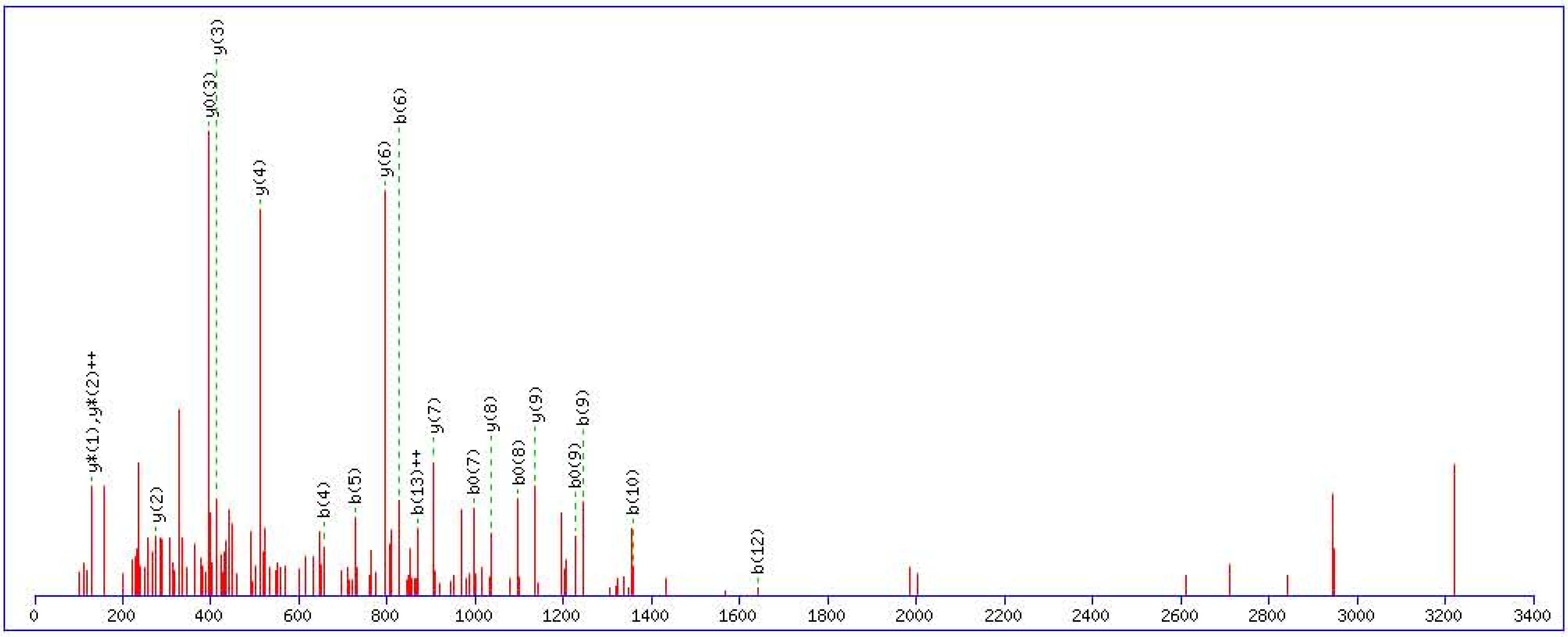
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGAQATWTELPWPHEK**
Found in **HEMO_HUMAN**, Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

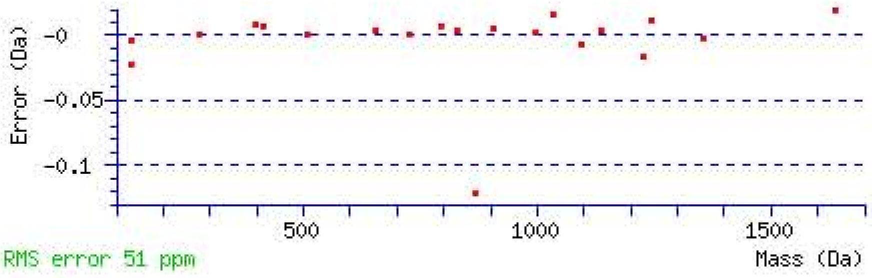
Match to Query 42288: 2148.056742 from(717.026190,3+) rtinseconds(2317) index(62305)
Title: Locus:1.1.1.1718.12 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

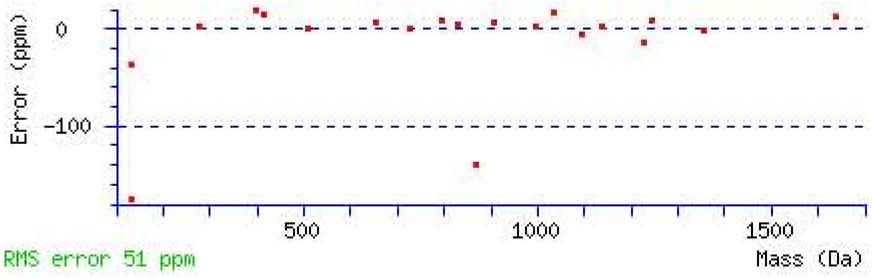
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2148.046234
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 43 **Expect:** 0.00012
Matches : 20/172 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							16
2	145.060768	73.034022			127.050203	64.028740	G	2062.021496	1031.514386	2044.994947	1023.001111	2044.010931	1022.509103	15
3	216.097882	108.552579			198.087317	99.547296	A	2005.000032	1003.003654	1987.973483	994.490380	1986.989467	993.998372	14
4	***655.323208***	328.165242	638.296659	319.651968	637.312643	319.159960	Q	1933.962918	967.485097	1916.936369	958.971823	1915.952353	958.479815	13
5	***726.360322***	363.683799	709.333773	355.170525	708.349757	354.678517	A	1494.737592	747.872434	1477.711043	739.359160	1476.727027	738.867152	12
6	***827.408001***	414.207639	810.381452	405.694364	809.397436	405.202356	T	1423.700478	712.353877	1406.673929	703.840603	1405.689913	703.348595	11
7	1013.487314	507.247295	996.460765	498.734020	995.476749	498.242012	W	1322.652799	661.830038	1305.626250	653.316763	1304.642234	652.824755	10
8	1114.534993	557.771135	1097.508444	549.257860	1096.524428	548.765852	T	***1136.573486***	568.790381	1119.546937	560.277107	1118.562921	559.785099	9
9	***1243.577586***	622.292431	1226.551037	613.779157	1225.567021	613.287149	E	***1035.525807***	518.266542	1018.499258	509.753267	1017.515242	509.261259	8
10	***1356.661650***	678.834463	1339.635101	670.321189	1338.651085	669.829181	L	***906.483214***	453.745245	889.456665	445.231971	888.472649	444.739963	7
11	1453.714414	727.360845	1436.687865	718.847571	1435.703849	718.355563	P	***793.399150***	397.203213	776.372601	388.689939	775.388585	388.197931	6
12	***1639.793727***	820.400502	1622.767178	811.887227	1621.783162	811.395219	W	696.346386	348.676831	679.319837	340.163557	678.335821	339.671549	5
13	1736.846491	868.926884	1719.819942	860.413609	1718.835926	859.921601	P	***510.267073***	255.637175	493.240524	247.123900	492.256508	246.631892	4
14	1873.905403	937.456340	1856.878854	928.943065	1855.894838	928.451057	H	***413.214309***	207.110793	396.187760	198.597518	395.203744	198.105510	3
15	2002.947996	1001.977636	1985.921447	993.464362	1984.937431	992.972354	E	***276.155397***	138.581337	259.128848	130.068062	258.144832	129.576054	2
16							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SGAQATWTELPWPHEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.5	2148.046234	0.010508	SGAQATWTELPWPHEK
0.5	2148.049408	0.007334	EPEGPAQAAVASGCLTRHAAR

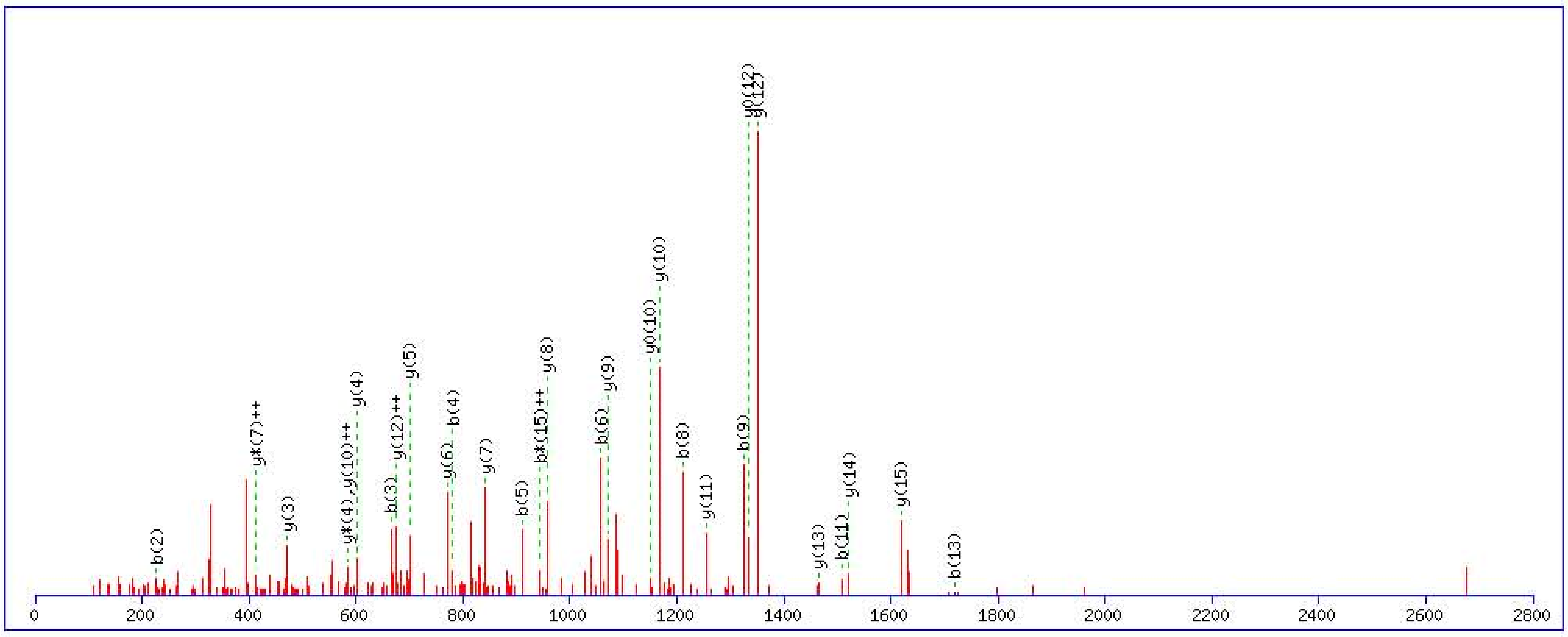
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLQDEFPGIPSPLDAAVECHR**
Found in **HEMO_HUMAN**, Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

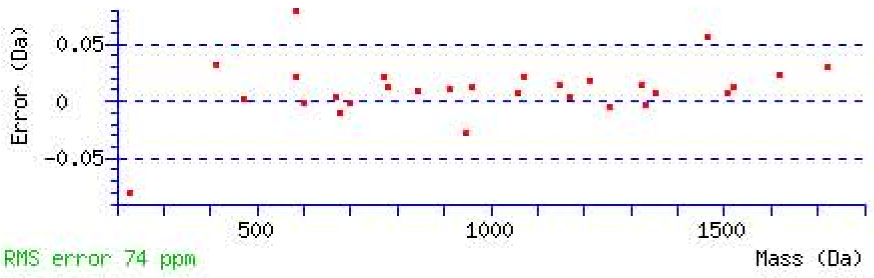
Match to Query 50162: 2674.346472 from(892.456100,3+) rtinseconds(2693) index(64372)
Title: Locus:1.1.1.1848.9 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

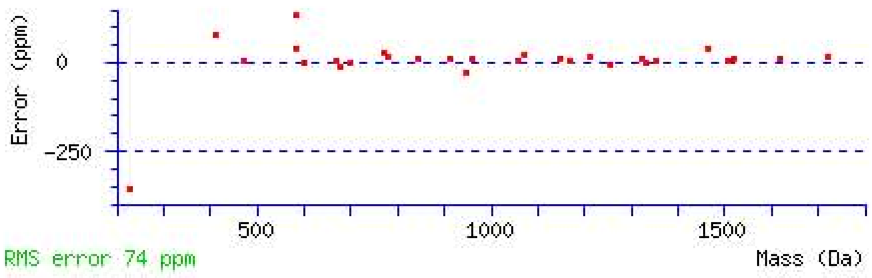
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2674.324722
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 80  Expect: 2.8e-007
Matches : 29/224 fragment ions using 51 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
80.0	2674.324722	0.021750	LLQDEFPGIPSPLDAAVECHR

Mascot: http://www.matrixscience.com/

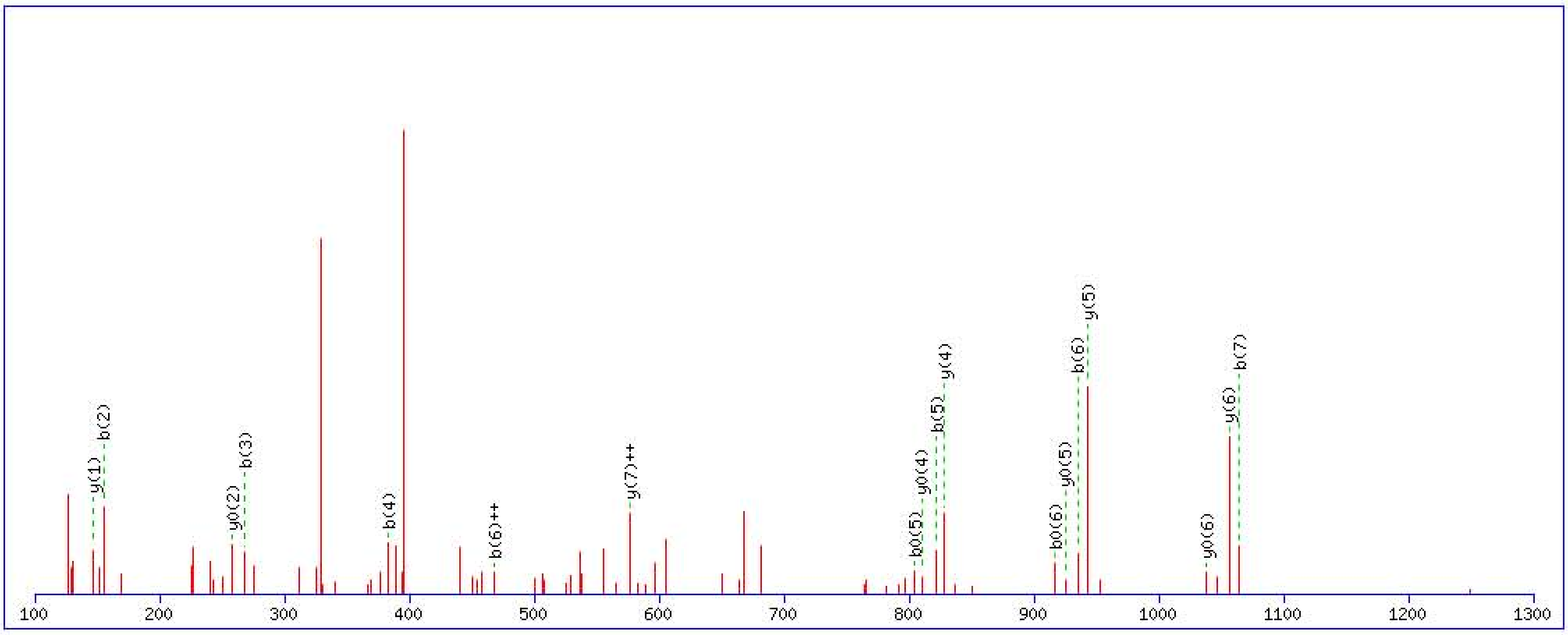
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPLDQLEK**
Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

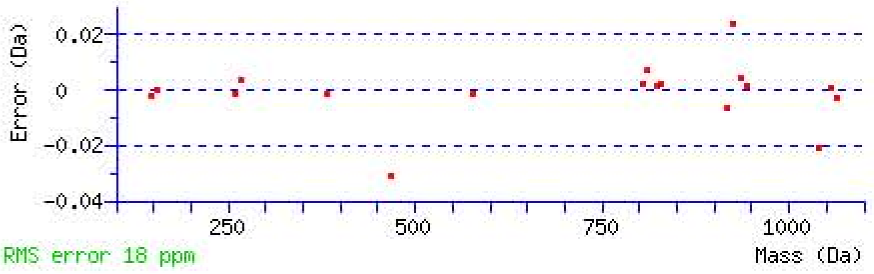
Match to Query 17960: 1209.640928 from(605.827740,2+) rtinseconds(2104) index(32473)
Title: Locus:1.1.1.3396.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

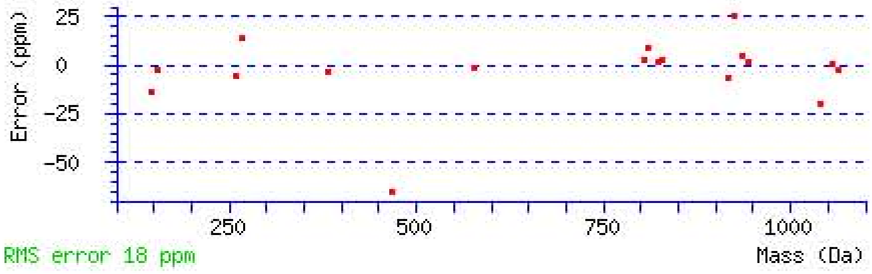
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1209.642731
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.009
Matches : 18/68 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							8
2	***155.081504***	78.044390					P	1153.628558	577.317917	1136.602009	568.804643	1135.617993	568.312635	7
3	***268.165568***	134.586422					L	**1056.575794**	528.791535	1039.549245	520.278261	1038.565229	519.786253	6
4	***383.192511***	192.099894			365.181946	183.094611	D	**943.491730**	472.249503	926.465181	463.736228	925.481165	463.244220	5
5	***822.417837***	411.712557	805.391288	403.199282	804.407272	402.707274	Q	**828.464787**	414.736032	811.438238	406.222757	810.454222	405.730749	4
6	***935.501901***	468.254589	918.475352	459.741314	917.491336	459.249306	L	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	3
7	***1064.544494***	532.775885	1047.517945	524.262611	1046.533929	523.770603	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
8							K	**147.112804**	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of GPLDQLEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.5	1209.642731	-0.001803	GPLDQLEK
9.1	1209.646545	-0.005617	EHNRLATELK
9.0	1209.628799	0.012129	TRFRIEMNK
4.3	1209.628815	0.012113	GLGHMPRAVEK
2.0	1209.642731	-0.001803	GTGEFIKALMK
0.4	1209.635330	0.005598	GPLAIREDPDK

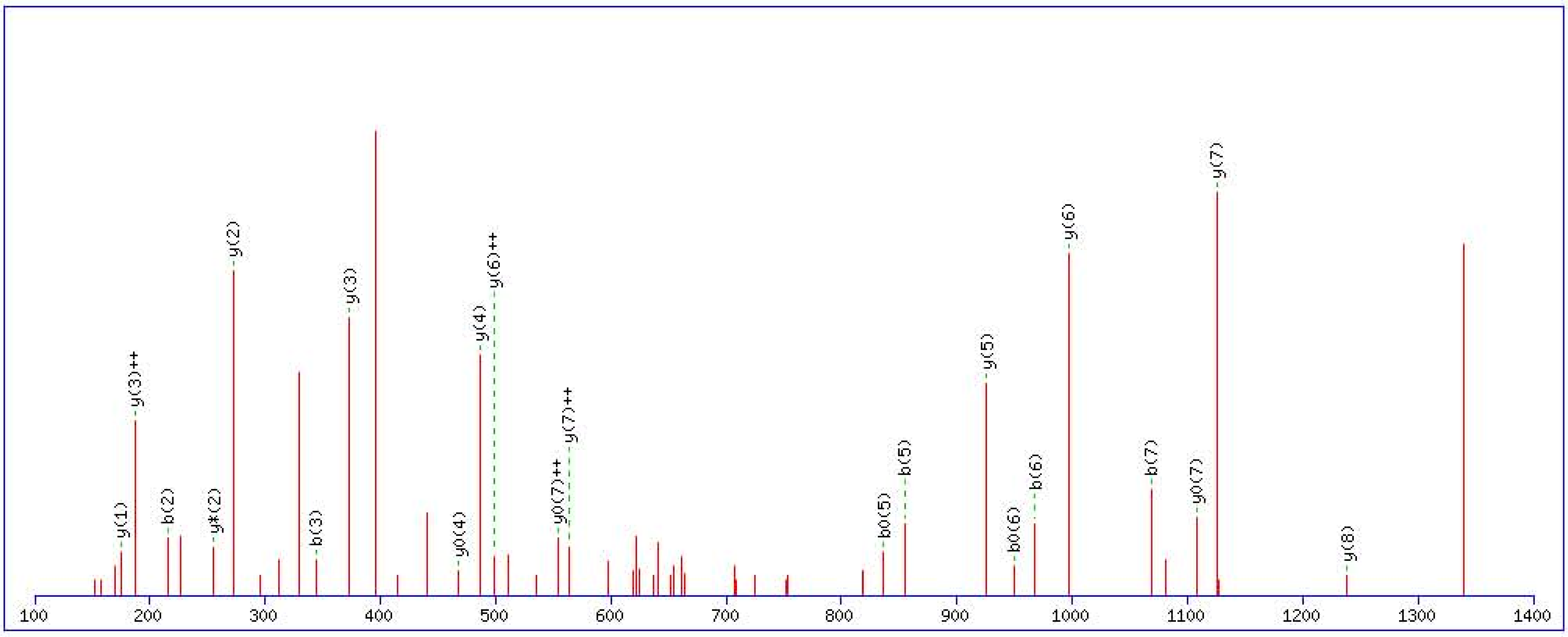
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLEAQLTPR**
Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

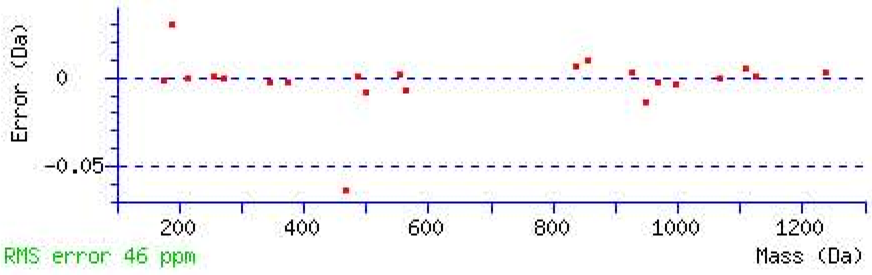
Match to Query 21093: 1338.722428 from(670.368490,2+) rtinseconds(1974) index(31671)
Title: Locus:1.1.1.3351.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

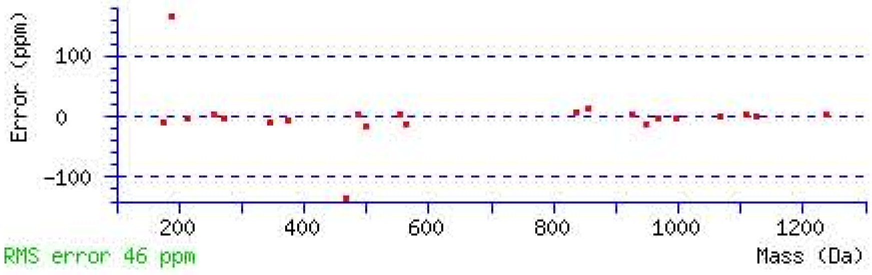
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1338.732941
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 8.8e-005
Matches : 22/84 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	102.054955	51.531116			84.044390	42.525833	T							9
2	**215.139019**	108.073147			197.128454	99.067865	L	***1238.692556***	619.849916	1221.666007	611.336642	1220.681991	610.844633	8
3	**344.181612**	172.594444			326.171047	163.589162	E	***1125.608492***	563.307884	1108.581943	554.794610	1107.597927	554.302602	7
4	415.218726	208.113001			397.208161	199.107719	A	***996.565899***	498.786588	979.539350	490.273313	978.555334	489.781305	6
5	**854.444052**	427.725664	837.417503	419.212390	836.433487	418.720382	Q	***925.528785***	463.268031	908.502236	454.754756	907.518220	454.262748	5
6	**967.528116**	484.267696	950.501567	475.754422	949.517551	475.262414	L	***486.303459***	243.655367	469.276910	235.142093	468.292894	234.650085	4
7	**1068.575795**	534.791536	1051.549246	526.278261	1050.565230	525.786253	T	***373.219395***	187.113335	356.192846	178.600061	355.208830	178.108053	3
8	1165.628559	583.317918	1148.602010	574.804643	1147.617994	574.312635	P	***272.171716***	136.589496	255.145167	128.076221			2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TLEAQLTPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.2	1338.732941	-0.010513	TLEAQLTPR
10.4	1338.711639	0.010789	DVPQAEVGRGRR
9.9	1338.732956	-0.010528	VDLQSLPTR
9.6	1338.725555	-0.003127	VDTVAAEHLTRK
5.4	1338.707809	0.014619	TLRPSPLCPGGGK
2.9	1338.715179	0.007249	QISTLAMHK
0.3	1338.732941	-0.010513	TDRIYAMKVVK

Mascot: http://www.matrixscience.com/

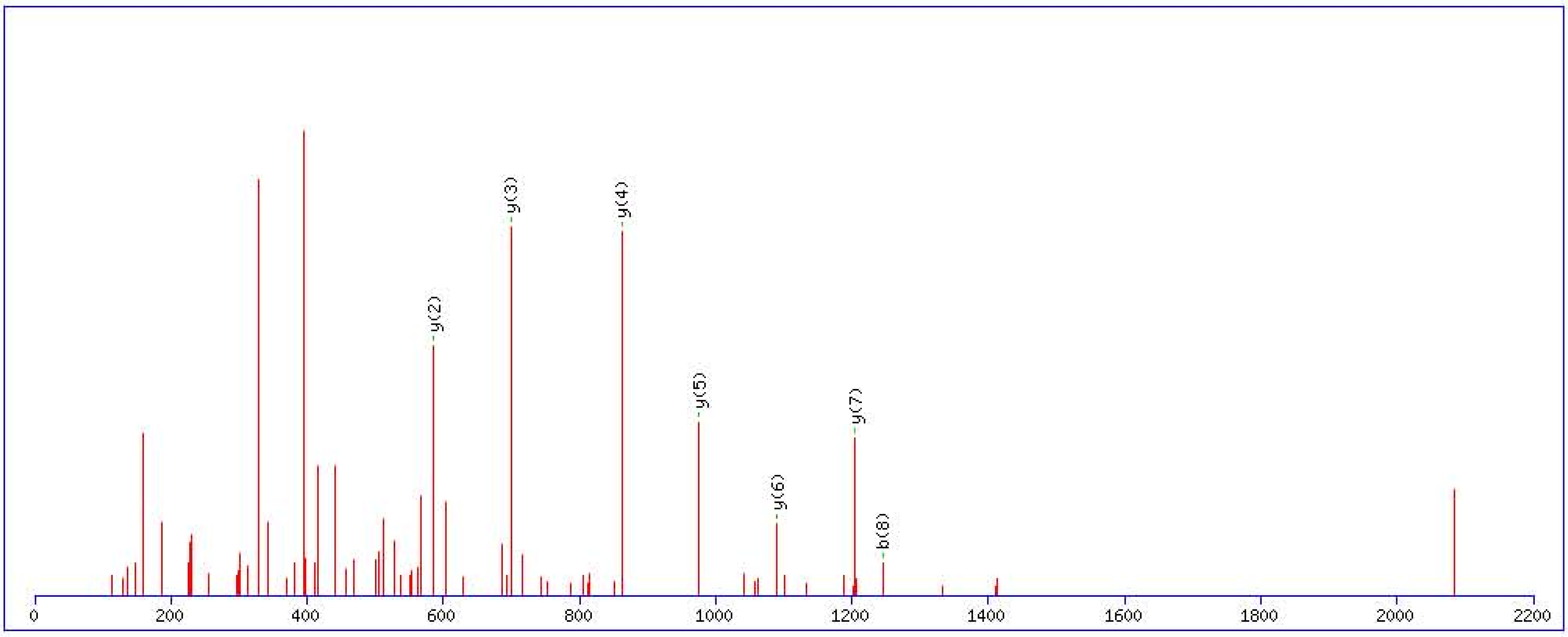
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVNDLYIQK**
Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

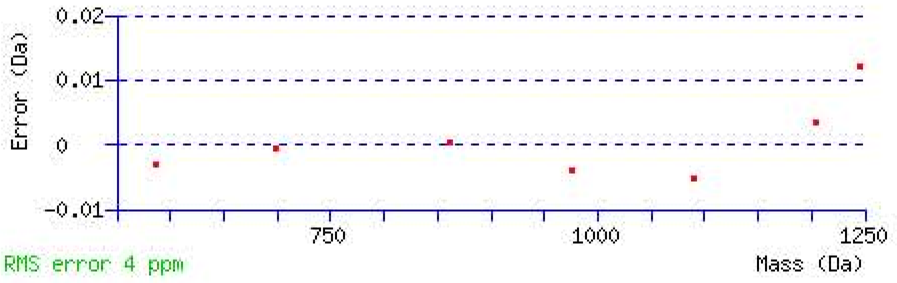
Match to Query 23260: 1389.727548 from(695.871050,2+) rtinseconds(1978) index(31697)
Title: Locus:1.1.1.3352.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

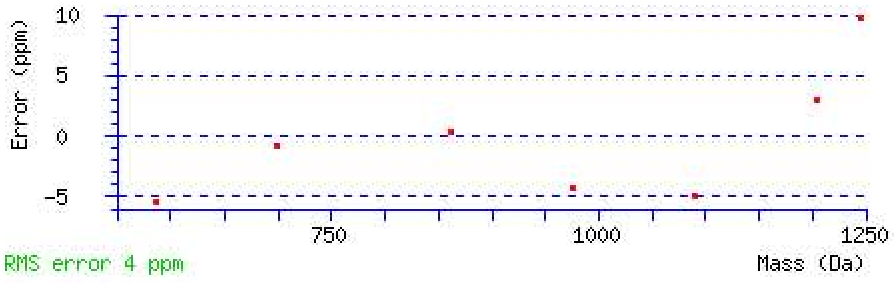
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1389.732605
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 36 **Expect:** 0.00099
Matches : 7/82 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	88.039304	44.523290			70.028739	35.518008	S							9
2	187.107718	94.057497			169.097153	85.052214	V	1303.707871	652.357573	1286.681322	643.844299	1285.697306	643.352291	8
3	301.150645	151.078960	284.124096	142.565686	283.140080	142.073678	N	*1204.639457*	602.823367	1187.612908	594.310092	1186.628892	593.818084	7
4	416.177588	208.592432	399.151039	200.079158	398.167023	199.587150	D	*1090.596530*	545.801903	1073.569981	537.288629	1072.585965	536.796621	6
5	529.261652	265.134464	512.235103	256.621190	511.251087	256.129182	L	*975.569587*	488.288432	958.543038	479.775157			5
6	692.324981	346.666129	675.298432	338.152854	674.314416	337.660846	Y	*862.485523*	431.746400	845.458974	423.233125			4
7	805.409045	403.208161	788.382496	394.694886	787.398480	394.202878	I	*699.422194*	350.214735	682.395645	341.701461			3
8	**1244.634371**	622.820823	1227.607822	614.307549	1226.623806	613.815541	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 SVNDLYIQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.2	1389.732605	-0.005057	SVNDLYIQK
3.9	1389.707458	0.020090	TKSMFQRTTYK
1.9	1389.735062	-0.007514	ISEAKEELKESK
1.7	1389.746323	-0.018775	TAKATLEQDSAKK
1.6	1389.713989	0.013559	LLPEPGPSDSPGPK
0.6	1389.728577	-0.001029	NMLTESLVALQR

Mascot: http://www.matrixscience.com/

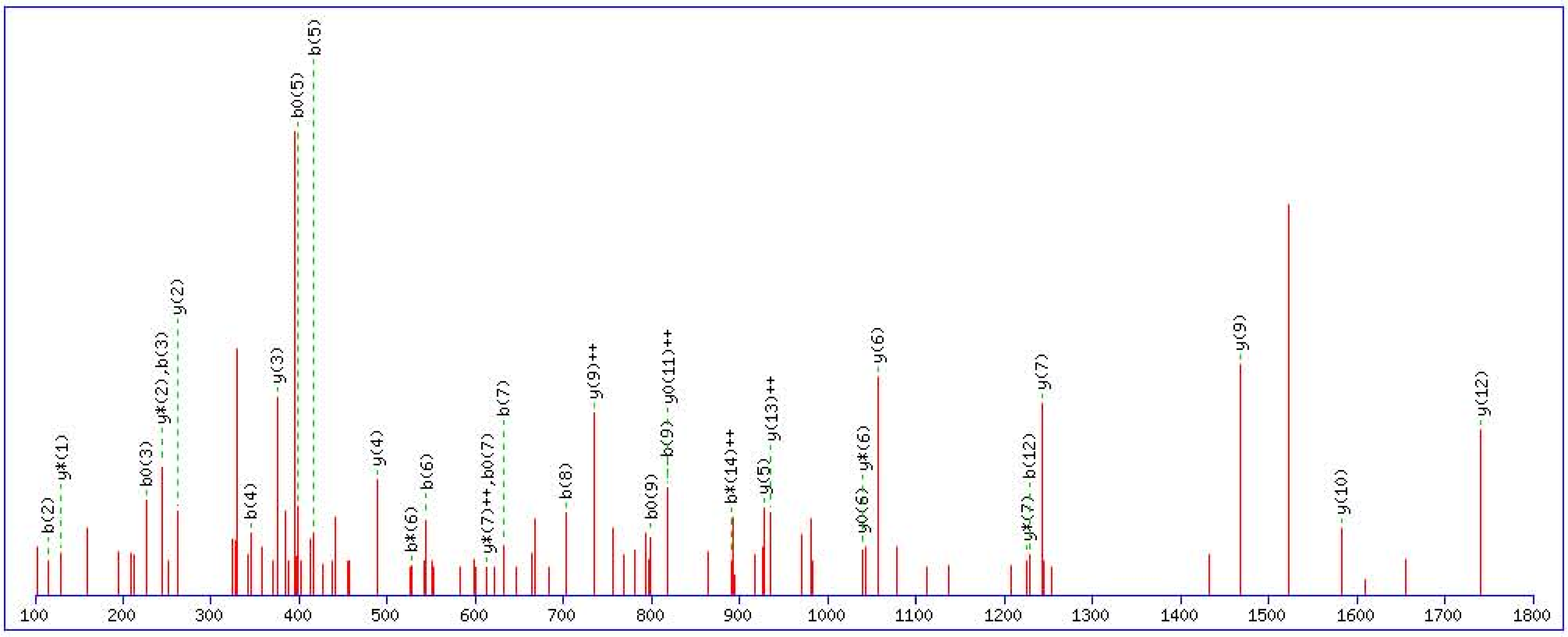
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGETAQSADPQWEQLNNK**
Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

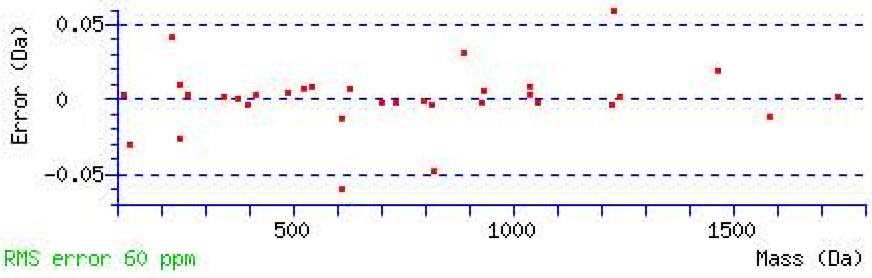
Match to Query 44775: 2283.047412 from(762.023080,3+) rtinseconds(1944) index(31422)
Title: Locus:1.1.1.3340.23 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

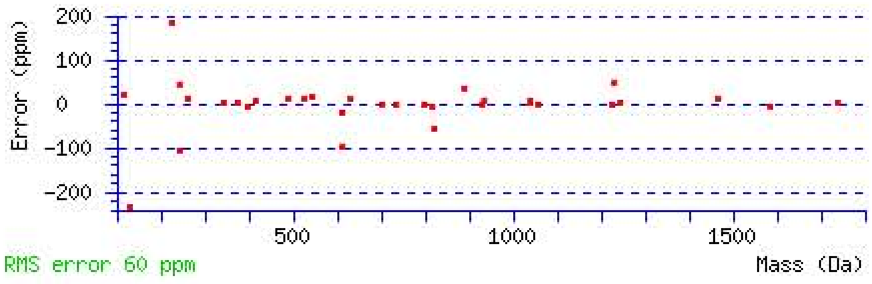
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2283.058975
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.00052
Matches : 33/180 fragment ions using 75 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							18
2	***115.050204***	58.028740					G	2227.044809	1114.026042	2210.018260	1105.512768	2209.034244	1105.020760	17
3	***244.092797***	122.550037			226.082232	113.544754	E	2170.023345	1085.515310	2152.996796	1077.002036	2152.012780	1076.510028	16
4	***345.140476***	173.073876			327.129911	164.068594	T	2040.980752	1020.994014	2023.954203	1012.480740	2022.970187	1011.988732	15
5	***416.177590***	208.592433			398.167025	199.587151	A	1939.933073	970.470175	1922.906524	961.956900	1921.922508	961.464892	14
6	***544.236168***	272.621722	527.209619	264.108448	526.225603	263.616440	Q	1868.895959	934.951618	1851.869410	926.438343	1850.885394	925.946335	13
7	***631.268196***	316.137736	614.241647	307.624462	613.257631	307.132454	S	***1740.837381***	870.922329	1723.810832	862.409054	1722.826816	861.917046	12
8	***702.305310***	351.656293	685.278761	343.143019	684.294745	342.651011	A	1653.805353	827.406315	1636.778804	818.893040	1635.794788	818.401032	11
9	***817.332253***	409.169765	800.305704	400.656490	799.321688	400.164482	D	***1582.768239***	791.887758	1565.741690	783.374483	1564.757674	782.882475	10
10	914.385017	457.696147	897.358468	449.182872	896.374452	448.690864	P	***1467.741296***	734.374286	1450.714747	725.861012	1449.730731	725.369004	9
11	1042.443595	521.725436	1025.417046	513.212161	1024.433030	512.720153	Q	1370.688532	685.847904	1353.661983	677.334630	1352.677967	676.842622	8
12	***1228.522908***	614.765092	1211.496359	606.251818	1210.512343	605.759809	W	***1242.629954***	621.818615	1225.603405	613.305341	1224.619389	612.813333	7
13	1357.565501	679.286388	1340.538952	670.773114	1339.554936	670.281106	E	***1056.550641***	528.778959	1039.524092	520.265684	1038.540076	519.773676	6
14	1796.790827	898.899052	1779.764278	890.385777	1778.780262	889.893769	Q	***927.508048***	464.257662	910.481499	455.744388			5
15	1909.874891	955.441083	1892.848342	946.927809	1891.864326	946.435801	L	***488.282722***	244.644999	471.256173	236.131725			4
16	2023.917818	1012.462547	2006.891269	1003.949273	2005.907253	1003.457265	N	***375.198658***	188.102967	358.172109	179.589693			3
17	2137.960745	1069.484010	2120.934196	1060.970736	2119.950180	1060.478728	N	***261.155731***	131.081504	244.129182	122.568229			2
18							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of GGETAQSADPQWEQLNNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.3	2283.058975	-0.011563	GGETAQSADPQWEQLNNK
20.9	2283.058975	-0.011563	GGETAQSADPQWEQLNNK

Mascot: http://www.matrixscience.com/

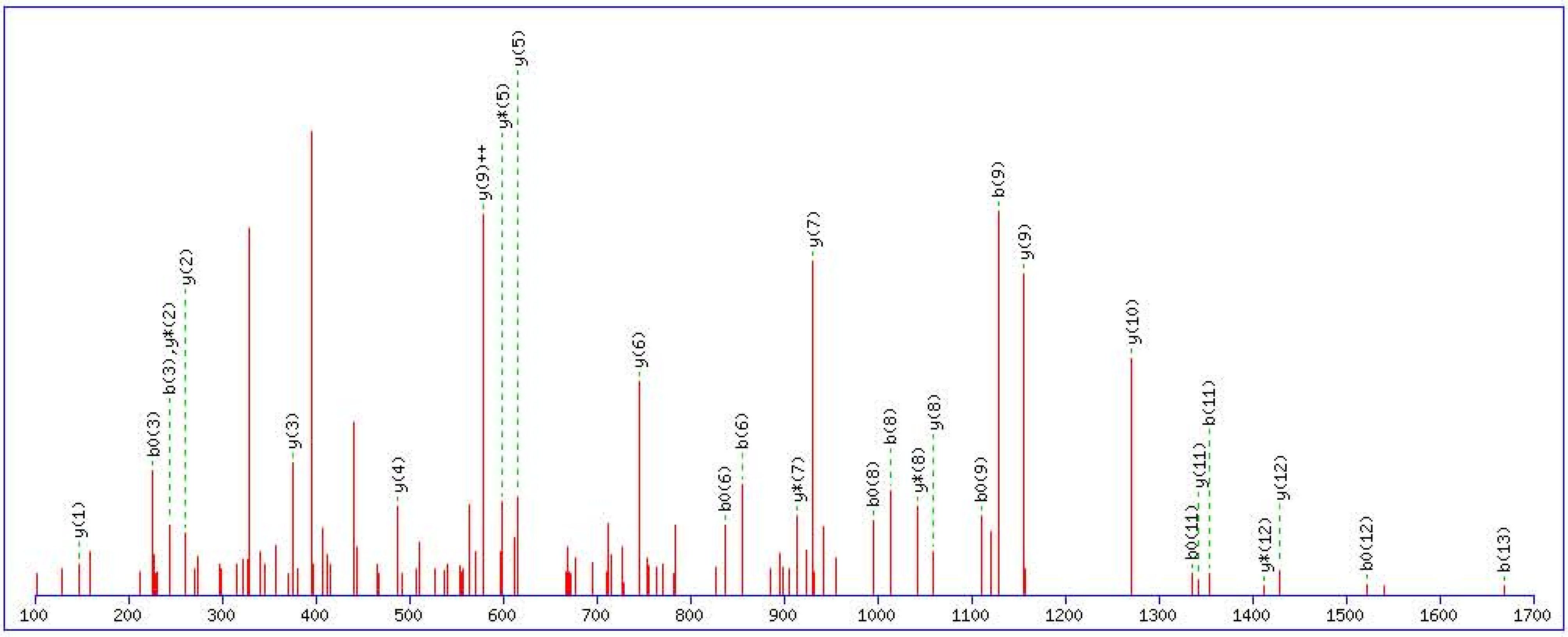
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGETAQSADPQWEQLNNK**
Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

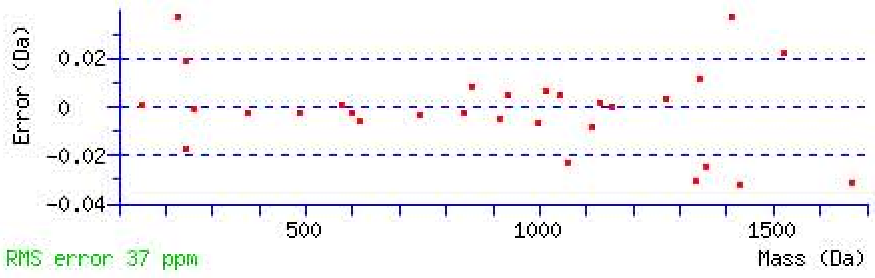
Match to Query 44777: 2283.055422 from(762.025750,3+) rtinseconds(1927) index(31288)
Title: Locus:1.1.1.3334.24 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

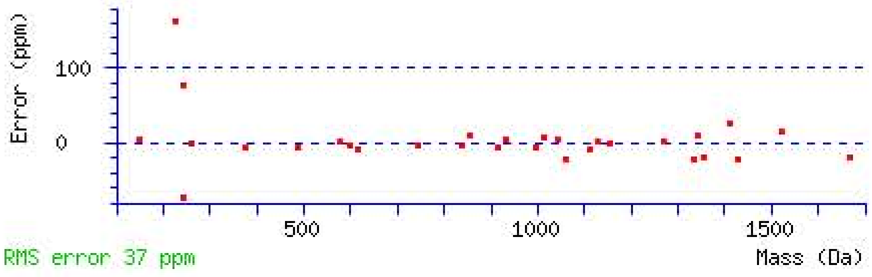
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2283.058975
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 83  Expect: 5.9e-008
Matches : 30/180 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	58.028740	29.518008					G							18
2	115.050204	58.028740					G	2227.044809	1114.026042	2210.018260	1105.512768	2209.034244	1105.020760	17
3	**244.092797**	122.550037			226.082232	113.544754	E	2170.023345	1085.515310	2152.996796	1077.002036	2152.012780	1076.510028	16
4	345.140476	173.073876			327.129911	164.068594	T	2040.980752	1020.994014	2023.954203	1012.480740	2022.970187	1011.988732	15
5	416.177590	208.592433			398.167025	199.587151	A	1939.933073	970.470175	1922.906524	961.956900	1921.922508	961.464892	14
6	**855.402916**	428.205096	838.376367	419.691822	837.392351	419.199814	Q	1868.895959	934.951618	1851.869410	926.438343	1850.885394	925.946335	13
7	942.434944	471.721110	925.408395	463.207836	924.424379	462.715828	S	***1429.670633***	715.338955	1412.644084	706.825680	1411.660068	706.333672	12
8	**1013.472058**	507.239667	996.445509	498.726393	995.461493	498.234385	A	***1342.638605***	671.822941	1325.612056	663.309666	1324.628040	662.817658	11
9	**1128.499001**	564.753139	1111.472452	556.239864	1110.488436	555.747856	D	***1271.601491***	636.304384	1254.574942	627.791109	1253.590926	627.299101	10
10	1225.551765	613.279521	1208.525216	604.766246	1207.541200	604.274238	P	***1156.574548***	578.790912	1139.547999	570.277638	1138.563983	569.785630	9
11	**1353.610343**	677.308810	1336.583794	668.795535	1335.599778	668.303527	Q	***1059.521784***	530.264530	1042.495235	521.751256	1041.511219	521.259248	8
12	1539.689656	770.348466	1522.663107	761.835192	1521.679091	761.343184	W	***931.463206***	466.235241	914.436657	457.721967	913.452641	457.229959	7
13	**1668.732249**	834.869762	1651.705700	826.356488	1650.721684	825.864480	E	***745.383893***	373.195585	728.357344	364.682310	727.373328	364.190302	6
14	1796.790827	898.899052	1779.764278	890.385777	1778.780262	889.893769	Q	***616.341300***	308.674288	599.314751	300.161014			5
15	1909.874891	955.441083	1892.848342	946.927809	1891.864326	946.435801	L	***488.282722***	244.644999	471.256173	236.131725			4
16	2023.917818	1012.462547	2006.891269	1003.949273	2005.907253	1003.457265	N	***375.198658***	188.102967	358.172109	179.589693			3
17	2137.960745	1069.484010	2120.934196	1060.970736	2119.950180	1060.478728	N	***261.155731***	131.081504	244.129182	122.568229			2
18							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of GGETAQSADPQWEQLNNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
83.2	2283.058975	-0.003553	GGETAQSADPQWEQLNNK
18.6	2283.058975	-0.003553	GGETAQSADPQWEQLNNK
0.6	2283.058975	-0.003553	GGETAQSADPQWEQLNNK

Mascot: http://www.matrixscience.com/

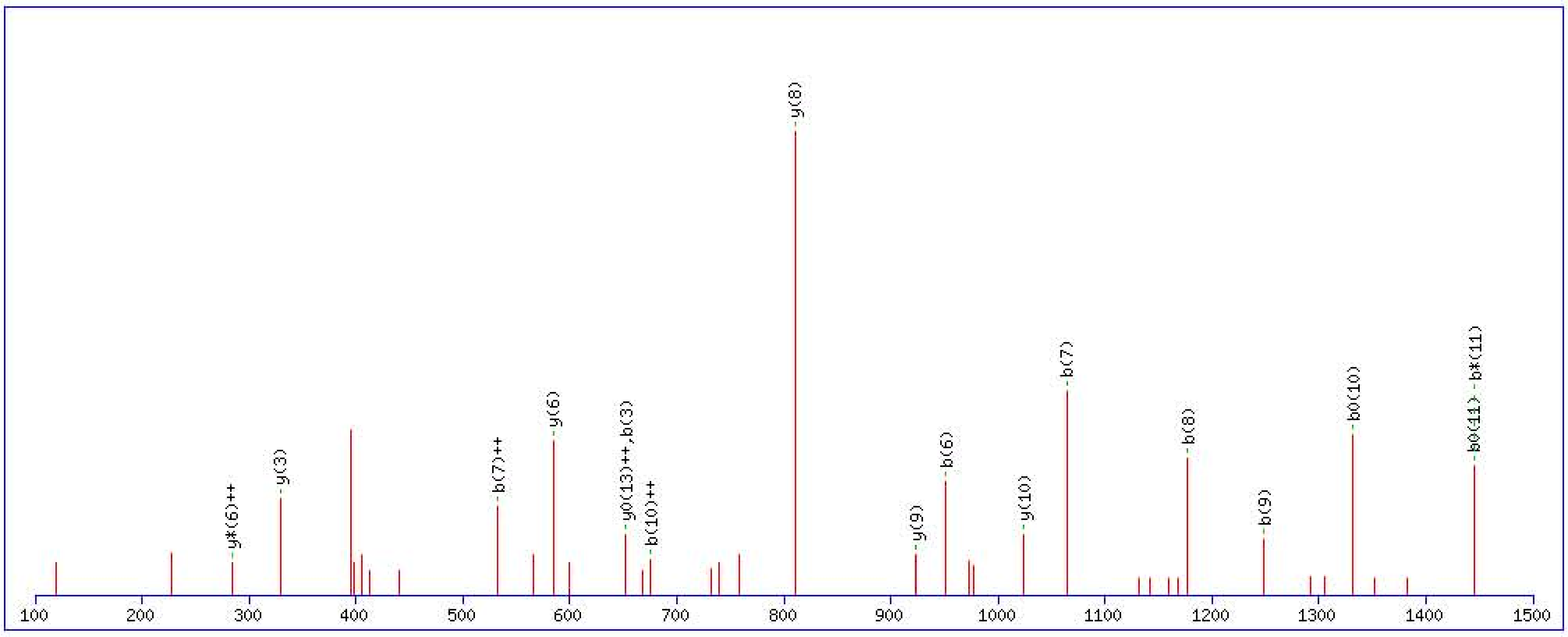
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQLSPDLLATLPEPASPGR**
Found in **HGFA_HUMAN**, Hepatocyte growth factor activator OS=Homo sapiens GN=HGFAC PE=1 SV=1

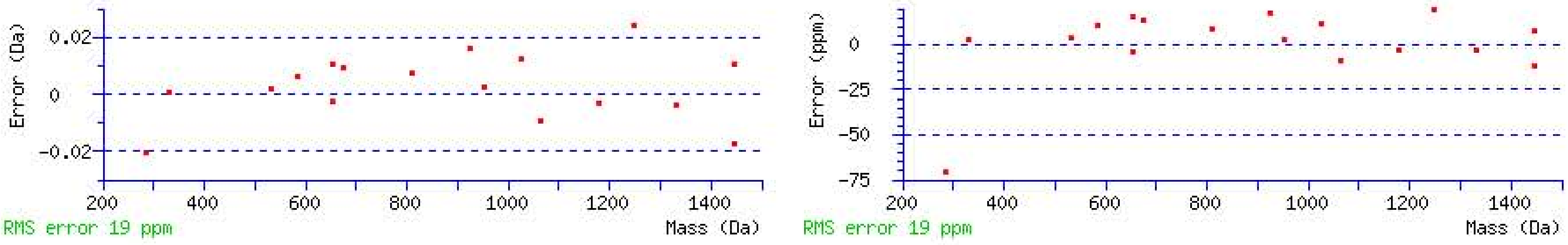
Match to Query 44546: 2271.231852 from(758.084560,3+) rtinseconds(2691) index(35753)
Title: Locus:1.1.1.3600.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 2271.229675
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 39 **Expect:** 0.0023
Matches : 17/202 fragment ions using 24 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	100.075690	50.541483					V							19
2	539.301016	270.154146	522.274467	261.640872			Q	2173.168553	1087.087914	2156.142004	1078.574640	2155.157988	1078.082632	18
3	***652.385080***	326.696178	635.358531	318.182904			L	1733.943227	867.475252	1716.916678	858.961977	1715.932662	858.469969	17
4	739.417108	370.212192	722.390559	361.698918	721.406543	361.206910	S	1620.859163	810.933219	1603.832614	802.419945	1602.848598	801.927937	16
5	836.469872	418.738574	819.443323	410.225300	818.459307	409.733292	P	1533.827135	767.417206	1516.800586	758.903931	1515.816570	758.411923	15
6	***951.496815***	476.252046	934.470266	467.738771	933.486250	467.246763	D	1436.774371	718.890824	1419.747822	710.377549	1418.763806	709.885541	14
7	***1064.580879***	**532.794078**	1047.554330	524.280803	1046.570314	523.788795	L	1321.747428	661.377352	1304.720879	652.864078	1303.736863	652.372069	13
8	***1177.664943***	589.336110	1160.638394	580.822835	1159.654378	580.330827	L	1208.663364	604.835320	1191.636815	596.322046	1190.652799	595.830038	12
9	***1248.702057***	624.854667	1231.675508	616.341392	1230.691492	615.849384	A	1095.579300	548.293288	1078.552751	539.780014	1077.568735	539.288006	11
10	1349.749736	**675.378506**	1332.723187	666.865232	1331.739171	666.373223	T	***1024.542186***	512.774731	1007.515637	504.261456	1006.531621	503.769448	10
11	1462.833800	731.920538	1445.807251	723.407264	1444.823235	722.915255	L	***923.494507***	462.250892	906.467958	453.737617	905.483942	453.245609	9
12	1559.886564	780.446920	1542.860015	771.933646	1541.875999	771.441637	P	***810.410443***	405.708860	793.383894	397.195585	792.399878	396.703577	8
13	1688.929157	844.968216	1671.902608	836.454942	1670.918592	835.962934	E	713.357679	357.182478	696.331130	348.669203	695.347114	348.177195	7
14	1785.981921	893.494598	1768.955372	884.981324	1767.971356	884.489316	P	***584.315086***	292.661181	567.288537	284.147907	566.304521	283.655899	6
15	1857.019035	929.013155	1839.992486	920.499881	1839.008470	920.007873	A	487.262322	244.134799	470.235773	235.621525	469.251757	235.129517	5
16	1944.051063	972.529169	1927.024514	964.015895	1926.040498	963.523887	S	416.225208	208.616242	399.198659	200.102968	398.214643	199.610960	4
17	2041.103827	1021.055552	2024.077278	1012.542277	2023.093262	1012.050269	P	***329.193180***	165.100228	312.166631	156.586954			3
18	2098.125291	1049.566283	2081.098742	1041.053009	2080.114726	1040.561001	G	232.140416	116.573846	215.113867	108.060572			2
19							R	175.118952	88.063114	158.092403	79.549839			1



NCBI **BLAST** search of VQLSPDLLATLPEPASPGR
(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	2271.229675	0.002177	VQLSPDLLATLPEPASPGR

Mascot: http://www.matrixscience.com/

{MATRIX SCIENCE}

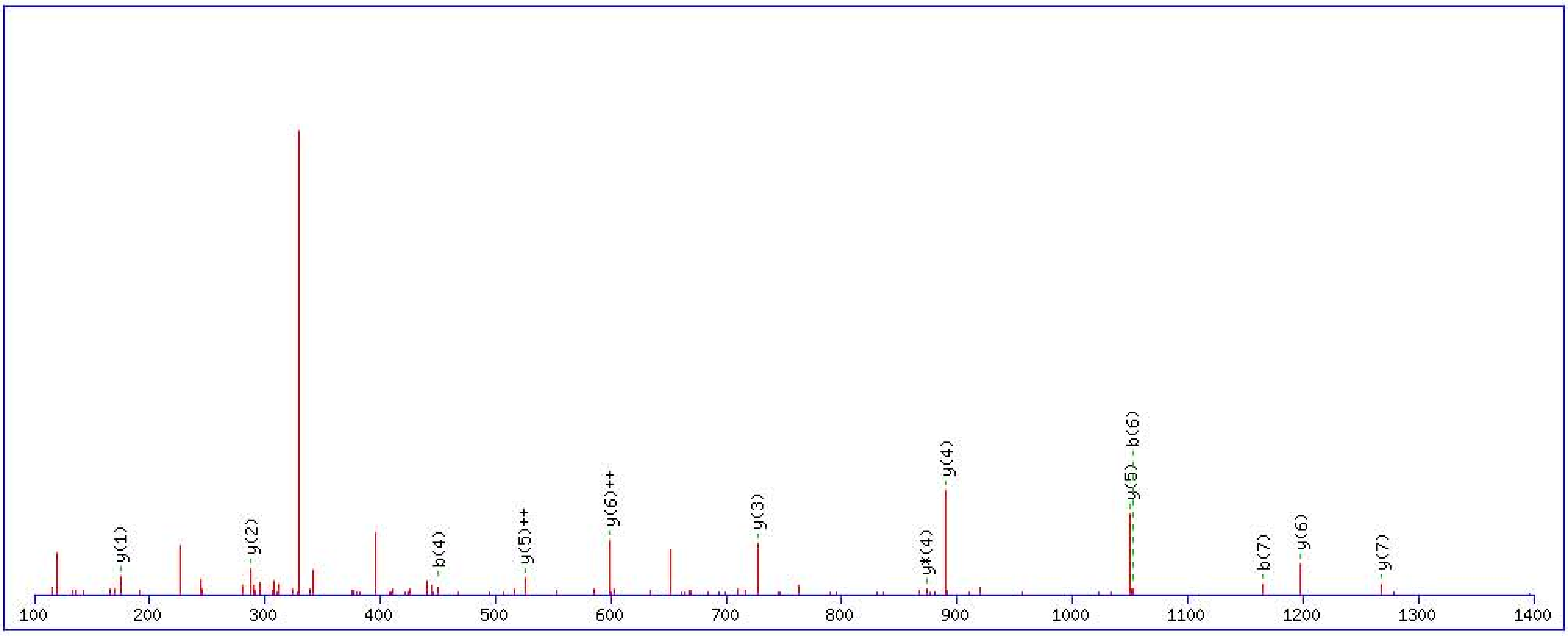
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAFCYQIR**
Found in **HGFL_HUMAN**, Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=2

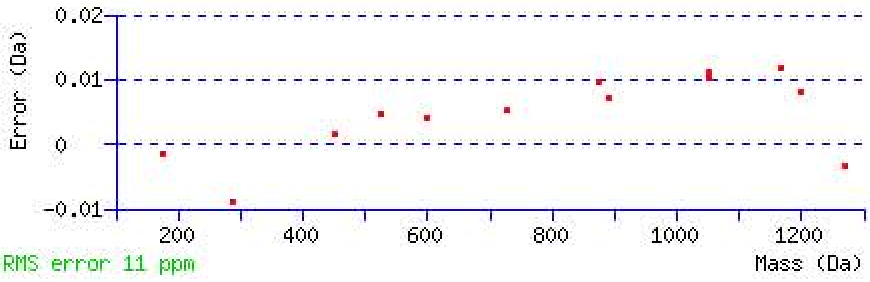
Match to Query 21088: 1338.669708 from(670.342130,2+) rtinseconds(2035) index(60809)
Title: Locus:1.1.1.1620.8 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

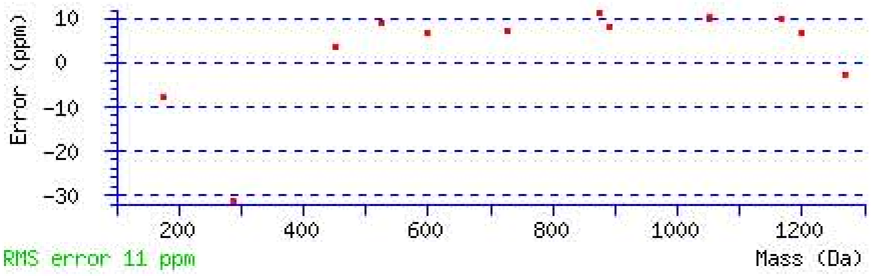
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1338.657669
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.0049
Matches : 13/46 fragment ions using 35 most intense peaks   (help)
```

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	72.044390	36.525833			A					8
2	143.081504	72.044390			A	*1268.627848*	634.817562	1251.601299	626.304288	7
3	290.149918	145.578597			F	*1197.590734*	599.299005	1180.564185	590.785731	6
4	**450.180567**	225.593922			C	*1050.522320*	525.764798	1033.495771	517.251524	5
5	613.243896	307.125586			Y	*890.491671*	445.749474	873.465122	437.236199	4
6	**1052.469222**	526.738249	1035.442673	518.224975	Q	*727.428342*	364.217809	710.401793	355.704534	3
7	**1165.553286**	583.280281	1148.526737	574.767007	I	*288.203016*	144.605146	271.176467	136.091871	2
8					R	*175.118952*	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of AAFCYQIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.8	1338.657669	0.012039	AAFCYQIR
2.1	1338.686661	-0.016953	QPQAWKDR
1.2	1338.678802	-0.009094	ALAMGFQSMVIR

Mascot: http://www.matrixscience.com/

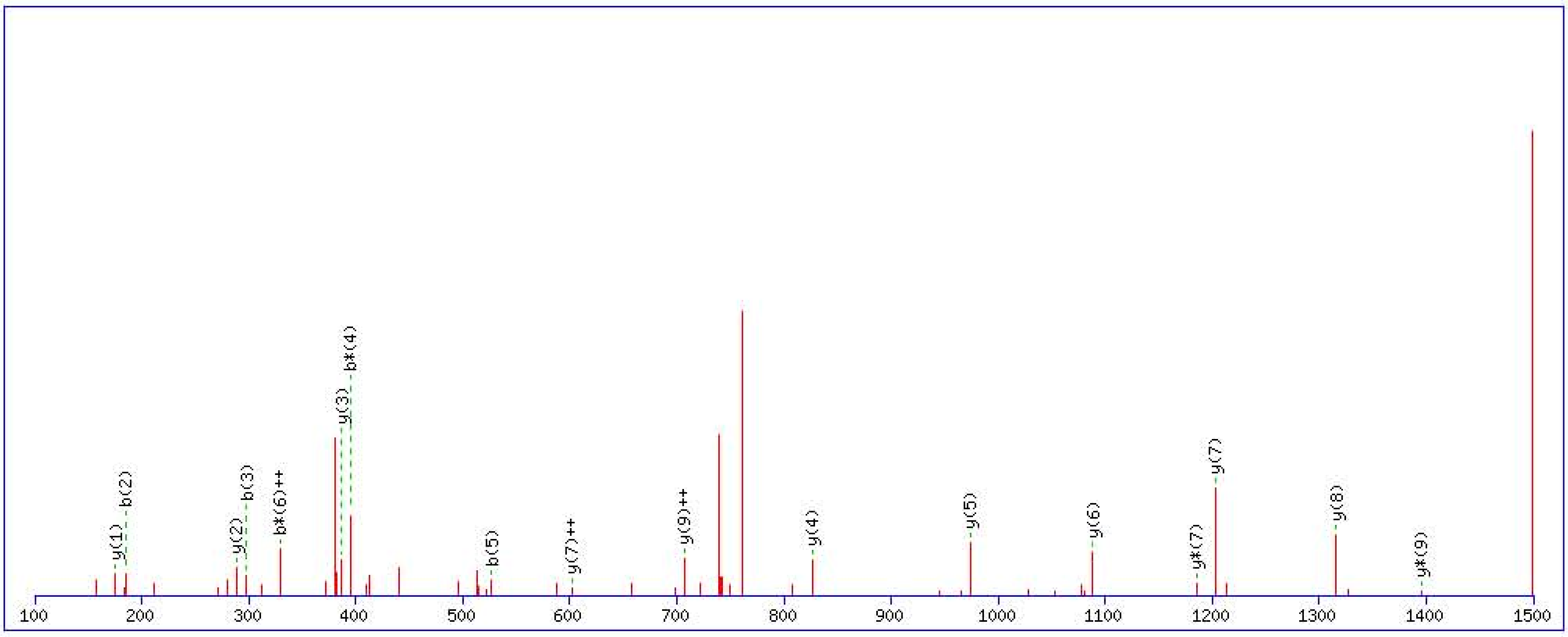
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPLNDFQVLR**
Found in **HGFL_HUMAN**, Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=2

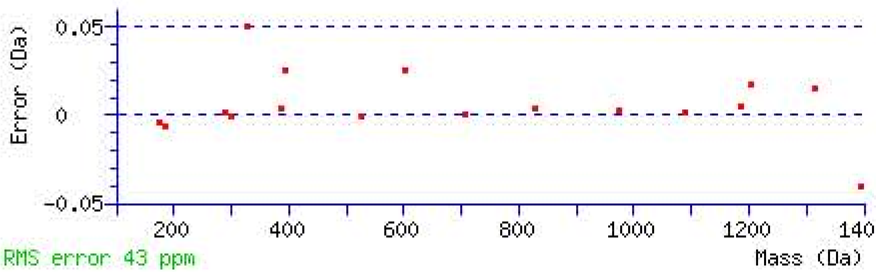
Match to Query 27082: 1498.806248 from(750.410400,2+) rtinseconds(2388) index(62663)
Title: Locus:1.1.1.1743.13 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

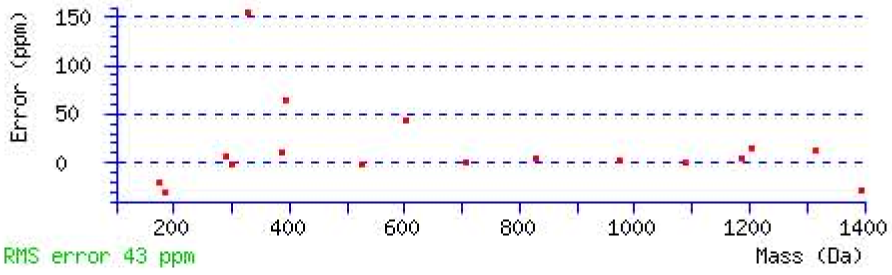
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1498.796616
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00016
Matches : 17/92 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							10
2	**185.092068**	93.049672			167.081503	84.044389	P	1412.771868	706.889572	1395.745319	698.376298	1394.761303	697.884290	9
3	**298.176132**	149.591704			280.165567	140.586422	L	***1315.719104***	658.363190	1298.692555	649.849916	1297.708539	649.357908	8
4	412.219059	206.613168	395.192510	198.099893	394.208494	197.607885	N	***1202.635040***	601.821158	1185.608491	593.307884	1184.624475	592.815876	7
5	**527.246002**	264.126639	510.219453	255.613365	509.235437	255.121357	D	***1088.592113***	544.799695	1071.565564	536.286420	1070.581548	535.794412	6
6	674.314416	337.660846	657.287867	329.147572	656.303851	328.655564	F	***973.565170***	487.286223	956.538621	478.772949			5
7	1113.539742	557.273509	1096.513193	548.760235	1095.529177	548.268227	Q	***826.496756***	413.752016	809.470207	405.238742			4
8	1212.608156	606.807716	1195.581607	598.294442	1194.597591	597.802434	V	***387.271430***	194.139353	370.244881	185.626078			3
9	1325.692220	663.349748	1308.665671	654.836474	1307.681655	654.344466	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 SPLNDFQVLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.5	1498.796616	0.009632	SPLNDFQVLR
5.7	1498.792572	0.013676	ALNITSLQMHSLR
2.6	1498.817749	-0.011501	LQGLPIVAGTMDIR
1.4	1498.787888	0.018360	ALSTTTSVDVSYKK
1.3	1498.796585	0.009663	LSLPTRAWEPAMK
1.1	1498.807846	-0.001598	ISGERVPQFR
0.8	1498.799103	0.007145	ALLNLPGTQTSGEAK
0.4	1498.799973	0.006275	ALLDQLMGTAR

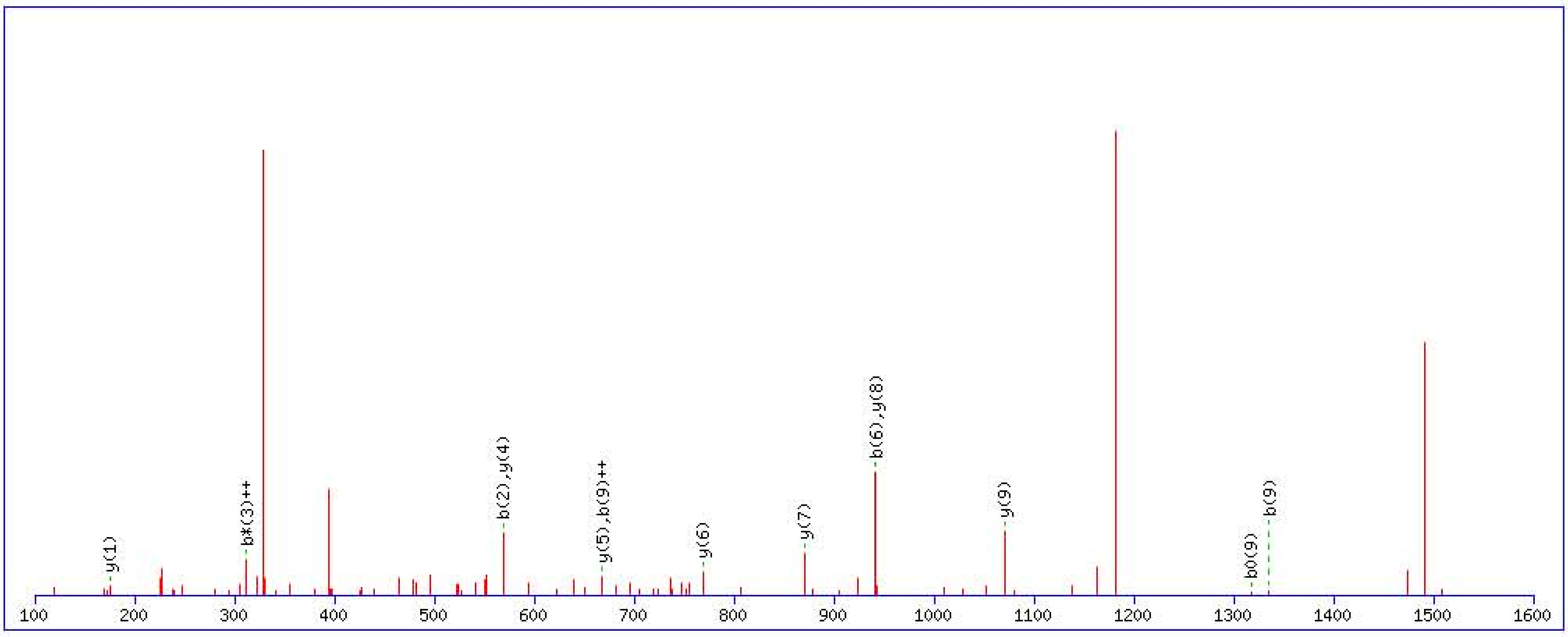
{MATRIX SCIENCE} Mascot Search Results

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

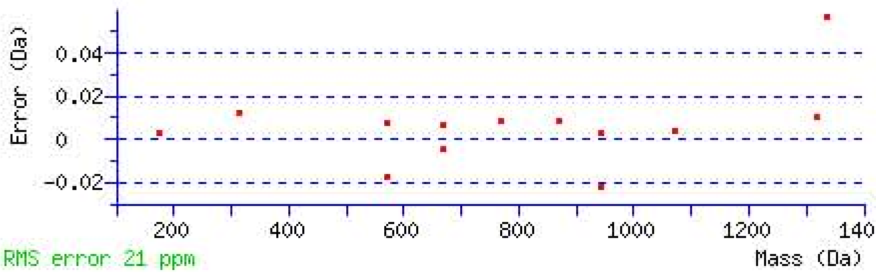
Match to Query 27453: 1508.714808 from(755.364680,2+) rtinseconds(1766) index(59275)
Title: Locus:1.1.1.1526.19 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

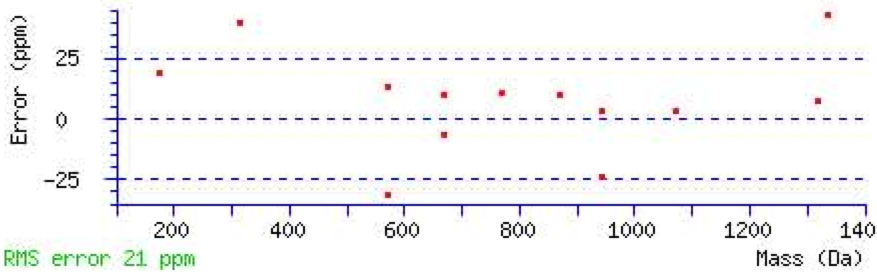
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1508.711578
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 55  Expect: 5.4e-005
Matches : 13/100 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	**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
55.0	1508.711578	0.003230	QEATTVSCFR
9.8	1508.726624	-0.011816	RDGQLQRMNYGR
6.7	1508.711380	0.003428	RTASGGRTEQGMSR
5.9	1508.708191	0.006617	EYGSMYTVHLGPR
3.7	1508.733154	-0.018346	APGSRLSSGGTNYSR
2.9	1508.736710	-0.021902	LKSSQMEQFT
2.0	1508.732681	-0.017873	KEAMKVSSQPCTK
1.4	1508.711548	0.003260	QMSKYPSGER
1.4	1508.715408	-0.000600	DHKSVDECKVHR
1.4	1508.701660	0.013148	MGAAWQEPHR

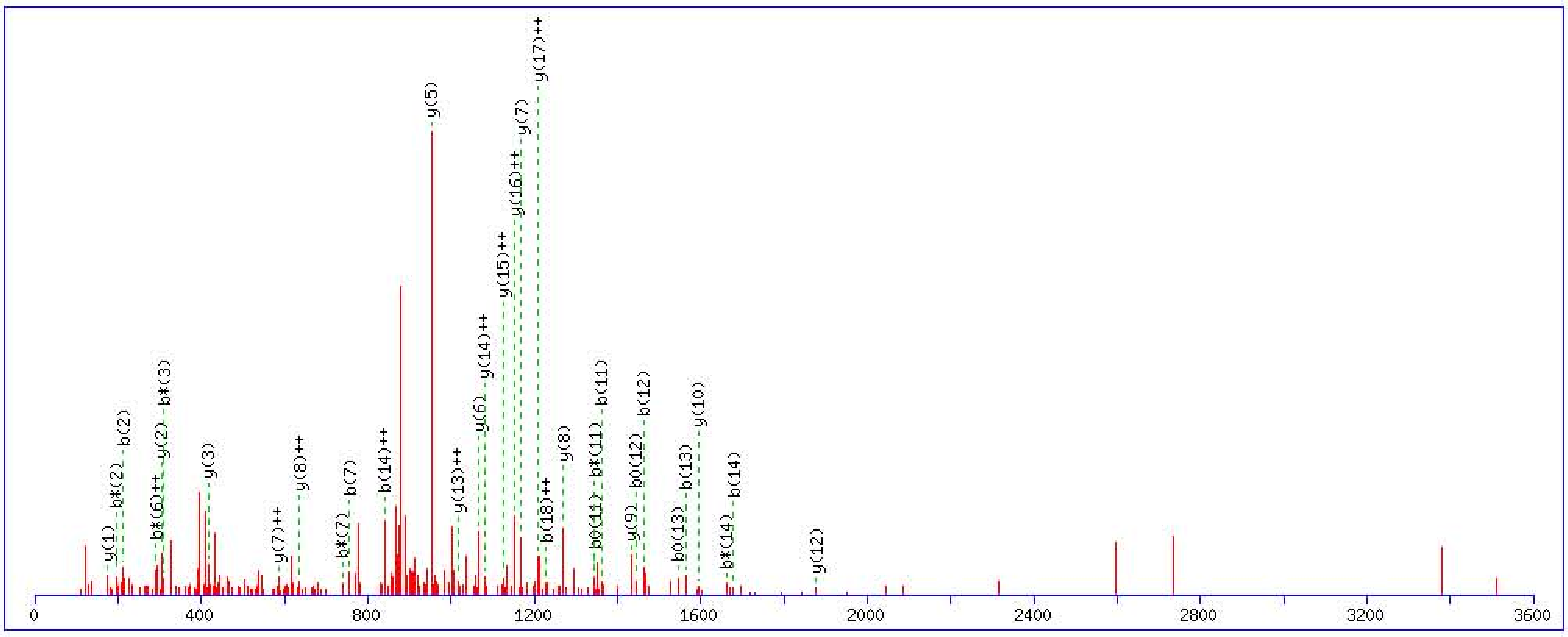
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPDGSERPWCYTTDPQIER**
Found in **HGFL_HUMAN**, Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=2

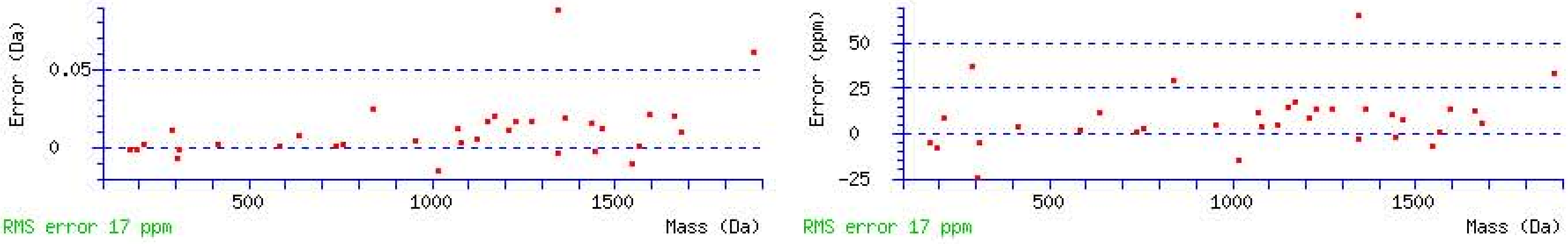
Match to Query 49800: 2631.196632 from(878.072820,3+) rtinseconds(2034) index(60802)
Title: Locus:1.1.1.1619.10 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2631.184601
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16     : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0025
Matches : 34/210 fragment ions using 90 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	2518.148958	1259.578117	2501.122409	1251.064842	2500.138393	1250.572834	18
3	327.129910	164.068593	310.103361	155.555319	309.119345	155.063311	D	2421.096194	1211.051735	2404.069645	1202.538460	2403.085629	1202.046452	17
4	384.151374	192.579325	367.124825	184.066050	366.140809	183.574042	G	2306.069251	1153.538263	2289.042702	1145.024989	2288.058686	1144.532981	16
5	471.183402	236.095339	454.156853	227.582064	453.172837	227.090056	S	2249.047787	1125.027531	2232.021238	1116.514257	2231.037222	1116.022249	15
6	600.225995	300.616636	583.199446	292.103361	582.215430	291.611353	E	2162.015759	1081.511517	2144.989210	1072.998243	2144.005194	1072.506235	14
7	**756.327106**	378.667191	739.300557	370.153916	738.316541	369.661908	R	2032.973166	1016.990221	2015.946617	1008.476947	2014.962601	1007.984939	13
8	853.379870	427.193573	836.353321	418.680298	835.369305	418.188290	P	***1876.872055***	938.939666	1859.845506	930.426391	1858.861490	929.934383	12
9	1039.459183	520.233229	1022.432634	511.719955	1021.448618	511.227947	W	1779.819291	890.413284	1762.792742	881.900009	1761.808726	881.408001	11
10	1199.489832	600.248554	1182.463283	591.735280	1181.479267	591.243271	C	***1593.739978***	797.373627	1576.713429	788.860353	1575.729413	788.368345	10
11	**1362.553161**	681.780219	1345.526612	673.266944	1344.542596	672.774936	Y	***1433.709329***	717.358303	1416.682780	708.845028	1415.698764	708.353020	9
12	**1463.600840**	732.304058	1446.574291	723.790784	1445.590275	723.298776	T	***1270.646000***	635.826638	1253.619451	627.313364	1252.635435	626.821356	8
13	**1564.648519**	782.827898	1547.621970	774.314623	1546.637954	773.822615	T	***1169.598321***	585.302799	1152.571772	576.789524	1151.587756	576.297516	7
14	**1679.675462**	**840.341369**	1662.648913	831.828095	1661.664897	831.336087	D	***1068.550642***	534.778959	1051.524093	526.265685	1050.540077	525.773677	6
15	1776.728226	888.867751	1759.701677	880.354477	1758.717661	879.862469	P	***953.523699***	477.265488	936.497150	468.752213	935.513134	468.260205	5
16	2215.953552	1108.480414	2198.927003	1099.967139	2197.942987	1099.475131	Q	856.470935	428.739106	839.444386	420.225831	838.460370	419.733823	4
17	2329.037616	1165.022446	2312.011067	1156.509171	2311.027051	1156.017163	I	***417.245609***	209.126443	400.219060	200.613168	399.235044	200.121160	3
18	2458.080209	**1229.543743**	2441.053660	1221.030468	2440.069644	1220.538460	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
19							R	***175.118952***	88.063114	158.092403	79.549839			1



NCBI **BLAST** search of NPDGSERPWCYTTDPQIER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.7	2631.184601	0.012031	NPDGSERPWCYTTDPQIER

Mascot: http://www.matrixscience.com/

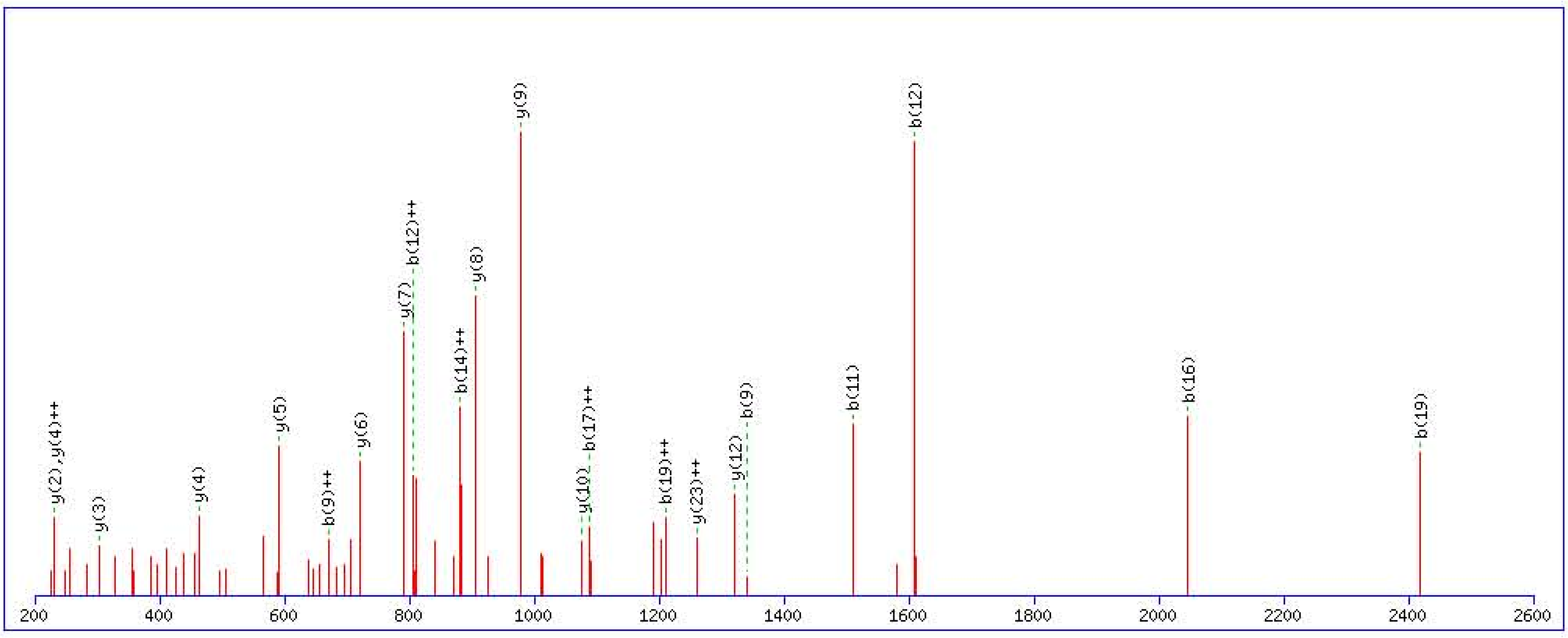
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTELQHLLHAVVPGPWQEDVADAEECAGR**
Found in **HGFL_HUMAN**, Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=2

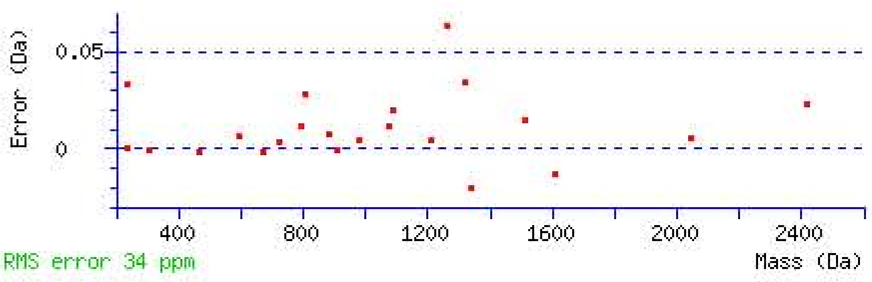
Match to Query 59523: 3494.699376 from(874.682120,4+) rtinseconds(2830) index(65484)
Title: Locus:1.1.1.1895.16 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

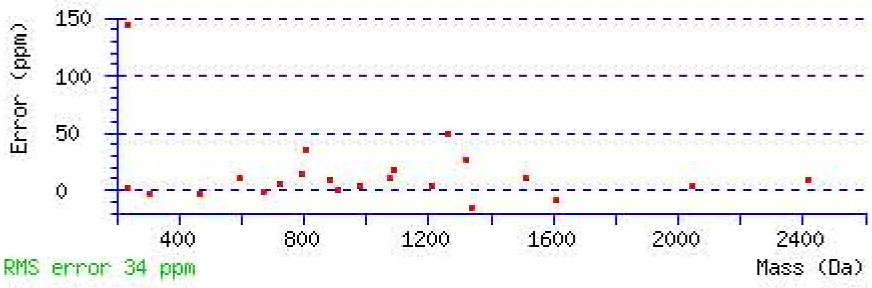
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3494.671112
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 7e-006
Matches : 22/318 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	58.028740	29.518008					G							29
2	159.076419	80.041847			141.065854	71.036565	T	3438.656925	1719.832100	3421.630376	1711.318826	3420.646360	1710.826818	28
3	288.119012	144.563144			270.108447	135.557862	E	3337.609246	1669.308261	3320.582697	1660.794986	3319.598681	1660.302978	27
4	401.203076	201.105176			383.192511	192.099894	L	3208.566653	1604.786964	3191.540104	1596.273690	3190.556088	1595.781682	26
5	840.428402	420.717839	823.401853	412.204565	822.417837	411.712557	Q	3095.482589	1548.244932	3078.456040	1539.731658	3077.472024	1539.239650	25
6	977.487314	489.247295	960.460765	480.734021	959.476749	480.242013	H	2656.257263	1328.632269	2639.230714	1320.118995	2638.246698	1319.626987	24
7	1090.571378	545.789327	1073.544829	537.276053	1072.560813	536.784045	L	2519.198351	1260.102813	2502.171802	1251.589539	2501.187786	1251.097531	23
8	1203.655442	602.331359	1186.628893	593.818085	1185.644877	593.326077	L	2406.114287	1203.560781	2389.087738	1195.047507	2388.103722	1194.555499	22
9	**1340.714354**	**670.860815**	1323.687805	662.347541	1322.703789	661.855532	H	2293.030223	1147.018749	2276.003674	1138.505475	2275.019658	1138.013467	21
10	1411.751468	706.379372	1394.724919	697.866098	1393.740903	697.374089	A	2155.971311	1078.489293	2138.944762	1069.976019	2137.960746	1069.484011	20
11	**1510.819882**	755.913579	1493.793333	747.400305	1492.809317	746.908297	V	2084.934197	1042.970736	2067.907648	1034.457462	2066.923632	1033.965454	19
12	**1609.888296**	**805.447786**	1592.861747	796.934512	1591.877731	796.442504	V	1985.865783	993.436530	1968.839234	984.923255	1967.855218	984.431247	18
13	1706.941060	853.974168	1689.914511	845.460894	1688.930495	844.968886	P	1886.797369	943.902323	1869.770820	935.389048	1868.786804	934.897040	17
14	1763.962524	**882.484900**	1746.935975	873.971626	1745.951959	873.479618	G	1789.744605	895.375941	1772.718056	886.862666	1771.734040	886.370658	16
15	1861.015288	931.011282	1843.988739	922.498008	1843.004723	922.006000	P	1732.723141	866.865209	1715.696592	858.351934	1714.712576	857.859926	15
16	**2047.094601**	1024.050939	2030.068052	1015.537664	2029.084036	1015.045656	W	1635.670377	818.338827	1618.643828	809.825552	1617.659812	809.333544	14
17	2175.153179	**1088.080227**	2158.126630	1079.566953	2157.142614	1079.074945	Q	1449.591064	725.299170	1432.564515	716.785896	1431.580499	716.293888	13
18	2304.195772	1152.601524	2287.169223	1144.088249	2286.185207	1143.596241	E	***1321.532486***	661.269881	1304.505937	652.756607	1303.521921	652.264599	12
19	**2419.222715**	**1210.114995**	2402.196166	1201.601721	2401.212150	1201.109713	D	1192.489893	596.748585	1175.463344	588.235310	1174.479328	587.743302	11
20	2518.291129	1259.649202	2501.264580	1251.135928	2500.280564	1250.643920	V	***1077.462950***	539.235113	1060.436401	530.721839	1059.452385	530.229831	10
21	2589.328243	1295.167759	2572.301694	1286.654485	2571.317678	1286.162477	A	***978.394536***	489.700906	961.367987	481.187632	960.383971	480.695624	9
22	2704.355186	1352.681231	2687.328637	1344.167956	2686.344621	1343.675948	D	***907.357422***	454.182349	890.330873	445.669075	889.346857	445.177067	8
23	2775.392300	1388.199788	2758.365751	1379.686513	2757.381735	1379.194505	A	***792.330479***	396.668878	775.303930	388.155603	774.319914	387.663595	7
24	2904.434893	1452.721085	2887.408344	1444.207810	2886.424328	1443.715802	E	***721.293365***	361.150321	704.266816	352.637046	703.282800	352.145038	6
25	3033.477486	1517.242381	3016.450937	1508.729106	3015.466921	1508.237099	E	***592.250772***	296.629024	575.224223	288.115750	574.240207	287.623742	5
26	3193.508135	1597.257705	3176.481586	1588.744431	3175.497570	1588.252423	C	***463.208179***	232.107727	446.181630	223.594453			4
27	3264.545249	1632.776263	3247.518700	1624.262988	3246.534684	1623.770980	A	***303.177530***	152.092403	286.150981	143.579129			3
28	3321.566713	1661.286995	3304.540164	1652.773720	3303.556148	1652.281712	G	***232.140416***	116.573846	215.113867	108.060571			2
29							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GTELQHLLHAVVPGPWQEDVADAEECAGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.3	3494.671112	0.028264	GTELQHLLHAVVPGPWQEDVADAEECAGR
42.5	3494.671112	0.028264	GTELQHLLHAVVPGPWQEDVADAEECAGR

Mascot: http://www.matrixscience.com/

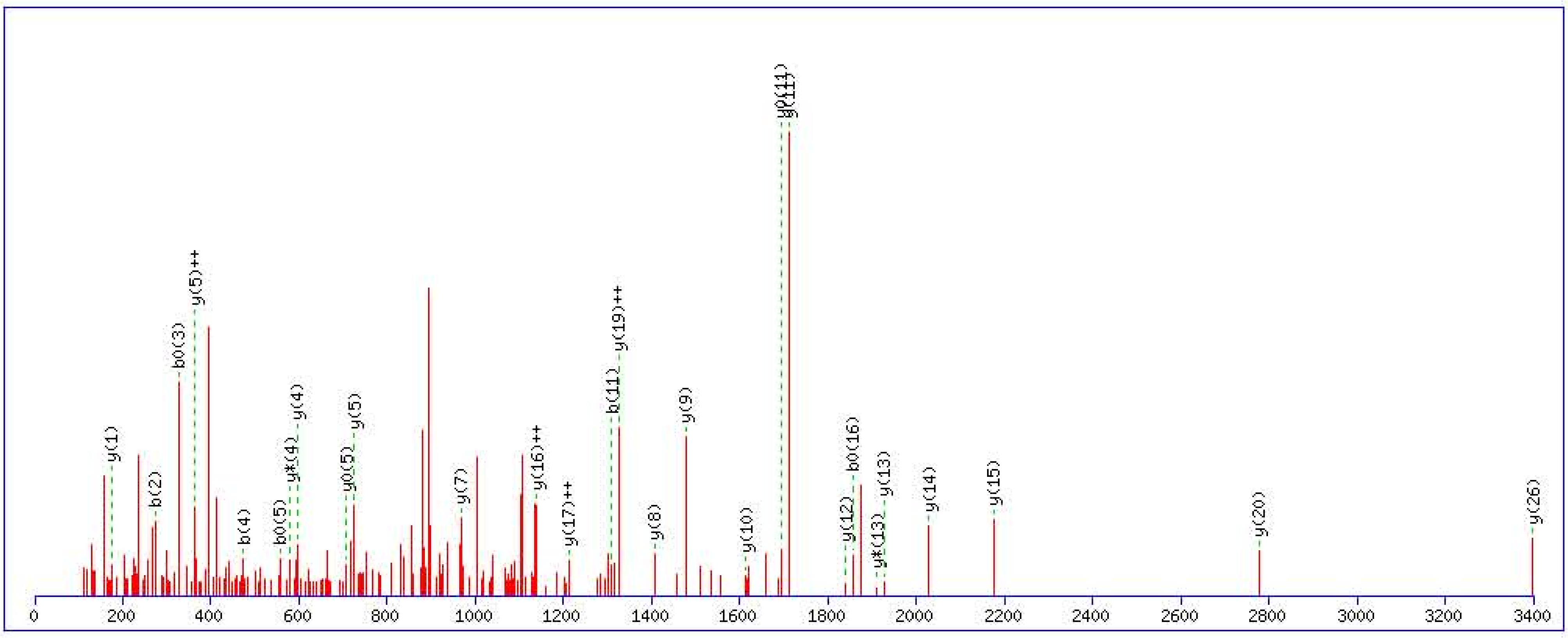
MATRIX SCIENCE Mascot Search Results

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

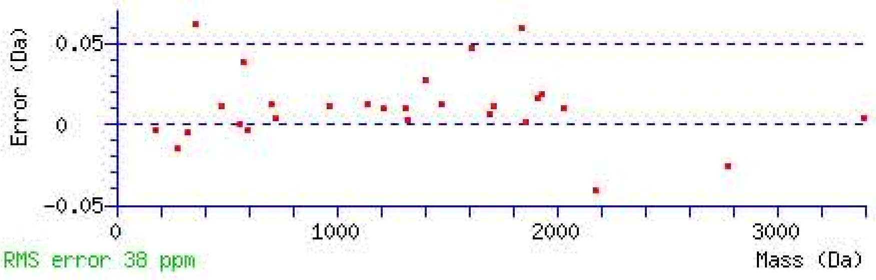
Match to Query 60354: 3584.680296 from(897.177350,4+) rtinseconds(2048) index(60855)
Title: Locus:1.1.1.1624.11 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

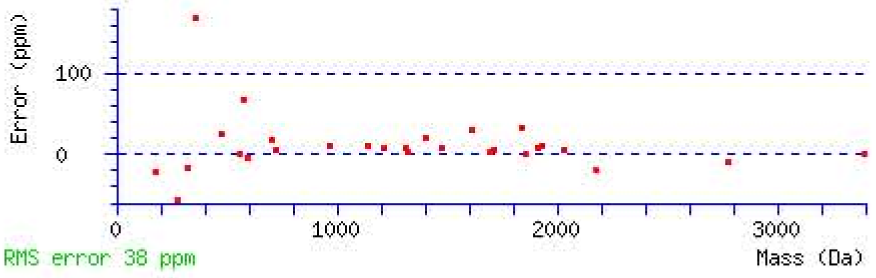
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 46  Expect: 0.00042
Matches : 28/288 fragment ions using 75 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
45.9	3584.660538	0.019758	WSAETPHKPQFTFTSEPHAQLEENFCR

Mascot: http://www.matrixscience.com/

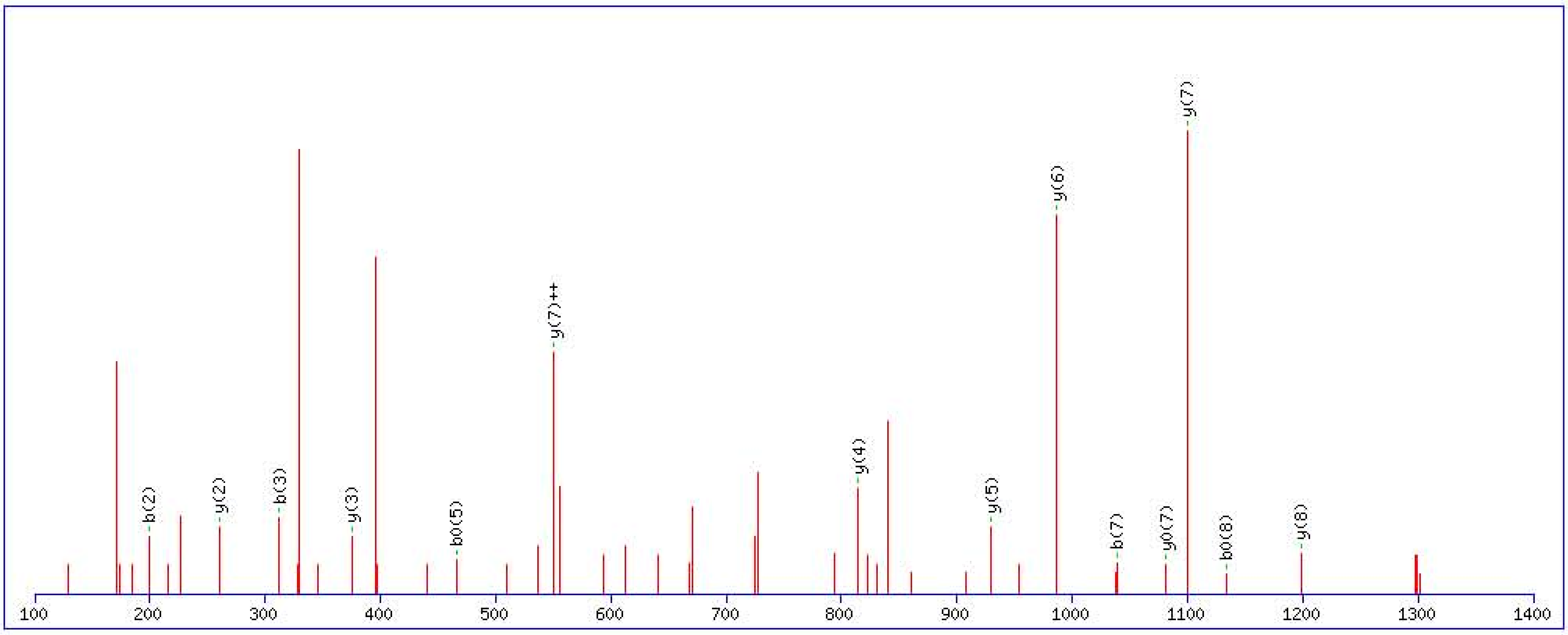
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVLGDQDLK**
Found in **HABP2_HUMAN**, Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1

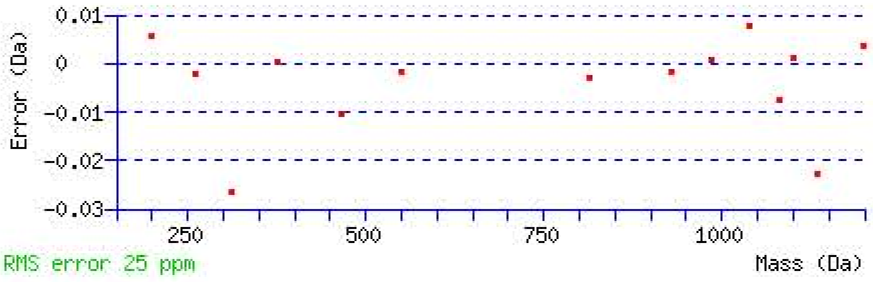
Match to Query 20283: 1296.711088 from(649.362820,2+) rtinseconds(1992) index(46005)
Title: Locus:1.1.1.3406.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

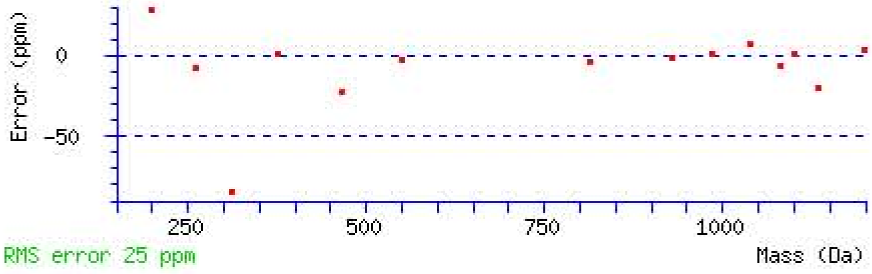
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1296.711166
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.00092
Matches : 14/74 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							9
2	**199.144104**	100.075690					V	***1198.650022***	599.828649	1181.623473	591.315374	1180.639457	590.823366	8
3	**312.228168**	156.617722					L	***1099.581608***	550.294442	1082.555059	541.781168	1081.571043	541.289159	7
4	369.249632	185.128454					G	***986.497544***	493.752410	969.470995	485.239135	968.486979	484.747127	6
5	484.276575	242.641925			466.266010	233.636643	D	***929.476080***	465.241678	912.449531	456.728403	911.465515	456.236395	5
6	923.501901	462.254589	906.475352	453.741314	905.491336	453.249306	Q	***814.449137***	407.728206	797.422588	399.214932	796.438572	398.722924	4
7	**1038.528844**	519.768060	1021.502295	511.254785	1020.518279	510.762777	D	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	3
8	1151.612908	576.310092	1134.586359	567.796817	1133.602343	567.304809	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 VVLGDQDLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.5	1296.711166	-0.000078	VVLGDQDLK
1.0	1296.692520	0.018568	EVDATNLPPTLK
0.1	1296.719025	-0.007937	VVSIHQDPKFK

{MATRIX SCIENCE}

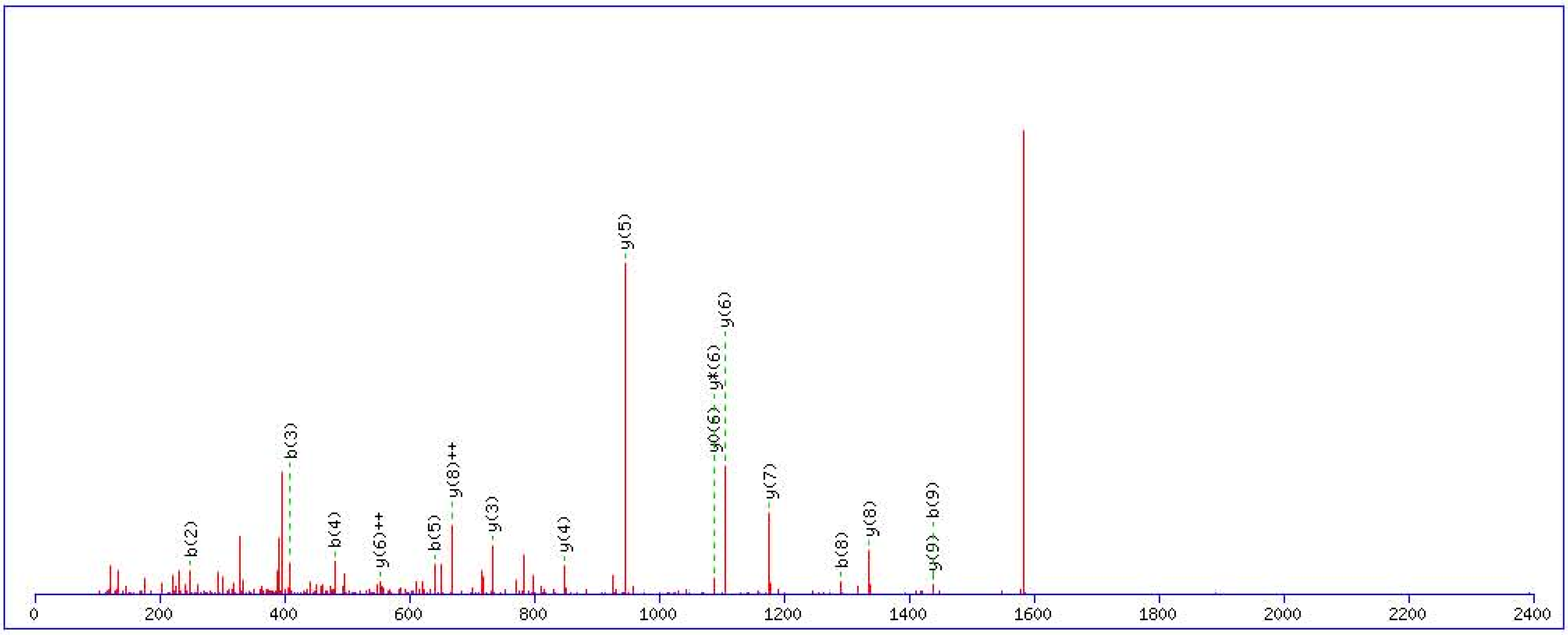
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FTCACPDQFK**
Found in **HABP2_HUMAN**, Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1

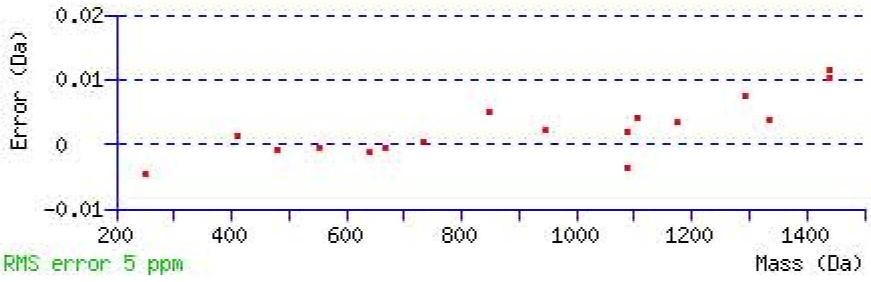
Match to Query 29876: 1583.693808 from(792.854180,2+) rtinseconds(1891) index(45236)
Title: Locus:1.1.1.3371.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

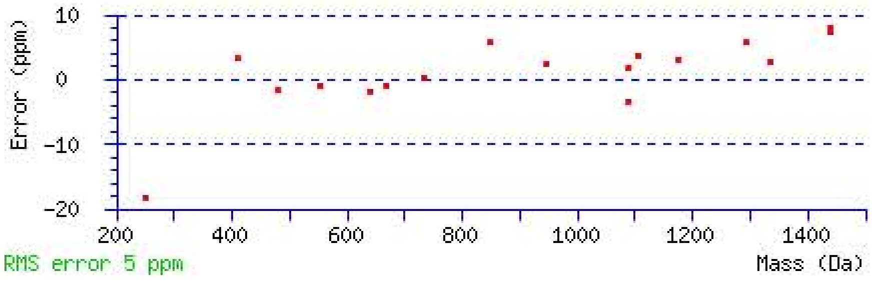
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1583.693497
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 5.1e-005
Matches : 17/86 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	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
47.5	1583.693497	0.000311	FTCACPDQFK
1.8	1583.700470	-0.006662	FGEYHKDDPSSFR

Mascot: http://www.matrixscience.com/

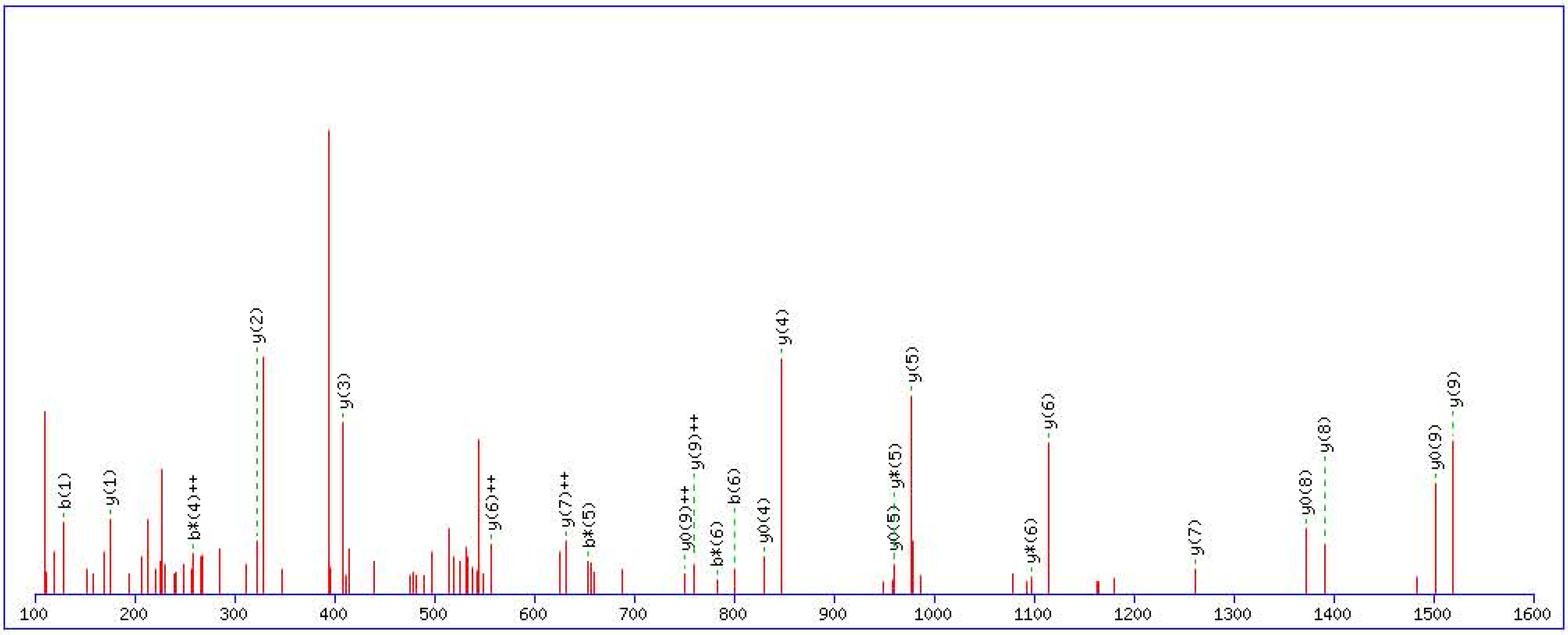
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KEEFHEQSFR**
Found in **HABP2_HUMAN**, Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1

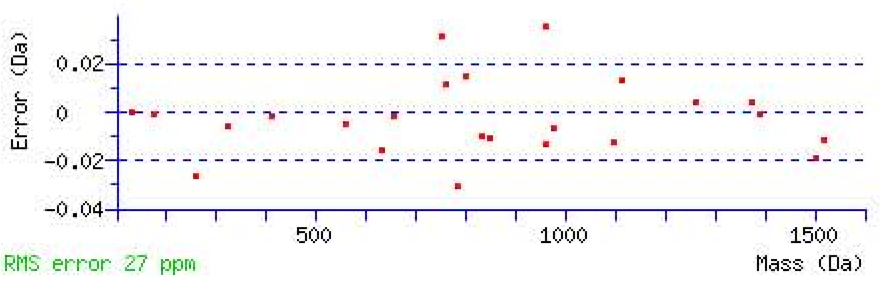
Match to Query 32617: 1646.782722 from(549.934850,3+) rtinseconds(1569) index(43295)
Title: Locus:1.1.1.3259.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

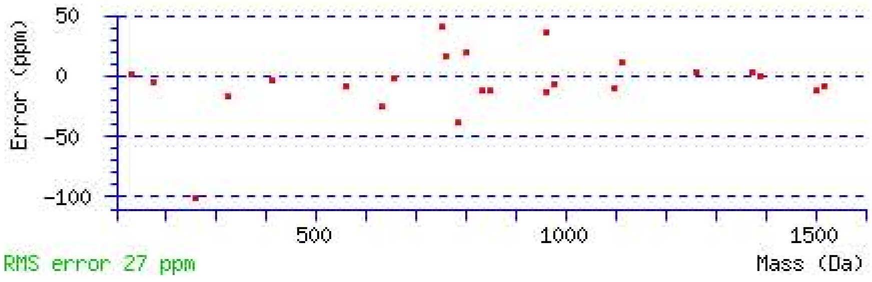
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1646.787491
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00014
Matches : 24/102 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	**129.102239**	65.054757	112.075690	56.541483			K							10
2	258.144832	129.576054	241.118283	121.062780	240.134267	120.570772	E	***1519.699825***	760.353551	1502.673276	751.840276	1501.689260	751.348268	9
3	387.187425	194.097351	370.160876	185.584076	369.176860	185.092068	E	***1390.657232***	695.832254	1373.630683	687.318980	1372.646667	686.826972	8
4	534.255839	267.631558	517.229290	259.118283	516.245274	258.626275	F	***1261.614639***	631.310958	1244.588090	622.797683	1243.604074	622.305675	7
5	671.314751	336.161014	654.288202	327.647739	653.304186	327.155731	H	***1114.546225***	557.776751	1097.519676	549.263476	1096.535660	548.771468	6
6	**800.357344**	400.682310	783.330795	392.169036	782.346779	391.677028	E	***977.487313***	489.247295	960.460764	480.734020	959.476748	480.242012	5
7	1239.582670	620.294973	1222.556121	611.781699	1221.572105	611.289691	Q	***848.444720***	424.725998	831.418171	416.212724	830.434155	415.720716	4
8	1326.614698	663.810987	1309.588149	655.297713	1308.604133	654.805705	S	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108053	3
9	1473.683112	737.345194	1456.656563	728.831920	1455.672547	728.339912	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 KEEFHEQSFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.1	1646.787491	-0.004769	KEEFHEQSFR
6.6	1646.763474	0.019248	KQEQKLDDEEEEK
2.8	1646.804596	-0.021874	QEILTALDRDASCR
1.8	1646.775589	0.007133	KPGLEEAVESACAMR

Mascot: http://www.matrixscience.com/

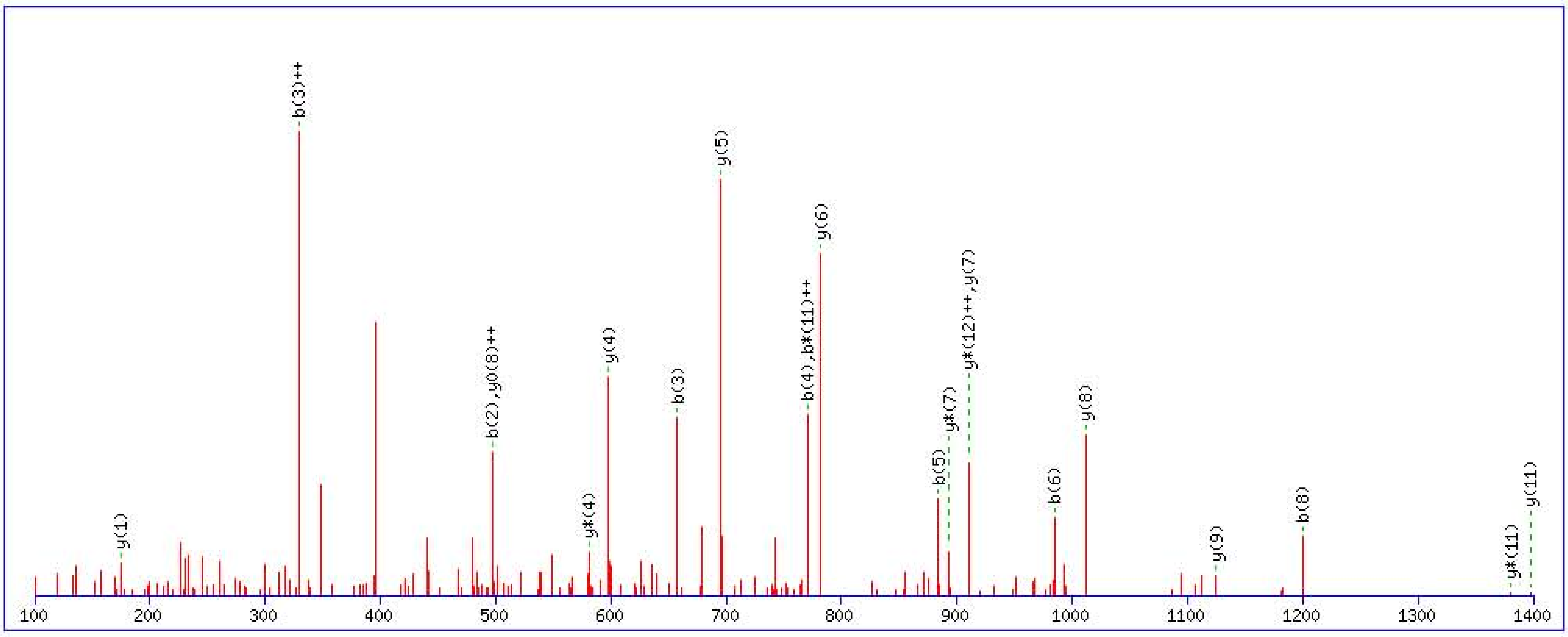
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQCLITQSPPYYR**
Found in **HABP2_HUMAN**, Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1

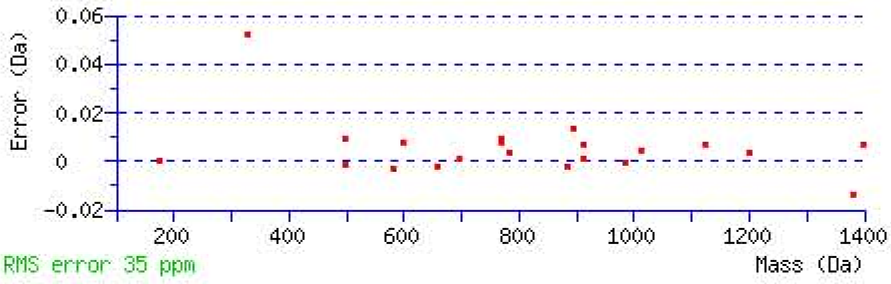
Match to Query 37316: 1892.929032 from(631.983620,3+) rtinseconds(2109) index(46656)
Title: Locus:1.1.1.3447.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

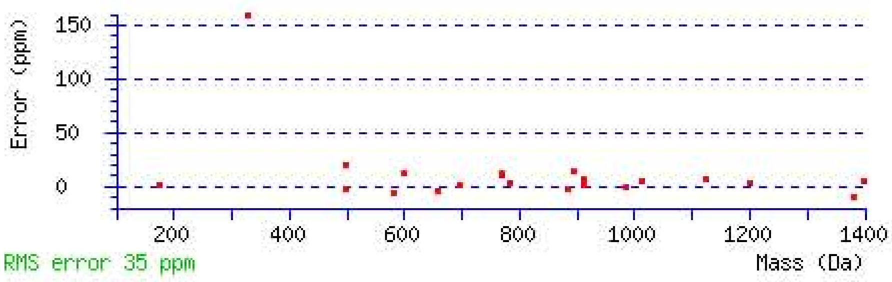


```
Monoisotopic mass of neutral peptide Mr(calc): 1892.927704
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 55  Expect: 8e-006
Matches : 21/122 fragment ions using 24 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							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



RMS error 35 ppm



RMS error 35 ppm

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
55.4	1892.927704	0.001328	GQCLITQSPPYYR
18.0	1892.927704	0.001328	GQCLITQSPPYYR
1.1	1892.942764	-0.013732	CLLLHPAGHAEPAAGSHR

Mascot: http://www.matrixscience.com/

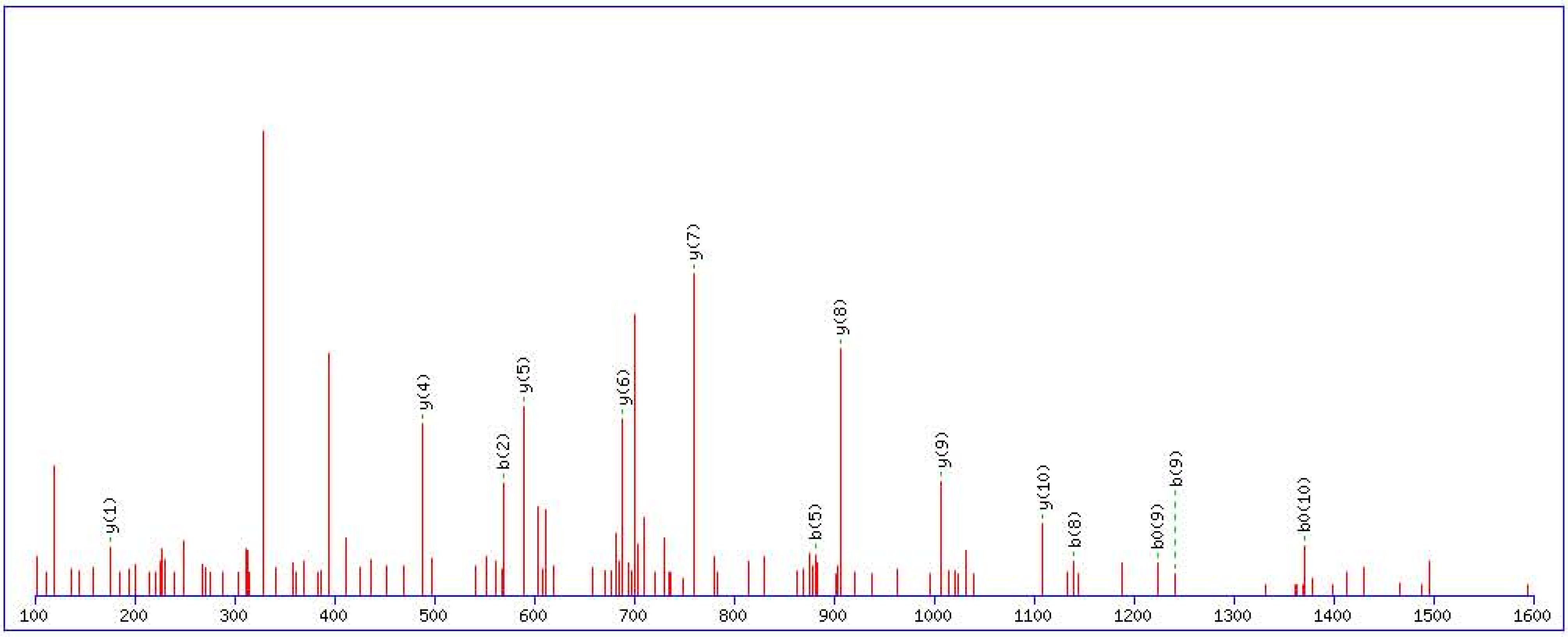
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QEPSQGTTTFAVTSILR**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

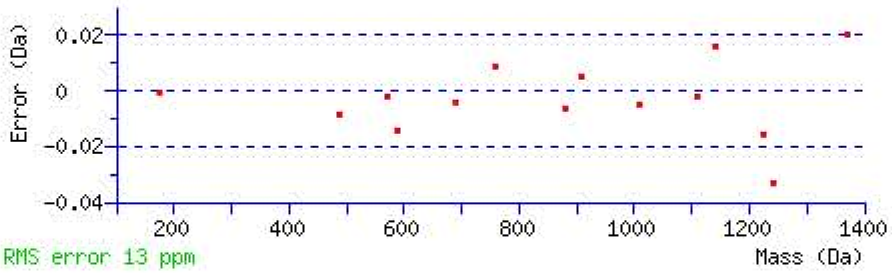
Match to Query 42252: 2146.103442 from(716.375090,3+) rtinseconds(2469) index(34375)
Title: Locus:1.1.1.3523.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

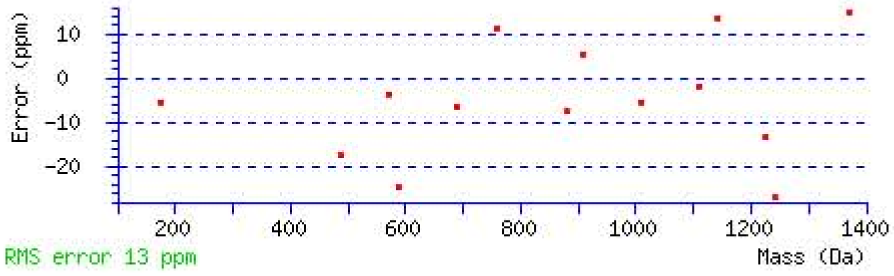
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2146.109253
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 37 **Expect:** 0.006
Matches : 14/184 fragment ions using 29 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	**569.275195**	285.141236	552.248646	276.627961	551.264630	276.135953	E	1707.891193	854.449235	1690.864644	845.935960	1689.880628	845.443952	16
3	666.327959	333.667618	649.301410	325.154343	648.317394	324.662335	P	1578.848600	789.927938	1561.822051	781.414664	1560.838035	780.922656	15
4	753.359987	377.183632	736.333438	368.670357	735.349422	368.178349	S	1481.795836	741.401556	1464.769287	732.888282	1463.785271	732.396274	14
5	**881.418565**	441.212921	864.392016	432.699646	863.408000	432.207638	Q	1394.763808	697.885542	1377.737259	689.372268	1376.753243	688.880260	13
6	938.440029	469.723653	921.413480	461.210378	920.429464	460.718370	G	1266.705230	633.856253	1249.678681	625.342979	1248.694665	624.850971	12
7	1039.487708	520.247492	1022.461159	511.734218	1021.477143	511.242210	T	1209.683766	605.345521	1192.657217	596.832247	1191.673201	596.340239	11
8	**1140.535387**	570.771332	1123.508838	562.258057	1122.524822	561.766049	T	***1108.636087***	554.821682	1091.609538	546.308407	1090.625522	545.816399	10
9	**1241.583066**	621.295171	1224.556517	612.781897	1223.572501	612.289889	T	***1007.588408***	504.297842	990.561859	495.784568	989.577843	495.292560	9
10	1388.651480	694.829378	1371.624931	686.316104	1370.640915	685.824096	F	***906.540729***	453.774003	889.514180	445.260728	888.530164	444.768720	8
11	1459.688594	730.347935	1442.662045	721.834661	1441.678029	721.342653	A	***759.472315***	380.239796	742.445766	371.726521	741.461750	371.234513	7
12	1558.757008	779.882142	1541.730459	771.368868	1540.746443	770.876860	V	***688.435201***	344.721239	671.408652	336.207964	670.424636	335.715956	6
13	1659.804687	830.405982	1642.778138	821.892707	1641.794122	821.400699	T	***589.366787***	295.187032	572.340238	286.673757	571.356222	286.181749	5
14	1746.836715	873.921996	1729.810166	865.408721	1728.826150	864.916713	S	***488.319108***	244.663192	471.292559	236.149918	470.308543	235.657910	4
15	1859.920779	930.464028	1842.894230	921.950753	1841.910214	921.458745	I	401.287080	201.147178	384.260531	192.633903			3
16	1973.004843	987.006060	1955.978294	978.492785	1954.994278	978.000777	L	288.203016	144.605146	271.176467	136.091872			2
17							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of QEPSQGTTTFAVTSILR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.7	2146.109253	-0.005811	QEPSQGTTTFAVTSILR
34.6	2146.109253	-0.005811	QEPSQGTTTFAVTSILR

Mascot: http://www.matrixscience.com/

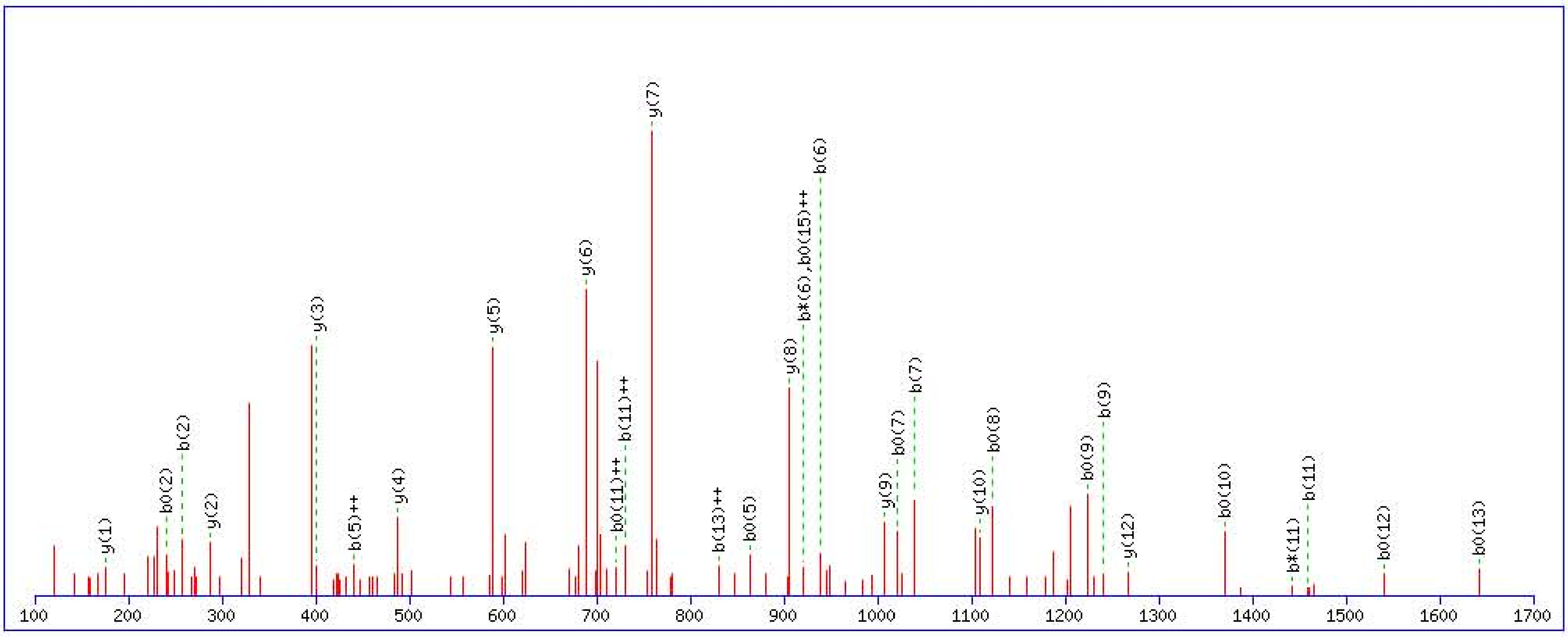
{MATRIX SCIENCE} **Mascot Search Results**

Peptide View

MS/MS Fragmentation of **QEPSQGTTTFAVTSILR**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

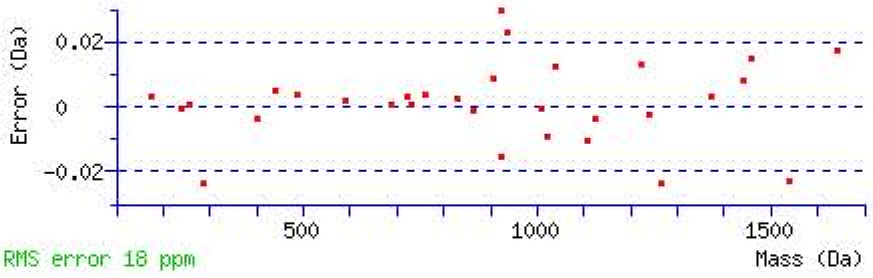
Match to Query 42253: 2146.106202 from(716.376010,3+) rtinseconds(2503) index(34614)
Title: Locus:1.1.1.3535.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

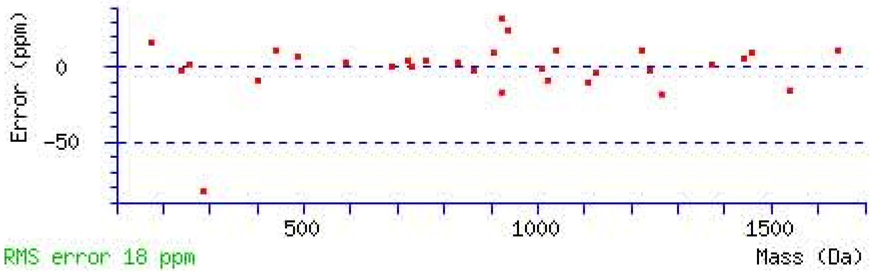
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2146.109253
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 59  Expect: 3.5e-005
Matches : 31/184 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	129.065854	65.036565	112.039305	56.523291			Q							17
2	**258.108447**	129.557862	241.081898	121.044587	240.097882	120.552579	E	2019.057941	1010.032609	2002.031392	1001.519334	2001.047376	1001.027326	16
3	355.161211	178.084244	338.134662	169.570969	337.150646	169.078961	P	1890.015348	945.511312	1872.988799	936.998038	1872.004783	936.506030	15
4	442.193239	221.600258	425.166690	213.086983	424.182674	212.594975	S	1792.962584	896.984930	1775.936035	888.471656	1774.952019	887.979648	14
5	881.418565	**441.212921**	864.392016	432.699646	863.408000	432.207638	Q	1705.930556	853.468916	1688.904007	844.955642	1687.919991	844.463634	13
6	**938.440029**	469.723653	921.413480	461.210378	920.429464	460.718370	G	***1266.705230***	633.856253	1249.678681	625.342979	1248.694665	624.850971	12
7	**1039.487708**	520.247492	1022.461159	511.734218	1021.477143	511.242210	T	1209.683766	605.345521	1192.657217	596.832247	1191.673201	596.340239	11
8	1140.535387	570.771332	1123.508838	562.258057	1122.524822	561.766049	T	***1108.636087***	554.821682	1091.609538	546.308407	1090.625522	545.816399	10
9	**1241.583066**	621.295171	1224.556517	612.781897	1223.572501	612.289889	T	***1007.588408***	504.297842	990.561859	495.784568	989.577843	495.292560	9
10	1388.651480	694.829378	1371.624931	686.316104	1370.640915	685.824096	F	***906.540729***	453.774003	889.514180	445.260728	888.530164	444.768720	8
11	**1459.688594**	**730.347935**	1442.662045	721.834661	1441.678029	721.342653	A	***759.472315***	380.239796	742.445766	371.726521	741.461750	371.234513	7
12	1558.757008	779.882142	1541.730459	771.368868	1540.746443	770.876860	V	***688.435201***	344.721239	671.408652	336.207964	670.424636	335.715956	6
13	1659.804687	**830.405982**	1642.778138	821.892707	1641.794122	821.400699	T	***589.366787***	295.187032	572.340238	286.673757	571.356222	286.181749	5
14	1746.836715	873.921996	1729.810166	865.408721	1728.826150	864.916713	S	***488.319108***	244.663192	471.292559	236.149918	470.308543	235.657910	4
15	1859.920779	930.464028	1842.894230	921.950753	1841.910214	921.458745	I	***401.287080***	201.147178	384.260531	192.633903			3
16	1973.004843	987.006060	1955.978294	978.492785	1954.994278	978.000777	L	***288.203016***	144.605146	271.176467	136.091872			2
17							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of QEPSQGTTTFAVTSILR
(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	2146.109253	-0.003051	QEPSQGTTTFAVTSILR
56.2	2146.109253	-0.003051	QEPSQGTTTFAVTSILR

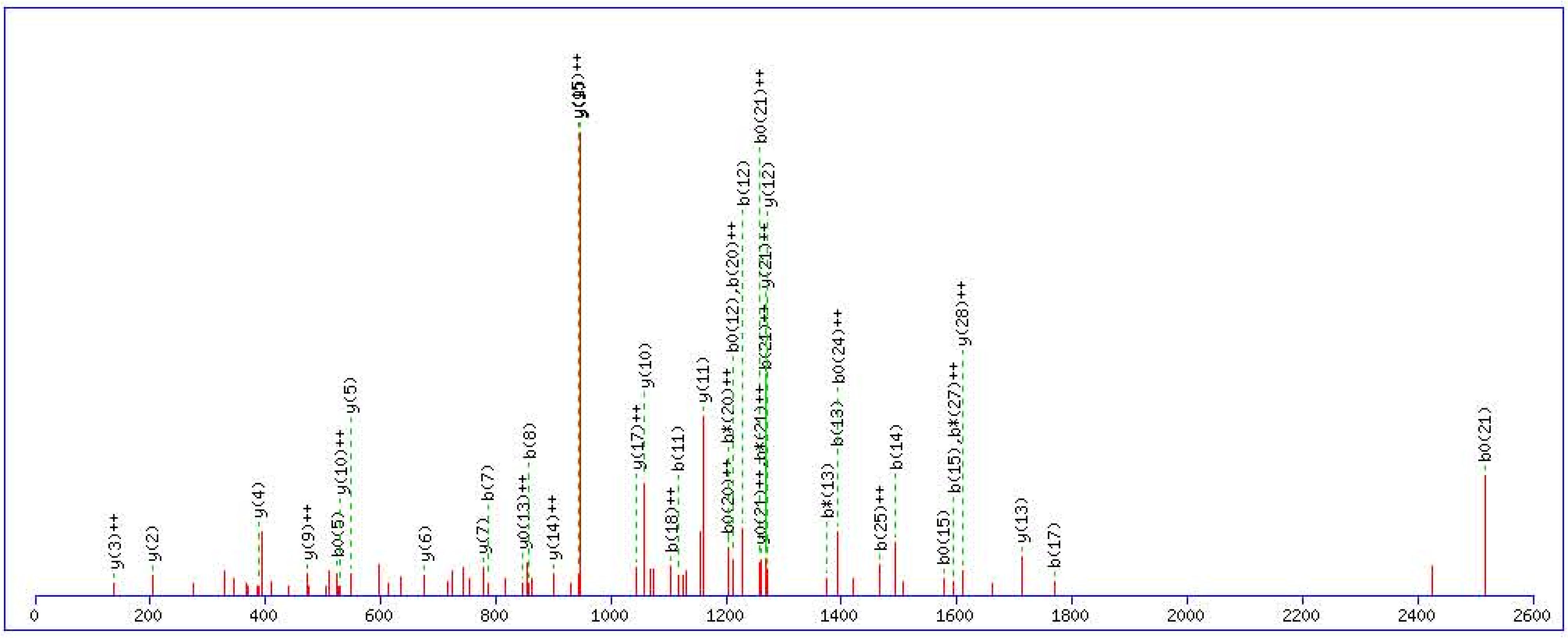
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NFPPSQDASGDLYTTSSQLTLPATQCLAGK**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

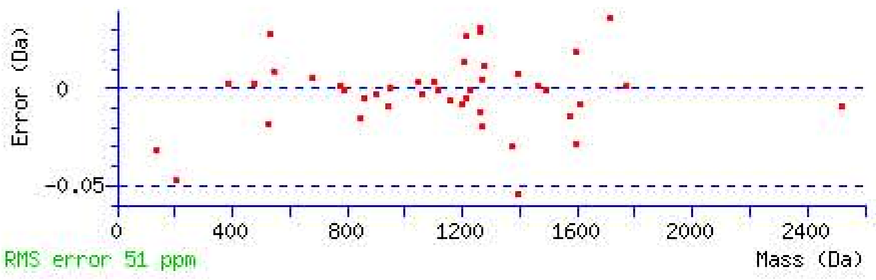
Match to Query 45404: 3478.661652 from(1160.561160,3+) rtinseconds(2582) index(35043)
Title: Locus:1.1.1.3562.24 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

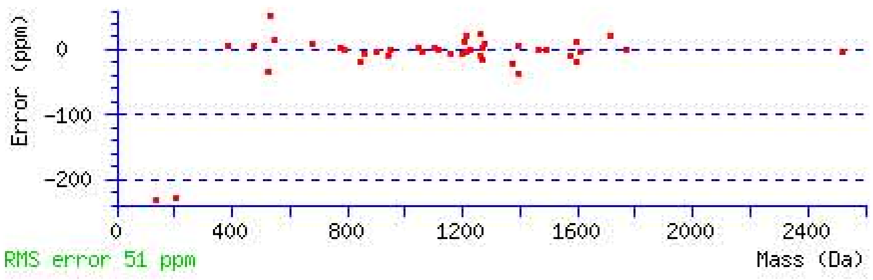
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3478.674866
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18    : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 8.6e-006
Matches : 43/328 fragment ions using 78 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							30
2	262.118617	131.562946	245.092068	123.049672			F	3365.639210	1683.323243	3348.612661	1674.809968	3347.628645	1674.317960	29
3	359.171381	180.089328	342.144832	171.576054			P	3218.570796	1609.789036	3201.544247	1601.275761	3200.560231	1600.783753	28
4	456.224145	228.615710	439.197596	220.102436			P	3121.518032	1561.262654	3104.491483	1552.749379	3103.507467	1552.257371	27
5	543.256173	272.131725	526.229624	263.618450	525.245608	263.126442	S	3024.465268	1512.736272	3007.438719	1504.222997	3006.454703	1503.730989	26
6	671.314751	336.161014	654.288202	327.647739	653.304186	327.155731	Q	2937.433240	1469.220258	2920.406691	1460.706983	2919.422675	1460.214975	25
7	***786.341694***	393.674485	769.315145	385.161210	768.331129	384.669202	D	2809.374662	1405.190969	2792.348113	1396.677694	2791.364097	1396.185686	24
8	***857.378808***	429.193042	840.352259	420.679767	839.368243	420.187759	A	2694.347719	1347.677497	2677.321170	1339.164223	2676.337154	1338.672215	23
9	944.410836	472.709056	927.384287	464.195781	926.400271	463.703773	S	2623.310605	1312.158941	2606.284056	1303.645666	2605.300040	1303.153658	22
10	1001.432300	501.219788	984.405751	492.706513	983.421735	492.214505	G	2536.278577	1268.642926	2519.252028	1260.129652	2518.268012	1259.637644	21
11	***1116.459243***	558.733260	1099.432694	550.219985	1098.448678	549.727977	D	2479.257113	1240.132195	2462.230564	1231.618920	2461.246548	1231.126912	20
12	***1229.543307***	615.275291	1212.516758	606.762017	1211.532742	606.270009	L	2364.230170	1182.618723	2347.203621	1174.105448	2346.219605	1173.613440	19
13	***1392.606636***	696.806956	1375.580087	688.293682	1374.596071	687.801673	Y	2251.146106	1126.076691	2234.119557	1117.563416	2233.135541	1117.071408	18
14	***1493.654315***	747.330796	1476.627766	738.817521	1475.643750	738.325513	T	2088.082777	1044.545026	2071.056228	1036.031752	2070.072212	1035.539744	17
15	***1594.701994***	797.854635	1577.675445	789.341361	1576.691429	788.849353	T	1987.035098	994.021187	1970.008549	985.507913	1969.024533	985.015905	16
16	1681.734022	841.370649	1664.707473	832.857375	1663.723457	832.365367	S	1885.987419	943.497348	1868.960870	934.984073	1867.976854	934.492065	15
17	***1768.766050***	884.886663	1751.739501	876.373389	1750.755485	875.881381	S	1798.955391	899.981334	1781.928842	891.468059	1780.944826	890.976051	14
18	2207.991376	**1104.499326**	2190.964827	1095.986051	2189.980811	1095.494043	Q	***1711.923363***	856.465320	1694.896814	847.952045	1693.912798	847.460037	13
19	2321.075440	1161.041358	2304.048891	1152.528083	2303.064875	1152.036075	L	***1272.698037***	636.852657	1255.671488	628.339382	1254.687472	627.847374	12
20	2422.123119	**1211.565197**	2405.096570	1203.051923	2404.112554	1202.559915	T	***1159.613973***	580.310625	1142.587424	571.797350	1141.603408	571.305342	11
21	2535.207183	**1268.107229**	2518.180634	1259.593955	2517.196618	1259.101947	L	***1058.566294***	529.786785	1041.539745	521.273511	1040.555729	520.781503	10
22	2632.259947	1316.633611	2615.233398	1308.120337	2614.249382	1307.628329	P	***945.482230***	473.244753	928.455681	464.731479	927.471665	464.239471	9
23	2703.297061	1352.152169	2686.270512	1343.638894	2685.286496	1343.146886	A	848.429466	424.718371	831.402917	416.205097	830.418901	415.713089	8
24	2804.344740	1402.676008	2787.318191	1394.162733	2786.334175	1393.670725	T	***777.392352***	389.199814	760.365803	380.686540	759.381787	380.194532	7
25	2932.403318	**1466.705297**	2915.376769	1458.192022	2914.392753	1457.700015	Q	***676.344673***	338.675975	659.318124	330.162700			6
26	3092.433967	1546.720621	3075.407418	1538.207347	3074.423402	1537.715339	C	***548.286095***	274.646686	531.259546	266.133411			5
27	3205.518031	1603.262653	3188.491482	1594.749379	3187.507466	1594.257371	L	***388.255446***	194.631361	371.228897	186.118087			4
28	3276.555145	1638.781211	3259.528596	1630.267936	3258.544580	1629.775928	A	275.171382	138.089329	258.144833	129.576055			3
29	3333.576609	1667.291943	3316.550060	1658.778668	3315.566044	1658.286660	G	***204.134268***	102.570772	187.107719	94.057497			2
30							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of NFPPSQDASGDLYTTSSQLTLPATQCLAGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.6	3478.674866	-0.013214	NFPPSQDASGDLYTTSSQLTLPATQCLAGK
20.2	3478.674866	-0.013214	NFPPSQDASGDLYTTSSQLTLPATQCLAGK
17.4	3478.674866	-0.013214	NFPPSQDASGDLYTTSSQLTLPATQCLAGK
0.5	3478.617325	0.044327	INRDPSFDLSYSFEYVILNEDCQTSR

Mascot: http://www.matrixscience.com/

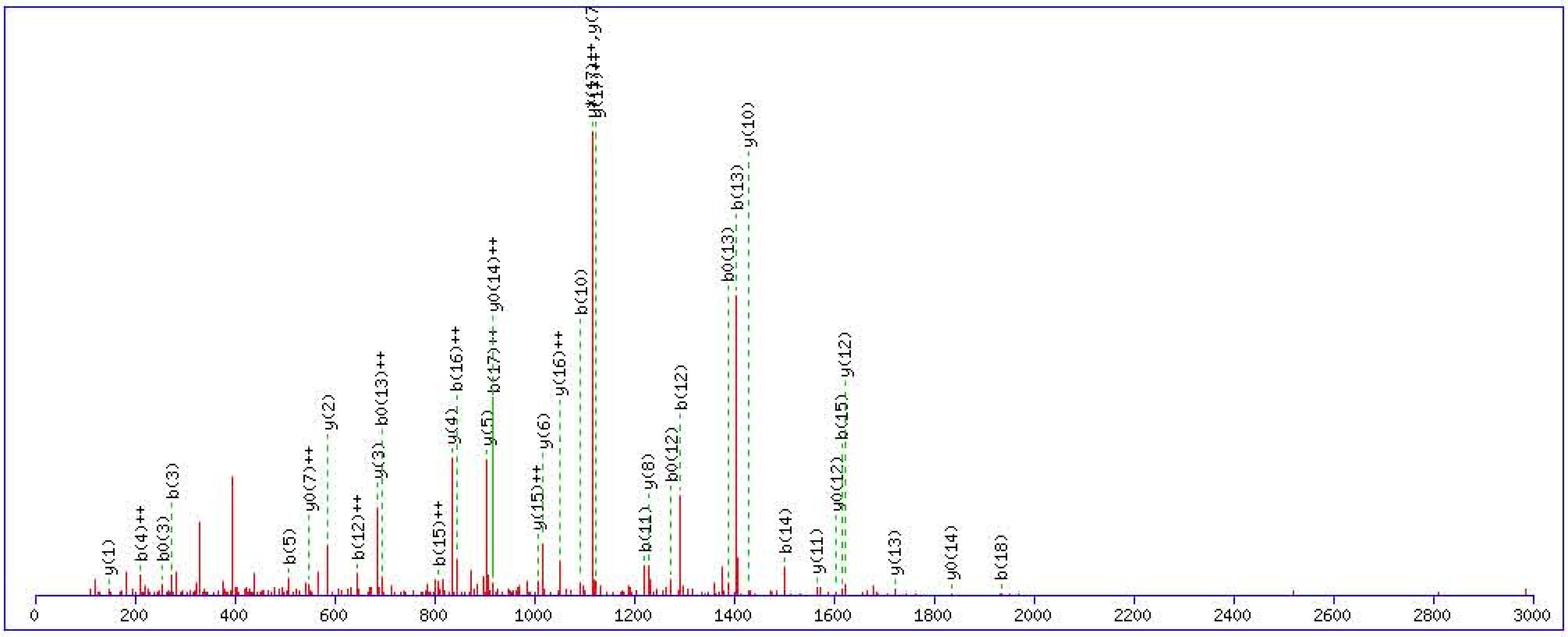
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GDTFSCMVGHEALPLAFTQK**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

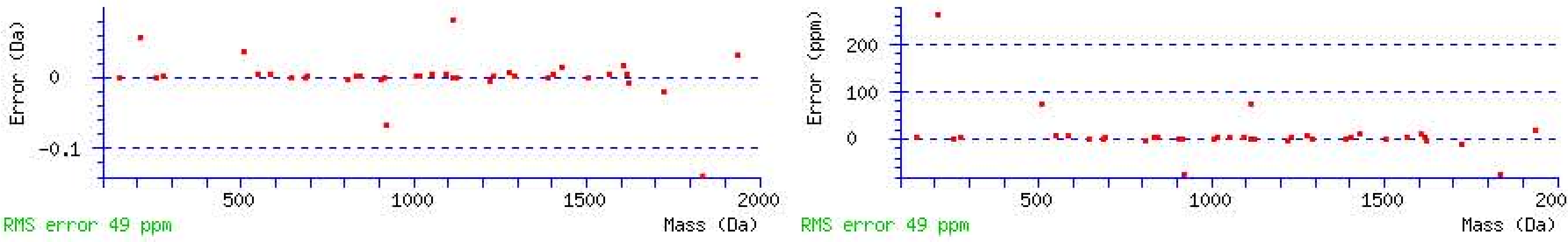
Match to Query 48765: 2519.197392 from(840.739740,3+) rtinseconds(2568) index(34971)
Title: Locus:1.1.1.3557.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 2519.201126
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q19    : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 2e-006
Matches : 38/186 fragment ions using 72 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							20
2	173.055683	87.031479			155.045118	78.026197	D	2463.186924	1232.097100	2446.160375	1223.583825	2445.176359	1223.091817	19
3	***274.103362***	137.555319			256.092797	128.550037	T	2348.159981	1174.583628	2331.133432	1166.070354	2330.149416	1165.578346	18
4	421.171776	**211.089526**			403.161211	202.084243	F	2247.112302	1124.059789	2230.085753	1115.546514	2229.101737	1115.054506	17
5	***508.203804***	254.605540			490.193239	245.600257	S	2100.043888	1050.525582	2083.017339	1042.012307	2082.033323	1041.520299	16
6	668.234453	334.620865			650.223888	325.615582	C	2013.011860	1007.009568	1995.985311	998.496294	1995.001295	998.004286	15
7	799.274938	400.141107			781.264373	391.135825	M	1852.981211	926.994244	1835.954662	918.480969	1834.970646	917.988961	14
8	898.343352	449.675314			880.332787	440.670031	V	***1721.940726***	861.474001	1704.914177	852.960727	1703.930161	852.468719	13
9	955.364816	478.186046			937.354251	469.180764	G	***1622.872312***	811.939794	1605.845763	803.426520	1604.861747	802.934512	12
10	***1092.423728***	546.715502			1074.413163	537.710219	H	***1565.850848***	783.429062	1548.824299	774.915788	1547.840283	774.423780	11
11	***1221.466321***	611.236799			1203.455756	602.231516	E	***1428.791936***	714.899606	1411.765387	706.386332	1410.781371	705.894324	10
12	***1292.503435***	**646.755356**			1274.492870	637.750073	A	1299.749343	650.378310	1282.722794	641.865035	1281.738778	641.373027	9
13	***1405.587499***	703.297388			1387.576934	694.292105	L	***1228.712229***	614.859753	1211.685680	606.346478	1210.701664	605.854470	8
14	***1502.640263***	751.823770			1484.629698	742.818487	P	***1115.628165***	558.317721	1098.601616	549.804446	1097.617600	549.312438	7
15	***1615.724327***	**808.365801**			1597.713762	799.360519	L	***1018.575401***	509.791339	1001.548852	501.278064	1000.564836	500.786056	6
16	1686.761441	**843.884358**			1668.750876	834.879076	A	***905.491337***	453.249307	888.464788	444.736032	887.480772	444.244024	5
17	1833.829855	**917.418566**			1815.819290	908.413283	F	***834.454223***	417.730750	817.427674	409.217475	816.443658	408.725467	4
18	***1934.877534***	967.942405			1916.866969	958.937122	T	***687.385809***	344.196543	670.359260	335.683268	669.375244	335.191260	3
19	2374.102860	1187.555068	2357.076311	1179.041793	2356.092295	1178.549785	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 GDTFSCMVGHEALPLAFTQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.6	2519.201126	-0.003734	GDTFSCMVGHEALPLAFTQK
0.9	2519.214783	-0.017391	KMQQENMKPQEQLTLEPYER
0.2	2519.196243	0.001149	EGSPHDNPTVQQIVQLSPVMQDT

Mascot: http://www.matrixscience.com/

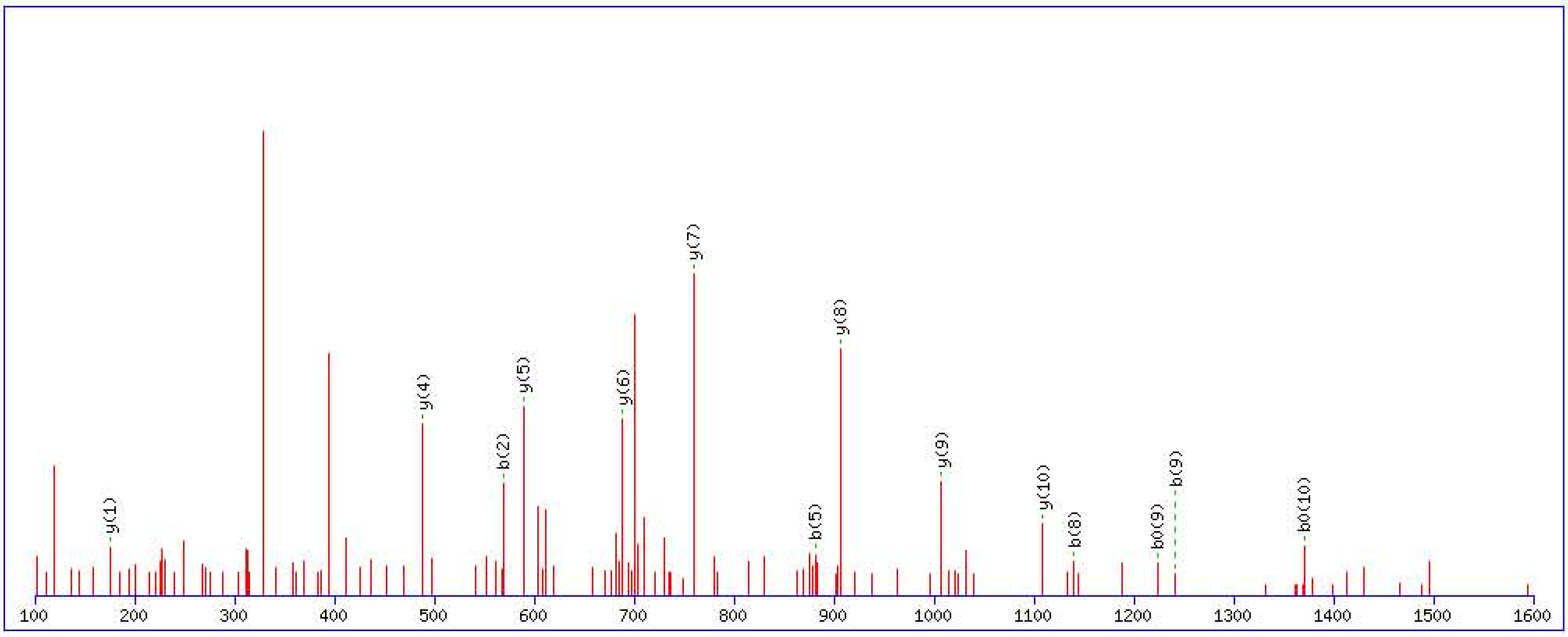
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QEPSQGTTTFAVTSILR**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

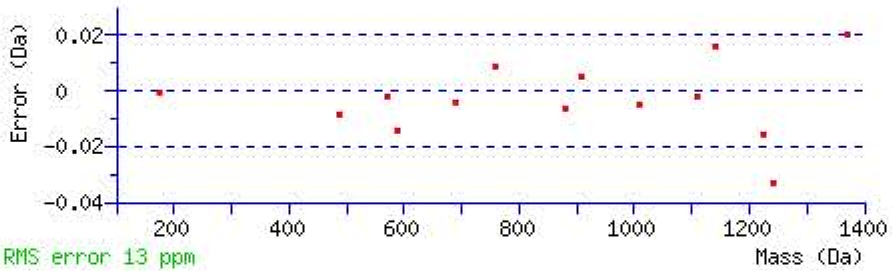
Match to Query 42252: 2146.103442 from(716.375090,3+) rtinseconds(2469) index(34375)
Title: Locus:1.1.1.3523.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

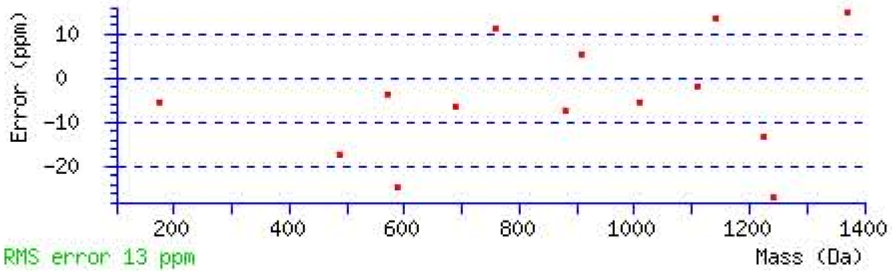
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2146.109253
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 37 **Expect:** 0.006
Matches : 14/184 fragment ions using 29 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	**569.275195**	285.141236	552.248646	276.627961	551.264630	276.135953	E	1707.891193	854.449235	1690.864644	845.935960	1689.880628	845.443952	16
3	666.327959	333.667618	649.301410	325.154343	648.317394	324.662335	P	1578.848600	789.927938	1561.822051	781.414664	1560.838035	780.922656	15
4	753.359987	377.183632	736.333438	368.670357	735.349422	368.178349	S	1481.795836	741.401556	1464.769287	732.888282	1463.785271	732.396274	14
5	**881.418565**	441.212921	864.392016	432.699646	863.408000	432.207638	Q	1394.763808	697.885542	1377.737259	689.372268	1376.753243	688.880260	13
6	938.440029	469.723653	921.413480	461.210378	920.429464	460.718370	G	1266.705230	633.856253	1249.678681	625.342979	1248.694665	624.850971	12
7	1039.487708	520.247492	1022.461159	511.734218	1021.477143	511.242210	T	1209.683766	605.345521	1192.657217	596.832247	1191.673201	596.340239	11
8	**1140.535387**	570.771332	1123.508838	562.258057	1122.524822	561.766049	T	***1108.636087***	554.821682	1091.609538	546.308407	1090.625522	545.816399	10
9	**1241.583066**	621.295171	1224.556517	612.781897	1223.572501	612.289889	T	***1007.588408***	504.297842	990.561859	495.784568	989.577843	495.292560	9
10	1388.651480	694.829378	1371.624931	686.316104	1370.640915	685.824096	F	***906.540729***	453.774003	889.514180	445.260728	888.530164	444.768720	8
11	1459.688594	730.347935	1442.662045	721.834661	1441.678029	721.342653	A	***759.472315***	380.239796	742.445766	371.726521	741.461750	371.234513	7
12	1558.757008	779.882142	1541.730459	771.368868	1540.746443	770.876860	V	***688.435201***	344.721239	671.408652	336.207964	670.424636	335.715956	6
13	1659.804687	830.405982	1642.778138	821.892707	1641.794122	821.400699	T	***589.366787***	295.187032	572.340238	286.673757	571.356222	286.181749	5
14	1746.836715	873.921996	1729.810166	865.408721	1728.826150	864.916713	S	***488.319108***	244.663192	471.292559	236.149918	470.308543	235.657910	4
15	1859.920779	930.464028	1842.894230	921.950753	1841.910214	921.458745	I	401.287080	201.147178	384.260531	192.633903			3
16	1973.004843	987.006060	1955.978294	978.492785	1954.994278	978.000777	L	288.203016	144.605146	271.176467	136.091872			2
17							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of QEPSQGTTTFAVTSILR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.7	2146.109253	-0.005811	QEPSQGTTTFAVTSILR
34.6	2146.109253	-0.005811	QEPSQGTTTFAVTSILR

Mascot: http://www.matrixscience.com/

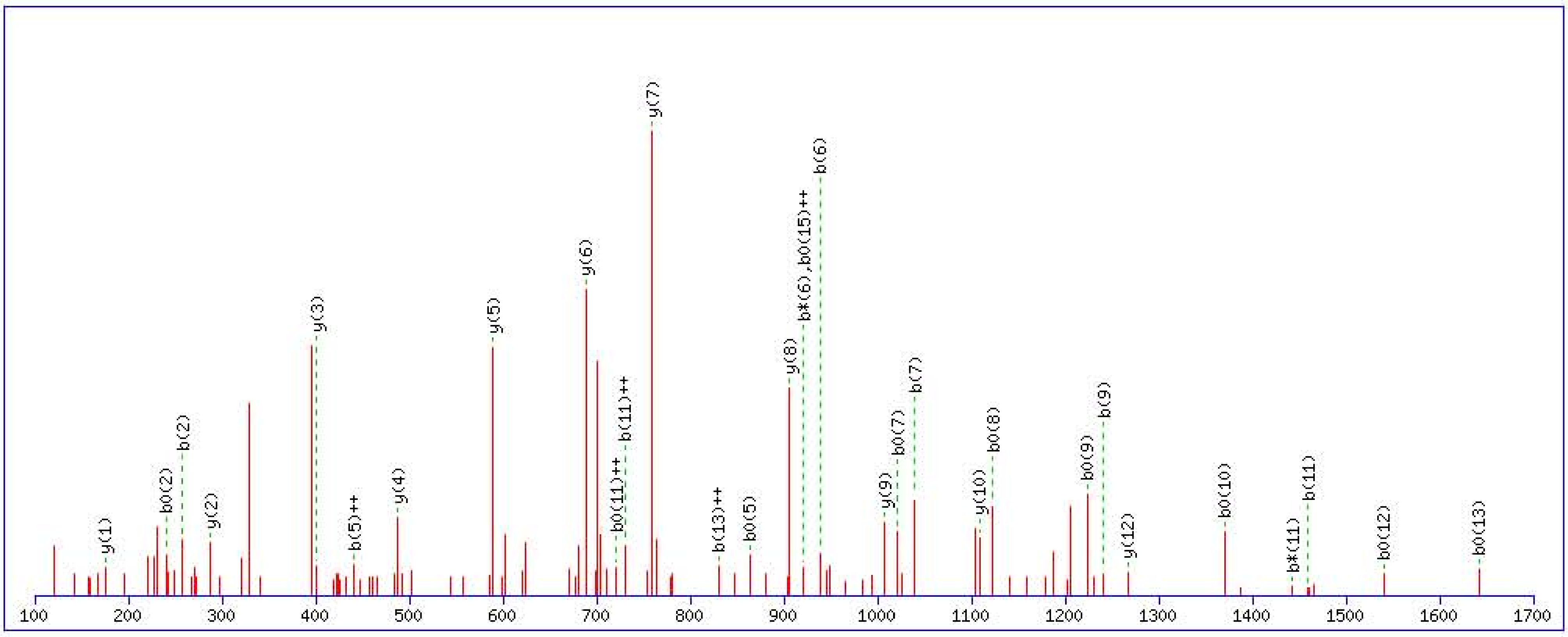
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QEPSQGTTTFAVTSILR**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

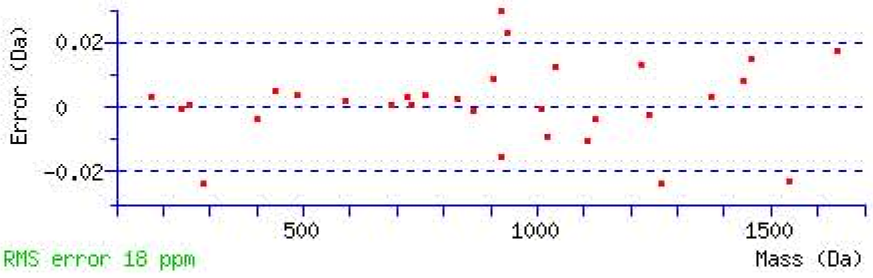
Match to Query 42253: 2146.106202 from(716.376010,3+) rtinseconds(2503) index(34614)
Title: Locus:1.1.1.3535.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

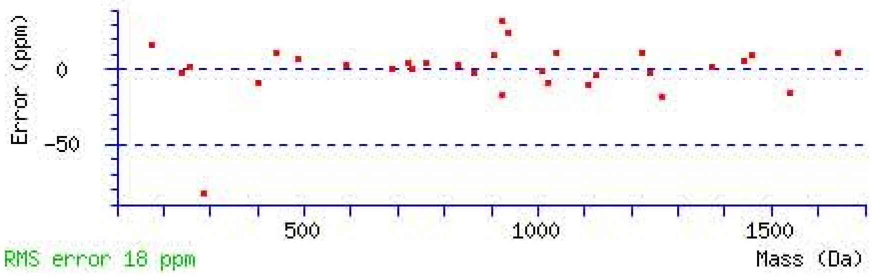
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2146.109253
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 59  Expect: 3.5e-005
Matches : 31/184 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	129.065854	65.036565	112.039305	56.523291			Q							17
2	**258.108447**	129.557862	241.081898	121.044587	240.097882	120.552579	E	2019.057941	1010.032609	2002.031392	1001.519334	2001.047376	1001.027326	16
3	355.161211	178.084244	338.134662	169.570969	337.150646	169.078961	P	1890.015348	945.511312	1872.988799	936.998038	1872.004783	936.506030	15
4	442.193239	221.600258	425.166690	213.086983	424.182674	212.594975	S	1792.962584	896.984930	1775.936035	888.471656	1774.952019	887.979648	14
5	881.418565	**441.212921**	864.392016	432.699646	863.408000	432.207638	Q	1705.930556	853.468916	1688.904007	844.955642	1687.919991	844.463634	13
6	**938.440029**	469.723653	921.413480	461.210378	920.429464	460.718370	G	***1266.705230***	633.856253	1249.678681	625.342979	1248.694665	624.850971	12
7	**1039.487708**	520.247492	1022.461159	511.734218	1021.477143	511.242210	T	1209.683766	605.345521	1192.657217	596.832247	1191.673201	596.340239	11
8	1140.535387	570.771332	1123.508838	562.258057	1122.524822	561.766049	T	***1108.636087***	554.821682	1091.609538	546.308407	1090.625522	545.816399	10
9	**1241.583066**	621.295171	1224.556517	612.781897	1223.572501	612.289889	T	***1007.588408***	504.297842	990.561859	495.784568	989.577843	495.292560	9
10	1388.651480	694.829378	1371.624931	686.316104	1370.640915	685.824096	F	***906.540729***	453.774003	889.514180	445.260728	888.530164	444.768720	8
11	**1459.688594**	**730.347935**	1442.662045	721.834661	1441.678029	721.342653	A	***759.472315***	380.239796	742.445766	371.726521	741.461750	371.234513	7
12	1558.757008	779.882142	1541.730459	771.368868	1540.746443	770.876860	V	***688.435201***	344.721239	671.408652	336.207964	670.424636	335.715956	6
13	1659.804687	**830.405982**	1642.778138	821.892707	1641.794122	821.400699	T	***589.366787***	295.187032	572.340238	286.673757	571.356222	286.181749	5
14	1746.836715	873.921996	1729.810166	865.408721	1728.826150	864.916713	S	***488.319108***	244.663192	471.292559	236.149918	470.308543	235.657910	4
15	1859.920779	930.464028	1842.894230	921.950753	1841.910214	921.458745	I	***401.287080***	201.147178	384.260531	192.633903			3
16	1973.004843	987.006060	1955.978294	978.492785	1954.994278	978.000777	L	***288.203016***	144.605146	271.176467	136.091872			2
17							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of QEPSQGTTTFAVTSILR
(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	2146.109253	-0.003051	QEPSQGTTTFAVTSILR
56.2	2146.109253	-0.003051	QEPSQGTTTFAVTSILR

Mascot: http://www.matrixscience.com/

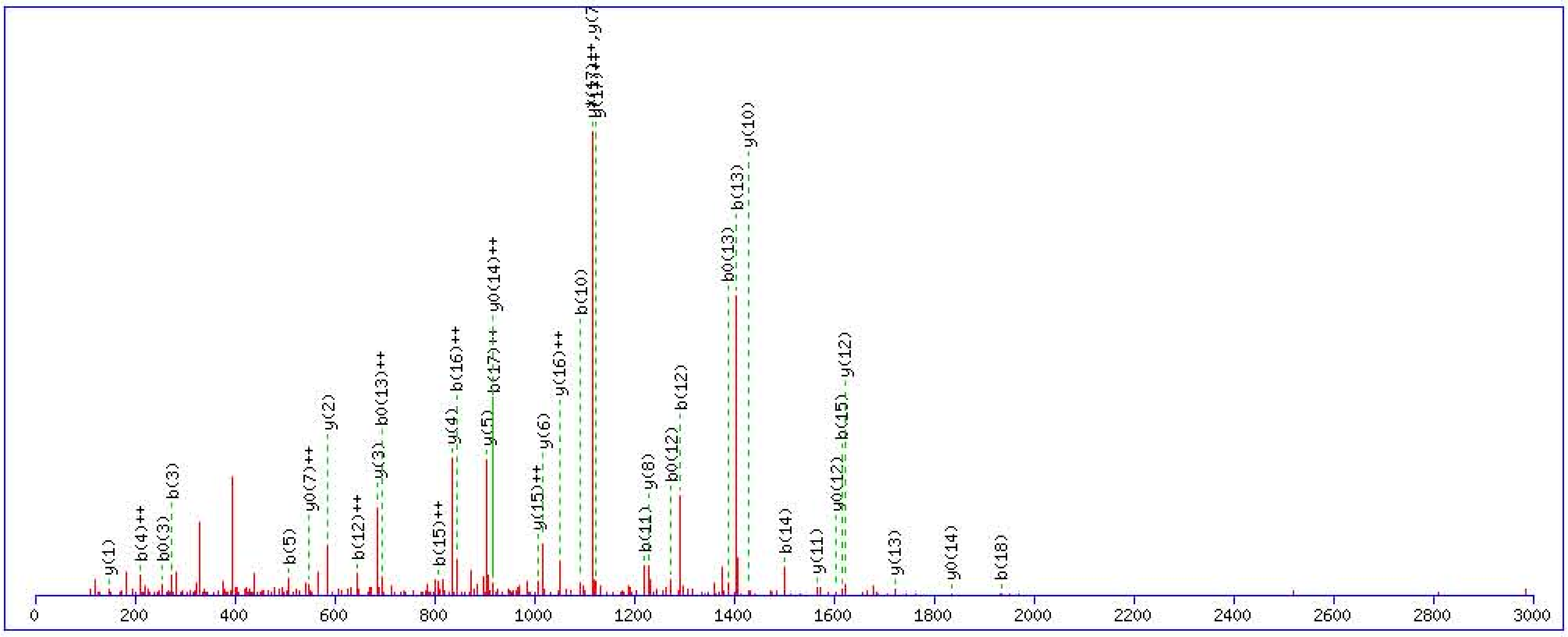
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GDTFSCMVGHEALPLAFTQK**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

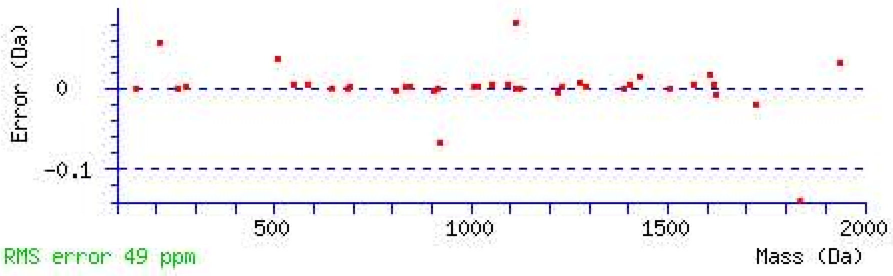
Match to Query 48765: 2519.197392 from(840.739740,3+) rtinseconds(2568) index(34971)
Title: Locus:1.1.1.3557.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

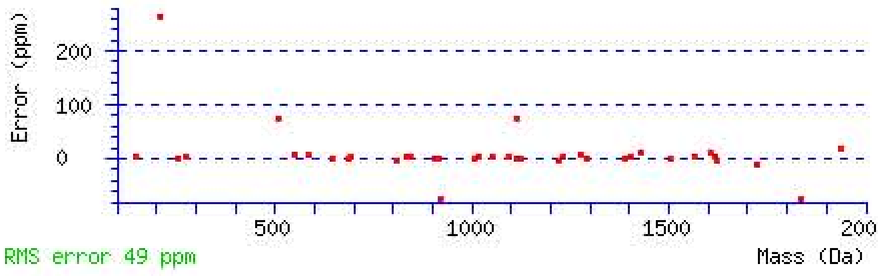
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [3000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2519.201126
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q19 : Biotin:Thermo-21345 (Q)
Ions Score: 62 **Expect:** 2e-006
Matches : 38/186 fragment ions using 72 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							20
2	173.055683	87.031479			155.045118	78.026197	D	2463.186924	1232.097100	2446.160375	1223.583825	2445.176359	1223.091817	19
3	***274.103362***	137.555319			256.092797	128.550037	T	2348.159981	1174.583628	2331.133432	1166.070354	2330.149416	1165.578346	18
4	421.171776	**211.089526**			403.161211	202.084243	F	2247.112302	1124.059789	2230.085753	1115.546514	2229.101737	1115.054506	17
5	***508.203804***	254.605540			490.193239	245.600257	S	2100.043888	1050.525582	2083.017339	1042.012307	2082.033323	1041.520299	16
6	668.234453	334.620865			650.223888	325.615582	C	2013.011860	1007.009568	1995.985311	998.496294	1995.001295	998.004286	15
7	799.274938	400.141107			781.264373	391.135825	M	1852.981211	926.994244	1835.954662	918.480969	1834.970646	917.988961	14
8	898.343352	449.675314			880.332787	440.670031	V	***1721.940726***	861.474001	1704.914177	852.960727	1703.930161	852.468719	13
9	955.364816	478.186046			937.354251	469.180764	G	***1622.872312***	811.939794	1605.845763	803.426520	1604.861747	802.934512	12
10	***1092.423728***	546.715502			1074.413163	537.710219	H	***1565.850848***	783.429062	1548.824299	774.915788	1547.840283	774.423780	11
11	***1221.466321***	611.236799			1203.455756	602.231516	E	***1428.791936***	714.899606	1411.765387	706.386332	1410.781371	705.894324	10
12	***1292.503435***	**646.755356**			1274.492870	637.750073	A	1299.749343	650.378310	1282.722794	641.865035	1281.738778	641.373027	9
13	***1405.587499***	703.297388			1387.576934	694.292105	L	***1228.712229***	614.859753	1211.685680	606.346478	1210.701664	605.854470	8
14	***1502.640263***	751.823770			1484.629698	742.818487	P	***1115.628165***	558.317721	1098.601616	549.804446	1097.617600	549.312438	7
15	***1615.724327***	**808.365801**			1597.713762	799.360519	L	***1018.575401***	509.791339	1001.548852	501.278064	1000.564836	500.786056	6
16	1686.761441	**843.884358**			1668.750876	834.879076	A	***905.491337***	453.249307	888.464788	444.736032	887.480772	444.244024	5
17	1833.829855	**917.418566**			1815.819290	908.413283	F	***834.454223***	417.730750	817.427674	409.217475	816.443658	408.725467	4
18	***1934.877534***	967.942405			1916.866969	958.937122	T	***687.385809***	344.196543	670.359260	335.683268	669.375244	335.191260	3
19	2374.102860	1187.555068	2357.076311	1179.041793	2356.092295	1178.549785	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 GDTFSCMVGHEALPLAFTQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.6	2519.201126	-0.003734	GDTFSCMVGHEALPLAFTQK
0.9	2519.214783	-0.017391	KMQQENMKPQEQLTLEPYER
0.2	2519.196243	0.001149	EGSPHDNPTVQQIVQLSPVMQDT

Mascot: http://www.matrixscience.com/

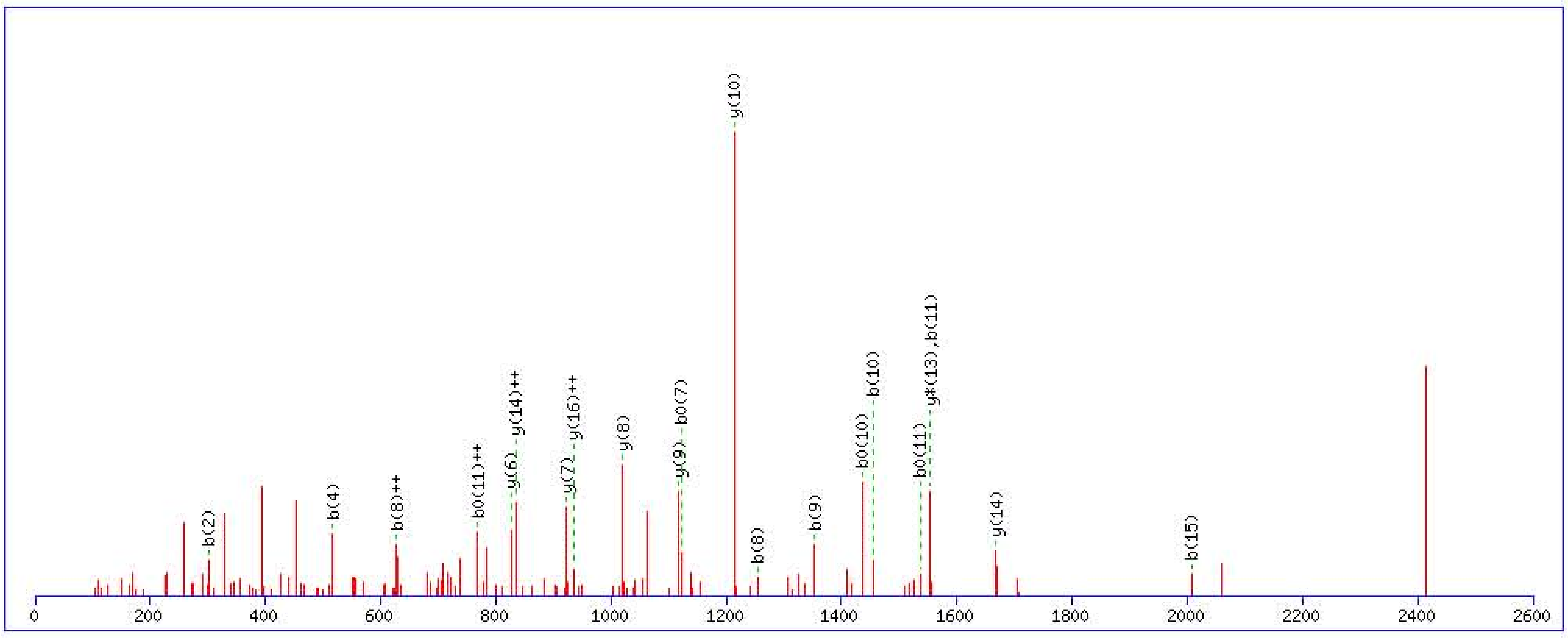
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HYTNPSQDVTVPCPVPPPPPCCHPR**
Found in **IGHA2_HUMAN**, Ig alpha-2 chain C region OS=Homo sapiens GN=IGHA2 PE=1 SV=3

