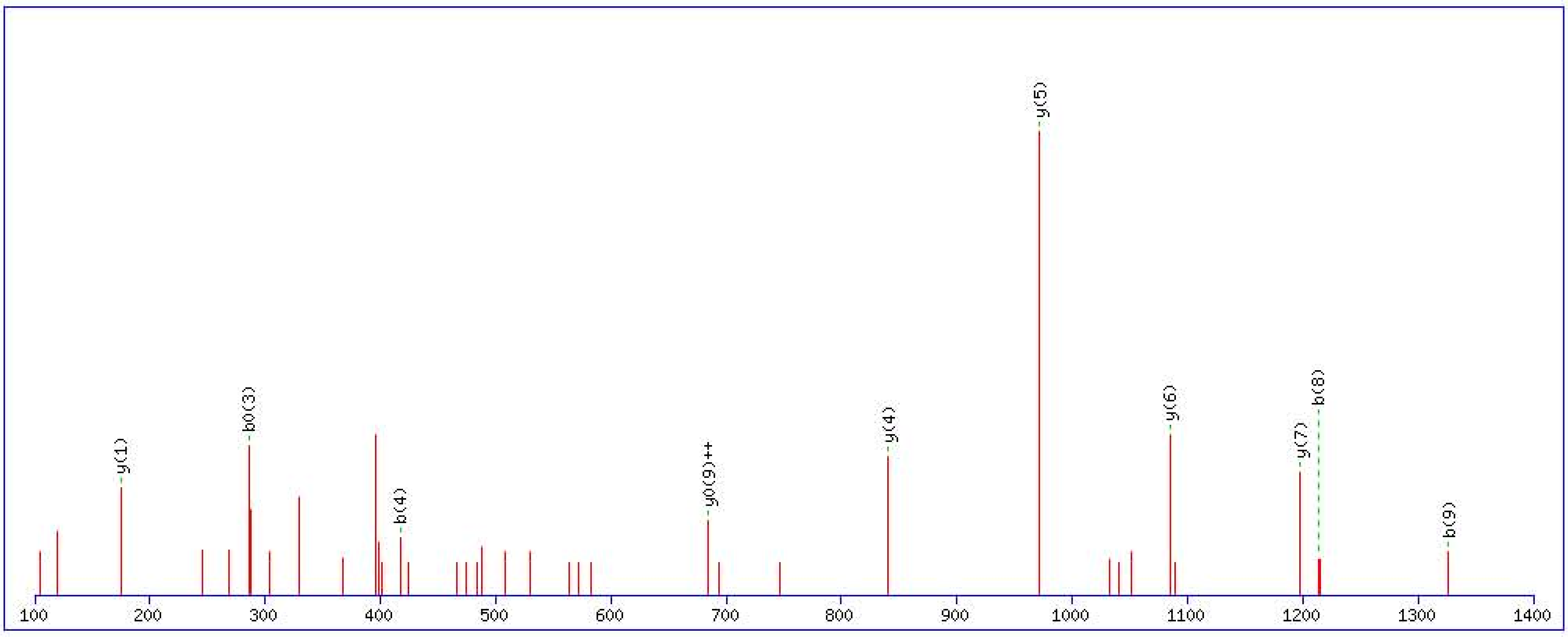
Mascot Search Results

Peptide View

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

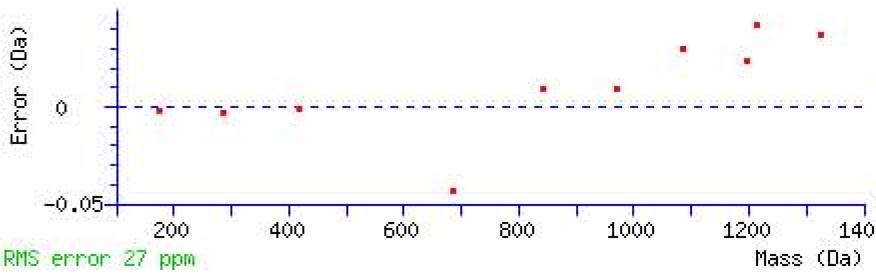
Match to Query 29889: 1499.841948 from(750.928250,2+) rtinseconds(2952) index(53690)
Title: Locus:1.1.1.3073.6 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

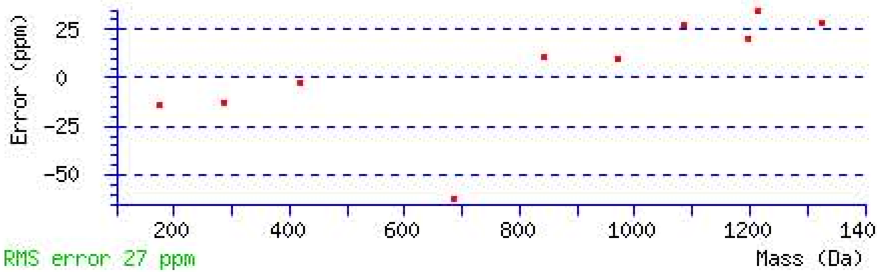
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1499.820374
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 36 **Expect:** 0.004
Matches : 10/82 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	116.034219	58.520748			98.023654	49.515465	D							10
2	203.066247	102.036761			185.055682	93.031479	S	1385.800726	693.404001	1368.774177	684.890726	1367.790161	684.398718	9
3	304.113926	152.560601			286.103361	143.555319	T	1298.768698	649.887987	1281.742149	641.374712	1280.758133	640.882704	8
4	**417.197990**	209.102633			399.187425	200.097351	L	***1197.721019***	599.364147	1180.694470	590.850873			7
5	530.282054	265.644665			512.271489	256.639383	I	***1084.636955***	542.822115	1067.610406	534.308841			6
6	661.322539	331.164908			643.311974	322.159625	M	***971.552891***	486.280083	954.526342	477.766809			5
7	1100.547865	550.777571	1083.521316	542.264296	1082.537300	541.772288	Q	***840.512406***	420.759841	823.485857	412.246566			4
8	**1213.631929**	607.319602	1196.605380	598.806328	1195.621364	598.314320	L	401.287080	201.147178	384.260531	192.633903			3
9	**1326.715993**	663.861634	1309.689444	655.348360	1308.705428	654.856352	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 DSTLIMQLLR
(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	1499.820374	0.021574	DSTLIMQLLR
19.0	1499.830719	0.011229	EEIVDKTRLIER
15.5	1499.860596	-0.018648	MTVGKKPVNLNKR
12.2	1499.819489	0.022459	SLSLVDNEIELLR
8.9	1499.824203	0.017745	MNKLGTRLVPAER
8.1	1499.830719	0.011229	IEALSSKVQQLER
7.8	1499.830704	0.011244	ALSSLQEELNKLR
7.8	1499.849350	-0.007402	LRLMNLLIDDIR
7.3	1499.845978	-0.004030	REPPSLLGYLSLR
7.2	1499.830704	0.011244	AQSENLELLSLKR

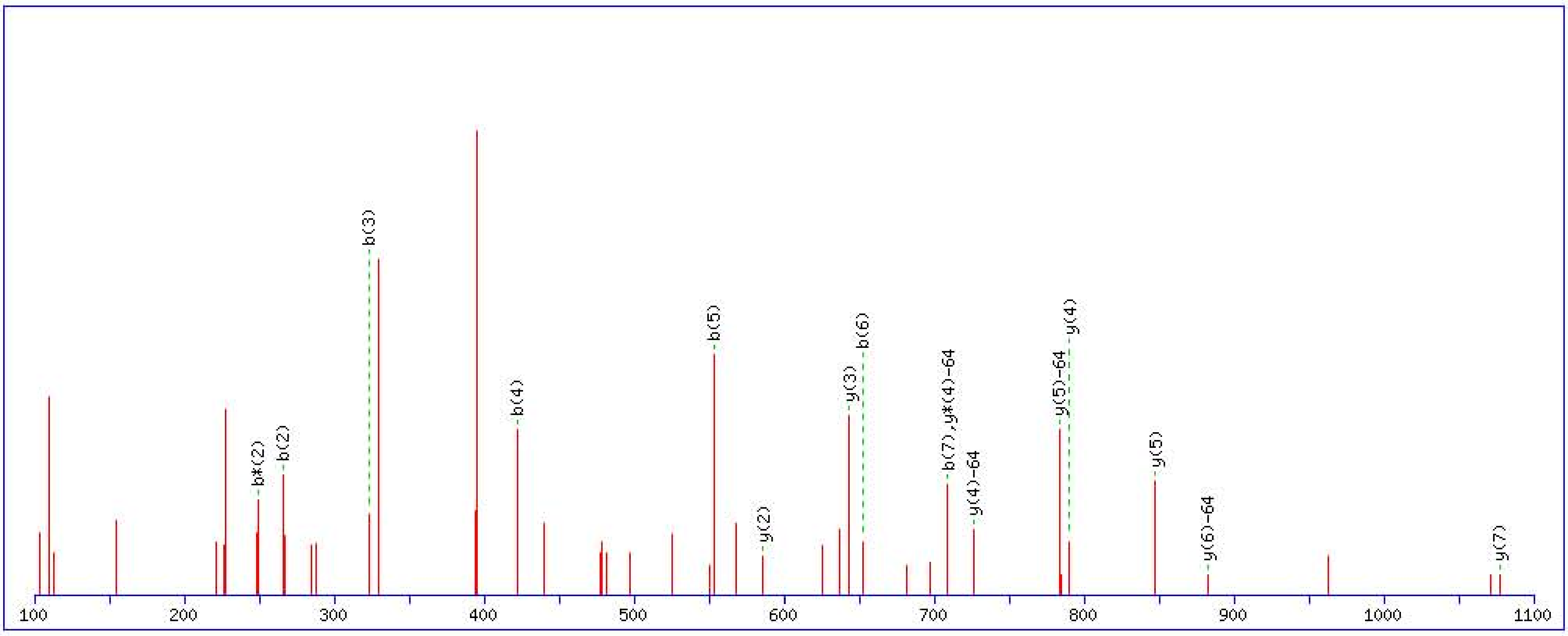
Mascot Search Results

Peptide View

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

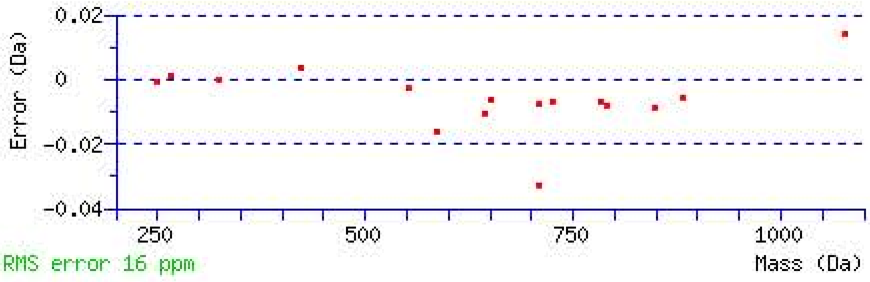
Match to Query 13460: 1497.722622 from(500.248150,3+) rtinseconds(1407) index(29670)
Title: Locus:1.1.1.3038.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

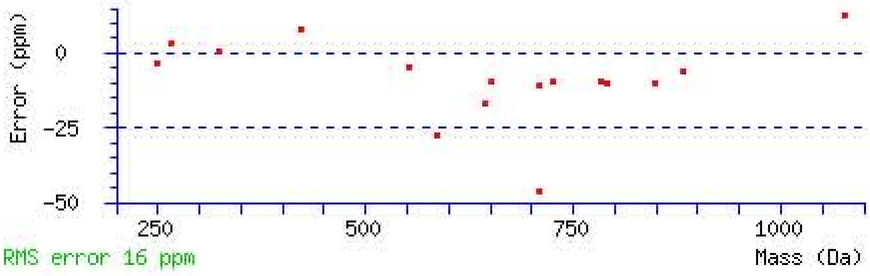
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1497.725464
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: 29  Expect: 0.053
Matches : 16/118 fragment ions using 33 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	1361.673813	681.340545	1344.647264	672.827270	10
3	***323.146230***	162.076753	306.119681	153.563478	G	1233.615235	617.311256	1216.588686	608.797981	9
4	***422.214644***	211.610960	405.188095	203.097685	V	1176.593771	588.800524	1159.567222	580.287249	8
5	***553.255129***	277.131203	536.228580	268.617928	M	***1077.525357***	539.266317	1060.498808	530.753042	7
6	***652.323543***	326.665410	635.296994	318.152135	V	946.484872	473.746074	929.458323	465.232800	6
7	***709.345007***	355.176142	692.318458	346.662867	G	***847.416458***	424.211867	830.389909	415.698593	5
8	856.380407	428.693842	839.353858	420.180567	M	***790.394994***	395.701135	773.368445	387.187861	4
9	913.401871	457.204574	896.375322	448.691299	G	***643.359594***	322.183435	626.333045	313.670161	3
10	1352.627197	676.817237	1335.600648	668.303962	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
28.9	1497.725464	-0.002842	HQGVMVGMGQK
1.5	1497.725464	-0.002842	HQGVMVGMGQK

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

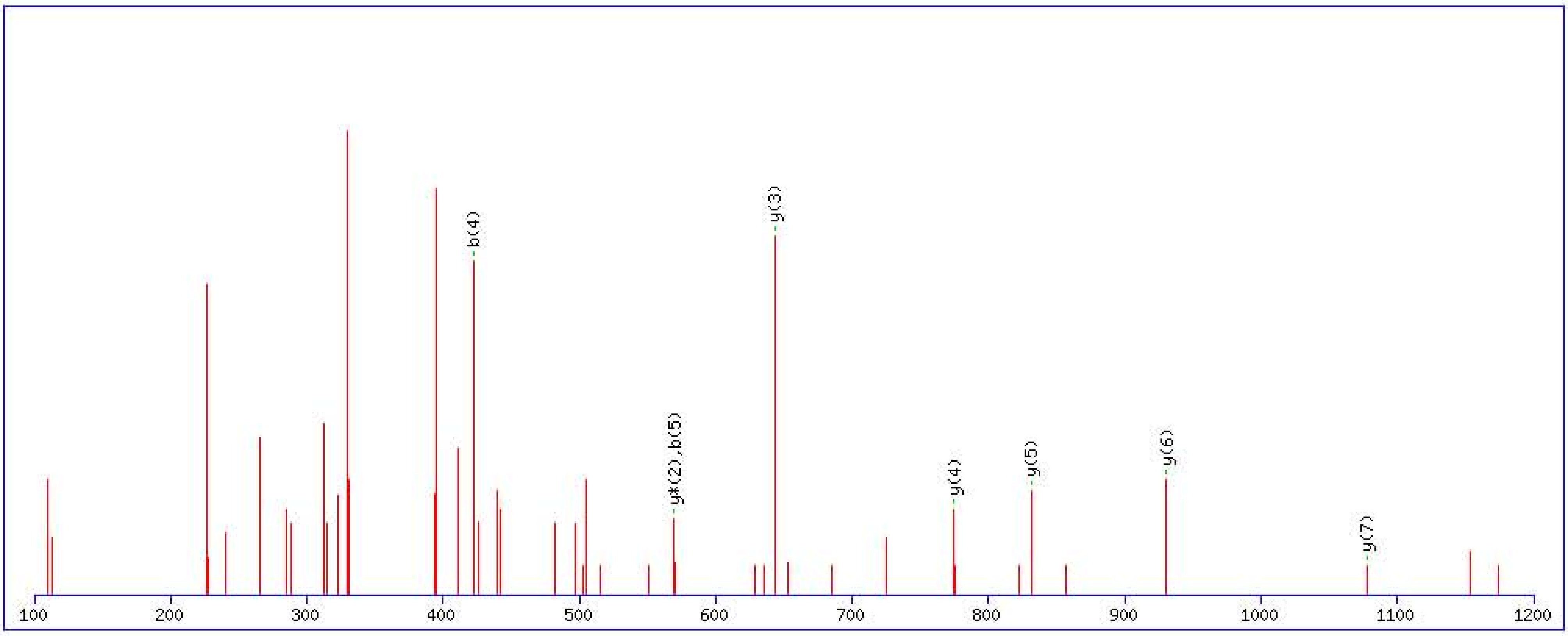
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

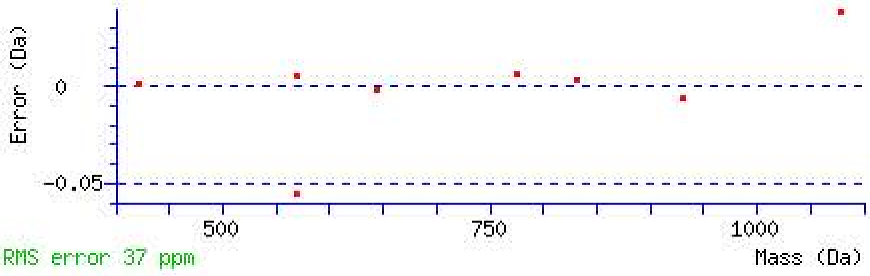
Match to Query 29848: 1497.727632 from(500.249820,3+) rtinseconds(1494) index(30242)
Title: Locus:1.1.1.3069.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

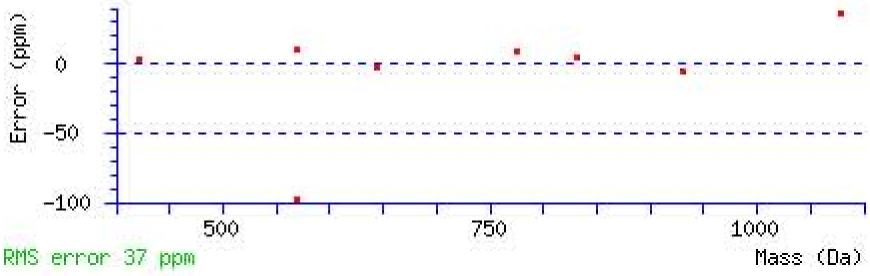
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1497.725464
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
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.019
Matches : 8/118 fragment ions using 11 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	1361.673813	681.340545	1344.647264	672.827270	10
3	323.146230	162.076753	306.119681	153.563478	G	1233.615235	617.311256	1216.588686	608.797981	9
4	**422.214644**	211.610960	405.188095	203.097685	V	1176.593771	588.800524	1159.567222	580.287249	8
5	**569.250044**	285.128660	552.223495	276.615386	M	***1077.525357***	539.266317	1060.498808	530.753042	7
6	668.318458	334.662867	651.291909	326.149592	V	***930.489957***	465.748617	913.463408	457.235342	6
7	725.339922	363.173599	708.313373	354.660325	G	***831.421543***	416.214410	814.394994	407.701135	5
8	856.380407	428.693842	839.353858	420.180567	M	***774.400079***	387.703678	757.373530	379.190403	4
9	913.401871	457.204574	896.375322	448.691299	G	***643.359594***	322.183435	626.333045	313.670161	3
10	1352.627197	676.817237	1335.600648	668.303962	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
28.9	1497.725464	0.002168	HQGVMVGMGQK
0.6	1497.725464	0.002168	HQGVMVGMGQK

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

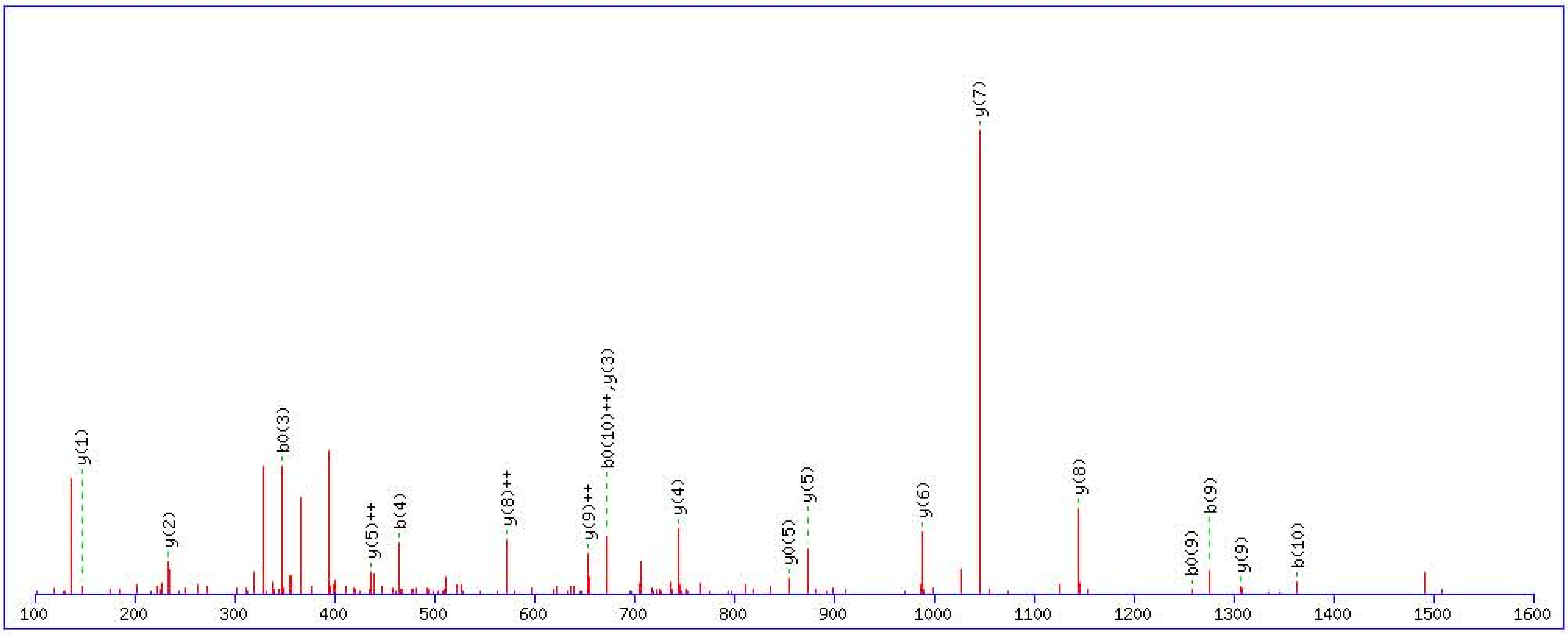
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

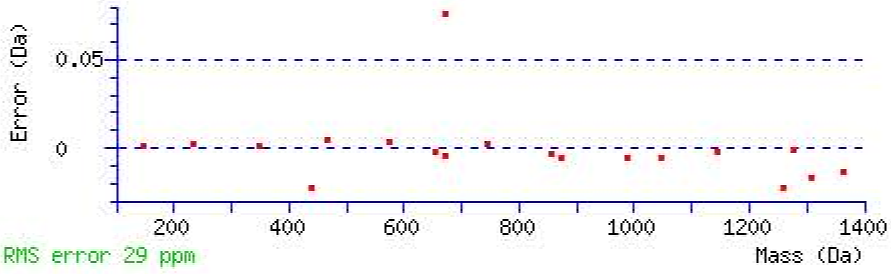
Match to Query 30200: 1508.677668 from(755.346110,2+) rtinseconds(1578) index(30725)
Title: Locus:1.1.1.3098.17 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

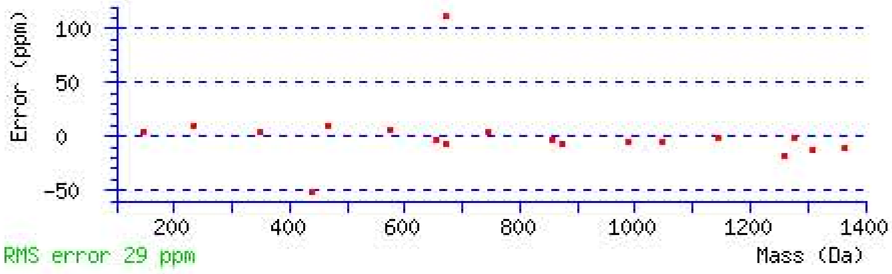
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 71 **Expect:** 8.8e-007
Matches : 19/102 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	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
70.5	1508.681702	-0.004034	DSYVGDEAQSK
9.4	1508.690277	-0.012609	GGRGGMGGSDRGGFNK
3.0	1508.659912	0.017756	QQAMPSTGMAEQSK

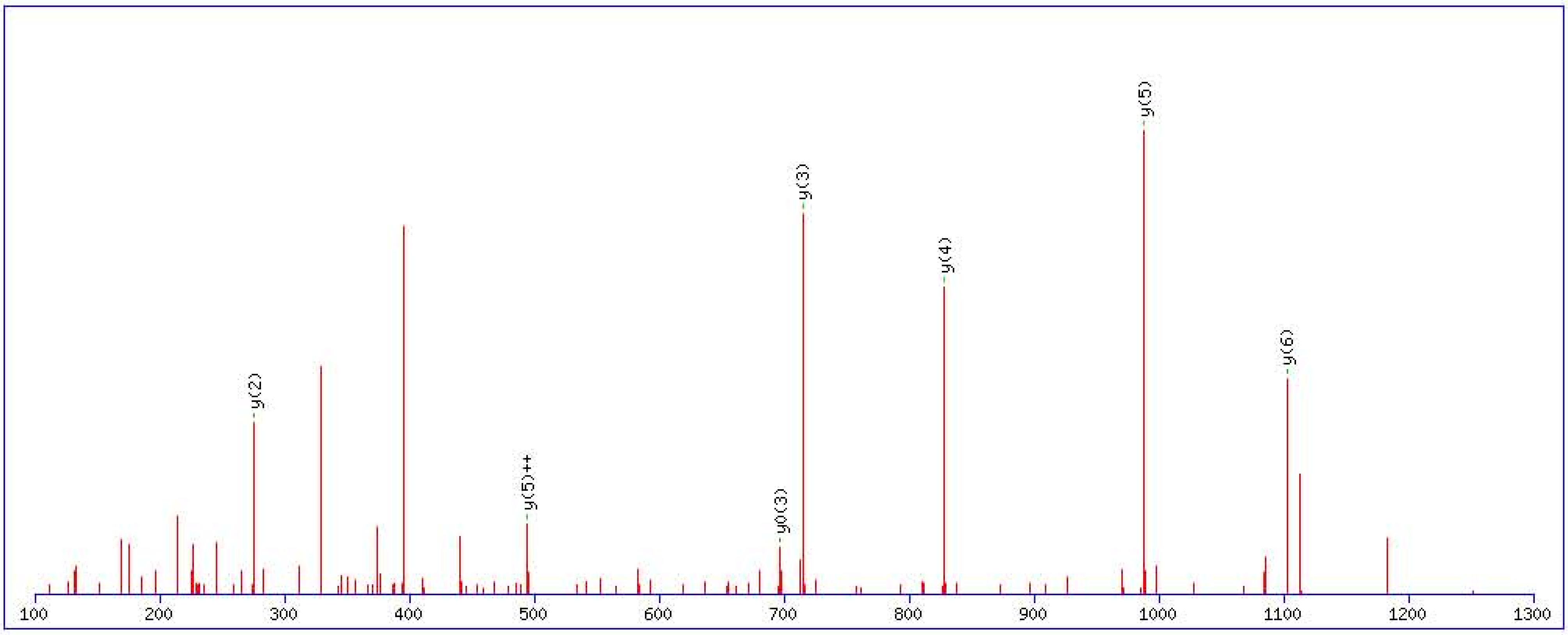
Mascot Search Results

Peptide View

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

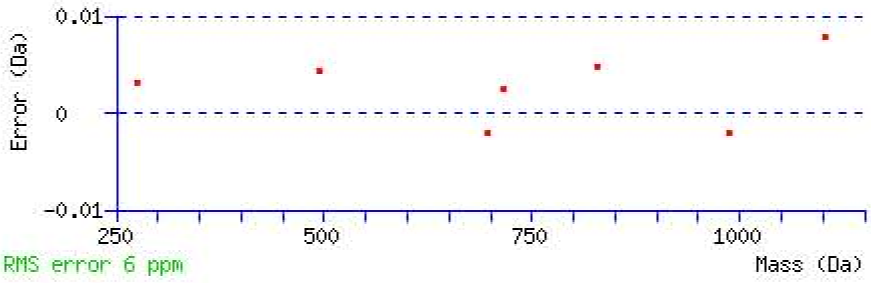
Match to Query 20350: 1200.609548 from(601.312050,2+) rtinseconds(1535) index(2293)
Title: Locus:1.1.1.3086.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

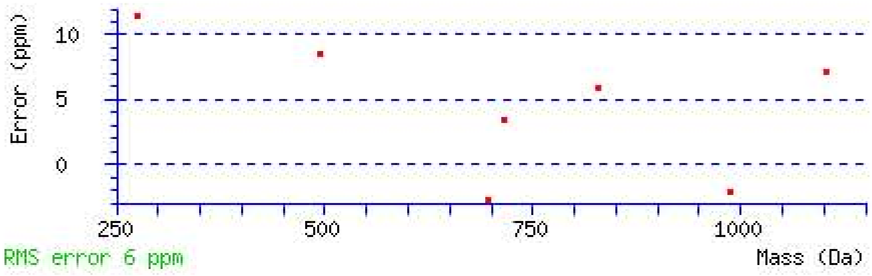
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1200.610733
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.003
Matches : 7/58 fragment ions using 11 most intense peaks    (help)
```

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





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.2	1200.610733	-0.001185	VNCLQTR
6.9	1200.621094	-0.011546	ESRPVQQTTR
5.4	1200.603333	0.006215	GRIAEPSVCGR
1.7	1200.592087	0.017461	SATEQQAR
1.3	1200.611191	-0.001643	HDSHLAKHTR
0.3	1200.621948	-0.012400	VNMLKHCKR

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

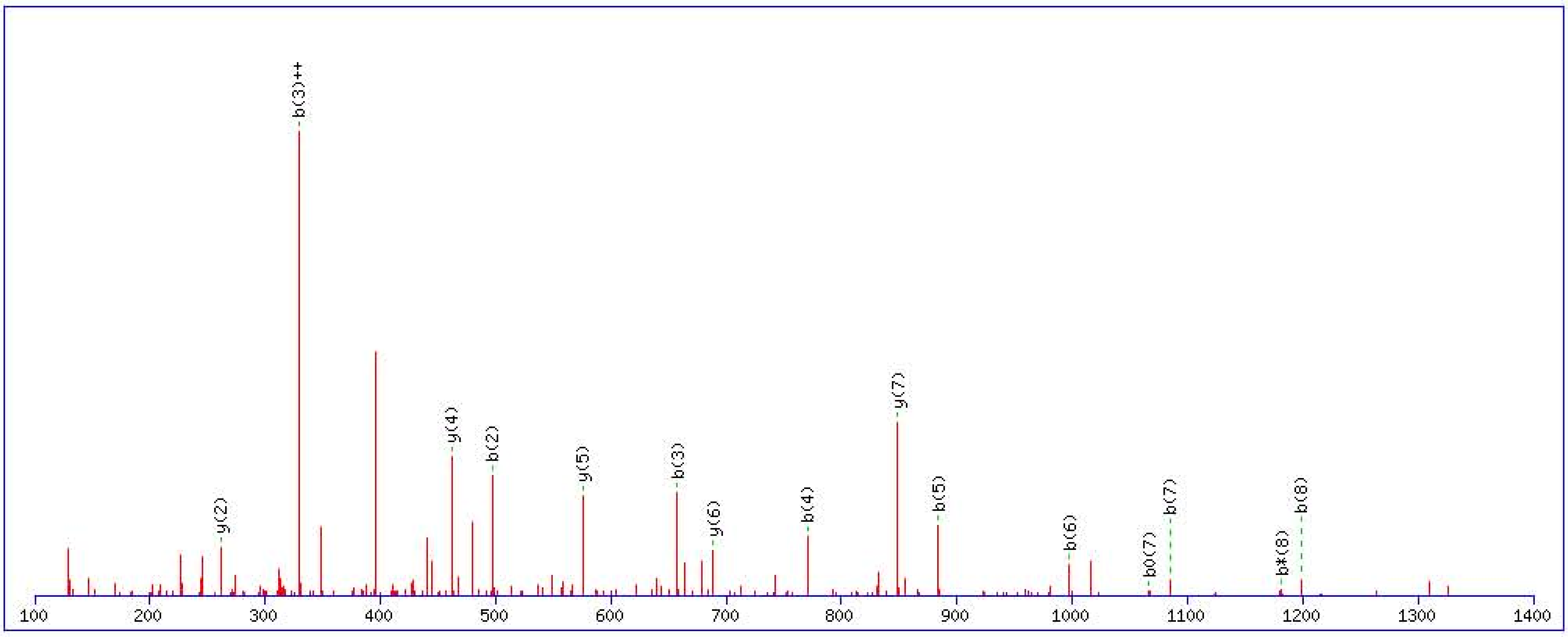
Mascot Search Results

Peptide View

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

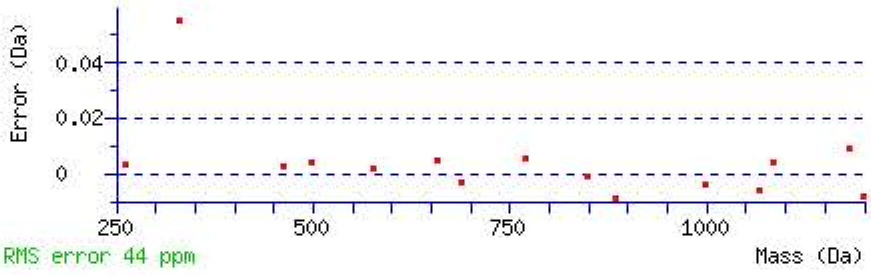
Match to Query 23867: 1343.667108 from(672.840830,2+) rtinseconds(1621) index(2863)
Title: Locus:1.1.1.3116.19 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

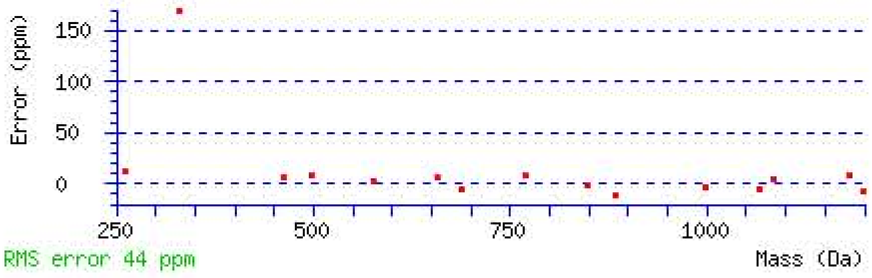
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1343.668961
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.00026
Matches : 15/78 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							9
2	*497.254066*	249.130671	480.227517	240.617397			Q	1287.654789	644.331033	1270.628240	635.817758	1269.644224	635.325750	8
3	*657.284715*	329.145996	640.258166	320.632721			C	**848.429463**	424.718370	831.402914	416.205095	830.418898	415.713087	7
4	*770.368779*	385.688028	753.342230	377.174753			I	**688.398814**	344.703045	671.372265	336.189771	670.388249	335.697763	6
5	*883.452843*	442.230060	866.426294	433.716785			I	**575.314750**	288.161013	558.288201	279.647739	557.304185	279.155731	5
6	*997.495770*	499.251523	980.469221	490.738249			N	**462.230686**	231.618981	445.204137	223.105706	444.220121	222.613698	4
7	*1084.527798*	542.767537	1067.501249	534.254263	1066.517233	533.762255	S	348.187759	174.597517	331.161210	166.084243	330.177194	165.592235	3
8	*1198.570725*	599.789001	1181.544176	591.275726	1180.560160	590.783718	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 GQCIINSNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.6	1343.668961	-0.001853	GQCIINSNK
9.8	1343.654358	0.012750	QSLNQFMAVYK
8.5	1343.661591	0.005517	GIGTGHTSMNKGGK
7.3	1343.661575	0.005533	KISSKGHCQGDK
6.1	1343.686707	-0.019599	QPSSAKSSNK
4.4	1343.657745	0.009363	QGGEPVSTMK
3.4	1343.679306	-0.012198	QAQSRAQEALDK
2.0	1343.675476	-0.008368	DKAEQLDSK
1.2	1343.650314	0.016794	EKLQEHMTSNK
1.2	1343.656876	0.010232	TNLDESDVQPVK

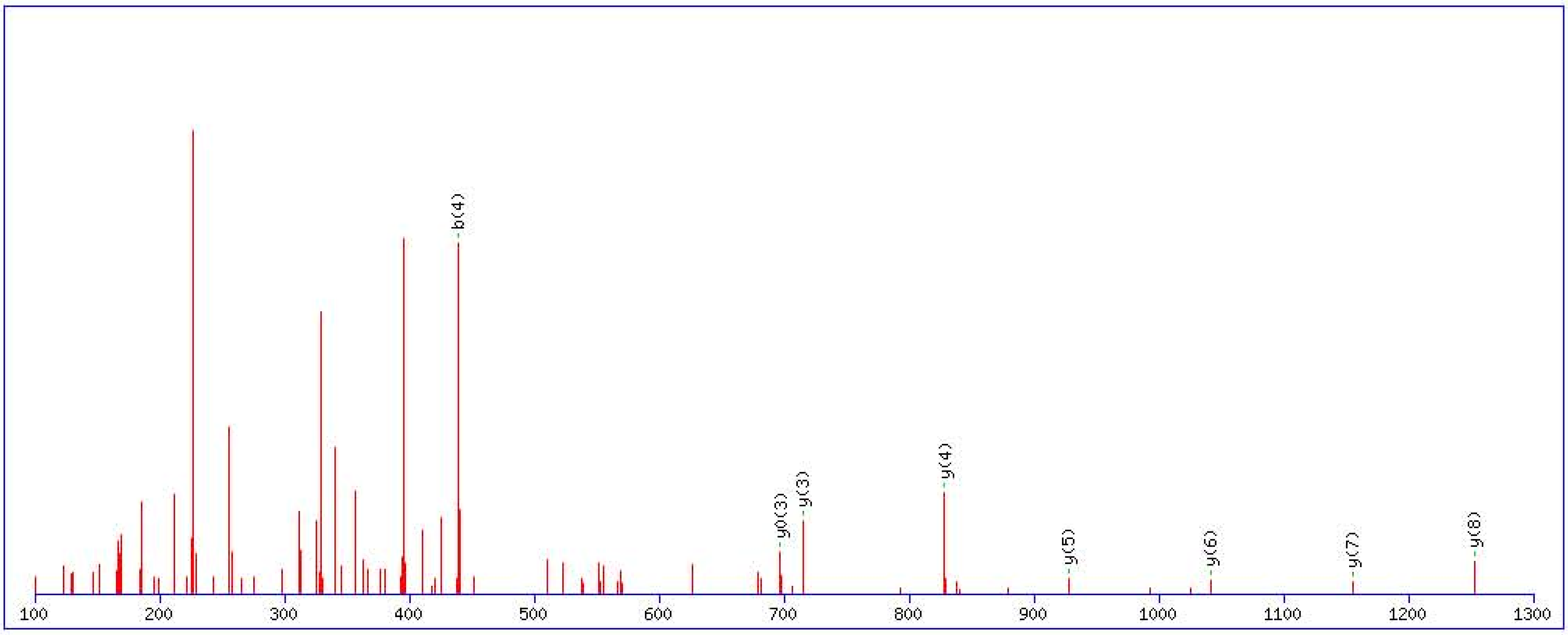
Mascot Search Results

Peptide View

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

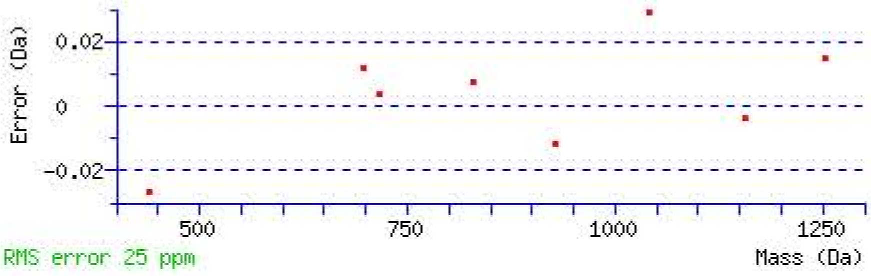
Match to Query 25235: 1364.749182 from(455.923670,3+) rtinseconds(1867) index(4068)
Title: Locus:1.1.1.3202.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

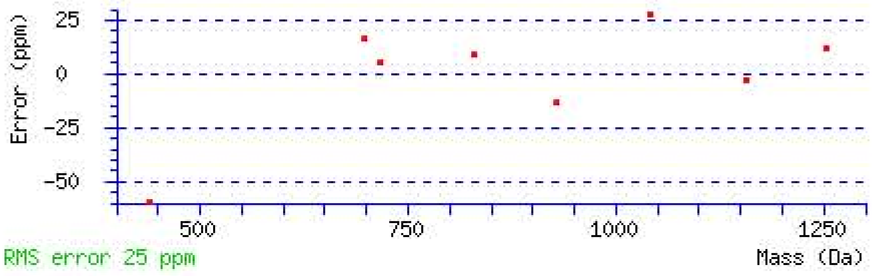
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1364.748581
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.0024
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	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
38.8	1364.748581	0.000601	LPNNVLQEK

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

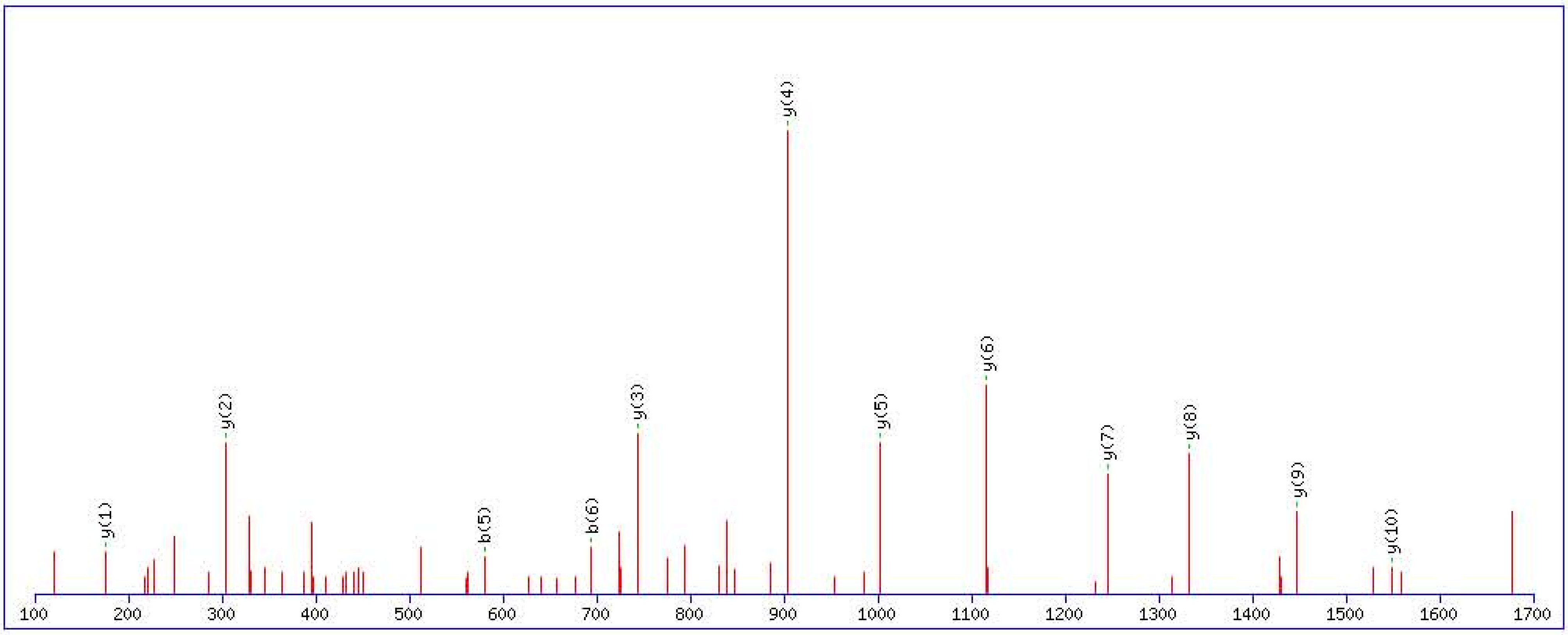
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

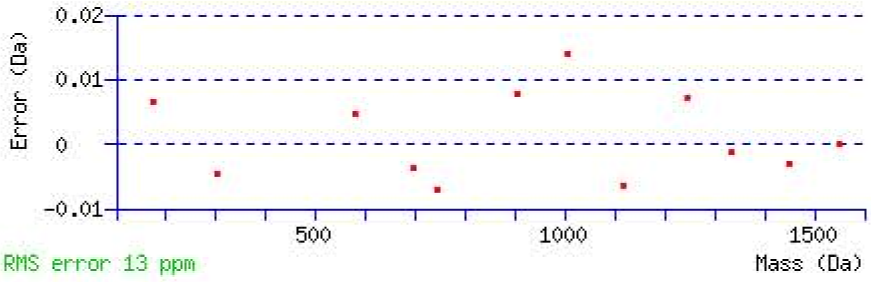
Match to Query 36308: 1694.735408 from(848.374980,2+) rtinseconds(1602) index(2695)
Title: Locus:1.1.1.3109.26 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

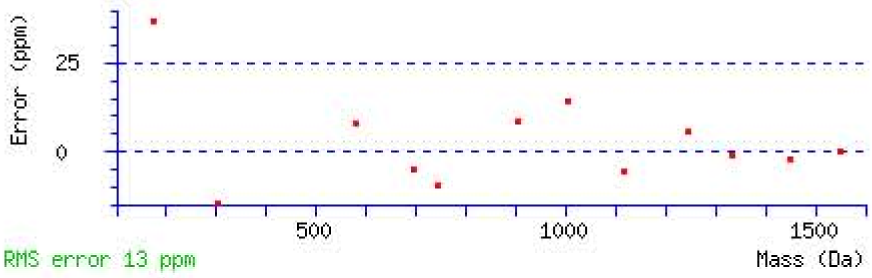
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1694.739243
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 97 **Expect:** 9.7e-010
Matches : 12/106 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	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





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
96.7	1694.739243	-0.003835	FTDSENVCQER
0.3	1694.710068	0.025340	RCVMDDDNEVRDR

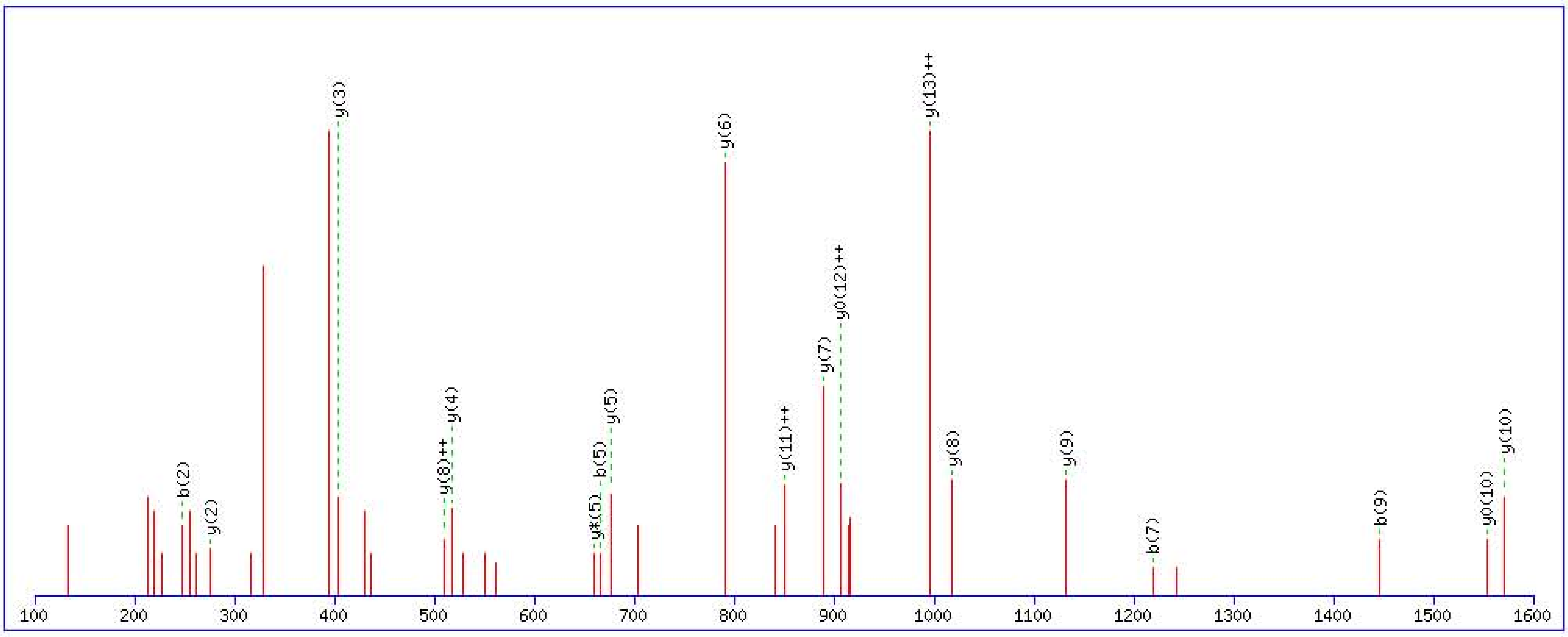
Mascot Search Results

Peptide View

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

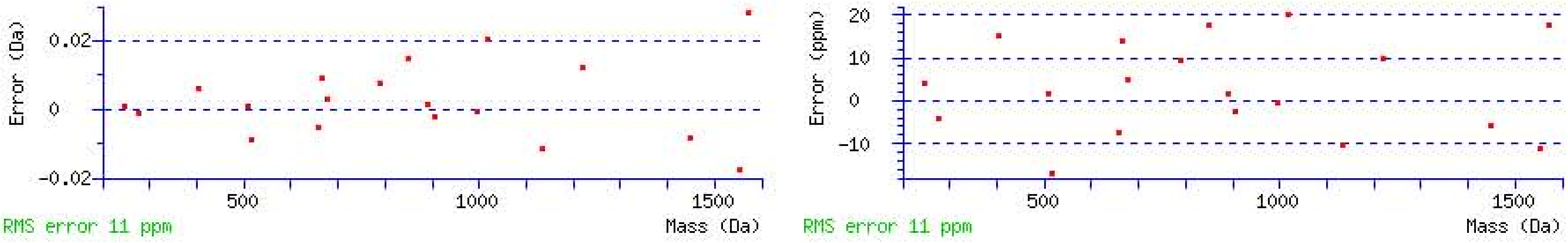
Match to Query 46660: 2235.981552 from(746.334460,3+) rtinseconds(1482) index(1903)
Title: Locus:1.1.1.3067.26 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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: 48 **Expect:** 8.9e-005
Matches : 19/156 fragment ions using 35 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							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
47.8	2235.985703	-0.004151	SCCEEQNKVNCLQTR
0.1	2235.985703	-0.004151	SCCEEQNKVNCLQTR

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

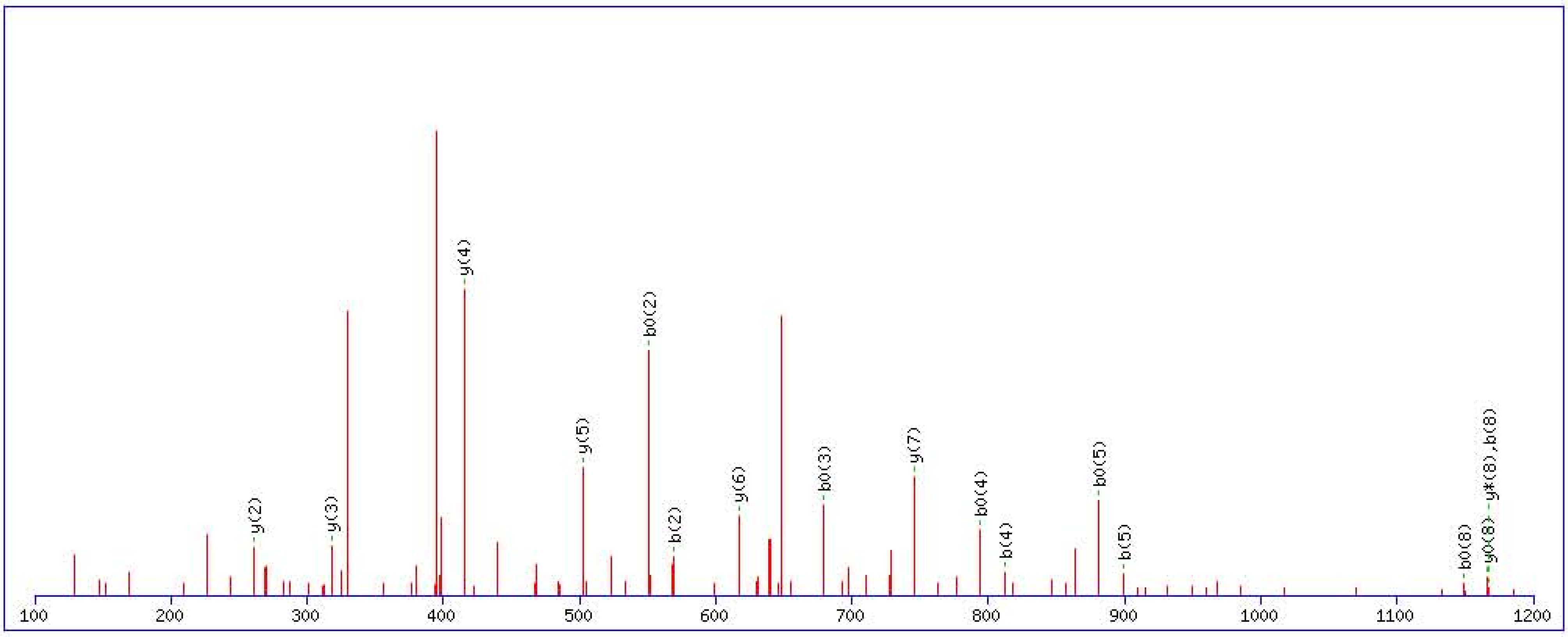
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

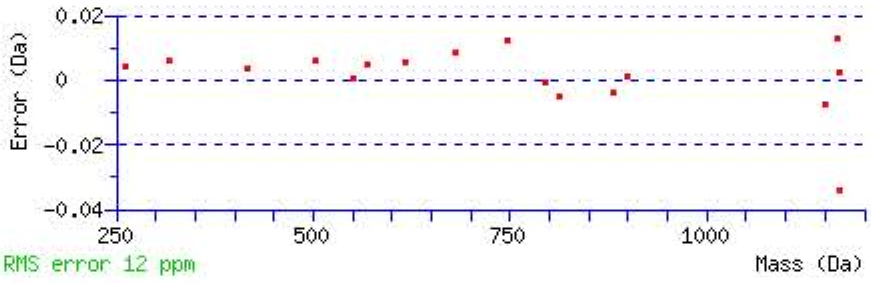
Match to Query 23266: 1312.611928 from(657.313240,2+) rtinseconds(1191) index(601)
Title: Locus:1.1.1.2966.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

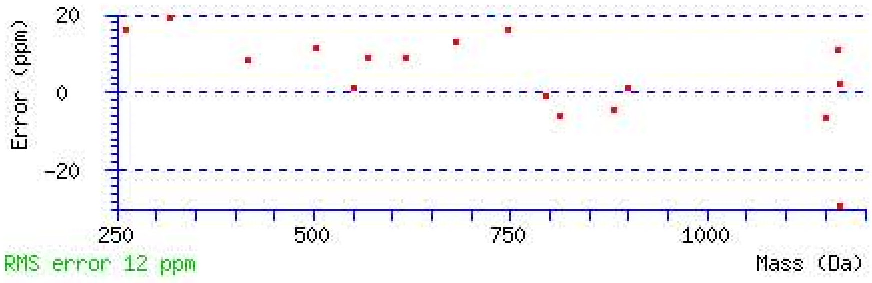
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 33 **Expect:** 0.0028
Matches : 17/86 fragment ions using 31 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	130.049869	65.528572			112.039304	56.523290	E							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
33.2	1312.608139	0.003789	EQQDSPGNK
20.0	1312.608139	0.003789	EQQDSPGNK
5.7	1312.625900	-0.013972	QEAVHTDSLEGK
4.9	1312.596878	0.015050	KYMEENDQLK
4.4	1312.626770	-0.014842	QQASPSCPK
3.9	1312.608124	0.003804	KDMNETFREK
3.7	1312.626770	-0.014842	QQASPSCPK
2.3	1312.596878	0.015050	YMEENDQLKK
1.2	1312.596909	0.015019	EPQEPEVCPTK
0.4	1312.601624	0.010304	CGECGKAFTRK

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

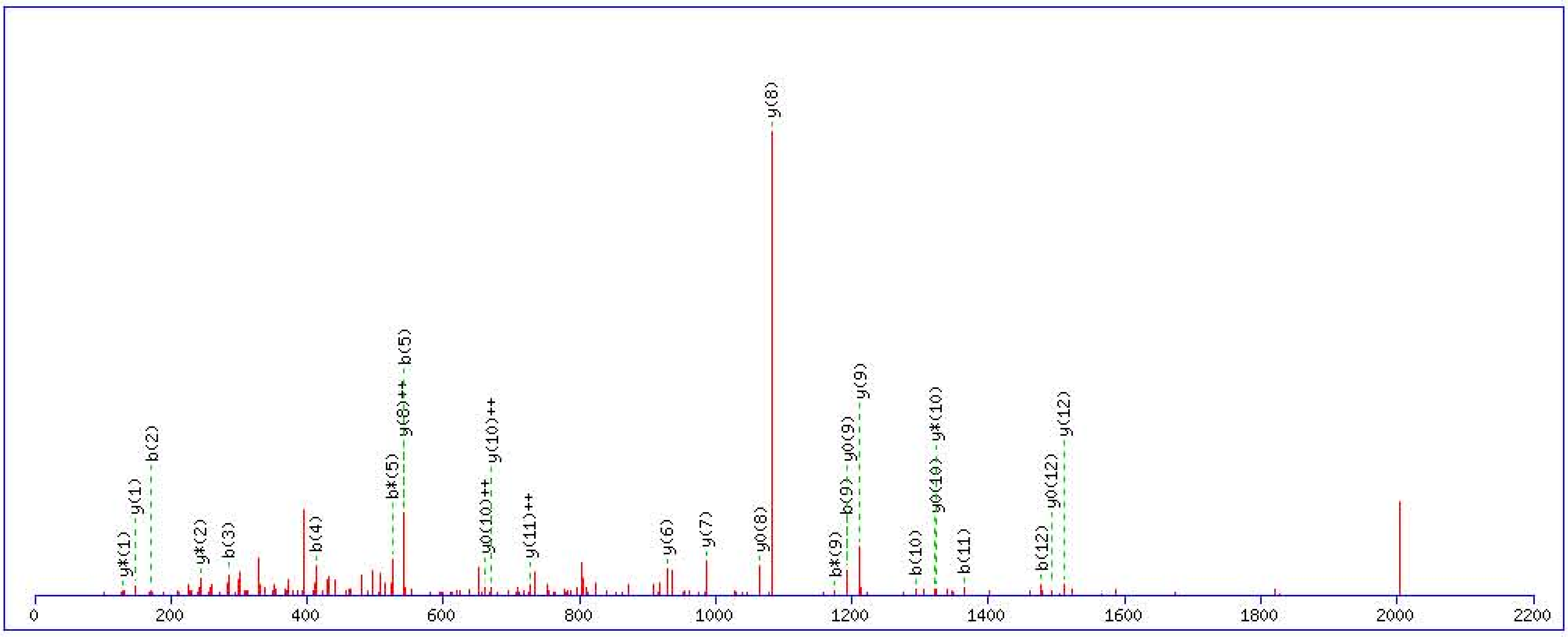
Mascot Search Results

Peptide View

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

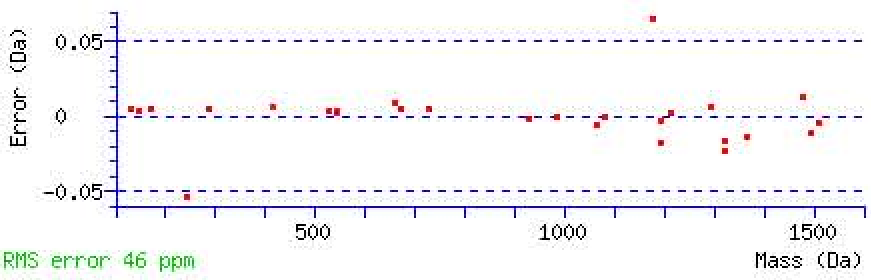
Match to Query 34261: 1622.846108 from(812.430330,2+) rtinseconds(1624) index(60585)
Title: Locus:1.1.1.3191.19 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

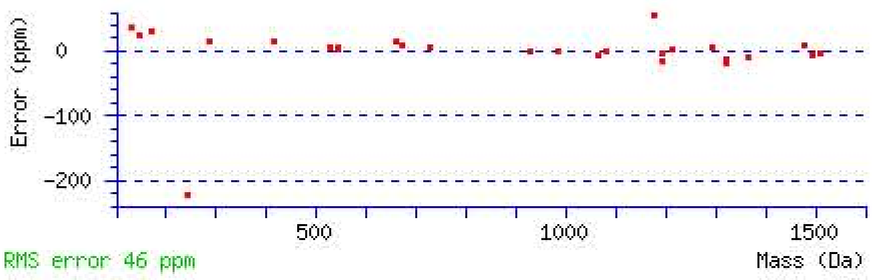
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1622.845016
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9     : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 4.3e-005
Matches : 27/126 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	114.091340	57.549308					L							13
2	***171.112804***	86.060040					G	***1510.768241***	755.887759	1493.741692	747.374484	1492.757676	746.882476	12
3	***285.155731***	143.081504	268.129182	134.568229			N	1453.746777	727.377027	1436.720228	718.863752	1435.736212	718.371744	11
4	***413.214309***	207.110793	396.187760	198.597518			Q	1339.703850	670.355563	1322.677301	661.842289	1321.693285	661.350281	10
5	***542.256902***	271.632089	525.230353	263.118815	524.246337	262.626807	E	***1211.645272***	606.326274	1194.618723	597.813000	1193.634707	597.320991	9
6	639.309666	320.158471	622.283117	311.645197	621.299101	311.153189	P	***1082.602679***	541.804978	1065.576130	533.291703	1064.592114	532.799695	8
7	696.331130	348.669203	679.304581	340.155929	678.320565	339.663921	G	***985.549915***	493.278596	968.523366	484.765321	967.539350	484.273313	7
8	753.352594	377.179935	736.326045	368.666661	735.342029	368.174653	G	***928.528451***	464.767864	911.501902	456.254589	910.517886	455.762581	6
9	***1192.577920***	596.792598	1175.551371	588.279324	1174.567355	587.787316	Q	871.506987	436.257132	854.480438	427.743857	853.496422	427.251849	5
10	***1293.625599***	647.316438	1276.599050	638.803163	1275.615034	638.311155	T	432.281661	216.644468	415.255112	208.131194	414.271096	207.639186	4
11	***1364.662713***	682.834995	1347.636164	674.321720	1346.652148	673.829712	A	331.233982	166.120629	314.207433	157.607354			3
12	***1477.746777***	739.377027	1460.720228	730.863752	1459.736212	730.371744	L	260.196868	130.602072	243.170319	122.088797			2
13							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.7	1622.845016	0.001092	LGNQEPGGQTALK
29.0	1622.845016	0.001092	LGNQEPGGQTALK
9.5	1622.858917	-0.012809	SVLLMELEVNYGLK
7.7	1622.849045	-0.002937	IPMPDFDLHLKGPK
7.5	1622.831085	0.015023	GLNPNPSHQMTKRK
7.5	1622.833771	0.012337	LDLAGRDLTDYLMK
3.5	1622.852890	-0.006782	QFEFVGSAPTRRTK
2.7	1622.863632	-0.017524	KRMILSTISWMGGK
2.2	1622.837601	0.008507	SQSEKQTYLEVRR
2.0	1622.864105	-0.017997	IWIPHSSGSSRLQR

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

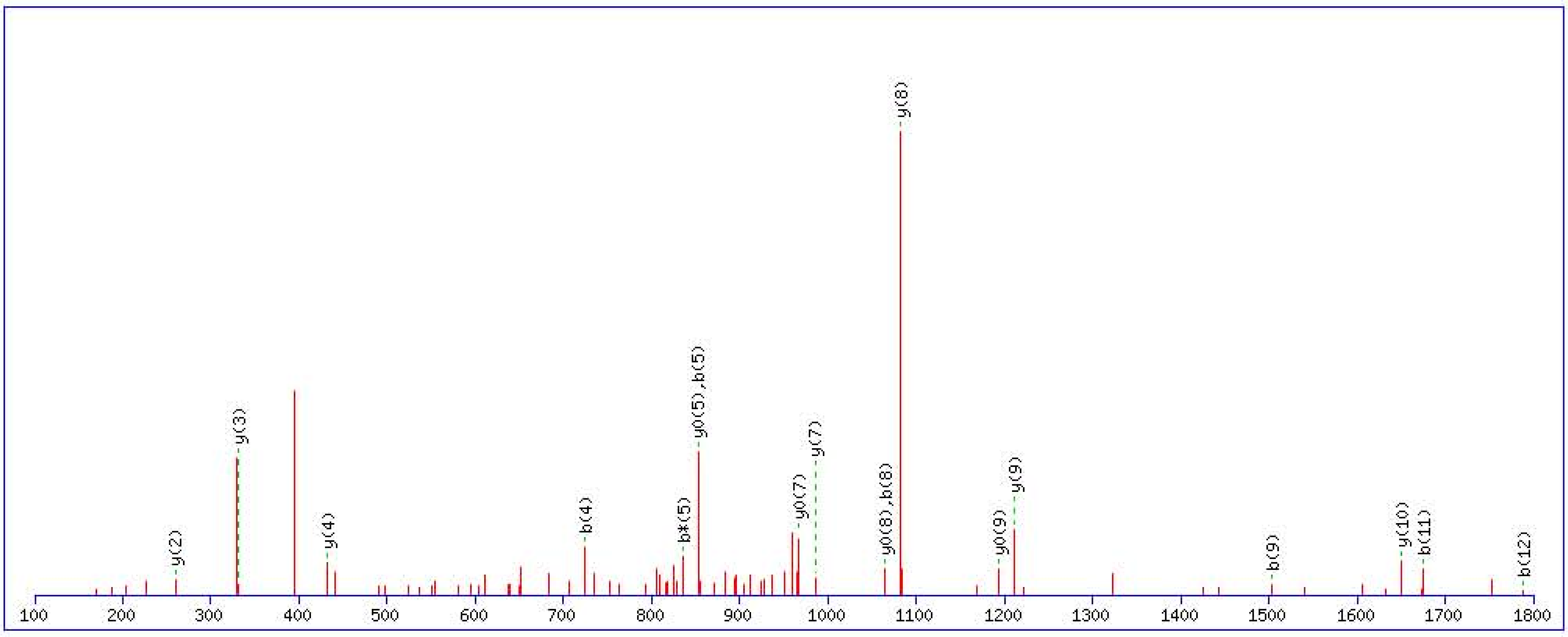
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

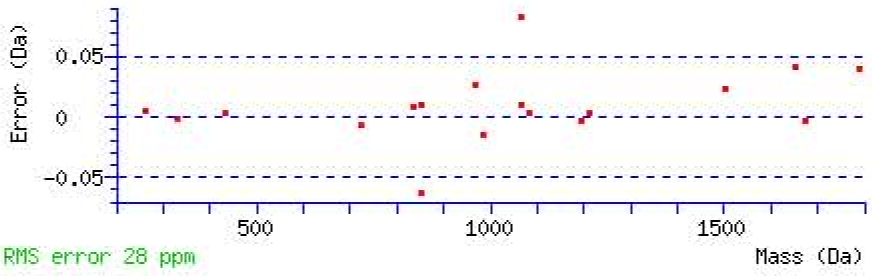
Match to Query 40833: 1934.008828 from(968.011690,2+) rtinseconds(1984) index(4871)
Title: Locus:1.1.1.3242.17 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

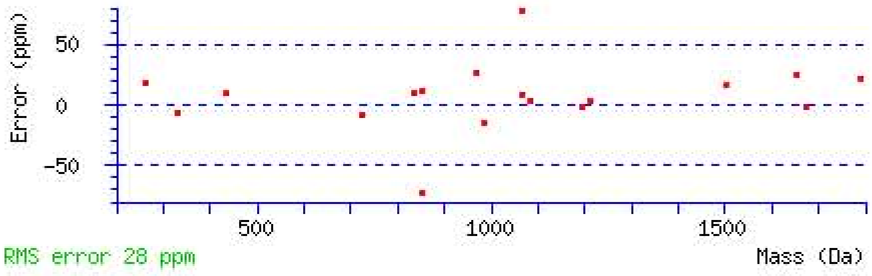
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 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: 39 **Expect:** 0.0059
Matches : 18/126 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							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
38.7	1934.011765	-0.002937	LGNQEPGGQTALK
9.3	1934.032867	-0.024039	KSRPLTGLMDLAKEMTK
9.2	1933.982758	0.026070	TVSKLNQEIWMMK
9.2	1933.982758	0.026070	TVSKLNQEIWMMK
5.5	1934.015594	-0.006766	RCRTTYSASQLHTLIK
1.3	1934.027008	-0.018180	VSFRLHITEPKMMFAK
0.7	1934.037369	-0.028541	NYLEGIYNVPVAAVRTR
0.2	1934.032867	-0.024039	KSRPLTGLMDLAKEMTK

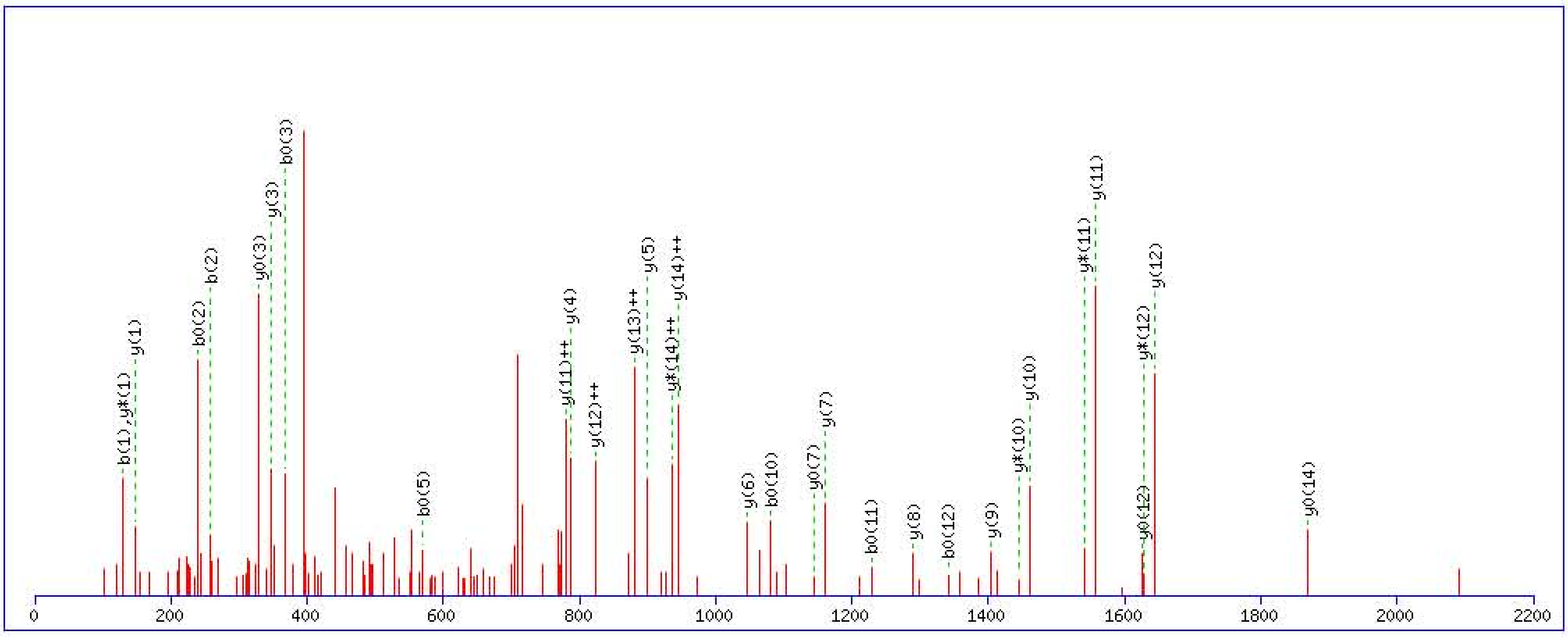
Mascot Search Results

Peptide View

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

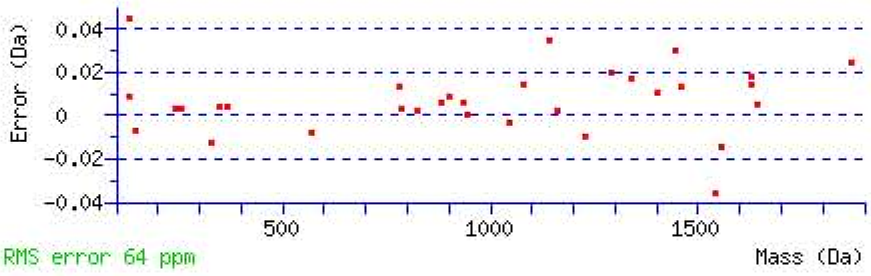
Match to Query 45066: 2144.061102 from(715.694310,3+) rtinseconds(2034) index(5130)
Title: Locus:1.1.1.3260.13 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

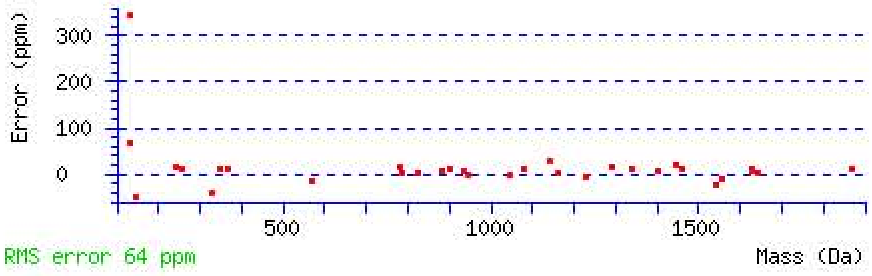
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 56  Expect: 6.6e-005
Matches : 32/174 fragment ions using 62 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							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
55.8	2144.057190	0.003912	EQQDSPGNKDFLQSLK

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

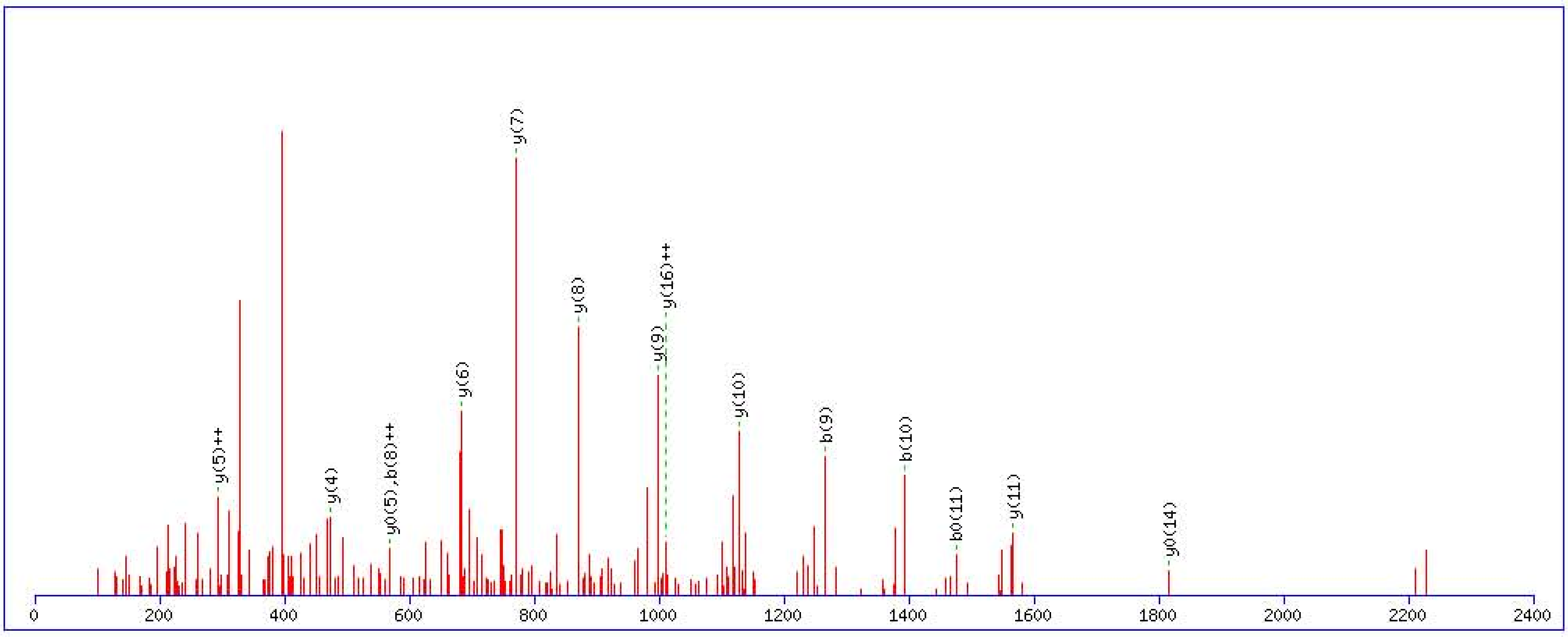
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

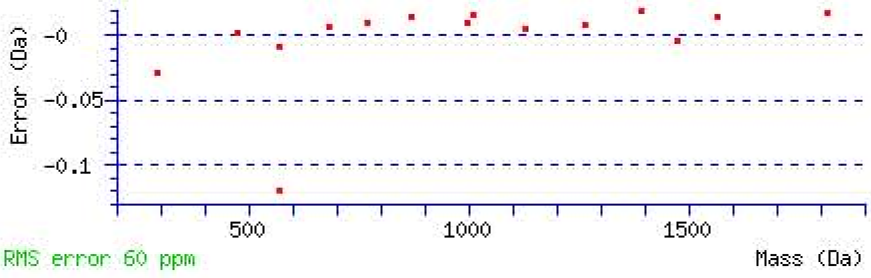
Match to Query 47154: 2263.236792 from(755.419540,3+) rtinseconds(2530) index(7730)
Title: Locus:1.1.1.3433.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

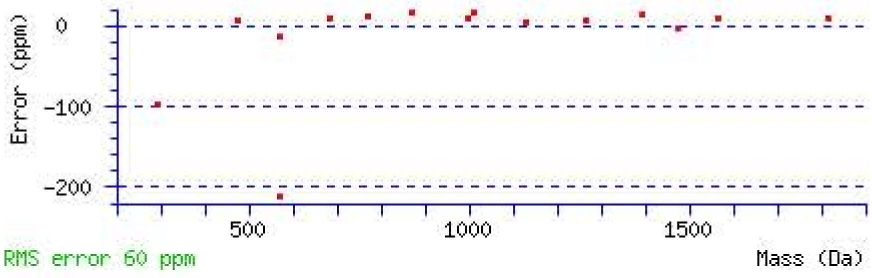
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2263.224594
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 53 **Expect:** 9.2e-005
Matches : 15/194 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
52.6	2263.224594	0.012198	QLTSGPNQEQVSPLTLLK
31.4	2263.224594	0.012198	QLTSGPNQEQVSPLTLLK
22.2	2263.224594	0.012198	QLTSGPNQEQVSPLTLLK
10.7	2263.224594	0.012198	GLALSSNKVKSVVMVVFDNEK

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

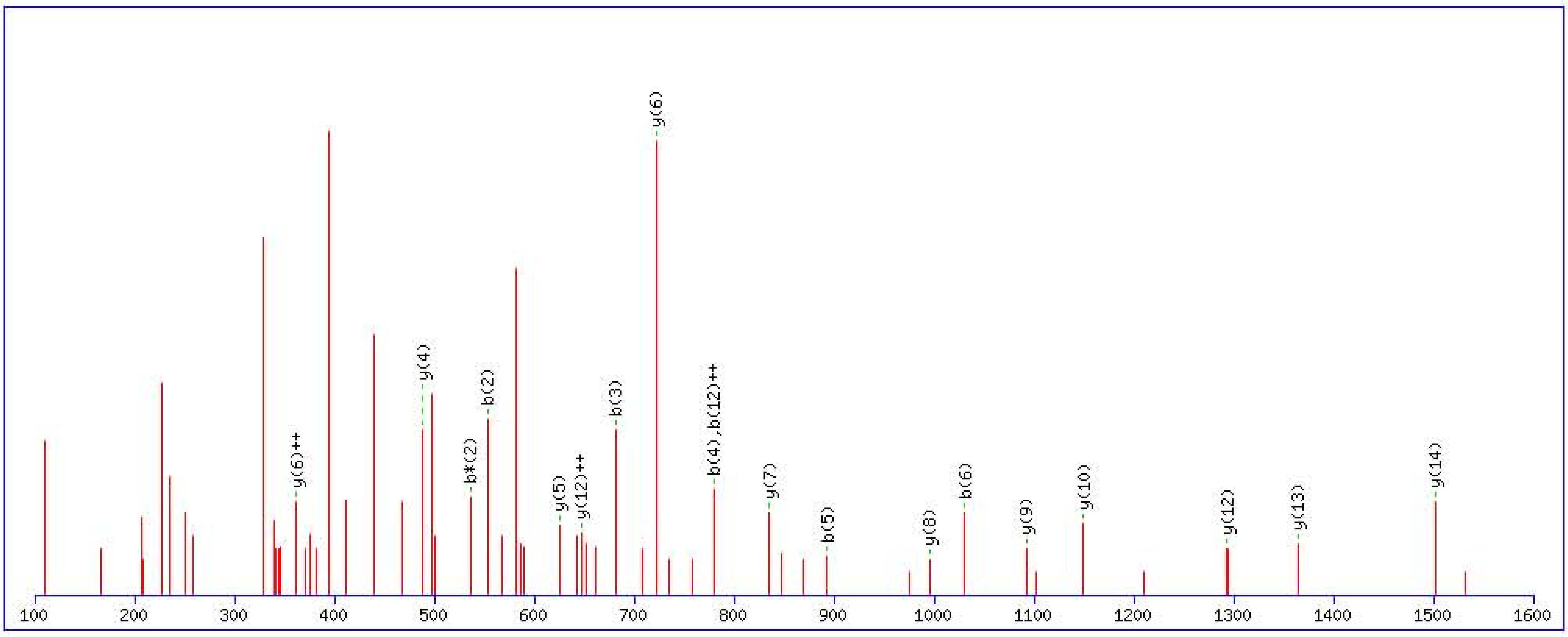
Mascot Search Results

Peptide View

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

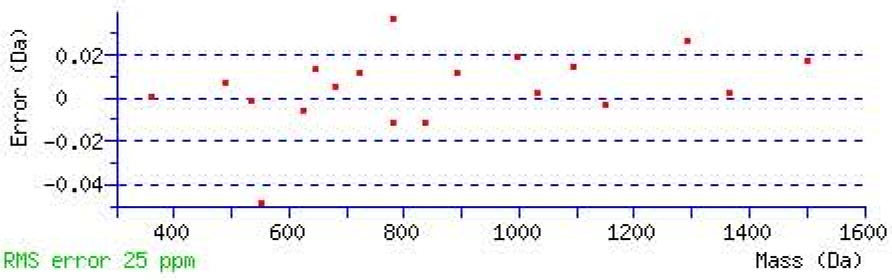
Match to Query 48962: 2393.286016 from(599.328780,4+) rtinseconds(2140) index(5722)
Title: Locus:1.1.1.3297.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

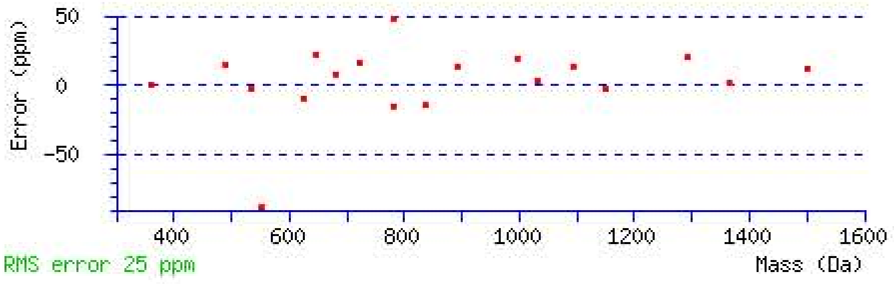
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2393.282410
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 50  Expect: 0.00019
Matches : 19/196 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							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
50.4	2393.282410	0.003606	LQQVLHAGSGPCLPHLLSR
46.4	2393.282410	0.003606	LQQVLHAGSGPCLPHLLSR

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

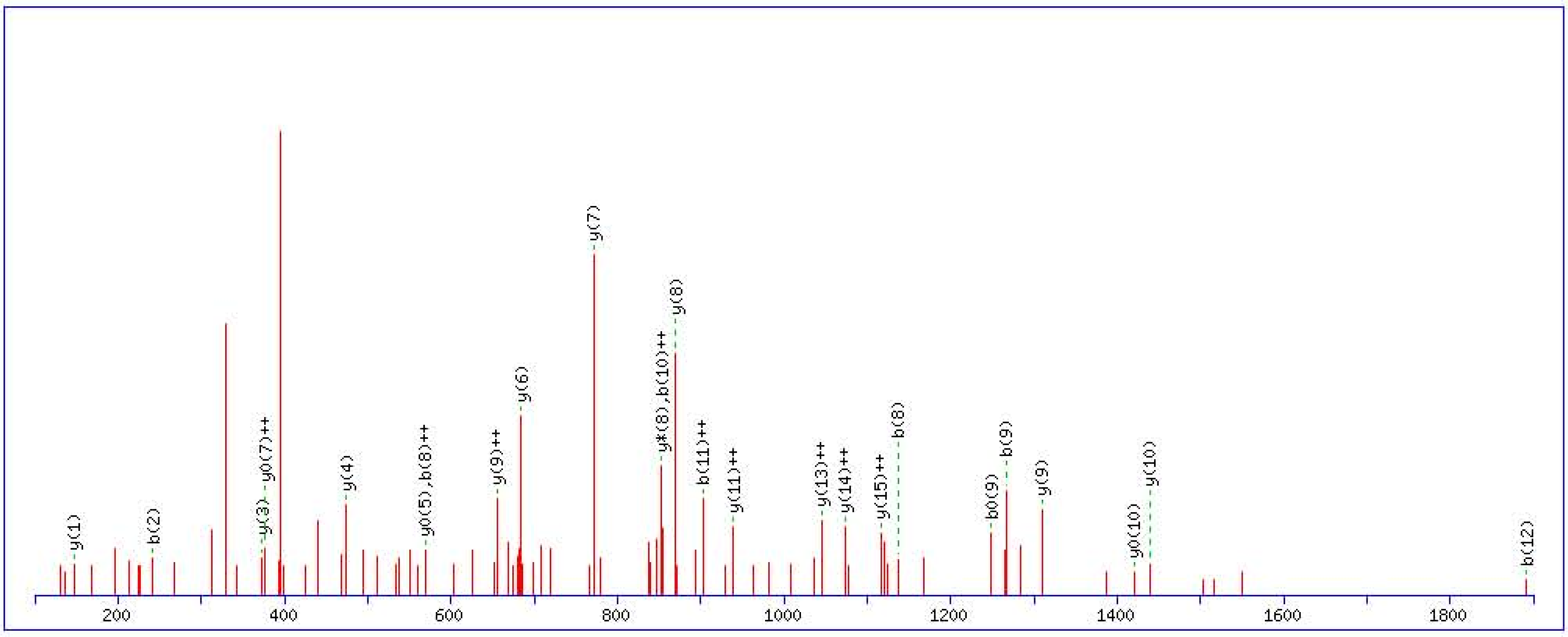
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

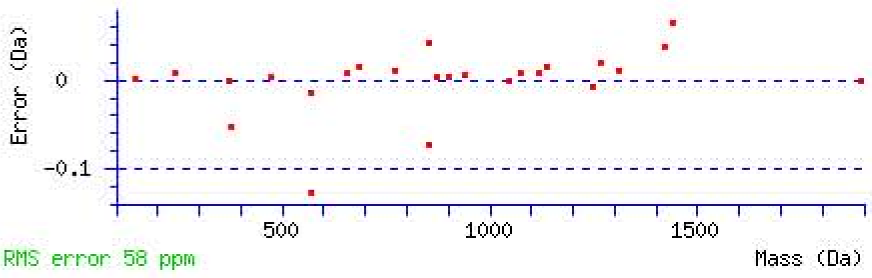
Match to Query 51875: 2574.402012 from(859.141280,3+) rtinseconds(2717) index(8927)
Title: Locus:1.1.1.3497.23 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

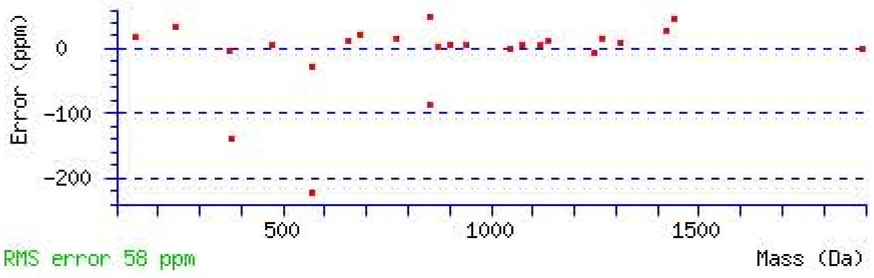
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 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: 40 **Expect:** 0.0014
Matches : 25/194 fragment ions using 42 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	129.065854	65.036565	112.039305	56.523291			Q							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
40.4	2574.391342	0.010670	QLTSGPNQEQVSPLTLLK
29.9	2574.391342	0.010670	QLTSGPNQEQVSPLTLLK
12.2	2574.391342	0.010670	QLTSGPNQEQVSPLTLLK

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

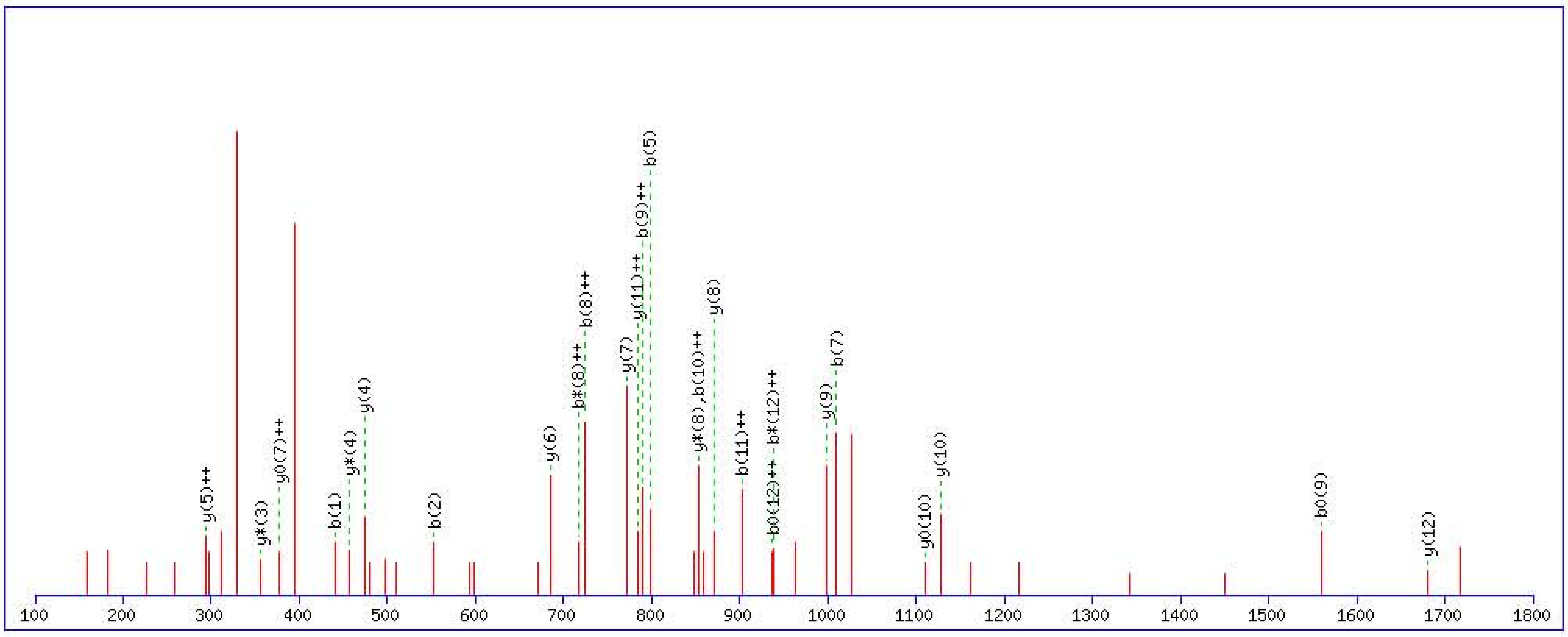
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

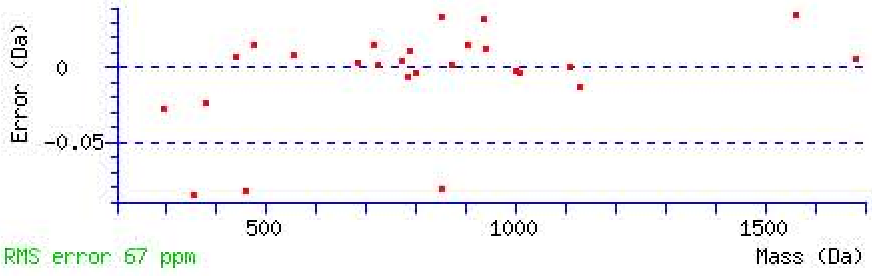
Match to Query 51877: 2574.406062 from(859.142630,3+) rtinseconds(2664) index(8478)
Title: Locus:1.1.1.3479.22 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

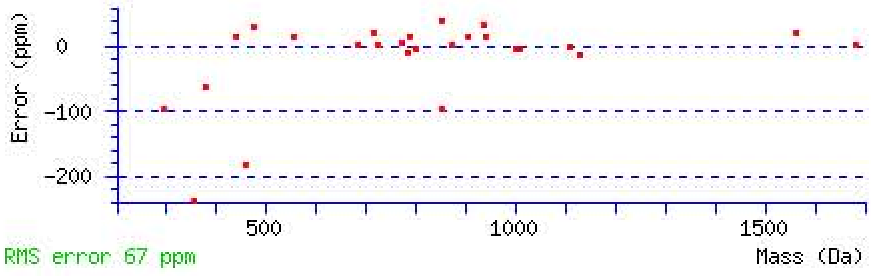
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 32  Expect: 0.0092
Matches : 26/194 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	***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





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
31.8	2574.391342	0.014720	QLTSGPNQEQVSPLTLLK
14.6	2574.391342	0.014720	QLTSGPNQEQVSPLTLLK
0.9	2574.391342	0.014720	QLTSGPNQEQVSPLTLLK

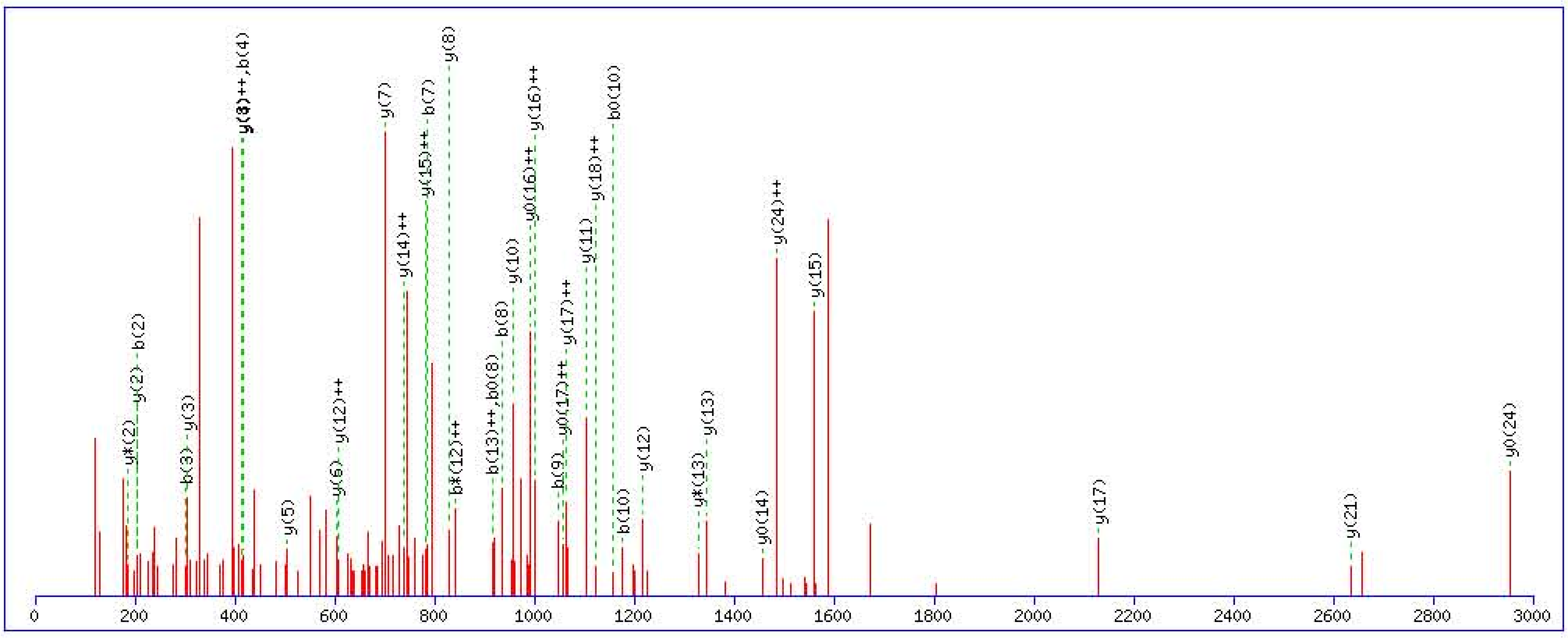
Mascot Search Results

Peptide View

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

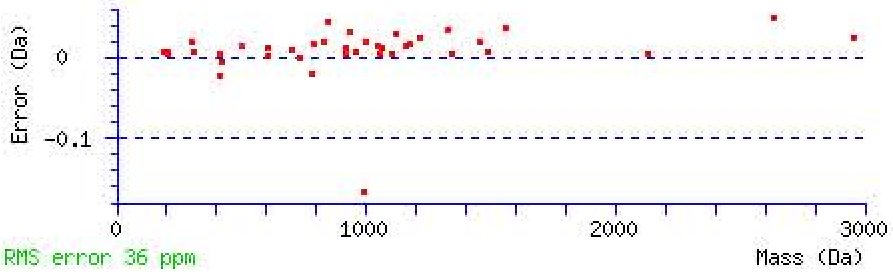
Match to Query 57440: 3175.681656 from(794.927690,4+) rtinseconds(2775) index(9342)
Title: Locus:1.1.1.3517.20 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

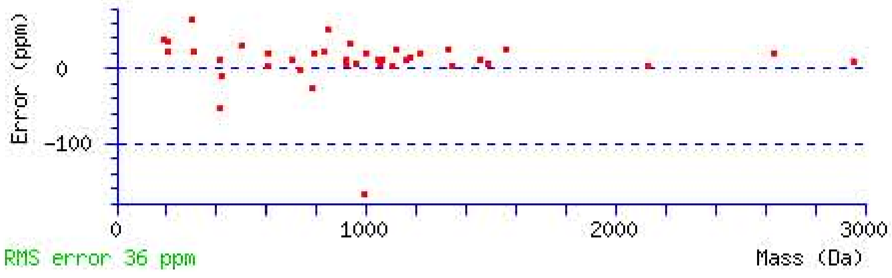


```
Monoisotopic mass of neutral peptide Mr(calc): 3175.662750
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 0.00014
Matches : 39/278 fragment ions using 107 most intense peaks   (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



RMS error 36 ppm



RMS error 36 ppm

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
51.6	3175.662750	0.018906	GFPIKEDFLEQSEQLFGAKPVSLTGK
34.3	3175.662750	0.018906	GFPIKEDFLEQSEQLFGAKPVSLTGK

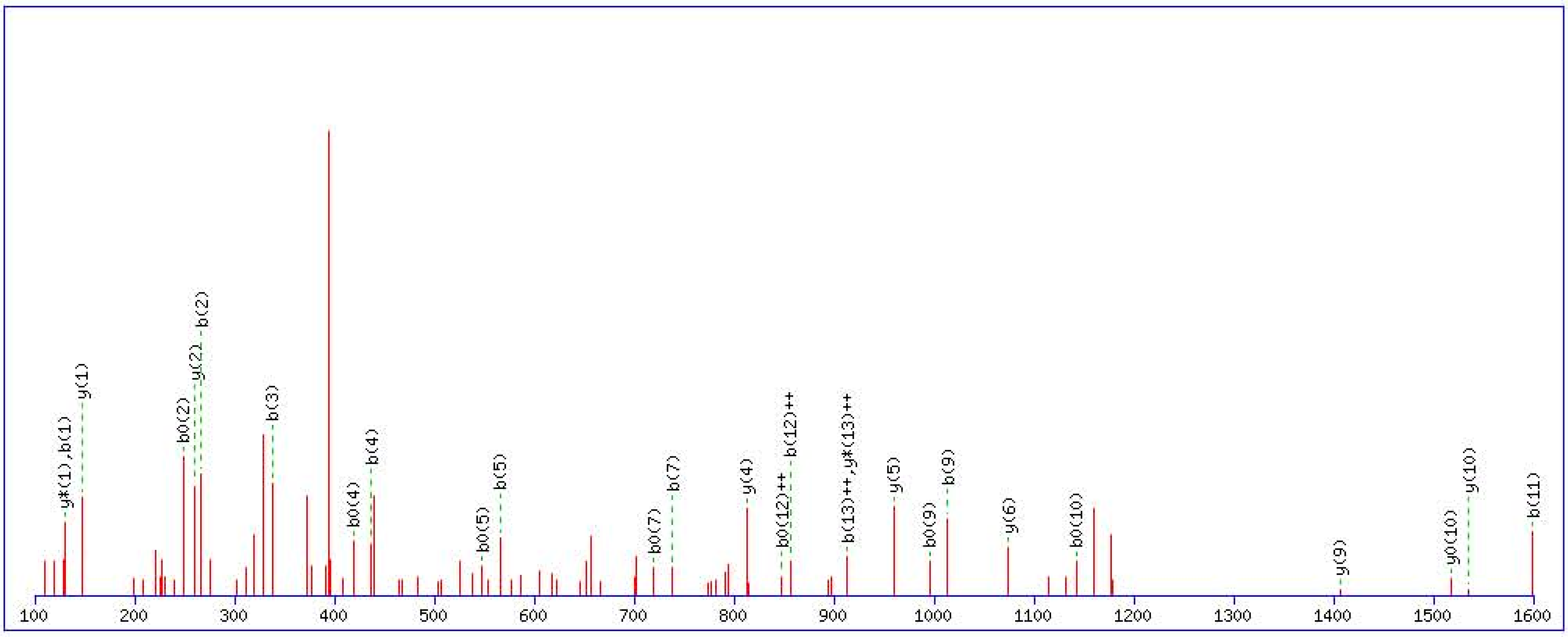
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

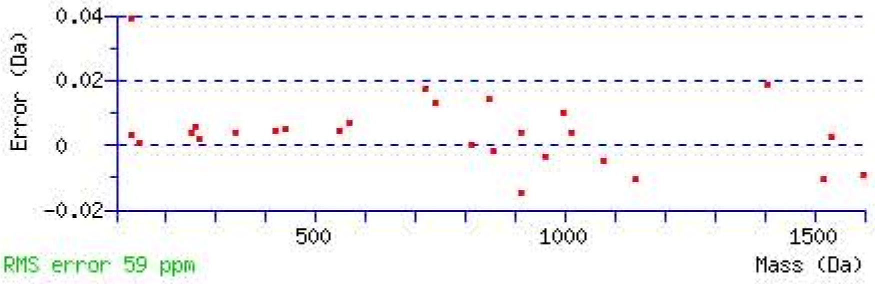
Match to Query 41549: 1970.921592 from(657.981140,3+) rtinseconds(2103) index(5485)
Title: Locus:1.1.1.3284.22 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

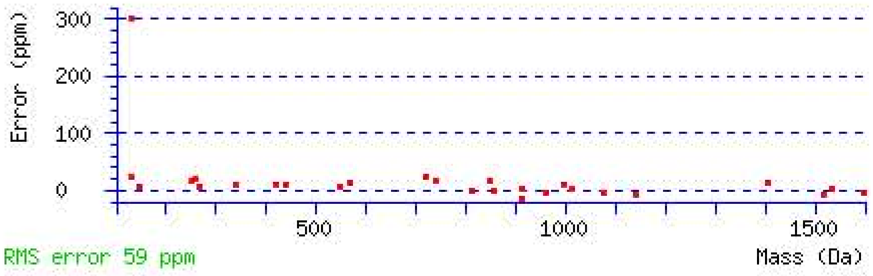
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1970.923019
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 63  Expect: 2.7e-006
Matches : 27/126 fragment ions using 36 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	***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
63.5	1970.923019	-0.001427	EHAVEGDCDFQLLK
4.1	1970.905258	0.016334	LDFNMTTNHSFMCLIK

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

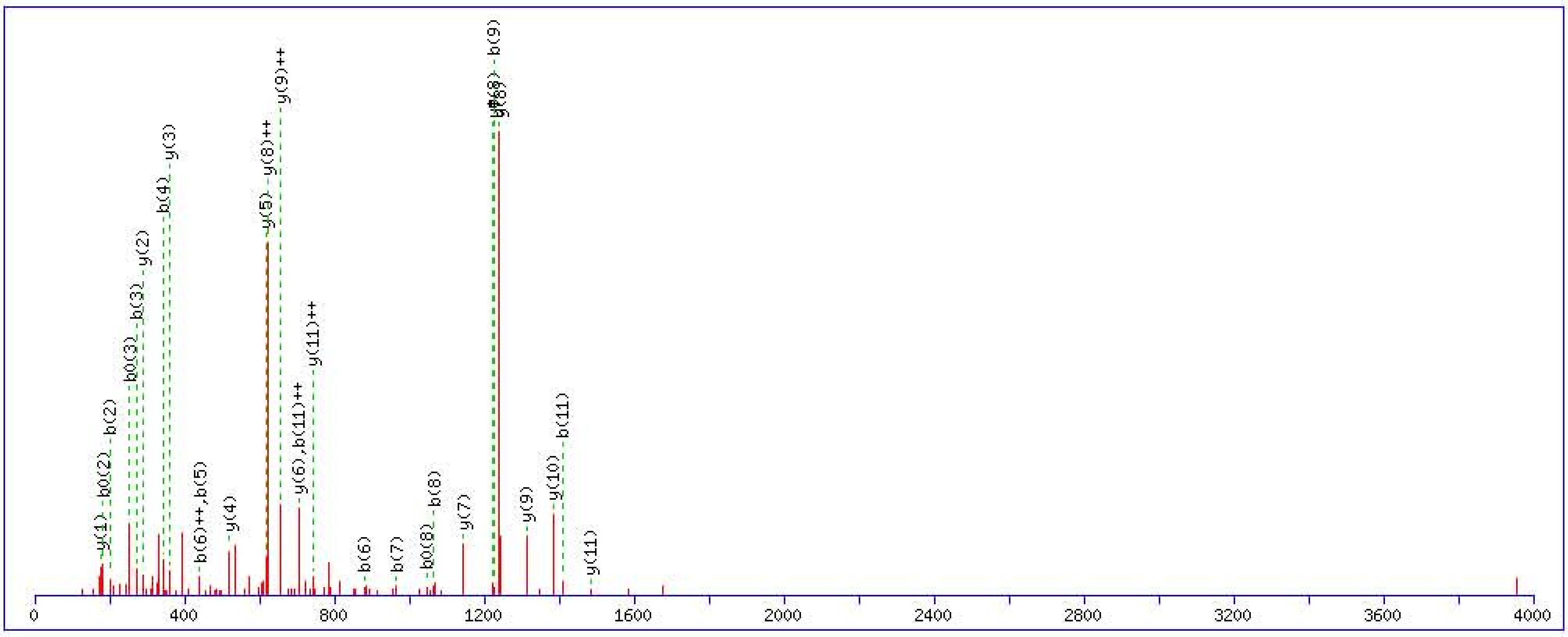
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

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

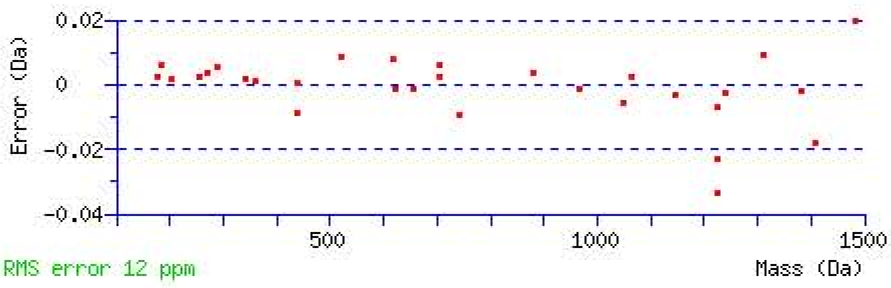
Match to Query 32362: 1582.843188 from(792.428870,2+) rtinseconds(1850) index(32147)
Title: Locus:1.1.1.3193.14 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

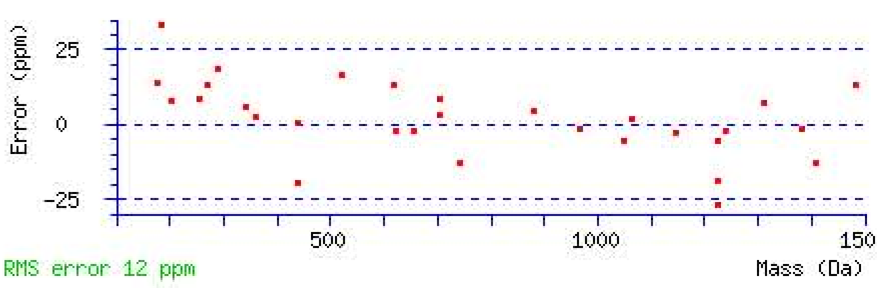
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1582.832352
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 77  Expect: 5.5e-007
Matches : 30/110 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							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
77.0	1582.832352	0.010836	VTAAPQSVCALR
11.4	1582.844040	-0.000852	APRHGPARDPGLPSR
8.7	1582.865356	-0.022168	QPAPGPVEKPPR
3.3	1582.821564	0.021624	LSKAVATWHANTER
2.9	1582.850067	-0.006879	AEQEASLQKLR
1.0	1582.821579	0.021609	IGGHGPTLKAYQEGR
0.6	1582.850098	-0.006910	VRSSPDKDQIK
0.6	1582.857956	-0.014768	LEDVKSQWVRPAR
0.2	1582.831482	0.011706	GIATNDVGIQKDGAPK

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

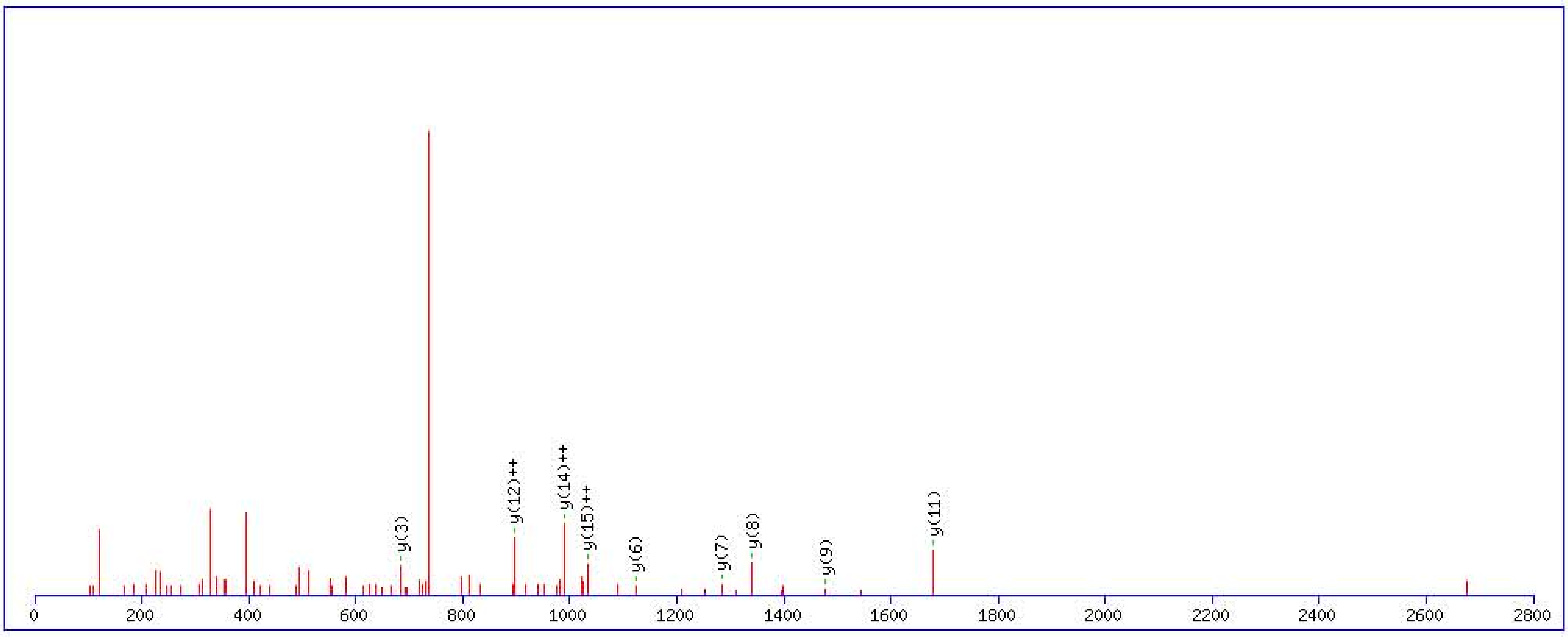
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

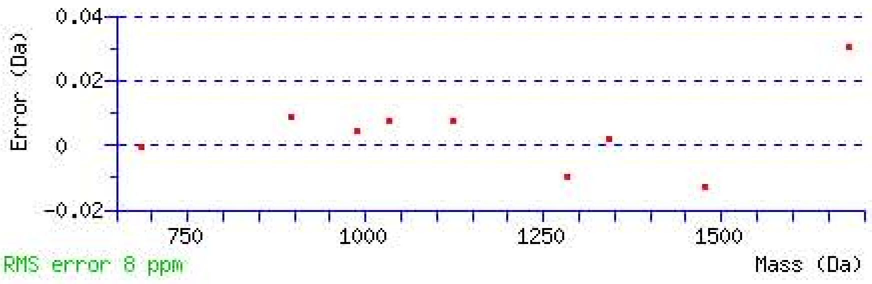
Match to Query 46121: 2210.045172 from(737.689000,3+) rtinseconds(1900) index(4225)
Title: Locus:1.1.1.3213.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

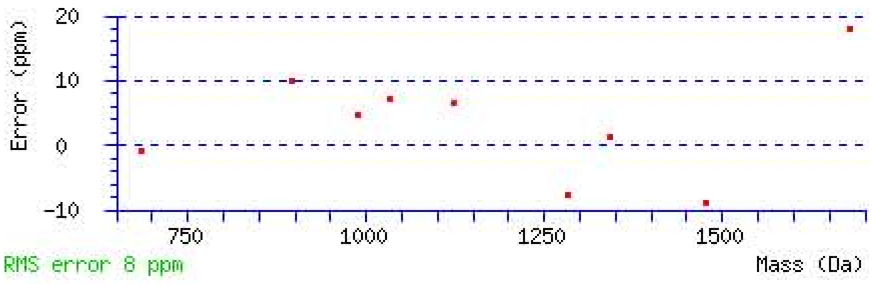
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2210.040131
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Biotin:Thermo-21345 (Q)
Ions Score: 30 **Expect:** 0.0025
Matches : 9/154 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							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
30.2	2210.040131	0.005041	FSGQLNSHGCFYQQVK
22.2	2210.040131	0.005041	FSGQLNSHGCFYQQVK
2.4	2210.045486	-0.000314	MSMKEVDEQMLAIQSK
2.4	2210.045486	-0.000314	MSMKEVDEQMLAIQSK
1.7	2210.045990	-0.000818	GKMISAGLPGEMGSPGEPGPPGR

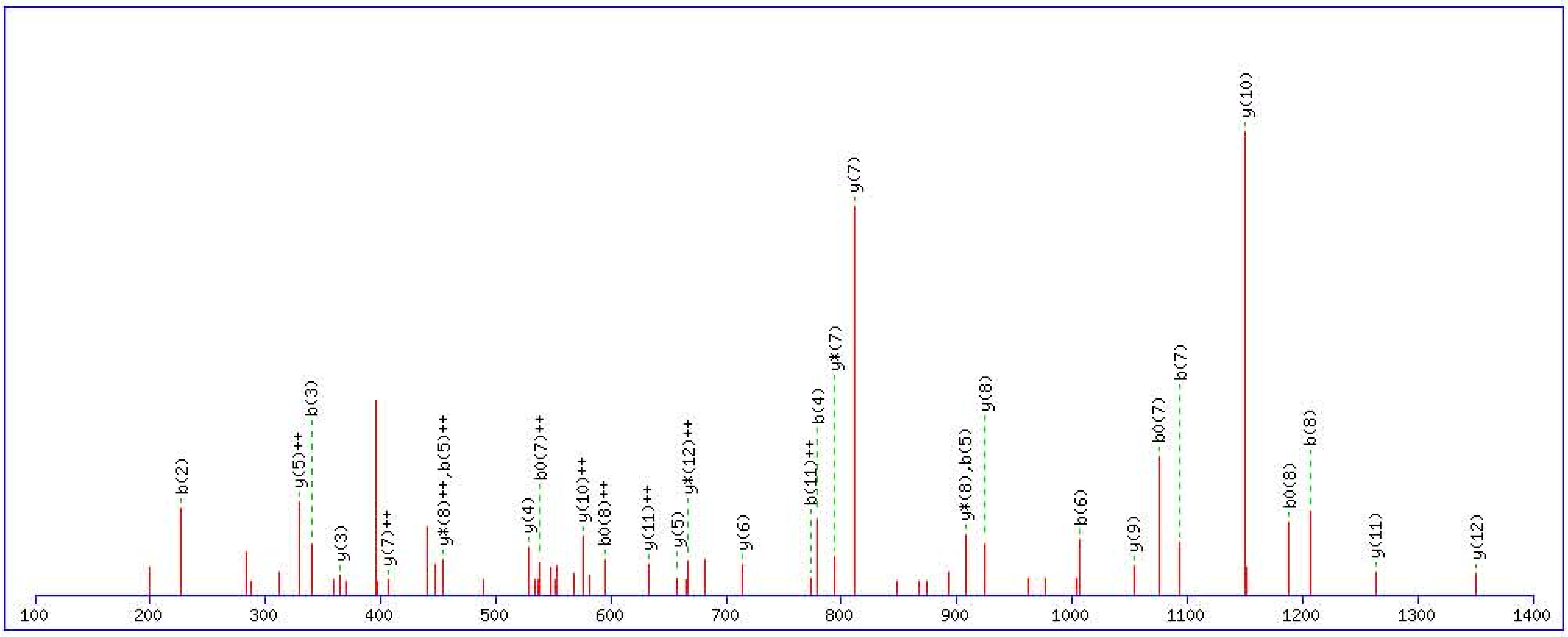
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

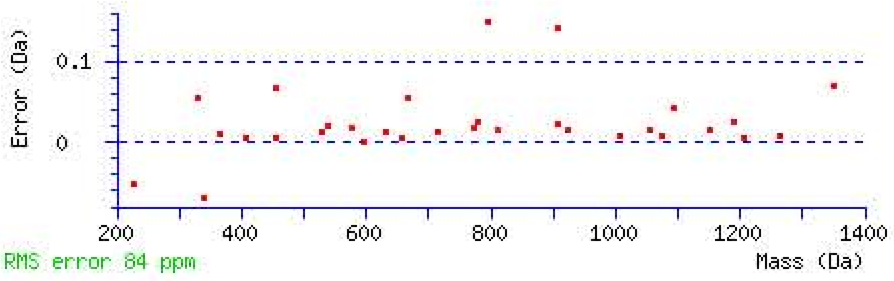
Match to Query 48579: 2355.290232 from(786.104020,3+) rtinseconds(2869) index(23911)
Title: Locus:1.1.1.3598.14 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

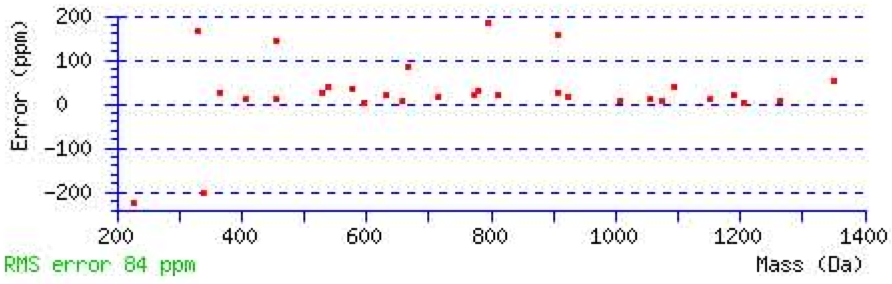
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2355.258179
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 65 **Expect:** 2e-006
Matches : 31/182 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	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
64.5	2355.258179	0.032053	LLLQQVSLPELPGEYSMK
56.4	2355.258179	0.032053	LLLQQVSLPELPGEYSMK
3.6	2355.288498	0.001734	LIQQERALLNFTEWKR
3.6	2355.288498	0.001734	LIQQERALLNFTEWKR
2.5	2355.273926	0.016306	LGLYTFVNLANFVKSWTNLR
0.1	2355.259354	0.030878	SQPRASGPPRSIQPQVSPR

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

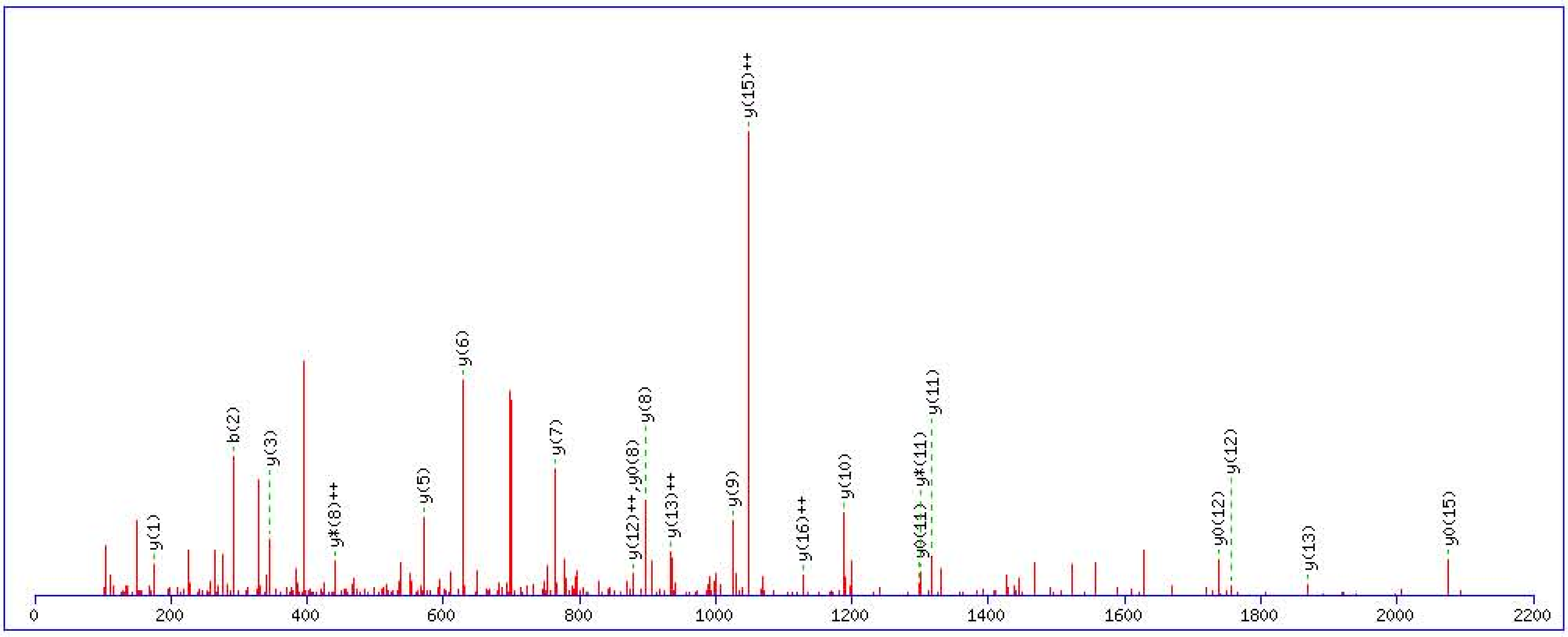
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

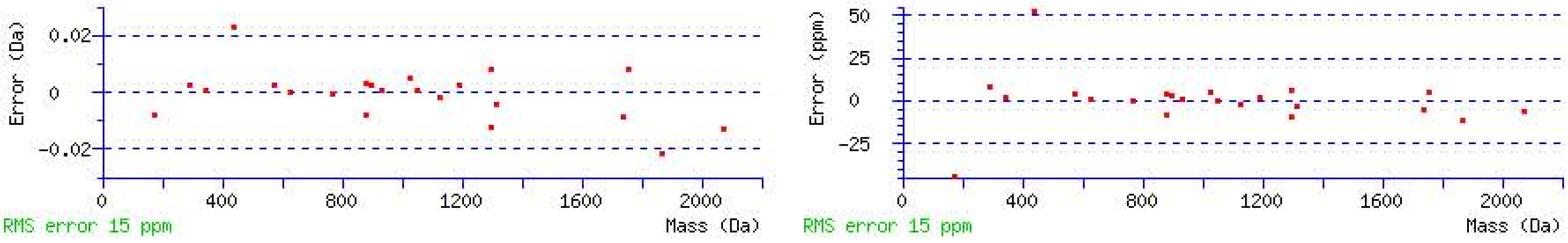
Match to Query 48826: 2384.091942 from(795.704590,3+) rtinseconds(2071) index(33549)
Title: Locus:1.1.1.3270.8 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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): 2384.089767
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.0018
Matches : 22/164 fragment ions using 60 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	132.047761	66.527518					M							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	1069.499142	535.253209	1052.472593	526.739935			Q	***1755.830524***	878.418900	1738.803975	869.905626	1737.819959	869.413618	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
38.0	2384.089767	0.002175	MCPQLQQYEMHGPEGLR
36.7	2384.089767	0.002175	MCPQLQQYEMHGPEGLR
36.5	2384.089767	0.002175	MCPQLQQYEMHGPEGLR

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

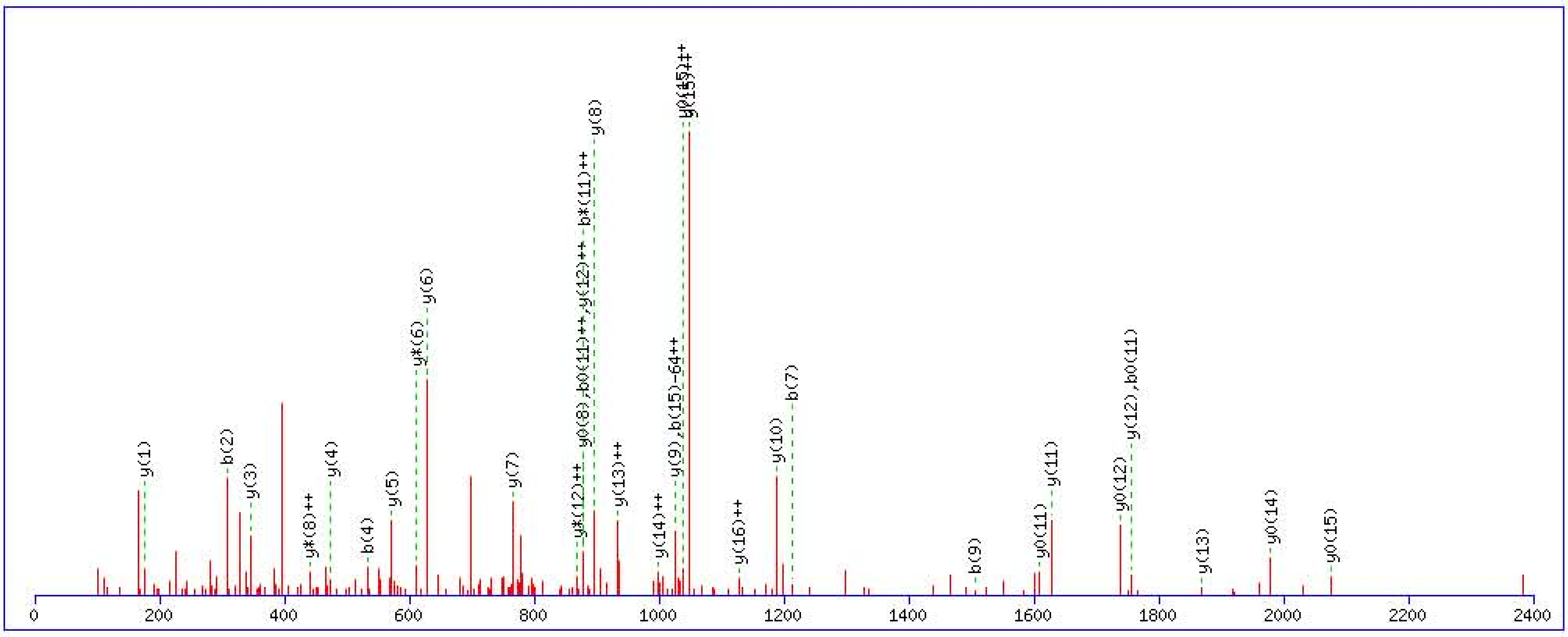
Mascot Search Results

Peptide View

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

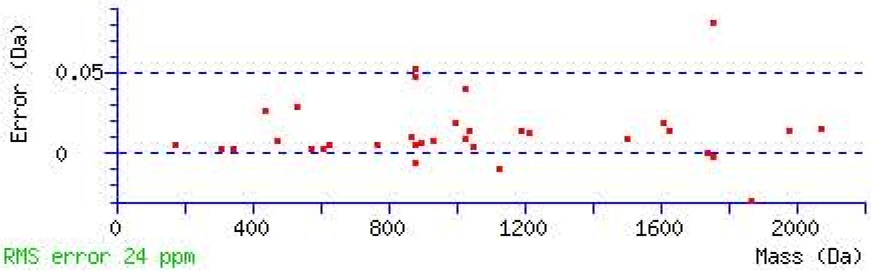
Match to Query 49080: 2400.086532 from(801.036120,3+) rtinseconds(1978) index(4842)
Title: Locus:1.1.1.3240.18 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

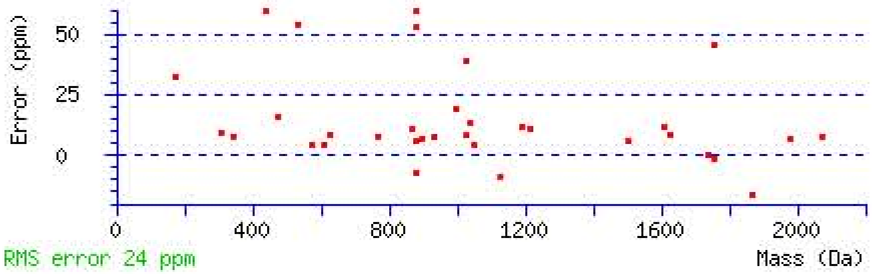
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 5.3e-005
Matches : 34/238 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	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	774.327309	387.667293	757.300760	379.154018			Q	***1755.830524***	878.418900	1738.803975	869.905626	1737.819959	869.413618	12
7	**1213.552635**	607.279956	1196.526086	598.766681			Q	***1627.771946***	814.389611	1610.745397	805.876337	1609.761381	805.384329	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
52.6	2400.084686	0.001846	MCPQLQQYEMHGPEGLR
43.5	2400.084686	0.001846	MCPQLQQYEMHGPEGLR
24.7	2400.084686	0.001846	MCPQLQQYEMHGPEGLR

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

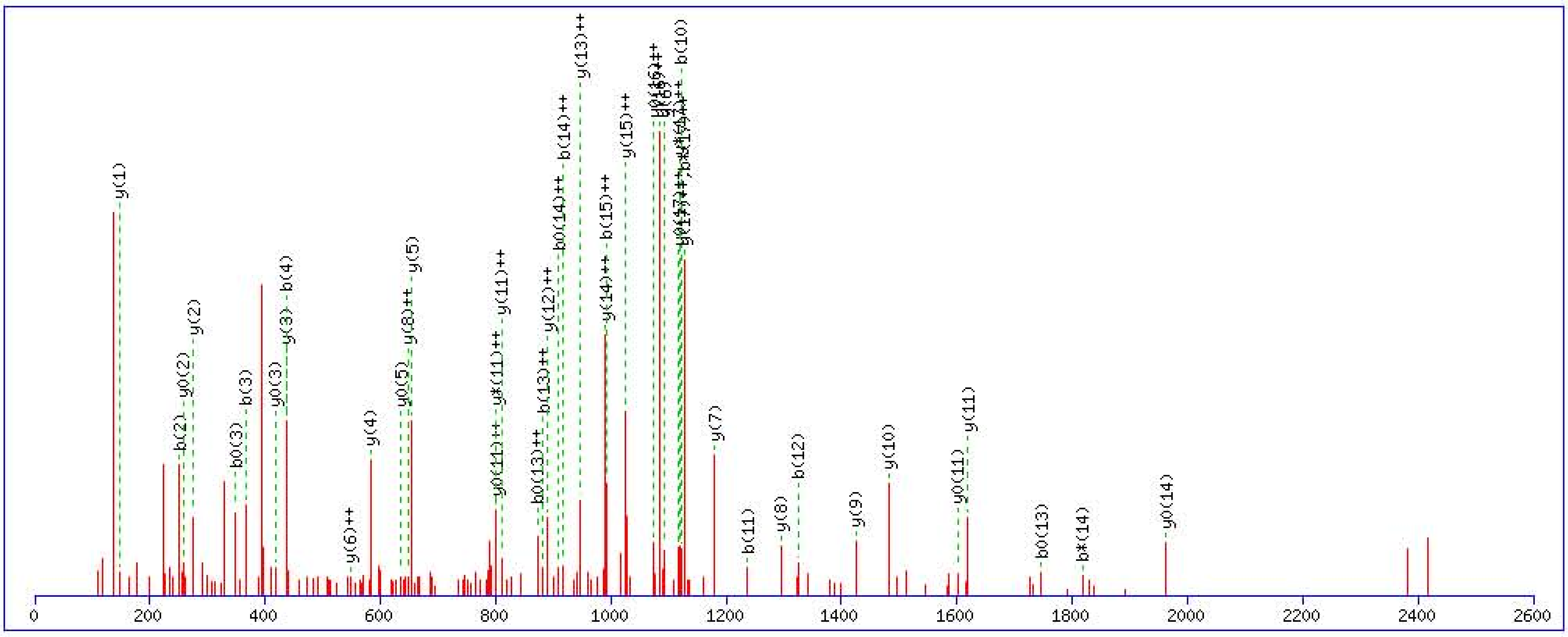
Mascot Search Results

Peptide View

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

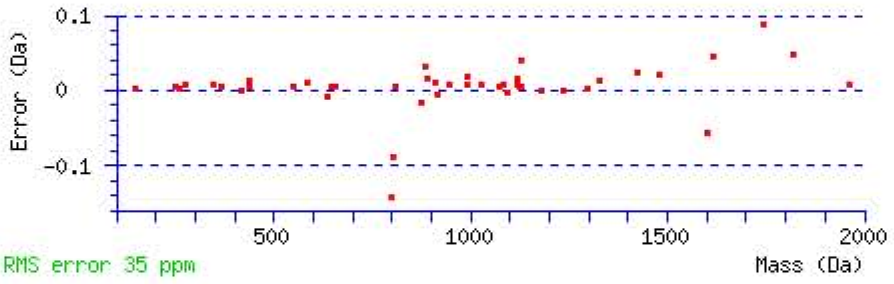
Match to Query 49365: 2415.952152 from(806.324660,3+) rtinseconds(1561) index(16285)
Title: Locus:1.1.1.3144.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

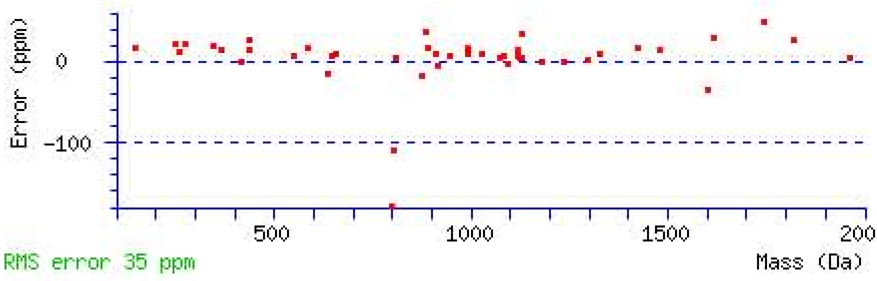
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 60  Expect: 9.4e-007
Matches : 45/176 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	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
60.3	2415.940598	0.011554	YSDASDCHGEDSQAFCEK

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

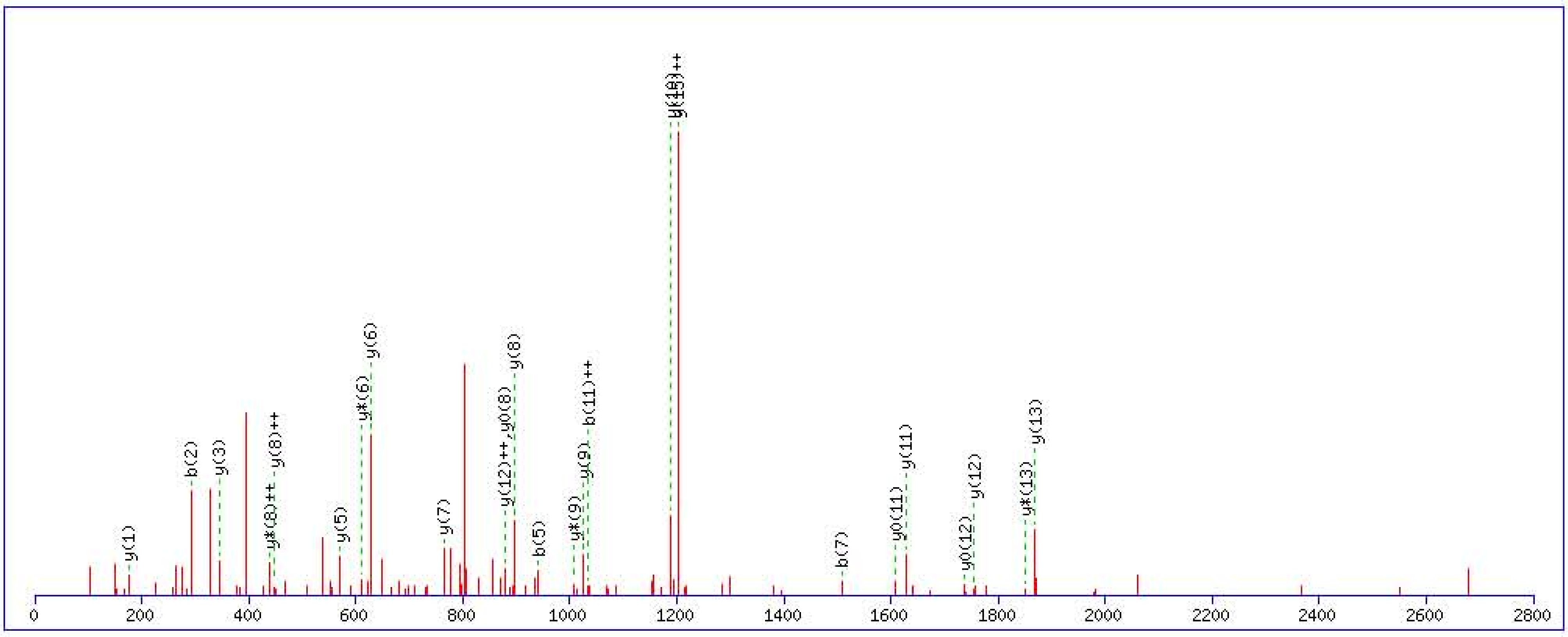
Mascot Search Results

Peptide View

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

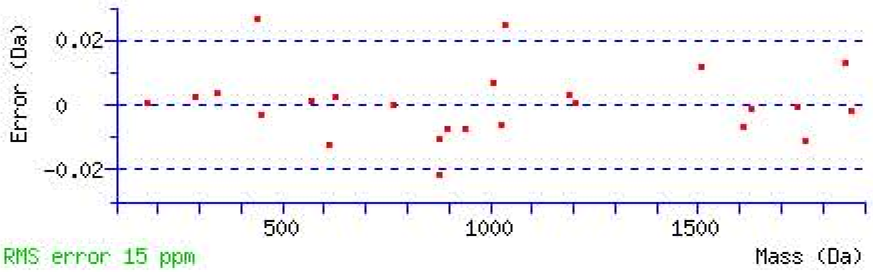
Match to Query 52700: 2695.263762 from(899.428530,3+) rtinseconds(2229) index(34458)
Title: Locus:1.1.1.3325.26 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

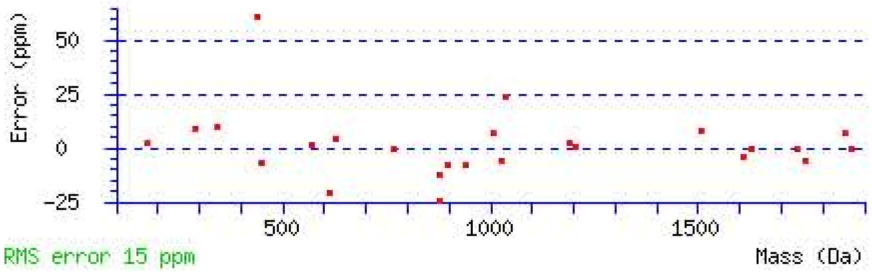


```
Monoisotopic mass of neutral peptide Mr(calc): 2695.256516
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4     : Biotin:Thermo-21345 (Q)
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.009
Matches : 25/164 fragment ions using 70 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	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



RMS error 15 ppm



RMS error 15 ppm

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
32.8	2695.256516	0.007246	MCPQLQQYEMHGPEGLR
26.7	2695.256516	0.007246	MCPQLQQYEMHGPEGLR
16.4	2695.256516	0.007246	MCPQLQQYEMHGPEGLR

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

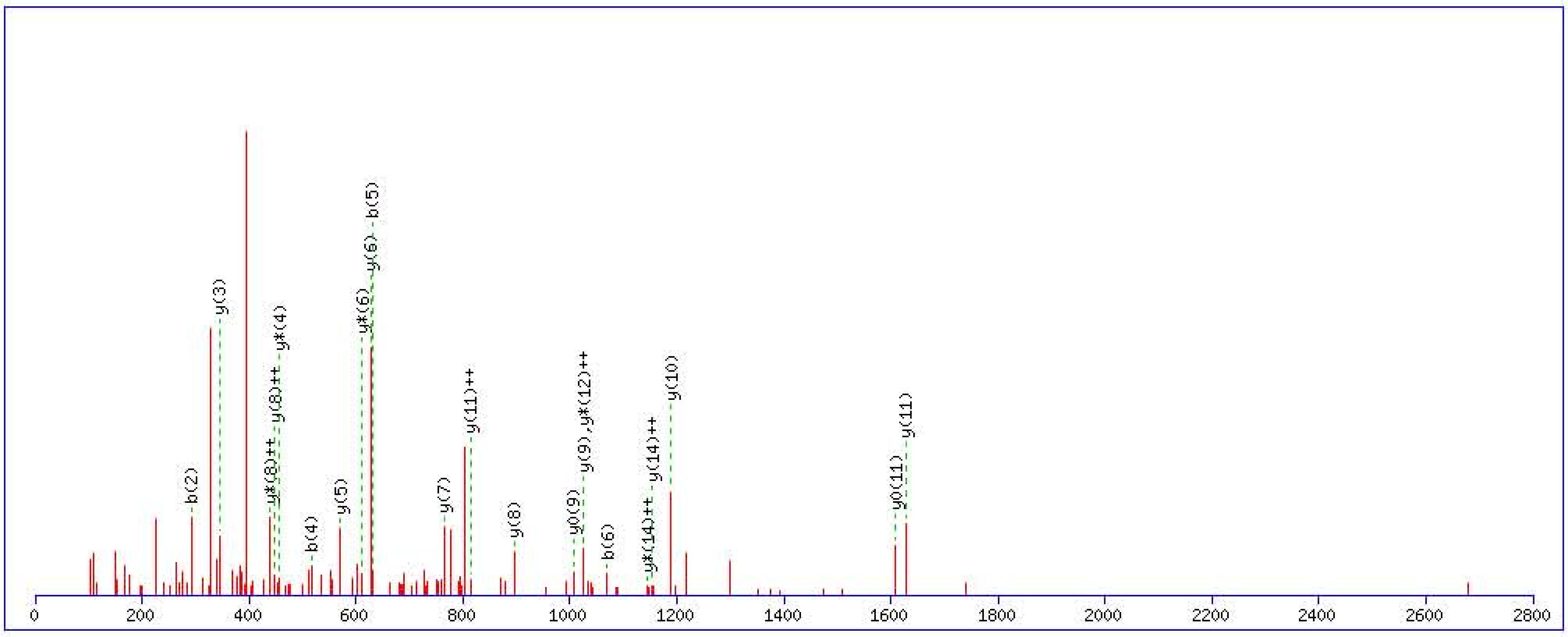
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

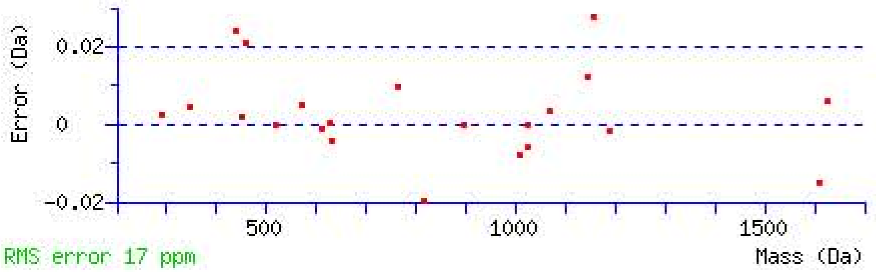
Match to Query 52706: 2695.264496 from(674.823400,4+) rtinseconds(2214) index(34323)
Title: Locus:1.1.1.3320.16 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

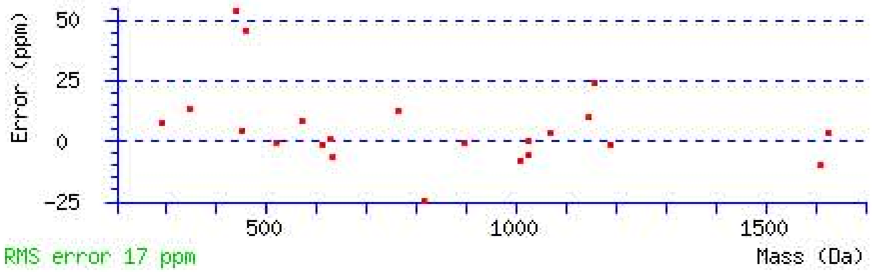


Monoisotopic mass of neutral peptide Mr(calc): 2695.256516
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 30 **Expect:** 0.019
Matches : 22/164 fragment ions using 45 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	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	***517.189752***	259.098514	500.163203	250.585240			Q	2308.139914	1154.573595	2291.113365	1146.060320	2290.129349	1145.568312	14
5	***630.273816***	315.640546	613.247267	307.127272			L	2180.081336	1090.544306	2163.054787	1082.031031	2162.070771	1081.539023	13
6	***1069.499142***	535.253209	1052.472593	526.739935			Q	2066.997272	1034.002274	2049.970723	1025.488999	2048.986707	1024.996991	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



RMS error 17 ppm



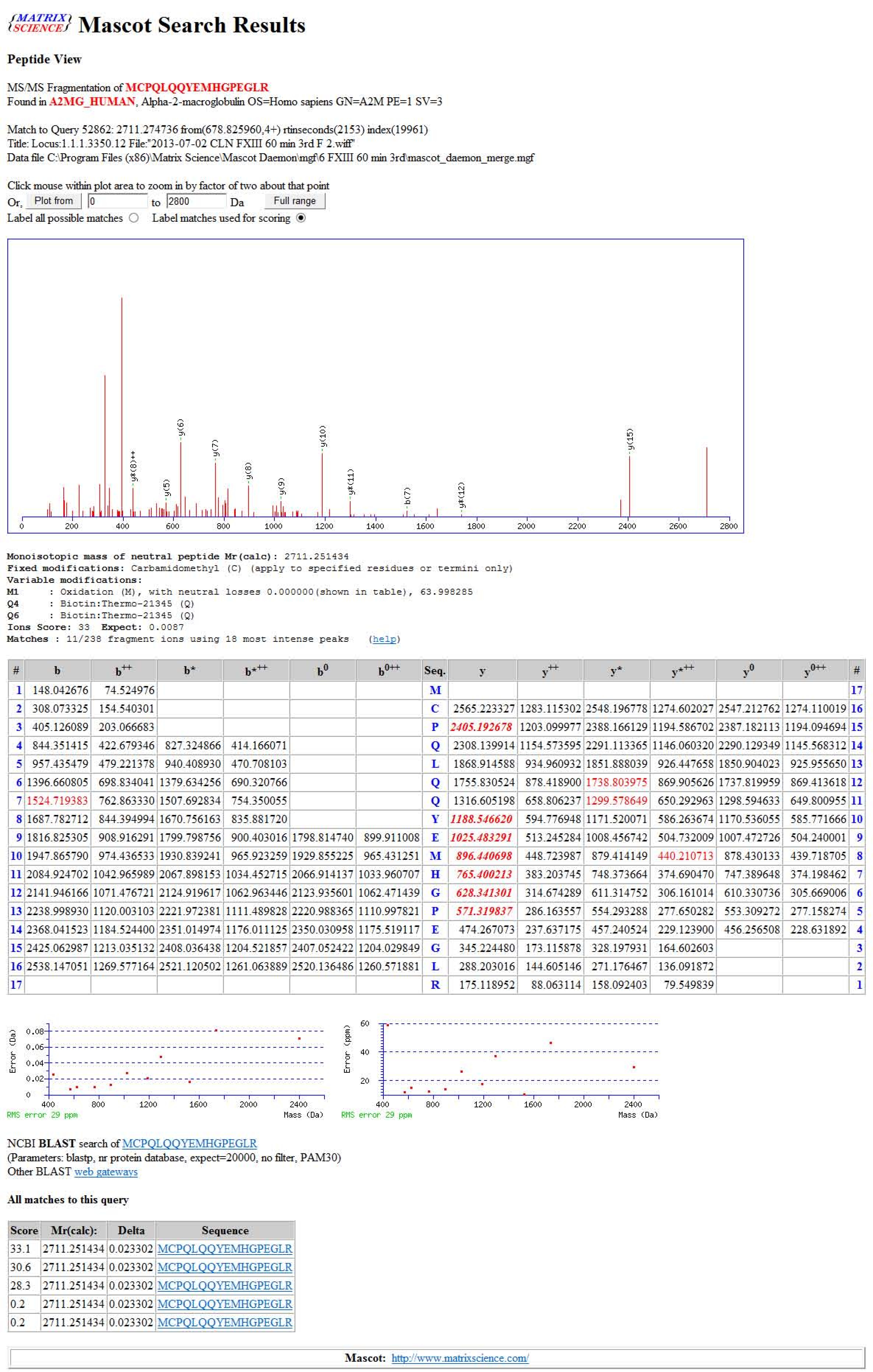
RMS error 17 ppm

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
29.6	2695.256516	0.007980	MCPQLQQYEMHGPEGLR
28.3	2695.256516	0.007980	MCPQLQQYEMHGPEGLR
17.6	2695.256516	0.007980	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 52862: 2711.274736 from(678.825960,4+) rtinseconds(2153) index(19961)
Title: Locus:1.1.1.3350.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 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: 33  Expect: 0.0087
Matches : 11/238 fragment ions using 18 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.042676	74.524976					M							17
2	308.073325	154.540301					C	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
33.1	2711.251434	0.023302	MCPQLQQYEMHGPEGLR
30.6	2711.251434	0.023302	MCPQLQQYEMHGPEGLR
28.3	2711.251434	0.023302	MCPQLQQYEMHGPEGLR
0.2	2711.251434	0.023302	MCPQLQQYEMHGPEGLR
0.2	2711.251434	0.023302	MCPQLQQYEMHGPEGLR

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

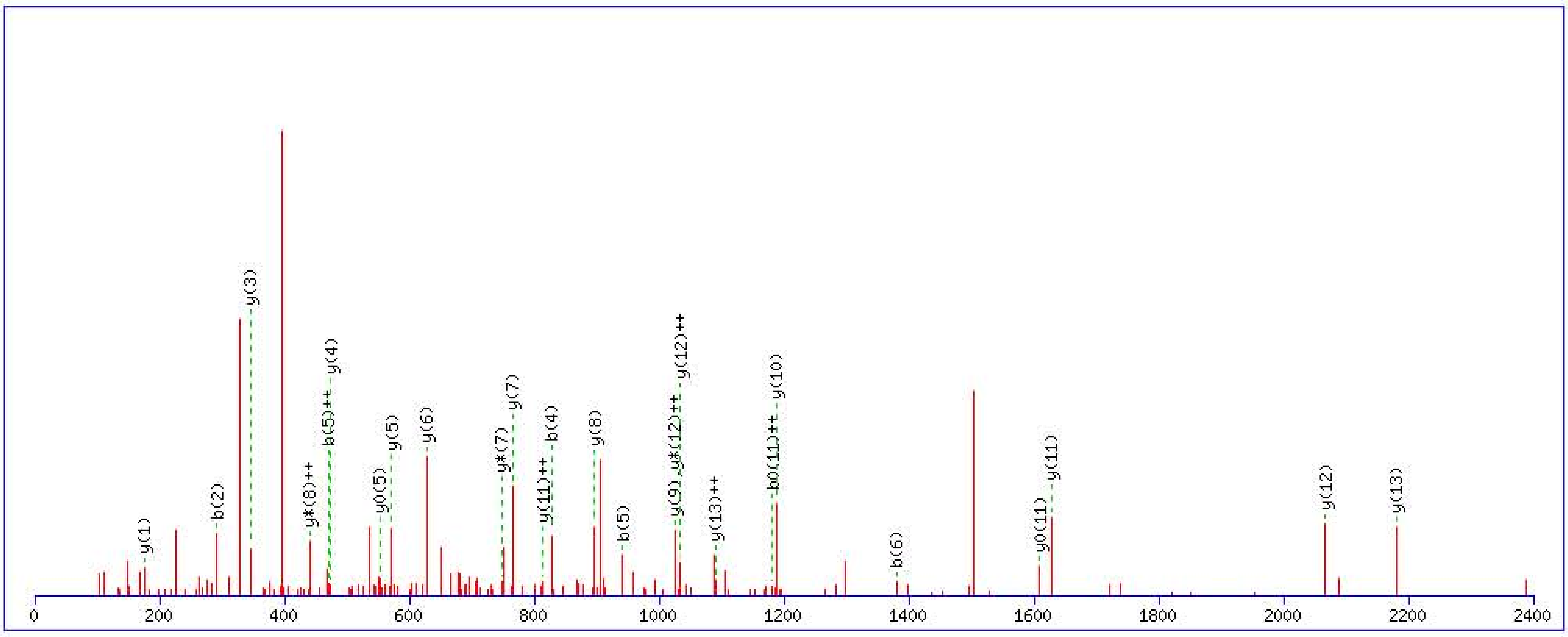
Mascot Search Results

Peptide View

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

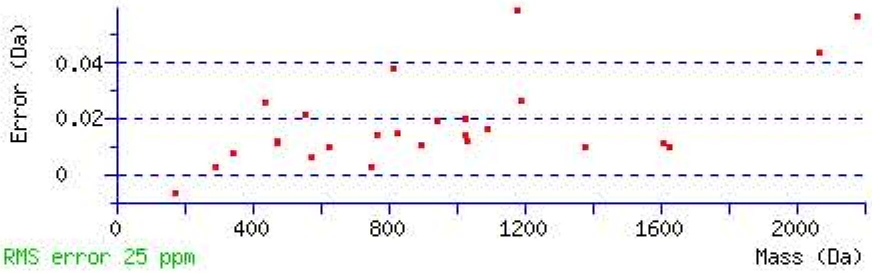
Match to Query 56142: 3006.459656 from(752.622190,4+) rtinseconds(2345) index(20963)
Title: Locus:1.1.1.3417.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

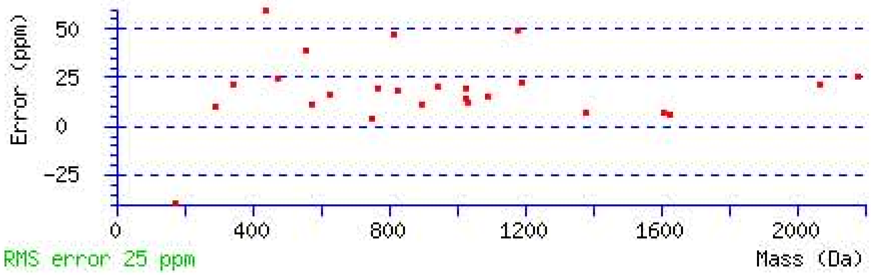
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 41  Expect: 0.0021
Matches : 26/164 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	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
41.1	3006.423264	0.036392	MCPQLQQYEMHGPEGLR

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

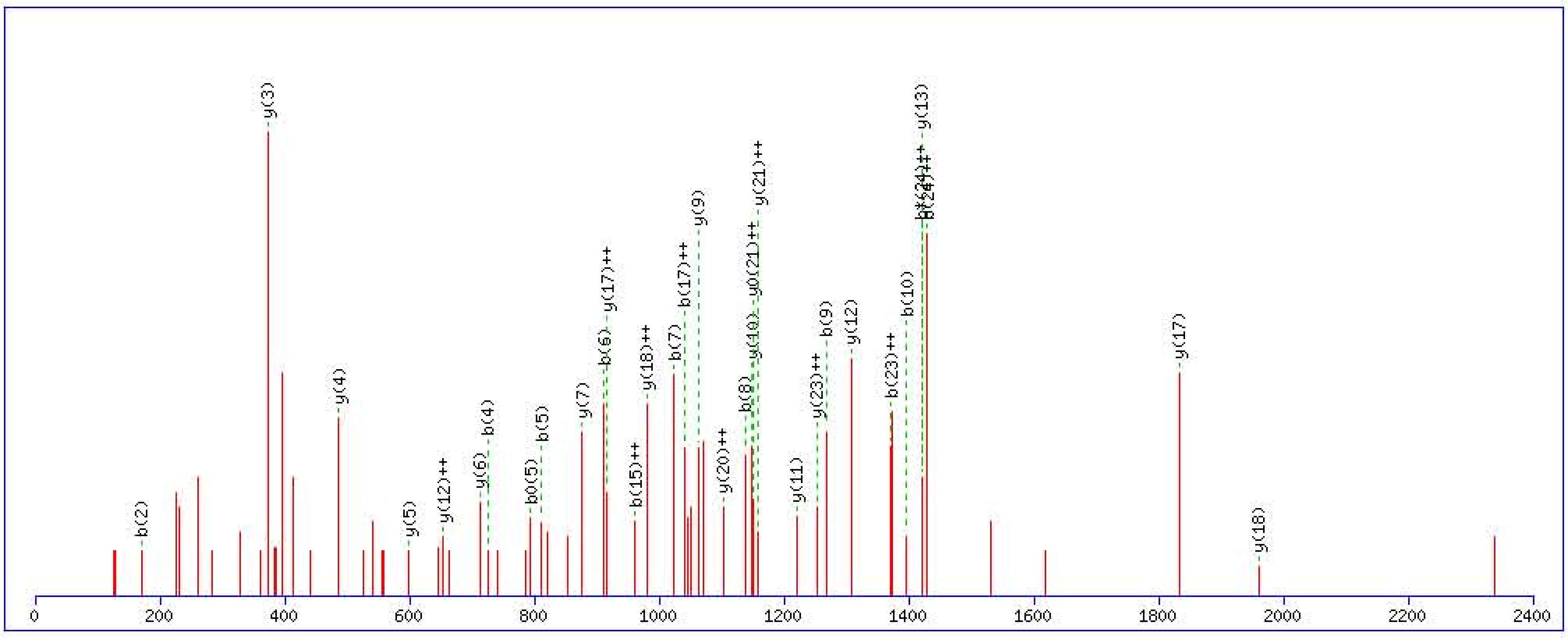
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

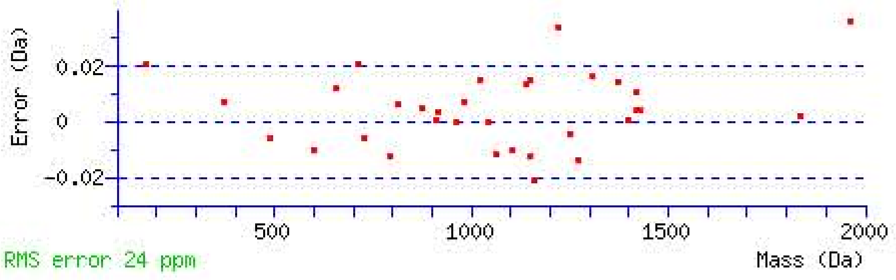
Match to Query 58592: 3227.692452 from(1076.904760,3+) rtinseconds(2776) index(37480)
Title: Locus:1.1.1.3514.26 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

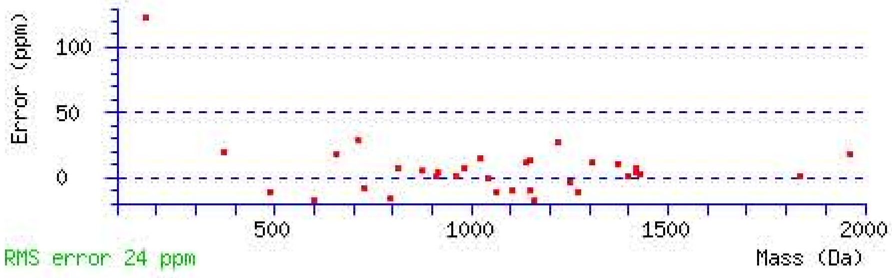
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3227.682129
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 63 **Expect:** 3.1e-006
Matches : 33/300 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	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





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
63.1	3227.682129	0.010323	AVDQSVLLMKPDAELSASSVYNLLPEK
4.4	3227.668900	0.023552	SQGRGKYDFYIGLGLAMSSSIFIGGSFILK

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

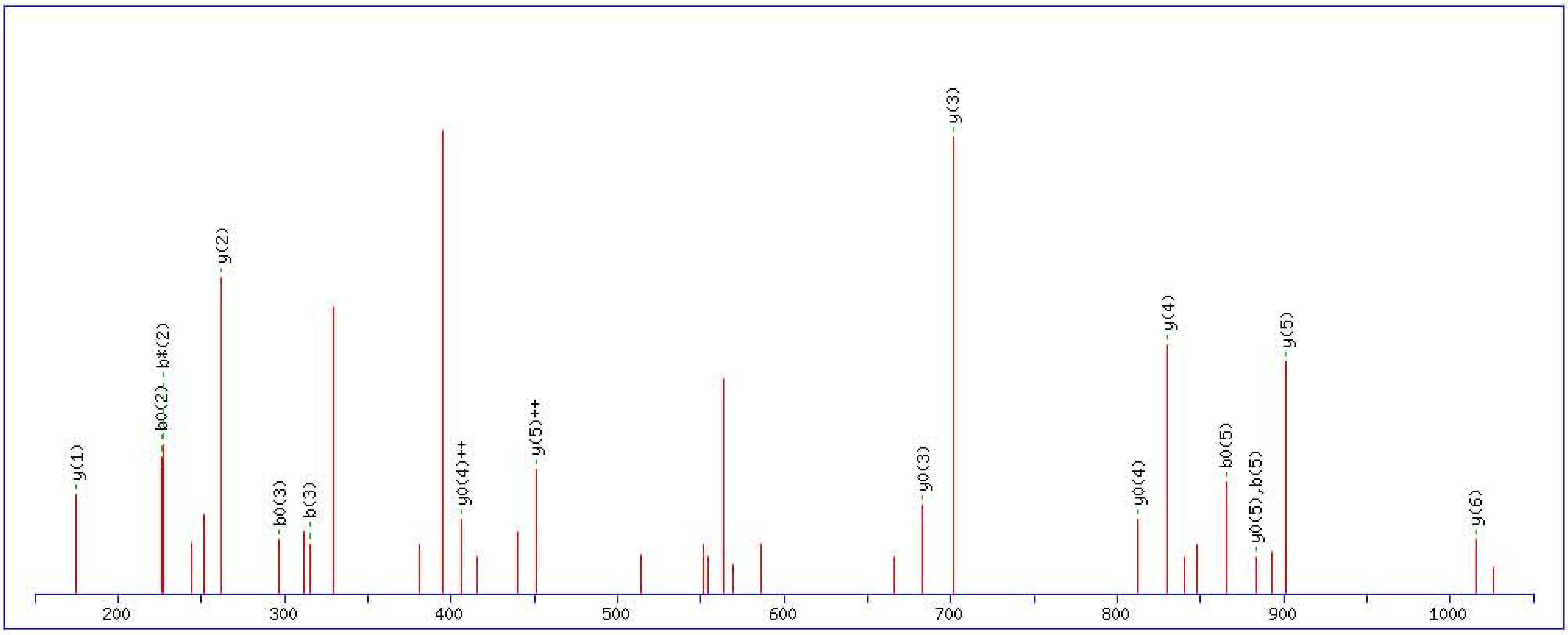
Mascot Search Results

Peptide View

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

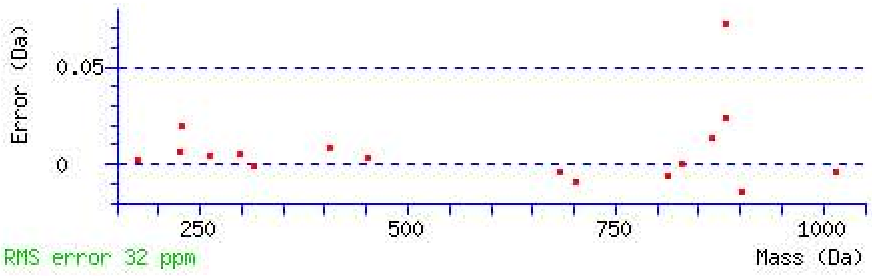
Match to Query 18634: 1143.532728 from(572.773640,2+) rtinseconds(1171) index(28680)
Title: Locus:1.1.1.2956.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

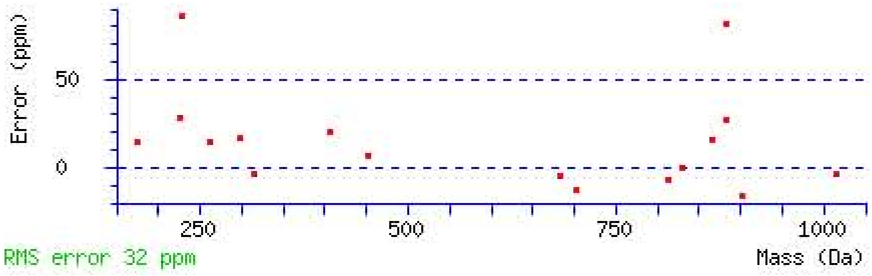
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1143.534225
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 37 **Expect:** 0.0022
Matches : 17/68 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	130.049869	65.528572			112.039304	56.523290	E							7
2	244.092796	122.550036	227.066247	114.036762	226.082231	113.544754	N	***1015.498940***	508.253108	998.472391	499.739834	997.488375	499.247826	6
3	**315.129910**	158.068593	298.103361	149.555319	297.119345	149.063311	A	***901.456013***	451.231645	884.429464	442.718370	883.445448	442.226362	5
4	444.172503	222.589890	427.145954	214.076615	426.161938	213.584607	E	***830.418899***	415.713088	813.392350	407.199813	812.408334	406.707805	4
5	**883.397829**	442.202553	866.371280	433.689278	865.387264	433.197270	Q	***701.376306***	351.191791	684.349757	342.678517	683.365741	342.186509	3
6	970.429857	485.718567	953.403308	477.205292	952.419292	476.713284	S	***262.150980***	131.579128	245.124431	123.065853	244.140415	122.573845	2
7							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.7	1143.534225	-0.001497	ENAEQSR
13.2	1143.549500	-0.016772	WQEQSR
0.0	1143.549500	-0.016772	KWESGHCLK

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

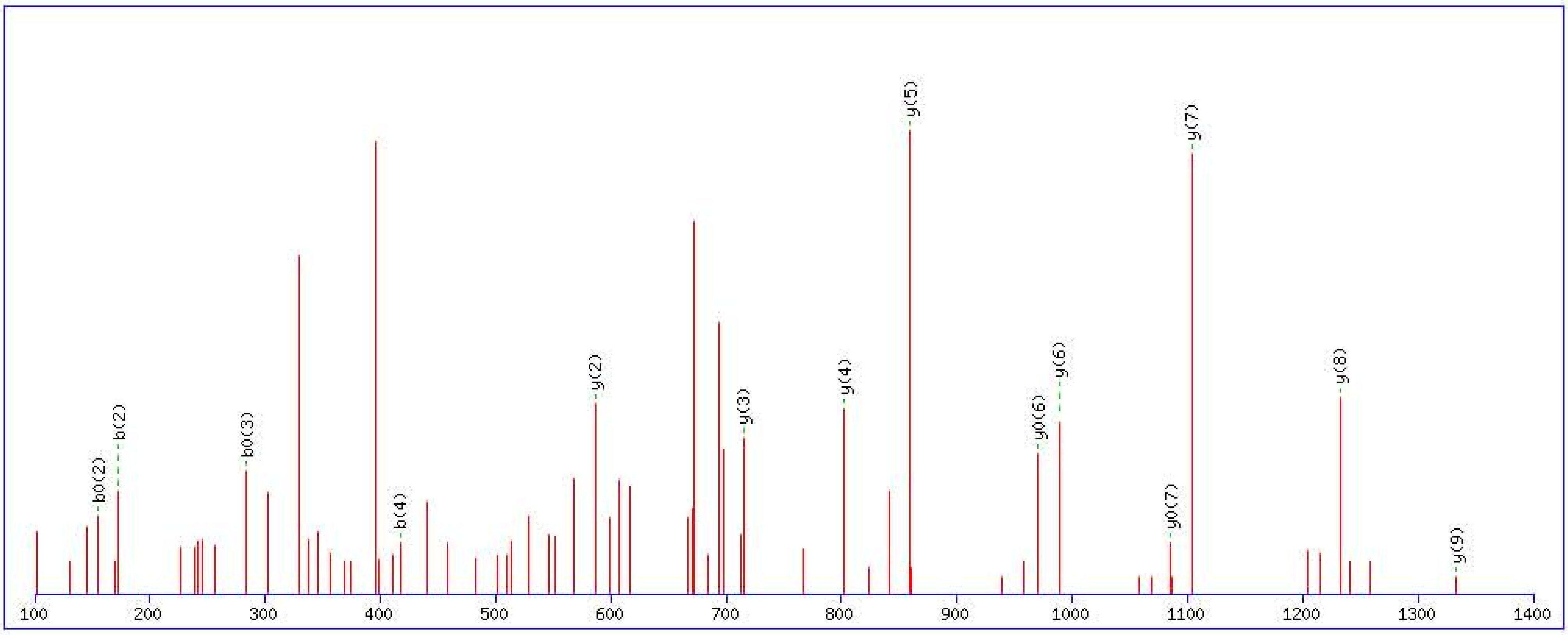
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

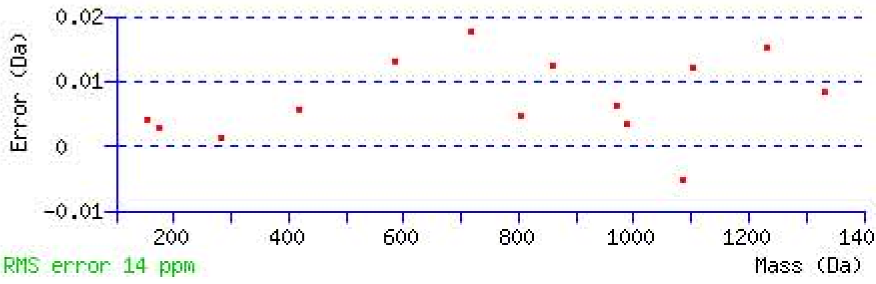
Match to Query 27018: 1403.634828 from(702.824690,2+) rtinseconds(1209) index(14378)
Title: Locus:1.1.1.3021.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

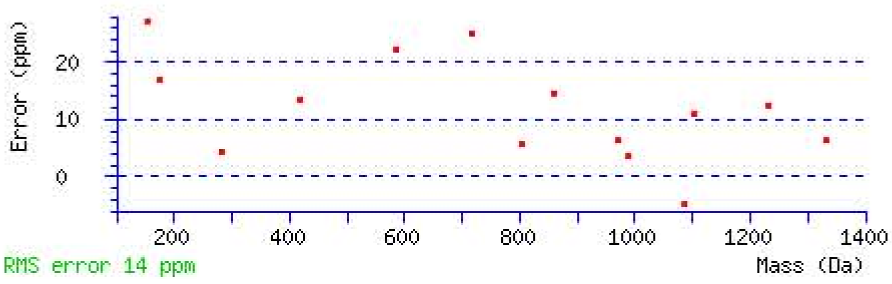
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1403.623840
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 56 **Expect:** 1.8e-005
Matches : 14/86 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							10
2	**173.092069**	87.049672			155.081504	78.044390	T	***1333.594023***	667.300650	1316.567474	658.787375	1315.583458	658.295367	9
3	302.134662	151.570969			284.124097	142.565687	E	***1232.546344***	616.776810	1215.519795	608.263536	1214.535779	607.771528	8
4	**417.161605**	209.084441			399.151040	200.079158	D	***1103.503751***	552.255514	1086.477202	543.742239	1085.493186	543.250231	7
5	546.204198	273.605737			528.193633	264.600455	E	***988.476808***	494.742042	971.450259	486.228768	970.466243	485.736760	6
6	603.225662	302.116469			585.215097	293.111187	G	***859.434215***	430.220746	842.407666	421.707471	841.423650	421.215463	5
7	690.257690	345.632483			672.247125	336.627201	S	***802.412751***	401.710014	785.386202	393.196739	784.402186	392.704731	4
8	819.300283	410.153780			801.289718	401.148497	E	***715.380723***	358.194000	698.354174	349.680725	697.370158	349.188717	3
9	1258.525609	629.766443	1241.499060	621.253168	1240.515044	620.761160	Q	***586.338130***	293.672703	569.311581	285.159428			2
10							K	147.112804	74.060040	130.086255	65.546765			1



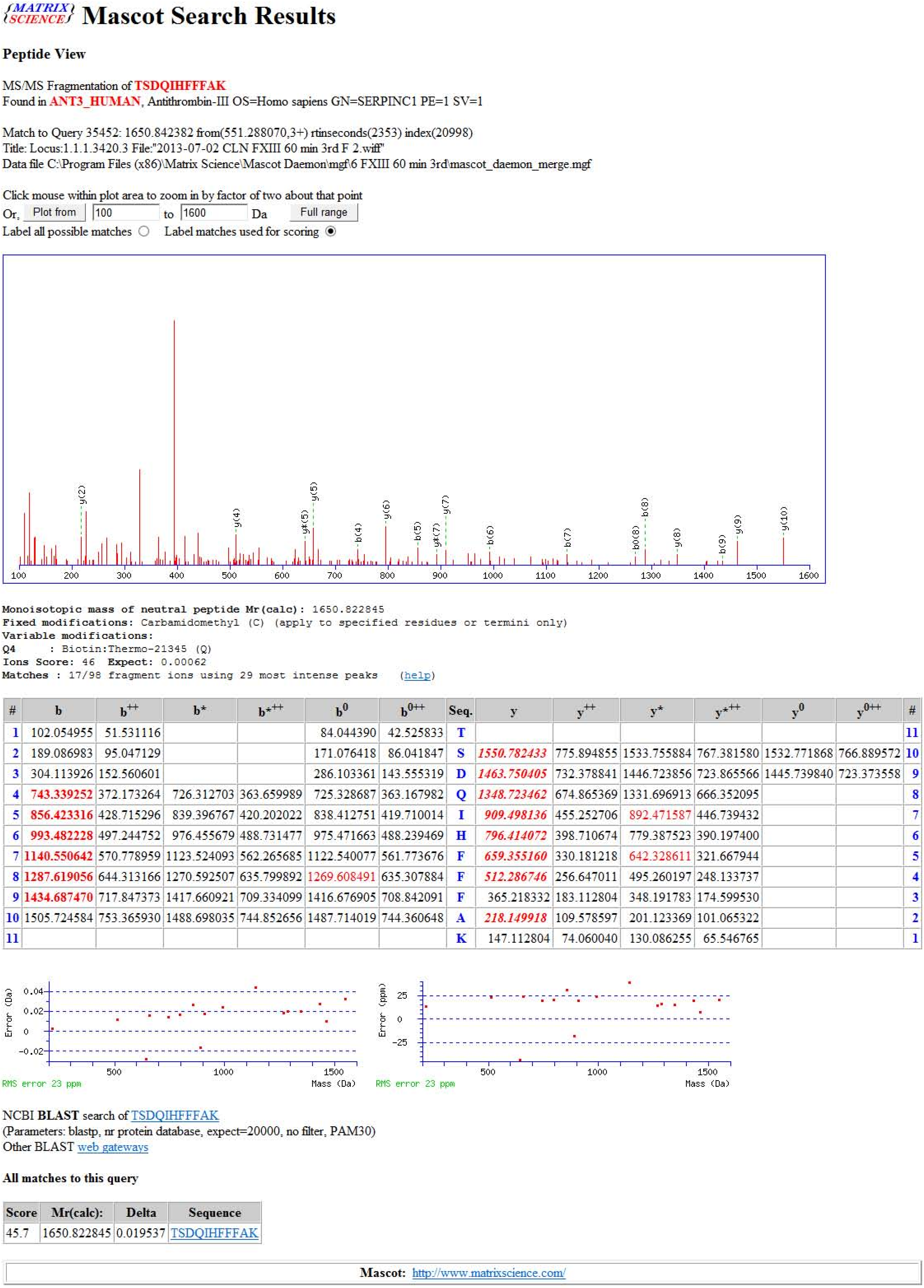


NCBI **BLAST** search of ATEDEGSEQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.3	1403.623840	0.010988	ATEDEGSEQK
14.2	1403.642929	-0.008101	EAESWSQIGNQR
4.7	1403.652832	-0.018004	LTSDEEGEPSGKR

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 35452: 1650.842382 from(551.288070,3+) rtinseconds(2353) index(20998)
Title: Locus:1.1.1.3420.3 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\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: 46  Expect: 0.00062
Matches : 17/98 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							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
45.7	1650.822845	0.019537	TSDQIHFFFAK

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

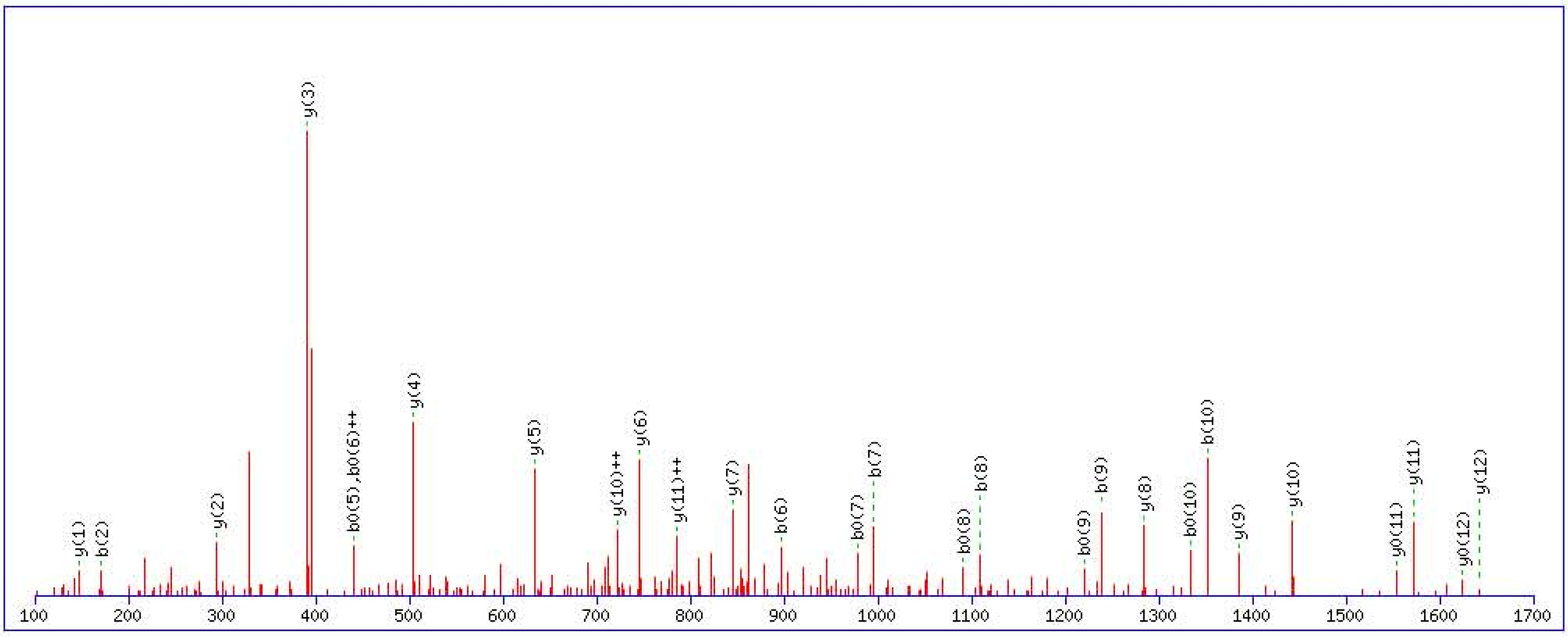
Mascot Search Results

Peptide View

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

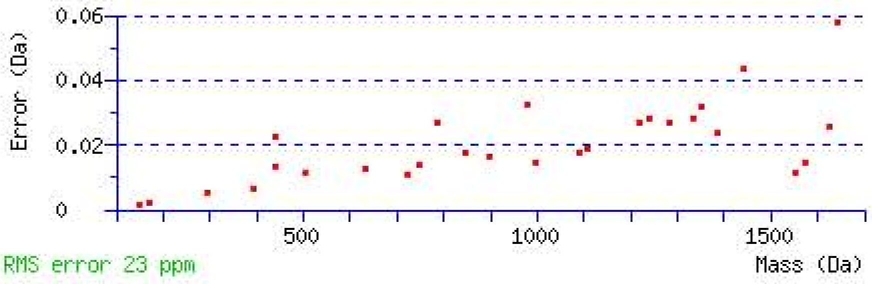
Match to Query 37221: 1740.974248 from(871.494400,2+) rtinseconds(2552) index(21961)
Title: Locus:1.1.1.3489.7 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

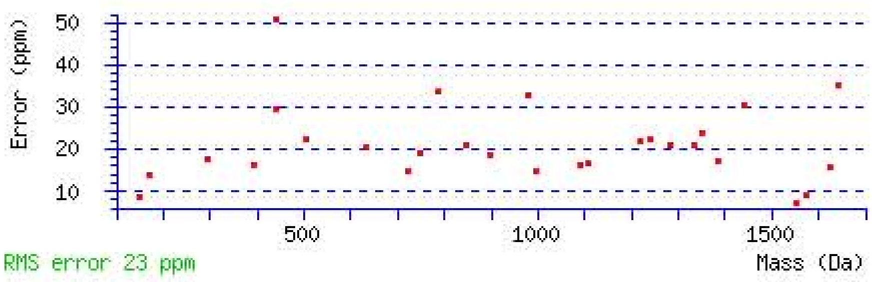
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1740.948425
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 84  Expect: 5.1e-008
Matches : 28/122 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	**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
84.2	1740.948425	0.025823	VAEGTQVLELPFK
9.8	1740.962982	0.011266	ISRQLAEEILMK
4.5	1740.980759	-0.006511	TKIDQLKQELSK

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

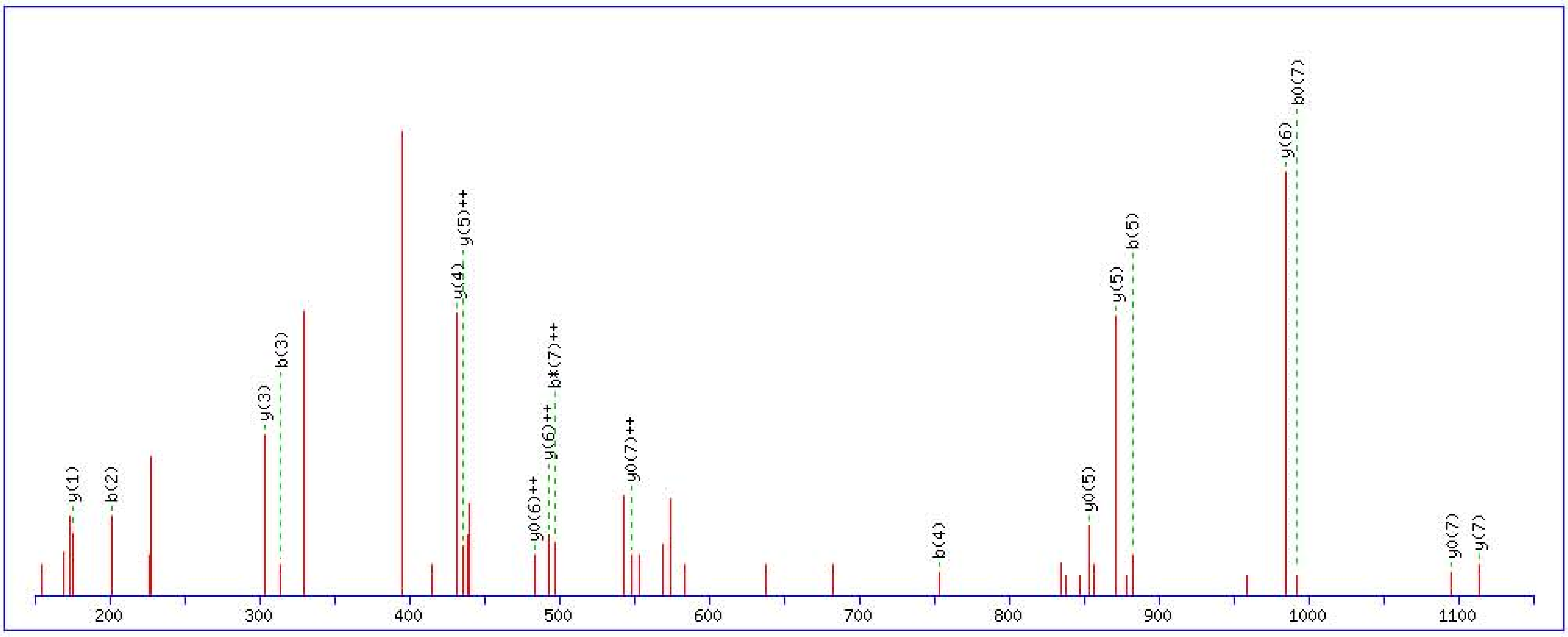
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

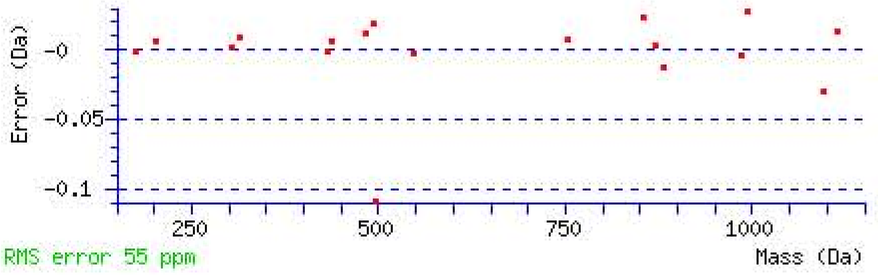
Match to Query 19964: 1183.602488 from(592.808520,2+) rtinseconds(1484) index(30177)
Title: Locus:1.1.1.3065.20 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

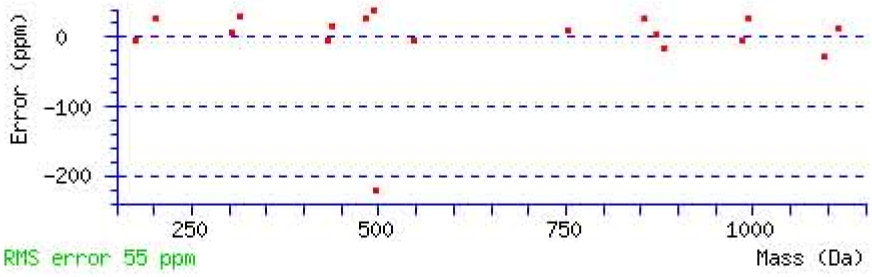
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [150] to [1150] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1183.601913
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.011
Matches : 18/70 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							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
31.9	1183.601913	0.000575	AELQEGAR
11.4	1183.601913	0.000575	EALEQQR
4.8	1183.587997	0.014491	EAKLDHCRR
4.7	1183.601913	0.000575	EALEQQR
4.1	1183.601913	0.000575	ELQAEAGR
3.4	1183.619690	-0.017202	TDPRPDAATIK
2.4	1183.595413	0.007075	AFCRMVTRK
2.3	1183.601913	0.000575	LEAEQQR
1.6	1183.619675	-0.017187	AAAASVPNADGLK

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

{MATRIX}
{SCIENCE}

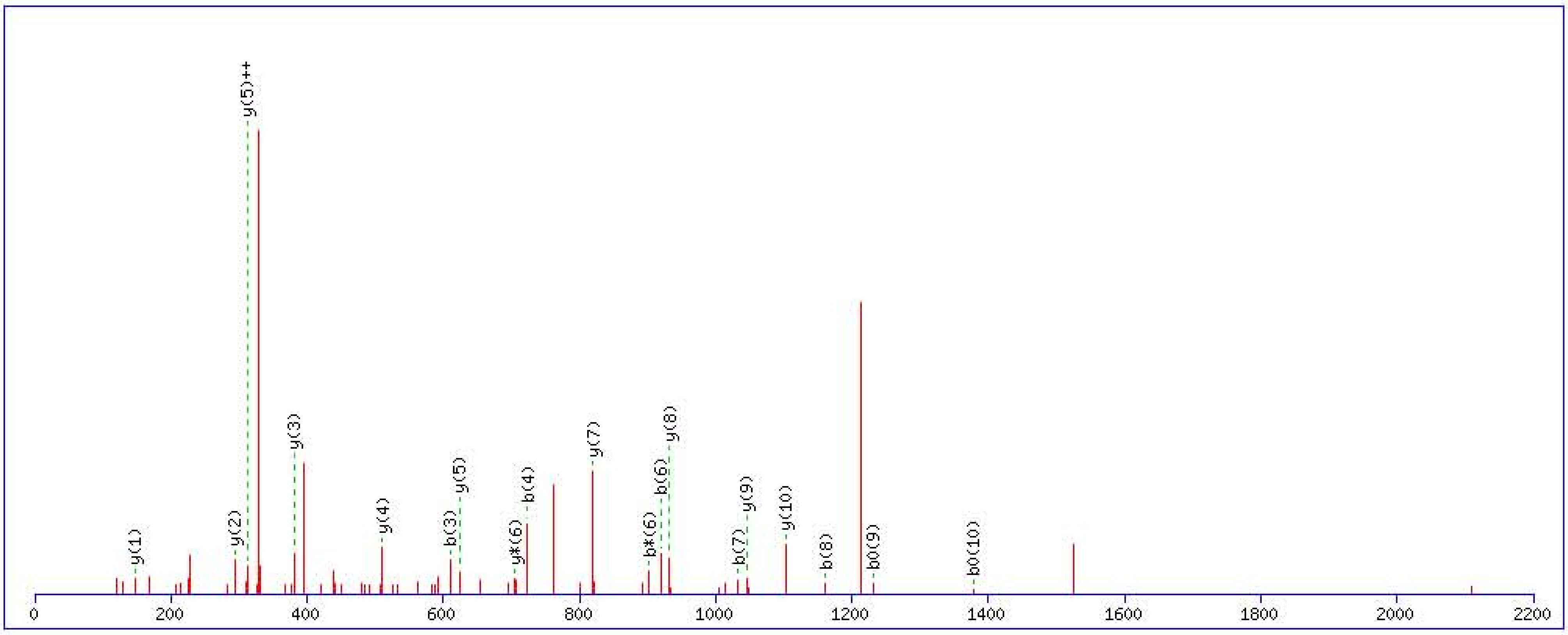
Mascot Search Results

Peptide View

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

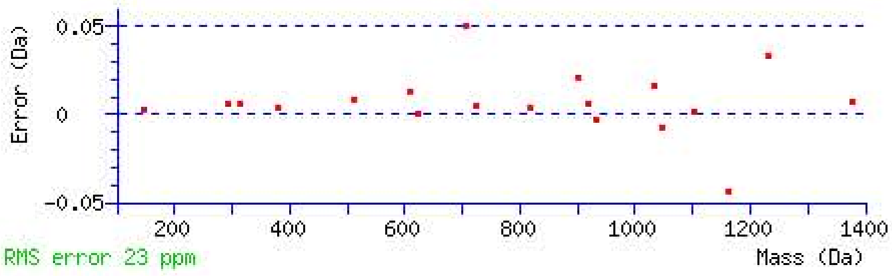
Match to Query 31029: 1540.874188 from(771.444370,2+) rtinseconds(2838) index(9661)
Title: Locus:1.1.1.3539.18 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

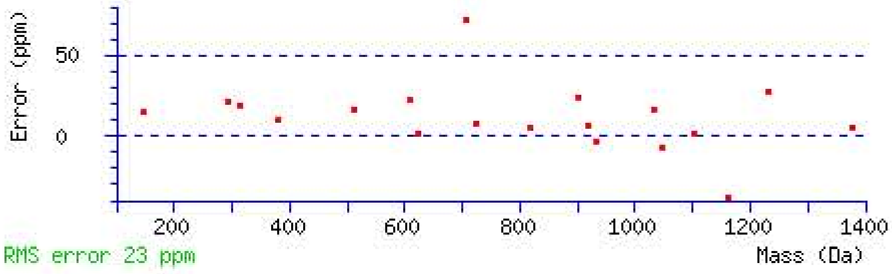
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1540.868713
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 2.6e-005
Matches : 19/102 fragment ions using 35 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
57.2	1540.868713	0.005475	QGLLPVLESFK
10.0	1540.894531	-0.020343	QAVLSMVRKAK

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

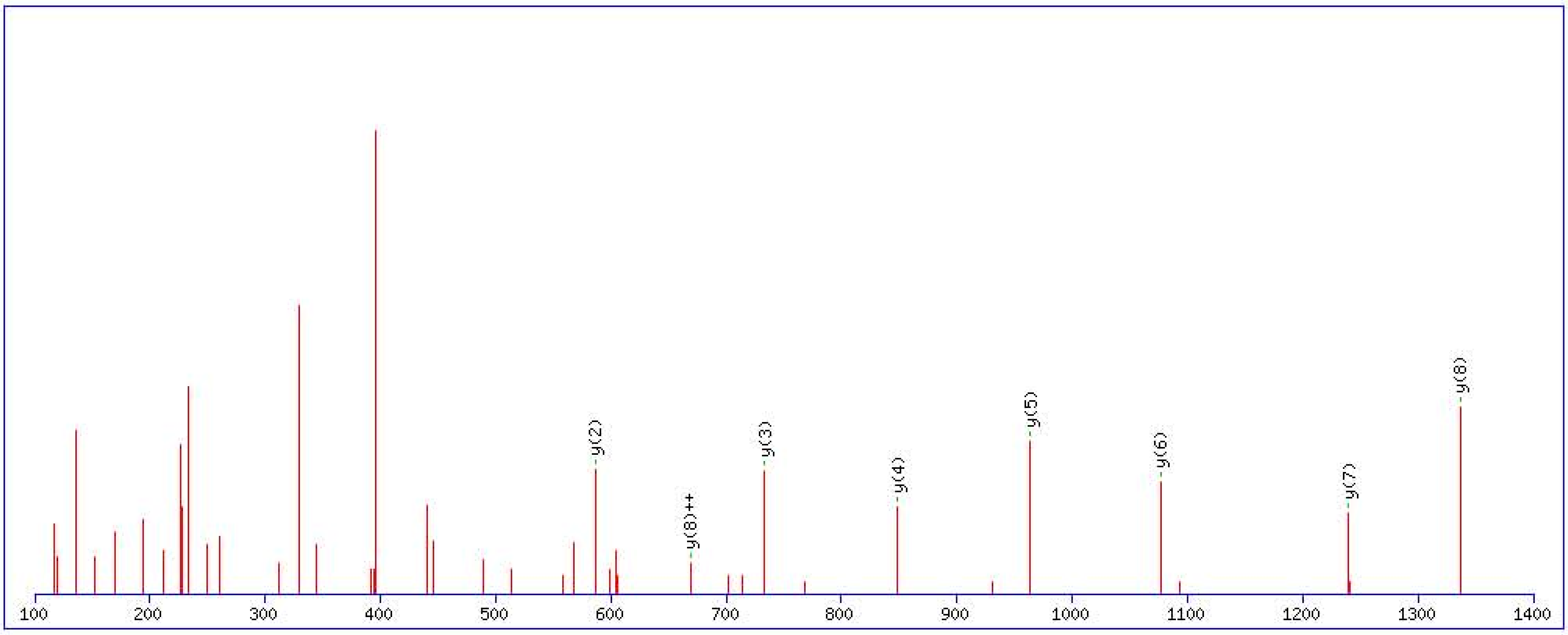
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

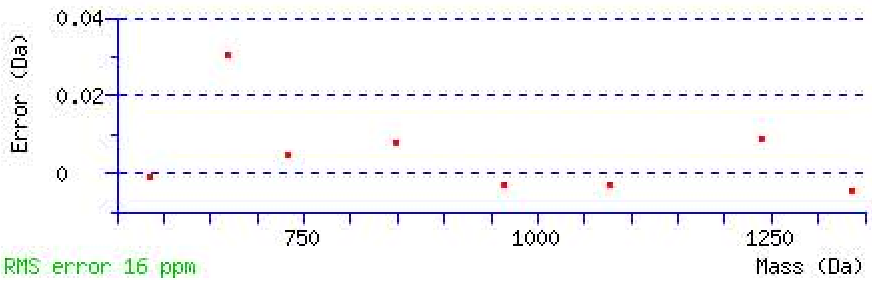
Match to Query 31534: 1562.785362 from(521.935730,3+) rtinseconds(2190) index(34172)
Title: Locus:1.1.1.3312.3 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

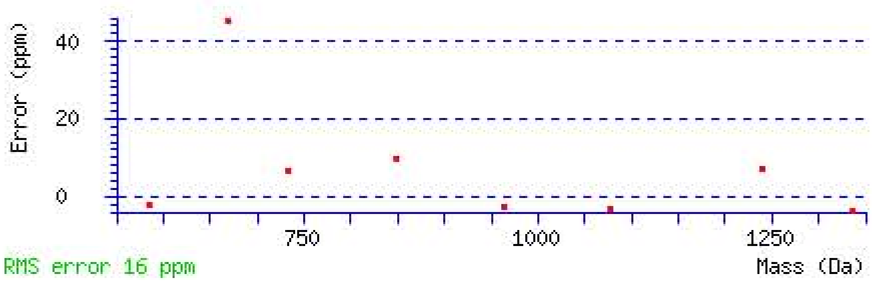
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1562.780304
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 4.6e-005
Matches : 8/90 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	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
49.3	1562.780304	0.005058	VQPYLDDFQK
3.0	1562.808624	-0.023262	LNSPTTTSQIMARK

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

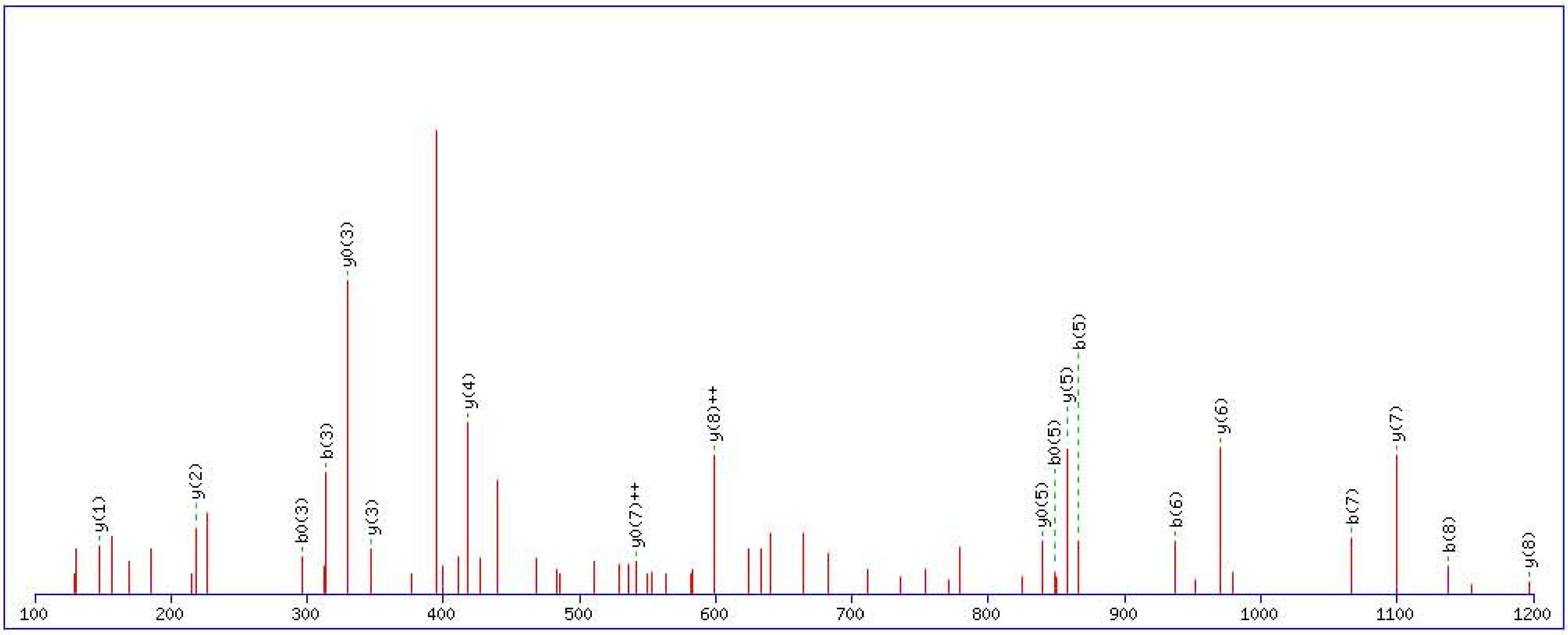
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

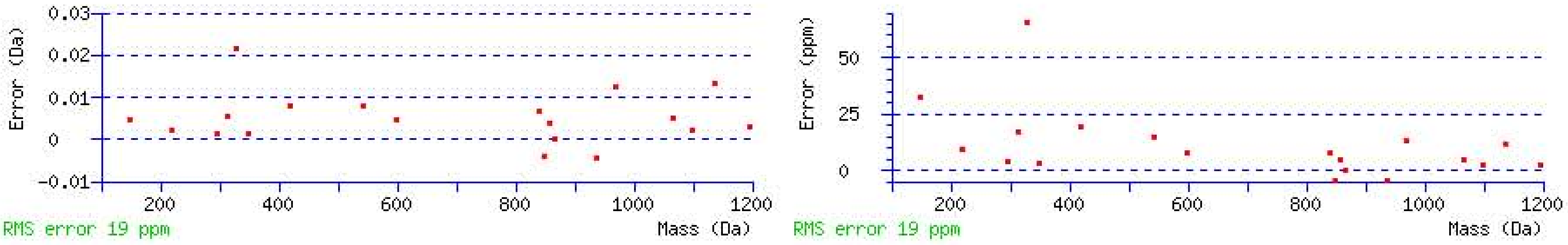
Match to Query 22614: 1282.649828 from(642.332190,2+) rtinseconds(1587) index(2584)
Title: Locus:1.1.1.3104.17 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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): 1282.659088
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00011
Matches : 19/84 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	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
46.3	1282.659088	-0.009260	SPELQAEAK
3.7	1282.662949	-0.013121	DLSDTQRHLAK
3.1	1282.641830	0.007998	SYPGHVQPATAR
1.8	1282.655716	-0.005888	ALEAEKYGFQK
1.0	1282.641815	0.008013	EIRFQPNDHK

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

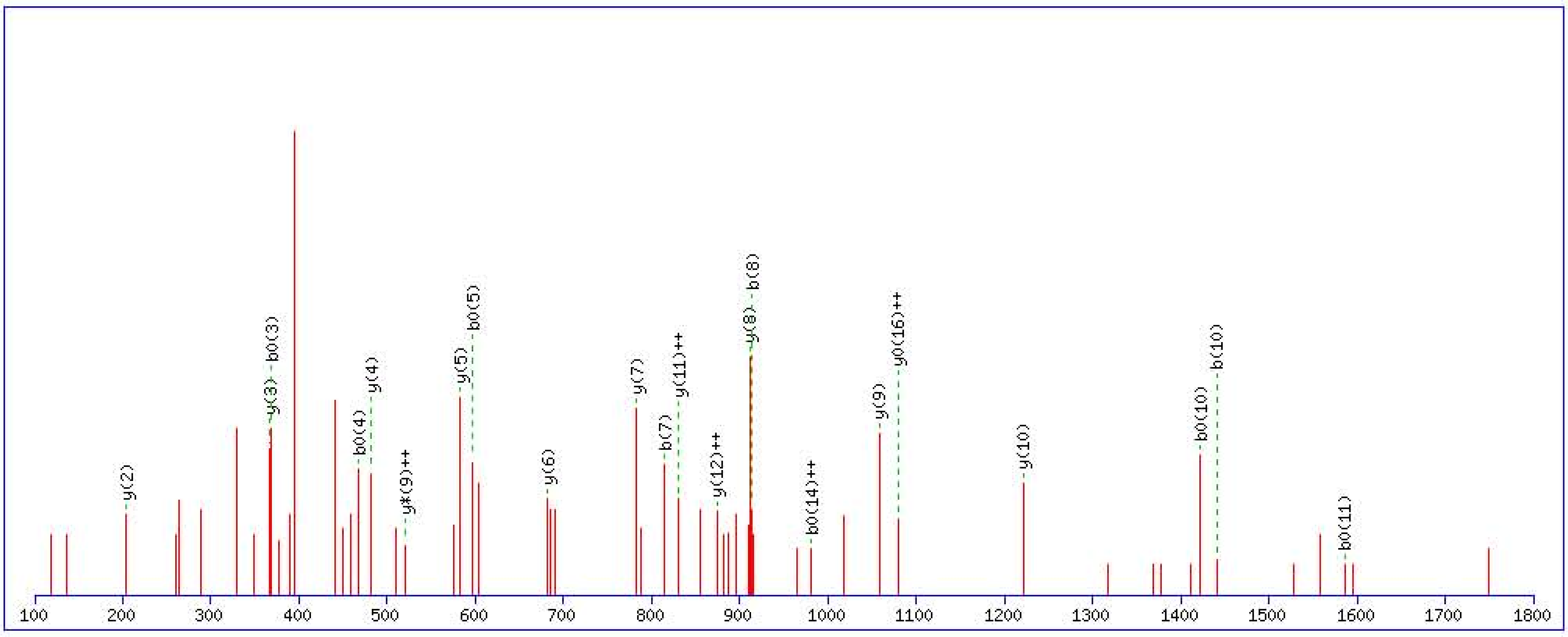
Mascot Search Results

Peptide View

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

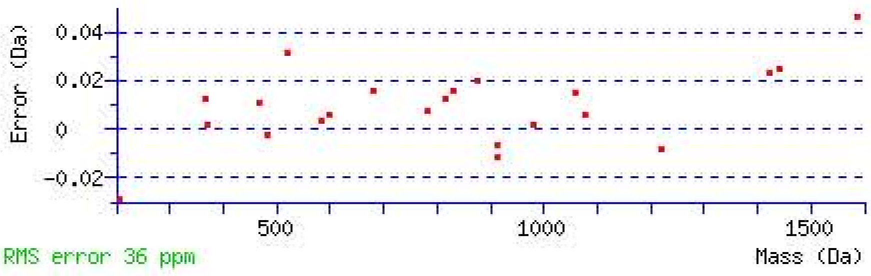
Match to Query 52452: 2660.260392 from(887.760740,3+) rtinseconds(3196) index(40147)
Title: Locus:1.1.1.3657.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

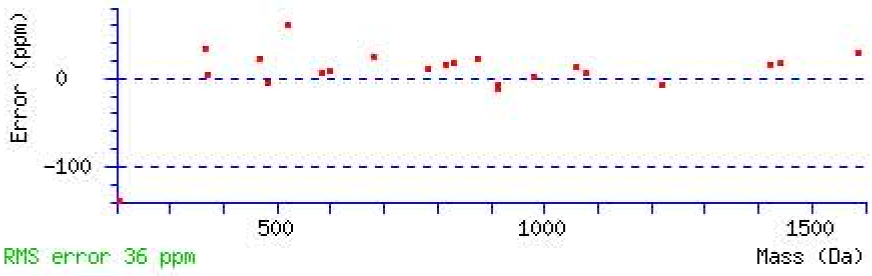
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2660.250244
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 34 **Expect:** 0.0078
Matches : 22/204 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							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
34.5	2660.250244	0.010148	EPCVESLVSQYFQTVTDYGK
19.5	2660.250244	0.010148	EPCVESLVSQYFQTVTDYGK

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

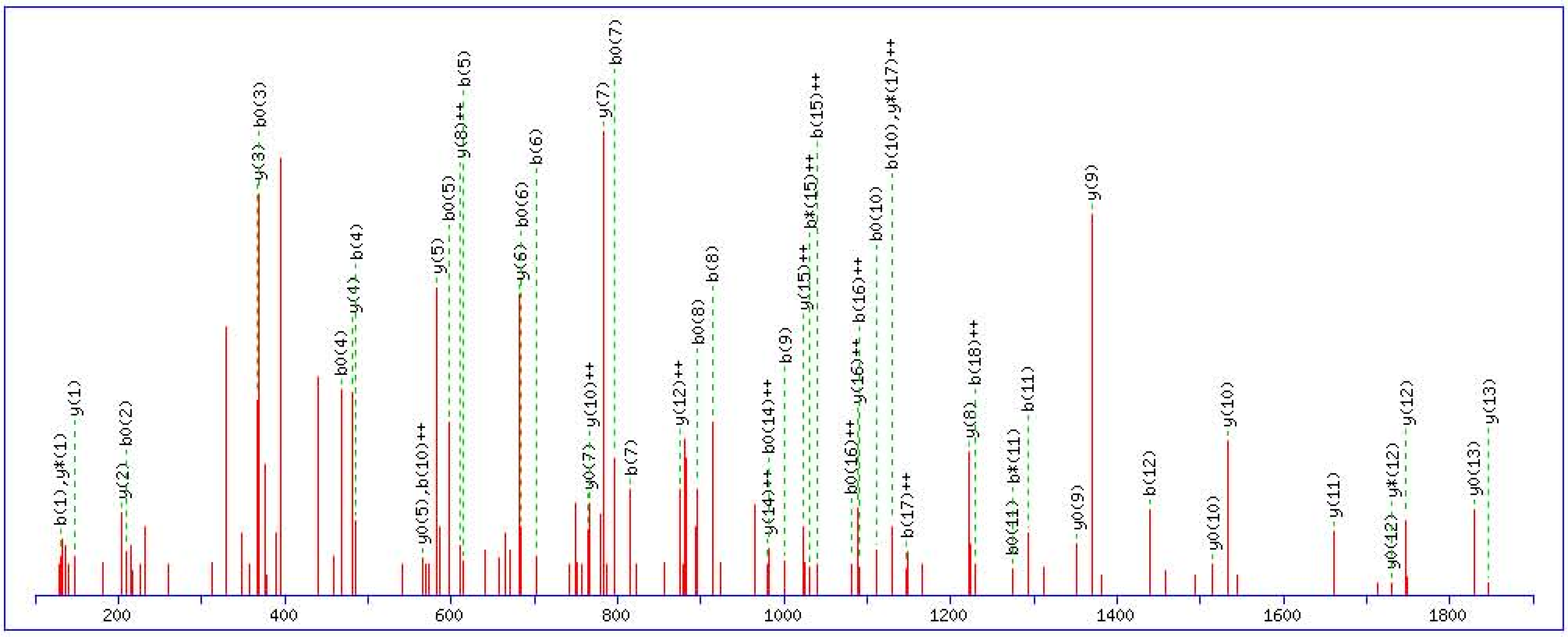
Mascot Search Results

Peptide View

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

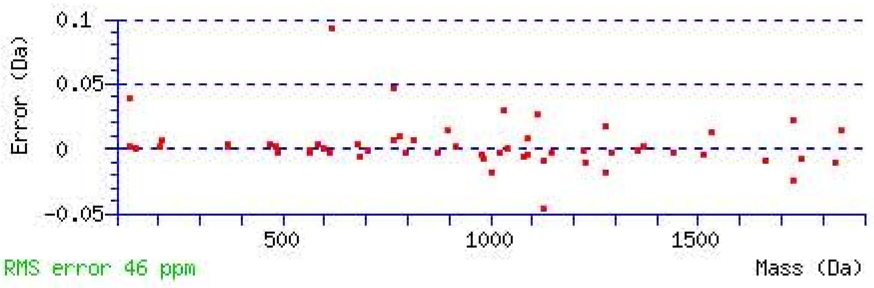
Match to Query 52456: 2660.261352 from(887.761060,3+) rtinseconds(3148) index(39931)
Title: Locus:1.1.1.3641.21 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

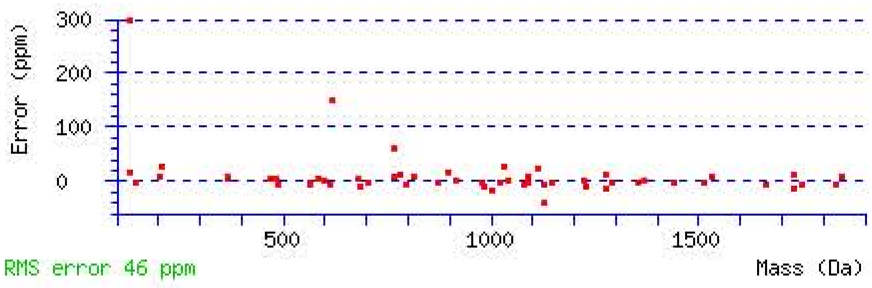
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2660.250244
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13 : Biotin:Thermo-21345 (Q)
Ions Score: 73 **Expect:** 9.8e-007
Matches : 56/204 fragment ions using 92 most intense peaks (help)

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





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
73.5	2660.250244	0.011108	EPCVESLVSQYFQTVTDYGK
39.9	2660.250244	0.011108	EPCVESLVSQYFQTVTDYGK

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

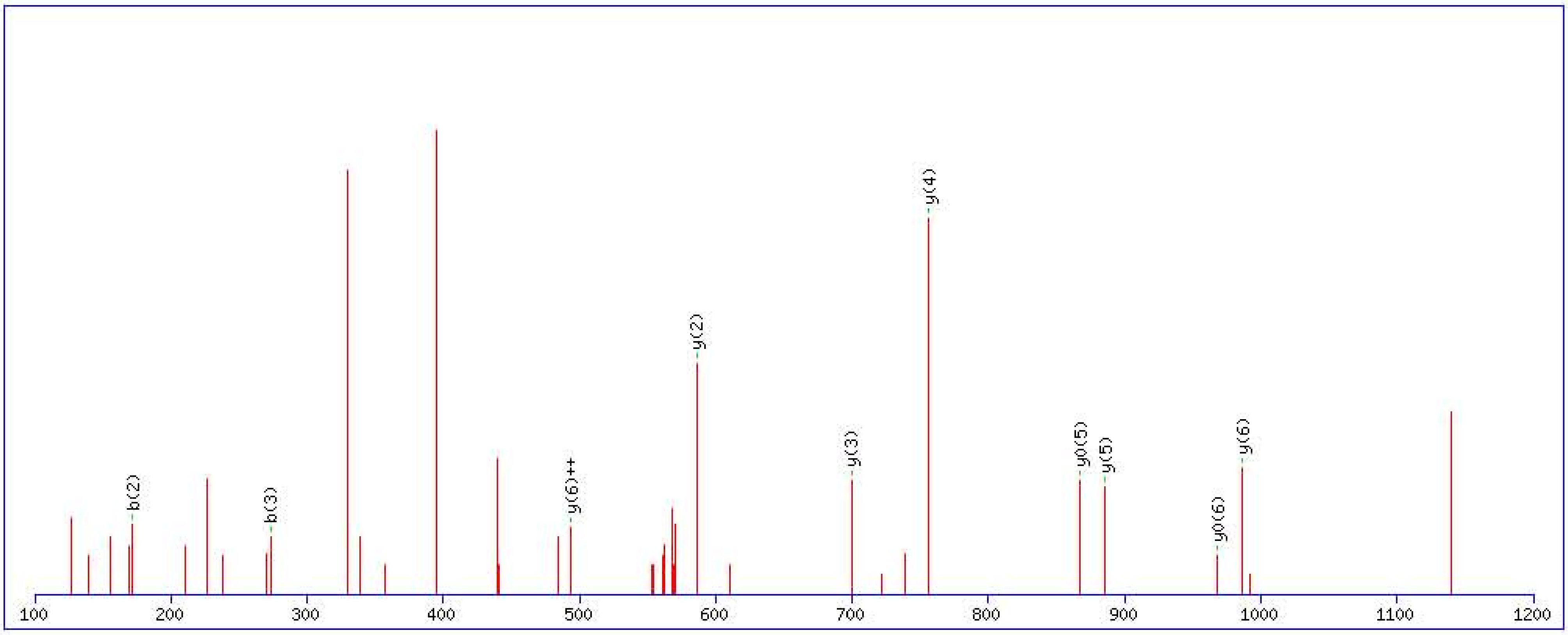
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

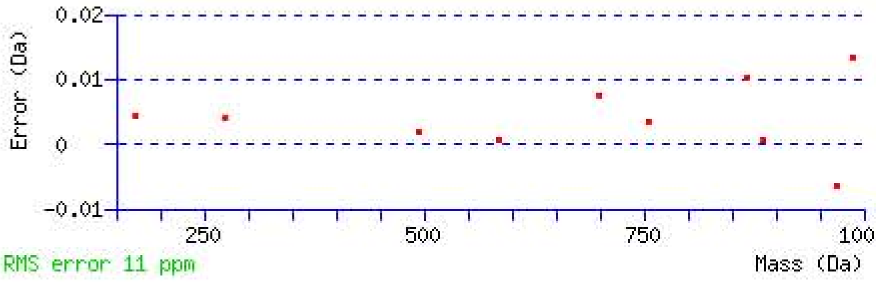
Match to Query 18992: 1156.589608 from(579.302080,2+) rtinseconds(1443) index(59431)
Title: Locus:1.1.1.3128.16 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

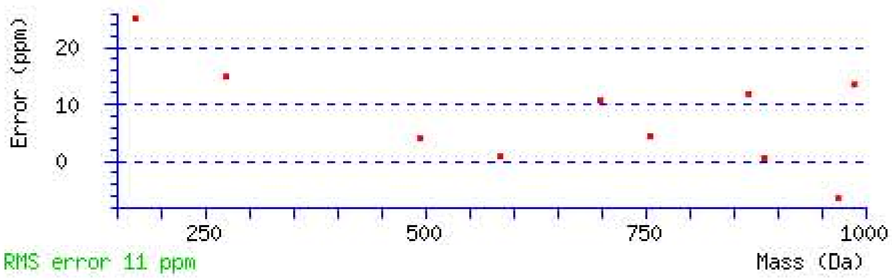


Monoisotopic mass of neutral peptide Mr(calc): 1156.591034
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 27 **Expect:** 0.042
Matches : 10/70 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							8
2	**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



RMS error 11 ppm



RMS error 11 ppm

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
26.6	1156.591034	-0.001426	GNTEGLQK

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

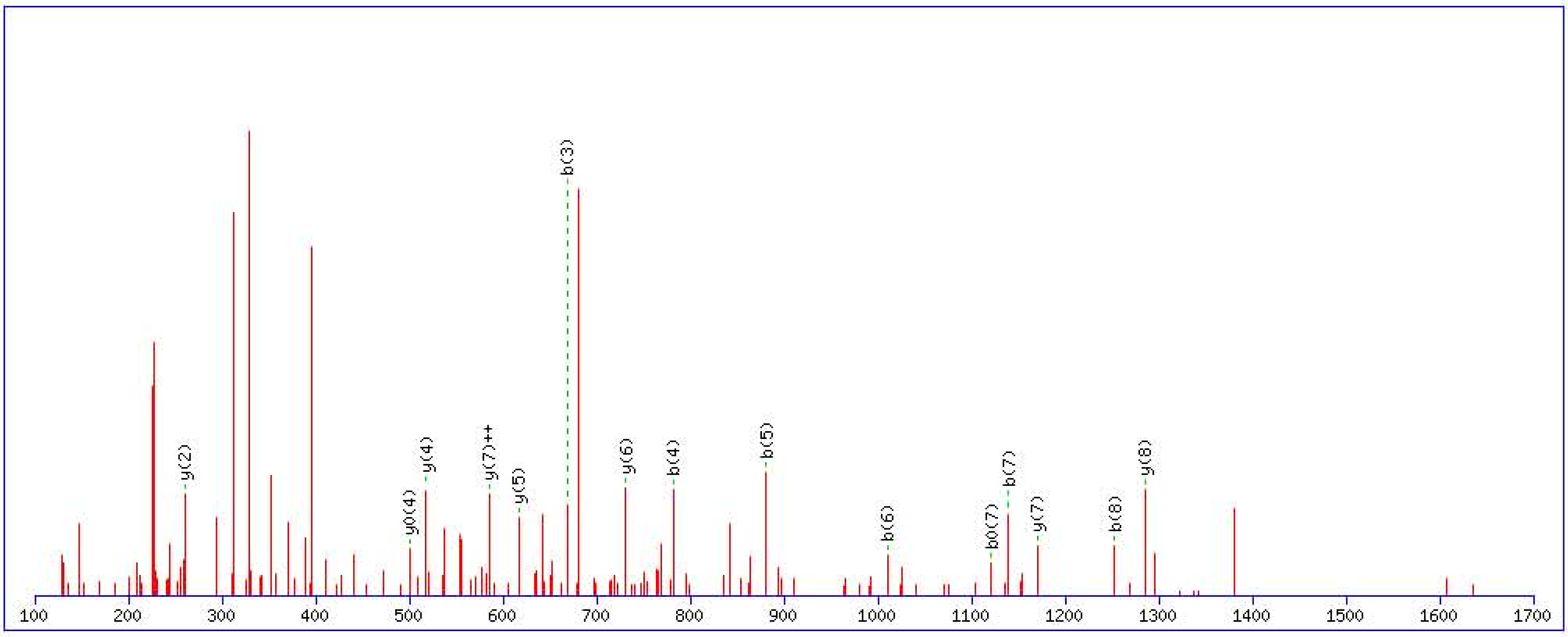
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

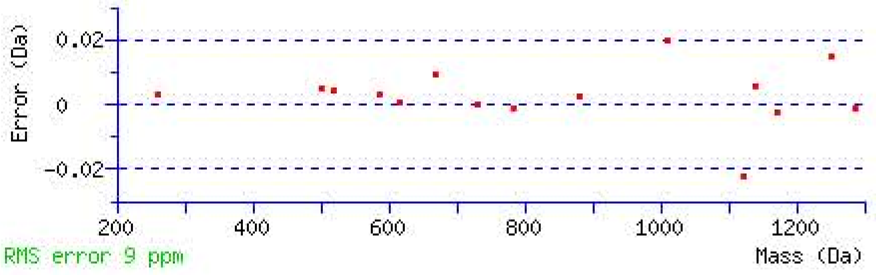
Match to Query 26290: 1397.725428 from(699.869990,2+) rtinseconds(1861) index(61658)
Title: Locus:1.1.1.3274.7 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

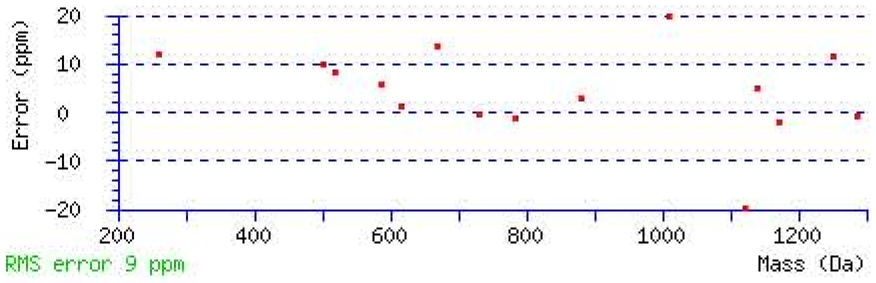
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1397.722427
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.0022
Matches : 15/86 fragment ions using 26 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308					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

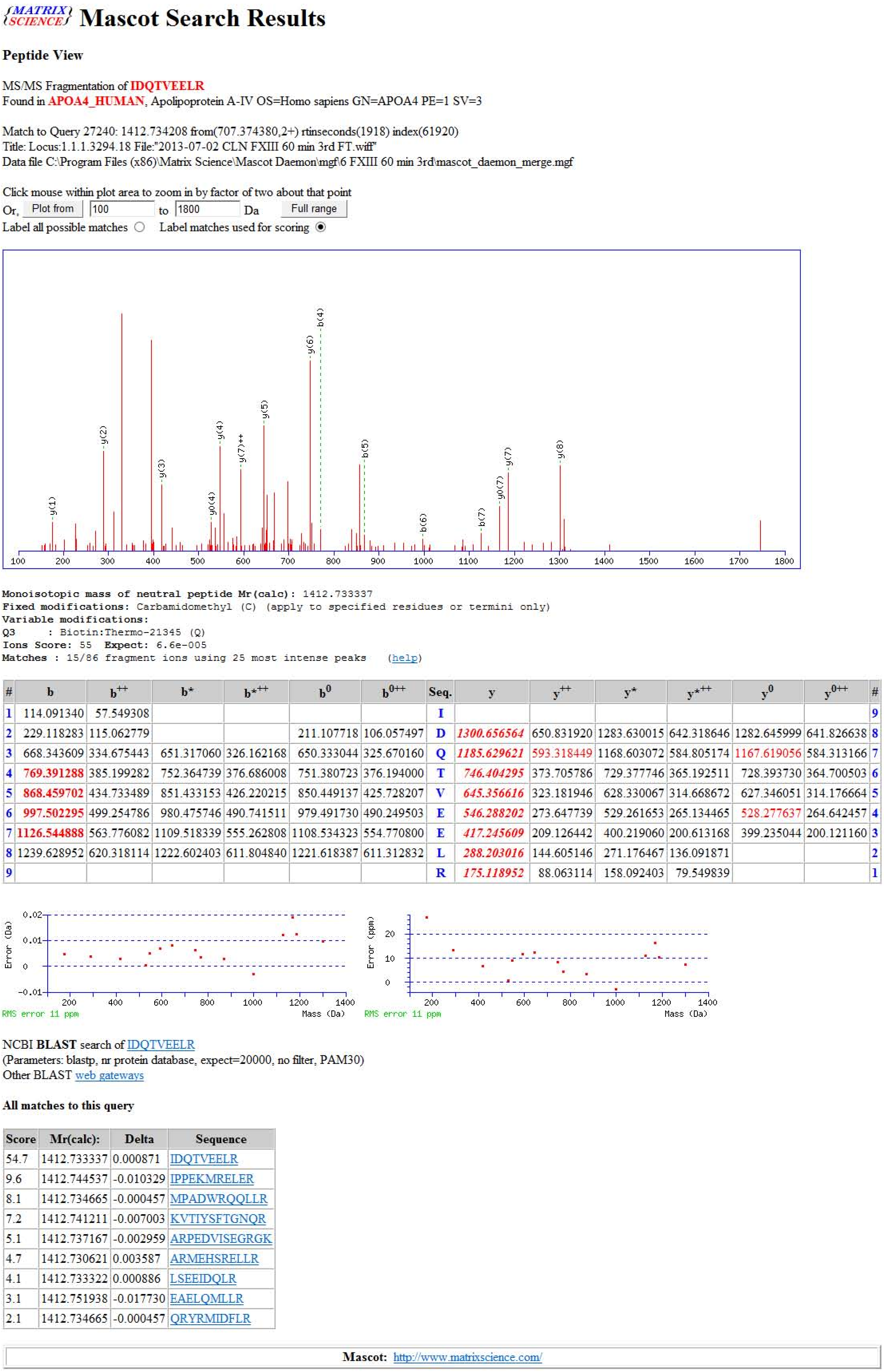




NCBI **BLAST** search of IDQNVEELK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.6	1397.722427	0.003001	IDQNVEELK
9.6	1397.744873	-0.019445	MLEKARHQELK
8.8	1397.744873	-0.019445	QRREEELK
3.1	1397.740204	-0.014776	VEGDLKGPEVDIK
3.1	1397.740204	-0.014776	VEGDLKGPEVDLK
2.5	1397.744873	-0.019445	QEERRELK
2.5	1397.744904	-0.019476	SSGPQRAGSLK
2.4	1397.737686	-0.012258	MYLNFLVSLGNK
2.0	1397.723785	0.001643	LFVSHMIDKHR
1.3	1397.708023	0.017405	KMALNSLMSLMK



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 27240: 1412.734208 from(707.374380,2+) rtinseconds(1918) index(61920)
Title: Locus:1.1.1.3294.18 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\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): 1412.733337
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 55  Expect: 6.6e-005
Matches : 15/86 fragment ions using 25 most intense peaks   (help)
```

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

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.7	1412.733337	0.000871	IDQTVEELR
9.6	1412.744537	-0.010329	IPPEKMRELER
8.1	1412.734665	-0.000457	MPADWRQQLLR
7.2	1412.741211	-0.007003	KVTIYSFTGNQR
5.1	1412.737167	-0.002959	ARPEDVISEGRGK
4.7	1412.730621	0.003587	ARMEHSRELLR
4.1	1412.733322	0.000886	LSEEIDQLR
3.1	1412.751938	-0.017730	EAELQMLLR
2.1	1412.734665	-0.000457	QRYRMIDFLR

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

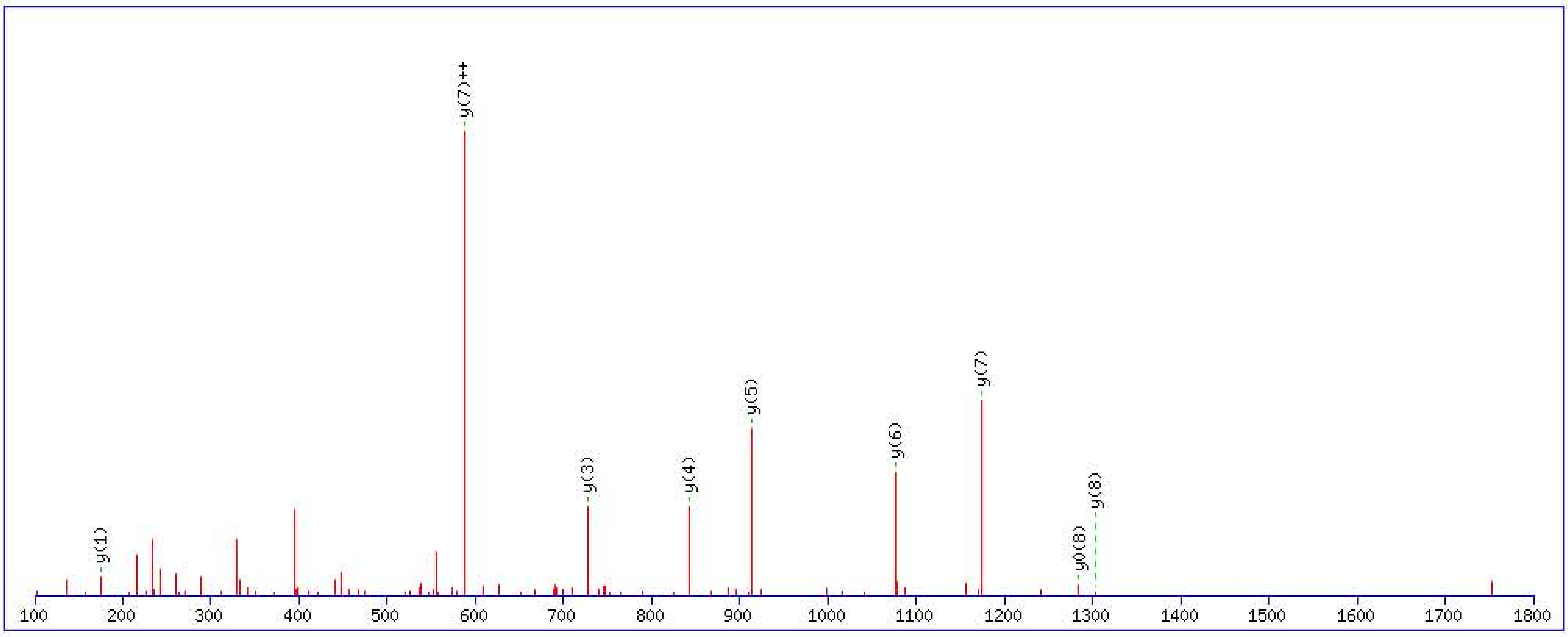
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

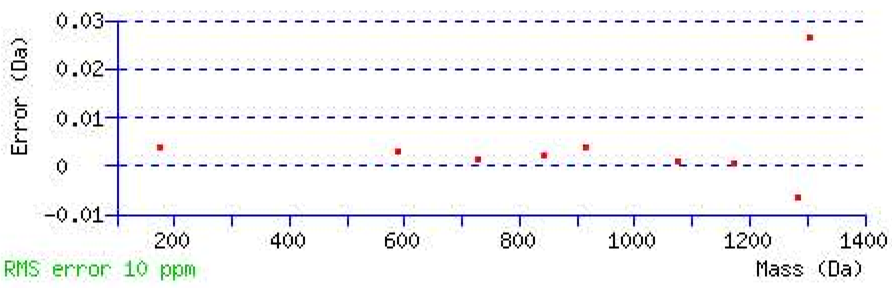
Match to Query 27260: 1414.726728 from(708.370640,2+) rtinseconds(1983) index(4866)
Title: Locus:1.1.1.3242.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

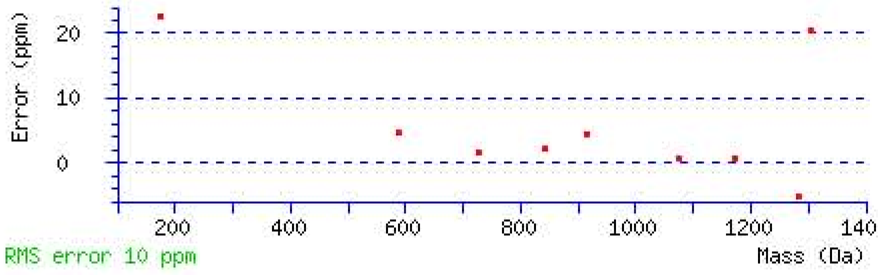
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 56  Expect: 4.5e-005
Matches : 9/76 fragment ions using 13 most intense peaks   (help)
```

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





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.8	1414.727844	-0.001116	LEPYADQLR
8.8	1414.716400	0.010328	LEEDARLEERR
7.9	1414.712585	0.014143	EISTEEQLR
4.7	1414.731689	-0.004961	NKAEFHQSVISR
2.9	1414.735062	-0.008334	IQLMQEVDRQR
2.5	1414.713943	0.012785	KLQCIADQFHR
1.9	1414.741547	-0.014819	LEKENLEERQK
1.2	1414.735077	-0.008349	SSMSGLHLVKQGR
0.6	1414.741577	-0.014849	LETVQADNIREK
0.4	1414.741577	-0.014849	ELDVEVSRLEAR

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

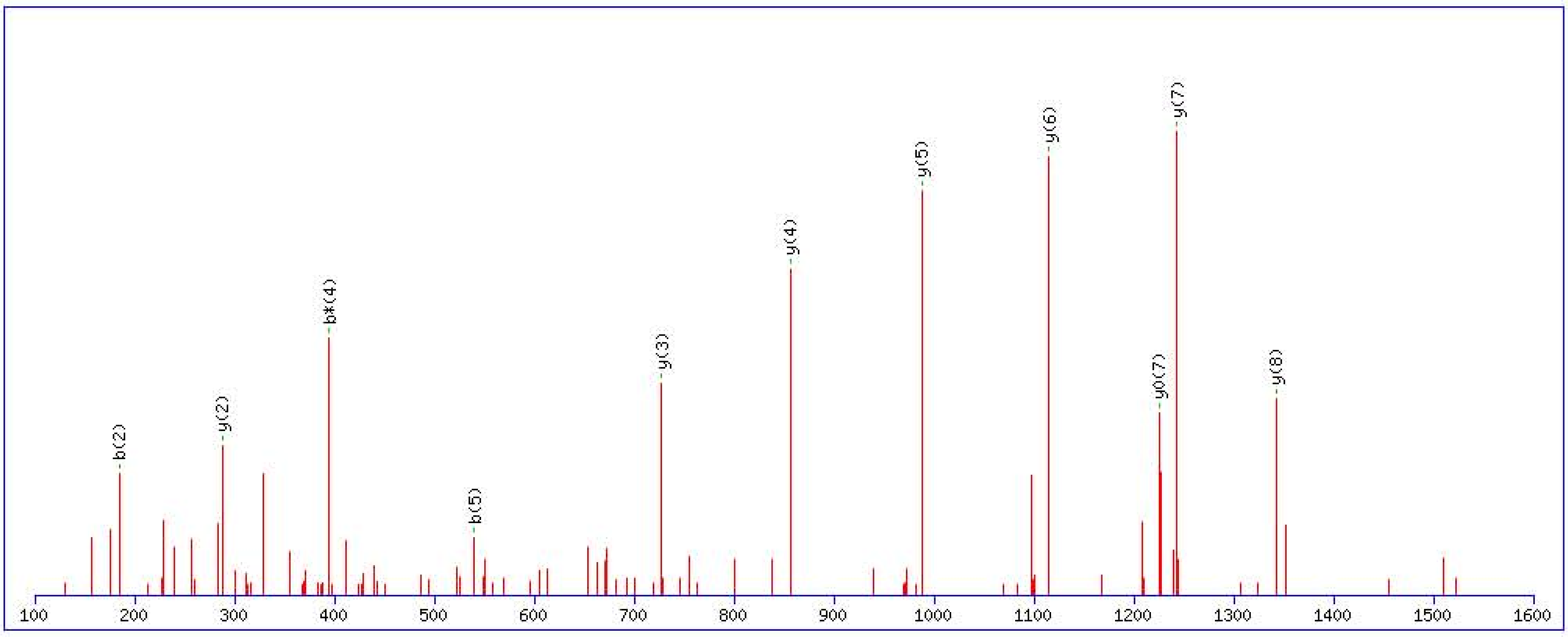
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

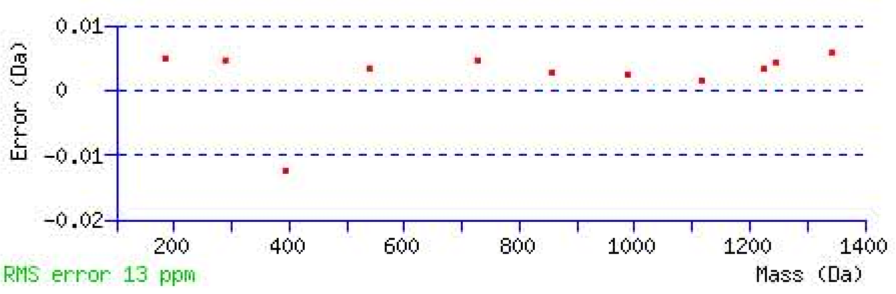
Match to Query 30736: 1525.807708 from(763.911130,2+) rtinseconds(2134) index(63333)
Title: Locus:1.1.1.3369.18 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

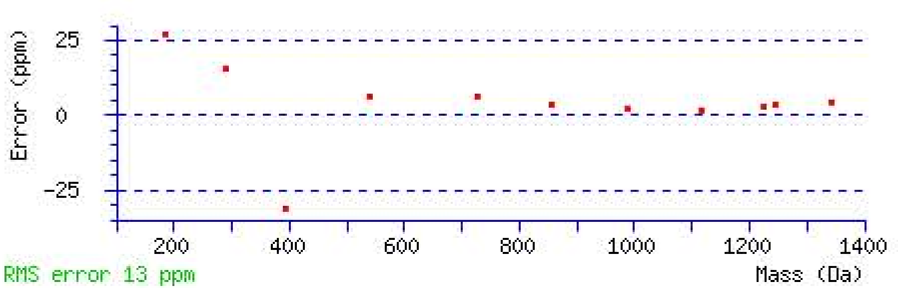
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1525.810867
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 66  Expect: 1.2e-005
Matches : 11/84 fragment ions using 14 most intense peaks   (help)
```

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





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.1	1525.810867	-0.003159	ALVQQMEQLR
23.4	1525.810867	-0.003159	ALVQQMEQLR
17.1	1525.792236	0.015472	ALTEQQEQLR
11.9	1525.810867	-0.003159	ALVQQMEQLR
11.1	1525.798752	0.008956	SPVKEEEKPQEVK
9.7	1525.800064	0.007644	ARALQSYYEAKAR
8.2	1525.807495	0.000213	WPPQQLMLSAALR
4.3	1525.784836	0.022872	LAQVATEEPERQR
4.3	1525.814697	-0.006989	ERQRTEQLR
4.1	1525.803482	0.004226	VNTPAGSSQKAR

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

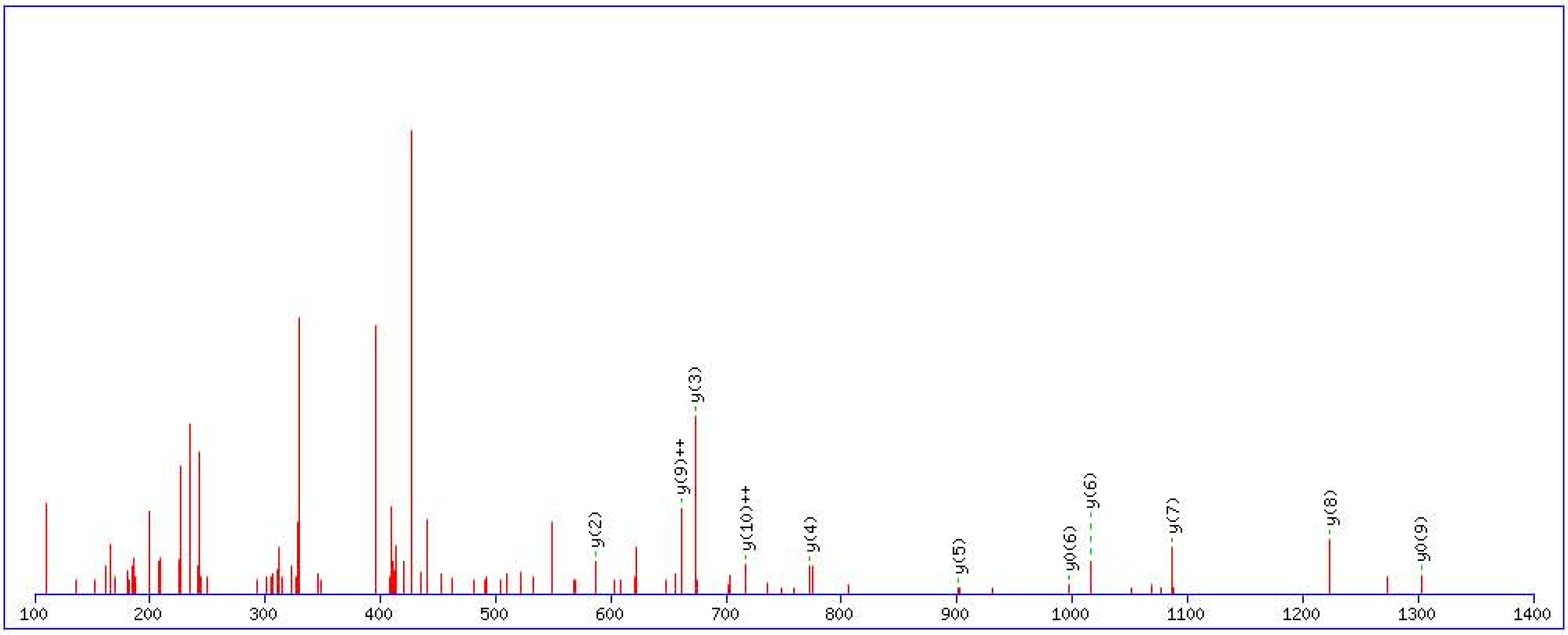
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

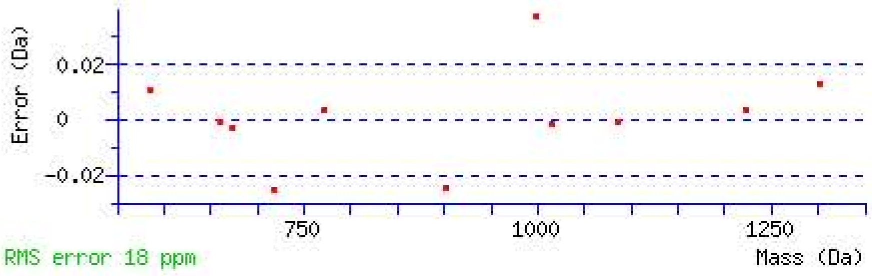
Match to Query 31104: 1545.831312 from(516.284380,3+) rtinseconds(1557) index(60148)
Title: Locus:1.1.1.3168.7 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

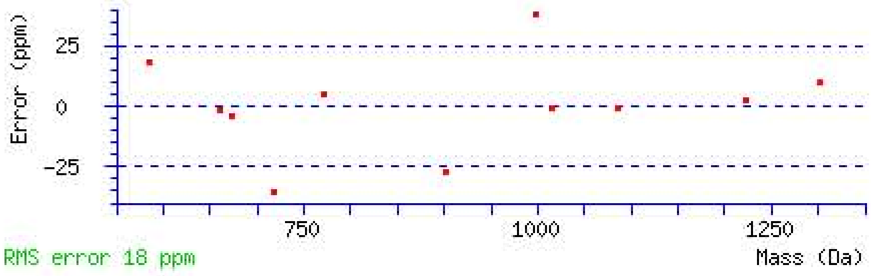
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 35 **Expect:** 0.0074
Matches : 11/94 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							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
34.7	1545.833710	-0.002398	LLPHANEVSQK

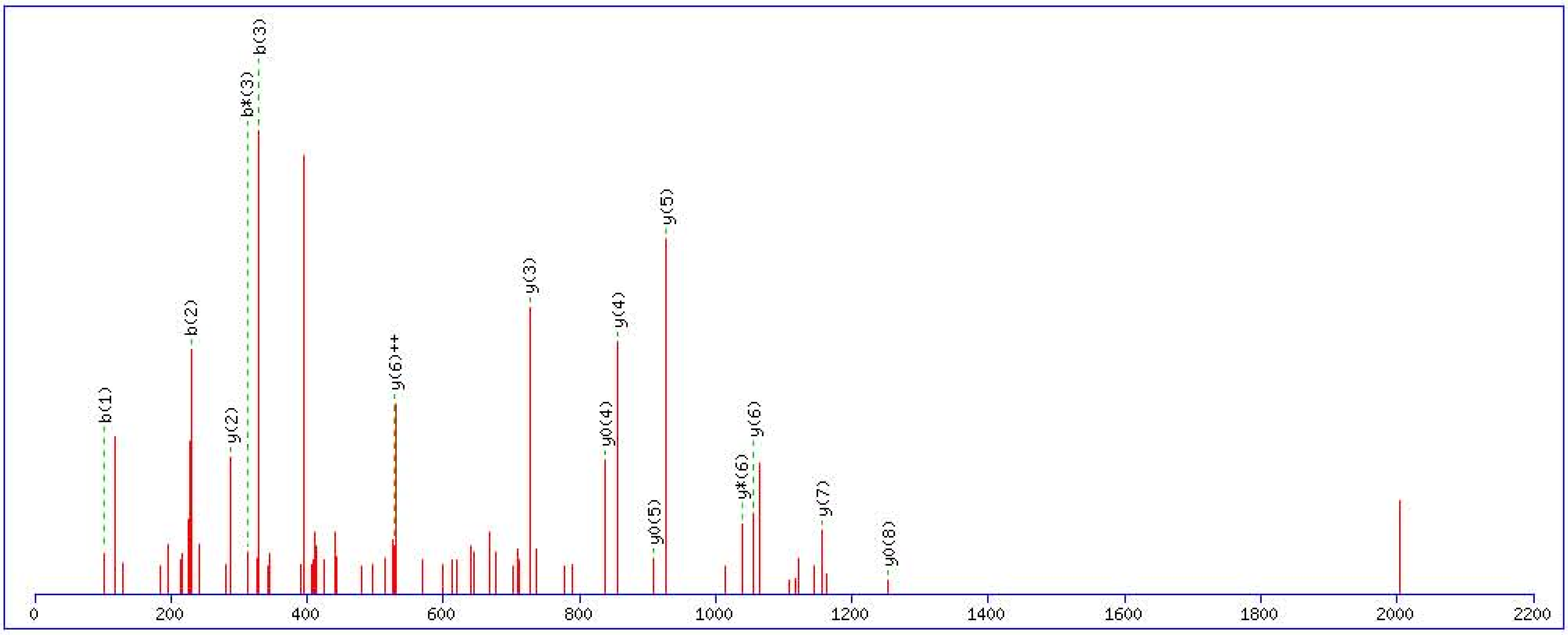
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

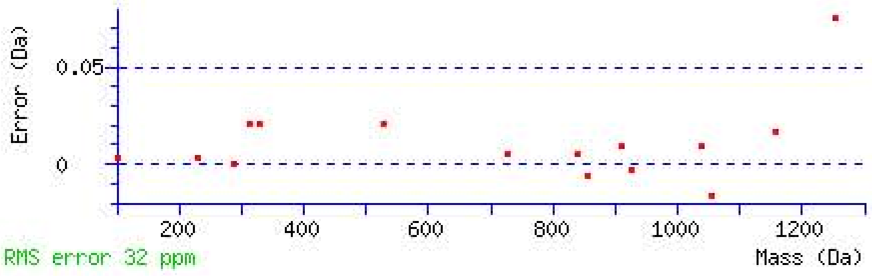
Match to Query 33221: 1597.822302 from(533.614710,3+) rtinseconds(1609) index(60490)
Title: Locus:1.1.1.3186.17 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

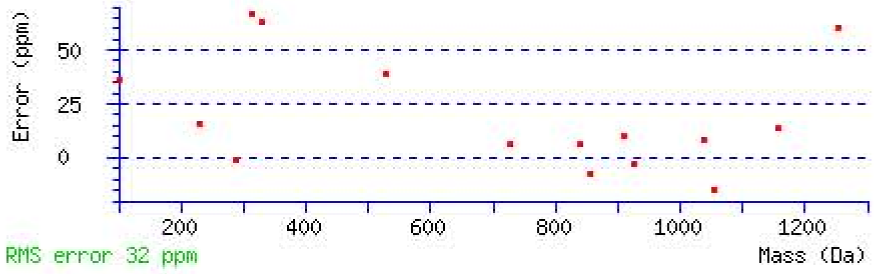
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1597.824615
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.0044
Matches : 15/112 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							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
26.8	1597.824615	-0.002313	TQVNTQAEQLR
6.1	1597.824615	-0.002313	TQVNTQAEQLR
1.7	1597.835846	-0.013544	TKAAATAGGQGGAAR