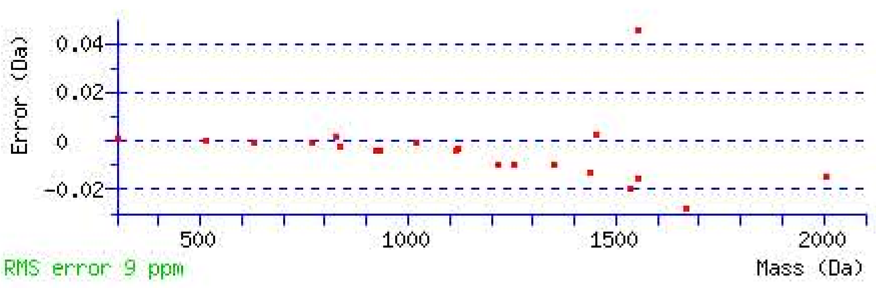
Match to Query 56325: 3219.465896 from(805.873750,4+) rtinseconds(1836) index(17931)
Title: Locus:1.1.1.3205.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

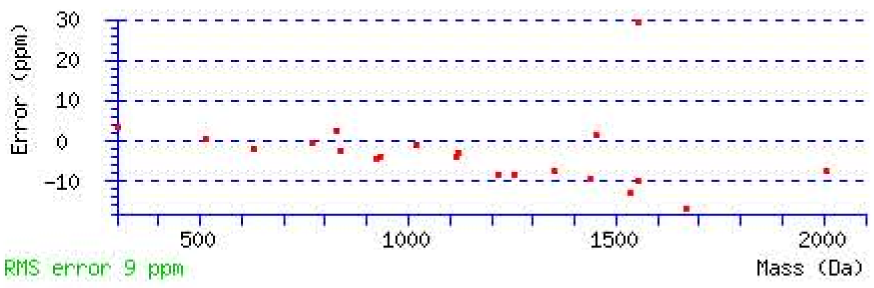
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3219.487518
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.0049
Matches : 21/248 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	138.066188	69.536732					H							25
2	***301.129517***	151.068397					Y	3083.435840	1542.221558	3066.409291	1533.708283	3065.425275	1533.216275	24
3	402.177196	201.592236			384.166631	192.586954	T	2920.372511	1460.689893	2903.345962	1452.176619	2902.361946	1451.684611	23
4	***516.220123***	258.613700	499.193574	250.100425	498.209558	249.608417	N	2819.324832	1410.166054	2802.298283	1401.652779	2801.314267	1401.160771	22
5	613.272887	307.140082	596.246338	298.626807	595.262322	298.134799	P	2705.281905	1353.144590	2688.255356	1344.631316	2687.271340	1344.139308	21
6	700.304915	350.656096	683.278366	342.142821	682.294350	341.650813	S	2608.229141	1304.618208	2591.202592	1296.104934	2590.218576	1295.612926	20
7	1139.530241	570.268759	1122.503692	561.755484	1121.519676	561.263476	Q	2521.197113	1261.102194	2504.170564	1252.588920	2503.186548	1252.096912	19
8	***1254.557184***	627.782230	1237.530635	619.268956	1236.546619	618.776948	D	2081.971787	1041.489531	2064.945238	1032.976257	2063.961222	1032.484249	18
9	***1353.625598***	677.316437	1336.599049	668.803163	1335.615033	668.311155	V	1966.944844	983.976060	1949.918295	975.462786	1948.934279	974.970778	17
10	***1454.673277***	727.840277	1437.646728	719.327002	1436.662712	718.834994	T	1867.876430	934.441853	1850.849881	925.928579	1849.865865	925.436571	16
11	***1553.741691***	777.374484	1536.715142	768.861209	1535.731126	768.369201	V	1766.828751	883.918014	1749.802202	875.404739			15
12	1650.794455	825.900866	1633.767906	817.387591	1632.783890	816.895583	P	***1667.760337***	834.383806	1650.733788	825.870532			14
13	1810.825104	905.916190	1793.798555	897.402916	1792.814539	896.910908	C	1570.707573	785.857424	1553.681024	777.344150			13
14	1907.877868	954.442572	1890.851319	945.929298	1889.867303	945.437290	P	1410.676924	705.842100	1393.650375	697.328825			12
15	***2006.946282***	1003.976779	1989.919733	995.463505	1988.935717	994.971497	V	1313.624160	657.315718	1296.597611	648.802443			11
16	2103.999046	1052.503161	2086.972497	1043.989887	2085.988481	1043.497879	P	***1214.555746***	607.781511	1197.529197	599.268236			10
17	2201.051810	1101.029543	2184.025261	1092.516269	2183.041245	1092.024261	P	***1117.502982***	559.255129	1100.476433	550.741854			9
18	2298.104574	1149.555925	2281.078025	1141.042651	2280.094009	1140.550643	P	***1020.450218***	510.728747	1003.423669	502.215472			8
19	2395.157338	1198.082307	2378.130789	1189.569033	2377.146773	1189.077025	P	***923.397454***	462.202365	906.370905	453.689090			7
20	2492.210102	1246.608689	2475.183553	1238.095415	2474.199537	1237.603407	P	***826.344690***	413.675983	809.318141	405.162708			6
21	2652.240751	1326.624014	2635.214202	1318.110739	2634.230186	1317.618731	C	729.291926	365.149601	712.265377	356.636326			5
22	2812.271400	1406.639338	2795.244851	1398.126063	2794.260835	1397.634055	C	569.261277	285.134276	552.234728	276.621002			4
23	2949.330312	1475.168794	2932.303763	1466.655519	2931.319747	1466.163511	H	409.230628	205.118952	392.204079	196.605677			3
24	3046.383076	1523.695176	3029.356527	1515.181901	3028.372511	1514.689893	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 HYTNPSQDVTVPCPVPPPPPCCHPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.4	3219.487518	-0.021622	HYTNPSQDVTVPCPVPPPPPCCHPR

Mascot: http://www.matrixscience.com/

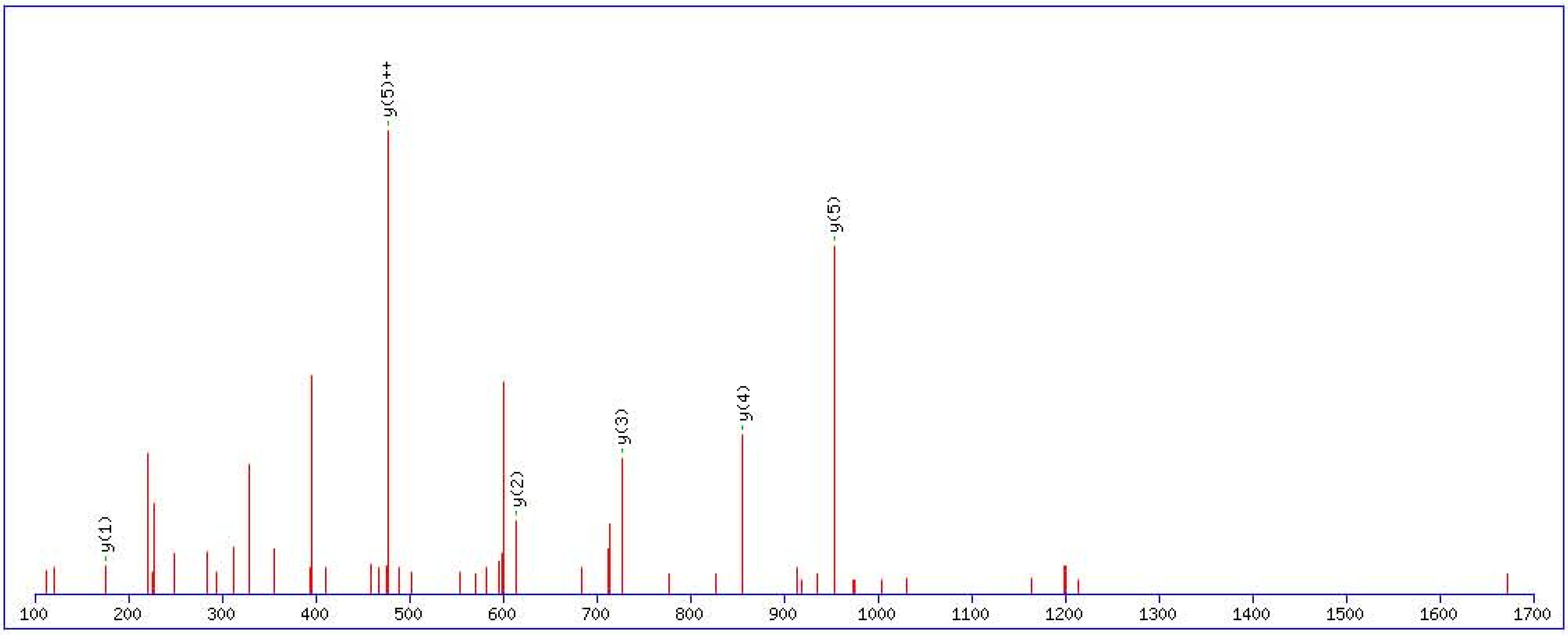
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TFPEIQR**
Found in **IGHD_HUMAN**, Ig delta chain C region OS=Homo sapiens GN=IGHD PE=1 SV=2

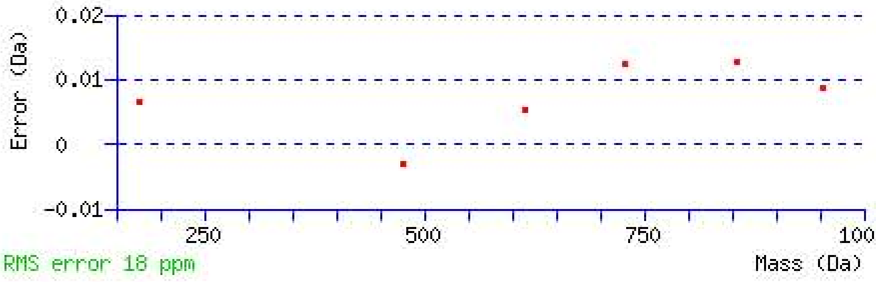
Match to Query 17764: 1200.631168 from(601.322860,2+) rtinseconds(1967) index(60398)
Title: Locus:1.1.1.1596.18 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

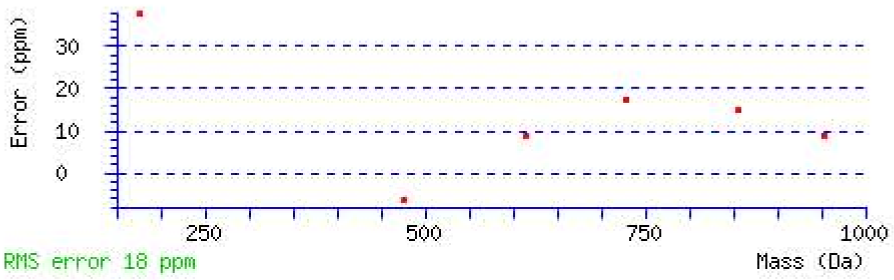
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1200.632507
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.0053
Matches : 6/56 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	102.054955	51.531116			84.044390	42.525833	T							7
2	249.123369	125.065322			231.112804	116.060040	F	1100.592113	550.799695	1083.565564	542.286420	1082.581548	541.794412	6
3	346.176133	173.591704			328.165568	164.586422	P	***953.523699***	477.265488	936.497150	468.752213	935.513134	468.260205	5
4	475.218726	238.113001			457.208161	229.107719	E	***856.470935***	428.739106	839.444386	420.225831	838.460370	419.733823	4
5	588.302790	294.655033			570.292225	285.649751	I	***727.428342***	364.217809	710.401793	355.704535			3
6	1027.528116	514.267696	1010.501567	505.754422	1009.517551	505.262414	Q	***614.344278***	307.675777	597.317729	299.162503			2
7							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TFPEIQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.1	1200.632507	-0.001339	TFPEIQR
6.4	1200.628464	0.002704	LLQLQEMGNR
0.2	1200.636353	-0.005185	TFTQKGNLHR

Mascot: http://www.matrixscience.com/

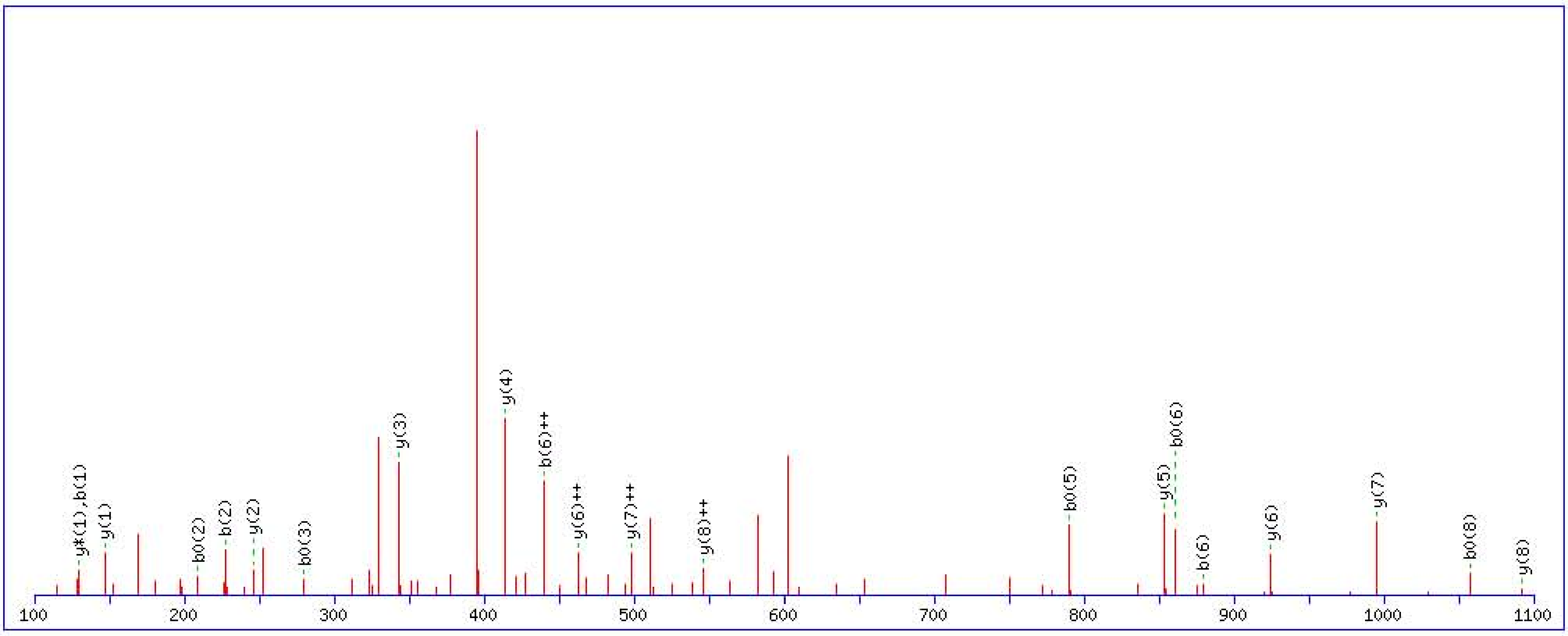
{MATRIX SCIENCE} Mascot Search Results

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

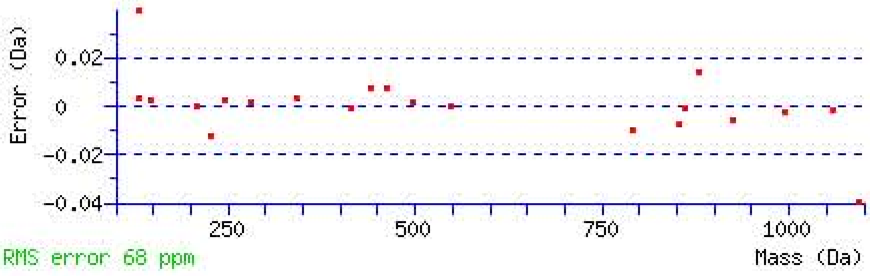
Match to Query 18169: 1220.656608 from(611.335580,2+) rtinseconds(1478) index(15719)
Title: Locus:1.1.1.3080.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

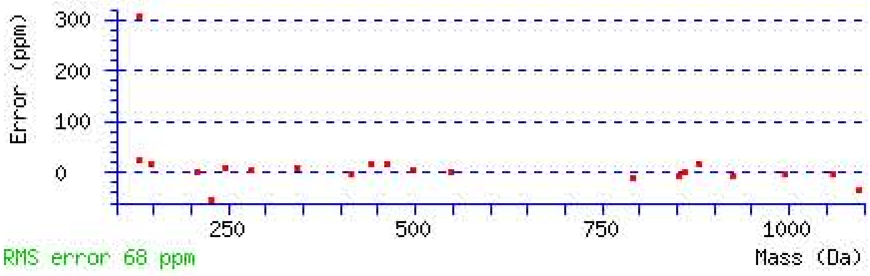
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1220.658707
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 0.00012
Matches : 21/72 fragment ions using 38 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
51.7	1220.658707	-0.002099	EPAAQAPVK
12.2	1220.658722	-0.002114	EQNVPVPK
2.3	1220.651321	0.005287	GQVLIAASSYGR
1.9	1220.666580	-0.009972	EPAIVRFFSR
0.9	1220.640076	0.016532	LLAEYTGAQQK

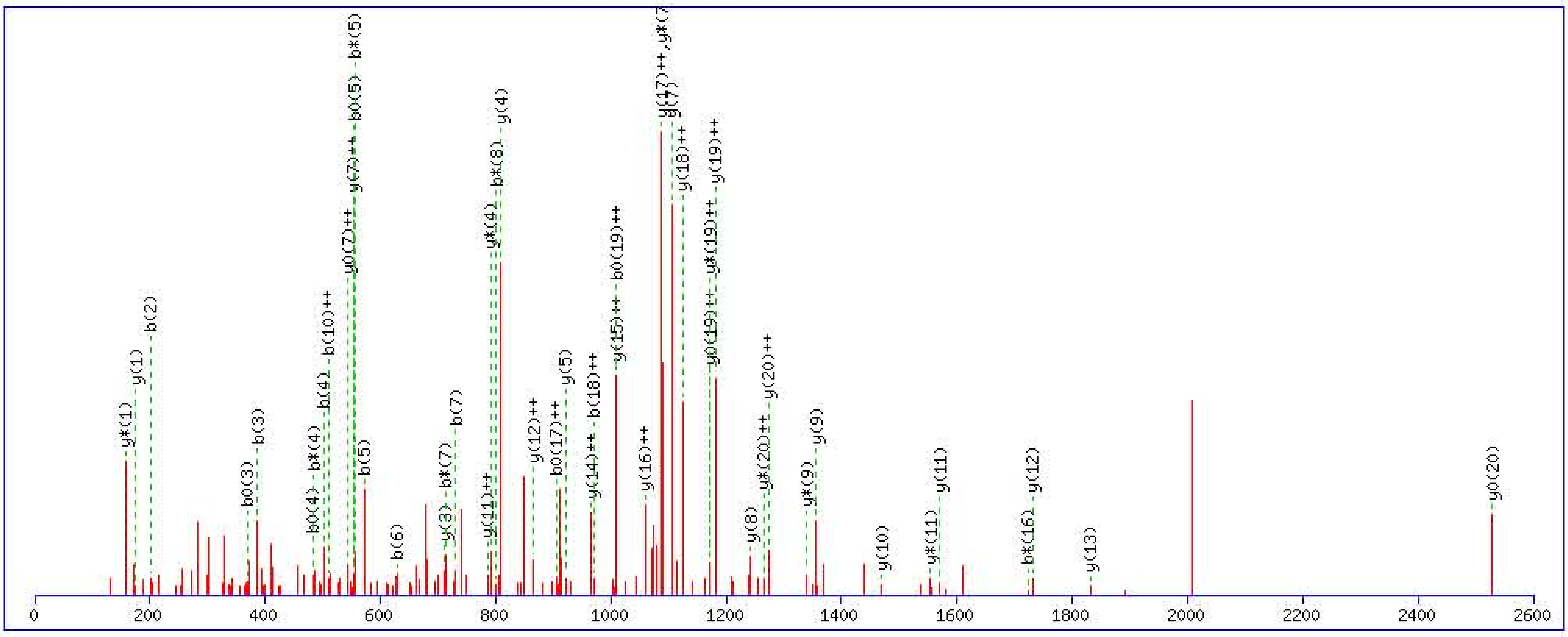
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLWNAGTSVTCTLNHPSLPPQR**
Found in **IGHD_HUMAN**, Ig delta chain C region OS=Homo sapiens GN=IGHD PE=1 SV=2

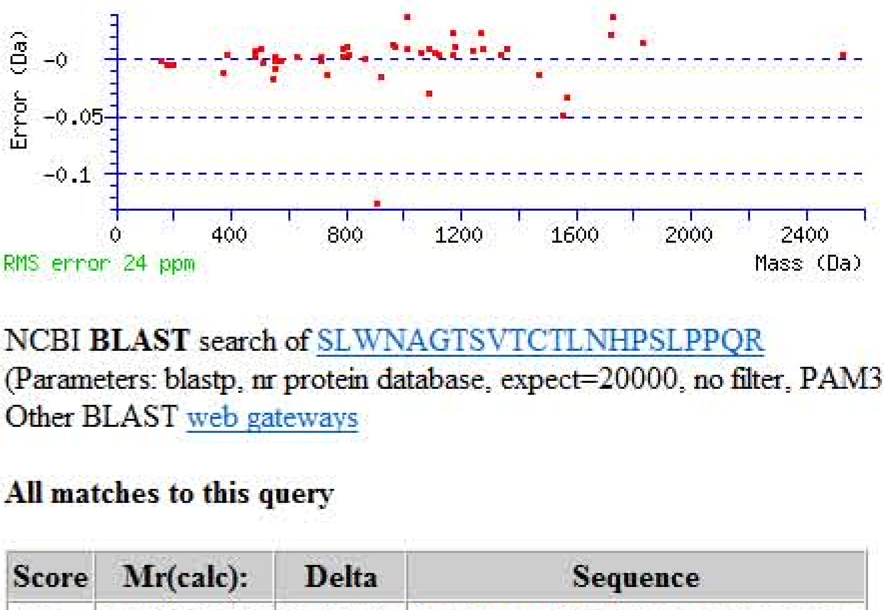
Match to Query 50896: 2746.385952 from(916.469260,3+) rtinseconds(2257) index(62050)
Title: Locus:1.1.1.1697.25 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

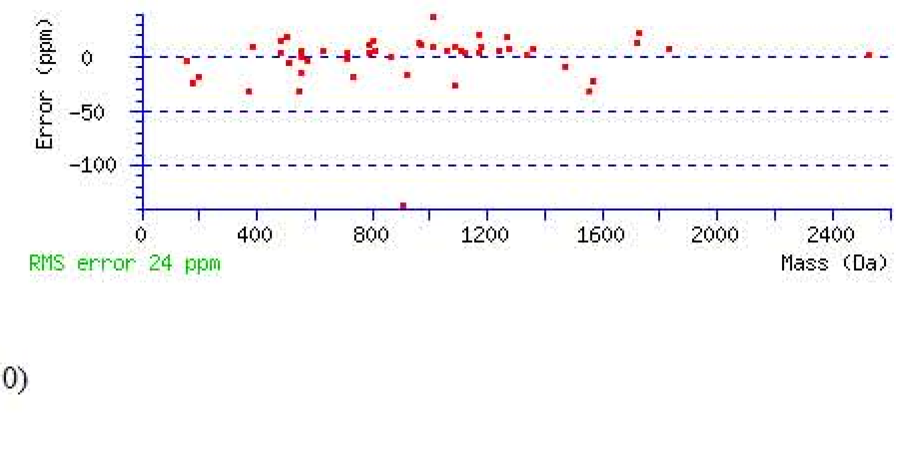
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2746.368332
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q21    : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.0017
Matches : 49/236 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	88.039304	44.523290			70.028739	35.518008	S							22
2	**201.123368**	101.065322			183.112803	92.060039	L	2660.343575	1330.675425	2643.317026	1322.162151	2642.333010	1321.670143	21
3	**387.202681**	194.104978			369.192116	185.099696	W	2547.259511	1274.133393	2530.232962	1265.620119	2529.248946	1265.128111	20
4	**501.245608**	251.126442	484.219059	242.613168	483.235043	242.121160	N	2361.180198	1181.093737	2344.153649	1172.580462	2343.169633	1172.088454	19
5	**572.282722**	286.644999	555.256173	278.131725	554.272157	277.639717	A	2247.137271	1124.072273	2230.110722	1115.558999	2229.126706	1115.066991	18
6	**629.304186**	315.155731	612.277637	306.642457	611.293621	306.150449	G	2176.100157	1088.553716	2159.073608	1080.040442	2158.089592	1079.548434	17
7	**730.351865**	365.679571	713.325316	357.166296	712.341300	356.674288	T	2119.078693	1060.042984	2102.052144	1051.529710	2101.068128	1051.037702	16
8	817.383893	409.195585	800.357344	400.682310	799.373328	400.190302	S	2018.031014	1009.519145	2001.004465	1001.005871	2000.020449	1000.513863	15
9	916.452307	458.729792	899.425758	450.216517	898.441742	449.724509	V	1930.998986	966.003131	1913.972437	957.489857	1912.988421	956.997849	14
10	1017.499986	509.253631	1000.473437	500.740357	999.489421	500.248349	T	***1831.930572***	916.468924	1814.904023	907.955650	1813.920007	907.463642	13
11	1177.530635	589.268956	1160.504086	580.755681	1159.520070	580.263673	C	***1730.882893***	865.945085	1713.856344	857.431810	1712.872328	856.939802	12
12	1278.578314	639.792795	1261.551765	631.279521	1260.567749	630.787513	T	***1570.852244***	785.929760	1553.825695	777.416486	1552.841679	776.924478	11
13	1391.662378	696.334827	1374.635829	687.821553	1373.651813	687.329545	L	***1469.804565***	735.405921	1452.778016	726.892646	1451.794000	726.400638	10
14	1505.705305	753.356291	1488.678756	744.843016	1487.694740	744.351008	N	***1356.720501***	678.863889	1339.693952	670.350614	1338.709936	669.858606	9
15	1642.764217	821.885746	1625.737668	813.372472	1624.753652	812.880464	H	***1242.677574***	621.842425	1225.651025	613.329151	1224.667009	612.837143	8
16	1739.816981	870.412128	1722.790432	861.898854	1721.806416	861.406846	P	***1105.618662***	553.312969	1088.592113	544.799695	1087.608097	544.307687	7
17	1826.849009	913.928143	1809.822460	905.414868	1808.838444	904.922860	S	1008.565898	504.786587	991.539349	496.273313	990.555333	495.781305	6
18	1939.933073	970.470174	1922.906524	961.956900	1921.922508	961.464892	L	***921.533870***	461.270573	904.507321	452.757299			5
19	2036.985837	1018.996557	2019.959288	1010.483282	2018.975272	1009.991274	P	***808.449806***	404.728541	791.423257	396.215267			4
20	2134.038601	1067.522938	2117.012052	1059.009664	2116.028036	1058.517656	P	***711.397042***	356.202159	694.370493	347.688885			3
21	2573.263927	1287.135601	2556.237378	1278.622327	2555.253362	1278.130319	Q	614.344278	307.675777	597.317729	299.162503			2
22							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SLWNAGTSVTCTLNHPSLPPQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.4	2746.368332	0.017620	SLWNAGTSVTCTLNHPSLPPQR

Mascot: http://www.matrixscience.com/

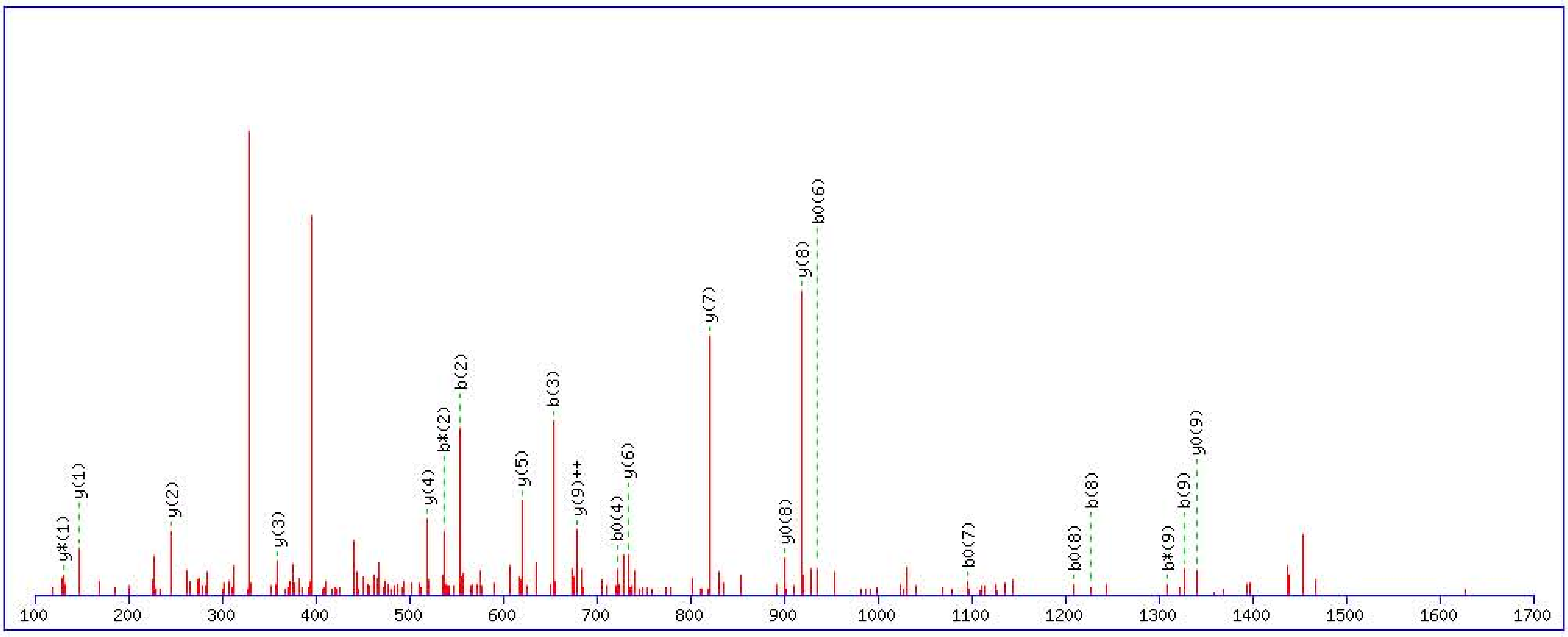
Mascot Search Results

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

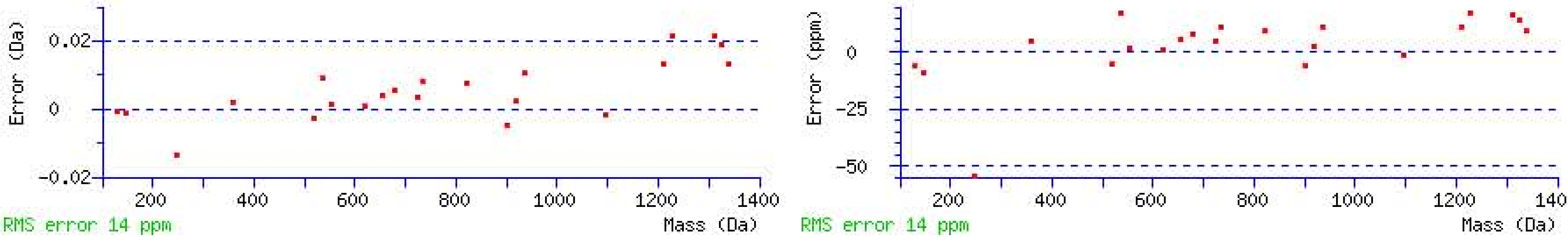
Match to Query 26441: 1471.795828 from(736.905190,2+) rtinseconds(2245) index(61966)
Title: Locus:1.1.1.1693.20 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 1471.789093
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 46 **Expect:** 0.00024
Matches : 22/94 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
45.5	1471.789093	0.006735	NQVSLTCLVK
6.4	1471.803467	-0.007639	EKQGPLLDLFGQK
5.1	1471.796921	-0.001093	YLIAACQHLQKK
4.1	1471.797592	-0.001764	KYFWDRAFLVK
3.8	1471.777847	0.017981	QLDMELVSVK
3.0	1471.806808	-0.010980	ESLLQIPRIEMK
2.8	1471.793106	0.002722	QPFMVDILAK
2.5	1471.799438	-0.003610	EVELDRLRDTVK
2.2	1471.814713	-0.018885	RQVIVGTWGESLK
0.1	1471.788162	0.007666	ELEAEKLQKEQK

Mascot: http://www.matrixscience.com/

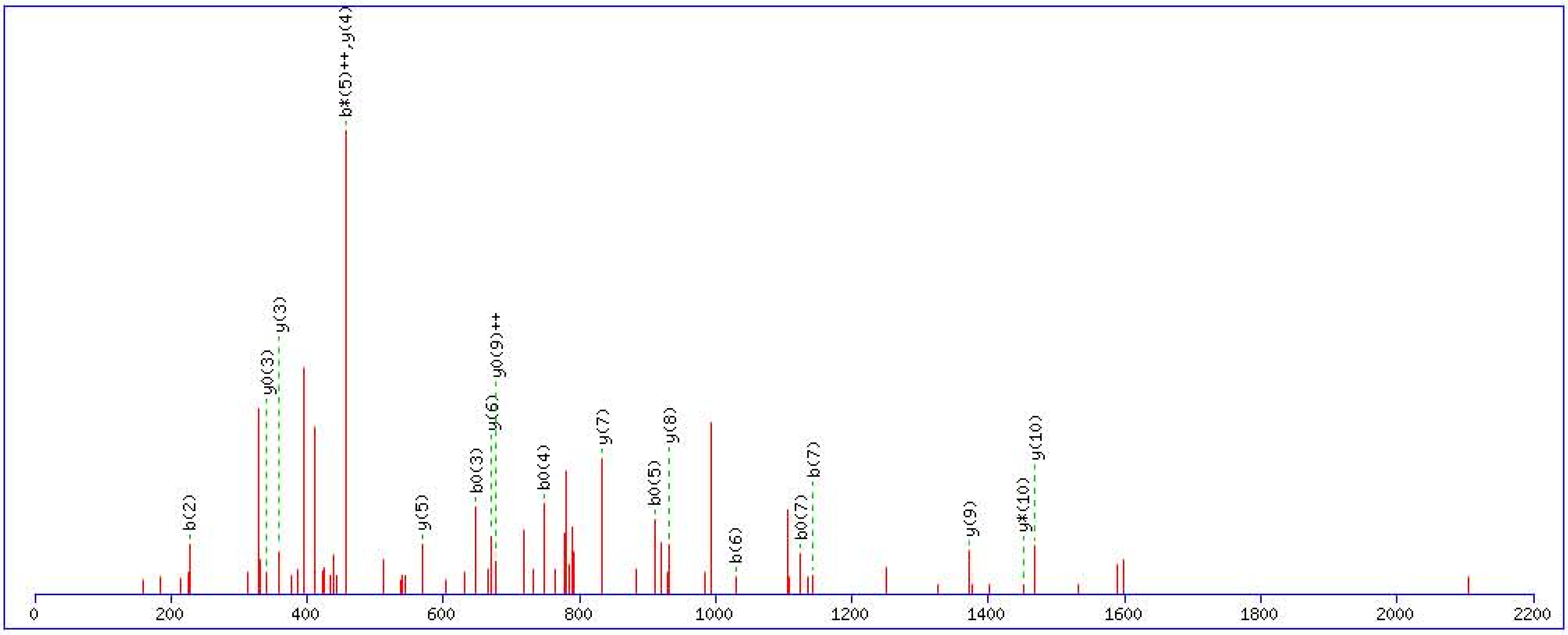
{MATRIX SCIENCE} Mascot Search Results

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

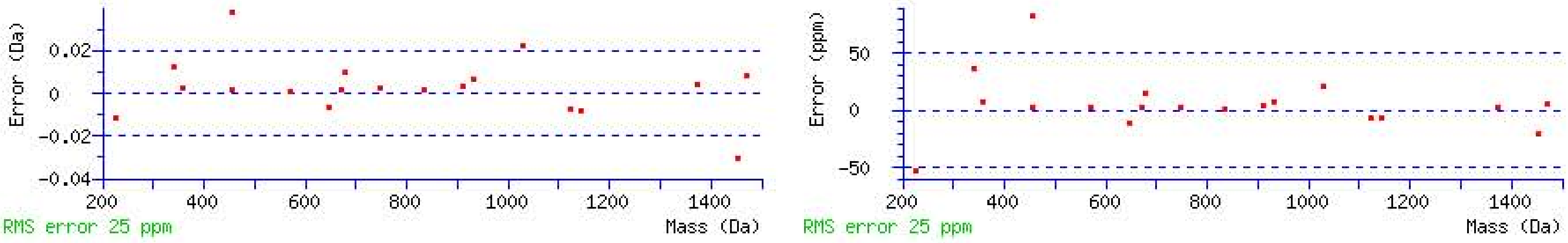
Match to Query 30487: 1596.834408 from(799.424480,2+) rtinseconds(2036) index(60816)
Title: Locus:1.1.1.1620.15 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 1596.833389
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.0012
Matches : 19/114 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	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
33.3	1596.833389	0.001019	EPQVYTLPPSR
2.3	1596.818115	0.016293	QEPEEKVVSNK
0.7	1596.851135	-0.016727	LLFHGENIEALDKV

Mascot: http://www.matrixscience.com/

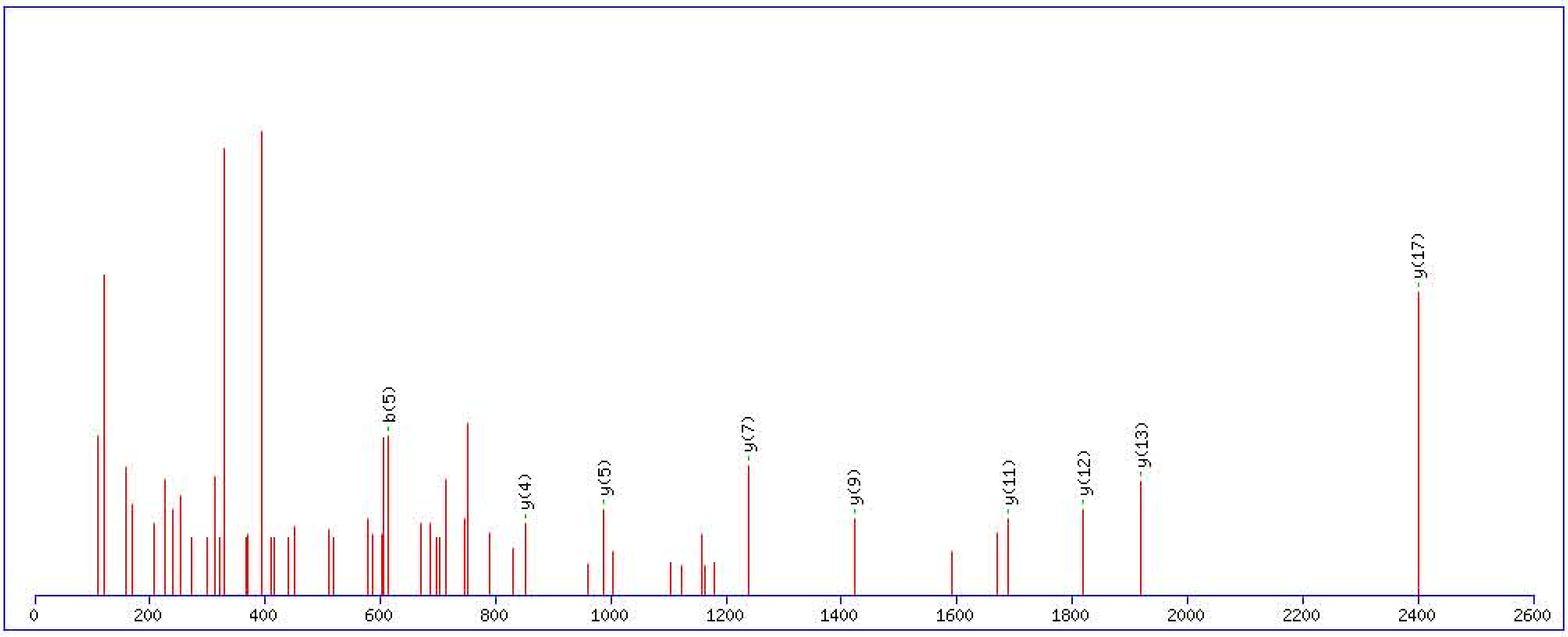
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WQQGNVFSCSVMHEALHNHYTQK**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

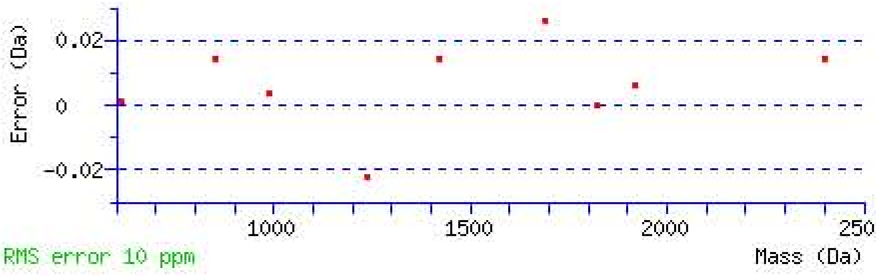
Match to Query 54772: 3111.419220 from(623.291120,5+) rtinseconds(2066) index(32261)
Title: Locus:1.1.1.3383.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

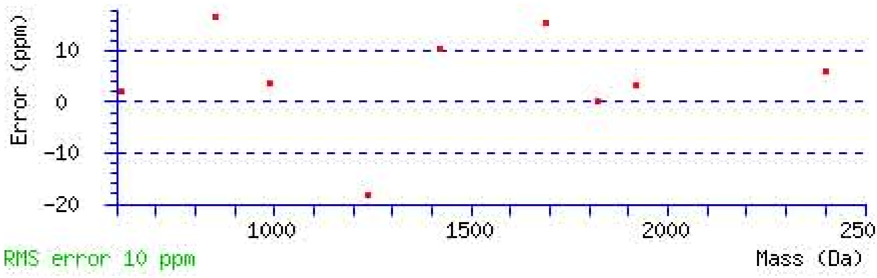
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3111.426590
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q22 : Biotin:Thermo-21345 (Q)
Ions Score: 33 **Expect:** 0.0061
Matches : 9/244 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	187.086589	94.046932					W							23
2	315.145167	158.076222	298.118618	149.562947			Q	2926.354551	1463.680913	2909.328002	1455.167639	2908.343986	1454.675631	22
3	443.203745	222.105511	426.177196	213.592236			Q	2798.295973	1399.651624	2781.269424	1391.138350	2780.285408	1390.646342	21
4	500.225209	250.616243	483.198660	242.102968			G	2670.237395	1335.622335	2653.210846	1327.109061	2652.226830	1326.617053	20
5	614.268136	307.637706	597.241587	299.124432			N	2613.215931	1307.111603	2596.189382	1298.598329	2595.205366	1298.106321	19
6	713.336550	357.171913	696.310001	348.658639			V	2499.173004	1250.090140	2482.146455	1241.576865	2481.162439	1241.084857	18
7	860.404964	430.706120	843.378415	422.192845			F	***2400.104590***	1200.555933	2383.078041	1192.042658	2382.094025	1191.550650	17
8	947.436992	474.222134	930.410443	465.708859	929.426427	465.216851	S	2253.036176	1127.021726	2236.009627	1118.508451	2235.025611	1118.016443	16
9	1107.467641	554.237459	1090.441092	545.724184	1089.457076	545.232176	C	2166.004148	1083.505712	2148.977599	1074.992437	2147.993583	1074.500429	15
10	1194.499669	597.753473	1177.473120	589.240198	1176.489104	588.748190	S	2005.973499	1003.490388	1988.946950	994.977113	1987.962934	994.485105	14
11	1293.568083	647.287680	1276.541534	638.774405	1275.557518	638.282397	V	***1918.941471***	959.974373	1901.914922	951.461099	1900.930906	950.969091	13
12	1424.608568	712.807922	1407.582019	704.294648	1406.598003	703.802640	M	***1819.873057***	910.440166	1802.846508	901.926892	1801.862492	901.434884	12
13	1561.667480	781.337378	1544.640931	772.824104	1543.656915	772.332096	H	***1688.832572***	844.919924	1671.806023	836.406649	1670.822007	835.914641	11
14	1690.710073	845.858675	1673.683524	837.345400	1672.699508	836.853392	E	1551.773660	776.390468	1534.747111	767.877193	1533.763095	767.385185	10
15	1761.747187	881.377231	1744.720638	872.863957	1743.736622	872.371949	A	***1422.731067***	711.869171	1405.704518	703.355897	1404.720502	702.863889	9
16	1874.831251	937.919263	1857.804702	929.405989	1856.820686	928.913981	L	1351.693953	676.350615	1334.667404	667.837340	1333.683388	667.345332	8
17	2011.890163	1006.448719	1994.863614	997.935445	1993.879598	997.443437	H	***1238.609889***	619.808583	1221.583340	611.295308	1220.599324	610.803300	7
18	2125.933090	1063.470183	2108.906541	1054.956908	2107.922525	1054.464900	N	1101.550977	551.279127	1084.524428	542.765852	1083.540412	542.273844	6
19	2262.992002	1131.999639	2245.965453	1123.486364	2244.981437	1122.994356	H	***987.508050***	494.257663	970.481501	485.744389	969.497485	485.252381	5
20	2426.055331	1213.531303	2409.028782	1205.018029	2408.044766	1204.526021	Y	***850.449138***	425.728207	833.422589	417.214933	832.438573	416.722925	4
21	2527.103010	1264.055143	2510.076461	1255.541868	2509.092445	1255.049860	T	687.385809	344.196543	670.359260	335.683268	669.375244	335.191260	3
22	2966.328336	1483.667806	2949.301787	1475.154531	2948.317771	1474.662523	Q	586.338130	293.672703	569.311581	285.159429			2
23							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of WQQGNVFSCSVMHEALHNHYTQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.0	3111.426590	-0.007370	WQQGNVFSCSVMHEALHNHYTQK

Mascot: http://www.matrixscience.com/

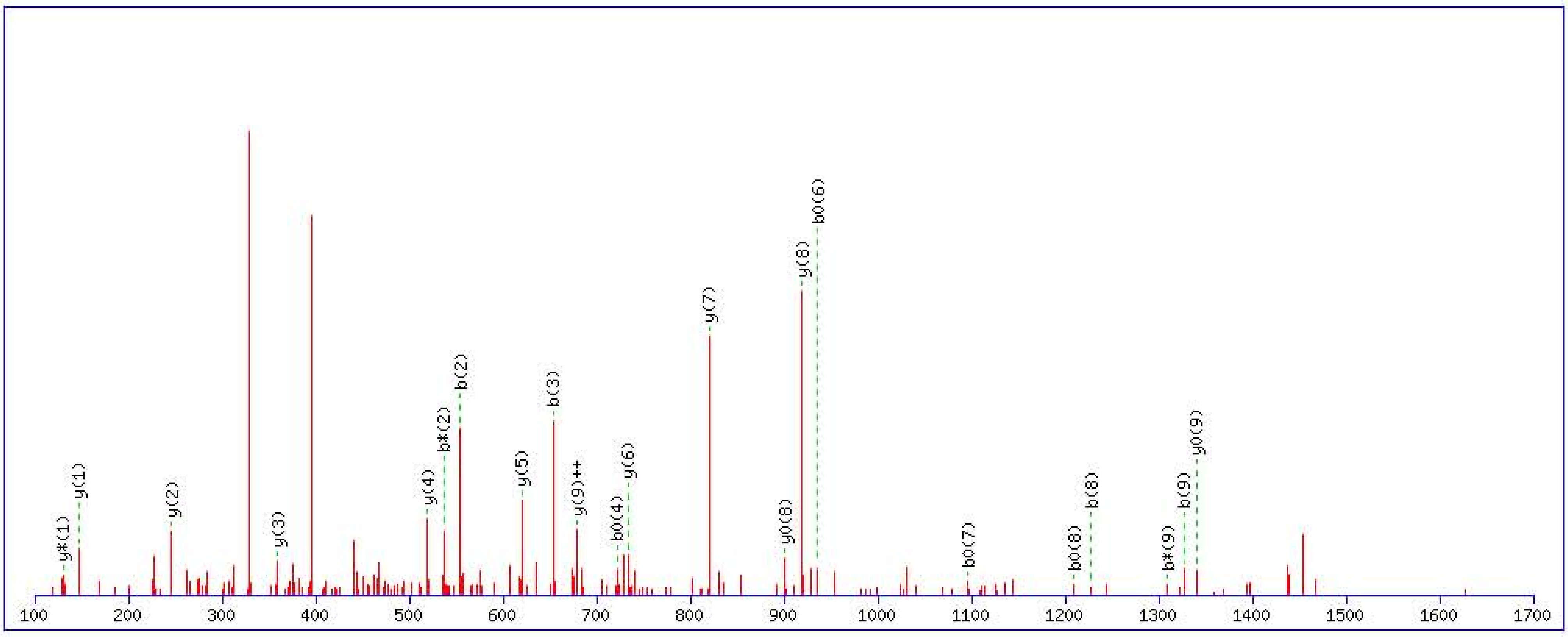
{MATRIX} {SCIENCE} Mascot Search Results

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 26441: 1471.795828 from(736.905190,2+) rtinseconds(2245) index(61966)
Title: Locus:1.1.1.1693.20 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\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 ●



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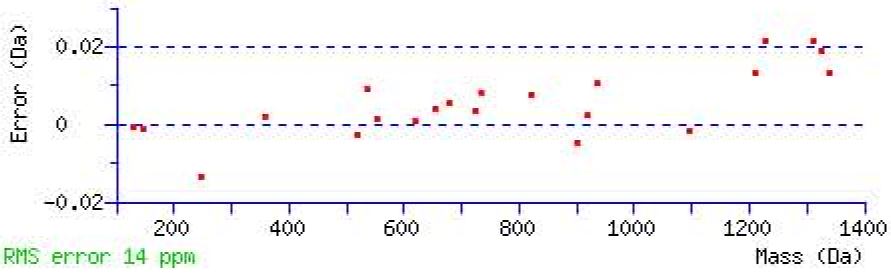
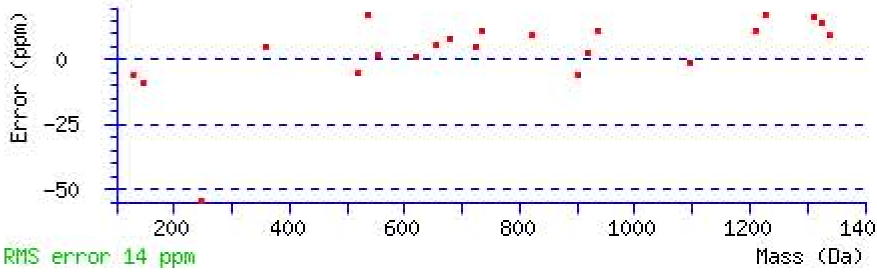
Monoisotopic mass of neutral peptide Mr(calc): 1471.789093
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00024
Matches : 22/94 fragment ions using 42 most intense peaks   (help)
```

#	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
45.5	1471.789093	0.006735	NQVSLTCLVK
6.4	1471.803467	-0.007639	EKQGPLLDLFGQK
5.1	1471.796921	-0.001093	YLIAACQHLQKK
4.1	1471.797592	-0.001764	KYFWDRAFLVK
3.8	1471.777847	0.017981	QLDMELVSVK
3.0	1471.806808	-0.010980	ESLLQIPRIEMK
2.8	1471.793106	0.002722	QPFMVDILAK
2.5	1471.799438	-0.003610	EVELDRLRDTVK
2.2	1471.814713	-0.018885	RQVIVGTWGESLK
0.1	1471.788162	0.007666	ELEAEKLQKEQK

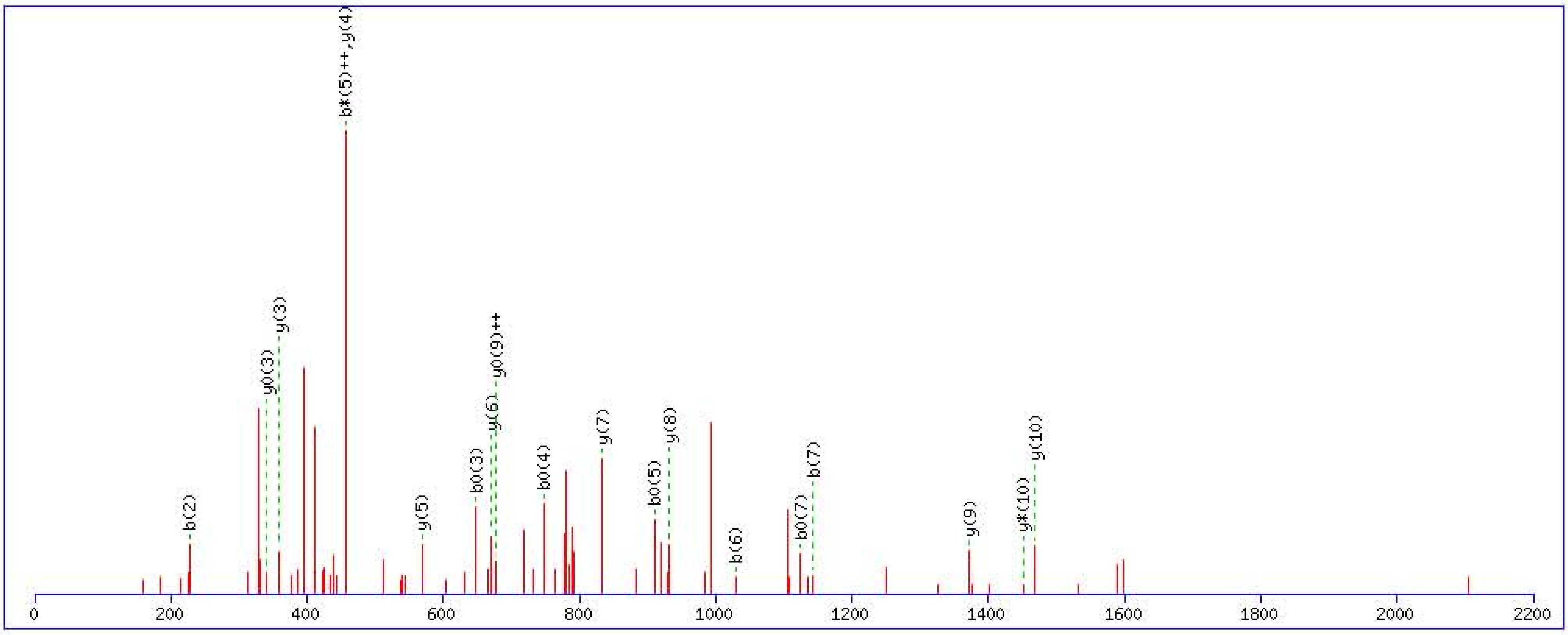
{MATRIX SCIENCE} Mascot Search Results

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

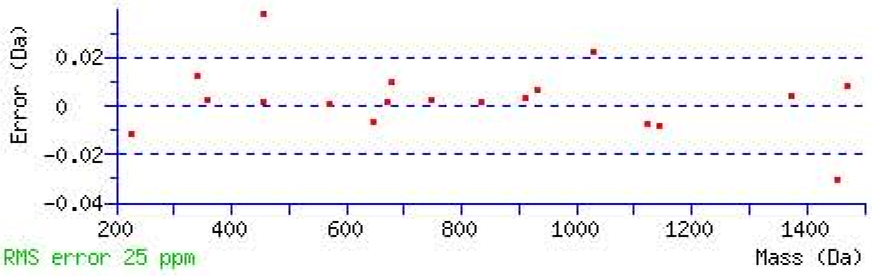
Match to Query 30487: 1596.834408 from(799.424480,2+) rtinseconds(2036) index(60816)
Title: Locus:1.1.1.1620.15 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

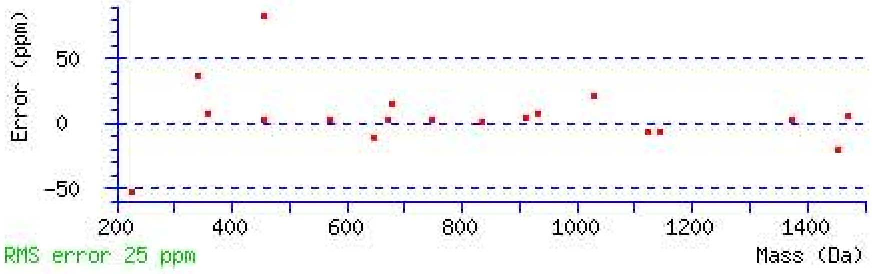
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1596.833389
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 33 **Expect:** 0.0012
Matches : 19/114 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	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
33.3	1596.833389	0.001019	EPQVYTLPPSR
2.3	1596.818115	0.016293	QEPEEKVVSNK
0.7	1596.851135	-0.016727	LLFHGENIEALDKV

Mascot: http://www.matrixscience.com/

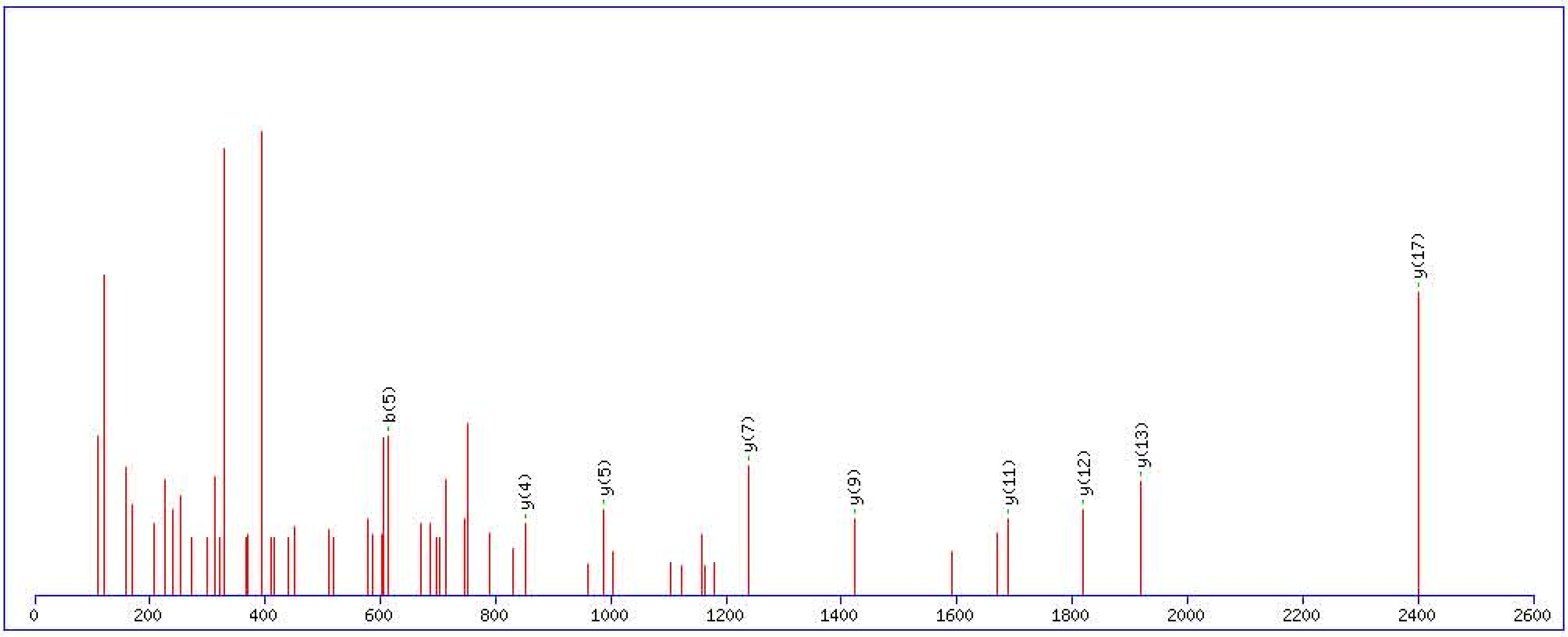
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WQQGNVFSCSVMHEALHNHYTQK**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

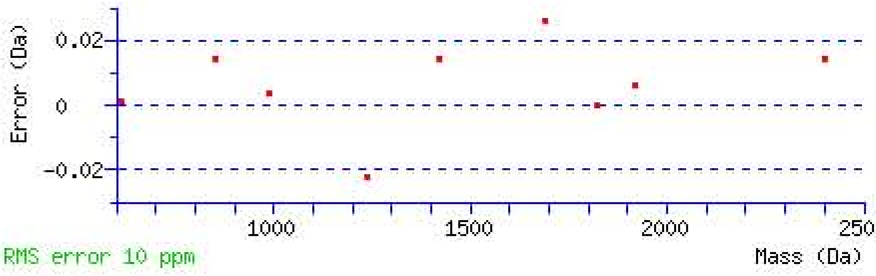
Match to Query 54772: 3111.419220 from(623.291120,5+) rtinseconds(2066) index(32261)
Title: Locus:1.1.1.3383.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

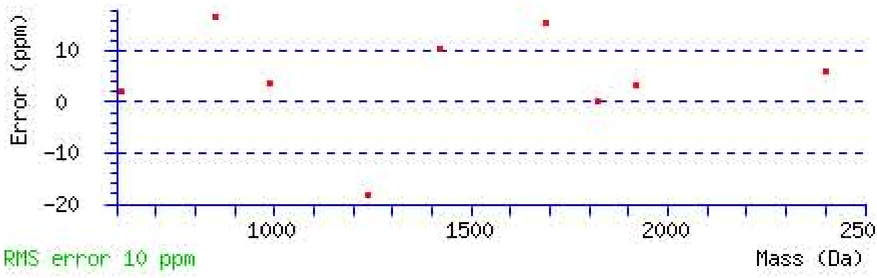
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3111.426590
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q22    : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.0061
Matches : 9/244 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	187.086589	94.046932					W							23
2	315.145167	158.076222	298.118618	149.562947			Q	2926.354551	1463.680913	2909.328002	1455.167639	2908.343986	1454.675631	22
3	443.203745	222.105511	426.177196	213.592236			Q	2798.295973	1399.651624	2781.269424	1391.138350	2780.285408	1390.646342	21
4	500.225209	250.616243	483.198660	242.102968			G	2670.237395	1335.622335	2653.210846	1327.109061	2652.226830	1326.617053	20
5	614.268136	307.637706	597.241587	299.124432			N	2613.215931	1307.111603	2596.189382	1298.598329	2595.205366	1298.106321	19
6	713.336550	357.171913	696.310001	348.658639			V	2499.173004	1250.090140	2482.146455	1241.576865	2481.162439	1241.084857	18
7	860.404964	430.706120	843.378415	422.192845			F	***2400.104590***	1200.555933	2383.078041	1192.042658	2382.094025	1191.550650	17
8	947.436992	474.222134	930.410443	465.708859	929.426427	465.216851	S	2253.036176	1127.021726	2236.009627	1118.508451	2235.025611	1118.016443	16
9	1107.467641	554.237459	1090.441092	545.724184	1089.457076	545.232176	C	2166.004148	1083.505712	2148.977599	1074.992437	2147.993583	1074.500429	15
10	1194.499669	597.753473	1177.473120	589.240198	1176.489104	588.748190	S	2005.973499	1003.490388	1988.946950	994.977113	1987.962934	994.485105	14
11	1293.568083	647.287680	1276.541534	638.774405	1275.557518	638.282397	V	***1918.941471***	959.974373	1901.914922	951.461099	1900.930906	950.969091	13
12	1424.608568	712.807922	1407.582019	704.294648	1406.598003	703.802640	M	***1819.873057***	910.440166	1802.846508	901.926892	1801.862492	901.434884	12
13	1561.667480	781.337378	1544.640931	772.824104	1543.656915	772.332096	H	***1688.832572***	844.919924	1671.806023	836.406649	1670.822007	835.914641	11
14	1690.710073	845.858675	1673.683524	837.345400	1672.699508	836.853392	E	1551.773660	776.390468	1534.747111	767.877193	1533.763095	767.385185	10
15	1761.747187	881.377231	1744.720638	872.863957	1743.736622	872.371949	A	***1422.731067***	711.869171	1405.704518	703.355897	1404.720502	702.863889	9
16	1874.831251	937.919263	1857.804702	929.405989	1856.820686	928.913981	L	1351.693953	676.350615	1334.667404	667.837340	1333.683388	667.345332	8
17	2011.890163	1006.448719	1994.863614	997.935445	1993.879598	997.443437	H	***1238.609889***	619.808583	1221.583340	611.295308	1220.599324	610.803300	7
18	2125.933090	1063.470183	2108.906541	1054.956908	2107.922525	1054.464900	N	1101.550977	551.279127	1084.524428	542.765852	1083.540412	542.273844	6
19	2262.992002	1131.999639	2245.965453	1123.486364	2244.981437	1122.994356	H	***987.508050***	494.257663	970.481501	485.744389	969.497485	485.252381	5
20	2426.055331	1213.531303	2409.028782	1205.018029	2408.044766	1204.526021	Y	***850.449138***	425.728207	833.422589	417.214933	832.438573	416.722925	4
21	2527.103010	1264.055143	2510.076461	1255.541868	2509.092445	1255.049860	T	687.385809	344.196543	670.359260	335.683268	669.375244	335.191260	3
22	2966.328336	1483.667806	2949.301787	1475.154531	2948.317771	1474.662523	Q	586.338130	293.672703	569.311581	285.159429			2
23							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of WQQGNVFSCSVMHEALHNHYTQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.0	3111.426590	-0.007370	WQQGNVFSCSVMHEALHNHYTQK

Mascot: http://www.matrixscience.com/

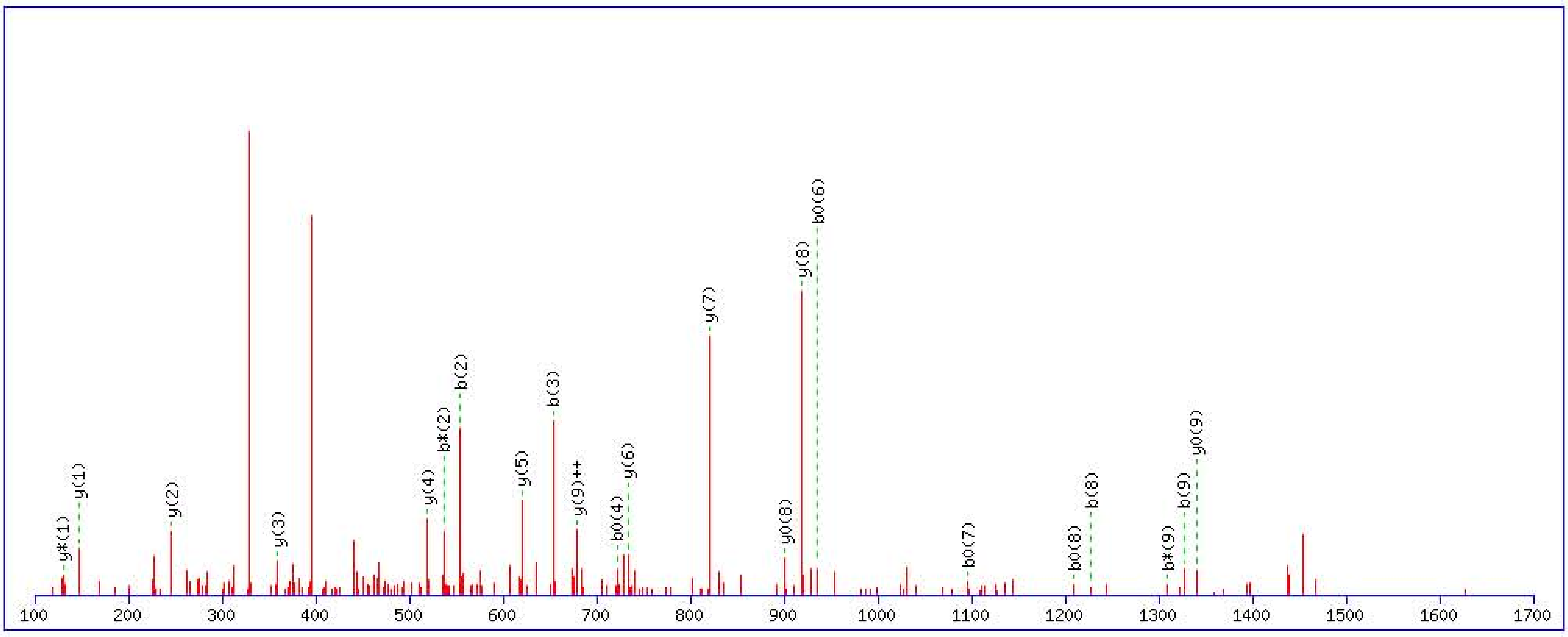
Mascot Search Results

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 26441: 1471.795828 from(736.905190,2+) rtinseconds(2245) index(61966)
Title: Locus:1.1.1.1693.20 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\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 ●



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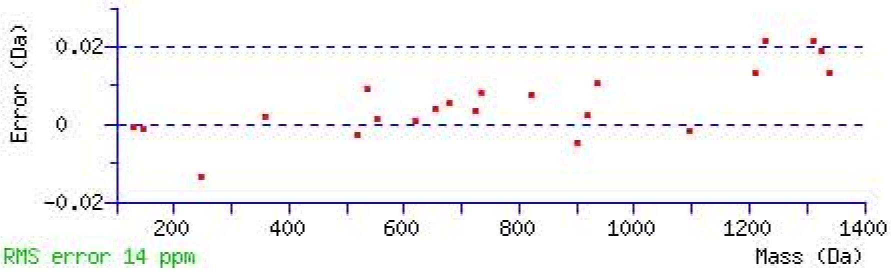
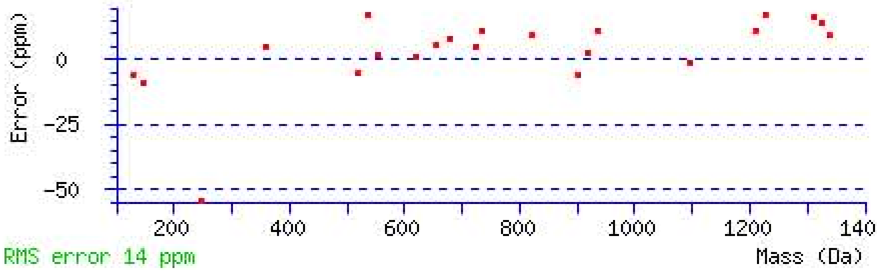
Monoisotopic mass of neutral peptide Mr(calc): 1471.789093
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00024
Matches : 22/94 fragment ions using 42 most intense peaks   (help)
```

#	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
45.5	1471.789093	0.006735	NQVSLTCLVK
6.4	1471.803467	-0.007639	EKQGPLLDLFGQK
5.1	1471.796921	-0.001093	YLIAACQHLQKK
4.1	1471.797592	-0.001764	KYFWDRAFLVK
3.8	1471.777847	0.017981	QLDMELVSVK
3.0	1471.806808	-0.010980	ESLLQIPRIEMK
2.8	1471.793106	0.002722	QPFMVDILAK
2.5	1471.799438	-0.003610	EVELDRLRDTVK
2.2	1471.814713	-0.018885	RQVIVGTWGESLK
0.1	1471.788162	0.007666	ELEAEKLQKEQK

Mascot: http://www.matrixscience.com/

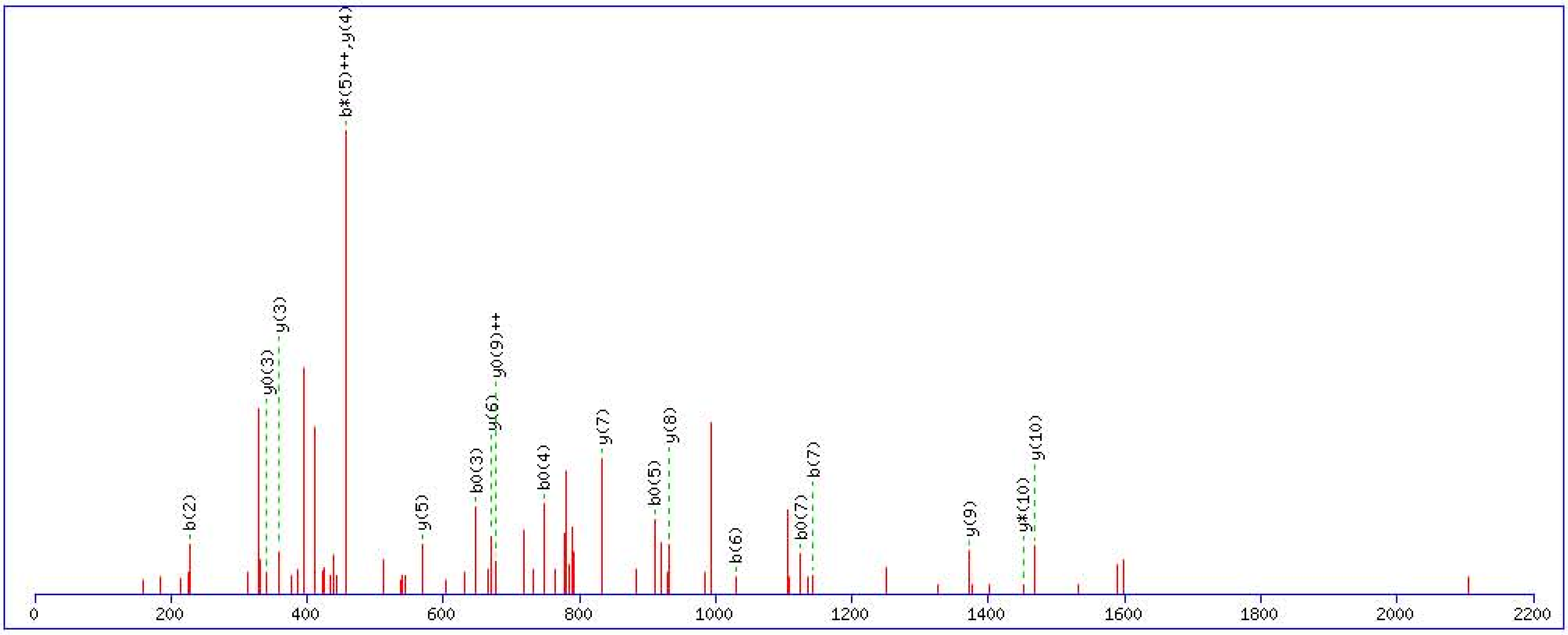
Mascot Search Results

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

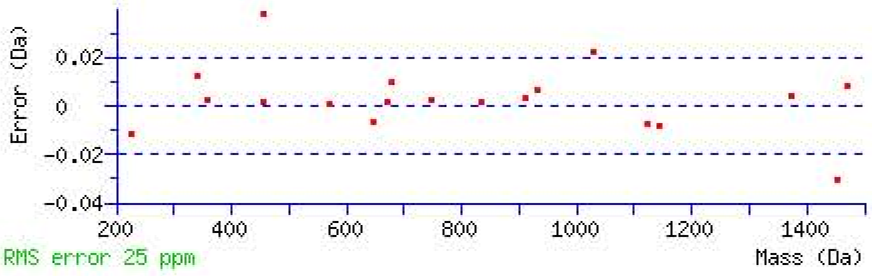
Match to Query 30487: 1596.834408 from(799.424480,2+) rtinseconds(2036) index(60816)
Title: Locus:1.1.1.1620.15 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

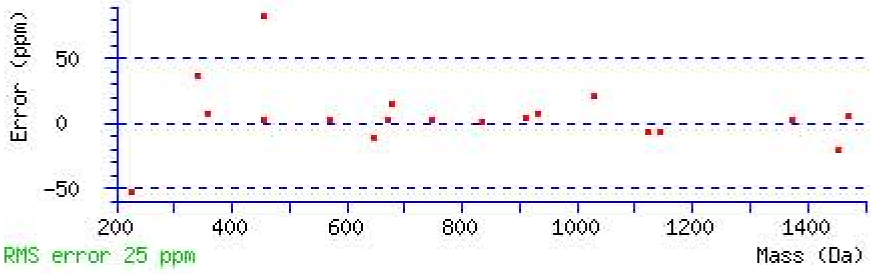
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1596.833389
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 33 **Expect:** 0.0012
Matches : 19/114 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	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
33.3	1596.833389	0.001019	EPQVYTLPPSR
2.3	1596.818115	0.016293	QEPEEKVVSNK
0.7	1596.851135	-0.016727	LLFHGENIEALDKV

Mascot: http://www.matrixscience.com/

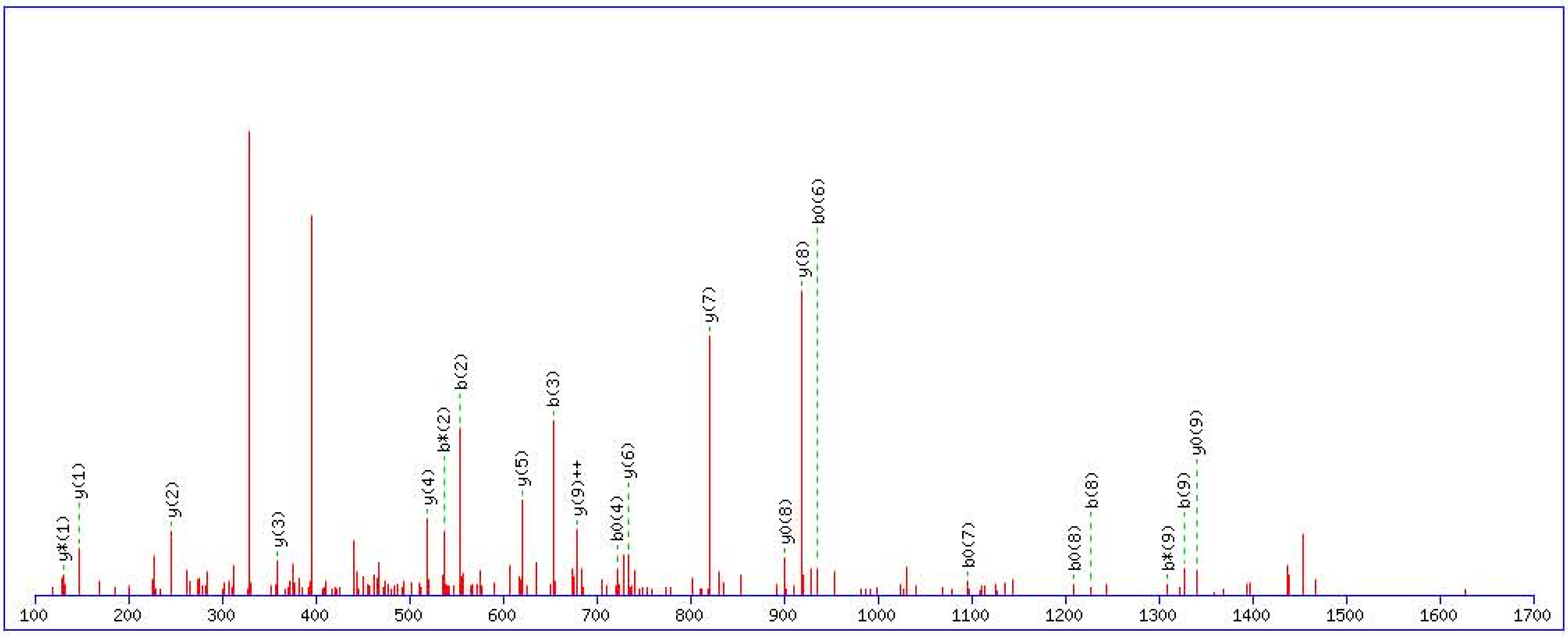
Mascot Search Results

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

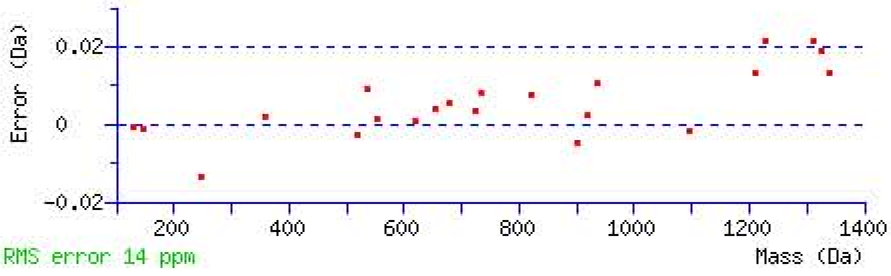
Match to Query 26441: 1471.795828 from(736.905190,2+) rtinseconds(2245) index(61966)
Title: Locus:1.1.1.1693.20 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

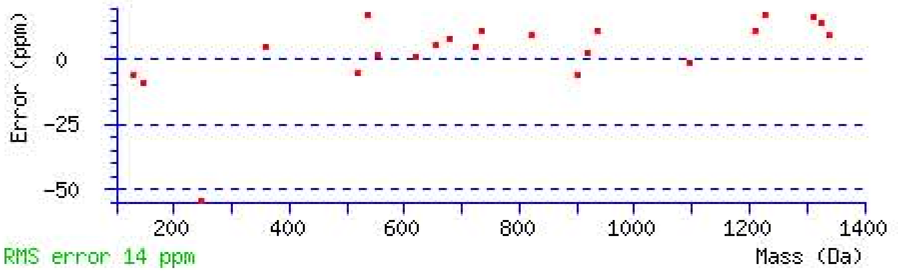
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1471.789093
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00024
Matches : 22/94 fragment ions using 42 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							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
45.5	1471.789093	0.006735	NQVSLTCLVK
6.4	1471.803467	-0.007639	EKQGPLLDLFGQK
5.1	1471.796921	-0.001093	YLIAACQHLQKK
4.1	1471.797592	-0.001764	KYFWDRAFLVK
3.8	1471.777847	0.017981	QLDMELVSVK
3.0	1471.806808	-0.010980	ESLLQIPRIEMK
2.8	1471.793106	0.002722	QPFMVDILAK
2.5	1471.799438	-0.003610	EVELDRLRDTVK
2.2	1471.814713	-0.018885	RQVIVGTWGESLK
0.1	1471.788162	0.007666	ELEAEKLQKEQK

Mascot: http://www.matrixscience.com/

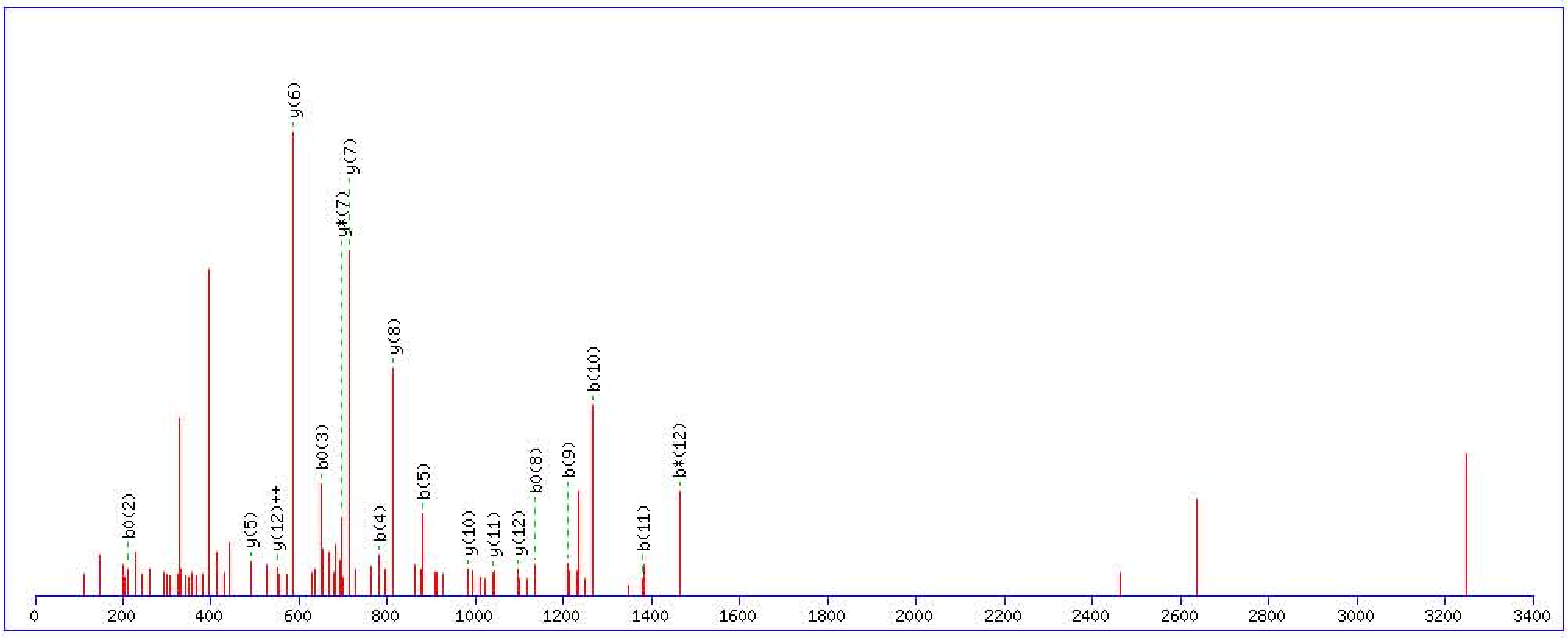
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVQLVESGGGLVQPGGSLR**
Found in **HV305_HUMAN**, Ig heavy chain V-III region BRO OS=Homo sapiens PE=1 SV=1

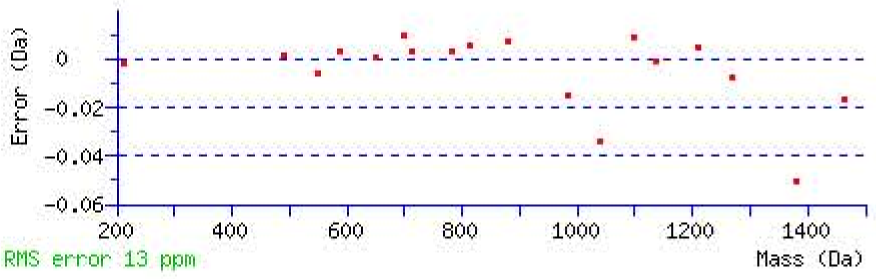
Match to Query 43131: 2192.151792 from(731.724540,3+) rtinseconds(2236) index(33283)
Title: Locus:1.1.1.3442.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

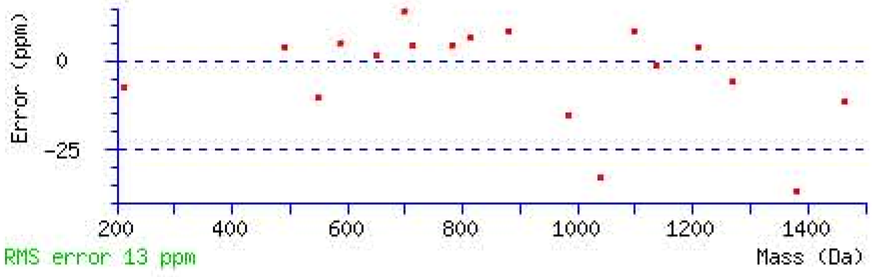
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2192.162354
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.0018
Matches : 18/208 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	130.049869	65.528572			112.039304	56.523290	E							19
2	229.118283	115.062780			211.107718	106.057497	V	2064.127023	1032.567149	2047.100474	1024.053875	2046.116458	1023.561867	18
3	668.343609	334.675443	651.317060	326.162168	650.333044	325.670160	Q	1965.058609	983.032942	1948.032060	974.519668	1947.048044	974.027660	17
4	***781.427673***	391.217475	764.401124	382.704200	763.417108	382.212192	L	1525.833283	763.420279	1508.806734	754.907005	1507.822718	754.414997	16
5	***880.496087***	440.751682	863.469538	432.238407	862.485522	431.746399	V	1412.749219	706.878248	1395.722670	698.364973	1394.738654	697.872965	15
6	1009.538680	505.272978	992.512131	496.759704	991.528115	496.267696	E	1313.680805	657.344041	1296.654256	648.830766	1295.670240	648.338758	14
7	1096.570708	548.788992	1079.544159	540.275718	1078.560143	539.783709	S	1184.638212	592.822744	1167.611663	584.309470	1166.627647	583.817462	13
8	1153.592172	577.299724	1136.565623	568.786450	1135.581607	568.294441	G	***1097.606184***	549.306730	1080.579635	540.793456	1079.595619	540.301447	12
9	***1210.613636***	605.810456	1193.587087	597.297181	1192.603071	596.805173	G	***1040.584720***	520.795998	1023.558171	512.282723	1022.574155	511.790716	11
10	***1267.635100***	634.321188	1250.608551	625.807913	1249.624535	625.315905	G	***983.563256***	492.285266	966.536707	483.771992	965.552691	483.279984	10
11	***1380.719164***	690.863220	1363.692615	682.349945	1362.708599	681.857937	L	926.541792	463.774534	909.515243	455.261260	908.531227	454.769252	9
12	1479.787578	740.397427	1462.761029	731.884152	1461.777013	731.392144	V	***813.457728***	407.232502	796.431179	398.719228	795.447163	398.227220	8
13	1607.846156	804.426716	1590.819607	795.913441	1589.835591	795.421433	Q	***714.389314***	357.698295	697.362765	349.185021	696.378749	348.693013	7
14	1704.898920	852.953098	1687.872371	844.439823	1686.888355	843.947815	P	***586.330736***	293.669006	569.304187	285.155732	568.320171	284.663724	6
15	1761.920384	881.463830	1744.893835	872.950555	1743.909819	872.458547	G	***489.277972***	245.142624	472.251423	236.629349	471.267407	236.137341	5
16	1818.941848	909.974562	1801.915299	901.461287	1800.931283	900.969279	G	432.256508	216.631892	415.229959	208.118618	414.245943	207.626610	4
17	1905.973876	953.490576	1888.947327	944.977301	1887.963311	944.485293	S	375.235044	188.121160	358.208495	179.607886	357.224479	179.115878	3
18	2019.057940	1010.032608	2002.031391	1001.519333	2001.047375	1001.027325	L	288.203016	144.605146	271.176467	136.091872			2
19							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of EVQLVESGGGLVQPGGSLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.4	2192.162354	-0.010562	EVQLVESGGGLVQPGGSLR
1.0	2192.131516	0.020276	CRQQRQQQK
1.0	2192.131516	0.020276	CRQQRQQQK
1.0	2192.131516	0.020276	CRQQRQQQK
1.0	2192.138031	0.013761	NQQTNDRKQK
0.2	2192.180908	-0.029116	IEEERLRLEQQK

Mascot: http://www.matrixscience.com/

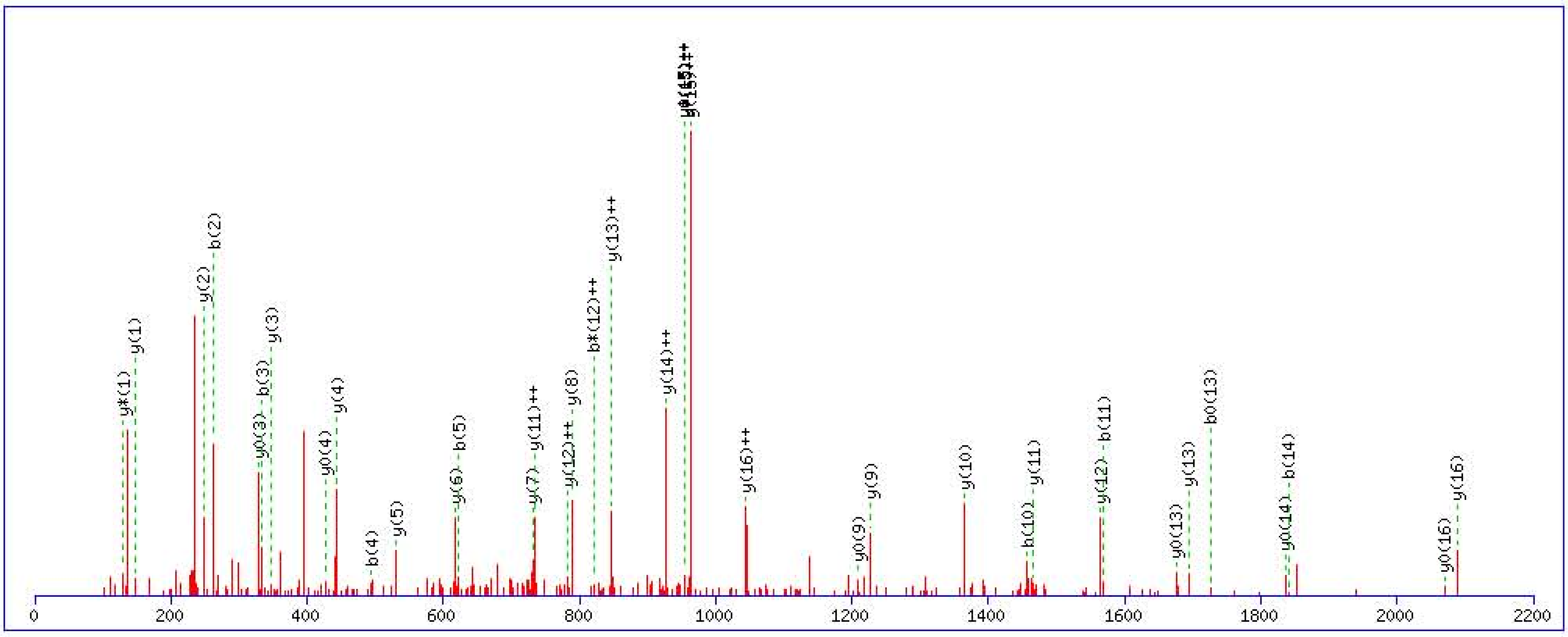
{MATRIX SCIENCE} Mascot Search Results

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

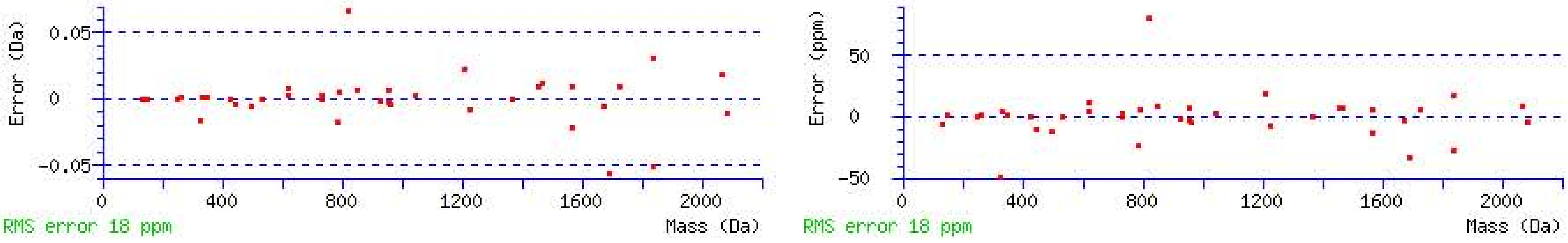
Match to Query 43031: 2186.080152 from(729.700660,3+) rtinseconds(1798) index(30587)
Title: Locus:1.1.1.3289.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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: 58  Expect: 4.2e-005
Matches : 38/166 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	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
58.1	2186.086411	-0.006259	VYACEVTHQGLSSPVTK

Mascot: http://www.matrixscience.com/

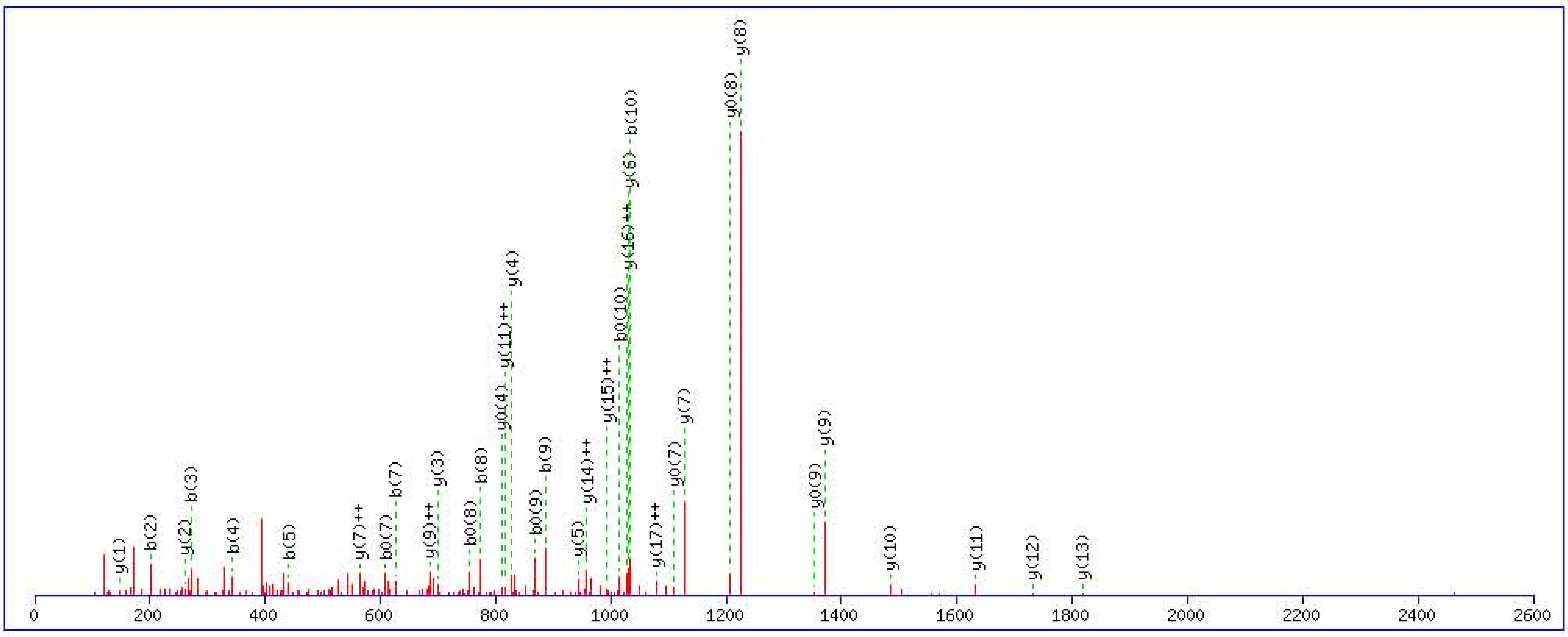
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVAAPSVFIFPPSDEQLK**
Found in **IGKC_HUMAN**, Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1

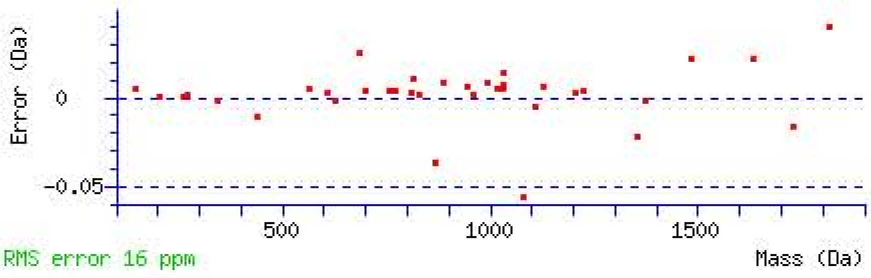
Match to Query 44190: 2256.185472 from(753.069100,3+) rtinseconds(2683) index(35694)
Title: Locus:1.1.1.3597.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

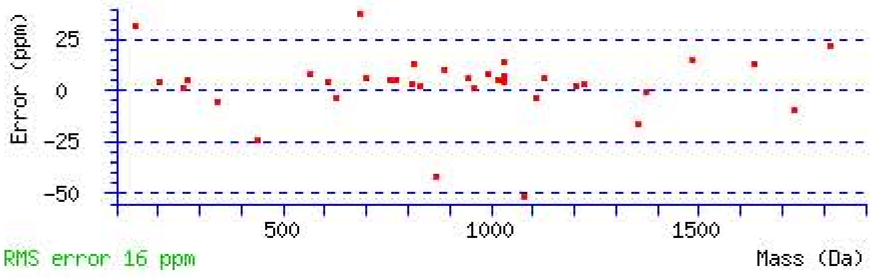
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2256.186432
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16    : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 8e-006
Matches : 36/168 fragment ions using 97 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							18
2	**201.123369**	101.065322			183.112804	92.060040	V	2156.146026	1078.576651	2139.119477	1070.063377	2138.135461	1069.571369	17
3	**272.160483**	136.583879			254.149918	127.578597	A	2057.077612	1029.042444	2040.051063	1020.529170	2039.067047	1020.037162	16
4	**343.197597**	172.102437			325.187032	163.097154	A	1986.040498	993.523887	1969.013949	985.010613	1968.029933	984.518605	15
5	**440.250361**	220.628819			422.239796	211.623536	P	1915.003384	958.005330	1897.976835	949.492056	1896.992819	949.000048	14
6	527.282389	264.144833			509.271824	255.139550	S	***1817.950620***	909.478948	1800.924071	900.965674	1799.940055	900.473666	13
7	**626.350803**	313.679040			608.340238	304.673757	V	***1730.918592***	865.962934	1713.892043	857.449660	1712.908027	856.957652	12
8	**773.419217**	387.213247			755.408652	378.207964	F	***1631.850178***	816.428727	1614.823629	807.915453	1613.839613	807.423445	11
9	**886.503281**	443.755279			868.492716	434.749996	I	***1484.781764***	742.894520	1467.755215	734.381246	1466.771199	733.889238	10
10	**1033.571695**	517.289486			1015.561130	508.284203	F	***1371.697700***	686.352488	1354.671151	677.839214	1353.687135	677.347206	9
11	1130.624459	565.815868			1112.613894	556.810585	P	***1224.629286***	612.818281	1207.602737	604.305007	1206.618721	603.812999	8
12	1227.677223	614.342250			1209.666658	605.336967	P	***1127.576522***	564.291899	1110.549973	555.778625	1109.565957	555.286617	7
13	1314.709251	657.858264			1296.698686	648.852981	S	***1030.523758***	515.765517	1013.497209	507.252243	1012.513193	506.760235	6
14	1429.736194	715.371735			1411.725629	706.366453	D	***943.491730***	472.249503	926.465181	463.736229	925.481165	463.244221	5
15	1558.778787	779.893032			1540.768222	770.887749	E	***828.464787***	414.736032	811.438238	406.222757	810.454222	405.730749	4
16	1998.004113	999.505695	1980.977564	990.992420	1979.993548	990.500412	Q	***699.422194***	350.214735	682.395645	341.701461			3
17	2111.088177	1056.047727	2094.061628	1047.534452	2093.077612	1047.042444	L	***260.196868***	130.602072	243.170319	122.088798			2
18							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TVAAPSVFIFPPSDEQLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.5	2256.186432	-0.000960	TVAAPSVFIFPPSDEQLK
0.1	2256.171860	0.013612	QVVCDLGNPMKAGTQLLAGLR

Mascot: http://www.matrixscience.com/

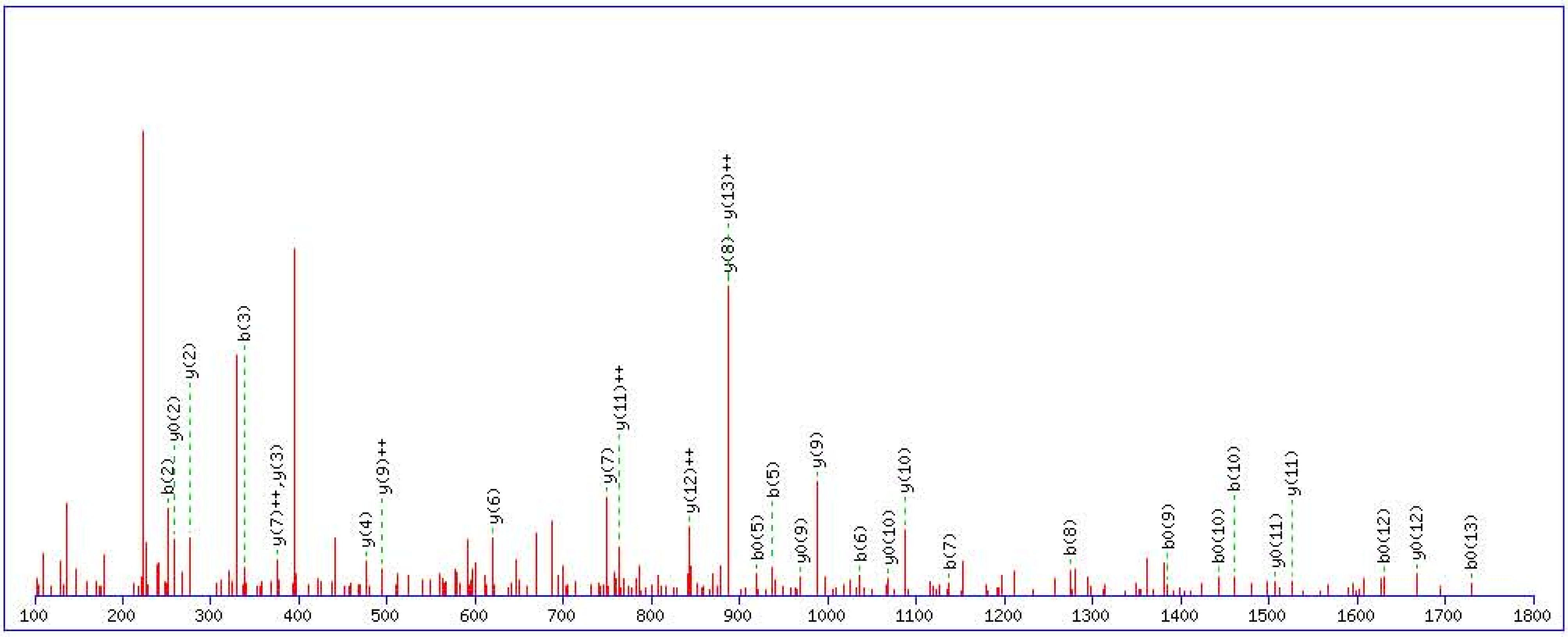
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SYSCQVTHEGSTVEK**
Found in **IGLL5_HUMAN**, Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2

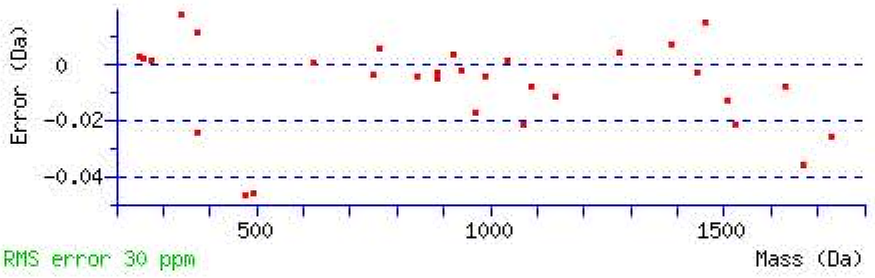
Match to Query 40228: 2021.908932 from(674.976920,3+) rtinseconds(1453) index(15568)
Title: Locus:1.1.1.3071.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

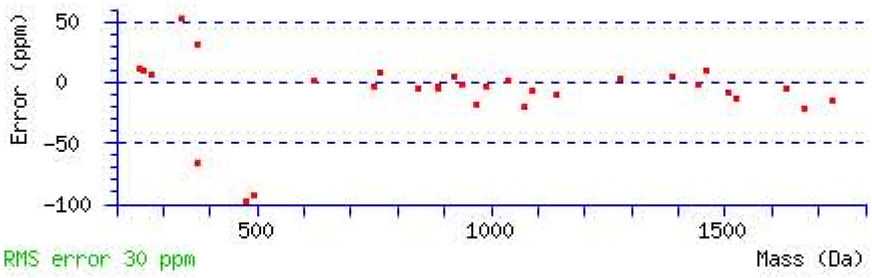
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2021.918671
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0026
Matches : 31/158 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	88.039304	44.523290			70.028739	35.518008	S							15
2	***251.102633***	126.054954			233.092068	117.049672	Y	1935.893912	968.450594	1918.867363	959.937320	1917.883347	959.445312	14
3	***338.134661***	169.570968			320.124096	160.565686	S	1772.830583	886.918930	1755.804034	878.405655	1754.820018	877.913647	13
4	498.165310	249.586293			480.154745	240.581011	C	1685.798555	843.402916	1668.772006	834.889641	1667.787990	834.397633	12
5	***937.390636***	469.198956	920.364087	460.685682	919.380071	460.193674	Q	***1525.767906***	763.387591	1508.741357	754.874317	1507.757341	754.382309	11
6	***1036.459050***	518.733163	1019.432501	510.219889	1018.448485	509.727881	V	***1086.542580***	543.774928	1069.516031	535.261654	1068.532015	534.769646	10
7	***1137.506729***	569.257003	1120.480180	560.743728	1119.496164	560.251720	T	***987.474166***	494.240721	970.447617	485.727447	969.463601	485.235439	9
8	***1274.565641***	637.786459	1257.539092	629.273184	1256.555076	628.781176	H	***886.426487***	443.716882	869.399938	435.203607	868.415922	434.711599	8
9	1403.608234	702.307755	1386.581685	693.794481	1385.597669	693.302473	E	***749.367575***	375.187426	732.341026	366.674151	731.357010	366.182143	7
10	***1460.629698***	730.818487	1443.603149	722.305213	1442.619133	721.813204	G	***620.324982***	310.666129	603.298433	302.152855	602.314417	301.660847	6
11	1547.661726	774.334501	1530.635177	765.821227	1529.651161	765.329219	S	563.303518	282.155397	546.276969	273.642123	545.292953	273.150115	5
12	1648.709405	824.858341	1631.682856	816.345066	1630.698840	815.853058	T	***476.271490***	238.639383	459.244941	230.126109	458.260925	229.634101	4
13	1747.777819	874.392548	1730.751270	865.879273	1729.767254	865.387265	V	***375.223811***	188.115544	358.197262	179.602269	357.213246	179.110261	3
14	1876.820412	938.913844	1859.793863	930.400570	1858.809847	929.908562	E	***276.155397***	138.581337	259.128848	130.068062	258.144832	129.576054	2
15							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SYSCQVTHEGSTVEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.4	2021.918671	-0.009739	SYSCQVTHEGSTVEK

Mascot: http://www.matrixscience.com/

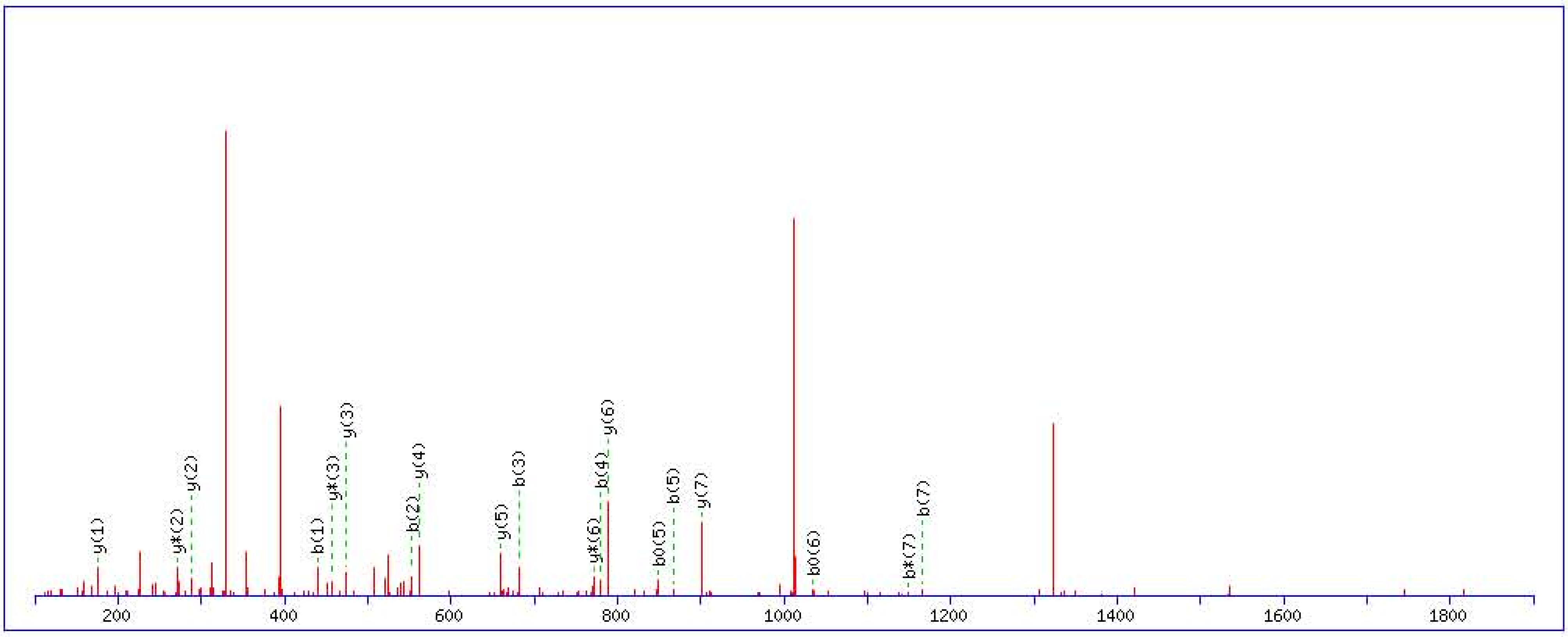
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QIQVSWLR**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

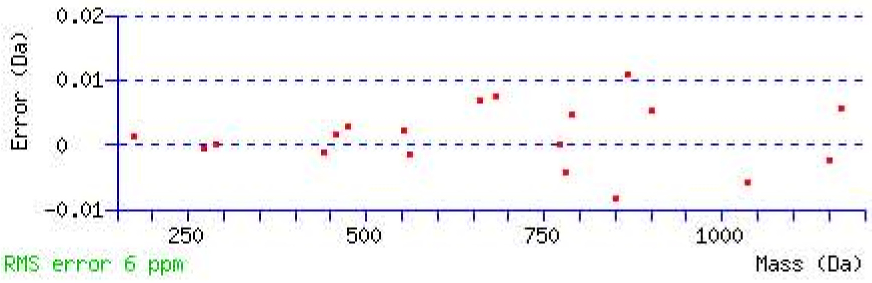
Match to Query 21116: 1339.740388 from(670.877470,2+) rtinseconds(2362) index(33882)
Title: Locus:1.1.1.3486.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

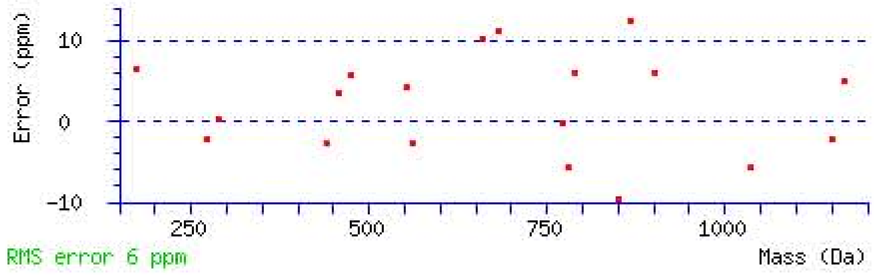
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1339.743454
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.035
Matches : 19/70 fragment ions using 48 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			I	***901.525413***	451.266344	884.498864	442.753070	883.514848	442.261062	7
3	**681.375244**	341.191260	664.348695	332.677986			Q	***788.441349***	394.724312	771.414800	386.211038	770.430784	385.719030	6
4	**780.443658**	390.725467	763.417109	382.212193			V	***660.382771***	330.695023	643.356222	322.181749	642.372206	321.689741	5
5	**867.475686**	434.241481	850.449137	425.728207	849.465121	425.236199	S	***561.314357***	281.160816	544.287808	272.647542	543.303792	272.155534	4
6	1053.554999	527.281138	1036.528450	518.767863	1035.544434	518.275855	W	***474.282329***	237.644802	457.255780	229.131528			3
7	**1166.639063**	583.823169	1149.612514	575.309895	1148.628498	574.817887	L	***288.203016***	144.605146	271.176467	136.091871			2
8							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of QIQVSWLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.8	1339.743454	-0.003066	QIQVSWLR
11.4	1339.753326	-0.012938	QLQISIAEK
11.3	1339.739426	0.000962	QLLRTDQR
11.3	1339.739410	0.000978	QLNRLETR
10.3	1339.735596	0.004792	QLQVAMPVK
8.8	1339.743454	-0.003066	QIQVSWLR
6.5	1339.739395	0.000993	QLAEKERR
6.5	1339.743439	-0.003051	QLSWLINR
6.5	1339.743454	-0.003066	QLTWLVNR
6.2	1339.728180	0.012208	IQQIEKDR

Mascot: http://www.matrixscience.com/

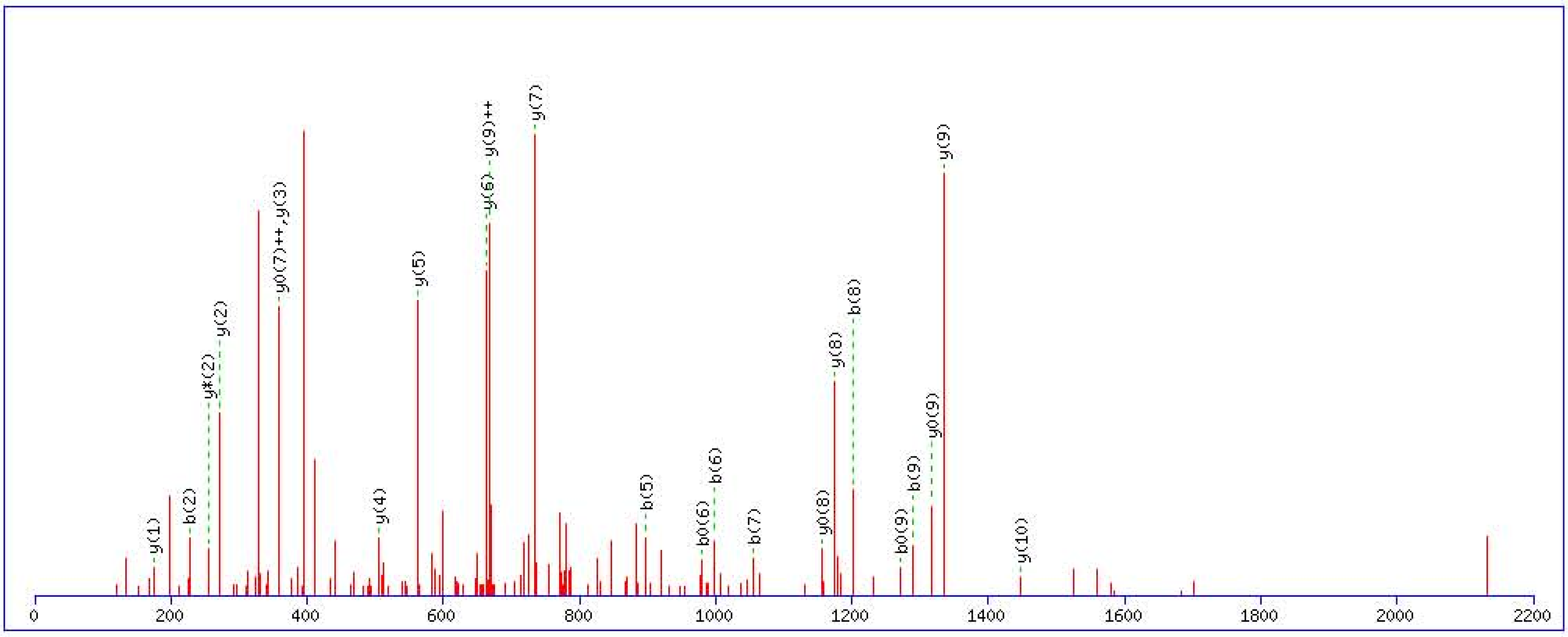
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LICQATGFSPR**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

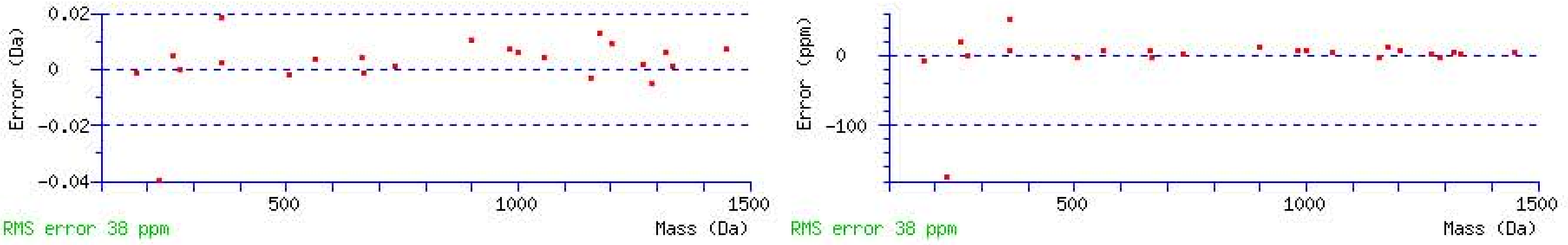
Match to Query 28738: 1559.793348 from(780.903950,2+) rtinseconds(2012) index(31987)
Title: Locus:1.1.1.3364.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 1559.795242
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 66 **Expect:** 4.8e-006
Matches : 23/100 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	114.091340	57.549308					L							11
2	**227.175404**	114.091340					I	***1447.718454***	724.362865	1430.691905	715.849591	1429.707889	715.357583	10
3	387.206053	194.106664					C	***1334.634390***	667.820833	1317.607841	659.307559	1316.623825	658.815551	9
4	826.431379	413.719328	809.404830	405.206053			Q	***1174.603741***	587.805509	1157.577192	579.292234	1156.593176	578.800226	8
5	**897.468493**	449.237885	880.441944	440.724610			A	***735.378415***	368.192846	718.351866	359.679571	717.367850	359.187563	7
6	**998.516172**	499.761724	981.489623	491.248449	980.505607	490.756441	T	***664.341301***	332.674289	647.314752	324.161014	646.330736	323.669006	6
7	**1055.537636**	528.272456	1038.511087	519.759182	1037.527071	519.267174	G	***563.293622***	282.150449	546.267073	273.637175	545.283057	273.145167	5
8	**1202.606050**	601.806663	1185.579501	593.293389	1184.595485	592.801381	F	***506.272158***	253.639717	489.245609	245.126443	488.261593	244.634435	4
9	**1289.638078**	645.322677	1272.611529	636.809403	1271.627513	636.317395	S	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
10	1386.690842	693.849059	1369.664293	685.335785	1368.680277	684.843777	P	***272.171716***	136.589496	255.145167	128.076221			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1



NCBI **BLAST** search of LICQATGFSPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.1	1559.795242	-0.001894	LICQATGFSPR
8.9	1559.808960	-0.015612	LDRLSGLADQMVAR
3.3	1559.770081	0.023267	ARCEVQFSPR
2.5	1559.808975	-0.015627	LLDRDACDTVRVK
1.7	1559.787827	0.005521	SLHPAMLPAADGAGPR

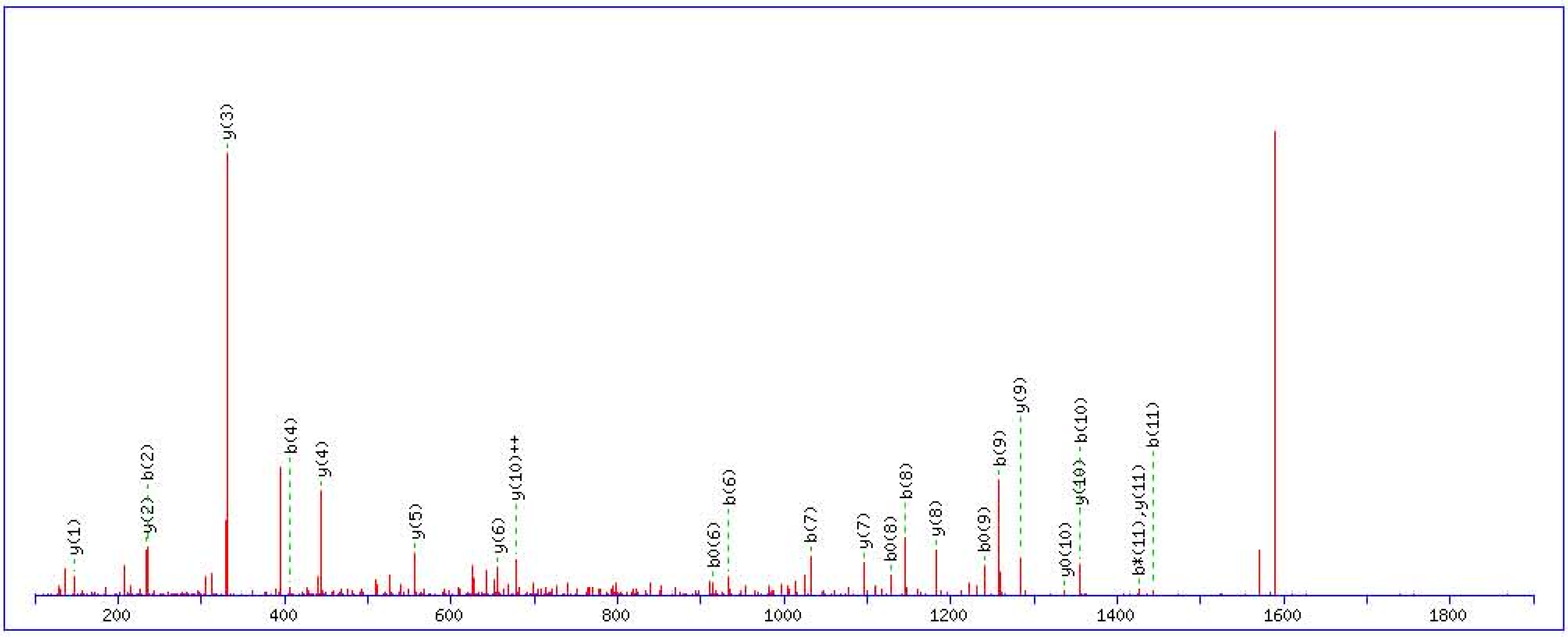
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YAATSQVLLPSK**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

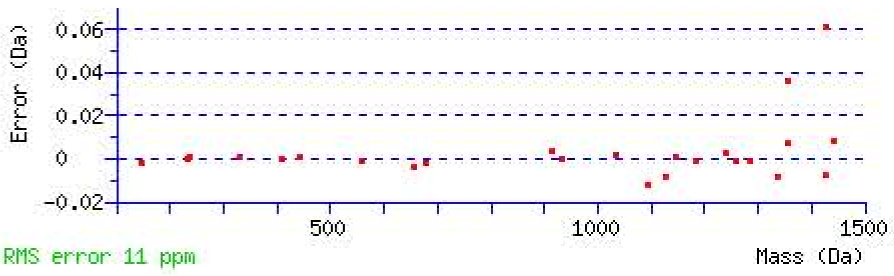
Match to Query 30020: 1587.867628 from(794.941090,2+) rtinseconds(2059) index(32220)
Title: Locus:1.1.1.3380.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

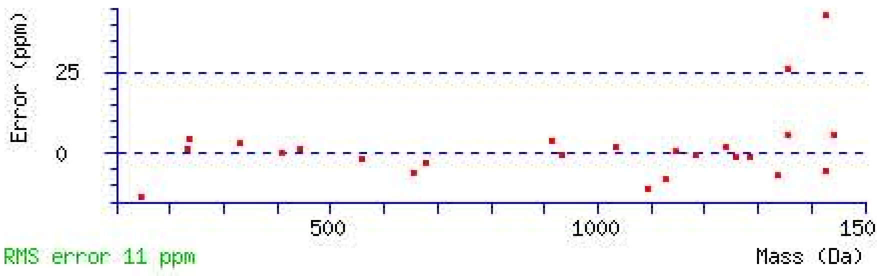
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1587.869431
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 72  Expect: 1.3e-006
Matches : 25/114 fragment ions using 45 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	**235.107719**	118.057498					A	***1425.813399***	713.410337	1408.786850	704.897063	1407.802834	704.405055	11
3	306.144833	153.576055					A	***1354.776285***	677.891780	1337.749736	669.378506	1336.765720	668.886498	10
4	**407.192512**	204.099894			389.181947	195.094612	T	***1283.739171***	642.373223	1266.712622	633.859949	1265.728606	633.367941	9
5	494.224540	247.615908			476.213975	238.610626	S	***1182.691492***	591.849384	1165.664943	583.336110	1164.680927	582.844101	8
6	**933.449866**	467.228571	916.423317	458.715297	915.439301	458.223289	Q	***1095.659464***	548.333370	1078.632915	539.820096	1077.648899	539.328088	7
7	**1032.518280**	516.762778	1015.491731	508.249504	1014.507715	507.757496	V	***656.434138***	328.720707	639.407589	320.207432	638.423573	319.715424	6
8	**1145.602344**	573.304810	1128.575795	564.791536	1127.591779	564.299527	L	***557.365724***	279.186500	540.339175	270.673226	539.355159	270.181218	5
9	**1258.686408**	629.846842	1241.659859	621.333567	1240.675843	620.841559	L	***444.281660***	222.644468	427.255111	214.131193	426.271095	213.639186	4
10	**1355.739172**	678.373224	1338.712623	669.859949	1337.728607	669.367941	P	***331.197596***	166.102436	314.171047	157.589162	313.187031	157.097154	3
11	**1442.771200**	721.889238	1425.744651	713.375964	1424.760635	712.883955	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
12							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of YAATSQVLLPSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
72.4	1587.869431	-0.001803	YAATSQVLLPSK
14.9	1587.862045	0.005583	VTGQNQEQFLLLAK
10.4	1587.862045	0.005583	DGASLSPATLFIQIR
5.5	1587.874603	-0.006975	SFAFRSAIIQHRR
4.8	1587.891220	-0.023592	TIQTIVFLYSLYK
4.8	1587.862030	0.005598	EDAKLSFKHVSSLK
4.6	1587.858002	0.009626	LSQEQTLQALRSSK
4.5	1587.846802	0.020826	KSDIDEIVLVGGSTR
3.7	1587.890533	-0.022905	EPTTKAEMLKIISK
3.5	1587.865402	0.002226	ENGLRDILAVLTMK

Mascot: http://www.matrixscience.com/

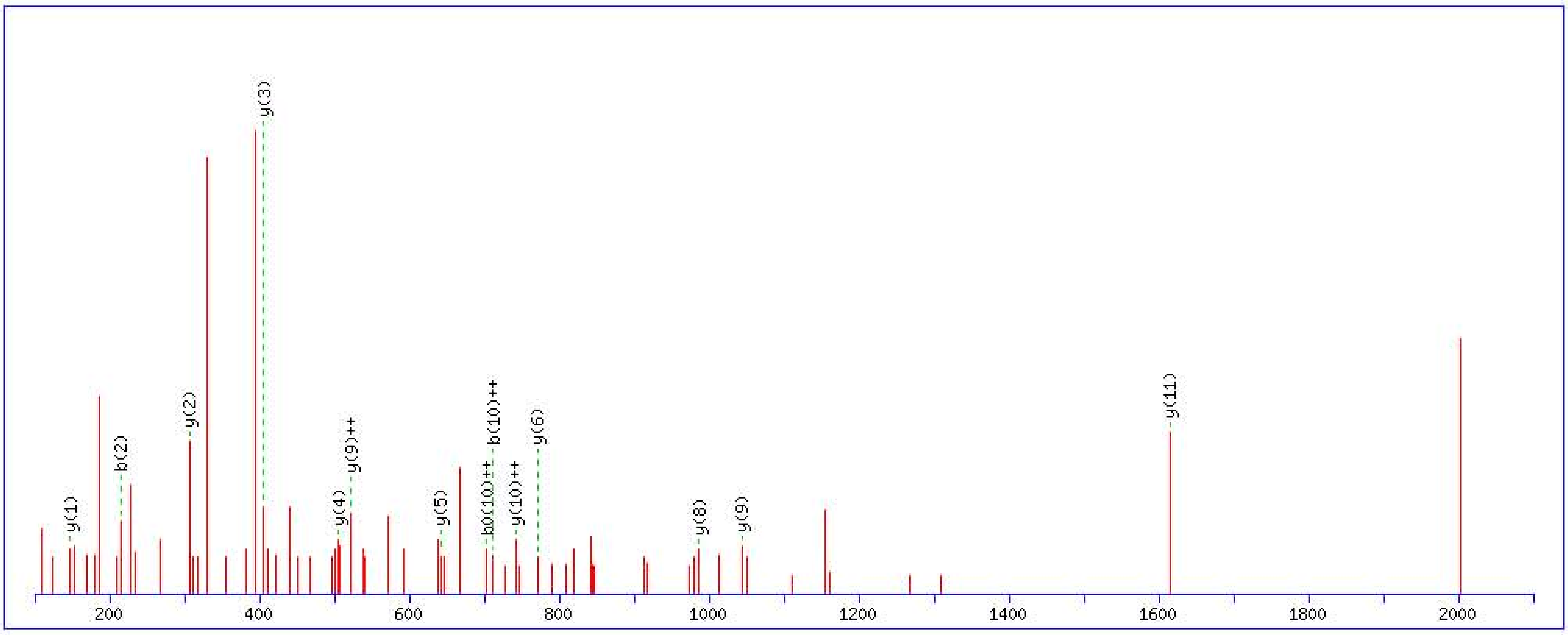
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DVMQGTDEHVVCK**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

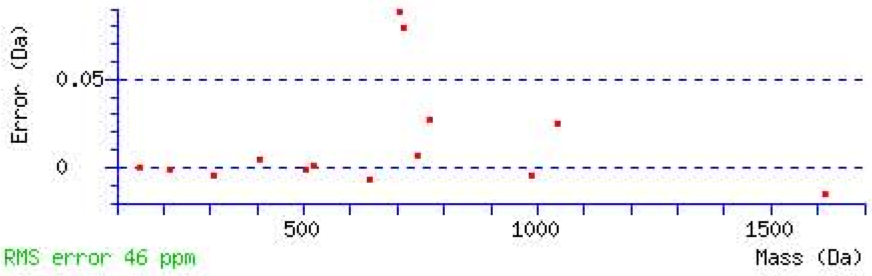
Match to Query 36287: 1827.822822 from(610.281550,3+) rtinseconds(1652) index(29794)
Title: Locus:1.1.1.3238.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

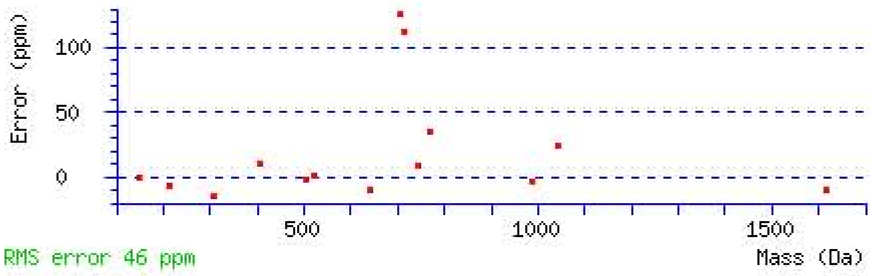
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1827.831787
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 25  Expect: 0.029
Matches : 14/128 fragment ions using 45 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	215.102633	108.054954			197.092068	99.049672	V	1713.812097	857.409687	1696.785548	848.896412	1695.801532	848.404404	12
3	346.143118	173.575197			328.132553	164.569915	M	***1614.743683***	807.875480	1597.717134	799.362205	1596.733118	798.870197	11
4	785.368444	393.187860	768.341895	384.674586	767.357879	384.182578	Q	1483.703198	742.355237	1466.676649	733.841963	1465.692633	733.349955	10
5	842.389908	421.698592	825.363359	413.185318	824.379343	412.693310	G	***1044.477872***	522.742574	1027.451323	514.229300	1026.467307	513.737292	9
6	943.437587	472.222432	926.411038	463.709157	925.427022	463.217149	T	***987.456408***	494.231842	970.429859	485.718568	969.445843	485.226560	8
7	1058.464530	529.735903	1041.437981	521.222629	1040.453965	520.730621	D	886.408729	443.708003	869.382180	435.194728	868.398164	434.702720	7
8	1187.507123	594.257200	1170.480574	585.743925	1169.496558	585.251917	E	***771.381786***	386.194531	754.355237	377.681257	753.371221	377.189249	6
9	1324.566035	662.786656	1307.539486	654.273381	1306.555470	653.781373	H	***642.339193***	321.673235	625.312644	313.159960			5
10	1423.634449	712.320863	1406.607900	703.807588	1405.623884	703.315580	V	***505.280281***	253.143779	488.253732	244.630504			4
11	1522.702863	761.855070	1505.676314	753.341795	1504.692298	752.849787	V	***406.211867***	203.609572	389.185318	195.096297			3
12	1682.733512	841.870394	1665.706963	833.357120	1664.722947	832.865112	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 DVMQGTDEHVVCK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.0	1827.831787	-0.008965	DVMQGTDEHVVCK

Mascot: http://www.matrixscience.com/

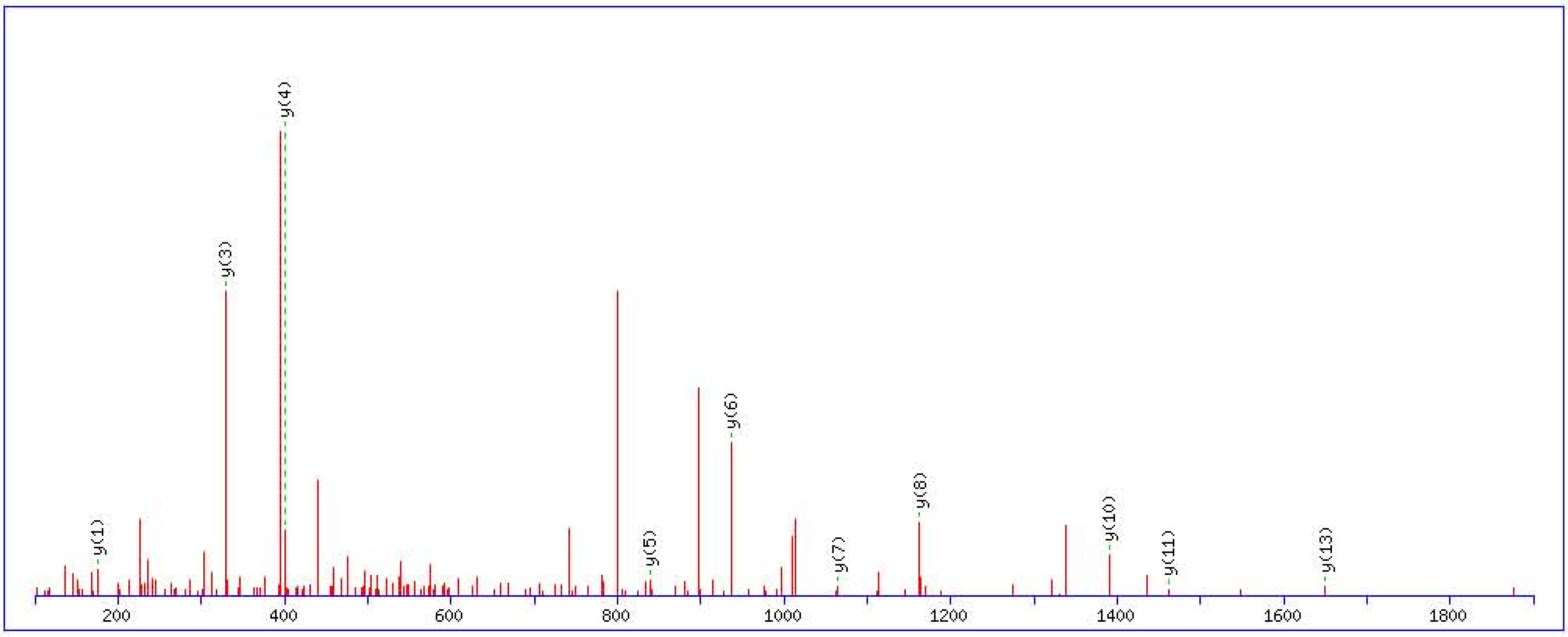
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YVTSAPMPEPQAPGR**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

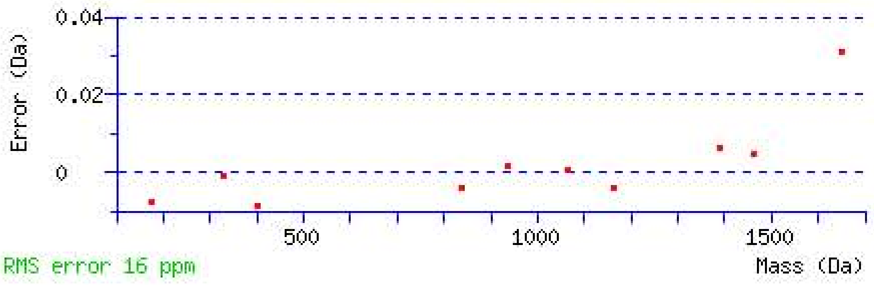
Match to Query 37641: 1910.930802 from(637.984210,3+) rtinseconds(1900) index(31109)
Title: Locus:1.1.1.3325.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

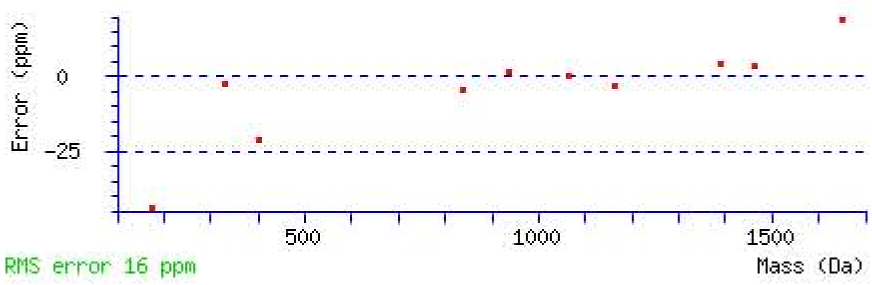
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1910.938263
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.02
Matches : 10/132 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	164.070605	82.538940					Y							15
2	263.139019	132.073148					V	1748.882225	874.944750	1731.855676	866.431476	1730.871660	865.939468	14
3	364.186698	182.596987			346.176133	173.591705	T	***1649.813811***	825.410543	1632.787262	816.897269	1631.803246	816.405261	13
4	451.218726	226.113001			433.208161	217.107719	S	1548.766132	774.886704	1531.739583	766.373430	1530.755567	765.881421	12
5	522.255840	261.631558			504.245275	252.626276	A	***1461.734104***	731.370690	1444.707555	722.857416	1443.723539	722.365407	11
6	619.308604	310.157940			601.298039	301.152658	P	***1390.696990***	695.852133	1373.670441	687.338859	1372.686425	686.846850	10
7	750.349089	375.678183			732.338524	366.672900	M	1293.644226	647.325751	1276.617677	638.812477	1275.633661	638.320468	9
8	847.401853	424.204565			829.391288	415.199282	P	***1162.603741***	581.805508	1145.577192	573.292234	1144.593176	572.800226	8
9	976.444446	488.725861			958.433881	479.720579	E	***1065.550977***	533.279126	1048.524428	524.765852	1047.540412	524.273844	7
10	1073.497210	537.252243			1055.486645	528.246961	P	***936.508384***	468.757830	919.481835	460.244555			6
11	1512.722536	756.864906	1495.695987	748.351632	1494.711971	747.859624	Q	***839.455620***	420.231448	822.429071	411.718173			5
12	1583.759650	792.383463	1566.733101	783.870189	1565.749085	783.378180	A	***400.230294***	200.618785	383.203745	192.105510			4
13	1680.812414	840.909845	1663.785865	832.396571	1662.801849	831.904563	P	***329.193180***	165.100228	312.166631	156.586953			3
14	1737.833878	869.420577	1720.807329	860.907303	1719.823313	860.415294	G	232.140416	116.573846	215.113867	108.060571			2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of YVTSAPMPEPQAPGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.6	1910.938263	-0.007461	YVTSAPMPEPQAPGR
22.6	1910.934265	-0.003463	SGSDEVQVGQQR
22.6	1910.934265	-0.003463	SGSDEVQVGQQR

Mascot: http://www.matrixscience.com/

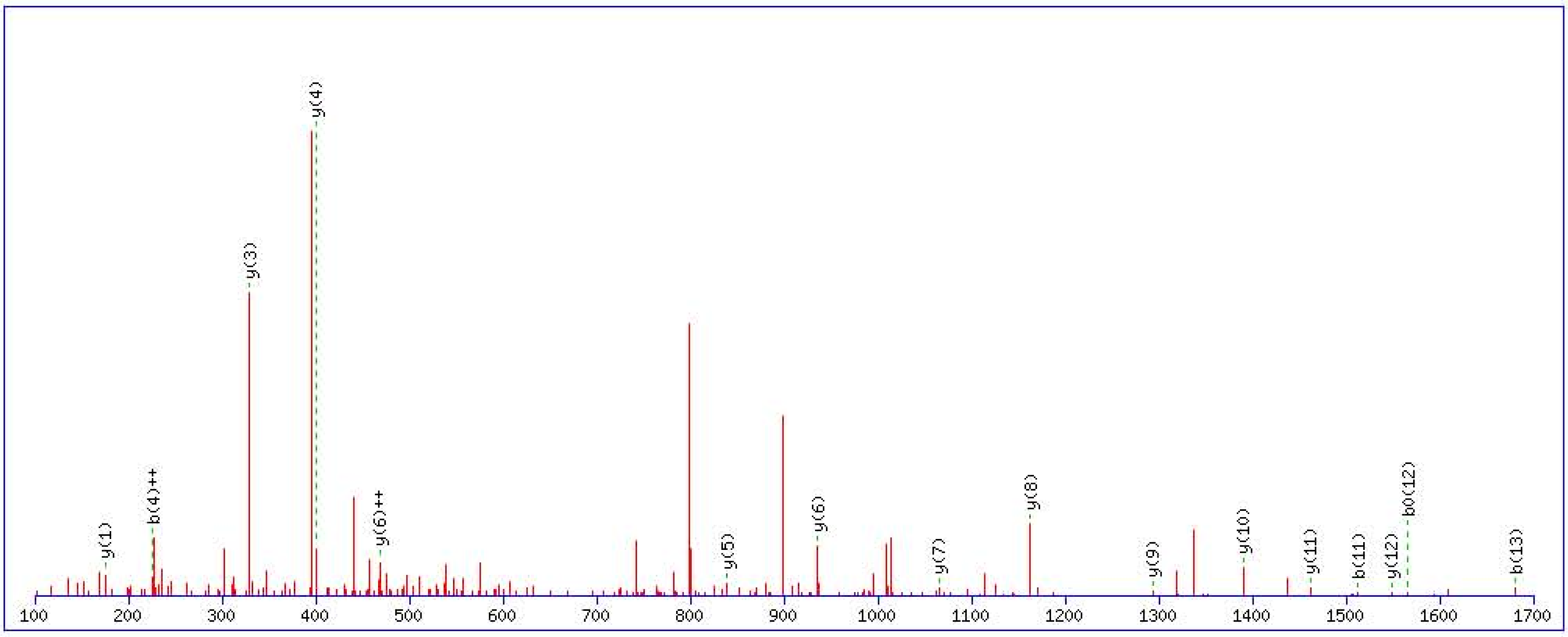
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YVTSAPMPEPQAPGR**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

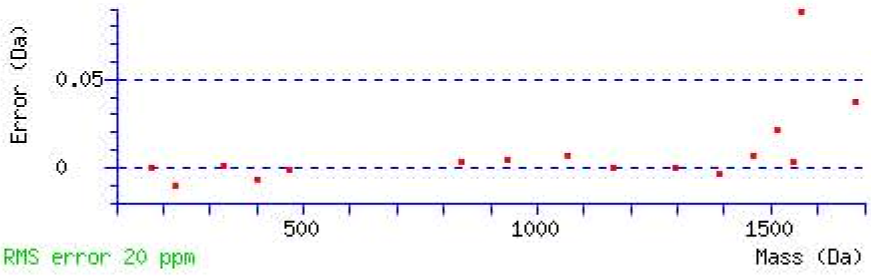
Match to Query 37642: 1910.930802 from(637.984210,3+) rtinseconds(1891) index(31052)
Title: Locus:1.1.1.3322.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

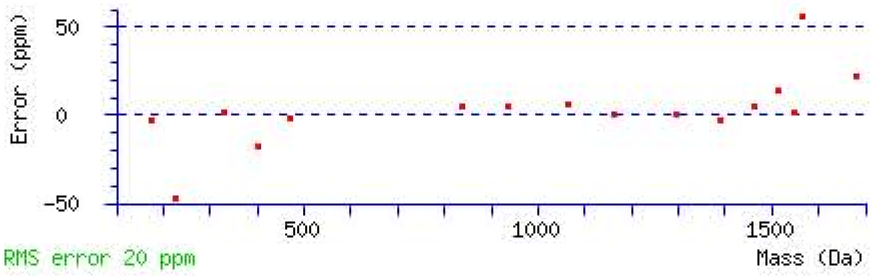
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1910.938263
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 33 **Expect:** 0.012
Matches : 16/132 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	164.070605	82.538940					Y							15
2	263.139019	132.073148					V	1748.882225	874.944750	1731.855676	866.431476	1730.871660	865.939468	14
3	364.186698	182.596987			346.176133	173.591705	T	1649.813811	825.410543	1632.787262	816.897269	1631.803246	816.405261	13
4	451.218726	226.113001			433.208161	217.107719	S	***1548.766132***	774.886704	1531.739583	766.373430	1530.755567	765.881421	12
5	522.255840	261.631558			504.245275	252.626276	A	***1461.734104***	731.370690	1444.707555	722.857416	1443.723539	722.365407	11
6	619.308604	310.157940			601.298039	301.152658	P	***1390.696990***	695.852133	1373.670441	687.338859	1372.686425	686.846850	10
7	750.349089	375.678183			732.338524	366.672900	M	***1293.644226***	647.325751	1276.617677	638.812477	1275.633661	638.320468	9
8	847.401853	424.204565			829.391288	415.199282	P	***1162.603741***	581.805508	1145.577192	573.292234	1144.593176	572.800226	8
9	976.444446	488.725861			958.433881	479.720579	E	***1065.550977***	533.279126	1048.524428	524.765852	1047.540412	524.273844	7
10	1073.497210	537.252243			1055.486645	528.246961	P	***936.508384***	468.757830	919.481835	460.244555			6
11	**1512.722536**	756.864906	1495.695987	748.351632	1494.711971	747.859624	Q	***839.455620***	420.231448	822.429071	411.718173			5
12	1583.759650	792.383463	1566.733101	783.870189	1565.749085	783.378180	A	***400.230294***	200.618785	383.203745	192.105510			4
13	**1680.812414**	840.909845	1663.785865	832.396571	1662.801849	831.904563	P	***329.193180***	165.100228	312.166631	156.586953			3
14	1737.833878	869.420577	1720.807329	860.907303	1719.823313	860.415294	G	232.140416	116.573846	215.113867	108.060571			2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of YVTSAPMPEPQAPGR
(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	1910.934265	-0.003463	SGSDEVQVGQQR
38.6	1910.934265	-0.003463	SGSDEVQVGQQR
32.7	1910.938263	-0.007461	YVTSAPMPEPQAPGR
1.6	1910.934265	-0.003463	SGSDEVQVGQQR

Mascot: http://www.matrixscience.com/

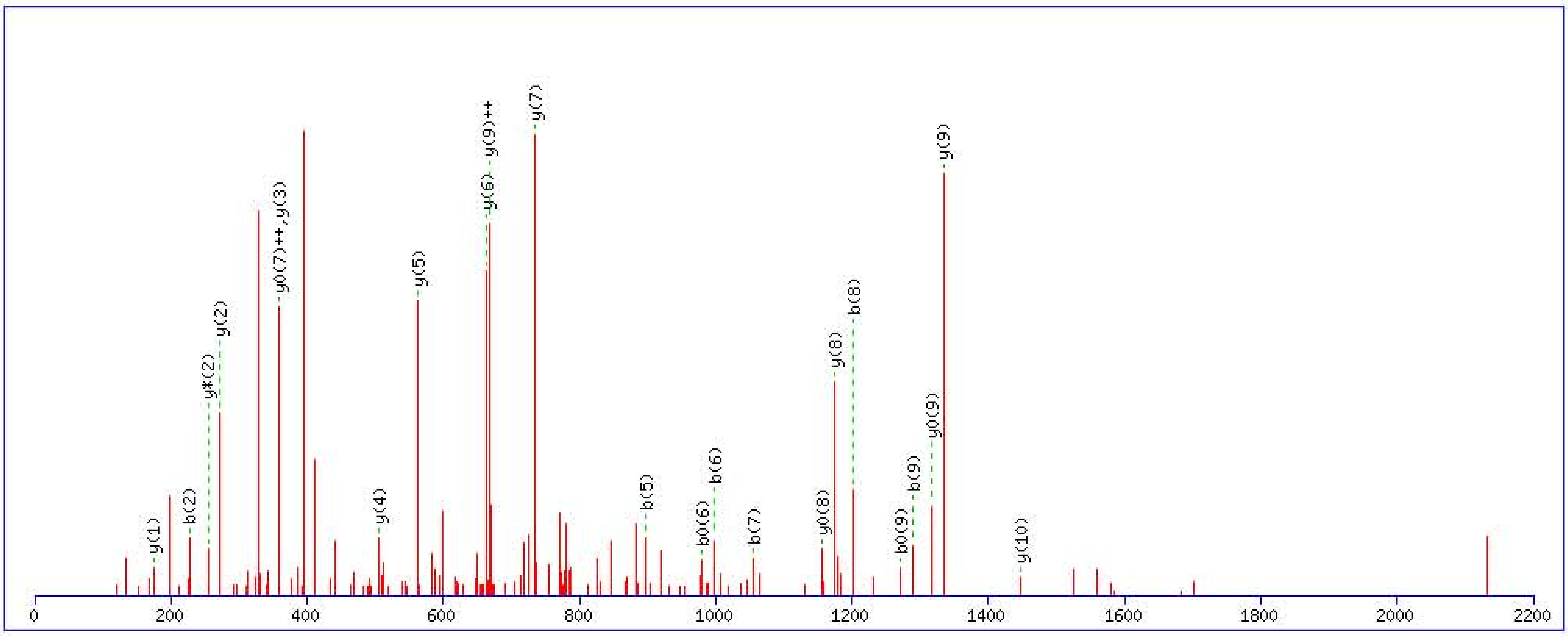
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LICQATGFSPR**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

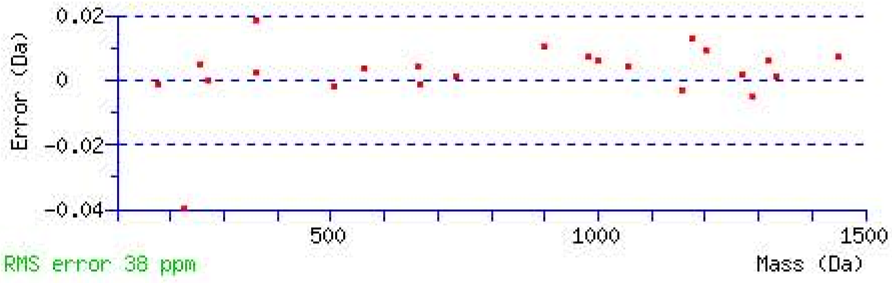
Match to Query 28738: 1559.793348 from(780.903950,2+) rtinseconds(2012) index(31987)
Title: Locus:1.1.1.3364.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

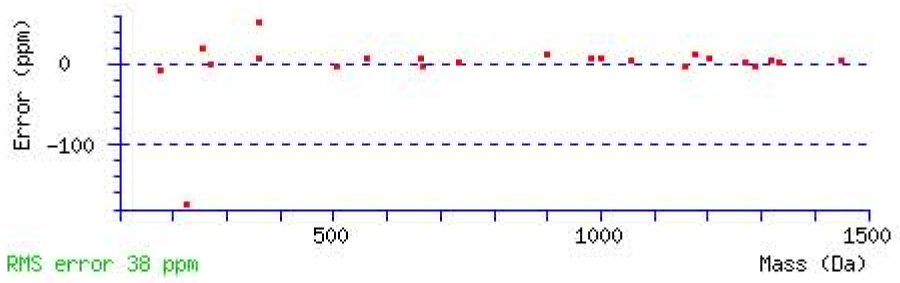
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1559.795242
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4     : Biotin:Thermo-21345 (Q)
Ions Score: 66  Expect: 4.8e-006
Matches : 23/100 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	114.091340	57.549308					L							11
2	**227.175404**	114.091340					I	***1447.718454***	724.362865	1430.691905	715.849591	1429.707889	715.357583	10
3	387.206053	194.106664					C	***1334.634390***	667.820833	1317.607841	659.307559	1316.623825	658.815551	9
4	826.431379	413.719328	809.404830	405.206053			Q	***1174.603741***	587.805509	1157.577192	579.292234	1156.593176	578.800226	8
5	**897.468493**	449.237885	880.441944	440.724610			A	***735.378415***	368.192846	718.351866	359.679571	717.367850	359.187563	7
6	**998.516172**	499.761724	981.489623	491.248449	980.505607	490.756441	T	***664.341301***	332.674289	647.314752	324.161014	646.330736	323.669006	6
7	**1055.537636**	528.272456	1038.511087	519.759182	1037.527071	519.267174	G	***563.293622***	282.150449	546.267073	273.637175	545.283057	273.145167	5
8	**1202.606050**	601.806663	1185.579501	593.293389	1184.595485	592.801381	F	***506.272158***	253.639717	489.245609	245.126443	488.261593	244.634435	4
9	**1289.638078**	645.322677	1272.611529	636.809403	1271.627513	636.317395	S	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
10	1386.690842	693.849059	1369.664293	685.335785	1368.680277	684.843777	P	***272.171716***	136.589496	255.145167	128.076221			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LICQATGFSPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.1	1559.795242	-0.001894	LICQATGFSPR
8.9	1559.808960	-0.015612	LDRLSGLADQMVAR
3.3	1559.770081	0.023267	ARCEVQFSPR
2.5	1559.808975	-0.015627	LLDRDACDTVRVK
1.7	1559.787827	0.005521	SLHPAMLPAADGAGPR

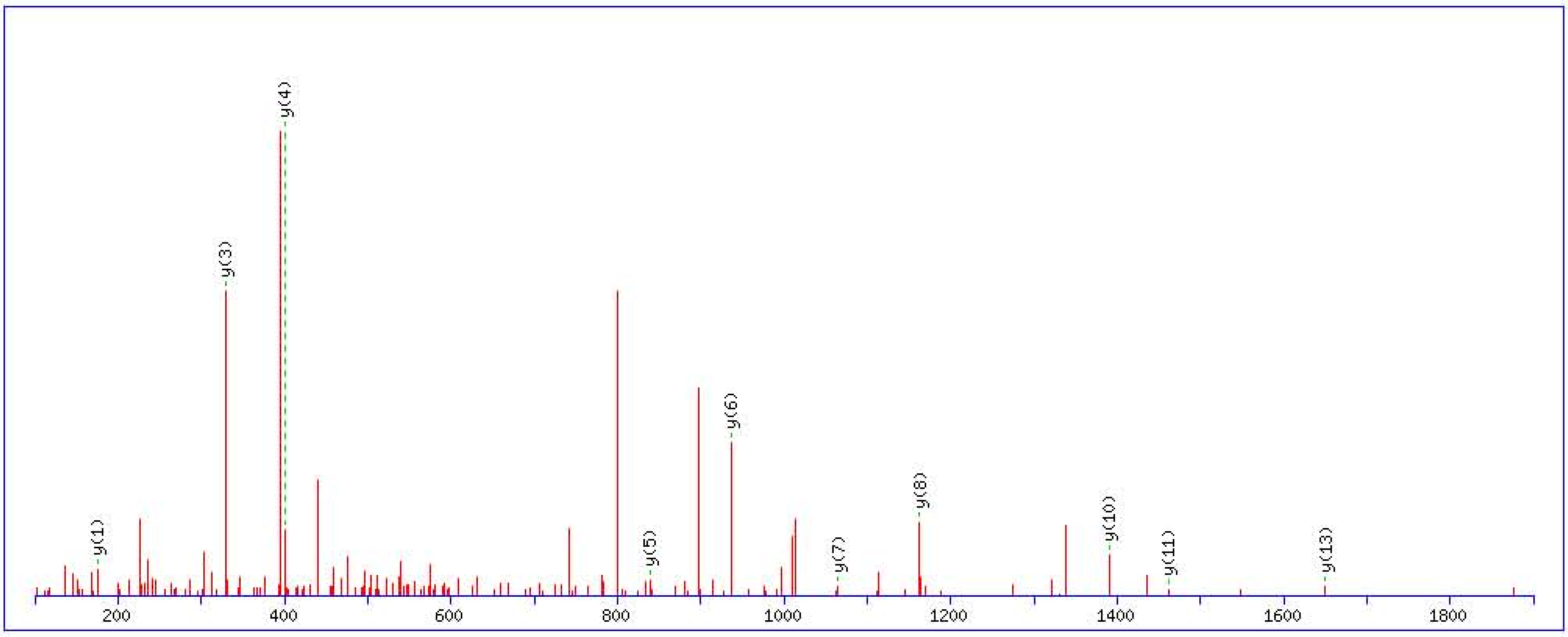
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YVTSAPMPEPQAPGR**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

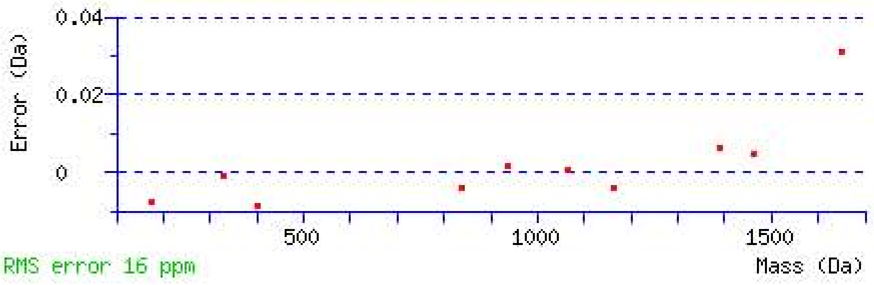
Match to Query 37641: 1910.930802 from(637.984210,3+) rtinseconds(1900) index(31109)
Title: Locus:1.1.1.3325.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

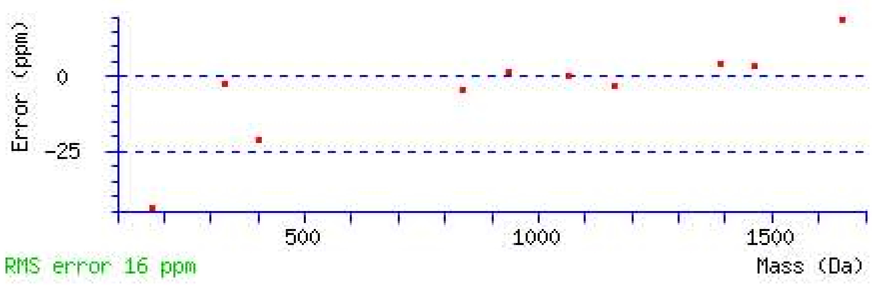
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1910.938263
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.02
Matches : 10/132 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	164.070605	82.538940					Y							15
2	263.139019	132.073148					V	1748.882225	874.944750	1731.855676	866.431476	1730.871660	865.939468	14
3	364.186698	182.596987			346.176133	173.591705	T	***1649.813811***	825.410543	1632.787262	816.897269	1631.803246	816.405261	13
4	451.218726	226.113001			433.208161	217.107719	S	1548.766132	774.886704	1531.739583	766.373430	1530.755567	765.881421	12
5	522.255840	261.631558			504.245275	252.626276	A	***1461.734104***	731.370690	1444.707555	722.857416	1443.723539	722.365407	11
6	619.308604	310.157940			601.298039	301.152658	P	***1390.696990***	695.852133	1373.670441	687.338859	1372.686425	686.846850	10
7	750.349089	375.678183			732.338524	366.672900	M	1293.644226	647.325751	1276.617677	638.812477	1275.633661	638.320468	9
8	847.401853	424.204565			829.391288	415.199282	P	***1162.603741***	581.805508	1145.577192	573.292234	1144.593176	572.800226	8
9	976.444446	488.725861			958.433881	479.720579	E	***1065.550977***	533.279126	1048.524428	524.765852	1047.540412	524.273844	7
10	1073.497210	537.252243			1055.486645	528.246961	P	***936.508384***	468.757830	919.481835	460.244555			6
11	1512.722536	756.864906	1495.695987	748.351632	1494.711971	747.859624	Q	***839.455620***	420.231448	822.429071	411.718173			5
12	1583.759650	792.383463	1566.733101	783.870189	1565.749085	783.378180	A	***400.230294***	200.618785	383.203745	192.105510			4
13	1680.812414	840.909845	1663.785865	832.396571	1662.801849	831.904563	P	***329.193180***	165.100228	312.166631	156.586953			3
14	1737.833878	869.420577	1720.807329	860.907303	1719.823313	860.415294	G	232.140416	116.573846	215.113867	108.060571			2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of YVTSAPMPEPQAPGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.6	1910.938263	-0.007461	YVTSAPMPEPQAPGR
22.6	1910.934265	-0.003463	SGSDEVQVGQQR
22.6	1910.934265	-0.003463	SGSDEVQVGQQR

Mascot: http://www.matrixscience.com/

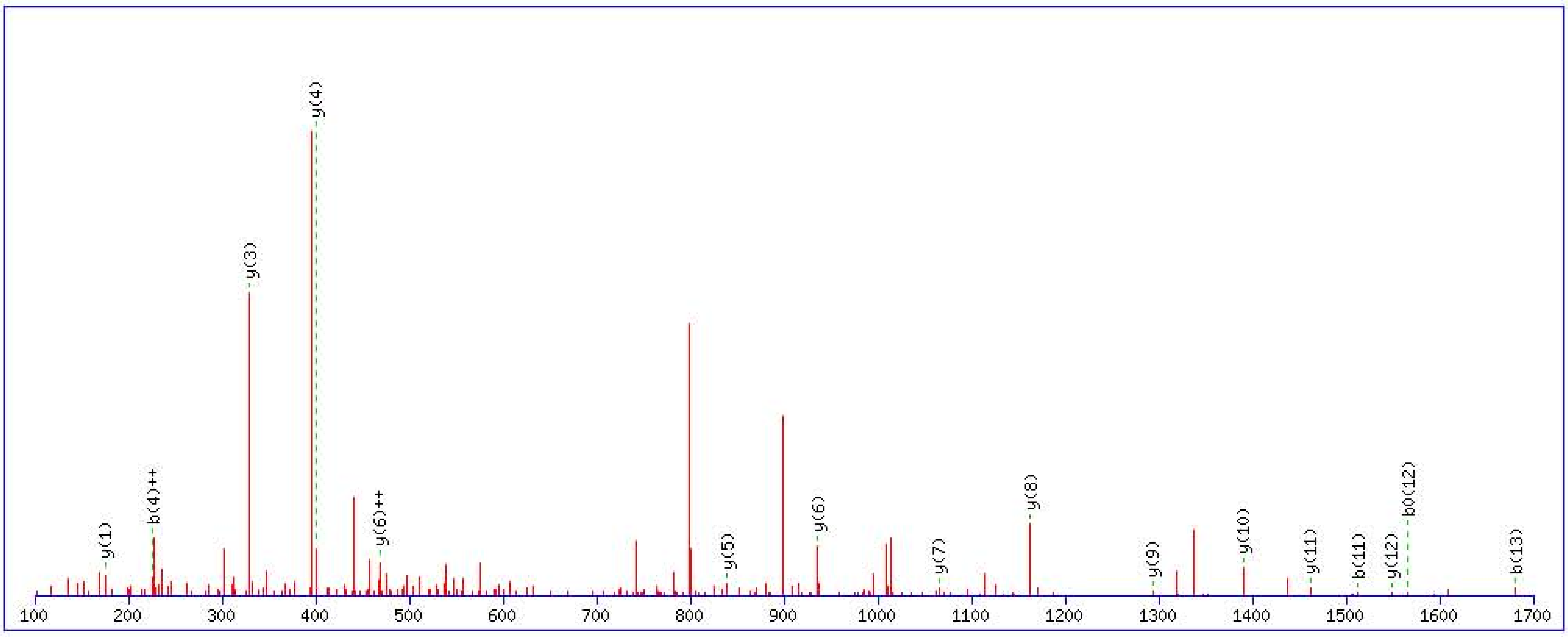
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YVTSAPMPEPQAPGR**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

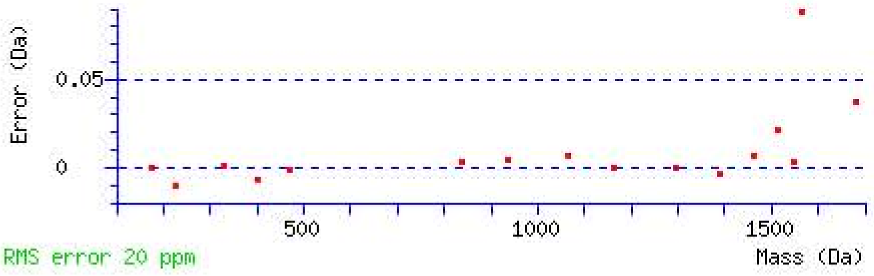
Match to Query 37642: 1910.930802 from(637.984210,3+) rtinseconds(1891) index(31052)
Title: Locus:1.1.1.3322.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

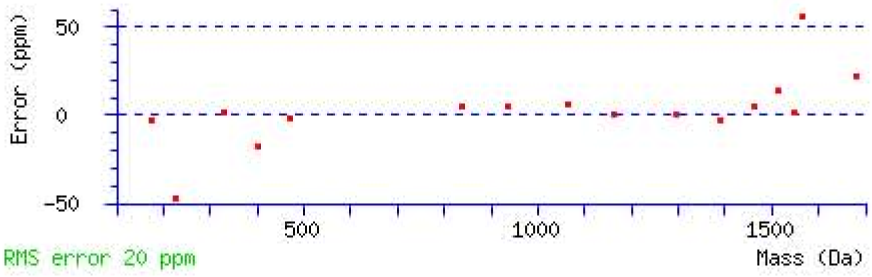
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1910.938263
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 33 **Expect:** 0.012
Matches : 16/132 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	164.070605	82.538940					Y							15
2	263.139019	132.073148					V	1748.882225	874.944750	1731.855676	866.431476	1730.871660	865.939468	14
3	364.186698	182.596987			346.176133	173.591705	T	1649.813811	825.410543	1632.787262	816.897269	1631.803246	816.405261	13
4	451.218726	226.113001			433.208161	217.107719	S	***1548.766132***	774.886704	1531.739583	766.373430	1530.755567	765.881421	12
5	522.255840	261.631558			504.245275	252.626276	A	***1461.734104***	731.370690	1444.707555	722.857416	1443.723539	722.365407	11
6	619.308604	310.157940			601.298039	301.152658	P	***1390.696990***	695.852133	1373.670441	687.338859	1372.686425	686.846850	10
7	750.349089	375.678183			732.338524	366.672900	M	***1293.644226***	647.325751	1276.617677	638.812477	1275.633661	638.320468	9
8	847.401853	424.204565			829.391288	415.199282	P	***1162.603741***	581.805508	1145.577192	573.292234	1144.593176	572.800226	8
9	976.444446	488.725861			958.433881	479.720579	E	***1065.550977***	533.279126	1048.524428	524.765852	1047.540412	524.273844	7
10	1073.497210	537.252243			1055.486645	528.246961	P	***936.508384***	468.757830	919.481835	460.244555			6
11	**1512.722536**	756.864906	1495.695987	748.351632	1494.711971	747.859624	Q	***839.455620***	420.231448	822.429071	411.718173			5
12	1583.759650	792.383463	1566.733101	783.870189	1565.749085	783.378180	A	***400.230294***	200.618785	383.203745	192.105510			4
13	**1680.812414**	840.909845	1663.785865	832.396571	1662.801849	831.904563	P	***329.193180***	165.100228	312.166631	156.586953			3
14	1737.833878	869.420577	1720.807329	860.907303	1719.823313	860.415294	G	232.140416	116.573846	215.113867	108.060571			2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of YVTSAPMPEPQAPGR
(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	1910.934265	-0.003463	SGSDEVQVGQQR
38.6	1910.934265	-0.003463	SGSDEVQVGQQR
32.7	1910.938263	-0.007461	YVTSAPMPEPQAPGR
1.6	1910.934265	-0.003463	SGSDEVQVGQQR

Mascot: http://www.matrixscience.com/

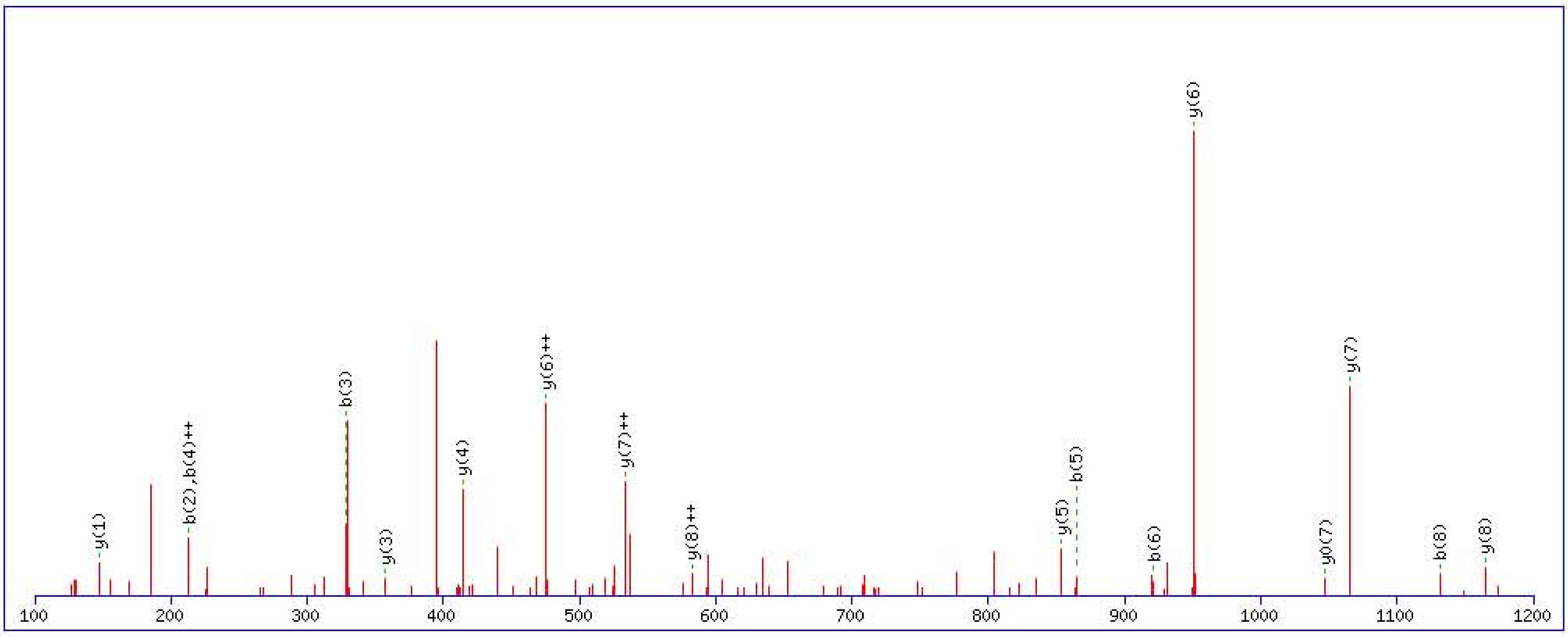
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVDPQGPLK**
Found in **FCGBP_HUMAN**, IgGFc-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3

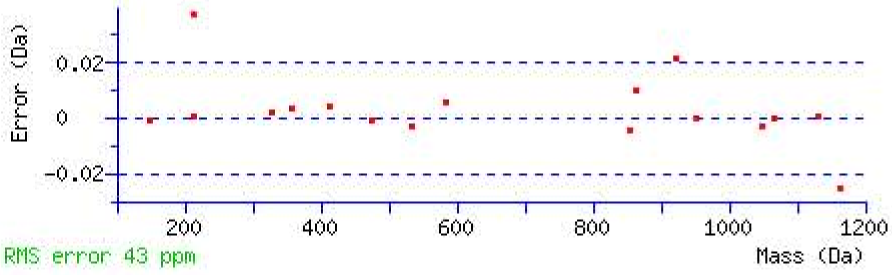
Match to Query 19711: 1276.716068 from(639.365310,2+) rtinseconds(1909) index(31157)
Title: Locus:1.1.1.3328.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

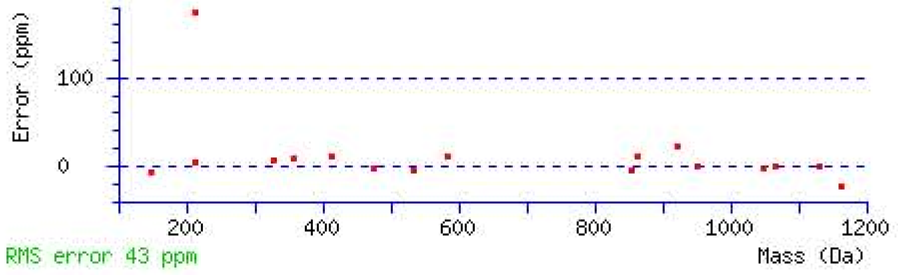
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1276.721329
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.041
Matches : 17/72 fragment ions using 51 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	213.159754	107.083515					V	*1164.644543*	582.825910	1147.617994	574.312635	1146.633978	573.820627	8
3	328.186697	164.596986			310.176132	155.591704	D	*1065.576129*	533.291703	1048.549580	524.778428	1047.565564	524.286420	7
4	425.239461	213.123368			407.228896	204.118086	P	*950.549186*	475.778231	933.522637	467.264956			6
5	864.464787	432.736032	847.438238	424.222757	846.454222	423.730749	Q	*853.496422*	427.251849	836.469873	418.738575			5
6	921.486251	461.246764	904.459702	452.733489	903.475686	452.241481	G	*414.271096*	207.639186	397.244547	199.125911			4
7	1018.539015	509.773146	1001.512466	501.259871	1000.528450	500.767863	P	*357.249632*	179.128454	340.223083	170.615179			3
8	1131.623079	566.315178	1114.596530	557.801903	1113.612514	557.309895	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 LVDPQGPLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.6	1276.721329	-0.005261	LVDPQGPLK
13.6	1276.706039	0.010029	IVKDLMSKAEK
12.7	1276.706726	0.009342	LVPDSLYVPFK
5.2	1276.713913	0.002155	VIDAKFETKAR
3.9	1276.717941	-0.001873	VLLYQPFELR
2.6	1276.698669	0.017399	KTGKSATTALGDK
0.8	1276.725128	-0.009060	QSLSRLAAYLR