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

{MATRIX SCIENCE}

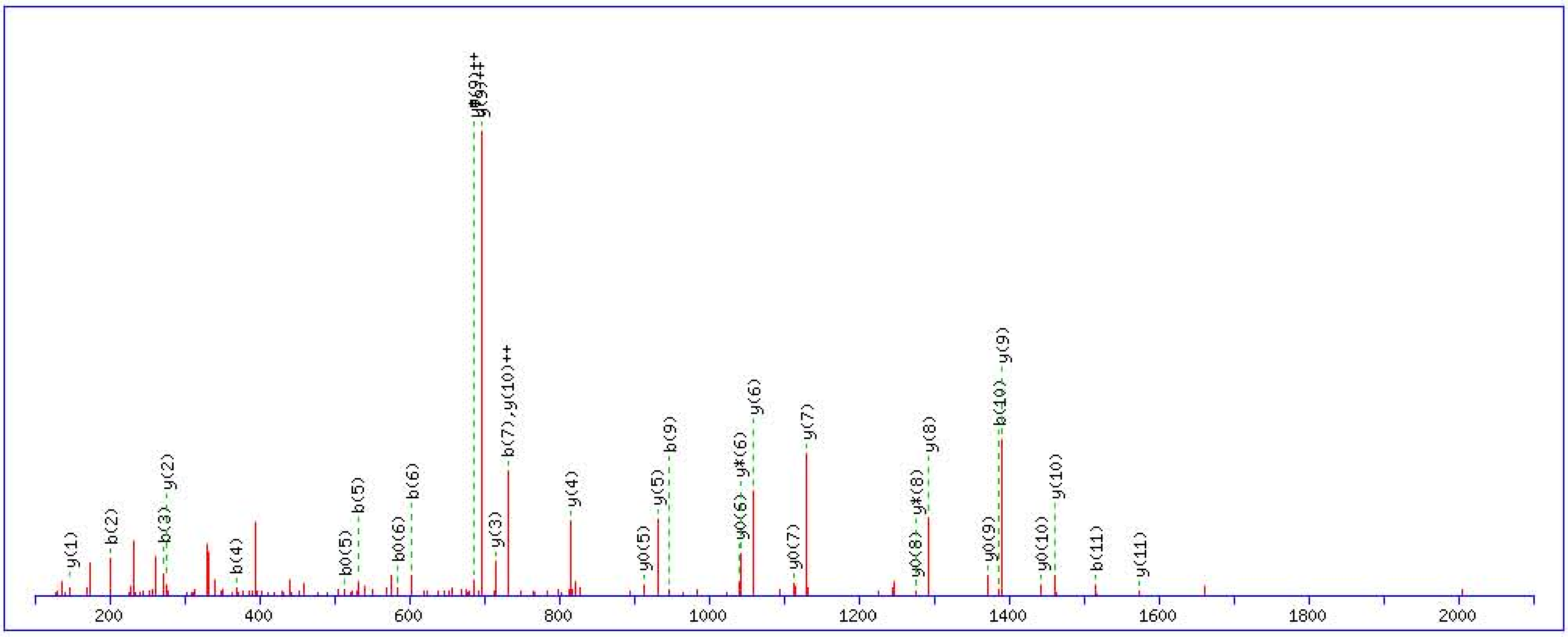
Mascot Search Results

Peptide View

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

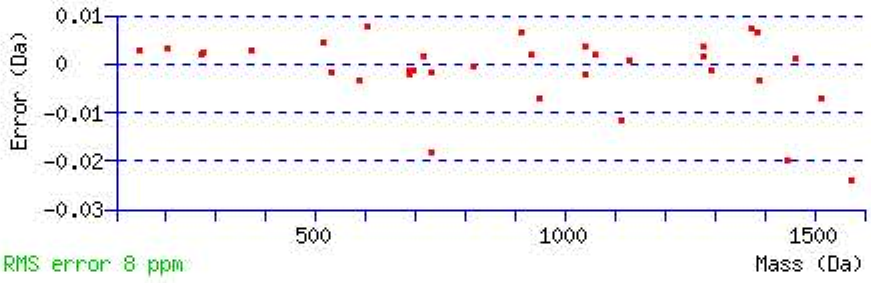
Match to Query 35636: 1660.815088 from(831.414820,2+) rtinseconds(1733) index(31564)
Title: Locus:1.1.1.3152.13 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

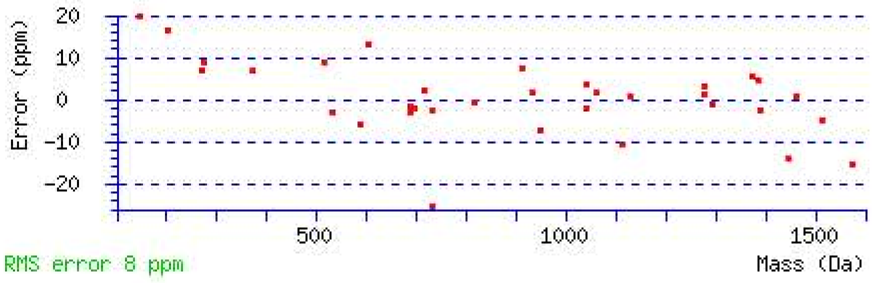
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [2100] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



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: 65 **Expect:** 6.4e-006
Matches : 34/118 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	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
65.5	1660.813034	0.002054	SLAPYAQDTQEK
34.7	1660.813034	0.002054	SLAPYAQDTQEK
10.4	1660.820908	-0.005820	SLARAGFYYTGVNDK
6.8	1660.826782	-0.011694	EAATQAQQTLGSTIDK
1.8	1660.813019	0.002069	EAALMAEFDNPNIVK

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

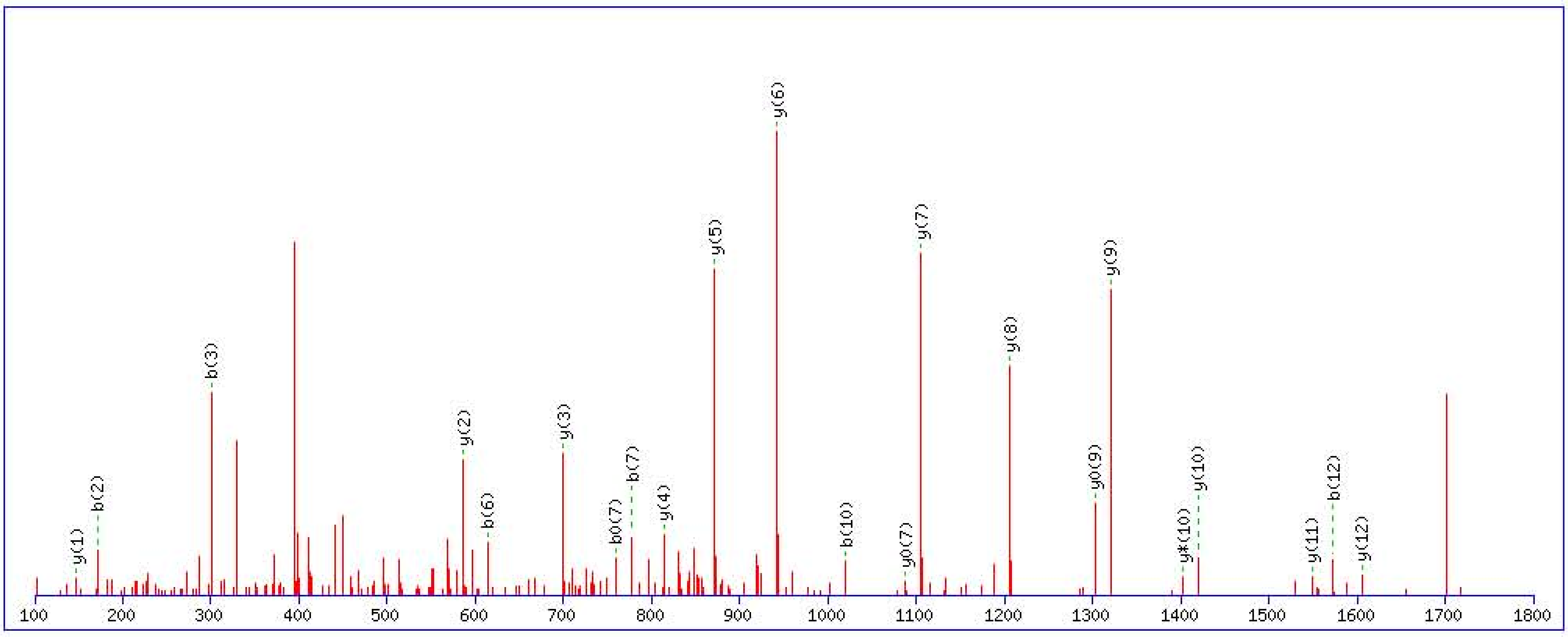
Mascot Search Results

Peptide View

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

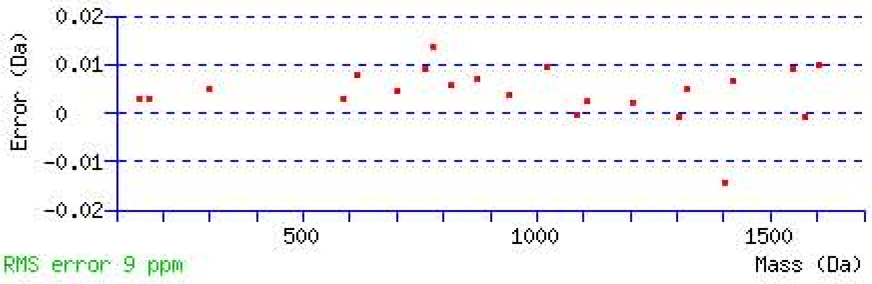
Match to Query 36791: 1717.875368 from(859.944960,2+) rtinseconds(2011) index(5017)
Title: Locus:1.1.1.3252.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

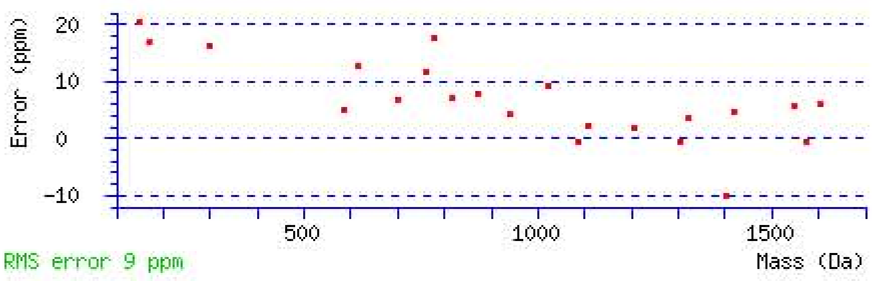
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1717.870895
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 103 **Expect:** 1.5e-009
Matches : 22/126 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							13
2	**171.112804**	86.060040					G	***1605.794121***	803.400699	1588.767572	794.887424	1587.783556	794.395416	12
3	**300.155397**	150.581336			282.144832	141.576054	E	***1548.772657***	774.889967	1531.746108	766.376692	1530.762092	765.884684	11
4	399.223811	200.115544			381.213246	191.110261	V	***1419.730064***	710.368670	1402.703515	701.855396	1401.719499	701.363388	10
5	513.266738	257.137007	496.240189	248.623733	495.256173	248.131725	N	***1320.661650***	660.834463	1303.635101	652.321189	1302.651085	651.829181	9
6	**614.314417**	307.660847	597.287868	299.147572	596.303852	298.655564	T	***1206.618723***	603.813000	1189.592174	595.299725	1188.608158	594.807717	8
7	**777.377746**	389.192511	760.351197	380.679237	759.367181	380.187229	Y	***1105.571044***	553.289160	1088.544495	544.775886	1087.560479	544.283878	7
8	848.414860	424.711068	831.388311	416.197794	830.404295	415.705786	A	***942.507715***	471.757496	925.481166	463.244221	924.497150	462.752213	6
9	905.436324	453.221800	888.409775	444.708526	887.425759	444.216518	G	***871.470601***	436.238939	854.444052	427.725664	853.460036	427.233656	5
10	**1020.463267**	510.735272	1003.436718	502.221997	1002.452702	501.729989	D	***814.449137***	407.728207	797.422588	399.214932	796.438572	398.722924	4
11	1133.547331	567.277304	1116.520782	558.764029	1115.536766	558.272021	L	***699.422194***	350.214735	682.395645	341.701461			3
12	**1572.772657**	786.889967	1555.746108	778.376692	1554.762092	777.884684	Q	***586.338130***	293.672703	569.311581	285.159429			2
13							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
102.5	1717.870895	0.004473	LGEVNTYAGDLQK
10.8	1717.866867	0.008501	IDAVNAETIREVCTK
5.1	1717.878067	-0.002699	RATEKEINNMGNTLK
2.5	1717.878754	-0.003386	IDAVAWNTTPYQLAR
1.1	1717.882126	-0.006758	NNKNFSTVDIQK
0.5	1717.856476	0.018892	GNMEQAILEMKK
0.3	1717.892014	-0.016646	LSTAVNIGKMDSPIEK

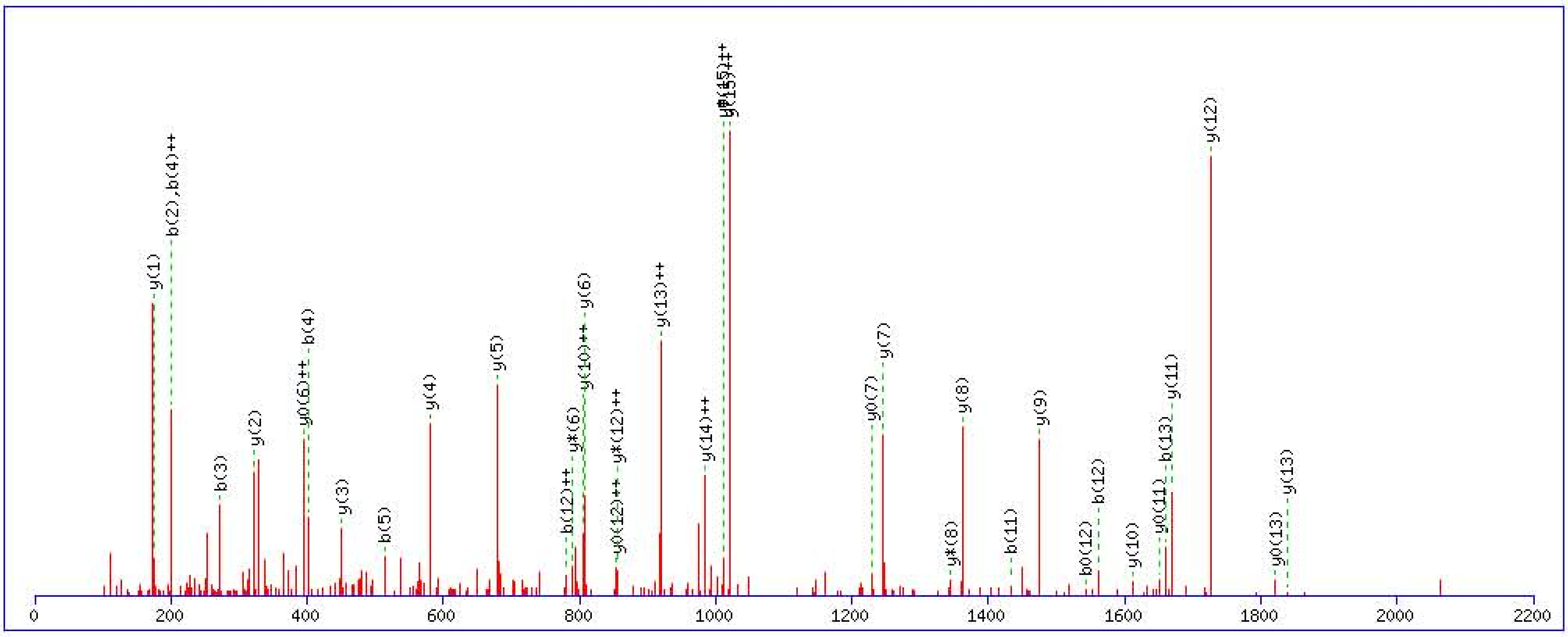
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

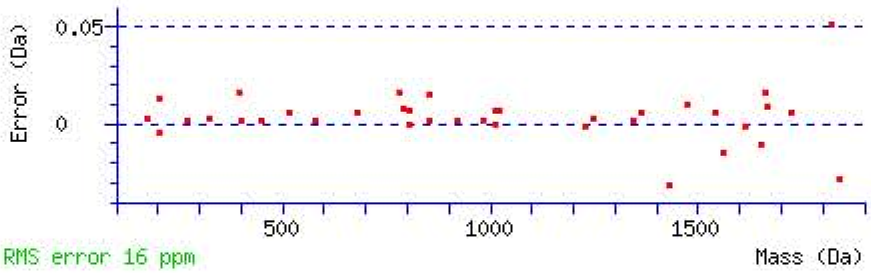
Match to Query 46685: 2238.118182 from(747.046670,3+) rtinseconds(2284) index(64176)
Title: Locus:1.1.1.3421.10 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

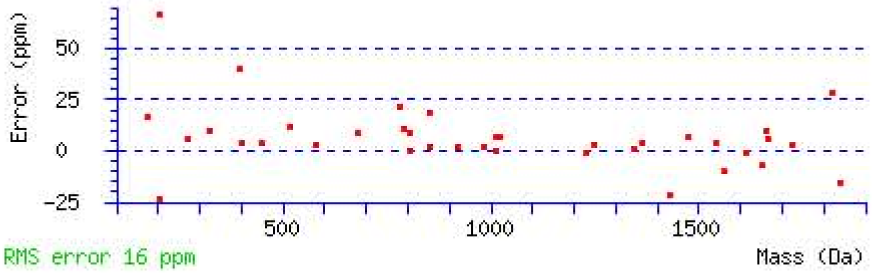
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2238.110291
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 69 **Expect:** 3.3e-006
Matches : 37/168 fragment ions using 72 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	**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
69.2	2238.110291	0.007891	SLAELGGHLDQQVEEFR
65.0	2238.110291	0.007891	SLAELGGHLDQQVEEFR

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

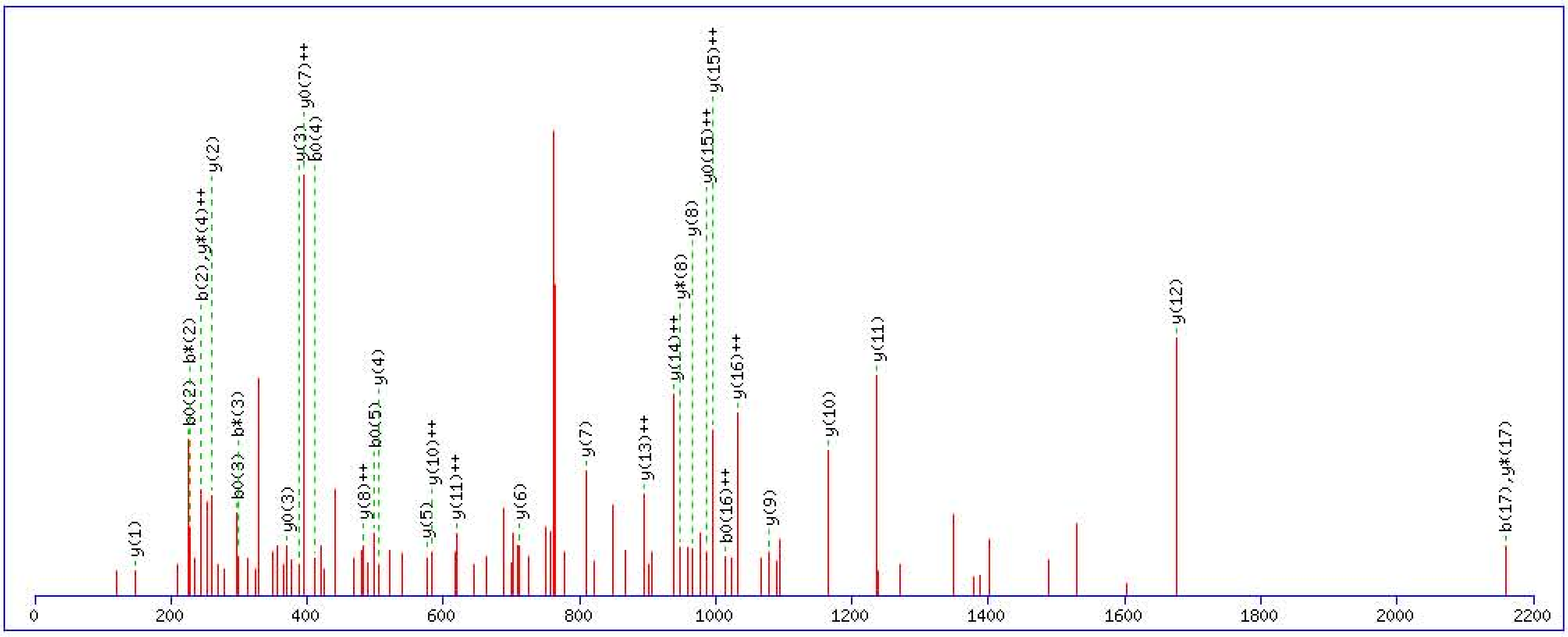
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

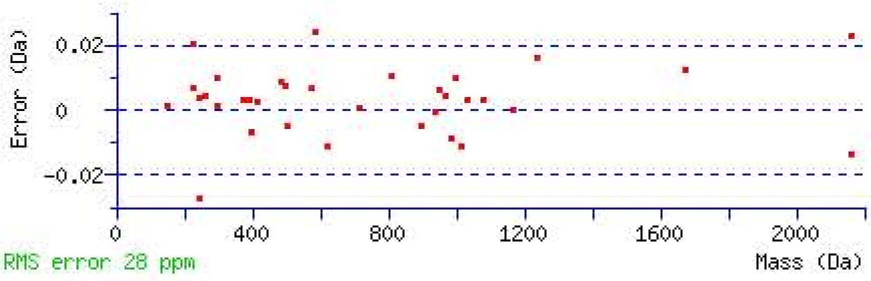
Match to Query 47870: 2304.162072 from(769.061300,3+) rtinseconds(1916) index(61902)
Title: Locus:1.1.1.3293.15 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

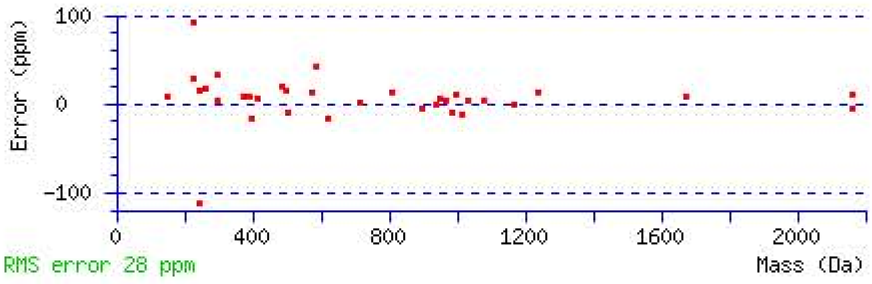
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2304.153183
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 44  Expect: 0.0011
Matches : 34/198 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	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
44.1	2304.153183	0.008889	ENADSLQASLRPHADELK

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

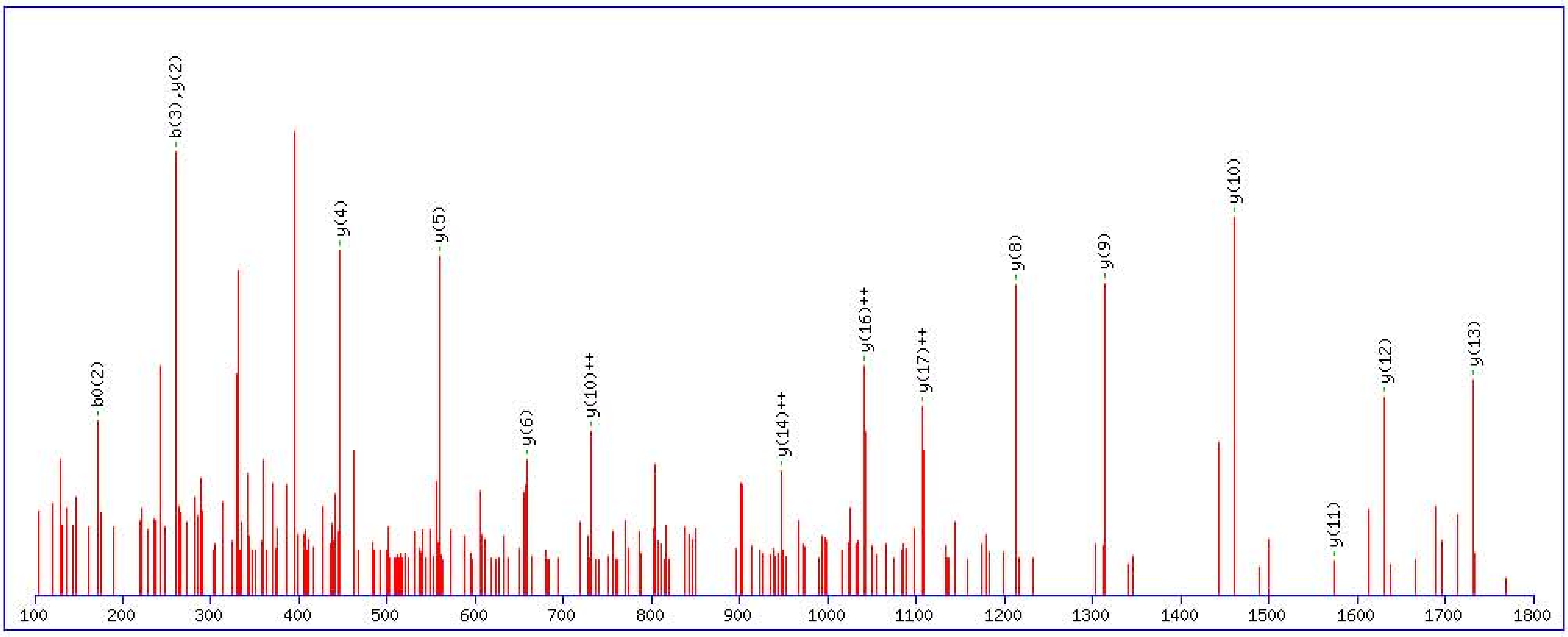
Mascot Search Results

Peptide View

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

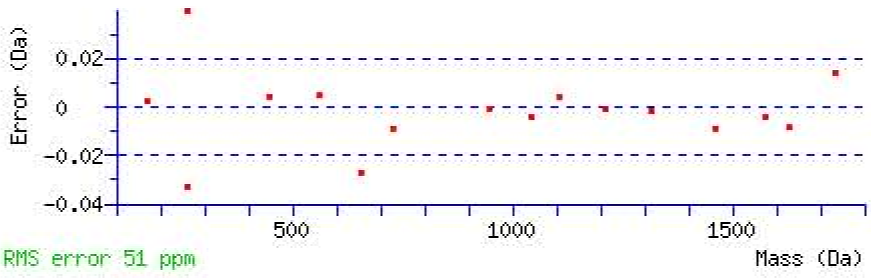
Match to Query 51650: 2543.308392 from(848.776740,3+) rtinseconds(3247) index(40266)
Title: Locus:1.1.1.3674.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

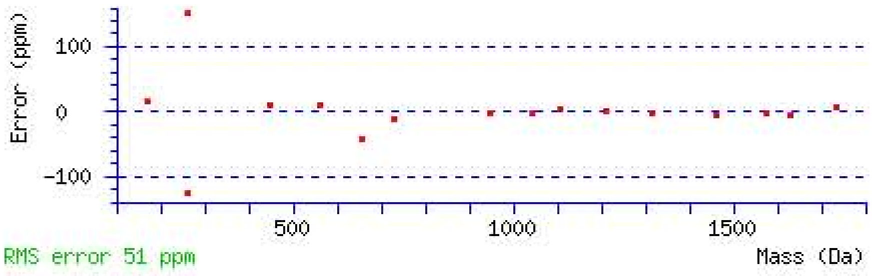
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2543.301544
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15     : Biotin:Thermo-21345 (Q)
Ions Score: 80  Expect: 3.1e-007
Matches : 16/206 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	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
79.7	2543.301544	0.006848	STAAMSTYTGIFTDQVLSVLK

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

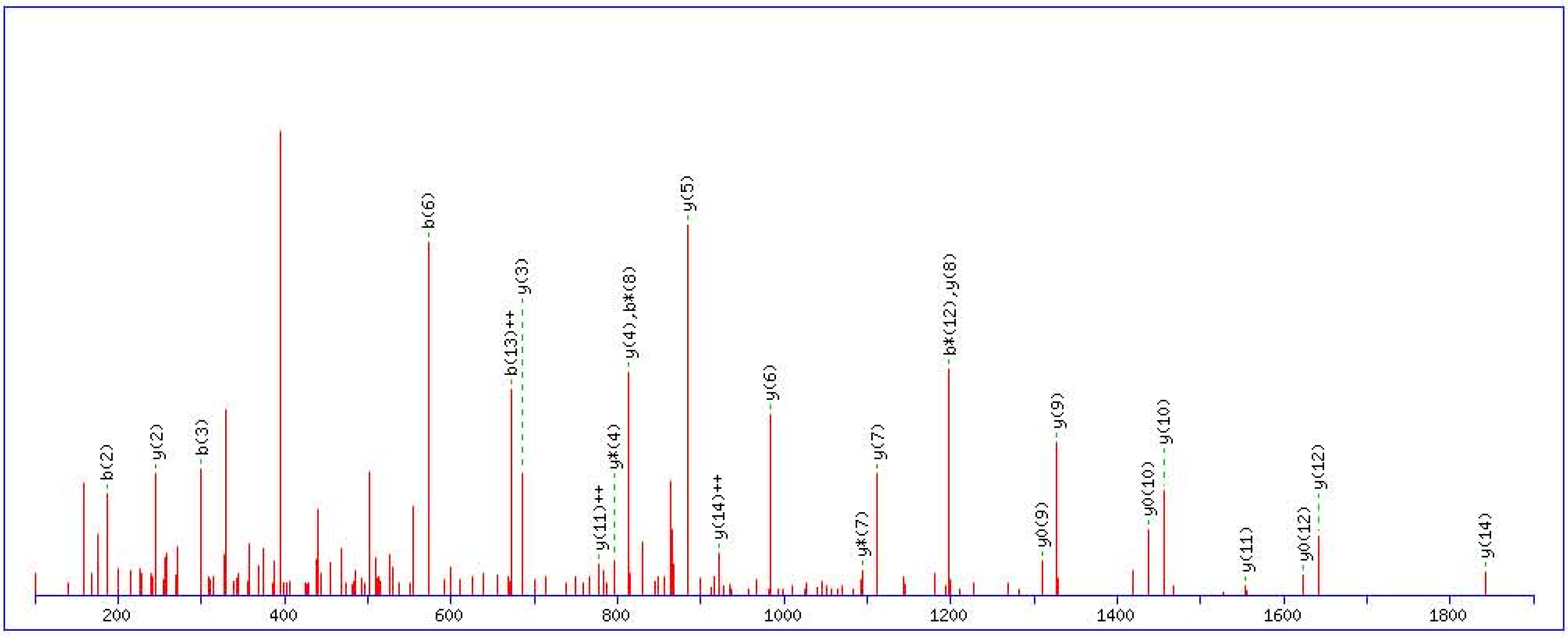
Mascot Search Results

Peptide View

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

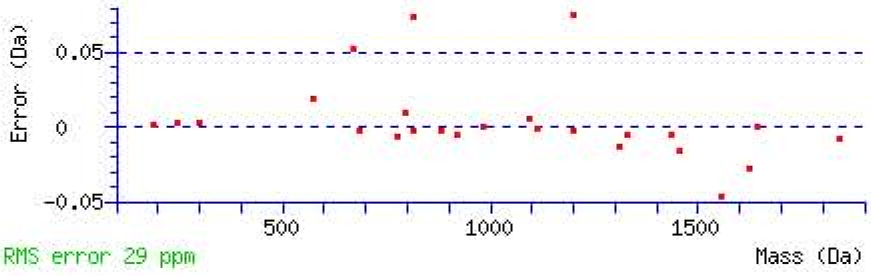
Match to Query 43136: 2027.012412 from(676.678080,3+) rtinseconds(1942) index(32758)
Title: Locus:1.1.1.3225.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

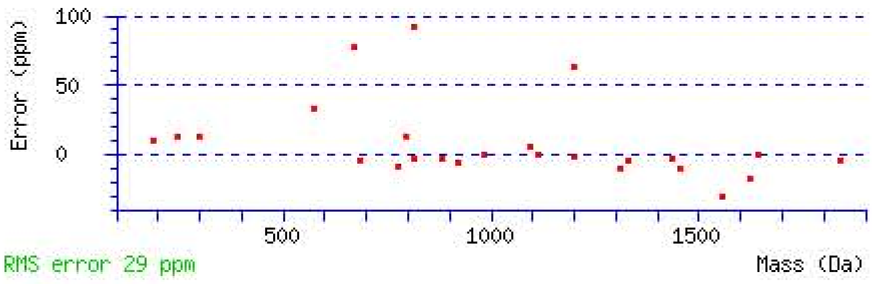
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2027.010574
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Biotin:Thermo-21345 (Q)
Ions Score: 90 **Expect:** 2.3e-008
Matches : 25/154 fragment ions using 33 most intense peaks (help)

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





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
90.4	2027.010574	0.001838	DALSSVQESQVAQQAR
80.0	2027.010574	0.001838	DALSSVQESQVAQQAR
75.0	2027.010574	0.001838	DALSSVQESQVAQQAR
37.4	2027.010574	0.001838	DALSSVQESQVAQQAR

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

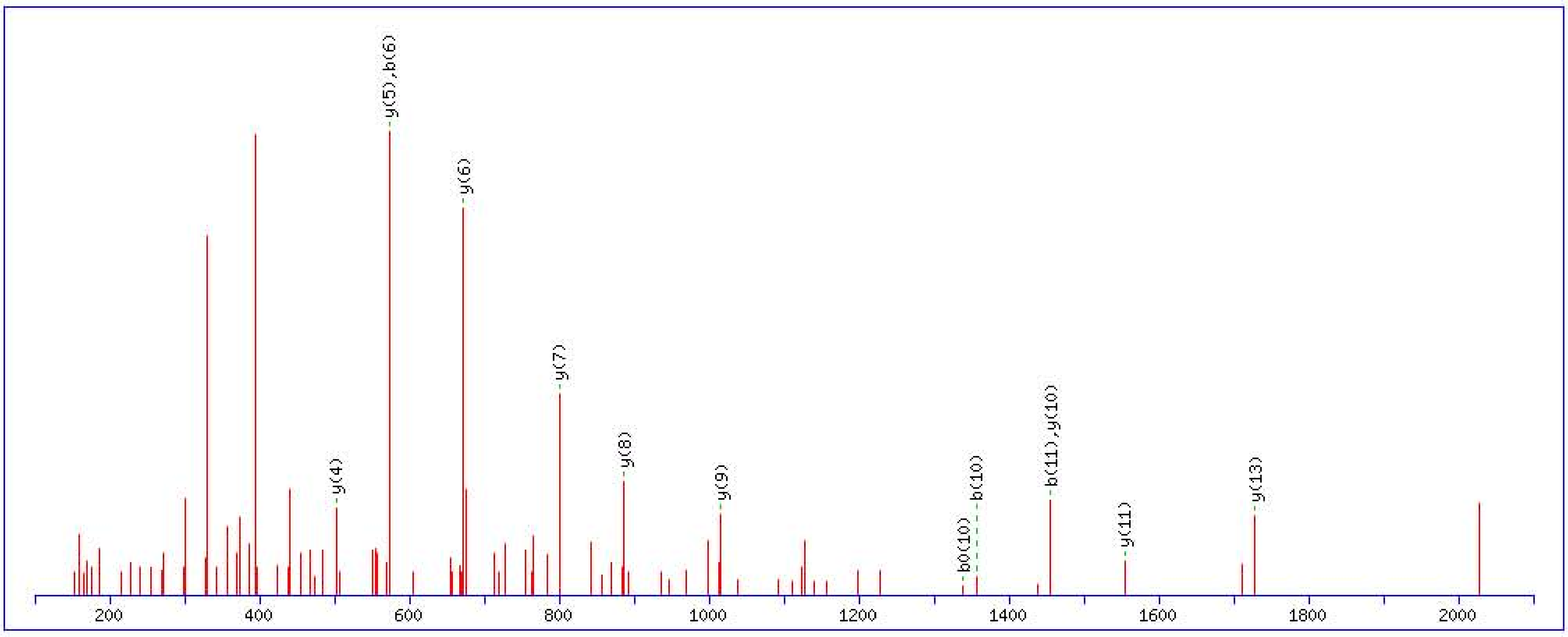
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

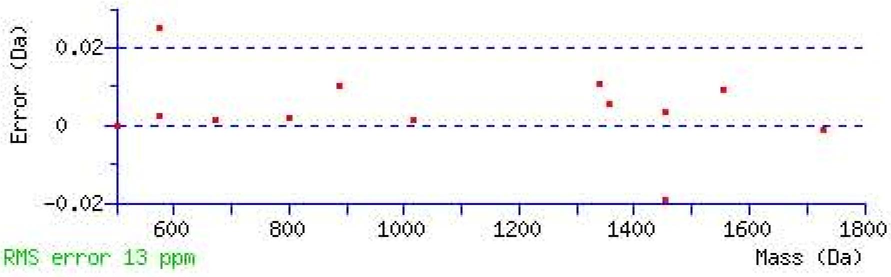
Match to Query 43138: 2027.012742 from(676.678190,3+) rtinseconds(1974) index(33013)
Title: Locus:1.1.1.3236.19 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

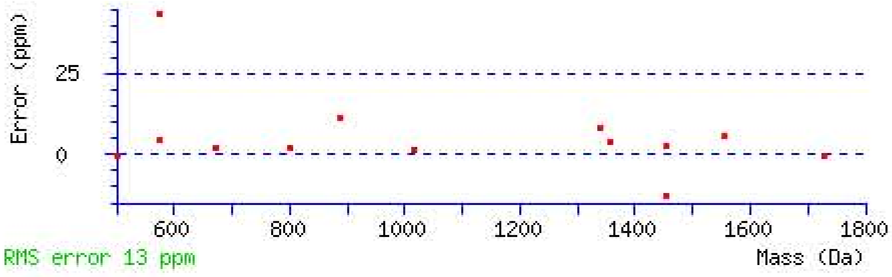
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2027.010574
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 66 **Expect:** 3.6e-006
Matches : 13/154 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	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
65.6	2027.010574	0.002168	DALSSVQESQVAQQAR
38.1	2027.010574	0.002168	DALSSVQESQVAQQAR
15.8	2027.010574	0.002168	DALSSVQESQVAQQAR
13.9	2027.010574	0.002168	DALSSVQESQVAQQAR
7.1	2027.010559	0.002183	LTGRGAEDSLADQAANK
0.7	2027.000870	0.011872	QMSEPNIPFPPQGFK

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

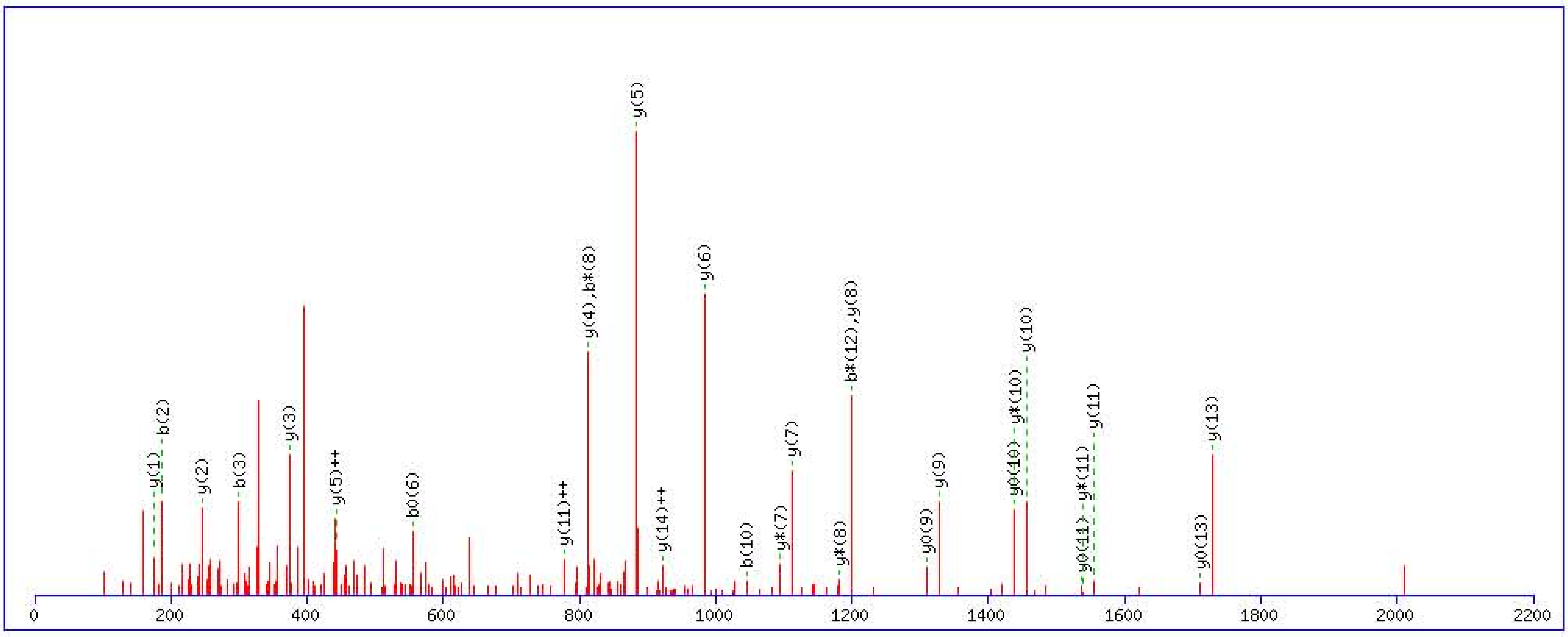
Mascot Search Results

Peptide View

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

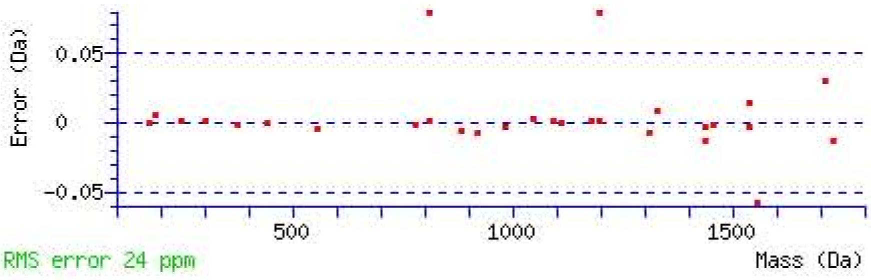
Match to Query 43141: 2027.014062 from(676.678630,3+) rtinseconds(1887) index(32320)
Title: Locus:1.1.1.3206.13 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

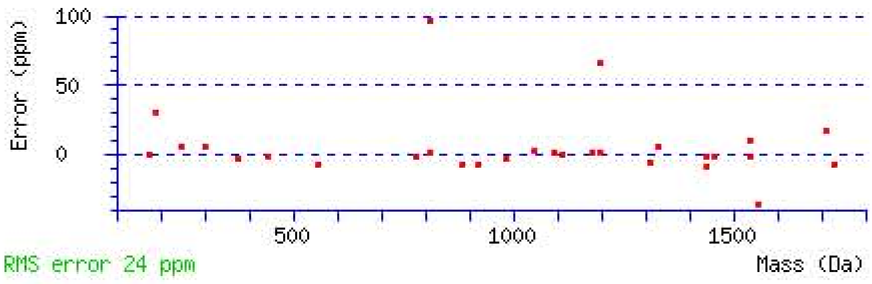
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2027.010574
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 79  Expect: 3.3e-007
Matches : 29/154 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	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
78.8	2027.010574	0.003488	DALSSVQESQVAQQAR
66.4	2027.010574	0.003488	DALSSVQESQVAQQAR
43.1	2027.010574	0.003488	DALSSVQESQVAQQAR
14.0	2027.010574	0.003488	DALSSVQESQVAQQAR

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

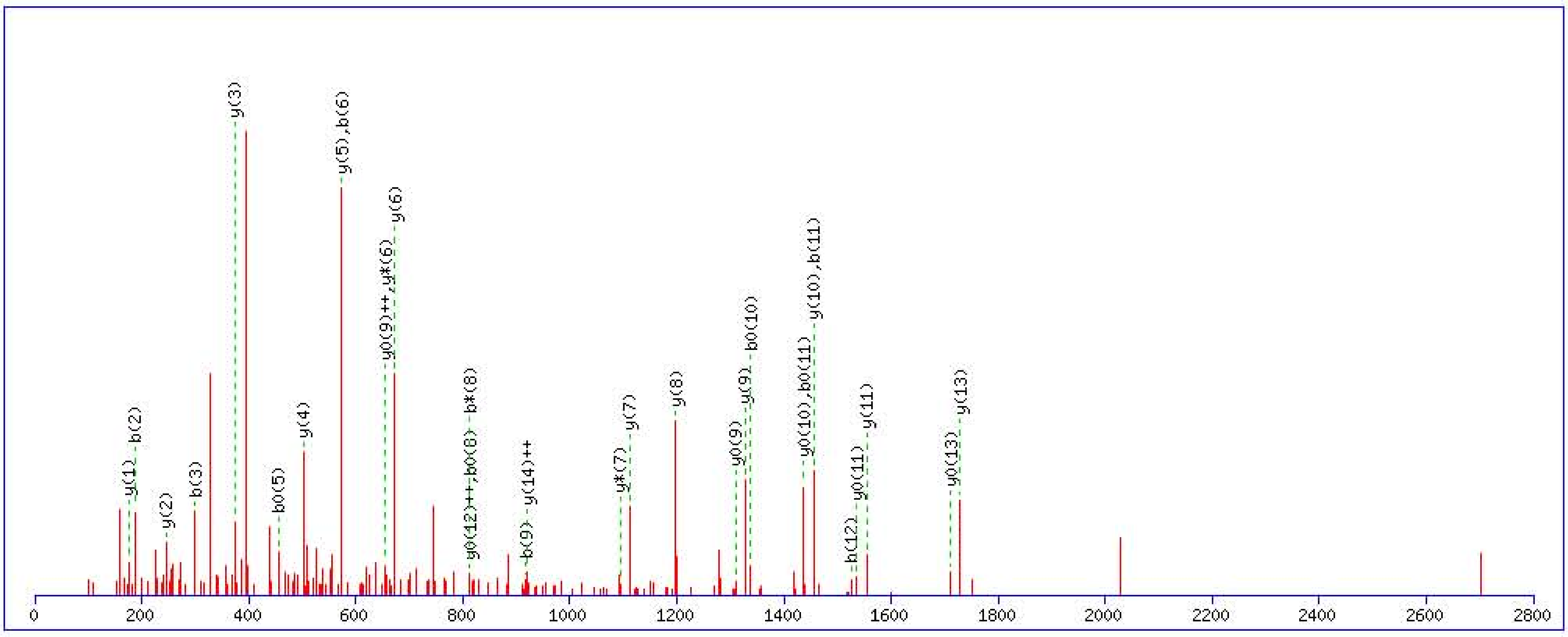
Mascot Search Results

Peptide View

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

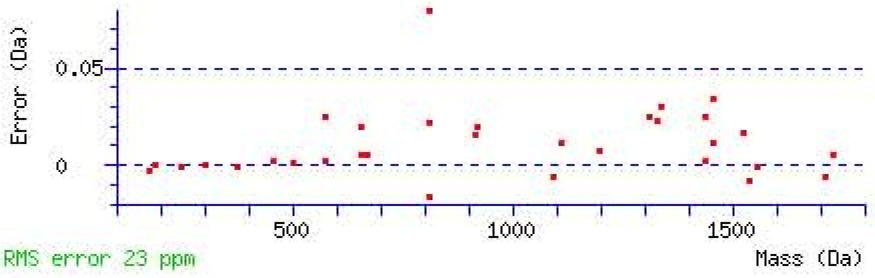
Match to Query 43146: 2027.022042 from(676.681290,3+) rtinseconds(1952) index(47087)
Title: Locus:1.1.1.2728.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

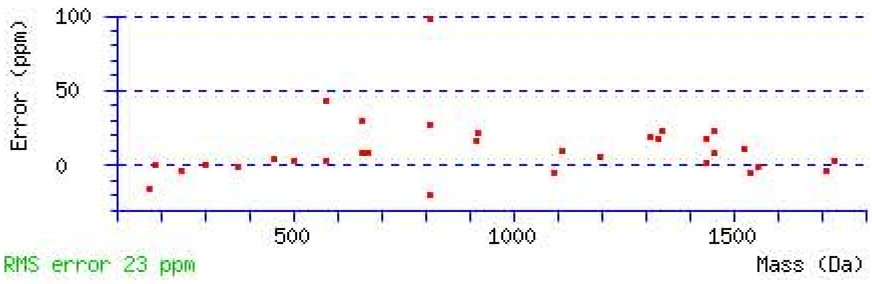
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 73 **Expect:** 2.4e-007
Matches : 32/154 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							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
73.2	2027.010574	0.011468	DALSSVQESQVAQQAR
68.8	2027.010574	0.011468	DALSSVQESQVAQQAR
57.8	2027.010574	0.011468	DALSSVQESQVAQQAR
35.9	2027.010574	0.011468	DALSSVQESQVAQQAR
2.6	2027.021805	0.000237	VASVESQGQEISGNRR
2.0	2027.017960	0.004082	MFELTLRGMSEALVDKR

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

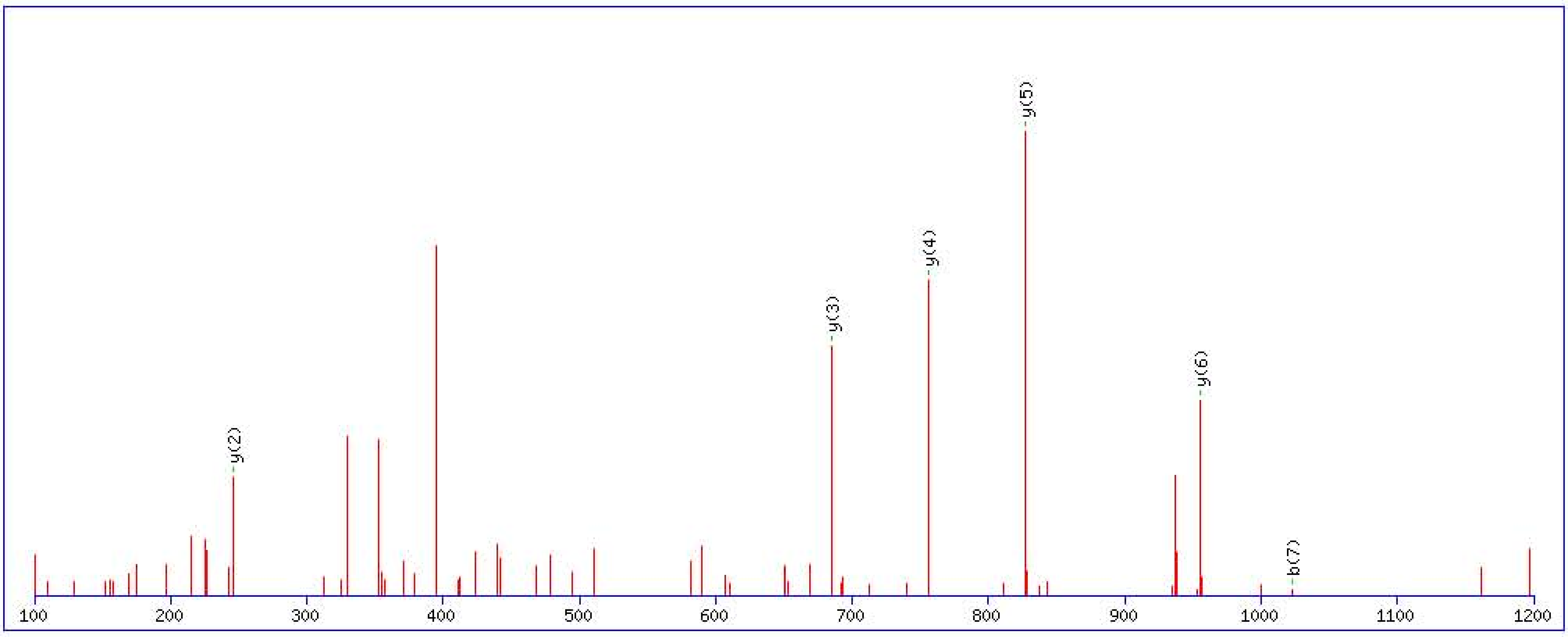
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

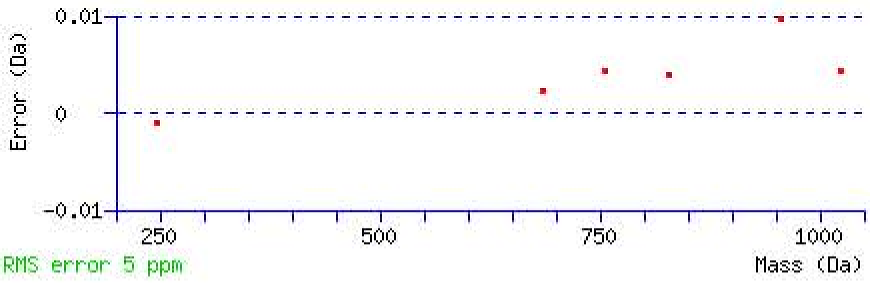
Match to Query 20281: 1196.630508 from(599.322530,2+) rtinseconds(1472) index(44045)
Title: Locus:1.1.1.2561.8 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

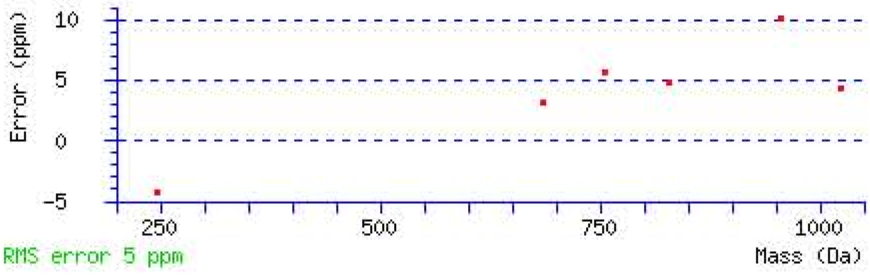


```
Monoisotopic mass of neutral peptide Mr(calc): 1196.633545
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0032
Matches : 6/66 fragment ions using 11 most intense peaks   (help)
```

#	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



RMS error 5 ppm



RMS error 5 ppm

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
37.0	1196.633545	-0.003037	ELQAAQAR
10.1	1196.614944	0.015564	EAIGPGGEVVNR
7.5	1196.633575	-0.003067	QASTQVPR
4.8	1196.614914	0.015594	ELQQAELPNR
3.9	1196.641434	-0.010926	STRPQAWVPR
2.6	1196.644775	-0.014267	KLDHEIRMR
2.5	1196.627029	0.003479	AGMPRQAR
2.5	1196.637390	-0.006882	TLRQAGAPNNR
2.4	1196.633560	-0.003052	GLAEVQNR
1.6	1196.641418	-0.010910	EAKKAGPGFHR

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

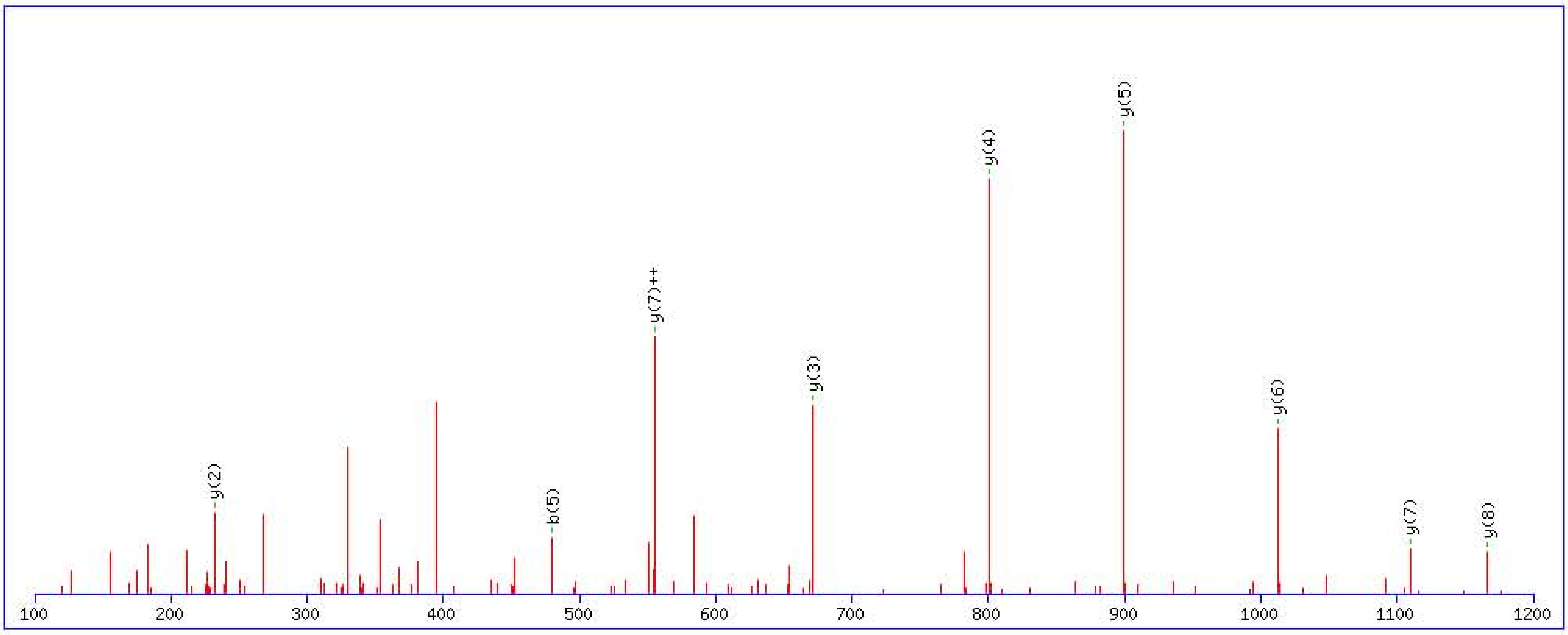
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

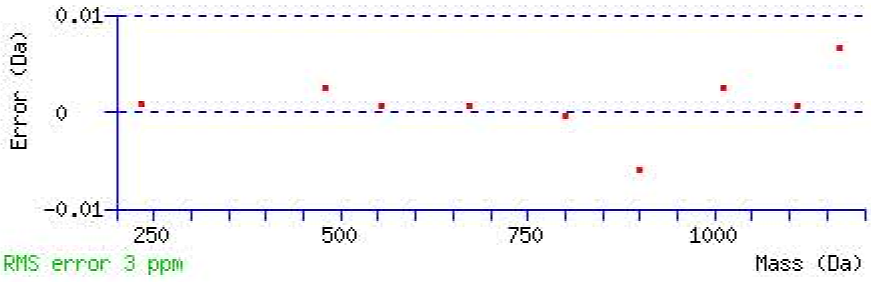
Match to Query 22385: 1278.713588 from(640.364070,2+) rtinseconds(1973) index(33010)
Title: Locus:1.1.1.3236.16 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

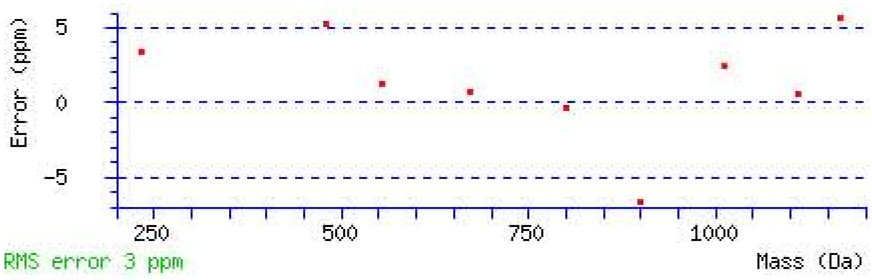
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1278.711823
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 64  Expect: 1.6e-006
Matches : 9/68 fragment ions using 11 most intense peaks   (help)
```

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





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.8	1278.711823	0.001765	LGPLVEQGR
2.0	1278.729584	-0.015996	IVIVPSLNPDGR

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

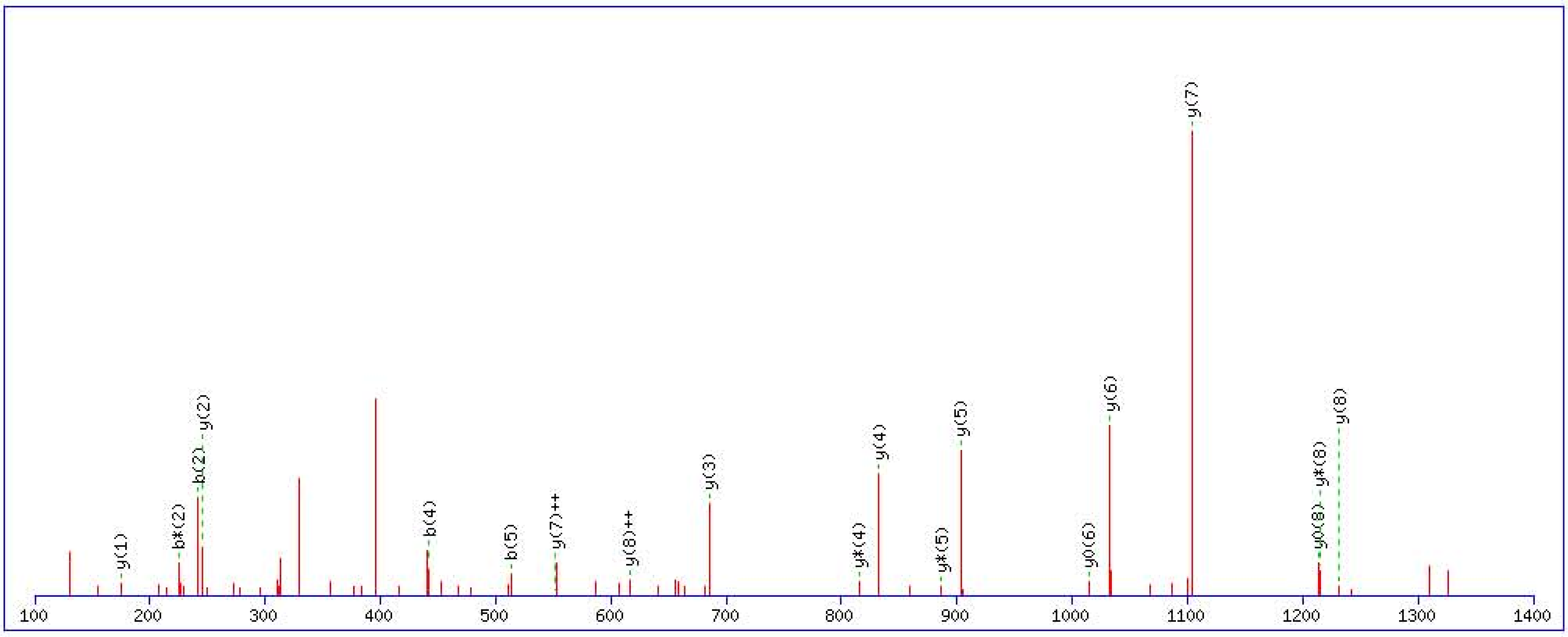
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

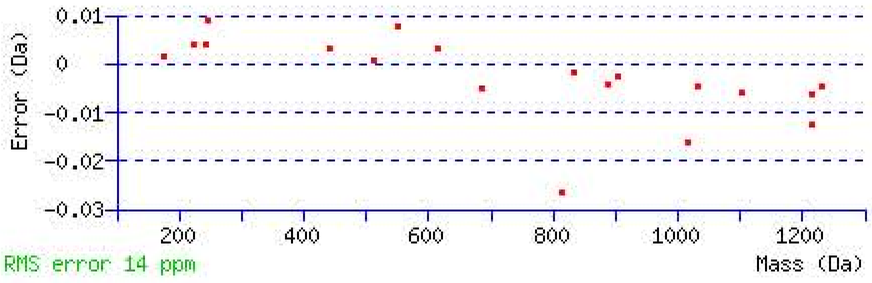
Match to Query 23881: 1343.708328 from(672.861440,2+) rtinseconds(1830) index(32053)
Title: Locus:1.1.1.3186.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

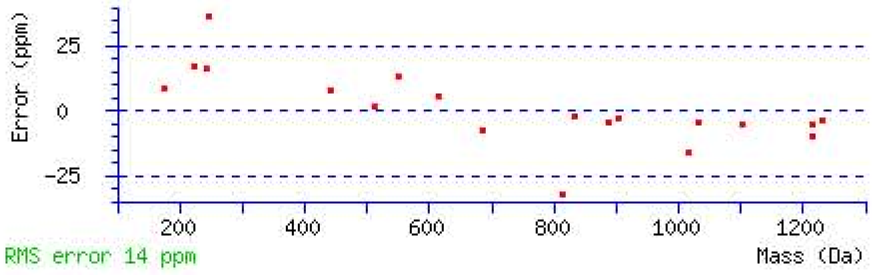
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1343.701965
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 2.2e-005
Matches : 19/78 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							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
60.4	1343.701965	0.006363	LQAEAFQAR
17.2	1343.715683	-0.007355	LKDSEAELQRR
11.7	1343.694107	0.014221	IQAMSEVQK
8.7	1343.704453	0.003875	IKGEELSEANVR
8.0	1343.704453	0.003875	IQEKKDEDIAR
5.7	1343.716583	-0.008255	LQQVMSRR
5.7	1343.693237	0.015091	LQDLELDLETR
5.5	1343.726929	-0.018601	LLNGDASTNRKR
5.2	1343.704453	0.003875	LQAANAEDIKSGK
3.6	1343.697952	0.010376	AMGTVREAAGLPR

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

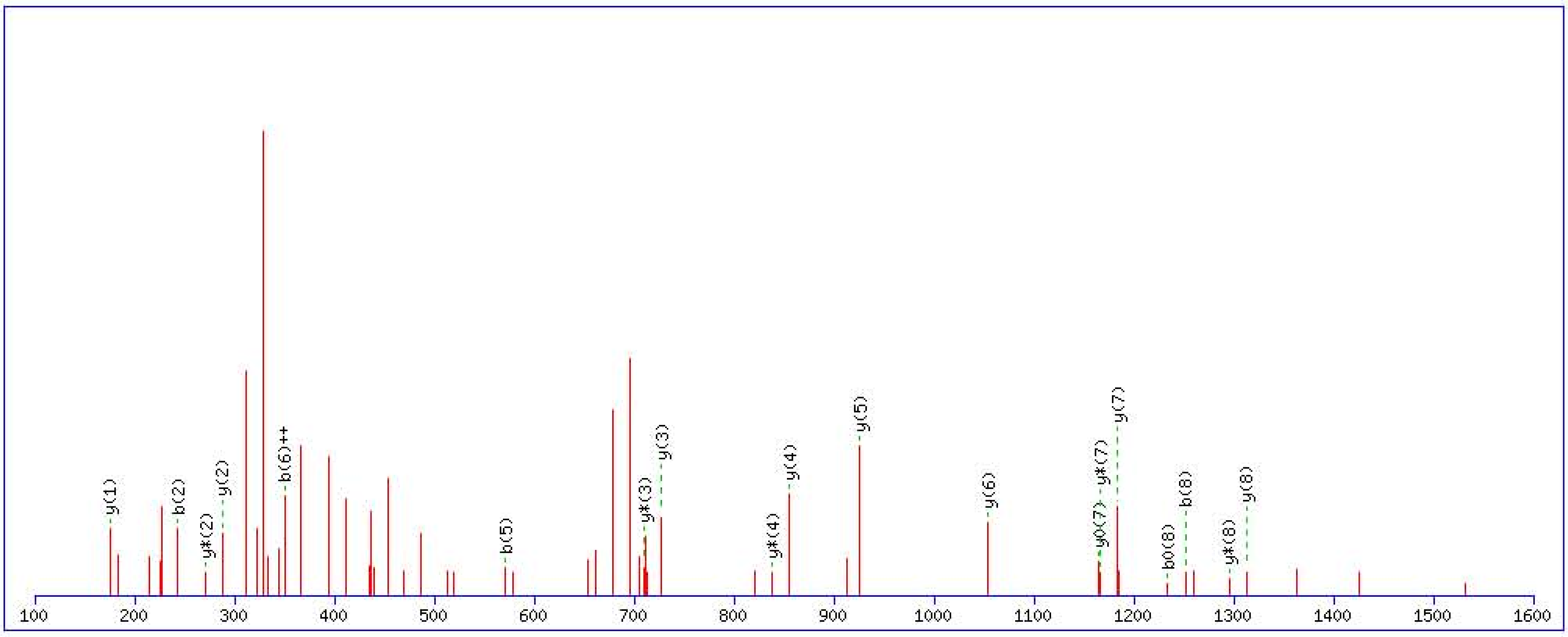
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

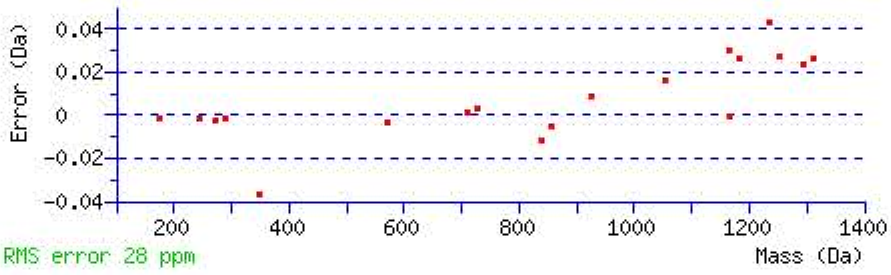
Match to Query 27826: 1424.734388 from(713.374470,2+) rtinseconds(1575) index(44684)
Title: Locus:1.1.1.2597.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

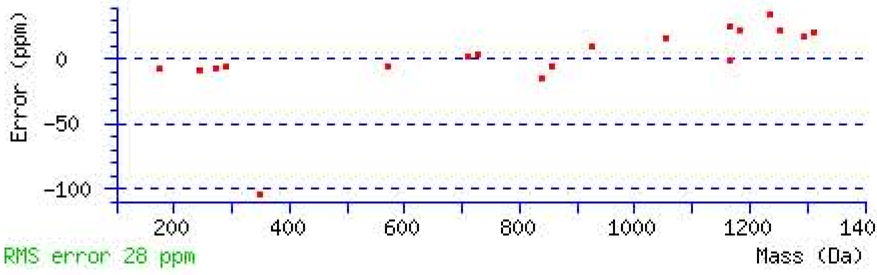
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1424.744553
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.0045
Matches : 19/76 fragment ions using 52 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	**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
32.7	1424.744553	-0.010165	LEEQAQQIR
23.4	1424.744553	-0.010165	LEEQAQQIR
7.2	1424.730667	0.003721	QPGCAVPQSGRLR
6.6	1424.744553	-0.010165	LEEQAQQIR
5.4	1424.745224	-0.010836	IITDKHFYFNK
4.1	1424.744583	-0.010195	QLSGDQPTIR
2.8	1424.733322	0.001066	LEQETEPLR
2.1	1424.726807	0.007581	QMNLQQQPK
0.4	1424.734680	-0.000292	WVLTAAHCLAQR

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

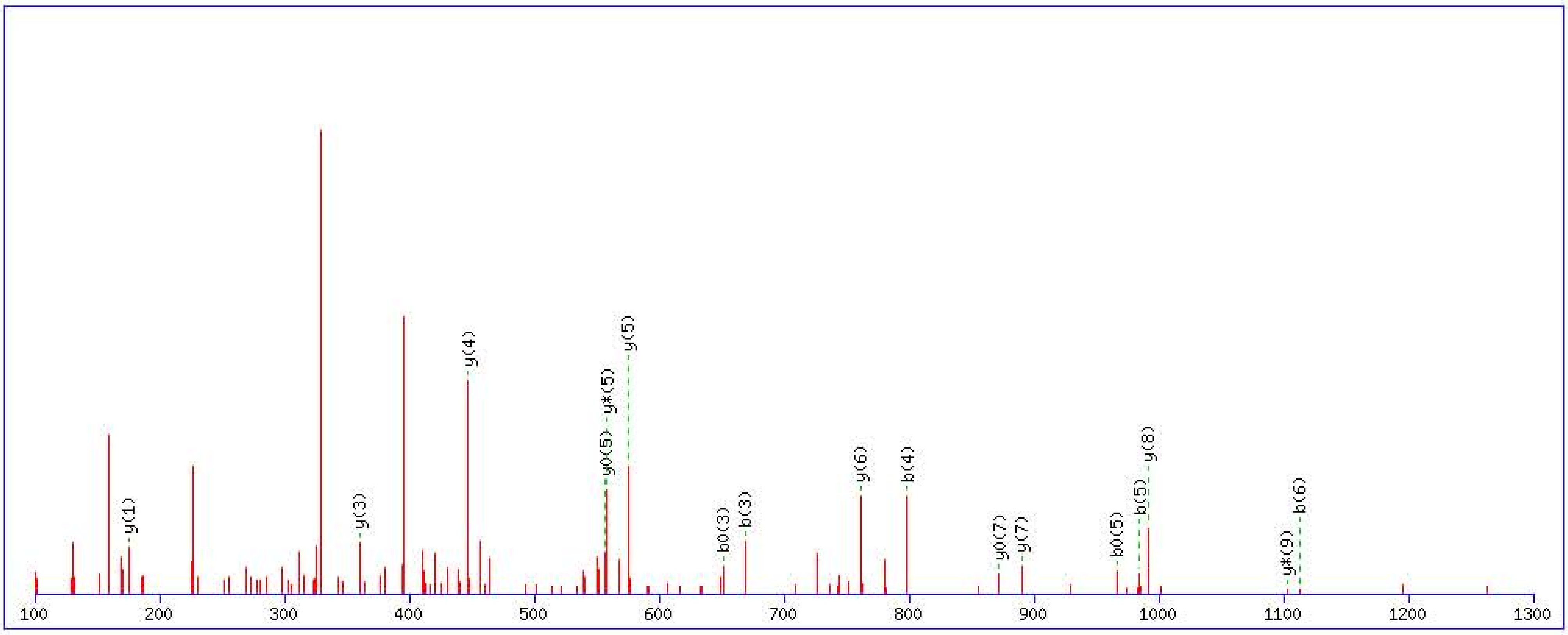
Mascot Search Results

Peptide View

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

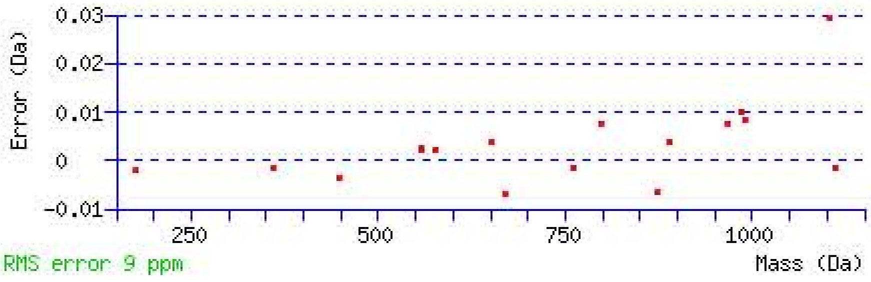
Match to Query 31310: 1557.731892 from(520.251240,3+) rtinseconds(1584) index(44746)
Title: Locus:1.1.1.2600.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

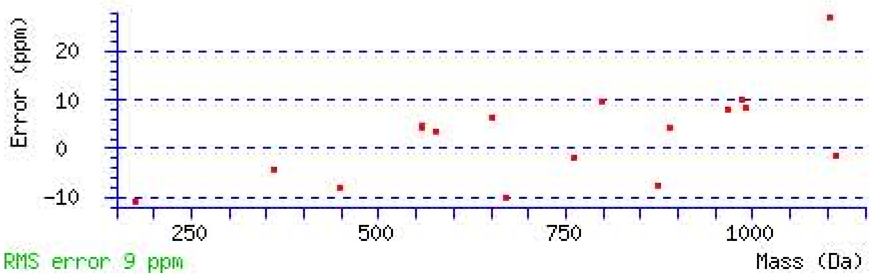
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1557.735809
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 34 **Expect:** 0.0019
Matches : 17/98 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	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
34.5	1557.735809	-0.003917	QQTEWQSGQR
33.0	1557.735809	-0.003917	QQTEWQSGQR
5.5	1557.745697	-0.013805	GSSLFMDTEKSGKR

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

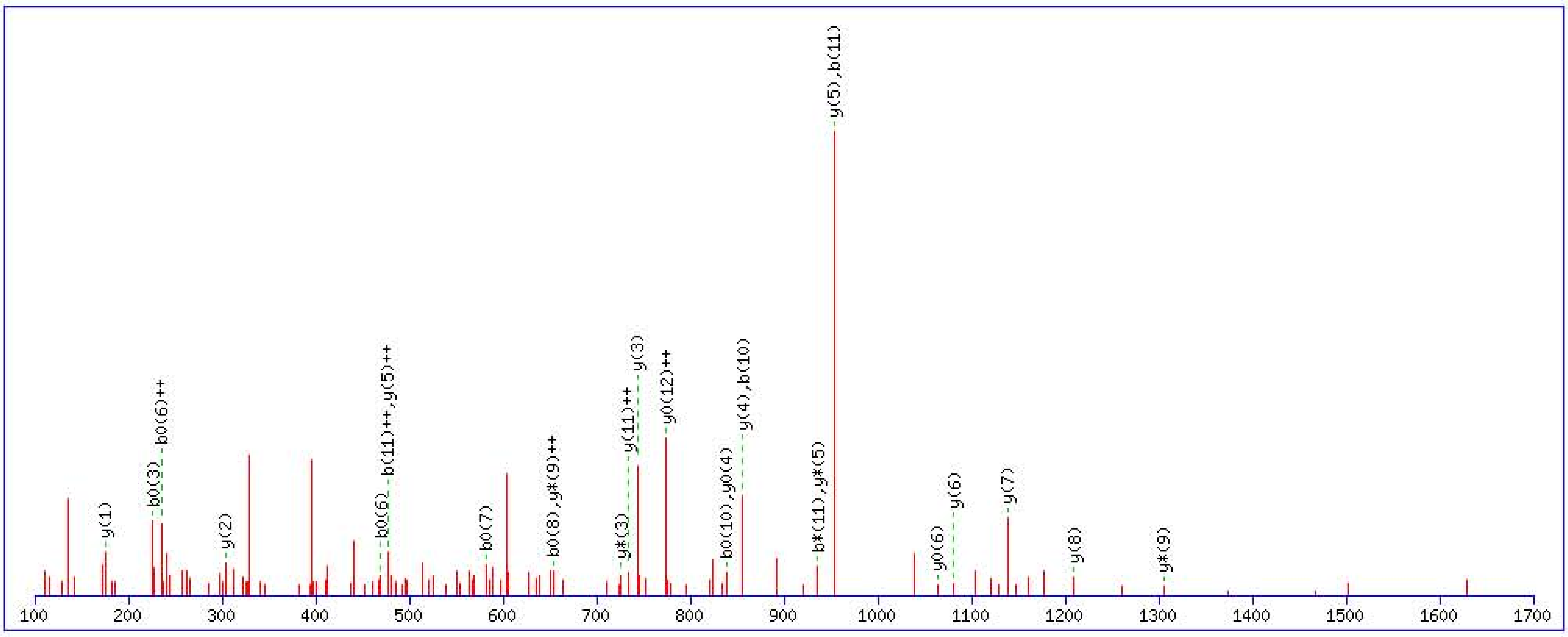
Mascot Search Results

Peptide View

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

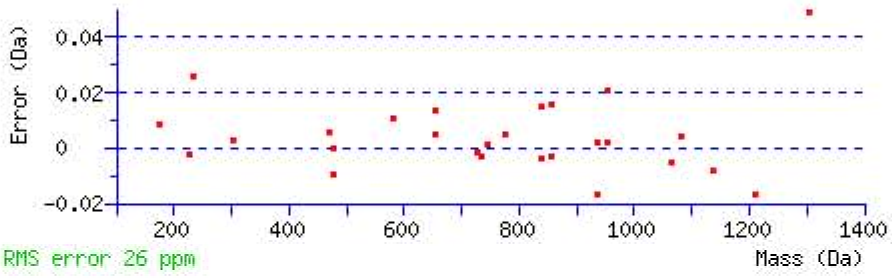
Match to Query 38620: 1807.960122 from(603.660650,3+) rtinseconds(1962) index(4734)
Title: Locus:1.1.1.3235.16 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

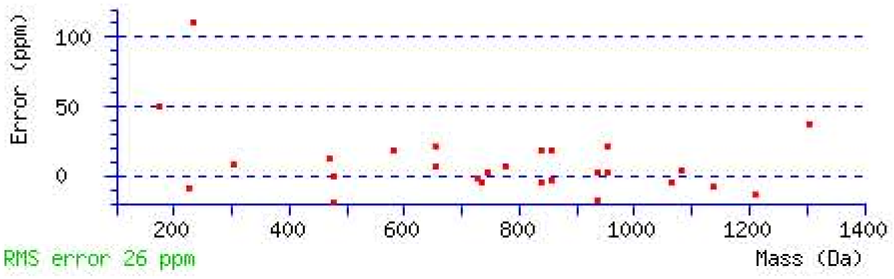
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1807.961441
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13 : Biotin:Thermo-21345 (Q)
Ions Score: 31 **Expect:** 0.01
Matches : 27/144 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	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
31.2	1807.961441	-0.001319	AATVGSLAGQPLQER
9.8	1807.947510	0.012612	VGLAQIAAMDISRGNHR
2.7	1807.961441	-0.001319	AATVGSLAGQPLQER

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

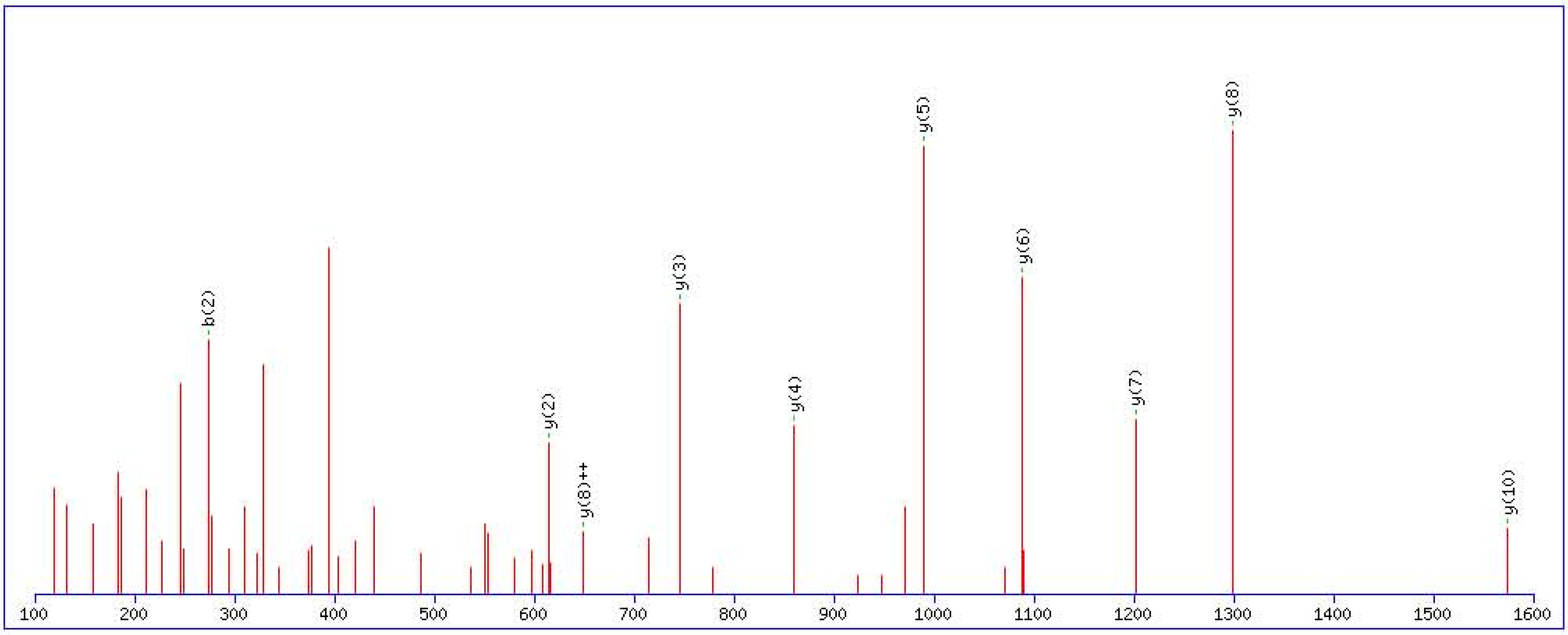
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

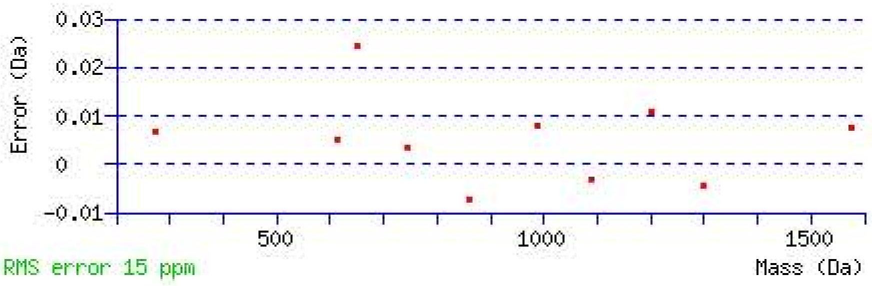
Match to Query 39310: 1846.885692 from(616.635840,3+) rtinseconds(2827) index(37903)
Title: Locus:1.1.1.3532.4 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

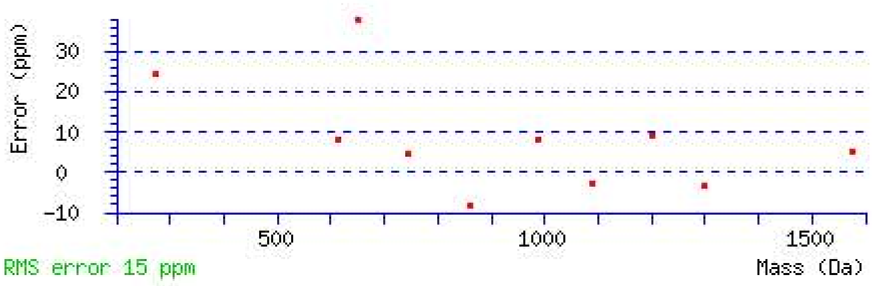
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1846.874603
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 65 **Expect:** 1.1e-006
Matches : 10/106 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							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
64.8	1846.874603	0.011089	SWFEPLVEDMQR
1.1	1846.895721	-0.010029	LQLEETMPSPYGR

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

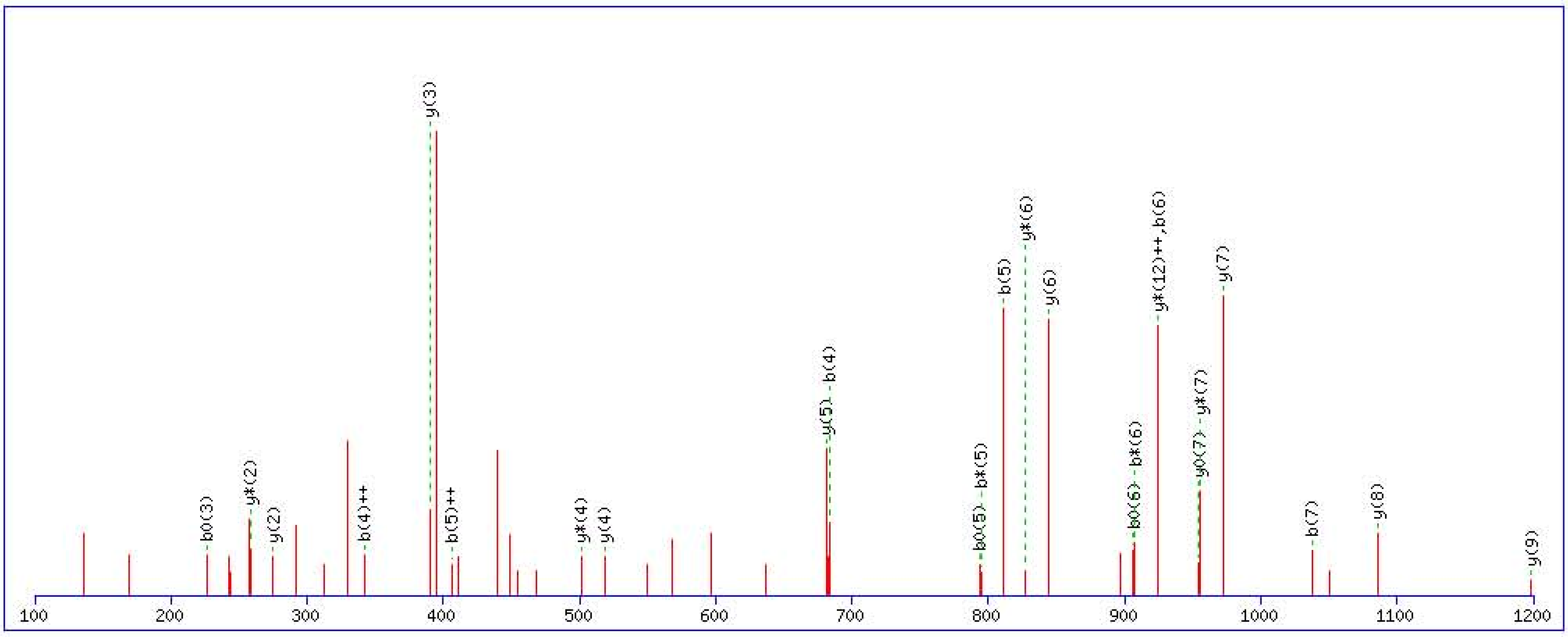
Mascot Search Results

Peptide View

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

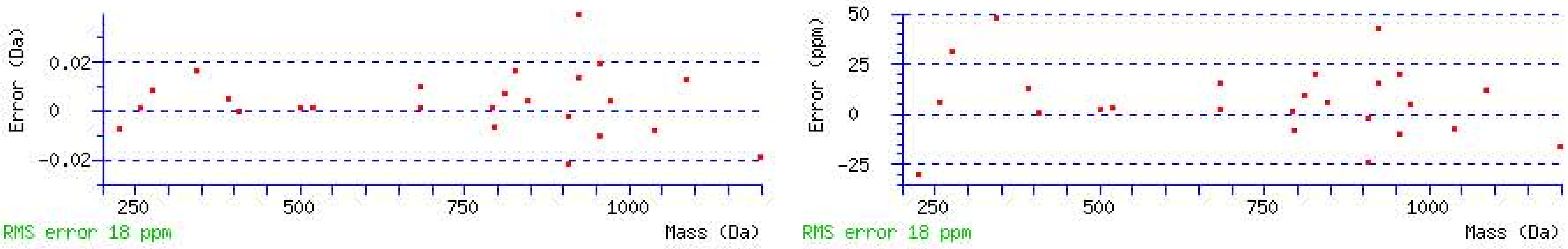
Match to Query 42848: 2008.018272 from(670.346700,3+) rtinseconds(2478) index(35609)
Title: Locus:1.1.1.3412.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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): 2008.008789
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 39 **Expect:** 0.0012
Matches : 25/146 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							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
38.8	2008.008789	0.009483	SGVQQLIQYYQDQK
34.9	2008.008789	0.009483	SGVQQLIQYYQDQK
7.2	2008.037308	-0.019036	VVPVSLSELYLLQCNMK
2.3	2008.026535	-0.008263	HYSNTLKALGISDEFVSK
1.4	2008.008789	0.009483	SGVQQLIQYYQDQK

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

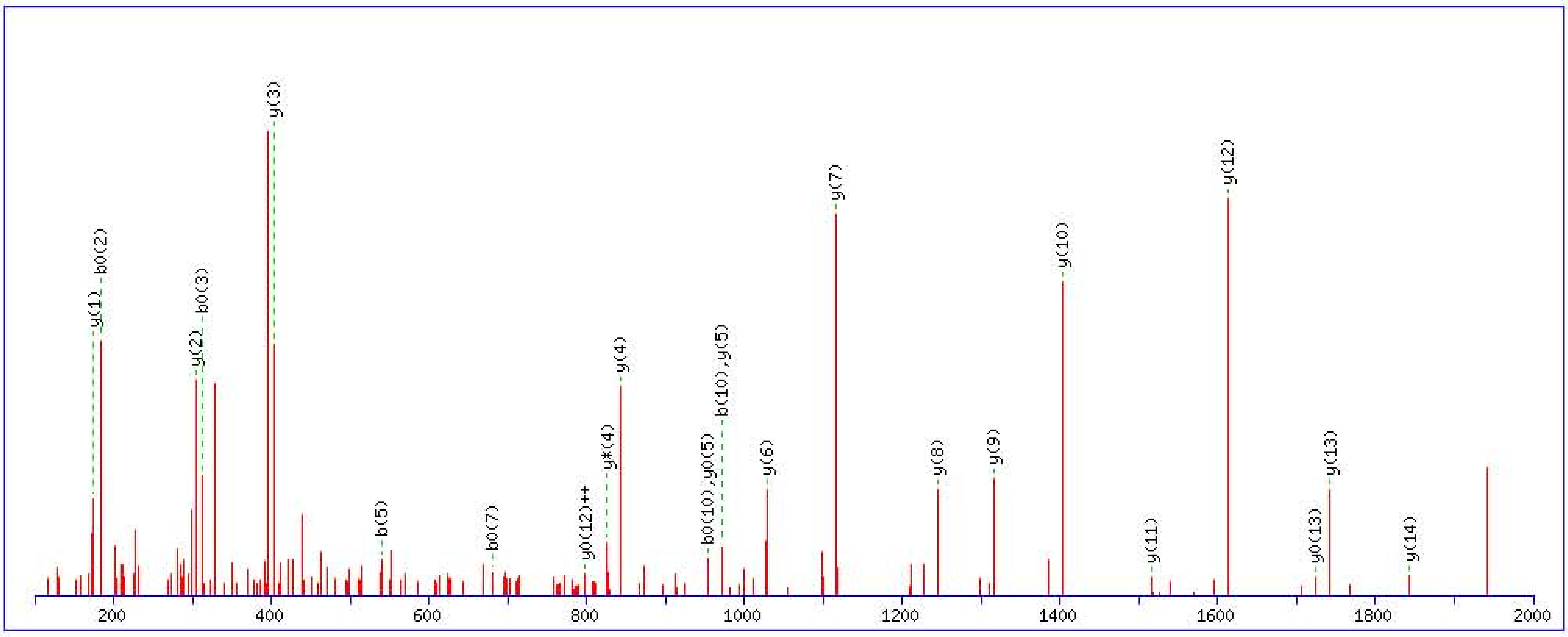
Mascot Search Results

Peptide View

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

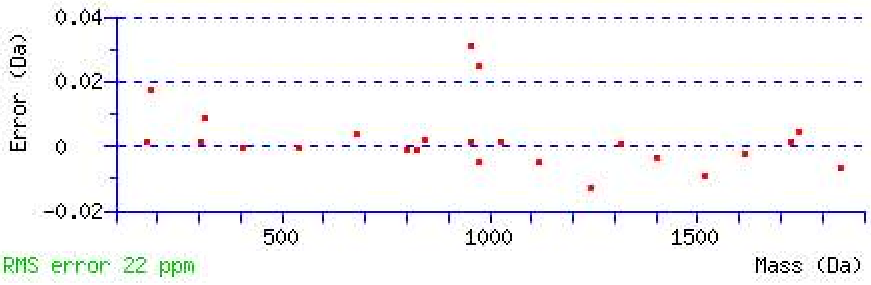
Match to Query 40937: 1940.950812 from(647.990880,3+) rtinseconds(1730) index(31548)
Title: Locus:1.1.1.3151.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

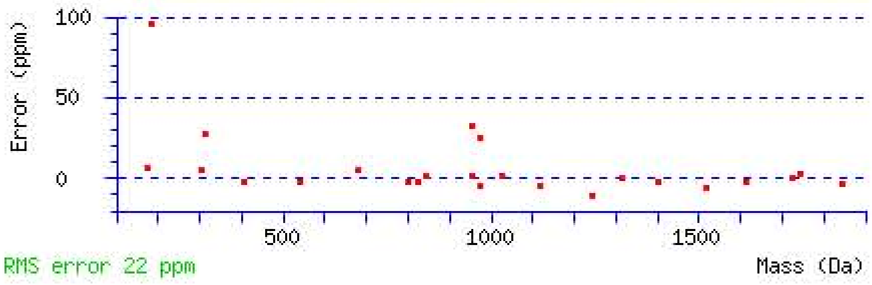
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1940.951324
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 118 **Expect:** 2.3e-011
Matches : 24/142 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	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
117.8	1940.951324	-0.000512	VTEPISAESGEQVER
4.3	1940.937378	0.013434	SNNLEREQEQLDR
2.8	1940.952698	-0.001886	IQSQTVGQGSDAHFR

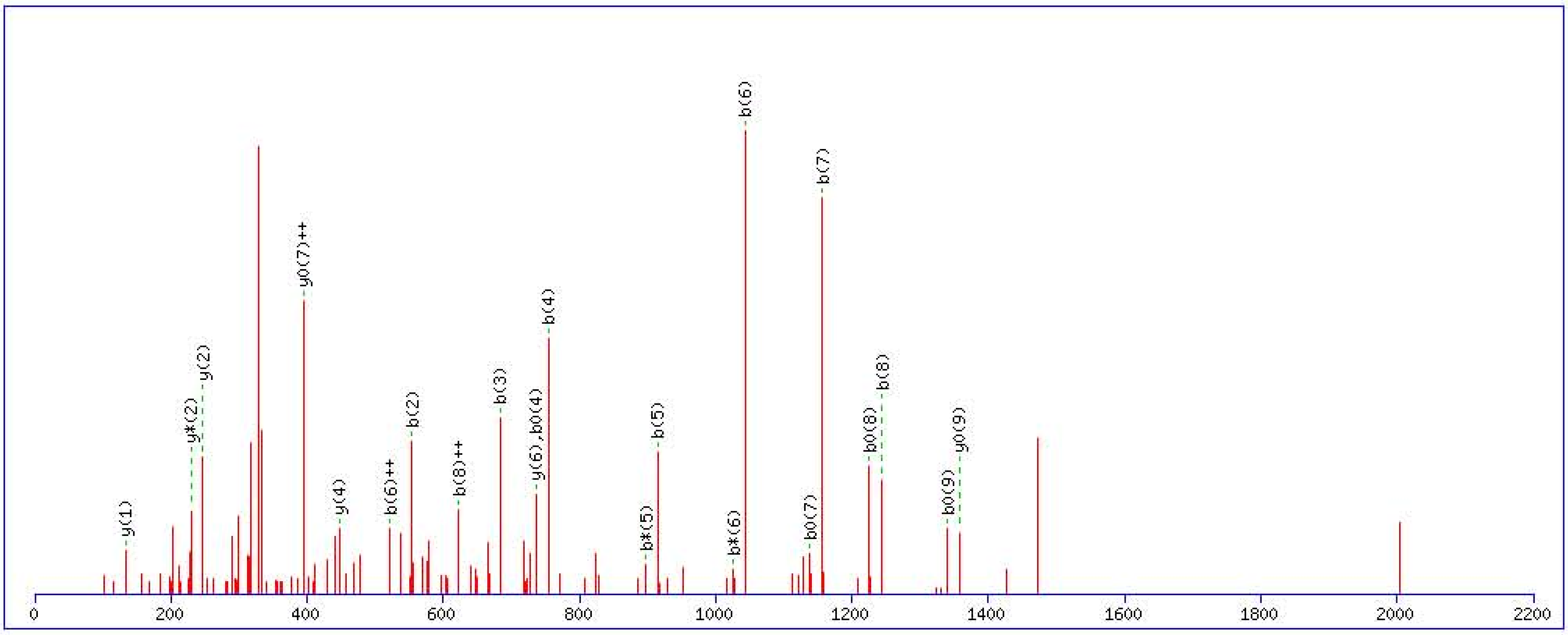
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

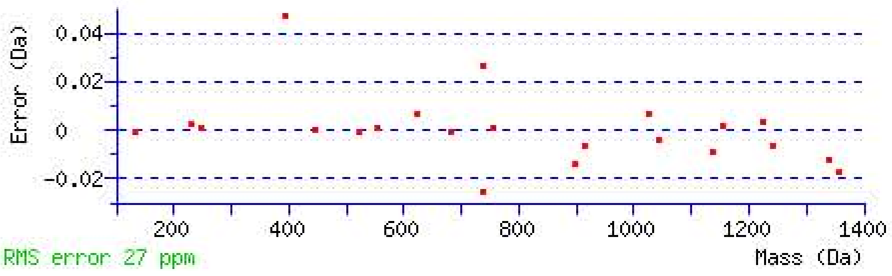
Match to Query 29663: 1488.639008 from(745.326780,2+) rtinseconds(1650) index(31154)
Title: Locus:1.1.1.3123.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

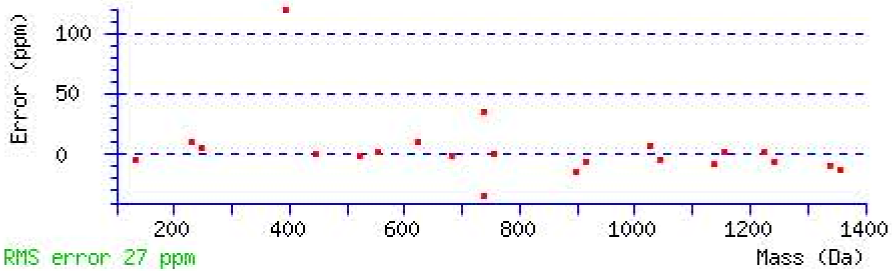
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1488.633682
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 64 **Expect:** 1.7e-006
Matches : 23/100 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	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
63.8	1488.633682	0.005326	NQEACELSNN

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

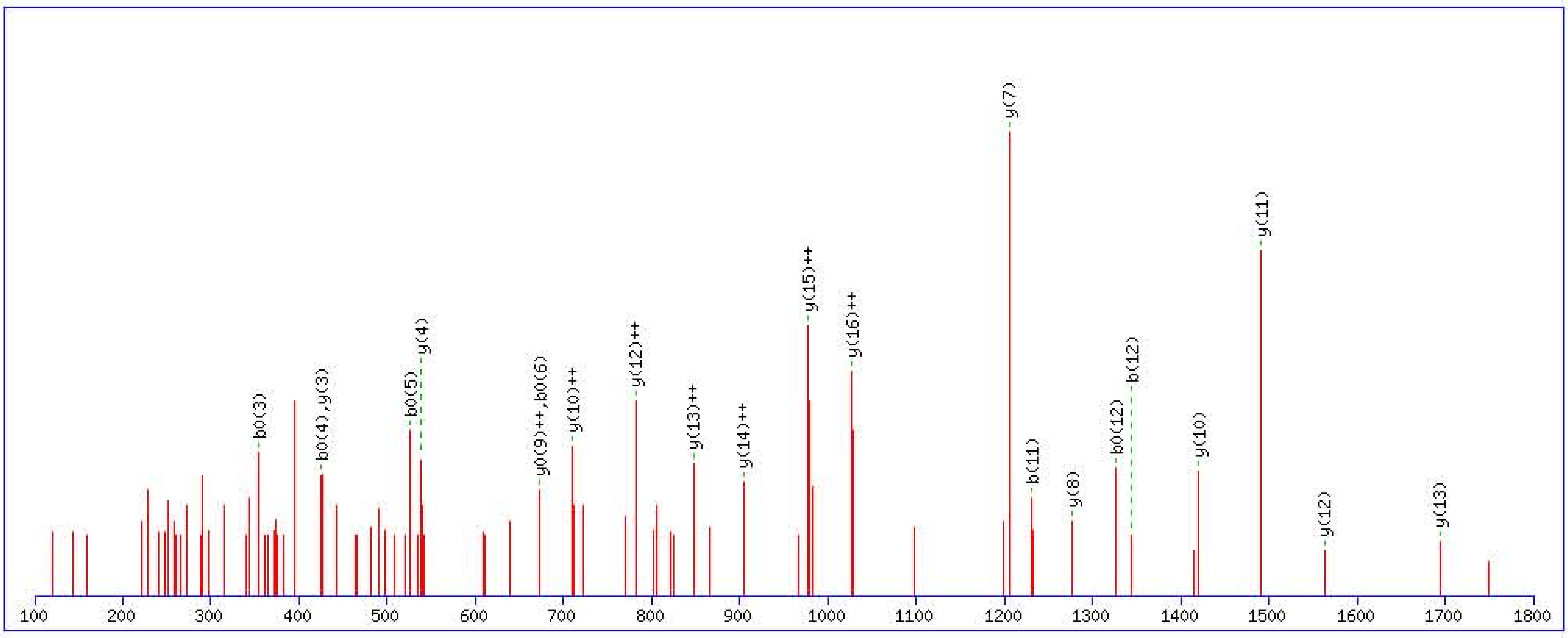
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

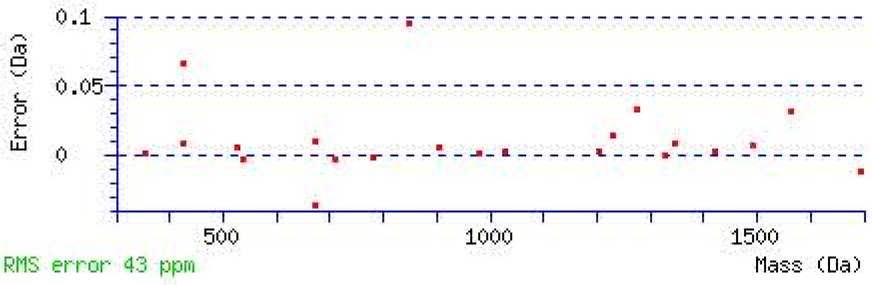
Match to Query 60714: 3396.682496 from(850.177900,4+) rtinseconds(3168) index(40041)
Title: Locus:1.1.1.3648.14 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

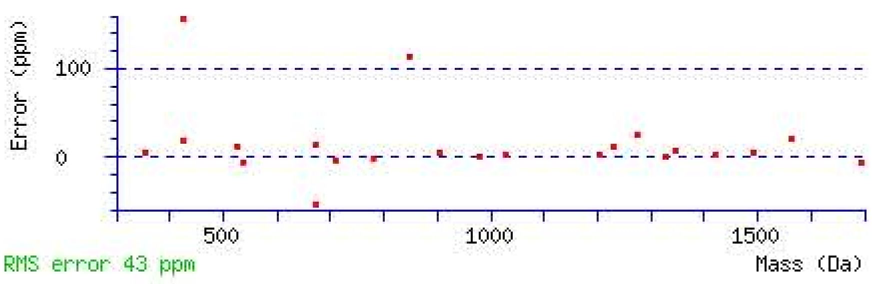
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3396.666855
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q24     : Biotin:Thermo-21345 (Q)
Ions Score: 45  Expect: 0.00091
Matches : 22/288 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							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
44.8	3396.666855	0.015641	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 41584: 1973.857572 from(658.959800,3+) rtinseconds(2006) index(4986)
Title: Locus:1.1.1.3250.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\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): 1973.854614
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0014
Matches : 23/130 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							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
35.3	1973.854614	0.002958	SCALDQNCQWEPR
13.2	1973.854614	0.002958	SCALDQNCQWEPR

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

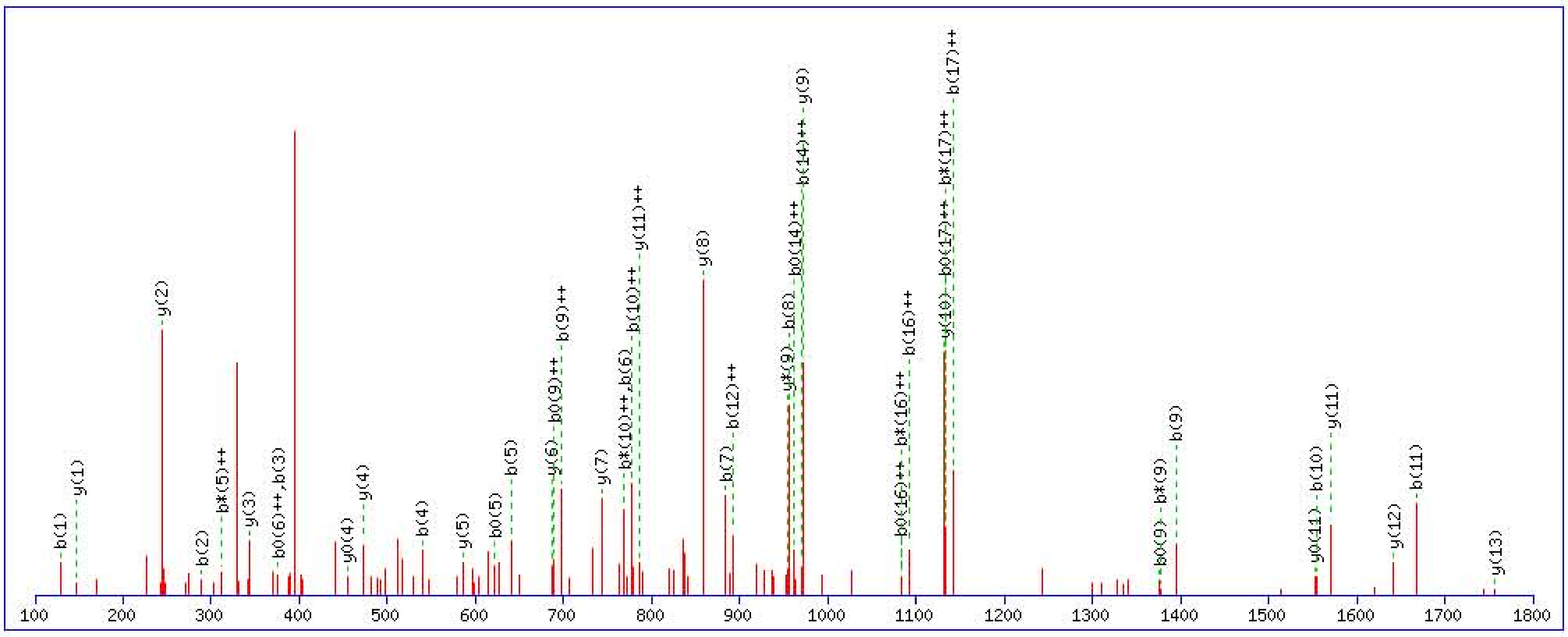
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

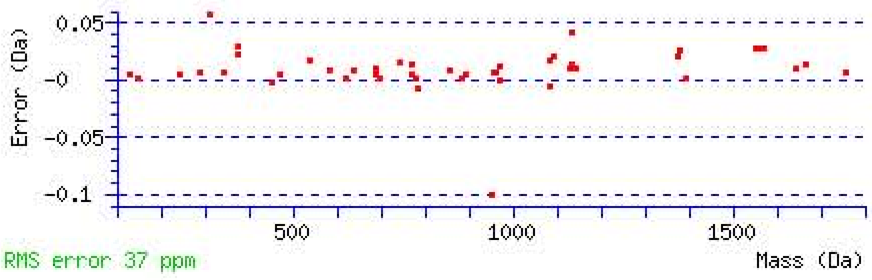
Match to Query 51475: 2524.171872 from(842.397900,3+) rtinseconds(2003) index(62602)
Title: Locus:1.1.1.3323.26 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

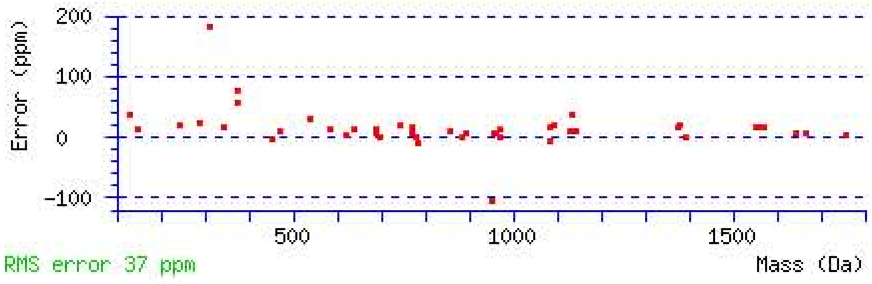
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 81  Expect: 1e-007
Matches : 46/206 fragment ions using 80 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***129.102239***	65.054757	112.075690	56.541483			K							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



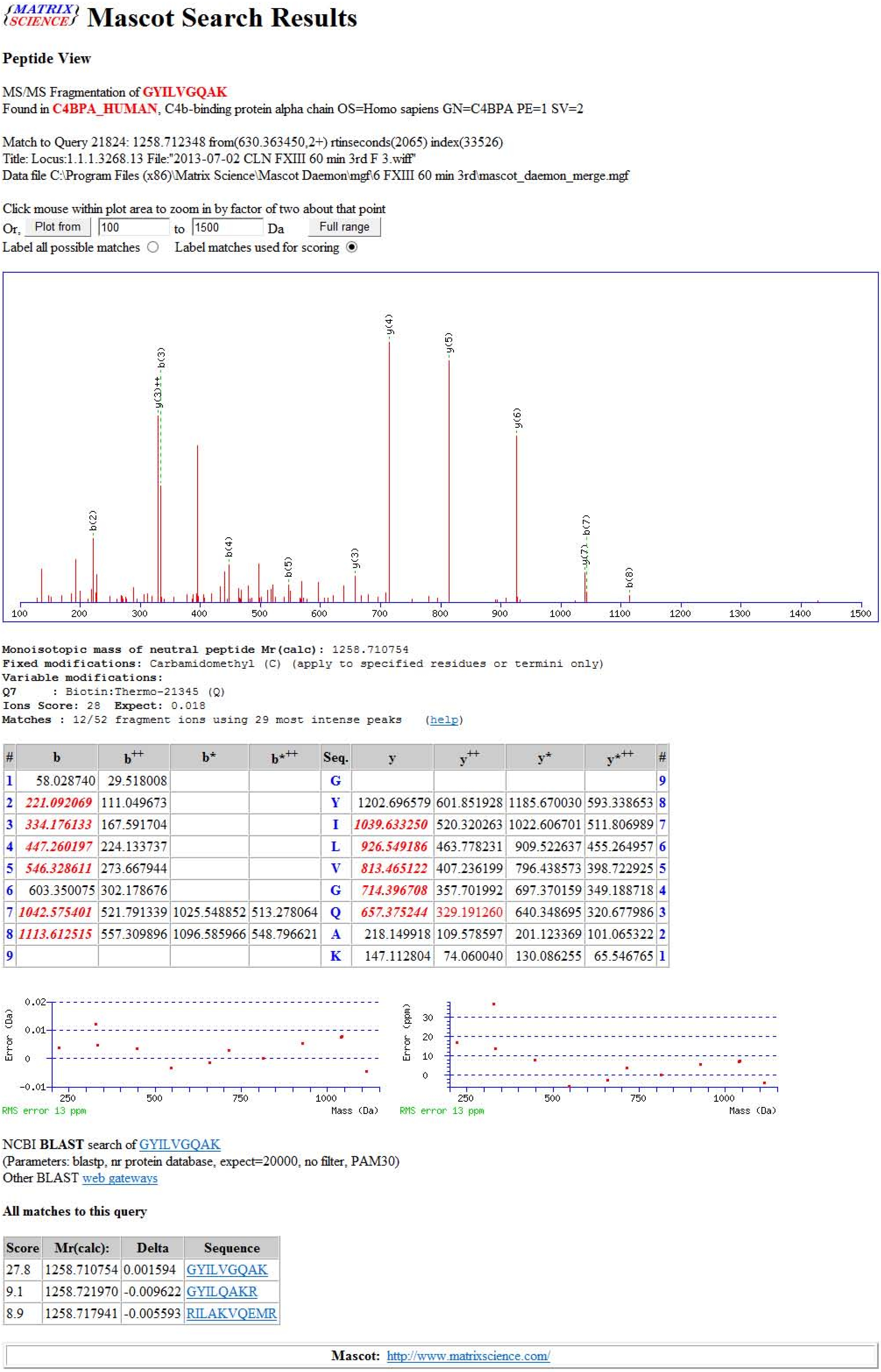


NCBI **BLAST** search of KCSYTEDAQCIDGTIEVPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
81.3	2524.164780	0.007092	KCSYTEDAQCIDGTIEVPK

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



Mascot Search Results

Peptide View

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

Match to Query 21824: 1258.712348 from(630.363450,2+) rtinseconds(2065) index(33526)
Title: Locus:1.1.1.3268.13 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\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): 1258.710754
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.018
Matches : 12/52 fragment ions using 29 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
27.8	1258.710754	0.001594	GYILVGQAK
9.1	1258.721970	-0.009622	GYILQAKR
8.9	1258.717941	-0.005593	RILAKVQEMR

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

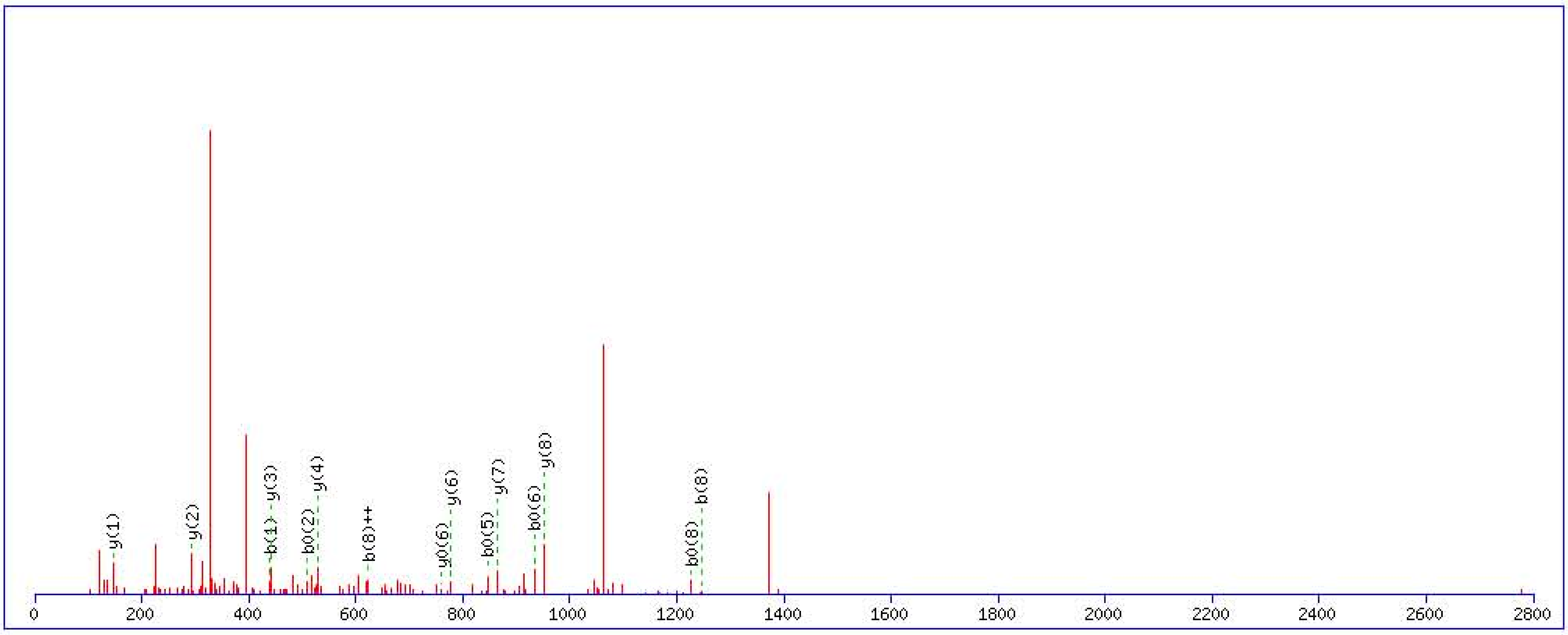
Mascot Search Results

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

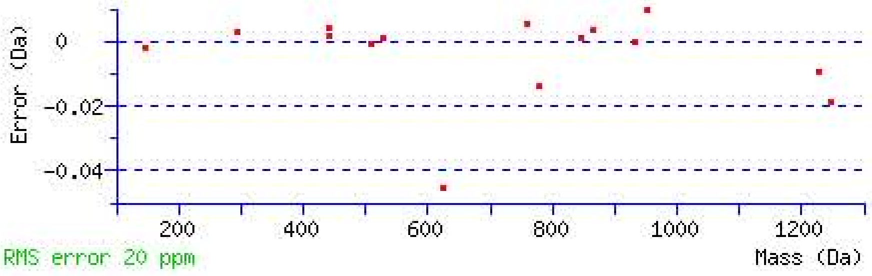
Match to Query 25948: 1390.663768 from(696.339160,2+) rtinseconds(2137) index(33923)
Title: Locus:1.1.1.3293.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

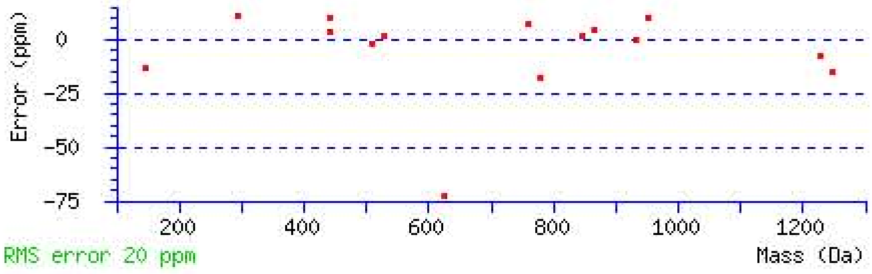
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1390.659119
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.0032
Matches : 15/88 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**							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
28.9	1390.659119	0.004649	QSSSYSFFK
2.1	1390.676208	-0.012440	AEKSSSTDQK
1.6	1390.669678	-0.005910	CAPASIRLMDNK
0.5	1390.673721	-0.009953	QPNCSSLFK

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

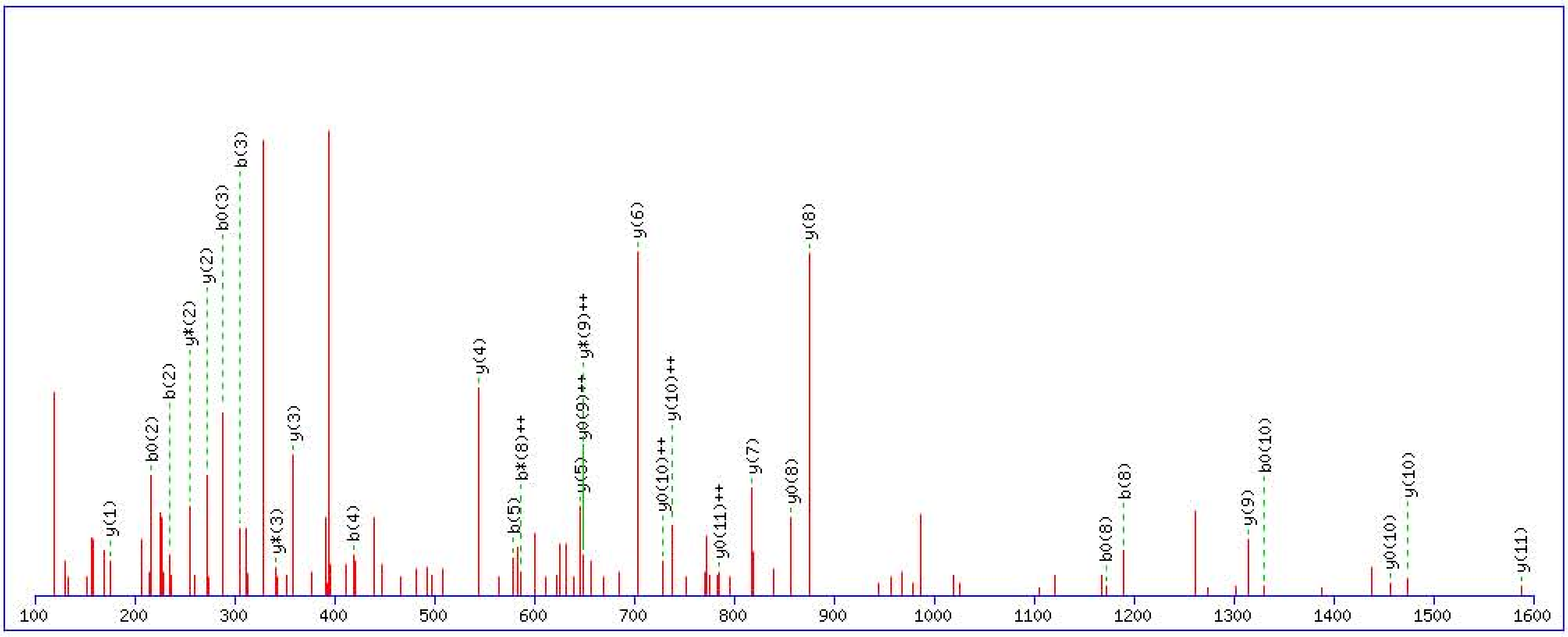
{MATRIX SCIENCE} Mascot Search Results

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

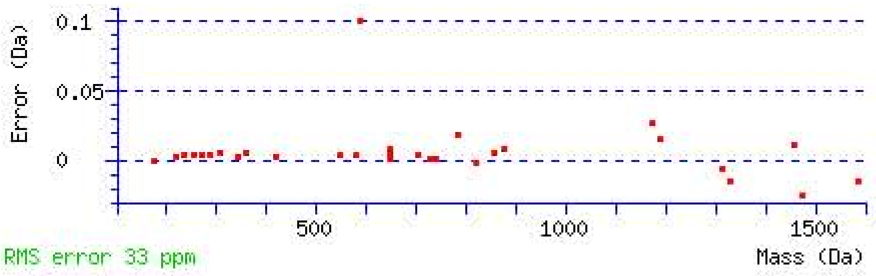
Match to Query 40090: 1891.884942 from(631.635590,3+) rtinseconds(2148) index(33971)
Title: Locus:1.1.1.3297.7 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

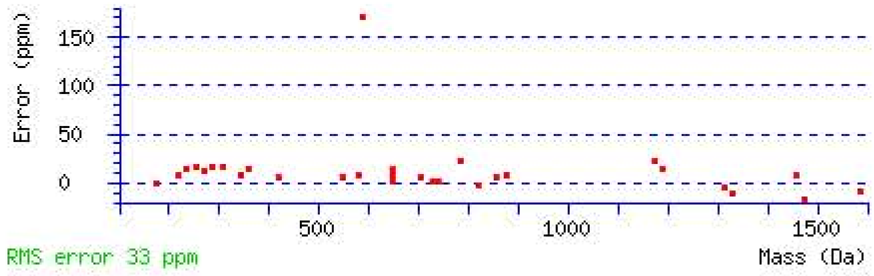
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1891.870941
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.001
Matches : 30/140 fragment ions using 81 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
41.5	1891.870941	0.014001	FSAICQGDGTWSPR

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

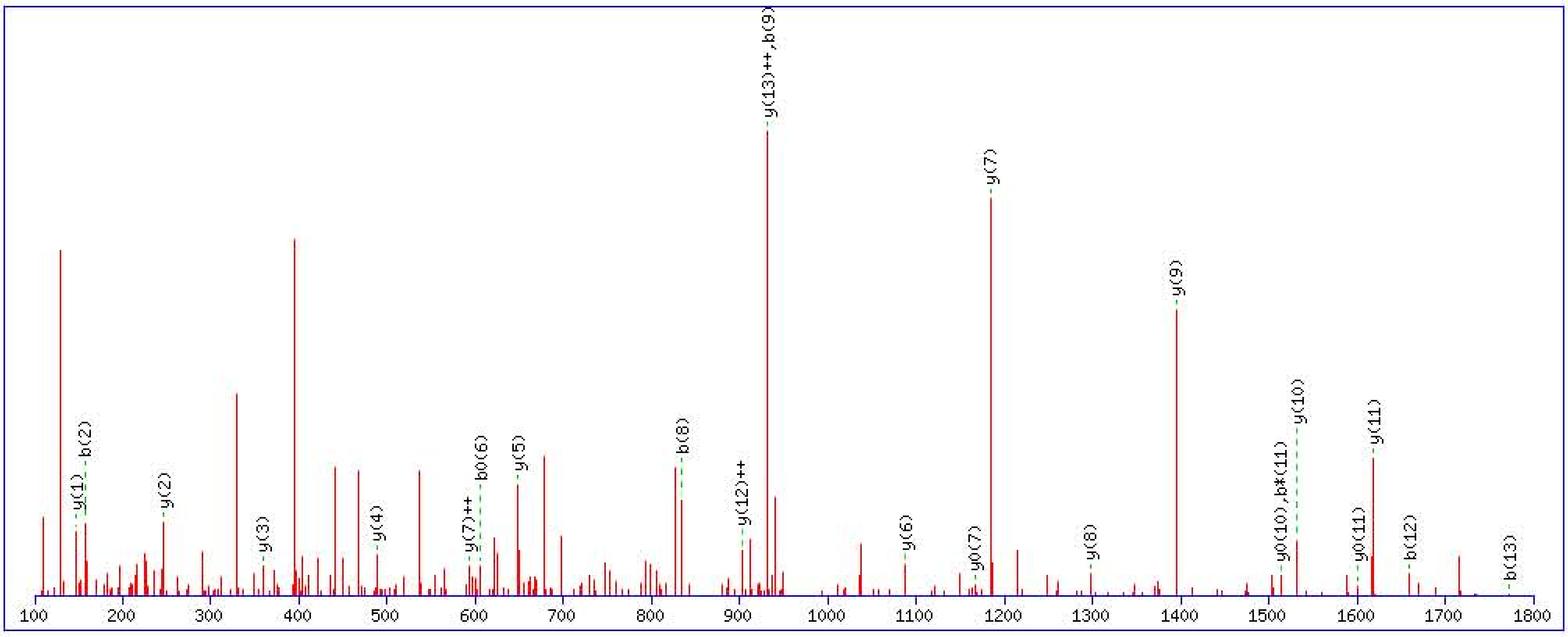
Mascot Search Results

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

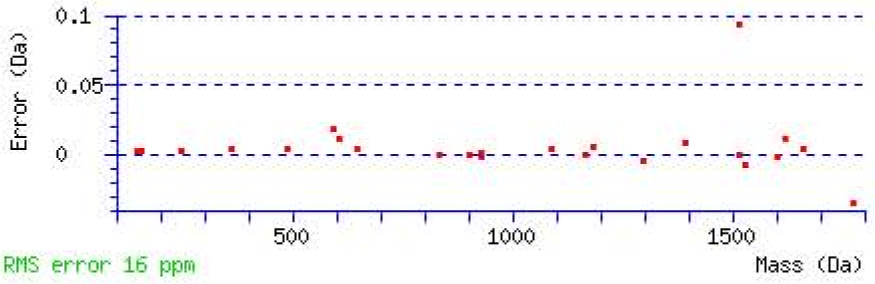
Match to Query 42980: 2017.032432 from(673.351420,3+) rtinseconds(2088) index(33630)
Title: Locus:1.1.1.3276.14 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

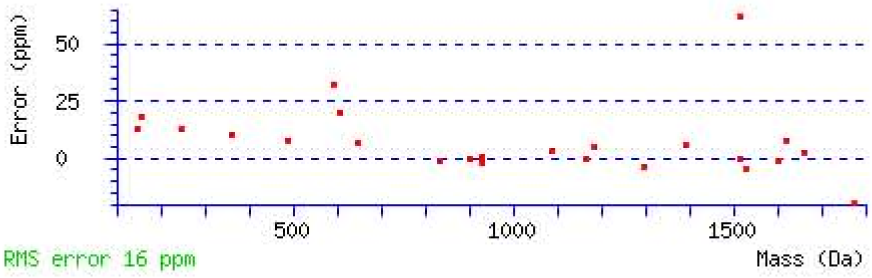
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 38  Expect: 0.0043
Matches : 24/136 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	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
38.5	2017.027771	0.004661	GVGWSHPLPQCEIVK

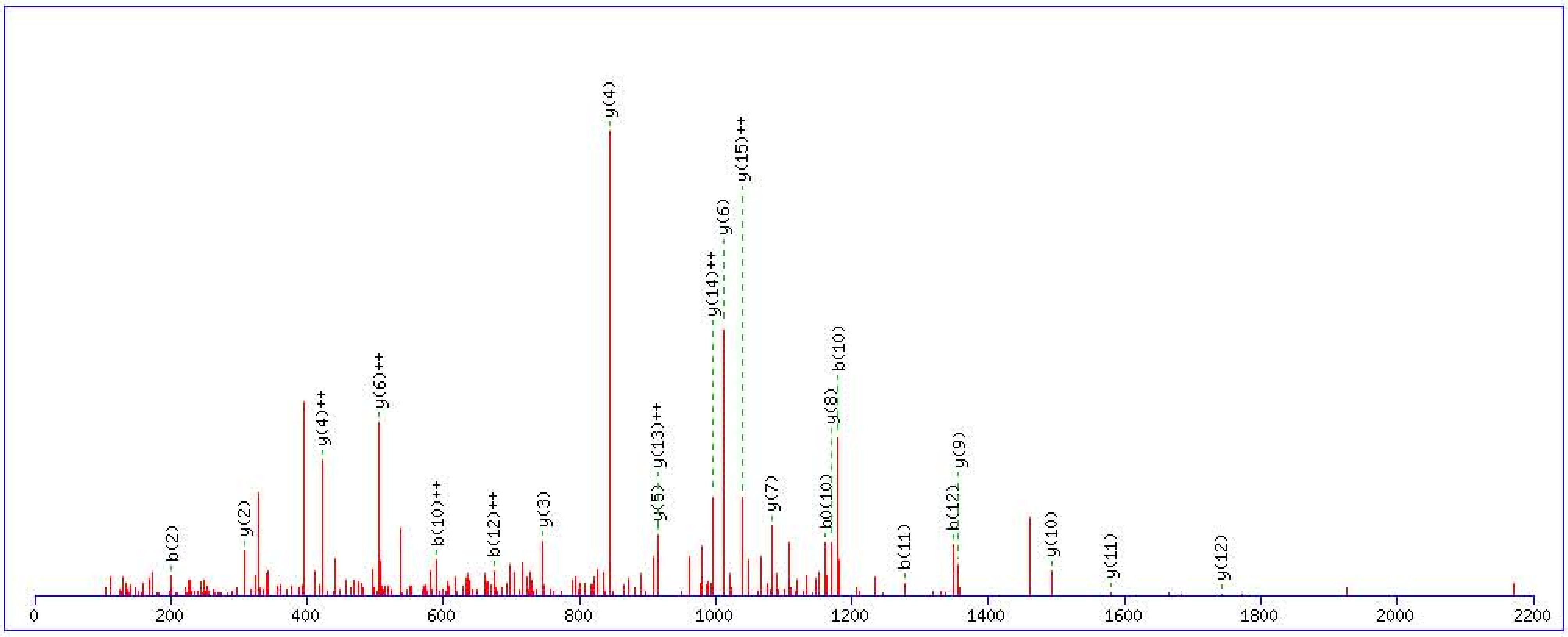
Mascot Search Results

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

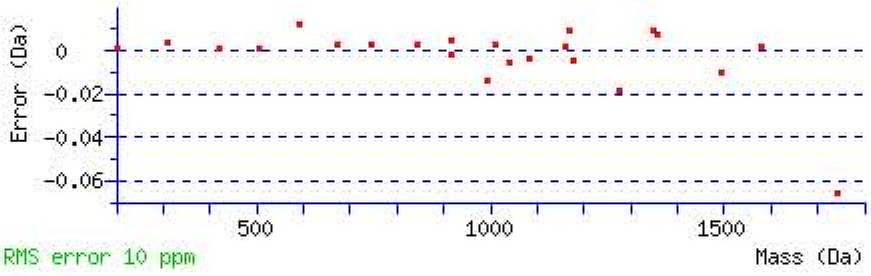
Match to Query 45864: 2188.989162 from(730.670330,3+) rtinseconds(1776) index(31813)
Title: Locus:1.1.1.3167.16 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

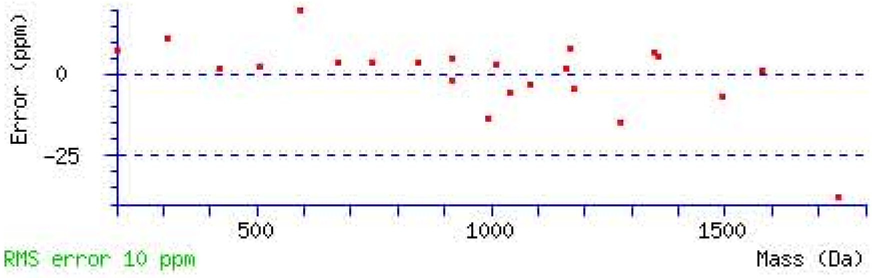
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2188.985626
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Biotin:Thermo-21345 (Q)
Ions Score: 56 **Expect:** 2.3e-005
Matches : 23/138 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	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
56.5	2188.985626	0.003536	LSCSYSHWSAPAPQCK

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

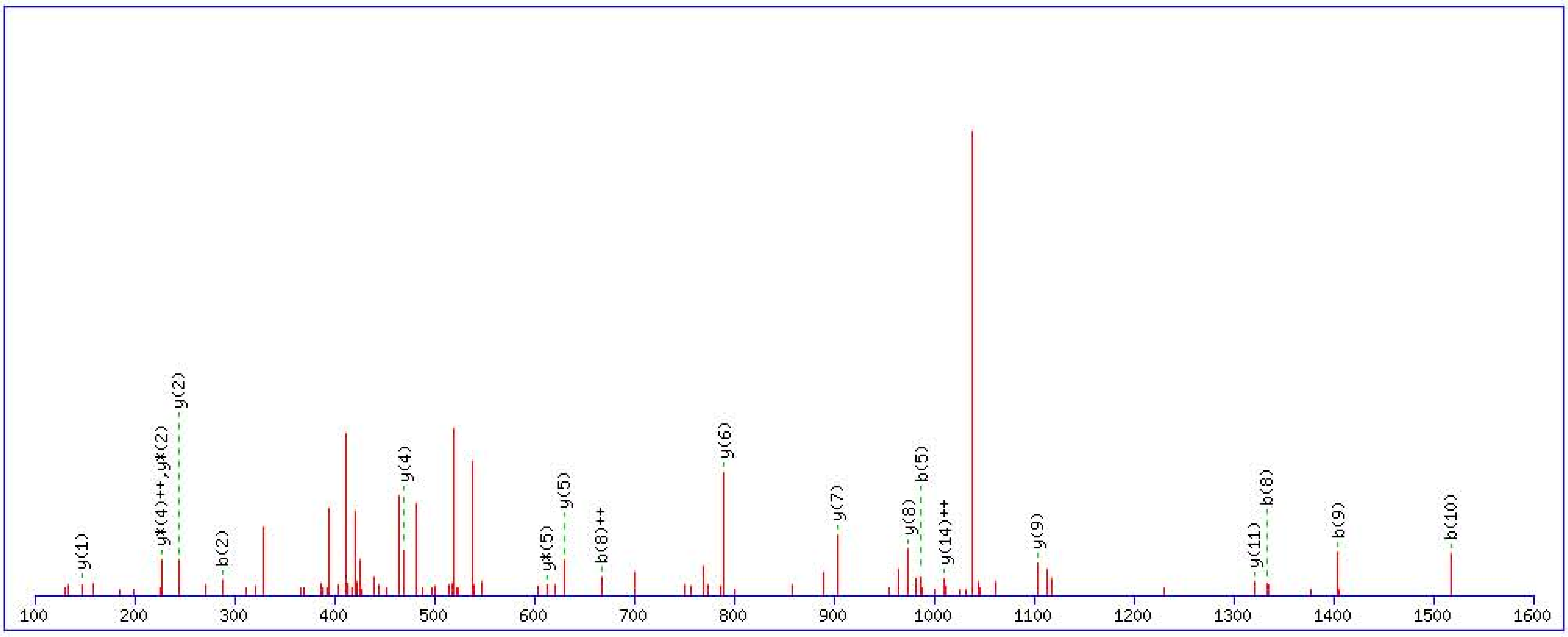
Mascot Search Results

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

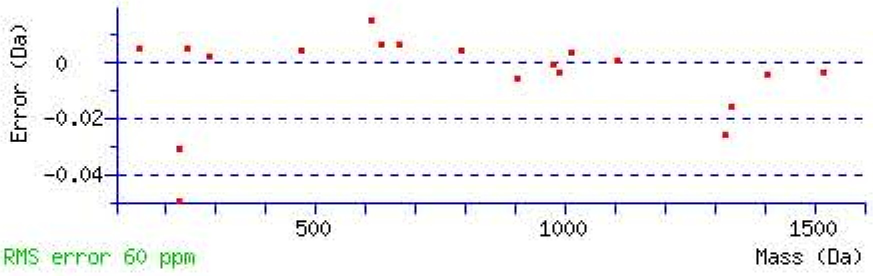
Match to Query 47904: 2306.007282 from(769.676370,3+) rtinseconds(2120) index(33830)
Title: Locus:1.1.1.3287.16 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

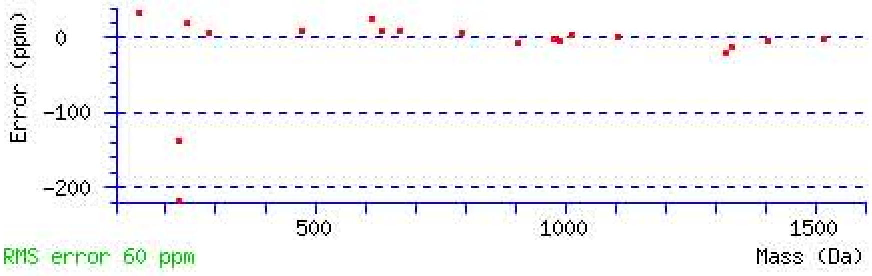
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2305.999237
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 28 **Expect:** 0.0074
Matches : 19/166 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	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
28.4	2305.999237	0.008045	WTPYQGCEALCCPEPK

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

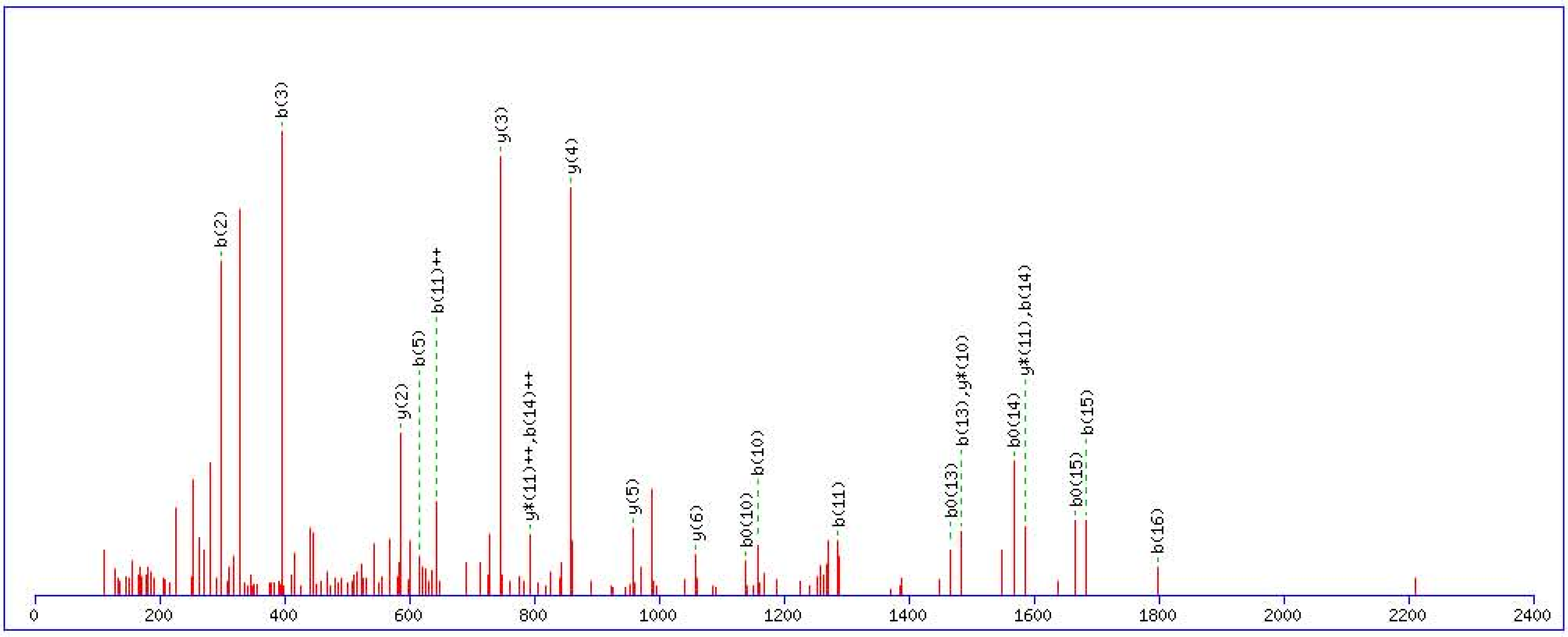
{MATRIX SCIENCE} Mascot Search Results

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

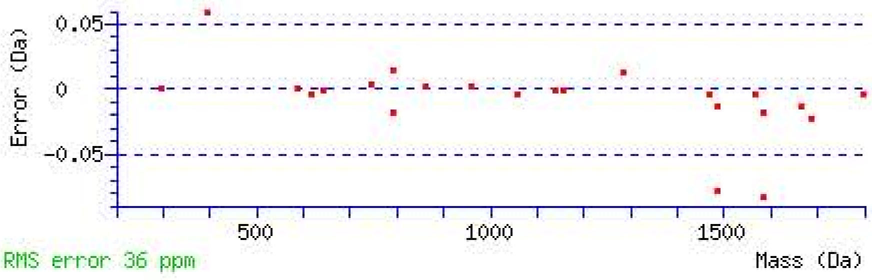
Match to Query 51637: 2542.206336 from(636.558860,4+) rtinseconds(1596) index(30863)
Title: Locus:1.1.1.3104.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

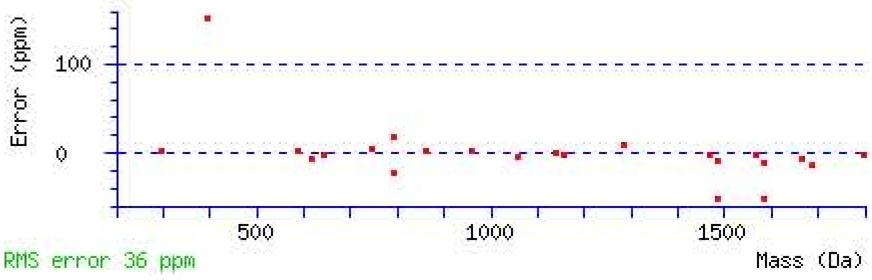
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 48  Expect: 0.00026
Matches : 23/182 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	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
48.4	2542.201859	0.004477	CHPGYKPTTDEPTTVICQK

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

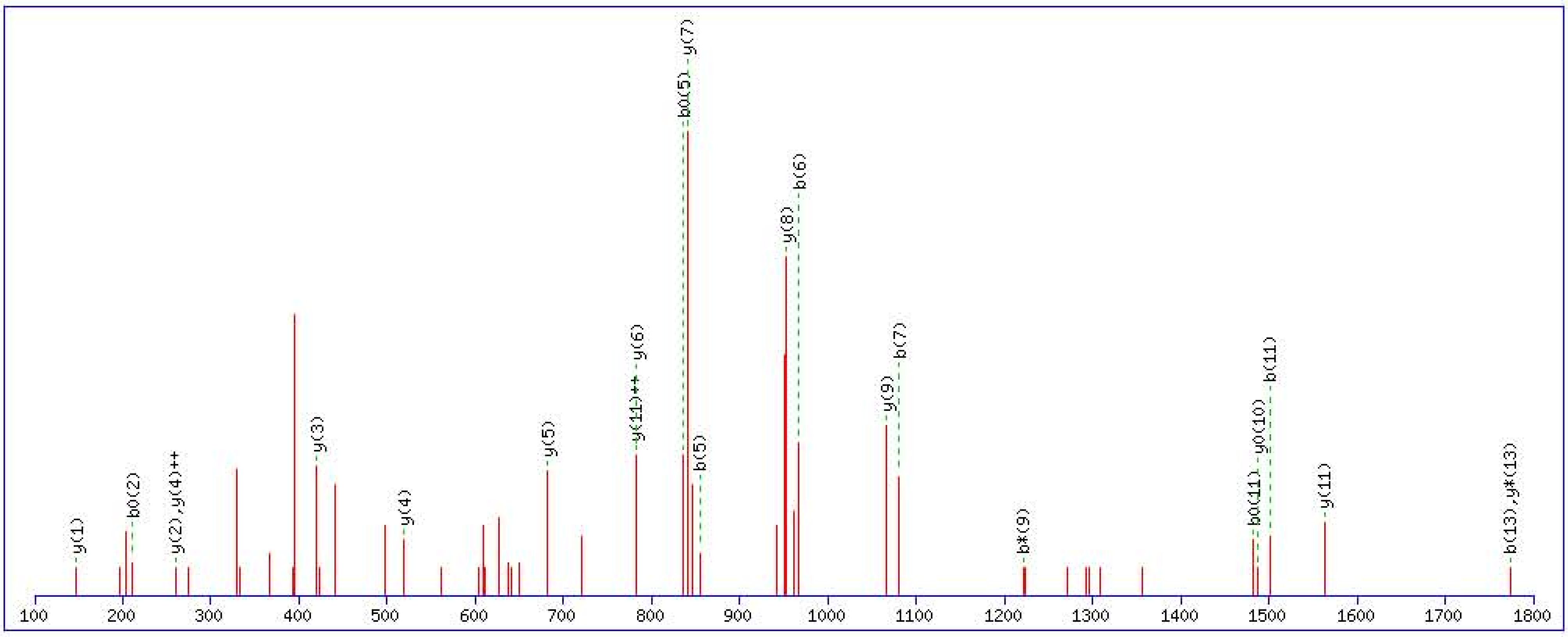
Mascot Search Results

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

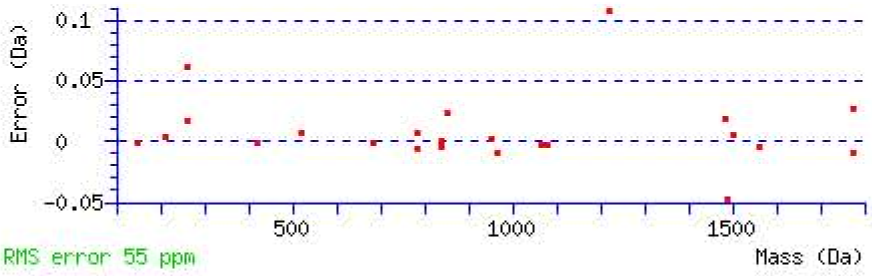
Match to Query 40555: 1919.000868 from(960.507710,2+) rtinseconds(2482) index(35644)
Title: Locus:1.1.1.3413.25 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

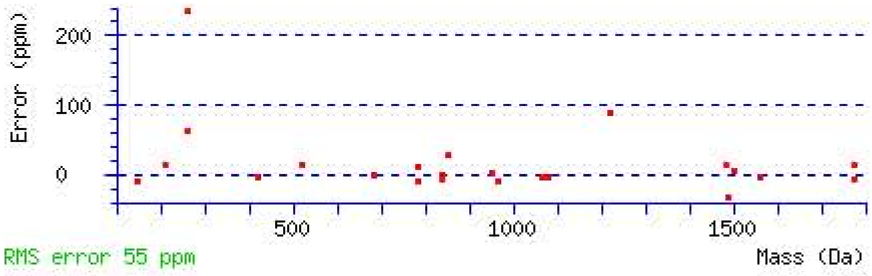
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1918.989639
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 55  Expect: 7.4e-005
Matches : 23/138 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	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
55.3	1918.989639	0.011229	EVEGQILGTYVCIK

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

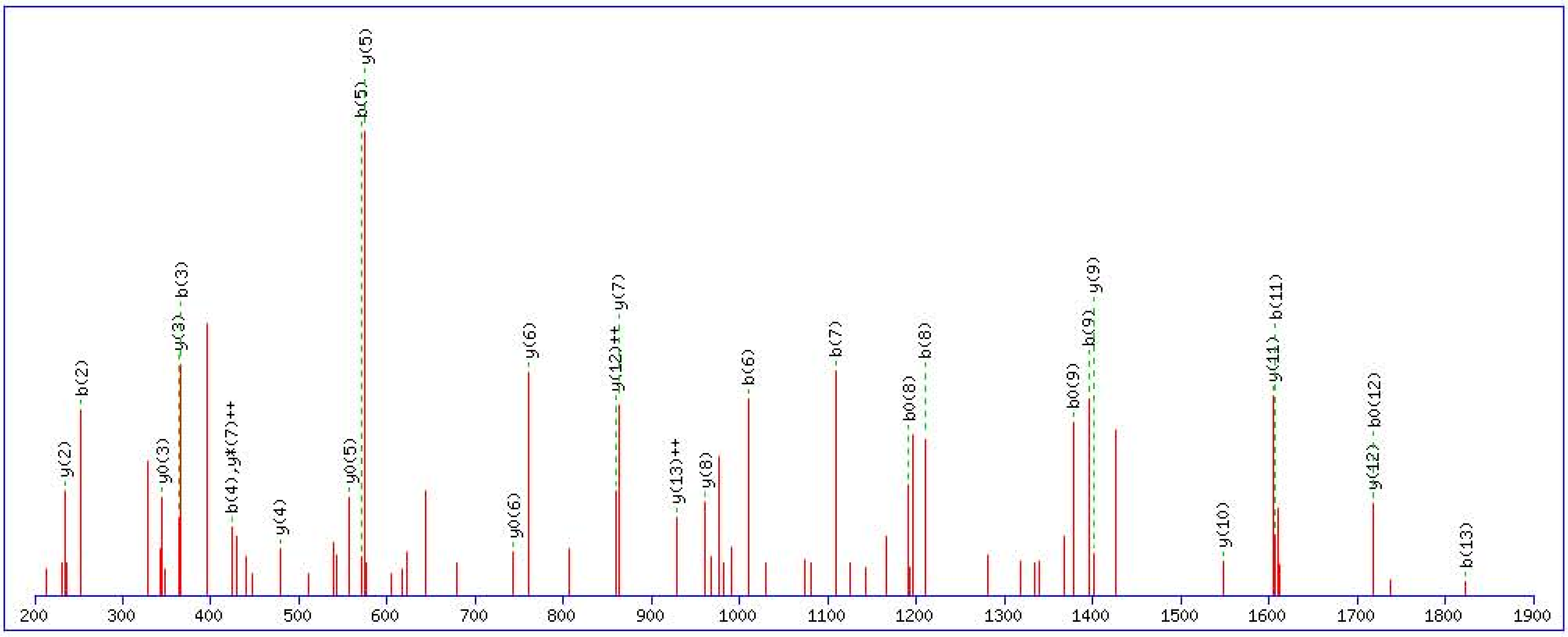
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

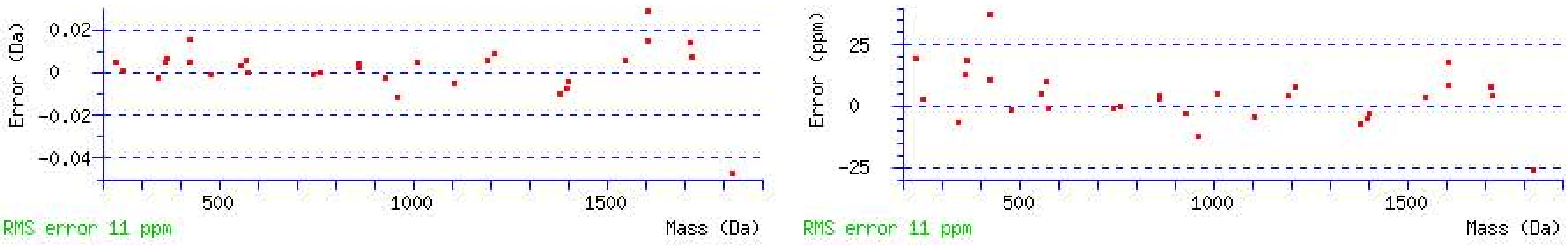
Match to Query 41514: 1968.963488 from(985.489020,2+) rtinseconds(2315) index(34901)
Title: Locus:1.1.1.3355.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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): 1968.940399
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 59  Expect: 1.2e-005
Matches : 30/144 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							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
58.8	1968.940399	0.023089	DHLGFQVTWPDESK
6.0	1968.949585	0.013903	EGQMESVEAAMSSKTLKK
2.0	1968.957458	0.006030	KFMAASVASTNRDEALDK

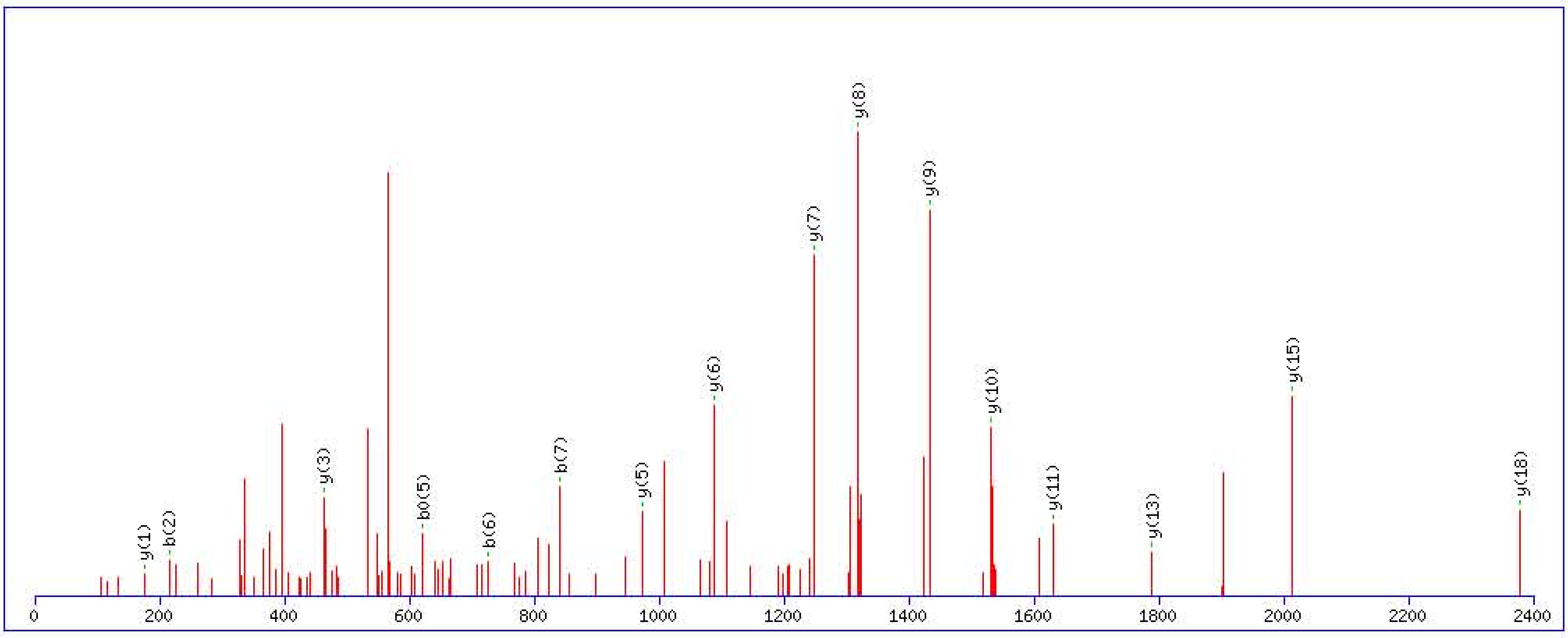
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

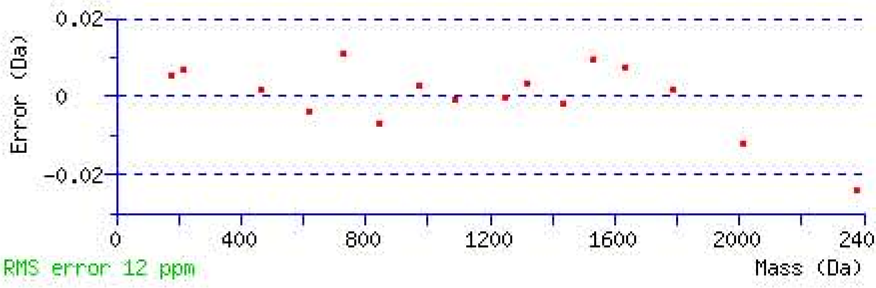
Match to Query 54668: 2854.260432 from(952.427420,3+) rtinseconds(2071) index(33551)
Title: Locus:1.1.1.3270.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

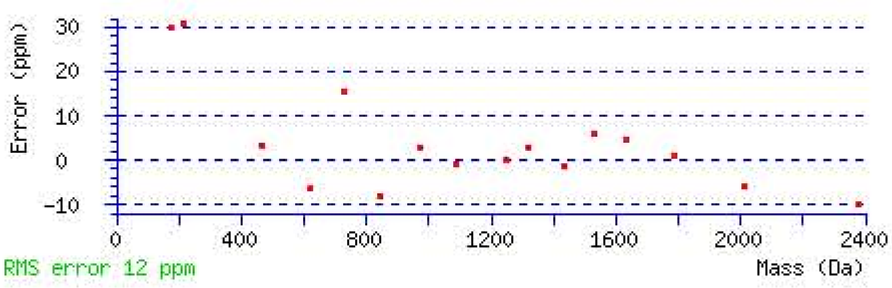
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2854.250671
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18     : Biotin:Thermo-21345 (Q)
Ions Score: 97  Expect: 1.1e-009
Matches : 16/240 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							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
97.2	2854.250671	0.009761	SQCTYSNPEGTVVLACDQAQCR
81.9	2854.250671	0.009761	SQCTYSNPEGTVVLACDQAQCR
3.3	2854.250671	0.009761	SQCTYSNPEGTVVLACDQAQCR

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

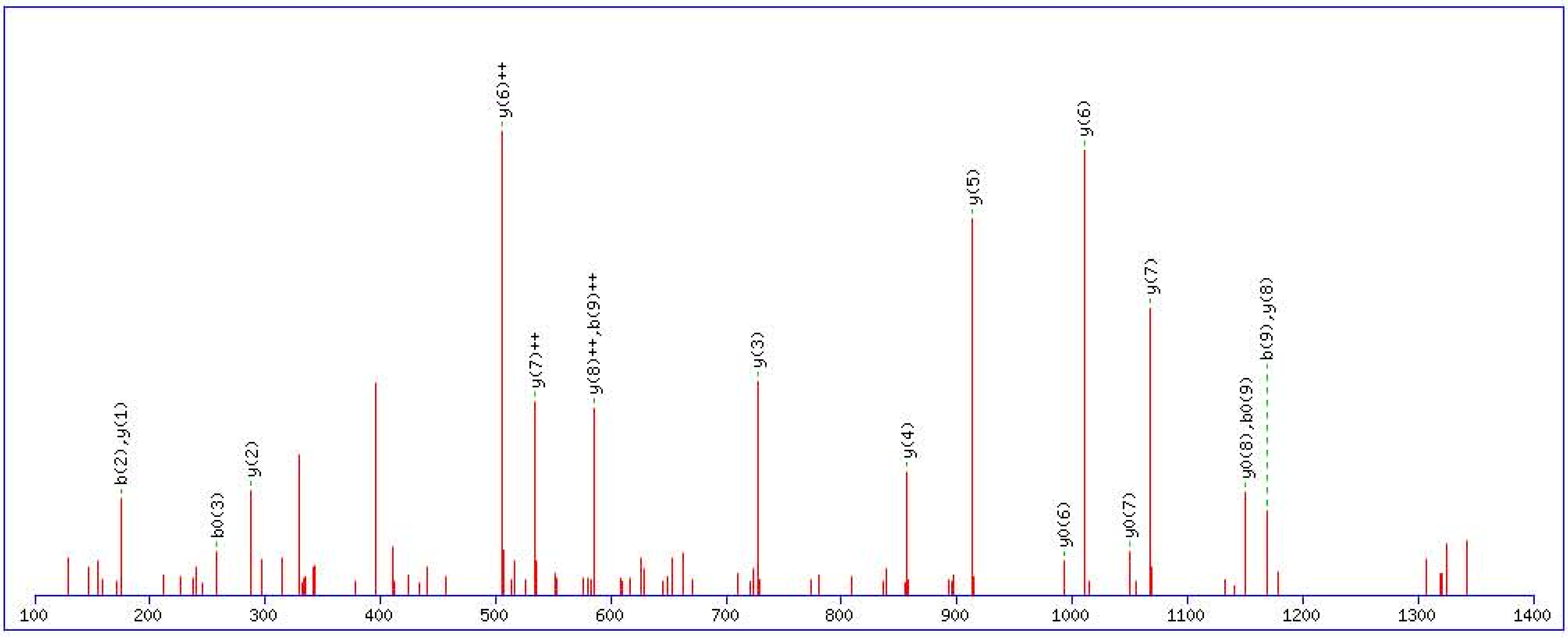
Mascot Search Results

Peptide View

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

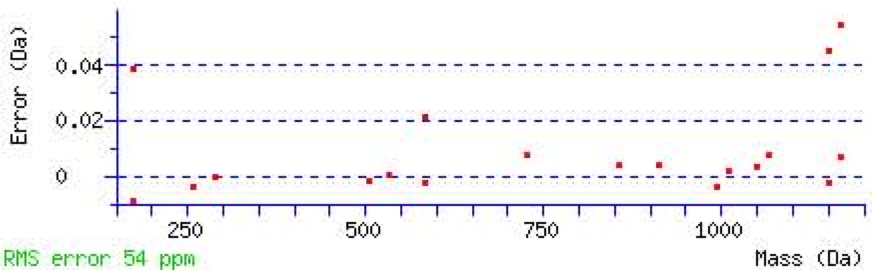
Match to Query 23845: 1341.673168 from(671.843860,2+) rtinseconds(1575) index(44683)
Title: Locus:1.1.1.2597.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

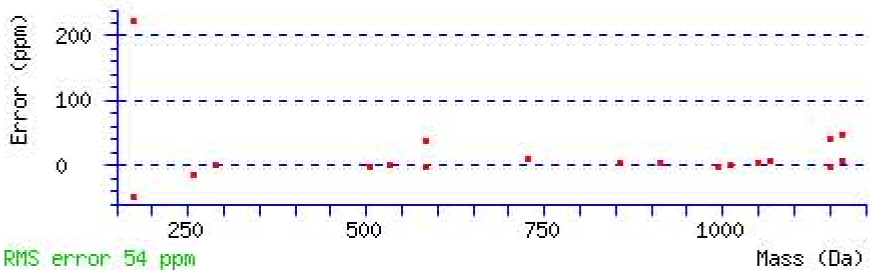
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1341.671082
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 66  Expect: 5.5e-006
Matches : 19/88 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	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
65.5	1341.671082	0.002086	SSTGPGEQLR
13.9	1341.674911	-0.001743	TSPERREPGTGR
8.2	1341.671036	0.002132	KEAEQEAAR
6.7	1341.663651	0.009517	ESARDPKPEASR
5.3	1341.653778	0.019390	QHRPSNAEFTR
5.0	1341.686127	-0.012959	QDDAGRIAARNR
4.9	1341.688828	-0.015660	DDAQLSGLPSALR
4.7	1341.680267	-0.007099	KFHEKHHSHR
2.9	1341.671082	0.002086	TSLPQDNTR
2.6	1341.653793	0.019375	GFAEHGKQQQGR

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

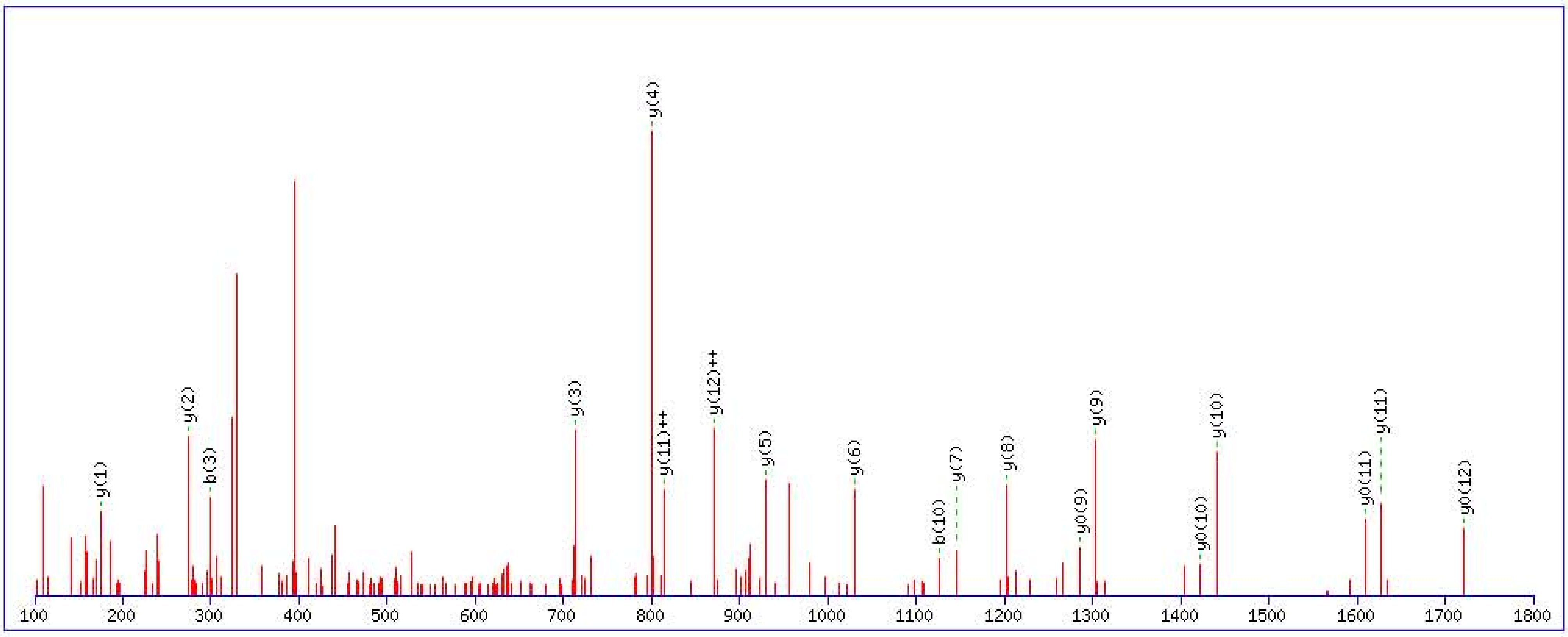
MATRIX SCIENCE Mascot Search Results

Peptide View

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

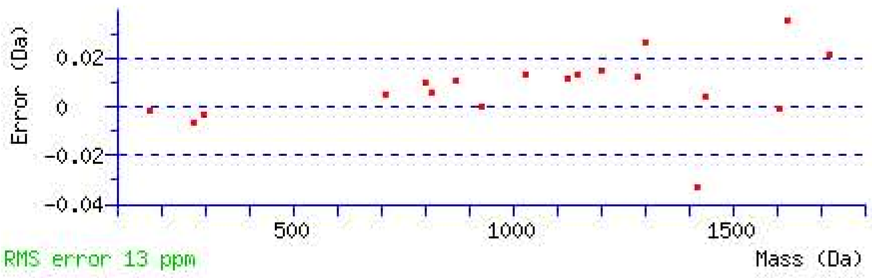
Match to Query 40652: 1923.934452 from(642.318760,3+) rtinseconds(1759) index(45843)
Title: Locus:1.1.1.2661.13 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

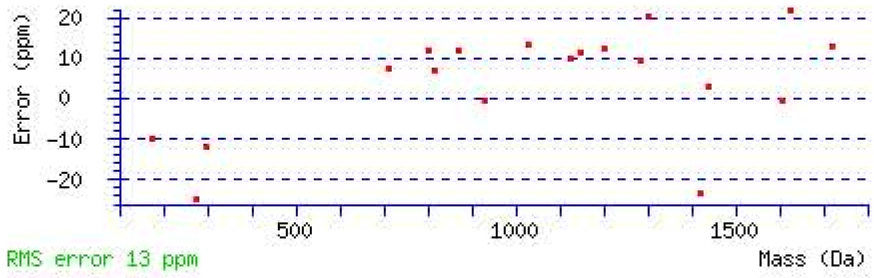
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1923.926132
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 73  Expect: 1.1e-006
Matches : 19/140 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	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
73.0	1923.926132	0.008320	NALWHTGDTESQVR

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

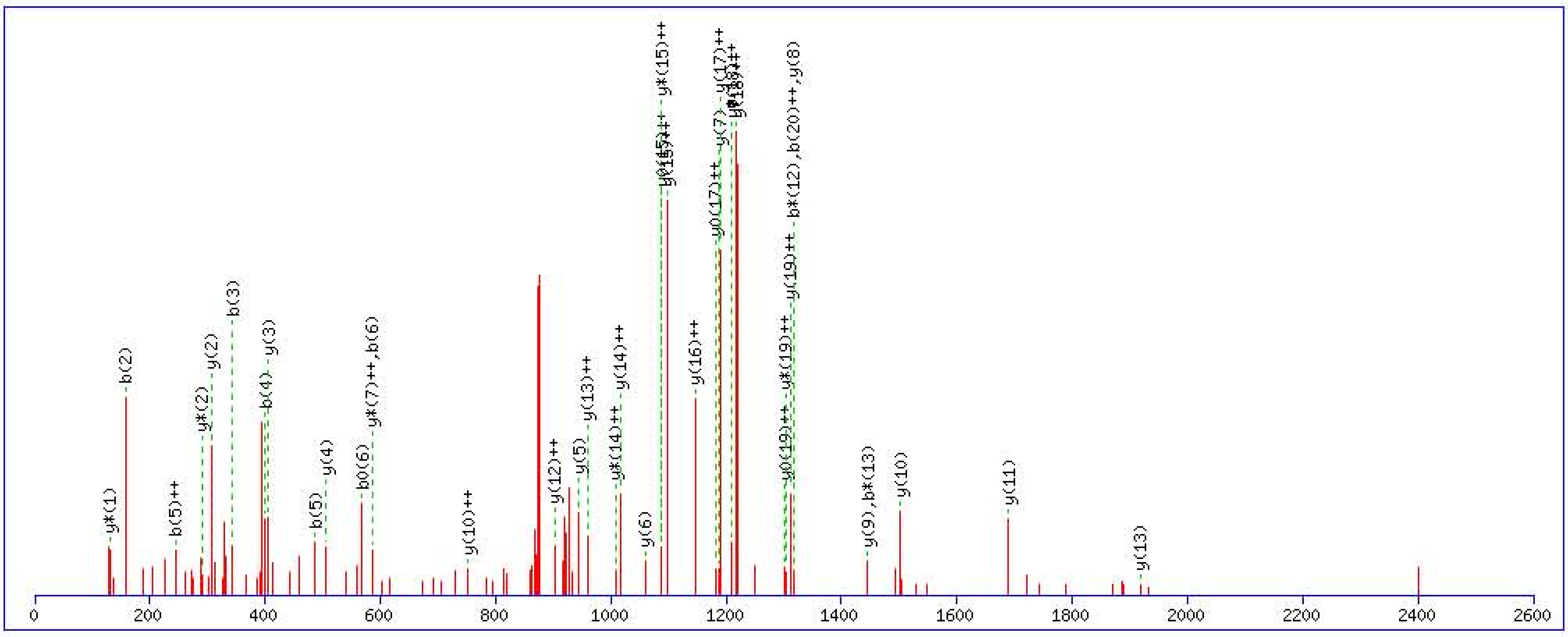
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

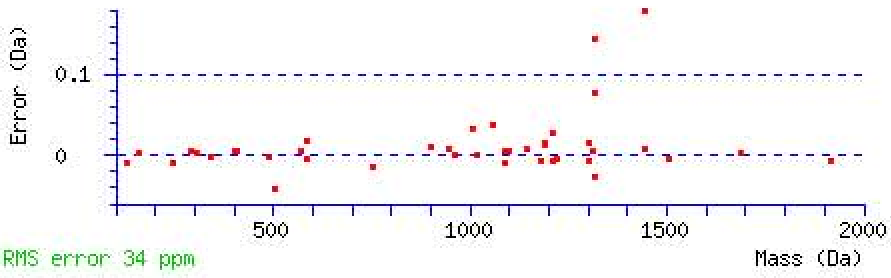
Match to Query 53517: 2777.240592 from(926.754140,3+) rtinseconds(2132) index(33897)
Title: Locus:1.1.1.3291.19 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

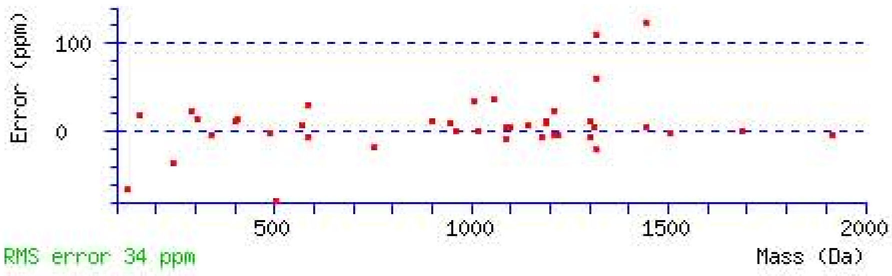


Monoisotopic mass of neutral peptide Mr(calc): 2777.224792
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q17 : Biotin:Thermo-21345 (Q)
Ions Score: 41 **Expect:** 0.00053
Matches : 41/204 fragment ions using 105 most intense peaks (help)

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



RMS error 34 ppm



RMS error 34 ppm

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
41.2	2777.224792	0.015800	GVWGSVCDDNWGEKEDQVVCK

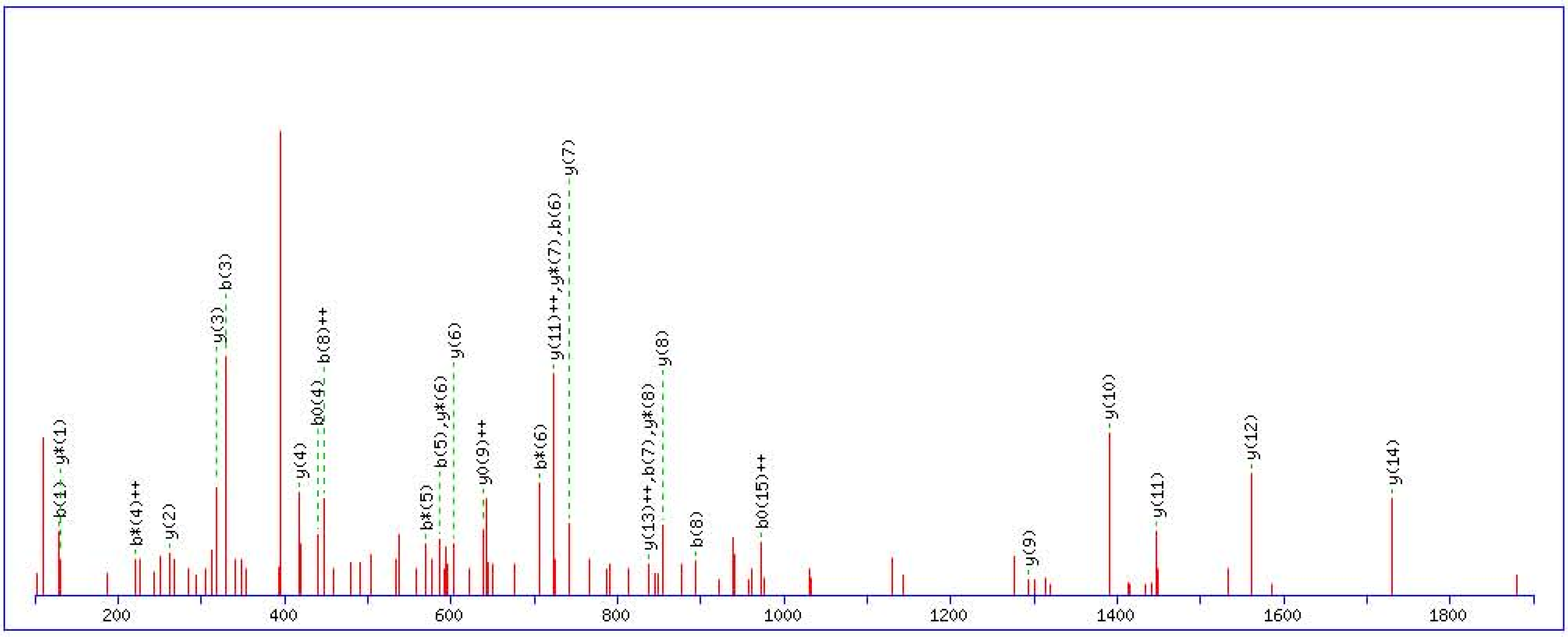
Mascot Search Results

Peptide View

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

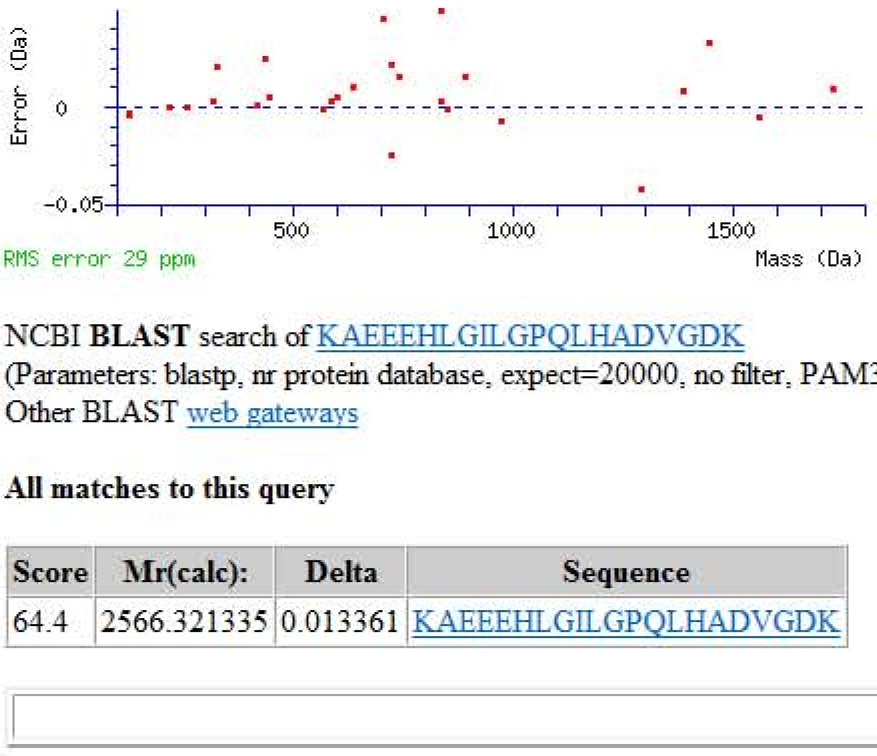
Match to Query 51783: 2566.334696 from(642.590950,4+) rtinseconds(1940) index(46985)
Title: Locus:1.1.1.2724.13 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

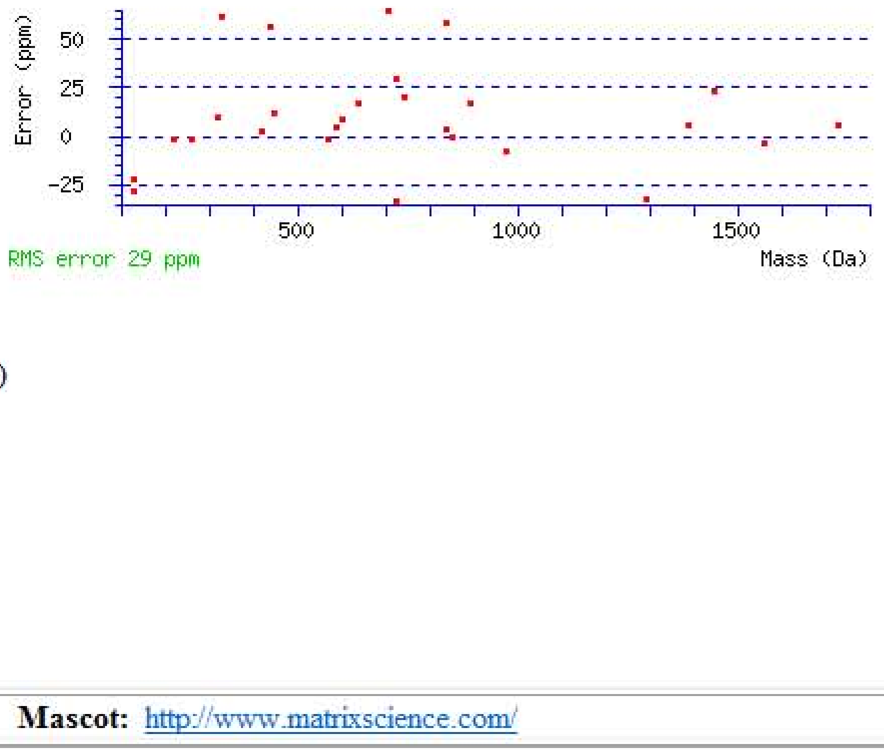


Monoisotopic mass of neutral peptide Mr(calc): 2566.321335
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13 : Biotin:Thermo-21345 (Q)
Ions Score: 64 **Expect:** 9.4e-006
Matches : 30/234 fragment ions using 45 most intense peaks (help)

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



RMS error 29 ppm



RMS error 29 ppm

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
64.4	2566.321335	0.013361	KAEEEHLGILGPQLHADVGDK

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

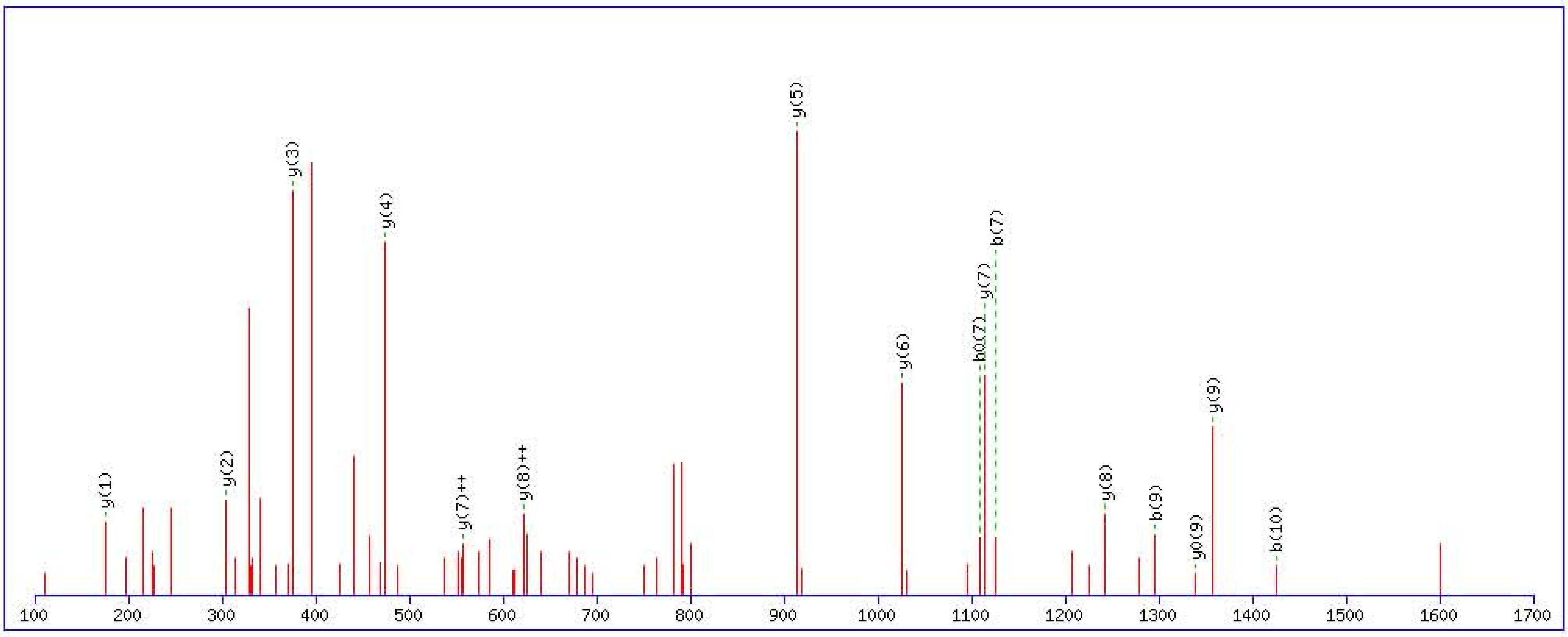
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

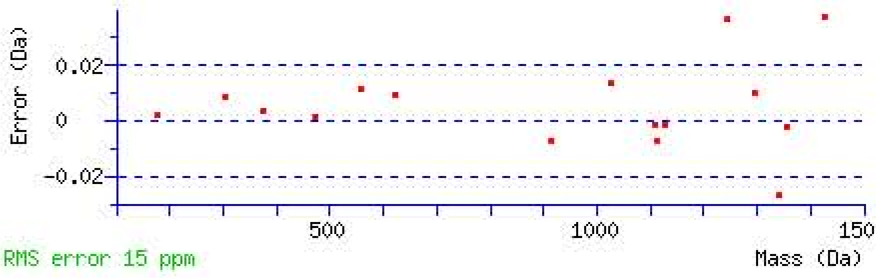
Match to Query 33254: 1598.796828 from(800.405690,2+) rtinseconds(1966) index(4768)
Title: Locus:1.1.1.3236.25 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

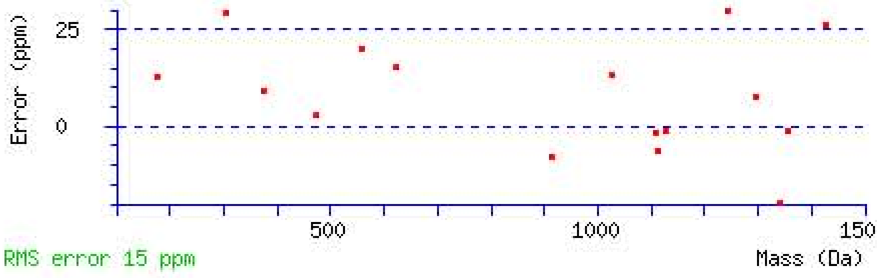
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1598.797379
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 71  Expect: 1.9e-006
Matches : 16/106 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	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
70.7	1598.797379	-0.000551	ELDESLQVAER
13.4	1598.787506	0.009322	AGGSWDLAVQER
7.8	1598.783478	0.013350	EDSVQRSTPNR
7.4	1598.817352	-0.020524	DRAALCQLWR
5.4	1598.797409	-0.000581	EDVDDLVSQLR
4.8	1598.802109	-0.005281	CQNALQQVTAR
4.5	1598.797379	-0.000551	LEESDVLQEAR
3.9	1598.802094	-0.005266	ELVSRCGEMLHIR
3.8	1598.794708	0.002120	GGRSRVDQEER
3.1	1598.812637	-0.015809	FINVGEKAYSCALK

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

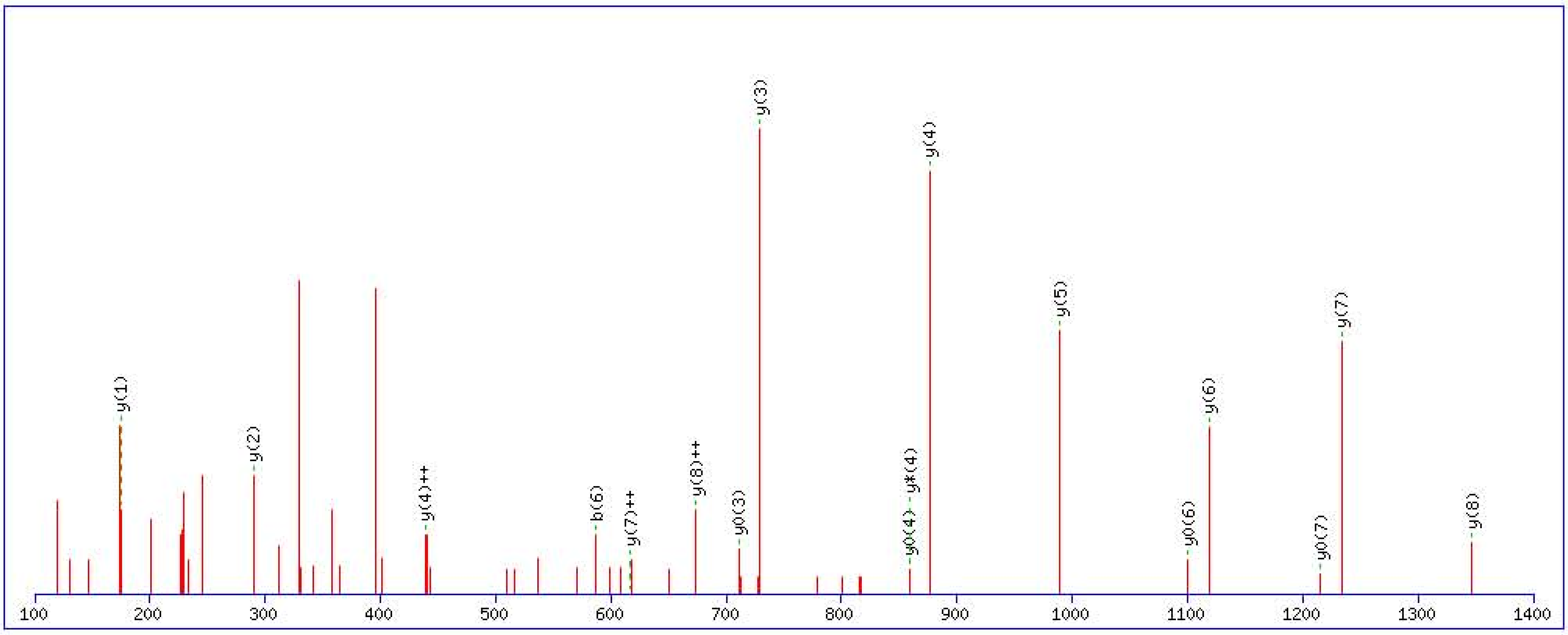
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

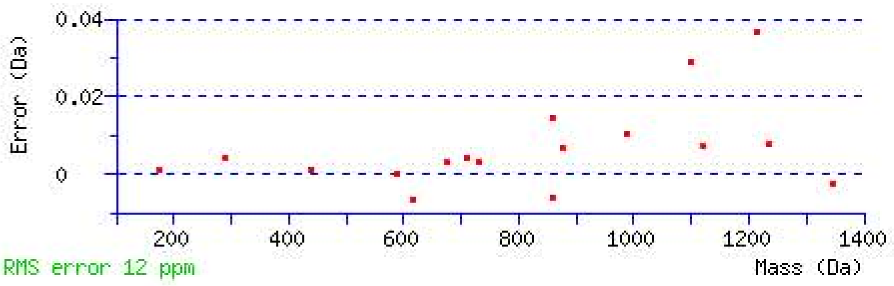
Match to Query 36535: 1703.860542 from(568.960790,3+) rtinseconds(2812) index(37781)
Title: Locus:1.1.1.3527.2 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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

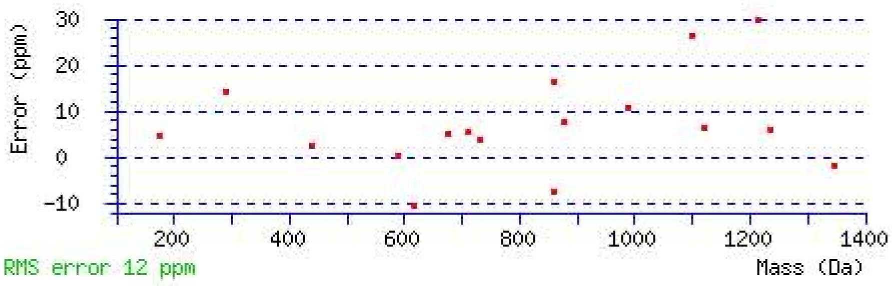


Monoisotopic mass of neutral peptide Mr(calc): 1703.855240
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 45 **Expect:** 5.7e-005
Matches : 17/110 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							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



RMS error 12 ppm



RMS error 12 ppm

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
45.5	1703.855240	0.005302	ASSIIDELFQDR
0.2	1703.859070	0.001472	RWDELETTTQAKAR

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

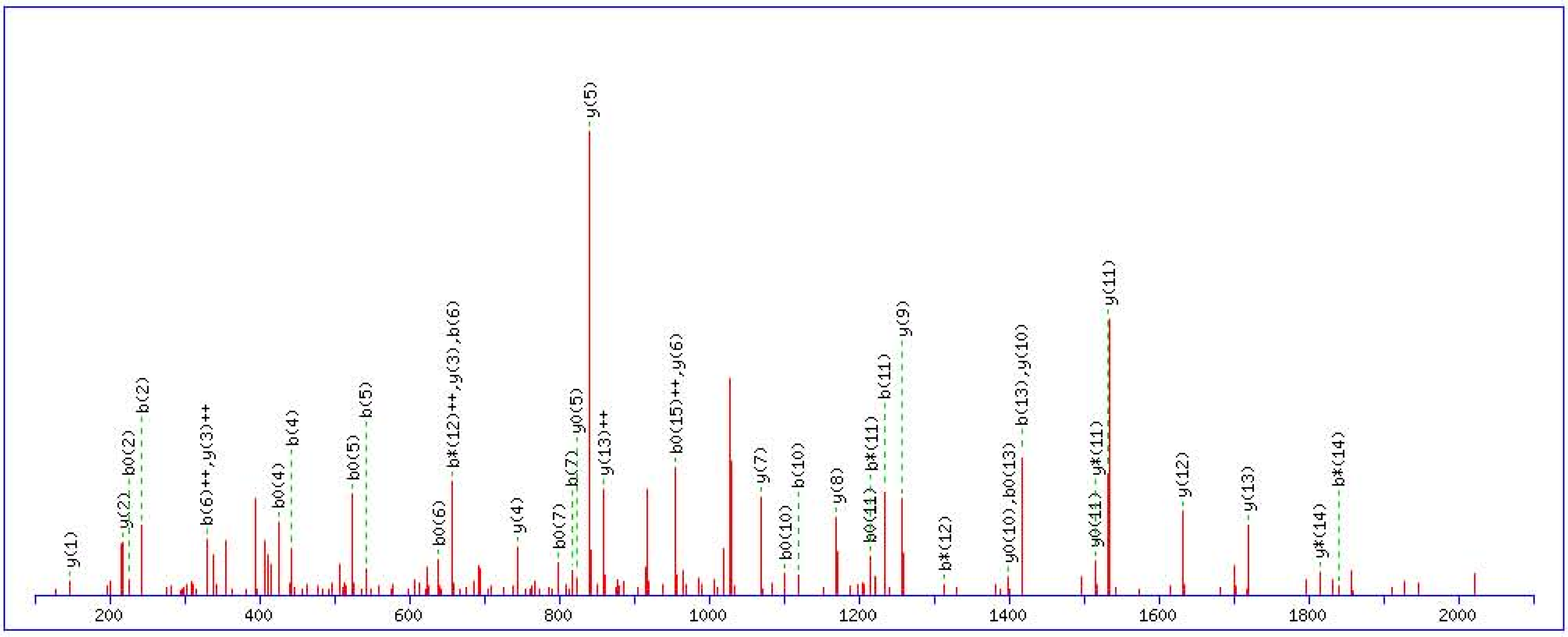
MATRIX SCIENCE Mascot Search Results

Peptide View

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

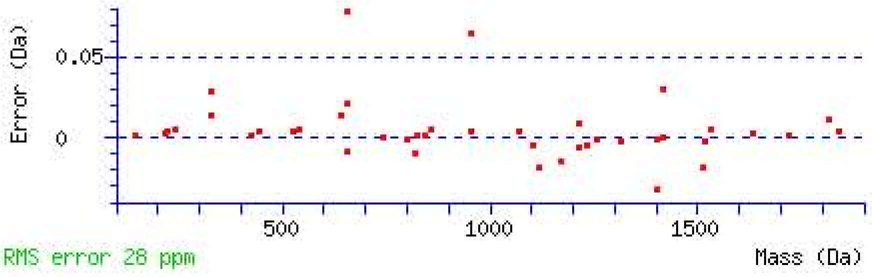
Match to Query 44082: 2072.993468 from(1037.504010,2+) rtinseconds(1813) index(31993)
Title: Locus:1.1.1.3180.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

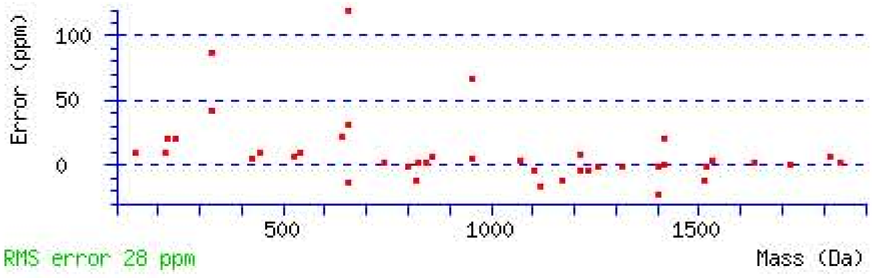
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 75 **Expect:** 1.2e-007
Matches : 42/156 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	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
75.2	2072.987061	0.006407	EILSVDCSTNNPSQAK
1.5	2072.994904	-0.001436	MQDPNADTEWNDILRKK
1.2	2072.985199	0.008269	KWVYPSEQMFWNAMLK
0.1	2073.023911	-0.030443	EAAAVFQETLRGGSQPDAAR

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

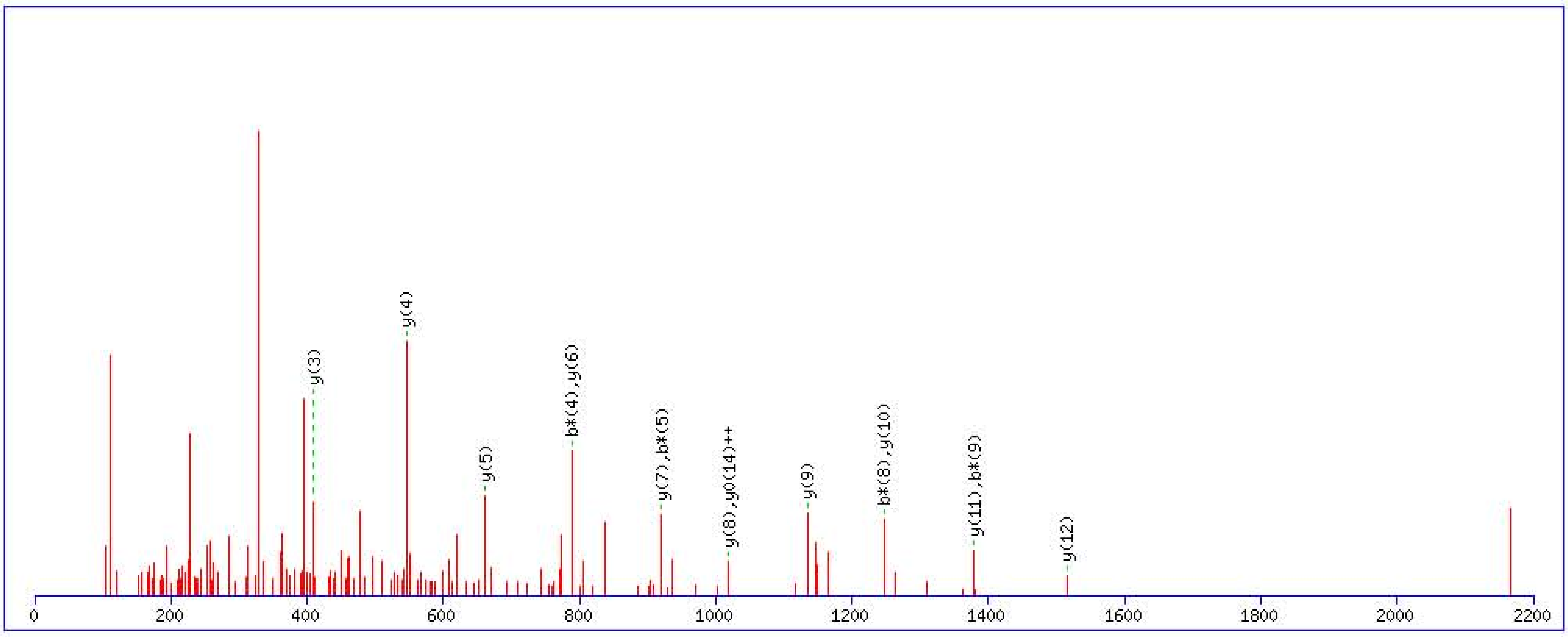
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

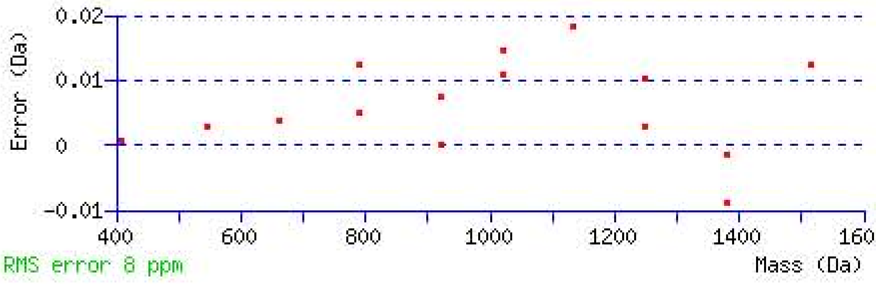
Match to Query 45730: 2183.011016 from(546.760030,4+) rtinseconds(2029) index(47598)
Title: Locus:1.1.1.2755.6 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

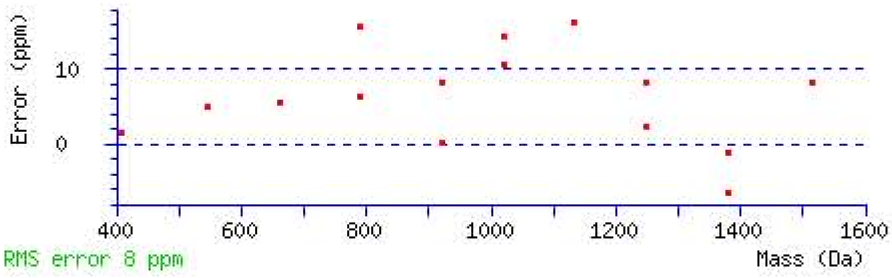
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2183.007446
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 78  Expect: 2.3e-007
Matches : 15/162 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	129.065854	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
77.6	2183.007446	0.003570	QQTHMLDVMQDHFSR
77.6	2183.007446	0.003570	QQTHMLDVMQDHFSR

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

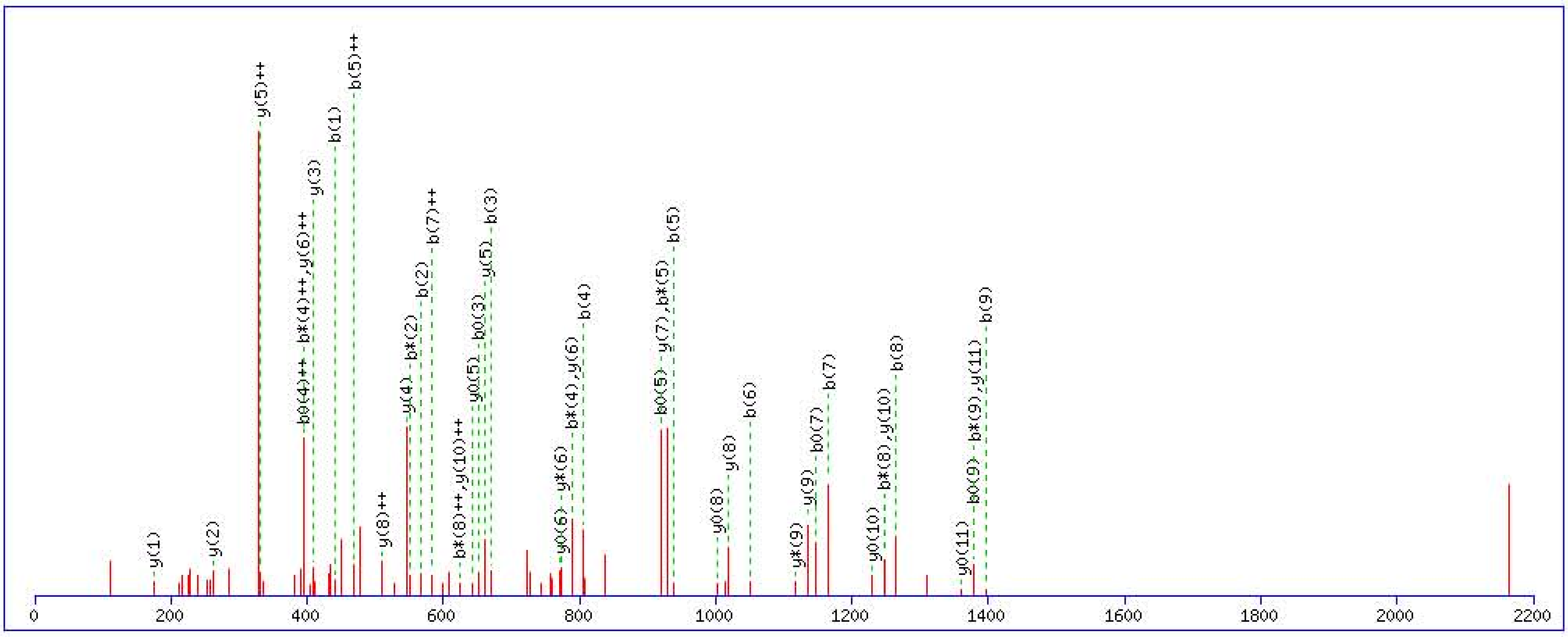
Mascot Search Results

Peptide View

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

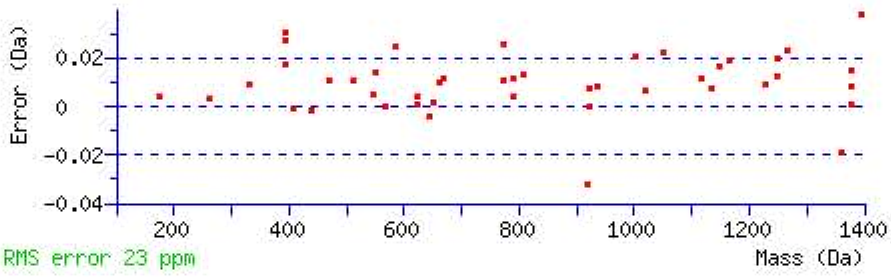
Match to Query 45735: 2183.016792 from(728.679540,3+) rtinseconds(2009) index(19131)
Title: Locus:1.1.1.3300.8 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

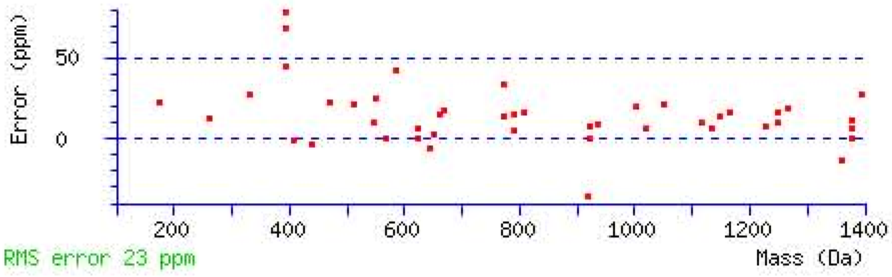


```
Monoisotopic mass of neutral peptide Mr(calc): 2183.007446
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 73  Expect: 1.7e-007
Matches : 45/162 fragment ions using 60 most intense peaks   (help)
```

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



RMS error 23 ppm



RMS error 23 ppm

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
73.3	2183.007446	0.009346	QQTHMLDVMQDHFSR
69.5	2183.007446	0.009346	QQTHMLDVMQDHFSR
1.1	2183.042465	-0.025673	EVYQKASVNMDQAMVK
0.4	2183.021149	-0.004357	GLAGEIVGEVRCHMEENQR

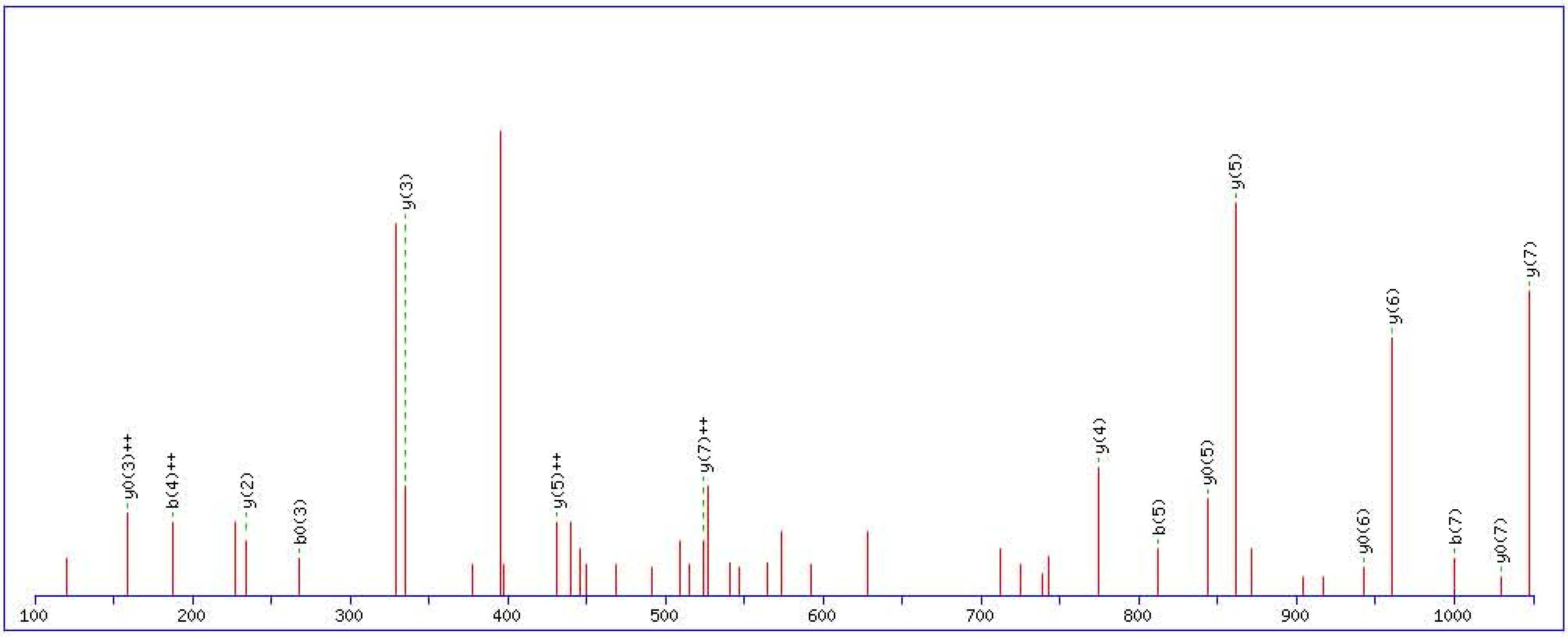
Mascot Search Results

Peptide View

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

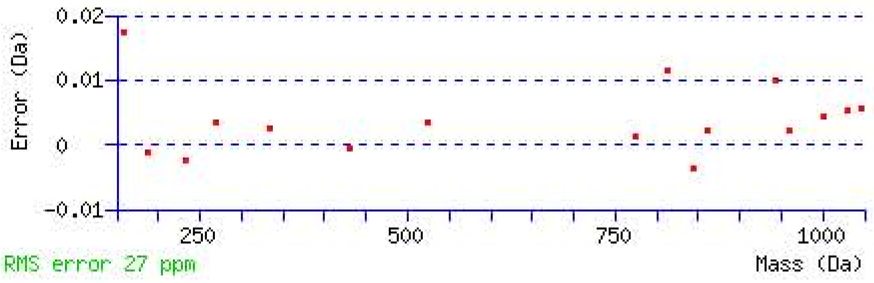
Match to Query 18684: 1145.611008 from(573.812780,2+) rtinseconds(1435) index(43767)
Title: Locus:1.1.1.2548.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

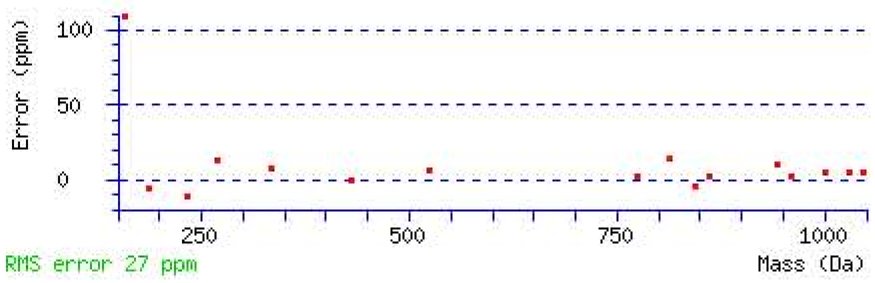
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1145.611450
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.00088
Matches : 17/72 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	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
35.3	1145.611450	-0.000442	VSVSQTSK
2.5	1145.622650	-0.011642	VKEALRDGMK
2.4	1145.623337	-0.012329	WVDGGKPLFK
1.7	1145.619278	-0.008270	WELQRSLSK
1.1	1145.622650	-0.011642	VSMDLRANLK
0.5	1145.611420	-0.000412	KSIMVQSPEK
0.2	1145.622650	-0.011642	VDNAMSRLLK

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

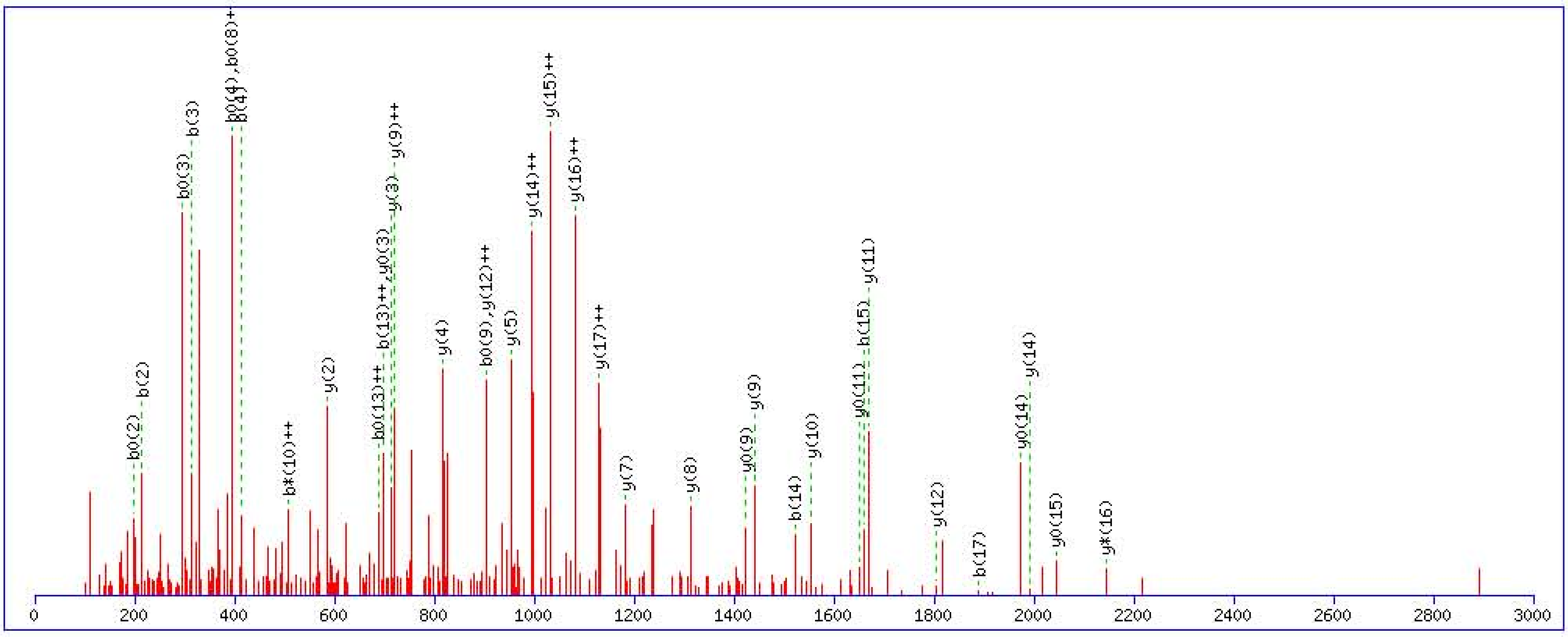
Mascot Search Results

Peptide View

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

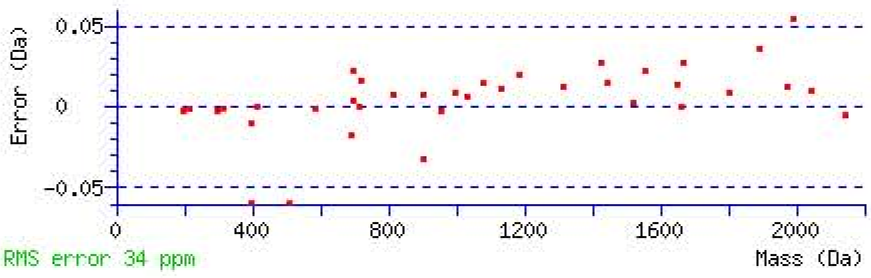
Match to Query 50435: 2474.224122 from(825.748650,3+) rtinseconds(1608) index(44915)
Title: Locus:1.1.1.2608.17 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

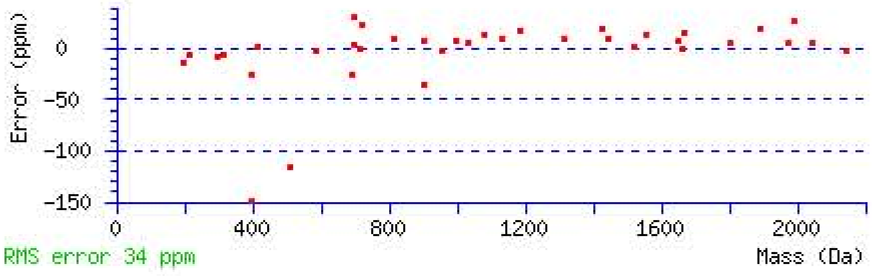
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2474.211121
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18     : Biotin:Thermo-21345 (Q)
Ions Score: 55  Expect: 8.1e-005
Matches : 37/194 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	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
55.1	2474.211121	0.013001	ITVVAGEHNIEETEHTEQK

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

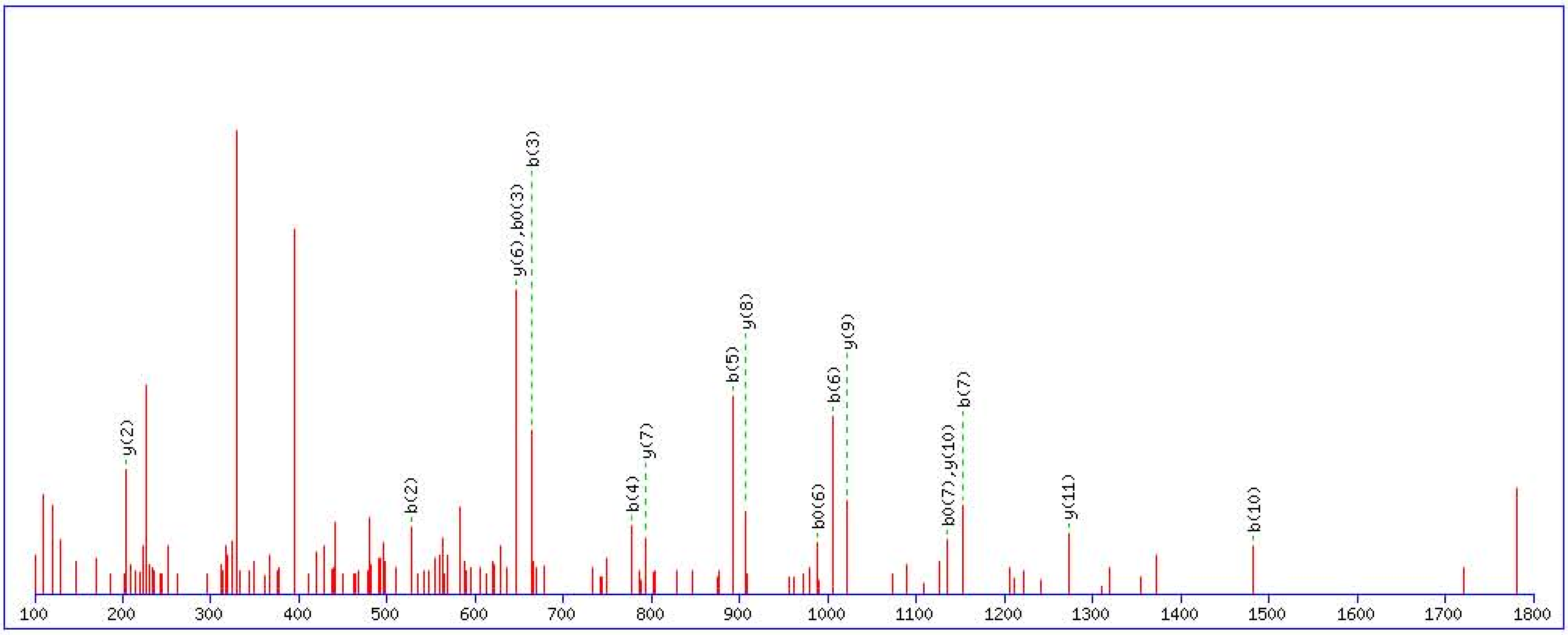
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

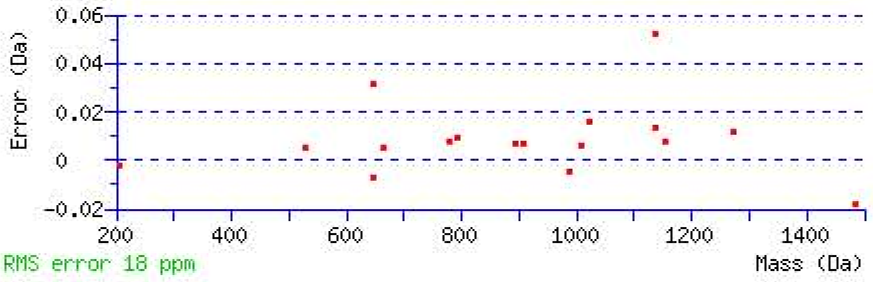
Match to Query 38451: 1797.890802 from(600.304210,3+) rtinseconds(1764) index(45869)
Title: Locus:1.1.1.2663.4 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

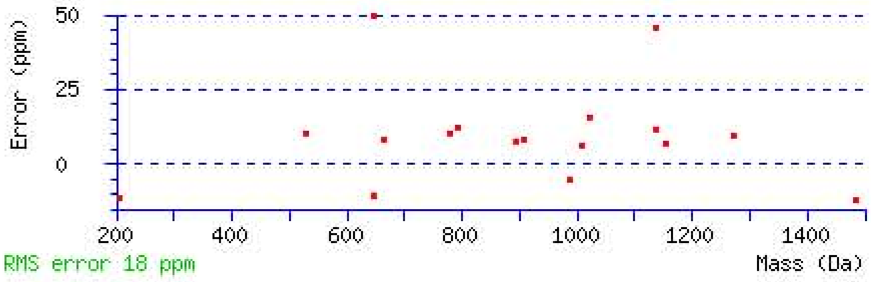
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1797.883194
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.0027
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
39.4	1797.883194	0.007608	SQHLDNFSNQIGK

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

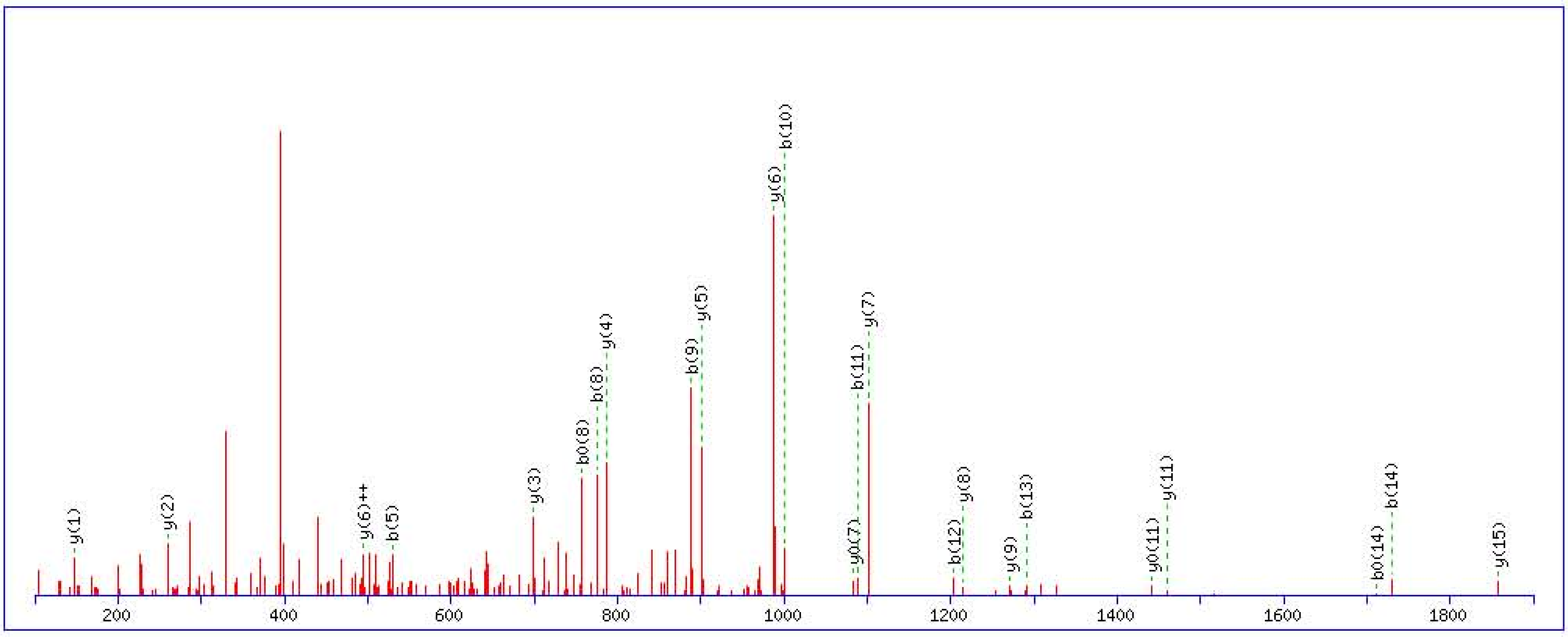
Mascot Search Results

Peptide View

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

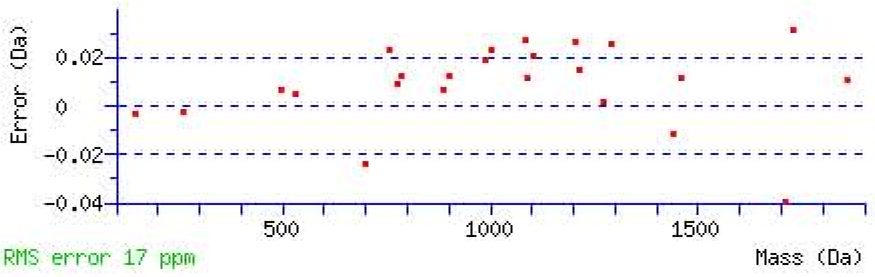
Match to Query 41786: 1988.031192 from(663.684340,3+) rtinseconds(2469) index(50083)
Title: Locus:1.1.1.2908.7 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

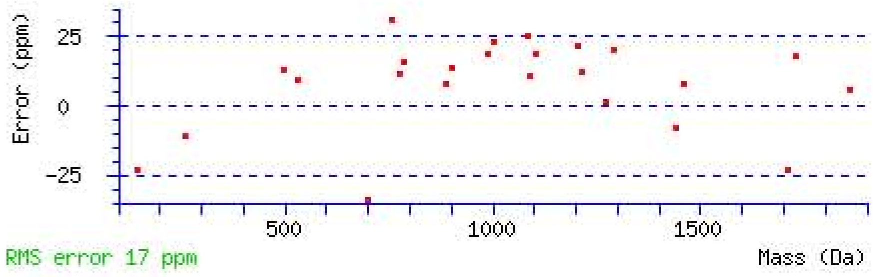
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1988.014465
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 66  Expect: 4.5e-006
Matches : 24/138 fragment ions using 43 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
65.8	1988.014465	0.016727	MPMGLSTGIISDSQIK
8.2	1988.054688	-0.023496	EVGKILCTDCATRPKLK
1.8	1988.047485	-0.016293	YDVSSQVISQLK
1.2	1988.051331	-0.020139	MTHKLVFLEDGTSQVRK
0.3	1988.055359	-0.024167	VVDYAQLVQPRFDK

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

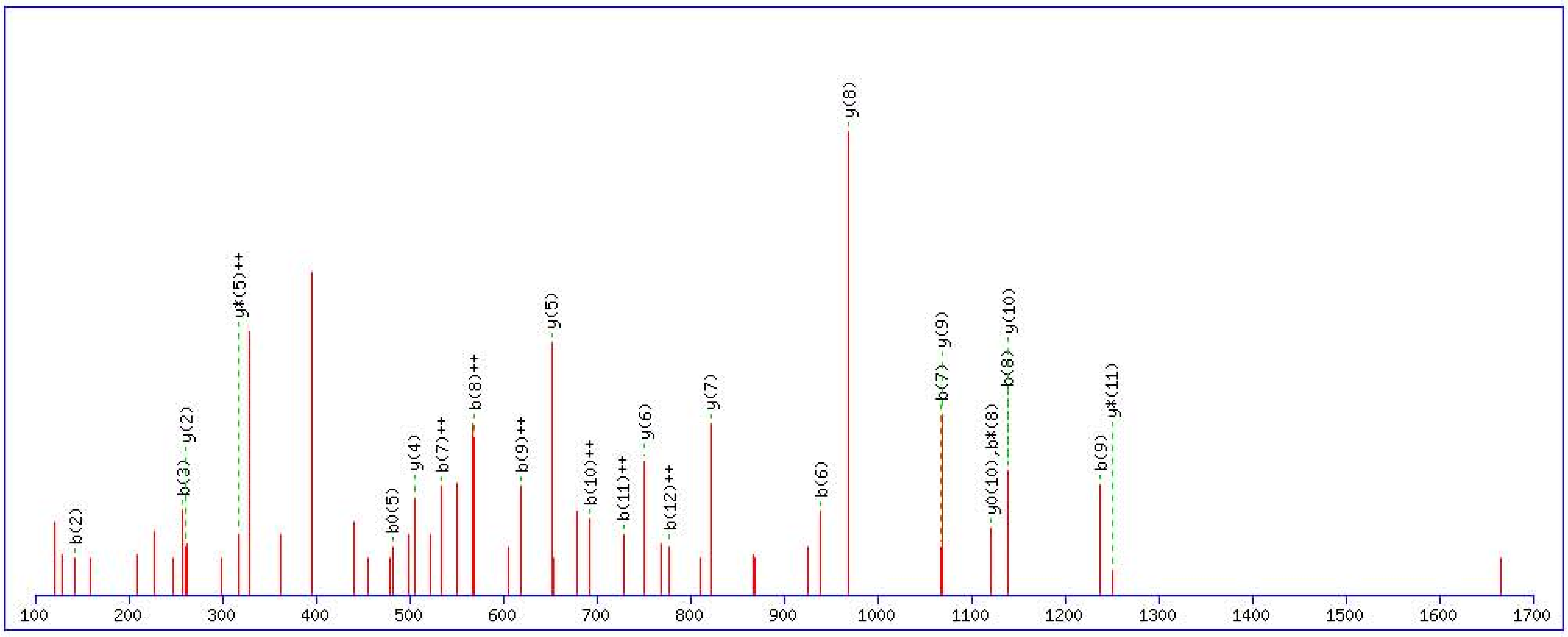
Mascot Search Results

Peptide View

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

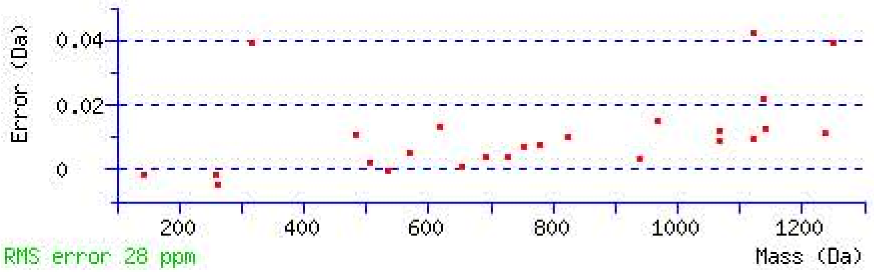
Match to Query 46071: 2205.103602 from(736.041810,3+) rtinseconds(2757) index(52064)
Title: Locus:1.1.1.3007.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

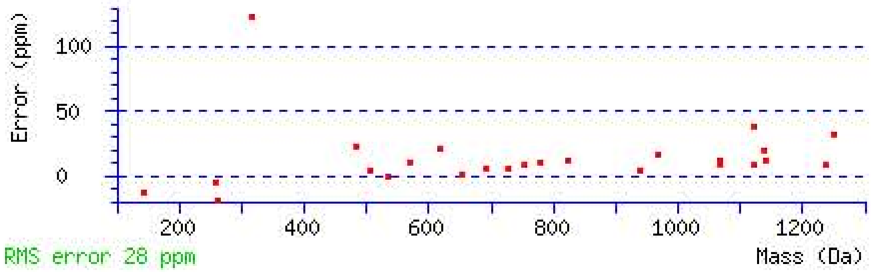
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2205.077591
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.00017
Matches : 25/174 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							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
41.6	2205.077591	0.026011	AADIEQQAVFAVFDENK
36.8	2205.077591	0.026011	AADIEQQAVFAVFDENK
1.4	2205.080063	0.023539	EKENDELDIQLKVFDENK
1.0	2205.129929	-0.026327	YPGRNGAQMMVHIVFKVAR

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

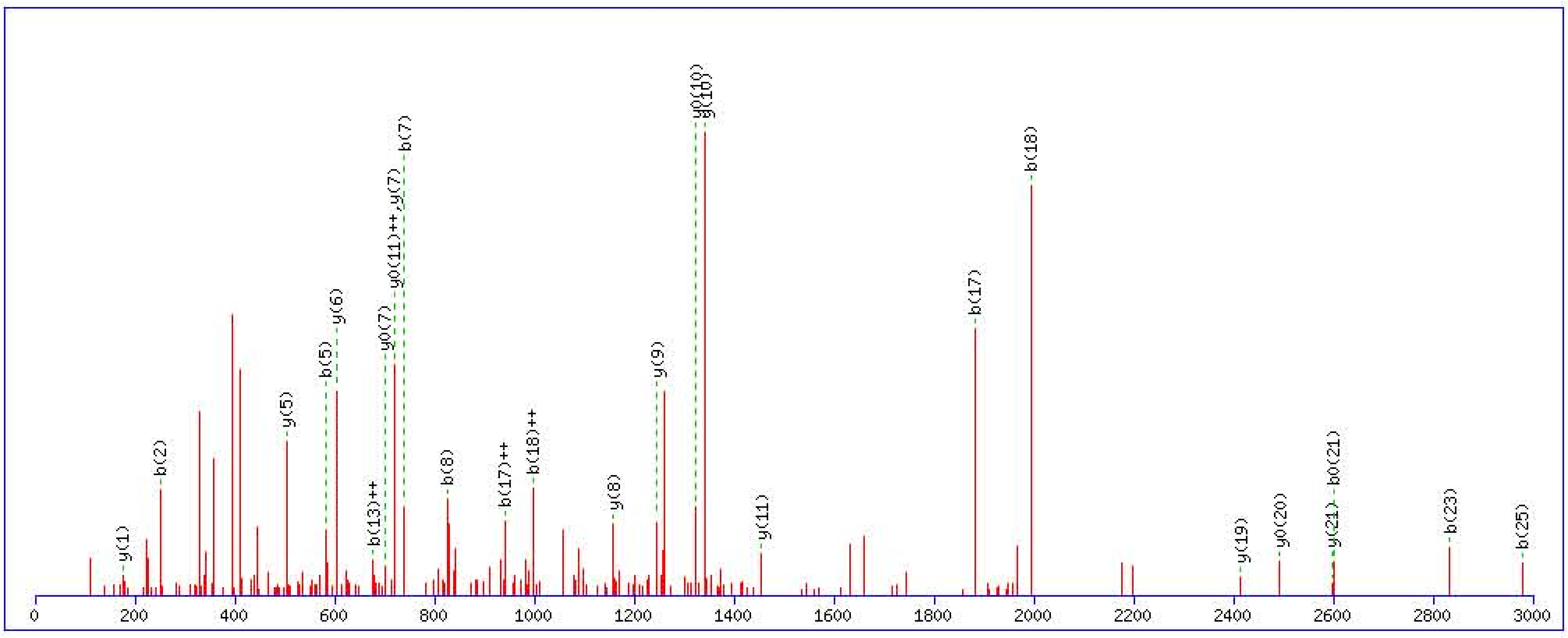
Mascot Search Results

Peptide View

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

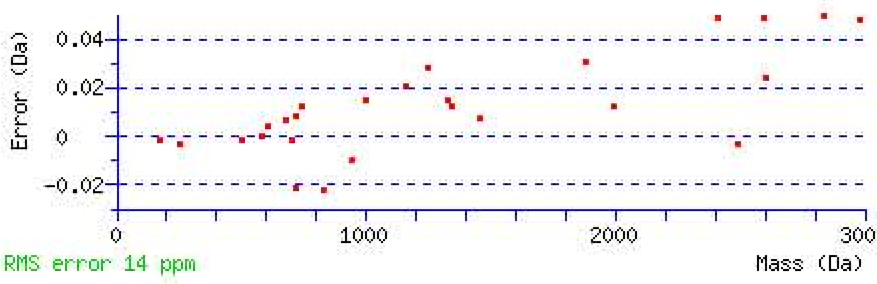
Match to Query 60331: 3335.565296 from(834.898600,4+) rtinseconds(2036) index(47636)
Title: Locus:1.1.1.2757.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

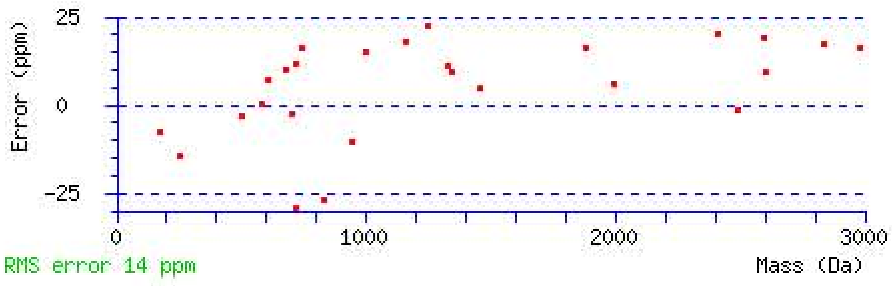
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3335.529938
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q21     : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 1e-005
Matches : 26/312 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	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	466.240858	233.624067	449.214309	225.110792	448.230293	224.618784	Q	2999.362197	1500.184736	2982.335648	1491.671462	2981.351632	1491.179454	25
5	***581.267801***	291.137539	564.241252	282.624264	563.257236	282.132256	D	2871.303619	1436.155447	2854.277070	1427.642173	2853.293054	1427.150165	24
6	682.315480	341.661378	665.288931	333.148103	664.304915	332.656095	T	2756.276676	1378.641976	2739.250127	1370.128701	2738.266111	1369.636693	23
7	***739.336944***	370.172110	722.310395	361.658836	721.326379	361.166828	G	2655.228997	1328.118136	2638.202448	1319.604862	2637.218432	1319.112854	22
8	***826.368972***	413.688124	809.342423	405.174849	808.358407	404.682841	S	***2598.207533***	1299.607404	2581.180984	1291.094130	2580.196968	1290.602122	21
9	923.421736	462.214506	906.395187	453.701232	905.411171	453.209224	P	2511.175505	1256.091390	2494.148956	1247.578116	2493.164940	1247.086108	20
10	1010.453764	505.730520	993.427215	497.217245	992.443199	496.725237	S	***2414.122741***	1207.565008	2397.096192	1199.051734	2396.112176	1198.559726	19
11	1067.475228	534.241252	1050.448679	525.727978	1049.464663	525.235970	G	2327.090713	1164.048994	2310.064164	1155.535720	2309.080148	1155.043712	18
12	1198.515713	599.761495	1181.489164	591.248220	1180.505148	590.756212	M	2270.069249	1135.538262	2253.042700	1127.024988	2252.058684	1126.532980	17
13	1354.616824	**677.812050**	1337.590275	669.298776	1336.606259	668.806767	R	2139.028764	1070.018020	2122.002215	1061.504745	2121.018199	1061.012737	16
14	1451.669588	726.338432	1434.643039	717.825158	1433.659023	717.333149	P	1982.927653	991.967465	1965.901104	983.454190	1964.917088	982.962182	15
15	1637.748901	819.378088	1620.722352	810.864814	1619.738336	810.372806	W	1885.874889	943.441082	1868.848340	934.927808	1867.864324	934.435800	14
16	1766.791494	883.899385	1749.764945	875.386110	1748.780929	874.894102	E	1699.795576	850.401426	1682.769027	841.888152	1681.785011	841.396143	13
17	***1881.818437***	**941.412856**	1864.791888	932.899582	1863.807872	932.407574	D	1570.752983	785.880130	1553.726434	777.366855	1552.742418	776.874847	12
18	***1994.902501***	**997.954888**	1977.875952	989.441614	1976.891936	988.949606	L	***1455.726040***	728.366658	1438.699491	719.853384	1437.715475	719.361376	11
19	2091.955265	1046.481270	2074.928716	1037.967996	2073.944700	1037.475988	P	***1342.641976***	671.824626	1325.615427	663.311352	1324.631411	662.819344	10
20	2178.987293	1089.997284	2161.960744	1081.484010	2160.976728	1080.992002	S	***1245.589212***	623.298244	1228.562663	614.784970	1227.578647	614.292962	9
21	2618.212619	1309.609947	2601.186070	1301.096673	2600.202054	1300.604665	Q	***1158.557184***	579.782230	1141.530635	571.268956	1140.546619	570.776948	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
54.2	3335.529938	0.035358	HLSQDTGSPSGMRPWEDLPSQDTGSPSR
7.2	3335.529938	0.035358	HLSQDTGSPSGMRPWEDLPSQDTGSPSR
1.0	3335.523605	0.041691	VQIDPYLEDSLCHICSSQPGPFFCR

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

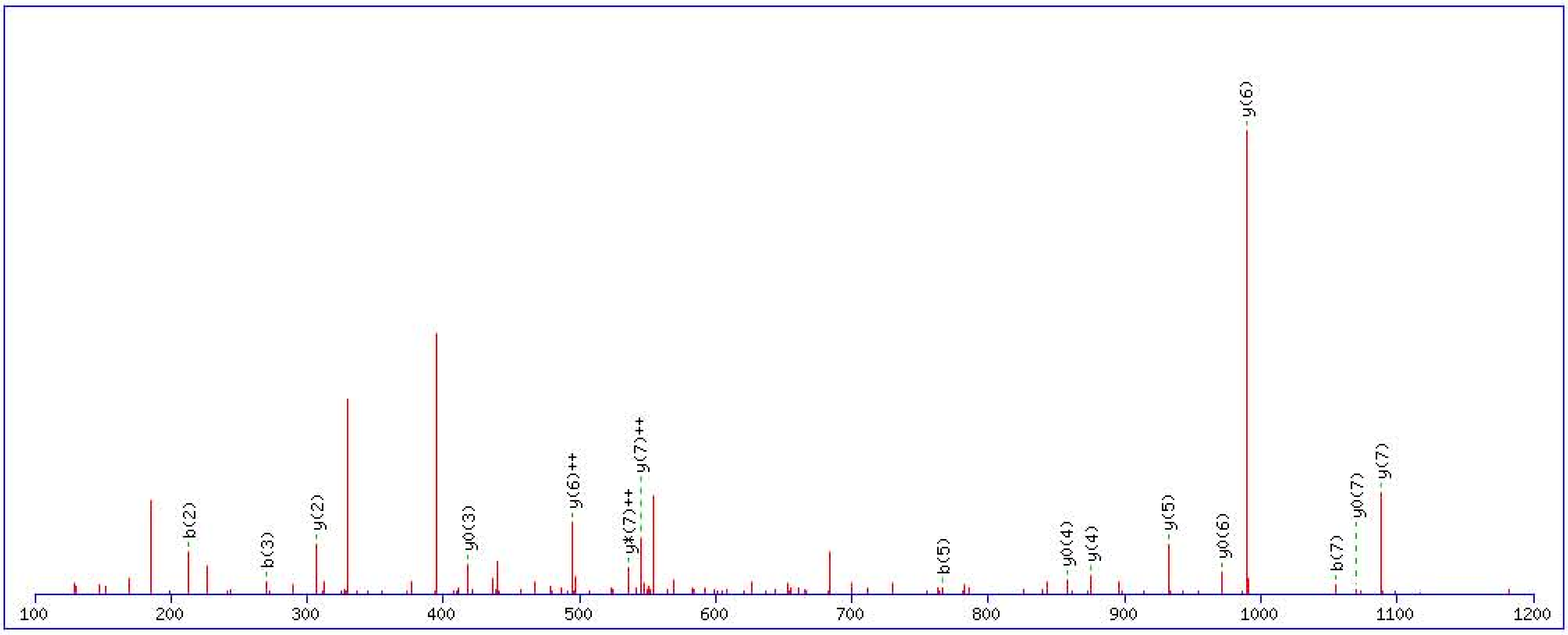
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

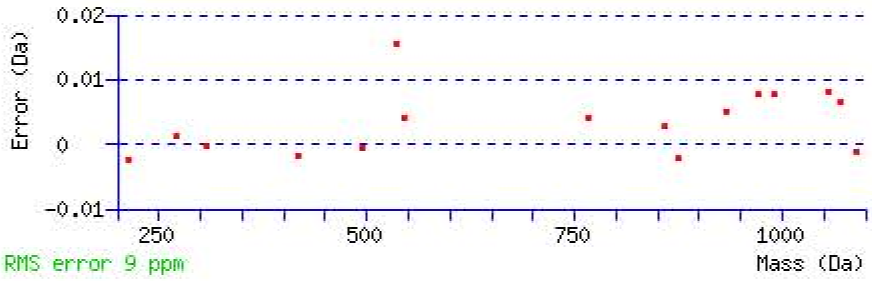
Match to Query 20349: 1200.599808 from(601.307180,2+) rtinseconds(1430) index(43745)
Title: Locus:1.1.1.2546.18 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

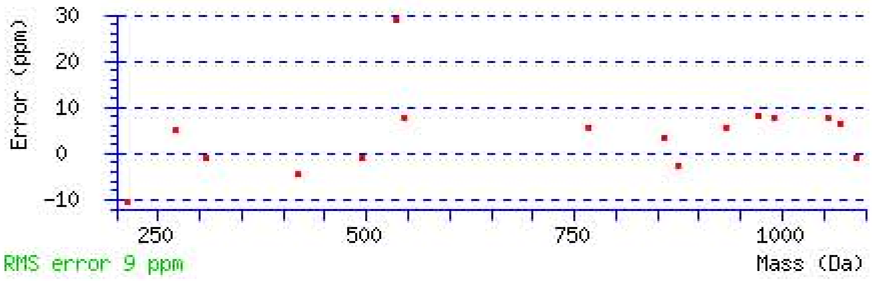
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1200.599503
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.0047
Matches : 16/62 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					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
27.7	1200.599503	0.000305	IVGGQECK
2.7	1200.598587	0.001221	ILADLEEENR
0.4	1200.596100	0.003708	LVKYMYDNR
0.3	1200.599503	0.000305	LIQGDGCK

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

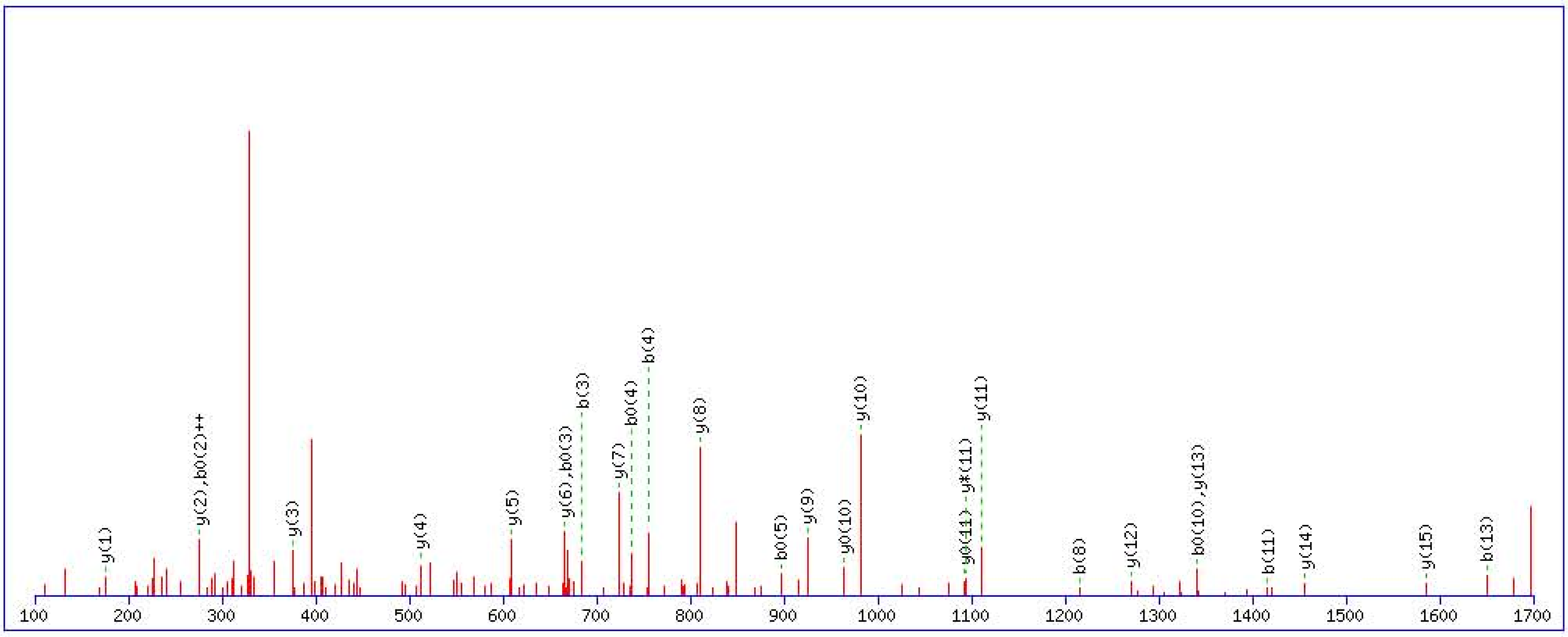
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

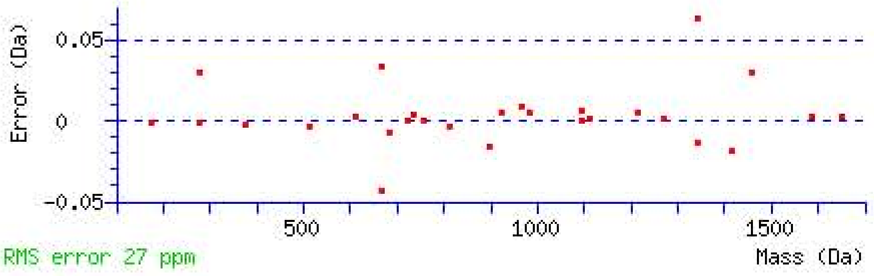
Match to Query 43078: 2023.886742 from(675.636190,3+) rtinseconds(1310) index(43089)
Title: Locus:1.1.1.2504.22 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

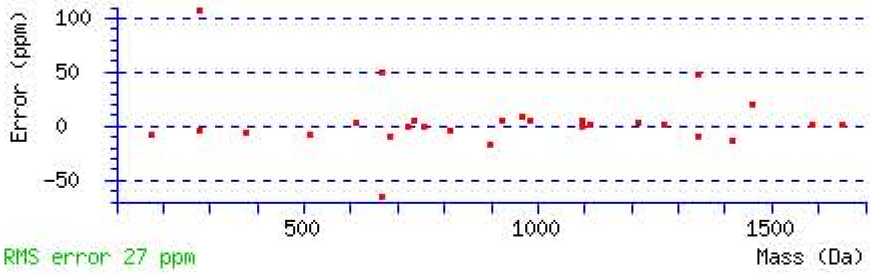
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2023.884033
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 111 **Expect:** 4.4e-011
Matches : 28/176 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							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
110.9	2023.884033	0.002709	QEDACQGDSGGPHVTR
54.5	2023.884033	0.002709	QEDACQGDSGGPHVTR
2.1	2023.864899	0.021843	QEGETAICSEMTADR

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

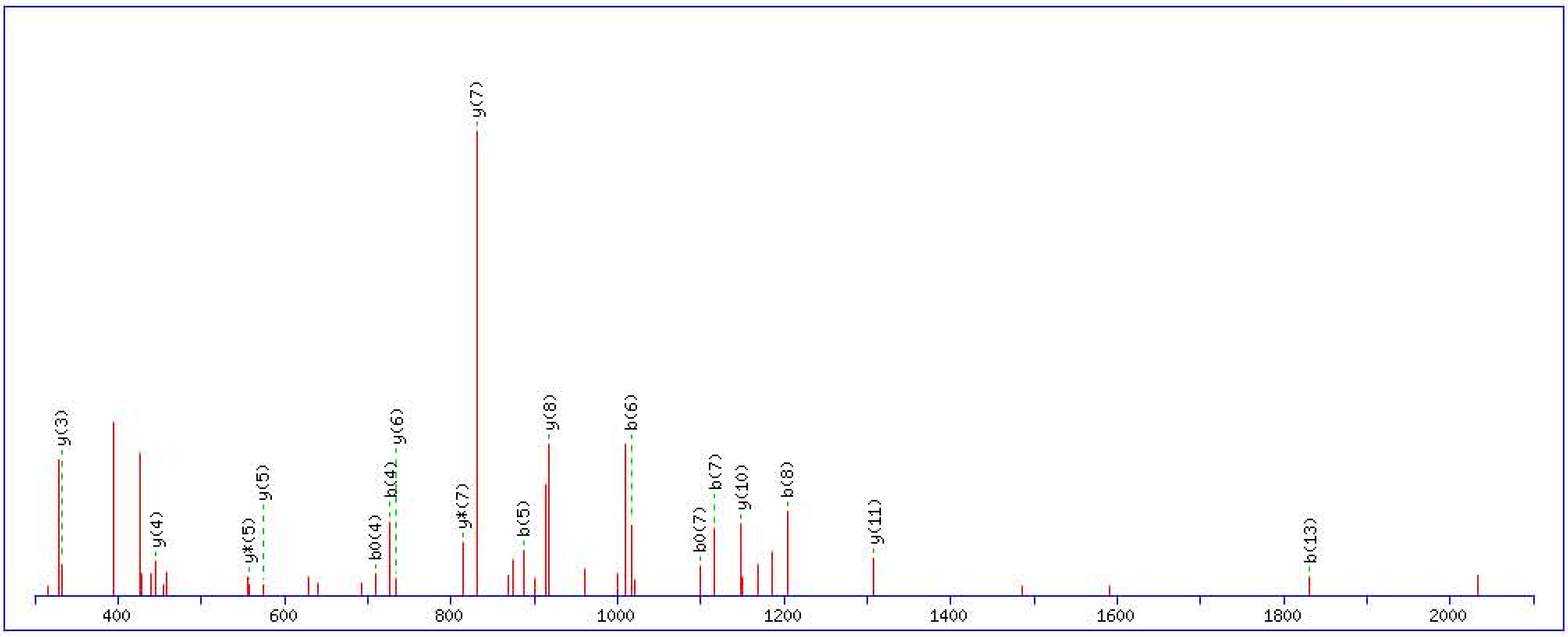
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

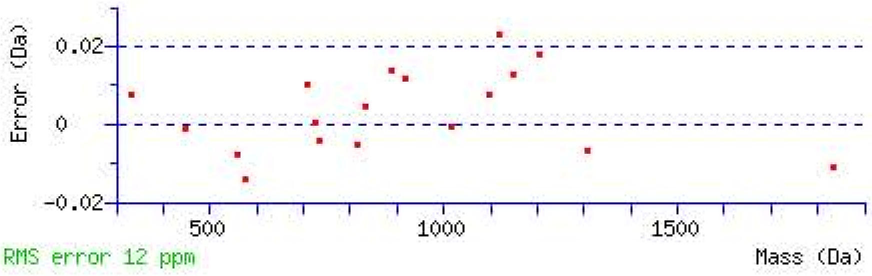
Match to Query 43279: 2033.831288 from(1017.922920,2+) rtinseconds(1341) index(43215)
Title: Locus:1.1.1.2515.13 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

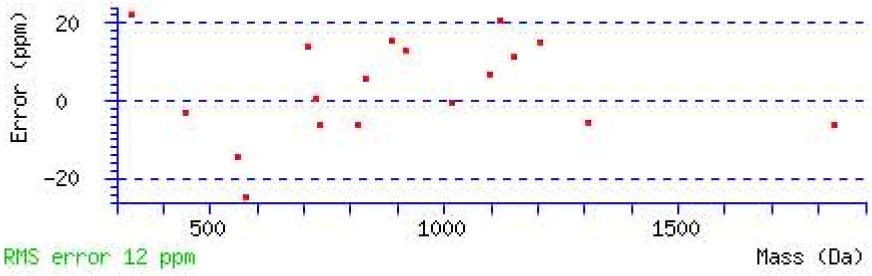
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2033.824127
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 50  Expect: 1.5e-005
Matches : 18/148 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	116.034219	58.520748			98.023654	49.515465	D							15
2	173.055683	87.031479			155.045118	78.026197	G	1919.804446	960.405861	1902.777897	951.892587	1901.793881	951.400579	14
3	288.082626	144.544951			270.072061	135.539669	D	1862.782982	931.895129	1845.756433	923.381855	1844.772417	922.889847	13
4	***727.307952***	364.157614	710.281403	355.644340	709.297387	355.152332	Q	1747.756039	874.381658	1730.729490	865.868383	1729.745474	865.376375	12
5	***887.338601***	444.172939	870.312052	435.659664	869.328036	435.167656	C	***1308.530713***	654.768995	1291.504164	646.255720	1290.520148	645.763712	11
6	***1016.381194***	508.694235	999.354645	500.180961	998.370629	499.688953	E	***1148.500064***	574.753670	1131.473515	566.240396	1130.489499	565.748388	10
7	***1117.428873***	559.218075	1100.402324	550.704800	1099.418308	550.212792	T	1019.457471	510.232374	1002.430922	501.719099	1001.446906	501.227091	9
8	***1204.460901***	602.734089	1187.434352	594.220814	1186.450336	593.728806	S	***918.409792***	459.708534	901.383243	451.195260	900.399227	450.703252	8
9	1301.513665	651.260471	1284.487116	642.747196	1283.503100	642.255188	P	***831.377764***	416.192520	814.351215	407.679246			7
10	1461.544314	731.275795	1444.517765	722.762521	1443.533749	722.270513	C	***734.325000***	367.666138	717.298451	359.152864			6
11	1589.602892	795.305084	1572.576343	786.791810	1571.592327	786.299802	Q	***574.294351***	287.650814	557.267802	279.137539			5
12	1703.645819	852.326548	1686.619270	843.813273	1685.635254	843.321265	N	***446.235773***	223.621524	429.209224	215.108250			4
13	***1831.704397***	916.355837	1814.677848	907.842562	1813.693832	907.350554	Q	***332.192846***	166.600061	315.166297	158.086787			3
14	1888.725861	944.866569	1871.699312	936.353294	1870.715296	935.861286	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 DGDQCETSPCQNQGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.1	2033.824127	0.007161	DGDQCETSPCQNQGK

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

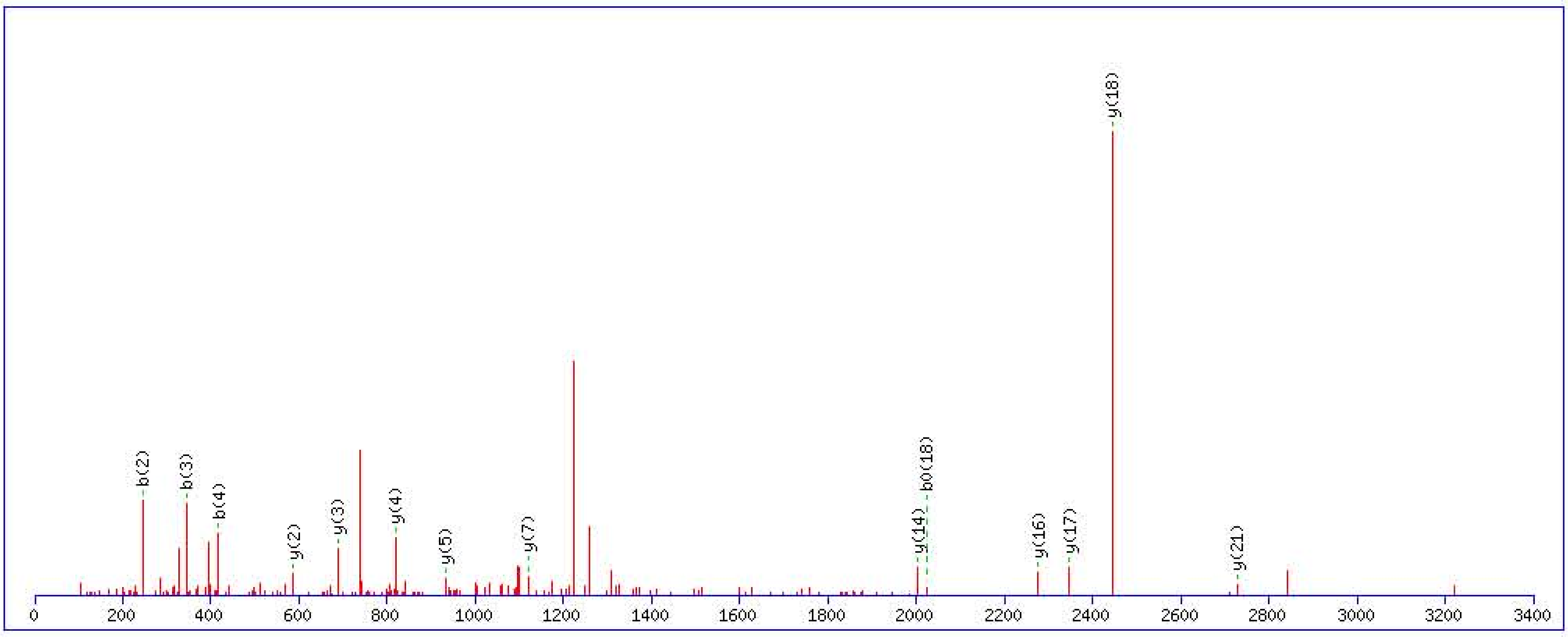
Mascot Search Results

Peptide View

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

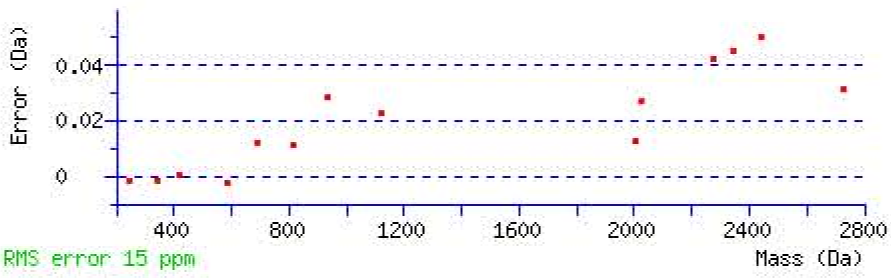
Match to Query 54748: 2858.399502 from(953.807110,3+) rtinseconds(2390) index(49728)
Title: Locus:1.1.1.2880.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

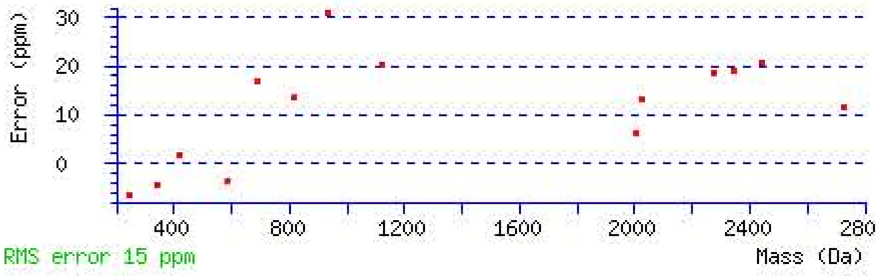
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [3400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2858.358719
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q21    : Biotin:Thermo-21345 (Q)
Ions Score: 59  Expect: 3.5e-005
Matches : 14/228 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							22
2	**246.090688**	123.548982	229.064139	115.035708			N	***2728.325542***	1364.666409	2711.298993	1356.153134	2710.314977	1355.661126	21
3	**345.159102**	173.083189	328.132553	164.569915			V	2614.282615	1307.644945	2597.256066	1299.131671	2596.272050	1298.639663	20
4	**416.196216**	208.601746	399.169667	200.088472			A	2515.214201	1258.110738	2498.187652	1249.597464	2497.203636	1249.105456	19
5	513.248980	257.128128	496.222431	248.614854			P	***2444.177087***	1222.592181	2427.150538	1214.078907	2426.166522	1213.586899	18
6	584.286094	292.646685	567.259545	284.133411			A	***2347.124323***	1174.065799	2330.097774	1165.552525	2329.113758	1165.060517	17
7	744.316743	372.662010	727.290194	364.148735			C	***2276.087209***	1138.547242	2259.060660	1130.033968	2258.076644	1129.541960	16
8	857.400807	429.204042	840.374258	420.690767			L	2116.056560	1058.531918	2099.030011	1050.018643	2098.045995	1049.526635	15
9	954.453571	477.730424	937.427022	469.217149			P	***2002.972496***	1001.989886	1985.945947	993.476612	1984.961931	992.984604	14
10	1083.496164	542.251720	1066.469615	533.738446	1065.485599	533.246438	E	1905.919732	953.463504	1888.893183	944.950230	1887.909167	944.458222	13
11	1239.597275	620.302276	1222.570726	611.789001	1221.586710	611.296993	R	1776.877139	888.942208	1759.850590	880.428933	1758.866574	879.936925	12
12	1354.624218	677.815747	1337.597669	669.302473	1336.613653	668.810465	D	1620.776028	810.891652	1603.749479	802.378378	1602.765463	801.886370	11
13	1540.703531	770.855404	1523.676982	762.342129	1522.692966	761.850121	W	1505.749085	753.378181	1488.722536	744.864906	1487.738520	744.372898	10
14	1611.740645	806.373961	1594.714096	797.860686	1593.730080	797.368678	A	1319.669772	660.338524	1302.643223	651.825250	1301.659207	651.333242	9
15	1740.783238	870.895257	1723.756689	862.381983	1722.772673	861.889975	E	1248.632658	624.819967	1231.606109	616.306693	1230.622093	615.814685	8
16	1827.815266	914.411271	1810.788717	905.897997	1809.804701	905.405989	S	***1119.590065***	560.298671	1102.563516	551.785396	1101.579500	551.293388	7
17	1928.862945	964.935111	1911.836396	956.421836	1910.852380	955.929828	T	1032.558037	516.782657	1015.531488	508.269382	1014.547472	507.777374	6
18	2041.947009	1021.477143	2024.920460	1012.963868	2023.936444	1012.471860	L	***931.510358***	466.258817	914.483809	457.745543	913.499793	457.253535	5
19	2172.987494	1086.997385	2155.960945	1078.484110	2154.976929	1077.992102	M	***818.426294***	409.716785	801.399745	401.203511	800.415729	400.711503	4
20	2274.035173	1137.521224	2257.008624	1129.007950	2256.024608	1128.515942	T	***687.385809***	344.196543	670.359260	335.683268	669.375244	335.191260	3
21	2713.260499	1357.133887	2696.233950	1348.620613	2695.249934	1348.128605	Q	***586.338130***	293.672703	569.311581	285.159429			2
22							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of MNVAPACLPERDWAESTLMTQK
(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	2858.358719	0.040783	MNVAPACLPERDWAESTLMTQK

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

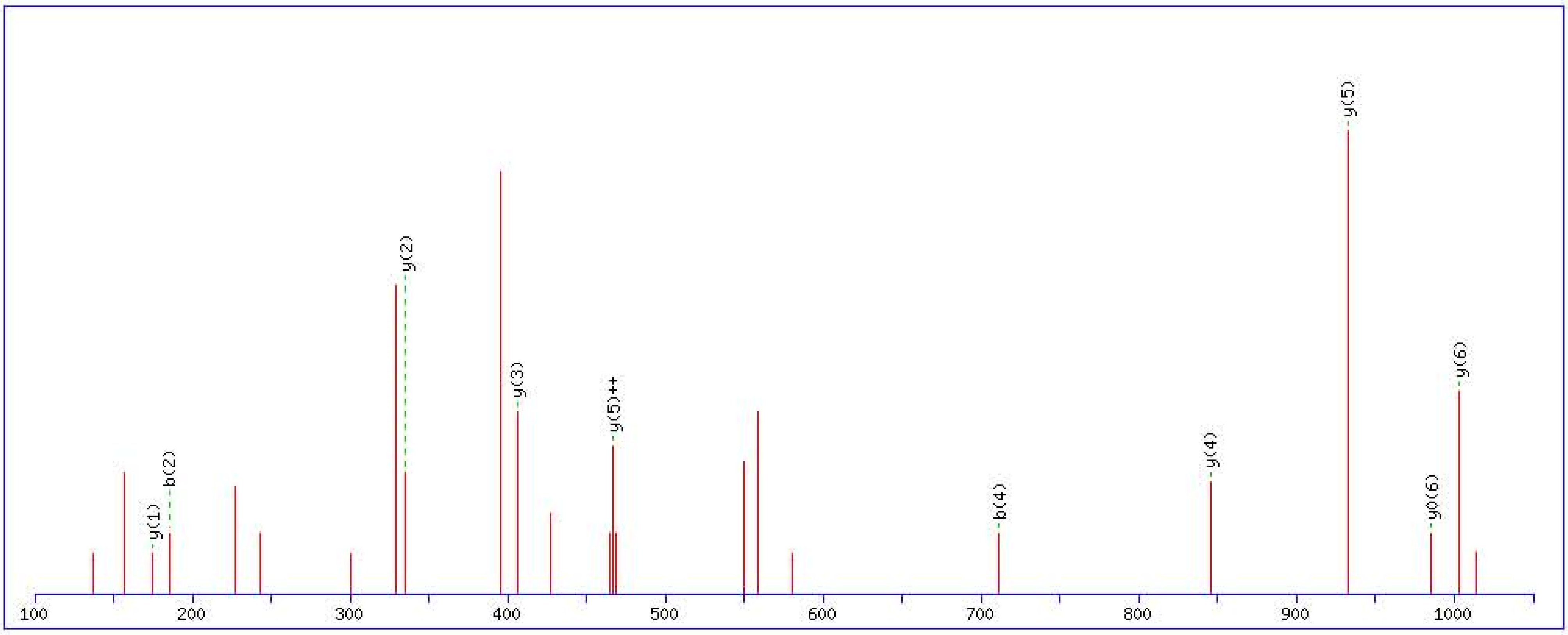
Mascot Search Results

Peptide View

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

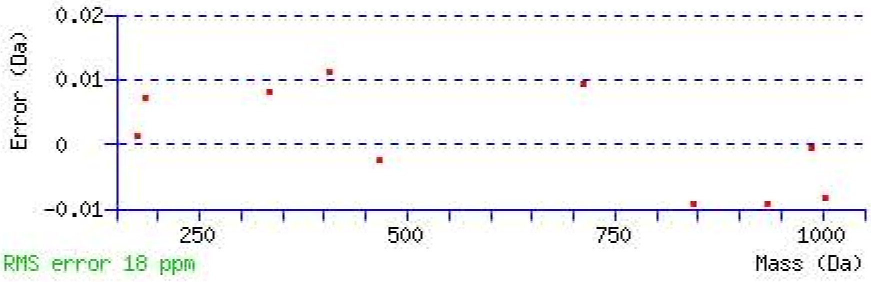
Match to Query 17079: 1115.554708 from(558.784630,2+) rtinseconds(1363) index(29411)
Title: Locus:1.1.1.3023.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

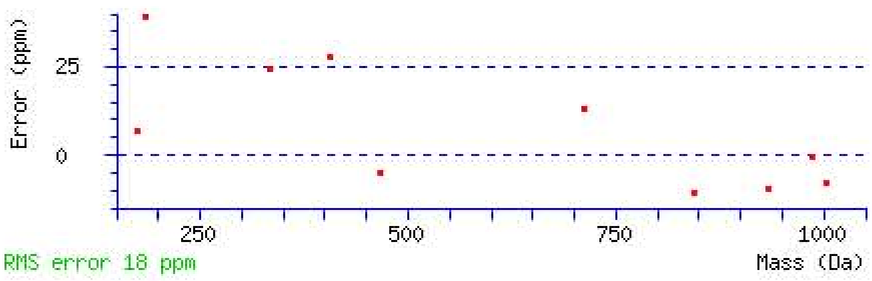
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1115.557953
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 30 **Expect:** 0.0035
Matches : 10/54 fragment ions using 24 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
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
30.3	1115.557953	-0.003245	LASQACR
4.0	1115.543350	0.011358	LEYKFCTR
2.3	1115.550552	0.004156	LAAGSRCPER
1.1	1115.546722	0.007986	LAQDACK

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

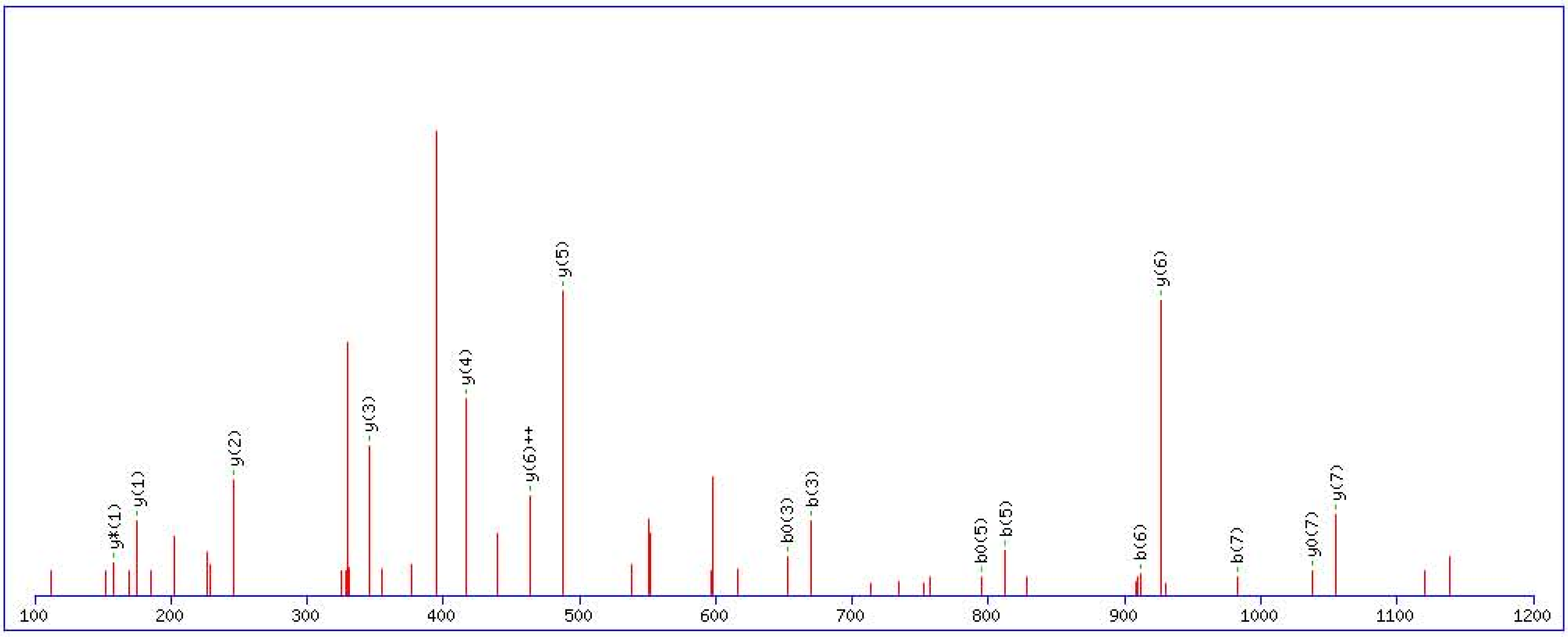
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

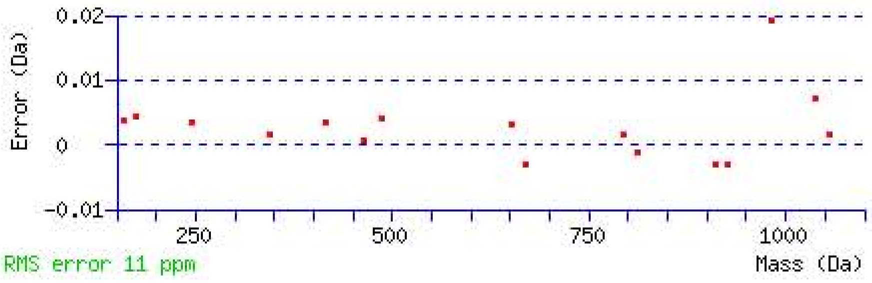
Match to Query 18975: 1155.606988 from(578.810770,2+) rtinseconds(1409) index(59236)
Title: Locus:1.1.1.3116.14 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

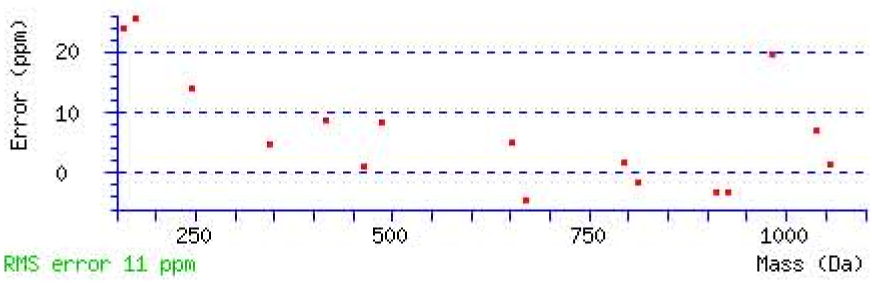
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1155.607010
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.001
Matches : 16/68 fragment ions using 31 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							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
43.4	1155.607010	-0.000022	TEQAAVAR
10.8	1155.589706	0.017282	EQWPERRR
8.3	1155.607025	-0.000037	VQDSAVAR
7.8	1155.610855	-0.003867	GAGAGLSRPGSAR
7.2	1155.607025	-0.000037	AMAAVPQDVVR
4.0	1155.599594	0.007394	TKESKHEAAR
2.8	1155.614883	-0.007895	RSGDWLLPGR
1.7	1155.607010	-0.000022	QQLETAR
1.5	1155.592422	0.014566	YTEFLTGLGR
1.2	1155.607040	-0.000052	TPACVPVSIGR

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

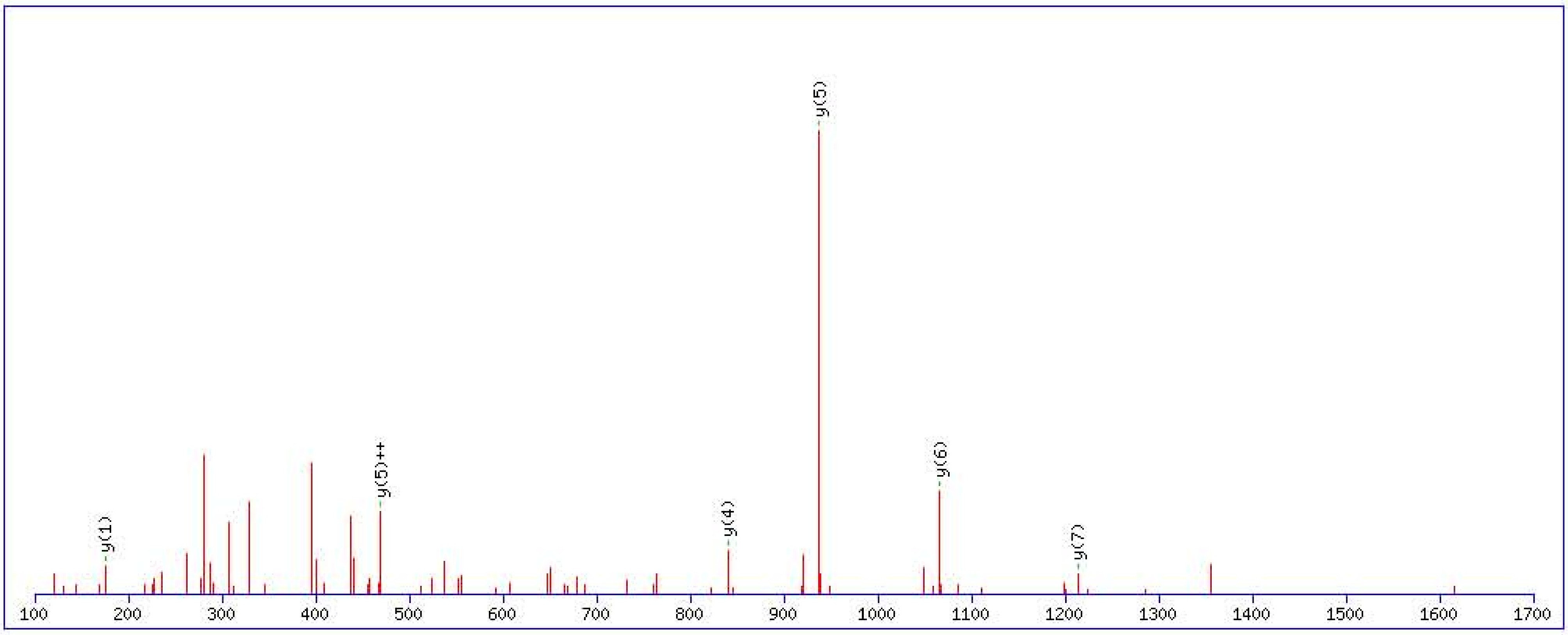
Mascot Search Results

Peptide View

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

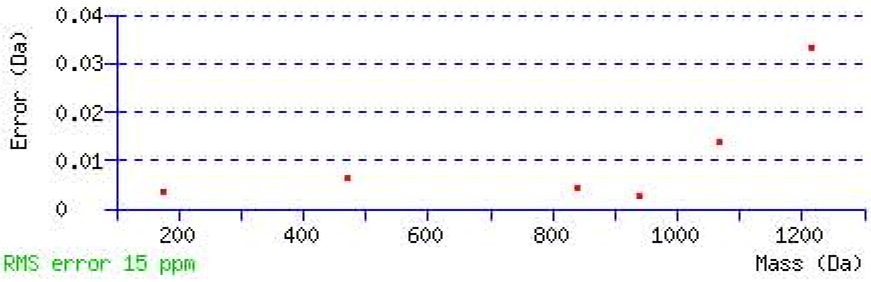
Match to Query 25472: 1372.701348 from(687.357950,2+) rtinseconds(2217) index(63769)
Title: Locus:1.1.1.3398.19 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

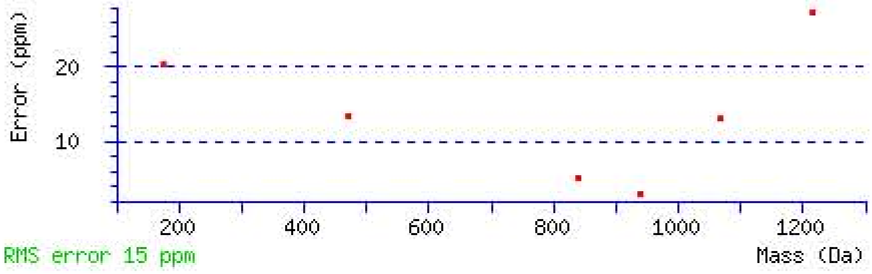
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1372.699539
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.012
Matches : 6/62 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	161.037925	81.022600					C							8
2	308.106339	154.556807					F	***1213.676177***	607.341726	1196.649628	598.828452	1195.665612	598.336444	7
3	437.148932	219.078104			419.138367	210.072822	E	***1066.607763***	533.807519	1049.581214	525.294245	1048.597198	524.802237	6
4	534.201696	267.604486			516.191131	258.599204	P	***937.565170***	469.286223	920.538621	460.772948			5
5	973.427022	487.217149	956.400473	478.703875	955.416457	478.211867	Q	***840.512406***	420.759841	823.485857	412.246566			4
6	1086.511086	543.759181	1069.484537	535.245907	1068.500521	534.753898	L	401.287080	201.147178	384.260531	192.633903			3
7	1199.595150	600.301213	1182.568601	591.787939	1181.584585	591.295930	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 CFEPQLLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.6	1372.699539	0.001809	CFEPQLLR
6.7	1372.710770	-0.009422	QPRMLDFR
1.1	1372.717331	-0.015983	QGLPVVMPVFDR
0.8	1372.703369	-0.002021	NPPKQEGHR

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

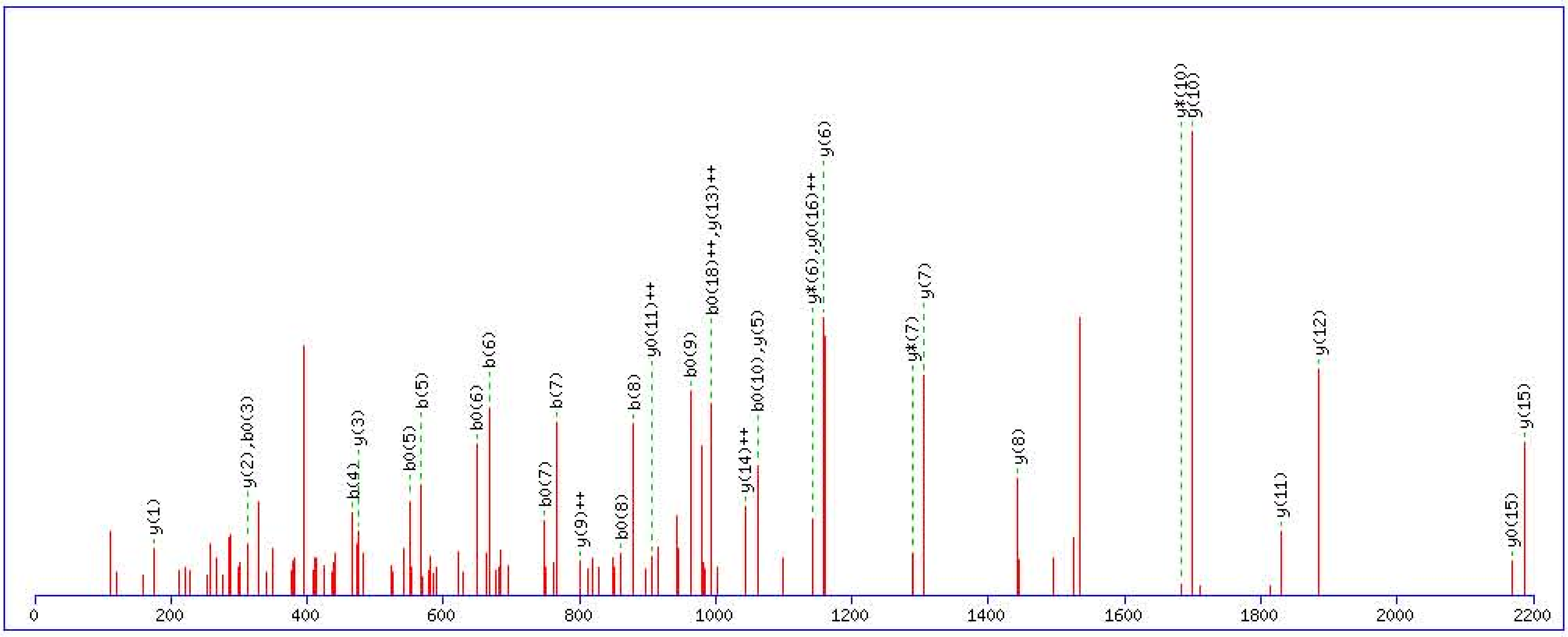
Mascot Search Results

Peptide View

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

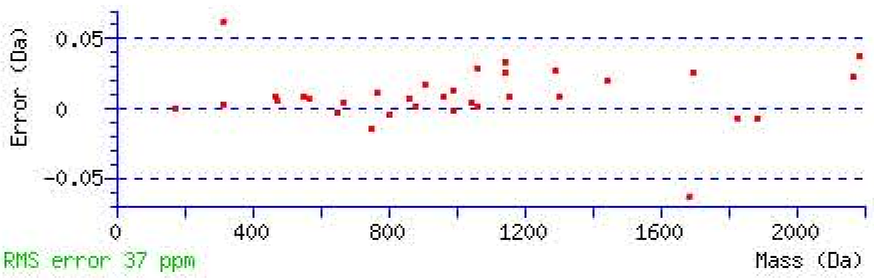
Match to Query 56487: 3064.478496 from(767.126900,4+) rtinseconds(2163) index(5852)
Title: Locus:1.1.1.3305.17 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

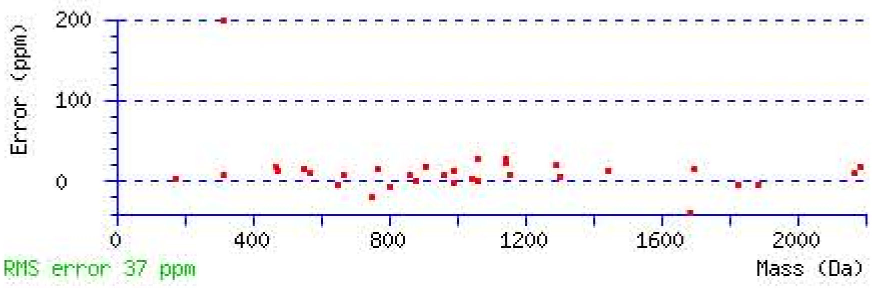
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3064.468796
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20     : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 2.1e-005
Matches : 33/204 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	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





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
60.5	3064.468796	0.009700	AEEHTVVLTVTGEPCHFPFQYHR

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

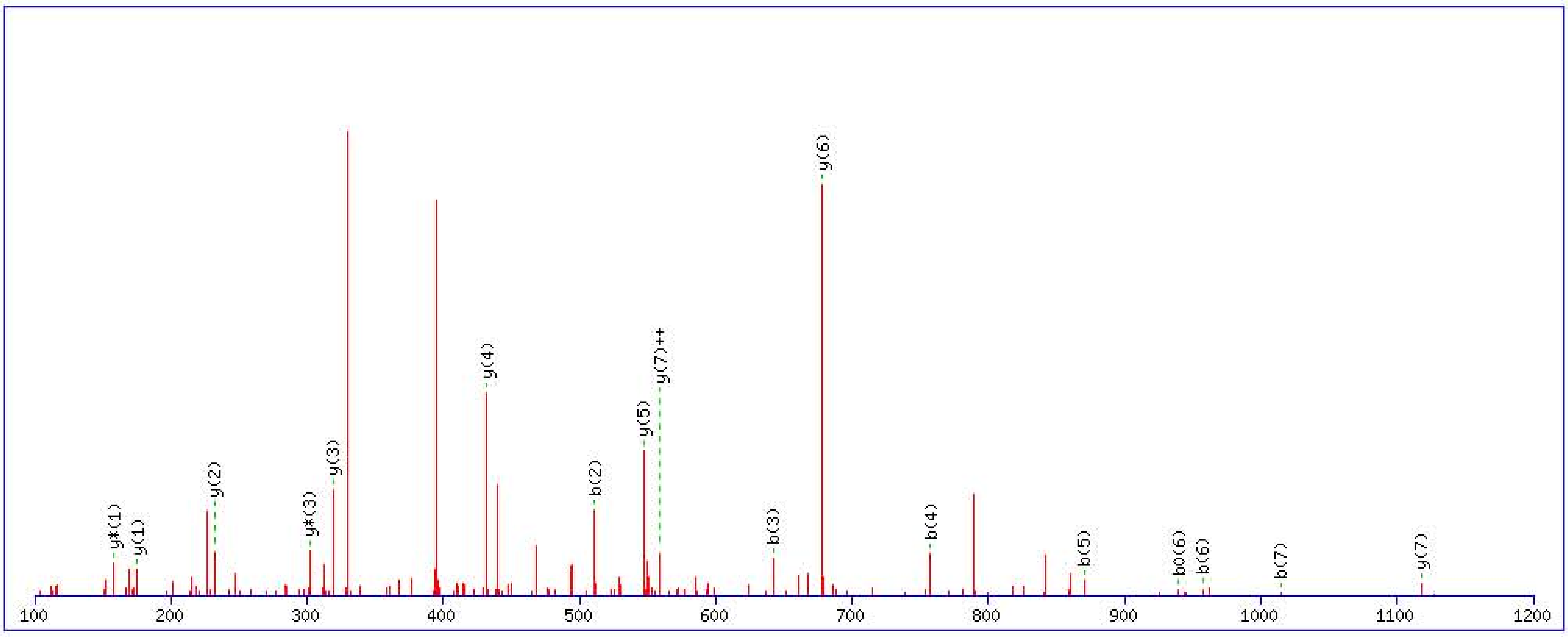
{MATRIX SCIENCE} Mascot Search Results

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

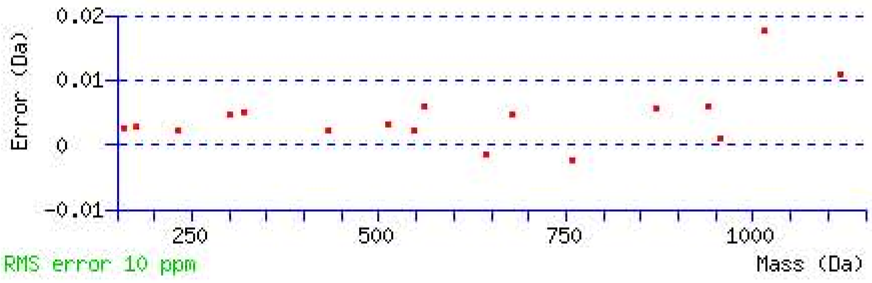
Match to Query 20057: 1187.578728 from(594.796640,2+) rtinseconds(1749) index(3533)
Title: Locus:1.1.1.3161.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

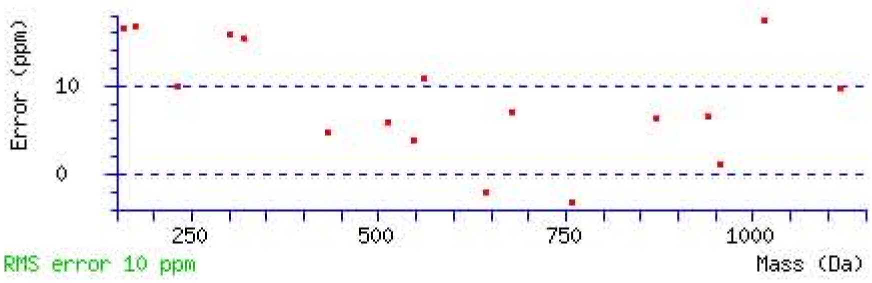
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 42  Expect: 0.001
Matches : 17/72 fragment ions using 30 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	**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
41.8	1187.579086	-0.000358	AQMDLSGR
9.6	1187.568314	0.010414	QREDIWEGR
9.1	1187.568344	0.010384	DHGFKVSADGR
8.6	1187.578201	0.000527	SSLENEPSLGR
7.0	1187.579086	-0.000358	QAAEVMGR
6.0	1187.575714	0.003014	YQDAAGPR
2.0	1187.593475	-0.014747	AESFPNTPLGR
0.9	1187.568314	0.010414	QYLEQHASGR

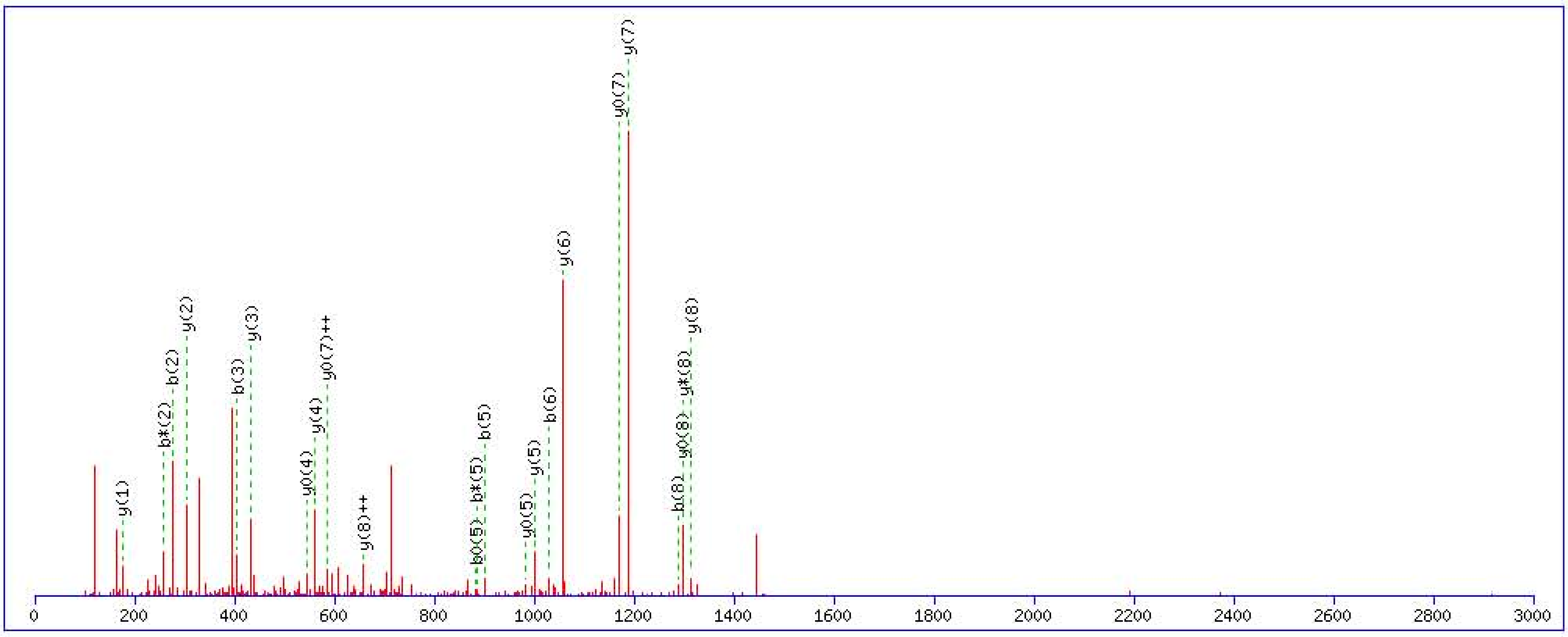
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

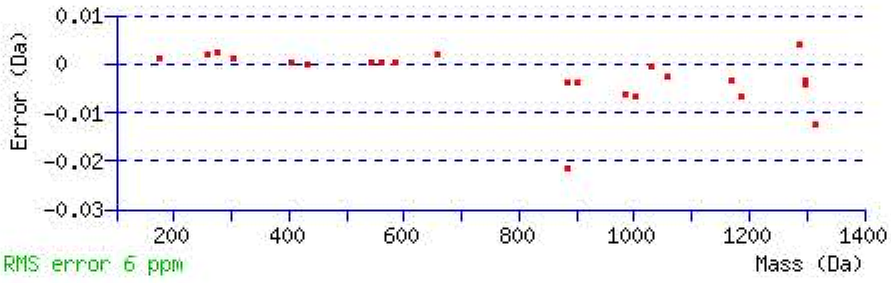
Match to Query 28894: 1461.655248 from(731.834900,2+) rtinseconds(1473) index(30088)
Title: Locus:1.1.1.3061.22 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

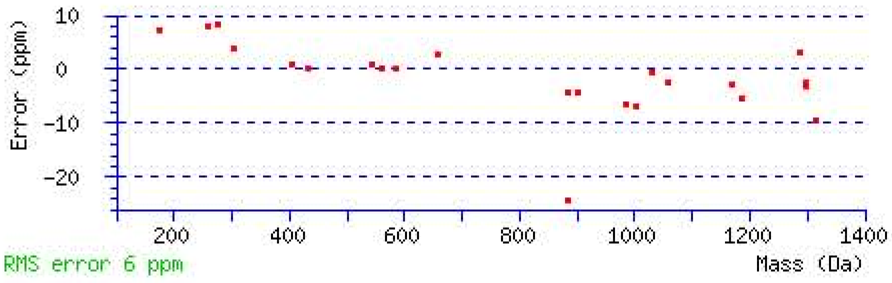
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 47  Expect: 0.00015
Matches : 23/88 fragment ions using 42 most intense peaks   (help)
```

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





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.0	1461.655807	-0.000559	FQEGQEEER
12.2	1461.640564	0.014684	NSGTQSDGEEK
10.3	1461.655807	-0.000559	FQEGQEEER
8.8	1461.640564	0.014684	VMTDVAGNPEEER
5.6	1461.648392	0.006856	HREELSDYEER
4.2	1461.637161	0.018087	ESELQWQEEER
1.4	1461.676956	-0.021708	MSGQVGDLSPSQEK

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

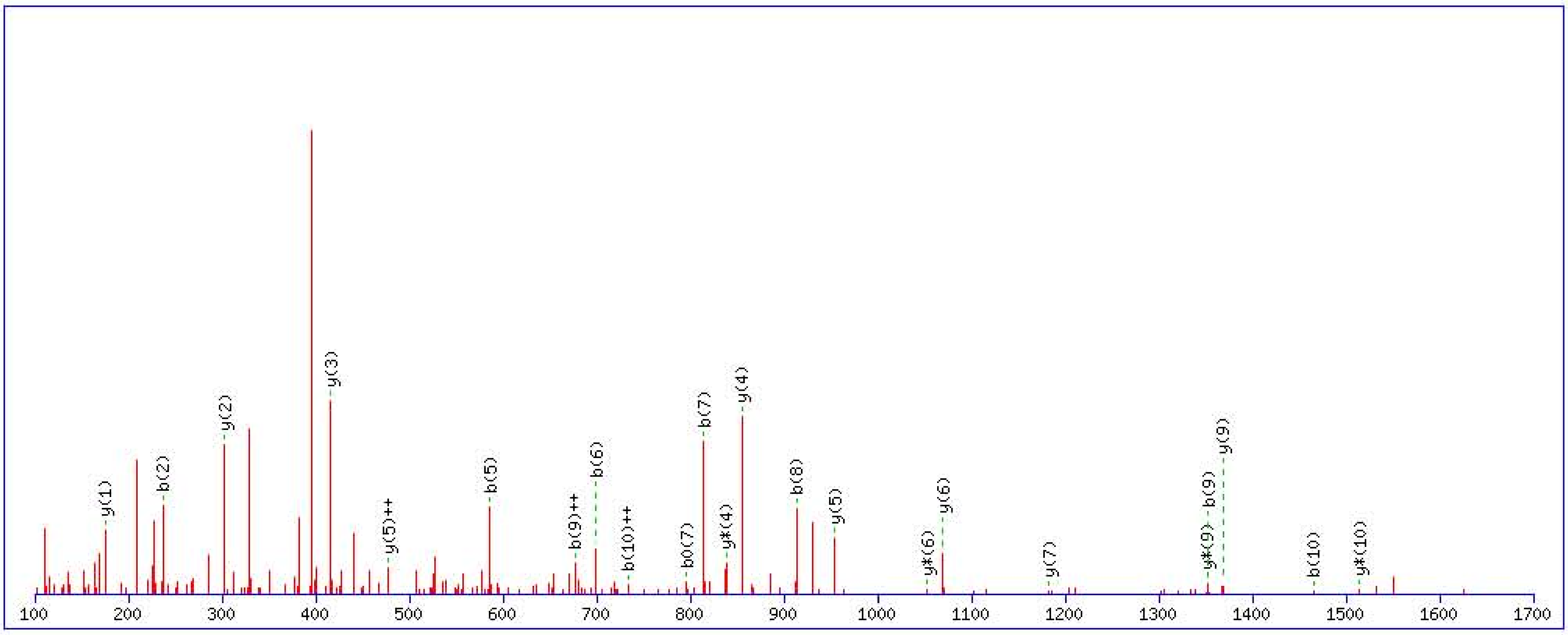
Mascot Search Results

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

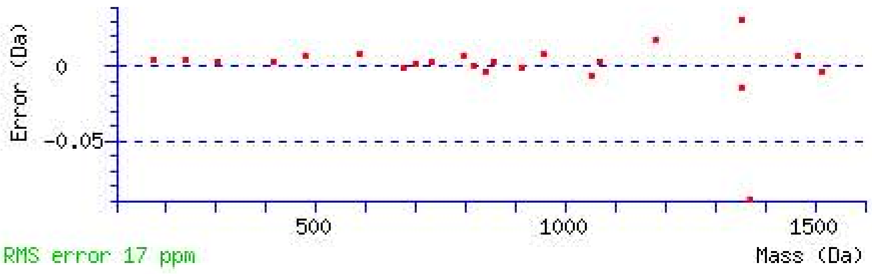
Match to Query 37843: 1766.913582 from(589.978470,3+) rtinseconds(1951) index(4633)
Title: Locus:1.1.1.3231.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

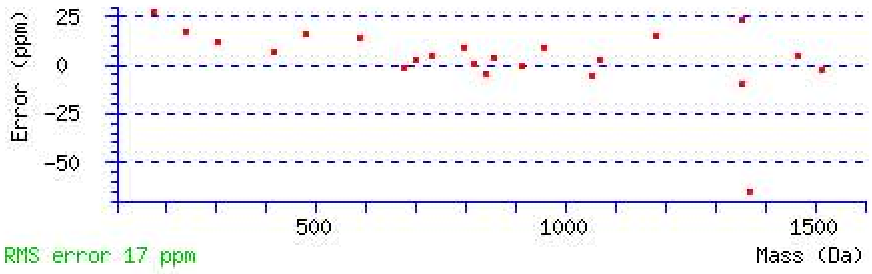
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1766.913773
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 39 **Expect:** 0.003
Matches : 23/98 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	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
39.3	1766.913773	-0.000191	HVYGELDVQIQR
16.7	1766.913773	-0.000191	HVYGELDVQIQR

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

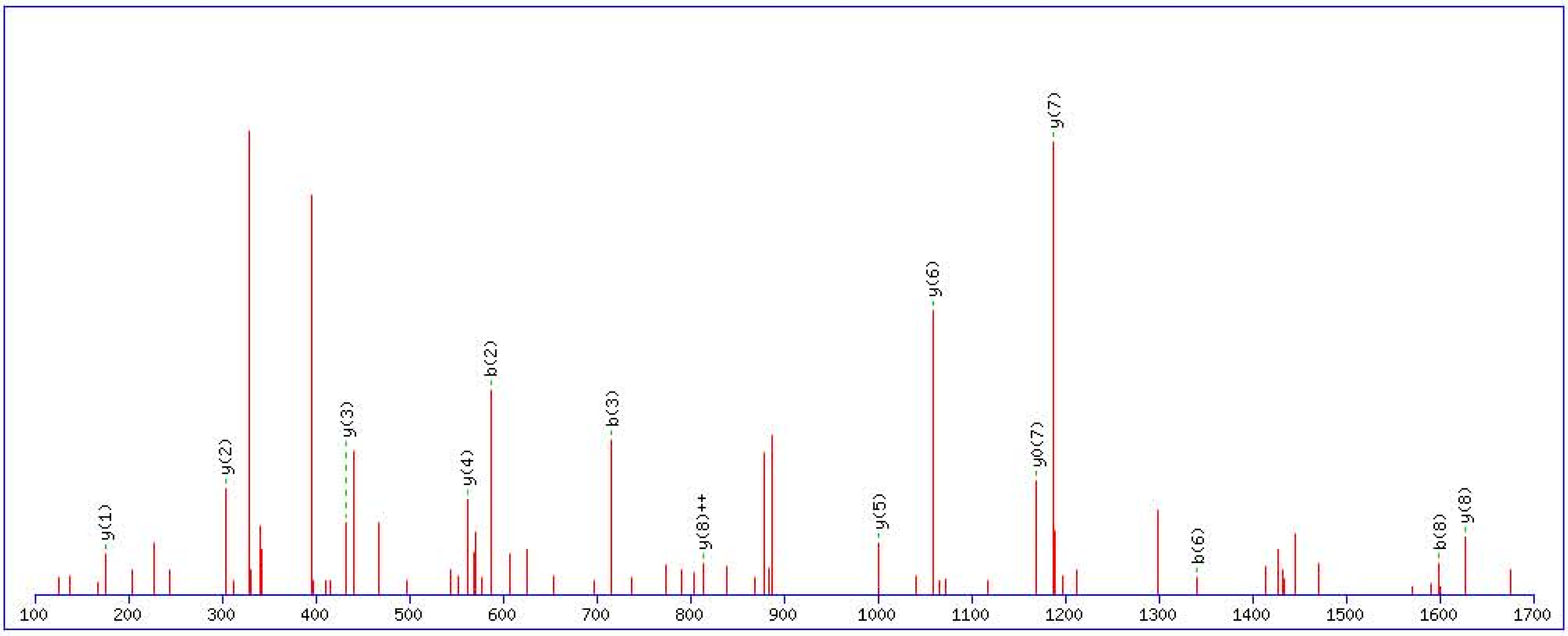
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

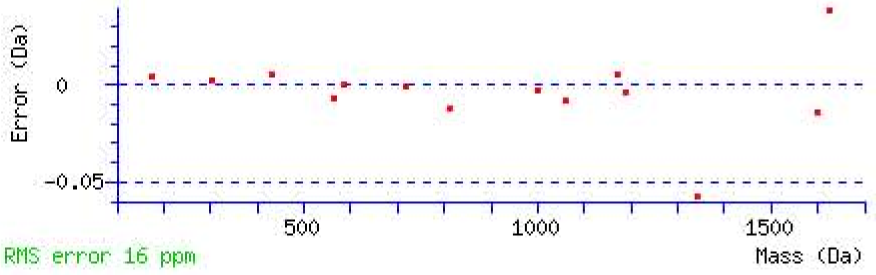
Match to Query 38009: 1772.815528 from(887.415040,2+) rtinseconds(1853) index(32159)
Title: Locus:1.1.1.3194.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

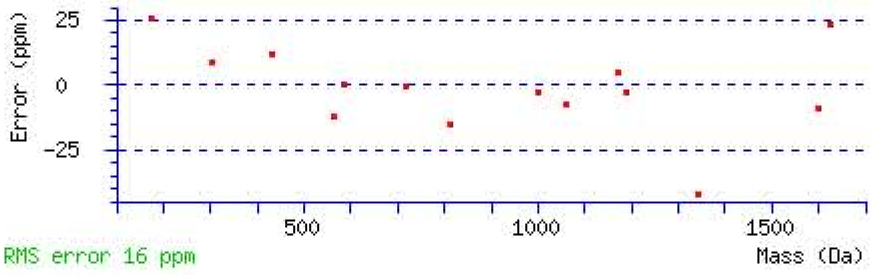
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1772.822556
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.0013
Matches : 14/88 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	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
39.5	1772.822556	-0.007028	FQEGQEEER
22.7	1772.803909	0.011619	ESELQWQEEER
6.1	1772.829727	-0.014199	QEEEEAMRRER
4.3	1772.798752	0.016776	HISSCMRWPGHYSR
3.8	1772.803909	0.011619	ESELQWQEEER
3.7	1772.828873	-0.013345	QAEQEATVAREEQER
3.7	1772.836288	-0.020760	ADGSLTGGGLEAAAMAPER
1.1	1772.811798	0.003730	YQTPPHQNFEDLER

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

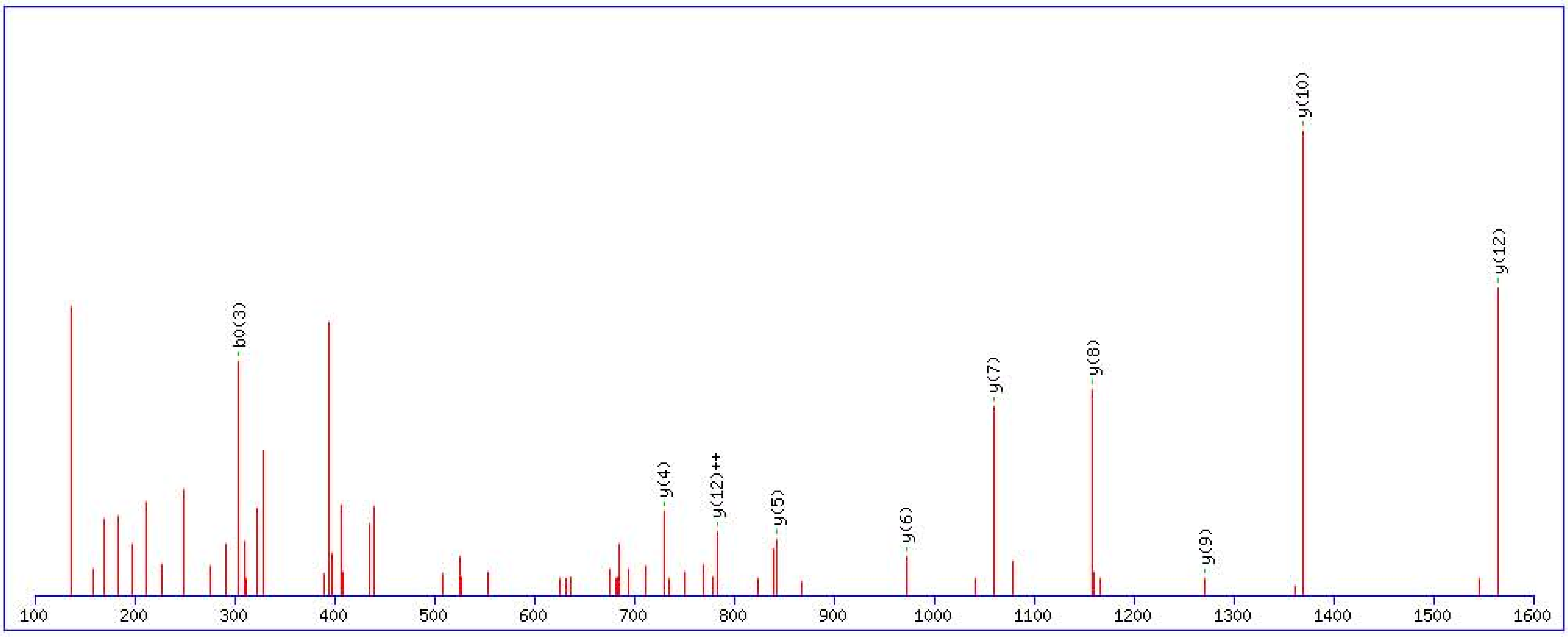
Mascot Search Results

Peptide View

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

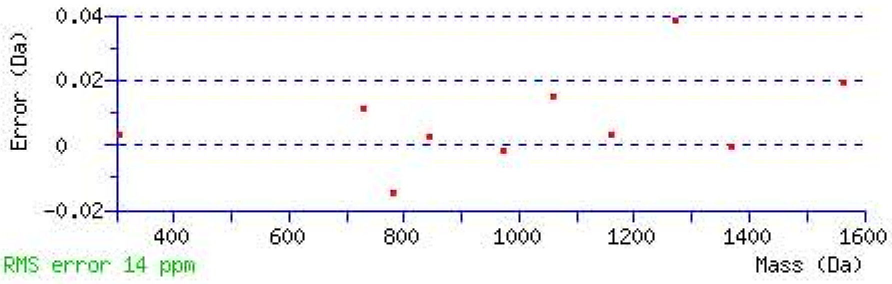
Match to Query 41987: 1998.094992 from(667.038940,3+) rtinseconds(2770) index(66806)
Title: Locus:1.1.1.3590.9 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

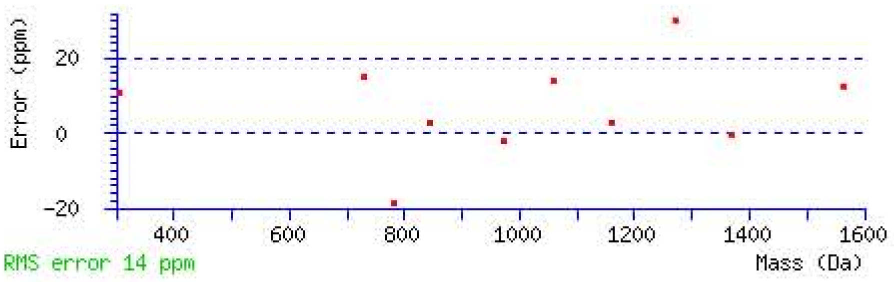
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 55  Expect: 1e-005
Matches : 10/150 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							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
54.9	1998.085983	0.009009	GTYIPVPIVSELQSGK
1.6	1998.099731	-0.004739	GDEVVVELVENGKKVTVGK

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

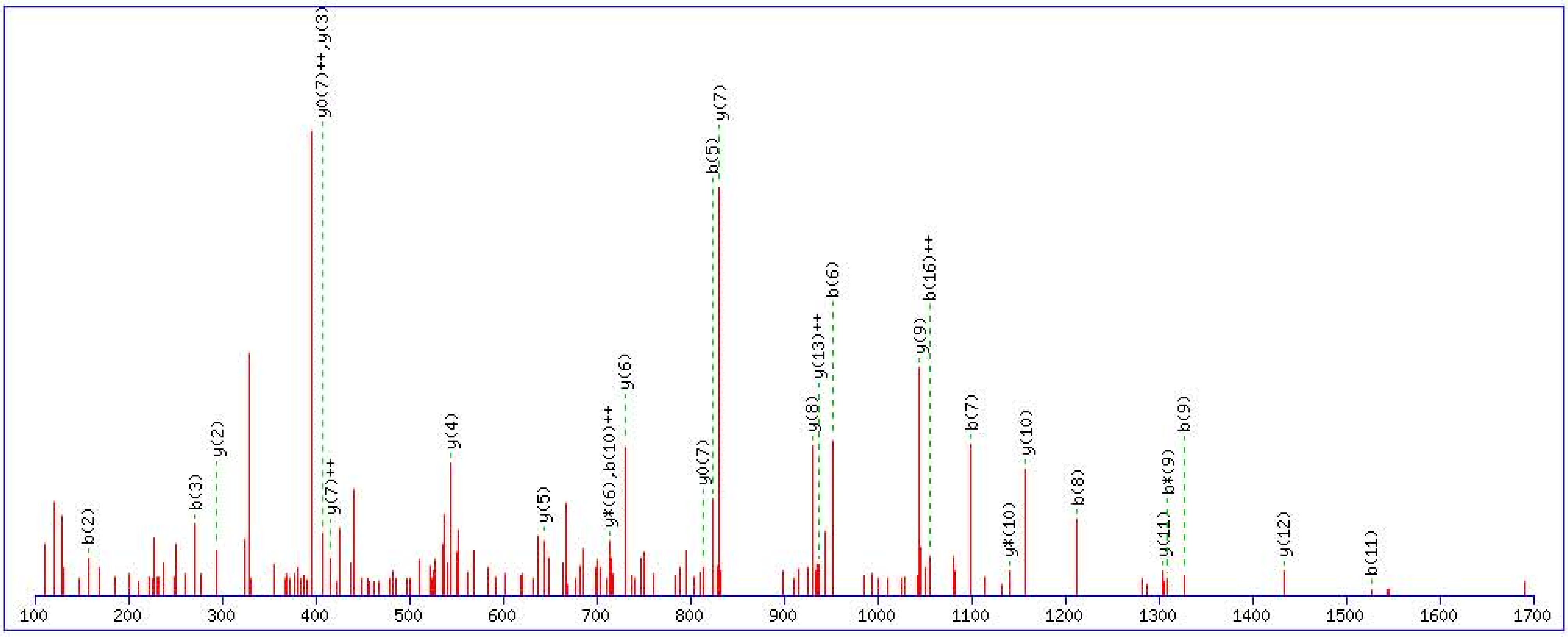
{MATRIX SCIENCE} Mascot Search Results

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

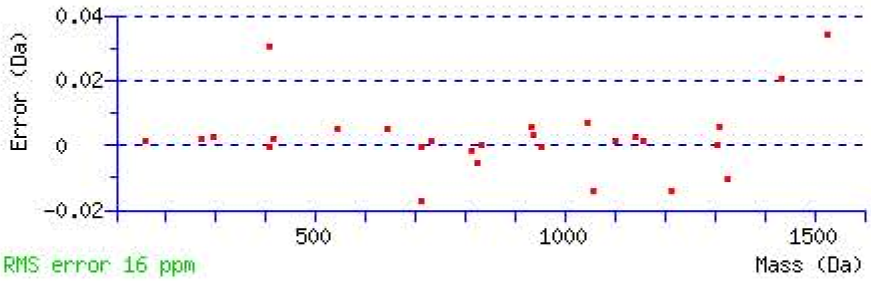
Match to Query 46948: 2255.223132 from(752.748320,3+) rtinseconds(3018) index(39162)
Title: Locus:1.1.1.3597.7 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

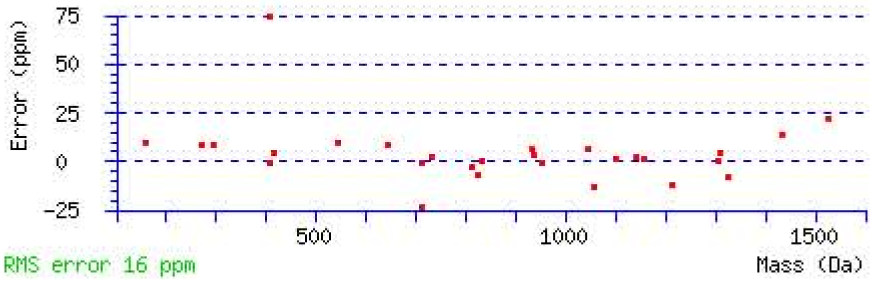
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2255.213654
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 0.00011
Matches : 28/168 fragment ions using 55 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
52.1	2255.213654	0.009478	GVNLQEFLNVTSVHLFK

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

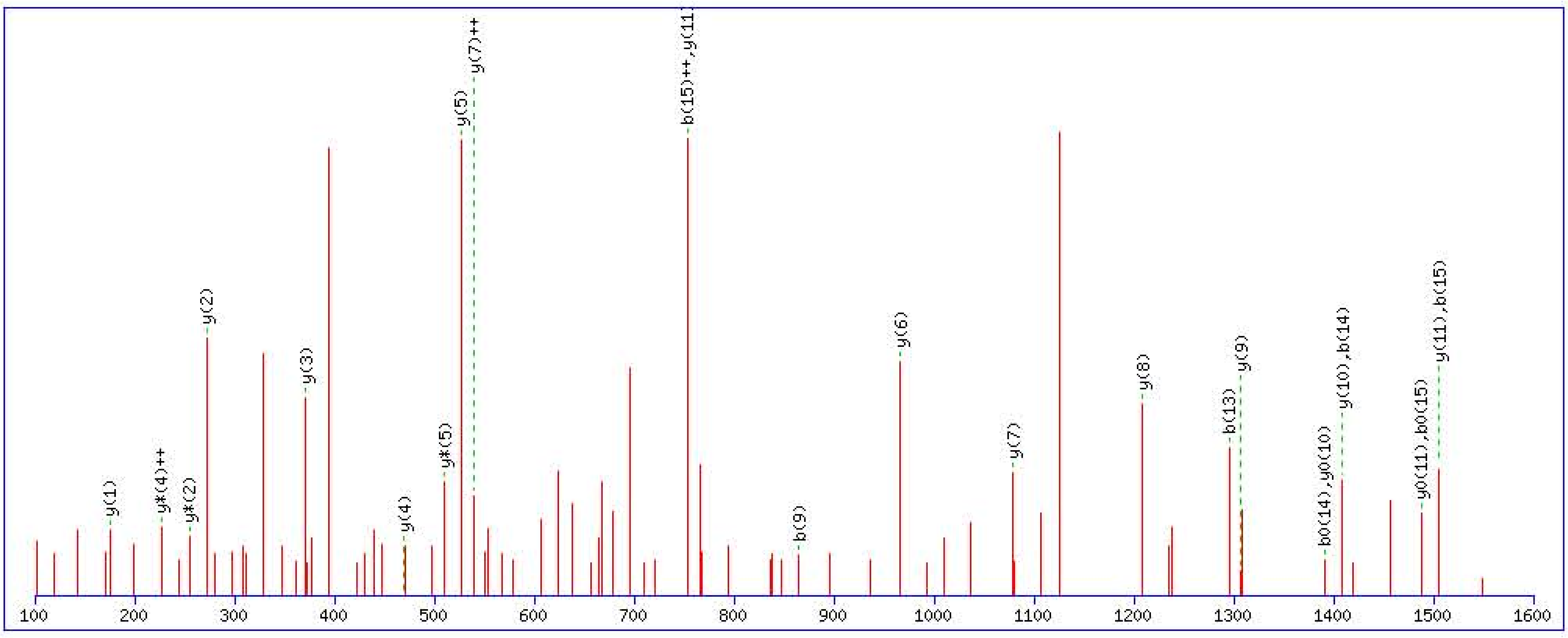
Mascot Search Results

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

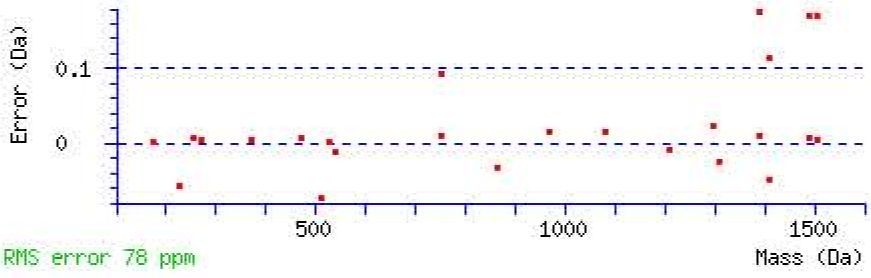
Match to Query 55304: 2912.483976 from(729.128270,4+) rtinseconds(2487) index(7417)
Title: Locus:1.1.1.3418.17 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

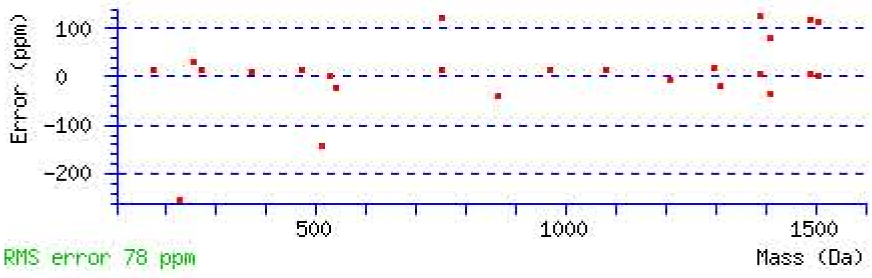
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2912.470200
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20    : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00011
Matches : 25/254 fragment ions using 44 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							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
48.2	2912.470200	0.013776	AVPPNNSNAAEDDLPTVELQGVVPR
5.6	2912.492661	-0.008685	TNHSSPEAQSKQTGRVLEPPVPSR
5.4	2912.492661	-0.008685	TNHSSPEAQSKQTGRVLEPPVPSR
1.0	2912.456650	0.027326	MRMATPLLMQALPMGALPQGPMQNATK
1.0	2912.456650	0.027326	MRMATPLLMQALPMGALPQGPMQNATK

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

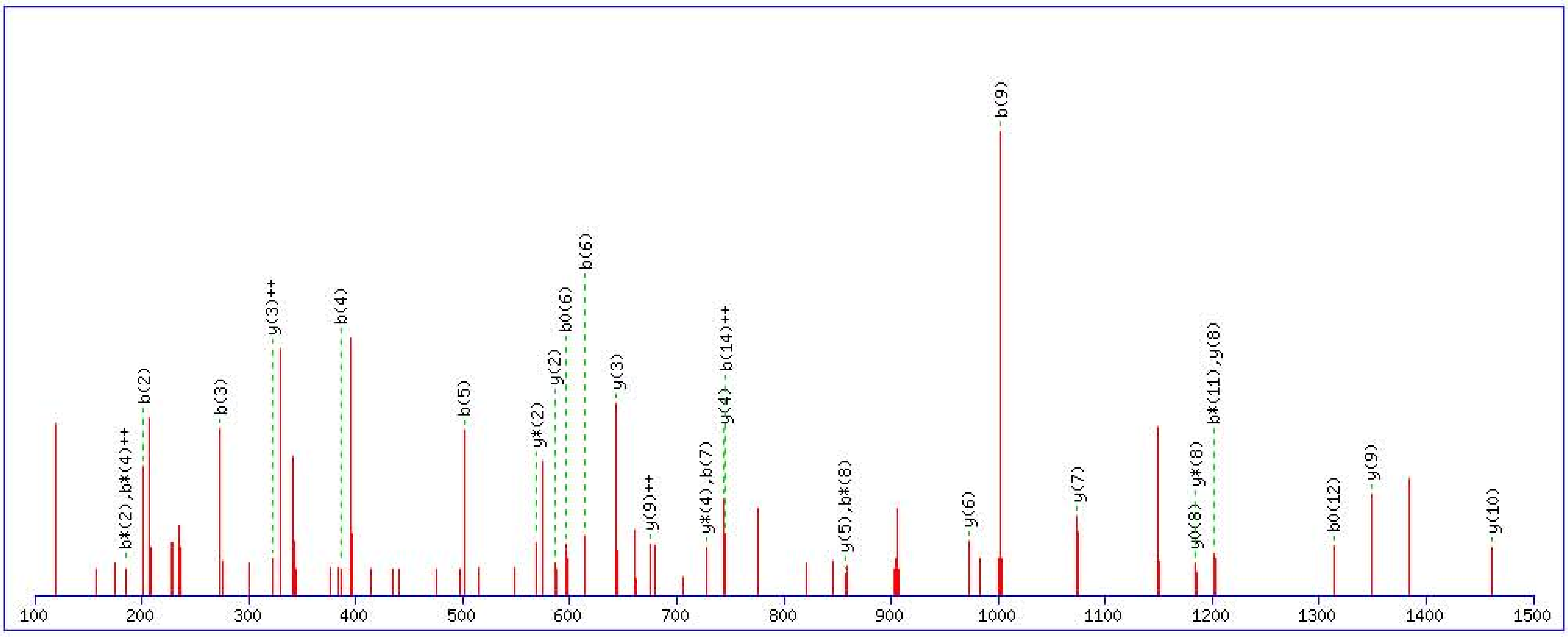
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SNALDIIFQTDLTGQK**
Found in **C1S_HUMAN**, Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1

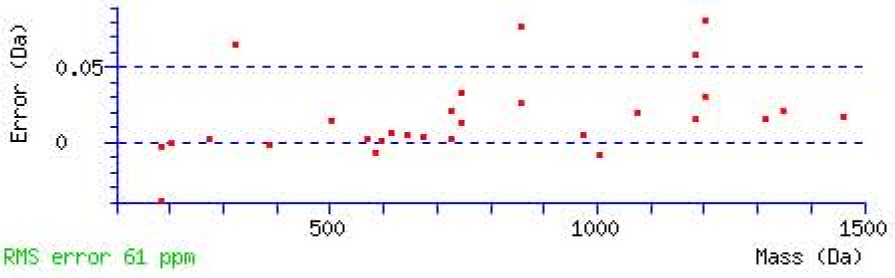
Match to Query 44112: 2074.100982 from(692.374270,3+) rtinseconds(2878) index(53069)
Title: Locus:1.1.1.3048.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

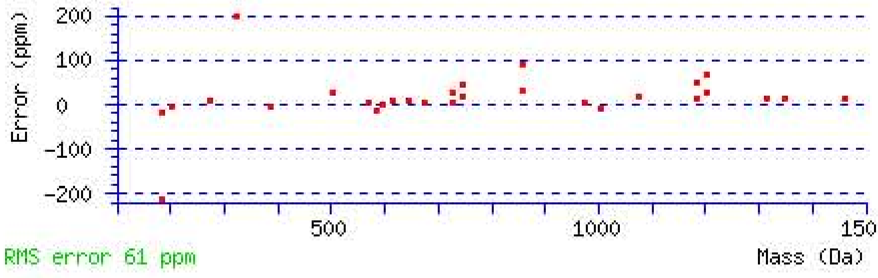
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 28 **Expect:** 0.042
Matches : 29/172 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	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
27.7	2074.076874	0.024108	SNALDIIFQTDLTGQK
10.7	2074.076874	0.024108	SNALDIIFQTDLTGQK

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

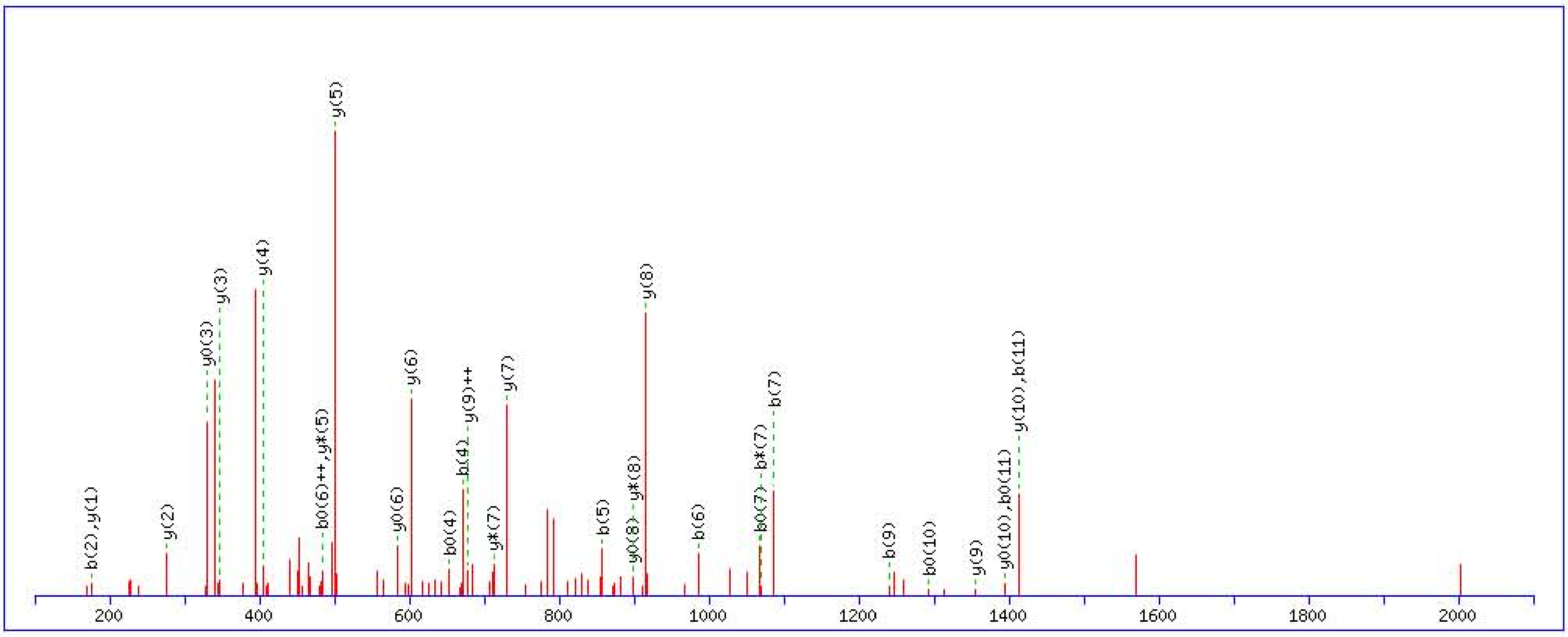
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSGQWQTPGATR**
Found in **CO2_HUMAN**, Complement C2 OS=Homo sapiens GN=C2 PE=1 SV=2

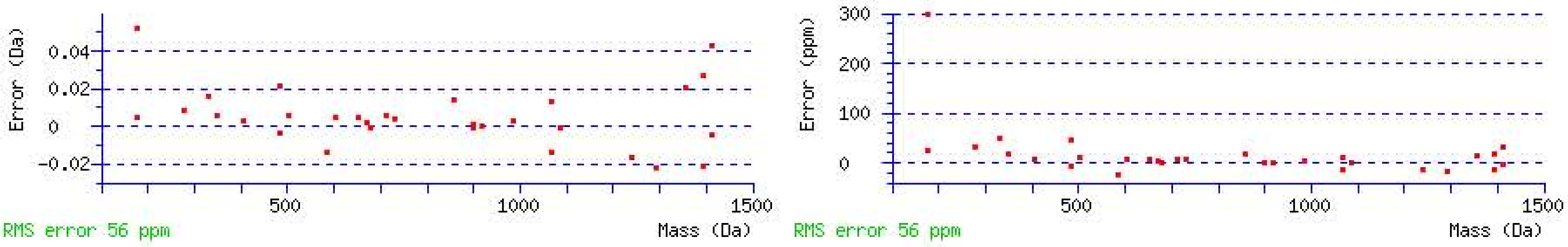
Match to Query 32617: 1585.766608 from(793.890580,2+) rtinseconds(1747) index(61085)
Title: Locus:1.1.1.3234.9 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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): 1585.767120
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 55 **Expect:** 3e-005
Matches : 31/124 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	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
55.4	1585.767120	-0.000512	SSGQWQTPGATR
27.6	1585.767120	-0.000512	SSGQWQTPGATR
6.8	1585.767075	-0.000467	AWENLGEQMGKAPR
6.2	1585.769592	-0.002984	ETDHKSLSSSPDKR
4.4	1585.751846	0.014762	LMDEPALRSPGGGDR
2.0	1585.766922	-0.000314	RTSNERPGSGQGQGR
1.1	1585.769653	-0.003045	GDVGTAGSVGGTGEPGLR

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

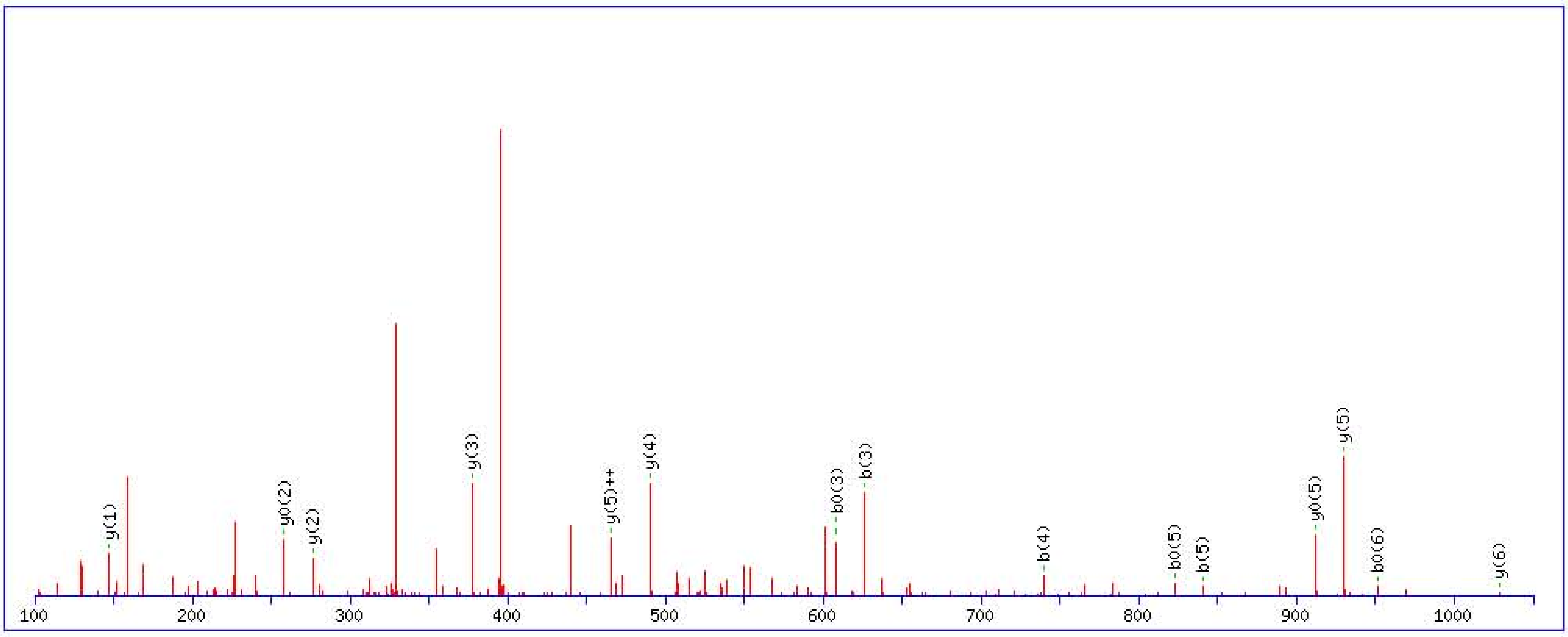
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

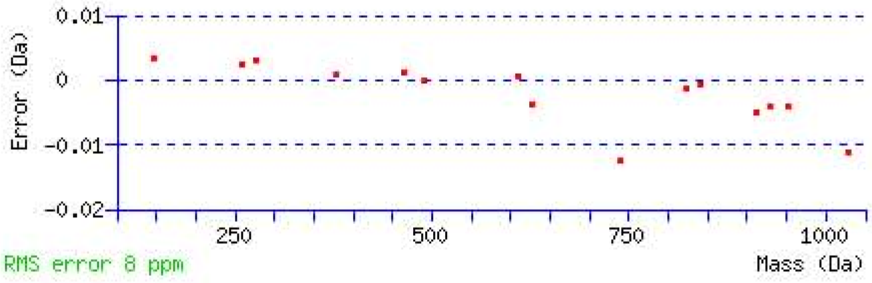
Match to Query 17067: 1114.602688 from(558.308620,2+) rtinseconds(1529) index(30442)
Title: Locus:1.1.1.3081.17 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

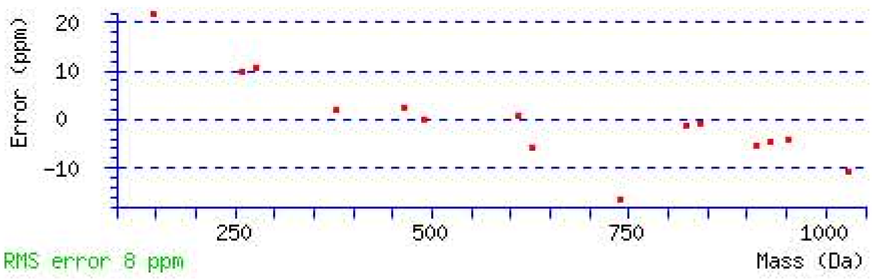
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 0.015
Matches : 15/66 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
32.0	1114.605621	-0.002933	SVQLTEK
14.8	1114.613480	-0.010792	SVFAKHGLEK
5.1	1114.591690	0.010998	ASVHSMISRK
4.6	1114.598236	0.004452	SAVITSLDPGR
4.3	1114.609451	-0.006763	SVARLSPETR
3.3	1114.609436	-0.006748	EGIKRQQEK
3.1	1114.588318	0.014370	YIVNRGEHK
2.5	1114.609451	-0.006763	LLQSALGGNSR
2.3	1114.605621	-0.002933	LQTSVEK
1.5	1114.616837	-0.014149	SPRLLCIEK

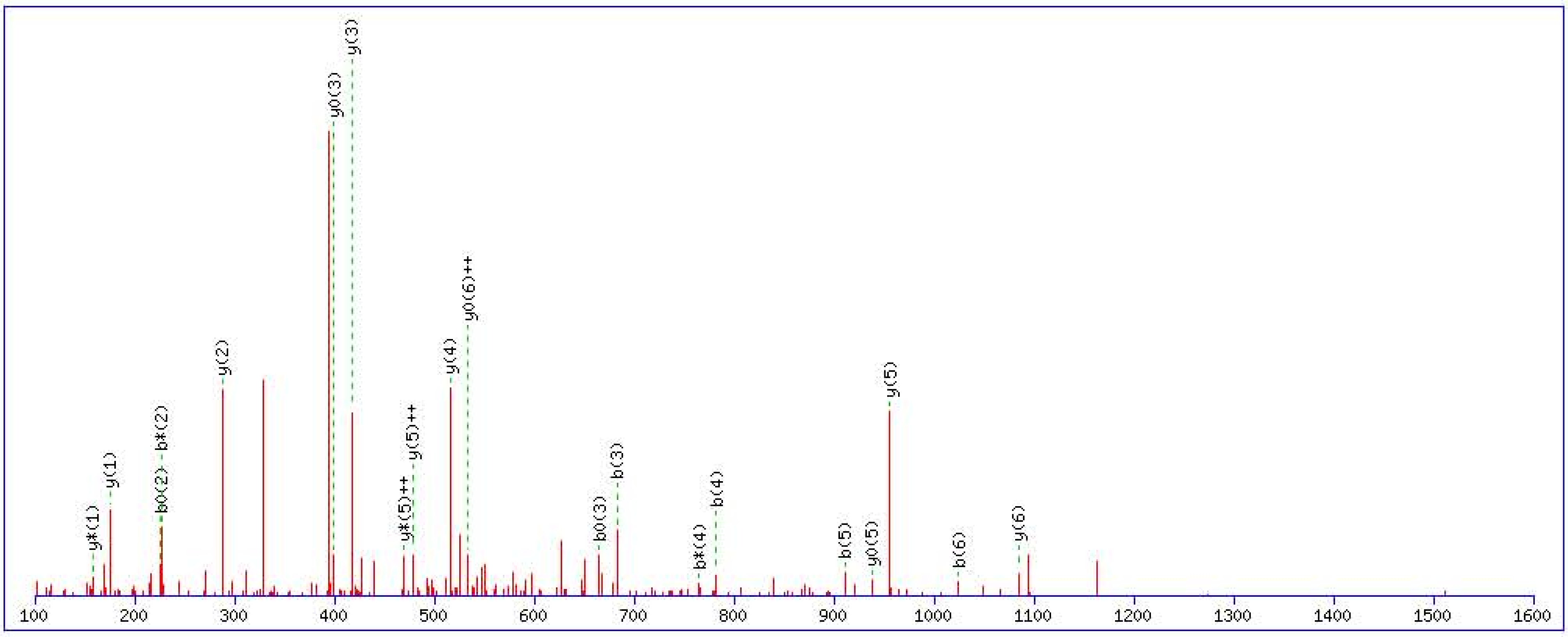
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

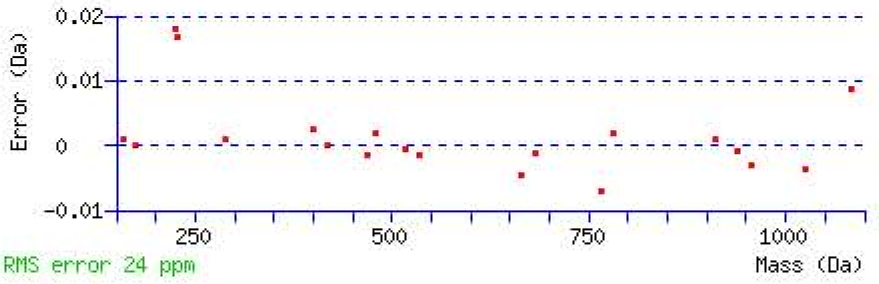
Match to Query 20294: 1197.616848 from(599.815700,2+) rtinseconds(1624) index(31042)
Title: Locus:1.1.1.3114.20 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

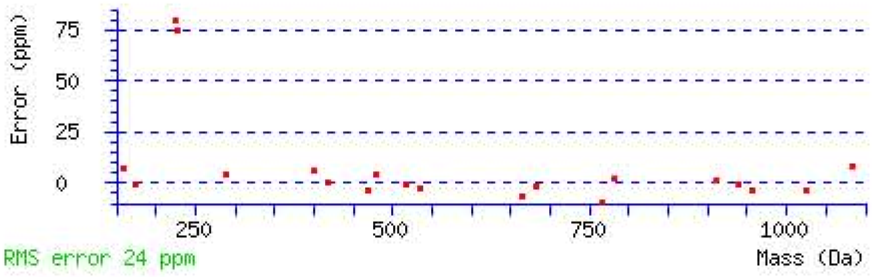
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1197.617569
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0037
Matches : 20/66 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	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
37.2	1197.617569	-0.000721	NEQVEIR
11.3	1197.617569	-0.000721	NQEDLLR
10.8	1197.598938	0.017910	AAQEGDLPELR
9.5	1197.617569	-0.000721	QEVNELR
8.6	1197.598953	0.017895	QDNLPDIEVR
8.2	1197.617569	-0.000721	LQDNELR
7.9	1197.598953	0.017895	EISPGSGPGEIR
6.3	1197.628815	-0.011967	QLSMQVHALR
6.2	1197.621399	-0.004551	EKHSTQAKNR
4.4	1197.598953	0.017895	VDNQPEELVR

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

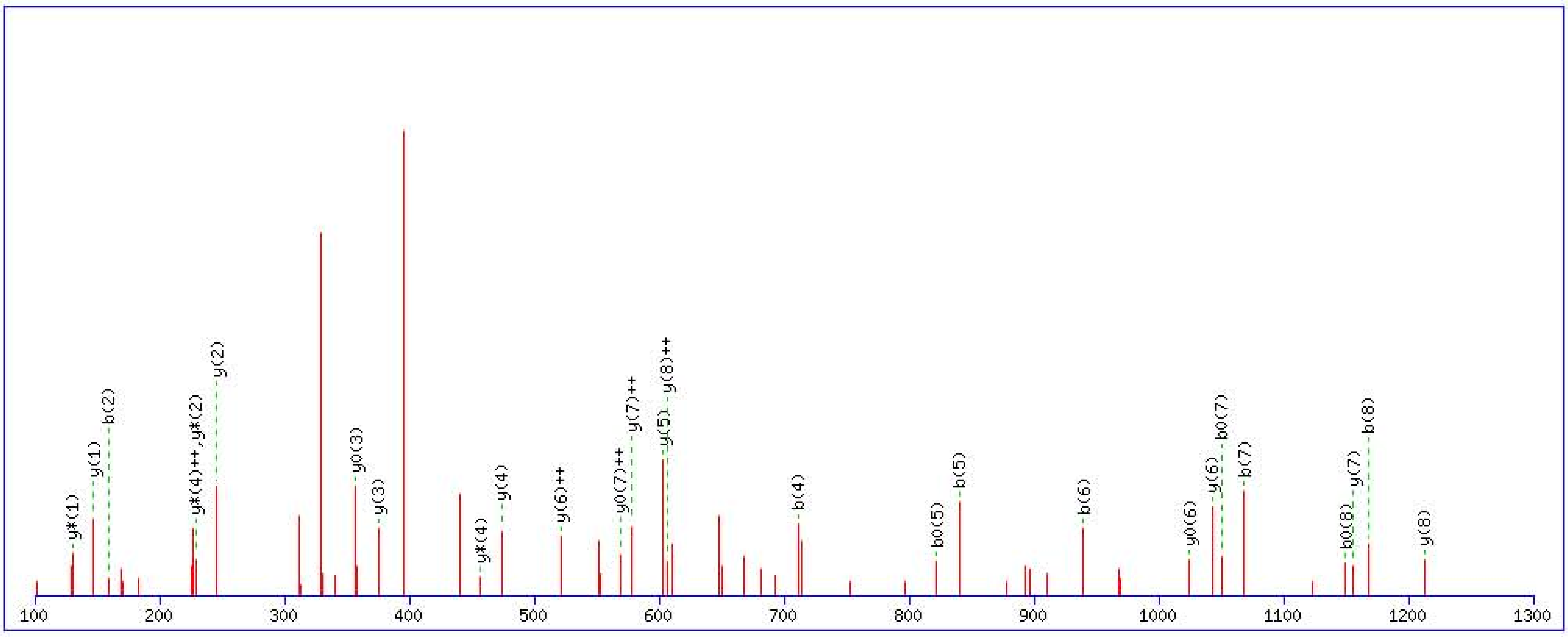
Mascot Search Results

Peptide View

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

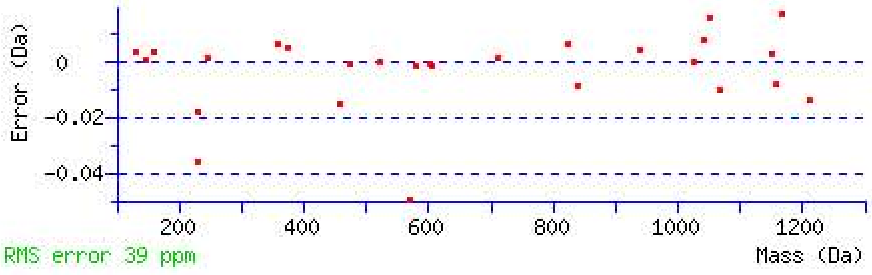
Match to Query 23275: 1312.707728 from(657.361140,2+) rtinseconds(1838) index(32088)
Title: Locus:1.1.1.3189.6 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

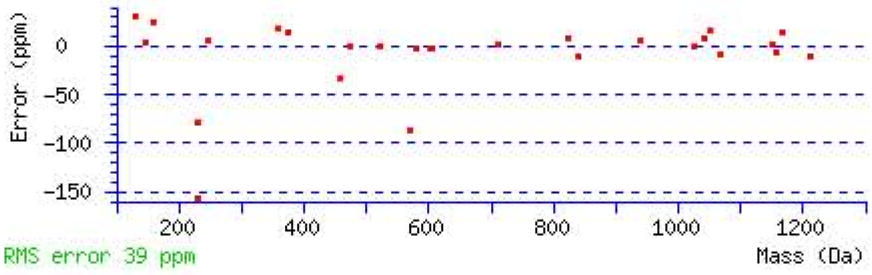
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 46  Expect: 0.00056
Matches : 27/86 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	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
46.4	1312.706070	0.001658	TGLQEVEVK
13.8	1312.699524	0.008204	TIMHLMINNVK
8.8	1312.721115	-0.013387	KKPQRDSQAQK
5.6	1312.706055	0.001673	QSAEEVIVK
5.3	1312.691422	0.016306	YKELYLEEVK
3.6	1312.702682	0.005046	IQYSLGKYDVK
3.2	1312.692139	0.015589	DRQSQIQK
3.0	1312.713913	-0.006185	KVFEKYTTAAR
1.7	1312.688766	0.018962	HKVHTGEKSYK
1.5	1312.692139	0.015589	EMLTHRNGLVK

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

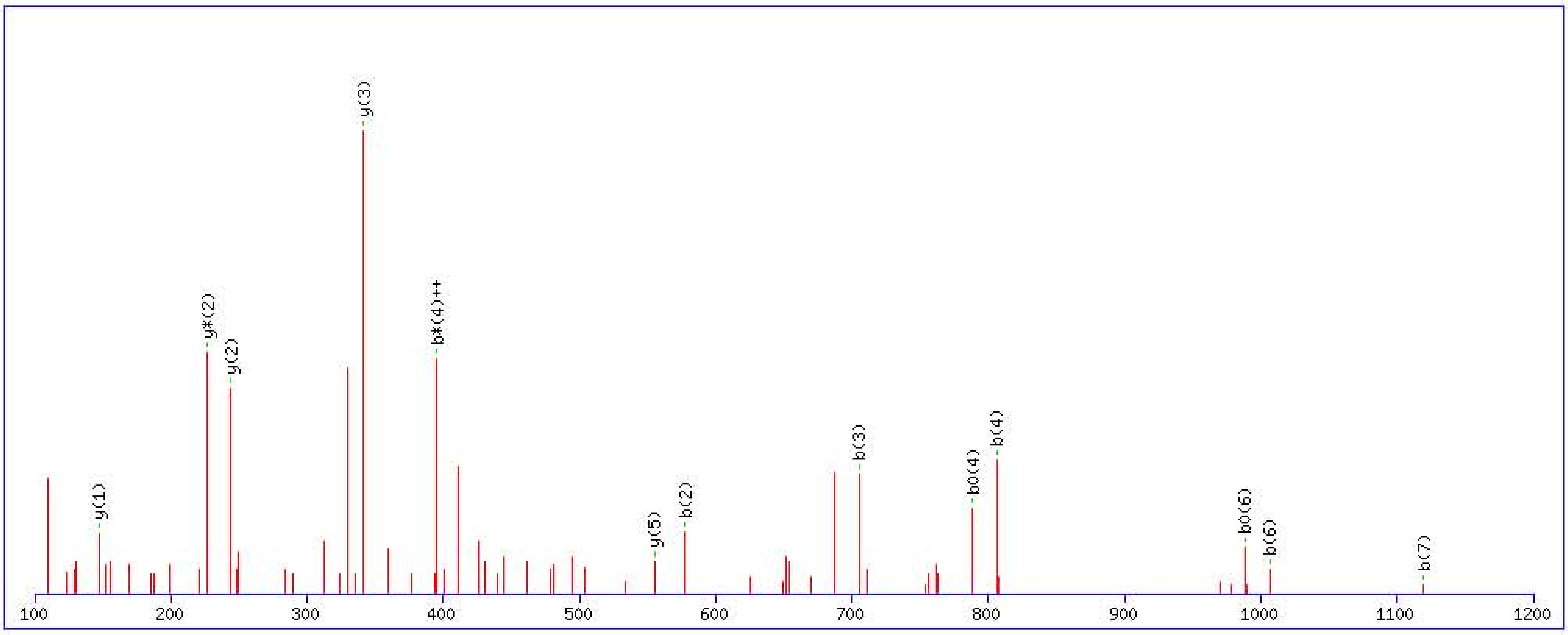
Mascot Search Results

Peptide View

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

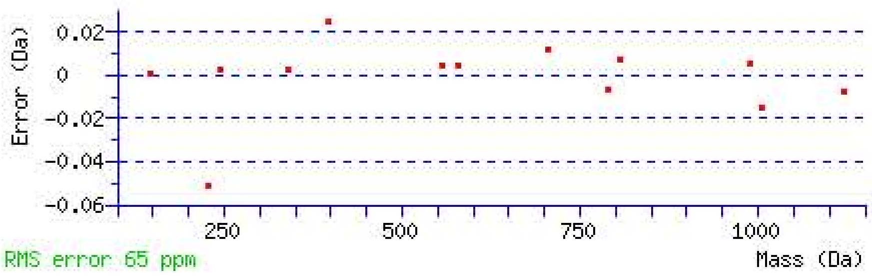
Match to Query 28844: 1458.798522 from(487.273450,3+) rtinseconds(1574) index(30697)
Title: Locus:1.1.1.3097.7 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

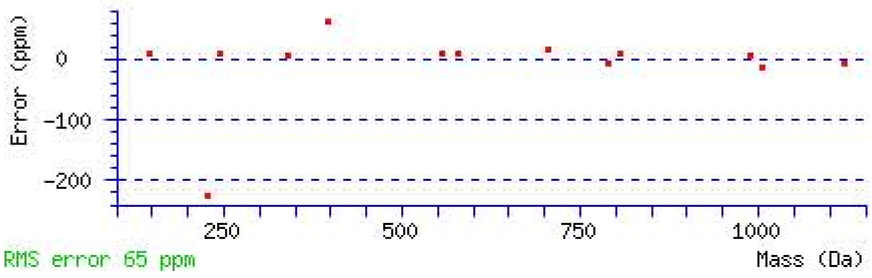
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1458.801712
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 44  Expect: 0.00089
Matches : 13/92 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	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
43.8	1458.801712	-0.003190	HQQTVTIPPK
33.8	1458.801712	-0.003190	HQQTVTIPPK

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

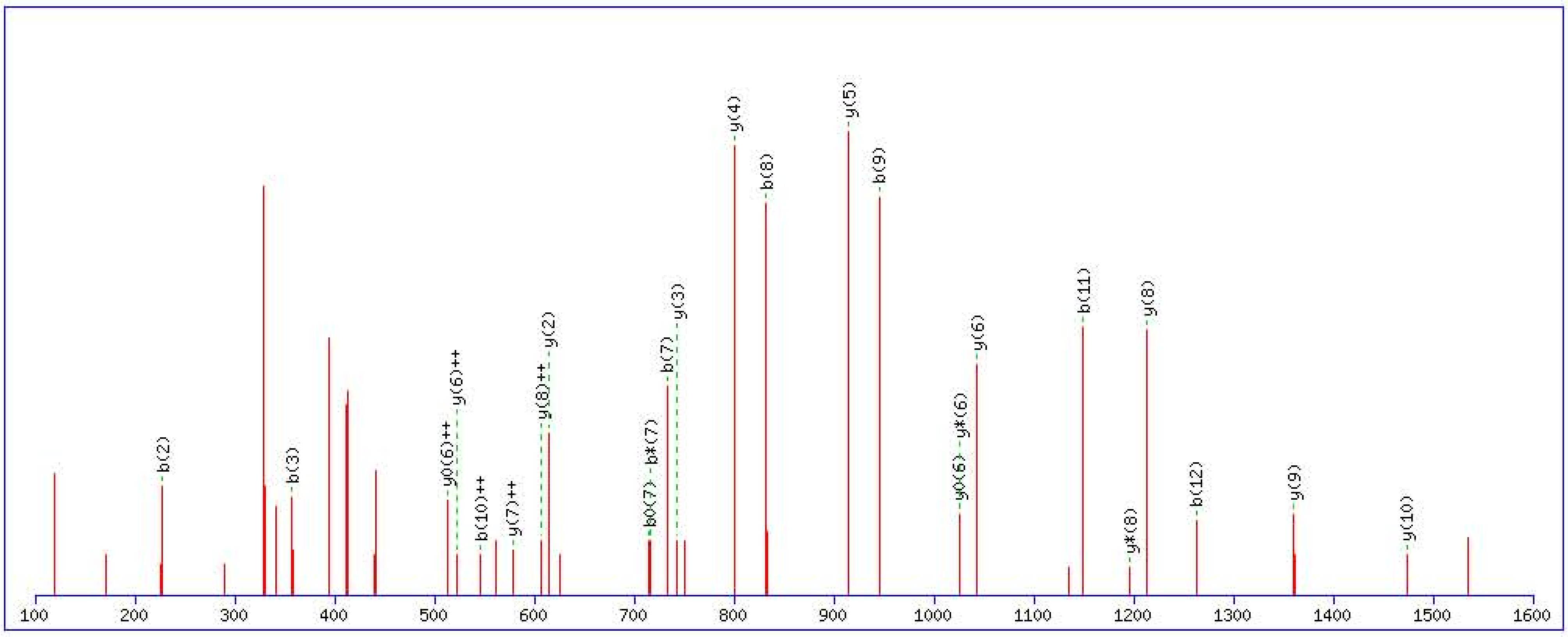
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

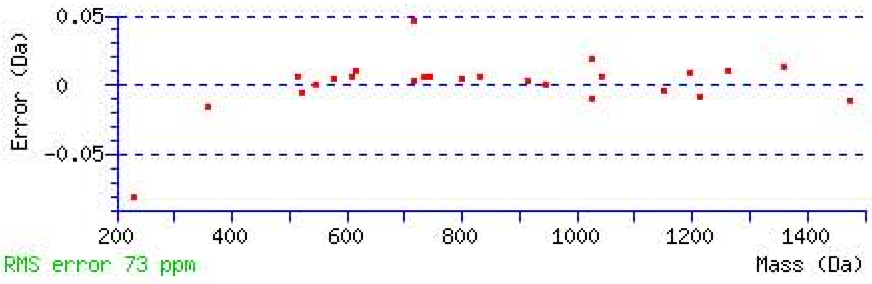
Match to Query 30938: 2304.200052 from(769.073960,3+) rtinseconds(2473) index(35579)
Title: Locus:1.1.1.3410.23 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

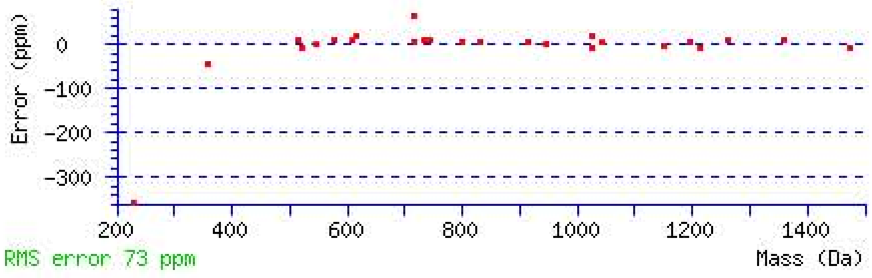
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 49 **Expect:** 0.0003
Matches : 25/196 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	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
49.3	2304.193649	0.006403	KVEGTAFVIFGIQDGEQR
25.2	2304.193649	0.006403	KVEGTAFVIFGIQDGEQR

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

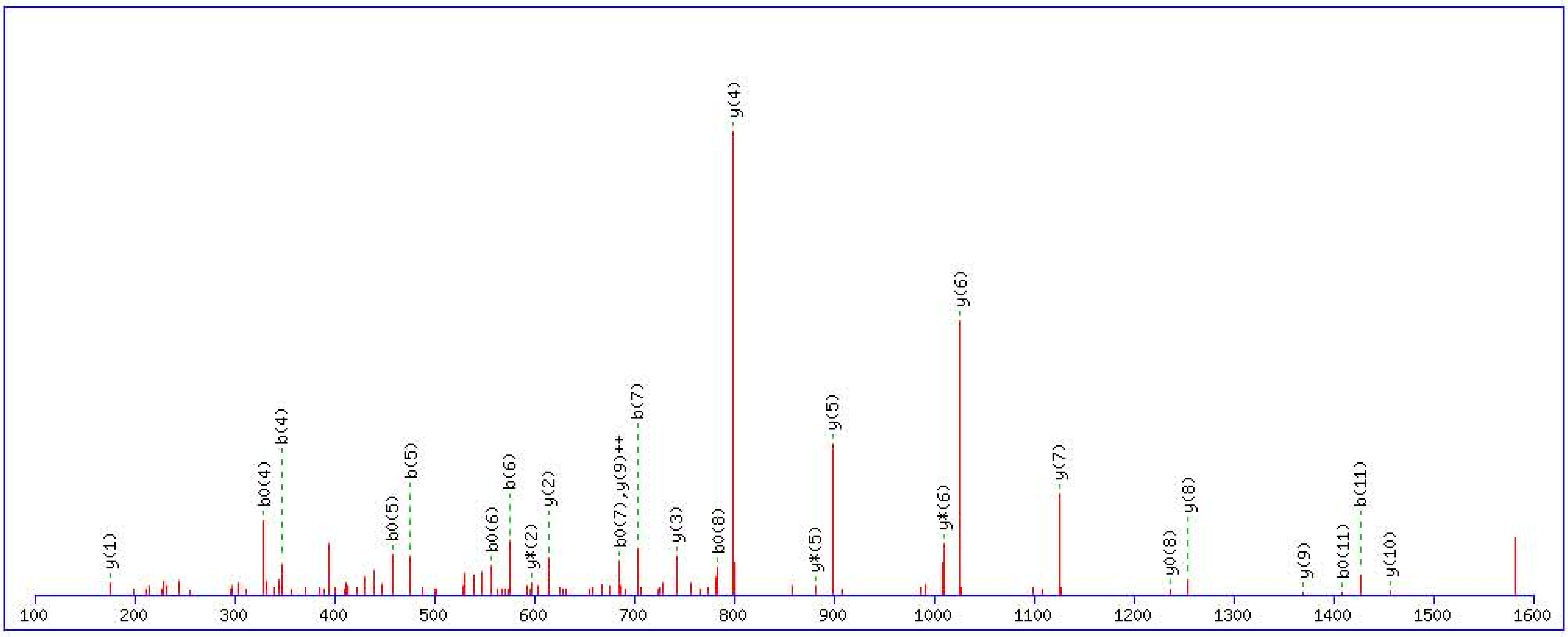
Mascot Search Results

Peptide View

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

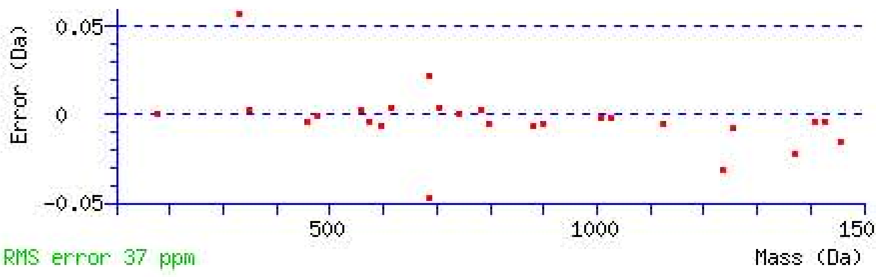
Match to Query 33271: 1599.763308 from(800.888930,2+) rtinseconds(1556) index(30586)
Title: Locus:1.1.1.3090.13 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

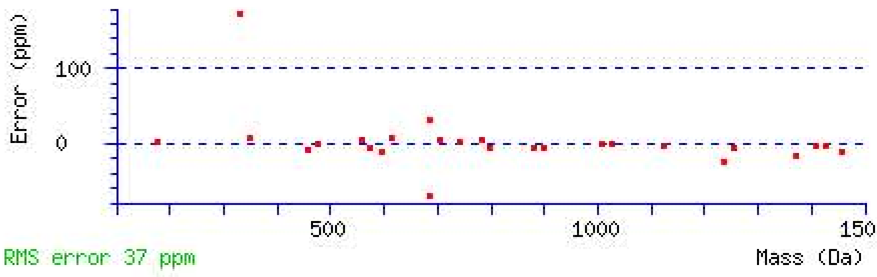
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1599.767517
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 78  Expect: 2.4e-007
Matches : 26/106 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	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





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
77.7	1599.767517	-0.004209	SGSDEVQVGQQR
62.4	1599.767517	-0.004209	SGSDEVQVGQQR
34.3	1599.767517	-0.004209	SGSDEVQVGQQR
9.9	1599.767471	-0.004163	AMNAANLNIPPSDTR
6.4	1599.779388	-0.016080	RFPDFSYITQNGR
3.5	1599.742325	0.020983	REGDQEERDR
1.8	1599.767502	-0.004194	EVCSEKTGHAEVVR
1.8	1599.753769	0.009539	ASTFSCIMQKWGGK
1.6	1599.767502	-0.004194	LHMLSSVDLNGQDR

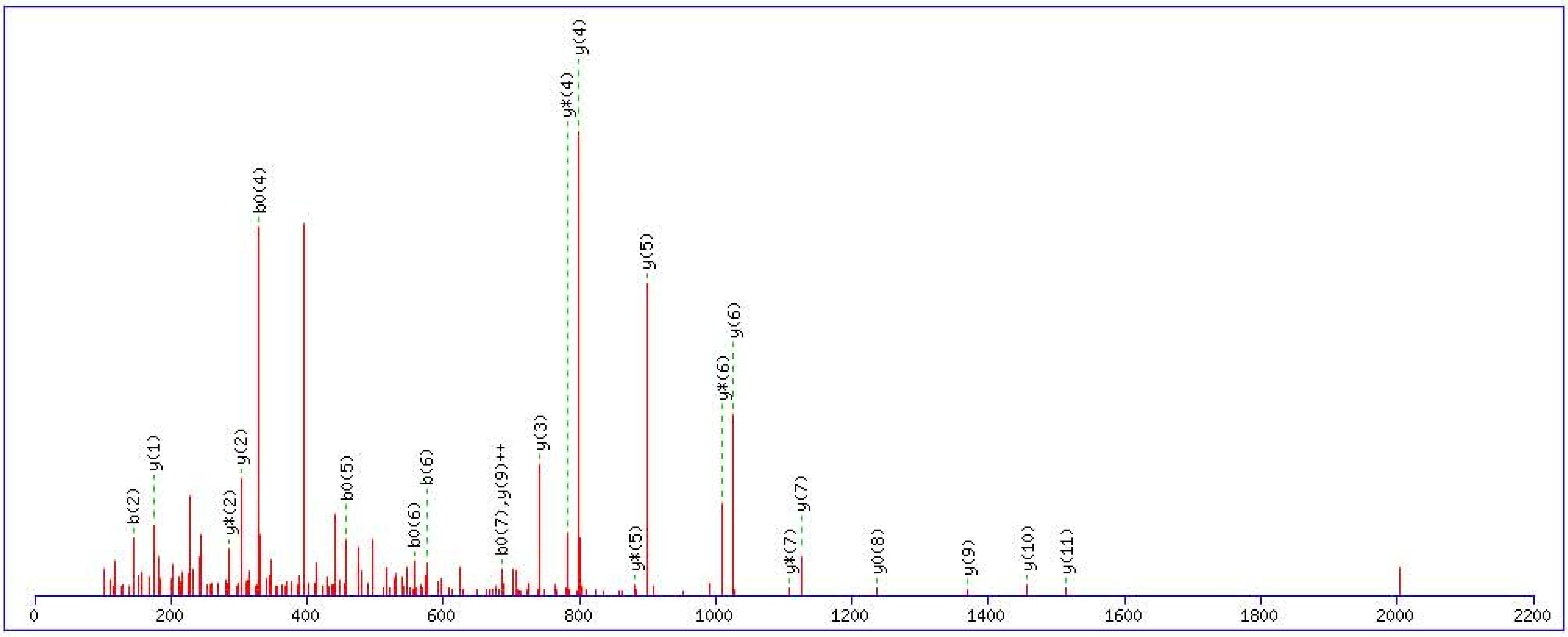
Mascot Search Results

Peptide View

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

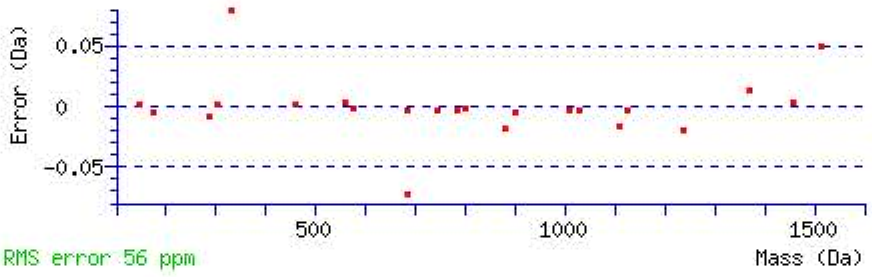
Match to Query 33272: 1599.763572 from(534.261800,3+) rtinseconds(1538) index(30490)
Title: Locus:1.1.1.3084.14 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

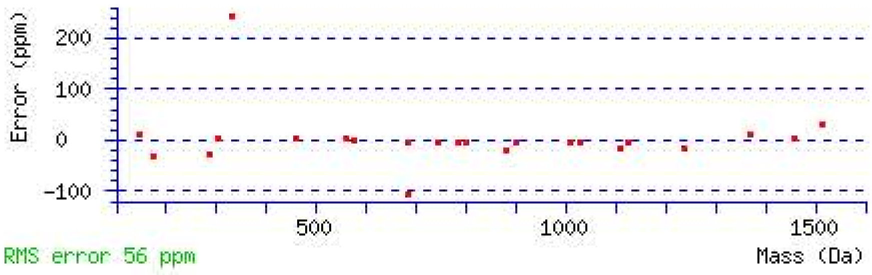


```
Monoisotopic mass of neutral peptide Mr(calc): 1599.767517
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 70  Expect: 1.4e-006
Matches : 23/106 fragment ions using 36 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							12
2	**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



RMS error 56 ppm



RMS error 56 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
70.0	1599.767517	-0.003945	SGSDEVQVGQQR
62.7	1599.767517	-0.003945	SGSDEVQVGQQR
28.6	1599.767517	-0.003945	SGSDEVQVGQQR

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

{MATRIX SCIENCE}

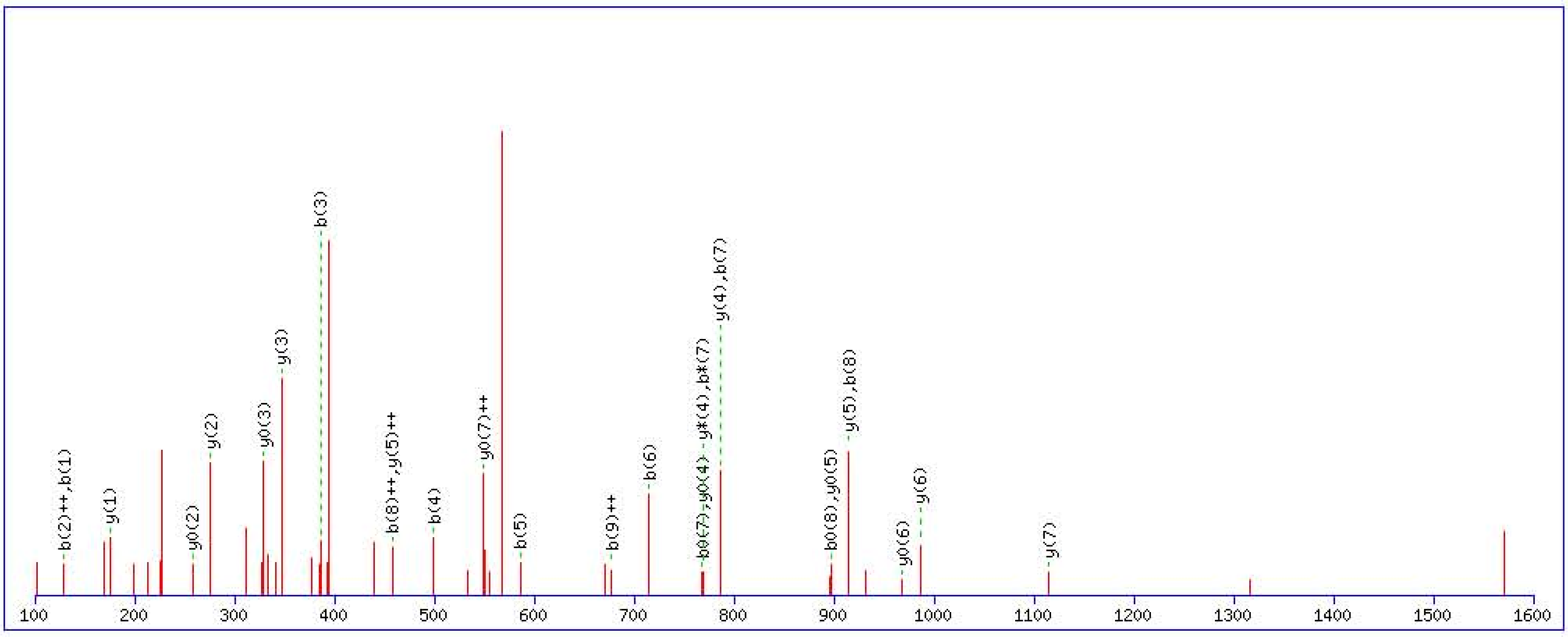
Mascot Search Results

Peptide View

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

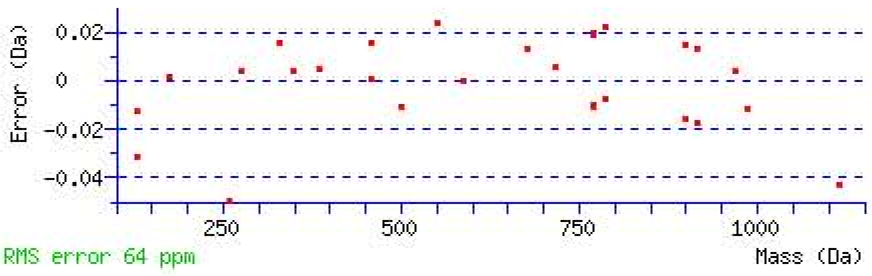
Match to Query 36417: 1699.852752 from(567.624860,3+) rtinseconds(1412) index(29685)
Title: Locus:1.1.1.3040.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

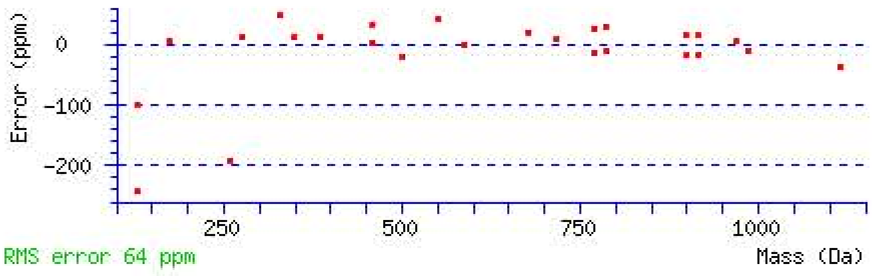
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1699.856277
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 41 **Expect:** 0.0025
Matches : 28/126 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							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
40.5	1699.856277	-0.003525	KQELSEAEQATR
14.0	1699.874039	-0.021287	KEISVNDLNESSIPR
7.7	1699.843063	0.009689	GKVSEGIDFVHHYGR
7.2	1699.856277	-0.003525	KQELSEAEQATR
5.7	1699.874924	-0.022172	SQGMLALSISPNR
5.7	1699.841705	0.011047	EKIDFADTVTKYDR
5.1	1699.845932	0.006820	QAMQEQLSK
4.4	1699.845932	0.006820	QAMQEQLSK
4.4	1699.838562	0.014190	EAPTQGLACVSTR
4.1	1699.848907	0.003845	TQATERVNSQPVNEK

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

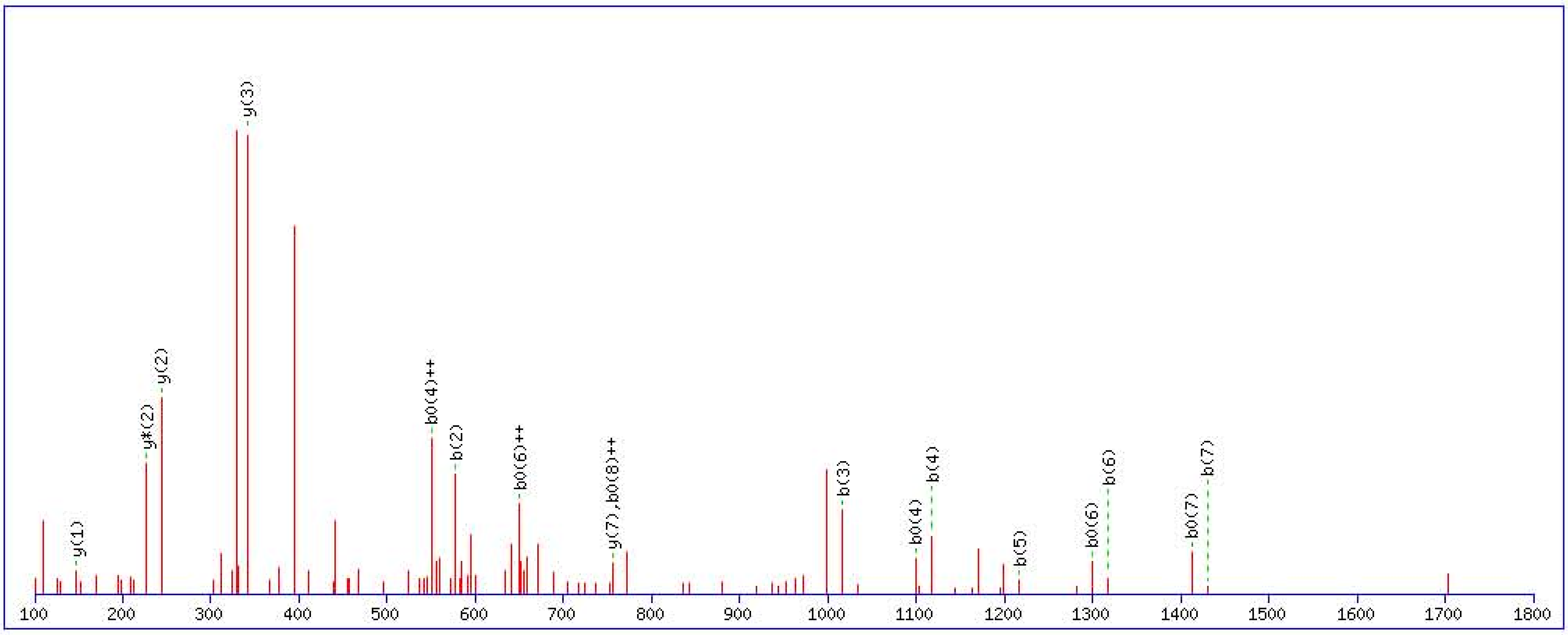
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

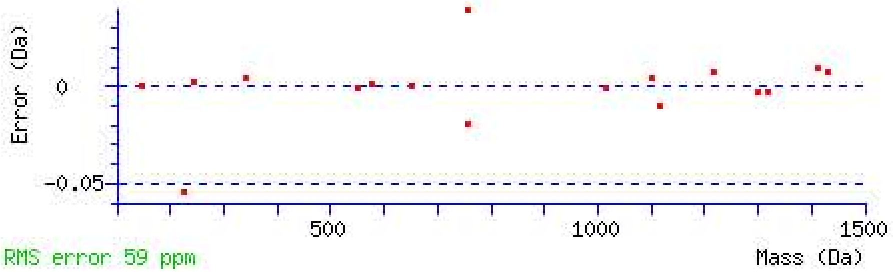
Match to Query 37956: 1769.969532 from(590.997120,3+) rtinseconds(1893) index(32360)
Title: Locus:1.1.1.3208.19 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

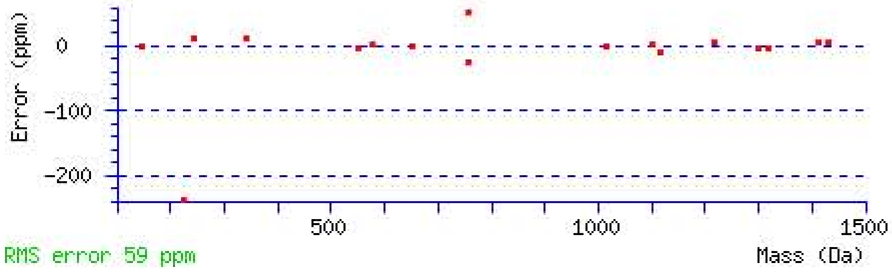
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 31  Expect: 0.0045
Matches : 17/92 fragment ions using 28 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
31.4	1769.968460	0.001072	HQQTVTIPPK
6.0	1769.961029	0.008503	WMLSRDRASTLPLPK
1.3	1769.978836	-0.009304	TPVRGEEPVFVVTGRK

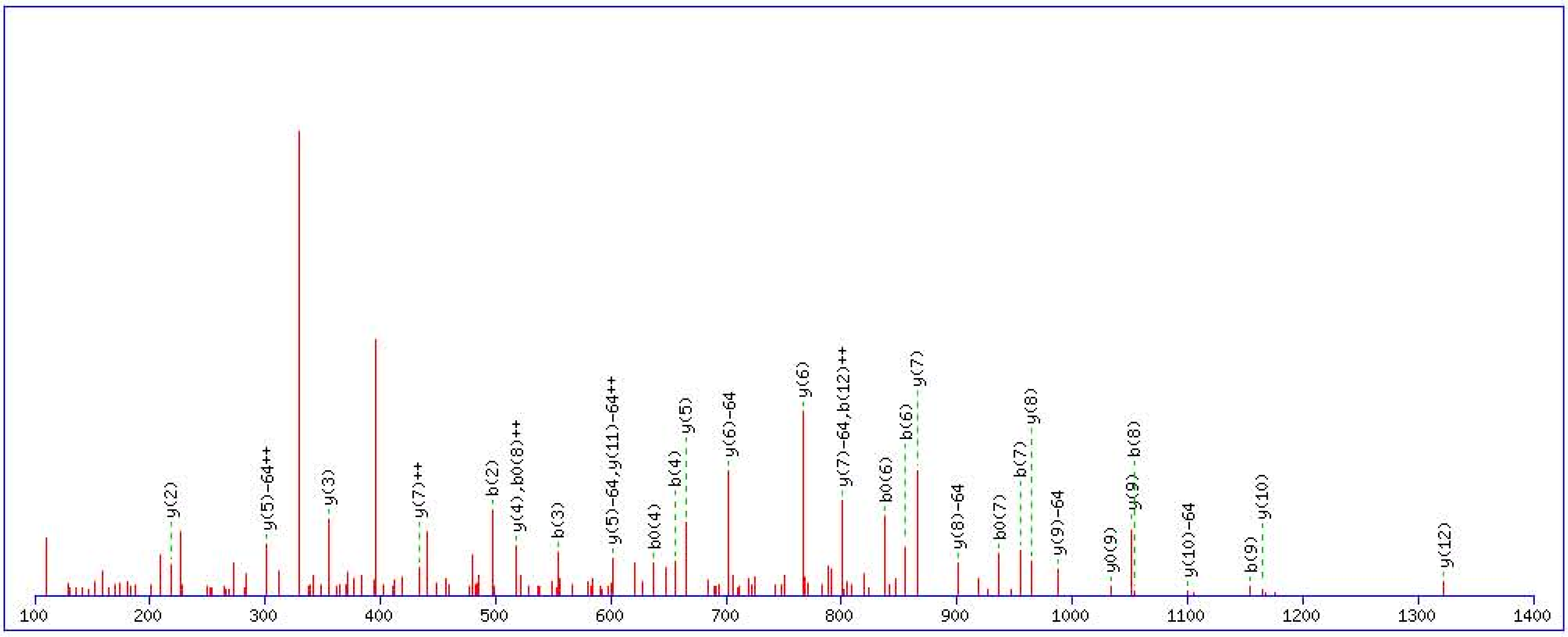
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

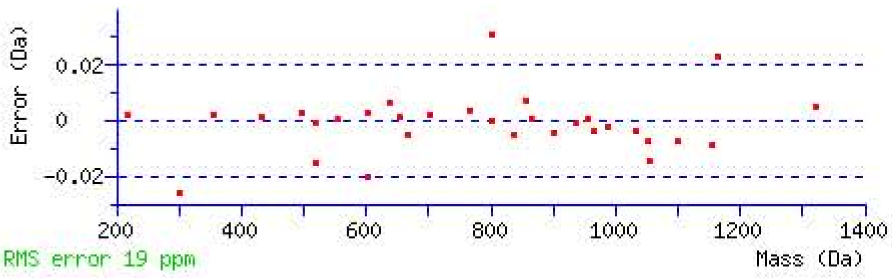
Match to Query 38886: 1817.919222 from(606.980350,3+) rtinseconds(1827) index(32042)
Title: Locus:1.1.1.3185.8 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

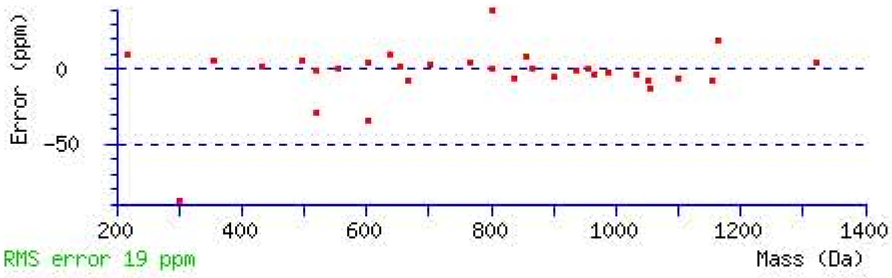
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 63  Expect: 1.7e-006
Matches : 32/214 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							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
63.2	1817.916824	0.002398	GQGTLSVVTMYHAK
1.8	1817.920181	-0.000959	QGGITAEVMMGILR

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

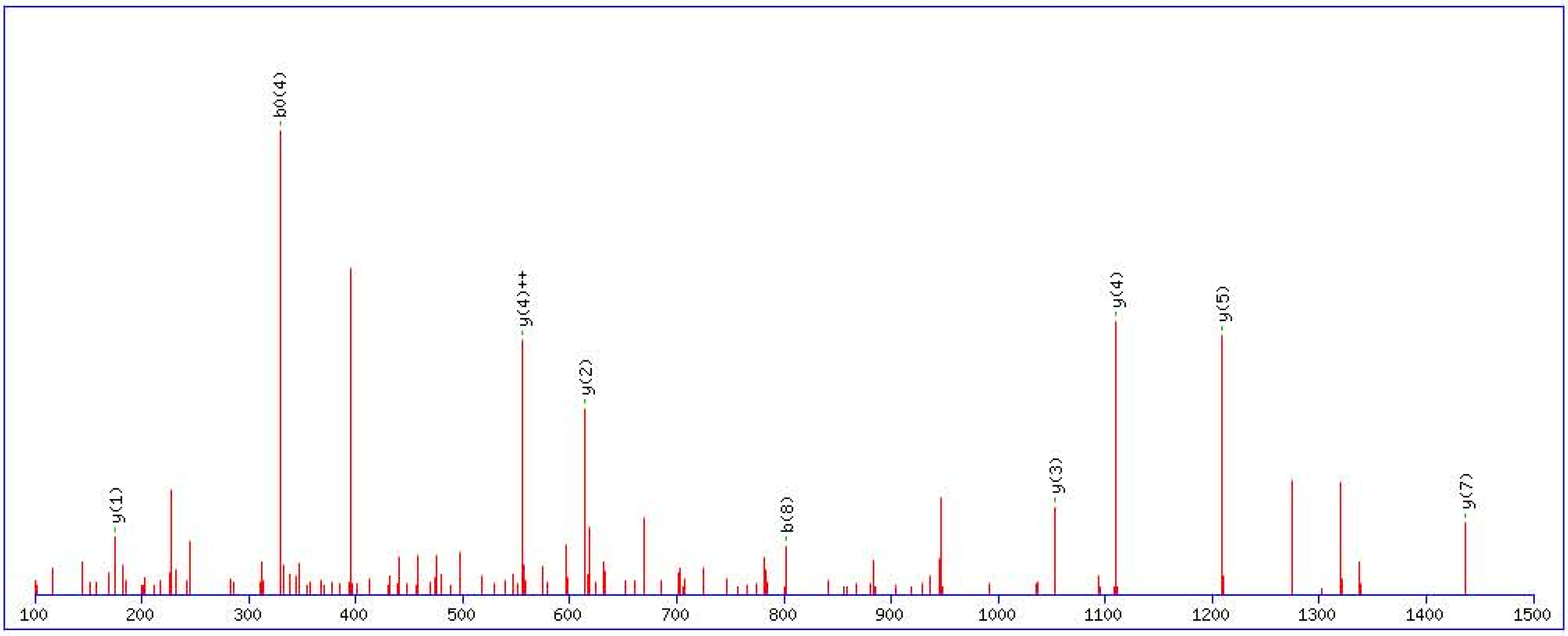
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

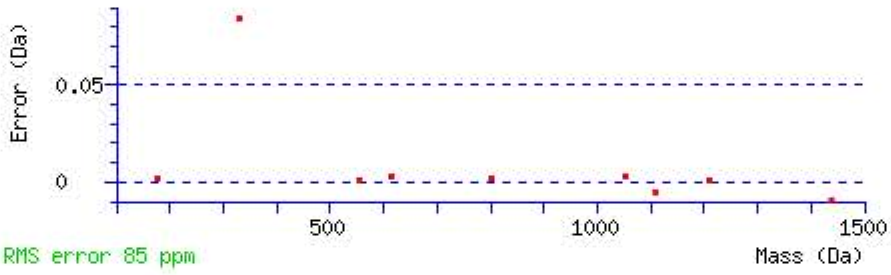
Match to Query 40432: 1910.938332 from(637.986720,3+) rtinseconds(1913) index(32514)
Title: Locus:1.1.1.3215.21 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

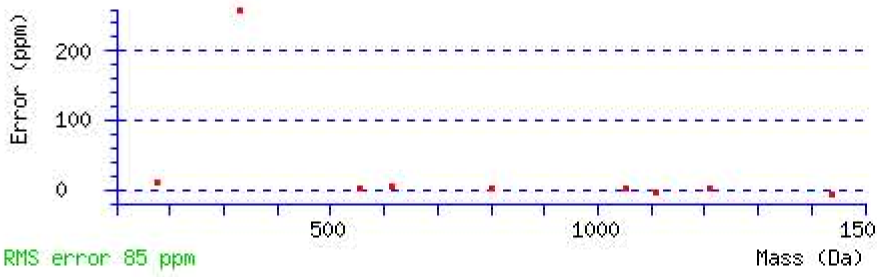
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 36  Expect: 0.0015
Matches : 9/106 fragment ions using 14 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	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
36.2	1910.934265	0.004067	SGSDEVQVGQQR
9.2	1910.934265	0.004067	SGSDEVQVGQQR
5.8	1910.958542	-0.020210	TDDYGRDLSSVQTLLTK
5.2	1910.934265	0.004067	SGSDEVQVGQQR
2.9	1910.960709	-0.022377	VGAPAWREAAQAMAR
0.8	1910.915619	0.022713	EDSGSGMKAELPPGPGAVGR

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

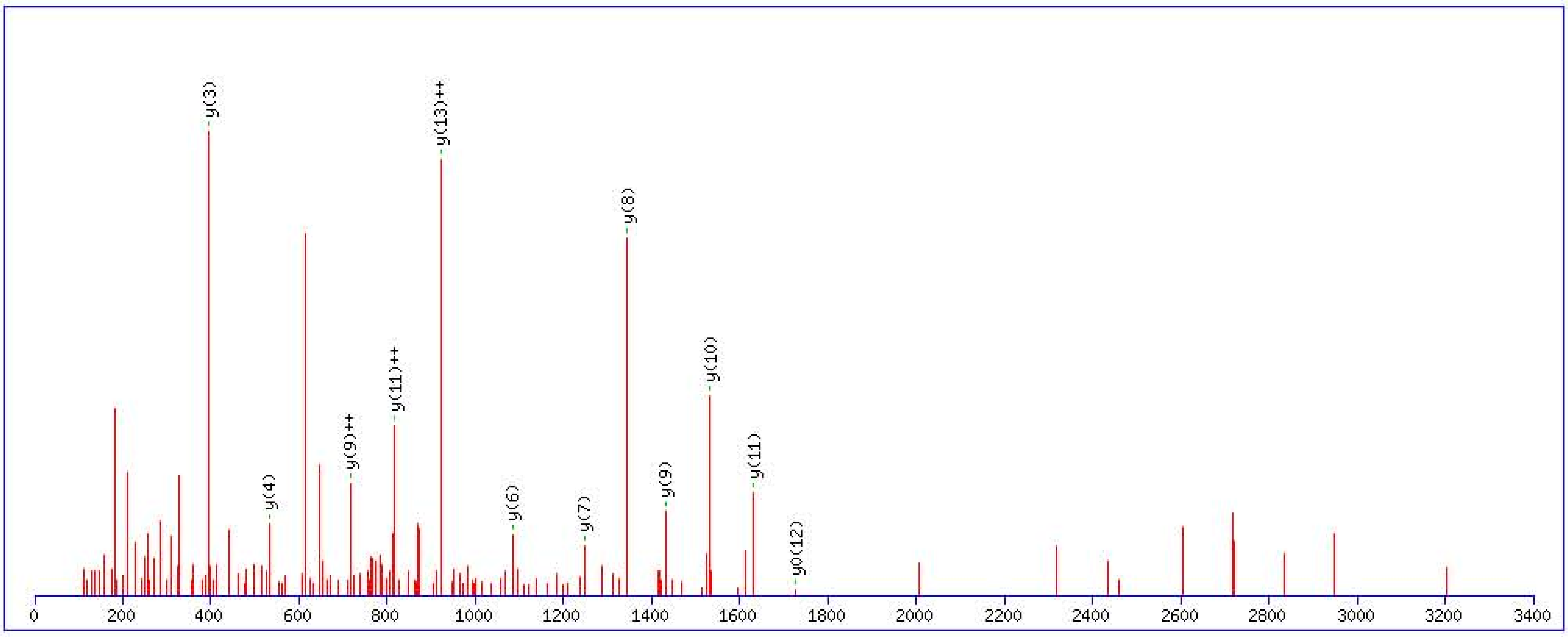
Mascot Search Results

Peptide View

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

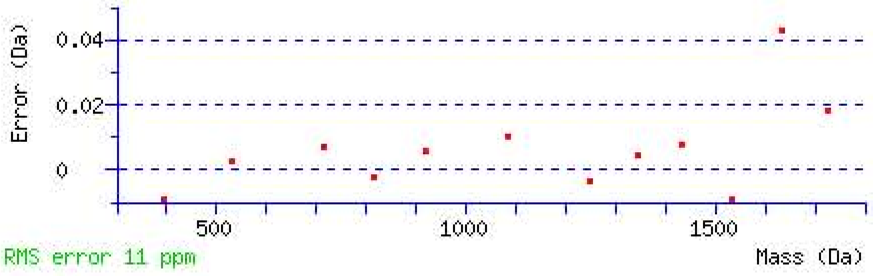
Match to Query 44435: 2098.137942 from(700.386590,3+) rtinseconds(2354) index(35027)
Title: Locus:1.1.1.3369.7 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

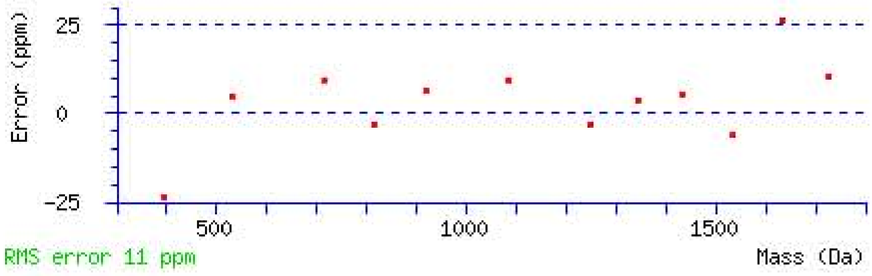
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2098.128525
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 53 **Expect:** 9.8e-005
Matches : 12/158 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							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
53.0	2098.128525	0.009417	SGIPIVTSPYQIHFTK

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

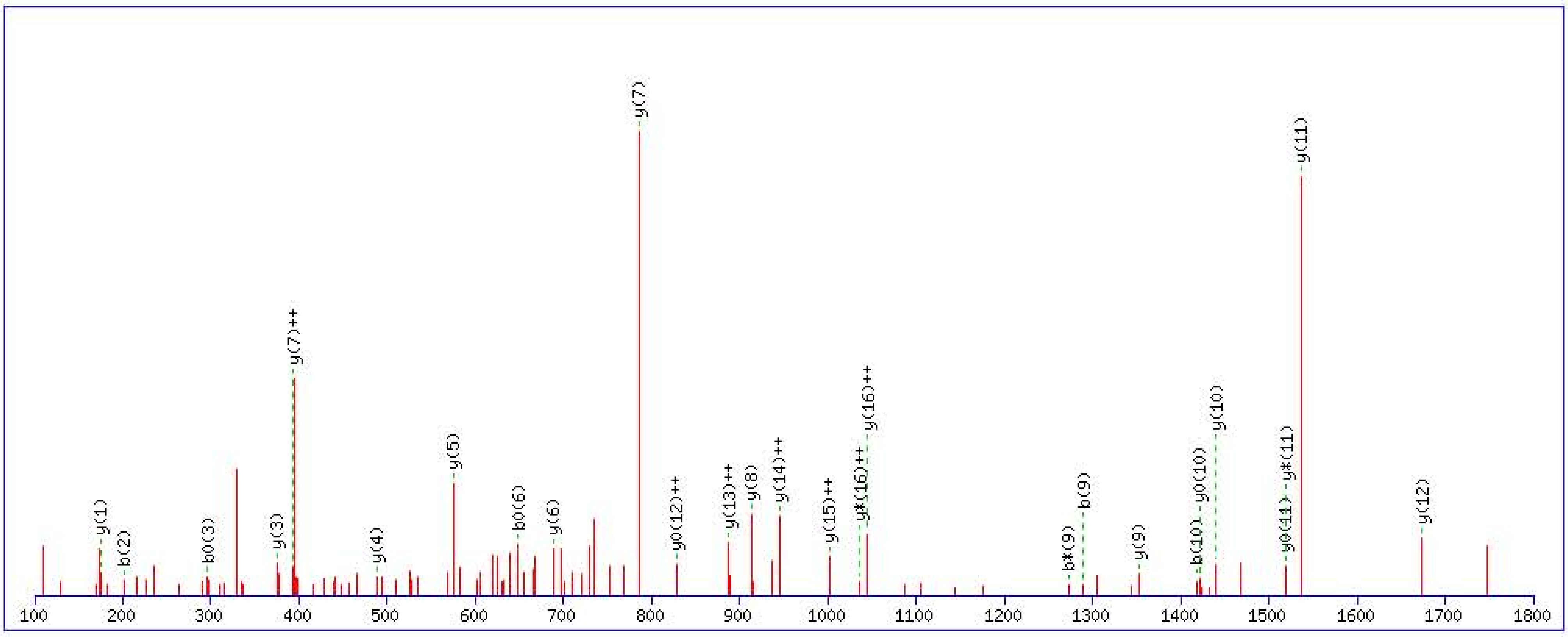
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

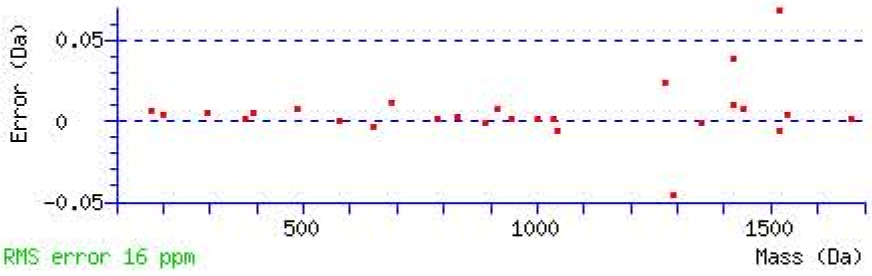
Match to Query 46022: 2201.238942 from(734.753590,3+) rtinseconds(1893) index(32366)
Title: Locus:1.1.1.3208.25 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

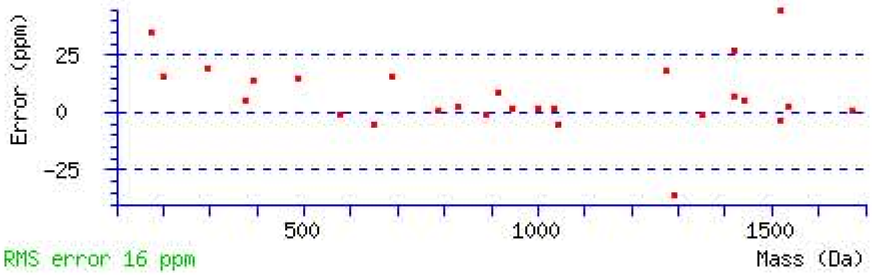
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2201.235428
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 1.7e-005
Matches : 27/180 fragment ions using 56 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							17
2	**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
57.0	2201.235428	0.003514	LSINTHPSQKPLSITVR

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

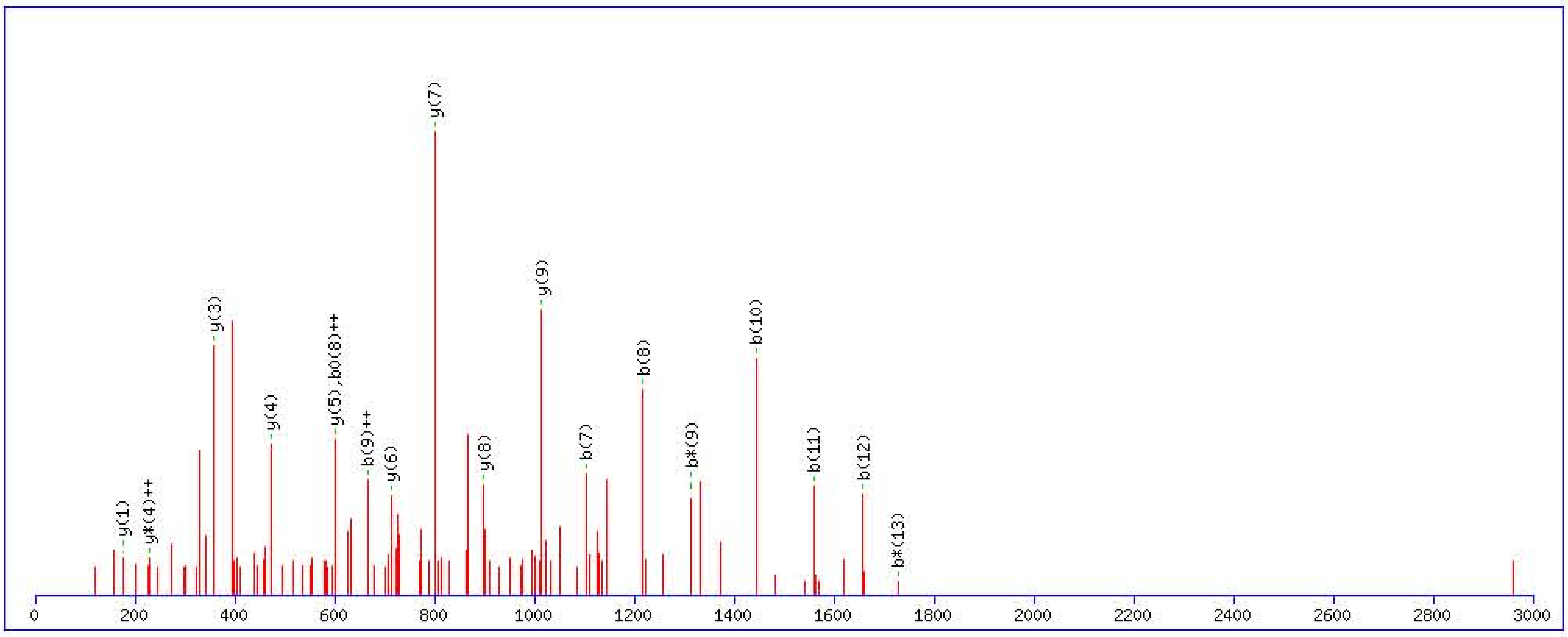
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

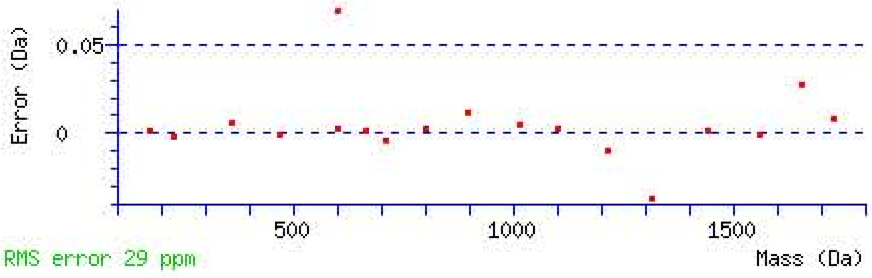
Match to Query 50048: 2457.244122 from(820.088650,3+) rtinseconds(2553) index(36060)
Title: Locus:1.1.1.3438.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

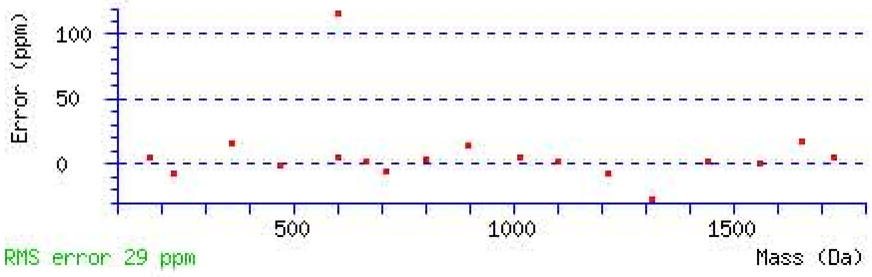
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2457.232193
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0047
Matches : 18/204 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	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
34.7	2457.232193	0.011929	DAPDHQELNLDVSLQLPSR
9.4	2457.243423	0.000699	TGLSDAFMILNPSPDVPESRRR
4.5	2457.278442	-0.034320	EPVSNSVTAEGMEALTKILAELR
0.5	2457.244080	0.000042	AKFHQTEGDHLTLLAVYNSWK

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

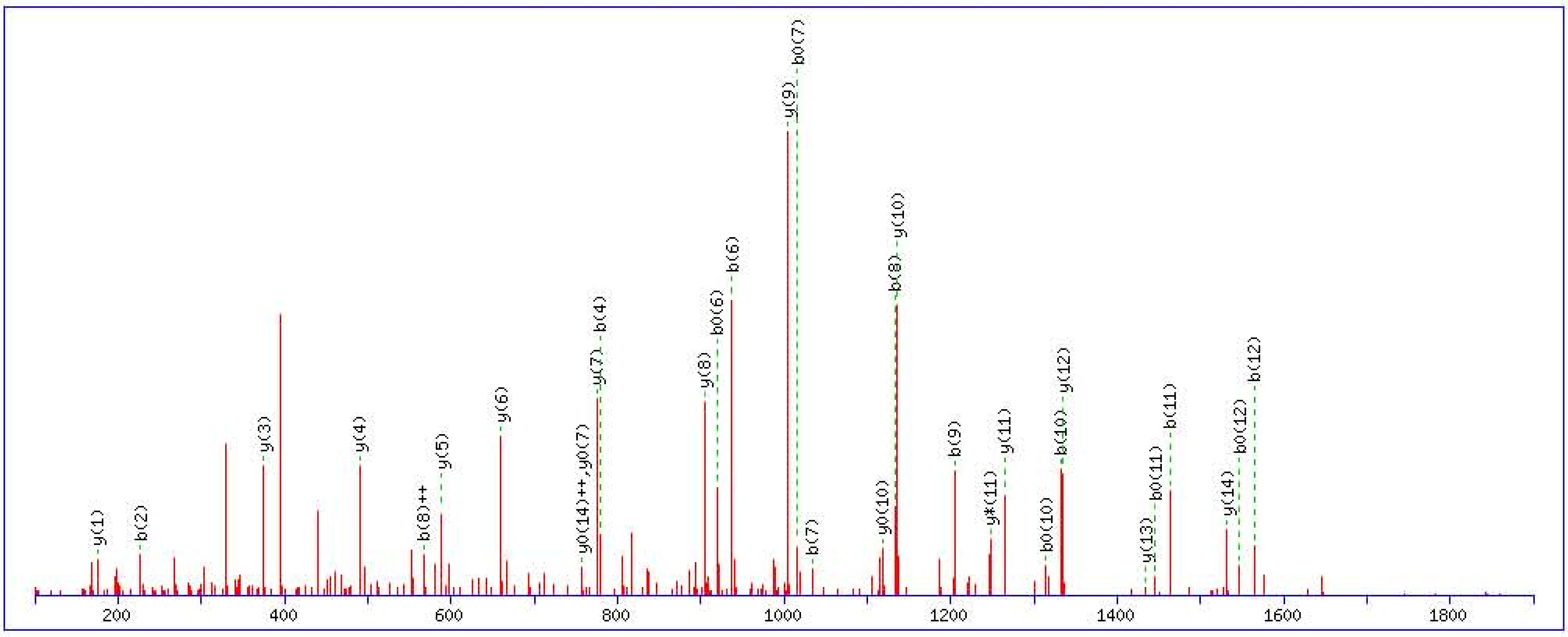
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

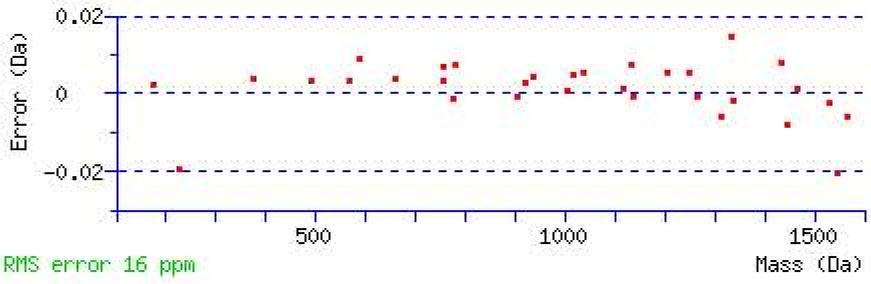
Match to Query 50261: 2467.253922 from(823.425250,3+) rtinseconds(2676) index(36685)
Title: Locus:1.1.1.3480.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

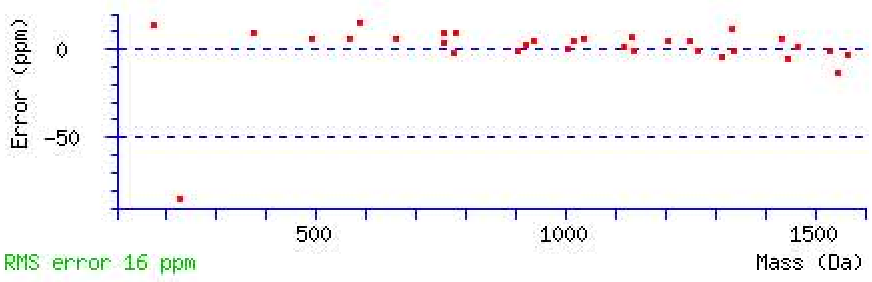
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 78 **Expect:** 4.8e-007
Matches : 32/210 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	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
78.0	2467.245071	0.008851	ILLQGTPVAQMTEDAVDAER
72.5	2467.245071	0.008851	ILLQGTPVAQMTEDAVDAER

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

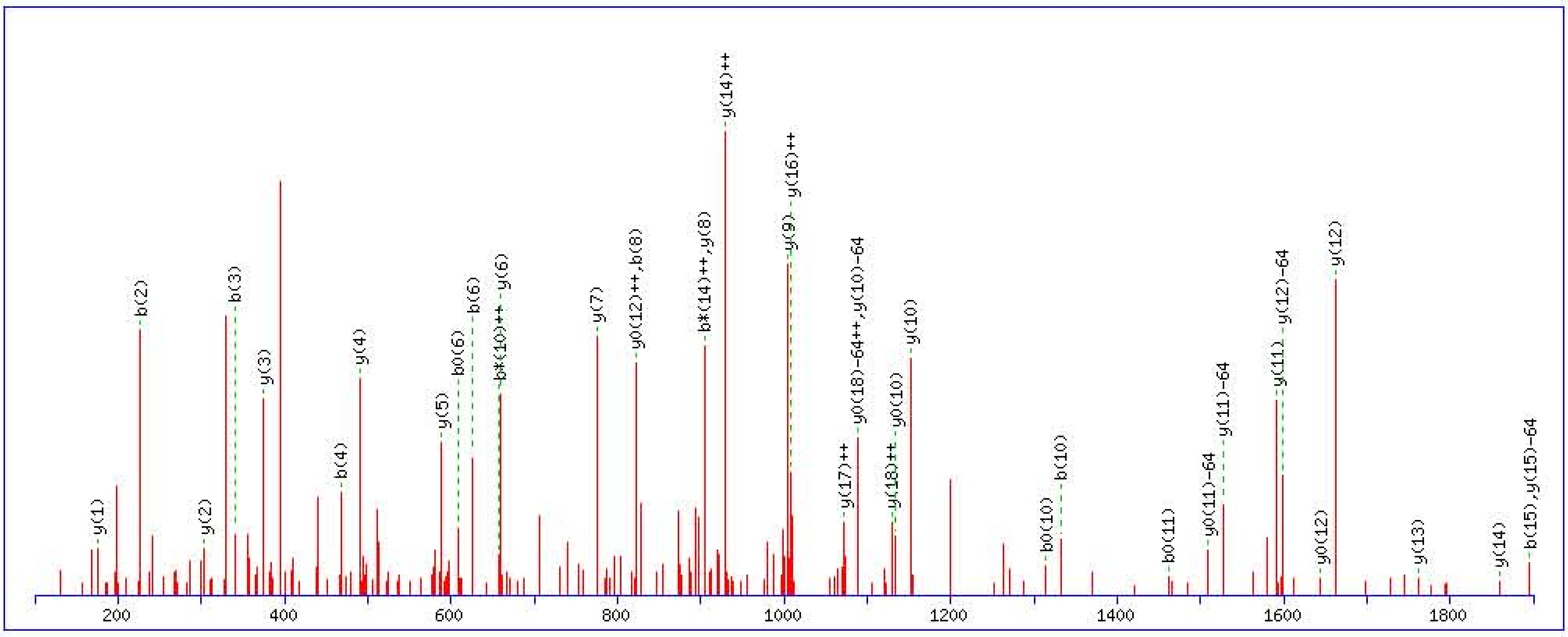
Mascot Search Results

Peptide View

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

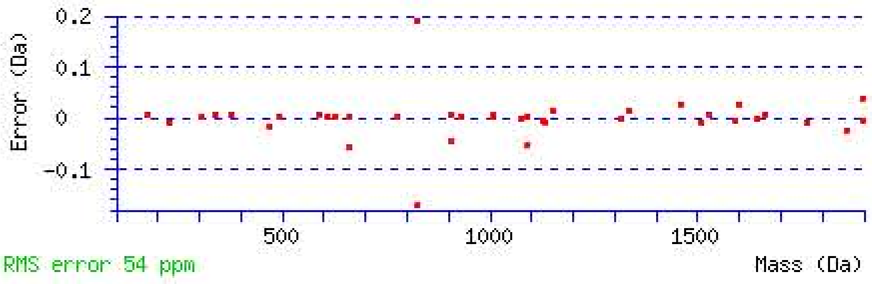
Match to Query 50662: 2483.248182 from(828.756670,3+) rtinseconds(2249) index(34600)
Title: Locus:1.1.1.3332.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

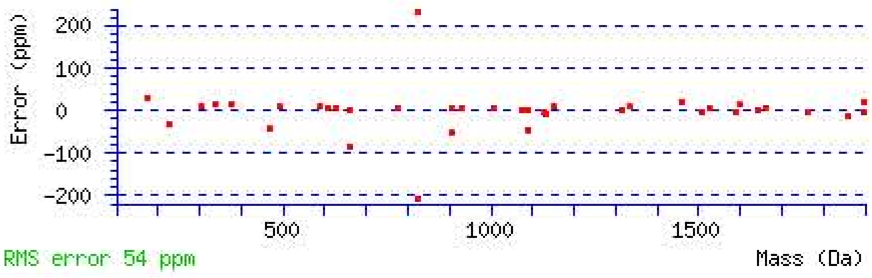
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2483.239990
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
M11 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 95 **Expect:** 9e-009
Matches : 39/324 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	114.091340	57.549308					I							20
2	**227.175404**	114.091340					L	2371.163212	1186.085244	2354.136663	1177.571969	2353.152647	1177.079961	19
3	**340.259468**	170.633372					L	2258.079148	1129.543212	2241.052599	1121.029938	2240.068583	1120.537930	18
4	**468.318046**	234.662661	451.291497	226.149386			Q	2144.995084	1073.001180	2127.968535	1064.487905	2126.984519	1063.995898	17
5	525.339510	263.173393	508.312961	254.660119			G	2016.936506	1008.971891	1999.909957	1000.458617	1998.925941	999.966609	16
6	**626.387189**	313.697233	609.360640	305.183958	608.376624	304.691950	T	1959.915042	980.461159	1942.888493	971.947885	1941.904477	971.455877	15
7	723.439953	362.223615	706.413404	353.710340	705.429388	353.218332	P	***1858.867363***	929.937320	1841.840814	921.424045	1840.856798	920.932037	14
8	**822.508367**	411.757822	805.481818	403.244547	804.497802	402.752539	V	***1761.814599***	881.410938	1744.788050	872.897663	1743.804034	872.405655	13
9	893.545481	447.276379	876.518932	438.763104	875.534916	438.271096	A	***1662.746185***	831.876731	1645.719636	823.363456	1644.735620	822.871448	12
10	**1332.770807**	666.889042	1315.744258	658.375767	1314.760242	657.883759	Q	***1591.709071***	796.358174	1574.682522	787.844899	1573.698506	787.352891	11
11	1479.806207	740.406742	1462.779658	731.893467	1461.795642	731.401459	M	***1152.483745***	576.745511	1135.457196	568.232236	1134.473180	567.740228	10
12	1580.853886	790.930581	1563.827337	782.417307	1562.843321	781.925299	T	***1005.448345***	503.227811	988.421796	494.714536	987.437780	494.222528	9
13	1709.896479	855.451878	1692.869930	846.938603	1691.885914	846.446595	E	***904.400666***	452.703971	887.374117	444.190697	886.390101	443.698689	8
14	1824.923422	912.965349	1807.896873	904.452075	1806.912857	903.960067	D	***775.358073***	388.182675	758.331524	379.669400	757.347508	379.177392	7
15	**1895.960536**	948.483906	1878.933987	939.970632	1877.949971	939.478624	A	***660.331130***	330.669203	643.304581	322.155929	642.320565	321.663921	6
16	1995.028950	998.018113	1978.002401	989.504839	1977.018385	989.012831	V	***589.294016***	295.150646	572.267467	286.637372	571.283451	286.145364	5
17	2110.055893	1055.531585	2093.029344	1047.018310	2092.045328	1046.526302	D	***490.225602***	245.616439	473.199053	237.103165	472.215037	236.611157	4
18	2181.093007	1091.050142	2164.066458	1082.536867	2163.082442	1082.044859	A	***375.198659***	188.102968	358.172110	179.589693	357.188094	179.097685	3
19	2310.135600	1155.571438	2293.109051	1147.058164	2292.125035	1146.566156	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
95.2	2483.239990	0.008192	ILLQGTPVAQMTEDAVDAER
37.4	2483.239990	0.008192	ILLQGTPVAQMTEDAVDAER

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

{MATRIX SCIENCE}

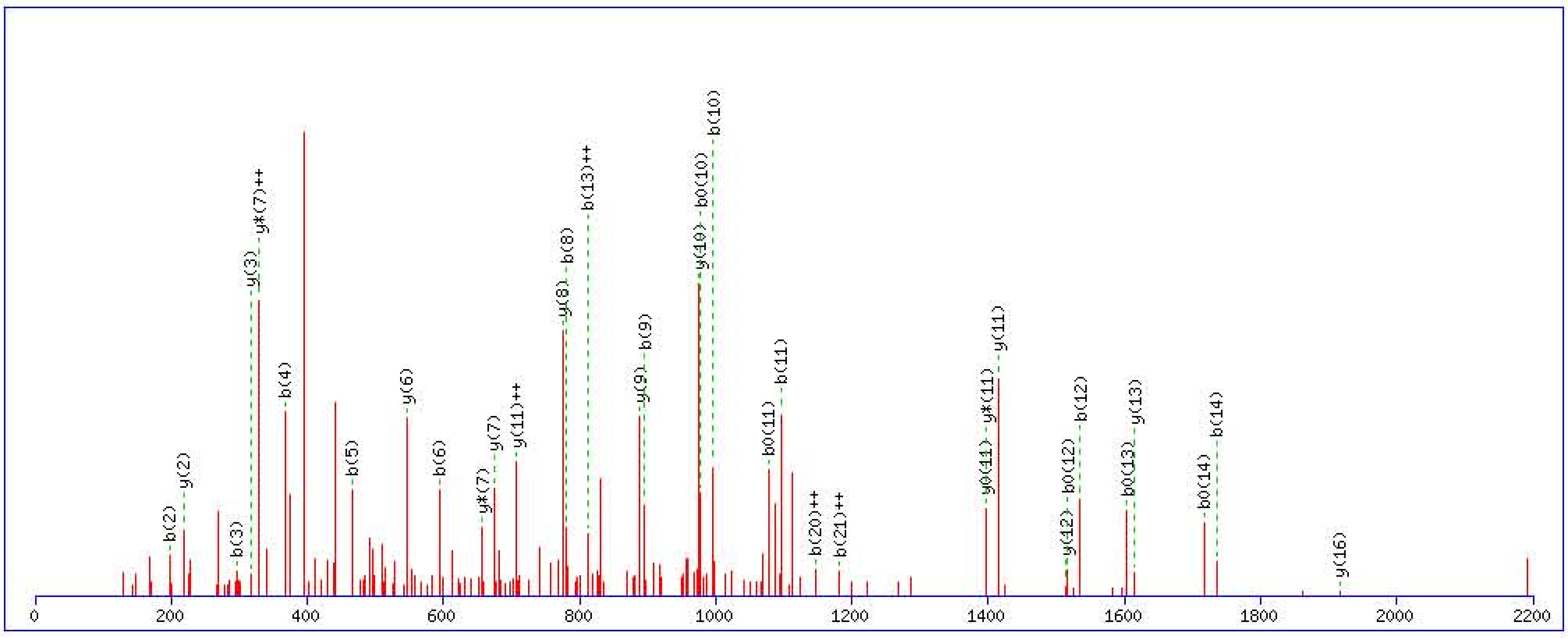
Mascot Search Results

Peptide View

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

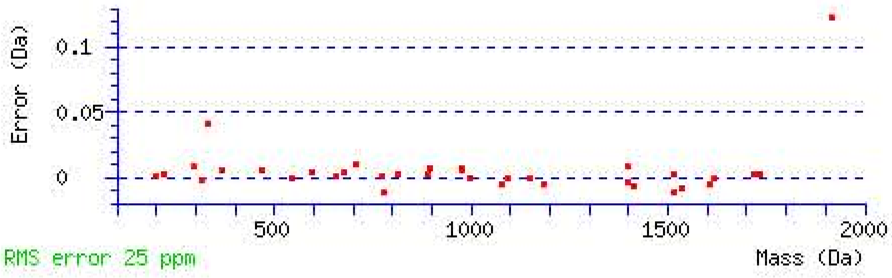
Match to Query 51297: 2508.298212 from(837.106680,3+) rtinseconds(2241) index(34556)
Title: Locus:1.1.1.3329.24 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

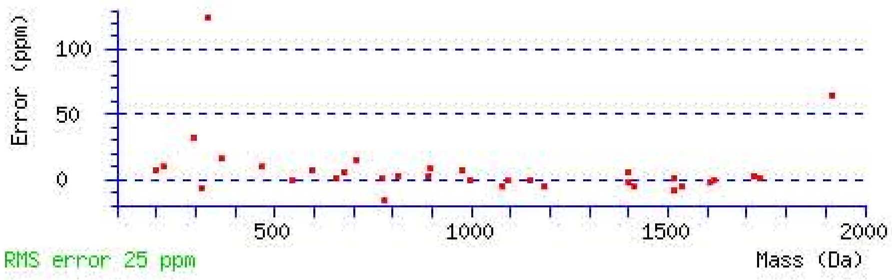
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2508.289429
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 93 **Expect:** 1.5e-008
Matches : 35/220 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							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
92.5	2508.289429	0.008783	VPVAVQGEDTVQSLTQGDGVAK
76.1	2508.289429	0.008783	VPVAVQGEDTVQSLTQGDGVAK
29.6	2508.289429	0.008783	VPVAVQGEDTVQSLTQGDGVAK

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

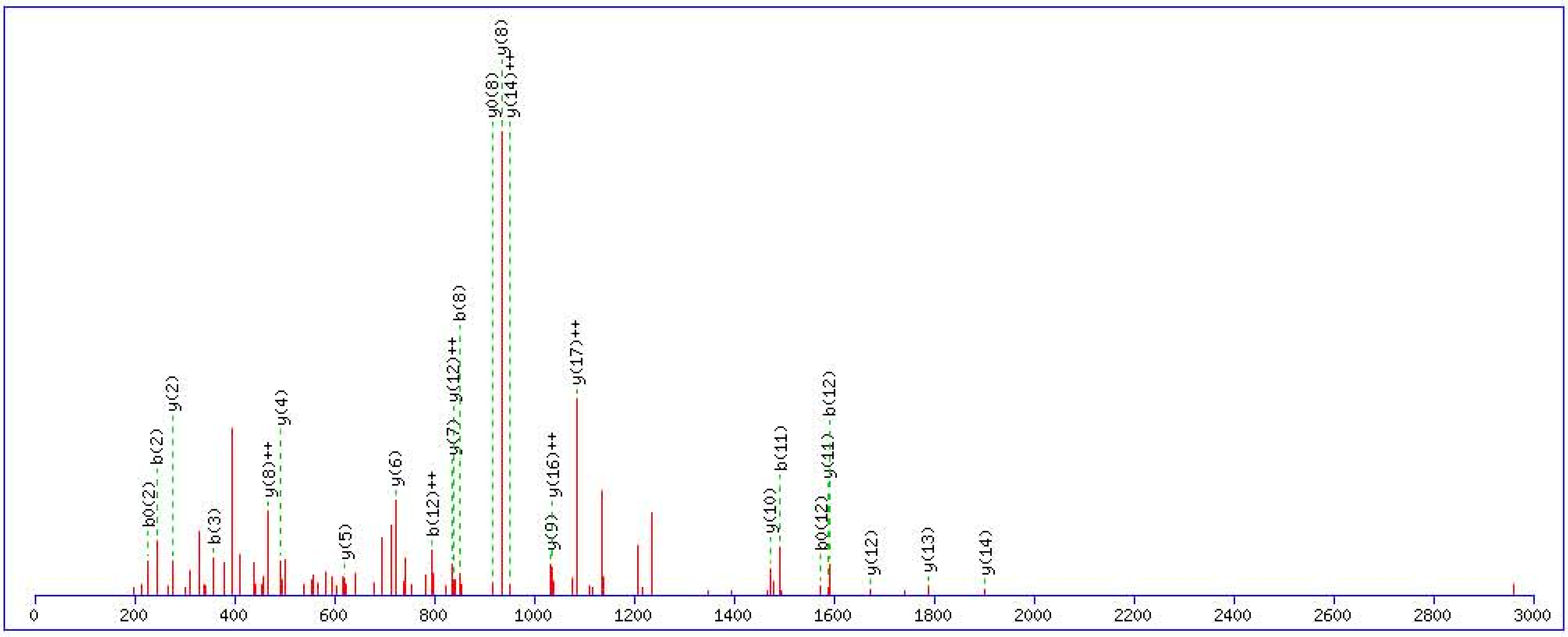
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

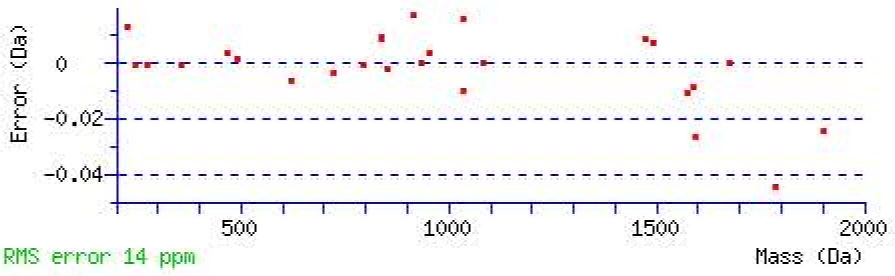
Match to Query 51476: 2524.172172 from(842.398000,3+) rtinseconds(2120) index(33831)
Title: Locus:1.1.1.3287.17 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

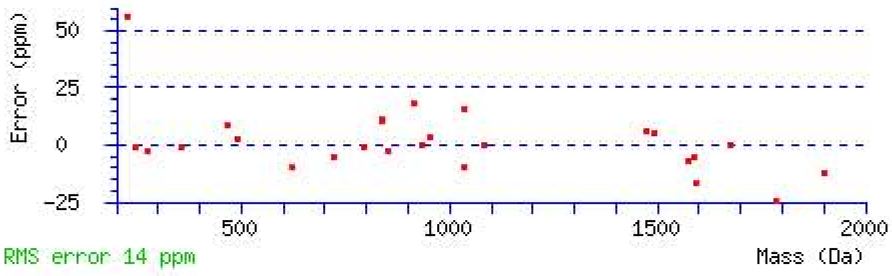
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2524.163910
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 4.9e-005
Matches : 26/206 fragment ions using 58 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							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
54.4	2524.163910	0.008262	EDIPPADLSDQVPDTESETR

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

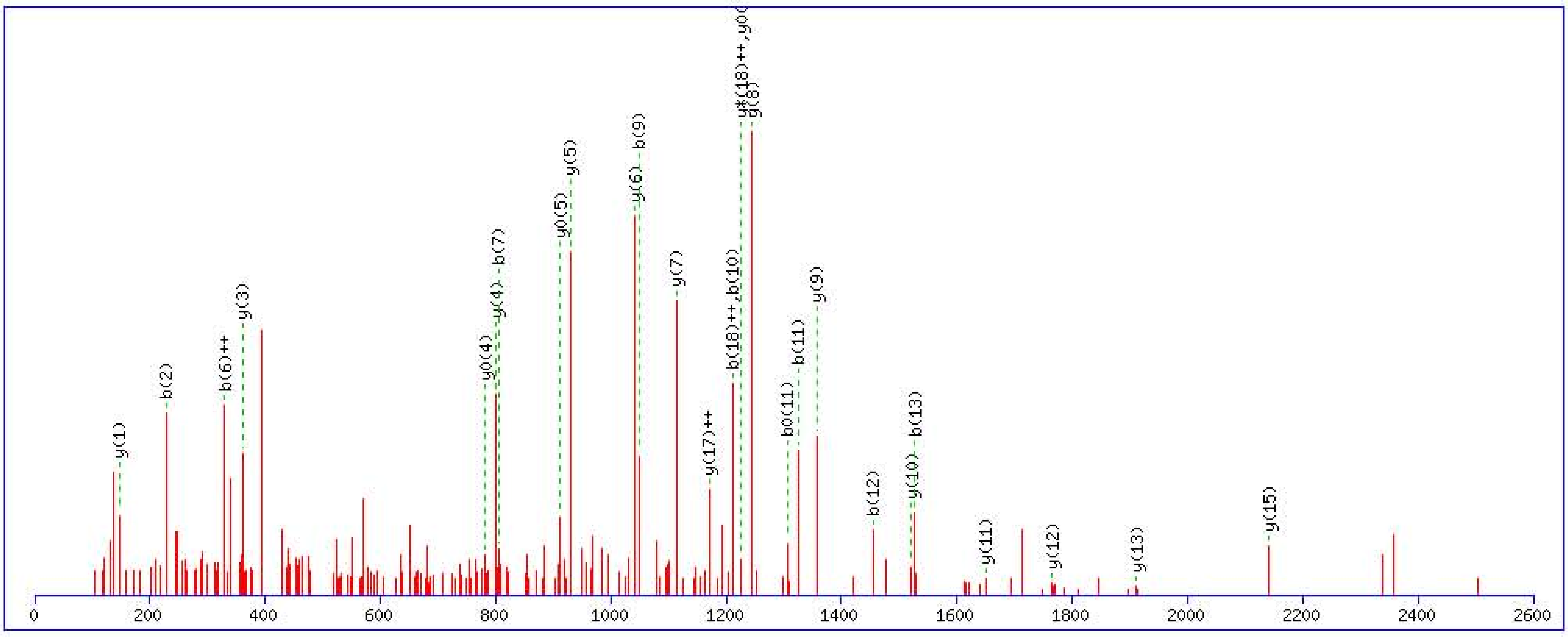
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

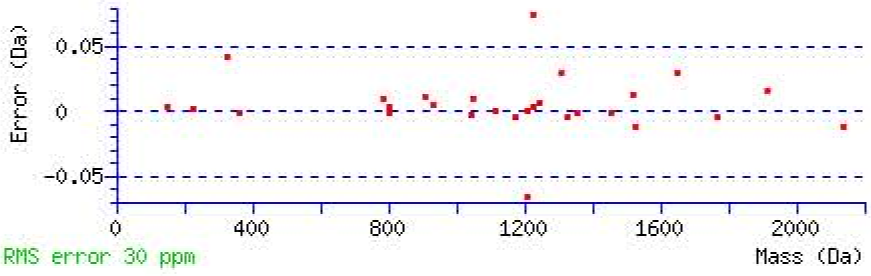
Match to Query 51790: 2567.270292 from(856.764040,3+) rtinseconds(3270) index(40352)
Title: Locus:1.1.1.3682.17 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

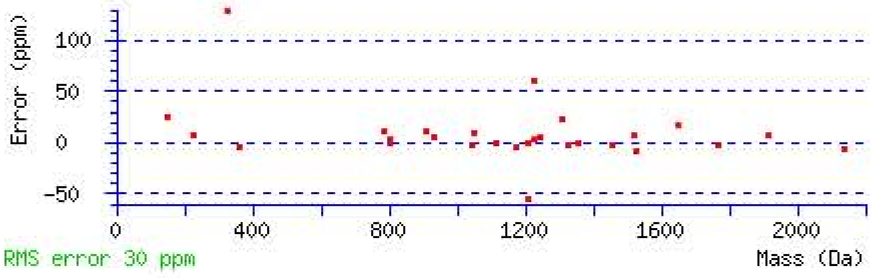
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2567.265121
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16 : Biotin:Thermo-21345 (Q)
Ions Score: 59 **Expect:** 3.1e-005
Matches : 28/204 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	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
59.4	2567.265121	0.005171	VQLSNDFDEYIMAIEQTIK

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

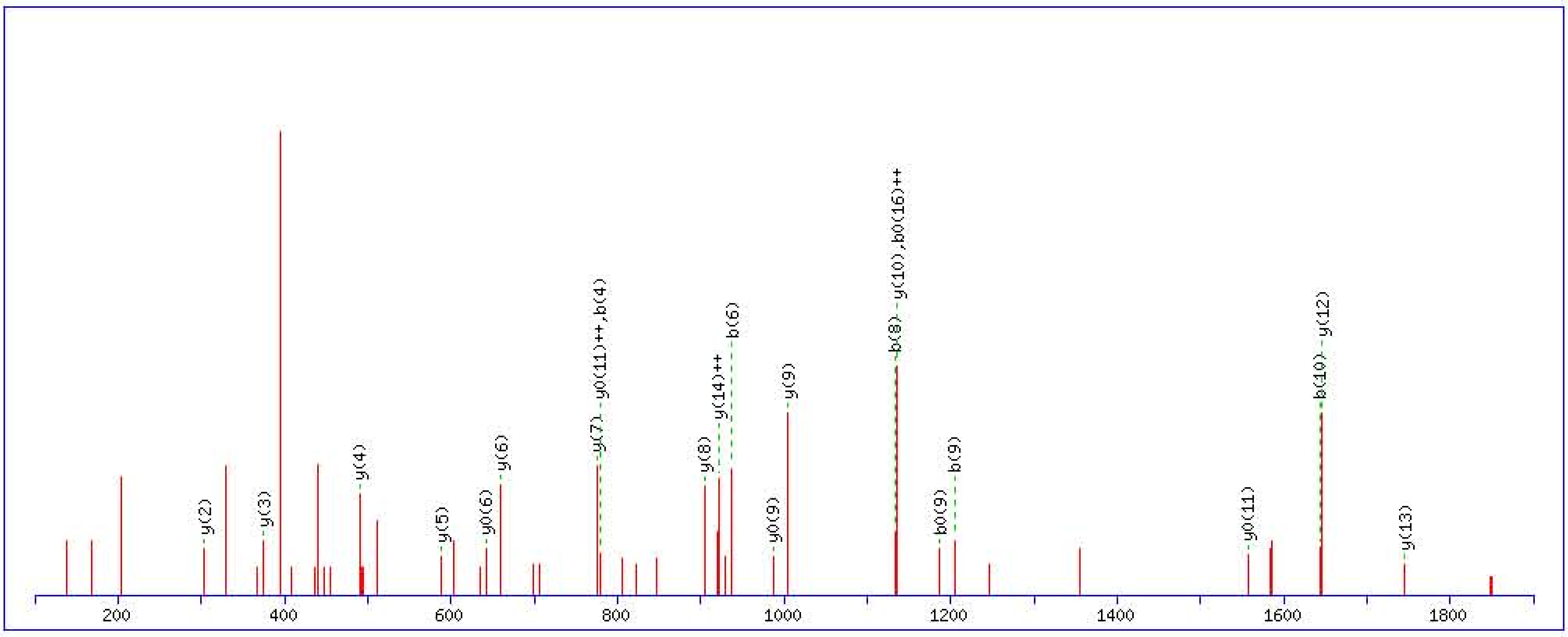
Mascot Search Results

Peptide View

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

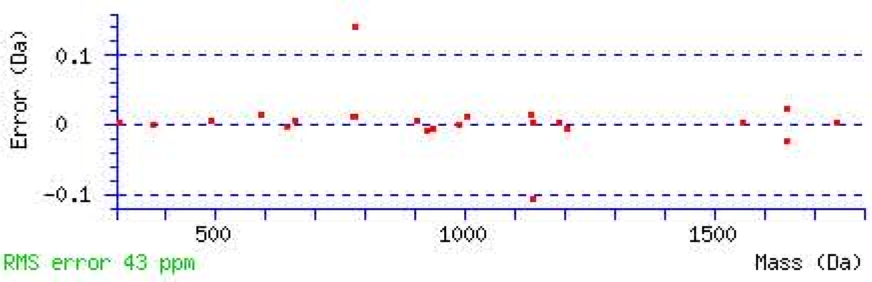
Match to Query 53528: 2778.426912 from(927.149580,3+) rtinseconds(2787) index(37575)
Title: Locus:1.1.1.3518.21 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

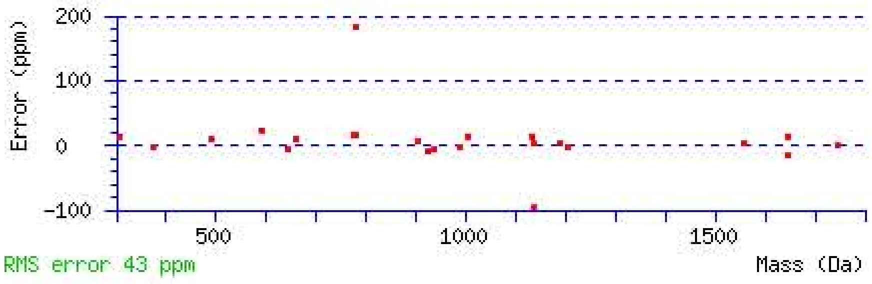
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 56  Expect: 5.5e-006
Matches : 23/210 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
56.2	2778.411819	0.015093	ILLQGTPVAQMTEDAVDAER
0.1	2778.401016	0.025896	AFAAALDERSTLLDMSSIFHQKAEK

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

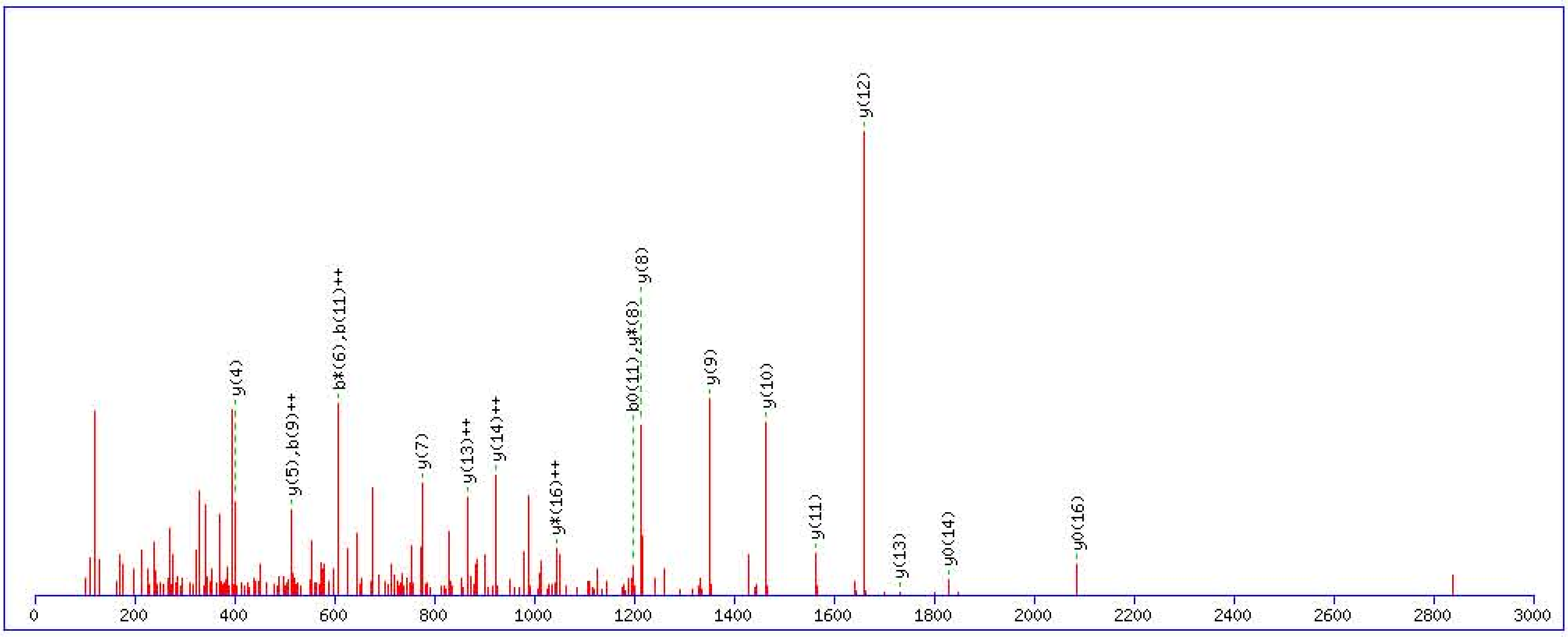
Mascot Search Results

Peptide View

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

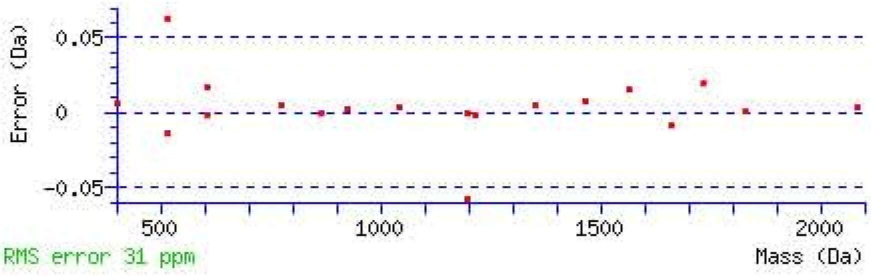
Match to Query 55022: 2874.461456 from(719.622640,4+) rtinseconds(2243) index(34571)
Title: Locus:1.1.1.3330.14 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

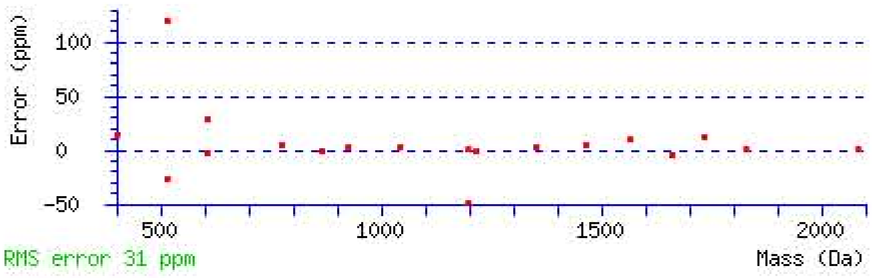
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 64  Expect: 1.2e-005
Matches : 19/246 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	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
64.0	2874.452057	0.009399	QKPDGVFQEDAPVIHQEMIGGLR

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

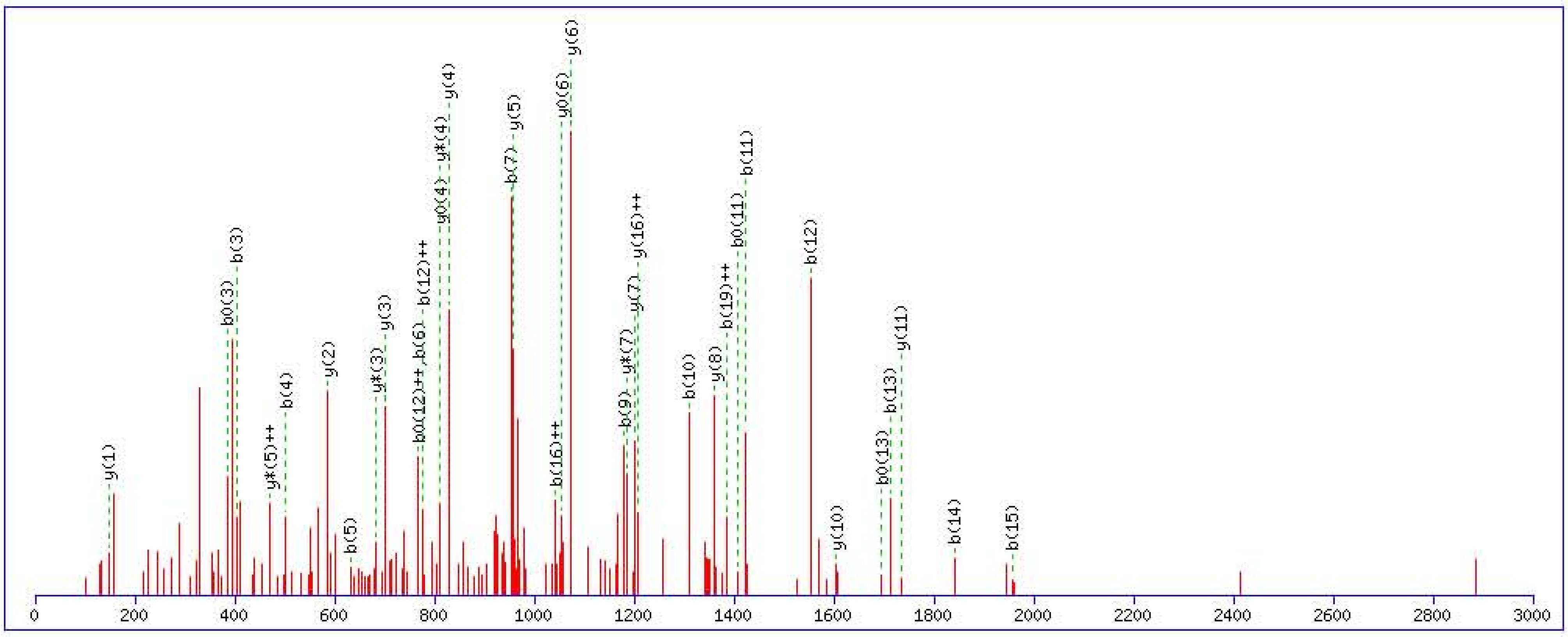
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

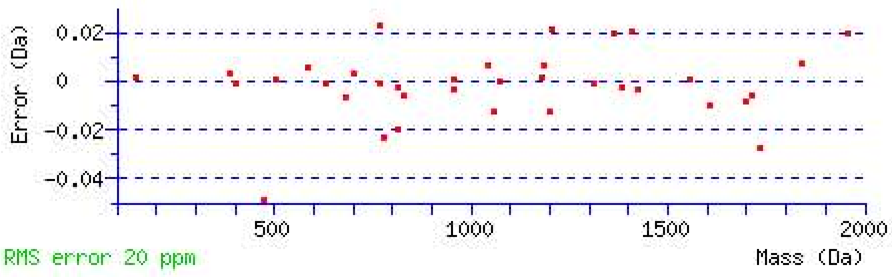
Match to Query 55332: 2913.194022 from(972.071950,3+) rtinseconds(2120) index(33832)
Title: Locus:1.1.1.3287.18 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

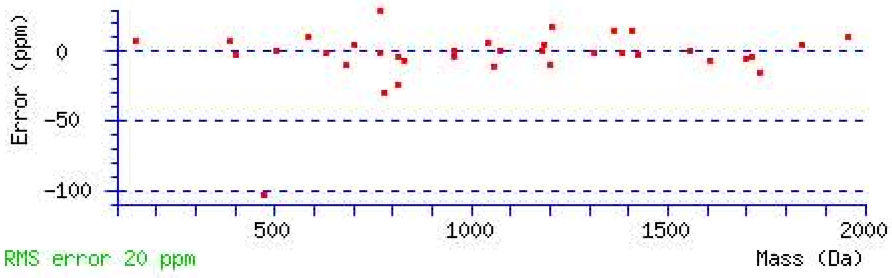
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2913.185776
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q19    : Biotin:Thermo-21345 (Q)
Ions Score: 73  Expect: 6.2e-008
Matches : 36/196 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	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





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
73.0	2913.185776	0.008246	DTWVEHWPEEDECQDEENQK
35.1	2913.185776	0.008246	DTWVEHWPEEDECQDEENQK

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

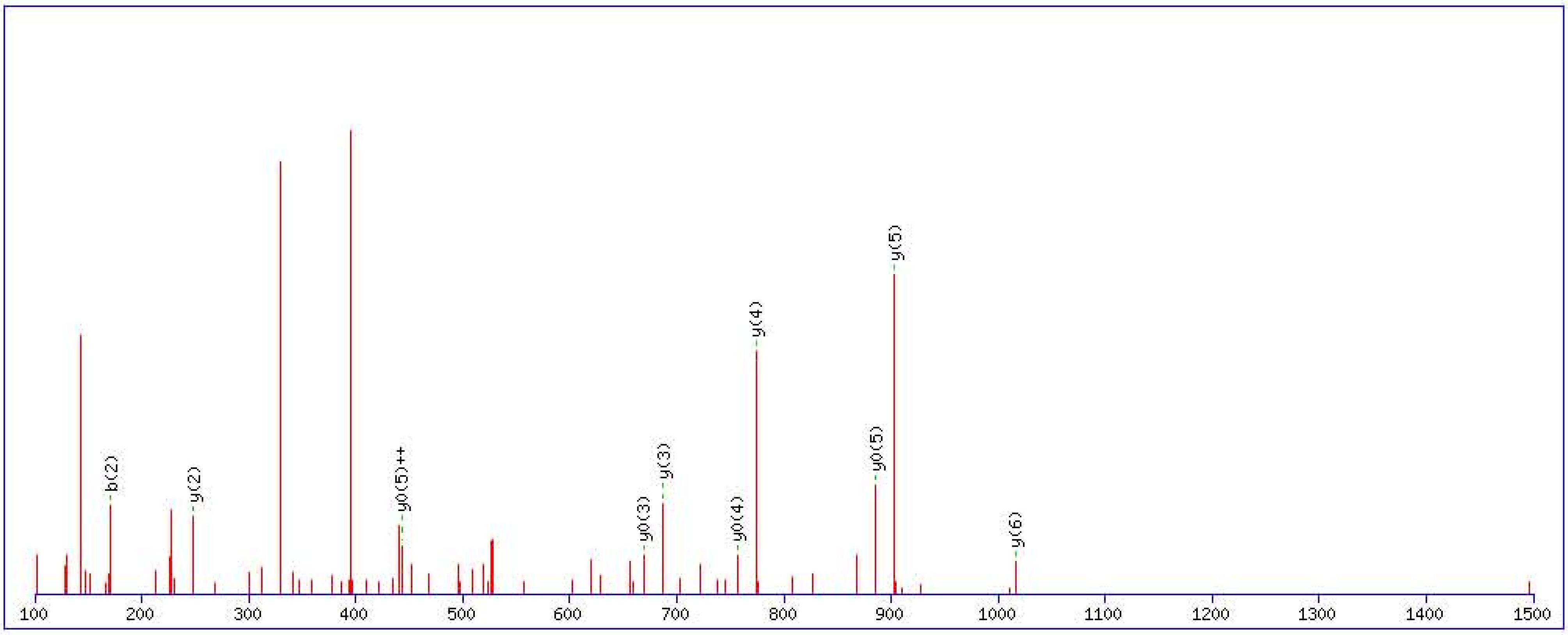
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

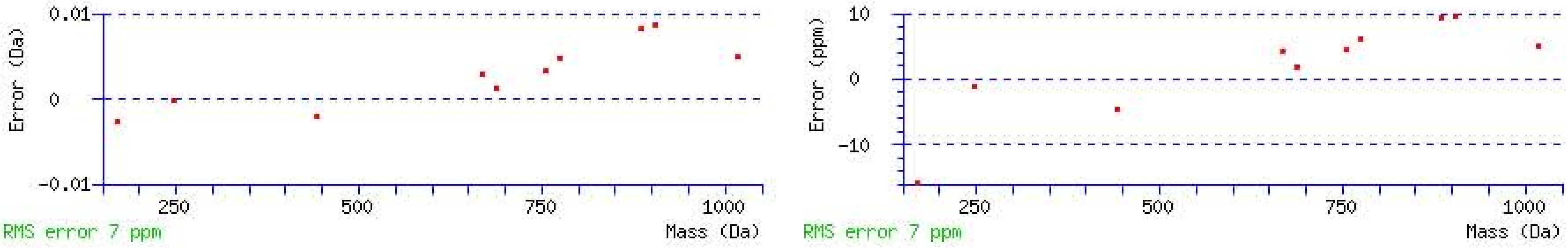
Match to Query 15590: 1072.557228 from(537.285890,2+) rtinseconds(1461) index(43956)
Title: Locus:1.1.1.2557.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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): 1072.558670
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.06
Matches : 10/58 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	58.028740	29.518008					G							7
2	171.112804	86.060040					L	***1016.544494***	508.775885	999.517945	500.262611	998.533929	499.770603	6
3	300.155397	150.581336			282.144832	141.576054	E	***903.460430***	452.233853	886.433881	443.720579	885.449865	443.228571	5
4	387.187425	194.097351			369.176860	185.092068	S	***774.417837***	387.712557	757.391288	379.199282	756.407272	378.707274	4
5	826.412751	413.710014	809.386202	405.196739	808.402186	404.704731	Q	***687.385809***	344.196543	670.359260	335.683268	669.375244	335.191260	3
6	927.460430	464.233853	910.433881	455.720579	909.449865	455.228571	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
7							K	147.112804	74.060040	130.086255	65.546765			1



NCBI **BLAST** search of GLESQTK
(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	1072.558670	-0.001442	GLESQTK
11.8	1072.558670	-0.001442	LGECPAVLSK
7.5	1072.558670	-0.001442	QSEGLTK
7.2	1072.551254	0.005974	KEAPRDETK
1.9	1072.551285	0.005943	GPRTTEPSTK
0.9	1072.566544	-0.009316	NHSLAFVGTK

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

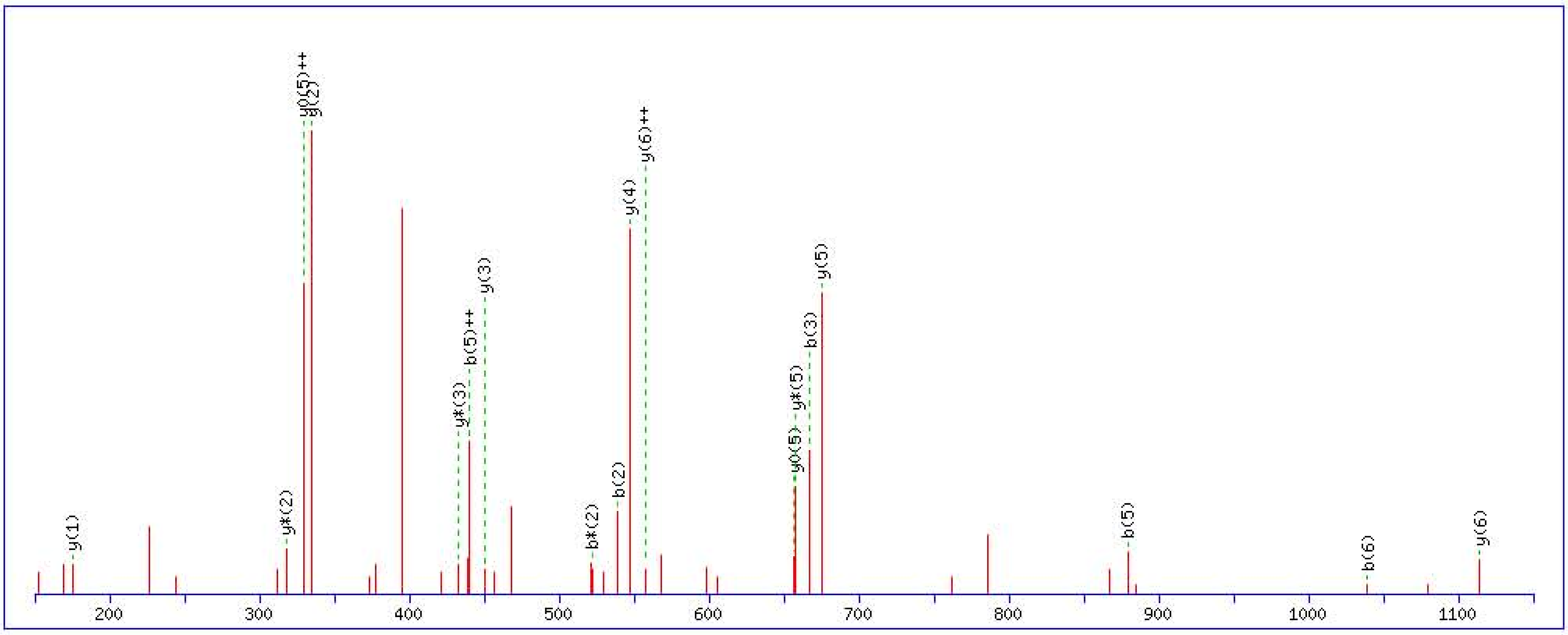
Mascot Search Results

Peptide View

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

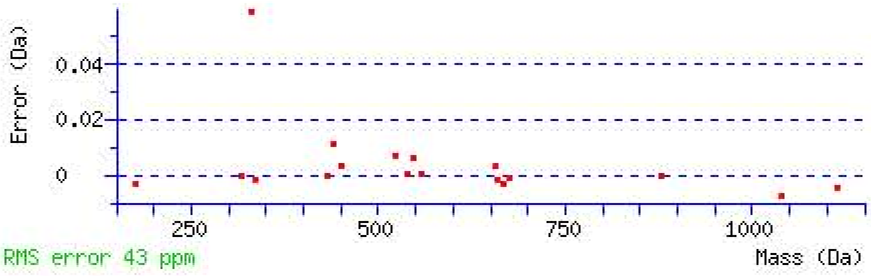
Match to Query 20591: 1212.574308 from(607.294430,2+) rtinseconds(1290) index(42994)
Title: Locus:1.1.1.2497.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

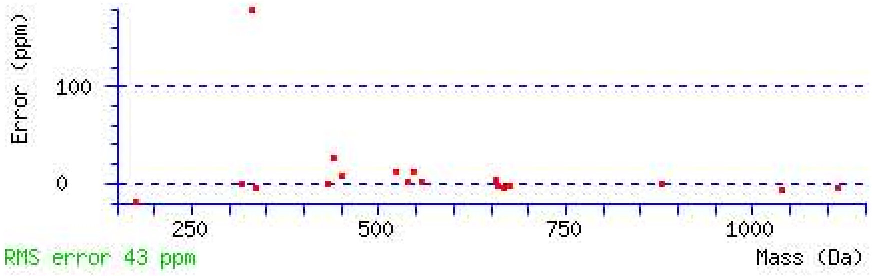
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1212.574356
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2     : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.0053
Matches : 18/58 fragment ions using 39 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							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
28.1	1212.574356	-0.000048	VQQPDCR
13.1	1212.574356	-0.000048	VQQPDCR
3.8	1212.592102	-0.017794	VQEDQQR
3.3	1212.582199	-0.007891	GRMPPSEFHR

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

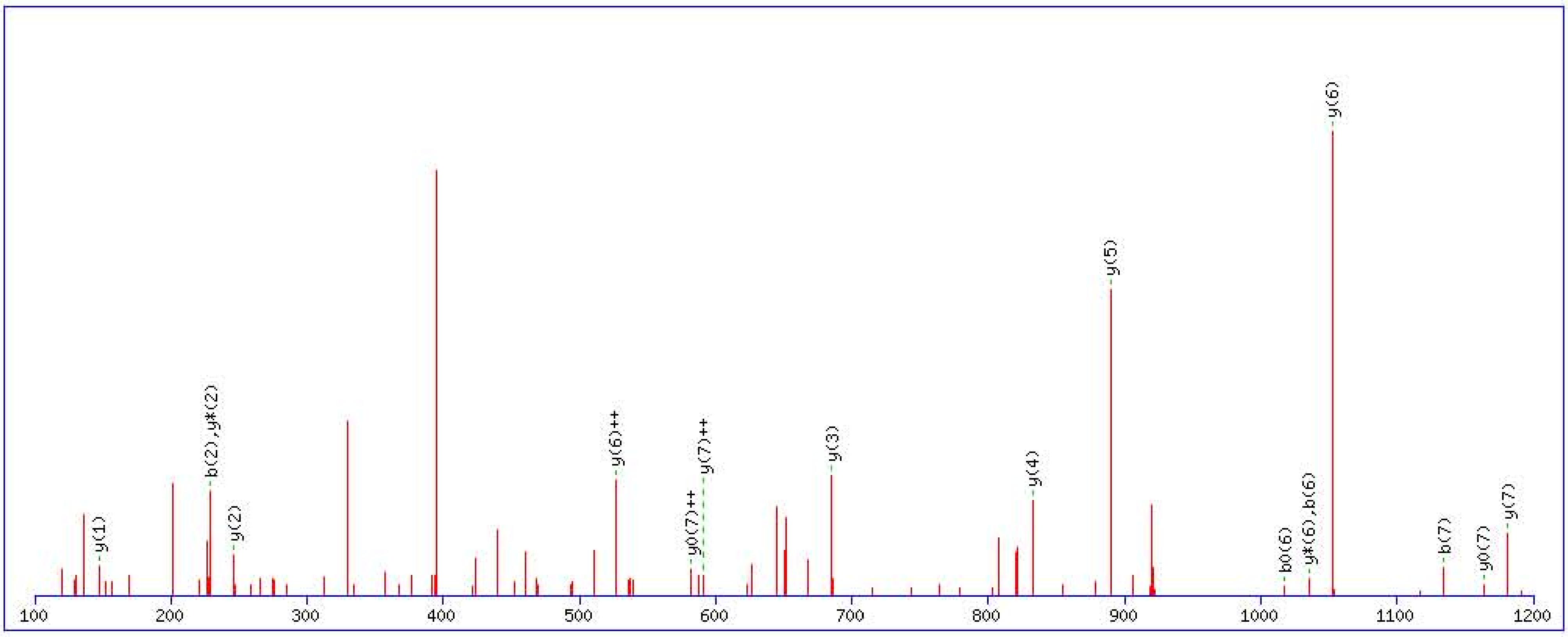
Mascot Search Results

Peptide View

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

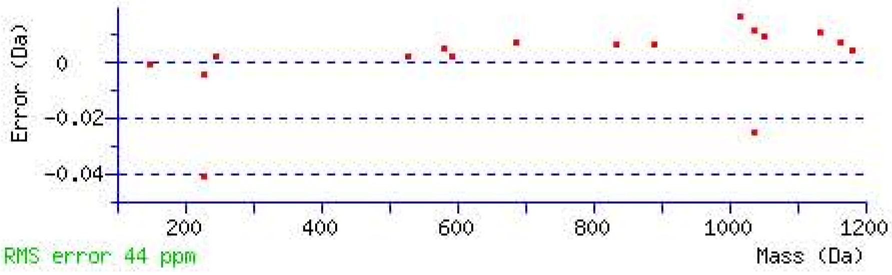
Match to Query 22437: 1279.669668 from(640.842110,2+) rtinseconds(1986) index(47365)
Title: Locus:1.1.1.2740.6 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

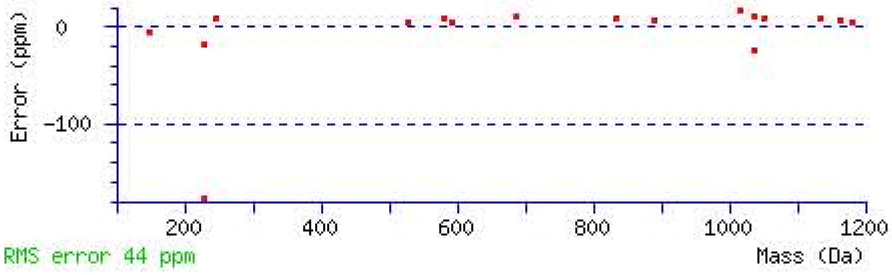
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 35  Expect: 0.005
Matches : 17/60 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	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
35.4	1279.663483	0.006185	VEYGFQVK
10.2	1279.684601	-0.014933	MSASAVFILDVK
6.0	1279.677216	-0.007548	VFKTEDTQGKK
5.1	1279.666824	0.002844	VKEWSLMIMK
5.1	1279.666824	0.002844	VKEWSLMIMK
4.2	1279.681229	-0.011561	EVTVKEWYVK
3.3	1279.687958	-0.018290	LIKSMESVMVK
3.0	1279.665955	0.003713	LDKYDSVEAIK
2.4	1279.670670	-0.001002	VEHKSNQK
2.2	1279.663483	0.006185	QFVGYLDK

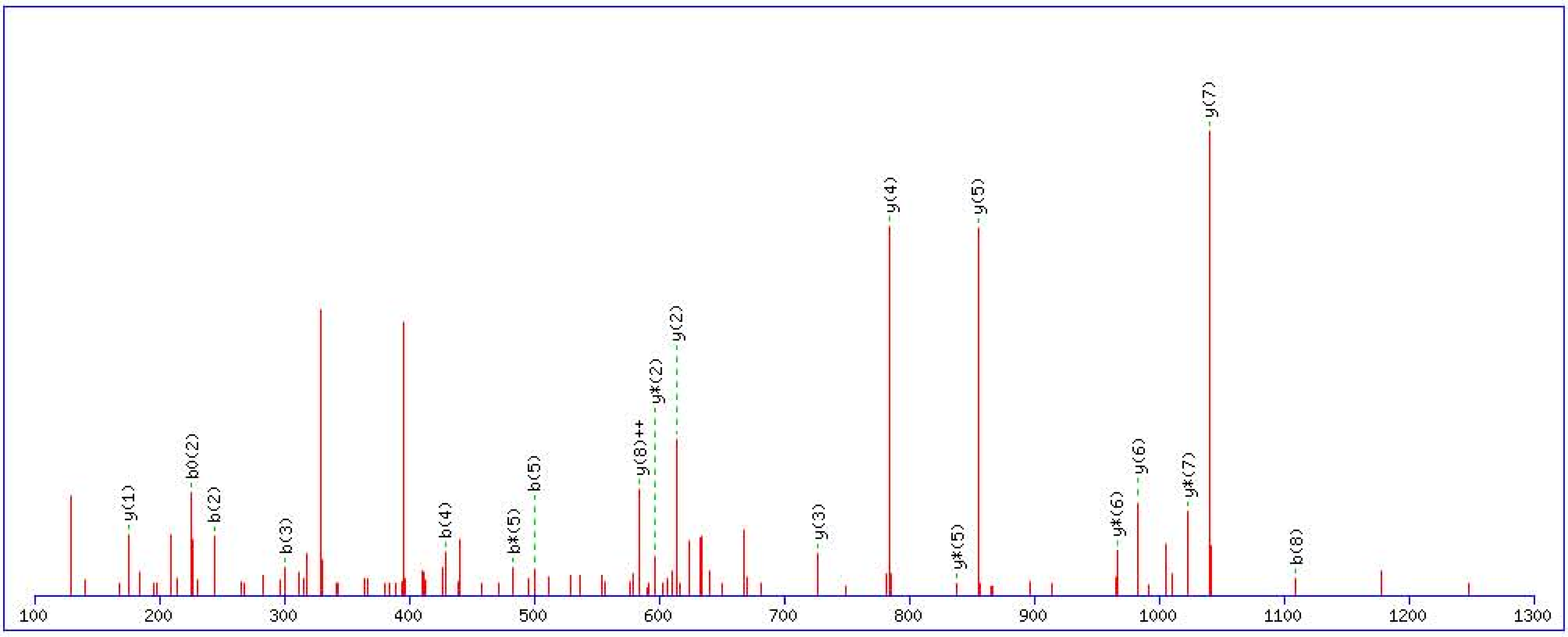
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

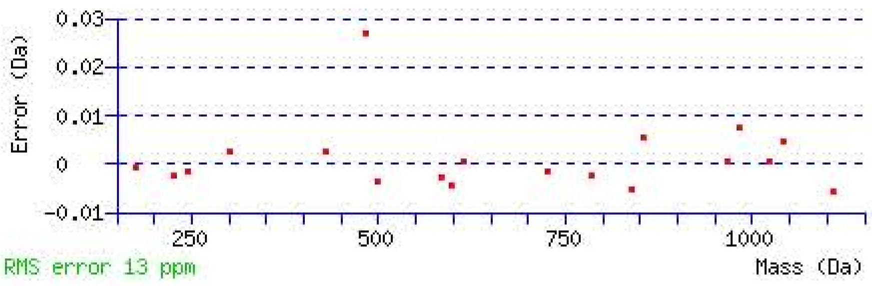
Match to Query 22621: 1282.684548 from(642.349550,2+) rtinseconds(1334) index(43190)
Title: Locus:1.1.1.2513.7 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

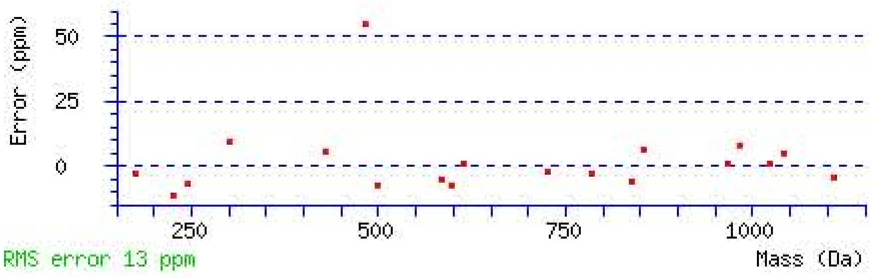
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1282.681580
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.0028
Matches : 19/78 fragment ions using 41 most intense peaks   (help)
```

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





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.6	1282.681580	0.002968	DKGQAGLQR
11.8	1282.670334	0.014214	ELEGQIQR
8.0	1282.674194	0.010354	QGEGQSRLVPGR
5.5	1282.674164	0.010384	NEGGKLGNPKNR
4.7	1282.681580	0.002968	DKGQAGLQR
4.3	1282.670349	0.014199	QIDLDVNR
4.0	1282.685623	-0.001075	VWVDGIQR
3.9	1282.670334	0.014214	QDLEAQIR
3.7	1282.688095	-0.003547	KPTKPESQSPGK
3.4	1282.692108	-0.007560	LEWVEIIEPR

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

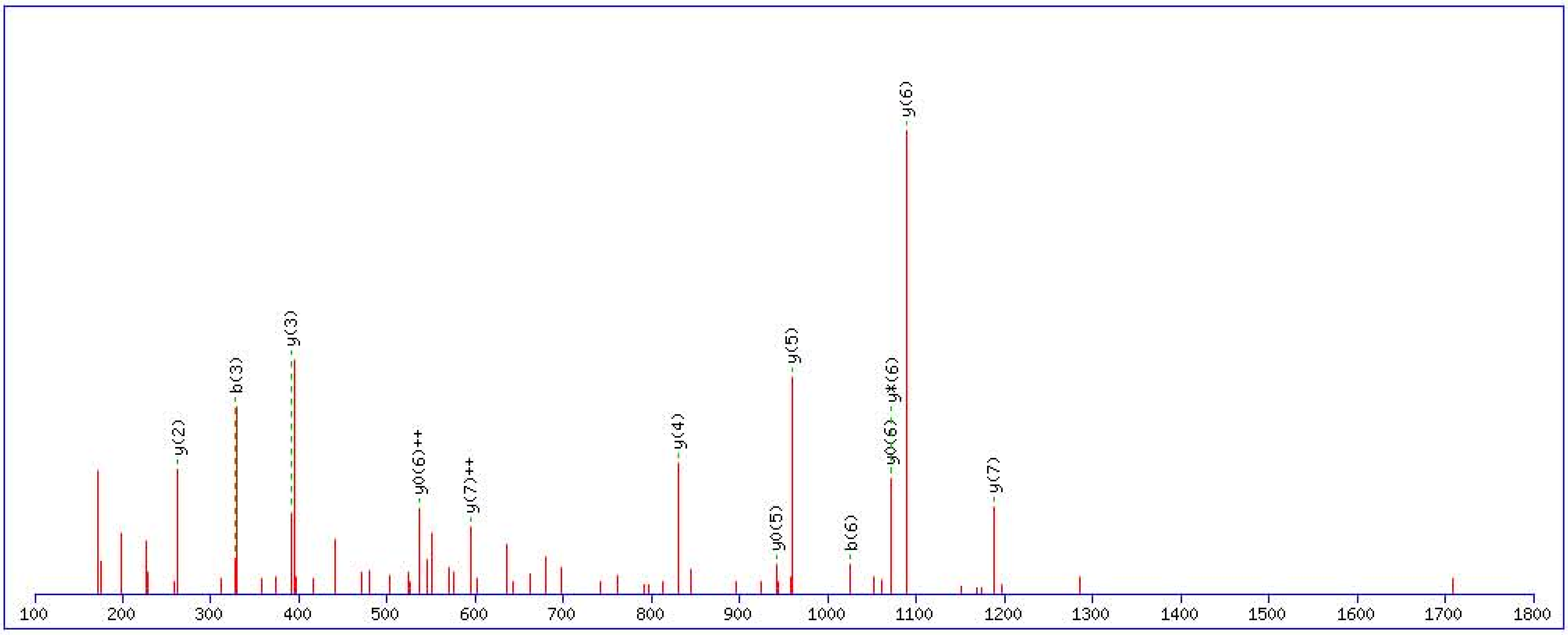
Mascot Search Results

Peptide View

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

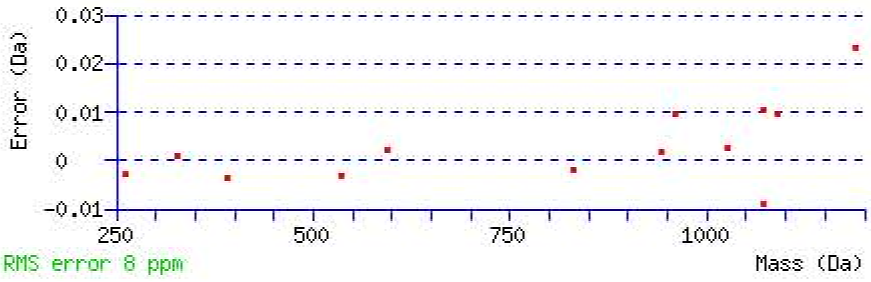
Match to Query 22733: 1285.636228 from(643.825390,2+) rtinseconds(1361) index(43302)
Title: Locus:1.1.1.2522.17 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

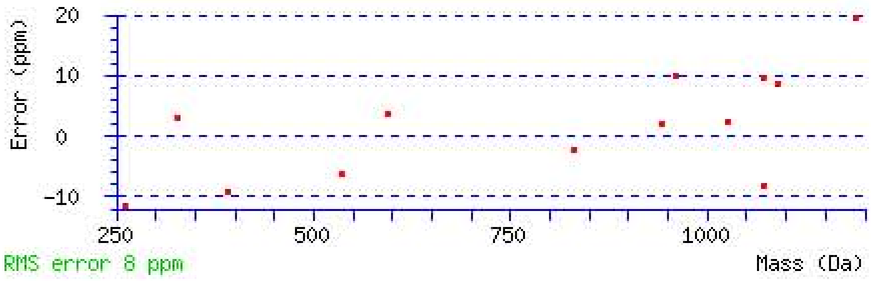
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1285.633621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 36 **Expect:** 0.00056
Matches : 13/70 fragment ions using 23 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	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
35.7	1285.633621	0.002607	VVEEQESR
1.0	1285.626236	0.009992	VETQEVNPGASR

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

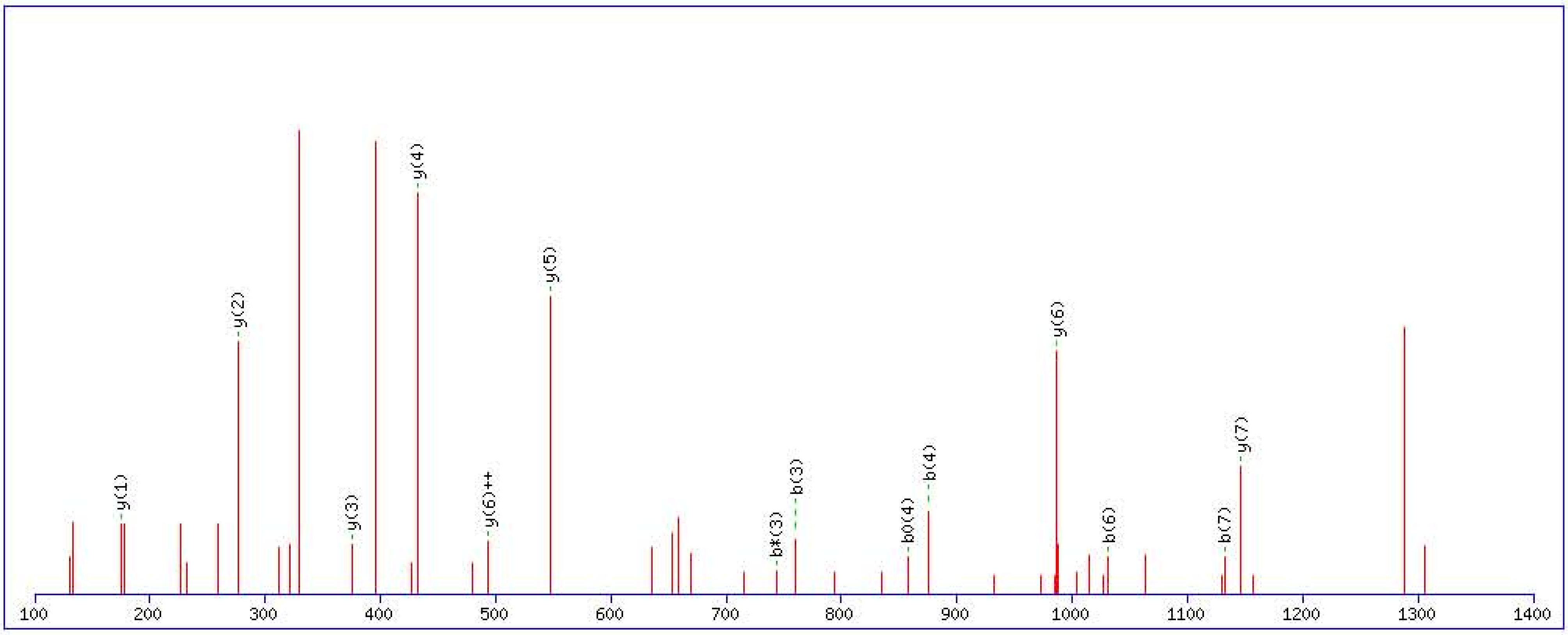
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

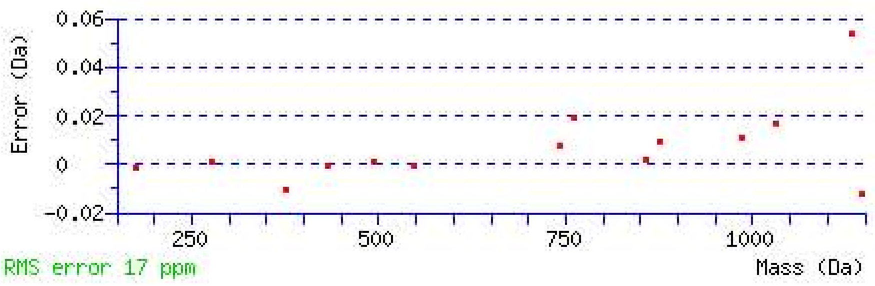
Match to Query 23136: 1305.570468 from(653.792510,2+) rtinseconds(1387) index(43448)
Title: Locus:1.1.1.2531.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

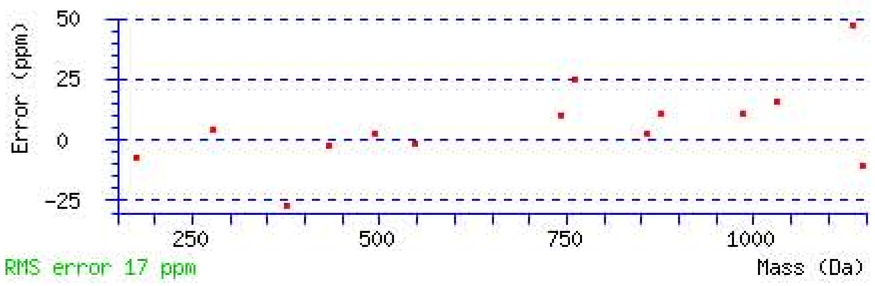
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1305.562820
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 5.7e-005
Matches : 14/72 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	161.037925	81.022600					C							8
2	321.068574	161.037925					C	***1146.539427***	573.773352	1129.512878	565.260077	1128.528862	564.768069	7
3	**760.293900**	380.650588	743.267351	372.137314			Q	***986.508778***	493.758027	969.482229	485.244753	968.498213	484.752745	6
4	**875.320843**	438.164060	858.294294	429.650785	857.310278	429.158777	D	***547.283452***	274.145364	530.256903	265.632090	529.272887	265.140082	5
5	932.342307	466.674792	915.315758	458.161517	914.331742	457.669509	G	***432.256509***	216.631893	415.229960	208.118618	414.245944	207.626610	4
6	**1031.410721**	516.208999	1014.384172	507.695724	1013.400156	507.203716	V	***375.235045***	188.121161	358.208496	179.607886	357.224480	179.115878	3
7	**1132.458400**	566.732838	1115.431851	558.219564	1114.447835	557.727556	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 CCQDGVTR
(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	1305.562820	0.007648	CCQDGVTR
14.1	1305.588409	-0.017941	CRSSTPADAWR
5.2	1305.577194	-0.006726	CDAGWLADGSVR
2.1	1305.569778	0.000690	SSWQGENQSQR
1.0	1305.583679	-0.013211	EQEPDFEEKR
0.6	1305.577148	-0.006680	MGQHYEEEKR

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

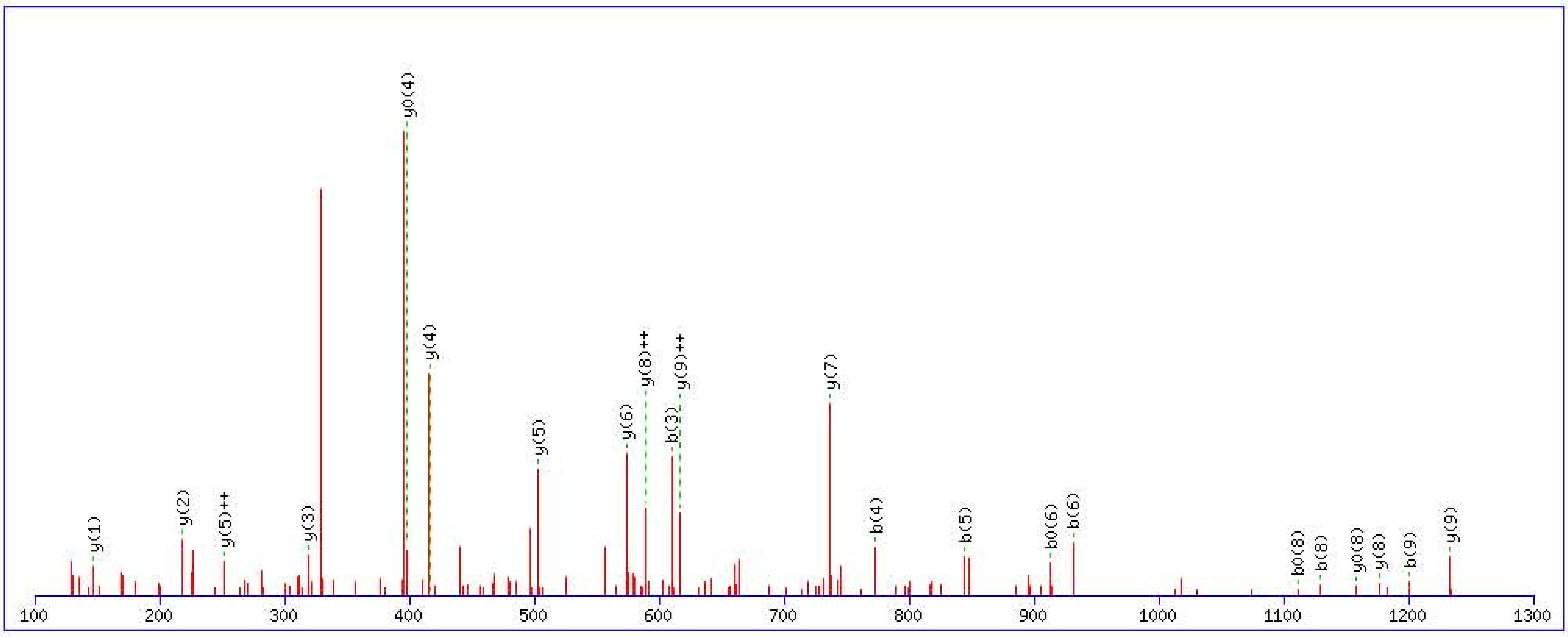
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

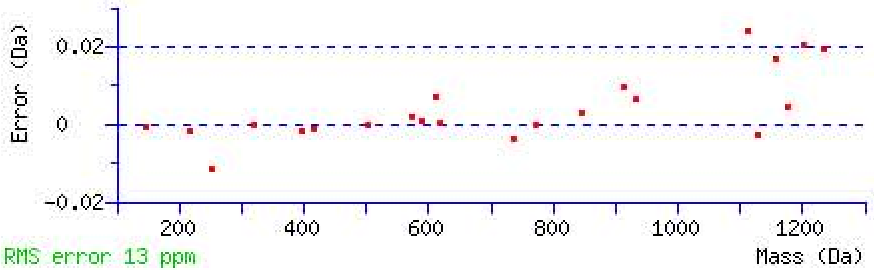
Match to Query 23941: 1345.710648 from(673.862600,2+) rtinseconds(1604) index(44889)
Title: Locus:1.1.1.2607.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

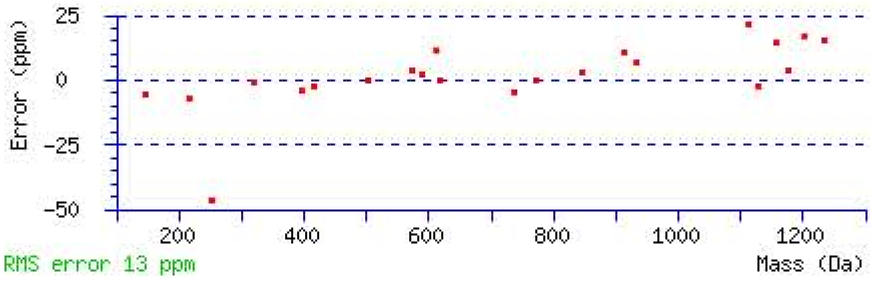
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1345.706390
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 53 **Expect:** 0.0001
Matches : 22/90 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							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
52.7	1345.706390	0.004258	LGQYASPTAK
9.4	1345.727509	-0.016861	LGLMDNEIKVAK
9.2	1345.692474	0.018174	VASCRYPALGPR
8.2	1345.706390	0.004258	LGQYDQALK
7.6	1345.724182	-0.013534	LGAVPATSGPTTFK
7.1	1345.706406	0.004242	QGLYTPQTK
0.4	1345.713608	-0.002960	NGMLLTGGGKDRK
0.3	1345.724152	-0.013504	QPLQTDIYGLAK

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

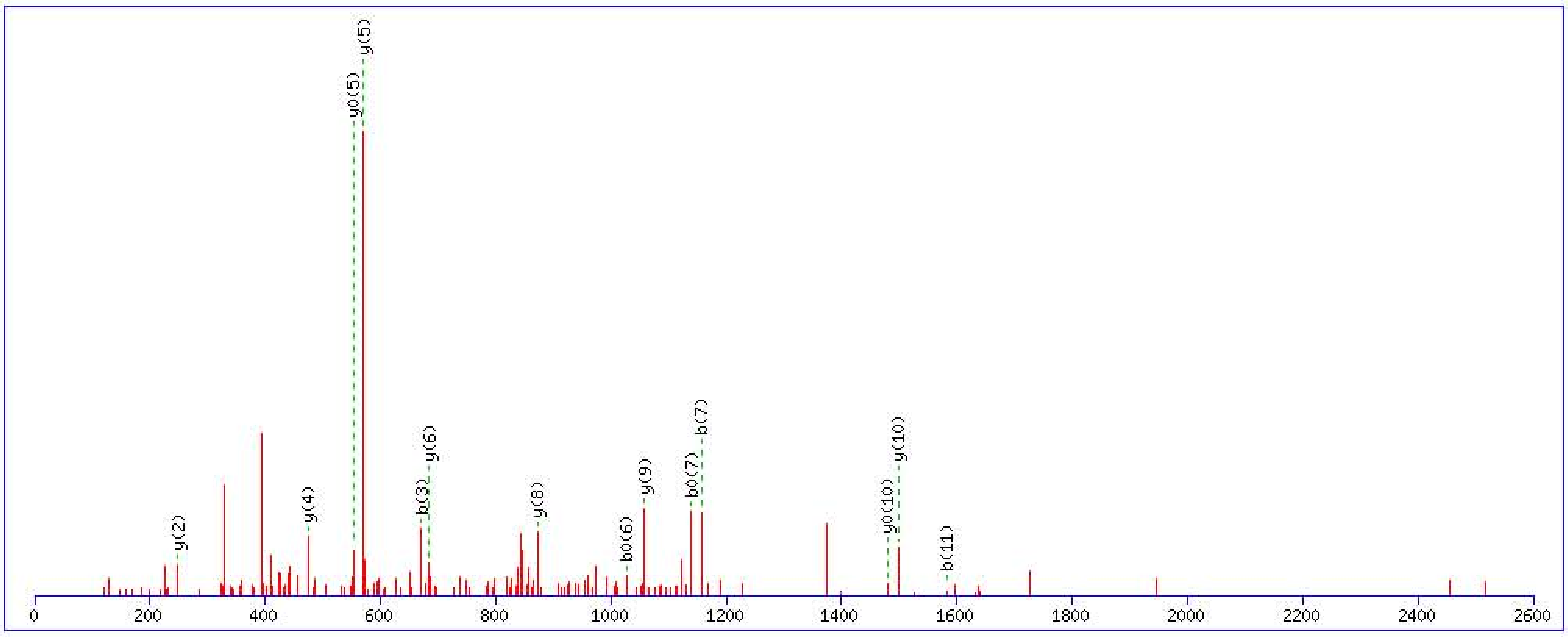
Mascot Search Results

Peptide View

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

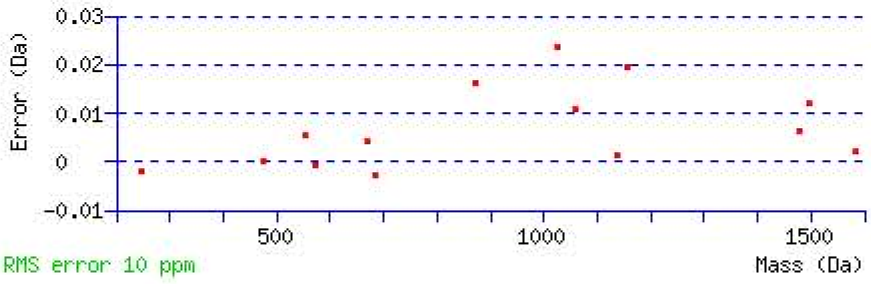
Match to Query 36950: 1726.873848 from(864.444200,2+) rtinseconds(2028) index(47589)
Title: Locus:1.1.1.2754.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

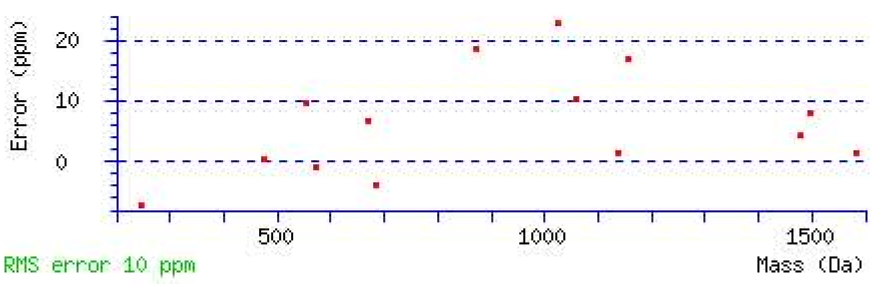


```
Monoisotopic mass of neutral peptide Mr(calc): 1726.860001
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.011
Matches : 14/126 fragment ions using 32 most intense peaks   (help)
```

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



RMS error 10 ppm



RMS error 10 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.1	1726.860001	0.013847	TEQWSTLPPETK
8.5	1726.871216	0.002632	NLNTKLQMYFQSPK
6.4	1726.867188	0.006660	KDHAEMQAVIDAKQK
2.2	1726.849960	0.023888	TERFGQGGAGPVGGQGPR
1.2	1726.874573	-0.000725	VTKNQEMMSQIKYK
0.4	1726.853485	0.020363	MASGHAFQPDLVK

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

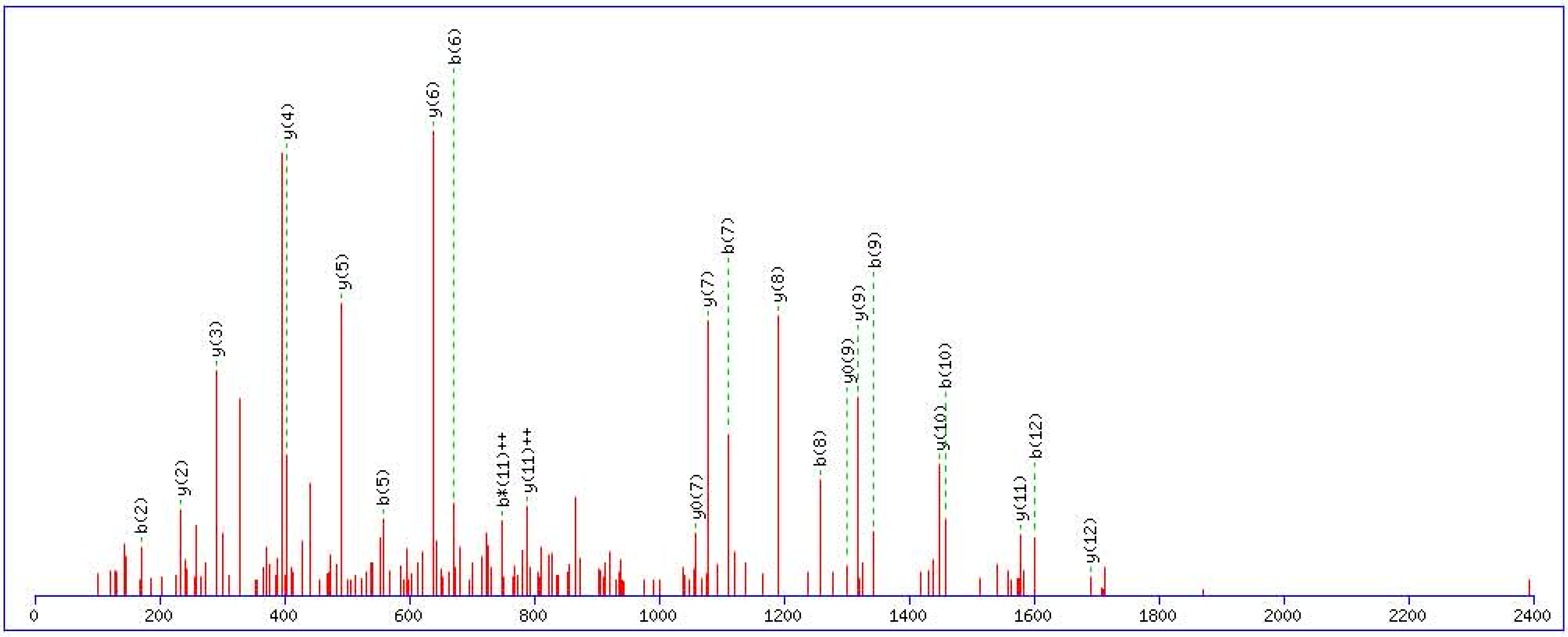
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