Mascot: http://www.matrixscience.com/

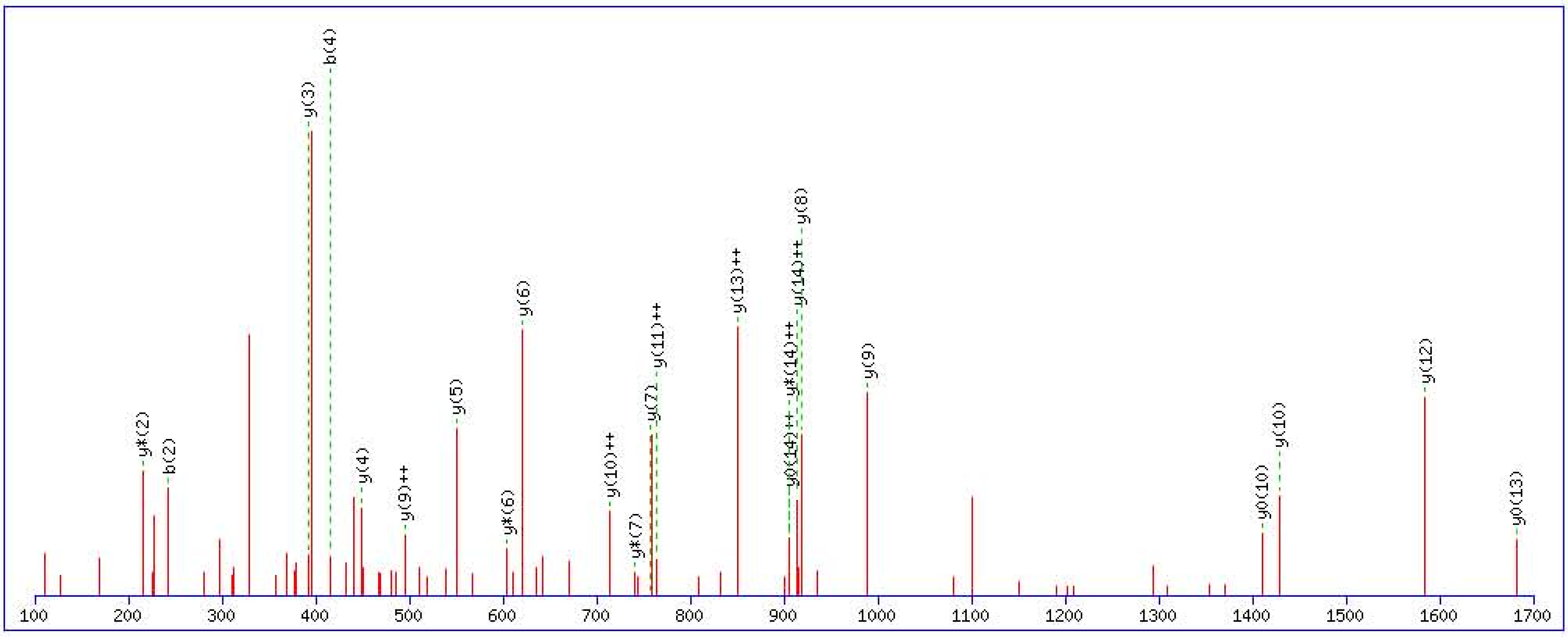
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEDGVQACHATGCGR**
Found in **FCGBP_HUMAN**, IgGFc-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3

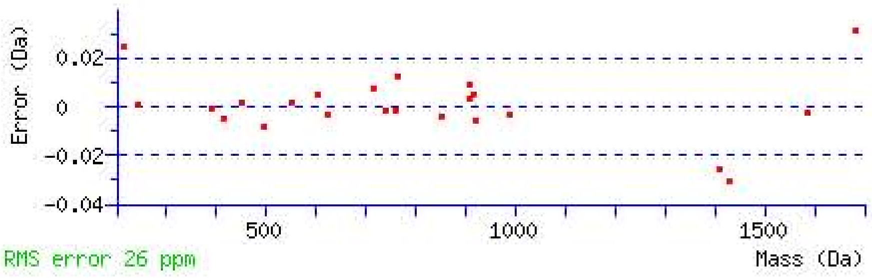
Match to Query 38176: 1940.862552 from(647.961460,3+) rtinseconds(1454) index(28510)
Title: Locus:1.1.1.3169.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

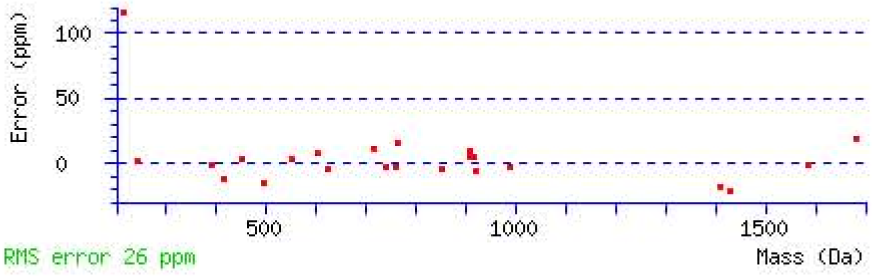
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1940.865540
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 44  Expect: 0.00025
Matches : 23/148 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							15
2	**243.133933**	122.070605			225.123368	113.065322	E	1828.788737	914.898006	1811.762188	906.384732	1810.778172	905.892724	14
3	358.160876	179.584076			340.150311	170.578794	D	1699.746144	850.376710	1682.719595	841.863435	1681.735579	841.371427	13
4	**415.182340**	208.094808			397.171775	199.089526	G	***1584.719201***	792.863238	1567.692652	784.349964	1566.708636	783.857956	12
5	514.250754	257.629015			496.240189	248.623733	V	1527.697737	764.352506	1510.671188	755.839232	1509.687172	755.347224	11
6	953.476080	477.241678	936.449531	468.728404	935.465515	468.236396	Q	***1428.629323***	714.818299	1411.602774	706.305025	1410.618758	705.813017	10
7	1024.513194	512.760235	1007.486645	504.246960	1006.502629	503.754952	A	***989.403997***	495.205636	972.377448	486.692362	971.393432	486.200354	9
8	1184.543843	592.775559	1167.517294	584.262285	1166.533278	583.770277	C	***918.366883***	459.687079	901.340334	451.173805	900.356318	450.681797	8
9	1321.602755	661.305015	1304.576206	652.791741	1303.592190	652.299733	H	***758.336234***	379.671755	741.309685	371.158480	740.325669	370.666472	7
10	1392.639869	696.823572	1375.613320	688.310298	1374.629304	687.818290	A	***621.277322***	311.142299	604.250773	302.629024	603.266757	302.137016	6
11	1493.687548	747.347412	1476.660999	738.834138	1475.676983	738.342129	T	***550.240208***	275.623742	533.213659	267.110467	532.229643	266.618459	5
12	1550.709012	775.858144	1533.682463	767.344869	1532.698447	766.852861	G	***449.192529***	225.099902	432.165980	216.586628			4
13	1710.739661	855.873468	1693.713112	847.360194	1692.729096	846.868186	C	***392.171065***	196.589170	375.144516	188.075896			3
14	1767.761125	884.384200	1750.734576	875.870926	1749.750560	875.378918	G	232.140416	116.573846	215.113867	108.060571			2
15							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LEDGVQACHATGCGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.8	1940.865540	-0.002988	LEDGVQACHATGCGR

Mascot: http://www.matrixscience.com/

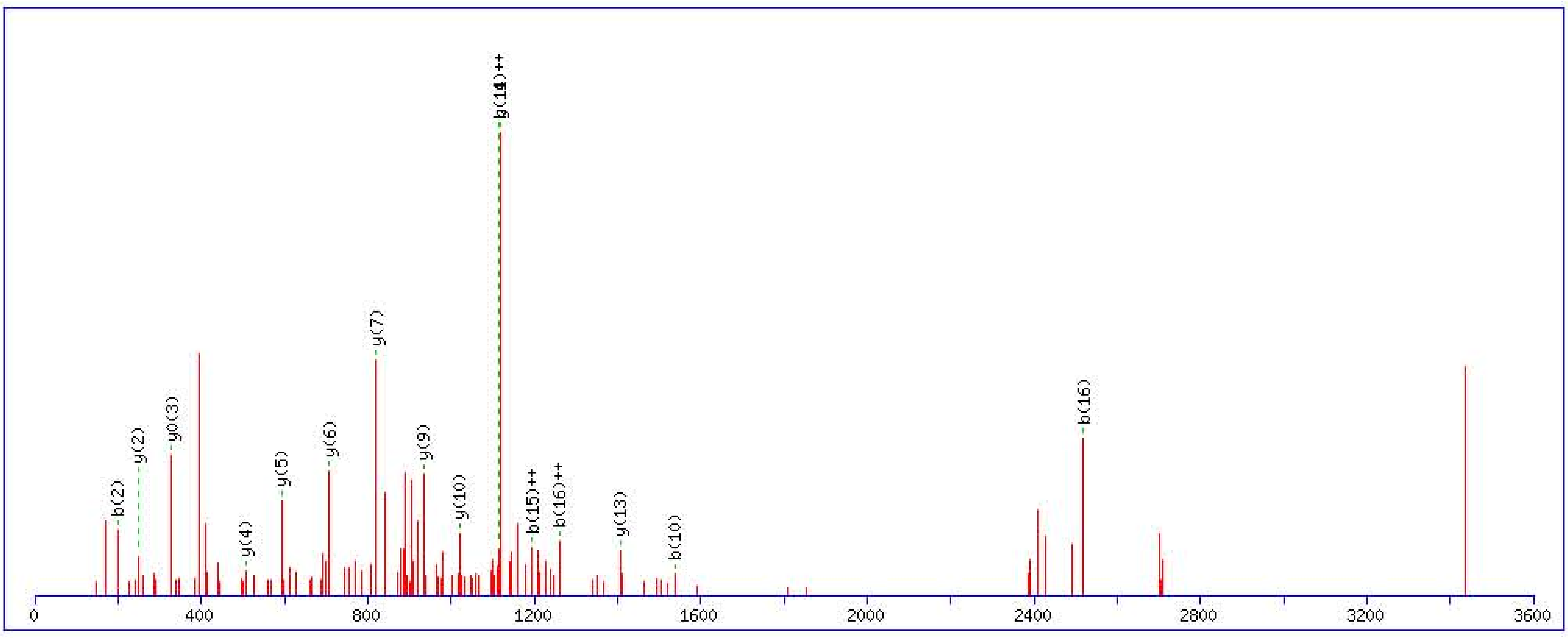
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVVCQEHSCKPGQVCQPSGGILSCVTK**
Found in **FCGBP_HUMAN**, IgGFc-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3

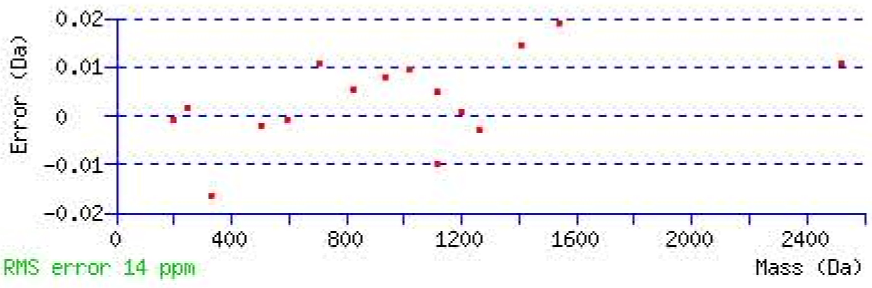
Match to Query 60612: 3635.747496 from(909.944150,4+) rtinseconds(2010) index(31976)
Title: Locus:1.1.1.3363.23 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

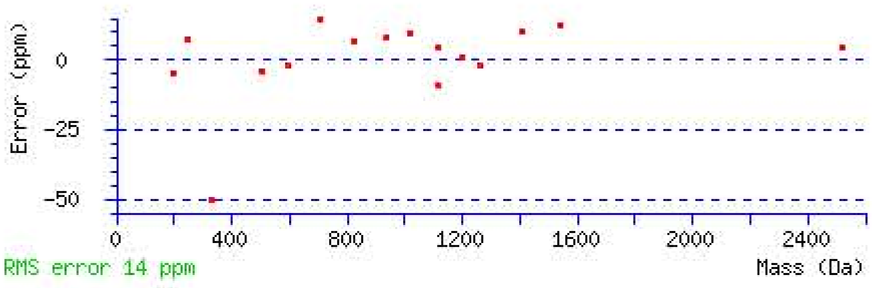
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [3600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3635.757751
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Q13 : Biotin:Thermo-21345 (Q)
Ions Score: 31 **Expect:** 0.016
Matches : 16/292 fragment ions using 38 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.075690	50.541483					V							27
2	**199.144104**	100.075690					V	3537.696565	1769.351920	3520.670016	1760.838646	3519.686000	1760.346638	26
3	298.212518	149.609897					V	3438.628151	1719.817713	3421.601602	1711.304439	3420.617586	1710.812431	25
4	458.243167	229.625222					C	3339.559737	1670.283506	3322.533188	1661.770232	3321.549172	1661.278224	24
5	897.468493	449.237885	880.441944	440.724610			Q	3179.529088	1590.268182	3162.502539	1581.754907	3161.518523	1581.262899	23
6	1026.511086	513.759181	1009.484537	505.245907	1008.500521	504.753899	E	2740.303762	1370.655519	2723.277213	1362.142244	2722.293197	1361.650236	22
7	1163.569998	582.288637	1146.543449	573.775363	1145.559433	573.283355	H	2611.261169	1306.134222	2594.234620	1297.620948	2593.250604	1297.128940	21
8	1250.602026	625.804651	1233.575477	617.291377	1232.591461	616.799369	S	2474.202257	1237.604766	2457.175708	1229.091492	2456.191692	1228.599484	20
9	1410.632675	705.819976	1393.606126	697.306701	1392.622110	696.814693	C	2387.170229	1194.088752	2370.143680	1185.575478	2369.159664	1185.083470	19
10	**1538.727638**	769.867457	1521.701089	761.354183	1520.717073	760.862175	K	2227.139580	1114.073428	2210.113031	1105.560153	2209.129015	1105.068145	18
11	1635.780402	818.393839	1618.753853	809.880565	1617.769837	809.388557	P	2099.044617	1050.025946	2082.018068	1041.512672	2081.034052	1041.020664	17
12	1692.801866	846.904571	1675.775317	838.391297	1674.791301	837.899289	G	2001.991853	1001.499564	1984.965304	992.986290	1983.981288	992.494282	16
13	2132.027192	1066.517234	2115.000643	1058.003959	2114.016627	1057.511951	Q	1944.970389	972.988832	1927.943840	964.475558	1926.959824	963.983550	15
14	2231.095606	**1116.051441**	2214.069057	1107.538166	2213.085041	1107.046158	V	1505.745063	753.376169	1488.718514	744.862895	1487.734498	744.370887	14
15	2391.126255	**1196.066765**	2374.099706	1187.553491	2373.115690	1187.061483	C	***1406.676649***	703.841962	1389.650100	695.328688	1388.666084	694.836680	13
16	**2519.184833**	**1260.096054**	2502.158284	1251.582780	2501.174268	1251.090772	Q	1246.646000	623.826638	1229.619451	615.313364	1228.635435	614.821355	12
17	2616.237597	1308.622436	2599.211048	1300.109162	2598.227032	1299.617154	P	***1118.587422***	559.797349	1101.560873	551.284074	1100.576857	550.792066	11
18	2703.269625	1352.138450	2686.243076	1343.625176	2685.259060	1343.133168	S	***1021.534658***	511.270967	1004.508109	502.757692	1003.524093	502.265684	10
19	2760.291089	1380.649182	2743.264540	1372.135908	2742.280524	1371.643900	G	***934.502630***	467.754953	917.476081	459.241678	916.492065	458.749670	9
20	2817.312553	1409.159914	2800.286004	1400.646640	2799.301988	1400.154632	G	877.481166	439.244221	860.454617	430.730946	859.470601	430.238938	8
21	2930.396617	1465.701946	2913.370068	1457.188672	2912.386052	1456.696664	I	***820.459702***	410.733489	803.433153	402.220214	802.449137	401.728206	7
22	3043.480681	1522.243978	3026.454132	1513.730704	3025.470116	1513.238696	L	***707.375638***	354.191457	690.349089	345.678182	689.365073	345.186174	6
23	3130.512709	1565.759993	3113.486160	1557.246718	3112.502144	1556.754710	S	***594.291574***	297.649425	577.265025	289.136150	576.281009	288.644142	5
24	3290.543358	1645.775317	3273.516809	1637.262042	3272.532793	1636.770034	C	***507.259546***	254.133411	490.232997	245.620136	489.248981	245.128128	4
25	3389.611772	1695.309524	3372.585223	1686.796249	3371.601207	1686.304241	V	347.228897	174.118086	330.202348	165.604812	329.218332	165.112804	3
26	3490.659451	1745.833363	3473.632902	1737.320089	3472.648886	1736.828081	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
27							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VVVCQEHSCKPGQVCQPSGGILSCVTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.4	3635.757751	-0.010255	VVVCQEHSCKPGQVCQPSGGILSCVTK
20.4	3635.757751	-0.010255	VVVCQEHSCKPGQVCQPSGGILSCVTK
20.3	3635.757751	-0.010255	VVVCQEHSCKPGQVCQPSGGILSCVTK

Mascot: http://www.matrixscience.com/

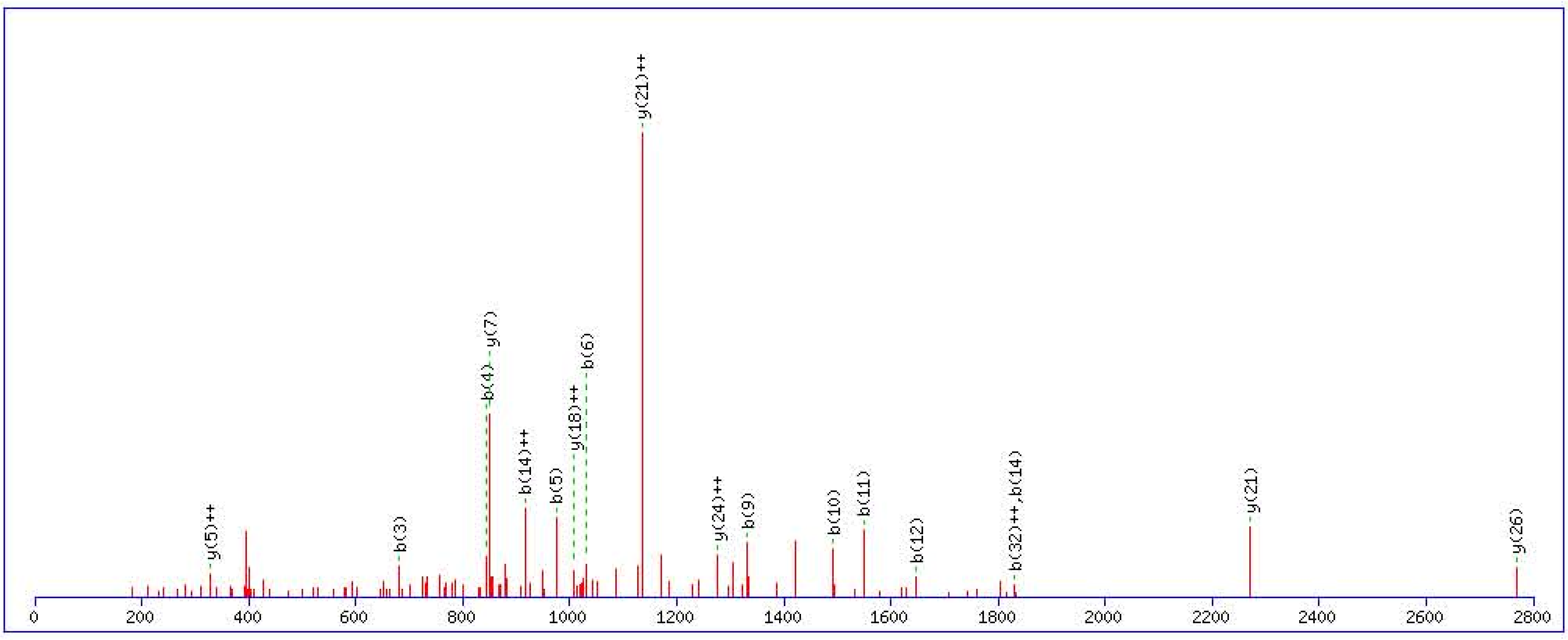
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEQYEGPGFCGPLAPGTGGPFTTCHAHVPPESFFK**
Found in **FCGBP_HUMAN**, IgGFc-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3

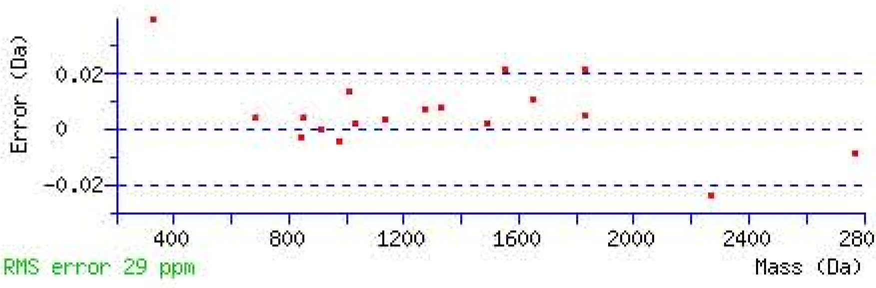
Match to Query 63728: 4099.908136 from(1025.984310,4+) rtinseconds(2513) index(34697)
Title: Locus:1.1.1.3538.26 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

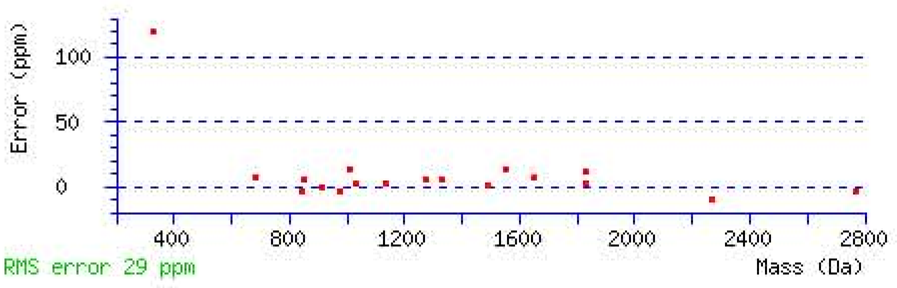
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 4099.905991
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.0089
Matches : 18/396 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	114.091340	57.549308					L							35
2	243.133933	122.070605			225.123368	113.065322	E	3987.829155	1994.418215	3970.802606	1985.904941	3969.818590	1985.412933	34
3	***682.359259***	341.683268	665.332710	333.169993	664.348694	332.677985	Q	3858.786562	1929.896919	3841.760013	1921.383644	3840.775997	1920.891636	33
4	***845.422588***	423.214932	828.396039	414.701658	827.412023	414.209650	Y	3419.561236	1710.284256	3402.534687	1701.770981	3401.550671	1701.278973	32
5	***974.465181***	487.736229	957.438632	479.222954	956.454616	478.730946	E	3256.497907	1628.752591	3239.471358	1620.239317	3238.487342	1619.747309	31
6	***1031.486645***	516.246961	1014.460096	507.733686	1013.476080	507.241678	G	3127.455314	1564.231295	3110.428765	1555.718020	3109.444749	1555.226012	30
7	1128.539409	564.773343	1111.512860	556.260068	1110.528844	555.768060	P	3070.433850	1535.720563	3053.407301	1527.207288	3052.423285	1526.715280	29
8	1185.560873	593.284075	1168.534324	584.770800	1167.550308	584.278792	G	2973.381086	1487.194181	2956.354537	1478.680906	2955.370521	1478.188898	28
9	***1332.629287***	666.818282	1315.602738	658.305007	1314.618722	657.812999	F	2916.359622	1458.683449	2899.333073	1450.170174	2898.349057	1449.678166	27
10	***1492.659936***	746.833606	1475.633387	738.320332	1474.649371	737.828324	C	**2769.291208**	1385.149242	2752.264659	1376.635967	2751.280643	1376.143959	26
11	***1549.681400***	775.344338	1532.654851	766.831064	1531.670835	766.339056	G	2609.260559	1305.133917	2592.234010	1296.620643	2591.249994	1296.128635	25
12	***1646.734164***	823.870720	1629.707615	815.357446	1628.723599	814.865438	P	2552.239095	1276.623185	2535.212546	1268.109911	2534.228530	1267.617903	24
13	1759.818228	880.412752	1742.791679	871.899478	1741.807663	871.407470	L	2455.186331	1228.096803	2438.159782	1219.583529	2437.175766	1219.091521	23
14	***1830.855342***	**915.931309**	1813.828793	907.418035	1812.844777	906.926027	A	2342.102267	1171.554771	2325.075718	1163.041497	2324.091702	1162.549489	22
15	1927.908106	964.457691	1910.881557	955.944417	1909.897541	955.452409	P	**2271.065153**	1136.036214	2254.038604	1127.522940	2253.054588	1127.030932	21
16	1984.929570	992.968423	1967.903021	984.455149	1966.919005	983.963141	G	2174.012389	1087.509832	2156.985840	1078.996558	2156.001824	1078.504550	20
17	2085.977249	1043.492262	2068.950700	1034.978988	2067.966684	1034.486980	T	2116.990925	1058.999100	2099.964376	1050.485826	2098.980360	1049.993818	19
18	2142.998713	1072.002994	2125.972164	1063.489720	2124.988148	1062.997712	G	2015.943246	1008.475261	1998.916697	999.961986	1997.932681	999.469978	18
19	2200.020177	1100.513726	2182.993628	1092.000452	2182.009612	1091.508444	G	1958.921782	979.964529	1941.895233	971.451254	1940.911217	970.959246	17
20	2297.072941	1149.040108	2280.046392	1140.526834	2279.062376	1140.034826	P	1901.900318	951.453797	1884.873769	942.940522	1883.889753	942.448514	16
21	2444.141355	1222.574315	2427.114806	1214.061041	2426.130790	1213.569033	F	1804.847554	902.927415	1787.821005	894.414140	1786.836989	893.922132	15
22	2545.189034	1273.098155	2528.162485	1264.584880	2527.178469	1264.092872	T	1657.779140	829.393208	1640.752591	820.879933	1639.768575	820.387925	14
23	2646.236713	1323.621994	2629.210164	1315.108720	2628.226148	1314.616712	T	1556.731461	778.869368	1539.704912	770.356094	1538.720896	769.864086	13
24	2806.267362	1403.637319	2789.240813	1395.124044	2788.256797	1394.632036	C	1455.683782	728.345529	1438.657233	719.832254	1437.673217	719.340246	12
25	2943.326274	1472.166775	2926.299725	1463.653500	2925.315709	1463.161492	H	1295.653133	648.330205	1278.626584	639.816930	1277.642568	639.324922	11
26	3014.363388	1507.685332	2997.336839	1499.172057	2996.352823	1498.680049	A	1158.594221	579.800749	1141.567672	571.287474	1140.583656	570.795466	10
27	3151.422300	1576.214788	3134.395751	1567.701513	3133.411735	1567.209505	H	1087.557107	544.282191	1070.530558	535.768917	1069.546542	535.276909	9
28	3250.490714	1625.748995	3233.464165	1617.235720	3232.480149	1616.743712	V	950.498195	475.752735	933.471646	467.239461	932.487630	466.747453	8
29	3347.543478	1674.275377	3330.516929	1665.762102	3329.532913	1665.270094	P	**851.429781**	426.218529	834.403232	417.705254	833.419216	417.213246	7
30	3444.596242	1722.801759	3427.569693	1714.288484	3426.585677	1713.796476	P	754.377017	377.692147	737.350468	369.178872	736.366452	368.686864	6
31	3573.638835	1787.323055	3556.612286	1778.809781	3555.628270	1778.317773	E	657.324253	329.165765	640.297704	320.652490	639.313688	320.160482	5
32	3660.670863	**1830.839069**	3643.644314	1822.325795	3642.660298	1821.833787	S	528.281660	264.644468	511.255111	256.131193	510.271095	255.639185	4
33	3807.739277	1904.373276	3790.712728	1895.860002	3789.728712	1895.367994	F	441.249632	221.128454	424.223083	212.615179			3
34	3954.807691	1977.907483	3937.781142	1969.394209	3936.797126	1968.902201	F	294.181218	147.594247	277.154669	139.080972			2
35							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LEQYEGPGFCGPLAPGTGGPFTTCHAHVPPESFFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.0	4099.905991	0.002145	LEQYEGPGFCGPLAPGTGGPFTTCHAHVPPESFFK

Mascot: http://www.matrixscience.com/

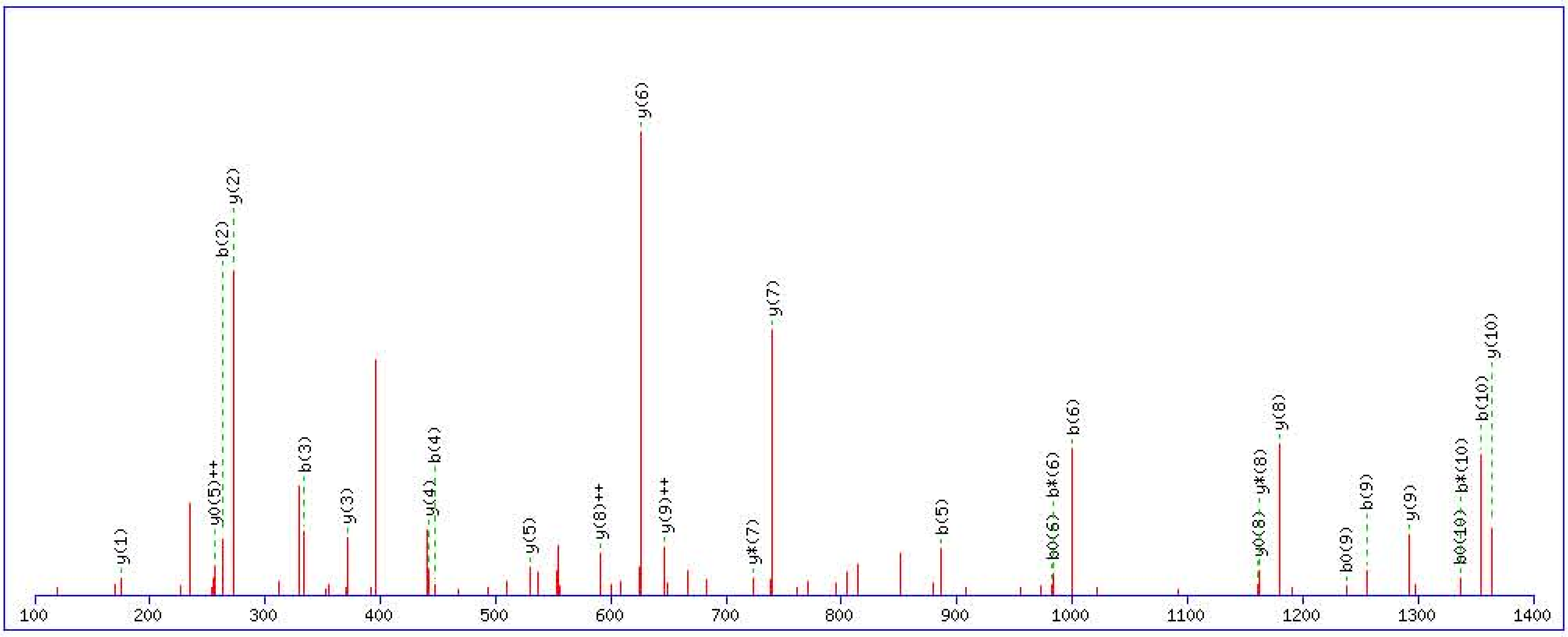
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DFALQNPSAVPR**
Found in **ALS_HUMAN**, Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1

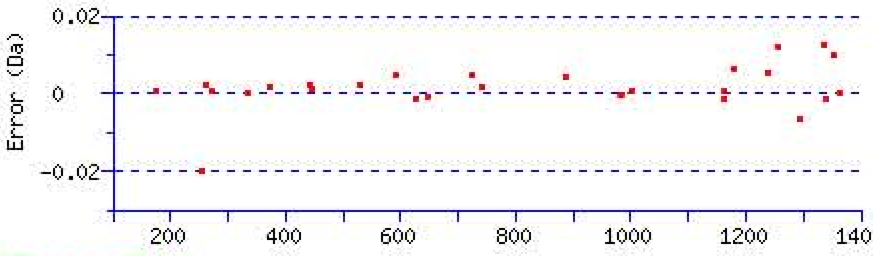
Match to Query 31602: 1624.832108 from(813.423330,2+) rtinseconds(2181) index(32936)
Title: Locus:1.1.1.3423.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

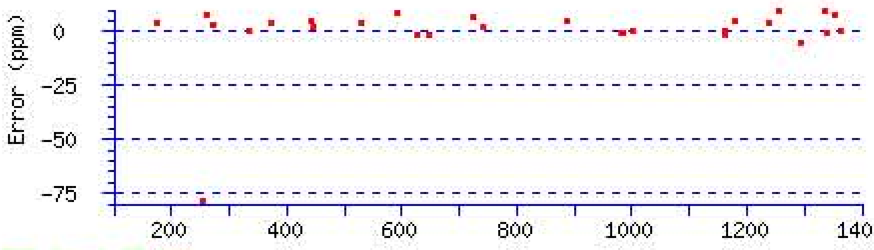


Monoisotopic mass of neutral peptide Mr(calc): 1624.839539
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 65 **Expect:** 7e-006
Matches : 28/116 fragment ions using 49 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							12
2	**263.102633**	132.054954			245.092068	123.049672	F	1510.819881	755.913579	1493.793332	747.400304	1492.809316	746.908296	11
3	**334.139747**	167.573512			316.129182	158.568229	A	***1363.751467***	682.379372	1346.724918	673.866097	1345.740902	673.374089	10
4	**447.223811**	224.115544			429.213246	215.110261	L	***1292.714353***	646.860815	1275.687804	638.347540	1274.703788	637.855532	9
5	**886.449137**	443.728207	869.422588	435.214932	868.438572	434.722924	Q	***1179.630289***	590.318783	1162.603740	581.805508	1161.619724	581.313500	8
6	**1000.492064**	500.749670	983.465515	492.236396	982.481499	491.744388	N	***740.404963***	370.706120	723.378414	362.192845	722.394398	361.700837	7
7	1097.544828	549.276052	1080.518279	540.762778	1079.534263	540.270770	P	***626.362036***	313.684656	609.335487	305.171382	608.351471	304.679374	6
8	1184.576856	592.792066	1167.550307	584.278792	1166.566291	583.786784	S	***529.309272***	265.158274	512.282723	256.645000	511.298707	256.152992	5
9	**1255.613970**	628.310623	1238.587421	619.797349	1237.603405	619.305341	A	***442.277244***	221.642260	425.250695	213.128986			4
10	**1354.682384**	677.844830	1337.655835	669.331556	1336.671819	668.839548	V	***371.240130***	186.123703	354.213581	177.610429			3
11	1451.735148	726.371212	1434.708599	717.857938	1433.724583	717.365930	P	***272.171716***	136.589496	255.145167	128.076221			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 15 ppm



RMS error 15 ppm

NCBI **BLAST** search of DFALQNPSAVPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.3	1624.839539	-0.007431	DFALQNPSAVPR
13.8	1624.853271	-0.021163	ASDPVRTGSEGLALPR
9.2	1624.816406	0.015702	SVMIGTALNTSEMKK
5.5	1624.854813	-0.022705	QWVAAGGHITFK
3.8	1624.832092	0.000016	AAAAAAALESWQAAAPR
2.4	1624.820892	0.011216	SSISNNYLNLTFPR
2.3	1624.829636	0.002472	NVDKWLWMLGAHR
2.2	1624.850296	-0.018188	QQLQMEVK
1.6	1624.817062	0.015046	GYYLEMLIGTPPQK
0.5	1624.850784	-0.018676	FCSFLQTSKVRPR

Mascot: http://www.matrixscience.com/

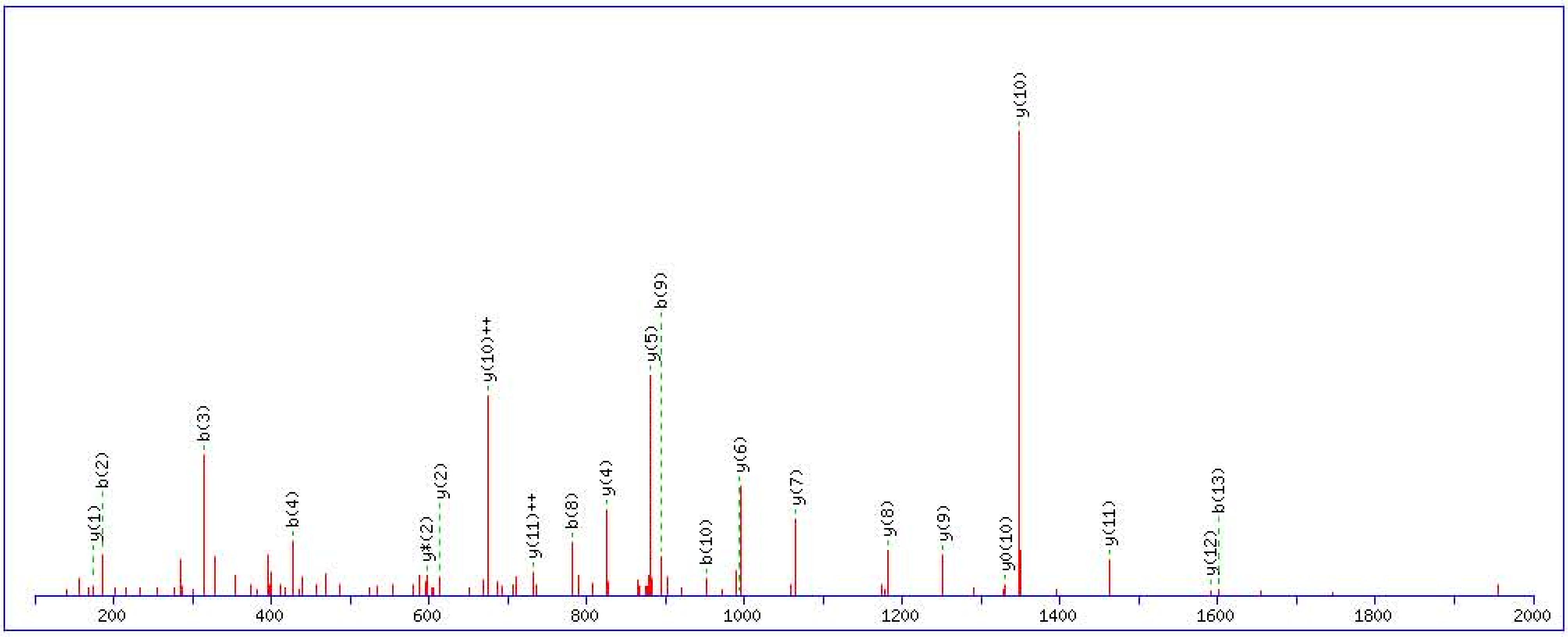
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAELPADALGPLQR**
Found in **ALS_HUMAN**, Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1

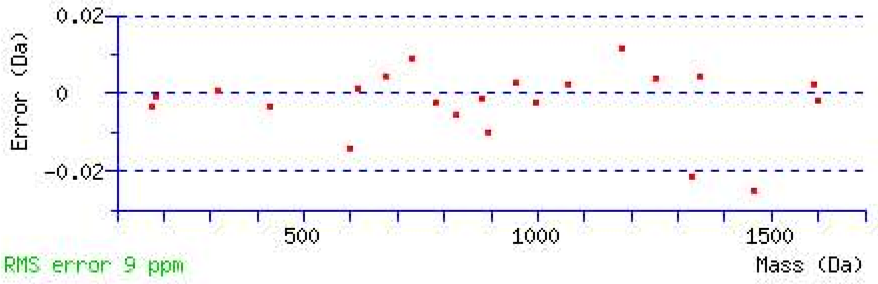
Match to Query 35240: 1773.978348 from(887.996450,2+) rtinseconds(2483) index(34445)
Title: Locus:1.1.1.3528.20 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

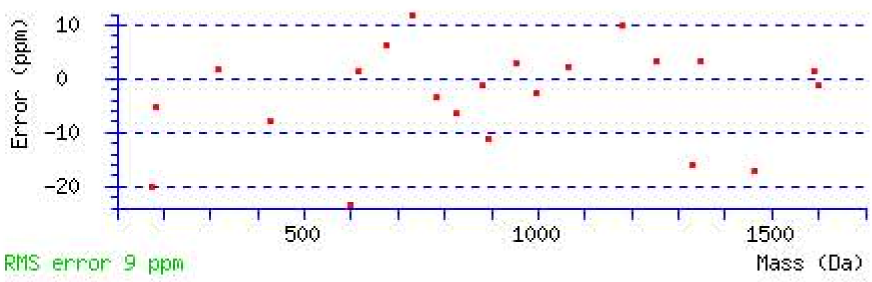
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1773.981094
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 70  Expect: 4.4e-007
Matches : 22/114 fragment ions using 44 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							14
2	**185.128454**	93.067865					A	1661.904340	831.455808	1644.877791	822.942534	1643.893775	822.450526	13
3	**314.171047**	157.589161			296.160482	148.583879	E	***1590.867226***	795.937251	1573.840677	787.423977	1572.856661	786.931969	12
4	**427.255111**	214.131193			409.244546	205.125911	L	***1461.824633***	731.415955	1444.798084	722.902680	1443.814068	722.410672	11
5	524.307875	262.657576			506.297310	253.652293	P	***1348.740569***	674.873922	1331.714020	666.360648	1330.730004	665.868640	10
6	595.344989	298.176133			577.334424	289.170850	A	***1251.687805***	626.347540	1234.661256	617.834266	1233.677240	617.342258	9
7	710.371932	355.689604			692.361367	346.684322	D	***1180.650691***	590.828984	1163.624142	582.315709	1162.640126	581.823701	8
8	**781.409046**	391.208161			763.398481	382.202879	A	***1065.623748***	533.315512	1048.597199	524.802238			7
9	**894.493110**	447.750193			876.482545	438.744911	L	***994.586634***	497.796955	977.560085	489.283681			6
10	**951.514574**	476.260925			933.504009	467.255643	G	***881.502570***	441.254923	864.476021	432.741649			5
11	1048.567338	524.787307			1030.556773	515.782025	P	***824.481106***	412.744191	807.454557	404.230916			4
12	1161.651402	581.329339			1143.640837	572.324056	L	727.428342	364.217809	710.401793	355.704534			3
13	**1600.876728**	800.942002	1583.850179	792.428728	1582.866163	791.936719	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 LAELPADALGPLQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.5	1773.981094	-0.002746	LAELPADALGPLQR
2.7	1773.963821	0.014527	ALEPPSGVLHFQPRAR

Mascot: http://www.matrixscience.com/

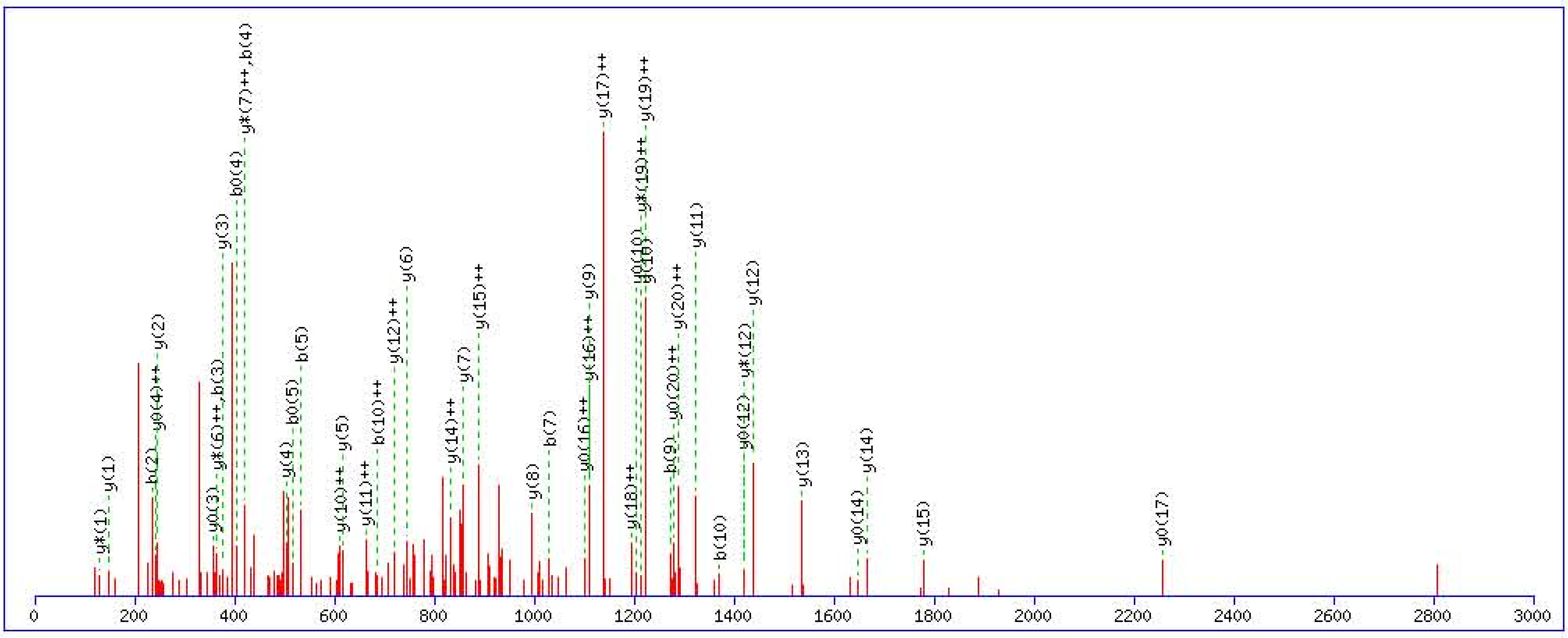
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFEGLGQLEVLTLDHNQLEVK**
Found in **ALS_HUMAN**, Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1

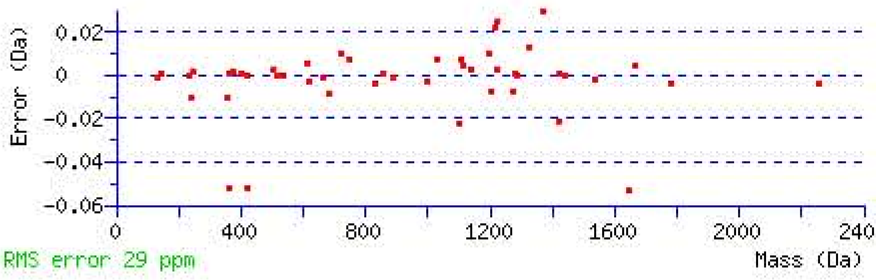
Match to Query 51637: 2807.452332 from(936.824720,3+) rtinseconds(2721) index(36005)
Title: Locus:1.1.1.3610.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

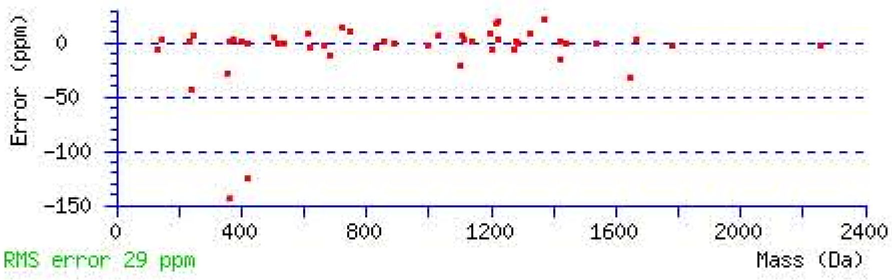
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2807.452759
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 77 **Expect:** 4.6e-007
Matches : 48/236 fragment ions using 94 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							22
2	**235.107718**	118.057497			217.097153	109.052214	F	2721.428016	1361.217646	2704.401467	1352.704371	2703.417451	1352.212363	21
3	**364.150311**	182.578793			346.139746	173.573511	E	2574.359602	1287.683439	2557.333053	1279.170164	2556.349037	1278.678156	20
4	**421.171775**	211.089525			403.161210	202.084243	G	2445.317009	1223.162142	2428.290460	1214.648868	2427.306444	1214.156860	19
5	**534.255839**	267.631558			516.245274	258.626275	L	2388.295545	1194.651410	2371.268996	1186.138136	2370.284980	1185.646128	18
6	591.277303	296.142290			573.266738	287.137007	G	2275.211481	1138.109378	2258.184932	1129.596104	2257.200916	1129.104096	17
7	**1030.502629**	515.754953	1013.476080	507.241678	1012.492064	506.749670	Q	2218.190017	1109.598646	2201.163468	1101.085372	2200.179452	1100.593364	16
8	1143.586693	572.296985	1126.560144	563.783710	1125.576128	563.291702	L	***1778.964691***	889.985984	1761.938142	881.472709	1760.954126	880.980701	15
9	**1272.629286**	636.818281	1255.602737	628.305007	1254.618721	627.812999	E	***1665.880627***	833.443952	1648.854078	824.930677	1647.870062	824.438669	14
10	**1371.697700**	686.352488	1354.671151	677.839214	1353.687135	677.347206	V	***1536.838034***	768.922655	1519.811485	760.409381	1518.827469	759.917373	13
11	1484.781764	742.894520	1467.755215	734.381246	1466.771199	733.889238	L	***1437.769620***	719.388448	1420.743071	710.875174	1419.759055	710.383166	12
12	1585.829443	793.418360	1568.802894	784.905085	1567.818878	784.413077	T	***1324.685556***	662.846416	1307.659007	654.333142	1306.674991	653.841134	11
13	1698.913507	849.960392	1681.886958	841.447117	1680.902942	840.955109	L	***1223.637877***	612.322577	1206.611328	603.809302	1205.627312	603.317294	10
14	1813.940450	907.473863	1796.913901	898.960589	1795.929885	898.468581	D	***1110.553813***	555.780545	1093.527264	547.267270	1092.543248	546.775262	9
15	1950.999362	976.003319	1933.972813	967.490045	1932.988797	966.998037	H	***995.526870***	498.267073	978.500321	489.753799	977.516305	489.261791	8
16	2065.042289	1033.024782	2048.015740	1024.511508	2047.031724	1024.019500	N	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	7
17	2193.100867	1097.054072	2176.074318	1088.540797	2175.090302	1088.048789	Q	***744.425031***	372.716154	727.398482	364.202879	726.414466	363.710871	6
18	2306.184931	1153.596104	2289.158382	1145.082829	2288.174366	1144.590821	L	***616.366453***	308.686865	599.339904	300.173590	598.355888	299.681582	5
19	2434.243509	1217.625393	2417.216960	1209.112118	2416.232944	1208.620110	Q	***503.282389***	252.144833	486.255840	243.631558	485.271824	243.139550	4
20	2563.286102	1282.146689	2546.259553	1273.633415	2545.275537	1273.141407	E	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	3
21	2662.354516	1331.680896	2645.327967	1323.167622	2644.343951	1322.675614	V	***246.181218***	123.594247	229.154669	115.080972			2
22							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SFEGLGQLEVLTLDHNQLEVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
77.3	2807.452759	-0.000427	SFEGLGQLEVLTLDHNQLEVK
6.9	2807.452759	-0.000427	SFEGLGQLEVLTLDHNQLEVK

Mascot: http://www.matrixscience.com/

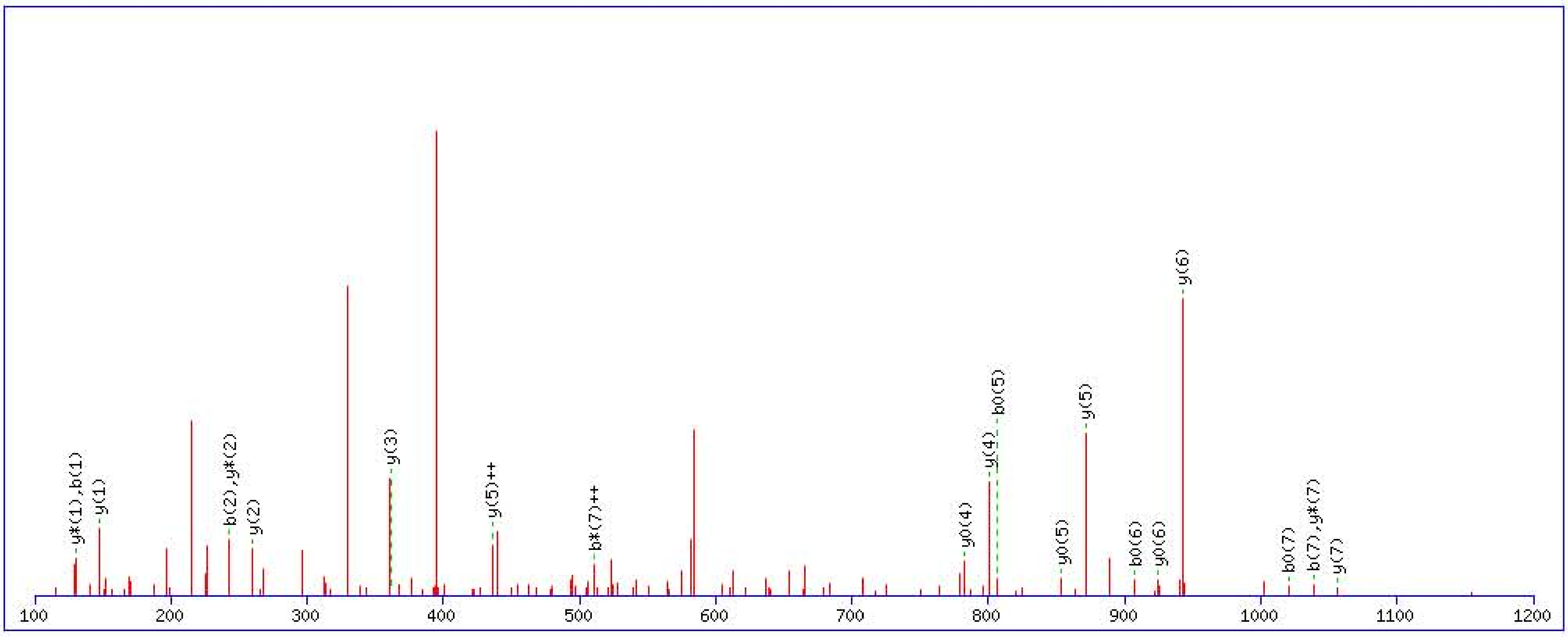
Mascot Search Results

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

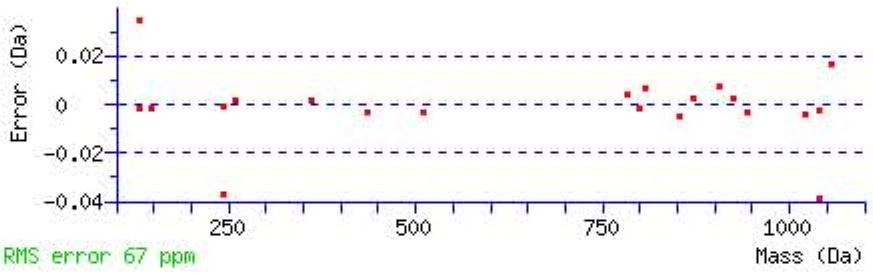
Match to Query 17365: 1183.662388 from(592.838470,2+) rtinseconds(1752) index(44431)
Title: Locus:1.1.1.3323.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

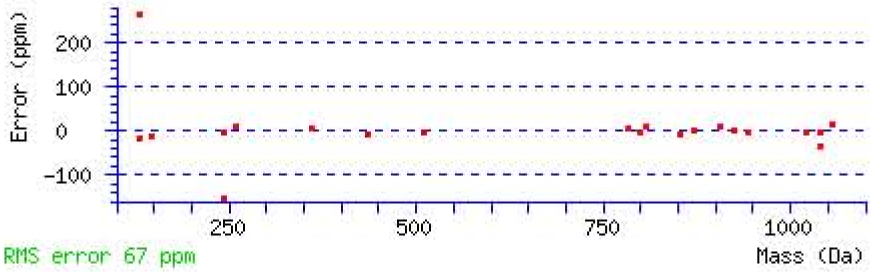
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 36  Expect: 0.0056
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
36.0	1183.663452	-0.001064	ELAAQTIK
29.4	1183.663452	-0.001064	ELAAQITK
8.6	1183.663452	-0.001064	LEQAATLK
7.8	1183.660080	0.002308	AIEAVAISPWK
7.8	1183.667282	-0.004894	GKQASEPALRK
5.5	1183.667297	-0.004909	EPTGRVEIRK
5.1	1183.656937	0.005451	MRPQTLK
5.0	1183.674683	-0.012295	ELRQLSK
4.8	1183.663452	-0.001064	EDLQKLK
4.6	1183.674698	-0.012310	TQVRELK

Mascot: http://www.matrixscience.com/

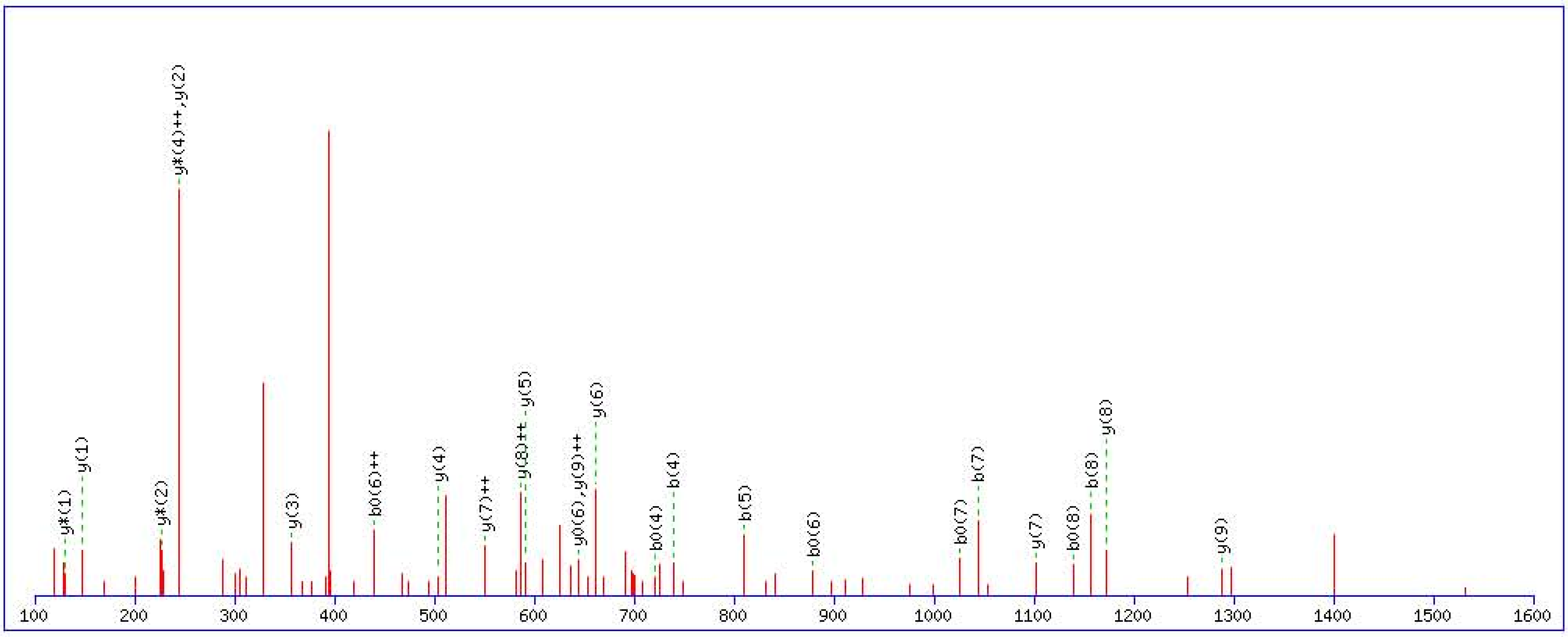
{MATRIX SCIENCE} Mascot Search Results

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

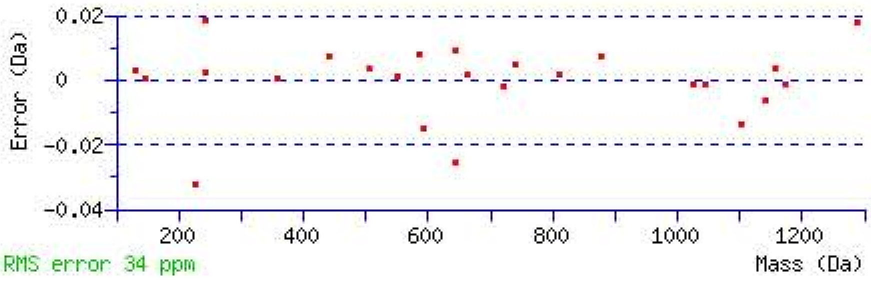
Match to Query 23605: 1399.755108 from(700.884830,2+) rtinseconds(2240) index(47481)
Title: Locus:1.1.1.3492.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

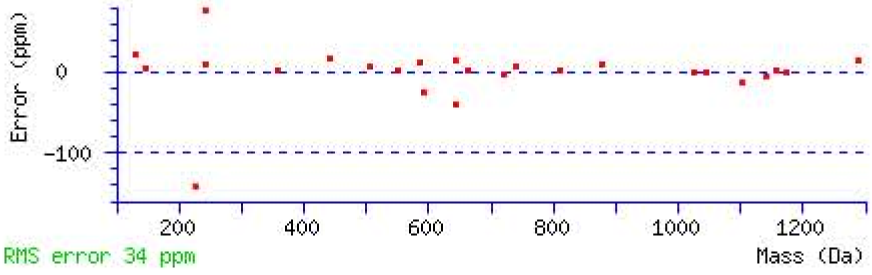
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1399.753342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 55  Expect: 5.1e-005
Matches : 25/92 fragment ions using 45 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
54.6	1399.753342	0.001766	LDAQASFLPK
8.3	1399.753342	0.001766	LLDFAASQPK
7.3	1399.745972	0.009136	IDAATGIPVTTWR
3.0	1399.746811	0.008297	FKMPKIHMSGPK
2.6	1399.771103	-0.015995	QKEPSVLFEVPK
2.4	1399.755814	-0.000706	KTELGPLKEEEK
1.4	1399.757156	-0.002048	IIGEKYHALNSR
1.2	1399.771973	-0.016865	IWQGMLTIK

Mascot: http://www.matrixscience.com/

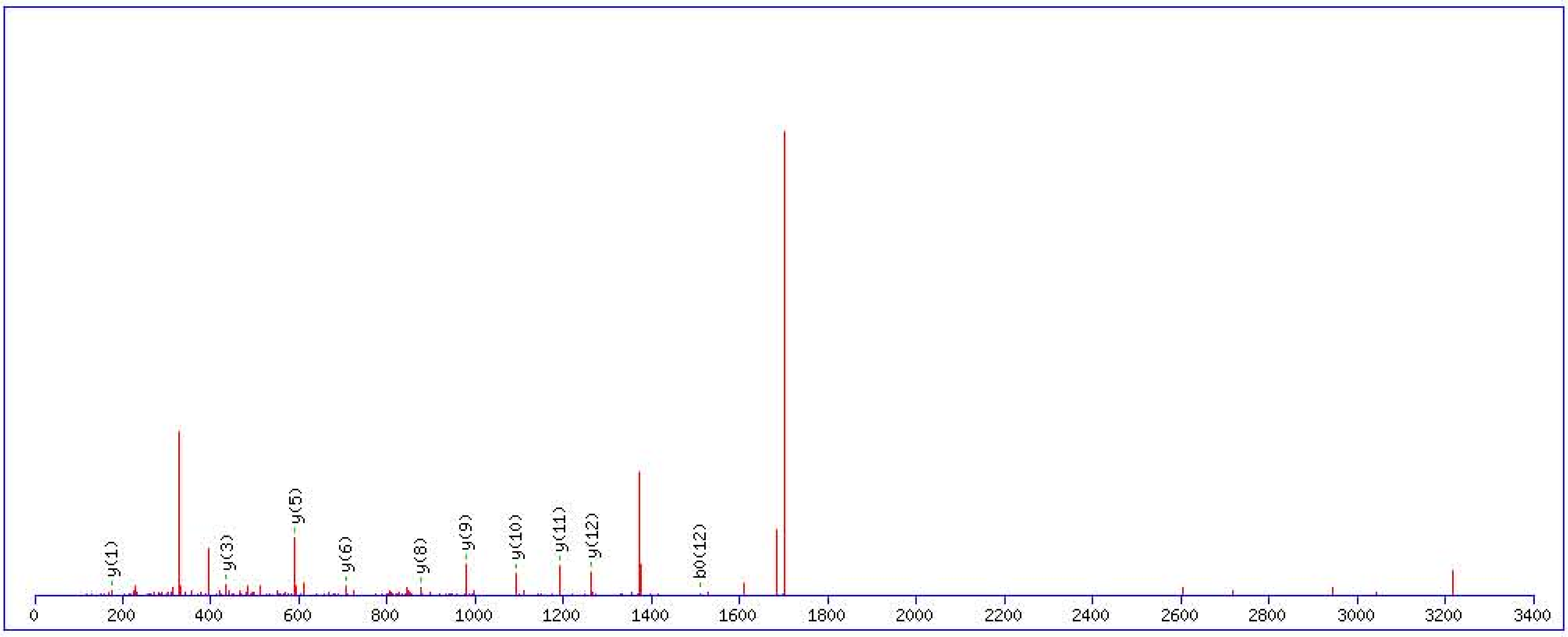
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QAVDTAVDGVFIR**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

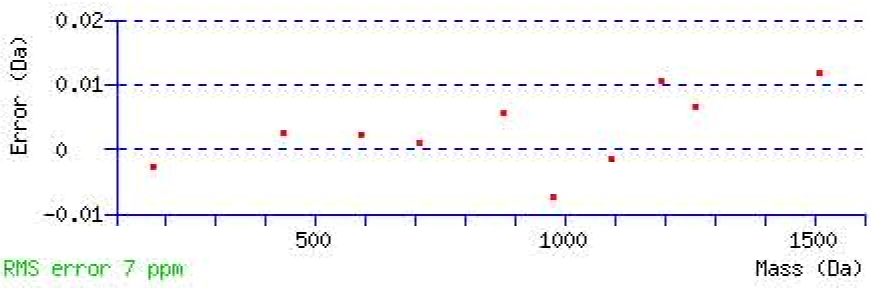
Match to Query 33655: 1700.888868 from(851.451710,2+) rtinseconds(2327) index(47970)
Title: Locus:1.1.1.3522.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

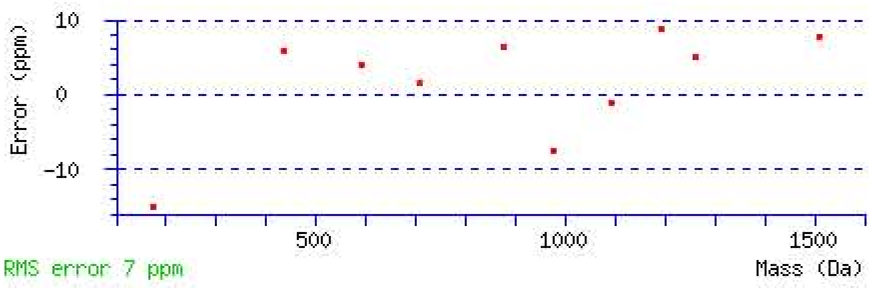
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1700.891998
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 66 **Expect:** 4.6e-006
Matches : 10/128 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	440.232602	220.619939	423.206053	212.106664			Q							13
2	511.269716	256.138496	494.243167	247.625221			A	***1262.673929***	631.840602	1245.647380	623.327328	1244.663364	622.835320	12
3	610.338130	305.672703	593.311581	297.159428			V	***1191.636815***	596.322045	1174.610266	587.808771	1173.626250	587.316763	11
4	725.365073	363.186174	708.338524	354.672900	707.354508	354.180892	D	***1092.568401***	546.787838	1075.541852	538.274564	1074.557836	537.782556	10
5	826.412752	413.710014	809.386203	405.196739	808.402187	404.704731	T	***977.541458***	489.274367	960.514909	480.761092	959.530893	480.269084	9
6	897.449866	449.228571	880.423317	440.715296	879.439301	440.223288	A	***876.493779***	438.750527	859.467230	430.237253	858.483214	429.745245	8
7	996.518280	498.762778	979.491731	490.249503	978.507715	489.757495	V	805.456665	403.231970	788.430116	394.718696	787.446100	394.226688	7
8	1111.545223	556.276249	1094.518674	547.762975	1093.534658	547.270967	D	***706.388251***	353.697764	689.361702	345.184489	688.377686	344.692481	6
9	1168.566687	584.786981	1151.540138	576.273707	1150.556122	575.781699	G	***591.361308***	296.184292	574.334759	287.671018			5
10	1267.635101	634.321188	1250.608552	625.807914	1249.624536	625.315906	V	534.339844	267.673560	517.313295	259.160286			4
11	1414.703515	707.855395	1397.676966	699.342121	1396.692950	698.850113	F	***435.271430***	218.139353	418.244881	209.626078			3
12	1527.787579	764.397427	1510.761030	755.884153	1509.777014	755.392145	I	288.203016	144.605146	271.176467	136.091871			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of QAVDTAVDGVFIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.6	1700.891998	-0.003130	QAVDTAVDGVFIR
8.1	1700.884109	0.004759	QALTTCDDILIK
3.1	1700.881424	0.007444	QAAVMGQKGGSKGR
0.8	1700.881882	0.006986	DNVGPRAPGRAPNQPR
0.7	1700.895813	-0.006945	VNPSVNPSISPAHGVAR
0.7	1700.863449	0.025419	GSKWEVYPAQVQGPR
0.5	1700.883224	0.005644	QLSLPETGELDSATLK
0.4	1700.880539	0.008329	KSLRINSTATPDQDR
0.4	1700.864120	0.024748	RENVNPRHPCLGPR
0.4	1700.905670	-0.016802	SLQEELSLARGTIER

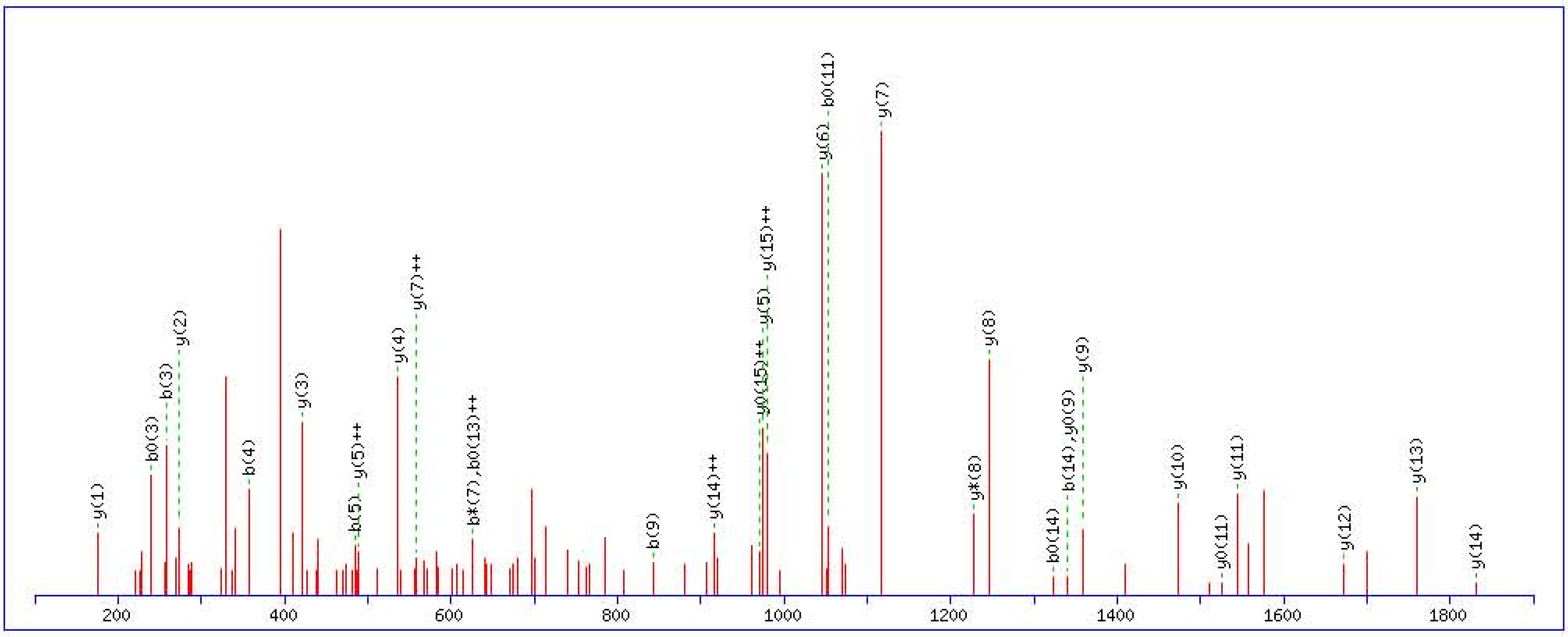
Mascot Search Results

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

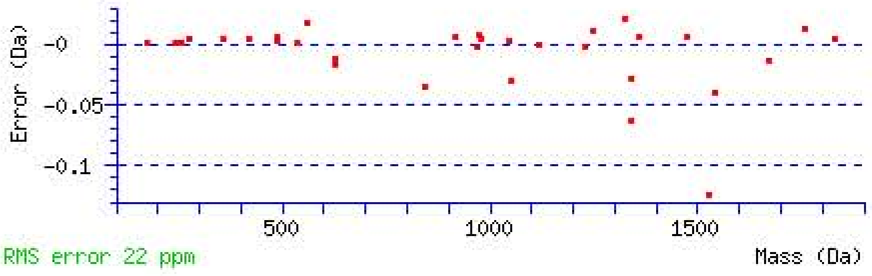
Match to Query 45325: 2314.180032 from(772.400620,3+) rtinseconds(2657) index(49707)
Title: Locus:1.1.1.3637.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

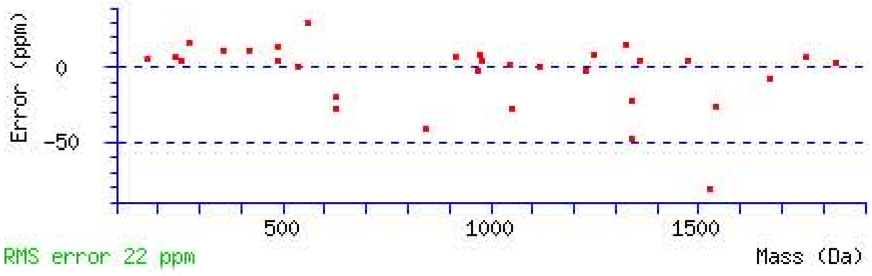
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2314.173950
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15 : Biotin:Thermo-21345 (Q)
Ions Score: 92 **Expect:** 1.9e-008
Matches : 32/200 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	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	1198.606242	599.806759	1181.579693	591.293485	1180.595677	590.801477	Q	***1245.640855***	623.324066	1228.614306	614.810791	1227.630290	614.318783	8
13	1269.643356	635.325316	1252.616807	626.812042	1251.632791	626.320034	A	***1117.582277***	559.294777	1100.555728	550.781502	1099.571712	550.289494	7
14	**1340.680470**	670.843873	1323.653921	662.330599	1322.669905	661.838591	A	***1046.545163***	523.776220	1029.518614	515.262945	1028.534598	514.770937	6
15	1779.905796	890.456536	1762.879247	881.943262	1761.895231	881.451254	Q	***975.508049***	488.257663	958.481500	479.744388	957.497484	479.252380	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
91.7	2314.173950	0.006082	GSLVQASEANLQAAQDFVR
52.9	2314.173950	0.006082	GSLVQASEANLQAAQDFVR

Mascot: http://www.matrixscience.com/

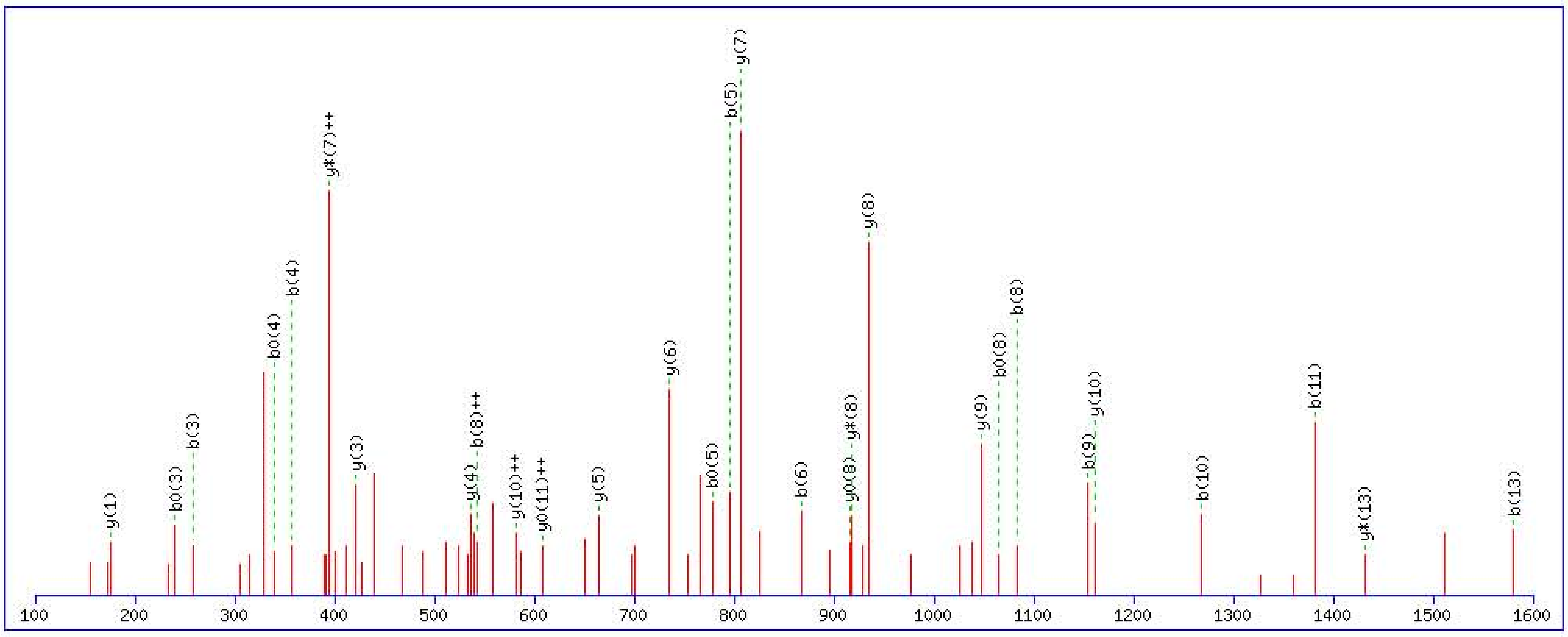
Mascot Search Results

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

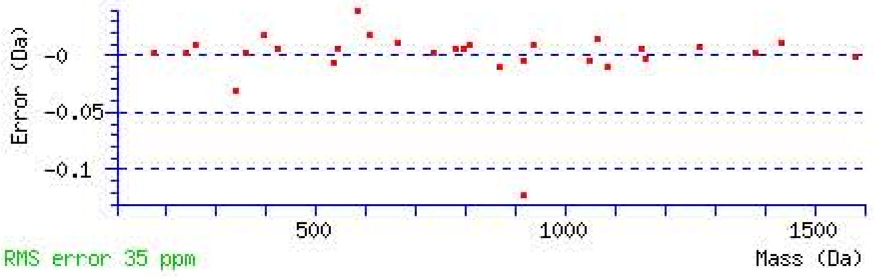
Match to Query 45326: 2314.181502 from(772.401110,3+) rtinseconds(2510) index(48884)
Title: Locus:1.1.1.3586.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

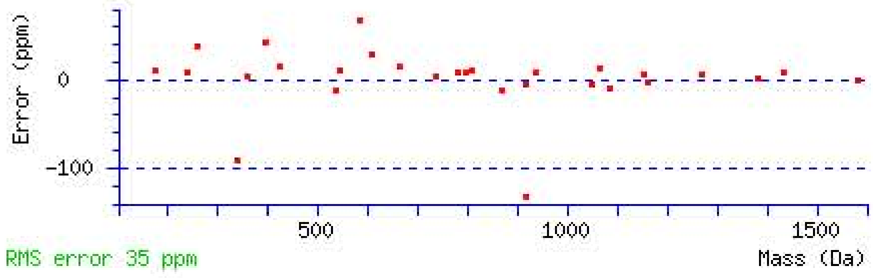
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 66  Expect: 1.1e-006
Matches : 29/200 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	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
65.7	2314.173950	0.007552	GSLVQASEANLQAAQDFVR
13.1	2314.173950	0.007552	GSLVQASEANLQAAQDFVR
2.3	2314.156662	0.024840	GPALTPIRDEEWGGHSPRSPR

Mascot: http://www.matrixscience.com/

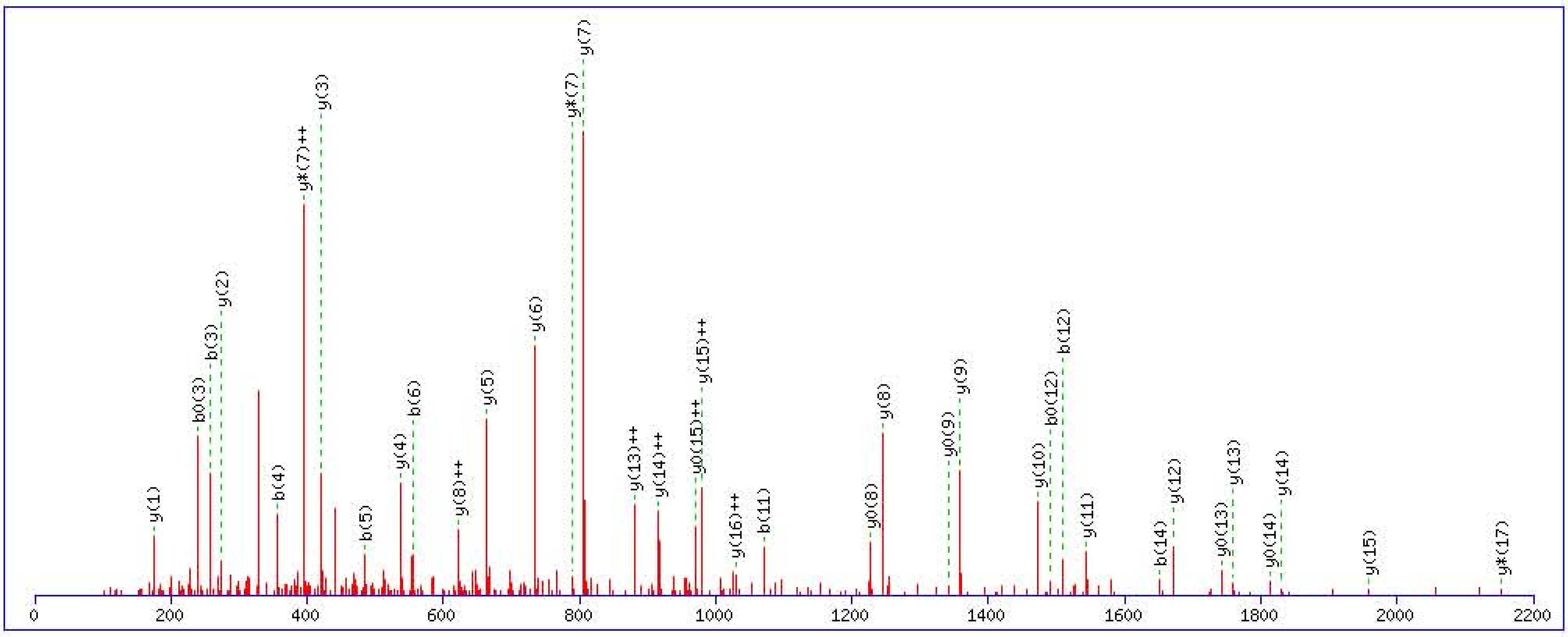
Mascot Search Results

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

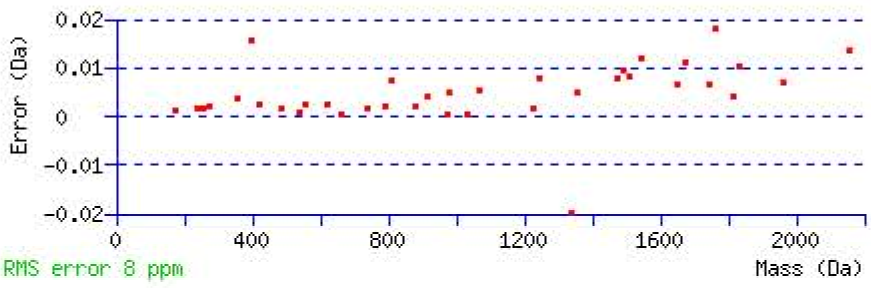
Match to Query 45327: 2314.188102 from(772.403310,3+) rtinseconds(2561) index(49081)
Title: Locus:1.1.1.3604.6 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

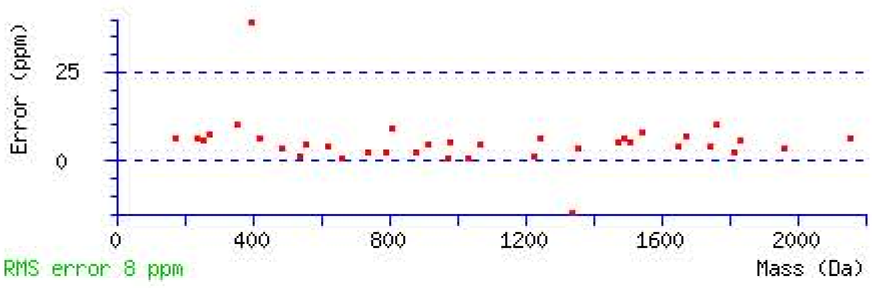
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 108  Expect: 5e-010
Matches : 37/200 fragment ions using 59 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
107.5	2314.173950	0.014152	GSLVQASEANLQAAQDFVR
60.7	2314.173950	0.014152	GSLVQASEANLQAAQDFVR
27.6	2314.173950	0.014152	GSLVQASEANLQAAQDFVR

Mascot: http://www.matrixscience.com/

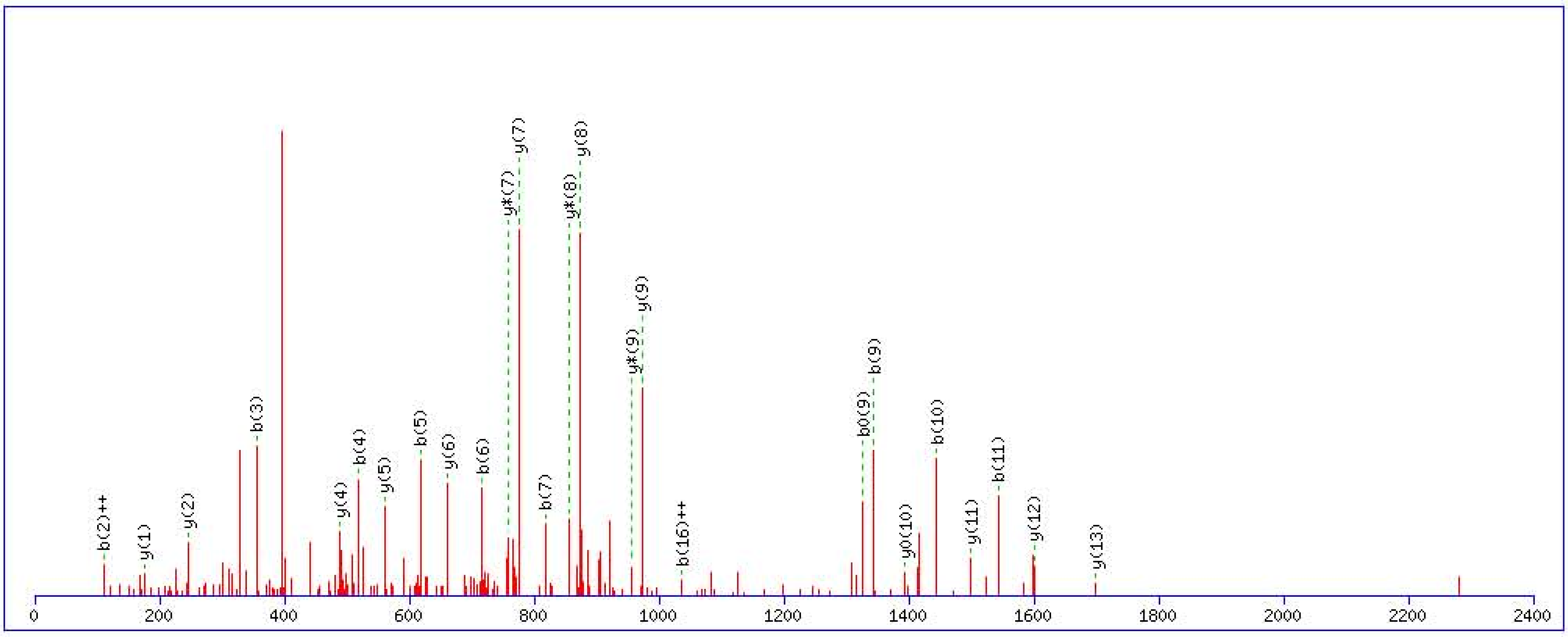
{MATRIX SCIENCE} Mascot Search Results

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

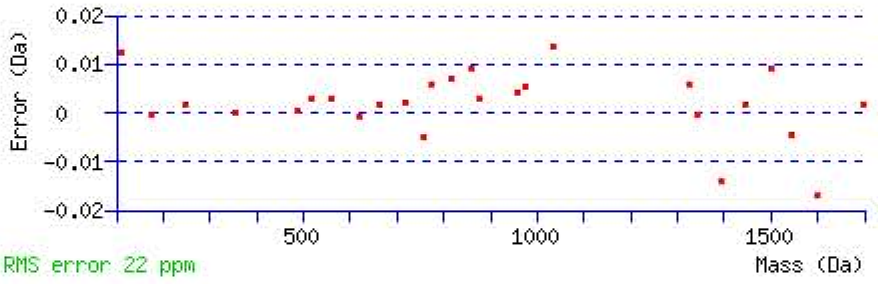
Match to Query 45358: 2316.167982 from(773.063270,3+) rtinseconds(1970) index(45811)
Title: Locus:1.1.1.3398.22 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

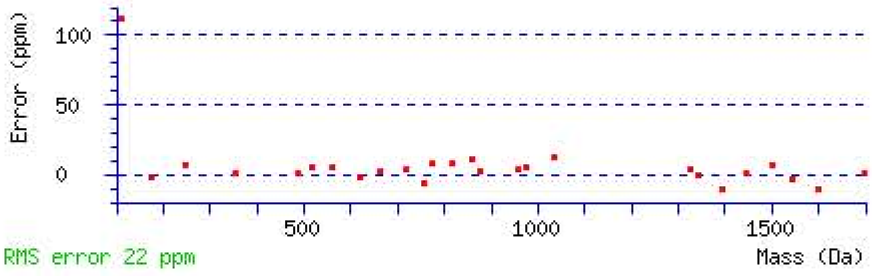
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2316.168488
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9     : Biotin:Thermo-21345 (Q)
Ions Score: 64  Expect: 1.1e-005
Matches : 26/172 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	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
63.7	2316.168488	-0.000506	FAHYVVTSQVVNTANEAR

Mascot: http://www.matrixscience.com/

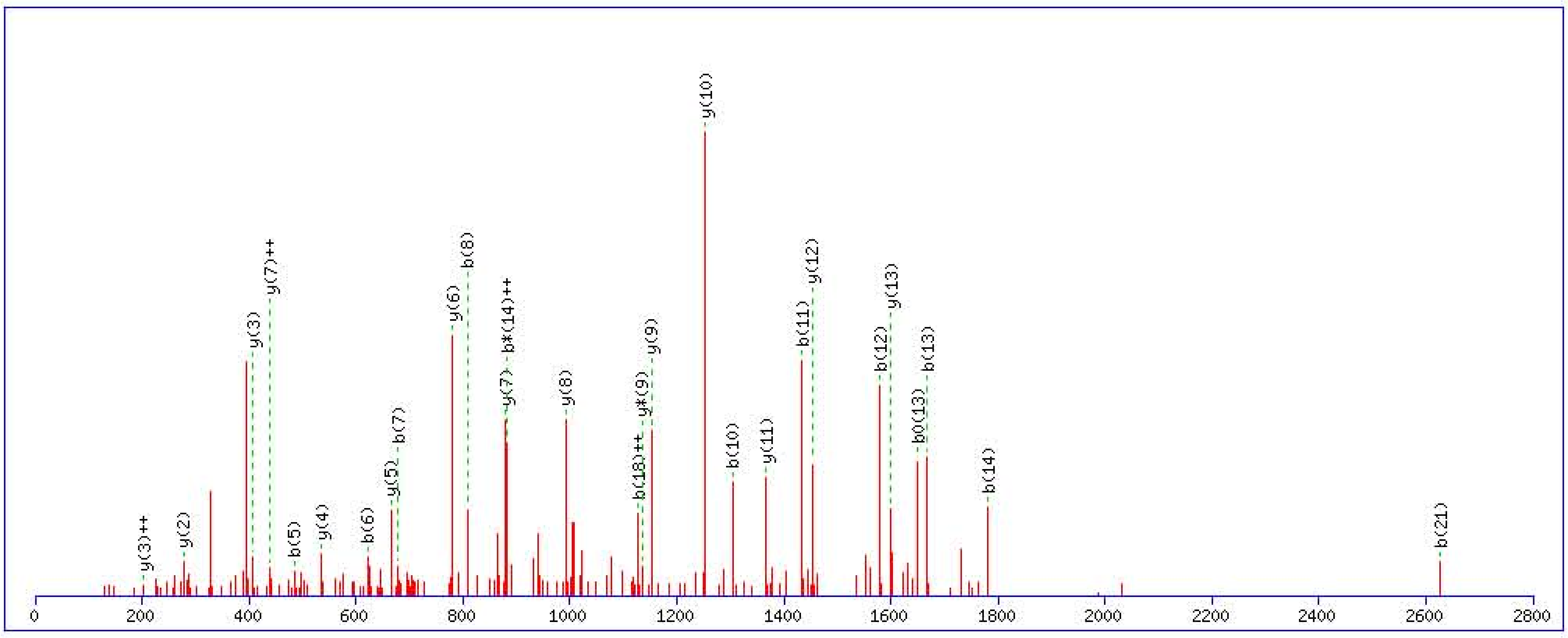
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADVQAHGEGQEFSITCLVDEEEMK**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

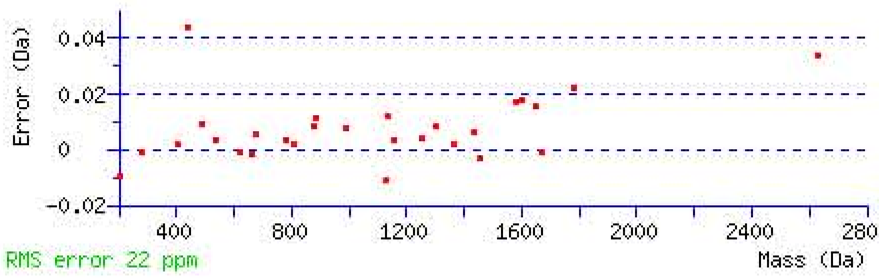
Match to Query 54231: 3032.359152 from(1011.793660,3+) rtinseconds(2519) index(48957)
Title: Locus:1.1.1.3589.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

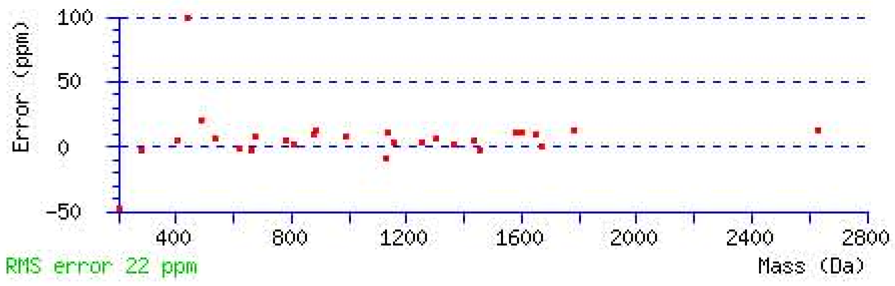
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3032.356552
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 100  Expect: 7.5e-010
Matches : 28/264 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	72.044390	36.525833					A							24
2	187.071333	94.039304			169.060768	85.034022	D	2962.326724	1481.667000	2945.300175	1473.153725	2944.316159	1472.661717	23
3	286.139747	143.573512			268.129182	134.568229	V	2847.299781	1424.153528	2830.273232	1415.640254	2829.289216	1415.148246	22
4	414.198325	207.602801	397.171776	199.089526	396.187760	198.597518	Q	2748.231367	1374.619321	2731.204818	1366.106047	2730.220802	1365.614039	21
5	***485.235439***	243.121357	468.208890	234.608083	467.224874	234.116075	A	2620.172789	1310.590032	2603.146240	1302.076758	2602.162224	1301.584750	20
6	***622.294351***	311.650814	605.267802	303.137539	604.283786	302.645531	H	2549.135675	1275.071475	2532.109126	1266.558201	2531.125110	1266.066193	19
7	***679.315815***	340.161546	662.289266	331.648271	661.305250	331.156263	G	2412.076763	1206.542019	2395.050214	1198.028745	2394.066198	1197.536737	18
8	***808.358408***	404.682842	791.331859	396.169568	790.347843	395.677560	E	2355.055299	1178.031287	2338.028750	1169.518013	2337.044734	1169.026005	17
9	865.379872	433.193574	848.353323	424.680300	847.369307	424.188292	G	2226.012706	1113.509991	2208.986157	1104.996716	2208.002141	1104.504708	16
10	***1304.605198***	652.806237	1287.578649	644.292963	1286.594633	643.800954	Q	2168.991242	1084.999259	2151.964693	1076.485984	2150.980677	1075.993976	15
11	***1433.647791***	717.327534	1416.621242	708.814259	1415.637226	708.322251	E	1729.765916	865.386596	1712.739367	856.873322	1711.755351	856.381314	14
12	***1580.716205***	790.861741	1563.689656	782.348466	1562.705640	781.856458	F	***1600.723323***	800.865300	1583.696774	792.352025	1582.712758	791.860017	13
13	***1667.748233***	834.377755	1650.721684	825.864480	1649.737668	825.372472	S	***1453.654909***	727.331093	1436.628360	718.817818	1435.644344	718.325810	12
14	***1780.832297***	890.919787	1763.805748	882.406512	1762.821732	881.914504	I	***1366.622881***	683.815079	1349.596332	675.301804	1348.612316	674.809796	11
15	1881.879976	941.443626	1864.853427	932.930352	1863.869411	932.438344	T	***1253.538817***	627.273047	1236.512268	618.759772	1235.528252	618.267764	10
16	2041.910625	1021.458951	2024.884076	1012.945676	2023.900060	1012.453668	C	***1152.491138***	576.749207	1135.464589	568.235933	1134.480573	567.743925	9
17	2154.994689	1078.000983	2137.968140	1069.487708	2136.984124	1068.995700	L	***992.460489***	496.733883	975.433940	488.220608	974.449924	487.728600	8
18	2254.063103	1127.535189	2237.036554	1119.021915	2236.052538	1118.529907	V	***879.376425***	440.191851	862.349876	431.678576	861.365860	431.186568	7
19	2369.090046	1185.048661	2352.063497	1176.535386	2351.079481	1176.043378	D	***780.308011***	390.657644	763.281462	382.144369	762.297446	381.652361	6
20	2498.132639	1249.569957	2481.106090	1241.056683	2480.122074	1240.564675	E	***665.281068***	333.144172	648.254519	324.630898	647.270503	324.138890	5
21	***2627.175232***	1314.091254	2610.148683	1305.577979	2609.164667	1305.085971	E	***536.238475***	268.622876	519.211926	260.109601	518.227910	259.617593	4
22	2756.217825	1378.612551	2739.191276	1370.099276	2738.207260	1369.607268	E	***407.195882***	204.101579	390.169333	195.588305	389.185317	195.096297	3
23	2887.258310	1444.132793	2870.231761	1435.619518	2869.247745	1435.127511	M	***278.153289***	139.580282	261.126740	131.067008			2
24							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ADVQAHGEGQEFSITCLVDEEEMK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
99.8	3032.356552	0.002600	ADVQAHGEGQEFSITCLVDEEEMK
73.3	3032.356552	0.002600	ADVQAHGEGQEFSITCLVDEEEMK

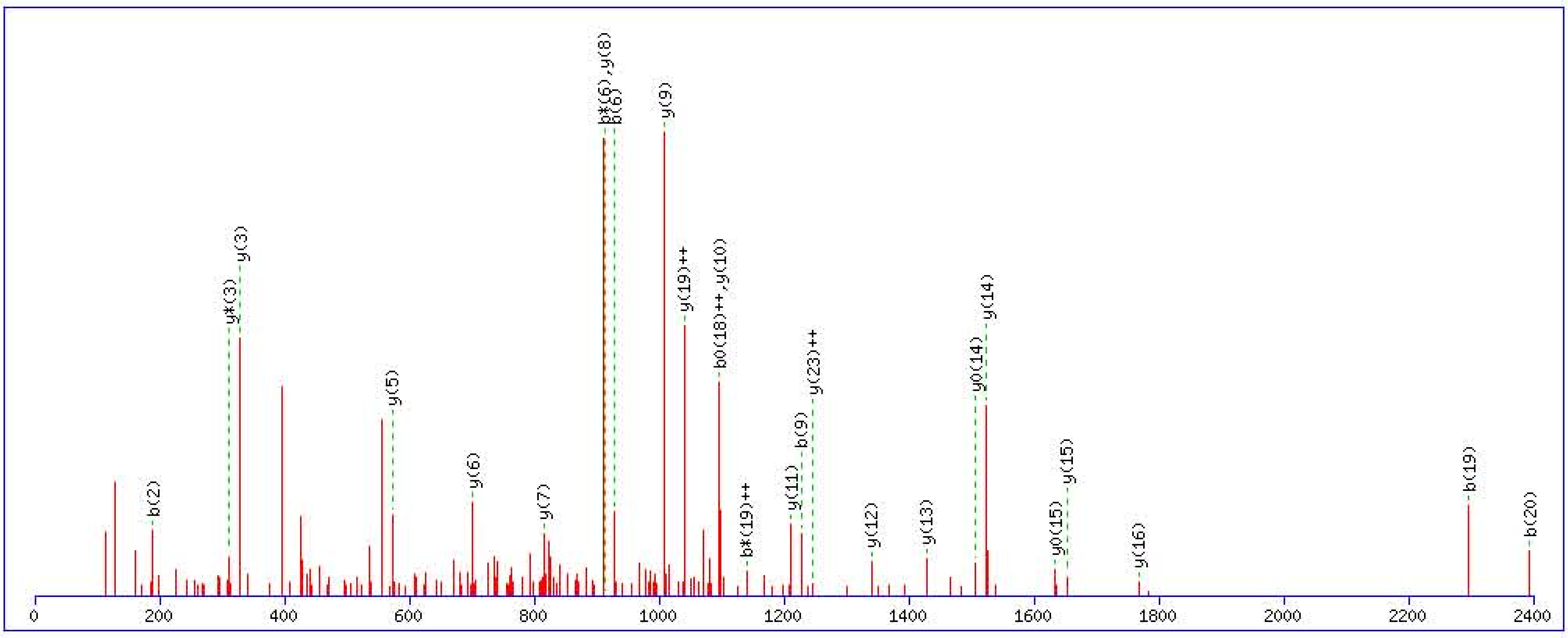
{MATRIX SCIENCE} Mascot Search Results

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

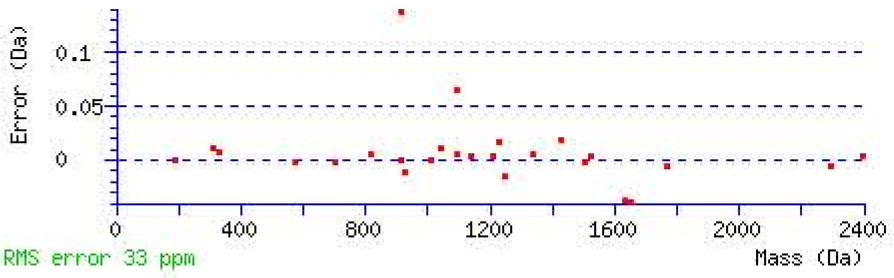
Match to Query 58186: 3304.619896 from(827.162250,4+) rtinseconds(2240) index(47487)
Title: Locus:1.1.1.3492.21 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

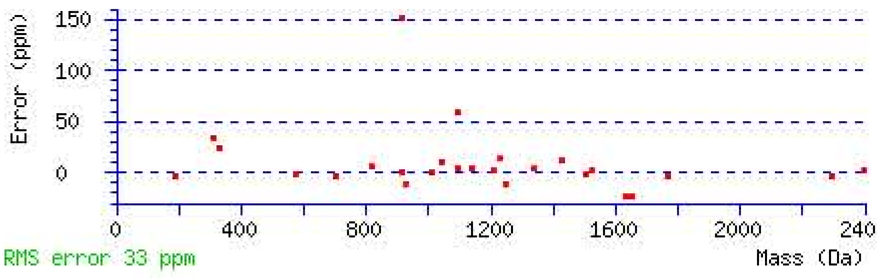
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3304.614151
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 85  Expect: 8.5e-008
Matches : 26/300 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	58.028740	29.518008					G							28
2	**189.069225**	95.038250					M	3248.599985	1624.803630	3231.573436	1616.290356	3230.589420	1615.798348	27
3	260.106339	130.556807					A	3117.559500	1559.283388	3100.532951	1550.770113	3099.548935	1550.278105	26
4	375.133282	188.070279			357.122717	179.064997	D	3046.522386	1523.764831	3029.495837	1515.251556	3028.511821	1514.759548	25
5	814.358608	407.682942	797.332059	399.169668	796.348043	398.677660	Q	2931.495443	1466.251359	2914.468894	1457.738085	2913.484878	1457.246077	24
6	**929.385551**	465.196414	912.359002	456.683139	911.374986	456.191131	D	2492.270117	1246.638696	2475.243568	1238.125422	2474.259552	1237.633414	23
7	986.407015	493.707146	969.380466	485.193871	968.396450	484.701863	G	2377.243174	1189.125225	2360.216625	1180.611950	2359.232609	1180.119942	22
8	1099.491079	550.249177	1082.464530	541.735903	1081.480514	541.243895	L	2320.221710	1160.614493	2303.195161	1152.101218	2302.211145	1151.609210	21
9	**1227.586042**	614.296659	1210.559493	605.783385	1209.575477	605.291376	K	2207.137646	1104.072461	2190.111097	1095.559186	2189.127081	1095.067178	20
10	1324.638806	662.823041	1307.612257	654.309767	1306.628241	653.817758	P	2079.042683	1040.024980	2062.016134	1031.511705	2061.032118	1031.019697	19
11	1425.686485	713.346881	1408.659936	704.833606	1407.675920	704.341598	T	1981.989919	991.498598	1964.963370	982.985323	1963.979354	982.493315	18
12	1538.770549	769.888912	1521.744000	761.375638	1520.759984	760.883630	I	1880.942240	940.974758	1863.915691	932.461484	1862.931675	931.969476	17
13	1653.797492	827.402384	1636.770943	818.889110	1635.786927	818.397101	D	***1767.858176***	884.432726	1750.831627	875.919452	1749.847611	875.427444	16
14	1781.892455	891.449865	1764.865906	882.936591	1763.881890	882.444583	K	***1652.831233***	826.919255	1635.804684	818.405980	1634.820668	817.913972	15
15	1878.945219	939.976248	1861.918670	931.462973	1860.934654	930.970965	P	***1524.736270***	762.871773	1507.709721	754.358499	1506.725705	753.866491	14
16	1965.977247	983.492262	1948.950698	974.978987	1947.966682	974.486979	S	***1427.683506***	714.345391	1410.656957	705.832117	1409.672941	705.340109	13
17	2095.019840	1048.013558	2077.993291	1039.500283	2077.009275	1039.008275	E	***1340.651478***	670.829377	1323.624929	662.316103	1322.640913	661.824095	12
18	2210.046783	1105.527029	2193.020234	1097.013755	2192.036218	1096.521747	D	***1211.608885***	606.308081	1194.582336	597.794806	1193.598320	597.302798	11
19	**2297.078811**	1149.043043	2280.052262	1140.529769	2279.068246	1140.037761	S	***1096.581942***	548.794609	1079.555393	540.281335	1078.571377	539.789327	10
20	**2394.131575**	1197.569425	2377.105026	1189.056151	2376.121010	1188.564143	P	***1009.549914***	505.278595	992.523365	496.765321	991.539349	496.273313	9
21	2491.184339	1246.095807	2474.157790	1237.582533	2473.173774	1237.090525	P	***912.497150***	456.752213	895.470601	448.238939	894.486585	447.746931	8
22	2604.268403	1302.637839	2587.241854	1294.124565	2586.257838	1293.632557	L	***815.444386***	408.225831	798.417837	399.712557	797.433821	399.220549	7
23	2733.310996	1367.159136	2716.284447	1358.645861	2715.300431	1358.153854	E	***702.360322***	351.683799	685.333773	343.170525	684.349757	342.678517	6
24	2864.351481	1432.679379	2847.324932	1424.166104	2846.340916	1423.674096	M	***573.317729***	287.162503	556.291180	278.649228			5
25	2977.435545	1489.221411	2960.408996	1480.708136	2959.424980	1480.216128	L	442.277244	221.642260	425.250695	213.128986			4
26	3034.457009	1517.732143	3017.430460	1509.218868	3016.446444	1508.726860	G	***329.193180***	165.100228	312.166631	156.586953			3
27	3131.509773	1566.258525	3114.483224	1557.745250	3113.499208	1557.253242	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
84.8	3304.614151	0.005745	GMADQDGLKPTIDKPSEDSPPLEMLGPR

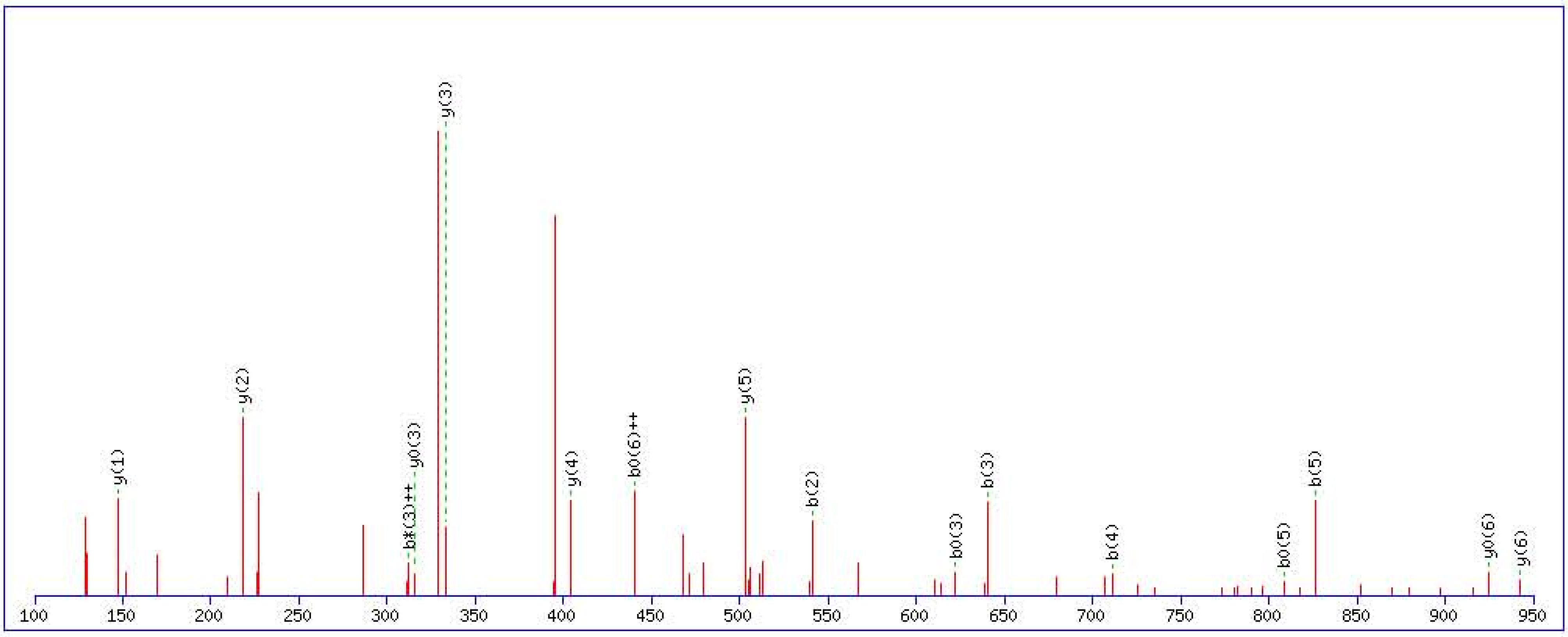
Mascot Search Results

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

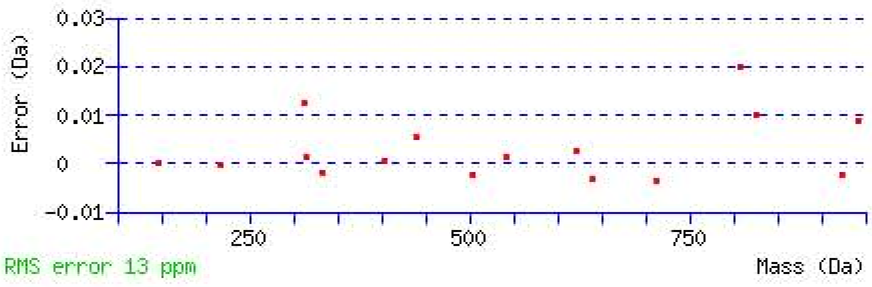
Match to Query 12688: 1042.544688 from(522.279620,2+) rtinseconds(1317) index(41902)
Title: Locus:1.1.1.3171.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

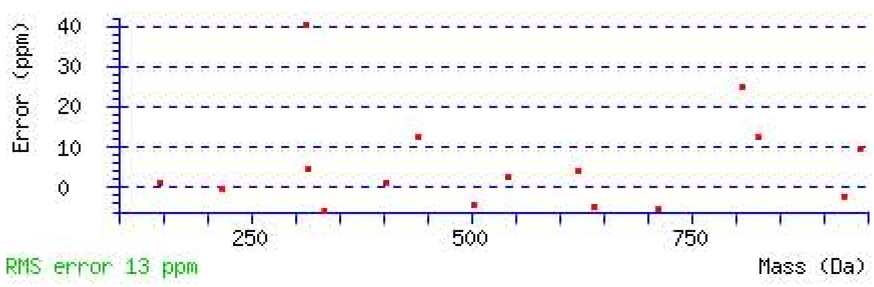
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 32  Expect: 0.016
Matches : 16/66 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	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
32.2	1042.548111	-0.003423	TQVADAK
16.7	1042.540726	0.003962	KPVSEVGDGR
11.1	1042.548096	-0.003408	SLQADAK
9.4	1042.540680	0.004008	EAEKRPADK
6.1	1042.559357	-0.014669	KTVPPCVSR
5.8	1042.529480	0.015208	TSPQPESGIK
4.9	1042.548080	-0.003392	KEQEAK
4.9	1042.548080	-0.003392	KQEEAK
4.2	1042.540710	0.003978	SLKSPPGSDR
3.8	1042.544724	-0.000036	WKGIEPGEK

Mascot: http://www.matrixscience.com/

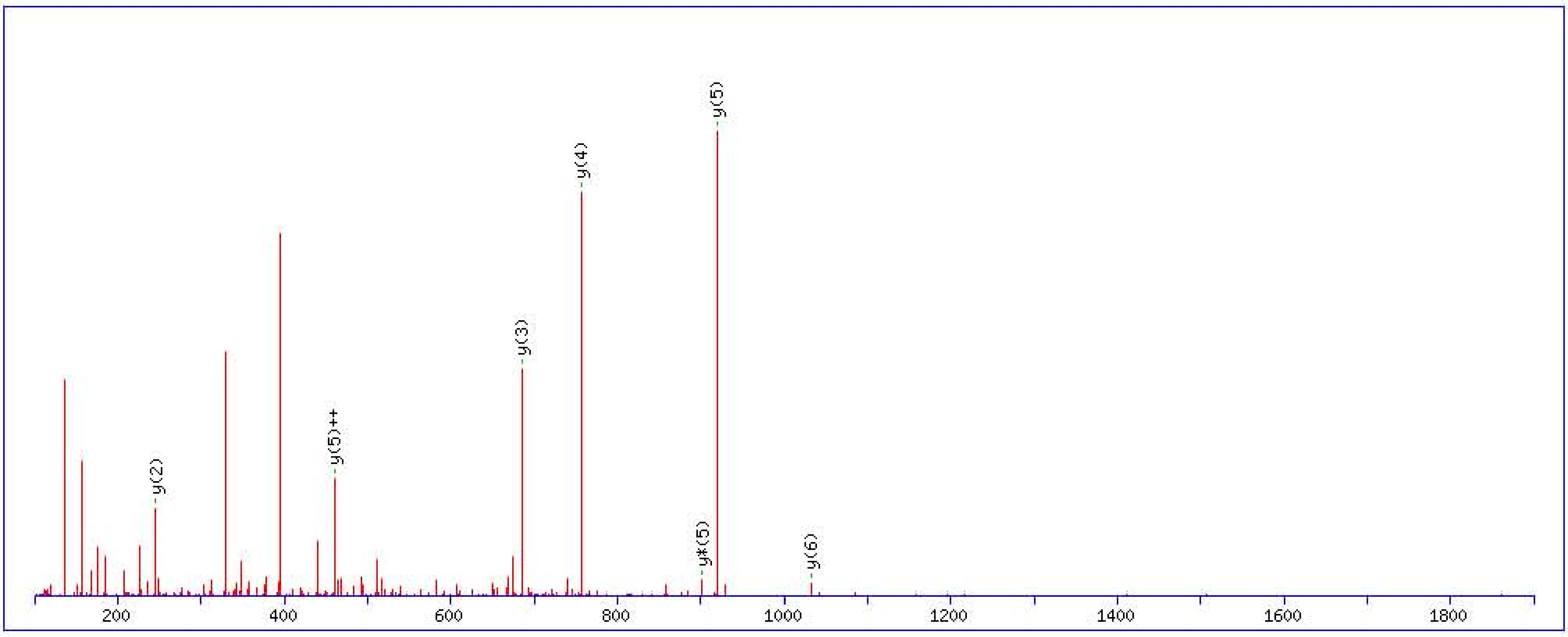
{MATRIX SCIENCE} Mascot Search Results

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

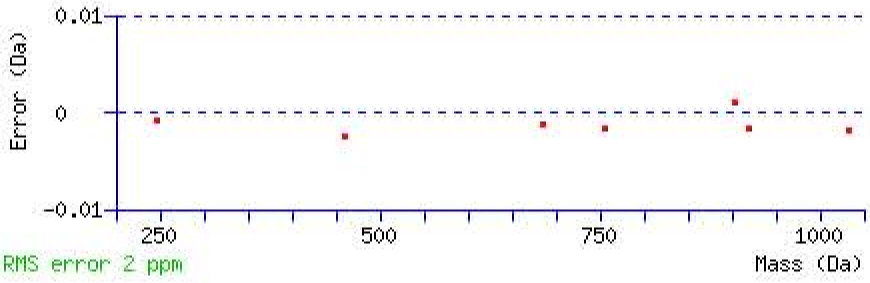
Match to Query 13868: 1102.592188 from(552.303370,2+) rtinseconds(1695) index(44115)
Title: Locus:1.1.1.3303.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

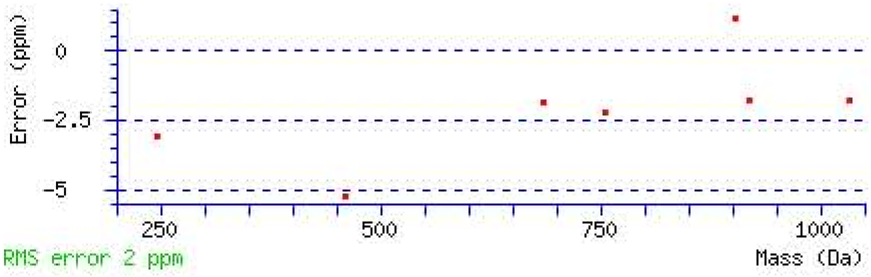
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1102.595703
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.004
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
37.8	1102.595703	-0.003515	ALYAQAR
11.8	1102.580460	0.011728	AMVENVTLAR
10.9	1102.602234	-0.010046	AIELGYNPVK
6.0	1102.591660	0.000528	AMKRLEEAR
5.0	1102.591690	0.000498	NMEVSLVRR
4.8	1102.588333	0.003855	SPYGLTPRGR
2.3	1102.580475	0.011713	SPQMVSAIVR
2.2	1102.580475	0.011713	ALSLVIGDCR
2.2	1102.602249	-0.010061	AIVLFNPDSK
1.8	1102.584305	0.007883	QSSQRGLTAR

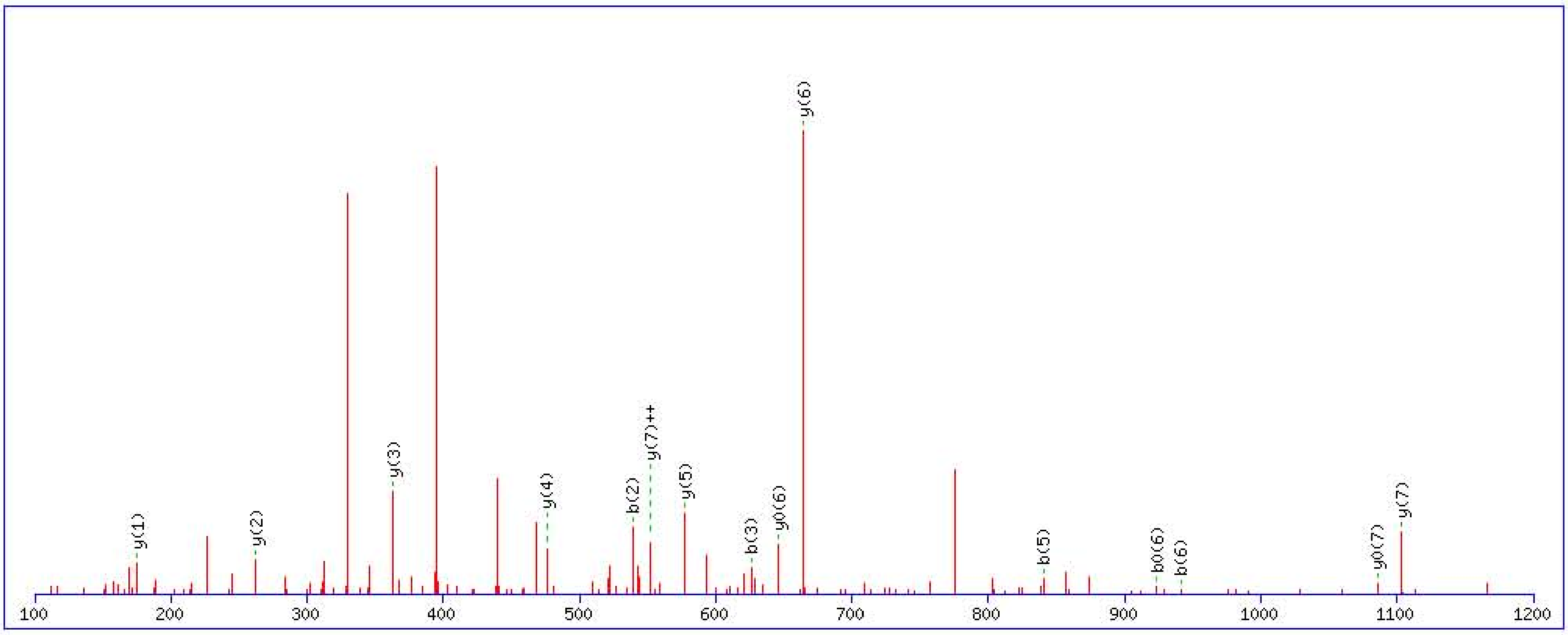
{MATRIX SCIENCE} Mascot Search Results

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

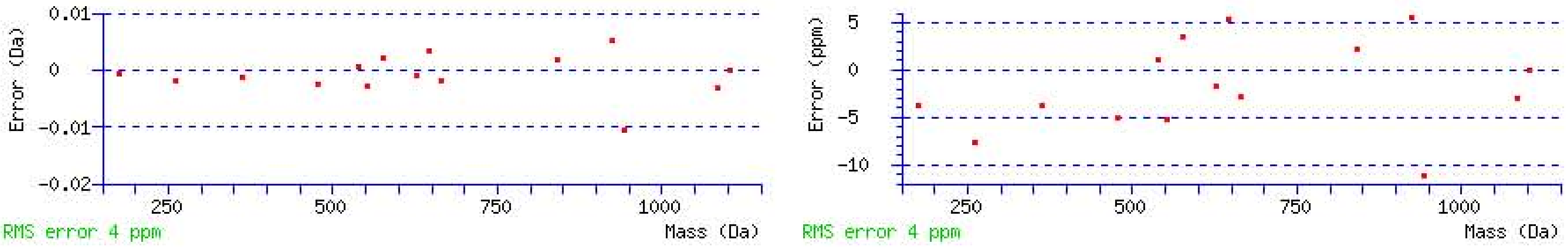
Match to Query 17787: 1201.644968 from(601.829760,2+) rtinseconds(1526) index(43051)
Title: Locus:1.1.1.3244.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 1201.648895
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 38 **Expect:** 0.0016
Matches : 15/76 fragment ions using 32 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
37.6	1201.648895	-0.003927	VQSTITSR
7.5	1201.638992	0.005976	VQPPSHAR
3.7	1201.641495	0.003473	NLTNVLGTQSR
3.5	1201.630249	0.014719	KLDAEDVIGSR
2.2	1201.638992	0.005976	VQGREFR

Mascot: http://www.matrixscience.com/

{MATRIX SCIENCE}

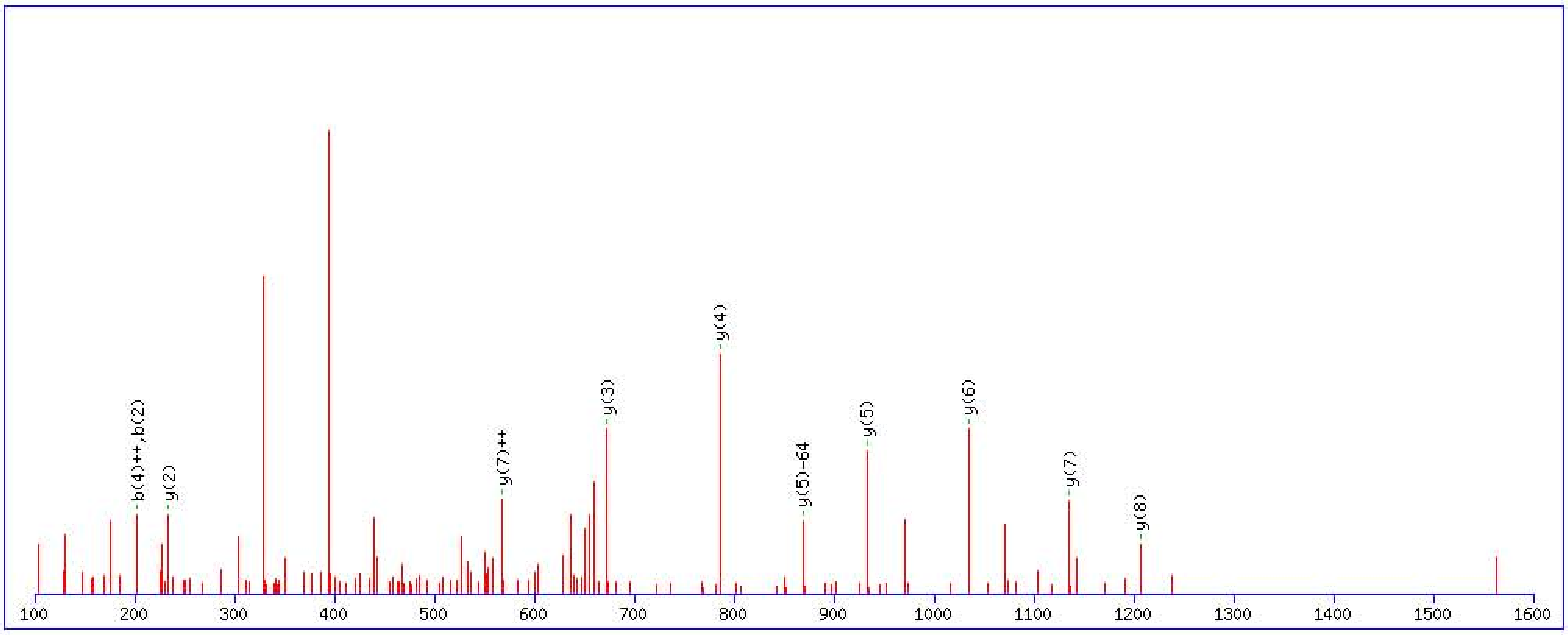
Mascot Search Results

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

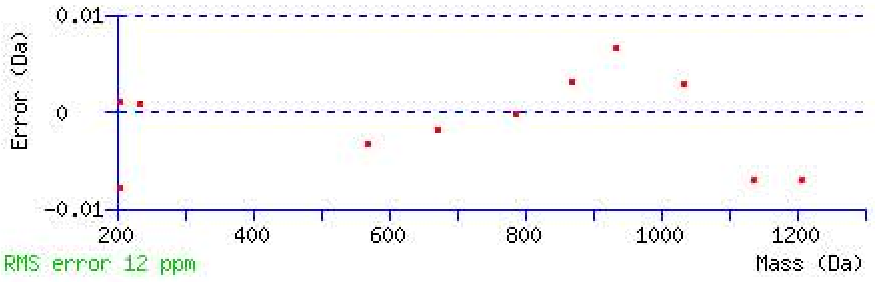
Match to Query 21042: 1336.652948 from(669.333750,2+) rtinseconds(1561) index(43255)
Title: Locus:1.1.1.3256.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

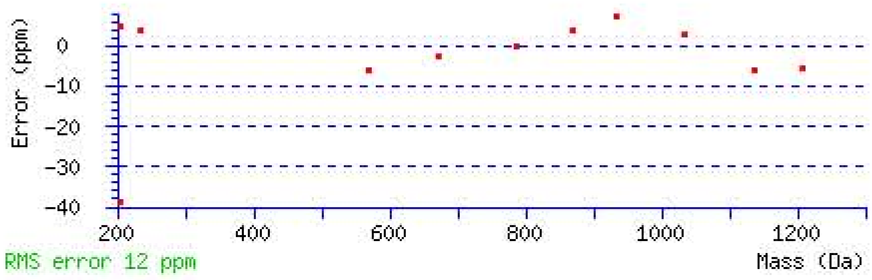
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1336.655289
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: 60  Expect: 1.5e-005
Matches : 11/122 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	132.047761	66.527518					M							9
2	**203.084875**	102.046075					A	***1206.622094***	603.814685	1189.595545	595.301411	1188.611529	594.809403	8
3	304.132554	152.569915			286.121989	143.564632	T	***1135.584980***	568.296128	1118.558431	559.782854	1117.574415	559.290846	7
4	405.180233	**203.093754**			387.169668	194.088472	T	***1034.537301***	517.772289	1017.510752	509.259014	1016.526736	508.767006	6
5	552.215633	276.611455			534.205068	267.606172	M	***933.489622***	467.248449	916.463073	458.735175	915.479057	458.243167	5
6	665.299697	333.153487			647.289132	324.148204	I	***786.454222***	393.730749	769.427673	385.217475	768.443657	384.725467	4
7	1104.525023	552.766149	1087.498474	544.252875	1086.514458	543.760867	Q	***673.370158***	337.188717	656.343609	328.675443	655.359593	328.183435	3
8	1191.557051	596.282164	1174.530502	587.768889	1173.546486	587.276881	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
59.8	1336.655289	-0.002341	MATTMIQSK
9.5	1336.647018	0.005930	SDSELVSKSTER
5.6	1336.662247	-0.009299	KAEELQATYER
3.8	1336.662308	-0.009360	KDTWGVVSSGSSK
1.5	1336.655289	-0.002341	MATTMIQSK

Mascot: http://www.matrixscience.com/

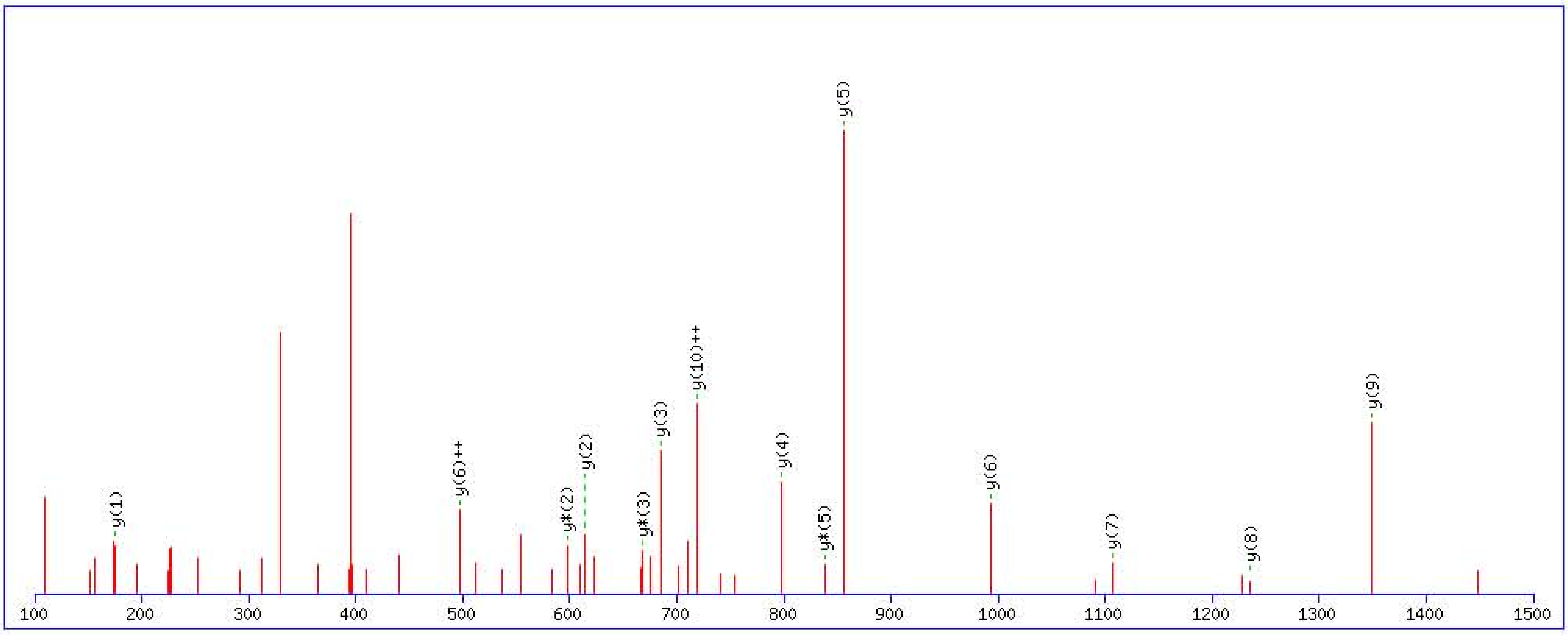
{MATRIX}{SCIENCE} Mascot Search Results

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

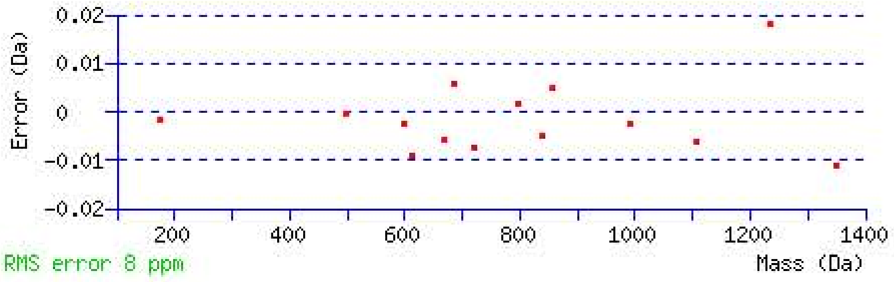
Match to Query 28465: 1548.775782 from(517.265870,3+) rtinseconds(1451) index(42582)
Title: Locus:1.1.1.3218.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

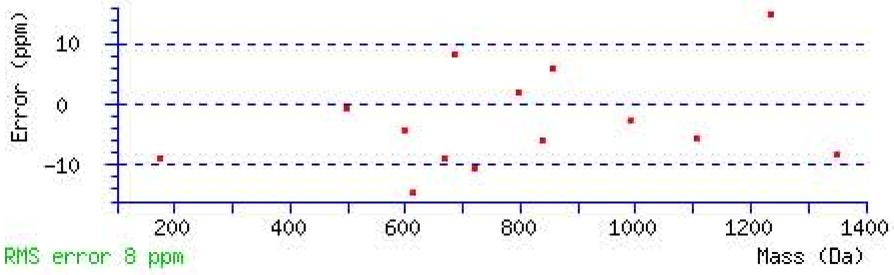
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1548.783066
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 2.5e-005
Matches : 14/100 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							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
52.2	1548.783066	-0.007284	LSNENHGIAQR
3.1	1548.798340	-0.022558	LSALRCGHLFGYR

Mascot: http://www.matrixscience.com/

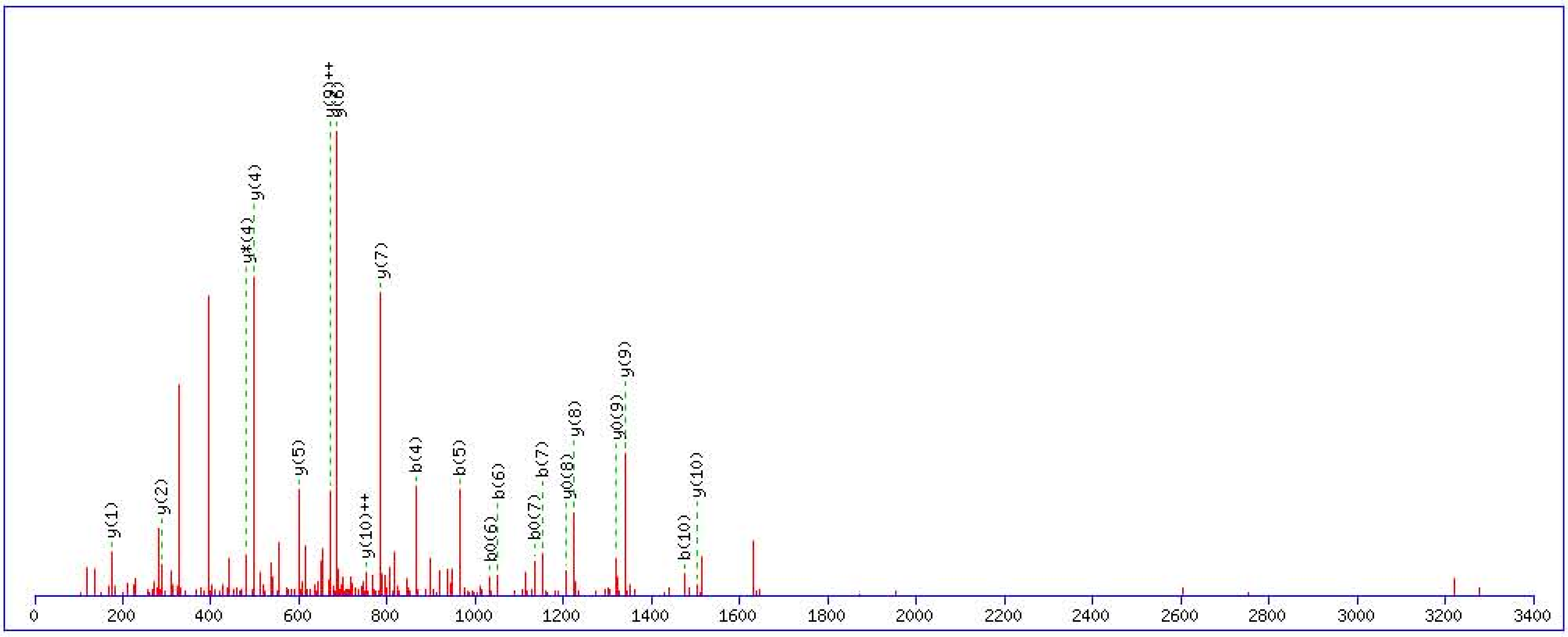
Mascot Search Results

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

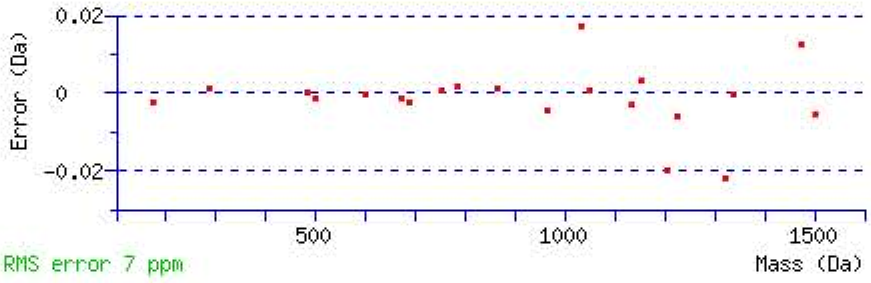
Match to Query 32647: 1647.873668 from(824.944110,2+) rtinseconds(2300) index(33613)
Title: Locus:1.1.1.3464.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

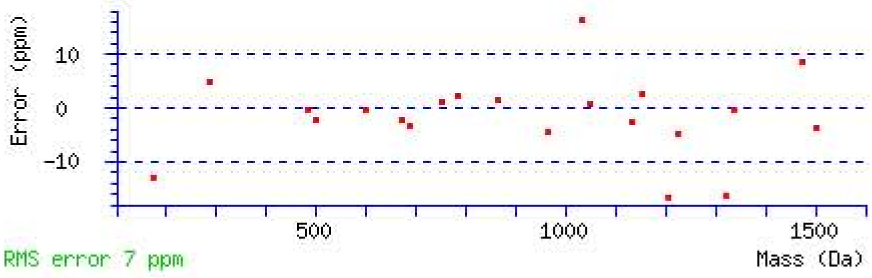
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1647.880676
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 68 **Expect:** 3.2e-006
Matches : 21/98 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	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
67.8	1647.880676	-0.007008	FYNQVSTPLLR
8.7	1647.873260	0.000408	AFKELPVNAQNYVR
6.1	1647.895264	-0.021596	MKPILLQGHER
4.5	1647.887878	-0.014210	TLNQQLTNHIR
2.8	1647.887878	-0.014210	TLNQQLTNHIR
1.6	1647.862015	0.011653	LSKQHLEKYPDYK
0.6	1647.894394	-0.020726	LSDNIQNVVLKSYR
0.0	1647.873260	0.000408	RQWQSELLQKYGL

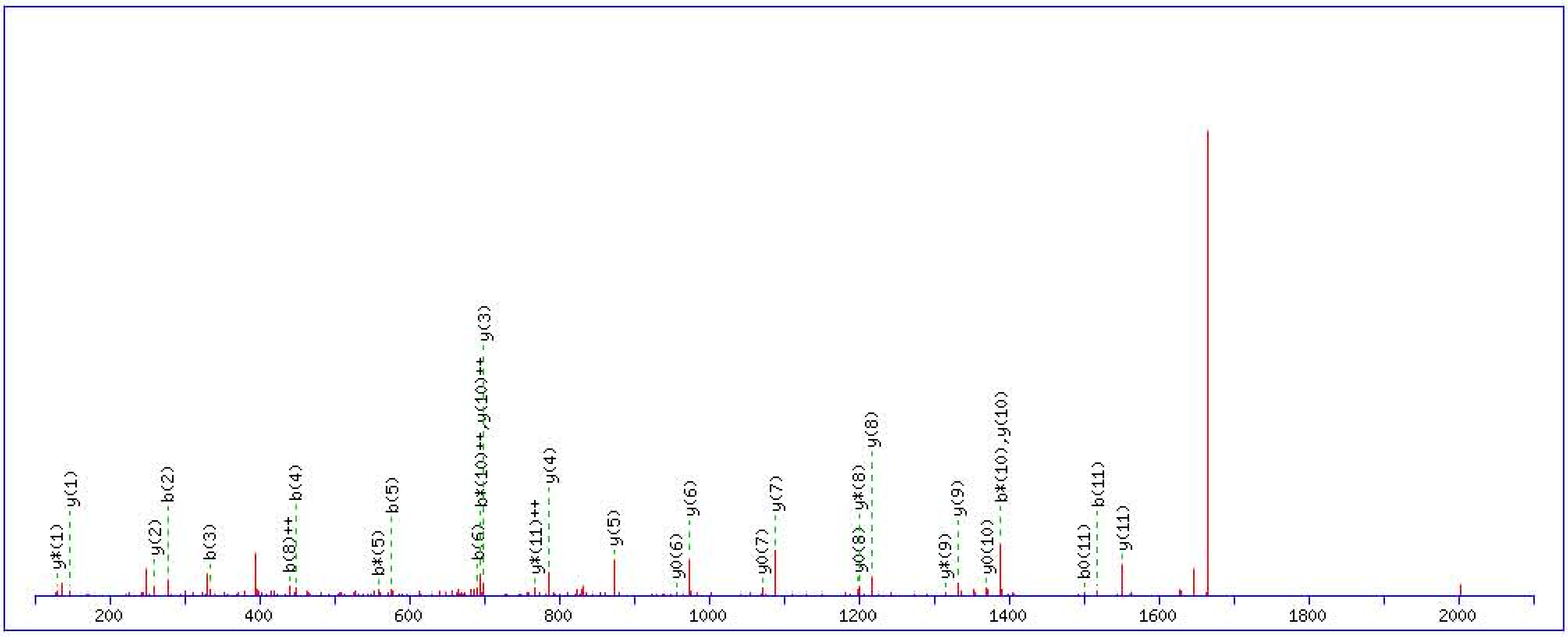
Mascot Search Results

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

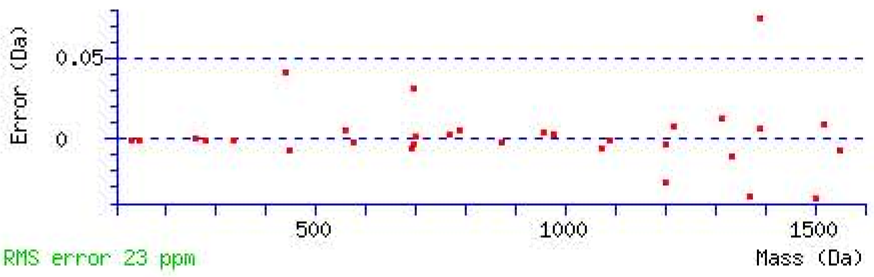
Match to Query 32956: 1663.819548 from(832.917050,2+) rtinseconds(1691) index(44094)
Title: Locus:1.1.1.3301.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

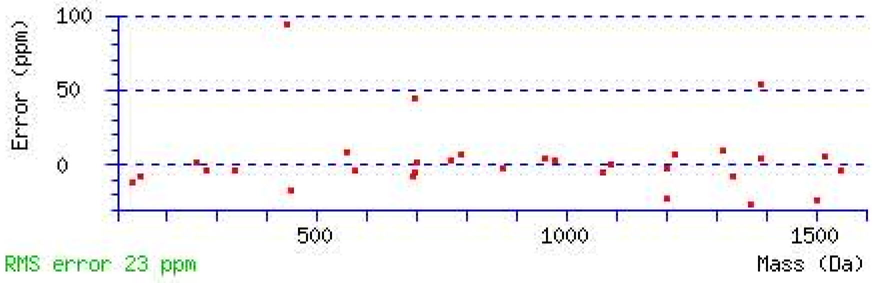
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1663.823944
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 84  Expect: 7.2e-008
Matches : 31/110 fragment ions using 47 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
83.5	1663.823944	-0.004396	IYGNQDTSSQLK
20.4	1663.823944	-0.004396	IYGNQDTSSQLK
7.0	1663.821442	-0.001894	LYGCFLRVYMQSK
3.1	1663.806183	0.013365	DLSMFSQNMTHIIK
2.1	1663.835175	-0.015627	DCSIIKWSVESGRK
2.0	1663.831345	-0.011797	QLTDCISEFLK

Mascot: http://www.matrixscience.com/

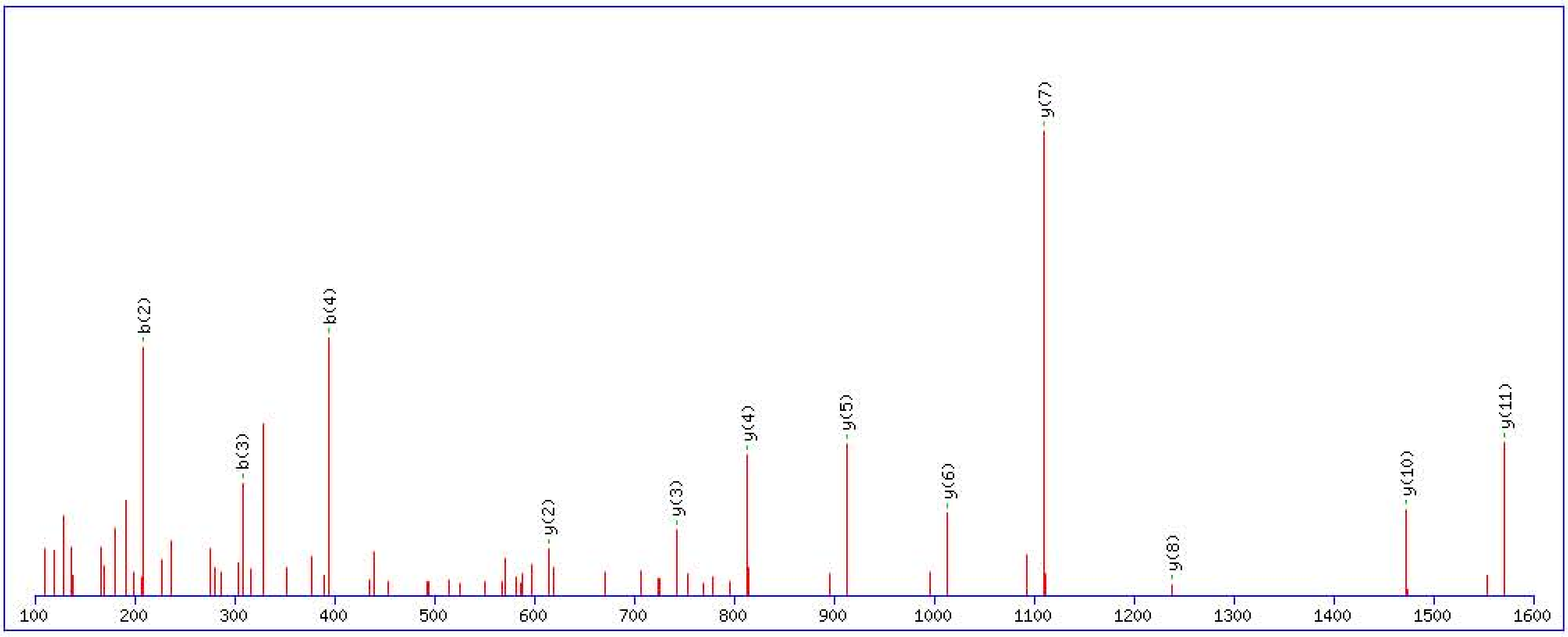
{MATRIX SCIENCE} Mascot Search Results

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

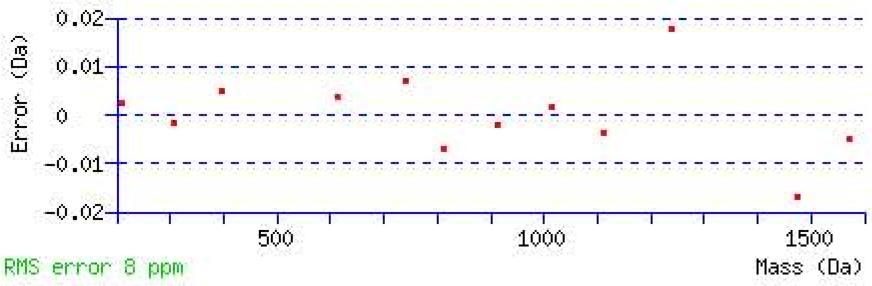
Match to Query 35306: 1778.956842 from(593.992890,3+) rtinseconds(1549) index(43194)
Title: Locus:1.1.1.3252.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

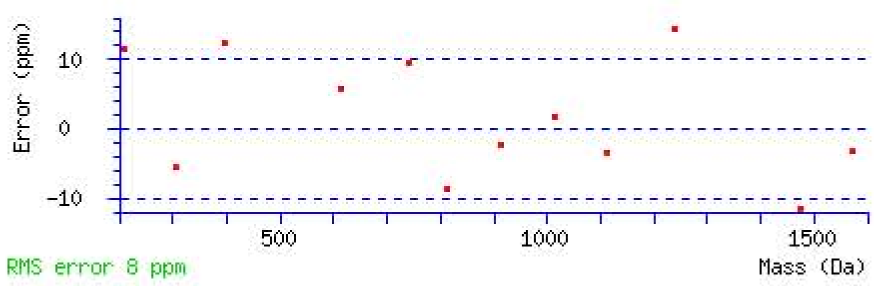
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1778.961395
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 82 **Expect:** 1.4e-007
Matches : 12/118 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							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
81.8	1778.961395	-0.004553	AHVSFKPTVAQQR
65.5	1778.961395	-0.004553	AHVSFKPTVAQQR

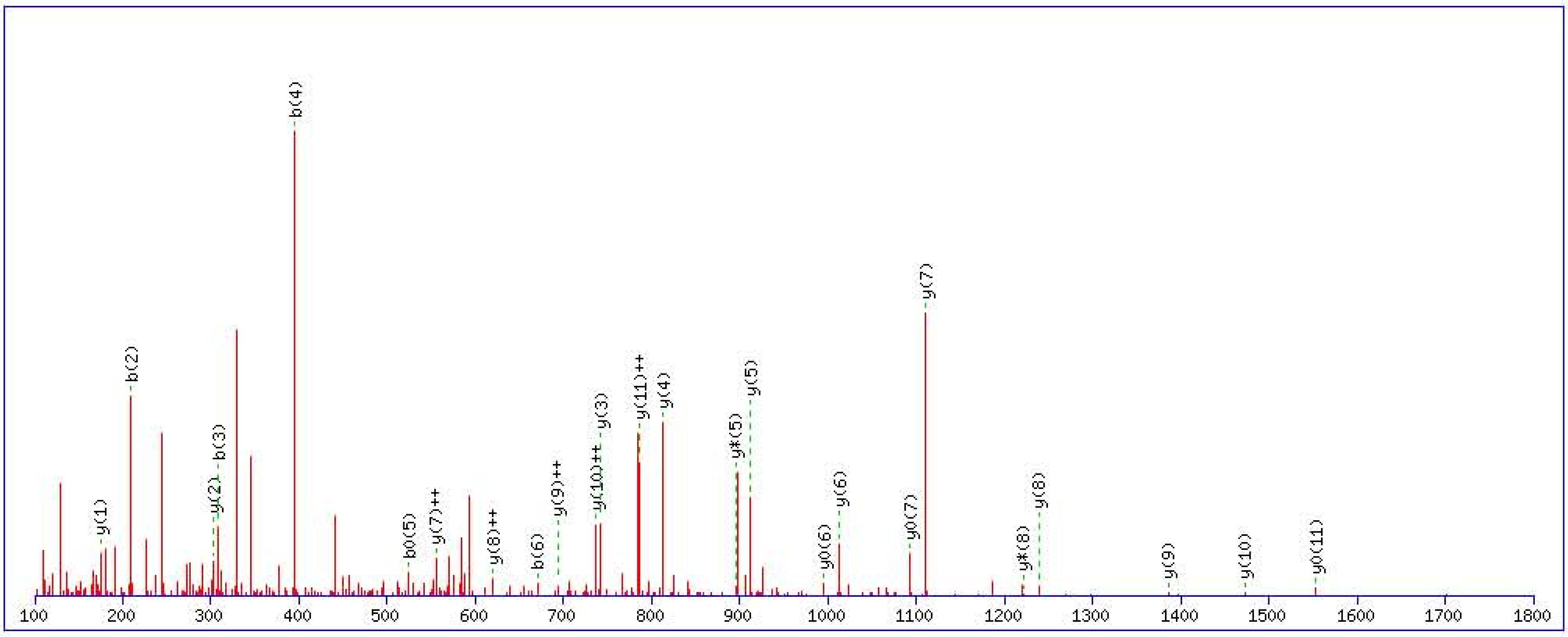
{MATRIX SCIENCE} Mascot Search Results

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

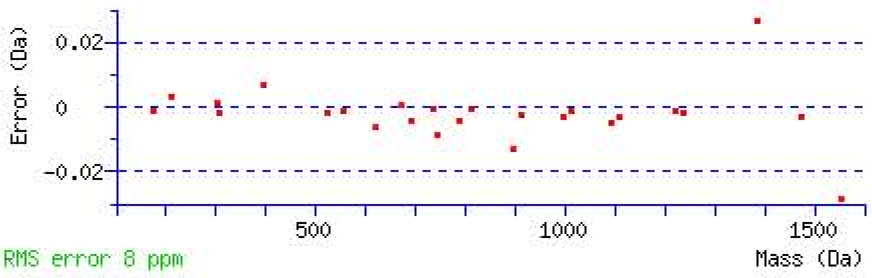
Match to Query 35307: 1778.956842 from(593.992890,3+) rtinseconds(1564) index(43268)
Title: Locus:1.1.1.3257.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

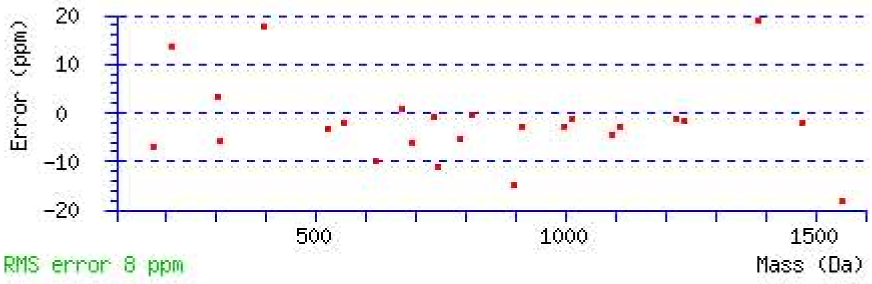
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1778.961395
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.00038
Matches : 25/118 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	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	1477.798418	739.402847	1460.771869	730.889573	1459.787853	730.397565	Q	***742.402856***	371.705066	725.376307	363.191792			3
12	1605.856996	803.432136	1588.830447	794.918862	1587.846431	794.426854	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 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
40.9	1778.961395	-0.004553	AHVSFKPTVAQQR
32.2	1778.961395	-0.004553	AHVSFKPTVAQQR
4.3	1778.982498	-0.025656	SRDAKLVLLNMPGPPR

Mascot: http://www.matrixscience.com/

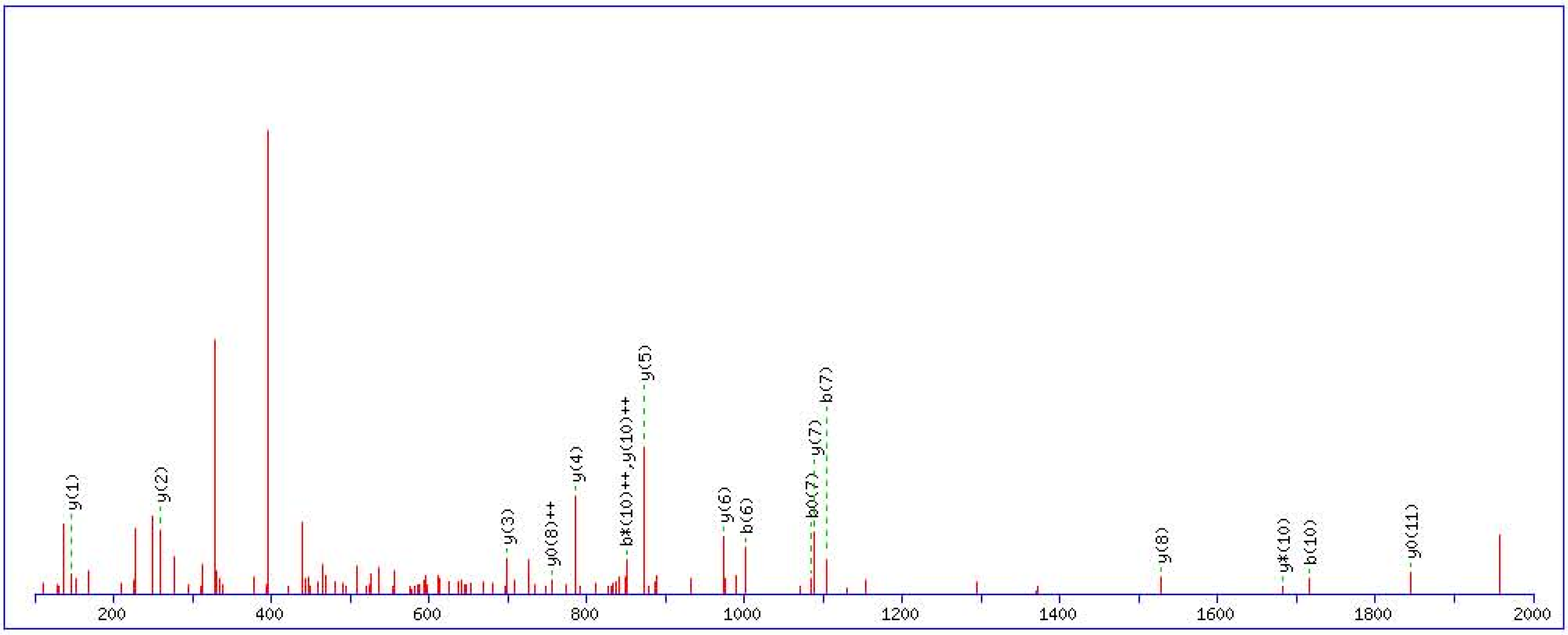
{MATRIX SCIENCE} Mascot Search Results

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

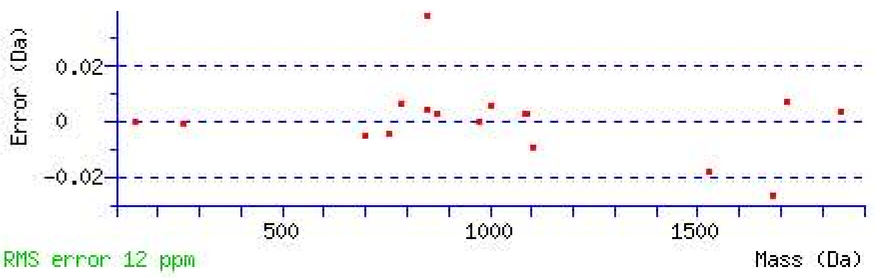
Match to Query 38876: 1974.993372 from(659.338400,3+) rtinseconds(2012) index(46169)
Title: Locus:1.1.1.3413.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

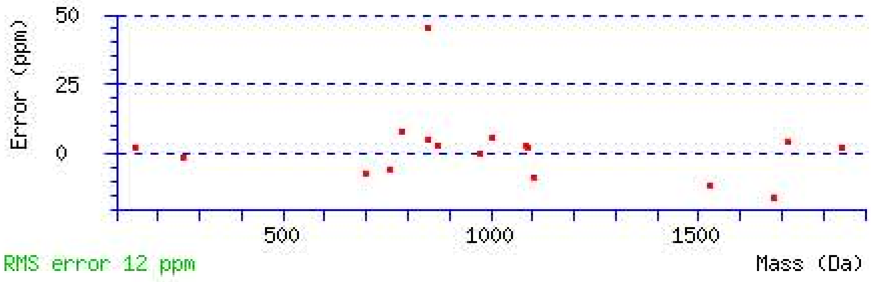
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 31  Expect: 0.02
Matches : 17/110 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	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
31.1	1974.990692	0.002680	IYGNQDTSSQLK

Mascot: http://www.matrixscience.com/

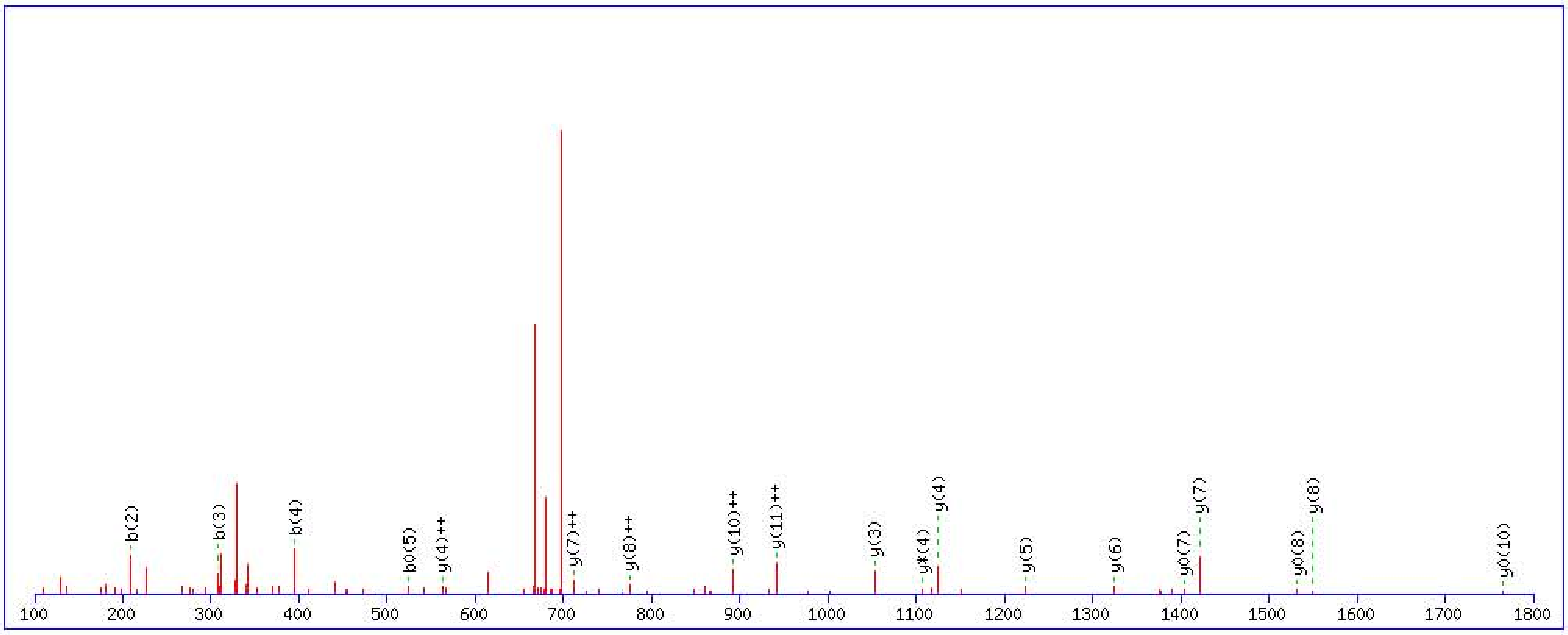
Mascot Search Results

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

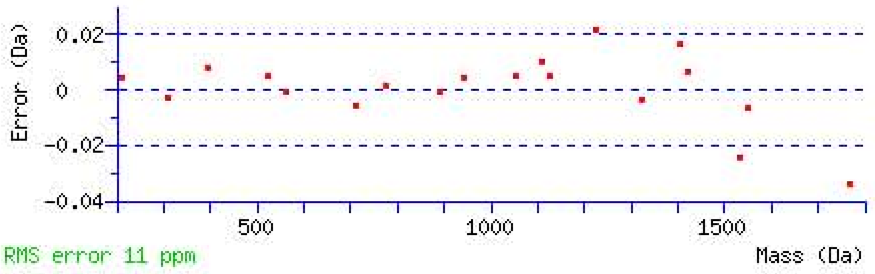
Match to Query 41448: 2090.128542 from(697.716790,3+) rtinseconds(1811) index(44829)
Title: Locus:1.1.1.3343.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

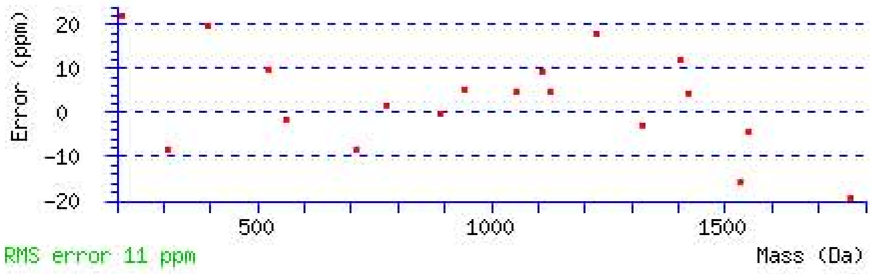
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2090.128143
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Q12    : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.018
Matches : 19/118 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	72.044390	36.525833					A							13
2	**209.103302**	105.055289					H	2020.098306	1010.552791	2003.071757	1002.039517	2002.087741	1001.547509	12
3	**308.171716**	154.589496					V	1883.039394	942.023335	1866.012845	933.510061	1865.028829	933.018053	11
4	**395.203744**	198.105510			377.193179	189.100227	S	1783.970980	892.489128	1766.944431	883.975854	1765.960415	883.483846	10
5	542.272158	271.639717			524.261593	262.634435	F	1696.938952	848.973114	1679.912403	840.459840	1678.928387	839.967832	9
6	670.367121	335.687199	653.340572	327.173924	652.356556	326.681916	K	***1549.870538***	775.438907	1532.843989	766.925633	1531.859973	766.433625	8
7	767.419885	384.213581	750.393336	375.700306	749.409320	375.208298	P	***1421.775575***	711.391426	1404.749026	702.878151	1403.765010	702.386143	7
8	868.467564	434.737420	851.441015	426.224146	850.456999	425.732138	T	***1324.722811***	662.865044	1307.696262	654.351769	1306.712246	653.859761	6
9	967.535978	484.271627	950.509429	475.758353	949.525413	475.266345	V	***1223.675132***	612.341204	1206.648583	603.827930			5
10	1038.573092	519.790184	1021.546543	511.276910	1020.562527	510.784902	A	***1124.606718***	562.806997	1107.580169	554.293723			4
11	1477.798418	739.402847	1460.771869	730.889573	1459.787853	730.397565	Q	***1053.569604***	527.288440	1036.543055	518.775166			3
12	1917.023744	959.015510	1899.997195	950.502236	1899.013179	950.010228	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
30.6	2090.128143	0.000399	AHVSFKPTVAQQR

Mascot: http://www.matrixscience.com/

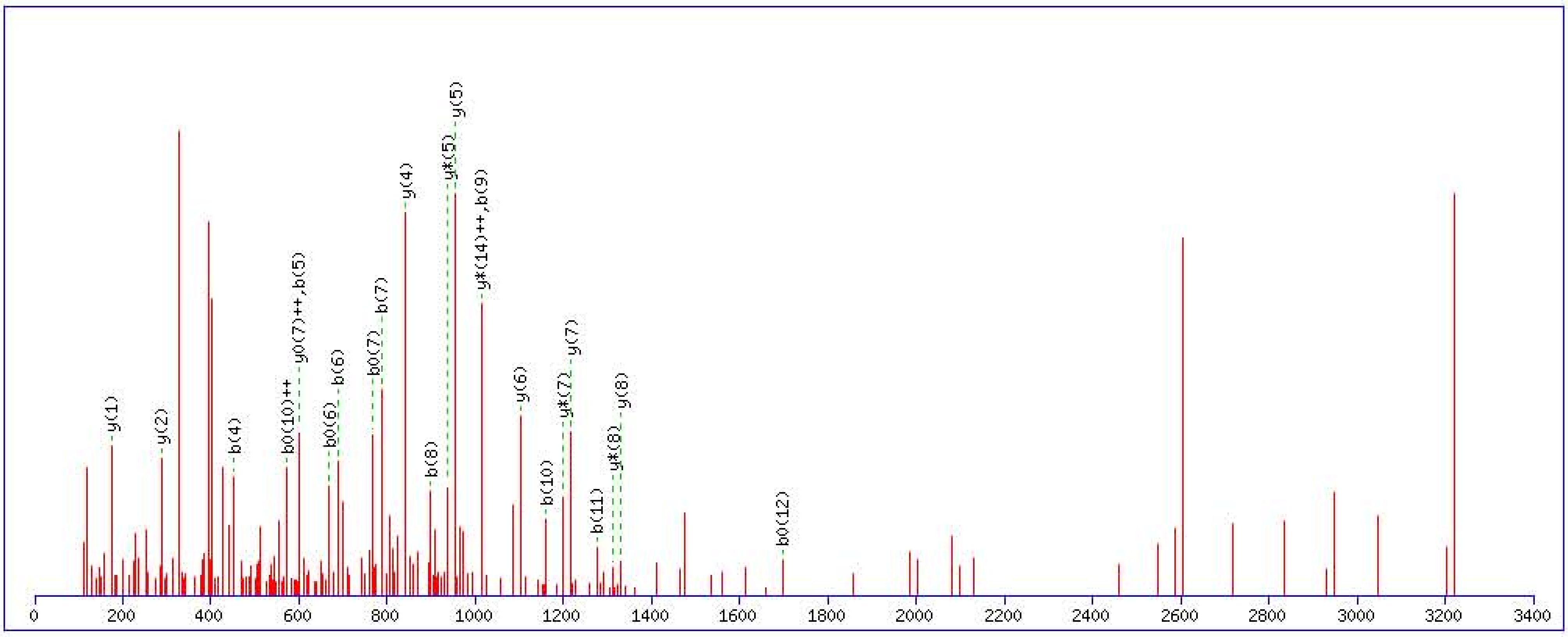
Mascot Search Results

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

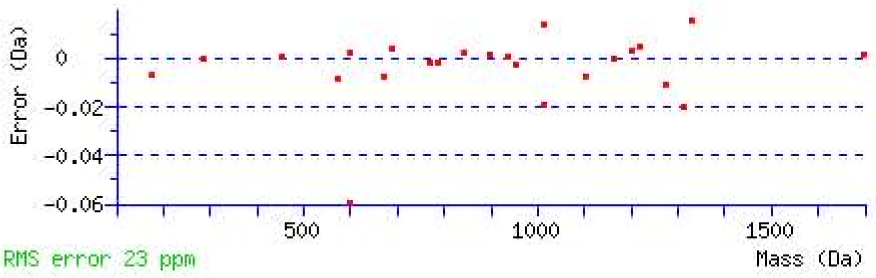
Match to Query 41805: 2115.013392 from(706.011740,3+) rtinseconds(2302) index(33623)
Title: Locus:1.1.1.3465.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

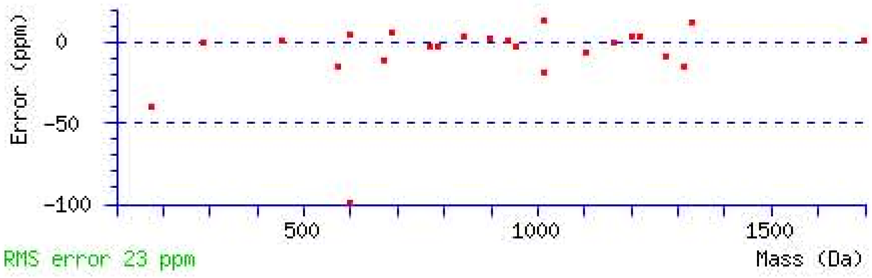
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [3400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2115.020752
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 50 **Expect:** 5.1e-005
Matches : 24/134 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	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
49.7	2115.020752	-0.007360	AEDHFSVIDFNQNIR
3.9	2115.033981	-0.020589	ESADRQVLMQEEEIK

Mascot: http://www.matrixscience.com/

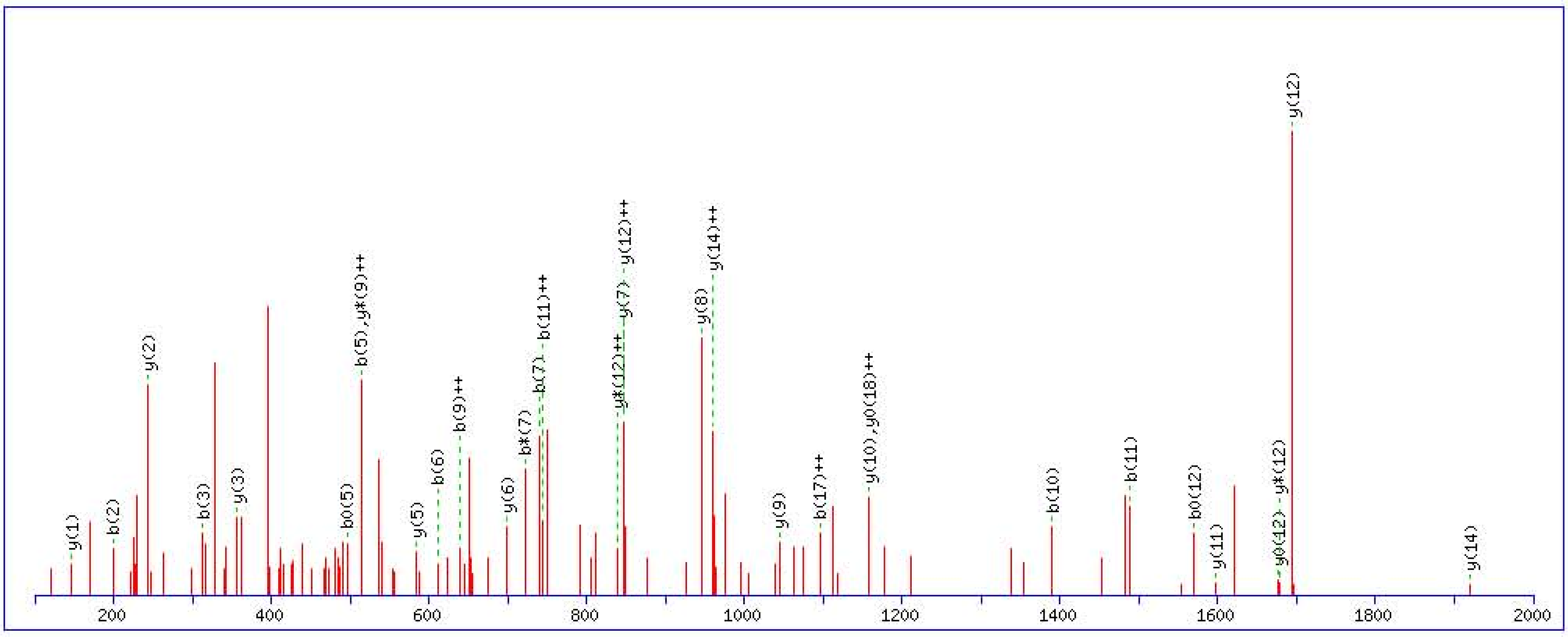
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVNNSPQPQNVVFDVQIPK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

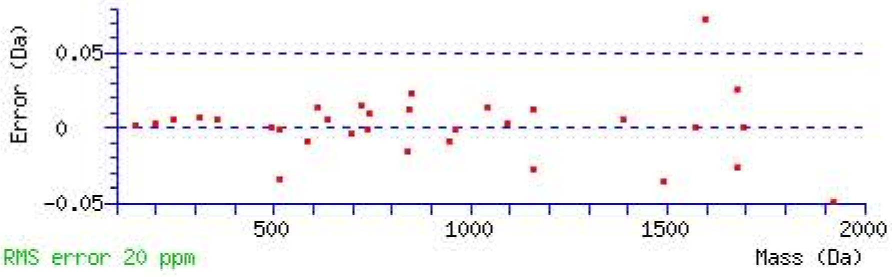
Match to Query 47015: 2432.289792 from(811.770540,3+) rtinseconds(2464) index(48631)
Title: Locus:1.1.1.3570.21 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

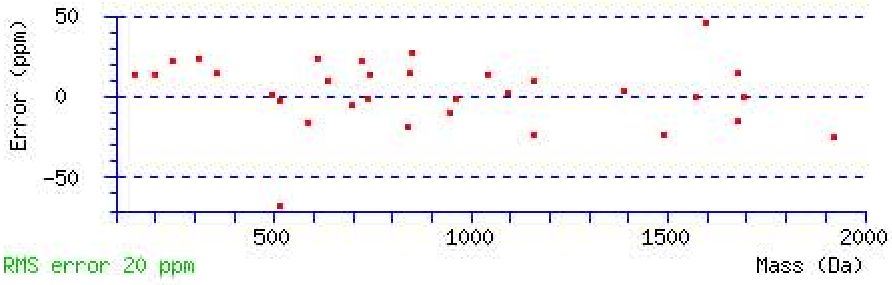
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2432.288620
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 1.6e-005
Matches : 32/194 fragment ions using 59 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	2334.227464	1167.617370	2317.200915	1159.104095	2316.216899	1158.612087	18
3	**313.187031**	157.097153	296.160482	148.583879			N	2235.159050	1118.083163	2218.132501	1109.569888	2217.148485	1109.077880	17
4	427.229958	214.118617	410.203409	205.605343			N	2121.116123	1061.061699	2104.089574	1052.548425	2103.105558	1052.056417	16
5	**514.261986**	257.634631	497.235437	249.121357	496.251421	248.629349	S	2007.073196	1004.040236	1990.046647	995.526962	1989.062631	995.034954	15
6	**611.314750**	306.161013	594.288201	297.647739	593.304185	297.155731	P	***1920.041168***	960.524222	1903.014619	952.010948	1902.030603	951.518940	14
7	**739.373328**	370.190302	722.346779	361.677028	721.362763	361.185020	Q	1822.988404	911.997840	1805.961855	903.484566	1804.977839	902.992558	13
8	836.426092	418.716684	819.399543	410.203410	818.415527	409.711402	P	***1694.929826***	847.968551	1677.903277	839.455277	1676.919261	838.963269	12
9	1275.651418	**638.329347**	1258.624869	629.816073	1257.640853	629.324065	Q	***1597.877062***	799.442169	1580.850513	790.928895	1579.866497	790.436887	11
10	**1389.694345**	695.350811	1372.667796	686.837536	1371.683780	686.345528	N	***1158.651736***	579.829506	1141.625187	571.316232	1140.641171	570.824224	10
11	**1488.762759**	**744.885018**	1471.736210	736.371743	1470.752194	735.879735	V	***1044.608809***	522.808043	1027.582260	514.294768	1026.598244	513.802760	9
12	1587.831173	794.419225	1570.804624	785.905950	1569.820608	785.413942	V	***945.540395***	473.273836	928.513846	464.760561	927.529830	464.268553	8
13	1734.899587	867.953432	1717.873038	859.440157	1716.889022	858.948149	F	***846.471981***	423.739629	829.445432	415.226354	828.461416	414.734346	7
14	1849.926530	925.466903	1832.899981	916.953629	1831.915965	916.461621	D	***699.403567***	350.205422	682.377018	341.692147	681.393002	341.200139	6
15	1948.994944	975.001110	1931.968395	966.487836	1930.984379	965.995828	V	***584.376624***	292.691950	567.350075	284.178676			5
16	2077.053522	1039.030399	2060.026973	1030.517124	2059.042957	1030.025117	Q	485.308210	243.157743	468.281661	234.644469			4
17	2190.137586	**1095.572431**	2173.111037	1087.059157	2172.127021	1086.567149	I	***357.249632***	179.128454	340.223083	170.615180			3
18	2287.190350	1144.098813	2270.163801	1135.585539	2269.179785	1135.093531	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 VVNNSPQPQNVVFDVQIPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.6	2432.288620	0.001172	VVNNSPQPQNVVFDVQIPK
33.9	2432.288620	0.001172	VVNNSPQPQNVVFDVQIPK
24.7	2432.288620	0.001172	VVNNSPQPQNVVFDVQIPK

Mascot: http://www.matrixscience.com/

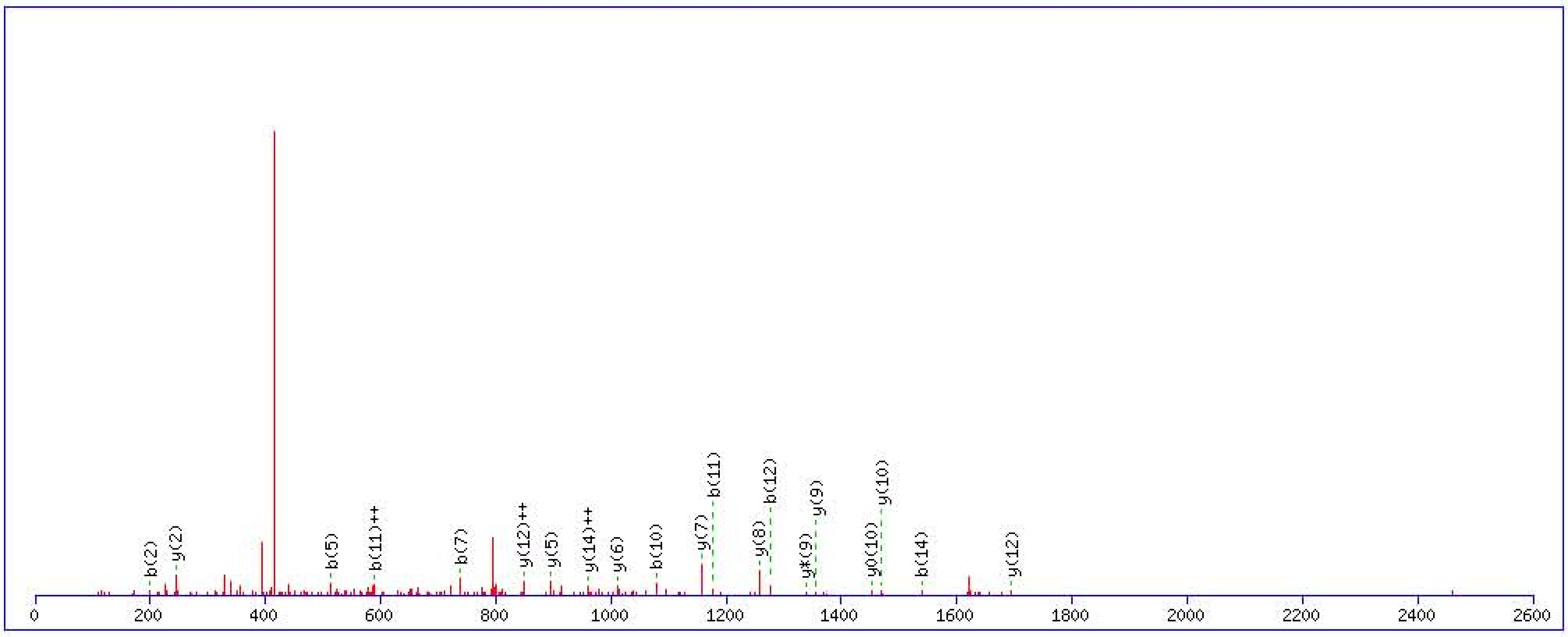
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVNNSPQPQNVVFDVQIPK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

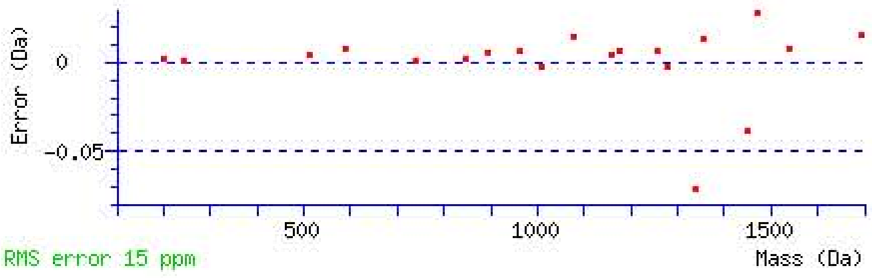
Match to Query 47016: 2432.290722 from(811.770850,3+) rtinseconds(2437) index(48521)
Title: Locus:1.1.1.3561.4 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

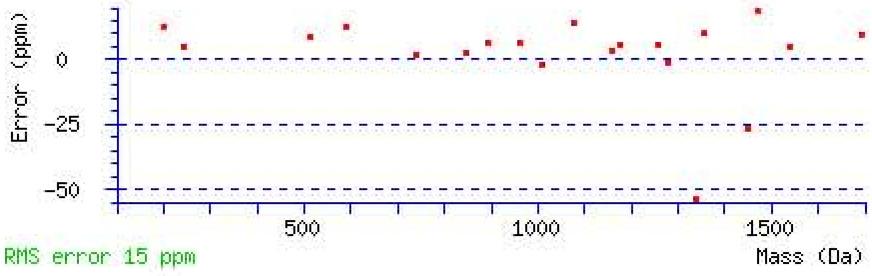
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2432.288620
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16 : Biotin:Thermo-21345 (Q)
Ions Score: 45 **Expect:** 0.00079
Matches : 20/194 fragment ions using 31 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	100.075690	50.541483					V							19
2	***199.144104***	100.075690					V	2334.227464	1167.617370	2317.200915	1159.104096	2316.216899	1158.612088	18
3	313.187031	157.097153	296.160482	148.583879			N	2235.159050	1118.083163	2218.132501	1109.569888	2217.148485	1109.077881	17
4	427.229958	214.118617	410.203409	205.605343			N	2121.116123	1061.061700	2104.089574	1052.548425	2103.105558	1052.056417	16
5	***514.261986***	257.634631	497.235437	249.121357	496.251421	248.629349	S	2007.073196	1004.040236	1990.046647	995.526962	1989.062631	995.034954	15
6	611.314750	306.161013	594.288201	297.647739	593.304185	297.155731	P	1920.041168	960.524222	1903.014619	952.010948	1902.030603	951.518940	14
7	***739.373328***	370.190302	722.346779	361.677028	721.362763	361.185020	Q	1822.988404	911.997840	1805.961855	903.484566	1804.977839	902.992558	13
8	836.426092	418.716684	819.399543	410.203410	818.415527	409.711402	P	***1694.929826***	847.968551	1677.903277	839.455277	1676.919261	838.963269	12
9	964.484670	482.745973	947.458121	474.232699	946.474105	473.740691	Q	1597.877062	799.442169	1580.850513	790.928895	1579.866497	790.436887	11
10	***1078.527597***	539.767437	1061.501048	531.254162	1060.517032	530.762154	N	***1469.818484***	735.412880	1452.791935	726.899606	1451.807919	726.407598	10
11	***1177.596011***	589.301644	1160.569462	580.788369	1159.585446	580.296361	V	***1355.775557***	678.391417	1338.749008	669.878142	1337.764992	669.386134	9
12	***1276.664425***	638.835851	1259.637876	630.322576	1258.653860	629.830568	V	***1256.707143***	628.857210	1239.680594	620.343935	1238.696578	619.851927	8
13	1423.732839	712.370058	1406.706290	703.856783	1405.722274	703.364775	F	***1157.638729***	579.323003	1140.612180	570.809728	1139.628164	570.317720	7
14	***1538.759782***	769.883529	1521.733233	761.370255	1520.749217	760.878247	D	***1010.570315***	505.788796	993.543766	497.275521	992.559750	496.783513	6
15	1637.828196	819.417736	1620.801647	810.904462	1619.817631	810.412454	V	***895.543372***	448.275324	878.516823	439.762050			5
16	2077.053522	1039.030399	2060.026973	1030.517125	2059.042957	1030.025117	Q	796.474958	398.741117	779.448409	390.227843			4
17	2190.137586	1095.572431	2173.111037	1087.059157	2172.127021	1086.567149	I	357.249632	179.128454	340.223083	170.615180			3
18	2287.190350	1144.098813	2270.163801	1135.585539	2269.179785	1135.093531	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 VVNNSPQPQNVVFDVQIPK
(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	2432.288620	0.002102	VVNNSPQPQNVVFDVQIPK
1.3	2432.288620	0.002102	VVNNSPQPQNVVFDVQIPK

{MATRIX} {SCIENCE}

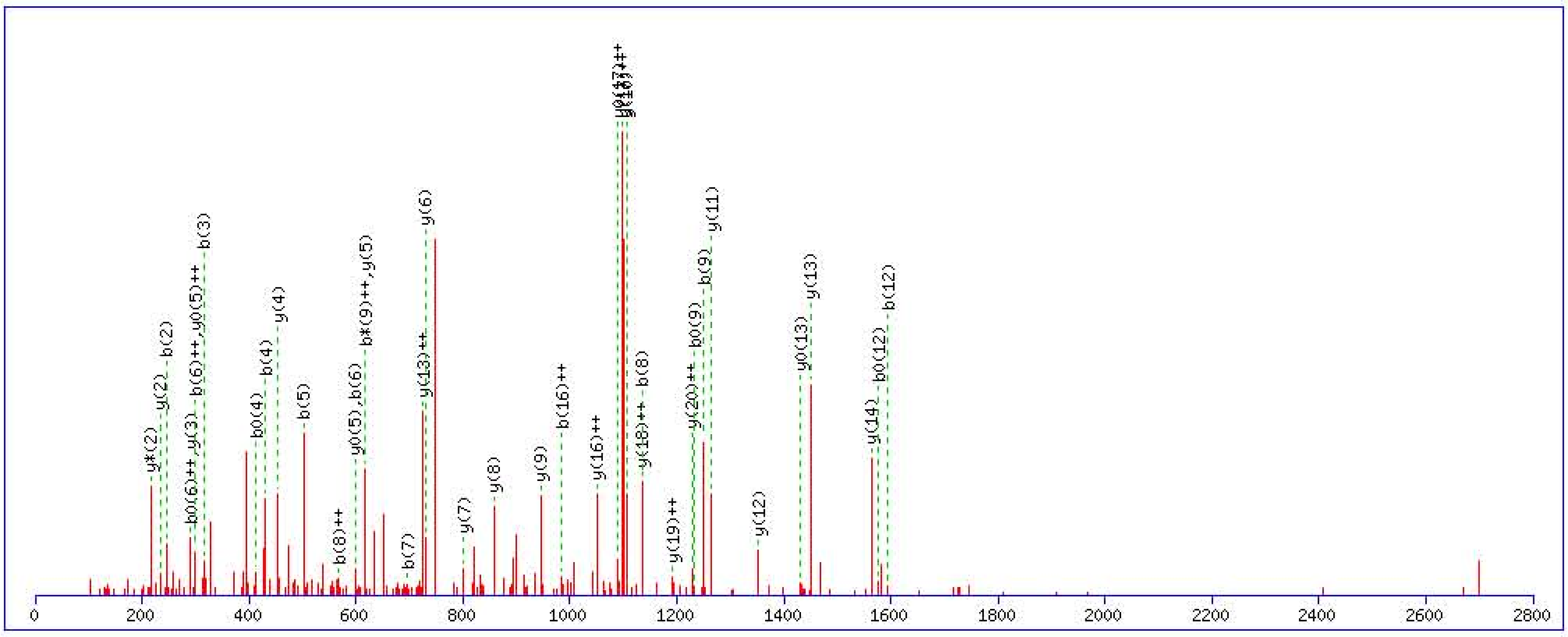
Mascot Search Results

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

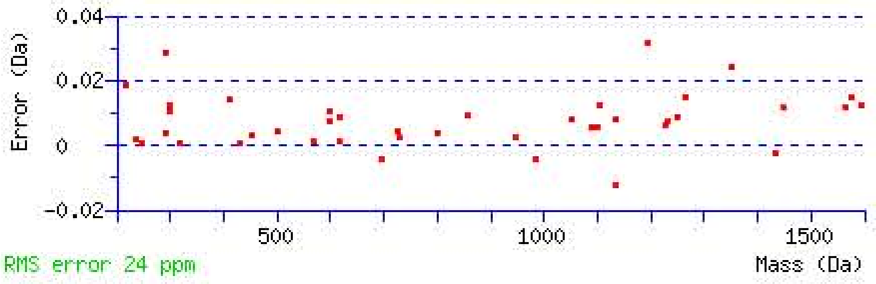
Match to Query 50354: 2698.196412 from(900.406080,3+) rtinseconds(2128) index(46774)
Title: Locus:1.1.1.3453.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

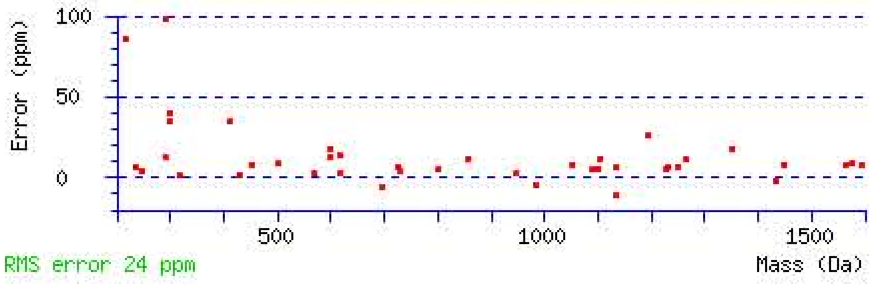
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2698.189941
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8     : Biotin:Thermo-21345 (Q)
Ions Score: 58  Expect: 1.2e-005
Matches : 41/230 fragment ions using 99 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
57.6	2698.189941	0.006471	MLADAPPQDPSCCSGALYYGSK

Mascot: http://www.matrixscience.com/

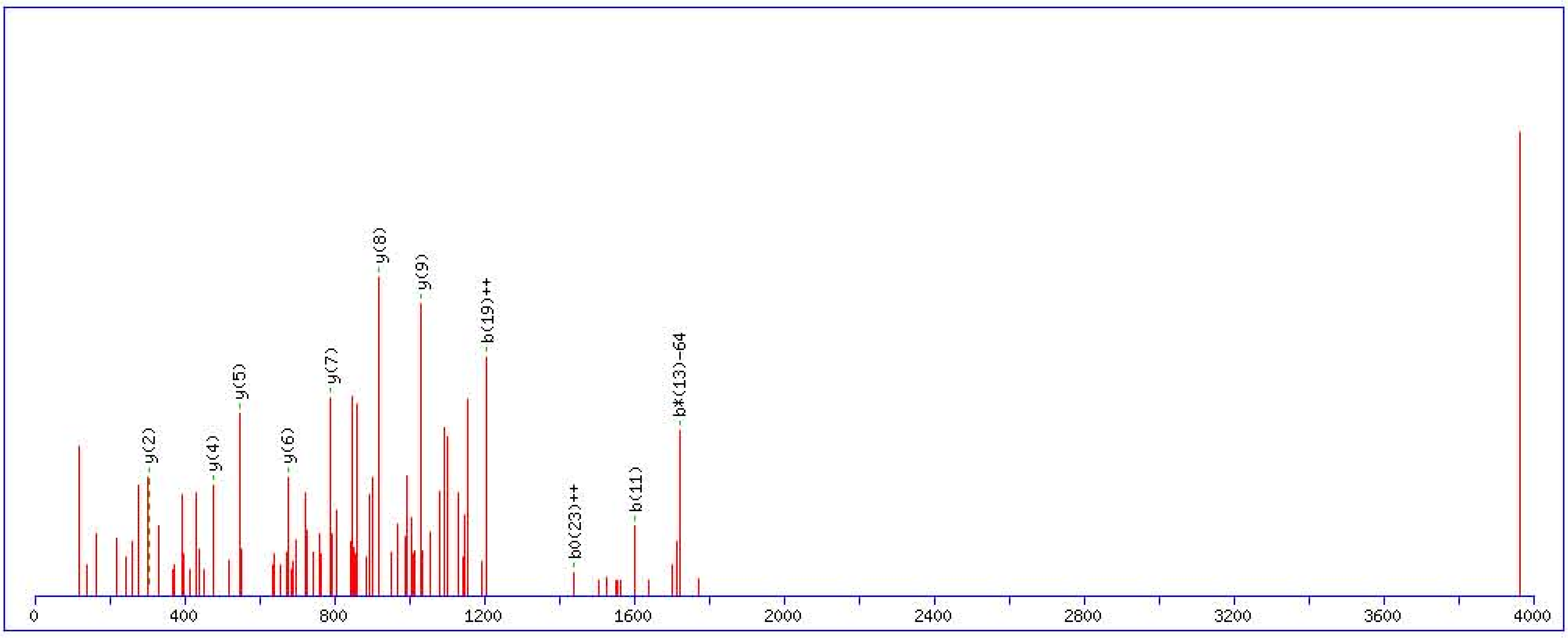
Mascot Search Results

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

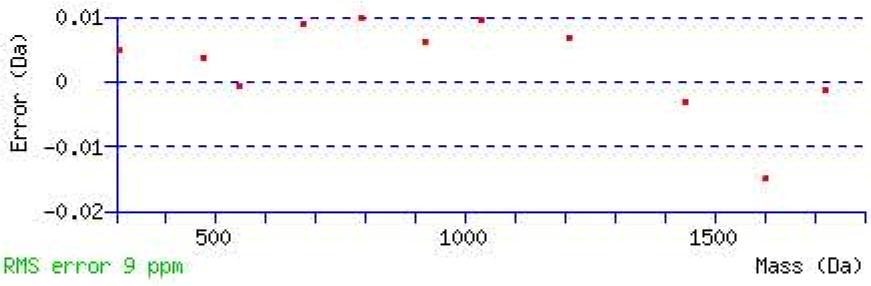
Match to Query 59131: 3443.751576 from(861.945170,4+) rtinseconds(2670) index(49816)
Title: Locus:1.1.1.3641.23 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

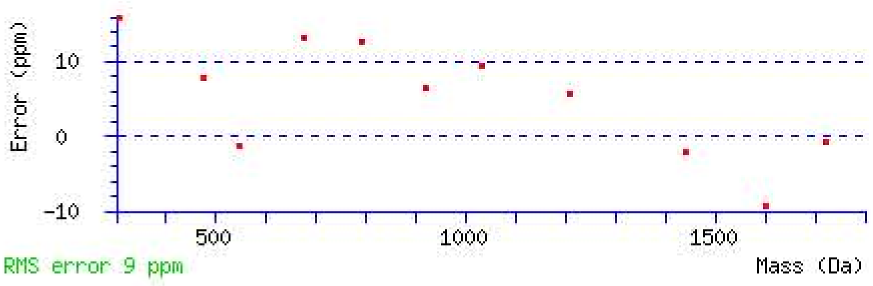
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 31 **Expect:** 0.02
Matches : 11/478 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	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
31.3	3443.742859	0.008717	SILQMSLDHHIVTPLTSLVIENEAGDER

Mascot: http://www.matrixscience.com/

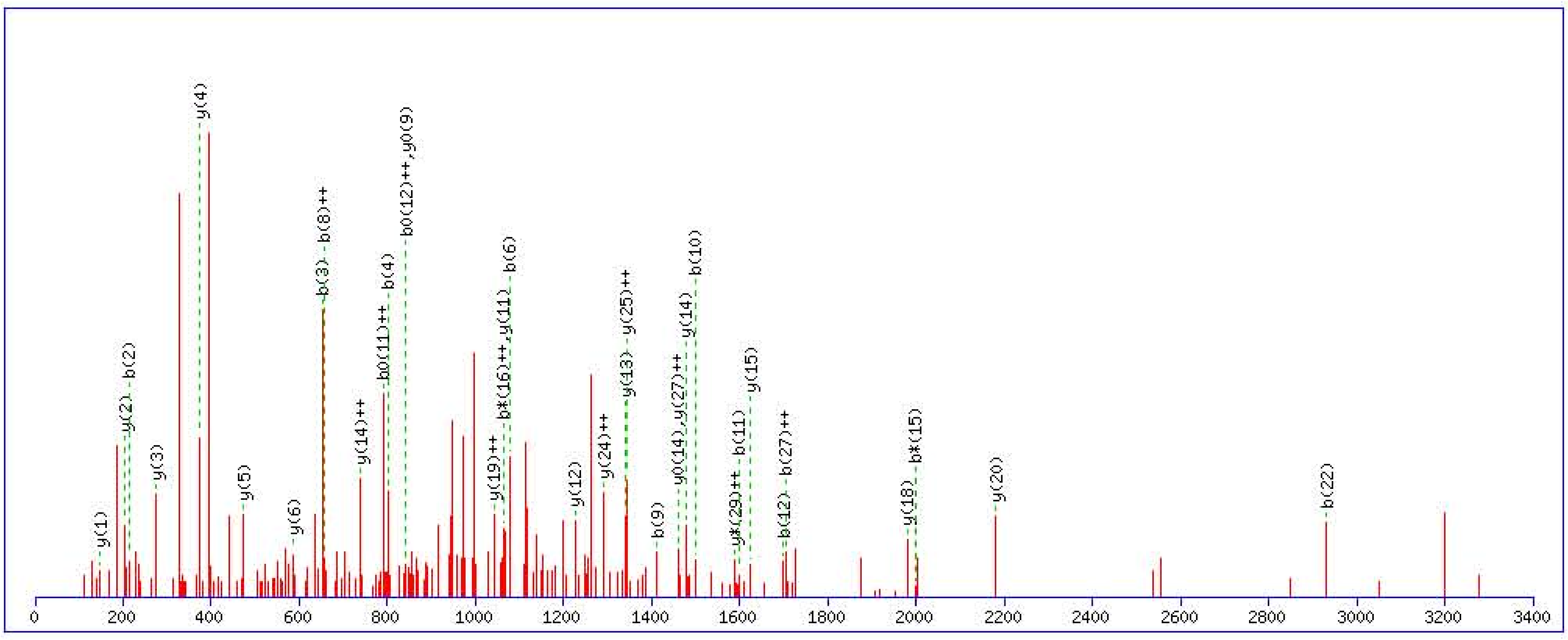
Mascot Search Results

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

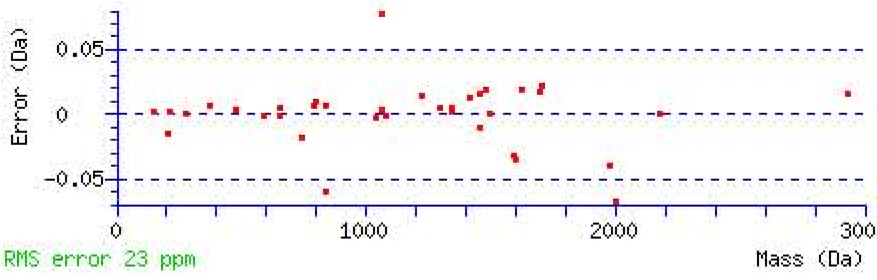
Match to Query 62282: 3993.921936 from(999.487760,4+) rtinseconds(2410) index(48416)
Title: Locus:1.1.1.3551.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

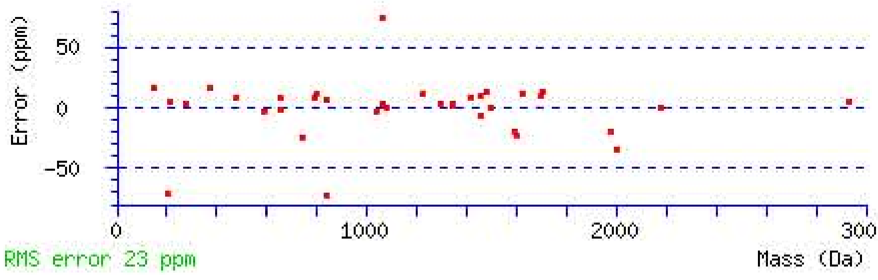
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3993.910858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.0013
Matches : 36/356 fragment ions using 100 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							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
42.2	3993.910858	0.011078	NVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGK
2.6	3993.910858	0.011078	NVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGK

Mascot: http://www.matrixscience.com/

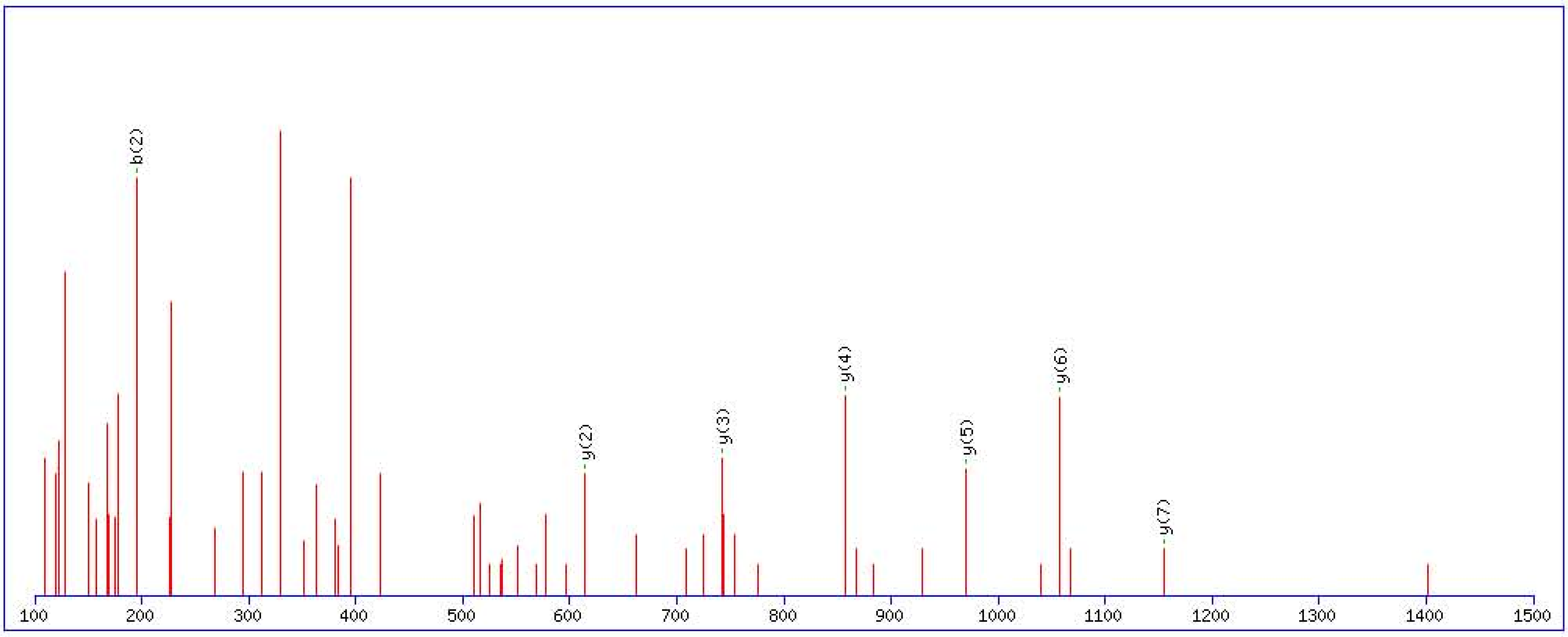
Mascot Search Results

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

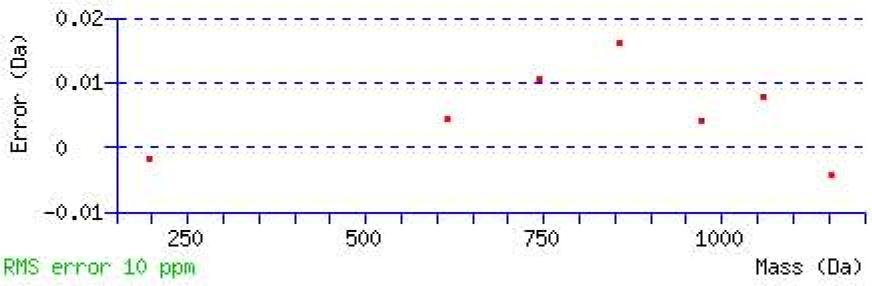
Match to Query 35900: 1808.928656 from(453.239440,4+) rtinseconds(1626) index(43698)
Title: Locus:1.1.1.3279.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

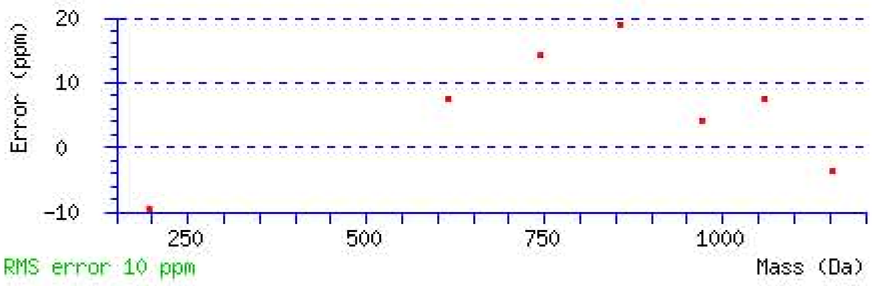
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1808.935577
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.012
Matches : 7/122 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							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
33.3	1808.935577	-0.006921	GHVSFKPSLDQQR
21.5	1808.935577	-0.006921	GHVSFKPSLDQQR

Mascot: http://www.matrixscience.com/

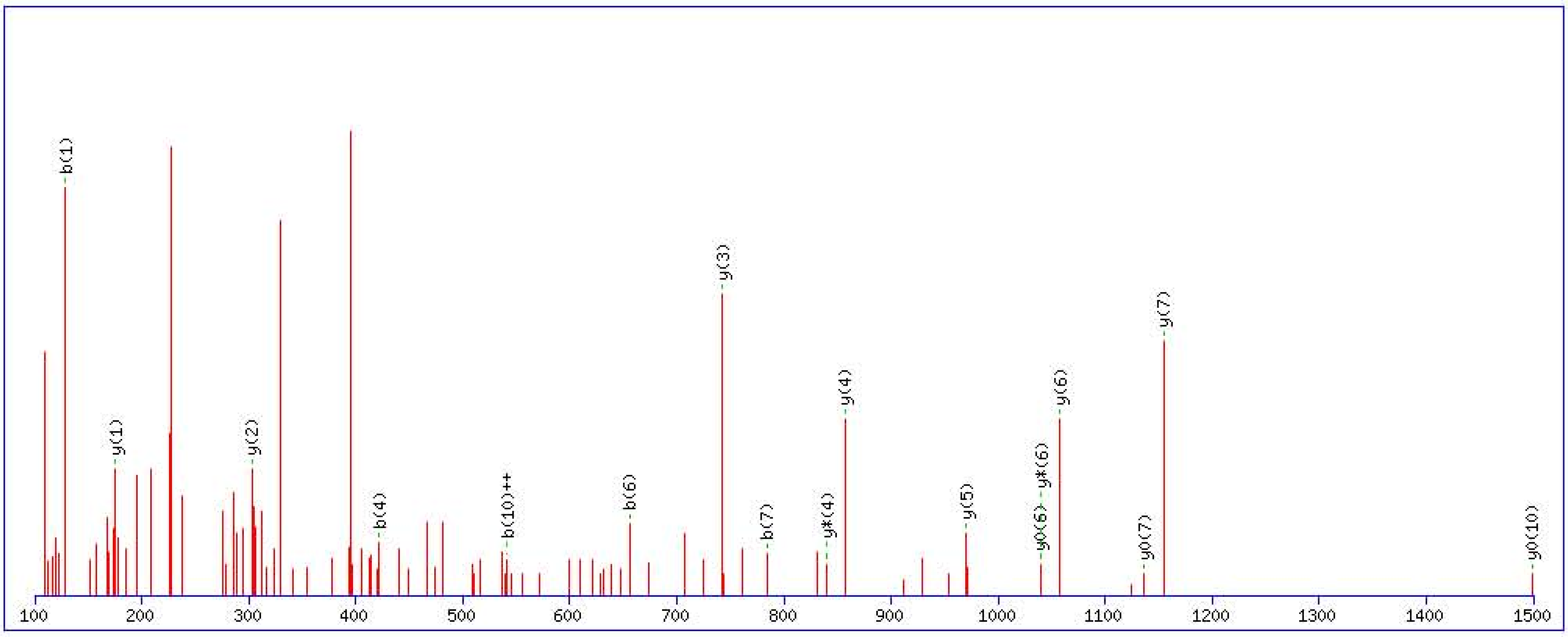
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KGHVSFKPSLDQQR**
Found in **ITIH3_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2

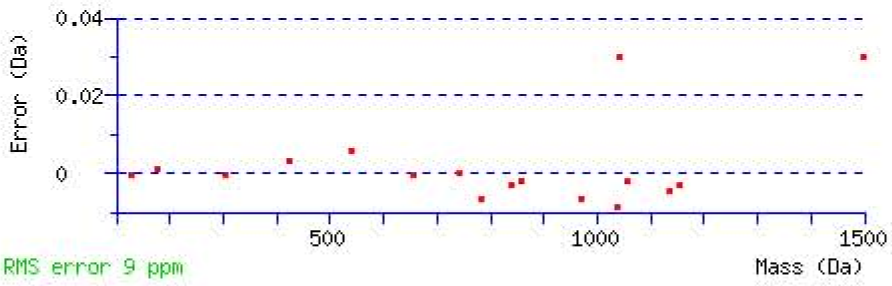
Match to Query 38130: 1937.024456 from(485.263390,4+) rtinseconds(1525) index(43047)
Title: Locus:1.1.1.3244.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

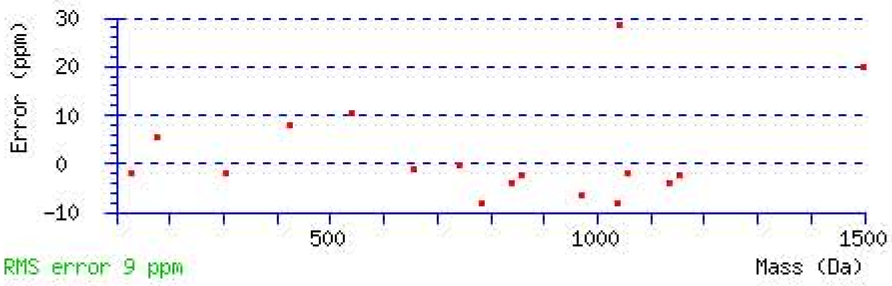
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1937.030533
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.0032
Matches : 17/142 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	***129.102239***	65.054757	112.075690	56.541483			K							14
2	186.123703	93.565489	169.097154	85.052215			G	1809.942850	905.475063	1792.916301	896.961789	1791.932285	896.469781	13
3	323.182615	162.094945	306.156066	153.581671			H	1752.921386	876.964331	1735.894837	868.451057	1734.910821	867.959049	12
4	***422.251029***	211.629153	405.224480	203.115878			V	1615.862474	808.434875	1598.835925	799.921601	1597.851909	799.429593	11
5	509.283057	255.145167	492.256508	246.631892	491.272492	246.139884	S	1516.794060	758.900668	1499.767511	750.387394	1498.783495	749.895386	10
6	***656.351471***	328.679374	639.324922	320.166099	638.340906	319.674091	F	1429.762032	715.384654	1412.735483	706.871380	1411.751467	706.379372	9
7	***784.446434***	392.726855	767.419885	384.213581	766.435869	383.721573	K	1282.693618	641.850447	1265.667069	633.337173	1264.683053	632.845165	8
8	881.499198	441.253237	864.472649	432.739963	863.488633	432.247955	P	***1154.598655***	577.802966	1137.572106	569.289691	1136.588090	568.797683	7
9	968.531226	484.769251	951.504677	476.255977	950.520661	475.763969	S	***1057.545891***	529.276584	1040.519342	520.763309	1039.535326	520.271301	6
10	1081.615290	541.311283	1064.588741	532.798009	1063.604725	532.306000	L	***970.513863***	485.760570	953.487314	477.247295	952.503298	476.755287	5
11	1196.642233	598.824755	1179.615684	590.311480	1178.631668	589.819472	D	***857.429799***	429.218538	840.403250	420.705263	839.419234	420.213255	4
12	1635.867559	818.437418	1618.841010	809.924143	1617.856994	809.432135	Q	***742.402856***	371.705066	725.376307	363.191792			3
13	1763.926137	882.466707	1746.899588	873.953432	1745.915572	873.461424	Q	***303.177530***	152.092403	286.150981	143.579129			2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of KGHVSFKPSLDQQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.7	1937.030533	-0.006077	KGHVSFKPSLDQQR
26.8	1937.030533	-0.006077	KGHVSFKPSLDQQR
4.9	1937.051620	-0.027164	QPLEREQCLALLALGAR
0.8	1937.008057	0.016399	QSKETPVGWQELPK

Mascot: http://www.matrixscience.com/

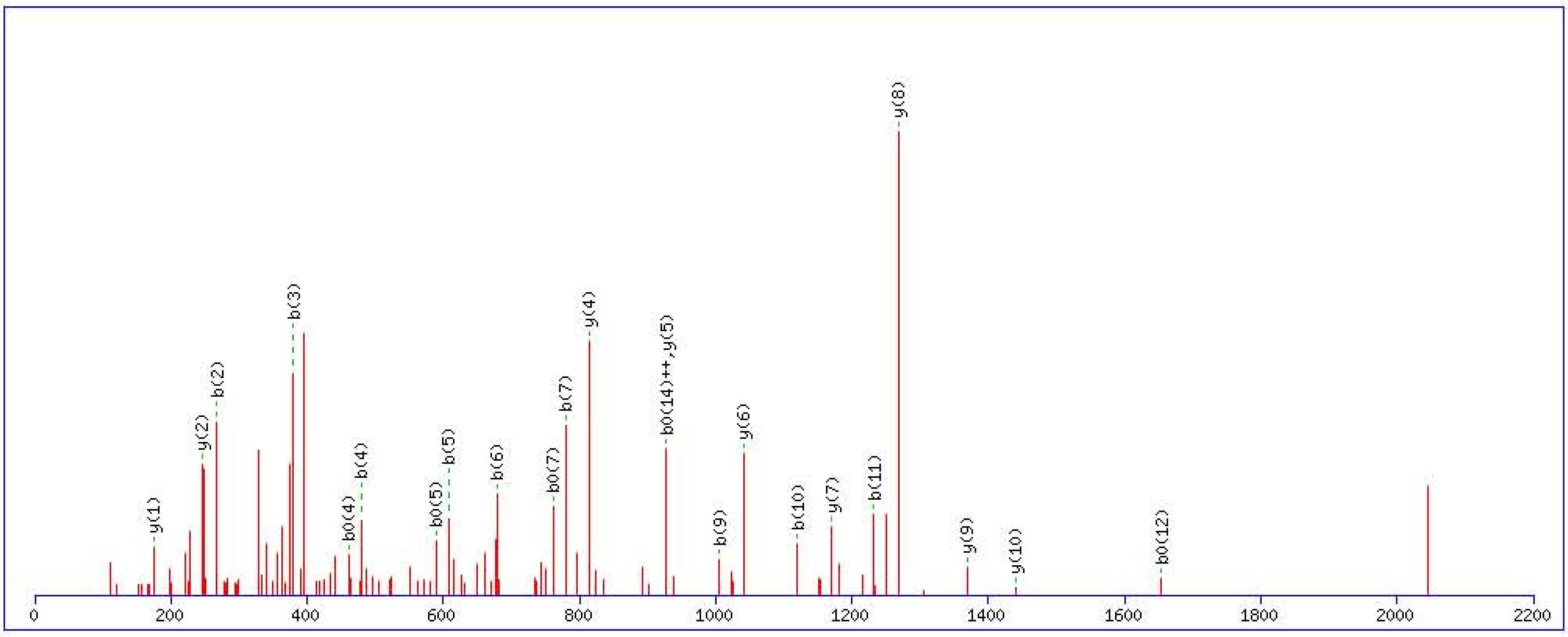
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EHLVQATPENLQEAR**
Found in **ITIH3_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2

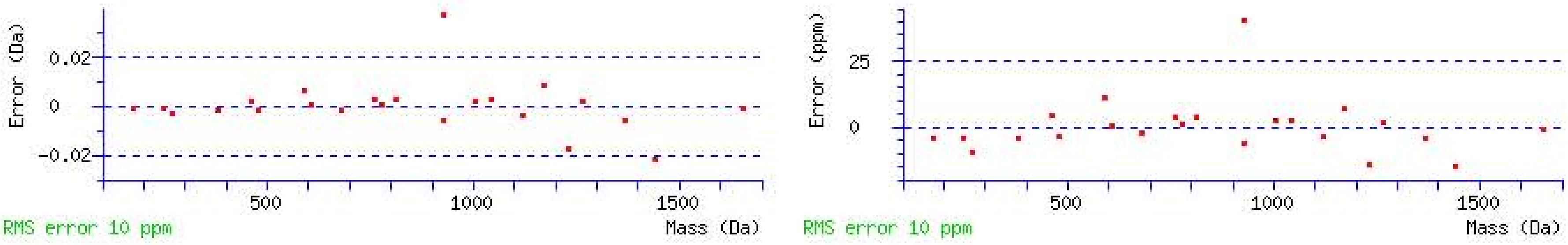
Match to Query 40718: 2045.035182 from(682.685670,3+) rtinseconds(1784) index(44651)
Title: Locus:1.1.1.3334.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 2045.036377
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 84  Expect: 3.2e-008
Matches : 23/156 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	130.049869	65.528572			112.039304	56.523290	E							15
2	***267.108781***	134.058028			249.098216	125.052746	H	1917.001094	959.004185	1899.974545	950.490911	1898.990529	949.998903	14
3	***380.192845***	190.600060			362.182280	181.594778	L	1779.942182	890.474729	1762.915633	881.961455	1761.931617	881.469447	13
4	***479.261259***	240.134267			461.250694	231.128985	V	1666.858118	833.932697	1649.831569	825.419423	1648.847553	824.927415	12
5	***607.319837***	304.163557	590.293288	295.650282	589.309272	295.158274	Q	1567.789704	784.398490	1550.763155	775.885216	1549.779139	775.393208	11
6	***678.356951***	339.682114	661.330402	331.168839	660.346386	330.676831	A	***1439.731126***	720.369201	1422.704577	711.855927	1421.720561	711.363919	10
7	***779.404630***	390.205953	762.378081	381.692679	761.394065	381.200671	T	***1368.694012***	684.850644	1351.667463	676.337370	1350.683447	675.845362	9
8	876.457394	438.732335	859.430845	430.219061	858.446829	429.727053	P	***1267.646333***	634.326805	1250.619784	625.813530	1249.635768	625.321522	8
9	***1005.499987***	503.253632	988.473438	494.740357	987.489422	494.248349	E	***1170.593569***	585.800423	1153.567020	577.287148	1152.583004	576.795140	7
10	***1119.542914***	560.275095	1102.516365	551.761821	1101.532349	551.269813	N	***1041.550976***	521.279126	1024.524427	512.765852	1023.540411	512.273844	6
11	***1232.626978***	616.817127	1215.600429	608.303853	1214.616413	607.811845	L	***927.508049***	464.257663	910.481500	455.744388	909.497484	455.252380	5
12	1671.852304	836.429790	1654.825755	827.916516	1653.841739	827.424508	Q	***814.423985***	407.715631	797.397436	399.202356	796.413420	398.710348	4
13	1800.894897	900.951087	1783.868348	892.437812	1782.884332	891.945804	E	375.198659	188.102968	358.172110	179.589693	357.188094	179.097685	3
14	1871.932011	936.469644	1854.905462	927.956369	1853.921446	927.464361	A	***246.156066***	123.581671	229.129517	115.068396			2
15							R	***175.118952***	88.063114	158.092403	79.549839			1



NCBI **BLAST** search of EHLVQATPENLQEAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
84.2	2045.036377	-0.001195	EHLVQATPENLQEAR
5.5	2045.036377	-0.001195	EHLVQATPENLQEAR
4.0	2045.064941	-0.029759	ASFSVVGMVKSLTRSSMVK
3.4	2045.035889	-0.000707	LNMEQLLQSASMELK
0.8	2045.014603	0.020579	GPRRMTVIIPGMSAENER
0.6	2045.022446	0.012736	EHNENMLRNILPSHVAR

Mascot: http://www.matrixscience.com/

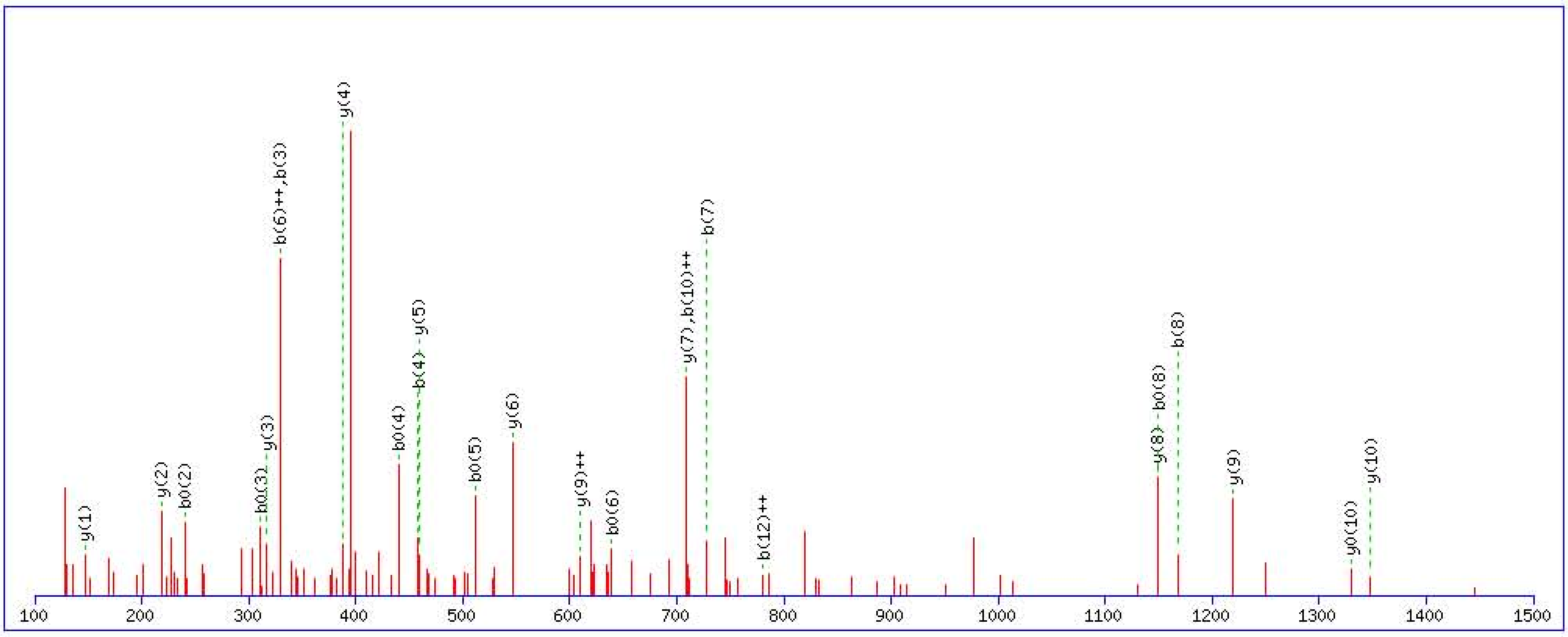
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EKAEAQAQYSAAVAK**
Found in **ITIH4_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4

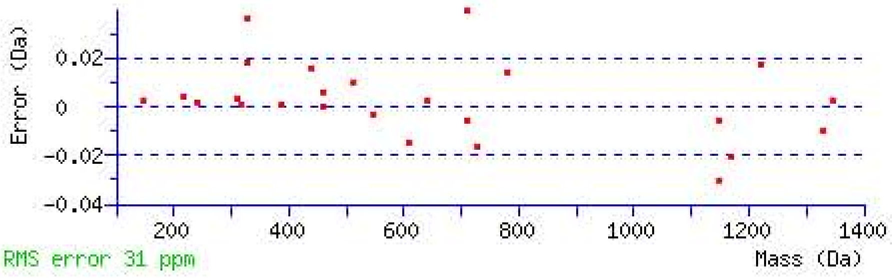
Match to Query 37130: 1874.947542 from(625.989790,3+) rtinseconds(1517) index(15964)
Title: Locus:1.1.1.3094.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

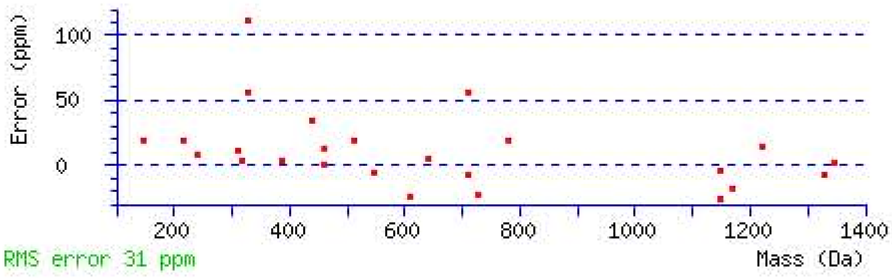
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1874.955978
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 55  Expect: 8.4e-005
Matches : 25/156 fragment ions using 44 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							15
2	258.144832	129.576054	241.118283	121.062780	240.134267	120.570772	K	1746.920719	873.963998	1729.894170	865.450723	1728.910154	864.958715	14
3	**329.181946**	165.094611	312.155397	156.581336	311.171381	156.089328	A	1618.825756	809.916516	1601.799207	801.403242	1600.815191	800.911233	13
4	**458.224539**	229.615907	441.197990	221.102633	440.213974	220.610625	E	1547.788642	774.397959	1530.762093	765.884685	1529.778077	765.392677	12
5	529.261653	265.134465	512.235104	256.621190	511.251088	256.129182	A	1418.746049	709.876663	1401.719500	701.363388	1400.735484	700.871380	11
6	657.320231	**329.163754**	640.293682	320.650479	639.309666	320.158471	Q	***1347.708935***	674.358106	1330.682386	665.844831	1329.698370	665.352823	10
7	**728.357345**	364.682311	711.330796	356.169036	710.346780	355.677028	A	***1219.650357***	610.328817	1202.623808	601.815542	1201.639792	601.323534	9
8	**1167.582671**	584.294973	1150.556122	575.781699	1149.572106	575.289691	Q	***1148.613243***	574.810260	1131.586694	566.296985	1130.602678	565.804977	8
9	1330.646000	665.826638	1313.619451	657.313364	1312.635435	656.821355	Y	***709.387917***	355.197597	692.361368	346.684322	691.377352	346.192314	7
10	1417.678028	**709.342652**	1400.651479	700.829378	1399.667463	700.337370	S	***546.324588***	273.665932	529.298039	265.152658	528.314023	264.660650	6
11	1488.715142	744.861209	1471.688593	736.347935	1470.704577	735.855927	A	***459.292560***	230.149918	442.266011	221.636643			5
12	1559.752256	**780.379766**	1542.725707	771.866492	1541.741691	771.374484	A	***388.255446***	194.631361	371.228897	186.118087			4
13	1658.820670	829.913973	1641.794121	821.400699	1640.810105	820.908691	V	***317.218332***	159.112804	300.191783	150.599530			3
14	1729.857784	865.432530	1712.831235	856.919256	1711.847219	856.427248	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 EKAEAQAQYSAAVAK
(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	1874.955978	-0.008436	EKAEAQAQYSAAVAK
38.8	1874.955978	-0.008436	EKAEAQAQYSAAVAK

Mascot: http://www.matrixscience.com/

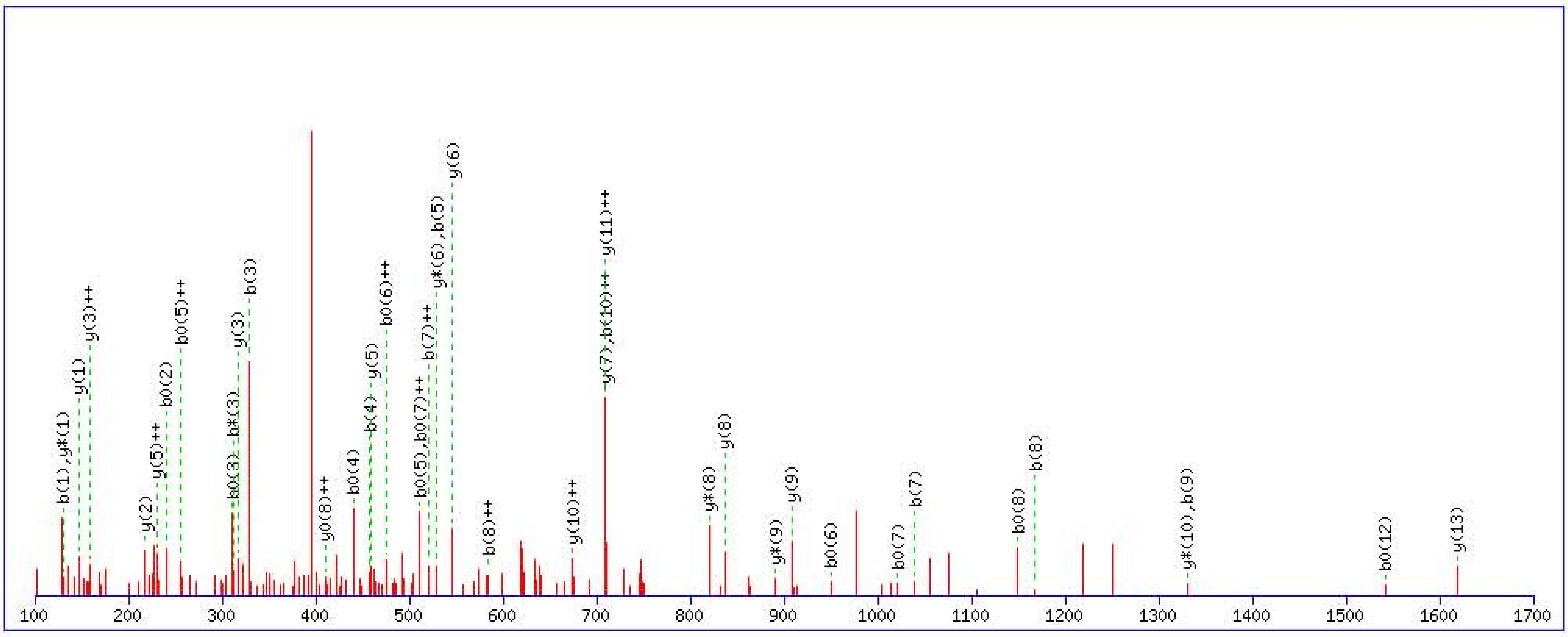
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EKAEAQAQYSAAVAK**
Found in **ITIH4_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4

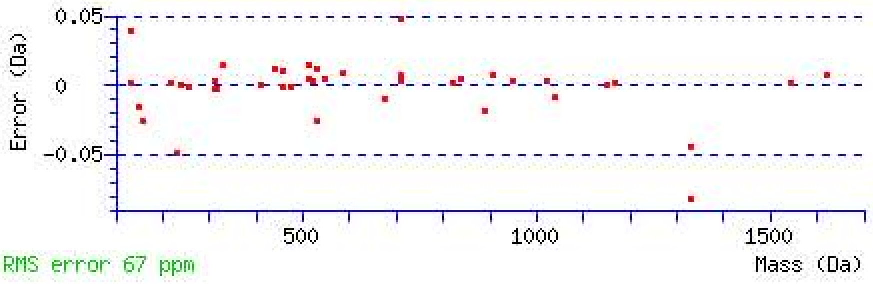
Match to Query 37131: 1874.966622 from(625.996150,3+) rtinseconds(1547) index(2323)
Title: Locus:1.1.1.3058.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

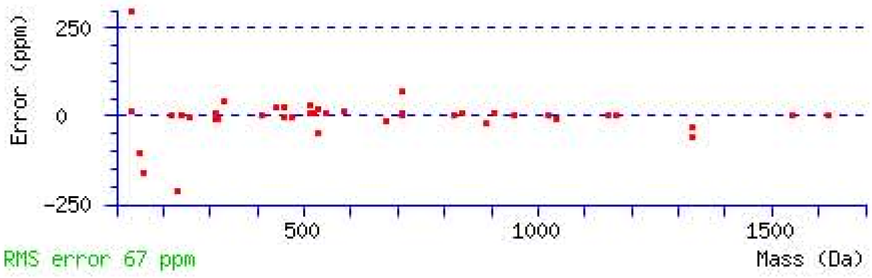
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1874.955978
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.0013
Matches : 41/156 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	***130.049869***	65.528572			112.039304	56.523290	E							15
2	258.144832	129.576054	241.118283	121.062780	240.134267	120.570772	K	1746.920719	873.963998	1729.894170	865.450723	1728.910154	864.958715	14
3	***329.181946***	165.094611	312.155397	156.581336	311.171381	156.089328	A	***1618.825756***	809.916516	1601.799207	801.403242	1600.815191	800.911233	13
4	***458.224539***	229.615907	441.197990	221.102633	440.213974	220.610625	E	1547.788642	774.397959	1530.762093	765.884685	1529.778077	765.392677	12
5	***529.261653***	265.134465	512.235104	256.621190	511.251088	256.129182	A	1418.746049	709.876663	1401.719500	701.363388	1400.735484	700.871380	11
6	968.486979	484.747128	951.460430	476.233853	950.476414	475.741845	Q	1347.708935	674.358106	1330.682386	665.844831	1329.698370	665.352823	10
7	***1039.524093***	**520.265685**	1022.497544	511.752410	1021.513528	511.260402	A	***908.483609***	454.745443	891.457060	446.232168	890.473044	445.740160	9
8	***1167.582671***	**584.294973**	1150.556122	575.781699	1149.572106	575.289691	Q	***837.446495***	419.226886	820.419946	410.713611	819.435930	410.221603	8
9	***1330.646000***	665.826638	1313.619451	657.313364	1312.635435	656.821355	Y	***709.387917***	355.197597	692.361368	346.684322	691.377352	346.192314	7
10	1417.678028	**709.342652**	1400.651479	700.829378	1399.667463	700.337370	S	***546.324588***	273.665932	529.298039	265.152658	528.314023	264.660650	6
11	1488.715142	744.861209	1471.688593	736.347935	1470.704577	735.855927	A	***459.292560***	230.149918	442.266011	221.636643			5
12	1559.752256	780.379766	1542.725707	771.866492	1541.741691	771.374484	A	388.255446	194.631361	371.228897	186.118087			4
13	1658.820670	829.913973	1641.794121	821.400699	1640.810105	820.908691	V	***317.218332***	159.112804	300.191783	150.599530			3
14	1729.857784	865.432530	1712.831235	856.919256	1711.847219	856.427248	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 EKAEAQAQYSAAVAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.0	1874.955978	0.010644	EKAEAQAQYSAAVAK
38.5	1874.955978	0.010644	EKAEAQAQYSAAVAK

Mascot: http://www.matrixscience.com/

{MATRIX SCIENCE}

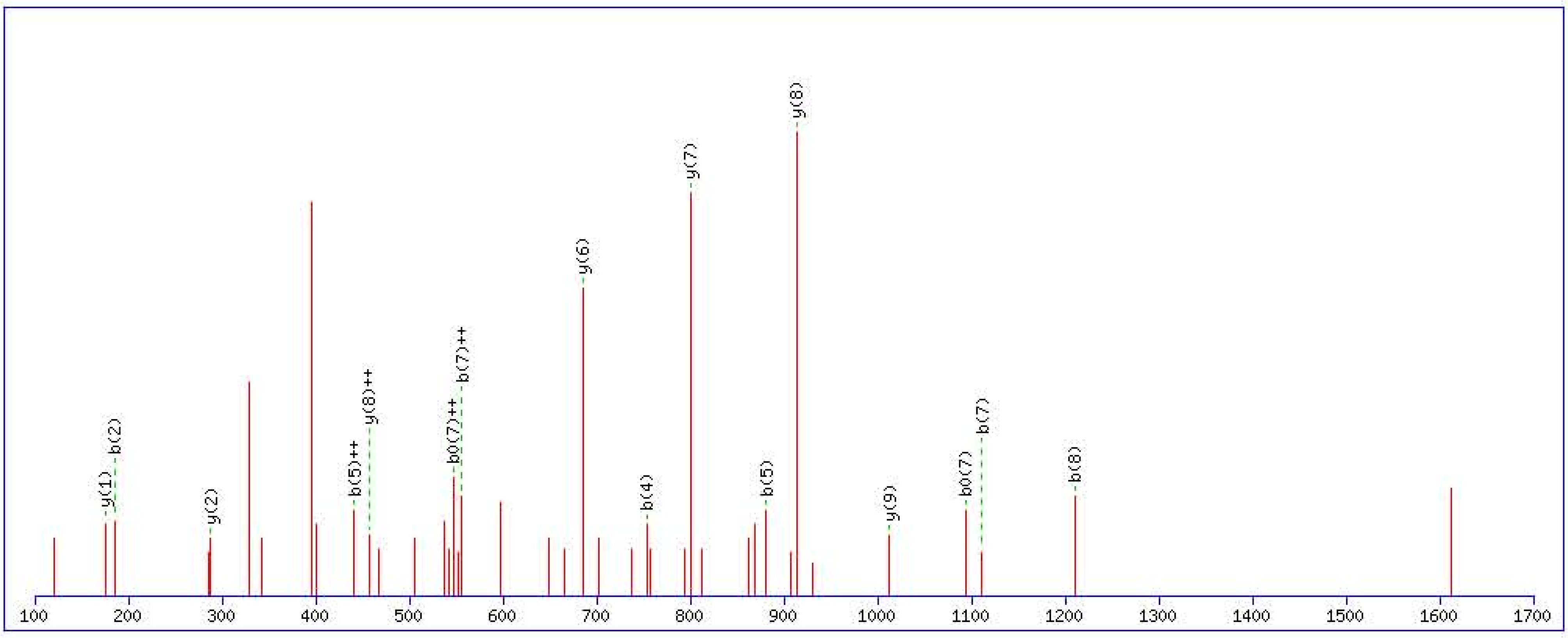
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPEQQETVLDGNLIIR**
Found in **ITIH4_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4

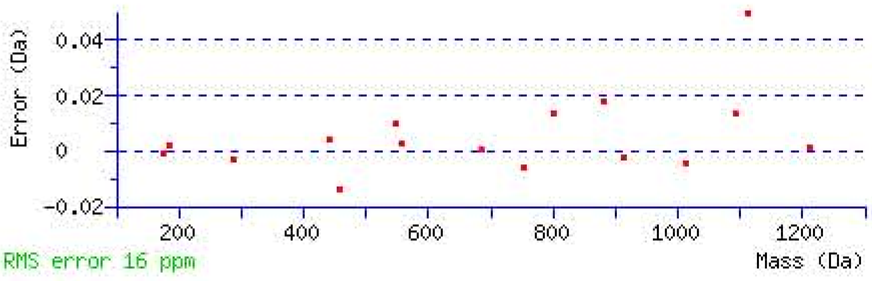
Match to Query 41897: 2122.128102 from(708.383310,3+) rtinseconds(2416) index(7144)
Title: Locus:1.1.1.3361.20 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

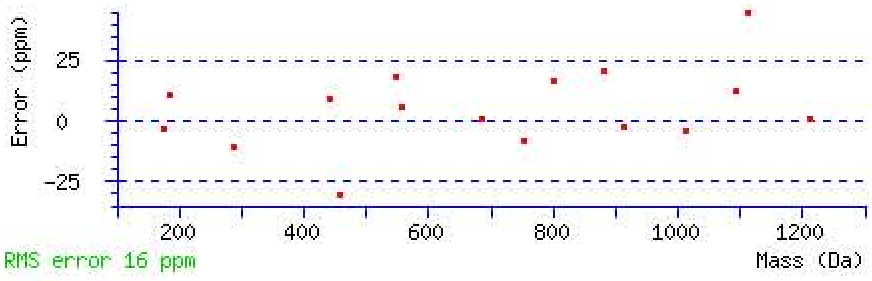
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1700 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2122.109222
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.00025
Matches : 16/162 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	88.039304	44.523290			70.028739	35.518008	S							16
2	***185.092068***	93.049672			167.081503	84.044389	P	2036.084489	1018.545882	2019.057940	1010.032608	2018.073924	1009.540600	15
3	314.134661	157.570968			296.124096	148.565686	E	1939.031725	970.019500	1922.005176	961.506226	1921.021160	961.014218	14
4	***753.359987***	377.183632	736.333438	368.670357	735.349422	368.178349	Q	1809.989132	905.498204	1792.962583	896.984929	1791.978567	896.492921	13
5	***881.418565***	**441.212921**	864.392016	432.699646	863.408000	432.207638	Q	1370.763806	685.885541	1353.737257	677.372266	1352.753241	676.880258	12
6	1010.461158	505.734217	993.434609	497.220943	992.450593	496.728935	E	1242.705228	621.856252	1225.678679	613.342977	1224.694663	612.850969	11
7	***1111.508837***	**556.258057**	1094.482288	547.744782	1093.498272	547.252774	T	1113.662635	557.334955	1096.636086	548.821681	1095.652070	548.329673	10
8	***1210.577251***	605.792264	1193.550702	597.278989	1192.566686	596.786981	V	***1012.614956***	506.811116	995.588407	498.297841	994.604391	497.805833	9
9	1323.661315	662.334296	1306.634766	653.821021	1305.650750	653.329013	L	***913.546542***	457.276909	896.519993	448.763634	895.535977	448.271626	8
10	1438.688258	719.847767	1421.661709	711.334493	1420.677693	710.842485	D	***800.462478***	400.734877	783.435929	392.221602	782.451913	391.729594	7
11	1495.709722	748.358499	1478.683173	739.845225	1477.699157	739.353217	G	***685.435535***	343.221405	668.408986	334.708131			6
12	1609.752649	805.379963	1592.726100	796.866688	1591.742084	796.374680	N	628.414071	314.710673	611.387522	306.197399			5
13	1722.836713	861.921994	1705.810164	853.408720	1704.826148	852.916712	L	514.371144	257.689210	497.344595	249.175935			4
14	1835.920777	918.464026	1818.894228	909.950752	1817.910212	909.458744	I	401.287080	201.147178	384.260531	192.633903			3
15	1949.004841	975.006058	1931.978292	966.492784	1930.994276	966.000776	I	***288.203016***	144.605146	271.176467	136.091871			2
16							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SPEQQETVLDGNLIIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.3	2122.109222	0.018880	SPEQQETVLDGNLIIR
34.9	2122.109222	0.018880	SPEQQETVLDGNLIIR
4.6	2122.099350	0.028752	IDLAVGDVVKTWRFSNMR
4.2	2122.100189	0.027913	MIAPQRWIDAQR
4.1	2122.139053	-0.010951	RRVYDALNVLMAMNIISK
4.1	2122.139053	-0.010951	RRVYDALNVLMAMNIISK
2.1	2122.135742	-0.007640	TQVSLTAVWIGAQGQPR
1.9	2122.120453	0.007649	TELLPGDRDNLAIQTR
1.5	2122.149612	-0.021510	LPALRLMNATITEELFFK
0.7	2122.100204	0.027898	QQGQCLLLWQAR

Mascot: http://www.matrixscience.com/

{MATRIX SCIENCE}

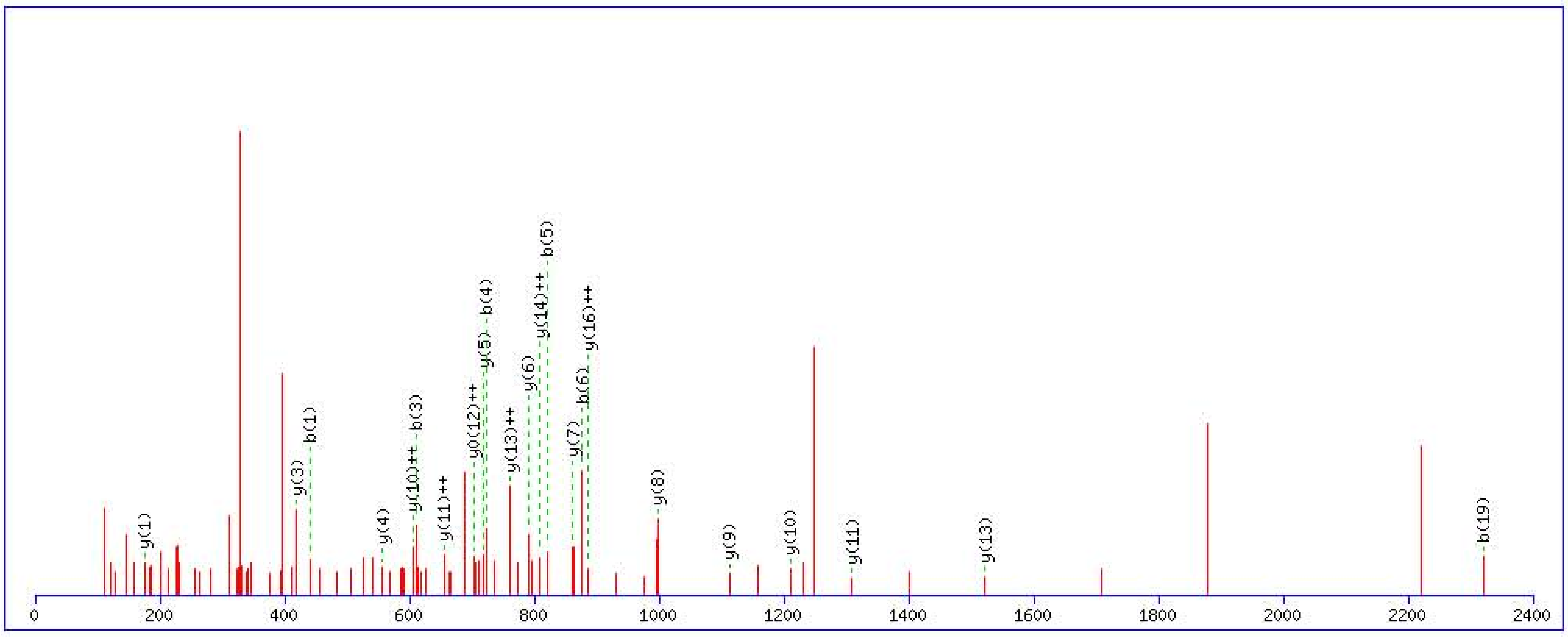
Mascot Search Results

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

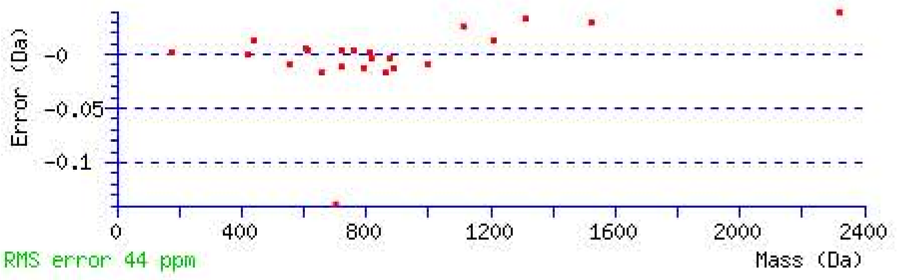
Match to Query 48392: 2494.244896 from(624.568500,4+) rtinseconds(2175) index(20073)
Title: Locus:1.1.1.3323.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

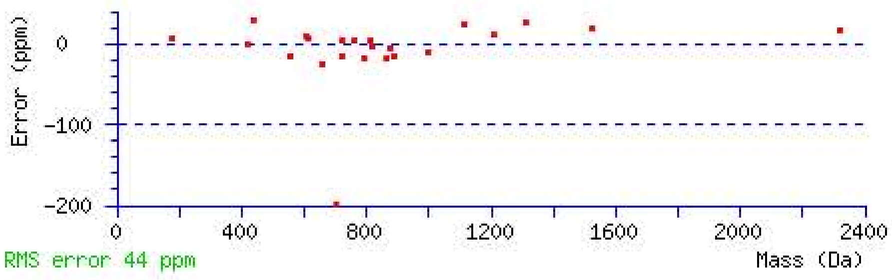
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2494.257980
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 50  Expect: 2.3e-005
Matches : 23/196 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	***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
49.9	2494.257980	-0.013084	QLGLPGPPDVPDHAAYHPFR
0.6	2494.270370	-0.025474	LLEVSDDPQVLAVAAHDVGEYVR

Mascot: http://www.matrixscience.com/

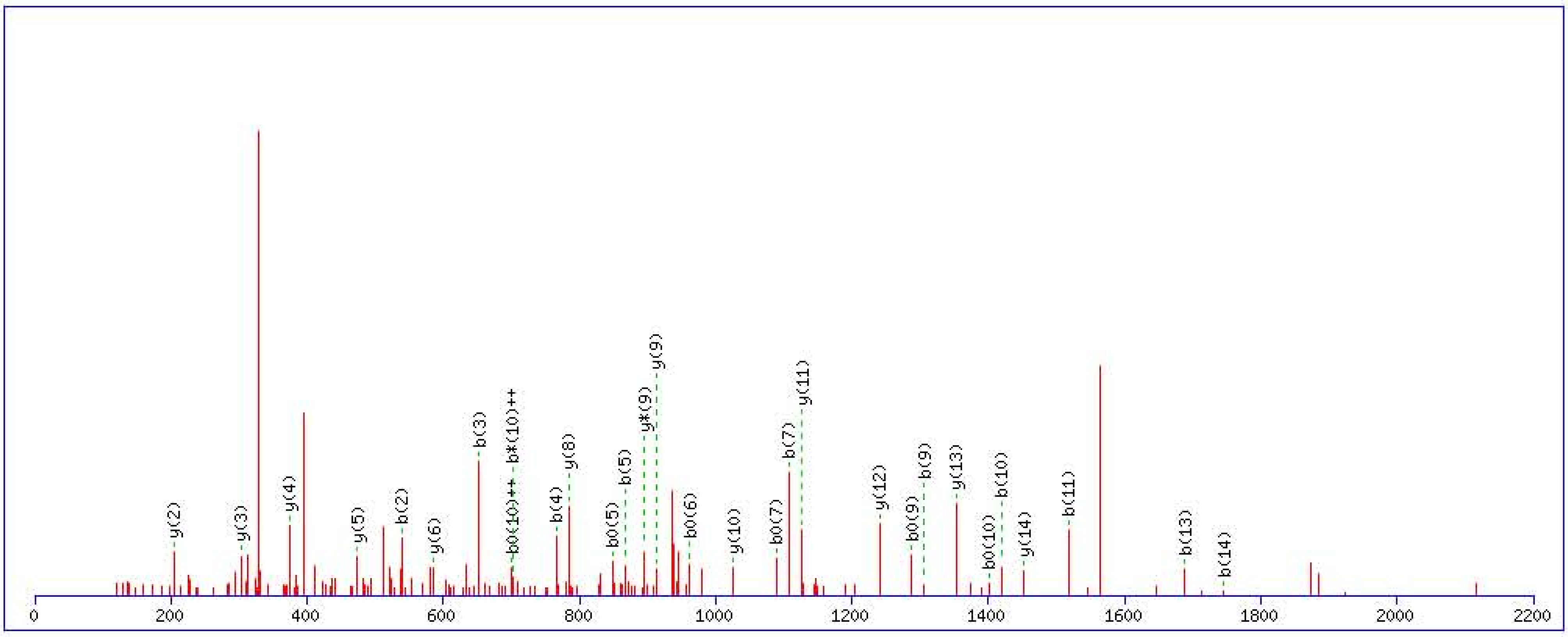
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QVILTLQPTLVAVGK**
Found in **ICAM2_HUMAN**, Intercellular adhesion molecule 2 OS=Homo sapiens GN=ICAM2 PE=1 SV=2

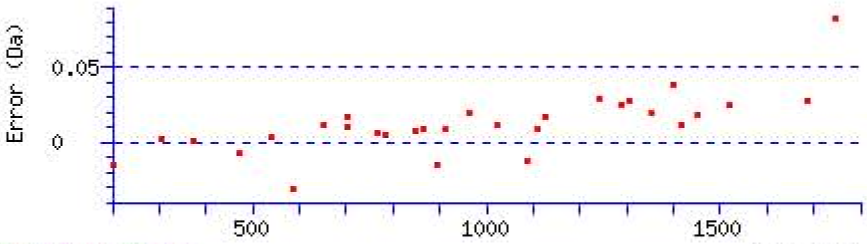
Match to Query 37285: 1890.157448 from(946.086000,2+) rtinseconds(2684) index(8620)
Title: Locus:1.1.1.3454.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

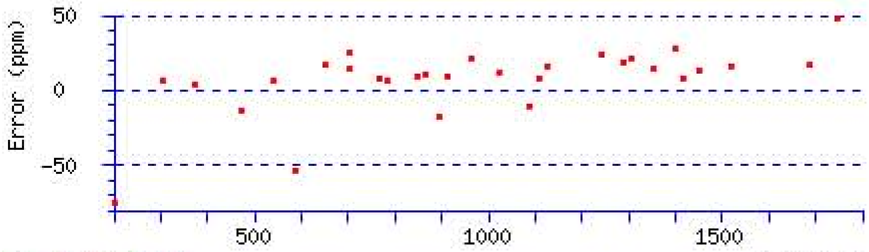


```
Monoisotopic mass of neutral peptide Mr(calc): 1890.137634
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 71  Expect: 8.8e-008
Matches : 30/148 fragment ions using 61 most intense peaks   (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							15
2	**539.301016**	270.154146	522.274467	261.640872			V	***1451.919580***	726.463428	1434.893031	717.950154	1433.909015	717.458146	14
3	**652.385080**	326.696178	635.358531	318.182904			I	***1352.851166***	676.929221	1335.824617	668.415947	1334.840601	667.923939	13
4	**765.469144**	383.238210	748.442595	374.724936			L	***1239.767102***	620.387189	1222.740553	611.873915	1221.756537	611.381907	12
5	**866.516823**	433.762050	849.490274	425.248775	848.506258	424.756767	T	***1126.683038***	563.845157	1109.656489	555.331883	1108.672473	554.839874	11
6	979.600887	490.304082	962.574338	481.790807	961.590322	481.298799	L	***1025.635359***	513.321318	1008.608810	504.808043	1007.624794	504.316035	10
7	**1107.659465**	554.333371	1090.632916	545.820096	1089.648900	545.328088	Q	***912.551295***	456.779286	895.524746	448.266011	894.540730	447.774003	9
8	1204.712229	602.859753	1187.685680	594.346478	1186.701664	593.854470	P	***784.492717***	392.749997	767.466168	384.236722	766.482152	383.744714	8
9	**1305.759908**	653.383592	1288.733359	644.870318	1287.749343	644.378310	T	687.439953	344.223615	670.413404	335.710340	669.429388	335.218332	7
10	**1418.843972**	709.925624	1401.817423	701.412350	1400.833407	700.920341	L	***586.392274***	293.699775	569.365725	285.186501			6
11	**1517.912386**	759.459831	1500.885837	750.946557	1499.901821	750.454548	V	***473.308210***	237.157743	456.281661	228.644469			5
12	1588.949500	794.978388	1571.922951	786.465114	1570.938935	785.973105	A	***374.239796***	187.623536	357.213247	179.110261			4
13	**1688.017914**	844.512595	1670.991365	835.999321	1670.007349	835.507313	V	***303.202682***	152.104979	286.176133	143.591704			3
14	**1745.039378**	873.023327	1728.012829	864.510053	1727.028813	864.018044	G	***204.134268***	102.570772	187.107719	94.057497			2
15							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 23 ppm



RMS error 23 ppm

NCBI **BLAST** search of QVILTLQPTLVAVGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.6	1890.137634	0.019814	QVILTLQPTLVAVGK
15.6	1890.137634	0.019814	QVILTLQPTLVAVGK

Mascot: http://www.matrixscience.com/

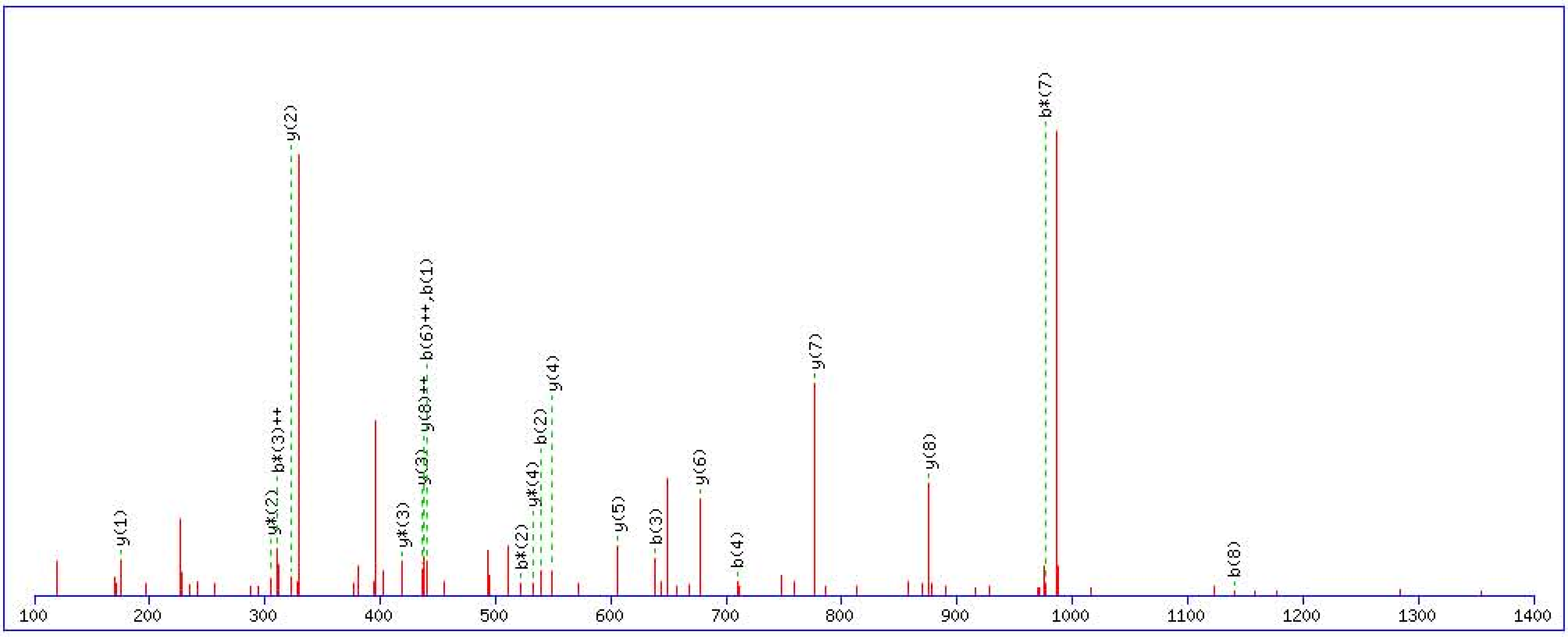
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QVVAGLNFR**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

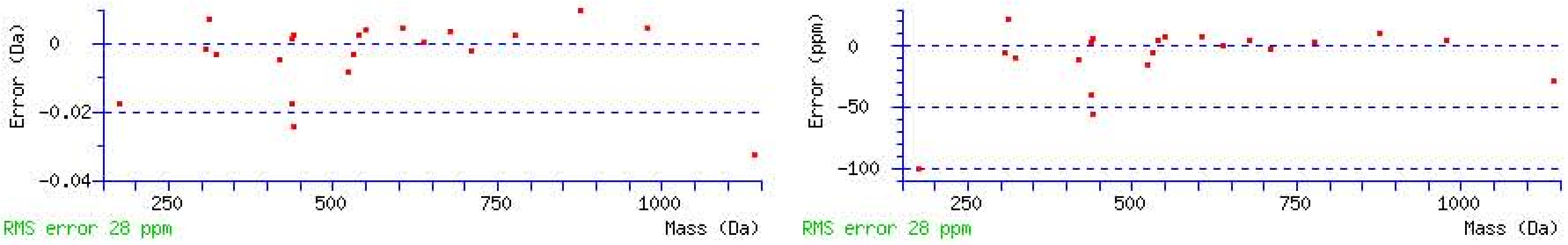
Match to Query 20595: 1313.729408 from(657.871980,2+) rtinseconds(2233) index(20403)
Title: Locus:1.1.1.3343.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 1313.727814
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.007
Matches : 21/64 fragment ions using 64 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	**440.232602**	220.619939	423.206053	212.106664	Q					9
2	**539.301016**	270.154146	522.274467	261.640872	V	***875.509763***	438.258520	858.483214	429.745245	8
3	**638.369430**	319.688353	621.342881	311.175078	V	***776.441349***	388.724313	759.414800	380.211038	7
4	**709.406544**	355.206910	692.379995	346.693635	A	***677.372935***	339.190106	660.346386	330.676831	6
5	766.428008	383.717642	749.401459	375.204367	G	***606.335821***	303.671549	589.309272	295.158274	5
6	879.512072	440.259674	862.485523	431.746400	L	***549.314357***	275.160817	532.287808	266.647542	4
7	993.554999	497.281138	976.528450	488.767863	N	***436.230293***	218.618784	419.203744	210.105510	3
8	**1140.623413**	570.815345	1123.596864	562.302070	F	***322.187366***	161.597321	305.160817	153.084047	2
9					R	***175.118952***	88.063114	158.092403	79.549839	1



NCBI **BLAST** search of QVVAGLNFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.7	1313.727814	0.001594	QVVAGLNFR
4.4	1313.748947	-0.019539	VLVQSVCIQIR
2.0	1313.730286	-0.000878	AKEDVLQKEVR
2.0	1313.731644	-0.002236	GEPPPPVRRPGR
2.0	1313.745575	-0.016167	GSLALQPFLVGGR
2.0	1313.727798	0.001610	KSLSVWQR
2.0	1313.730301	-0.000893	LSQTLQVQLER
2.0	1313.741516	-0.012108	NLTRLDLSLNR
2.0	1313.730286	-0.000878	QVTKEEGLALAR
2.0	1313.723755	0.005653	SLKMLPERGQR

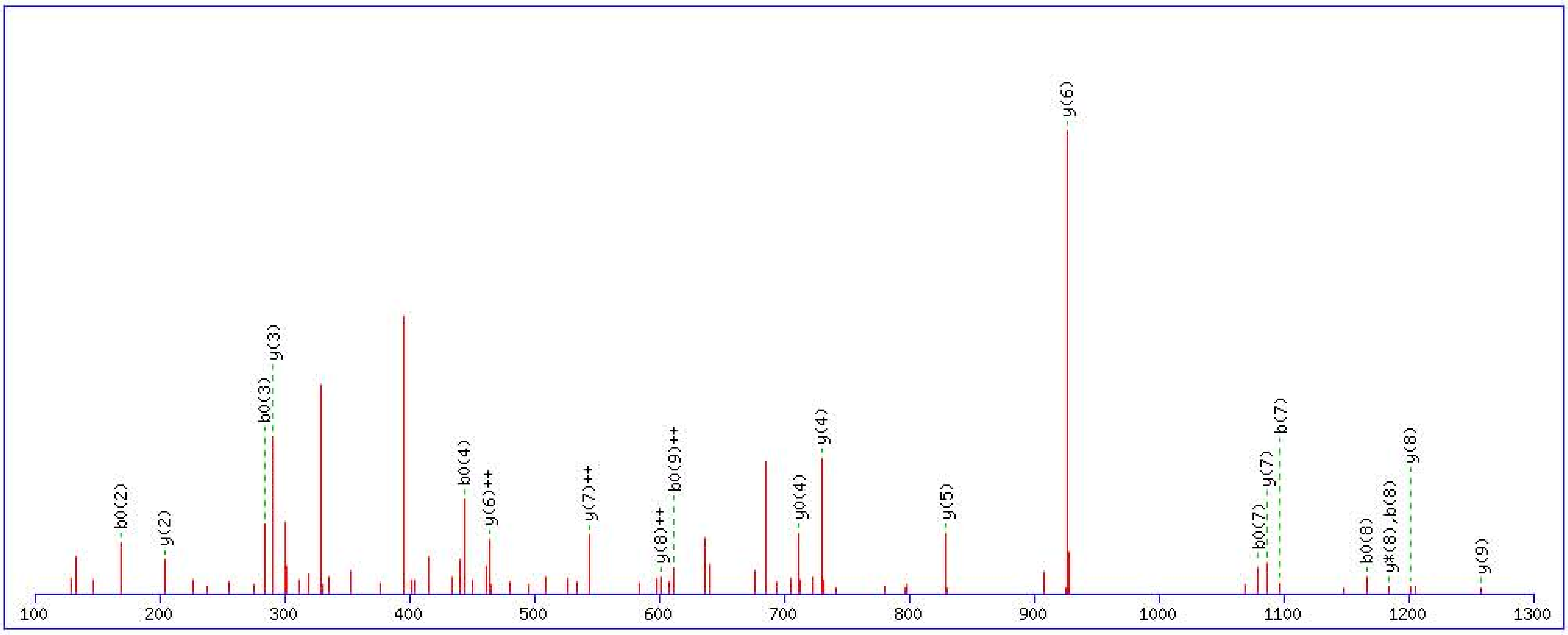
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGDCPVQSGK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

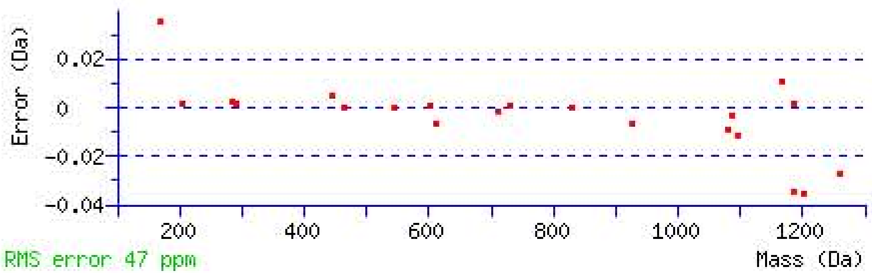
Match to Query 23067: 1386.620748 from(694.317650,2+) rtinseconds(1421) index(15369)
Title: Locus:1.1.1.3060.24 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

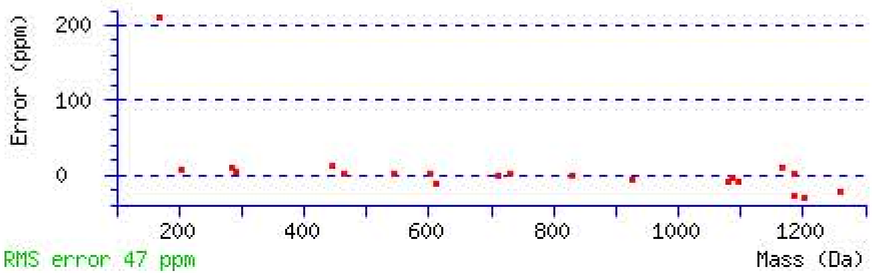
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1386.627182
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 58  Expect: 9.7e-006
Matches : 21/92 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	130.049869	65.528572			112.039304	56.523290	E							10
2	187.071333	94.039305			169.060768	85.034022	G	***1258.591856***	629.799566	1241.565307	621.286292	1240.581291	620.794284	9
3	302.098276	151.552776			284.087711	142.547494	D	***1201.570392***	601.288834	1184.543843	592.775560	1183.559827	592.283552	8
4	462.128925	231.568101			444.118360	222.562818	C	***1086.543449***	543.775363	1069.516900	535.262088	1068.532884	534.770080	7
5	559.181689	280.094483			541.171124	271.089200	P	***926.512800***	463.760038	909.486251	455.246764	908.502235	454.754756	6
6	658.250103	329.628690			640.239538	320.623407	V	***829.460036***	415.233656	812.433487	406.720382	811.449471	406.228374	5
7	**1097.475429**	549.241353	1080.448880	540.728078	1079.464864	540.236070	Q	***730.391622***	365.699449	713.365073	357.186175	712.381057	356.694167	4
8	**1184.507457**	592.757367	1167.480908	584.244092	1166.496892	583.752084	S	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	3
9	1241.528921	621.268099	1224.502372	612.754824	1223.518356	612.262816	G	***204.134268***	102.570772	187.107719	94.057497			2
10							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of EGDCPVQSGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.6	1386.627182	-0.006434	EGDCPVQSGK
5.4	1386.619766	0.000982	QMQQQEHDSLK

Mascot: http://www.matrixscience.com/

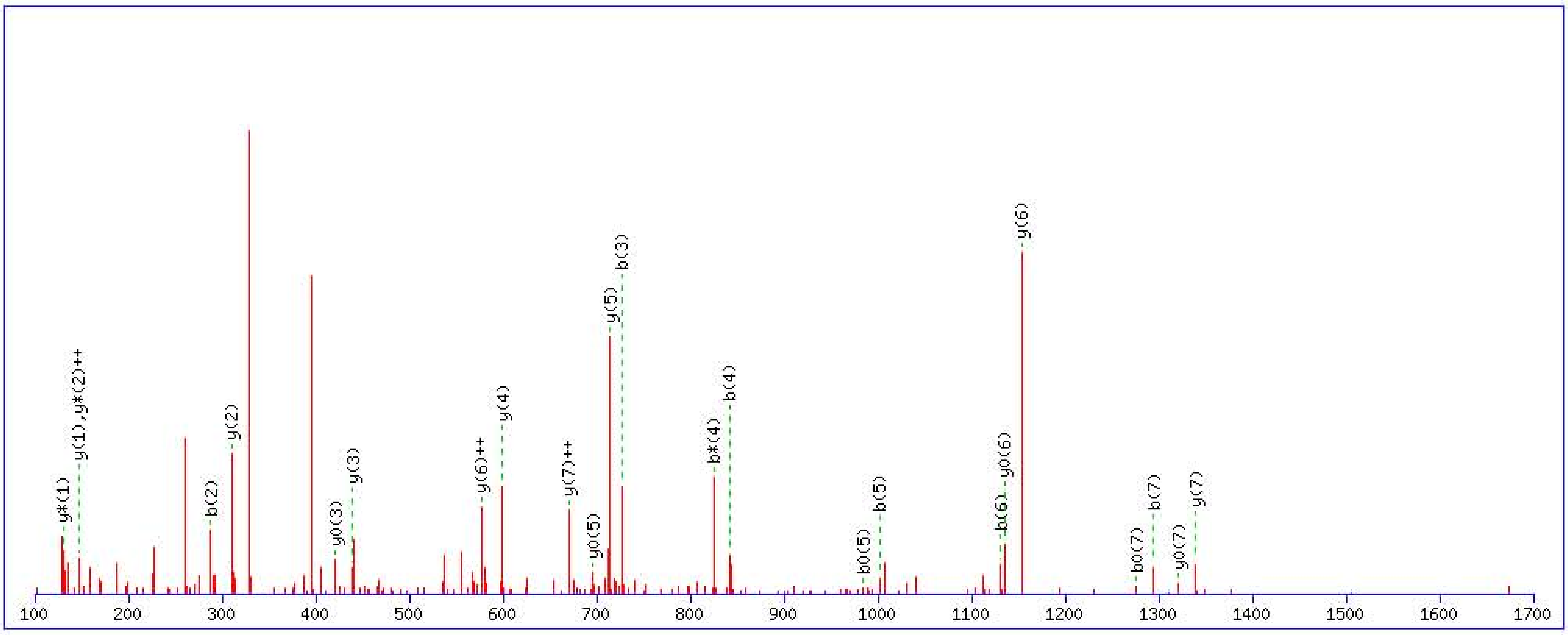
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TWQDCEYK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

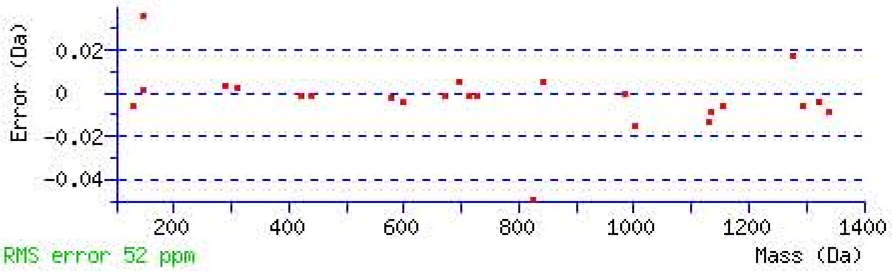
Match to Query 25574: 1439.615508 from(720.815030,2+) rtinseconds(1799) index(17731)
Title: Locus:1.1.1.3192.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

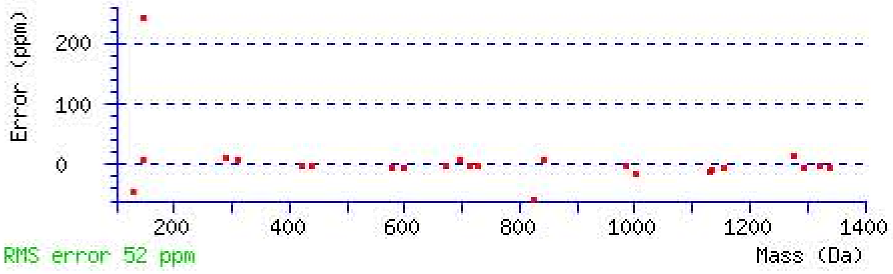
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1439.621353
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.0036
Matches : 24/76 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	102.054955	51.531116			84.044390	42.525833	T							8
2	**288.134268**	144.570772			270.123703	135.565490	W	***1339.580957***	670.294117	1322.554408	661.780842	1321.570392	661.288834	7
3	**727.359594**	364.183435	710.333045	355.670161	709.349029	355.178153	Q	***1153.501644***	577.254460	1136.475095	568.741186	1135.491079	568.249178	6
4	**842.386537**	421.696907	825.359988	413.183632	824.375972	412.691624	D	***714.276318***	357.641797	697.249769	349.128523	696.265753	348.636515	5
5	**1002.417186**	501.712231	985.390637	493.198957	984.406621	492.706949	C	***599.249375***	300.128326	582.222826	291.615051	581.238810	291.123043	4
6	**1131.459779**	566.233528	1114.433230	557.720253	1113.449214	557.228245	E	***439.218726***	220.113001	422.192177	211.599727	421.208161	211.107719	3
7	**1294.523108**	647.765192	1277.496559	639.251918	1276.512543	638.759910	Y	***310.176133***	155.591705	293.149584	147.078430			2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TWQDCEYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.1	1439.621353	-0.005845	TWQDCEYK
5.0	1439.602036	0.013472	EQMEEEQKAMR

Mascot: http://www.matrixscience.com/

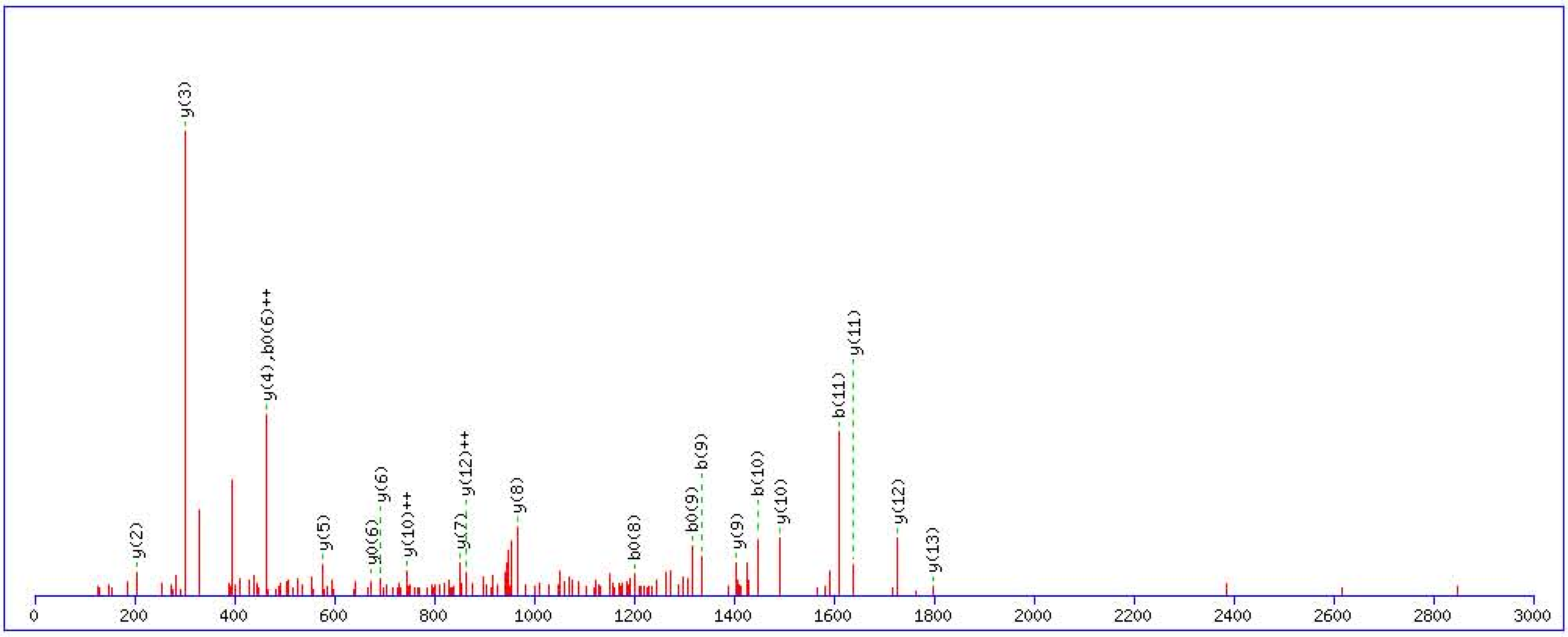
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IASFSQNCDIYPGK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

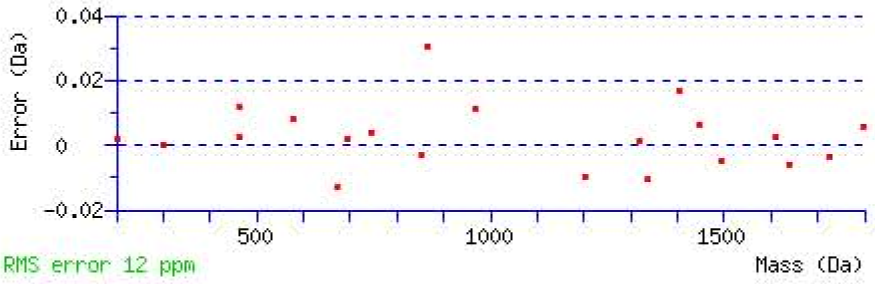
Match to Query 37614: 1909.890968 from(955.952760,2+) rtinseconds(2064) index(19397)
Title: Locus:1.1.1.3284.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

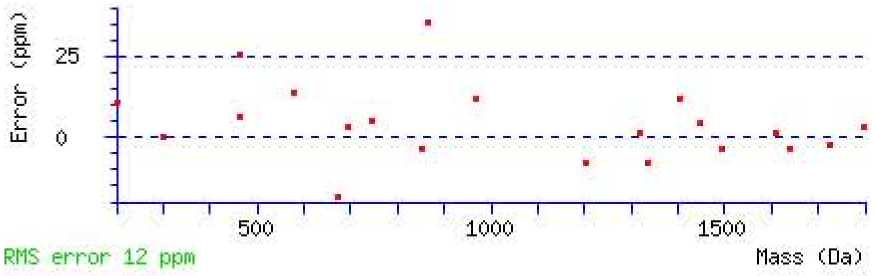
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1909.906631
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 85  Expect: 4.6e-008
Matches : 21/132 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							14
2	185.128454	93.067865					A	***1797.829854***	899.418565	1780.803305	890.905291	1779.819289	890.413283	13
3	272.160482	136.583879			254.149917	127.578596	S	***1726.792740***	863.900008	1709.766191	855.386734	1708.782175	854.894726	12
4	419.228896	210.118086			401.218331	201.112803	F	***1639.760712***	820.383994	1622.734163	811.870720	1621.750147	811.378712	11
5	506.260924	253.634100			488.250359	244.628817	S	***1492.692298***	746.849787	1475.665749	738.336513	1474.681733	737.844505	10
6	945.486250	473.246763	928.459701	464.733488	927.475685	464.241480	Q	***1405.660270***	703.333773	1388.633721	694.820499	1387.649705	694.328491	9
7	1059.529177	530.268226	1042.502628	521.754952	1041.518612	521.262944	N	***966.434944***	483.721110	949.408395	475.207836	948.424379	474.715828	8
8	1219.559826	610.283551	1202.533277	601.770277	1201.549261	601.278268	C	***852.392017***	426.699647	835.365468	418.186372	834.381452	417.694364	7
9	**1334.586769**	667.797023	1317.560220	659.283748	1316.576204	658.791740	D	***692.361368***	346.684322	675.334819	338.171048	674.350803	337.679040	6
10	**1447.670833**	724.339054	1430.644284	715.825780	1429.660268	715.333772	I	***577.334425***	289.170851	560.307876	280.657576			5
11	**1610.734162**	805.870719	1593.707613	797.357445	1592.723597	796.865436	Y	***464.250361***	232.628818	447.223812	224.115544			4
12	1707.786926	854.397101	1690.760377	845.883827	1689.776361	845.391819	P	***301.187032***	151.097154	284.160483	142.583879			3
13	1764.808390	882.907833	1747.781841	874.394559	1746.797825	873.902550	G	***204.134268***	102.570772	187.107719	94.057497			2
14							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of IASFSQNCDIYPGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
85.1	1909.906631	-0.015663	IASFSQNCDIYPGK
6.9	1909.877441	0.013527	IAREAPSECNCPAGPPGK

Mascot: http://www.matrixscience.com/

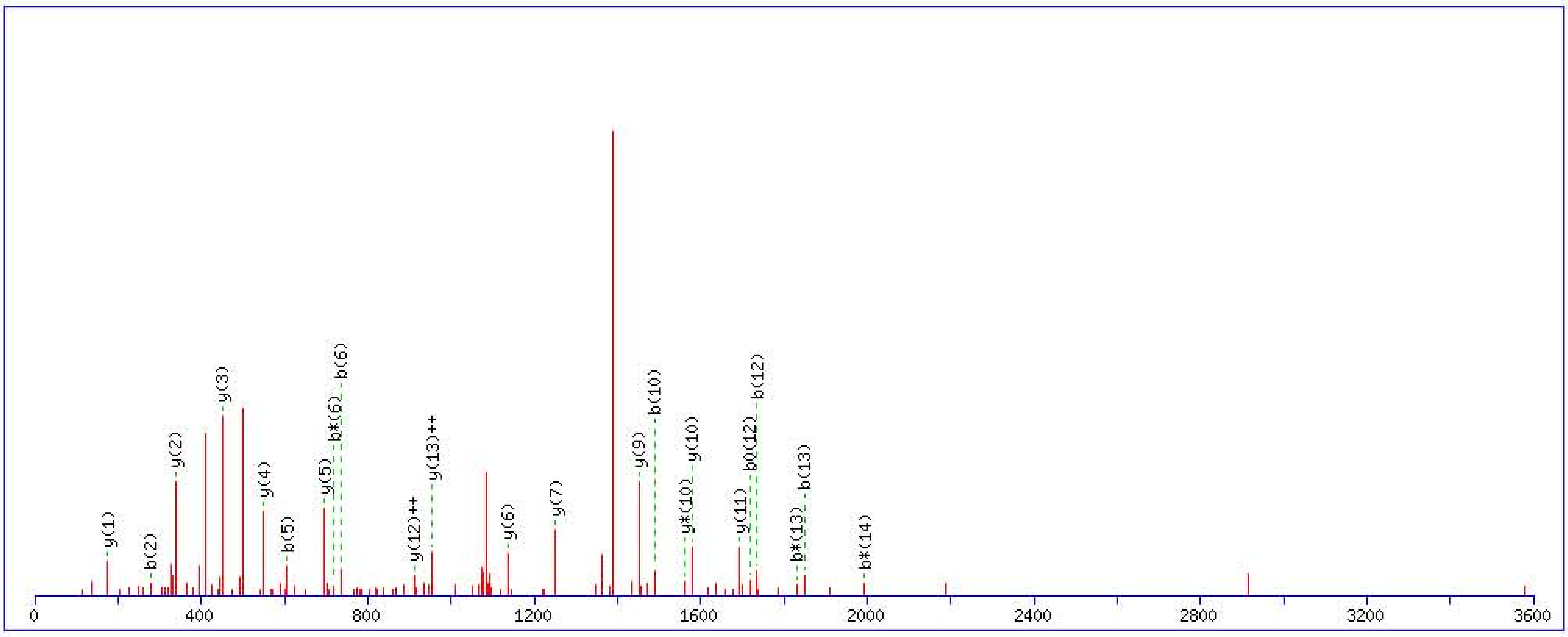
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YNSQNQSNNQFVLYR**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

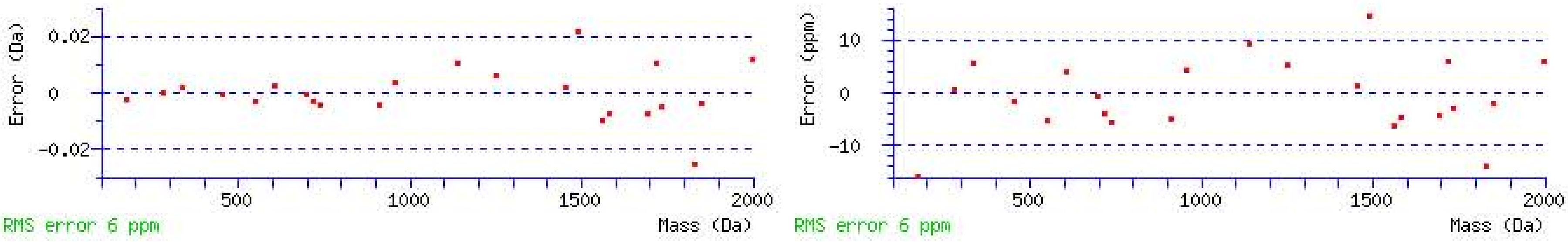
Match to Query 43004: 2185.020628 from(1093.517590,2+) rtinseconds(2145) index(32713)
Title: Locus:1.1.1.3410.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2185.037445
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10    : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 1.3e-006
Matches : 23/146 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	164.070605	82.538940					Y							15
2	**278.113532**	139.560404	261.086983	131.047130			N	2022.981419	1011.994348	2005.954870	1003.481073	2004.970854	1002.989065	14
3	365.145560	183.076418	348.119011	174.563144	347.134995	174.071136	S	1908.938492	954.972884	1891.911943	946.459610	1890.927927	945.967602	13
4	493.204138	247.105707	476.177589	238.592433	475.193573	238.100425	Q	1821.906464	911.456870	1804.879915	902.943596	1803.895899	902.451588	12
5	**607.247065**	304.127171	590.220516	295.613896	589.236500	295.121888	N	***1693.847886***	847.427581	1676.821337	838.914307	1675.837321	838.422299	11
6	**735.305643**	368.156460	718.279094	359.643185	717.295078	359.151177	Q	***1579.804959***	790.406118	1562.778410	781.892843	1561.794394	781.400835	10
7	822.337671	411.672474	805.311122	403.159199	804.327106	402.667191	S	***1451.746381***	726.376829	1434.719832	717.863554	1433.735816	717.371546	9
8	936.380598	468.693937	919.354049	460.180662	918.370033	459.688654	N	1364.714353	682.860815	1347.687804	674.347540			8
9	1050.423525	525.715400	1033.396976	517.202126	1032.412960	516.710118	N	***1250.671426***	625.839351	1233.644877	617.326077			7
10	**1489.648851**	745.328064	1472.622302	736.814789	1471.638286	736.322781	Q	***1136.628499***	568.817888	1119.601950	560.304613			6
11	1636.717265	818.862271	1619.690716	810.348996	1618.706700	809.856988	F	***697.403173***	349.205225	680.376624	340.691950			5
12	**1735.785679**	868.396478	1718.759130	859.883203	1717.775114	859.391195	V	***550.334759***	275.671018	533.308210	267.157743			4
13	**1848.869743**	924.938510	1831.843194	916.425235	1830.859178	915.933227	L	***451.266345***	226.136811	434.239796	217.623536			3
14	2011.933072	1006.470174	1994.906523	997.956900	1993.922507	997.464892	Y	***338.182281***	169.594779	321.155732	161.081504			2
15							R	***175.118952***	88.063114	158.092403	79.549840			1



NCBI **BLAST** search of YNSQNQSNNQFVLYR
(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	2185.037445	-0.016817	YNSQNQSNNQFVLYR
28.8	2185.037445	-0.016817	YNSQNQSNNQFVLYR
13.4	2185.037445	-0.016817	YNSQNQSNNQFVLYR

Mascot: http://www.matrixscience.com/

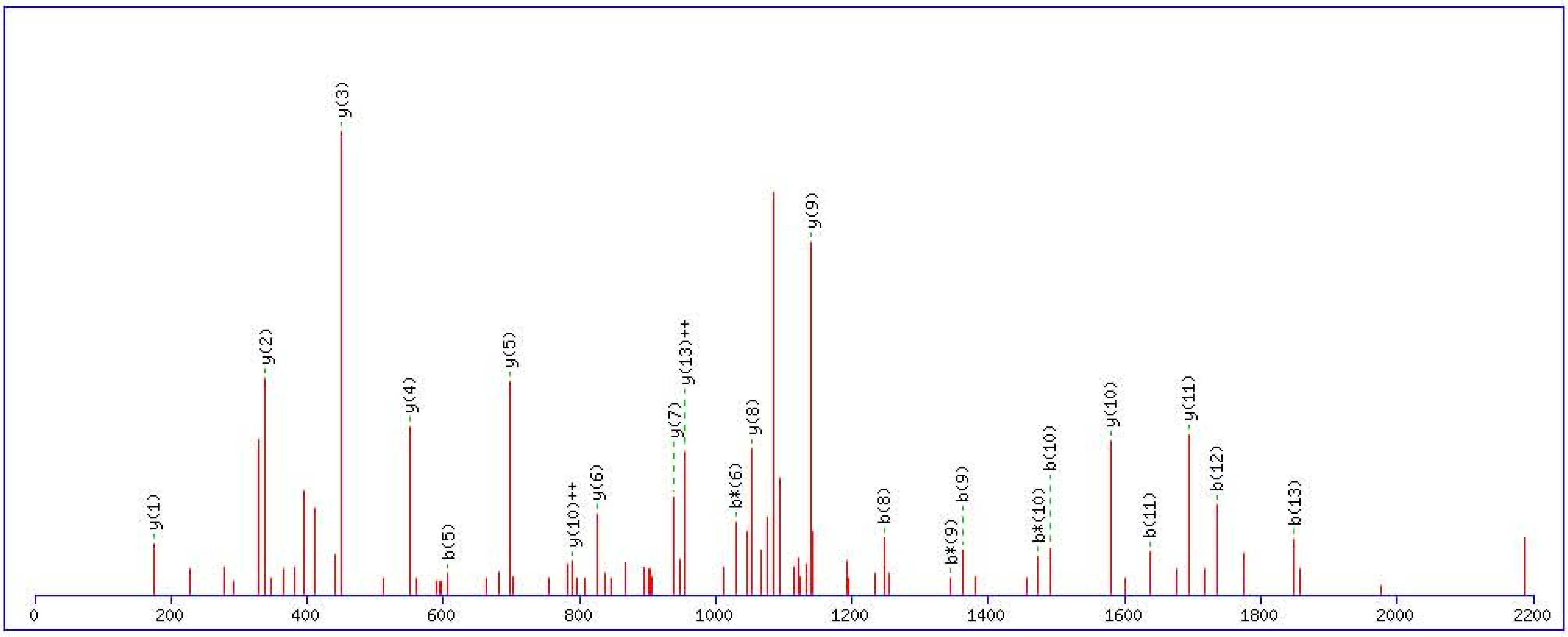
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YNSQNQSNNQFVLYR**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

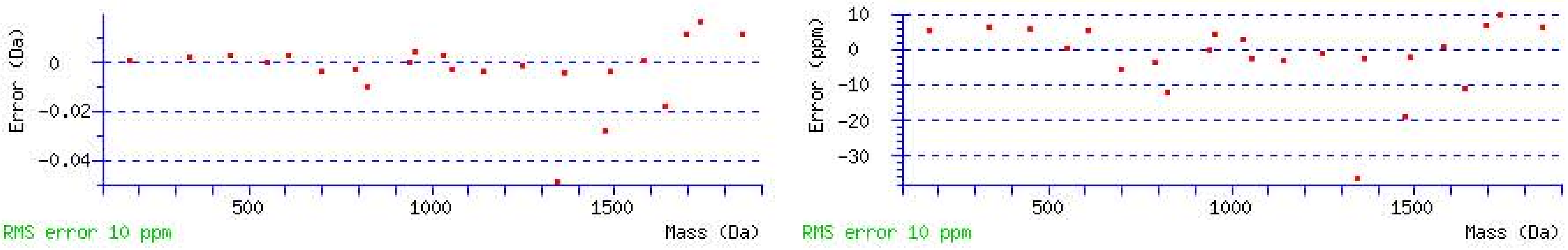
Match to Query 43005: 2185.031248 from(1093.522900,2+) rtinseconds(2062) index(19385)
Title: Locus:1.1.1.3283.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 2185.037445
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 81  Expect: 2.8e-008
Matches : 23/146 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	164.070605	82.538940					Y							15
2	278.113532	139.560404	261.086983	131.047130			N	2022.981419	1011.994348	2005.954870	1003.481073	2004.970854	1002.989065	14
3	365.145560	183.076418	348.119011	174.563144	347.134995	174.071136	S	1908.938492	954.972884	1891.911943	946.459610	1890.927927	945.967602	13
4	493.204138	247.105707	476.177589	238.592433	475.193573	238.100425	Q	1821.906464	911.456870	1804.879915	902.943596	1803.895899	902.451588	12
5	**607.247065**	304.127171	590.220516	295.613896	589.236500	295.121888	N	***1693.847886***	847.427581	1676.821337	838.914307	1675.837321	838.422299	11
6	1046.472391	523.739834	1029.445842	515.226559	1028.461826	514.734551	Q	***1579.804959***	790.406118	1562.778410	781.892843	1561.794394	781.400835	10
7	1133.504419	567.255848	1116.477870	558.742573	1115.493854	558.250565	S	***1140.579633***	570.793455	1123.553084	562.280180	1122.569068	561.788172	9
8	**1247.547346**	624.277311	1230.520797	615.764037	1229.536781	615.272029	N	***1053.547605***	527.277441	1036.521056	518.764166			8
9	**1361.590273**	681.298775	1344.563724	672.785500	1343.579708	672.293492	N	***939.504678***	470.255977	922.478129	461.742703			7
10	**1489.648851**	745.328064	1472.622302	736.814789	1471.638286	736.322781	Q	***825.461751***	413.234514	808.435202	404.721239			6
11	**1636.717265**	818.862271	1619.690716	810.348996	1618.706700	809.856988	F	***697.403173***	349.205225	680.376624	340.691950			5
12	**1735.785679**	868.396478	1718.759130	859.883203	1717.775114	859.391195	V	***550.334759***	275.671018	533.308210	267.157743			4
13	**1848.869743**	924.938510	1831.843194	916.425235	1830.859178	915.933227	L	***451.266345***	226.136811	434.239796	217.623536			3
14	2011.933072	1006.470174	1994.906523	997.956900	1993.922507	997.464892	Y	***338.182281***	169.594779	321.155732	161.081504			2
15							R	***175.118952***	88.063114	158.092403	79.549840			1



NCBI **BLAST** search of YNSQNQSNNQFVLYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
81.1	2185.037445	-0.006197	YNSQNQSNNQFVLYR
50.0	2185.037445	-0.006197	YNSQNQSNNQFVLYR
43.1	2185.037445	-0.006197	YNSQNQSNNQFVLYR
0.6	2185.040604	-0.009356	ERAAAAAAAAQMHAKNGGGSSSR
0.5	2185.047348	-0.016100	HLSSLTDNEQADIFER

Mascot: http://www.matrixscience.com/

{MATRIX} {SCIENCE}

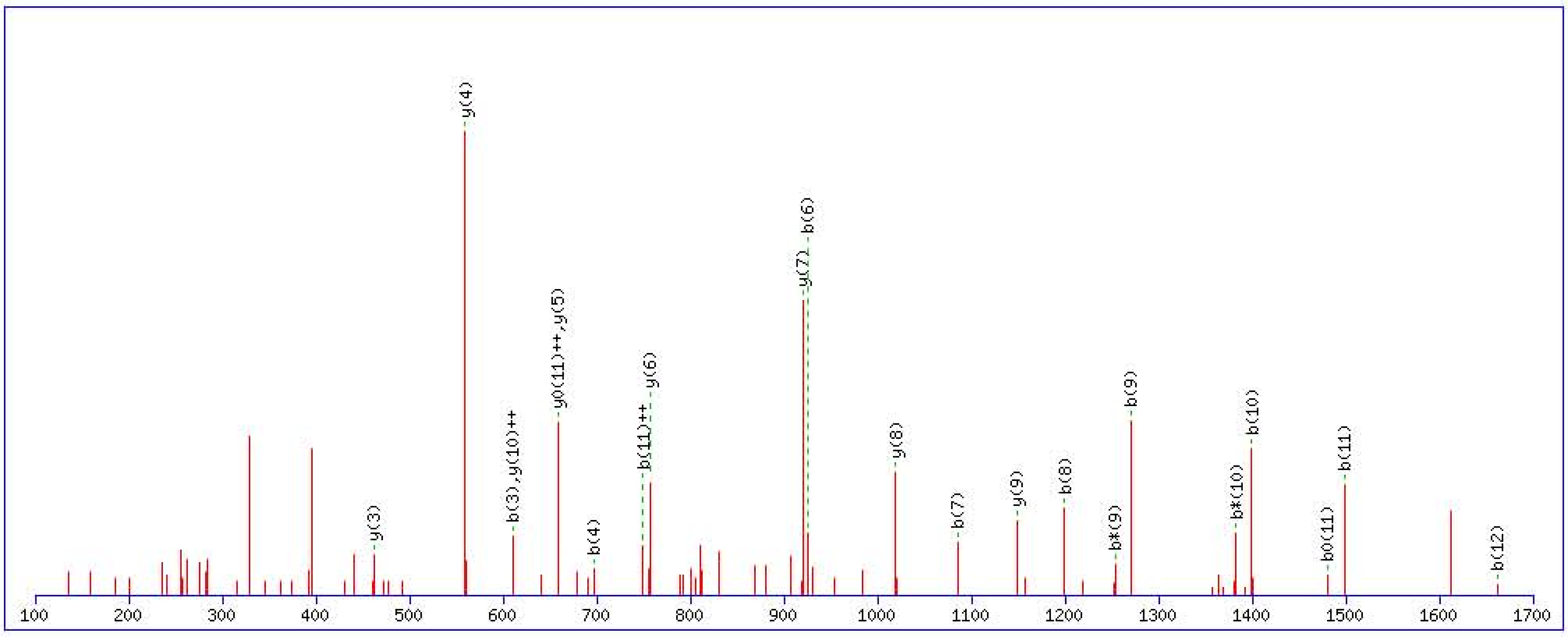
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGQSLDCNAEVYVVPWEK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

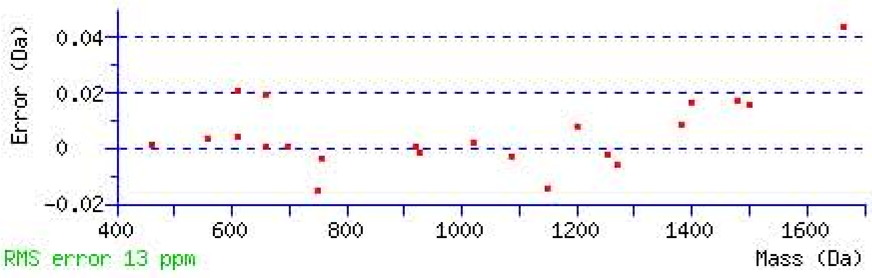
Match to Query 46747: 2417.172252 from(806.731360,3+) rtinseconds(2581) index(35035)
Title: Locus:1.1.1.3562.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

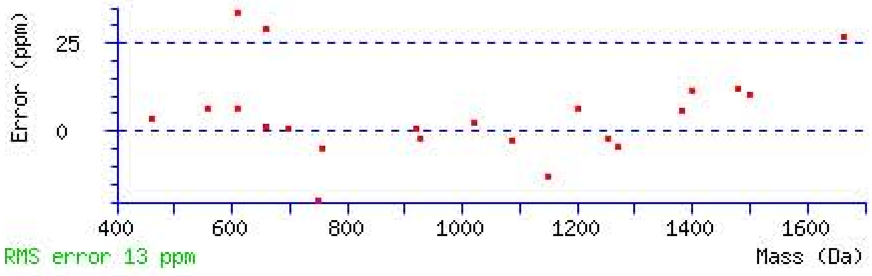
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2417.175934
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 60 **Expect:** 3.1e-006
Matches : 22/192 fragment ions using 29 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							18
2	171.112804	86.060040					G	2305.099153	1153.053214	2288.072604	1144.539940	2287.088588	1144.047932	17
3	***610.338130***	305.672703	593.311581	297.159429			Q	2248.077689	1124.542482	2231.051140	1116.029208	2230.067124	1115.537200	16
4	***697.370158***	349.188717	680.343609	340.675443	679.359593	340.183435	S	1808.852363	904.929820	1791.825814	896.416545	1790.841798	895.924537	15
5	810.454222	405.730749	793.427673	397.217475	792.443657	396.725467	L	1721.820335	861.413806	1704.793786	852.900531	1703.809770	852.408523	14
6	***925.481165***	463.244221	908.454616	454.730946	907.470600	454.238938	D	1608.736271	804.871774	1591.709722	796.358499	1590.725706	795.866491	13
7	***1085.511814***	543.259545	1068.485265	534.746271	1067.501249	534.254262	C	1493.709328	747.358302	1476.682779	738.845028	1475.698763	738.353020	12
8	***1199.554741***	600.281008	1182.528192	591.767734	1181.544176	591.275726	N	1333.678679	667.342978	1316.652130	658.829703	1315.668114	658.337695	11
9	***1270.591855***	635.799565	1253.565306	627.286291	1252.581290	626.794283	A	1219.635752	610.321514	1202.609203	601.808240	1201.625187	601.316232	10
10	***1399.634448***	700.320862	1382.607899	691.807588	1381.623883	691.315580	E	***1148.598638***	574.802957	1131.572089	566.289683	1130.588073	565.797675	9
11	***1498.702862***	749.855069	1481.676313	741.341795	1480.692297	740.849787	V	***1019.556045***	510.281661	1002.529496	501.768386	1001.545480	501.276378	8
12	***1661.766191***	831.386734	1644.739642	822.873459	1643.755626	822.381451	Y	***920.487631***	460.747454	903.461082	452.234179	902.477066	451.742171	7
13	1760.834605	880.920941	1743.808056	872.407666	1742.824040	871.915658	V	***757.424302***	379.215789	740.397753	370.702515	739.413737	370.210507	6
14	1859.903019	930.455148	1842.876470	921.941873	1841.892454	921.449865	V	***658.355888***	329.681582	641.329339	321.168308	640.345323	320.676300	5
15	1956.955783	978.981530	1939.929234	970.468255	1938.945218	969.976247	P	***559.287474***	280.147375	542.260925	271.634101	541.276909	271.142093	4
16	2143.035096	1072.021186	2126.008547	1063.507911	2125.024531	1063.015903	W	***462.234710***	231.620993	445.208161	223.107719	444.224145	222.615711	3
17	2272.077689	1136.542483	2255.051140	1128.029208	2254.067124	1127.537200	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
18							K	147.112804	74.060040	130.086255	65.546765			1

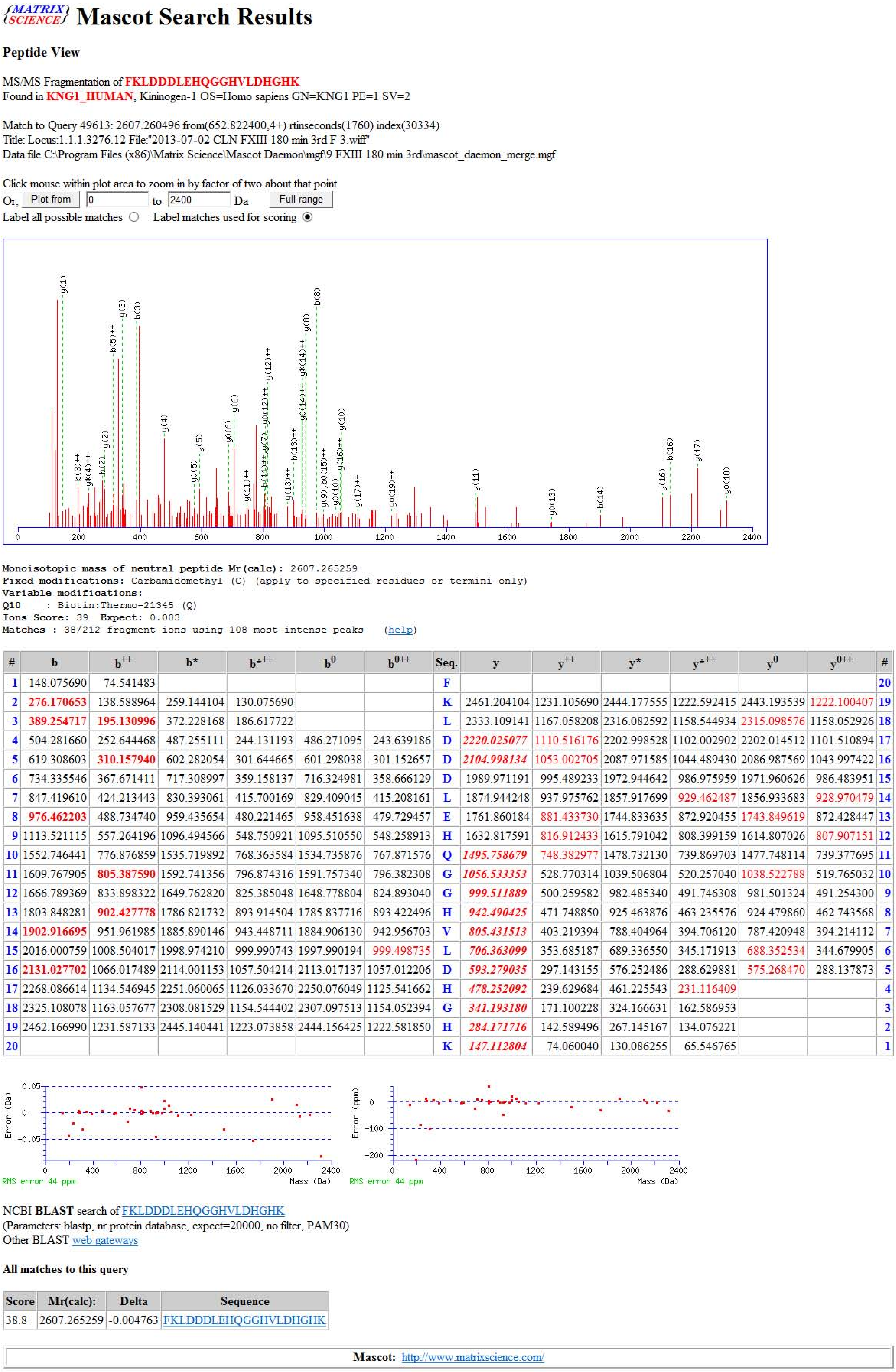




NCBI **BLAST** search of LGQSLDCNAEVYVVPWEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.2	2417.175934	-0.003682	LGQSLDCNAEVYVVPWEK
1.4	2417.149246	0.023006	DEVSGAQMNSSLLPQDAVSSNLR
1.1	2417.146713	0.025539	AMSIREQIGHPDYILEEMNR



Mascot Search Results

Peptide View

MS/MS Fragmentation of **FKLDDDLEHQGGHVLDHGHK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

Match to Query 49613: 2607.260496 from(652.822400,4+) rtinseconds(1760) index(30334)
Title: Locus:1.1.1.3276.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\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): 2607.265259
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10    : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.003
Matches : 38/212 fragment ions using 108 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	**276.170653**	138.588964	259.144104	130.075690			K	2461.204104	1231.105690	2444.177555	1222.592415	2443.193539	1222.100407	19
3	**389.254717**	**195.130996**	372.228168	186.617722			L	2333.109141	1167.058208	2316.082592	1158.544934	2315.098576	1158.052926	18
4	504.281660	252.644468	487.255111	244.131193	486.271095	243.639186	D	***2220.025077***	1110.516176	2202.998528	1102.002902	2202.014512	1101.510894	17
5	619.308603	**310.157940**	602.282054	301.644665	601.298038	301.152657	D	***2104.998134***	1053.002705	2087.971585	1044.489430	2086.987569	1043.997422	16
6	734.335546	367.671411	717.308997	359.158137	716.324981	358.666129	D	1989.971191	995.489233	1972.944642	986.975959	1971.960626	986.483951	15
7	847.419610	424.213443	830.393061	415.700169	829.409045	415.208161	L	1874.944248	937.975762	1857.917699	929.462487	1856.933683	928.970479	14
8	**976.462203**	488.734740	959.435654	480.221465	958.451638	479.729457	E	1761.860184	881.433730	1744.833635	872.920455	1743.849619	872.428447	13
9	1113.521115	557.264196	1096.494566	548.750921	1095.510550	548.258913	H	1632.817591	816.912433	1615.791042	808.399159	1614.807026	807.907151	12
10	1552.746441	776.876859	1535.719892	768.363584	1534.735876	767.871576	Q	***1495.758679***	748.382977	1478.732130	739.869703	1477.748114	739.377695	11
11	1609.767905	**805.387590**	1592.741356	796.874316	1591.757340	796.382308	G	***1056.533353***	528.770314	1039.506804	520.257040	1038.522788	519.765032	10
12	1666.789369	833.898322	1649.762820	825.385048	1648.778804	824.893040	G	***999.511889***	500.259582	982.485340	491.746308	981.501324	491.254300	9
13	1803.848281	**902.427778**	1786.821732	893.914504	1785.837716	893.422496	H	***942.490425***	471.748850	925.463876	463.235576	924.479860	462.743568	8
14	**1902.916695**	951.961985	1885.890146	943.448711	1884.906130	942.956703	V	***805.431513***	403.219394	788.404964	394.706120	787.420948	394.214112	7
15	2016.000759	1008.504017	1998.974210	999.990743	1997.990194	999.498735	L	***706.363099***	353.685187	689.336550	345.171913	688.352534	344.679905	6
16	**2131.027702**	1066.017489	2114.001153	1057.504214	2113.017137	1057.012206	D	***593.279035***	297.143155	576.252486	288.629881	575.268470	288.137873	5
17	2268.086614	1134.546945	2251.060065	1126.033670	2250.076049	1125.541662	H	***478.252092***	239.629684	461.225543	231.116409			4
18	2325.108078	1163.057677	2308.081529	1154.544402	2307.097513	1154.052394	G	***341.193180***	171.100228	324.166631	162.586953			3
19	2462.166990	1231.587133	2445.140441	1223.073858	2444.156425	1222.581850	H	***284.171716***	142.589496	267.145167	134.076221			2
20							K	***147.112804***	74.060040	130.086255	65.546765			1

NCBI **BLAST** search of FKLDDDLEHQGGHVLDHGHK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.8	2607.265259	-0.004763	FKLDDDLEHQGGHVLDHGHK

Mascot: http://www.matrixscience.com/

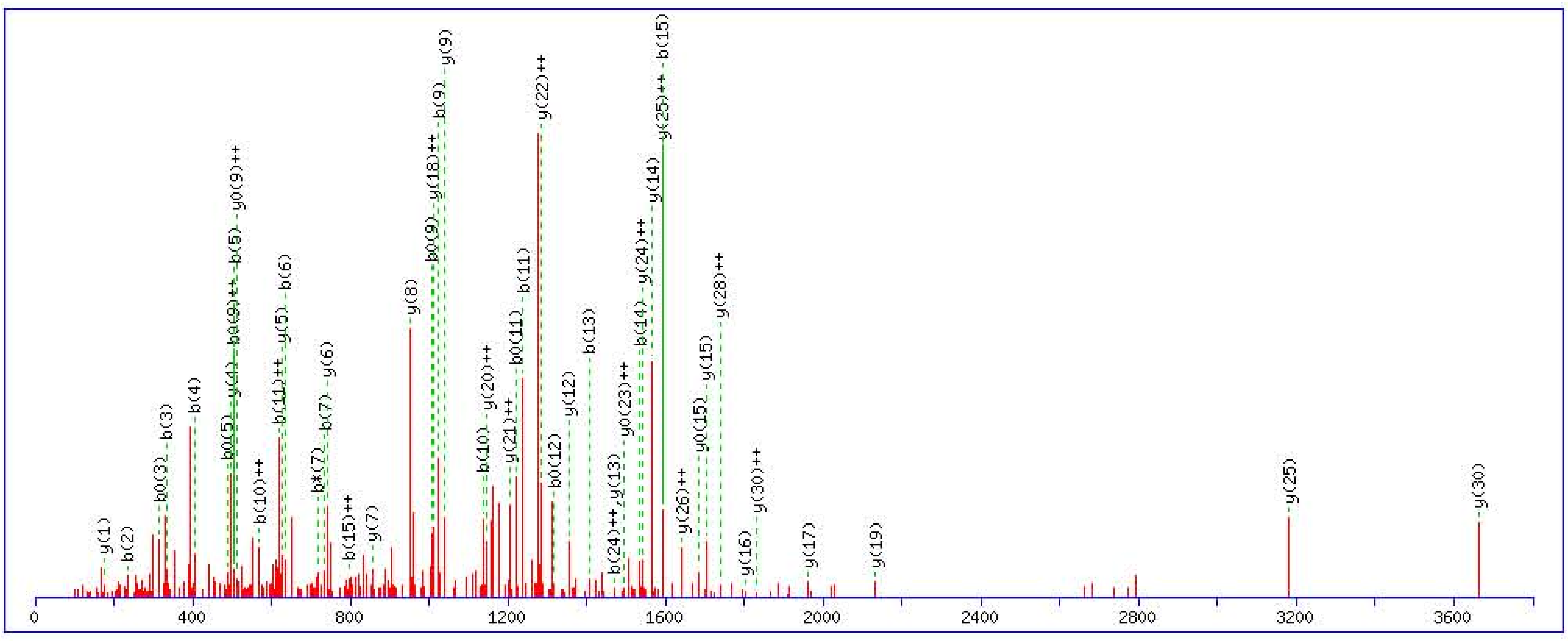
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

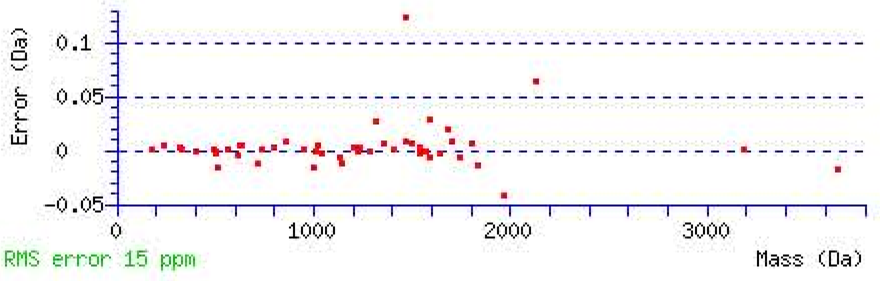
Match to Query 67670: 5066.469570 from(1014.301190,5+) rtinseconds(2672) index(35656)
Title: Locus:1.1.1.3593.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

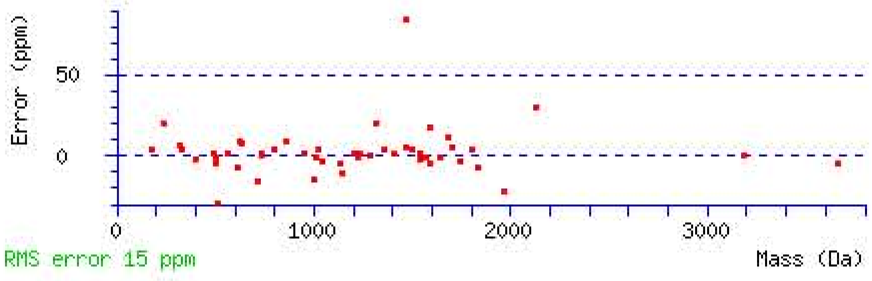
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 5066.465057
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q21     : Biotin:Thermo-21345 (Q)
Ions Score: 59  Expect: 2.5e-005
Matches : 51/484 fragment ions using 140 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							43
2	***235.107718***	118.057497			217.097153	109.052214	S	4920.403881	2460.705578	4903.377332	2452.192304	4902.393316	2451.700296	42
3	***334.176132***	167.591704			316.165567	158.586422	V	4833.371853	2417.189565	4816.345304	2408.676290	4815.361288	2408.184282	41
4	***405.213246***	203.110261			387.202681	194.104978	A	4734.303439	2367.655357	4717.276890	2359.142083	4716.292874	2358.650075	40
5	***506.260925***	253.634100			488.250360	244.628818	T	4663.266325	2332.136800	4646.239776	2323.623526	4645.255760	2323.131518	39
6	***634.319503***	317.663390	617.292954	309.150115	616.308938	308.658107	Q	4562.218646	2281.612961	4545.192097	2273.099686	4544.208081	2272.607679	38
7	***735.367182***	368.187229	718.340633	359.673955	717.356617	359.181947	T	4434.160068	2217.583672	4417.133519	2209.070397	4416.149503	2208.578390	37
8	895.397831	448.202554	878.371282	439.689279	877.387266	439.197271	C	4333.112389	2167.059833	4316.085840	2158.546558	4315.101824	2158.054550	36
9	***1023.456409***	512.231843	1006.429860	503.718568	1005.445844	503.226560	Q	4173.081740	2087.044508	4156.055191	2078.531233	4155.071175	2078.039226	35
10	***1136.540473***	**568.773875**	1119.513924	560.260600	1118.529908	559.768592	I	4045.023162	2023.015219	4027.996613	2014.501944	4027.012597	2014.009936	34
11	***1237.588152***	**619.297714**	1220.561603	610.784440	1219.577587	610.292432	T	3931.939098	1966.473187	3914.912549	1957.959912	3913.928533	1957.467904	33
12	1334.640916	667.824096	1317.614367	659.310822	1316.630351	658.818814	P	3830.891419	1915.949347	3813.864870	1907.436073	3812.880854	1906.944065	32
13	***1405.678030***	703.342653	1388.651481	694.829379	1387.667465	694.337371	A	3733.838655	1867.422965	3716.812106	1858.909691	3715.828090	1858.417683	31
14	***1534.720623***	767.863949	1517.694074	759.350675	1516.710058	758.858667	E	***3662.801541***	1831.904408	3645.774992	1823.391134	3644.790976	1822.899126	30
15	***1591.742087***	**796.374681**	1574.715538	787.861407	1573.731522	787.369399	G	3533.758948	1767.383112	3516.732399	1758.869837	3515.748383	1758.377829	29
16	1688.794851	844.901063	1671.768302	836.387789	1670.784286	835.895781	P	3476.737484	1738.872380	3459.710935	1730.359105	3458.726919	1729.867097	28
17	1787.863265	894.435271	1770.836716	885.921996	1769.852700	885.429988	V	3379.684720	1690.345998	3362.658171	1681.832723	3361.674155	1681.340715	27
18	1886.931679	943.969478	1869.905130	935.456203	1868.921114	934.964195	V	3280.616306	1640.811791	3263.589757	1632.298516	3262.605741	1631.806508	26
19	1987.979358	994.493317	1970.952809	985.980043	1969.968793	985.488035	T	***3181.547892***	1591.277584	3164.521343	1582.764309	3163.537327	1582.272301	25
20	2059.016472	1030.011874	2041.989923	1021.498600	2041.005907	1021.006591	A	3080.500213	1540.753744	3063.473664	1532.240470	3062.489648	1531.748462	24
21	2498.241798	1249.624537	2481.215249	1241.111262	2480.231233	1240.619254	Q	3009.463099	1505.235187	2992.436550	1496.721913	2991.452534	1496.229905	23
22	2661.305127	1331.156202	2644.278578	1322.642927	2643.294562	1322.150919	Y	2570.237773	1285.622524	2553.211224	1277.109250	2552.227208	1276.617242	22
23	2776.332070	1388.669673	2759.305521	1380.156398	2758.321505	1379.664390	D	2407.174444	1204.090860	2390.147895	1195.577585	2389.163879	1195.085577	21
24	2936.362719	**1468.684997**	2919.336170	1460.171723	2918.352154	1459.679715	C	2292.147501	1146.577388	2275.120952	1138.064114	2274.136936	1137.572106	20
25	3049.446783	1525.227029	3032.420234	1516.713755	3031.436218	1516.221747	L	***2132.116852***	1066.562064	2115.090303	1058.048789	2114.106287	1057.556781	19
26	3106.468247	1553.737761	3089.441698	1545.224487	3088.457682	1544.732479	G	2019.032788	1010.020032	2002.006239	1001.506757	2001.022223	1001.014749	18
27	3266.498896	1633.753086	3249.472347	1625.239811	3248.488331	1624.747803	C	***1962.011324***	981.509300	1944.984775	972.996025	1944.000759	972.504017	17
28	3365.567310	1683.287293	3348.540761	1674.774018	3347.556745	1674.282010	V	***1801.980675***	901.493975	1784.954126	892.980701	1783.970110	892.488693	16
29	3502.626222	1751.816749	3485.599673	1743.303474	3484.615657	1742.811466	H	***1702.912261***	851.959768	1685.885712	843.446494	1684.901696	842.954486	15
30	3599.678986	1800.343131	3582.652437	1791.829856	3581.668421	1791.337848	P	***1565.853349***	783.430312	1548.826800	774.917038	1547.842784	774.425030	14
31	3712.763050	1856.885163	3695.736501	1848.371888	3694.752485	1847.879880	I	***1468.800585***	734.903930	1451.774036	726.390656	1450.790020	725.898648	13
32	3799.795078	1900.401177	3782.768529	1891.887902	3781.784513	1891.395894	S	***1355.716521***	678.361898	1338.689972	669.848624	1337.705956	669.356616	12
33	3900.842757	1950.925016	3883.816208	1942.411742	3882.832192	1941.919734	T	1268.684493	634.845884	1251.657944	626.332610	1250.673928	625.840602	11
34	4028.901335	2014.954305	4011.874786	2006.441031	4010.890770	2005.949023	Q	1167.636814	584.322045	1150.610265	575.808770	1149.626249	575.316762	10
35	4115.933363	2058.470320	4098.906814	2049.957045	4097.922798	2049.465037	S	***1039.578236***	520.292756	1022.551687	511.779481	1021.567671	511.287473	9
36	4212.986127	2106.996702	4195.959578	2098.483427	4194.975562	2097.991419	P	***952.546208***	476.776742	935.519659	468.263467	934.535643	467.771459	8
37	4328.013070	2164.510173	4310.986521	2155.996899	4310.002505	2155.504891	D	***855.493444***	428.250360	838.466895	419.737085	837.482879	419.245077	7
38	4441.097134	2221.052205	4424.070585	2212.538930	4423.086569	2212.046923	L	***740.466501***	370.736888	723.439952	362.223614	722.455936	361.731606	6
39	4570.139727	2285.573502	4553.113178	2277.060227	4552.129162	2276.568219	E	***627.382437***	314.194856	610.355888	305.681582	609.371872	305.189574	5
40	4667.192491	2334.099884	4650.165942	2325.586609	4649.181926	2325.094601	P	***498.339844***	249.673560	481.313295	241.160285			4
41	4780.276555	2390.641915	4763.250006	2382.128641	4762.265990	2381.636633	I	401.287080	201.147178	384.260531	192.633903			3
42	4893.360619	2447.183947	4876.334070	2438.670673	4875.350054	2438.178665	L	288.203016	144.605146	271.176467	136.091871			2
43							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.6	5066.465057	0.004513	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR
21.8	5066.465057	0.004513	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR
21.8	5066.465057	0.004513	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR
21.1	5066.465057	0.004513	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR

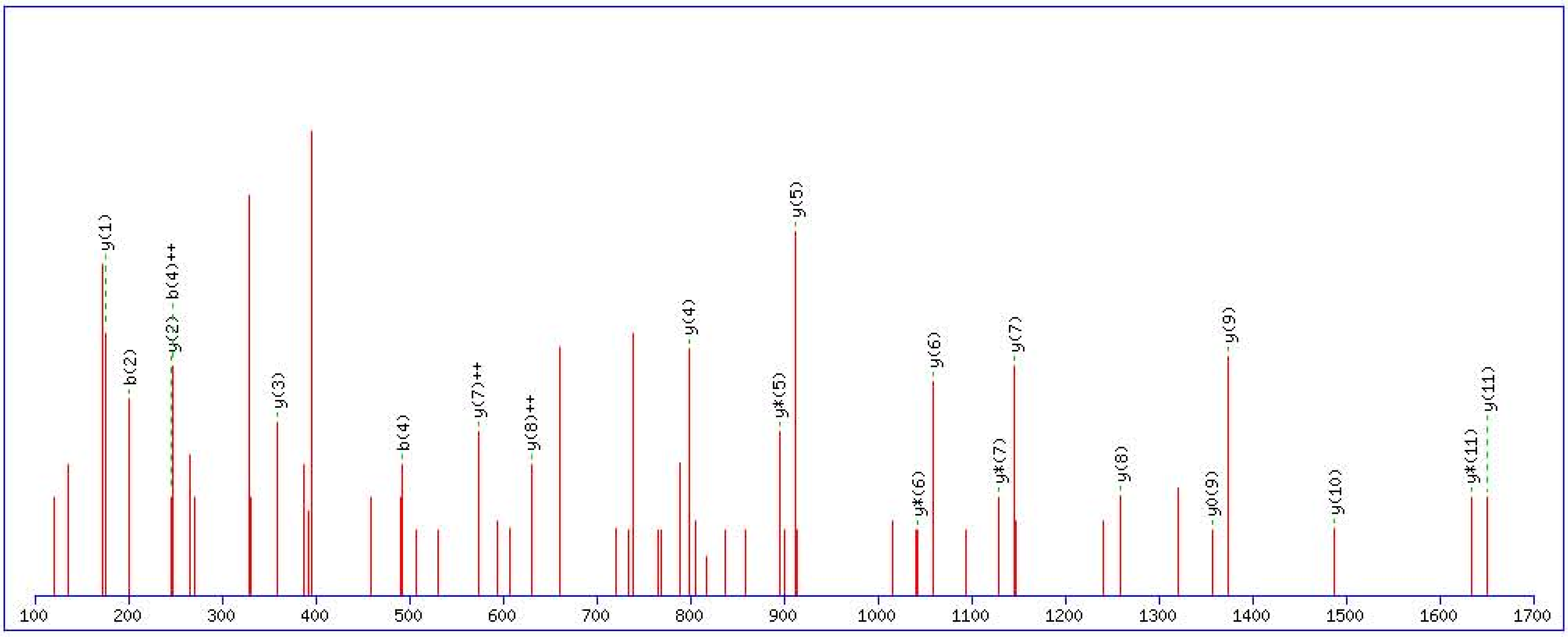
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLEYLDLSFNQIAR**
Found in **LUM_HUMAN**, Lumican OS=Homo sapiens GN=LUM PE=1 SV=2

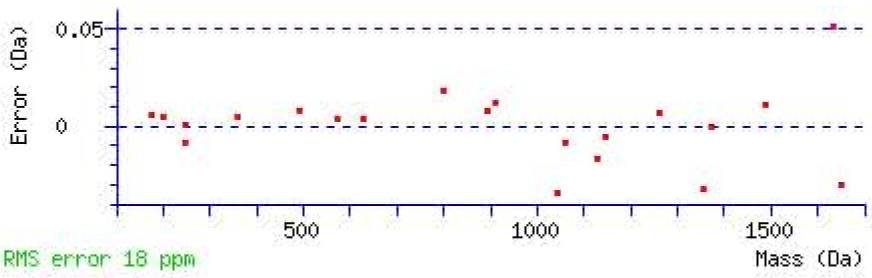
Match to Query 38944: 1979.026212 from(660.682680,3+) rtinseconds(2763) index(50466)
Title: Locus:1.1.1.3673.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

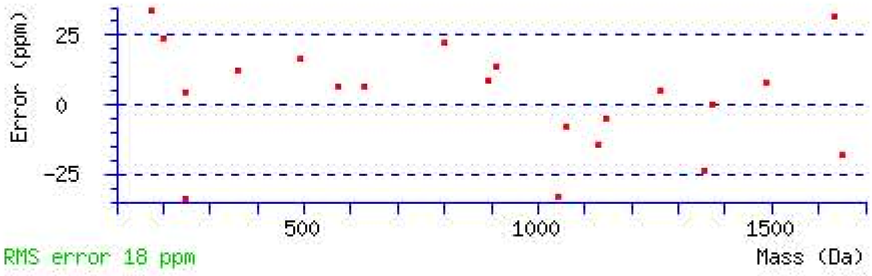
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1979.018600
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 68  Expect: 6.9e-007
Matches : 21/126 fragment ions using 38 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							14
2	**201.123368**	101.065322			183.112803	92.060039	L	1892.993882	947.000579	1875.967333	938.487305	1874.983317	937.995296	13
3	330.165961	165.586618			312.155396	156.581336	E	1779.909818	890.458547	1762.883269	881.945273	1761.899253	881.453265	12
4	**493.229290**	247.118283			475.218725	238.113001	Y	***1650.867225***	825.937251	1633.840676	817.423976	1632.856660	816.931968	11
5	606.313354	303.660315			588.302789	294.655033	L	***1487.803896***	744.405586	1470.777347	735.892312	1469.793331	735.400304	10
6	721.340297	361.173787			703.329732	352.168504	D	***1374.719832***	687.863554	1357.693283	679.350280	1356.709267	678.858272	9
7	834.424361	417.715819			816.413796	408.710536	L	***1259.692889***	630.350083	1242.666340	621.836808	1241.682324	621.344800	8
8	921.456389	461.231833			903.445824	452.226550	S	***1146.608825***	573.808051	1129.582276	565.294776	1128.598260	564.802768	7
9	1068.524803	534.766040			1050.514238	525.760757	F	***1059.576797***	530.292037	1042.550248	521.778762			6
10	1182.567730	591.787503	1165.541181	583.274229	1164.557165	582.782220	N	***912.508383***	456.757830	895.481834	448.244555			5
11	1621.793056	811.400166	1604.766507	802.886892	1603.782491	802.394884	Q	***798.465456***	399.736366	781.438907	391.223092			4
12	1734.877120	867.942198	1717.850571	859.428924	1716.866555	858.936916	I	***359.240130***	180.123703	342.213581	171.610428			3
13	1805.914234	903.460755	1788.887685	894.947481	1787.903669	894.455473	A	***246.156066***	123.581671	229.129517	115.068396			2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SLEYLDLSFNQIAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.5	1979.018600	0.007612	SLEYLDLSFNQIAR
1.8	1979.025787	0.000425	HQNLQEKLAEEMLGLAR

Mascot: http://www.matrixscience.com/

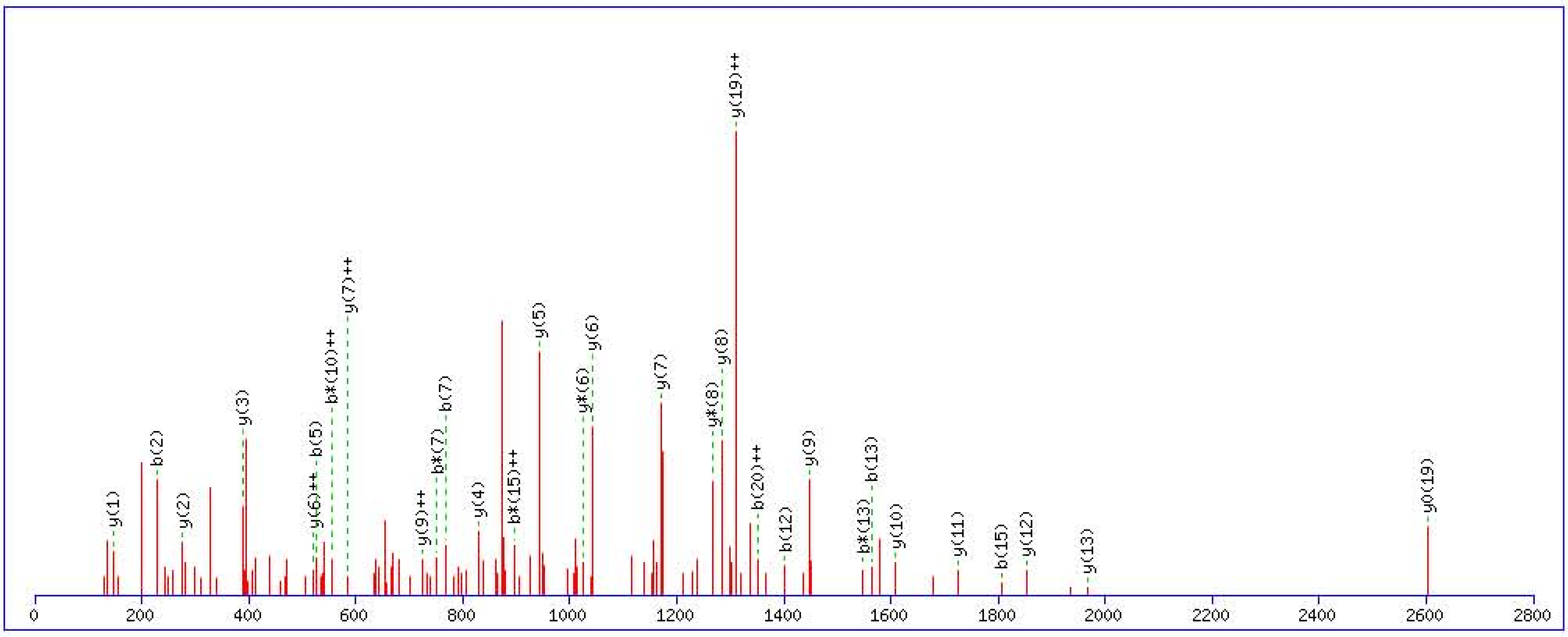
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NIPTVNENLENYYLEVNQLEK**
Found in **LUM_HUMAN**, Lumican OS=Homo sapiens GN=LUM PE=1 SV=2

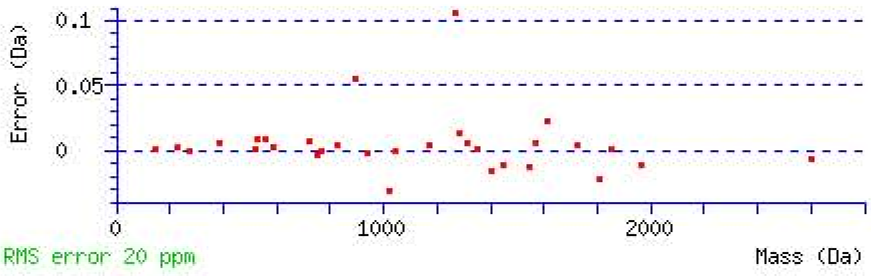
Match to Query 52172: 2846.425182 from(949.815670,3+) rtinseconds(2694) index(50015)
Title: Locus:1.1.1.3649.22 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

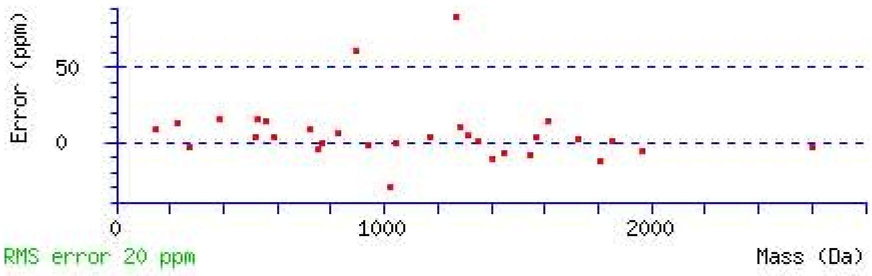
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2846.415985
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18     : Biotin:Thermo-21345 (Q)
Ions Score: 58  Expect: 4.6e-005
Matches : 31/232 fragment ions using 66 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							21
2	**228.134267**	114.570771	211.107718	106.057497			I	2733.380395	1367.193835	2716.353846	1358.680561	2715.369830	1358.188553	20
3	325.187031	163.097153	308.160482	154.583879			P	2620.296331	1310.651803	2603.269782	1302.138529	2602.285766	1301.646521	19
4	426.234710	213.620993	409.208161	205.107719	408.224145	204.615711	T	2523.243567	1262.125421	2506.217018	1253.612147	2505.233002	1253.120139	18
5	**525.303124**	263.155200	508.276575	254.641926	507.292559	254.149918	V	2422.195888	1211.601582	2405.169339	1203.088307	2404.185323	1202.596299	17
6	639.346051	320.176664	622.319502	311.663389	621.335486	311.171381	N	2323.127474	1162.067375	2306.100925	1153.554100	2305.116909	1153.062092	16
7	**768.388644**	384.697960	751.362095	376.184686	750.378079	375.692678	E	2209.084547	1105.045911	2192.057998	1096.532637	2191.073982	1096.040629	15
8	882.431571	441.719424	865.405022	433.206149	864.421006	432.714141	N	2080.041954	1040.524615	2063.015405	1032.011340	2062.031389	1031.519332	14
9	995.515635	498.261456	978.489086	489.748181	977.505070	489.256173	L	***1965.999027***	983.503152	1948.972478	974.989877	1947.988462	974.497869	13
10	1124.558228	562.782752	1107.531679	554.269478	1106.547663	553.777470	E	***1852.914963***	926.961120	1835.888414	918.447845	1834.904398	917.955837	12
11	1238.601155	619.804216	1221.574606	611.290941	1220.590590	610.798933	N	***1723.872370***	862.439823	1706.845821	853.926549	1705.861805	853.434541	11
12	**1401.664484**	701.335880	1384.637935	692.822606	1383.653919	692.330598	Y	***1609.829443***	805.418360	1592.802894	796.905085	1591.818878	796.413077	10
13	**1564.727813**	782.867545	1547.701264	774.354270	1546.717248	773.862262	Y	***1446.766114***	723.886695	1429.739565	715.373421	1428.755549	714.881413	9
14	1677.811877	839.409577	1660.785328	830.896302	1659.801312	830.404294	L	***1283.702785***	642.355031	1266.676236	633.841756	1265.692220	633.349748	8
15	**1806.854470**	903.930873	1789.827921	895.417599	1788.843905	894.925591	E	***1170.618721***	585.812999	1153.592172	577.299724	1152.608156	576.807716	7
16	1905.922884	953.465080	1888.896335	944.951806	1887.912319	944.459798	V	***1041.576128***	521.291702	1024.549579	512.778428	1023.565563	512.286420	6
17	2019.965811	1010.486544	2002.939262	1001.973269	2001.955246	1001.481261	N	***942.507714***	471.757495	925.481165	463.244221	924.497149	462.752213	5
18	2459.191137	1230.099206	2442.164588	1221.585932	2441.180572	1221.093924	Q	***828.464787***	414.736032	811.438238	406.222757	810.454222	405.730749	4
19	2572.275201	1286.641238	2555.248652	1278.127964	2554.264636	1277.635956	L	***389.239461***	195.123369	372.212912	186.610094	371.228896	186.118086	3
20	2701.317794	1351.162535	2684.291245	1342.649260	2683.307229	1342.157252	E	***276.155397***	138.581337	259.128848	130.068062	258.144832	129.576054	2
21							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of NIPTVNENLENYYLEVNQLEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.7	2846.415985	0.009197	NIPTVNENLENYYLEVNQLEK

Mascot: http://www.matrixscience.com/

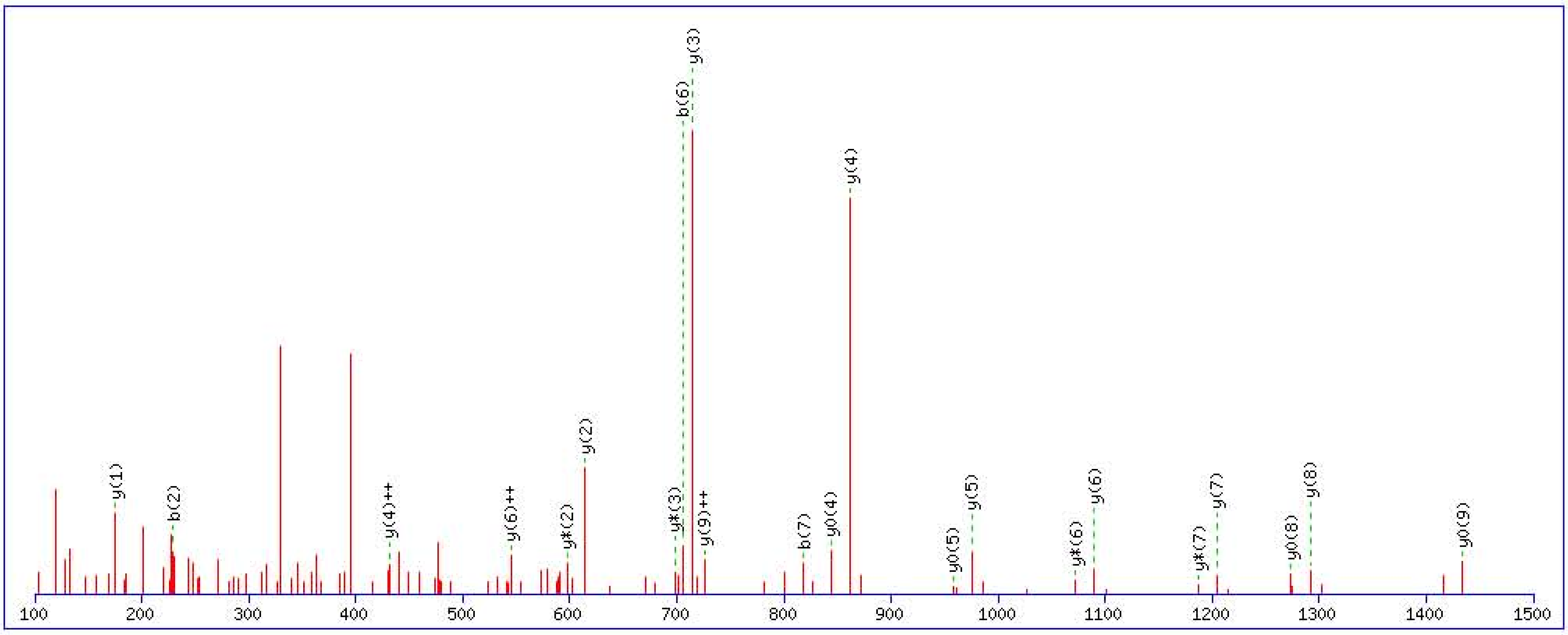
Mascot Search Results

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

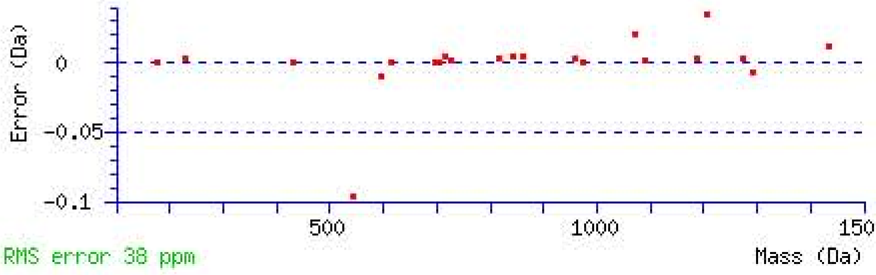
Match to Query 33272: 1678.780212 from(560.600680,3+) rtinseconds(2115) index(46685)
Title: Locus:1.1.1.3449.3 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

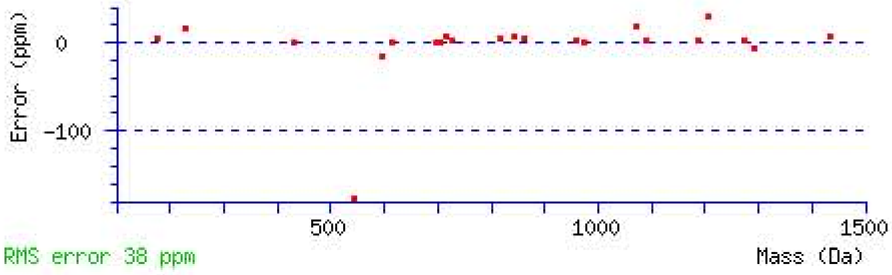
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1678.780716
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 47 **Expect:** 7.4e-005
Matches : 22/104 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	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
47.0	1678.780716	-0.000504	VECSDNLFTQR
3.0	1678.769455	0.010757	VWDKEGEMEVAMQK

Mascot: http://www.matrixscience.com/

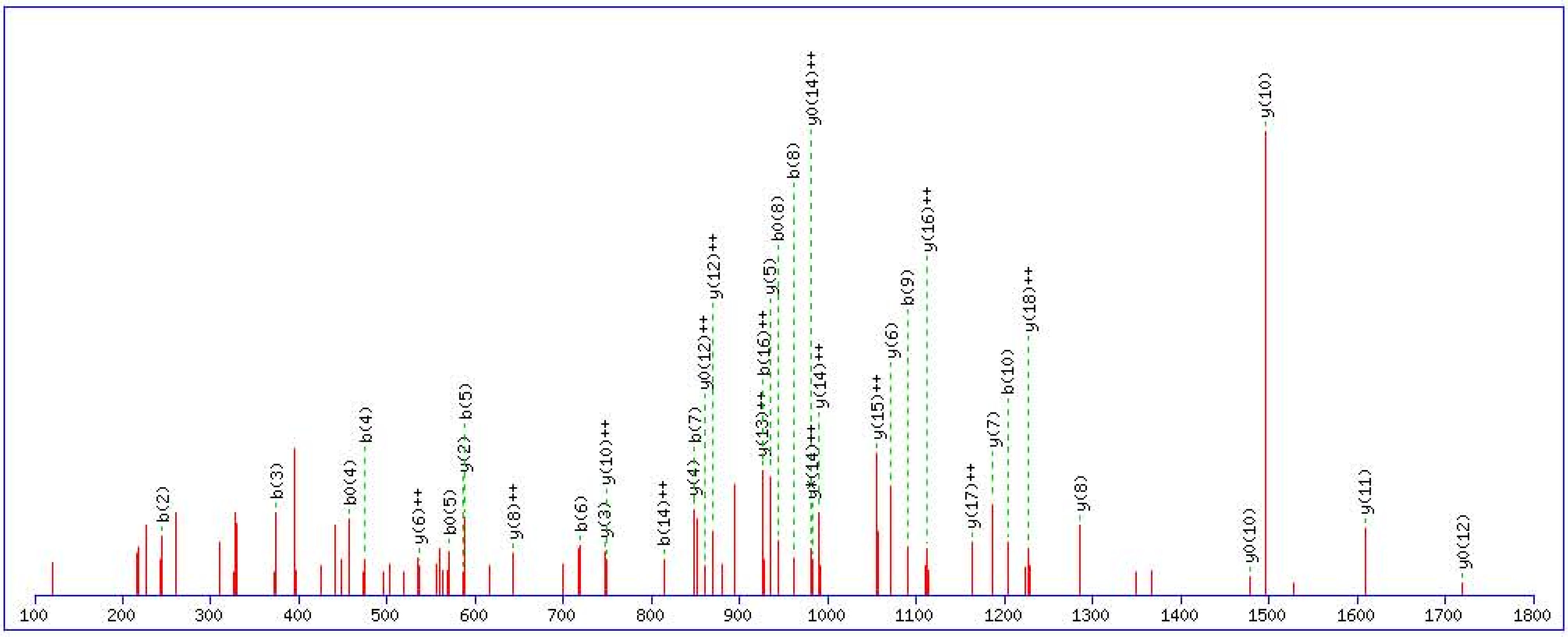
{MATRIX} {SCIENCE} Mascot Search Results

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 50346: 2697.328992 from(900.116940,3+) rtinseconds(2770) index(50523)
Title: Locus:1.1.1.3675.22 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\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): 2697.321609

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

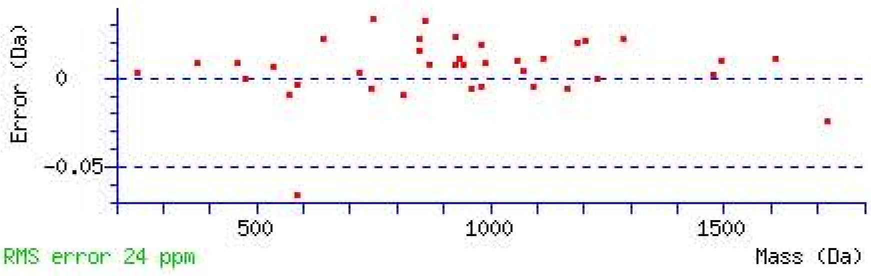
Variable modifications:

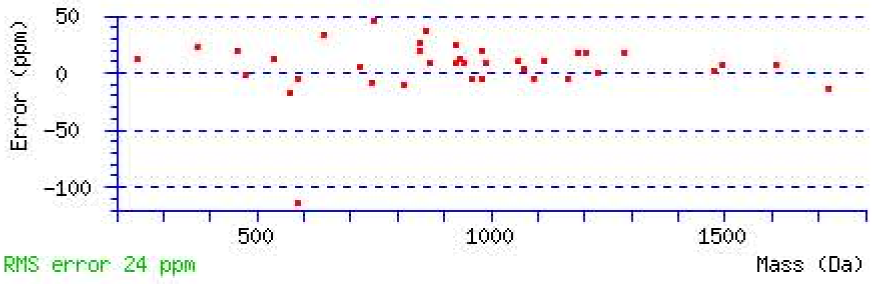
Q19 : Biotin:Thermo-21345 (Q)

Ions Score: 51 **Expect:** 0.00021

Matches : 38/182 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	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
51.3	2697.321609	0.007383	FPETLMEIEIPIVDHSTCQK

Mascot: http://www.matrixscience.com/

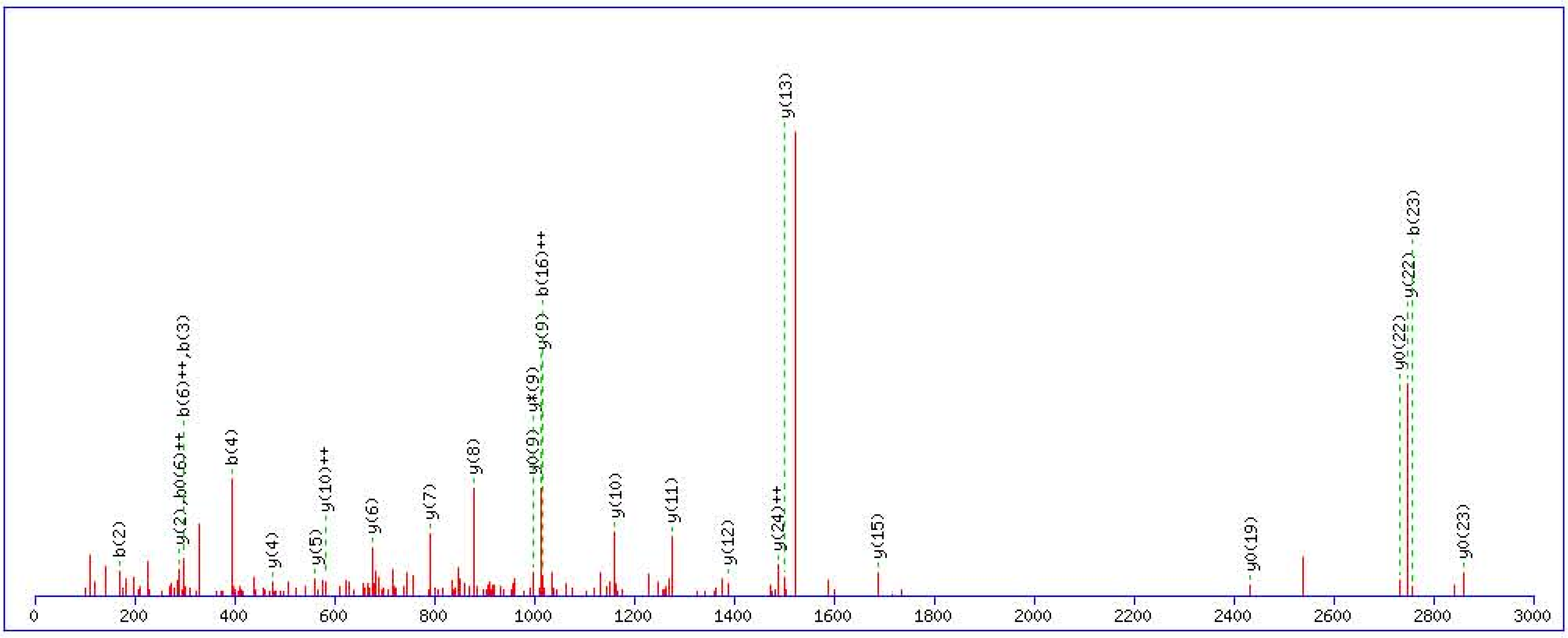
Mascot Search Results

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

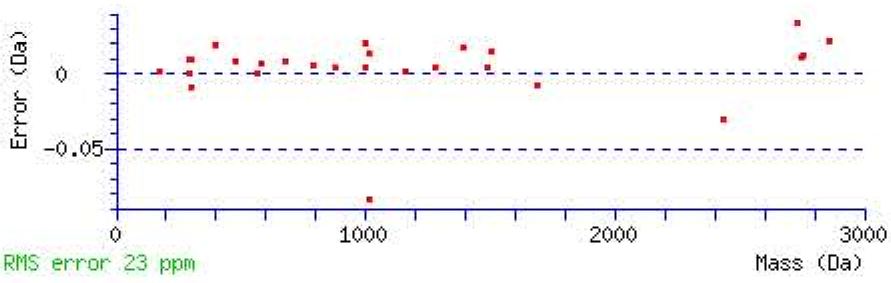
Match to Query 54365: 3045.503456 from(762.383140,4+) rtinseconds(2289) index(47792)
Title: Locus:1.1.1.3509.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

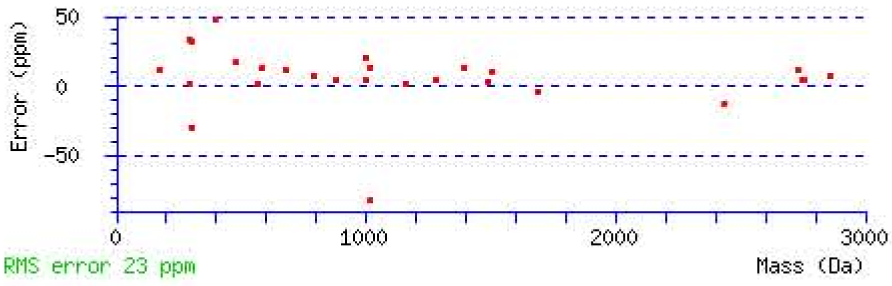
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3045.497803
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 2.9e-005
Matches : 27/266 fragment ions using 57 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
59.9	3045.497803	0.005653	APEPISTQSHSVLILFHSDNSGENR

Mascot: http://www.matrixscience.com/

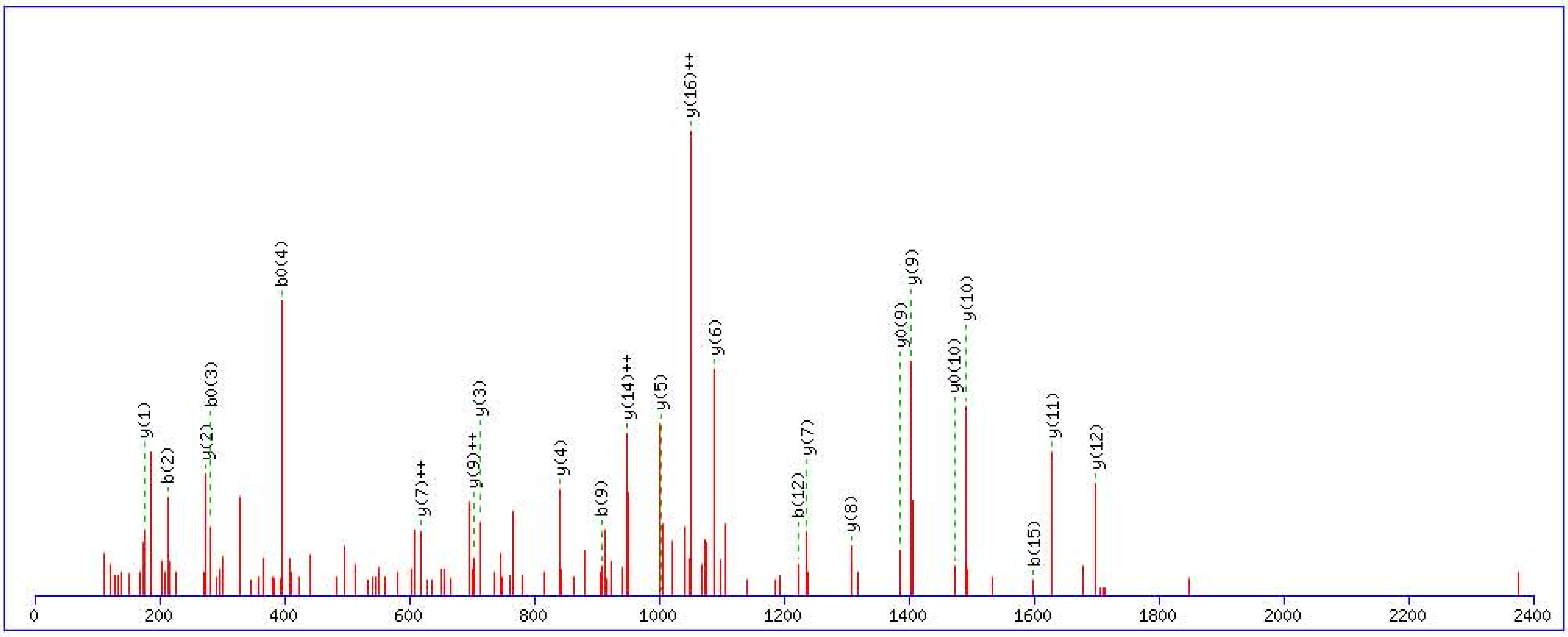
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLSIAQAHSPAFSCEQVR**
Found in **CD14_HUMAN**, Monocyte differentiation antigen CD14 OS=Homo sapiens GN=CD14 PE=1 SV=2

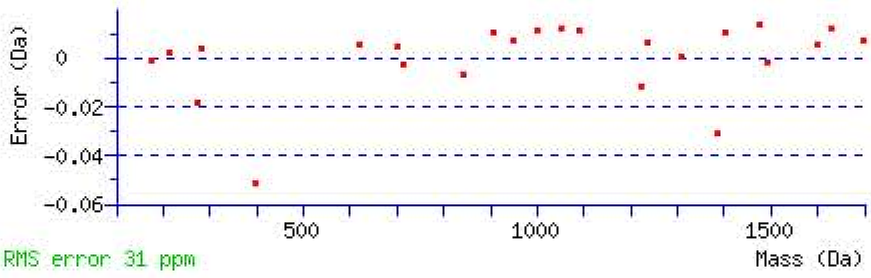
Match to Query 45272: 2310.156132 from(771.059320,3+) rtinseconds(2001) index(31897)
Title: Locus:1.1.1.3360.19 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

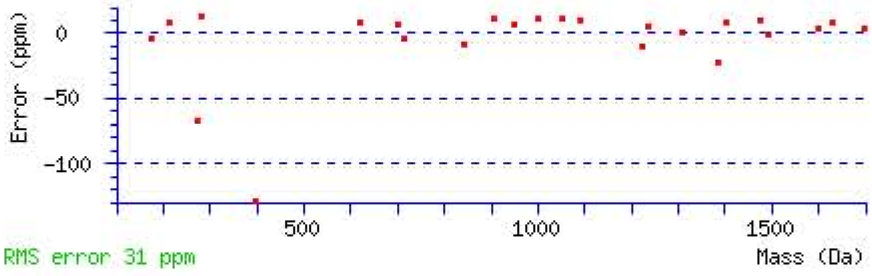
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2310.161285
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16 : Biotin:Thermo-21345 (Q)
Ions Score: 64 **Expect:** 1.1e-005
Matches : 24/184 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							18
2	**213.159754**	107.083515					L	2212.100156	1106.553716	2195.073607	1098.040441	2194.089591	1097.548433	17
3	300.191782	150.599529			282.181217	141.594247	S	2099.016092	1050.011684	2081.989543	1041.498409	2081.005527	1041.006401	16
4	413.275846	207.141561			395.265281	198.136279	I	2011.984064	1006.495670	1994.957515	997.982396	1993.973499	997.490388	15
5	484.312960	242.660118			466.302395	233.654836	A	1898.900000	949.953638	1881.873451	941.440364	1880.889435	940.948356	14
6	612.371538	306.689407	595.344989	298.176133	594.360973	297.684125	Q	1827.862886	914.435081	1810.836337	905.921807	1809.852321	905.429799	13
7	683.408652	342.207964	666.382103	333.694690	665.398087	333.202682	A	***1699.804308***	850.405792	1682.777759	841.892518	1681.793743	841.400510	12
8	820.467564	410.737420	803.441015	402.224146	802.456999	401.732138	H	***1628.767194***	814.887235	1611.740645	806.373961	1610.756629	805.881953	11
9	**907.499592**	454.253434	890.473043	445.740160	889.489027	445.248152	S	***1491.708282***	746.357779	1474.681733	737.844505	1473.697717	737.352497	10
10	1004.552356	502.779816	987.525807	494.266542	986.541791	493.774534	P	***1404.676254***	702.841765	1387.649705	694.328491	1386.665689	693.836483	9
11	1075.589470	538.298373	1058.562921	529.785099	1057.578905	529.293091	A	***1307.623490***	654.315383	1290.596941	645.802109	1289.612925	645.310101	8
12	**1222.657884**	611.832580	1205.631335	603.319306	1204.647319	602.827298	F	***1236.586376***	618.796826	1219.559827	610.283552	1218.575811	609.791544	7
13	1309.689912	655.348594	1292.663363	646.835320	1291.679347	646.343312	S	***1089.517962***	545.262619	1072.491413	536.749345	1071.507397	536.257337	6
14	1469.720561	735.363919	1452.694012	726.850644	1451.709996	726.358636	C	***1002.485934***	501.746605	985.459385	493.233331	984.475369	492.741323	5
15	**1598.763154**	799.885215	1581.736605	791.371941	1580.752589	790.879933	E	***842.455285***	421.731281	825.428736	413.218006	824.444720	412.725998	4
16	2037.988480	1019.497878	2020.961931	1010.984604	2019.977915	1010.492596	Q	***713.412692***	357.209984	696.386143	348.696710			3
17	2137.056894	1069.032085	2120.030345	1060.518811	2119.046329	1060.026803	V	***274.187366***	137.597321	257.160817	129.084046			2
18							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VLSIAQAHSPAFSCEQVR
(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	2310.161285	-0.005153	VLSIAQAHSPAFSCEQVR

Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSQTQSHPDLGTEGCWDQLSAPR**
Found in **PGRP2_HUMAN**, N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens GN=PGLYRP2 PE=1 SV=1

Match to Query 52010: 2837.298702 from(946.773510,3+) rtinseconds(2073) index(60976)
Title: Locus:1.1.1.1633.10 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\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): 2837.286133
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18     : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 2.4e-005
Matches : 29/252 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	58.028740	29.518008					G							23
2	145.060768	73.034022			127.050203	64.028740	S	2781.271927	1391.139601	2764.245378	1382.626327	2763.261362	1382.134319	22
3	273.119346	137.063311	256.092797	128.550037	255.108781	128.058029	Q	2694.239899	1347.623587	2677.213350	1339.110313	2676.229334	1338.618305	21
4	374.167025	187.587151	357.140476	179.073876	356.156460	178.581868	T	2566.181321	1283.594298	2549.154772	1275.081024	2548.170756	1274.589016	20
5	502.225603	251.616440	485.199054	243.103165	484.215038	242.611157	Q	2465.133642	1233.070459	2448.107093	1224.557184	2447.123077	1224.065176	19
6	589.257631	295.132454	572.231082	286.619179	571.247066	286.127171	S	2337.075064	1169.041170	2320.048515	1160.527895	2319.064499	1160.035887	18
7	**726.316543**	363.661910	709.289994	355.148635	708.305978	354.656627	H	2250.043036	1125.525156	2233.016487	1117.011881	2232.032471	1116.519873	17
8	823.369307	412.188292	806.342758	403.675017	805.358742	403.183009	P	2112.984124	1056.995700	2095.957575	1048.482425	2094.973559	1047.990417	16
9	**938.396250**	469.701763	921.369701	461.188489	920.385685	460.696481	D	2015.931360	1008.469318	1998.904811	999.956044	1997.920795	999.464036	15
10	**1051.480314**	526.243795	1034.453765	517.730521	1033.469749	517.238512	L	1900.904417	950.955847	1883.877868	942.442572	1882.893852	941.950564	14
11	1108.501778	554.754527	1091.475229	546.241252	1090.491213	545.749244	G	1787.820353	894.413815	1770.793804	885.900540	1769.809788	885.408532	13
12	1209.549457	605.278366	1192.522908	596.765092	1191.538892	596.273084	T	1730.798889	865.903083	1713.772340	857.389808	1712.788324	856.897800	12
13	1338.592050	669.799663	1321.565501	661.286389	1320.581485	660.794380	E	***1629.751210***	815.379243	1612.724661	806.865969	1611.740645	806.373961	11
14	1395.613514	698.310395	1378.586965	689.797121	1377.602949	689.305112	G	***1500.708617***	750.857947	1483.682068	742.344672	1482.698052	741.852664	10
15	1555.644163	778.325719	1538.617614	769.812445	1537.633598	769.320437	C	***1443.687153***	722.347215	1426.660604	713.833940	1425.676588	713.341932	9
16	**1741.723476**	871.365376	1724.696927	862.852102	1723.712911	862.360093	W	***1283.656504***	642.331890	1266.629955	633.818616	1265.645939	633.326608	8
17	**1856.750419**	928.878848	1839.723870	920.365573	1838.739854	919.873565	D	***1097.577191***	549.292234	1080.550642	540.778959	1079.566626	540.286951	7
18	2295.975745	**1148.491510**	2278.949196	1139.978236	2277.965180	1139.486228	Q	***982.550248***	491.778762	965.523699	483.265488	964.539683	482.773480	6
19	2409.059809	**1205.033542**	2392.033260	1196.520268	2391.049244	1196.028260	L	***543.324922***	272.166099	526.298373	263.652825	525.314357	263.160817	5
20	2496.091837	1248.549556	2479.065288	1240.036282	2478.081272	1239.544274	S	***430.240858***	215.624067	413.214309	207.110793	412.230293	206.618785	4
21	**2567.128951**	1284.068114	2550.102402	1275.554839	2549.118386	1275.062831	A	***343.208830***	172.108053	326.182281	163.594779			3
22	2664.181715	1332.594496	2647.155166	1324.081221	2646.171150	1323.589213	P	***272.171716***	136.589496	255.145167	128.076221			2
23							R	175.118952	88.063114	158.092403	79.549839			1

NCBI **BLAST** search of GSQTQSHPDLGTEGCWDQLSAPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.8	2837.286133	0.012569	GSQTQSHPDLGTEGCWDQLSAPR
1.8	2837.286133	0.012569	GSQTQSHPDLGTEGCWDQLSAPR
1.6	2837.286133	0.012569	GSQTQSHPDLGTEGCWDQLSAPR

Mascot: http://www.matrixscience.com/

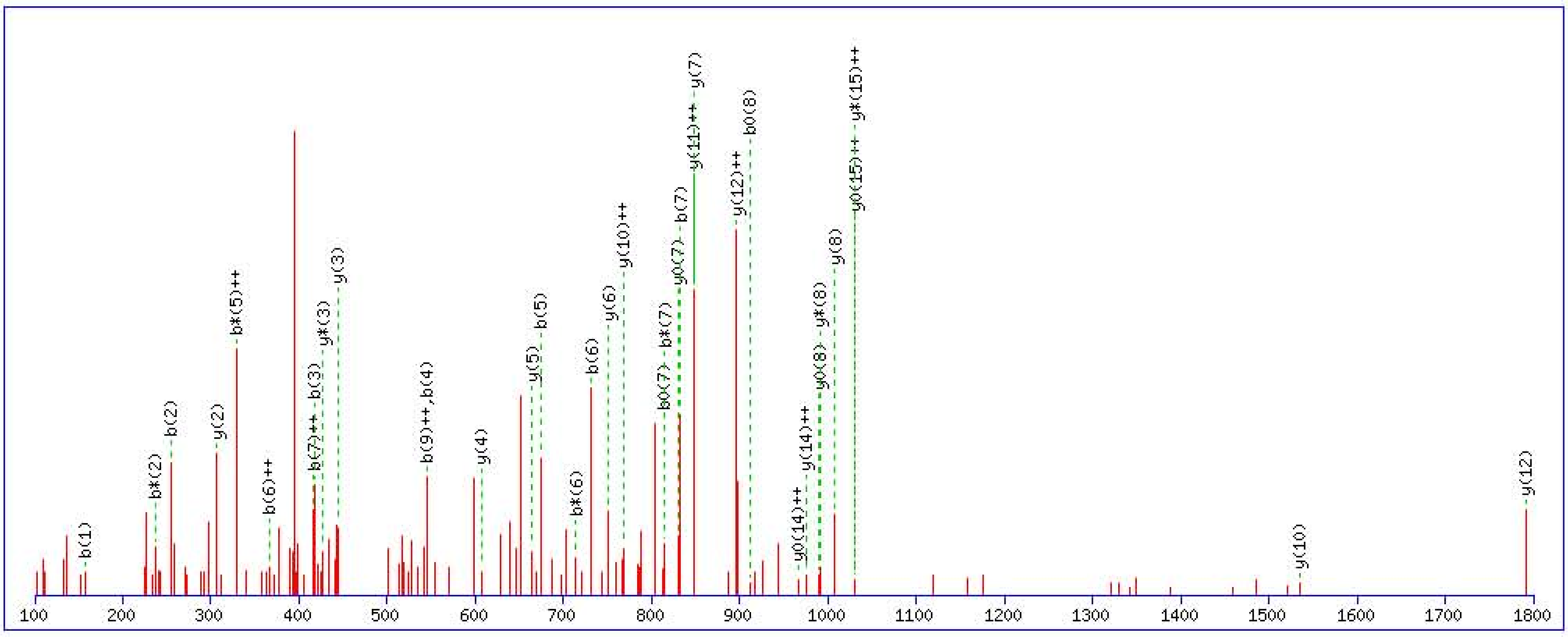
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPYQEGTPCSQCPSGYHCK**
Found in **PI16_HUMAN**, Peptidase inhibitor 16 OS=Homo sapiens GN=PI16 PE=1 SV=1

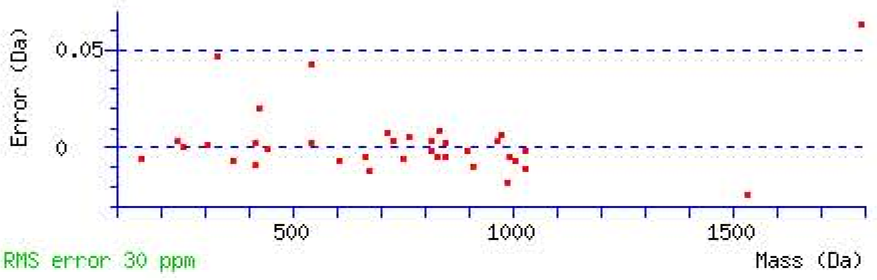
Match to Query 49714: 2622.116616 from(656.536430,4+) rtinseconds(1363) index(28048)
Title: Locus:1.1.1.3137.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

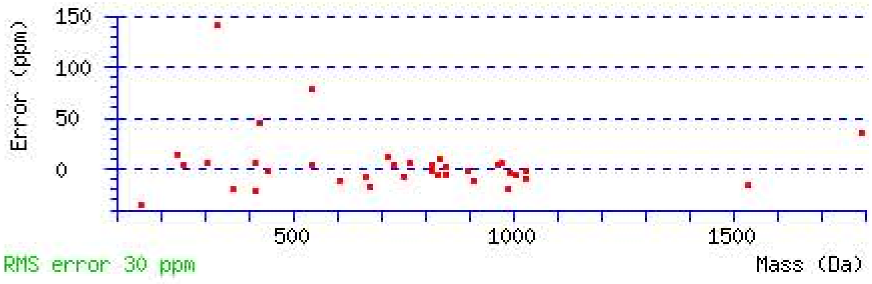
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2622.123611
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 31 **Expect:** 0.0023
Matches : 36/198 fragment ions using 94 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							19
2	***254.161151***	127.584213	237.134602	119.070939			P	2467.029773	1234.018524	2450.003224	1225.505250	2449.019208	1225.013242	18
3	***417.224480***	209.115878	400.197931	200.602604			Y	2369.977009	1185.492142	2352.950460	1176.978868	2351.966444	1176.486860	17
4	***545.283058***	273.145167	528.256509	264.631893			Q	2206.913680	1103.960478	2189.887131	1095.447203	2188.903115	1094.955195	16
5	***674.325651***	337.666464	657.299102	329.153189	656.315086	328.661181	E	2078.855102	1039.931189	2061.828553	1031.417914	2060.844537	1030.925906	15
6	***731.347115***	**366.177196**	714.320566	357.663921	713.336550	357.171913	G	1949.812509	975.409892	1932.785960	966.896618	1931.801944	966.404610	14
7	***832.394794***	**416.701035**	815.368245	408.187761	814.384229	407.695753	T	1892.791045	946.899160	1875.764496	938.385886	1874.780480	937.893878	13
8	929.447558	465.227417	912.421009	456.714143	911.436993	456.222135	P	***1791.743366***	896.375321	1774.716817	887.862047	1773.732801	887.370038	12
9	1089.478207	**545.242742**	1072.451658	536.729467	1071.467642	536.237459	C	1694.690602	847.848939	1677.664053	839.335665	1676.680037	838.843656	11
10	1176.510235	588.758756	1159.483686	580.245481	1158.499670	579.753473	S	***1534.659953***	767.833614	1517.633404	759.320340	1516.649388	758.828332	10
11	1615.735561	808.371419	1598.709012	799.858144	1597.724996	799.366136	Q	1447.627925	724.317600	1430.601376	715.804326	1429.617360	715.312318	9
12	1775.766210	888.386743	1758.739661	879.873469	1757.755645	879.381461	C	***1008.402599***	504.704937	991.376050	496.191663	990.392034	495.699655	8
13	1872.818974	936.913125	1855.792425	928.399851	1854.808409	927.907843	P	***848.371950***	424.689613	831.345401	416.176338	830.361385	415.684330	7
14	1959.851002	980.429139	1942.824453	971.915865	1941.840437	971.423857	S	***751.319186***	376.163231	734.292637	367.649956	733.308621	367.157948	6
15	2016.872466	1008.939871	1999.845917	1000.426597	1998.861901	999.934589	G	***664.287158***	332.647217	647.260609	324.133942			5
16	2179.935795	1090.471535	2162.909246	1081.958261	2161.925230	1081.466253	Y	***607.265694***	304.136485	590.239145	295.623210			4
17	2316.994707	1159.000991	2299.968158	1150.487717	2298.984142	1149.995709	H	***444.202365***	222.604820	427.175816	214.091546			3
18	2477.025356	1239.016316	2459.998807	1230.503041	2459.014791	1230.011033	C	***307.143453***	154.075364	290.116904	145.562090			2
19							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of RPYQEGTPCSQCPSGYHCK
(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	2622.123611	-0.006995	RPYQEGTPCSQCPSGYHCK

Mascot: http://www.matrixscience.com/

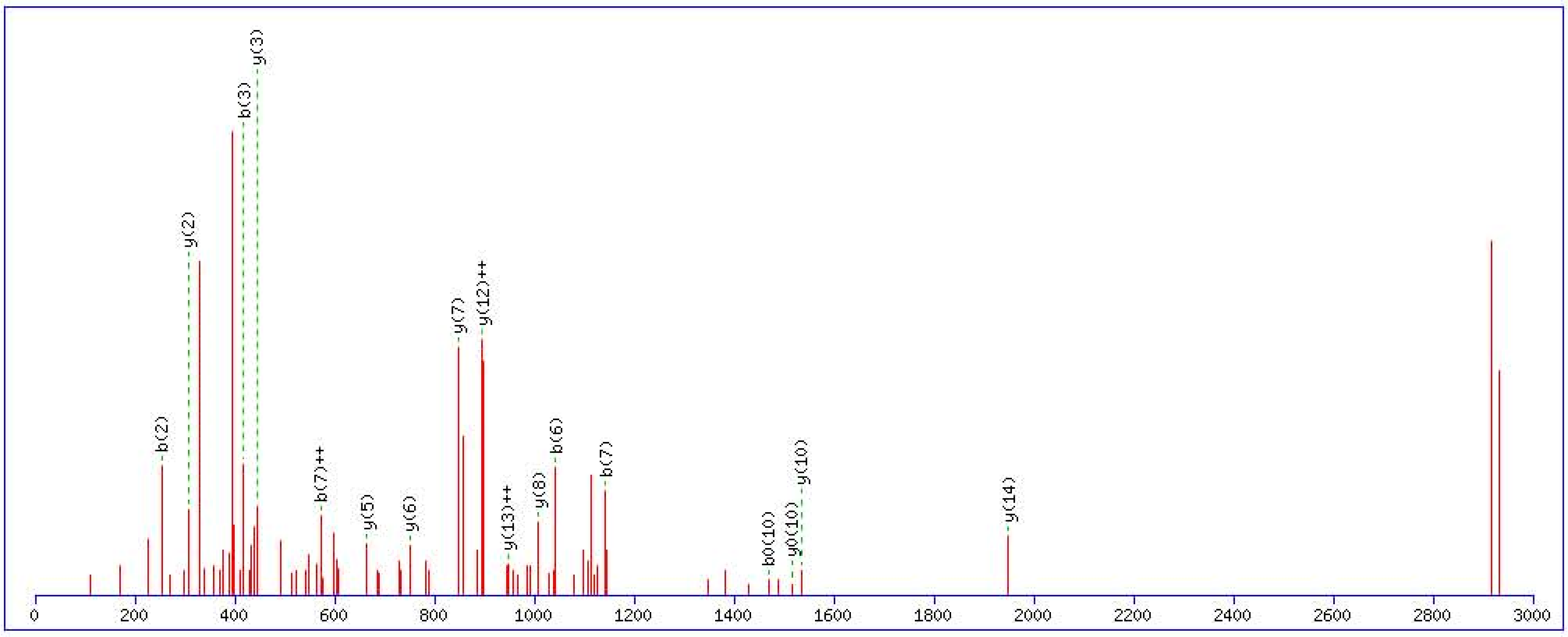
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPYQEGTPCSQCPSGYHCK**
Found in **PI16_HUMAN**, Peptidase inhibitor 16 OS=Homo sapiens GN=PI16 PE=1 SV=1

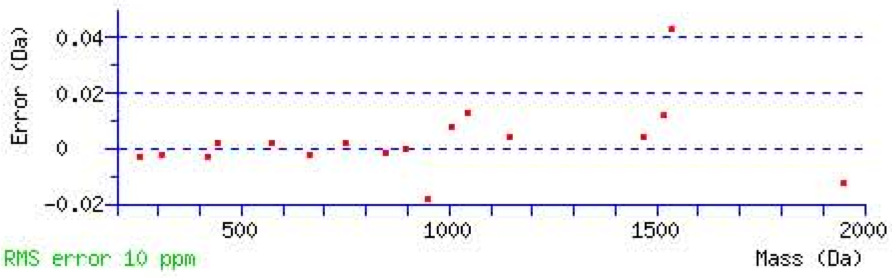
Match to Query 53346: 2933.274696 from(734.325950,4+) rtinseconds(1609) index(29468)
Title: Locus:1.1.1.3223.20 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

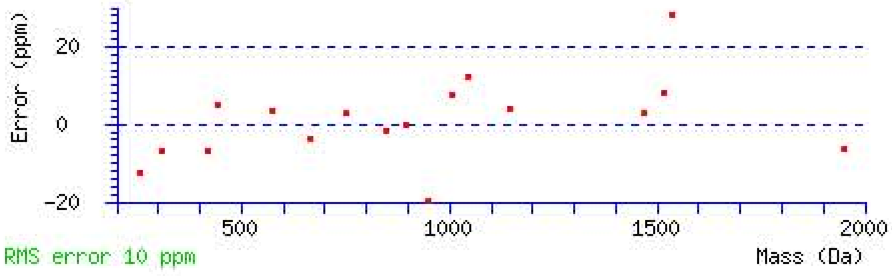