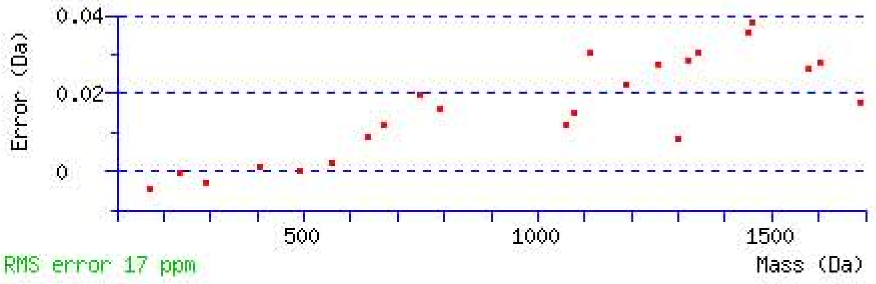
Match to Query 37441: 1746.905928 from(874.460240,2+) rtinseconds(2557) index(50641)
Title: Locus:1.1.1.2938.6 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

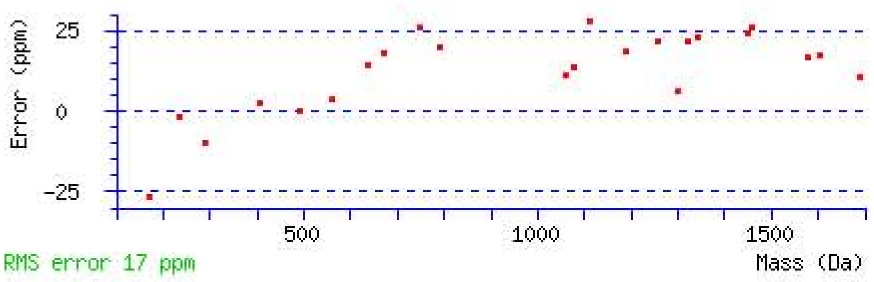
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 89  Expect: 8.7e-009
Matches : 23/126 fragment ions using 33 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	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
89.4	1746.886200	0.019728	GLEEELQFSLGSK
3.4	1746.887558	0.018370	AVQSKAFCAGGLAPGWK
1.4	1746.918533	-0.012605	AKLQMTEAALALSEQK

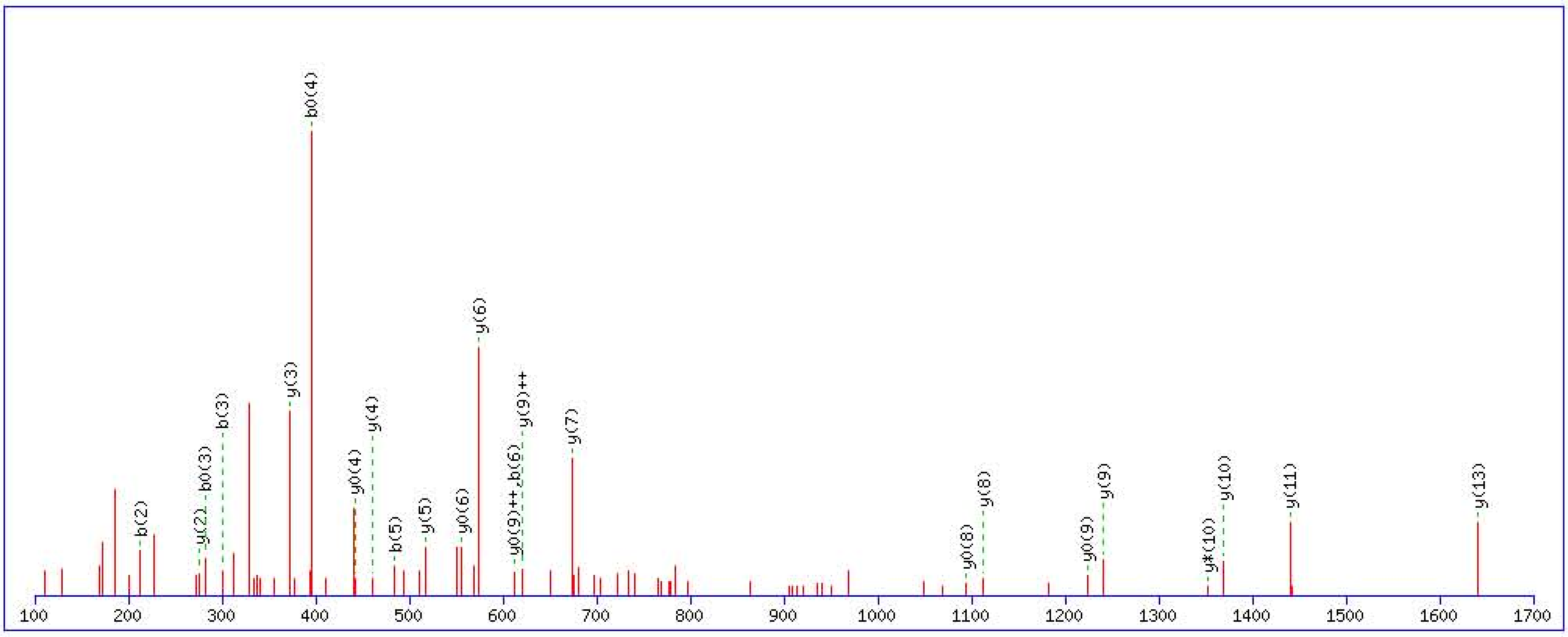
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

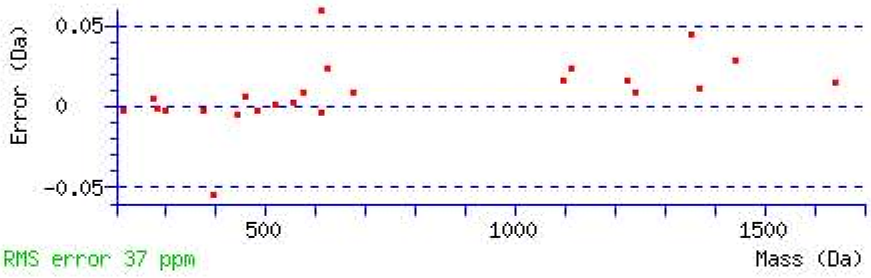
Match to Query 39377: 1851.983712 from(618.335180,3+) rtinseconds(1978) index(47293)
Title: Locus:1.1.1.2737.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

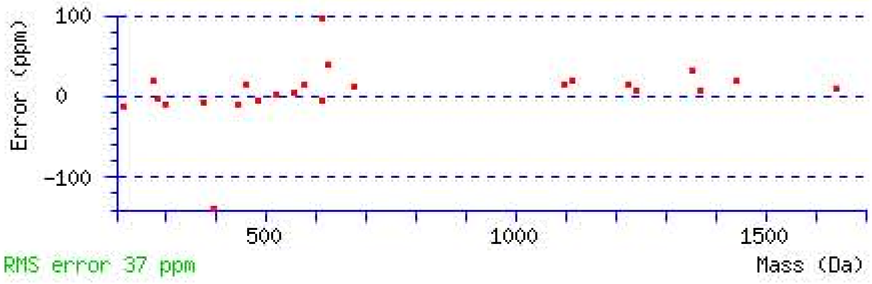
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 53  Expect: 1.4e-005
Matches : 24/152 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							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
53.1	1851.976425	0.007287	VLSLAQEQVGGSPEK
34.0	1851.976425	0.007287	VLSLAQEQVGGSPEK
1.4	1852.005402	-0.021690	LQLEQQVATGPALDNKK

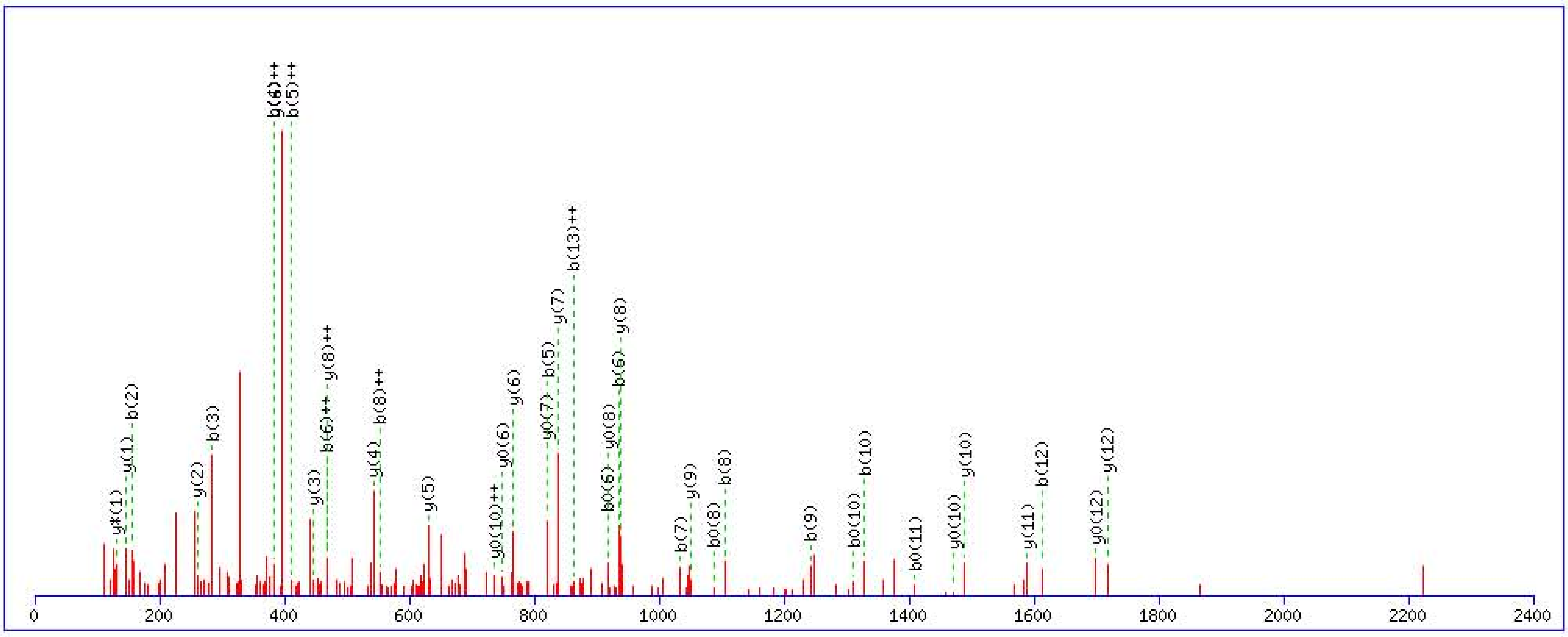
Mascot Search Results

Peptide View

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

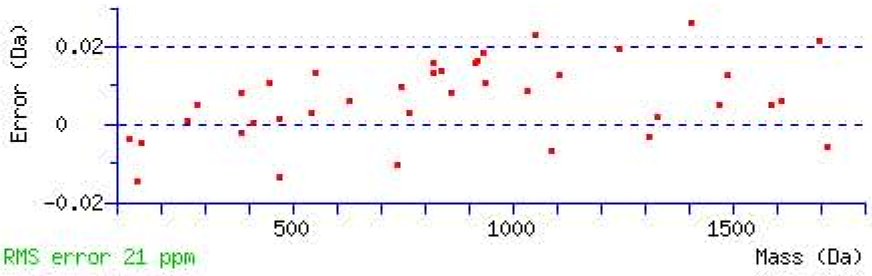
Match to Query 39870: 1871.022912 from(624.681580,3+) rtinseconds(2231) index(48816)
Title: Locus:1.1.1.2825.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

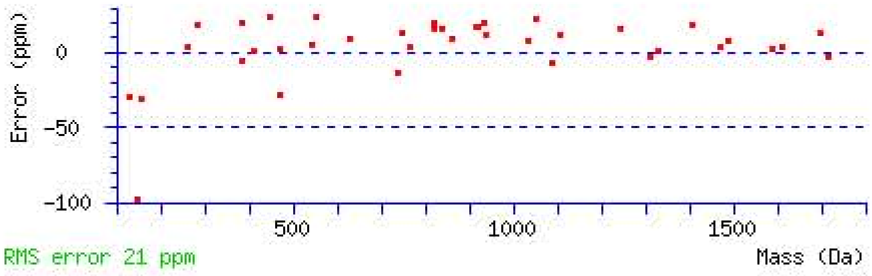
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1871.012756
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 47 **Expect:** 0.00038
Matches : 39/136 fragment ions using 106 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	**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
47.2	1871.012756	0.010156	GPEVQLVAHSPWLK

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

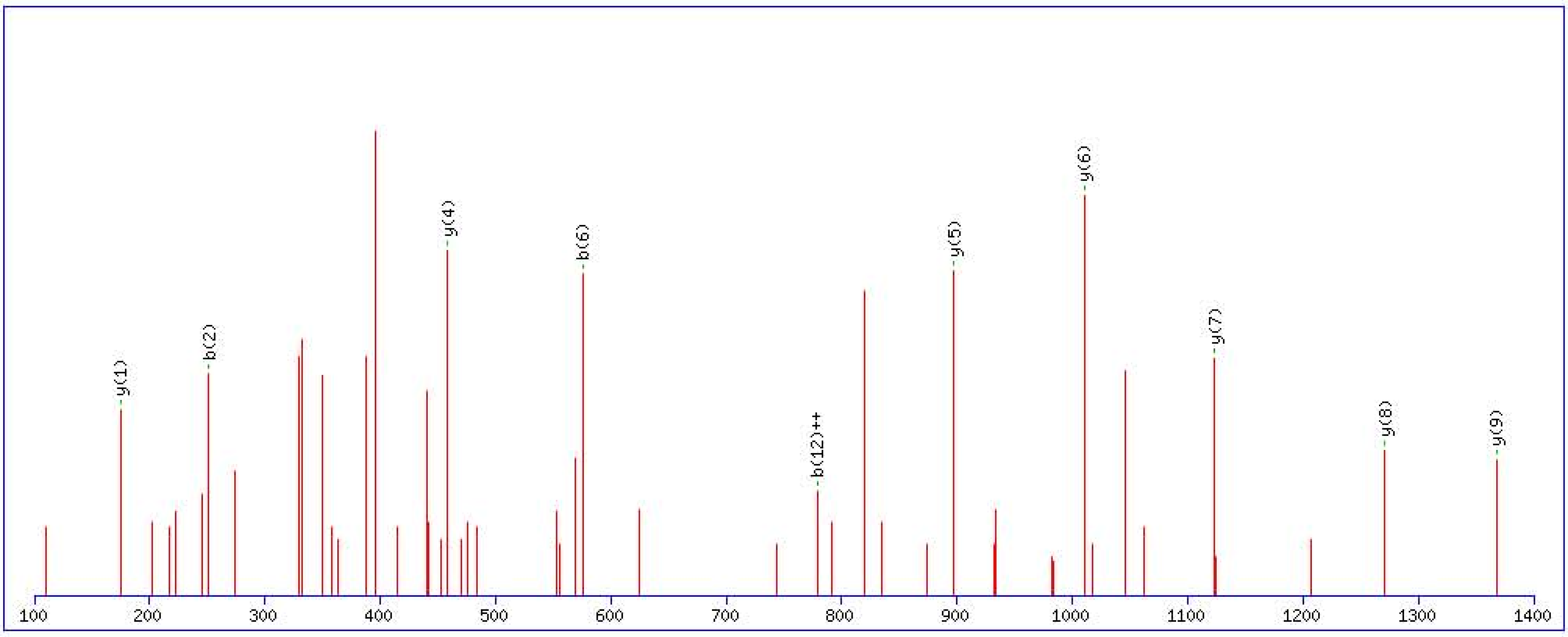
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

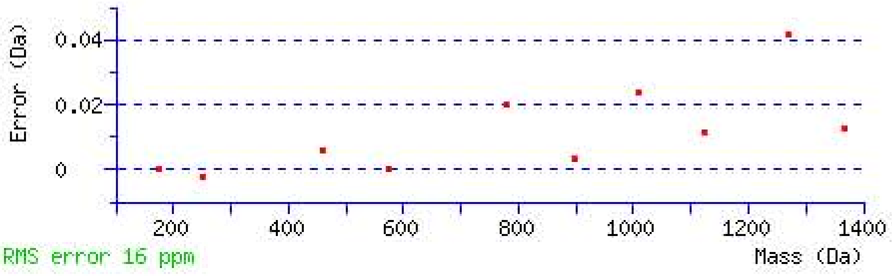
Match to Query 40950: 1941.156402 from(648.059410,3+) rtinseconds(2868) index(52987)
Title: Locus:1.1.1.3045.3 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

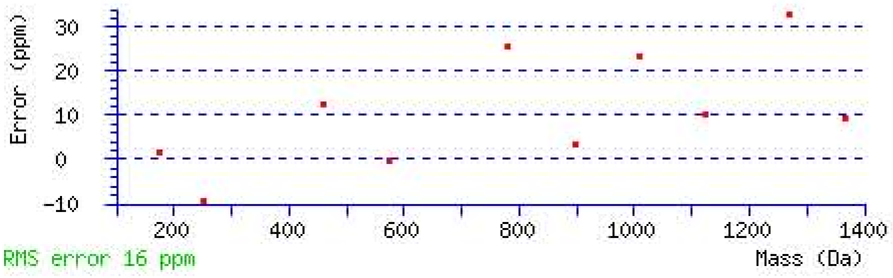
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1941.138626
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 52 **Expect:** 1.2e-005
Matches : 10/92 fragment ions using 13 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
51.6	1941.138626	0.017776	HLVPGAPFLLQALVR

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

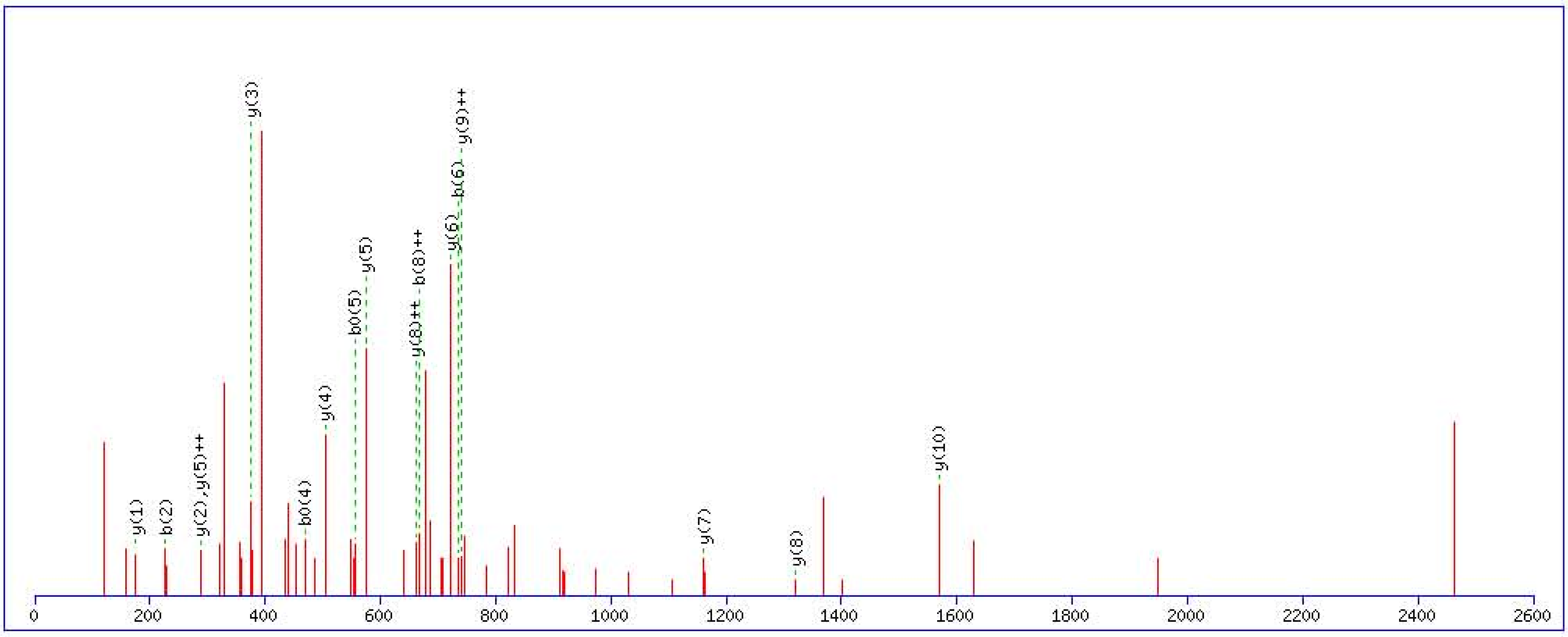
Mascot Search Results

Peptide View

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

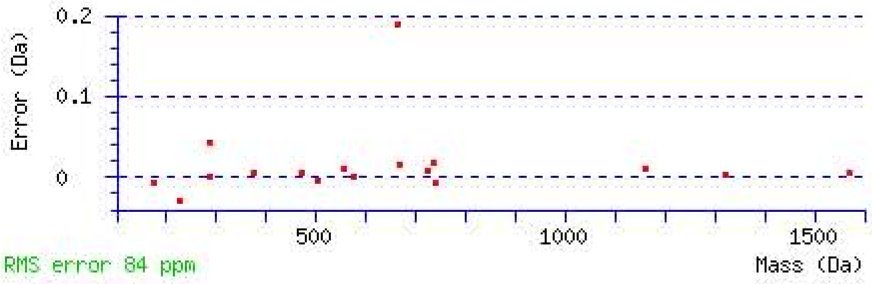
Match to Query 43769: 2053.964232 from(685.662020,3+) rtinseconds(2492) index(50229)
Title: Locus:1.1.1.2916.14 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

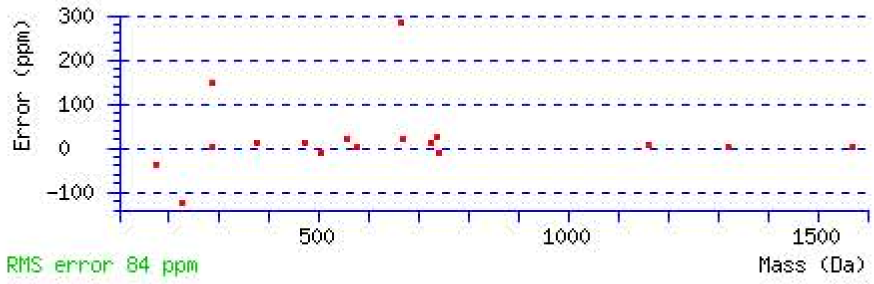
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2053.942368
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.00081
Matches : 17/138 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
33.8	2053.942368	0.021864	EPFLSCCQFAESLR
0.9	2053.948227	0.016005	EKSTCSMGSELLPMISPR

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

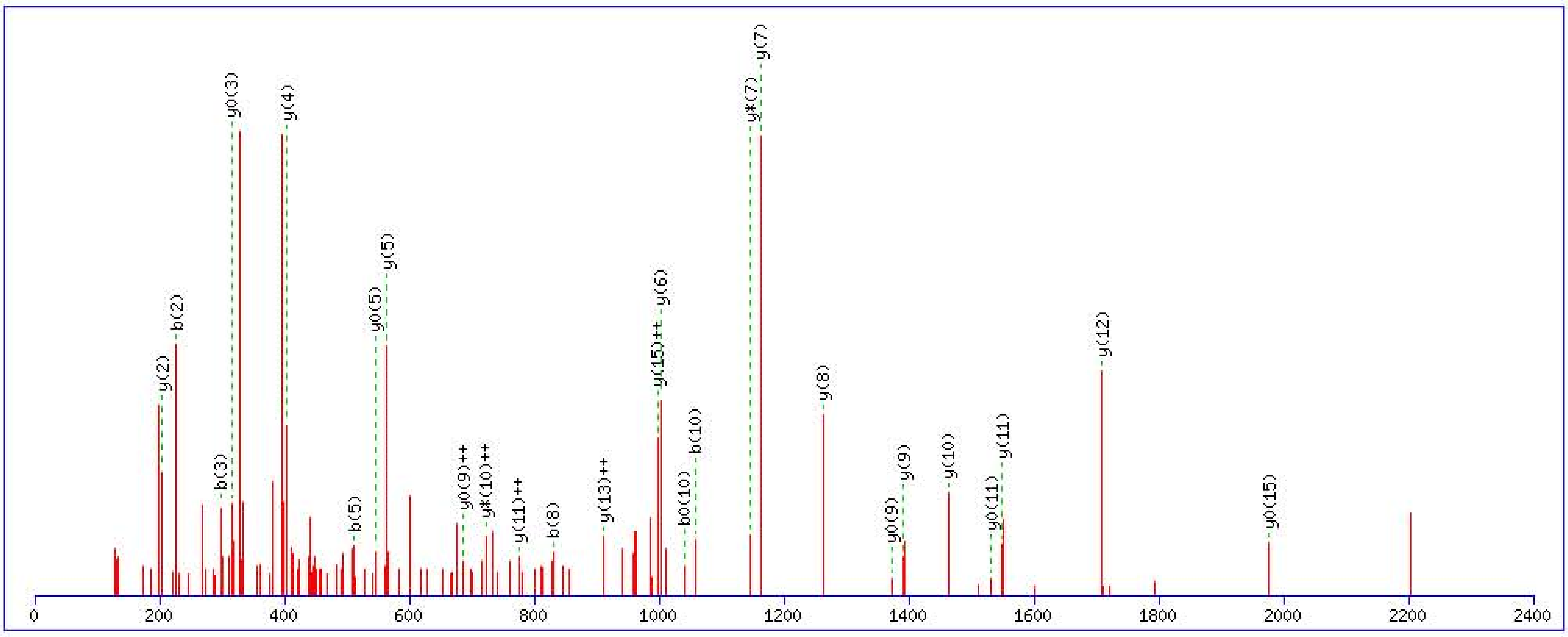
Mascot Search Results

Peptide View

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

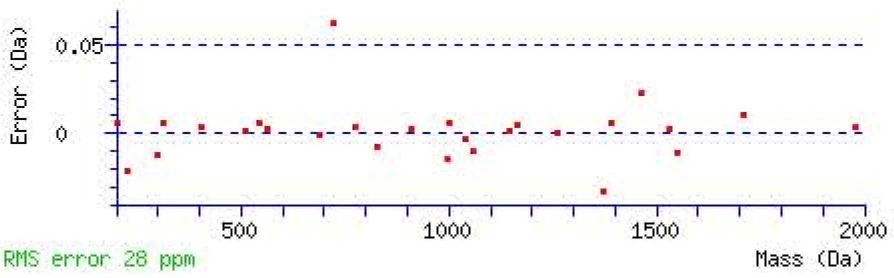
Match to Query 46405: 2220.049032 from(741.023620,3+) rtinseconds(2140) index(63359)
Title: Locus:1.1.1.3371.11 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

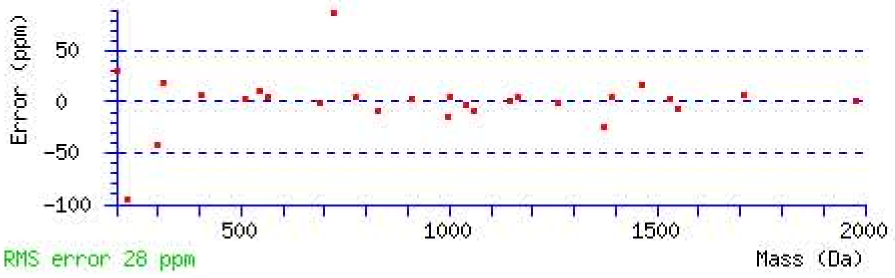
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 51 **Expect:** 2.7e-005
Matches : 27/160 fragment ions using 50 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
51.3	2220.041092	0.007940	LLATLCSAEVCQCAEGK
2.5	2220.048080	0.000952	EPQEGAELPEATGTTSHR

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

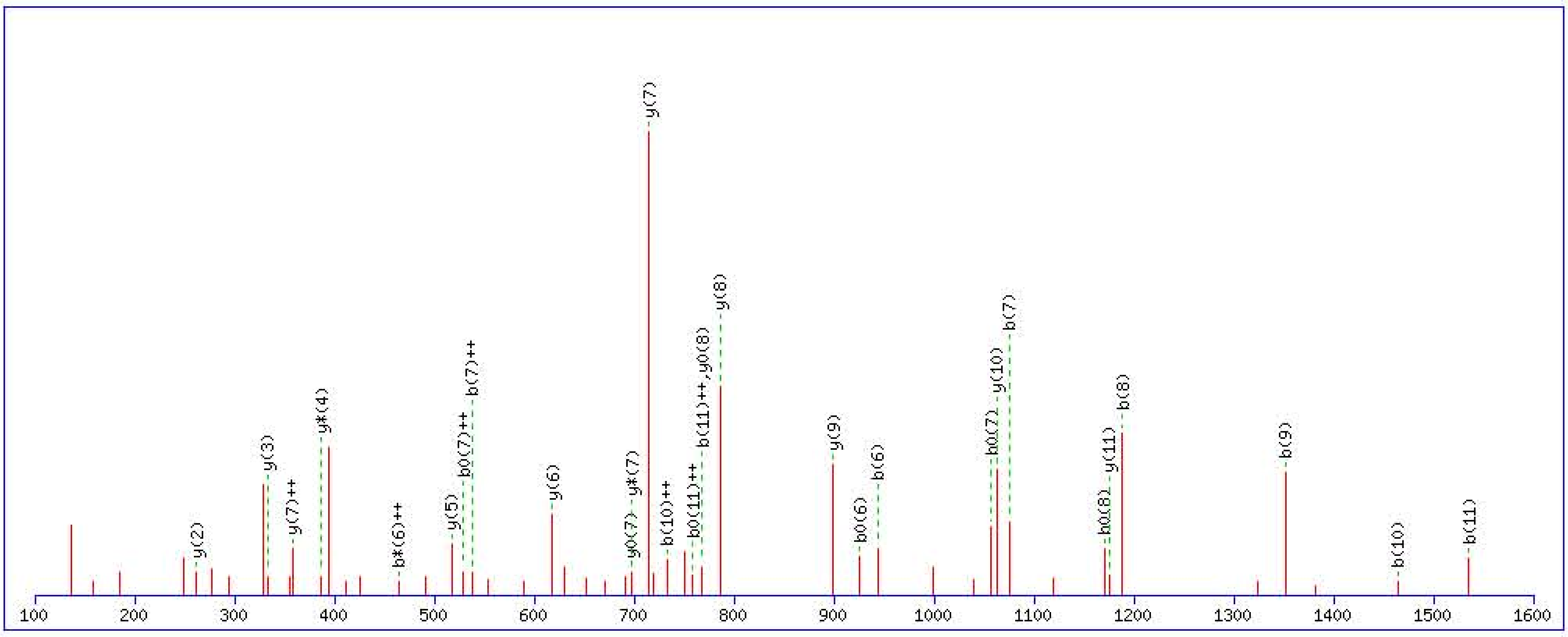
Mascot Search Results

Peptide View

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

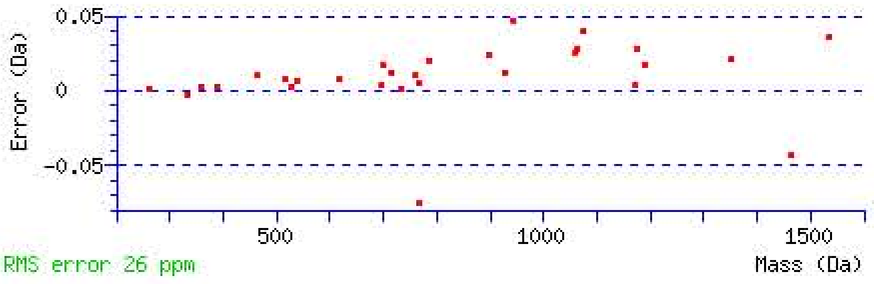
Match to Query 46845: 2249.129682 from(750.717170,3+) rtinseconds(2504) index(50330)
Title: Locus:1.1.1.2920.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

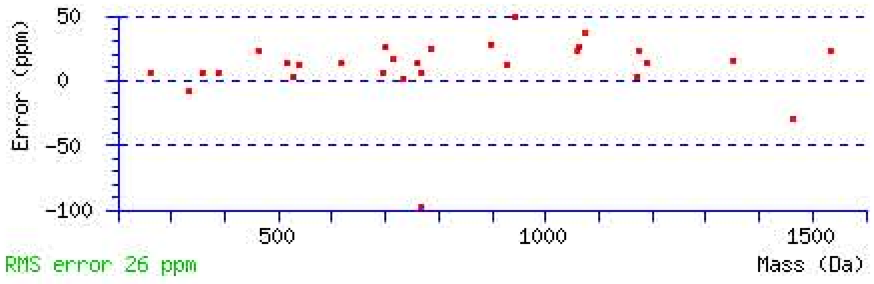
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2249.100647
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.00079
Matches : 29/188 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							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
41.4	2249.100647	0.029035	GCGEQTMIYLAPTLAASR
7.8	2249.115051	0.014631	YSTSLYASPSMVHEGVAVVPR
1.3	2249.143570	-0.013888	TPPPQPPLISSMDSISQK
1.3	2249.104492	0.025190	AQLQQHNLEMVGEGTRQ
0.3	2249.137527	-0.007845	QKFERPICVSWSTDVKGGR

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

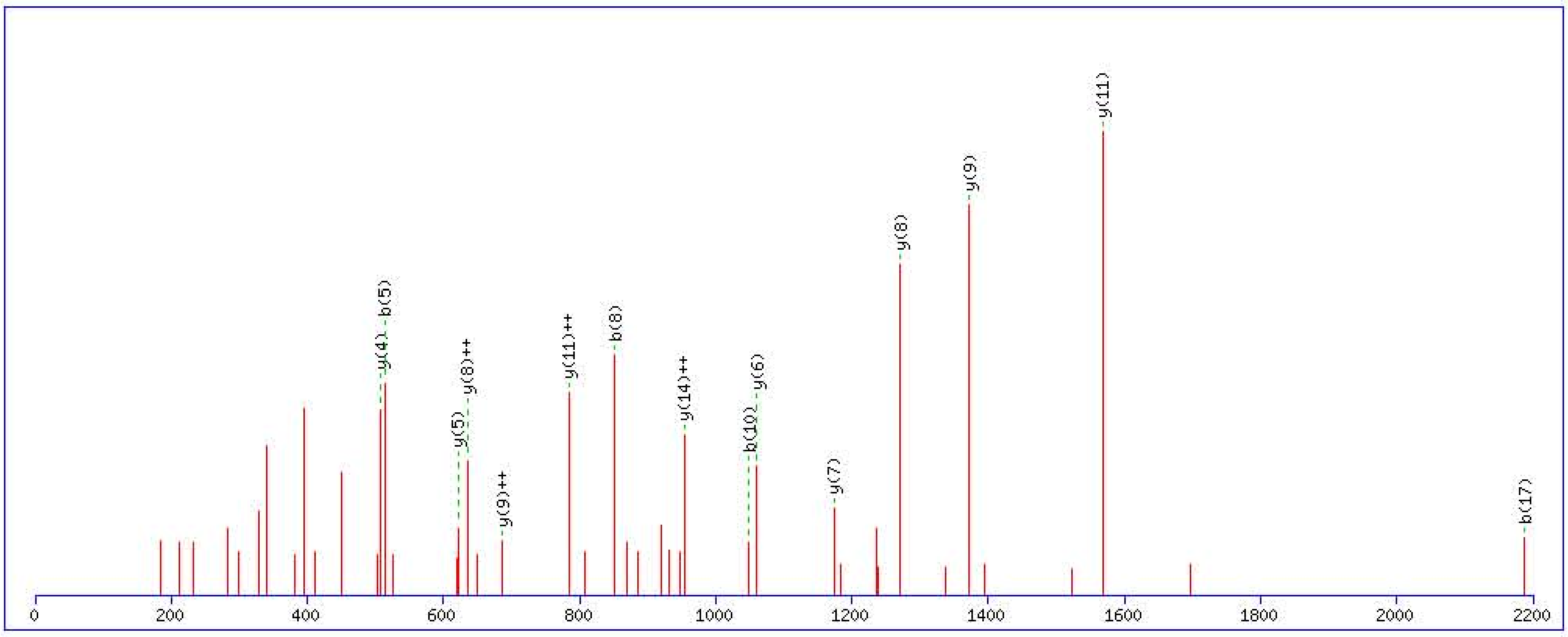
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

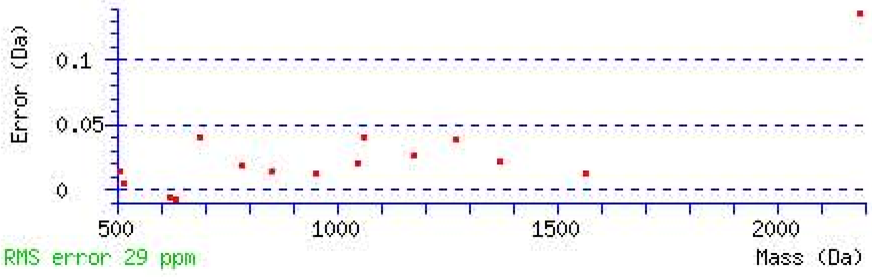
Match to Query 49443: 2418.255432 from(807.092420,3+) rtinseconds(3006) index(54069)
Title: Locus:1.1.1.3091.18 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

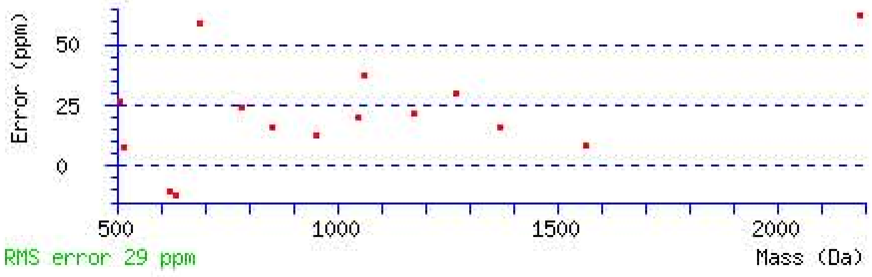
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2418.225342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14    : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.0011
Matches : 15/198 fragment ions using 29 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
32.4	2418.225342	0.030090	DDPDAPLQPVTPLQLFEGR
0.8	2418.259033	-0.003601	QQQRALLGPWLSGPQGTDR
0.8	2418.259033	-0.003601	QQQRALLGPWLSGPQGTDR
0.8	2418.259033	-0.003601	QQQRALLGPWLSGPQGTDR

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

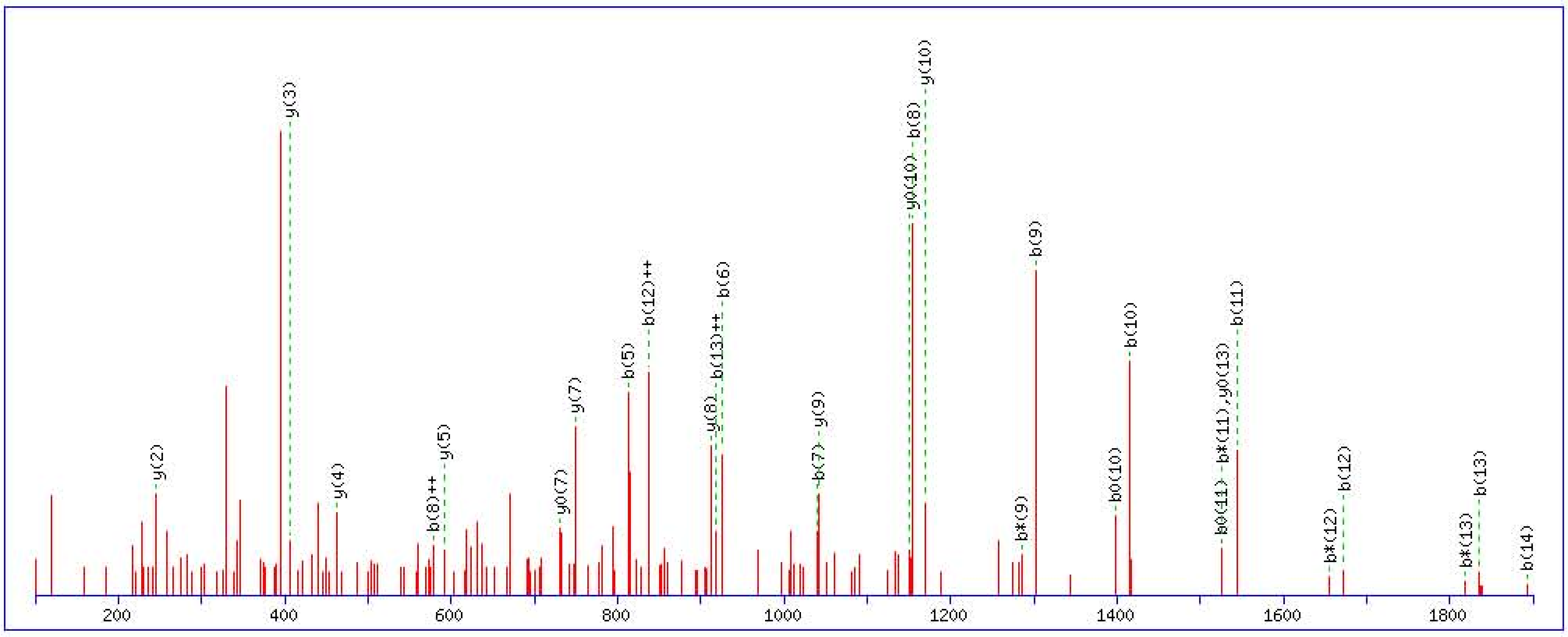
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

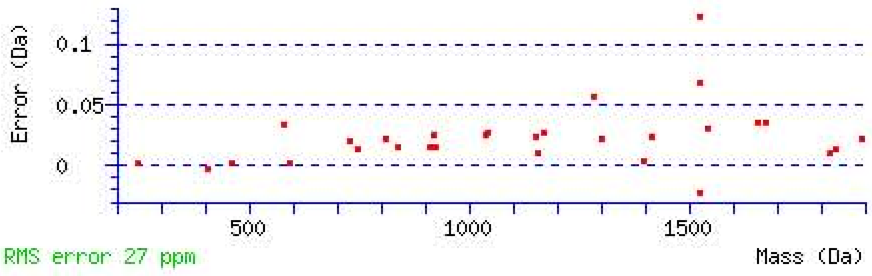
Match to Query 51933: 2583.191832 from(862.071220,3+) rtinseconds(2732) index(51870)
Title: Locus:1.1.1.2998.21 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

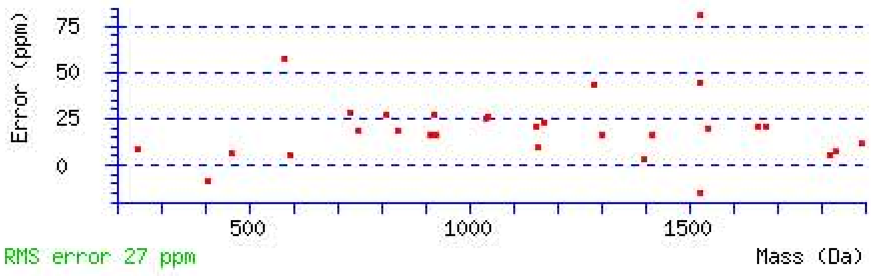
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2583.155624
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 7.5e-006
Matches : 30/194 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							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
62.5	2583.155624	0.036208	AACAQLNDFLQEYGTQGCQV
15.1	2583.155624	0.036208	AACAQLNDFLQEYGTQGCQV

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

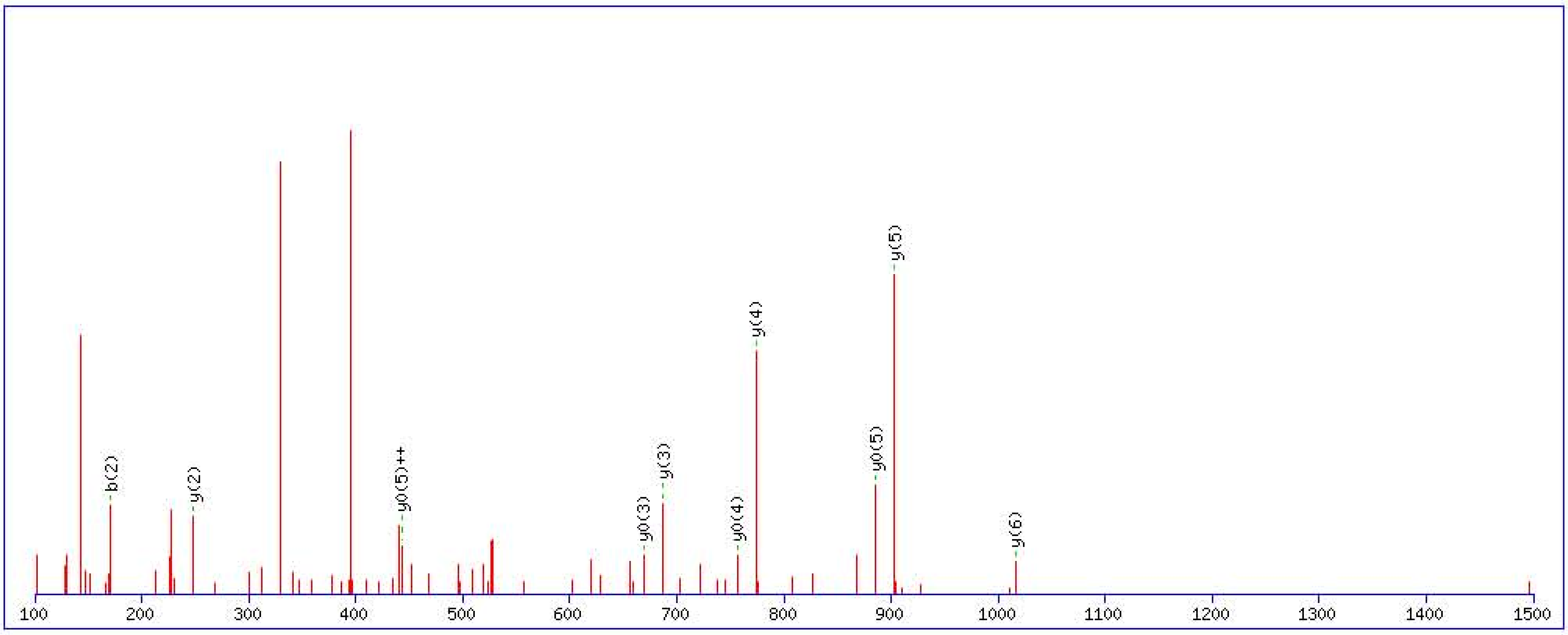
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

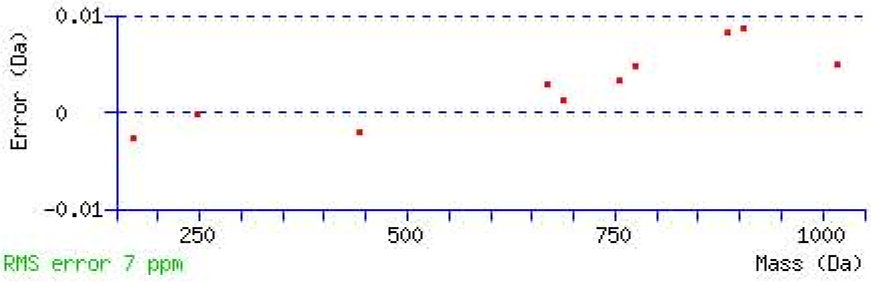
Match to Query 15590: 1072.557228 from(537.285890,2+) rtinseconds(1461) index(43956)
Title: Locus:1.1.1.2557.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

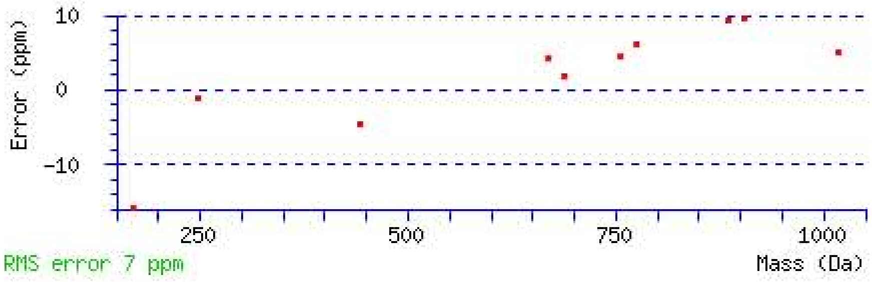
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1072.558670
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.06
Matches : 10/58 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	58.028740	29.518008					G							7
2	171.112804	86.060040					L	***1016.544494***	508.775885	999.517945	500.262611	998.533929	499.770603	6
3	300.155397	150.581336			282.144832	141.576054	E	***903.460430***	452.233853	886.433881	443.720579	885.449865	443.228571	5
4	387.187425	194.097351			369.176860	185.092068	S	***774.417837***	387.712557	757.391288	379.199282	756.407272	378.707274	4
5	826.412751	413.710014	809.386202	405.196739	808.402186	404.704731	Q	***687.385809***	344.196543	670.359260	335.683268	669.375244	335.191260	3
6	927.460430	464.233853	910.433881	455.720579	909.449865	455.228571	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
7							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of GLESQTK
(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	1072.558670	-0.001442	GLESQTK
11.8	1072.558670	-0.001442	LGECPAVLSK
7.5	1072.558670	-0.001442	QSEGLTK
7.2	1072.551254	0.005974	KEAPRDETK
1.9	1072.551285	0.005943	GPRTTEPSTK
0.9	1072.566544	-0.009316	NHSLAFVGTK

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

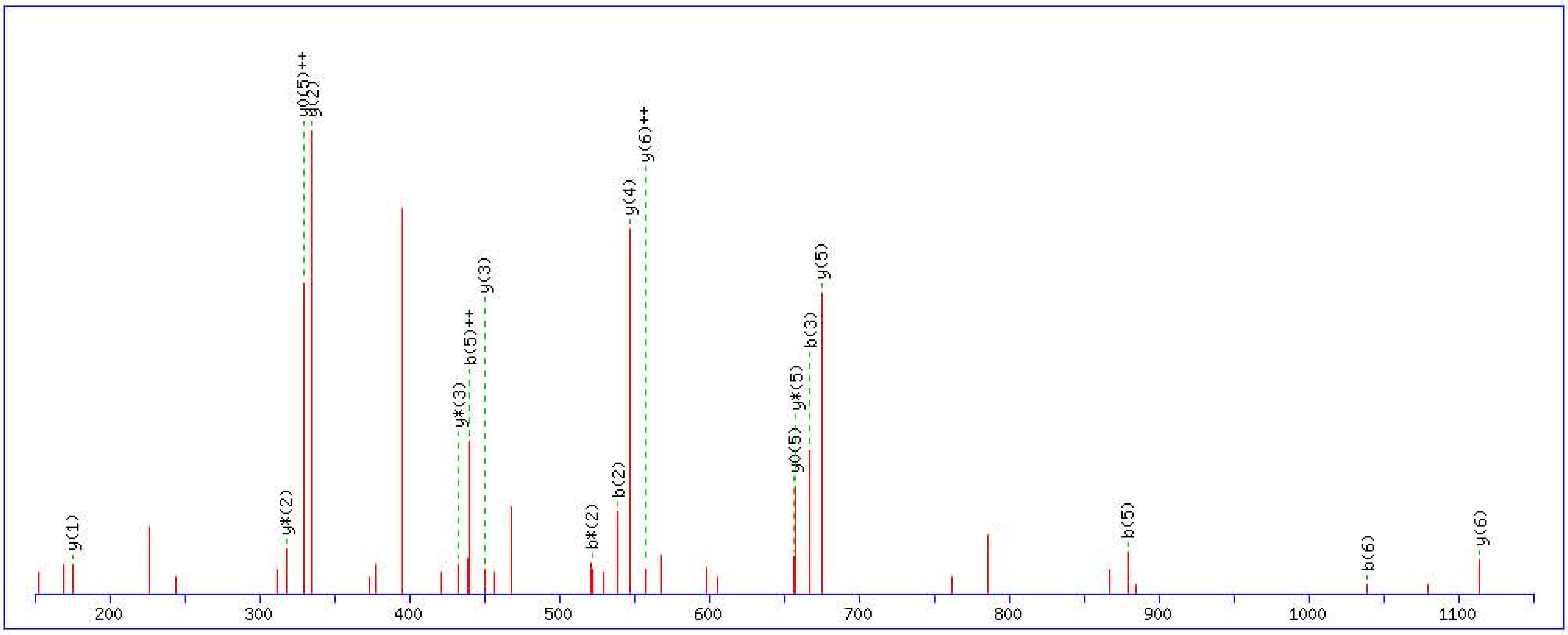
Mascot Search Results

Peptide View

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

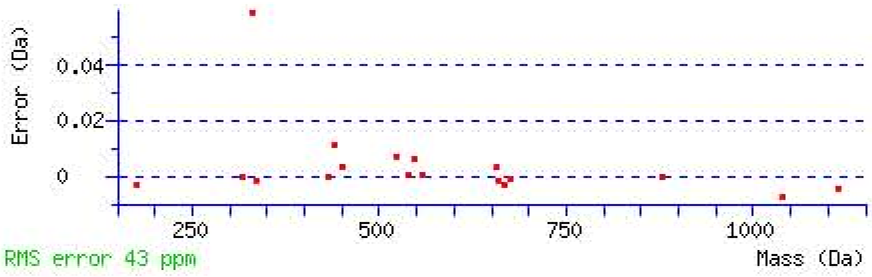
Match to Query 20591: 1212.574308 from(607.294430,2+) rtinseconds(1290) index(42994)
Title: Locus:1.1.1.2497.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

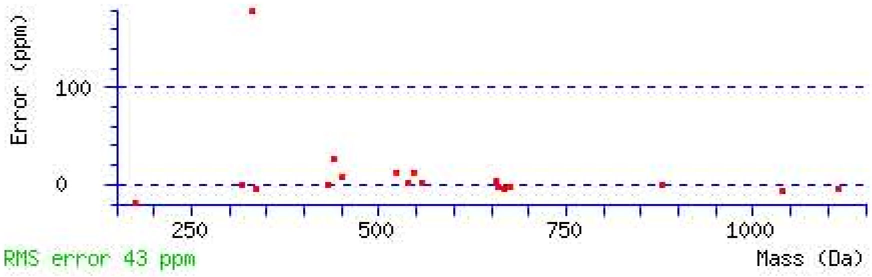
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1212.574356
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 28 **Expect:** 0.0053
Matches : 18/58 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							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
28.1	1212.574356	-0.000048	VQQPDCR
13.1	1212.574356	-0.000048	VQQPDCR
3.8	1212.592102	-0.017794	VQEDQQR
3.3	1212.582199	-0.007891	GRMPPSEFHR

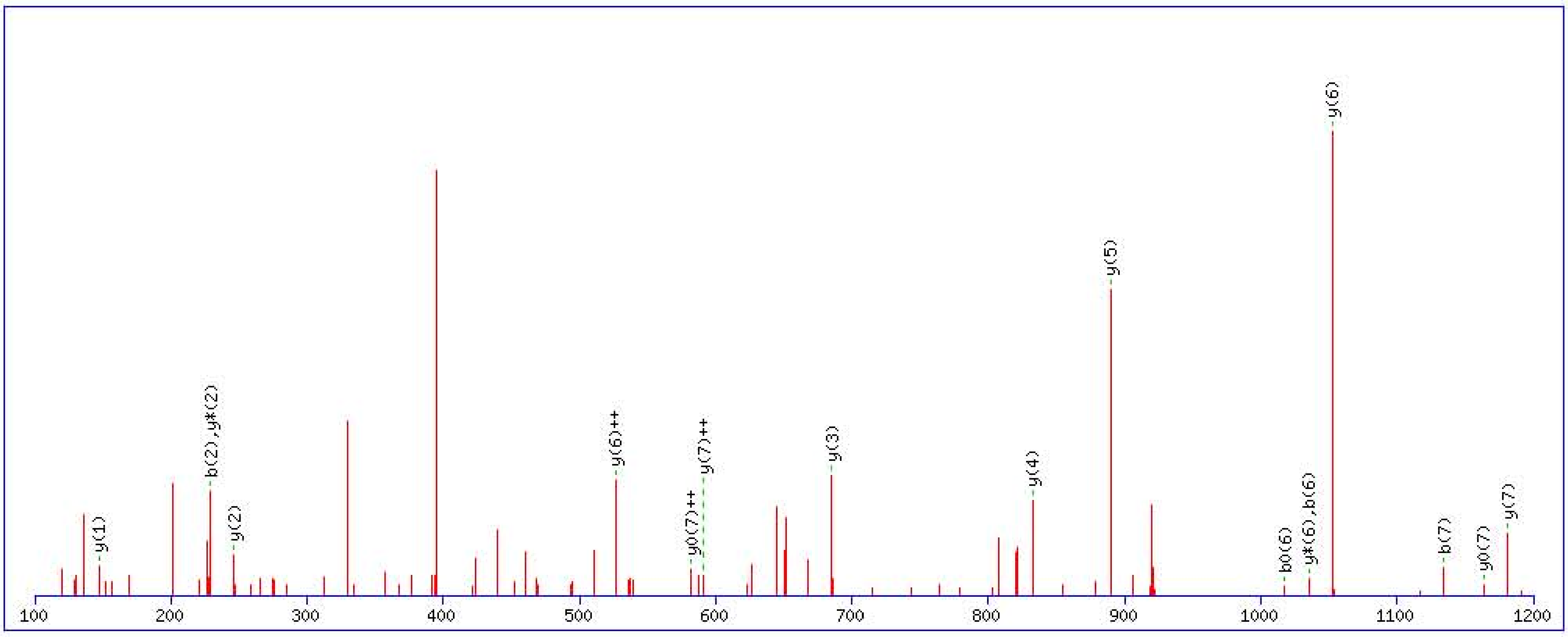
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

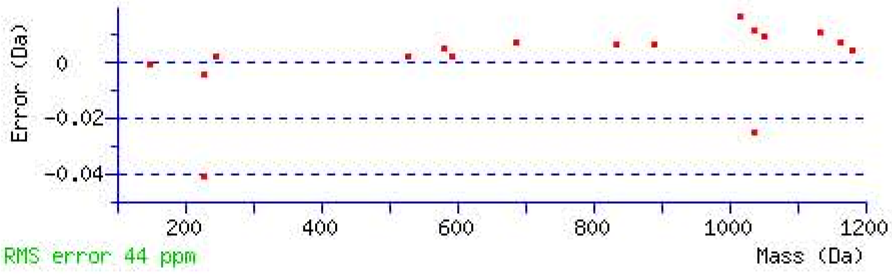
Match to Query 22437: 1279.669668 from(640.842110,2+) rtinseconds(1986) index(47365)
Title: Locus:1.1.1.2740.6 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

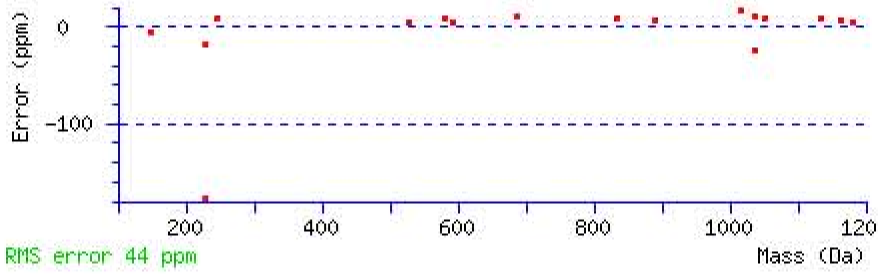
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 35  Expect: 0.005
Matches : 17/60 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	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
35.4	1279.663483	0.006185	VEYGFQVK
10.2	1279.684601	-0.014933	MSASAVFILDVK
6.0	1279.677216	-0.007548	VFKTEDTQGKK
5.1	1279.666824	0.002844	VKEWSLMIMK
5.1	1279.666824	0.002844	VKEWSLMIMK
4.2	1279.681229	-0.011561	EVTVKEWYVK
3.3	1279.687958	-0.018290	LIKSMESVMVK
3.0	1279.665955	0.003713	LDKYDSVEAIK
2.4	1279.670670	-0.001002	VEHKSNQK
2.2	1279.663483	0.006185	QFVGYLDK

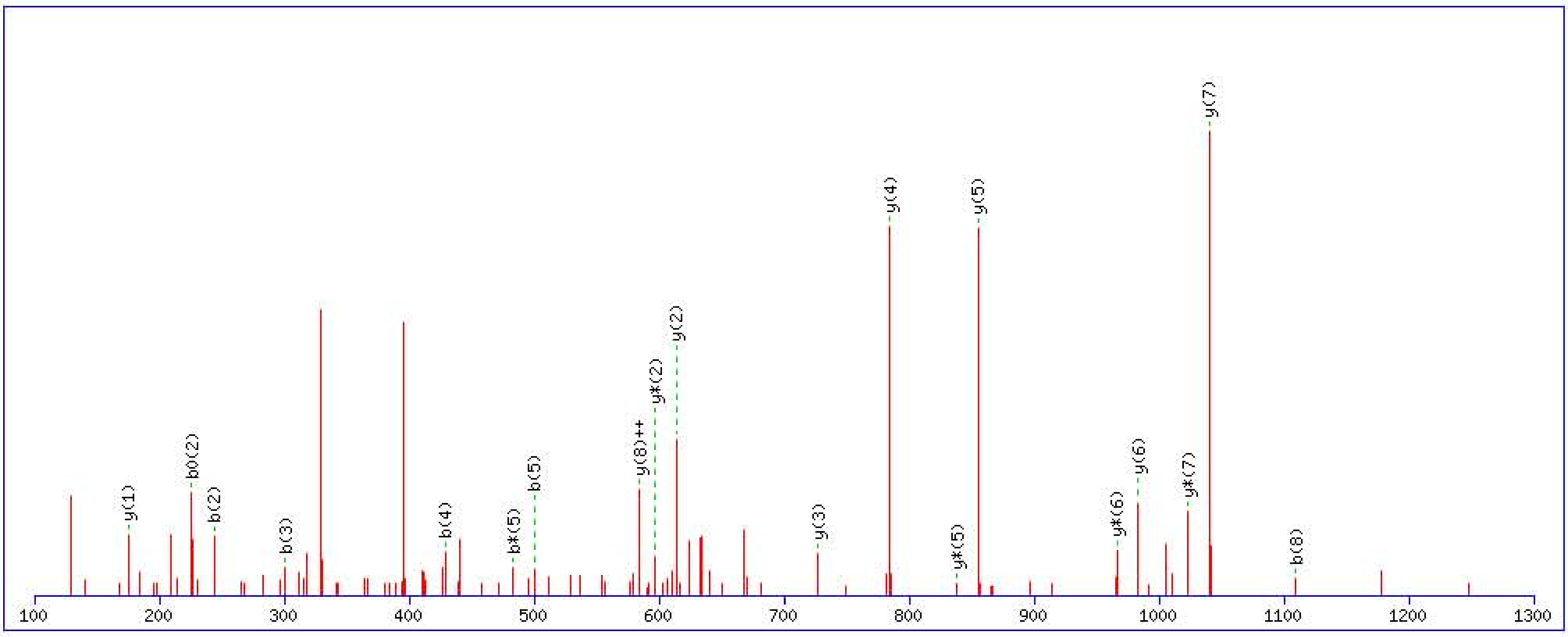
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

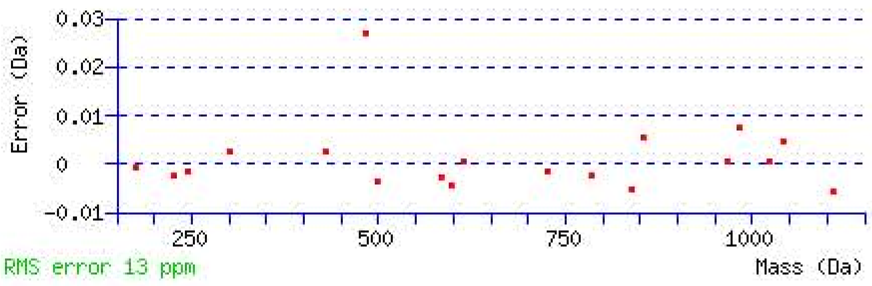
Match to Query 22621: 1282.684548 from(642.349550,2+) rtinseconds(1334) index(43190)
Title: Locus:1.1.1.2513.7 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

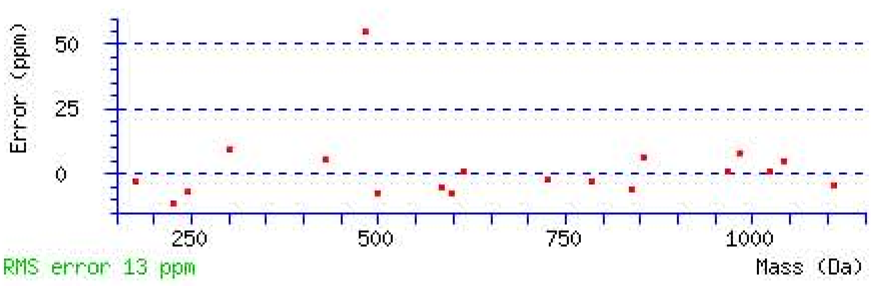
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1282.681580
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 39 **Expect:** 0.0028
Matches : 19/78 fragment ions using 41 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	116.034219	58.520748			98.023654	49.515465	D					9
2	**244.129182**	122.568229	227.102633	114.054955	226.118617	113.562947	K	1168.661925	584.834600	1151.635376	576.321326	8
3	**301.150646**	151.078961	284.124097	142.565687	283.140081	142.073679	G	***1040.566962***	520.787119	1023.540413	512.273844	7
4	**429.209224**	215.108250	412.182675	206.594976	411.198659	206.102968	Q	***983.545498***	492.276387	966.518949	483.763112	6
5	**500.246338**	250.626807	483.219789	242.113532	482.235773	241.621524	A	***855.486920***	428.247098	838.460371	419.733823	5
6	557.267802	279.137539	540.241253	270.624265	539.257237	270.132257	G	***784.449806***	392.728541	767.423257	384.215266	4
7	670.351866	335.679571	653.325317	327.166297	652.341301	326.674289	L	***727.428342***	364.217809	710.401793	355.704534	3
8	**1109.577192**	555.292234	1092.550643	546.778960	1091.566627	546.286951	Q	***614.344278***	307.675777	597.317729	299.162502	2
9							R	***175.118952***	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.6	1282.681580	0.002968	DKGQAGLQR
11.8	1282.670334	0.014214	ELEGQIQR
8.0	1282.674194	0.010354	QGEGQSRLVPGR
5.5	1282.674164	0.010384	NEGGKLGNPKNR
4.7	1282.681580	0.002968	DKGQAGLQR
4.3	1282.670349	0.014199	QIDLDVNR
4.0	1282.685623	-0.001075	VWVDGIQR
3.9	1282.670334	0.014214	QDLEAQIR
3.7	1282.688095	-0.003547	KPTKPESQSPGK
3.4	1282.692108	-0.007560	LEWVEIIEPR

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

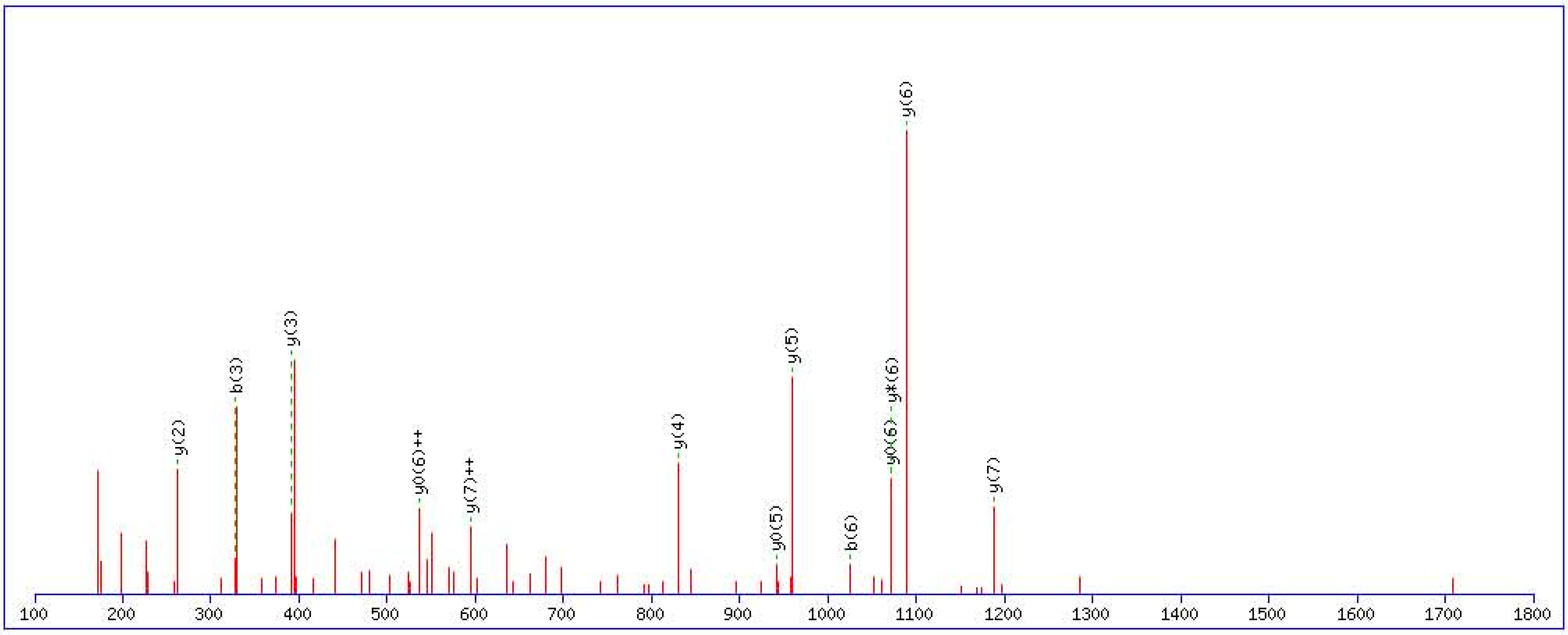
Mascot Search Results

Peptide View

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

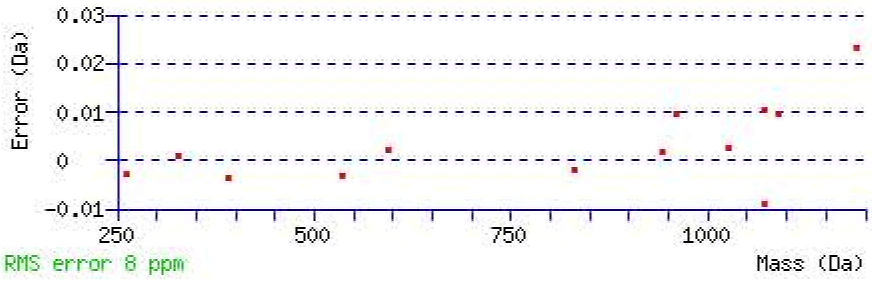
Match to Query 22733: 1285.636228 from(643.825390,2+) rtinseconds(1361) index(43302)
Title: Locus:1.1.1.2522.17 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

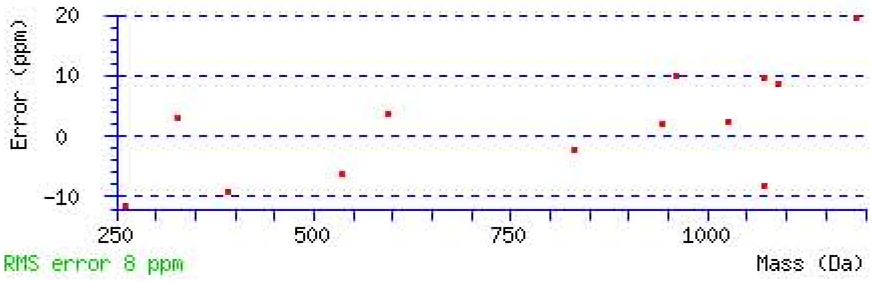
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1285.633621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 36 **Expect:** 0.00056
Matches : 13/70 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	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
35.7	1285.633621	0.002607	VVEEQESR
1.0	1285.626236	0.009992	VETQEVNPGASR

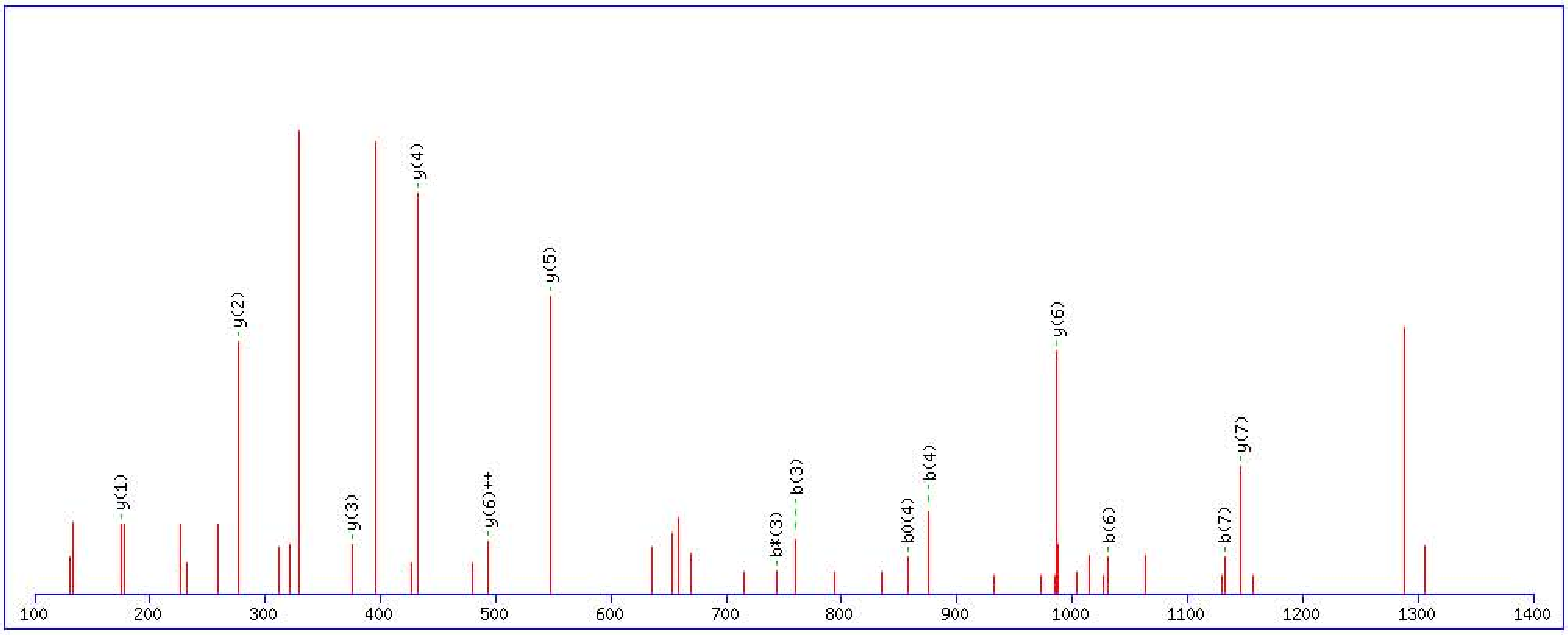
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

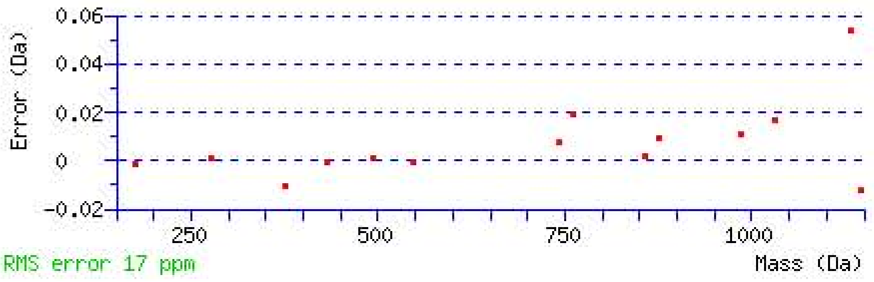
Match to Query 23136: 1305.570468 from(653.792510,2+) rtinseconds(1387) index(43448)
Title: Locus:1.1.1.2531.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

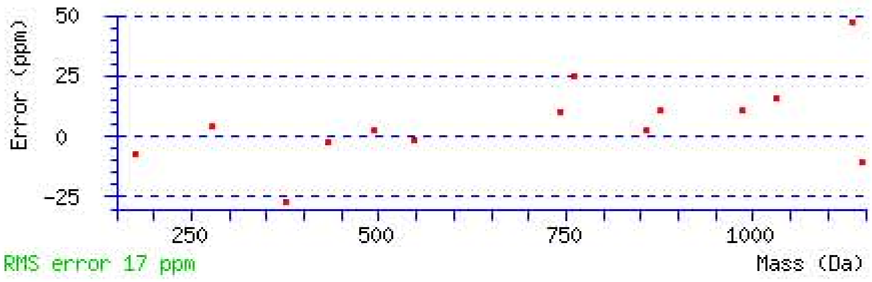
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1305.562820
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 5.7e-005
Matches : 14/72 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	161.037925	81.022600					C							8
2	321.068574	161.037925					C	***1146.539427***	573.773352	1129.512878	565.260077	1128.528862	564.768069	7
3	**760.293900**	380.650588	743.267351	372.137314			Q	***986.508778***	493.758027	969.482229	485.244753	968.498213	484.752745	6
4	**875.320843**	438.164060	858.294294	429.650785	857.310278	429.158777	D	***547.283452***	274.145364	530.256903	265.632090	529.272887	265.140082	5
5	932.342307	466.674792	915.315758	458.161517	914.331742	457.669509	G	***432.256509***	216.631893	415.229960	208.118618	414.245944	207.626610	4
6	**1031.410721**	516.208999	1014.384172	507.695724	1013.400156	507.203716	V	***375.235045***	188.121161	358.208496	179.607886	357.224480	179.115878	3
7	**1132.458400**	566.732838	1115.431851	558.219564	1114.447835	557.727556	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 CCQDGVTR
(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	1305.562820	0.007648	CCQDGVTR
14.1	1305.588409	-0.017941	CRSSTPADAWR
5.2	1305.577194	-0.006726	CDAGWLADGSVR
2.1	1305.569778	0.000690	SSWQGENQSQR
1.0	1305.583679	-0.013211	EQEPDFEEKR
0.6	1305.577148	-0.006680	MGQHYEEEKR

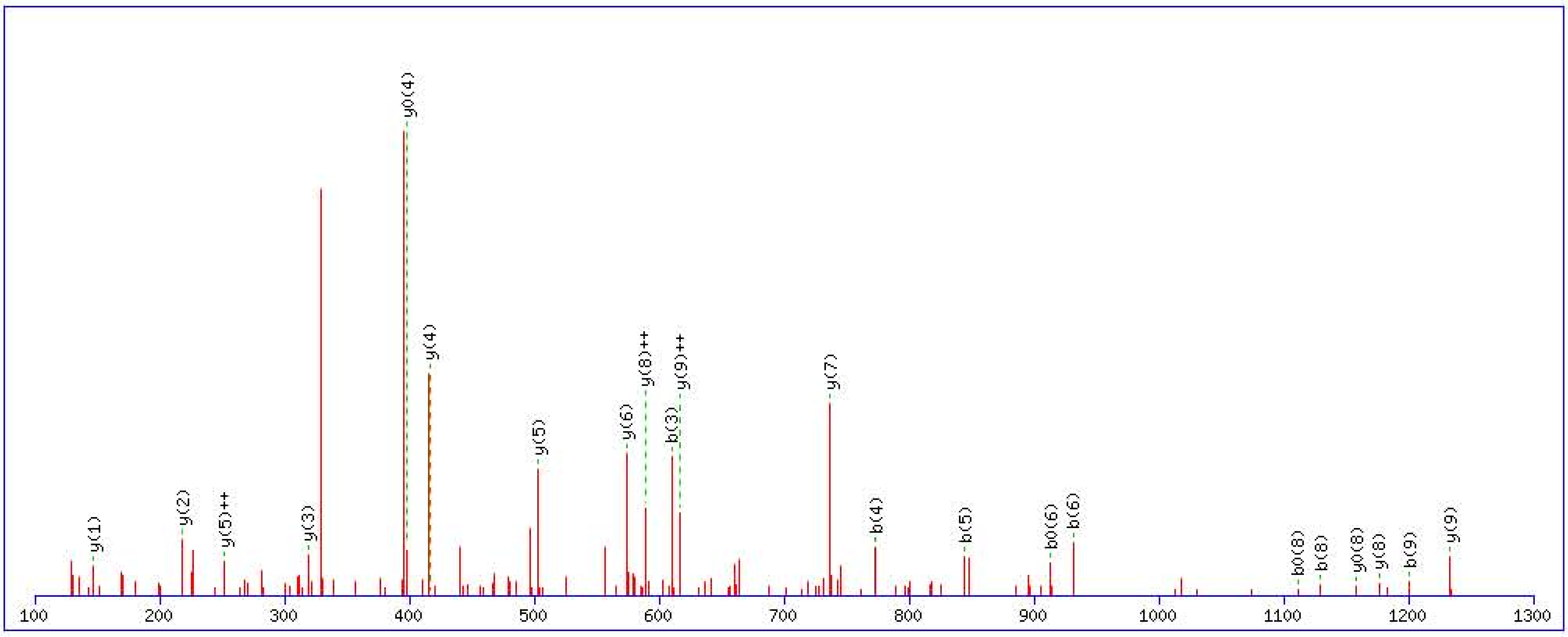
Mascot Search Results

Peptide View

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

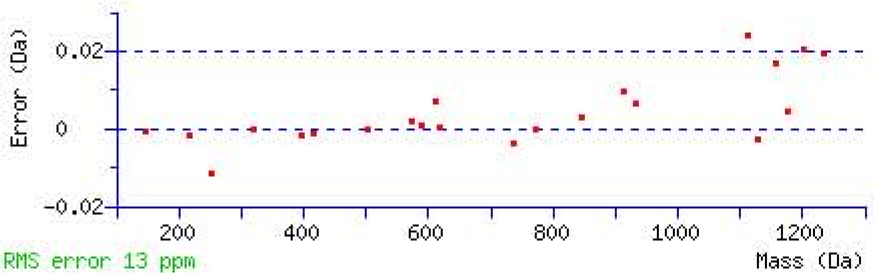
Match to Query 23941: 1345.710648 from(673.862600,2+) rtinseconds(1604) index(44889)
Title: Locus:1.1.1.2607.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

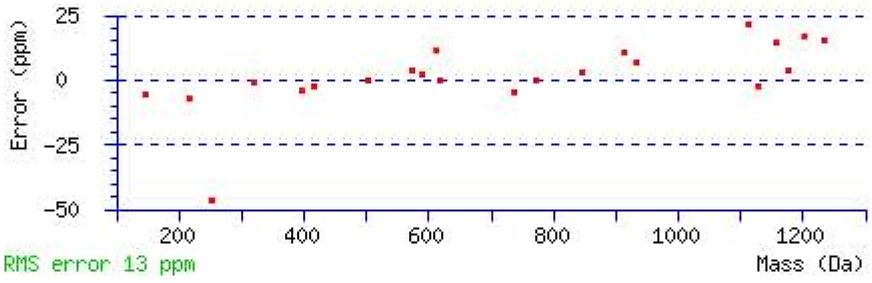
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1345.706390
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 53 **Expect:** 0.0001
Matches : 22/90 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**							**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
52.7	1345.706390	0.004258	LGQYASPTAK
9.4	1345.727509	-0.016861	LGLMDNEIKVAK
9.2	1345.692474	0.018174	VASCRYPALGPR
8.2	1345.706390	0.004258	LGQYDQALK
7.6	1345.724182	-0.013534	LGAVPATSGPTTFK
7.1	1345.706406	0.004242	QGLYTPQTK
0.4	1345.713608	-0.002960	NGMLLTGGGKDRK
0.3	1345.724152	-0.013504	QPLQTDIYGLAK

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

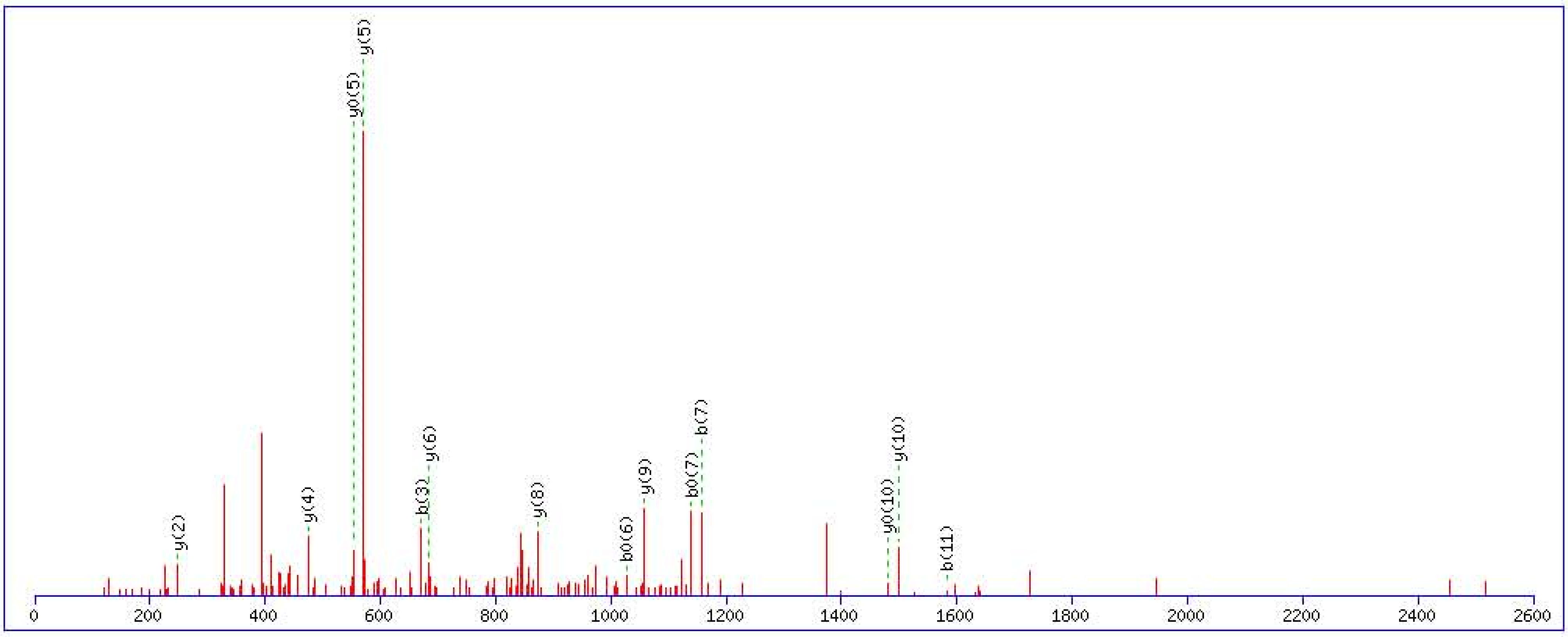
Mascot Search Results

Peptide View

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

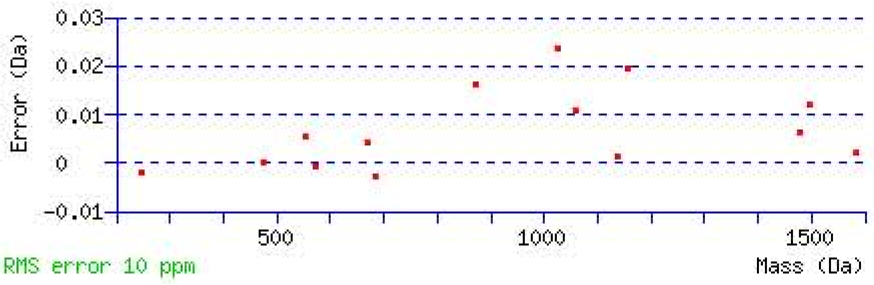
Match to Query 36950: 1726.873848 from(864.444200,2+) rtinseconds(2028) index(47589)
Title: Locus:1.1.1.2754.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

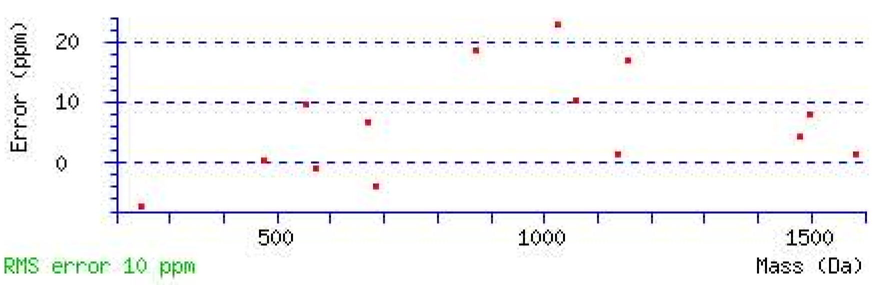
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1726.860001
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 30 **Expect:** 0.011
Matches : 14/126 fragment ions using 32 most intense peaks (help)

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





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.1	1726.860001	0.013847	TEQWSTLPPETK
8.5	1726.871216	0.002632	NLNTKLQMYFQSPK
6.4	1726.867188	0.006660	KDHAEMQAVIDAKQK
2.2	1726.849960	0.023888	TERFGQGGAGPVGGQGPR
1.2	1726.874573	-0.000725	VTKNQEMMSQIKYK
0.4	1726.853485	0.020363	MASGHAFQPDLVK

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

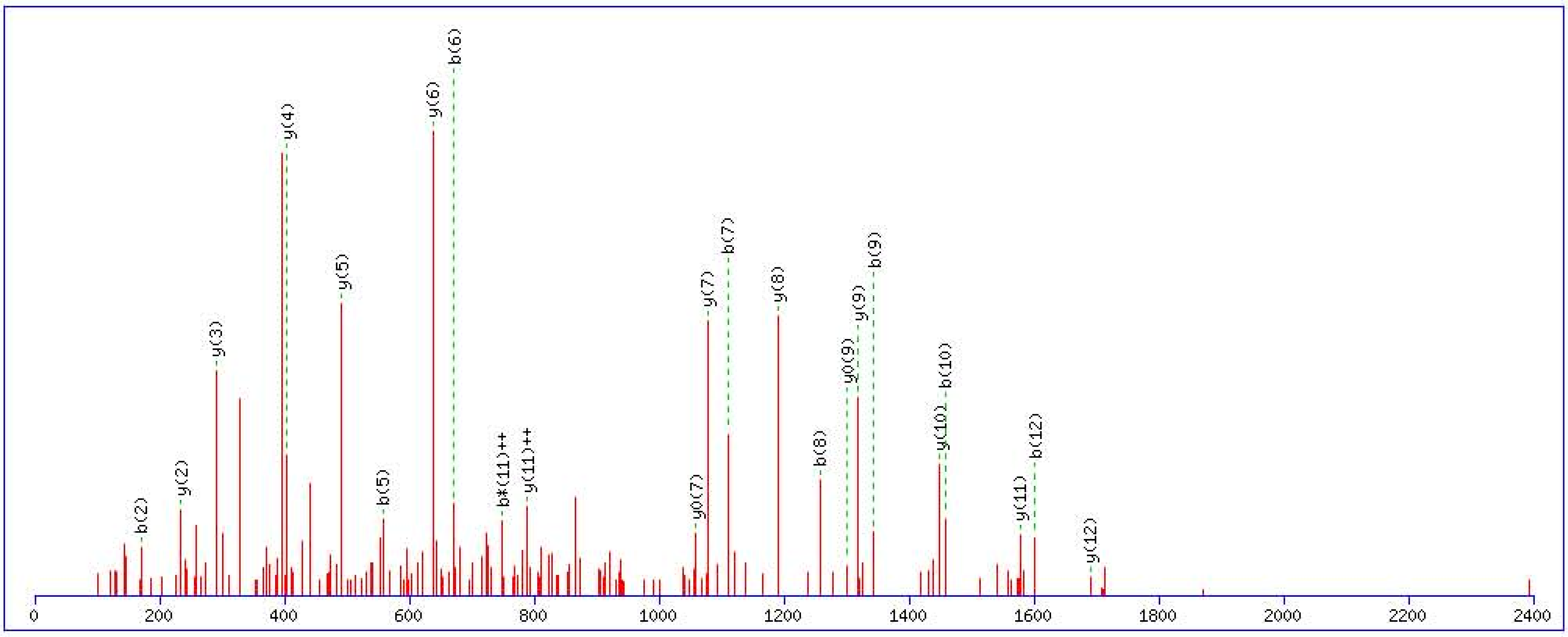
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

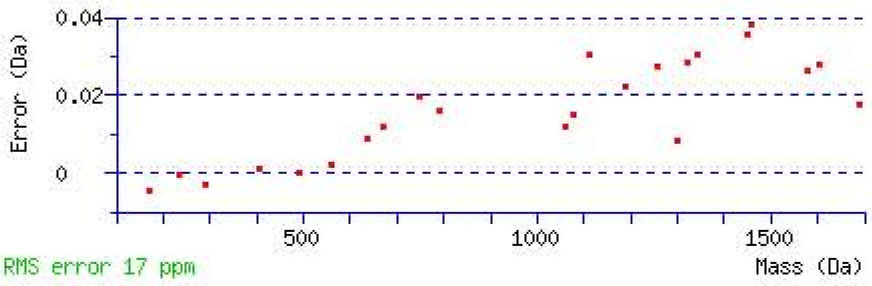
Match to Query 37441: 1746.905928 from(874.460240,2+) rtinseconds(2557) index(50641)
Title: Locus:1.1.1.2938.6 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

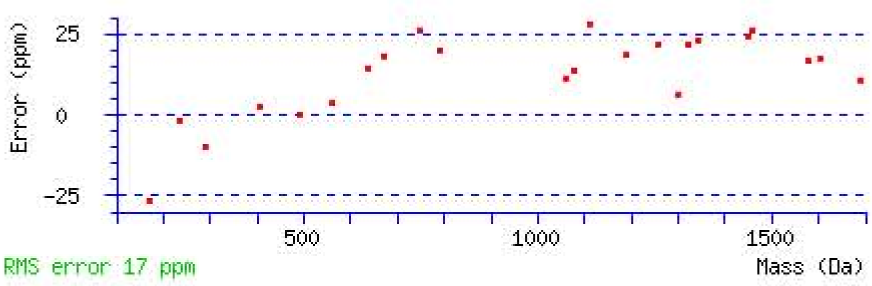
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 89  Expect: 8.7e-009
Matches : 23/126 fragment ions using 33 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	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
89.4	1746.886200	0.019728	GLEEELQFSLGSK
3.4	1746.887558	0.018370	AVQSKAFCAGGLAPGWK
1.4	1746.918533	-0.012605	AKLQMTEAALALSEQK

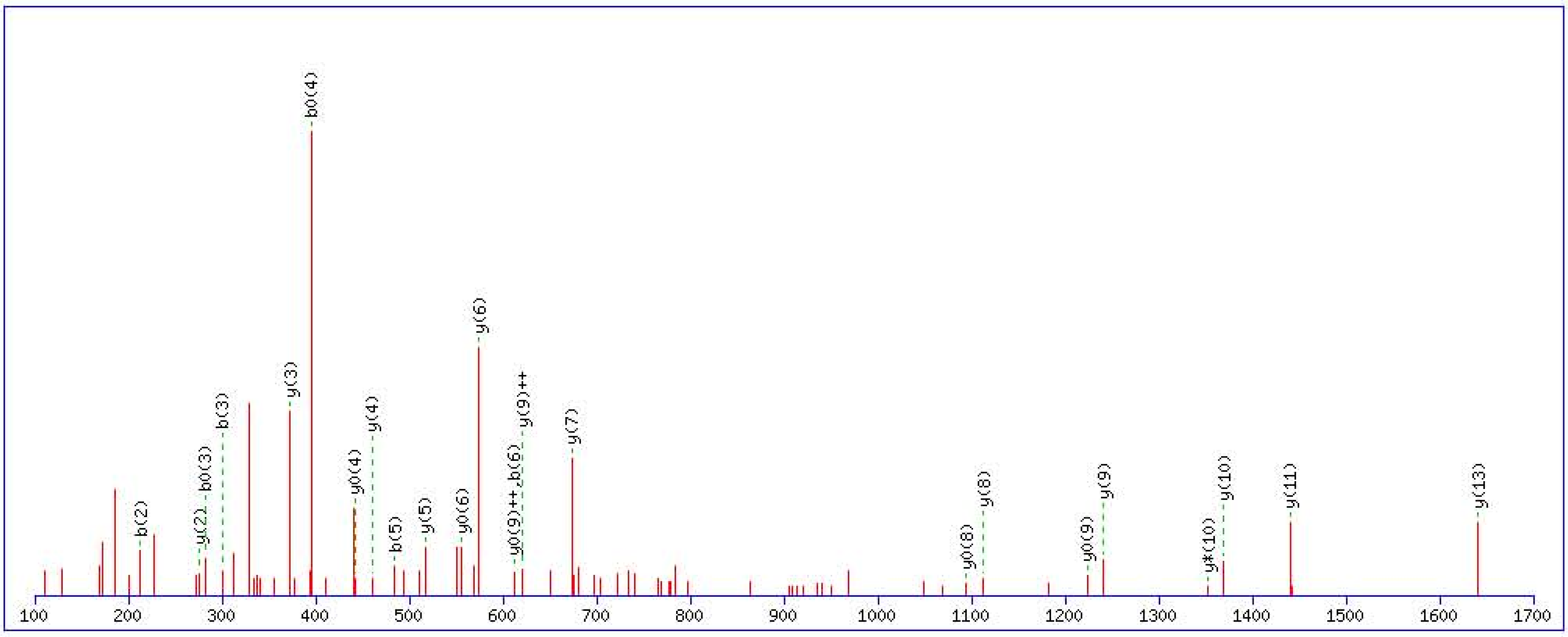
Mascot Search Results

Peptide View

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

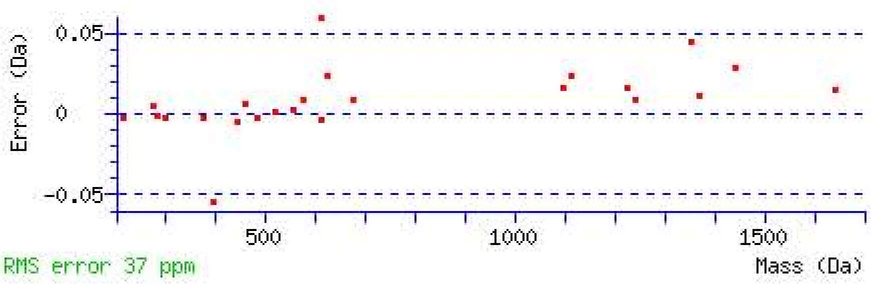
Match to Query 39377: 1851.983712 from(618.335180,3+) rtinseconds(1978) index(47293)
Title: Locus:1.1.1.2737.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

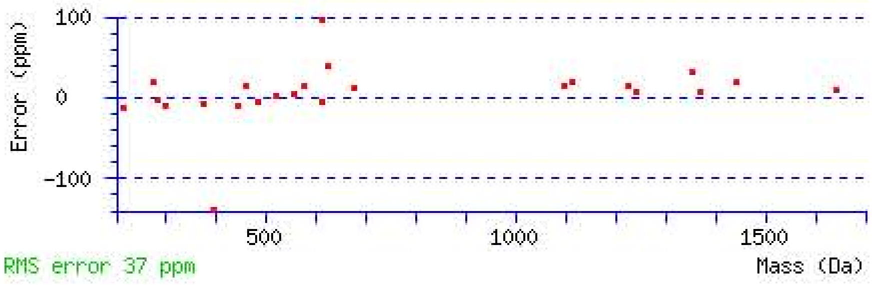


Monoisotopic mass of neutral peptide Mr(calc): 1851.976425
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 53 **Expect:** 1.4e-005
Matches : 24/152 fragment ions using 56 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							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



RMS error 37 ppm



RMS error 37 ppm

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
53.1	1851.976425	0.007287	VLSLAQEQVGGSPEK
34.0	1851.976425	0.007287	VLSLAQEQVGGSPEK
1.4	1852.005402	-0.021690	LQLEQQVATGPALDNKK

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

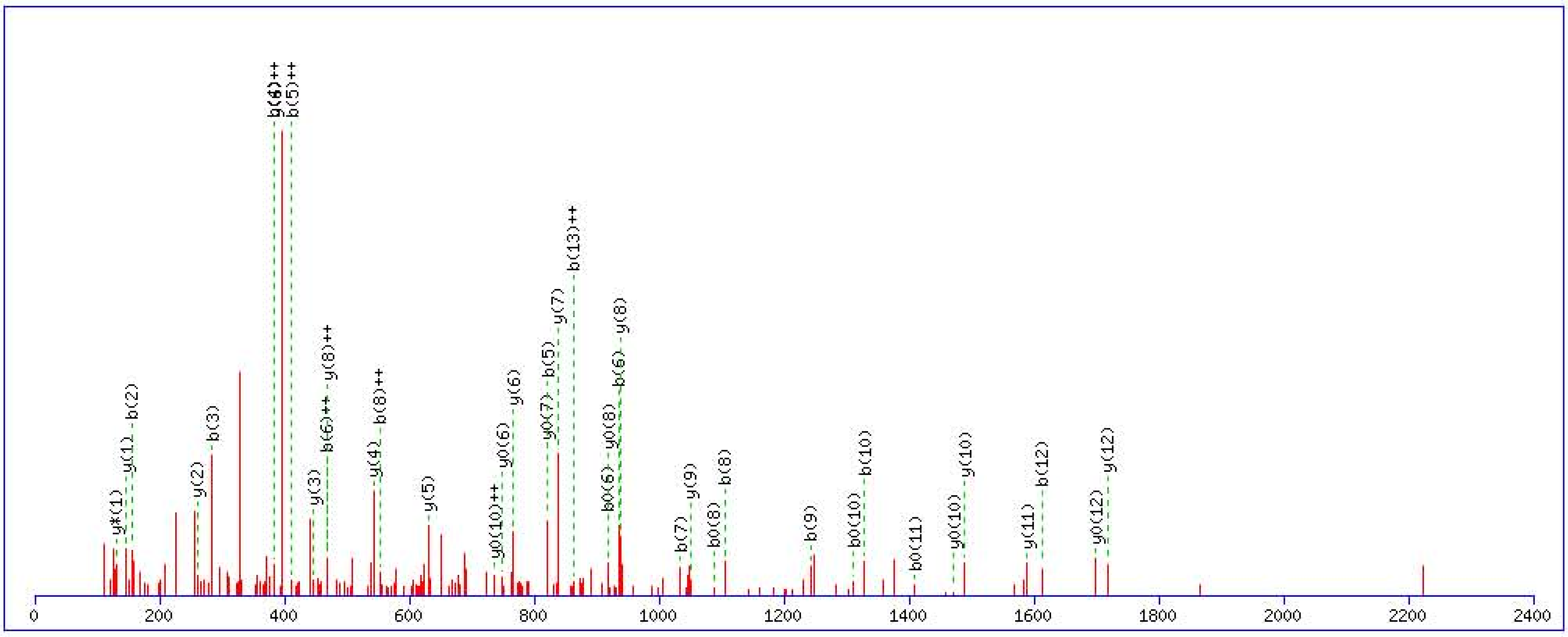
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

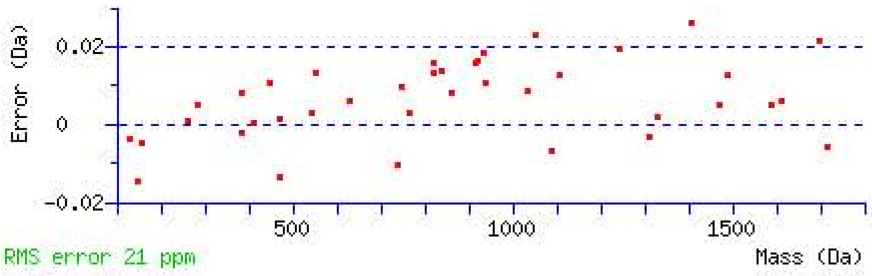
Match to Query 39870: 1871.022912 from(624.681580,3+) rtinseconds(2231) index(48816)
Title: Locus:1.1.1.2825.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

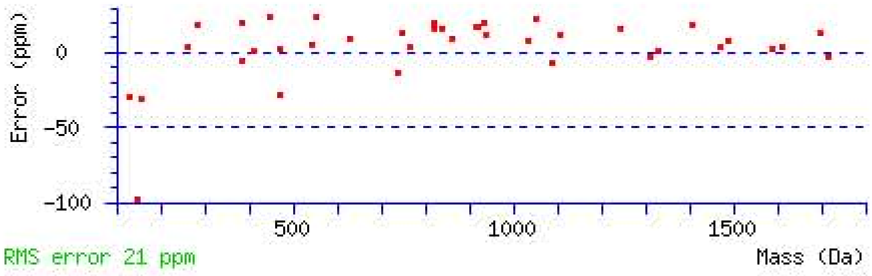
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1871.012756
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 0.00038
Matches : 39/136 fragment ions using 106 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	**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
47.2	1871.012756	0.010156	GPEVQLVAHSPWLK

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

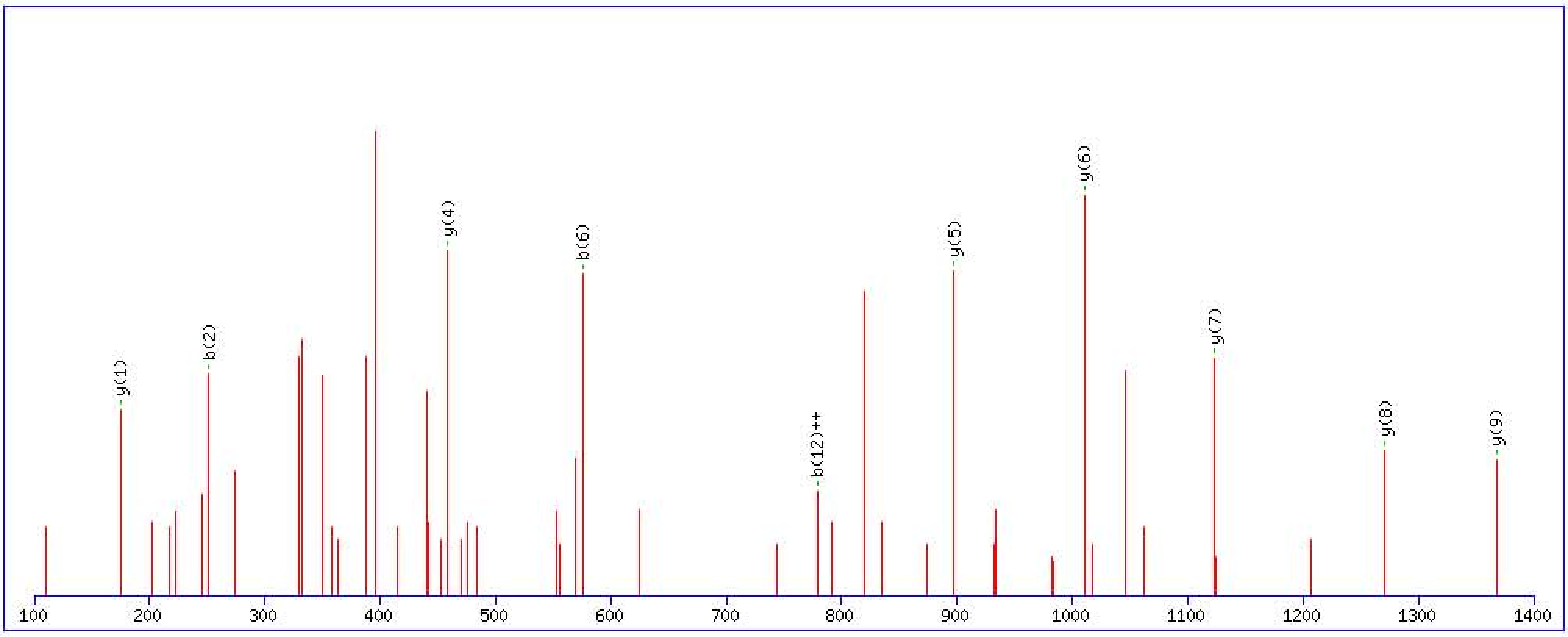
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

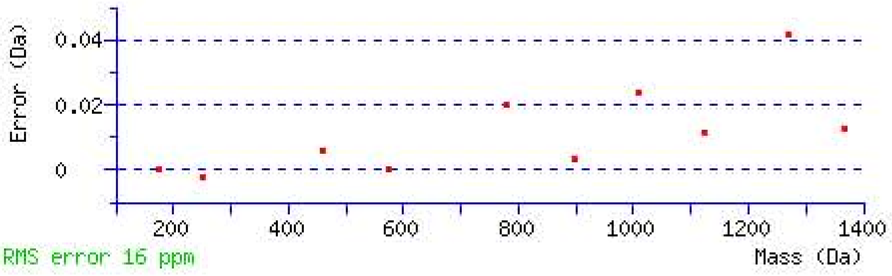
Match to Query 40950: 1941.156402 from(648.059410,3+) rtinseconds(2868) index(52987)
Title: Locus:1.1.1.3045.3 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

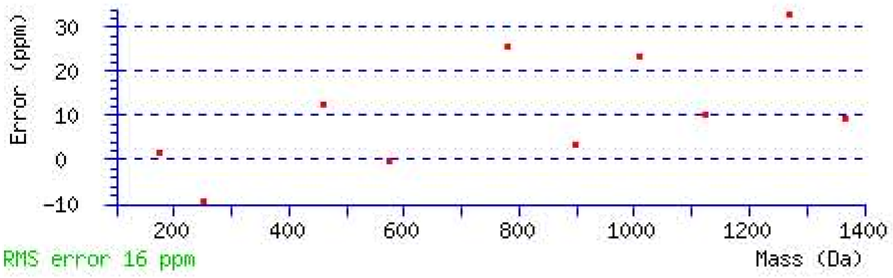
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1941.138626
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 52 **Expect:** 1.2e-005
Matches : 10/92 fragment ions using 13 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
51.6	1941.138626	0.017776	HLVPGAPFLLQALVR

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

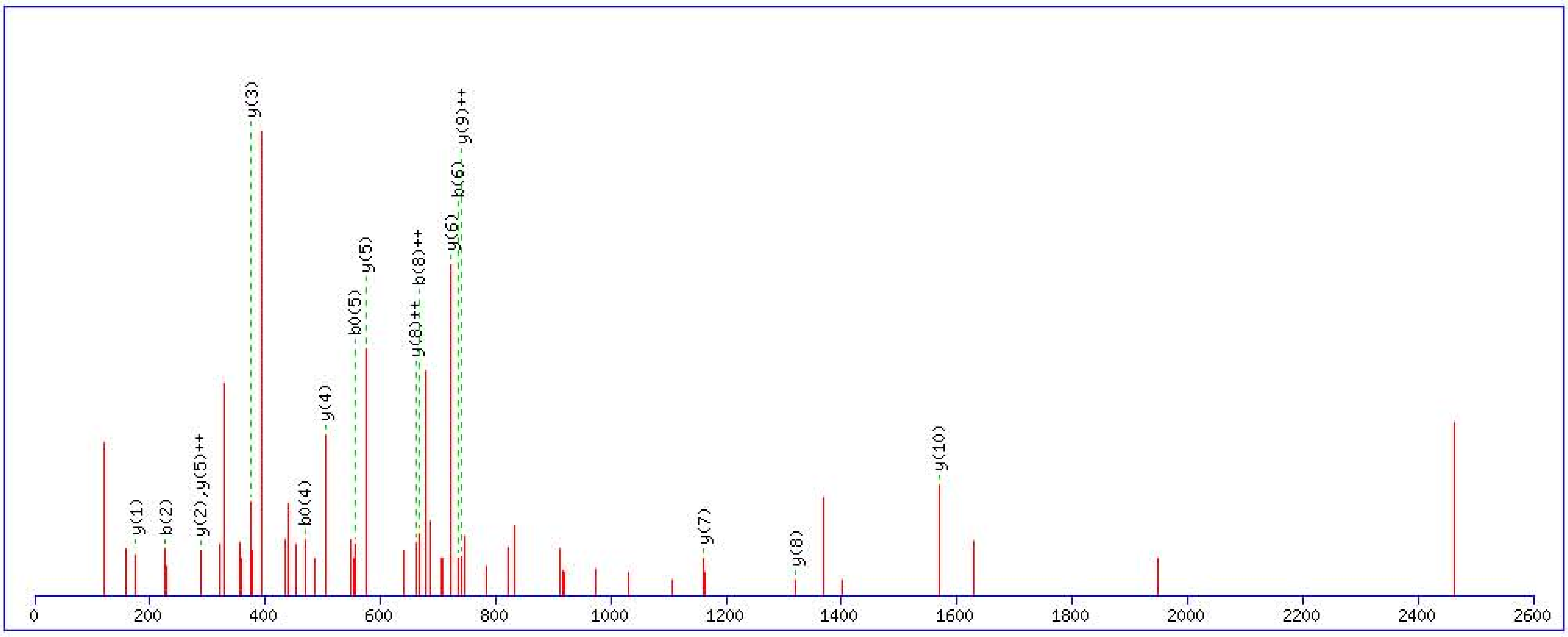
Mascot Search Results

Peptide View

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

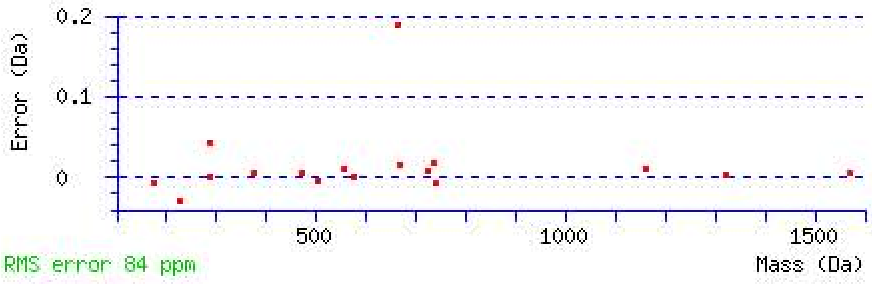
Match to Query 43769: 2053.964232 from(685.662020,3+) rtinseconds(2492) index(50229)
Title: Locus:1.1.1.2916.14 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

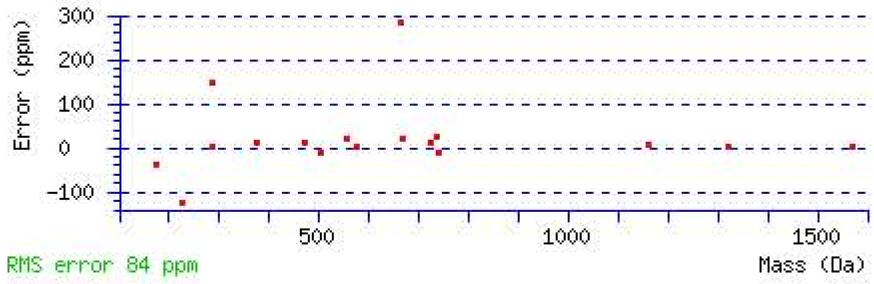
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2053.942368
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.00081
Matches : 17/138 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
33.8	2053.942368	0.021864	EPFLSCCQFAESLR
0.9	2053.948227	0.016005	EKSTCSMGSELLPMISPR

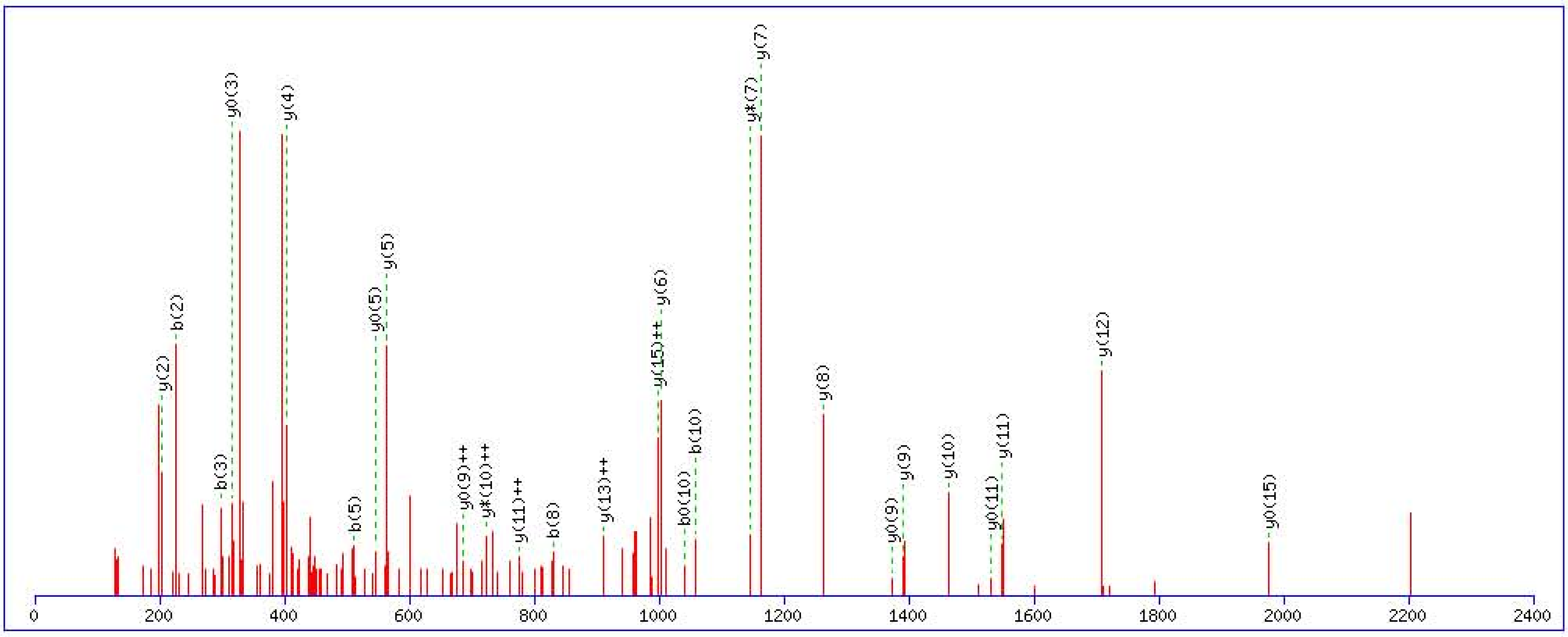
Mascot Search Results

Peptide View

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

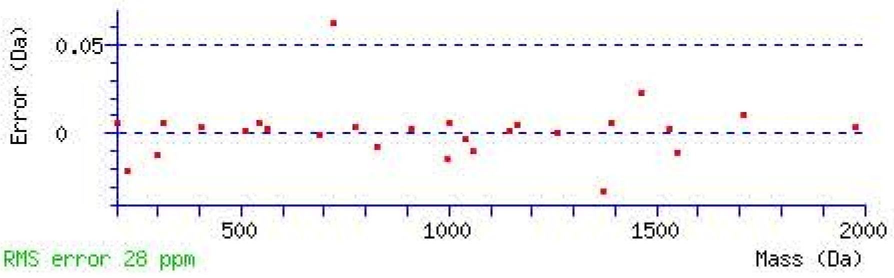
Match to Query 46405: 2220.049032 from(741.023620,3+) rtinseconds(2140) index(63359)
Title: Locus:1.1.1.3371.11 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

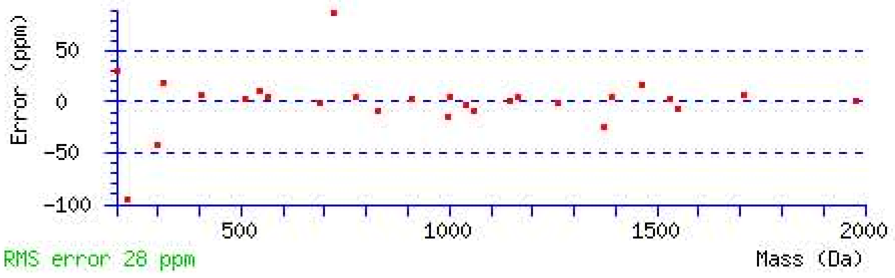
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 51  Expect: 2.7e-005
Matches : 27/160 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	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
51.3	2220.041092	0.007940	LLATLCSAEVCQCAEGK
2.5	2220.048080	0.000952	EPQEGAELPEATGTTSHR

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

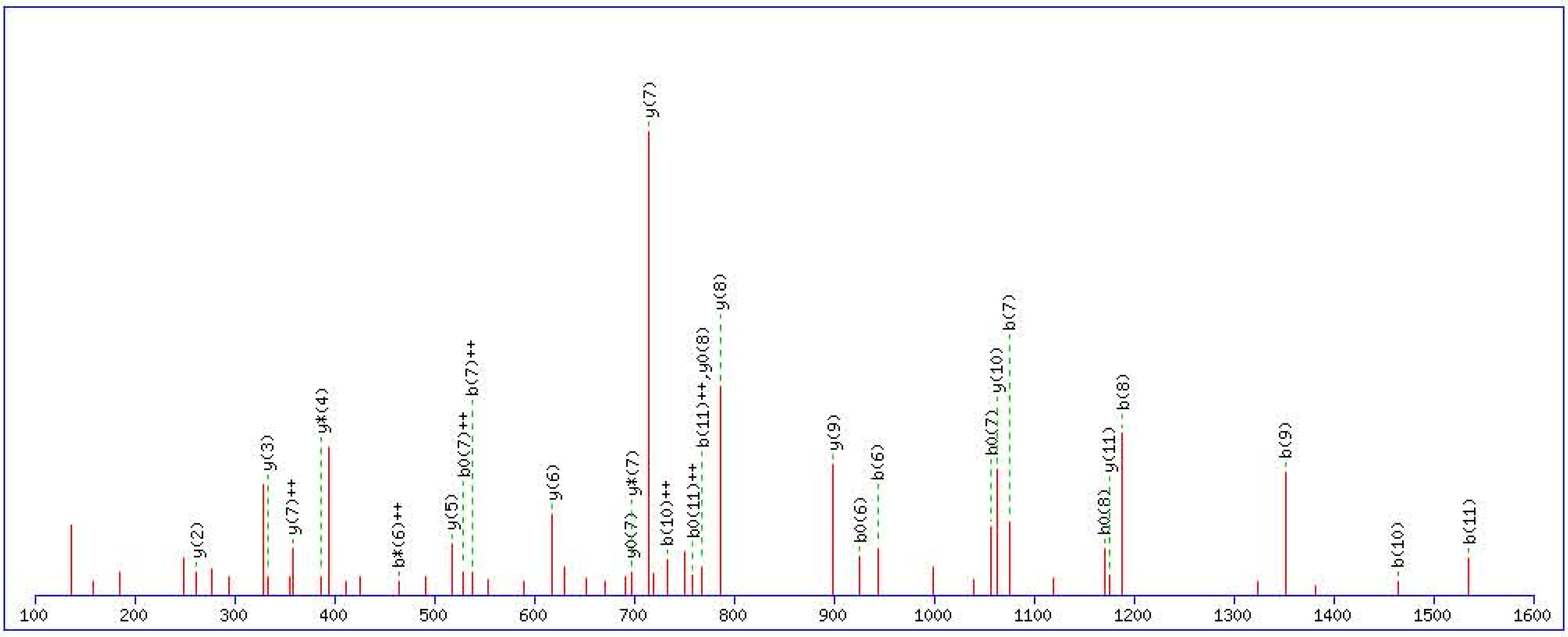
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

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

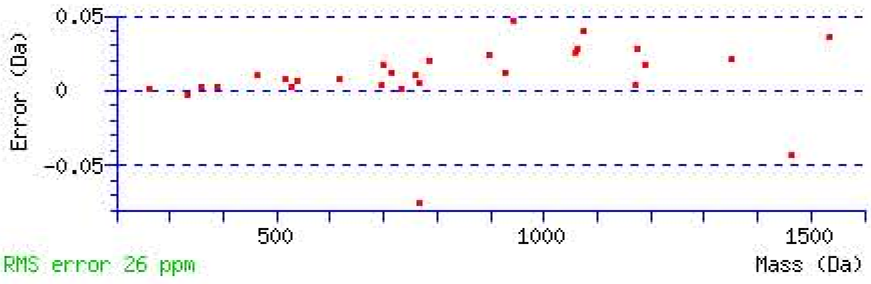
Match to Query 46845: 2249.129682 from(750.717170,3+) rtinseconds(2504) index(50330)
Title: Locus:1.1.1.2920.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

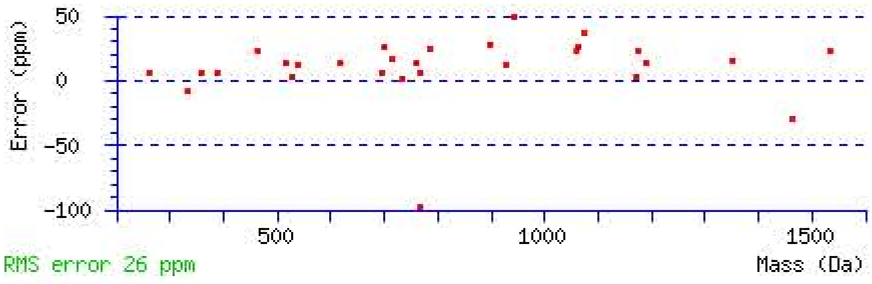
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2249.100647
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.00079
Matches : 29/188 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							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
41.4	2249.100647	0.029035	GCGEQTMIYLAPTLAASR
7.8	2249.115051	0.014631	YSTSLYASPSMVHEGVAVVPR
1.3	2249.143570	-0.013888	TPPPQPPLISSMDSISQK
1.3	2249.104492	0.025190	AQLQQHNLEMVGEGTRQ
0.3	2249.137527	-0.007845	QKFERPICVSWSTDVKGGR

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

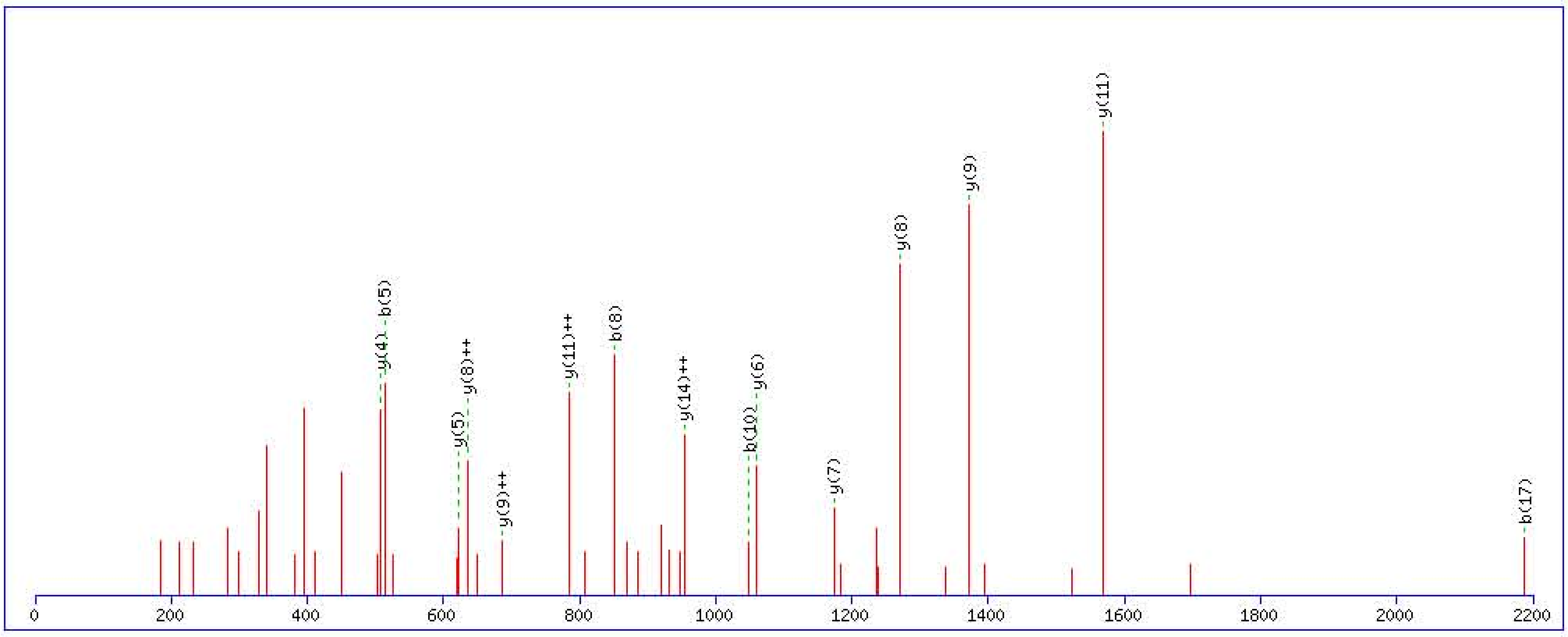
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

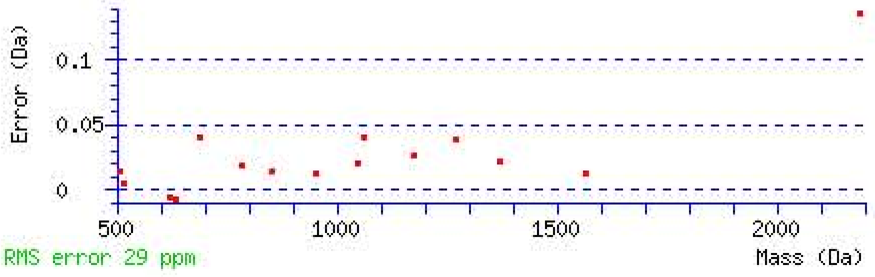
Match to Query 49443: 2418.255432 from(807.092420,3+) rtinseconds(3006) index(54069)
Title: Locus:1.1.1.3091.18 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

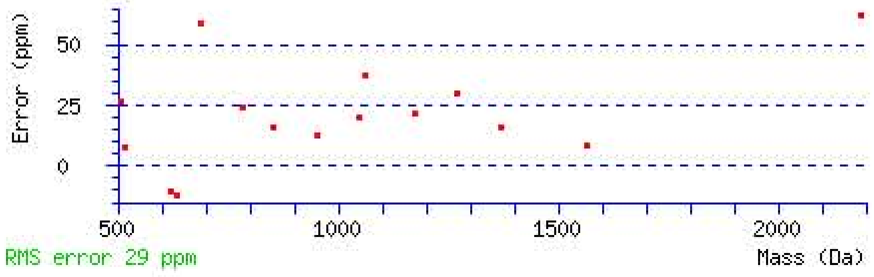
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2418.225342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14    : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.0011
Matches : 15/198 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	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
32.4	2418.225342	0.030090	DDPDAPLQPVTPLQLFEGR
0.8	2418.259033	-0.003601	QQQRALLGPWLSGPQGTDR
0.8	2418.259033	-0.003601	QQQRALLGPWLSGPQGTDR
0.8	2418.259033	-0.003601	QQQRALLGPWLSGPQGTDR

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

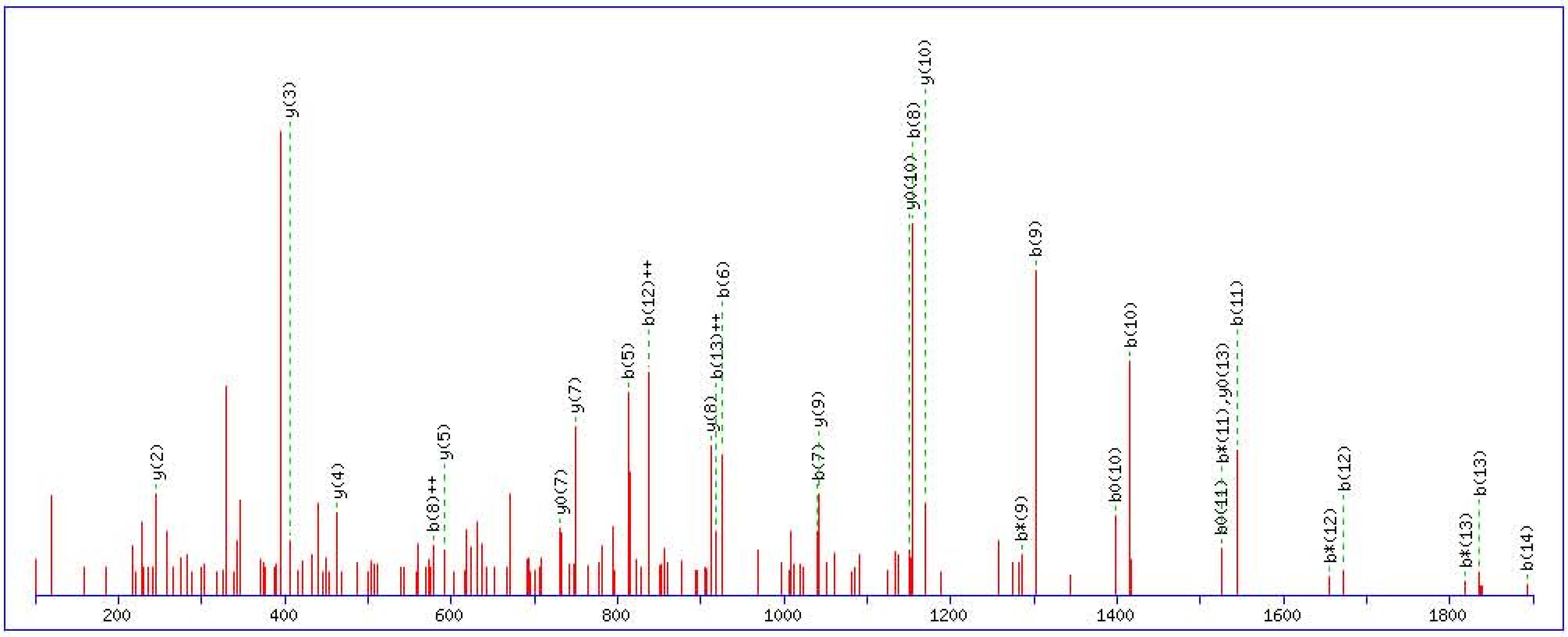
Mascot Search Results

Peptide View

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

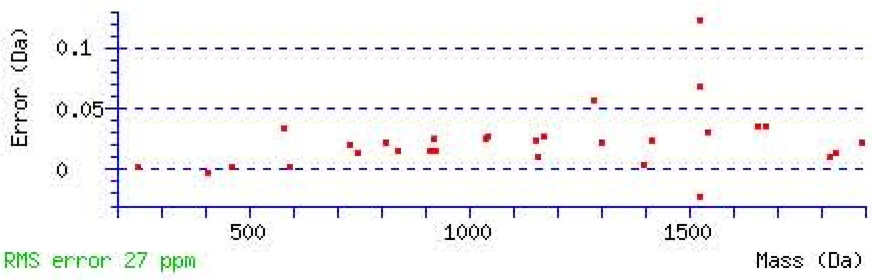
Match to Query 51933: 2583.191832 from(862.071220,3+) rtinseconds(2732) index(51870)
Title: Locus:1.1.1.2998.21 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

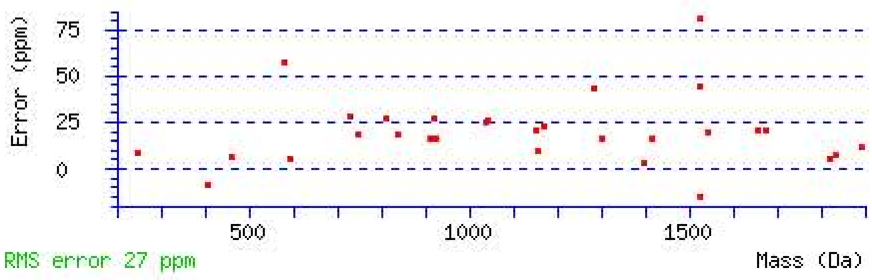
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2583.155624
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 7.5e-006
Matches : 30/194 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	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
62.5	2583.155624	0.036208	AACAQLNDFLQEYGTQGCQV
15.1	2583.155624	0.036208	AACAQLNDFLQEYGTQGCQV

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

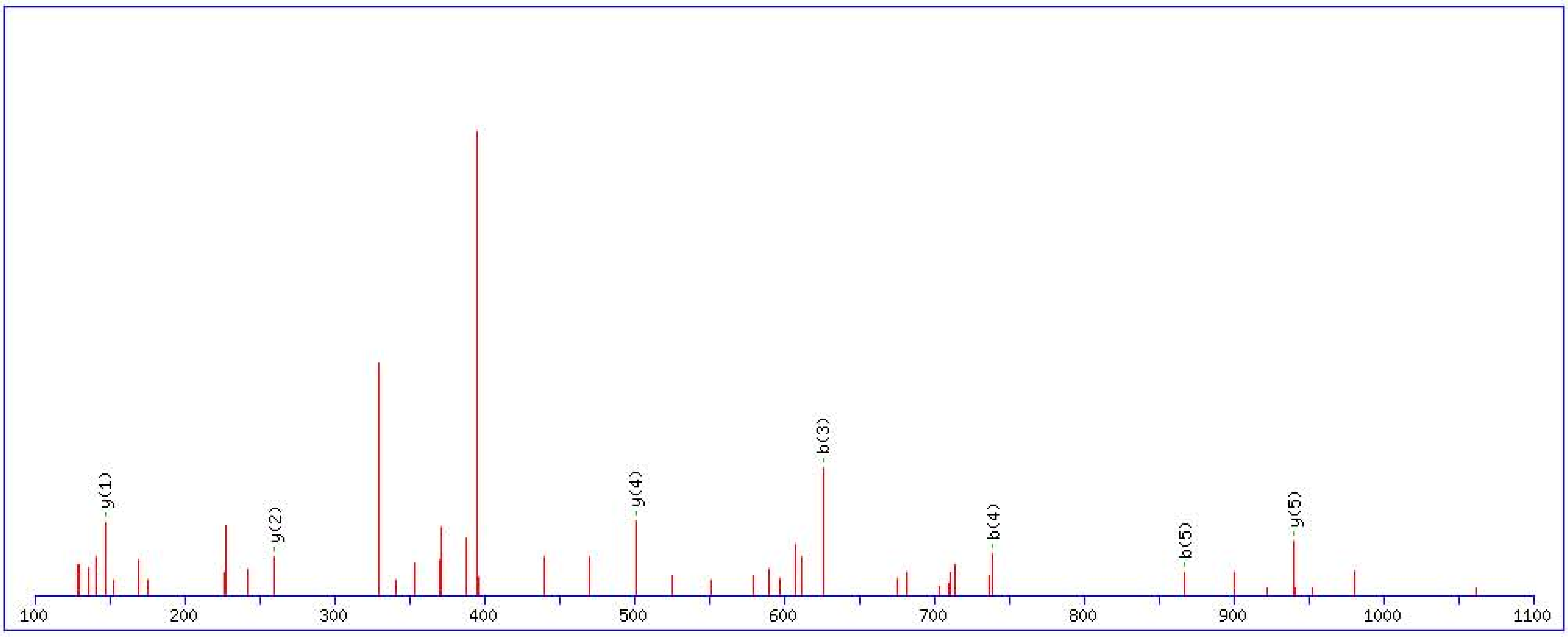
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GEQIQLK**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

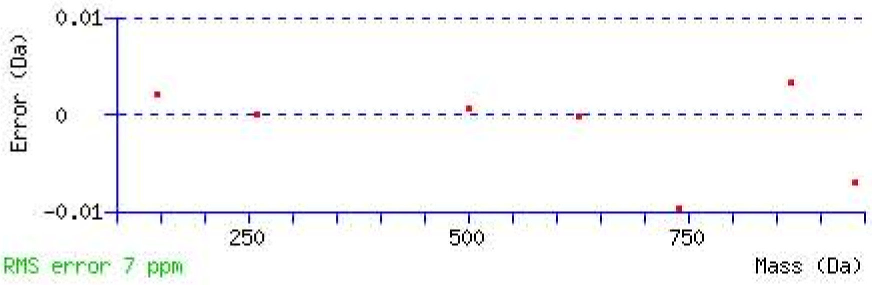
Match to Query 17403: 1125.622228 from(563.818390,2+) rtinseconds(1752) index(31676)
Title: Locus:1.1.1.3159.13 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

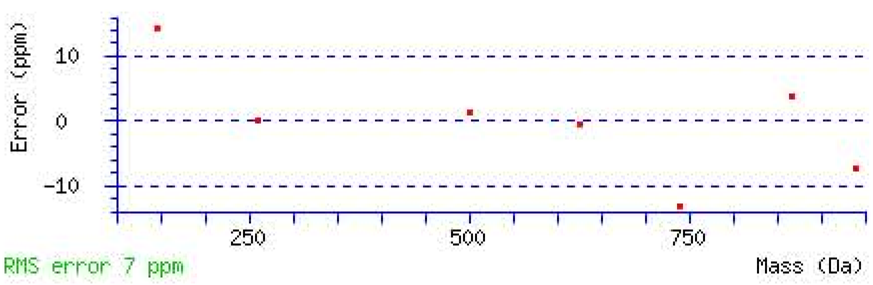
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1125.621597
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 25  Expect: 0.039
Matches : 7/56 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							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
25.2	1125.621597	0.000631	GEQIQLK
9.5	1125.632828	-0.010600	KLCLSHLQK
8.9	1125.607666	0.014562	QMDRHAKIK
7.2	1125.636856	-0.014628	WAAQVIK
6.8	1125.633499	-0.011271	VSHFLPWIK
6.0	1125.629486	-0.007258	RVDGWPVGLK
4.9	1125.606979	0.015249	LKEAFDYIK
4.8	1125.621597	0.000631	GEQIQLK
3.7	1125.621597	0.000631	GQELIQK
3.2	1125.622940	-0.000712	WQLGRR

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

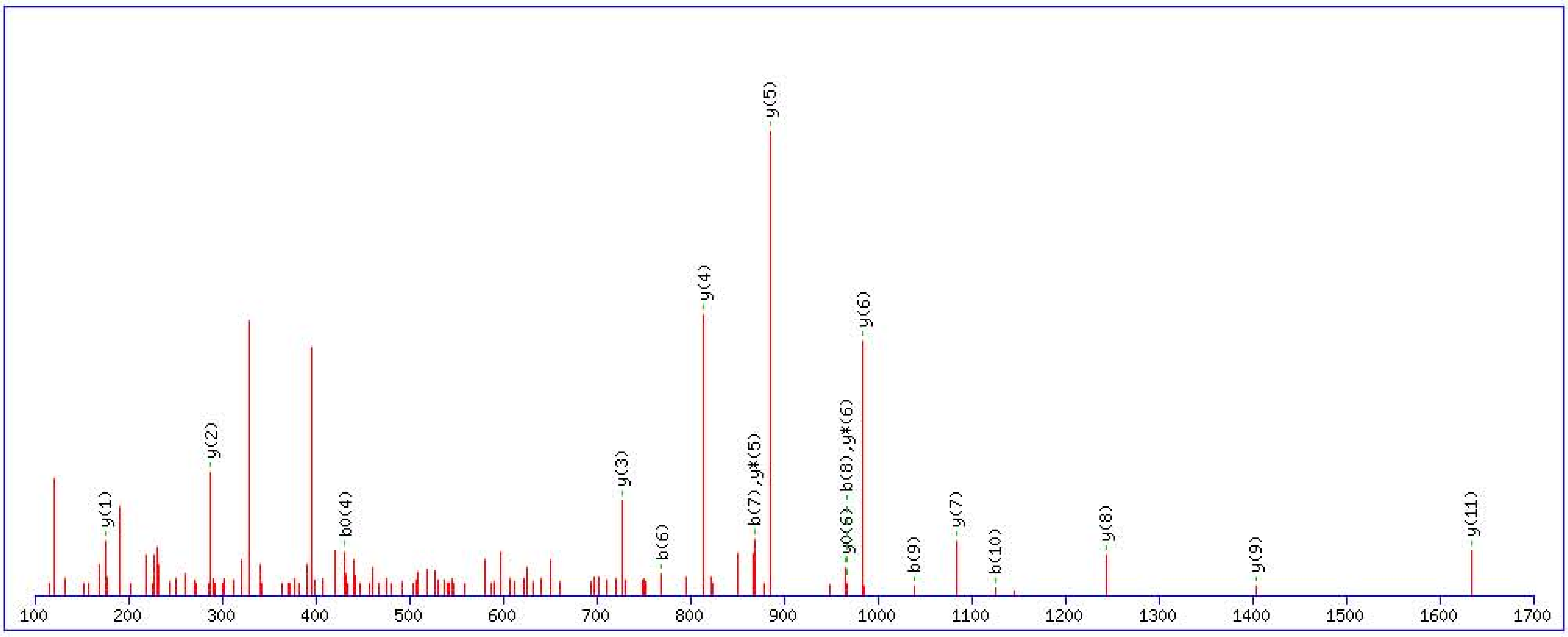
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFTECCVVASQLR**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

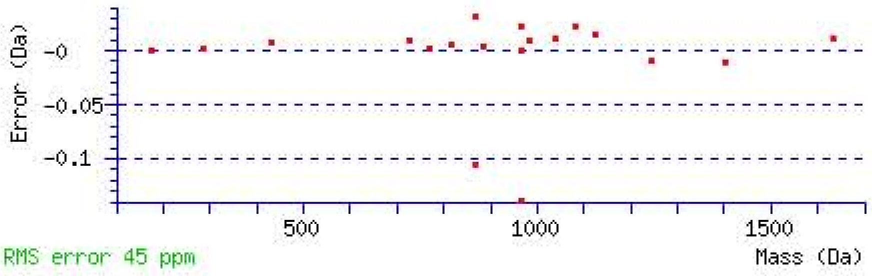
Match to Query 39370: 1850.894082 from(617.971970,3+) rtinseconds(2188) index(34165)
Title: Locus:1.1.1.3311.7 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

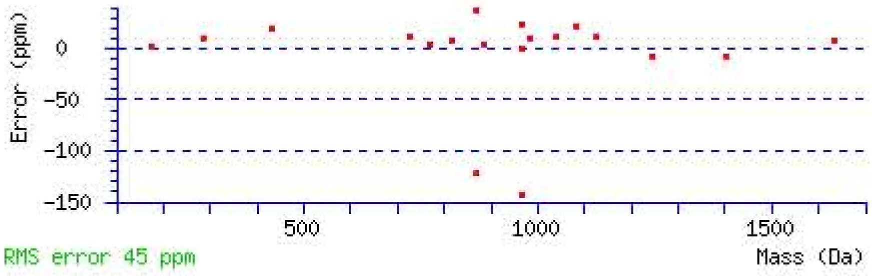
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1850.884140
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 8.8e-006
Matches : 19/114 fragment ions using 35 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	72.044390	36.525833					A							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
57.1	1850.884140	0.009942	AFTECCVVASQLR
3.2	1850.893127	0.000955	AMESTATAAVAAELVSADK

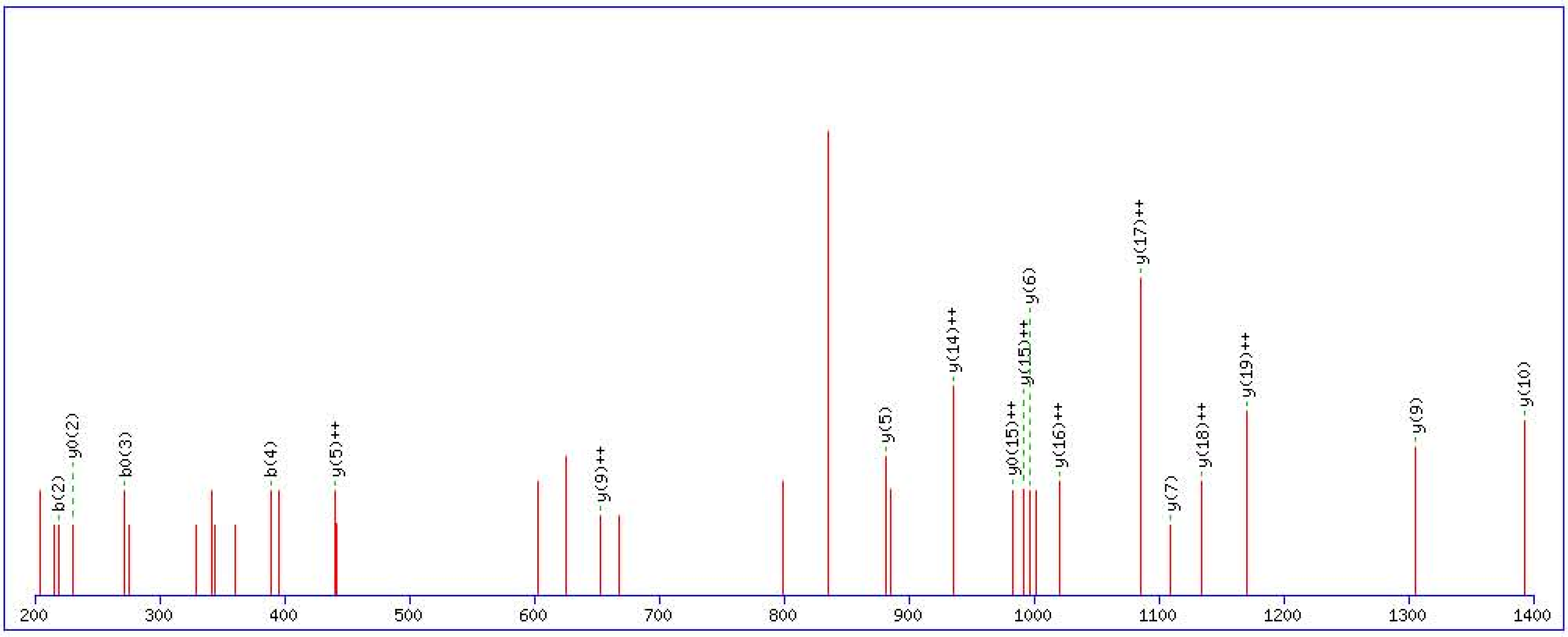
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MSAVEGICTSESPVIDHQGTK**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

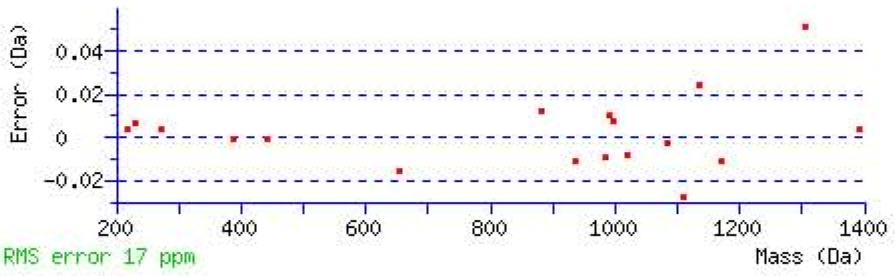
Match to Query 51717: 2556.200082 from(853.073970,3+) rtinseconds(1957) index(32868)
Title: Locus:1.1.1.3230.24 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

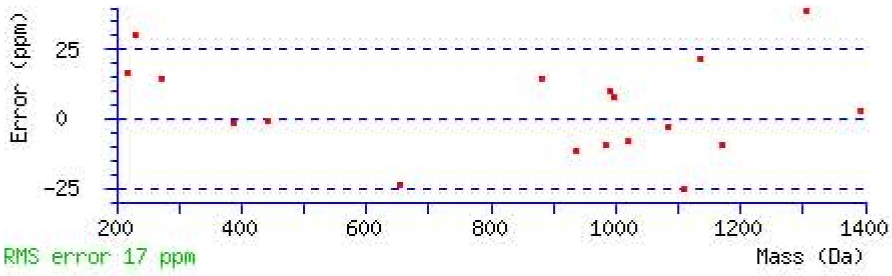
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 39  Expect: 0.0025
Matches : 18/202 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	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





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
38.7	2556.202240	-0.002158	MSAVEGICTSESPVIDHQGTK

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

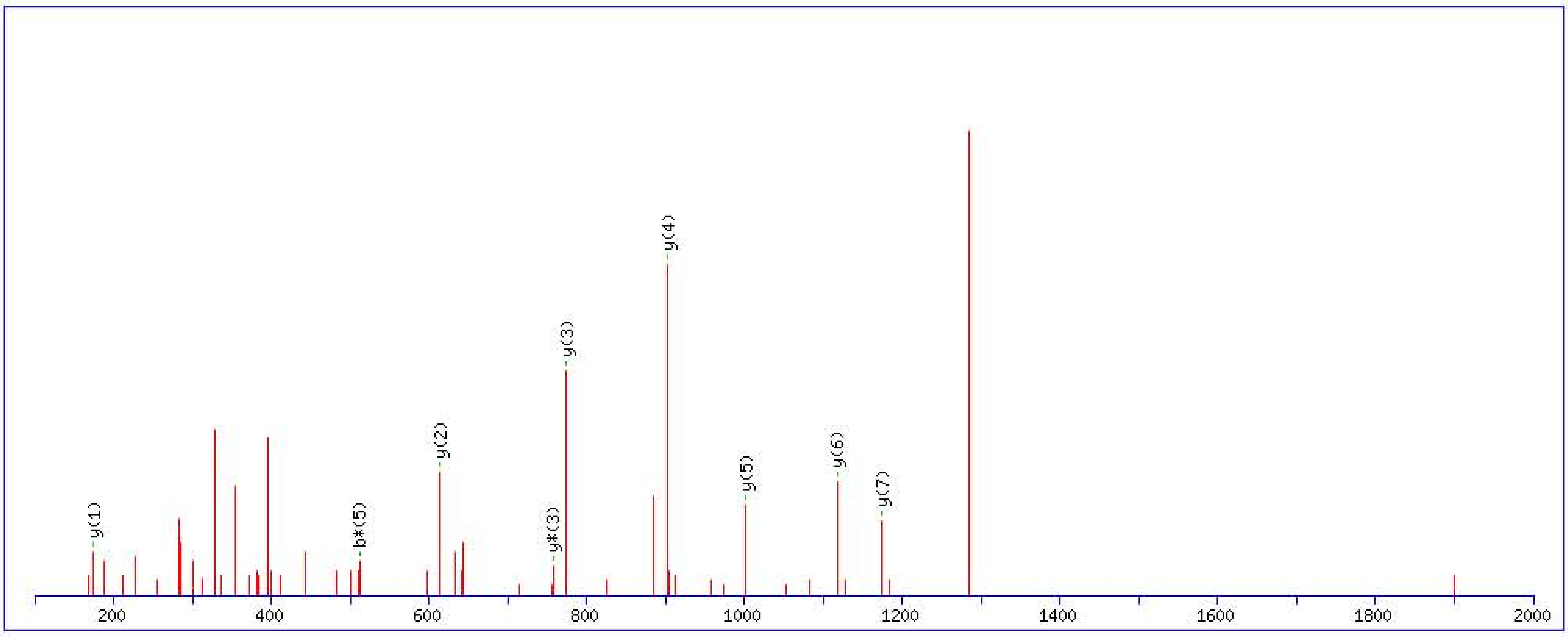
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QGDVECQR**
Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

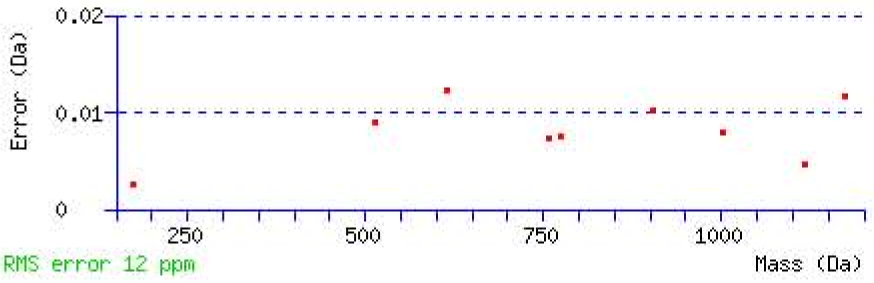
Match to Query 23073: 1301.596568 from(651.805560,2+) rtinseconds(1363) index(14952)
Title: Locus:1.1.1.3075.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

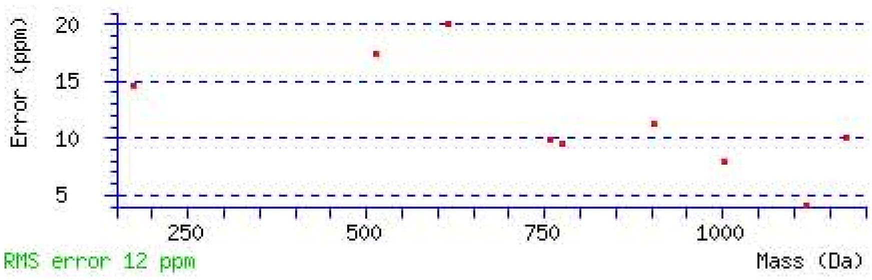
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1301.585648
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 7.8e-006
Matches : 9/74 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
59.9	1301.585648	0.010920	QGDVECQR
15.3	1301.584763	0.011805	KATEDAEGGDGPR
11.1	1301.584747	0.011821	QESPSQENIDR
10.1	1301.604263	-0.007695	CPAAMTVMHLR
6.4	1301.604263	-0.007695	CPAAMTVMHLR
4.1	1301.584747	0.011821	ESENLASGDQPR
3.0	1301.614609	-0.018041	LGNPEEGQRMR

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

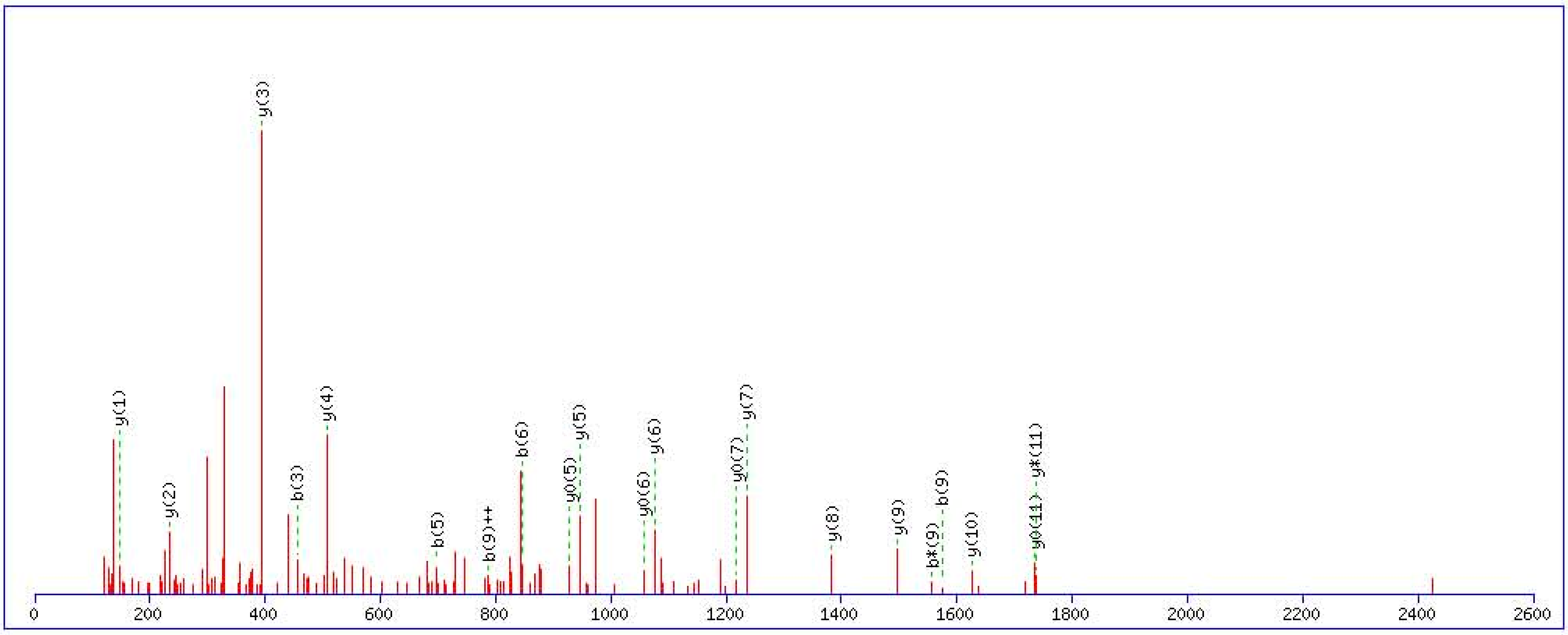
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YYQENFCEQICSK**
Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

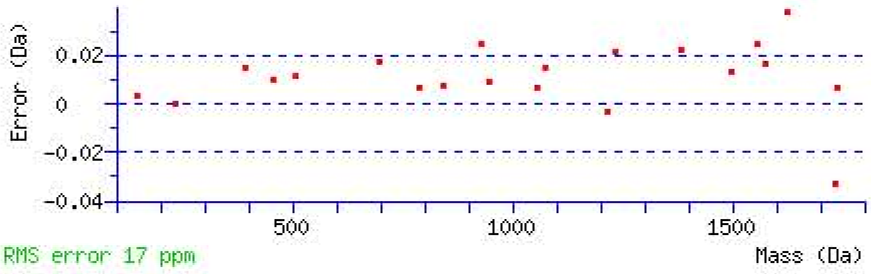
Match to Query 44169: 2078.907882 from(693.976570,3+) rtinseconds(2047) index(19351)
Title: Locus:1.1.1.3313.13 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

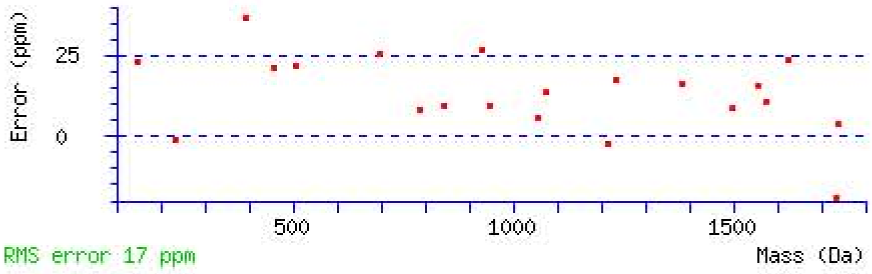
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2078.889984
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 8.9e-005
Matches : 21/132 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	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
48.0	2078.889984	0.017898	YYQENFCEQICSK

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

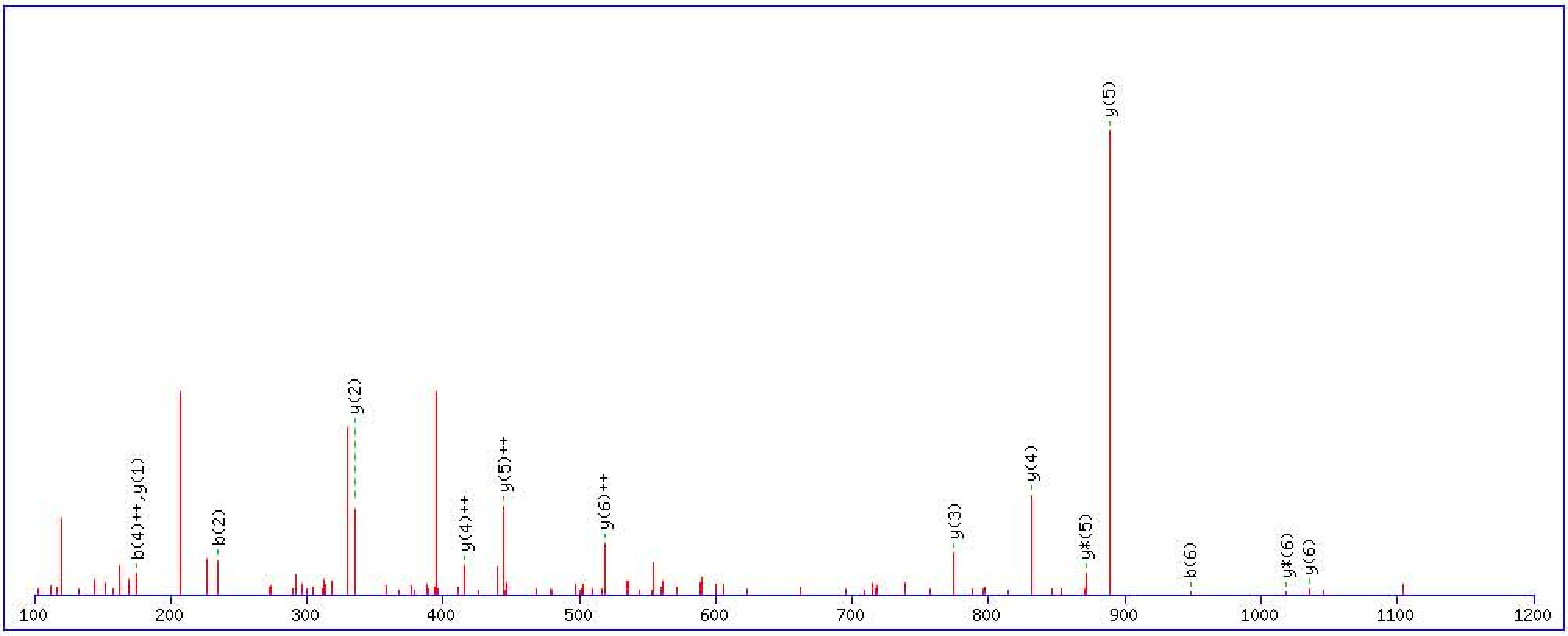
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