```
Monoisotopic mass of neutral peptide Mr(calc): 2933.290359
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.0004
Matches : 17/198 fragment ions using 30 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			R							19
2	***254.161151***	127.584213	237.134602	119.070939			P	2778.196521	1389.601898	2761.169972	1381.088624	2760.185956	1380.596616	18
3	***417.224480***	209.115878	400.197931	200.602604			Y	2681.143757	1341.075516	2664.117208	1332.562242	2663.133192	1332.070234	17
4	856.449806	428.728541	839.423257	420.215267			Q	2518.080428	1259.543852	2501.053879	1251.030577	2500.069863	1250.538569	16
5	985.492399	493.249838	968.465850	484.736563	967.481834	484.244555	E	2078.855102	1039.931189	2061.828553	1031.417914	2060.844537	1030.925906	15
6	***1042.513863***	521.760570	1025.487314	513.247295	1024.503298	512.755287	G	***1949.812509***	975.409893	1932.785960	966.896618	1931.801944	966.404610	14
7	***1143.561542***	572.284409	1126.534993	563.771135	1125.550977	563.279127	T	1892.791045	946.899160	1875.764496	938.385886	1874.780480	937.893878	13
8	1240.614306	620.810791	1223.587757	612.297517	1222.603741	611.805509	P	1791.743366	896.375321	1774.716817	887.862047	1773.732801	887.370038	12
9	1400.644955	700.826116	1383.618406	692.312841	1382.634390	691.820833	C	1694.690602	847.848939	1677.664053	839.335665	1676.680037	838.843656	11
10	1487.676983	744.342130	1470.650434	735.828855	1469.666418	735.336847	S	***1534.659953***	767.833614	1517.633404	759.320340	1516.649388	758.828332	10
11	1926.902309	963.954793	1909.875760	955.441518	1908.891744	954.949510	Q	1447.627925	724.317600	1430.601376	715.804326	1429.617360	715.312318	9
12	2086.932958	1043.970117	2069.906409	1035.456842	2068.922393	1034.964834	C	***1008.402599***	504.704937	991.376050	496.191663	990.392034	495.699655	8
13	2183.985722	1092.496499	2166.959173	1083.983224	2165.975157	1083.491216	P	***848.371950***	424.689613	831.345401	416.176338	830.361385	415.684330	7
14	2271.017750	1136.012513	2253.991201	1127.499238	2253.007185	1127.007230	S	***751.319186***	376.163231	734.292637	367.649956	733.308621	367.157948	6
15	2328.039214	1164.523245	2311.012665	1156.009970	2310.028649	1155.517962	G	***664.287158***	332.647217	647.260609	324.133942			5
16	2491.102543	1246.054909	2474.075994	1237.541635	2473.091978	1237.049627	Y	607.265694	304.136485	590.239145	295.623210			4
17	2628.161455	1314.584365	2611.134906	1306.071091	2610.150890	1305.579083	H	***444.202365***	222.604820	427.175816	214.091546			3
18	2788.192104	1394.599690	2771.165555	1386.086415	2770.181539	1385.594407	C	***307.143453***	154.075364	290.116904	145.562090			2
19							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 10 ppm



RMS error 10 ppm

NCBI **BLAST** search of RPYQEGTPCSQCPSGYHCK
(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	2933.290359	-0.015663	RPYQEGTPCSQCPSGYHCK

Mascot: http://www.matrixscience.com/

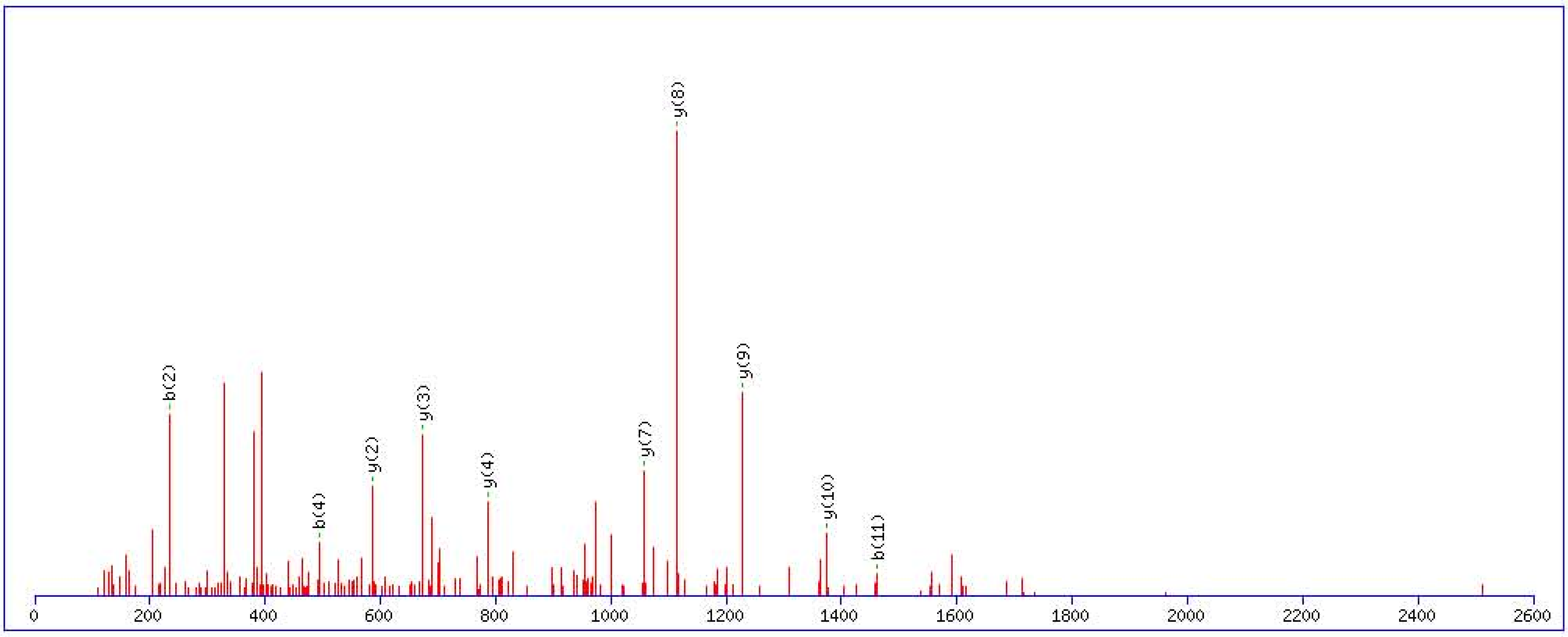
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TMFIGGSQLSQK**
Found in **PHLD_HUMAN**, Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens GN=GPLD1 PE=1 SV=3

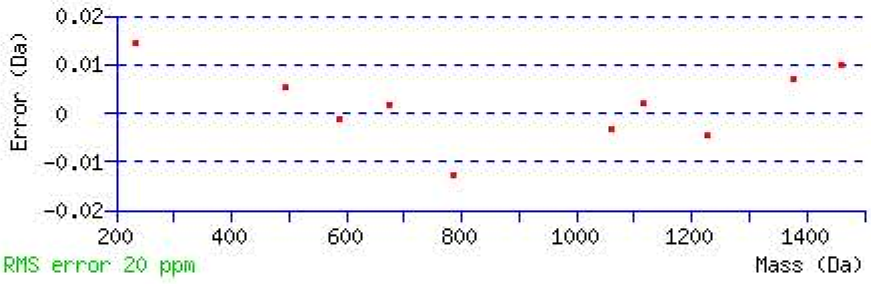
Match to Query 30750: 1606.810428 from(804.412490,2+) rtinseconds(2131) index(32624)
Title: Locus:1.1.1.3405.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

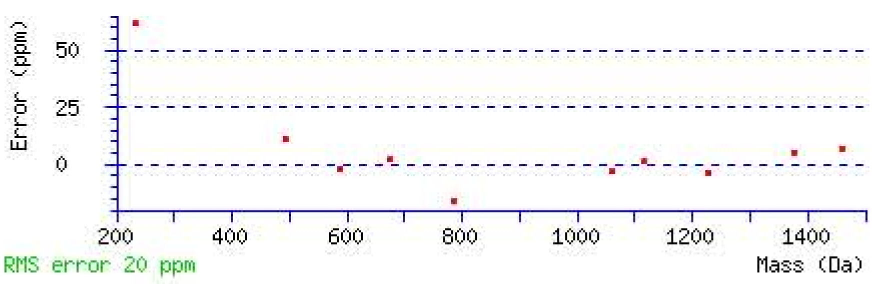
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1606.821121
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 2.4e-005
Matches : 10/114 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	102.054955	51.531116			84.044390	42.525833	T							12
2	**233.095440**	117.051358			215.084875	108.046076	M	1506.780719	753.893998	1489.754170	745.380723	1488.770154	744.888715	11
3	380.163854	190.585565			362.153289	181.580282	F	***1375.740234***	688.373755	1358.713685	679.860481	1357.729669	679.368473	10
4	**493.247918**	247.127597			475.237353	238.122314	I	***1228.671820***	614.839548	1211.645271	606.326274	1210.661255	605.834266	9
5	550.269382	275.638329			532.258817	266.633047	G	***1115.587756***	558.297516	1098.561207	549.784242	1097.577191	549.292234	8
6	607.290846	304.149061			589.280281	295.143779	G	***1058.566292***	529.786784	1041.539743	521.273510	1040.555727	520.781502	7
7	694.322874	347.665075			676.312309	338.659793	S	1001.544828	501.276052	984.518279	492.762778	983.534263	492.270770	6
8	822.381452	411.694364	805.354903	403.181090	804.370887	402.689082	Q	914.512800	457.760038	897.486251	449.246764	896.502235	448.754756	5
9	935.465516	468.236396	918.438967	459.723122	917.454951	459.231114	L	***786.454222***	393.730749	769.427673	385.217475	768.443657	384.725467	4
10	1022.497544	511.752410	1005.470995	503.239136	1004.486979	502.747128	S	***673.370158***	337.188717	656.343609	328.675443	655.359593	328.183435	3
11	**1461.722870**	731.365073	1444.696321	722.851799	1443.712305	722.359791	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 TMFIGGSQLSQK
(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	1606.821121	-0.010693	TMFIGGSQLSQK
19.1	1606.821121	-0.010693	TMFIGGSQLSQK
2.2	1606.795959	0.014469	VFMDRATNQSK
2.1	1606.798447	0.011981	KSNTILGSQEGNTMK
0.8	1606.809692	0.000736	KAIQRTVSSSGCEGK
0.6	1606.809860	0.000568	AIPEYMTISQK

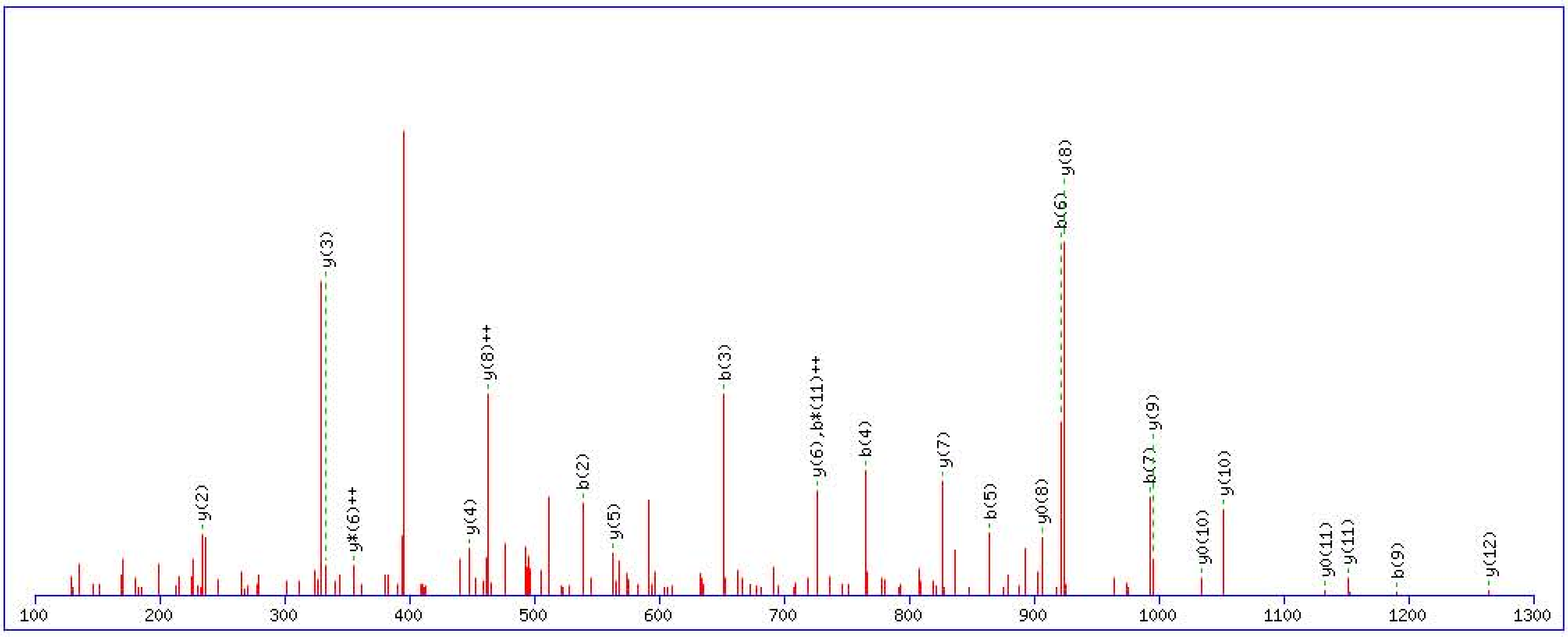
Mascot Search Results

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

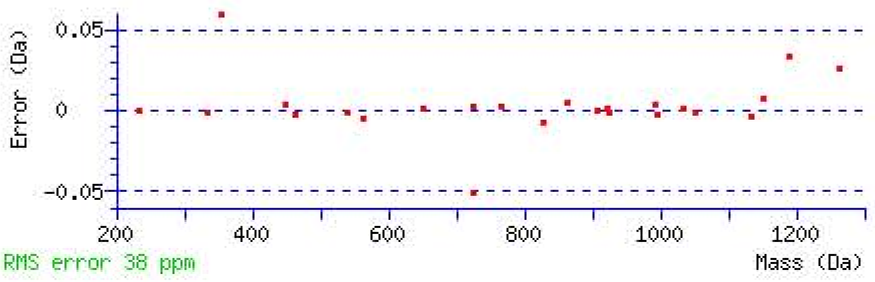
Match to Query 37719: 1915.005582 from(639.342470,3+) rtinseconds(2318) index(33696)
Title: Locus:1.1.1.3471.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

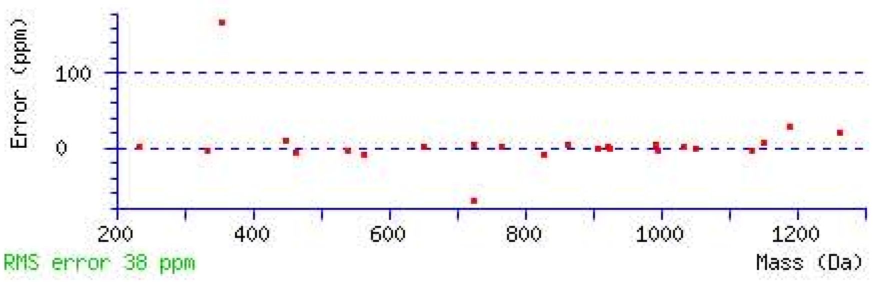
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1915.012497
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 1.1e-005
Matches : 24/150 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	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
54.1	1915.012497	-0.006915	QVLLVGAPTYDDVSK
1.4	1914.998550	0.007032	LLAPEAGSHPQQTQK
1.4	1914.998550	0.007032	LLAPEAGSHPQQTQK
1.4	1914.998550	0.007032	LLAPEAGSHPQQTQK
0.2	1915.027710	-0.022128	DYPIYLLKFKQCLSK
0.2	1915.008438	-0.002856	VIQKNQEETTSISK

Mascot: http://www.matrixscience.com/

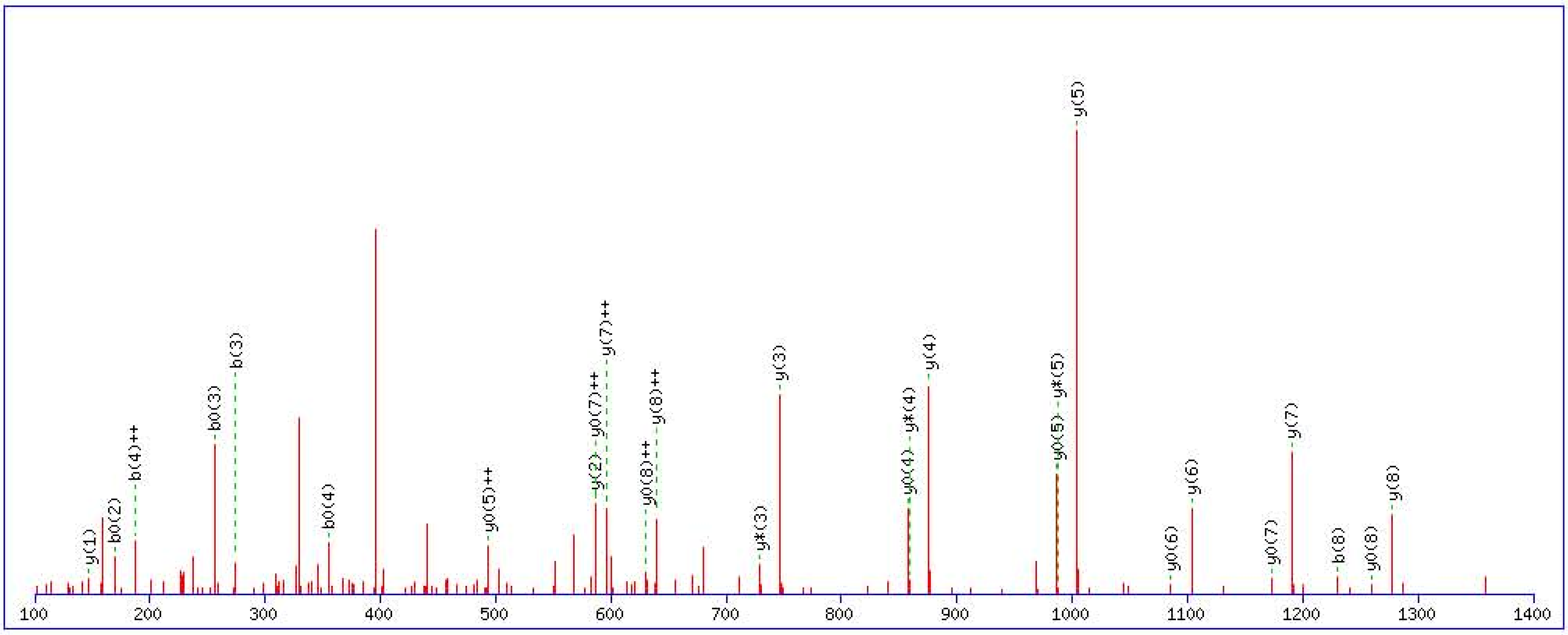
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSSVEECQK**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

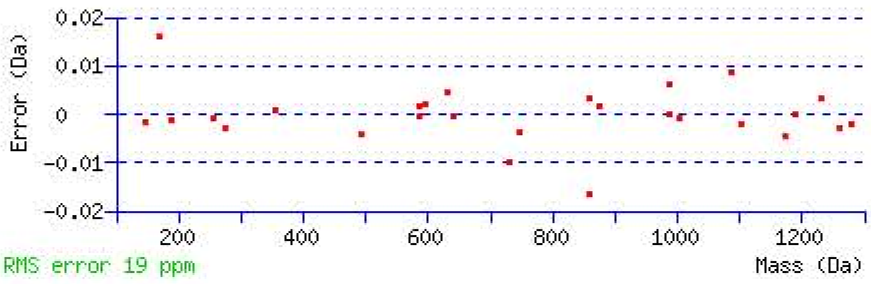
Match to Query 22803: 1375.646888 from(688.830720,2+) rtinseconds(1402) index(57313)
Title: Locus:1.1.1.1399.20 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

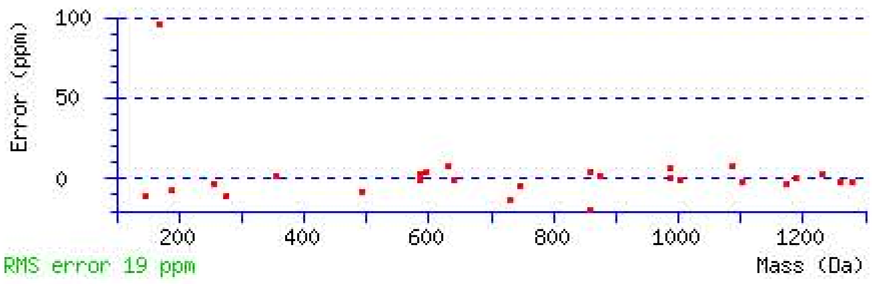
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 49  Expect: 0.00019
Matches : 28/74 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	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
48.8	1375.647568	-0.000680	VSSVEECQK
9.8	1375.662827	-0.015939	GFSIPECQK
2.6	1375.665329	-0.018441	ADVSLPSMQGDLK
0.5	1375.665314	-0.018426	VSLMTSSEEIHK

Mascot: http://www.matrixscience.com/

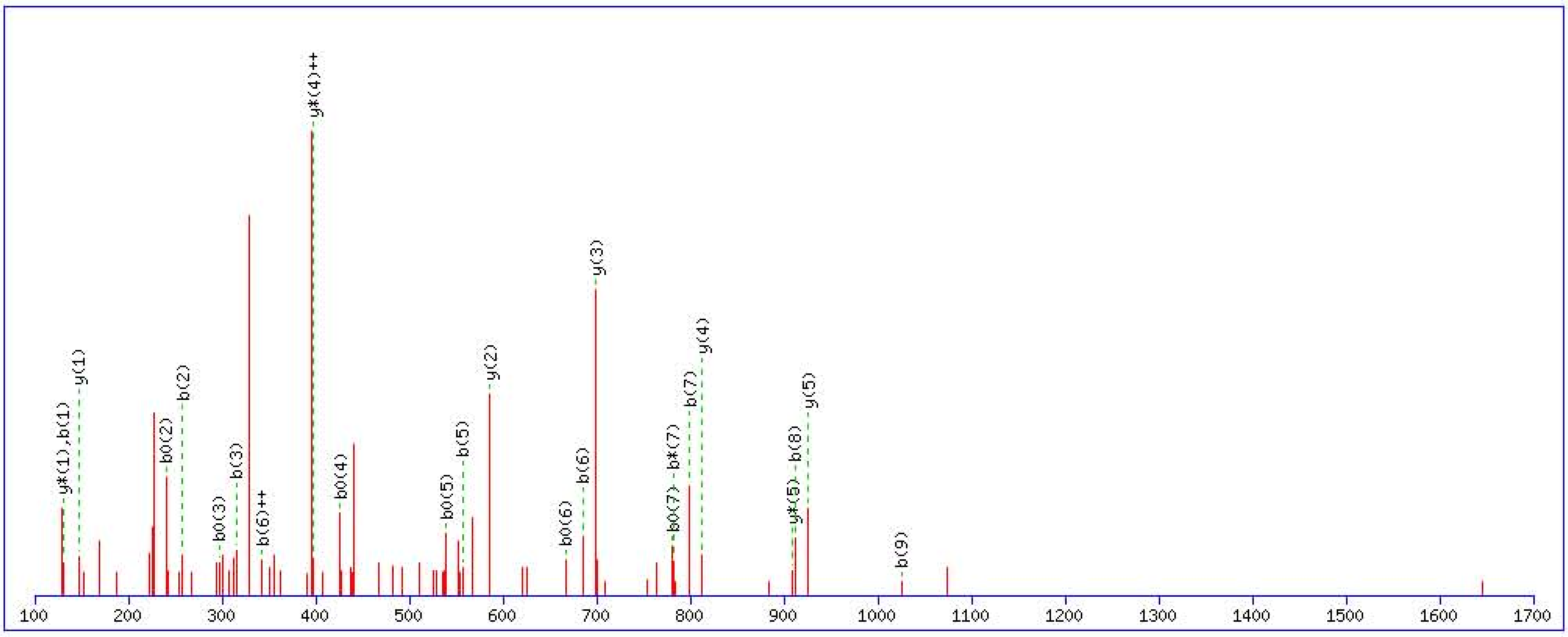
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EKGEIQNILQK**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

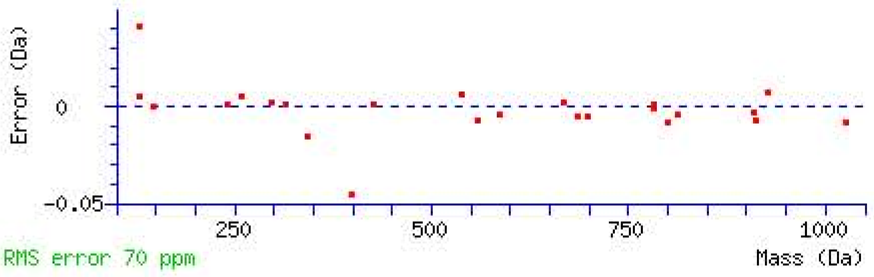
Match to Query 30908: 1609.881912 from(537.634580,3+) rtinseconds(1887) index(18203)
Title: Locus:1.1.1.3223.4 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

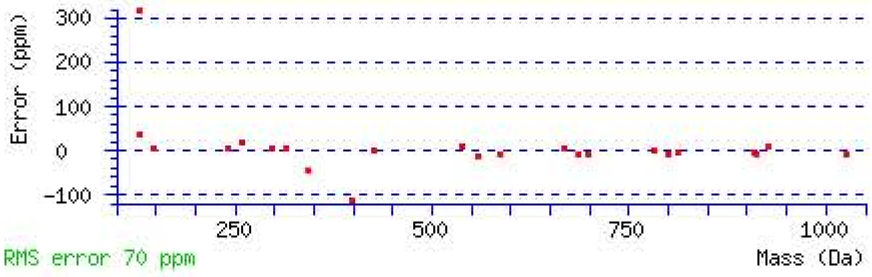
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1609.886124
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 32 **Expect:** 0.013
Matches : 24/104 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	***130.049869***	65.528572			112.039304	56.523290	E							11
2	***258.144832***	129.576054	241.118283	121.062780	240.134267	120.570772	K	1481.850847	741.429061	1464.824298	732.915787	1463.840282	732.423779	10
3	***315.166296***	158.086786	298.139747	149.573512	297.155731	149.081504	G	1353.755884	677.381580	1336.729335	668.868306	1335.745319	668.376297	9
4	444.208889	222.608082	427.182340	214.094808	426.198324	213.602800	E	1296.734420	648.870848	1279.707871	640.357574	1278.723855	639.865566	8
5	***557.292953***	279.150115	540.266404	270.636840	539.282388	270.144832	I	1167.691827	584.349552	1150.665278	575.836277			7
6	***685.351531***	343.179404	668.324982	334.666129	667.340966	334.174121	Q	1054.607763	527.807520	1037.581214	519.294245			6
7	***799.394458***	400.200867	782.367909	391.687592	781.383893	391.195585	N	**926.549185**	463.778231	909.522636	455.264956			5
8	***912.478522***	456.742899	895.451973	448.229625	894.467957	447.737617	I	**812.506258**	406.756767	795.479709	398.243493			4
9	***1025.562586***	513.284931	1008.536037	504.771657	1007.552021	504.279649	L	**699.422194**	350.214735	682.395645	341.701461			3
10	1464.787912	732.897594	1447.761363	724.384320	1446.777347	723.892312	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 EKGEIQNILQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.1	1609.886124	-0.004212	EKGEIQNILQK
14.7	1609.872192	0.009720	QEAERALKQAR
2.8	1609.897400	-0.015488	TNLRIVDVGGQK
1.9	1609.878754	0.003158	AGPLTVNTEAQQLLR
1.1	1609.886154	-0.004242	KTVTAMDVVYALKR
0.9	1609.868393	0.013519	TKVQEQQK
0.3	1609.890839	-0.008927	RIHMMSLGVLNLAR

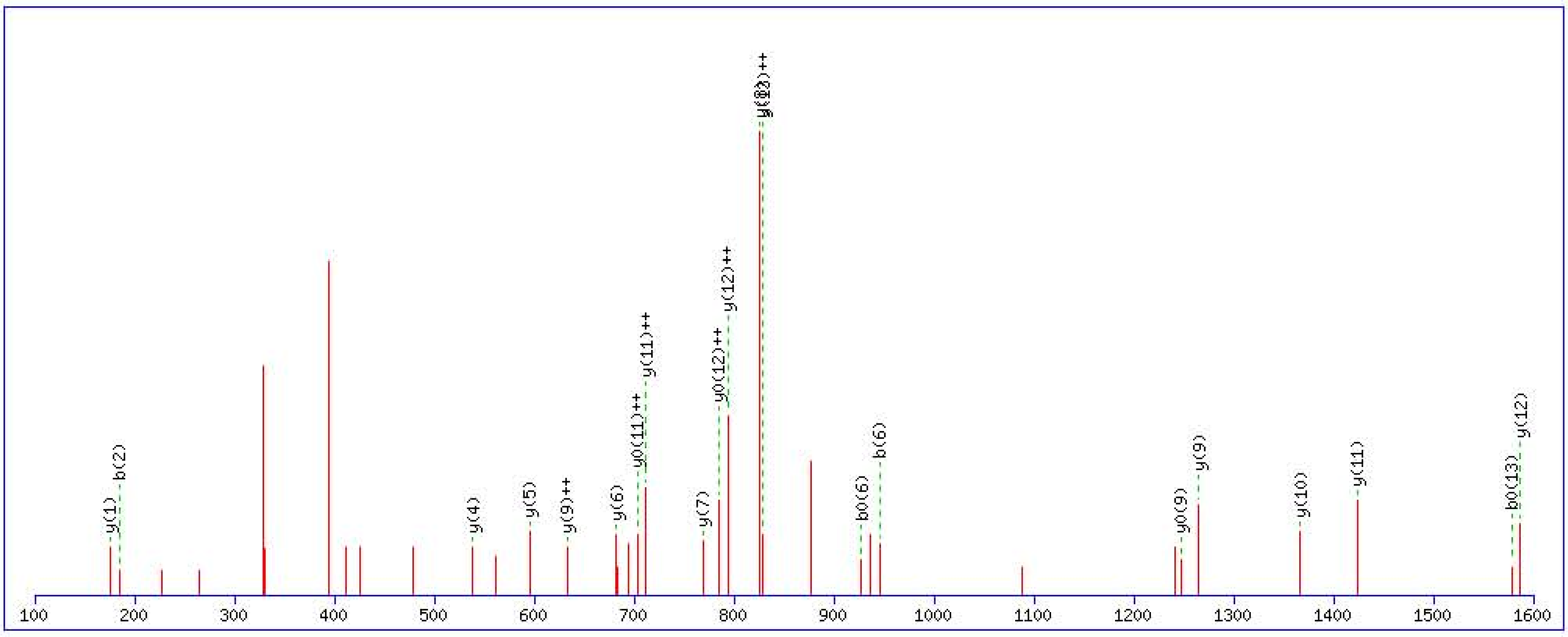
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IAYGTQGSSGYSLR**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

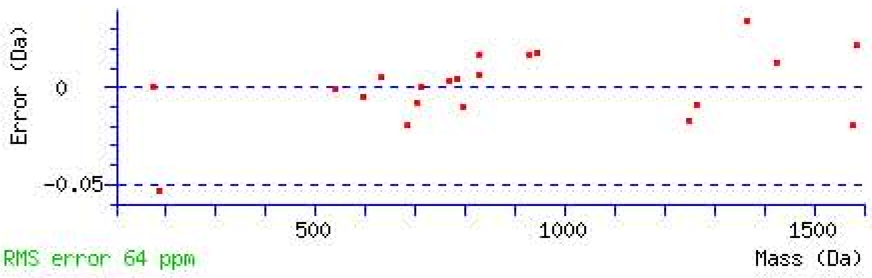
Match to Query 35090: 1769.884768 from(885.949660,2+) rtinseconds(1918) index(59981)
Title: Locus:1.1.1.1579.25 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

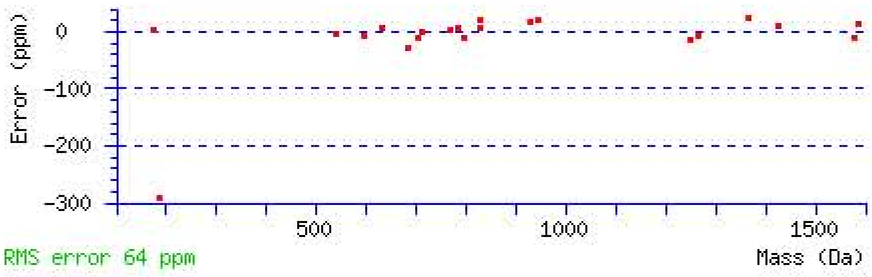
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1769.877045
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 72  Expect: 4.2e-007
Matches : 21/134 fragment ions using 34 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					I							14
2	**185.128454**	93.067865					A	1657.800269	829.403773	1640.773720	820.890498	1639.789704	820.398490	13
3	348.191783	174.599529					Y	***1586.763155***	793.885216	1569.736606	785.371941	1568.752590	784.879933	12
4	405.213247	203.110261					G	***1423.699826***	712.353551	1406.673277	703.840277	1405.689261	703.348269	11
5	506.260926	253.634101			488.250361	244.628818	T	***1366.678362***	683.842819	1349.651813	675.329545	1348.667797	674.837537	10
6	**945.486252**	473.246764	928.459703	464.733490	927.475687	464.241482	Q	***1265.630683***	633.318980	1248.604134	624.805705	1247.620118	624.313697	9
7	1002.507716	501.757496	985.481167	493.244222	984.497151	492.752214	G	***826.405357***	413.706317	809.378808	405.193042	808.394792	404.701034	8
8	1089.539744	545.273510	1072.513195	536.760236	1071.529179	536.268228	S	***769.383893***	385.195585	752.357344	376.682310	751.373328	376.190302	7
9	1176.571772	588.789524	1159.545223	580.276250	1158.561207	579.784242	S	***682.351865***	341.679571	665.325316	333.166296	664.341300	332.674288	6
10	1233.593236	617.300256	1216.566687	608.786982	1215.582671	608.294974	G	***595.319837***	298.163557	578.293288	289.650282	577.309272	289.158274	5
11	1396.656565	698.831921	1379.630016	690.318646	1378.646000	689.826638	Y	***538.298373***	269.652825	521.271824	261.139550	520.287808	260.647542	4
12	1483.688593	742.347935	1466.662044	733.834660	1465.678028	733.342652	S	375.235044	188.121160	358.208495	179.607885	357.224479	179.115877	3
13	1596.772657	798.889967	1579.746108	790.376692	1578.762092	789.884684	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 IAYGTQGSSGYSLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
72.5	1769.877045	0.007723	IAYGTQGSSGYSLR
4.2	1769.909424	-0.024656	LATDAAQVQGATGTR
1.5	1769.880402	0.004366	ALSQTPMPAPEMPKTR
1.5	1769.872299	0.012469	LAYSEAGDYLVAIEEK
0.7	1769.875717	0.009051	TSGMLTVLEEEAVFTK
0.0	1769.884247	0.000521	TELQEVRAQLCNPGR

Mascot: http://www.matrixscience.com/

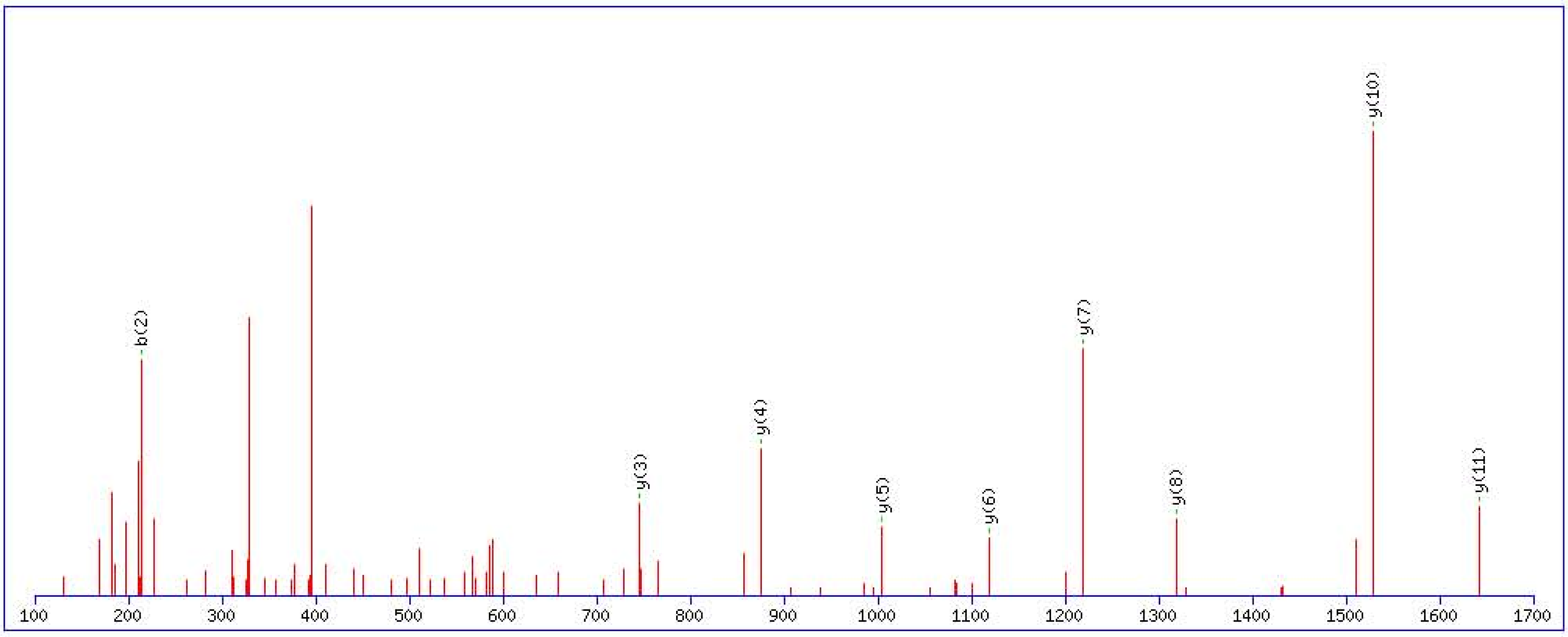
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNIPLVTNEECQK**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

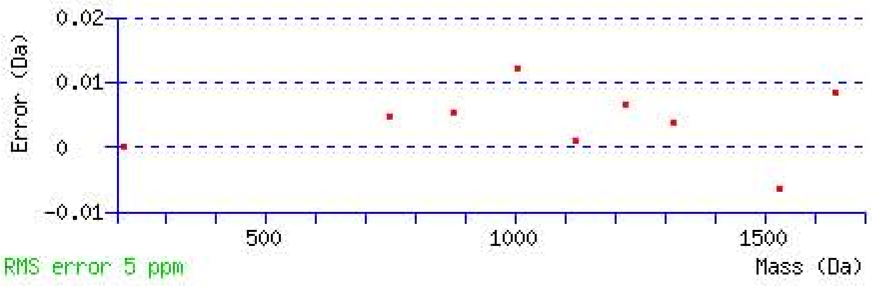
Match to Query 36790: 1853.935782 from(618.985870,3+) rtinseconds(2172) index(20038)
Title: Locus:1.1.1.3322.3 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

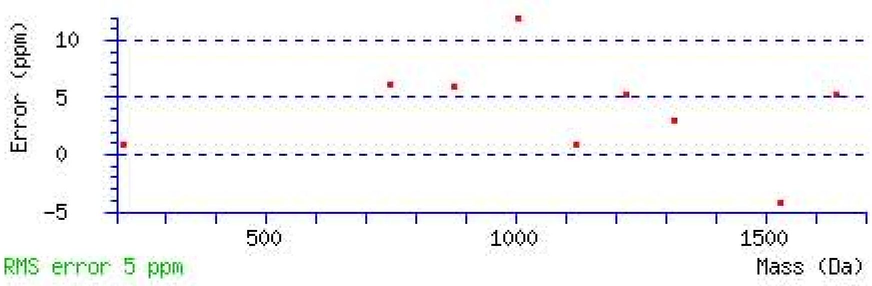
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1853.937927
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 3.6e-005
Matches : 9/124 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	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
56.9	1853.937927	-0.002145	VNIPLVTNEECQK
9.0	1853.934341	0.001441	RGLSNPNELQAAIDSNR
3.0	1853.909424	0.026358	CFNTLTNSFQPSLLGR

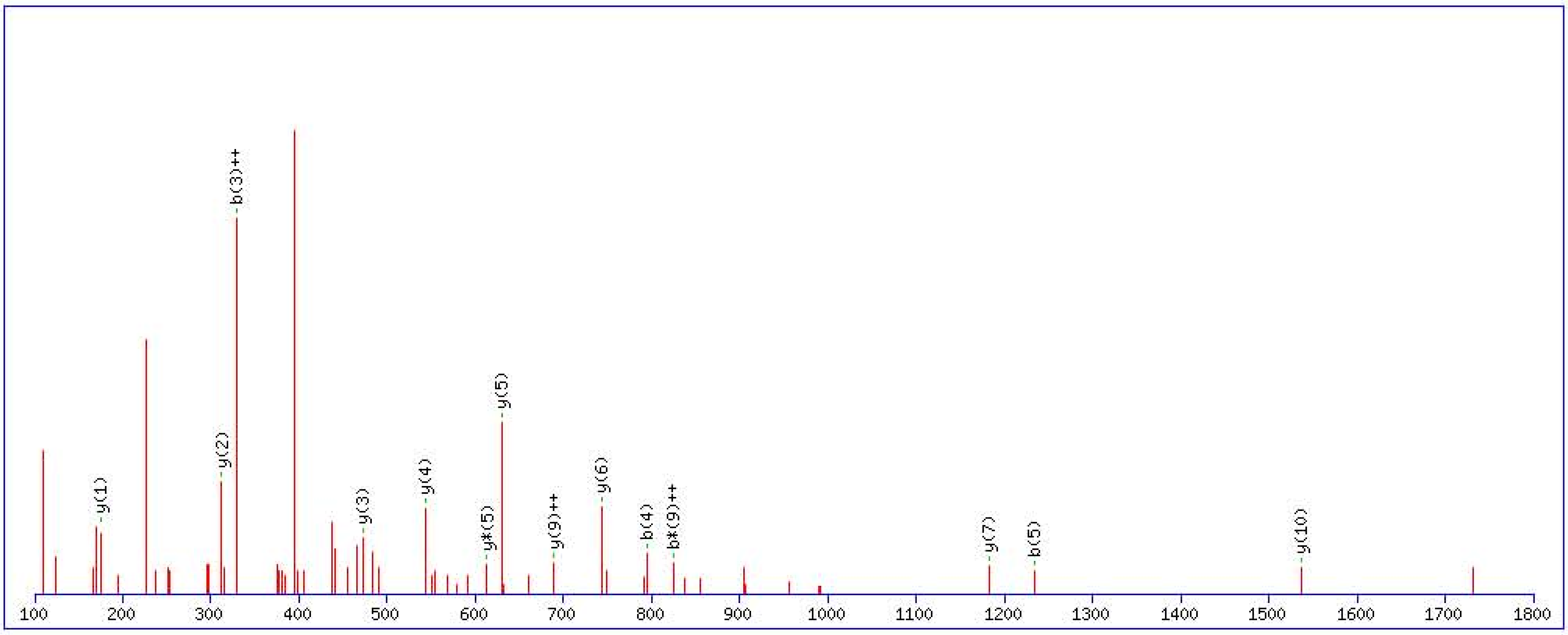
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QCGHQISACHR**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

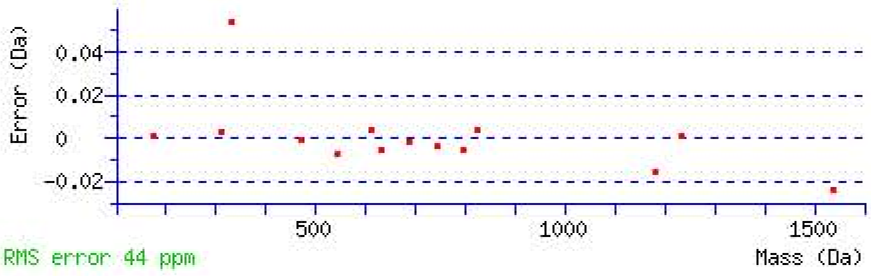
Match to Query 38868: 1974.909616 from(494.734680,4+) rtinseconds(1497) index(28805)
Title: Locus:1.1.1.3184.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

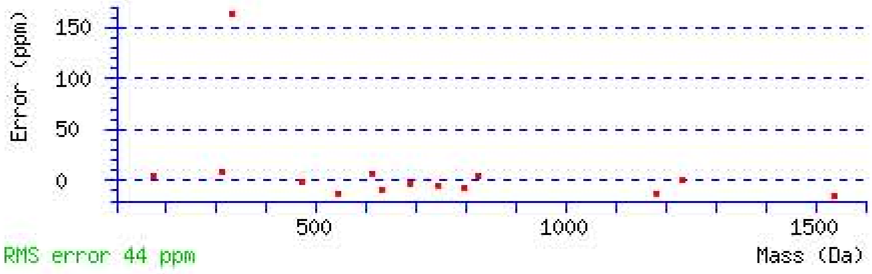
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 33  Expect: 0.0057
Matches : 14/100 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	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
33.4	1974.916122	-0.006506	QCGHQISACHR

Mascot: http://www.matrixscience.com/

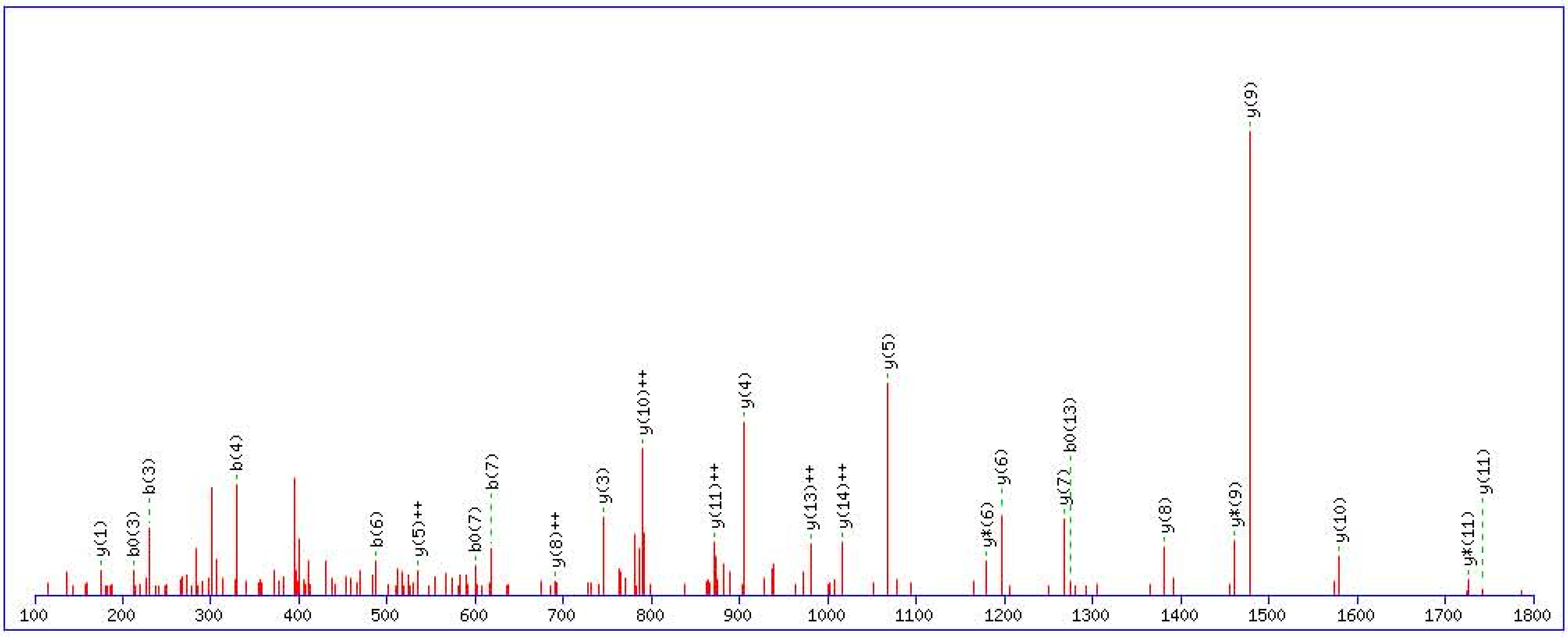
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGDVASMYTPNAQYCQMR**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

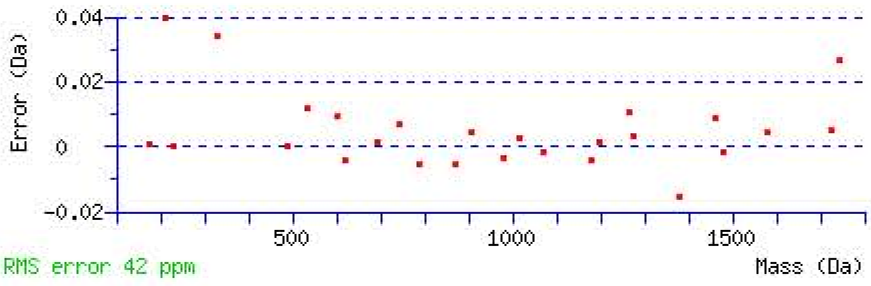
Match to Query 45932: 2359.021602 from(787.347810,3+) rtinseconds(2076) index(32325)
Title: Locus:1.1.1.3386.19 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

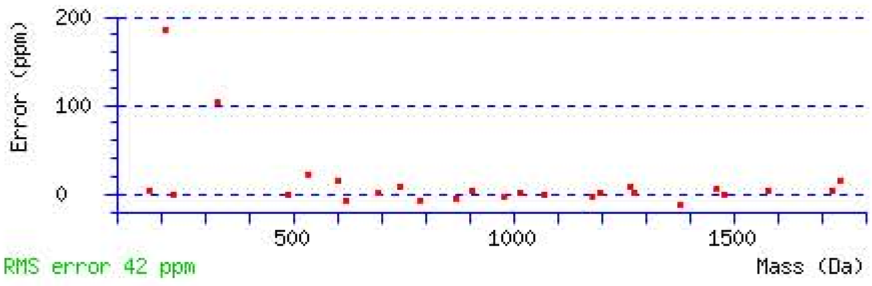
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2359.021759
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16    : Biotin:Thermo-21345 (Q)
Ions Score: 76  Expect: 1.1e-007
Matches : 26/162 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							18
2	115.050204	58.028740					G	2303.007580	1152.007428	2285.981031	1143.494153	2284.997015	1143.002145	17
3	**230.077147**	115.542211			212.066582	106.536929	D	2245.986116	1123.496696	2228.959567	1114.983421	2227.975551	1114.491413	16
4	**329.145561**	165.076418			311.134996	156.071136	V	2130.959173	1065.983224	2113.932624	1057.469950	2112.948608	1056.977942	15
5	400.182675	200.594975			382.172110	191.589693	A	2031.890759	1016.449018	2014.864210	1007.935743	2013.880194	1007.443735	14
6	**487.214703**	244.110989			469.204138	235.105707	S	1960.853645	980.930461	1943.827096	972.417186	1942.843080	971.925178	13
7	**618.255188**	309.631232			600.244623	300.625949	M	1873.821617	937.414447	1856.795068	928.901172	1855.811052	928.409164	12
8	781.318517	391.162896			763.307952	382.157614	Y	***1742.781132***	871.894204	1725.754583	863.380930	1724.770567	862.888922	11
9	882.366196	441.686736			864.355631	432.681453	T	***1579.717803***	790.362540	1562.691254	781.849265	1561.707238	781.357257	10
10	979.418960	490.213118			961.408395	481.207835	P	***1478.670124***	739.838700	1461.643575	731.325426			9
11	1093.461887	547.234581	1076.435338	538.721307	1075.451322	538.229299	N	***1381.617360***	691.312318	1364.590811	682.799044			8
12	1164.499001	582.753138	1147.472452	574.239864	1146.488436	573.747856	A	***1267.574433***	634.290855	1250.547884	625.777580			7
13	1292.557579	646.782428	1275.531030	638.269153	1274.547014	637.777145	Q	***1196.537319***	598.772298	1179.510770	590.259023			6
14	1455.620908	728.314092	1438.594359	719.800818	1437.610343	719.308810	Y	***1068.478741***	534.743009	1051.452192	526.229734			5
15	1615.651557	808.329417	1598.625008	799.816142	1597.640992	799.324134	C	***905.415412***	453.211344	888.388863	444.698070			4
16	2054.876883	1027.942079	2037.850334	1019.428805	2036.866318	1018.936797	Q	***745.384763***	373.196020	728.358214	364.682745			3
17	2185.917368	1093.462322	2168.890819	1084.949047	2167.906803	1084.457039	M	306.159437	153.583356	289.132888	145.070082			2
18							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GGDVASMYTPNAQYCQMR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
76.3	2359.021759	-0.000157	GGDVASMYTPNAQYCQMR
44.2	2359.021759	-0.000157	GGDVASMYTPNAQYCQMR

Mascot: http://www.matrixscience.com/

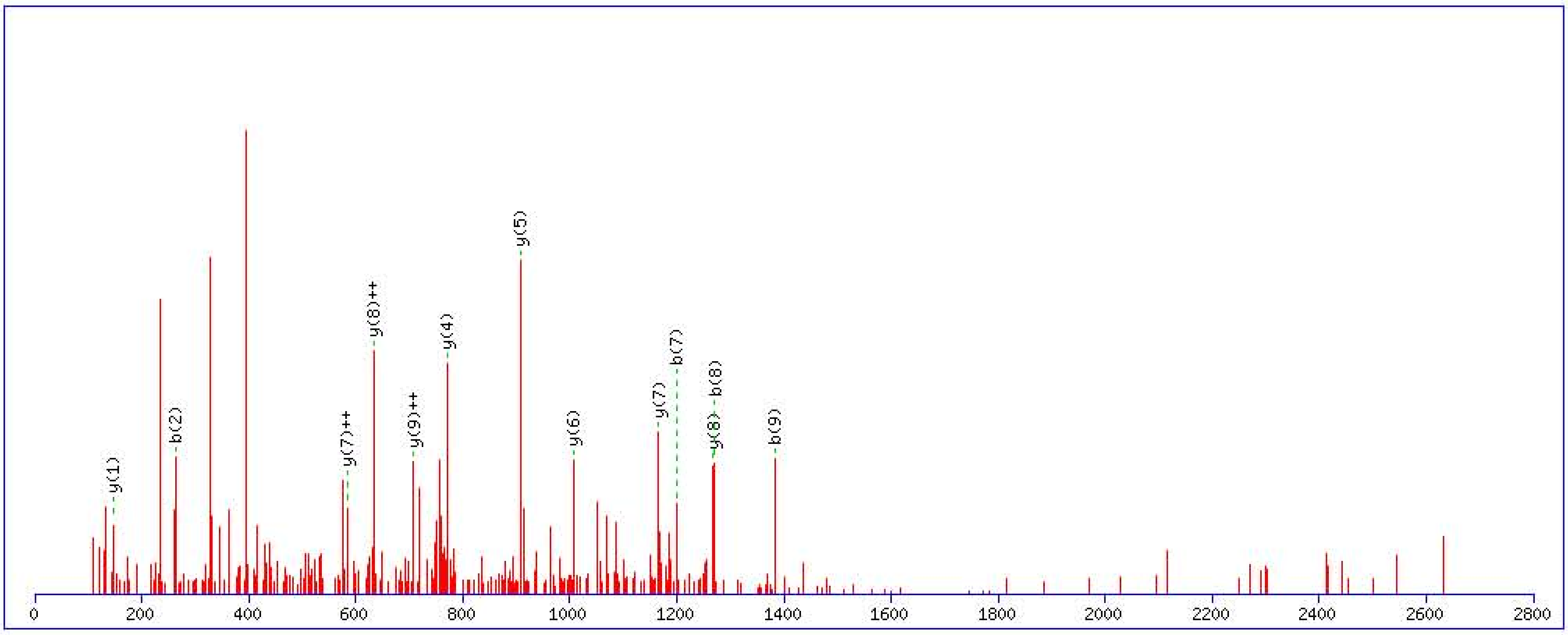
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DFTCVHQALK**
Found in **IC1_HUMAN**, Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2

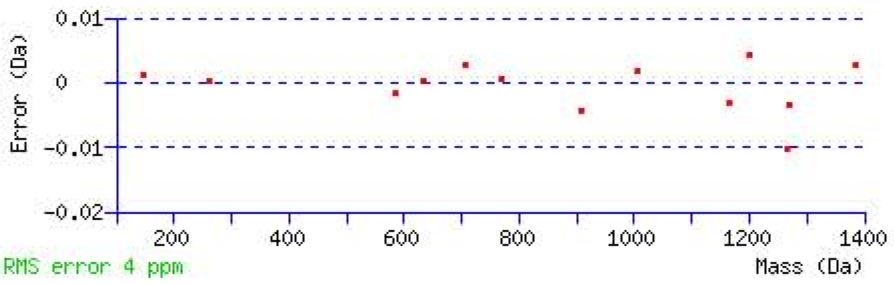
Match to Query 28044: 1528.749188 from(765.381870,2+) rtinseconds(1830) index(30780)
Title: Locus:1.1.1.3300.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

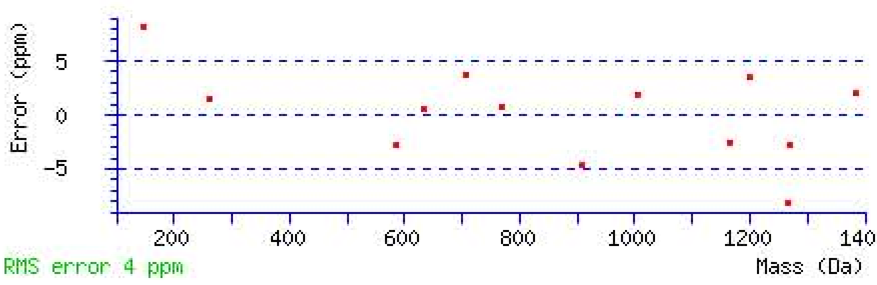
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1528.753052
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 28 **Expect:** 0.0037
Matches : 13/82 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							10
2	***263.102633***	132.054954			245.092068	123.049672	F	1414.733376	707.870326	1397.706827	699.357051	1396.722811	698.865043	9
3	364.150312	182.578794			346.139747	173.573512	T	***1267.664962***	634.336119	1250.638413	625.822844	1249.654397	625.330836	8
4	524.180961	262.594119			506.170396	253.588836	C	***1166.617283***	583.812279	1149.590734	575.299005			7
5	623.249375	312.128326			605.238810	303.123043	V	***1006.586634***	503.796955	989.560085	495.283680			6
6	760.308287	380.657782			742.297722	371.652499	H	***907.518220***	454.262748	890.491671	445.749473			5
7	***1199.533613***	600.270444	1182.507064	591.757170	1181.523048	591.265162	Q	***770.459308***	385.733292	753.432759	377.220017			4
8	***1270.570727***	635.789001	1253.544178	627.275727	1252.560162	626.783719	A	331.233982	166.120629	314.207433	157.607354			3
9	***1383.654791***	692.331033	1366.628242	683.817759	1365.644226	683.325751	L	260.196868	130.602072	243.170319	122.088797			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of DFTCVHQALK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.4	1528.753052	-0.003864	DFTCVHQALK
2.5	1528.740936	0.008252	VYESIGQYGGETVK

Mascot: http://www.matrixscience.com/

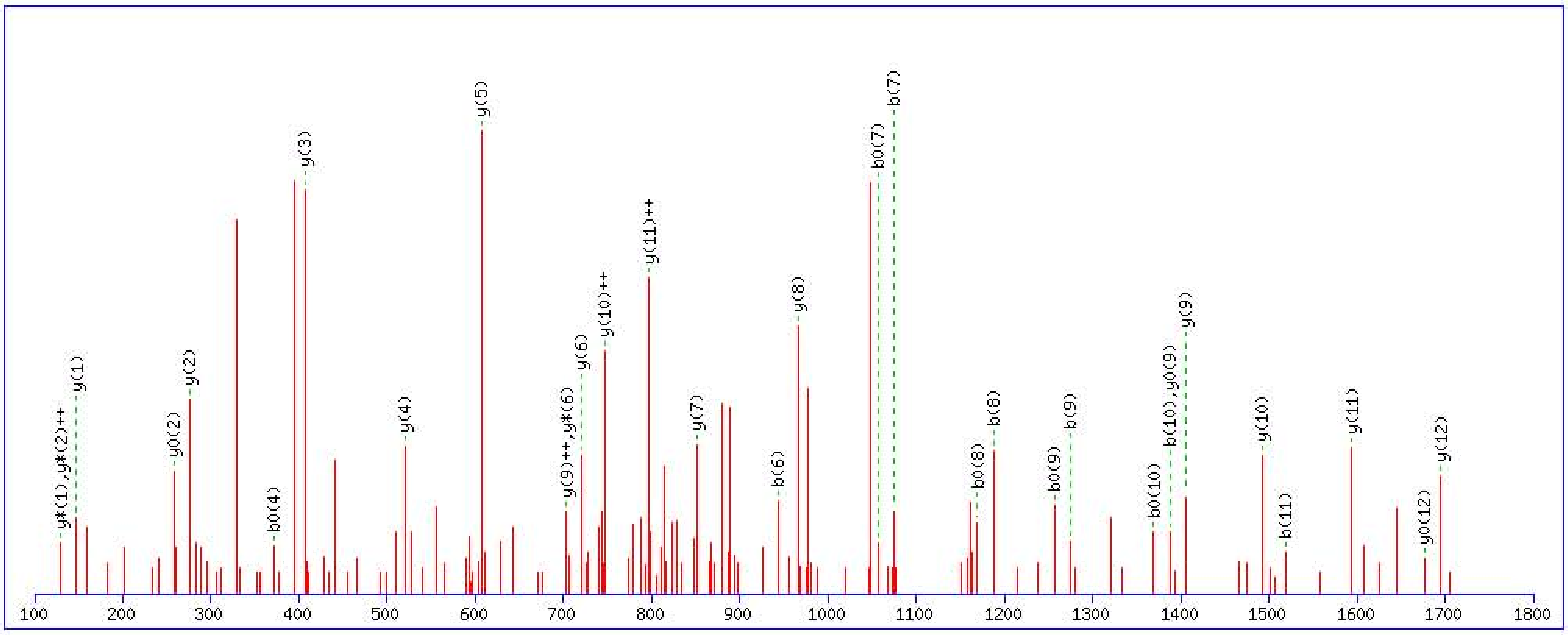
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTTSQDMLSIMEK**
Found in **IC1_HUMAN**, Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2

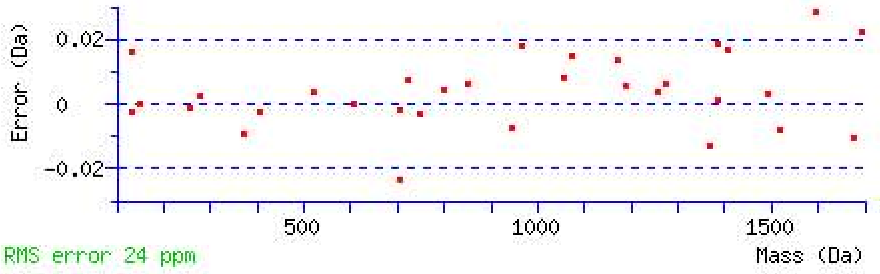
Match to Query 35568: 1792.871568 from(897.443060,2+) rtinseconds(2389) index(34021)
Title: Locus:1.1.1.3495.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

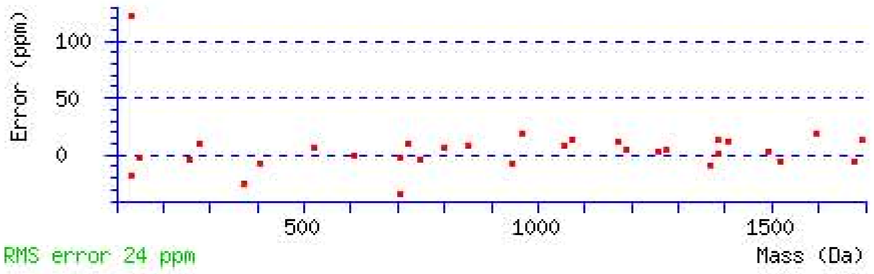
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1792.877304
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 86  Expect: 5e-008
Matches : 32/132 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	100.075690	50.541483					V							13
2	201.123369	101.065322			183.112804	92.060040	T	***1694.816178***	847.911727	1677.789629	839.398453	1676.805613	838.906445	12
3	302.171048	151.589162			284.160483	142.583879	T	***1593.768499***	797.387888	1576.741950	788.874613	1575.757934	788.382605	11
4	389.203076	195.105176			371.192511	186.099893	S	***1492.720820***	746.864048	1475.694271	738.350774	1474.710255	737.858766	10
5	828.428402	414.717839	811.401853	406.204565	810.417837	405.712557	Q	***1405.688792***	703.348034	1388.662243	694.834760	1387.678227	694.342752	9
6	**943.455345**	472.231311	926.428796	463.718036	925.444780	463.226028	D	***966.463466***	483.735371	949.436917	475.222097	948.452901	474.730089	8
7	**1074.495830**	537.751553	1057.469281	529.238279	1056.485265	528.746271	M	***851.436523***	426.221900	834.409974	417.708625	833.425958	417.216617	7
8	**1187.579894**	594.293585	1170.553345	585.780311	1169.569329	585.288302	L	***720.396038***	360.701657	703.369489	352.188383	702.385473	351.696375	6
9	**1274.611922**	637.809599	1257.585373	629.296325	1256.601357	628.804317	S	***607.311974***	304.159625	590.285425	295.646351	589.301409	295.154343	5
10	**1387.695986**	694.351631	1370.669437	685.838357	1369.685421	685.346348	I	***520.279946***	260.643611	503.253397	252.130337	502.269381	251.638329	4
11	**1518.736471**	759.871873	1501.709922	751.358599	1500.725906	750.866591	M	***407.195882***	204.101579	390.169333	195.588305	389.185317	195.096297	3
12	1647.779064	824.393170	1630.752515	815.879896	1629.768499	815.387888	E	***276.155397***	138.581337	259.128848	130.068062	258.144832	129.576054	2
13							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VTTSQDMLSIMEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
86.5	1792.877304	-0.005736	VTTSQDMLSIMEK

Mascot: http://www.matrixscience.com/

{MATRIX SCIENCE}

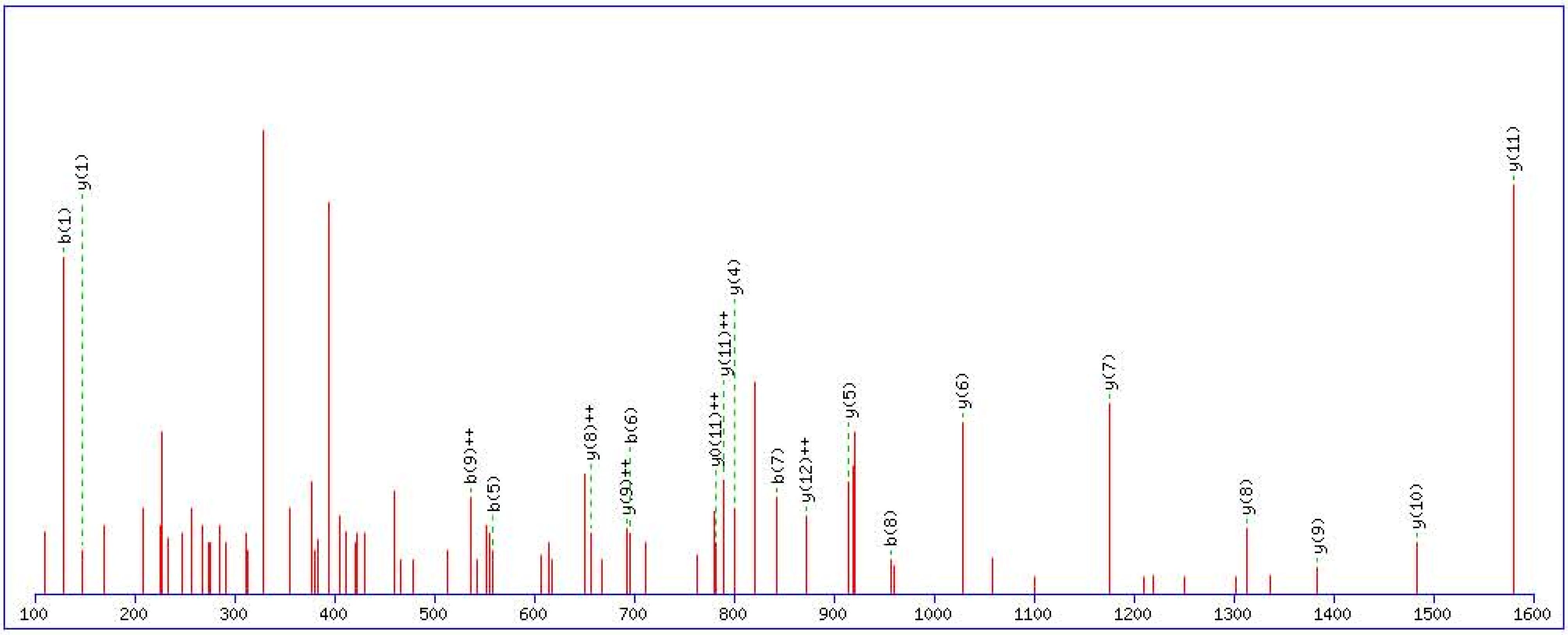
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KYPVAHFIDQTLK**
Found in **IC1_HUMAN**, Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2

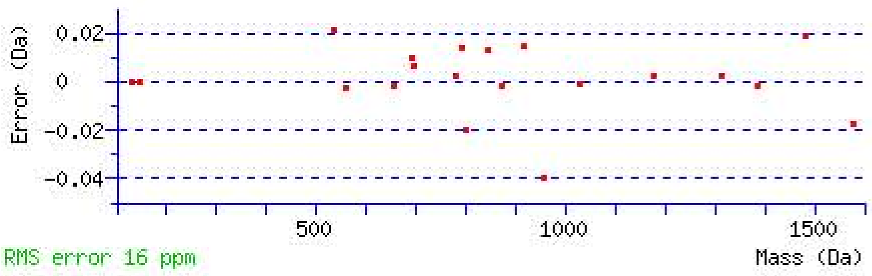
Match to Query 37033: 1870.009872 from(624.343900,3+) rtinseconds(2035) index(32090)
Title: Locus:1.1.1.3372.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

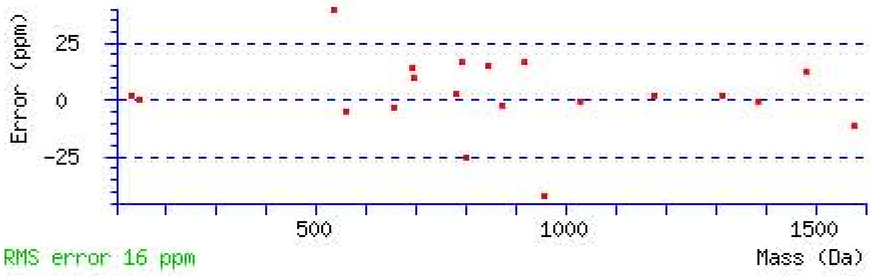
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1870.017502
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.024
Matches : 20/124 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	**129.102239**	65.054757	112.075690	56.541483			K							13
2	292.165568	146.586422	275.139019	138.073148			Y	1742.929827	871.968552	1725.903278	863.455277	1724.919262	862.963269	12
3	389.218332	195.112804	372.191783	186.599529			P	***1579.866498***	790.436887	1562.839949	781.923613	1561.855933	781.431605	11
4	488.286746	244.647011	471.260197	236.133737			V	***1482.813734***	741.910505	1465.787185	733.397231	1464.803169	732.905223	10
5	**559.323860**	280.165568	542.297311	271.652294			A	***1383.745320***	692.376298	1366.718771	683.863024	1365.734755	683.371016	9
6	**696.382772**	348.695024	679.356223	340.181750			H	***1312.708206***	656.857741	1295.681657	648.344467	1294.697641	647.852459	8
7	**843.451186**	422.229231	826.424637	413.715957			F	***1175.649294***	588.328285	1158.622745	579.815011	1157.638729	579.323003	7
8	**956.535250**	478.771263	939.508701	470.257989			I	***1028.580880***	514.794078	1011.554331	506.280804	1010.570315	505.788796	6
9	1071.562193	536.284735	1054.535644	527.771460	1053.551628	527.279452	D	***915.496816***	458.252046	898.470267	449.738772	897.486251	449.246764	5
10	1510.787519	755.897398	1493.760970	747.384123	1492.776954	746.892115	Q	***800.469873***	400.738575	783.443324	392.225300	782.459308	391.733292	4
11	1611.835198	806.421237	1594.808649	797.907963	1593.824633	797.415955	T	361.244547	181.125911	344.217998	172.612637	343.233982	172.120629	3
12	1724.919262	862.963269	1707.892713	854.449995	1706.908697	853.957987	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 KYPVAHFIDQTLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.6	1870.017502	-0.007630	KYPVAHFIDQTLK

Mascot: http://www.matrixscience.com/

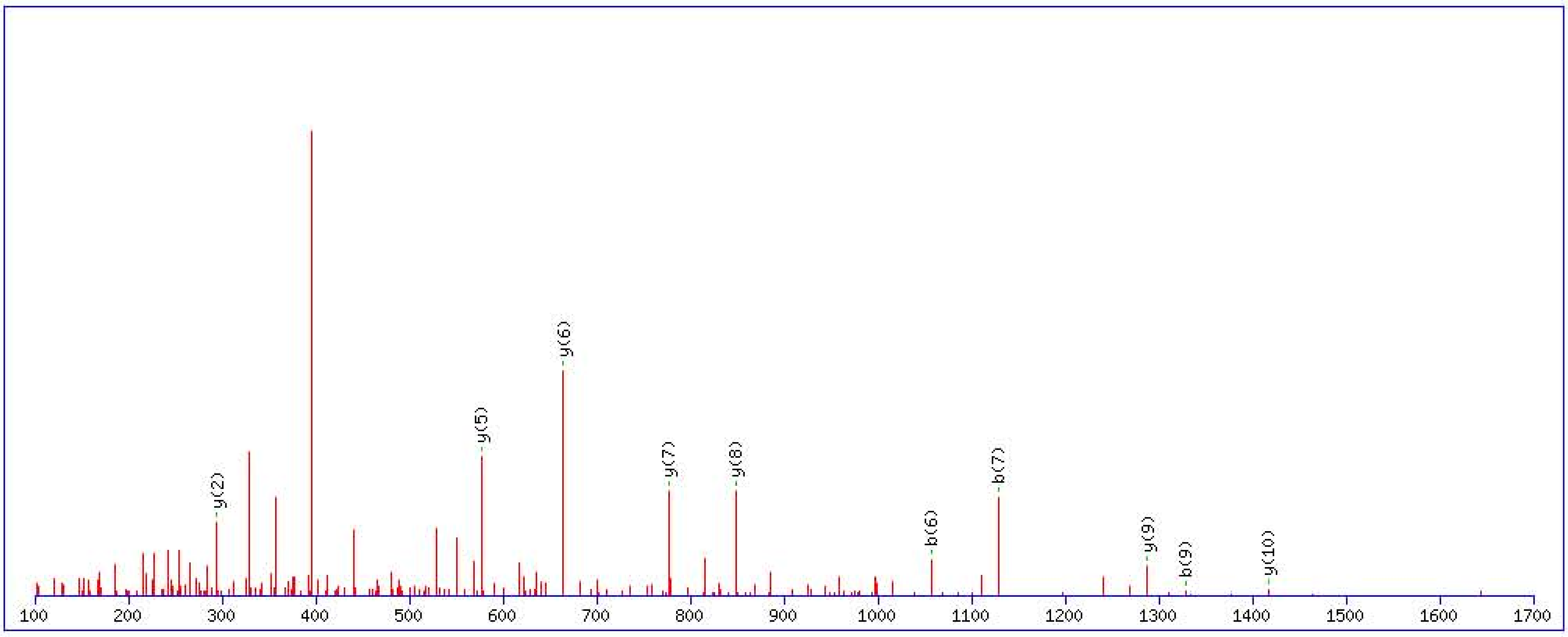
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEDMEQALSPSVFK**
Found in **IC1_HUMAN**, Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2

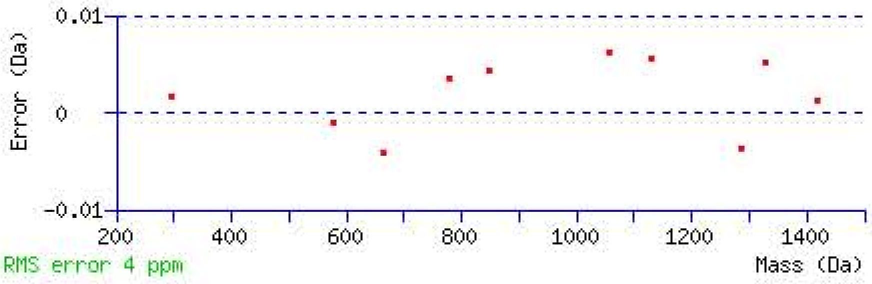
Match to Query 37455: 1903.938102 from(635.653310,3+) rtinseconds(2448) index(34301)
Title: Locus:1.1.1.3516.4 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

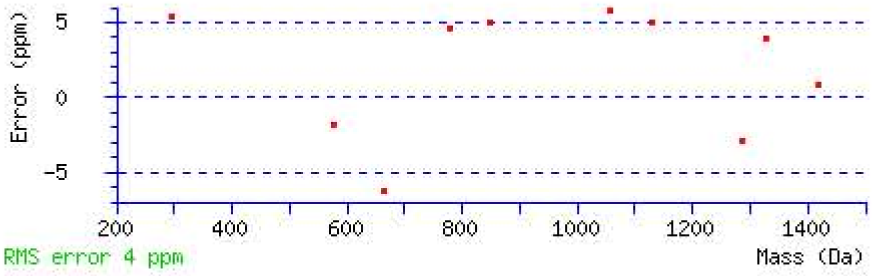
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1903.942337
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 45 **Expect:** 0.00014
Matches : 10/138 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	114.091340	57.549308					L							14
2	243.133933	122.070605			225.123368	113.065322	E	1791.865570	896.436423	1774.839021	887.923149	1773.855005	887.431141	13
3	358.160876	179.584076			340.150311	170.578794	D	1662.822977	831.915127	1645.796428	823.401852	1644.812412	822.909844	12
4	489.201361	245.104319			471.190796	236.099036	M	1547.796034	774.401655	1530.769485	765.888381	1529.785469	765.396373	11
5	618.243954	309.625615			600.233389	300.620333	E	***1416.755549***	708.881413	1399.729000	700.368138	1398.744984	699.876130	10
6	**1057.469280**	529.238278	1040.442731	520.725004	1039.458715	520.232996	Q	***1287.712956***	644.360116	1270.686407	635.846842	1269.702391	635.354834	9
7	**1128.506394**	564.756835	1111.479845	556.243561	1110.495829	555.751553	A	***848.487630***	424.747453	831.461081	416.234179	830.477065	415.742171	8
8	1241.590458	621.298867	1224.563909	612.785593	1223.579893	612.293584	L	***777.450516***	389.228896	760.423967	380.715622	759.439951	380.223614	7
9	**1328.622486**	664.814881	1311.595937	656.301607	1310.611921	655.809598	S	***664.366452***	332.686864	647.339903	324.173590	646.355887	323.681582	6
10	1425.675250	713.341263	1408.648701	704.827989	1407.664685	704.335981	P	***577.334424***	289.170850	560.307875	280.657576	559.323859	280.165568	5
11	1512.707278	756.857277	1495.680729	748.344003	1494.696713	747.851995	S	480.281660	240.644468	463.255111	232.131194	462.271095	231.639186	4
12	1611.775692	806.391484	1594.749143	797.878210	1593.765127	797.386202	V	393.249632	197.128454	376.223083	188.615180			3
13	1758.844106	879.925691	1741.817557	871.412417	1740.833541	870.920409	F	***294.181218***	147.594247	277.154669	139.080973			2
14							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LEDMEQALSPSVFK
(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	1903.942337	-0.004235	LEDMEQALSPSVFK
3.6	1903.924377	0.013725	LQSQRPSMASELMPSSR

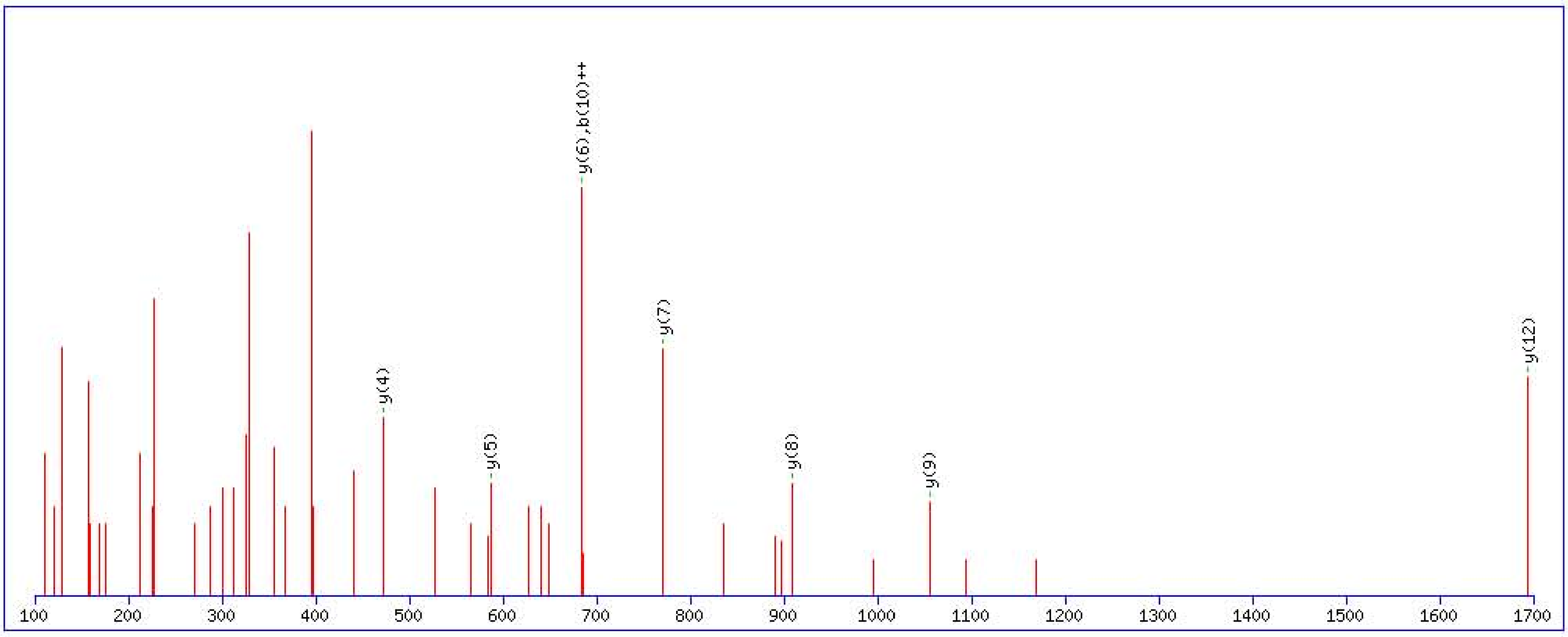
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVTSVSQIFHSPDLAIR**
Found in **IC1_HUMAN**, Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2

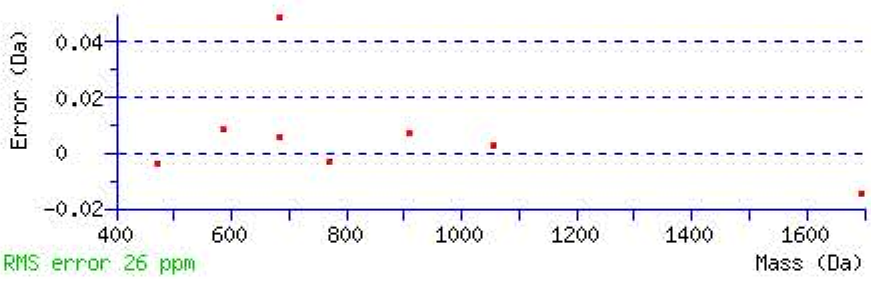
Match to Query 42160: 2137.133216 from(535.290580,4+) rtinseconds(2342) index(33791)
Title: Locus:1.1.1.3479.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

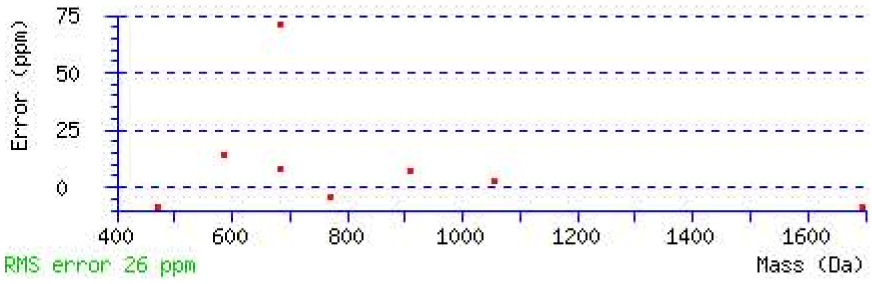
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2137.135406
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 41 **Expect:** 0.0019
Matches : 8/168 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							17
2	157.097154	79.052215					V	2081.121208	1041.064242	2064.094659	1032.550967	2063.110643	1032.058959	16
3	258.144833	129.576055			240.134268	120.570772	T	1982.052794	991.530035	1965.026245	983.016761	1964.042229	982.524753	15
4	345.176861	173.092068			327.166296	164.086786	S	1881.005115	941.006196	1863.978566	932.492921	1862.994550	932.000913	14
5	444.245275	222.626275			426.234710	213.620993	V	1793.973087	897.490182	1776.946538	888.976907	1775.962522	888.484899	13
6	531.277303	266.142290			513.266738	257.137007	S	***1694.904673***	847.955975	1677.878124	839.442700	1676.894108	838.950692	12
7	970.502629	485.754953	953.476080	477.241678	952.492064	476.749670	Q	1607.872645	804.439961	1590.846096	795.926686	1589.862080	795.434678	11
8	1083.586693	542.296985	1066.560144	533.783710	1065.576128	533.291702	I	1168.647319	584.827298	1151.620770	576.314023	1150.636754	575.822015	10
9	1230.655107	615.831192	1213.628558	607.317917	1212.644542	606.825909	F	***1055.563255***	528.285266	1038.536706	519.771991	1037.552690	519.279983	9
10	1367.714019	**684.360648**	1350.687470	675.847373	1349.703454	675.355365	H	***908.494841***	454.751059	891.468292	446.237784	890.484276	445.745776	8
11	1454.746047	727.876662	1437.719498	719.363387	1436.735482	718.871379	S	***771.435929***	386.221603	754.409380	377.708328	753.425364	377.216320	7
12	1551.798811	776.403044	1534.772262	767.889769	1533.788246	767.397761	P	***684.403901***	342.705589	667.377352	334.192314	666.393336	333.700306	6
13	1666.825754	833.916515	1649.799205	825.403241	1648.815189	824.911233	D	***587.351137***	294.179207	570.324588	285.665932	569.340572	285.173924	5
14	1779.909818	890.458547	1762.883269	881.945273	1761.899253	881.453265	L	***472.324194***	236.665735	455.297645	228.152460			4
15	1850.946932	925.977104	1833.920383	917.463830	1832.936367	916.971822	A	359.240130	180.123703	342.213581	171.610429			3
16	1964.030996	982.519136	1947.004447	974.005862	1946.020431	973.513853	I	288.203016	144.605146	271.176467	136.091872			2
17							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of GVTSVSQIFHSPDLAIR
(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	2137.135406	-0.002190	GVTSVSQIFHSPDLAIR

Mascot: http://www.matrixscience.com/

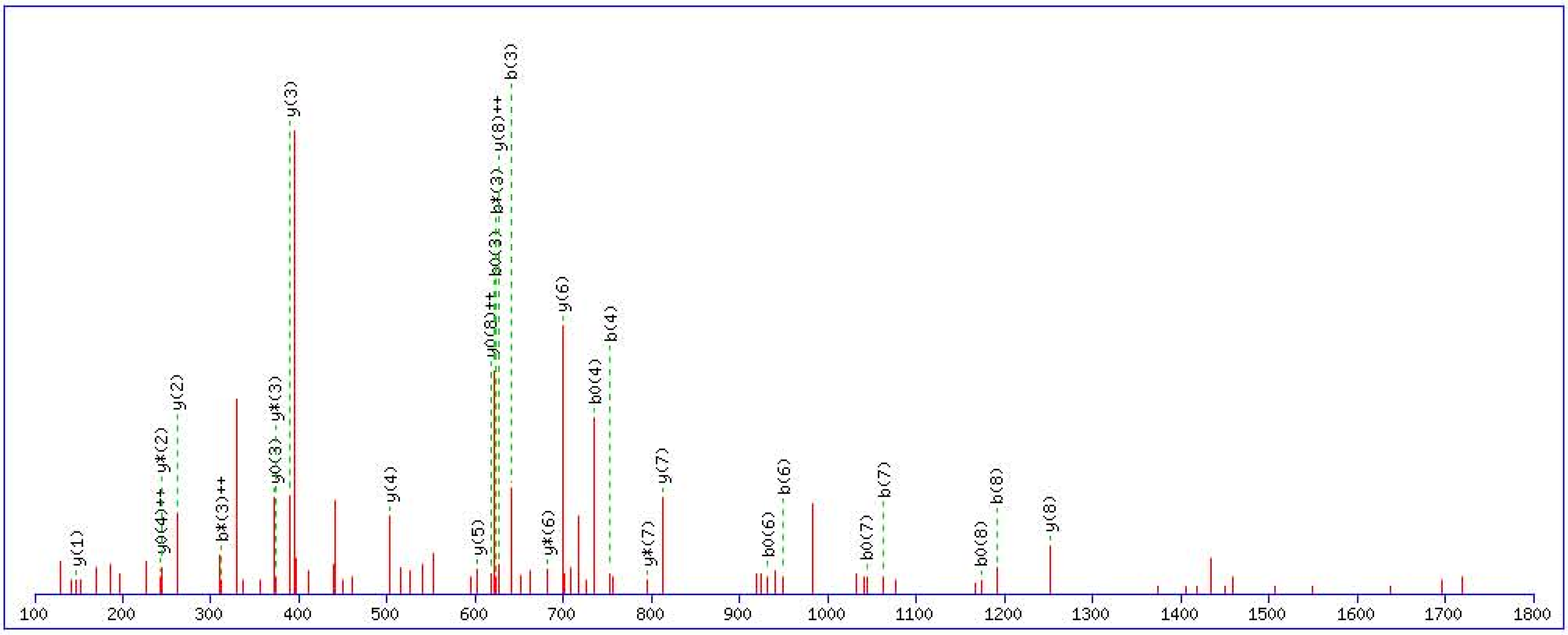
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAQLPVIENK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

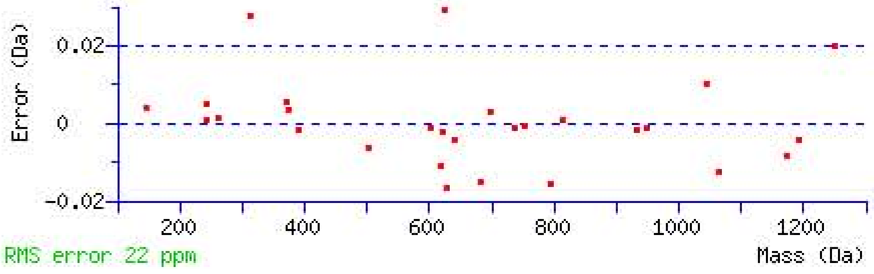
Match to Query 25893: 1450.782108 from(726.398330,2+) rtinseconds(1991) index(19030)
Title: Locus:1.1.1.3259.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

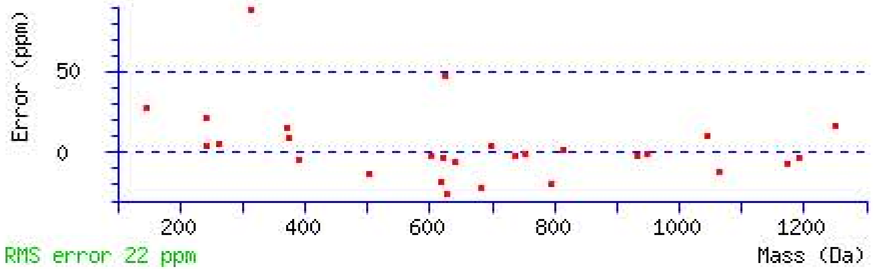
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1450.785355
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 32 **Expect:** 0.014
Matches : 28/100 fragment ions using 71 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
31.6	1450.785355	-0.003247	EAQLPVIENK

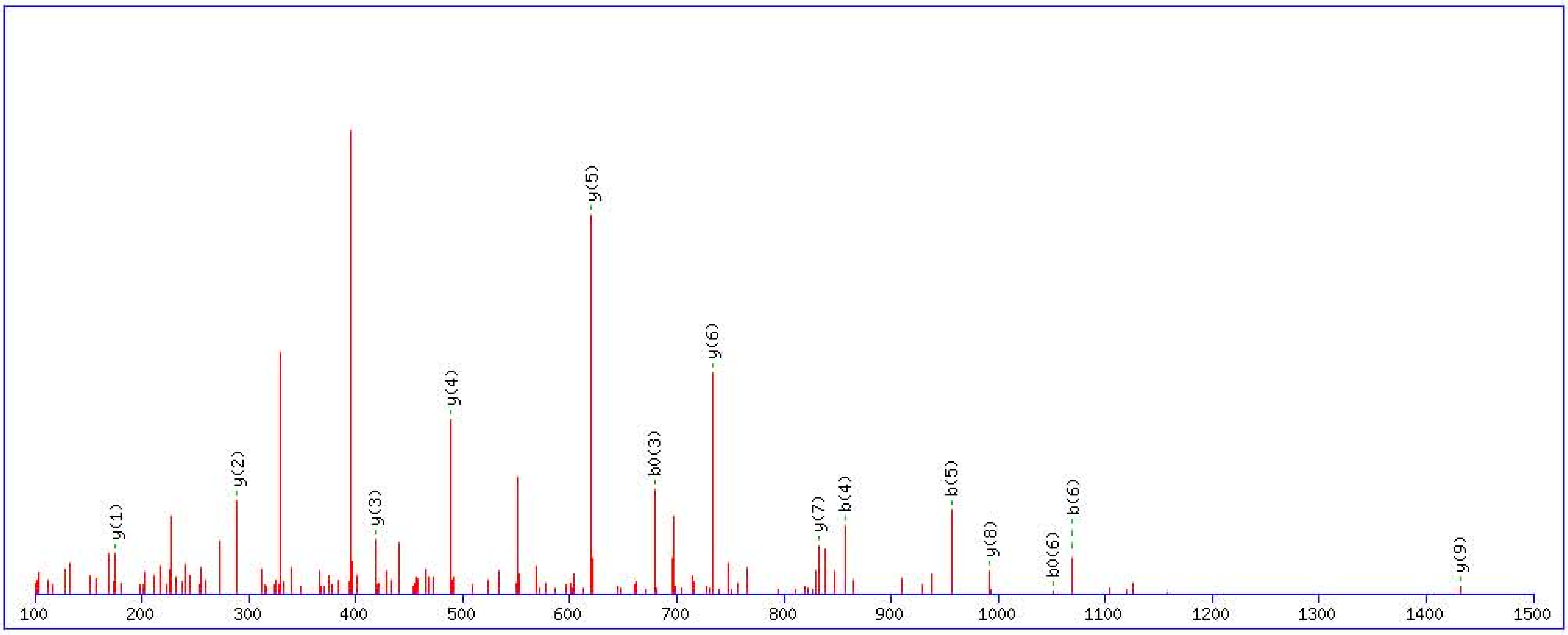
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQQCVIMAENR**
Found in **PLGB_HUMAN**, Plasminogen-like protein B OS=Homo sapiens GN=PLGLB1 PE=1 SV=1

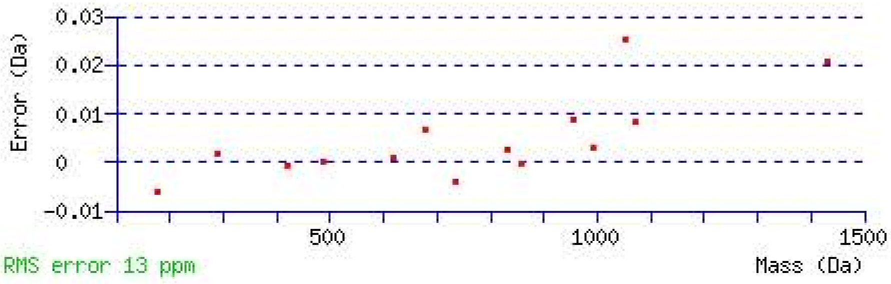
Match to Query 33449: 1687.784052 from(563.601960,3+) rtinseconds(1830) index(59592)
Title: Locus:1.1.1.1549.4 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

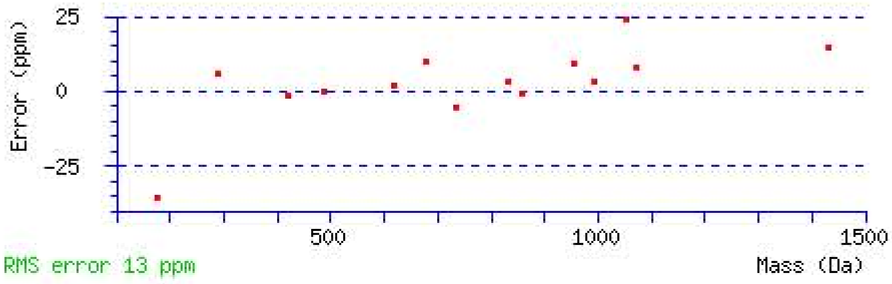
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1687.784393
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 1.9e-006
Matches : 14/114 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	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
61.5	1687.784393	-0.000341	EQQCVIMAENR
59.7	1687.784393	-0.000341	EQQCVIMAENR
0.4	1687.787552	-0.003500	GASEDGEYFLMIRGK

Mascot: http://www.matrixscience.com/

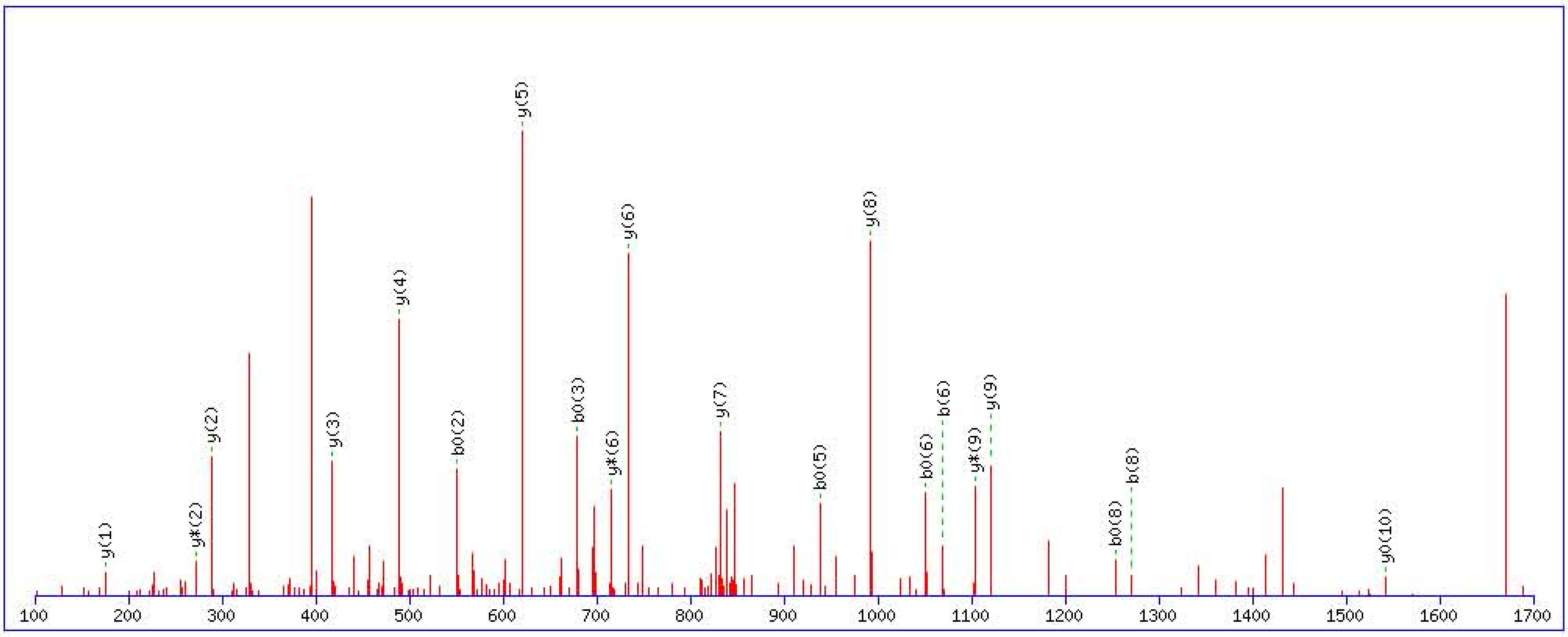
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQQCVIMAENR**
Found in **PLGB_HUMAN**, Plasminogen-like protein B OS=Homo sapiens GN=PLGLB1 PE=1 SV=1

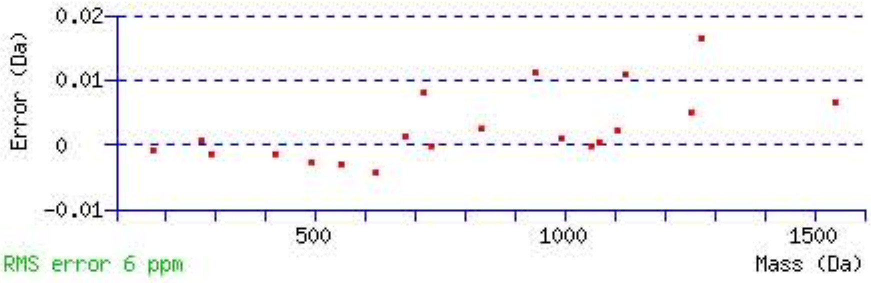
Match to Query 33450: 1687.789148 from(844.901850,2+) rtinseconds(1824) index(59571)
Title: Locus:1.1.1.1546.10 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

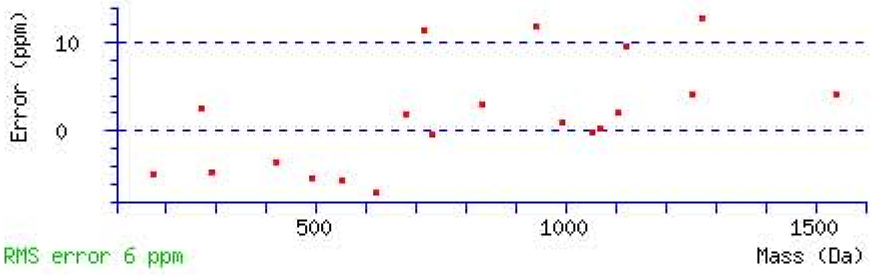
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1687.784393
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 64 **Expect:** 2.7e-006
Matches : 20/114 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	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
63.9	1687.784393	0.004755	EQQCVIMAENR
61.5	1687.784393	0.004755	EQQCVIMAENR
4.2	1687.781006	0.008142	ELMAWNQAENR
2.9	1687.773193	0.015955	FGAVCTCMEKATGLK
1.8	1687.776093	0.013055	QQEEAQAAAAAASAESR
1.5	1687.773666	0.015482	TTGPPSGQMPDNPPHR
0.0	1687.813370	-0.024222	MKQSPALAPEERCR

Mascot: http://www.matrixscience.com/

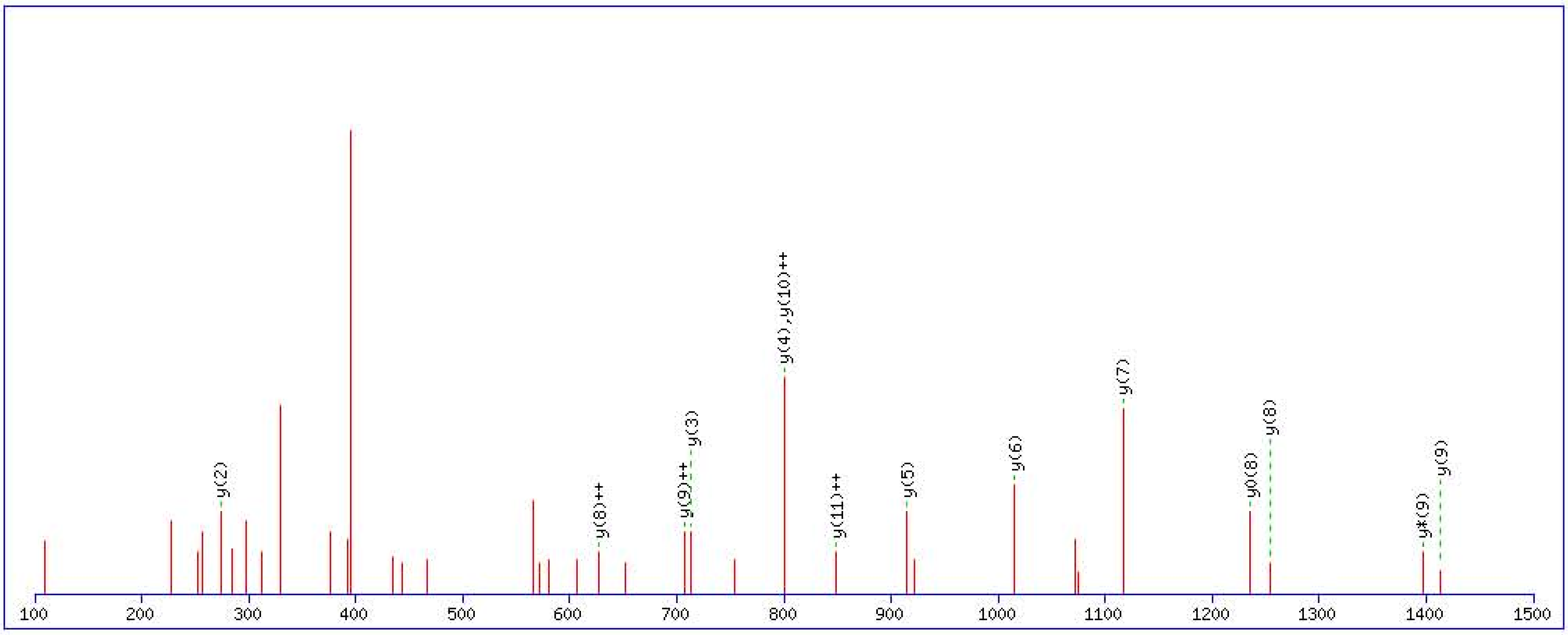
Mascot Search Results

Peptide View

MS/MS Fragmentation of **APWCHTTNSQVR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

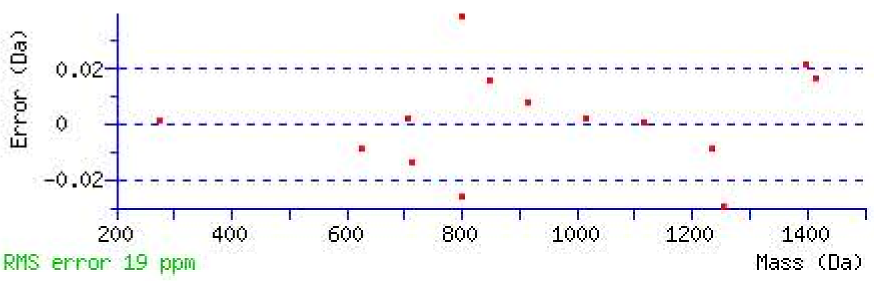
Match to Query 34984: 1766.825922 from(589.949250,3+) rtinseconds(1568) index(29194)
Title: Locus:1.1.1.3209.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

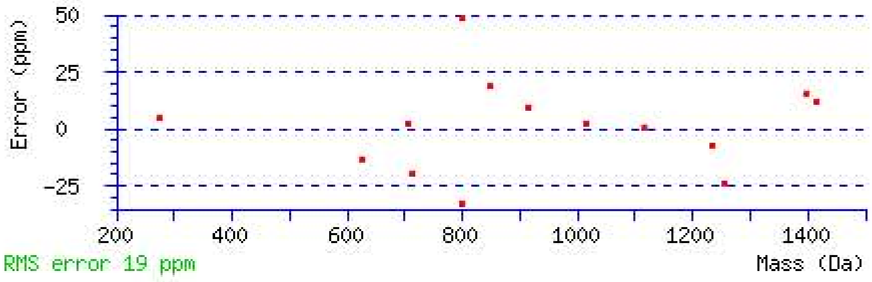
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1766.834488
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10    : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.00019
Matches : 14/102 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	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
49.0	1766.834488	-0.008566	APWCHTTNSQVR

Mascot: http://www.matrixscience.com/

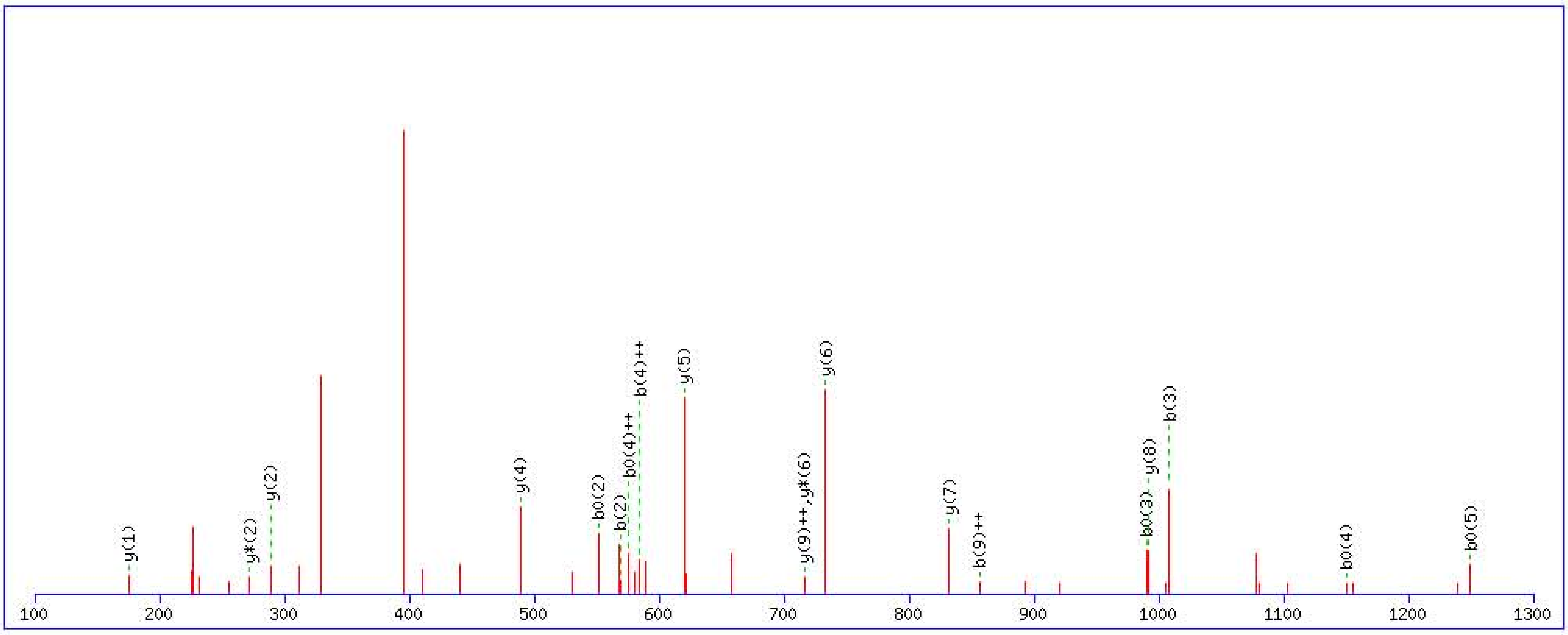
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQQCVIMAENR**
Found in **PLGB_HUMAN**, Plasminogen-like protein B OS=Homo sapiens GN=PLGLB1 PE=1 SV=1

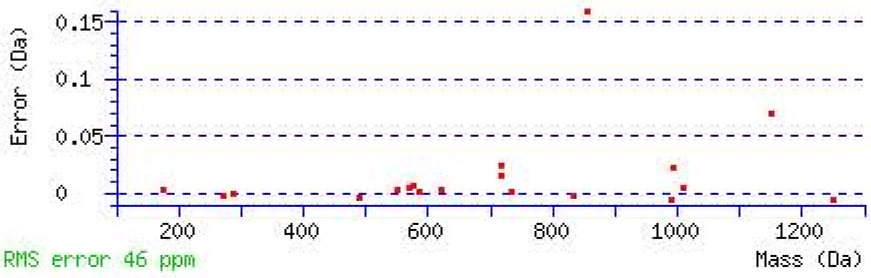
Match to Query 39281: 1998.957132 from(667.326320,3+) rtinseconds(2139) index(61312)
Title: Locus:1.1.1.1656.17 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

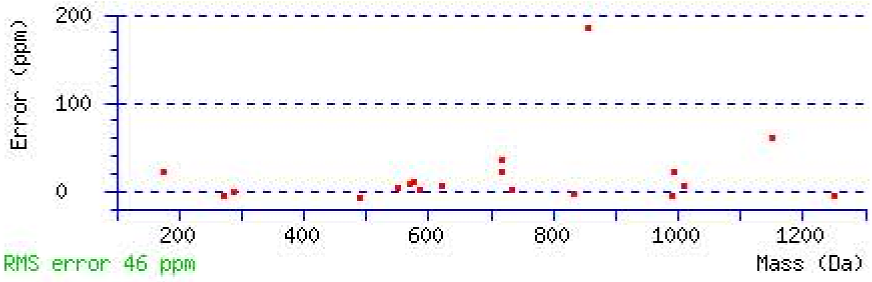
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 28  Expect: 0.0028
Matches : 19/114 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	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
28.2	1998.951141	0.005991	EQQCVIMAENR
1.0	1998.929138	0.027994	YEMLQDNVEGYRR
0.1	1998.932526	0.024606	NVMNKVSEMSSFQR

Mascot: http://www.matrixscience.com/

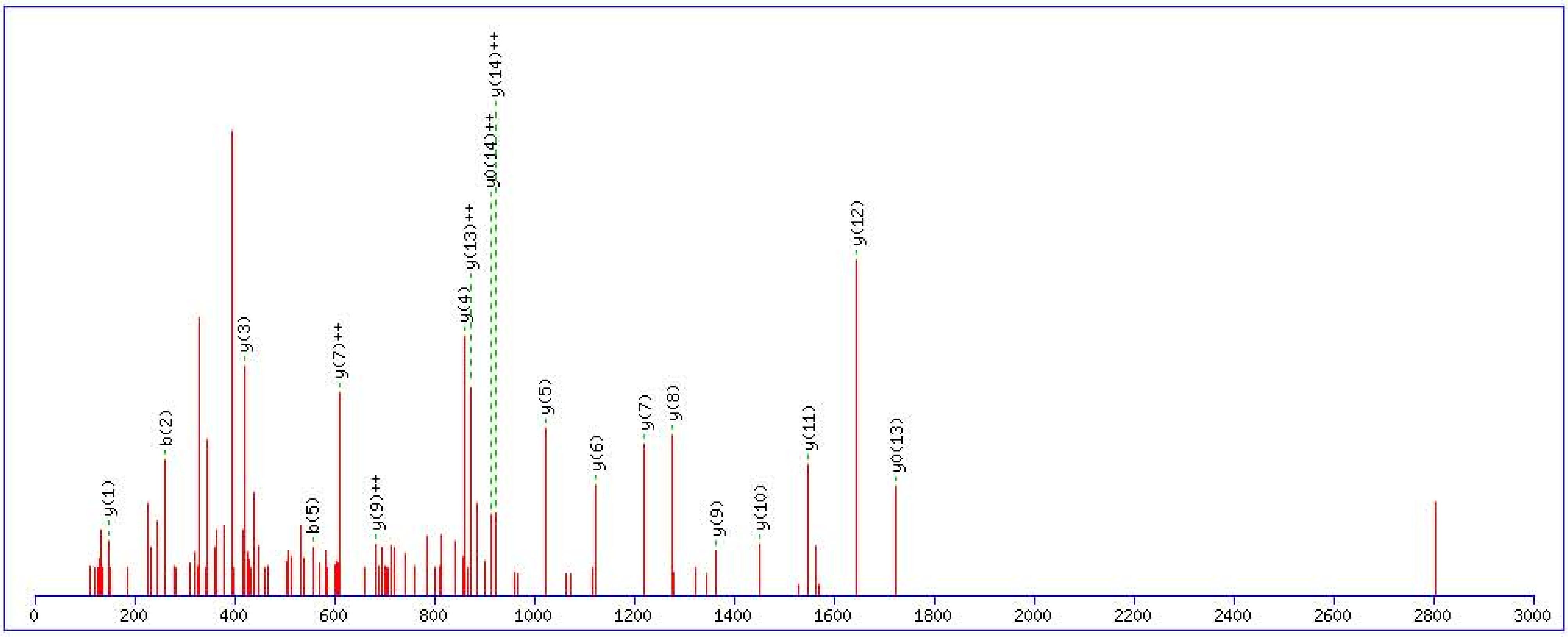
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **CTTPPPSSGPTYQCLK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

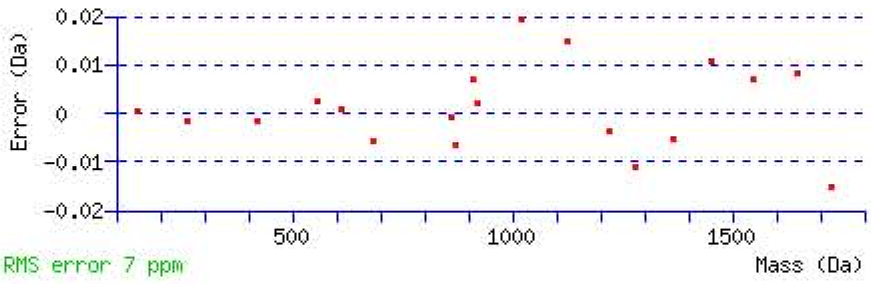
Match to Query 41683: 2103.980472 from(702.334100,3+) rtinseconds(1757) index(59225)
Title: Locus:1.1.1.1523.9 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

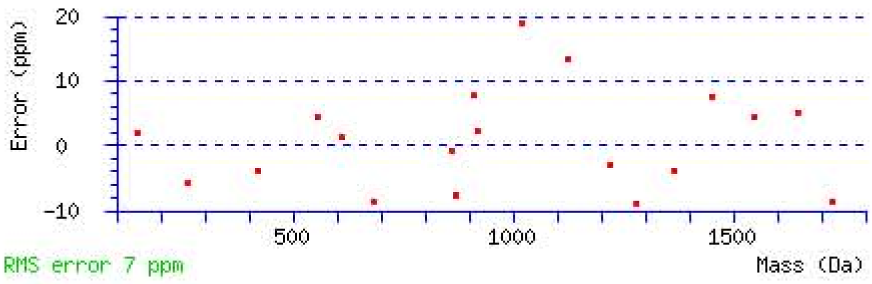
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2103.979172
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 75  Expect: 4.2e-007
Matches : 19/144 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	161.037925	81.022600					C							16
2	**262.085604**	131.546440			244.075039	122.541158	T	1944.955785	972.981531	1927.929236	964.468256	1926.945220	963.976248	15
3	363.133283	182.070280			345.122718	173.064997	T	1843.908106	922.457691	1826.881557	913.944417	1825.897541	913.452409	14
4	460.186047	230.596661			442.175482	221.591379	P	1742.860427	871.933852	1725.833878	863.420577	1724.849862	862.928569	13
5	**557.238811**	279.123044			539.228246	270.117761	P	***1645.807663***	823.407470	1628.781114	814.894195	1627.797098	814.402187	12
6	654.291575	327.649426			636.281010	318.644143	P	***1548.754899***	774.881088	1531.728350	766.367813	1530.744334	765.875805	11
7	741.323603	371.165440			723.313038	362.160157	S	***1451.702135***	726.354706	1434.675586	717.841431	1433.691570	717.349423	10
8	828.355631	414.681454			810.345066	405.676171	S	***1364.670107***	682.838692	1347.643558	674.325417	1346.659542	673.833409	9
9	885.377095	443.192186			867.366530	434.186903	G	***1277.638079***	639.322678	1260.611530	630.809403	1259.627514	630.317395	8
10	982.429859	491.718568			964.419294	482.713285	P	***1220.616615***	610.811946	1203.590066	602.298671	1202.606050	601.806663	7
11	1083.477538	542.242407			1065.466973	533.237125	T	***1123.563851***	562.285564	1106.537302	553.772289	1105.553286	553.280281	6
12	1246.540867	623.774072			1228.530302	614.768789	Y	***1022.516172***	511.761724	1005.489623	503.248450			5
13	1685.766193	843.386735	1668.739644	834.873460	1667.755628	834.381452	Q	***859.452843***	430.230060	842.426294	421.716785			4
14	1845.796842	923.402059	1828.770293	914.888785	1827.786277	914.396777	C	***420.227517***	210.617396	403.200968	202.104122			3
15	1958.880906	979.944091	1941.854357	971.430817	1940.870341	970.938809	L	260.196868	130.602072	243.170319	122.088797			2
16							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of CTTPPPSSGPTYQCLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
75.1	2103.979172	0.001300	CTTPPPSSGPTYQCLK
7.0	2103.964554	0.015918	TAADTPAIMNWDLFFTMK

Mascot: http://www.matrixscience.com/

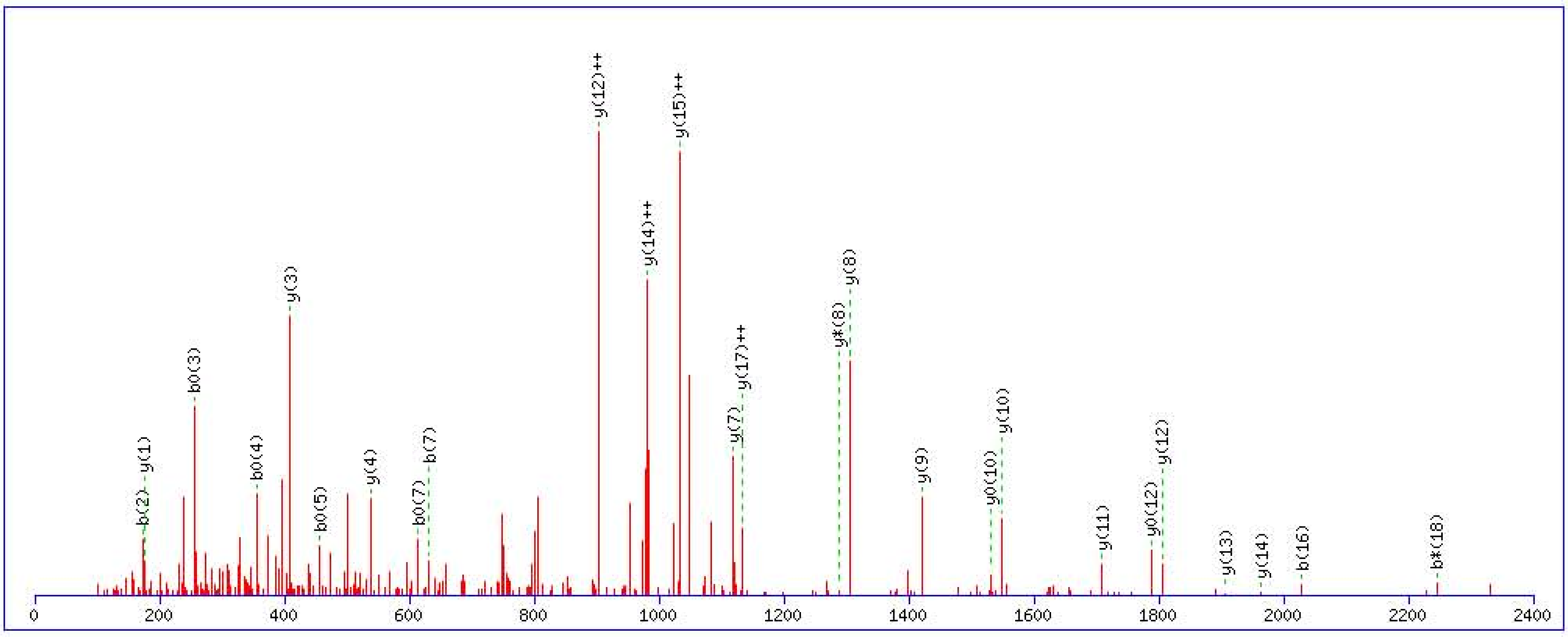
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ATTVTGTPCQDWAAQEPHR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

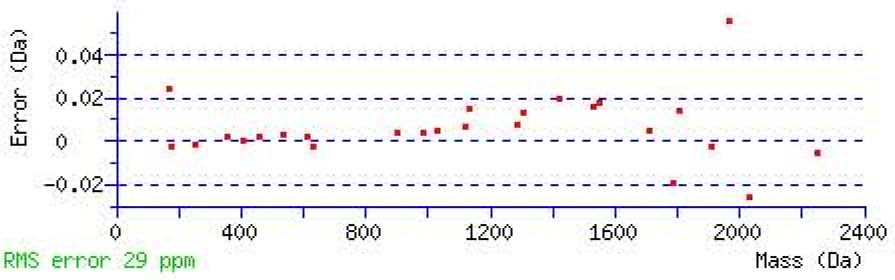
Match to Query 47056: 2436.139272 from(813.053700,3+) rtinseconds(1875) index(59749)
Title: Locus:1.1.1.1564.10 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

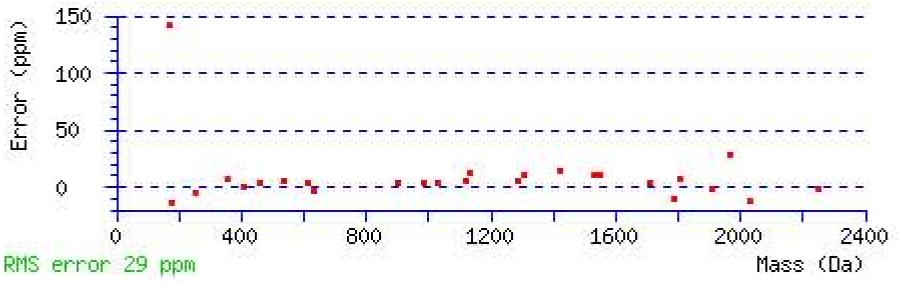
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 67  Expect: 3.3e-006
Matches : 26/190 fragment ions using 42 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
66.8	2436.131470	0.007802	ATTVTGTPCQDWAAQEPHR
35.0	2436.131470	0.007802	ATTVTGTPCQDWAAQEPHR

Mascot: http://www.matrixscience.com/

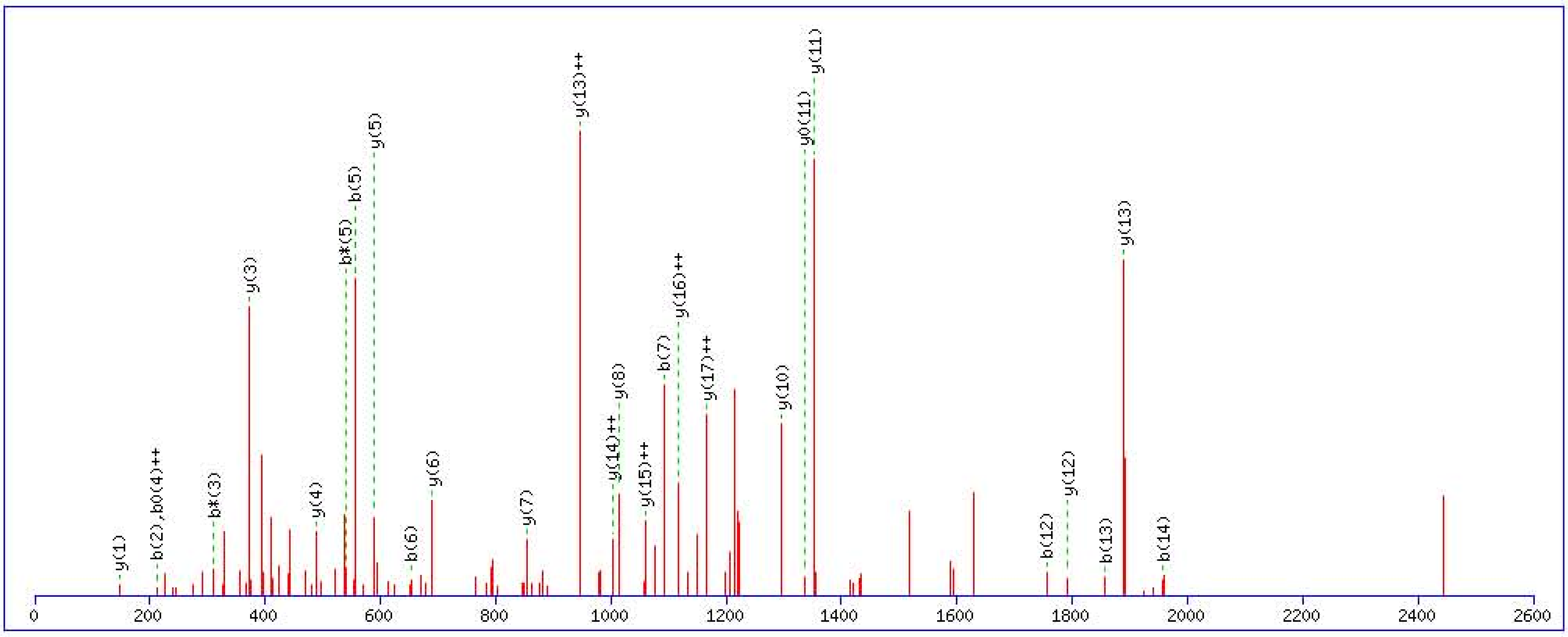
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPDNDPQGPWCYTTDPEK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

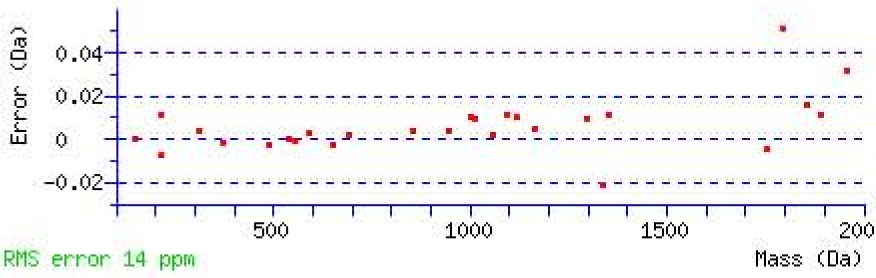
Match to Query 47178: 2444.045488 from(1223.030020,2+) rtinseconds(2102) index(61114)
Title: Locus:1.1.1.1643.11 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

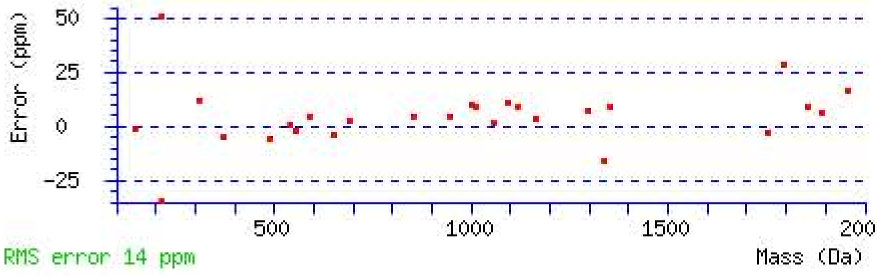
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2444.041306
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 5.8e-006
Matches : 27/198 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	115.050203	58.028740	98.023654	49.515465			N							18
2	**212.102967**	106.555121	195.076418	98.041847			P	2331.005648	1166.006462	2313.979099	1157.493187	2312.995083	1157.001179	17
3	327.129910	164.068593	310.103361	155.555319	309.119345	155.063311	D	2233.952884	1117.480080	2216.926335	1108.966805	2215.942319	1108.474797	16
4	441.172837	221.090057	424.146288	212.576782	423.162272	212.084774	N	2118.925941	1059.966608	2101.899392	1051.453334	2100.915376	1050.961326	15
5	**556.199780**	278.603528	539.173231	270.090254	538.189215	269.598246	D	2004.883014	1002.945145	1987.856465	994.431871	1986.872449	993.939863	14
6	**653.252544**	327.129910	636.225995	318.616636	635.241979	318.124628	P	***1889.856071***	945.431673	1872.829522	936.918399	1871.845506	936.426391	13
7	**1092.477870**	546.742573	1075.451321	538.229299	1074.467305	537.737290	Q	***1792.803307***	896.905291	1775.776758	888.392017	1774.792742	887.900009	12
8	1149.499334	575.253305	1132.472785	566.740030	1131.488769	566.248022	G	***1353.577981***	677.292629	1336.551432	668.779354	1335.567416	668.287346	11
9	1246.552098	623.779687	1229.525549	615.266413	1228.541533	614.774404	P	***1296.556517***	648.781897	1279.529968	640.268622	1278.545952	639.776614	10
10	1432.631411	716.819343	1415.604862	708.306069	1414.620846	707.814061	W	1199.503753	600.255515	1182.477204	591.742240	1181.493188	591.250232	9
11	1592.662060	796.834668	1575.635511	788.321394	1574.651495	787.829385	C	***1013.424440***	507.215858	996.397891	498.702584	995.413875	498.210576	8
12	**1755.725389**	878.366333	1738.698840	869.853058	1737.714824	869.361050	Y	***853.393791***	427.200534	836.367242	418.687259	835.383226	418.195251	7
13	**1856.773068**	928.890172	1839.746519	920.376898	1838.762503	919.884889	T	***690.330462***	345.668869	673.303913	337.155595	672.319897	336.663587	6
14	**1957.820747**	979.414012	1940.794198	970.900737	1939.810182	970.408729	T	***589.282783***	295.145030	572.256234	286.631755	571.272218	286.139747	5
15	2072.847690	1036.927483	2055.821141	1028.414208	2054.837125	1027.922200	D	***488.235104***	244.621190	471.208555	236.107915	470.224539	235.615907	4
16	2169.900454	1085.453865	2152.873905	1076.940590	2151.889889	1076.448582	P	***373.208161***	187.107719	356.181612	178.594444	355.197596	178.102436	3
17	2298.943047	1149.975161	2281.916498	1141.461887	2280.932482	1140.969879	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
18							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of NPDNDPQGPWCYTTDPEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.7	2444.041306	0.004182	NPDNDPQGPWCYTTDPEK

Mascot: http://www.matrixscience.com/

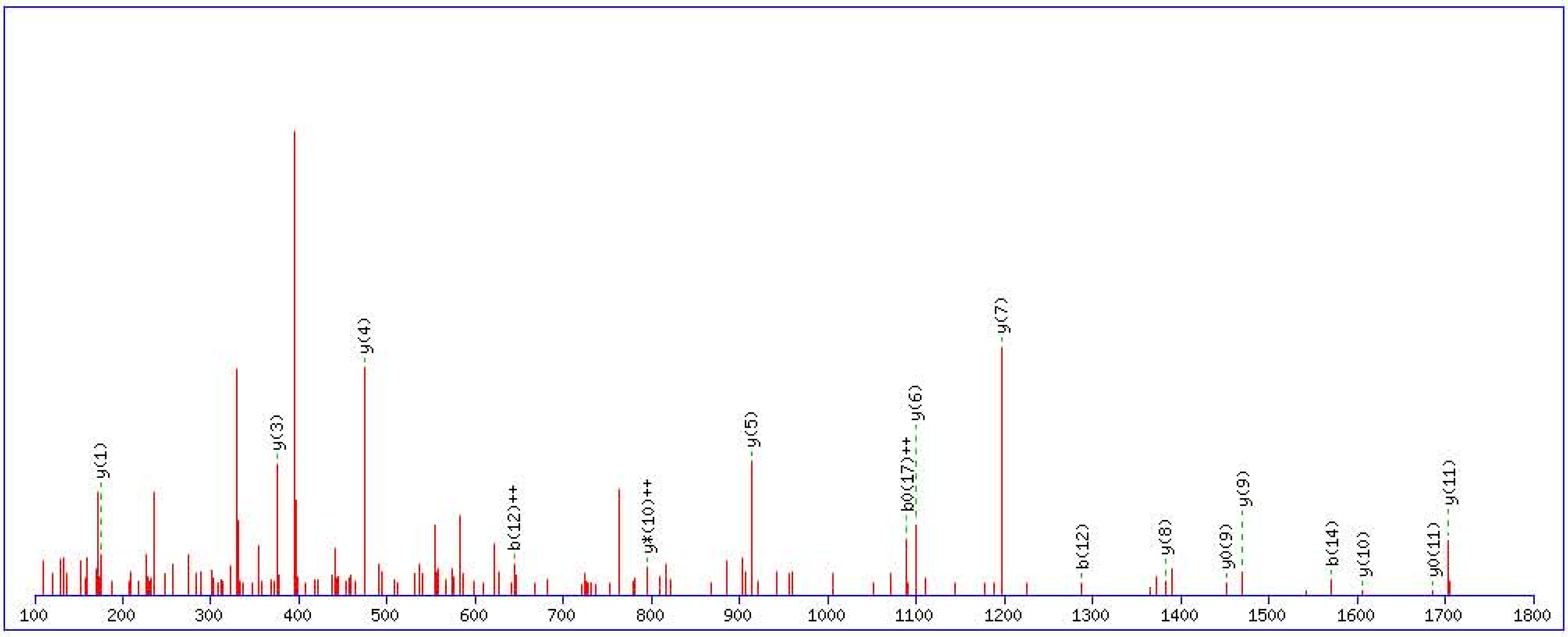
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVGGCVAHPHSWPWQVSLR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

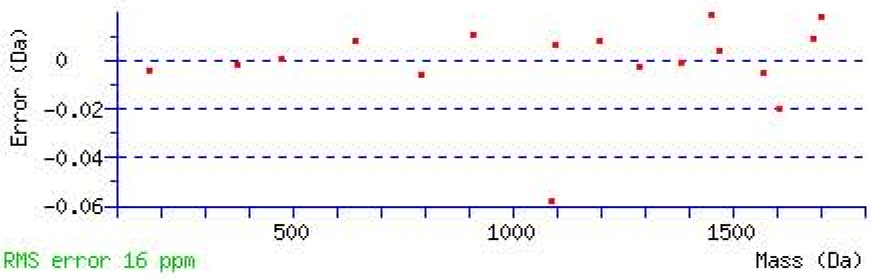
Match to Query 47998: 2482.254616 from(621.570930,4+) rtinseconds(2213) index(61710)
Title: Locus:1.1.1.1682.12 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

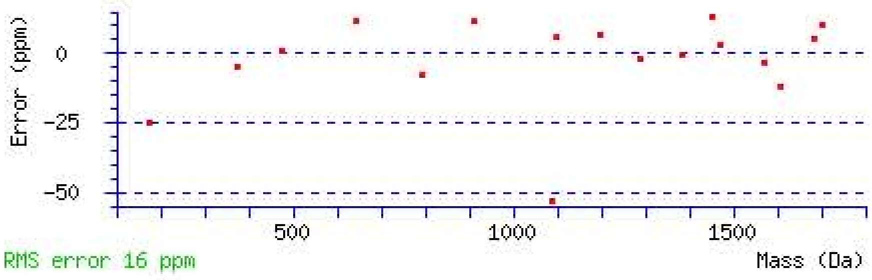
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2482.251480
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15     : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.00068
Matches : 17/164 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	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
35.6	2482.251480	0.003136	VVGGCVAHPHSWPWQVSLR
1.8	2482.232178	0.022438	SFCAAVLQGASFVRLGGRSCSPR

Mascot: http://www.matrixscience.com/

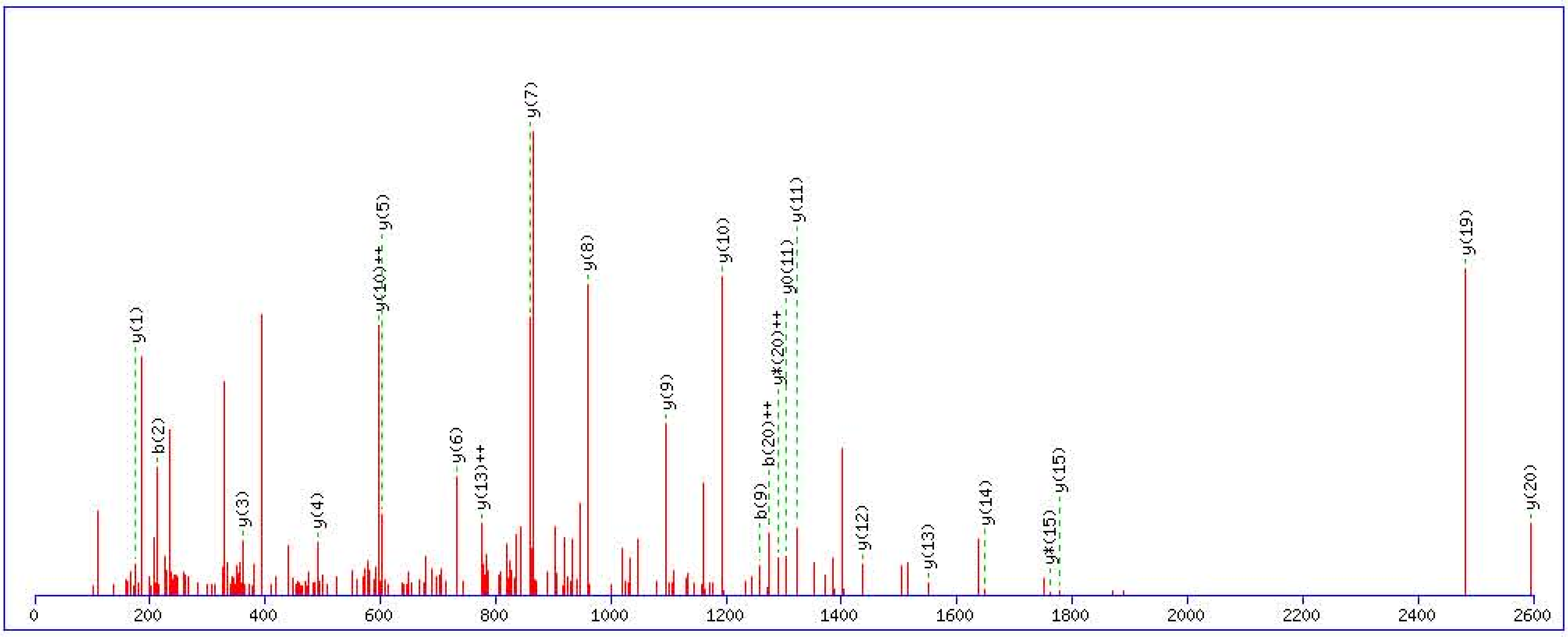
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VILGAHQEVNLEPHVQEIEVSR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

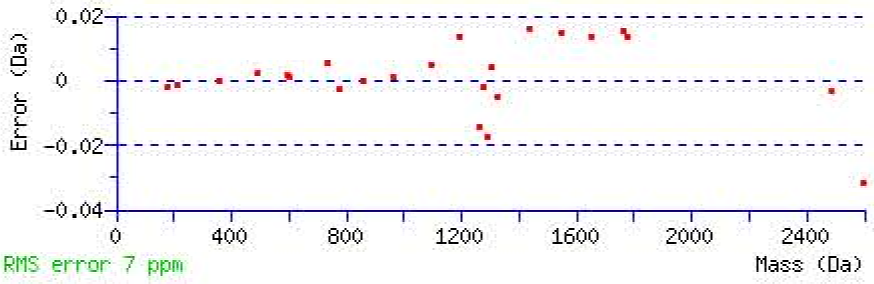
Match to Query 51626: 2806.488416 from(702.629380,4+) rtinseconds(2109) index(61151)
Title: Locus:1.1.1.1646.6 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

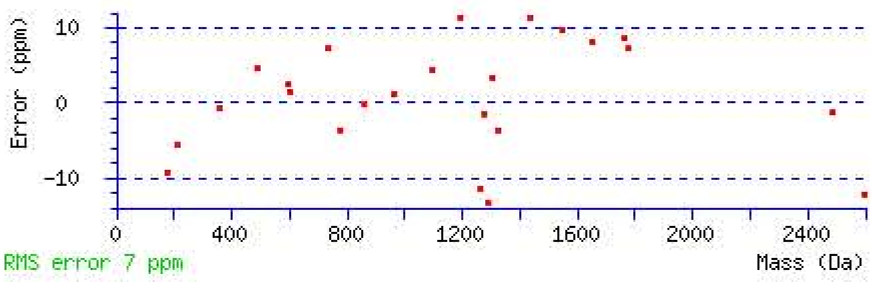
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2806.479965
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 84  Expect: 8.2e-008
Matches : 24/224 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	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	1030.586634	515.796955	1013.560085	507.283681			Q	2217.133229	1109.070252	2200.106680	1100.556978	2199.122664	1100.064970	16
8	1159.629227	580.318252	1142.602678	571.804977	1141.618662	571.312969	E	***1777.907903***	889.457590	1760.881354	880.944315	1759.897338	880.452307	15
9	**1258.697641**	629.852459	1241.671092	621.339184	1240.687076	620.847176	V	***1648.865310***	824.936293	1631.838761	816.423019	1630.854745	815.931011	14
10	1372.740568	686.873922	1355.714019	678.360648	1354.730003	677.868640	N	***1549.796896***	775.402086	1532.770347	766.888812	1531.786331	766.396804	13
11	1485.824632	743.415954	1468.798083	734.902680	1467.814067	734.410672	L	***1435.753969***	718.380623	1418.727420	709.867348	1417.743404	709.375340	12
12	1614.867225	807.937251	1597.840676	799.423976	1596.856660	798.931968	E	***1322.669905***	661.838591	1305.643356	653.325316	1304.659340	652.833308	11
13	1711.919989	856.463633	1694.893440	847.950358	1693.909424	847.458350	P	***1193.627312***	597.317294	1176.600763	588.804020	1175.616747	588.312012	10
14	1848.978901	924.993089	1831.952352	916.479814	1830.968336	915.987806	H	***1096.574548***	548.790912	1079.547999	540.277638	1078.563983	539.785630	9
15	1948.047315	974.527296	1931.020766	966.014021	1930.036750	965.522013	V	***959.515636***	480.261456	942.489087	471.748182	941.505071	471.256174	8
16	2076.105893	1038.556584	2059.079344	1030.043310	2058.095328	1029.551302	Q	***860.447222***	430.727249	843.420673	422.213975	842.436657	421.721967	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
84.0	2806.479965	0.008451	VILGAHQEVNLEPHVQEIEVSR
12.0	2806.479965	0.008451	VILGAHQEVNLEPHVQEIEVSR

Mascot: http://www.matrixscience.com/

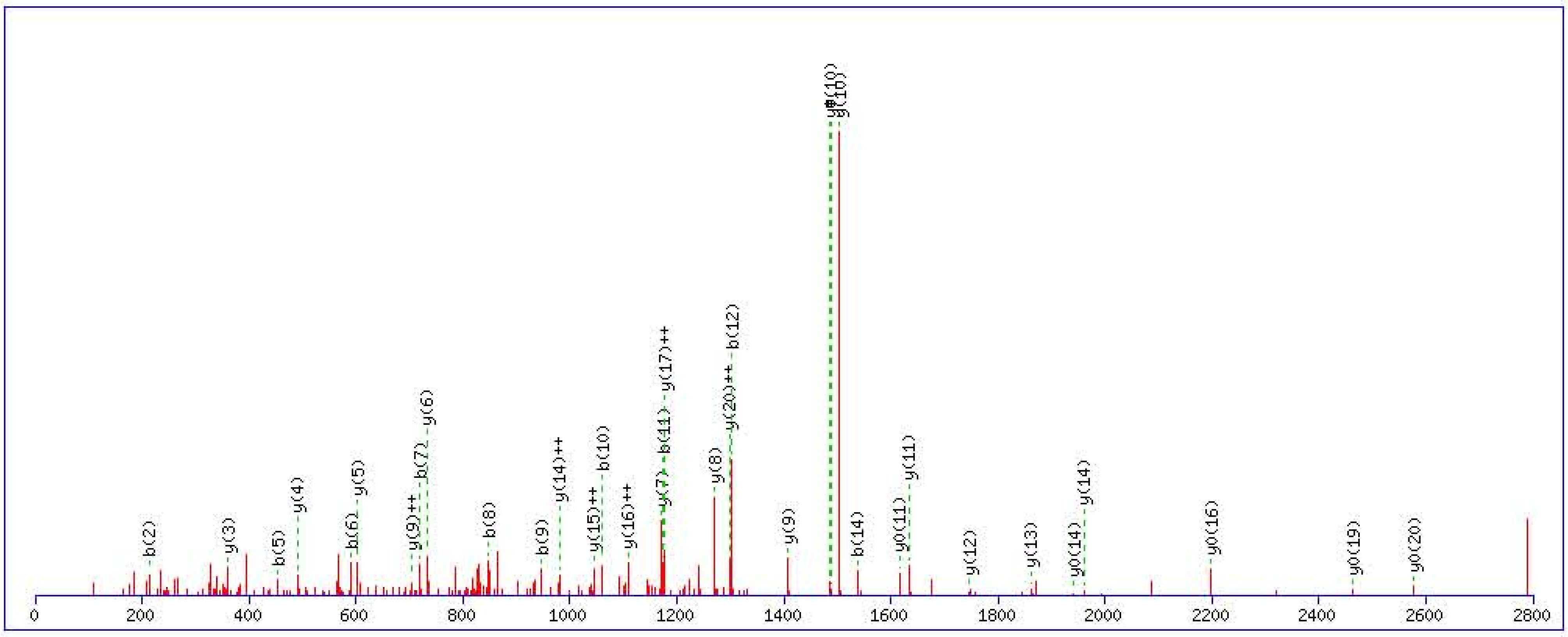
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VILGAHQEVNLEPHVQEIEVSR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

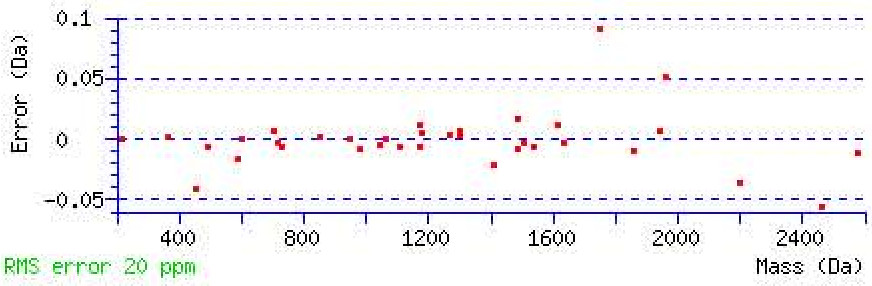
Match to Query 51628: 2806.491132 from(936.504320,3+) rtinseconds(2068) index(60951)
Title: Locus:1.1.1.1631.15 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

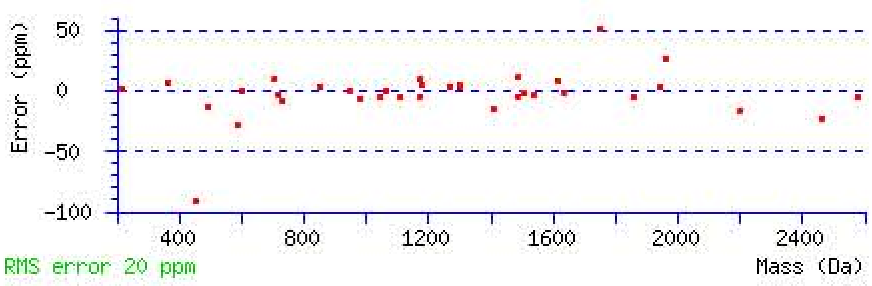
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2806.479965
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16     : Biotin:Thermo-21345 (Q)
Ions Score: 73  Expect: 1.6e-007
Matches : 35/224 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	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
72.7	2806.479965	0.011167	VILGAHQEVNLEPHVQEIEVSR
0.1	2806.476791	0.014341	LYLYAAHDVTFIPLLMTLGIFDHK

Mascot: http://www.matrixscience.com/

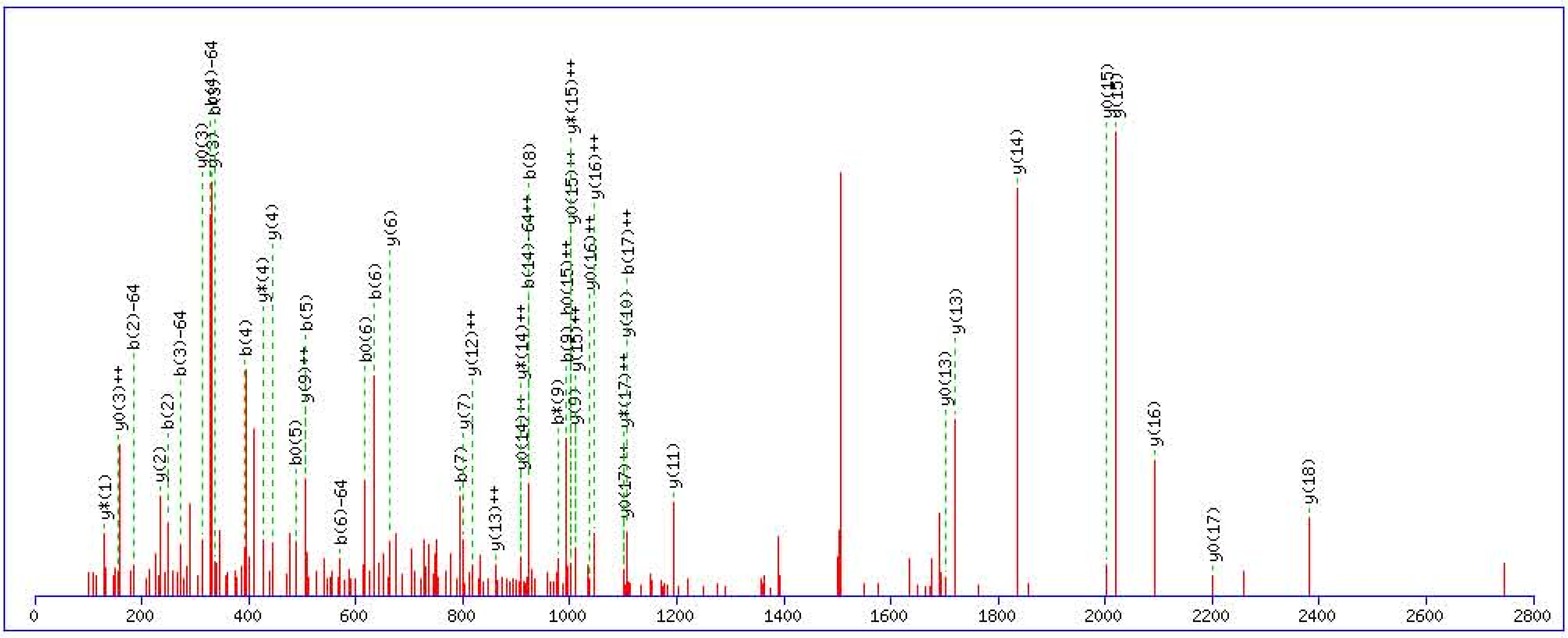
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TMSGLECQAWDSQSPHAHGYIPSK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

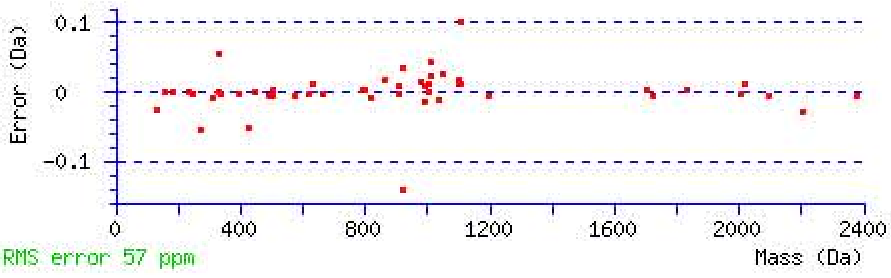
Match to Query 54098: 3013.365016 from(754.348530,4+) rtinseconds(1872) index(59739)
Title: Locus:1.1.1.1563.9 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

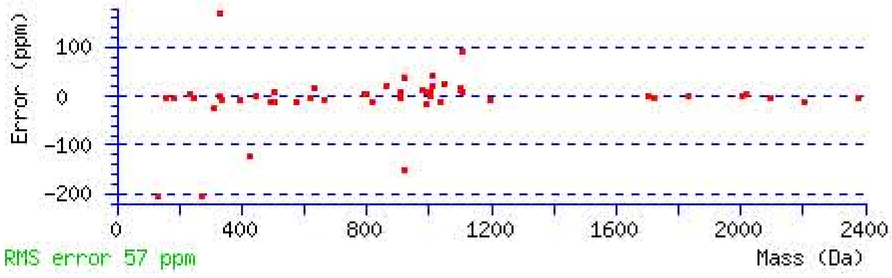
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3013.352081
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
Q13 : Biotin:Thermo-21345 (Q)
Ions Score: 46 **Expect:** 0.0003
Matches : 50/386 fragment ions using 129 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	***249.090355***	125.048815			231.079790	116.043533	M	2913.311683	1457.159480	2896.285134	1448.646205	2895.301118	1448.154197	23
3	***336.122383***	168.564829			318.111818	159.559547	S	2766.276283	1383.641780	2749.249734	1375.128505	2748.265718	1374.636497	22
4	***393.143847***	197.075561			375.133282	188.070279	G	2679.244255	1340.125765	2662.217706	1331.612491	2661.233690	1331.120483	21
5	***506.227911***	253.617593			488.217346	244.612311	L	2622.222791	1311.615034	2605.196242	1303.101759	2604.212226	1302.609751	20
6	***635.270504***	318.138890			617.259939	309.133608	E	2509.138727	1255.073001	2492.112178	1246.559727	2491.128162	1246.067719	19
7	***795.301153***	398.154215			777.290588	389.148932	C	***2380.096134***	1190.551705	2363.069585	1182.038430	2362.085569	1181.546422	18
8	***923.359731***	462.183504	906.333182	453.670229	905.349166	453.178221	Q	2220.065485	1110.536381	2203.038936	1102.023106	2202.054920	1101.531098	17
9	***994.396845***	497.702061	977.370296	489.188786	976.386280	488.696778	A	***2092.006907***	1046.507091	2074.980358	1037.993817	2073.996342	1037.501809	16
10	1180.476158	590.741717	1163.449609	582.228443	1162.465593	581.736435	W	***2020.969793***	1010.988535	2003.943244	1002.475260	2002.959228	1001.983252	15
11	1295.503101	648.255189	1278.476552	639.741914	1277.492536	639.249906	D	***1834.890480***	917.948878	1817.863931	909.435604	1816.879915	908.943596	14
12	1382.535129	691.771203	1365.508580	683.257928	1364.524564	682.765920	S	***1719.863537***	860.435407	1702.836988	851.922132	1701.852972	851.430124	13
13	1821.760455	911.383866	1804.733906	902.870591	1803.749890	902.378583	Q	1632.831509	816.919393	1615.804960	808.406118	1614.820944	807.914110	12
14	1908.792483	954.899880	1891.765934	946.386605	1890.781918	945.894597	S	***1193.606183***	597.306730	1176.579634	588.793455	1175.595618	588.301447	11
15	2005.845247	1003.426262	1988.818698	994.912987	1987.834682	994.420979	P	***1106.574155***	553.790716	1089.547606	545.277441	1088.563590	544.785433	10
16	2142.904159	1071.955718	2125.877610	1063.442443	2124.893594	1062.950435	H	***1009.521391***	505.264334	992.494842	496.751059	991.510826	496.259051	9
17	2213.941273	1107.474275	2196.914724	1098.961000	2195.930708	1098.468992	A	872.462479	436.734878	855.435930	428.221603	854.451914	427.729595	8
18	2351.000185	1176.003731	2333.973636	1167.490456	2332.989620	1166.998448	H	***801.425365***	401.216321	784.398816	392.703046	783.414800	392.211038	7
19	2408.021649	1204.514463	2390.995100	1196.001188	2390.011084	1195.509180	G	***664.366453***	332.686865	647.339904	324.173590	646.355888	323.681582	6
20	2571.084978	1286.046127	2554.058429	1277.532853	2553.074413	1277.040845	Y	607.344989	304.176133	590.318440	295.662858	589.334424	295.170850	5
21	2684.169042	1342.588159	2667.142493	1334.074885	2666.158477	1333.582877	I	***444.281660***	222.644468	427.255111	214.131194	426.271095	213.639186	4
22	2781.221806	1391.114541	2764.195257	1382.601267	2763.211241	1382.109259	P	***331.197596***	166.102436	314.171047	157.589162	313.187031	157.097154	3
23	2868.253834	1434.630555	2851.227285	1426.117281	2850.243269	1425.625273	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
45.8	3013.352081	0.012935	TMSGLECQAWDSQSPHAHGYIPSK
18.0	3013.352081	0.012935	TMSGLECQAWDSQSPHAHGYIPSK

Mascot: http://www.matrixscience.com/

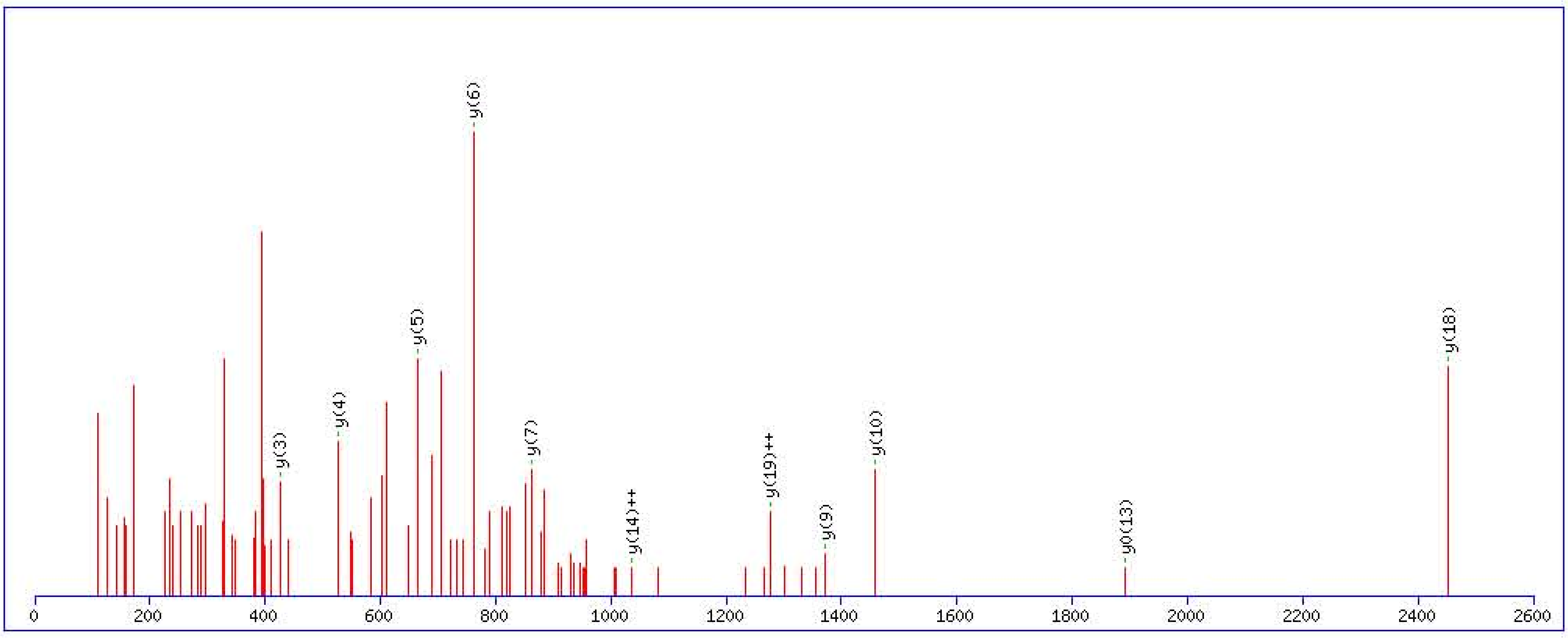
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNVAVTVSGHTCQHWSAQTPHTHNR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

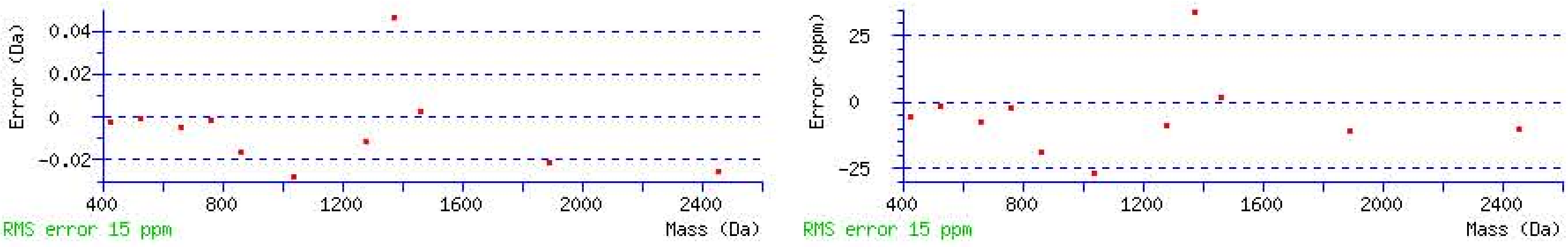
Match to Query 54684: 3092.452770 from(619.497830,5+) rtinseconds(1437) index(57574)
Title: Locus:1.1.1.1411.15 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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): 3092.457016
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18 : Biotin:Thermo-21345 (Q)
Ions Score: 50 **Expect:** 0.0002
Matches : 11/270 fragment ions using 15 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
49.5	3092.457016	-0.004246	GNVAVTVSGHTCQHWSAQTPHTHNR
26.3	3092.457016	-0.004246	GNVAVTVSGHTCQHWSAQTPHTHNR

Mascot: http://www.matrixscience.com/

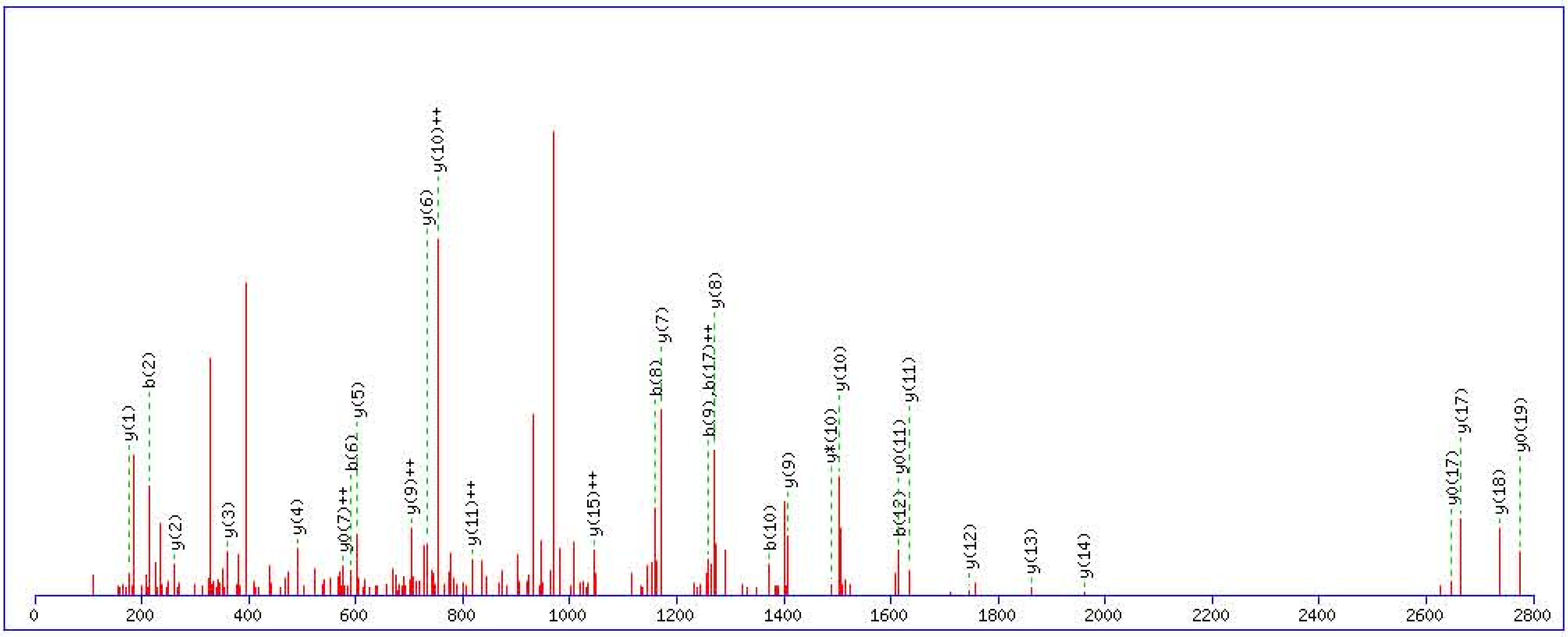
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VILGAHQEVNLEPHVQEIEVSR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

Match to Query 54796: 3117.662536 from(780.422910,4+) rtinseconds(2245) index(61967)
Title: Locus:1.1.1.1693.21 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\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 ●



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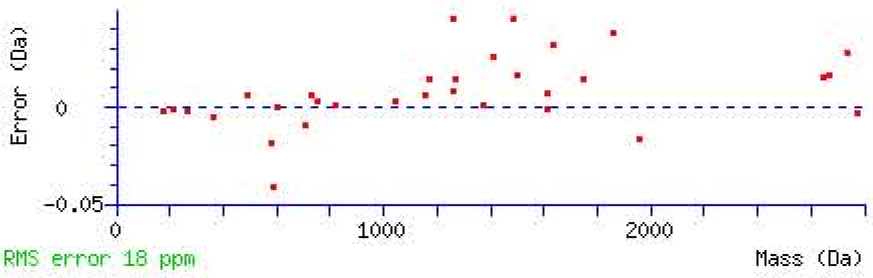
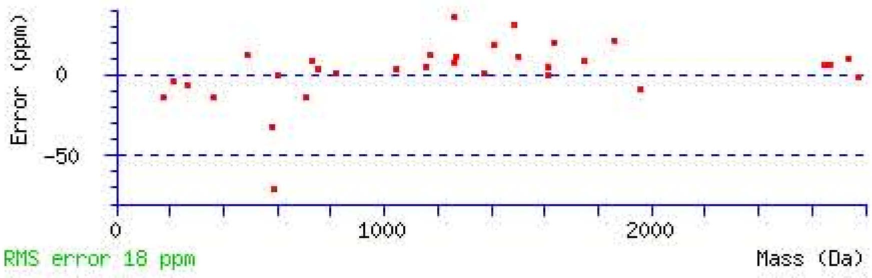
Monoisotopic mass of neutral peptide Mr(calc): 3117.646713
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Q16     : Biotin:Thermo-21345 (Q)
Ions Score: 73  Expect: 7.4e-007
Matches : 32/224 fragment ions using 72 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	3019.585595	1510.296435	3002.559046	1501.783161	3001.575030	1501.291153	21
3	326.243818	163.625547					L	2906.501531	1453.754403	2889.474982	1445.241129	2888.490966	1444.749121	20
4	383.265282	192.136279					G	2793.417467	1397.212371	2776.390918	1388.699097	2775.406902	1388.207089	19
5	454.302396	227.654836					A	2736.396003	1368.701639	2719.369454	1360.188365	2718.385438	1359.696357	18
6	591.361308	296.184292					H	2665.358889	1333.183082	2648.332340	1324.669808	2647.348324	1324.177800	17
7	1030.586634	515.796955	1013.560085	507.283681			Q	2528.299977	1264.653627	2511.273428	1256.140352	2510.289412	1255.648344	16
8	1159.629227	580.318252	1142.602678	571.804977	1141.618662	571.312969	E	2089.074651	1045.040963	2072.048102	1036.527689	2071.064086	1036.035681	15
9	1258.697641	629.852459	1241.671092	621.339184	1240.687076	620.847176	V	1960.032058	980.519667	1943.005509	972.006393	1942.021493	971.514385	14
10	1372.740568	686.873922	1355.714019	678.360648	1354.730003	677.868640	N	1860.963644	930.985460	1843.937095	922.472186	1842.953079	921.980178	13
11	1485.824632	743.415954	1468.798083	734.902680	1467.814067	734.410672	L	1746.920717	873.963997	1729.894168	865.450722	1728.910152	864.958714	12
12	1614.867225	807.937251	1597.840676	799.423976	1596.856660	798.931968	E	1633.836653	817.421965	1616.810104	808.908690	1615.826088	808.416682	11
13	1711.919989	856.463633	1694.893440	847.950358	1693.909424	847.458350	P	1504.794060	752.900668	1487.767511	744.387394	1486.783495	743.895386	10
14	1848.978901	924.993089	1831.952352	916.479814	1830.968336	915.987806	H	1407.741296	704.374286	1390.714747	695.861012	1389.730731	695.369004	9
15	1948.047315	974.527296	1931.020766	966.014021	1930.036750	965.522013	V	1270.682384	635.844830	1253.655835	627.331556	1252.671819	626.839548	8
16	2387.272641	1194.139958	2370.246092	1185.626684	2369.262076	1185.134676	Q	1171.613970	586.310623	1154.587421	577.797349	1153.603405	577.305341	7
17	2516.315234	1258.661255	2499.288685	1250.147980	2498.304669	1249.655973	E	732.388644	366.697960	715.362095	358.184686	714.378079	357.692678	6
18	2629.399298	1315.203287	2612.372749	1306.690013	2611.388733	1306.198005	I	603.346051	302.176664	586.319502	293.663389	585.335486	293.171381	5
19	2758.441891	1379.724584	2741.415342	1371.211309	2740.431326	1370.719301	E	490.261987	245.634631	473.235438	237.121357	472.251422	236.629349	4
20	2857.510305	1429.258791	2840.483756	1420.745516	2839.499740	1420.253508	V	361.219394	181.113335	344.192845	172.600060	343.208829	172.108052	3
21	2944.542333	1472.774805	2927.515784	1464.261530	2926.531768	1463.769522	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
73.4	3117.646713	0.015823	VILGAHQEVNLEPHVQEIEVSR

Mascot: http://www.matrixscience.com/

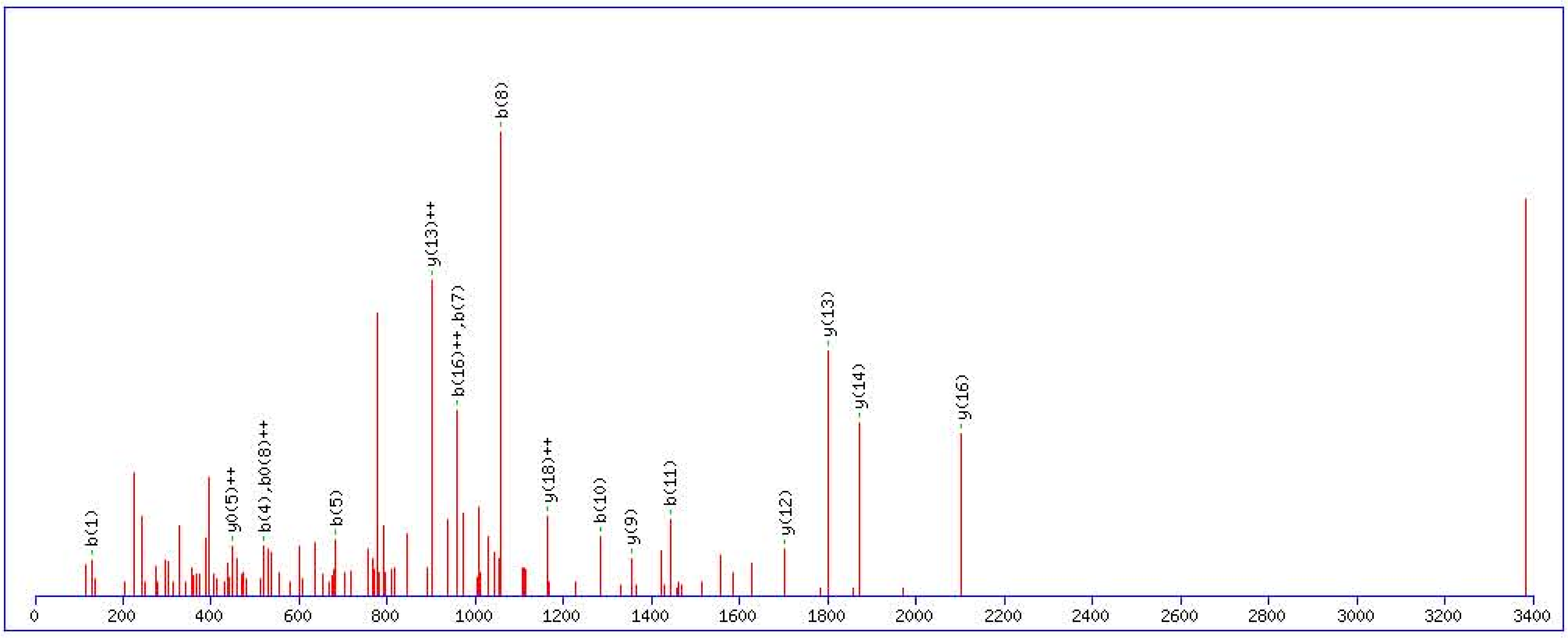
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLYDYCDVPQCAAPSFDCGKPQVEPK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

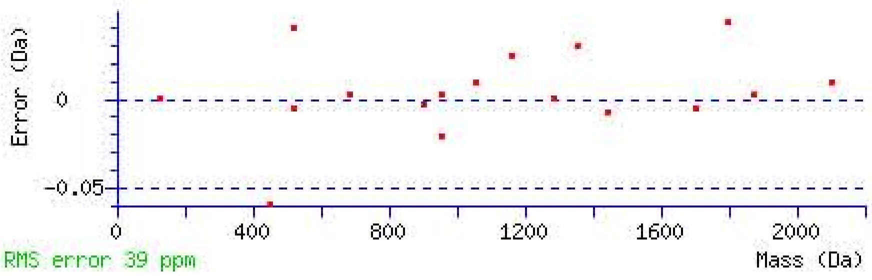
Match to Query 58613: 3382.563456 from(846.648140,4+) rtinseconds(1944) index(60206)
Title: Locus:1.1.1.1588.26 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

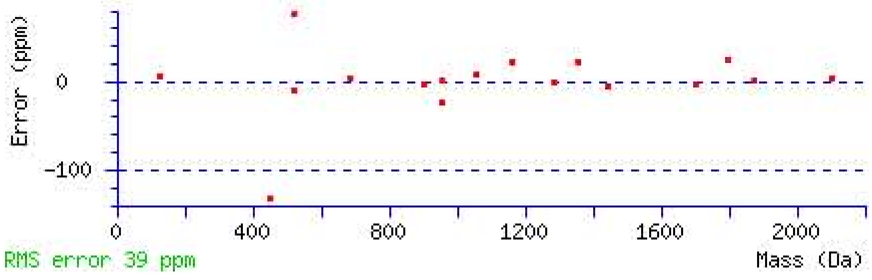
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3382.549469
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q22    : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 0.00028
Matches : 17/290 fragment ions using 21 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							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	1262.095089	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	***1282.577252***	641.792264	1265.550703	633.278990	1264.566687	632.786982	Q	2230.045345	1115.526310	2213.018796	1107.013036	2212.034780	1106.521028	17
11	***1442.607901***	721.807589	1425.581352	713.294314	1424.597336	712.802306	C	***2101.986767***	1051.497021	2084.960218	1042.983747	2083.976202	1042.491739	16
12	1513.645015	757.326146	1496.618466	748.812871	1495.634450	748.320863	A	1941.956118	971.481697	1924.929569	962.968423	1923.945553	962.476415	15
13	1584.682129	792.844703	1567.655580	784.331428	1566.671564	783.839420	A	***1870.919004***	935.963140	1853.892455	927.449866	1852.908439	926.957858	14
14	1681.734893	841.371085	1664.708344	832.857810	1663.724328	832.365802	P	***1799.881890***	900.444583	1782.855341	891.931309	1781.871325	891.439301	13
15	1768.766921	884.887099	1751.740372	876.373824	1750.756356	875.881816	S	***1702.829126***	851.918201	1685.802577	843.404927	1684.818561	842.912919	12
16	1915.835335	958.421306	1898.808786	949.908031	1897.824770	949.416023	F	1615.797098	808.402187	1598.770549	799.888913	1597.786533	799.396905	11
17	2030.862278	1015.934777	2013.835729	1007.421503	2012.851713	1006.929495	D	1468.728684	734.867980	1451.702135	726.354706	1450.718119	725.862698	10
18	2190.892927	1095.950102	2173.866378	1087.436827	2172.882362	1086.944819	C	***1353.701741***	677.354509	1336.675192	668.841234	1335.691176	668.349226	9
19	2247.914391	1124.460834	2230.887842	1115.947559	2229.903826	1115.455551	G	1193.671092	597.339184	1176.644543	588.825910	1175.660527	588.333902	8
20	2376.009354	1188.508315	2358.982805	1179.995041	2357.998789	1179.503033	K	1136.649628	568.828452	1119.623079	560.315178	1118.639063	559.823170	7
21	2473.062118	1237.034697	2456.035569	1228.521423	2455.051553	1228.029415	P	1008.554665	504.780971	991.528116	496.267696	990.544100	495.775688	6
22	2912.287444	1456.647360	2895.260895	1448.134086	2894.276879	1447.642078	Q	911.501901	456.254589	894.475352	447.741314	893.491336	447.249306	5
23	3011.355858	1506.181567	2994.329309	1497.668293	2993.345293	1497.176285	V	472.276575	236.641925	455.250026	228.128651	454.266010	227.636643	4
24	3140.398451	1570.702864	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	1619.229246	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
46.5	3382.549469	0.013987	KLYDYCDVPQCAAPSFDCGKPQVEPK
4.4	3382.549469	0.013987	KLYDYCDVPQCAAPSFDCGKPQVEPK

Mascot: http://www.matrixscience.com/

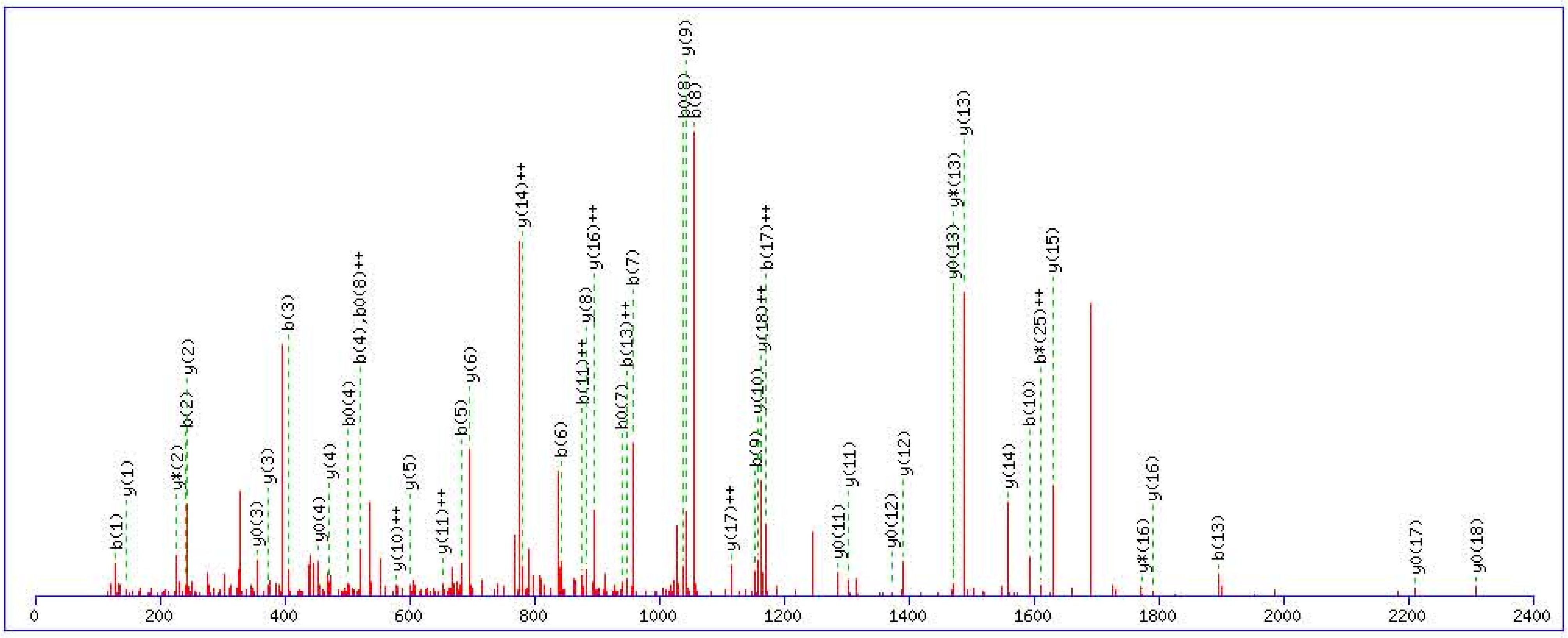
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLYDYCDVPQCAAPSFDCGKPQVEPK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

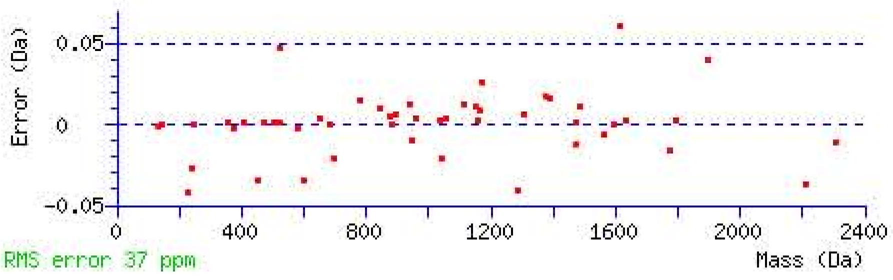
Match to Query 58614: 3382.568056 from(846.649290,4+) rtinseconds(1996) index(60612)
Title: Locus:1.1.1.1606.25 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

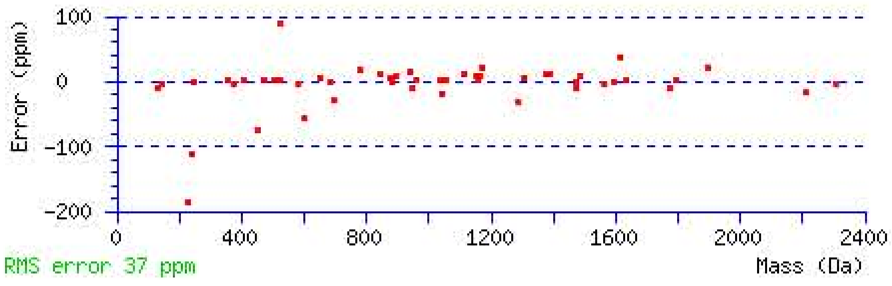
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3382.549469
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 1.3e-005
Matches : 50/290 fragment ions using 151 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
60.0	3382.549469	0.018587	KLYDYCDVPQCAAPSFDCGKPQVEPK
6.2	3382.549469	0.018587	KLYDYCDVPQCAAPSFDCGKPQVEPK

Mascot: http://www.matrixscience.com/

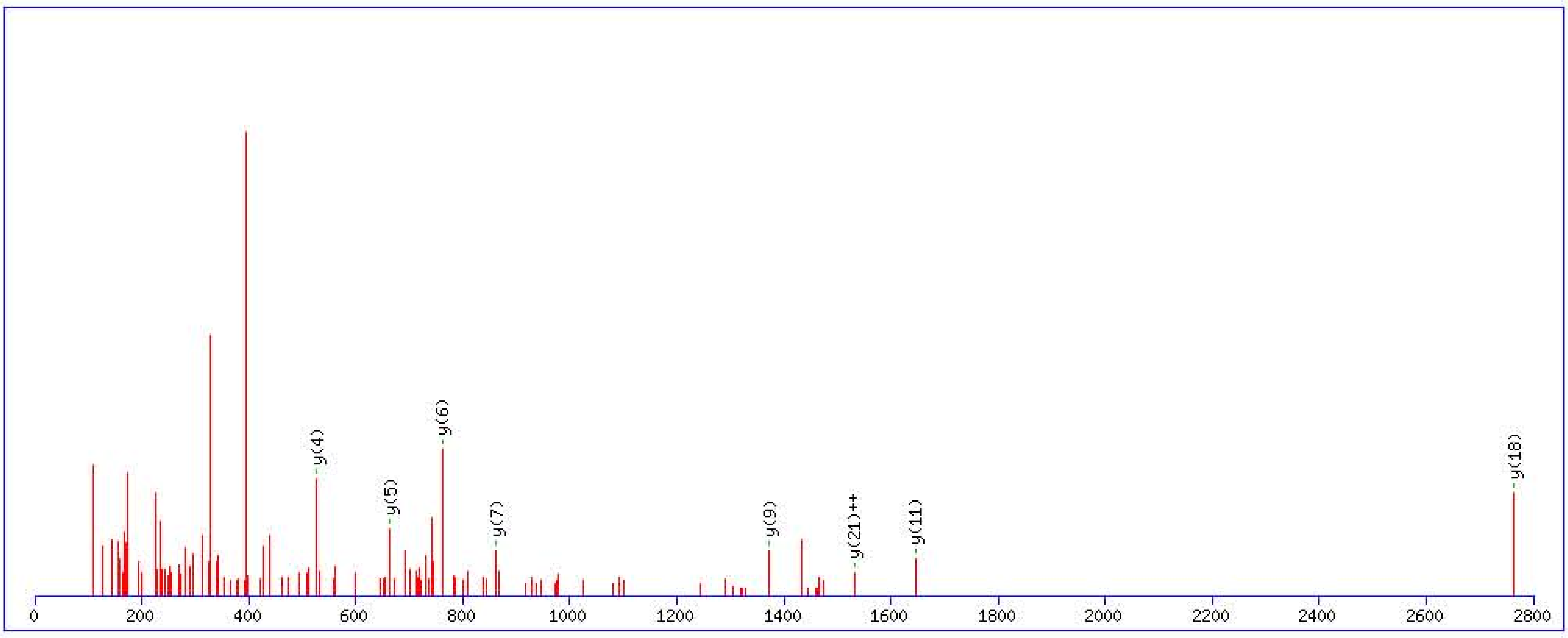
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNVAVTVSGHTCQHWSAQTPHTHNR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

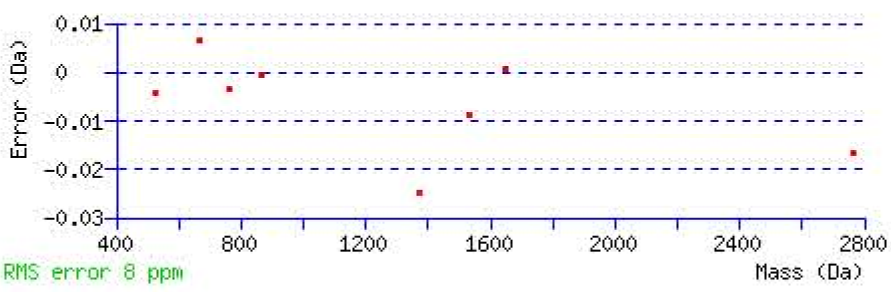
Match to Query 58836: 3403.620444 from(568.277350,6+) rtinseconds(1678) index(58845)
Title: Locus:1.1.1.1496.5 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

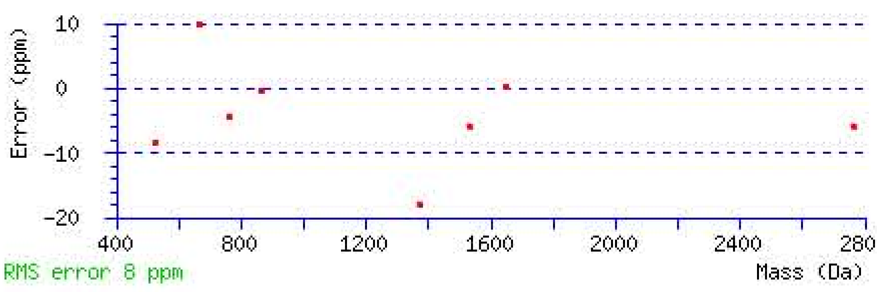
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 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: 25 **Expect:** 0.073
Matches : 8/270 fragment ions using 16 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
25.1	3403.623764	-0.003320	GNVAVTVSGHTCQHWSAQTPHTHNR

Mascot: http://www.matrixscience.com/

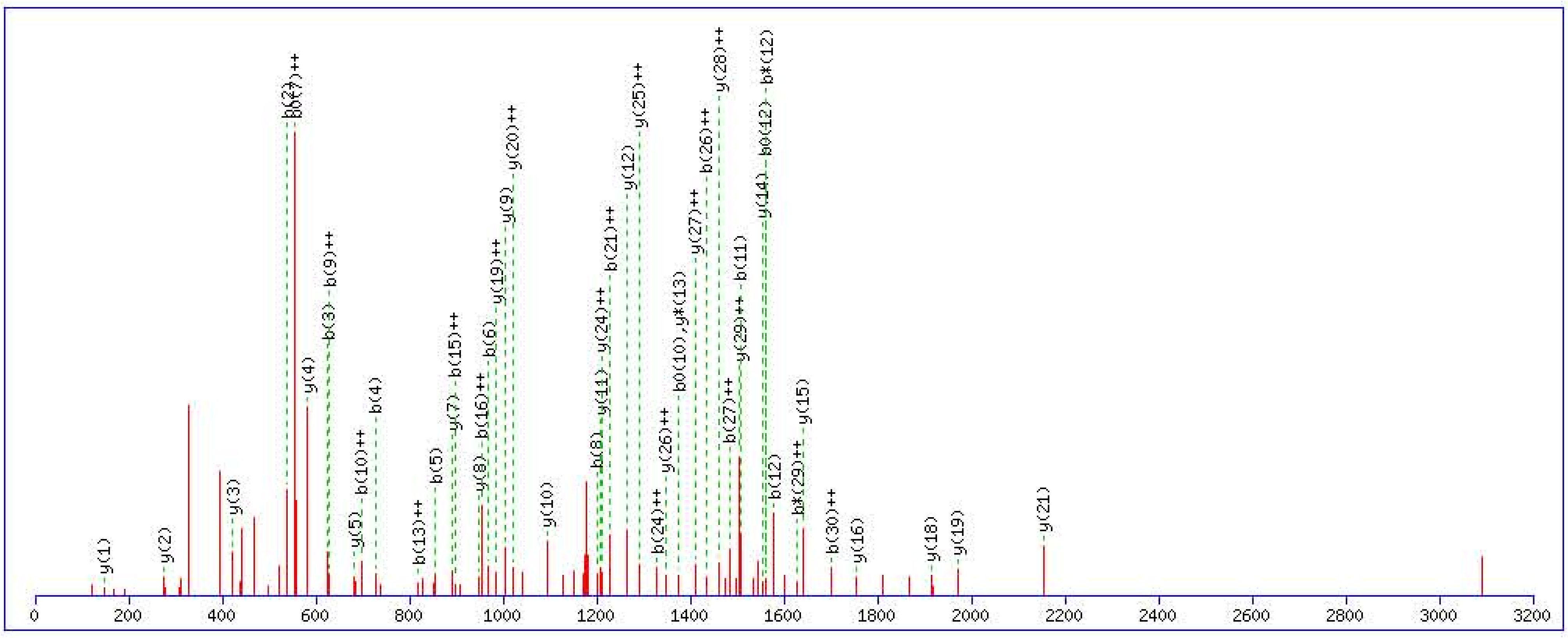
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQSTELCAGHLAGGTDSCQGDSGGPLVCFEK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

Match to Query 59885: 3547.630632 from(1183.550820,3+) rtinseconds(2180) index(61552)
Title: Locus:1.1.1.1670.13 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\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 ●



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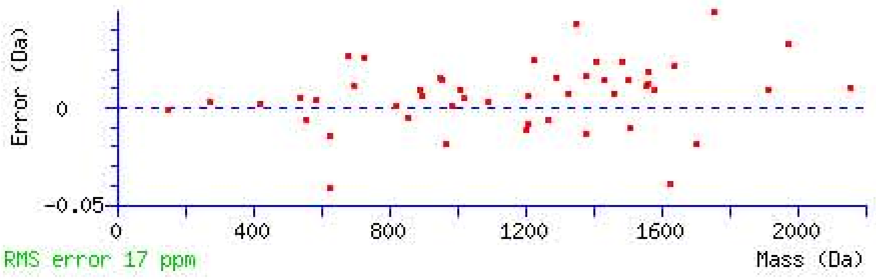
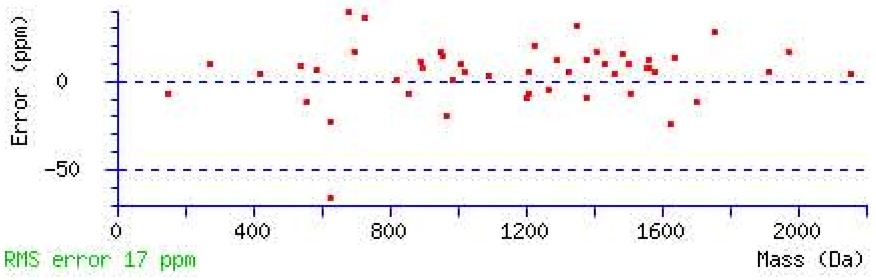
Monoisotopic mass of neutral peptide Mr(calc): 3547.584061
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2     : Biotin:Thermo-21345 (Q)
Ions Score: 83  Expect: 6.8e-008
Matches : 49/352 fragment ions using 103 most intense peaks   (help)
```

#	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
82.6	3547.584061	0.046571	VQSTELCAGHLAGGTDSCQGDSGGPLVCFEK
4.9	3547.584061	0.046571	VQSTELCAGHLAGGTDSCQGDSGGPLVCFEK

Mascot: http://www.matrixscience.com/

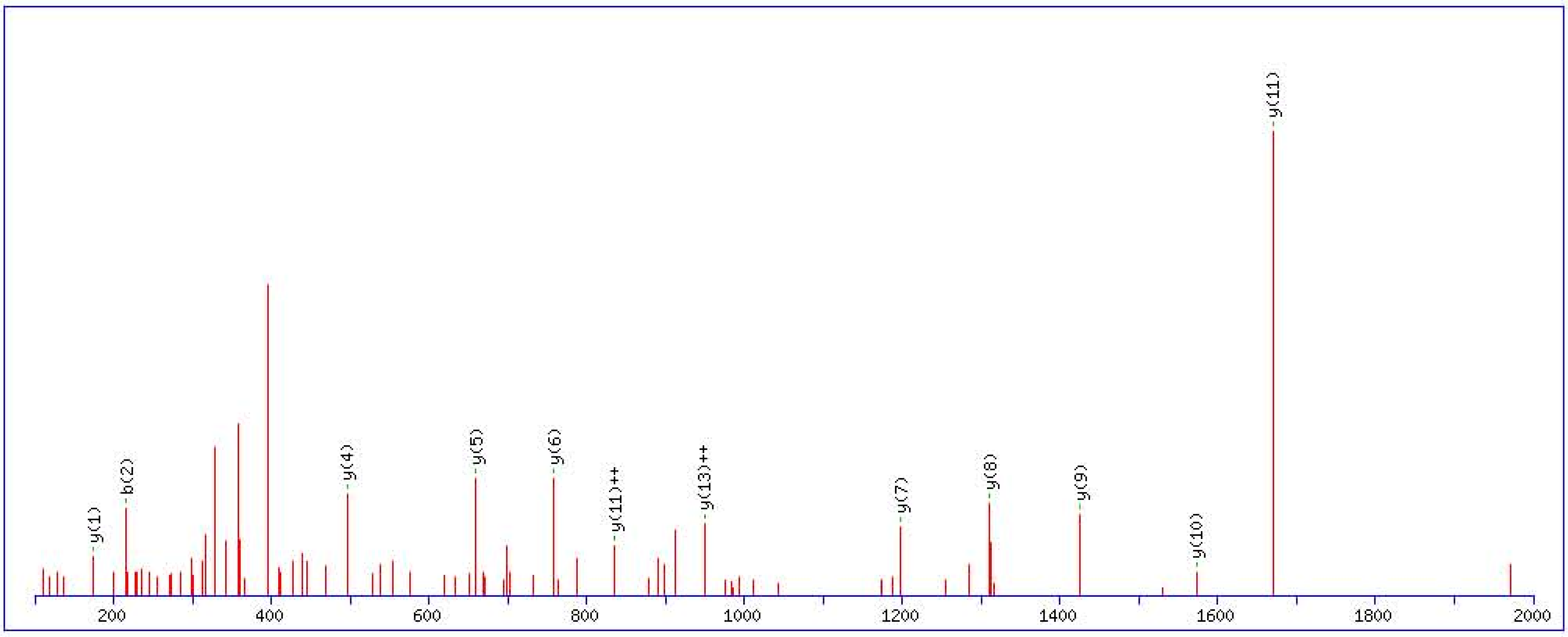
{MATRIX SCIENCE} Mascot Search Results

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

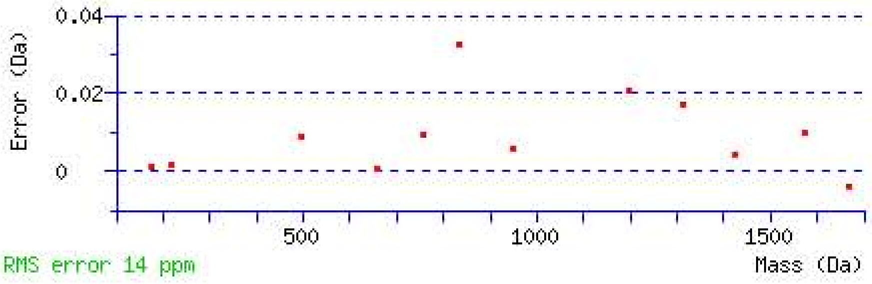
Match to Query 41792: 2113.047342 from(705.356390,3+) rtinseconds(2116) index(46692)
Title: Locus:1.1.1.3449.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

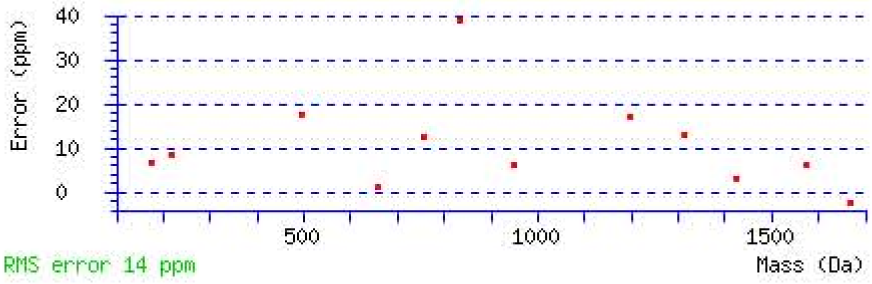
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2113.041504
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9     : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 1.7e-005
Matches : 12/164 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	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
61.9	2113.041504	0.005838	TNTQPFDLQVYHPSR
5.0	2113.041504	0.005838	TNTQPFDLQVYHPSR

Mascot: http://www.matrixscience.com/

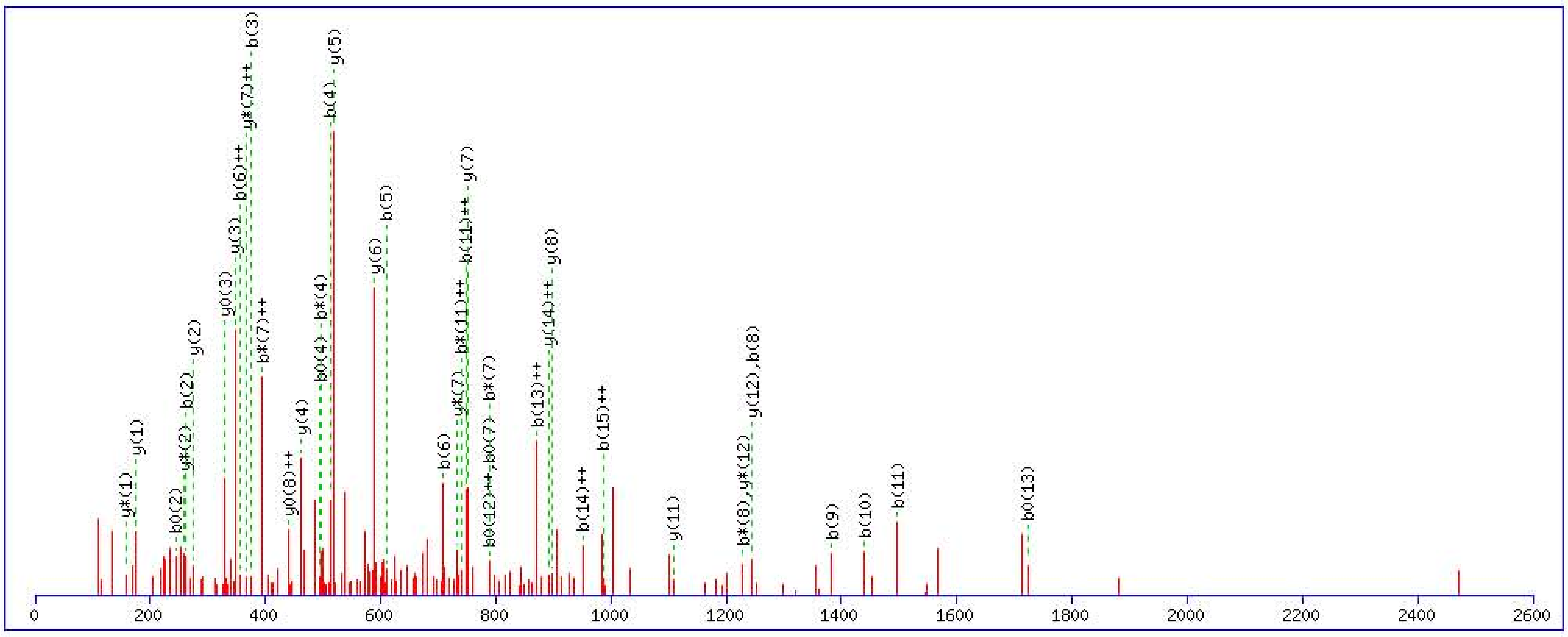
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TCNHPVPQHGGPFCAGDATR**
Found in **PROP_HUMAN**, Properdin OS=Homo sapiens GN=CFP PE=1 SV=2

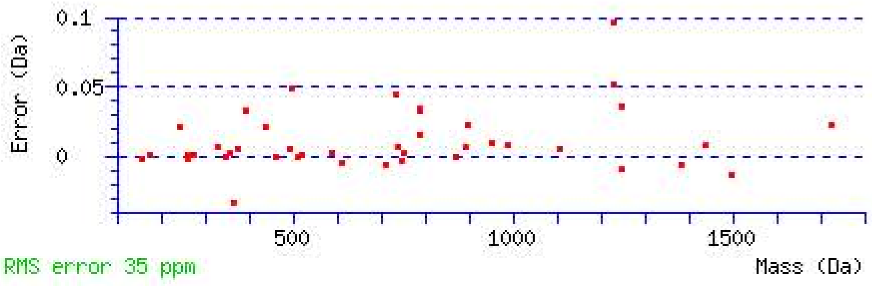
Match to Query 48194: 2489.111296 from(623.285100,4+) rtinseconds(1528) index(58124)
Title: Locus:1.1.1.1443.16 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

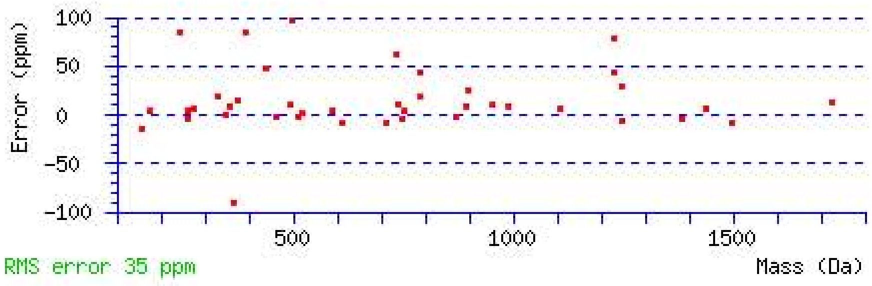
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2489.115128
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 45 **Expect:** 0.00022
Matches : 42/222 fragment ions using 108 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							20
2	***262.085604***	131.546440			244.075039	122.541158	C	2389.074689	1195.040982	2372.048140	1186.527708	2371.064124	1186.035700	19
3	***376.128531***	188.567904	359.101982	180.054629	358.117966	179.562621	N	2229.044040	1115.025658	2212.017491	1106.512383	2211.033475	1106.020375	18
4	***513.187443***	257.097360	496.160894	248.584085	495.176878	248.092077	H	2115.001113	1058.004194	2097.974564	1049.490920	2096.990548	1048.998912	17
5	***610.240207***	305.623742	593.213658	297.110467	592.229642	296.618459	P	1977.942201	989.474739	1960.915652	980.961464	1959.931636	980.469456	16
6	***709.308621***	**355.157949**	692.282072	346.644674	691.298056	346.152666	V	1880.889437	940.948357	1863.862888	932.435082	1862.878872	931.943074	15
7	806.361385	403.684331	789.334836	395.171056	788.350820	394.679048	P	1781.821023	891.414150	1764.794474	882.900875	1763.810458	882.408867	14
8	***1245.586711***	623.296994	1228.560162	614.783719	1227.576146	614.291711	Q	1684.768259	842.887768	1667.741710	834.374493	1666.757694	833.882485	13
9	***1382.645623***	691.826450	1365.619074	683.313175	1364.635058	682.821167	H	***1245.542933***	623.275105	1228.516384	614.761830	1227.532368	614.269822	12
10	***1439.667087***	720.337182	1422.640538	711.823907	1421.656522	711.331899	G	***1108.484021***	554.745649	1091.457472	546.232374	1090.473456	545.740366	11
11	***1496.688551***	**748.847914**	1479.662002	740.334639	1478.677986	739.842631	G	1051.462557	526.234917	1034.436008	517.721642	1033.451992	517.229634	10
12	1593.741315	797.374296	1576.714766	788.861021	1575.730750	788.369013	P	994.441093	497.724185	977.414544	489.210910	976.430528	488.718902	9
13	1740.809729	**870.908503**	1723.783180	862.395228	1722.799164	861.903220	F	***897.388329***	449.197803	880.361780	440.684528	879.377764	440.192520	8
14	1900.840378	**950.923827**	1883.813829	942.410553	1882.829813	941.918545	C	***750.319915***	375.663596	733.293366	367.150321	732.309350	366.658313	7
15	1971.877492	**986.442384**	1954.850943	977.929110	1953.866927	977.437102	A	***590.289266***	295.648271	573.262717	287.134997	572.278701	286.642989	6
16	2028.898956	1014.953116	2011.872407	1006.439842	2010.888391	1005.947834	G	***519.252152***	260.129714	502.225603	251.616440	501.241587	251.124432	5
17	2143.925899	1072.466587	2126.899350	1063.953313	2125.915334	1063.461305	D	***462.230688***	231.618982	445.204139	223.105707	444.220123	222.613700	4
18	2214.963013	1107.985144	2197.936464	1099.471870	2196.952448	1098.979862	A	***347.203745***	174.105510	330.177196	165.592236	329.193180	165.100228	3
19	2316.010692	1158.508984	2298.984143	1149.995709	2298.000127	1149.503701	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
20							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TCNHPVPQHGGPFCAGDATR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.1	2489.115128	-0.003832	TCNHPVPQHGGPFCAGDATR

Mascot: http://www.matrixscience.com/

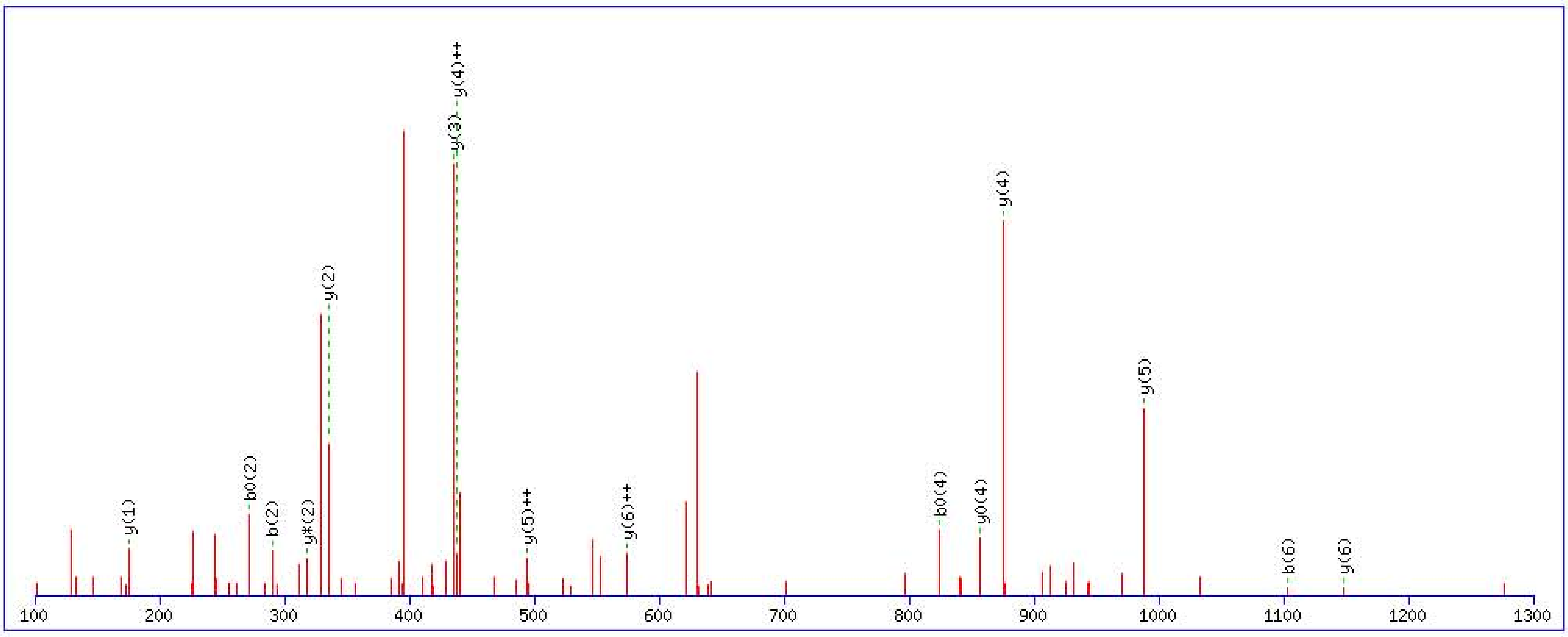
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of ECLQTCR
Found in AMBP_HUMAN, Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

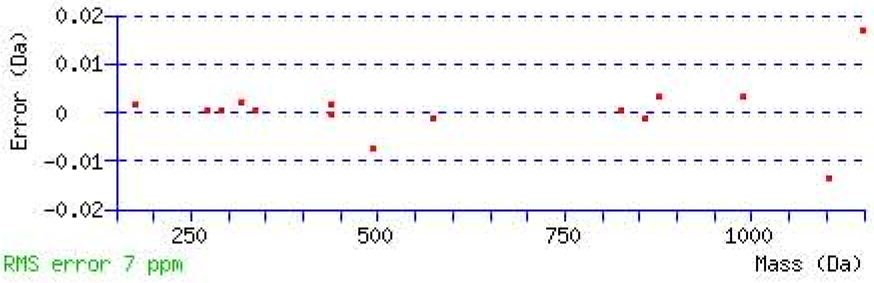
Match to Query 19690: 1276.565768 from(639.290160,2+) rtinseconds(1500) index(28834)
Title: Locus:1.1.1.3185.20 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

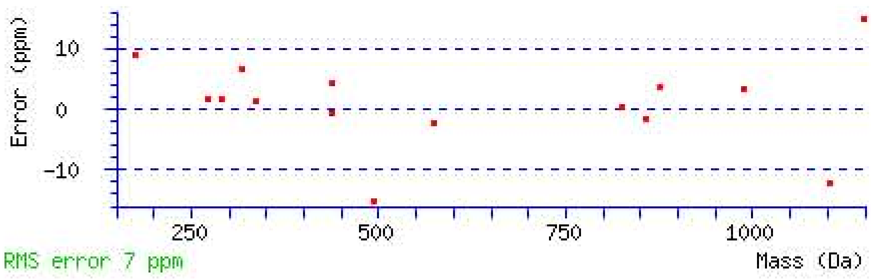
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1300] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1276.572632
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.016
Matches : 15/62 fragment ions using 37 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							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
28.2	1276.572632	-0.006864	ECLQTCR
8.5	1276.583862	-0.018094	KMSLSCHVCR
6.2	1276.571762	-0.005994	AGAESPTMSVDGR
6.0	1276.553116	0.012652	EDLDNASKDDR
5.5	1276.569229	-0.003461	MTGRYEMYAR
5.2	1276.579605	-0.013837	EEQRSPFNDR
1.5	1276.560516	0.005252	DEAEMSPVVER
1.5	1276.560516	0.005252	QQVPSEDSMEK

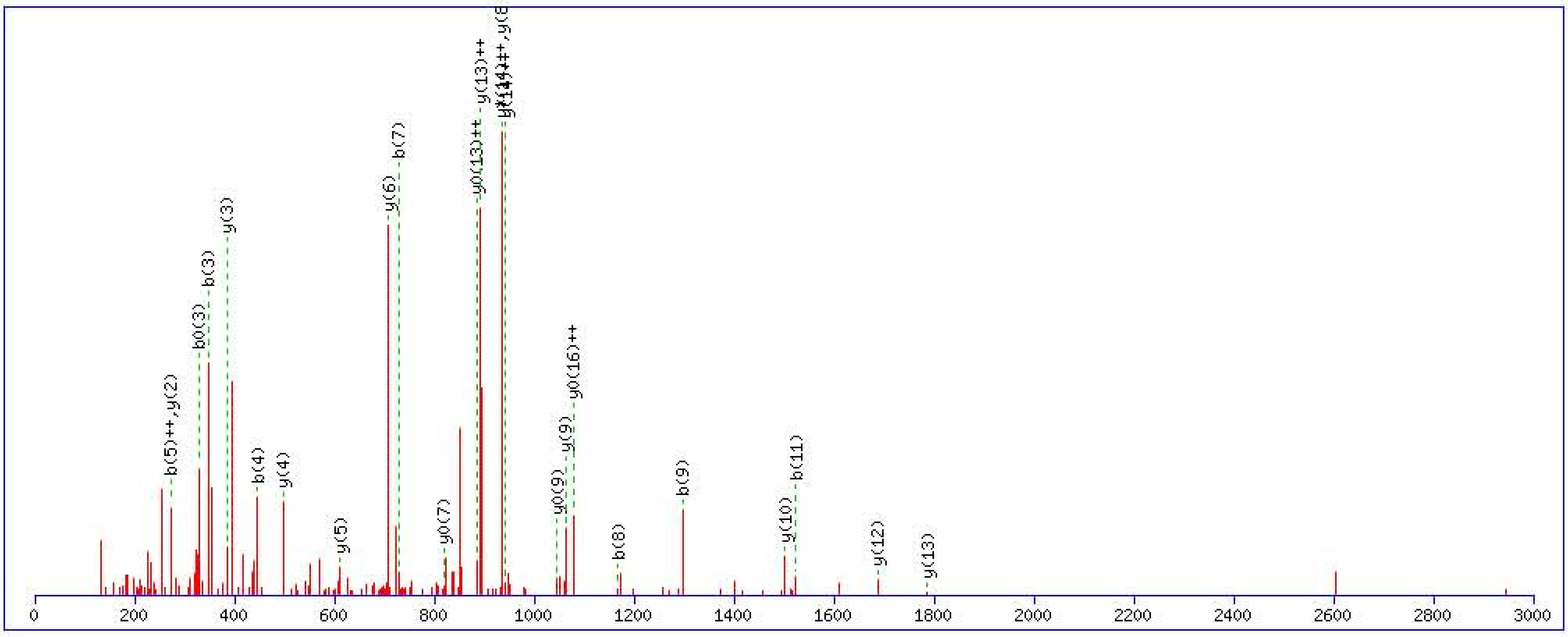
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GECVPGEQEPEPILIPR**
Found in **AMBP_HUMAN**, Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

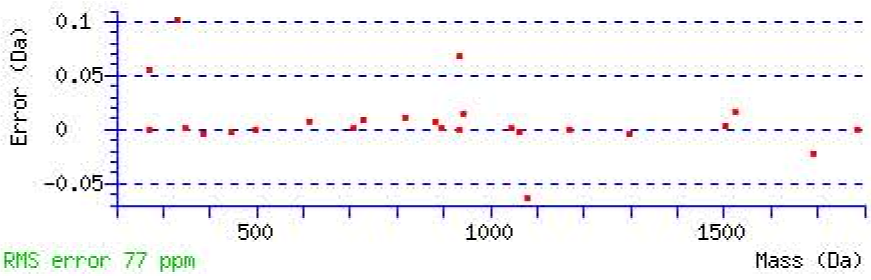
Match to Query 43791: 2230.108152 from(744.376660,3+) rtinseconds(2303) index(33625)
Title: Locus:1.1.1.3465.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

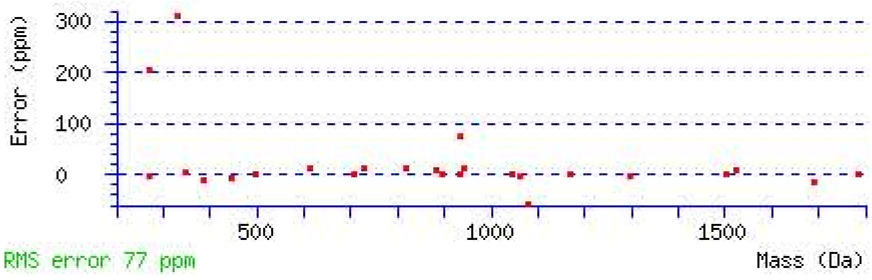
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2230.112595
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8     : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.00049
Matches : 25/164 fragment ions using 59 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	187.071333	94.039305			169.060768	85.034022	E	2174.098425	1087.552850	2157.071876	1079.039576	2156.087860	1078.547568	16
3	**347.101982**	174.054629			329.091417	165.049347	C	2045.055832	1023.031554	2028.029283	1014.518279	2027.045267	1014.026271	15
4	**446.170396**	223.588836			428.159831	214.583554	V	1885.025183	943.016229	1867.998634	934.502955	1867.014618	934.010947	14
5	543.223160	272.115218			525.212595	263.109936	P	***1785.956769***	893.482022	1768.930220	884.968748	1767.946204	884.476740	13
6	600.244624	300.625950			582.234059	291.620668	G	***1688.904005***	844.955640	1671.877456	836.442366	1670.893440	835.950358	12
7	**729.287217**	365.147247			711.276652	356.141964	E	1631.882541	816.444908	1614.855992	807.931634	1613.871976	807.439626	11
8	**1168.512543**	584.759910	1151.485994	576.246635	1150.501978	575.754627	Q	***1502.839948***	751.923612	1485.813399	743.410337	1484.829383	742.918329	10
9	**1297.555136**	649.281206	1280.528587	640.767932	1279.544571	640.275924	E	***1063.614622***	532.310949	1046.588073	523.797674	1045.604057	523.305666	9
10	1394.607900	697.807588	1377.581351	689.294314	1376.597335	688.802306	P	***934.572029***	467.789652	917.545480	459.276378	916.561464	458.784370	8
11	**1523.650493**	762.328885	1506.623944	753.815610	1505.639928	753.323602	E	837.519265	419.263270	820.492716	410.749996	819.508700	410.257988	7
12	1620.703257	810.855267	1603.676708	802.341992	1602.692692	801.849984	P	***708.476672***	354.741974	691.450123	346.228699			6
13	1733.787321	867.397299	1716.760772	858.884024	1715.776756	858.392016	I	***611.423908***	306.215592	594.397359	297.702317			5
14	1846.871385	923.939331	1829.844836	915.426056	1828.860820	914.934048	L	***498.339844***	249.673560	481.313295	241.160285			4
15	1959.955449	980.481363	1942.928900	971.968088	1941.944884	971.476080	I	***385.255780***	193.131528	368.229231	184.618253			3
16	2057.008213	1029.007744	2039.981664	1020.494470	2038.997648	1020.002462	P	***272.171716***	136.589496	255.145167	128.076221			2
17							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GECVPGEQEPEPILIPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.2	2230.112595	-0.004443	GECVPGEQEPEPILIPR
2.8	2230.090591	0.017561	AELGERPEPVDFSFNPLADK
1.5	2230.122971	-0.014819	QFLGPEGNVDVELIDKSTNR

Mascot: http://www.matrixscience.com/

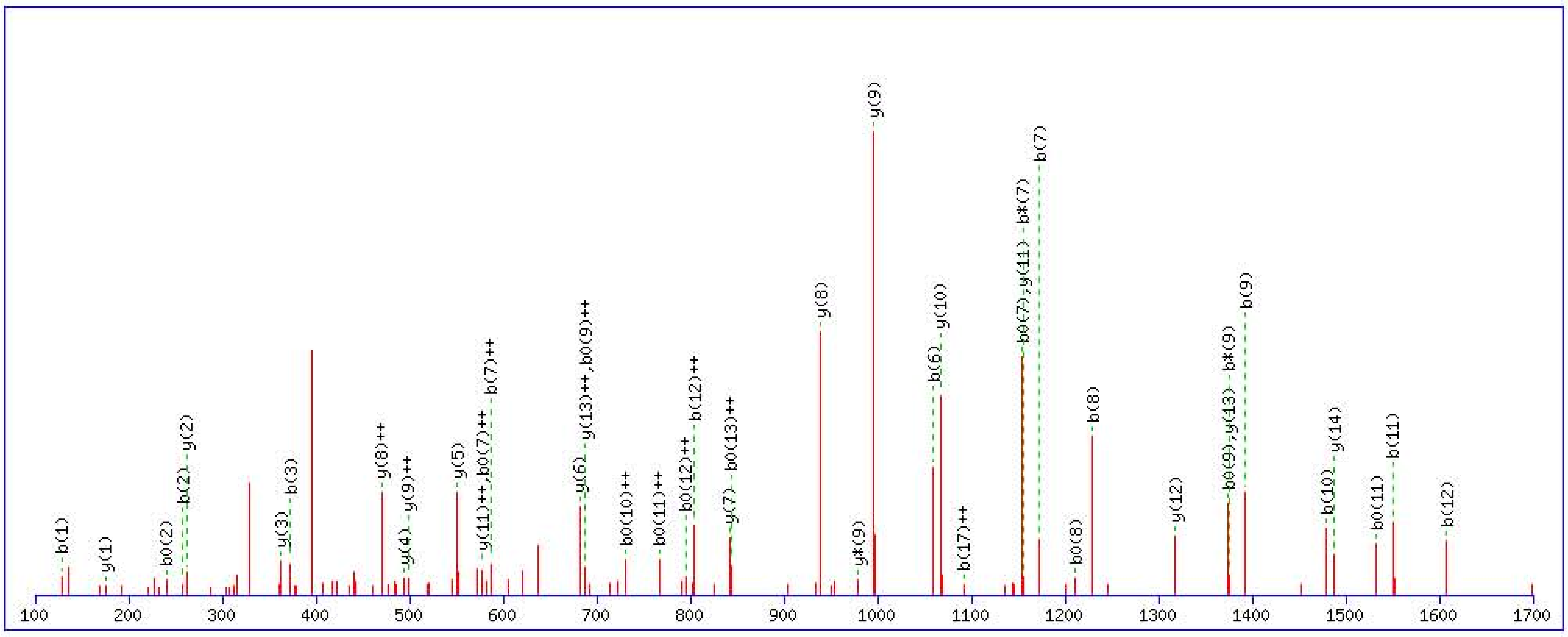
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **KEDSCQLGYSAGPCMGMTSR**
Found in **AMBP_HUMAN**, Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

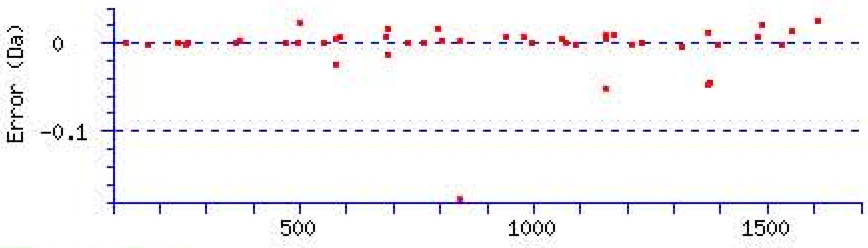
Match to Query 49018: 2545.089612 from(849.370480,3+) rtinseconds(1914) index(45347)
Title: Locus:1.1.1.3379.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

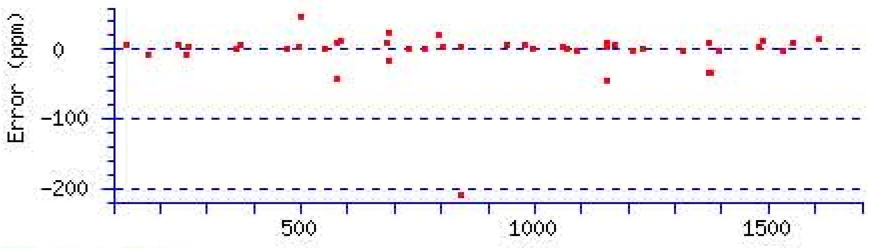
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2545.089188
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 89 **Expect:** 3.8e-009
Matches : 45/224 fragment ions using 67 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							20
2	***258.144832***	129.576054	241.118283	121.062780	240.134267	120.570772	E	2418.001508	1209.504392	2400.974959	1200.991117	2399.990943	1200.499109	19
3	***373.171775***	187.089526	356.145226	178.576251	355.161210	178.084243	D	2288.958915	1144.983095	2271.932366	1136.469821	2270.948350	1135.977813	18
4	460.203803	230.605540	443.177254	222.092265	442.193238	221.600257	S	2173.931972	1087.469624	2156.905423	1078.956349	2155.921407	1078.464341	17
5	620.234452	310.620864	603.207903	302.107590	602.223887	301.615582	C	2086.899944	1043.953610	2069.873395	1035.440335	2068.889379	1034.948327	16
6	***1059.459778***	530.233527	1042.433229	521.720253	1041.449213	521.228245	Q	1926.869295	963.938286	1909.842746	955.425011	1908.858730	954.933003	15
7	***1172.543842***	**586.775559**	1155.517293	578.262285	1154.533277	577.770277	L	***1487.643969***	744.325623	1470.617420	735.812348	1469.633404	735.320340	14
8	***1229.565306***	615.286291	1212.538757	606.773017	1211.554741	606.281008	G	***1374.559905***	687.783591	1357.533356	679.270316	1356.549340	678.778308	13
9	***1392.628635***	696.817956	1375.602086	688.304681	1374.618070	687.812673	Y	***1317.538441***	659.272859	1300.511892	650.759584	1299.527876	650.267576	12
10	***1479.660663***	740.333970	1462.634114	731.820695	1461.650098	731.328687	S	***1154.475112***	577.741194	1137.448563	569.227920	1136.464547	568.735912	11
11	***1550.697777***	775.852527	1533.671228	767.339252	1532.687212	766.847244	A	***1067.443084***	534.225180	1050.416535	525.711906	1049.432519	525.219898	10
12	***1607.719241***	**804.363259**	1590.692692	795.849984	1589.708676	795.357976	G	***996.405970***	498.706623	979.379421	490.193349	978.395405	489.701341	9
13	1704.772005	852.889641	1687.745456	844.376366	1686.761440	843.884358	P	***939.384506***	470.195891	922.357957	461.682617	921.373941	461.190609	8
14	1864.802654	932.904965	1847.776105	924.391691	1846.792089	923.899683	C	***842.331742***	421.669509	825.305193	413.156235	824.321177	412.664227	7
15	1995.843139	998.425208	1978.816590	989.911933	1977.832574	989.419925	M	***682.301093***	341.654185	665.274544	333.140910	664.290528	332.648902	6
16	2052.864603	1026.935939	2035.838054	1018.422665	2034.854038	1017.930657	G	***551.260608***	276.133942	534.234059	267.620668	533.250043	267.128660	5
17	2183.905088	**1092.456182**	2166.878539	1083.942907	2165.894523	1083.450899	M	***494.239144***	247.623210	477.212595	239.109935	476.228579	238.617927	4
18	2284.952767	1142.980021	2267.926218	1134.466747	2266.942202	1133.974739	T	***363.198659***	182.102967	346.172110	173.589693	345.188094	173.097685	3
19	2371.984795	1186.496035	2354.958246	1177.982761	2353.974230	1177.490753	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
89.4	2545.089188	0.000424	KEDSCQLGYSAGPCMGMTSR
1.2	2545.110138	-0.020526	QDGSCEASVSFEDVTVDFSR

Mascot: http://www.matrixscience.com/

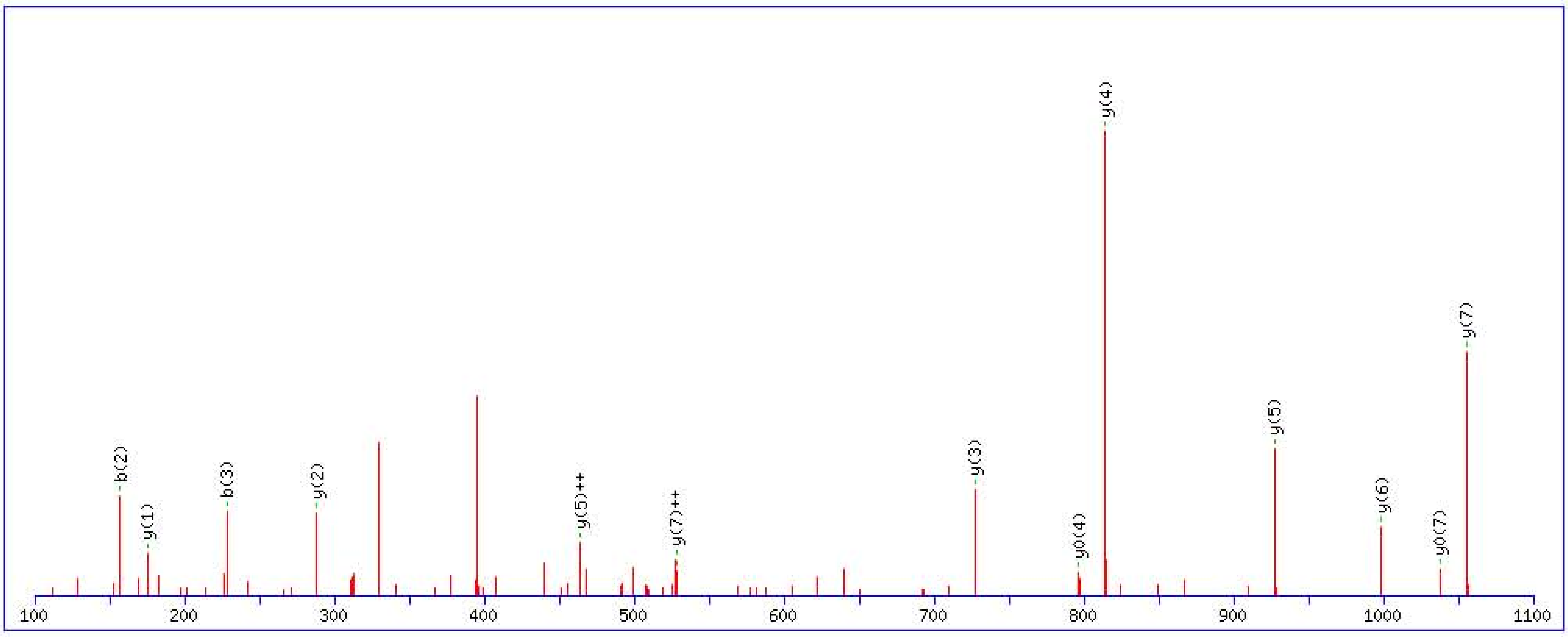
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGALSQLR**
Found in **MENT_HUMAN**, Protein MENT OS=Homo sapiens GN=MENT PE=2 SV=1

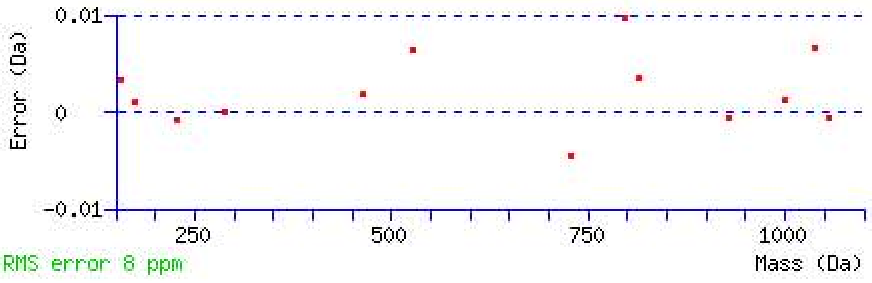
Match to Query 16375: 1153.660008 from(577.837280,2+) rtinseconds(1963) index(31583)
Title: Locus:1.1.1.3347.13 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

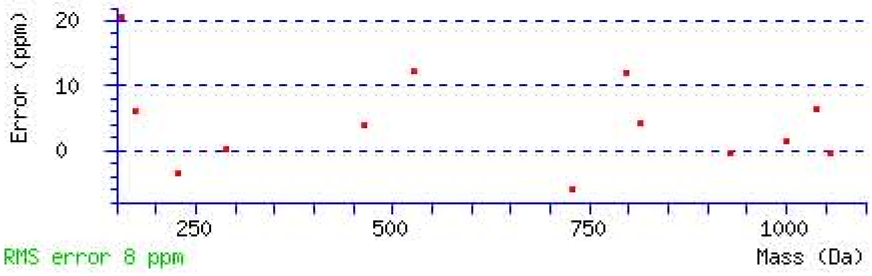
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1153.664139
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 7.6e-005
Matches : 13/60 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	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
53.3	1153.664139	-0.004131	VGALSQLR
14.4	1153.664124	-0.004116	VKQEALR
13.1	1153.675354	-0.015346	RALLSQR
13.1	1153.675369	-0.015361	RALTVQR
11.0	1153.645477	0.014531	RALAAPVAEEK
9.2	1153.667953	-0.007945	RANPNSIRVK
6.2	1153.656723	0.003285	RPSADPGKKAK
3.5	1153.642822	0.017186	RAPIGQSGRGR
2.5	1153.675369	-0.015361	QTVRALR
1.9	1153.645493	0.014515	NLLKLDPADR

Mascot: http://www.matrixscience.com/

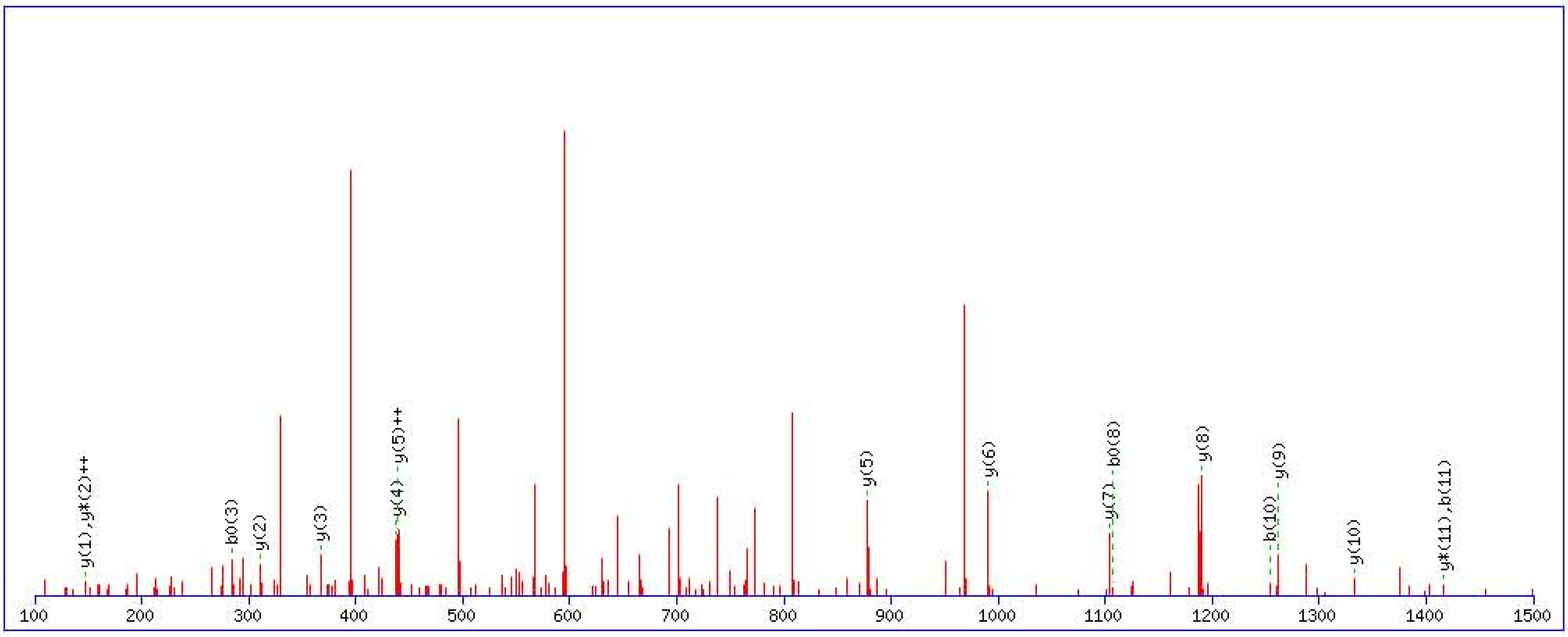
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ETAASLLQAGYK**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

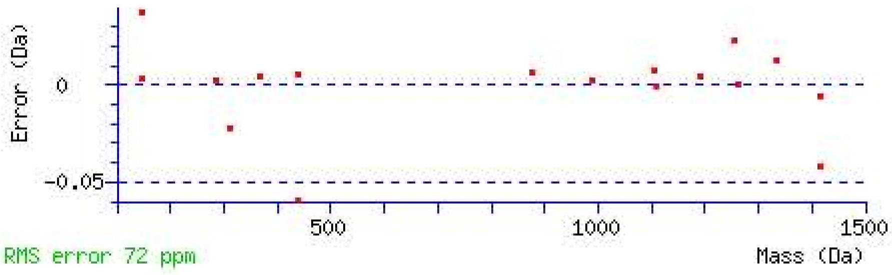
Match to Query 28801: 1561.812528 from(781.913540,2+) rtinseconds(2139) index(46847)
Title: Locus:1.1.1.3457.18 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

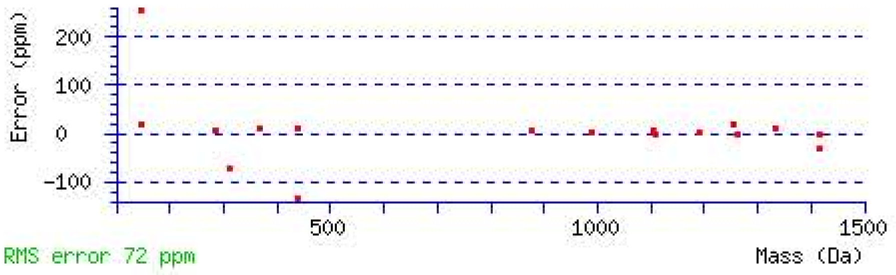
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1561.817383
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.0016
Matches : 17/104 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	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
33.3	1561.817383	-0.004855	ETAASLLQAGYK
3.3	1561.828613	-0.016085	QLASRYASVEK
1.2	1561.821243	-0.008715	TEKHPPVSPGRTEK

Mascot: http://www.matrixscience.com/

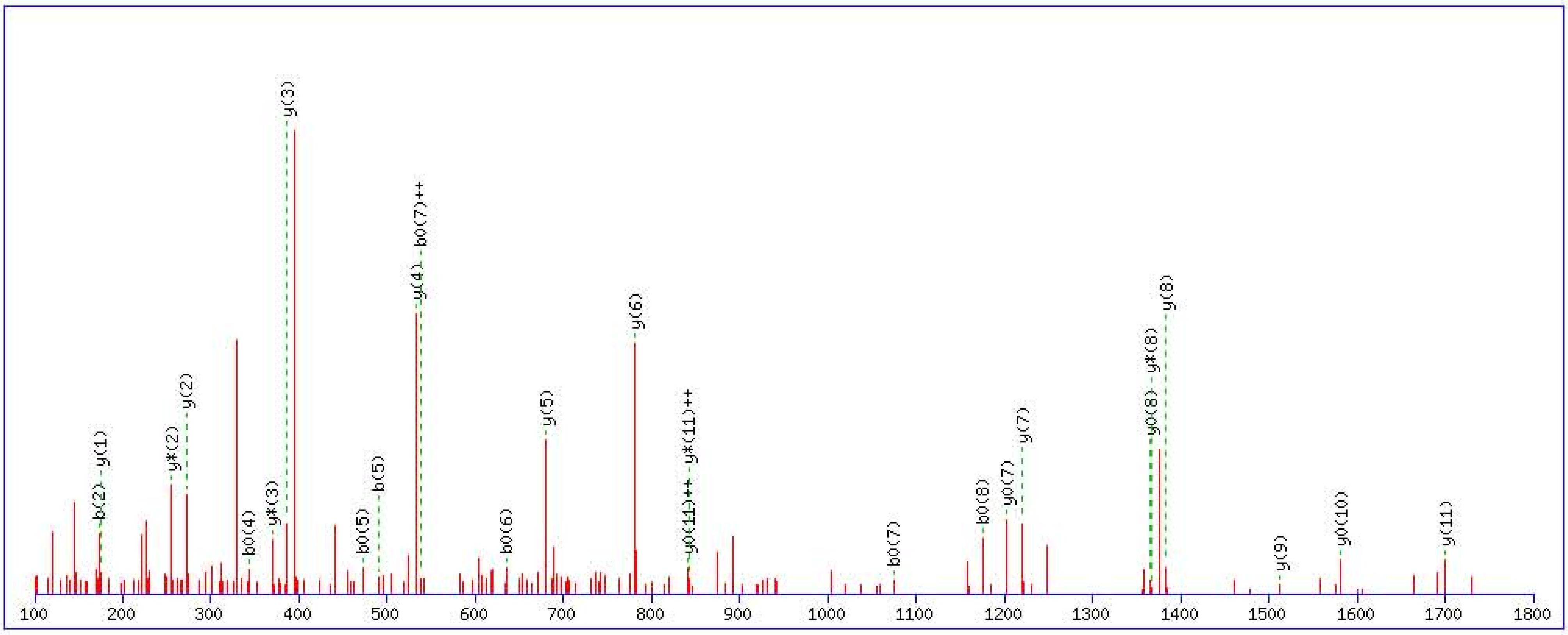
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TATSEYQTFFNPR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

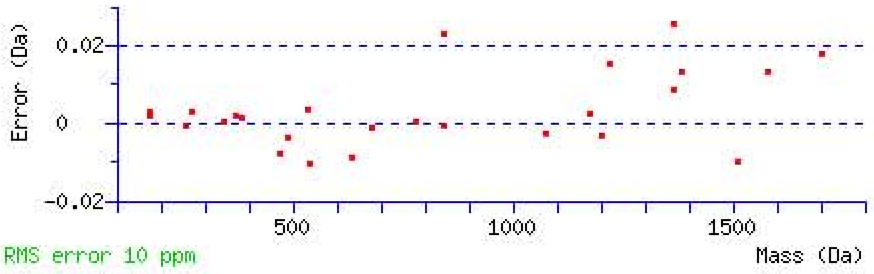
Match to Query 37067: 1871.887692 from(624.969840,3+) rtinseconds(2291) index(47802)
Title: Locus:1.1.1.3510.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

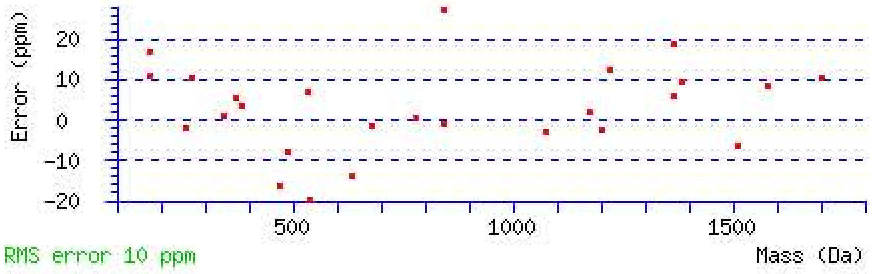
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1871.887619
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.016
Matches : 26/122 fragment ions using 87 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
30.2	1871.887619	0.000073	TATSEYQTFFNPR

Mascot: http://www.matrixscience.com/

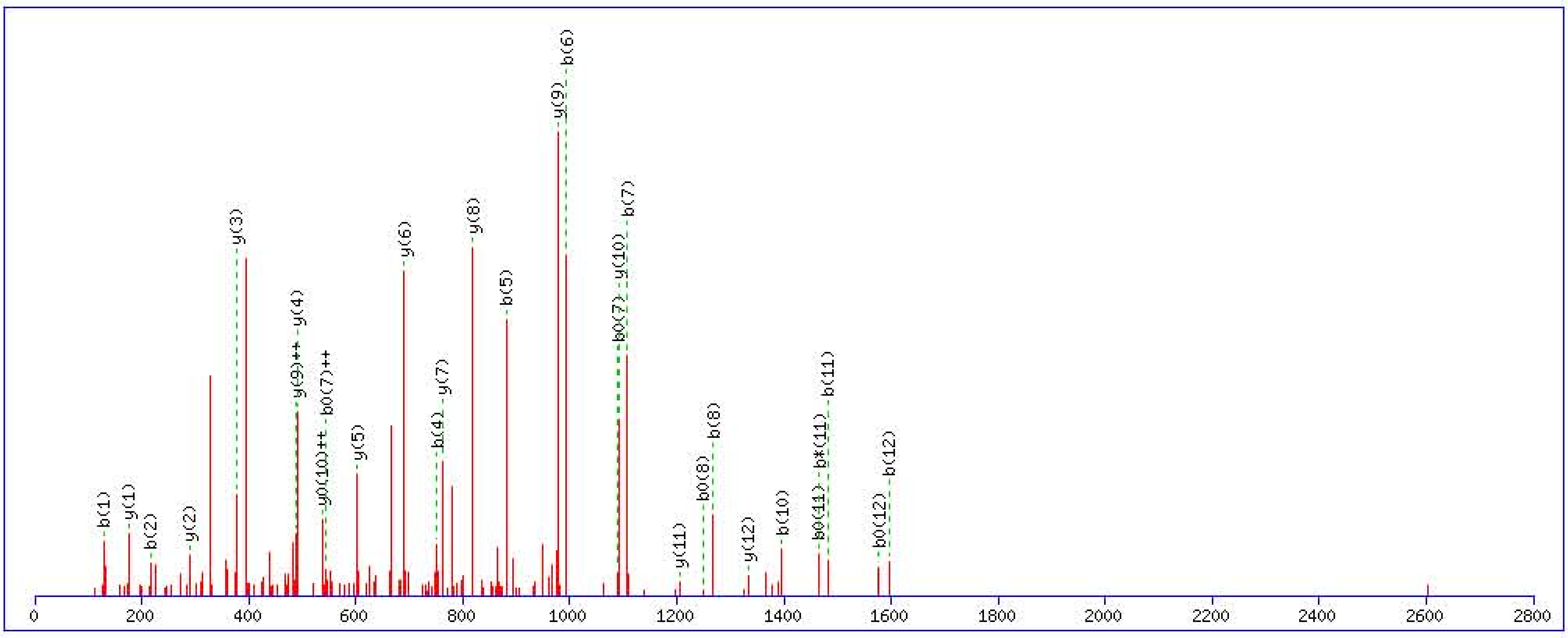
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KSPQELLCGASLISDR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

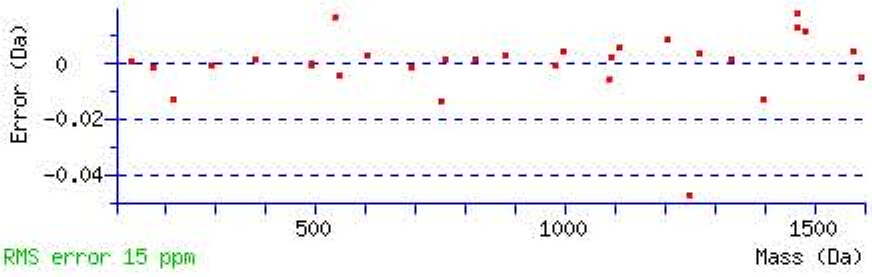
Match to Query 41354: 2084.075982 from(695.699270,3+) rtinseconds(2291) index(47804)
Title: Locus:1.1.1.3510.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

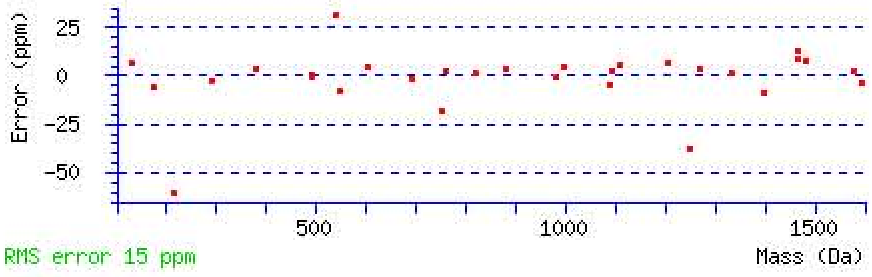
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2084.075806
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4     : Biotin:Thermo-21345 (Q)
Ions Score: 90  Expect: 2.6e-008
Matches : 30/176 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	***129.102239***	65.054757	112.075690	56.541483			K							16
2	***216.134267***	108.570771	199.107718	100.057497	198.123702	99.565489	S	1956.988145	978.997711	1939.961596	970.484436	1938.977580	969.992428	15
3	313.187031	157.097153	296.160482	148.583879	295.176466	148.091871	P	1869.956117	935.481697	1852.929568	926.968422	1851.945552	926.476414	14
4	***752.412357***	376.709817	735.385808	368.196542	734.401792	367.704534	Q	1772.903353	886.955314	1755.876804	878.442040	1754.892788	877.950032	13
5	***881.454950***	441.231113	864.428401	432.717839	863.444385	432.225831	E	***1333.678027***	667.342652	1316.651478	658.829377	1315.667462	658.337369	12
6	***994.539014***	497.773145	977.512465	489.259871	976.528449	488.767863	L	***1204.635434***	602.821355	1187.608885	594.308081	1186.624869	593.816073	11
7	***1107.623078***	554.315177	1090.596529	545.801903	1089.612513	545.309895	L	***1091.551370***	546.279323	1074.524821	537.766049	1073.540805	537.274040	10
8	***1267.653727***	634.330502	1250.627178	625.817227	1249.643162	625.325219	C	***978.467306***	489.737291	961.440757	481.224017	960.456741	480.732009	9
9	1324.675191	662.841234	1307.648642	654.327959	1306.664626	653.835951	G	***818.436657***	409.721967	801.410108	401.208692	800.426092	400.716684	8
10	***1395.712305***	698.359791	1378.685756	689.846516	1377.701740	689.354508	A	***761.415193***	381.211235	744.388644	372.697960	743.404628	372.205952	7
11	***1482.744333***	741.875805	1465.717784	733.362530	1464.733768	732.870522	S	***690.378079***	345.692678	673.351530	337.179403	672.367514	336.687395	6
12	***1595.828397***	798.417837	1578.801848	789.904562	1577.817832	789.412554	L	***603.346051***	302.176664	586.319502	293.663389	585.335486	293.171381	5
13	1708.912461	854.959868	1691.885912	846.446594	1690.901896	845.954586	I	***490.261987***	245.634631	473.235438	237.121357	472.251422	236.629349	4
14	1795.944489	898.475883	1778.917940	889.962608	1777.933924	889.470600	S	***377.177923***	189.092600	360.151374	180.579325	359.167358	180.087317	3
15	1910.971432	955.989354	1893.944883	947.476080	1892.960867	946.984072	D	***290.145895***	145.576585	273.119346	137.063311	272.135330	136.571303	2
16							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of KSPQELLCGASLISDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
90.5	2084.075806	0.000176	KSPQELLCGASLISDR
10.7	2084.050659	0.025323	EGSSEISQRVQSR
10.6	2084.090225	-0.014243	SKYDVPGPPLNVTITDVNR
6.4	2084.097565	-0.021583	KEFIMAELIQTEKAYVR
6.4	2084.097565	-0.021583	KEFIMAELLQTEKAYVR
5.7	2084.045959	0.030023	EDQLDTVLAVLEDSAR
4.6	2084.101425	-0.025443	KAILRVAELSSDDFHLDR
2.0	2084.083679	-0.007697	EDLISFLCGKVPPPRNSR
0.8	2084.071091	0.004891	LAPSEITEELPSSQLMPVK

Mascot: http://www.matrixscience.com/

MATRIX SCIENCE

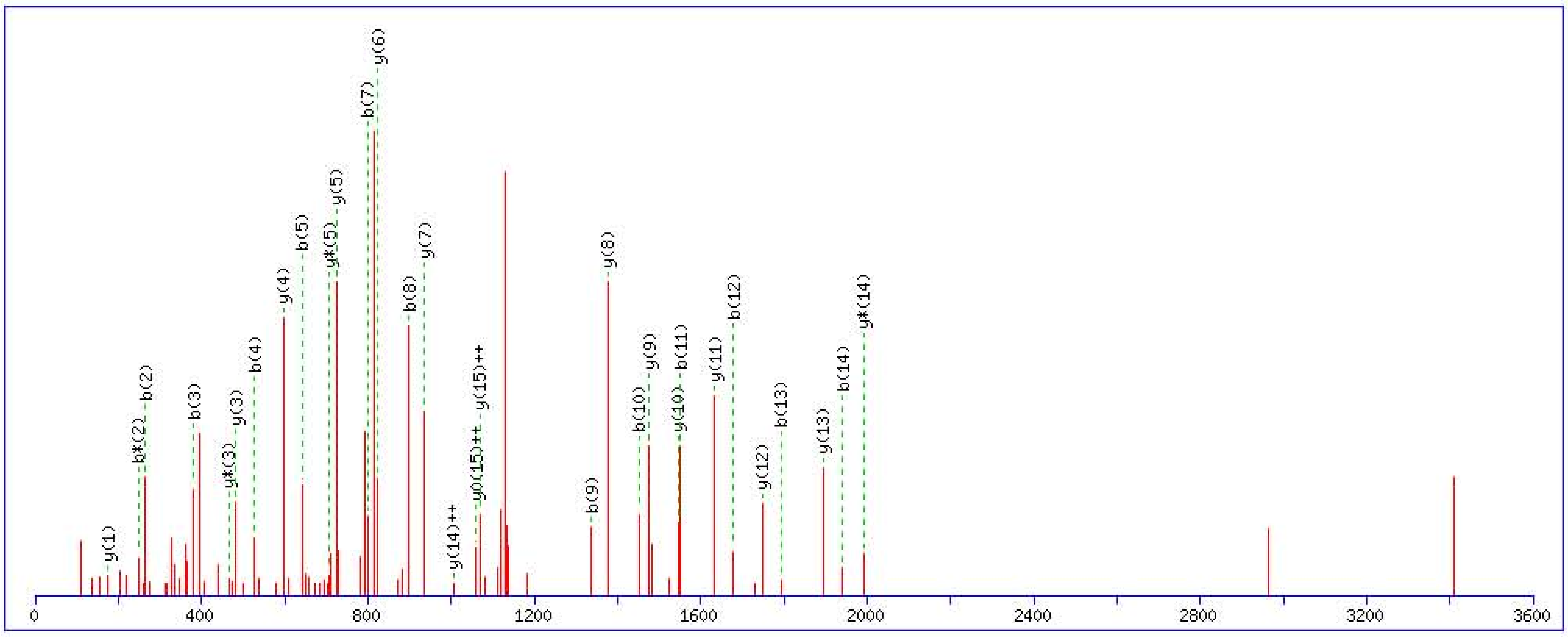
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQDFNSAVQLVENFCR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

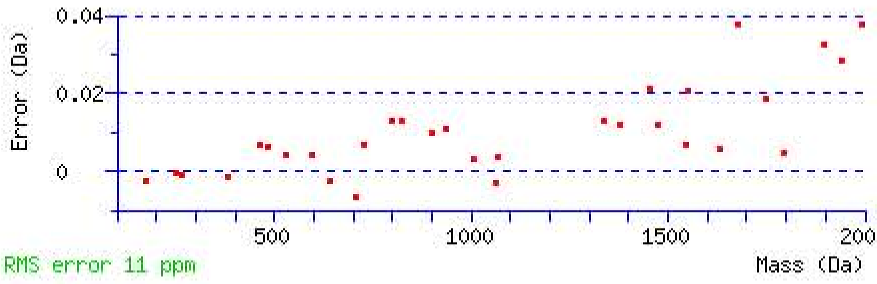
Match to Query 44597: 2274.088308 from(1138.051430,2+) rtinseconds(2469) index(62995)
Title: Locus:1.1.1.1771.12 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

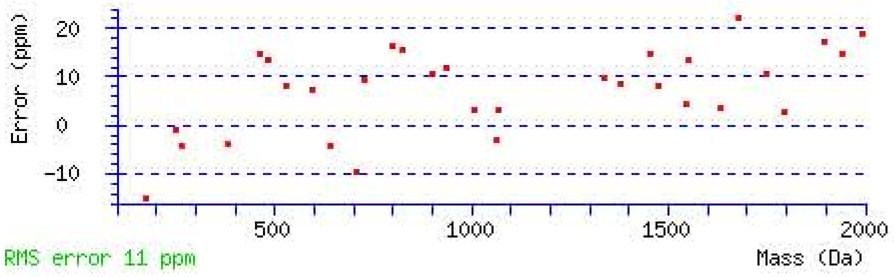
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 89 **Expect:** 2.8e-008
Matches : 31/166 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	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
89.1	2274.067398	0.020910	HQDFNSAVQLVENFCR
14.4	2274.067398	0.020910	HQDFNSAVQLVENFCR

Mascot: http://www.matrixscience.com/

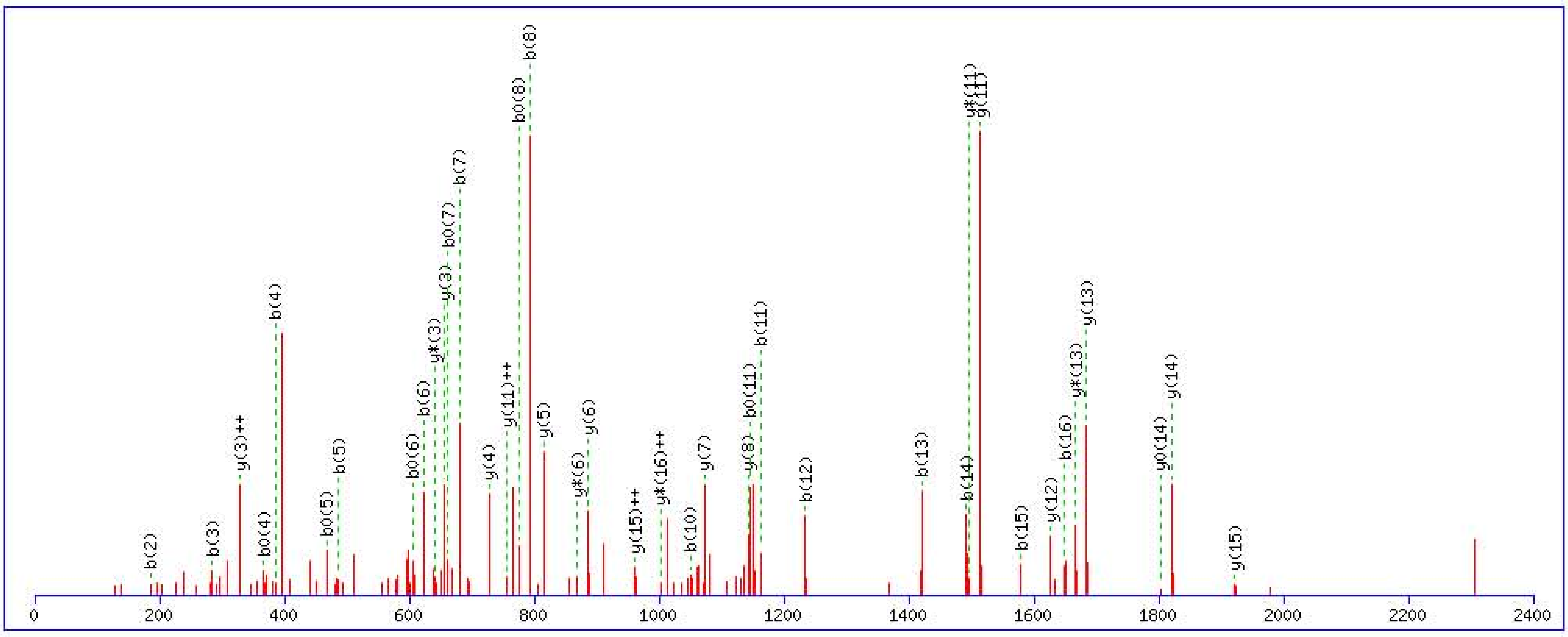
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAVTTHGLPCLAWASAQAK**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

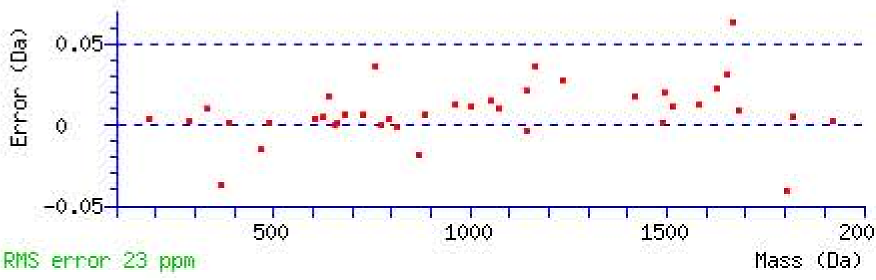
Match to Query 45189: 2305.219168 from(1153.616860,2+) rtinseconds(2367) index(48139)
Title: Locus:1.1.1.3536.23 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

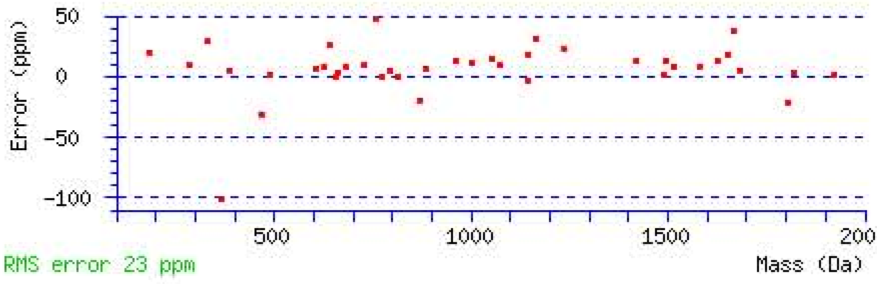
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2305.207504
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q17 : Biotin:Thermo-21345 (Q)
Ions Score: 53 **Expect:** 0.00014
Matches : 40/170 fragment ions using 122 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
52.5	2305.207504	0.011664	LAVTTHGLPCLAWASAQAK

Mascot: http://www.matrixscience.com/

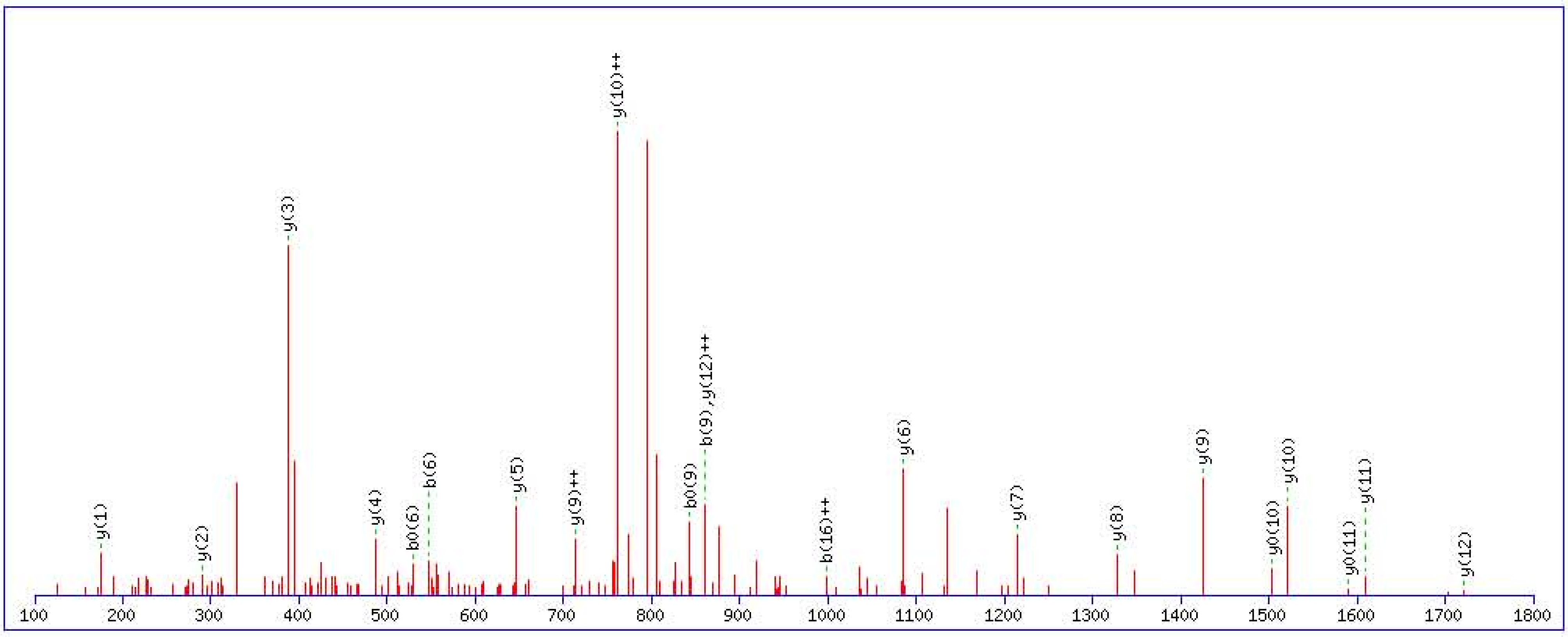
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SEGSSVNLSPPLEQCVPDR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

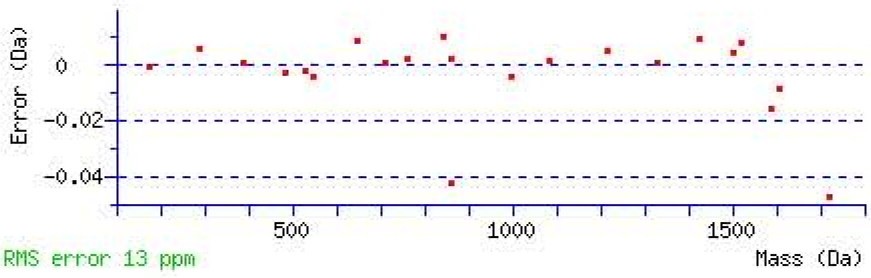
Match to Query 46125: 2381.140572 from(794.720800,3+) rtinseconds(2202) index(47255)
Title: Locus:1.1.1.3479.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

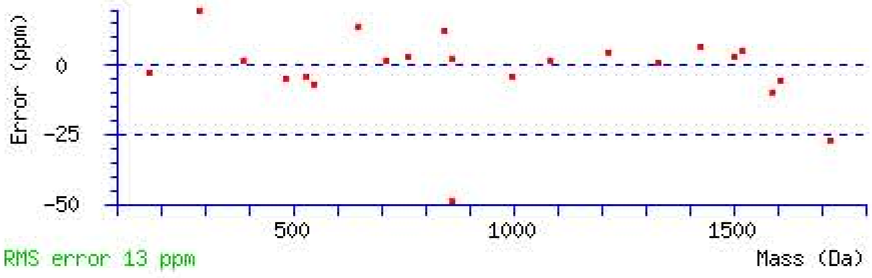
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2381.135529
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 84  Expect: 1.7e-008
Matches : 22/202 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							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
84.1	2381.135529	0.005043	SEGSSVNLSPPLEQCVPDR
1.2	2381.158005	-0.017433	HPKPSTVKDCPTLCKQTDNR

Mascot: http://www.matrixscience.com/

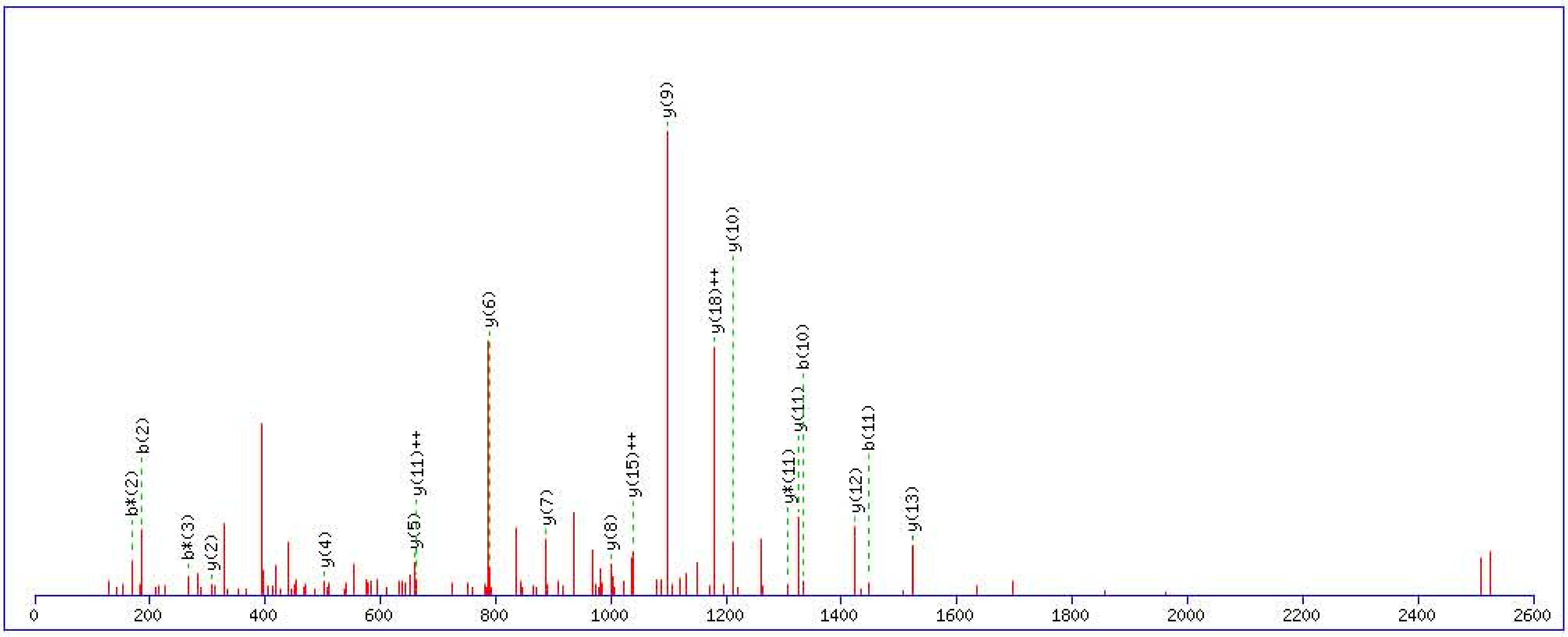
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQPSVLQVVNLPIVERPVCK**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

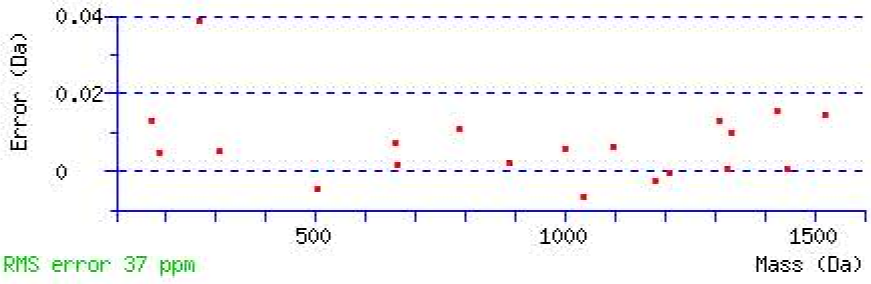
Match to Query 48982: 2542.420992 from(848.480940,3+) rtinseconds(2516) index(48939)
Title: Locus:1.1.1.3588.20 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

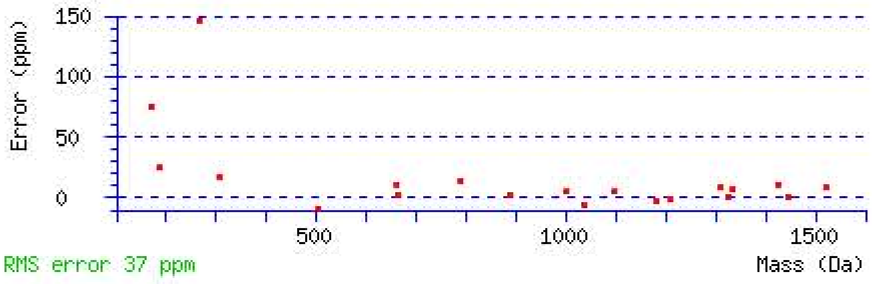
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2542.412766
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 6.8e-005
Matches : 20/210 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	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
51.0	2542.412766	0.008226	GQPSVLQVVNLPIVERPVCK
41.4	2542.412766	0.008226	GQPSVLQVVNLPIVERPVCK

Mascot: http://www.matrixscience.com/

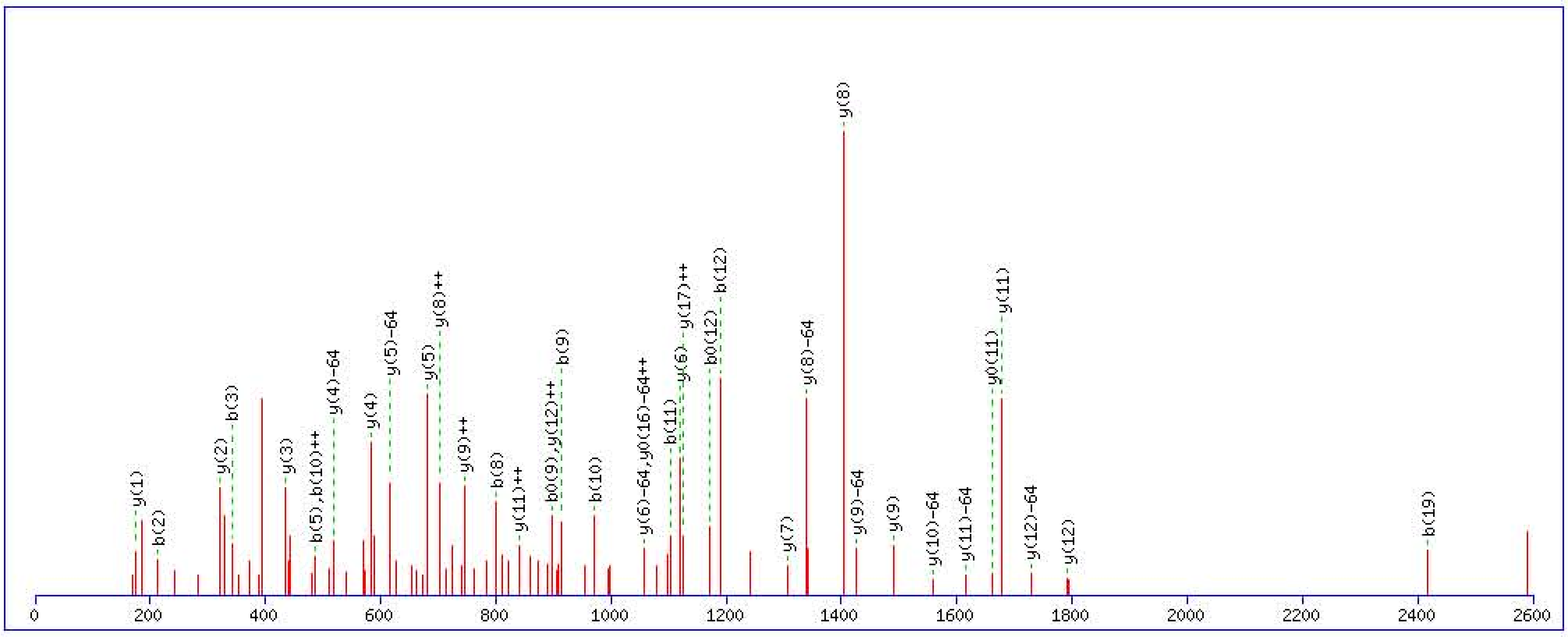
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVEGSDAEIGMSPWQVMLFR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

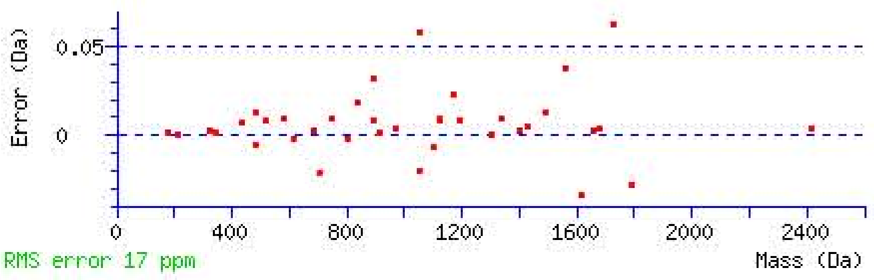
Match to Query 49434: 2591.271192 from(864.764340,3+) rtinseconds(2876) index(51385)
Title: Locus:1.1.1.3711.20 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

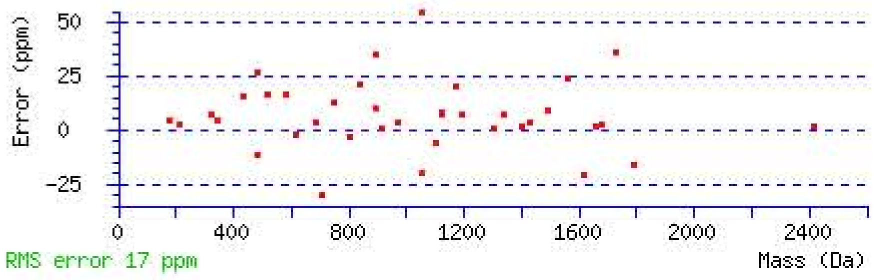
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2591.258621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15     : Biotin:Thermo-21345 (Q)
M17     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 81  Expect: 2.3e-007
Matches : 38/284 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							20
2	***213.159754***	107.083515					V	2479.181837	1240.094556	2462.155288	1231.581282	2461.171272	1231.089274	19
3	***342.202347***	171.604811			324.191782	162.599529	E	2380.113423	1190.560349	2363.086874	1182.047075	2362.102858	1181.555067	18
4	399.223811	200.115543			381.213246	191.110261	G	2251.070830	1126.039053	2234.044281	1117.525778	2233.060265	1117.033770	17
5	***486.255839***	243.631557			468.245274	234.626275	S	2194.049366	1097.528321	2177.022817	1089.015046	2176.038801	1088.523038	16
6	601.282782	301.145029			583.272217	292.139747	D	2107.017338	1054.012307	2089.990789	1045.499032	2089.006773	1045.007024	15
7	672.319896	336.663586			654.309331	327.658303	A	1991.990395	996.498836	1974.963846	987.985561	1973.979830	987.493553	14
8	***801.362489***	401.184883			783.351924	392.179600	E	1920.953281	960.980279	1903.926732	952.467004	1902.942716	951.974996	13
9	***914.446553***	457.726915			896.435988	448.721632	I	***1791.910688***	896.458982	1774.884139	887.945708	1773.900123	887.453700	12
10	***971.468017***	486.237647			953.457452	477.232364	G	***1678.826624***	839.916950	1661.800075	831.403676	1660.816059	830.911668	11
11	***1102.508502***	551.757889			1084.497937	542.752606	M	1621.805160	811.406218	1604.778611	802.892944	1603.794595	802.400936	10
12	***1189.540530***	595.273903			1171.529965	586.268621	S	***1490.764675***	745.885976	1473.738126	737.372701	1472.754110	736.880693	9
13	1286.593294	643.800285			1268.582729	634.795003	P	***1403.732647***	702.369962	1386.706098	693.856687			8
14	1472.672607	736.839942			1454.662042	727.834659	W	***1306.679883***	653.843580	1289.653334	645.330305			7
15	1911.897933	956.452605	1894.871384	947.939330	1893.887368	947.447322	Q	***1120.600570***	560.803923	1103.574021	552.290649			6
16	2010.966347	1005.986812	1993.939798	997.473537	1992.955782	996.981529	V	***681.375244***	341.191260	664.348695	332.677986			5
17	2158.001747	1079.504511	2140.975198	1070.991237	2139.991182	1070.499229	M	***582.306830***	291.657053	565.280281	283.143779			4
18	2271.085811	1136.046543	2254.059262	1127.533269	2253.075246	1127.041261	L	***435.271430***	218.139353	418.244881	209.626078			3
19	***2418.154225***	1209.580750	2401.127676	1201.067476	2400.143660	1200.575468	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 IVEGSDAEIGMSPWQVMLFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
80.7	2591.258621	0.012571	IVEGSDAEIGMSPWQVMLFR
16.4	2591.258621	0.012571	IVEGSDAEIGMSPWQVMLFR

Mascot: http://www.matrixscience.com/

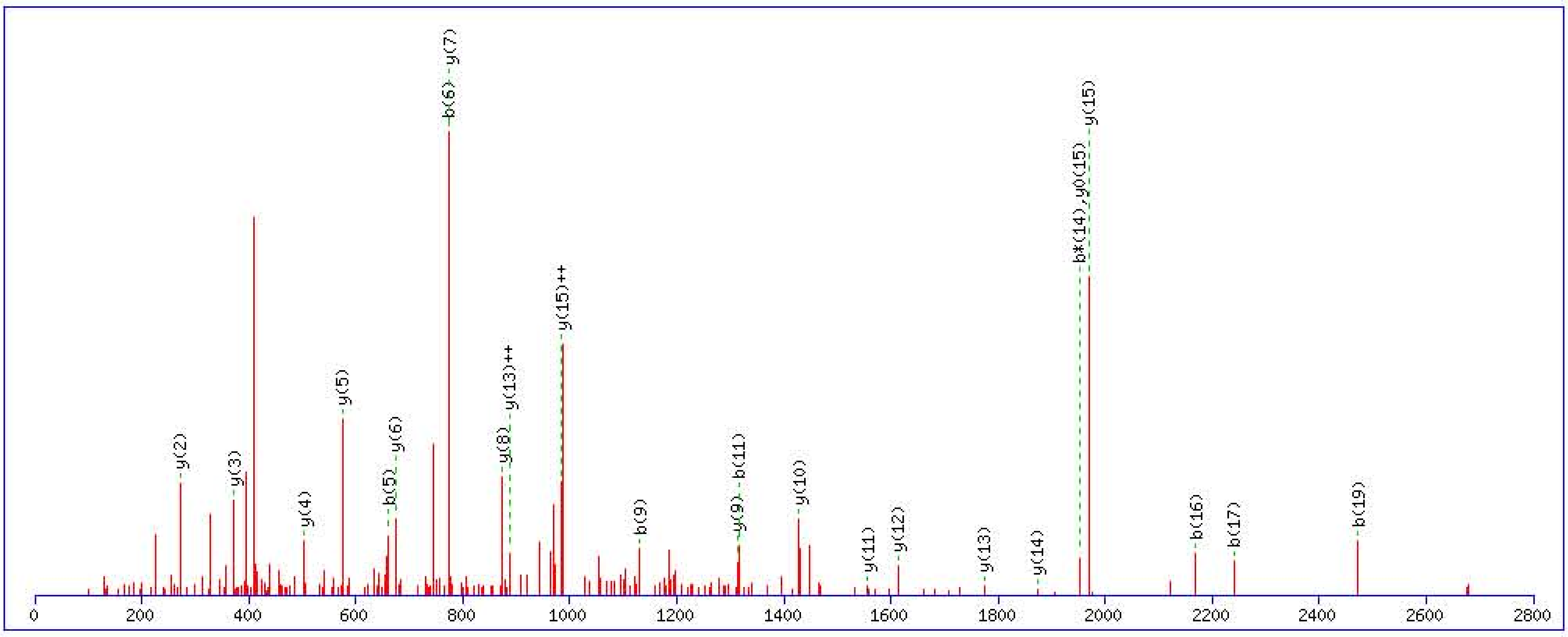
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RQECSIPVCGQDQVTVAMTPR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

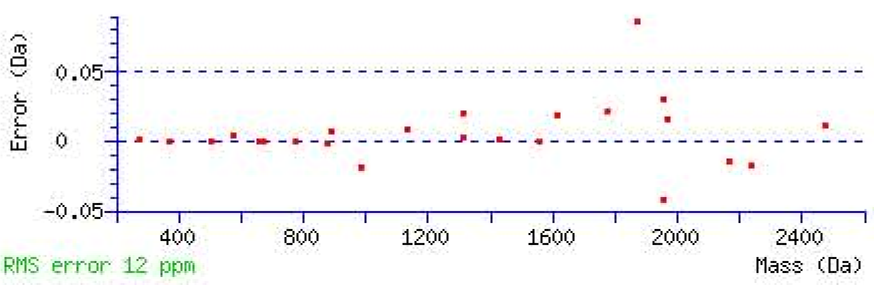
Match to Query 50843: 2742.306642 from(915.109490,3+) rtinseconds(2048) index(46328)
Title: Locus:1.1.1.3425.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

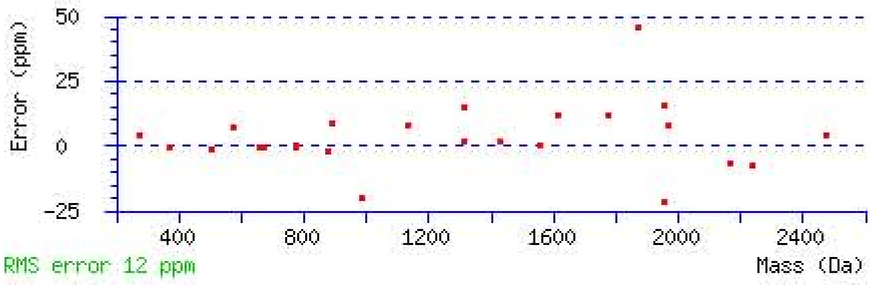
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2742.307404
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 85  Expect: 6.6e-008
Matches : 25/232 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	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
85.4	2742.307404	-0.000762	RQECSIPVCGQDQVTVAMTPR
60.1	2742.307404	-0.000762	RQECSIPVCGQDQVTVAMTPR
12.6	2742.307404	-0.000762	RQECSIPVCGQDQVTVAMTPR

Mascot: http://www.matrixscience.com/

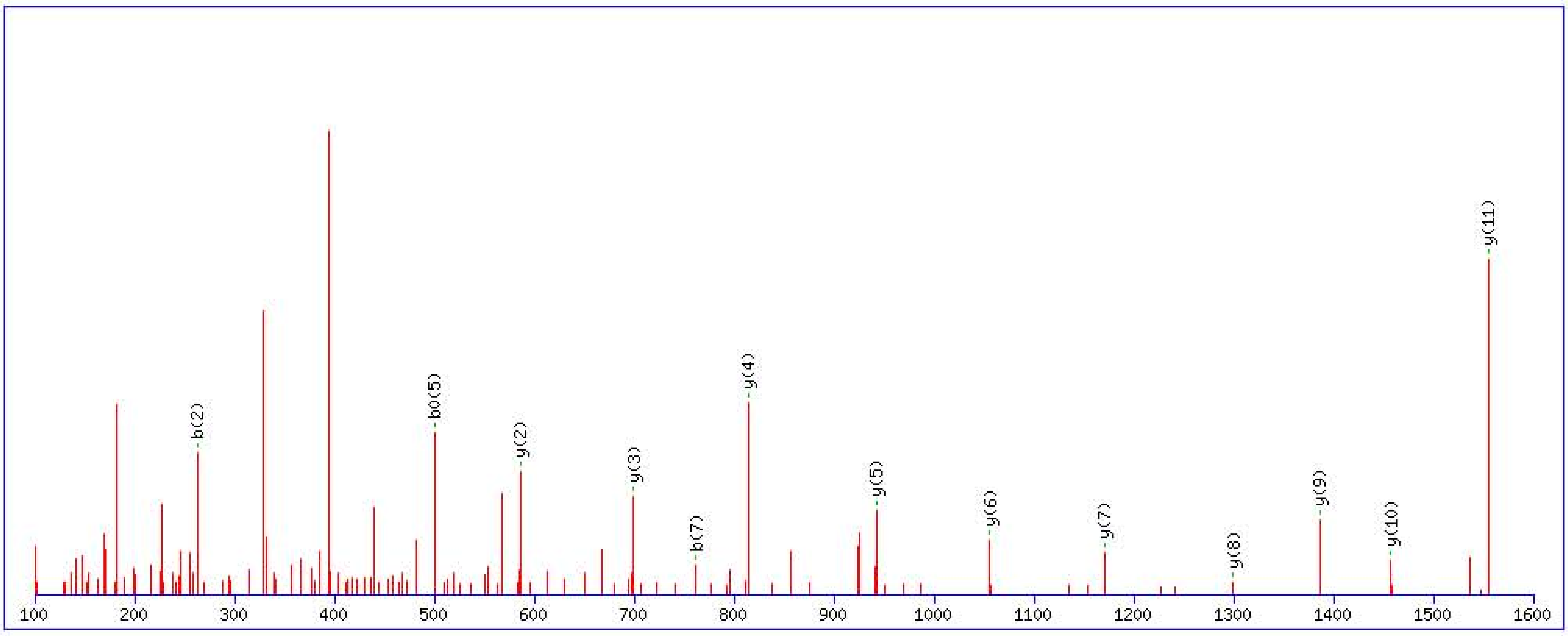
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DMPASEDLQDLQK**
Found in **SEPP1_HUMAN**, Selenoprotein P OS=Homo sapiens GN=SEPP1 PE=1 SV=3

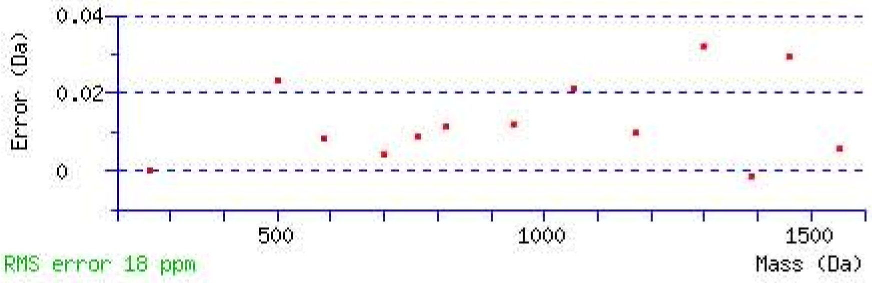
Match to Query 36059: 1815.843102 from(606.288310,3+) rtinseconds(2085) index(5389)
Title: Locus:1.1.1.3246.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

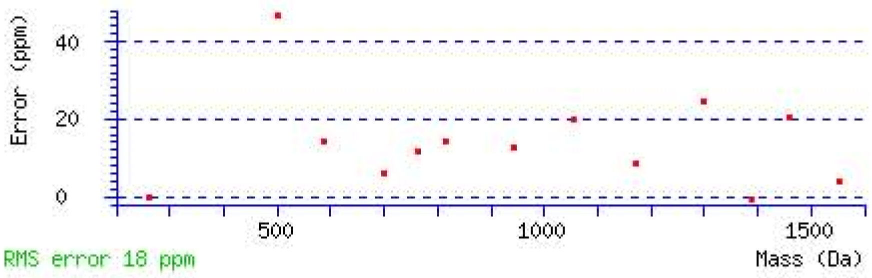
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1815.838272
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
Q12    : Biotin:Thermo-21345 (Q)
Ions Score: 93  Expect: 7.3e-009
Matches : 13/180 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	116.034219	58.520748			98.023654	49.515465	D							13
2	**263.069619**	132.038447			245.059054	123.033165	M	1701.818621	851.412948	1684.792072	842.899674	1683.808056	842.407666	12
3	360.122383	180.564829			342.111818	171.559547	P	***1554.783221***	777.895248	1537.756672	769.381974	1536.772656	768.889966	11
4	431.159497	216.083386			413.148932	207.078104	A	***1457.730457***	729.368866	1440.703908	720.855592	1439.719892	720.363584	10
5	518.191525	259.599401			500.180960	250.594118	S	***1386.693343***	693.850310	1369.666794	685.337035	1368.682778	684.845027	9
6	647.234118	324.120697			629.223553	315.115414	E	***1299.661315***	650.334296	1282.634766	641.821021	1281.650750	641.329013	8
7	**762.261061**	381.634168			744.250496	372.628886	D	***1170.618722***	585.812999	1153.592173	577.299725	1152.608157	576.807716	7
8	875.345125	438.176200			857.334560	429.170918	L	***1055.591779***	528.299528	1038.565230	519.786253	1037.581214	519.294245	6
9	1003.403703	502.205490	986.377154	493.692215	985.393138	493.200207	Q	***942.507715***	471.757496	925.481166	463.244221	924.497150	462.752213	5
10	1118.430646	559.718961	1101.404097	551.205687	1100.420081	550.713679	D	***814.449137***	407.728207	797.422588	399.214932	796.438572	398.722924	4
11	1231.514710	616.260993	1214.488161	607.747719	1213.504145	607.255710	L	***699.422194***	350.214735	682.395645	341.701461			3
12	1670.740036	835.873656	1653.713487	827.360382	1652.729471	826.868373	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
92.5	1815.838272	0.004830	DMPASEDLQDLQK
44.6	1815.838272	0.004830	DMPASEDLQDLQK

Mascot: http://www.matrixscience.com/

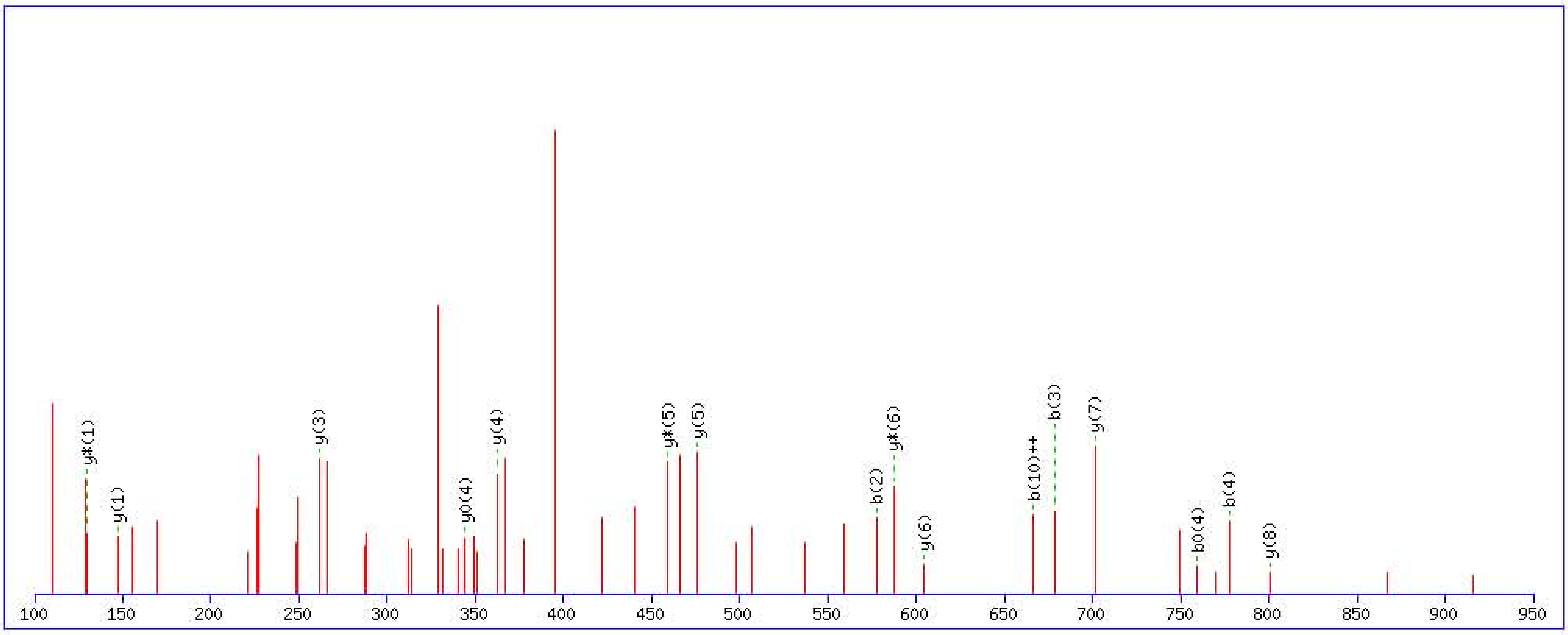
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQTVPQNTGGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

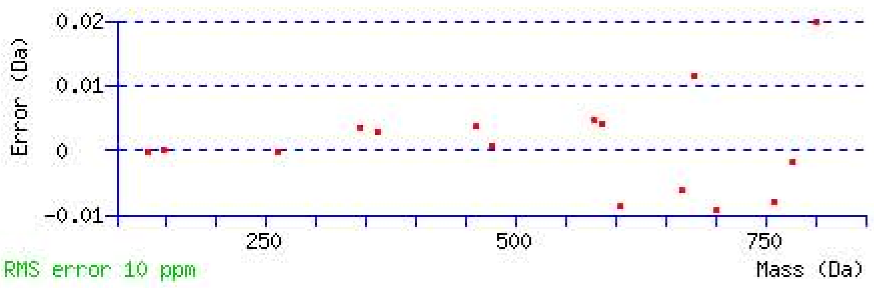
Match to Query 26562: 1476.747612 from(493.256480,3+) rtinseconds(1240) index(56652)
Title: Locus:1.1.1.1343.5 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

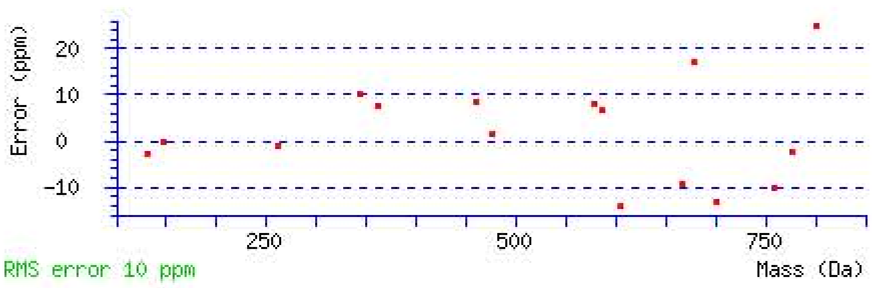
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1476.750748
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 26 **Expect:** 0.0089
Matches : 16/108 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	138.066188	69.536732					H							11
2	**577.291514**	289.149395	560.264965	280.636121			Q	1340.699099	670.853187	1323.672550	662.339913	1322.688534	661.847905	10
3	**678.339193**	339.673235	661.312644	331.159960	660.328628	330.667952	T	901.473773	451.240524	884.447224	442.727250	883.463208	442.235242	9
4	**777.407607**	389.207442	760.381058	380.694167	759.397042	380.202159	V	***800.426094***	400.716685	783.399545	392.203410	782.415529	391.711402	8
5	874.460371	437.733824	857.433822	429.220549	856.449806	428.728541	P	***701.357680***	351.182478	684.331131	342.669203	683.347115	342.177195	7
6	1002.518949	501.763113	985.492400	493.249838	984.508384	492.757830	Q	***604.304916***	302.656096	587.278367	294.142821	586.294351	293.650813	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
26.5	1476.750748	-0.003136	HQTVPQNTGGK
16.3	1476.750748	-0.003136	HQTVPQNTGGK
4.6	1476.736115	0.011497	HQEALIGQSFYGK

Mascot: http://www.matrixscience.com/

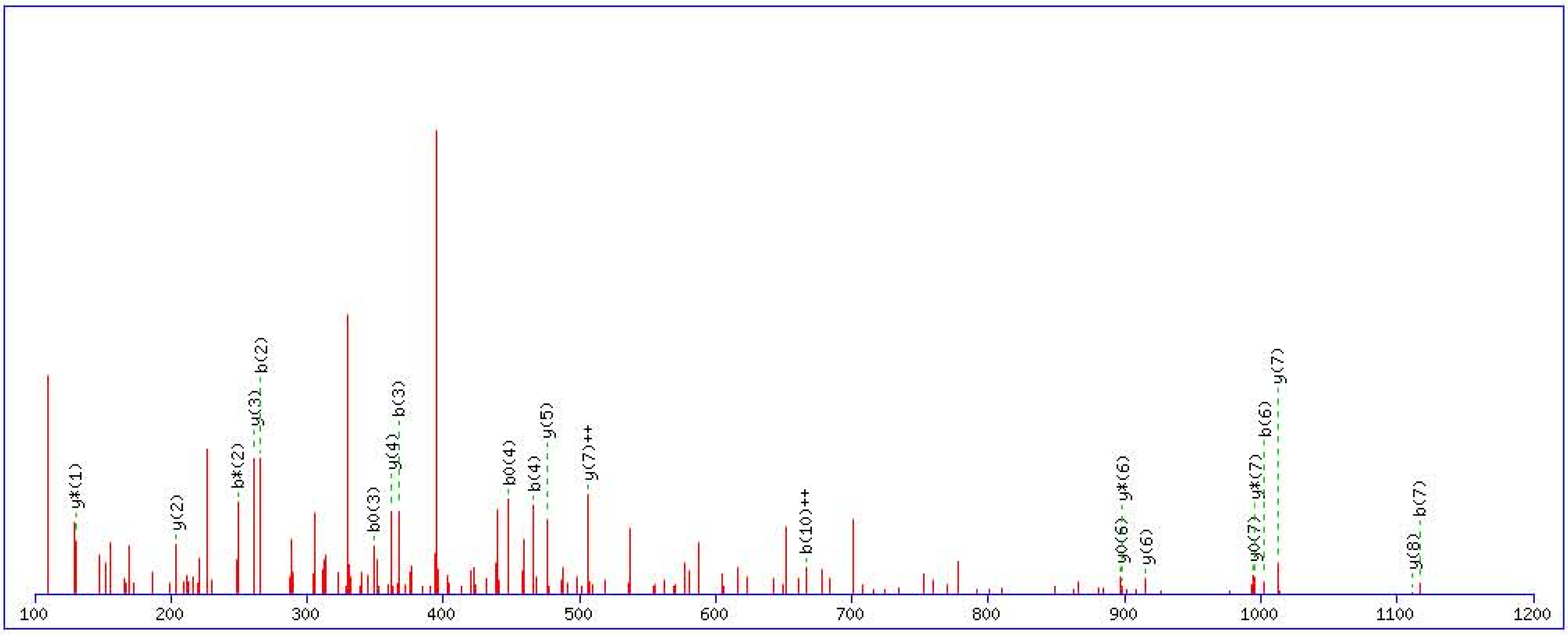
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQTVPQNTGGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

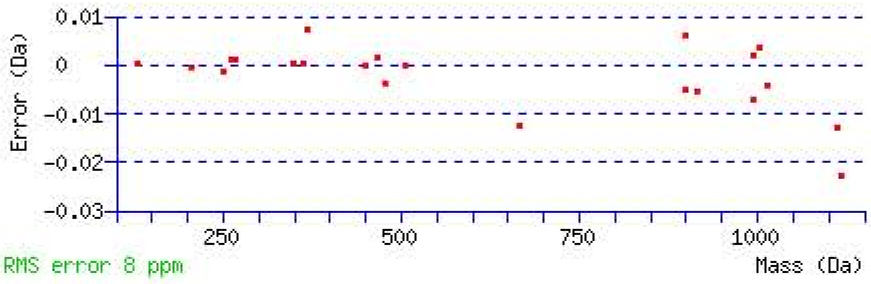
Match to Query 26564: 1476.748692 from(493.256840,3+) rtinseconds(1222) index(56607)
Title: Locus:1.1.1.1337.3 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

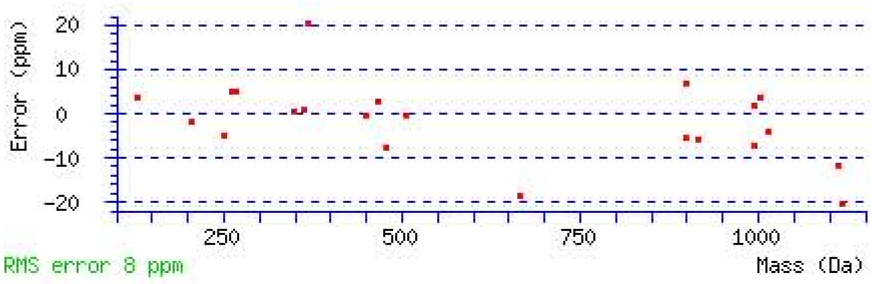
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1476.750748
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 25  Expect: 0.015
Matches : 22/108 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							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
25.1	1476.750748	-0.002056	HQTVPQNTGGK
24.2	1476.750748	-0.002056	HQTVPQNTGGK
5.7	1476.736115	0.012577	HQEALIGQSFYGK

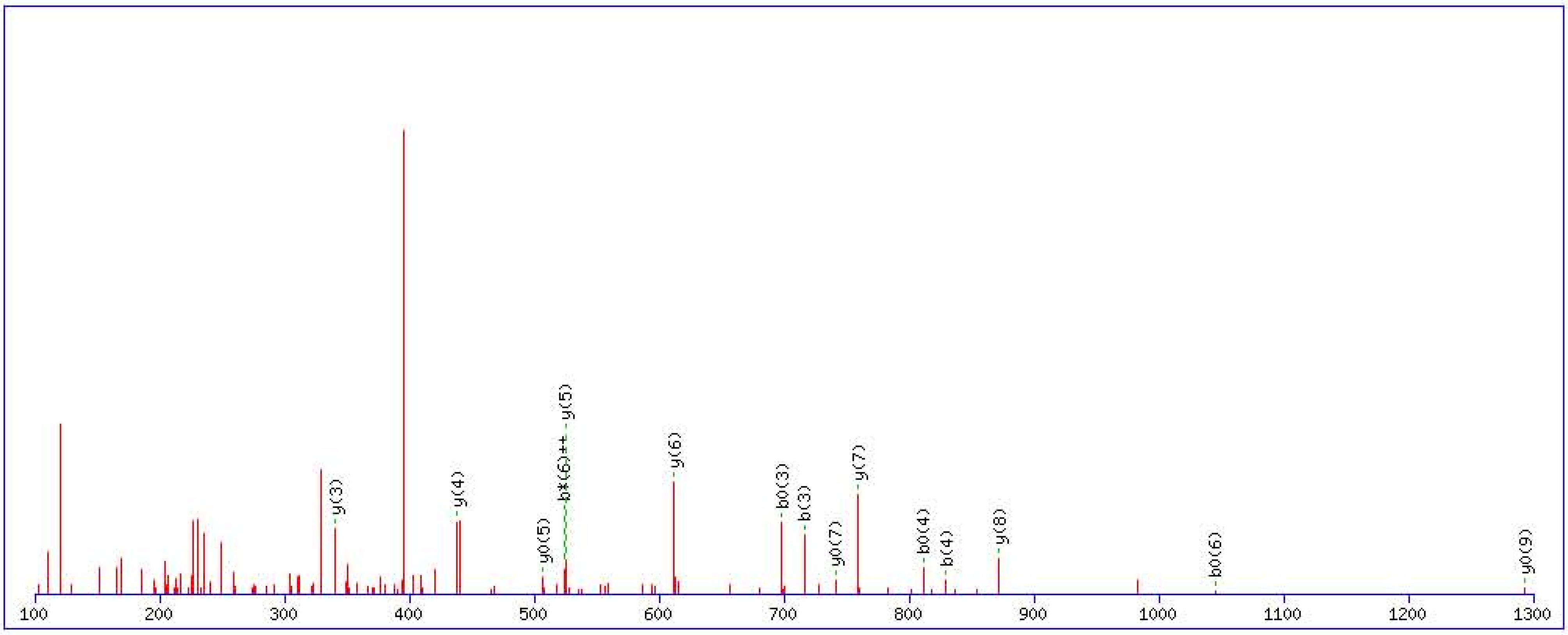
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EFQLFSSPHGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

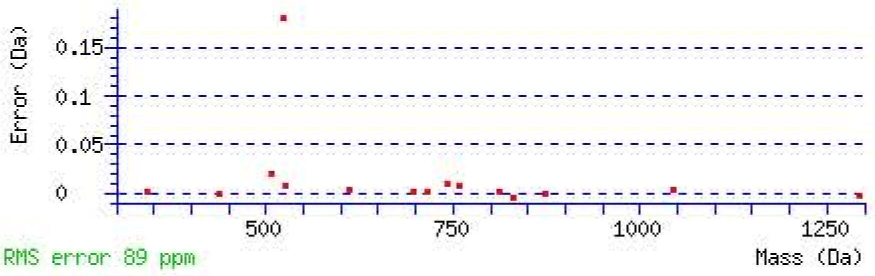
Match to Query 29990: 1586.792142 from(529.937990,3+) rtinseconds(2078) index(60999)
Title: Locus:1.1.1.1635.5 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

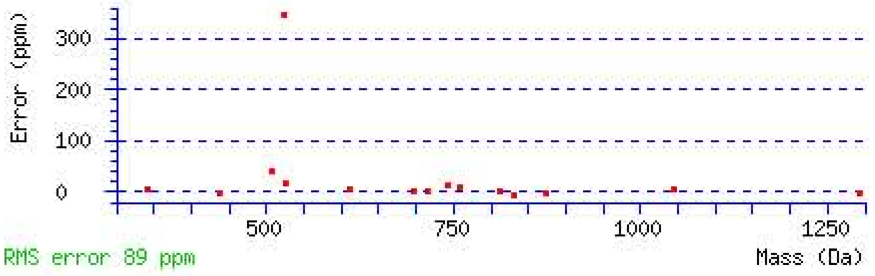
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1586.791534
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.0036
Matches : 15/108 fragment ions using 27 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	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
28.0	1586.791534	0.000608	EFQLFSSPHGK
1.9	1586.813980	-0.021838	FTQNHMLIYHKR

Mascot: http://www.matrixscience.com/

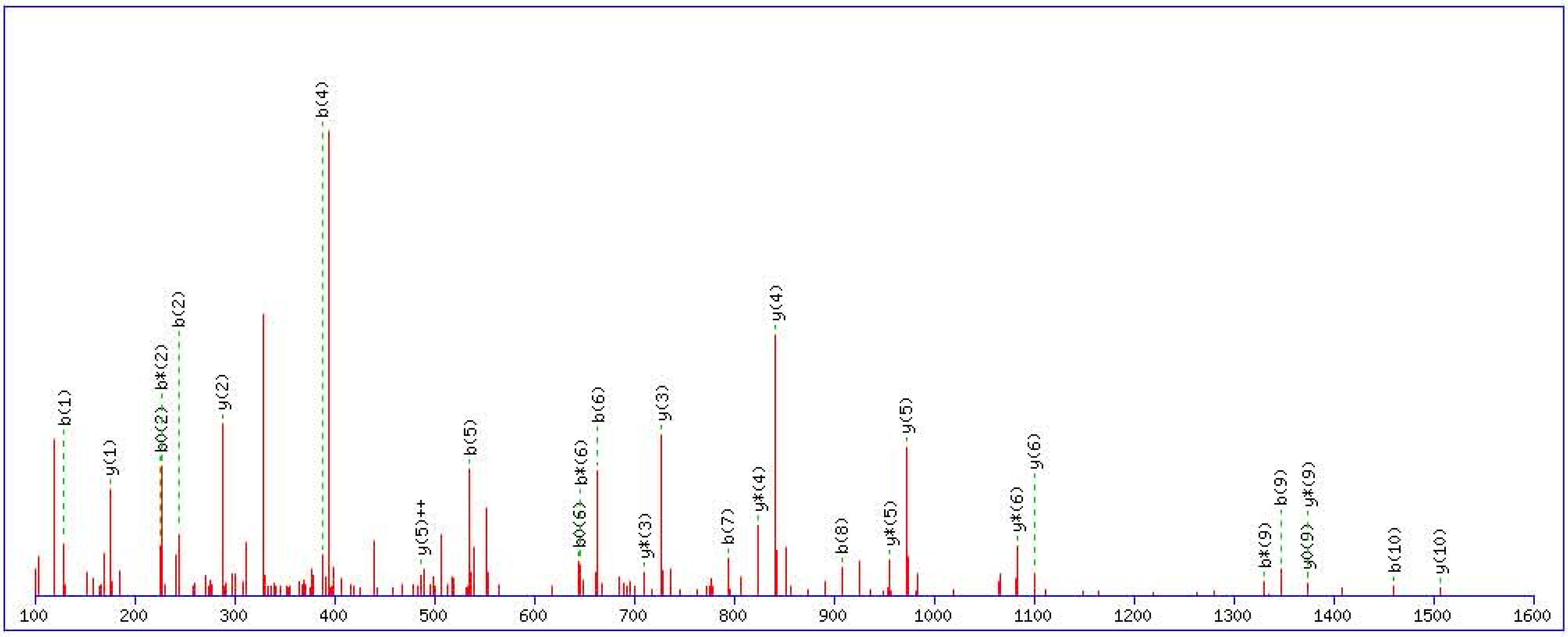
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KDSGFQMNQLR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

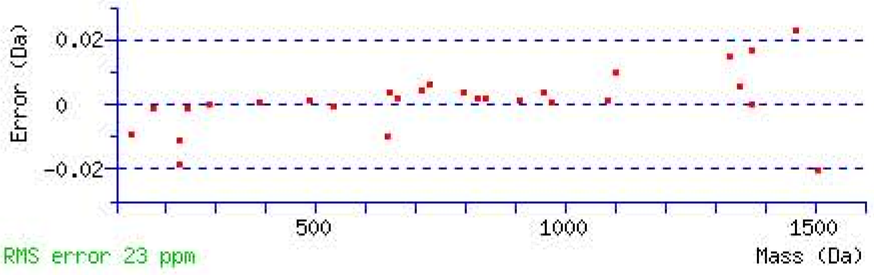
Match to Query 32303: 1633.801062 from(545.607630,3+) rtinseconds(1868) index(59720)
Title: Locus:1.1.1.1562.9 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

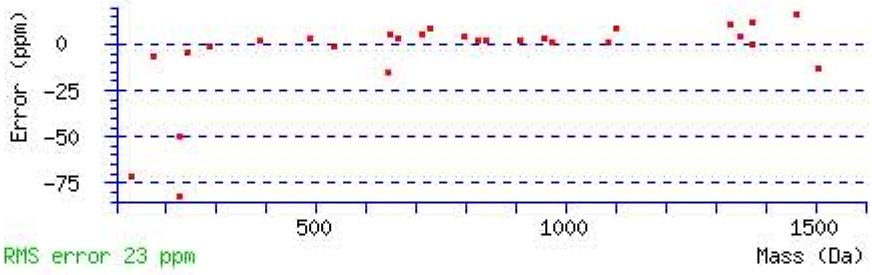
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1633.806854
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 38 **Expect:** 0.001
Matches : 28/102 fragment ions using 65 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							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	*663.309666*	332.158471	646.283117	323.645197	645.299101	323.153189	Q	**1100.570332**	550.788804	1083.543783	542.275530			6
7	*794.350151*	397.678714	777.323602	389.165439	776.339586	388.673431	M	**972.511754**	486.759515	955.485205	478.246240			5
8	*908.393078*	454.700177	891.366529	446.186903	890.382513	445.694895	N	**841.471269**	421.239272	824.444720	412.725998			4
9	*1347.618404*	674.312840	1330.591855	665.799566	1329.607839	665.307558	Q	**727.428342**	364.217809	710.401793	355.704534			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
38.0	1633.806854	-0.005792	KDSGFQMNQLR
16.8	1633.806854	-0.005792	KDSGFQMNQLR
5.7	1633.798096	0.002966	QDQEKDNMIEKLK
2.4	1633.824615	-0.023553	AGGAFLMAGQVAEQLR
2.3	1633.817184	-0.016122	HLHEGAKSASAEELR
1.5	1633.809311	-0.008249	GLSEEERSEKAMLR
1.5	1633.795609	0.005453	KFMEDEQQLR
1.2	1633.799454	0.001608	DANSFKSRDQR

Mascot: http://www.matrixscience.com/

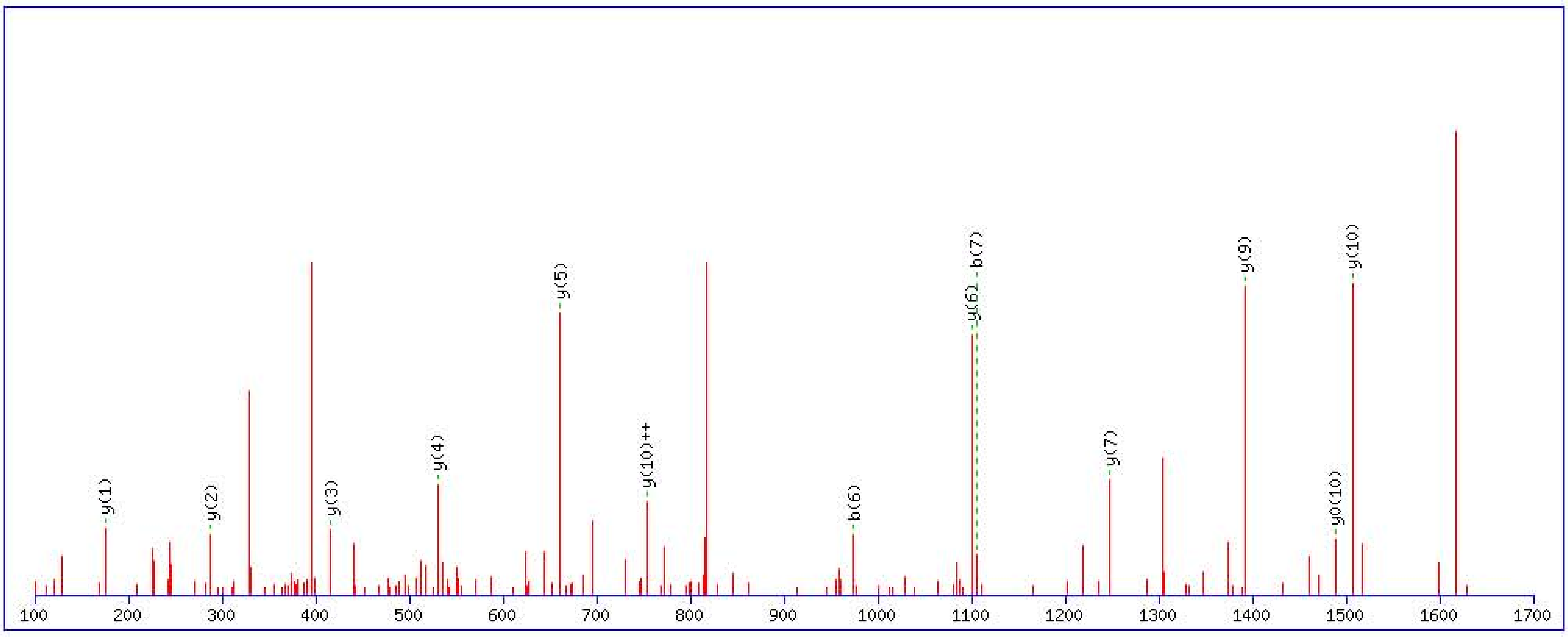
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KDSGFQMNQLR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

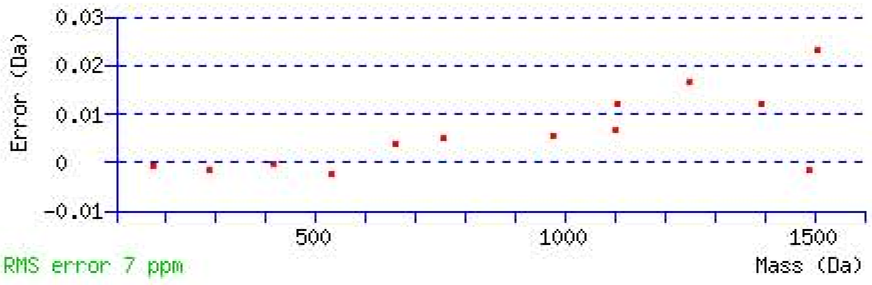
Match to Query 32313: 1633.812748 from(817.913650,2+) rtinseconds(1769) index(59302)
Title: Locus:1.1.1.1527.23 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

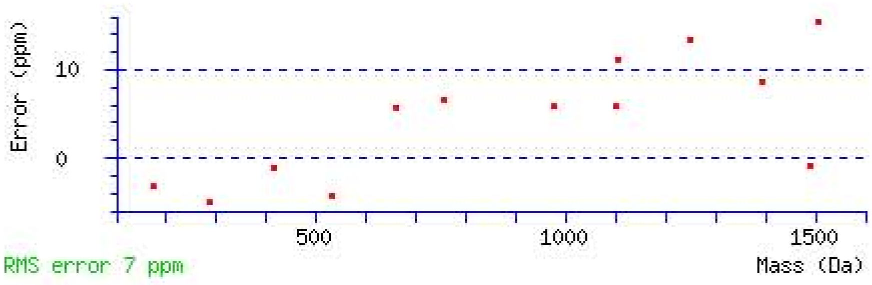
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 80 **Expect:** 2.2e-007
Matches : 13/102 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	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
80.2	1633.806854	0.005894	KDSGFQMNQLR
32.6	1633.806854	0.005894	KDSGFQMNQLR
12.6	1633.824615	-0.011867	AGGAFLMAGQVAEQLR
10.6	1633.795609	0.017139	KFMEDEQQLR
7.2	1633.798096	0.014652	QDQEKDNMIEKLK
6.4	1633.832443	-0.019695	NRYINILAYDHSR
6.3	1633.810669	0.002079	AGLENMDRAAQRFR
4.8	1633.805954	0.006794	LFREENDINESIR
4.7	1633.799454	0.013294	GPDNSMGFGAERKIR
4.6	1633.824585	-0.011837	EQAARFCAEIKSPK

Mascot: http://www.matrixscience.com/

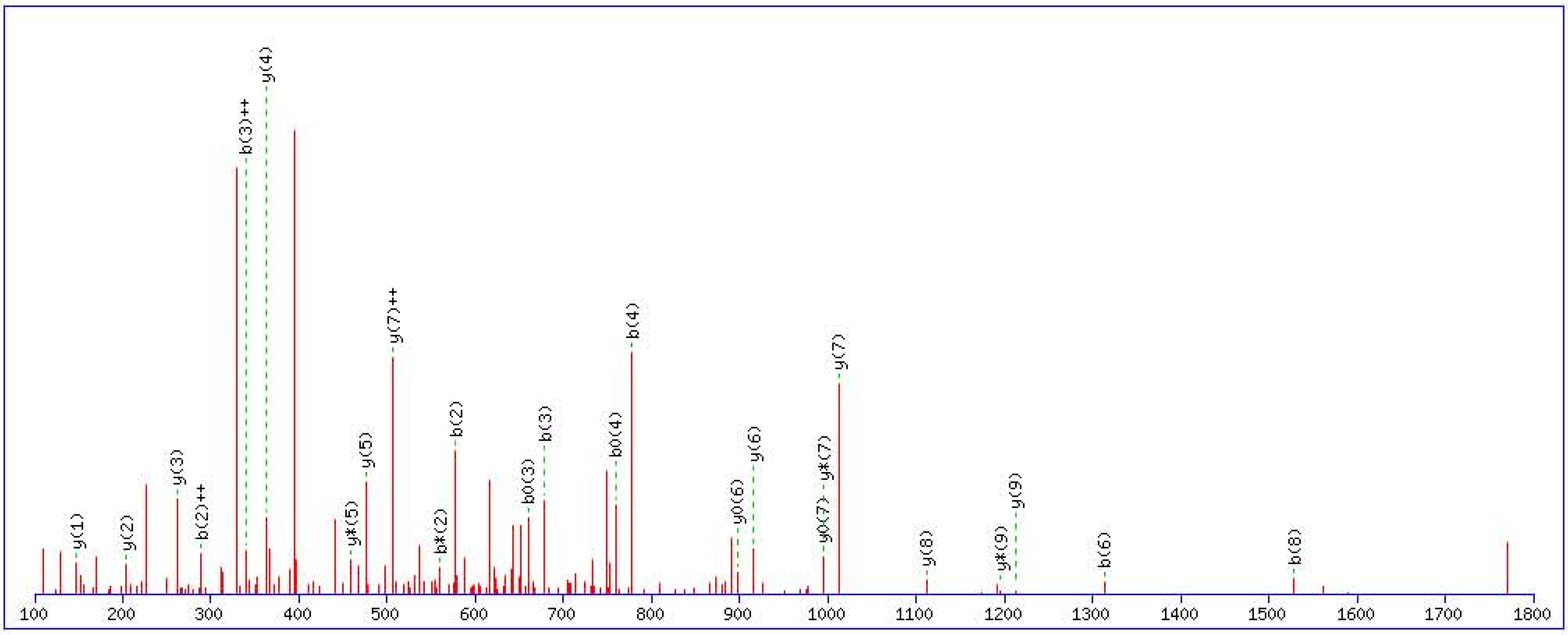
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQTVPQNTGGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

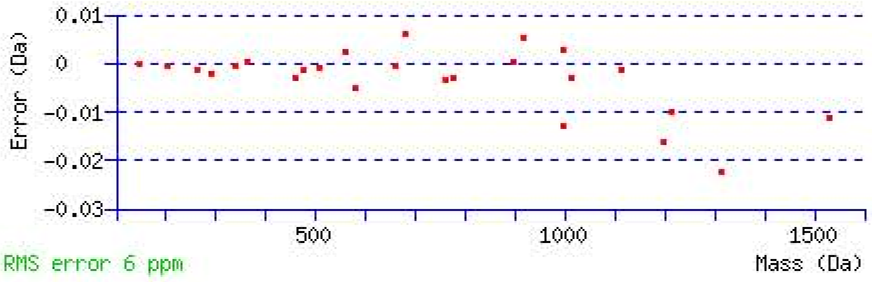
Match to Query 35463: 1787.914152 from(596.978660,3+) rtinseconds(1613) index(58595)
Title: Locus:1.1.1.1473.10 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

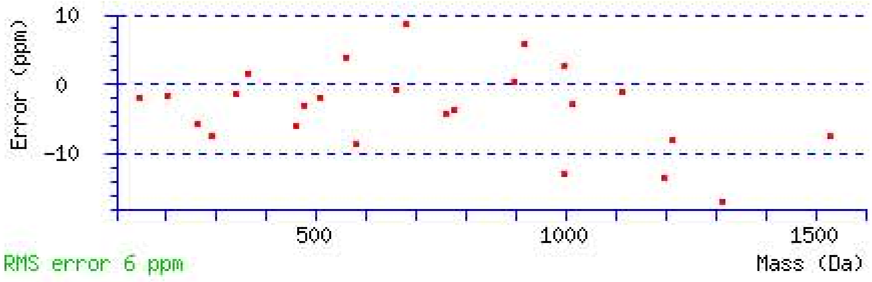
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1787.917496
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: 37 **Expect:** 0.00059
Matches : 25/108 fragment ions using 59 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	**577.291514**	**289.149395**	560.264965	280.636121			Q	1651.865847	826.436562	1634.839298	817.923287	1633.855282	817.431279	10
3	**678.339193**	**339.673235**	661.312644	331.159960	660.328628	330.667952	T	***1212.640521***	606.823899	1195.613972	598.310624	1194.629956	597.818616	9
4	**777.407607**	389.207442	760.381058	380.694167	759.397042	380.202159	V	***1111.592842***	556.300059	1094.566293	547.786785	1093.582277	547.294777	8
5	874.460371	437.733824	857.433822	429.220549	856.449806	428.728541	P	***1012.524428***	506.765852	995.497879	498.252578	994.513863	497.760570	7
6	**1313.685697**	657.346487	1296.659148	648.833212	1295.675132	648.341204	Q	***915.471664***	458.239470	898.445115	449.726196	897.461099	449.234188	6
7	1427.728624	714.367950	1410.702075	705.854676	1409.718059	705.362668	N	***476.246338***	238.626807	459.219789	230.113532	458.235773	229.621524	5
8	**1528.776303**	764.891790	1511.749754	756.378515	1510.765738	755.886507	T	***362.203411***	181.605343	345.176862	173.092069	344.192846	172.600061	4
9	1585.797767	793.402522	1568.771218	784.889247	1567.787202	784.397239	G	***261.155732***	131.081504	244.129183	122.568229			3
10	1642.819231	821.913254	1625.792682	813.399979	1624.808666	812.907971	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
36.5	1787.917496	-0.003344	HQTVPQNTGGK
2.1	1787.923996	-0.009844	VPLQGFAALEGMNGIQK
2.0	1787.935211	-0.021059	ARAYGPGIEPTGNMVKK

Mascot: http://www.matrixscience.com/

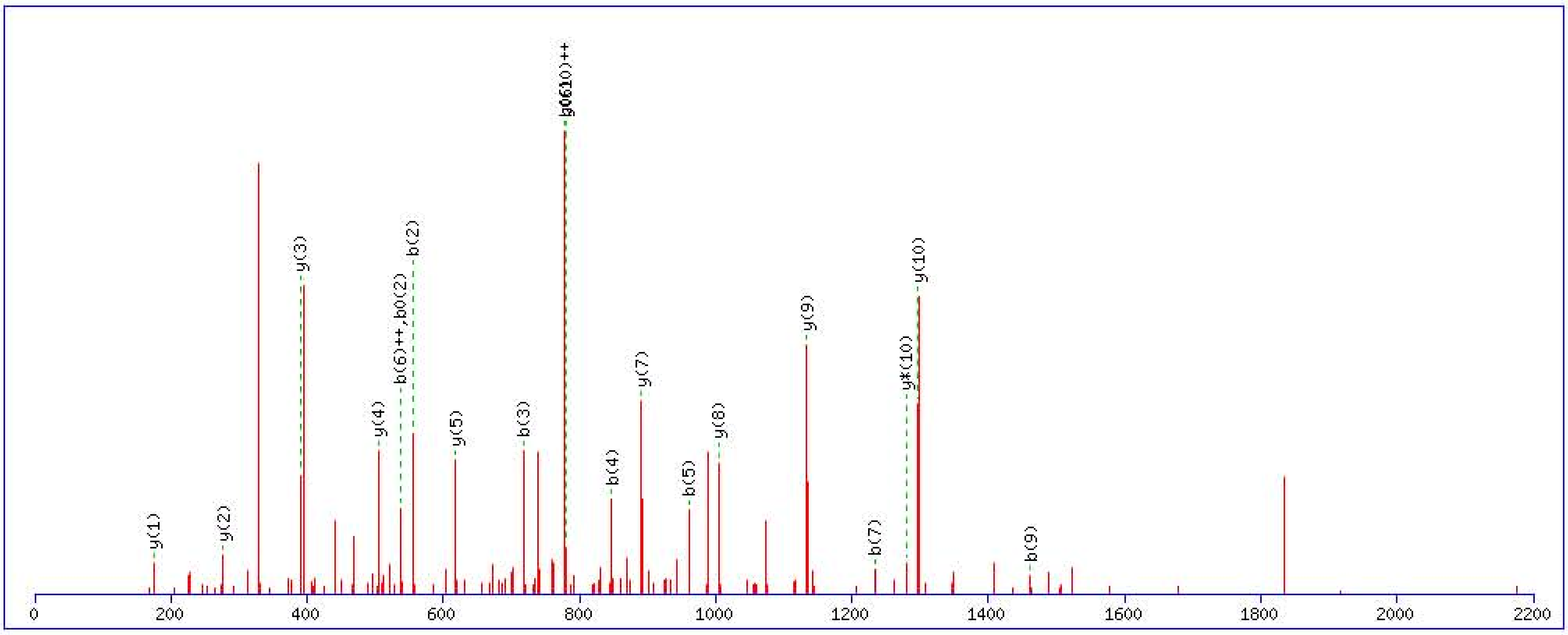
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DQYELLCLDNTR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

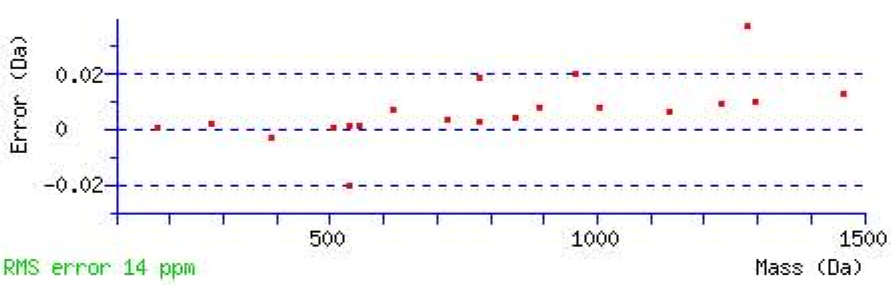
Match to Query 36618: 1849.884028 from(925.949290,2+) rtinseconds(2458) index(62960)
Title: Locus:1.1.1.1767.14 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

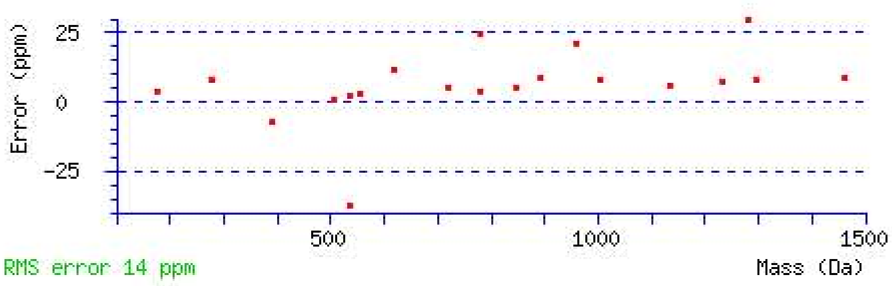
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1849.870239
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 50  Expect: 3.4e-005
Matches : 20/128 fragment ions using 45 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							12
2	**555.259545**	278.133411	538.232996	269.620136	537.248980	269.128128	Q	1735.850590	868.428933	1718.824041	859.915659	1717.840025	859.423651	11
3	**718.322874**	359.665075	701.296325	351.151801	700.312309	350.659793	Y	***1296.625264***	648.816270	1279.598715	640.302996	1278.614699	639.810988	10
4	**847.365467**	424.186372	830.338918	415.673097	829.354902	415.181089	E	***1133.561935***	567.284606	1116.535386	558.771331	1115.551370	558.279323	9
5	**960.449531**	480.728404	943.422982	472.215129	942.438966	471.723121	L	***1004.519342***	502.763309	987.492793	494.250034	986.508777	493.758026	8
6	1073.533595	537.270436	1056.507046	528.757161	1055.523030	528.265153	L	***891.435278***	446.221277	874.408729	437.708002	873.424713	437.215994	7
7	**1233.564244**	617.285760	1216.537695	608.772486	1215.553679	608.280478	C	***778.351214***	389.679245	761.324665	381.165971	760.340649	380.673963	6
8	1346.648308	673.827792	1329.621759	665.314518	1328.637743	664.822510	L	***618.320565***	309.663921	601.294016	301.150646	600.310000	300.658638	5
9	**1461.675251**	731.341264	1444.648702	722.827989	1443.664686	722.335981	D	***505.236501***	253.121888	488.209952	244.608614	487.225936	244.116606	4
10	1575.718178	788.362727	1558.691629	779.849453	1557.707613	779.357445	N	***390.209558***	195.608417	373.183009	187.095142	372.198993	186.603134	3
11	1676.765857	838.886567	1659.739308	830.373292	1658.755292	829.881284	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 DQYELLCLDNTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.4	1849.870239	0.013789	DQYELLCLDNTR
2.8	1849.858810	0.025218	ISQETEQRCESLNTR

Mascot: http://www.matrixscience.com/

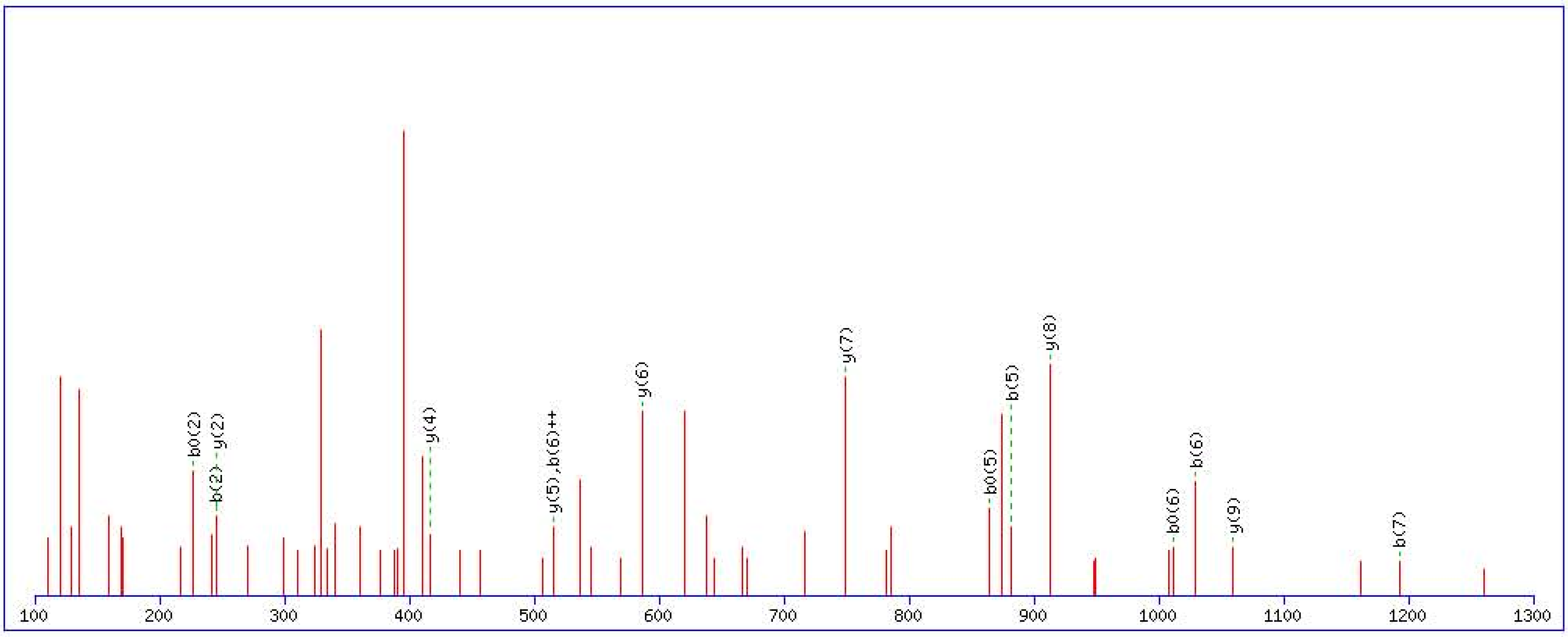
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EDPQTFYYAVAVVK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

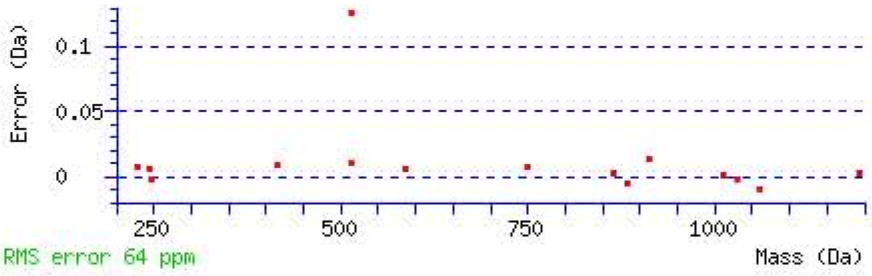
Match to Query 38169: 1939.984152 from(647.668660,3+) rtinseconds(2589) index(63757)
Title: Locus:1.1.1.1813.8 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

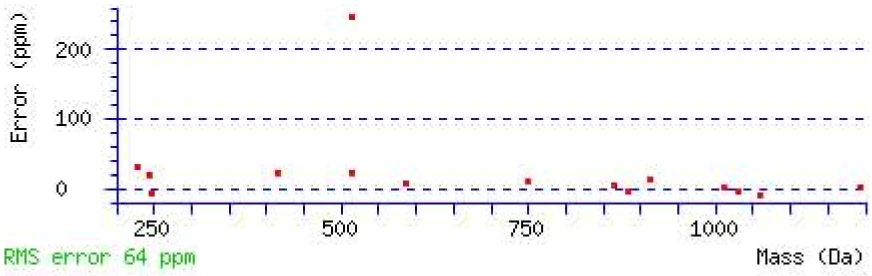
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1939.975372
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 26 **Expect:** 0.077
Matches : 15/132 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							14
2	**245.076812**	123.042044			227.066247	114.036762	D	1811.940058	906.473667	1794.913509	897.960393	1793.929493	897.468385	13
3	342.129576	171.568426			324.119011	162.563144	P	1696.913115	848.960196	1679.886566	840.446921	1678.902550	839.954913	12
4	781.354902	391.181089	764.328353	382.667815	763.344337	382.175807	Q	1599.860351	800.433814	1582.833802	791.920539	1581.849786	791.428531	11
5	**882.402581**	441.704929	865.376032	433.191654	864.392016	432.699646	T	1160.635025	580.821151	1143.608476	572.307876	1142.624460	571.815868	10
6	**1029.470995**	515.239136	1012.444446	506.725861	1011.460430	506.233853	F	***1059.587346***	530.297311	1042.560797	521.784037			9
7	**1192.534324**	596.770800	1175.507775	588.257526	1174.523759	587.765518	Y	***912.518932***	456.763104	895.492383	448.249830			8
8	1355.597653	678.302465	1338.571104	669.789190	1337.587088	669.297182	Y	***749.455603***	375.231440	732.429054	366.718165			7
9	1426.634767	713.821022	1409.608218	705.307747	1408.624202	704.815739	A	***586.392274***	293.699775	569.365725	285.186501			6
10	1525.703181	763.355229	1508.676632	754.841954	1507.692616	754.349946	V	***515.355160***	258.181218	498.328611	249.667944			5
11	1596.740295	798.873786	1579.713746	790.360511	1578.729730	789.868503	A	***416.286746***	208.647011	399.260197	200.133737			4
12	1695.808709	848.407993	1678.782160	839.894718	1677.798144	839.402710	V	345.249632	173.128454	328.223083	164.615180			3
13	1794.877123	897.942200	1777.850574	889.428925	1776.866558	888.936917	V	***246.181218***	123.594247	229.154669	115.080973			2
14							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of EDPQTFYYAVAVVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.1	1939.975372	0.008780	EDPQTFYYAVAVVK

Mascot: http://www.matrixscience.com/

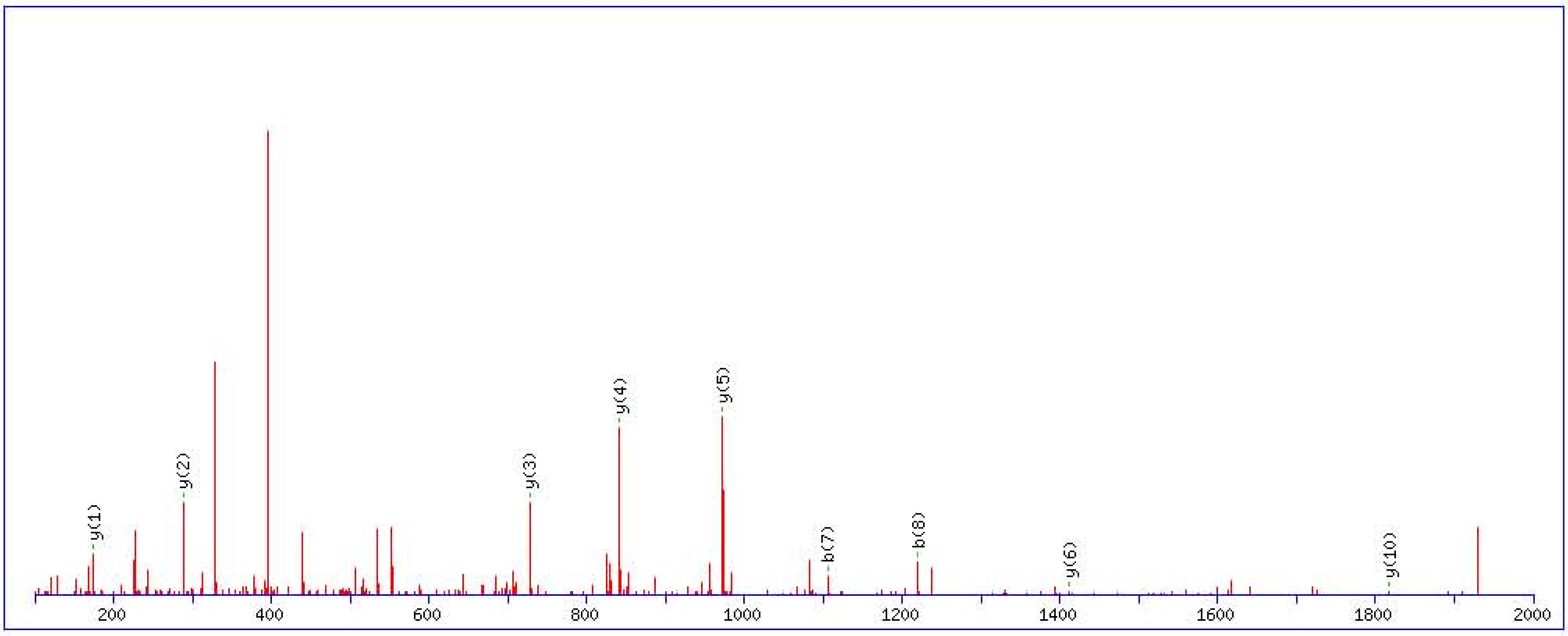
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KDSGFQMNQLR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

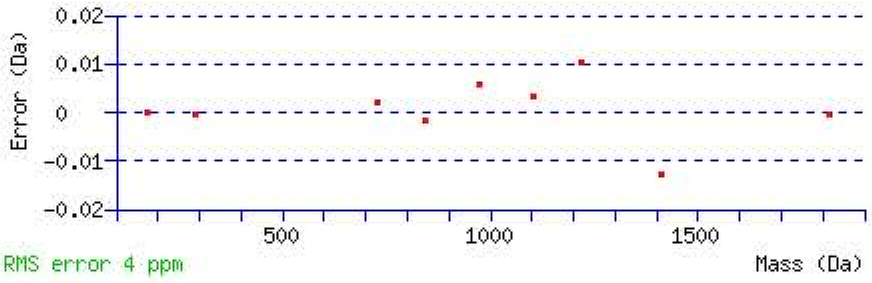
Match to Query 38243: 1944.974442 from(649.332090,3+) rtinseconds(2082) index(61018)
Title: Locus:1.1.1.1636.12 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

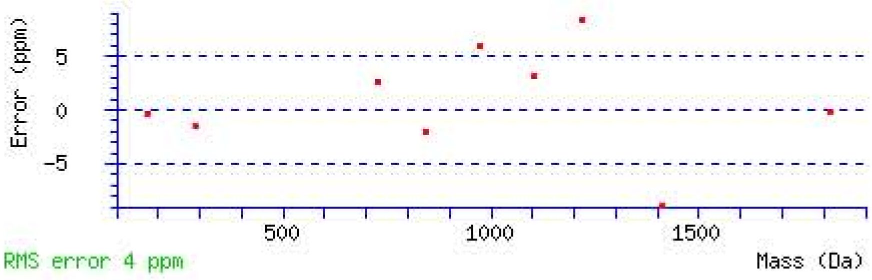
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1944.973602
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Q9     : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.0014
Matches : 9/102 fragment ions using 19 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							11
2	244.129182	122.568229	227.102633	114.054955	226.118617	113.562947	D	*1817.885929*	909.446603	1800.859380	900.933328	1799.875364	900.441320	10
3	331.161210	166.084243	314.134661	157.570969	313.150645	157.078961	S	1702.858986	851.933131	1685.832437	843.419857	1684.848421	842.927848	9
4	388.182674	194.594975	371.156125	186.081701	370.172109	185.589693	G	1615.826958	808.417117	1598.800409	799.903843			8
5	535.251088	268.129182	518.224539	259.615908	517.240523	259.123900	F	1558.805494	779.906385	1541.778945	771.393111			7
6	974.476414	487.741845	957.449865	479.228571	956.465849	478.736563	Q	*1411.737080*	706.372178	1394.710531	697.858904			6
7	**1105.516899**	553.262088	1088.490350	544.748813	1087.506334	544.256805	M	*972.511754*	486.759515	955.485205	478.246241			5
8	**1219.559826**	610.283551	1202.533277	601.770277	1201.549261	601.278268	N	*841.471269*	421.239273	824.444720	412.725998			4
9	1658.785152	829.896214	1641.758603	821.382940	1640.774587	820.890932	Q	*727.428342*	364.217809	710.401793	355.704535			3
10	1771.869216	886.438246	1754.842667	877.924972	1753.858651	877.432964	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
35.6	1944.973602	0.000840	KDSGFQMNQLR
5.0	1944.962357	0.012085	KFMEDEQQLR
4.9	1944.991364	-0.016922	AGGAFLMAGQVAEQLR
1.8	1944.981461	-0.007019	KFPPMTSYHRMLLHR

{MATRIX SCIENCE}

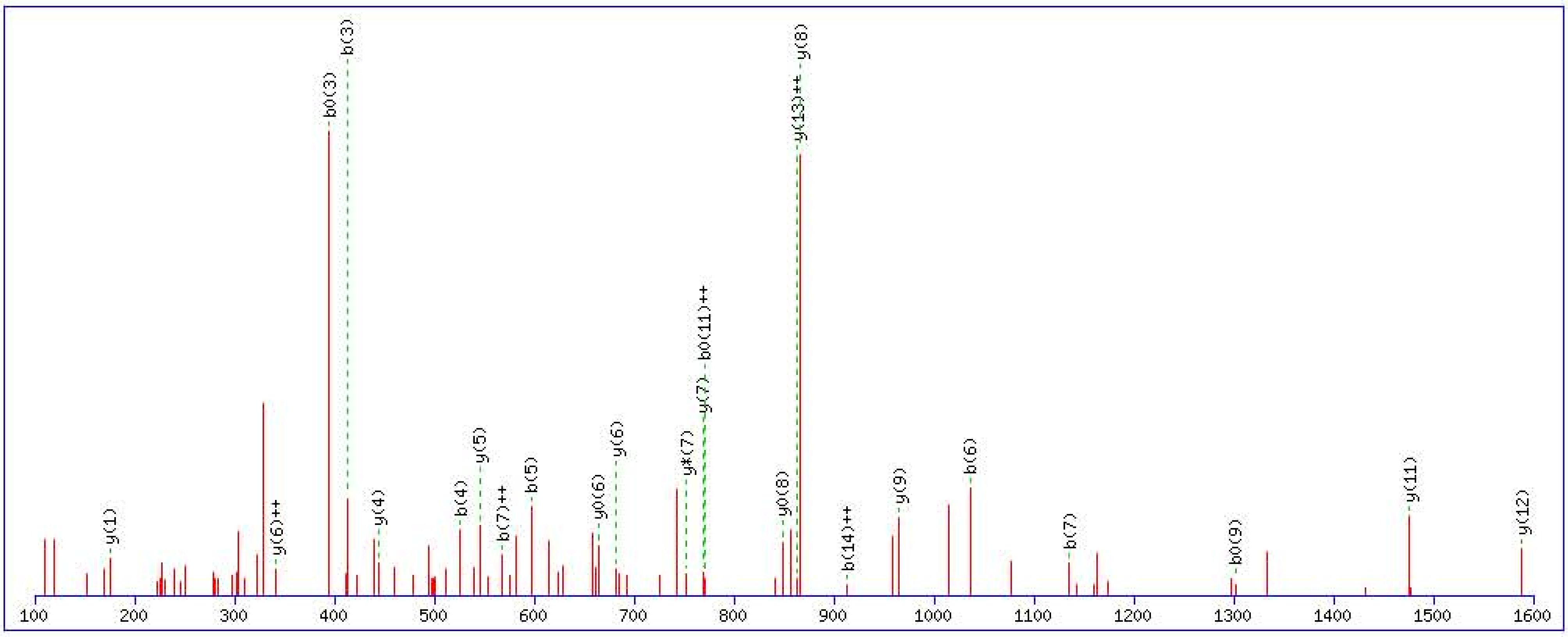
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DCHLAQVPSHTVVAR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

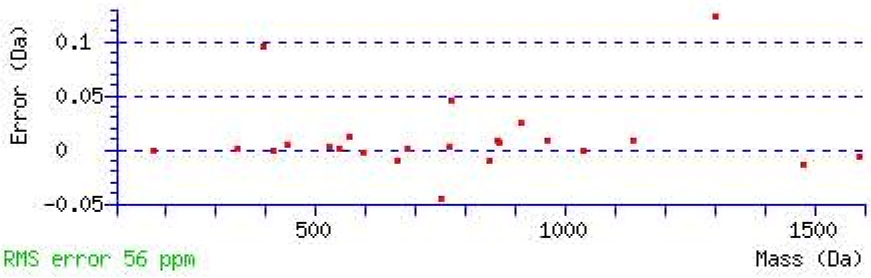
Match to Query 39303: 2000.004852 from(667.675560,3+) rtinseconds(1657) index(2988)
Title: Locus:1.1.1.3096.22 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

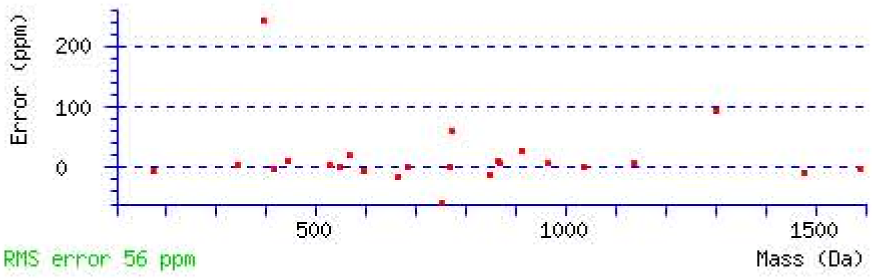
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2000.008438
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.0017
Matches : 24/150 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	116.034219	58.520748			98.023654	49.515465	D							15
2	276.064868	138.536072			258.054303	129.530790	C	1885.988756	943.498016	1868.962207	934.984742	1867.978191	934.492734	14
3	**413.123780**	207.065528			395.113215	198.060245	H	1725.958107	863.482692	1708.931558	854.969417	1707.947542	854.477409	13
4	**526.207844**	263.607560			508.197279	254.602278	L	***1588.899195***	794.953236	1571.872646	786.439961	1570.888630	785.947953	12
5	**597.244958**	299.126117			579.234393	290.120835	A	***1475.815131***	738.411204	1458.788582	729.897929	1457.804566	729.405921	11
6	**1036.470284**	518.738780	1019.443735	510.225506	1018.459719	509.733498	Q	1404.778017	702.892647	1387.751468	694.379372	1386.767452	693.887364	10
7	**1135.538698**	**568.272987**	1118.512149	559.759713	1117.528133	559.267705	V	***965.552691***	483.279984	948.526142	474.766709	947.542126	474.274701	9
8	1232.591462	616.799369	1215.564913	608.286095	1214.580897	607.794087	P	***866.484277***	433.745777	849.457728	425.232502	848.473712	424.740494	8
9	1319.623490	660.315383	1302.596941	651.802109	1301.612925	651.310101	S	***769.431513***	385.219395	752.404964	376.706120	751.420948	376.214112	7
10	1456.682402	728.844839	1439.655853	720.331565	1438.671837	719.839557	H	***682.399485***	341.703381	665.372936	333.190106	664.388920	332.698098	6
11	1557.730081	779.368679	1540.703532	770.855404	1539.719516	770.363396	T	***545.340573***	273.173925	528.314024	264.660650	527.330008	264.168642	5
12	1656.798495	828.902886	1639.771946	820.389611	1638.787930	819.897603	V	***444.292894***	222.650085	427.266345	214.136811			4
13	1755.866909	878.437093	1738.840360	869.923818	1737.856344	869.431810	V	345.224480	173.115878	328.197931	164.602603			3
14	1826.904023	**913.955650**	1809.877474	905.442375	1808.893458	904.950367	A	246.156066	123.581671	229.129517	115.068396			2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of DCHLAQVPSHTVVAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.3	2000.008438	-0.003586	DCHLAQVPSHTVVAR
2.6	1999.997162	0.007690	ECGKAFAHMSVLIKHEK
0.5	1999.978561	0.026291	GFTAASDSDLLAQTHR

Mascot: http://www.matrixscience.com/

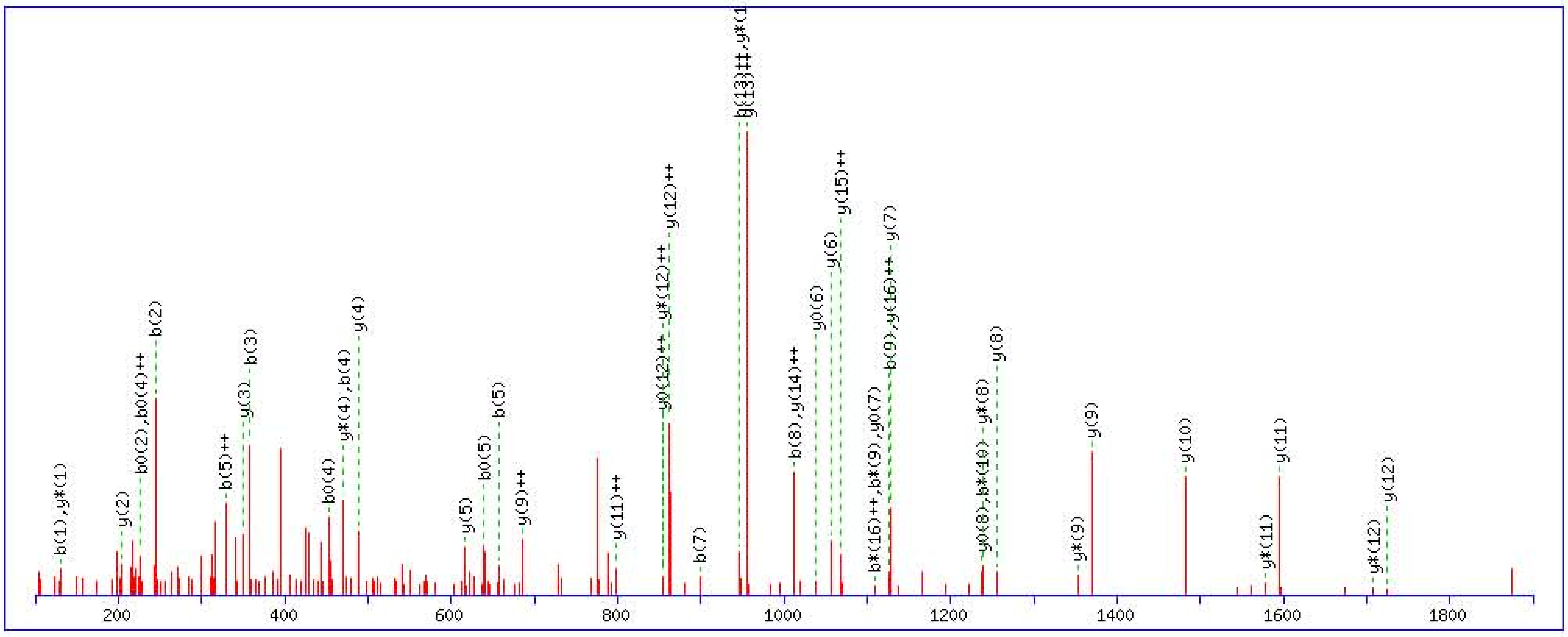
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EDLIWELLNQAQEHFGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

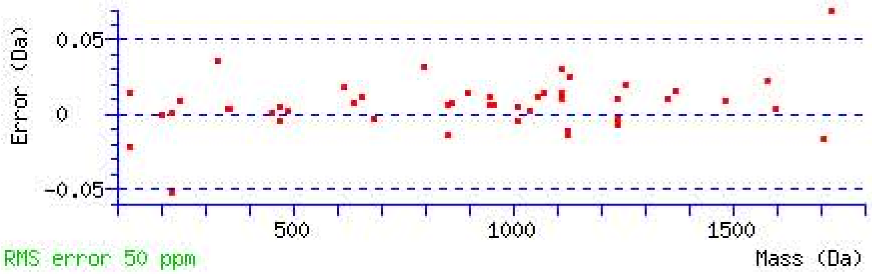
Match to Query 46112: 2380.204452 from(794.408760,3+) rtinseconds(3303) index(67804)
Title: Locus:1.1.1.2055.7 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

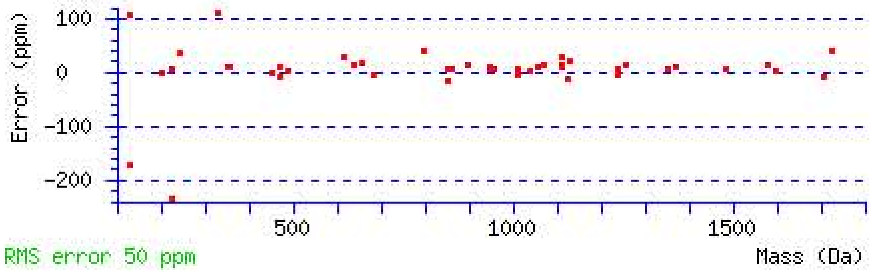
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2380.188522
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 59  Expect: 7.8e-006
Matches : 47/168 fragment ions using 72 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							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	1254.636479	627.821878	1237.609930	619.308603	1236.625914	618.816595	Q	***1255.625205***	628.316240	1238.598656	619.802966	1237.614640	619.310958	8
11	1325.673593	663.340435	1308.647044	654.827160	1307.663028	654.335152	A	***1127.566627***	564.286951	1110.540078	555.773677	1109.556062	555.281669	7
12	1764.898919	882.953098	1747.872370	874.439823	1746.888354	873.947815	Q	***1056.529513***	528.768395	1039.502964	520.255120	1038.518948	519.763112	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
59.0	2380.188522	0.015930	EDLIWELLNQAQEHFGK
44.4	2380.188522	0.015930	EDLIWELLNQAQEHFGK
4.6	2380.212997	-0.008545	ELTLEHMETERLELAQK

Mascot: http://www.matrixscience.com/

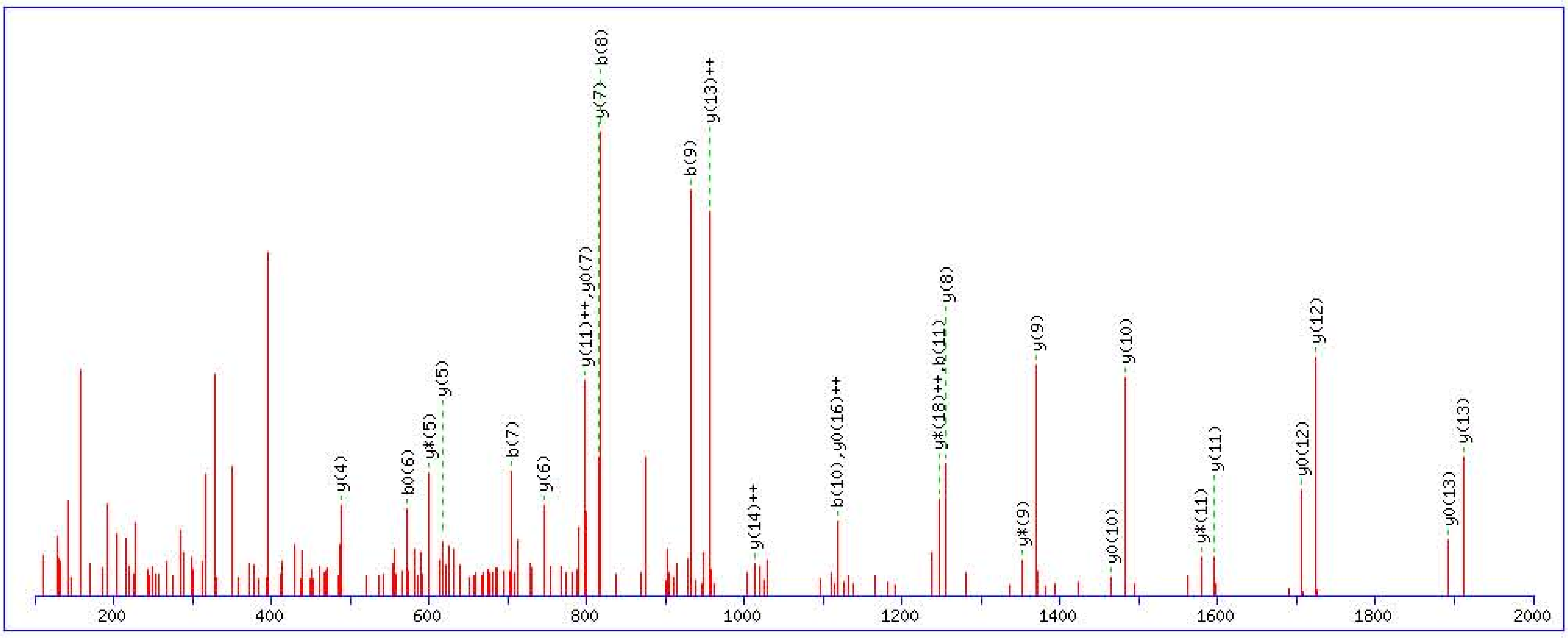
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SMGGKEDLIWELLNQAQEHFGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

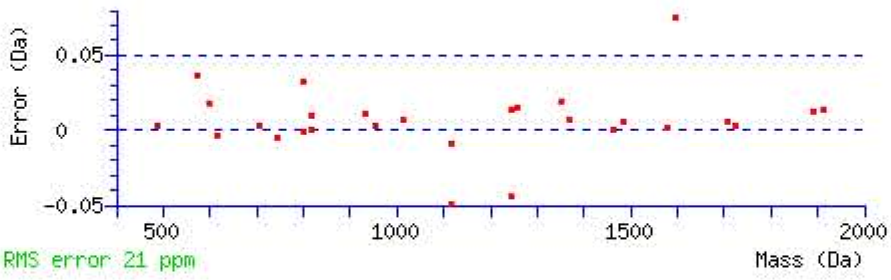
Match to Query 52080: 2840.414816 from(711.110980,4+) rtinseconds(3018) index(66772)
Title: Locus:1.1.1.1959.4 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

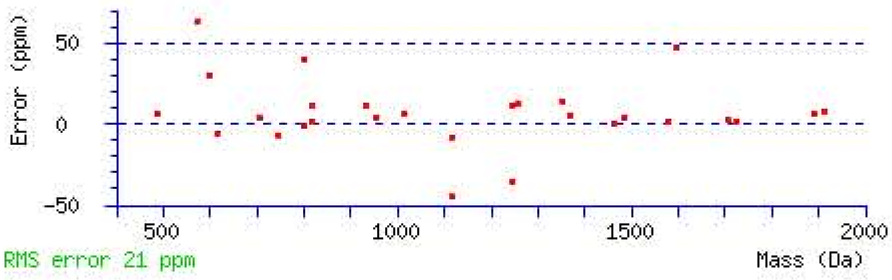