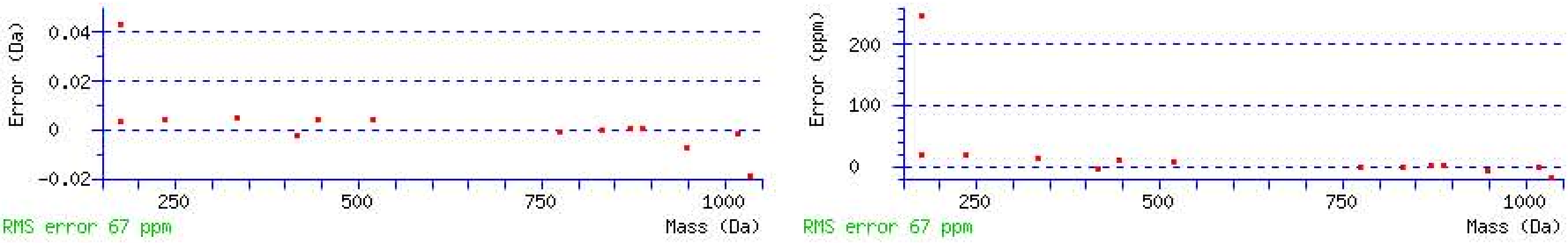
Match to Query 17316: 1121.508208 from(561.761380,2+) rtinseconds(1564) index(2446)
Title: Locus:1.1.1.3096.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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): 1121.511032
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.0038
Matches : 14/52 fragment ions using 29 most intense peaks    (help)
```

#	b	b++	b*	b*++	b0	b0++	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
30.7	1121.511032	-0.002824	SFGGQCR
4.8	1121.500259	0.007949	HPGFHQEDR
4.7	1121.513535	-0.005327	MGSGGDSLLGGR
1.8	1121.502274	0.005934	MSVEEQIDR

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

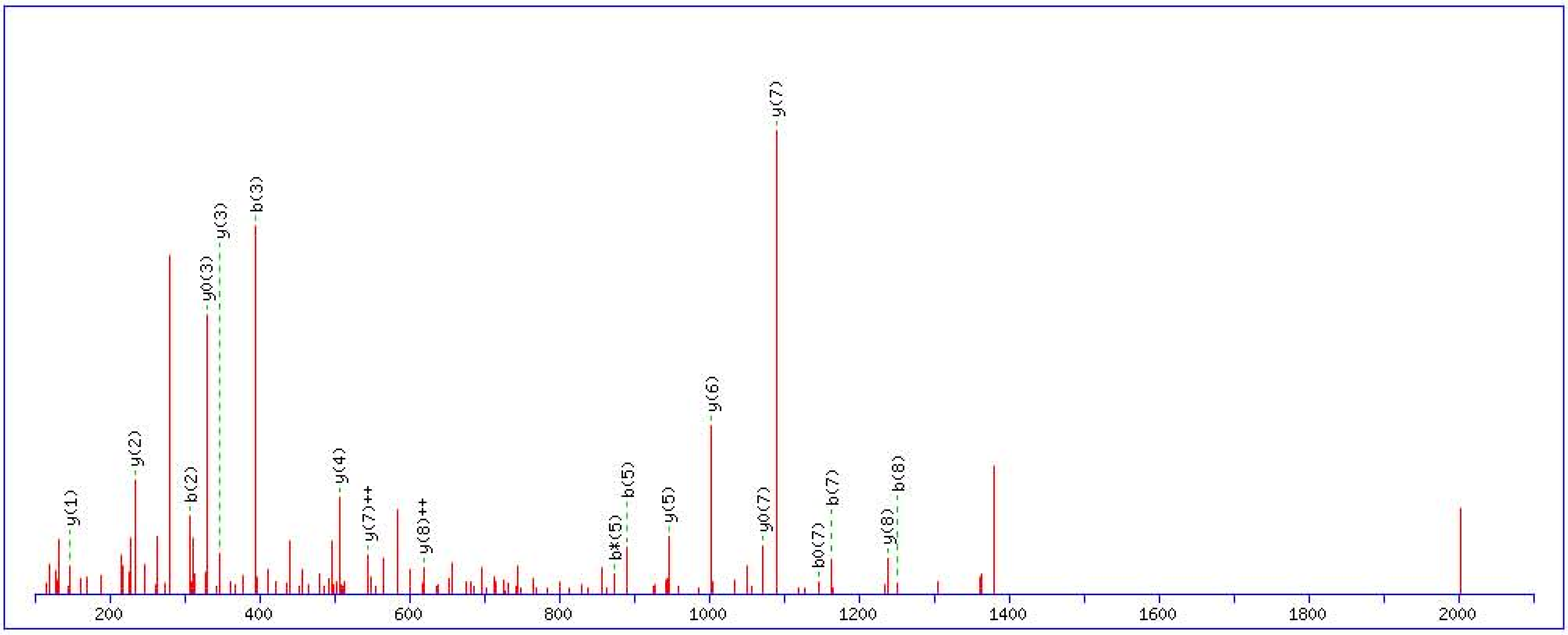
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

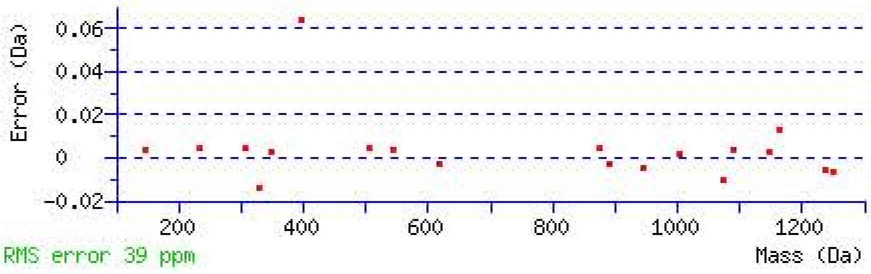
Match to Query 26264: 1396.629708 from(699.322130,2+) rtinseconds(1656) index(3072)
Title: Locus:1.1.1.3128.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

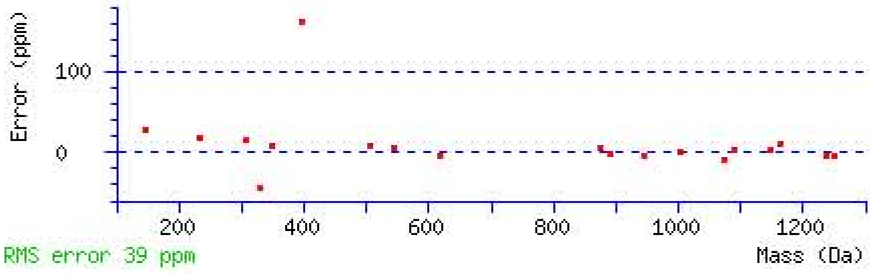
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1396.630157
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00012
Matches : 19/82 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	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
48.5	1396.630157	-0.000449	CFSGQCISK
16.0	1396.629272	0.000436	QLSQAEATDFCK

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

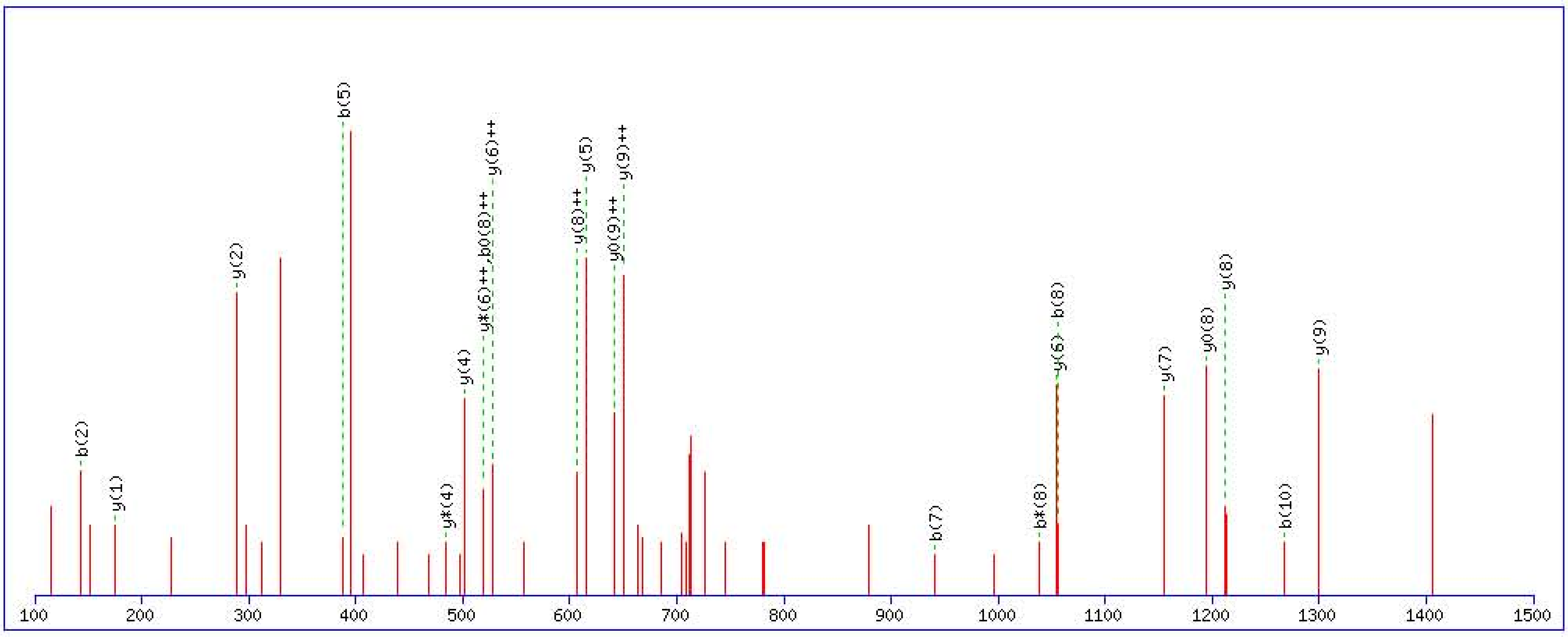
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

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

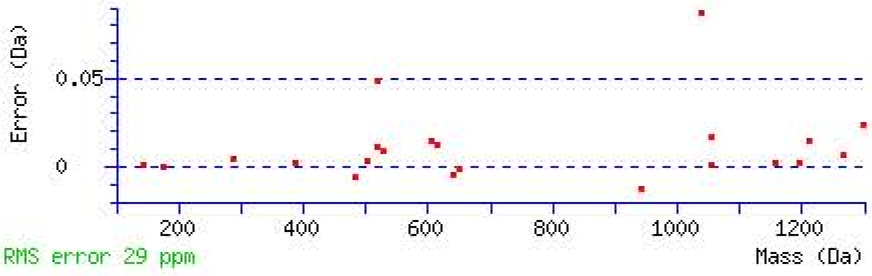
Match to Query 28370: 1440.759128 from(721.386840,2+) rtinseconds(1593) index(16535)
Title: Locus:1.1.1.3155.18 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

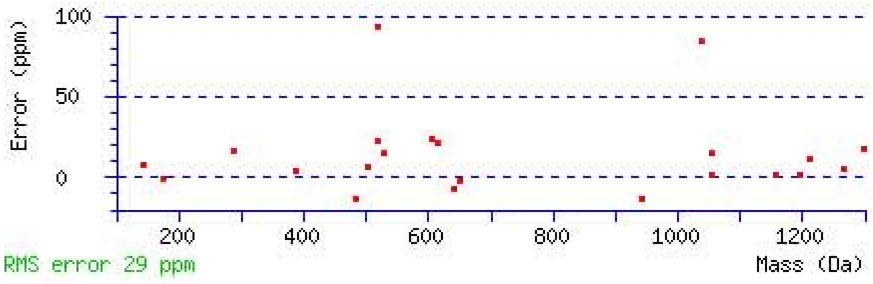
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1440.750717
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 48 **Expect:** 0.00022
Matches : 22/94 fragment ions using 41 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	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
48.3	1440.750717	0.008411	AASGTQNNVLR
8.7	1440.765961	-0.006833	VMHANNPKYVLR
4.6	1440.739471	0.019657	EEKCPLGTAPALR
3.8	1440.750717	0.008411	LDQLDASRGR
3.6	1440.769318	-0.010190	RMQEMLHKIQK
3.0	1440.757217	0.001911	NNLLEIEVNDLR
2.5	1440.754715	0.004413	MAAWSPAAAAPLLR
1.9	1440.757202	0.001926	NNLLQAELEELR
1.0	1440.761963	-0.002835	THTVRLAMGNGLR
0.1	1440.739487	0.019641	AAVTGQDEAIR

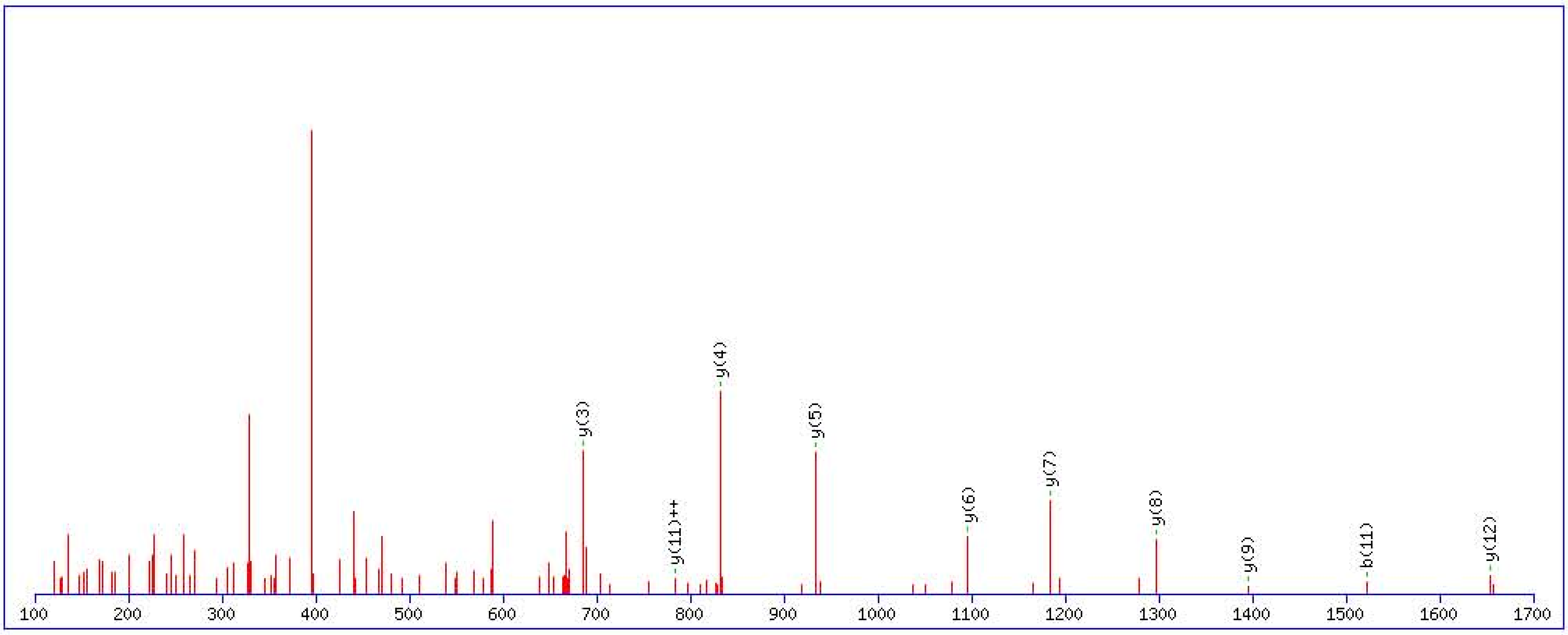
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

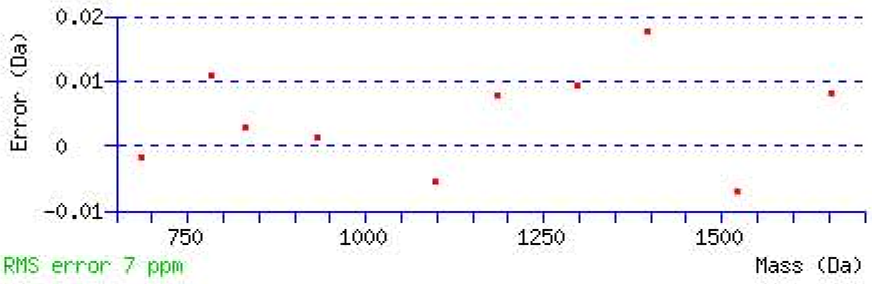
Match to Query 37805: 1765.950672 from(589.657500,3+) rtinseconds(2495) index(7487)
Title: Locus:1.1.1.3421.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

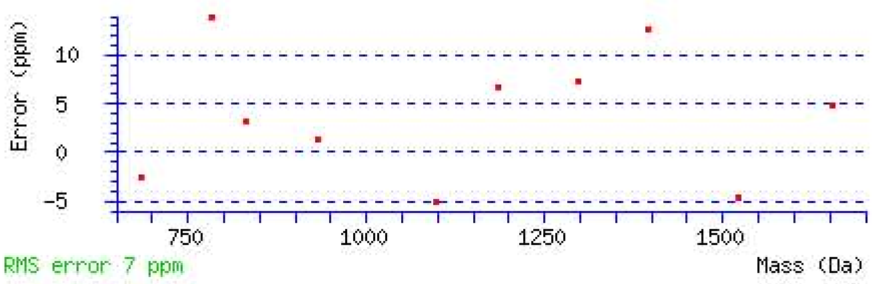
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1765.943680
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 50 **Expect:** 0.00025
Matches : 10/128 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	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
49.6	1765.943680	0.006992	LSGNVLSYTFQVK

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

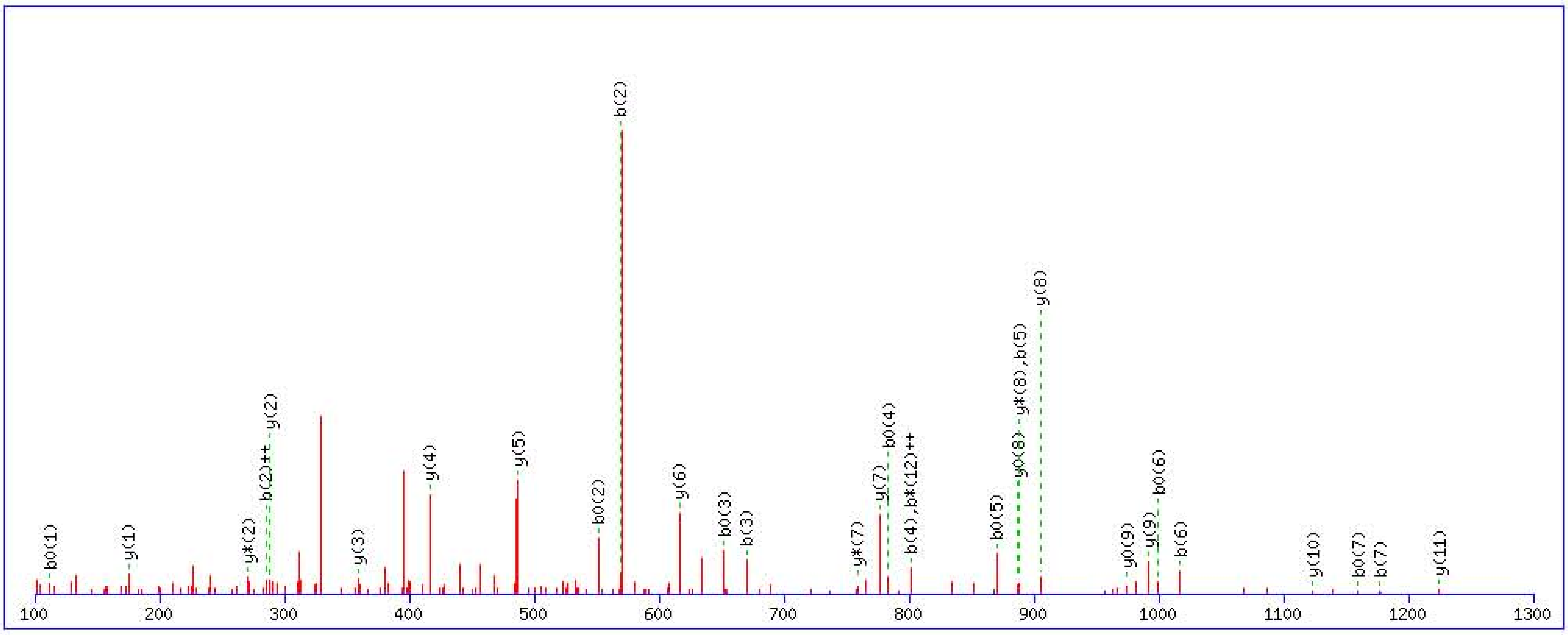
Mascot Search Results

Peptide View

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

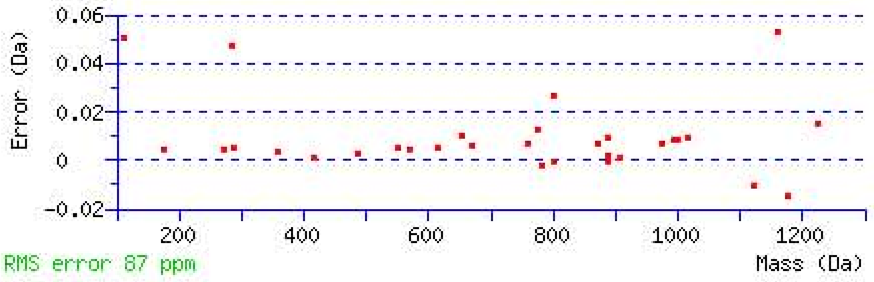
Match to Query 38354: 1791.796692 from(598.272840,3+) rtinseconds(1767) index(3625)
Title: Locus:1.1.1.3167.13 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

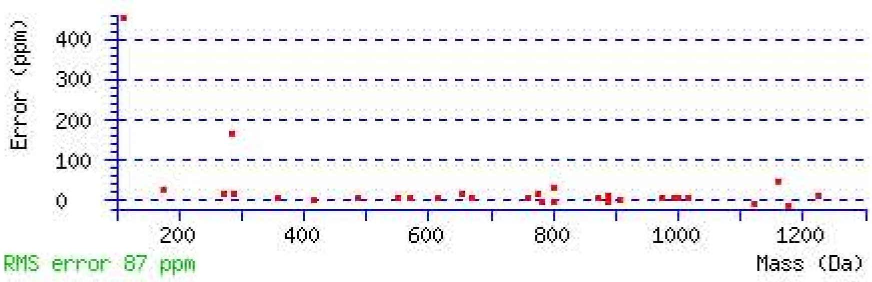
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1791.795349
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 62 **Expect:** 5.1e-006
Matches : 31/132 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	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
61.9	1791.795349	0.001343	EQTMSECEAGALR

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

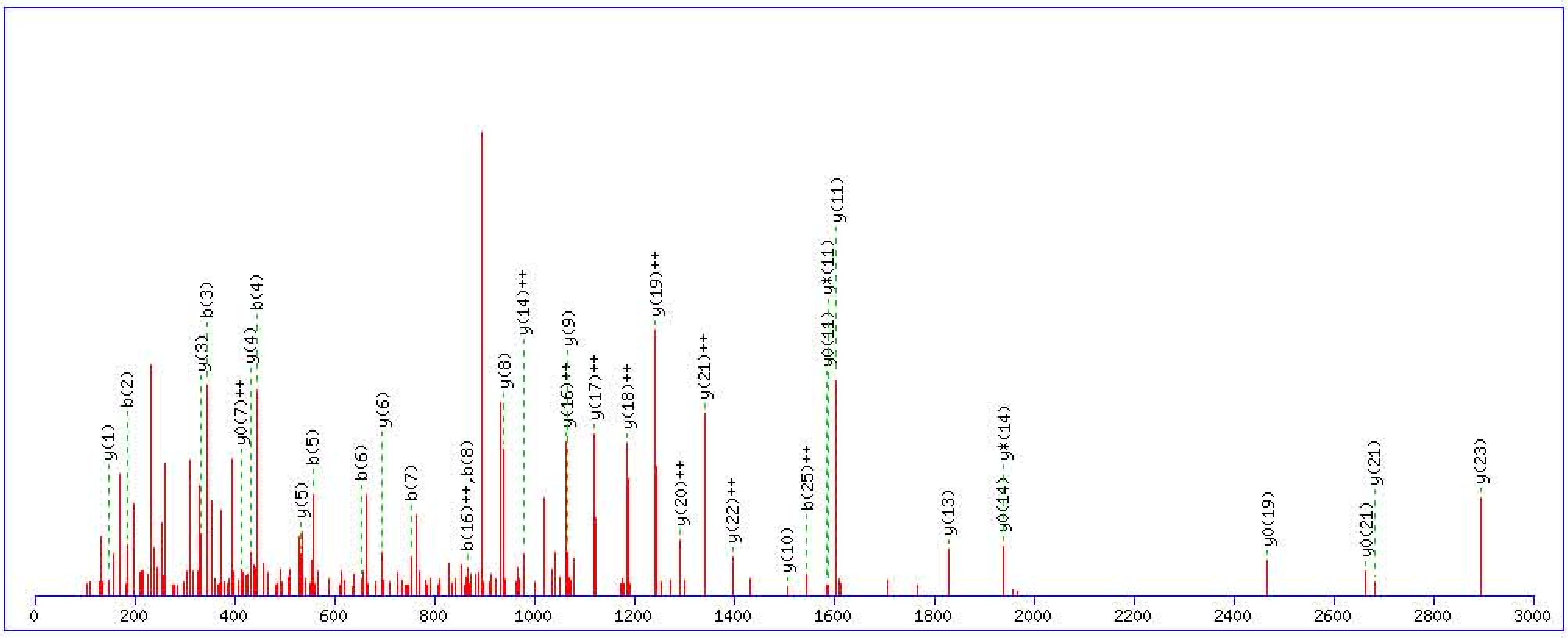
Mascot Search Results

Peptide View

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

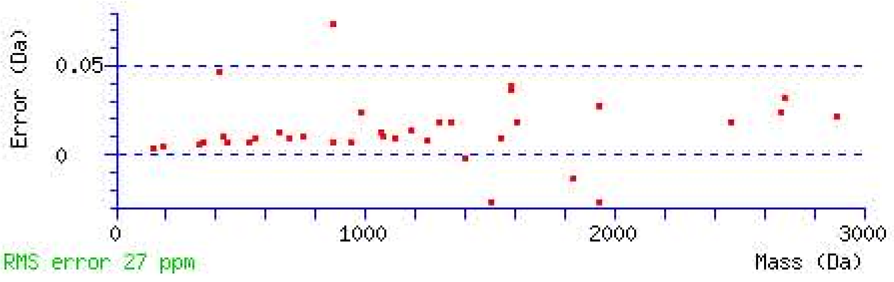
Match to Query 58922: 3237.696136 from(810.431310,4+) rtinseconds(2592) index(8038)
Title: Locus:1.1.1.3454.22 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

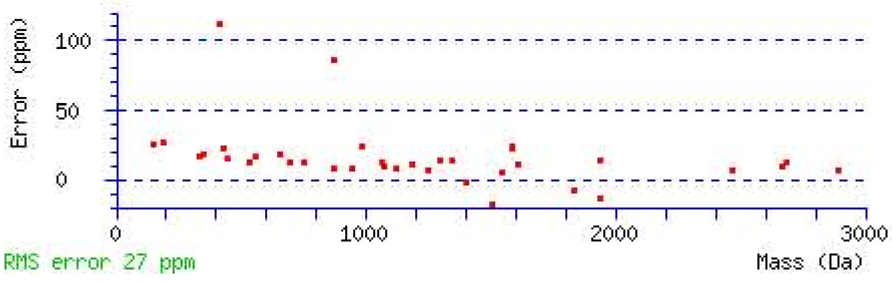
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 38  Expect: 0.00029
Matches : 36/256 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	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
38.0	3237.675262	0.020874	IACVLPVLMDGIQSHPQKPFYTVGEK
26.4	3237.675262	0.020874	IACVLPVLMDGIQSHPQKPFYTVGEK
0.3	3237.724503	-0.028367	QNFLQNVEGTKSSQPLTSNSLLPLTPVINV

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

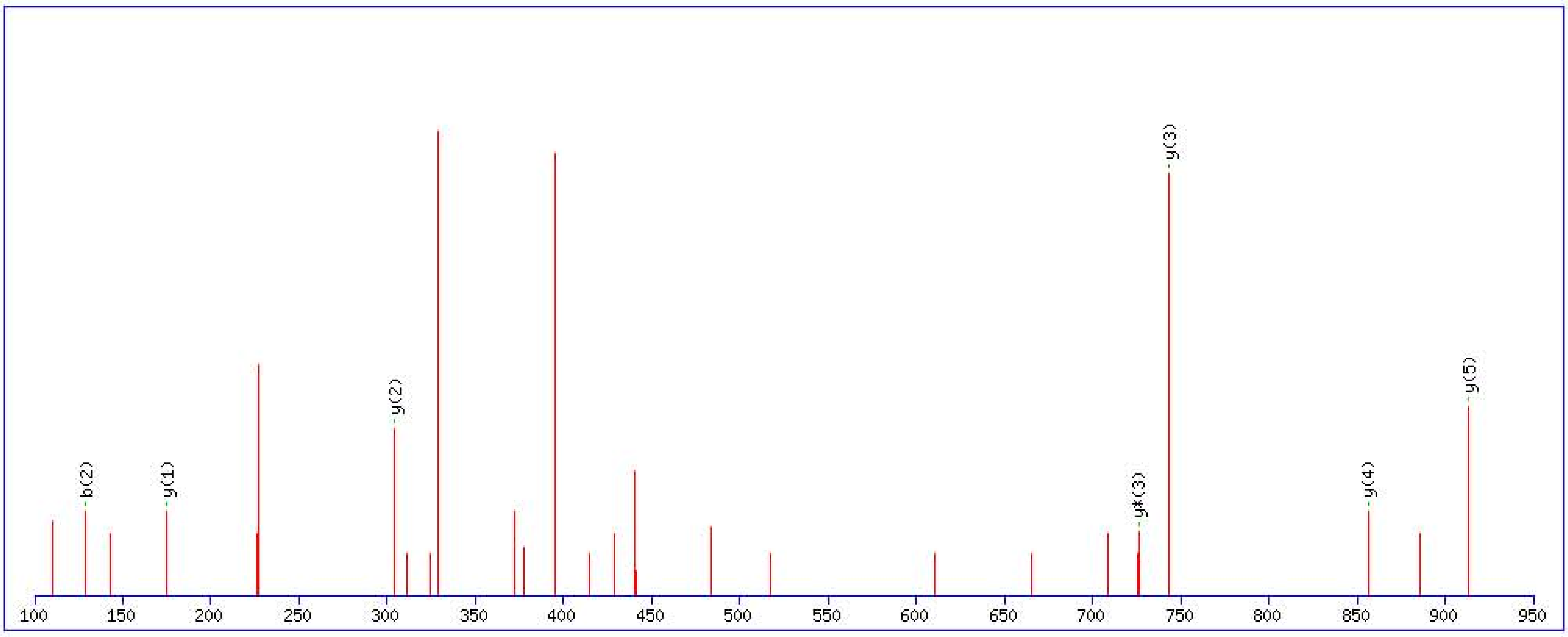
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

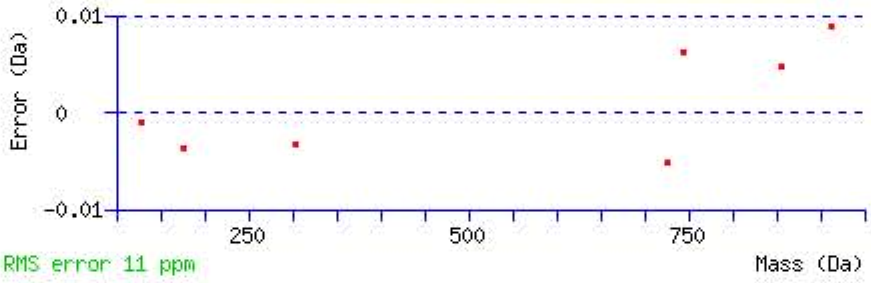
Match to Query 13203: 983.519968 from(492.767260,2+) rtinseconds(1426) index(43710)
Title: Locus:1.1.1.2545.8 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

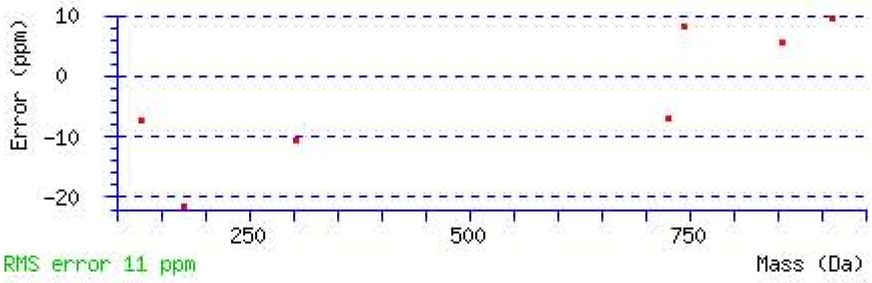
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [950] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
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: 27  Expect: 0.044
Matches : 7/44 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	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
26.6	983.522217	-0.002249	AGIQER
15.5	983.522217	-0.002249	AGLEQR
15.4	983.522217	-0.002249	QIQER
15.4	983.522217	-0.002249	QLQER
9.2	983.514816	0.005152	QPVREAER
7.0	983.522202	-0.002234	KLMENPPR
7.0	983.522217	-0.002249	QLEQR
6.4	983.522217	-0.002249	IQQER
6.4	983.522217	-0.002249	LQQER
5.2	983.530090	-0.010122	QLLNHFGR

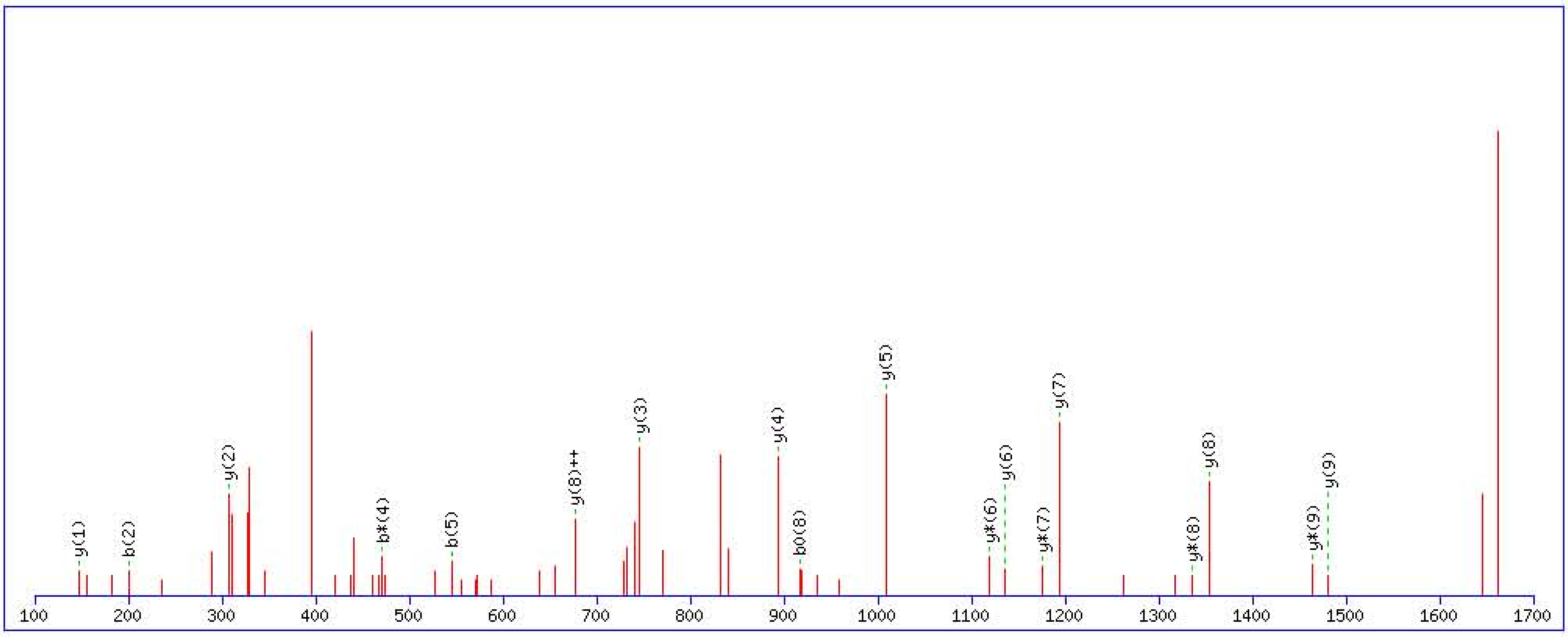
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

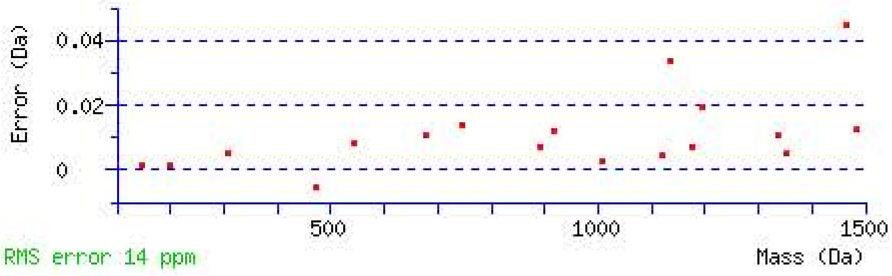
Match to Query 36039: 1679.732888 from(840.873720,2+) rtinseconds(1535) index(16123)
Title: Locus:1.1.1.3135.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

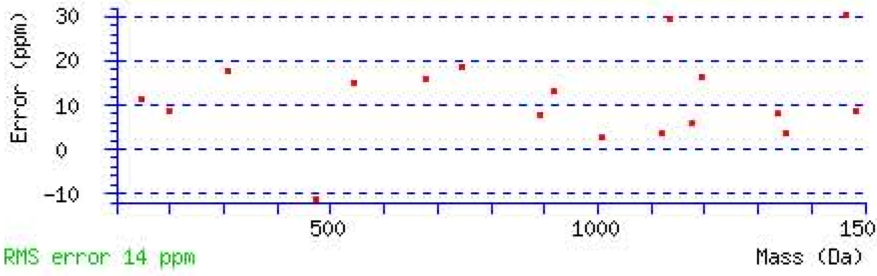
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1679.721832
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 68  Expect: 8.2e-007
Matches : 18/100 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	129.065854	65.036565	112.039305	56.523291			Q							11
2	**200.102968**	100.555122	183.076419	92.041848			A	1552.670519	776.838898	1535.643970	768.325623	1534.659954	767.833615	10
3	328.161546	164.584411	311.134997	156.071136			Q	***1481.633405***	741.320341	1464.606856	732.807066	1463.622840	732.315058	9
4	488.192195	244.599736	471.165646	236.086461			C	***1353.574827***	677.291052	1336.548278	668.777777	1335.564262	668.285769	8
5	**545.213659**	273.110468	528.187110	264.597193			G	***1193.544178***	597.275727	1176.517629	588.762453	1175.533613	588.270445	7
6	673.272237	337.139757	656.245688	328.626482			Q	***1136.522714***	568.764995	1119.496165	560.251721	1118.512149	559.759713	6
7	788.299180	394.653228	771.272631	386.139954	770.288615	385.647946	D	***1008.464136***	504.735706	991.437587	496.222432	990.453571	495.730424	5
8	935.367594	468.187435	918.341045	459.674161	917.357029	459.182153	F	***893.437193***	447.222235	876.410644	438.708960			4
9	1374.592920	687.800098	1357.566371	679.286824	1356.582355	678.794816	Q	***746.368779***	373.688028	729.342230	365.174753			3
10	1534.623569	767.815423	1517.597020	759.302148	1516.613004	758.810140	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 QAQCGQDFQCK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.1	1679.721832	0.011056	QAQCGQDFQCK
29.9	1679.721832	0.011056	QAQCGQDFQCK
7.2	1679.713074	0.019814	QSASMTSDNADDK
6.2	1679.733063	-0.000175	HMIMHTGDGPHKCK
0.3	1679.721832	0.011056	QAQCGQDFQCK

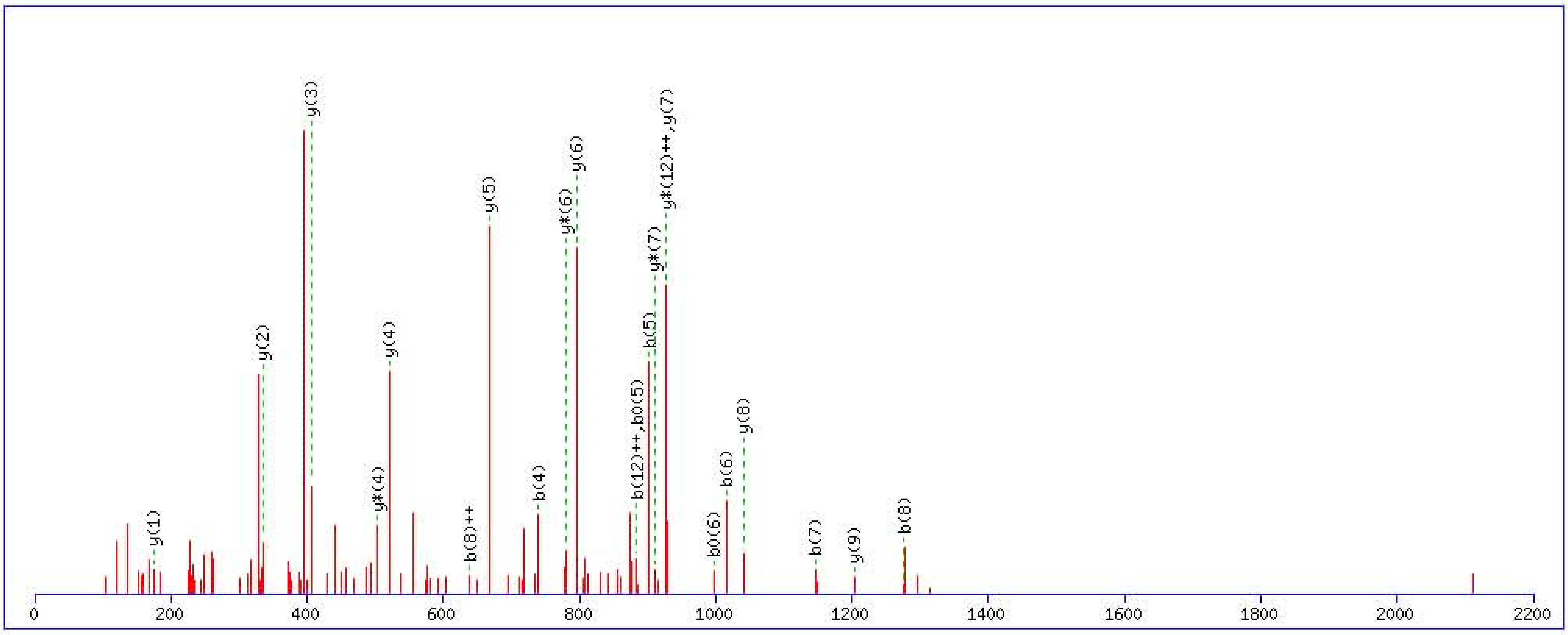
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

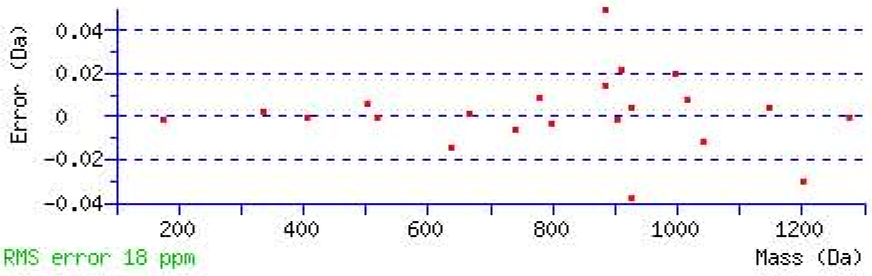
Match to Query 40932: 1940.903832 from(647.975220,3+) rtinseconds(2561) index(36081)
Title: Locus:1.1.1.3441.6 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

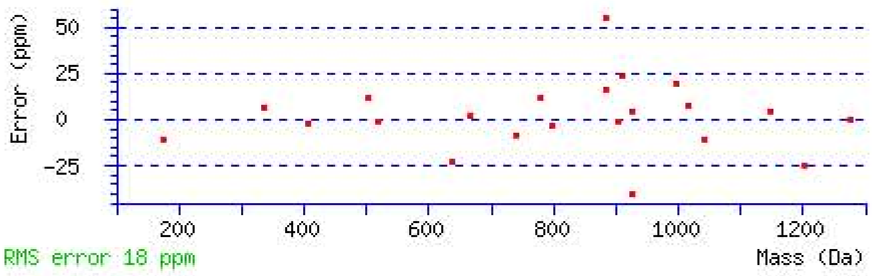
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1940.894669
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.0016
Matches : 22/124 fragment ions using 47 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							13
2	185.128454	93.067865					L	1870.864860	935.936068	1853.838311	927.422794	1852.854295	926.930786	12
3	300.155397	150.581336			282.144832	141.576054	D	1757.780796	879.394036	1740.754247	870.880762	1739.770231	870.388754	11
4	**739.380723**	370.194000	722.354174	361.680725	721.370158	361.188717	Q	1642.753853	821.880565	1625.727304	813.367290	1624.743288	812.875282	10
5	**902.444052**	451.725664	885.417503	443.212390	884.433487	442.720382	Y	***1203.528527***	602.267902	1186.501978	593.754627	1185.517962	593.262619	9
6	**1015.528116**	508.267696	998.501567	499.754422	997.517551	499.262414	L	***1040.465198***	520.736237	1023.438649	512.222963	1022.454633	511.730955	8
7	**1146.568601**	573.787939	1129.542052	565.274664	1128.558036	564.782656	M	***927.381134***	464.194205	910.354585	455.680931	909.370569	455.188923	7
8	**1275.611194**	**638.309235**	1258.584645	629.795961	1257.600629	629.303953	E	***796.340649***	398.673963	779.314100	390.160688	778.330084	389.668680	6
9	1422.679608	711.843442	1405.653059	703.330168	1404.669043	702.838160	F	***667.298056***	334.152666	650.271507	325.639392			5
10	1536.722535	768.864906	1519.695986	760.351631	1518.711970	759.859623	N	***520.229642***	260.618459	503.203093	252.105185			4
11	1607.759649	804.383463	1590.733100	795.870188	1589.749084	795.378180	A	***406.186715***	203.596995	389.160166	195.083721			3
12	1767.790298	**884.398787**	1750.763749	875.885513	1749.779733	875.393505	C	***335.149601***	168.078438	318.123052	159.565164			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ALDQYLMEFNACR
(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	1940.894669	0.009163	ALDQYLMEFNACR

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

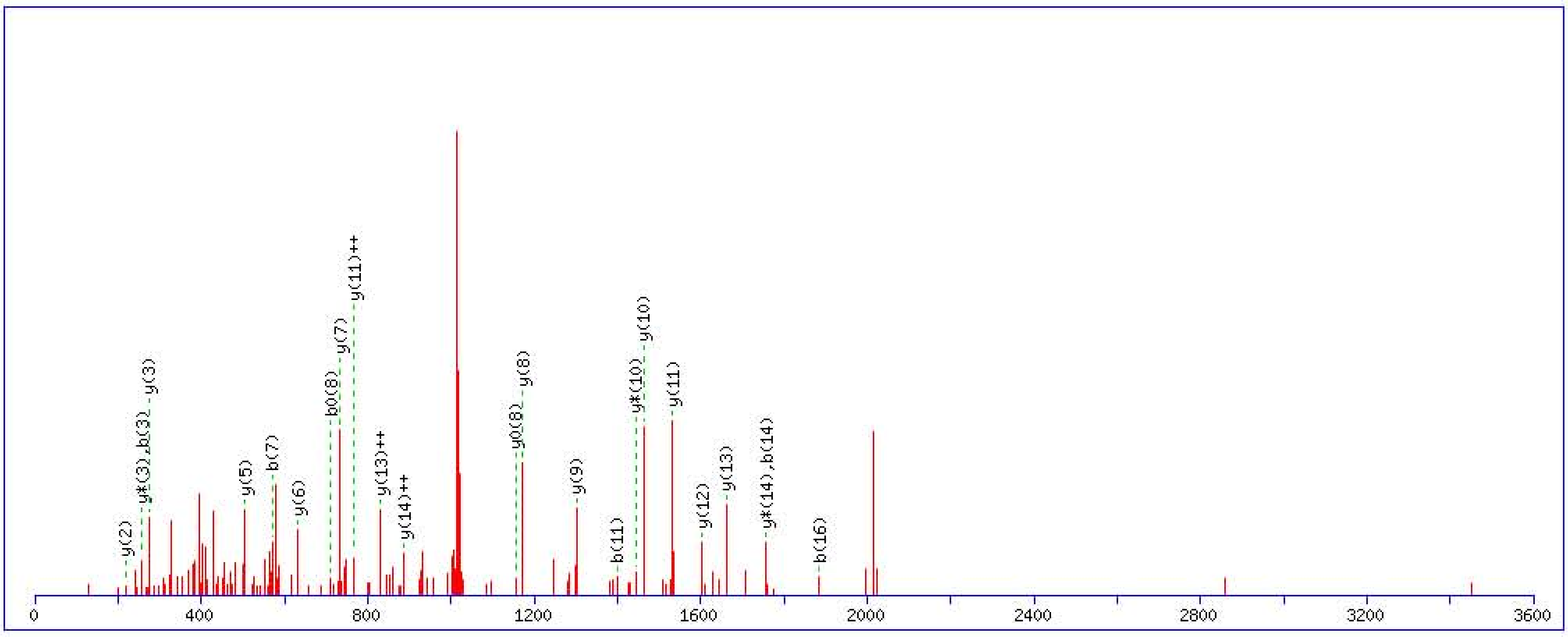
{MATRIX SCIENCE} Mascot Search Results

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

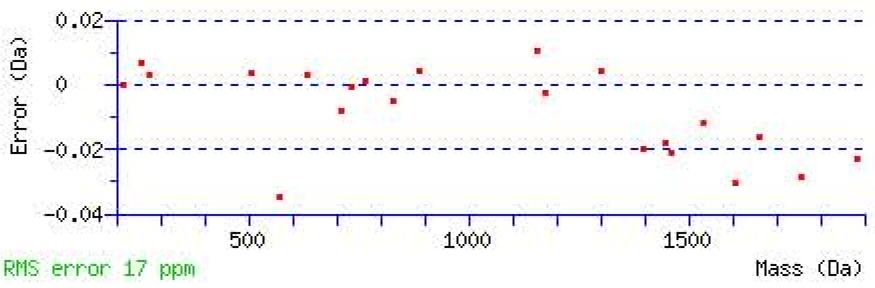
Match to Query 43237: 2030.974008 from(1016.494280,2+) rtinseconds(1724) index(31513)
Title: Locus:1.1.1.3149.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

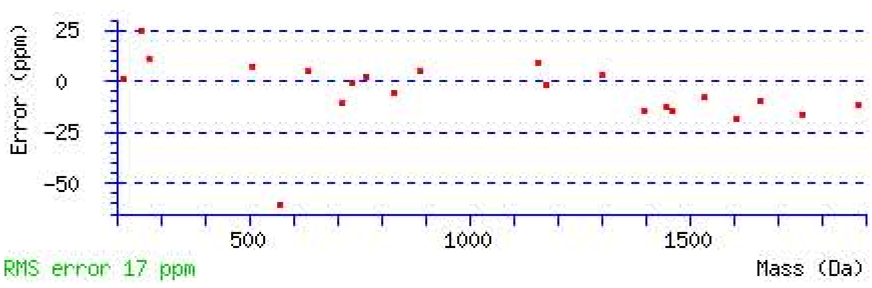
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2030.976501
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 75 **Expect:** 2.7e-007
Matches : 24/164 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							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
74.7	2030.976501	-0.002493	LGSLGAACEQTQTEGAK
48.2	2030.976501	-0.002493	LGSLGAACEQTQTEGAK
4.4	2031.000748	-0.026740	LEQQVEDLESSLEQEKK
1.7	2030.958710	0.015298	QPMNAASGAAMSLAGAEK
0.3	2030.973099	0.000909	QFEEAEQQANTNLAK

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

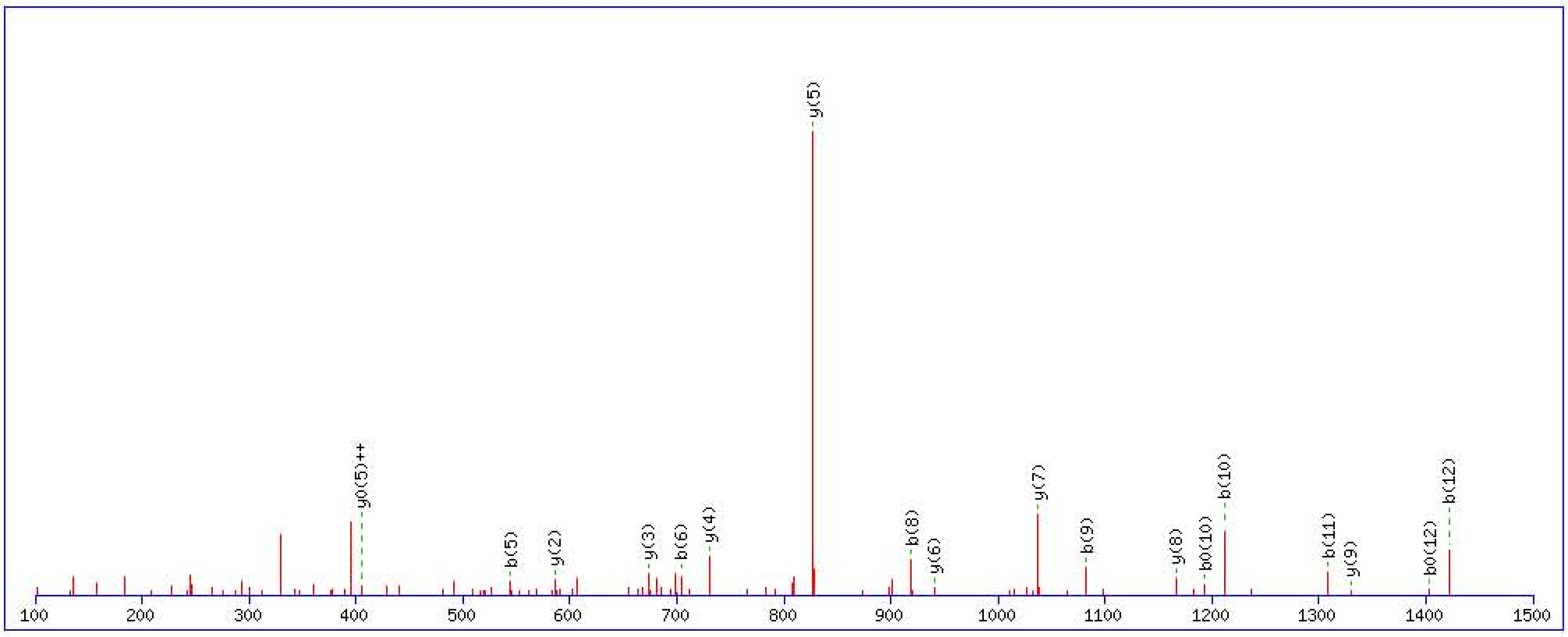
{MATRIX SCIENCE} Mascot Search Results

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

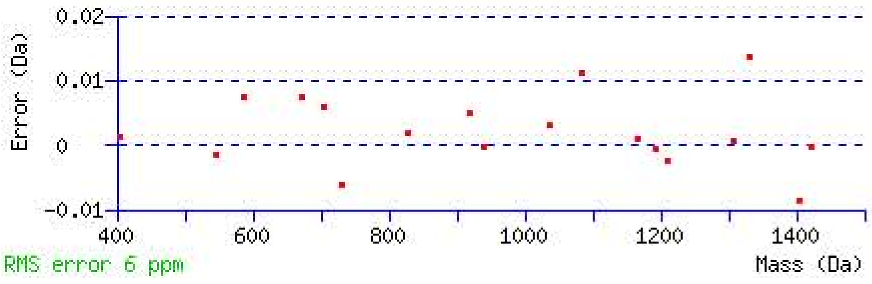
Match to Query 46819: 2247.023622 from(750.015150,3+) rtinseconds(1896) index(32391)
Title: Locus:1.1.1.3209.25 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

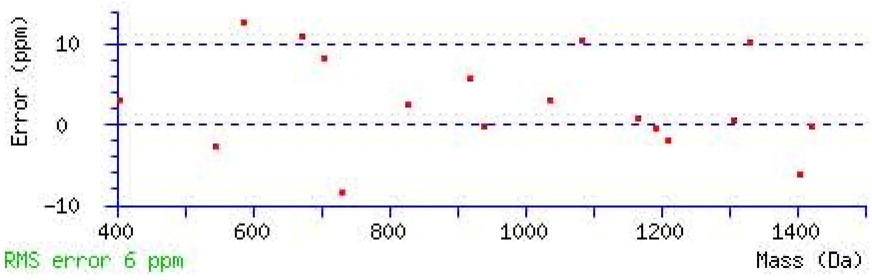
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1500 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



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: 54 **Expect:** 9.4e-006
Matches : 18/170 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	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
54.1	2247.018753	0.004869	AIDEDCSQYEPIPGSQK
0.5	2247.048630	-0.025008	LVDQDKTMFICKSSWSMR
0.3	2247.047760	-0.024138	NGSDDPSYNGAIIVSGDQK
0.2	2247.048615	-0.024993	NPGYPQSEGLLGECMIR

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

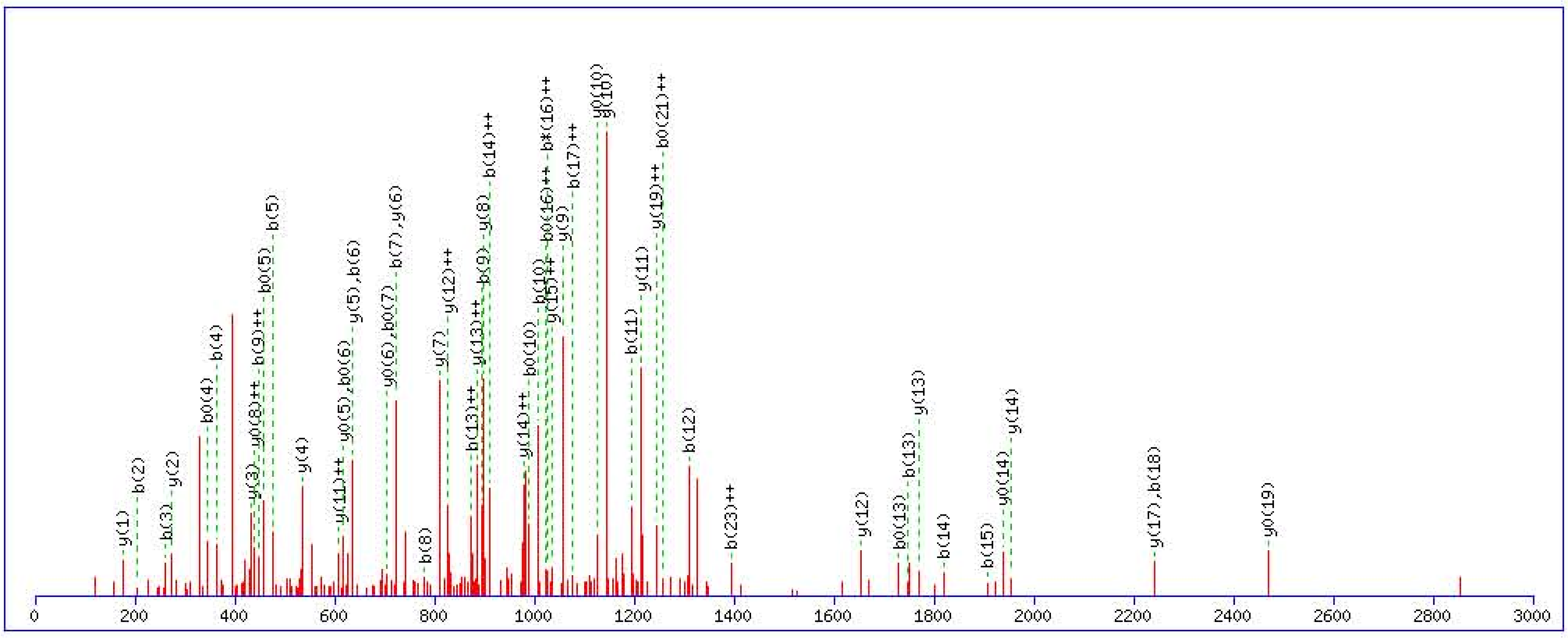
Mascot Search Results

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

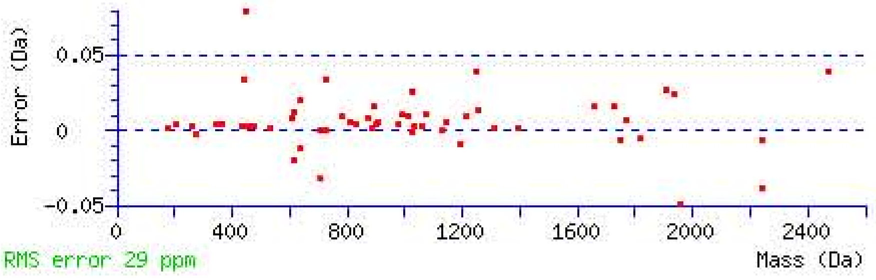
Match to Query 55815: 2962.295802 from(988.439210,3+) rtinseconds(2378) index(35137)
Title: Locus:1.1.1.3377.21 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

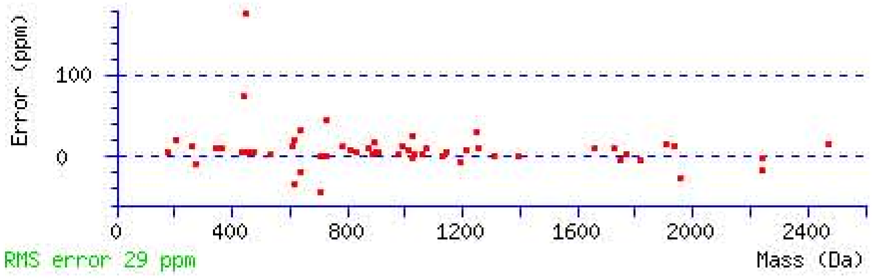
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2962.271835
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 97  Expect: 1e-009
Matches : 56/240 fragment ions using 96 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
97.4	2962.271835	0.023967	FGGTICSGDIWDQASCSSSTTCVR
2.1	2962.308167	-0.012365	VNELCVEALCRMEQANCSFQVFDK

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

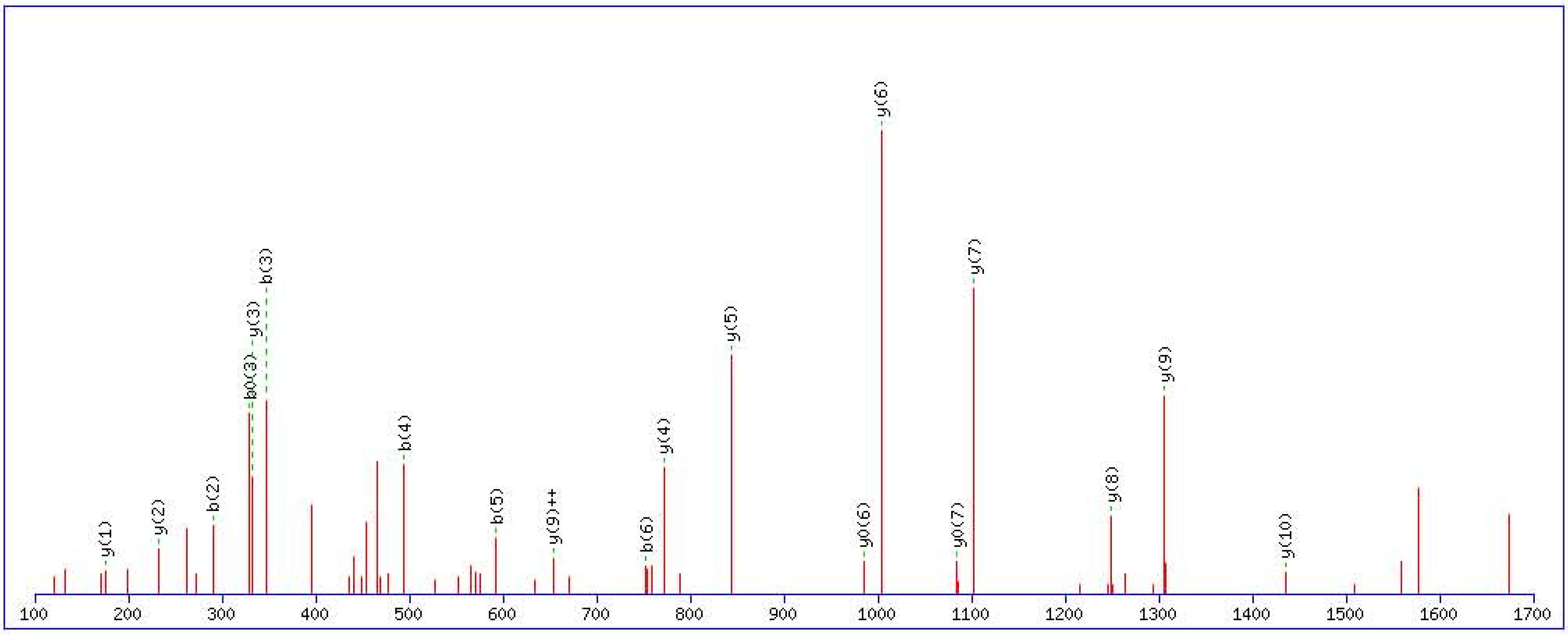
Mascot Search Results

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

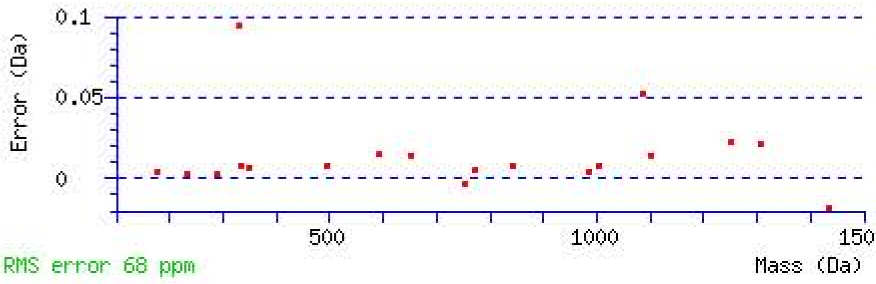
Match to Query 32996: 1594.713188 from(798.363870,2+) rtinseconds(1788) index(17666)
Title: Locus:1.1.1.3223.18 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

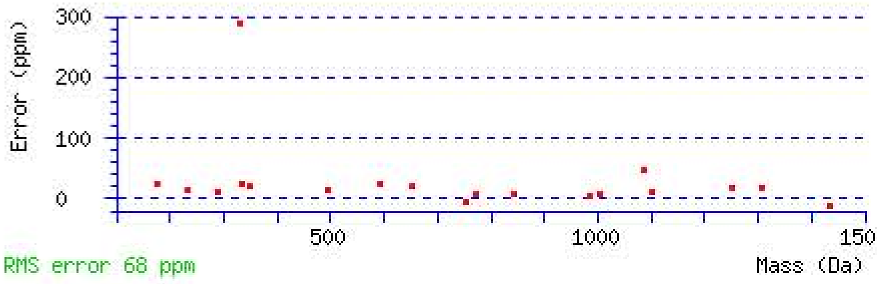
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1594.705460
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 68 **Expect:** 1.3e-006
Matches : 19/100 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	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
67.6	1594.705460	0.007728	CEGFVCAQTGR

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

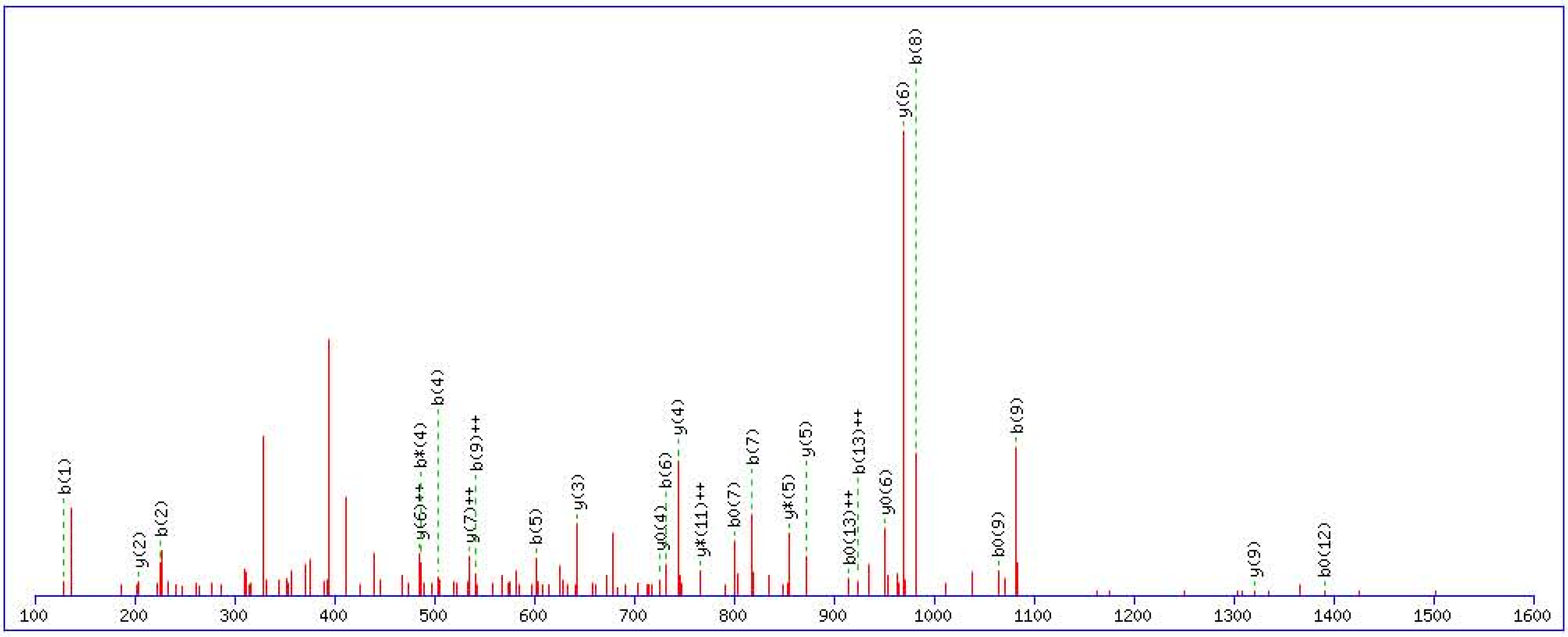
Mascot Search Results

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

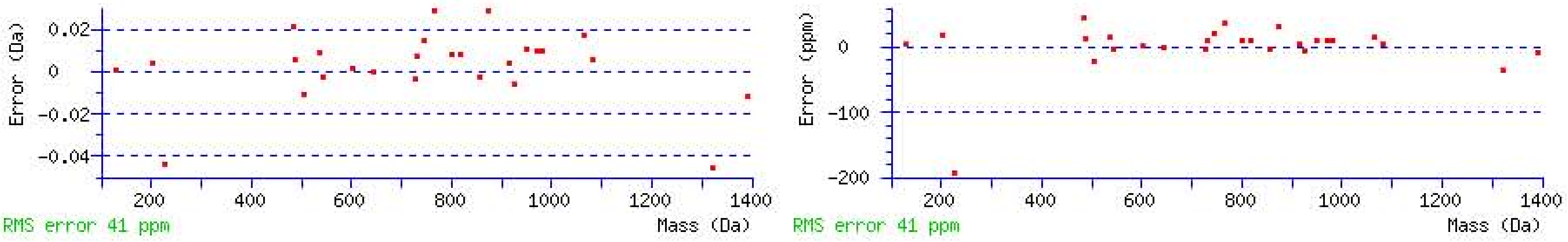
Match to Query 43705: 2050.030032 from(684.350620,3+) rtinseconds(1604) index(16605)
Title: Locus:1.1.1.3159.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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): 2050.019348
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.00054
Matches : 27/152 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	***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



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
37.0	2050.019348	0.010684	KPYNVESYTPQTQGK
24.4	2050.019348	0.010684	KPYNVESYTPQTQGK
2.2	2050.026566	0.003466	LFVGMLNKQQSEDDVRR

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

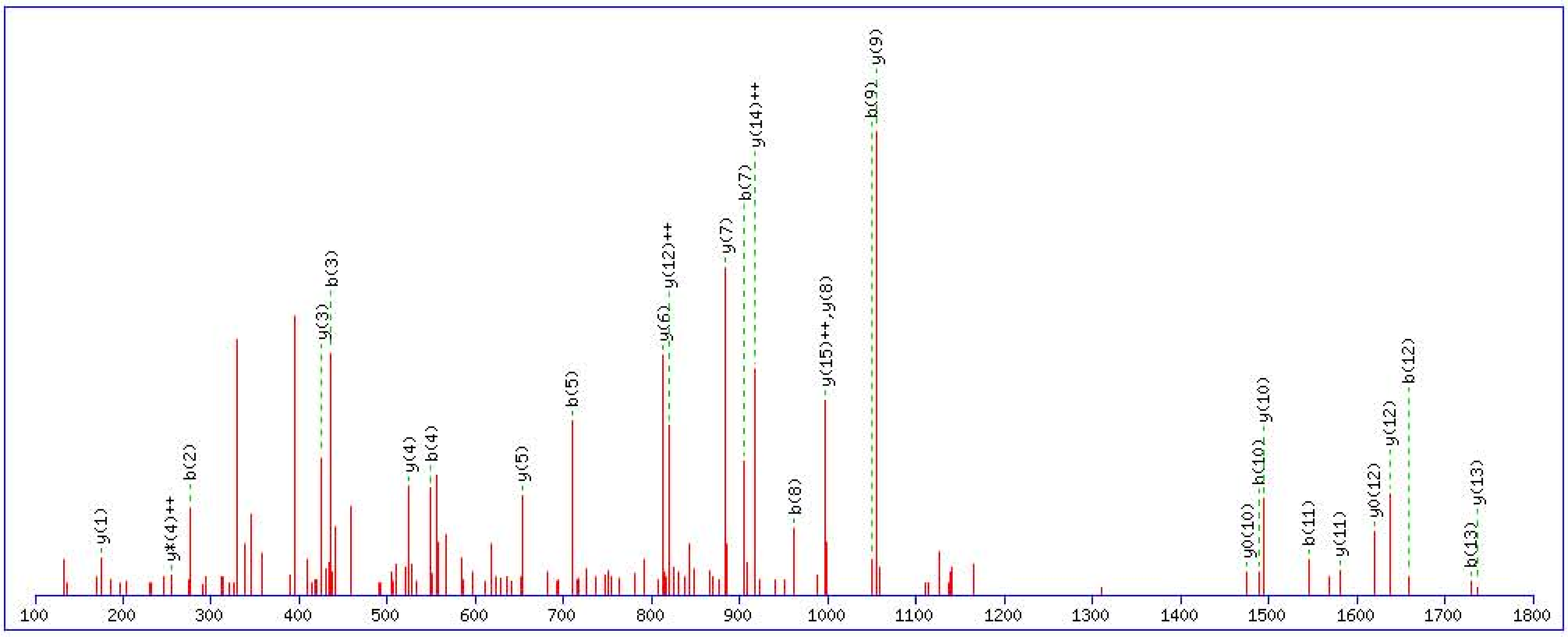
{MATRIX SCIENCE} Mascot Search Results

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

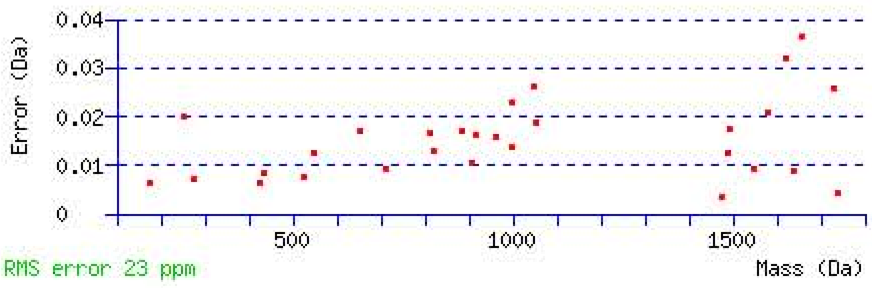
Match to Query 51628: 2541.124332 from(848.048720,3+) rtinseconds(2168) index(20066)
Title: Locus:1.1.1.3355.16 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

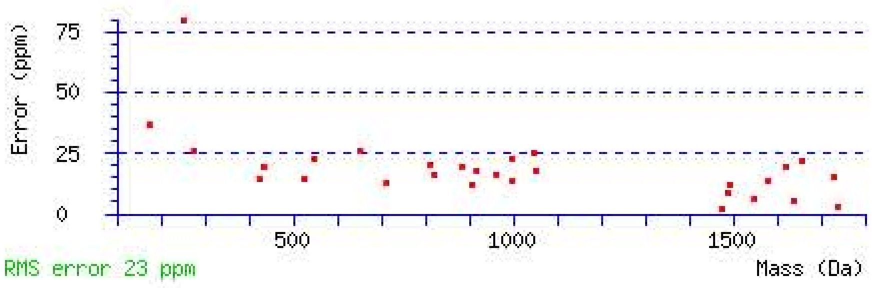
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2541.094299
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 92  Expect: 4e-009
Matches : 29/192 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	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
92.4	2541.094299	0.030033	CDCICPVGSQGLACEVSYR

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

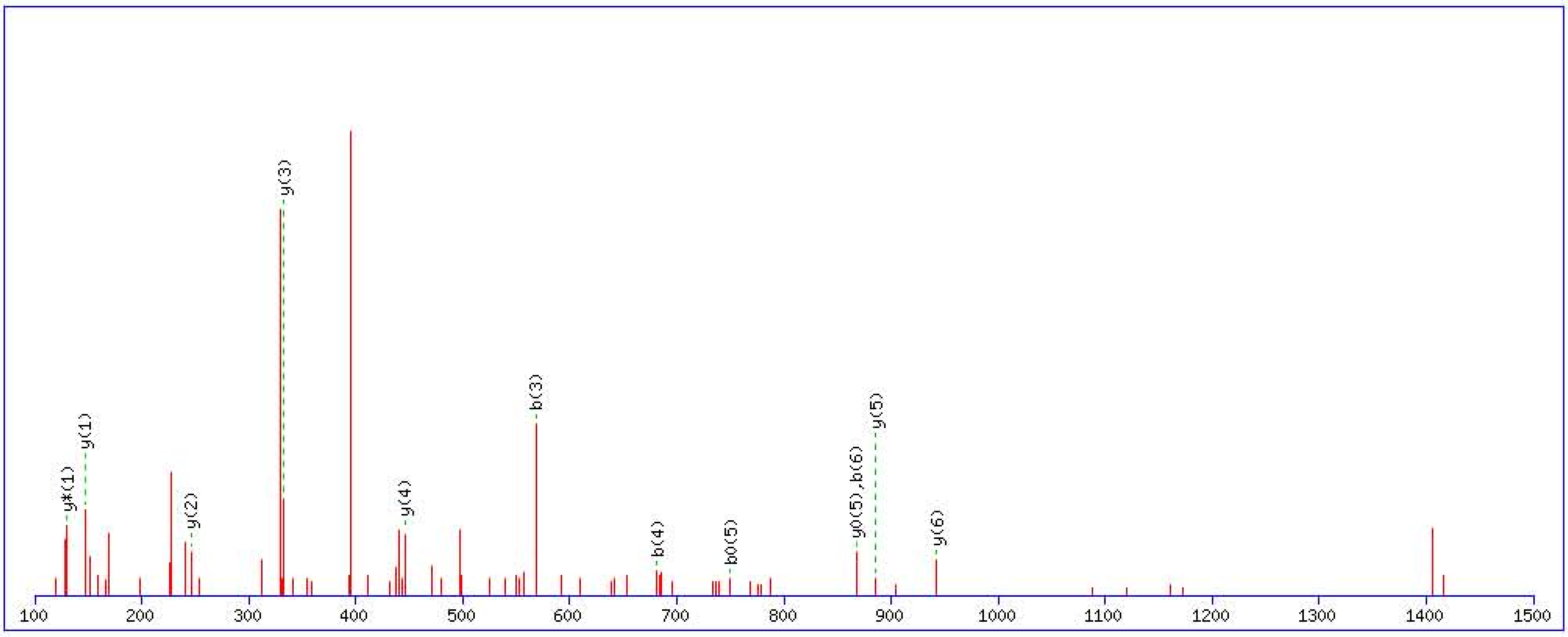
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGQLSVK**
Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

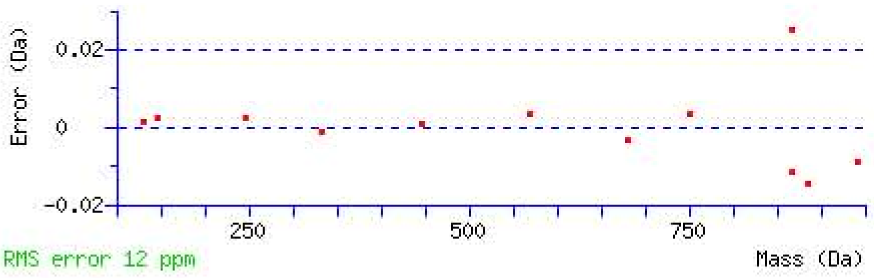
Match to Query 13746: 1012.573548 from(507.294050,2+) rtinseconds(1592) index(30838)
Title: Locus:1.1.1.3103.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

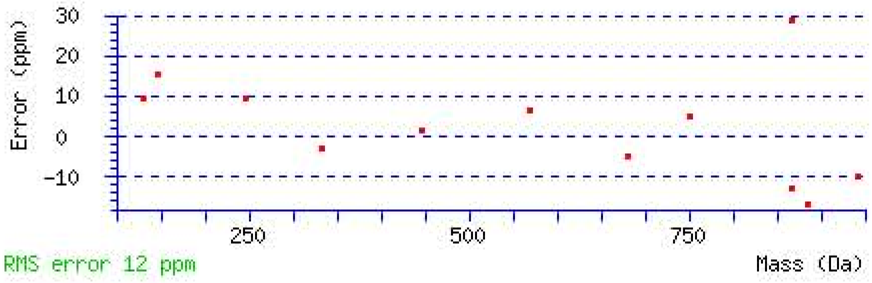
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1012.573929
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.025
Matches : 12/56 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							7
2	129.065854	65.036565					G	*942.544100*	471.775688	925.517551	463.262414	924.533535	462.770406	6
3	**568.291180**	284.649228	551.264631	276.135954			Q	*885.522636*	443.264956	868.496087	434.751682	867.512071	434.259674	5
4	**681.375244**	341.191260	664.348695	332.677986			L	*446.297310*	223.652293	429.270761	215.139018	428.286745	214.647010	4
5	768.407272	384.707274	751.380723	376.194000	750.396707	375.701992	S	*333.213246*	167.110261	316.186697	158.596986	315.202681	158.104978	3
6	**867.475686**	434.241481	850.449137	425.728207	849.465121	425.236199	V	*246.181218*	123.594247	229.154669	115.080972			2
7							K	*147.112804*	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of AGQLSVK
(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	1012.573929	-0.000381	AGQLSVK
19.3	1012.573929	-0.000381	QAGLVSK
19.3	1012.573914	-0.000366	QKLEGK
11.2	1012.573914	-0.000366	KEAQVK
8.3	1012.573914	-0.000366	QKADIK
8.3	1012.573914	-0.000366	QKADLK
8.3	1012.573914	-0.000366	QKEGIK
8.3	1012.585144	-0.011596	QKNGKK
6.9	1012.573914	-0.000366	KQDLAK
6.3	1012.573914	-0.000366	AKEVQK

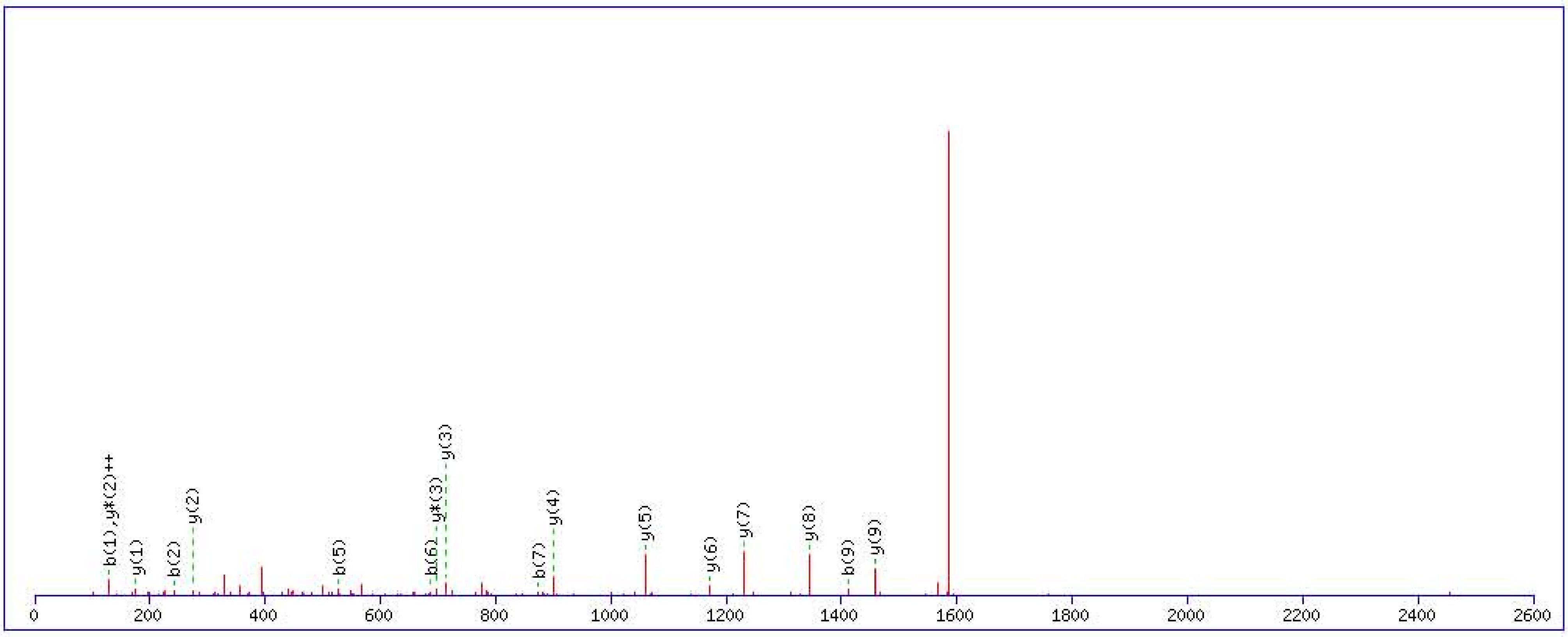
{MATRIX SCIENCE} Mascot Search Results

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

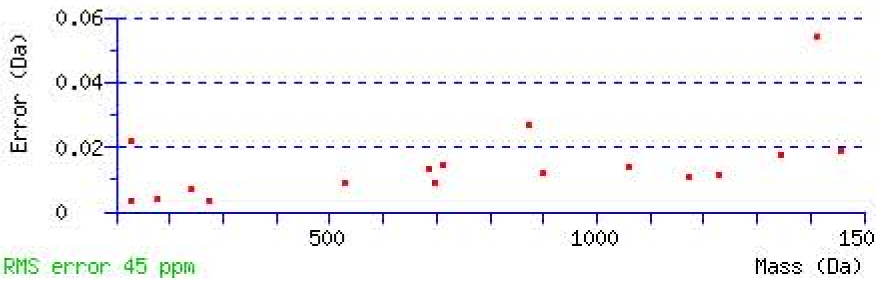
Match to Query 32590: 1584.841748 from(793.428150,2+) rtinseconds(2073) index(19475)
Title: Locus:1.1.1.3322.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

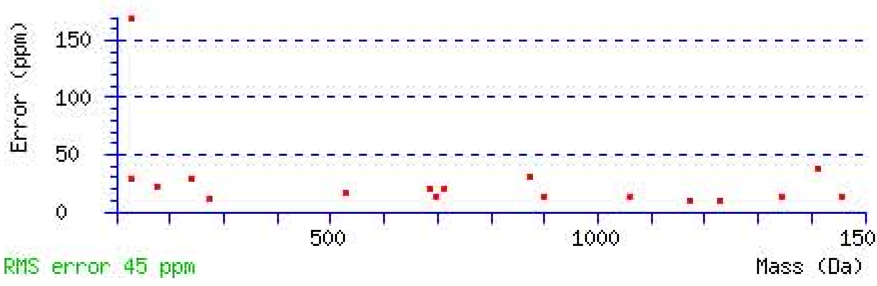
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1584.826874
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 2.2e-005
Matches : 17/90 fragment ions using 30 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							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
61.0	1584.826874	0.014874	KLDGICWQVR
20.7	1584.858353	-0.016605	QLDGLAGLKGEGSRGK
11.5	1584.858337	-0.016589	LKSNDGEERLAVVR
7.4	1584.822830	0.018918	QLDQKCKQAR
7.3	1584.822830	0.018918	QLDQKCKQAR
6.7	1584.859222	-0.017474	KLSDVCQLRR
6.3	1584.819458	0.022290	QITRSWQEAR
6.3	1584.841278	0.000470	QLAWVGDGVWVSIR
4.1	1584.818100	0.023648	KQQTLEAEEAK
3.0	1584.851791	-0.010043	KQLRAQEIAMQNR

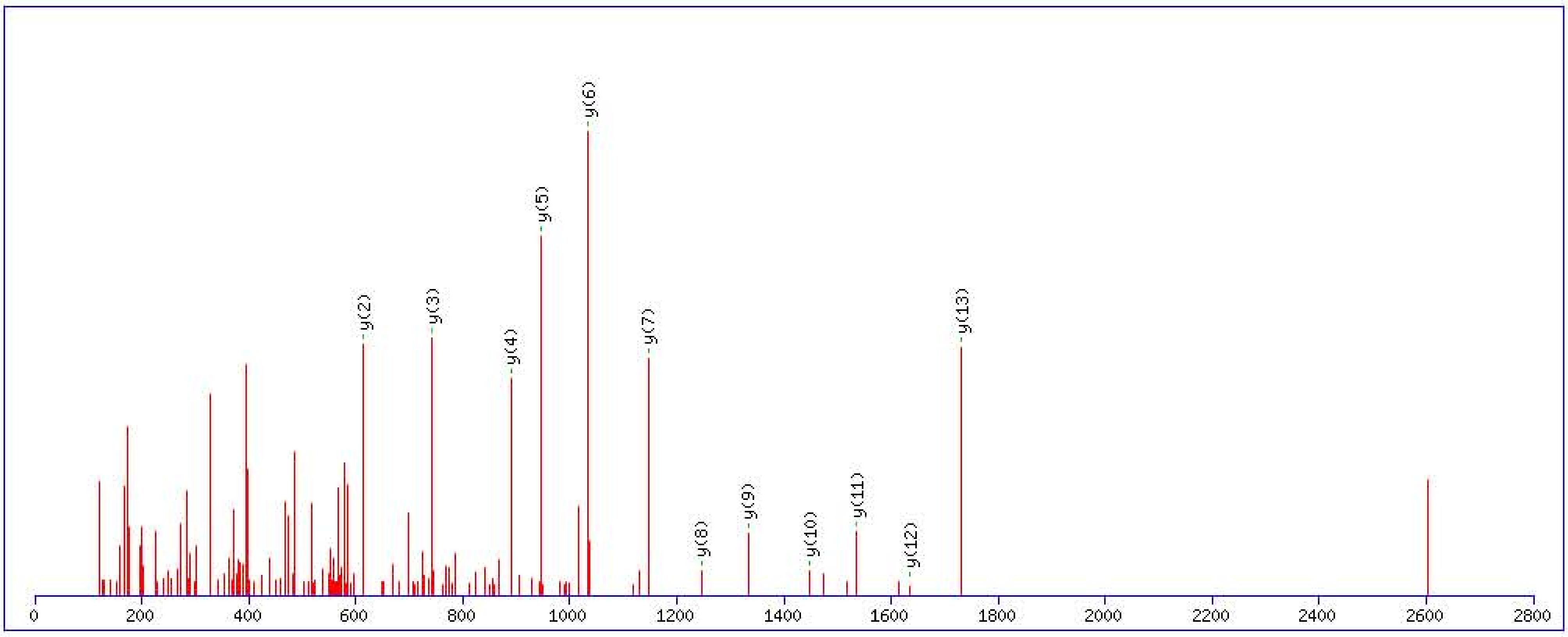
{MATRIX SCIENCE} Mascot Search Results

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

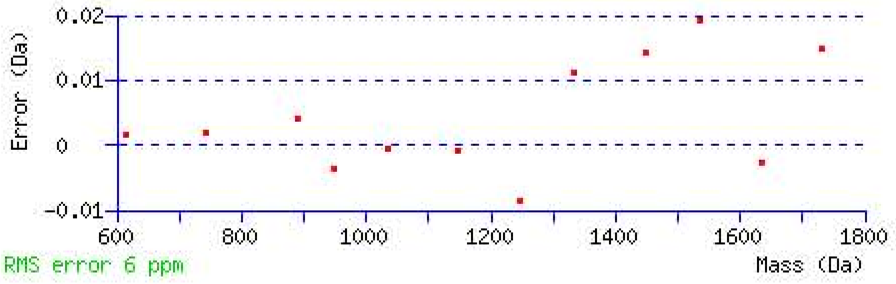
Match to Query 40743: 1930.992072 from(644.671300,3+) rtinseconds(2512) index(35904)
Title: Locus:1.1.1.3424.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

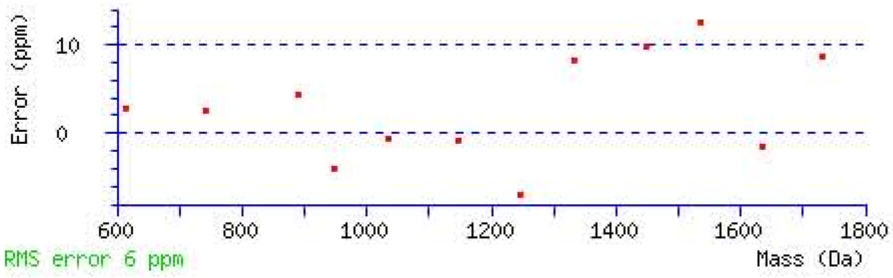
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 104 **Expect:** 2.4e-010
Matches : 12/138 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	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
103.6	1930.982254	0.009818	SLPVSDSVLSGFEQR
0.9	1931.000885	-0.008813	LSPVTACAGQTLQFK

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

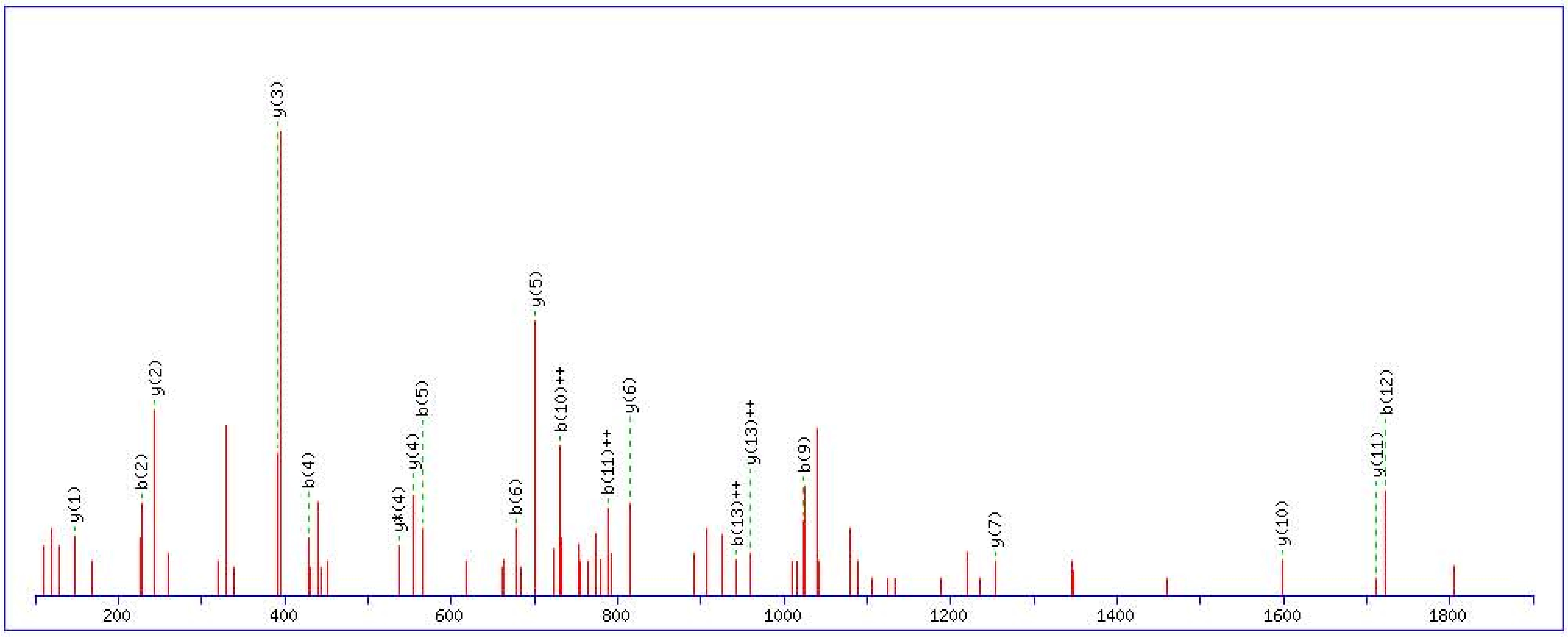
{MATRIX SCIENCE} Mascot Search Results

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

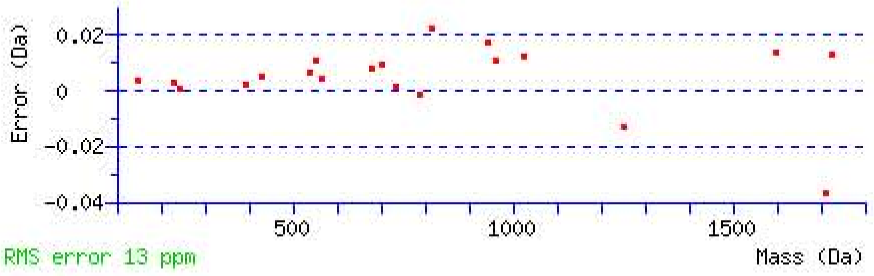
Match to Query 47378: 2275.150872 from(759.390900,3+) rtinseconds(2400) index(35257)
Title: Locus:1.1.1.3385.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

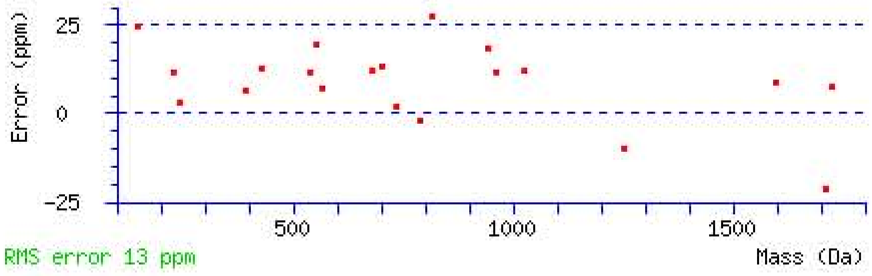
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2275.134720
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.0049
Matches : 20/160 fragment ions using 43 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	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
38.0	2275.134720	0.016152	VQEAHLTEDQIFYFPK
12.8	2275.134720	0.016152	VQEAHLTEDQIFYFPK

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

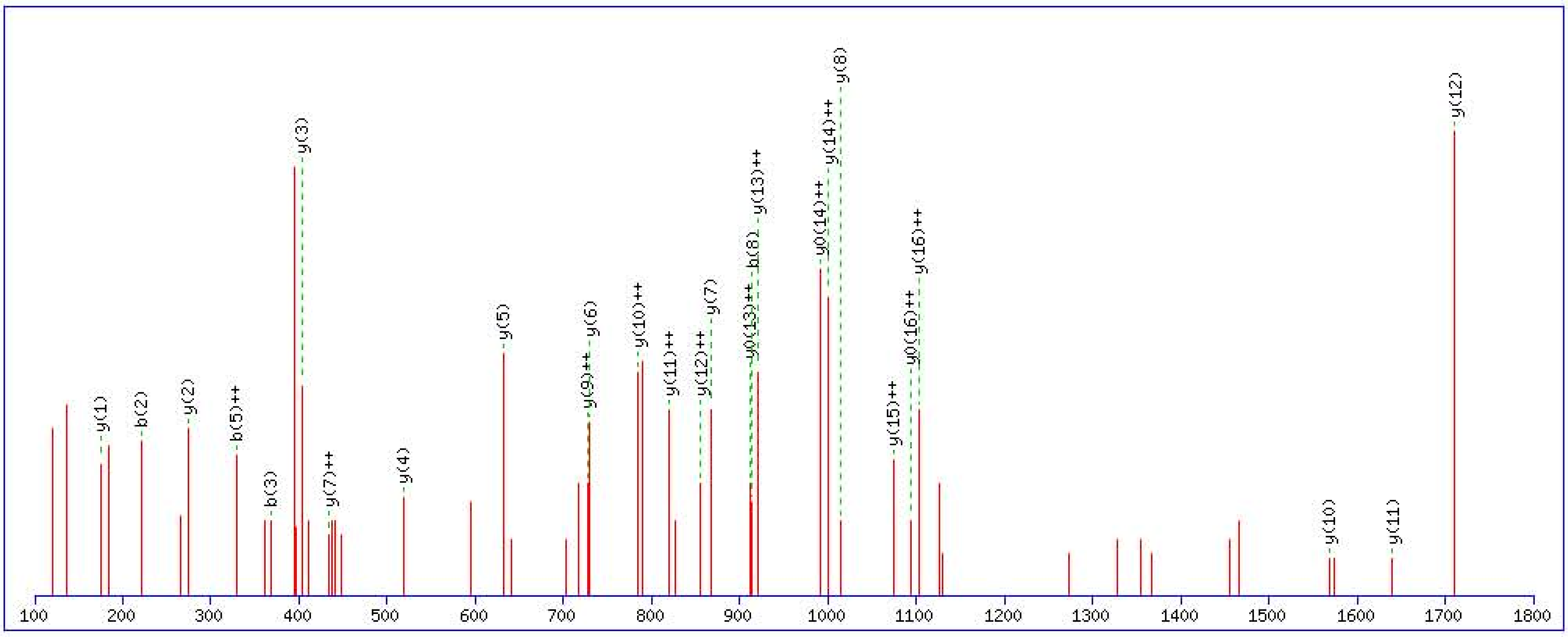
{MATRIX}{SCIENCE} Mascot Search Results

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

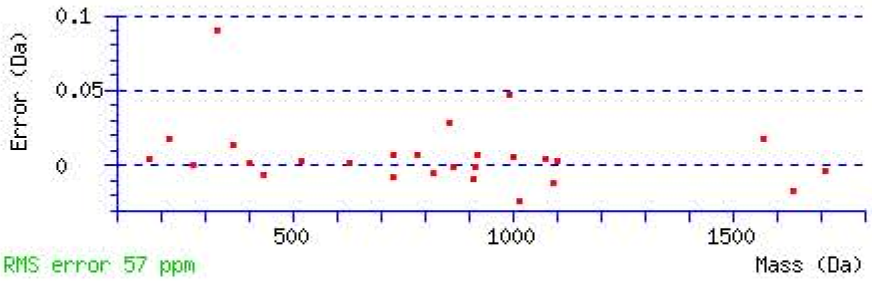
Match to Query 48672: 2366.096022 from(789.705950,3+) rtinseconds(2582) index(36186)
Title: Locus:1.1.1.3448.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

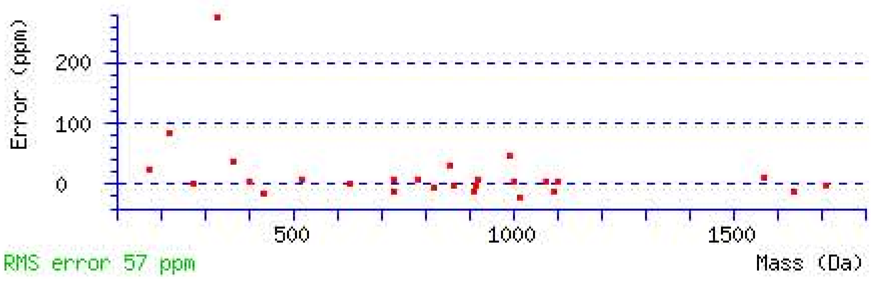
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2366.082382
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 64 **Expect:** 5.5e-006
Matches : 27/164 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	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
64.5	2366.082382	0.013640	YGFCEAADQFHVLDEVR

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

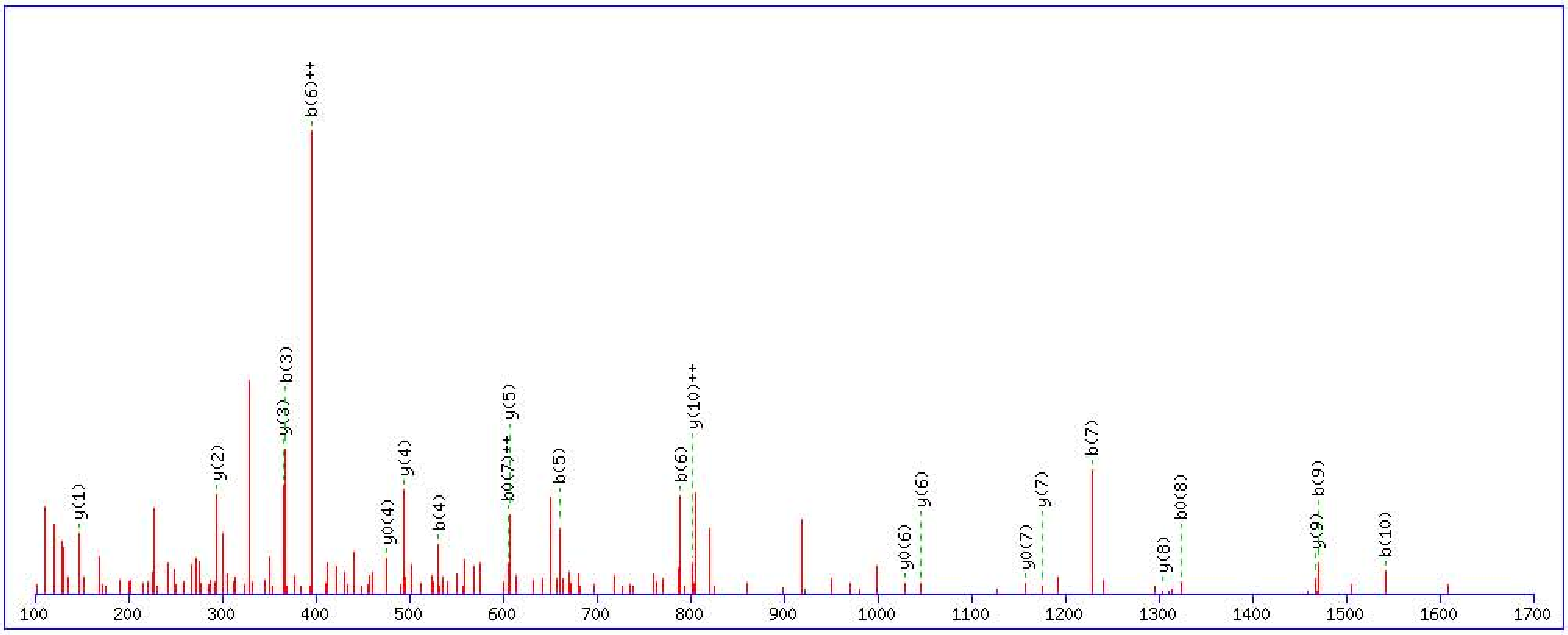
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEHYEEQIEAFK**
Found in **CO9_HUMAN**, Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2

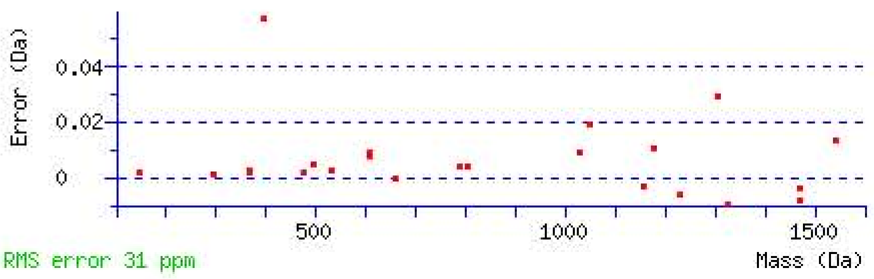
Match to Query 39107: 1833.866742 from(612.296190,3+) rtinseconds(1986) index(33117)
Title: Locus:1.1.1.3240.23 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

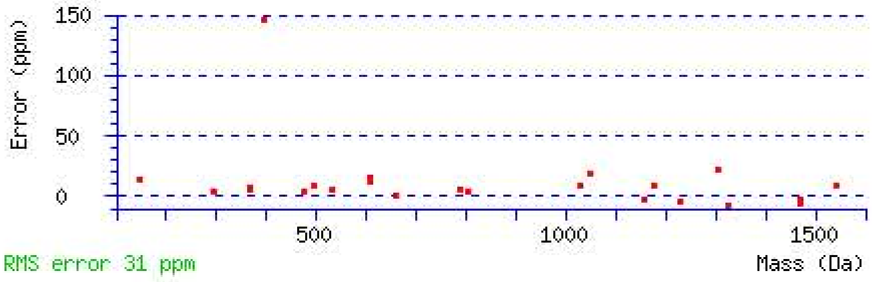
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1833.860703
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0018
Matches : 23/114 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	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





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
34.4	1833.860703	0.006039	TEHYEEQIEAFK
5.2	1833.860031	0.006711	KMAALECEDPERELK

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

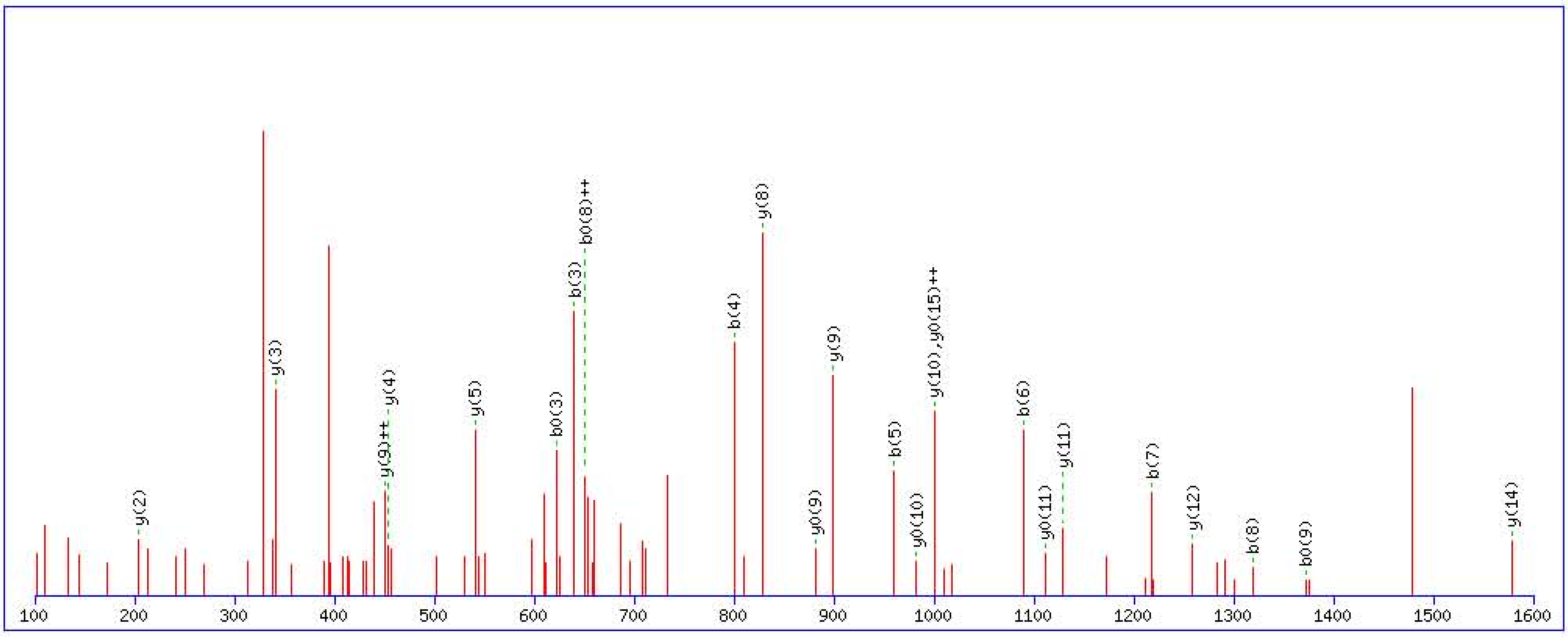
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEQCCEETASSISLHGK**
Found in **CO9_HUMAN**, Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2

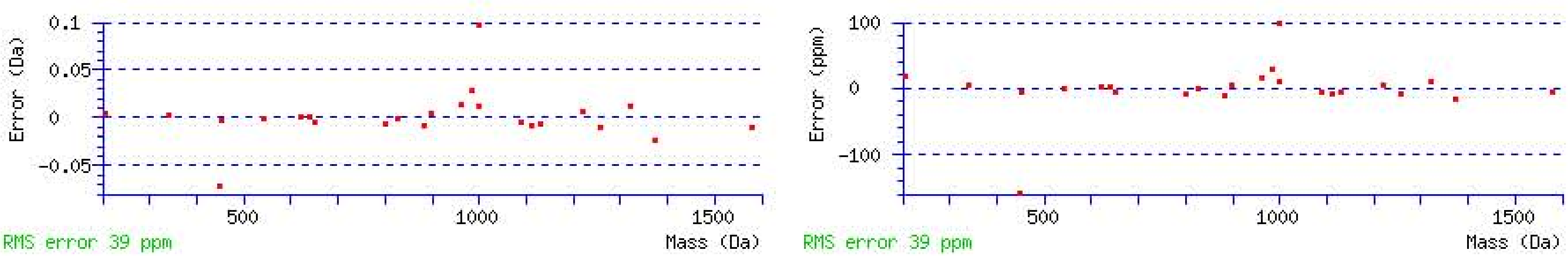
Match to Query 46325: 2216.980812 from(740.000880,3+) rtinseconds(1584) index(30777)
Title: Locus:1.1.1.3100.26 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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): 2216.986404
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 55 **Expect:** 2.6e-005
Matches : 24/178 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	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
54.6	2216.986404	-0.005592	AEQCCEETASSISLHGK

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

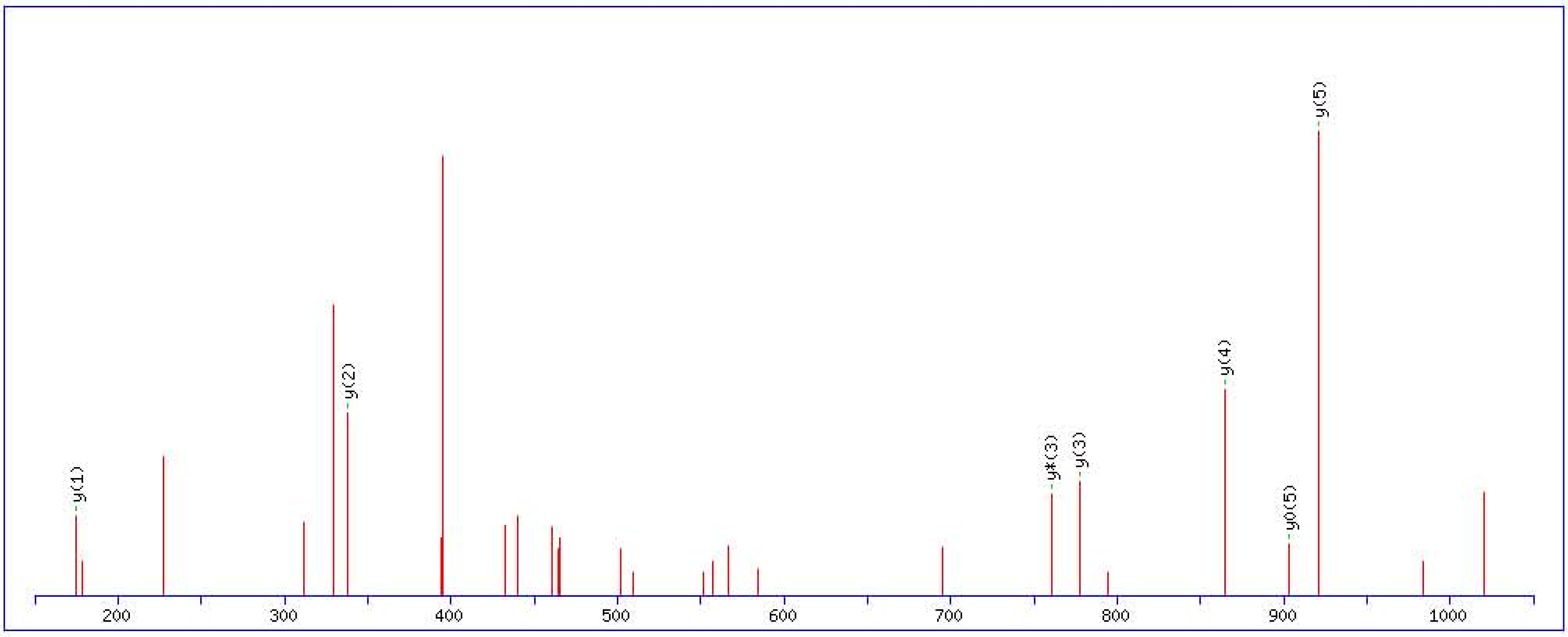
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

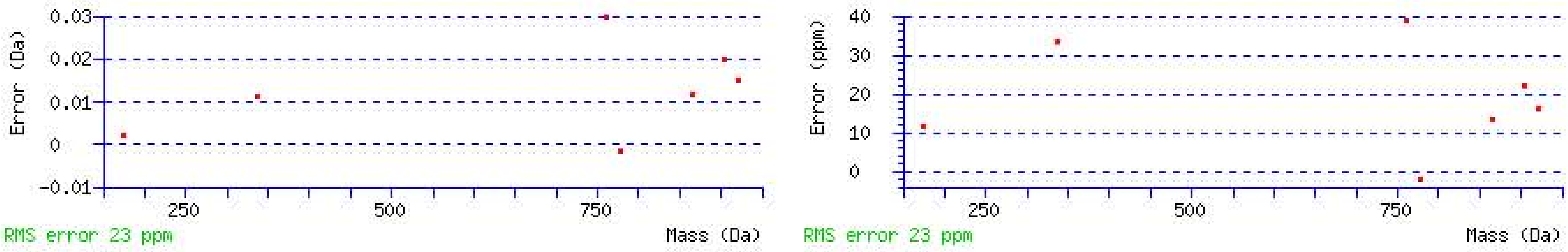
Match to Query 14161: 1019.525848 from(510.770200,2+) rtinseconds(1412) index(15266)
Title: Locus:1.1.1.3092.17 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 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: 28  Expect: 0.054
Matches : 7/44 fragment ions using 16 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							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
28.4	1019.522232	0.003616	VGSQYR
13.9	1019.533447	-0.007599	RSQYR
12.3	1019.539993	-0.014145	VGEAFALTGR
7.2	1019.510818	0.015030	RSSVSSGGAGR
6.5	1019.539993	-0.014145	VDLAAFQTR
4.9	1019.512146	0.013702	RSRGHHDR
4.7	1019.526047	-0.000199	SRERGPYR
4.3	1019.539978	-0.014130	DGLLLYNGR
1.6	1019.533463	-0.007615	VSLMWRGR
0.1	1019.530090	-0.004242	SPLPWQHR

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

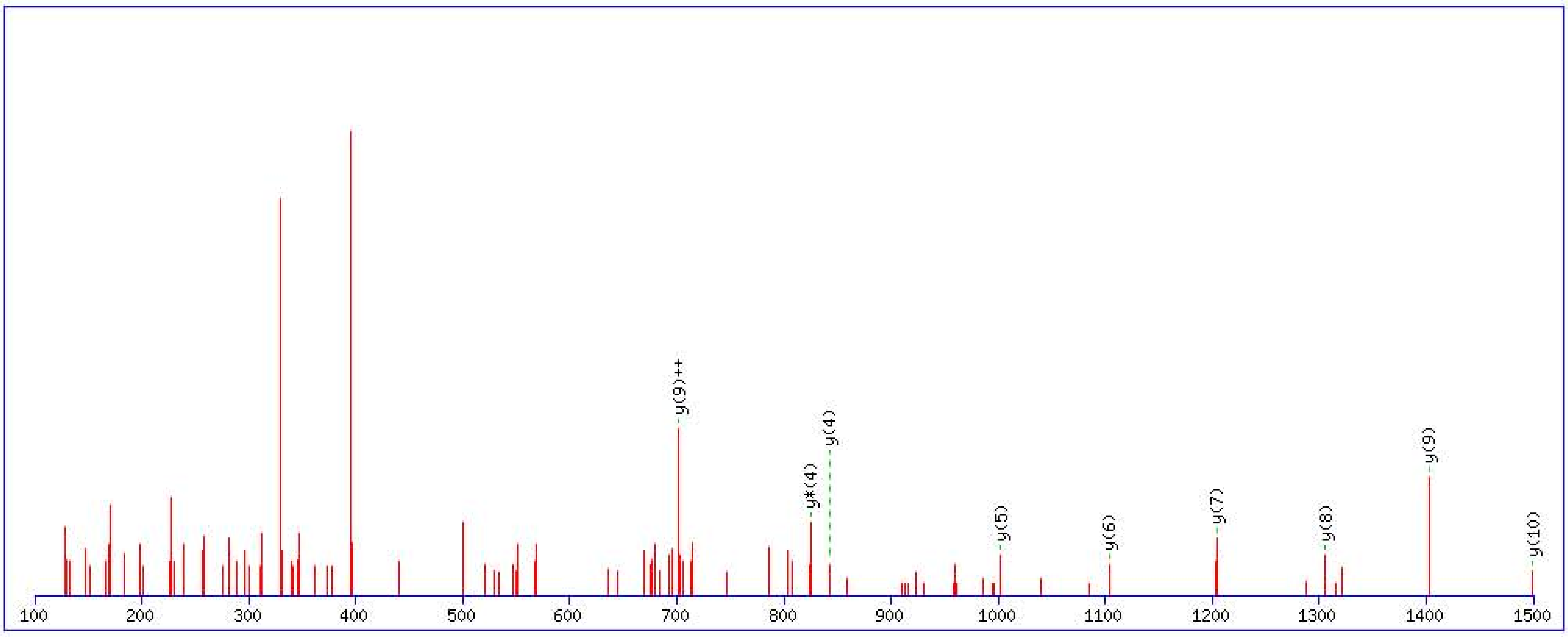
Mascot Search Results

Peptide View

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

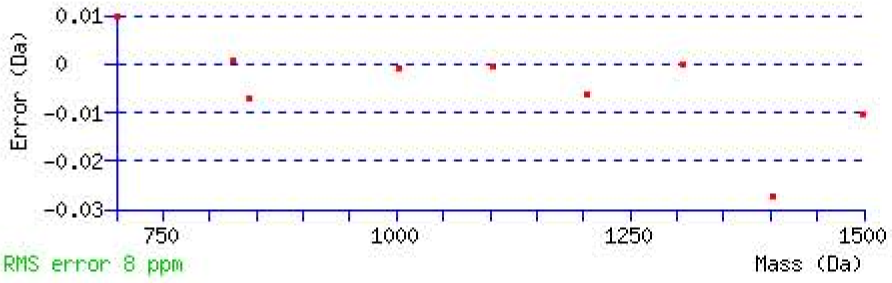
Match to Query 33775: 1611.811152 from(538.277660,3+) rtinseconds(1463) index(1773)
Title: Locus:1.1.1.3061.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

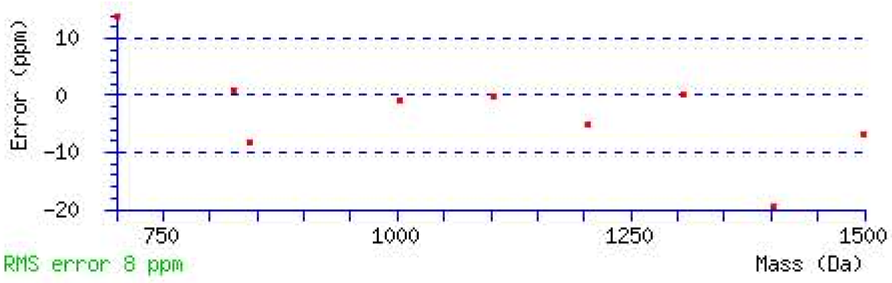
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 44  Expect: 0.00041
Matches : 9/90 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
44.3	1611.811295	-0.000143	LPPTTTCQQQK
44.3	1611.811295	-0.000143	LPPTTTCQQQK
44.3	1611.811295	-0.000143	LPPTTTCQQQK
7.7	1611.815094	-0.003942	NDVEGAKMHLRQAK
2.0	1611.803406	0.007746	TPIKMGISASTMTMK
0.1	1611.803864	0.007288	HQEMEDVIRLAQK

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

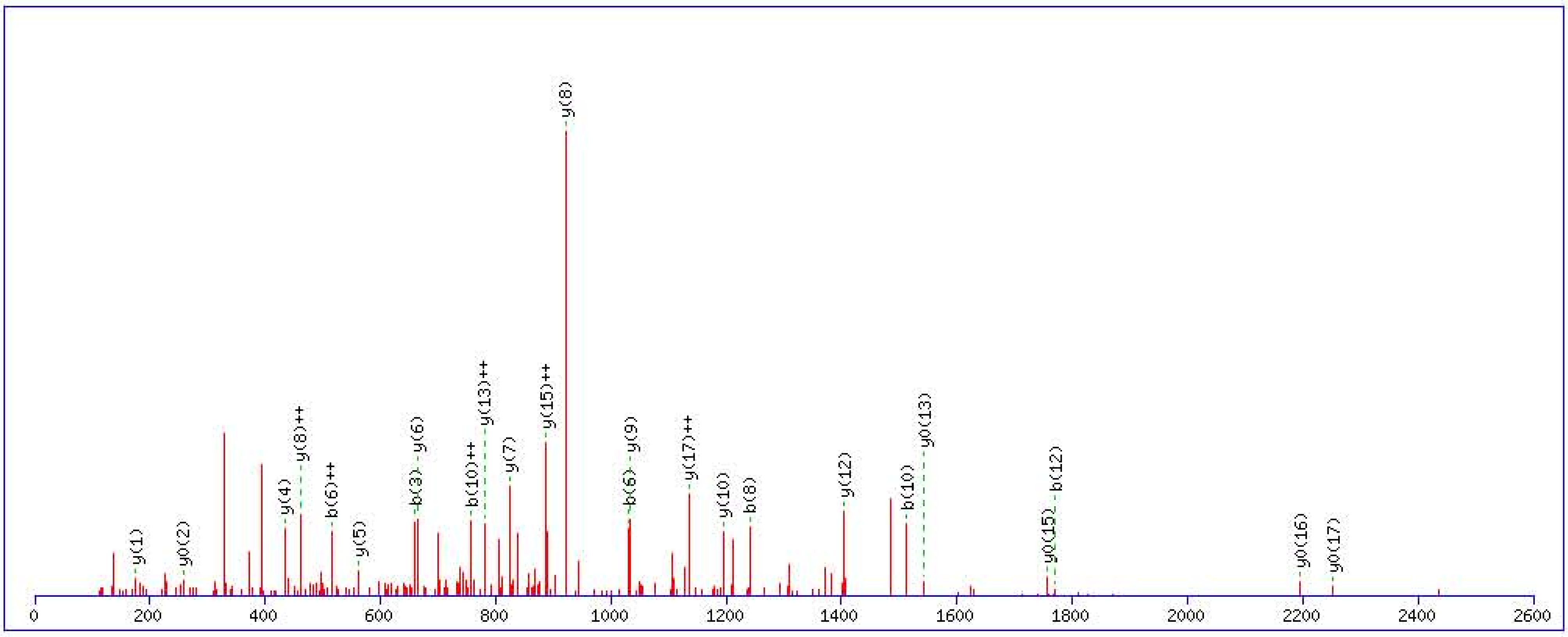
Mascot Search Results

Peptide View

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

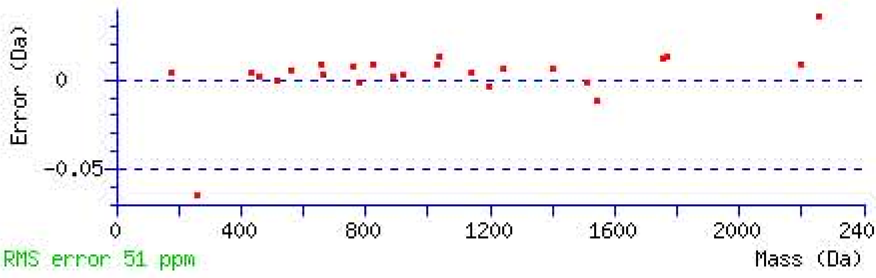
Match to Query 49672: 2433.198162 from(812.073330,3+) rtinseconds(2089) index(5389)
Title: Locus:1.1.1.3279.16 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

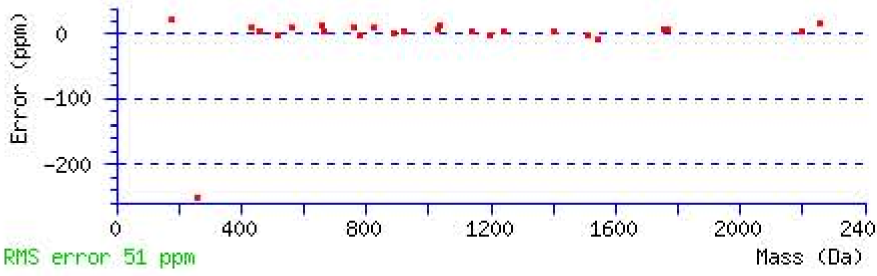
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2433.196701
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 0.00015
Matches : 25/192 fragment ions using 38 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
52.2	2433.196701	0.001461	YGQTIRPICLPCTEGTTR

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

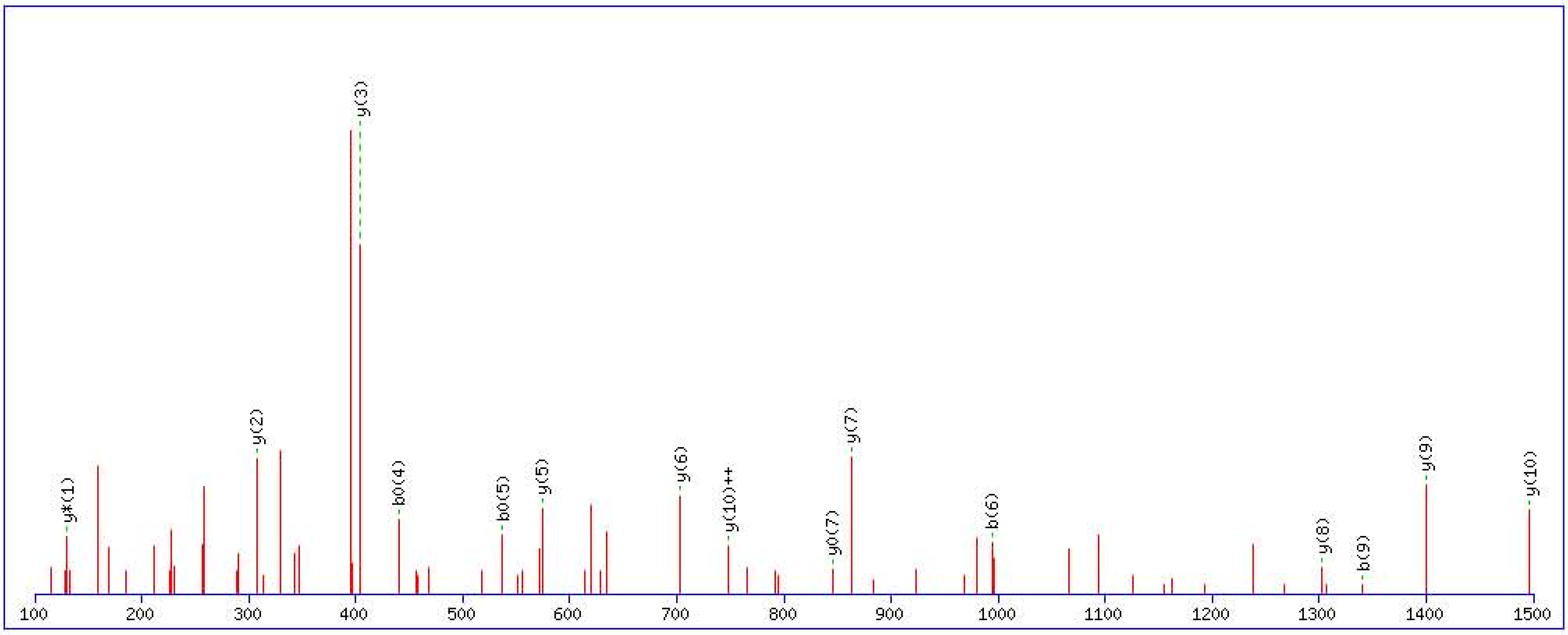
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **WSSPPQCEGLPCK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

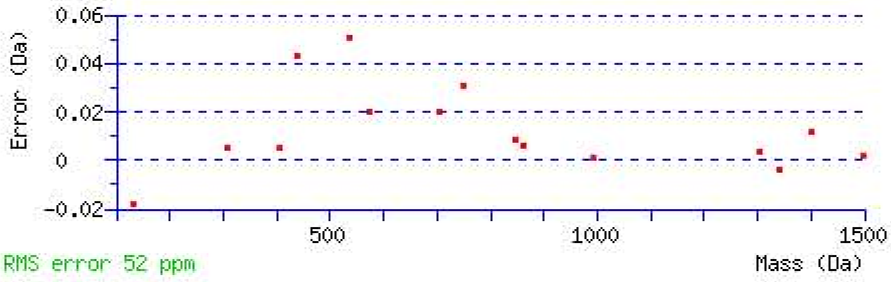
Match to Query 39626: 1855.855482 from(619.625770,3+) rtinseconds(1919) index(18483)
Title: Locus:1.1.1.3269.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

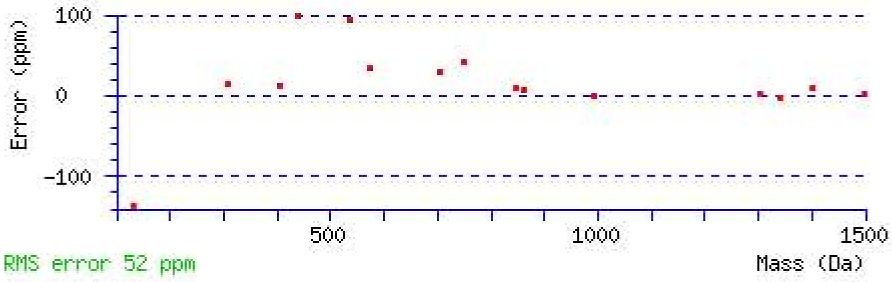
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1855.841934
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.00056
Matches : 15/122 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	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
43.2	1855.841934	0.013548	WSSPPQCEGLPCK

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

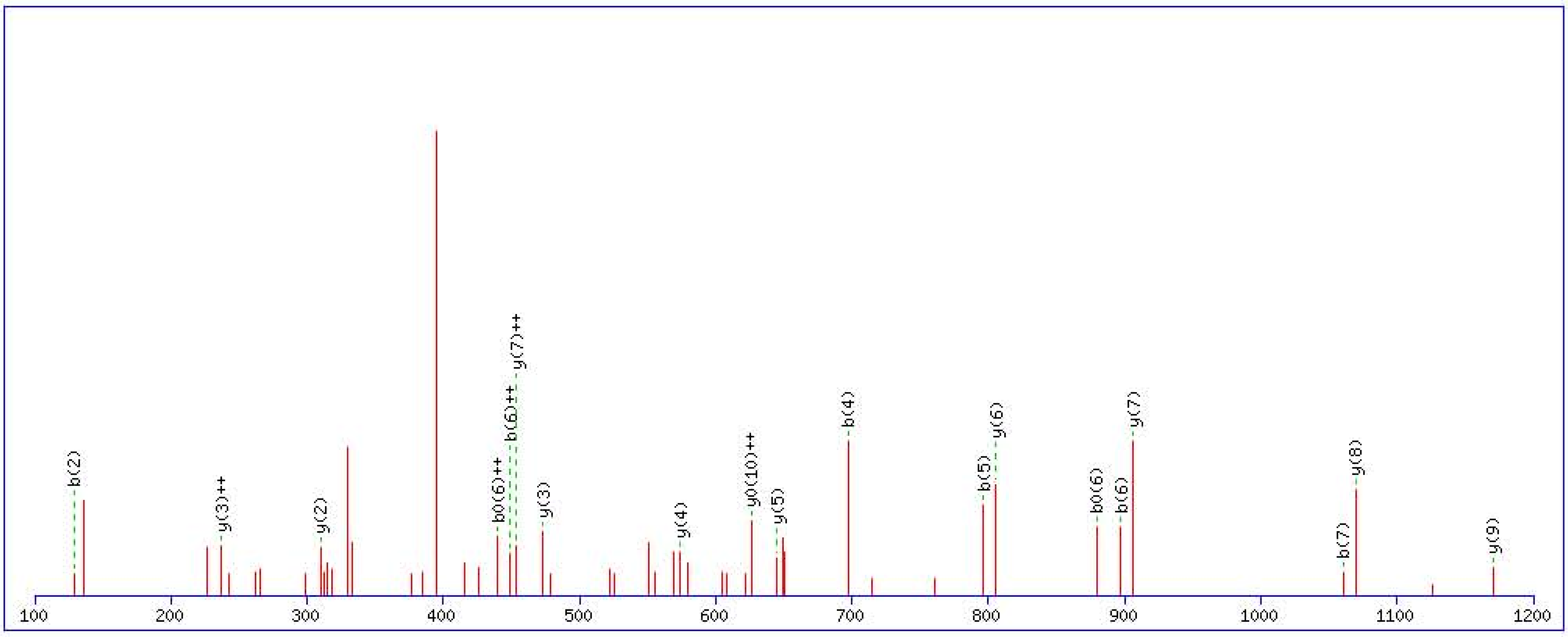
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGEQVTYTCATYYK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

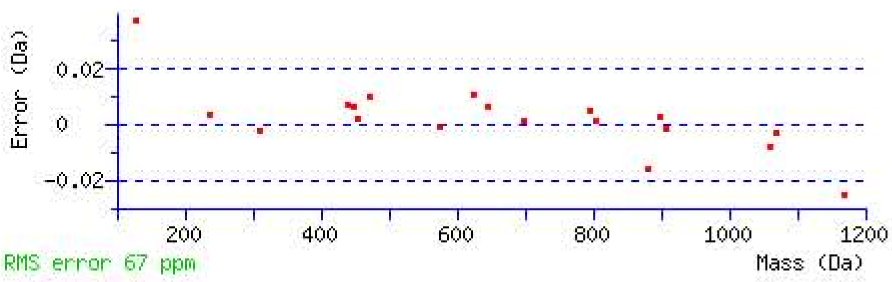
Match to Query 41410: 1964.907402 from(655.976410,3+) rtinseconds(1881) index(32285)
Title: Locus:1.1.1.3204.8 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

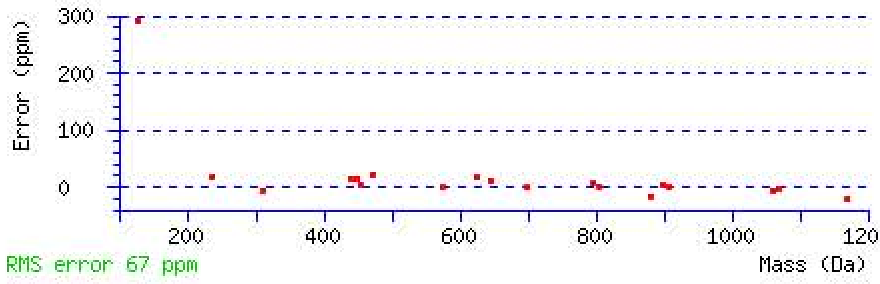
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1964.901215
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.00072
Matches : 19/140 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	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
42.5	1964.901215	0.006187	AGEQVTYTCATYYK

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

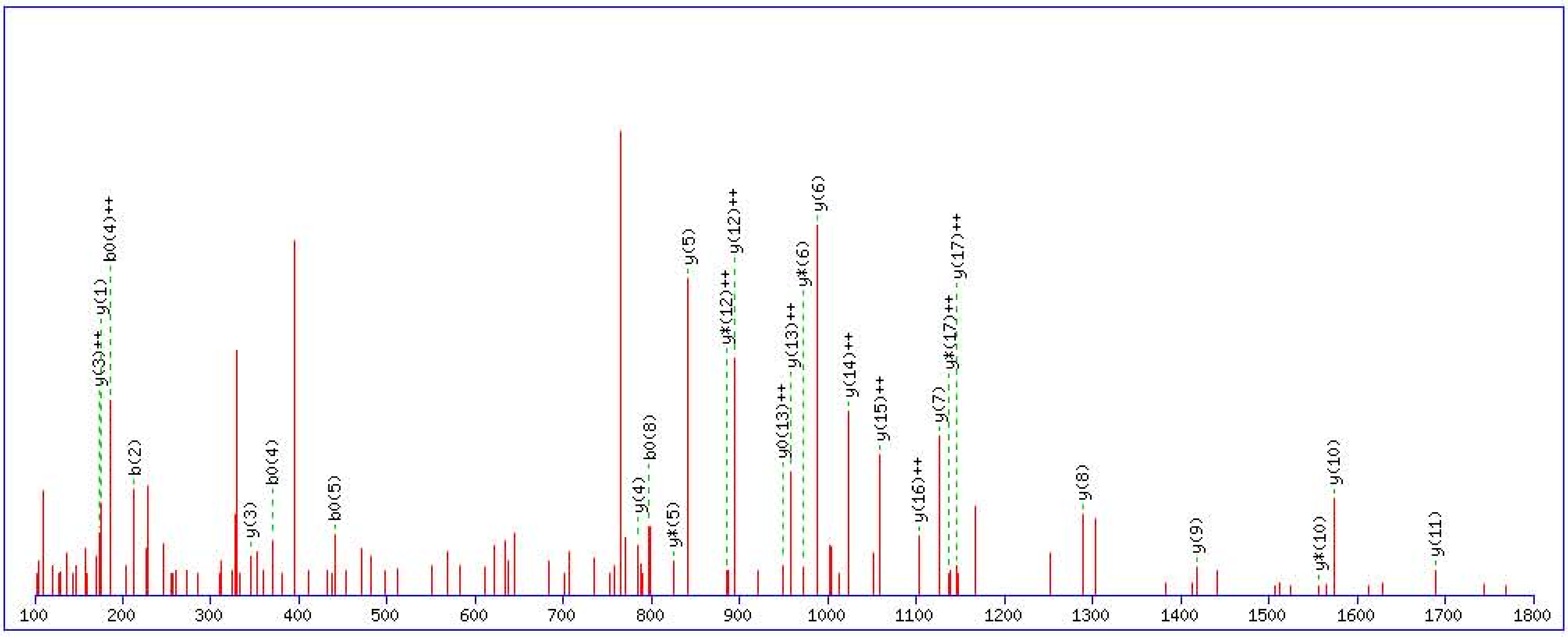
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVSSAMEPDREYHFGQAVR**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

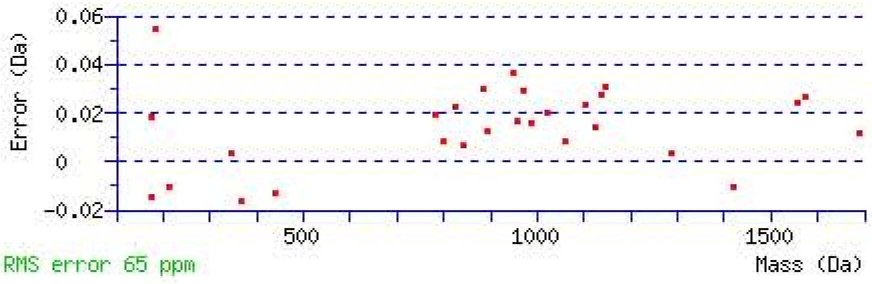
Match to Query 51182: 2502.233136 from(626.565560,4+) rtinseconds(1864) index(18073)
Title: Locus:1.1.1.3250.7 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

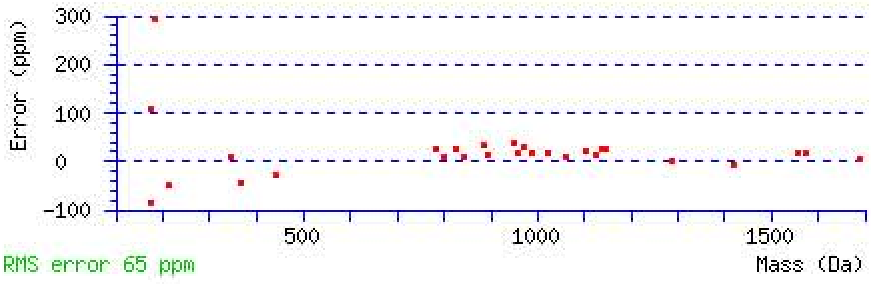
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2502.214767
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16    : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.027
Matches : 28/178 fragment ions using 93 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
29.7	2502.214767	0.018369	IVSSAMEPDREYHFGQAVR

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

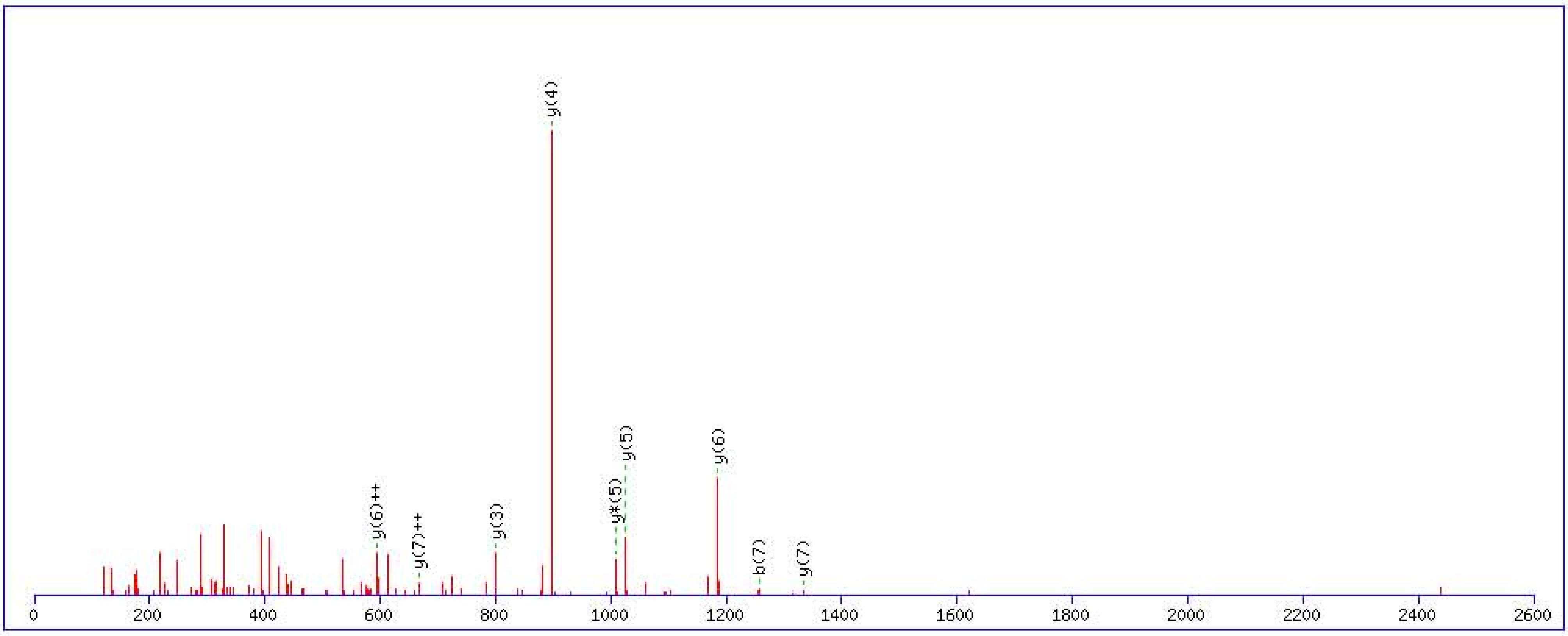
Mascot Search Results

Peptide View

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

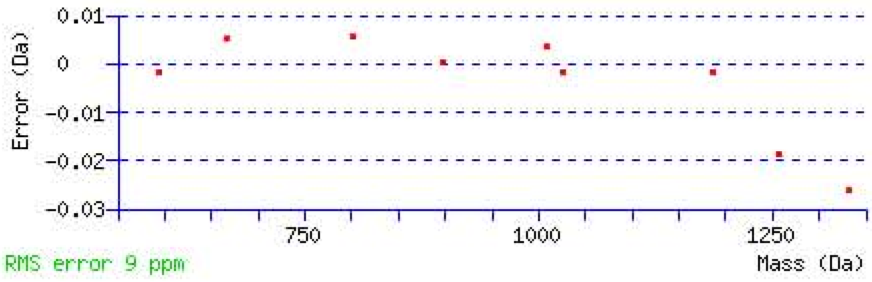
Match to Query 28048: 1430.696708 from(716.355630,2+) rtinseconds(2074) index(62953)
Title: Locus:1.1.1.3348.10 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

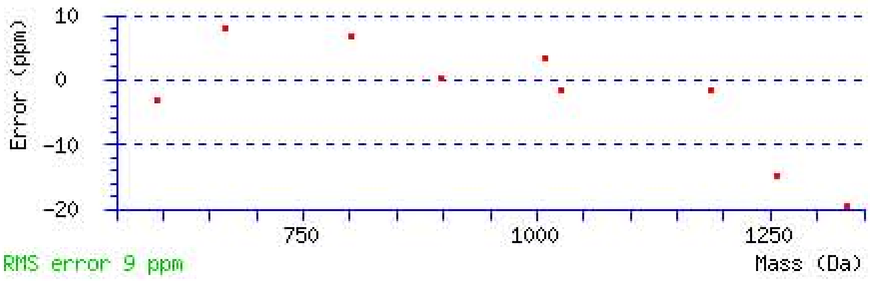
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1430.695145
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.00095
Matches : 9/50 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
32.9	1430.695145	0.001563	VFCQPWQR
7.5	1430.695145	0.001563	VFCQPWQR
0.6	1430.693619	0.003089	QLQTLSMPGGGGNR
0.6	1430.700989	-0.004281	NMPQADAMVLVAR
0.1	1430.711319	-0.014611	RAKAEDENETLR

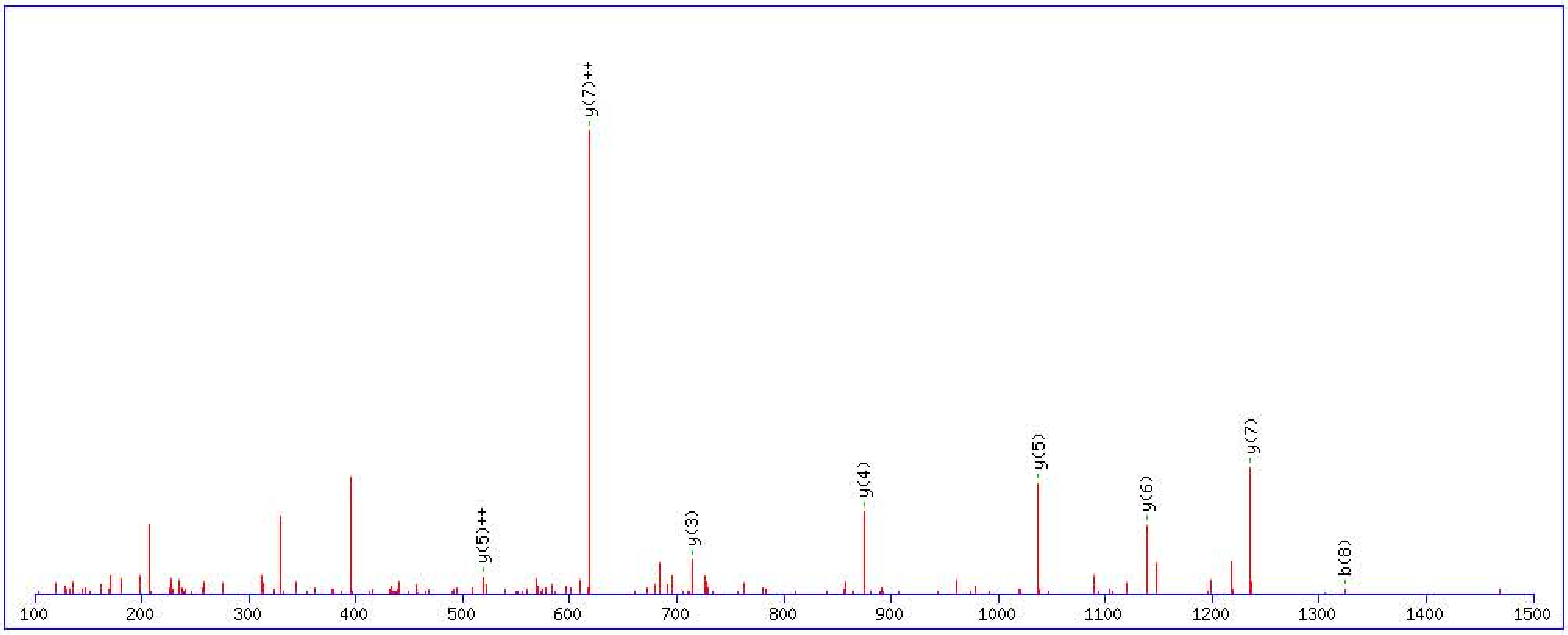
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

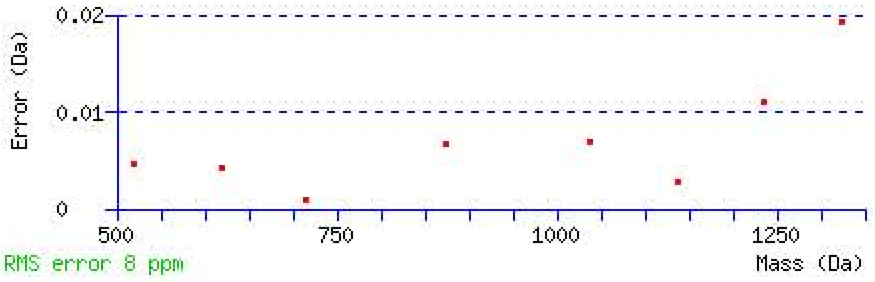
Match to Query 29122: 1468.685288 from(735.349920,2+) rtinseconds(1859) index(61652)
Title: Locus:1.1.1.3273.11 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

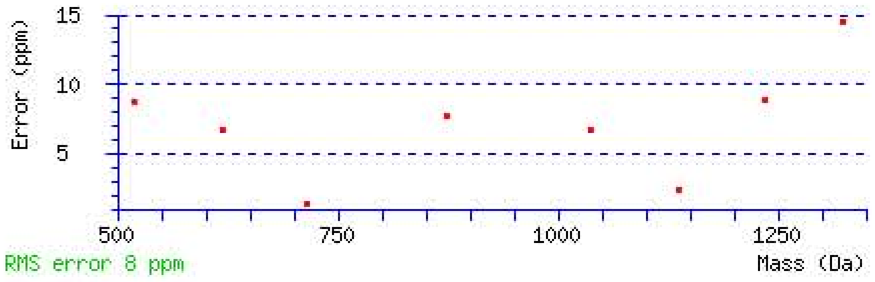
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1468.684296
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 30 **Expect:** 0.0055
Matches : 8/74 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	88.039304	44.523290			70.028739	35.518008	S							9
2	235.107718	118.057497			217.097153	109.052214	F	1382.659543	691.833410	1365.632994	683.320135	1364.648978	682.828127	8
3	332.160482	166.583879			314.149917	157.578596	P	*1235.591129*	618.299203	1218.564580	609.785928	1217.580564	609.293920	7
4	433.208161	217.107718			415.197596	208.102436	T	*1138.538365*	569.772821	1121.511816	561.259546	1120.527800	560.767538	6
5	596.271490	298.639383			578.260925	289.634101	Y	*1037.490686*	519.248981	1020.464137	510.735707			5
6	756.302139	378.654708			738.291574	369.649425	C	*874.427357*	437.717317	857.400808	429.204042			4
7	884.360717	442.683997	867.334168	434.170722	866.350152	433.678714	Q	*714.396708*	357.701992	697.370159	349.188718			3
8	**1323.586043**	662.296660	1306.559494	653.783385	1305.575478	653.291377	Q	586.338130	293.672703	569.311581	285.159428			2
9							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.1	1468.684296	0.000992	SFPTYCQQK
30.1	1468.684296	0.000992	SFPTYCQQK
5.6	1468.671524	0.013764	MEAETGSSVETGKK
0.9	1468.688126	-0.002838	FSIPSMTEHHAGR
0.2	1468.680252	0.005036	YAKGNGDCALLCK

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

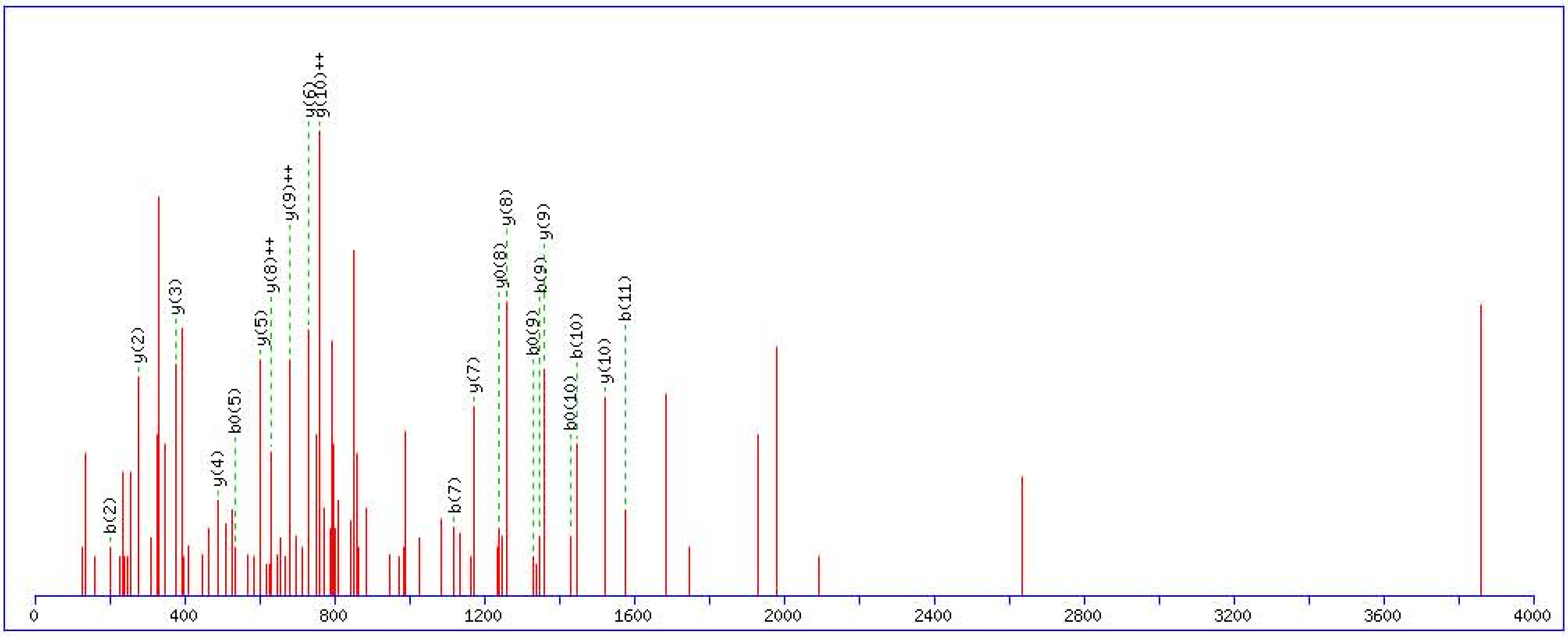
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

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

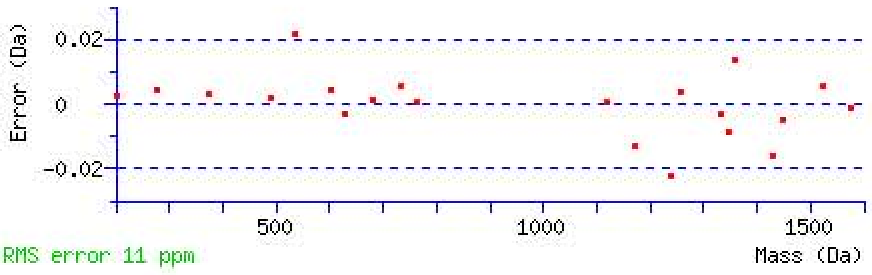
Match to Query 36856: 1721.841028 from(861.927790,2+) rtinseconds(1910) index(61868)
Title: Locus:1.1.1.3291.12 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

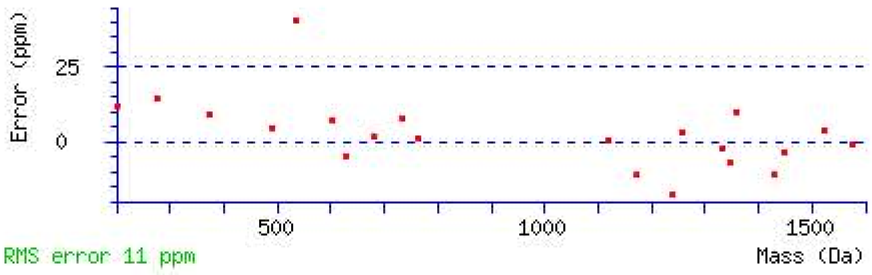
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1721.854584
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 6.4e-005
Matches : 21/118 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	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
48.2	1721.854584	-0.013556	VTYTSQEDLVEK
3.2	1721.858414	-0.017386	DRVYQVTEQQISEK
3.2	1721.830292	0.010736	MQNICNFLVEK
0.7	1721.847122	-0.006094	EAYDQKIAEEEAKAK

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

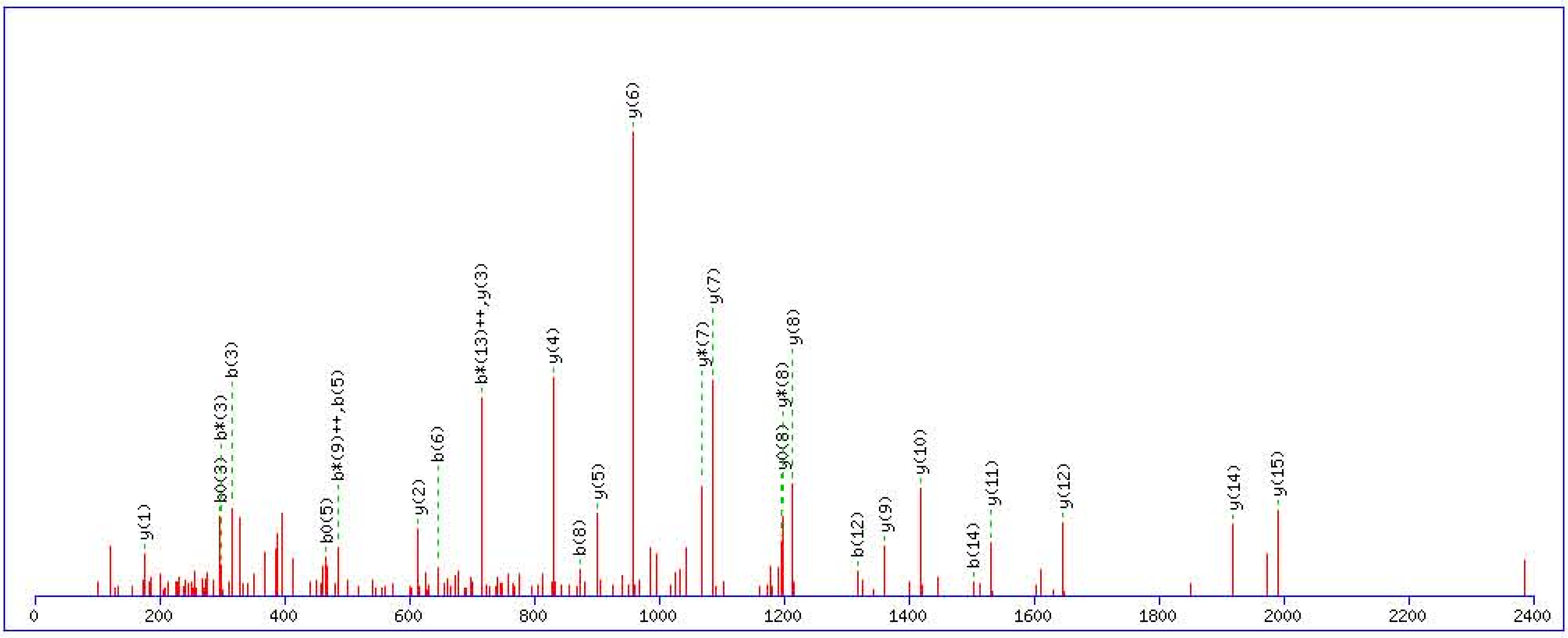
MATRIX SCIENCE Mascot Search Results

Peptide View

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

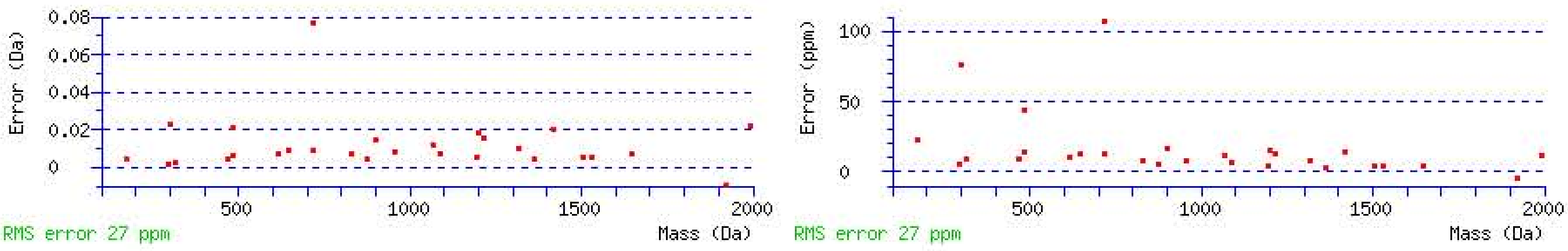
Match to Query 49180: 2403.139392 from(802.053740,3+) rtinseconds(2297) index(64243)
Title: Locus:1.1.1.3426.10 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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): 2403.131119
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18    : Biotin:Thermo-21345 (Q)
Ions Score: 116  Expect: 5.2e-011
Matches : 28/208 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	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
115.8	2403.131119	0.008273	EANVACLDLGFQQGADTQR
48.4	2403.131119	0.008273	EANVACLDLGFQQGADTQR
35.5	2403.131119	0.008273	EANVACLDLGFQQGADTQR
7.5	2403.171967	-0.032575	HAGEEVFTSKEEANFFIHRR
4.8	2403.157135	-0.017743	QAMMKTDFPGDLGSQR
0.6	2403.104553	0.034839	ESSMEPKAAEEEAGSEQKR

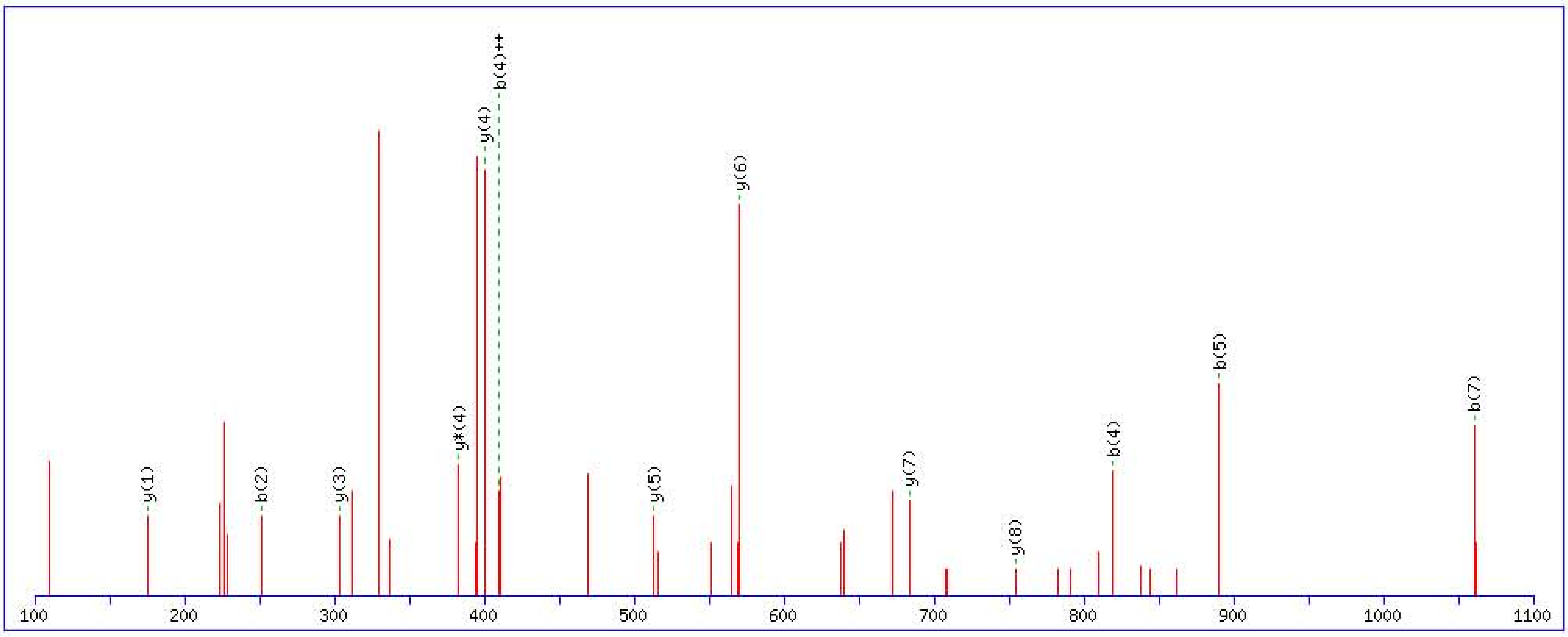
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HLQEALGLPAGR**
Found in **CLC11_HUMAN**, C-type lectin domain family 11 member A OS=Homo sapiens GN=CLEC11A PE=1 SV=1

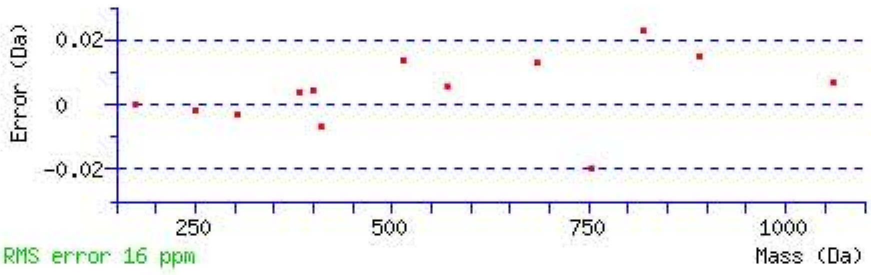
Match to Query 31864: 1571.864862 from(524.962230,3+) rtinseconds(1937) index(46954)
Title: Locus:1.1.1.2723.7 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

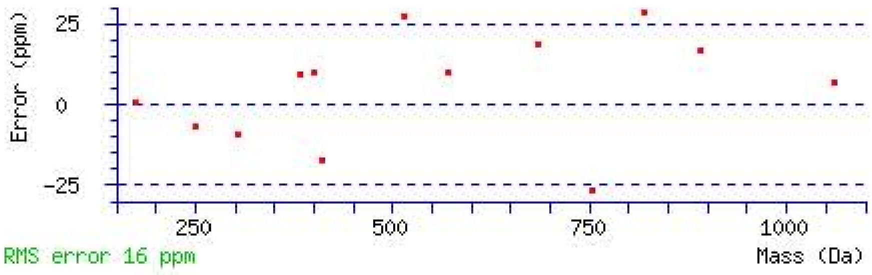
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1571.860596
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.0055
Matches : 13/106 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	138.066188	69.536732					H							12
2	**251.150252**	126.078764					L	1435.808983	718.408129	1418.782434	709.894855	1417.798418	709.402847	11
3	690.375578	345.691427	673.349029	337.178153			Q	1322.724919	661.866098	1305.698370	653.352823	1304.714354	652.860815	10
4	**819.418171**	410.212724	802.391622	401.699449	801.407606	401.207441	E	883.499593	442.253434	866.473044	433.740160	865.489028	433.248152	9
5	**890.455285**	445.731281	873.428736	437.218006	872.444720	436.725998	A	***754.457000***	377.732138	737.430451	369.218863			8
6	1003.539349	502.273313	986.512800	493.760038	985.528784	493.268030	L	***683.419886***	342.213581	666.393337	333.700306			7
7	**1060.560813**	530.784045	1043.534264	522.270770	1042.550248	521.778762	G	***570.335822***	285.671549	553.309273	277.158274			6
8	1173.644877	587.326077	1156.618328	578.812802	1155.634312	578.320794	L	***513.314358***	257.160817	496.287809	248.647542			5
9	1270.697641	635.852459	1253.671092	627.339184	1252.687076	626.847176	P	***400.230294***	200.618785	383.203745	192.105510			4
10	1341.734755	671.371016	1324.708206	662.857741	1323.724190	662.365733	A	***303.177530***	152.092403	286.150981	143.579128			3
11	1398.756219	699.881747	1381.729670	691.368473	1380.745654	690.876465	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 HLQEALGLPAGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.3	1571.860596	0.004266	HLQEALGLPAGR
5.8	1571.856567	0.008295	QVRELQMRLDIR
0.7	1571.857224	0.007638	VNWLGSKEGLRWK
0.7	1571.878372	-0.013510	LTGRVLALSFDAPGR
0.3	1571.857239	0.007623	GRSPLAFIPFSAGPR

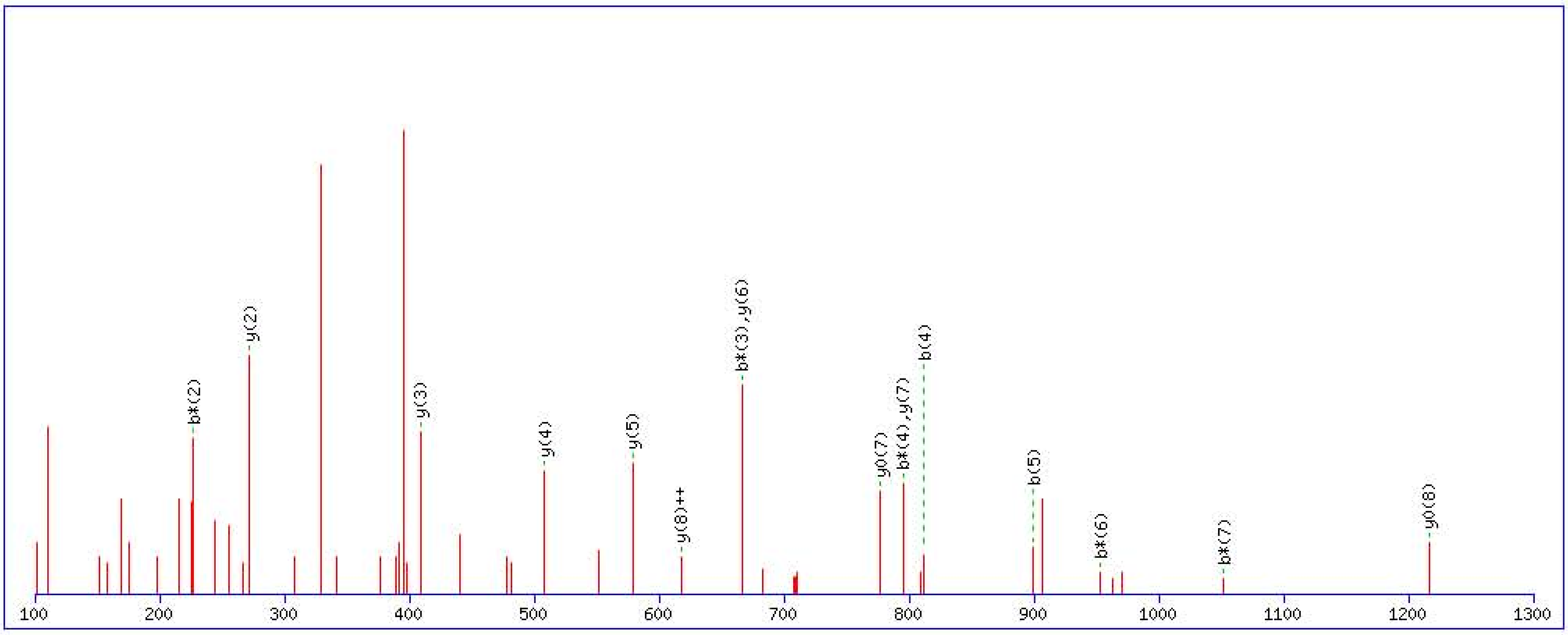
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NEQESAVHPR**
Found in **DBNL_HUMAN**, Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1

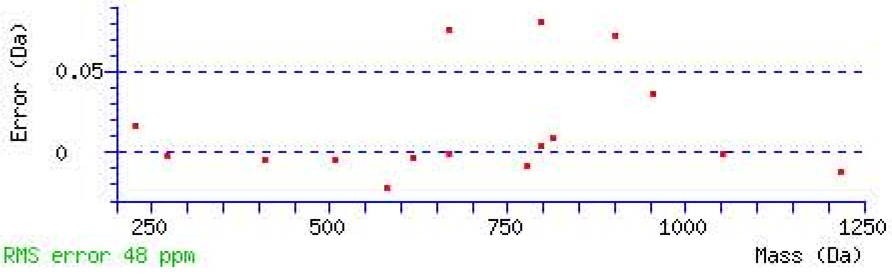
Match to Query 29345: 1476.713172 from(493.245000,3+) rtinseconds(1289) index(42988)
Title: Locus:1.1.1.2497.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

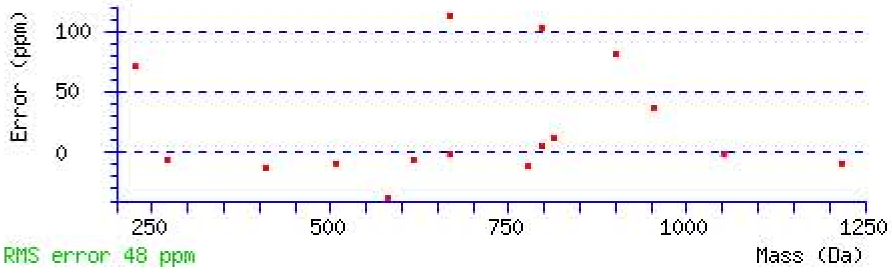
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1476.714325
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 37 **Expect:** 0.0042
Matches : 16/96 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	115.050203	58.028740	98.023654	49.515465			N							10
2	244.092796	122.550036	227.066247	114.036762	226.082231	113.544754	E	1363.678696	682.342986	1346.652147	673.829712	1345.668131	673.337704	9
3	683.318122	342.162699	666.291573	333.649425	665.307557	333.157417	Q	1234.636103	617.821690	1217.609554	609.308415	1216.625538	608.816407	8
4	**812.360715**	406.683996	795.334166	398.170721	794.350150	397.678713	E	***795.410777***	398.209027	778.384228	389.695752	777.400212	389.203744	7
5	**899.392743**	450.200010	882.366194	441.686735	881.382178	441.194727	S	***666.368184***	333.687730	649.341635	325.174456	648.357619	324.682448	6
6	970.429857	485.718567	953.403308	477.205292	952.419292	476.713284	A	***579.336156***	290.171716	562.309607	281.658442			5
7	1069.498271	535.252774	1052.471722	526.739499	1051.487706	526.247491	V	***508.299042***	254.653159	491.272493	246.139884			4
8	1206.557183	603.782230	1189.530634	595.268955	1188.546618	594.776947	H	***409.230628***	205.118952	392.204079	196.605677			3
9	1303.609947	652.308612	1286.583398	643.795337	1285.599382	643.303329	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 NEQESAVHPR
(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	1476.714325	-0.001153	NEQESAVHPR

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

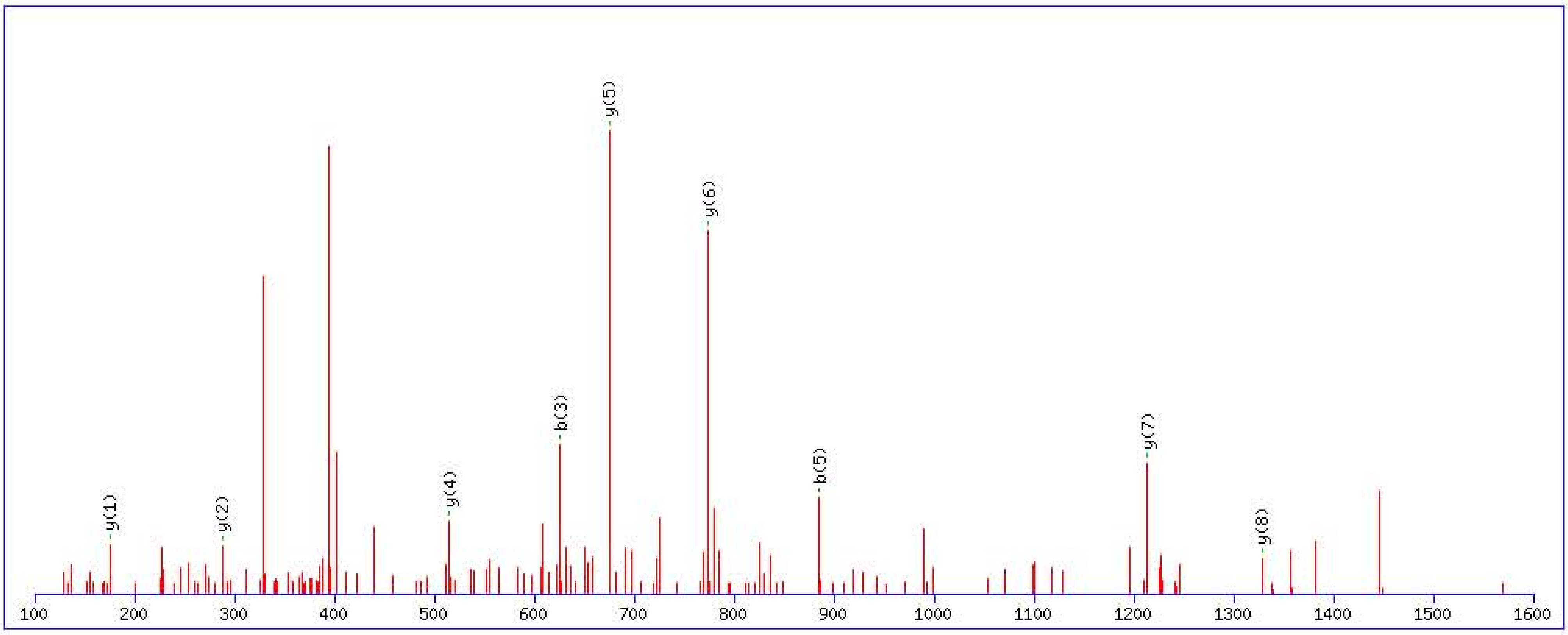
{MATRIX SCIENCE} Mascot Search Results

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

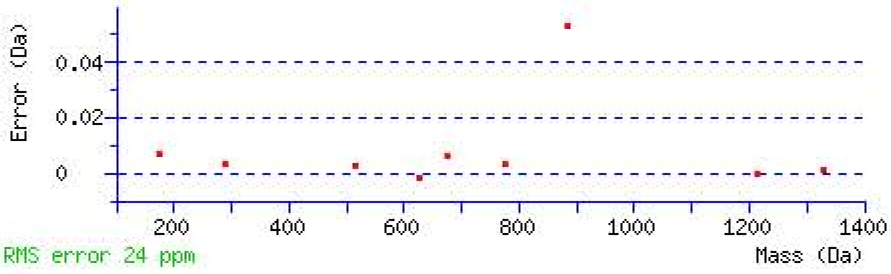
Match to Query 26314: 1398.726068 from(700.370310,2+) rtinseconds(2028) index(33335)
Title: Locus:1.1.1.3255.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

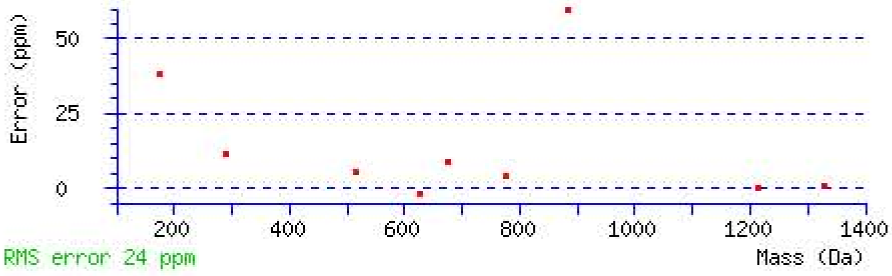
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1398.711166
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 7.5e-006
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
56.5	1398.711166	0.014902	ADQVCINLR
1.8	1398.729584	-0.003516	WLAPDGLIFPDR
1.6	1398.746643	-0.020575	EEIEREVNILR
1.3	1398.746674	-0.020606	APTASLAPTSQSLR

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

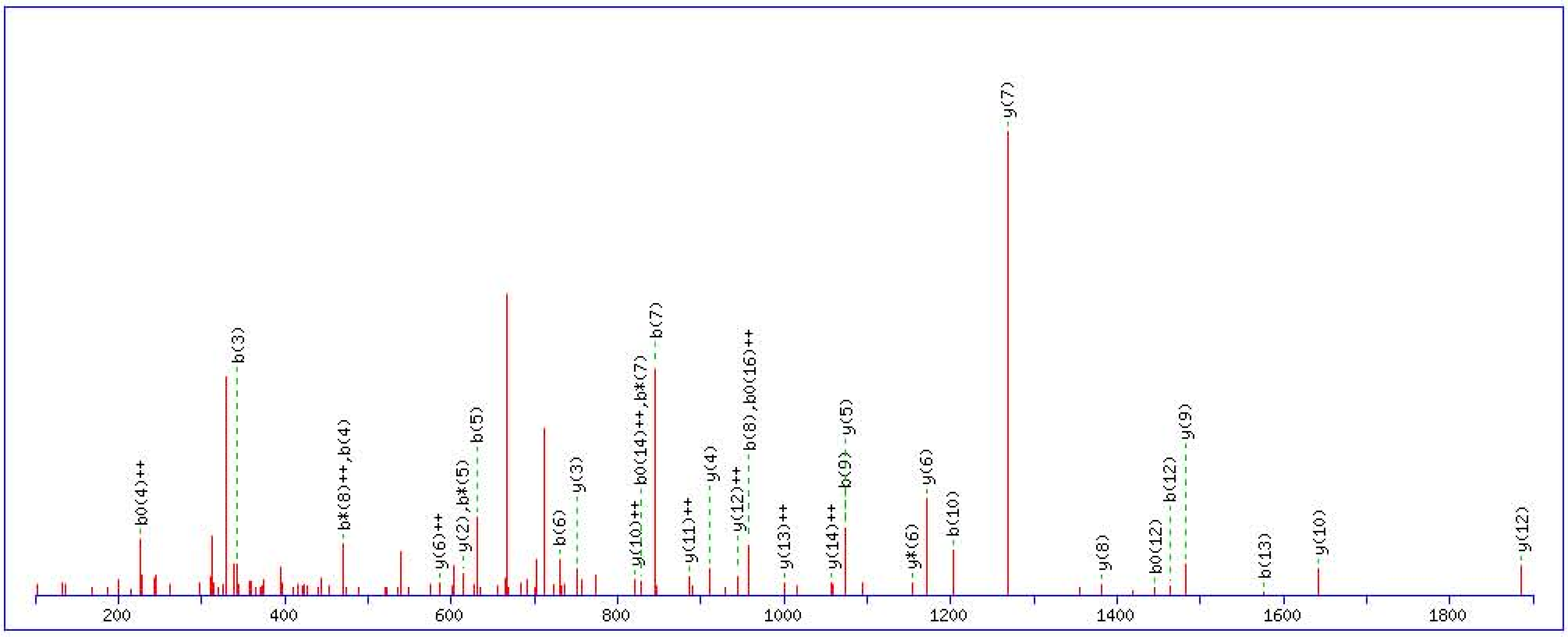
Mascot Search Results

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

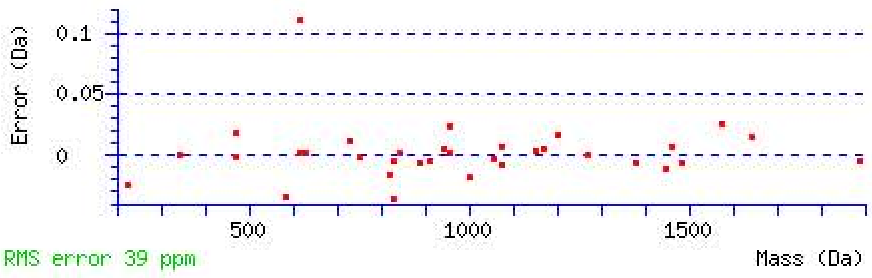
Match to Query 54366: 2843.270176 from(711.824820,4+) rtinseconds(1773) index(31796)
Title: Locus:1.1.1.3166.13 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

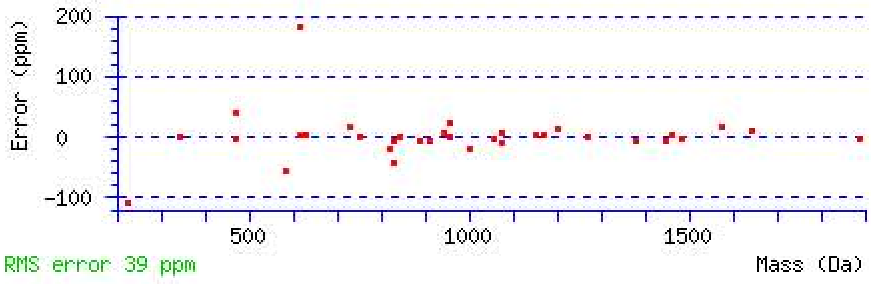
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2843.261169
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q19    : Biotin:Thermo-21345 (Q)
Ions Score: 69  Expect: 8.4e-007
Matches : 34/208 fragment ions using 53 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
69.1	2843.261169	0.009007	RGEQCVDIDECTIPPYCHQR

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

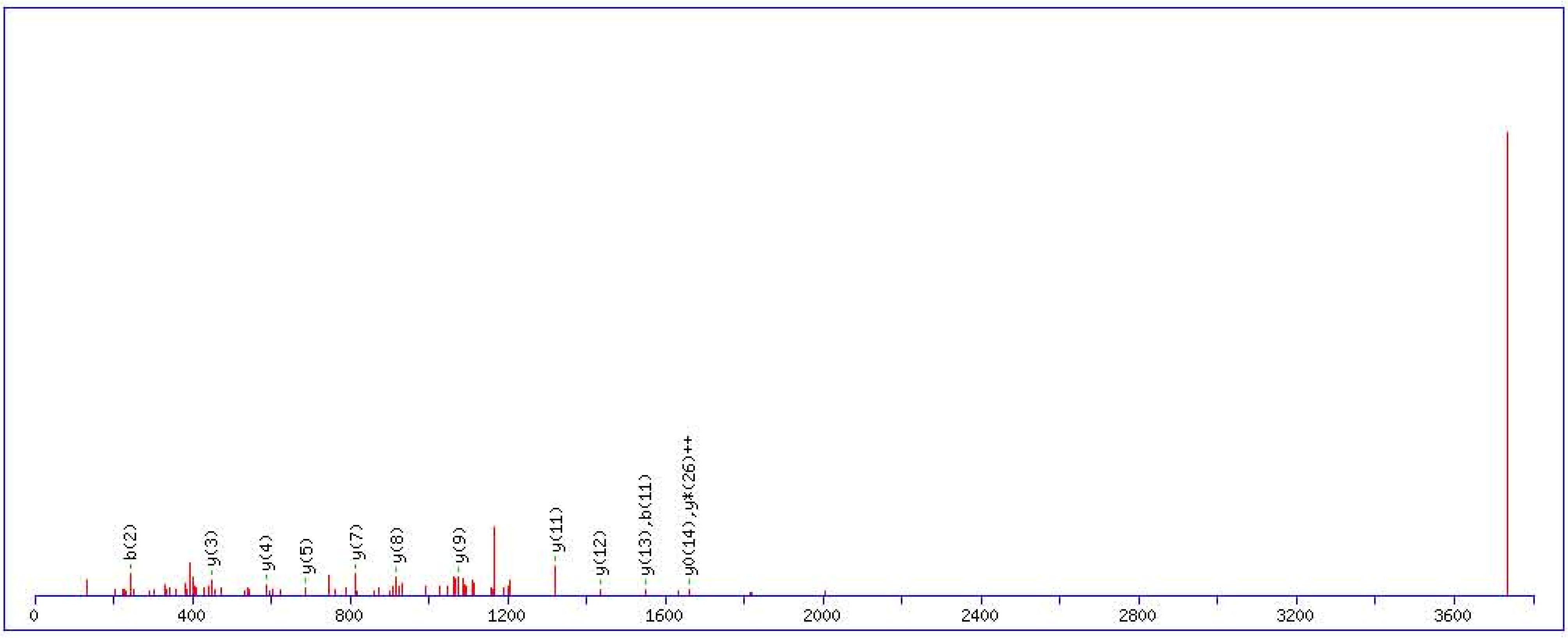
Mascot Search Results

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

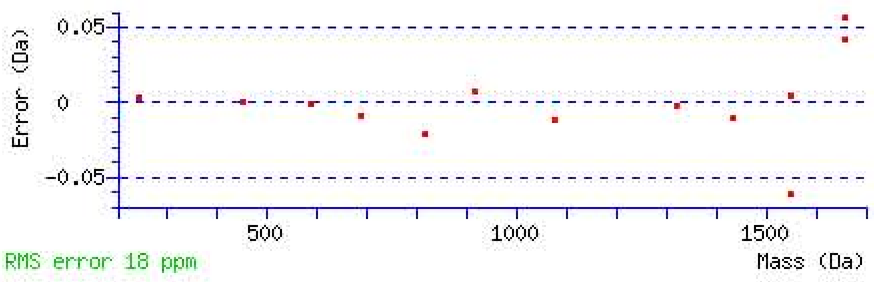
Match to Query 62779: 3733.546616 from(934.393930,4+) rtinseconds(1748) index(31647)
Title: Locus:1.1.1.3157.19 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

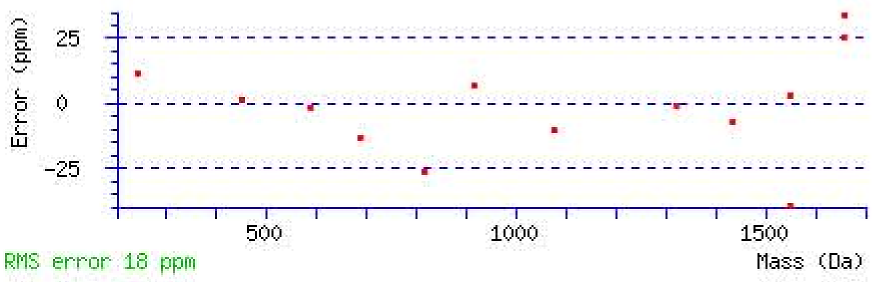
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3733.543625
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9     : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 1.9e-005
Matches : 13/312 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					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
49.0	3733.543625	0.002991	IQCAAGYEQSEHNVCQDIDECTAGTHNCR
45.9	3733.543625	0.002991	IQCAAGYEQSEHNVCQDIDECTAGTHNCR
45.3	3733.543625	0.002991	IQCAAGYEQSEHNVCQDIDECTAGTHNCR

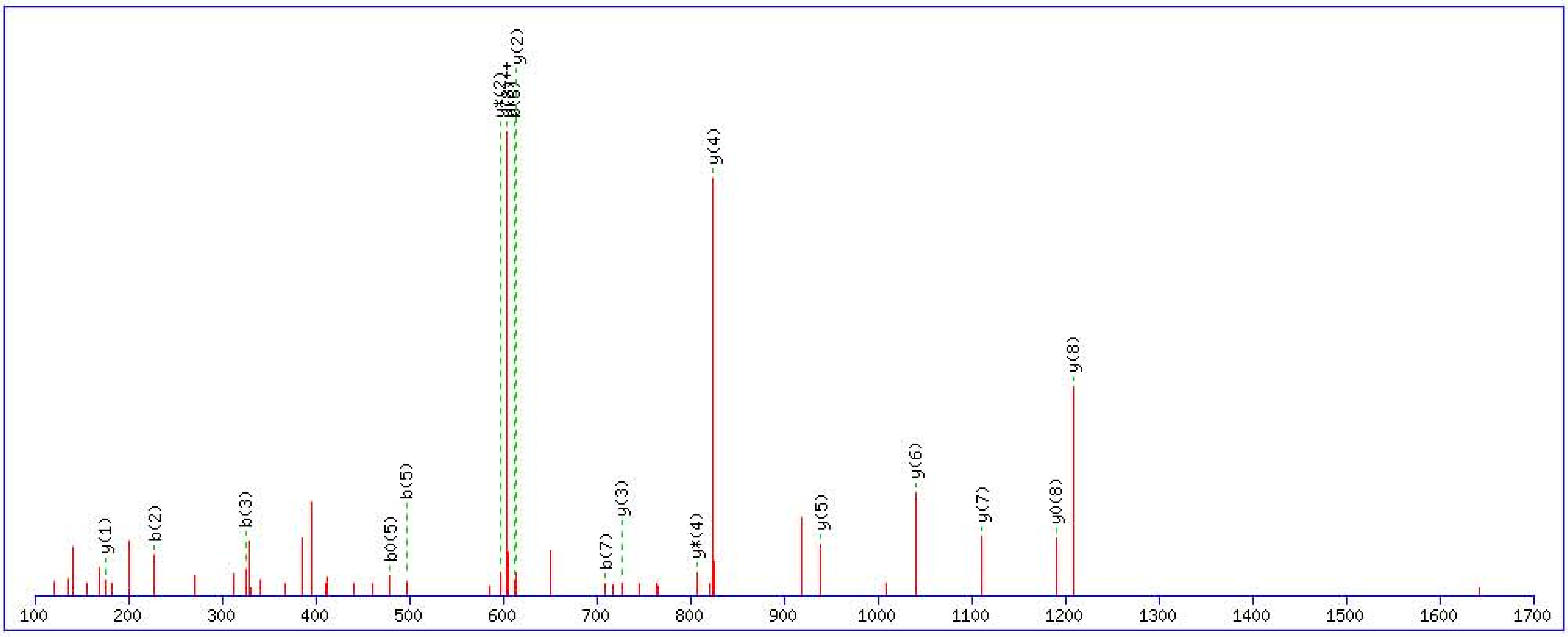
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

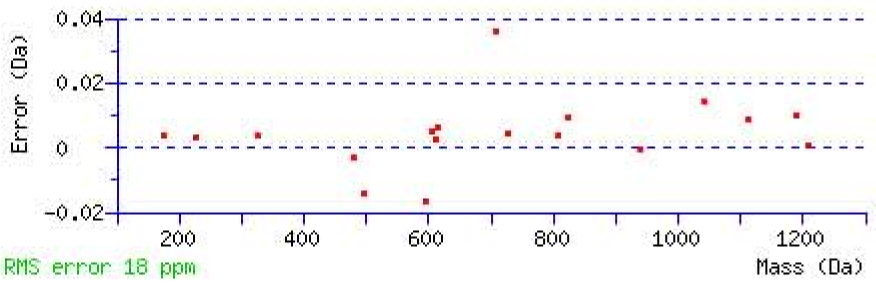
Match to Query 28239: 1434.776588 from(718.395570,2+) rtinseconds(1989) index(4910)
Title: Locus:1.1.1.3244.23 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

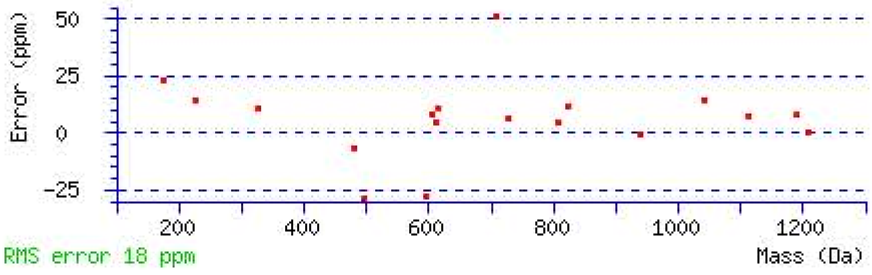
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1434.765305
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.00048
Matches : 18/92 fragment ions using 41 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							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
41.8	1434.765305	0.011283	NLPATDPLQR
6.0	1434.757889	0.018699	NLIRQISSGEYR
2.6	1434.761932	0.014656	NLDYPFGNVLRK
1.0	1434.761932	0.014656	NIFPSNLVSAAFR
0.1	1434.757919	0.018669	VQQAELHTGSLPR

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

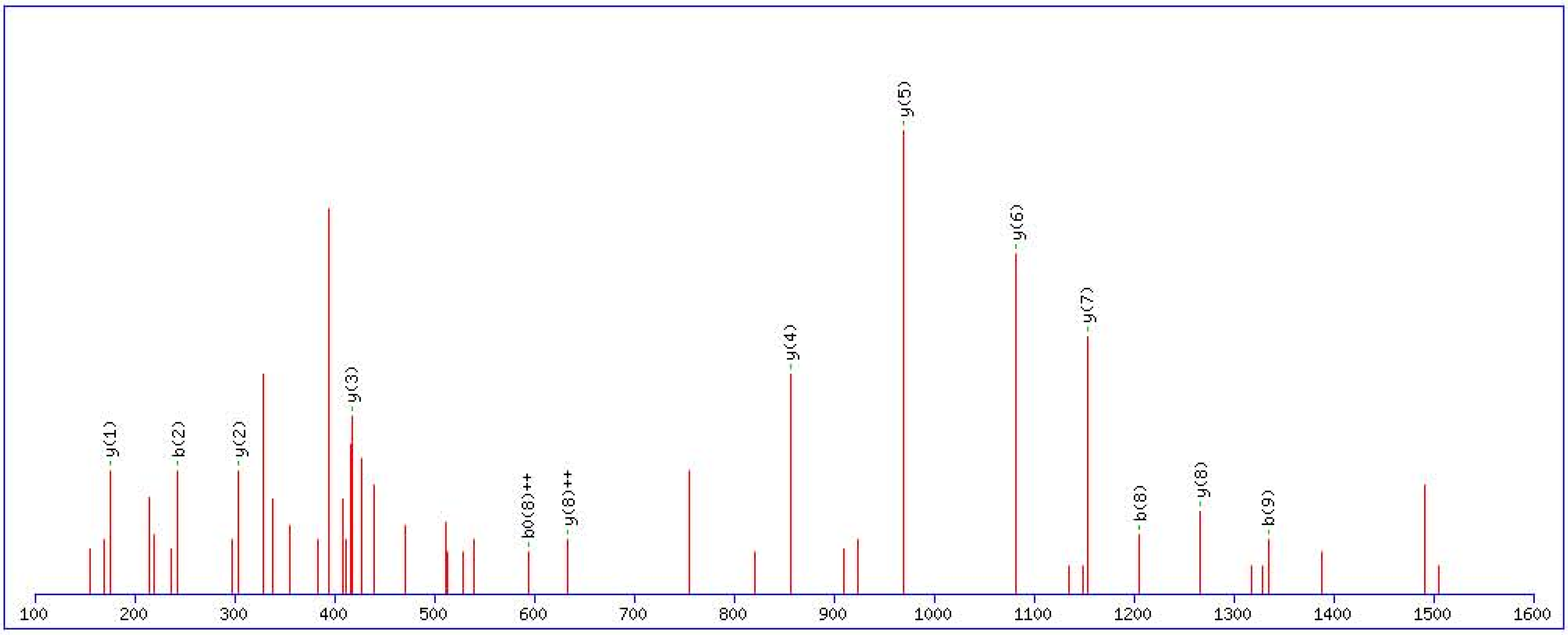
Mascot Search Results

Peptide View

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

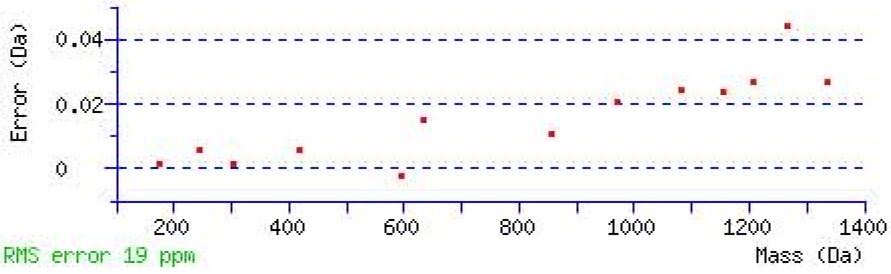
Match to Query 30177: 1507.899788 from(754.957170,2+) rtinseconds(2762) index(23323)
Title: Locus:1.1.1.3561.17 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

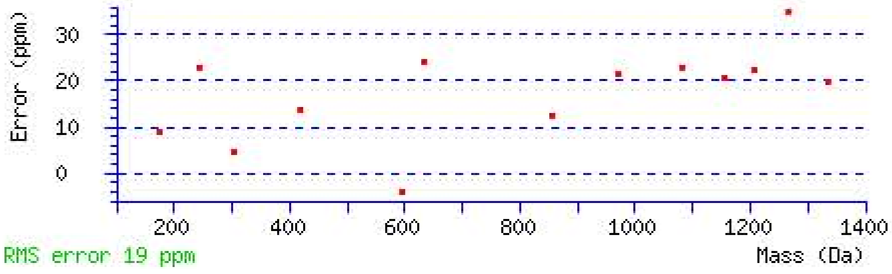
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 53  Expect: 2.2e-005
Matches : 13/94 fragment ions using 23 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	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
52.6	1507.879578	0.020210	ELLALIQLER

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

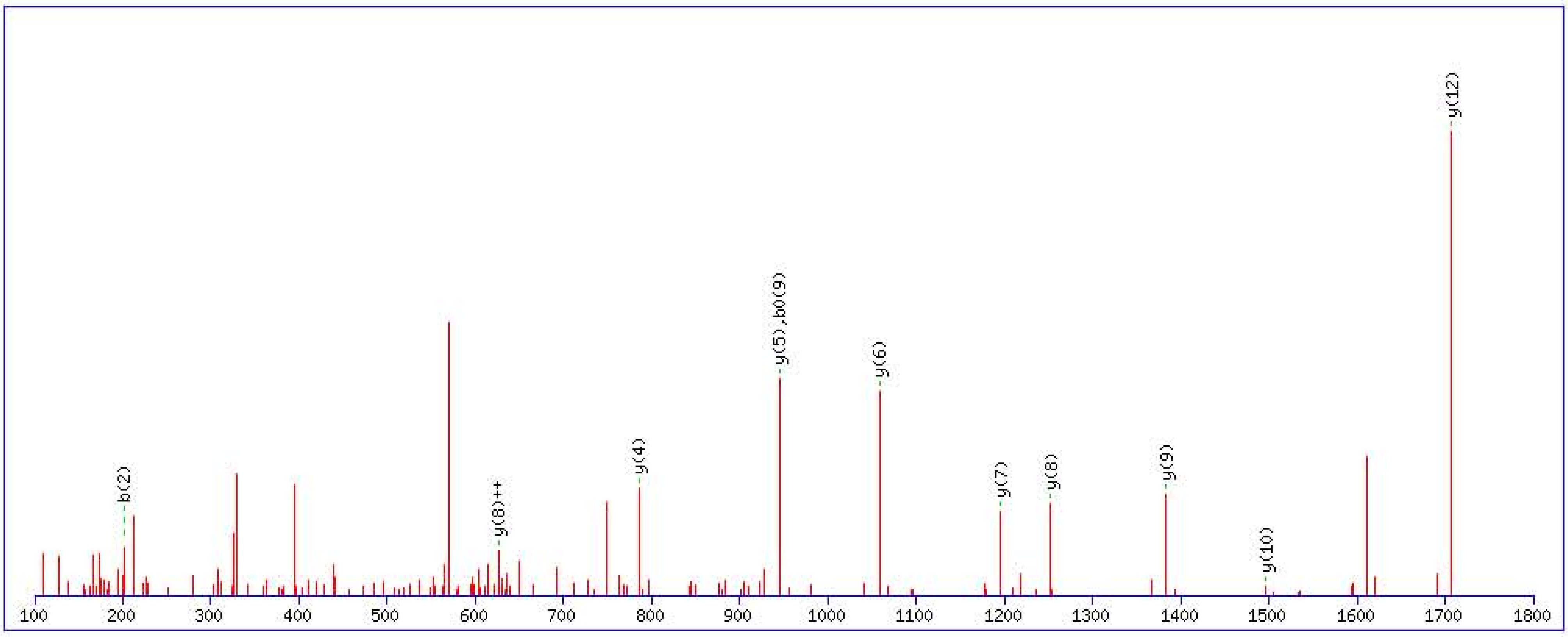
Mascot Search Results

Peptide View

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

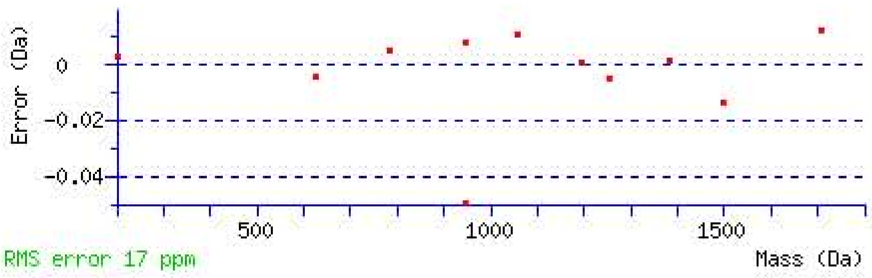
Match to Query 40327: 1906.932462 from(636.651430,3+) rtinseconds(1919) index(4361)
Title: Locus:1.1.1.3220.18 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

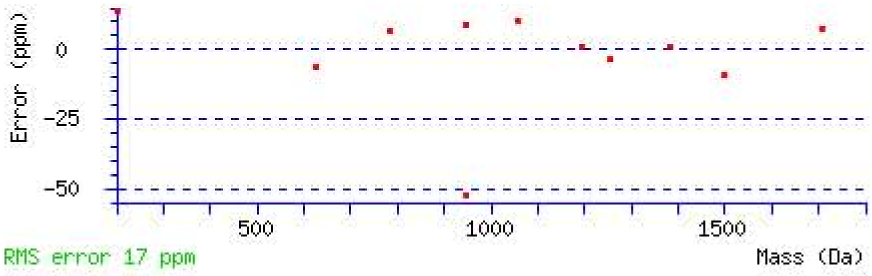
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1906.932816
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 0.00044
Matches : 11/124 fragment ions using 16 most intense peaks   (help)
```

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





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.0	1906.932816	-0.000354	VTPNLMGHLCGNQR

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

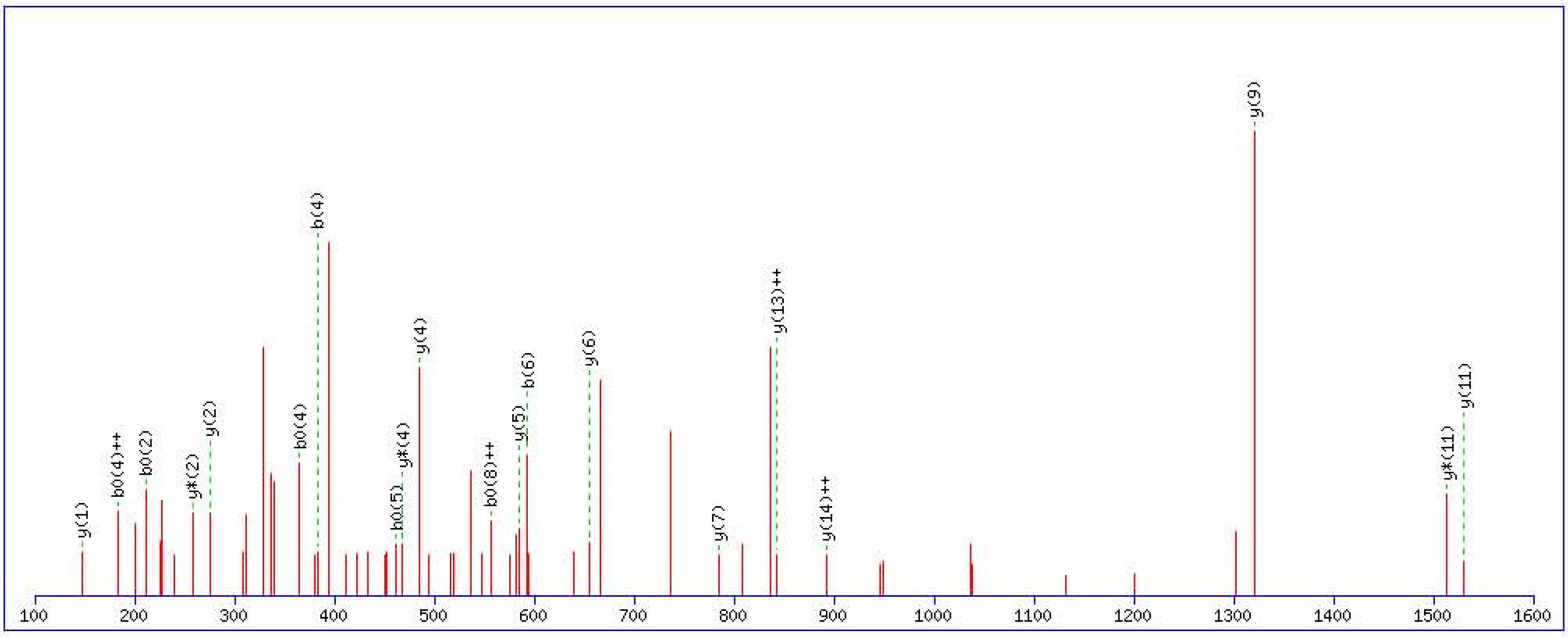
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

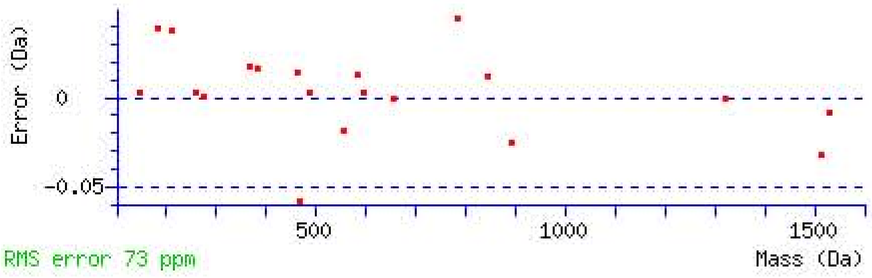
Match to Query 40484: 1912.053042 from(638.358290,3+) rtinseconds(2241) index(6302)
Title: Locus:1.1.1.3332.18 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

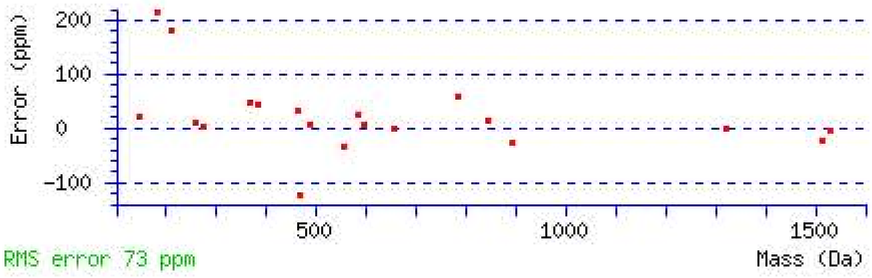
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1912.049194
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.012
Matches : 20/142 fragment ions using 48 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	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
31.4	1912.049194	0.003848	EVGPPLPQEAVPLQK

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

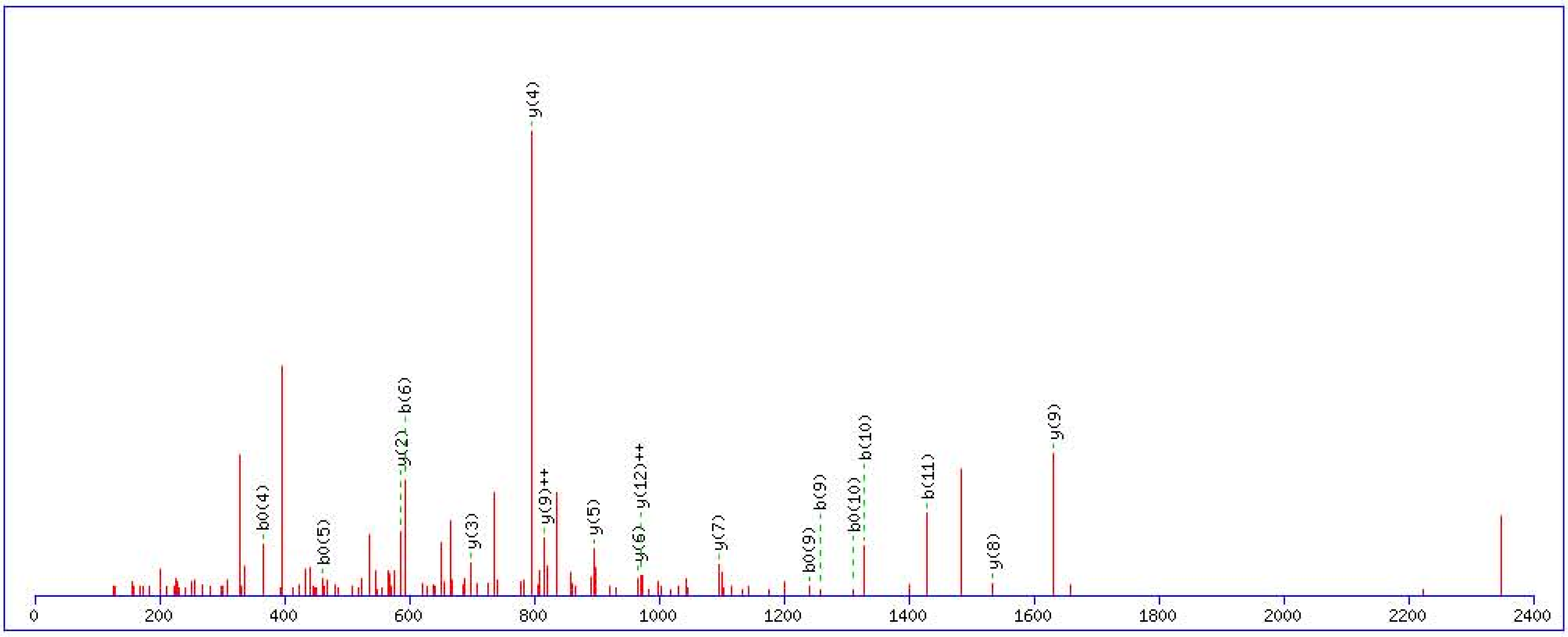
Mascot Search Results

Peptide View

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

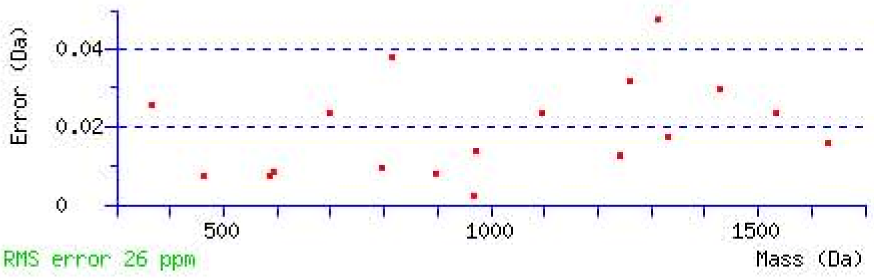
Match to Query 46456: 2223.245592 from(742.089140,3+) rtinseconds(2449) index(21411)
Title: Locus:1.1.1.3453.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

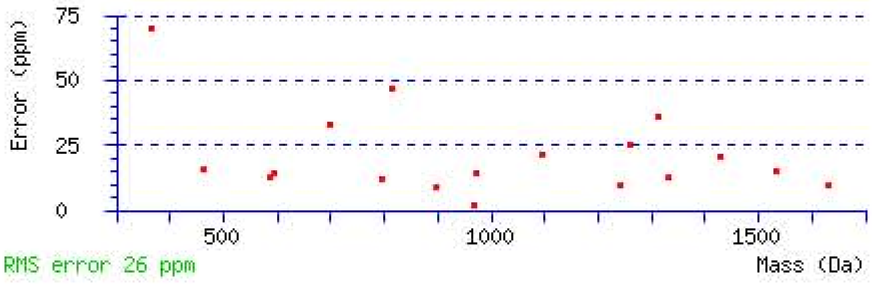


```
Monoisotopic mass of neutral peptide Mr(calc): 2223.215942
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.016
Matches : 18/142 fragment ions using 44 most intense peaks   (help)
```

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



RMS error 26 ppm



RMS error 26 ppm

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
28.1	2223.215942	0.029650	EVGPPLPQEAVPLQK

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

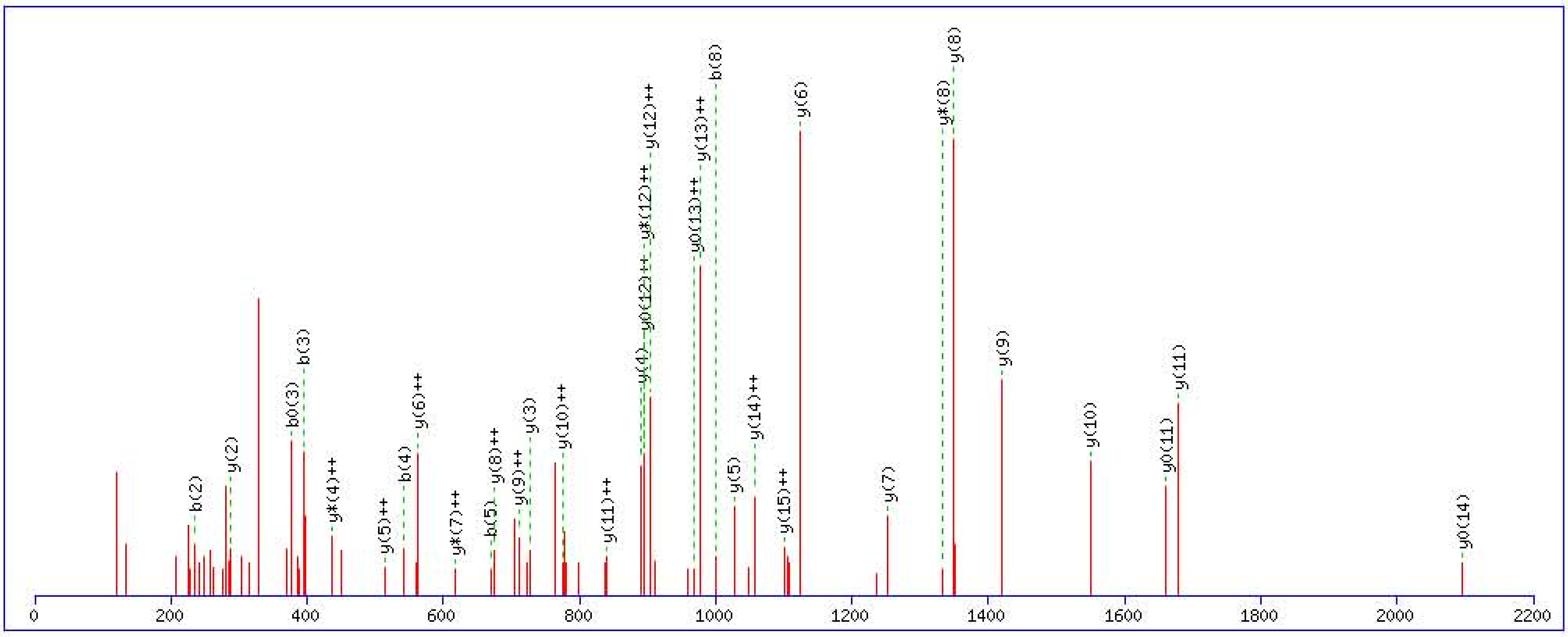
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

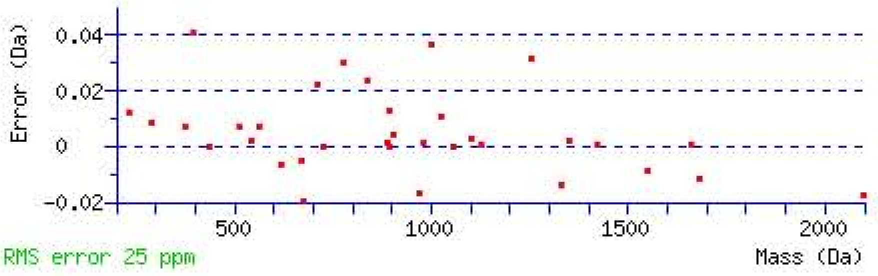
Match to Query 48504: 2347.085652 from(783.369160,3+) rtinseconds(1957) index(4693)
Title: Locus:1.1.1.3233.25 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

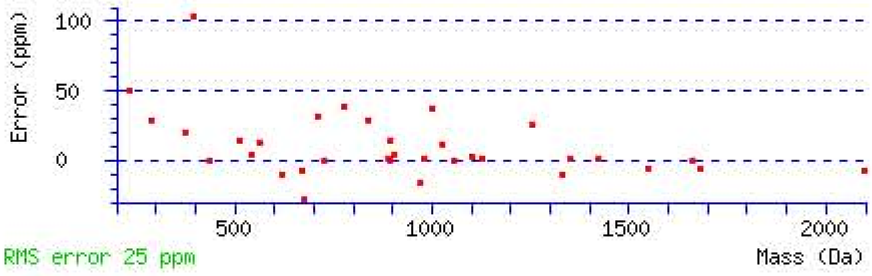
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2347.087784
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 67  Expect: 3.1e-006
Matches : 34/152 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	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
66.7	2347.087784	-0.002132	FSCFQEEAPQPHYQLR
29.8	2347.087784	-0.002132	FSCFQEEAPQPHYQLR

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

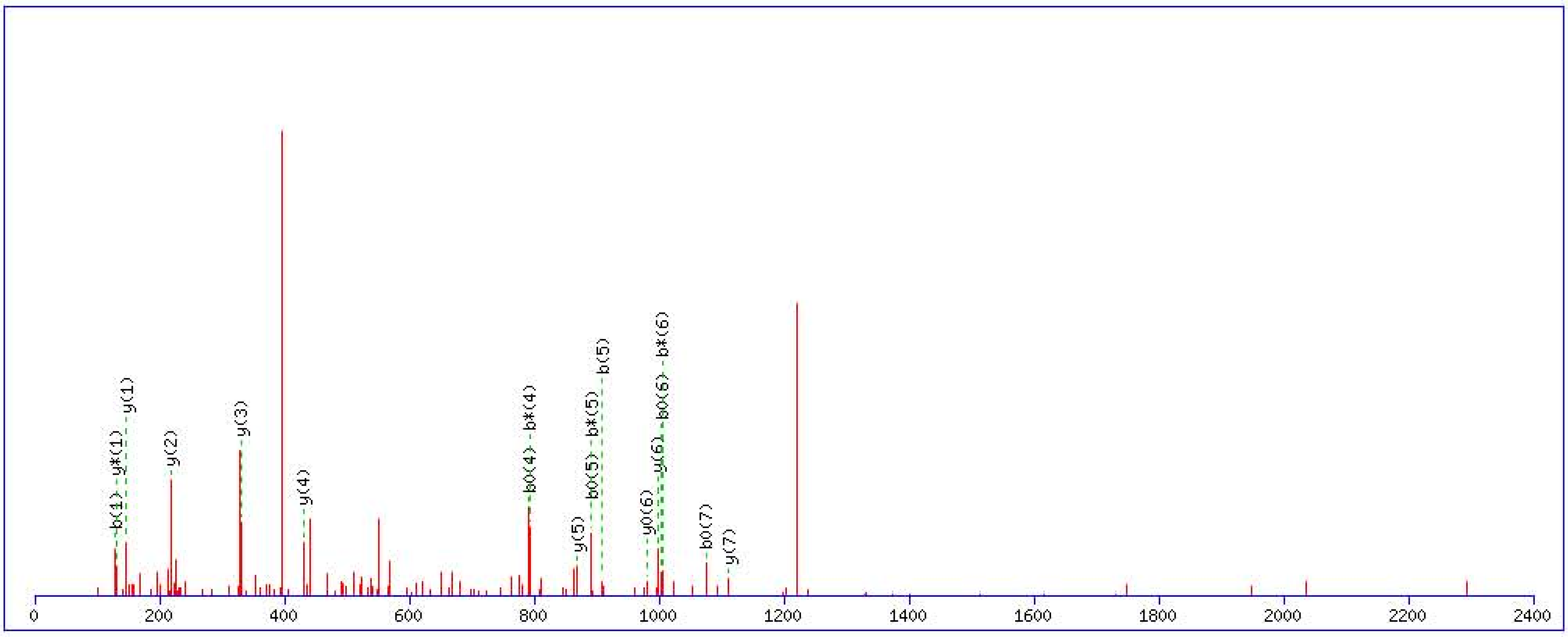
Mascot Search Results

Peptide View

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

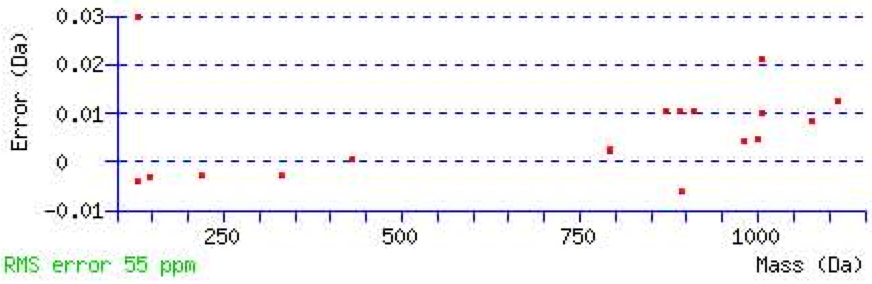
Match to Query 21295: 1238.712648 from(620.363600,2+) rtinseconds(1782) index(45970)
Title: Locus:1.1.1.2669.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

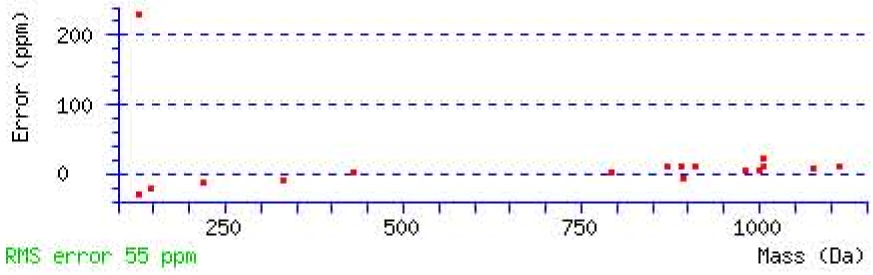
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1238.705658
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.00095
Matches : 18/70 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	**129.065854**	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
41.7	1238.705658	0.006990	QLEQVIAK
18.9	1238.705658	0.006990	QLEQVIAK
11.9	1238.698257	0.014391	IHADASSKVLAK
10.0	1238.716904	-0.004256	DRVQVAIK
8.0	1238.702301	0.010347	DVFKKGFSIAK
5.9	1238.698273	0.014375	GHVTQLKESLK
5.3	1238.728119	-0.015471	QEVRRLK
5.1	1238.705658	0.006990	QIAQEIVK
3.6	1238.709473	0.003175	NDLRPANKLAK
2.4	1238.716888	-0.004240	KRILCPLDPK

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

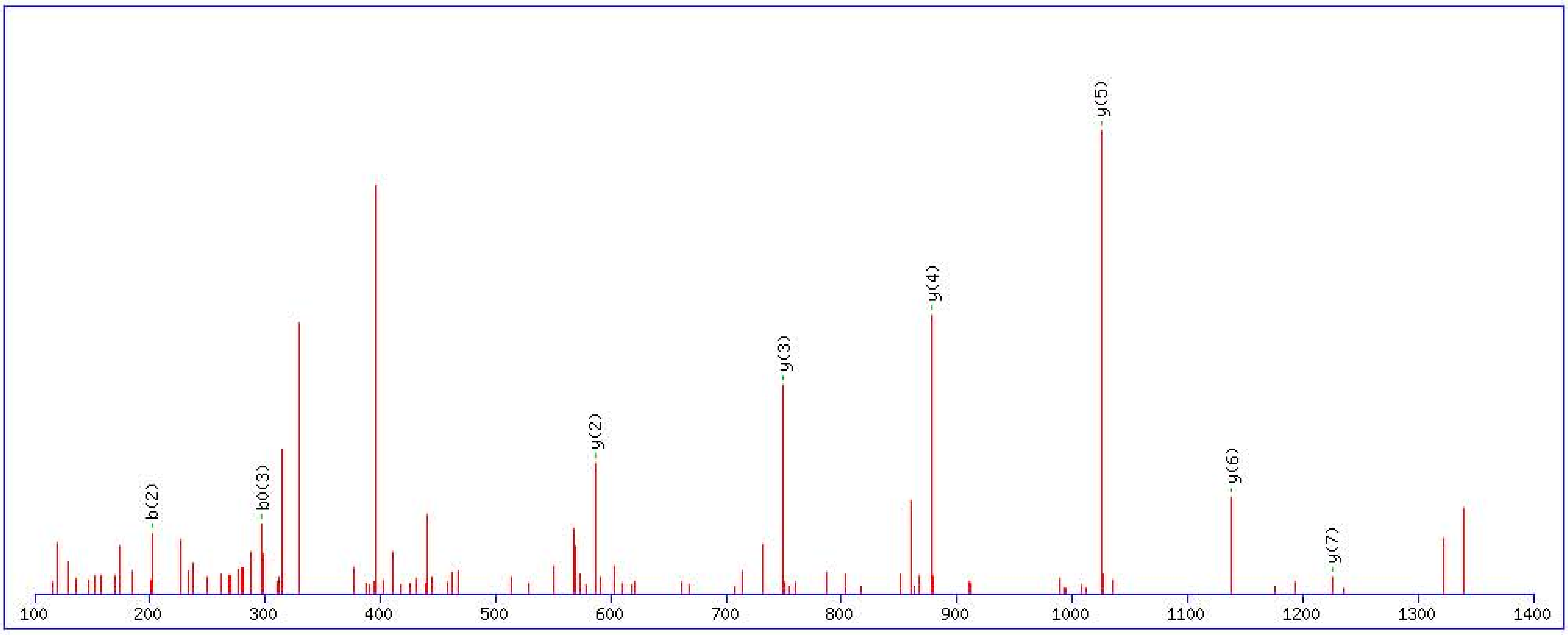
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

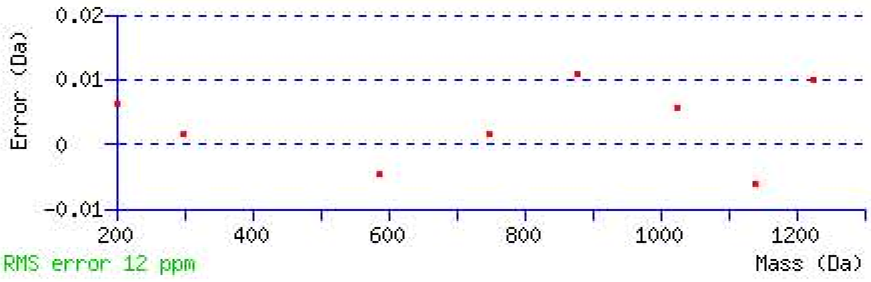
Match to Query 23761: 1338.667048 from(670.340800,2+) rtinseconds(2094) index(5418)
Title: Locus:1.1.1.3281.14 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

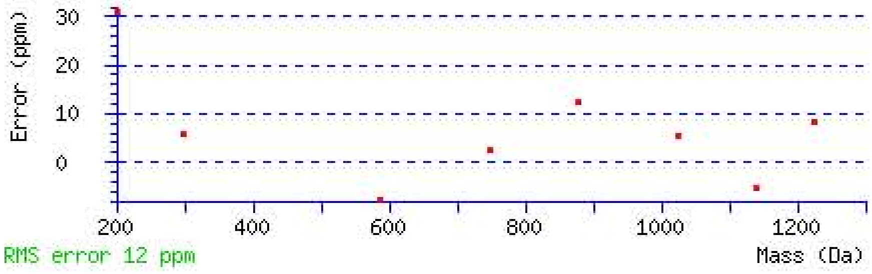
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1338.664185
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.00063
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	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
42.6	1338.664185	0.002863	NSLFEYQK
8.2	1338.660172	0.006876	NSMFTAGKGVAEK
6.9	1338.660172	0.006876	BTVYLQMBSLR
5.8	1338.666687	0.000361	SKVEEKYVDDK
4.5	1338.682632	-0.015584	NLSRMQSRFGK

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

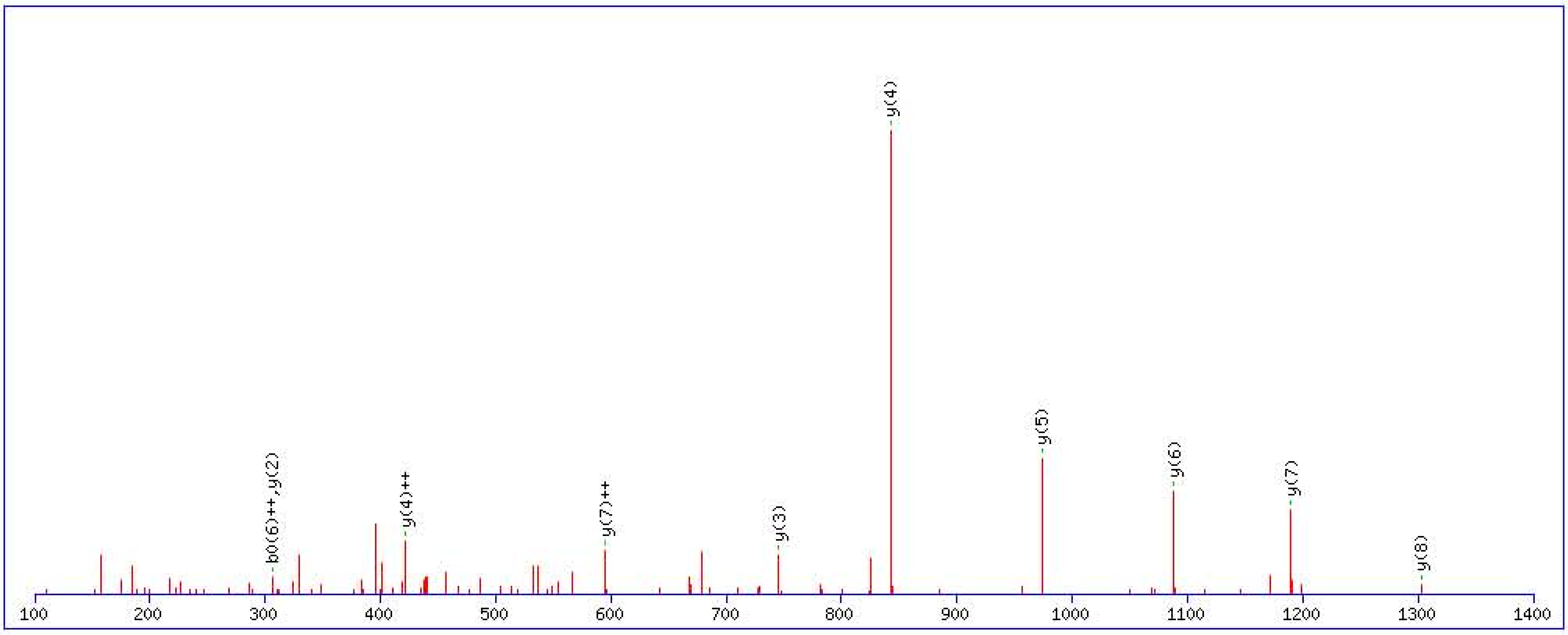
Mascot Search Results

Peptide View

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

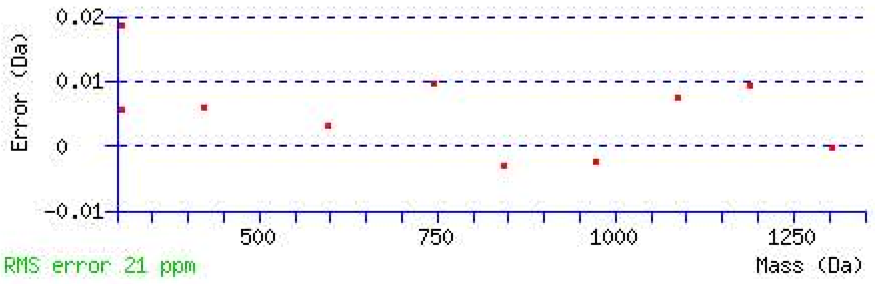
Match to Query 25447: 1372.667868 from(687.341210,2+) rtinseconds(2072) index(5313)
Title: Locus:1.1.1.3273.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

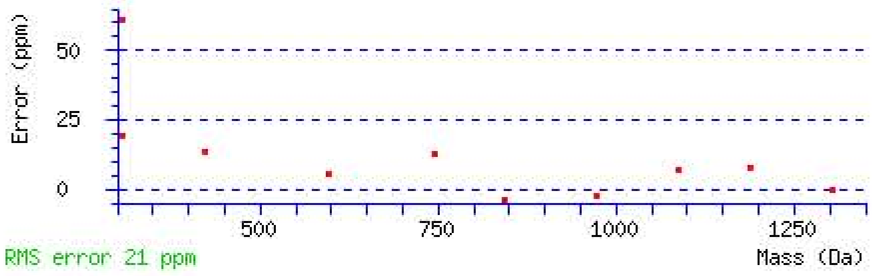
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1372.666519
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 63  Expect: 2.4e-006
Matches : 10/70 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							9
2	185.128454	93.067865					L	***1302.636698***	651.821987	1285.610149	643.308713	1284.626133	642.816705	8
3	286.176133	143.591704			268.165568	134.586422	T	***1189.552634***	595.279955	1172.526085	586.766681	1171.542069	586.274672	7
4	401.203076	201.105176			383.192511	192.099894	D	***1088.504955***	544.756116	1071.478406	536.242841	1070.494390	535.750833	6
5	532.243561	266.625419			514.232996	257.620136	M	***973.478012***	487.242644	956.451463	478.729370			5
6	629.296325	315.151801			611.285760	306.146518	P	***842.437527***	421.722402	825.410978	413.209127			4
7	1068.521651	534.764464	1051.495102	526.251189	1050.511086	525.759181	Q	***745.384763***	373.196020	728.358214	364.682745			3
8	1199.562136	600.284706	1182.535587	591.771432	1181.551571	591.279424	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
62.7	1372.666519	0.001349	ALTDMPQMR
2.6	1372.663620	0.004248	AGREHFAFGEPR
0.9	1372.665649	0.002219	SEMTASPLVGPER
0.7	1372.681610	-0.013742	RMGVMTDVHRR
0.7	1372.681610	-0.013742	RMGVMTDVHRR

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

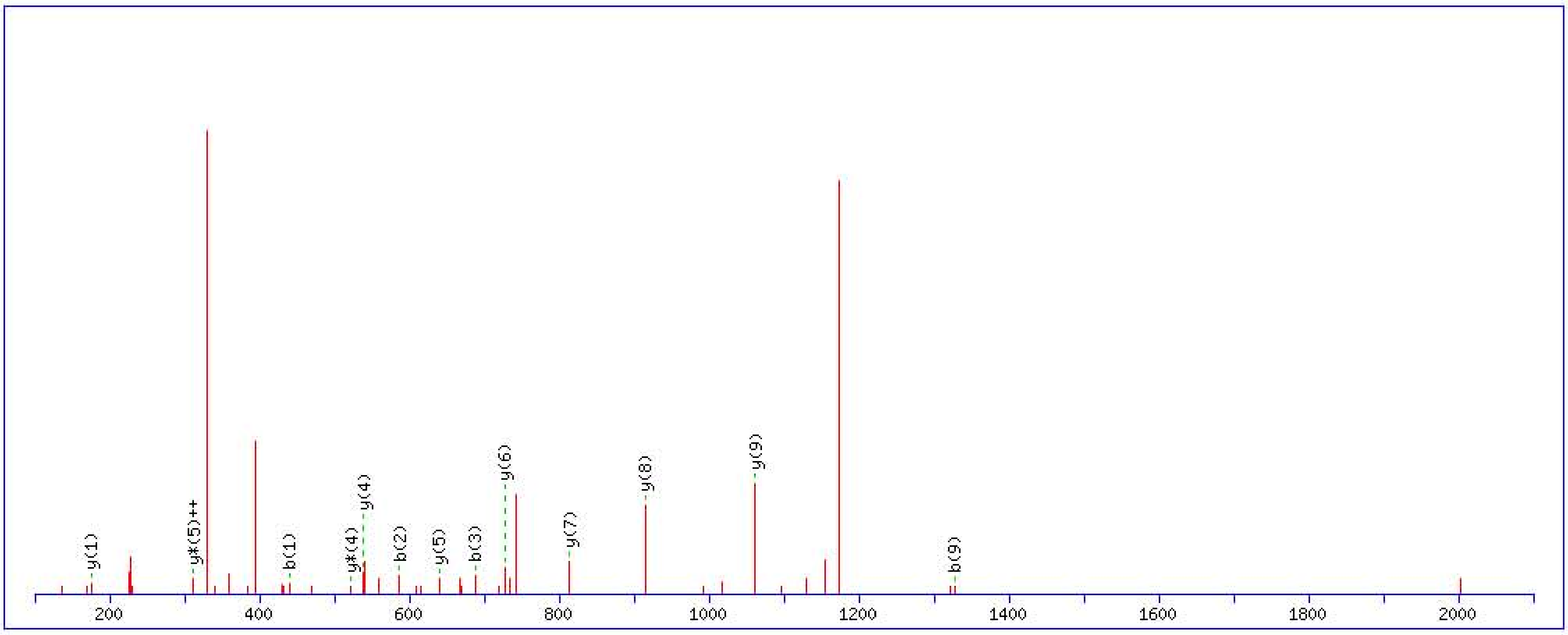
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

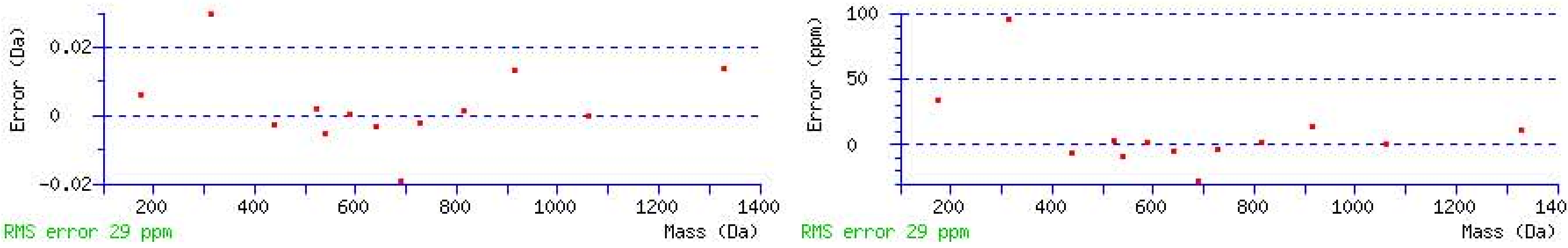
Match to Query 29894: 1500.701268 from(751.357910,2+) rtinseconds(1599) index(30888)
Title: Locus:1.1.1.3105.25 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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): 1500.703110
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.0058
Matches : 13/98 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	**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
26.7	1500.703110	-0.001842	QFTSSTSYNR
2.9	1500.703110	-0.001842	DAEGWETVQR

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

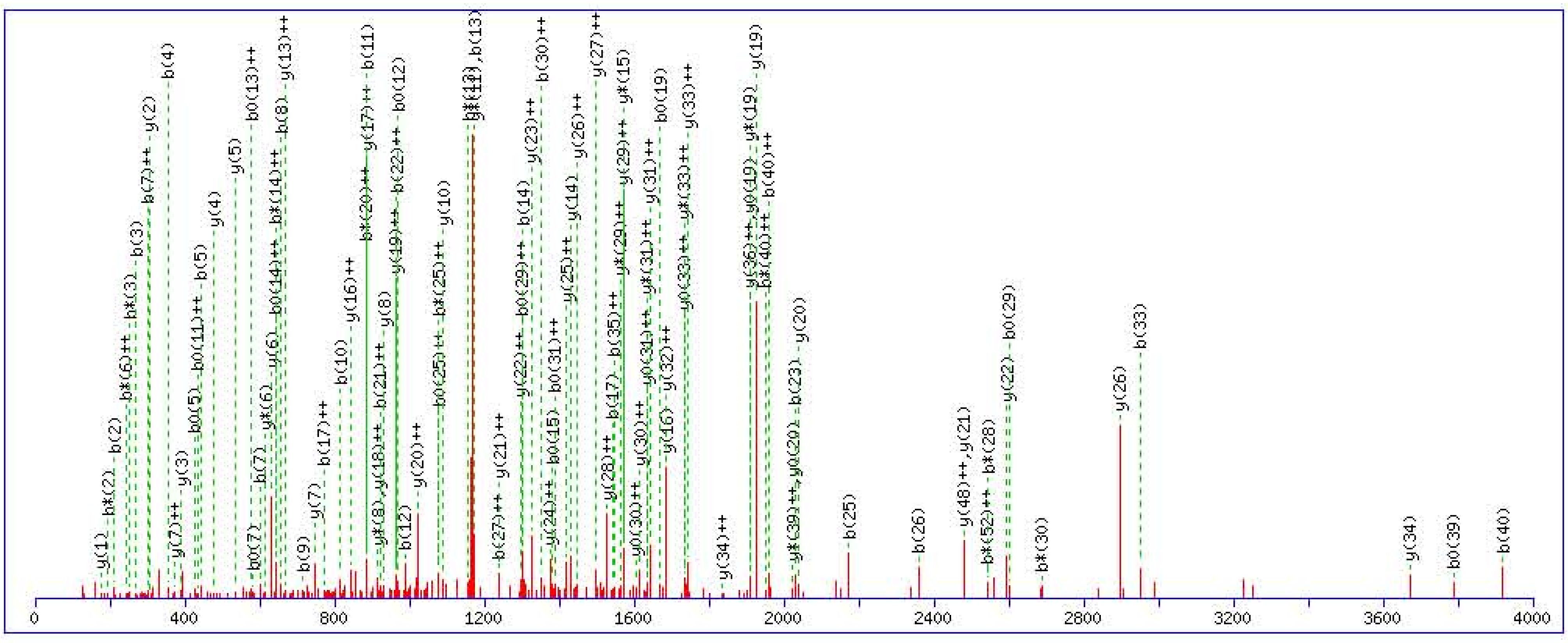
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

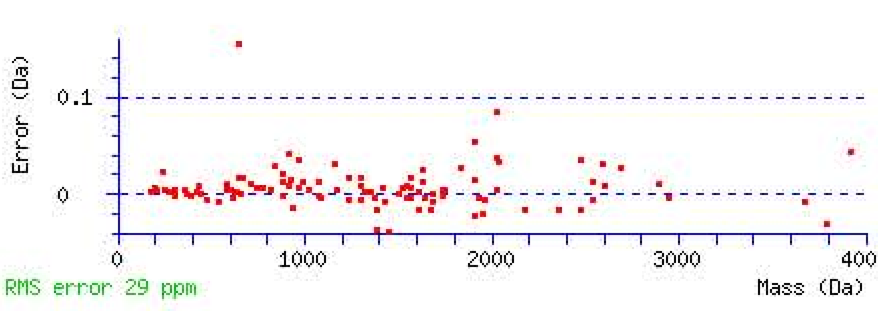
Match to Query 70229: 5844.622820 from(1169.931840,5+) rtinseconds(1774) index(3659)
Title: Locus:1.1.1.3169.17 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

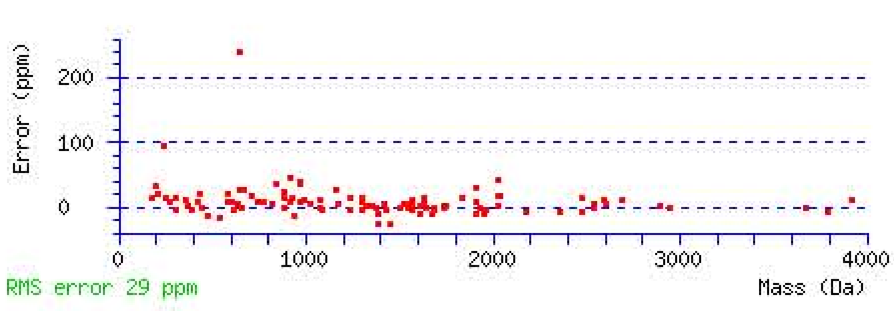
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 117 **Expect:** 7.9e-012
Matches : 104/688 fragment ions using 198 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
117.4	5844.608032	0.014788	NPGSSGTGGTATWKPGSSGPGSTGSWNSGSSGTGSTGNQNPGSPRPGSTGTWNPGSSER

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

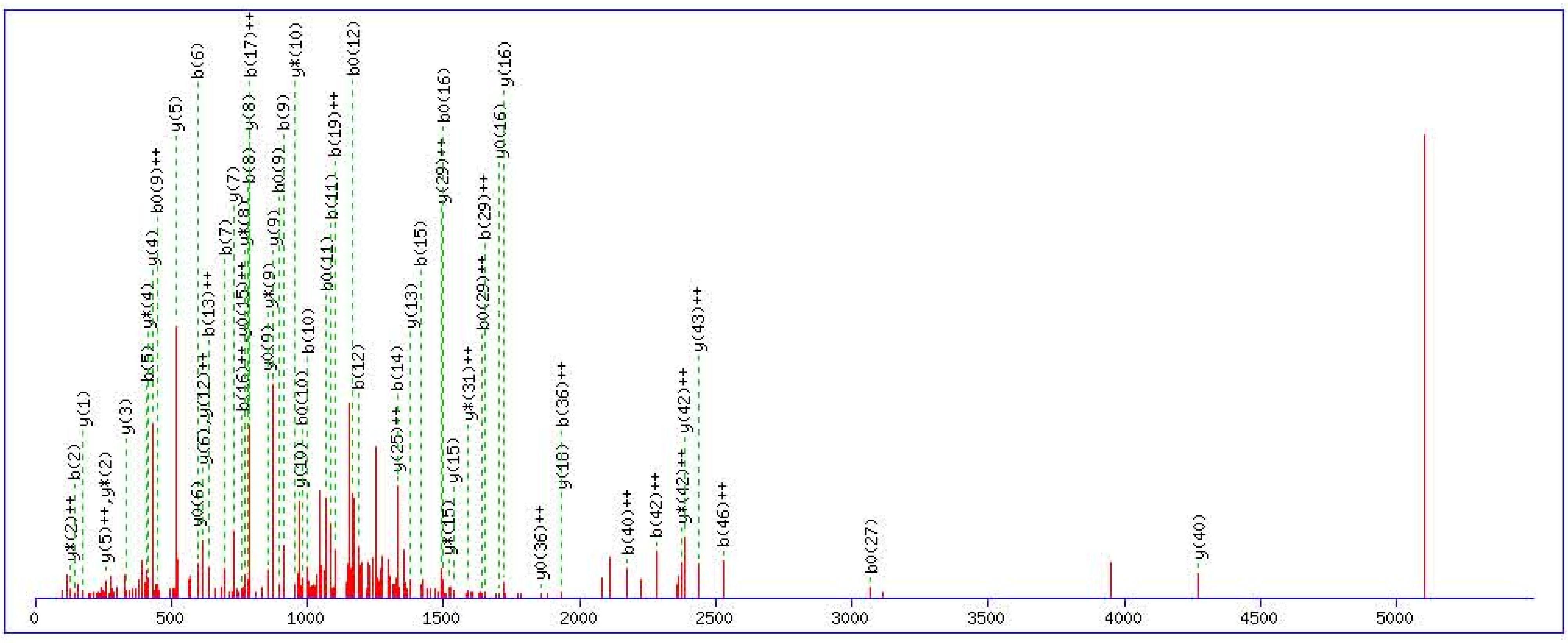
Mascot Search Results

Peptide View

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

Match to Query 70434: 6284.805384 from(1048.474840,6+) rtinseconds(2083) index(5363)
Title: Locus:1.1.1.3277.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 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 ●



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Monoisotopic mass of neutral peptide Mr(calc): 6284.792847
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18    : Biotin:Thermo-21345 (Q)
Ions Score: 44  Expect: 0.00017
Matches : 62/646 fragment ions using 154 most intense peaks   (help)
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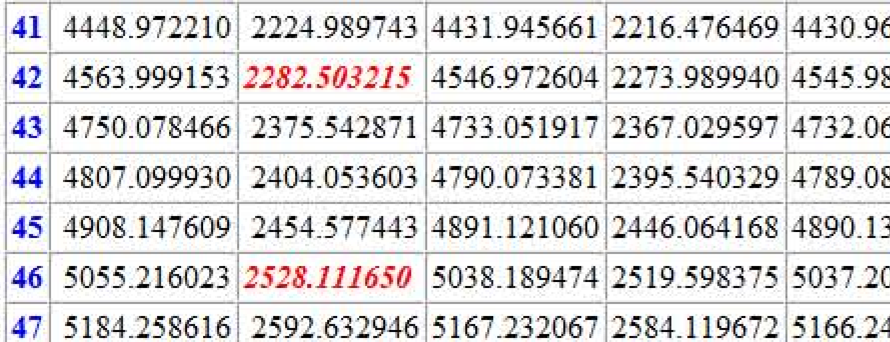
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							58
2	***145.060768***	73.034022			127.050203	64.028740	S	6228.778603	3114.892940	6211.752054	3106.379665	6210.768038	3105.887657	57
3	216.097882	108.552579			198.087317	99.547296	A	6141.746575	3071.376926	6124.720026	3062.863651	6123.736010	3062.371643	56
4	273.119346	137.063311			255.108781	128.058029	G	6070.709461	3035.858369	6053.682912	3027.345094	6052.698896	3026.853086	55
5	***410.178258***	205.592767			392.167693	196.587484	H	6013.687997	3007.347637	5996.661448	2998.834362	5995.677432	2998.342354	54
6	***596.257571***	298.632424			578.247006	289.627141	W	5876.629085	2938.818181	5859.602536	2930.304906	5858.618520	2929.812898	53
7	***697.305250***	349.156263			679.294685	340.150981	T	5690.549772	2845.778524	5673.523223	2837.265250	5672.539207	2836.773242	52
8	***784.337278***	392.672277			766.326713	383.666995	S	5589.502093	2795.254685	5572.475544	2786.741410	5571.491528	2786.249402	51
9	***913.379871***	457.193574			895.369306	448.188291	E	5502.470065	2751.738671	5485.443516	2743.225396	5484.459500	2742.733388	50
10	***1000.411899***	500.709588			982.401334	491.704305	S	5373.427472	2687.217374	5356.400923	2678.704100	5355.416907	2678.212092	49
11	***1087.443927***	544.225602			1069.433362	535.220319	S	5286.395444	2643.701360	5269.368895	2635.188086	5268.384879	2634.696078	48
12	***1186.512341***	593.759809			1168.501776	584.754526	V	5199.363416	2600.185346	5182.336867	2591.672072	5181.352851	2591.180064	47
13	1273.544369	***637.275823***			1255.533804	628.270540	S	5100.295002	2550.651139	5083.268453	2542.137865	5082.284437	2541.645857	46
14	***1330.565833***	665.786555			1312.555268	656.781272	G	5013.262974	2507.135125	4996.236425	2498.621851	4995.252409	2498.129843	45
15	***1417.597861***	709.302569			1399.587296	700.297286	S	4956.241510	2478.624393	4939.214961	2470.111119	4938.230945	2469.619111	44
16	1518.645540	***759.826408***			1500.634975	750.821126	T	4869.209482	2435.108379	4852.182933	2426.595105	4851.198917	2426.103097	43
17	1575.667004	***788.337140***			1557.656439	779.331858	G	4768.161803	2384.584540	4751.135254	2376.071265	4750.151238	2375.579257	42
18	2014.892330	1007.949803	1997.865781	999.436529	1996.881765	998.944521	Q	4711.140339	2356.073808	4694.113790	2347.560533	4693.129774	2347.068525	41
19	2200.971643	***1100.989460***	2183.945094	1092.476185	2182.961078	1091.984177	W	***4271.915013***	2136.461145	4254.888464	2127.947870	4253.904448	2127.455862	40
20	2338.030555	1169.518916	2321.004006	1161.005641	2320.019990	1160.513633	H	4085.835700	2043.421488	4068.809151	2034.908214	4067.825135	2034.416206	39
21	2425.062583	1213.034930	2408.036034	1204.521655	2407.052018	1204.029647	S	3948.776788	1974.892032	3931.750239	1966.378758	3930.766223	1965.886750	38
22	2554.105176	1277.556226	2537.078627	1269.042952	2536.094611	1268.550944	E	3861.744760	1931.376018	3844.718211	1922.862744	3843.734195	1922.370736	37
23	2641.137204	1321.072240	2624.110655	1312.558966	2623.126639	1312.066958	S	3732.702167	1866.854722	3715.675618	1858.341447	3714.691602	1857.849439	36
24	2698.158668	1349.582972	2681.132119	1341.069698	2680.148103	1340.577690	G	3645.670139	1823.338708	3628.643590	1814.825433	3627.659574	1814.333425	35
25	2785.190696	1393.098986	2768.164147	1384.585712	2767.180131	1384.093704	S	3588.648675	1794.827976	3571.622126	1786.314701	3570.638110	1785.822693	34
26	2932.259110	1466.633193	2915.232561	1458.119919	2914.248545	1457.627911	F	3501.616647	1751.311962	3484.590098	1742.798687	3483.606082	1742.306679	33
27	3088.360221	1544.683749	3071.333672	1536.170474	3070.349656	1535.678466	R	3354.548233	1677.777755	3337.521684	1669.264480	3336.537668	1668.772472	32
28	3185.412985	1593.210131	3168.386436	1584.696856	3167.402420	1584.204848	P	3198.447122	1599.727199	3181.420573	1591.213925	3180.436557	1590.721917	31
29	3300.439928	***1650.723602***	3283.413379	1642.210327	3282.429363	1641.718320	D	3101.394358	1551.200817	3084.367809	1542.687543	3083.383793	1542.195535	30
30	3387.471956	1694.239616	3370.445407	1685.726342	3369.461391	1685.234334	S	2986.367415	1493.687346	2969.340866	1485.174071	2968.356850	1484.682063	29
31	3484.524720	1742.765998	3467.498171	1734.252724	3466.514155	1733.760716	P	2899.335387	1450.171332	2882.308838	1441.658057	2881.324822	1441.166049	28
32	3541.546184	1771.276730	3524.519635	1762.763456	3523.535619	1762.271448	G	2802.282623	1401.644950	2785.256074	1393.131675	2784.272058	1392.639667	27
33	3628.578212	1814.792744	3611.551663	1806.279470	3610.567647	1805.787462	S	2745.261159	1373.134218	2728.234610	1364.620943	2727.250594	1364.128935	26
34	3685.599676	1843.303476	3668.573127	1834.790202	3667.589111	1834.298194	G	2658.229131	1329.618204	2641.202582	1321.104929	2640.218566	1320.612921	25
35	3799.642603	1900.324940	3782.616054	1891.811665	3781.632038	1891.319657	N	2601.207667	1301.107472	2584.181118	1292.594197	2583.197102	1292.102189	24
36	3870.679717	***1935.843497***	3853.653168	1927.330222	3852.669152	1926.838214	A	2487.164740	1244.086008	2470.138191	1235.572734	2469.154175	1235.080726	23
37	4026.780828	2013.894052	4009.754279	2005.380778	4008.770263	2004.888770	R	2416.127626	1208.567451	2399.101077	1200.054177	2398.117061	1199.562169	22
38	4123.833592	2062.420434	4106.807043	2053.907160	4105.823027	2053.415152	P	2260.026515	1130.516896	2242.999966	1122.003621	2242.015950	1121.511613	21
39	4237.876519	2119.441898	4220.849970	2110.928623	4219.865954	2110.436615	N	2162.973751	1081.990514	2145.947202	1073.477239	2144.963186	1072.985231	20
40	4351.919446	***2176.463361***	4334.892897	2167.950087	4333.908881	2167.458079	N	2048.930824	1024.969050	2031.904275	1016.455776	2030.920259	1015.963768	19
41	4448.972210	2224.989743	4431.945661	2216.476469	4430.961645	2215.984461	P	***1934.887897***	967.947587	1917.861348	959.434312	1916.877332	958.942304	18
42	4563.999153	***2282.503215***	4546.972604	2273.989940	4545.988588	2273.497932	D	1837.835133	919.421205	1820.808584	910.907930	1819.824568	910.415922	17
43	4750.078466	2375.542871	4733.051917	2367.029597	4732.067901	2366.537589	W	***1722.808190***	861.907733	1705.781641	853.394459	1704.797625	852.902451	16
44	4807.099930	2404.053603	4790.073381	2395.540329	4789.089365	2395.048321	G	***1536.728877***	768.868077	1519.702328	760.354802	1518.718312	759.862794	15
45	4908.147609	2454.577443	4891.121060	2446.064168	4890.137044	2445.572160	T	1479.707413	740.357345	1462.680864	731.844070	1461.696848	731.352062	14
46	5055.216023	***2528.111650***	5038.189474	2519.598375	5037.205458	2519.106367	F	***1378.659734***	689.833505	1361.633185	681.320231	1360.649169	680.828223	13
47	5184.258616	2592.632946	5167.232067	2584.119672	5166.248051	2583.627664	E	1231.591320	616.299298	1214.564771	607.786024	1213.580755	607.294016	12
48	5313.301209	2657.154243	5296.274660	2648.640968	5295.290644	2648.148960	E	1102.548727	551.778002	1085.522178	543.264727	1084.538162	542.772719	11
49	5412.369623	2706.688450	5395.343074	2698.175175	5394.359058	2697.683167	V	***973.506134***	487.256705	956.479585	478.743431	955.495569	478.251423	10
50	5499.401651	2750.204464	5482.375102	2741.691189	5481.391086	2741.199181	S	***874.437720***	437.722498	857.411171	429.209224	856.427155	428.717216	9
51	5556.423115	2778.715196	5539.396566	2770.201921	5538.412550	2769.709913	G	***787.405692***	394.206484	770.379143	385.693210	769.395127	385.201202	8
52	5670.466042	2835.736659	5653.439493	2827.223385	5652.455477	2826.731377	N	***730.384228***	365.695752	713.357679	357.182478	712.373663	356.690470	7
53	5769.534456	2885.270866	5752.507907	2876.757592	5751.523891	2876.265584	V	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	6
54	5856.566484	2928.786880	5839.539935	2920.273606	5838.555919	2919.781598	S	***517.272887***	259.140082	500.246338	250.626807	499.262322	250.134799	5
55	5953.619248	2977.313262	5936.592699	2968.799988	5935.608683	2968.307980	P	***430.240859***	215.624068	413.214310	207.110793	412.230294	206.618785	4
56	6010.640712	3005.823994	5993.614163	2997.310720	5992.630147	2996.818712	G	***333.188095***	167.097686	316.161546	158.584411	315.177530	158.092403	3
57	6111.688391	3056.347834	6094.661842	3047.834559	6093.677826	3047.342551	T	276.166631	138.586954	259.140082	130.073679	258.156066	129.581671	2
58							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.0	6284.792847	0.012537	GSAGHWTSESSVSGSTGQWHSESGSFRPDSPGSGNARPNNPDWGTFEEVSGNVSPGTR

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

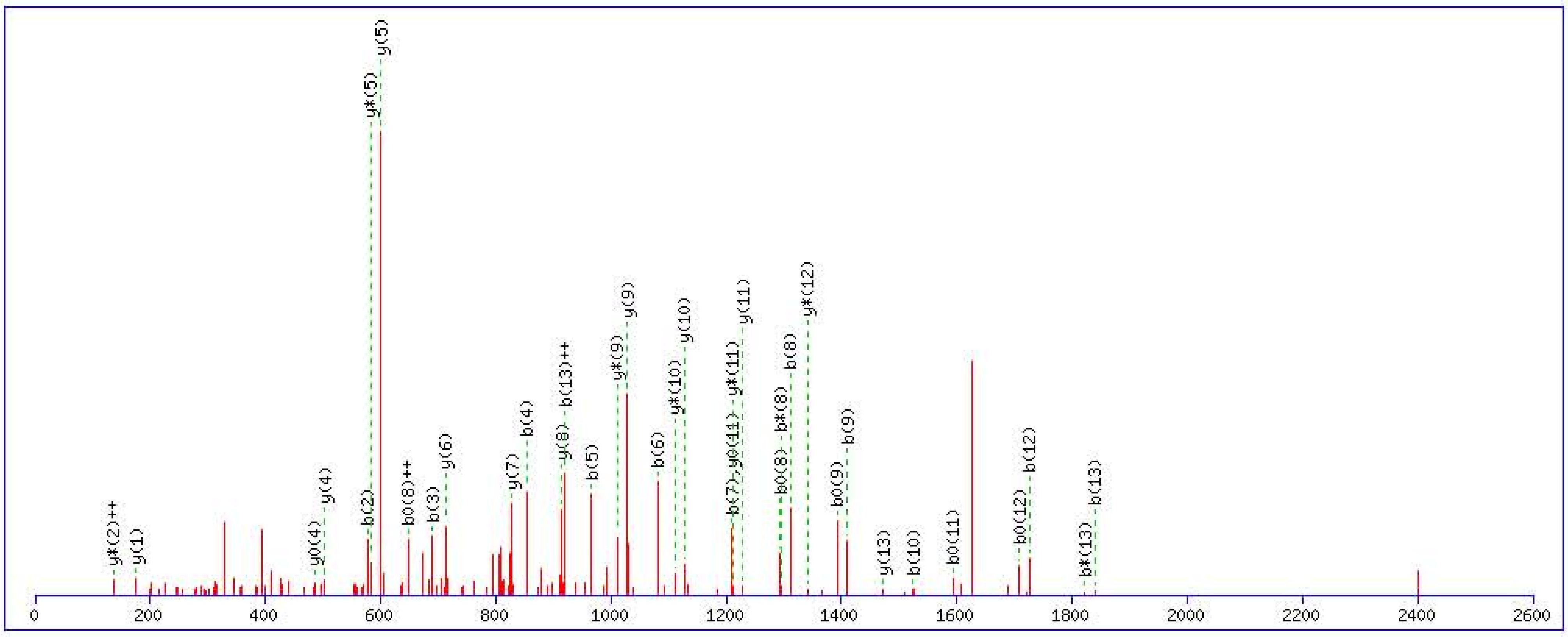
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

Match to Query 49723: 2437.266372 from(813.429400,3+) rtinseconds(2157) index(48383)
Title: Locus:1.1.1.2799.21 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 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 ●



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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: 82  Expect: 3.5e-008
Matches : 37/186 fragment ions using 51 most intense peaks   (help)
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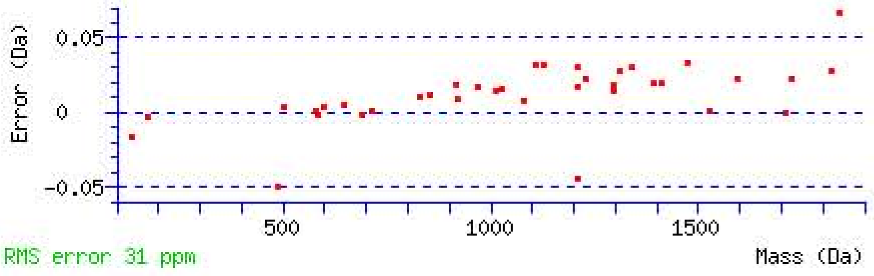
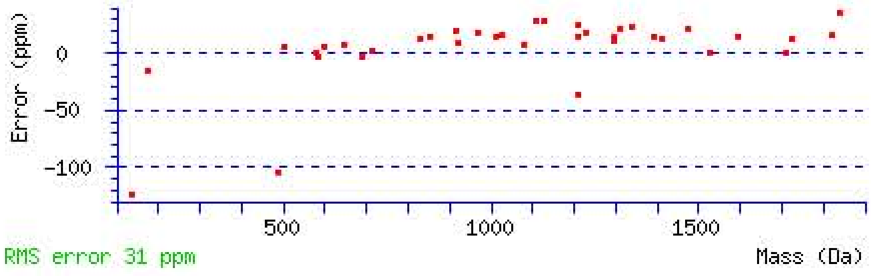
#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	138.066188	69.536732					H							18
2	***577.291514***	289.149395	560.264965	280.636121			Q	2301.190744	1151.099010	2284.164195	1142.585735	2283.180179	1142.093727	17
3	***690.375578***	345.691427	673.349029	337.178153			L	1861.965418	931.486347	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
82.4	2437.242355	0.024017	HQLYIDETVNSNIPTNLR
2.7	2437.253586	0.012786	DEASGFCYLNDAVLGILRLRR
1.8	2437.289520	-0.023148	VPEIMGVICAQLSIISQPR
0.2	2437.279617	-0.013245	GMLHQDHITFAMLLARIK

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

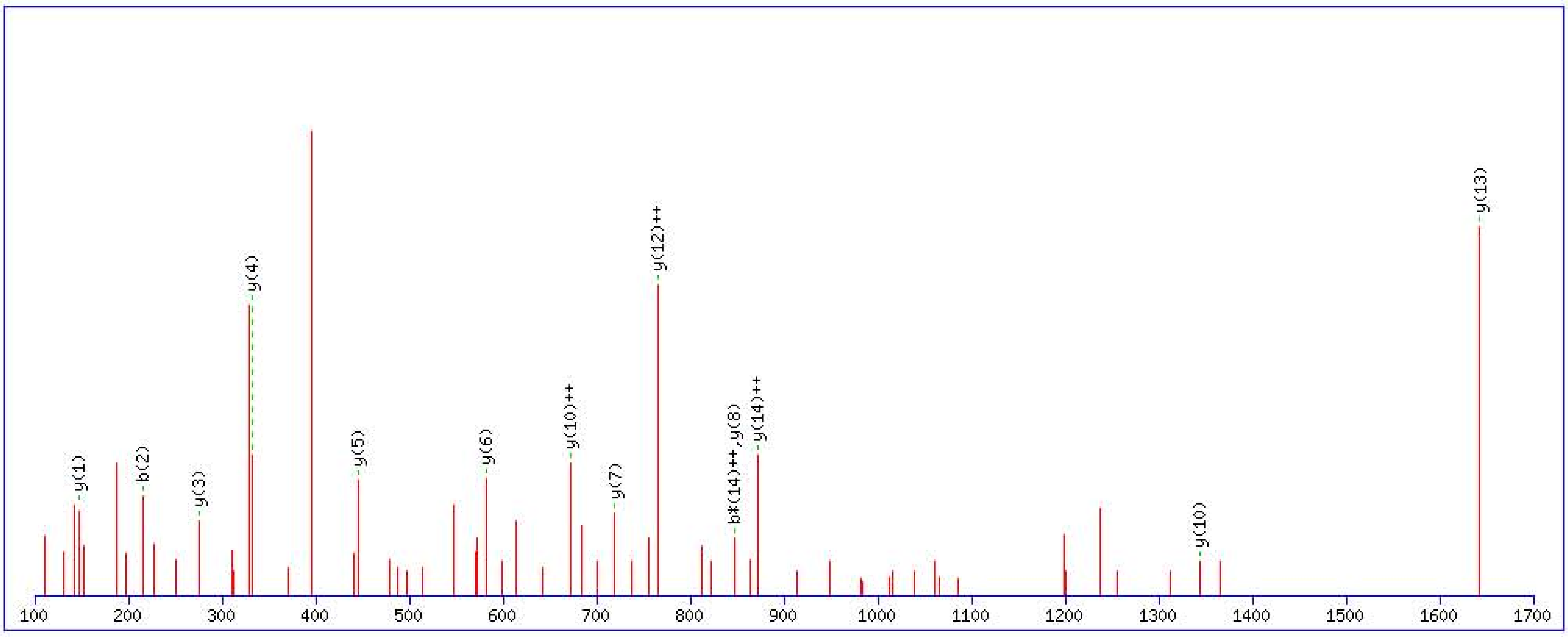
Mascot Search Results

Peptide View

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

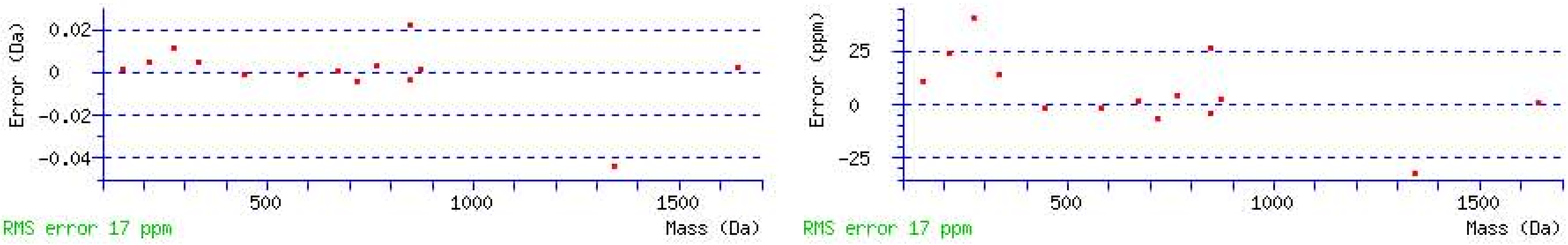
Match to Query 39637: 1855.969092 from(619.663640,3+) rtinseconds(1547) index(2357)
Title: Locus:1.1.1.3090.16 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 1855.972687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 35 **Expect:** 0.0011
Matches : 14/134 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							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
35.0	1855.972687	-0.003595	LTIGEGQQHHLGGAK
28.4	1855.972687	-0.003595	LTIGEGQQHHLGGAK
3.3	1855.979202	-0.010110	ITIVENVGSVEGLAYHR

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

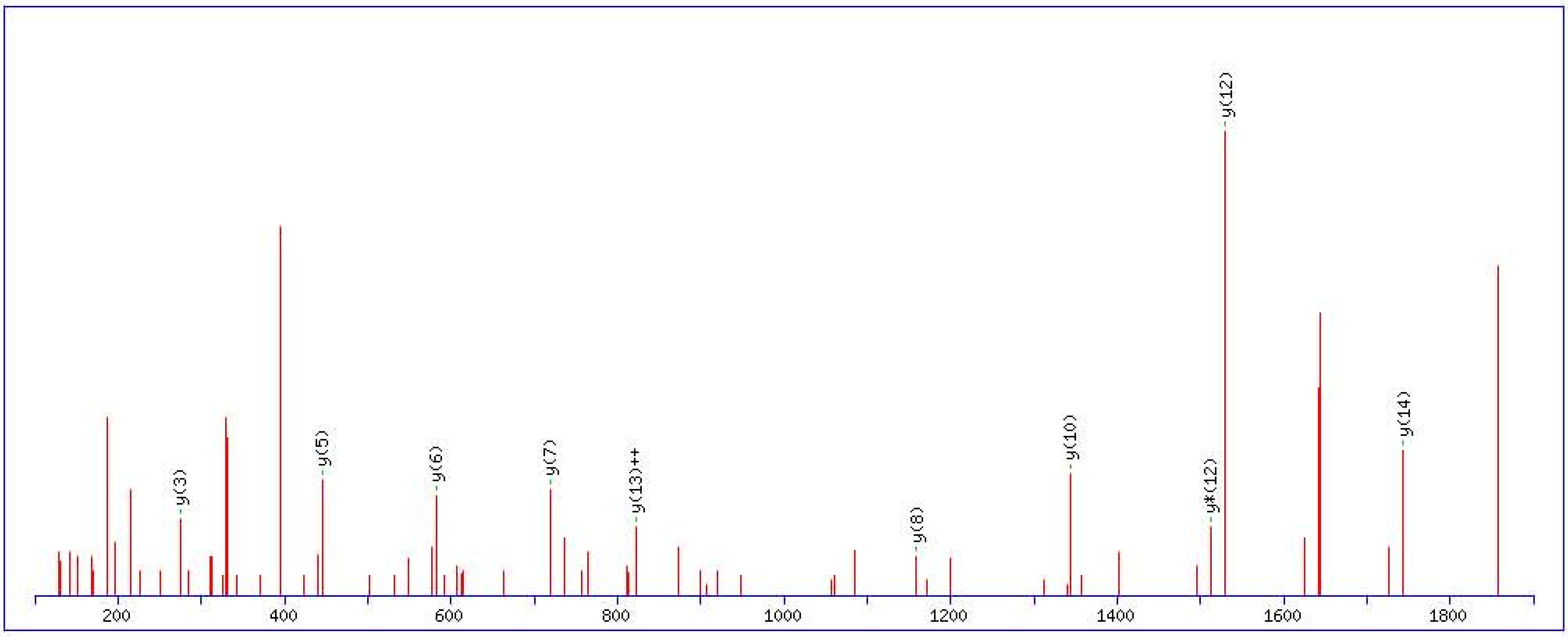
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

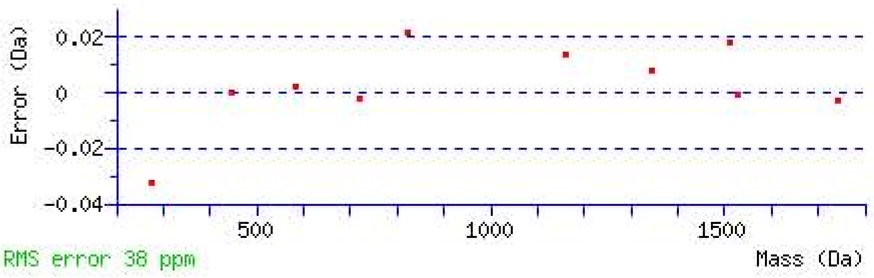
Match to Query 39649: 1855.975992 from(619.665940,3+) rtinseconds(1503) index(44212)
Title: Locus:1.1.1.2572.8 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

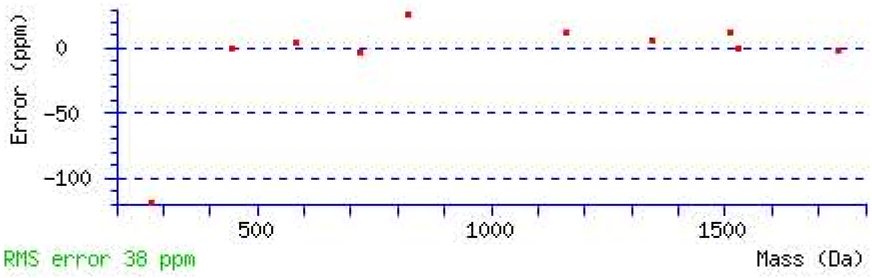
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1855.972687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 9.7e-005
Matches : 10/134 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							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
48.1	1855.972687	0.003305	LTIGEGQQHHLGGAK
37.9	1855.972687	0.003305	LTIGEGQQHHLGGAK
5.3	1855.979202	-0.003210	ITIVENVGSVEGLAYHR

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

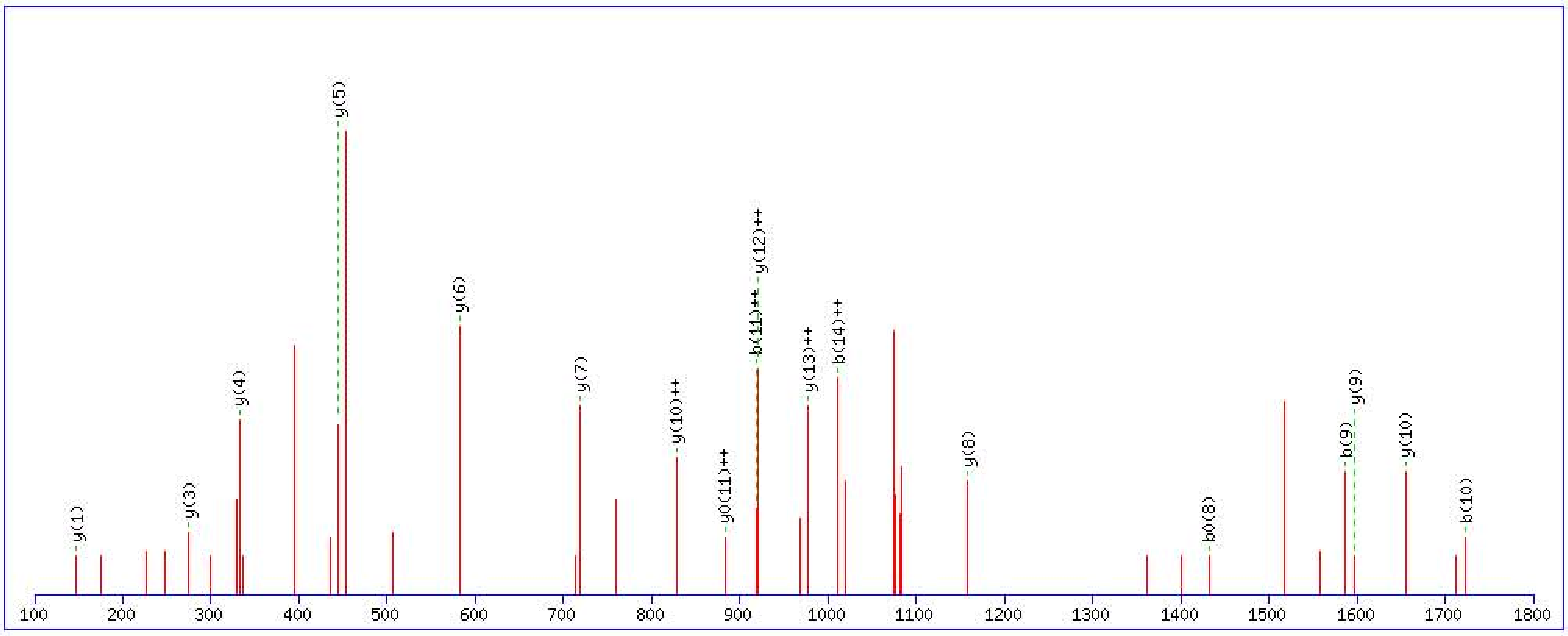
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

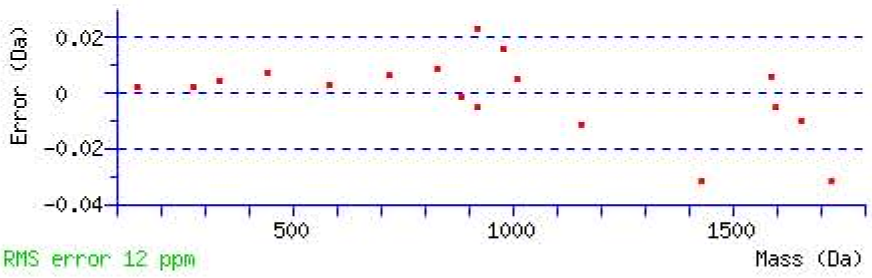
Match to Query 45461: 2167.147008 from(1084.580780,2+) rtinseconds(1805) index(3840)
Title: Locus:1.1.1.3180.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

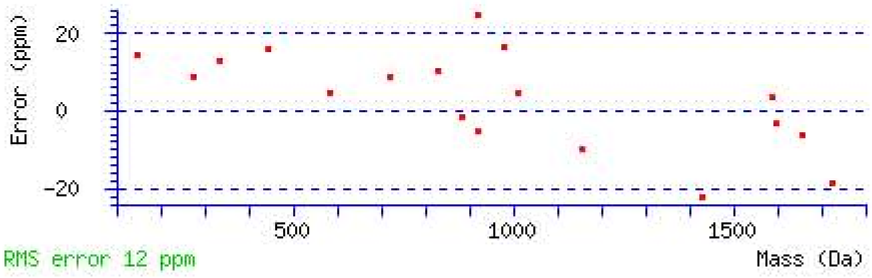
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2167.139435
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 4.7e-005
Matches : 18/134 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							15
2	215.139019	108.073147			197.128454	99.067865	T	2055.062650	1028.034963	2038.036101	1019.521688	2037.052085	1019.029680	14
3	328.223083	164.615179			310.212518	155.609897	I	1954.014971	977.511123	1936.988422	968.997849	1936.004406	968.505841	13
4	385.244547	193.125911			367.233982	184.120629	G	1840.930907	920.969091	1823.904358	912.455817	1822.920342	911.963809	12
5	514.287140	257.647208			496.276575	248.641926	E	1783.909443	892.458359	1766.882894	883.945085	1765.898878	883.453077	11
6	571.308604	286.157940			553.298039	277.152658	G	***1654.866850***	827.937063	1637.840301	819.423788			10
7	1010.533930	505.770603	993.507381	497.257329	992.523365	496.765321	Q	***1597.845386***	799.426331	1580.818837	790.913056			9
8	1449.759256	725.383266	1432.732707	716.869992	1431.748691	716.377984	Q	***1158.620060***	579.813668	1141.593511	571.300393			8
9	**1586.818168**	793.912722	1569.791619	785.399448	1568.807603	784.907440	H	***719.394734***	360.201005	702.368185	351.687730			7
10	**1723.877080**	862.442178	1706.850531	853.928904	1705.866515	853.436895	H	***582.335822***	291.671549	565.309273	283.158274			6
11	1836.961144	**918.984210**	1819.934595	910.470936	1818.950579	909.978927	L	***445.276910***	223.142093	428.250361	214.628818			5
12	1893.982608	947.494942	1876.956059	938.981667	1875.972043	938.489659	G	***332.192846***	166.600061	315.166297	158.086786			4
13	1951.004072	976.005674	1933.977523	967.492399	1932.993507	967.000391	G	***275.171382***	138.089329	258.144833	129.576054			3
14	2022.041186	**1011.524231**	2005.014637	1003.010956	2004.030621	1002.518948	A	218.149918	109.578597	201.123369	101.065322			2
15							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.4	2167.139435	0.007573	LTIGEGQQHHLGGAK
3.1	2167.177612	-0.030604	EEPPEPVPSPIIPILPSTAGK
1.3	2167.127304	0.019704	LQNTSLYDSKIWTTKNQK

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

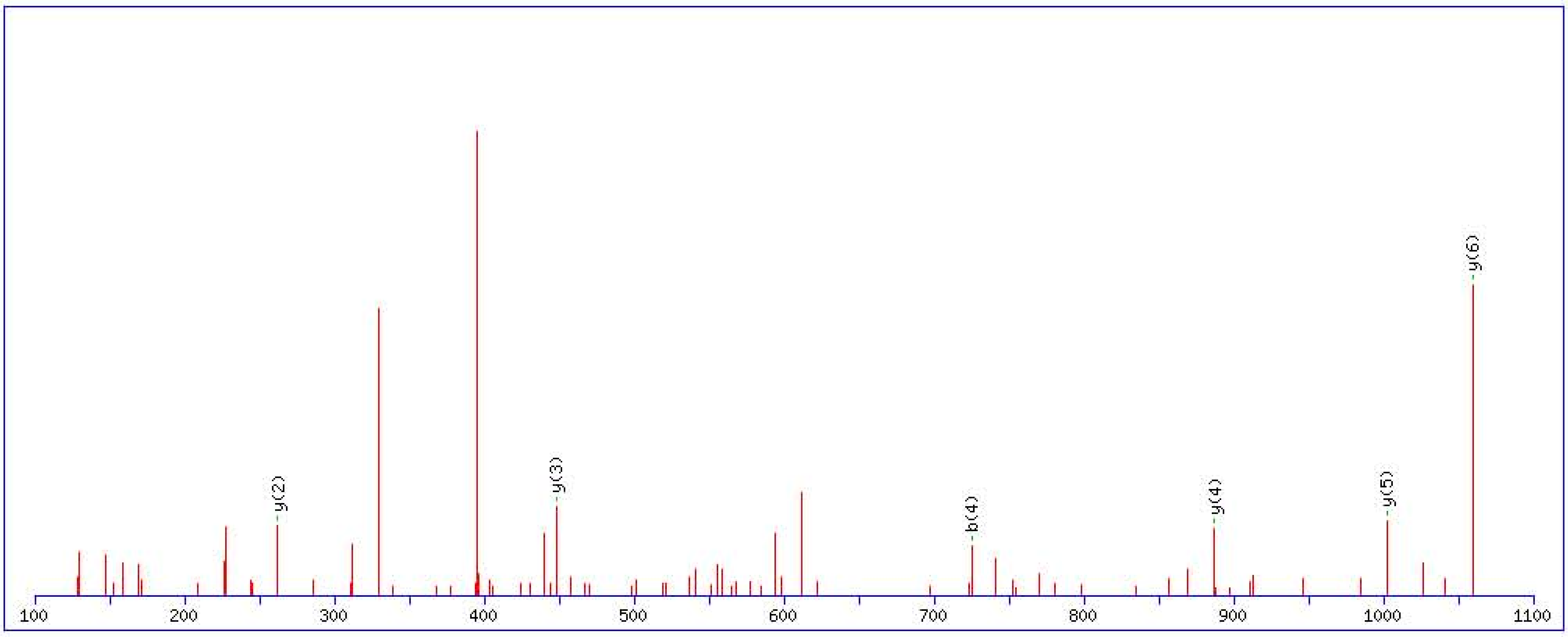
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

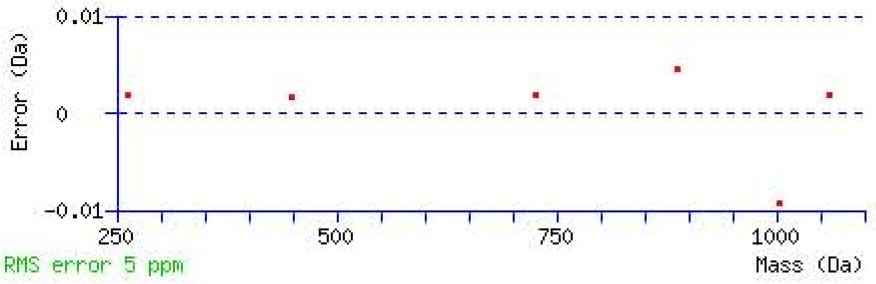
Match to Query 19490: 1171.570968 from(586.792760,2+) rtinseconds(1824) index(32029)
Title: Locus:1.1.1.3184.8 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

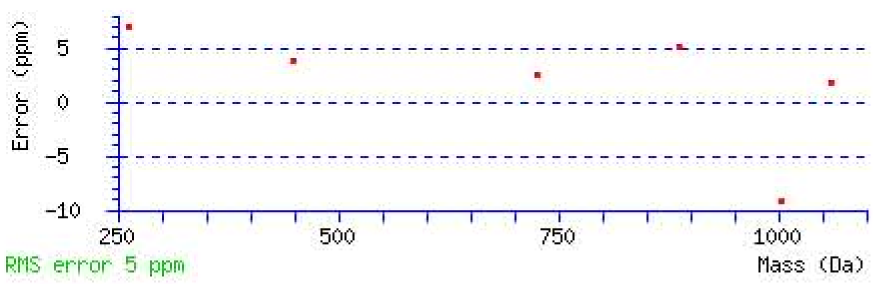
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 0.013
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
31.1	1171.569580	0.001388	IGDQWDK
11.6	1171.583328	-0.012360	GEVGDPGQKGTK
8.7	1171.576096	-0.005128	LYFSDATLDK
5.3	1171.554337	0.016631	ALCDTPGVDPK
3.2	1171.573410	-0.002442	RAPDPGFQER
3.1	1171.565536	0.005432	VASHINEMQK
3.0	1171.572067	-0.001099	LGSGPDGAEEIK
2.5	1171.565536	0.005432	MGSGEPNPAGKK
1.5	1171.572037	-0.001069	ENPEVKAEEK
0.6	1171.565536	0.005432	MNGSLHQELK

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

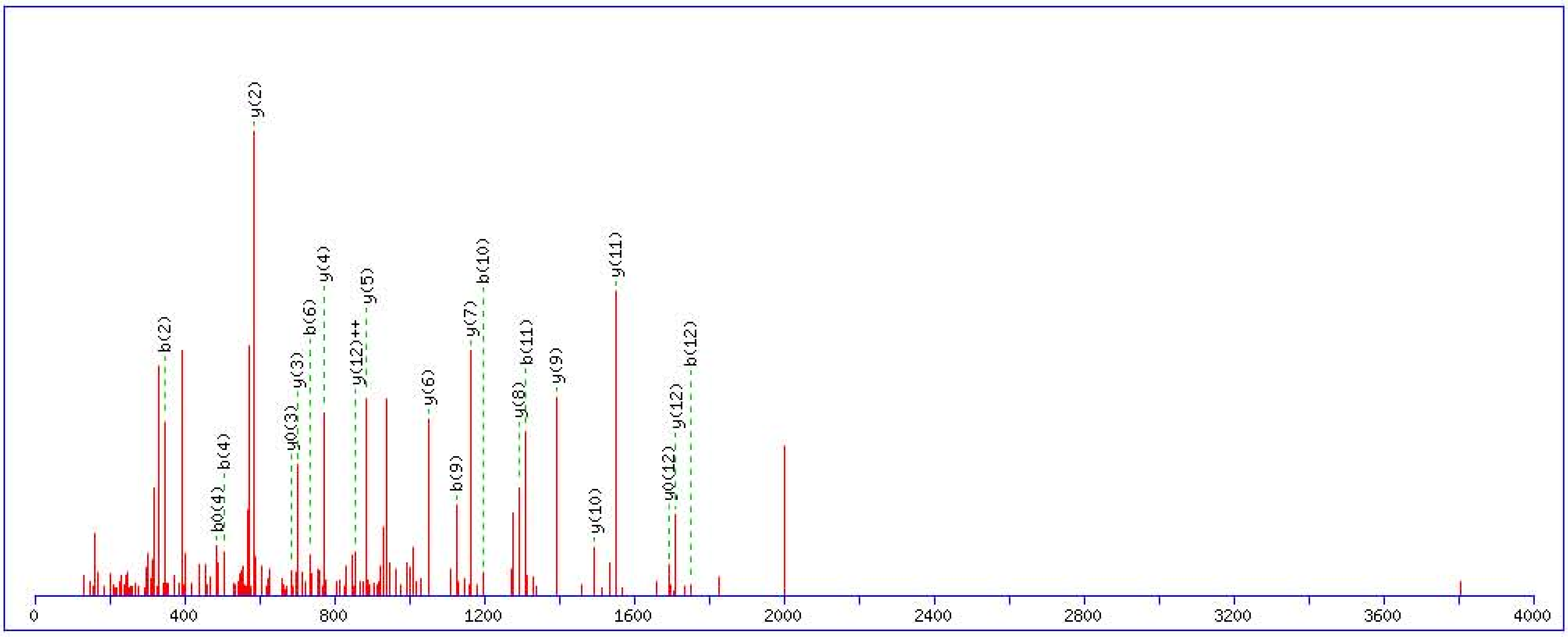
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

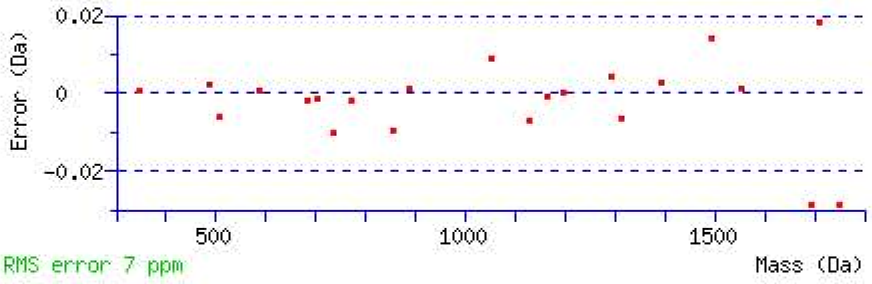
Match to Query 40134: 1896.816508 from(949.415530,2+) rtinseconds(1673) index(31247)
Title: Locus:1.1.1.3131.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

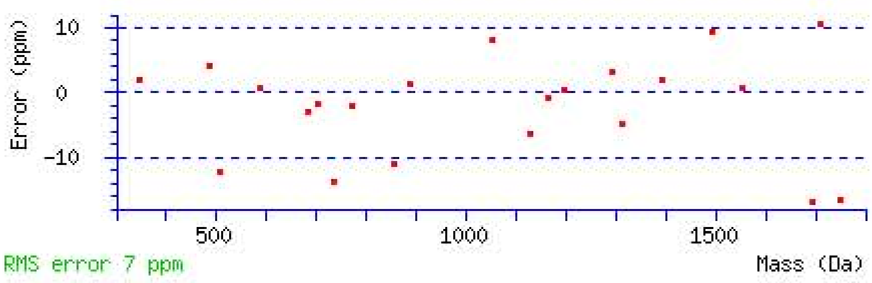
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1896.813477
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 81  Expect: 3.3e-008
Matches : 22/124 fragment ions using 34 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
81.3	1896.813477	0.003031	WCGTTQNYDADQK
11.4	1896.813477	0.003031	WCGTTQNYDADQK

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

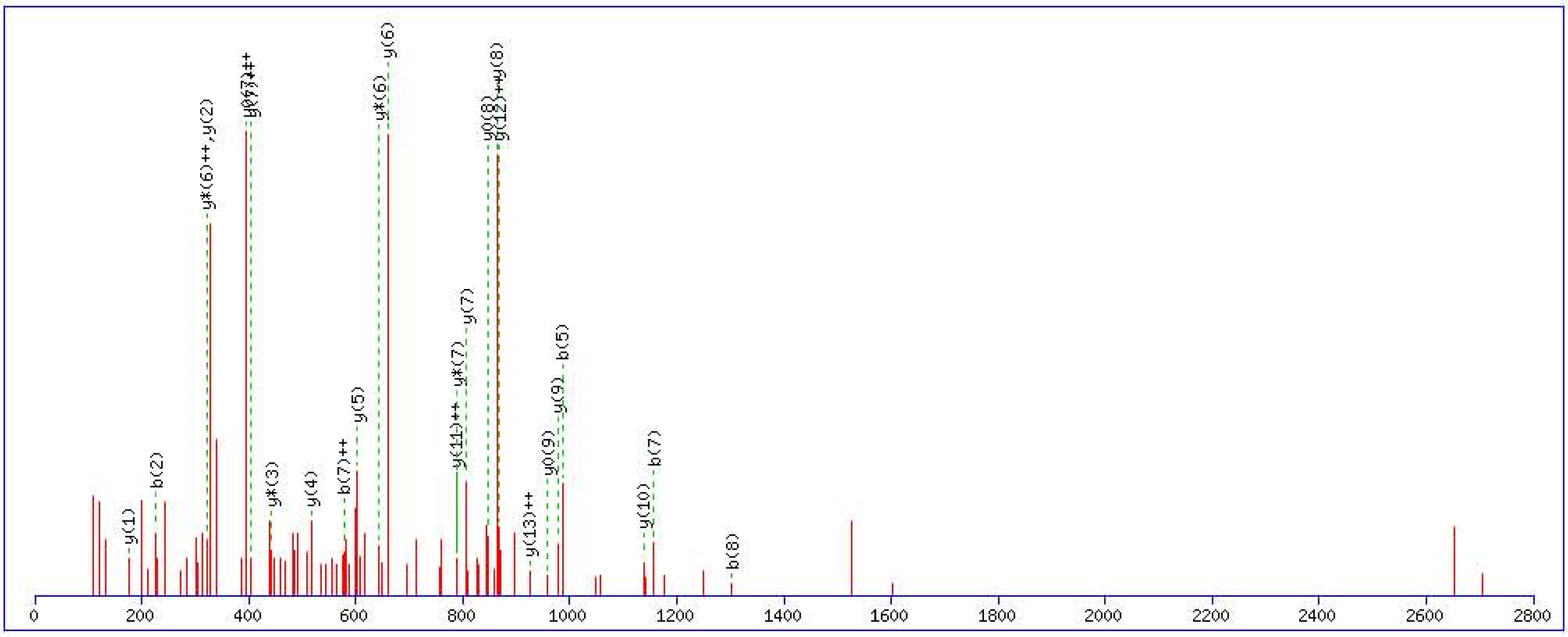
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

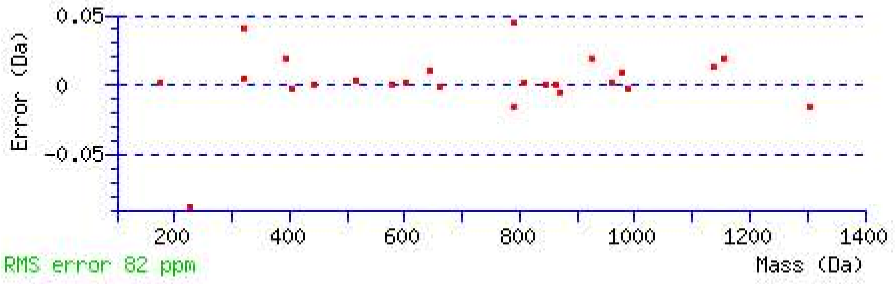
Match to Query 41322: 1961.952702 from(654.991510,3+) rtinseconds(2190) index(34177)
Title: Locus:1.1.1.3312.8 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

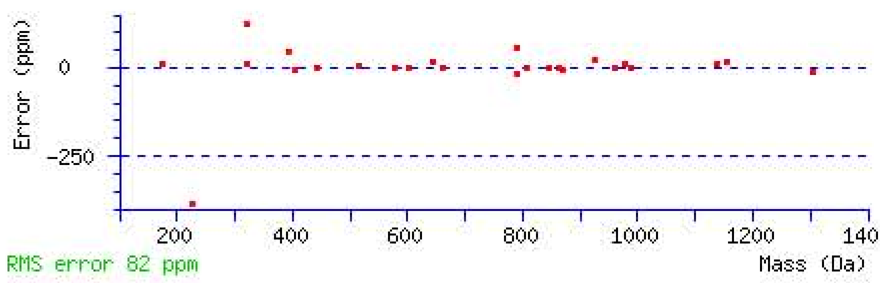
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1961.942673
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.001
Matches : 25/124 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	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
32.8	1961.942673	0.010029	LLCQCLGFGSGHFR
0.8	1961.970779	-0.018077	DAGREGLRSDVFPGPSFR

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

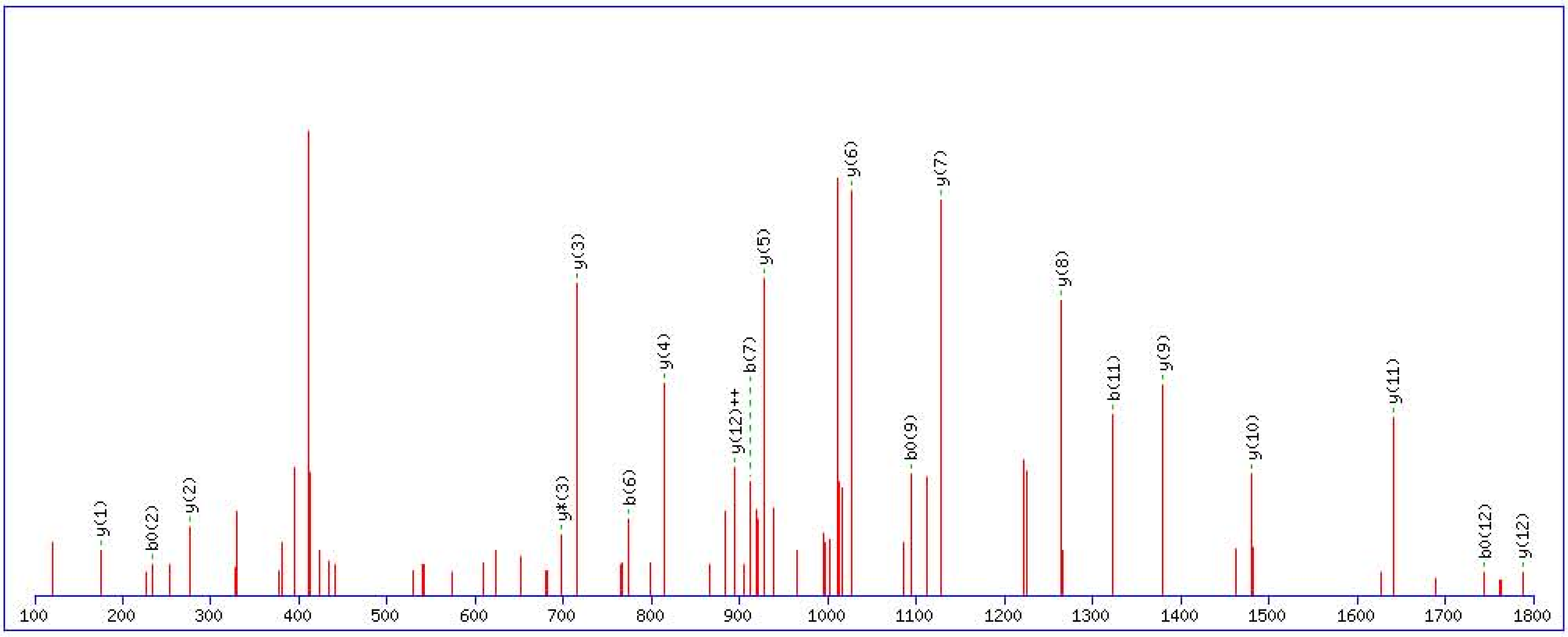
Mascot Search Results

Peptide View

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

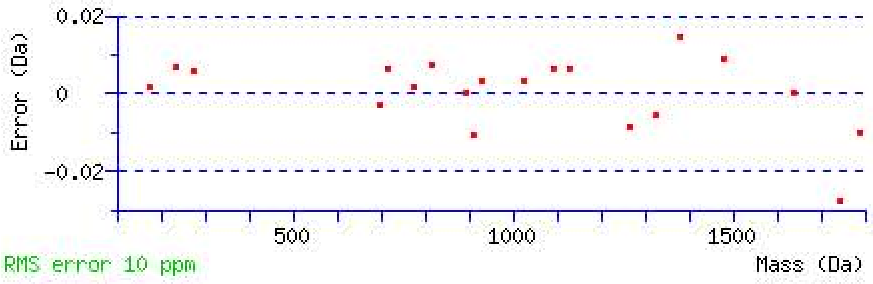
Match to Query 43334: 2036.980708 from(1019.497630,2+) rtinseconds(2023) index(33312)
Title: Locus:1.1.1.3253.18 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

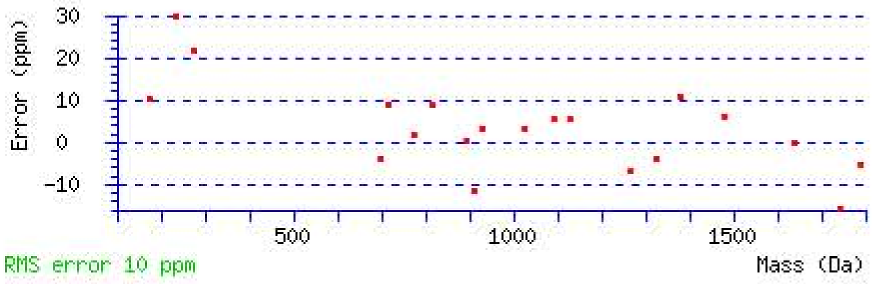


```
Monoisotopic mass of neutral peptide Mr(calc): 2036.981232
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 90  Expect: 6.6e-009
Matches : 20/130 fragment ions using 31 most intense peaks    (help)
```

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



RMS error 10 ppm



RMS error 10 ppm

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
89.9	2036.981232	-0.000524	YSFCTDHTVLVQTR
2.6	2037.006180	-0.025472	TVSEDRPQAVSSGHTR
1.1	2036.969818	0.010890	GSMGDPGLPGPQGLRGDVGDR

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

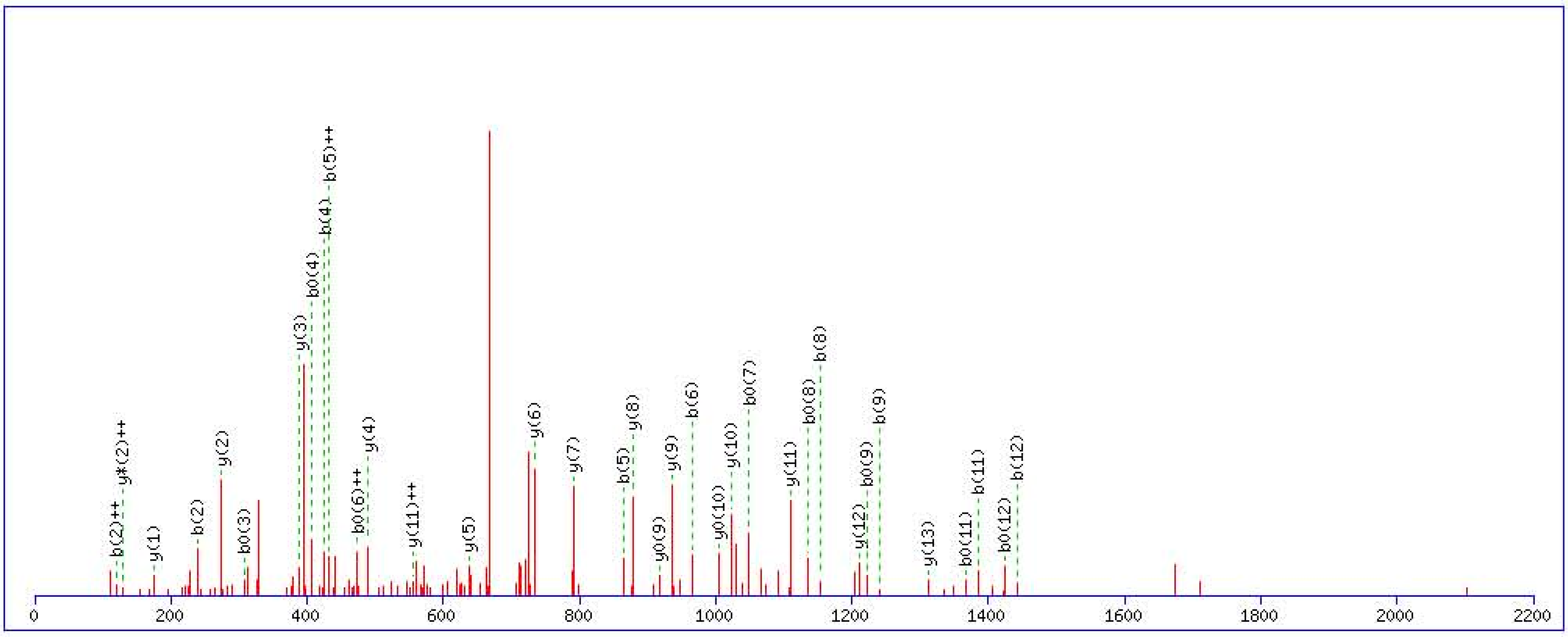
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

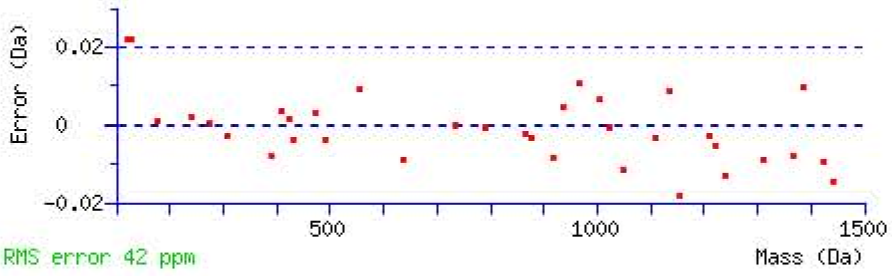
Match to Query 45595: 2174.042502 from(725.688110,3+) rtinseconds(1667) index(31216)
Title: Locus:1.1.1.3129.14 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

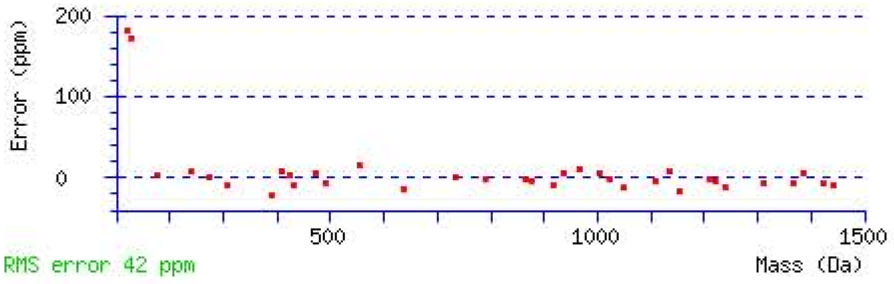
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2174.042664
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 82  Expect: 1.3e-007
Matches : 35/190 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	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
81.8	2174.042664	-0.000162	HTSVQTTSSGSGPFTDVR

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

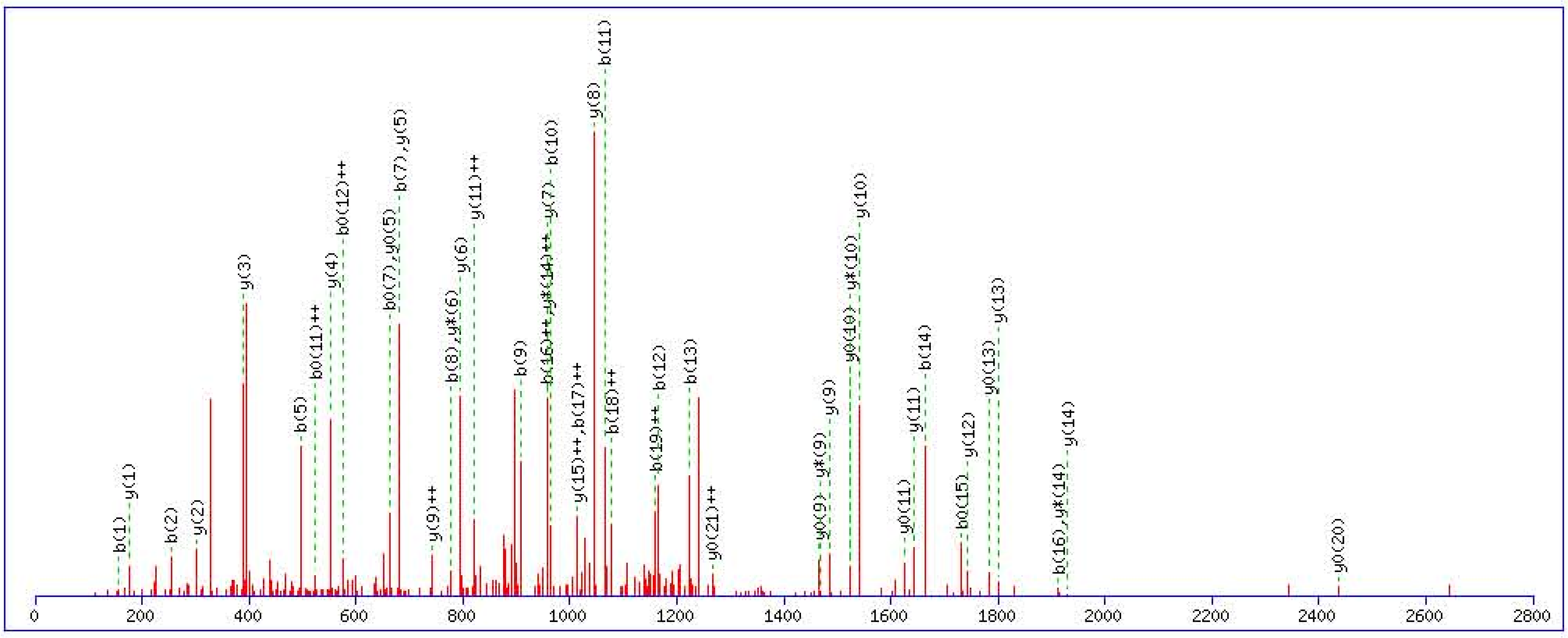
MATRIX SCIENCE Mascot Search Results

Peptide View

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

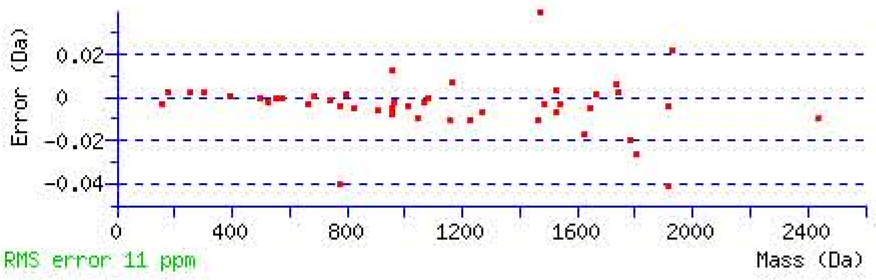
Match to Query 52767: 2706.234552 from(903.085460,3+) rtinseconds(1533) index(30460)
Title: Locus:1.1.1.3082.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

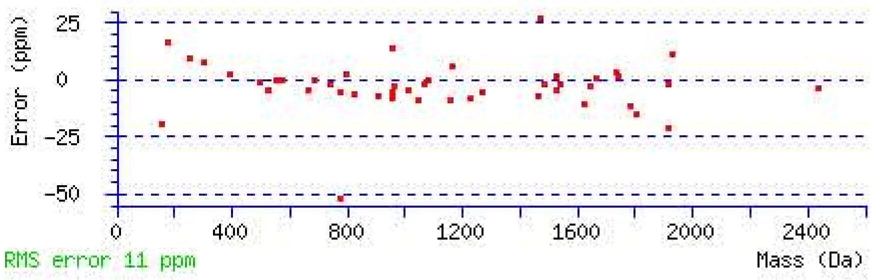
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2706.245621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 83  Expect: 2.2e-008
Matches : 50/240 fragment ions using 75 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	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
83.4	2706.245621	-0.011069	RPGGEPSPEGTTGQSYNQYSQR
61.1	2706.245621	-0.011069	RPGGEPSPEGTTGQSYNQYSQR
41.8	2706.245621	-0.011069	RPGGEPSPEGTTGQSYNQYSQR
1.7	2706.246658	-0.012106	MAQKMSFGFYKYSNMEFVR

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

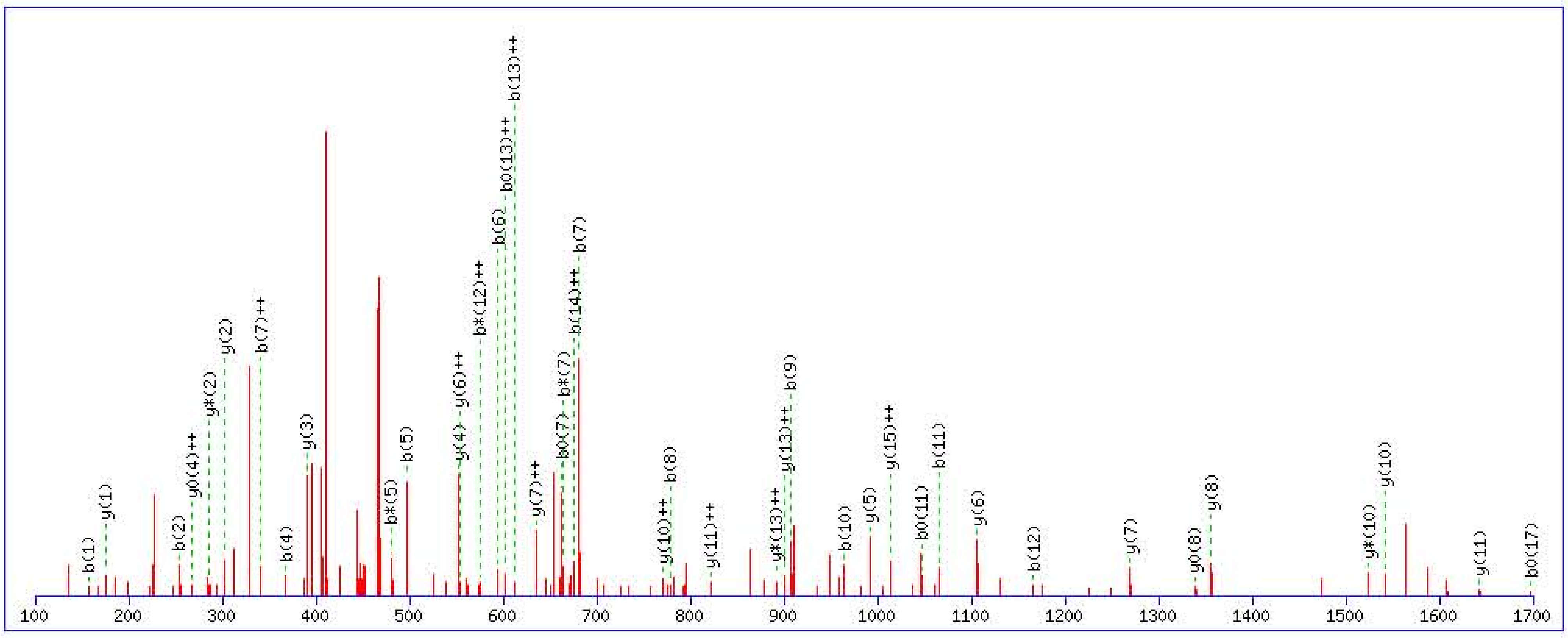
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

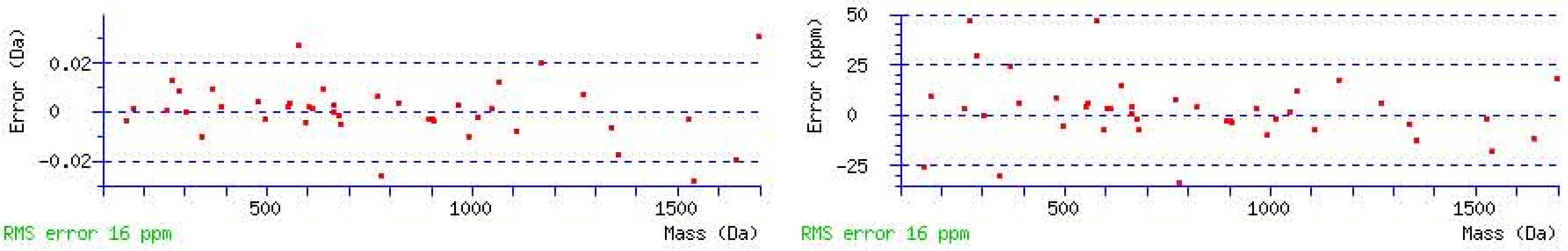
Match to Query 52768: 2706.237376 from(677.566620,4+) rtinseconds(1515) index(30360)
Title: Locus:1.1.1.3076.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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): 2706.245621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18     : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 6.4e-005
Matches : 42/240 fragment ions using 109 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	1351.623685	**676.315480**	1334.597136	667.802206	1333.613120	667.310198	Q	1484.695075	742.851176	1467.668526	734.337901	1466.684510	733.845893	9
15	1438.655713	719.831494	1421.629164	711.318220	1420.645148	710.826212	S	***1356.636497***	678.821887	1339.609948	670.308612	1338.625932	669.816604	8
16	1601.719042	801.363159	1584.692493	792.849885	1583.708477	792.357876	Y	***1269.604469***	635.305873	1252.577920	626.792598	1251.593904	626.300590	7
17	1715.761969	858.384622	1698.735420	849.871348	1697.751404	849.379340	N	***1106.541140***	553.774208	1089.514591	545.260934	1088.530575	544.768926	6
18	2154.987295	1077.997285	2137.960746	1069.484011	2136.976730	1068.992003	Q	***992.498213***	496.752745	975.471664	488.239470	974.487648	487.747462	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
52.7	2706.245621	-0.008245	RPGGEPSPEGTTGQSYNQYSQR
38.0	2706.245621	-0.008245	RPGGEPSPEGTTGQSYNQYSQR
32.3	2706.245621	-0.008245	RPGGEPSPEGTTGQSYNQYSQR

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

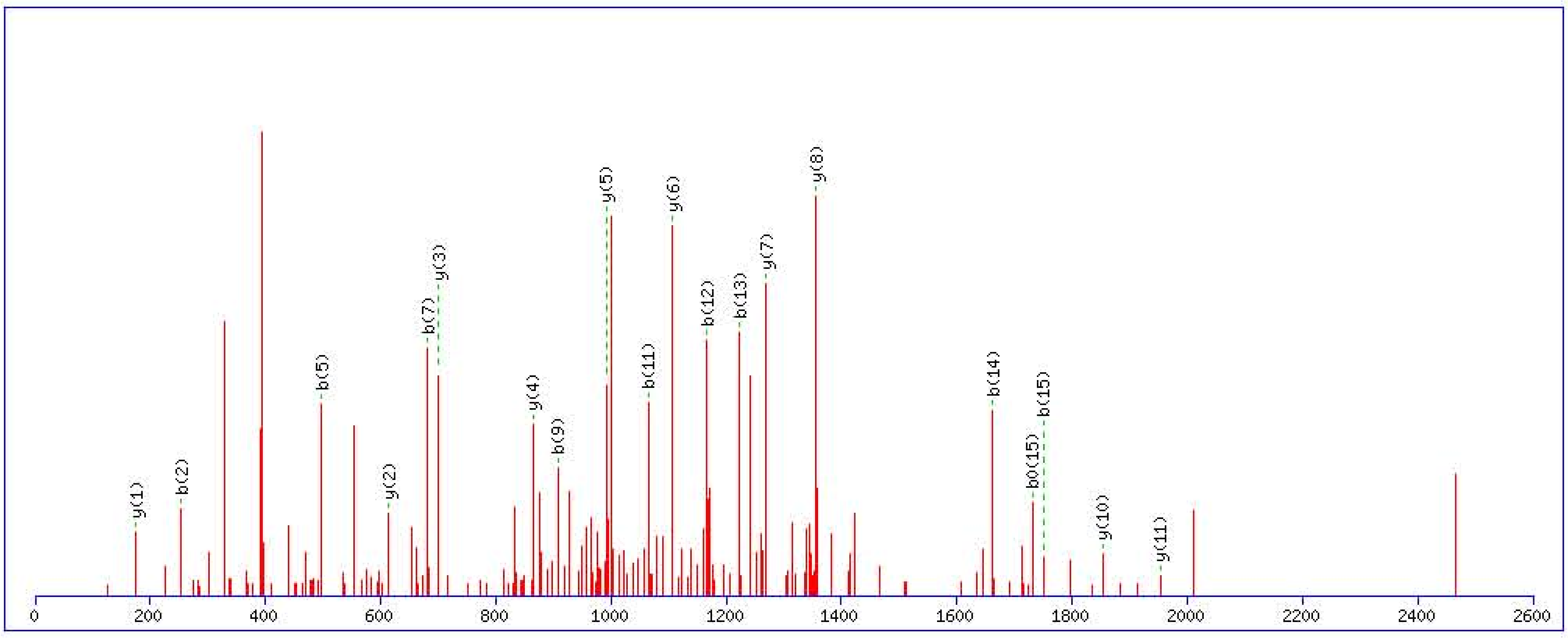
Mascot Search Results

Peptide View

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

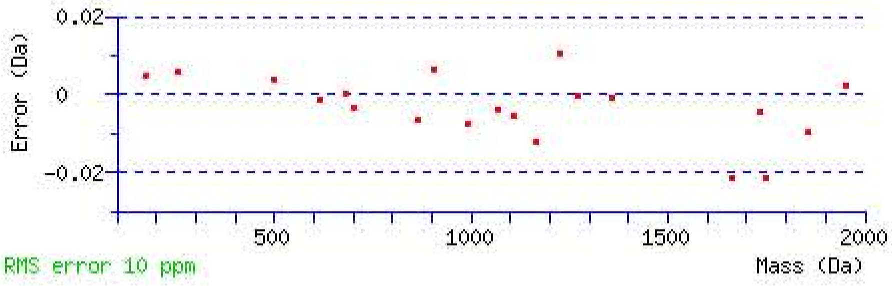
Match to Query 56201: 3017.415912 from(1006.812580,3+) rtinseconds(1811) index(31979)
Title: Locus:1.1.1.3179.13 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

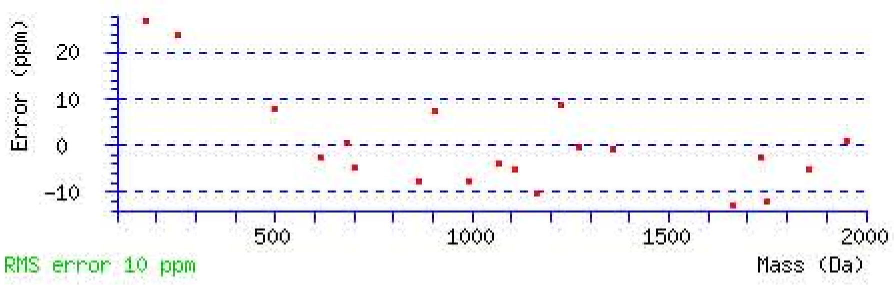
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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)
Q21     : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 1e-005
Matches : 20/240 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	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	2154.987295	1077.997285	2137.960746	1069.484011	2136.976730	1068.992003	Q	***992.498213***	496.752745	975.471664	488.239470	974.487648	487.747462	5
19	2318.050624	1159.528950	2301.024075	1151.015675	2300.040059	1150.523667	Y	***864.439635***	432.723456	847.413086	424.210181	846.429070	423.718173	4
20	2405.082652	1203.044964	2388.056103	1194.531689	2387.072087	1194.039681	S	***701.376306***	351.191791	684.349757	342.678517	683.365741	342.186509	3
21	2844.307978	1422.657627	2827.281429	1414.144353	2826.297413	1413.652345	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
62.4	3017.412369	0.003543	RPGGEPSPEGTTGQSYNQYSQR
60.5	3017.412369	0.003543	RPGGEPSPEGTTGQSYNQYSQR
27.3	3017.412369	0.003543	RPGGEPSPEGTTGQSYNQYSQR

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

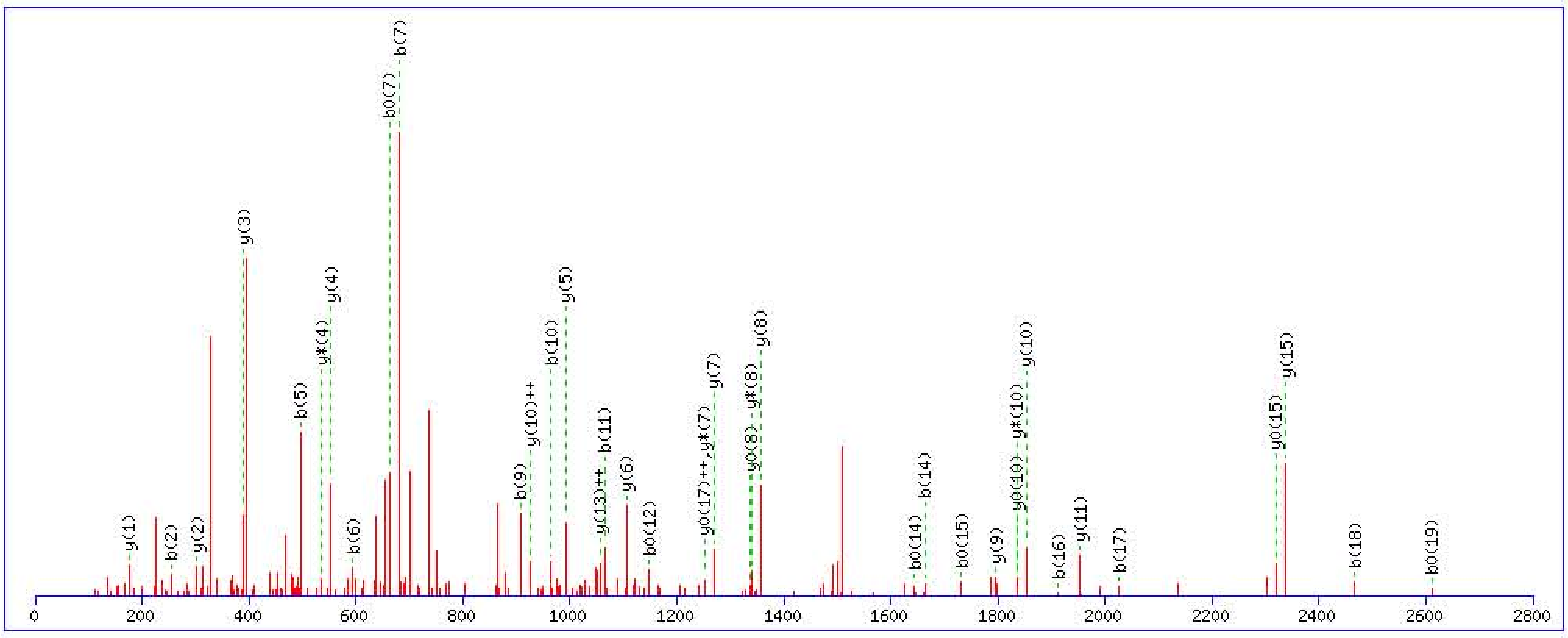
Mascot Search Results

Peptide View

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

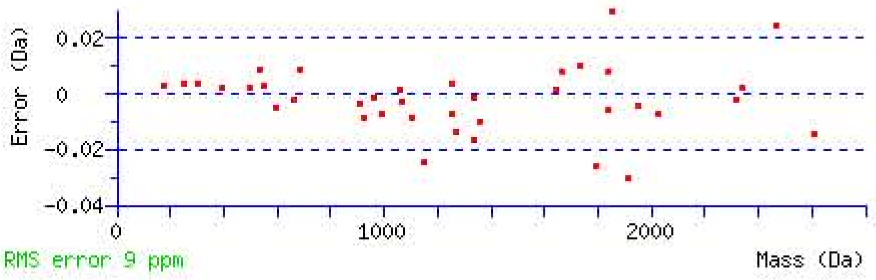
Match to Query 56203: 3017.419016 from(755.362030,4+) rtinseconds(1810) index(31975)
Title: Locus:1.1.1.3179.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

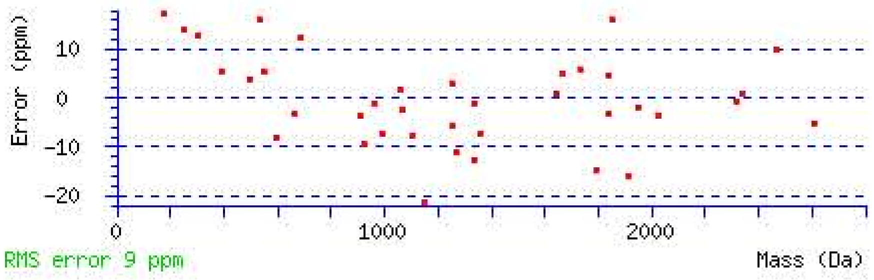
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 81  Expect: 1.4e-007
Matches : 38/240 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	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
81.2	3017.412369	0.006647	RPGGEPSPEGTTGQSYNQYSQR
67.3	3017.412369	0.006647	RPGGEPSPEGTTGQSYNQYSQR
26.8	3017.412369	0.006647	RPGGEPSPEGTTGQSYNQYSQR