```
Monoisotopic mass of neutral peptide Mr(calc): 2840.398926
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15     : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 2.3e-006
Matches : 28/236 fragment ions using 36 most intense peaks   (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							22
2	219.079789	110.043532			201.069224	101.038250	M	2754.374206	1377.690741	2737.347657	1369.177466	2736.363641	1368.685458	21
3	276.101253	138.554264			258.090688	129.548982	G	2623.333721	1312.170498	2606.307172	1303.657224	2605.323156	1303.165216	20
4	333.122717	167.064996			315.112152	158.059714	G	2566.312257	1283.659766	2549.285708	1275.146492	2548.301692	1274.654484	19
5	461.217680	231.112478	444.191131	222.599203	443.207115	222.107195	K	2509.290793	1255.149034	2492.264244	1246.635760	2491.280228	1246.143752	18
6	590.260273	295.633775	573.233724	287.120500	572.249708	286.628492	E	2381.195830	1191.101553	2364.169281	1182.588278	2363.185265	1182.096270	17
7	**705.287216**	353.147246	688.260667	344.633972	687.276651	344.141964	D	2252.153237	1126.580256	2235.126688	1118.066982	2234.142672	1117.574974	16
8	**818.371280**	409.689278	801.344731	401.176004	800.360715	400.683996	L	2137.126294	1069.066785	2120.099745	1060.553510	2119.115729	1060.061502	15
9	**931.455344**	466.231310	914.428795	457.718036	913.444779	457.226028	I	2024.042230	1012.524753	2007.015681	1004.011479	2006.031665	1003.519471	14
10	**1117.534657**	559.270967	1100.508108	550.757692	1099.524092	550.265684	W	***1910.958166***	955.982721	1893.931617	947.469447	1892.947601	946.977439	13
11	**1246.577250**	623.792263	1229.550701	615.278989	1228.566685	614.786981	E	***1724.878853***	862.943065	1707.852304	854.429790	1706.868288	853.937782	12
12	1359.661314	680.334295	1342.634765	671.821021	1341.650749	671.329012	L	***1595.836260***	798.421768	1578.809711	789.908494	1577.825695	789.416486	11
13	1472.745378	736.876327	1455.718829	728.363052	1454.734813	727.871044	L	***1482.752196***	741.879736	1465.725647	733.366462	1464.741631	732.874454	10
14	1586.788305	793.897790	1569.761756	785.384516	1568.777740	784.892508	N	***1369.668132***	685.337704	1352.641583	676.824430	1351.657567	676.332422	9
15	2026.013631	1013.510454	2008.987082	1004.997179	2008.003066	1004.505171	Q	***1255.625205***	628.316241	1238.598656	619.802966	1237.614640	619.310958	8
16	2097.050745	1049.029010	2080.024196	1040.515736	2079.040180	1040.023728	A	***816.399879***	408.703578	799.373330	400.190303	798.389314	399.698295	7
17	2225.109323	1113.058300	2208.082774	1104.545025	2207.098758	1104.053017	Q	***745.362765***	373.185021	728.336216	364.671746	727.352200	364.179738	6
18	2354.151916	1177.579596	2337.125367	1169.066322	2336.141351	1168.574314	E	***617.304187***	309.155732	600.277638	300.642457	599.293622	300.150449	5
19	2491.210828	1246.109052	2474.184279	1237.595777	2473.200263	1237.103770	H	***488.261594***	244.634435	471.235045	236.121160			4
20	2638.279242	1319.643259	2621.252693	1311.129984	2620.268677	1310.637976	F	351.202682	176.104979	334.176133	167.591704			3
21	2695.300706	1348.153991	2678.274157	1339.640716	2677.290141	1339.148708	G	204.134268	102.570772	187.107719	94.057497			2
22							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 21 ppm



RMS error 21 ppm

NCBI **BLAST** search of SMGGKEDLIWELLNQAQEHFGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.0	2840.398926	0.015890	SMGGKEDLIWELLNQAQEHFGK
42.0	2840.398926	0.015890	SMGGKEDLIWELLNQAQEHFGK
0.8	2840.394440	0.020376	MNNQTKTLDCLMAASIPAVEIFMVK
0.1	2840.380539	0.034277	SLGTIQQCCDAIDHLCRIIEK

Mascot: http://www.matrixscience.com/

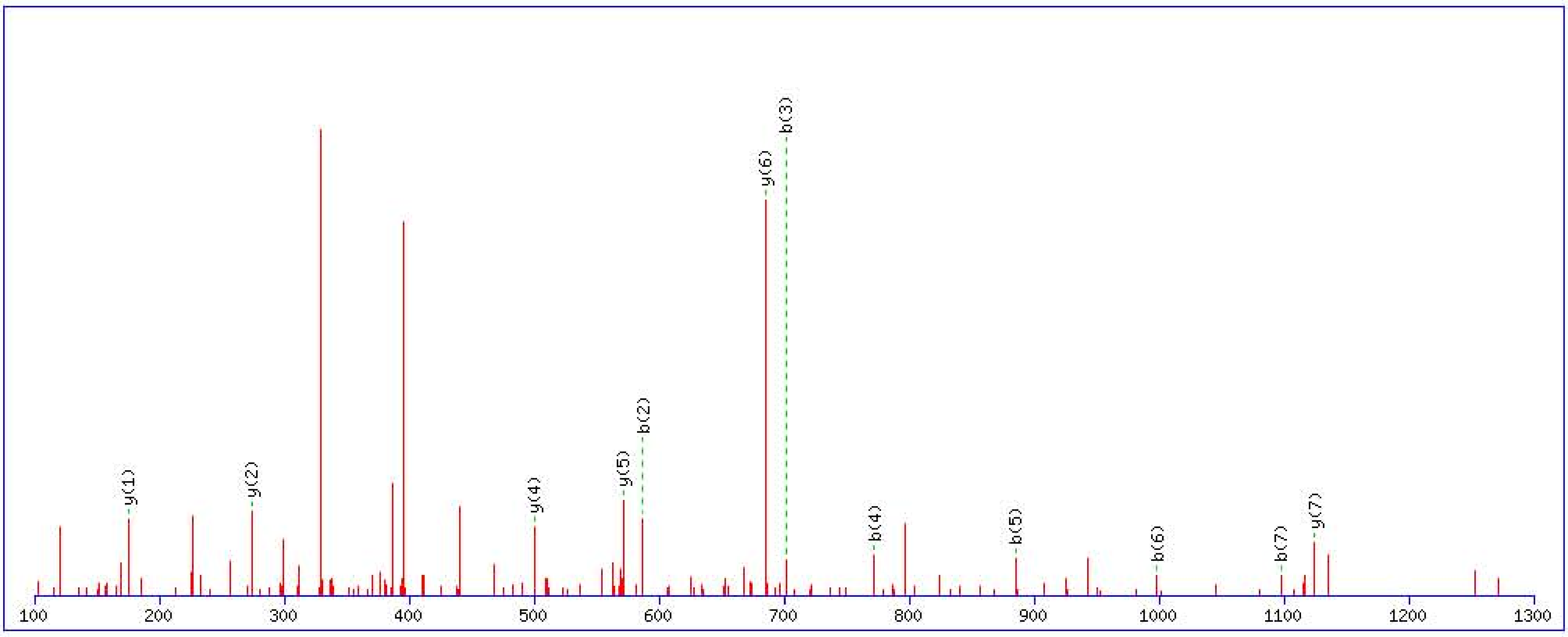
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FQNALLVR**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

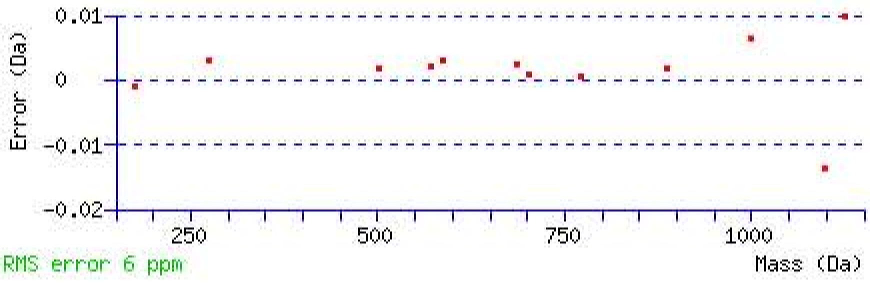
Match to Query 19562: 1270.718108 from(636.366330,2+) rtinseconds(2129) index(32617)
Title: Locus:1.1.1.3405.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

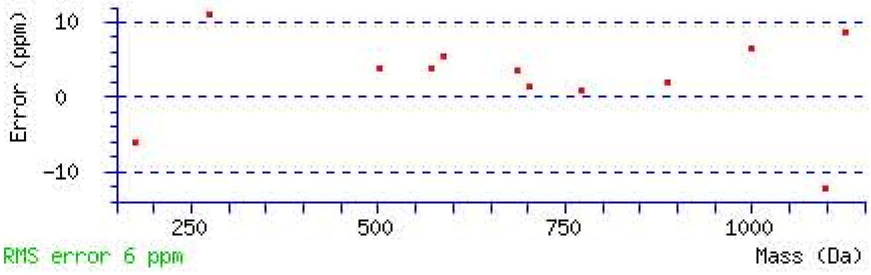
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1270.721985
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 38 **Expect:** 0.0061
Matches : 12/54 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	148.075690	74.541483			F					8
2	***587.301016***	294.154146	570.274467	285.640872	Q	***1124.660861***	562.834068	1107.634312	554.320794	7
3	***701.343943***	351.175610	684.317394	342.662335	N	***685.435535***	343.221406	668.408986	334.708131	6
4	***772.381057***	386.694166	755.354508	378.180892	A	***571.392608***	286.199942	554.366059	277.686668	5
5	***885.465121***	443.236199	868.438572	434.722924	L	***500.355494***	250.681385	483.328945	242.168110	4
6	***998.549185***	499.778231	981.522636	491.264956	L	387.271430	194.139353	370.244881	185.626078	3
7	***1097.617599***	549.312437	1080.591050	540.799163	V	***274.187366***	137.597321	257.160817	129.084046	2
8					R	***175.118952***	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of FQNALLVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.8	1270.721985	-0.003877	FQNALLVR
16.2	1270.722000	-0.003892	FQIAQVVR
14.3	1270.699295	0.018813	QEAEERKLLR
13.0	1270.735687	-0.017579	KEAELRSGIIR
11.7	1270.699341	0.018767	AVTLRSGSEPVR
9.1	1270.699295	0.018813	AEKLERELQR
8.2	1270.706696	0.011412	LPALLEKNAMR
6.7	1270.725357	-0.007249	QKVMAIVR
6.7	1270.733215	-0.015107	FQRQILR
6.6	1270.733215	-0.015107	MFHIRAVILR

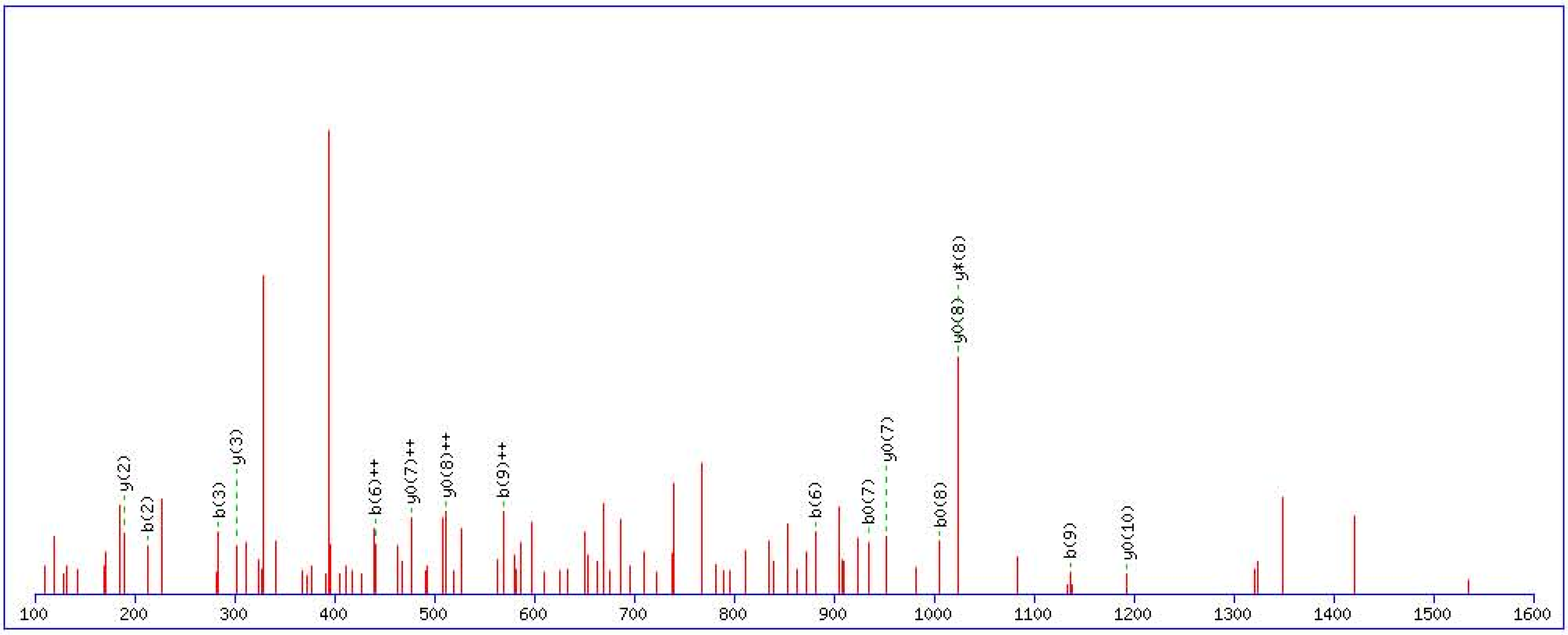
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVAASQAALGL**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

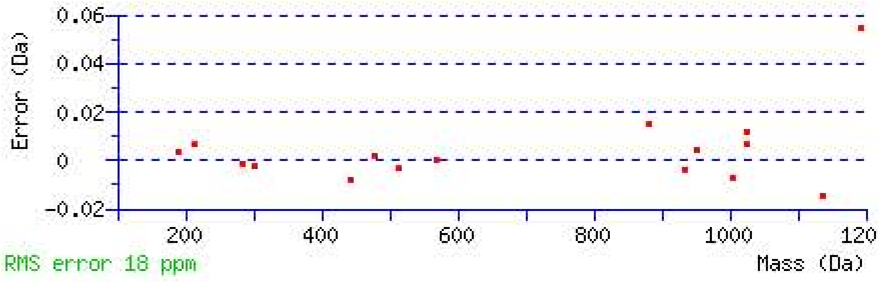
Match to Query 20764: 1323.759728 from(662.887140,2+) rtinseconds(2532) index(34860)
Title: Locus:1.1.1.3545.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

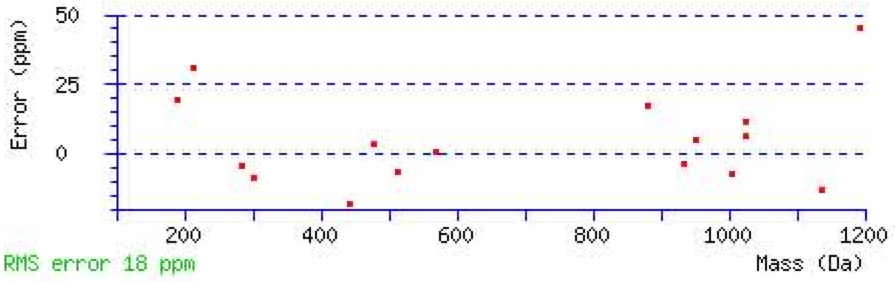
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1323.758423
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.022
Matches : 21/80 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							11
2	***213.159754***	107.083515					V	1211.681657	606.344466	1194.655108	597.831192	1193.671092	597.339184	10
3	***284.196868***	142.602072					A	1112.613243	556.810259	1095.586694	548.296985	1094.602678	547.804977	9
4	355.233982	178.120629					A	1041.576129	521.291702	1024.549580	512.778428	1023.565564	512.286420	8
5	442.266010	221.636643			424.255445	212.631361	S	970.539015	485.773145	953.512466	477.259871	952.528450	476.767863	7
6	***881.491336***	**441.249306**	864.464787	432.736032	863.480771	432.244024	Q	883.506987	442.257131	866.480438	433.743857			6
7	***952.528450***	**476.767863**	935.501901	468.254589	934.517885	467.762581	A	444.281661	222.644468					5
8	***1023.565564***	**512.286420**	1006.539015	503.773146	1005.554999	503.281138	A	373.244547	187.125911					4
9	***1136.649628***	**568.828452**	1119.623079	560.315178	1118.639063	559.823169	L	**302.207433**	151.607354					3
10	***1193.671092***	597.339184	1176.644543	588.825909	1175.660527	588.333901	G	**189.123369**	95.065322					2
11							L	132.101905	66.554590					1





NCBI **BLAST** search of LVAASQAALGL
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.5	1323.758423	0.001305	LVAASQAALGL

Mascot: http://www.matrixscience.com/

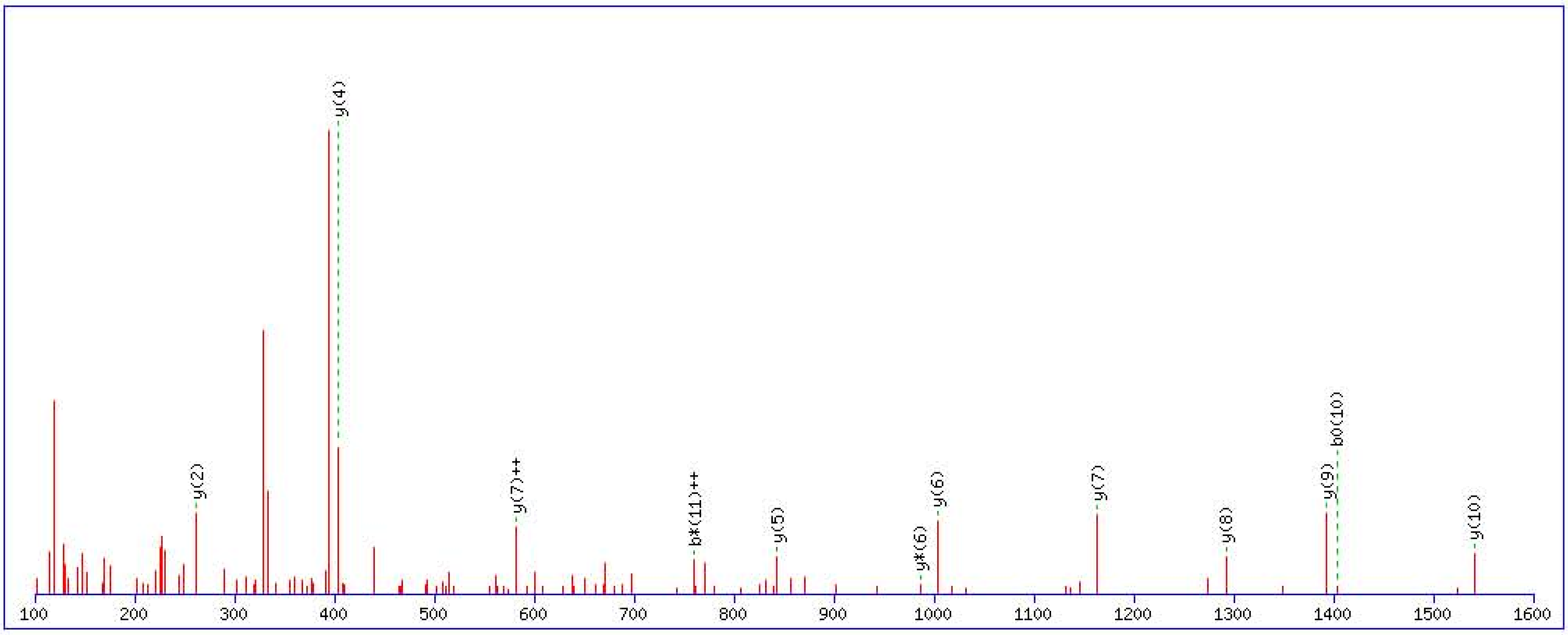
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAFTECCQAADK**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

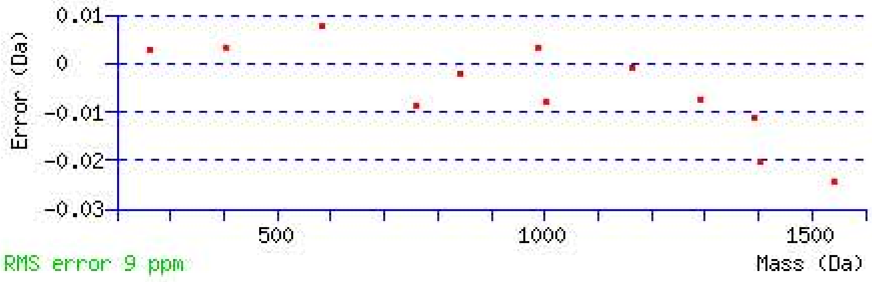
Match to Query 33341: 1681.718202 from(561.580010,3+) rtinseconds(1635) index(16742)
Title: Locus:1.1.1.3135.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

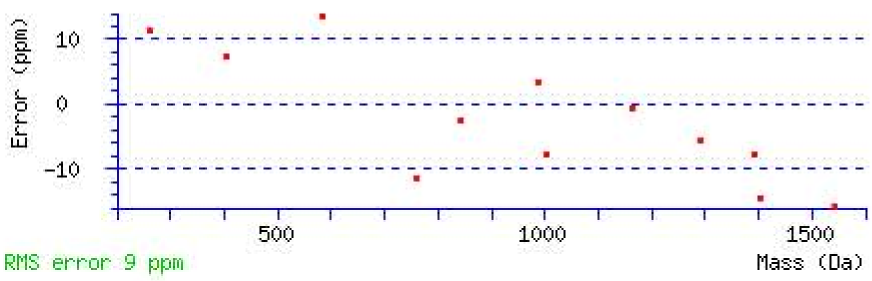
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1681.726227
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 53 **Expect:** 1.8e-005
Matches : 12/110 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							12
2	143.081504	72.044390					A	1611.696399	806.351838	1594.669850	797.838563	1593.685834	797.346555	11
3	290.149918	145.578597					F	***1540.659285***	770.833281	1523.632736	762.320006	1522.648720	761.827998	10
4	391.197597	196.102437			373.187032	187.097154	T	***1393.590871***	697.299074	1376.564322	688.785799	1375.580306	688.293791	9
5	520.240190	260.623733			502.229625	251.618451	E	***1292.543192***	646.775234	1275.516643	638.261960	1274.532627	637.769952	8
6	680.270839	340.639058			662.260274	331.633775	C	***1163.500599***	582.253938	1146.474050	573.740663	1145.490034	573.248655	7
7	840.301488	420.654382			822.290923	411.649100	C	***1003.469950***	502.238613	986.443401	493.725339	985.459385	493.233331	6
8	1279.526814	640.267045	1262.500265	631.753771	1261.516249	631.261763	Q	***843.439301***	422.223289	826.412752	413.710014	825.428736	413.218006	5
9	1350.563928	675.785602	1333.537379	667.272328	1332.553363	666.780320	A	***404.213975***	202.610626	387.187426	194.097351	386.203410	193.605343	4
10	1421.601042	711.304159	1404.574493	702.790885	1403.590477	702.298877	A	333.176861	167.092069	316.150312	158.578794	315.166296	158.086786	3
11	1536.627985	768.817631	1519.601436	760.304356	1518.617420	759.812348	D	***262.139747***	131.573512	245.113198	123.060237	244.129182	122.568229	2
12							K	147.112804	74.060040	130.086255	65.546765			1



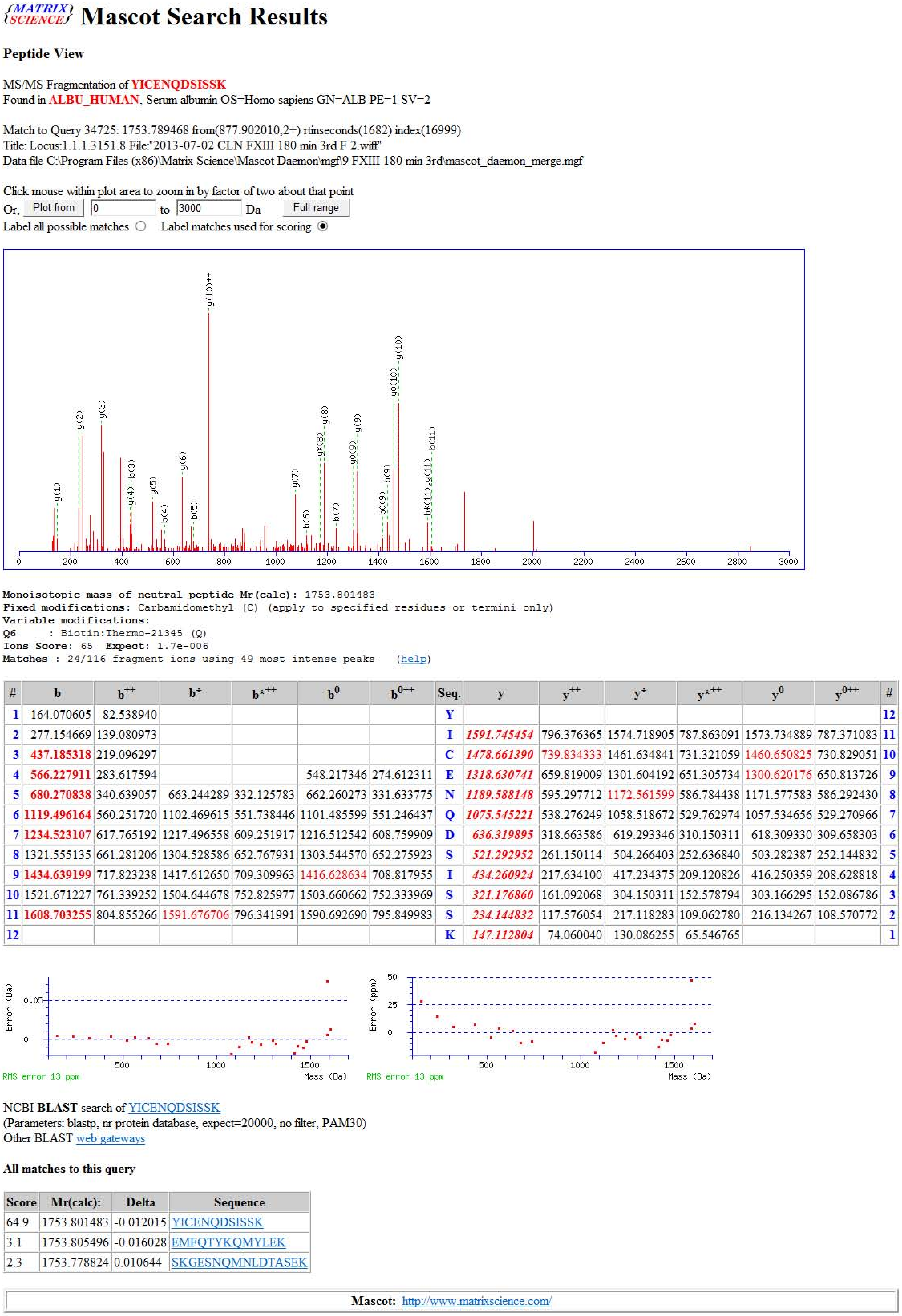


NCBI **BLAST** search of AAFTECCQAADK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.0	1681.726227	-0.008025	AAFTECCQAADK

Mascot: http://www.matrixscience.com/



{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of YICENQDSISSK
Found in ALBU_HUMAN, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

Match to Query 34725: 1753.789468 from(877.902010,2+) rtinseconds(1682) index(16999)
Title: Locus:1.1.1.3151.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\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): 1753.801483
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 1.7e-006
Matches : 24/116 fragment ions using 49 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	164.070605	82.538940					Y							12
2	277.154669	139.080973					I	***1591.745454***	796.376365	1574.718905	787.863091	1573.734889	787.371083	11
3	**437.185318**	219.096297					C	***1478.661390***	739.834333	1461.634841	731.321059	1460.650825	730.829051	10
4	**566.227911**	283.617594			548.217346	274.612311	E	***1318.630741***	659.819009	1301.604192	651.305734	1300.620176	650.813726	9
5	**680.270838**	340.639057	663.244289	332.125783	662.260273	331.633775	N	***1189.588148***	595.297712	1172.561599	586.784438	1171.577583	586.292430	8
6	**1119.496164**	560.251720	1102.469615	551.738446	1101.485599	551.246437	Q	***1075.545221***	538.276249	1058.518672	529.762974	1057.534656	529.270966	7
7	**1234.523107**	617.765192	1217.496558	609.251917	1216.512542	608.759909	D	***636.319895***	318.663586	619.293346	310.150311	618.309330	309.658303	6
8	1321.555135	661.281206	1304.528586	652.767931	1303.544570	652.275923	S	***521.292952***	261.150114	504.266403	252.636840	503.282387	252.144832	5
9	**1434.639199**	717.823238	1417.612650	709.309963	1416.628634	708.817955	I	***434.260924***	217.634100	417.234375	209.120826	416.250359	208.628818	4
10	1521.671227	761.339252	1504.644678	752.825977	1503.660662	752.333969	S	***321.176860***	161.092068	304.150311	152.578794	303.166295	152.086786	3
11	**1608.703255**	804.855266	1591.676706	796.341991	1590.692690	795.849983	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
12							K	***147.112804***	74.060040	130.086255	65.546765			1

NCBI **BLAST** search of YICENQDSISSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.9	1753.801483	-0.012015	YICENQDSISSK
3.1	1753.805496	-0.016028	EMFQTYKQMYLEK
2.3	1753.778824	0.010644	SKGESNQMNLDTASEK

Mascot: http://www.matrixscience.com/

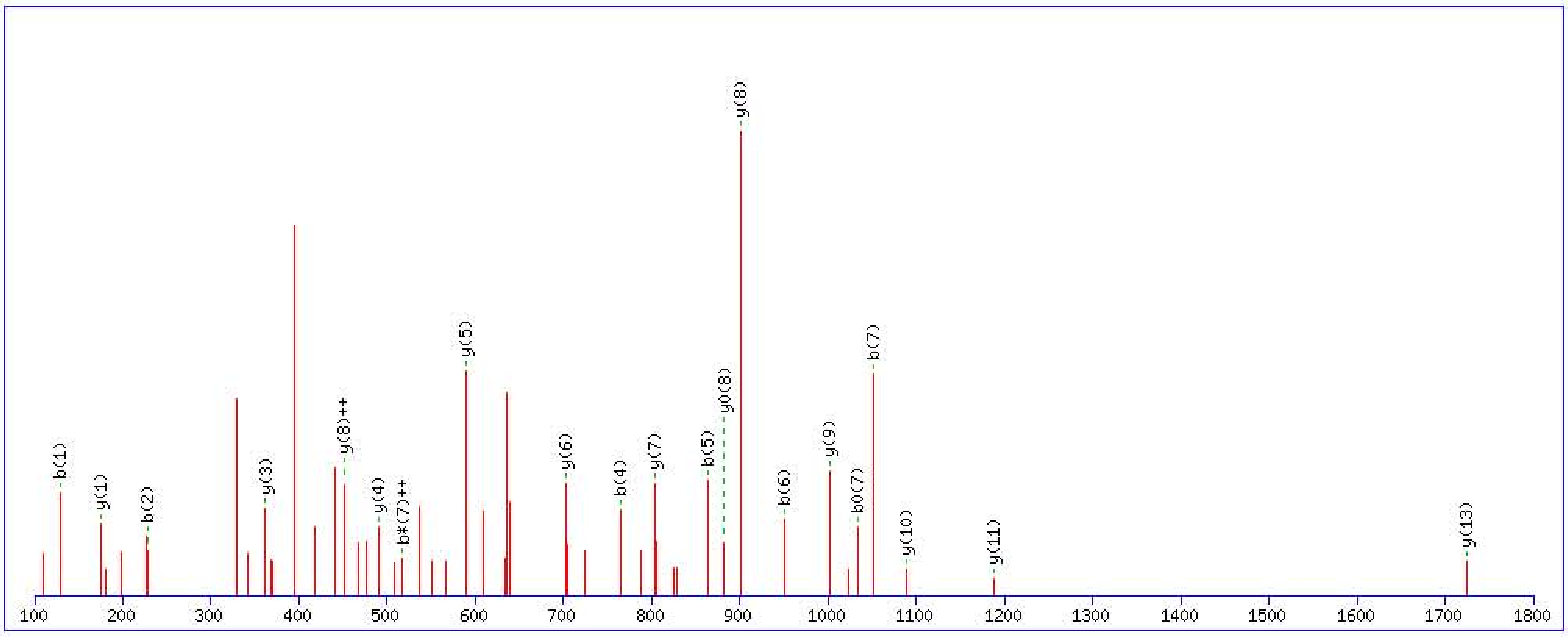
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KVPQVSTPTLVEVSR**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

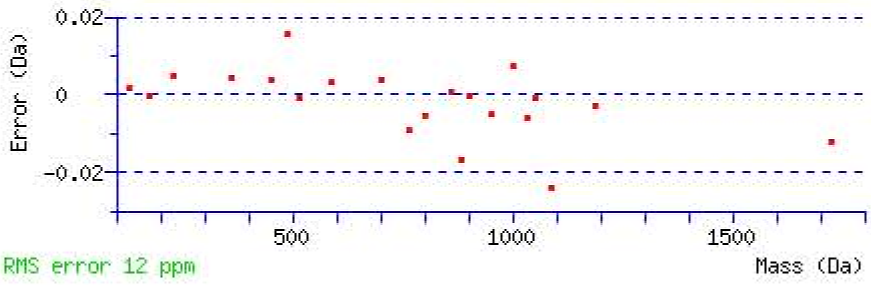
Match to Query 38333: 1950.089322 from(651.037050,3+) rtinseconds(1957) index(31532)
Title: Locus:1.1.1.3345.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

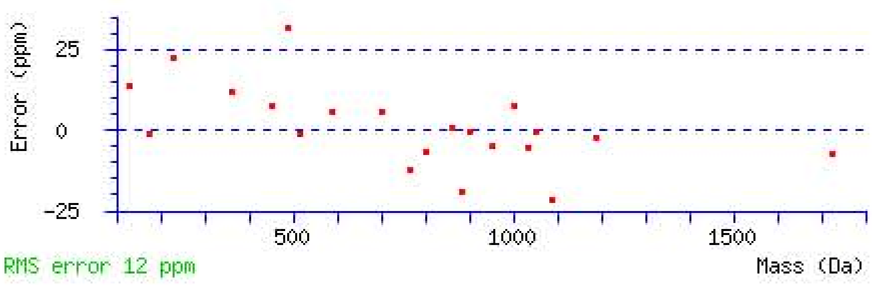
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1950.097229
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 67 **Expect:** 2.7e-006
Matches : 21/156 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	**129.102239**	65.054757	112.075690	56.541483			K							15
2	**228.170653**	114.588965	211.144104	106.075690			V	1823.009533	912.008404	1805.982984	903.495130	1804.998968	903.003122	14
3	325.223417	163.115346	308.196868	154.602072			P	***1723.941119***	862.474197	1706.914570	853.960923	1705.930554	853.468915	13
4	**764.448743**	382.728010	747.422194	374.214735			Q	1626.888355	813.947815	1609.861806	805.434541	1608.877790	804.942533	12
5	**863.517157**	432.262217	846.490608	423.748942			V	***1187.663029***	594.335153	1170.636480	585.821878	1169.652464	585.329870	11
6	**950.549185**	475.778231	933.522636	467.264956	932.538620	466.772948	S	***1088.594615***	544.800946	1071.568066	536.287671	1070.584050	535.795663	10
7	**1051.596864**	526.302070	1034.570315	517.788795	1033.586299	517.296787	T	***1001.562587***	501.284932	984.536038	492.771657	983.552022	492.279649	9
8	1148.649628	574.828452	1131.623079	566.315178	1130.639063	565.823169	P	***900.514908***	450.761092	883.488359	442.247818	882.504343	441.755810	8
9	1249.697307	625.352291	1232.670758	616.839017	1231.686742	616.347009	T	***803.462144***	402.234710	786.435595	393.721436	785.451579	393.229428	7
10	1362.781371	681.894323	1345.754822	673.381049	1344.770806	672.889041	L	***702.414465***	351.710871	685.387916	343.197596	684.403900	342.705588	6
11	1461.849785	731.428530	1444.823236	722.915256	1443.839220	722.423248	V	***589.330401***	295.168839	572.303852	286.655564	571.319836	286.163556	5
12	1590.892378	795.949827	1573.865829	787.436552	1572.881813	786.944544	E	***490.261987***	245.634631	473.235438	237.121357	472.251422	236.629349	4
13	1689.960792	845.484034	1672.934243	836.970759	1671.950227	836.478751	V	***361.219394***	181.113335	344.192845	172.600061	343.208829	172.108053	3
14	1776.992820	889.000048	1759.966271	880.486774	1758.982255	879.994765	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 KVPQVSTPTLVEVSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.6	1950.097229	-0.007907	KVPQVSTPTLVEVSR
9.7	1950.060791	0.028531	QPITEAEMLKGVIKEHK
1.3	1950.065521	0.023801	QAQTDRVNLRK

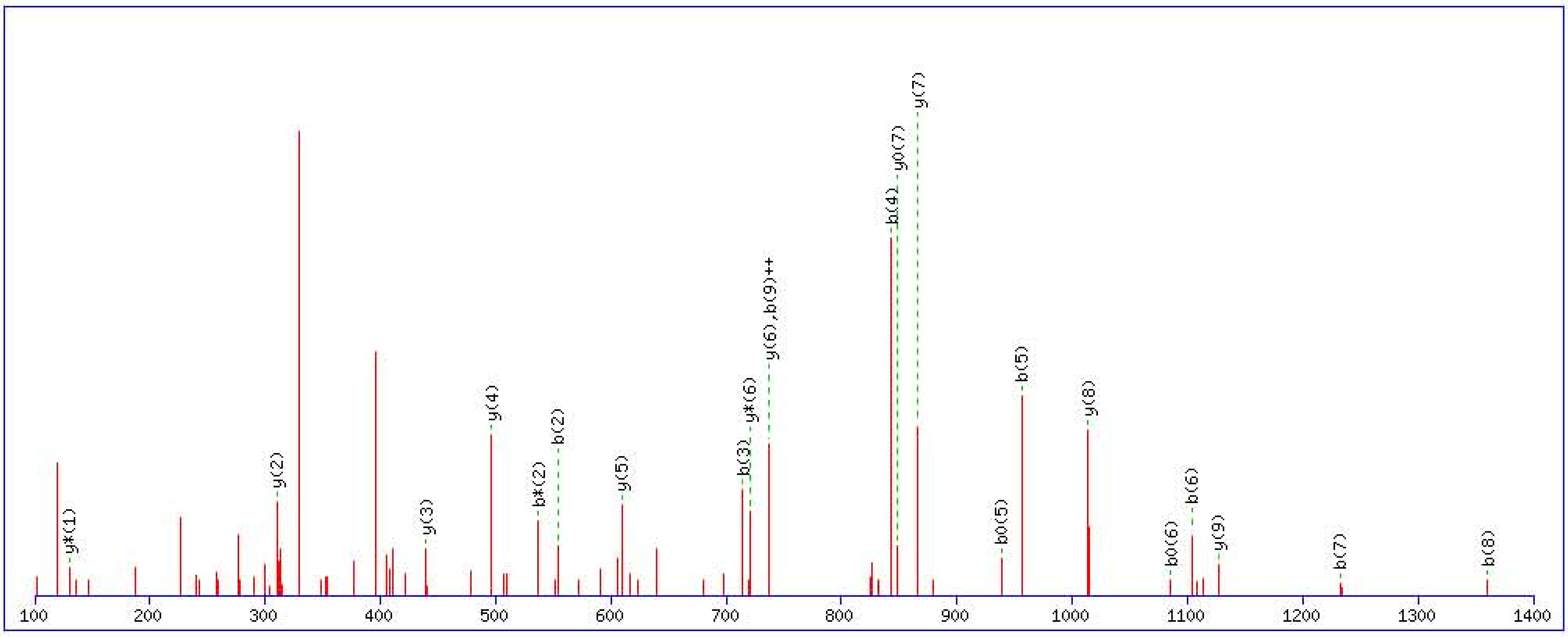
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QNCELFEQLGEYK**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

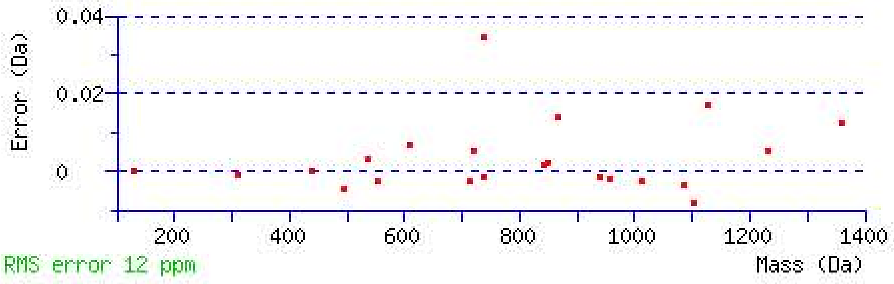
Match to Query 38753: 1967.918202 from(656.980010,3+) rtinseconds(2410) index(21295)
Title: Locus:1.1.1.3405.4 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

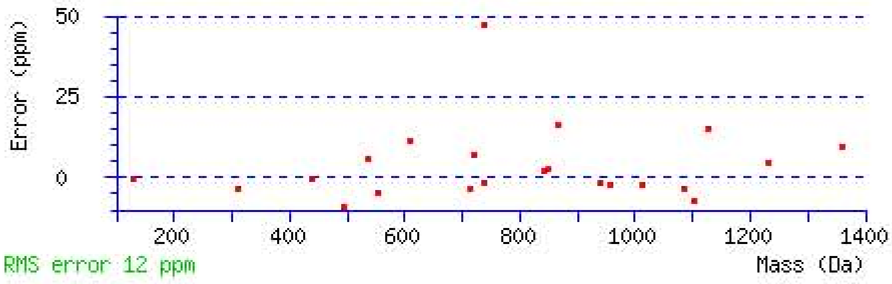
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1967.912094
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1     : Biotin:Thermo-21345 (Q)
Ions Score: 50  Expect: 2.5e-005
Matches : 22/134 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							13
2	***554.275529***	277.641403	537.248980	269.128128			N	1529.694072	765.350674	1512.667523	756.837400	1511.683507	756.345392	12
3	***714.306178***	357.656727	697.279629	349.143453			C	1415.651145	708.329211	1398.624596	699.815936	1397.640580	699.323928	11
4	***843.348771***	422.178024	826.322222	413.664749	825.338206	413.172741	E	1255.620496	628.313886	1238.593947	619.800612	1237.609931	619.308604	10
5	***956.432835***	478.720056	939.406286	470.206781	938.422270	469.714773	L	***1126.577903***	563.792590	1109.551354	555.279315	1108.567338	554.787307	9
6	***1103.501249***	552.254263	1086.474700	543.740988	1085.490684	543.248980	F	***1013.493839***	507.250558	996.467290	498.737283	995.483274	498.245275	8
7	***1232.543842***	616.775559	1215.517293	608.262285	1214.533277	607.770277	E	***866.425425***	433.716351	849.398876	425.203076	848.414860	424.711068	7
8	***1360.602420***	680.804848	1343.575871	672.291574	1342.591855	671.799566	Q	***737.382832***	369.195054	720.356283	360.681780	719.372267	360.189772	6
9	1473.686484	737.346880	1456.659935	728.833606	1455.675919	728.341598	L	***609.324254***	305.165765	592.297705	296.652490	591.313689	296.160482	5
10	1530.707948	765.857612	1513.681399	757.344338	1512.697383	756.852330	G	***496.240190***	248.623733	479.213641	240.110458	478.229625	239.618450	4
11	1659.750541	830.378909	1642.723992	821.865634	1641.739976	821.373626	E	***439.218726***	220.113001	422.192177	211.599726	421.208161	211.107718	3
12	1822.813870	911.910573	1805.787321	903.397299	1804.803305	902.905291	Y	***310.176133***	155.591705	293.149584	147.078430			2
13							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of QNCELFEQLGEYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.2	1967.912094	0.006108	QNCELFEQLGEYK
1.1	1967.930069	-0.011867	TQQRMKEMESVMK
1.1	1967.930069	-0.011867	TQQRMKEMESVMK

Mascot: http://www.matrixscience.com/

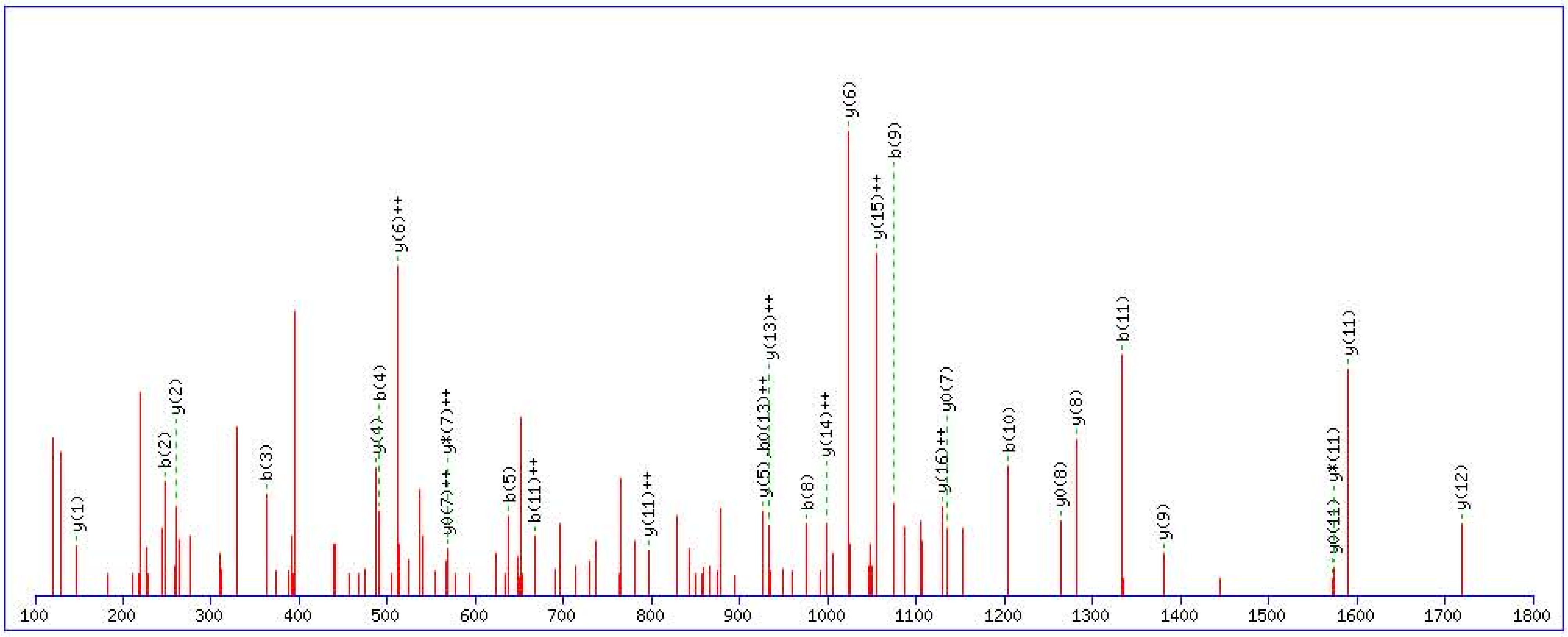
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VFDEFKPLVEEPQNLIK**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

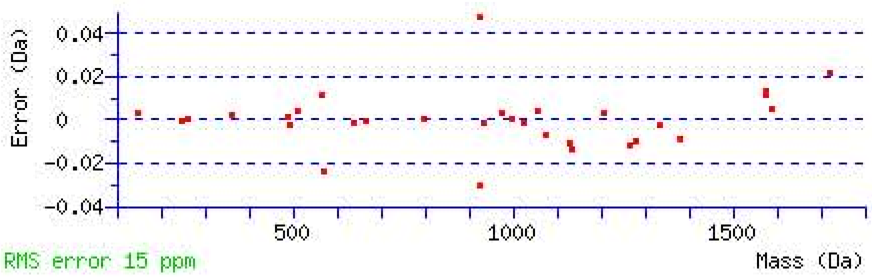
Match to Query 45897: 2355.253782 from(786.091870,3+) rtinseconds(2628) index(35430)
Title: Locus:1.1.1.3578.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

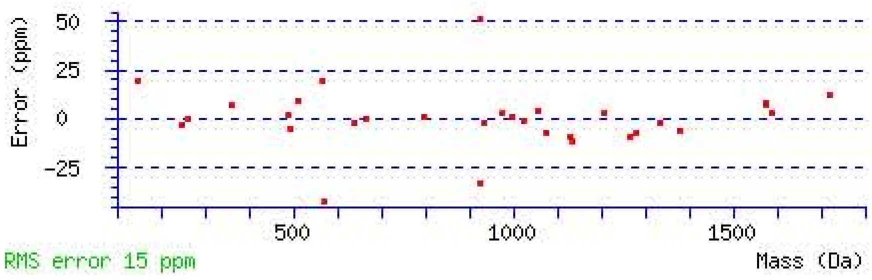
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2355.254822
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.0003
Matches : 31/166 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	100.075690	50.541483					V							17
2	***247.144104***	124.075690					F	2257.193704	1129.100490	2240.167155	1120.587216	2239.183139	1120.095208	16
3	***362.171047***	181.589161			344.160482	172.583879	D	2110.125290	1055.566283	2093.098741	1047.053008	2092.114725	1046.561000	15
4	***491.213640***	246.110458			473.203075	237.105176	E	1995.098347	998.052812	1978.071798	989.539537	1977.087782	989.047529	14
5	***638.282054***	319.644665			620.271489	310.639383	F	1866.055754	933.531515	1849.029205	925.018241	1848.045189	924.526233	13
6	766.377017	383.692147	749.350468	375.178872	748.366452	374.686864	K	***1718.987340***	859.997308	1701.960791	851.484034	1700.976775	850.992026	12
7	863.429781	432.218529	846.403232	423.705254	845.419216	423.213246	P	***1590.892377***	795.949827	1573.865828	787.436552	1572.881812	786.944544	11
8	***976.513845***	488.760561	959.487296	480.247286	958.503280	479.755278	L	1493.839613	747.423445	1476.813064	738.910170	1475.829048	738.418162	10
9	***1075.582259***	538.294768	1058.555710	529.781493	1057.571694	529.289485	V	***1380.755549***	690.881413	1363.729000	682.368138	1362.744984	681.876130	9
10	***1204.624852***	602.816064	1187.598303	594.302790	1186.614287	593.810782	E	***1281.687135***	641.347206	1264.660586	632.833931	1263.676570	632.341923	8
11	***1333.667445***	667.337361	1316.640896	658.824086	1315.656880	658.332078	E	1152.644542	576.825909	1135.617993	568.312635	1134.633977	567.820627	7
12	1430.720209	715.863743	1413.693660	707.350468	1412.709644	706.858460	P	***1023.601949***	512.304613	1006.575400	503.791338			6
13	1869.945535	935.476406	1852.918986	926.963131	1851.934970	926.471123	Q	***926.549185***	463.778231	909.522636	455.264956			5
14	1983.988462	992.497869	1966.961913	983.984595	1965.977897	983.492587	N	***487.323859***	244.165568	470.297310	235.652293			4
15	2097.072526	1049.039901	2080.045977	1040.526627	2079.061961	1040.034619	L	373.280932	187.144104	356.254383	178.630830			3
16	2210.156590	1105.581933	2193.130041	1097.068659	2192.146025	1096.576651	I	***260.196868***	130.602072	243.170319	122.088798			2
17							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VFDEFKPLVEEPQNLIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.4	2355.254822	-0.001040	VFDEFKPLVEEPQNLIK

Mascot: http://www.matrixscience.com/

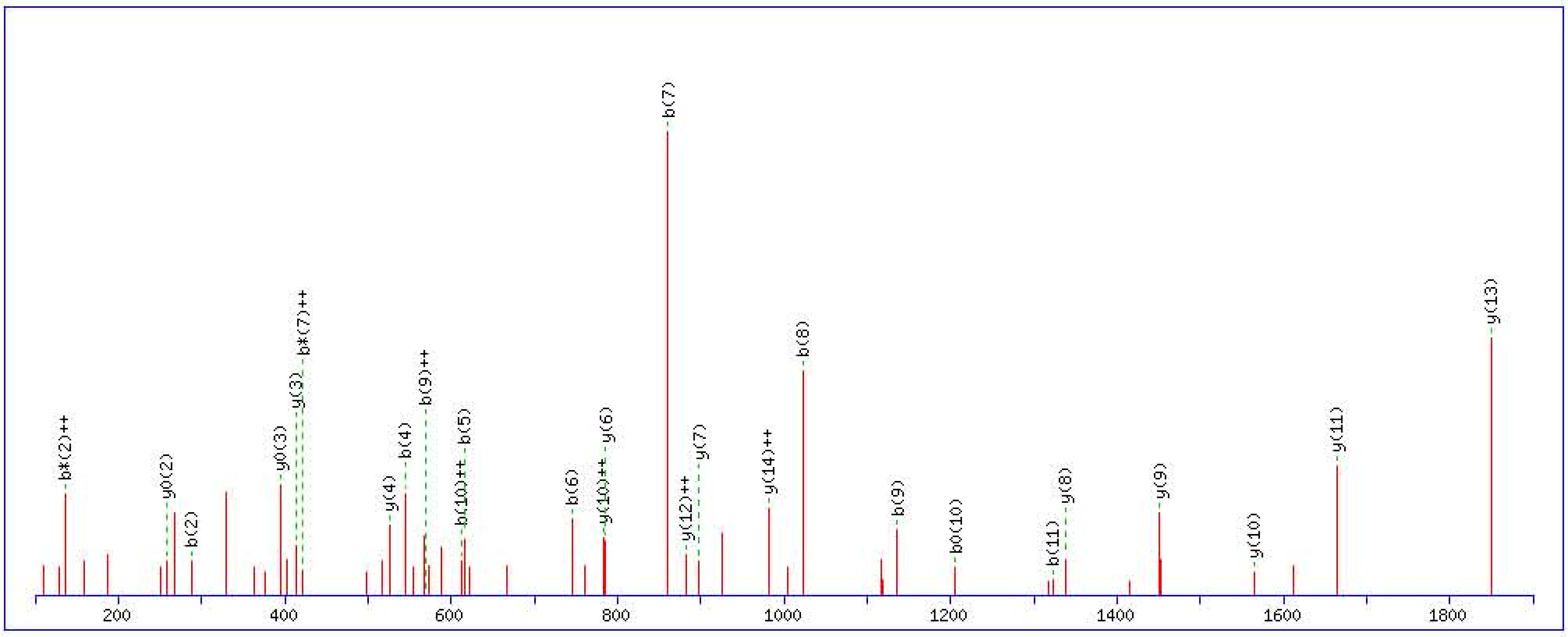
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RMPCAEDYLSVVLNQLCVLHEK**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

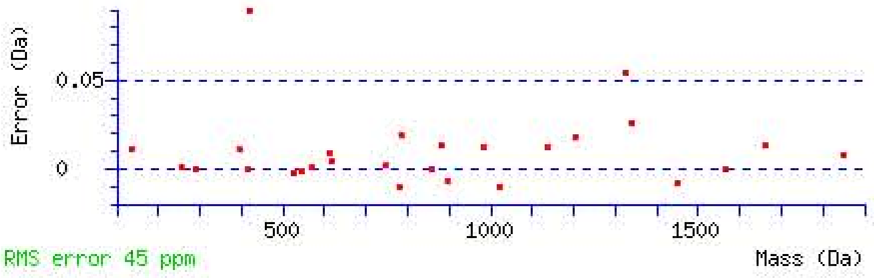
Match to Query 53895: 2984.474256 from(747.125840,4+) rtinseconds(3096) index(38676)
Title: Locus:1.1.1.3738.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

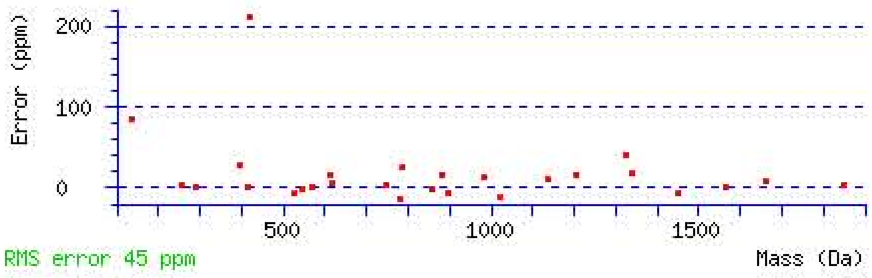
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2984.474426
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15 : Biotin:Thermo-21345 (Q)
Ions Score: 69 **Expect:** 1.1e-006
Matches : 27/240 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	157.108387	79.057831	140.081838	70.544557			R							22
2	***288.148872***	144.578074	271.122323	136.064799			M	2829.380614	1415.193945	2812.354065	1406.680670	2811.370049	1406.188662	21
3	385.201636	193.104456	368.175087	184.591181			P	2698.340129	1349.673702	2681.313580	1341.160428	2680.329564	1340.668420	20
4	***545.232285***	273.119781	528.205736	264.606506			C	2601.287365	1301.147320	2584.260816	1292.634046	2583.276800	1292.142038	19
5	***616.269399***	308.638338	599.242850	300.125063			A	2441.256716	1221.131996	2424.230167	1212.618721	2423.246151	1212.126713	18
6	***745.311992***	373.159634	728.285443	364.646360	727.301427	364.154352	E	2370.219602	1185.613439	2353.193053	1177.100164	2352.209037	1176.608156	17
7	***860.338935***	430.673106	843.312386	422.159831	842.328370	421.667823	D	2241.177009	1121.092142	2224.150460	1112.578868	2223.166444	1112.086860	16
8	***1023.402264***	512.204770	1006.375715	503.691496	1005.391699	503.199488	Y	2126.150066	1063.578671	2109.123517	1055.065396	2108.139501	1054.573388	15
9	***1136.486328***	**568.746802**	1119.459779	560.233528	1118.475763	559.741519	L	1963.086737	982.047007	1946.060188	973.533732	1945.076172	973.041724	14
10	1223.518356	**612.262816**	1206.491807	603.749542	1205.507791	603.257534	S	***1850.002673***	925.504975	1832.976124	916.991700	1831.992108	916.499692	13
11	***1322.586770***	661.797023	1305.560221	653.283749	1304.576205	652.791741	V	1762.970645	881.988961	1745.944096	873.475686	1744.960080	872.983678	12
12	1421.655184	711.331230	1404.628635	702.817956	1403.644619	702.325948	V	***1663.902231***	832.454754	1646.875682	823.941479	1645.891666	823.449471	11
13	1534.739248	767.873262	1517.712699	759.359988	1516.728683	758.867980	L	***1564.833817***	782.920547	1547.807268	774.407272	1546.823252	773.915264	10
14	1648.782175	824.894726	1631.755626	816.381451	1630.771610	815.889443	N	***1451.749753***	726.378515	1434.723204	717.865240	1433.739188	717.373232	9
15	2088.007501	1044.507388	2070.980952	1035.994114	2069.996936	1035.502106	Q	***1337.706826***	669.357051	1320.680277	660.843777	1319.696261	660.351769	8
16	2201.091565	1101.049421	2184.065016	1092.536146	2183.081000	1092.044138	L	***898.481500***	449.744388	881.454951	441.231114	880.470935	440.739106	7
17	2361.122214	1181.064745	2344.095665	1172.551470	2343.111649	1172.059462	C	***785.397436***	393.202356	768.370887	384.689081	767.386871	384.197073	6
18	2460.190628	1230.598952	2443.164079	1222.085677	2442.180063	1221.593669	V	625.366787	313.187032	608.340238	304.673757	607.356222	304.181749	5
19	2573.274692	1287.140984	2556.248143	1278.627709	2555.264127	1278.135701	L	***526.298373***	263.652825	509.271824	255.139550	508.287808	254.647542	4
20	2710.333604	1355.670440	2693.307055	1347.157165	2692.323039	1346.665157	H	***413.214309***	207.110793	396.187760	198.597518	395.203744	198.105510	3
21	2839.376197	1420.191736	2822.349648	1411.678462	2821.365632	1411.186454	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
22							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of RMPCAEDYLSVVLNQLCVLHEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.2	2984.474426	-0.000170	RMPCAEDYLSVVLNQLCVLHEK
5.6	2984.466171	0.008085	QQMNGLTSFLDASTVYGSSPALERQLR

Mascot: http://www.matrixscience.com/

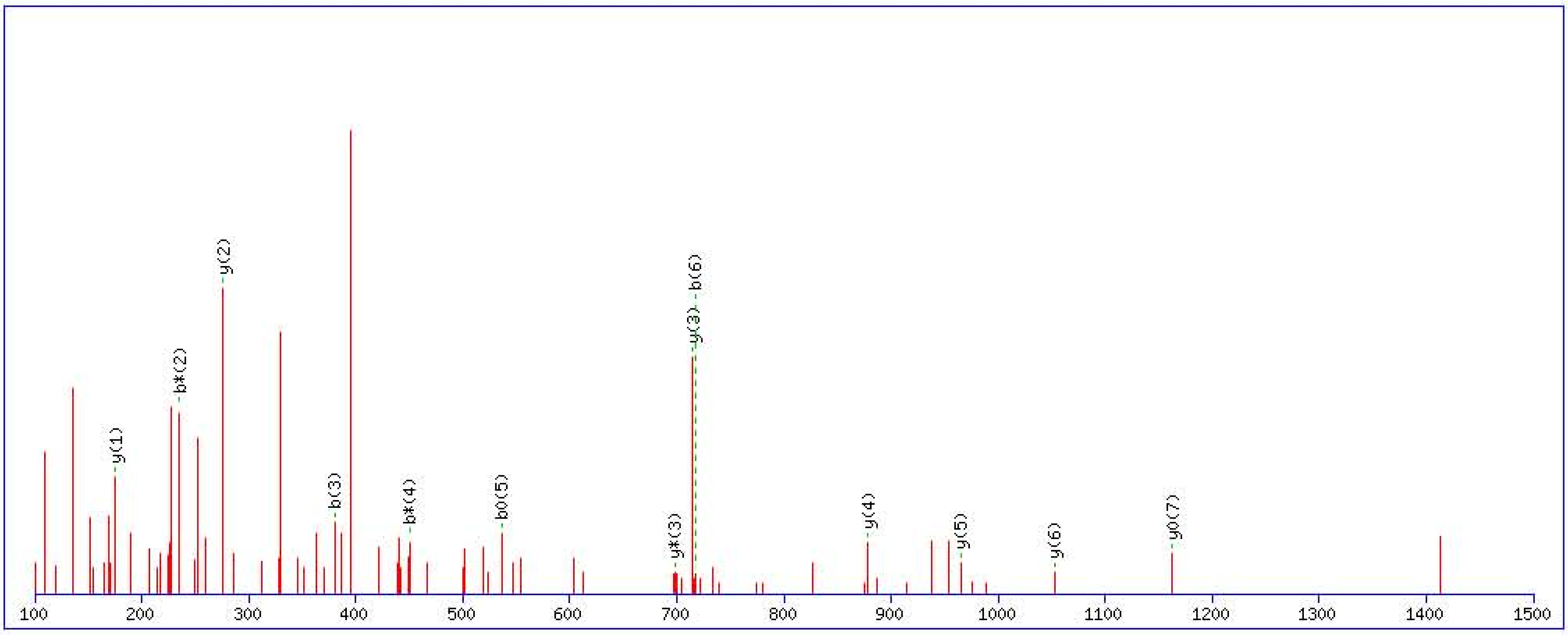
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NHQSSYQTR**
Found in **PON1_HUMAN**, Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3

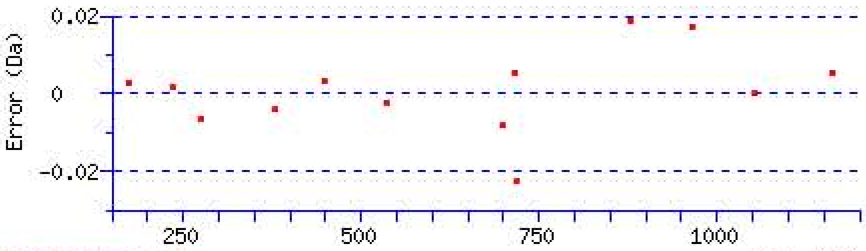
Match to Query 25312: 1430.671092 from(477.897640,3+) rtinseconds(1211) index(27513)
Title: Locus:1.1.1.3084.7 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

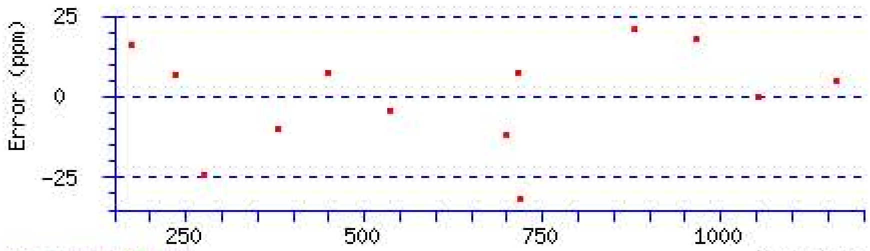


```
Monoisotopic mass of neutral peptide Mr(calc): 1430.672470
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.0079
Matches : 13/88 fragment ions using 30 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.050203	58.028740	98.023654	49.515465			N							9
2	252.109115	126.558195	235.082566	118.044921			H	1317.636832	659.322054	1300.610283	650.808780	1299.626267	650.316772	8
3	**380.167693**	190.587484	363.141144	182.074210			Q	1180.577920	590.792598	1163.551371	582.279324	1162.567355	581.787316	7
4	467.199721	234.103499	450.173172	225.590224	449.189156	225.098216	S	***1052.519342***	526.763309	1035.492793	518.250035	1034.508777	517.758027	6
5	554.231749	277.619513	537.205200	269.106238	536.221184	268.614230	S	***965.487314***	483.247295	948.460765	474.734021	947.476749	474.242013	5
6	**717.295078**	359.151177	700.268529	350.637903	699.284513	350.145895	Y	***878.455286***	439.731281	861.428737	431.218007	860.444721	430.725999	4
7	1156.520404	578.763840	1139.493855	570.250566	1138.509839	569.758558	Q	***715.391957***	358.199617	698.365408	349.686342	697.381392	349.194334	3
8	1257.568083	629.287680	1240.541534	620.774405	1239.557518	620.282397	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
9							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 15 ppm



RMS error 15 ppm

NCBI **BLAST** search of NHQSSYQTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.6	1430.672470	-0.001378	NHQSSYQTR
3.2	1430.686371	-0.015279	LICESLYASGYR

Mascot: http://www.matrixscience.com/

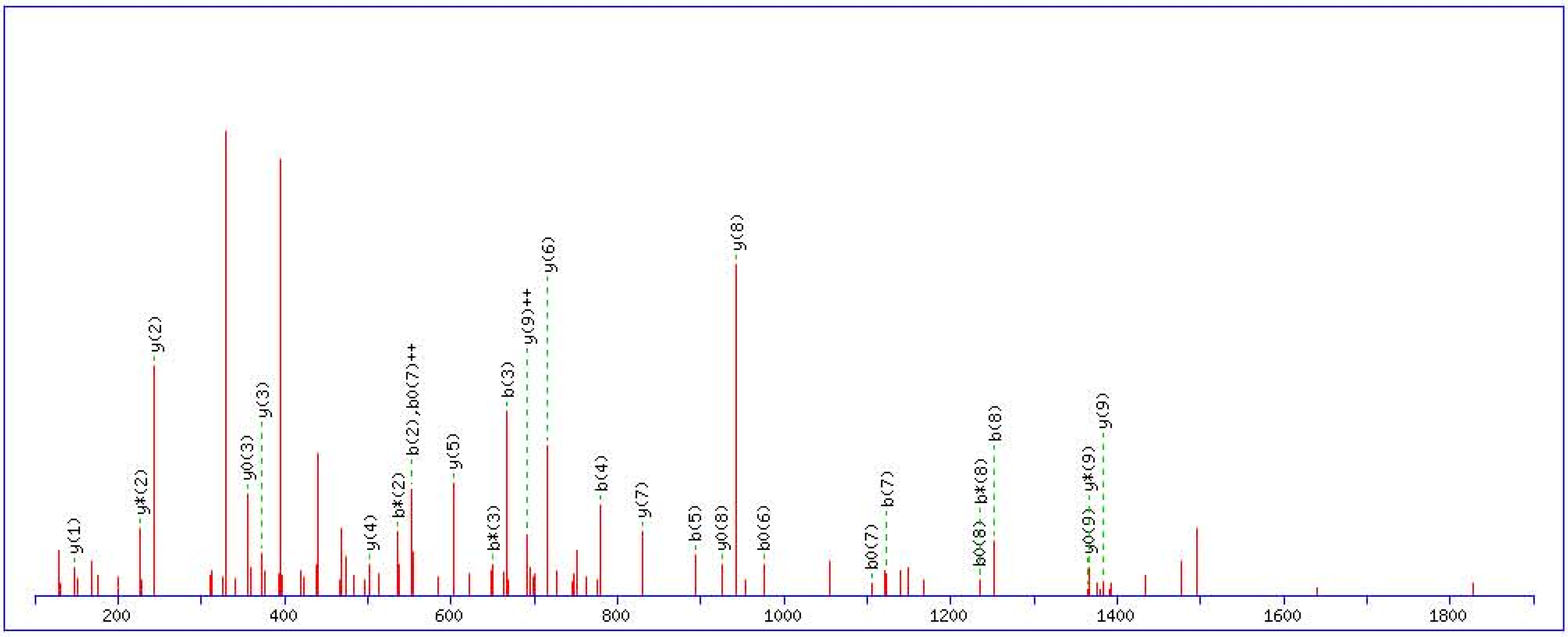
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQNILTEEPK**
Found in **PON1_HUMAN**, Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3

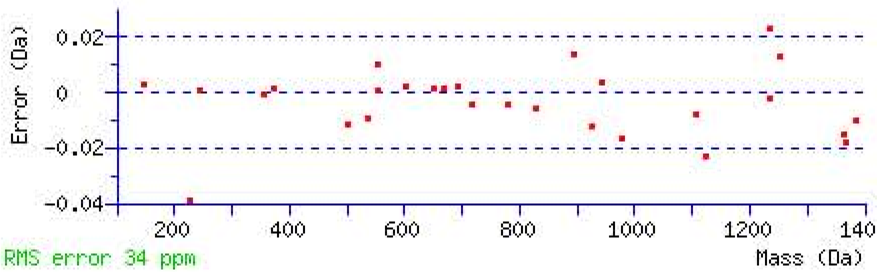
Match to Query 27033: 1494.814468 from(748.414510,2+) rtinseconds(2065) index(46421)
Title: Locus:1.1.1.3431.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

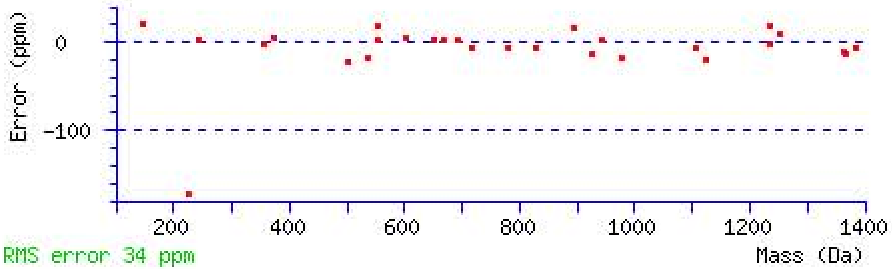
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1494.811569
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 45  Expect: 0.00015
Matches : 28/92 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	114.091340	57.549308					I							10
2	**553.316666**	277.161971	536.290117	268.648697			Q	***1382.734814***	691.871045	1365.708265	683.357771	1364.724249	682.865763	9
3	**667.359593**	334.183435	650.333044	325.670160			N	***943.509488***	472.258382	926.482939	463.745108	925.498923	463.253100	8
4	**780.443657**	390.725467	763.417108	382.212192			I	***829.466561***	415.236919	812.440012	406.723644	811.455996	406.231636	7
5	**893.527721**	447.267499	876.501172	438.754224			L	***716.382497***	358.694887	699.355948	350.181612	698.371932	349.689604	6
6	994.575400	497.791338	977.548851	489.278064	976.564835	488.786056	T	***603.298433***	302.152855	586.271884	293.639580	585.287868	293.147572	5
7	**1123.617993**	562.312635	1106.591444	553.799360	1105.607428	553.307352	E	***502.250754***	251.629015	485.224205	243.115741	484.240189	242.623733	4
8	**1252.660586**	626.833931	1235.634037	618.320657	1234.650021	617.828649	E	***373.208161***	187.107719	356.181612	178.594444	355.197556	178.102436	3
9	1349.713350	675.360313	1332.686801	666.847039	1331.702785	666.355031	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 IQNILTEEPK
(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	1494.811569	0.002899	IQNILTEEPK
3.8	1494.809097	0.005371	LQLYVFVMR
3.7	1494.805054	0.009414	KSIPLKMCYVTR
3.0	1494.815430	-0.000962	KGSTKDSGHLQIPK
2.6	1494.797668	0.016800	KMVTHTAASPALPR
1.9	1494.834030	-0.019562	QLNAIRDNIK

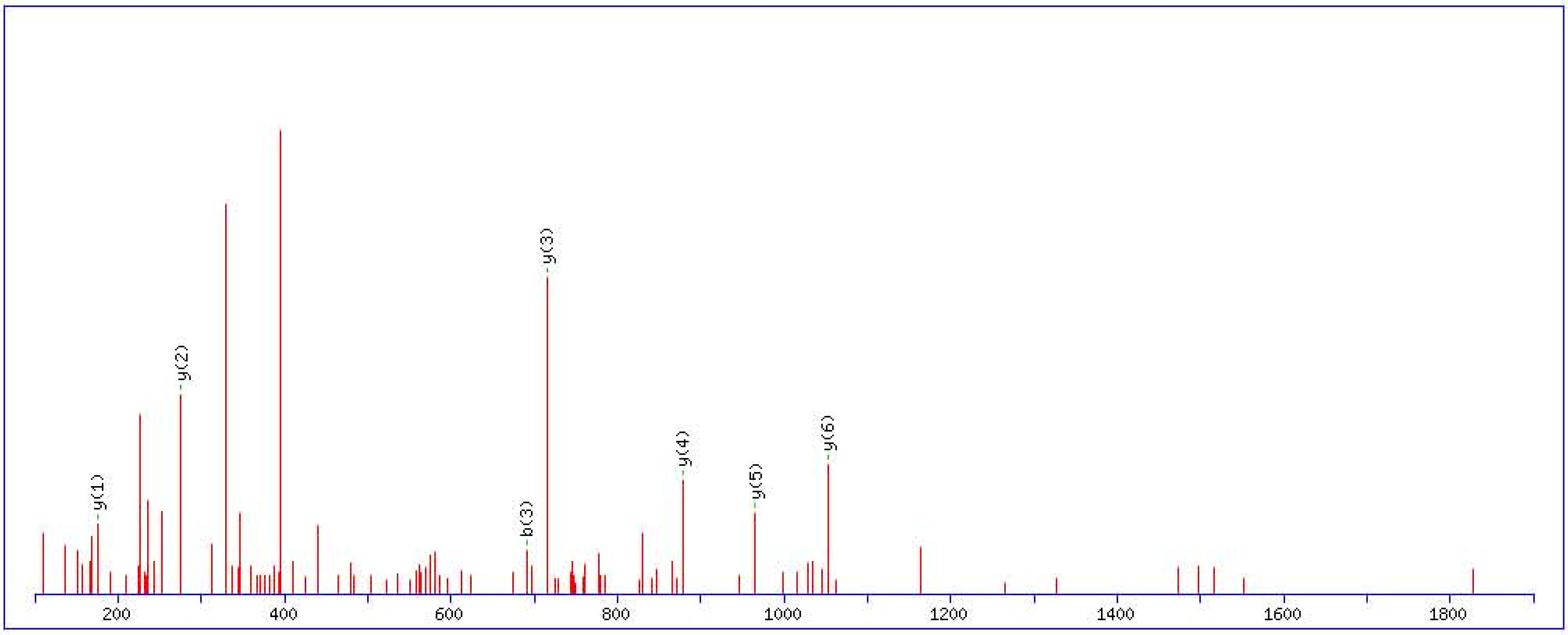
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NHQSSYQTR**
Found in **PON1_HUMAN**, Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3

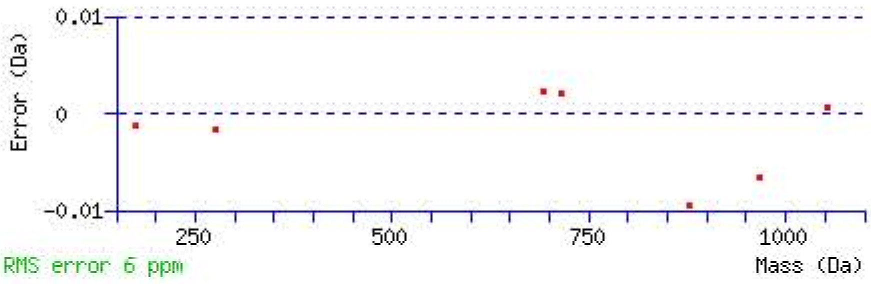
Match to Query 34407: 1741.833222 from(581.618350,3+) rtinseconds(1606) index(43539)
Title: Locus:1.1.1.3272.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

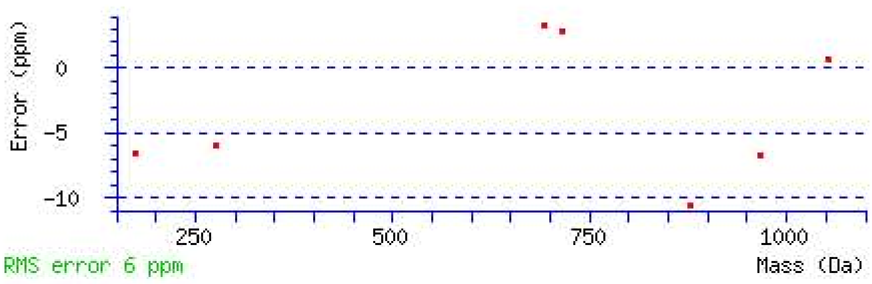
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1741.839218
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 26 **Expect:** 0.049
Matches : 7/88 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	115.050203	58.028740	98.023654	49.515465			N							9
2	252.109115	126.558195	235.082566	118.044921			H	1628.803580	814.905428	1611.777031	806.392154	1610.793015	805.900146	8
3	691.334441	346.170859	674.307892	337.657584			Q	1491.744668	746.375972	1474.718119	737.862698	1473.734103	737.370690	7
4	778.366469	389.686872	761.339920	381.173598	760.355904	380.681590	S	***1052.519342***	526.763309	1035.492793	518.250035	1034.508777	517.758027	6
5	865.398497	433.202886	848.371948	424.689612	847.387932	424.197604	S	***965.487314***	483.247295	948.460765	474.734021	947.476749	474.242013	5
6	1028.461826	514.734551	1011.435277	506.221276	1010.451261	505.729268	Y	***878.455286***	439.731281	861.428737	431.218007	860.444721	430.725999	4
7	1467.687152	734.347214	1450.660603	725.833940	1449.676587	725.341932	Q	***715.391957***	358.199617	698.365408	349.686342	697.381392	349.194334	3
8	1568.734831	784.871054	1551.708282	776.357779	1550.724266	775.865771	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of NHQSSYQTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.6	1741.839218	-0.005996	NHQSSYQTR

Mascot: http://www.matrixscience.com/

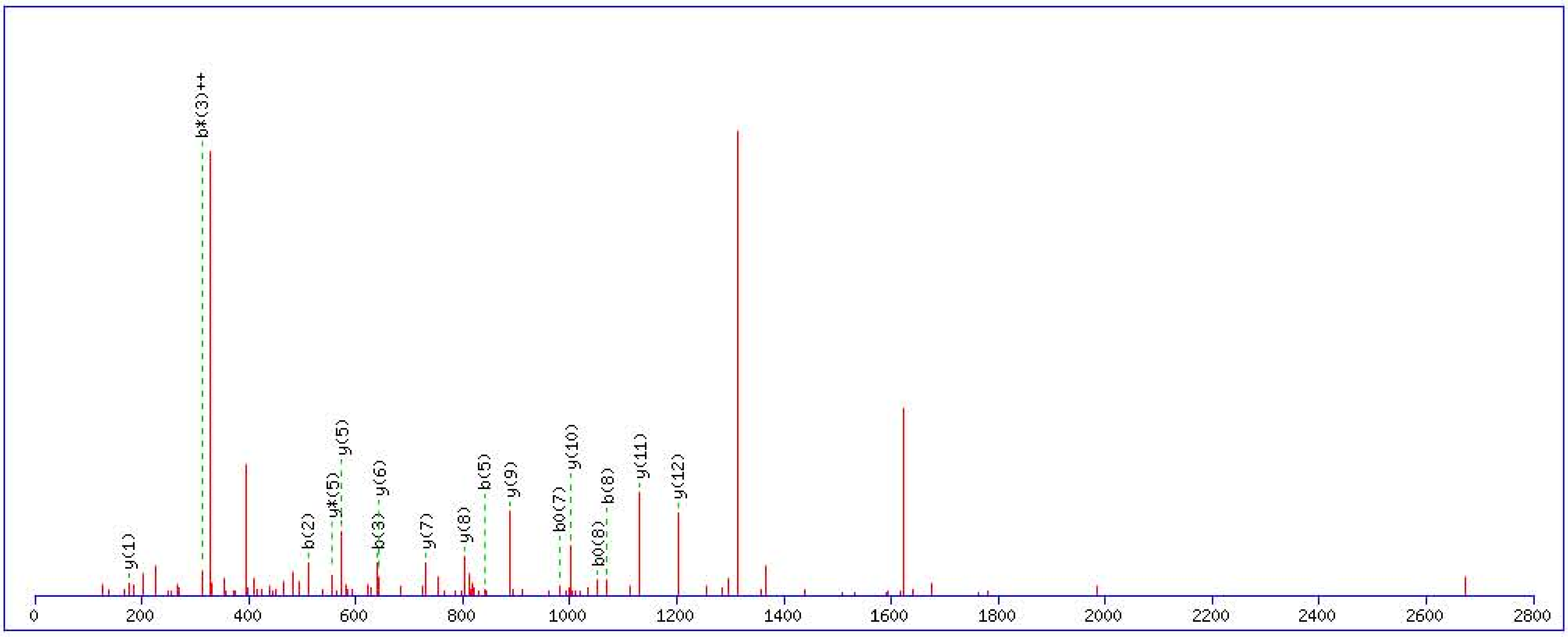
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QAEISASAPTSLR**
Found in **SHBG_HUMAN**, Sex hormone-binding globulin OS=Homo sapiens GN=SHBG PE=1 SV=2

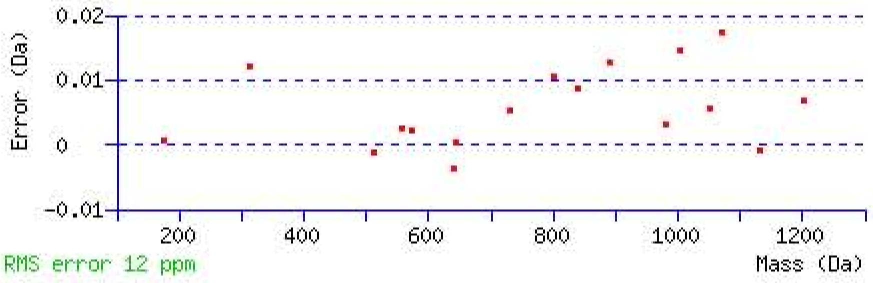
Match to Query 32544: 1640.864388 from(821.439470,2+) rtinseconds(1926) index(4360)
Title: Locus:1.1.1.3190.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

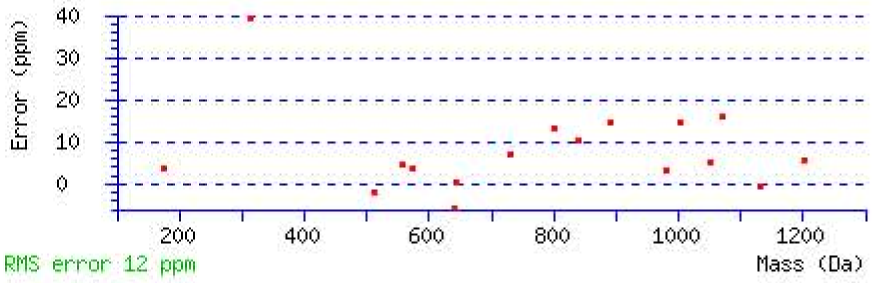
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1640.855560
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 5.9e-006
Matches : 17/136 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	440.232602	220.619939	423.206053	212.106664			Q							13
2	**511.269716**	256.138496	494.243167	247.625221			A	***1202.637542***	601.822409	1185.610993	593.309135	1184.626977	592.817126	12
3	**640.312309**	320.659793	623.285760	312.146518	622.301744	311.654510	E	***1131.600428***	566.303852	1114.573879	557.790578	1113.589863	557.298569	11
4	753.396373	377.201825	736.369824	368.688550	735.385808	368.196542	I	***1002.557835***	501.782556	985.531286	493.269281	984.547270	492.777273	10
5	**840.428401**	420.717839	823.401852	412.204564	822.417836	411.712556	S	***889.473771***	445.240523	872.447222	436.727249	871.463206	436.235241	9
6	911.465515	456.236396	894.438966	447.723121	893.454950	447.231113	A	***802.441743***	401.724510	785.415194	393.211235	784.431178	392.719227	8
7	998.497543	499.752410	981.470994	491.239135	980.486978	490.747127	S	***731.404629***	366.205953	714.378080	357.692678	713.394064	357.200670	7
8	**1069.534657**	535.270966	1052.508108	526.757692	1051.524092	526.265684	A	***644.372601***	322.689939	627.346052	314.176664	626.362036	313.684656	6
9	1166.587421	583.797349	1149.560872	575.284074	1148.576856	574.792066	P	***573.335487***	287.171382	556.308938	278.658107	555.324922	278.166099	5
10	1267.635100	634.321188	1250.608551	625.807914	1249.624535	625.315905	T	476.282723	238.644999	459.256174	230.131725	458.272158	229.639717	4
11	1354.667128	677.837202	1337.640579	669.323928	1336.656563	668.831920	S	375.235044	188.121160	358.208495	179.607885	357.224479	179.115877	3
12	1467.751192	734.379234	1450.724643	725.865960	1449.740627	725.373951	L	288.203016	144.605146	271.176467	136.091871			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of QAEISASAPTSLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.1	1640.855560	0.008828	QAEISASAPTSLR
1.3	1640.884521	-0.020133	EAQKKPAESQKIER
1.2	1640.848160	0.016228	LQRILEGEGNQEAGK
0.8	1640.880707	-0.016319	KLSPELMNQLVPEK

Mascot: http://www.matrixscience.com/

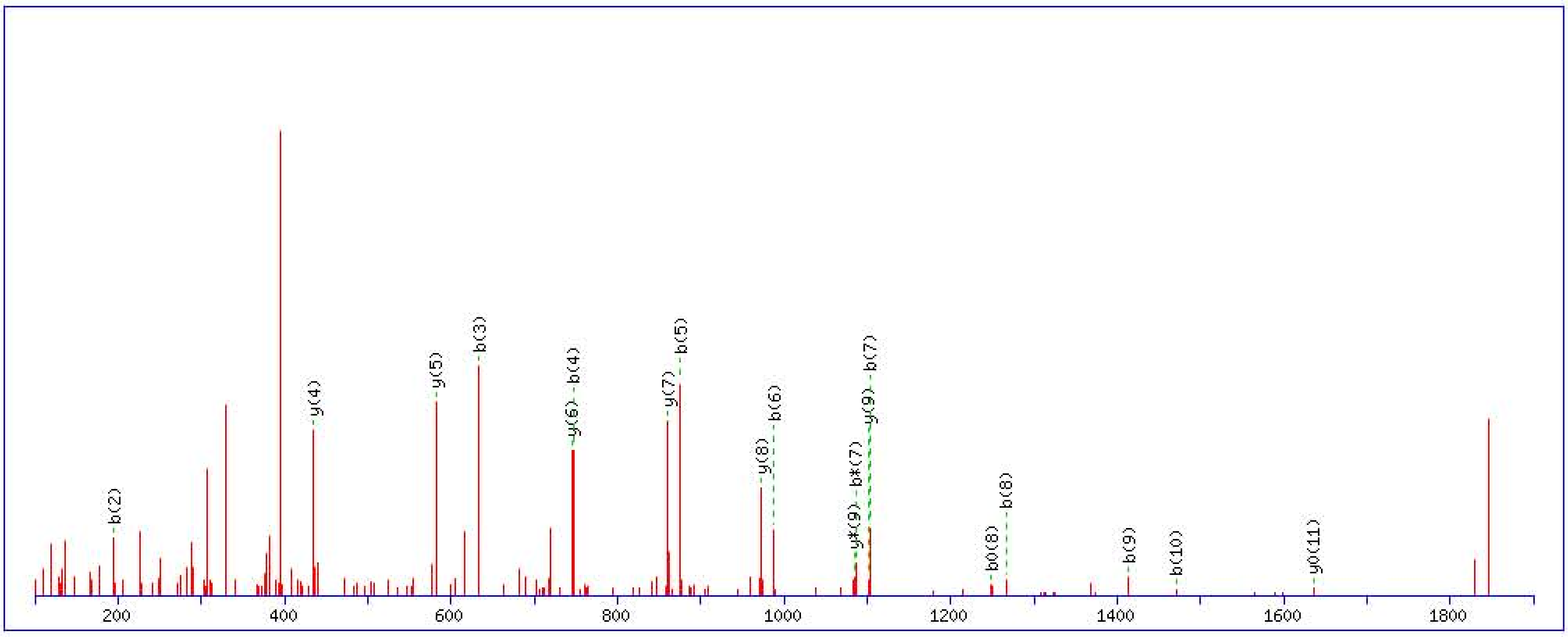
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GHQLQLDYFGACK**
Found in **SPRL1_HUMAN**, SPARC-like protein 1 OS=Homo sapiens GN=SPARCL1 PE=1 SV=2

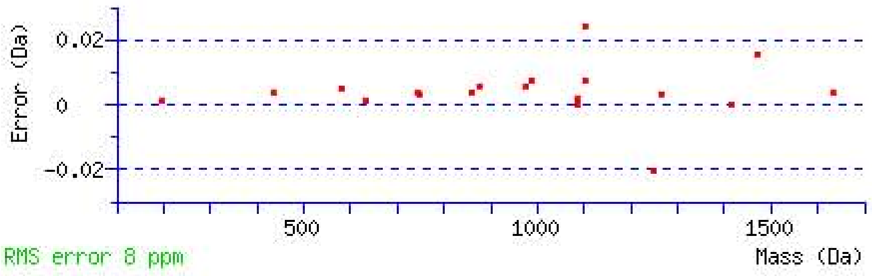
Match to Query 36560: 1846.887072 from(616.636300,3+) rtinseconds(2147) index(46895)
Title: Locus:1.1.1.3460.5 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

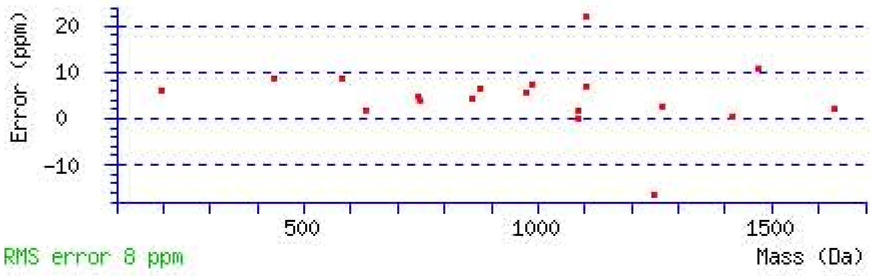
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 56  Expect: 1.2e-005
Matches : 19/116 fragment ions using 33 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	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
55.8	1846.885849	0.001223	GHQLQLDYFGACK
30.0	1846.885849	0.001223	GHQLQLDYFGACK
3.5	1846.906082	-0.019010	DLNTGVFNNQENEILK

Mascot: http://www.matrixscience.com/

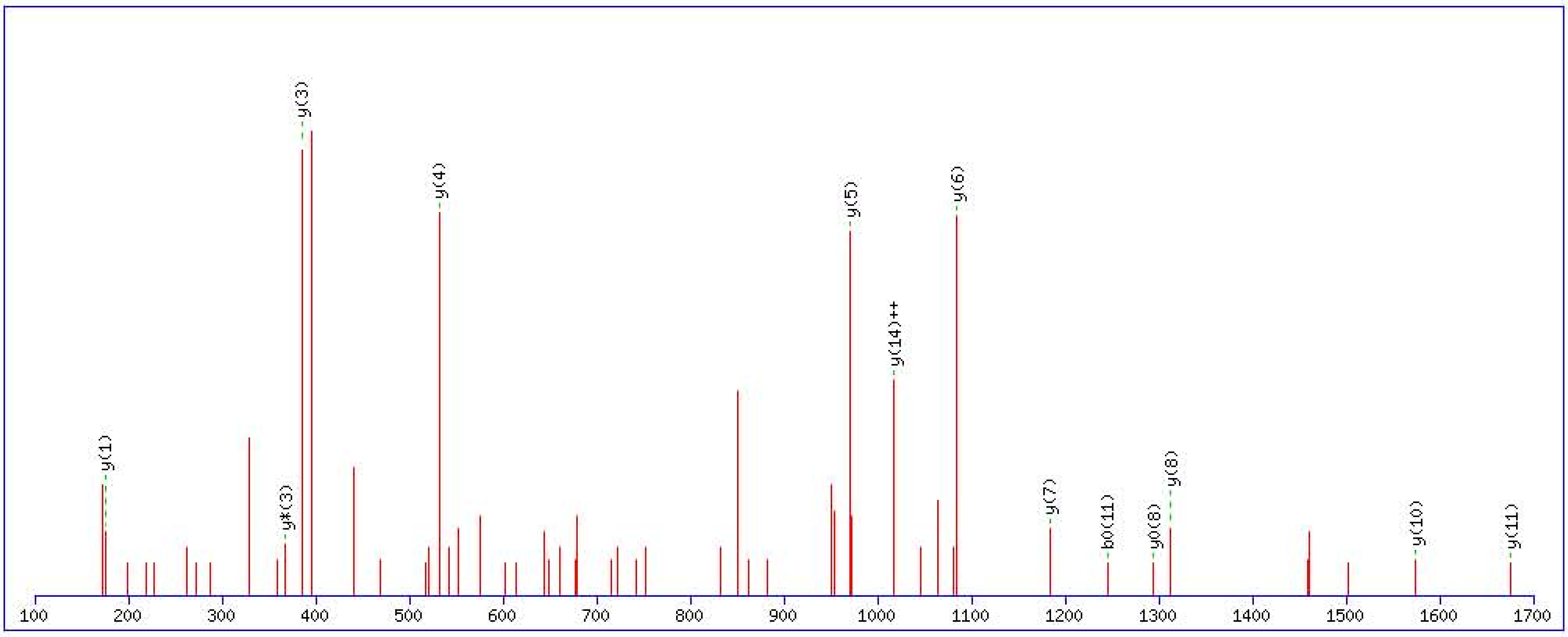
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SIPTCTDFEVIQFPLR**
Found in **SPRL1_HUMAN**, SPARC-like protein 1 OS=Homo sapiens GN=SPARCL1 PE=1 SV=2

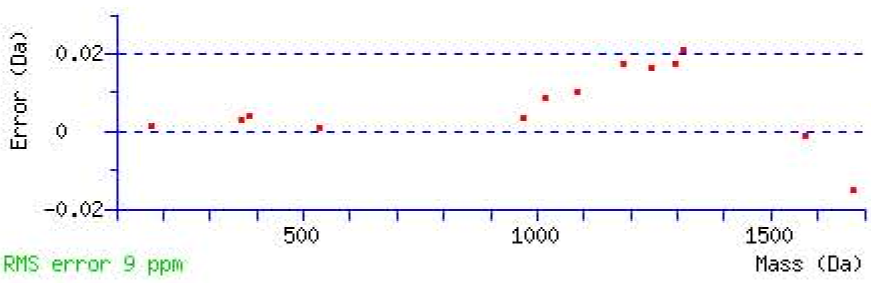
Match to Query 43856: 2233.134462 from(745.385430,3+) rtinseconds(2822) index(50941)
Title: Locus:1.1.1.3693.11 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

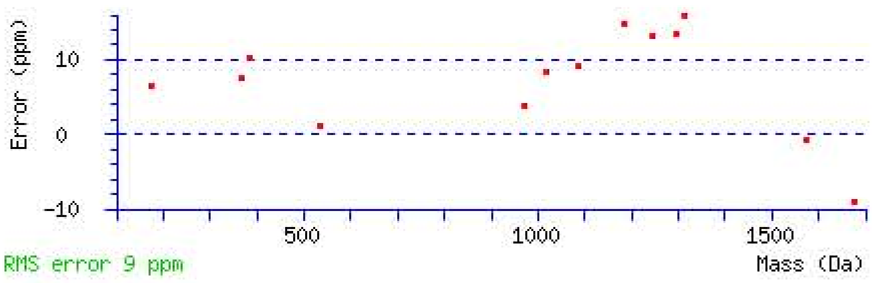
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2233.127548
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.00052
Matches : 13/144 fragment ions using 29 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	201.123368	101.065322			183.112803	92.060039	I	2147.102783	1074.055029	2130.076234	1065.541755	2129.092218	1065.049747	15
3	298.176132	149.591704			280.165567	140.586422	P	2034.018719	1017.512998	2016.992170	1008.999723	2016.008154	1008.507715	14
4	399.223811	200.115544			381.213246	191.110261	T	1936.965955	968.986616	1919.939406	960.473341	1918.955390	959.981333	13
5	559.254460	280.130868			541.243895	271.125586	C	1835.918276	918.462776	1818.891727	909.949502	1817.907711	909.457494	12
6	660.302139	330.654708			642.291574	321.649425	T	***1675.887627***	838.447452	1658.861078	829.934177	1657.877062	829.442169	11
7	775.329082	388.168179			757.318517	379.162897	D	***1574.839948***	787.923612	1557.813399	779.410338	1556.829383	778.918330	10
8	922.397496	461.702386			904.386931	452.697104	F	1459.813005	730.410141	1442.786456	721.896866	1441.802440	721.404858	9
9	1051.440089	526.223683			1033.429524	517.218400	E	***1312.744591***	656.875934	1295.718042	648.362659	1294.734026	647.870651	8
10	1150.508503	575.757890			1132.497938	566.752607	V	***1183.701998***	592.354637	1166.675449	583.841363			7
11	1263.592567	632.299921			1245.582002	623.294639	I	***1084.633584***	542.820430	1067.607035	534.307156			6
12	1702.817893	851.912585	1685.791344	843.399310	1684.807328	842.907302	Q	***971.549520***	486.278398	954.522971	477.765124			5
13	1849.886307	925.446792	1832.859758	916.933517	1831.875742	916.441509	F	***532.324194***	266.665735	515.297645	258.152461			4
14	1946.939071	973.973174	1929.912522	965.459899	1928.928506	964.967891	P	***385.255780***	193.131528	368.229231	184.618253			3
15	2060.023135	1030.515205	2042.996586	1022.001931	2042.012570	1021.509923	L	288.203016	144.605146	271.176467	136.091871			2
16							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SIPTCTDFEVIQFPLR
(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	2233.127548	0.006914	SIPTCTDFEVIQFPLR
3.9	2233.141861	-0.007399	FELPLDIPEEEARYWAKK
0.4	2233.108704	0.025758	AQLGSWGKGSSGGAKASETDALR

Mascot: http://www.matrixscience.com/

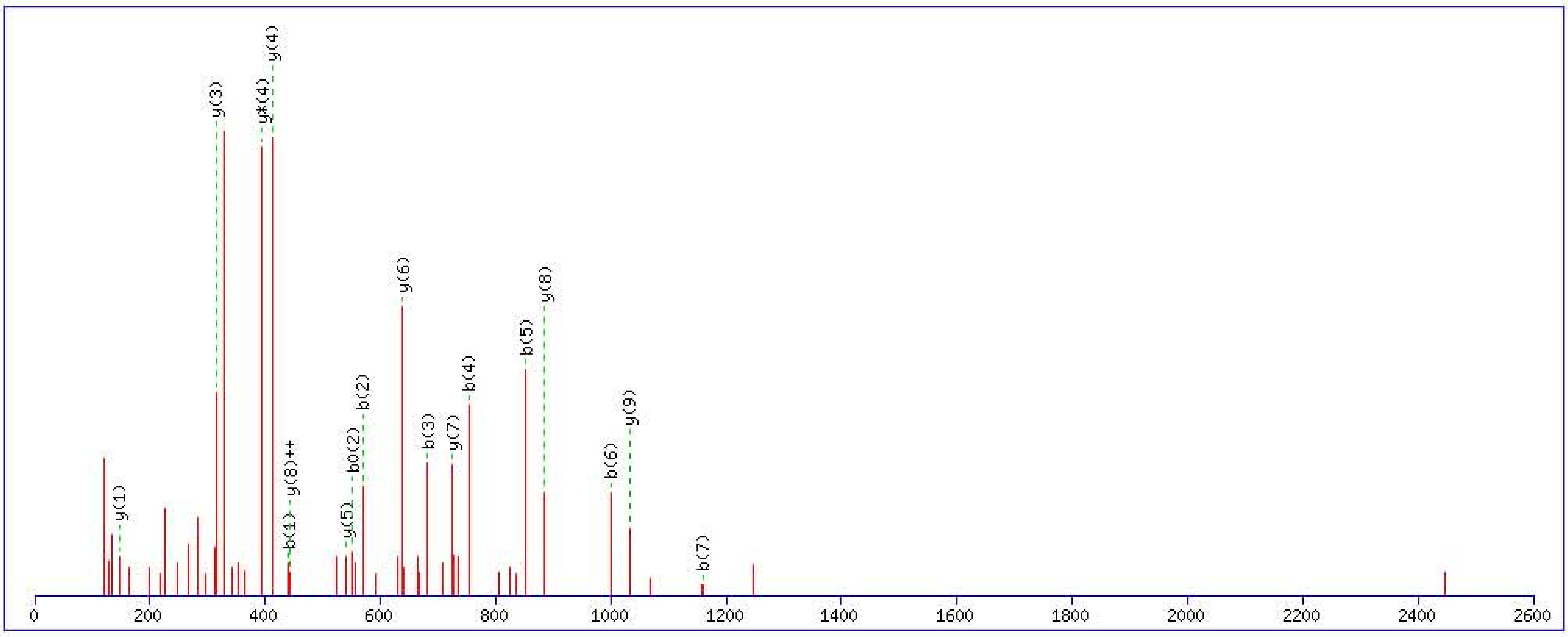
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QELAVFCSPEPPAK**
Found in **TLN1_HUMAN**, Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3

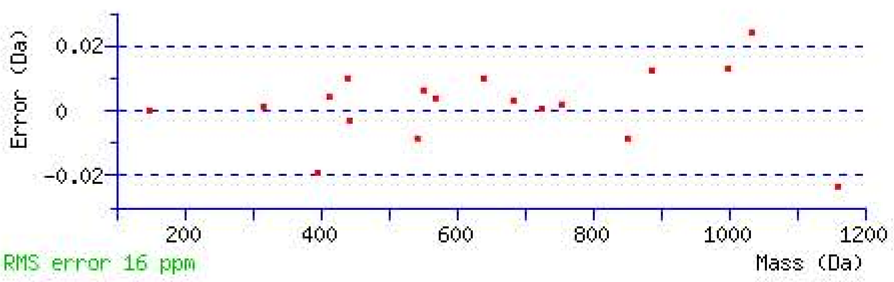
Match to Query 37214: 1882.938882 from(628.653570,3+) rtinseconds(2259) index(47613)
Title: Locus:1.1.1.3499.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

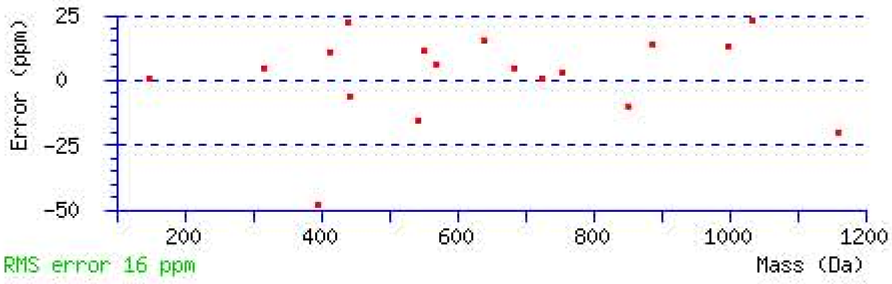
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1882.932114
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 63  Expect: 1.7e-006
Matches : 18/146 fragment ions using 29 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							14
2	***569.275195***	285.141236	552.248646	276.627961	551.264630	276.135953	E	1444.714079	722.860678	1427.687530	714.347403	1426.703514	713.855395	13
3	***682.359259***	341.683268	665.332710	333.169993	664.348694	332.677985	L	1315.671486	658.339381	1298.644937	649.826107	1297.660921	649.334098	12
4	***753.396373***	377.201825	736.369824	368.688550	735.385808	368.196542	A	1202.587422	601.797349	1185.560873	593.284075	1184.576857	592.792067	11
5	***852.464787***	426.736032	835.438238	418.222757	834.454222	417.730749	V	1131.550308	566.278792	1114.523759	557.765518	1113.539743	557.273510	10
6	***999.533201***	500.270239	982.506652	491.756964	981.522636	491.264956	F	***1032.481894***	516.744585	1015.455345	508.231311	1014.471329	507.739303	9
7	***1159.563850***	580.285563	1142.537301	571.772289	1141.553285	571.280281	C	***885.413480***	443.210378	868.386931	434.697104	867.402915	434.205096	8
8	1246.595878	623.801577	1229.569329	615.288303	1228.585313	614.796295	S	***725.382831***	363.195054	708.356282	354.681779	707.372266	354.189771	7
9	1343.648642	672.327959	1326.622093	663.814685	1325.638077	663.322677	P	***638.350803***	319.679040	621.324254	311.165765	620.340238	310.673757	6
10	1472.691235	736.849256	1455.664686	728.335981	1454.680670	727.843973	E	***541.298039***	271.152658	524.271490	262.639383	523.287474	262.147375	5
11	1569.743999	785.375638	1552.717450	776.862363	1551.733434	776.370355	P	***412.255446***	206.631361	395.228897	198.118087			4
12	1666.796763	833.902020	1649.770214	825.388745	1648.786198	824.896737	P	***315.202682***	158.104979	298.176133	149.591704			3
13	1737.833877	869.420577	1720.807328	860.907302	1719.823312	860.415294	A	218.149918	109.578597	201.123369	101.065322			2
14							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of QELAVFCSPEPPAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.6	1882.932114	0.006768	QELAVFCSPEPPAK
1.1	1882.949875	-0.010993	ISGHVGIIFSMSYLESK

Mascot: http://www.matrixscience.com/

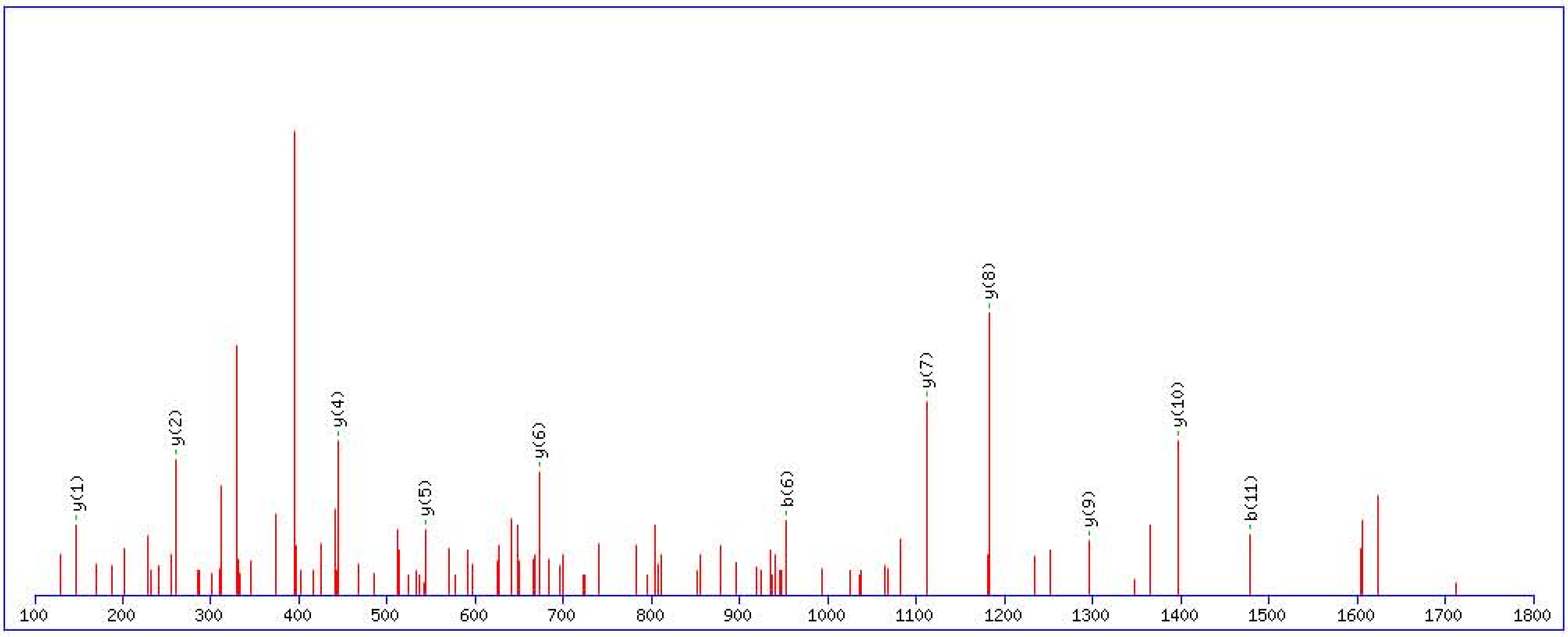
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDTLAQEVALLK**
Found in **TETN_HUMAN**, Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=3

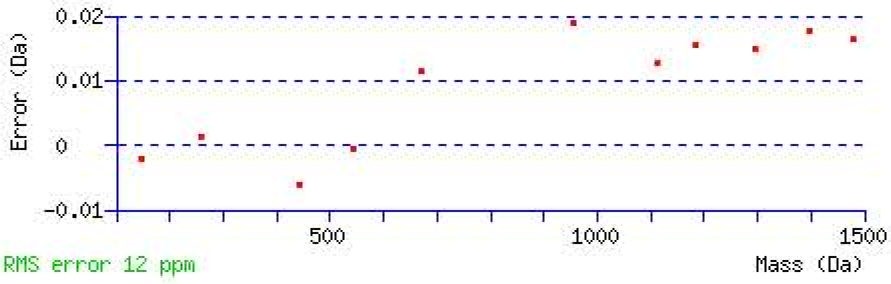
Match to Query 31588: 1623.942548 from(812.978550,2+) rtinseconds(2629) index(8320)
Title: Locus:1.1.1.3435.19 File:"2013-07-02 CLN FXIII 180 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

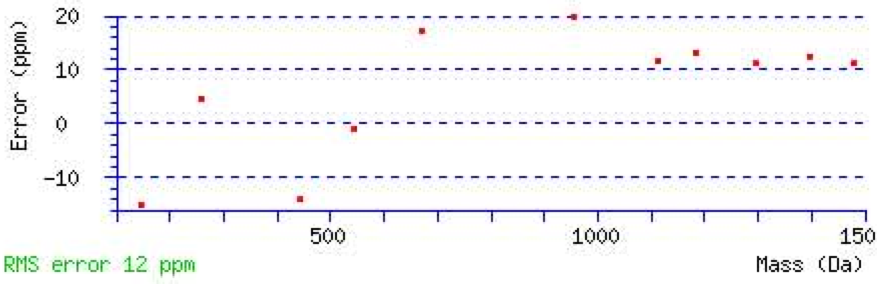
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monospace mass of neutral peptide Mr(calc): 1623.926941
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 83 **Expect:** 3.9e-008
Matches : 11/110 fragment ions using 15 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	114.091340	57.549308					L							12
2	229.118283	115.062779			211.107718	106.057497	D	1511.850179	756.428728	1494.823630	747.915453	1493.839614	747.423445	11
3	330.165962	165.586619			312.155397	156.581336	T	***1396.823236***	698.915256	1379.796687	690.401982	1378.812671	689.909973	10
4	443.250026	222.128651			425.239461	213.123369	L	***1295.775557***	648.391416	1278.749008	639.878142	1277.764992	639.386134	9
5	514.287140	257.647208			496.276575	248.641926	A	***1182.691493***	591.849385	1165.664944	583.336110	1164.680928	582.844102	8
6	**953.512466**	477.259871	936.485917	468.746597	935.501901	468.254589	Q	***1111.654379***	556.330827	1094.627830	547.817553	1093.643814	547.325545	7
7	1082.555059	541.781168	1065.528510	533.267893	1064.544494	532.775885	E	***672.429053***	336.718165	655.402504	328.204890	654.418488	327.712882	6
8	1181.623473	591.315375	1164.596924	582.802100	1163.612908	582.310092	V	***543.386460***	272.196868	526.359911	263.683593			5
9	1252.660587	626.833932	1235.634038	618.320657	1234.650022	617.828649	A	***444.318046***	222.662661	427.291497	214.149386			4
10	1365.744651	683.375964	1348.718102	674.862689	1347.734086	674.370681	L	373.280932	187.144104	356.254383	178.630829			3
11	**1478.828715**	739.917995	1461.802166	731.404721	1460.818150	730.912713	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 LDTLAQEVALLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
82.6	1623.926941	0.015607	LDTLAQEVALLK
5.5	1623.919556	0.022992	EVSPEPIVSTVARLK
5.3	1623.928268	0.014280	EVQRLYHKLK
2.8	1623.944702	-0.002154	EVELIIQVTPKDIK
1.9	1623.942001	0.000547	ESKPGGLPRRSSIIK
1.9	1623.919540	0.023008	KLSLGTAEPQVKEPK
1.5	1623.934799	0.007749	FIQKFSQASSKILK
1.3	1623.955933	-0.013385	GAAVNLTLVTPEKAIK
1.0	1623.957245	-0.014697	ERQLLWLELLRR

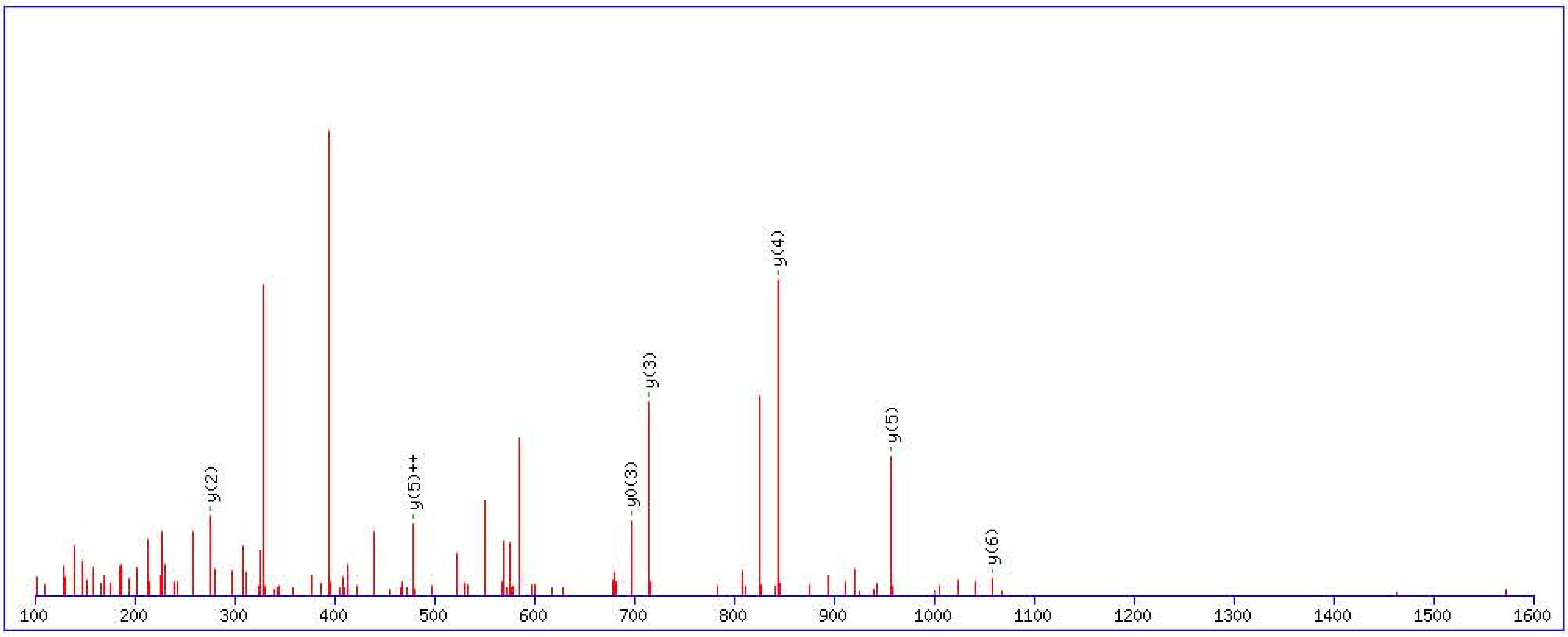
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ETIEQEK**
Found in **TYB10_HUMAN**, Thymosin beta-10 OS=Homo sapiens GN=TMSB10 PE=1 SV=2

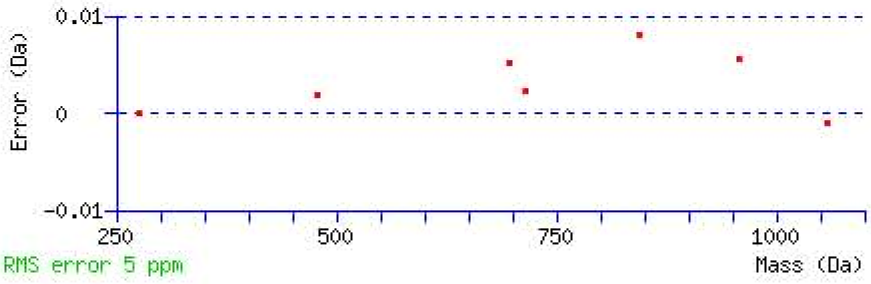
Match to Query 17448: 1186.587848 from(594.301200,2+) rtinseconds(1459) index(57724)
Title: Locus:1.1.1.1419.14 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

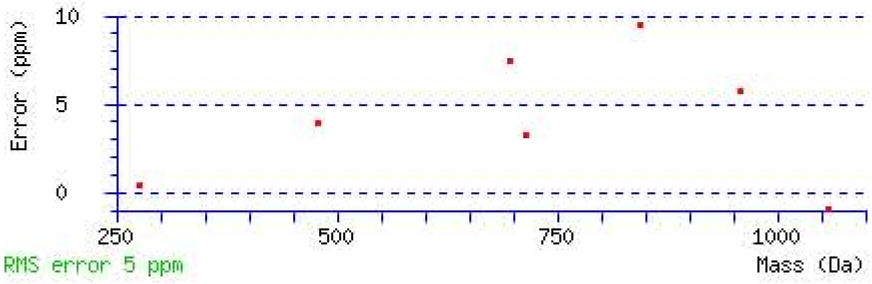
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1186.590347
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.0018
Matches : 7/62 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	130.049869	65.528572			112.039304	56.523290	E							7
2	231.097548	116.052412			213.086983	107.047130	T	***1058.555059***	529.781168	1041.528510	521.267893	1040.544494	520.775885	6
3	344.181612	172.594444			326.171047	163.589162	I	***957.507380***	479.257328	940.480831	470.744054	939.496815	470.252046	5
4	473.224205	237.115741			455.213640	228.110458	E	***844.423316***	422.715296	827.396767	414.202022	826.412751	413.710014	4
5	912.449531	456.728404	895.422982	448.215129	894.438966	447.723121	Q	***715.380723***	358.194000	698.354174	349.680725	697.370158	349.188717	3
6	1041.492124	521.249700	1024.465575	512.736426	1023.481559	512.244418	E	***276.155397***	138.581336	259.128848	130.068062	258.144832	129.576054	2
7							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ETIEQEK
(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	1186.590347	-0.002499	ETIEQEK
8.5	1186.572586	0.015262	KEMMKETFK
6.0	1186.601578	-0.013730	TNEKQEK
6.0	1186.601578	-0.013730	QEQKESK
5.2	1186.586960	0.000888	KLYSQYEEK
5.0	1186.605392	-0.017544	KEAEQEAARR
4.8	1186.572586	0.015262	KEMMKETFK
4.8	1186.591721	-0.003873	KTVGFHSHMK
4.6	1186.590347	-0.002499	QEEELTK
3.4	1186.605408	-0.017560	EVRQENREK

Mascot: http://www.matrixscience.com/

{MATRIX} {SCIENCE}

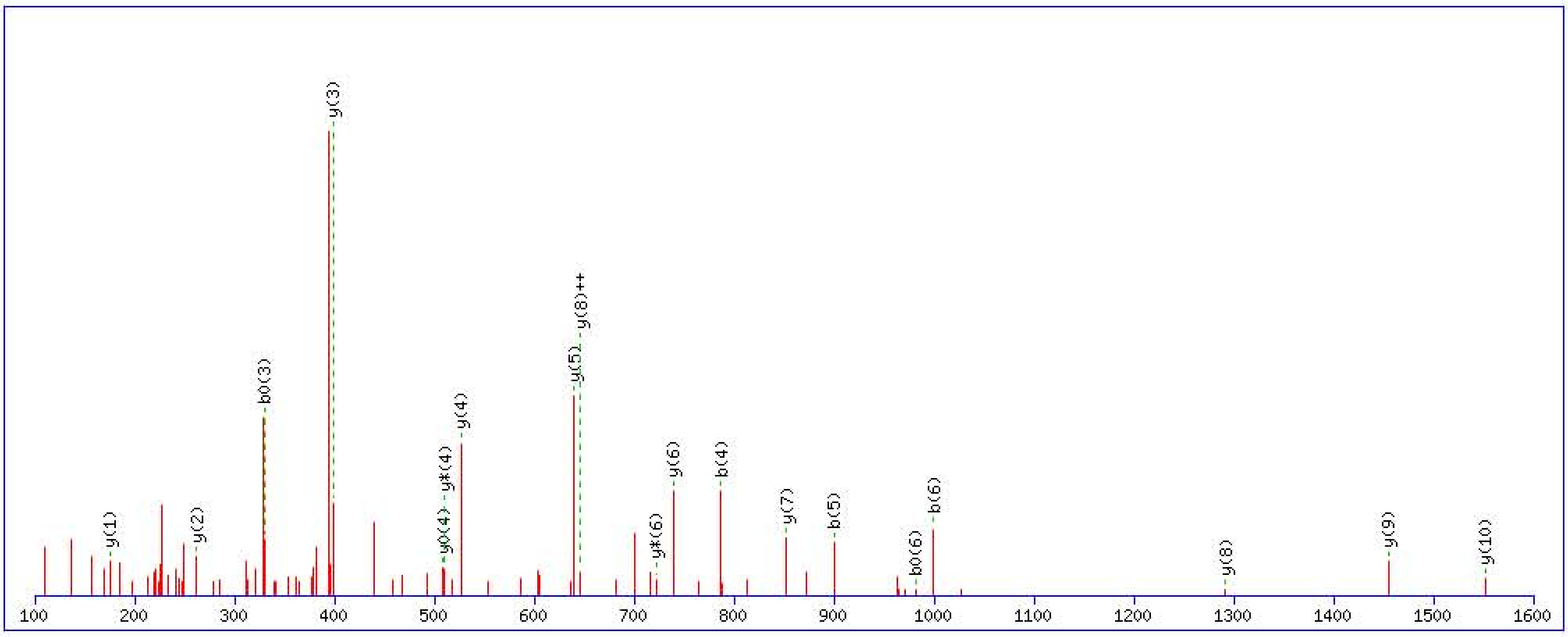
Mascot Search Results

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

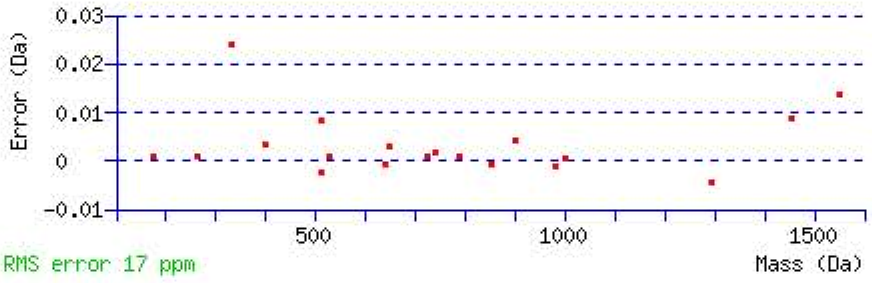
Match to Query 32441: 1637.864832 from(546.962220,3+) rtinseconds(1929) index(31304)
Title: Locus:1.1.1.3335.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

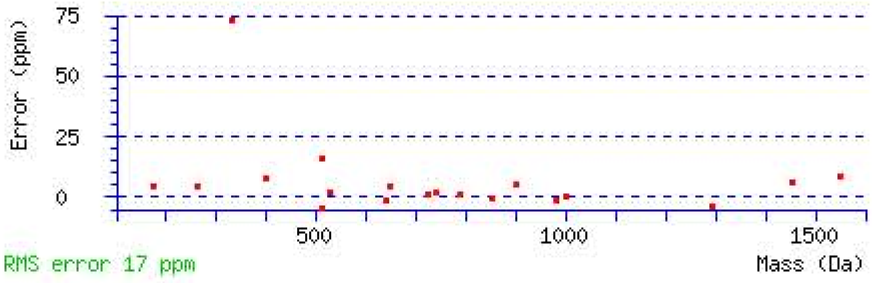
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1637.871170
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 6.9e-006
Matches : 19/112 fragment ions using 40 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							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
55.8	1637.871170	-0.006338	SPYQLVLQHSR
3.4	1637.871170	-0.006338	SPYQLVLQHSR
0.7	1637.855911	0.008921	RTAYSGVPMTILSSR

Mascot: http://www.matrixscience.com/

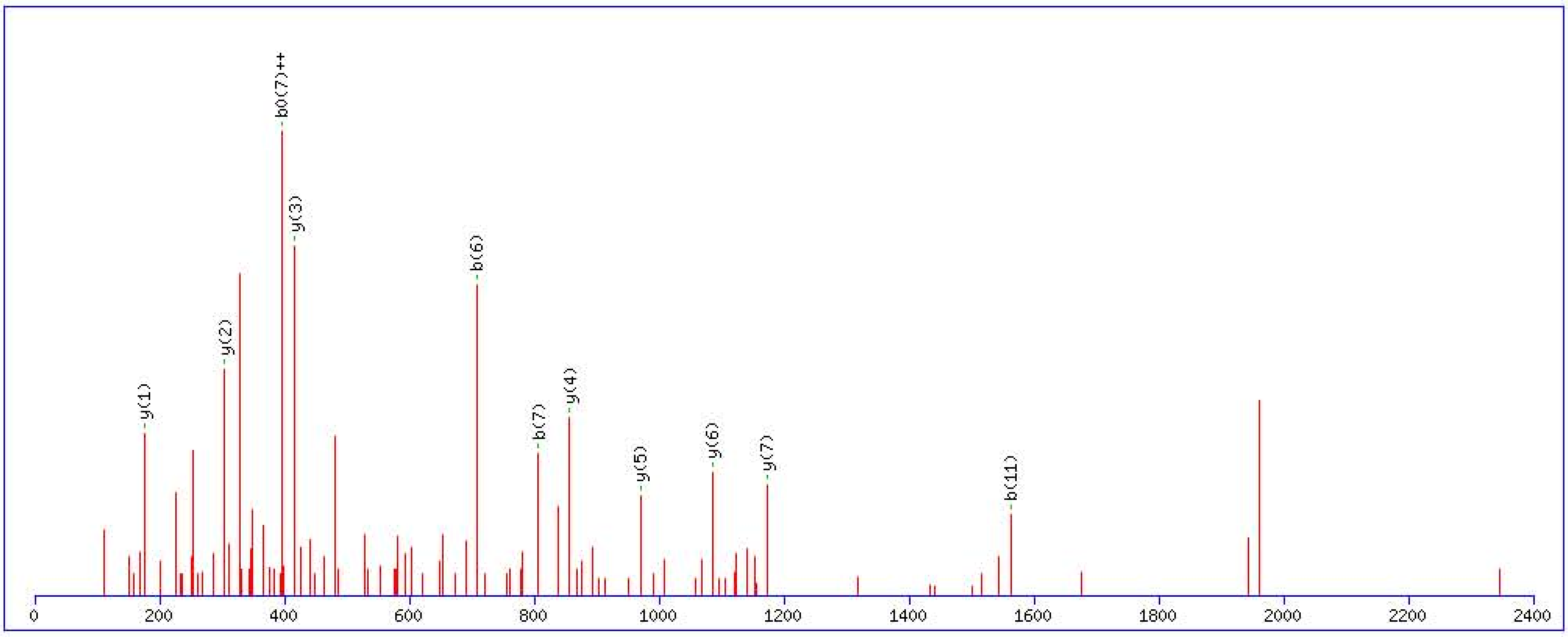
{MATRIX SCIENCE} **Mascot Search Results**

Peptide View

MS/MS Fragmentation of **NLHDLDVSDNQLER**
Found in **VASN_HUMAN**, Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1

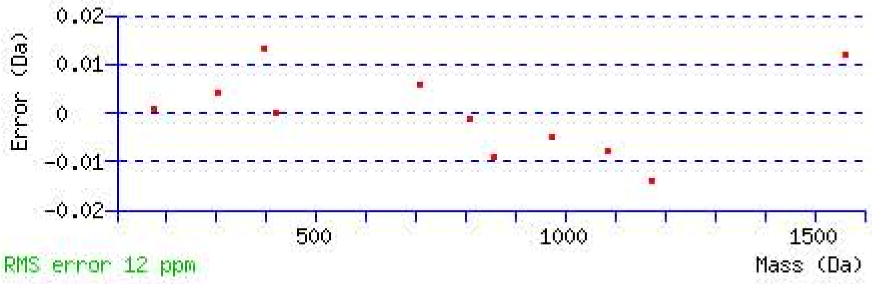
Match to Query 38911: 1977.948522 from(660.323450,3+) rtinseconds(1954) index(18785)
Title: Locus:1.1.1.3246.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

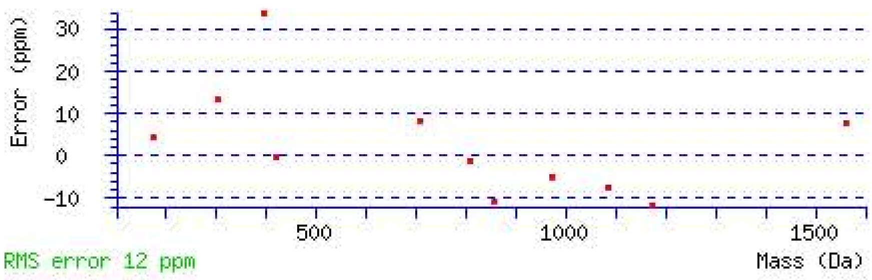


```
Monoisotopic mass of neutral peptide Mr(calc): 1977.957809
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 50  Expect: 0.00021
Matches : 11/148 fragment ions using 16 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							14
2	228.134267	114.570771	211.107718	106.057497			L	1864.922173	932.964724	1847.895624	924.451450	1846.911608	923.959442	13
3	365.193179	183.100227	348.166630	174.586953			H	1751.838109	876.422692	1734.811560	867.909418	1733.827544	867.417410	12
4	480.220122	240.613699	463.193573	232.100425	462.209557	231.608417	D	1614.779197	807.893236	1597.752648	799.379962	1596.768632	798.887954	11
5	593.304186	297.155731	576.277637	288.642457	575.293621	288.150449	L	1499.752254	750.379765	1482.725705	741.866490	1481.741689	741.374482	10
6	**708.331129**	354.669203	691.304580	346.155928	690.320564	345.663920	D	1386.668190	693.837733	1369.641641	685.324458	1368.657625	684.832450	9
7	**807.399543**	404.203410	790.372994	395.690135	789.388978	395.198127	V	1271.641247	636.324261	1254.614698	627.810987	1253.630682	627.318979	8
8	894.431571	447.719424	877.405022	439.206149	876.421006	438.714141	S	***1172.572833***	586.790054	1155.546284	578.276780	1154.562268	577.784772	7
9	1009.458514	505.232895	992.431965	496.719620	991.447949	496.227612	D	***1085.540805***	543.274040	1068.514256	534.760766	1067.530240	534.268758	6
10	1123.501441	562.254358	1106.474892	553.741084	1105.490876	553.249076	N	***970.513862***	485.760569	953.487313	477.247294	952.503297	476.755286	5
11	**1562.726767**	781.867021	1545.700218	773.353747	1544.716202	772.861739	Q	***856.470935***	428.739105	839.444386	420.225831	838.460370	419.733823	4
12	1675.810831	838.409053	1658.784282	829.895779	1657.800266	829.403771	L	***417.245609***	209.126442	400.219060	200.613168	399.235044	200.121160	3
13	1804.853424	902.930350	1787.826875	894.417075	1786.842859	893.925067	E	***304.161545***	152.584410	287.134996	144.071136	286.150980	143.579128	2
14							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 12 ppm



RMS error 12 ppm

NCBI **BLAST** search of NLHDLDVSDNQLER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.8	1977.957809	-0.009287	NLHDLDVSDNQLER

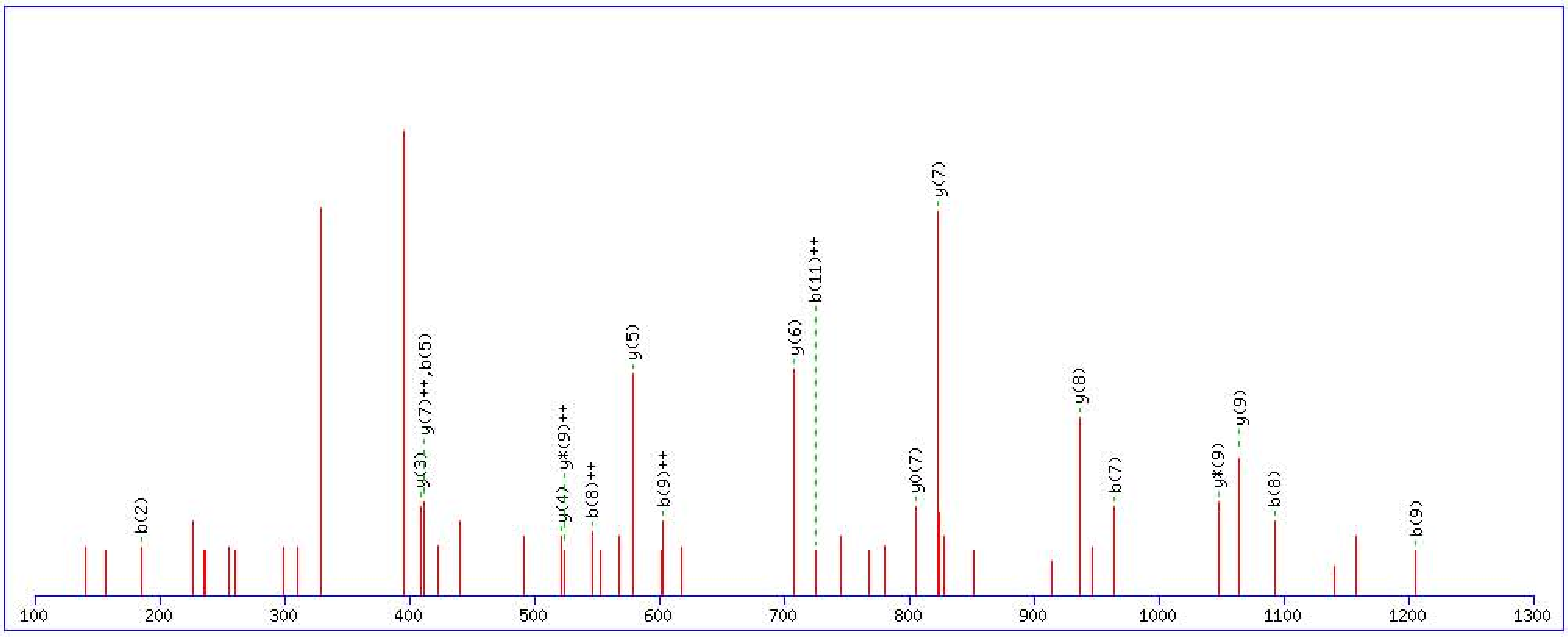
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAGLGLQQLDEGLFSR**
Found in **VASN_HUMAN**, Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1

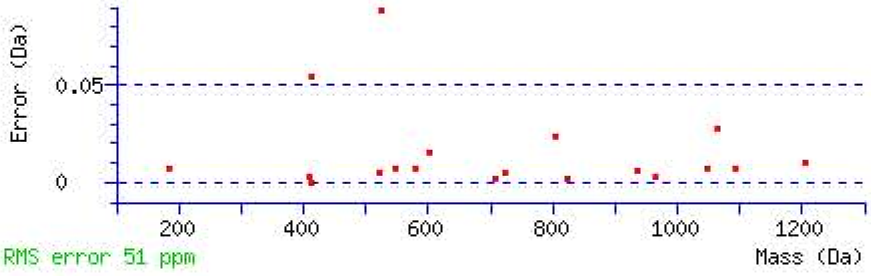
Match to Query 40328: 2027.088852 from(676.703560,3+) rtinseconds(2838) index(23948)
Title: Locus:1.1.1.3552.4 File:"2013-07-02 CLN FXIII 180 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