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

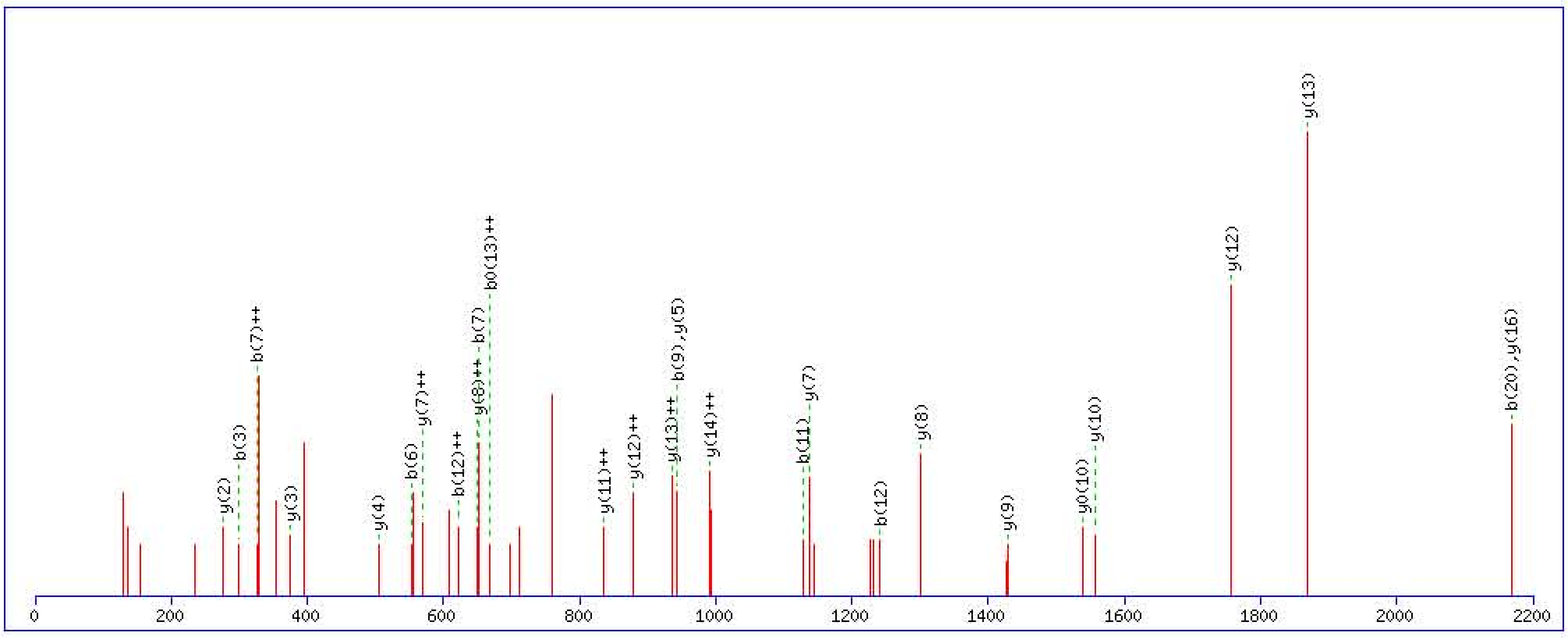
Mascot Search Results

Peptide View

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

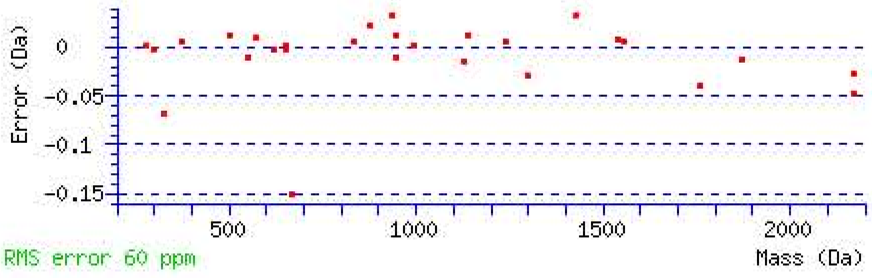
Match to Query 56797: 3109.651136 from(778.420060,4+) rtinseconds(2208) index(34278)
Title: Locus:1.1.1.3318.18 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

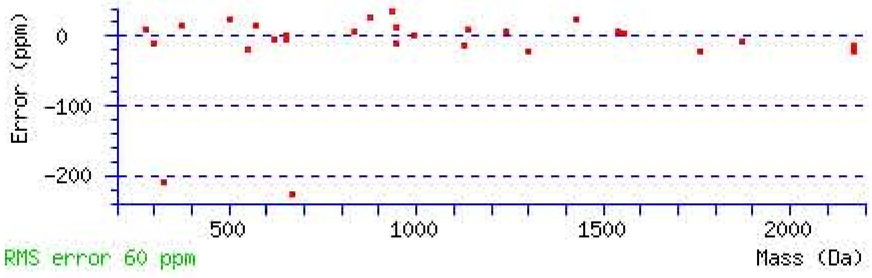


Monoisotopic mass of neutral peptide Mr(calc): 3109.638275
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q21 : Biotin:Thermo-21345 (Q)
Ions Score: 65 **Expect:** 5.9e-006
Matches : 28/266 fragment ions using 43 most intense peaks (help)

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



RMS error 60 ppm



RMS error 60 ppm

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
65.2	3109.638275	0.012861	GLKPGVVYEGQLISIQQYGHQEVTR
39.5	3109.638275	0.012861	GLKPGVVYEGQLISIQQYGHQEVTR
32.9	3109.638275	0.012861	GLKPGVVYEGQLISIQQYGHQEVTR
3.7	3109.638275	0.012861	GLKPGVVYEGQLISIQQYGHQEVTR

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

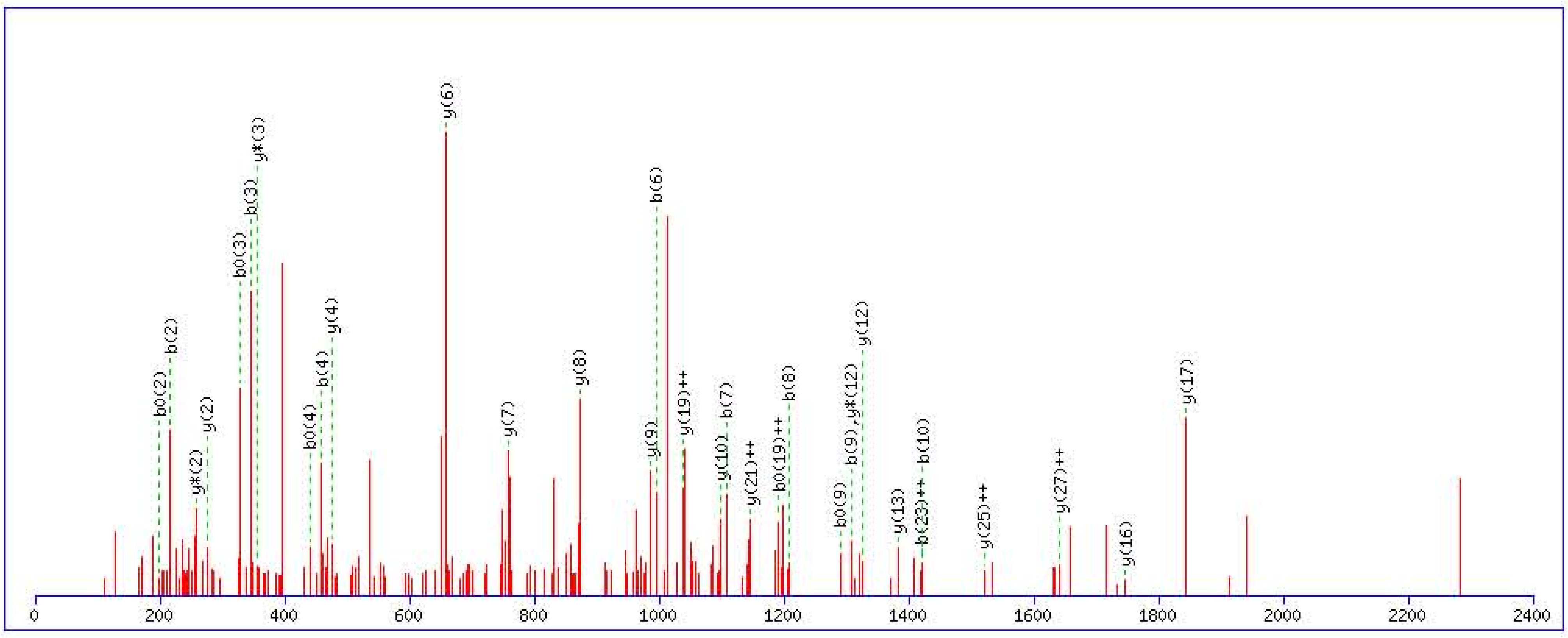
Mascot Search Results

Peptide View

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

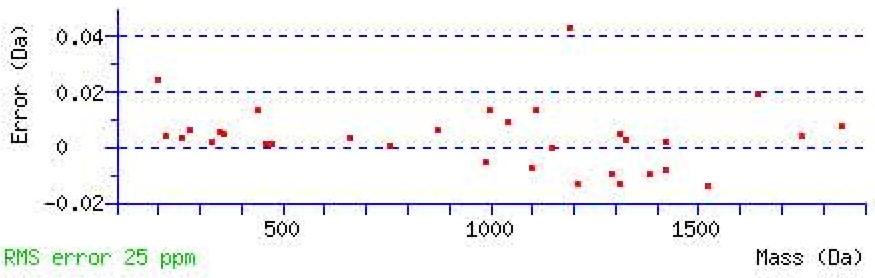
Match to Query 61368: 3497.879016 from(875.477030,4+) rtinseconds(2606) index(36376)
Title: Locus:1.1.1.3456.23 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

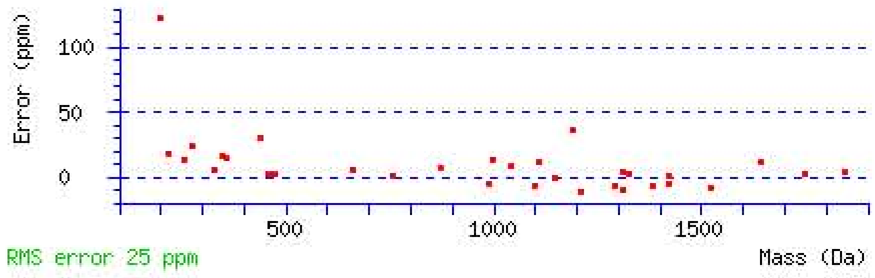
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3497.859238
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.0089
Matches : 32/320 fragment ions using 105 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
31.9	3497.859238	0.019778	TDELPQLVTLPHPNLHGPEILDVPSTVQK

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

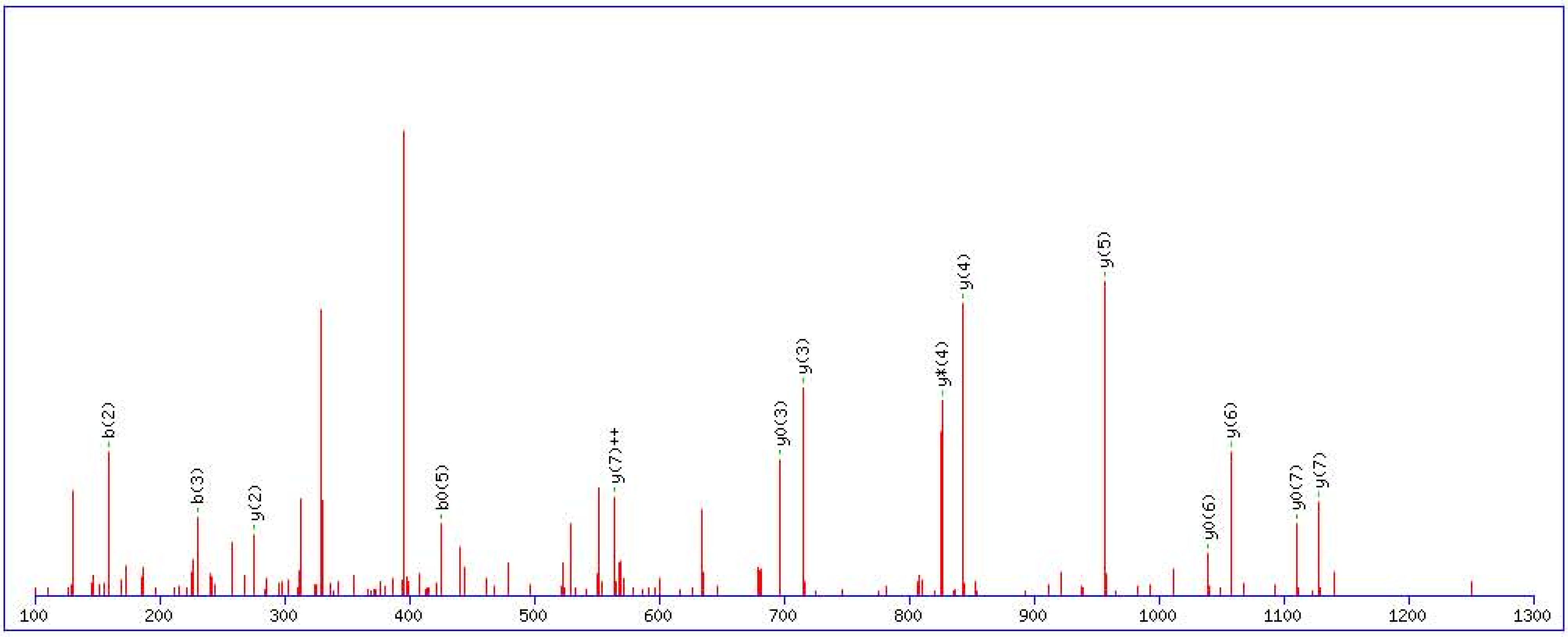
Mascot Search Results

Peptide View

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

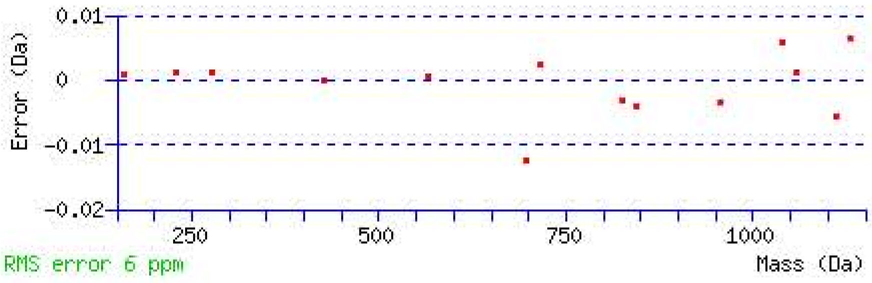
Match to Query 22736: 1285.668568 from(643.841560,2+) rtinseconds(1498) index(30265)
Title: Locus:1.1.1.3070.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

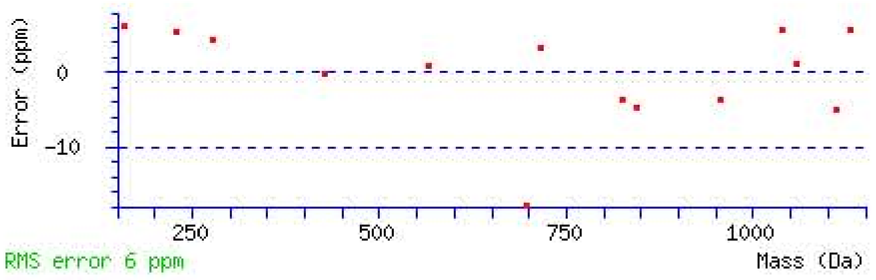
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1285.669998
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.0037
Matches : 14/84 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							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
38.5	1285.669998	-0.001430	SAATLQQEK
29.1	1285.669998	-0.001430	SAATLQQEK
11.8	1285.651367	0.017201	LLQAVENGDAEK
6.3	1285.652237	0.016331	AMQIQEQK
5.0	1285.669998	-0.001430	ASLDQGKEK
4.2	1285.649582	0.018986	SVPCPRCVRR
3.4	1285.658752	0.009816	IESLEQEK
3.4	1285.658768	0.009800	VTELEQEK
2.9	1285.673859	-0.005291	NDVGGQRSLVNK
1.6	1285.687759	-0.019191	SNQQLVDIIEK

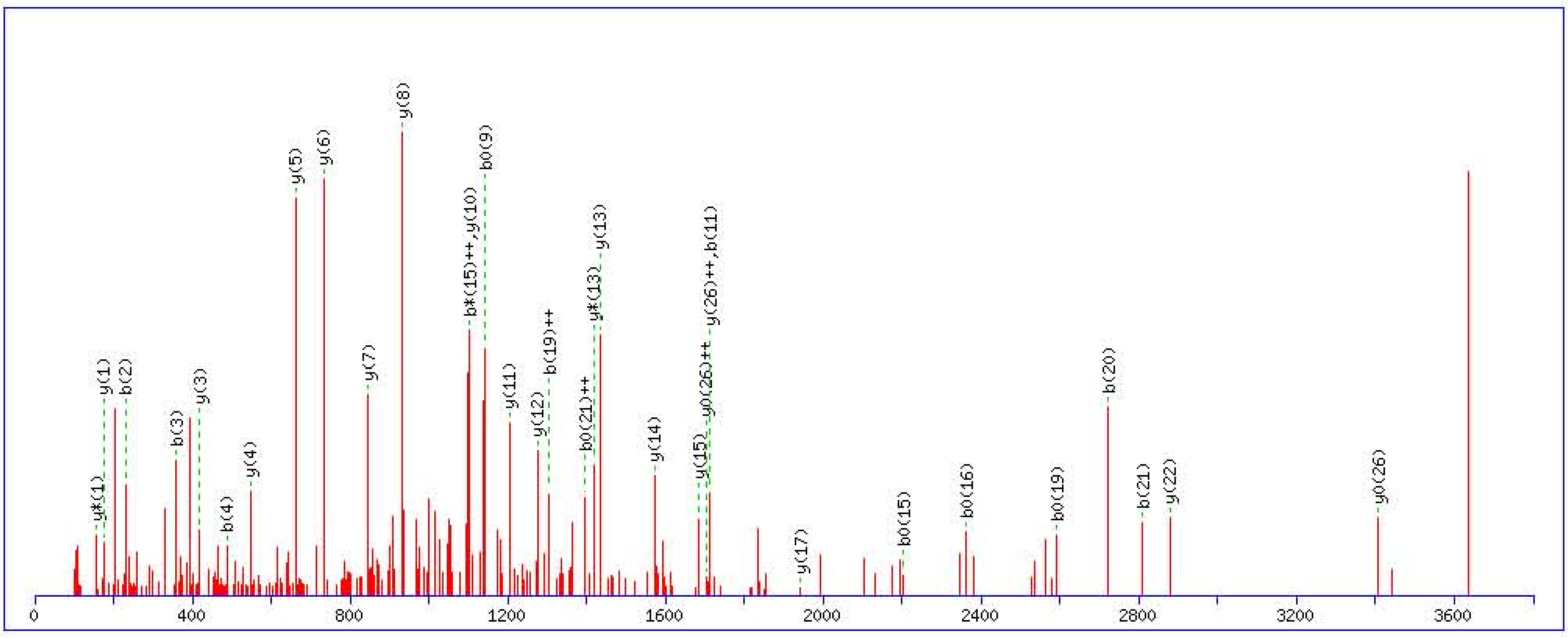
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

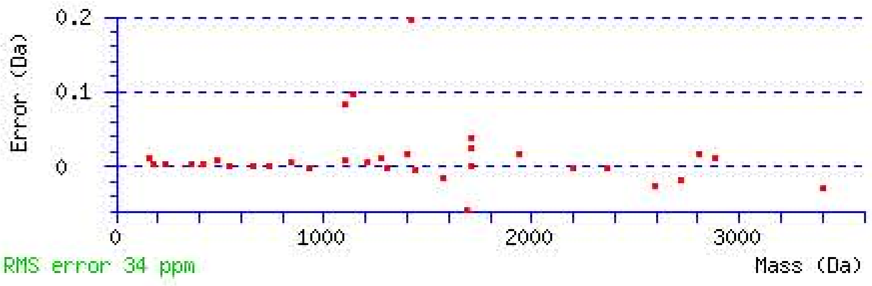
Match to Query 62387: 3653.622896 from(914.413000,4+) rtinseconds(2091) index(33658)
Title: Locus:1.1.1.3277.19 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

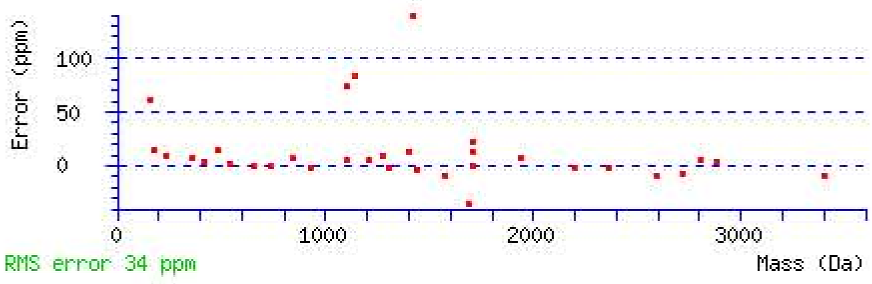
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 88 **Expect:** 1.2e-008
Matches : 33/312 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	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
88.0	3653.615311	0.007585	MVQEQCCHSQLEELHCATGISLANEQDR
74.6	3653.615311	0.007585	MVQEQCCHSQLEELHCATGISLANEQDR
70.7	3653.615311	0.007585	MVQEQCCHSQLEELHCATGISLANEQDR

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

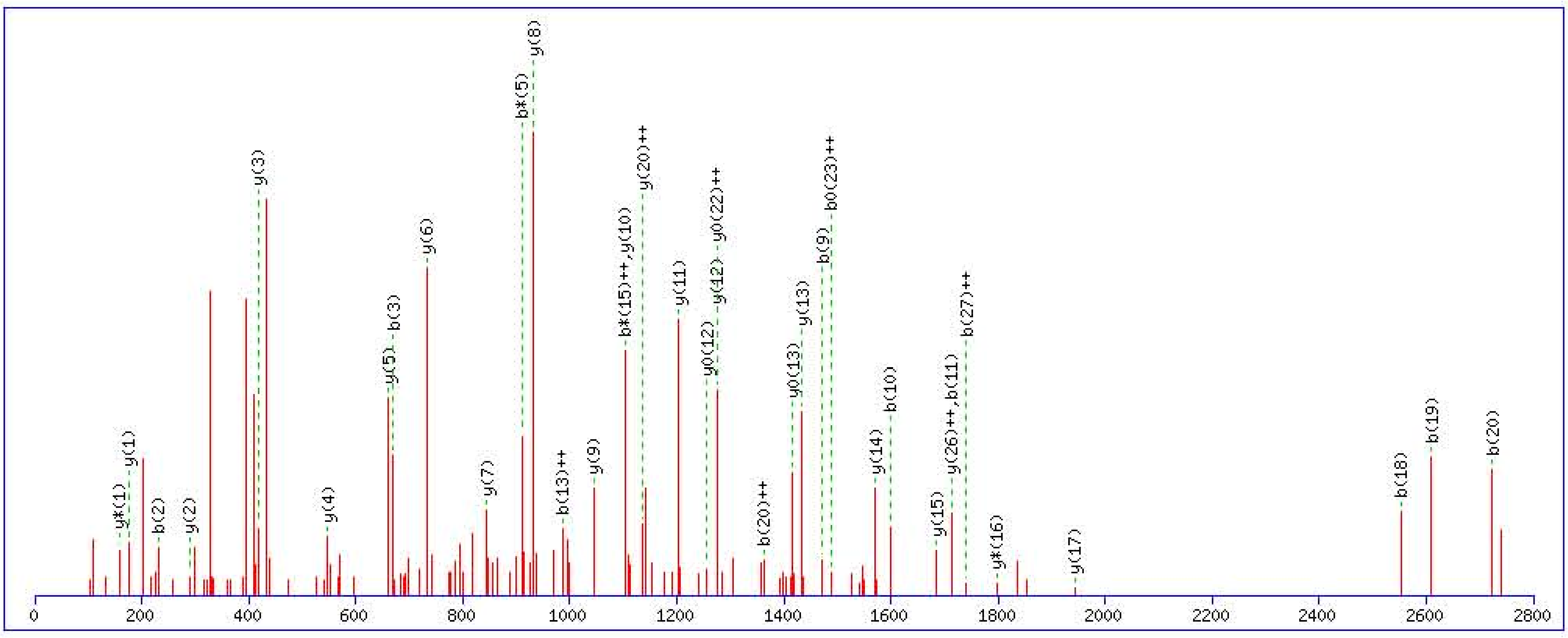
Mascot Search Results

Peptide View

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

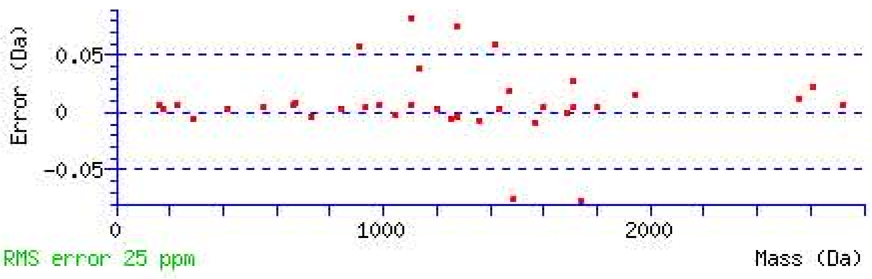
Match to Query 62388: 3653.625736 from(914.413710,4+) rtinseconds(1996) index(33180)
Title: Locus:1.1.1.3244.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

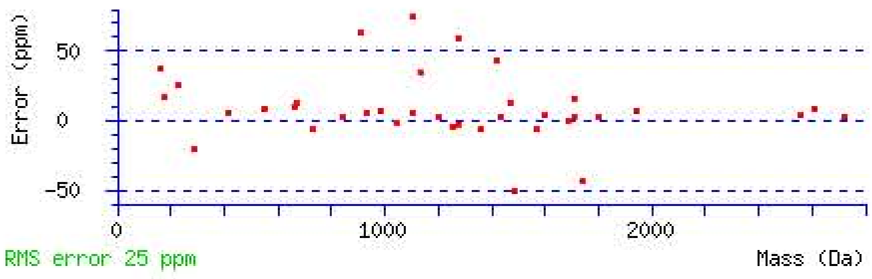
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3653.615311
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 78  Expect: 1.3e-007
Matches : 37/312 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	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
77.8	3653.615311	0.010425	MVQEQCCHSQLEELHCATGISLANEQDR
76.0	3653.615311	0.010425	MVQEQCCHSQLEELHCATGISLANEQDR
71.2	3653.615311	0.010425	MVQEQCCHSQLEELHCATGISLANEQDR

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

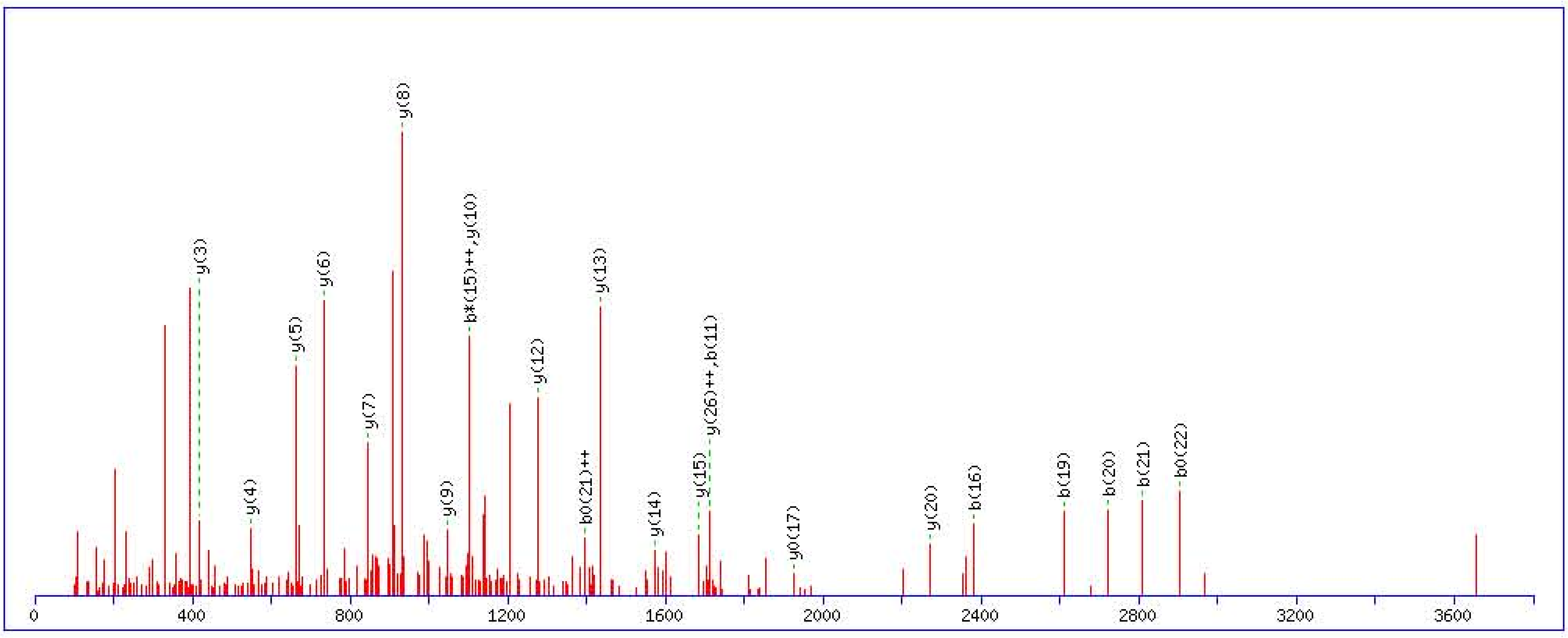
Mascot Search Results

Peptide View

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

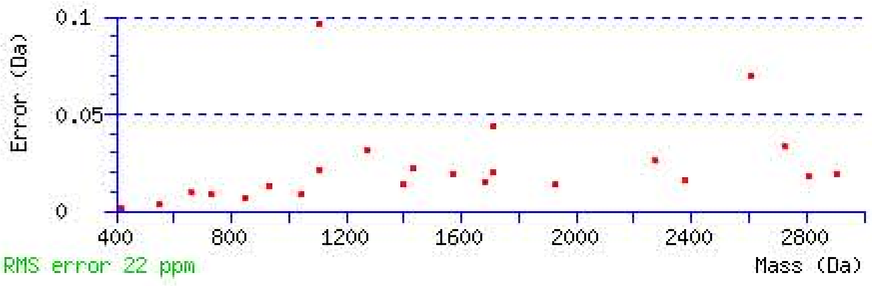
Match to Query 62391: 3653.662456 from(914.422890,4+) rtinseconds(1970) index(47231)
Title: Locus:1.1.1.2734.22 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

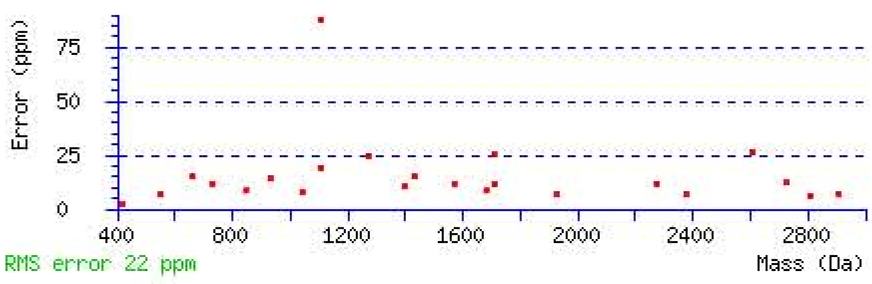
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3653.615311
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 102 **Expect:** 7.3e-010
Matches : 23/312 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	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
102.0	3653.615311	0.047145	MVQEQCCHSQLEELHCATGISLANEQDR
102.0	3653.615311	0.047145	MVQEQCCHSQLEELHCATGISLANEQDR
87.4	3653.615311	0.047145	MVQEQCCHSQLEELHCATGISLANEQDR

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

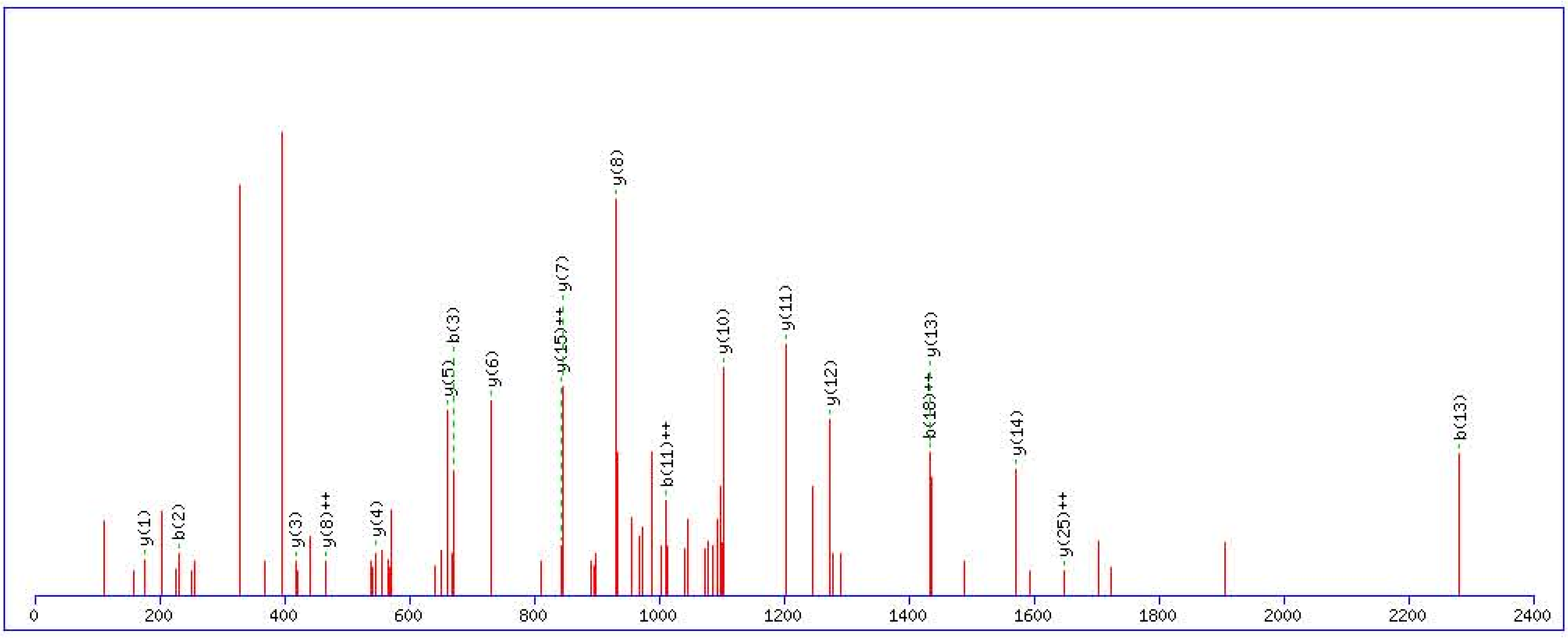
Mascot Search Results

Peptide View

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

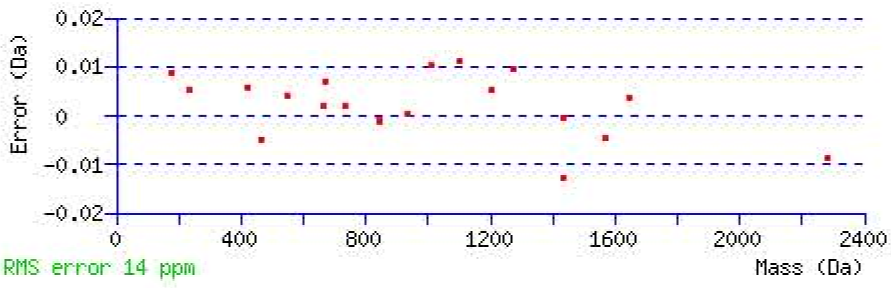
Match to Query 63773: 3964.794816 from(992.205980,4+) rtinseconds(2215) index(34333)
Title: Locus:1.1.1.3320.26 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

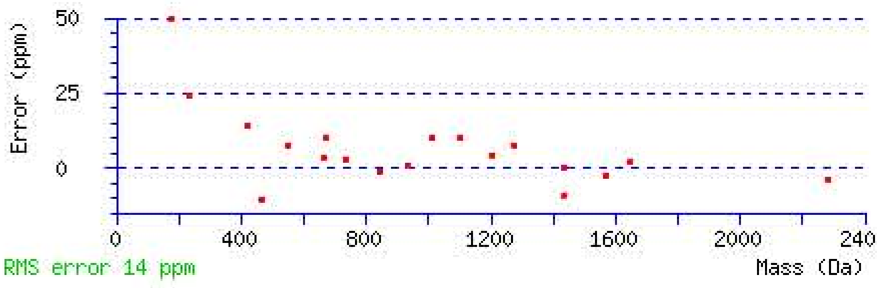


```
Monoisotopic mass of neutral peptide Mr(calc): 3964.782059
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Q10    : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 9e-005
Matches : 20/312 fragment ions using 43 most intense peaks   (help)
```

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



RMS error 14 ppm



RMS error 14 ppm

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
50.5	3964.782059	0.012757	MVQEQCCHSQLEELHCATGISLANEQDR
50.5	3964.782059	0.012757	MVQEQCCHSQLEELHCATGISLANEQDR
48.1	3964.782059	0.012757	MVQEQCCHSQLEELHCATGISLANEQDR

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

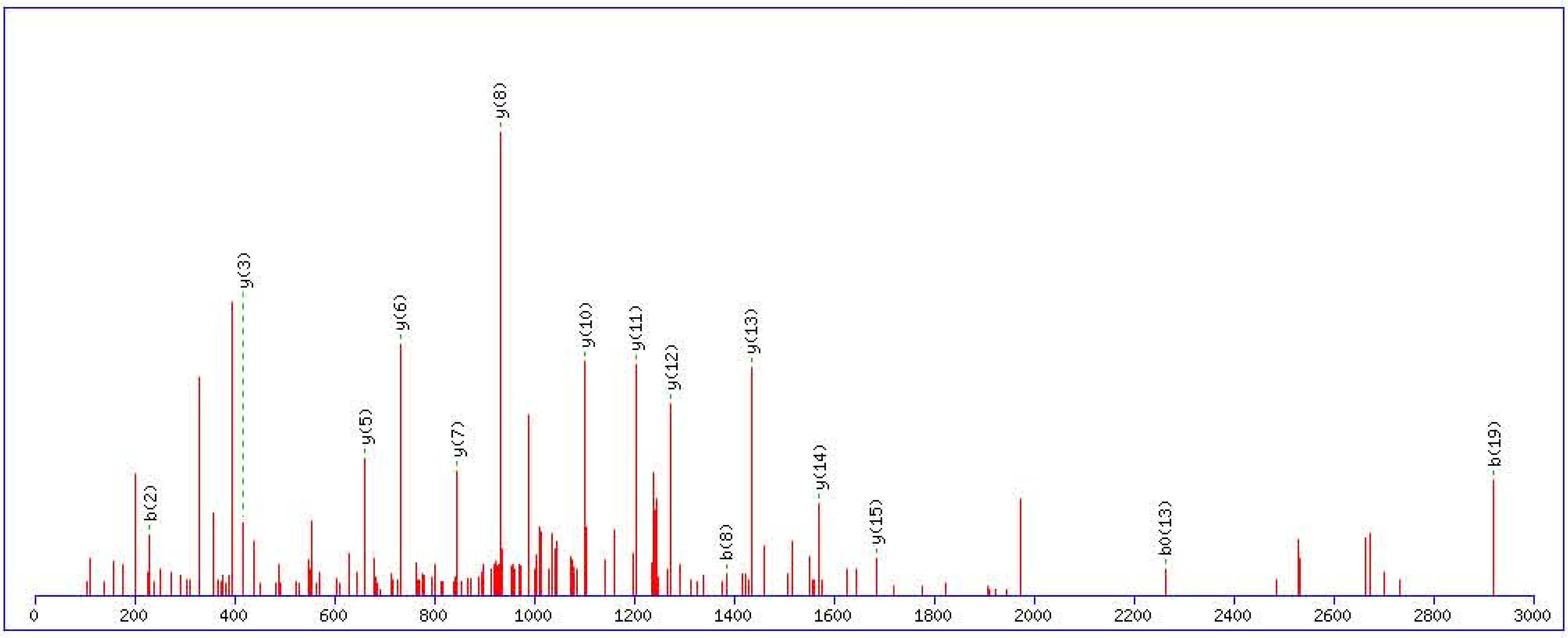
Mascot Search Results

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 63774: 3964.794816 from(992.205980,4+) rtinseconds(2206) index(34261)
Title: Locus:1.1.1.3317.19 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 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 ●



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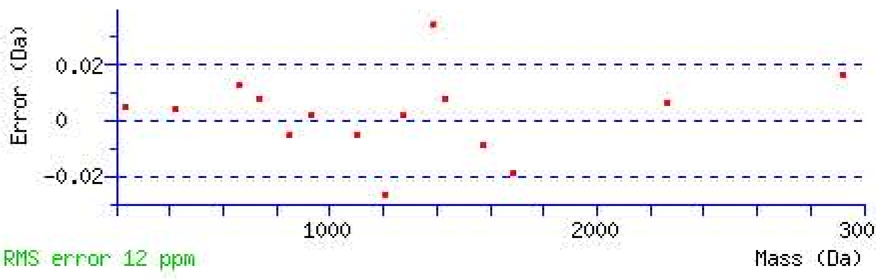
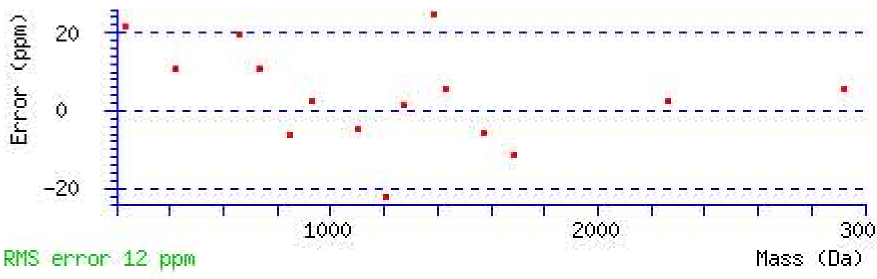
Monoisotopic mass of neutral peptide Mr(calc): 3964.782059
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 63  Expect: 5.2e-006
Matches : 15/312 fragment ions 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	3834.748870	1917.878073	3817.722321	1909.364798	3816.738305	1908.872790	27
3	359.174753	180.091015	342.148204	171.577740			Q	3735.680456	1868.343866	3718.653907	1859.830591	3717.669891	1859.338583	26
4	488.217346	244.612311	471.190797	236.099037	470.206781	235.607029	E	3607.621878	1804.314577	3590.595329	1795.801302	3589.611313	1795.309294	25
5	927.442672	464.224974	910.416123	455.711700	909.432107	455.219692	Q	3478.579285	1739.793280	3461.552736	1731.280006	3460.568720	1730.787998	24
6	1087.473321	544.240298	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	615.250340	C	2879.323310	1440.165293	2862.296761	1431.652018	2861.312745	1431.160011	22
8	**1384.562882**	692.785079	1367.536333	684.271805	1366.552317	683.779796	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
62.9	3964.782059	0.012757	MVQEQCCHSQLEELHCATGISLANEQDR
62.9	3964.782059	0.012757	MVQEQCCHSQLEELHCATGISLANEQDR
60.2	3964.782059	0.012757	MVQEQCCHSQLEELHCATGISLANEQDR

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

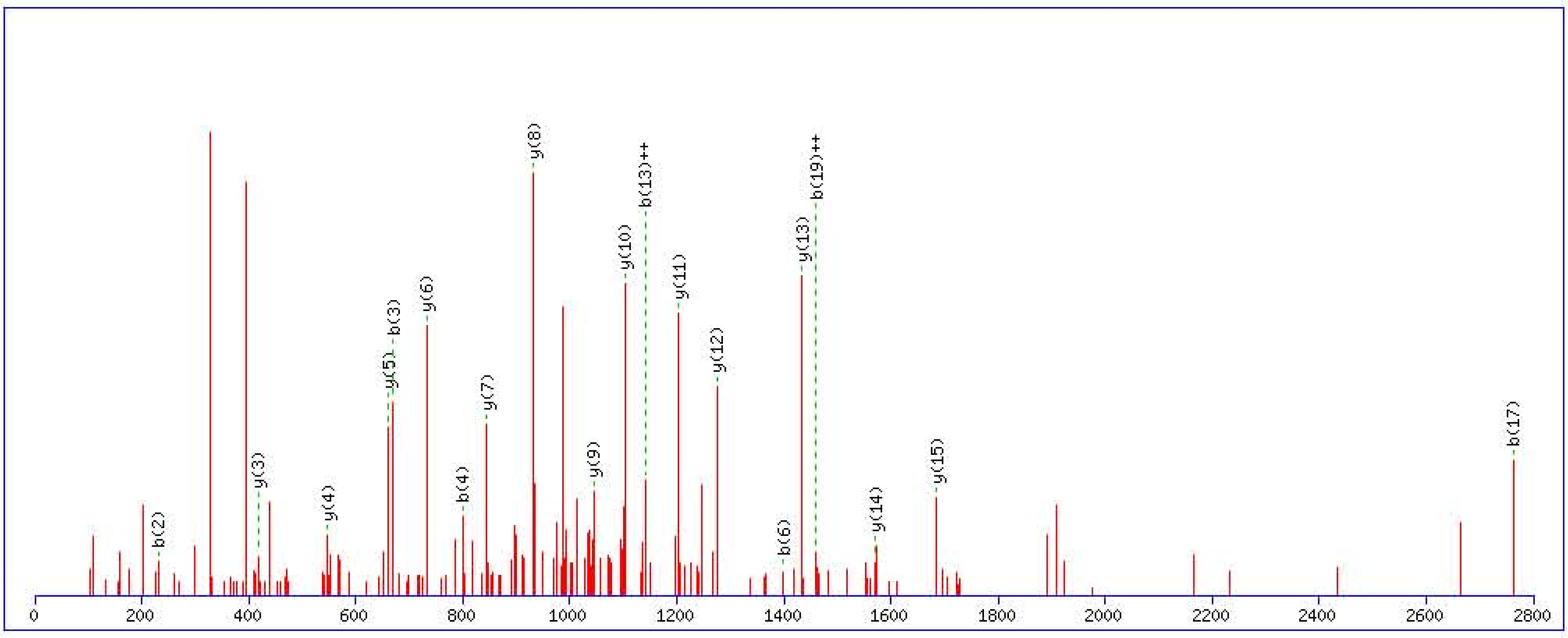
MATRIX SCIENCE Mascot Search Results

Peptide View

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

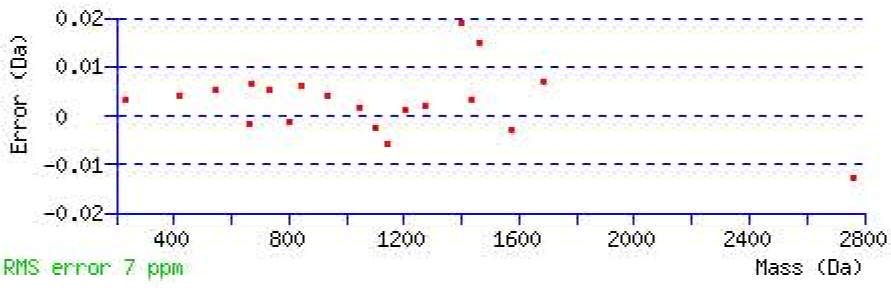
Match to Query 63776: 3964.801576 from(992.207670,4+) rtinseconds(2132) index(33899)
Title: Locus:1.1.1.3291.21 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

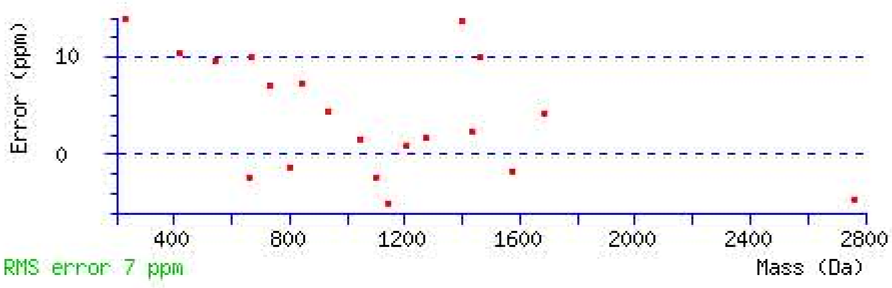
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 59  Expect: 1.4e-005
Matches : 20/312 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	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
58.9	3964.782059	0.019517	MVQEQCCHSQLEELHCATGISLANEQDR
56.9	3964.782059	0.019517	MVQEQCCHSQLEELHCATGISLANEQDR
52.4	3964.782059	0.019517	MVQEQCCHSQLEELHCATGISLANEQDR

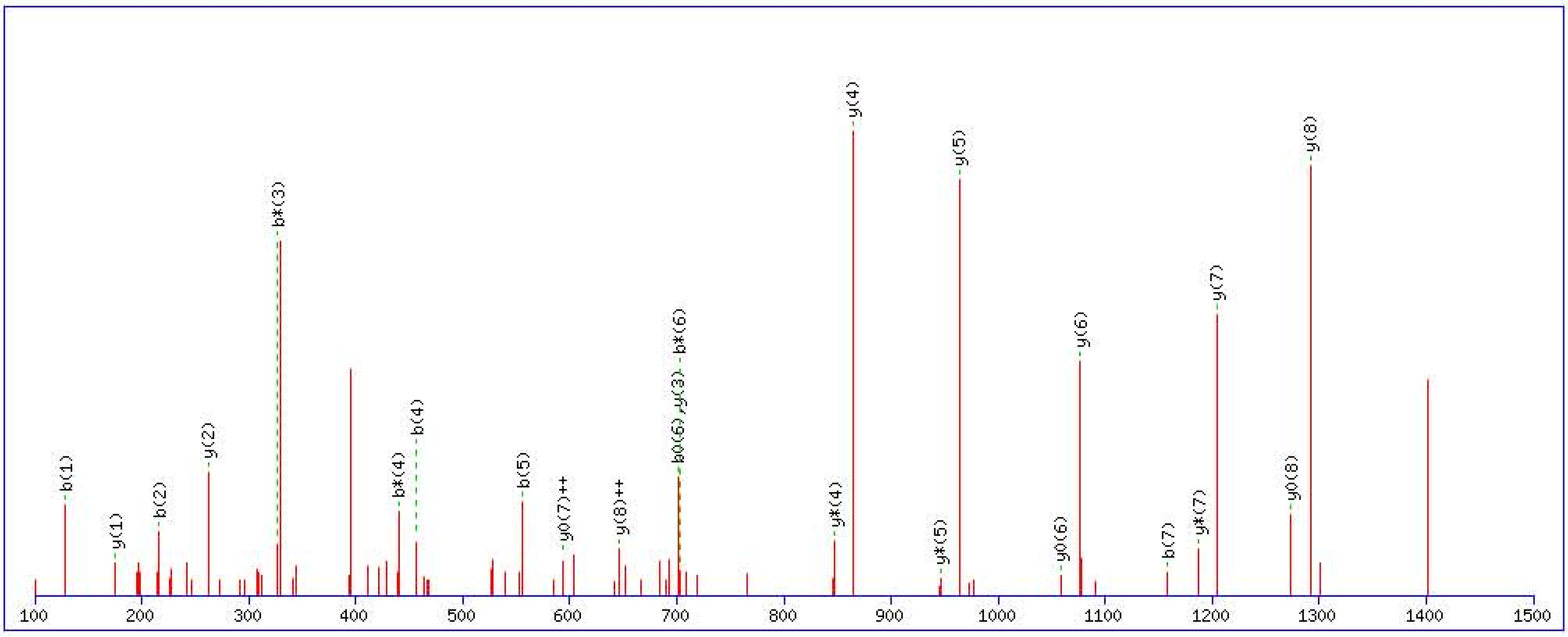
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

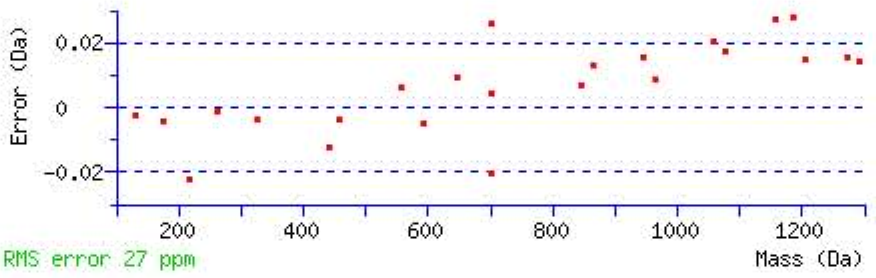
Match to Query 27371: 1418.776328 from(710.395440,2+) rtinseconds(1504) index(44215)
Title: Locus:1.1.1.2572.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

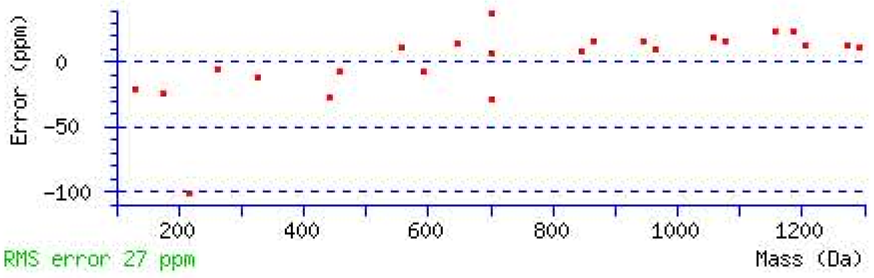
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 53  Expect: 4.8e-005
Matches : 24/92 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	**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
53.1	1418.770386	0.005942	KSQLVYQSR
16.2	1418.770386	0.005942	KSQLVYQSR
6.7	1418.780273	-0.003945	TNQLMETLKTIK
5.6	1418.767044	0.009284	SQGLAGLFAGVFPR
5.2	1418.788147	-0.011819	QSQVDRLYVALK
4.2	1418.776886	-0.000558	EKAKALEDLAGFK
2.3	1418.763000	0.013328	IKGEQGAPGLQGHK
0.8	1418.787659	-0.011331	KEILLAMLMVDK
0.7	1418.778259	-0.001931	RVSLPQWPPPSR

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

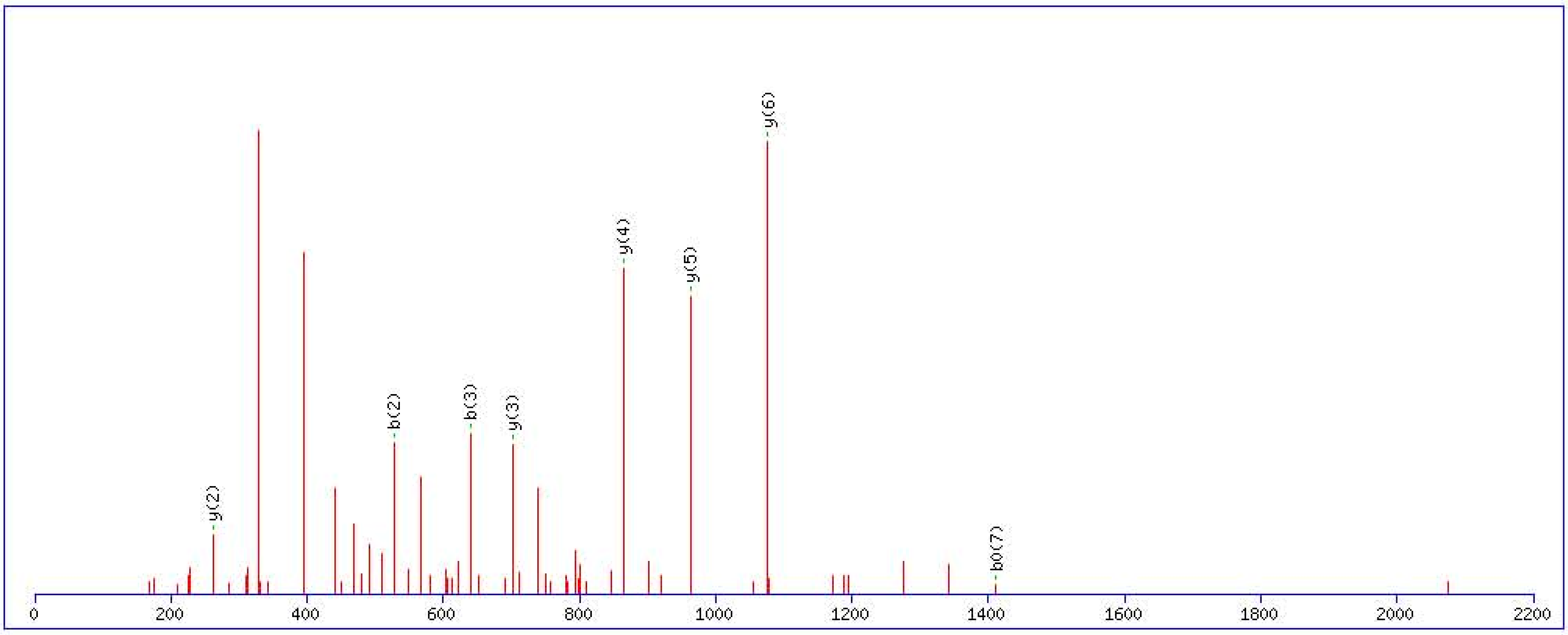
Mascot Search Results

Peptide View

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

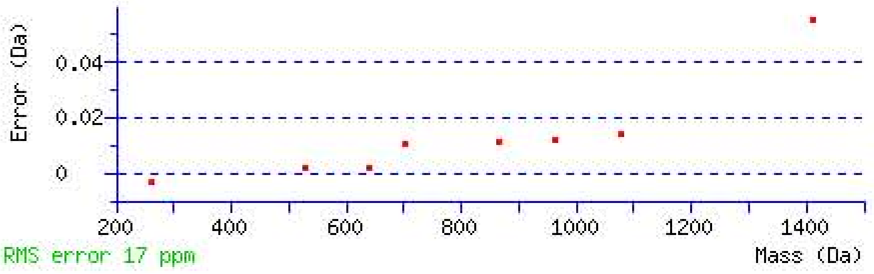
Match to Query 33324: 1601.849188 from(801.931870,2+) rtinseconds(2076) index(47831)
Title: Locus:1.1.1.2771.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

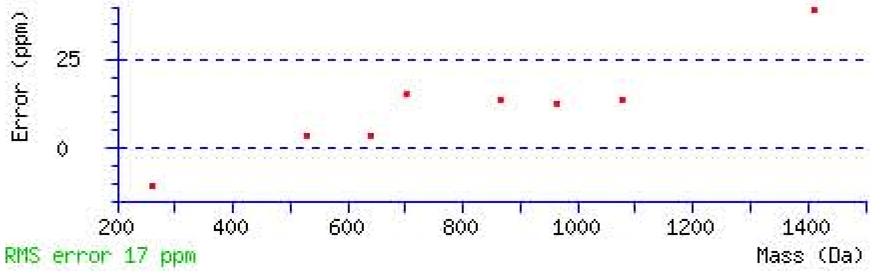
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 29  Expect: 0.01
Matches : 8/80 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							8
2	**527.264630**	264.135953	510.238081	255.622679	509.254065	255.130671	Q	1515.817439	758.412358	1498.790890	749.899083	1497.806874	749.407075	7
3	**640.348694**	320.677985	623.322145	312.164711	622.338129	311.672703	L	***1076.592113***	538.799695	1059.565564	530.286420	1058.581548	529.794412	6
4	739.417108	370.212192	722.390559	361.698917	721.406543	361.206909	V	***963.508049***	482.257663	946.481500	473.744388	945.497484	473.252380	5
5	902.480437	451.743856	885.453888	443.230582	884.469872	442.738574	Y	***864.439635***	432.723456	847.413086	424.210181	846.429070	423.718173	4
6	1341.705763	671.356520	1324.679214	662.843245	1323.695198	662.351237	Q	***701.376306***	351.191791	684.349757	342.678517	683.365741	342.186509	3
7	1428.737791	714.872534	1411.711242	706.359259	1410.727226	705.867251	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
8							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.9	1601.842178	0.007010	SQLVYQSR
7.3	1601.846024	0.003164	RFVLSCSLLSHQR
2.0	1601.834763	0.014425	QMLEALNFLHSKR
1.5	1601.855881	-0.006693	ELQRLQQAETMKK
1.5	1601.852051	-0.002863	SQISELNLLMK

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

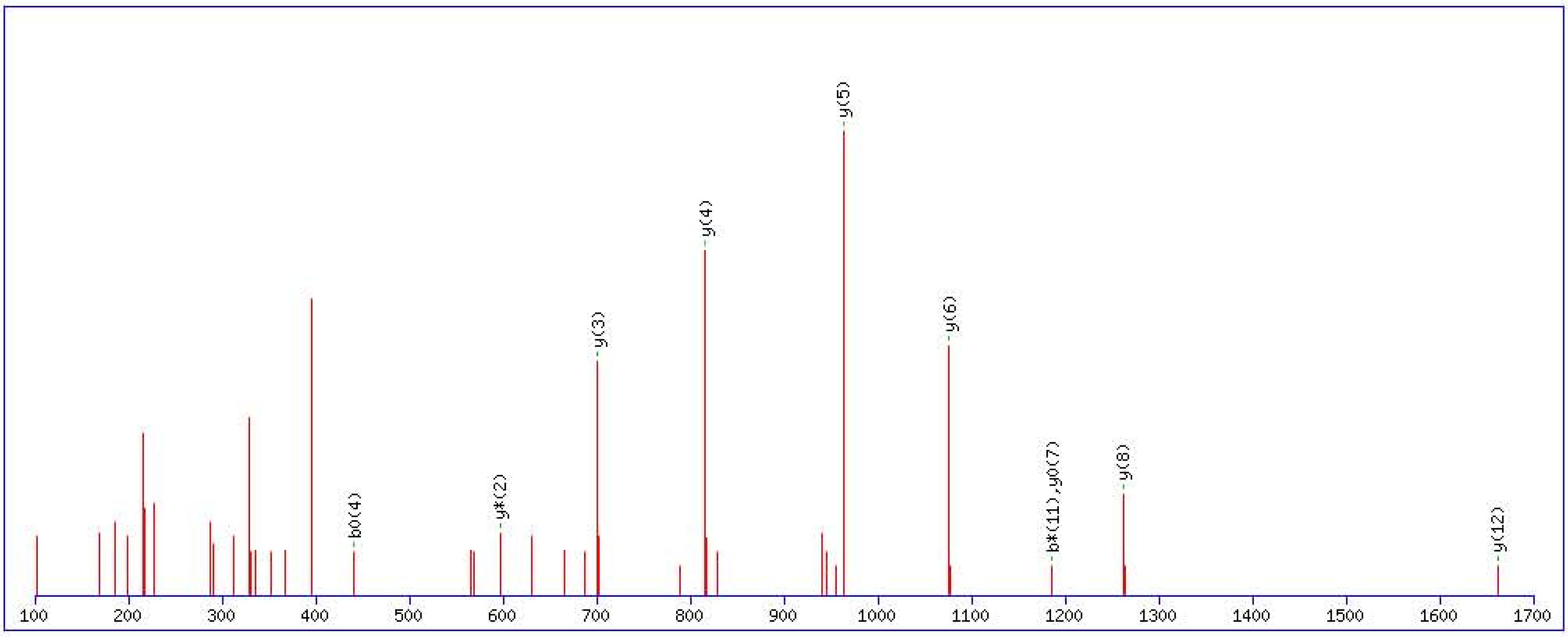
Mascot Search Results

Peptide View

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

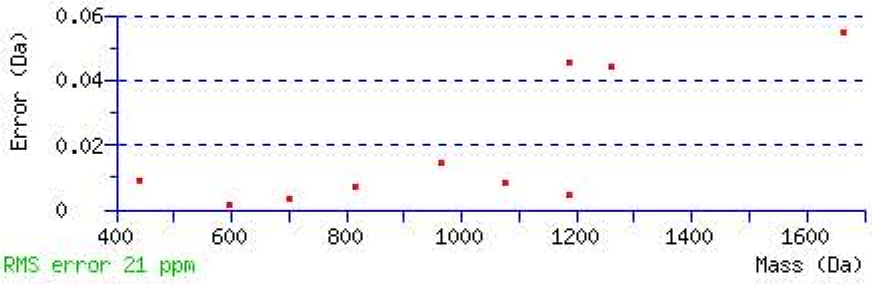
Match to Query 40239: 1902.963852 from(635.328560,3+) rtinseconds(2698) index(51595)
Title: Locus:1.1.1.2987.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

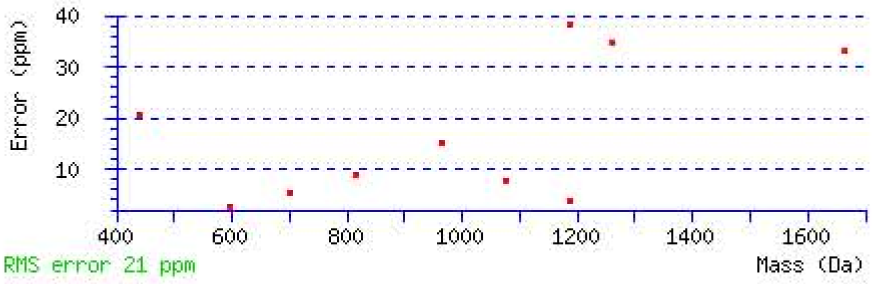
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1902.950928
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.00043
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
36.1	1902.950928	0.012924	ELSEALGQIFDSQR
0.3	1902.947739	0.016113	MKEQLREMENLR

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

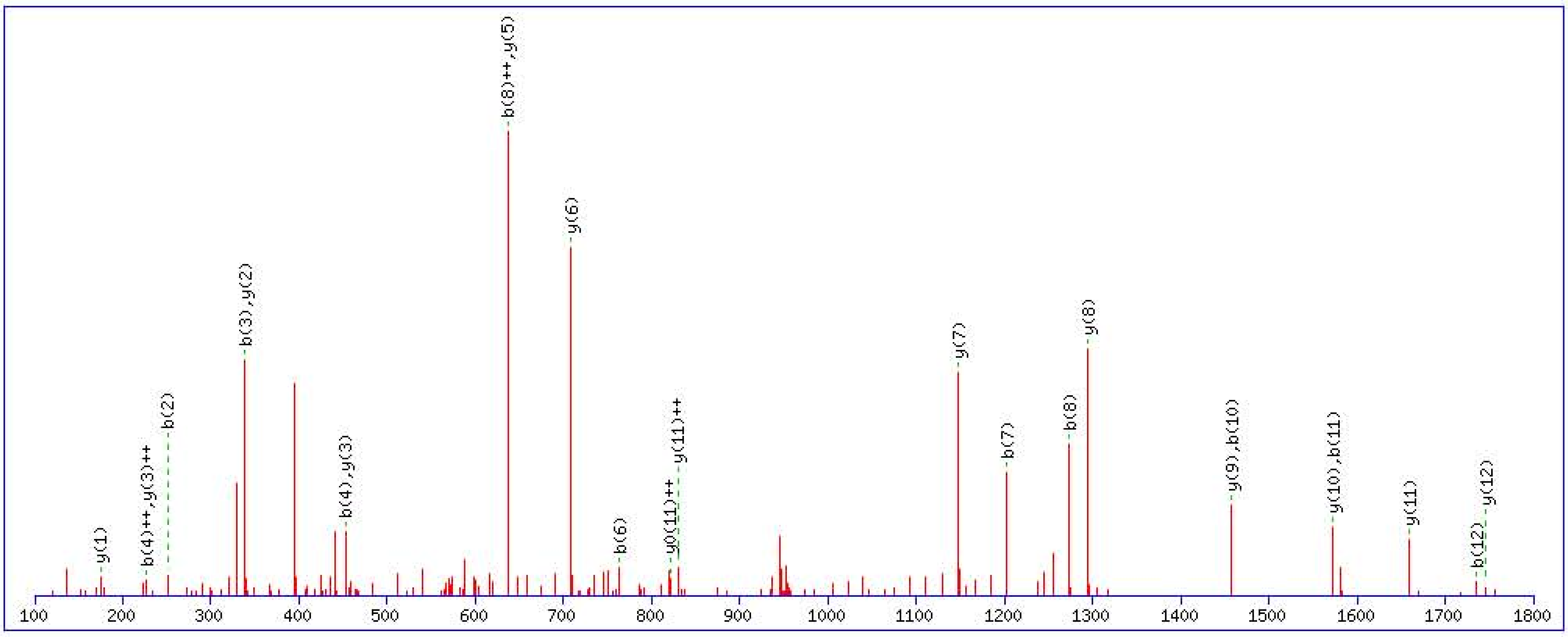
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

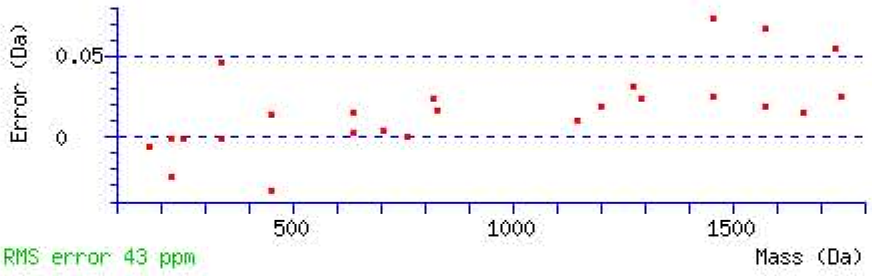
Match to Query 40361: 1908.863048 from(955.438800,2+) rtinseconds(2088) index(47915)
Title: Locus:1.1.1.2775.19 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

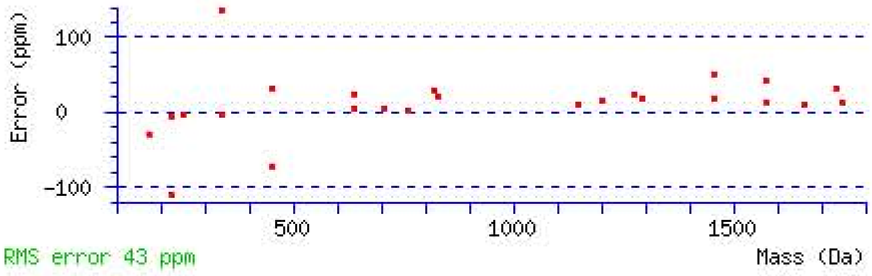
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1908.835236
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 81  Expect: 4.3e-008
Matches : 25/126 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	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
80.9	1908.835236	0.027812	YSSDYFQAPSDYR
2.3	1908.868927	-0.005879	YSSYRSHDHYQR

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

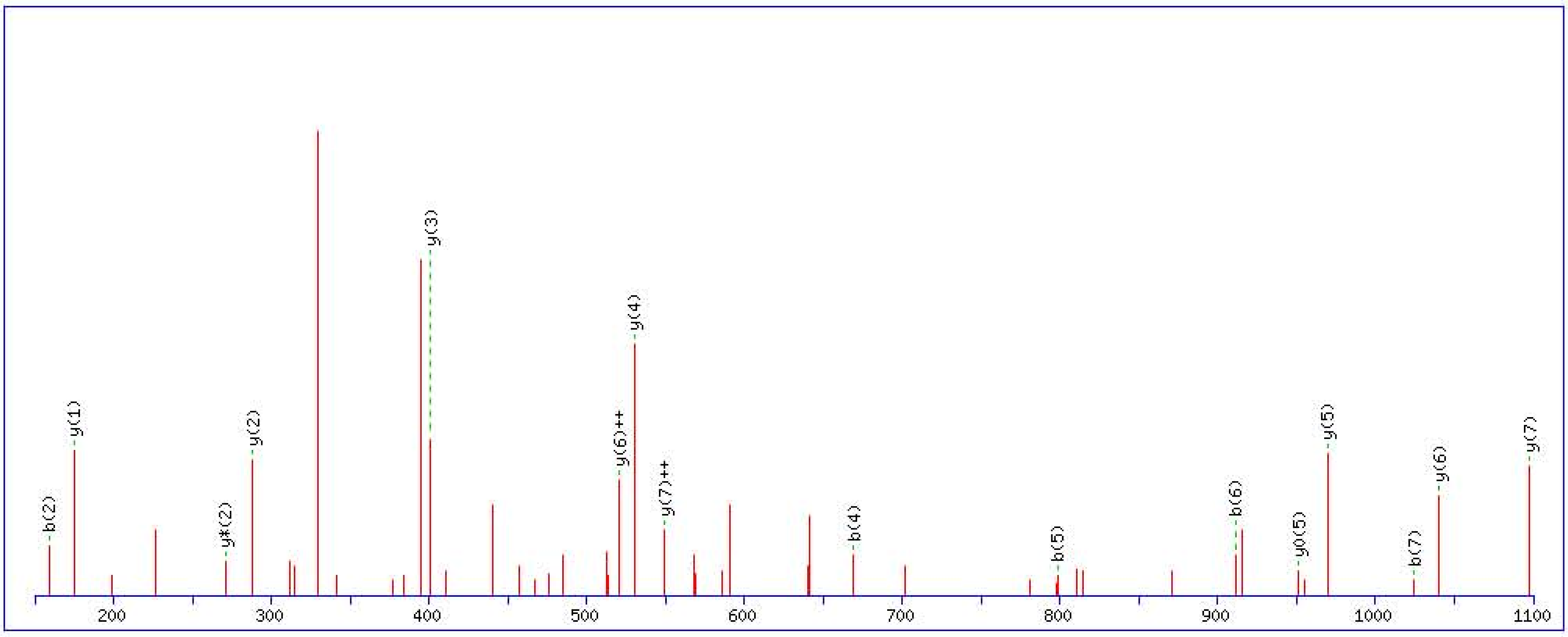
Mascot Search Results

Peptide View

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

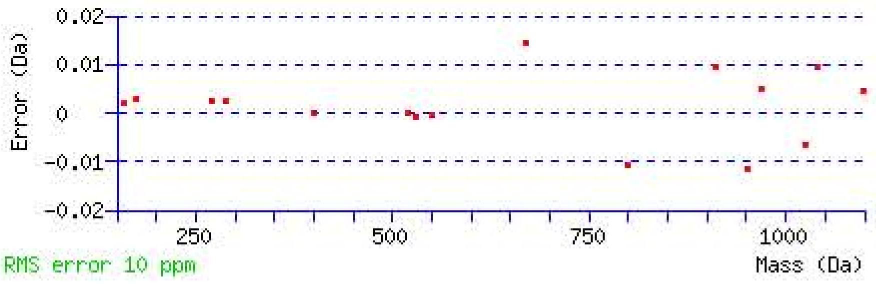
Match to Query 20300: 1197.656568 from(599.835560,2+) rtinseconds(1916) index(4340)
Title: Locus:1.1.1.3219.22 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

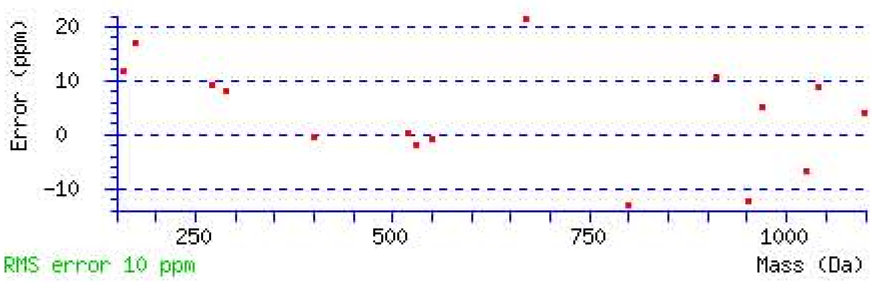
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 49  Expect: 0.00034
Matches : 16/72 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	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
48.6	1197.653961	0.002607	TGAQELLR
21.8	1197.653961	0.002607	QTQEILR
21.4	1197.653961	0.002607	TQQLLER
20.4	1197.653961	0.002607	QTQEILR
14.0	1197.653961	0.002607	QQEITIR
13.9	1197.646545	0.010023	RSPQEAEILR
11.0	1197.671692	-0.015124	LGLENAEALR
10.1	1197.653961	0.002607	TQQLLER
9.9	1197.653961	0.002607	QTEQLLR
9.9	1197.653961	0.002607	QTEQLLR

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

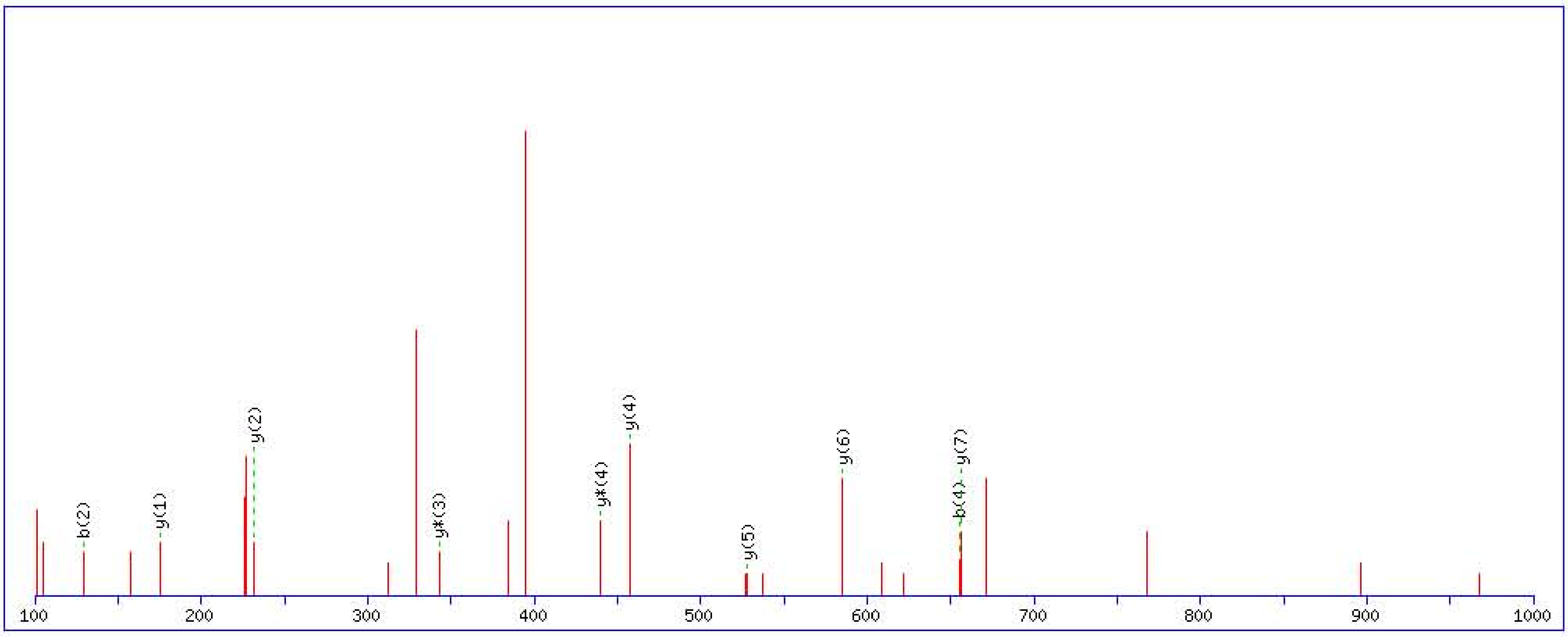
Mascot Search Results

Peptide View

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

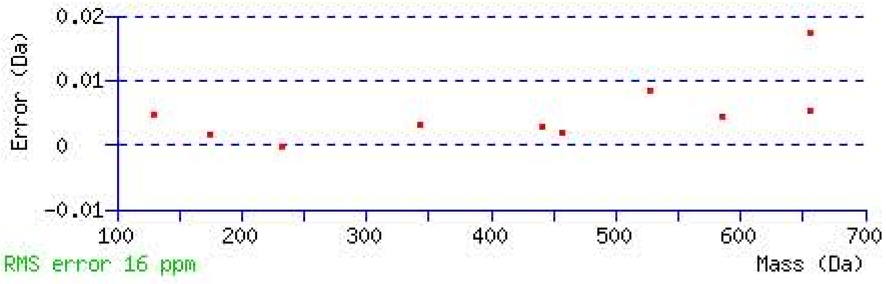
Match to Query 23210: 1309.658022 from(437.559950,3+) rtinseconds(1267) index(826)
Title: Locus:1.1.1.2993.3 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

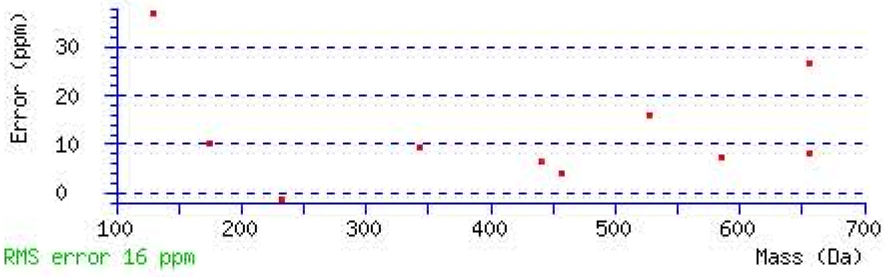
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1309.656097
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 27 **Expect:** 0.015
Matches : 10/94 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							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	**655.323208**	328.165242	638.296659	319.651968	637.312643	319.159960	Q	1095.572776	548.290026	1078.546227	539.776752			8
5	726.360322	363.683799	709.333773	355.170525	708.349757	354.678517	A	***656.347450***	328.677363	639.320901	320.164088			7
6	783.381786	392.194531	766.355237	383.681257	765.371221	383.189249	G	***585.310336***	293.158806	568.283787	284.645532			6
7	854.418900	427.713088	837.392351	419.199814	836.408335	418.707806	A	***528.288872***	264.648074	511.262323	256.134799			5
8	951.471664	476.239470	934.445115	467.726196	933.461099	467.234188	P	***457.251758***	229.129517	440.225209	220.616242			4
9	1079.530242	540.268759	1062.503693	531.755485	1061.519677	531.263477	Q	360.198994	180.603135	343.172445	172.089860			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
26.7	1309.656097	0.001925	GASQAGAPQGR
24.2	1309.656097	0.001925	GASQAGAPQGR
7.0	1309.669998	-0.011976	LIETQMERFK
0.5	1309.648895	0.009127	WDIFQVMISR

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

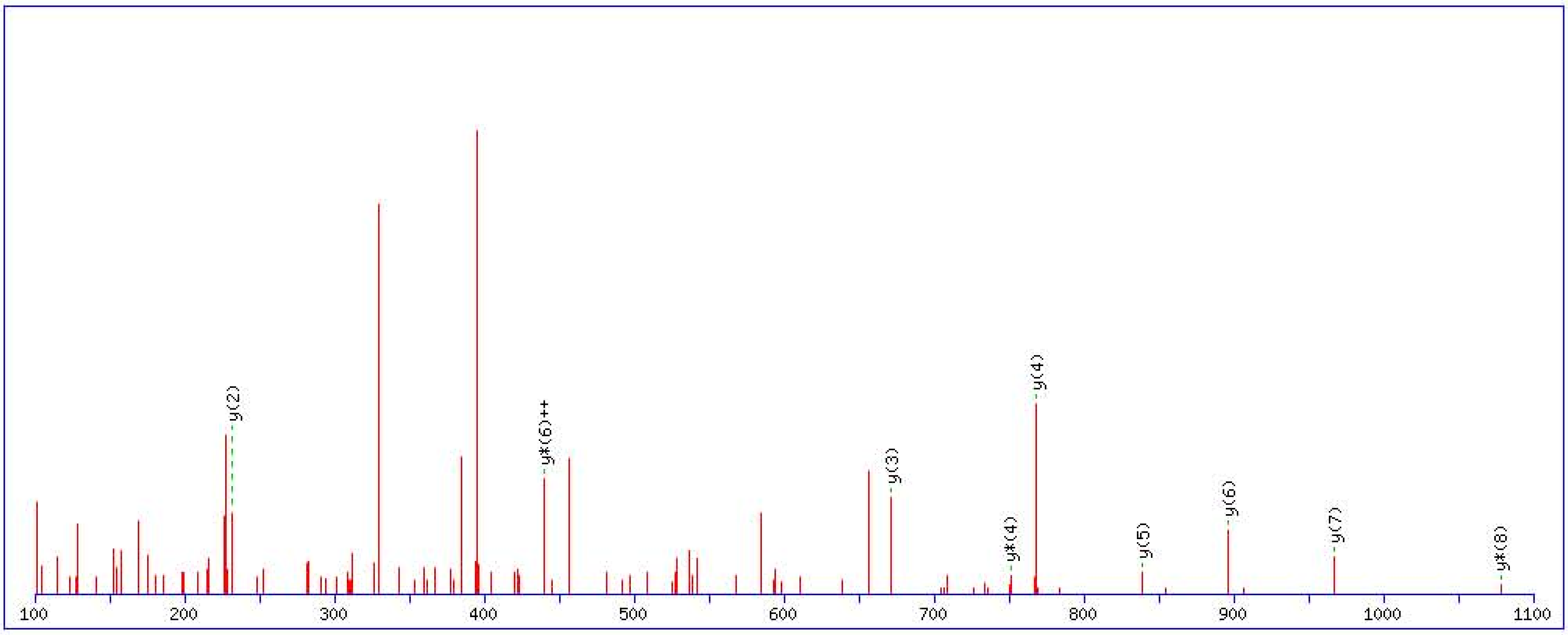
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

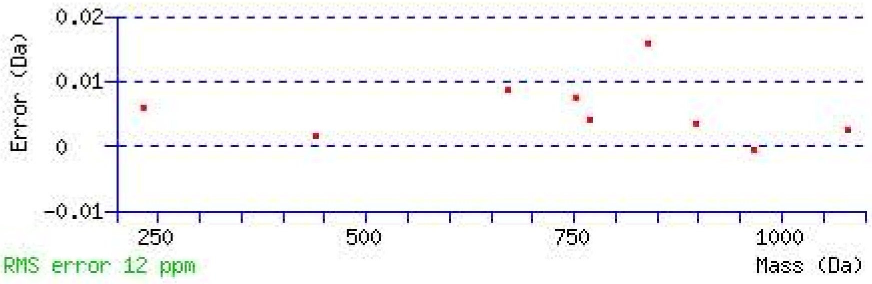
Match to Query 23212: 1309.658022 from(437.559950,3+) rtinseconds(1276) index(853)
Title: Locus:1.1.1.2996.2 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

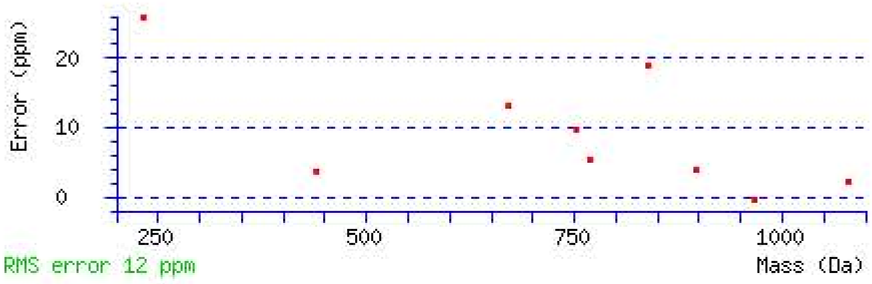
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1309.656097
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 29 **Expect:** 0.002
Matches : 9/94 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					**G**							**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
29.0	1309.656097	0.001925	GASQAGAPQGR
18.6	1309.656097	0.001925	GASQAGAPQGR
0.1	1309.669998	-0.011976	LIETQMERFK

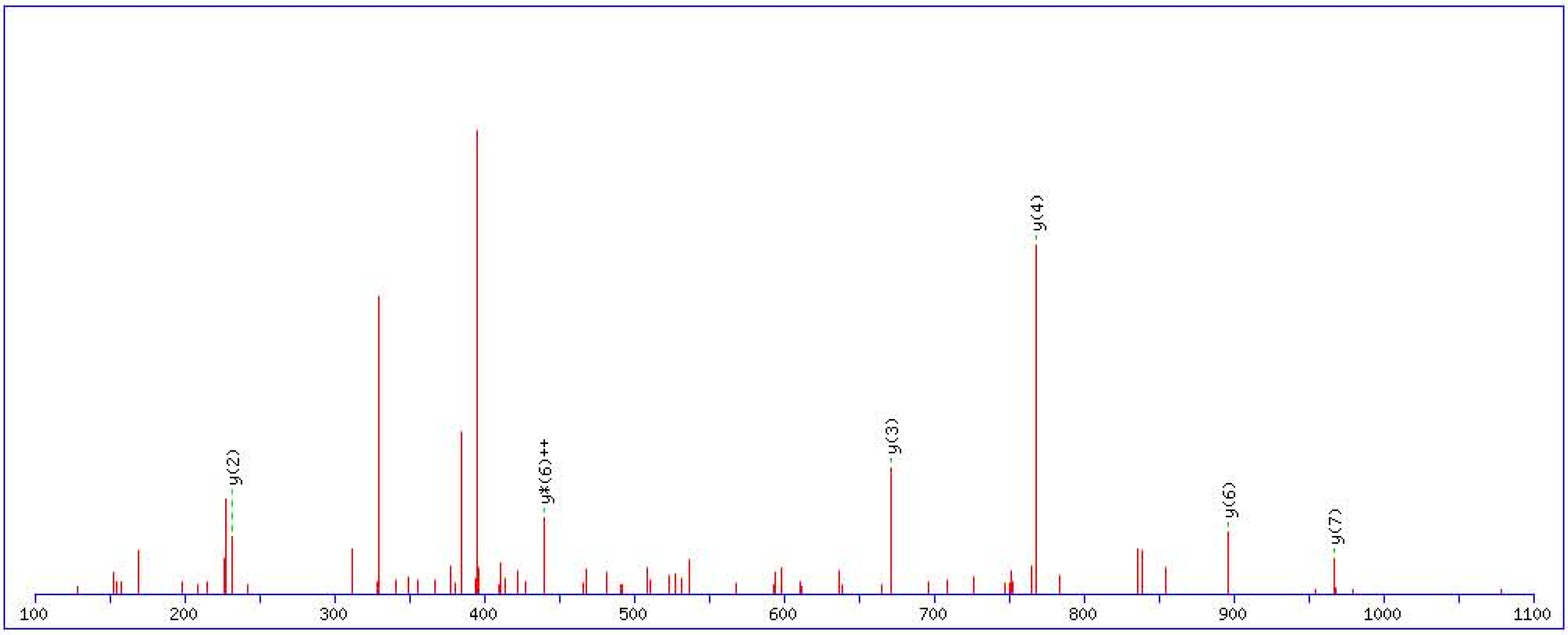
{MATRIX} *{SCIENCE}* Mascot Search Results

Peptide View

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

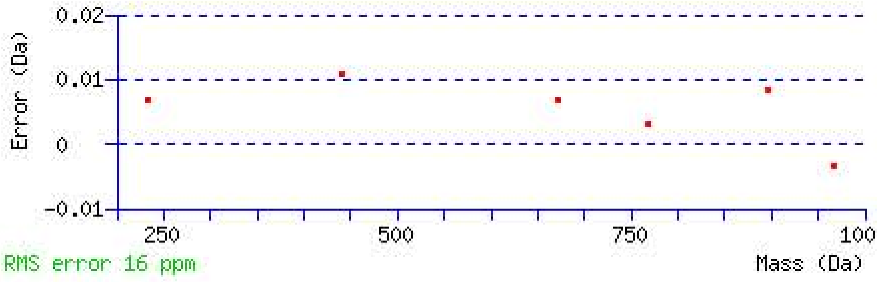
Match to Query 34092: 1620.824142 from(541.281990,3+) rtinseconds(1695) index(3235)
Title: Locus:1.1.1.3142.5 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

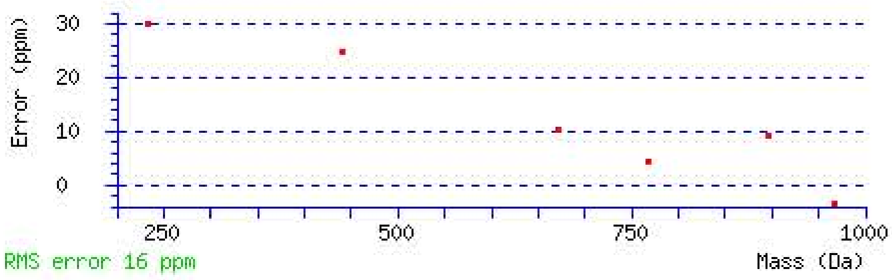
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 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: 28 **Expect:** 0.0041
Matches : 6/94 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							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





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
28.1	1620.822845	0.001297	GASQAGAPQGR
2.6	1620.815430	0.008712	SLQAQEDARHR

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

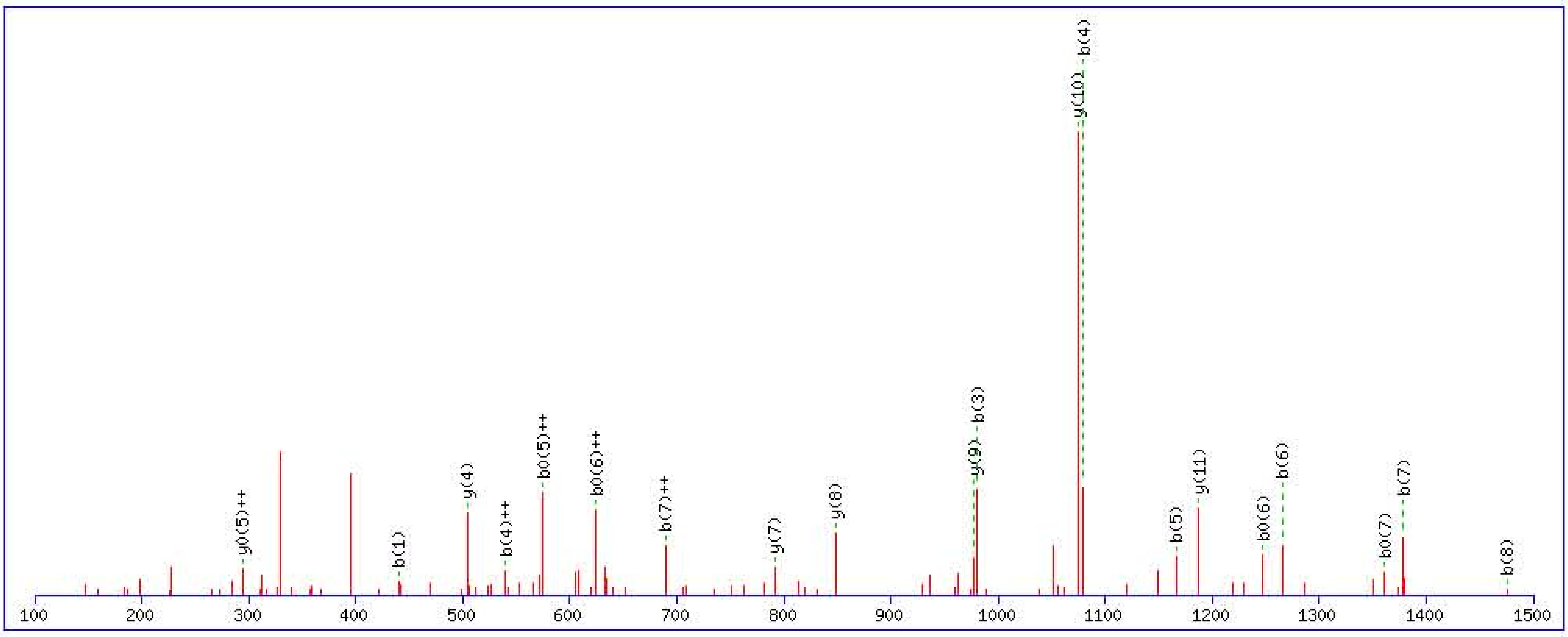
Mascot Search Results

Peptide View

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

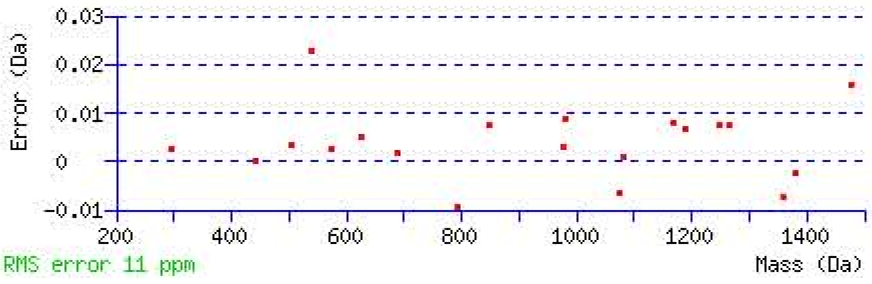
Match to Query 49930: 2451.299832 from(818.107220,3+) rtinseconds(2614) index(36446)
Title: Locus:1.1.1.3459.18 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

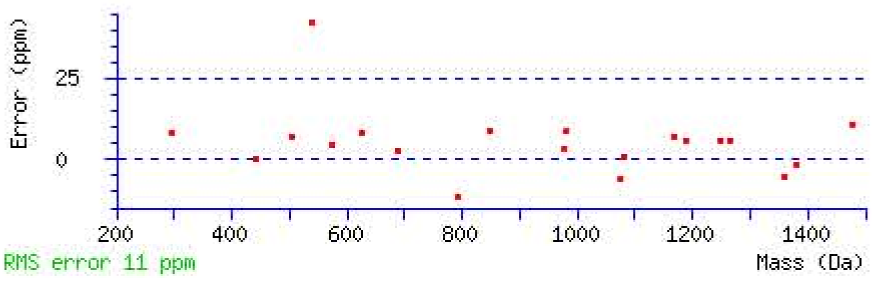
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 59  Expect: 9.2e-006
Matches : 21/182 fragment ions using 27 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							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
59.4	2451.290588	0.009244	QTQVSVLPEGGETPLFK
5.5	2451.277130	0.022702	GFPSDTQLLDLRRNHFPSVPR
3.7	2451.330780	-0.030948	RQFQSQLADLQQLPDILK
3.7	2451.330780	-0.030948	RQFQSQLADLQQLPDILK
2.0	2451.301590	-0.001758	ATKRISHMPSRPELSAVATDLR

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

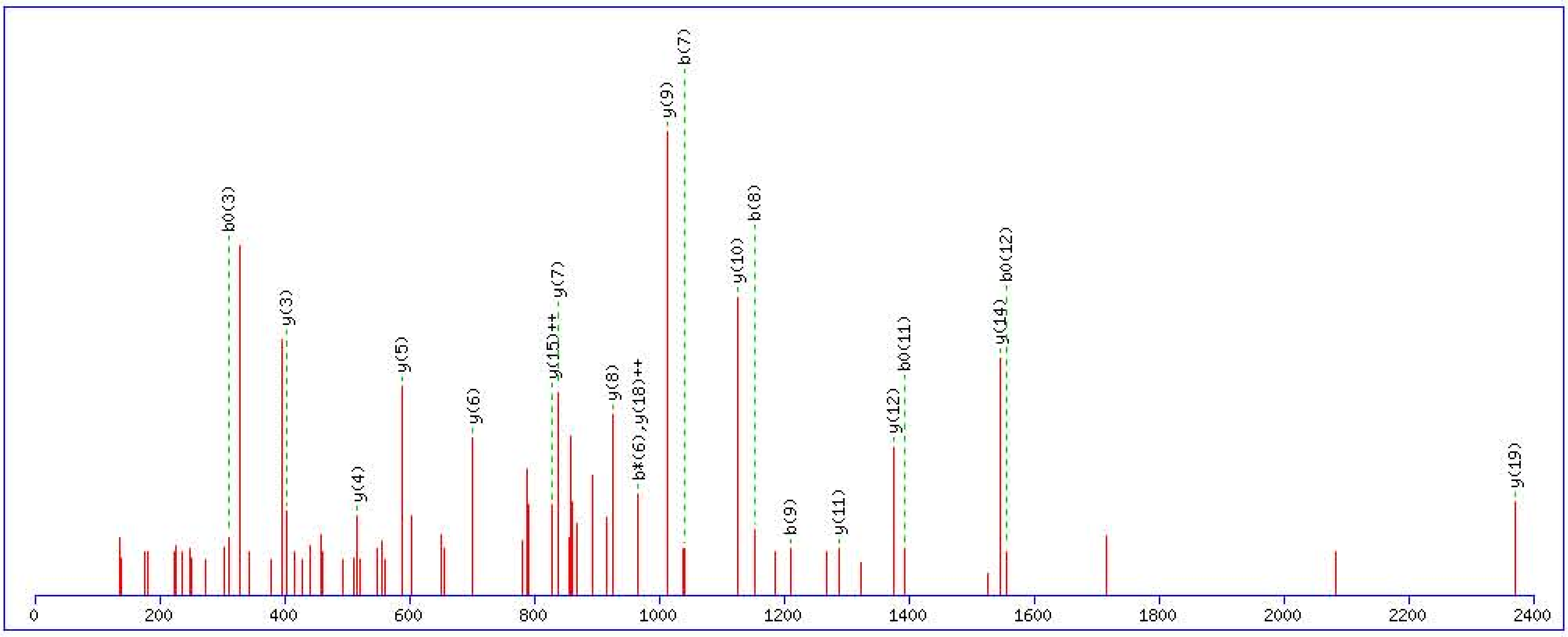
Mascot Search Results

Peptide View

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

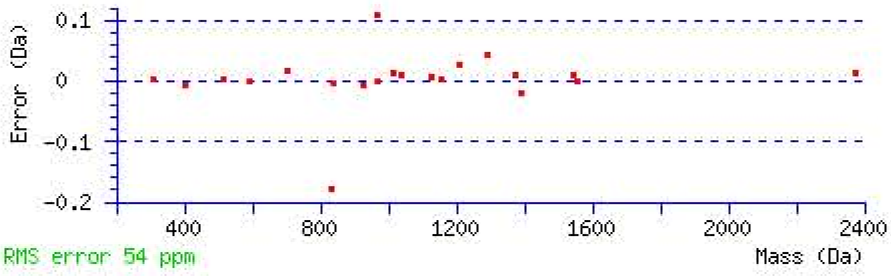
Match to Query 52731: 2697.327612 from(900.116480,3+) rtinseconds(2568) index(36105)
Title: Locus:1.1.1.3443.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

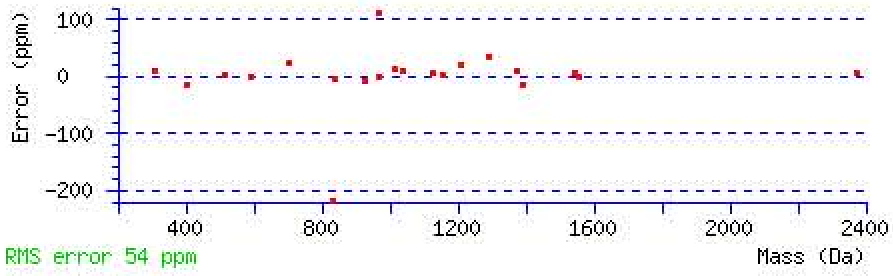
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2697.306824
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 78  Expect: 4.2e-007
Matches : 21/244 fragment ions using 32 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							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
78.2	2697.306824	0.020788	DPDQTDGLGLSYLSSHIANVER

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

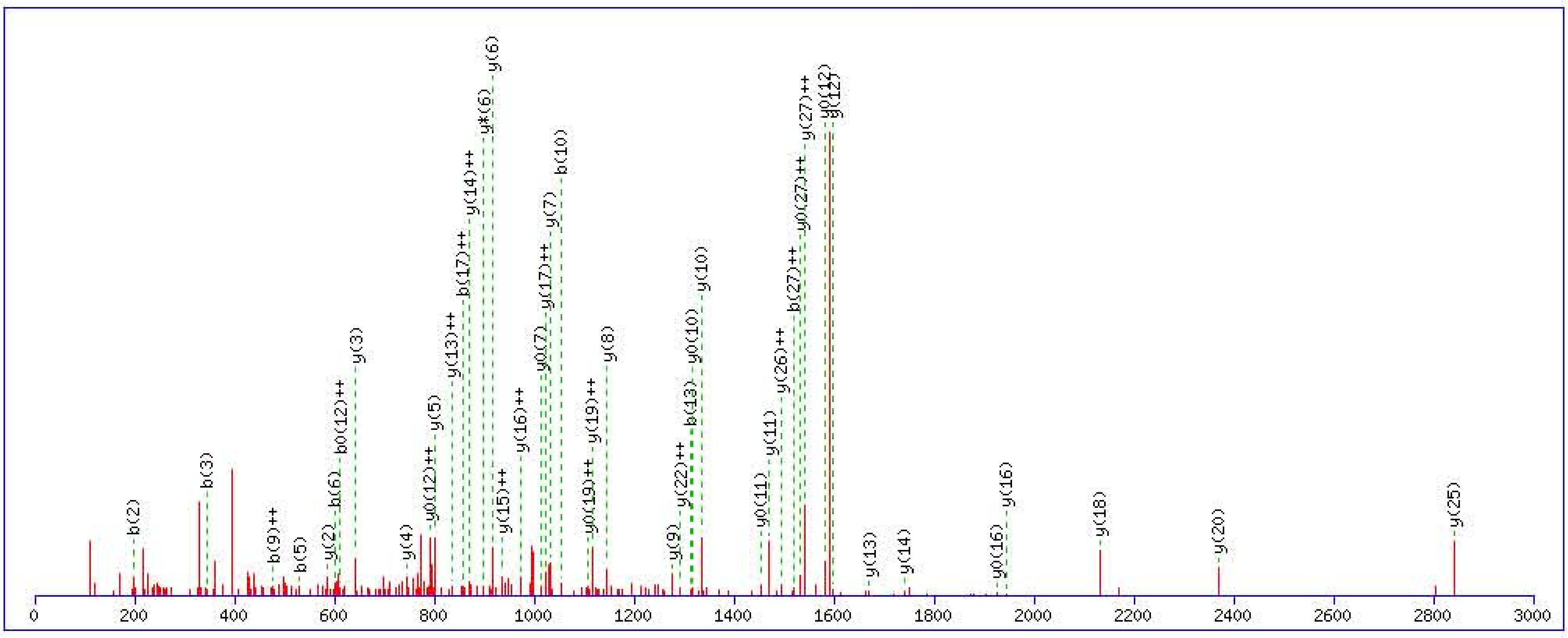
Mascot Search Results

Peptide View

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

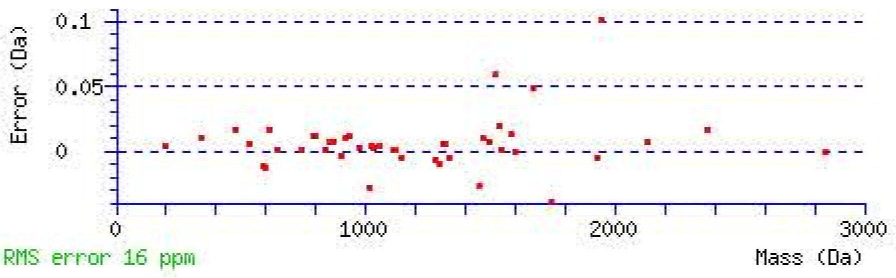
Match to Query 57487: 3183.445896 from(796.868750,4+) rtinseconds(1972) index(4799)
Title: Locus:1.1.1.3238.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

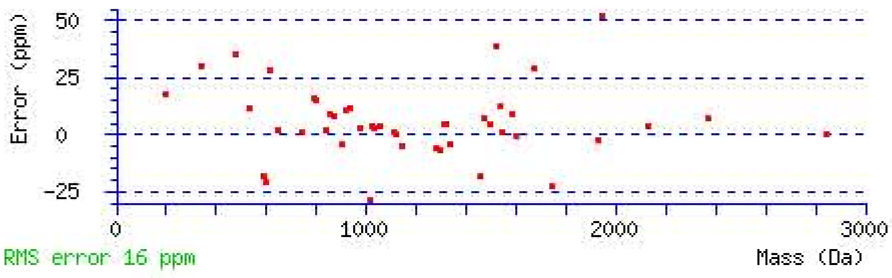
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3183.442383
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q27 : Biotin:Thermo-21345 (Q)
Ions Score: 59 **Expect:** 1.4e-005
Matches : 45/280 fragment ions using 148 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
59.1	3183.442383	0.003513	VPFDAATLHTSTAMAAQHGMDDDGTGQK
15.0	3183.442383	0.003513	VPFDAATLHTSTAMAAQHGMDDDGTGQK

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

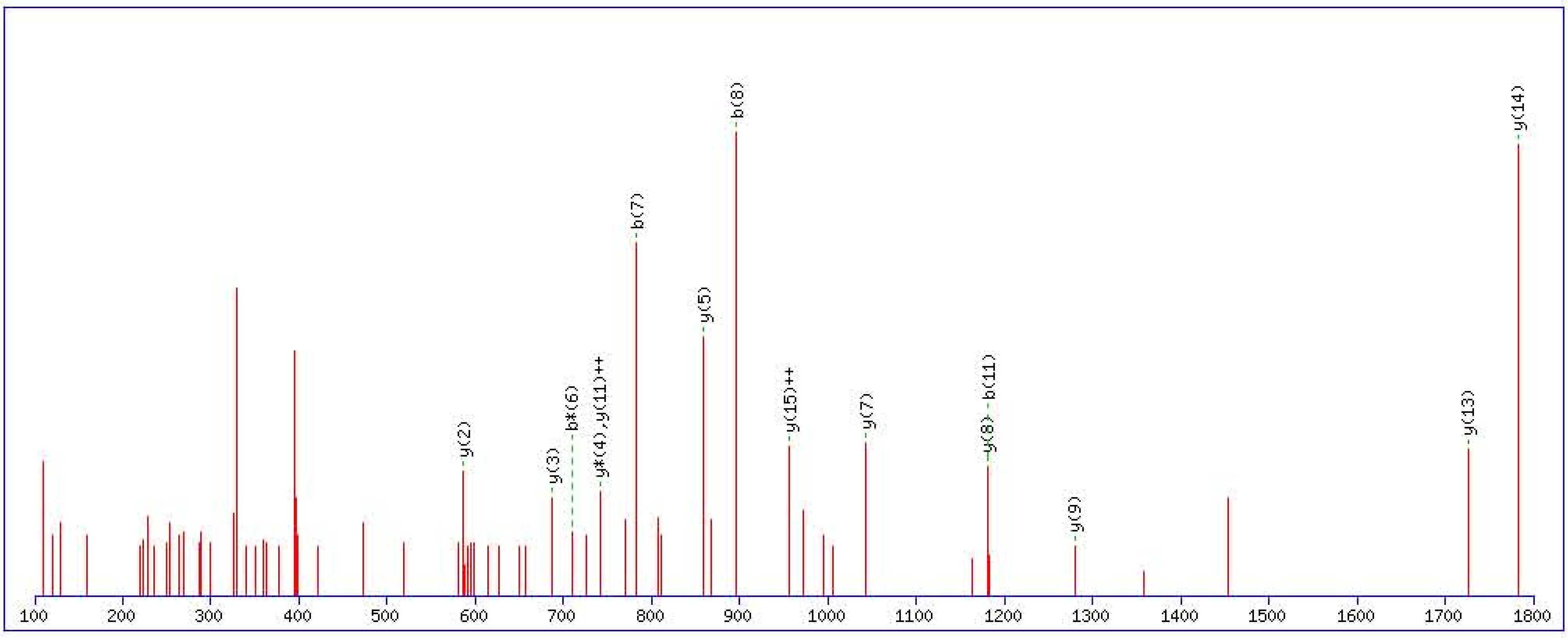
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VIHDNFGIVEGLMTTVHAITATQK**
Found in **G3P_HUMAN**, Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3

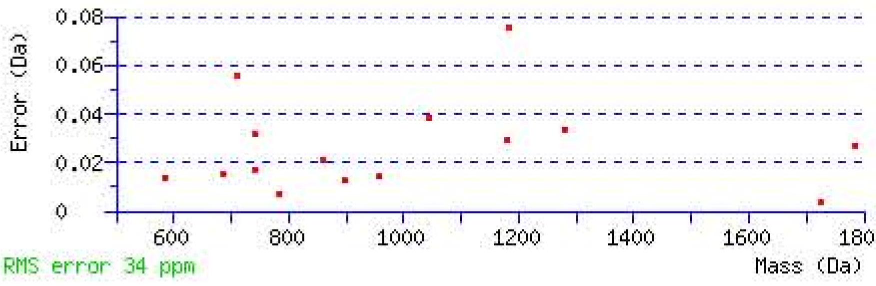
Match to Query 55282: 2905.553696 from(727.395700,4+) rtinseconds(3118) index(54674)
Title: Locus:1.1.1.3130.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

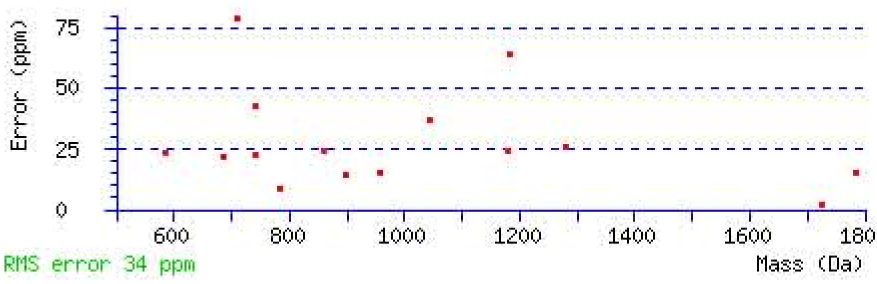
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2905.519424
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q23    : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.0012
Matches : 15/258 fragment ions using 26 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
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
37.6	2905.519424	0.034272	VIHDNFGIVEGLMTTVHAITATQK
6.5	2905.511490	0.042206	TLQEIFQAENTIMLLERSIMAK
2.4	2905.511490	0.042206	TLQEIFQAENTIMLLERSIMAK

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

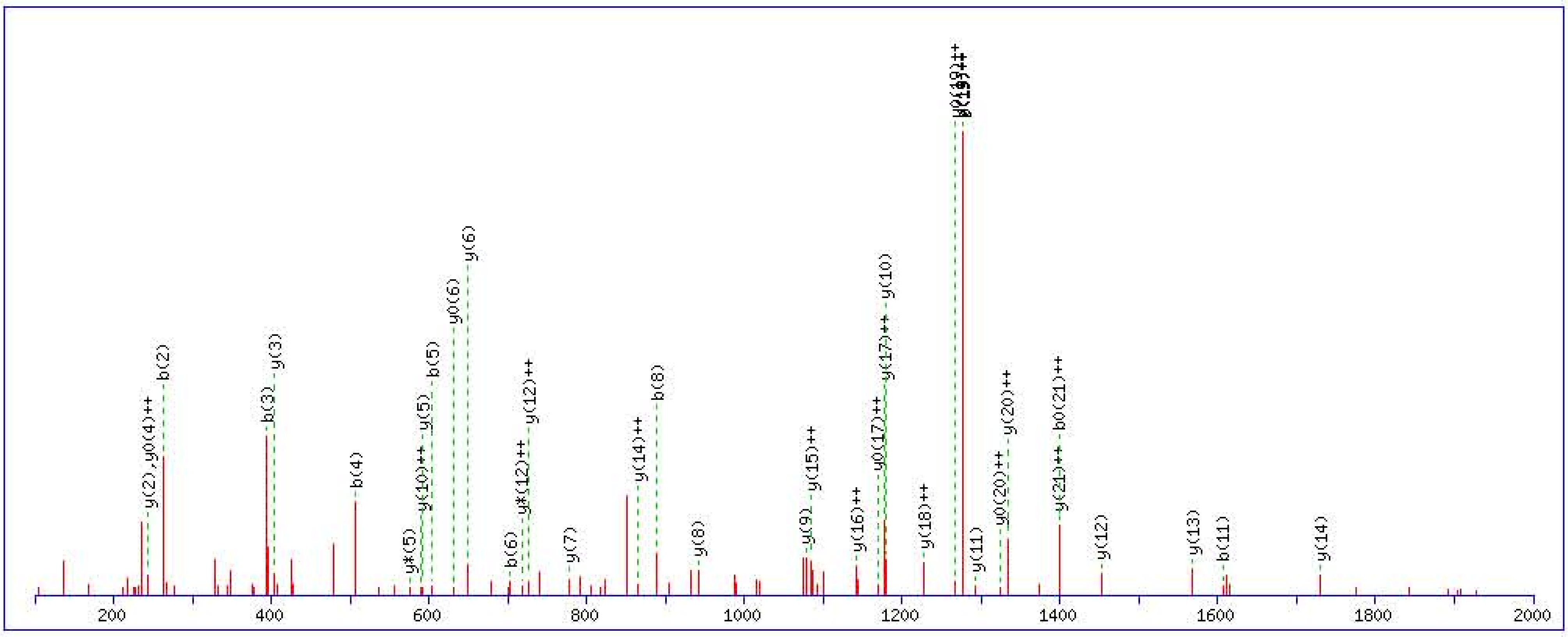
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YVMLPVADQYDCITHYEGSTCPK**
Found in **HPTR_HUMAN**, Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=1 SV=2

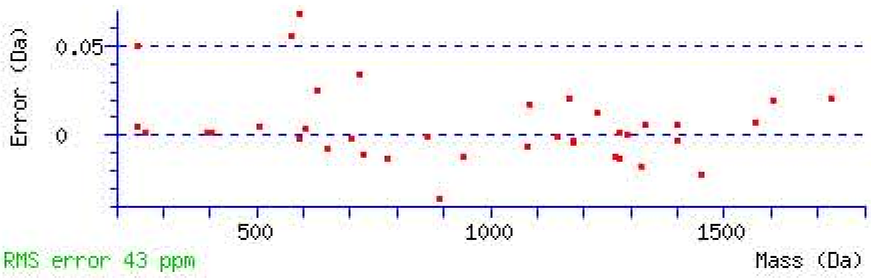
Match to Query 56471: 3057.389382 from(1020.137070,3+) rtinseconds(2456) index(35470)
Title: Locus:1.1.1.3404.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

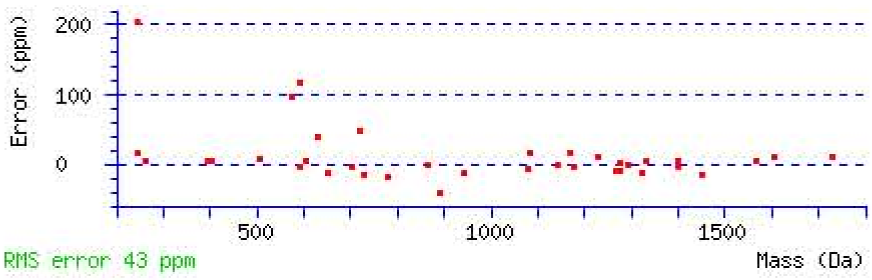
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3057.374466
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 54 **Expect:** 4.5e-005
Matches : 38/228 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	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
53.6	3057.374466	0.014916	YVMLPVADQYDCITHYEGSTCPK

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

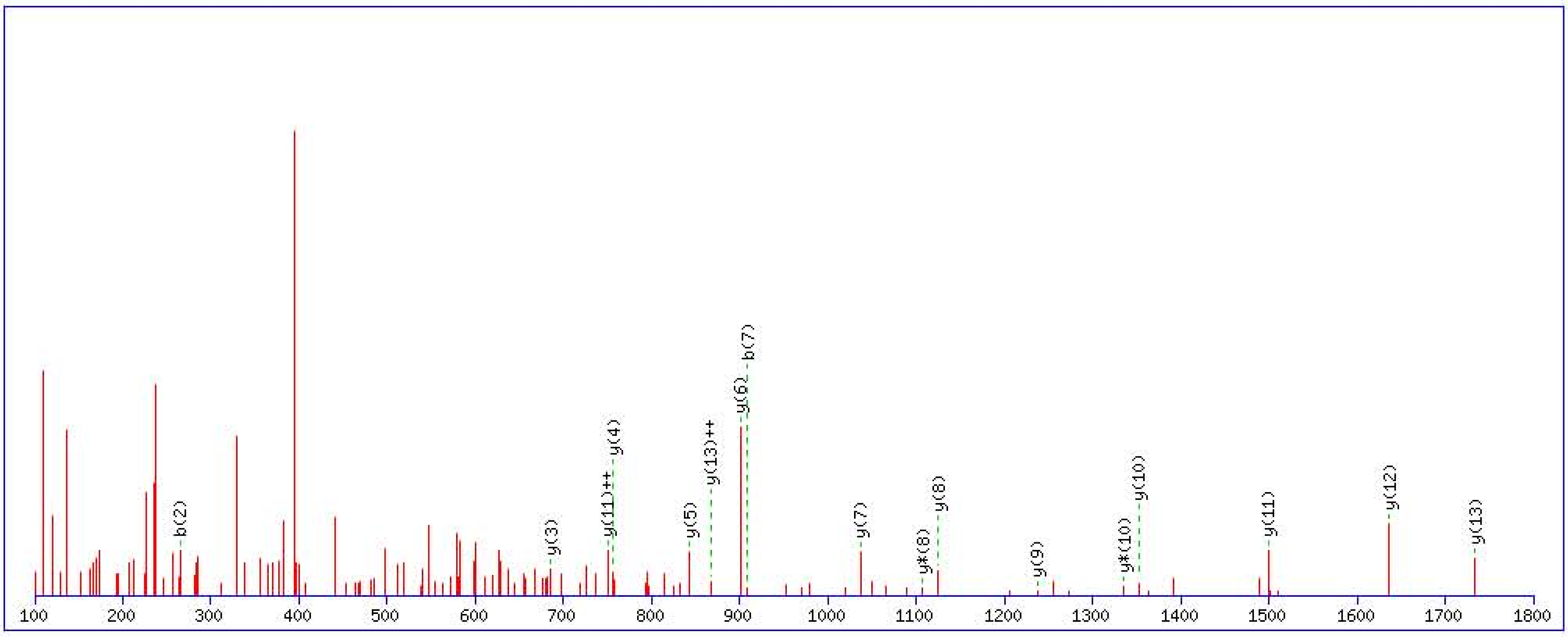
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TYFPHFDLSHGSAQVK**
Found in **HBA_HUMAN**, Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2

Match to Query 45062: 2144.051296 from(537.020100,4+) rtinseconds(2097) index(5434)
Title: Locus:1.1.1.3282.13 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\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 ●



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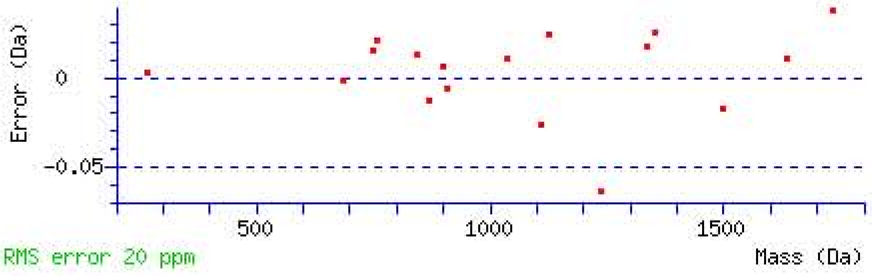
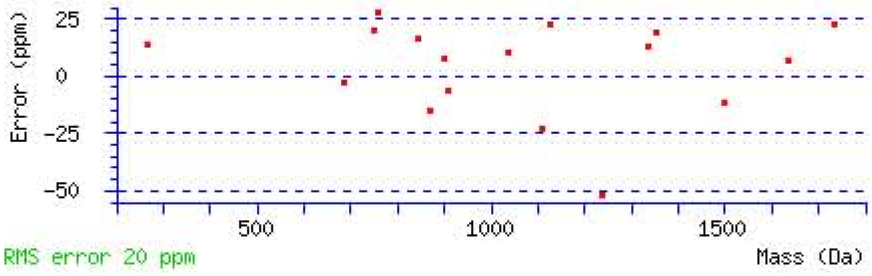
Monoisotopic mass of neutral peptide Mr(calc): 2144.051346
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0071
Matches : 17/146 fragment ions using 56 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	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
35.3	2144.051346	-0.000050	TYFPHFDLSHGSAQVK

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

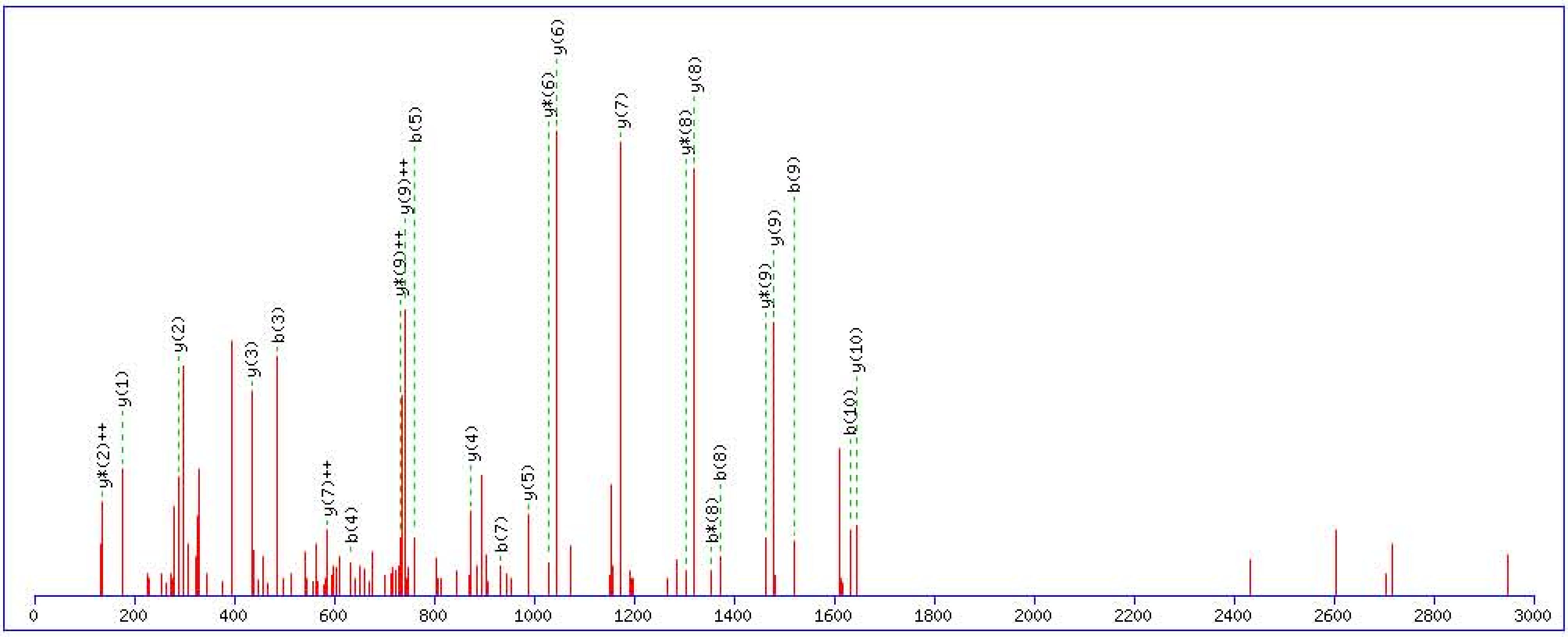
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YYCFQGNQFLR**
Found in **HEMO_HUMAN**, Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

Match to Query 38572: 1805.857648 from(903.936100,2+) rtinseconds(2332) index(64392)
Title: Locus:1.1.1.3438.15 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 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 ●



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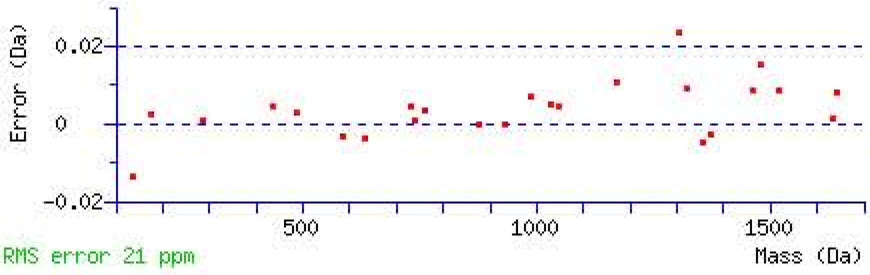
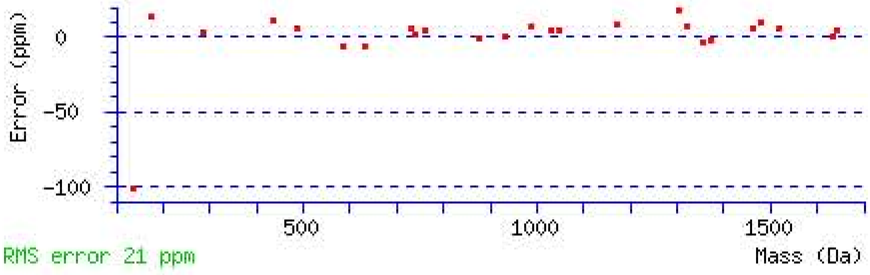
Monoisotopic mass of neutral peptide Mr(calc): 1805.838165
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 1.7e-005
Matches : 25/72 fragment ions using 46 most intense peaks   (help)
```

#	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
59.6	1805.838165	0.019483	YYCFQGNQFLR
56.1	1805.838165	0.019483	YYCFQGNQFLR
7.5	1805.844055	0.013593	LLQAPFTDCGDGPMLR
3.9	1805.845383	0.012265	WGTRGGFNGQMER
3.9	1805.873886	-0.016238	QMFQERSSR
3.9	1805.873032	-0.015384	VSTGDNWNGIMKDTLR
2.0	1805.866013	-0.008365	SMKMQQEVVEMR

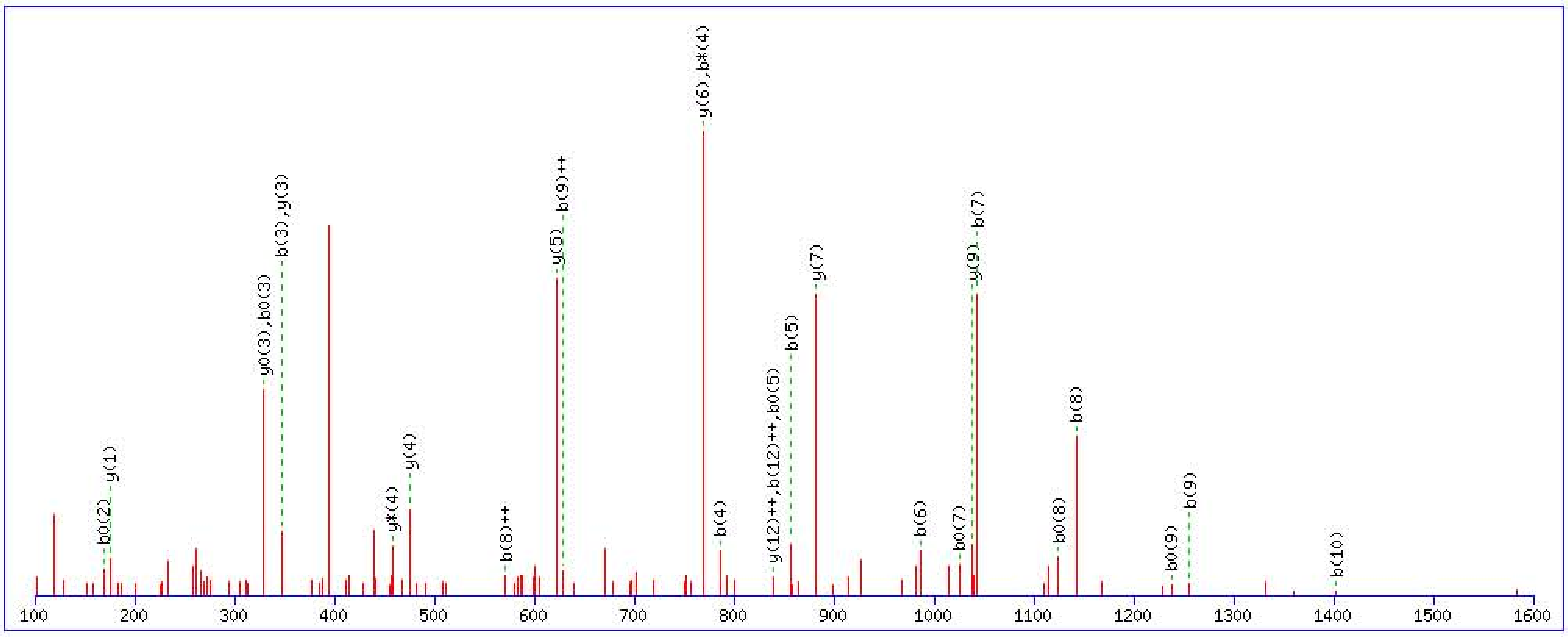
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GECQAEGVLFFQGDR**
Found in **HEMO_HUMAN**, Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

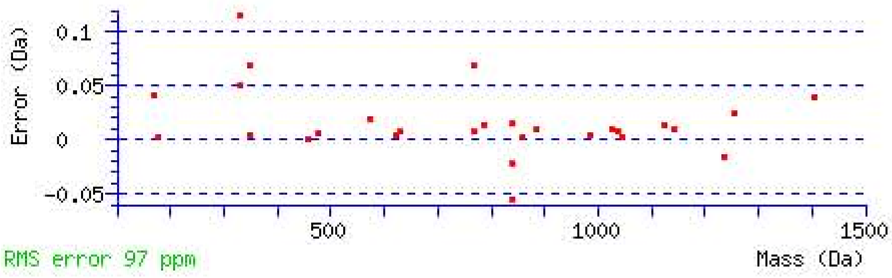
Match to Query 43064: 2022.944802 from(675.322210,3+) rtinseconds(2423) index(64809)
Title: Locus:1.1.1.3470.10 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

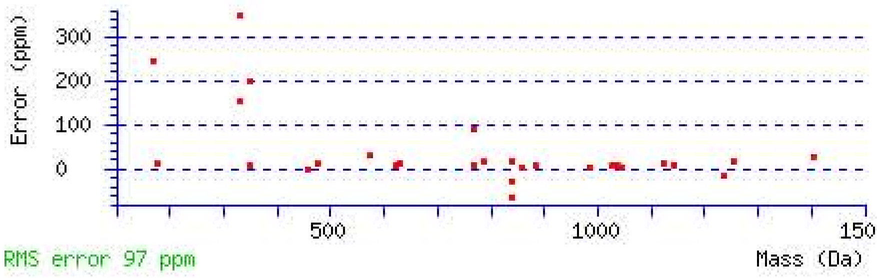
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2022.929184
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 0.00034
Matches : 28/158 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	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
46.5	2022.929184	0.015618	GECQAEGVLFFQGDR

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

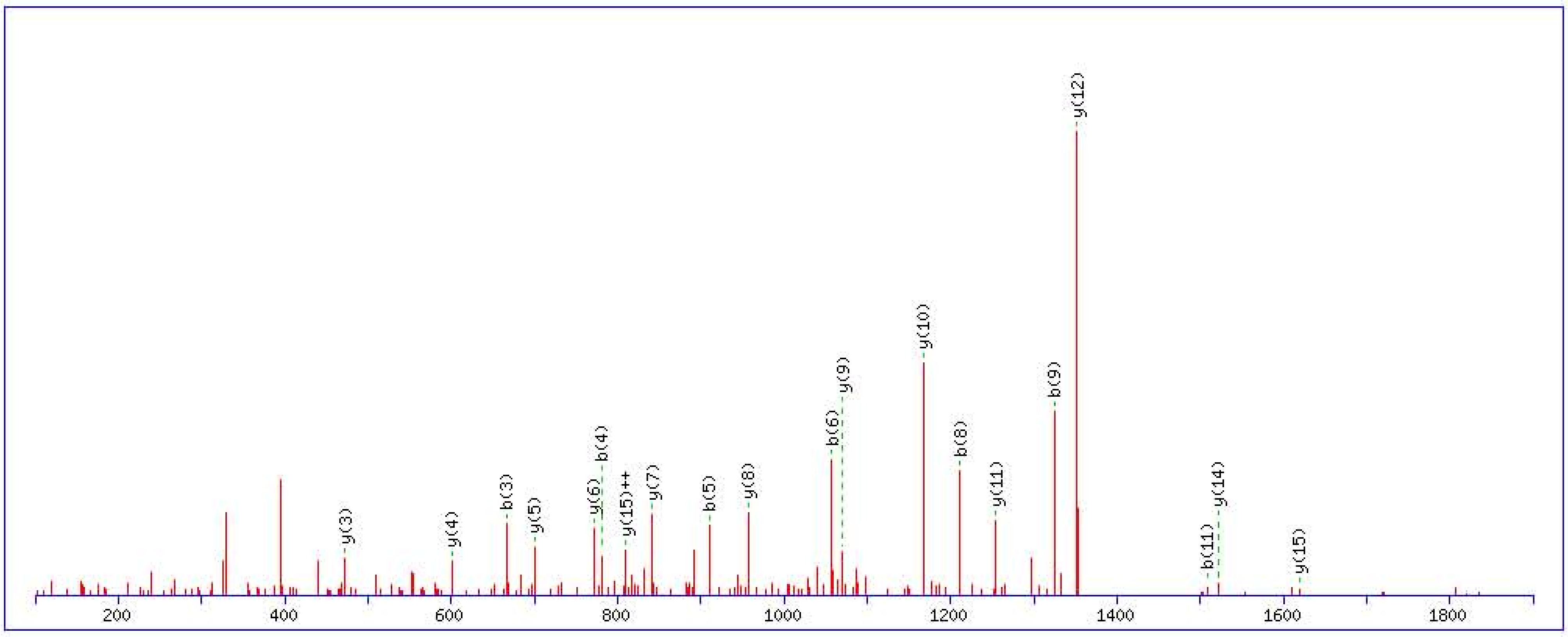
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLQDEFPGIPSPLDAAVECHR**
Found in **HEMO_HUMAN**, Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

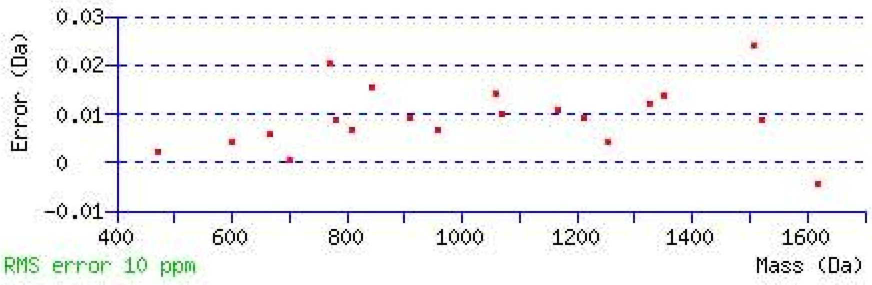
Match to Query 52541: 2674.337562 from(892.453130,3+) rtinseconds(2678) index(66101)
Title: Locus:1.1.1.3558.10 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

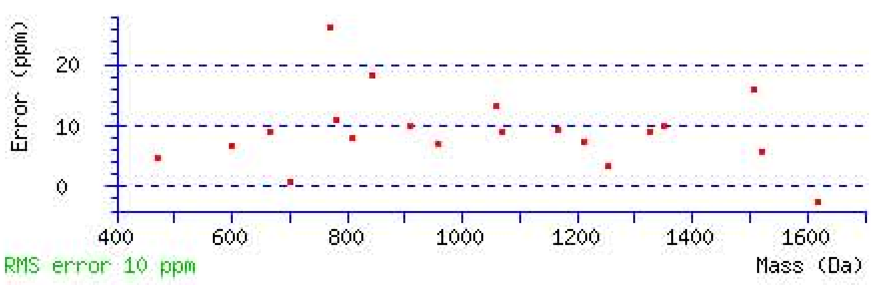
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2674.324722
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 73  Expect: 1.4e-006
Matches : 20/224 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							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
72.9	2674.324722	0.012840	LLQDEFPGIPSPLDAAVECHR

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

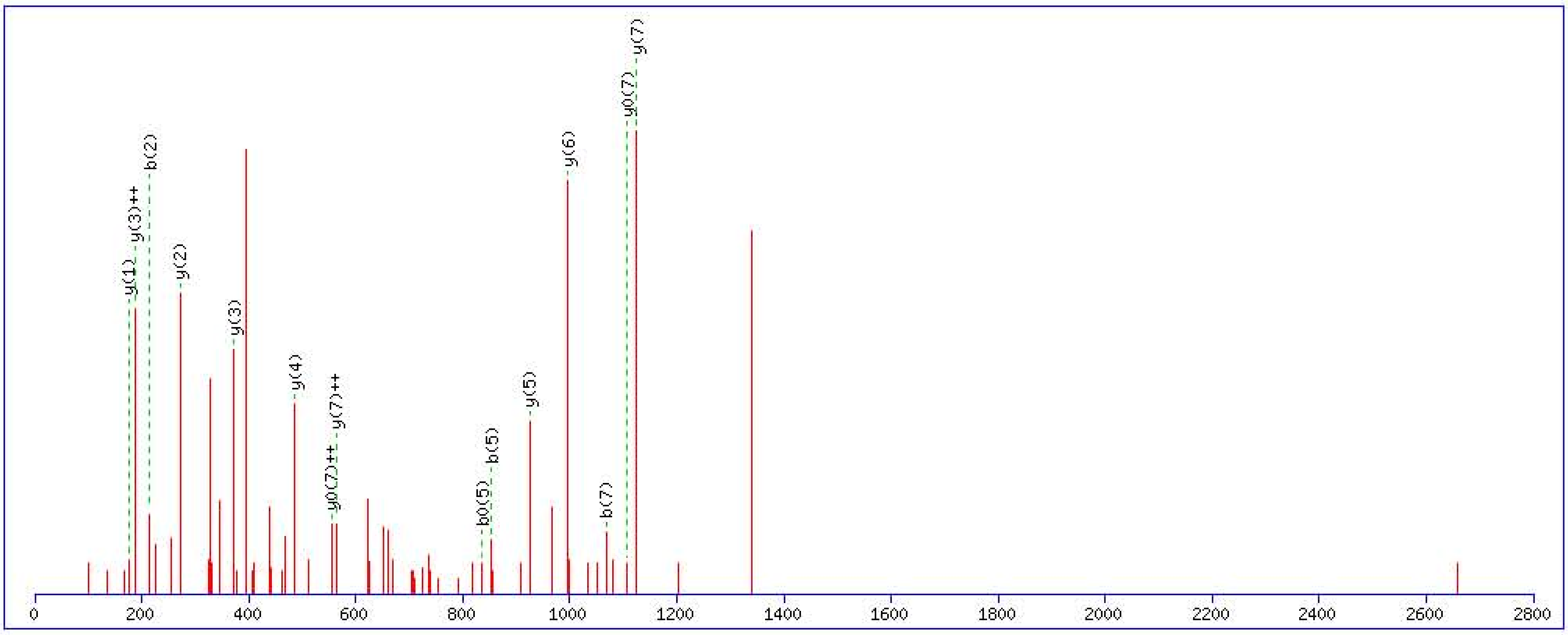
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLEAQLTPR**
Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

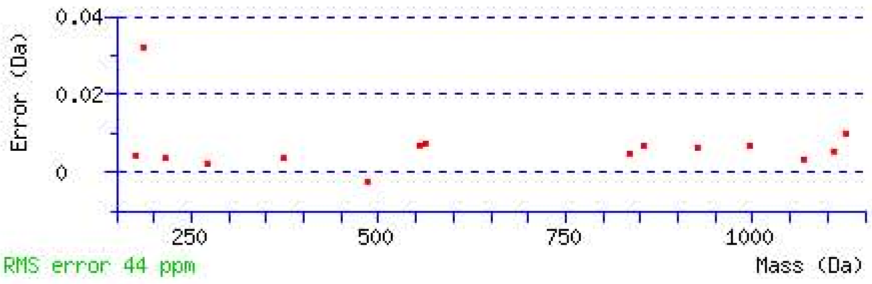
Match to Query 23773: 1338.736928 from(670.375740,2+) rtinseconds(1959) index(32889)
Title: Locus:1.1.1.3231.20 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

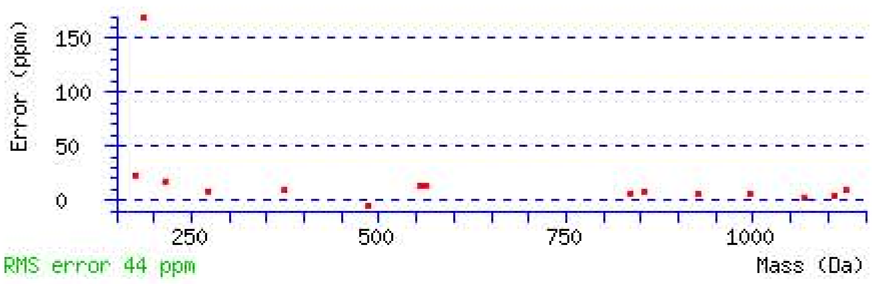
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1338.732941
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 0.00015
Matches : 15/84 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	**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
50.8	1338.732941	0.003987	TLEAQLTPR
15.0	1338.732956	0.003972	VDLQSLPTR
5.2	1338.725555	0.011373	VDTVAAEHLTRK
1.5	1338.726883	0.010045	ASAVRGSRPWPR
1.5	1338.725555	0.011373	RSPTVEPSTLPR

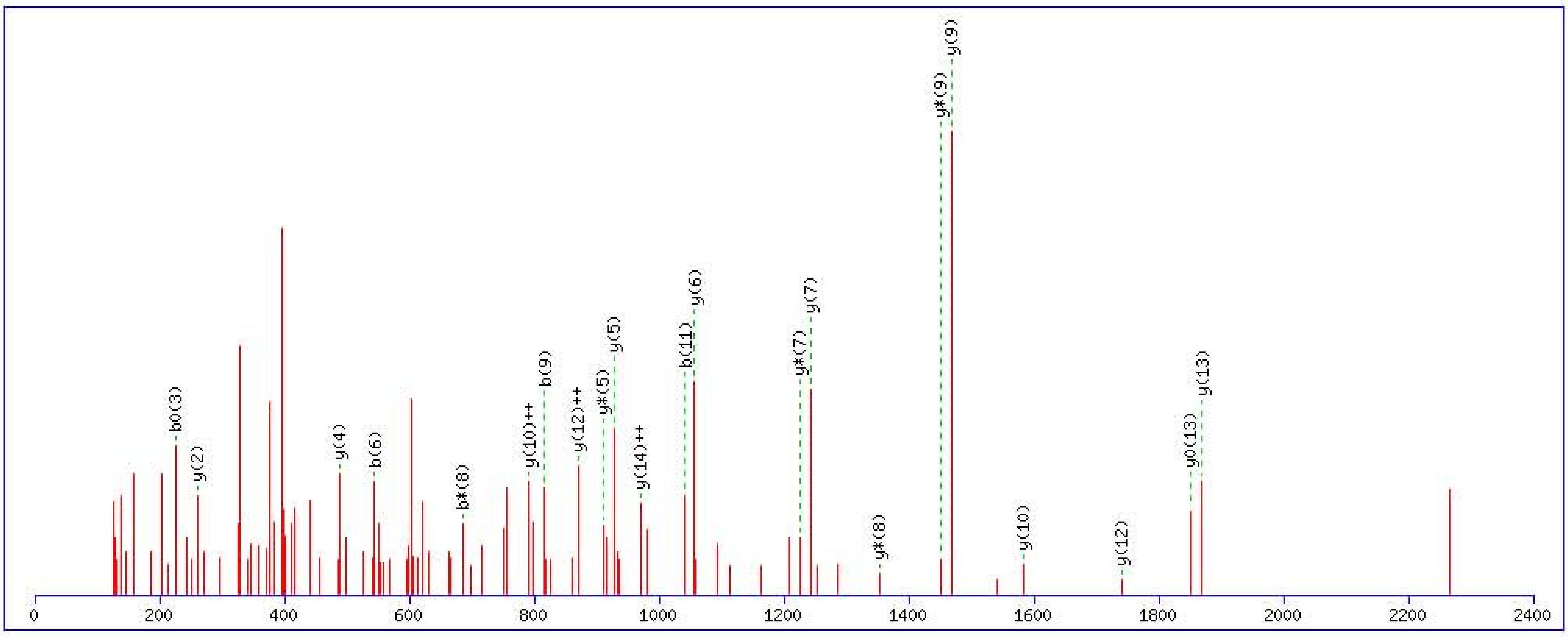
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGETAQSADPQWEQLNNK**
Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

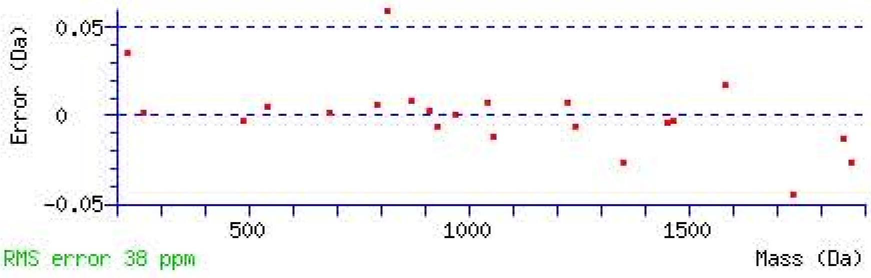
Match to Query 47504: 2283.060792 from(762.027540,3+) rtinseconds(1933) index(32684)
Title: Locus:1.1.1.3222.16 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

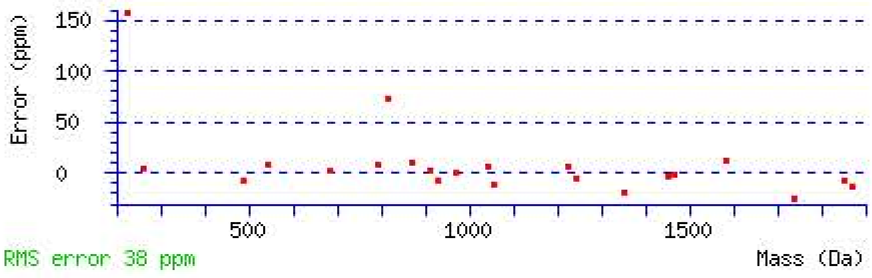
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2283.058975
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 55  Expect: 4.3e-005
Matches : 22/180 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	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
55.0	2283.058975	0.001817	GGETAQSADPQWEQLNNK
27.7	2283.058975	0.001817	GGETAQSADPQWEQLNNK
6.1	2283.058975	0.001817	GGETAQSADPQWEQLNNK

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

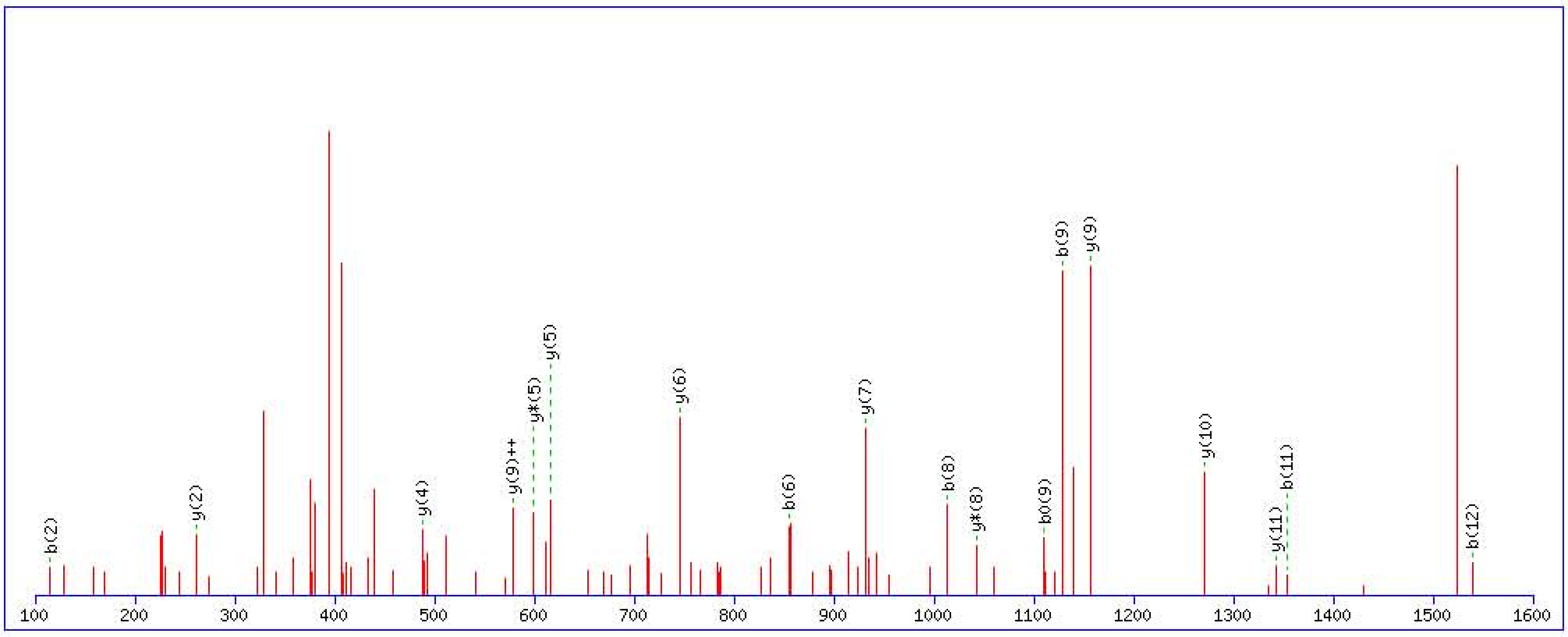
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGETAQSADPQWEQLNNK**
Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

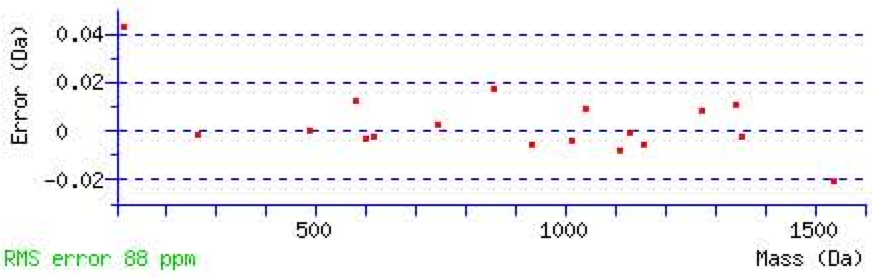
Match to Query 47505: 2283.065142 from(762.028990,3+) rtinseconds(1914) index(32519)
Title: Locus:1.1.1.3215.26 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

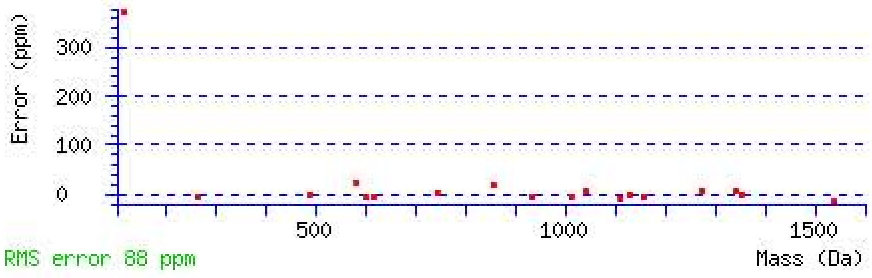
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2283.058975
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 47 **Expect:** 0.00031
Matches : 18/180 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							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
46.7	2283.058975	0.006167	GGETAQSADPQWEQLNNK
7.4	2283.058975	0.006167	GGETAQSADPQWEQLNNK

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

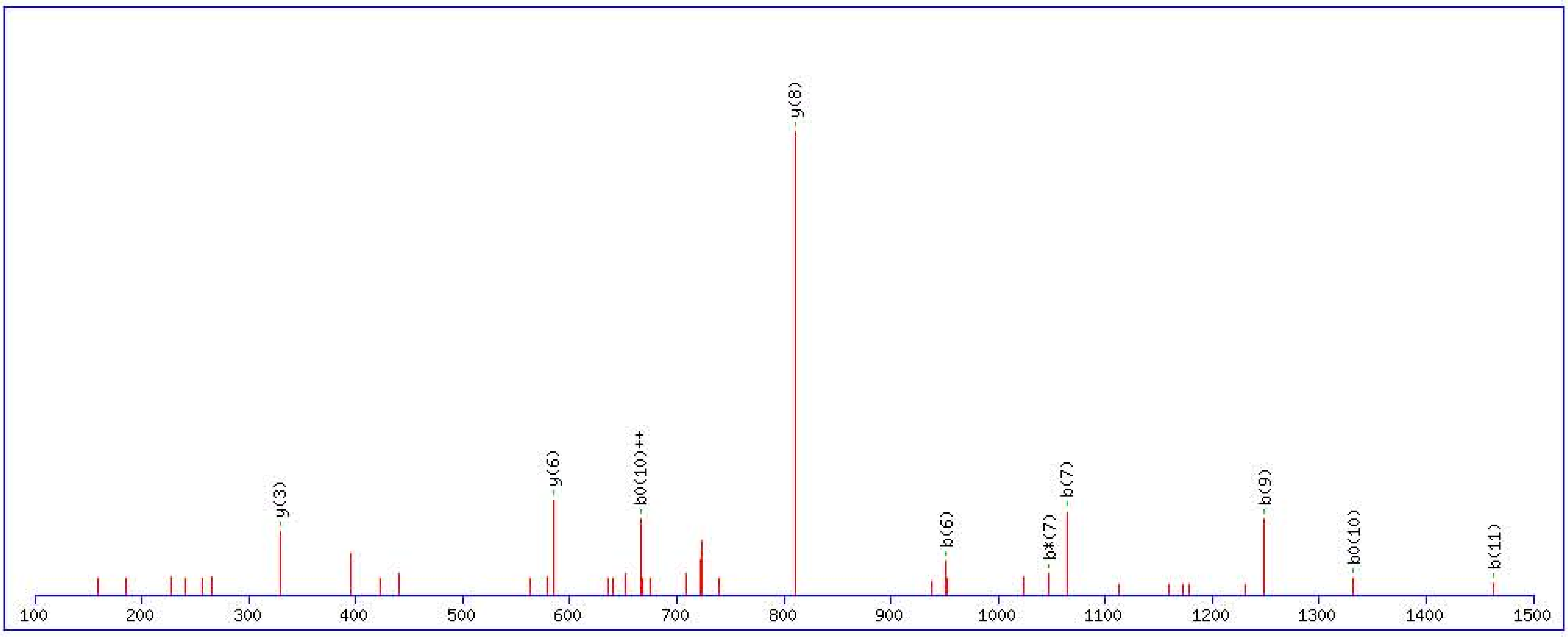
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQLSPDLLATLPEPASPGR**
Found in **HGFA_HUMAN**, Hepatocyte growth factor activator OS=Homo sapiens GN=HGFAC PE=1 SV=1

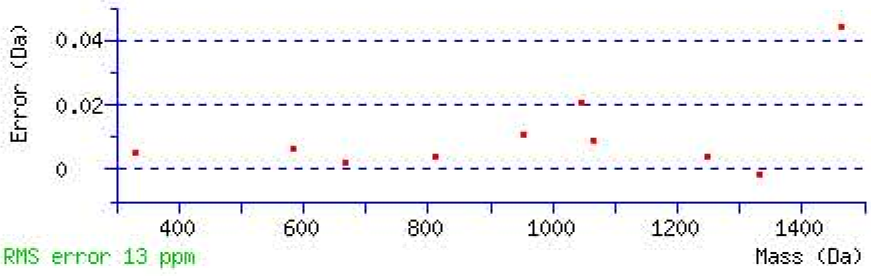
Match to Query 47286: 2271.242232 from(758.088020,3+) rtinseconds(2684) index(8650)
Title: Locus:1.1.1.3486.21 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

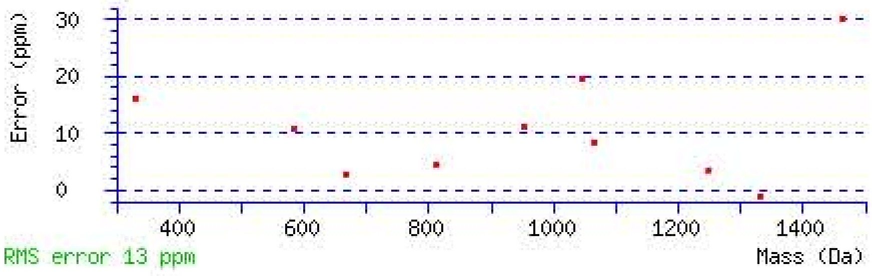
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 31  Expect: 0.0028
Matches : 10/202 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	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

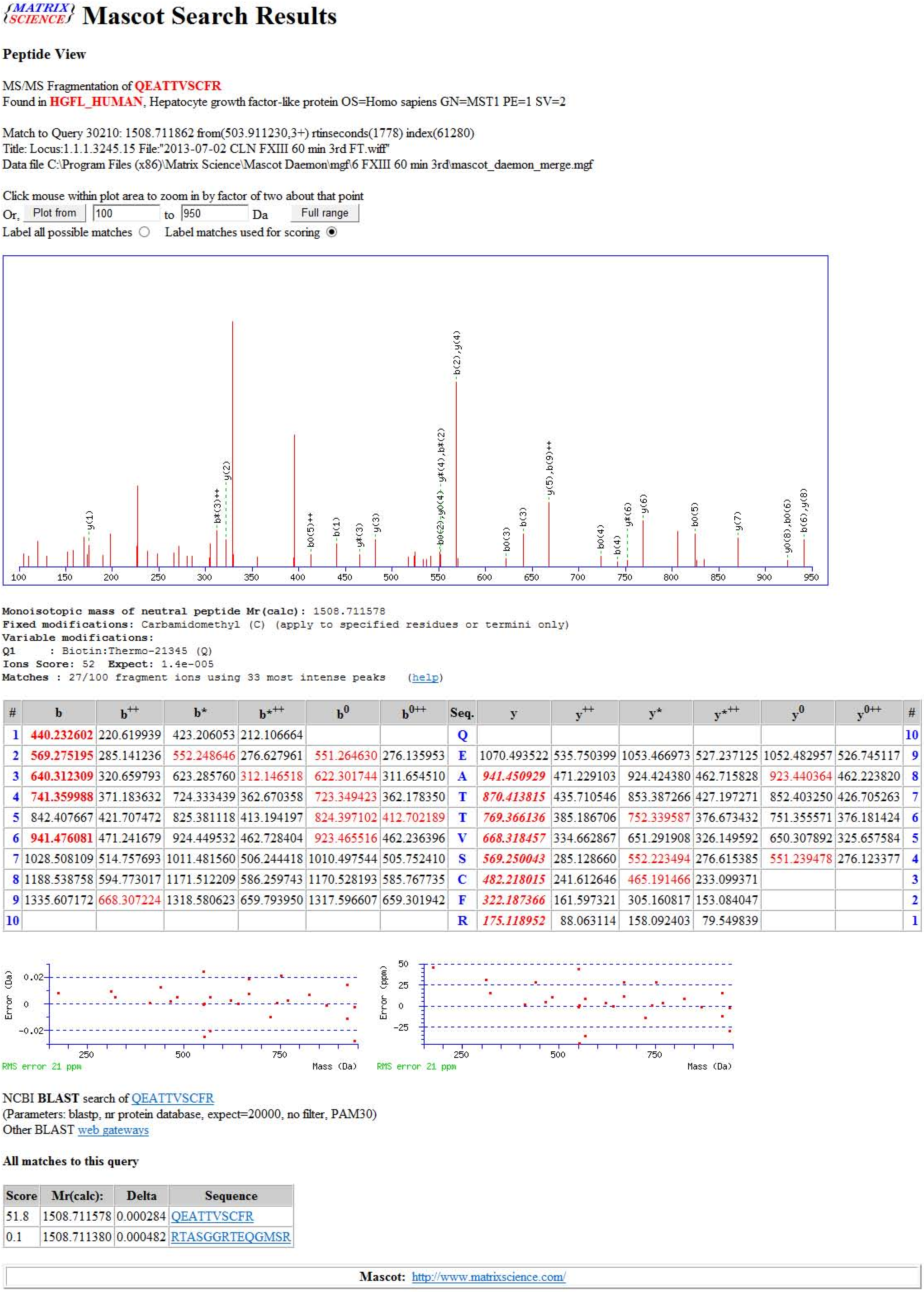




NCBI **BLAST** search of VQLSPDLLATLPEPASPGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.3	2271.229675	0.012557	VQLSPDLLATLPEPASPGR
4.0	2271.230530	0.011702	LAVSQMKQQKYPTK
4.0	2271.230530	0.011702	LAVSQMKQQKYPTK
2.0	2271.226303	0.015929	IAKSDPPTLLTPSKWSVEFR



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 30210: 1508.711862 from(503.911230,3+) rtinseconds(1778) index(61280)
Title: Locus:1.1.1.3245.15 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\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): 1508.711578
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 1.4e-005
Matches : 27/100 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	**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
51.8	1508.711578	0.000284	QEATTVSCFR
0.1	1508.711380	0.000482	RTASGGRTEQGMSR

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

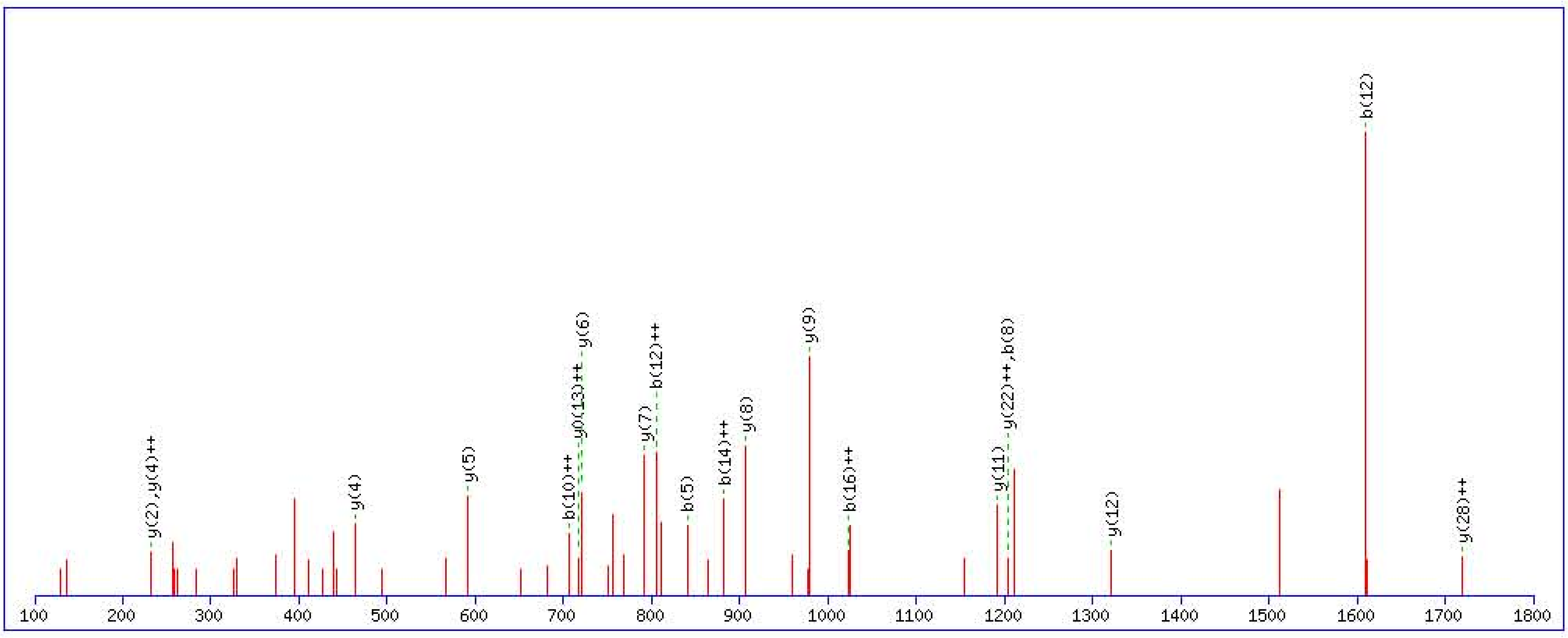
Mascot Search Results

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

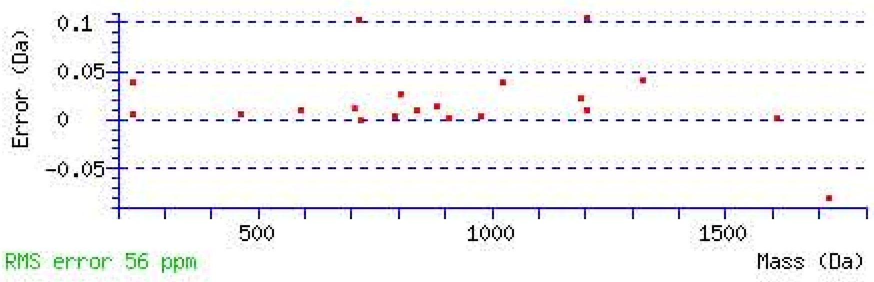
Match to Query 61337: 3494.686696 from(874.678950,4+) rtinseconds(2846) index(67443)
Title: Locus:1.1.1.3615.21 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

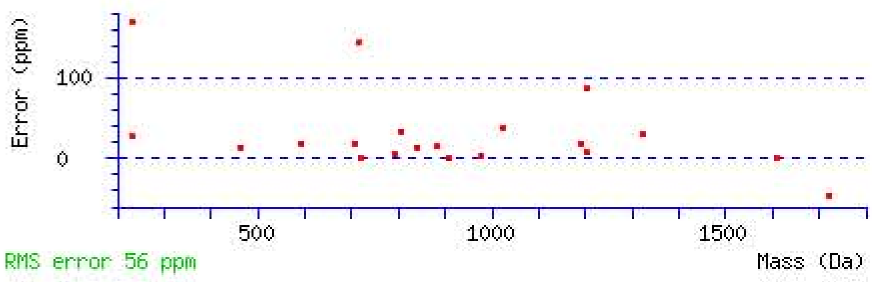
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3494.671112
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.0016
Matches : 20/318 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							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
41.2	3494.671112	0.015584	GTELQHLLHAVVPGPWQEDVADAEECAGR
34.2	3494.671112	0.015584	GTELQHLLHAVVPGPWQEDVADAEECAGR

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

MATRIX SCIENCE

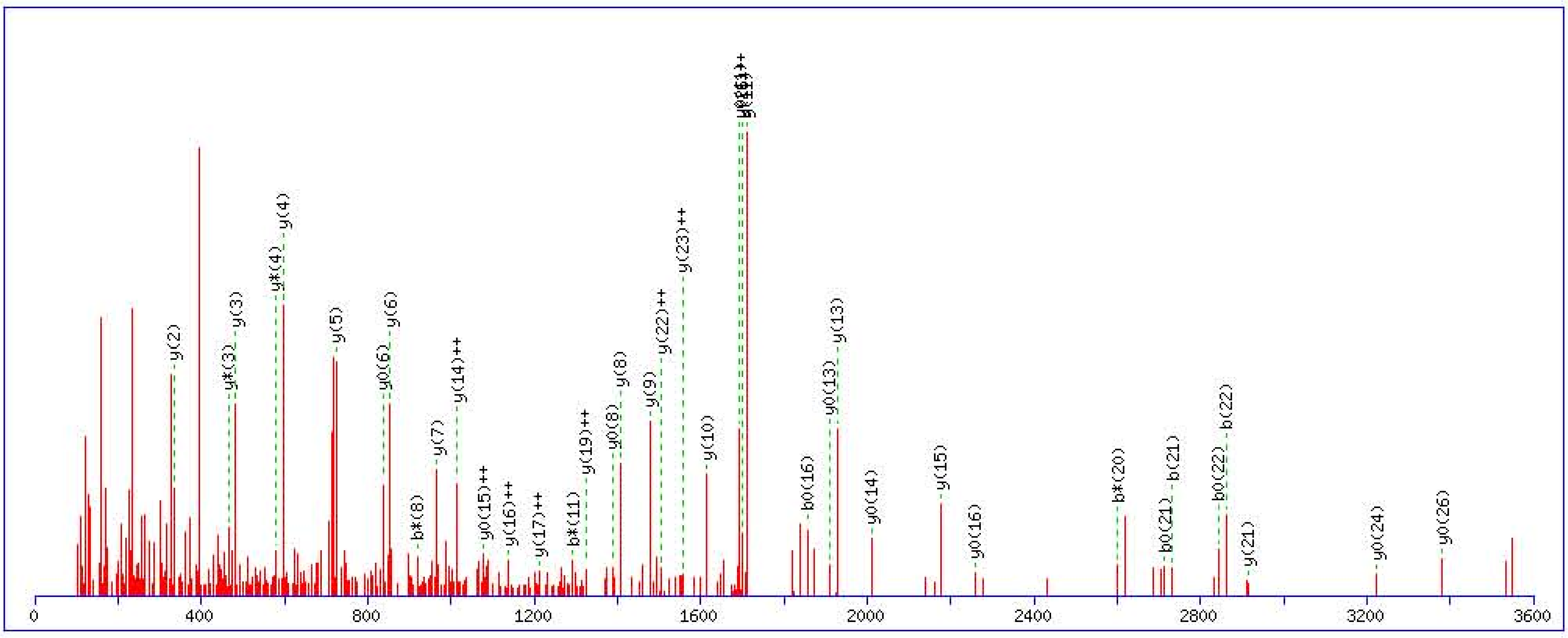
Mascot Search Results

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

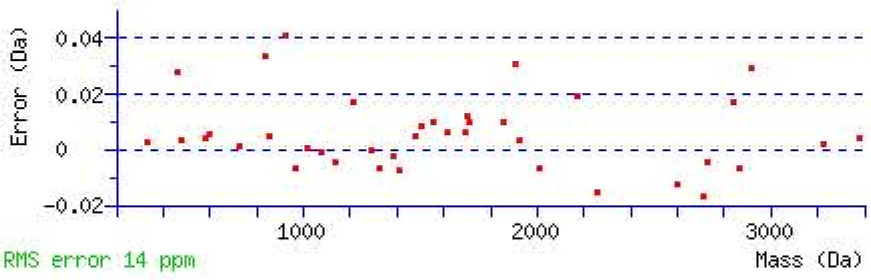
Match to Query 62102: 3584.666120 from(717.940500,5+) rtinseconds(2054) index(62851)
Title: Locus:1.1.1.3341.10 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

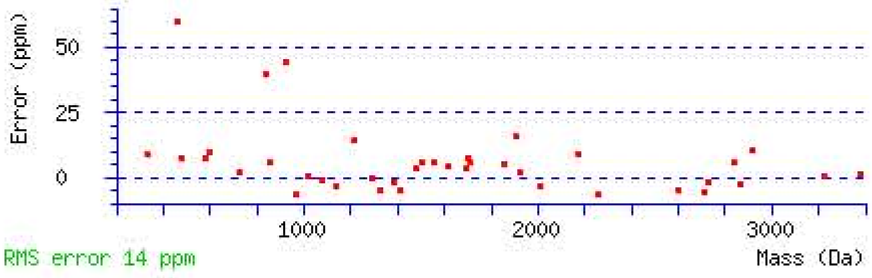
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3584.660538
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20     : Biotin:Thermo-21345 (Q)
Ions Score: 63  Expect: 8.1e-006
Matches : 39/288 fragment ions using 79 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
62.6	3584.660538	0.005582	WSAETPHKPQFTFTSEPHAQLEENFCR
6.9	3584.660538	0.005582	WSAETPHKPQFTFTSEPHAQLEENFCR

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

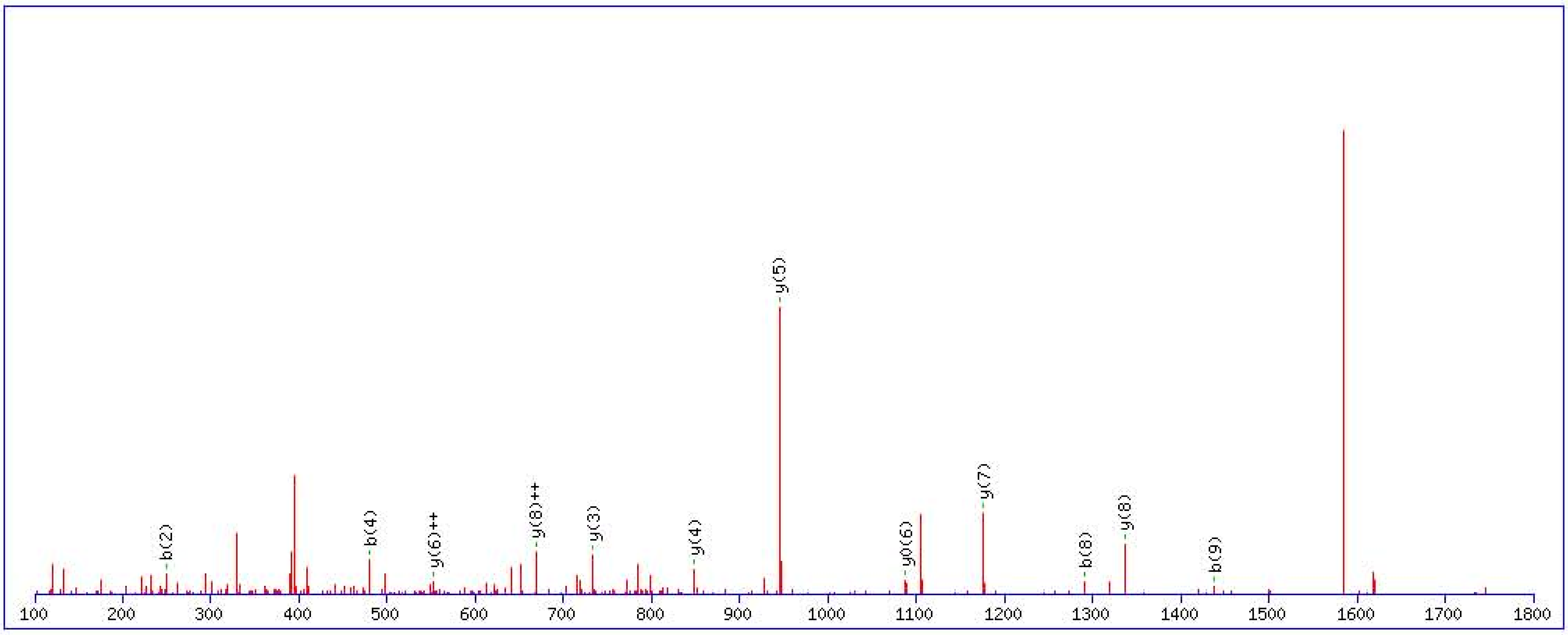
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FTCACPDQFK**
Found in **HABP2_HUMAN**, Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1

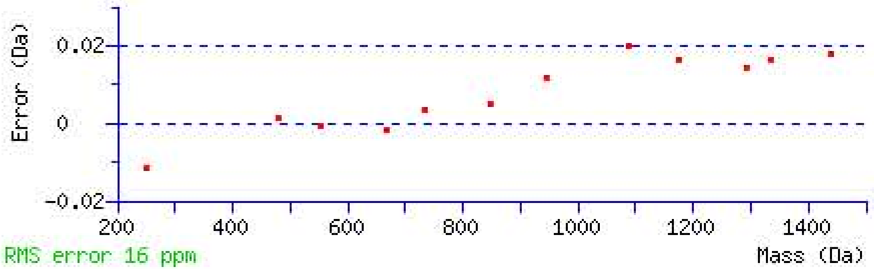
Match to Query 32538: 1583.708088 from(792.861320,2+) rtinseconds(1862) index(46383)
Title: Locus:1.1.1.2697.7 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

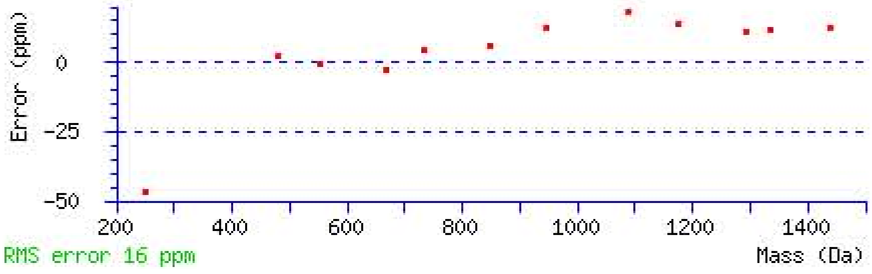
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1583.693497
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 0.00015
Matches : 12/86 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							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
47.3	1583.693497	0.014591	FTCACPDQFK

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

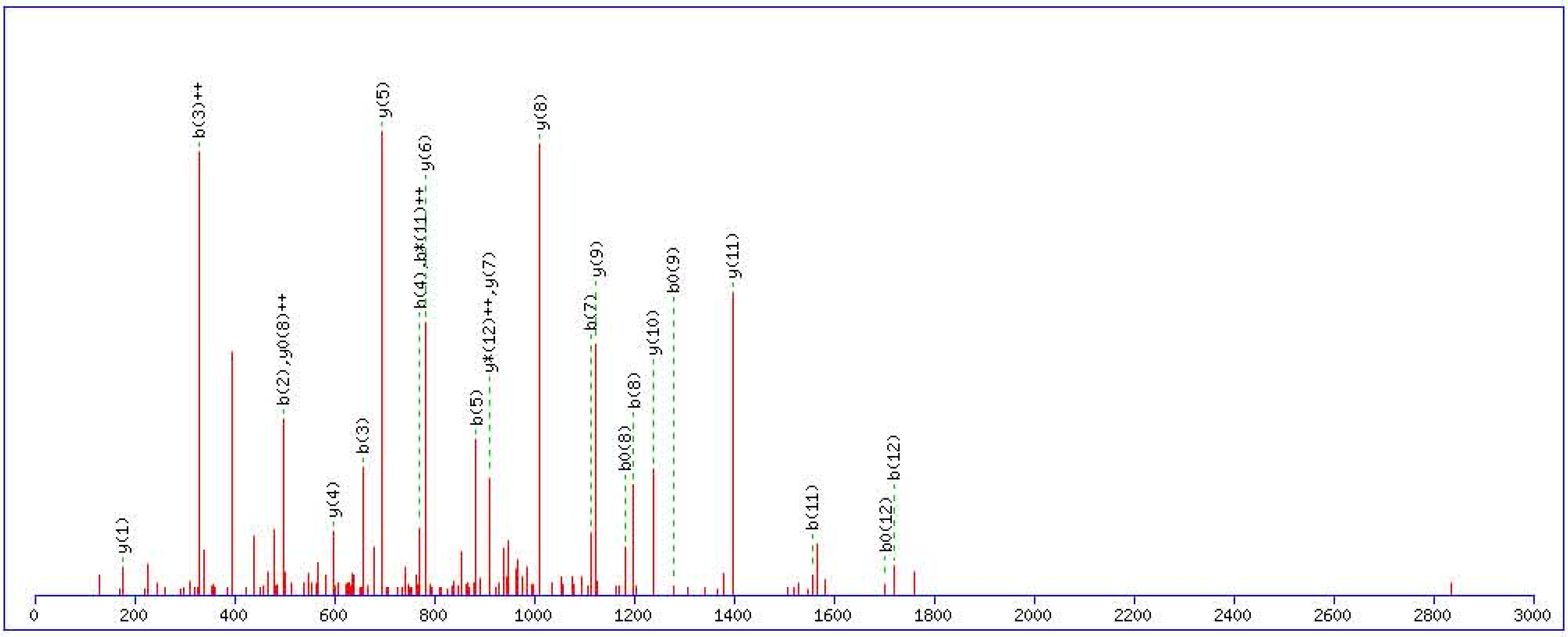
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQCLITQSPPYYR**
Found in **HABP2_HUMAN**, Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1

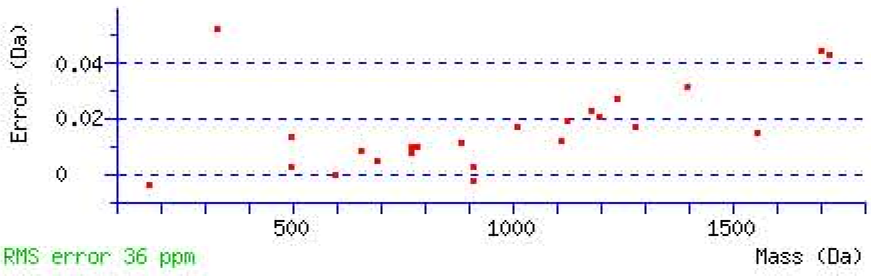
Match to Query 40101: 1892.954688 from(947.484620,2+) rtinseconds(2091) index(47936)
Title: Locus:1.1.1.2776.16 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

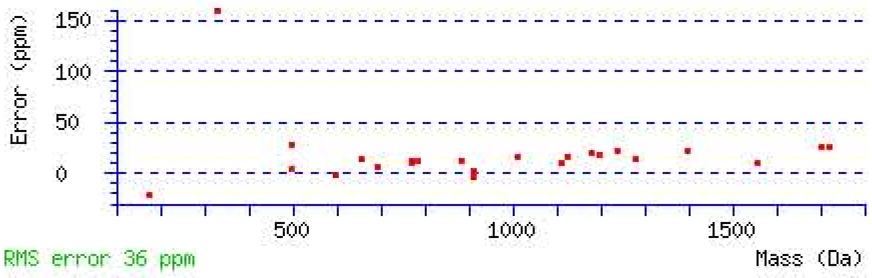
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1892.927704
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 59 **Expect:** 1.2e-005
Matches : 24/122 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							13
2	***497.254066***	249.130671	480.227517	240.617397			Q	1836.913526	918.960401	1819.886977	910.447127	1818.902961	909.955119	12
3	***657.284715***	329.145996	640.258166	320.632721			C	***1397.688200***	699.347738	1380.661651	690.834464	1379.677635	690.342456	11
4	***770.368779***	385.688028	753.342230	377.174753			L	***1237.657551***	619.332414	1220.631002	610.819139	1219.646986	610.327131	10
5	***883.452843***	442.230060	866.426294	433.716785			I	***1124.573487***	562.790382	1107.546938	554.277107	1106.562922	553.785099	9
6	984.500522	492.753899	967.473973	484.240625	966.489957	483.748617	T	***1011.489423***	506.248350	994.462874	497.735075	993.478858	497.243067	8
7	***1112.559100***	556.783188	1095.532551	548.269914	1094.548535	547.777906	Q	***910.441744***	455.724510	893.415195	447.211236	892.431179	446.719228	7
8	***1199.591128***	600.299202	1182.564579	591.785928	1181.580563	591.293920	S	***782.383166***	391.695221	765.356617	383.181947	764.372601	382.689939	6
9	1296.643892	648.825584	1279.617343	640.312310	1278.633327	639.820302	P	***695.351138***	348.179207	678.324589	339.665933			5
10	1393.696656	697.351966	1376.670107	688.838692	1375.686091	688.346684	P	***598.298374***	299.652825	581.271825	291.139551			4
11	***1556.759985***	778.883631	1539.733436	770.370356	1538.749420	769.878348	Y	501.245610	251.126443	484.219061	242.613169			3
12	***1719.823314***	860.415295	1702.796765	851.902021	1701.812749	851.410013	Y	338.182281	169.594778	321.155732	161.081504			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.5	1892.927704	0.026984	GQCLITQSPPYYR
11.5	1892.927704	0.026984	GQCLITQSPPYYR
5.5	1892.974411	-0.019723	EALLDESRPLFERYR
4.0	1892.934921	0.019767	QGSQAGPGPQLAQGMR
2.9	1892.977844	-0.023156	QVZLVZSGGGAVZPGR
2.7	1892.977844	-0.023156	QVZLVZSGGGAVZPGR
2.5	1892.963882	-0.009194	RTQQEESNLGKHR
1.7	1892.977844	-0.023156	QVZLVZSGGGAVZPGR
1.7	1892.977844	-0.023156	QVZLVZSGGGAVZPGR
0.1	1892.938065	0.016623	AQESVGFLDPAPAANPGPR

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

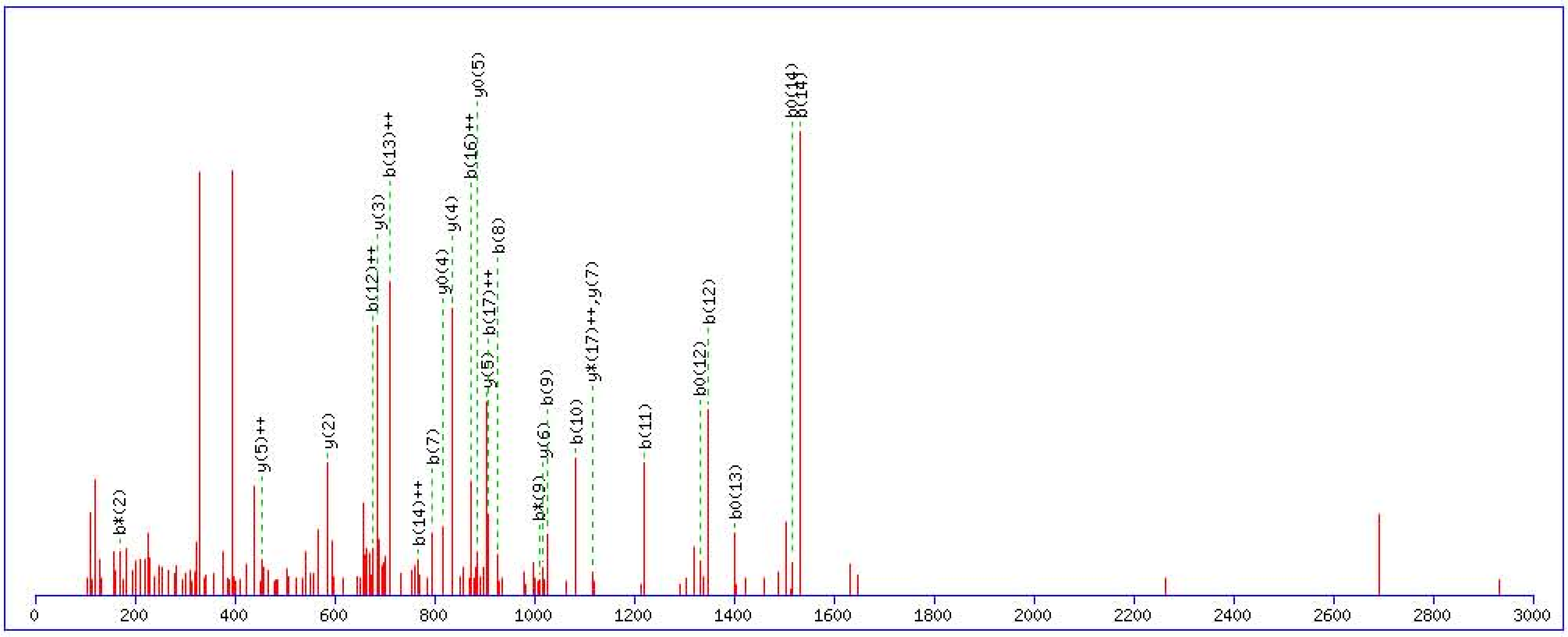
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KGDTFSCMVGHEALPLAFTQK**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

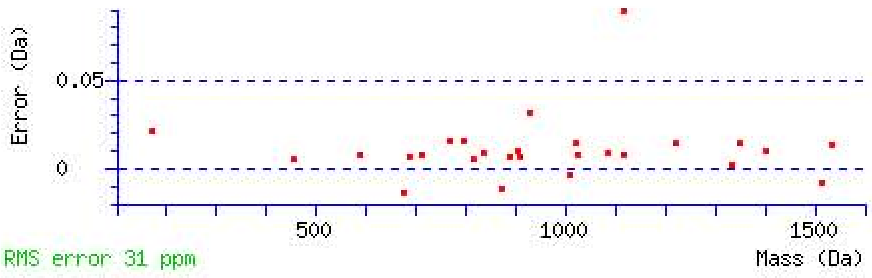
Match to Query 52390: 2647.309856 from(662.834740,4+) rtinseconds(2367) index(6838)
Title: Locus:1.1.1.3376.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

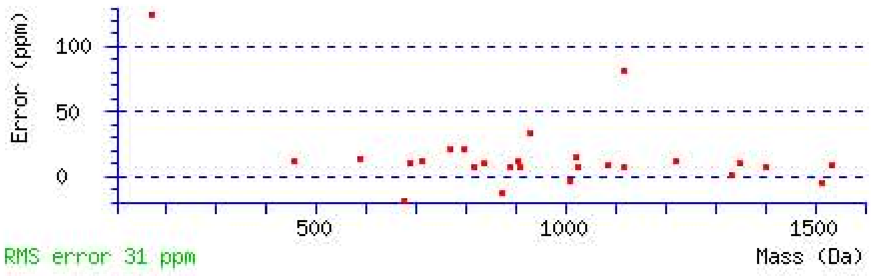
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2647.296082
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20     : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.046
Matches : 27/232 fragment ions using 61 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							21
2	186.123703	93.565489	169.097154	85.052215			G	2520.208388	1260.607832	2503.181839	1252.094557	2502.197823	1251.602549	20
3	301.150646	151.078961	284.124097	142.565687	283.140081	142.073679	D	2463.186924	1232.097100	2446.160375	1223.583825	2445.176359	1223.091817	19
4	402.198325	201.602801	385.171776	193.089526	384.187760	192.597518	T	2348.159981	1174.583628	2331.133432	1166.070354	2330.149416	1165.578346	18
5	549.266739	275.137008	532.240190	266.623733	531.256174	266.131725	F	2247.112302	1124.059789	2230.085753	1115.546514	2229.101737	1115.054506	17
6	636.298767	318.653022	619.272218	310.139747	618.288202	309.647739	S	2100.043888	1050.525582	2083.017339	1042.012307	2082.033323	1041.520299	16
7	***796.329416***	398.668346	779.302867	390.155072	778.318851	389.663064	C	2013.011860	1007.009568	1995.985311	998.496294	1995.001295	998.004286	15
8	***927.369901***	464.188589	910.343352	455.675314	909.359336	455.183306	M	1852.981211	926.994244	1835.954662	918.480969	1834.970646	917.988961	14
9	***1026.438315***	513.722796	1009.411766	505.209521	1008.427750	504.717513	V	1721.940726	861.474001	1704.914177	852.960727	1703.930161	852.468719	13
10	***1083.459779***	542.233528	1066.433230	533.720253	1065.449214	533.228245	G	1622.872312	811.939794	1605.845763	803.426520	1604.861747	802.934512	12
11	***1220.518691***	610.762984	1203.492142	602.249709	1202.508126	601.757701	H	1565.850848	783.429062	1548.824299	774.915788	1547.840283	774.423780	11
12	***1349.561284***	**675.284280**	1332.534735	666.771006	1331.550719	666.278998	E	1428.791936	714.899606	1411.765387	706.386332	1410.781371	705.894324	10
13	1420.598398	**710.802837**	1403.571849	702.289563	1402.587833	701.797555	A	1299.749343	650.378310	1282.722794	641.865035	1281.738778	641.373027	9
14	***1533.682462***	**767.344869**	1516.655913	758.831595	1515.671897	758.339587	L	1228.712229	614.859753	1211.685680	606.346478	1210.701664	605.854470	8
15	1630.735226	815.871251	1613.708677	807.357977	1612.724661	806.865969	P	***1115.628165***	558.317721	1098.601616	549.804446	1097.617600	549.312438	7
16	1743.819290	**872.413283**	1726.792741	863.900009	1725.808725	863.408000	L	***1018.575401***	509.791339	1001.548852	501.278064	1000.564836	500.786056	6
17	1814.856404	**907.931840**	1797.829855	899.418566	1796.845839	898.926557	A	***905.491337***	453.249307	888.464788	444.736032	887.480772	444.244024	5
18	1961.924818	981.466047	1944.898269	972.952773	1943.914253	972.460764	F	***834.454223***	417.730750	817.427674	409.217475	816.443658	408.725467	4
19	2062.972497	1031.989886	2045.945948	1023.476612	2044.961932	1022.984604	T	***687.385809***	344.196543	670.359260	335.683268	669.375244	335.191260	3
20	2502.197823	1251.602549	2485.171274	1243.089275	2484.187258	1242.597267	Q	***586.338130***	293.672703	569.311581	285.159429			2
21							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.0	2647.296082	0.013774	KGDTFSCMVGHEALPLAFTQK

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

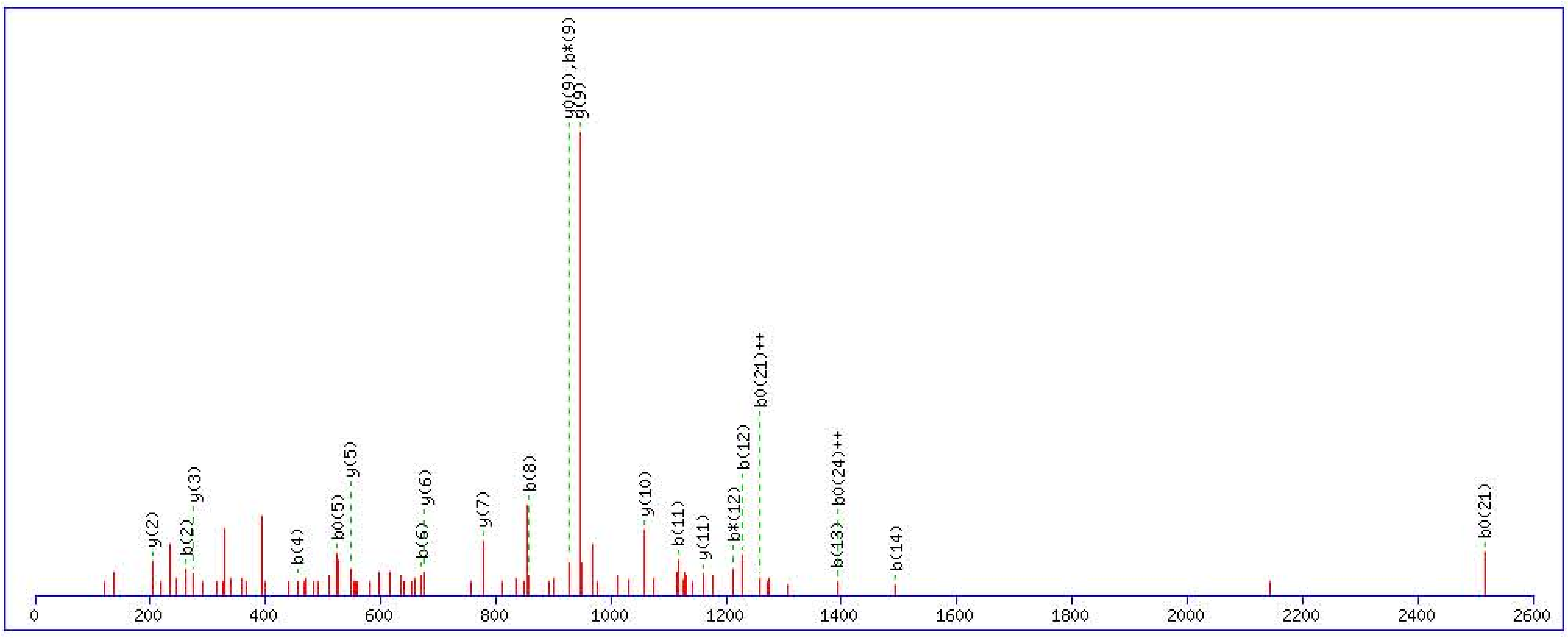
Mascot Search Results

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

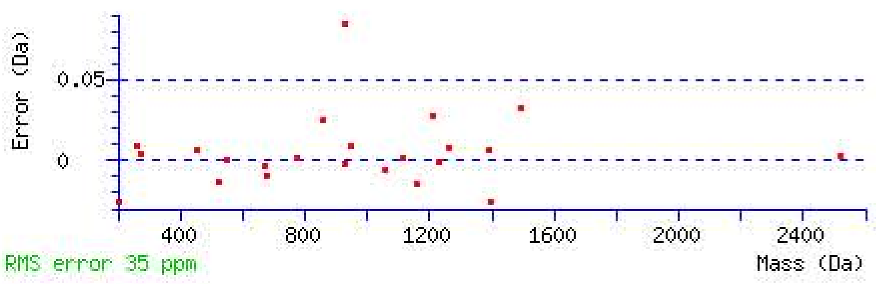
Match to Query 61216: 3478.691816 from(870.680230,4+) rtinseconds(2597) index(36303)
Title: Locus:1.1.1.3453.25 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

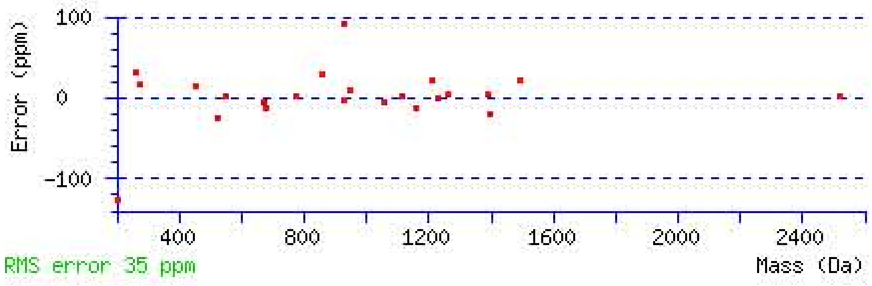
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 54  Expect: 8.3e-005
Matches : 23/328 fragment ions using 41 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							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
54.4	3478.674866	0.016950	NFPPSQDASGDLYTTSSQLTLPATQCLAGK
21.6	3478.674866	0.016950	NFPPSQDASGDLYTTSSQLTLPATQCLAGK
21.5	3478.674866	0.016950	NFPPSQDASGDLYTTSSQLTLPATQCLAGK

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

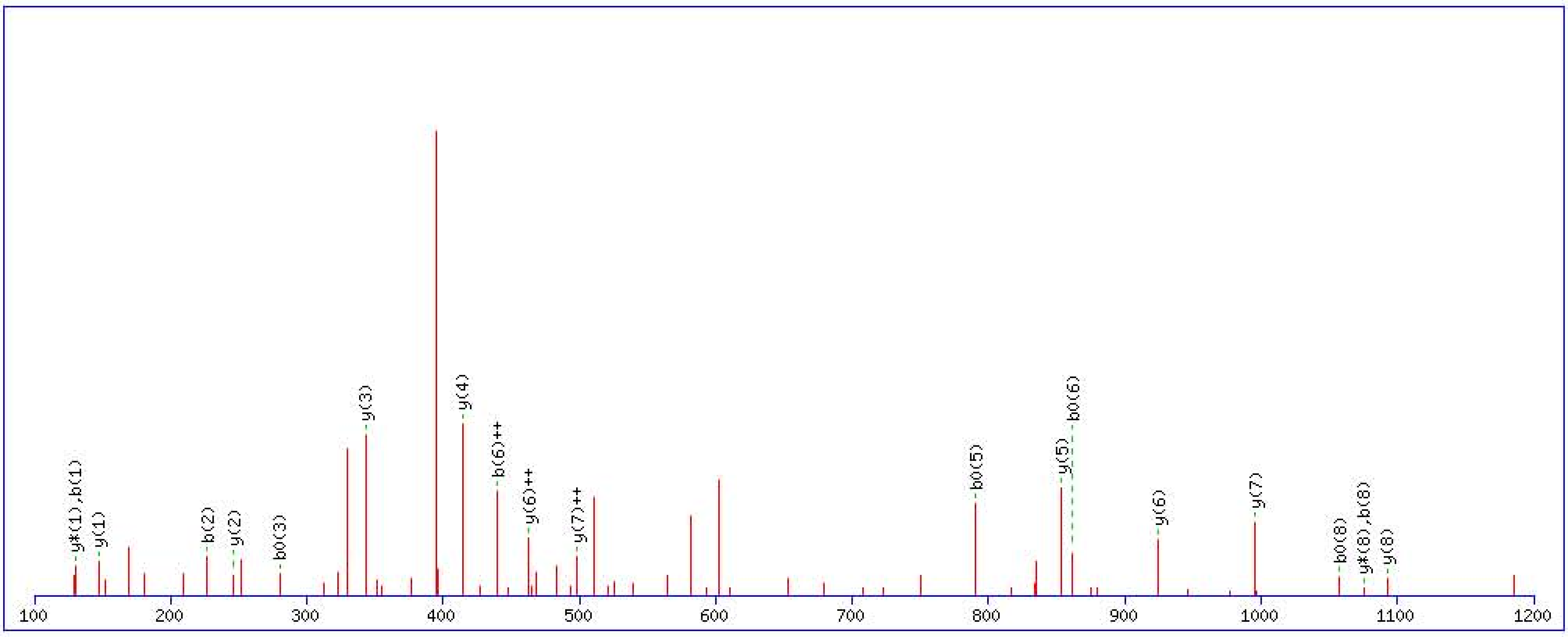
Mascot Search Results

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

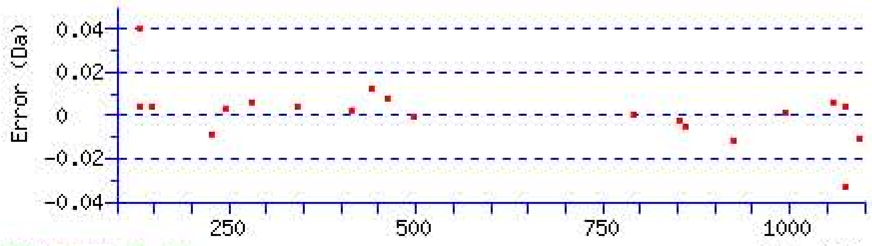
Match to Query 20767: 1220.657028 from(611.335790,2+) rtinseconds(1449) index(59469)
Title: Locus:1.1.1.3130.17 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

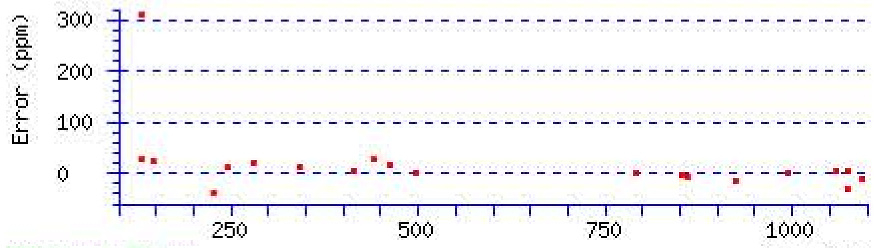
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1220.658707
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.00022
Matches : 20/72 fragment ions using 39 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	**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
49.2	1220.658707	-0.001679	EPAAQAPVK
16.9	1220.658722	-0.001694	EQNVPVPK
2.6	1220.654678	0.002350	SVRMLSGSKEK
2.3	1220.651321	0.005707	GQVLIAASSYGR
2.1	1220.651291	0.005737	EYIKQRGAEK
1.6	1220.644806	0.012222	GGHVQREK
1.6	1220.669937	-0.012909	IIAHSNQK
1.6	1220.640076	0.016952	LLAEYTGAQQK
1.4	1220.647491	0.009537	ETLFSVMPGLK
1.4	1220.666580	-0.009552	EPAIVRFFSR

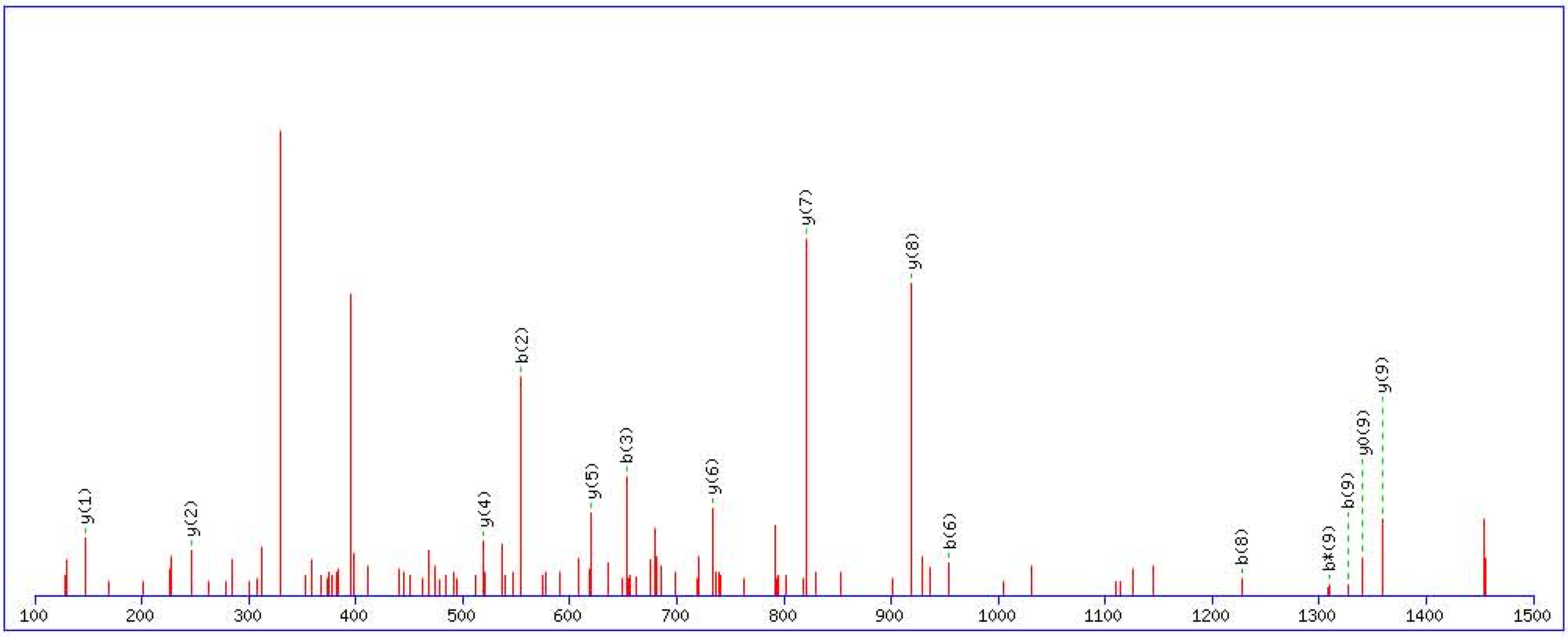
{MATRIX SCIENCE} Mascot Search Results

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

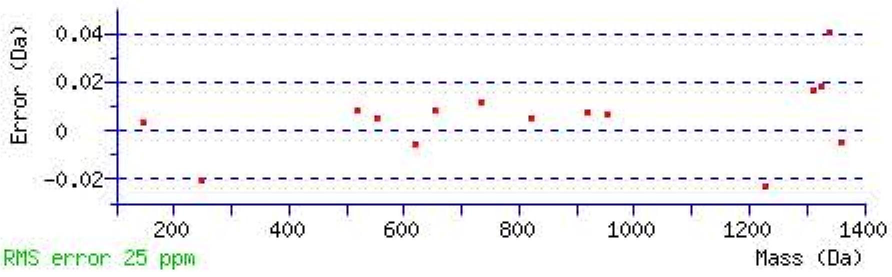
Match to Query 29231: 1471.791608 from(736.903080,2+) rtinseconds(2257) index(64048)
Title: Locus:1.1.1.3412.10 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

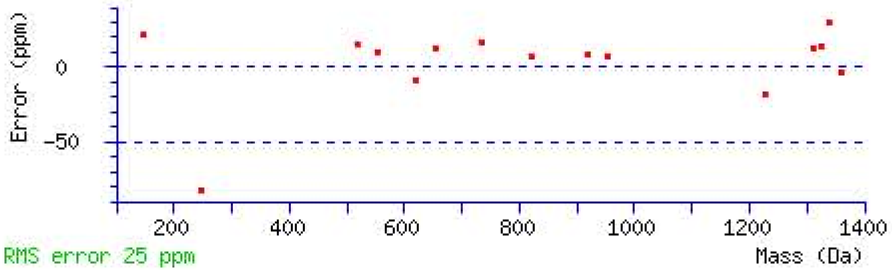


Monoisotopic mass of neutral peptide Mr(calc): 1471.789093
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 52 **Expect:** 4.7e-005
Matches : 15/94 fragment ions using 28 most intense peaks (help)

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



RMS error 25 ppm



RMS error 25 ppm

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
51.9	1471.789093	0.002515	NQVSLTCLVK
5.4	1471.803467	-0.011859	EKQGPLLDLFGQK
5.2	1471.806839	-0.015231	VANSPTMVNLLLGK
4.8	1471.799438	-0.007830	EVELDRLRDTVK
4.1	1471.796921	-0.005313	YLIAACQHLQKK
3.6	1471.796265	-0.004657	ELFEYFVVVSLK
2.8	1471.797592	-0.005984	KYFWDRAFLVK
2.4	1471.770447	0.021161	QPTTAEKSATK
1.1	1471.778305	0.013303	NVQKGKGLEGWEK

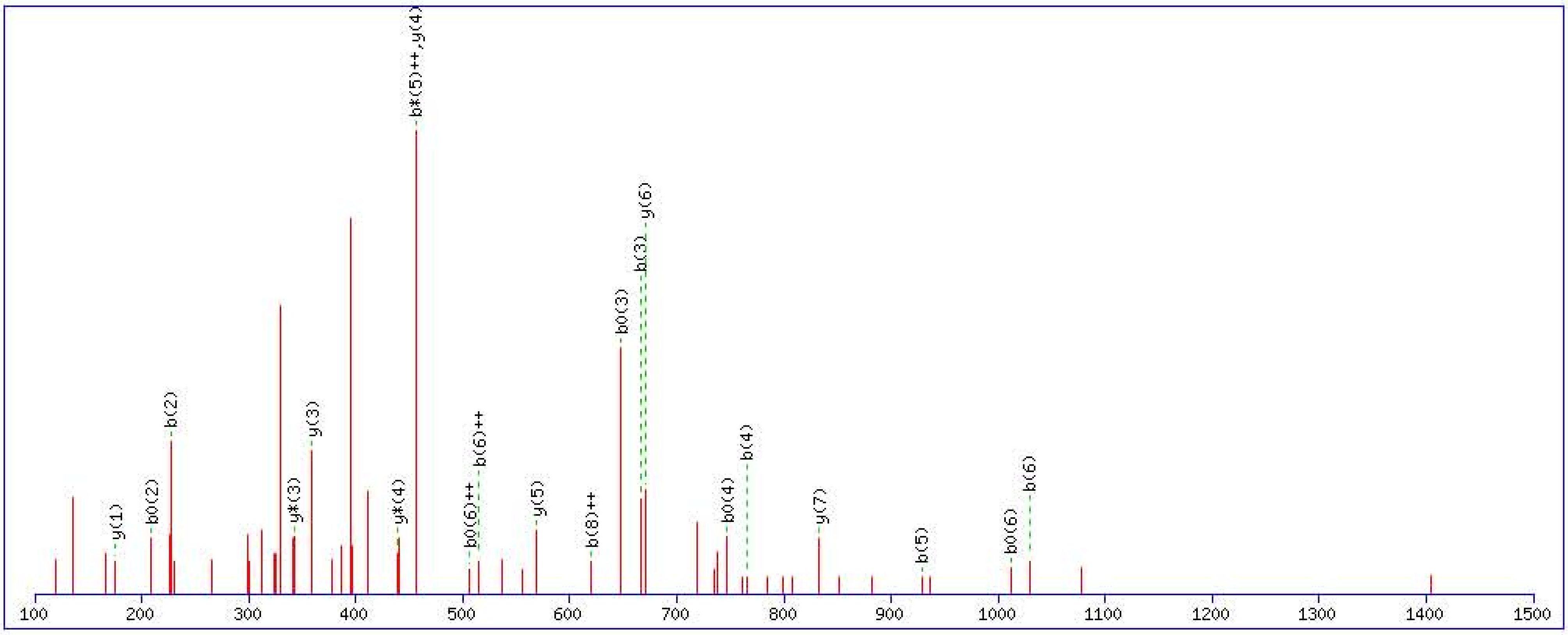
Mascot Search Results

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

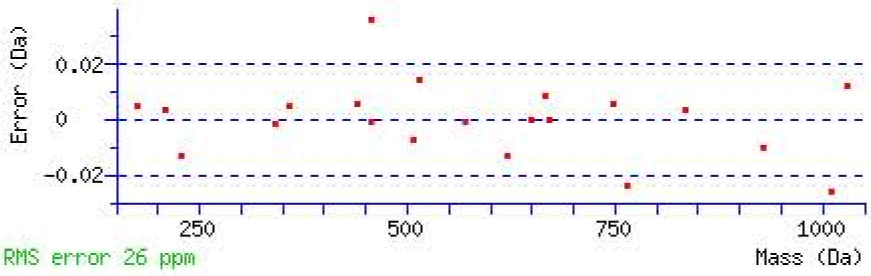
Match to Query 33190: 1596.828912 from(533.283580,3+) rtinseconds(1996) index(62540)
Title: Locus:1.1.1.3321.14 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

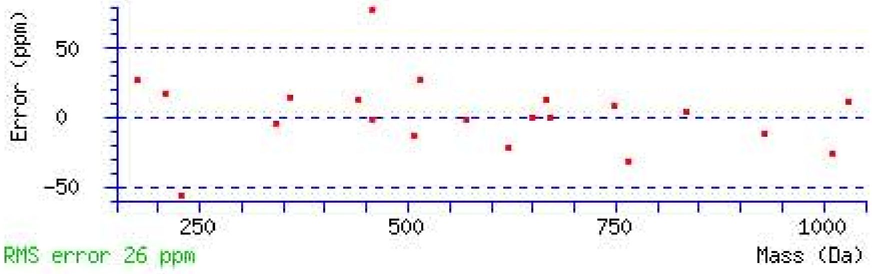
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1596.833389
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 27 **Expect:** 0.0031
Matches : 21/114 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	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
27.4	1596.833389	-0.004477	EPQVYTLPPSR
0.6	1596.847122	-0.018210	ATPSSSPGTATALPALR

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

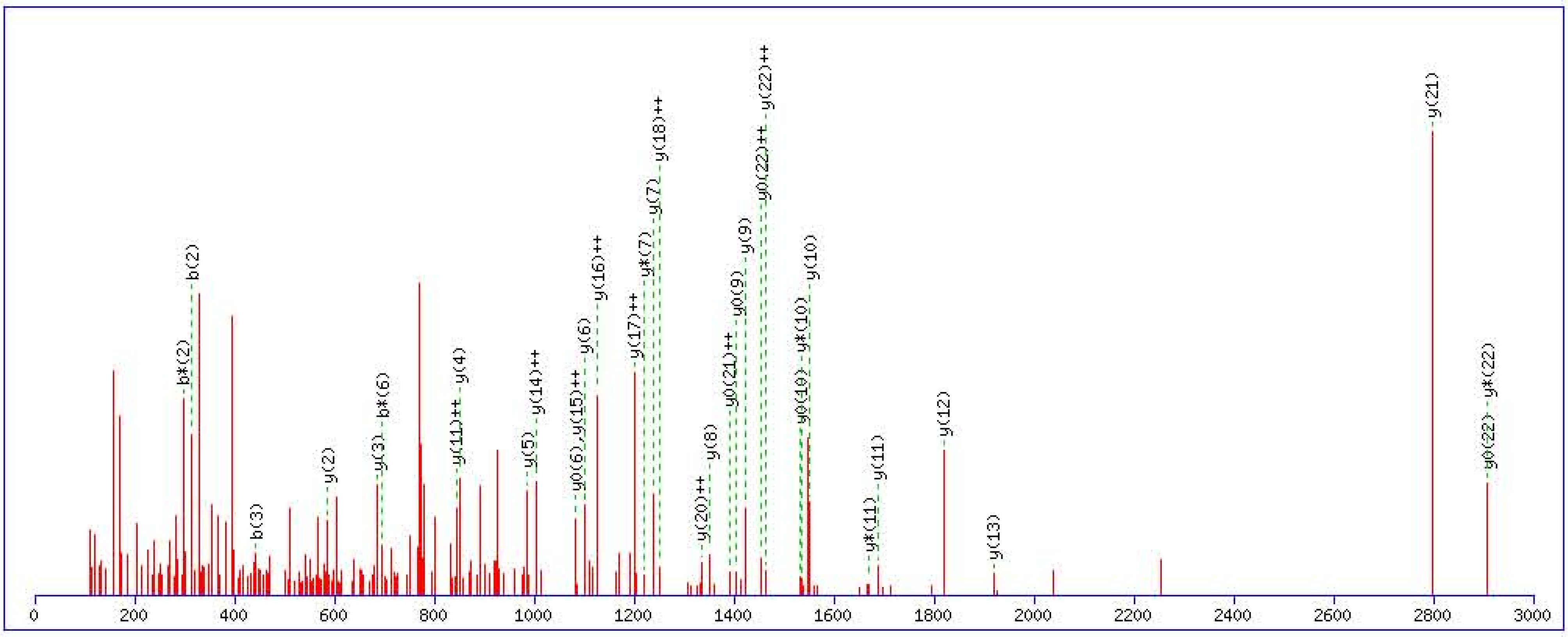
{MATRIX SCIENCE} Mascot Search Results

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

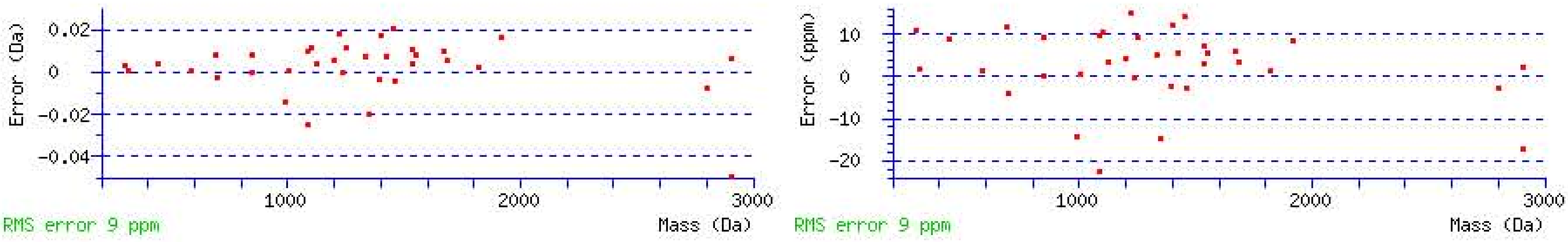
Match to Query 56804: 3111.434616 from(778.865930,4+) rtinseconds(2094) index(63044)
Title: Locus:1.1.1.3355.13 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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): 3111.426590
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q22     : Biotin:Thermo-21345 (Q)
Ions Score: 66  Expect: 3.6e-006
Matches : 35/244 fragment ions using 76 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	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
66.0	3111.426590	0.008026	WQQGNVFSCSVMHEALHNHYTQK

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

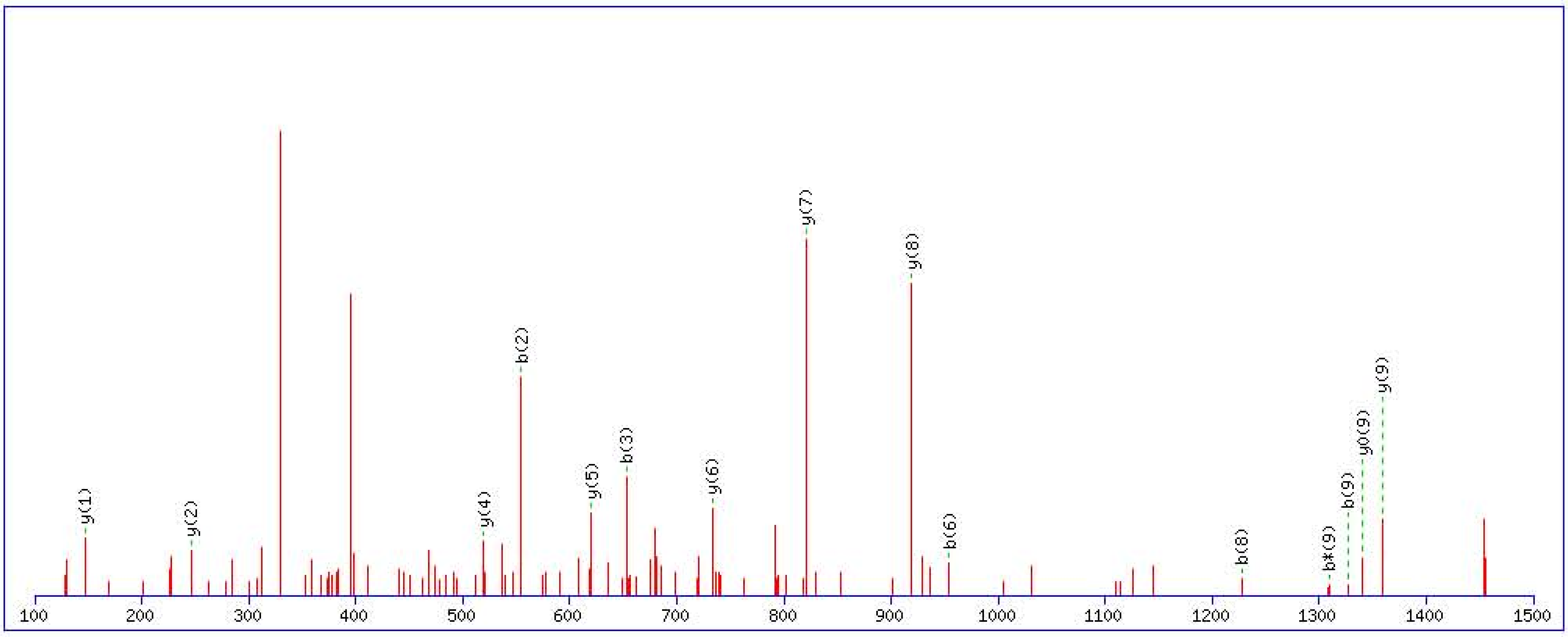
Mascot Search Results

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

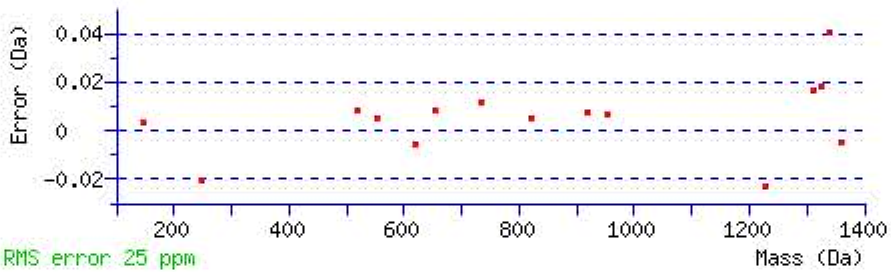
Match to Query 29231: 1471.791608 from(736.903080,2+) rtinseconds(2257) index(64048)
Title: Locus:1.1.1.3412.10 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

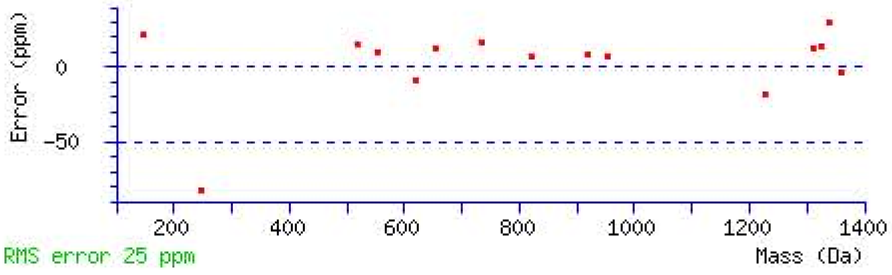
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1471.789093
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 52 **Expect:** 4.7e-005
Matches : 15/94 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	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
51.9	1471.789093	0.002515	NQVSLTCLVK
5.4	1471.803467	-0.011859	EKQGPLLDLFGQK
5.2	1471.806839	-0.015231	VANSPTMVNLLLGK
4.8	1471.799438	-0.007830	EVELDRLRDTVK
4.1	1471.796921	-0.005313	YLIAACQHLQKK
3.6	1471.796265	-0.004657	ELFEYFVVVSLK
2.8	1471.797592	-0.005984	KYFWDRAFLVK
2.4	1471.770447	0.021161	QPTTAEKSATK
1.1	1471.778305	0.013303	NVQKGKGLEGWEK

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

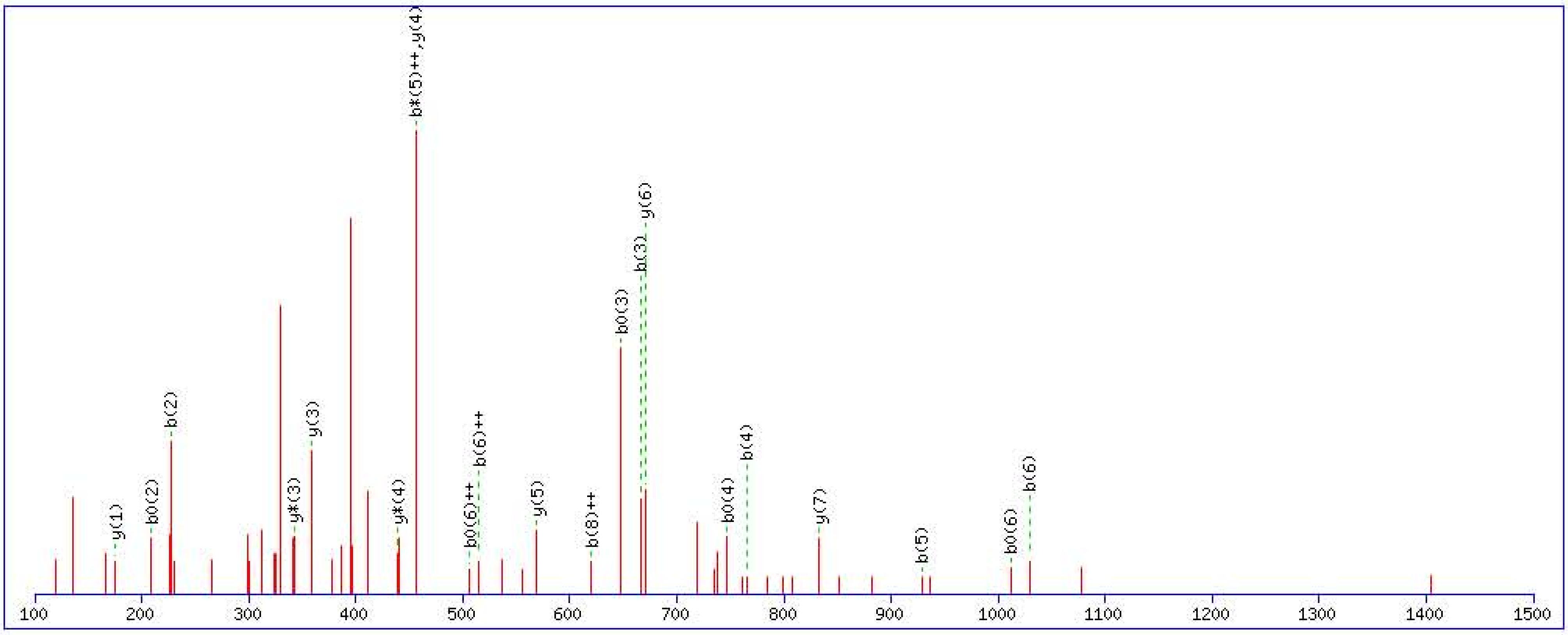
Mascot Search Results

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

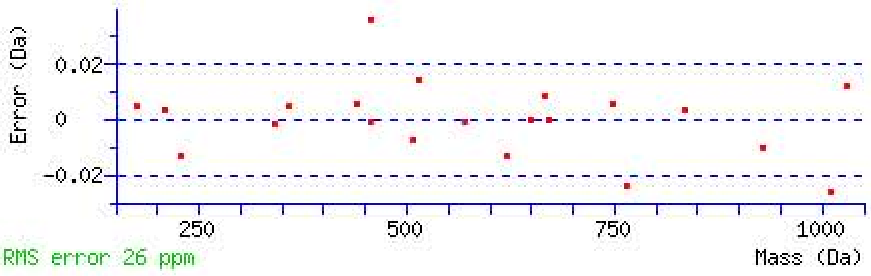
Match to Query 33190: 1596.828912 from(533.283580,3+) rtinseconds(1996) index(62540)
Title: Locus:1.1.1.3321.14 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

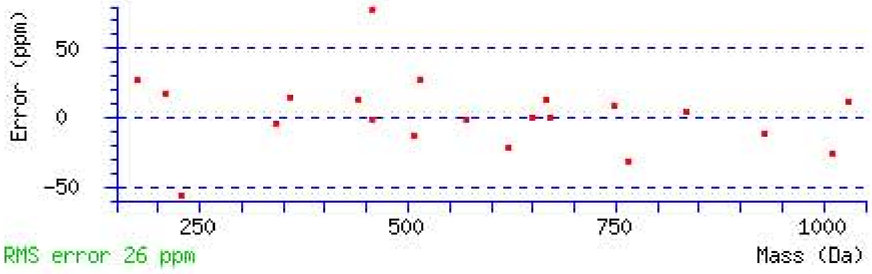
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1596.833389
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 27 **Expect:** 0.0031
Matches : 21/114 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	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
27.4	1596.833389	-0.004477	EPQVYTLPPSR
0.6	1596.847122	-0.018210	ATPSSSPGTATALPALR

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

MATRIX SCIENCE

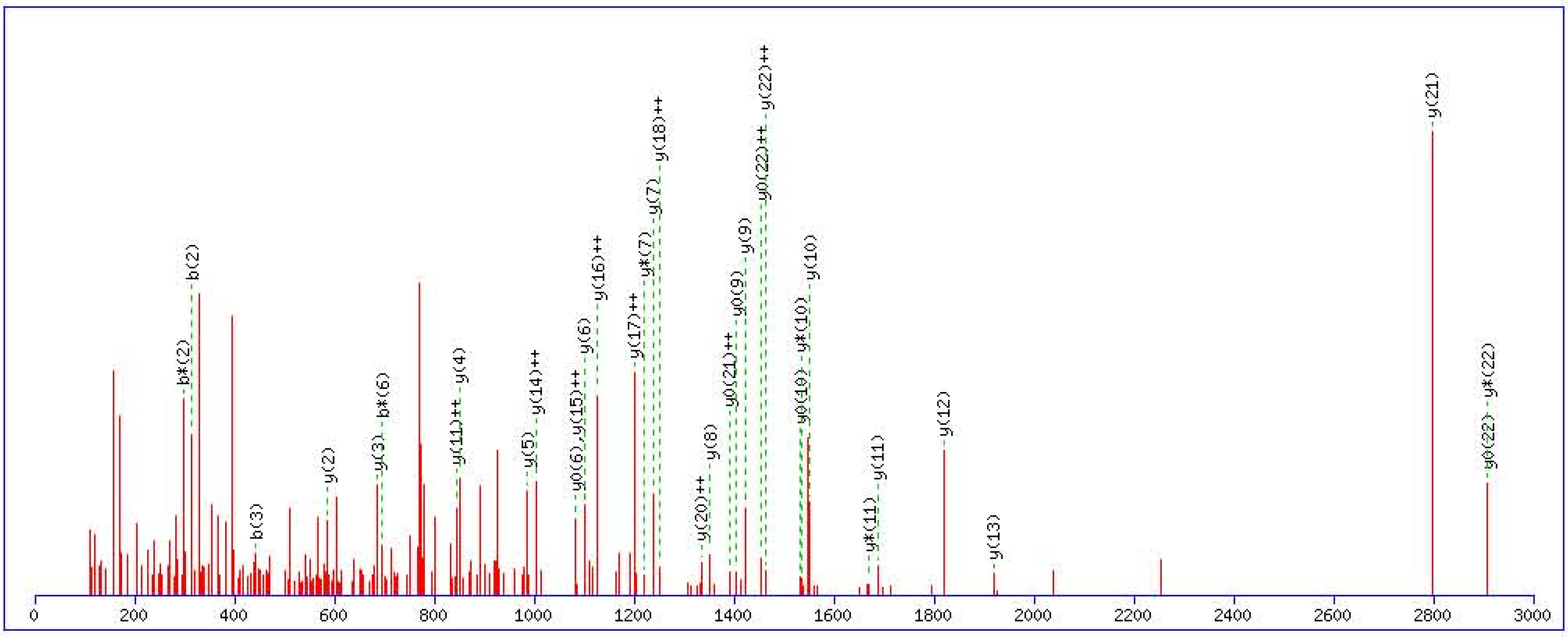
Mascot Search Results

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

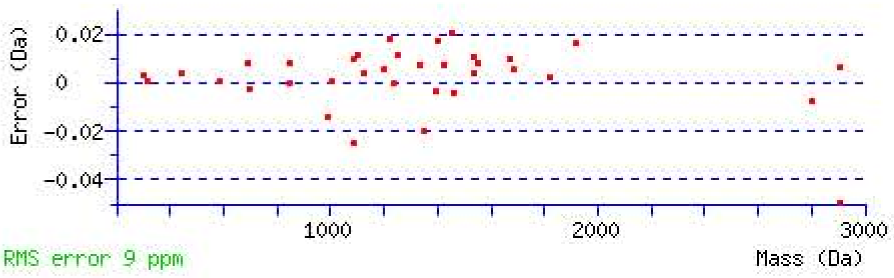
Match to Query 56804: 3111.434616 from(778.865930,4+) rtinseconds(2094) index(63044)
Title: Locus:1.1.1.3355.13 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

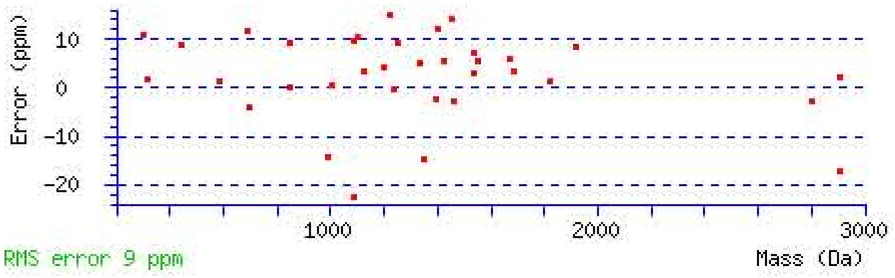
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3111.426590
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q22     : Biotin:Thermo-21345 (Q)
Ions Score: 66  Expect: 3.6e-006
Matches : 35/244 fragment ions using 76 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	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
66.0	3111.426590	0.008026	WQQGNVFSCSVMHEALHNHYTQK

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

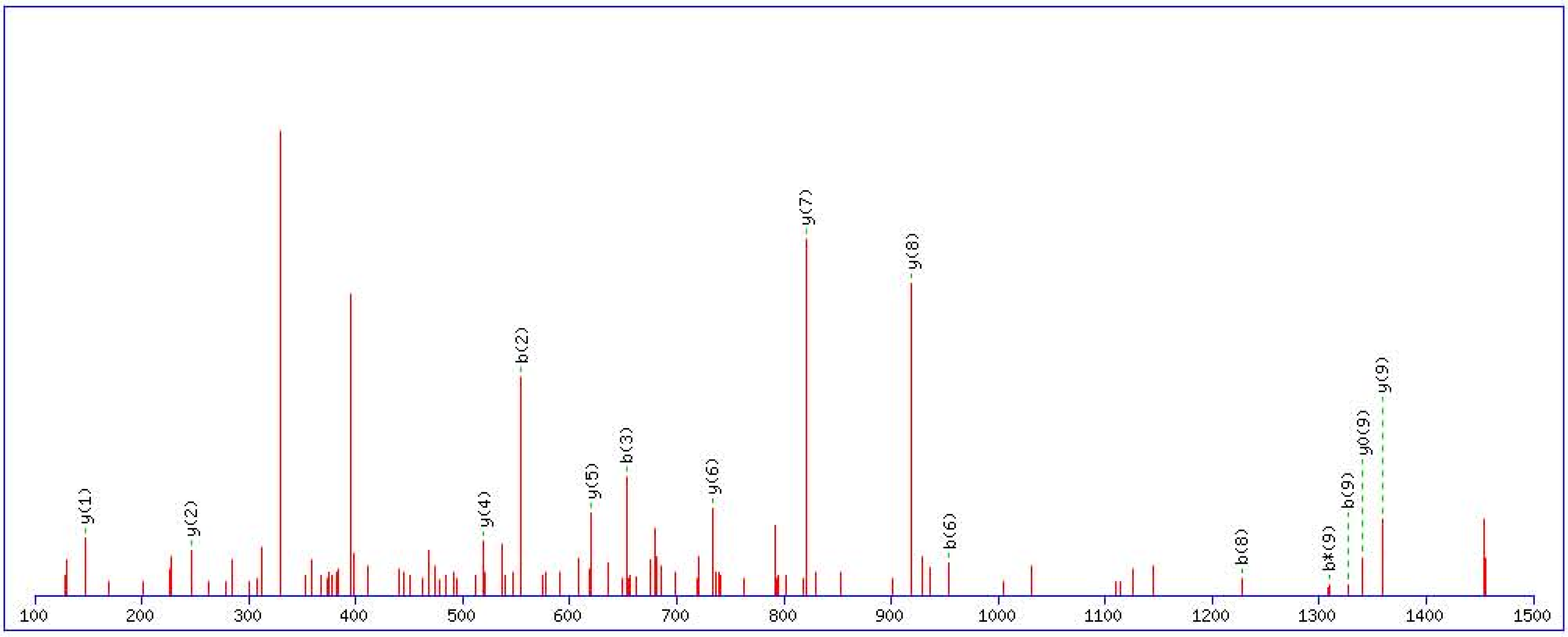
{MATRIX SCIENCE} Mascot Search Results

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

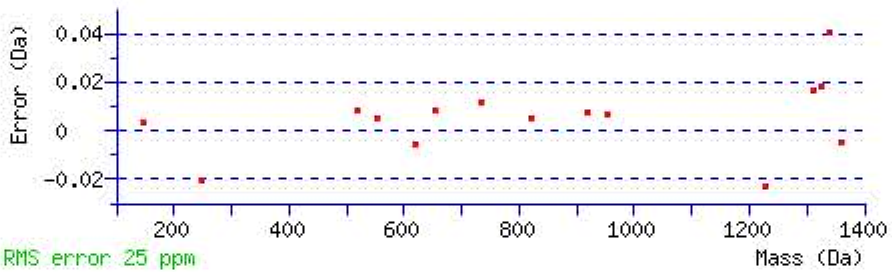
Match to Query 29231: 1471.791608 from(736.903080,2+) rtinseconds(2257) index(64048)
Title: Locus:1.1.1.3412.10 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

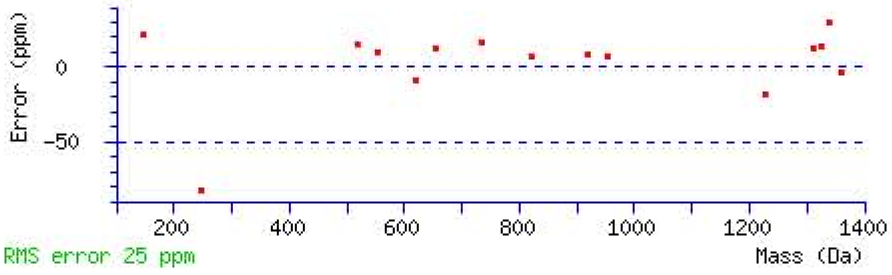
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1471.789093
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 4.7e-005
Matches : 15/94 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	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
51.9	1471.789093	0.002515	NQVSLTCLVK
5.4	1471.803467	-0.011859	EKQGPLLDLFGQK
5.2	1471.806839	-0.015231	VANSPTMVNLLLGK
4.8	1471.799438	-0.007830	EVELDRLRDTVK
4.1	1471.796921	-0.005313	YLIAACQHLQKK
3.6	1471.796265	-0.004657	ELFEYFVVVSLK
2.8	1471.797592	-0.005984	KYFWDRAFLVK
2.4	1471.770447	0.021161	QPTTAEKSATK
1.1	1471.778305	0.013303	NVQKGKGLEGWEK

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

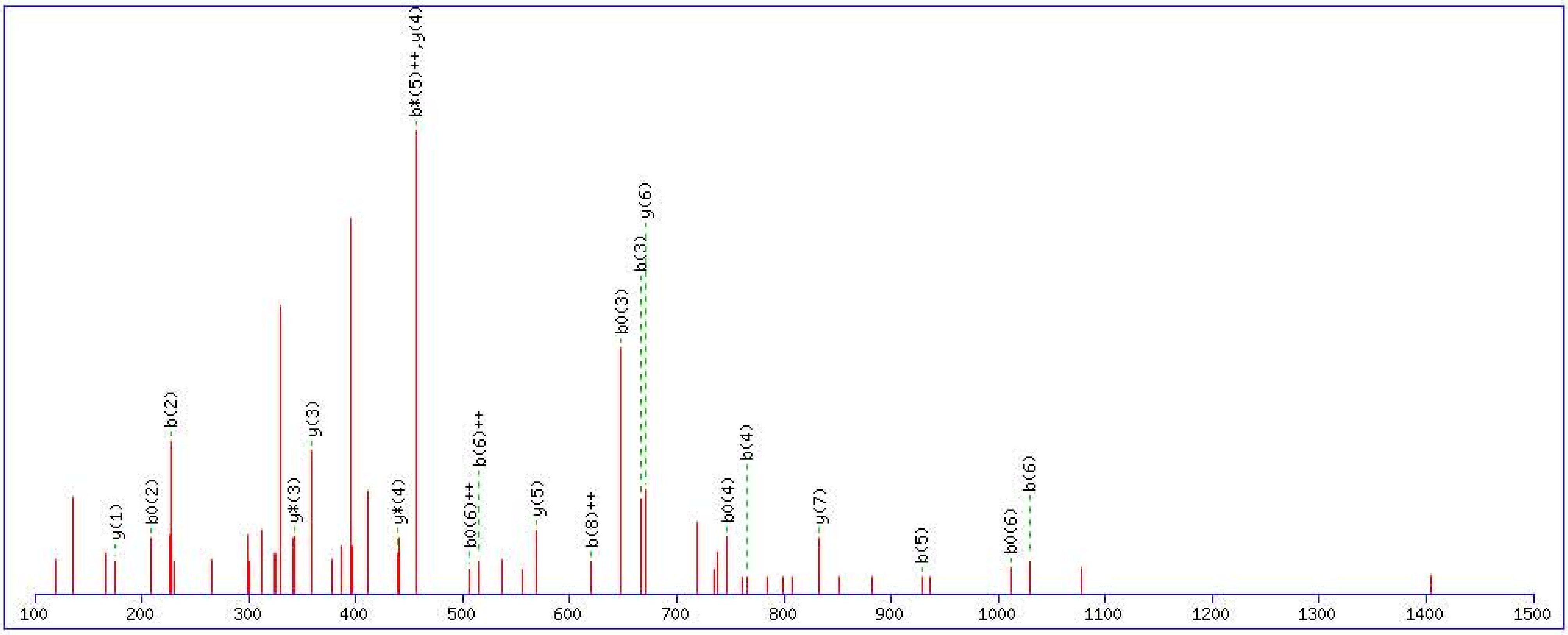
Mascot Search Results

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

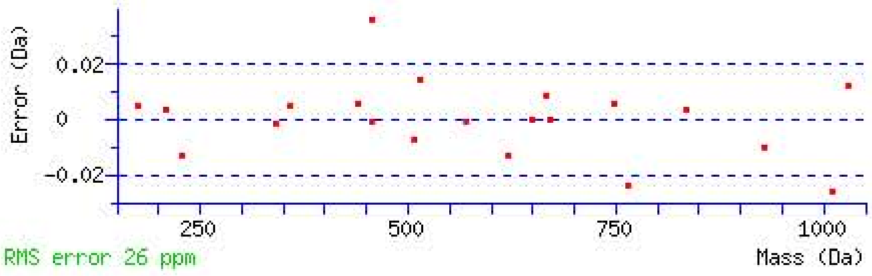
Match to Query 33190: 1596.828912 from(533.283580,3+) rtinseconds(1996) index(62540)
Title: Locus:1.1.1.3321.14 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

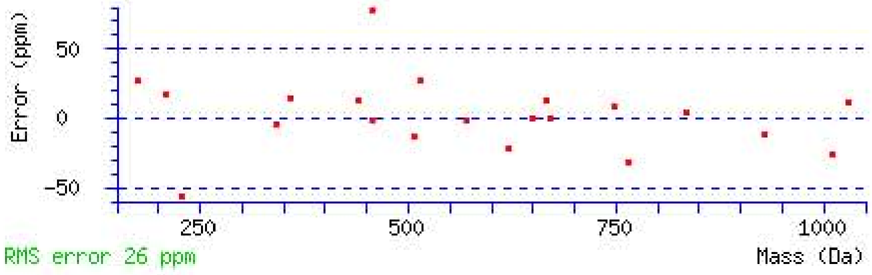


Monoisotopic mass of neutral peptide Mr(calc): 1596.833389
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 27 **Expect:** 0.0031
Matches : 21/114 fragment ions using 42 most intense peaks (help)

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



RMS error 26 ppm



RMS error 26 ppm

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
27.4	1596.833389	-0.004477	EPQVYTLPPSR
0.6	1596.847122	-0.018210	ATPSSSPGTATALPALR

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

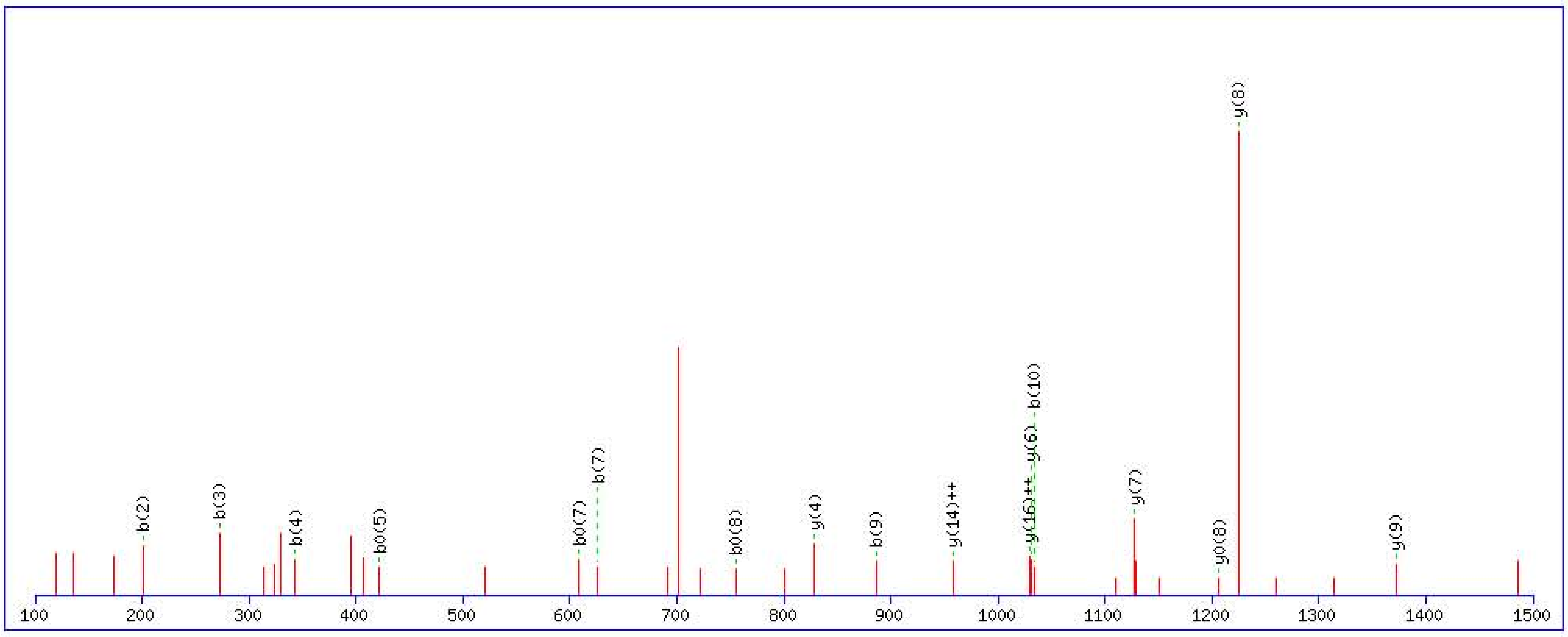
{MATRIX SCIENCE} Mascot Search Results

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

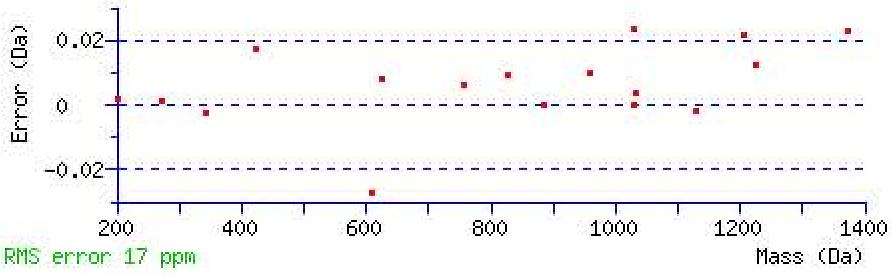
Match to Query 46971: 2256.196992 from(753.072940,3+) rtinseconds(2697) index(66221)
Title: Locus:1.1.1.3565.12 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

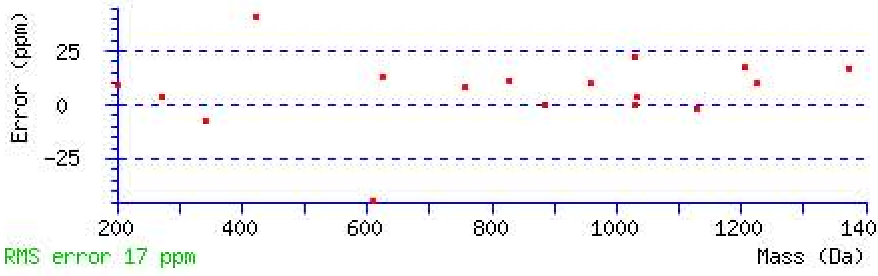
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2256.186432
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16     : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.0028
Matches : 17/168 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	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
27.8	2256.186432	0.010560	TVAAPSVFIFPPSDEQLK
0.6	2256.211365	-0.014373	ELEQLHLGLYGTSDRLTLAK
0.5	2256.179016	0.017976	TFLVPEIKSLDQYDFSRAK

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

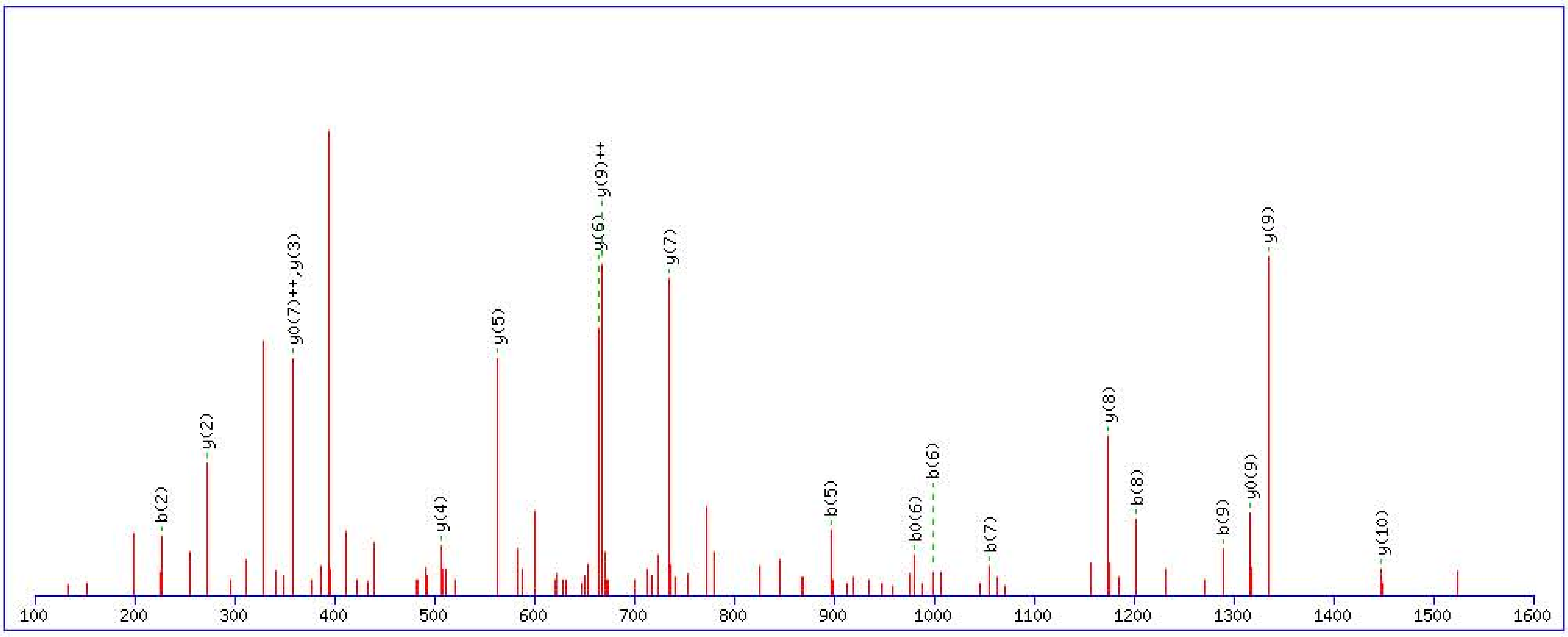
Mascot Search Results

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

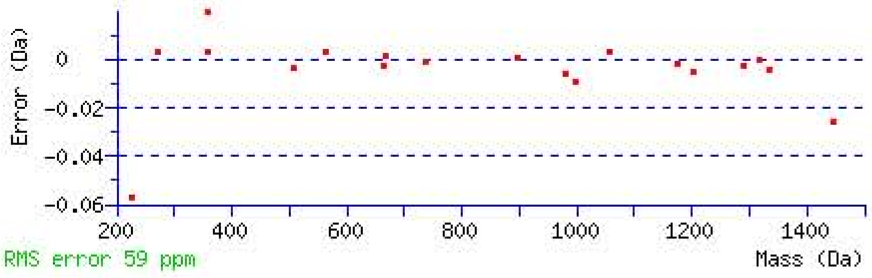
Match to Query 31367: 1559.800348 from(780.907450,2+) rtinseconds(1999) index(33195)
Title: Locus:1.1.1.3245.8 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

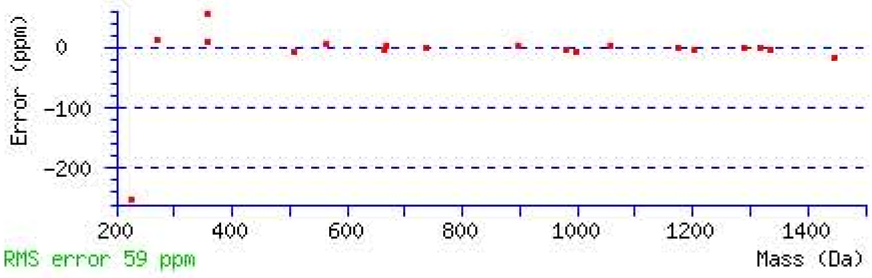
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1559.795242
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 67  Expect: 1.9e-006
Matches : 19/100 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							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
66.6	1559.795242	0.005106	LICQATGFSPR
5.4	1559.820190	-0.019842	MTRSATQAAKQVPR
4.3	1559.808960	-0.008612	LDRLSGLADQMVAR
3.0	1559.808975	-0.008627	LLDRDACDTVRVK

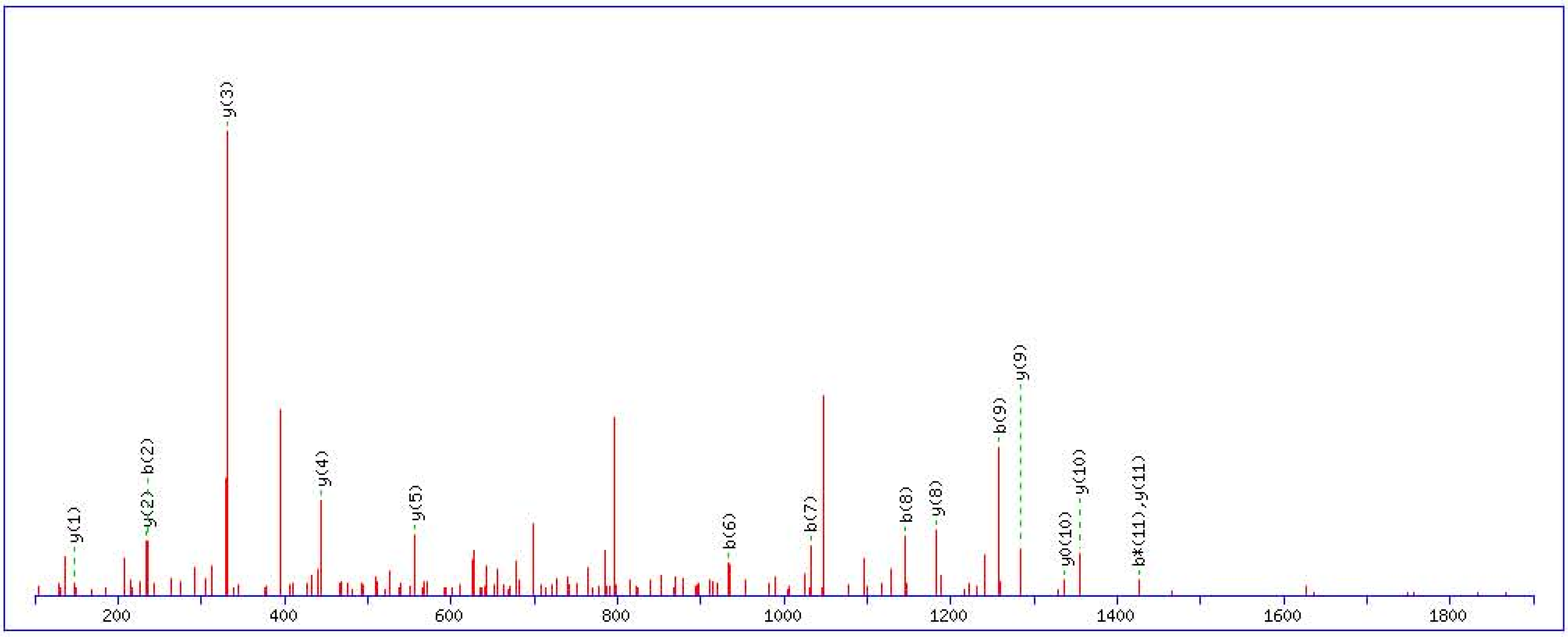
{MATRIX SCIENCE} Mascot Search Results

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

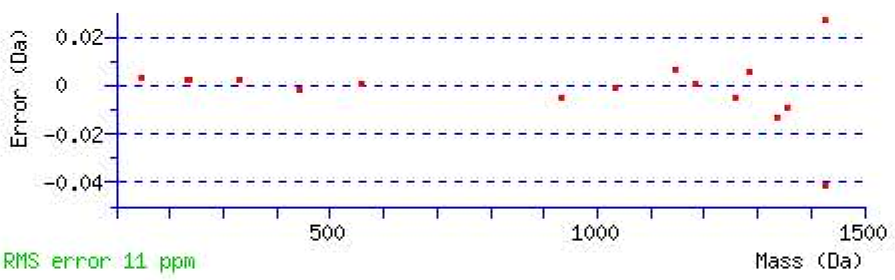
Match to Query 32676: 1587.861308 from(794.937930,2+) rtinseconds(2045) index(33415)
Title: Locus:1.1.1.3261.17 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

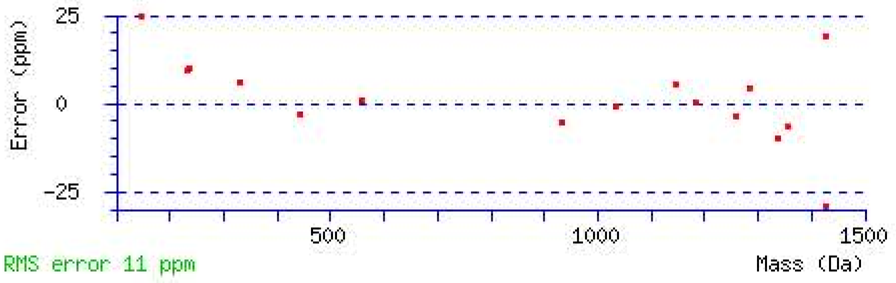
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 58 **Expect:** 5.4e-005
Matches : 16/114 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	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
58.4	1587.869431	-0.008123	YAATSQVLLPSK
12.1	1587.862045	-0.000737	VTGQNQEQFLLLAK
10.5	1587.841599	0.019709	QSTHLKDHRR
4.7	1587.874603	-0.013295	SFAFRSAIIQHRR
1.1	1587.862045	-0.000737	DGASLSPATLFIQIR
0.8	1587.840286	0.021022	DATRVLQMVLDGVR

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

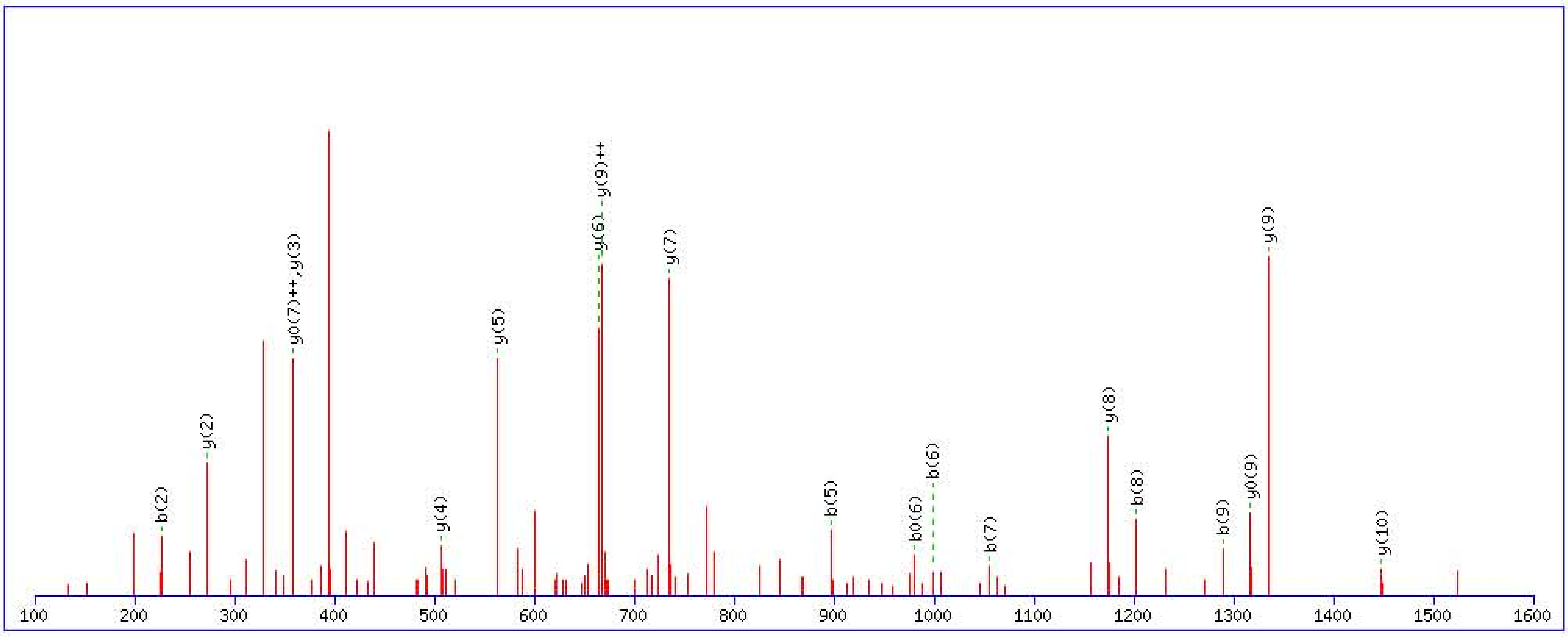
{MATRIX SCIENCE} Mascot Search Results

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

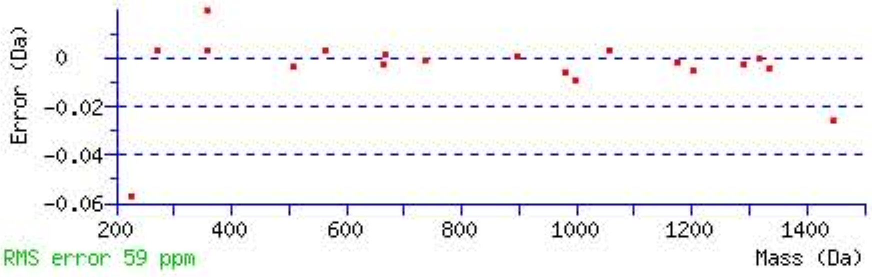
Match to Query 31367: 1559.800348 from(780.907450,2+) rtinseconds(1999) index(33195)
Title: Locus:1.1.1.3245.8 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

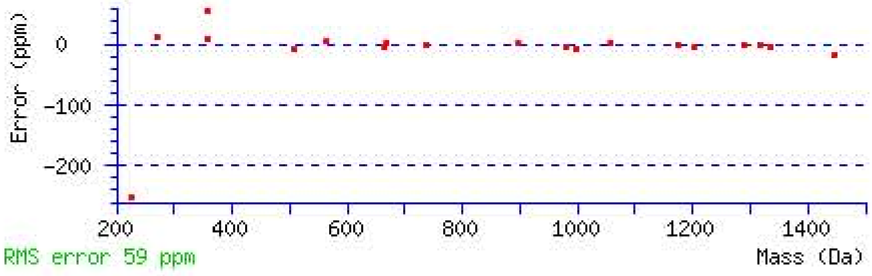
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1559.795242
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 67  Expect: 1.9e-006
Matches : 19/100 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							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
66.6	1559.795242	0.005106	LICQATGFSPR
5.4	1559.820190	-0.019842	MTRSATQAAKQVPR
4.3	1559.808960	-0.008612	LDRLSGLADQMVAR
3.0	1559.808975	-0.008627	LLDRDACDTVRVK

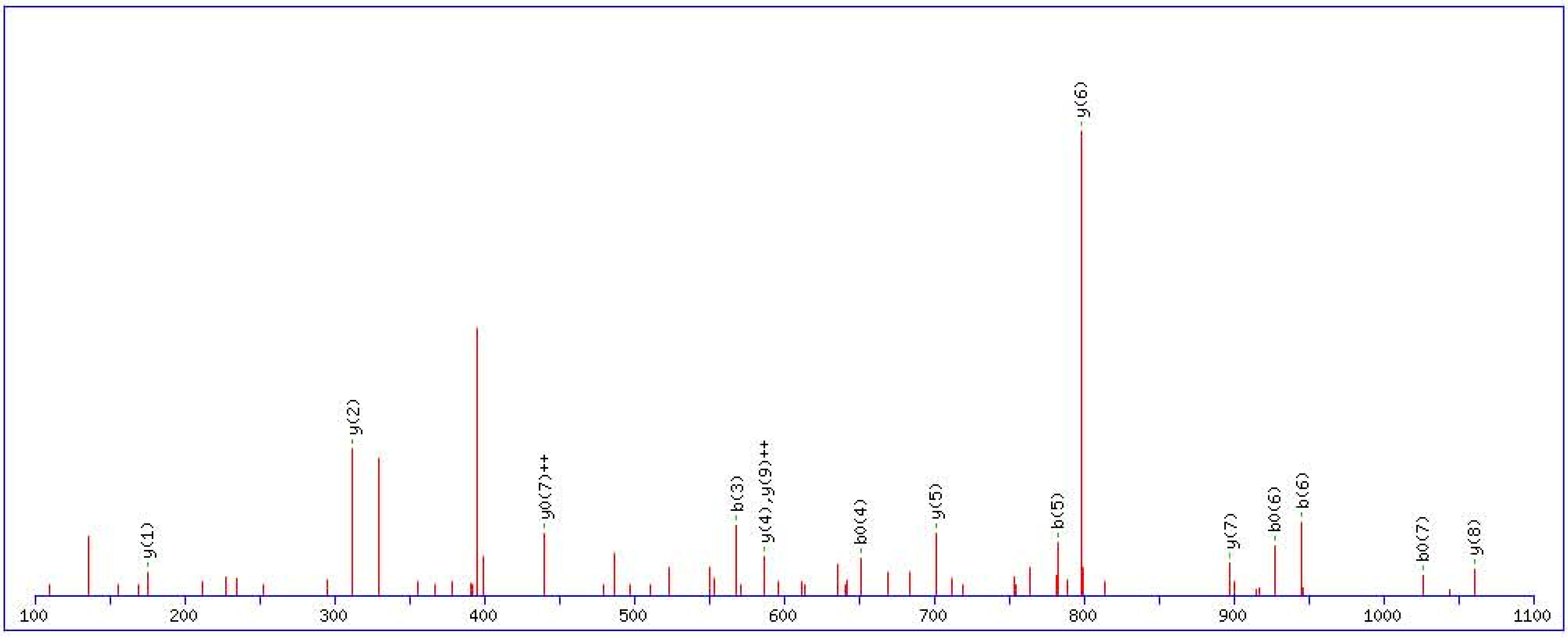
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GAQTLYVPNCDHR**
Found in **IBP6_HUMAN**, Insulin-like growth factor-binding protein 6 OS=Homo sapiens GN=IGFBP6 PE=1 SV=1

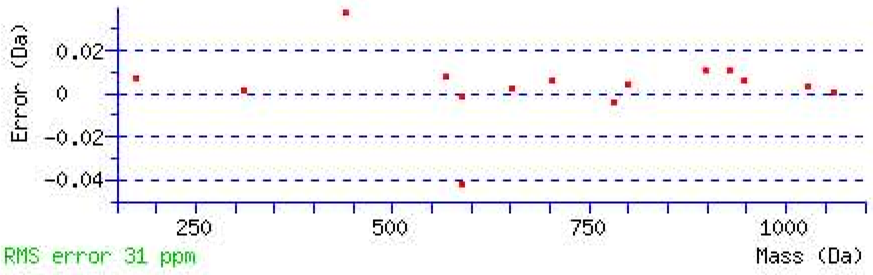
Match to Query 39231: 1840.872762 from(614.631530,3+) rtinseconds(1772) index(61231)
Title: Locus:1.1.1.3243.14 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

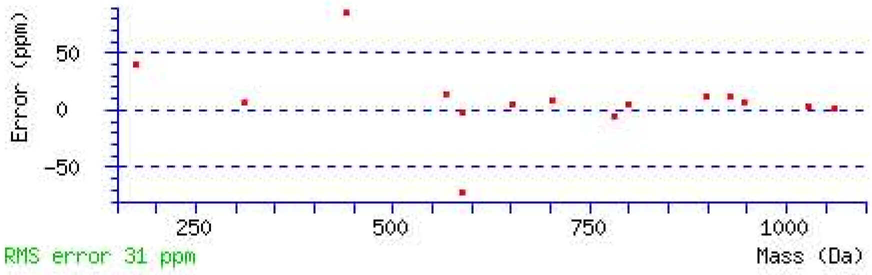
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1840.871262
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 47 **Expect:** 0.0003
Matches : 15/130 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							13
2	129.065854	65.036565					A	1784.857073	892.932175	1767.830524	884.418900	1766.846508	883.926892	12
3	**568.291180**	284.649228	551.264631	276.135954			Q	1713.819959	857.413618	1696.793410	848.900343	1695.809394	848.408335	11
4	669.338859	335.173068	652.312310	326.659793	651.328294	326.167785	T	1274.594633	637.800955	1257.568084	629.287680	1256.584068	628.795672	10
5	**782.422923**	391.715100	765.396374	383.201825	764.412358	382.709817	L	1173.546954	587.277115	1156.520405	578.763841	1155.536389	578.271833	9
6	**945.486252**	473.246764	928.459703	464.733490	927.475687	464.241482	Y	***1060.462890***	530.735083	1043.436341	522.221809	1042.452325	521.729801	8
7	1044.554666	522.780971	1027.528117	514.267697	1026.544101	513.775689	V	***897.399561***	449.203419	880.373012	440.690144	879.388996	440.198136	7
8	1141.607430	571.307353	1124.580881	562.794079	1123.596865	562.302071	P	***798.331147***	399.669212	781.304598	391.155937	780.320582	390.663929	6
9	1255.650357	628.328817	1238.623808	619.815542	1237.639792	619.323534	N	***701.278383***	351.142830	684.251834	342.629555	683.267818	342.137547	5
10	1415.681006	708.344141	1398.654457	699.830867	1397.670441	699.338859	C	***587.235456***	294.121366	570.208907	285.608092	569.224891	285.116084	4
11	1530.707949	765.857613	1513.681400	757.344338	1512.697384	756.852330	D	427.204807	214.106041	410.178258	205.592767	409.194242	205.100759	3
12	1667.766861	834.387069	1650.740312	825.873794	1649.756296	825.381786	H	***312.177864***	156.592570	295.151315	148.079295			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.2	1840.871262	0.001500	GAQTLYVPNCDHR
10.1	1840.887650	-0.014888	AALSASEGEEVPQDK
1.5	1840.873734	-0.000972	PEMTENETPTKKQHR
1.2	1840.892365	-0.019603	NNSPMAANQTPTLR

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

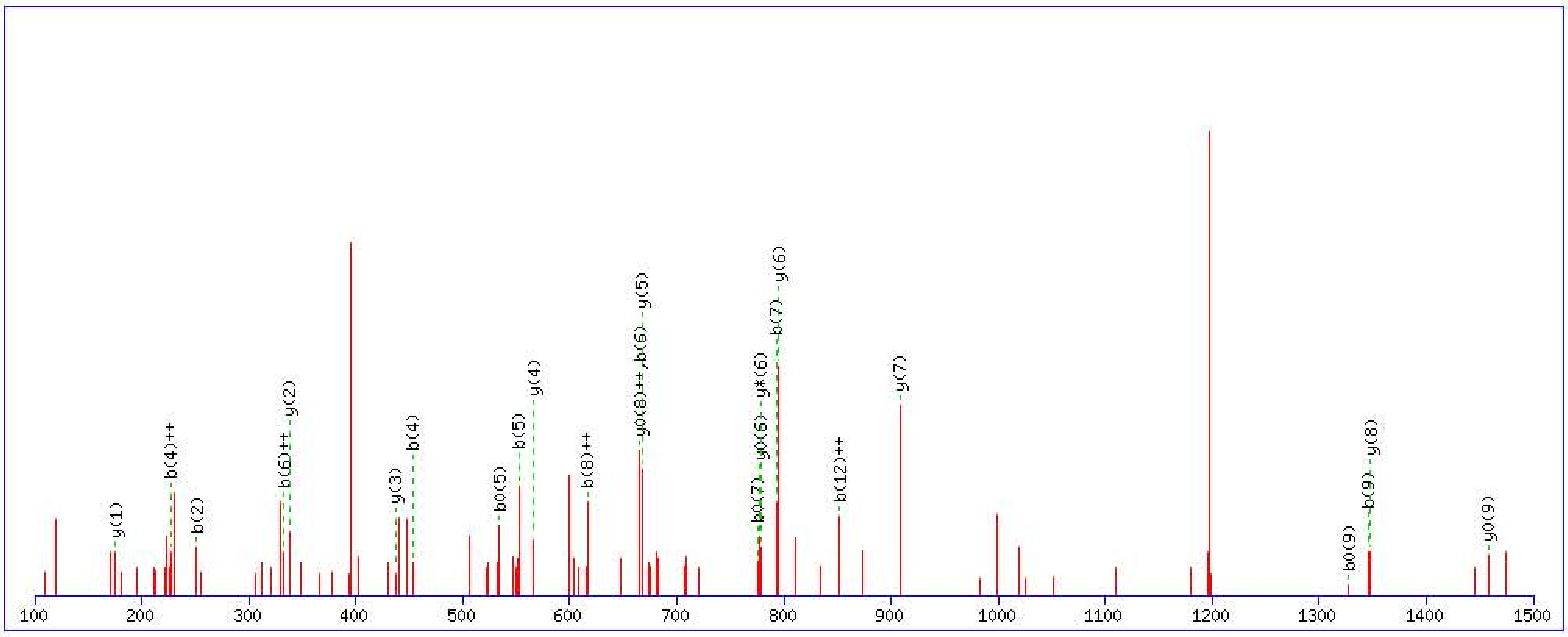
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HLDSVLQQLQTEVYR**
Found in **IBP6_HUMAN**, Insulin-like growth factor-binding protein 6 OS=Homo sapiens GN=IGFBP6 PE=1 SV=1

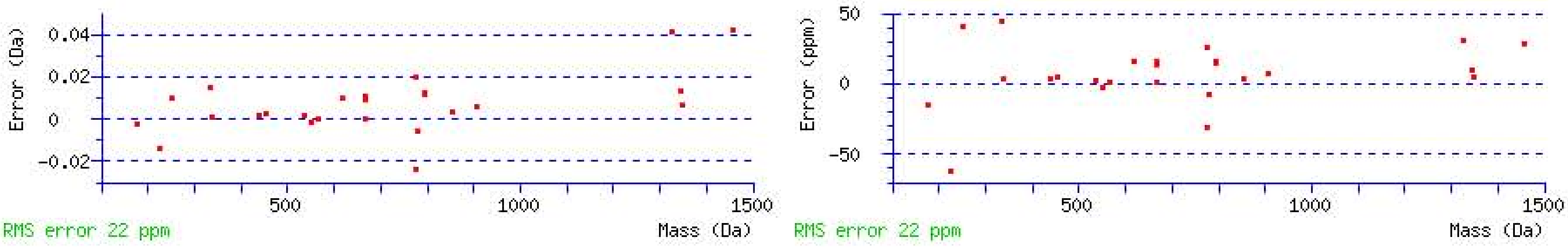
Match to Query 45027: 2139.118782 from(714.046870,3+) rtinseconds(2601) index(65762)
Title: Locus:1.1.1.3532.12 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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): 2139.114655
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.025
Matches : 25/146 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	138.066188	69.536732					H							15
2	***251.150252***	126.078764					L	2003.063026	1002.035151	1986.036477	993.521877	1985.052461	993.029869	14
3	366.177195	183.592235			348.166630	174.586953	D	1889.978962	945.493119	1872.952413	936.979845	1871.968397	936.487836	13
4	***453.209223***	**227.108250**			435.198658	218.102967	S	1774.952019	887.979648	1757.925470	879.466373	1756.941454	878.974365	12
5	***552.277637***	276.642457			534.267072	267.637174	V	1687.919991	844.463634	1670.893442	835.950359	1669.909426	835.458351	11
6	***665.361701***	**333.184489**			647.351136	324.179206	L	1588.851577	794.929427	1571.825028	786.416152	1570.841012	785.924144	10
7	***793.420279***	397.213778	776.393730	388.700503	775.409714	388.208495	Q	1475.767513	738.387395	1458.740964	729.874120	1457.756948	729.382112	9
8	1232.645605	**616.826440**	1215.619056	608.313166	1214.635040	607.821158	Q	***1347.708935***	674.358105	1330.682386	665.844831	1329.698370	665.352823	8
9	***1345.729669***	673.368472	1328.703120	664.855198	1327.719104	664.363190	L	***908.483609***	454.745443	891.457060	446.232168	890.473044	445.740160	7
10	1473.788247	737.397761	1456.761698	728.884487	1455.777682	728.392479	Q	***795.399545***	398.203411	778.372996	389.690136	777.388980	389.198128	6
11	1574.835926	787.921601	1557.809377	779.408326	1556.825361	778.916318	T	***667.340967***	334.174122	650.314418	325.660847	649.330402	325.168839	5
12	1703.878519	**852.442897**	1686.851970	843.929623	1685.867954	843.437615	E	***566.293288***	283.650282	549.266739	275.137008	548.282723	274.645000	4
13	1802.946933	901.977104	1785.920384	893.463830	1784.936368	892.971822	V	***437.250695***	219.128986	420.224146	210.615711			3
14	1966.010262	983.508769	1948.983713	974.995494	1947.999697	974.503486	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 HLDSVLQQLQTEVYR
(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	2139.114655	0.004127	HLDSVLQQLQTEVYR
21.8	2139.114655	0.004127	HLDSVLQQLQTEVYR
11.9	2139.114655	0.004127	HLDSVLQQLQTEVYR

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

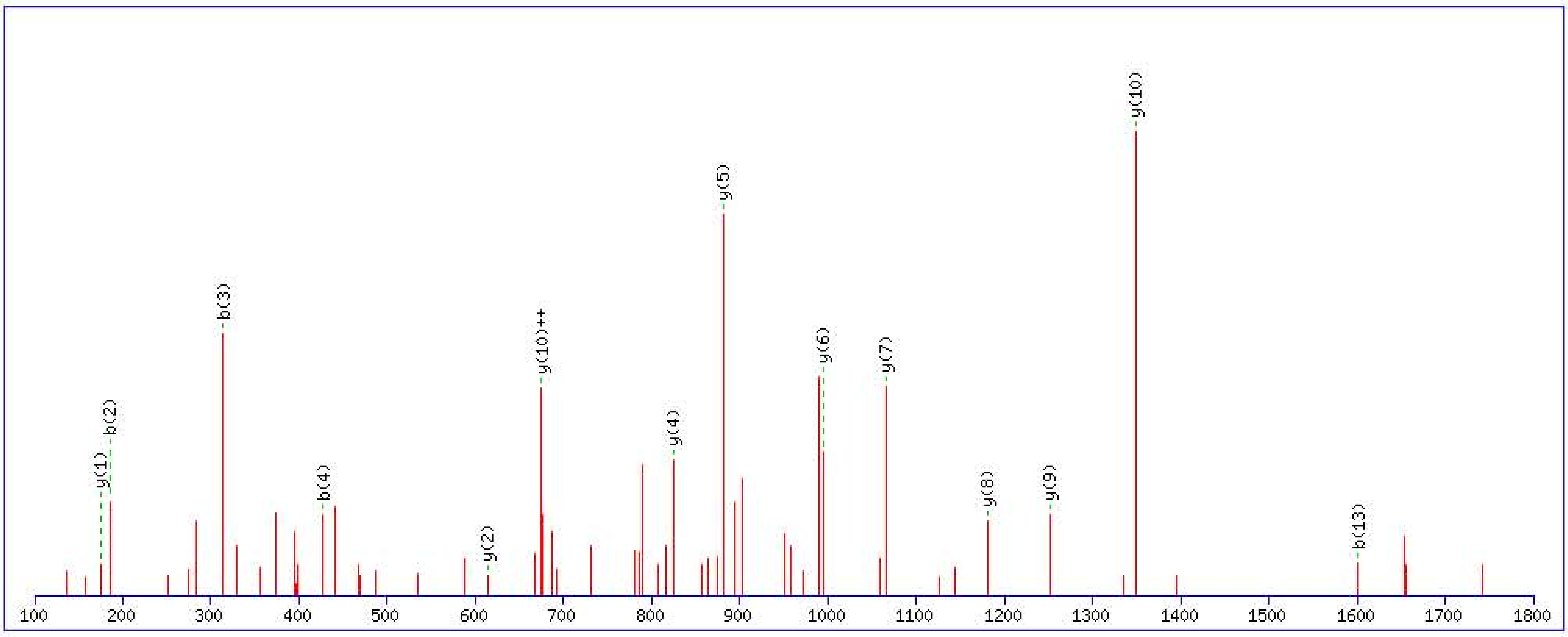
{MATRIX SCIENCE} Mascot Search Results

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

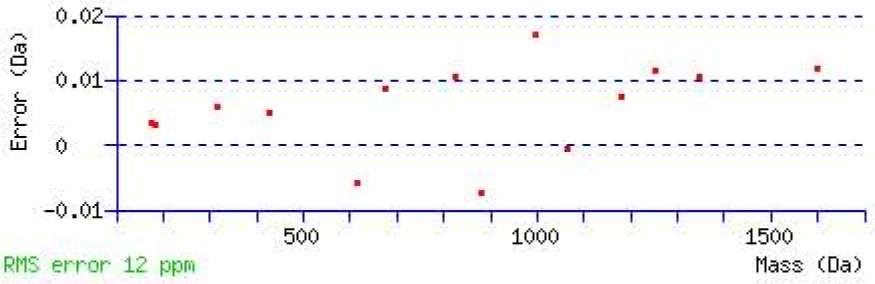
Match to Query 38064: 1773.990048 from(888.002300,2+) rtinseconds(2466) index(35528)
Title: Locus:1.1.1.3408.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

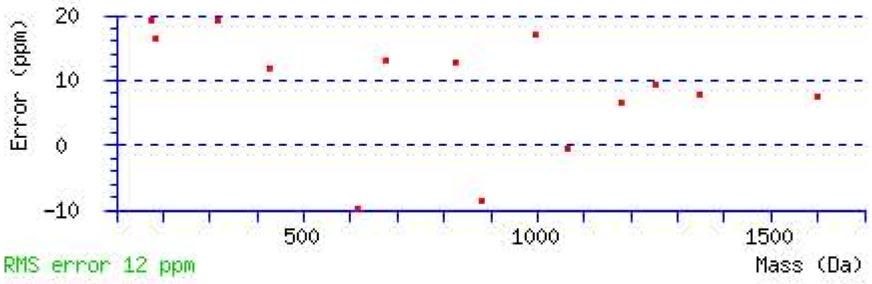
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1773.981094
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.00019
Matches : 14/114 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							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
48.6	1773.981094	0.008954	LAELPADALGPLQR

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

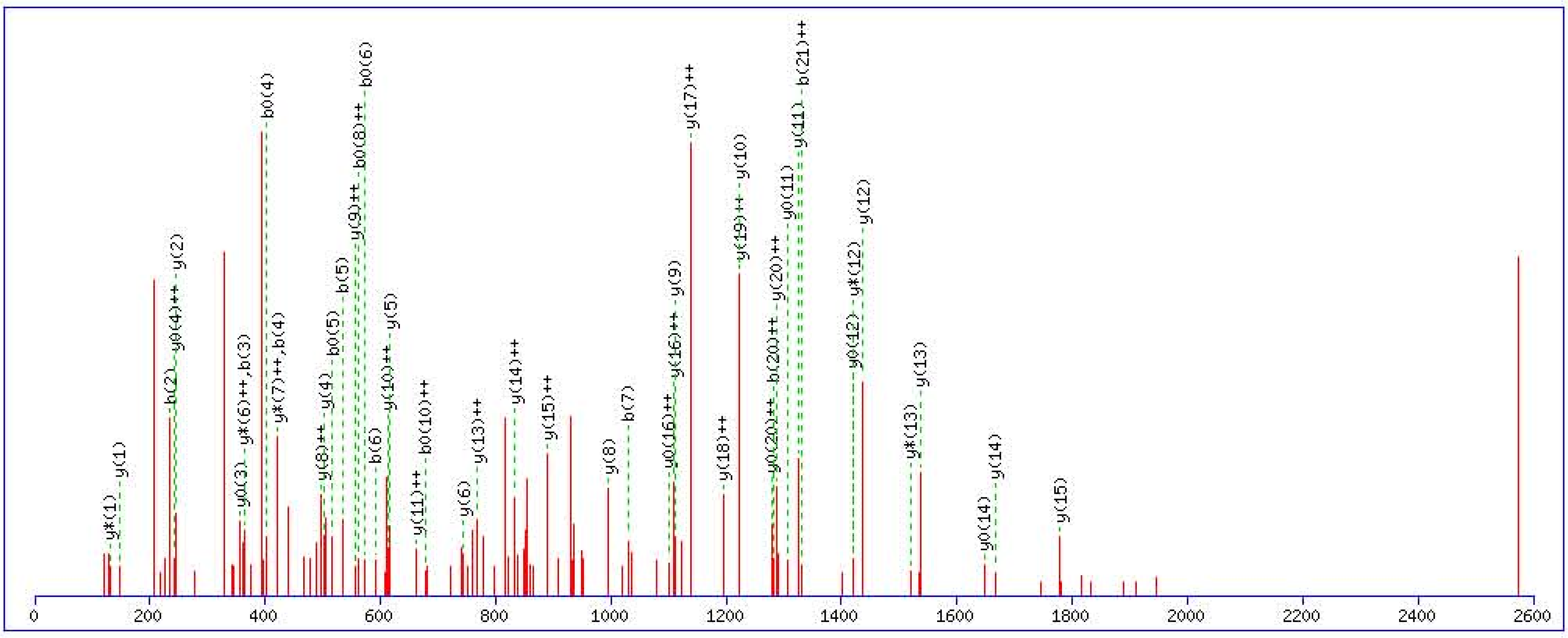
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFEGLGQLEVLTLDHNQLQEVK**
Found in **ALS_HUMAN**, Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1

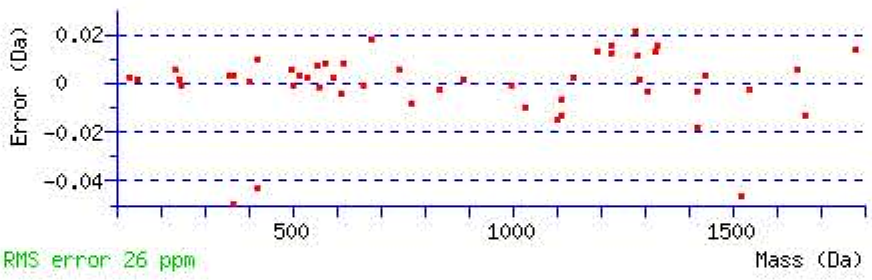
Match to Query 53865: 2807.467872 from(936.829900,3+) rtinseconds(2722) index(37025)
Title: Locus:1.1.1.3496.21 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

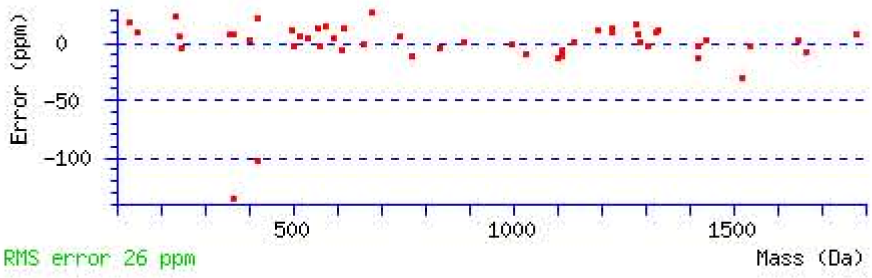
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2807.452759
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 64  Expect: 8.9e-006
Matches : 50/236 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	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 SFEGLGQLEVLTLDHNQLQEVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.3	2807.452759	0.015113	SFEGLGQLEVLTLDHNQLQEVK
9.0	2807.452759	0.015113	SFEGLGQLEVLTLDHNQLQEVK

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

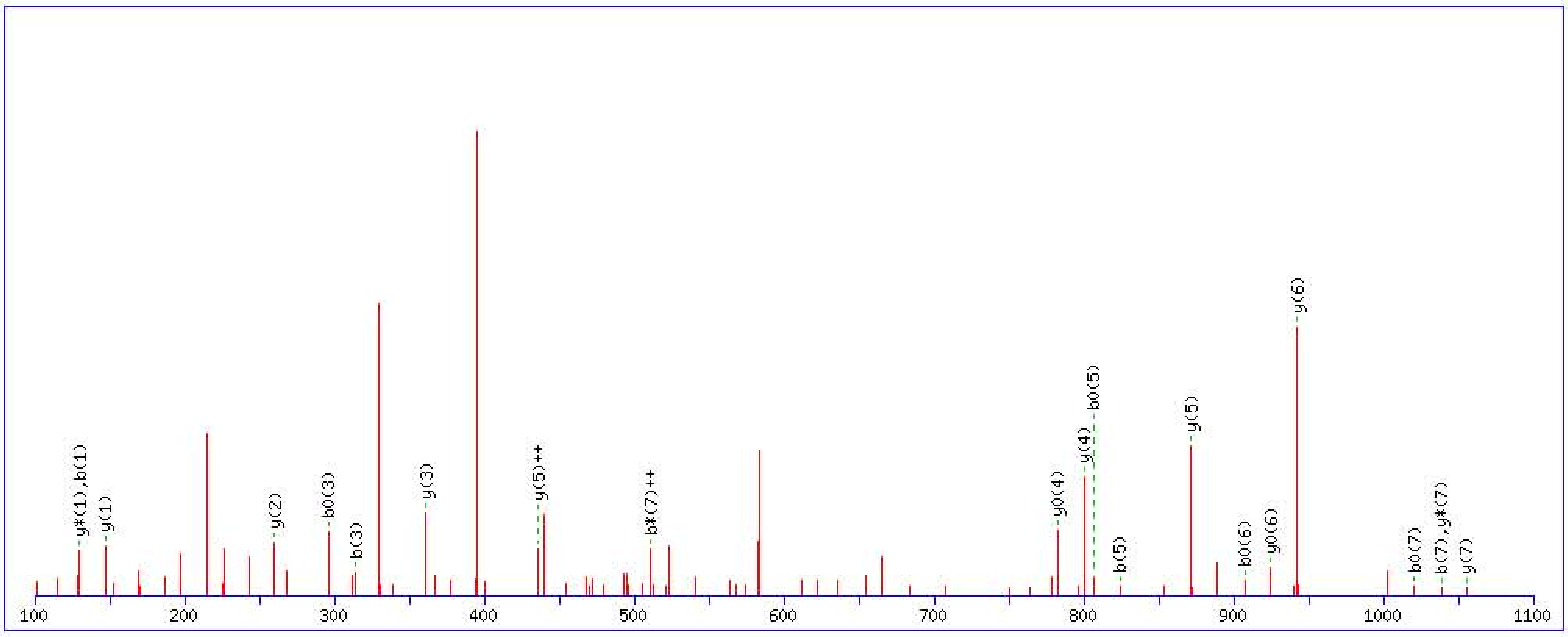
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELAAQTIK**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

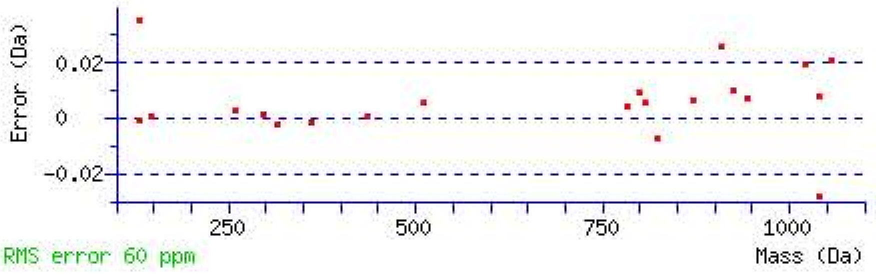
Match to Query 19966: 1183.664828 from(592.839690,2+) rtinseconds(1718) index(45556)
Title: Locus:1.1.1.2647.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

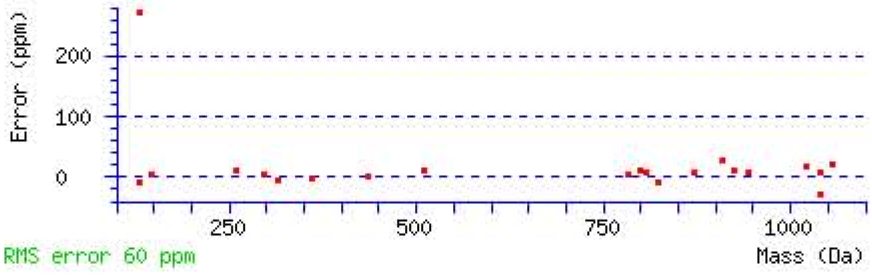
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1183.663452
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.0055
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	0.001376	ELAAQTIK
24.8	1183.663452	0.001376	ELAAQITK
7.8	1183.681198	-0.016370	LEALLEAAGIGK
7.4	1183.663452	0.001376	LEQAATLK
7.0	1183.660080	0.004748	AIEAVAISPWK
7.0	1183.667282	-0.002454	GKQASEPALRK
6.3	1183.656937	0.007891	MRPQTLK
5.7	1183.667297	-0.002469	EPTGRVEIRK
5.0	1183.681229	-0.016401	NTLAIPLTDVK
4.1	1183.667282	-0.002454	QLLRALEEGR

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

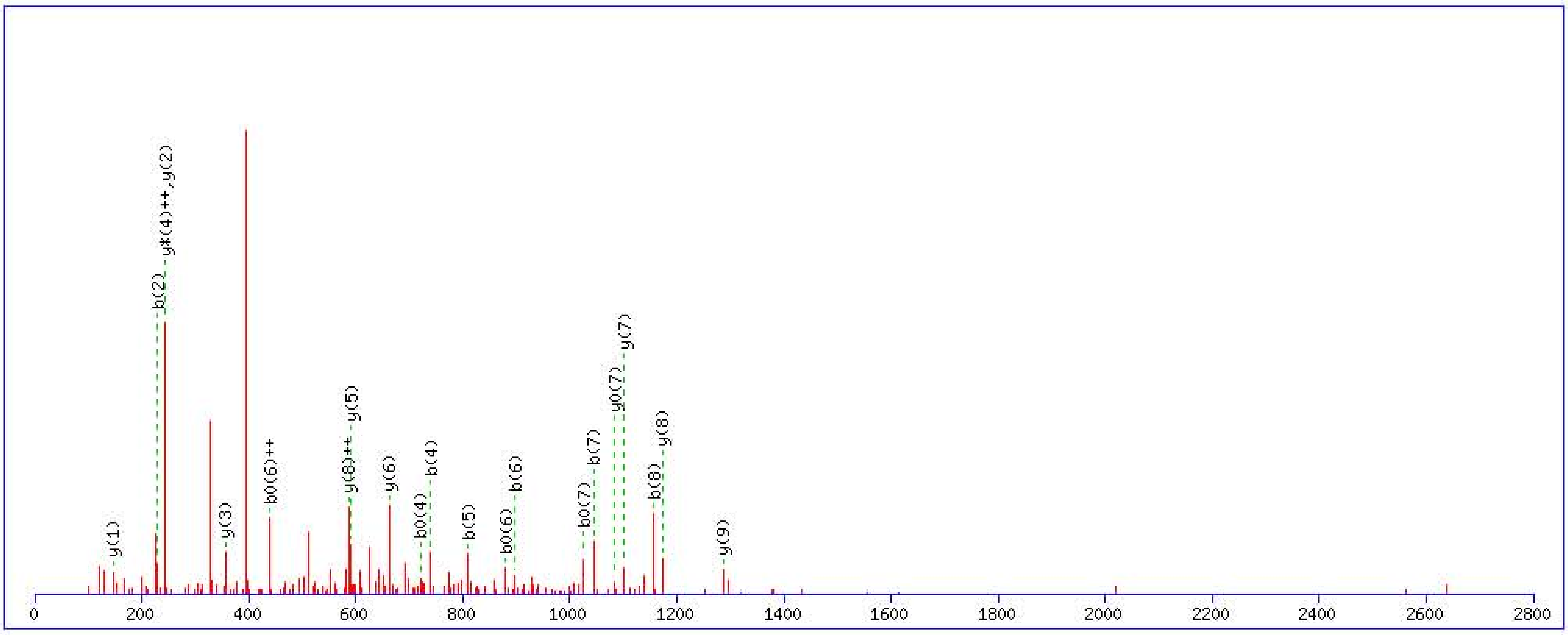
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDAQASFLPK**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

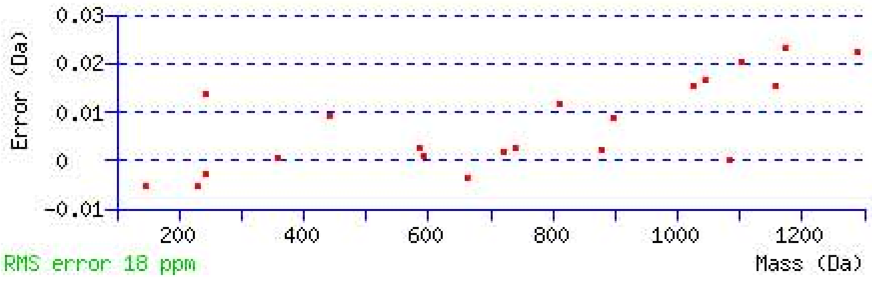
Match to Query 26332: 1399.764468 from(700.889510,2+) rtinseconds(2219) index(48728)
Title: Locus:1.1.1.2821.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

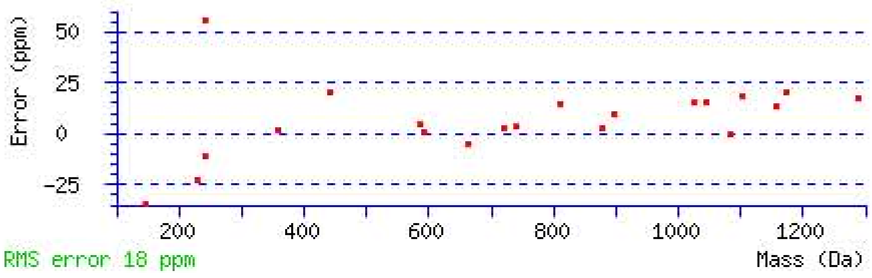
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1399.753342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 44  Expect: 0.00049
Matches : 21/92 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					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
44.3	1399.753342	0.011126	LDAQASFLPK
8.6	1399.745972	0.018496	IDAATGIPVTTWR
3.0	1399.778275	-0.013807	LSRLQEKEELR
2.1	1399.767059	-0.002591	EKAVTDEKPKQK

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

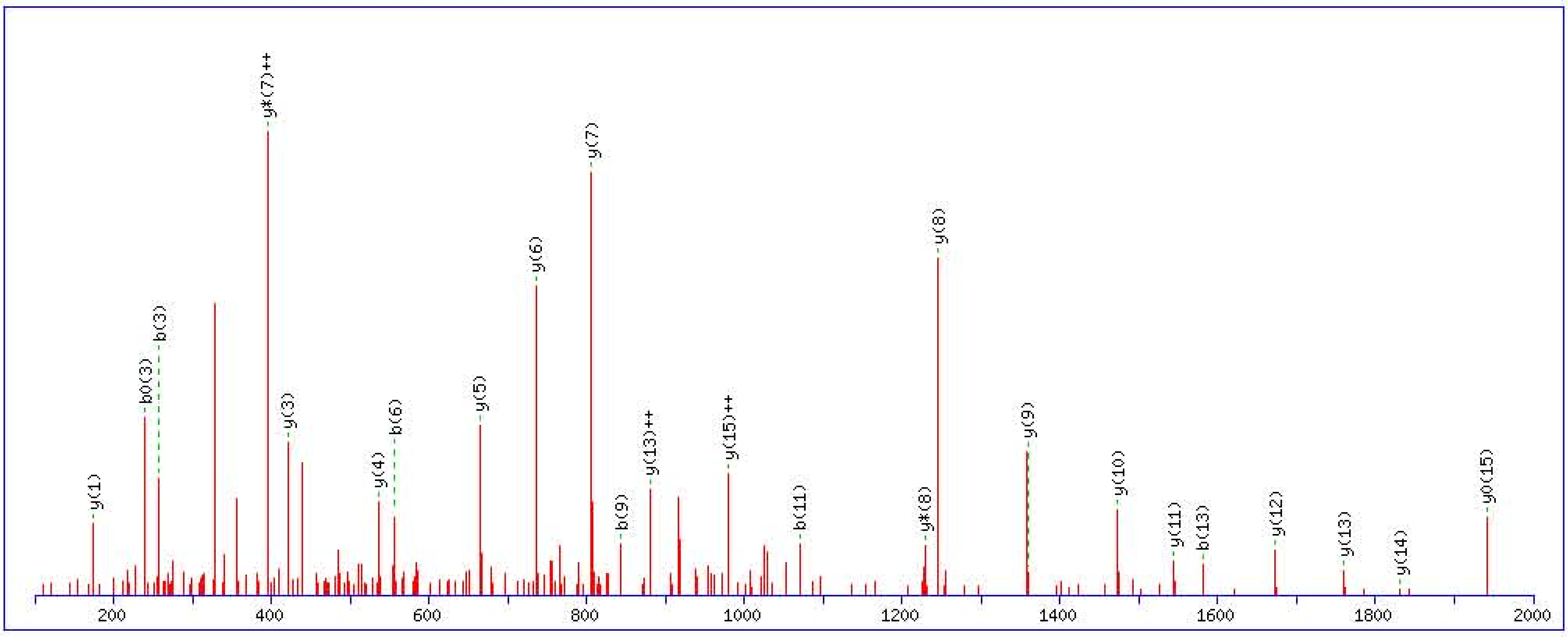
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSLVQASEANLQAAQDFVR**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

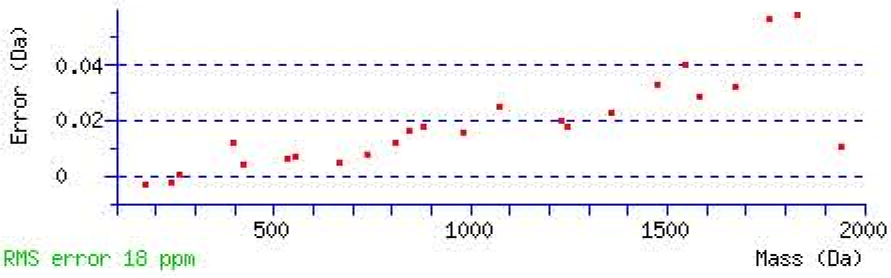
Match to Query 48008: 2314.204092 from(772.408640,3+) rtinseconds(2550) index(50621)
Title: Locus:1.1.1.2936.8 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

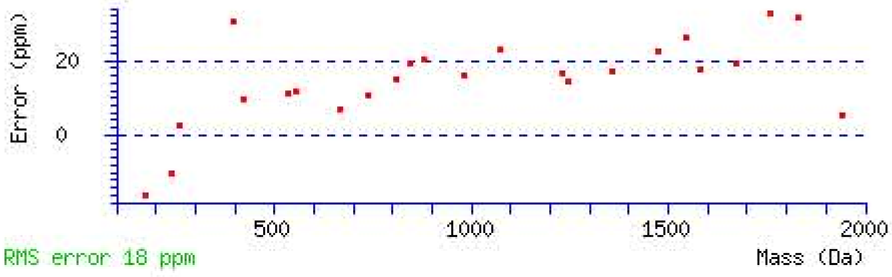
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2314.173950
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12    : Biotin:Thermo-21345 (Q)
Ions Score: 95  Expect: 2e-009
Matches : 24/200 fragment ions using 37 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							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
95.1	2314.173950	0.030142	GSLVQASEANLQAAQDFVR
56.9	2314.173950	0.030142	GSLVQASEANLQAAQDFVR
15.6	2314.173950	0.030142	GSLVQASEANLQAAQDFVR
2.2	2314.178635	0.025457	NKDRPAMQLYQPGARSR

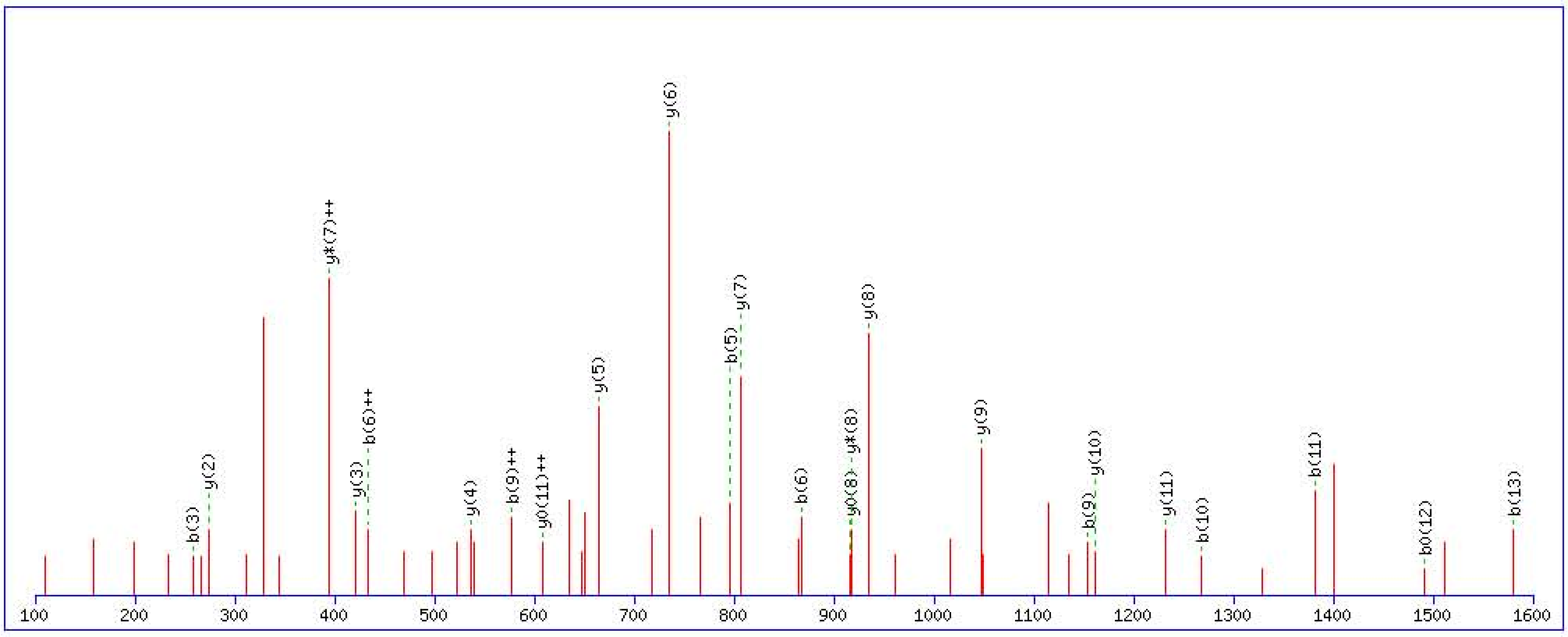
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSLVQASEANLQAAQDFVR**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

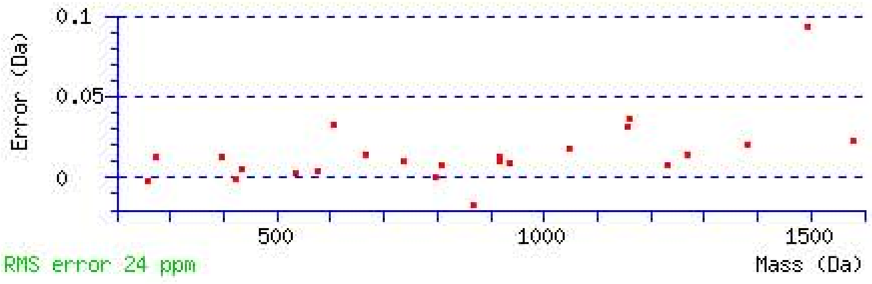
Match to Query 48009: 2314.206282 from(772.409370,3+) rtinseconds(2504) index(50333)
Title: Locus:1.1.1.2920.18 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

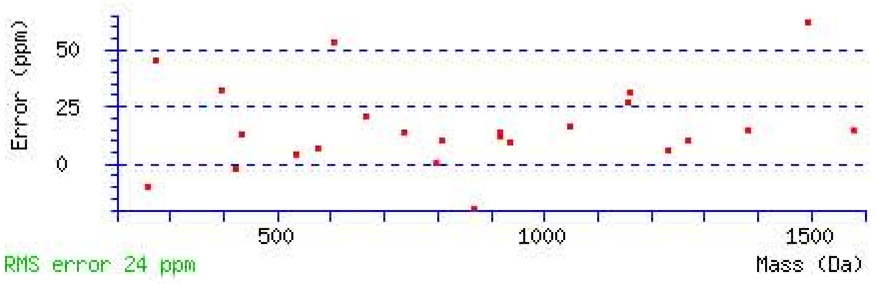
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 64  Expect: 1.2e-005
Matches : 24/200 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	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
63.6	2314.173950	0.032332	GSLVQASEANLQAAQDFVR
13.4	2314.173950	0.032332	GSLVQASEANLQAAQDFVR

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

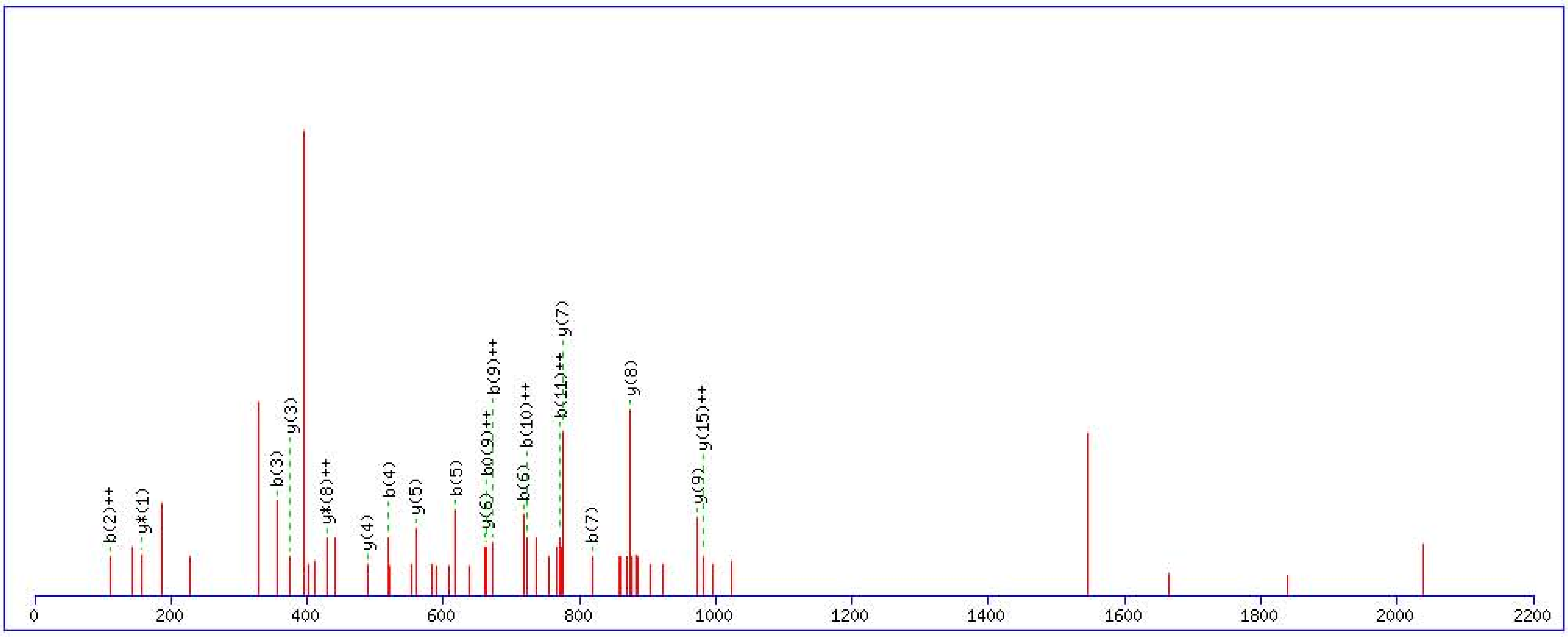
Mascot Search Results

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

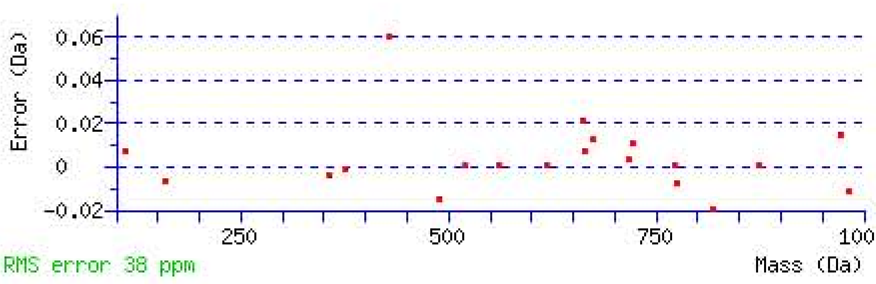
Match to Query 48039: 2316.183582 from(773.068470,3+) rtinseconds(1953) index(47093)
Title: Locus:1.1.1.2728.21 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

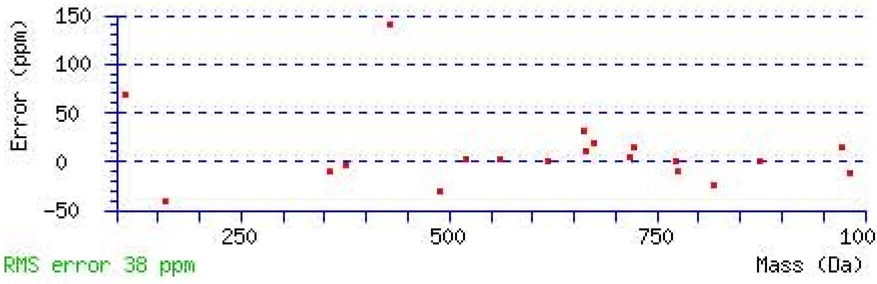
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2316.168488
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9     : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.014
Matches : 20/172 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	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
32.8	2316.168488	0.015094	FAHYVVTSQVVNTANEAR

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

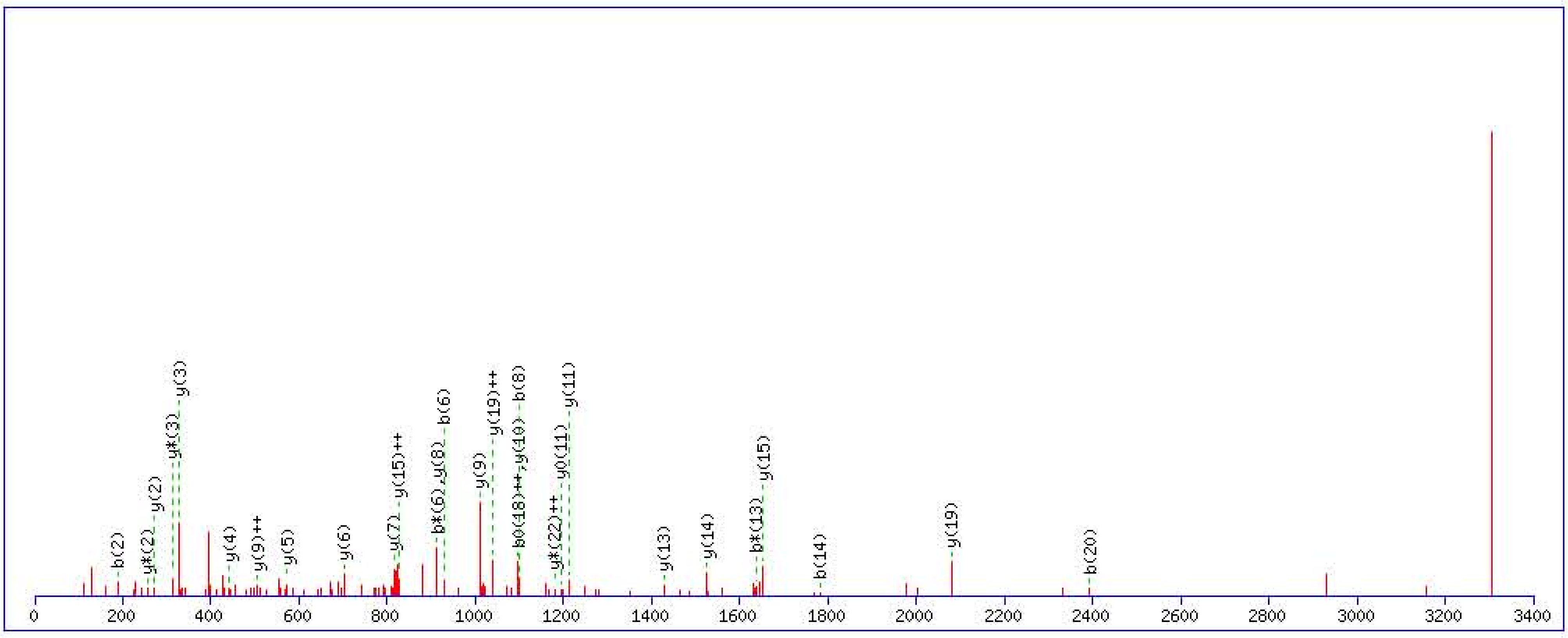
MATRIX SCIENCE Mascot Search Results

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

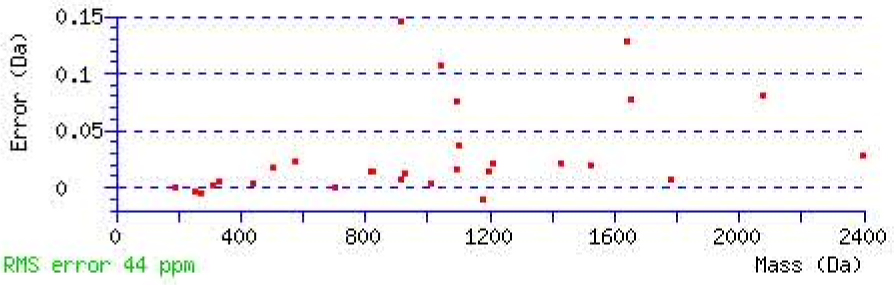
Match to Query 60222: 3304.652816 from(827.170480,4+) rtinseconds(2221) index(48741)
Title: Locus:1.1.1.2821.23 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

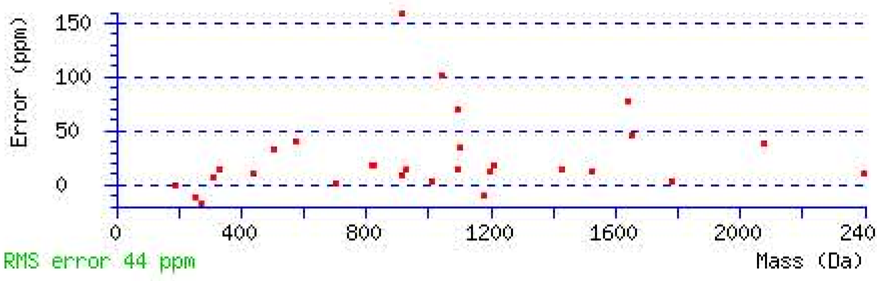
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3304.614151
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 35 **Expect:** 0.0094
Matches : 29/300 fragment ions using 107 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
34.9	3304.614151	0.038665	GMADQDGLKPTIDKPSEDSPPLEMLGPR

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

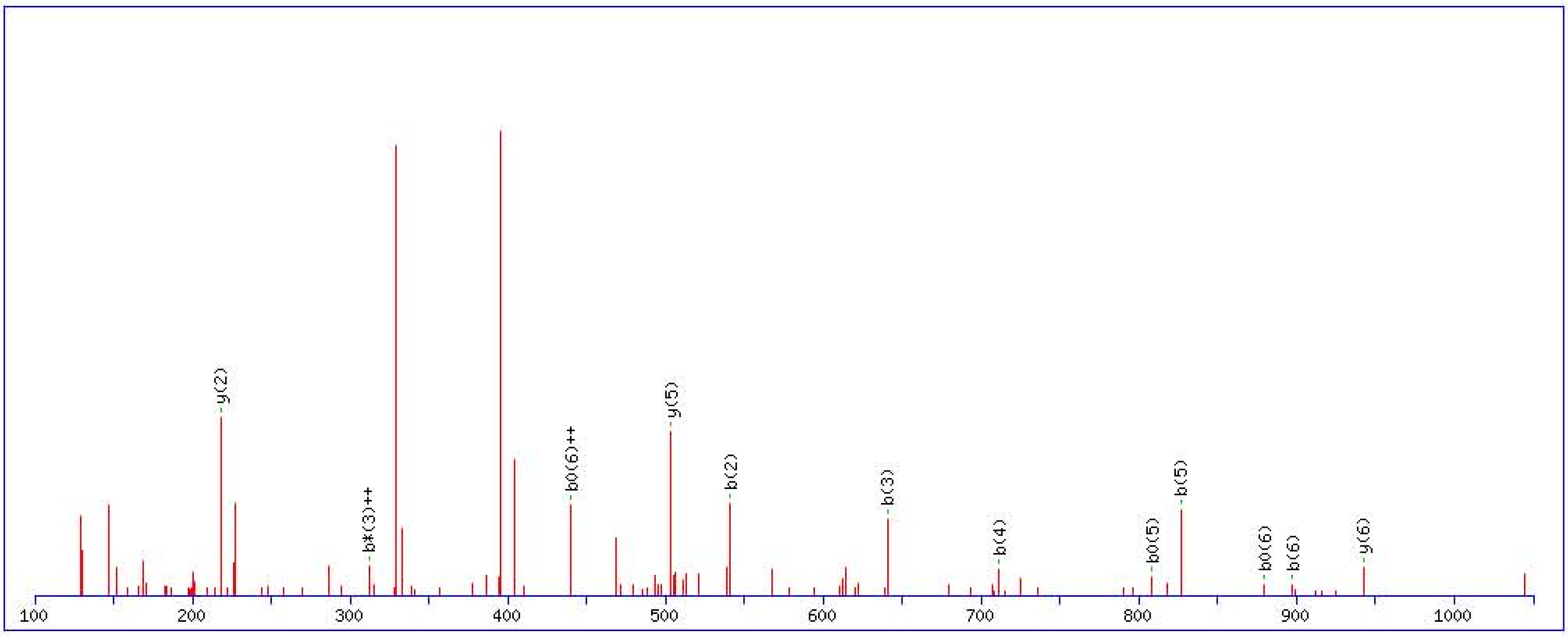
Mascot Search Results

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

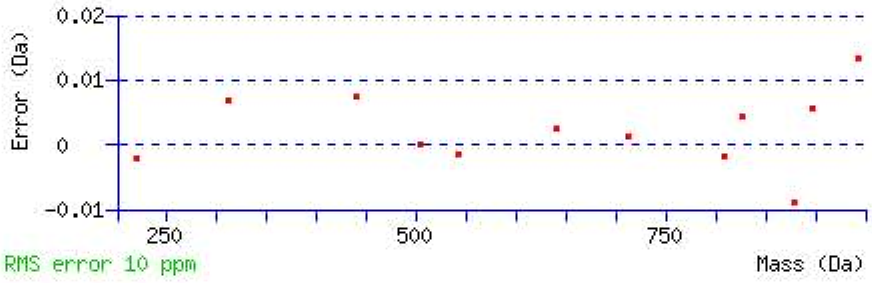
Match to Query 14872: 1042.545688 from(522.280120,2+) rtinseconds(1300) index(43036)
Title: Locus:1.1.1.2501.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

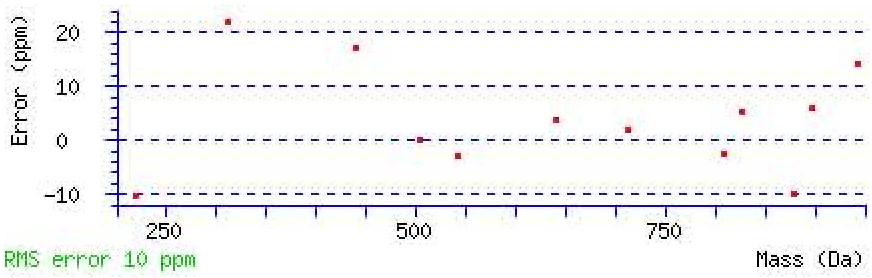
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1042.548111
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.013
Matches : 12/66 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							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
32.9	1042.548111	-0.002423	TQVADAK
14.5	1042.548096	-0.002408	SLQADAK
10.8	1042.534164	0.011524	QEAHKRMK
8.9	1042.540726	0.004962	KPVSEVGDGR
8.0	1042.538223	0.007465	SCKHVVWK
6.0	1042.544739	0.000949	GLEWVGSPAK
6.0	1042.544724	0.000964	WKGIEPGEK
5.2	1042.548096	-0.002408	QEAGLSK
4.8	1042.548080	-0.002392	KEQEAK
4.7	1042.540680	0.005008	EAEKRPADK

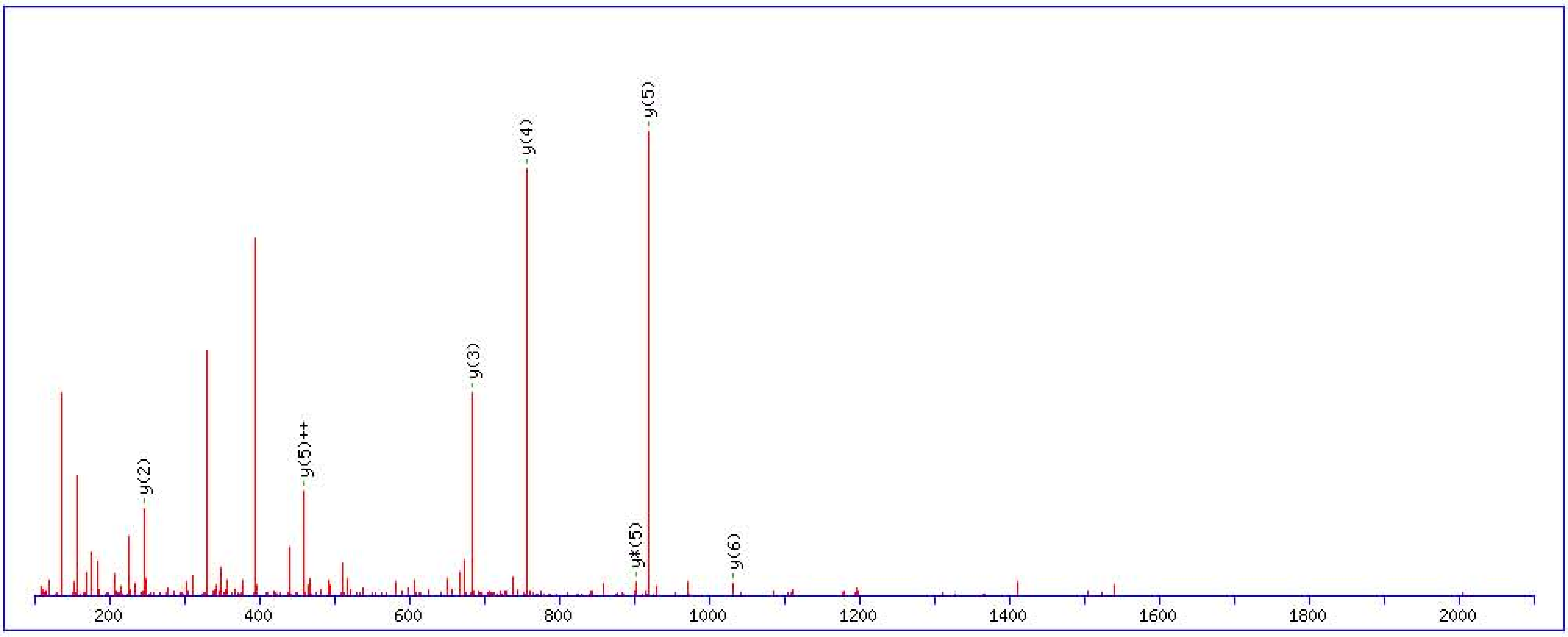
Mascot Search Results

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

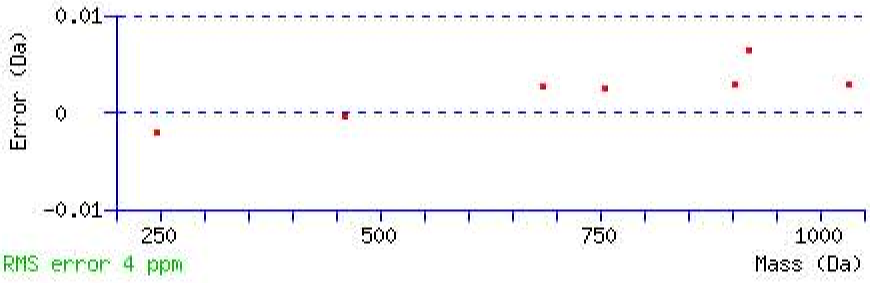
Match to Query 16206: 1102.594728 from(552.304640,2+) rtinseconds(1633) index(45054)
Title: Locus:1.1.1.2617.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

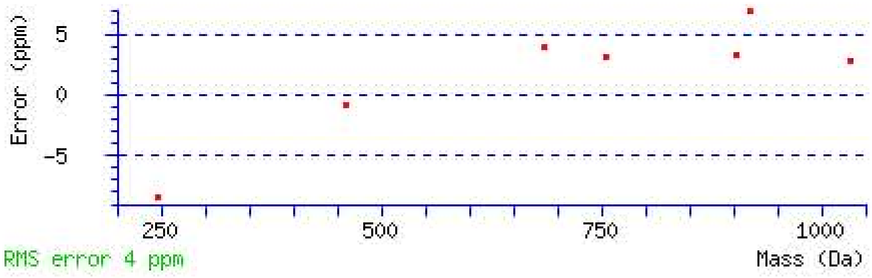
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1102.595703
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.0035
Matches : 7/40 fragment ions using 10 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	#
1	72.044390	36.525833			A					7
2	185.128454	93.067865			L	***1032.565899***	516.786588	1015.539350	508.273313	6
3	348.191783	174.599529			Y	***919.481835***	460.244556	902.455286	451.731281	5
4	419.228897	210.118087			A	***756.418506***	378.712891	739.391957	370.199617	4
5	858.454223	429.730750	841.427674	421.217475	Q	***685.381392***	343.194334	668.354843	334.681060	3
6	929.491337	465.249307	912.464788	456.736032	A	***246.156066***	123.581671	229.129517	115.068397	2
7					R	175.118952	88.063114	158.092403	79.549840	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.7	1102.595703	-0.000975	ALYAQAR
10.9	1102.602234	-0.007506	AIELGYNPVK
8.5	1102.580460	0.014268	AMVENVTLAR
6.1	1102.591660	0.003068	AMKRLEEAR
5.7	1102.598221	-0.003493	LAGSLATDLSR
5.5	1102.588333	0.006395	SPYGLTPRGR
3.8	1102.591690	0.003038	NMEVSLVRR
3.6	1102.598221	-0.003493	DDLKATLTAR
3.6	1102.584305	0.010423	QSSQRGLTAR
3.0	1102.610321	-0.015593	ALGMMGLVRR

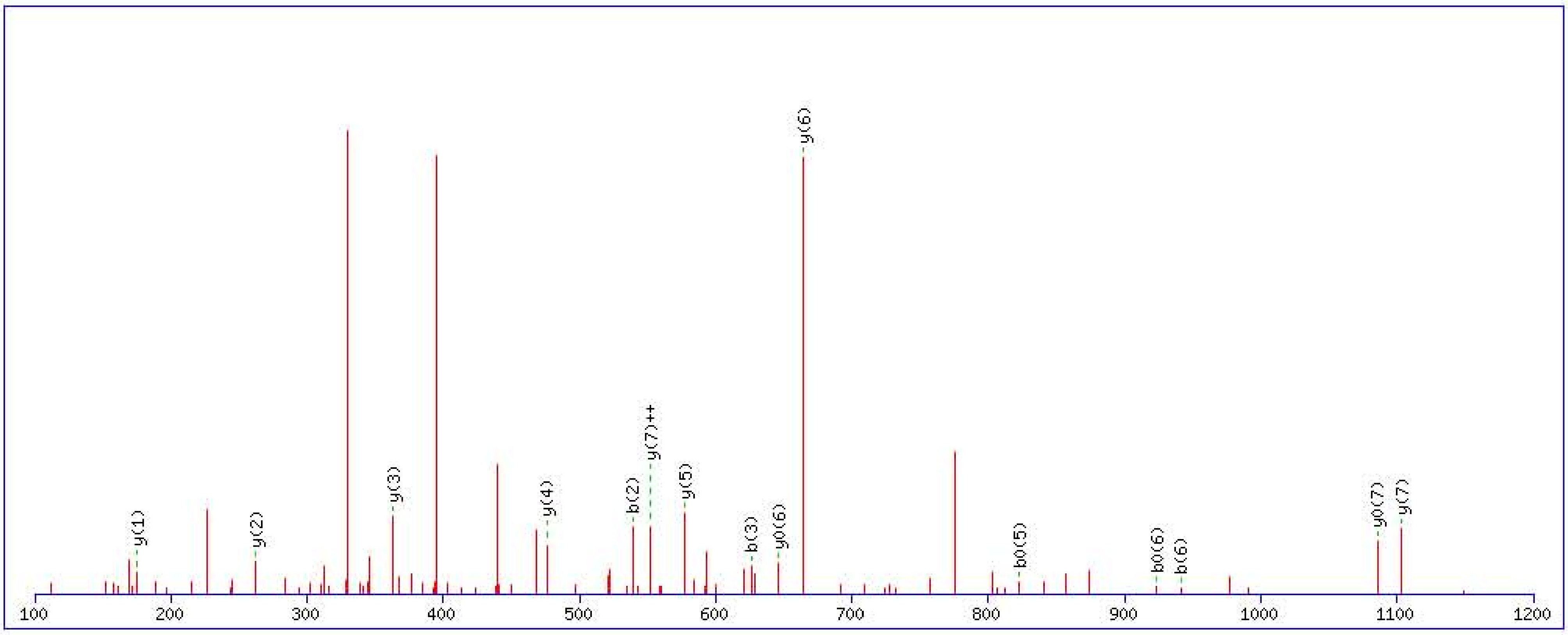
{MATRIX SCIENCE} Mascot Search Results

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

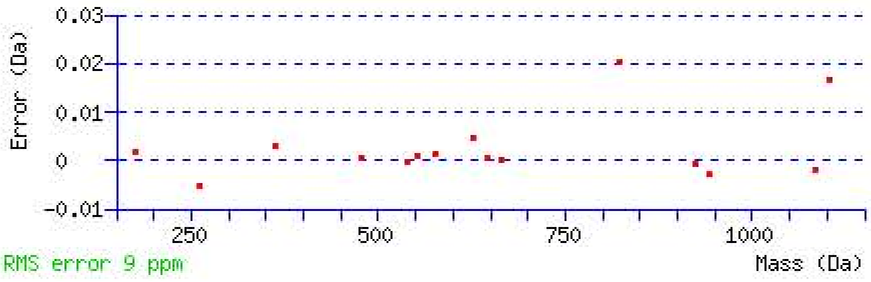
Match to Query 20361: 1201.649908 from(601.832230,2+) rtinseconds(1495) index(44169)
Title: Locus:1.1.1.2569.7 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

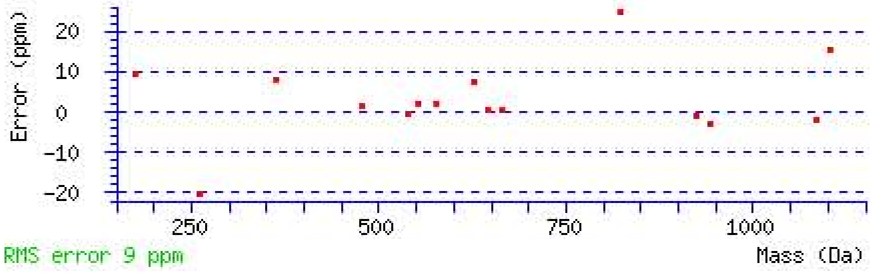
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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:** 0.00072
Matches : 15/76 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							8
2	**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



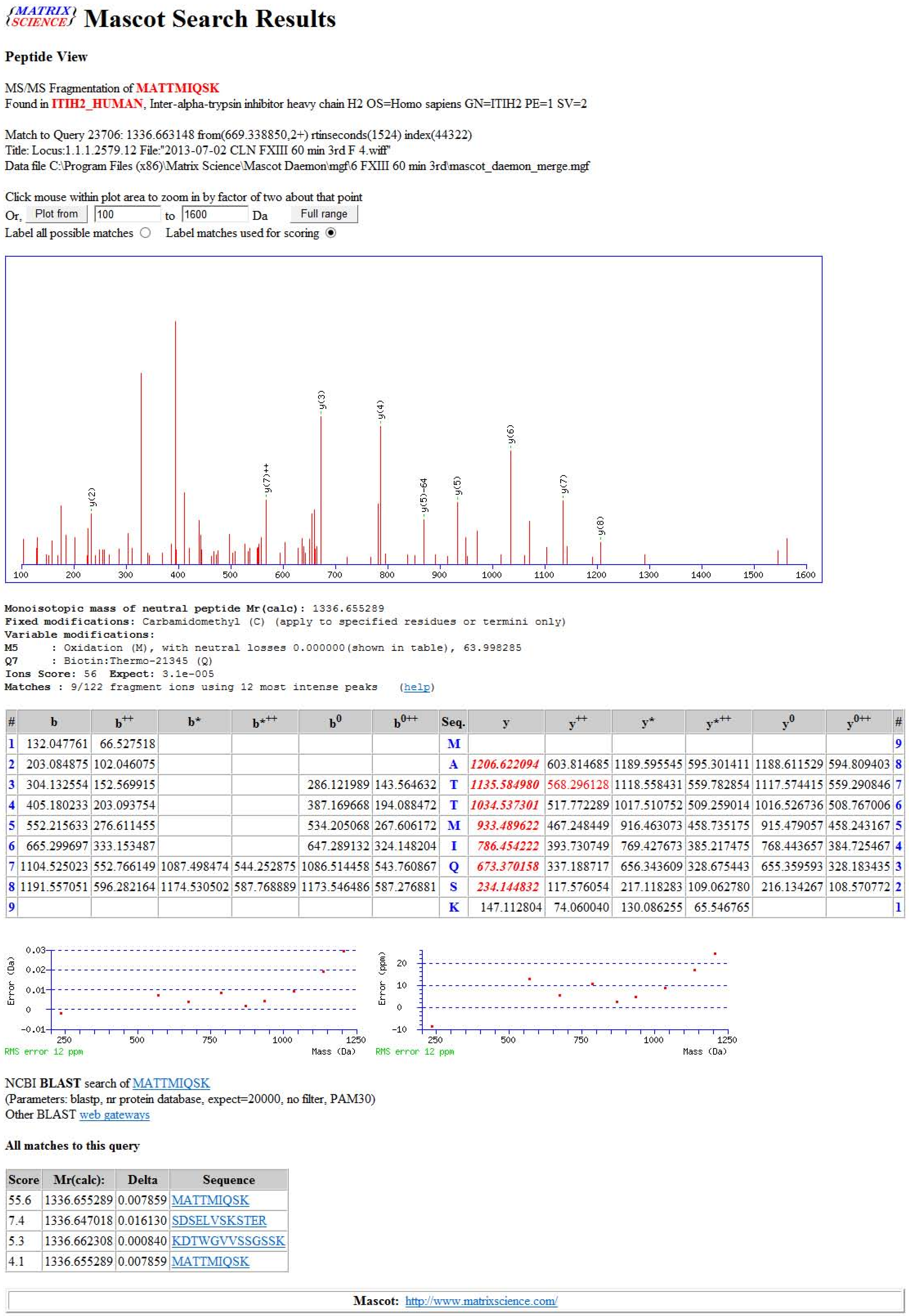


NCBI **BLAST** search of VQSTITSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.9	1201.648895	0.001013	VQSTITSR
4.1	1201.638992	0.010916	VQPPSHAR
1.2	1201.660767	-0.010859	VWKPQLFER
0.0	1201.638992	0.010916	VQGREFR

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



Mascot Search Results

Peptide View

MS/MS Fragmentation of **MATTMIQSK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

Match to Query 23706: 1336.663148 from(669.338850,2+) rtinseconds(1524) index(44322)
Title: Locus:1.1.1.2579.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\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: 56 **Expect:** 3.1e-005
Matches : 9/122 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

RMS error 12 ppm

RMS error 12 ppm

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
55.6	1336.655289	0.007859	MATTMIQSK
7.4	1336.647018	0.016130	SDSELVSKSTER
5.3	1336.662308	0.000840	KDTWGVVSSGSSK
4.1	1336.655289	0.007859	MATTMIQSK

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

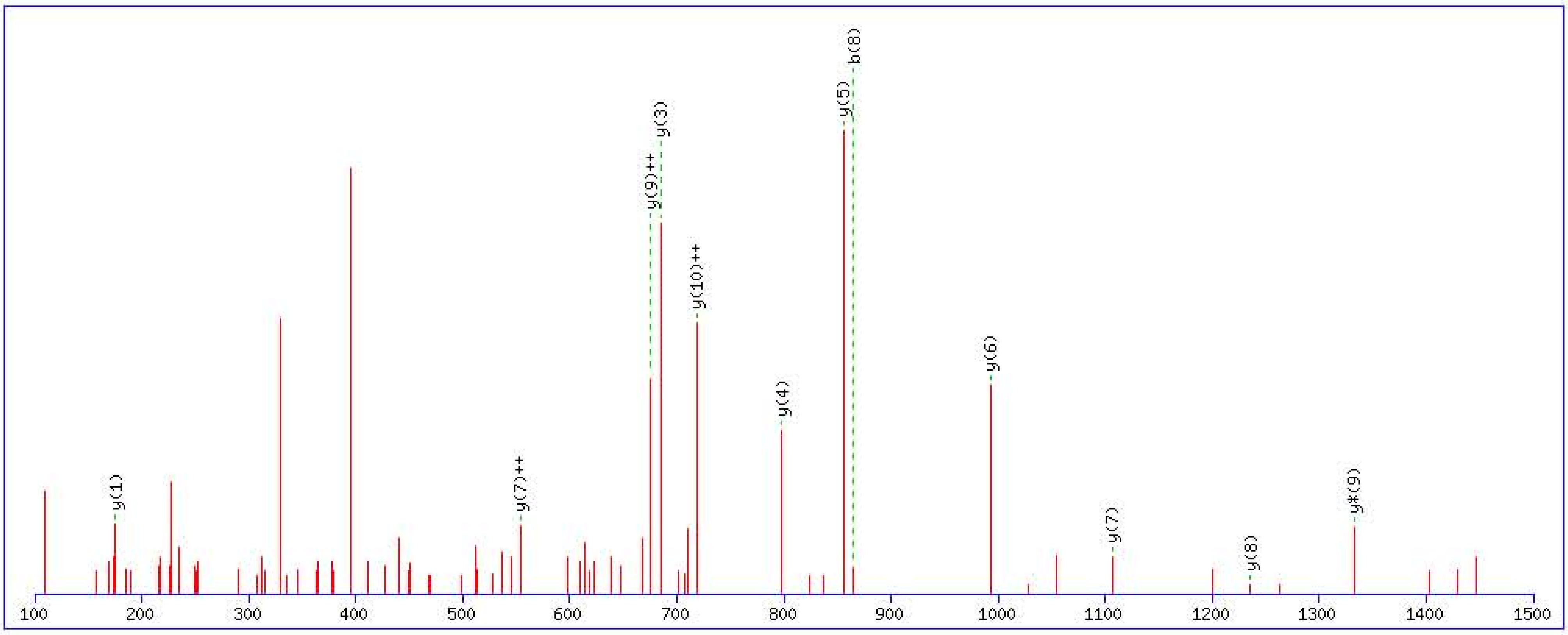
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSNENHGIAQR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

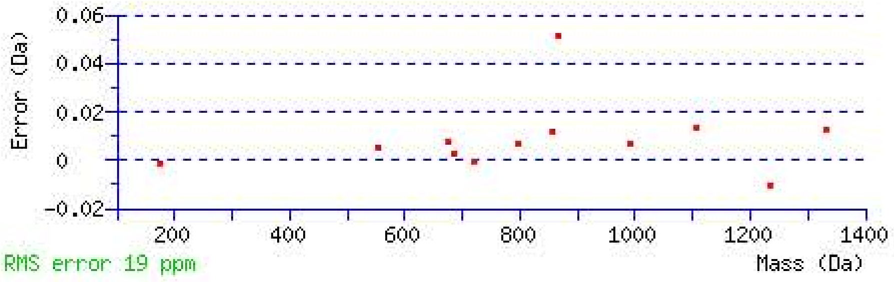
Match to Query 31128: 1548.765582 from(517.262470,3+) rtinseconds(1418) index(43645)
Title: Locus:1.1.1.2542.16 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

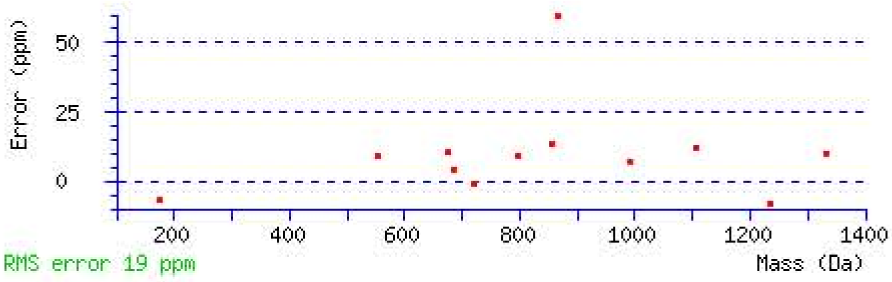
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 34  Expect: 0.00073
Matches : 12/100 fragment ions using 26 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							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
33.9	1548.783066	-0.017484	LSNENHGIAQR
0.4	1548.782394	-0.016812	IIPPYTDDAFEIR

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

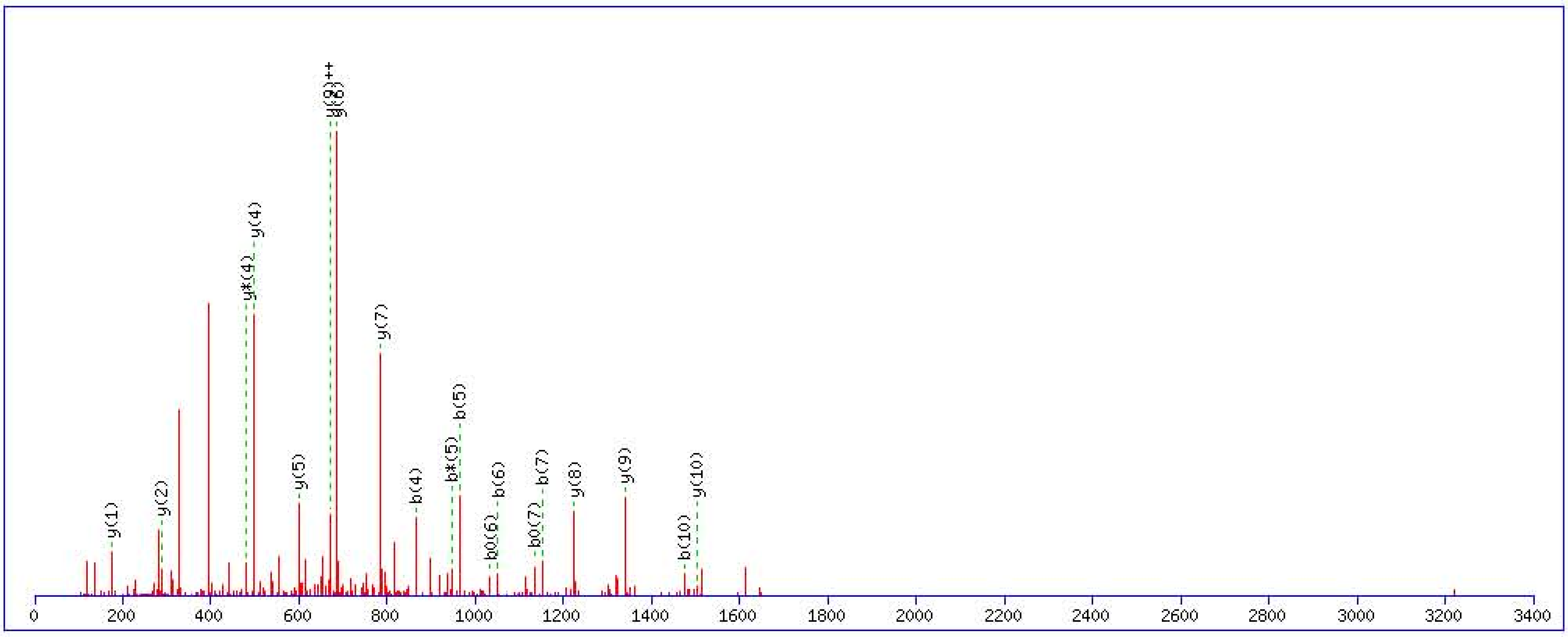
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FYNQVSTPLLR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

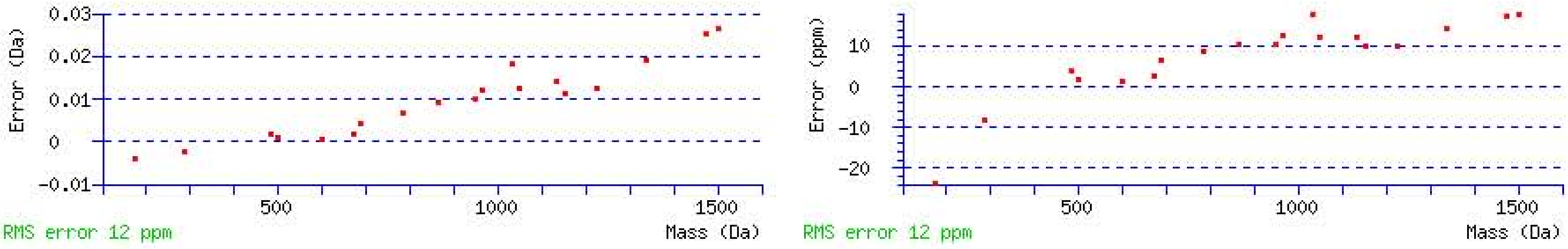
Match to Query 35402: 1647.899528 from(824.957040,2+) rtinseconds(2278) index(49112)
Title: Locus:1.1.1.2841.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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: 62 **Expect:** 9.4e-006
Matches : 19/98 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
61.5	1647.880676	0.018852	FYNQVSTPLLR
7.4	1647.903137	-0.003609	EVRIMRWFGLVSR
6.0	1647.895264	0.004264	MKPILLQGHER
3.8	1647.887878	0.011650	TLNQQLTNHIR
3.0	1647.910339	-0.010811	LMRPRREGGPPGGLR
2.6	1647.887878	0.011650	TLNQQLTNHIR
0.3	1647.894394	0.005134	LSDNIQNVVLKSYR

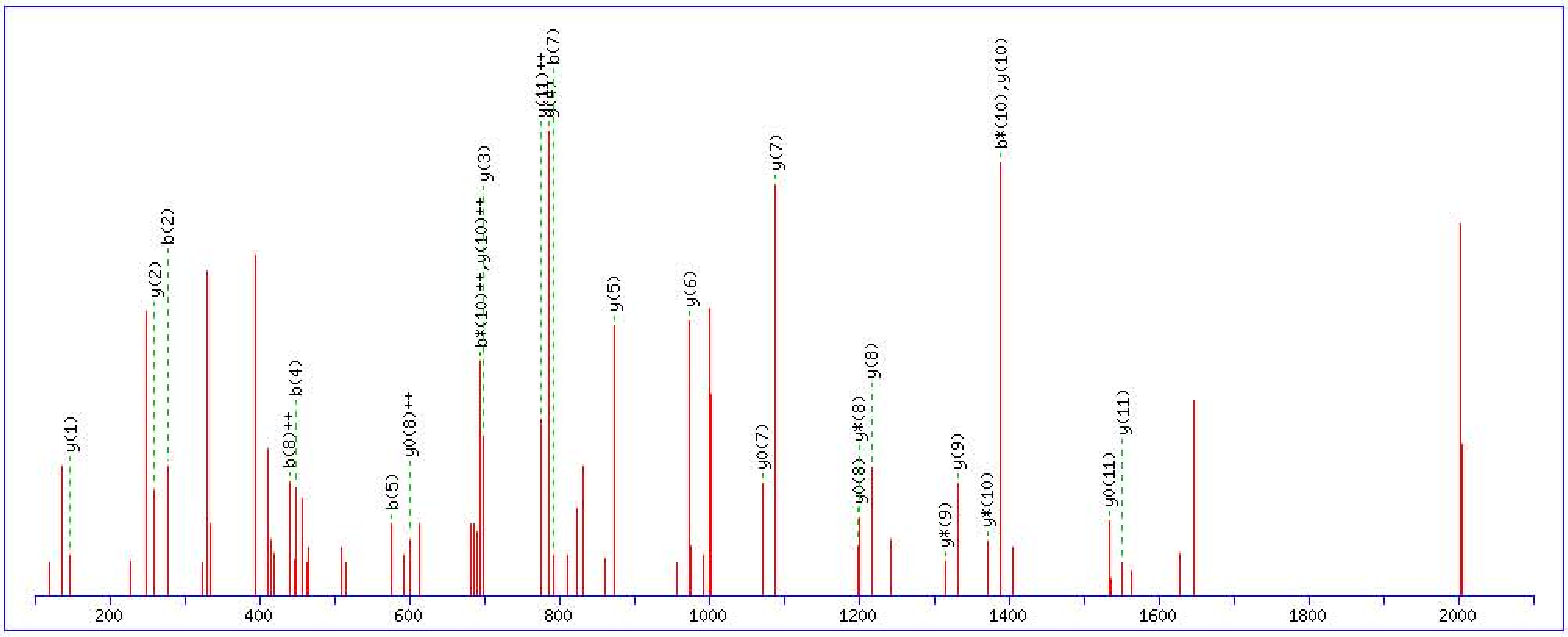
{MATRIX SCIENCE} Mascot Search Results

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

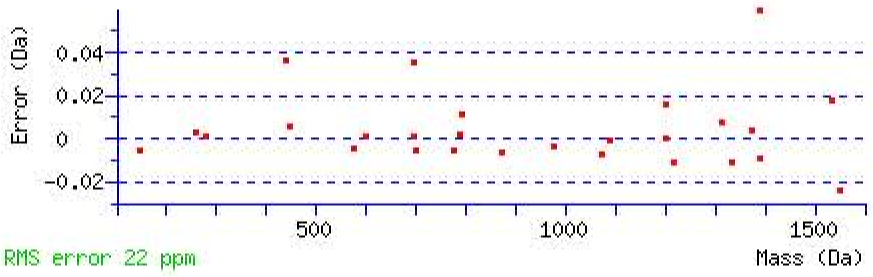
Match to Query 35702: 1663.829348 from(832.921950,2+) rtinseconds(1642) index(31118)
Title: Locus:1.1.1.3120.20 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

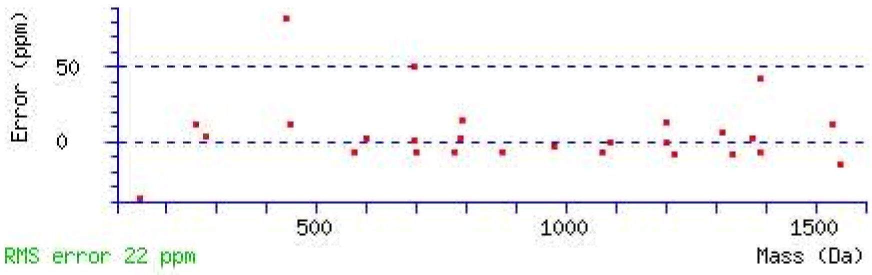
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 82  Expect: 6.4e-008
Matches : 27/110 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							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
82.2	1663.823944	0.005404	IYGNQDTSSQLK
22.8	1663.823944	0.005404	IYGNQDTSSQLK
5.2	1663.821442	0.007906	LYGCFLRVYMQSK
2.7	1663.806183	0.023165	DLSMFSQNMTHIIK
1.4	1663.836029	-0.006681	LADWKKMACLLCR

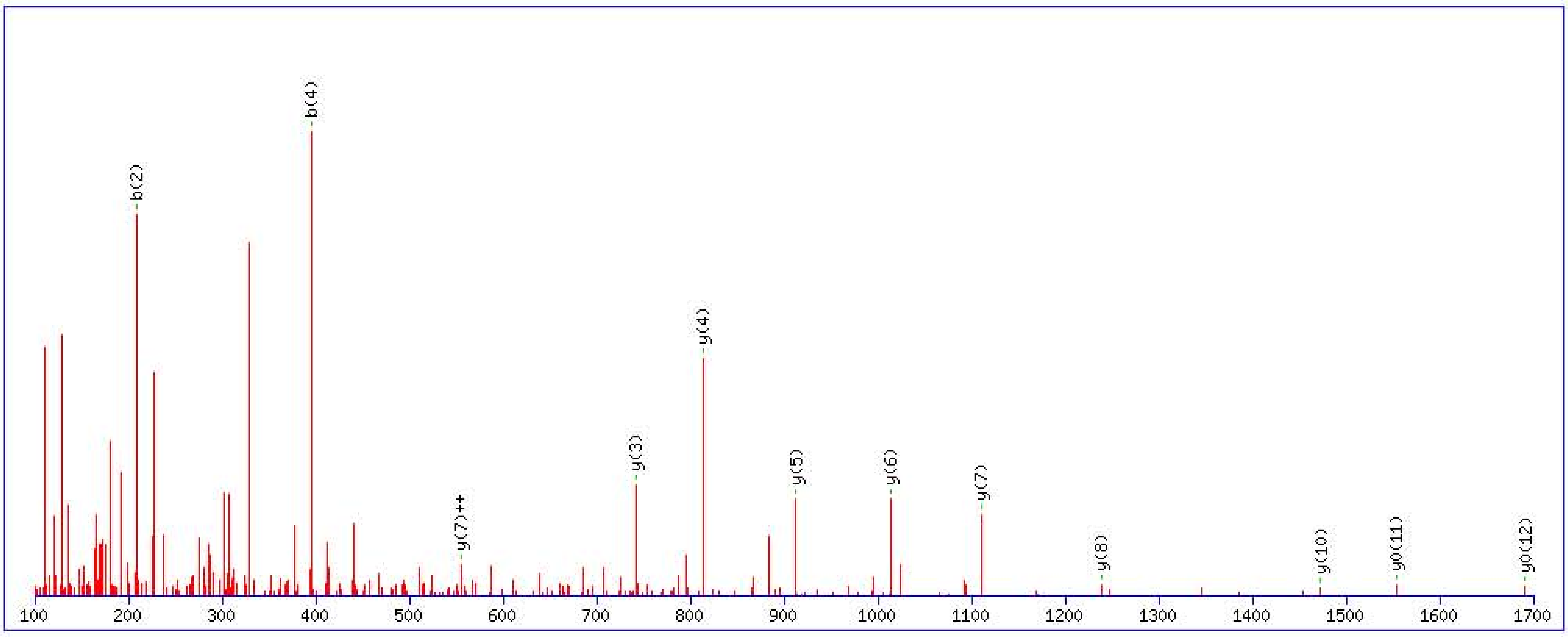
{MATRIX SCIENCE} Mascot Search Results

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

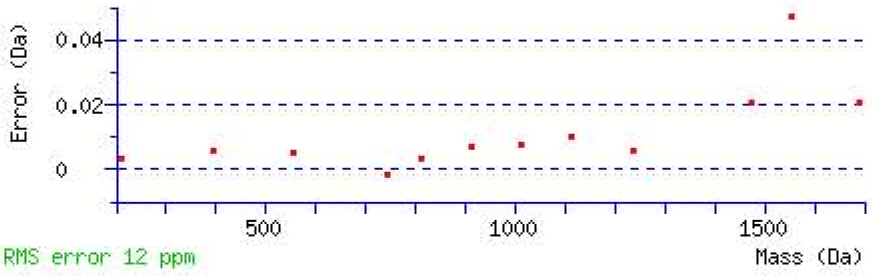
Match to Query 38124: 1778.955256 from(445.746090,4+) rtinseconds(1524) index(44319)
Title: Locus:1.1.1.2579.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

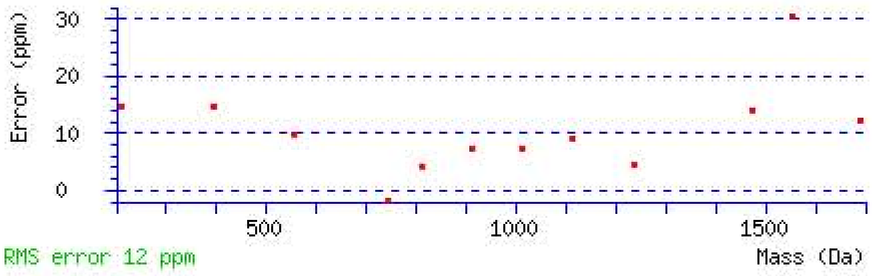
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1778.961395
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 46 **Expect:** 0.00047
Matches : 12/118 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	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
46.5	1778.961395	-0.006139	AHVSFKPTVAQQR
46.5	1778.961395	-0.006139	AHVSFKPTVAQQR

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

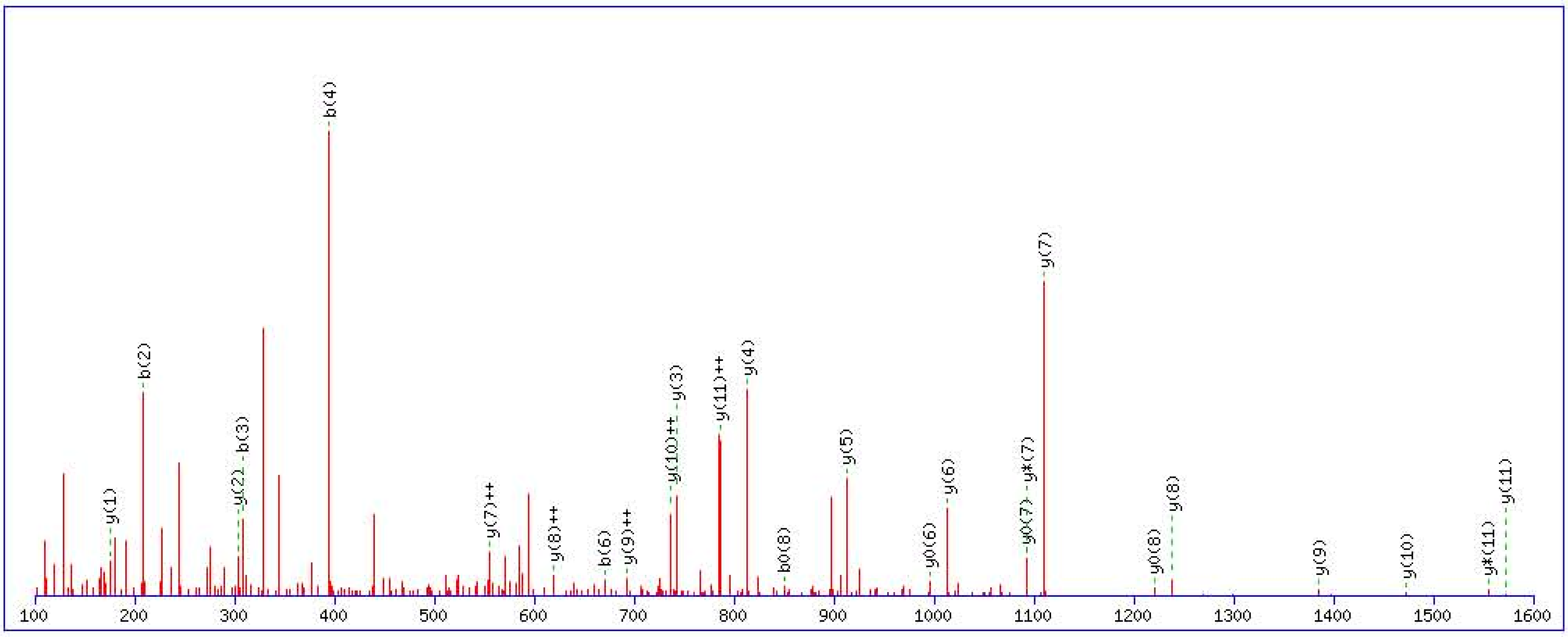
{MATRIX SCIENCE} Mascot Search Results

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

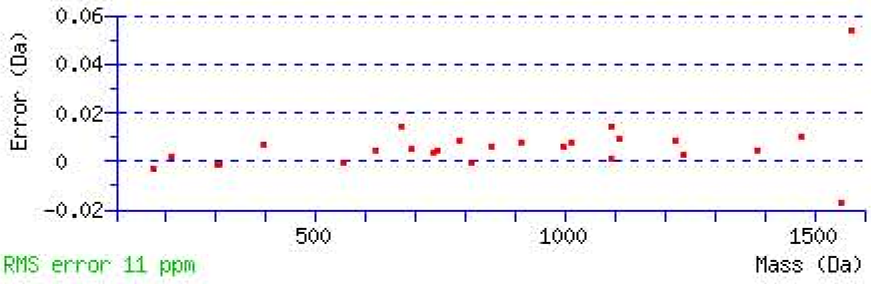
Match to Query 38126: 1778.960862 from(593.994230,3+) rtinseconds(1524) index(44321)
Title: Locus:1.1.1.2579.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

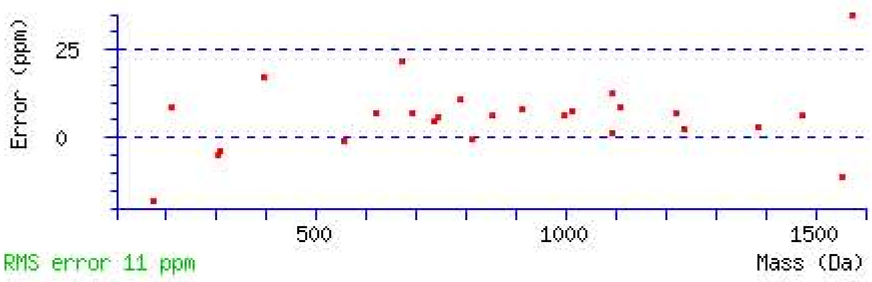
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1778.961395
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 1.9e-005
Matches : 26/118 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							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
53.0	1778.961395	-0.000533	AHVSFKPTVAQQR
46.3	1778.961395	-0.000533	AHVSFKPTVAQQR
2.6	1778.982498	-0.021636	SRDAKLVLLNMPGPPR

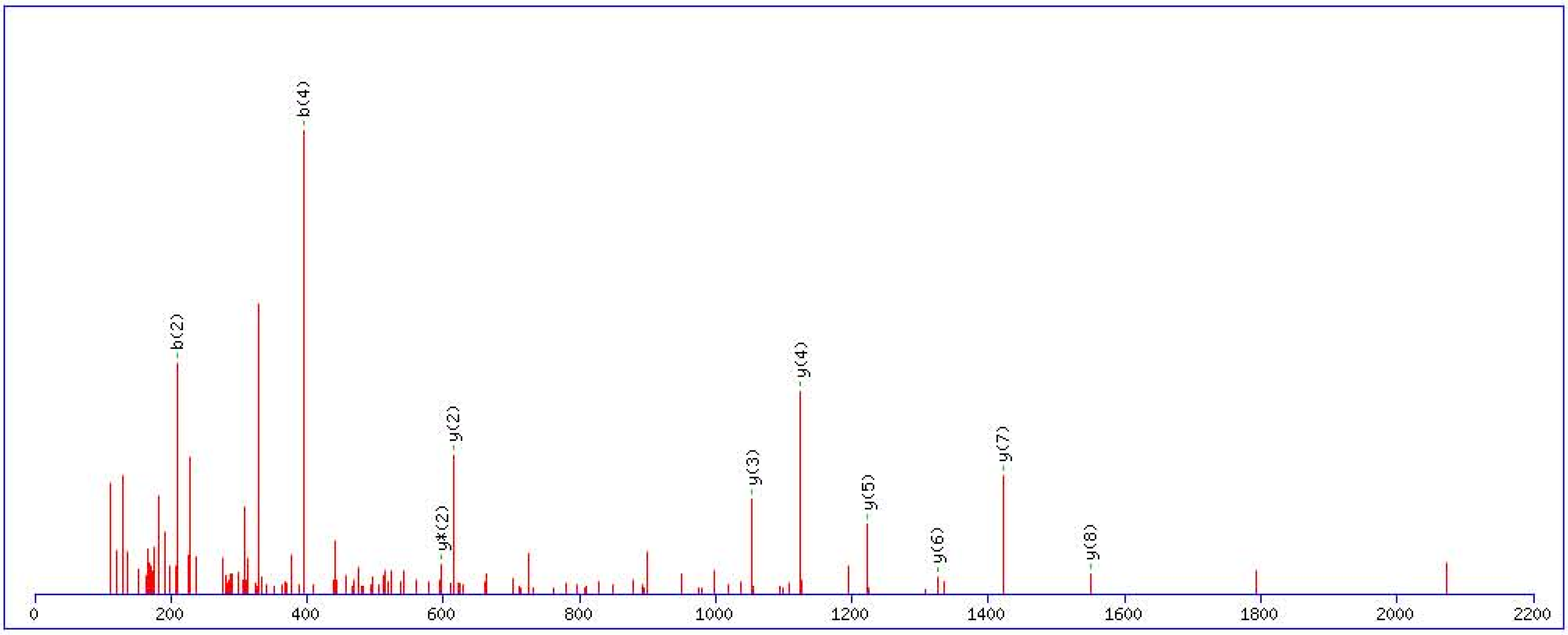
Mascot Search Results

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

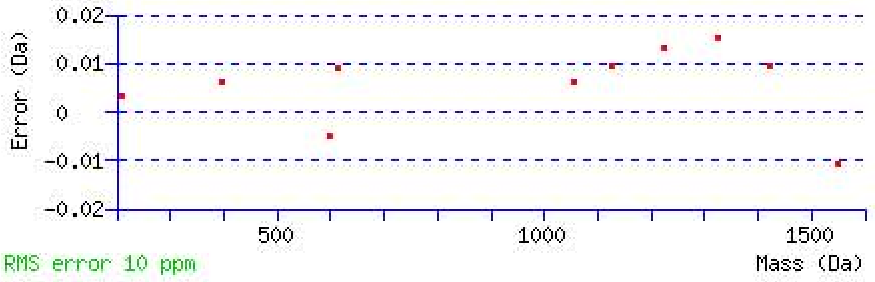
Match to Query 44343: 2090.130216 from(523.539830,4+) rtinseconds(1767) index(45890)
Title: Locus:1.1.1.2664.8 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

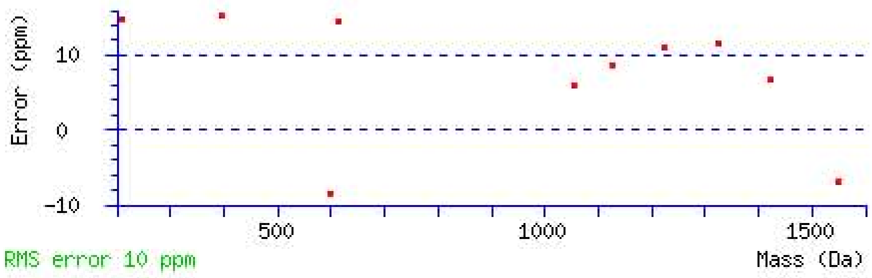
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 41  Expect: 0.0018
Matches : 10/118 fragment ions using 17 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							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
40.5	2090.128143	0.002073	AHVSFKPTVAQQR

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

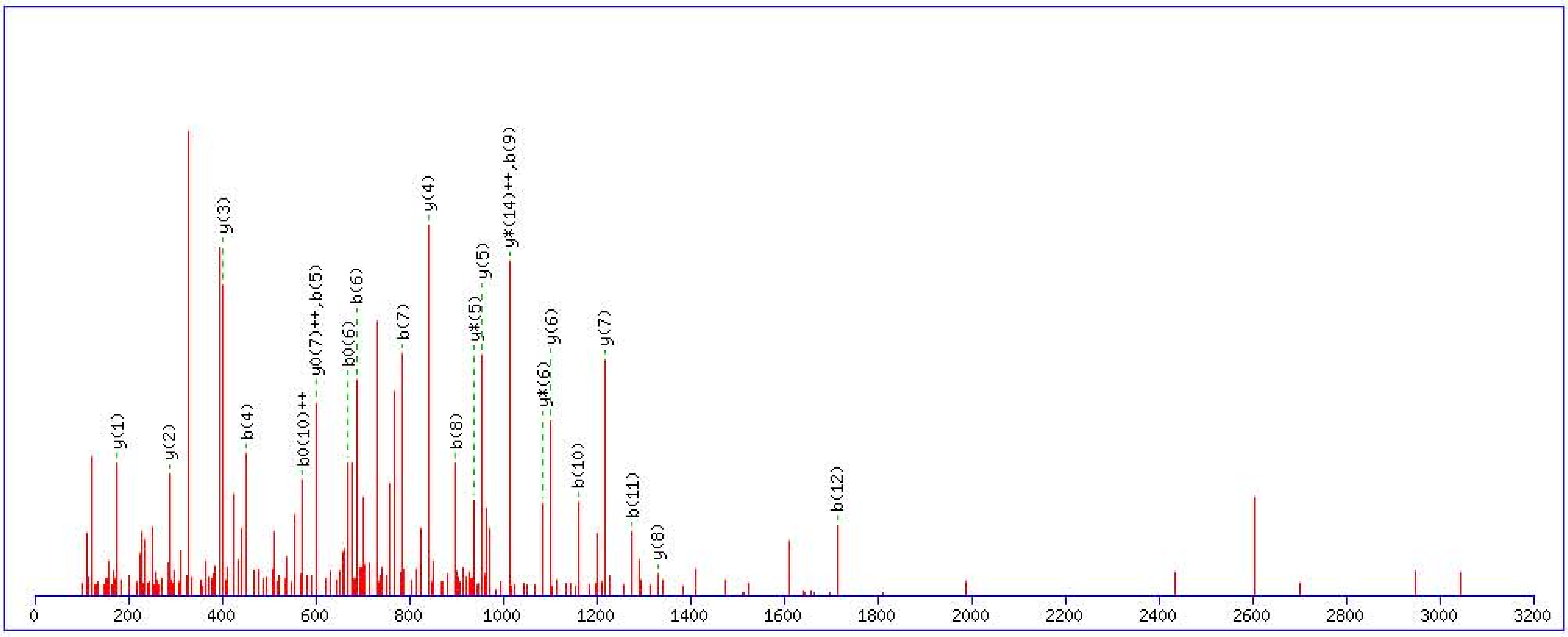
Mascot Search Results

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

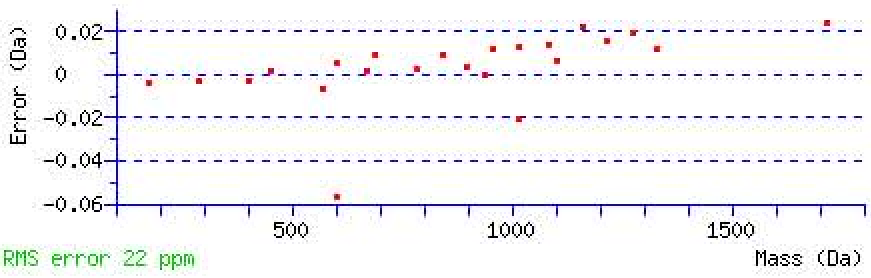
Match to Query 44683: 2115.034362 from(706.018730,3+) rtinseconds(2277) index(49110)
Title: Locus:1.1.1.2841.8 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

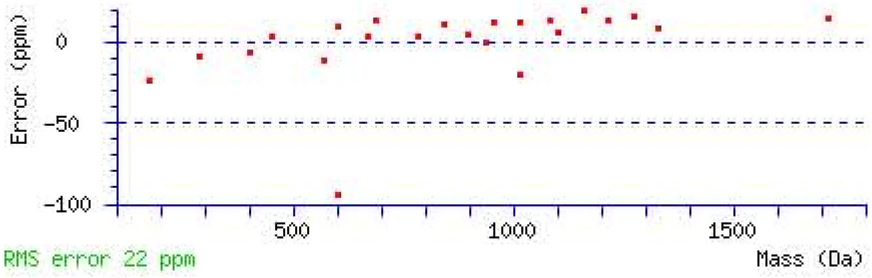
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2115.020752
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 6.8e-006
Matches : 23/134 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	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
57.2	2115.020752	0.013610	AEDHFSVIDFNQNIR
2.1	2115.033981	0.000381	ESADRQVLMQEEEIK

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

{MATRIX SCIENCE}

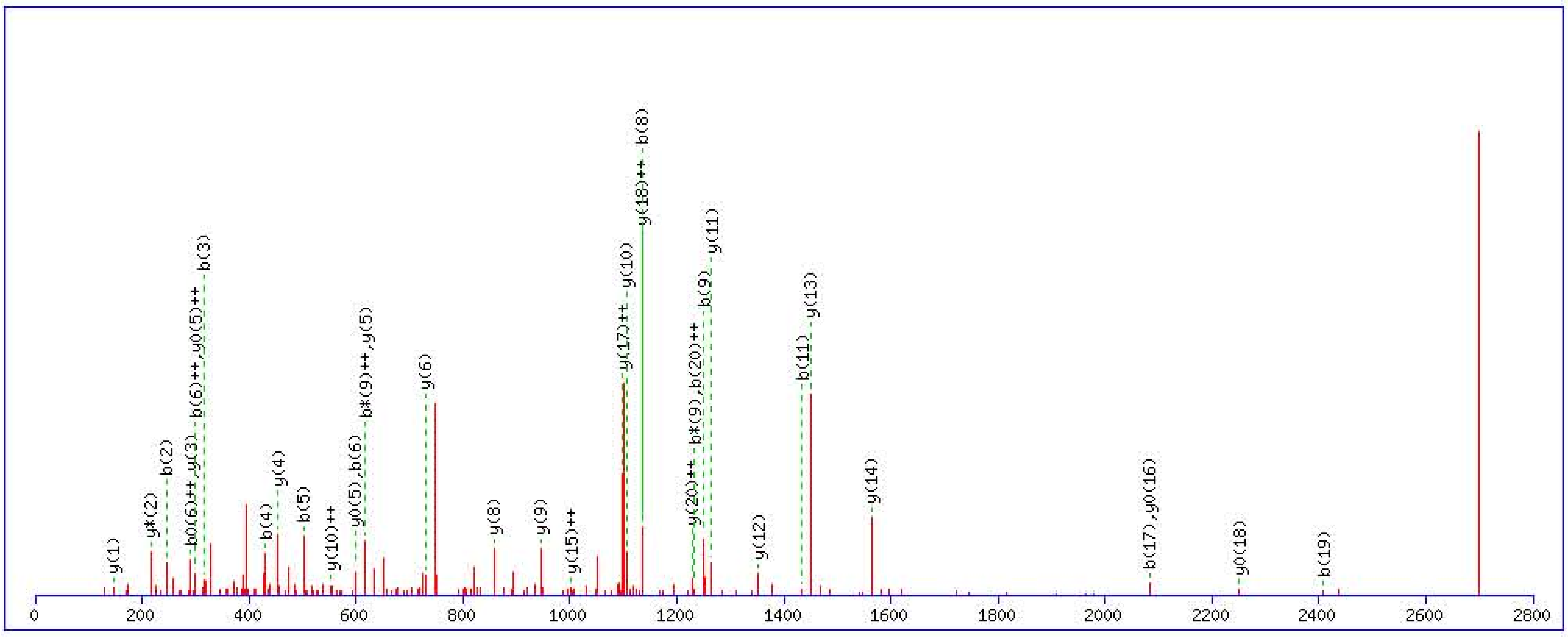
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MLADAPPQDPSCCSGALYYGSK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

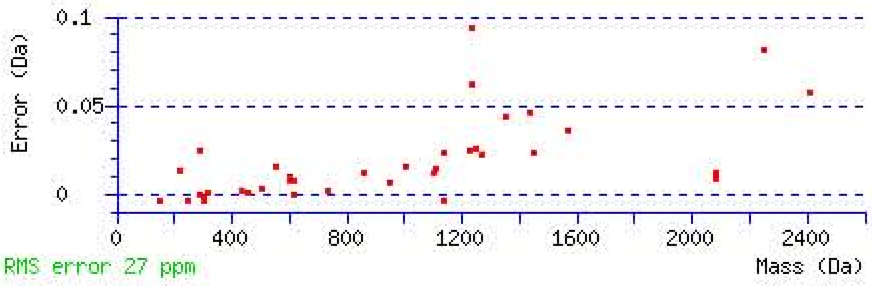
Match to Query 52741: 2698.225002 from(900.415610,3+) rtinseconds(2105) index(48024)
Title: Locus:1.1.1.2781.19 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

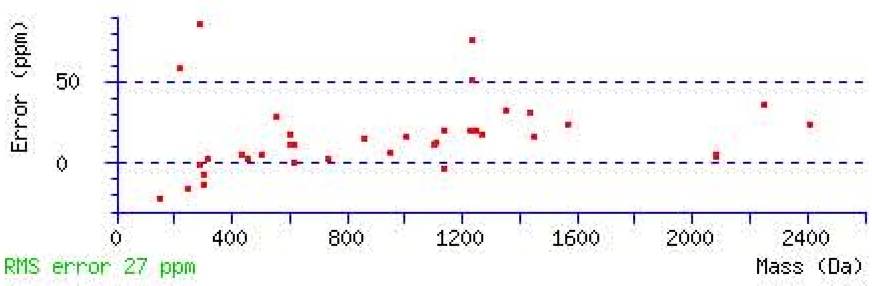


Monoisotopic mass of neutral peptide Mr(calc): 2698.189941
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 51 **Expect:** 7.8e-005
Matches : 37/230 fragment ions using 84 most intense peaks (help)

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



RMS error 27 ppm



RMS error 27 ppm

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
51.4	2698.189941	0.035061	MLADAPPQDPSCCSGALYYGSK

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

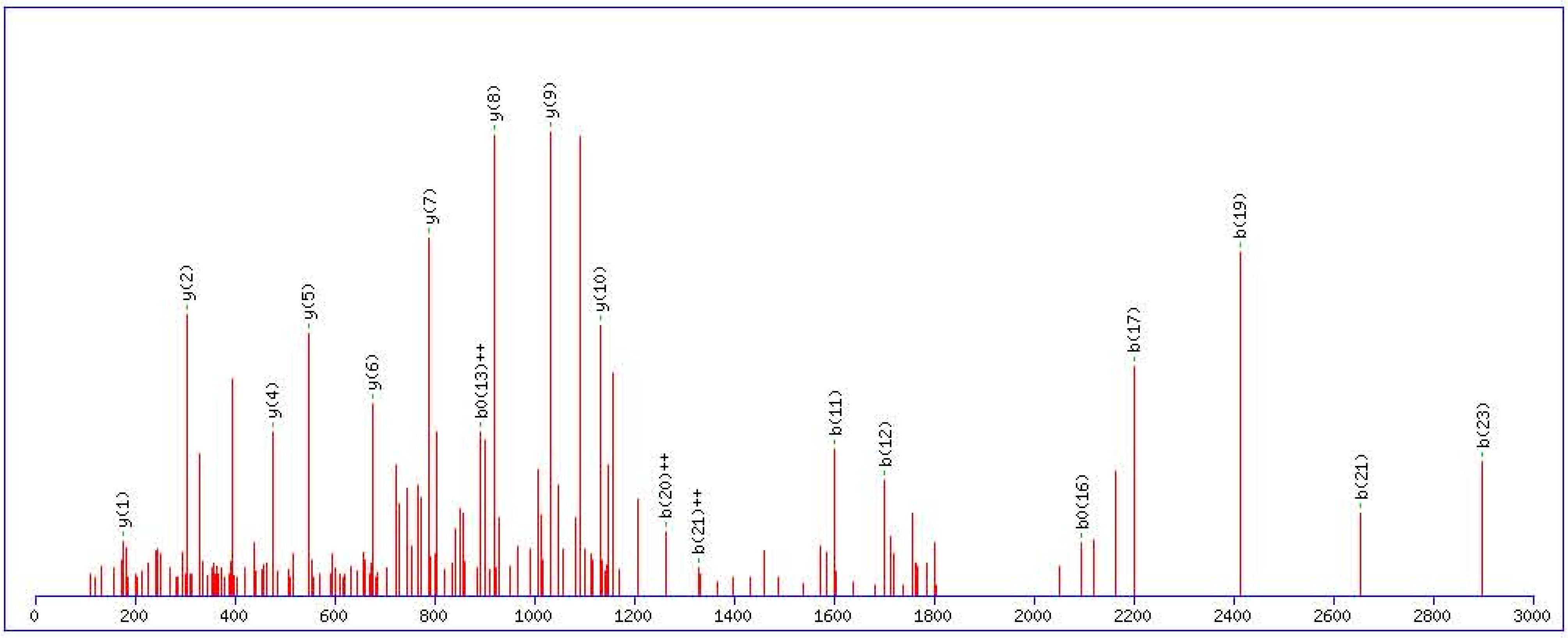
Mascot Search Results

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

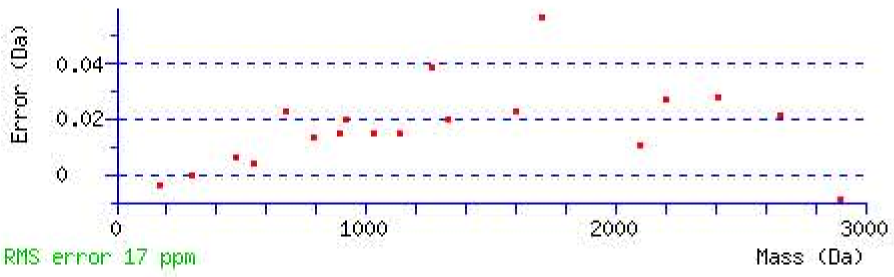
Match to Query 61038: 3443.790656 from(861.954940,4+) rtinseconds(2676) index(51408)
Title: Locus:1.1.1.2979.23 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

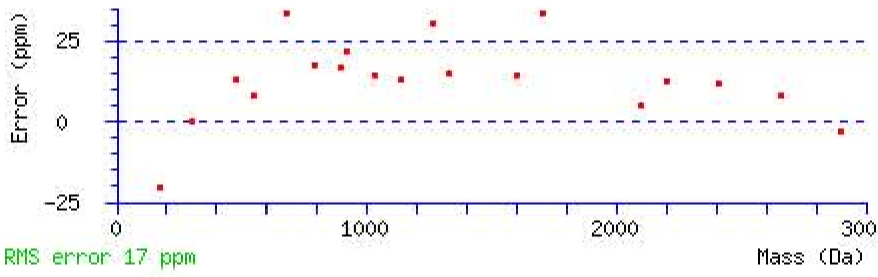
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 70  Expect: 2.3e-006
Matches : 19/478 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							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
70.0	3443.742859	0.047797	SILQMSLDHHIVTPLTSLVIENEAGDER

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

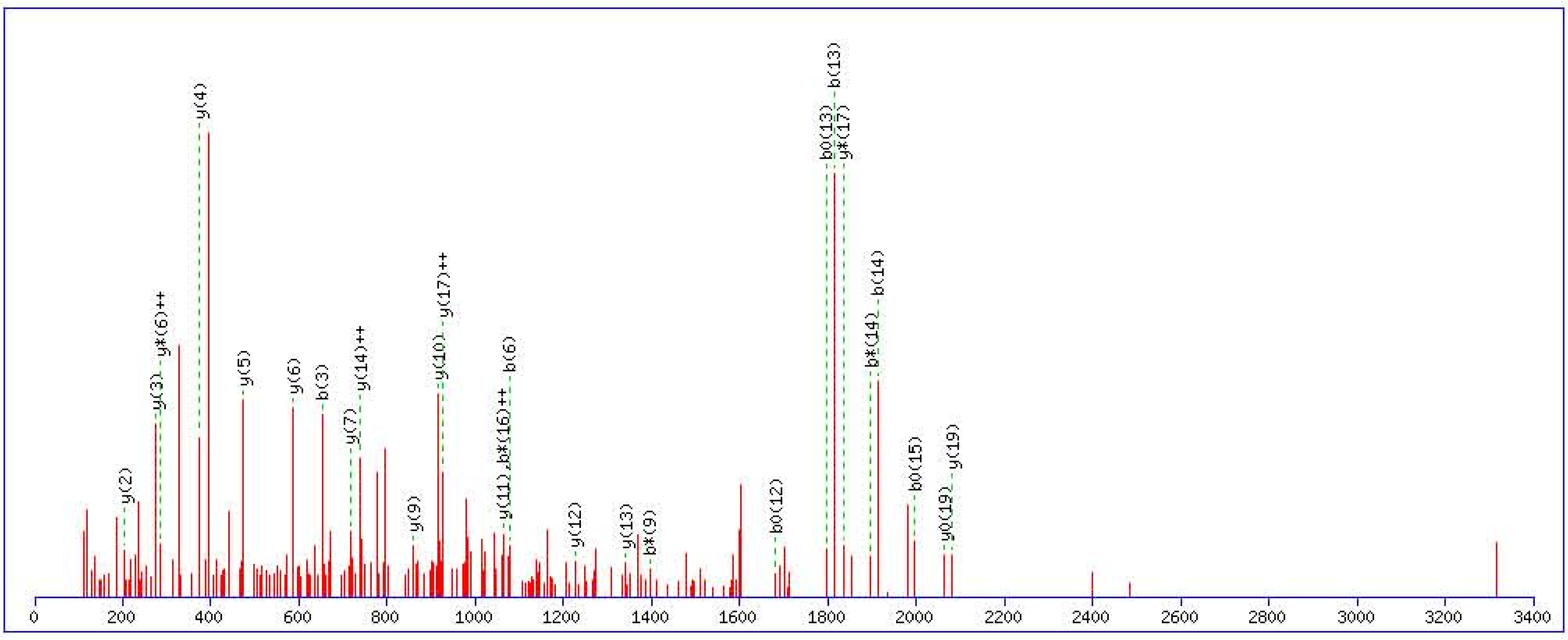
Mascot Search Results

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

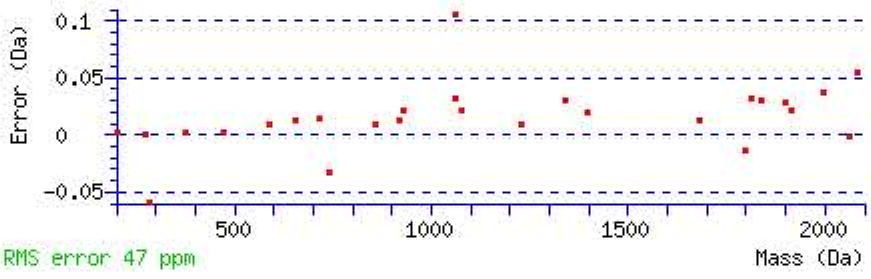
Match to Query 63942: 3993.957920 from(799.798860,5+) rtinseconds(2389) index(49726)
Title: Locus:1.1.1.2880.8 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

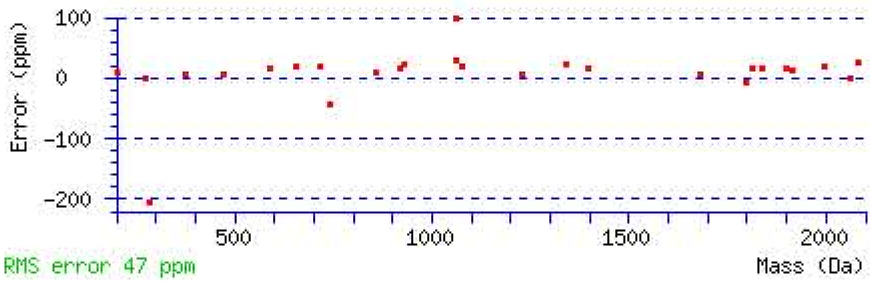
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 28 **Expect:** 0.037
Matches : 27/356 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	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
28.0	3993.910858	0.047062	NVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGK
13.7	3993.910858	0.047062	NVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGK

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

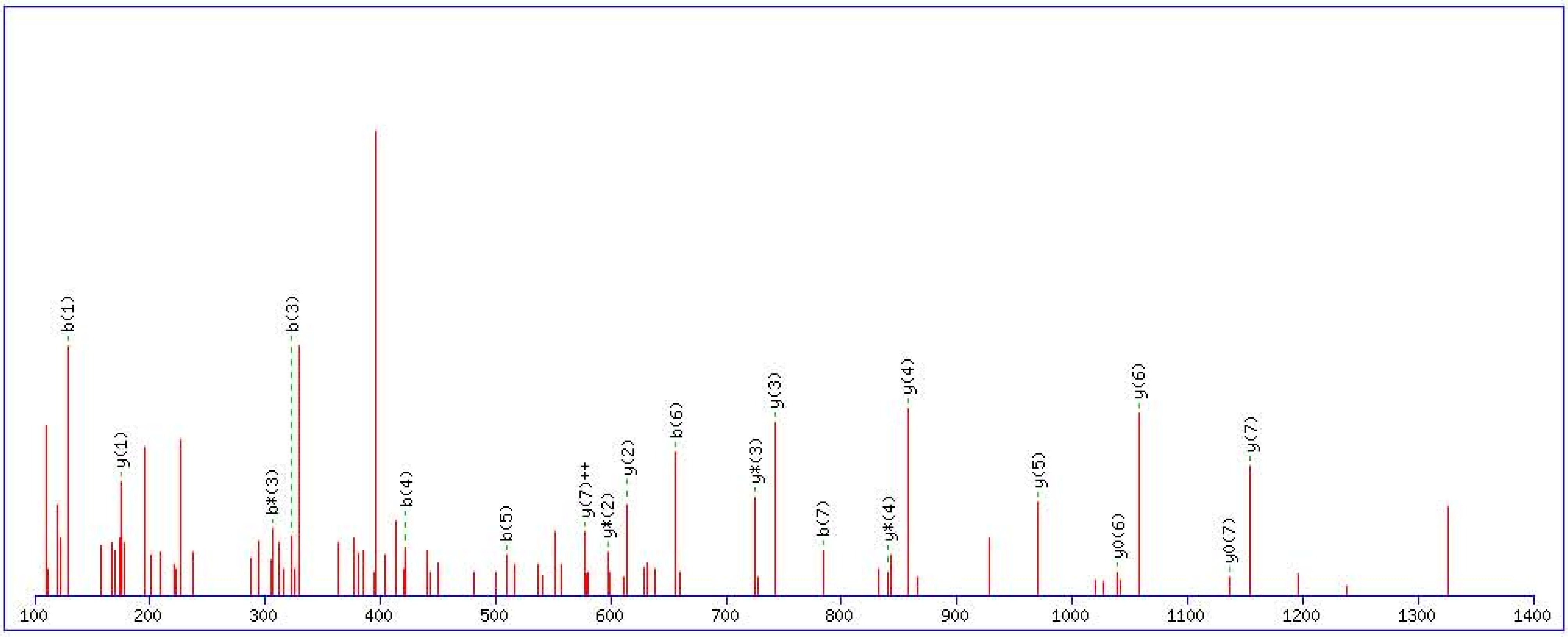
{MATRIX SCIENCE} Mascot Search Results

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

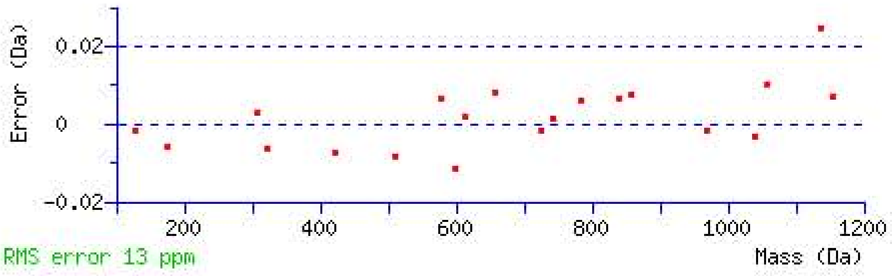
Match to Query 40876: 1937.023536 from(485.263160,4+) rtinseconds(1458) index(43930)
Title: Locus:1.1.1.2556.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

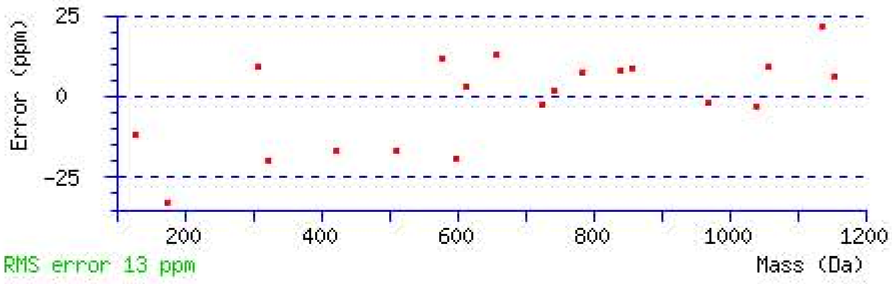
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1937.030533
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.00036
Matches : 20/142 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							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	1324.700811	662.854043	1307.674262	654.340769	1306.690246	653.848761	Q	***742.402856***	371.705066	725.376307	363.191792			3
13	1763.926137	882.466707	1746.899588	873.953432	1745.915572	873.461424	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 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
39.7	1937.030533	-0.006997	KGHVSFKPSLDQQR
30.9	1937.030533	-0.006997	KGHVSFKPSLDQQR
3.0	1937.051620	-0.028084	QPLEREQCLALLALGAR

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

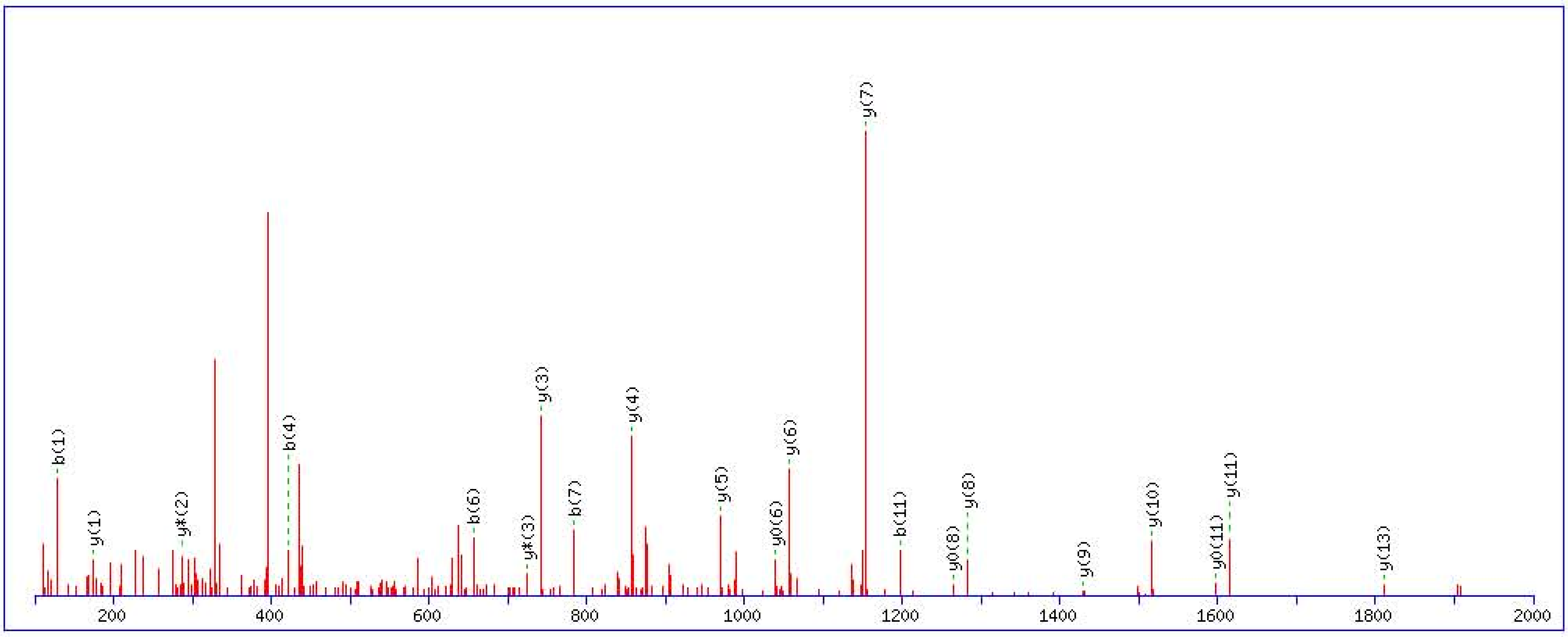
{MATRIX SCIENCE} Mascot Search Results

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

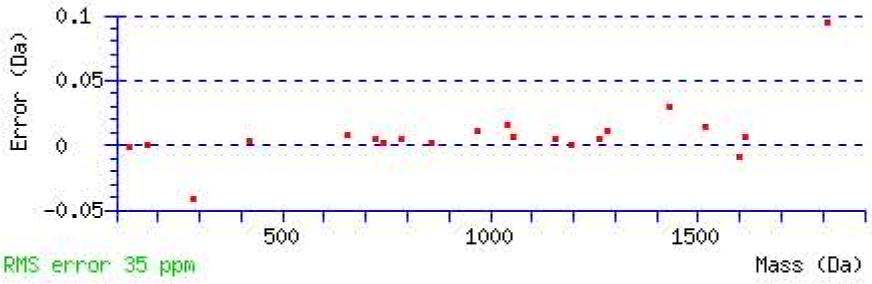
Match to Query 40881: 1937.034732 from(646.685520,3+) rtinseconds(1487) index(44117)
Title: Locus:1.1.1.2566.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

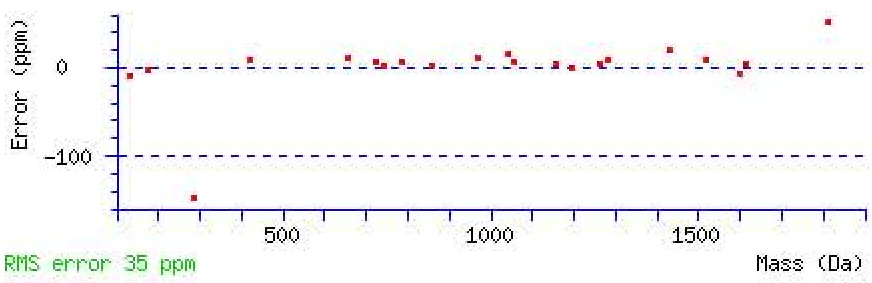
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1937.030533
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 5e-005
Matches : 21/142 fragment ions using 49 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							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
56.5	1937.030533	0.004199	KGHVSFKPSLDQQR
56.2	1937.030533	0.004199	KGHVSFKPSLDQQR

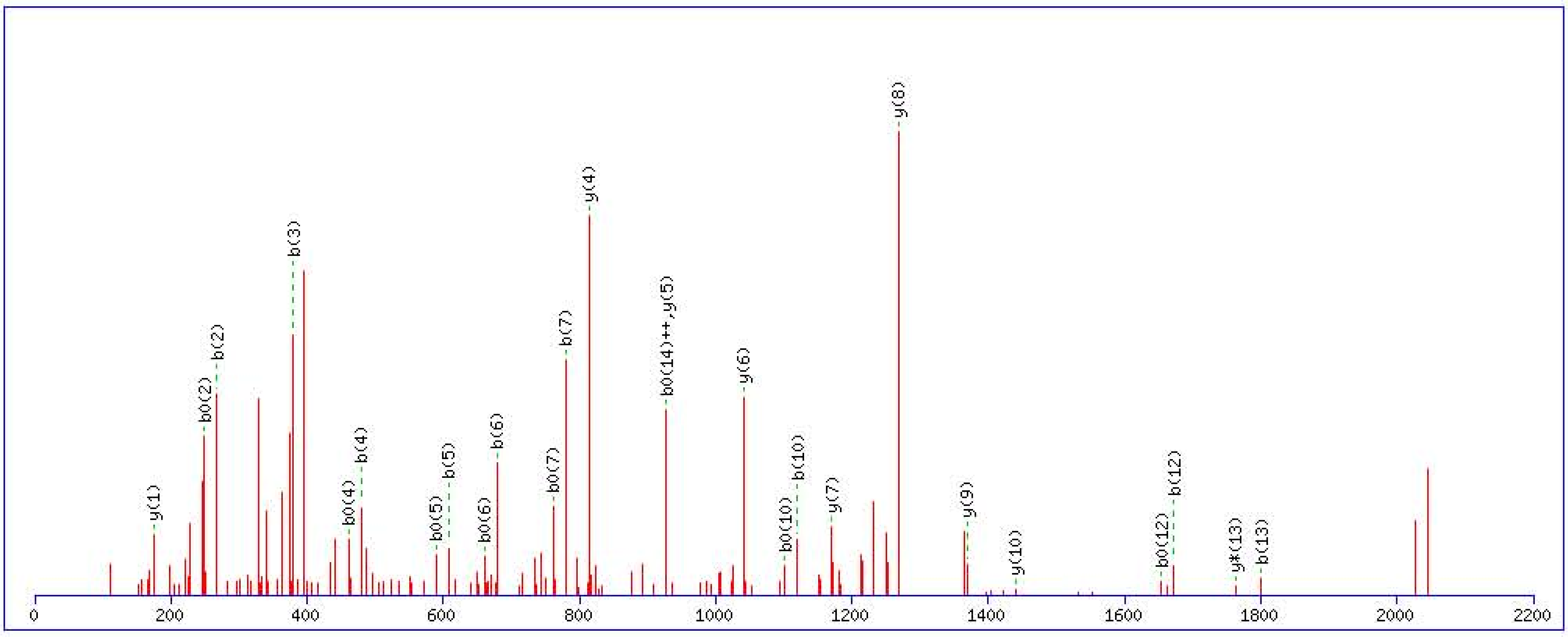
{MATRIX SCIENCE} Mascot Search Results

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

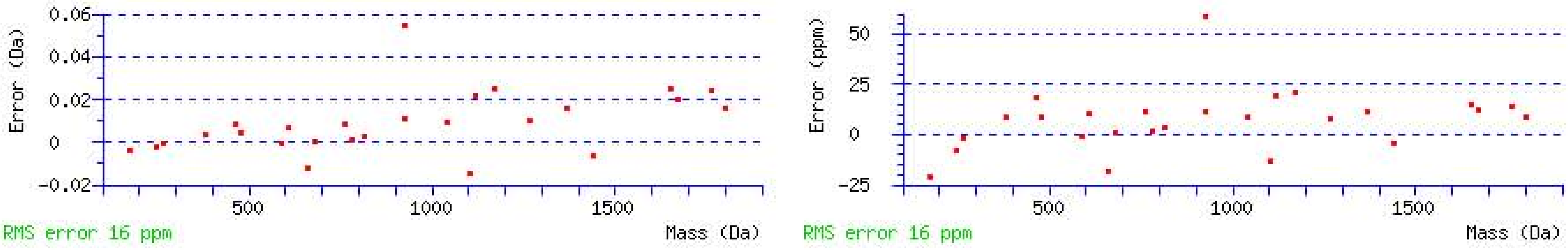
Match to Query 43561: 2045.043642 from(682.688490,3+) rtinseconds(1730) index(45637)
Title: Locus:1.1.1.2651.8 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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: 78  Expect: 2.2e-007
Matches : 26/156 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							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
78.2	2045.036377	0.007265	EHLVQATPENLQEAR
7.7	2045.036377	0.007265	EHLVQATPENLQEAR
6.9	2045.035889	0.007753	LNMEQLLQSASMELK
5.4	2045.022446	0.021196	EHNENMLRNILPSHVAR
3.9	2045.021118	0.022524	VSLVGADDLRKMQEEEAR

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

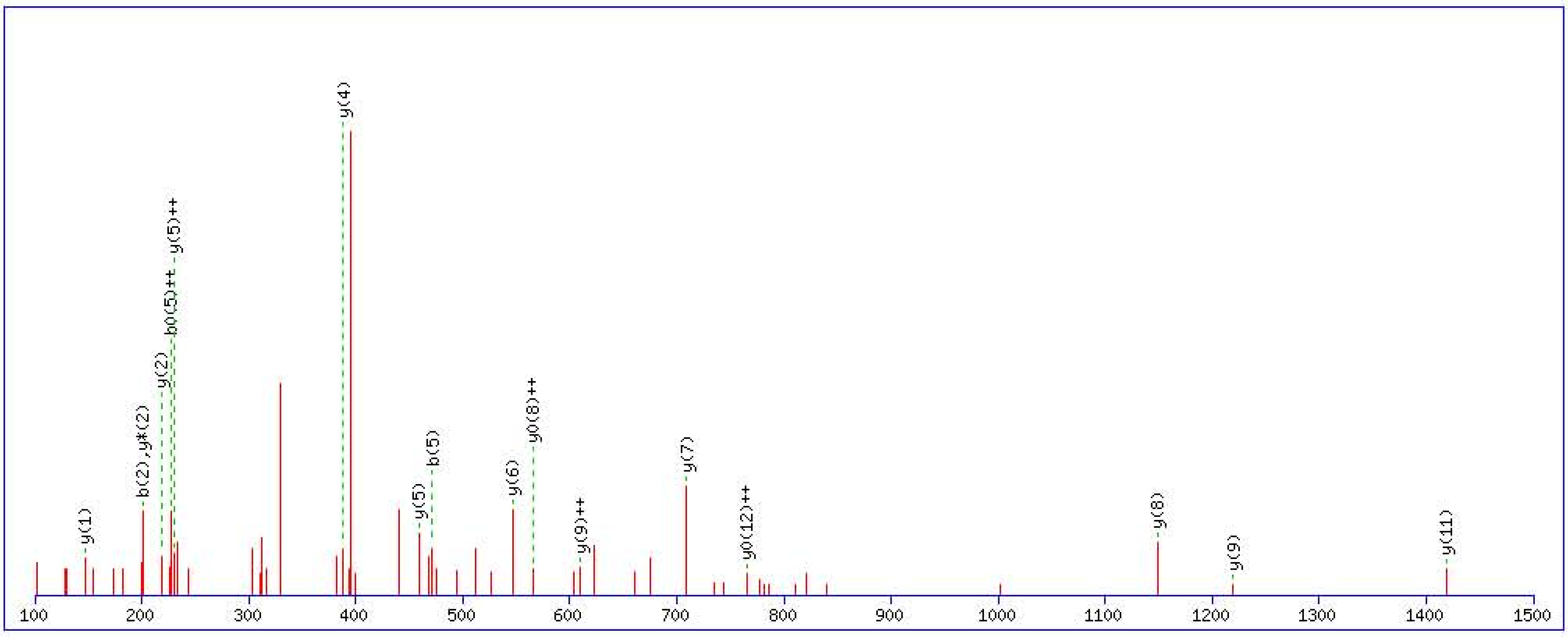
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEAQAQYSAAVAK**
Found in **ITIH4_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4

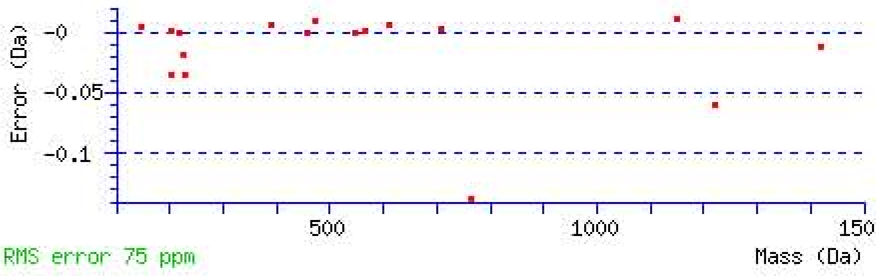
Match to Query 34036: 1617.816882 from(540.279570,3+) rtinseconds(1613) index(2788)
Title: Locus:1.1.1.3113.19 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

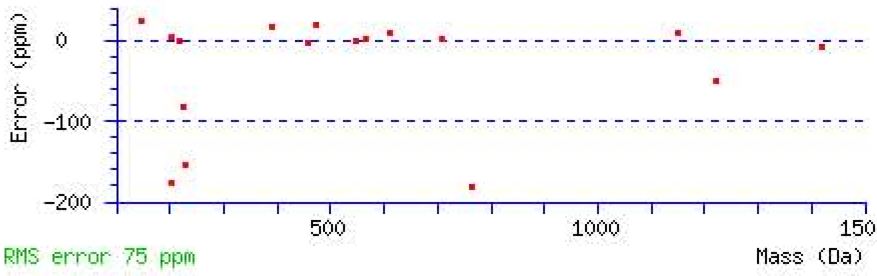
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1617.818436
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 5.2e-005
Matches : 17/126 fragment ions using 35 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							13
2	**201.086983**	101.047130			183.076418	92.041847	E	1547.788642	774.397959	1530.762093	765.884685	1529.778077	765.392677	12
3	272.124097	136.565687			254.113532	127.560404	A	***1418.746049***	709.876663	1401.719500	701.363388	1400.735484	700.871380	11
4	400.182675	200.594976	383.156126	192.081701	382.172110	191.589693	Q	1347.708935	674.358106	1330.682386	665.844831	1329.698370	665.352823	10
5	**471.219789**	236.113533	454.193240	227.600258	453.209224	227.108250	A	***1219.650357***	610.328817	1202.623808	601.815542	1201.639792	601.323534	9
6	910.445115	455.726196	893.418566	447.212921	892.434550	446.720913	Q	***1148.613243***	574.810260	1131.586694	566.296985	1130.602678	565.804977	8
7	1073.508444	537.257860	1056.481895	528.744586	1055.497879	528.252578	Y	***709.387917***	355.197597	692.361368	346.684322	691.377352	346.192314	7
8	1160.540472	580.773874	1143.513923	572.260600	1142.529907	571.768592	S	***546.324588***	273.665932	529.298039	265.152658	528.314023	264.660650	6
9	1231.577586	616.292431	1214.551037	607.779157	1213.567021	607.287149	A	***459.292560***	230.149918	442.266011	221.636643			5
10	1302.614700	651.810988	1285.588151	643.297714	1284.604135	642.805706	A	***388.255446***	194.631361	371.228897	186.118087			4
11	1401.683114	701.345195	1384.656565	692.831921	1383.672549	692.339913	V	317.218332	159.112804	300.191783	150.599530			3
12	1472.720228	736.863752	1455.693679	728.350478	1454.709663	727.858470	A	***218.149918***	109.578597	201.123369	101.065322			2
13							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of AEAQAQYSAAVAK
(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	1617.818436	-0.001554	AEAQAQYSAAVAK
21.1	1617.818436	-0.001554	AEAQAQYSAAVAK
1.9	1617.807220	0.009662	WVPGLKESAEEMVK
1.4	1617.820953	-0.004071	SETGVLDKKEGEQAK
1.1	1617.803162	0.013720	EATEINMKNEALQK
1.0	1617.829712	-0.012830	EGGHRVLIFSQMTK
0.6	1617.829681	-0.012799	NDVMIRKEAYVHK

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

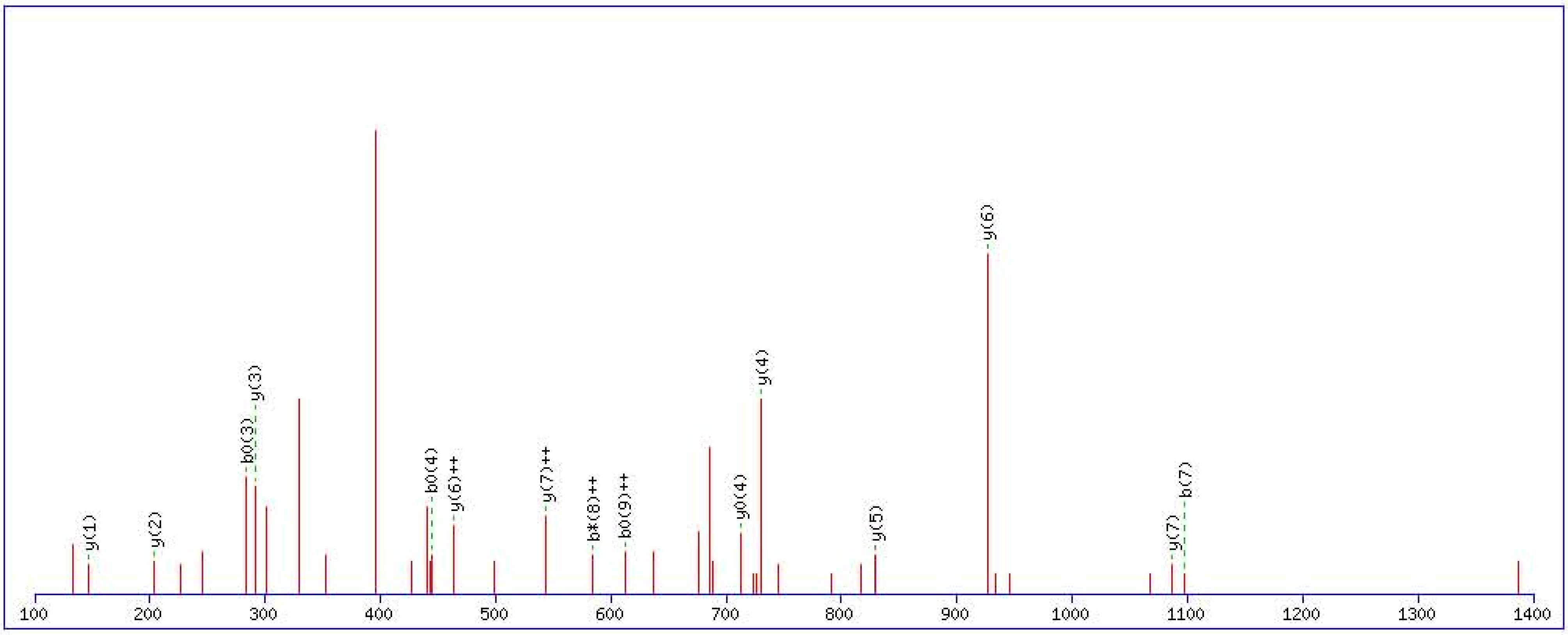
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGDCPVQSGK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

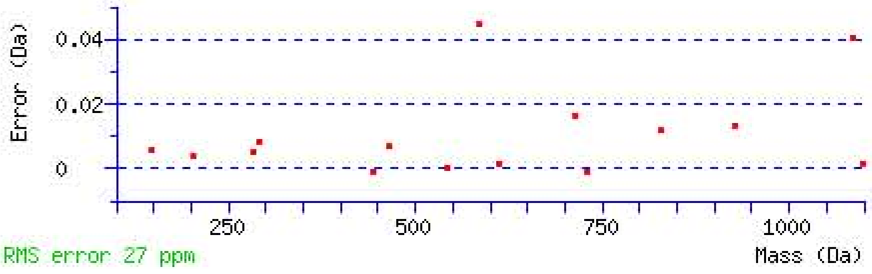
Match to Query 25743: 1386.634928 from(694.324740,2+) rtinseconds(1399) index(15170)
Title: Locus:1.1.1.3087.18 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

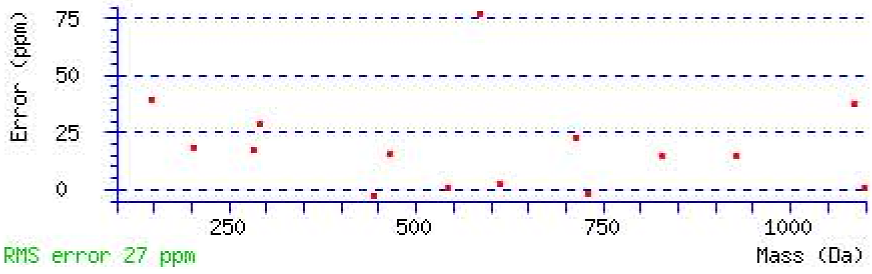
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1386.627182
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 29 **Expect:** 0.011
Matches : 15/92 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	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
28.8	1386.627182	0.007746	EGDCPVQSGK

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

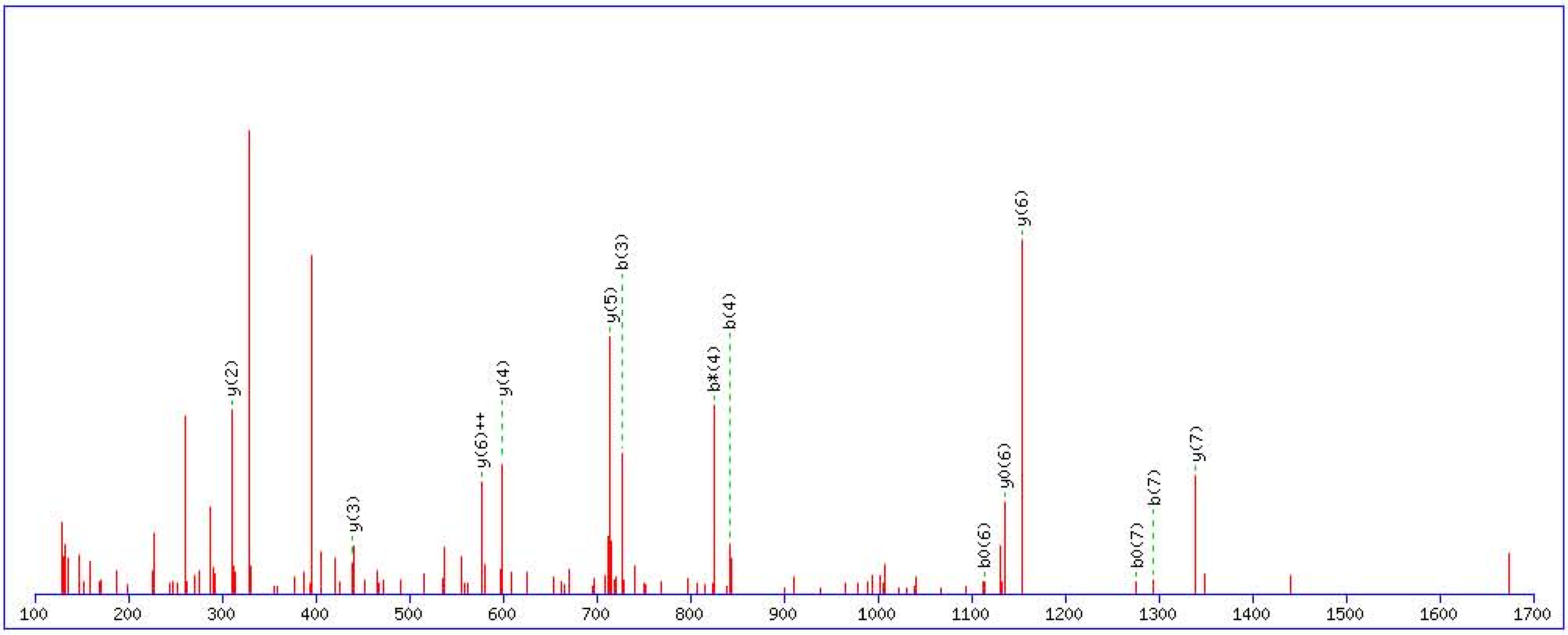
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TWQDCEYK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

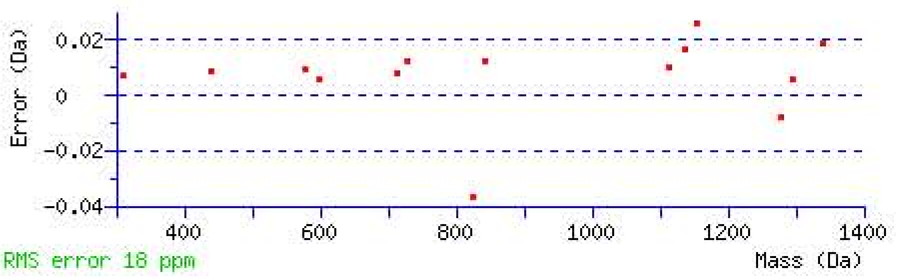
Match to Query 28302: 1439.638648 from(720.826600,2+) rtinseconds(1780) index(17617)
Title: Locus:1.1.1.3220.17 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

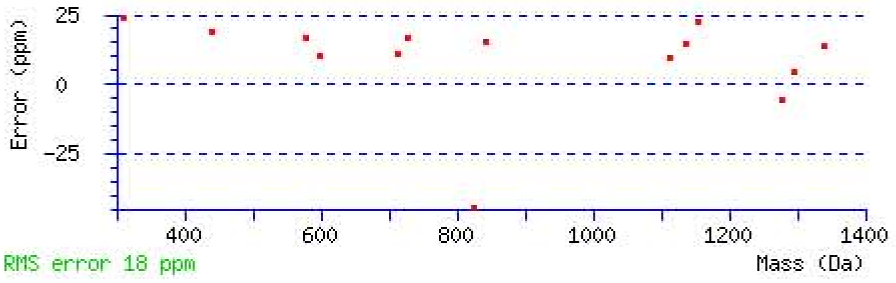
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 29 **Expect:** 0.0025
Matches : 14/76 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	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
29.4	1439.621353	0.017295	TWQDCEYK
1.7	1439.653702	-0.015054	MPNGMYDGSALIR
1.5	1439.653702	-0.015054	MPNGMYDGSALIR

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

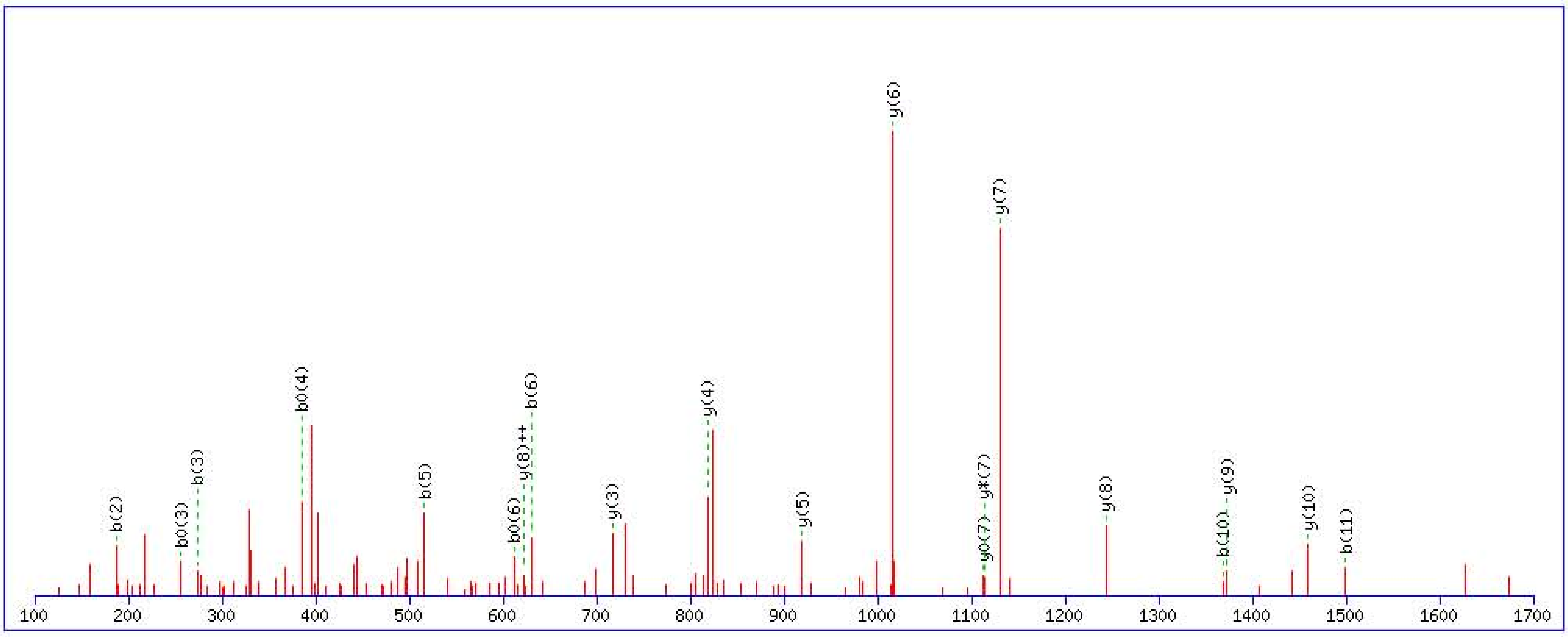
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVSEINPTTQMK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

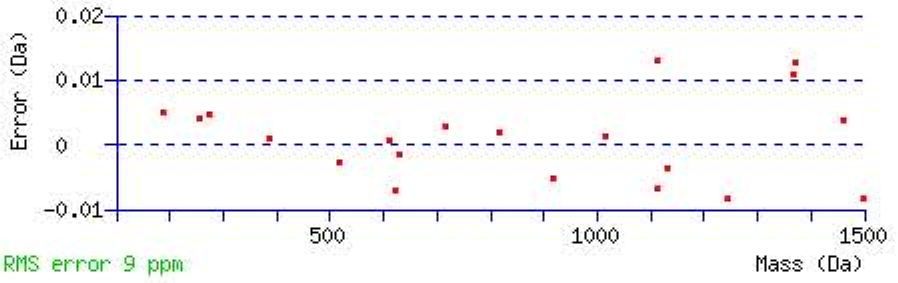
Match to Query 35349: 1644.819248 from(823.416900,2+) rtinseconds(1847) index(32131)
Title: Locus:1.1.1.3192.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

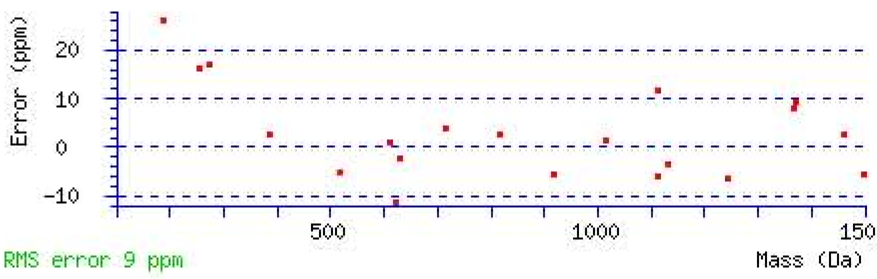


```
Monoisotopic mass of neutral peptide Mr(calc): 1644.821503
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 4.1e-006
Matches : 20/116 fragment ions using 28 most intense peaks   (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							12
2	***187.107718***	94.057497			169.097153	85.052214	V	1558.796763	779.902020	1541.770214	771.388745	1540.786198	770.896737	11
3	***274.139746***	137.573511			256.129181	128.568229	S	***1459.728349***	730.367813	1442.701800	721.854538	1441.717784	721.362530	10
4	403.182339	202.094808			385.171774	193.089525	E	***1372.696321***	686.851799	1355.669772	678.338524	1354.685756	677.846516	9
5	***516.266403***	258.636840			498.255838	249.631557	I	***1243.653728***	622.330502	1226.627179	613.817228	1225.643163	613.325220	8
6	***630.309330***	315.658303	613.282781	307.145029	612.298765	306.653021	N	***1130.569664***	565.788470	1113.543115	557.275196	1112.559099	556.783188	7
7	727.362094	364.184685	710.335545	355.671411	709.351529	355.179403	P	***1016.526737***	508.767007	999.500188	500.253732	998.516172	499.761724	6
8	828.409773	414.708525	811.383224	406.195250	810.399208	405.703242	T	***919.473973***	460.240625	902.447424	451.727350	901.463408	451.235342	5
9	929.457452	465.232364	912.430903	456.719090	911.446887	456.227082	T	***818.426294***	409.716785	801.399745	401.203511	800.415729	400.711503	4
10	***1368.682778***	684.845027	1351.656229	676.331753	1350.672213	675.839745	Q	***717.378615***	359.192946	700.352066	350.679671			3
11	***1499.723263***	750.365270	1482.696714	741.851995	1481.712698	741.359987	M	278.153289	139.580282	261.126740	131.067008			2
12							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 9 ppm



RMS error 9 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.9	1644.821503	-0.002255	SVSEINPTTQMK
3.3	1644.814133	0.005115	VTDQGSPPMSATAIVR
1.1	1644.803757	0.015491	TISTMKVMQFQGMK
0.3	1644.810745	0.008503	VSDGENVIISHFNSK

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

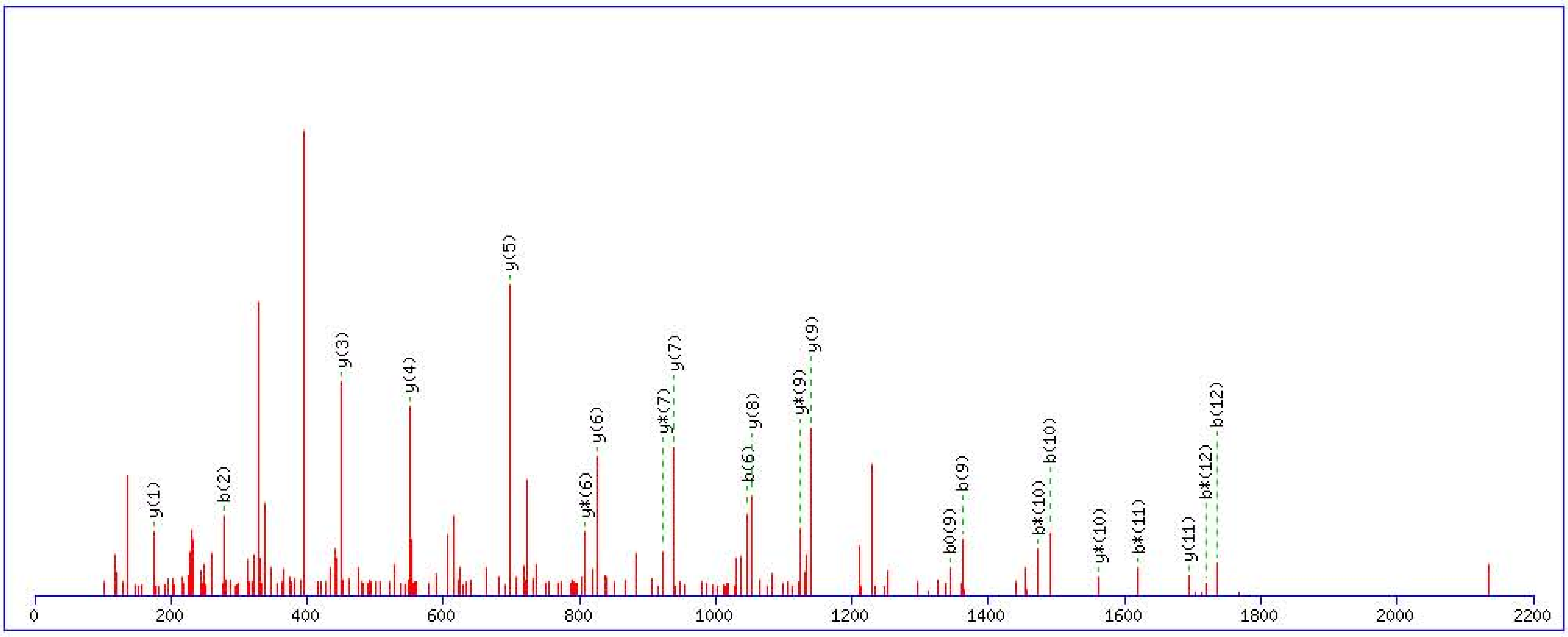
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YNSQNQSNNQFVLYR**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

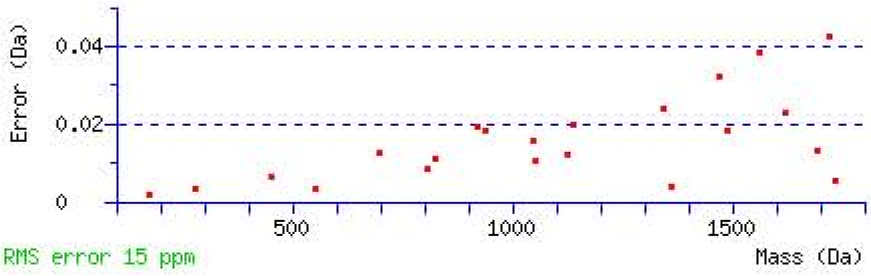
Match to Query 45795: 2185.057872 from(729.359900,3+) rtinseconds(2056) index(19393)
Title: Locus:1.1.1.3316.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

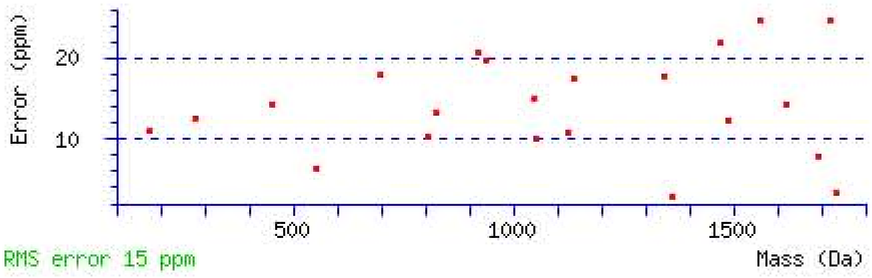
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
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: 54  Expect: 8.9e-005
Matches : 22/146 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
53.7	2185.037445	0.020427	YNSQNQSNNQFVLYR
41.4	2185.037445	0.020427	YNSQNQSNNQFVLYR
9.9	2185.037445	0.020427	YNSQNQSNNQFVLYR

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

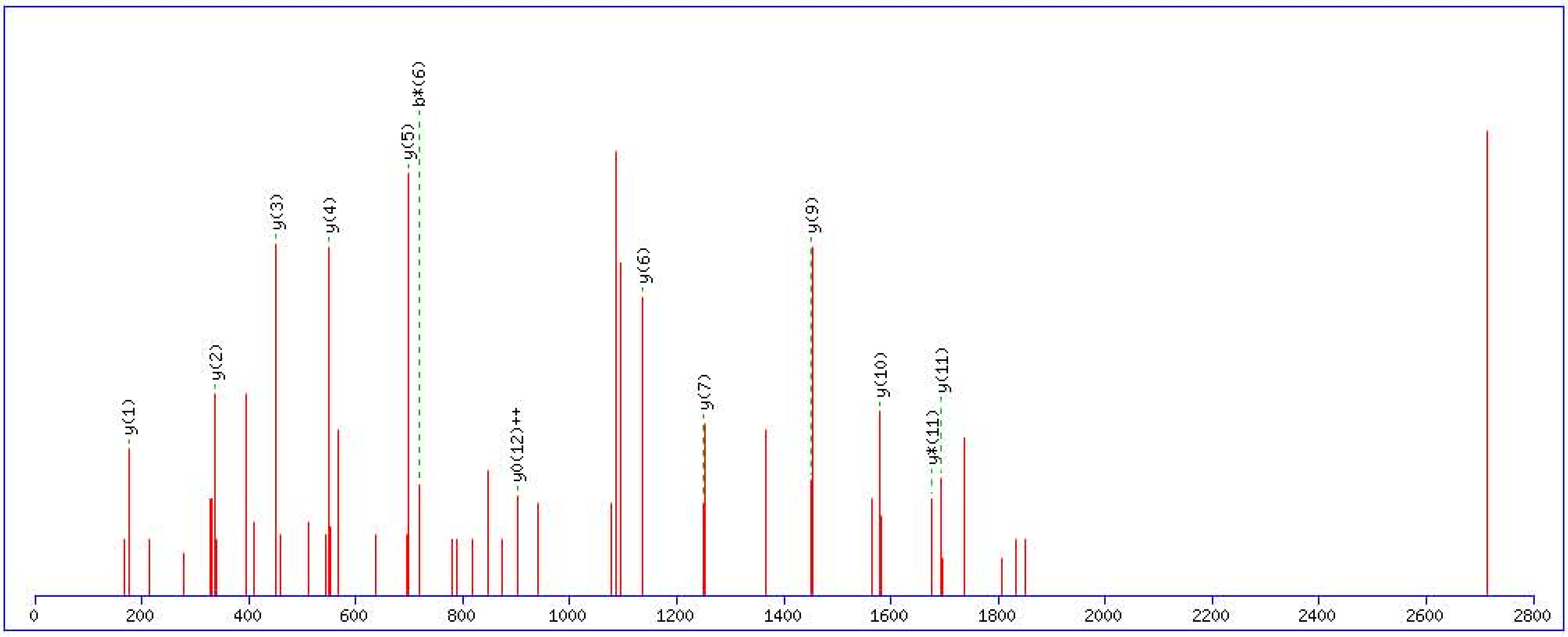
{MATRIX SCIENCE} Mascot Search Results

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 45797: 2185.063028 from(1093.538790,2+) rtinseconds(2143) index(19887)
Title: Locus:1.1.1.3346.20 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 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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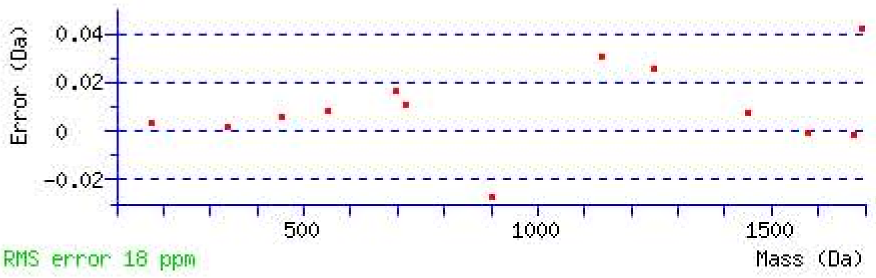
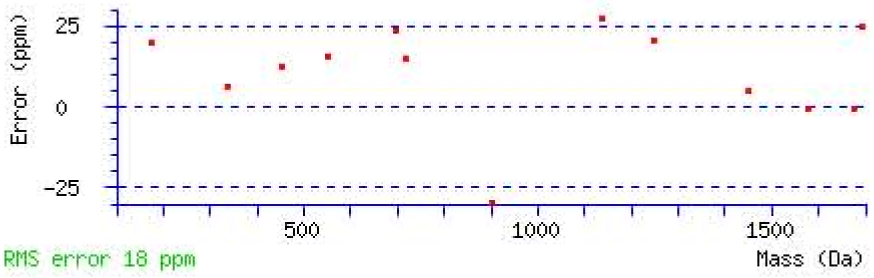
Monoisotopic mass of neutral peptide Mr(calc): 2185.037445
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0047
Matches : 13/146 fragment ions using 40 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	164.070605	82.538940					Y							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
36.8	2185.037445	0.025583	YNSQNQSNNQFVLYR
26.1	2185.037445	0.025583	YNSQNQSNNQFVLYR
19.7	2185.037445	0.025583	YNSQNQSNNQFVLYR

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

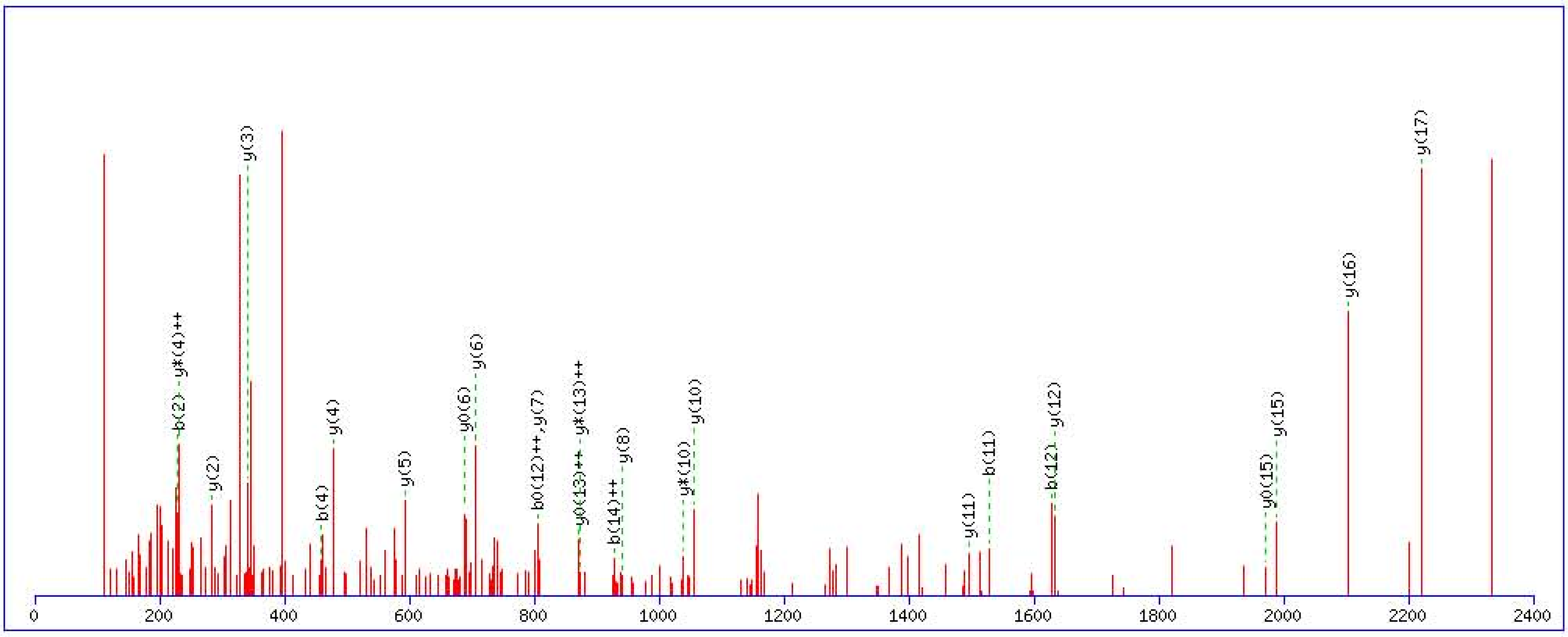
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDDDLEHQGGHVLDHGHK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

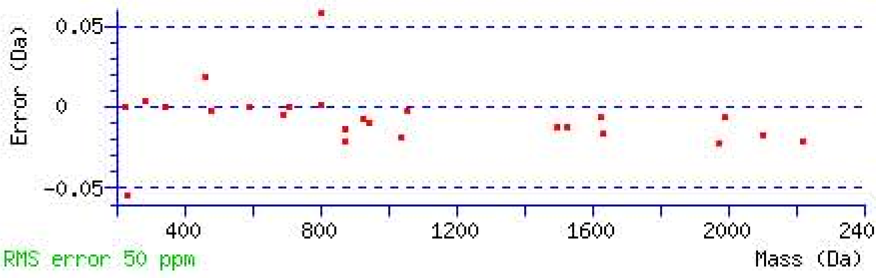
Match to Query 48332: 2332.093776 from(584.030720,4+) rtinseconds(1543) index(30517)
Title: Locus:1.1.1.3086.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

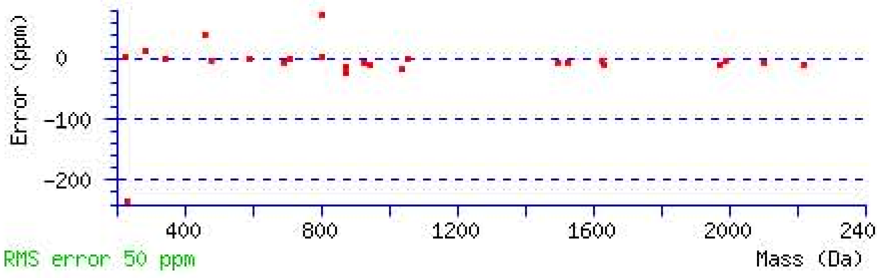
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2332.101883
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8     : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00027
Matches : 25/180 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	**229.118283**	115.062779			211.107718	106.057497	D	***2220.025077***	1110.516176	2202.998528	1102.002902	2202.014512	1101.510894	17
3	344.145226	172.576251			326.134661	163.570968	D	***2104.998134***	1053.002705	2087.971585	1044.489430	2086.987569	1043.997422	16
4	**459.172169**	230.089722			441.161604	221.084440	D	***1989.971191***	995.489234	1972.944642	986.975959	1971.960626	986.483951	15
5	572.256233	286.631755			554.245668	277.626472	L	1874.944248	937.975762	1857.917699	929.462488	1856.933683	928.970480	14
6	701.298826	351.153051			683.288261	342.147769	E	1761.860184	881.433730	1744.833635	872.920456	1743.849619	872.428448	13
7	838.357738	419.682507			820.347173	410.677225	H	***1632.817591***	816.912434	1615.791042	808.399159	1614.807026	807.907151	12
8	1277.583064	639.295170	1260.556515	630.781896	1259.572499	630.289888	Q	***1495.758679***	748.382978	1478.732130	739.869703	1477.748114	739.377695	11
9	1334.604528	667.805902	1317.577979	659.292628	1316.593963	658.800620	G	***1056.533353***	528.770315	1039.506804	520.257040	1038.522788	519.765032	10
10	1391.625992	696.316634	1374.599443	687.803360	1373.615427	687.311352	G	999.511889	500.259583	982.485340	491.746308	981.501324	491.254300	9
11	**1528.684904**	764.846090	1511.658355	756.332816	1510.674339	755.840807	H	***942.490425***	471.748851	925.463876	463.235576	924.479860	462.743568	8
12	**1627.753318**	814.380297	1610.726769	805.867023	1609.742753	805.375015	V	***805.431513***	403.219395	788.404964	394.706120	787.420948	394.214112	7
13	1740.837382	870.922329	1723.810833	862.409055	1722.826817	861.917046	L	***706.363099***	353.685188	689.336550	345.171913	688.352534	344.679905	6
14	1855.864325	928.435801	1838.837776	919.922526	1837.853760	919.430518	D	***593.279035***	297.143156	576.252486	288.629881	575.268470	288.137873	5
15	1992.923237	996.965257	1975.896688	988.451982	1974.912672	987.959974	H	***478.252092***	239.629684	461.225543	231.116410			4
16	2049.944701	1025.475988	2032.918152	1016.962714	2031.934136	1016.470706	G	***341.193180***	171.100228	324.166631	162.586954			3
17	2187.003613	1094.005444	2169.977064	1085.492170	2168.993048	1085.000162	H	***284.171716***	142.589496	267.145167	134.076221			2
18							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LDDDLEHQGGHVLDHGHK
(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	2332.101883	-0.008107	LDDDLEHQGGHVLDHGHK

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

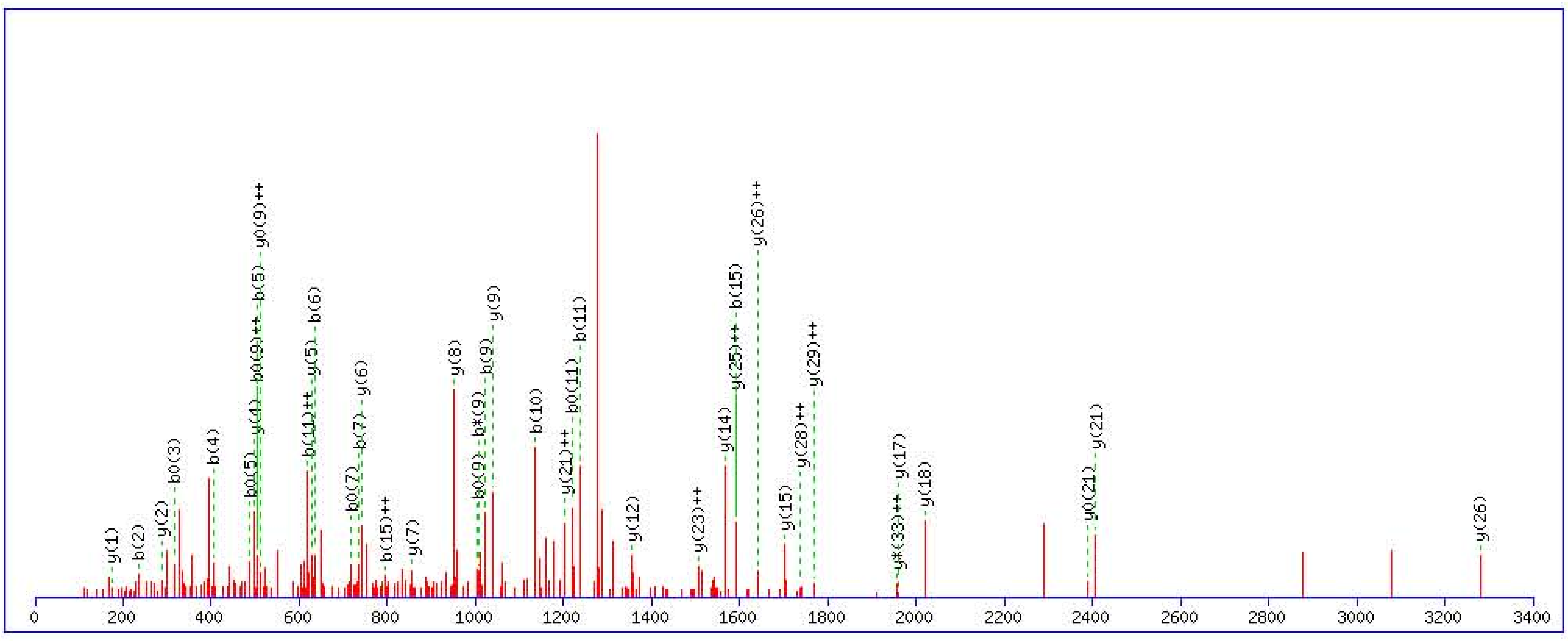
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

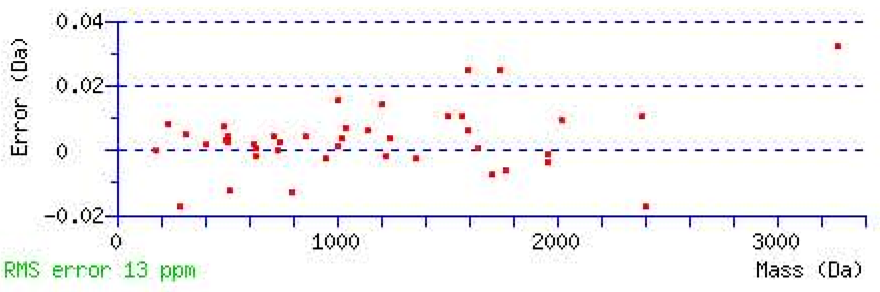
Match to Query 69282: 5066.484070 from(1014.304090,5+) rtinseconds(2673) index(36676)
Title: Locus:1.1.1.3479.17 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

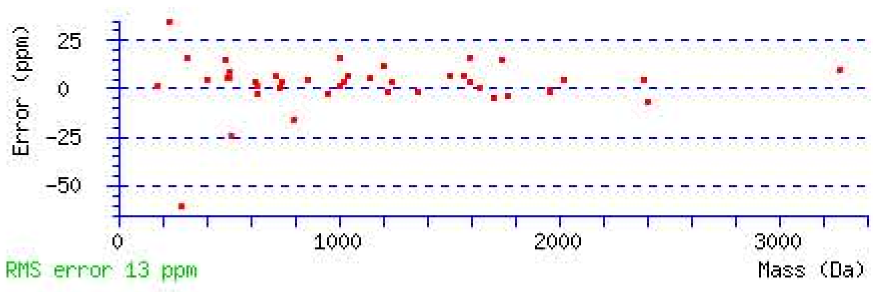


Monoisotopic mass of neutral peptide Mr(calc): 5066.465057
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q21 : Biotin:Thermo-21345 (Q)
Ions Score: 60 **Expect:** 1.9e-005
Matches : 42/484 fragment ions using 96 most intense peaks (help)

#	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



RMS error 13 ppm



RMS error 13 ppm

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
60.1	5066.465057	0.019013	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR
25.0	5066.465057	0.019013	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR
22.1	5066.465057	0.019013	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR
19.8	5066.465057	0.019013	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR

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

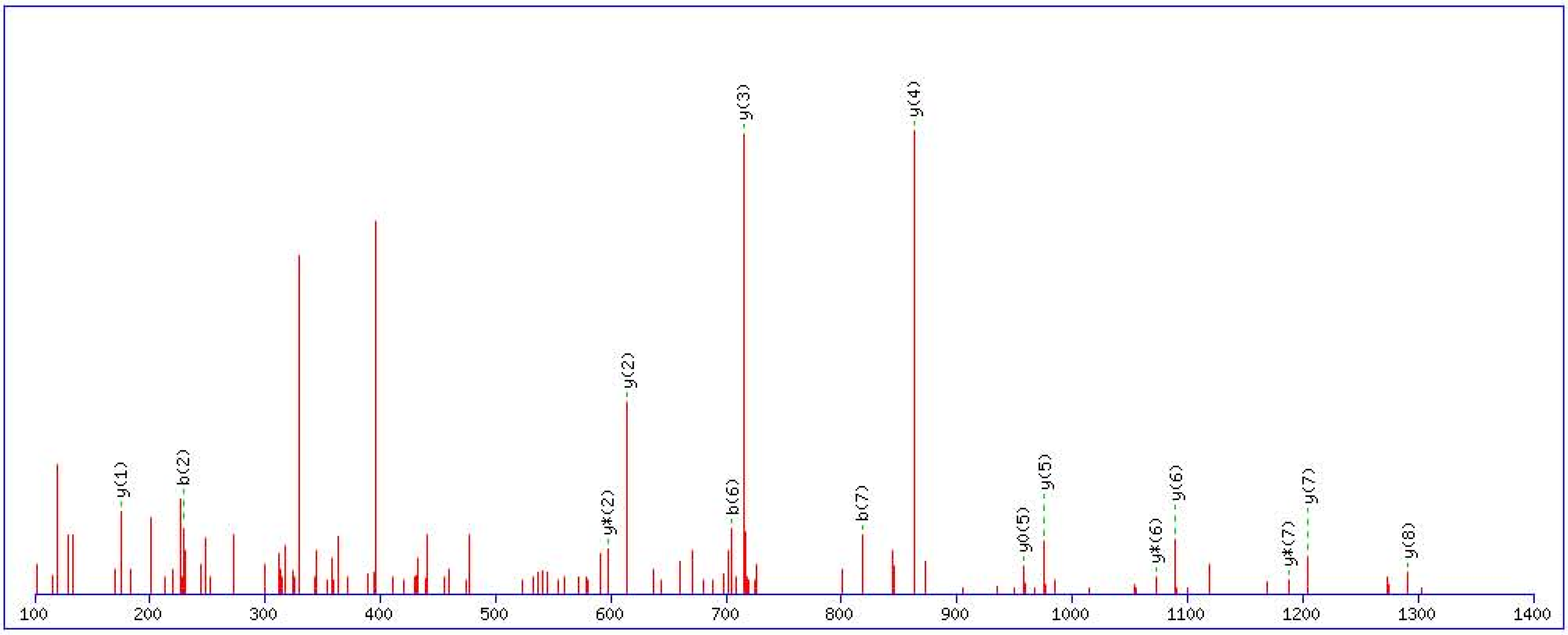
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VECSDNLFTQR**
Found in **MASP1_HUMAN**, Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3

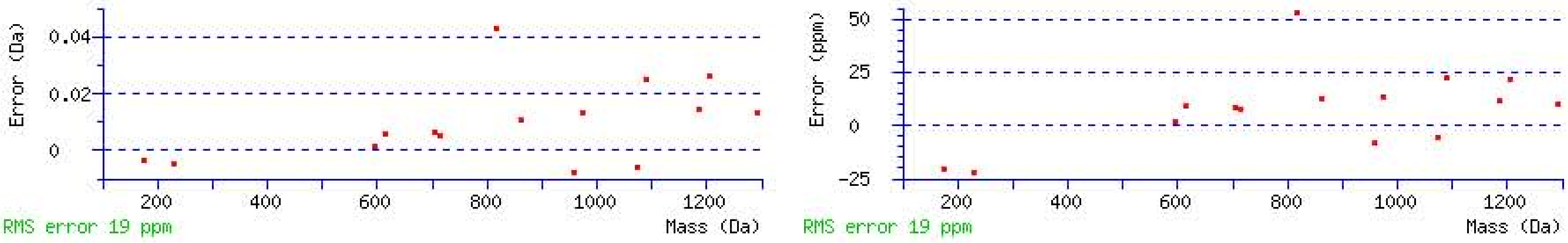
Match to Query 36031: 1678.783422 from(560.601750,3+) rtinseconds(2095) index(47966)
Title: Locus:1.1.1.2778.4 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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



```
Monoisotopic mass of neutral peptide Mr(calc): 1678.780716
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 50  Expect: 0.00015
Matches : 15/104 fragment ions using 25 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							11
2	**229.118283**	115.062780			211.107718	106.057497	E	1580.719575	790.863426	1563.693026	782.350151	1562.709010	781.858143	10
3	389.148932	195.078104			371.138367	186.072822	C	1451.676982	726.342129	1434.650433	717.828855	1433.666417	717.336847	9
4	476.180960	238.594118			458.170395	229.588835	S	***1291.646333***	646.326805	1274.619784	637.813530	1273.635768	637.321522	8
5	591.207903	296.107590			573.197338	287.102307	D	***1204.614305***	602.810791	1187.587756	594.297516	1186.603740	593.805508	7
6	**705.250830**	353.129053	688.224281	344.615778	687.240265	344.123770	N	***1089.587362***	545.297319	1072.560813	536.784045	1071.576797	536.292037	6
7	**818.334894**	409.671085	801.308345	401.157810	800.324329	400.665802	L	***975.544435***	488.275856	958.517886	479.762581	957.533870	479.270573	5
8	965.403308	483.205292	948.376759	474.692017	947.392743	474.200009	F	***862.460371***	431.733824	845.433822	423.220549	844.449806	422.728541	4
9	1066.450987	533.729131	1049.424438	525.215857	1048.440422	524.723849	T	***715.391957***	358.199617	698.365408	349.686342	697.381392	349.194334	3
10	1505.676313	753.341795	1488.649764	744.828520	1487.665748	744.336512	Q	***614.344278***	307.675777	597.317729	299.162503			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.5	1678.780716	0.002706	VECSDNLFTQR

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

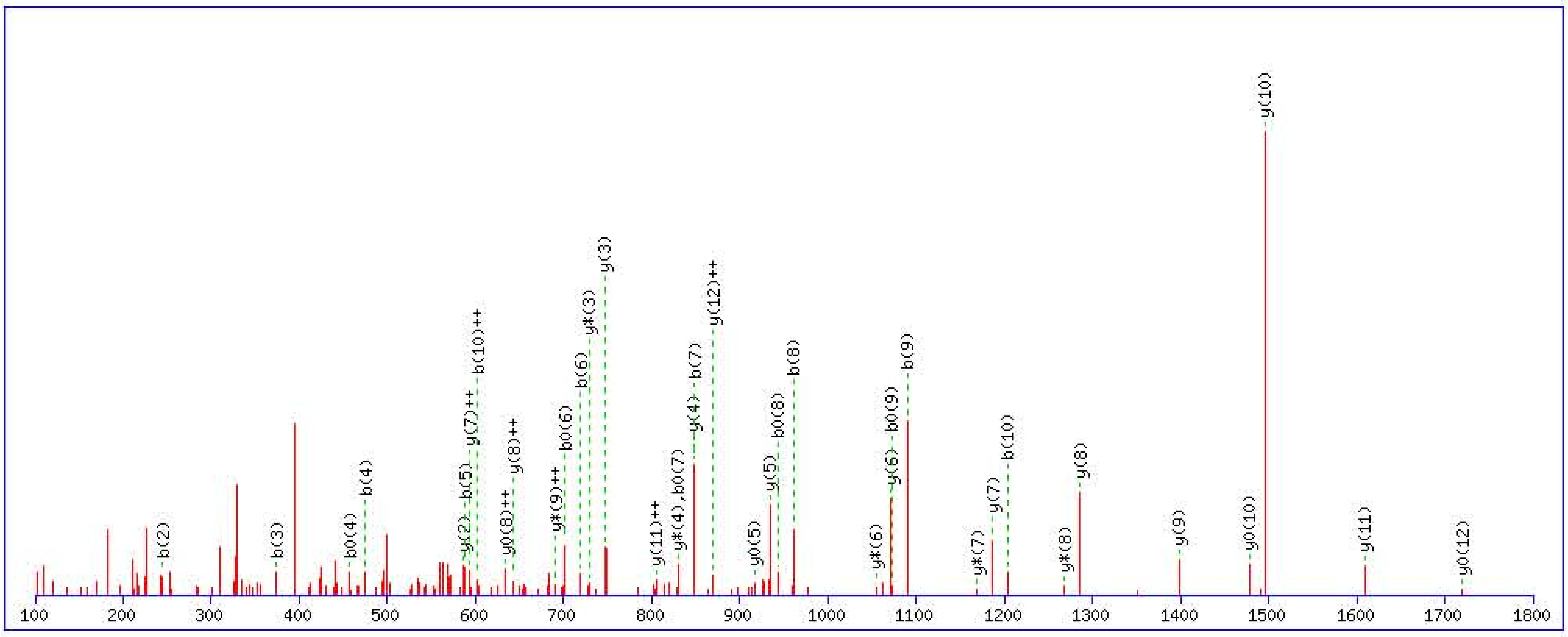
{MATRIX SCIENCE} Mascot Search Results

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

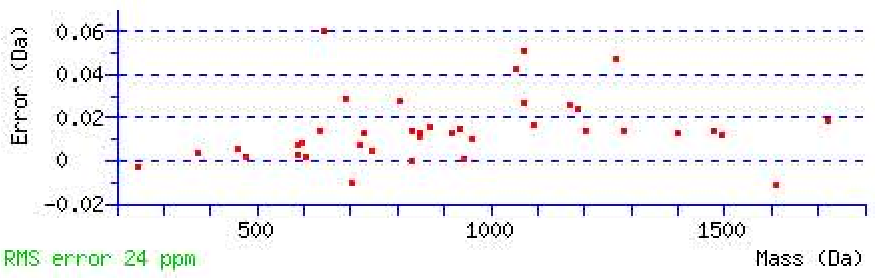
Match to Query 52735: 2697.349696 from(675.344700,4+) rtinseconds(2751) index(52029)
Title: Locus:1.1.1.3005.5 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

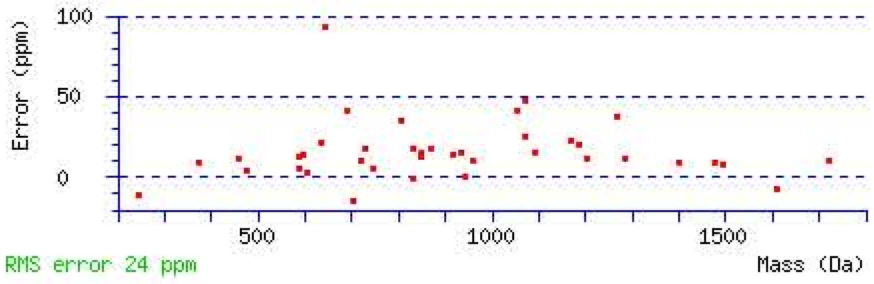
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 56  Expect: 9.8e-006
Matches : 39/182 fragment ions using 80 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
55.9	2697.321609	0.028087	FPETLMEIEIPIVDHSTCQK
2.4	2697.379593	-0.029897	LVVLFSQMRLANFQTDSQESIQK
0.9	2697.363159	-0.013463	RRGYAPLLYLQSHCDVPADR

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

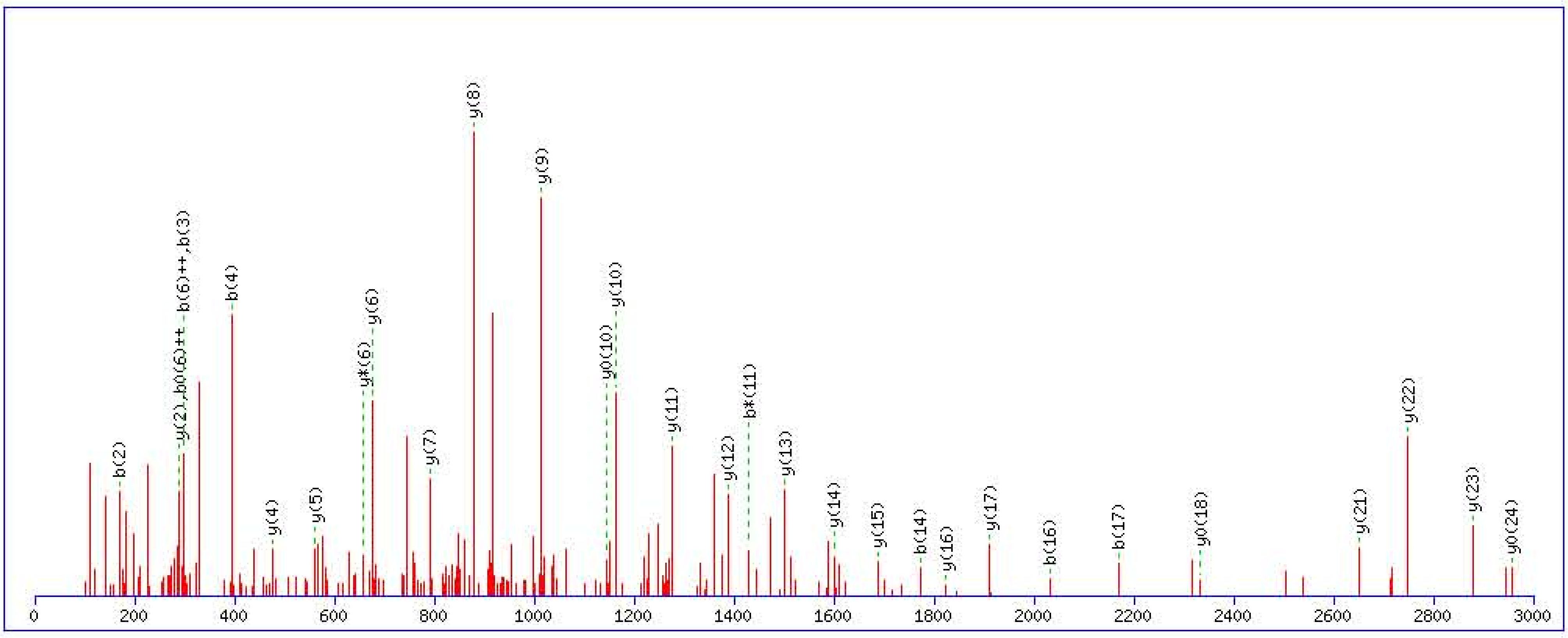
MATRIX SCIENCE Mascot Search Results

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

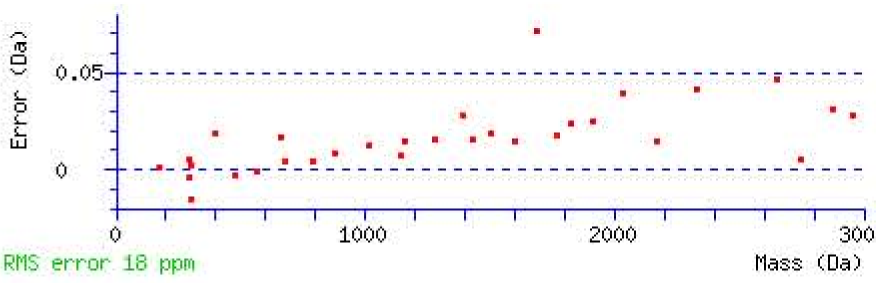
Match to Query 56401: 3045.524056 from(762.388290,4+) rtinseconds(2249) index(48968)
Title: Locus:1.1.1.2831.15 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

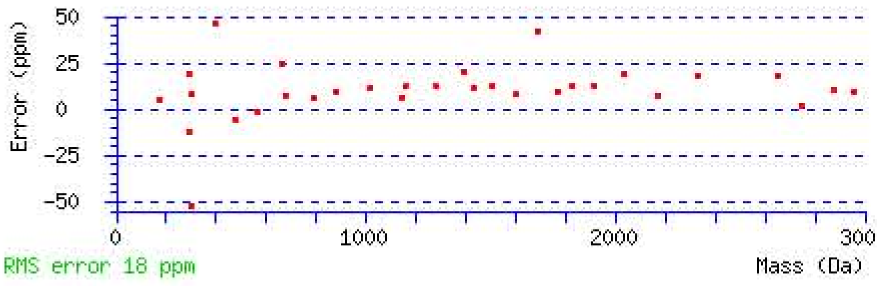