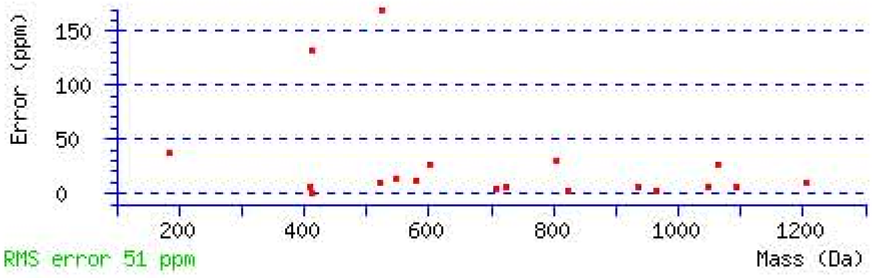
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2027.087372
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0046
Matches : 19/148 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	114.091340	57.549308					L							16
2	**185.128454**	93.067865					A	1915.010596	958.008936	1897.984047	949.495662	1897.000031	949.003654	15
3	242.149918	121.578597					G	1843.973482	922.490379	1826.946933	913.977105	1825.962917	913.485097	14
4	355.233982	178.120629					L	1786.952018	893.979647	1769.925469	885.466373	1768.941453	884.974364	13
5	**412.255446**	206.631361					G	1673.867954	837.437615	1656.841405	828.924341	1655.857389	828.432333	12
6	525.339510	263.173393					L	1616.846490	808.926883	1599.819941	800.413609	1598.835925	799.921601	11
7	**964.564836**	482.786056	947.538287	474.272782			Q	1503.762426	752.384851	1486.735877	743.871577	1485.751861	743.379569	10
8	**1092.623414**	**546.815345**	1075.596865	538.302071			Q	***1064.537100***	532.772188	1047.510551	524.258914	1046.526535	523.766906	9
9	**1205.707478**	**603.357377**	1188.680929	594.844102			L	***936.478522***	468.742899	919.451973	460.229625	918.467957	459.737617	8
10	1320.734421	660.870848	1303.707872	652.357574	1302.723856	651.865566	D	***823.394458***	412.200867	806.367909	403.687593	805.383893	403.195585	7
11	1449.777014	**725.392145**	1432.750465	716.878871	1431.766449	716.386863	E	***708.367515***	354.687396	691.340966	346.174121	690.356950	345.682113	6
12	1506.798478	753.902877	1489.771929	745.389603	1488.787913	744.897594	G	***579.324922***	290.166099	562.298373	281.652825	561.314357	281.160817	5
13	1619.882542	810.444909	1602.855993	801.931634	1601.871977	801.439626	L	***522.303458***	261.655367	505.276909	253.142093	504.292893	252.650085	4
14	1766.950956	883.979116	1749.924407	875.465842	1748.940391	874.973833	F	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108053	3
15	1853.982984	927.495130	1836.956435	918.981856	1835.972419	918.489848	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
16							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LAGLGLQQLDEGLFSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.7	2027.087372	0.001480	LAGLGLQQLDEGLFSR
22.5	2027.087372	0.001480	LAGLGLQQLDEGLFSR

Mascot: http://www.matrixscience.com/

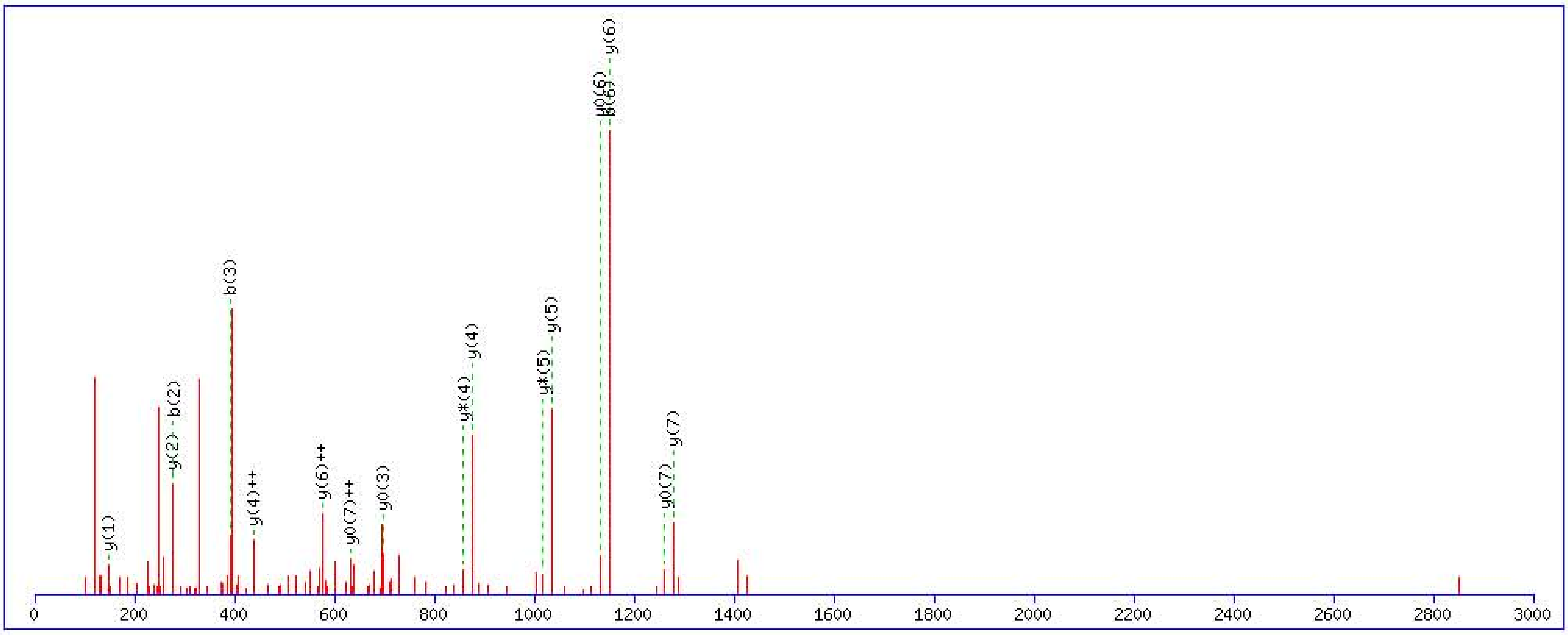
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FEDCCQEK**
Found in **VTDB_HUMAN**, Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

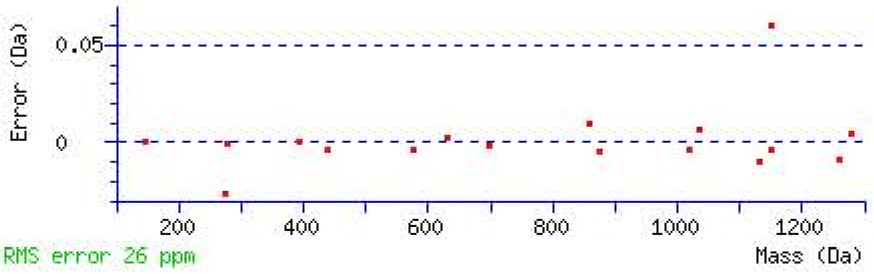
Match to Query 25123: 1425.568248 from(713.791400,2+) rtinseconds(1492) index(28763)
Title: Locus:1.1.1.3182.15 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

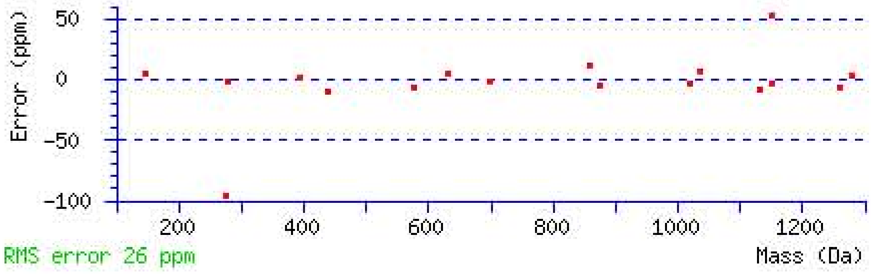
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1425.572693
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.0014
Matches : 17/70 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	148.075690	74.541483					F							8
2	**277.118283**	139.062779			259.107718	130.057497	E	***1279.511557***	640.259417	1262.485008	631.746142	1261.500992	631.254134	7
3	**392.145226**	196.576251			374.134661	187.570968	D	***1150.468964***	575.738120	1133.442415	567.224846	1132.458399	566.732838	6
4	552.175875	276.591576			534.165310	267.586293	C	***1035.442021***	518.224649	1018.415472	509.711374	1017.431456	509.219366	5
5	712.206524	356.606900			694.195959	347.601618	C	***875.411372***	438.209324	858.384823	429.696050	857.400807	429.204042	4
6	**1151.431850**	576.219563	1134.405301	567.706289	1133.421285	567.214281	Q	715.380723	358.194000	698.354174	349.680725	697.370158	349.188717	3
7	1280.474443	640.740860	1263.447894	632.227585	1262.463878	631.735577	E	***276.155397***	138.581337	259.128848	130.068062	258.144832	129.576054	2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of FEDCCQEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.4	1425.572693	-0.004445	FEDCCQEK

Mascot: http://www.matrixscience.com/

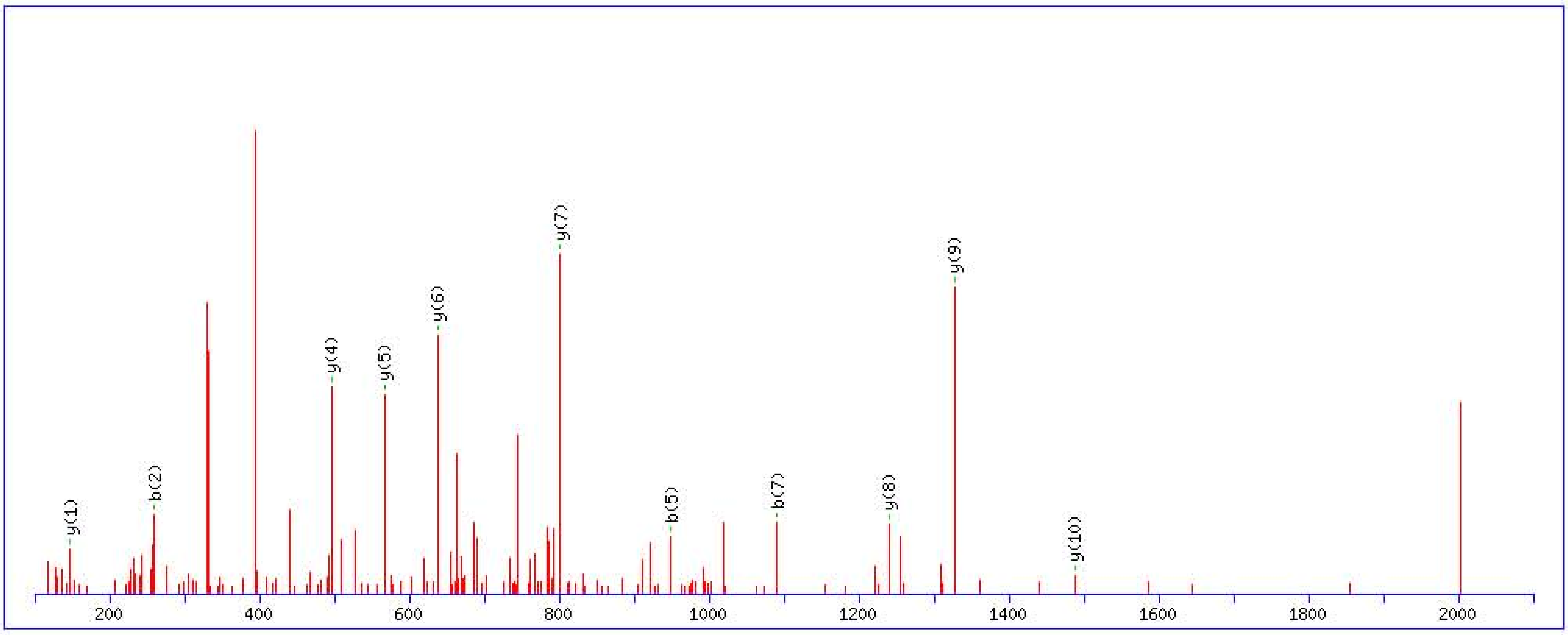
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VCSQYAAYGEK**
Found in **VTDB_HUMAN**, Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

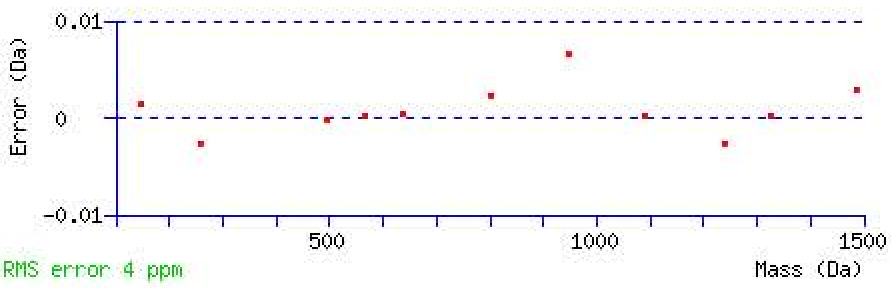
Match to Query 29956: 1585.728728 from(793.871640,2+) rtinseconds(1658) index(58775)
Title: Locus:1.1.1.1488.12 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

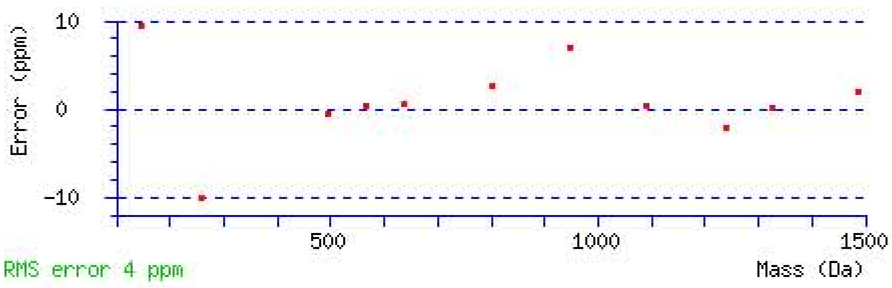
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [2100] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1585.726868
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 66  Expect: 2.4e-006
Matches : 11/108 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	100.075690	50.541483					V							11
2	**260.106339**	130.556807					C	***1487.665750***	744.336513	1470.639201	735.823239	1469.655185	735.331231	10
3	347.138367	174.072821			329.127802	165.067539	S	***1327.635101***	664.321189	1310.608552	655.807914	1309.624536	655.315906	9
4	786.363693	393.685485	769.337144	385.172210	768.353128	384.680202	Q	***1240.603073***	620.805175	1223.576524	612.291900	1222.592508	611.799892	8
5	**949.427022**	475.217149	932.400473	466.703875	931.416457	466.211867	Y	***801.377747***	401.192512	784.351198	392.679237	783.367182	392.187229	7
6	1020.464136	510.735706	1003.437587	502.222432	1002.453571	501.730424	A	***638.314418***	319.660847	621.287869	311.147573	620.303853	310.655565	6
7	**1091.501250**	546.254263	1074.474701	537.740989	1073.490685	537.248981	A	***567.277304***	284.142290	550.250755	275.629016	549.266739	275.137008	5
8	1254.564579	627.785928	1237.538030	619.272653	1236.554014	618.780645	Y	***496.240190***	248.623733	479.213641	240.110459	478.229625	239.618451	4
9	1311.586043	656.296660	1294.559494	647.783385	1293.575478	647.291377	G	333.176861	167.092069	316.150312	158.578794	315.166296	158.086786	3
10	1440.628636	720.817956	1423.602087	712.304682	1422.618071	711.812674	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
11							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VCSQYAAYGEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.1	1585.726868	0.001860	VCSQYAAYGEK
21.9	1585.744614	-0.015886	MSVNYAAGLSPYADK
3.8	1585.747986	-0.019258	MKMGQEFVESKEK

Mascot: http://www.matrixscience.com/

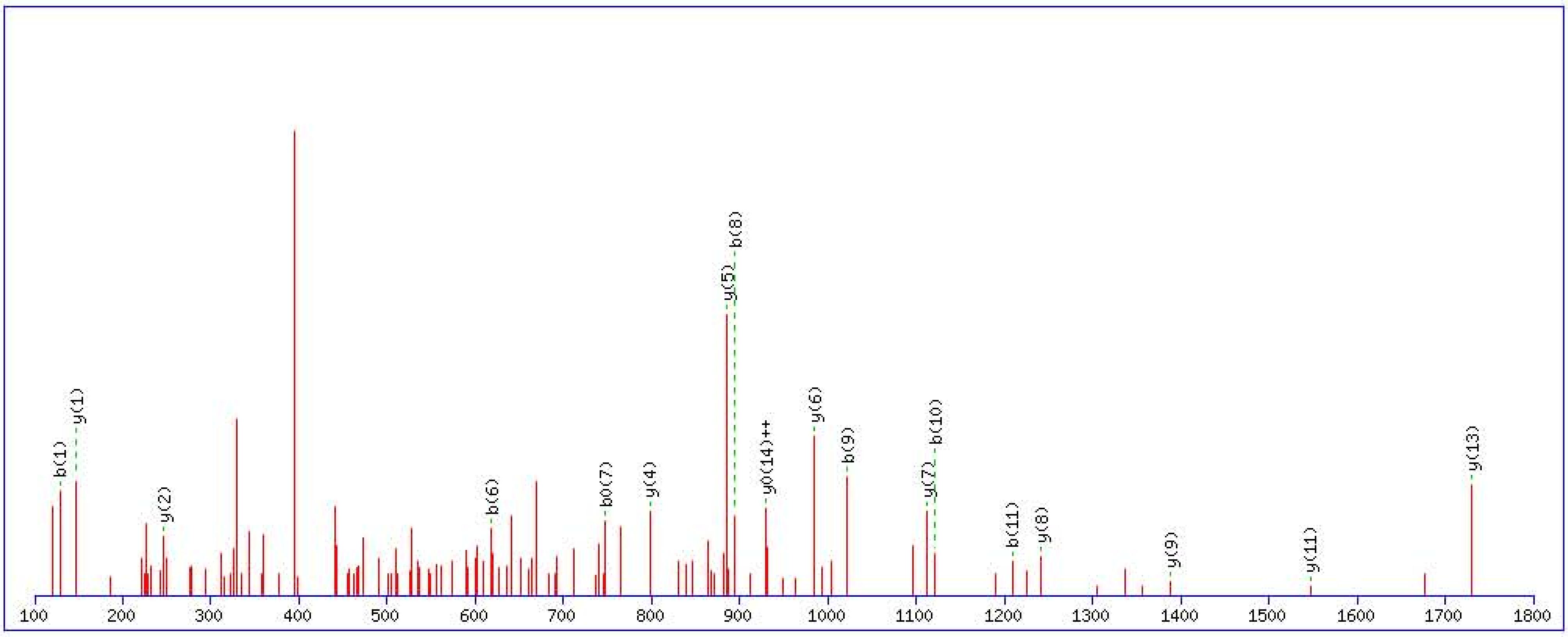
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KFPSGTFEQVSQLVK**
Found in **VTDB_HUMAN**, Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

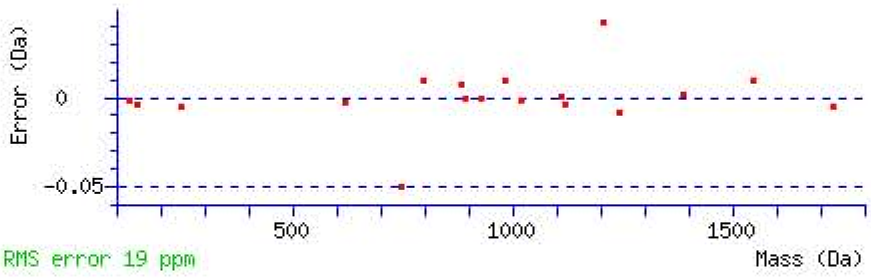
Match to Query 39974: 2005.075032 from(669.365620,3+) rtinseconds(2242) index(61938)
Title: Locus:1.1.1.1692.17 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

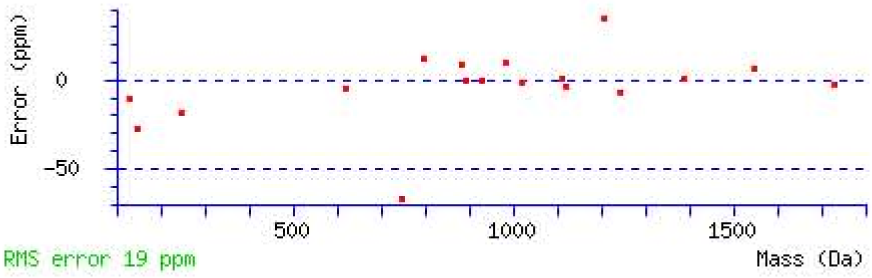
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2005.070679
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12    : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 7e-006
Matches : 19/154 fragment ions using 29 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							15
2	276.170653	138.588964	259.144104	130.075690			F	1877.982984	939.495130	1860.956435	930.981856	1859.972419	930.489848	14
3	373.223417	187.115346	356.196868	178.602072			P	***1730.914570***	865.960923	1713.888021	857.447649	1712.904005	856.955641	13
4	460.255445	230.631360	443.228896	222.118086	442.244880	221.626078	S	1633.861806	817.434541	1616.835257	808.921267	1615.851241	808.429259	12
5	517.276909	259.142093	500.250360	250.628818	499.266344	250.136810	G	***1546.829778***	773.918527	1529.803229	765.405253	1528.819213	764.913245	11
6	**618.324588**	309.665932	601.298039	301.152658	600.314023	300.660650	T	1489.808314	745.407795	1472.781765	736.894521	1471.797749	736.402513	10
7	765.393002	383.200139	748.366453	374.686865	747.382437	374.194857	F	***1388.760635***	694.883956	1371.734086	686.370681	1370.750070	685.878673	9
8	**894.435595**	447.721436	877.409046	439.208161	876.425030	438.716153	E	***1241.692221***	621.349749	1224.665672	612.836474	1223.681656	612.344466	8
9	**1022.494173**	511.750725	1005.467624	503.237450	1004.483608	502.745442	Q	***1112.649628***	556.828452	1095.623079	548.315178	1094.639063	547.823170	7
10	**1121.562587**	561.284932	1104.536038	552.771657	1103.552022	552.279649	V	***984.591050***	492.799163	967.564501	484.285889	966.580485	483.793881	6
11	**1208.594615**	604.800946	1191.568066	596.287671	1190.584050	595.795663	S	***885.522636***	443.264956	868.496087	434.751682	867.512071	434.259674	5
12	1647.819941	824.413609	1630.793392	815.900334	1629.809376	815.408326	Q	***798.490608***	399.748942	781.464059	391.235668			4
13	1760.904005	880.955641	1743.877456	872.442366	1742.893440	871.950358	L	359.265282	180.136279	342.238733	171.623004			3
14	1859.972419	930.489848	1842.945870	921.976573	1841.961854	921.484565	V	***246.181218***	123.594247	229.154669	115.080973			2
15							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of KFPSGTFEQVSQLVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.9	2005.070679	0.004353	KFPSGTFEQVSQLVK
25.1	2005.070679	0.004353	KFPSGTFEQVSQLVK

Mascot: http://www.matrixscience.com/

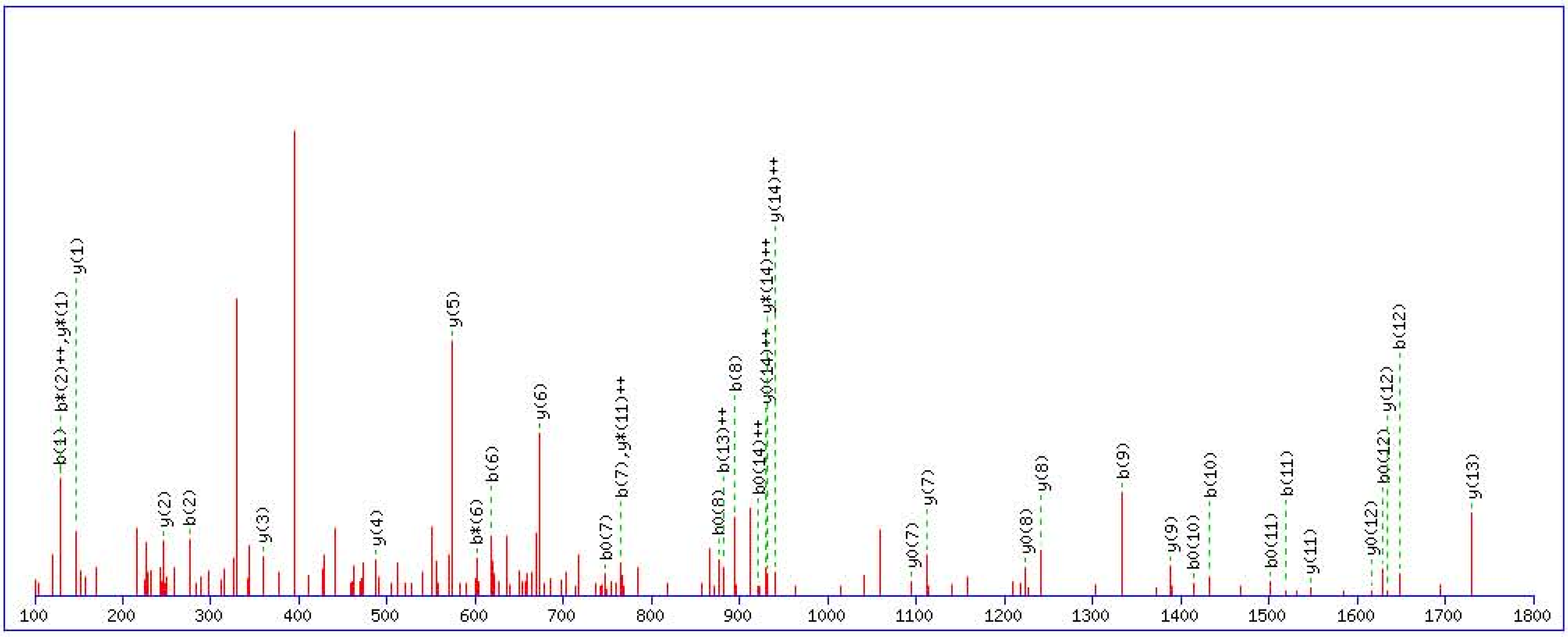
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KFPSGTFEQVSQLVK**
Found in **VTDB_HUMAN**, Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

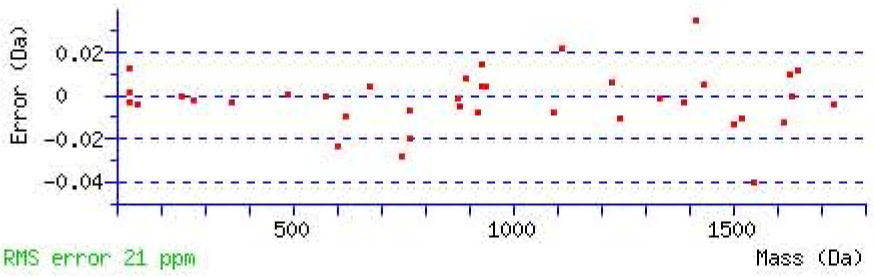
Match to Query 39976: 2005.076172 from(669.366000,3+) rtinseconds(2305) index(62257)
Title: Locus:1.1.1.1714.10 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

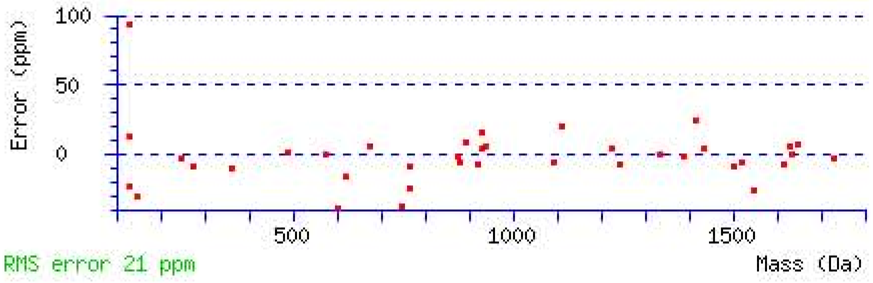


```
Monoisotopic mass of neutral peptide Mr(calc): 2005.070679
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 55  Expect: 1e-005
Matches : 39/154 fragment ions using 79 most intense peaks   (help)
```

#	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							15
2	**276.170653**	138.588964	259.144104	130.075690			F	1877.982984	939.495130	1860.956435	930.981856	1859.972419	930.489848	14
3	373.223417	187.115346	356.196868	178.602072			P	***1730.914570***	865.960923	1713.888021	857.447649	1712.904005	856.955641	13
4	460.255445	230.631360	443.228896	222.118086	442.244880	221.626078	S	***1633.861806***	817.434541	1616.835257	808.921267	1615.851241	808.429259	12
5	517.276909	259.142093	500.250360	250.628818	499.266344	250.136810	G	***1546.829778***	773.918527	1529.803229	765.405253	1528.819213	764.913245	11
6	**618.324588**	309.665932	601.298039	301.152658	600.314023	300.660650	T	1489.808314	745.407795	1472.781765	736.894521	1471.797749	736.402513	10
7	**765.393002**	383.200139	748.366453	374.686865	747.382437	374.194857	F	***1388.760635***	694.883955	1371.734086	686.370681	1370.750070	685.878673	9
8	**894.435595**	447.721436	877.409046	439.208161	876.425030	438.716153	E	***1241.692221***	621.349749	1224.665672	612.836474	1223.681656	612.344466	8
9	**1333.660921**	667.334098	1316.634372	658.820824	1315.650356	658.328816	Q	***1112.649628***	556.828452	1095.623079	548.315178	1094.639063	547.823169	7
10	**1432.729335**	716.868306	1415.702786	708.355031	1414.718770	707.863023	V	***673.424302***	337.215789	656.397753	328.702515	655.413737	328.210507	6
11	**1519.761363**	760.384320	1502.734814	751.871045	1501.750798	751.379037	S	***574.355888***	287.681582	557.329339	279.168308	556.345323	278.676300	5
12	**1647.819941**	824.413609	1630.793392	815.900334	1629.809376	815.408326	Q	***487.323860***	244.165568	470.297311	235.652293			4
13	1760.904005	**880.955640**	1743.877456	872.442366	1742.893440	871.950358	L	***359.265282***	180.136279	342.238733	171.623004			3
14	1859.972419	**930.489848**	1842.945870	921.976573	1841.961854	921.484565	V	***246.181218***	123.594247	229.154669	115.080973			2
15							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 21 ppm



RMS error 21 ppm

NCBI **BLAST** search of KFPSGTFEQVSQLVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.0	2005.070679	0.005493	KFPSGTFEQVSQLVK
25.2	2005.070679	0.005493	KFPSGTFEQVSQLVK
1.8	2005.048874	0.027298	KTMSKPGNGQPPVPEK
1.8	2005.079193	-0.003021	RATWLHQALREGTR

Mascot: http://www.matrixscience.com/

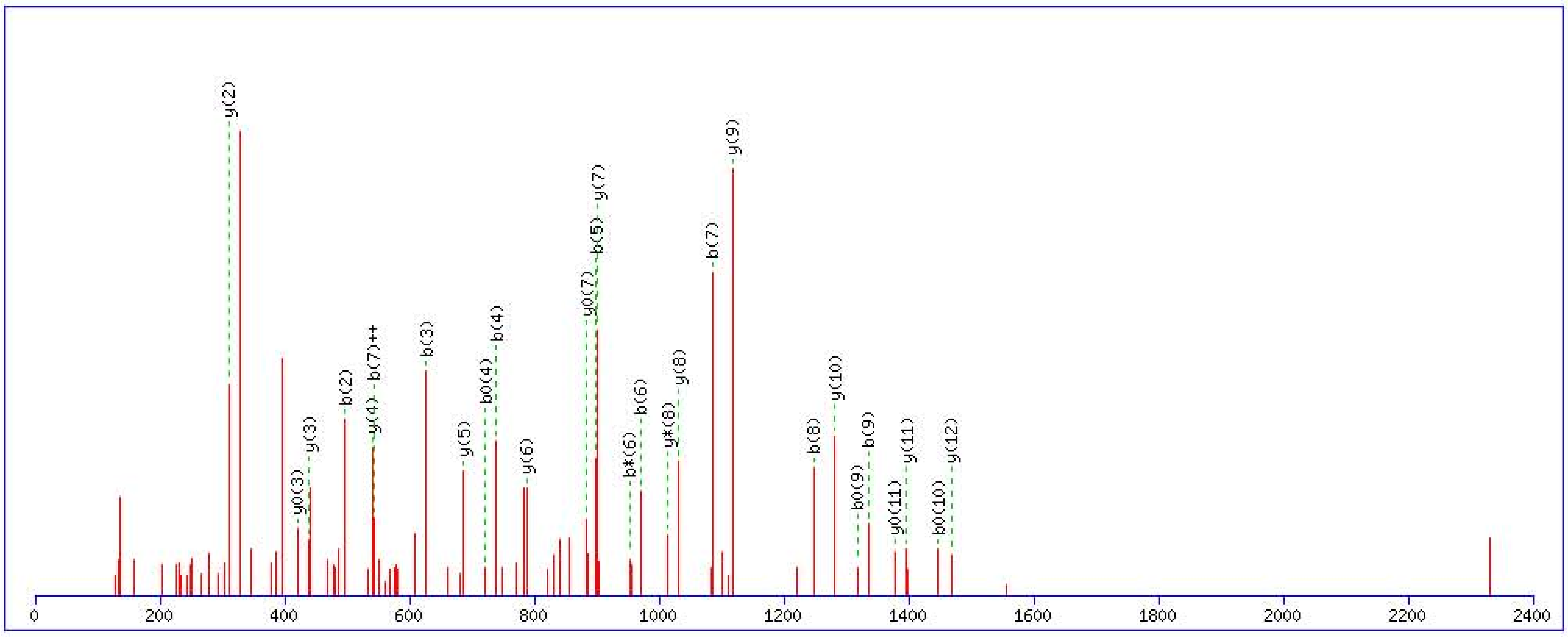
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQELCADYSENTFTEYK**
Found in **VTDB_HUMAN**, Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

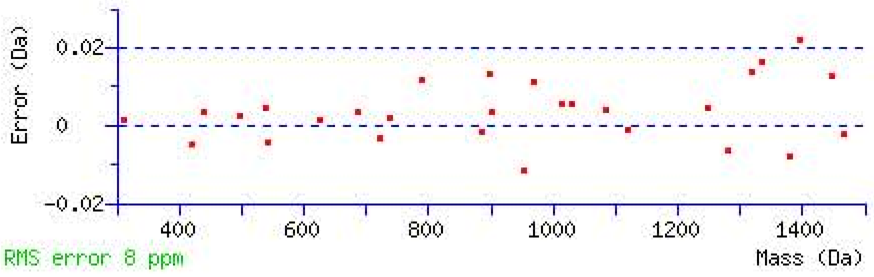
Match to Query 45972: 2365.019022 from(789.346950,3+) rtinseconds(2171) index(32858)
Title: Locus:1.1.1.3419.24 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

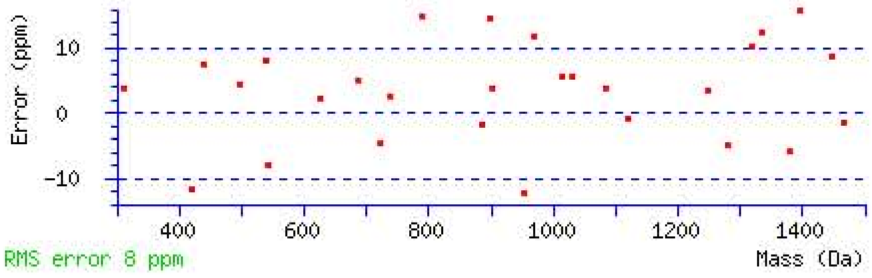
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2365.024231
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 78  Expect: 4.6e-008
Matches : 28/182 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	58.028740	29.518008					G							17
2	***497.254066***	249.130671	480.227517	240.617397			Q	2309.010064	1155.008670	2291.983515	1146.495395	2290.999499	1146.003387	16
3	***626.296659***	313.651968	609.270110	305.138693	608.286094	304.646685	E	1869.784738	935.396007	1852.758189	926.882733	1851.774173	926.390725	15
4	***739.380723***	370.194000	722.354174	361.680725	721.370158	361.188717	L	1740.742145	870.874711	1723.715596	862.361436	1722.731580	861.869428	14
5	***899.411372***	450.209324	882.384823	441.696050	881.400807	441.204042	C	1627.658081	814.332679	1610.631532	805.819404	1609.647516	805.327396	13
6	***970.448486***	485.727881	953.421937	477.214607	952.437921	476.722599	A	***1467.627432***	734.317354	1450.600883	725.804080	1449.616867	725.312072	12
7	***1085.475429***	543.241353	1068.448880	534.728078	1067.464864	534.236070	D	***1396.590318***	698.798797	1379.563769	690.285523	1378.579753	689.793515	11
8	***1248.538758***	624.773017	1231.512209	616.259743	1230.528193	615.767735	Y	***1281.563375***	641.285326	1264.536826	632.772051	1263.552810	632.280043	10
9	***1335.570786***	668.289031	1318.544237	659.775757	1317.560221	659.283749	S	***1118.500046***	559.753661	1101.473497	551.240387	1100.489481	550.748379	9
10	1464.613379	732.810328	1447.586830	724.297053	1446.602814	723.805045	E	***1031.468018***	516.237647	1014.441469	507.724373	1013.457453	507.232365	8
11	1578.656306	789.831791	1561.629757	781.318517	1560.645741	780.826509	N	***902.425425***	451.716351	885.398876	443.203076	884.414860	442.711068	7
12	1679.703985	840.355631	1662.677436	831.842356	1661.693420	831.350348	T	***788.382498***	394.694887	771.355949	386.181613	770.371933	385.689605	6
13	1826.772399	913.889838	1809.745850	905.376563	1808.761834	904.884555	F	***687.334819***	344.171048	670.308270	335.657773	669.324254	335.165765	5
14	1927.820078	964.413677	1910.793529	955.900403	1909.809513	955.408395	T	***540.266405***	270.636841	523.239856	262.123566	522.255840	261.631558	4
15	2056.862671	1028.934973	2039.836122	1020.421699	2038.852106	1019.929691	E	***439.218726***	220.113001	422.192177	211.599726	421.208161	211.107718	3
16	2219.926000	1110.466638	2202.899451	1101.953363	2201.915435	1101.461355	Y	***310.176133***	155.591705	293.149584	147.078430			2
17							K	147.112804	74.060040	130.086255	65.546765			1



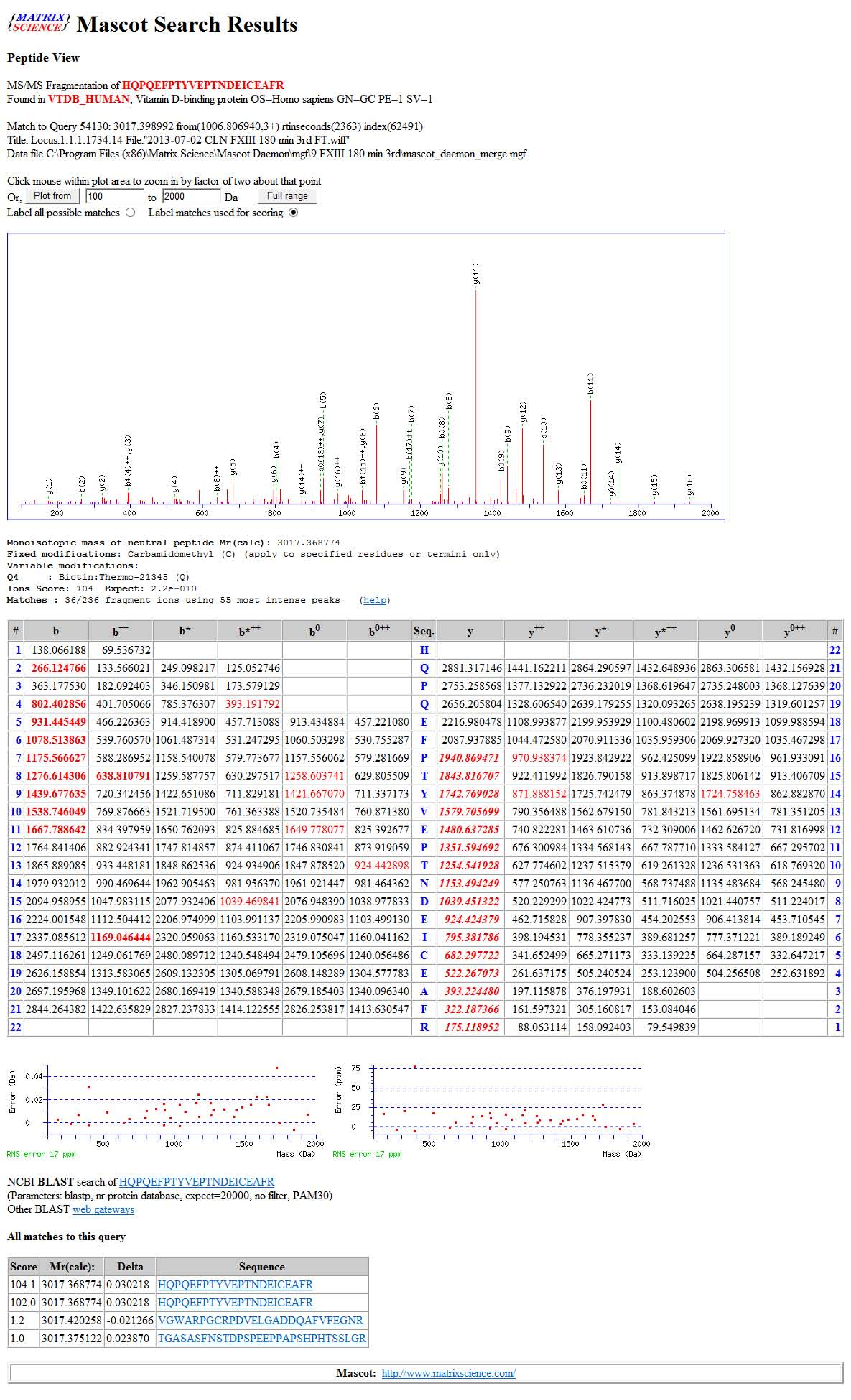


NCBI **BLAST** search of GQELCADYSENTFTEYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
78.2	2365.024231	-0.005209	GQELCADYSENTFTEYK

Mascot: http://www.matrixscience.com/



Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQPQEFPTYVEPTNDEICEAFR**
Found in **VTDB_HUMAN**, Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

Match to Query 54130: 3017.398992 from(1006.806940,3+) rtinseconds(2363) index(62491)
Title: Locus:1.1.1.1734.14 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\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): 3017.368774
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 104  Expect: 2.2e-010
Matches : 36/236 fragment ions using 55 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	138.066188	69.536732					H							22
2	**266.124766**	133.566021	249.098217	125.052746			Q	2881.317146	1441.162211	2864.290597	1432.648936	2863.306581	1432.156928	21
3	363.177530	182.092403	346.150981	173.579129			P	2753.258568	1377.132922	2736.232019	1368.619647	2735.248003	1368.127639	20
4	**802.402856**	401.705066	785.376307	393.191792			Q	2656.205804	1328.606540	2639.179255	1320.093265	2638.195239	1319.601257	19
5	**931.445449**	466.226363	914.418900	457.713088	913.434884	457.221080	E	2216.980478	1108.993877	2199.953929	1100.480602	2198.969913	1099.988594	18
6	**1078.513863**	539.760570	1061.487314	531.247295	1060.503298	530.755287	F	2087.937885	1044.472580	2070.911336	1035.959306	2069.927320	1035.467298	17
7	**1175.566627**	588.286952	1158.540078	579.773677	1157.556062	579.281669	P	***1940.869471***	970.938374	1923.842922	962.425099	1922.858906	961.933091	16
8	**1276.614306**	**638.810791**	1259.587757	630.297517	1258.603741	629.805509	T	***1843.816707***	922.411992	1826.790158	913.898717	1825.806142	913.406709	15
9	**1439.677635**	720.342456	1422.651086	711.829181	1421.667070	711.337173	Y	***1742.769028***	871.888152	1725.742479	863.374878	1724.758463	862.882870	14
10	**1538.746049**	769.876663	1521.719500	761.363388	1520.735484	760.871380	V	***1579.705699***	790.356488	1562.679150	781.843213	1561.695134	781.351205	13
11	**1667.788642**	834.397959	1650.762093	825.884685	1649.778077	825.392677	E	***1480.637285***	740.822281	1463.610736	732.309006	1462.626720	731.816998	12
12	1764.841406	882.924341	1747.814857	874.411067	1746.830841	873.919059	P	***1351.594692***	676.300984	1334.568143	667.787710	1333.584127	667.295702	11
13	1865.889085	933.448181	1848.862536	924.934906	1847.878520	924.442898	T	***1254.541928***	627.774602	1237.515379	619.261328	1236.531363	618.769320	10
14	1979.932012	990.469644	1962.905463	981.956370	1961.921447	981.464362	N	***1153.494249***	577.250763	1136.467700	568.737488	1135.483684	568.245480	9
15	2094.958955	1047.983115	2077.932406	1039.469841	2076.948390	1038.977833	D	***1039.451322***	520.229299	1022.424773	511.716025	1021.440757	511.224017	8
16	2224.001548	1112.504412	2206.974999	1103.991137	2205.990983	1103.499130	E	***924.424379***	462.715828	907.397830	454.202553	906.413814	453.710545	7
17	2337.085612	**1169.046444**	2320.059063	1160.533170	2319.075047	1160.041162	I	***795.381786***	398.194531	778.355237	389.681257	777.371221	389.189249	6
18	2497.116261	1249.061769	2480.089712	1240.548494	2479.105696	1240.056486	C	***682.297722***	341.652499	665.271173	333.139225	664.287157	332.647217	5
19	2626.158854	1313.583065	2609.132305	1305.069791	2608.148289	1304.577783	E	***522.267073***	261.637175	505.240524	253.123900	504.256508	252.631892	4
20	2697.195968	1349.101622	2680.169419	1340.588348	2679.185403	1340.096340	A	***393.224480***	197.115878	376.197931	188.602603			3
21	2844.264382	1422.635829	2827.237833	1414.122555	2826.253817	1413.630547	F	***322.187366***	161.597321	305.160817	153.084046			2
22							R	***175.118952***	88.063114	158.092403	79.549839			1

NCBI **BLAST** search of HQPQEFPTYVEPTNDEICEAFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
104.1	3017.368774	0.030218	HQPQEFPTYVEPTNDEICEAFR
102.0	3017.368774	0.030218	HQPQEFPTYVEPTNDEICEAFR
1.2	3017.420258	-0.021266	VGWARPGCRPDVELGADDQAFVFEGNR
1.0	3017.375122	0.023870	TGASASFNSTDPSPEEPPAPSHPHTSSLGR

Mascot: http://www.matrixscience.com/

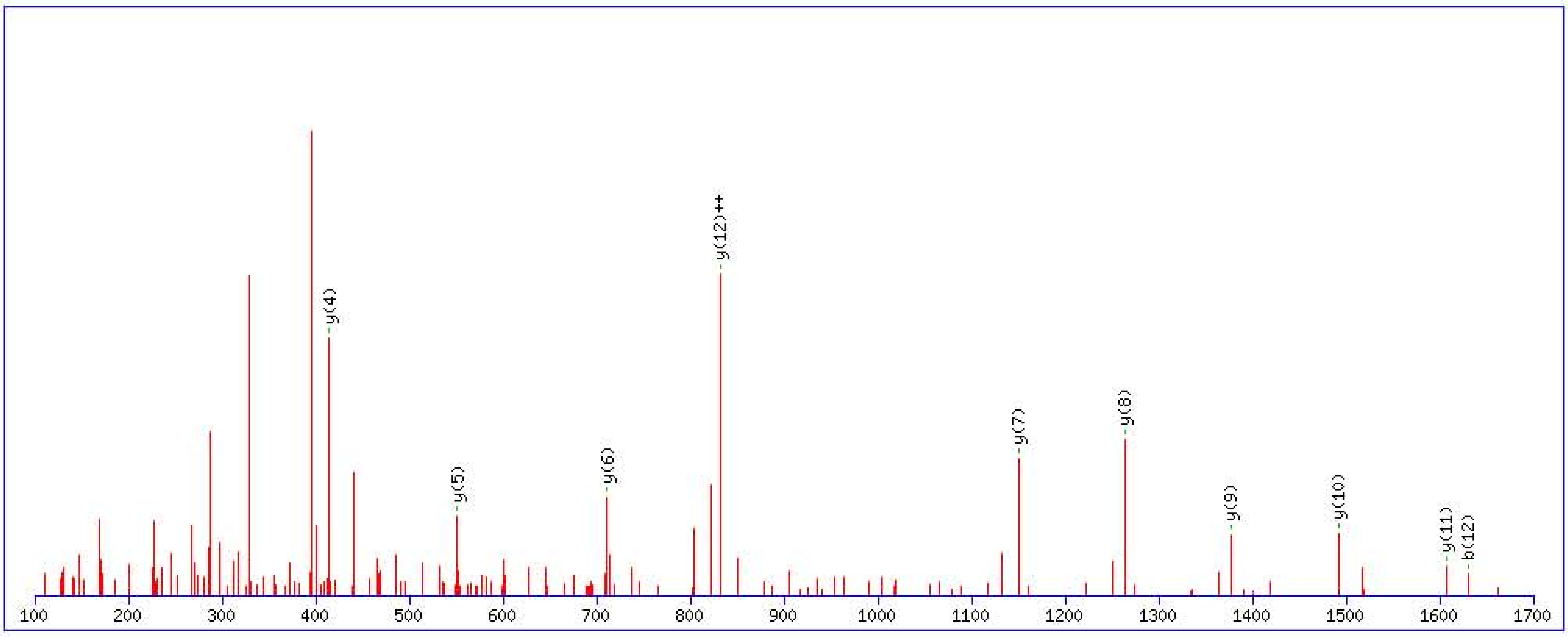
{MATRIX SCIENCE} Mascot Search Results

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

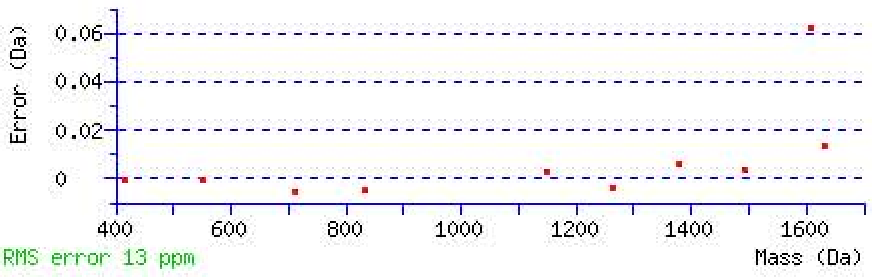
Match to Query 35272: 1775.905782 from(592.975870,3+) rtinseconds(1983) index(45924)
Title: Locus:1.1.1.3403.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

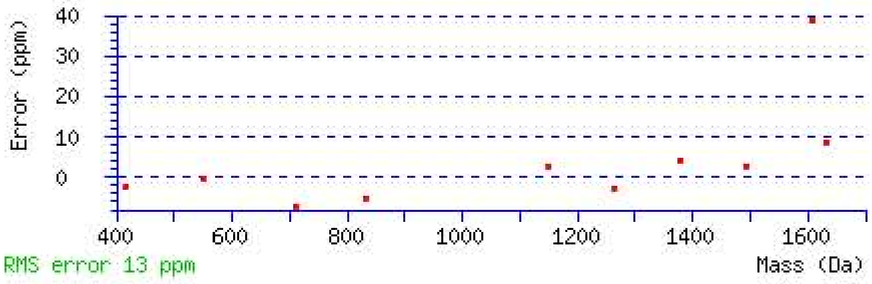
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 48 **Expect:** 4.3e-005
Matches : 10/110 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
47.8	1775.906250	-0.000468	LGDDLLQCHPAVK
1.1	1775.879761	0.026021	VASMDSIGNLMVSPPVK

Mascot: http://www.matrixscience.com/

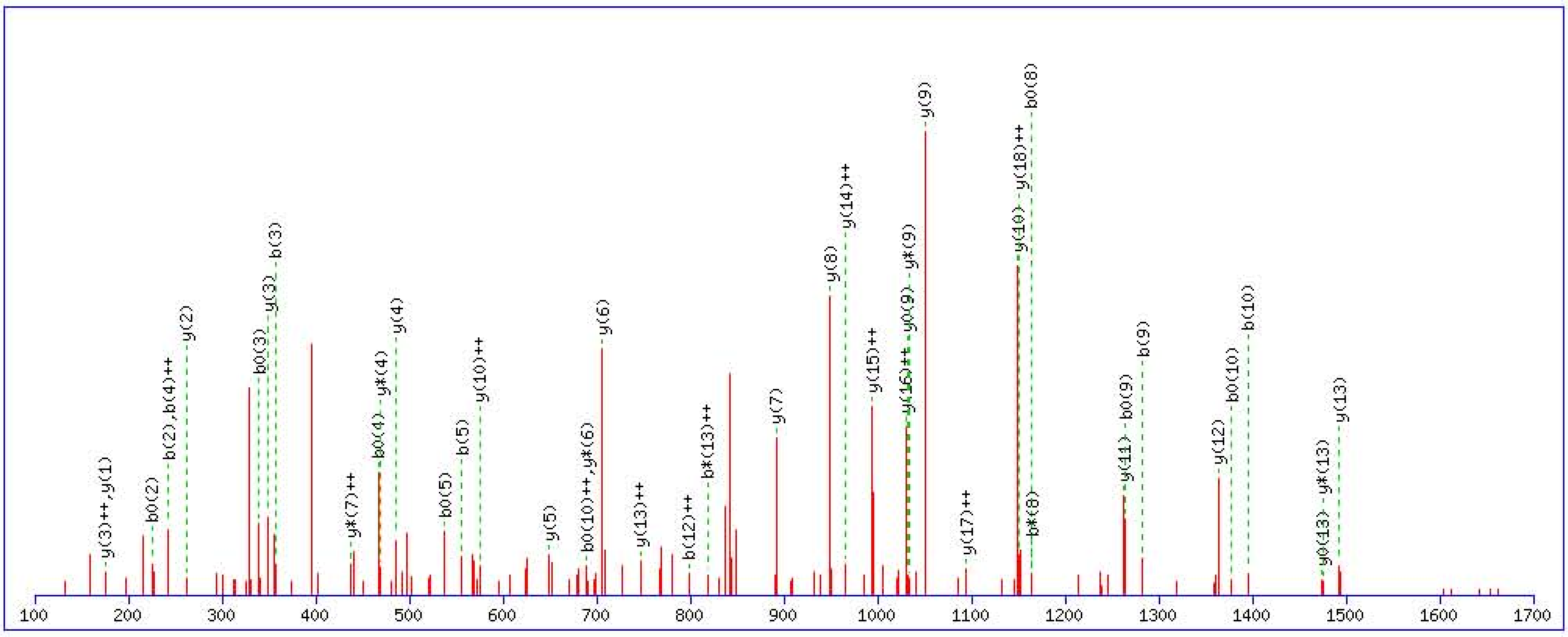
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELNQAGQETLVTGWGYHSSR**
Found in **PROC_HUMAN**, Vitamin K-dependent protein C OS=Homo sapiens GN=PROC PE=1 SV=1

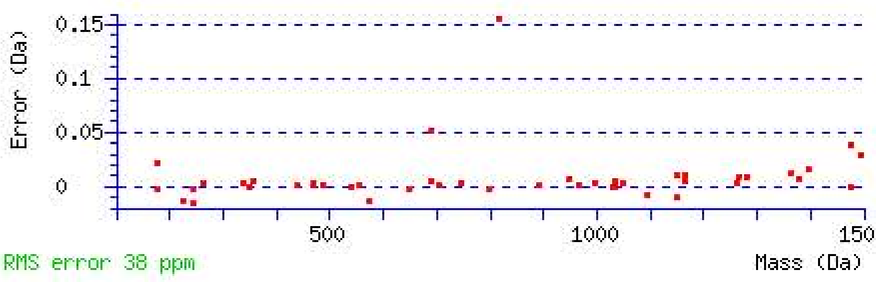
Match to Query 48989: 2543.229282 from(848.750370,3+) rtinseconds(2186) index(47175)
Title: Locus:1.1.1.3473.22 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

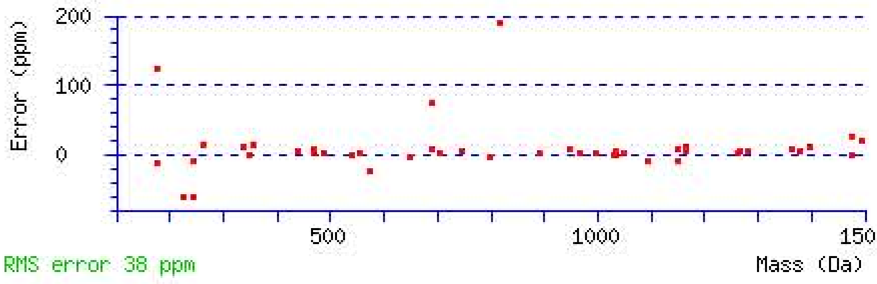
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2543.222702
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 1.9e-005
Matches : 45/222 fragment ions using 86 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	**243.133933**	122.070605			225.123368	113.065322	L	2415.187392	1208.097334	2398.160843	1199.584059	2397.176827	1199.092051	19
3	**357.176860**	179.092068	340.150311	170.578794	339.166295	170.086786	N	2302.103328	1151.555302	2285.076779	1143.042027	2284.092763	1142.550019	18
4	485.235438	**243.121357**	468.208889	234.608083	467.224873	234.116075	Q	2188.060401	1094.533838	2171.033852	1086.020564	2170.049836	1085.528556	17
5	**556.272552**	278.639914	539.246003	270.126640	538.261987	269.634632	A	2060.001823	1030.504549	2042.975274	1021.991275	2041.991258	1021.499267	16
6	613.294016	307.150646	596.267467	298.637372	595.283451	298.145364	G	1988.964709	994.985993	1971.938160	986.472718	1970.954144	985.980710	15
7	1052.519342	526.763309	1035.492793	518.250035	1034.508777	517.758027	Q	1931.943245	966.475261	1914.916696	957.961986	1913.932680	957.469978	14
8	1181.561935	591.284606	1164.535386	582.771331	1163.551370	582.279323	E	***1492.717919***	746.862597	1475.691370	738.349323	1474.707354	737.857315	13
9	**1282.609614**	641.808445	1265.583065	633.295171	1264.599049	632.803163	T	***1363.675326***	682.341301	1346.648777	673.828026	1345.664761	673.336018	12
10	**1395.693678**	698.350477	1378.667129	689.837203	1377.683113	689.345195	L	***1262.627647***	631.817461	1245.601098	623.304187	1244.617082	622.812179	11
11	1494.762092	747.884684	1477.735543	739.371410	1476.751527	738.879402	V	***1149.543583***	575.275429	1132.517034	566.762155	1131.533018	566.270147	10
12	1595.809771	**798.408524**	1578.783222	789.895249	1577.799206	789.403241	T	***1050.475169***	525.741222	1033.448620	517.227948	1032.464604	516.735940	9
13	1652.831235	826.919256	1635.804686	818.405981	1634.820670	817.913973	G	***949.427490***	475.217383	932.400941	466.704108	931.416925	466.212100	8
14	1838.910548	919.958912	1821.883999	911.445638	1820.899983	910.953630	W	***892.406026***	446.706651	875.379477	438.193376	874.395461	437.701368	7
15	1895.932012	948.469644	1878.905463	939.956370	1877.921447	939.464362	G	***706.326713***	353.666994	689.300164	345.153720	688.316148	344.661712	6
16	2058.995341	1030.001308	2041.968792	1021.488034	2040.984776	1020.996026	Y	***649.305249***	325.156263	632.278700	316.642988	631.294684	316.150980	5
17	2196.054253	1098.530764	2179.027704	1090.017490	2178.043688	1089.525482	H	***486.241920***	243.624598	469.215371	235.111324	468.231355	234.619316	4
18	2283.086281	1142.046778	2266.059732	1133.533504	2265.075716	1133.041496	S	***349.183008***	175.095142	332.156459	166.581868	331.172443	166.089860	3
19	2370.118309	1185.562792	2353.091760	1177.049518	2352.107744	1176.557510	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 ELNQAGQETLVTGWGYHSSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.0	2543.222702	0.006580	ELNQAGQETLVTGWGYHSSR
53.7	2543.222702	0.006580	ELNQAGQETLVTGWGYHSSR

Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View

MS/MS Fragmentation of **STTDNDIALLHLAQPATLSQTIVPICLPDSGLAER**
Found in **PROC_HUMAN**, Vitamin K-dependent protein C OS=Homo sapiens GN=PROC PE=1 SV=1

Match to Query 62651: 4041.114056 from(1011.285790,4+) rtinseconds(2981) index(52204)
Title: Locus:1.1.1.3746.22 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\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): 4041.091476
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20    : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 9.6e-005
Matches : 49/398 fragment ions using 101 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							35
2	***189.086983***	95.047129			171.076418	86.041847	T	3955.066740	1978.037008	3938.040191	1969.523733	3937.056175	1969.031725	34
3	290.134662	145.570969			272.124097	136.565687	T	3854.019061	1927.513168	3836.992512	1918.999894	3836.008496	1918.507886	33
4	405.161605	203.084441			387.151040	194.079158	D	3752.971382	1876.989329	3735.944833	1868.476054	3734.960817	1867.984046	32
5	519.204532	260.105904	502.177983	251.592630	501.193967	251.100622	N	3637.944439	1819.475857	3620.917890	1810.962583	3619.933874	1810.470575	31
6	***634.231475***	317.619376	617.204926	309.106101	616.220910	308.614093	D	3523.901512	1762.454394	3506.874963	1753.941119	3505.890947	1753.449111	30
7	***747.315539***	374.161408	730.288990	365.648133	729.304974	365.156125	I	3408.874569	1704.940922	3391.848020	1696.427648	3390.864004	1695.935640	29
8	818.352653	409.679965	801.326104	401.166690	800.342088	400.674682	A	3295.790505	1648.398890	3278.763956	1639.885616	3277.779940	1639.393608	28
9	931.436717	466.221997	914.410168	457.708722	913.426152	457.216714	L	3224.753391	1612.880333	3207.726842	1604.367059	3206.742826	1603.875051	27
10	***1044.520781***	522.764028	1027.494232	514.250754	1026.510216	513.758746	L	3111.669327	1556.338301	3094.642778	1547.825027	3093.658762	1547.333019	26
11	1181.579693	591.293484	1164.553144	582.780210	1163.569128	582.288202	H	2998.585263	1499.796269	2981.558714	1491.282995	2980.574698	1490.790987	25
12	1294.663757	647.835516	1277.637208	639.322242	1276.653192	638.830234	L	2861.526351	1431.266813	2844.499802	1422.753539	2843.515786	1422.261531	24
13	***1365.700871***	683.354073	1348.674322	674.840799	1347.690306	674.348791	A	2748.442287	1374.724781	2731.415738	1366.211507	2730.431722	1365.719499	23
14	***1493.759449***	**747.383362**	1476.732900	738.870088	1475.748884	738.378080	Q	2677.405173	1339.206224	2660.378624	1330.692950	2659.394608	1330.200942	22
15	1590.812213	795.909744	1573.785664	787.396470	1572.801648	786.904462	P	2549.346595	1275.176935	2532.320046	1266.663661	2531.336030	1266.171653	21
16	1661.849327	831.428301	1644.822778	822.915027	1643.838762	822.423019	A	2452.293831	1226.650553	2435.267282	1218.137279	2434.283266	1217.645271	20
17	***1762.897006***	881.952141	1745.870457	873.438867	1744.886441	872.946858	T	2381.256717	1191.131996	2364.230168	1182.618722	2363.246152	1182.126714	19
18	***1875.981070***	**938.494173**	1858.954521	929.980898	1857.970505	929.488890	L	2280.209038	1140.608157	2263.182489	1132.094882	2262.198473	1131.602874	18
19	1963.013098	982.010187	1945.986549	973.496913	1945.002533	973.004904	S	2167.124974	1084.066125	2150.098425	1075.552850	2149.114409	1075.060842	17
20	2402.238424	1201.622850	2385.211875	1193.109575	2384.227859	1192.617567	Q	2080.092946	1040.550111	2063.066397	1032.036836	2062.082381	1031.544828	16
21	2503.286103	1252.146689	2486.259554	1243.633415	2485.275538	1243.141407	T	***1640.867620***	820.937448	1623.841071	812.424174	1622.857055	811.932166	15
22	2616.370167	**1308.688721**	2599.343618	1300.175447	2598.359602	1299.683439	I	***1539.819941***	770.413609	1522.793392	761.900334	1521.809376	761.408326	14
23	***2715.438581***	**1358.222928**	2698.412032	1349.709654	2697.428016	1349.217646	V	***1426.735877***	713.871577	1409.709328	705.358302	1408.725312	704.866294	13
24	2812.491345	1406.749310	2795.464796	1398.236036	2794.480780	1397.744028	P	***1327.667463***	664.337370	1310.640914	655.824095	1309.656898	655.332087	12
25	2925.575409	1463.291342	2908.548860	1454.778068	2907.564844	1454.286060	I	***1230.614699***	615.810988	1213.588150	607.297713	1212.604134	606.805705	11
26	3085.606058	1543.306667	3068.579509	1534.793392	3067.595493	1534.301384	C	***1117.530635***	559.268956	1100.504086	550.755681	1099.520070	550.263673	10
27	3198.690122	**1599.848699**	3181.663573	1591.335424	3180.679557	1590.843416	L	***957.499986***	479.253631	940.473437	470.740357	939.489421	470.248349	9
28	3295.742886	1648.375081	3278.716337	1639.861806	3277.732321	1639.369798	P	***844.415922***	422.711599	827.389373	414.198325	826.405357	413.706317	8
29	3410.769829	1705.888552	3393.743280	1697.375278	3392.759264	1696.883270	D	***747.363158***	374.185217	730.336609	365.671943	729.352593	365.179935	7
30	3497.801857	1749.404566	3480.775308	1740.891292	3479.791292	1740.399284	S	***632.336215***	316.671746	615.309666	308.158471	614.325650	307.666463	6
31	3554.823321	1777.915298	3537.796772	1769.402024	3536.812756	1768.910016	G	***545.304187***	273.155732	528.277638	264.642457	527.293622	264.150449	5
32	3667.907385	1834.457330	3650.880836	1825.944056	3649.896820	1825.452048	L	488.282723	244.645000	471.256174	236.131725	470.272158	235.639717	4
33	3738.944499	1869.975887	3721.917950	1861.462613	3720.933934	1860.970605	A	375.198659	188.102968	358.172110	179.589693	357.188094	179.097685	3
34	3867.987092	1934.497184	3850.960543	1925.983909	3849.976527	1925.491901	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
35							R	***175.118952***	88.063114	158.092403	79.549839			1

NCBI **BLAST** search of STTDNDIALLHLAQPATLSQTIVPICLPDSGLAER
(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	4041.091476	0.022580	STTDNDIALLHLAQPATLSQTIVPICLPDSGLAER
31.5	4041.091476	0.022580	STTDNDIALLHLAQPATLSQTIVPICLPDSGLAER

Mascot: http://www.matrixscience.com/

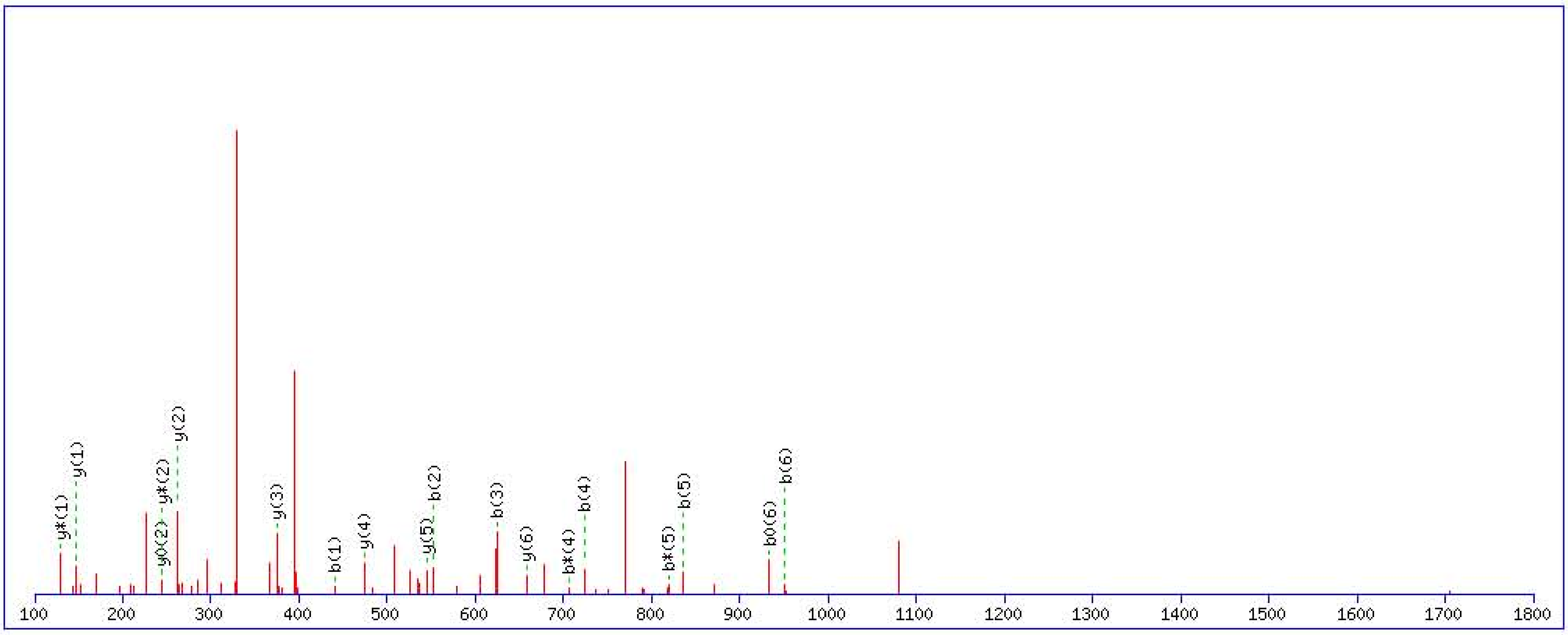
{MATRIX SCIENCE} Mascot Search Results

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

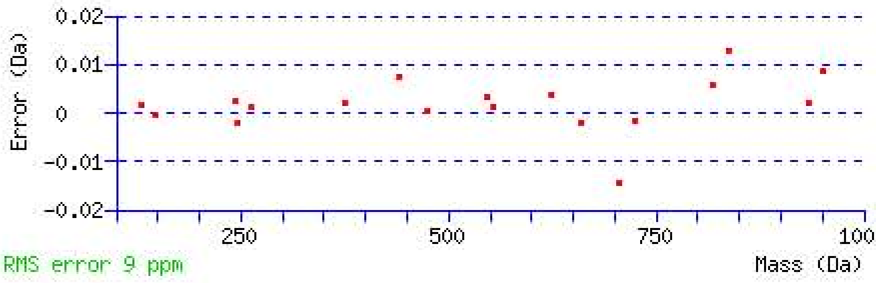
Match to Query 13790: 1096.631228 from(549.322890,2+) rtinseconds(1985) index(45943)
Title: Locus:1.1.1.3404.4 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

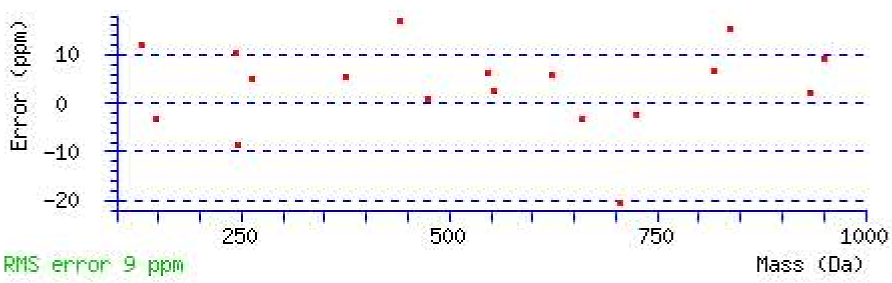
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1096.631439
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 26 **Expect:** 0.036
Matches : 18/60 fragment ions using 41 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							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
26.4	1096.631439	-0.000211	QLAVLDK
15.5	1096.624054	0.007174	KPVDSVPLSR
9.0	1096.624023	0.007205	IPRENLLDK
6.7	1096.631439	-0.000211	GILQLDK
4.4	1096.639297	-0.008069	AHVSPLFKAK
3.8	1096.635269	-0.004041	SSSLVIHKAR
1.8	1096.631439	-0.000211	ILGLDQK

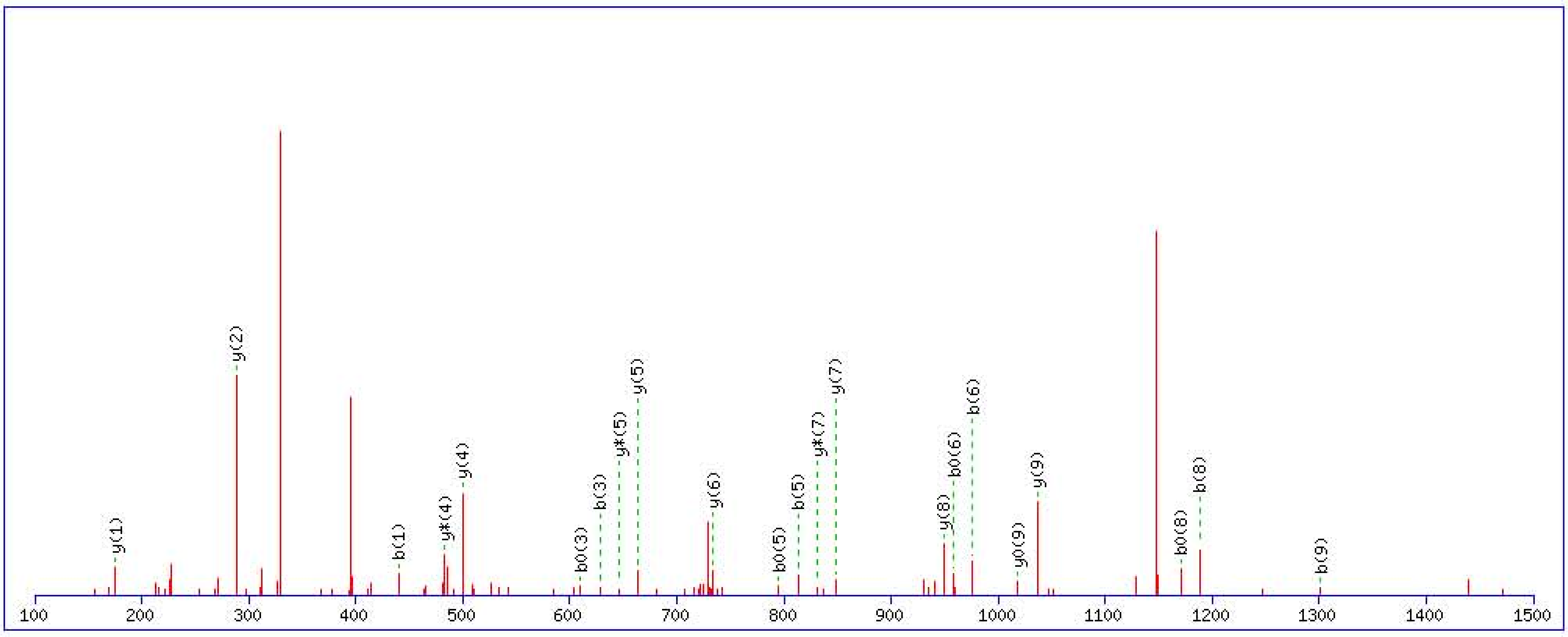
{MATRIX SCIENCE} Mascot Search Results

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

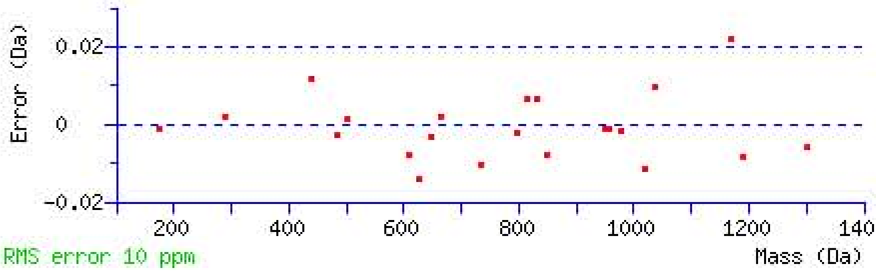
Match to Query 26499: 1474.720948 from(738.367750,2+) rtinseconds(1789) index(30533)
Title: Locus:1.1.1.3286.20 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

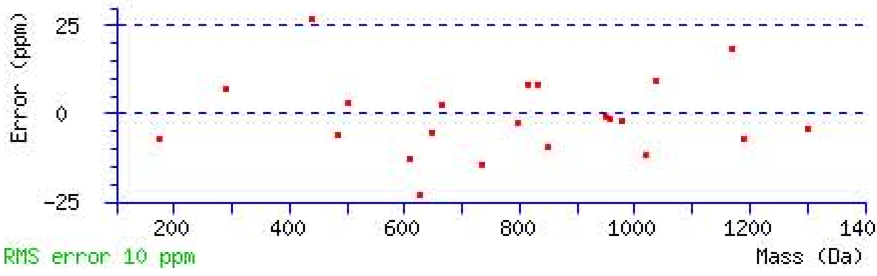
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1474.723831
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 43 **Expect:** 0.00093
Matches : 22/102 fragment ions using 45 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
43.3	1474.723831	-0.002883	QSTNAYPDLR
14.9	1474.741592	-0.020644	SSLEHGSDVYLLR
12.8	1474.721161	-0.000213	QSTHGERGHR
7.2	1474.735092	-0.014144	SFCVLSQLTQHR
6.1	1474.719803	0.001145	CVASNAAGADSLAIR
5.1	1474.742462	-0.021514	QCKSEFPIR
3.8	1474.738419	-0.017471	NNMEGLNVMGKLR
3.5	1474.719788	0.001160	QQEELEQMRLR
3.3	1474.716461	0.004487	AFSDSSQLTVHQR
3.2	1474.723846	-0.002898	QQDGELVGYR

Mascot: http://www.matrixscience.com/

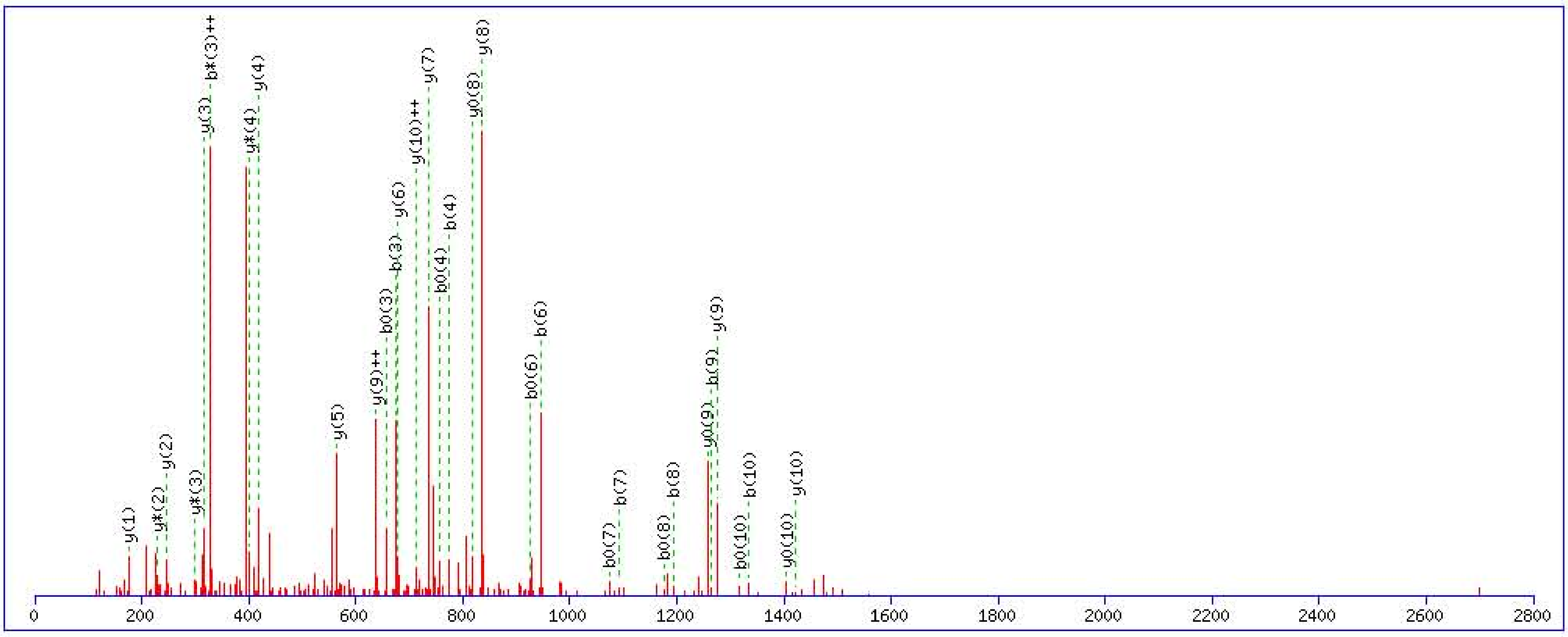
{MATRIX SCIENCE} Mascot Search Results

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

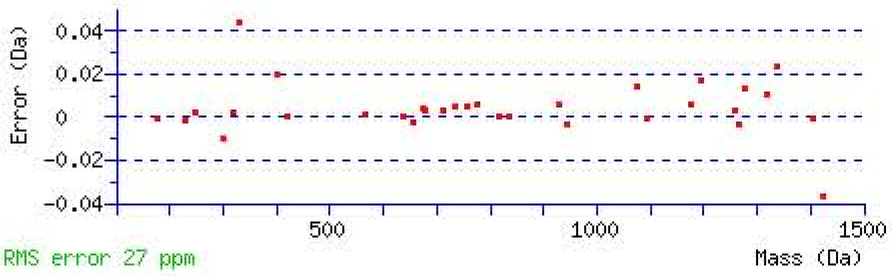
Match to Query 27494: 1508.776428 from(755.395490,2+) rtinseconds(2323) index(47953)
Title: Locus:1.1.1.3521.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

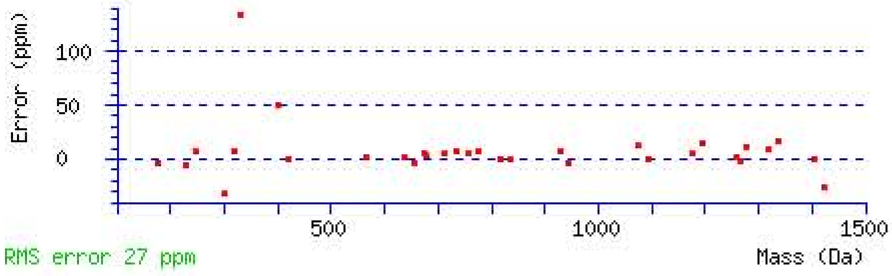
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 55  Expect: 2.2e-005
Matches : 32/110 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	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
55.0	1508.780975	-0.004547	SFQTGLFTAAR
5.0	1508.762344	0.014084	EDFVPFTGEKKGR
3.9	1508.798721	-0.022293	SSYGVAAPVDFLRK
3.5	1508.776932	-0.000504	LMGADSLQLFRSR
0.3	1508.759186	0.017242	QVHCGSEILR
0.1	1508.765701	0.010727	TKPLSMLYVDNGR

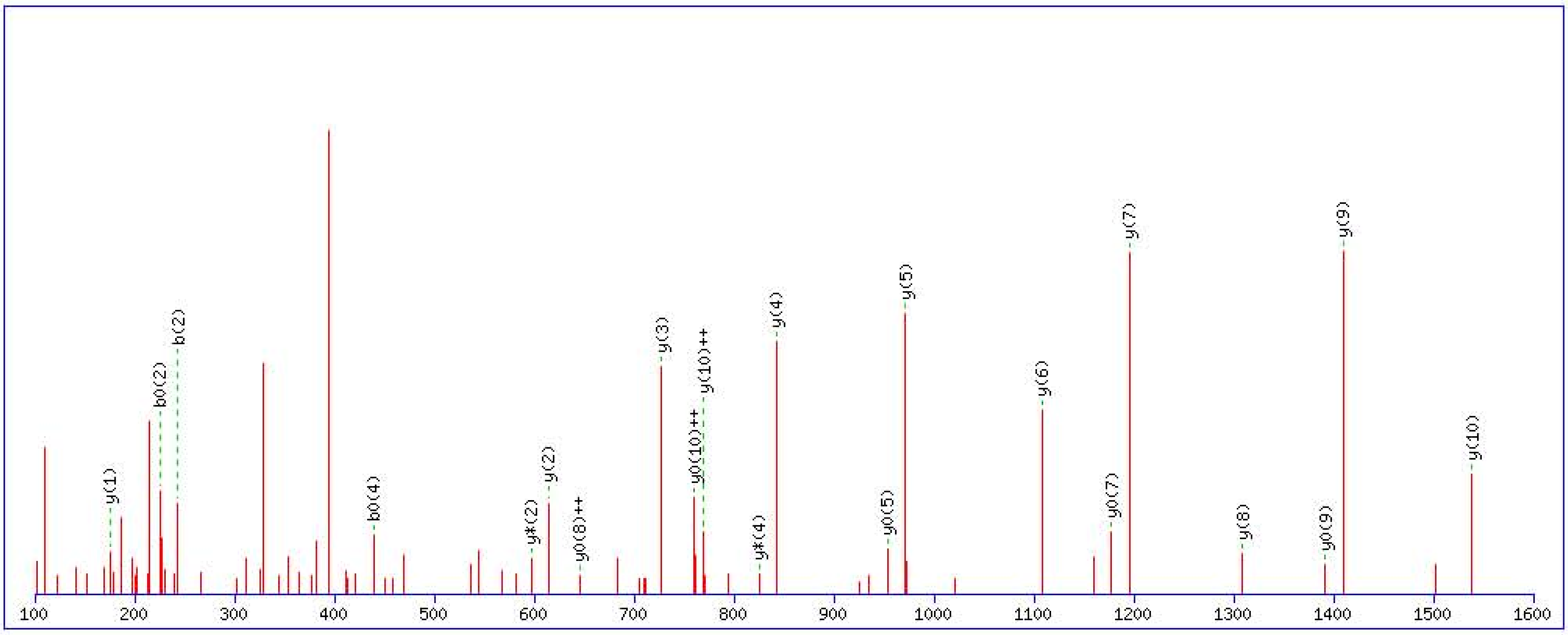
Mascot Search Results

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

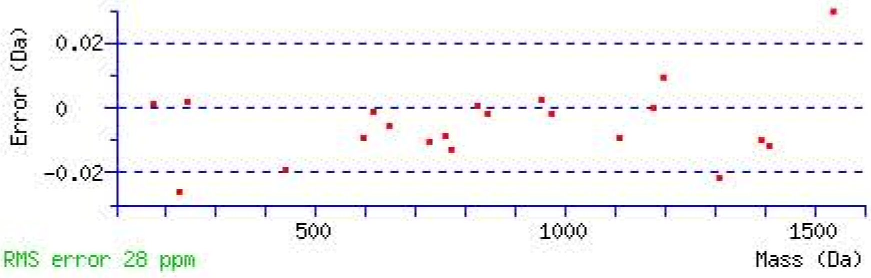
Match to Query 32719: 1650.833022 from(551.284950,3+) rtinseconds(1648) index(29771)
Title: Locus:1.1.1.3237.14 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

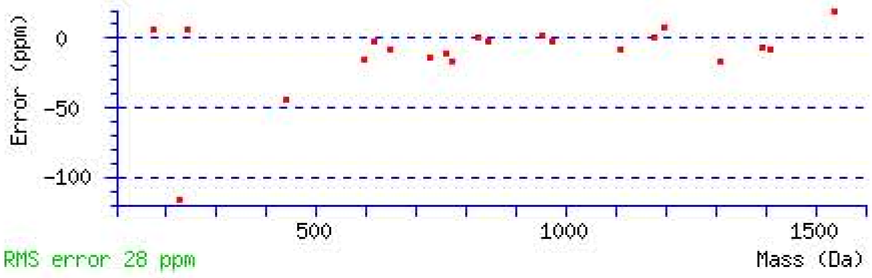
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1650.839920
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 3.6e-006
Matches : 21/94 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	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
61.7	1650.839920	-0.006898	IETISHEDLQR
3.5	1650.847305	-0.014283	LLFQELMSMSIAPR
3.0	1650.821274	0.011748	ELSRLDKELDDYR

Mascot: http://www.matrixscience.com/

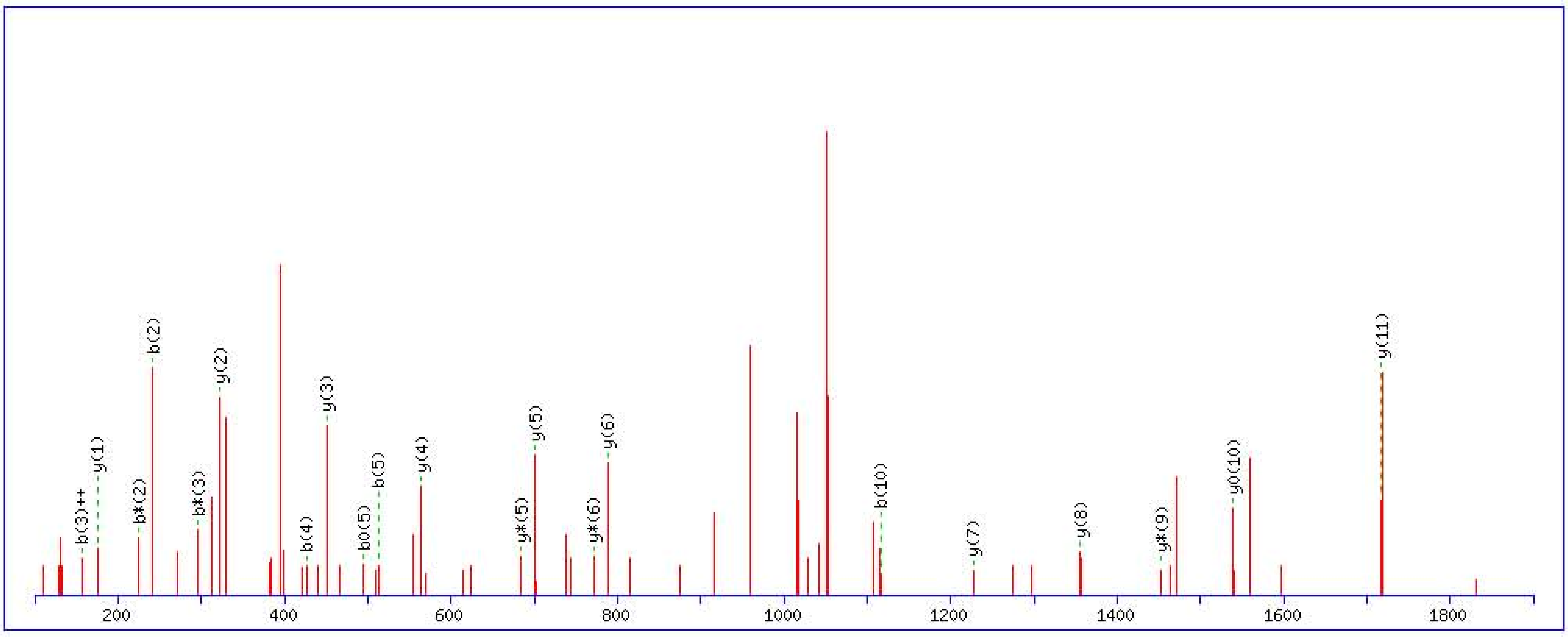
Mascot Search Results

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

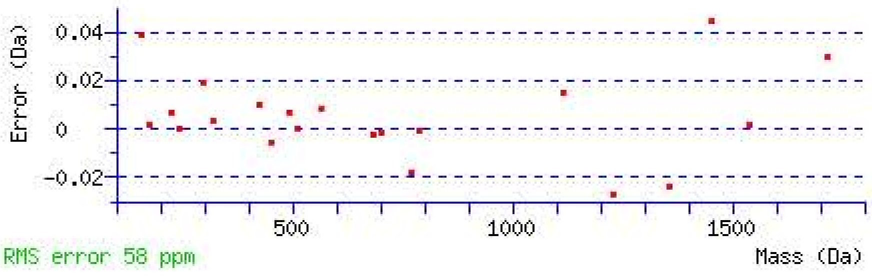
Match to Query 45751: 2342.152902 from(781.724910,3+) rtinseconds(2246) index(47540)
Title: Locus:1.1.1.3494.24 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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 ●

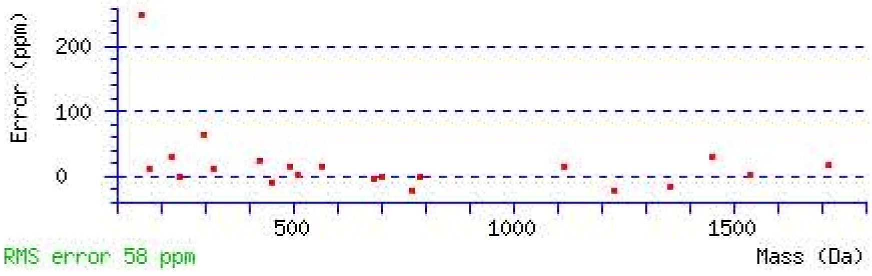


Monoisotopic mass of neutral peptide Mr(calc): 2342.151108
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 33 **Expect:** 0.014
Matches : 21/178 fragment ions using 47 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	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



RMS error 58 ppm



RMS error 58 ppm

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
33.1	2342.151108	0.001794	IQALSLCSDQQSHLEFR
30.5	2342.151108	0.001794	IQALSLCSDQQSHLEFR
10.2	2342.151108	0.001794	IQALSLCSDQQSHLEFR

Mascot: http://www.matrixscience.com/

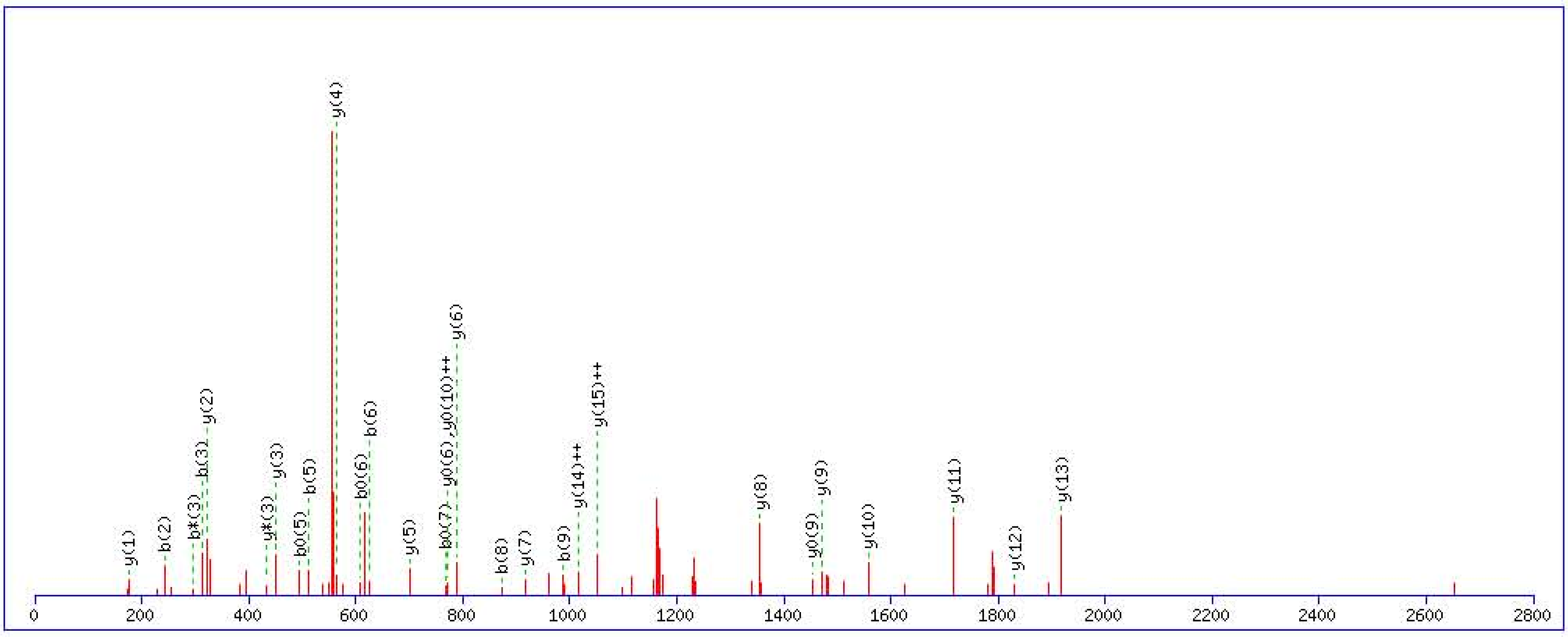
{MATRIX SCIENCE} Mascot Search Results

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

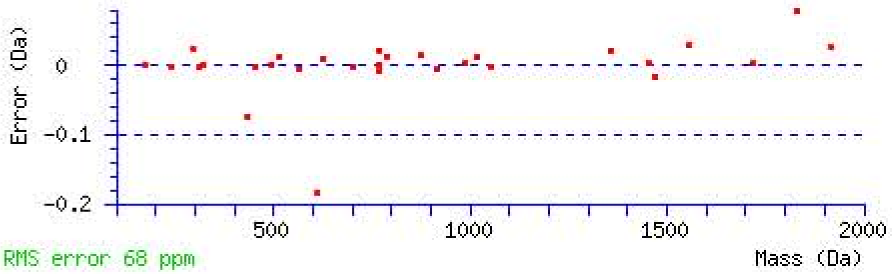
Match to Query 45756: 2342.177428 from(1172.095990,2+) rtinseconds(2194) index(61620)
Title: Locus:1.1.1.1675.22 File:"2013-07-02 CLN FXIII 180 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

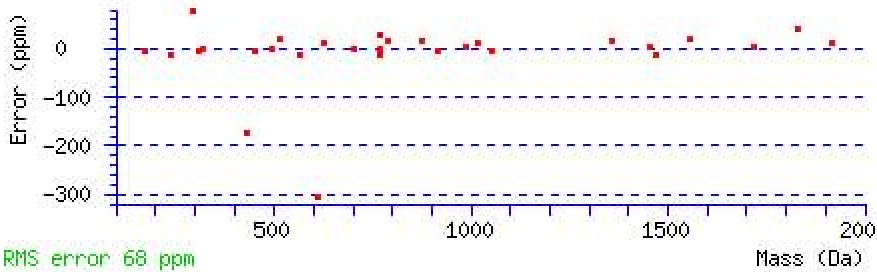
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2342.151108
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 : 29/178 fragment ions using 74 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	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
54.4	2342.151108	0.026320	IQALSLCSDQQSHLEFR
46.4	2342.151108	0.026320	IQALSLCSDQQSHLEFR
6.8	2342.151108	0.026320	IQALSLCSDQQSHLEFR

Mascot: http://www.matrixscience.com/

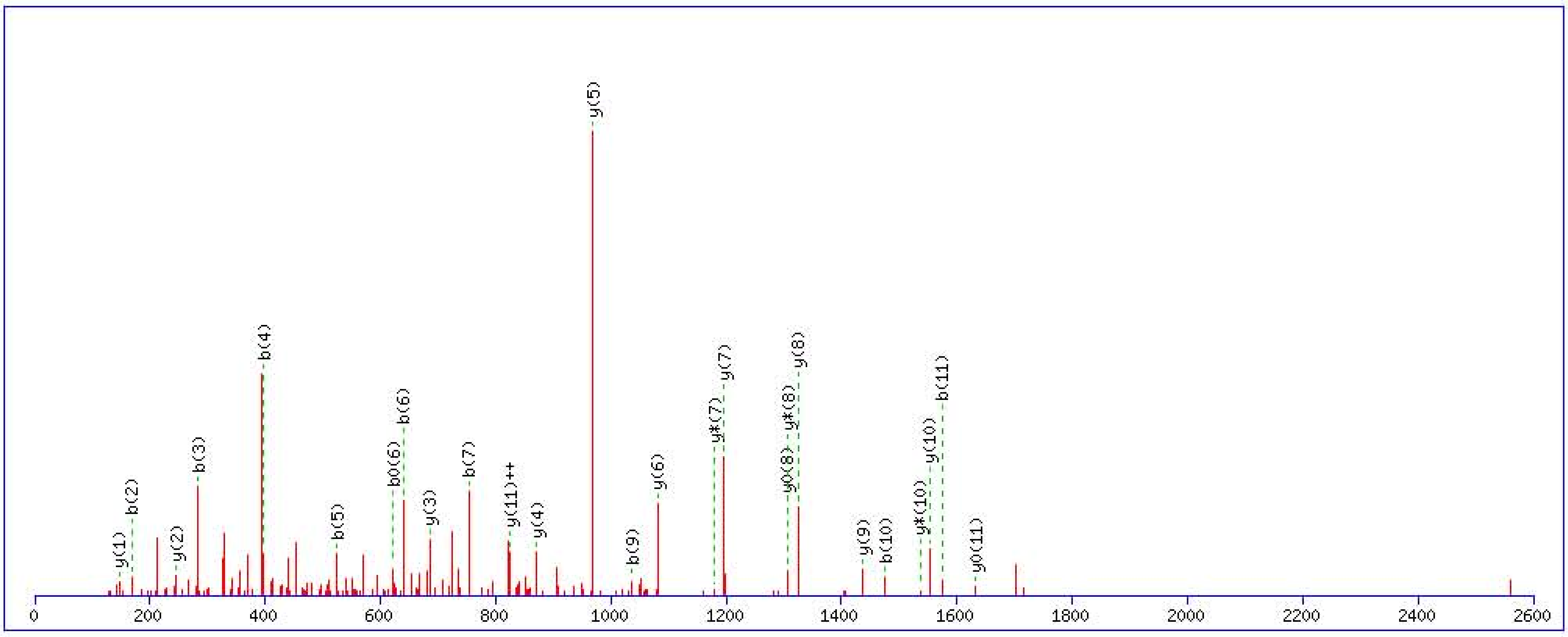
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **APDLQDLPWQVK**
Found in **PROZ_HUMAN**, Vitamin K-dependent protein Z OS=Homo sapiens GN=PROZ PE=1 SV=2

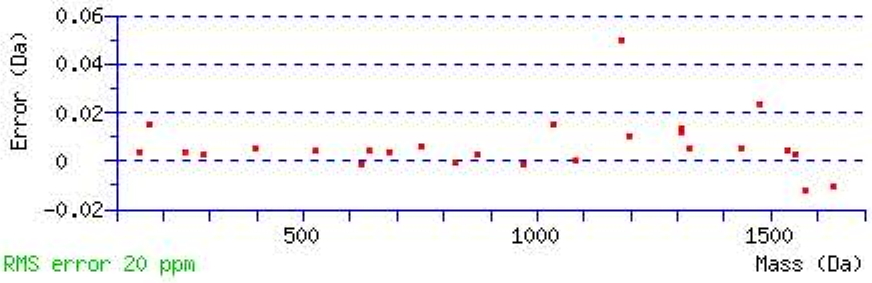
Match to Query 34059: 1719.909528 from(860.962040,2+) rtinseconds(2544) index(49039)
Title: Locus:1.1.1.3598.4 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

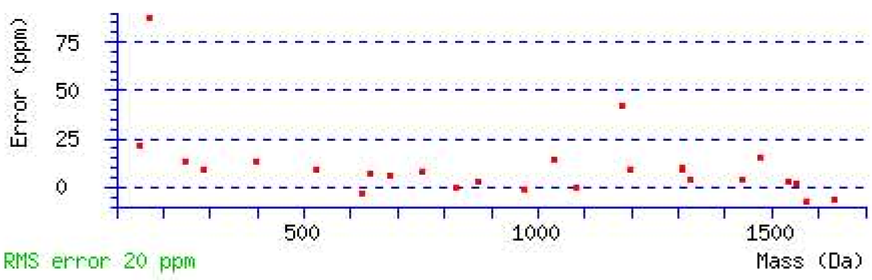
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1719.901810
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 63 **Expect:** 1.1e-005
Matches : 26/108 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	72.044390	36.525833					A							12
2	**169.097154**	85.052215					P	1649.871977	825.439627	1632.845428	816.926352	1631.861412	816.434344	11
3	**284.124097**	142.565687			266.113532	133.560404	D	***1552.819213***	776.913245	1535.792664	768.399970	1534.808648	767.907962	10
4	**397.208161**	199.107719			379.197596	190.102436	L	***1437.792270***	719.399773	1420.765721	710.886499	1419.781705	710.394491	9
5	**525.266739**	263.137008	508.240190	254.623733	507.256174	254.131725	Q	***1324.708206***	662.857741	1307.681657	654.344467	1306.697641	653.852459	8
6	**640.293682**	320.650479	623.267133	312.137205	622.283117	311.645197	D	***1196.649628***	598.828452	1179.623079	590.315178	1178.639063	589.823170	7
7	**753.377746**	377.192511	736.351197	368.679237	735.367181	368.187229	L	***1081.622685***	541.314981	1064.596136	532.801706			6
8	850.430510	425.718893	833.403961	417.205619	832.419945	416.713611	P	***968.538621***	484.772949	951.512072	476.259674			5
9	**1036.509823**	518.758550	1019.483274	510.245275	1018.499258	509.753267	W	***871.485857***	436.246567	854.459308	427.733292			4
10	**1475.735149**	738.371213	1458.708600	729.857938	1457.724584	729.365930	Q	***685.406544***	343.206910	668.379995	334.693636			3
11	**1574.803563**	787.905420	1557.777014	779.392145	1556.792998	778.900137	V	***246.181218***	123.594247	229.154669	115.080973			2
12							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of APDLQDLPWQVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.8	1719.901810	0.007718	APDLQDLPWQVK
16.0	1719.901810	0.007718	APDLQDLPWQVK
11.8	1719.907715	0.001813	VLAGVVMTTGTDVKDAK
4.3	1719.897766	0.011762	LVHNKPPTMKPEGEK

Mascot: http://www.matrixscience.com/

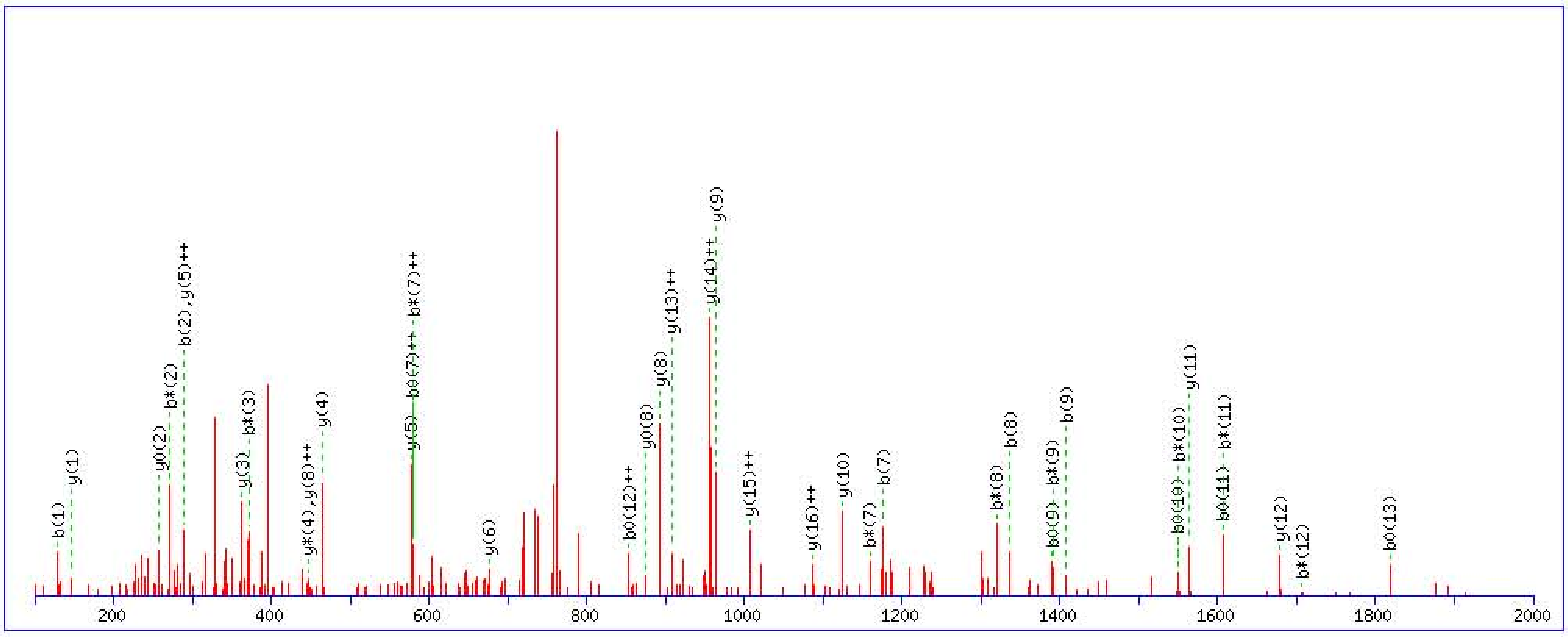
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QCVPHDQCACGVLTSEK**
Found in **PROZ_HUMAN**, Vitamin K-dependent protein Z OS=Homo sapiens GN=PROZ PE=1 SV=2

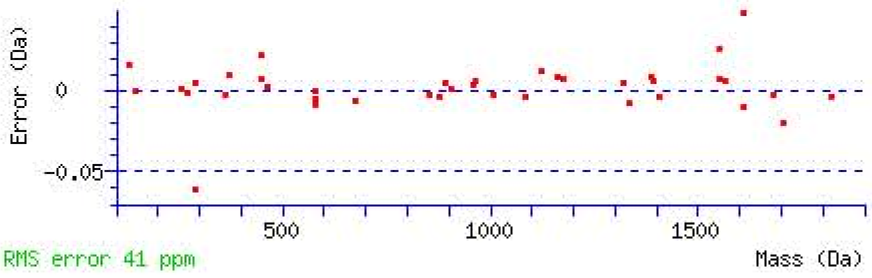
Match to Query 45084: 2299.016742 from(767.346190,3+) rtinseconds(1658) index(43917)
Title: Locus:1.1.1.3290.8 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

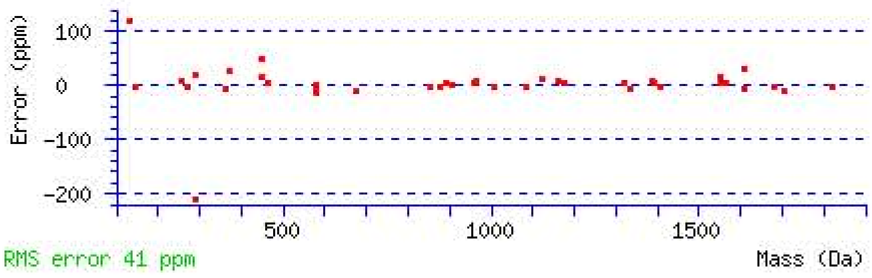
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2299.021790
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00012
Matches : 39/180 fragment ions using 72 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							17
2	**289.096503**	145.051890	272.069954	136.538615			C	2171.970466	1086.488871	2154.943917	1077.975596	2153.959901	1077.483588	16
3	388.164917	194.586097	371.138368	186.072822			V	2011.939817	1006.473547	1994.913268	997.960272	1993.929252	997.468264	15
4	485.217681	243.112479	468.191132	234.599204			P	1912.871403	956.939340	1895.844854	948.426065	1894.860838	947.934057	14
5	622.276593	311.641935	605.250044	303.128660			H	1815.818639	908.412958	1798.792090	899.899683	1797.808074	899.407675	13
6	737.303536	369.155406	720.276987	360.642132	719.292971	360.150124	D	***1678.759727***	839.883502	1661.733178	831.370227	1660.749162	830.878219	12
7	**1176.528862**	588.768069	1159.502313	580.254795	1158.518297	579.762786	Q	***1563.732784***	782.370030	1546.706235	773.856756	1545.722219	773.364748	11
8	**1336.559511**	668.783393	1319.532962	660.270119	1318.548946	659.778111	C	***1124.507458***	562.757367	1107.480909	554.244093	1106.496893	553.752085	10
9	**1407.596625**	704.301950	1390.570076	695.788676	1389.586060	695.296668	A	***964.476809***	482.742043	947.450260	474.228768	946.466244	473.736760	9
10	1567.627274	784.317275	1550.600725	775.804001	1549.616709	775.311992	C	***893.439695***	447.223486	876.413146	438.710211	875.429130	438.218203	8
11	1624.648738	812.828007	1607.622189	804.314732	1606.638173	803.822724	G	733.409046	367.208161	716.382497	358.694887	715.398481	358.202879	7
12	1723.717152	862.362214	1706.690603	853.848940	1705.706587	853.356931	V	***676.387582***	338.697429	659.361033	330.184155	658.377017	329.692147	6
13	1836.801216	918.904246	1819.774667	910.390971	1818.790651	909.898963	L	***577.319168***	289.163222	560.292619	280.649948	559.308603	280.157940	5
14	1937.848895	969.428085	1920.822346	960.914811	1919.838330	960.422803	T	***464.235104***	232.621190	447.208555	224.107916	446.224539	223.615908	4
15	2024.880923	1012.944100	2007.854374	1004.430825	2006.870358	1003.938817	S	***363.187425***	182.097351	346.160876	173.584076	345.176860	173.092068	3
16	2153.923516	1077.465396	2136.896967	1068.952121	2135.912951	1068.460113	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
17							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of QCVPHDQCACGVLTSEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.5	2299.021790	-0.005048	QCVPHDQCACGVLTSEK
24.6	2299.021790	-0.005048	QCVPHDQCACGVLTSEK

Mascot: http://www.matrixscience.com/

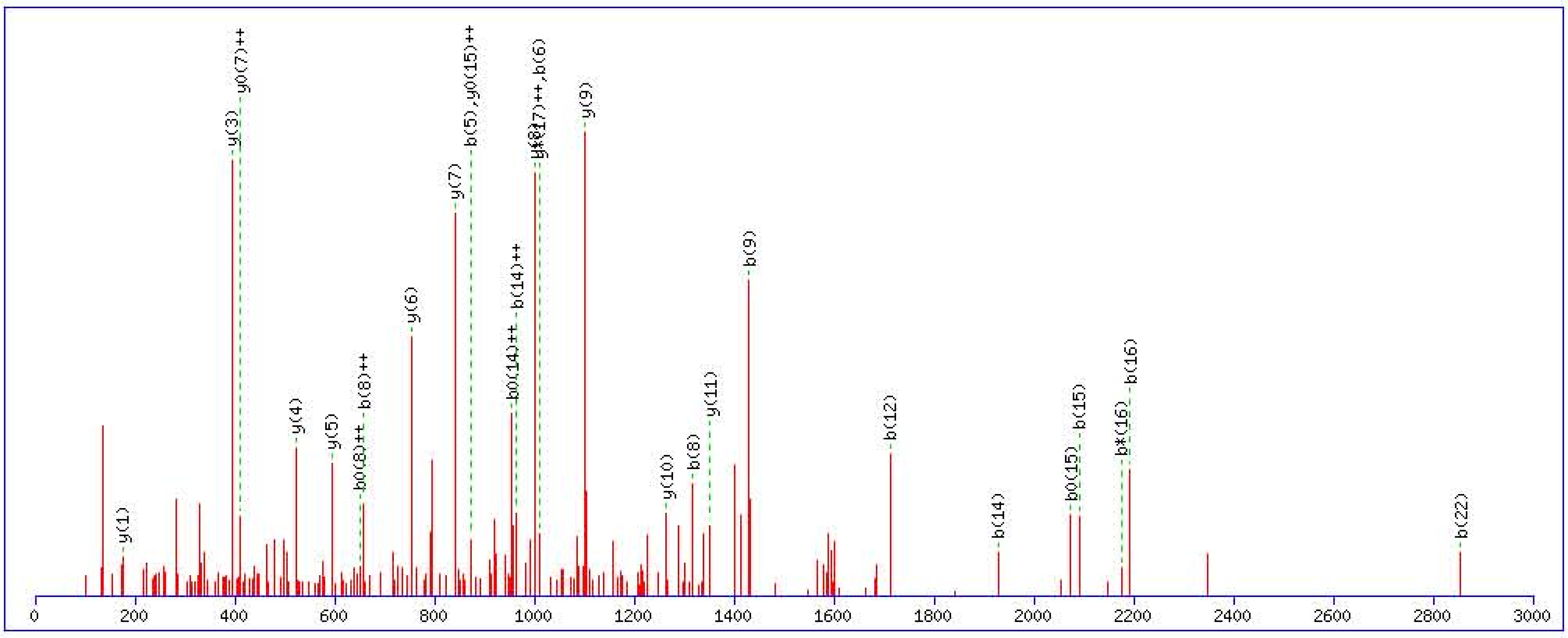
{MATRIX SCIENCE} Mascot Search Results

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

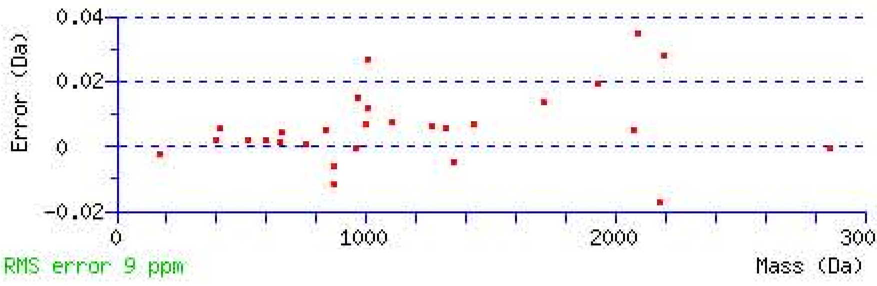
Match to Query 55417: 3192.305616 from(799.083680,4+) rtinseconds(2067) index(46433)
Title: Locus:1.1.1.3432.12 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

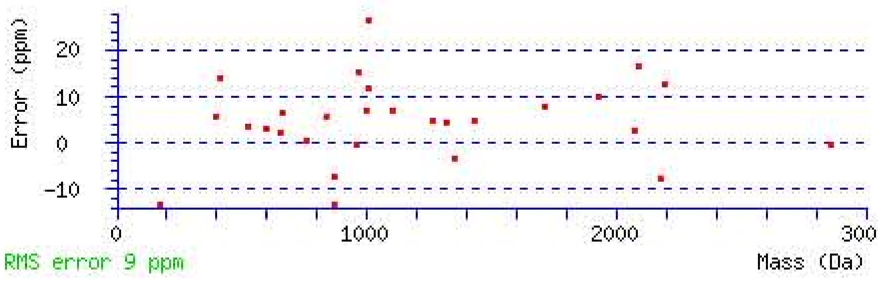
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3192.298050
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 74  Expect: 4.7e-008
Matches : 28/256 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	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



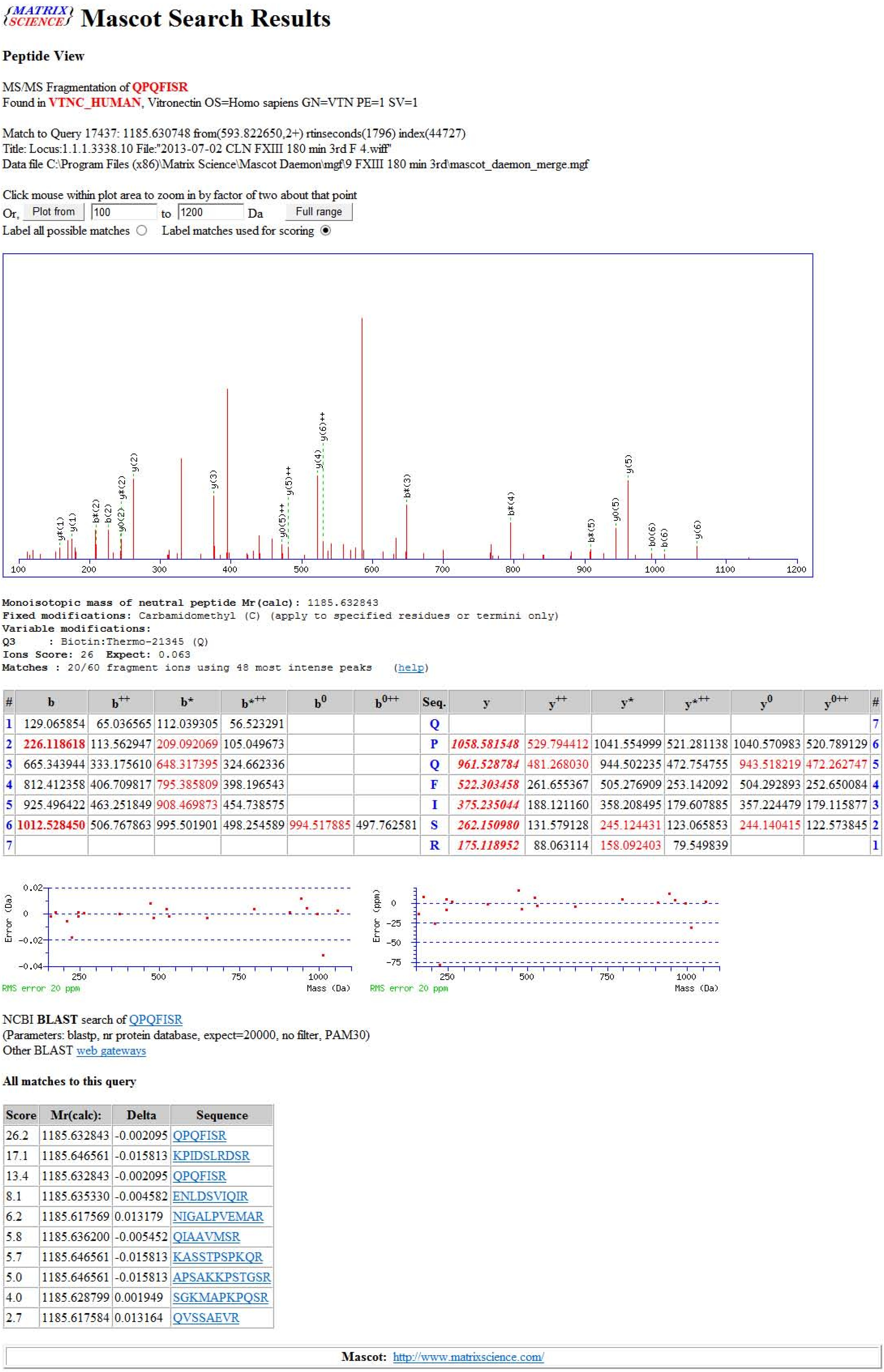


NCBI **BLAST** search of TDGCQHFCLPGQESYTCSCAQGYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
73.9	3192.298050	0.007566	TDGCQHFCLPGQESYTCSCAQGYR
41.5	3192.298050	0.007566	TDGCQHFCLPGQESYTCSCAQGYR

Mascot: http://www.matrixscience.com/



Mascot Search Results

Peptide View

MS/MS Fragmentation of **QPQFISR**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

Match to Query 17437: 1185.630748 from(593.822650,2+) rtinseconds(1796) index(44727)
Title: Locus:1.1.1.3338.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\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): 1185.632843
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.063
Matches : 20/60 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	129.065854	65.036565	112.039305	56.523291			Q							7
2	**226.118618**	113.562947	209.092069	105.049673			P	***1058.581548***	529.794412	1041.554999	521.281138	1040.570983	520.789129	6
3	665.343944	333.175610	648.317395	324.662336			Q	***961.528784***	481.268030	944.502235	472.754755	943.518219	472.262747	5
4	812.412358	406.709817	795.385809	398.196543			F	***522.303458***	261.655367	505.276909	253.142092	504.292893	252.650084	4
5	925.496422	463.251849	908.469873	454.738575			I	***375.235044***	188.121160	358.208495	179.607885	357.224479	179.115877	3
6	**1012.528450**	506.767863	995.501901	498.254589	994.517885	497.762581	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 QPQFISR
(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	1185.632843	-0.002095	QPQFISR
17.1	1185.646561	-0.015813	KPIDSLRDSR
13.4	1185.632843	-0.002095	QPQFISR
8.1	1185.635330	-0.004582	ENLDSVIQIR
6.2	1185.617569	0.013179	NIGALPVEMAR
5.8	1185.636200	-0.005452	QIAAVMSR
5.7	1185.646561	-0.015813	KASSTPSPKQR
5.0	1185.646561	-0.015813	APSAKKPSTGSR
4.0	1185.628799	0.001949	SGKMAPKPQSR
2.7	1185.617584	0.013164	QVSSAEVR

Mascot: http://www.matrixscience.com/

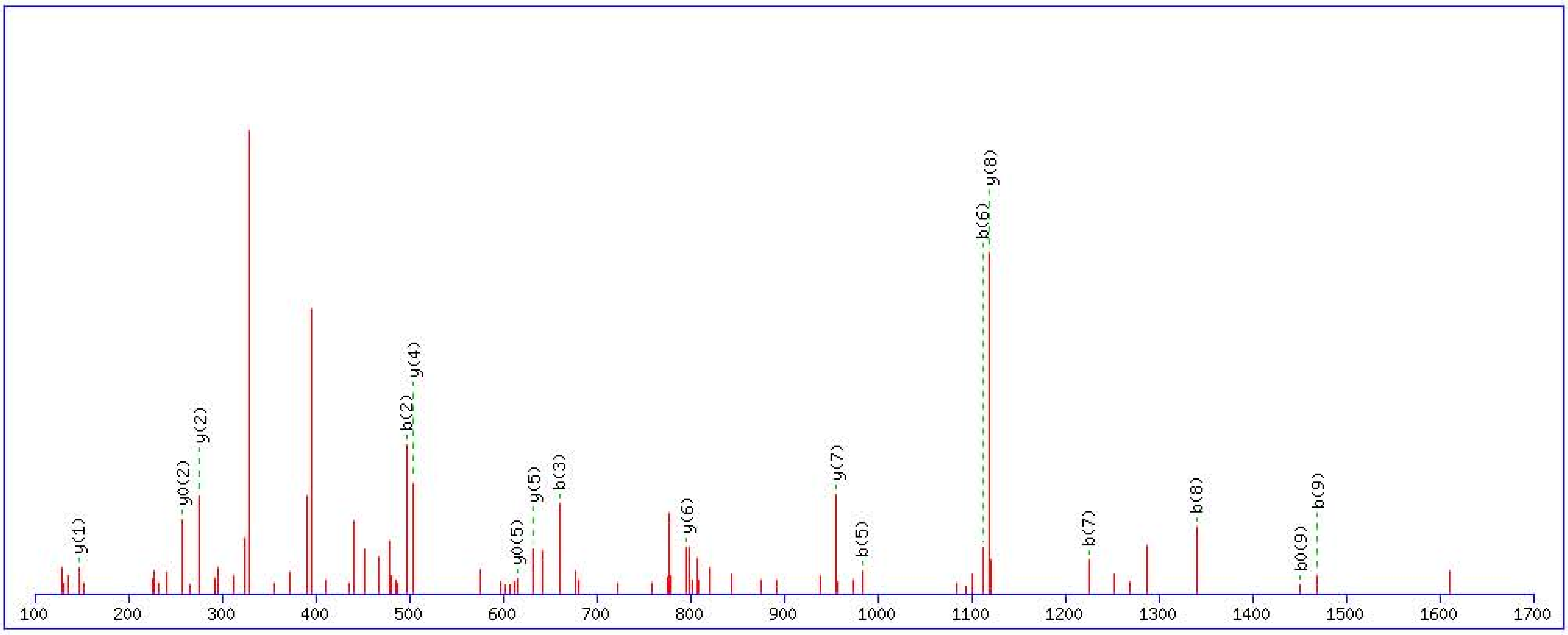
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQYCYELDEK**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

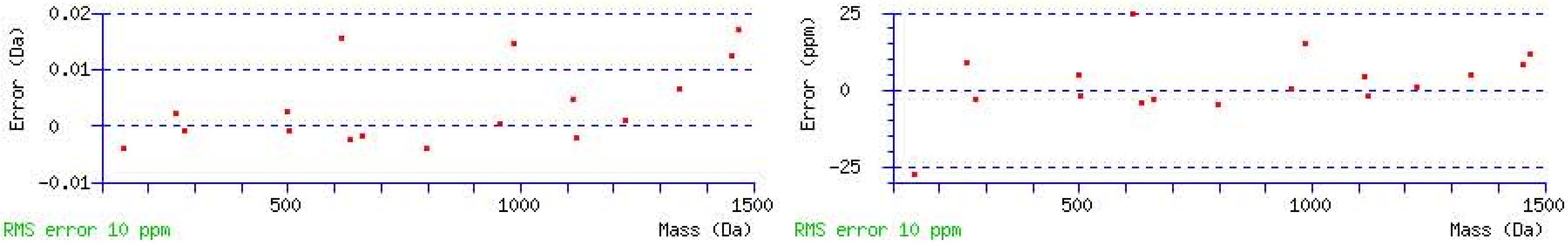
Match to Query 31100: 1614.708108 from(808.361330,2+) rtinseconds(1914) index(45346)
Title: Locus:1.1.1.3379.17 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

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: 47 **Expect:** 8.4e-005
Matches : 17/94 fragment ions using 27 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
46.8	1614.705795	0.002313	GQYCYELDEK
6.1	1614.717010	-0.008902	EYFRMELMHAEK
1.6	1614.692566	0.015542	QFFDCGHWYDLK
0.3	1614.701767	0.006341	KAEQLMSDENCFK

Mascot: http://www.matrixscience.com/

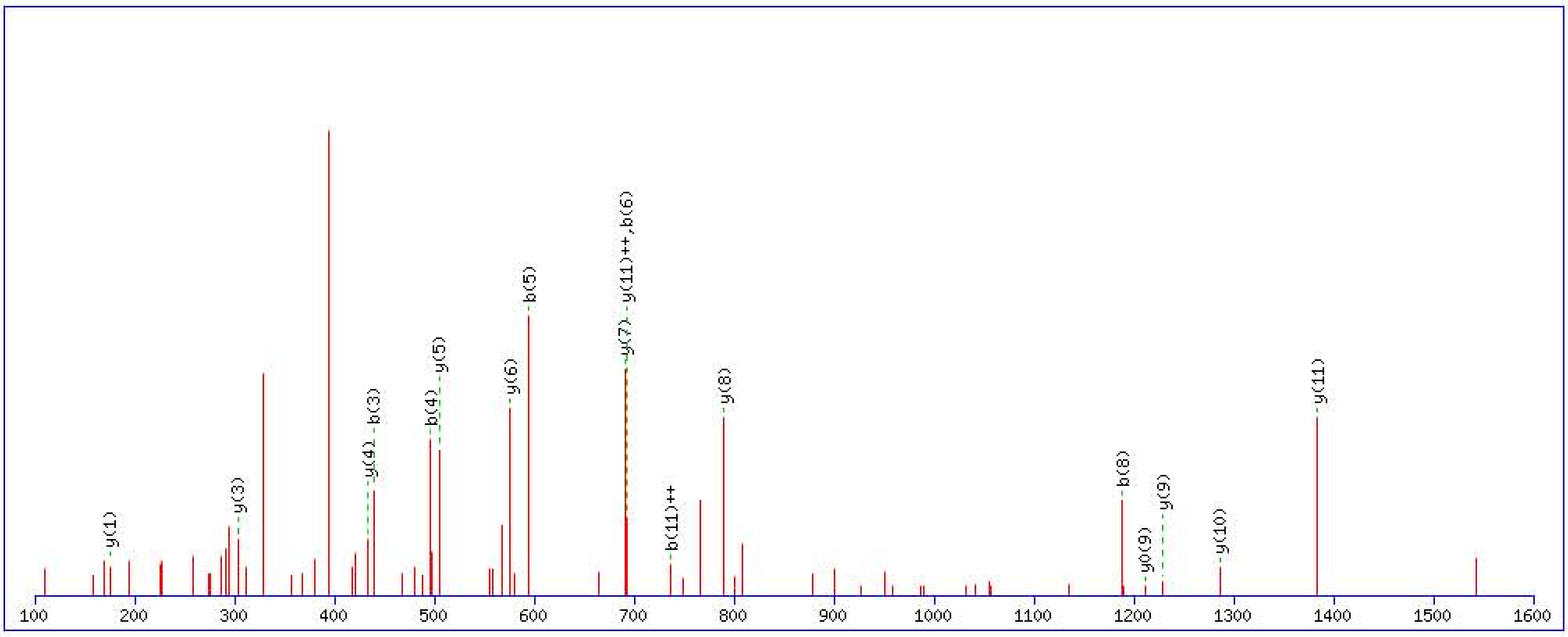
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DWHGVPGQVDAAMAGR**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

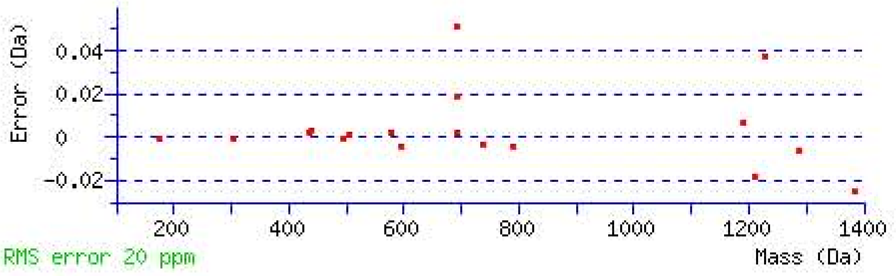
Match to Query 38902: 1976.933772 from(659.985200,3+) rtinseconds(2178) index(32912)
Title: Locus:1.1.1.3422.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

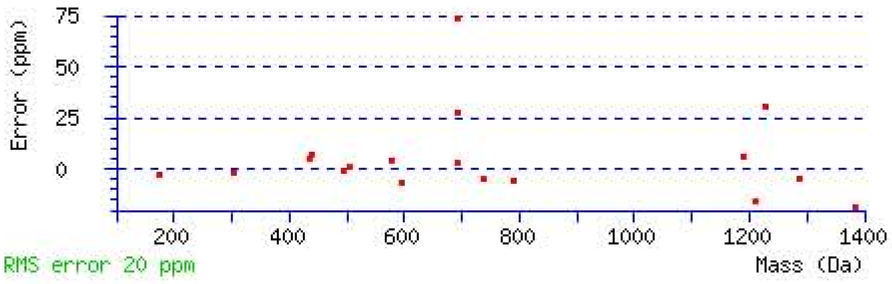
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1976.934937
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.00051
Matches : 18/154 fragment ions using 45 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
42.9	1976.934937	-0.001165	DWHGVPGQVDAAMAGR
7.8	1976.918793	0.014979	DDGLQYRPDVKDASDQR

Mascot: http://www.matrixscience.com/

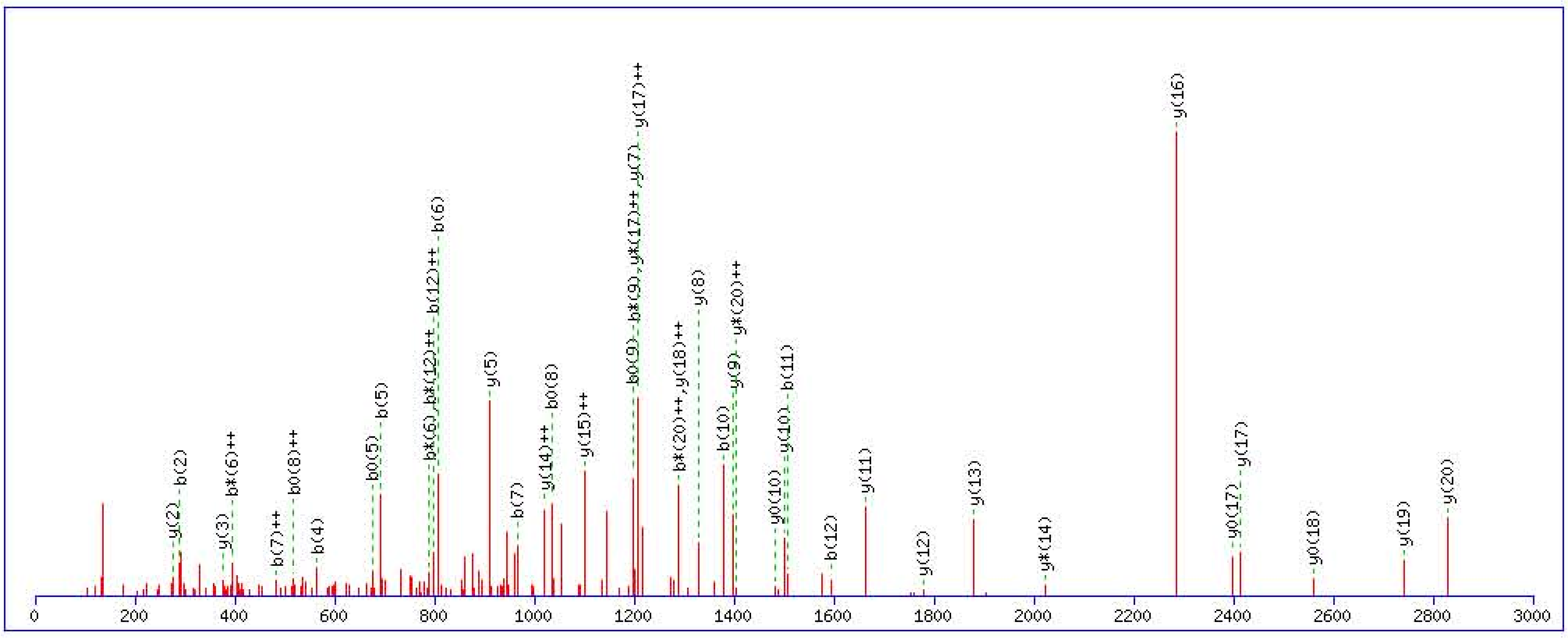
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CQCDELCSYYQSCCTDYTAECKPQVTR**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

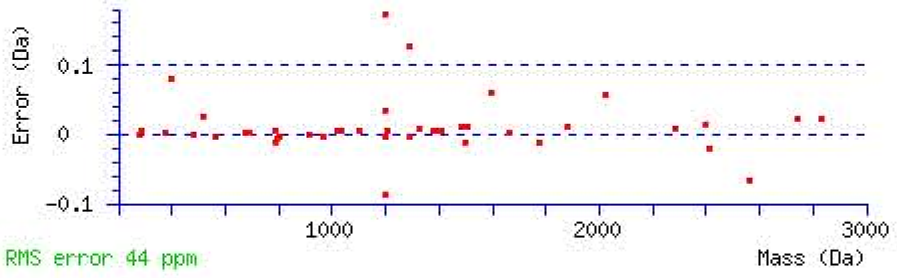
Match to Query 61264: 3792.513656 from(949.135690,4+) rtinseconds(1967) index(45788)
Title: Locus:1.1.1.3397.24 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

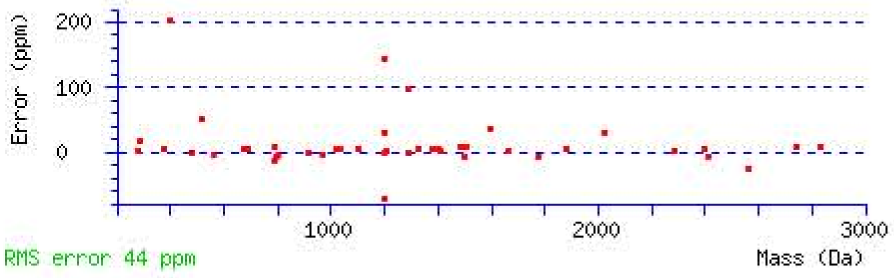
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [3000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3792.511536
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q24     : Biotin:Thermo-21345 (Q)
Ions Score: 86  Expect: 2.5e-009
Matches : 43/302 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							27
2	***289.096503***	145.051890	272.069954	136.538615			Q	3633.488150	1817.247713	3616.461601	1808.734438	3615.477585	1808.242431	26
3	449.127152	225.067214	432.100603	216.553940			C	3505.429572	1753.218424	3488.403023	1744.705149	3487.419007	1744.213141	25
4	***564.154095***	282.580686	547.127546	274.067411	546.143530	273.575403	D	3345.398923	1673.203099	3328.372374	1664.689825	3327.388358	1664.197817	24
5	***693.196688***	347.101982	676.170139	338.588708	675.186123	338.096700	E	3230.371980	1615.689628	3213.345431	1607.176353	3212.361415	1606.684345	23
6	***806.280752***	403.644014	789.254203	395.130740	788.270187	394.638732	L	3101.329387	1551.168331	3084.302838	1542.655057	3083.318822	1542.163049	22
7	***966.311401***	**483.659339**	949.284852	475.146064	948.300836	474.654056	C	2988.245323	1494.626299	2971.218774	1486.113025	2970.234758	1485.621017	21
8	1053.343429	527.175353	1036.316880	518.662078	1035.332864	518.170070	S	***2828.214674***	1414.610975	2811.188125	1406.097700	2810.204109	1405.605692	20
9	1216.406758	608.707017	1199.380209	600.193743	1198.396193	599.701735	Y	***2741.182646***	1371.094961	2724.156097	1362.581686	2723.172081	1362.089678	19
10	***1379.470087***	690.238682	1362.443538	681.725407	1361.459522	681.233399	Y	2578.119317	1289.563296	2561.092768	1281.050022	2560.108752	1280.558014	18
11	***1507.528665***	754.267971	1490.502116	745.754696	1489.518100	745.262688	Q	***2415.055988***	1208.031632	2398.029439	1199.518357	2397.045423	1199.026349	17
12	***1594.560693***	**797.783985**	1577.534144	789.270710	1576.550128	788.778702	S	***2286.997410***	1144.002343	2269.970861	1135.489068	2268.986845	1134.997060	16
13	1754.591342	877.799309	1737.564793	869.286035	1736.580777	868.794027	C	2199.965382	1100.486329	2182.938833	1091.973054	2181.954817	1091.481046	15
14	1914.621991	957.814634	1897.595442	949.301359	1896.611426	948.809351	C	2039.934733	1020.471005	2022.908184	1011.957730	2021.924168	1011.465722	14
15	2015.669670	1008.338473	1998.643121	999.825199	1997.659105	999.333191	T	***1879.904084***	940.455680	1862.877535	931.942406	1861.893519	931.450398	13
16	2130.696613	1065.851945	2113.670064	1057.338670	2112.686048	1056.846662	D	***1778.856405***	889.931841	1761.829856	881.418566	1760.845840	880.926558	12
17	2293.759942	1147.383609	2276.733393	1138.870335	2275.749377	1138.378327	Y	***1663.829462***	832.418369	1646.802913	823.905095	1645.818897	823.413086	11
18	2394.807621	1197.907449	2377.781072	1189.394174	2376.797056	1188.902166	T	***1500.766133***	750.886704	1483.739584	742.373430	1482.755568	741.881422	10
19	2465.844735	1233.426006	2448.818186	1224.912731	2447.834170	1224.420723	A	***1399.718454***	700.362865	1382.691905	691.849591	1381.707889	691.357583	9
20	2594.887328	1297.947302	2577.860779	1289.434028	2576.876763	1288.942020	E	***1328.681340***	664.844308	1311.654791	656.331033	1310.670775	655.839025	8
21	2754.917977	1377.962627	2737.891428	1369.449352	2736.907412	1368.957344	C	***1199.638747***	600.323011	1182.612198	591.809737	1181.628182	591.317729	7
22	2883.012940	1442.010108	2865.986391	1433.496834	2865.002375	1433.004826	K	1039.608098	520.307687	1022.581549	511.794412	1021.597533	511.302404	6
23	2980.065704	1490.536490	2963.039155	1482.023216	2962.055139	1481.531208	P	***911.513135***	456.260205	894.486586	447.746931	893.502570	447.254923	5
24	3419.291030	1710.149153	3402.264481	1701.635879	3401.280465	1701.143871	Q	814.460371	407.733823	797.433822	399.220549	796.449806	398.728541	4
25	3518.359444	1759.683360	3501.332895	1751.170086	3500.348879	1750.678078	V	***375.235045***	188.121160	358.208496	179.607886	357.224480	179.115878	3
26	3619.407123	1810.207200	3602.380574	1801.693925	3601.396558	1801.201917	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 CQCDELCSYYQSCCTDYTAECKPQVTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
86.0	3792.511536	0.002120	CQCDELCSYYQSCCTDYTAECKPQVTR
20.5	3792.511536	0.002120	CQCDELCSYYQSCCTDYTAECKPQVTR

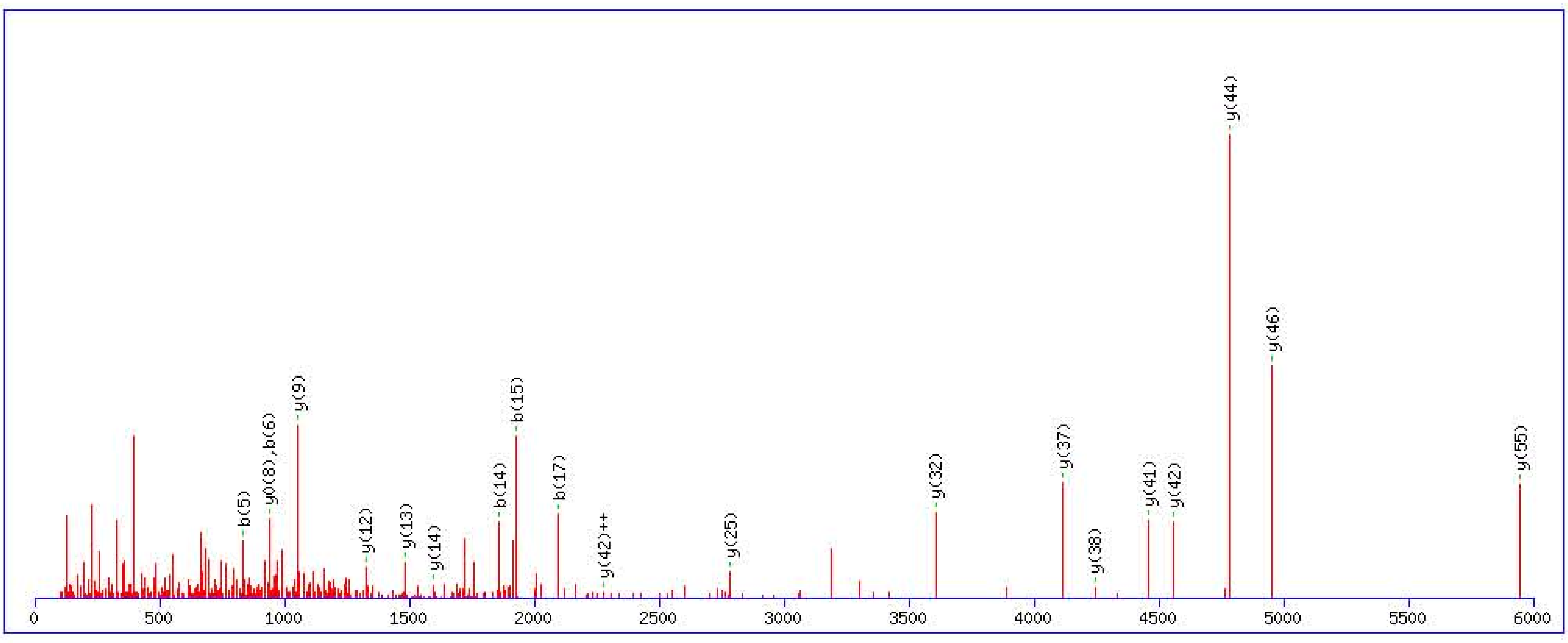
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNPEQTPVLKPEEEAPAPEVGASKPEGIDSRPETLHPGRPQPPAEEELCSGKPFDAFTDLK**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

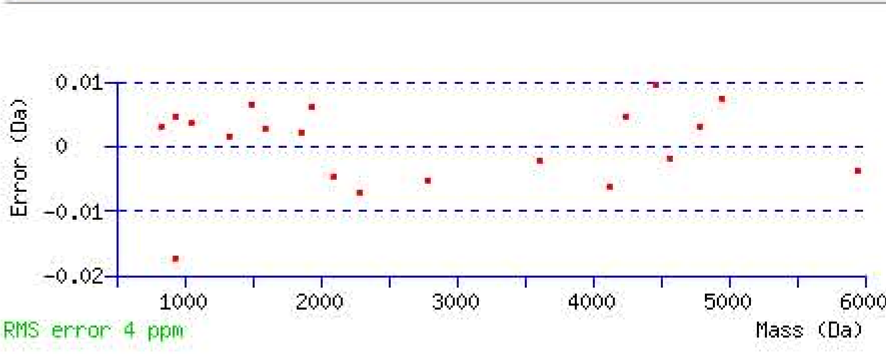
Match to Query 69089: 6883.379552 from(861.429720,8+) rtinseconds(2104) index(32479)
Title: Locus:1.1.1.3396.16 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

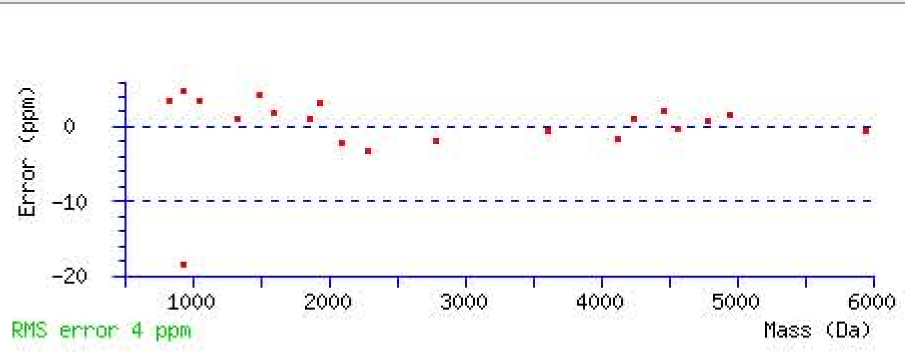
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 6000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 44  Expect: 0.00052
Matches : 20/708 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	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
43.5	6883.374893	0.004659	GNPEQTPVLKPEEEAPAPEVGASKPEGIDSRPETLHPGRPQPPAEEELCSGKPFDAFTDLK
1.0	6883.374893	0.004659	GNPEQTPVLKPEEEAPAPEVGASKPEGIDSRPETLHPGRPQPPAEEELCSGKPFDAFTDLK

Mascot: http://www.matrixscience.com/

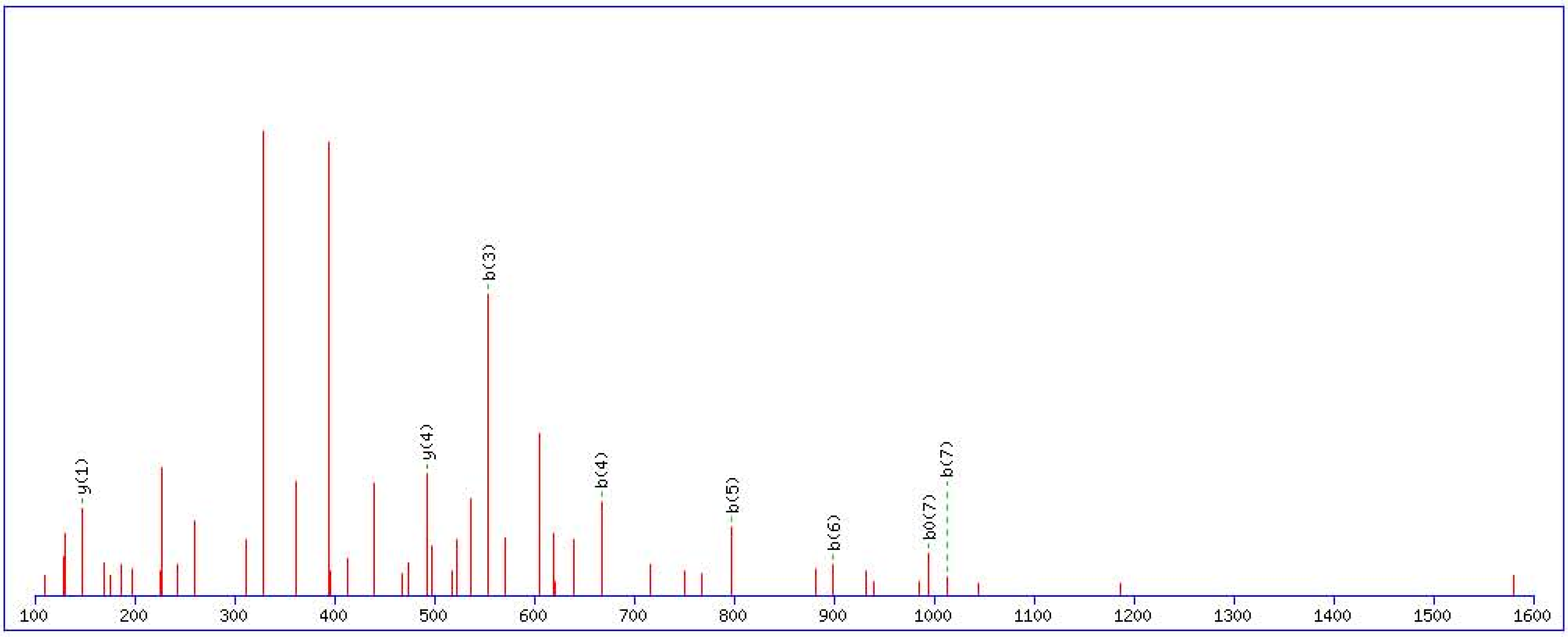
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGQIMTLK**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

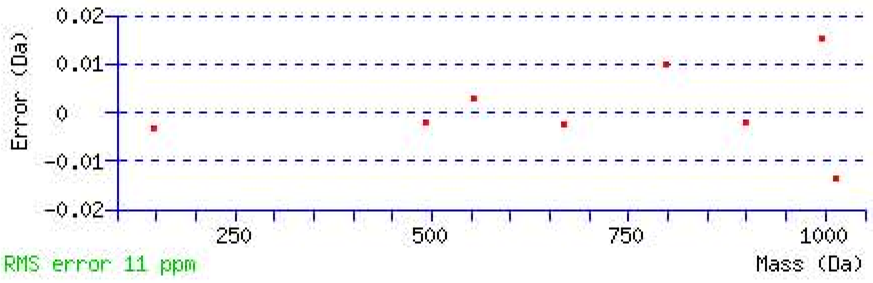
Match to Query 16446: 1157.625008 from(579.819780,2+) rtinseconds(1935) index(31358)
Title: Locus:1.1.1.3337.19 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

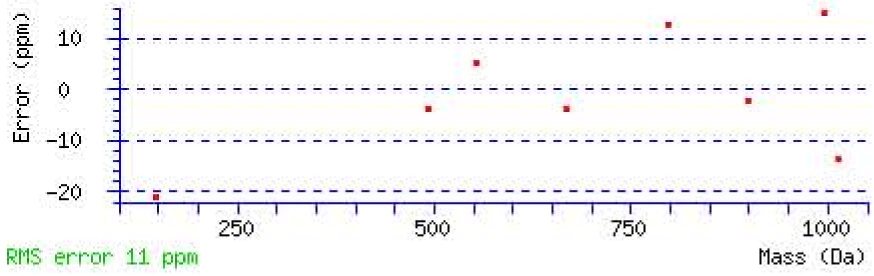
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 37  Expect: 0.0055
Matches : 8/66 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	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
37.2	1157.630066	-0.005058	GGQIMTLK
17.3	1157.630051	-0.005043	QLSQMLK
11.5	1157.640411	-0.015403	SPGKNSSIQLK
9.5	1157.636566	-0.011558	ILVEEMAPLK
9.4	1157.619293	0.005715	TNFEGPPRLK
8.5	1157.640411	-0.015403	AQQLLSSGNLK
8.2	1157.629196	-0.004188	EPQTITQLTK
7.5	1157.622665	0.002343	QRTDSLK
7.4	1157.611420	0.013588	MKLDVPEQAK
6.6	1157.636566	-0.011558	LLAIMPDELK

Mascot: http://www.matrixscience.com/

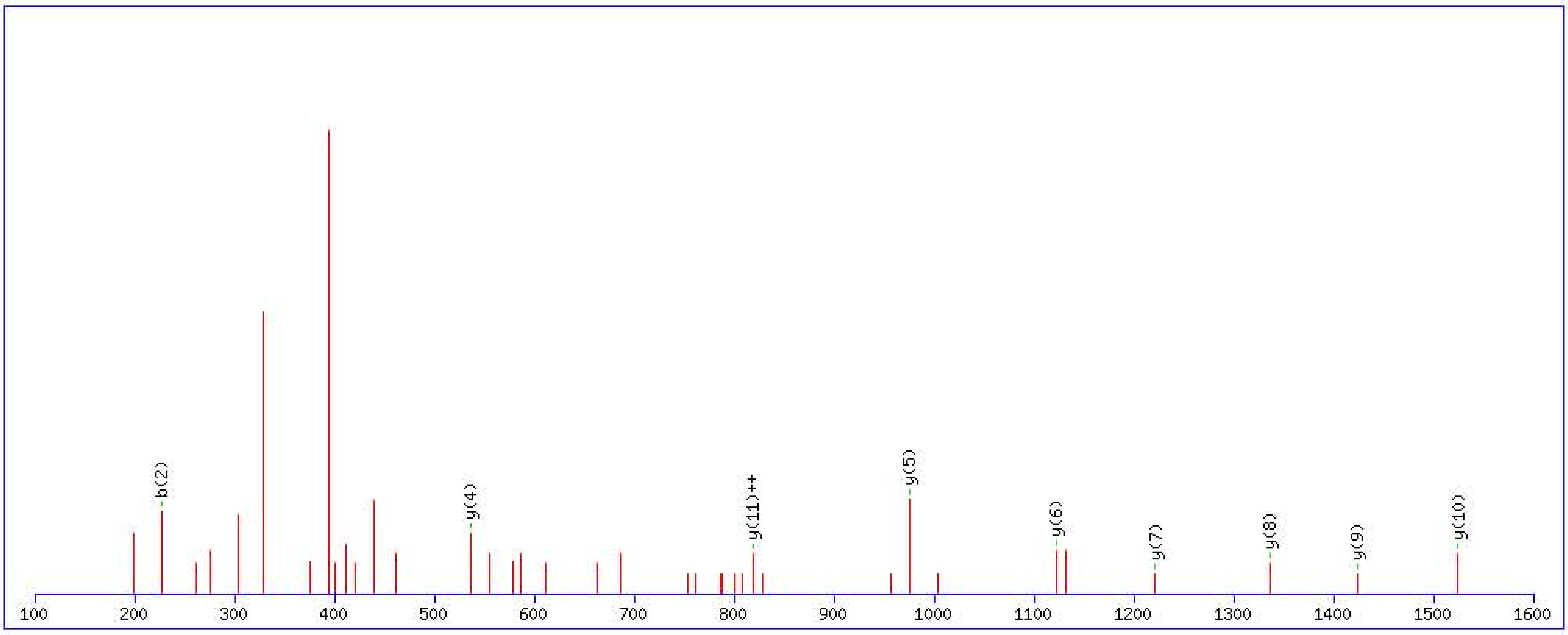
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILTSDVFQDCNK**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

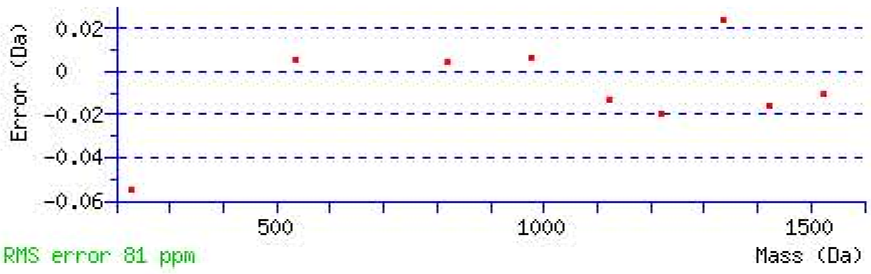
Match to Query 16776: 1749.848862 from(584.290230,3+) rtinseconds(2167) index(47022)
Title: Locus:1.1.1.3467.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

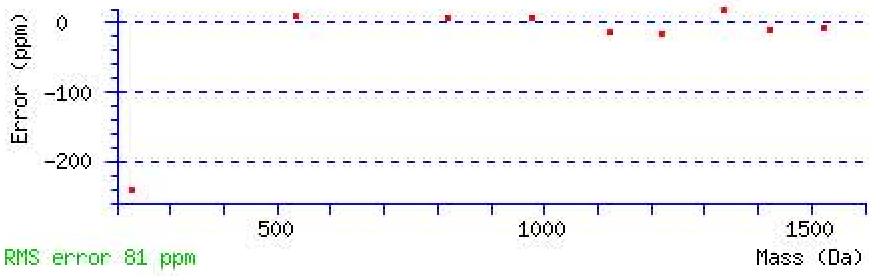
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1749.842987
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 45  Expect: 0.0019
Matches : 9/108 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	114.091340	57.549308					I							12
2	**227.175404**	114.091340					L	1637.766191	819.386734	1620.739642	810.873459	1619.755626	810.381451	11
3	328.223083	164.615179			310.212518	155.609897	T	***1524.682127***	762.844702	1507.655578	754.331427	1506.671562	753.839419	10
4	415.255111	208.131193			397.244546	199.125911	S	***1423.634448***	712.320862	1406.607899	703.807588	1405.623883	703.315580	9
5	530.282054	265.644665			512.271489	256.639383	D	***1336.602420***	668.804848	1319.575871	660.291574	1318.591855	659.799565	8
6	629.350468	315.178872			611.339903	306.173589	V	***1221.575477***	611.291377	1204.548928	602.778102	1203.564912	602.286094	7
7	776.418882	388.713079			758.408317	379.707796	F	***1122.507063***	561.757170	1105.480514	553.243895	1104.496498	552.751887	6
8	1215.644208	608.325742	1198.617659	599.812468	1197.633643	599.320459	Q	***975.438649***	488.222963	958.412100	479.709688	957.428084	479.217680	5
9	1330.671151	665.839214	1313.644602	657.325939	1312.660586	656.833931	D	***536.213323***	268.610300	519.186774	260.097025	518.202758	259.605017	4
10	1490.701800	745.854538	1473.675251	737.341264	1472.691235	736.849256	C	421.186380	211.096828	404.159831	202.583553			3
11	1604.744727	802.876002	1587.718178	794.362727	1586.734162	793.870719	N	261.155731	131.081503	244.129182	122.568229			2
12							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ILTSDVFQDCNK
(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	1749.842987	0.005875	ILTSDVFQDCNK

Mascot: http://www.matrixscience.com/

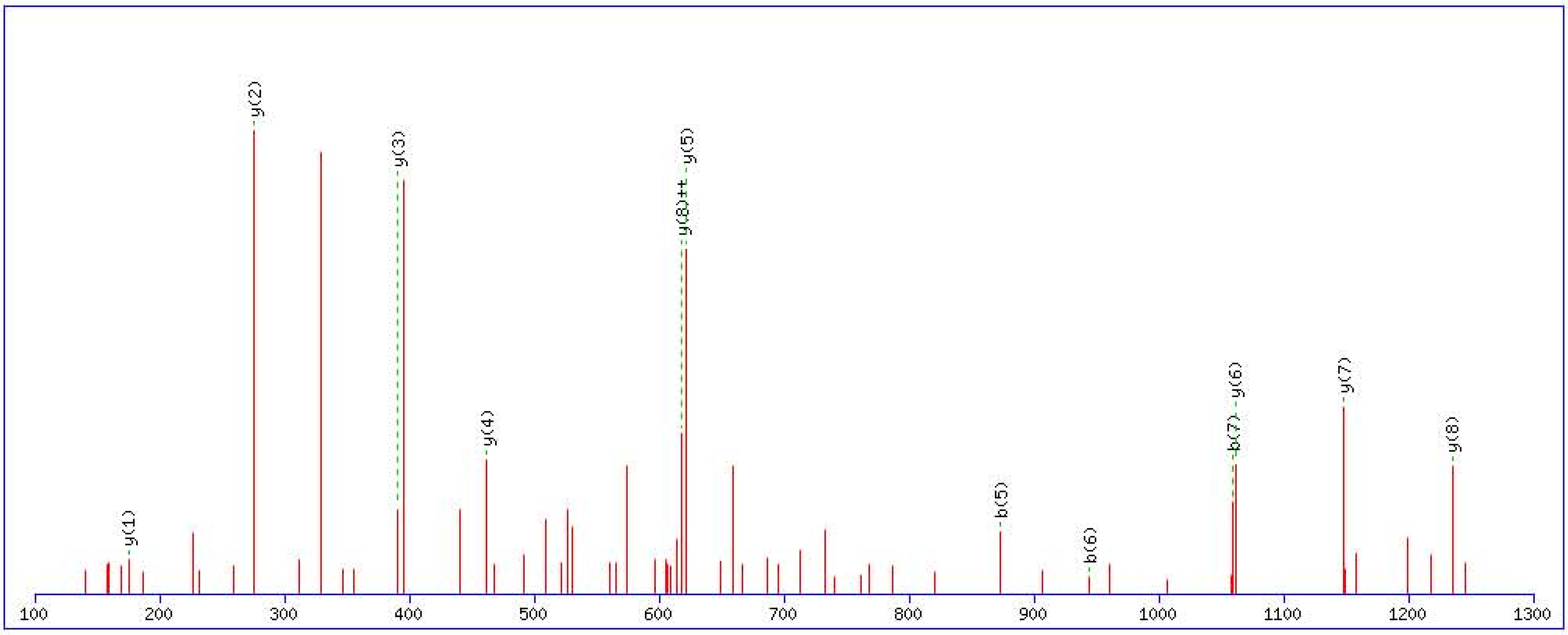
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSSQCADTR**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

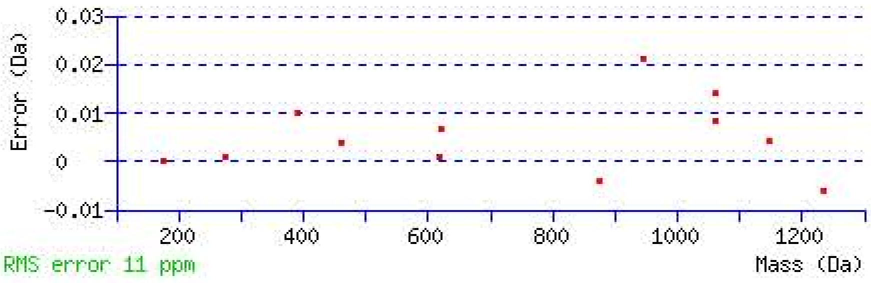
Match to Query 20958: 1333.610088 from(667.812320,2+) rtinseconds(1300) index(27758)
Title: Locus:1.1.1.3115.9 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

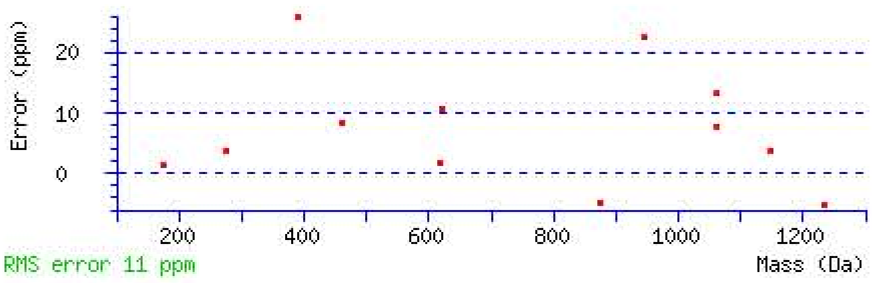
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1333.611862
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 51 **Expect:** 1.6e-005
Matches : 12/86 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	100.075690	50.541483					V							9
2	187.107718	94.057497			169.097153	85.052214	S	*1235.550719*	618.278998	1218.524170	609.765723	1217.540154	609.273715	8
3	274.139746	137.573511			256.129181	128.568229	S	*1148.518691*	574.762984	1131.492142	566.249709	1130.508126	565.757701	7
4	713.365072	357.186174	696.338523	348.672900	695.354507	348.180892	Q	*1061.486663*	531.246970	1044.460114	522.733695	1043.476098	522.241687	6
5	**873.395721**	437.201499	856.369172	428.688224	855.385156	428.196216	C	*622.261337*	311.634307	605.234788	303.121032	604.250772	302.629024	5
6	**944.432835**	472.720056	927.406286	464.206781	926.422270	463.714773	A	*462.230688*	231.618982	445.204139	223.105707	444.220123	222.613700	4
7	**1059.459778**	530.233527	1042.433229	521.720253	1041.449213	521.228245	D	*391.193574*	196.100425	374.167025	187.587151	373.183009	187.095143	3
8	1160.507457	580.757367	1143.480908	572.244092	1142.496892	571.752084	T	*276.166631*	138.586953	259.140082	130.073679	258.156066	129.581671	2
9							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VSSQCADTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.4	1333.611862	-0.001774	VSSQCADTR
0.3	1333.590729	0.019359	CFSRAGSVYCK

Mascot: http://www.matrixscience.com/

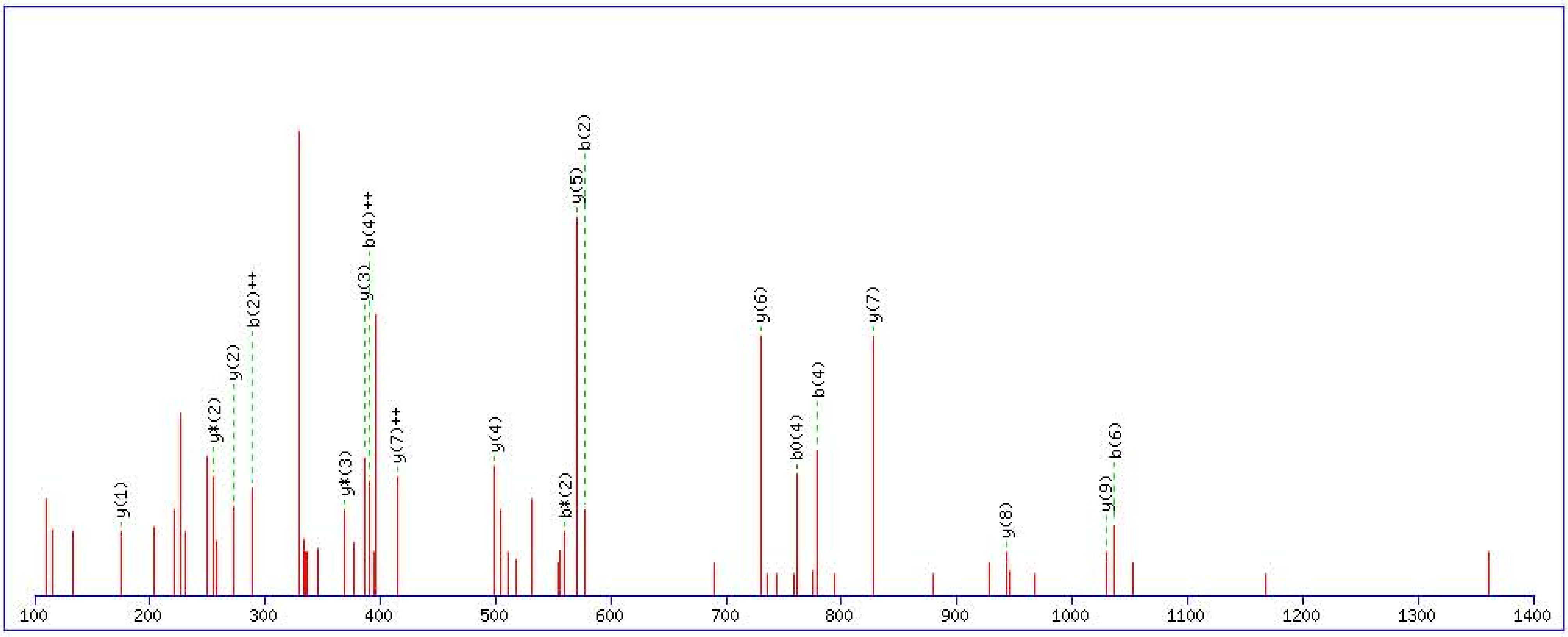
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QHSDPCALNPR**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

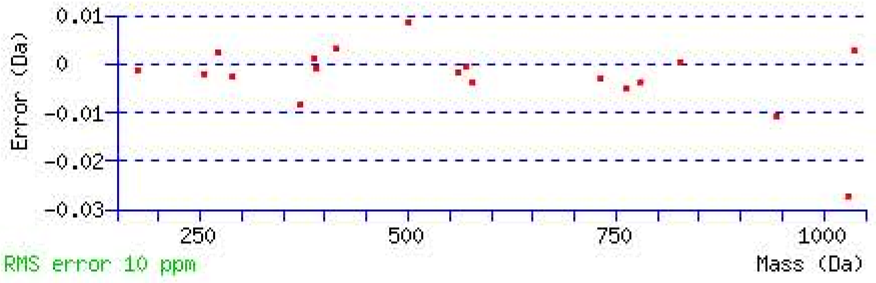
Match to Query 30690: 1604.748282 from(535.923370,3+) rtinseconds(1456) index(28522)
Title: Locus:1.1.1.3170.10 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

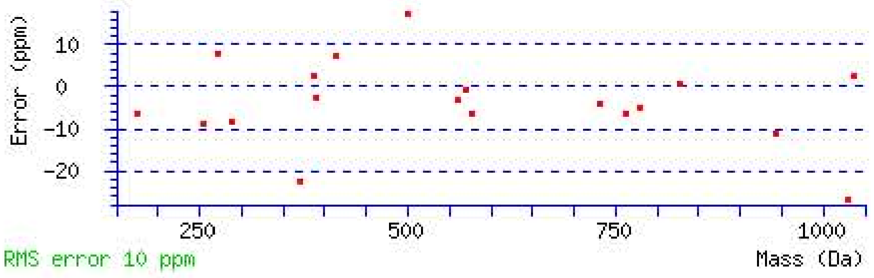
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1604.755157
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00014
Matches : 19/102 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	440.232602	220.619939	423.206053	212.106664			Q							11
2	**577.291514**	**289.149395**	560.264965	280.636121			H	1166.537117	583.772196	1149.510568	575.258922	1148.526552	574.766914	10
3	664.323542	332.665409	647.296993	324.152134	646.312977	323.660126	S	***1029.478205***	515.242740	1012.451656	506.729466	1011.467640	506.237458	9
4	**779.350485**	**390.178880**	762.323936	381.665606	761.339920	381.173598	D	***942.446177***	471.726726	925.419628	463.213452	924.435612	462.721444	8
5	876.403249	438.705263	859.376700	430.191988	858.392684	429.699980	P	***827.419234***	414.213255	810.392685	405.699980			7
6	**1036.433898**	518.720587	1019.407349	510.207313	1018.423333	509.715305	C	***730.366470***	365.686873	713.339921	357.173598			6
7	1107.471012	554.239144	1090.444463	545.725870	1089.460447	545.233861	A	***570.335821***	285.671548	553.309272	277.158274			5
8	1220.555076	610.781176	1203.528527	602.267901	1202.544511	601.775893	L	***499.298707***	250.152991	482.272158	241.639717			4
9	1334.598003	667.802639	1317.571454	659.289365	1316.587438	658.797357	N	***386.214643***	193.610959	369.188094	185.097685			3
10	1431.650767	716.329021	1414.624218	707.815747	1413.640202	707.323739	P	***272.171716***	136.589496	255.145167	128.076221			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of QHSDPCALNPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.2	1604.755157	-0.006875	QHSDPCALNPR
4.9	1604.747726	0.000556	IHNEERSYKCNR
0.7	1604.754288	-0.006006	GPSPASSSSSSPPAHPR
0.4	1604.732529	0.015753	GDVGDRGDKQQGMAR

Mascot: http://www.matrixscience.com/

{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILDELLQTCVDPEDCPVCEVAGR**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

Match to Query 53976: 2998.395192 from(1000.472340,3+) rtinseconds(2623) index(35388)
Title: Locus:1.1.1.3576.25 File:"2013-07-02 CLN FXIII 180 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\9 FXIII 180 min 3rd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 2998.390854
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 80  Expect: 4.3e-008
Matches : 25/240 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	114.091340	57.549308					I							23
2	***227.175404***	114.091340					L	2886.314052	1443.660664	2869.287503	1435.147389	2868.303487	1434.655381	22
3	***342.202347***	171.604811			324.191782	162.599529	D	2773.229988	1387.118632	2756.203439	1378.605357	2755.219423	1378.113349	21
4	***471.244940***	236.126108			453.234375	227.120826	E	2658.203045	1329.605160	2641.176496	1321.091886	2640.192480	1320.599878	20
5	***584.329004***	292.668140			566.318439	283.662858	L	2529.160452	1265.083864	2512.133903	1256.570589	2511.149887	1256.078581	19
6	***697.413068***	349.210172			679.402503	340.204890	L	2416.076388	1208.541832	2399.049839	1200.028557	2398.065823	1199.536549	18
7	***1136.638394***	568.822835	1119.611845	560.309561	1118.627829	559.817553	Q	2302.992324	1151.999800	2285.965775	1143.486525	2284.981759	1142.994517	17
8	***1237.686073***	619.346675	1220.659524	610.833400	1219.675508	610.341392	T	1863.766998	932.387137	1846.740449	923.873863	1845.756433	923.381855	16
9	1397.716722	699.361999	1380.690173	690.848725	1379.706157	690.356717	C	1762.719319	881.863298	1745.692770	873.350023	1744.708754	872.858015	15
10	1496.785136	748.896206	1479.758587	740.382932	1478.774571	739.890924	V	***1602.688670***	801.847973	1585.662121	793.334699	1584.678105	792.842691	14
11	***1611.812079***	806.409678	1594.785530	797.896403	1593.801514	797.404395	D	***1503.620256***	752.313766	1486.593707	743.800492	1485.609691	743.308483	13
12	1708.864843	854.936060	1691.838294	846.422785	1690.854278	845.930777	P	***1388.593313***	694.800294	1371.566764	686.287020	1370.582748	685.795012	12
13	1837.907436	919.457356	1820.880887	910.944082	1819.896871	910.452074	E	***1291.540549***	646.273912	1274.514000	637.760638	1273.529984	637.268630	11
14	1952.934379	976.970828	1935.907830	968.457553	1934.923814	967.965545	D	***1162.497956***	581.752616	1145.471407	573.239342	1144.487391	572.747333	10
15	2112.965028	1056.986152	2095.938479	1048.472877	2094.954463	1047.980869	C	***1047.471013***	524.239144	1030.444464	515.725870	1029.460448	515.233862	9
16	2210.017792	1105.512534	2192.991243	1096.999259	2192.007227	1096.507251	P	***887.440364***	444.223820	870.413815	435.710545	869.429799	435.218537	8
17	2309.086206	1155.046741	2292.059657	1146.533466	2291.075641	1146.041458	V	790.387600	395.697438	773.361051	387.184163	772.377035	386.692155	7
18	2469.116855	1235.062065	2452.090306	1226.548791	2451.106290	1226.056783	C	***691.319186***	346.163231	674.292637	337.649956	673.308621	337.157948	6
19	2598.159448	1299.583362	2581.132899	1291.070087	2580.148883	1290.578079	E	***531.288537***	266.147907	514.261988	257.634632	513.277972	257.142624	5
20	2697.227862	1349.117569	2680.201313	1340.604294	2679.217297	1340.112286	V	402.245944	201.626610	385.219395	193.113335			4
21	2768.264976	1384.636126	2751.238427	1376.122851	2750.254411	1375.630843	A	***303.177530***	152.092403	286.150981	143.579129			3
22	2825.286440	1413.146858	2808.259891	1404.633583	2807.275875	1404.141575	G	232.140416	116.573846	215.113867	108.060571			2
23							R	175.118952	88.063114	158.092403	79.549839			1

NCBI **BLAST** search of ILDELLQTCVDPEDCPVCEVAGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
80.1	2998.390854	0.004338	ILDELLQTCVDPEDCPVCEVAGR
1.5	2998.398026	-0.002834	VFQTYDPEDNGFIPDSLLEDVMK

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