```
Monoisotopic mass of neutral peptide Mr(calc): 3045.497803
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 98  Expect: 4.8e-009
Matches : 31/266 fragment ions using 68 most intense peaks   (help)
```

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



RMS error 18 ppm



RMS error 18 ppm

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
97.6	3045.497803	0.026253	APEPISTQSHSVLILFHSDNSGENR

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

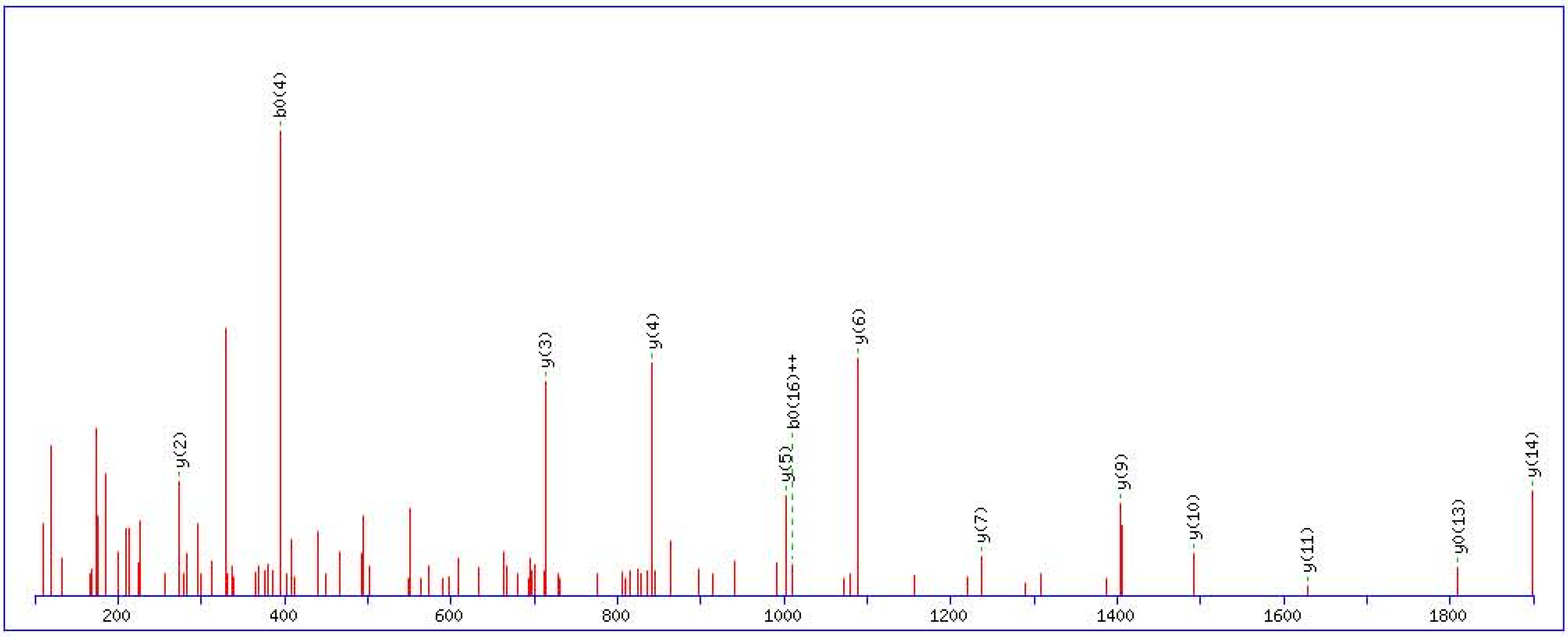
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLSIAQAHSPAFSCEQVR**
Found in **CD14_HUMAN**, Monocyte differentiation antigen CD14 OS=Homo sapiens GN=CD14 PE=1 SV=2

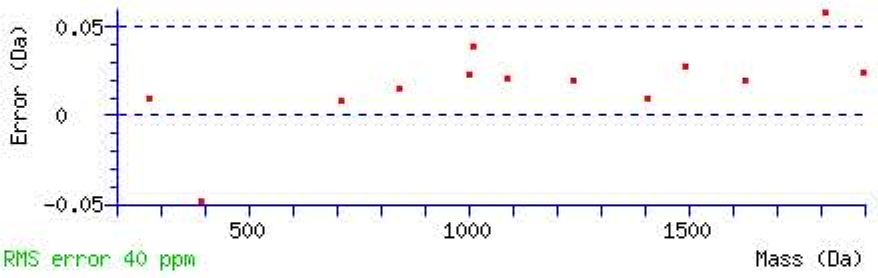
Match to Query 47959: 2310.180896 from(578.552500,4+) rtinseconds(1986) index(18994)
Title: Locus:1.1.1.3292.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

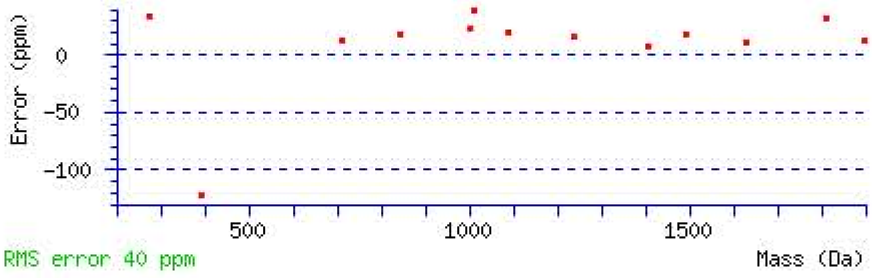
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2310.161285
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16 : Biotin:Thermo-21345 (Q)
Ions Score: 45 **Expect:** 0.00092
Matches : 13/184 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							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
44.9	2310.161285	0.019611	VLSIAQAHSPAFSCEQVR

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

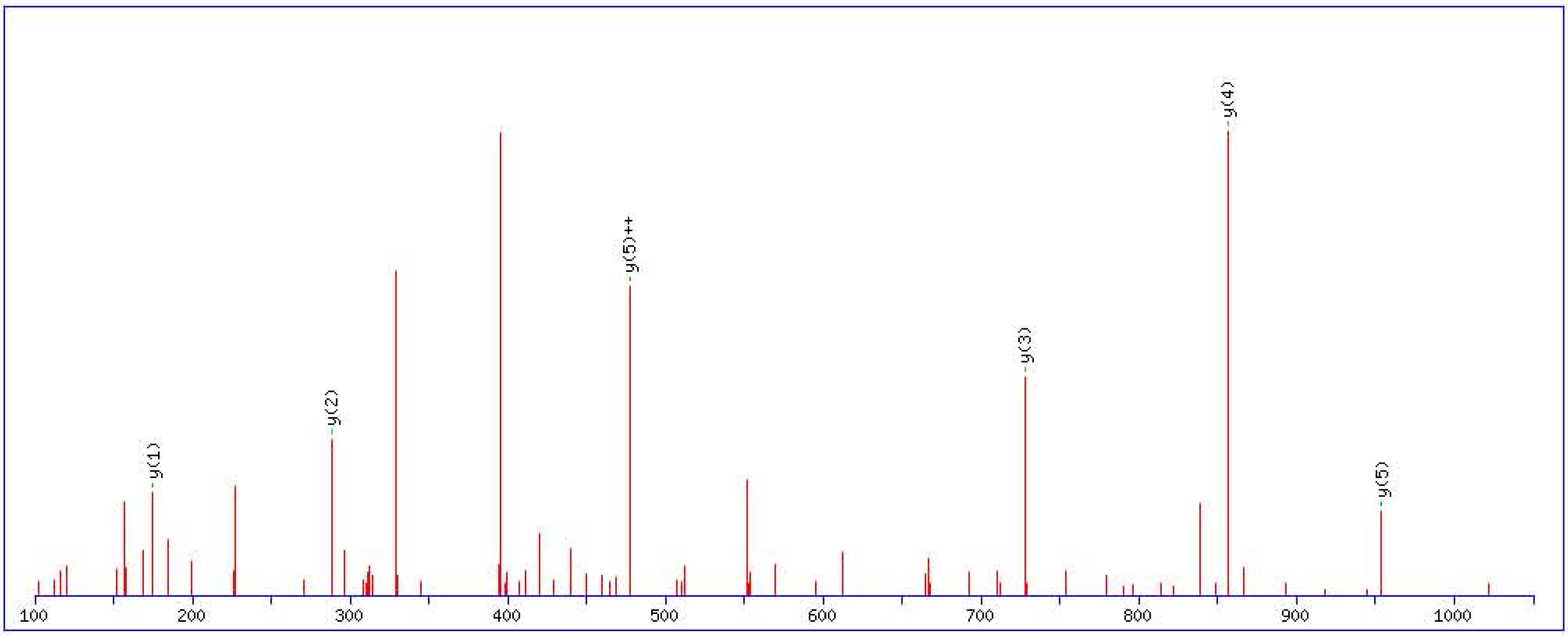
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPEQLR**
Found in **GNPTG_HUMAN**, N-acetylglucosamine-1-phosphotransferase subunit gamma OS=Homo sapiens GN=GNPTG PE=1 SV=1

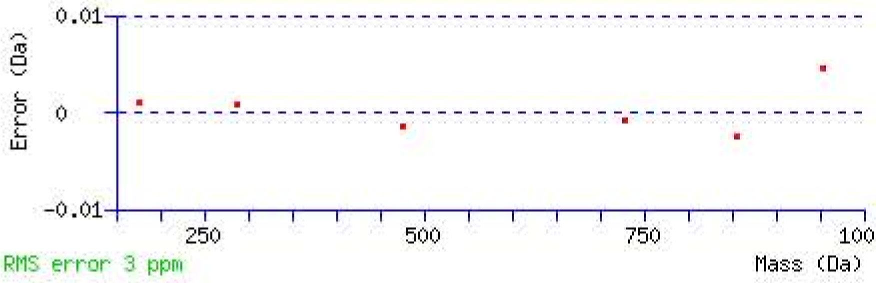
Match to Query 14811: 1039.556168 from(520.785360,2+) rtinseconds(1506) index(30312)
Title: Locus:1.1.1.3073.7 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

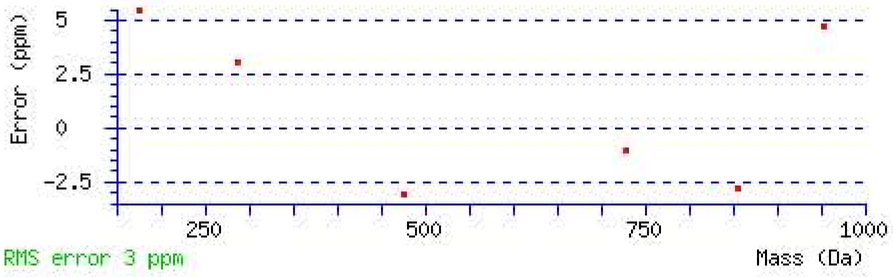
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1039.548431
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0063
Matches : 6/48 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	88.039304	44.523290			70.028739	35.518008	S							6
2	185.092068	93.049672			167.081503	84.044389	P	***953.523699***	477.265488	936.497150	468.752213	935.513134	468.260205	5
3	314.134661	157.570968			296.124096	148.565686	E	***856.470935***	428.739106	839.444386	420.225831	838.460370	419.733823	4
4	753.359987	377.183632	736.333438	368.670357	735.349422	368.178349	Q	***727.428342***	364.217809	710.401793	355.704535			3
5	866.444051	433.725664	849.417502	425.212389	848.433486	424.720381	L	***288.203016***	144.605146	271.176467	136.091872			2
6							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of SPEQLR
(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	1039.548431	0.007737	SPEQLR
20.8	1039.548431	0.007737	SPEIQR
17.2	1039.541031	0.015137	ALESNHTLR
12.8	1039.567535	-0.011367	SSLVWHRR
11.5	1039.563492	-0.007324	SSLERHRR
9.8	1039.567535	-0.011367	SPPPPHRPR
8.1	1039.570892	-0.014724	SMGRLAHIR
5.8	1039.541061	0.015107	SSRVTFSTR
5.5	1039.563492	-0.007324	SSHLRERR
4.7	1039.541046	0.015122	ALQSGPPQSR

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

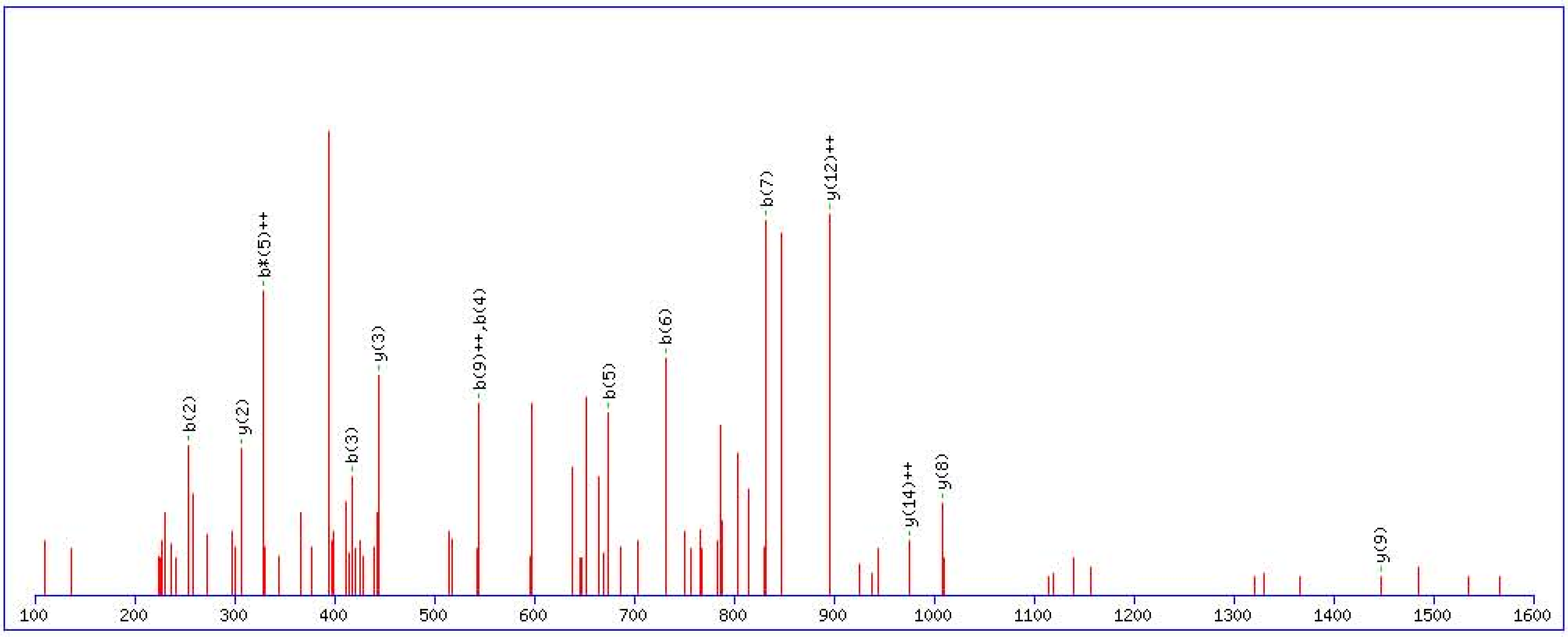
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPYQEGTPCSQCPSGYHCK**
Found in **PI16_HUMAN**, Peptidase inhibitor 16 OS=Homo sapiens GN=PI16 PE=1 SV=1

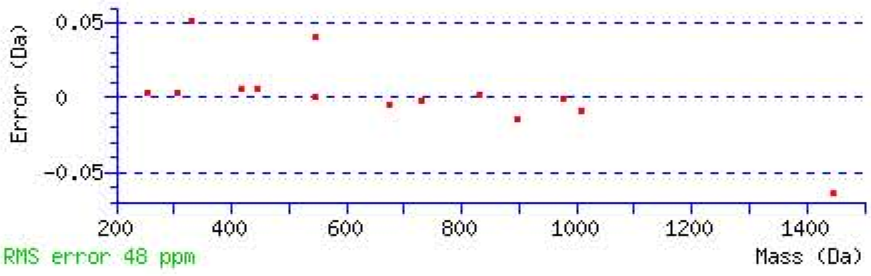
Match to Query 52244: 2622.115056 from(656.536040,4+) rtinseconds(1338) index(29283)
Title: Locus:1.1.1.3014.17 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

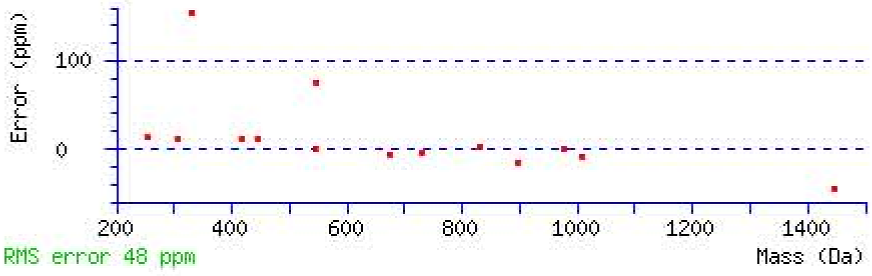
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2622.123611
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.0068
Matches : 14/198 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	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
26.4	2622.123611	-0.008555	RPYQEGTPCSQCPSGYHCK

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

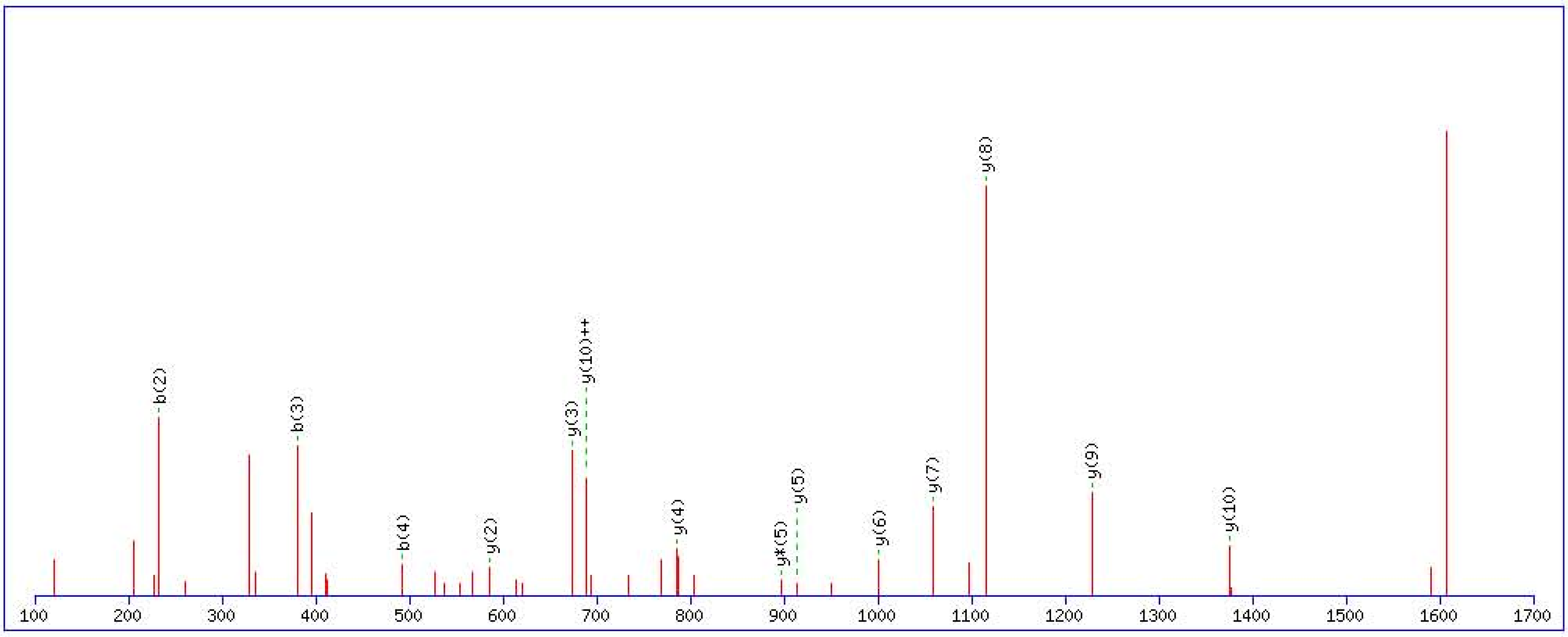
Mascot Search Results

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

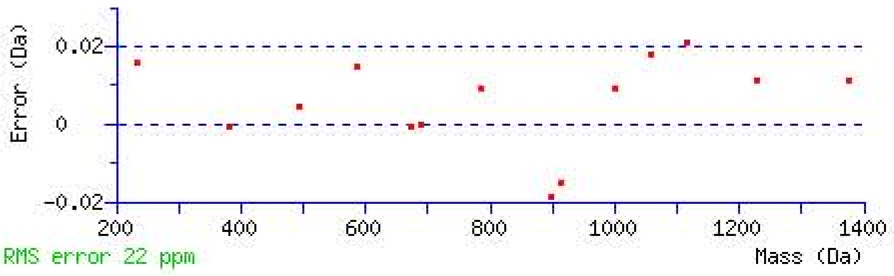
Match to Query 33445: 1606.842548 from(804.428550,2+) rtinseconds(2120) index(48139)
Title: Locus:1.1.1.2786.17 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

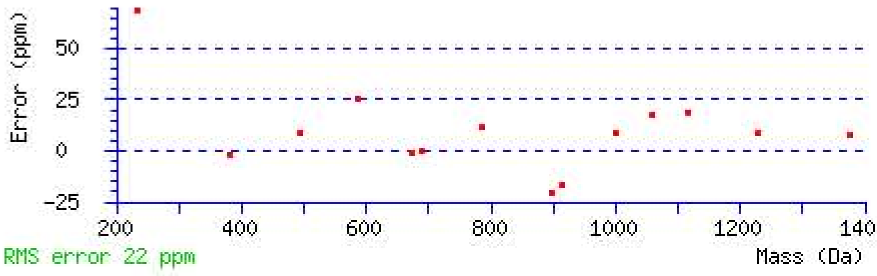
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1606.821121
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 66  Expect: 6.2e-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	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
65.8	1606.821121	0.021427	TMFIGGSQLSQK
31.5	1606.821121	0.021427	TMFIGGSQLSQK

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

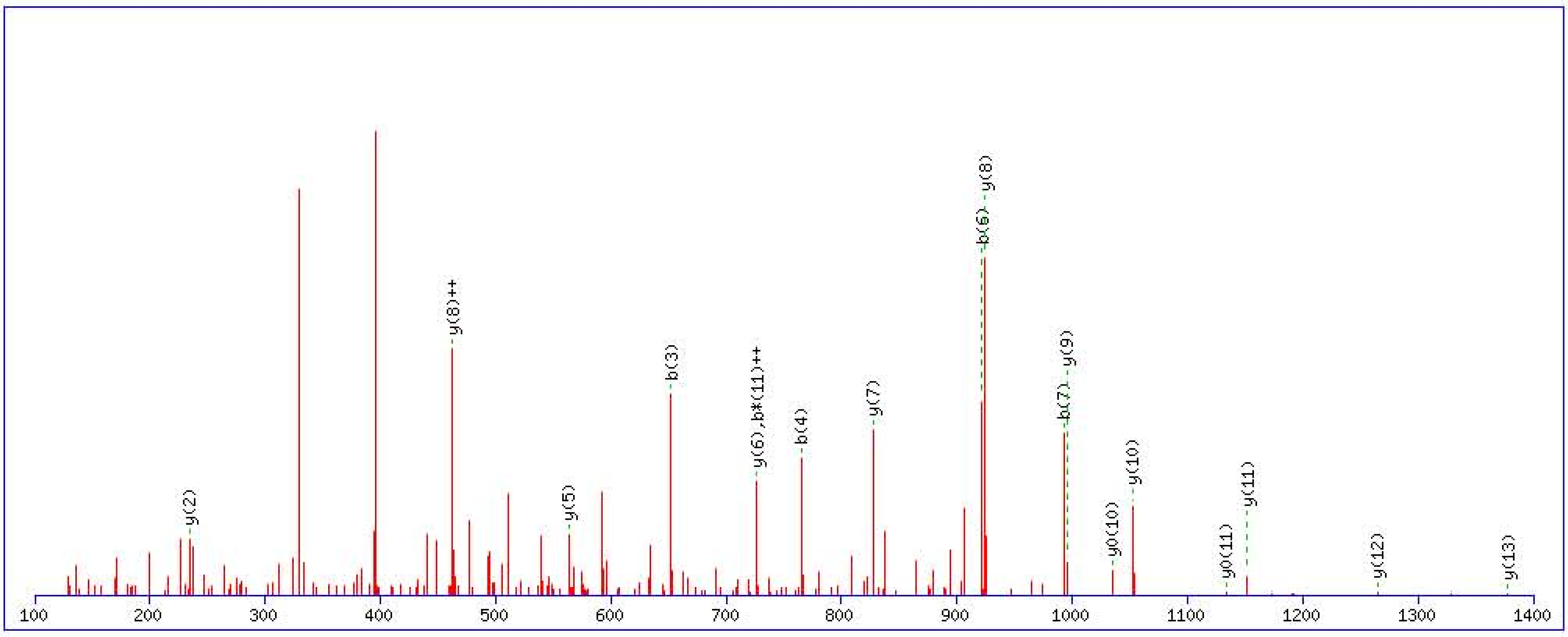
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QVLLVGAPTYDDVSK**
Found in **PHLD_HUMAN**, Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens GN=GPLD1 PE=1 SV=3

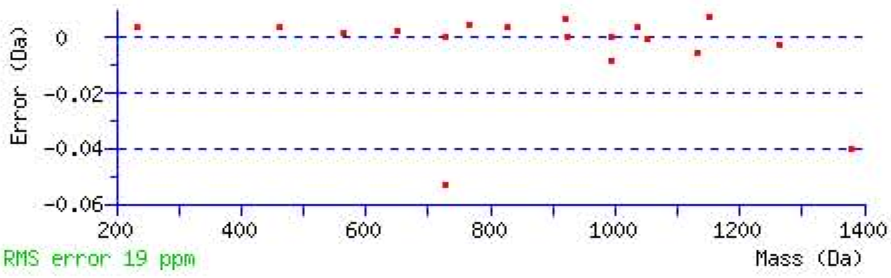
Match to Query 40510: 1915.016352 from(639.346060,3+) rtinseconds(2320) index(34918)
Title: Locus:1.1.1.3357.5 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

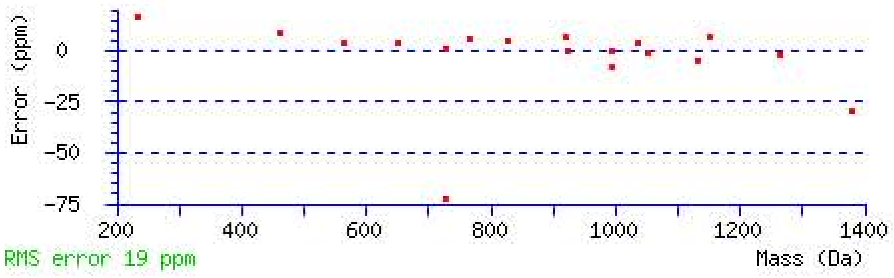
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1915.012497
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 68  Expect: 7.2e-007
Matches : 18/150 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							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
68.2	1915.012497	0.003855	QVLLVGAPTYDDVSK
2.5	1915.002411	0.013941	SQHEGRVEVQIGGPGPLR
0.5	1914.998550	0.017802	LLAPEAGSHPQQTQK
0.5	1914.998550	0.017802	LLAPEAGSHPQQTQK
0.5	1914.998550	0.017802	LLAPEAGSHPQQTQK

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

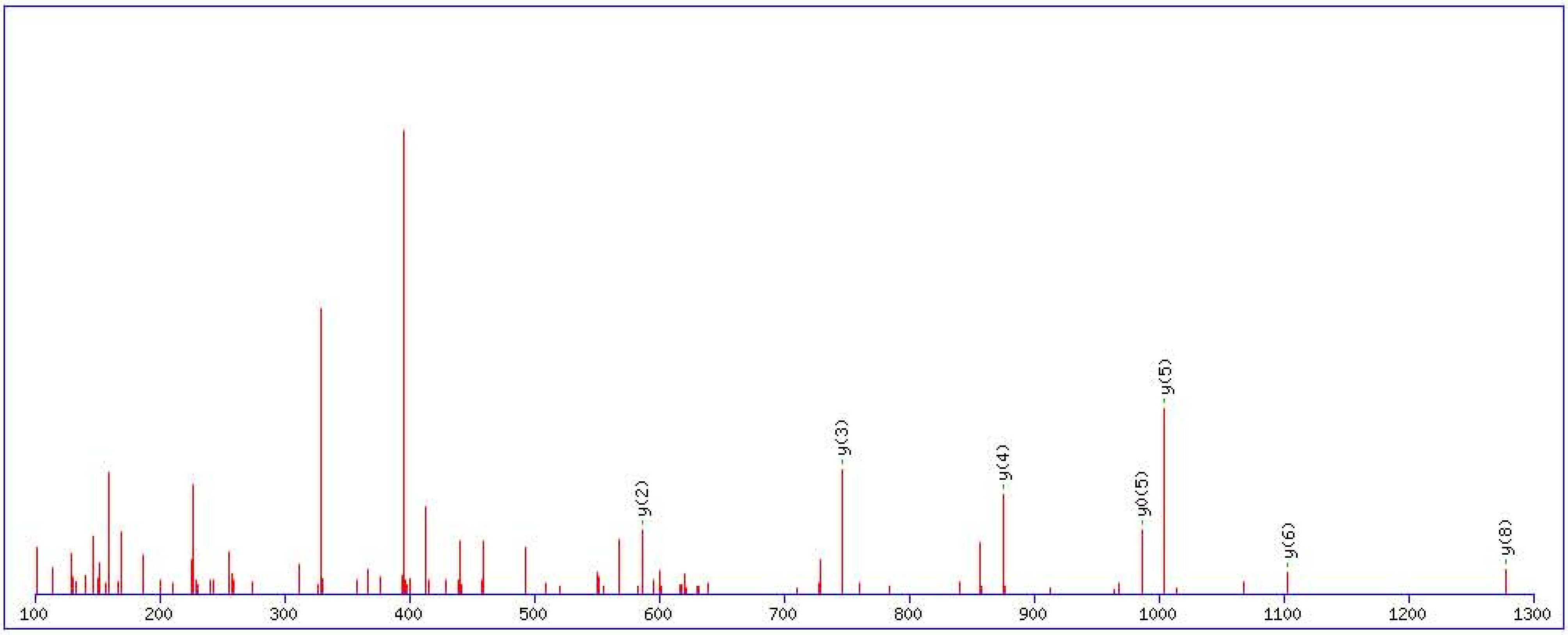
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSSVEECQK**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

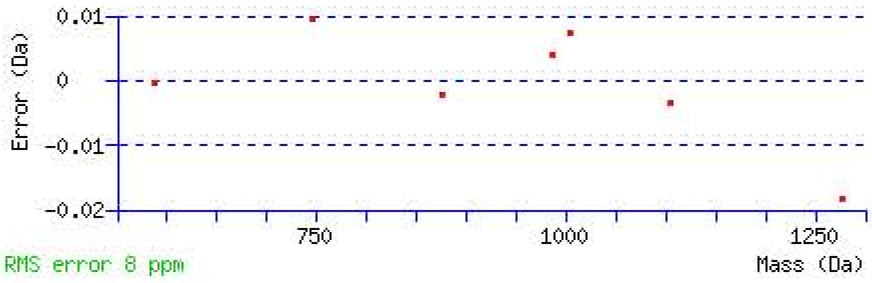
Match to Query 25529: 1375.647672 from(459.556500,3+) rtinseconds(1405) index(59219)
Title: Locus:1.1.1.3115.5 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

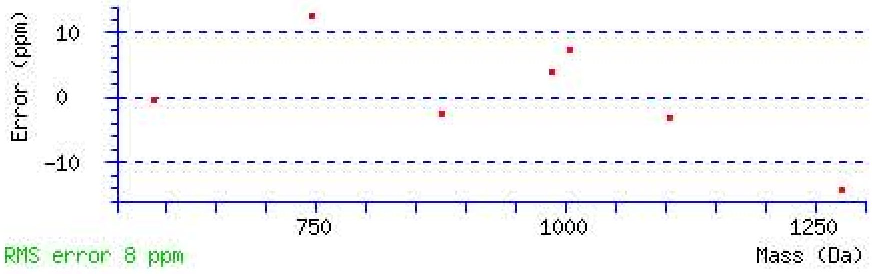
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1375.647568
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.00064
Matches : 7/74 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	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
36.4	1375.647568	0.000104	VSSVEECQK
2.3	1375.662827	-0.015155	GFSIPECQK

Mascot: http://www.matrixscience.com/

{MATRIX SCIENCE}

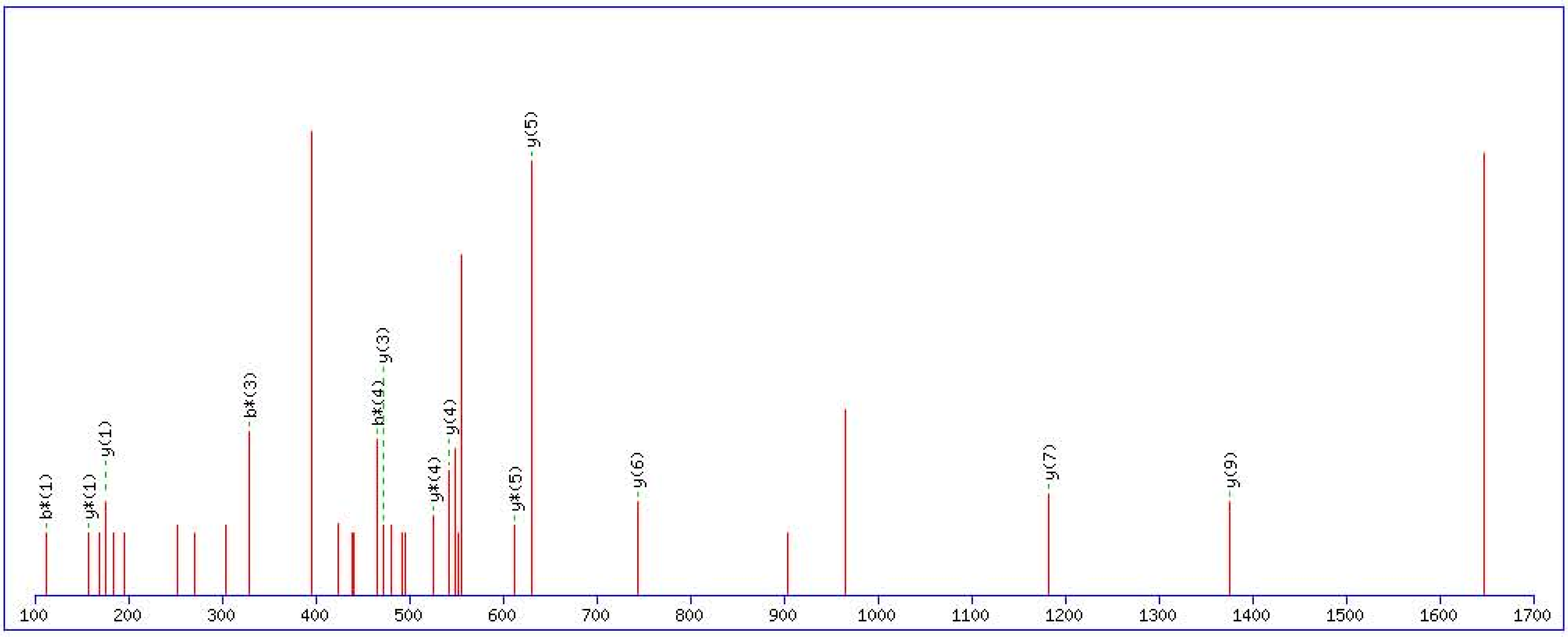
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QCGHQISACHR**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

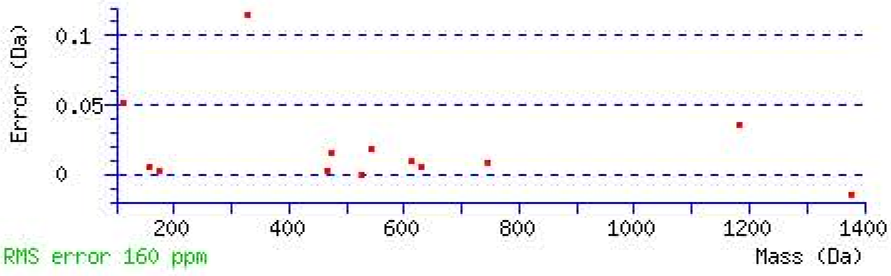
Match to Query 35694: 1663.752342 from(555.591390,3+) rtinseconds(1127) index(58265)
Title: Locus:1.1.1.3018.13 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

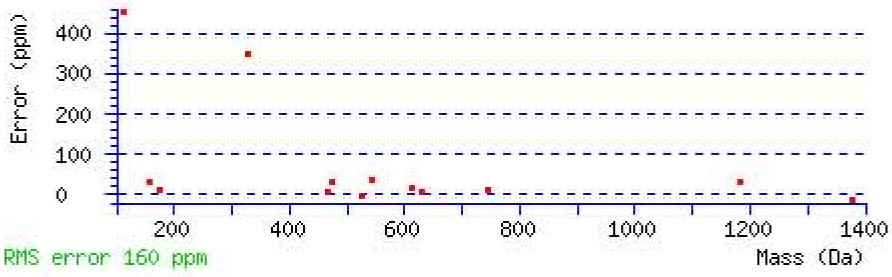
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1663.749374
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0016
Matches : 13/100 fragment ions using 25 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							11
2	289.096503	145.051890	272.069954	136.538615			C	1536.698070	768.852673	1519.671521	760.339399	1518.687505	759.847391	10
3	346.117967	173.562622	329.091418	165.049347			G	***1376.667421***	688.837348	1359.640872	680.324074	1358.656856	679.832066	9
4	483.176879	242.092078	466.150330	233.578803			H	1319.645957	660.326617	1302.619408	651.813342	1301.635392	651.321334	8
5	922.402205	461.704741	905.375656	453.191466			Q	***1182.587045***	591.797161	1165.560496	583.283886	1164.576480	582.791878	7
6	1035.486269	518.246773	1018.459720	509.733498			I	***743.361719***	372.184498	726.335170	363.671223	725.351154	363.179215	6
7	1122.518297	561.762787	1105.491748	553.249512	1104.507732	552.757504	S	***630.277655***	315.642466	613.251106	307.129191	612.267090	306.637183	5
8	1193.555411	597.281344	1176.528862	588.768069	1175.544846	588.276061	A	***543.245627***	272.126452	526.219078	263.613177			4
9	1353.586060	677.296668	1336.559511	668.783394	1335.575495	668.291386	C	***472.208513***	236.607894	455.181964	228.094620			3
10	1490.644972	745.826124	1473.618423	737.312850	1472.634407	736.820842	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
33.8	1663.749374	0.002968	QCGHQISACHR
15.9	1663.749374	0.002968	QCGHQISACHR
3.7	1663.768906	-0.016564	QLSVEPYSQEEAER
2.2	1663.744675	0.007667	QCQALVIWTDCDR
2.0	1663.737213	0.015129	EQWAEREREMER
0.6	1663.774521	-0.022179	RMQWAMQTGGR
0.1	1663.740616	0.011726	ESPMVRSARDDMDR
0.0	1663.772278	-0.019936	NLTEEMAALDESVAR
0.0	1663.773651	-0.021309	AGSDGAKIGNCPFSQR

Mascot: http://www.matrixscience.com/

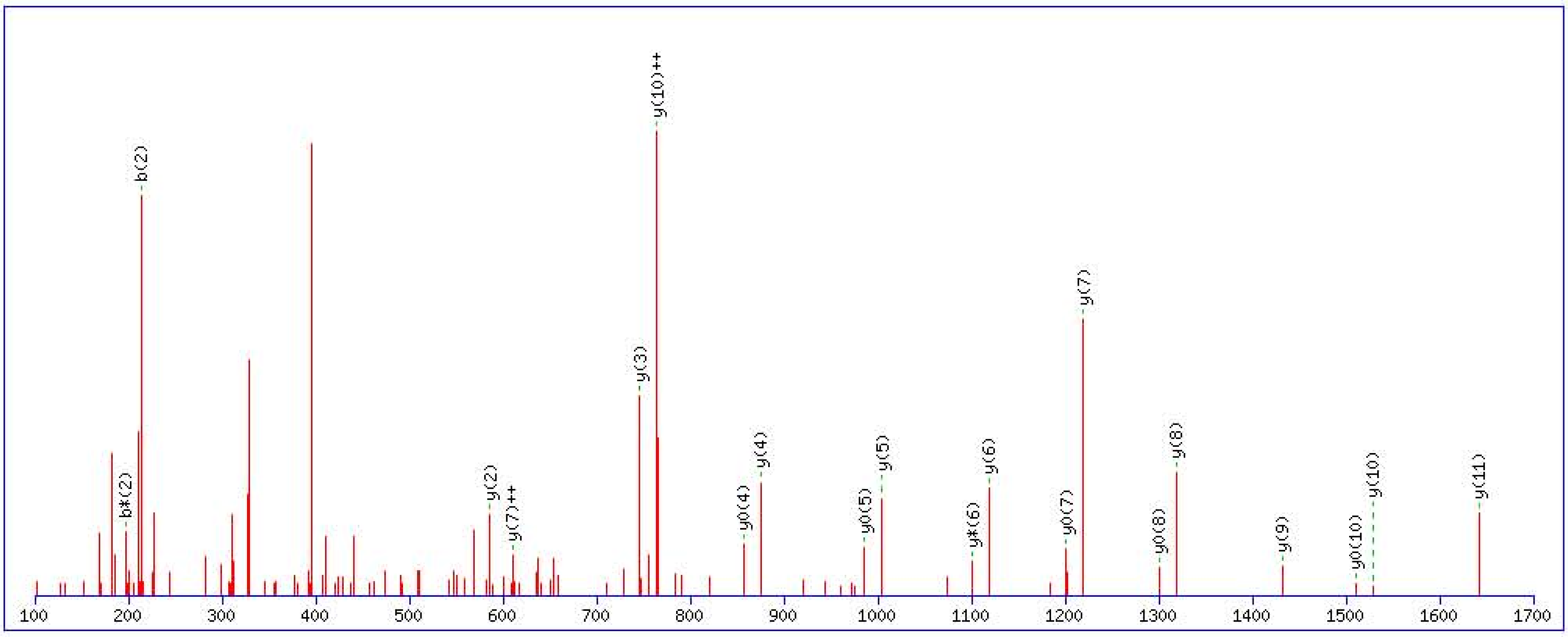
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNIPLVTNEECQK**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

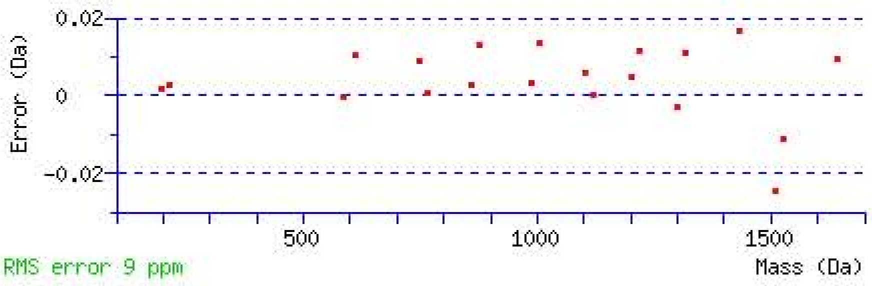
Match to Query 39531: 1853.941272 from(618.987700,3+) rtinseconds(2165) index(63498)
Title: Locus:1.1.1.3380.15 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

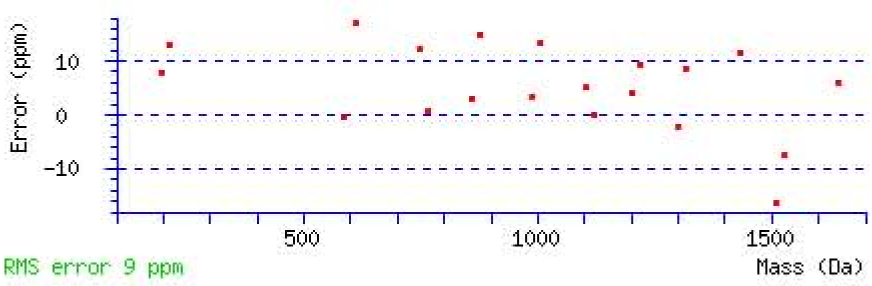
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 66 **Expect:** 1.5e-006
Matches : 20/124 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	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
65.7	1853.937927	0.003345	VNIPLVTNEECQK
3.7	1853.934341	0.006931	RGLSNPNELQAAIDSNR

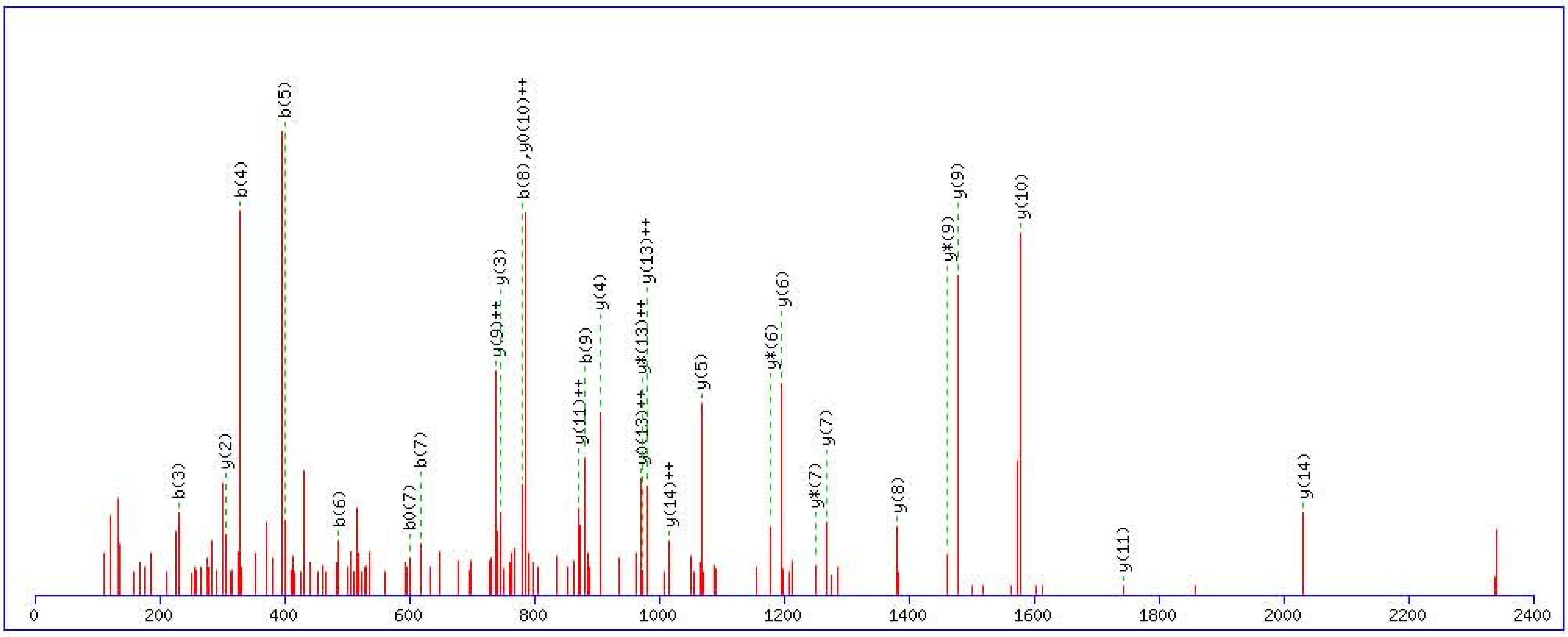
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGDVASMYTPNAQYCQMR**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

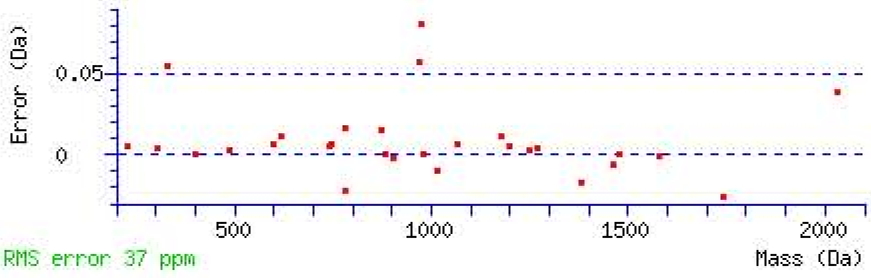
Match to Query 48621: 2359.037112 from(787.352980,3+) rtinseconds(2094) index(63046)
Title: Locus:1.1.1.3355.15 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

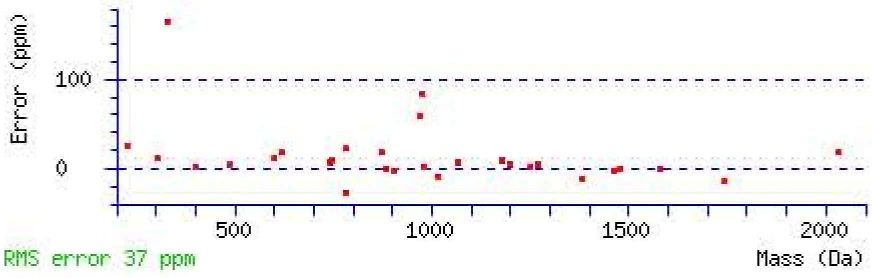


Monoisotopic mass of neutral peptide Mr(calc): 2359.021759
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16 : Biotin:Thermo-21345 (Q)
Ions Score: 50 **Expect:** 6.6e-005
Matches : 29/162 fragment ions using 63 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.028740	29.518008					G							18
2	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



RMS error 37 ppm



RMS error 37 ppm

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
49.6	2359.021759	0.015353	GGDVASMYTPNAQYCQMR
30.2	2359.021759	0.015353	GGDVASMYTPNAQYCQMR

Mascot: http://www.matrixscience.com/

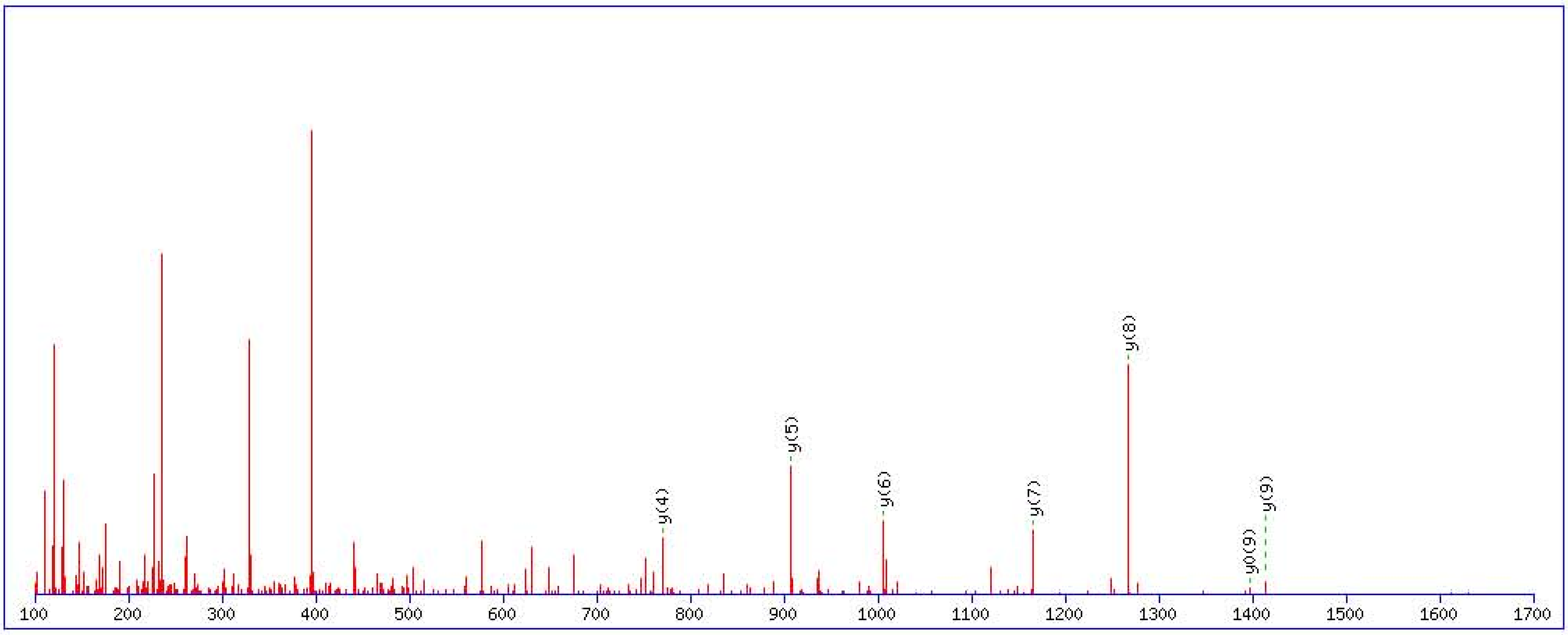
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DFTCVHQALK**
Found in **IC1_HUMAN**, Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2

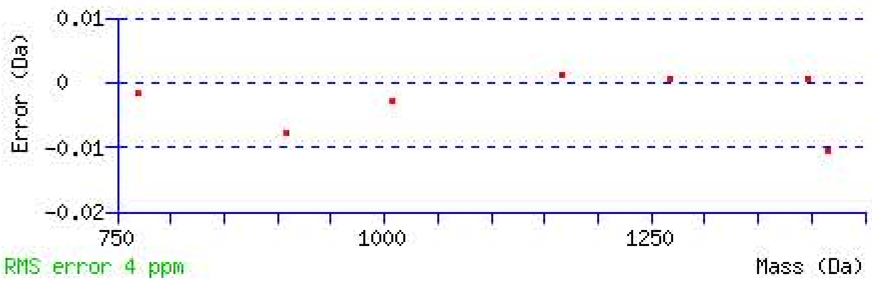
Match to Query 30790: 1528.755912 from(510.592580,3+) rtinseconds(1823) index(32026)
Title: Locus:1.1.1.3184.5 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

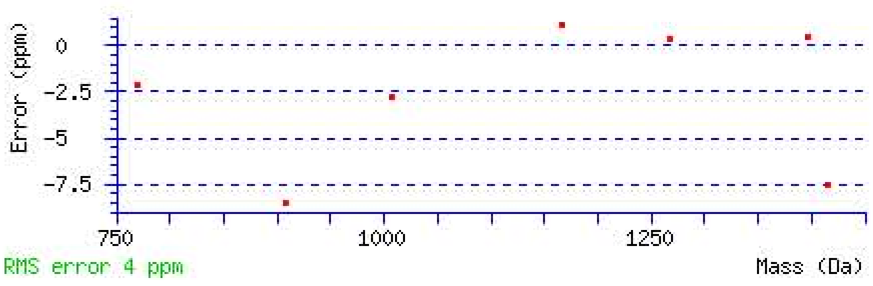
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1528.753052
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.0035
Matches : 7/82 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							10
2	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
29.7	1528.753052	0.002860	DFTCVHQALK
3.5	1528.764084	-0.008172	HTRQMRNTVAGSR

Mascot: http://www.matrixscience.com/

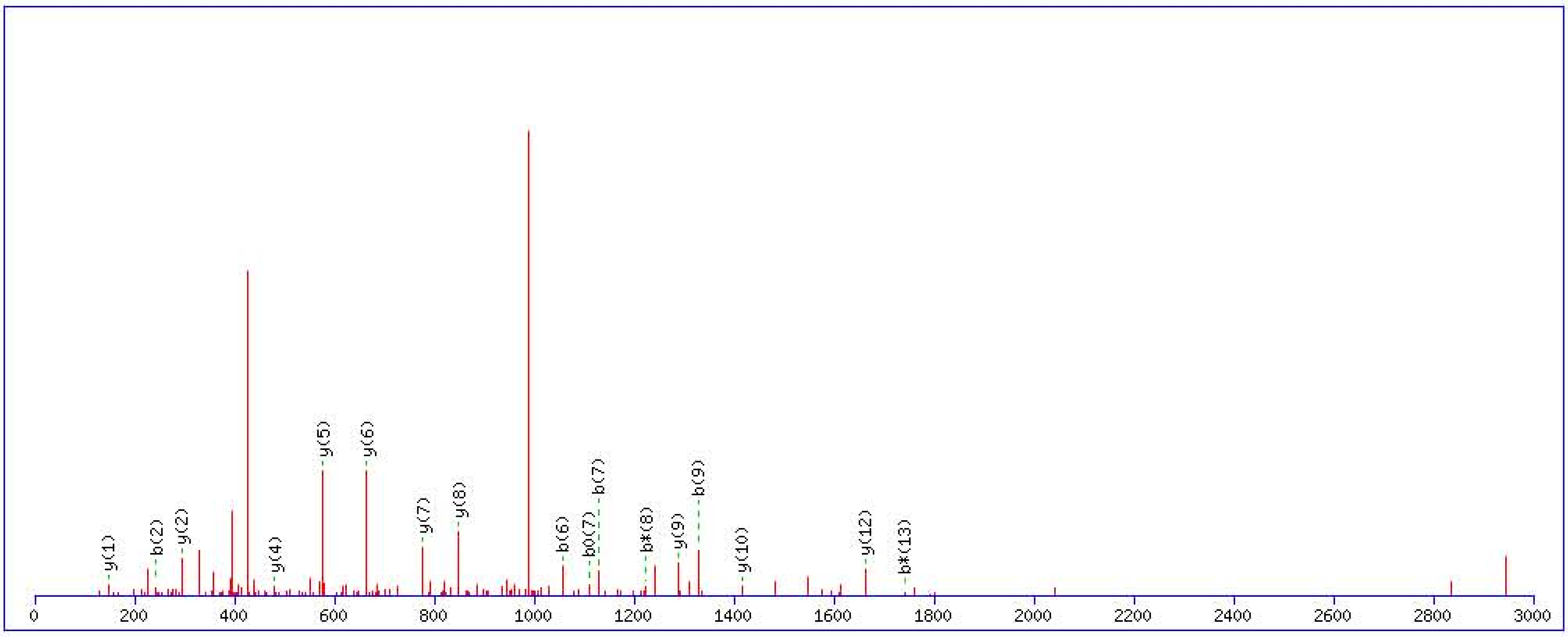
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEDMEQALSPSVFK**
Found in **IC1_HUMAN**, Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2

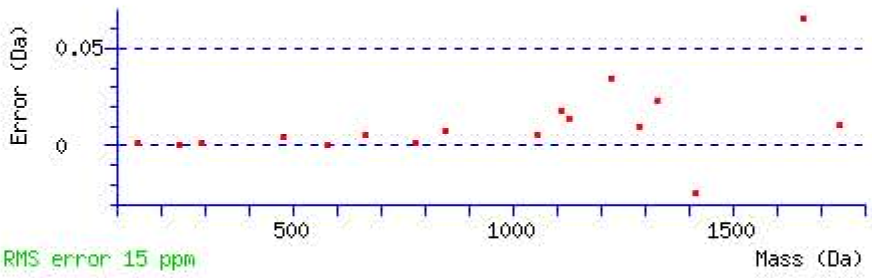
Match to Query 40248: 1903.952468 from(952.983510,2+) rtinseconds(2439) index(35396)
Title: Locus:1.1.1.3398.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

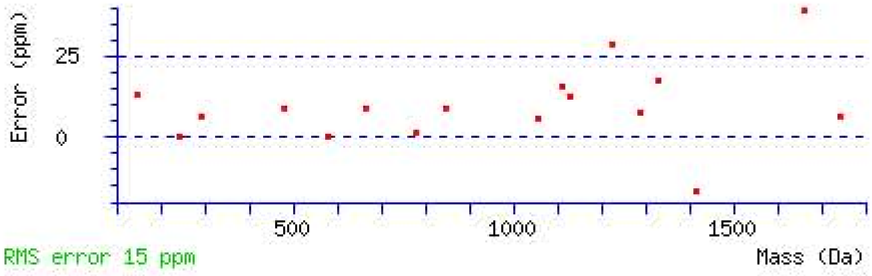
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1903.942337
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0051
Matches : 17/138 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							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
37.3	1903.942337	0.010131	LEDMEQALSPSVFK

Mascot: http://www.matrixscience.com/

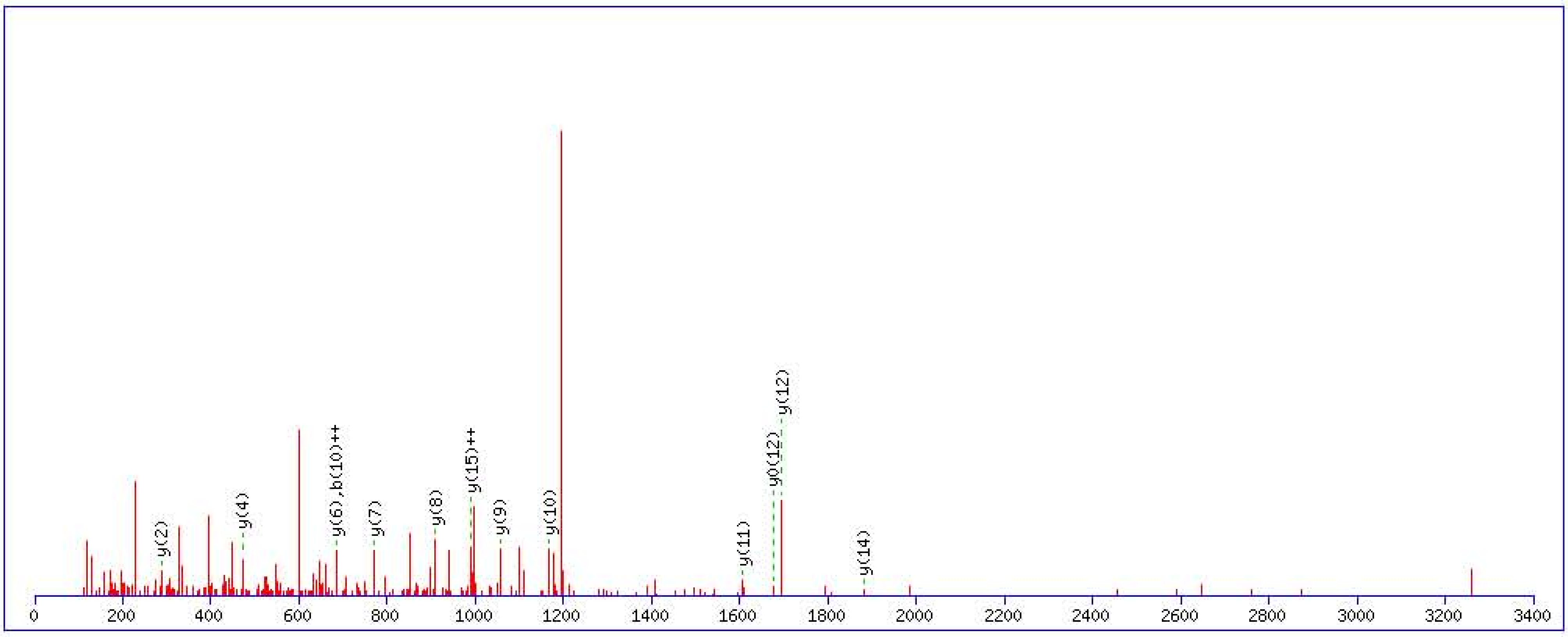
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVTSVSQIFHSPDLAIR**
Found in **IC1_HUMAN**, Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2

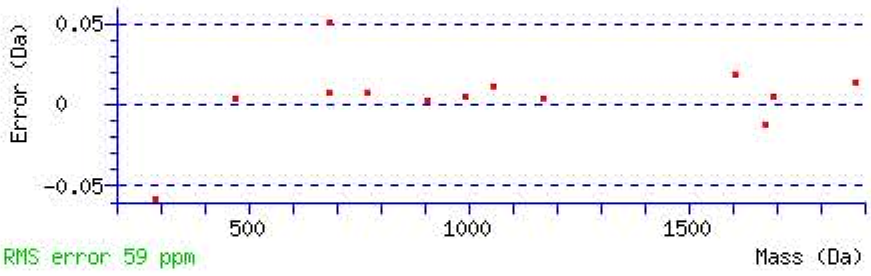
Match to Query 45002: 2137.146252 from(713.389360,3+) rtinseconds(2366) index(35074)
Title: Locus:1.1.1.3373.6 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

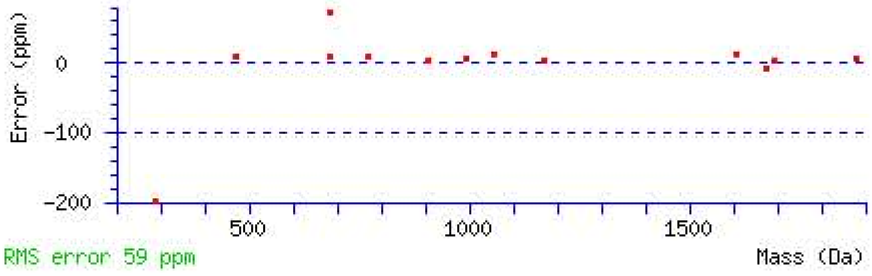
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2137.135406
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 35 **Expect:** 0.0061
Matches : 13/168 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							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
35.2	2137.135406	0.010846	GVTSVSQIFHSPDLAIR

Mascot: http://www.matrixscience.com/

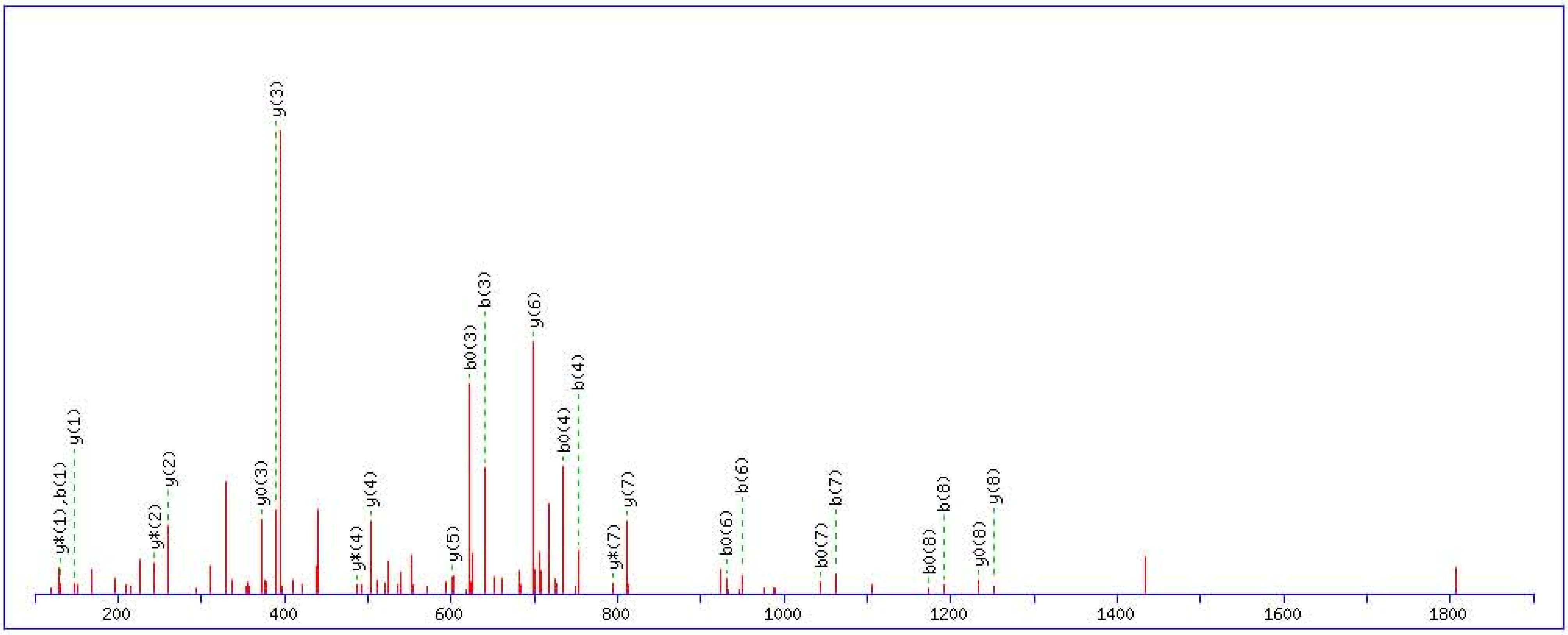
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAQLPVIENK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

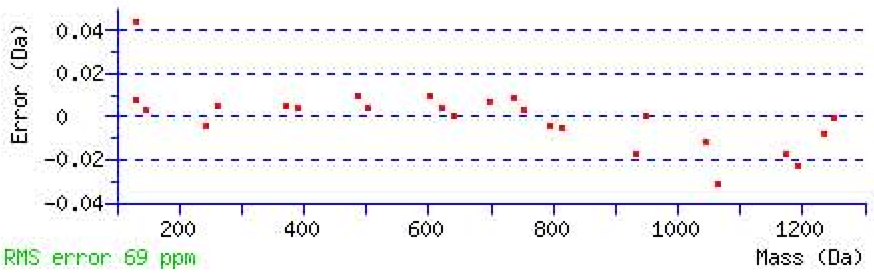
Match to Query 28627: 1450.785728 from(726.400140,2+) rtinseconds(1983) index(4868)
Title: Locus:1.1.1.3242.14 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

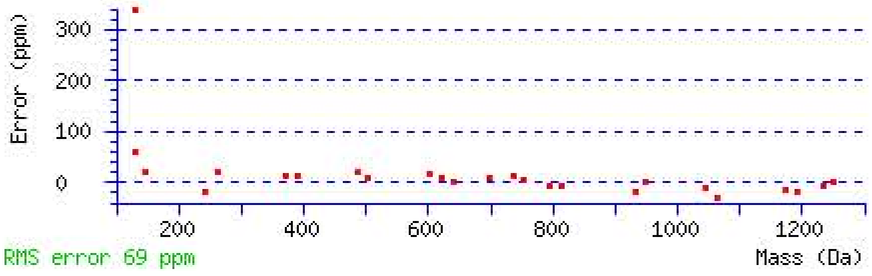
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1450.785355
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.00014
Matches : 25/100 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							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
42.8	1450.785355	0.000373	EAQLPVIENK
1.7	1450.764236	0.021492	EIFHPEIQK
1.0	1450.790527	-0.004799	QNIWRHNRLSK

Mascot: http://www.matrixscience.com/

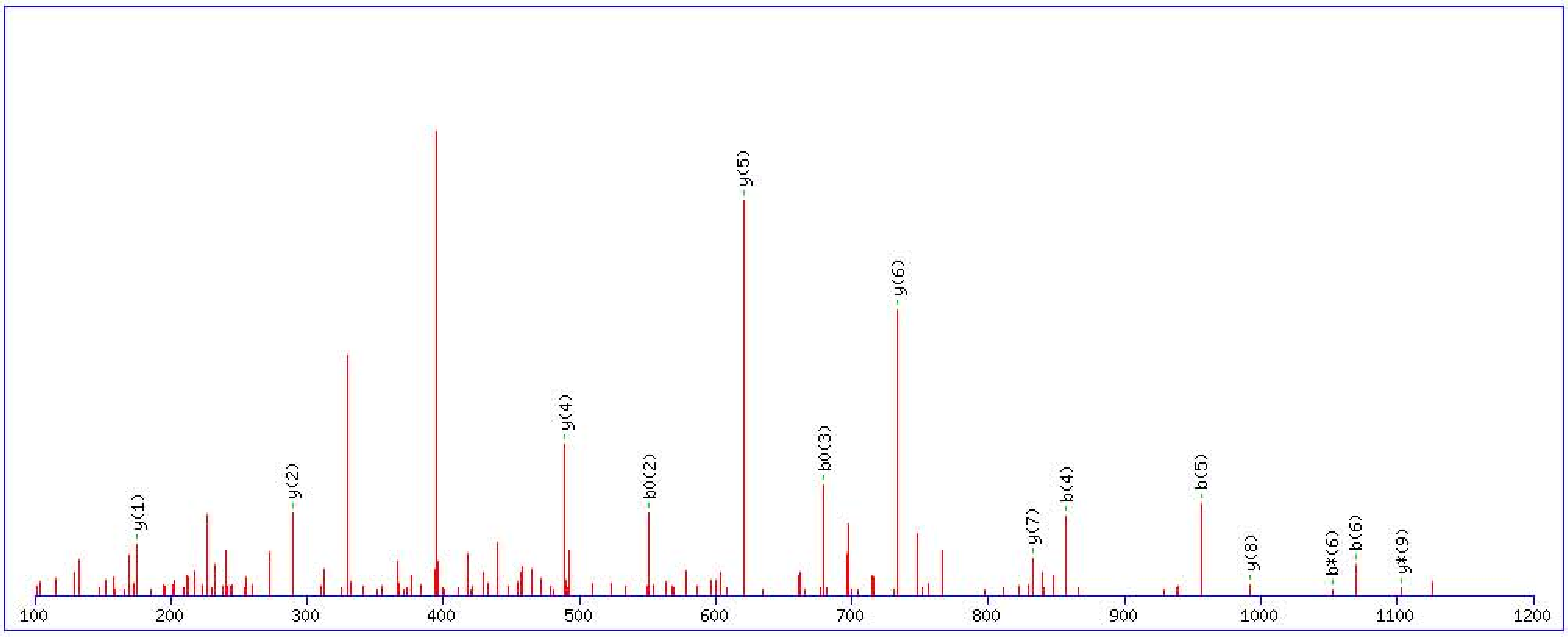
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQQCVIMAENR**
Found in **PLGB_HUMAN**, Plasminogen-like protein B OS=Homo sapiens GN=PLGLB1 PE=1 SV=1

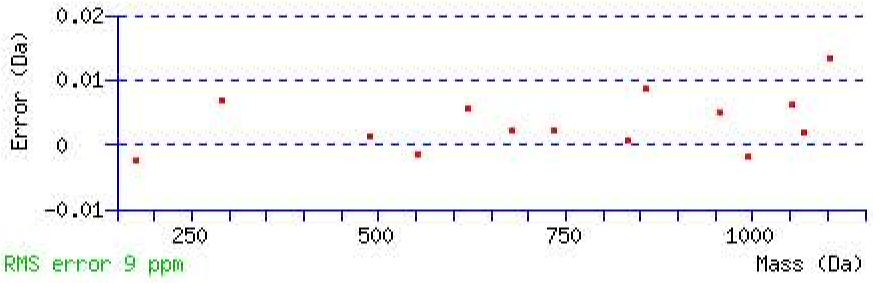
Match to Query 36215: 1687.785312 from(563.602380,3+) rtinseconds(1832) index(61552)
Title: Locus:1.1.1.3264.5 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

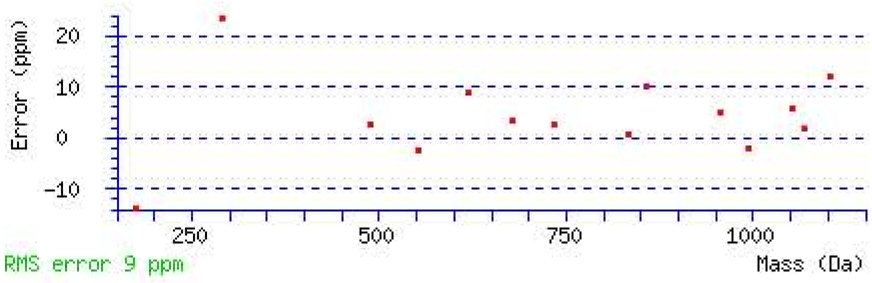


```
Monoisotopic mass of neutral peptide Mr(calc): 1687.784393
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.00023
Matches : 14/114 fragment ions using 22 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	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



RMS error 9 ppm



RMS error 9 ppm

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
43.1	1687.784393	0.000919	EQQCVIMAENR
38.6	1687.784393	0.000919	EQQCVIMAENR
4.0	1687.773666	0.011646	TTGPPSGQMPDNPPHR
1.7	1687.776093	0.009219	QQEEAQAAAAAASAESR
1.4	1687.787552	-0.002240	GASEDGEYFLMIRGK
0.1	1687.765778	0.019534	NVMNKVSEMSSFQR

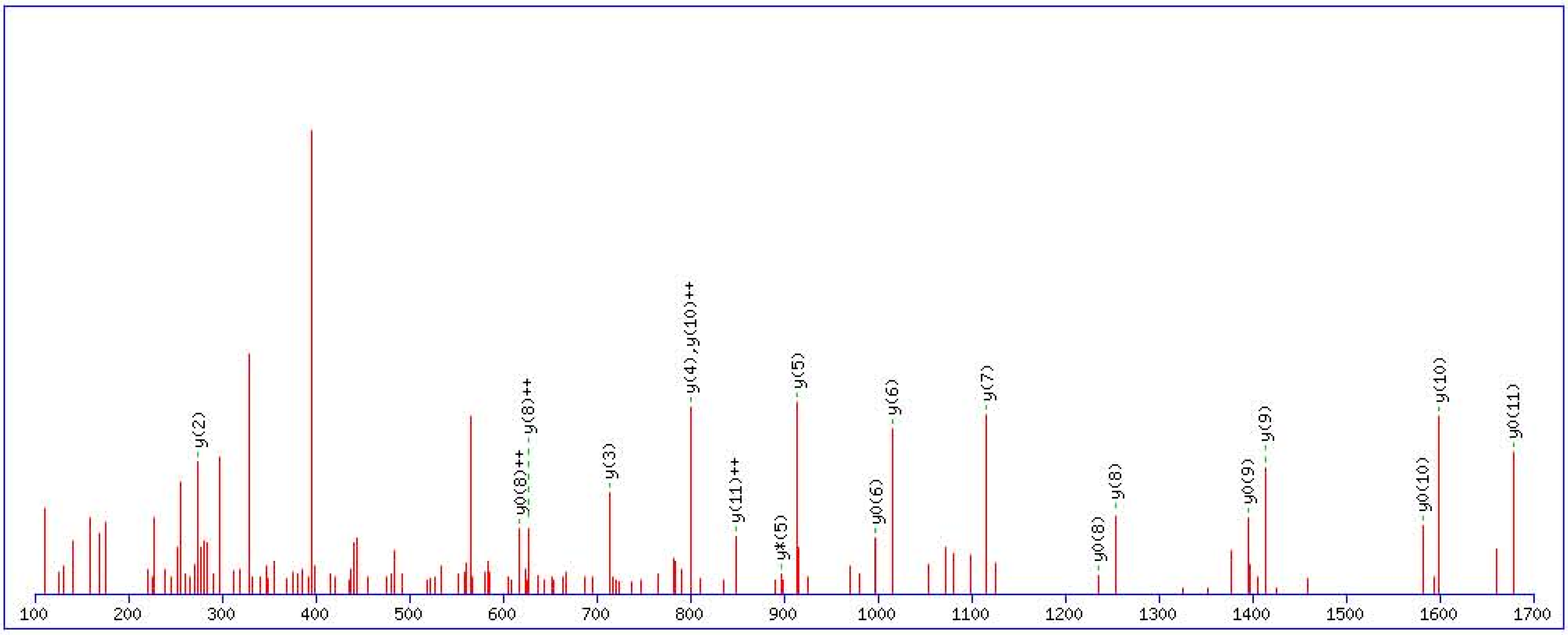
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **APWCHTTNSQVR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

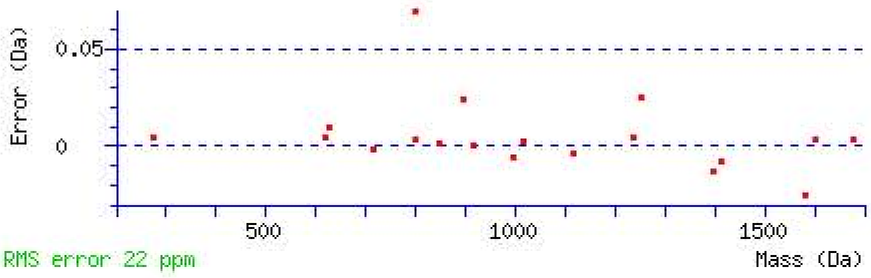
Match to Query 37832: 1766.831292 from(589.951040,3+) rtinseconds(1540) index(60064)
Title: Locus:1.1.1.3162.12 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

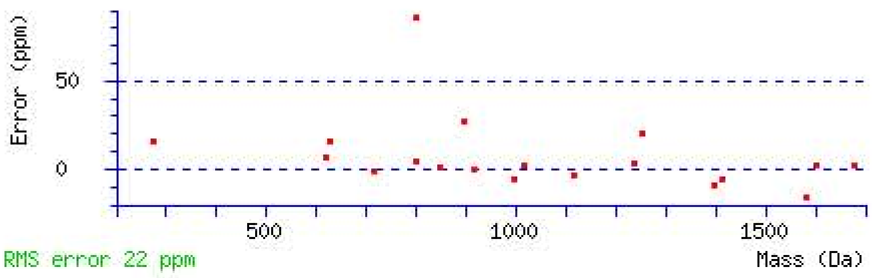
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1766.834488
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 54 **Expect:** 5.9e-005
Matches : 19/102 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							12
2	169.097154	85.052215					P	1696.804643	848.905960	1679.778094	840.392685	1678.794078	839.900677	11
3	355.176467	178.091872					W	***1599.751879***	800.379578	1582.725330	791.866303	1581.741314	791.374295	10
4	515.207116	258.107196					C	***1413.672566***	707.339921	1396.646017	698.826647	1395.662001	698.334639	9
5	652.266028	326.636652					H	***1253.641917***	627.324597	1236.615368	618.811322	1235.631352	618.319314	8
6	753.313707	377.160492			735.303142	368.155209	T	***1116.583005***	558.795141	1099.556456	550.281866	1098.572440	549.789858	7
7	854.361386	427.684331			836.350821	418.679049	T	***1015.535326***	508.271301	998.508777	499.758027	997.524761	499.266019	6
8	968.404313	484.705795	951.377764	476.192520	950.393748	475.700512	N	***914.487647***	457.747462	897.461098	449.234187	896.477082	448.742179	5
9	1055.436341	528.221809	1038.409792	519.708534	1037.425776	519.216526	S	***800.444720***	400.725998	783.418171	392.212724	782.434155	391.720716	4
10	1494.661667	747.834472	1477.635118	739.321197	1476.651102	738.829189	Q	***713.412692***	357.209984	696.386143	348.696710			3
11	1593.730081	797.368679	1576.703532	788.855404	1575.719516	788.363396	V	***274.187366***	137.597321	257.160817	129.084047			2
12							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of APWCHTTNSQVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.3	1766.834488	-0.003196	APWCHTTNSQVR

Mascot: http://www.matrixscience.com/

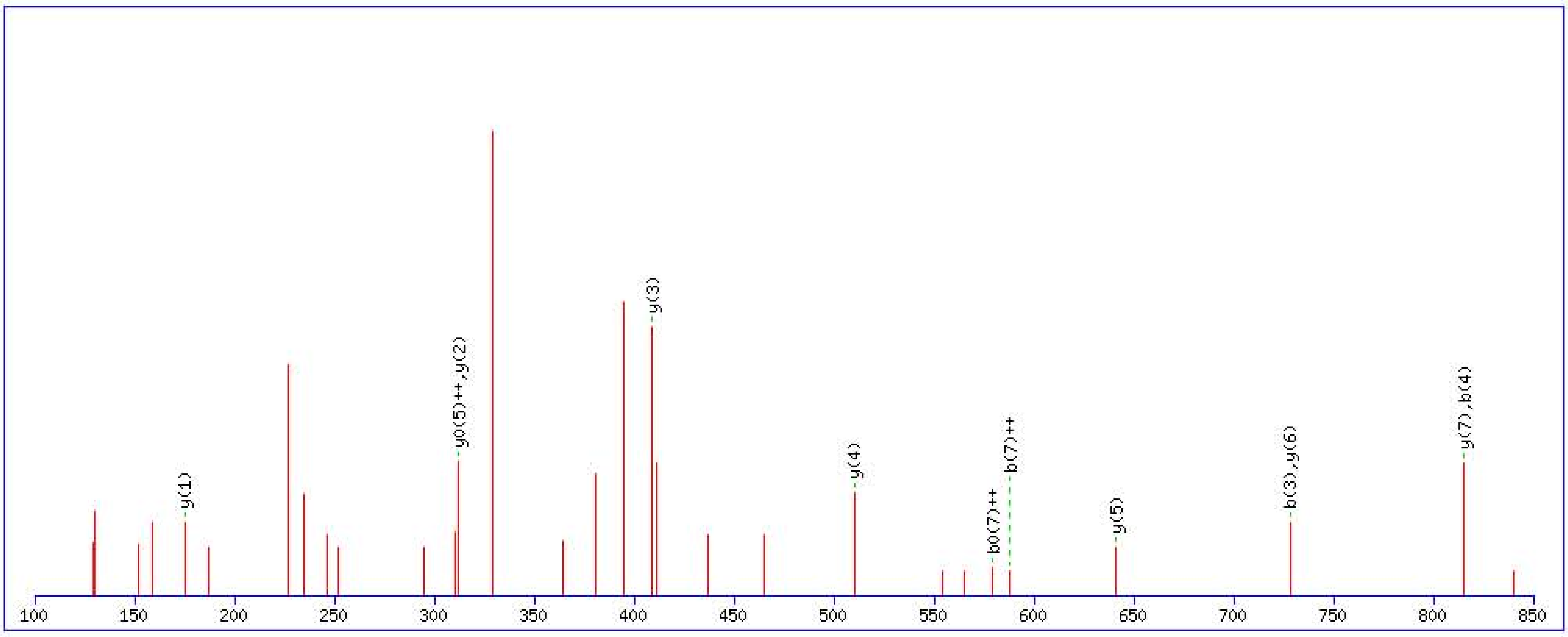
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KCQSWSSMTPHR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

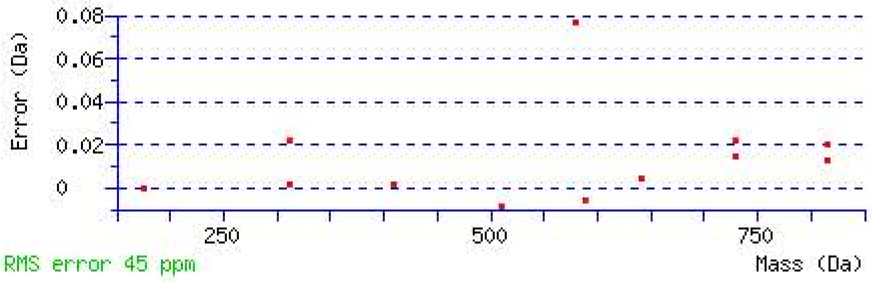
Match to Query 38829: 1814.836616 from(454.716430,4+) rtinseconds(1594) index(60356)
Title: Locus:1.1.1.3181.8 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

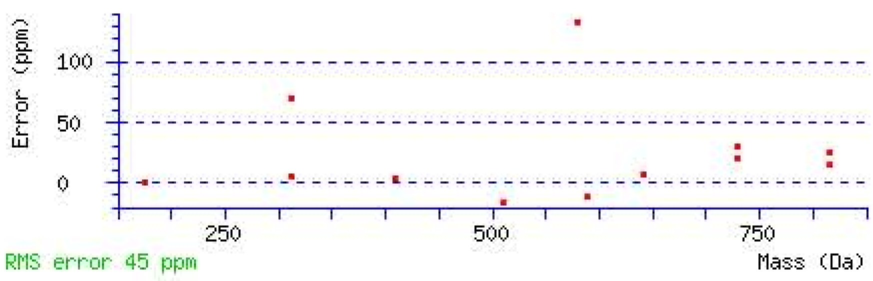
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1814.837845
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 33 **Expect:** 0.0064
Matches : 12/120 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	129.102239	65.054757	112.075690	56.541483			K							12
2	289.132888	145.070082	272.106339	136.556808			C	1687.750164	844.378720	1670.723615	835.865446	1669.739599	835.373438	11
3	**728.358214**	364.682745	711.331665	356.169471			Q	1527.719515	764.363396	1510.692966	755.850121	1509.708950	755.358113	10
4	**815.390242**	408.198759	798.363693	399.685485	797.379677	399.193477	S	1088.494189	544.750733	1071.467640	536.237458	1070.483624	535.745450	9
5	1001.469555	501.238416	984.443006	492.725141	983.458990	492.233133	W	1001.462161	501.234719	984.435612	492.721444	983.451596	492.229436	8
6	1088.501583	544.754430	1071.475034	536.241155	1070.491018	535.749147	S	***815.382848***	408.195062	798.356299	399.681788	797.372283	399.189780	7
7	1175.533611	588.270444	1158.507062	579.757169	1157.523046	579.265161	S	***728.350820***	364.679048	711.324271	356.165774	710.340255	355.673766	6
8	1306.574096	653.790686	1289.547547	645.277412	1288.563531	644.785404	M	***641.318792***	321.163034	624.292243	312.649760	623.308227	312.157752	5
9	1407.621775	704.314526	1390.595226	695.801251	1389.611210	695.309243	T	***510.278307***	255.642791	493.251758	247.129517	492.267742	246.637509	4
10	1504.674539	752.840908	1487.647990	744.327633	1486.663974	743.835625	P	***409.230628***	205.118952	392.204079	196.605677			3
11	1641.733451	821.370364	1624.706902	812.857089	1623.722886	812.365081	H	***312.177864***	156.592570	295.151315	148.079295			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of KCQSWSSMTPHR
(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	1814.837845	-0.001229	KCQSWSSMTPHR
9.5	1814.811371	0.025245	EVVAMDCEMVGLGPHR
3.5	1814.811371	0.025245	EVVAMDCEMVGLGPHR

Mascot: http://www.matrixscience.com/

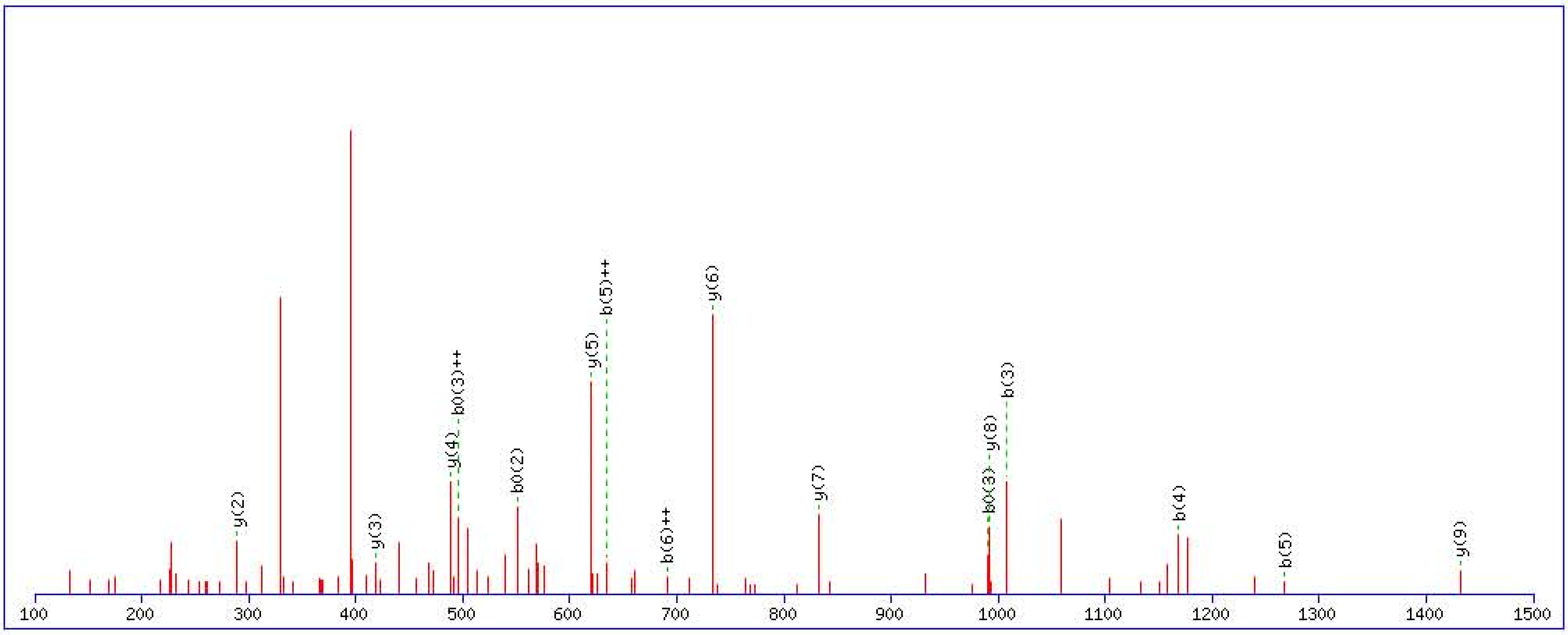
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQQCVIMAENR**
Found in **PLGB_HUMAN**, Plasminogen-like protein B OS=Homo sapiens GN=PLGLB1 PE=1 SV=1

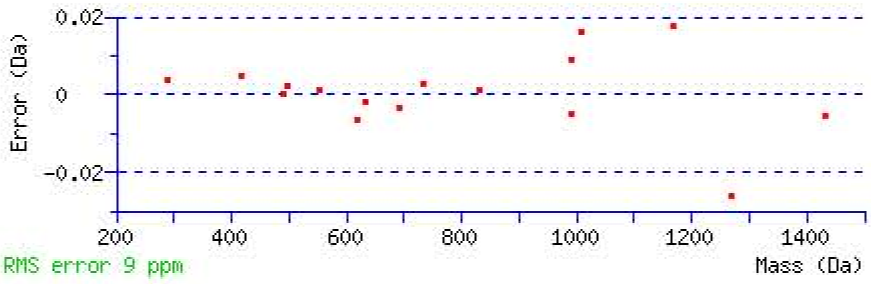
Match to Query 42014: 1998.953292 from(667.325040,3+) rtinseconds(2145) index(63386)
Title: Locus:1.1.1.3373.11 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

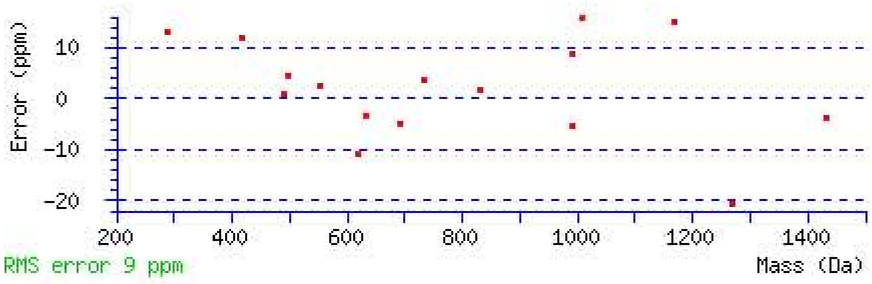
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 36  Expect: 0.0048
Matches : 16/114 fragment ions using 34 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	569.275195	285.141236	552.248646	276.627961	551.264630	276.135953	Q	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
36.1	1998.951141	0.002151	EQQCVIMAENR

Mascot: http://www.matrixscience.com/

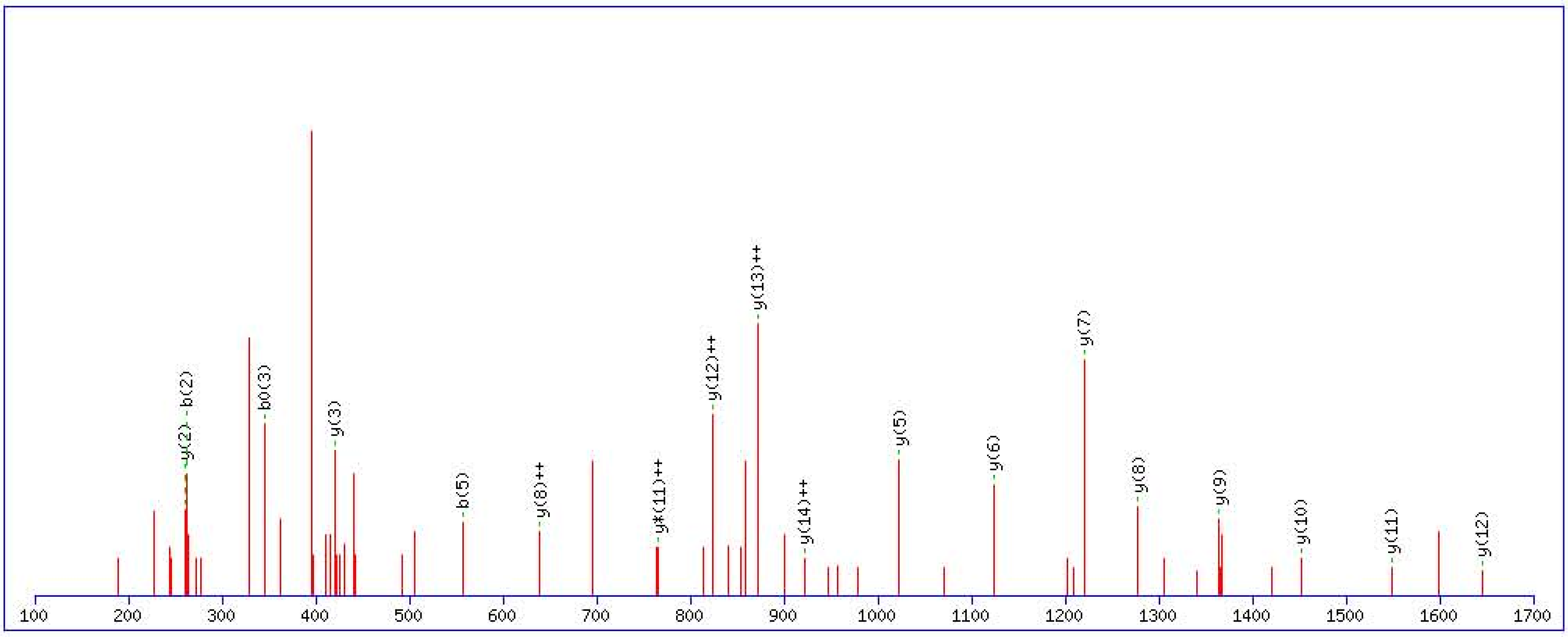
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **CTTPPPSSGPTYQCLK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

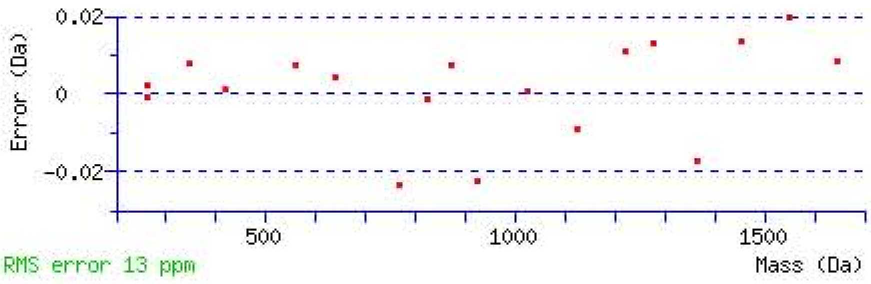
Match to Query 44550: 2103.981552 from(702.334460,3+) rtinseconds(1787) index(61351)
Title: Locus:1.1.1.3248.18 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

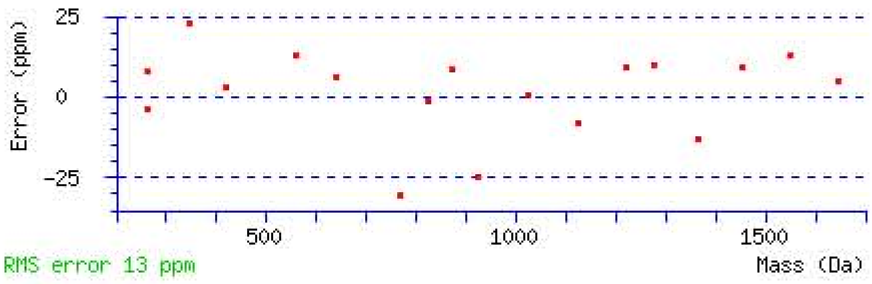
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2103.979172
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 68  Expect: 1.5e-006
Matches : 18/144 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	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
68.0	2103.979172	0.002380	CTTPPPSSGPTYQCLK
6.0	2103.964554	0.016998	TAADTPAIMNWDLFFTMK

Mascot: http://www.matrixscience.com/

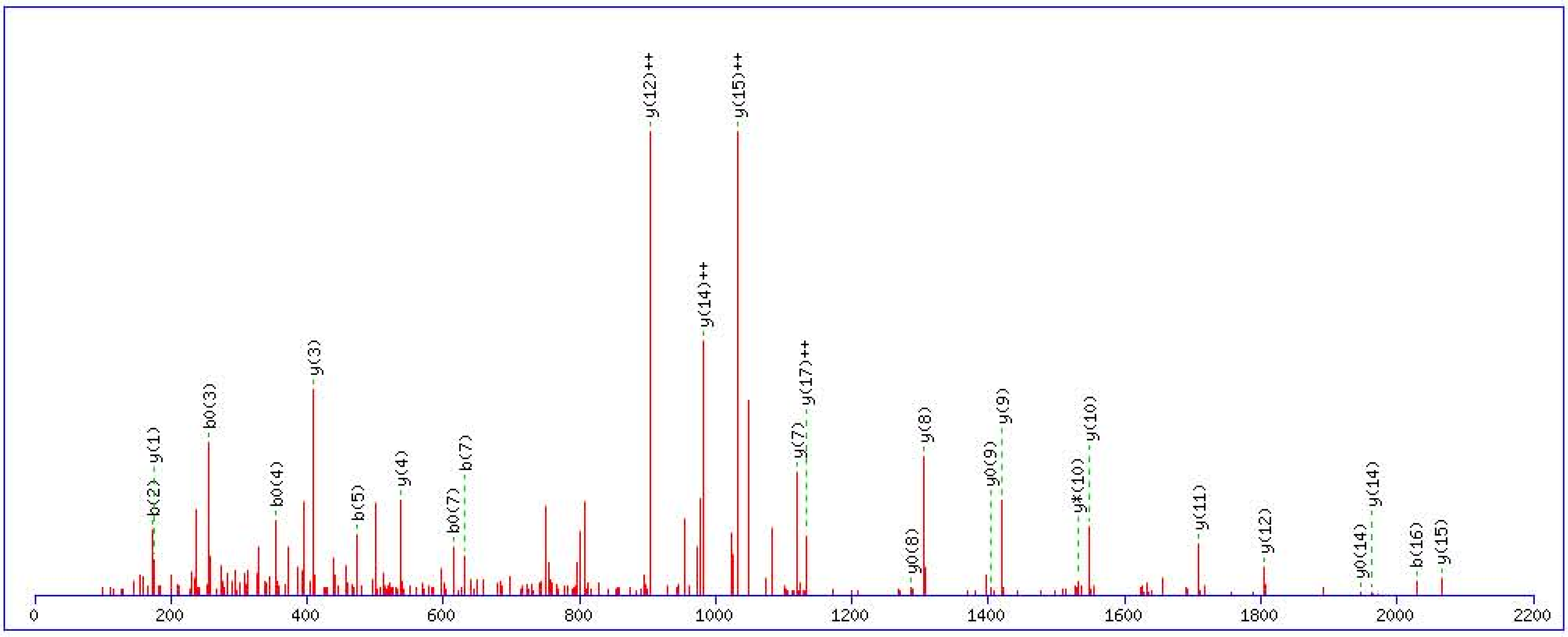
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ATTVTGTPCQDWAAQEPHR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

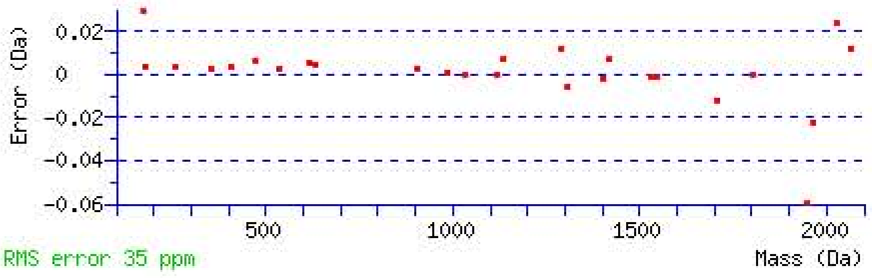
Match to Query 49702: 2436.134892 from(813.052240,3+) rtinseconds(1885) index(61746)
Title: Locus:1.1.1.3282.9 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

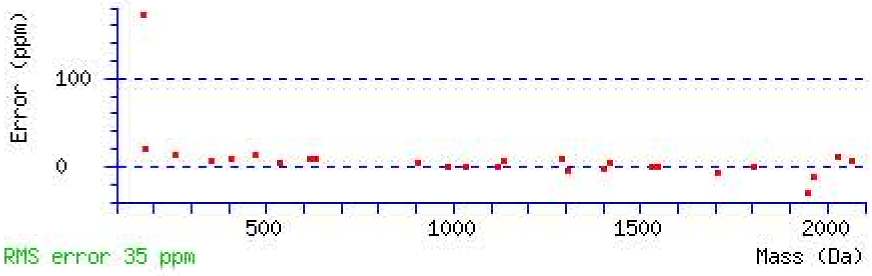


Monoisotopic mass of neutral peptide Mr(calc): 2436.131470
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15 : Biotin:Thermo-21345 (Q)
Ions Score: 70 **Expect:** 6e-007
Matches : 26/190 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							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



RMS error 35 ppm



RMS error 35 ppm

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
70.1	2436.131470	0.003422	ATTVTGTPCQDWAAQEPHR
35.9	2436.131470	0.003422	ATTVTGTPCQDWAAQEPHR
3.7	2436.162506	-0.027614	CLVVCDSSPSADGAVTSSLGISVR

Mascot: http://www.matrixscience.com/

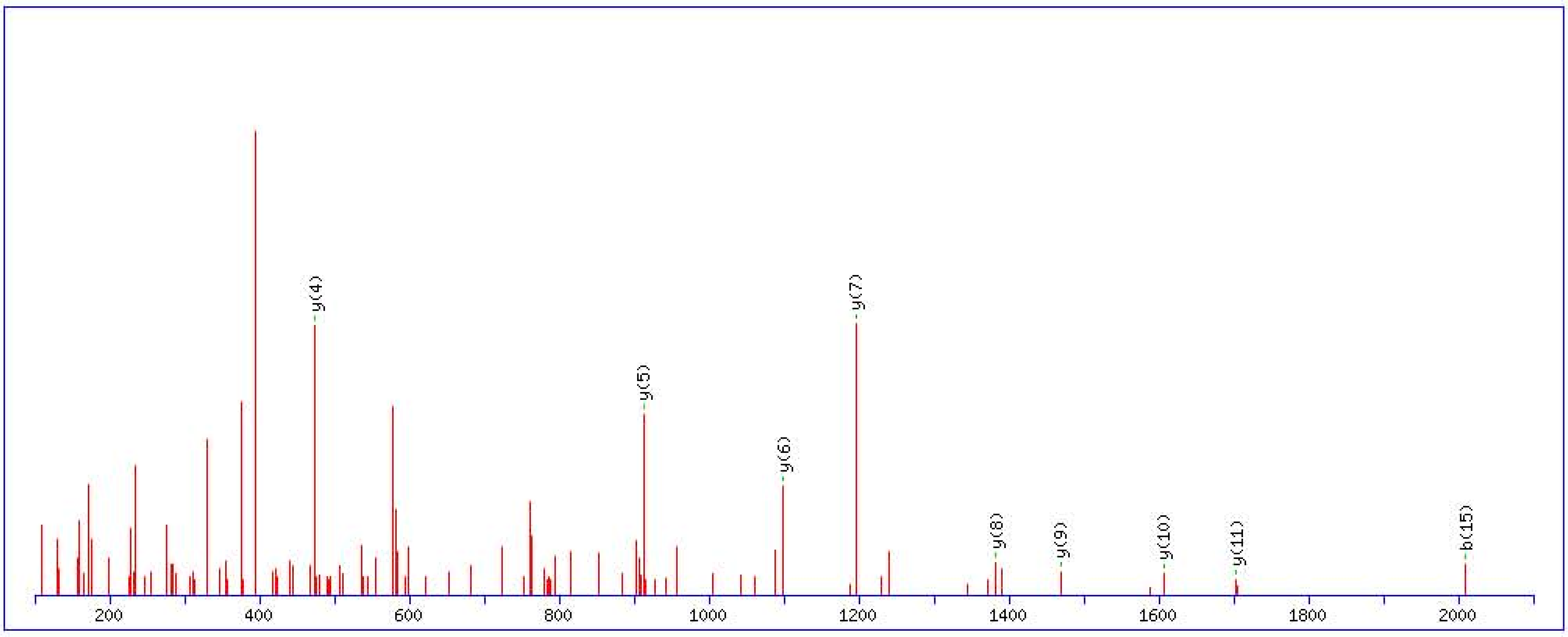
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVGGCVAHPHSWPWQVSLR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

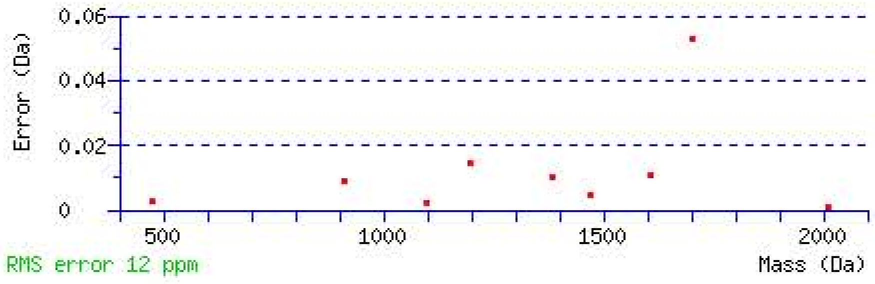
Match to Query 50628: 2482.255016 from(621.571030,4+) rtinseconds(2231) index(63859)
Title: Locus:1.1.1.3403.10 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

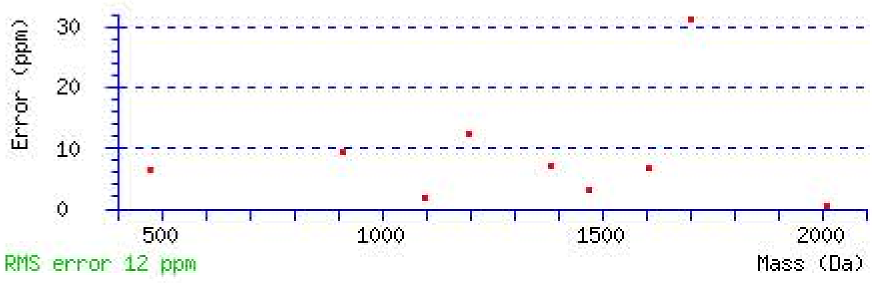
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2482.251480
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15 : Biotin:Thermo-21345 (Q)
Ions Score: 38 **Expect:** 0.0045
Matches : 9/164 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	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
38.3	2482.251480	0.003536	VVGGCVAHPHSWPWQVSLR

Mascot: http://www.matrixscience.com/

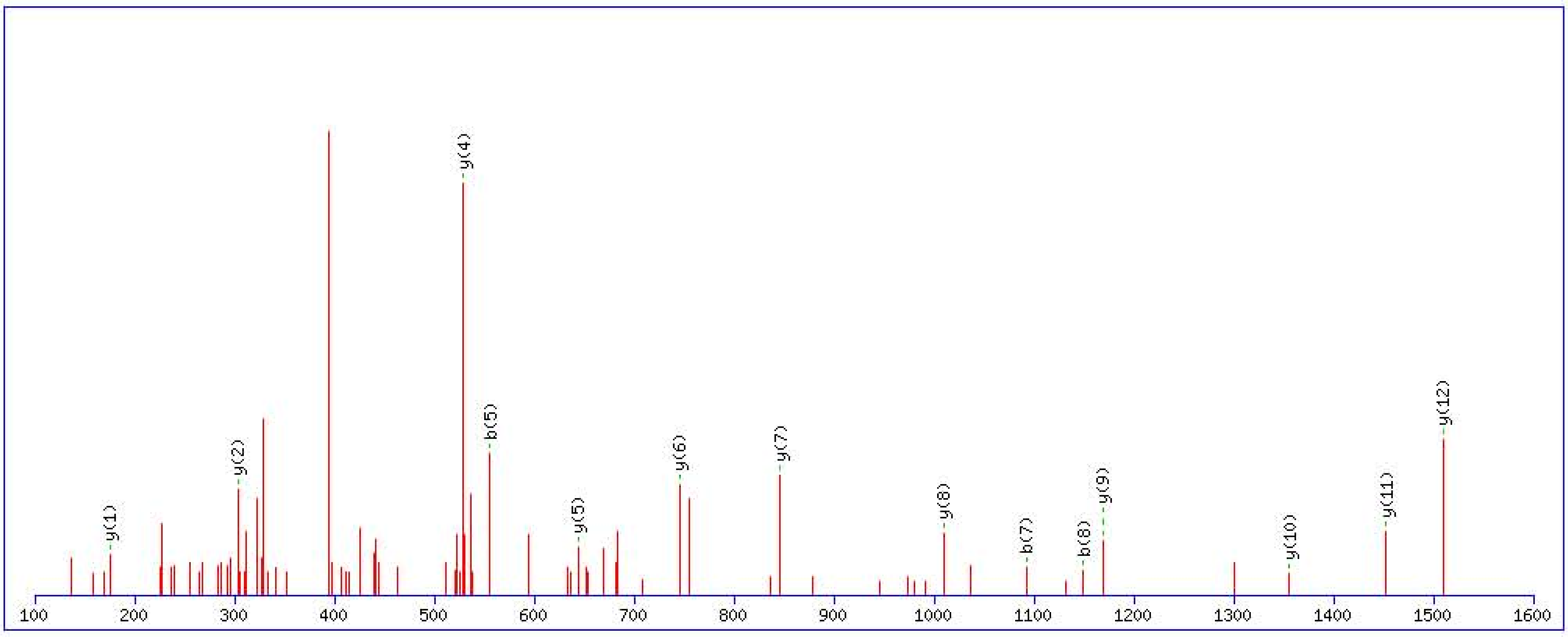
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPDNDPQGPWCYTTDPEKR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

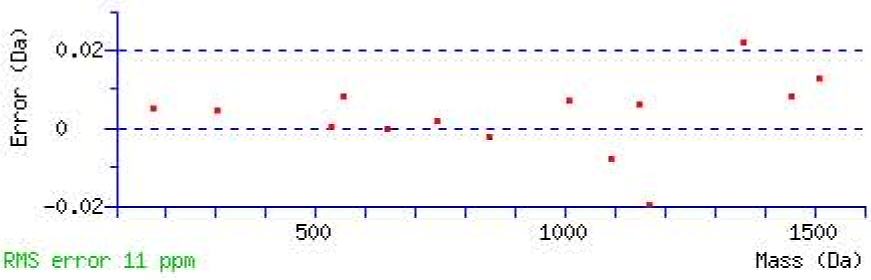
Match to Query 52101: 2600.143696 from(651.043200,4+) rtinseconds(1973) index(62344)
Title: Locus:1.1.1.3313.18 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

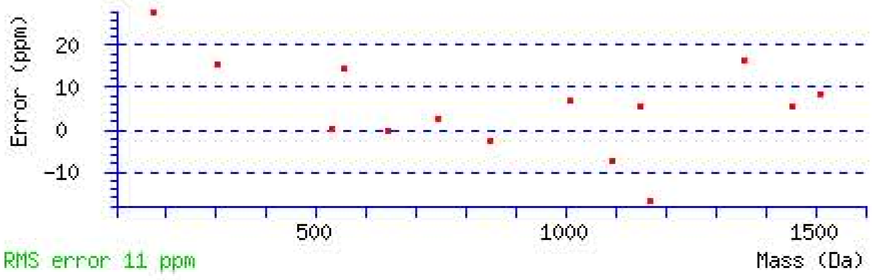
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2600.142410
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 65 **Expect:** 1.8e-006
Matches : 14/208 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							19
2	212.102967	106.555121	195.076418	98.041847			P	2487.106759	1244.057017	2470.080210	1235.543743	2469.096194	1235.051735	18
3	327.129910	164.068593	310.103361	155.555319	309.119345	155.063311	D	2390.053995	1195.530635	2373.027446	1187.017361	2372.043430	1186.525353	17
4	441.172837	221.090057	424.146288	212.576782	423.162272	212.084774	N	2275.027052	1138.017164	2258.000503	1129.503889	2257.016487	1129.011881	16
5	**556.199780**	278.603528	539.173231	270.090254	538.189215	269.598246	D	2160.984125	1080.995700	2143.957576	1072.482426	2142.973560	1071.990418	15
6	653.252544	327.129910	636.225995	318.616636	635.241979	318.124628	P	2045.957182	1023.482229	2028.930633	1014.968955	2027.946617	1014.476946	14
7	**1092.477870**	546.742573	1075.451321	538.229299	1074.467305	537.737290	Q	1948.904418	974.955847	1931.877869	966.442572	1930.893853	965.950564	13
8	**1149.499334**	575.253305	1132.472785	566.740030	1131.488769	566.248022	G	***1509.679092***	755.343184	1492.652543	746.829910	1491.668527	746.337902	12
9	1246.552098	623.779687	1229.525549	615.266413	1228.541533	614.774404	P	***1452.657628***	726.832452	1435.631079	718.319178	1434.647063	717.827170	11
10	1432.631411	716.819343	1415.604862	708.306069	1414.620846	707.814061	W	***1355.604864***	678.306070	1338.578315	669.792796	1337.594299	669.300788	10
11	1592.662060	796.834668	1575.635511	788.321394	1574.651495	787.829385	C	***1169.525551***	585.266414	1152.499002	576.753139	1151.514986	576.261131	9
12	1755.725389	878.366333	1738.698840	869.853058	1737.714824	869.361050	Y	***1009.494902***	505.251089	992.468353	496.737815	991.484337	496.245807	8
13	1856.773068	928.890172	1839.746519	920.376898	1838.762503	919.884889	T	***846.431573***	423.719425	829.405024	415.206150	828.421008	414.714142	7
14	1957.820747	979.414012	1940.794198	970.900737	1939.810182	970.408729	T	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	6
15	2072.847690	1036.927483	2055.821141	1028.414208	2054.837125	1027.922200	D	***644.336215***	322.671746	627.309666	314.158471	626.325650	313.666463	5
16	2169.900454	1085.453865	2152.873905	1076.940590	2151.889889	1076.448582	P	***529.309272***	265.158274	512.282723	256.645000	511.298707	256.152992	4
17	2298.943047	1149.975161	2281.916498	1141.461887	2280.932482	1140.969879	E	432.256508	216.631892	415.229959	208.118618	414.245943	207.626610	3
18	2427.038010	1214.022643	2410.011461	1205.509368	2409.027445	1205.017360	K	***303.213915***	152.110595	286.187366	143.597321			2
19							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of NPDNDPQGPWCYTTDPEKR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.3	2600.142410	0.001286	NPDNDPQGPWCYTTDPEKR

Mascot: http://www.matrixscience.com/

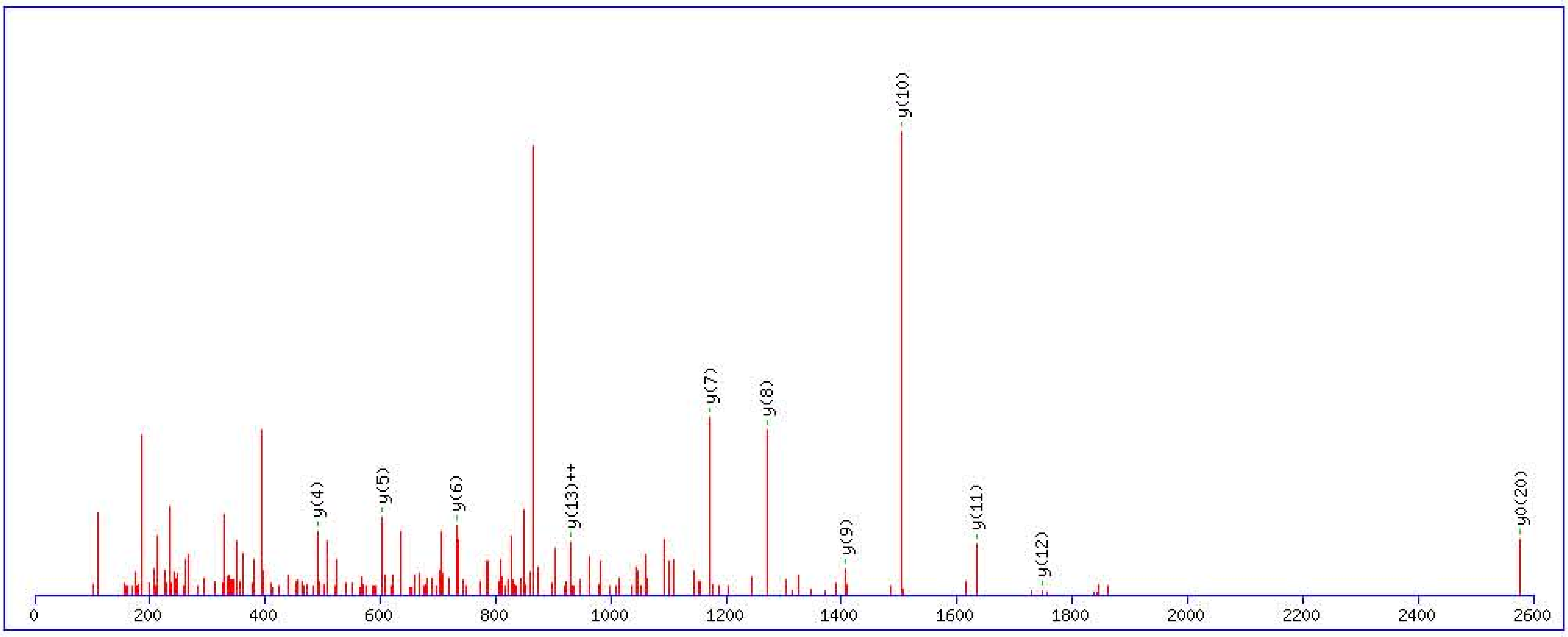
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VILGAHQEVNLEPHVQEIEVSR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

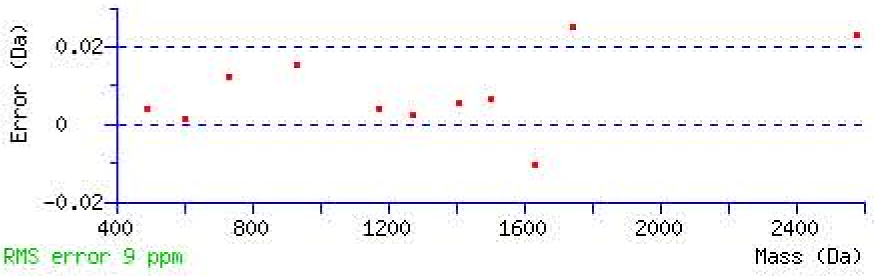
Match to Query 53854: 2806.483136 from(702.628060,4+) rtinseconds(2088) index(63016)
Title: Locus:1.1.1.3353.11 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

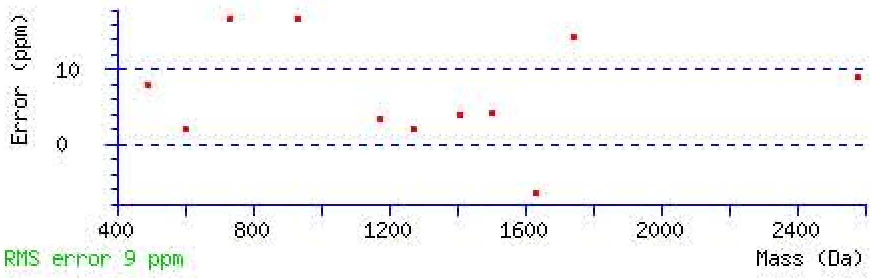
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2806.479965
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16    : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 0.00042
Matches : 11/224 fragment ions using 19 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							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
47.1	2806.479965	0.003171	VILGAHQEVNLEPHVQEIEVSR

Mascot: http://www.matrixscience.com/

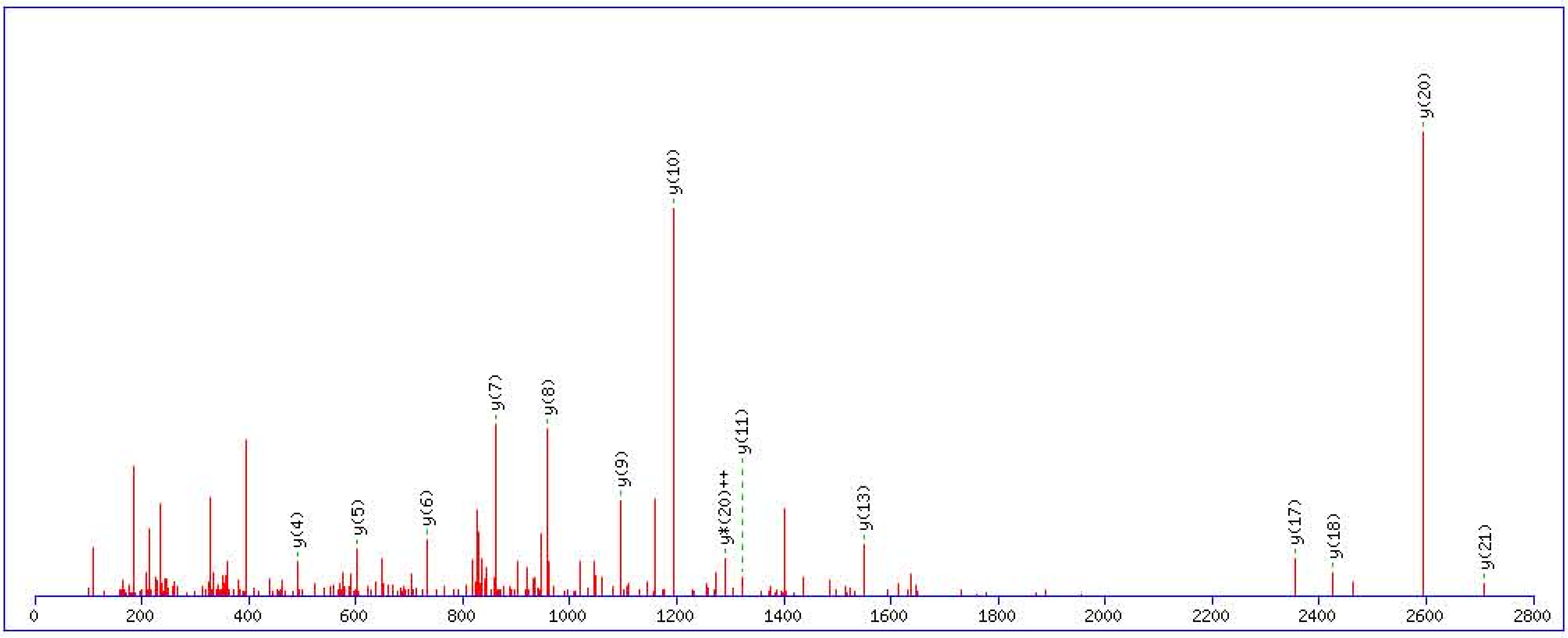
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VILGAHQEVNLEPHVQEIEVSR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

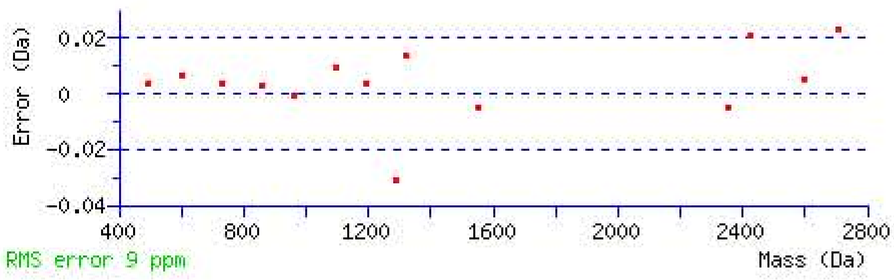
Match to Query 53856: 2806.485576 from(702.628670,4+) rtinseconds(2117) index(63230)
Title: Locus:1.1.1.3363.22 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

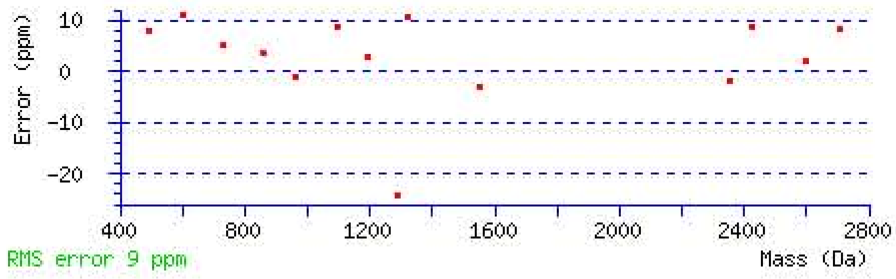
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2806.479965
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 91 **Expect:** 4.8e-009
Matches : 14/224 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							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
90.8	2806.479965	0.005611	VILGAHQEVNLEPHVQEIEVSR
24.0	2806.479965	0.005611	VILGAHQEVNLEPHVQEIEVSR
2.0	2806.516327	-0.030751	VLLGVIQELEKGEAHREGLSYR

Mascot: http://www.matrixscience.com/

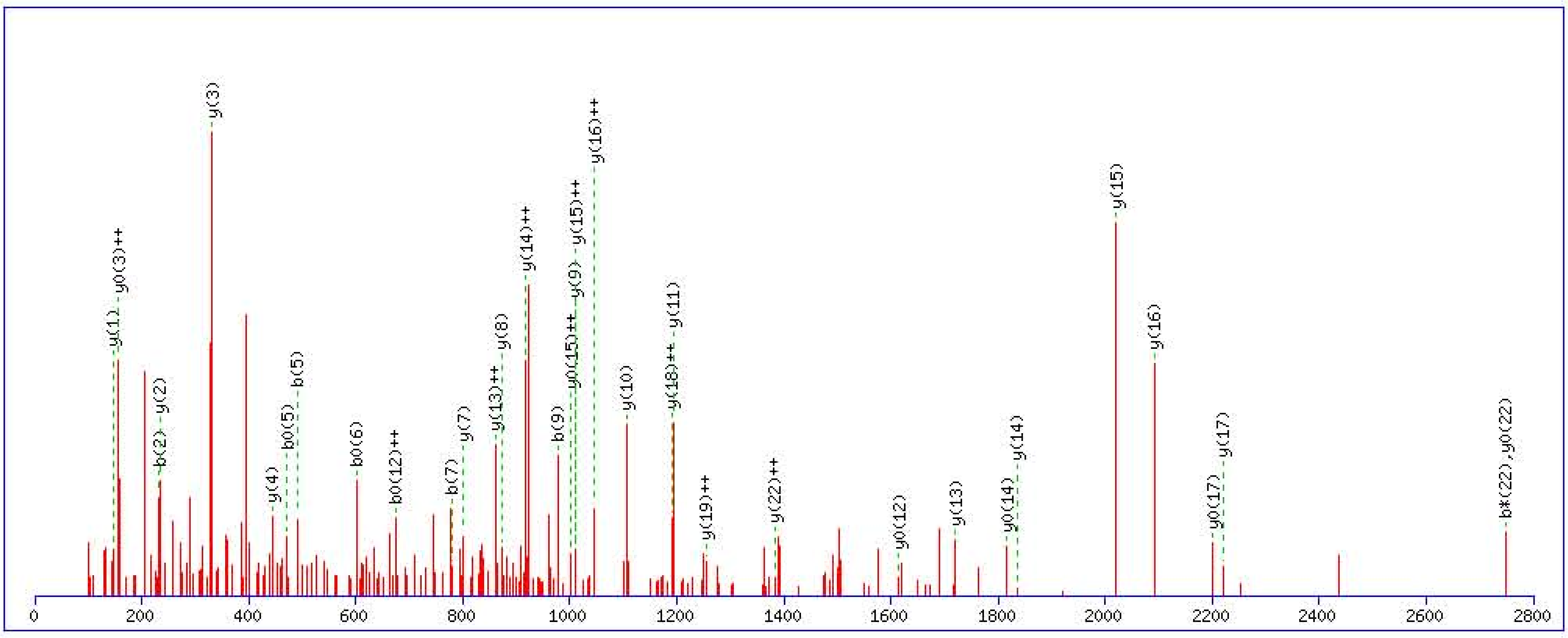
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TMSGLECQAWDSQSPHAHGYIPSK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

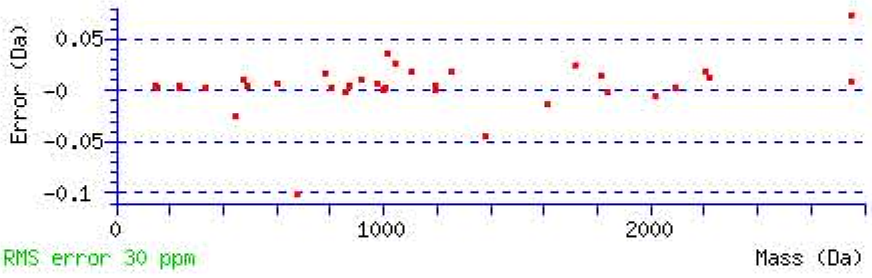
Match to Query 56043: 2997.361296 from(750.347600,4+) rtinseconds(1985) index(4883)
Title: Locus:1.1.1.3243.13 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

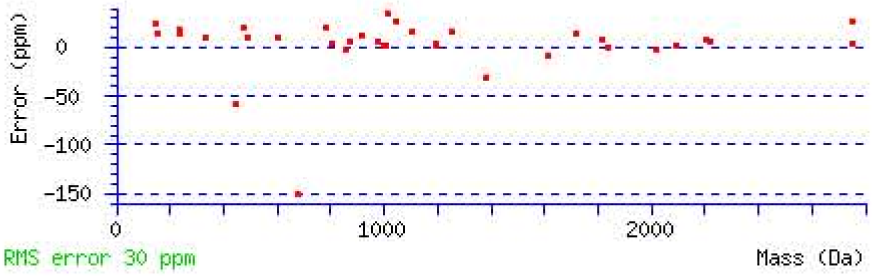


```
Monoisotopic mass of neutral peptide Mr(calc): 2997.357162
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00017
Matches : 35/260 fragment ions using 94 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	102.054955	51.531116			84.044390	42.525833	T							24
2	**233.095440**	117.051358			215.084875	108.046076	M	2897.316768	1449.162022	2880.290219	1440.648748	2879.306203	1440.156740	23
3	320.127468	160.567372			302.116903	151.562089	S	2766.276283	1383.641780	2749.249734	1375.128505	2748.265718	1374.636497	22
4	377.148932	189.078104			359.138367	180.072821	G	2679.244255	1340.125766	2662.217706	1331.612491	2661.233690	1331.120483	21
5	**490.232996**	245.620136			472.222431	236.614853	L	2622.222791	1311.615034	2605.196242	1303.101759	2604.212226	1302.609751	20
6	619.275589	310.141433			601.265024	301.136150	E	2509.138727	1255.073002	2492.112178	1246.559727	2491.128162	1246.067719	19
7	**779.306238**	390.156757			761.295673	381.151475	C	2380.096134	1190.551705	2363.069585	1182.038431	2362.085569	1181.546423	18
8	907.364816	454.186046	890.338267	445.672772	889.354251	445.180764	Q	***2220.065485***	1110.536381	2203.038936	1102.023106	2202.054920	1101.531098	17
9	**978.401930**	489.704603	961.375381	481.191329	960.391365	480.699321	A	***2092.006907***	1046.507092	2074.980358	1037.993817	2073.996342	1037.501809	16
10	1164.481243	582.744260	1147.454694	574.230985	1146.470678	573.738977	W	***2020.969793***	1010.988535	2003.943244	1002.475260	2002.959228	1001.983252	15
11	1279.508186	640.257731	1262.481637	631.744457	1261.497621	631.252449	D	***1834.890480***	917.948878	1817.863931	909.435604	1816.879915	908.943596	14
12	1366.540214	683.773745	1349.513665	675.260471	1348.529649	674.768463	S	***1719.863537***	860.435407	1702.836988	851.922132	1701.852972	851.430124	13
13	1805.765540	903.386408	1788.738991	894.873134	1787.754975	894.381126	Q	1632.831509	816.919393	1615.804960	808.406118	1614.820944	807.914110	12
14	1892.797568	946.902422	1875.771019	938.389148	1874.787003	937.897140	S	***1193.606183***	597.306730	1176.579634	588.793455	1175.595618	588.301447	11
15	1989.850332	995.428804	1972.823783	986.915530	1971.839767	986.423522	P	***1106.574155***	553.790716	1089.547606	545.277441	1088.563590	544.785433	10
16	2126.909244	1063.958260	2109.882695	1055.444986	2108.898679	1054.952978	H	***1009.521391***	505.264334	992.494842	496.751059	991.510826	496.259051	9
17	2197.946358	1099.476817	2180.919809	1090.963543	2179.935793	1090.471535	A	***872.462479***	436.734878	855.435930	428.221603	854.451914	427.729595	8
18	2335.005270	1168.006273	2317.978721	1159.492999	2316.994705	1159.000991	H	***801.425365***	401.216321	784.398816	392.703046	783.414800	392.211038	7
19	2392.026734	1196.517005	2375.000185	1188.003731	2374.016169	1187.511723	G	664.366453	332.686865	647.339904	324.173590	646.355888	323.681582	6
20	2555.090063	1278.048670	2538.063514	1269.535395	2537.079498	1269.043387	Y	607.344989	304.176133	590.318440	295.662858	589.334424	295.170850	5
21	2668.174127	1334.590702	2651.147578	1326.077427	2650.163562	1325.585419	I	***444.281660***	222.644468	427.255111	214.131194	426.271095	213.639186	4
22	2765.226891	1383.117084	2748.200342	1374.603809	2747.216326	1374.111801	P	***331.197596***	166.102436	314.171047	157.589162	313.187031	157.097154	3
23	2852.258919	1426.633098	2835.232370	1418.119823	2834.248354	1417.627815	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
24							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 30 ppm



RMS error 30 ppm

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
48.0	2997.357162	0.004134	TMSGLECQAWDSQSPHAHGYIPSK
15.2	2997.357162	0.004134	TMSGLECQAWDSQSPHAHGYIPSK

Mascot: http://www.matrixscience.com/

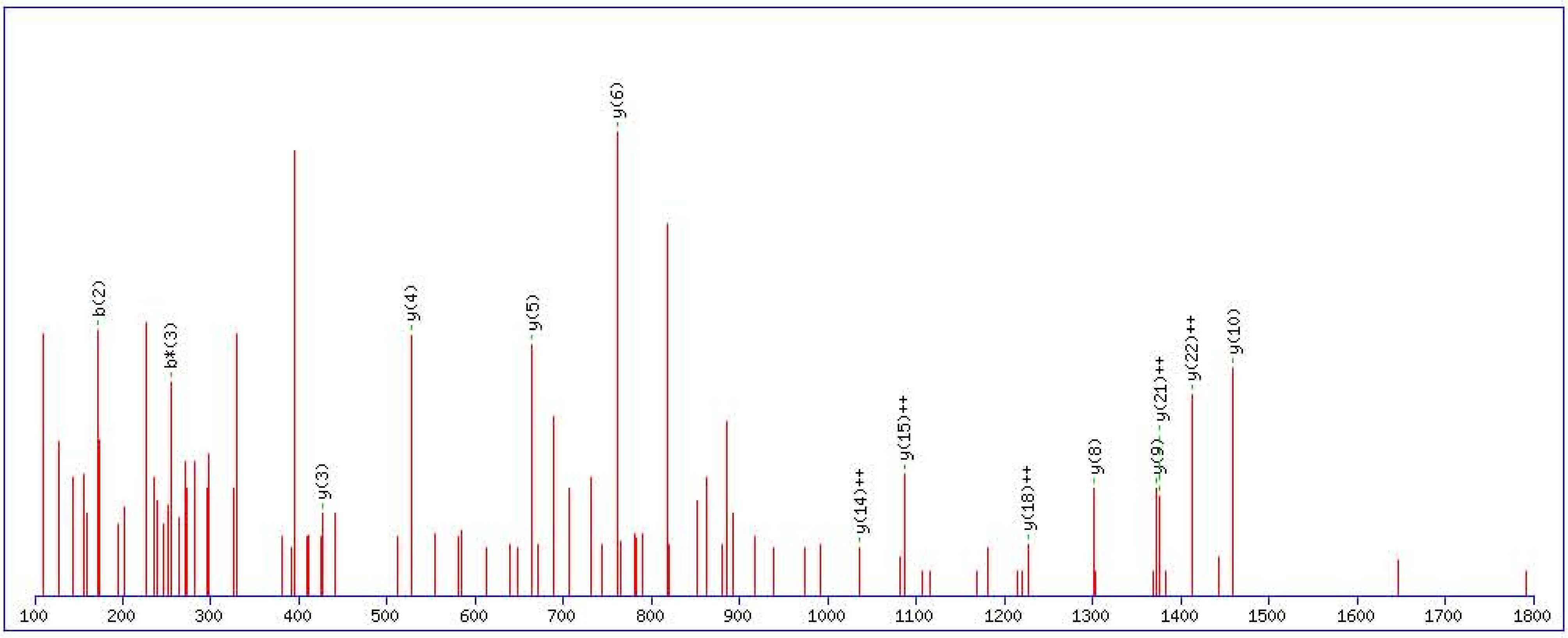
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNVAVTVSGHTCQHWSAQTPHTHNR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

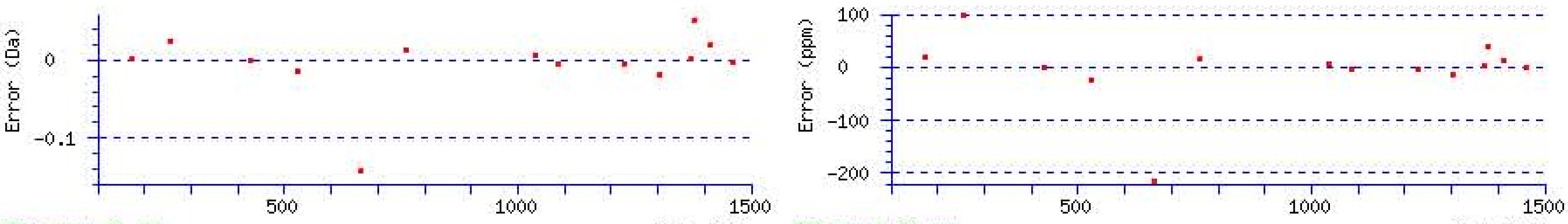
Match to Query 56688: 3092.451220 from(619.497520,5+) rtinseconds(1441) index(59414)
Title: Locus:1.1.1.3127.21 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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): 3092.457016
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18    : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.021
Matches : 14/270 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							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
29.1	3092.457016	-0.005796	GNVAVTVSGHTCQHWSAQTPHTHNR
12.4	3092.457016	-0.005796	GNVAVTVSGHTCQHWSAQTPHTHNR

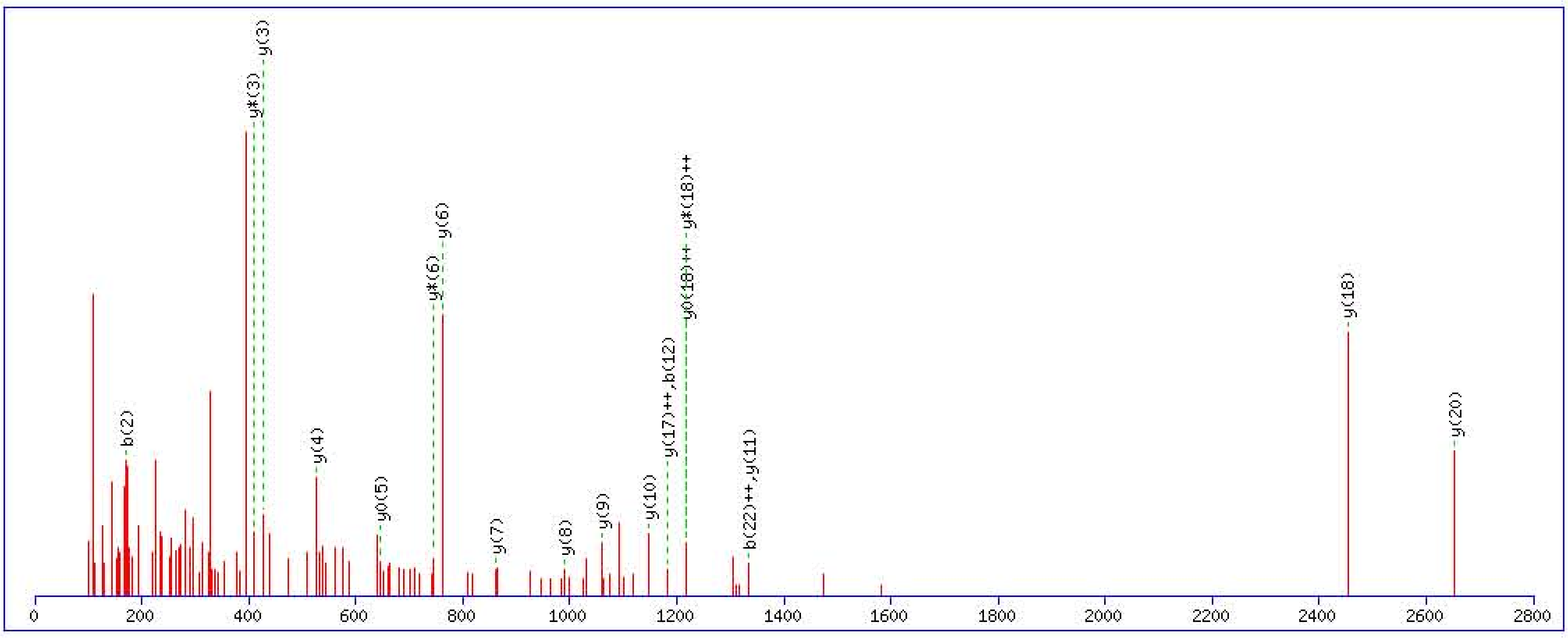
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNVAVTVSGHTCQHWSAQTPHTHNR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

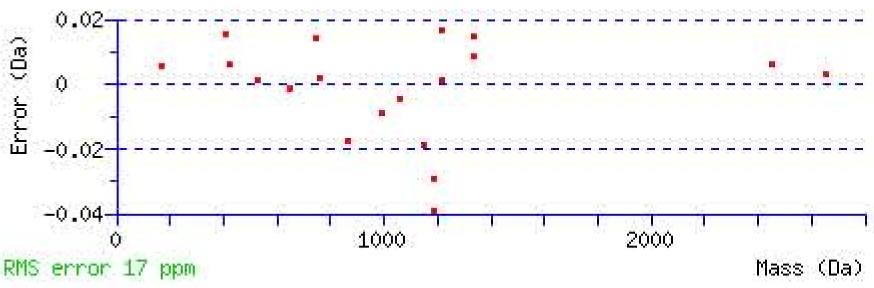
Match to Query 56693: 3092.453244 from(516.416150,6+) rtinseconds(1486) index(59755)
Title: Locus:1.1.1.3143.14 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

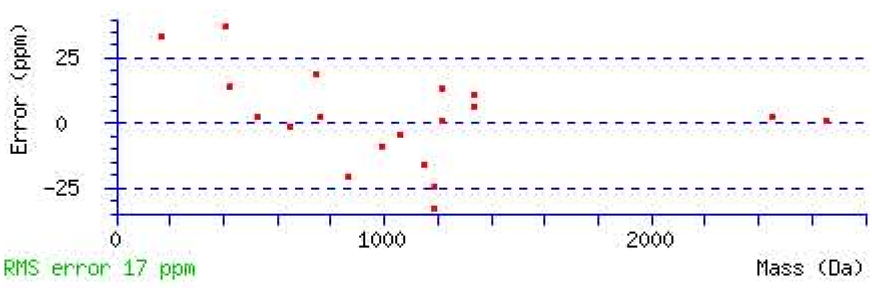
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3092.457016
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13 : Biotin:Thermo-21345 (Q)
Ions Score: 51 **Expect:** 0.00013
Matches : 19/270 fragment ions using 30 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	1622.777760	811.892518	1605.751211	803.379244	1604.767195	802.887236	Q	1910.919096	955.963186	1893.892547	947.449911	1892.908531	946.957903	13
14	1759.836672	880.421974	1742.810123	871.908700	1741.826107	871.416692	H	1471.693770	736.350523	1454.667221	727.837248	1453.683205	727.345240	12
15	1945.915985	973.461631	1928.889436	964.948356	1927.905420	964.456348	W	***1334.634858***	667.821067	1317.608309	659.307792	1316.624293	658.815784	11
16	2032.948013	1016.977645	2015.921464	1008.464370	2014.937448	1007.972362	S	***1148.555545***	574.781410	1131.528996	566.268136	1130.544980	565.776128	10
17	2103.985127	1052.496201	2086.958578	1043.982927	2085.974562	1043.490919	A	***1061.523517***	531.265396	1044.496968	522.752122	1043.512952	522.260114	9
18	2232.043705	1116.525490	2215.017156	1108.012216	2214.033140	1107.520208	Q	***990.486403***	495.746839	973.459854	487.233565	972.475838	486.741557	8
19	2333.091384	1167.049330	2316.064835	1158.536055	2315.080819	1158.044047	T	***862.427825***	431.717550	845.401276	423.204276	844.417260	422.712268	7
20	2430.144148	1215.575712	2413.117599	1207.062437	2412.133583	1206.570429	P	***761.380146***	381.193711	744.353597	372.680436	743.369581	372.188428	6
21	2567.203060	1284.105168	2550.176511	1275.591893	2549.192495	1275.099885	H	664.327382	332.667329	647.300833	324.154054	646.316817	323.662046	5
22	2668.250739	1334.629007	2651.224190	1326.115733	2650.240174	1325.623725	T	***527.268470***	264.137873	510.241921	255.624598	509.257905	255.132590	4
23	2805.309651	1403.158463	2788.283102	1394.645189	2787.299086	1394.153181	H	***426.220791***	213.614033	409.194242	205.100759			3
24	2919.352578	1460.179927	2902.326029	1451.666652	2901.342013	1451.174644	N	289.161879	145.084577	272.135330	136.571303			2
25							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GNVAVTVSGHTCQHWSAQTPHTHNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.3	3092.457016	-0.003772	GNVAVTVSGHTCQHWSAQTPHTHNR
16.0	3092.457016	-0.003772	GNVAVTVSGHTCQHWSAQTPHTHNR

Mascot: http://www.matrixscience.com/

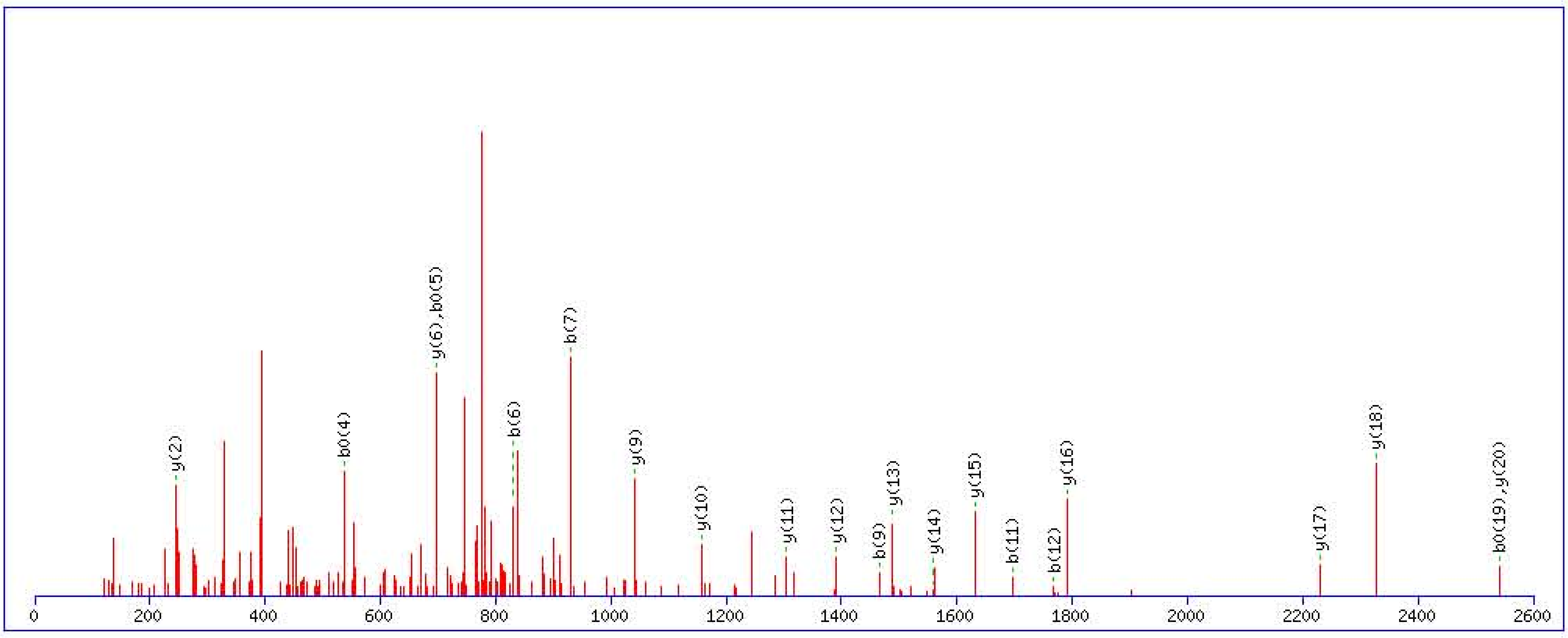
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LYDYCDVPQCAAPSFDCGKPQVEPK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

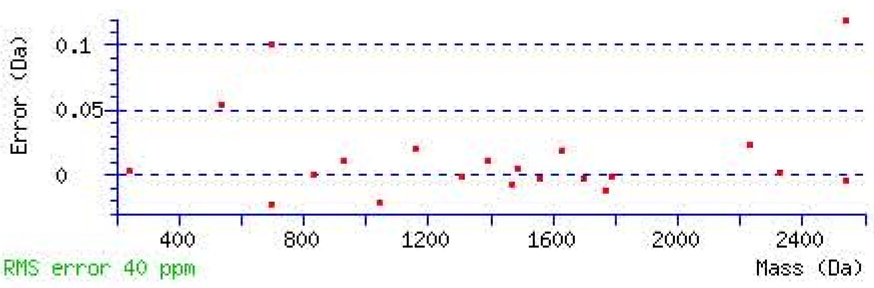
Match to Query 59426: 3254.463376 from(814.623120,4+) rtinseconds(2111) index(63177)
Title: Locus:1.1.1.3361.19 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

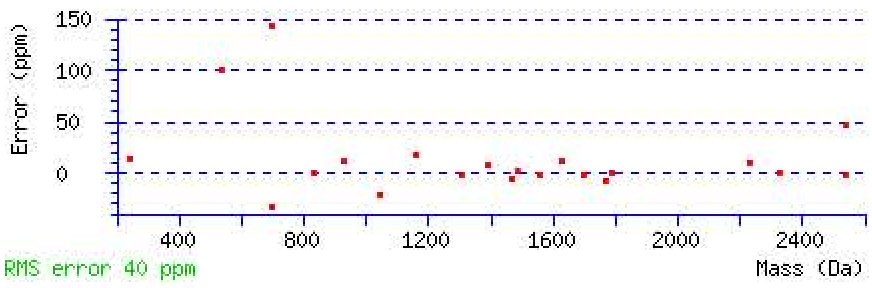
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3254.454514
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 67 **Expect:** 1.9e-006
Matches : 21/264 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							25
2	277.154669	139.080973					Y	3142.377716	1571.692496	3125.351167	1563.179221	3124.367151	1562.687213	24
3	392.181612	196.594444			374.171047	187.589162	D	2979.314387	1490.160831	2962.287838	1481.647557	2961.303822	1481.155549	23
4	555.244941	278.126109			537.234376	269.120826	Y	2864.287444	1432.647360	2847.260895	1424.134085	2846.276879	1423.642077	22
5	715.275590	358.141433			697.265025	349.136151	C	2701.224115	1351.115695	2684.197566	1342.602421	2683.213550	1342.110413	21
6	**830.302533**	415.654905			812.291968	406.649622	D	***2541.193466***	1271.100371	2524.166917	1262.587096	2523.182901	1262.095088	20
7	**929.370947**	465.189112			911.360382	456.183829	V	2426.166523	1213.586899	2409.139974	1205.073625	2408.155958	1204.581617	19
8	1026.423711	513.715494			1008.413146	504.710211	P	***2327.098109***	1164.052692	2310.071560	1155.539418	2309.087544	1155.047410	18
9	**1465.649037**	733.328157	1448.622488	724.814882	1447.638472	724.322874	Q	***2230.045345***	1115.526310	2213.018796	1107.013036	2212.034780	1106.521028	17
10	1625.679686	813.343481	1608.653137	804.830207	1607.669121	804.338199	C	***1790.820019***	895.913648	1773.793470	887.400373	1772.809454	886.908365	16
11	**1696.716800**	848.862038	1679.690251	840.348764	1678.706235	839.856756	A	***1630.789370***	815.898323	1613.762821	807.385049	1612.778805	806.893040	15
12	**1767.753914**	884.380595	1750.727365	875.867321	1749.743349	875.375313	A	***1559.752256***	780.379766	1542.725707	771.866492	1541.741691	771.374484	14
13	1864.806678	932.906977	1847.780129	924.393703	1846.796113	923.901695	P	***1488.715142***	744.861209	1471.688593	736.347935	1470.704577	735.855927	13
14	1951.838706	976.422991	1934.812157	967.909717	1933.828141	967.417709	S	***1391.662378***	696.334827	1374.635829	687.821553	1373.651813	687.329545	12
15	2098.907120	1049.957198	2081.880571	1041.443924	2080.896555	1040.951916	F	***1304.630350***	652.818813	1287.603801	644.305539	1286.619785	643.813530	11
16	2213.934063	1107.470670	2196.907514	1098.957395	2195.923498	1098.465387	D	***1157.561936***	579.284606	1140.535387	570.771331	1139.551371	570.279323	10
17	2373.964712	1187.485994	2356.938163	1178.972719	2355.954147	1178.480711	C	***1042.534993***	521.771135	1025.508444	513.257860	1024.524428	512.765852	9
18	2430.986176	1215.996726	2413.959627	1207.483451	2412.975611	1206.991443	G	882.504344	441.755810	865.477795	433.242536	864.493779	432.750528	8
19	2559.081139	1280.044207	2542.054590	1271.530933	2541.070574	1271.038925	K	825.482880	413.245078	808.456331	404.731804	807.472315	404.239796	7
20	2656.133903	1328.570589	2639.107354	1320.057315	2638.123338	1319.565307	P	***697.387917***	349.197597	680.361368	340.684322	679.377352	340.192314	6
21	2784.192481	1392.599878	2767.165932	1384.086604	2766.181916	1383.594596	Q	600.335153	300.671215	583.308604	292.157940	582.324588	291.665932	5
22	2883.260895	1442.134085	2866.234346	1433.620811	2865.250330	1433.128803	V	472.276575	236.641925	455.250026	228.128651	454.266010	227.636643	4
23	3012.303488	1506.655382	2995.276939	1498.142107	2994.292923	1497.650099	E	373.208161	187.107719	356.181612	178.594444	355.197596	178.102436	3
24	3109.356252	1555.181764	3092.329703	1546.668489	3091.345687	1546.176481	P	***244.165568***	122.586422	227.139019	114.073148			2
25							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LYDYCDVPQCAAPSFDCGKPQVEPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.7	3254.454514	0.008862	LYDYCDVPQCAAPSFDCGKPQVEPK
6.5	3254.454514	0.008862	LYDYCDVPQCAAPSFDCGKPQVEPK

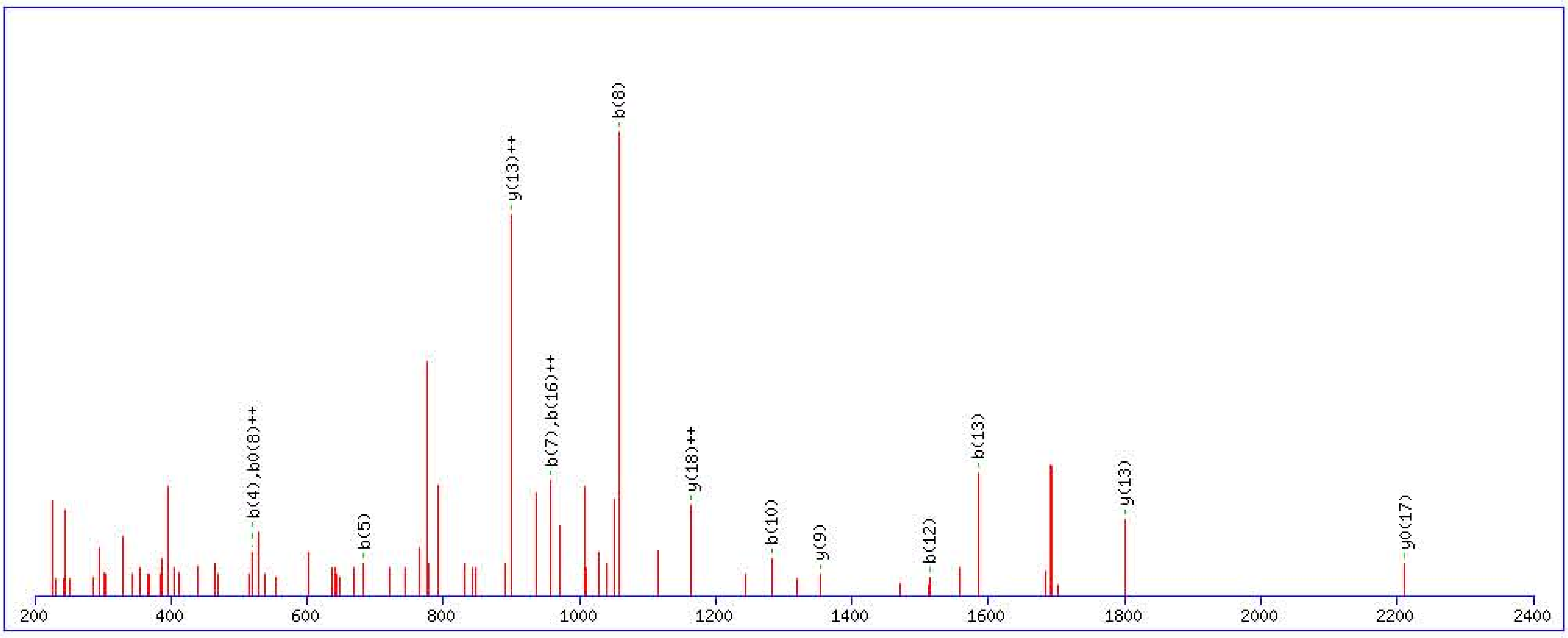
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLYDYCDVPQCAAPSFDCGKPQVEPK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

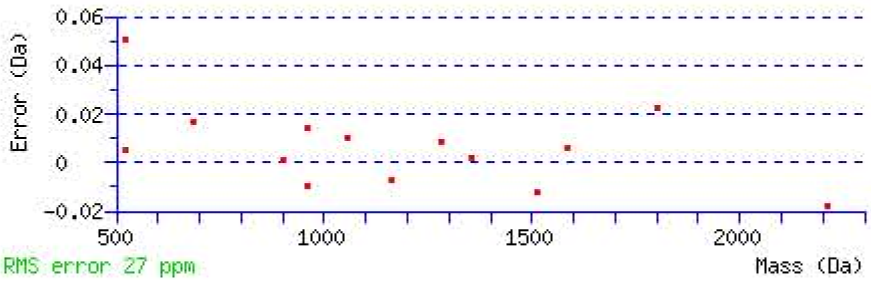
Match to Query 60573: 3382.550456 from(846.644890,4+) rtinseconds(1968) index(62301)
Title: Locus:1.1.1.3311.25 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

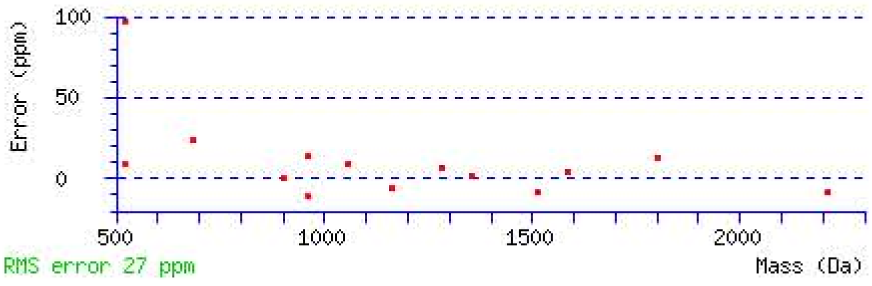
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3382.549469
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q22     : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.0016
Matches : 14/290 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	129.102239	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
38.4	3382.549469	0.000987	KLYDYCDVPQCAAPSFDCGKPQVEPK
2.6	3382.549469	0.000987	KLYDYCDVPQCAAPSFDCGKPQVEPK

Mascot: http://www.matrixscience.com/

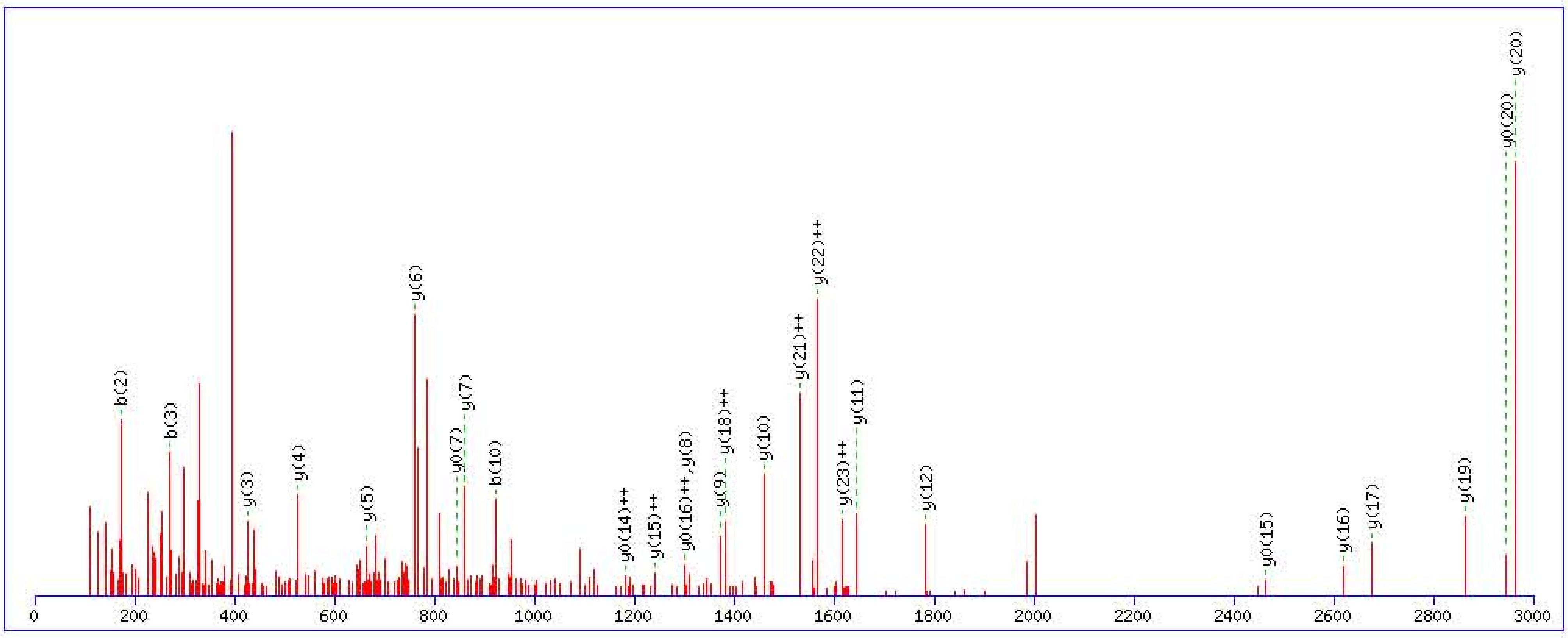
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNVAVTVSGHTCQHWSAQTPHTHNR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

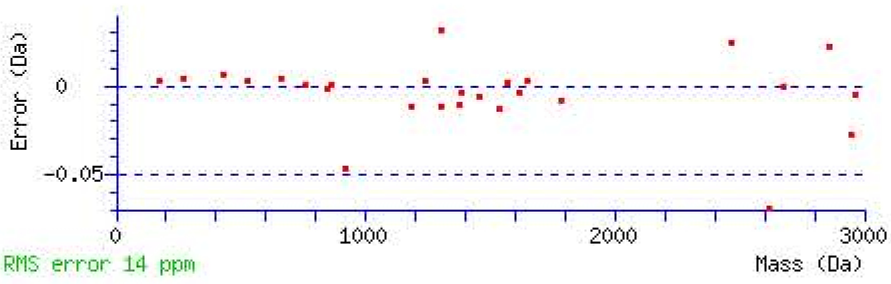
Match to Query 60785: 3403.626970 from(681.732670,5+) rtinseconds(1699) index(60864)
Title: Locus:1.1.1.3217.13 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

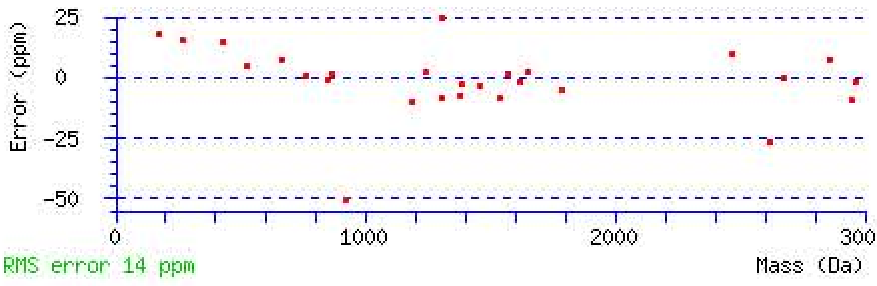


Monoisotopic mass of neutral peptide Mr(calc): 3403.623764
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13 : Biotin:Thermo-21345 (Q)
Q18 : Biotin:Thermo-21345 (Q)
Ions Score: 80 **Expect:** 2.5e-007
Matches : 27/270 fragment ions using 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							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



RMS error 14 ppm



RMS error 14 ppm

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
79.8	3403.623764	0.003206	GNVAVTVSGHTCQHWSAQTPHTHNR

Mascot: http://www.matrixscience.com/

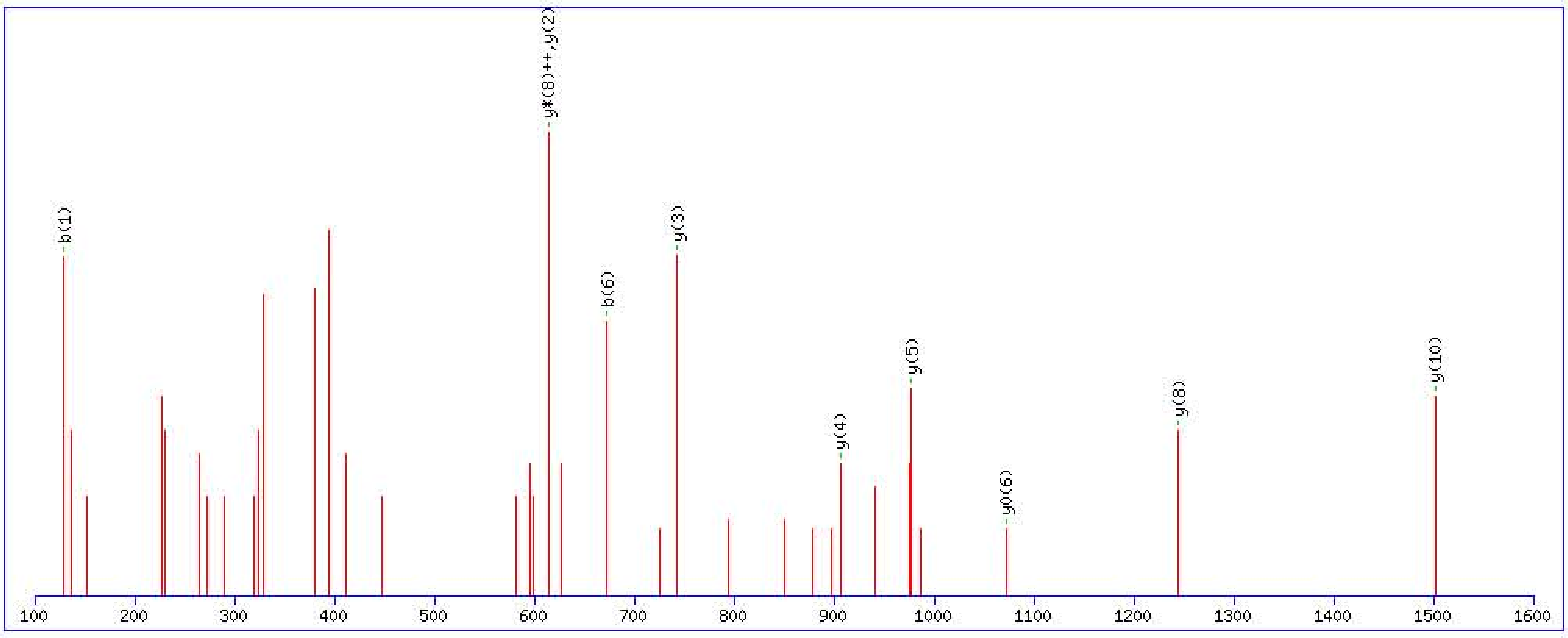
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KCSAPEPSQKPPGKPCPGLAYEQR**
Found in **PROP_HUMAN**, Properdin OS=Homo sapiens GN=CFP PE=1 SV=2

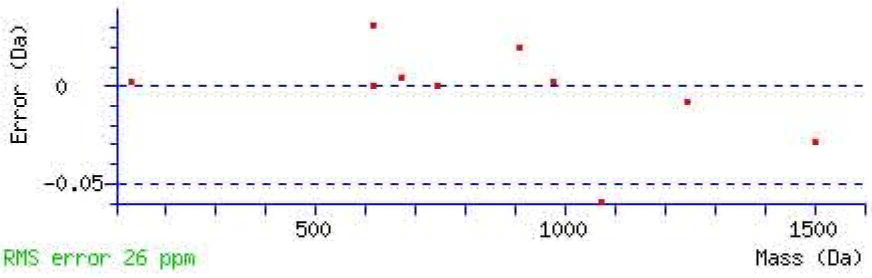
Match to Query 56004: 2992.467920 from(599.500860,5+) rtinseconds(1472) index(59649)
Title: Locus:1.1.1.3138.20 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

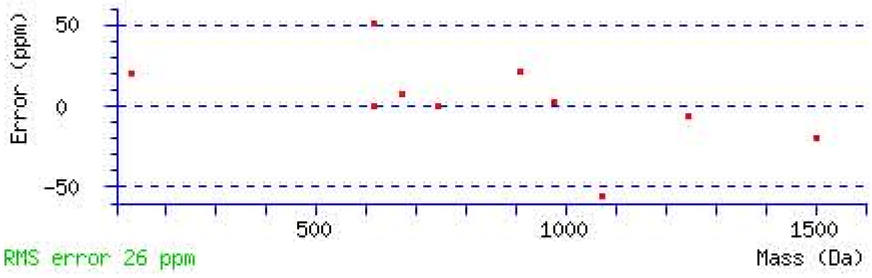
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2992.472107
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q23     : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.00042
Matches : 10/268 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	**129.102239**	65.054757	112.075690	56.541483			K							24
2	289.132888	145.070082	272.106339	136.556808			C	2865.384455	1433.195865	2848.357906	1424.682591	2847.373890	1424.190583	23
3	376.164916	188.586096	359.138367	180.072822	358.154351	179.580814	S	2705.353806	1353.180541	2688.327257	1344.667266	2687.343241	1344.175258	22
4	447.202030	224.104653	430.175481	215.591378	429.191465	215.099370	A	2618.321778	1309.664527	2601.295229	1301.151252	2600.311213	1300.659244	21
5	544.254794	272.631035	527.228245	264.117761	526.244229	263.625753	P	2547.284664	1274.145970	2530.258115	1265.632695	2529.274099	1265.140687	20
6	**673.297387**	337.152332	656.270838	328.639057	655.286822	328.147049	E	2450.231900	1225.619588	2433.205351	1217.106313	2432.221335	1216.614305	19
7	770.350151	385.678714	753.323602	377.165439	752.339586	376.673431	P	2321.189307	1161.098292	2304.162758	1152.585017	2303.178742	1152.093009	18
8	857.382179	429.194728	840.355630	420.681453	839.371614	420.189445	S	2224.136543	1112.571909	2207.109994	1104.058635	2206.125978	1103.566627	17
9	985.440757	493.224017	968.414208	484.710742	967.430192	484.218734	Q	2137.104515	1069.055895	2120.077966	1060.542621	2119.093950	1060.050613	16
10	1113.535720	557.271498	1096.509171	548.758224	1095.525155	548.266216	K	2009.045937	1005.026607	1992.019388	996.513332	1991.035372	996.021324	15
11	1210.588484	605.797880	1193.561935	597.284606	1192.577919	596.792598	P	1880.950974	940.979125	1863.924425	932.465851	1862.940409	931.973843	14
12	1307.641248	654.324262	1290.614699	645.810988	1289.630683	645.318980	P	1783.898210	892.452743	1766.871661	883.939469	1765.887645	883.447461	13
13	1364.662712	682.834994	1347.636163	674.321720	1346.652147	673.829712	G	1686.845446	843.926361	1669.818897	835.413087	1668.834881	834.921079	12
14	1492.757675	746.882476	1475.731126	738.369201	1474.747110	737.877193	K	1629.823982	815.415629	1612.797433	806.902355	1611.813417	806.410347	11
15	1589.810439	795.408858	1572.783890	786.895583	1571.799874	786.403575	P	***1501.729019***	751.368148	1484.702470	742.854873	1483.718454	742.362865	10
16	1749.841088	875.424182	1732.814539	866.910908	1731.830523	866.418900	C	1404.676255	702.841766	1387.649706	694.328491	1386.665690	693.836483	9
17	1846.893852	923.950564	1829.867303	915.437290	1828.883287	914.945282	P	***1244.645606***	622.826441	1227.619057	614.313167	1226.635041	613.821159	8
18	1903.915316	952.461296	1886.888767	943.948022	1885.904751	943.456014	G	1147.592842	574.300059	1130.566293	565.786785	1129.582277	565.294777	7
19	2016.999380	1009.003328	1999.972831	1000.490054	1998.988815	999.998045	L	1090.571378	545.789327	1073.544829	537.276053	1072.560813	536.784045	6
20	2088.036494	1044.521885	2071.009945	1036.008610	2070.025929	1035.516602	A	***977.487314***	489.247295	960.460765	480.734021	959.476749	480.242013	5
21	2251.099823	1126.053549	2234.073274	1117.540275	2233.089258	1117.048267	Y	***906.450200***	453.728738	889.423651	445.215464	888.439635	444.723456	4
22	2380.142416	1190.574846	2363.115867	1182.061571	2362.131851	1181.569564	E	***743.386871***	372.197074	726.360322	363.683799	725.376306	363.191791	3
23	2819.367742	1410.187509	2802.341193	1401.674235	2801.357177	1401.182227	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 KCSAPEPSQKPPGKPCPGLAYEQR
(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	2992.472107	-0.004187	KCSAPEPSQKPPGKPCPGLAYEQR
0.5	2992.492355	-0.024435	ESSRSHAVFTITIESMEKSNEIVNIR

Mascot: http://www.matrixscience.com/

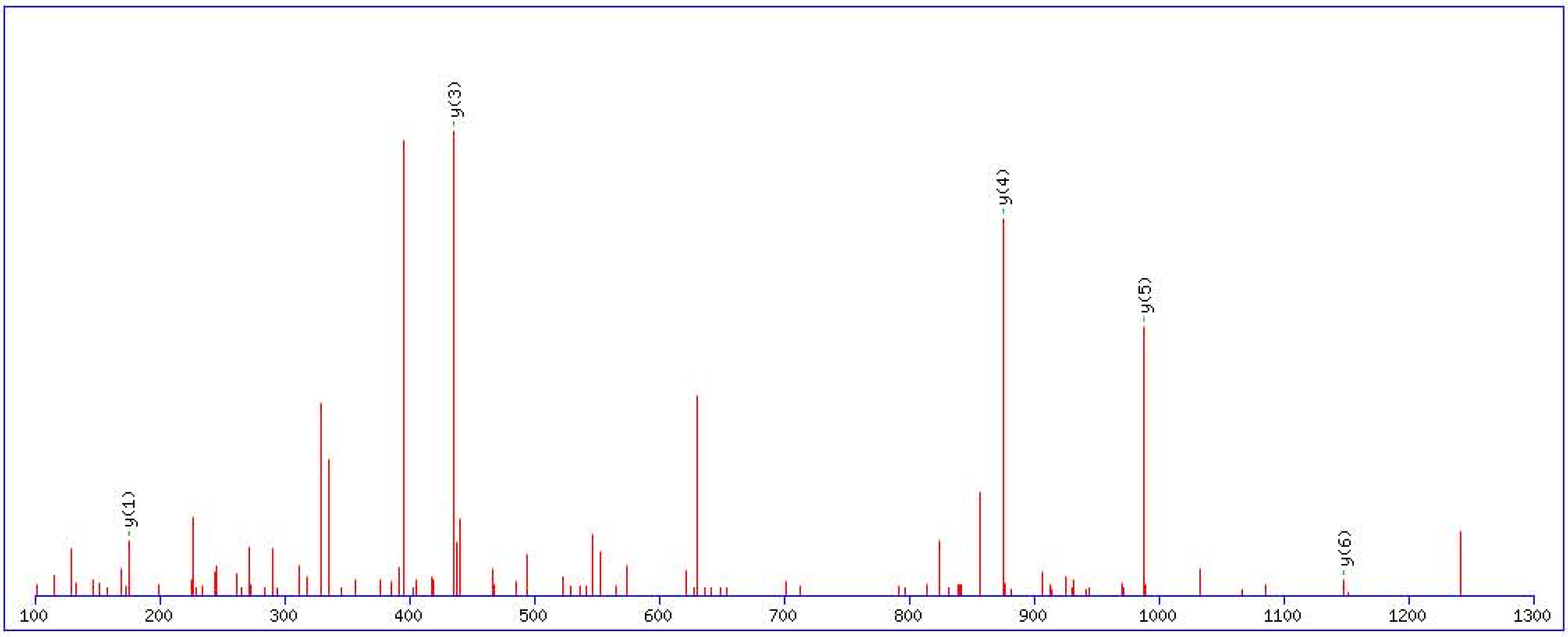
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ECLQTCR**
Found in **AMBP_HUMAN**, Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

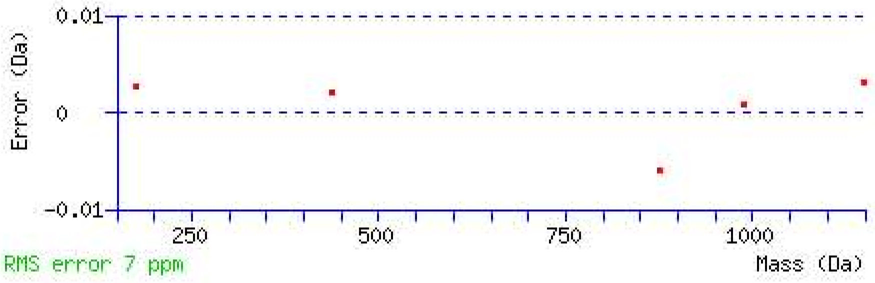
Match to Query 22342: 1276.570548 from(639.292550,2+) rtinseconds(1472) index(30086)
Title: Locus:1.1.1.3061.20 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

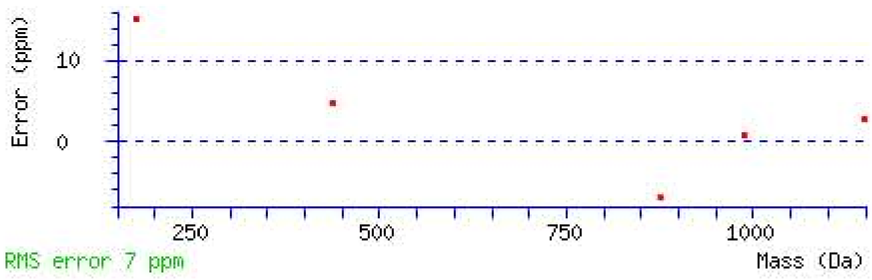
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 0.0099
Matches : 5/62 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							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
27.8	1276.572632	-0.002084	ECLQTCR
10.1	1276.553116	0.017432	EDLDNASKDDR
5.3	1276.587006	-0.016458	EDGTWAPMRSK
4.8	1276.579605	-0.009057	EEQRSPFNDR
2.6	1276.582977	-0.012429	EMQLGREDQR
2.1	1276.572388	-0.001840	EDSYANYFIR
1.7	1276.569229	0.001319	MTGRYEMYAR
0.3	1276.560516	0.010032	QQVPSEDSMEK

Mascot: http://www.matrixscience.com/

{MATRIX SCIENCE}

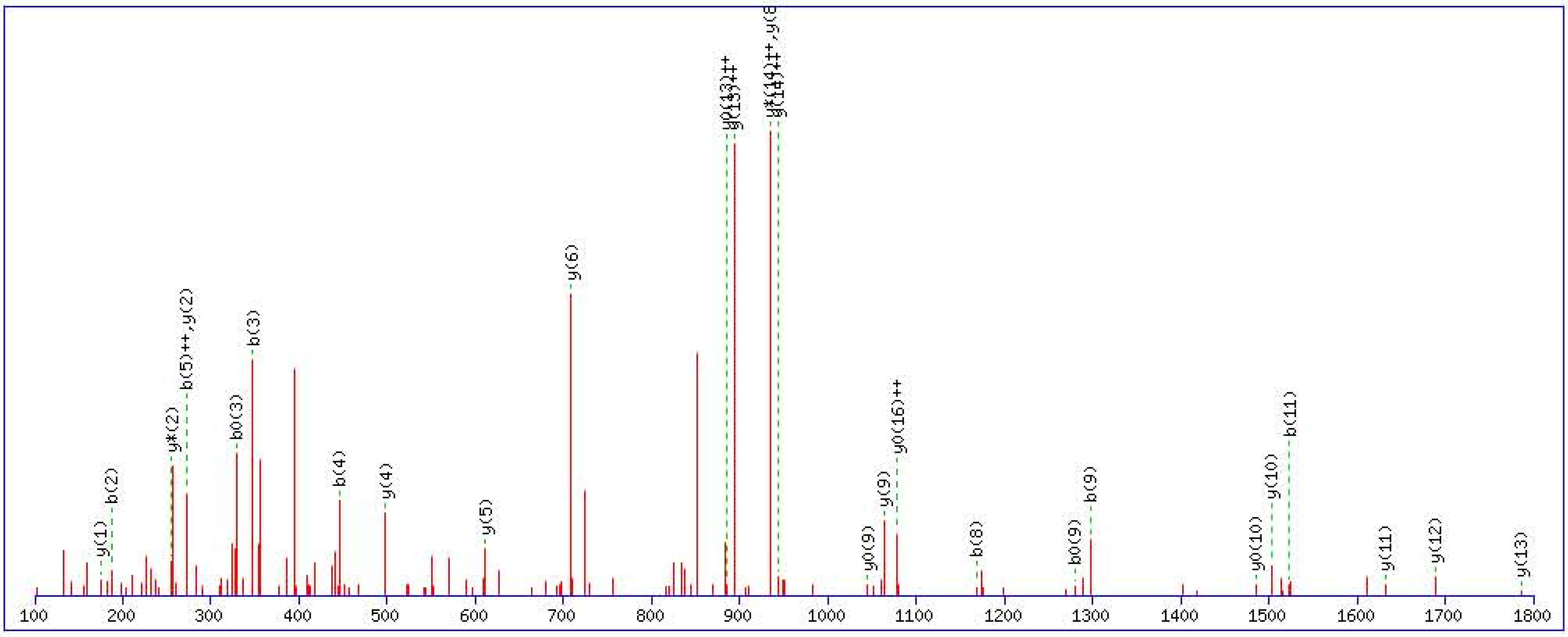
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GECVPGEQEPEPILIPR**
Found in **AMBP_HUMAN**, Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

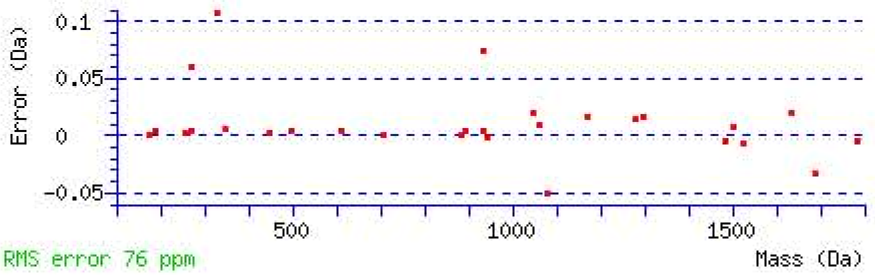
Match to Query 46569: 2230.119312 from(744.380380,3+) rtinseconds(2304) index(6605)
Title: Locus:1.1.1.3354.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

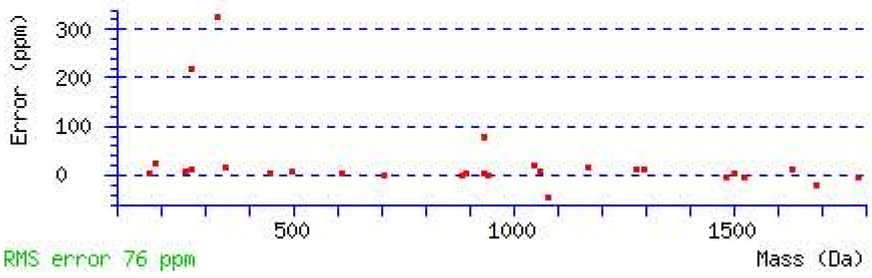
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2230.112595
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 50  Expect: 0.00034
Matches : 28/164 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
49.5	2230.112595	0.006717	GECVPGEQEPEPILIPR

Mascot: http://www.matrixscience.com/

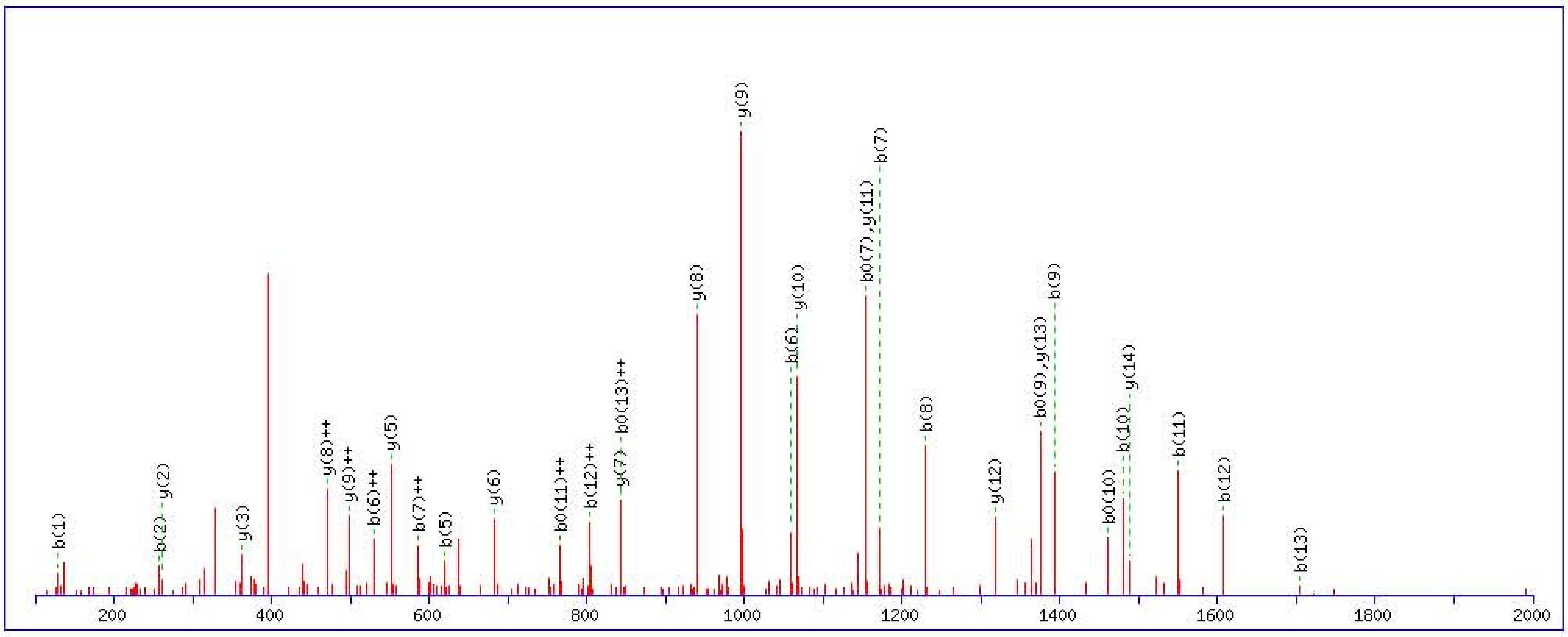
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KEDSCQLGYSAGPCMGMTSR**
Found in **AMBP_HUMAN**, Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

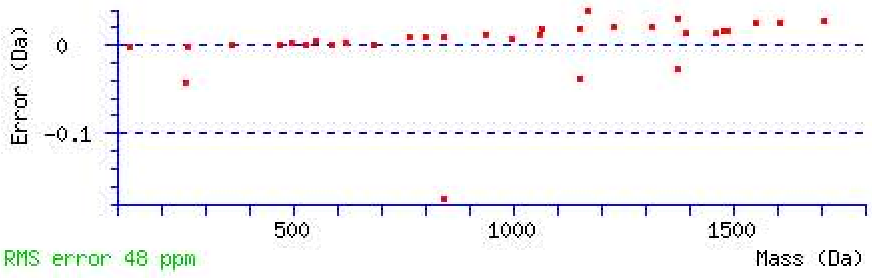
Match to Query 51669: 2545.121022 from(849.380950,3+) rtinseconds(1872) index(46434)
Title: Locus:1.1.1.2700.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

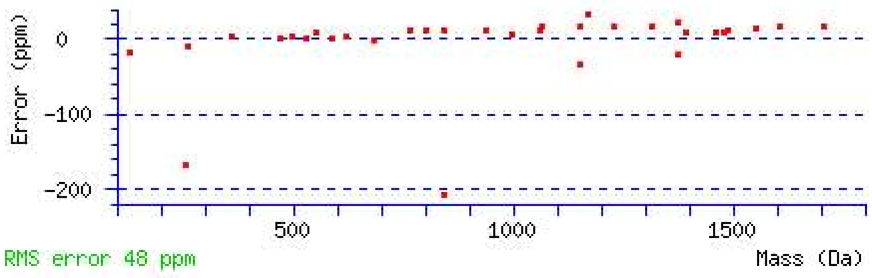
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2545.089188
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 86  Expect: 1.4e-008
Matches : 33/224 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	***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
85.8	2545.089188	0.031834	KEDSCQLGYSAGPCMGMTSR

Mascot: http://www.matrixscience.com/

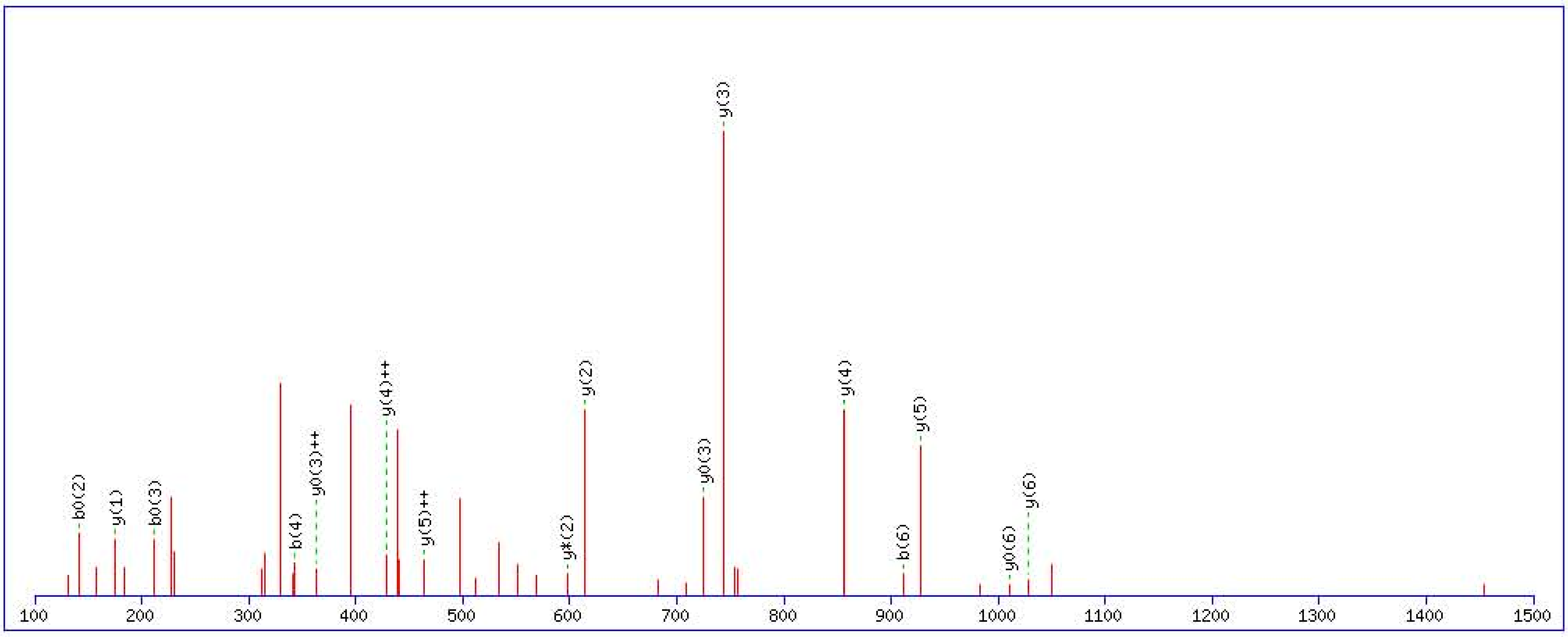
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTAIEQR**
Found in **HEG1_HUMAN**, Protein HEG homolog 1 OS=Homo sapiens GN=HEG1 PE=1 SV=3

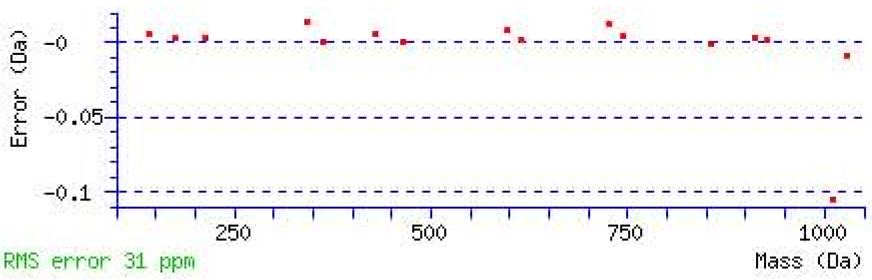
Match to Query 15868: 1084.567848 from(543.291200,2+) rtinseconds(1470) index(30062)
Title: Locus:1.1.1.3060.21 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

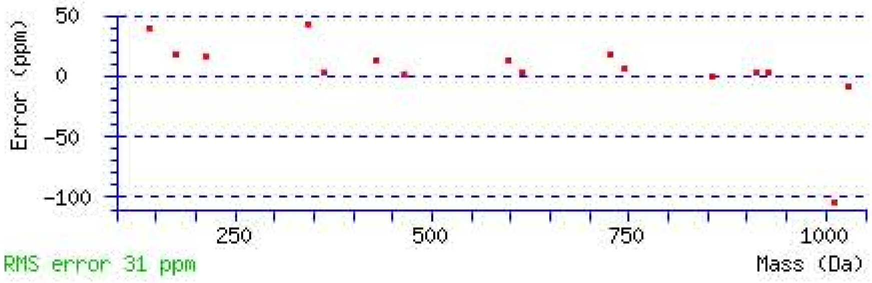
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1084.569901
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 35 **Expect:** 0.0061
Matches : 16/56 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							7
2	159.076419	80.041847			141.065854	71.036565	T	***1028.555728***	514.781502	1011.529179	506.268228	1010.545163	505.776220	6
3	230.113533	115.560404			212.102968	106.555122	A	***927.508049***	464.257663	910.481500	455.744388	909.497484	455.252380	5
4	**343.197597**	172.102436			325.187032	163.097154	I	***856.470935***	428.739106	839.444386	420.225831	838.460370	419.733823	4
5	472.240190	236.623733			454.229625	227.618450	E	***743.386871***	372.197074	726.360322	363.683799	725.376306	363.191791	3
6	**911.465516**	456.236396	894.438967	447.723122	893.454951	447.231114	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 GTAIEQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.9	1084.569901	-0.002053	GTAIEQR
10.6	1084.569885	-0.002037	ASAEIQR
7.9	1084.573730	-0.005882	RGELPRDSR
6.3	1084.569916	-0.002068	TKMDLGGHVK
6.3	1084.569885	-0.002037	QELAASR
6.3	1084.569901	-0.002053	QELAGTR
3.1	1084.566559	0.001289	DGGVLFHVNK
3.1	1084.573715	-0.005867	ARTREAEPR
1.2	1084.573746	-0.005898	TGRHSIASTR
1.0	1084.562485	0.005363	RSEALEAGPR

Mascot: http://www.matrixscience.com/

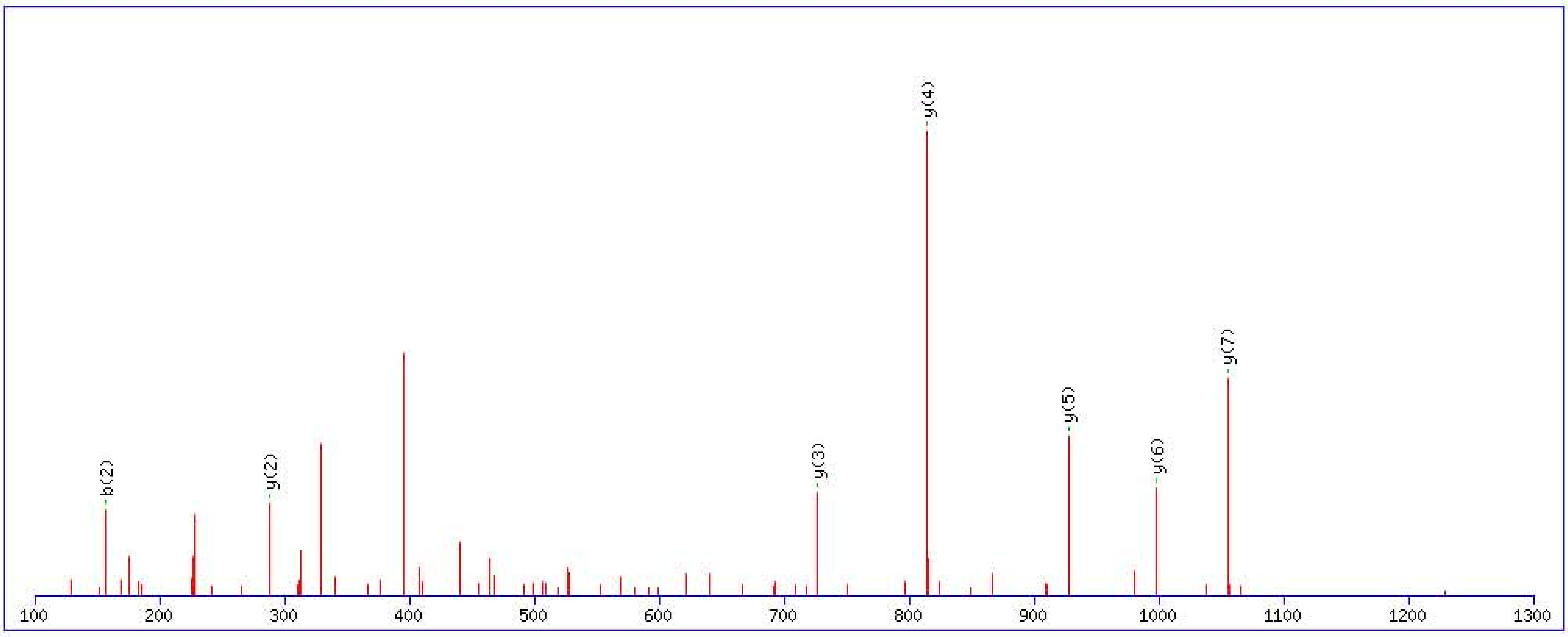
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGALSQLR**
Found in **MENT_HUMAN**, Protein MENT OS=Homo sapiens GN=MENT PE=2 SV=1

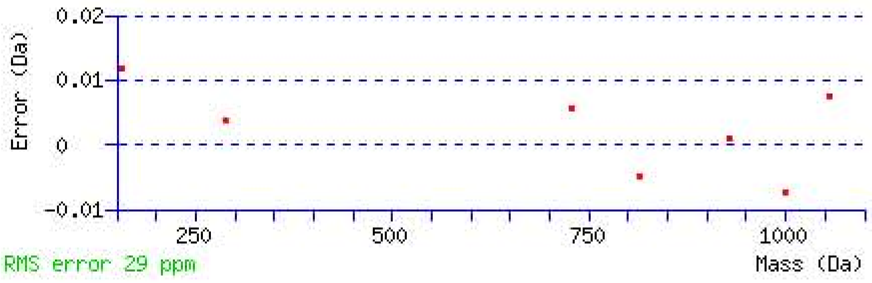
Match to Query 18957: 1153.664988 from(577.839770,2+) rtinseconds(1935) index(32703)
Title: Locus:1.1.1.3223.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

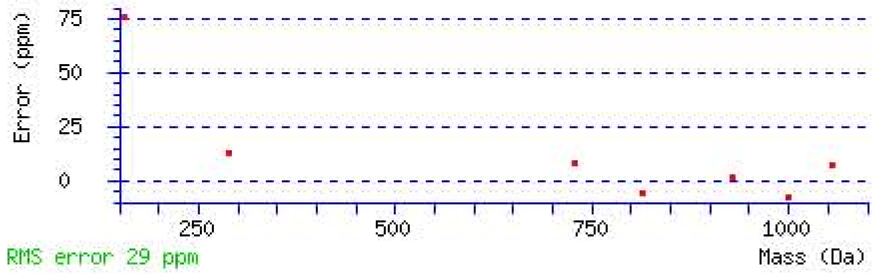
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1153.664139
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00023
Matches : 7/60 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	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
48.3	1153.664139	0.000849	VGALSQLR
15.9	1153.667953	-0.002965	RANPNSIRVK
12.3	1153.681870	-0.016882	RALENLLPTK
11.1	1153.681885	-0.016897	VQEKTALPLR
10.9	1153.664124	0.000864	VKQEALR
10.4	1153.675354	-0.010366	RALLSQR
10.4	1153.675369	-0.010381	RALTVQR
5.2	1153.664139	0.000849	VTQINLR
4.3	1153.660767	0.004221	VPTAAGAWLLR
4.3	1153.675369	-0.010381	QTVRALR

Mascot: http://www.matrixscience.com/

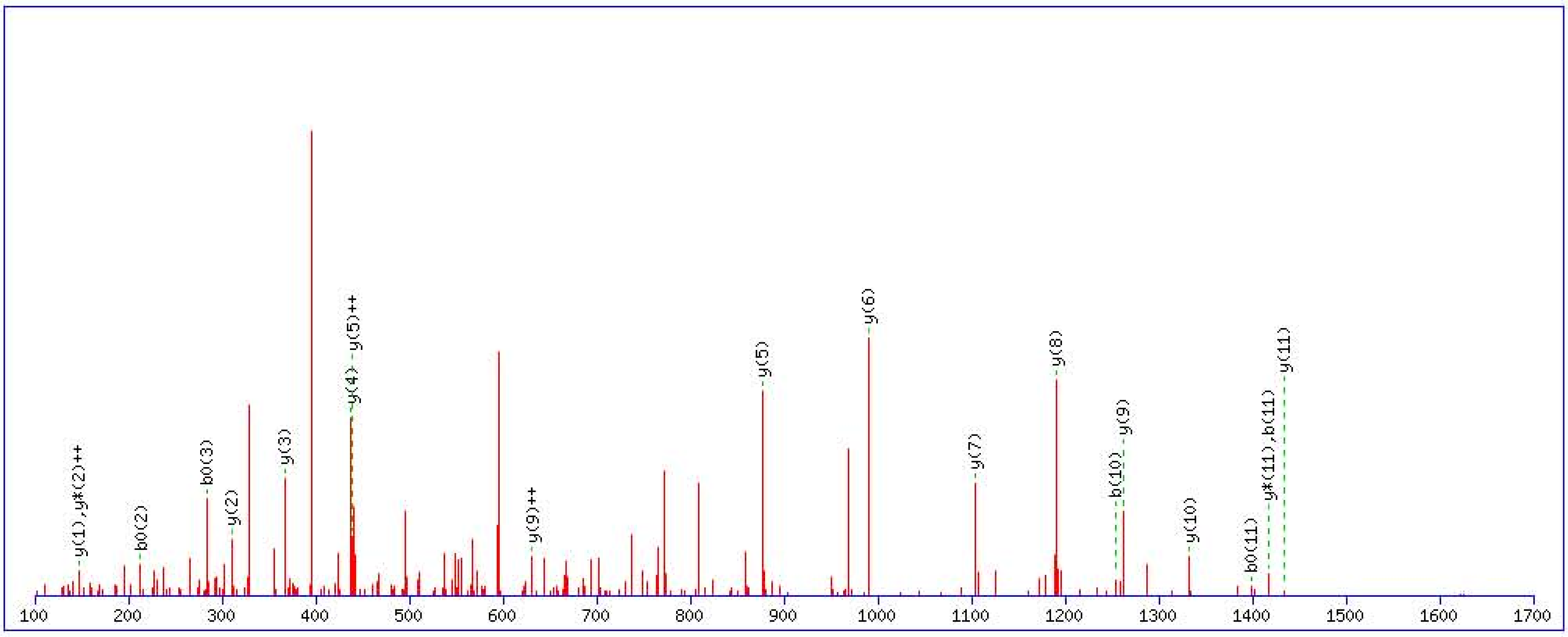
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ETAASLLQAGYK**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

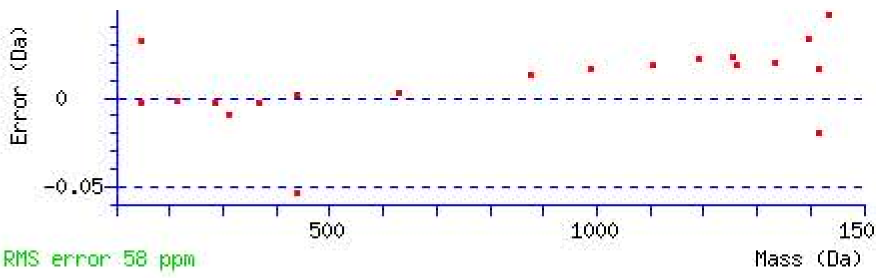
Match to Query 31437: 1561.831408 from(781.922980,2+) rtinseconds(2125) index(48175)
Title: Locus:1.1.1.2788.16 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

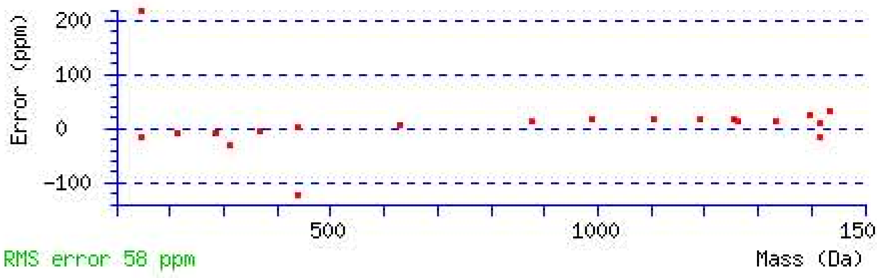
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1561.817383
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 51 **Expect:** 2.5e-005
Matches : 20/104 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
51.5	1561.817383	0.014025	ETAASLLQAGYK
2.2	1561.817398	0.014010	VLPEVLEKQCGYK
0.3	1561.843903	-0.012495	HLSGLSWPQVK

Mascot: http://www.matrixscience.com/

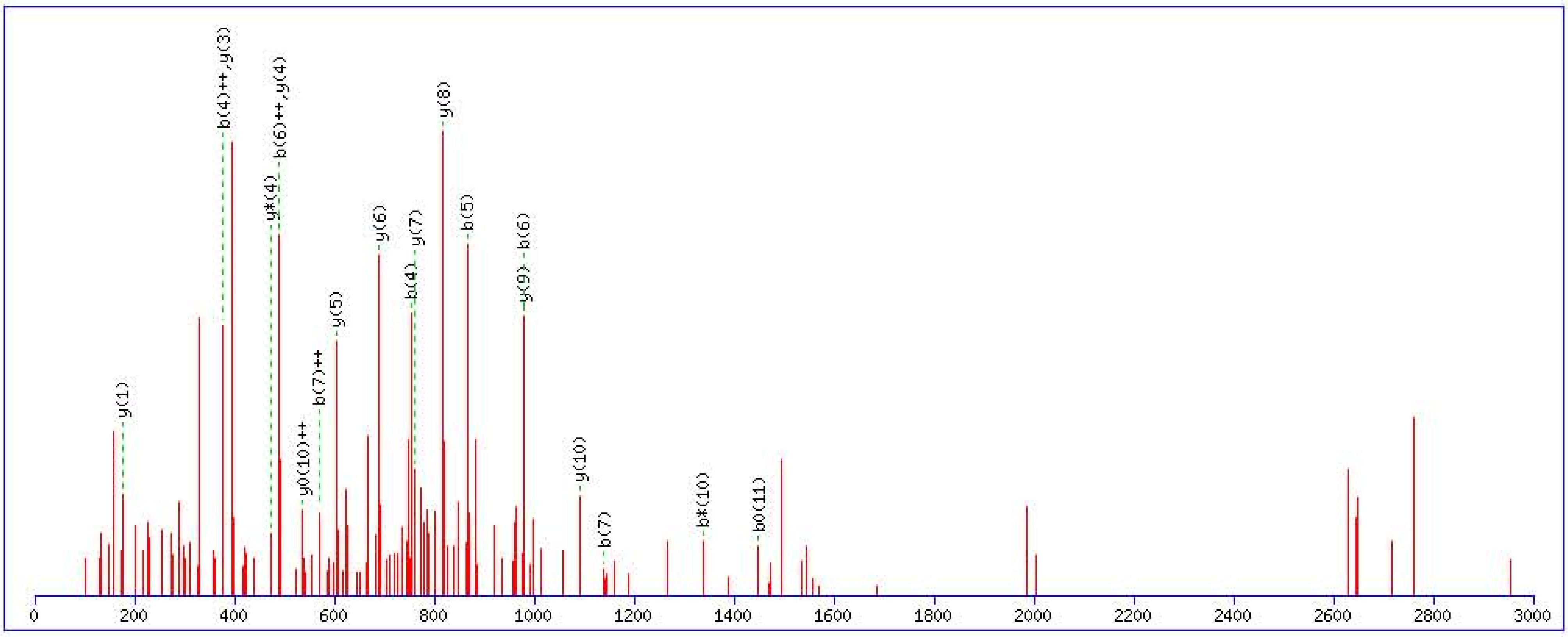
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPQELLCGASLISDR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

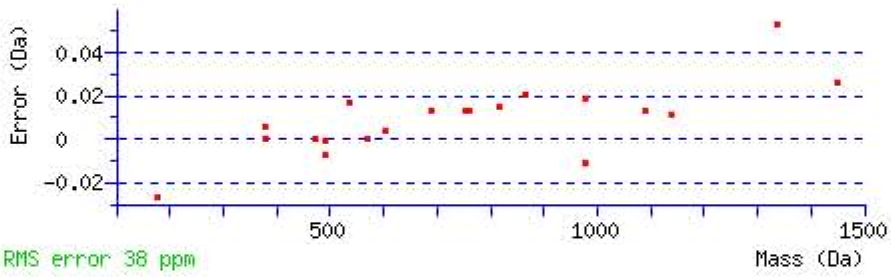
Match to Query 41172: 1956.003852 from(653.008560,3+) rtinseconds(2490) index(50209)
Title: Locus:1.1.1.2915.19 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

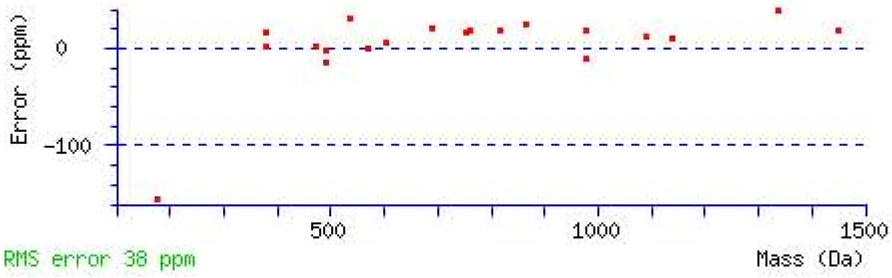
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1955.980850
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.0045
Matches : 20/162 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	88.039304	44.523290			70.028739	35.518008	S							15
2	185.092068	93.049672			167.081503	84.044389	P	1869.956117	935.481697	1852.929568	926.968422	1851.945552	926.476414	14
3	624.317394	312.662335	607.290845	304.149061	606.306829	303.657053	Q	1772.903353	886.955314	1755.876804	878.442040	1754.892788	877.950032	13
4	**753.359987**	**377.183632**	736.333438	368.670357	735.349422	368.178349	E	1333.678027	667.342652	1316.651478	658.829377	1315.667462	658.337369	12
5	**866.444051**	433.725664	849.417502	425.212389	848.433486	424.720381	L	1204.635434	602.821355	1187.608885	594.308081	1186.624869	593.816073	11
6	**979.528115**	**490.267696**	962.501566	481.754421	961.517550	481.262413	L	***1091.551370***	546.279323	1074.524821	537.766049	1073.540805	537.274040	10
7	**1139.558764**	**570.283020**	1122.532215	561.769746	1121.548199	561.277738	C	***978.467306***	489.737291	961.440757	481.224017	960.456741	480.732009	9
8	1196.580228	598.793752	1179.553679	590.280478	1178.569663	589.788470	G	***818.436657***	409.721967	801.410108	401.208692	800.426092	400.716684	8
9	1267.617342	634.312309	1250.590793	625.799035	1249.606777	625.307027	A	***761.415193***	381.211235	744.388644	372.697960	743.404628	372.205952	7
10	1354.649370	677.828323	1337.622821	669.315049	1336.638805	668.823041	S	***690.378079***	345.692678	673.351530	337.179403	672.367514	336.687395	6
11	1467.733434	734.370355	1450.706885	725.857081	1449.722869	725.365073	L	***603.346051***	302.176664	586.319502	293.663389	585.335486	293.171381	5
12	1580.817498	790.912387	1563.790949	782.399113	1562.806933	781.907104	I	***490.261987***	245.634631	473.235438	237.121357	472.251422	236.629349	4
13	1667.849526	834.428401	1650.822977	825.915127	1649.838961	825.423118	S	***377.177923***	189.092600	360.151374	180.579325	359.167358	180.087317	3
14	1782.876469	891.941873	1765.849920	883.428598	1764.865904	882.936590	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SPQELLCGASLISDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.9	1955.980850	0.023002	SPQELLCGASLISDR

Mascot: http://www.matrixscience.com/

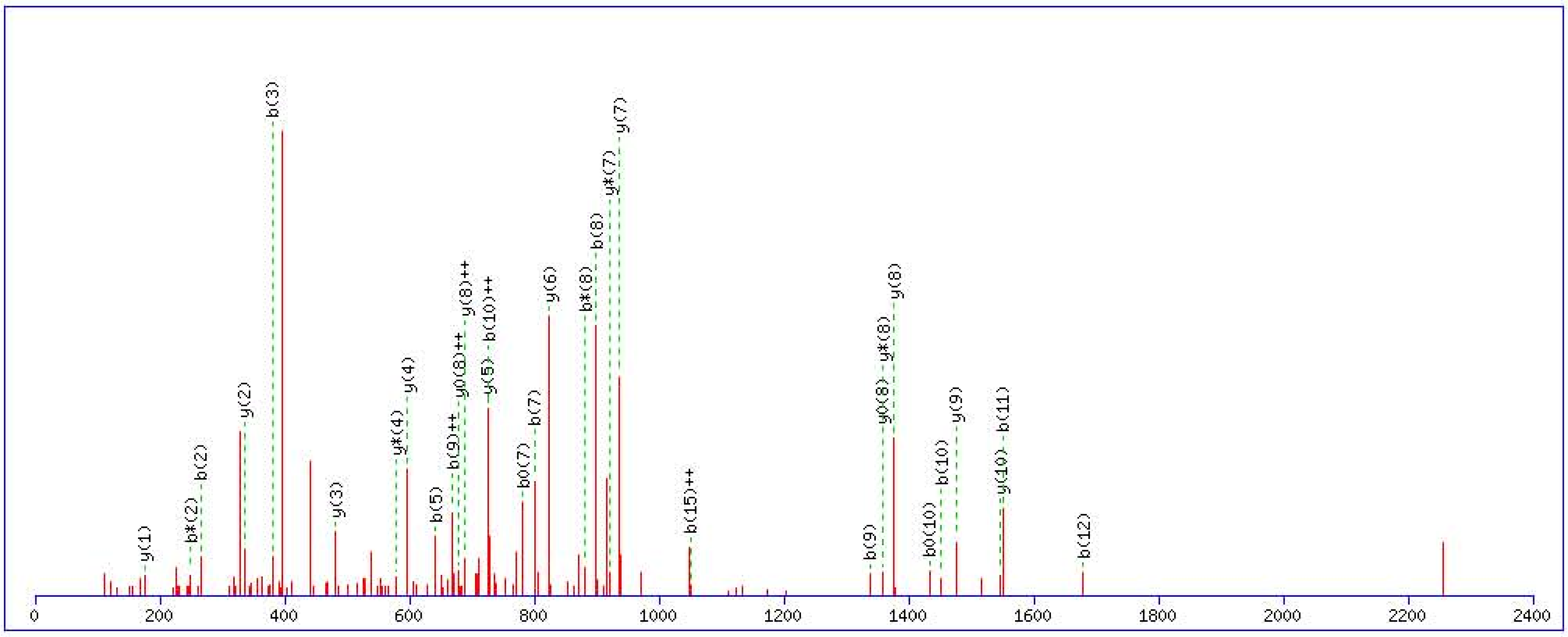
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQDFNSAVQLVENFCR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

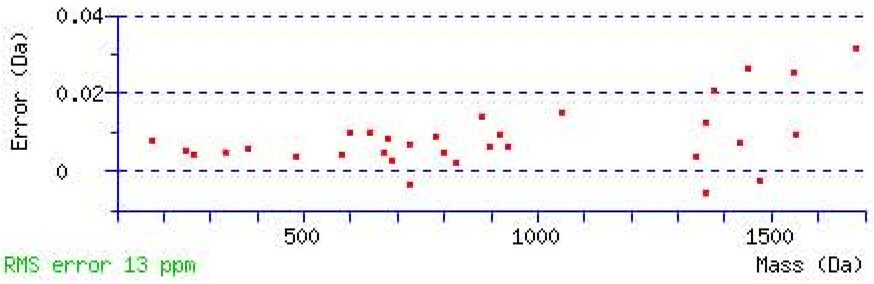
Match to Query 47303: 2274.078792 from(759.033540,3+) rtinseconds(2480) index(65007)
Title: Locus:1.1.1.3490.11 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

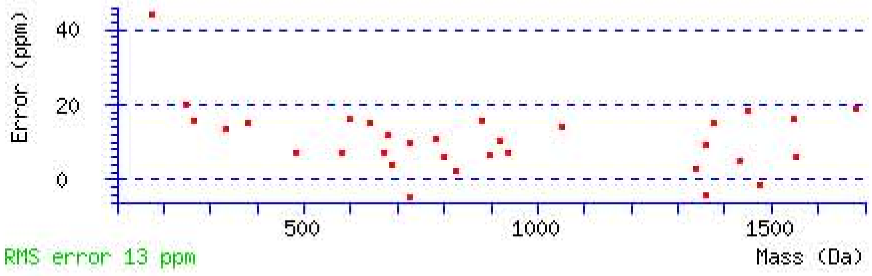
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2274.067398
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 61 **Expect:** 1.5e-005
Matches : 32/166 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	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
61.2	2274.067398	0.011394	HQDFNSAVQLVENFCR
22.0	2274.067398	0.011394	HQDFNSAVQLVENFCR

Mascot: http://www.matrixscience.com/

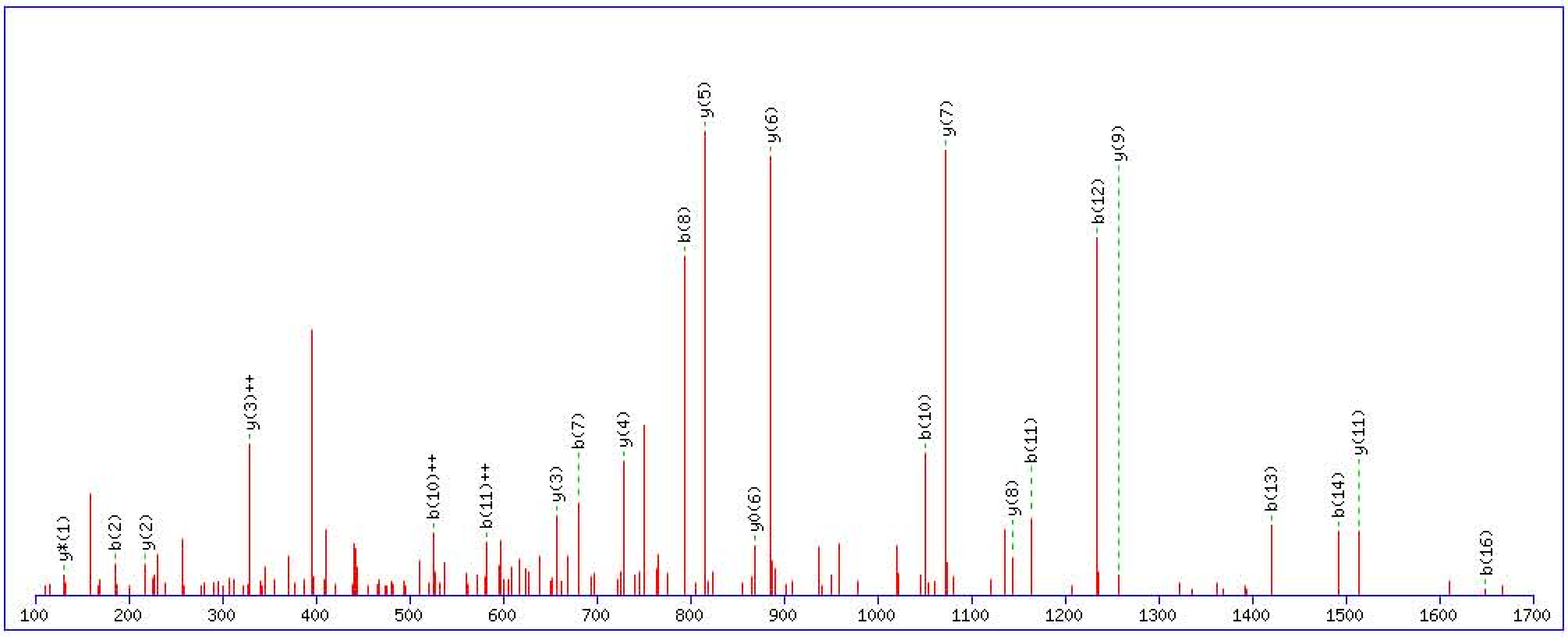
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAVTTHGLPCLAWASAQAK**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

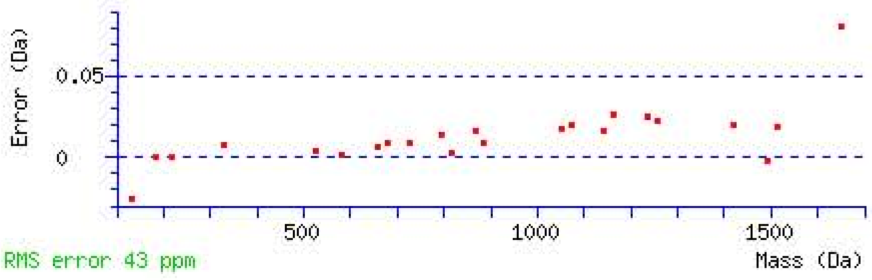
Match to Query 47894: 2305.235082 from(769.418970,3+) rtinseconds(2343) index(49456)
Title: Locus:1.1.1.2864.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

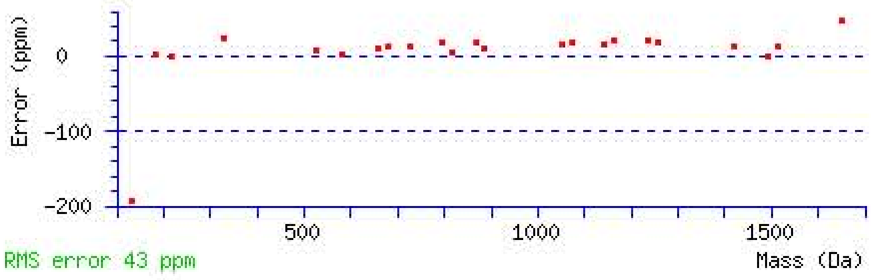
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2305.207504
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q17 : Biotin:Thermo-21345 (Q)
Ions Score: 49 **Expect:** 0.00027
Matches : 23/170 fragment ions using 46 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
49.0	2305.207504	0.027578	LAVTTHGLPCLAWASAQAK

Mascot: http://www.matrixscience.com/

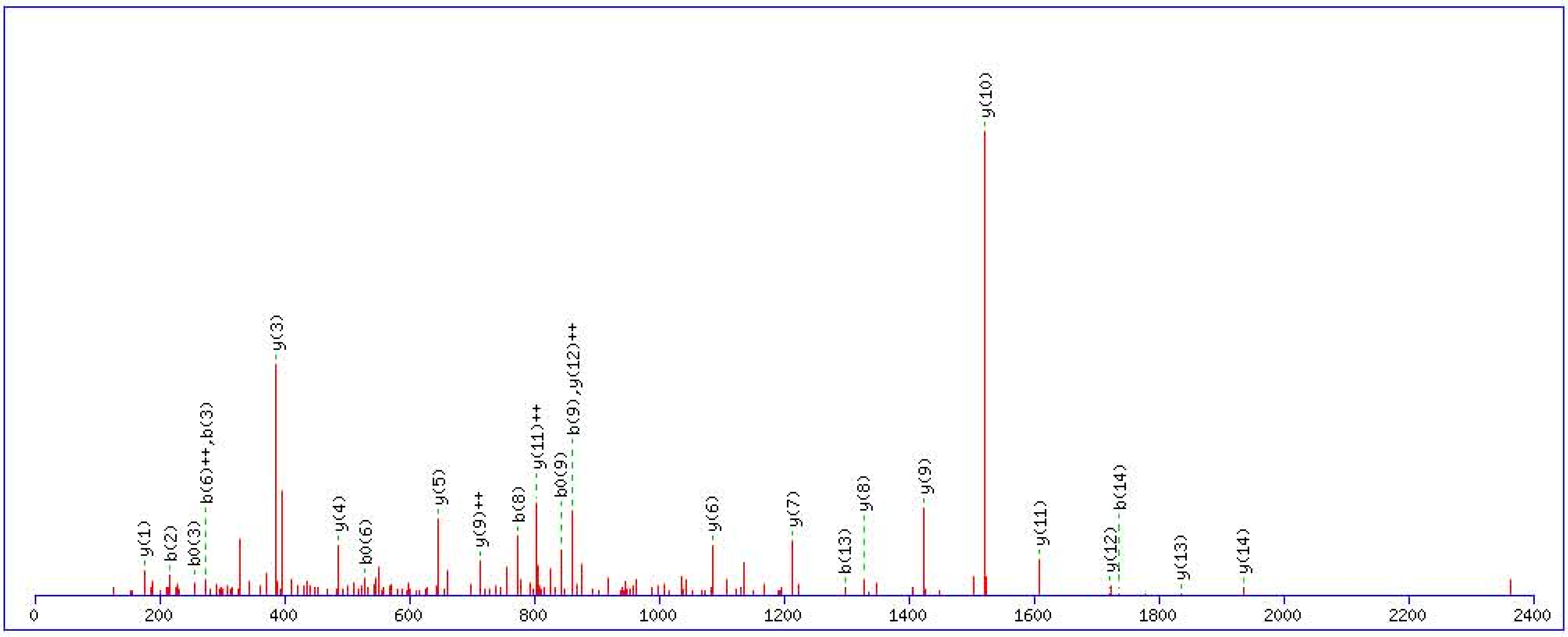
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SEGSSVNLSPPLEQCVPDR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

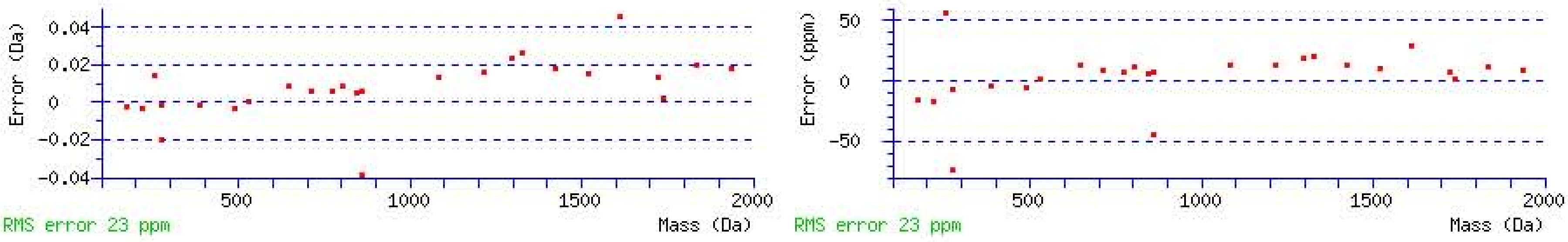
Match to Query 48793: 2381.159262 from(794.727030,3+) rtinseconds(2157) index(48381)
Title: Locus:1.1.1.2799.19 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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): 2381.135529
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 101  Expect: 2.2e-009
Matches : 26/202 fragment ions using 35 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							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
100.7	2381.135529	0.023733	SEGSSVNLSPPLEQCVPDR
8.1	2381.168564	-0.009302	GNAVVGYLQCFDLEGESGLVVR
2.0	2381.160675	-0.001413	IPSTVEFCSTPAEKMAETVLR

Mascot: http://www.matrixscience.com/

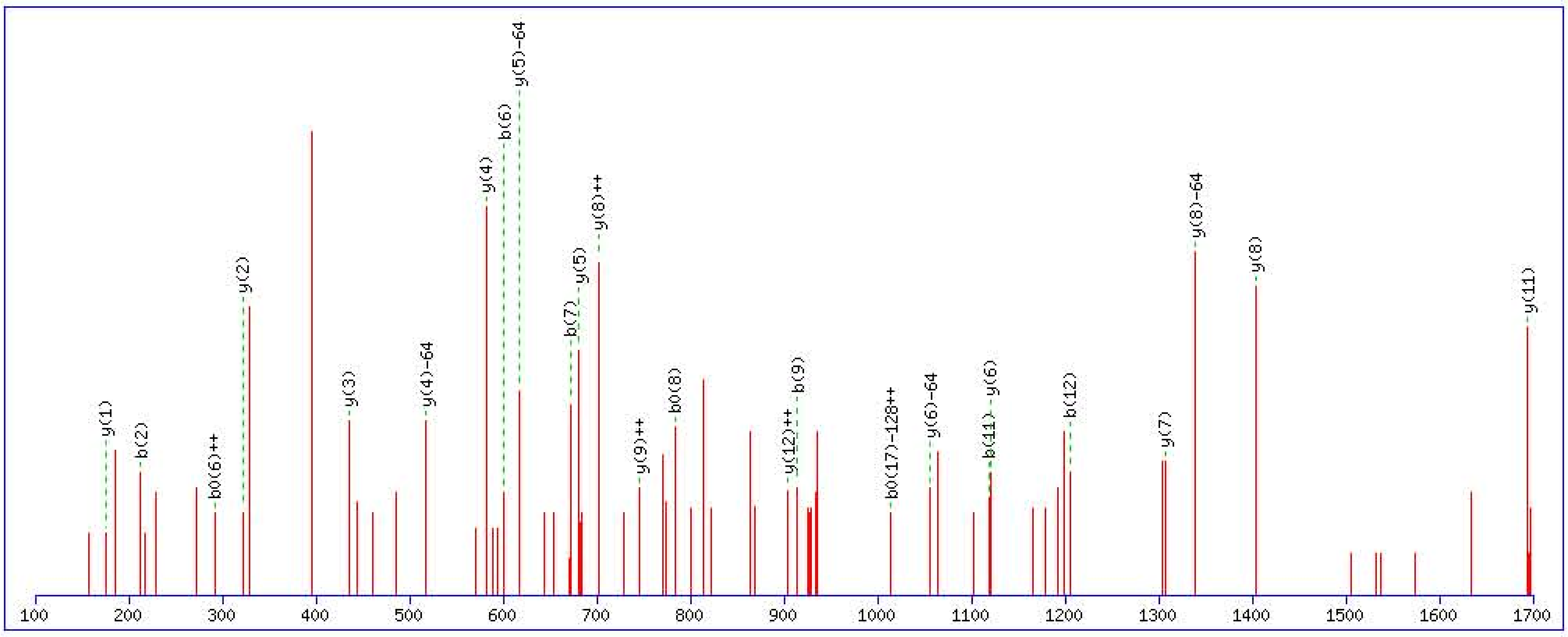
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVEGSDAEIGMSPWQVMLFR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

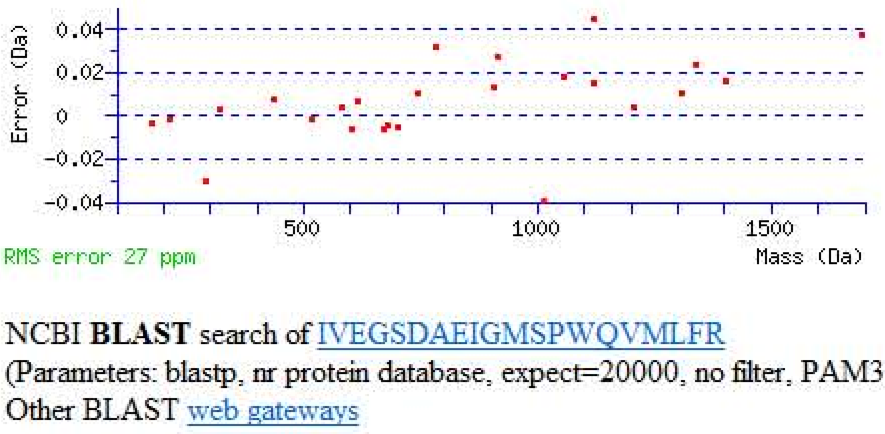
Match to Query 52165: 2607.285552 from(870.102460,3+) rtinseconds(2738) index(51922)
Title: Locus:1.1.1.3000.23 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

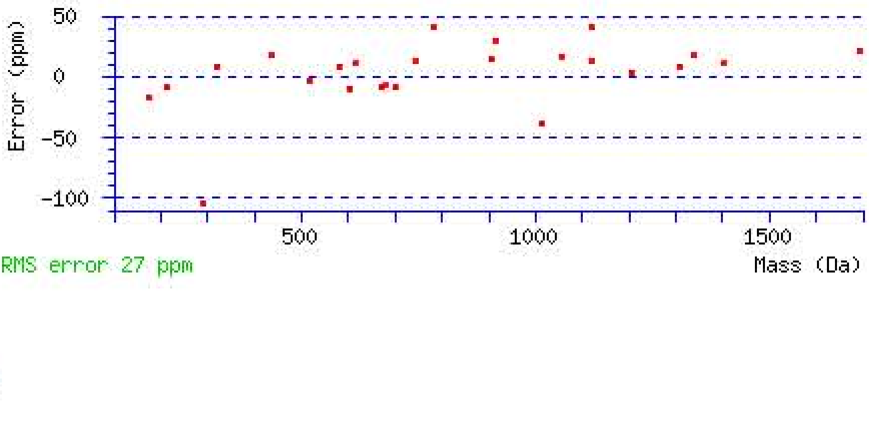
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2607.253540
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M11    : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q15    : Biotin:Thermo-21345 (Q)
M17    : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 41  Expect: 0.0023
Matches : 25/312 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					I							20
2	***213.159754***	107.083515					V	2495.176752	1248.092014	2478.150203	1239.578739	2477.166187	1239.086731	19
3	342.202347	171.604811			324.191782	162.599529	E	2396.108338	1198.557807	2379.081789	1190.044532	2378.097773	1189.552524	18
4	399.223811	200.115543			381.213246	191.110261	G	2267.065745	1134.036510	2250.039196	1125.523236	2249.055180	1125.031228	17
5	486.255839	243.631557			468.245274	234.626275	S	2210.044281	1105.525778	2193.017732	1097.012504	2192.033716	1096.520496	16
6	***601.282782***	301.145029			583.272217	292.139747	D	2123.012253	1062.009764	2105.985704	1053.496490	2105.001688	1053.004482	15
7	***672.319896***	336.663586			654.309331	327.658303	A	2007.985310	1004.496293	1990.958761	995.983019	1989.974745	995.491011	14
8	801.362489	401.184883			783.351924	392.179600	E	1936.948196	968.977736	1919.921647	960.464462	1918.937631	959.972454	13
9	***914.446553***	457.726915			896.435988	448.721632	I	1807.905603	904.456440	1790.879054	895.943165	1789.895038	895.451157	12
10	971.468017	486.237647			953.457452	477.232364	G	***1694.821539***	847.914408	1677.794990	839.401133	1676.810974	838.909125	11
11	***1118.503417***	559.755346			1100.492852	550.750064	M	1637.800075	819.403676	1620.773526	810.890401	1619.789510	810.398393	10
12	***1205.535445***	603.271361			1187.524880	594.266078	S	1490.764675	745.885976	1473.738126	737.372701	1472.754110	736.880693	9
13	1302.588209	651.797743			1284.577644	642.792460	P	***1403.732647***	702.369962	1386.706098	693.856687			8
14	1488.667522	744.837399			1470.656957	735.832116	W	***1306.679883***	653.843580	1289.653334	645.330305			7
15	1927.892848	964.450062	1910.866299	955.936788	1909.882283	955.444780	Q	***1120.600570***	560.803923	1103.574021	552.290649			6
16	2026.961262	1013.984269	2009.934713	1005.470995	2008.950697	1004.978987	V	***681.375244***	341.191260	664.348695	332.677986			5
17	2173.996662	1087.501969	2156.970113	1078.988694	2155.986097	1078.496686	M	***582.306830***	291.657053	565.280281	283.143779			4
18	2287.080726	1144.044001	2270.054177	1135.530726	2269.070161	1135.038719	L	***435.271430***	218.139353	418.244881	209.626078			3
19	2434.149140	1217.578208	2417.122591	1209.064933	2416.138575	1208.572925	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
40.6	2607.253540	0.032012	IVEGSDAEIGMSPWQVMLFR

Mascot: http://www.matrixscience.com/

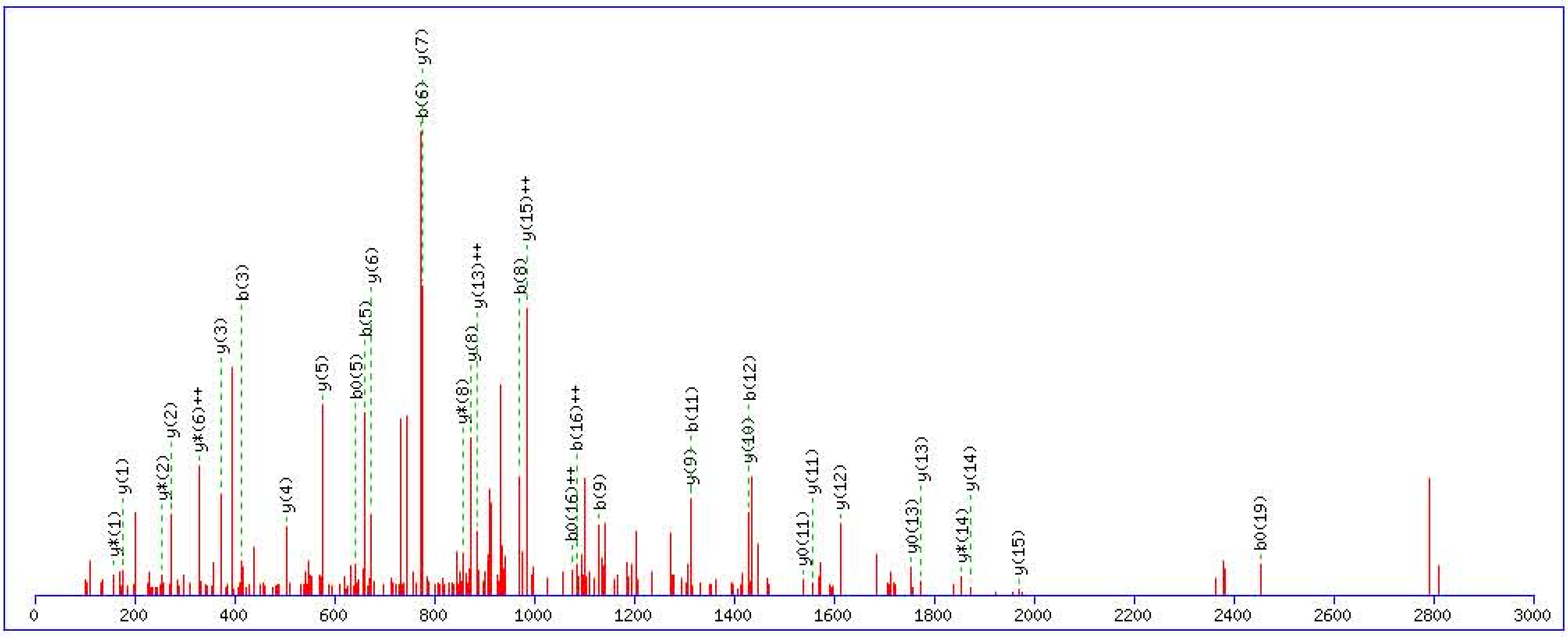
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RQECSIPVCGQDQVTVAMTPR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

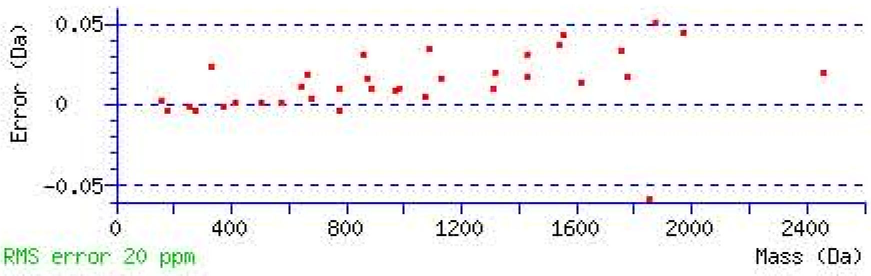
Match to Query 53189: 2742.337542 from(915.119790,3+) rtinseconds(1967) index(47205)
Title: Locus:1.1.1.2733.21 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

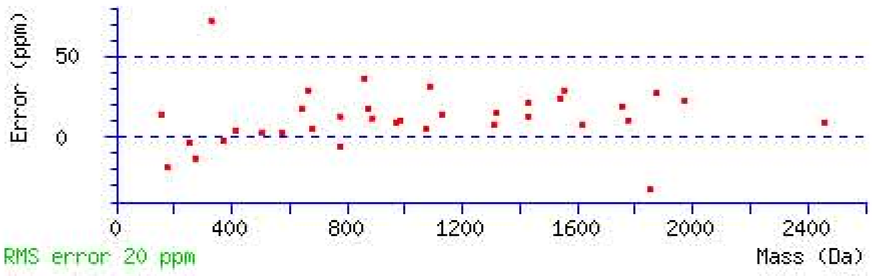
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2742.307404
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 72  Expect: 1.7e-006
Matches : 35/232 fragment ions using 77 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			R							21
2	285.166965	143.087121	268.140416	134.573846			Q	2587.213551	1294.110413	2570.187002	1285.597139	2569.202986	1285.105131	20
3	**414.209558**	207.608417	397.183009	199.095143	396.198993	198.603135	E	2459.154973	1230.081124	2442.128424	1221.567850	2441.144408	1221.075842	19
4	574.240207	287.623742	557.213658	279.110467	556.229642	278.618459	C	2330.112380	1165.559828	2313.085831	1157.046553	2312.101815	1156.554545	18
5	**661.272235**	331.139756	644.245686	322.626481	643.261670	322.134473	S	2170.081731	1085.544503	2153.055182	1077.031229	2152.071166	1076.539221	17
6	**774.356299**	387.681788	757.329750	379.168513	756.345734	378.676505	I	2083.049703	1042.028489	2066.023154	1033.515215	2065.039138	1033.023207	16
7	871.409063	436.208170	854.382514	427.694895	853.398498	427.202887	P	***1969.965639***	985.486458	1952.939090	976.973183	1951.955074	976.481175	15
8	**970.477477**	485.742377	953.450928	477.229102	952.466912	476.737094	V	***1872.912875***	936.960076	1855.886326	928.446801	1854.902310	927.954793	14
9	**1130.508126**	565.757701	1113.481577	557.244427	1112.497561	556.752418	C	***1773.844461***	887.425868	1756.817912	878.912594	1755.833896	878.420586	13
10	1187.529590	594.268433	1170.503041	585.755158	1169.519025	585.263150	G	***1613.813812***	807.410544	1596.787263	798.897270	1595.803247	798.405262	12
11	**1315.588168**	658.297722	1298.561619	649.784448	1297.577603	649.292440	Q	***1556.792348***	778.899812	1539.765799	770.386538	1538.781783	769.894530	11
12	**1430.615111**	715.811194	1413.588562	707.297919	1412.604546	706.805911	D	***1428.733770***	714.870523	1411.707221	706.357249	1410.723205	705.865241	10
13	1869.840437	935.423857	1852.813888	926.910582	1851.829872	926.418574	Q	***1313.706827***	657.357052	1296.680278	648.843777	1295.696262	648.351769	9
14	1968.908851	984.958064	1951.882302	976.444789	1950.898286	975.952781	V	***874.481501***	437.744389	857.454952	429.231114	856.470936	428.739106	8
15	2069.956530	1035.481903	2052.929981	1026.968628	2051.945965	1026.476620	T	***775.413087***	388.210181	758.386538	379.696907	757.402522	379.204899	7
16	2169.024944	1085.016110	2151.998395	1076.502835	2151.014379	1076.010827	V	***674.365408***	337.686342	657.338859	329.173067	656.354843	328.681059	6
17	2240.062058	1120.534667	2223.035509	1112.021392	2222.051493	1111.529384	A	***575.296994***	288.152135	558.270445	279.638861	557.286429	279.146853	5
18	2371.102543	1186.054909	2354.075994	1177.541635	2353.091978	1177.049627	M	***504.259880***	252.633578	487.233331	244.120303	486.249315	243.628295	4
19	2472.150222	1236.578749	2455.123673	1228.065474	2454.139657	1227.573466	T	***373.219395***	187.113335	356.192846	178.600061	355.208830	178.108053	3
20	2569.202986	1285.105131	2552.176437	1276.591856	2551.192421	1276.099848	P	***272.171716***	136.589496	255.145167	128.076221			2
21							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of RQECSIPVCGQDQVTVAMTPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
72.1	2742.307404	0.030138	RQECSIPVCGQDQVTVAMTPR
50.6	2742.307404	0.030138	RQECSIPVCGQDQVTVAMTPR
10.1	2742.307404	0.030138	RQECSIPVCGQDQVTVAMTPR

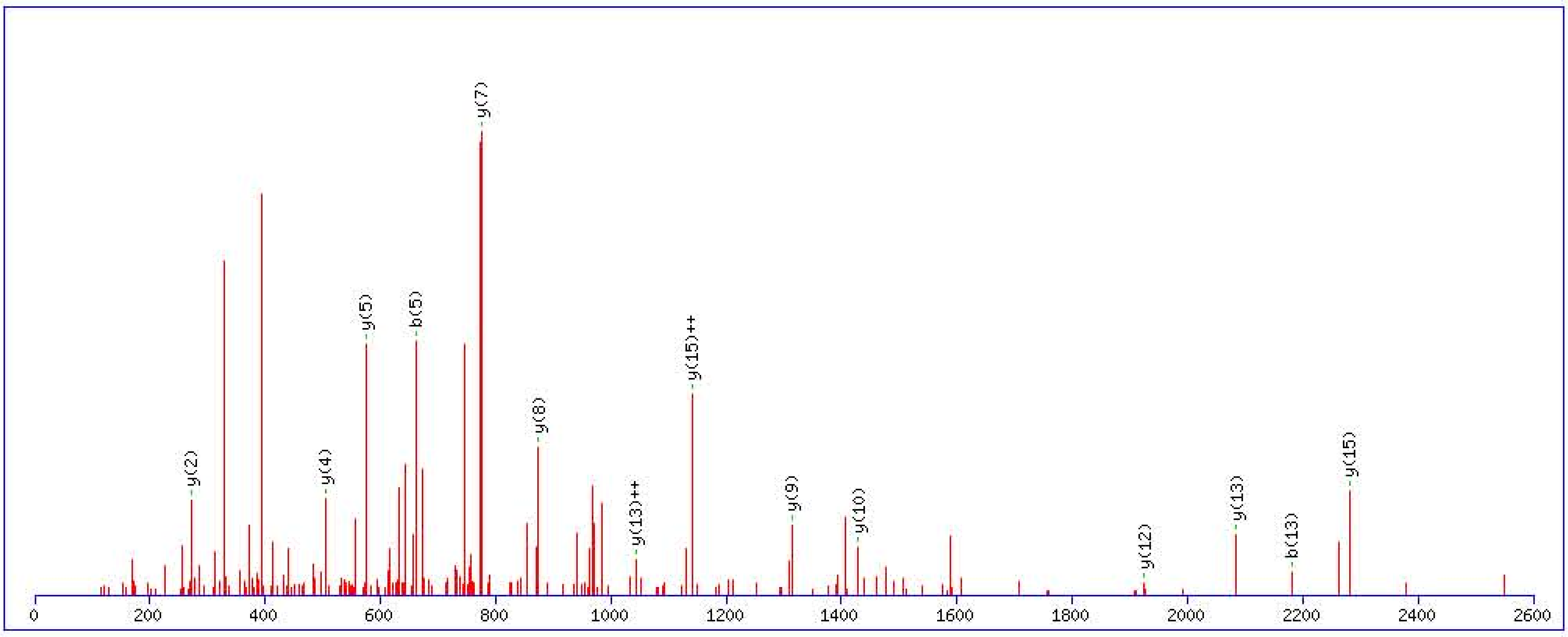
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RQECSIPVCGQDQVTVAMTPR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

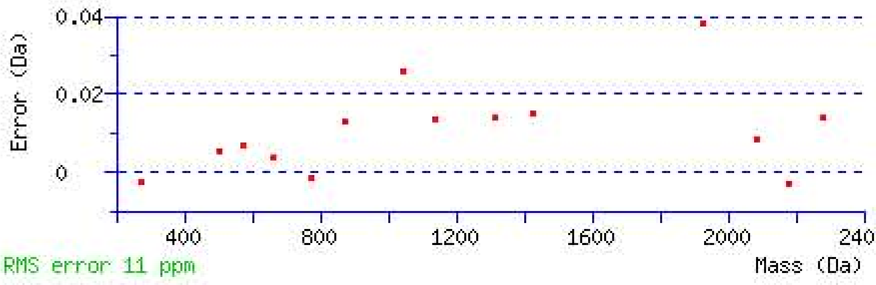
Match to Query 56433: 3053.498336 from(764.381860,4+) rtinseconds(2205) index(48628)
Title: Locus:1.1.1.2816.7 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

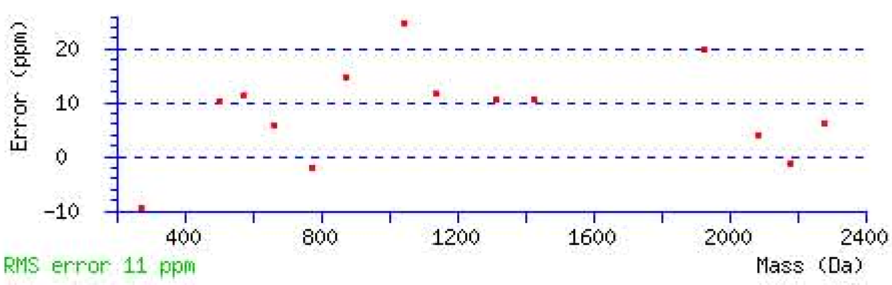
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3053.474152
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 55  Expect: 8.3e-005
Matches : 14/232 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	157.108387	79.057831	140.081838	70.544557			R							21
2	285.166965	143.087121	268.140416	134.573846			Q	2898.380299	1449.693787	2881.353750	1441.180513	2880.369734	1440.688505	20
3	414.209558	207.608417	397.183009	199.095143	396.198993	198.603135	E	2770.321721	1385.664498	2753.295172	1377.151224	2752.311156	1376.659216	19
4	574.240207	287.623742	557.213658	279.110467	556.229642	278.618459	C	2641.279128	1321.143202	2624.252579	1312.629927	2623.268563	1312.137919	18
5	**661.272235**	331.139756	644.245686	322.626481	643.261670	322.134473	S	2481.248479	1241.127877	2464.221930	1232.614603	2463.237914	1232.122595	17
6	774.356299	387.681788	757.329750	379.168513	756.345734	378.676505	I	2394.216451	1197.611863	2377.189902	1189.098589	2376.205886	1188.606581	16
7	871.409063	436.208170	854.382514	427.694895	853.398498	427.202887	P	***2281.132387***	1141.069831	2264.105838	1132.556557	2263.121822	1132.064549	15
8	970.477477	485.742377	953.450928	477.229102	952.466912	476.737094	V	2184.079623	1092.543449	2167.053074	1084.030175	2166.069058	1083.538167	14
9	1130.508126	565.757701	1113.481577	557.244427	1112.497561	556.752418	C	***2085.011209***	1043.009242	2067.984660	1034.495968	2067.000644	1034.003960	13
10	1187.529590	594.268433	1170.503041	585.755158	1169.519025	585.263150	G	***1924.980560***	962.993918	1907.954011	954.480643	1906.969995	953.988635	12
11	1626.754916	813.881096	1609.728367	805.367822	1608.744351	804.875814	Q	1867.959096	934.483186	1850.932547	925.969911	1849.948531	925.477903	11
12	1741.781859	871.394568	1724.755310	862.881293	1723.771294	862.389285	D	***1428.733770***	714.870523	1411.707221	706.357248	1410.723205	705.865240	10
13	**2181.007185**	1091.007230	2163.980636	1082.493956	2162.996620	1082.001948	Q	***1313.706827***	657.357051	1296.680278	648.843777	1295.696262	648.351769	9
14	2280.075599	1140.541437	2263.049050	1132.028163	2262.065034	1131.536155	V	***874.481501***	437.744388	857.454952	429.231114	856.470936	428.739106	8
15	2381.123278	1191.065277	2364.096729	1182.552002	2363.112713	1182.059994	T	***775.413087***	388.210181	758.386538	379.696907	757.402522	379.204899	7
16	2480.191692	1240.599484	2463.165143	1232.086209	2462.181127	1231.594201	V	674.365408	337.686342	657.338859	329.173067	656.354843	328.681059	6
17	2551.228806	1276.118041	2534.202257	1267.604766	2533.218241	1267.112758	A	***575.296994***	288.152135	558.270445	279.638861	557.286429	279.146853	5
18	2682.269291	1341.638283	2665.242742	1333.125009	2664.258726	1332.633001	M	***504.259880***	252.633578	487.233331	244.120303	486.249315	243.628295	4
19	2783.316970	1392.162123	2766.290421	1383.648848	2765.306405	1383.156840	T	373.219395	187.113335	356.192846	178.600061	355.208830	178.108053	3
20	2880.369734	1440.688505	2863.343185	1432.175230	2862.359169	1431.683222	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
55.5	3053.474152	0.024184	RQECSIPVCGQDQVTVAMTPR
18.8	3053.474152	0.024184	RQECSIPVCGQDQVTVAMTPR
4.0	3053.474152	0.024184	RQECSIPVCGQDQVTVAMTPR

Mascot: http://www.matrixscience.com/

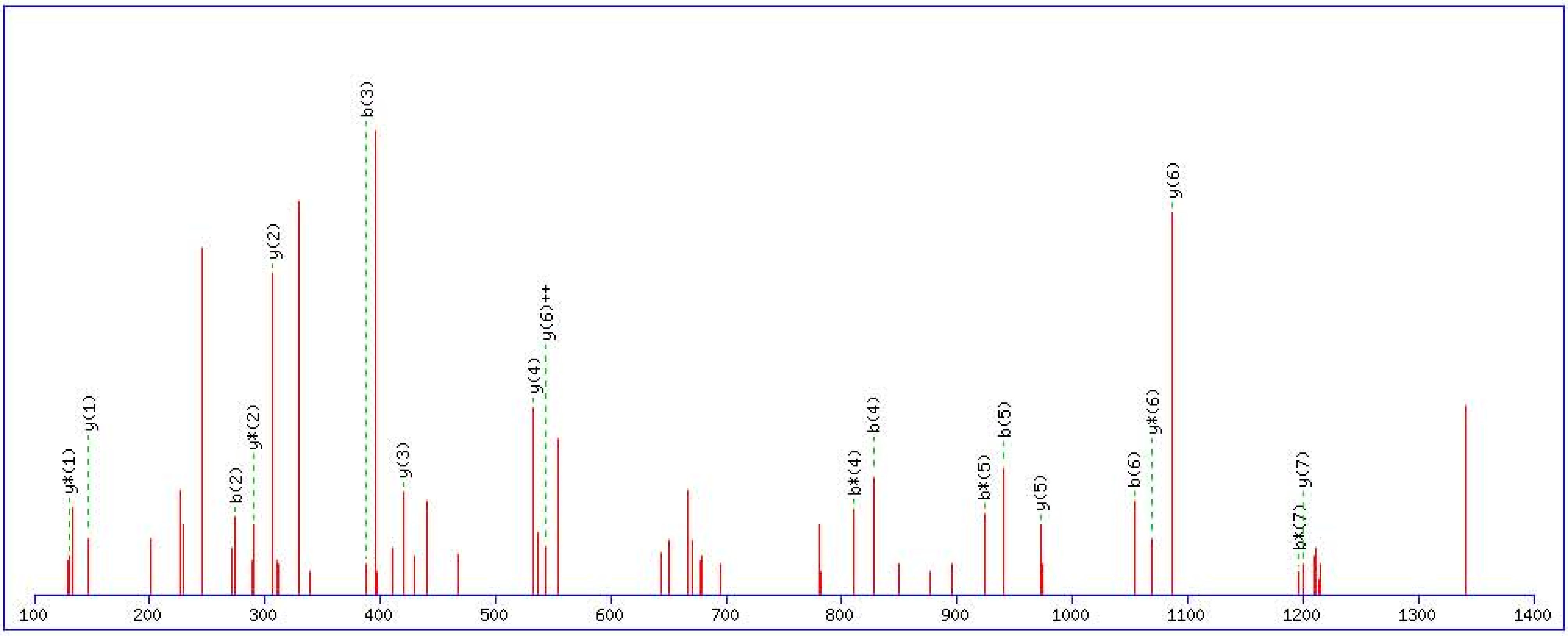
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **CINQLLCK**
Found in **SEPP1_HUMAN**, Selenoprotein P OS=Homo sapiens GN=SEPP1 PE=1 SV=3

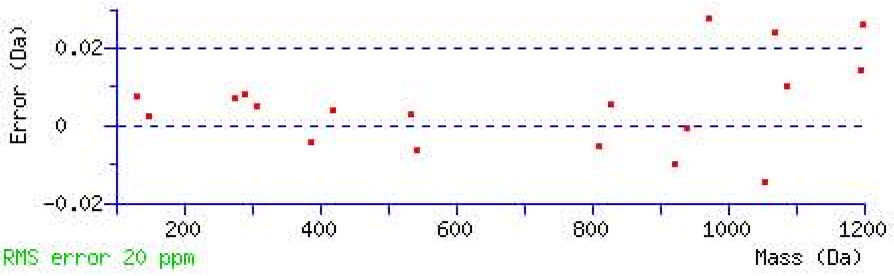
Match to Query 24921: 1358.684108 from(680.349330,2+) rtinseconds(2005) index(62621)
Title: Locus:1.1.1.3324.20 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

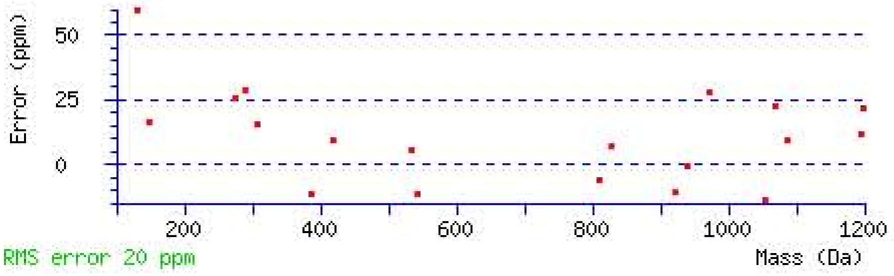
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1358.687256
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.0063
Matches : 19/52 fragment ions using 48 most intense peaks   (help)
```

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	161.037925	81.022600			C					8
2	**274.121989**	137.564632			I	***1199.663898***	600.335587	1182.637349	591.822313	7
3	**388.164916**	194.586096	371.138367	186.072822	N	***1086.579834***	543.793555	1069.553285	535.280281	6
4	**827.390242**	414.198759	810.363693	405.685485	Q	***972.536907***	486.772092	955.510358	478.258817	5
5	**940.474306**	470.740791	923.447757	462.227517	L	***533.311581***	267.159429	516.285032	258.646154	4
6	**1053.558370**	527.282823	1036.531821	518.769549	L	***420.227517***	210.617396	403.200968	202.104122	3
7	1213.589019	607.298148	1196.562470	598.784873	C	***307.143453***	154.075365	290.116904	145.562090	2
8					K	***147.112804***	74.060040	130.086255	65.546765	1





NCBI **BLAST** search of CINQLLCK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.5	1358.687256	-0.003148	CINQLLCK
4.0	1358.701630	-0.017522	KKIYAMGGGSYGK

Mascot: http://www.matrixscience.com/

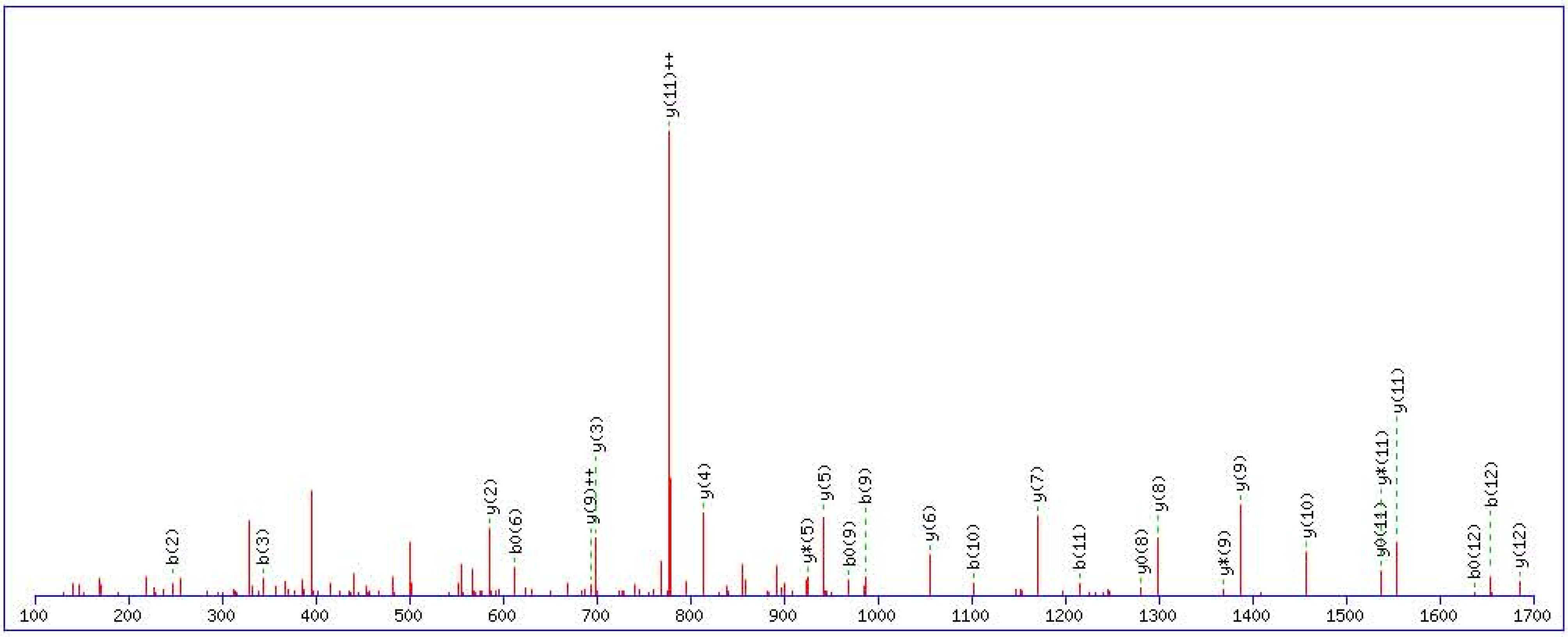
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DMPASEDLQDLQK**
Found in **SEPP1_HUMAN**, Selenoprotein P OS=Homo sapiens GN=SEPP1 PE=1 SV=3

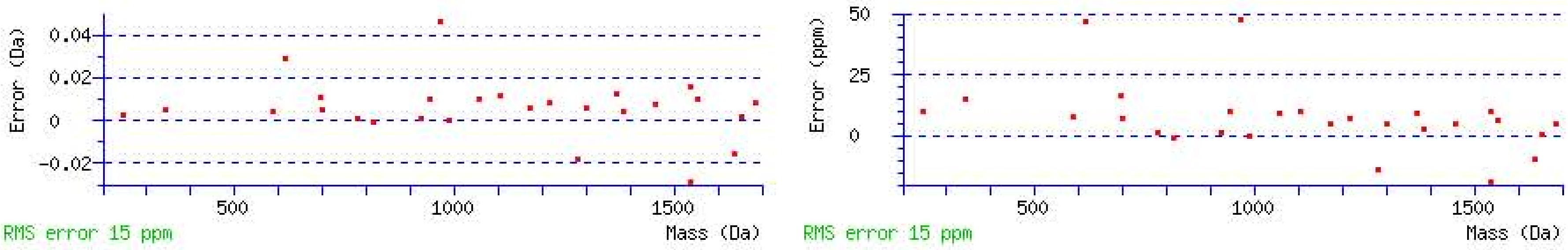
Match to Query 38485: 1799.852368 from(900.933460,2+) rtinseconds(2189) index(34168)
Title: Locus:1.1.1.3311.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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): 1799.843353
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 74  Expect: 2.1e-007
Matches : 27/122 fragment ions using 46 most intense peaks    (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	116.034219	58.520748			98.023654	49.515465	D							13
2	**247.074704**	124.040990			229.064139	115.035708	M	***1685.823706***	843.415491	1668.797157	834.902217	1667.813141	834.410209	12
3	**344.127468**	172.567372			326.116903	163.562089	P	***1554.783221***	777.895249	1537.756672	769.381974	1536.772656	768.889966	11
4	415.164582	208.085929			397.154017	199.080646	A	***1457.730457***	729.368867	1440.703908	720.855592	1439.719892	720.363584	10
5	502.196610	251.601943			484.186045	242.596660	S	***1386.693343***	693.850310	1369.666794	685.337035	1368.682778	684.845027	9
6	631.239203	316.123240			613.228638	307.117957	E	***1299.661315***	650.334296	1282.634766	641.821021	1281.650750	641.329013	8
7	746.266146	373.636711			728.255581	364.631428	D	***1170.618722***	585.812999	1153.592173	577.299725	1152.608157	576.807717	7
8	859.350210	430.178743			841.339645	421.173460	L	***1055.591779***	528.299528	1038.565230	519.786253	1037.581214	519.294245	6
9	**987.408788**	494.208032	970.382239	485.694757	969.398223	485.202749	Q	***942.507715***	471.757496	925.481166	463.244221	924.497150	462.752213	5
10	**1102.435731**	551.721504	1085.409182	543.208229	1084.425166	542.716221	D	***814.449137***	407.728207	797.422588	399.214932	796.438572	398.722924	4
11	**1215.519795**	608.263535	1198.493246	599.750261	1197.509230	599.258253	L	***699.422194***	350.214735	682.395645	341.701461			3
12	**1654.745121**	827.876199	1637.718572	819.362924	1636.734556	818.870916	Q	***586.338130***	293.672703	569.311581	285.159429			2
13							K	147.112804	74.060040	130.086255	65.546765			1



NCBI **BLAST** search of DMPASEDLQDLQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
73.6	1799.843353	0.009015	DMPASEDLQDLQK
36.8	1799.843353	0.009015	DMPASEDLQDLQK
2.3	1799.855057	-0.002689	GDETPREPSSWGARAGK

Mascot: http://www.matrixscience.com/

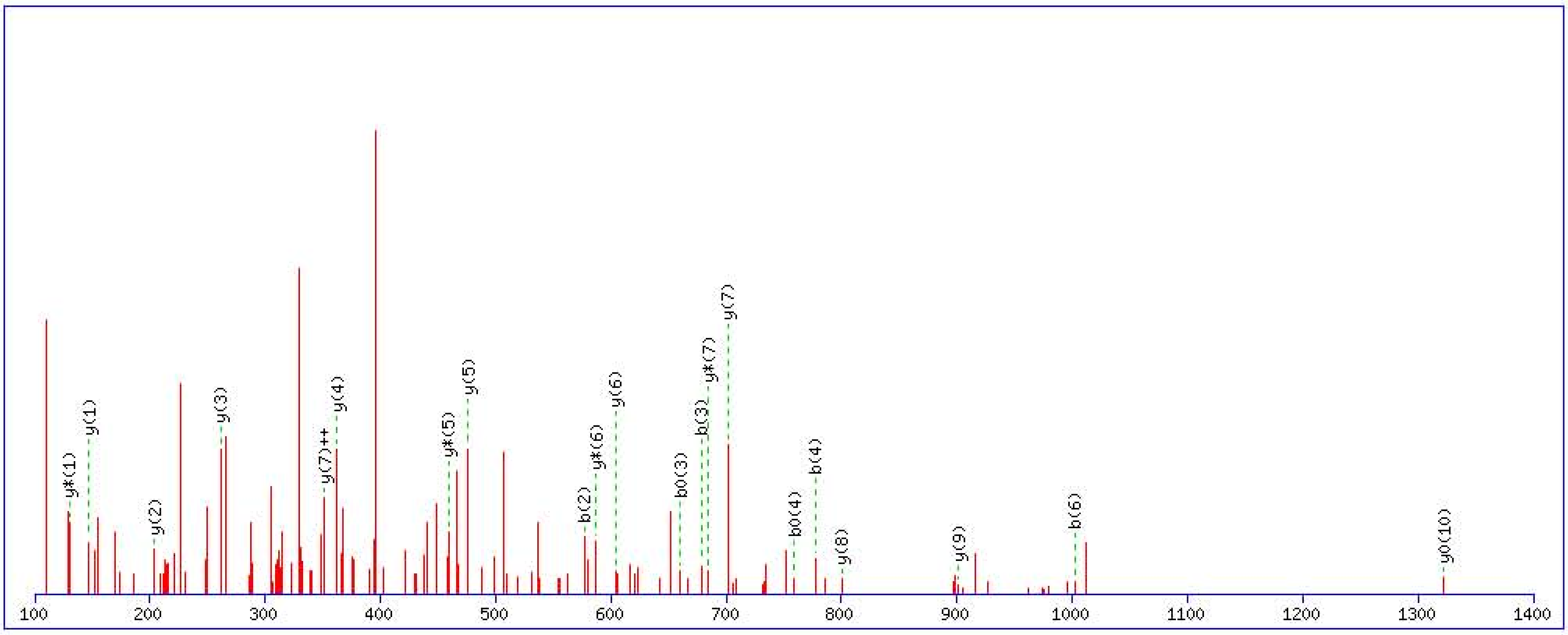
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQTVPQNTGGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

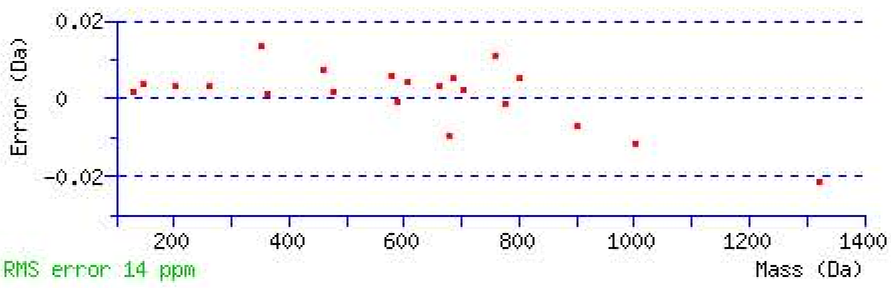
Match to Query 29354: 1476.752712 from(493.258180,3+) rtinseconds(1227) index(58532)
Title: Locus:1.1.1.3053.4 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

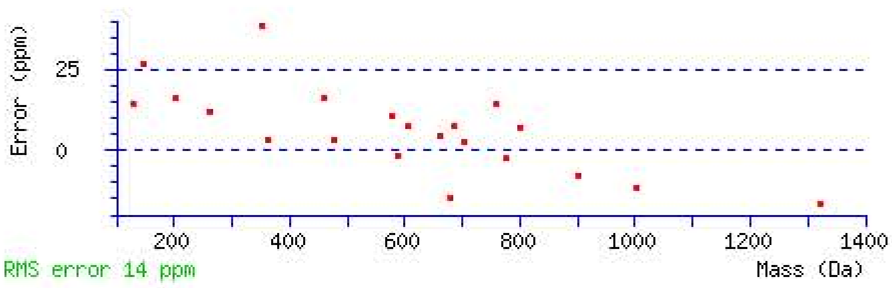


Monoisotopic mass of neutral peptide Mr(calc): 1476.750748
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 31 **Expect:** 0.003
Matches : 21/108 fragment ions using 62 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	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



RMS error 14 ppm



RMS error 14 ppm

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
31.3	1476.750748	0.001964	HQTVPQNTGGK
19.5	1476.750748	0.001964	HQTVPQNTGGK
4.3	1476.736115	0.016597	HQEALIGQSFYGK

Mascot: http://www.matrixscience.com/

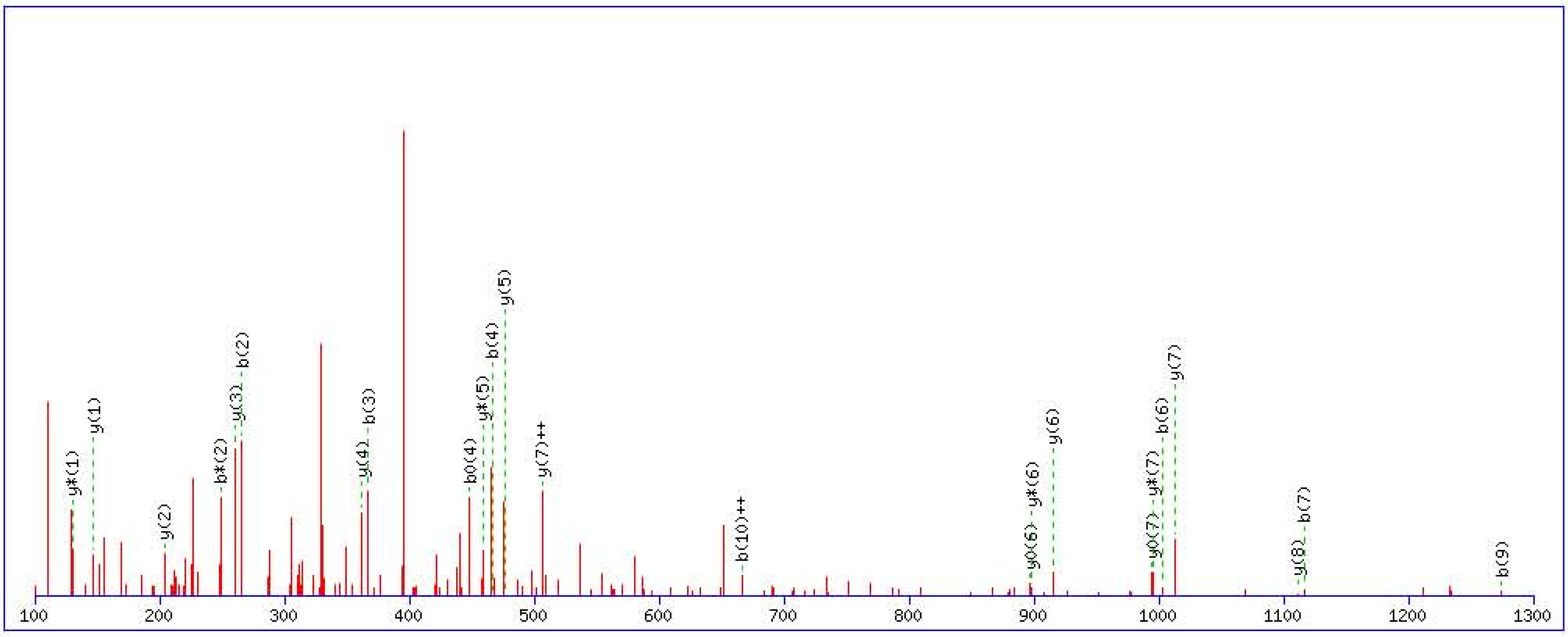
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQTVPQNTGGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

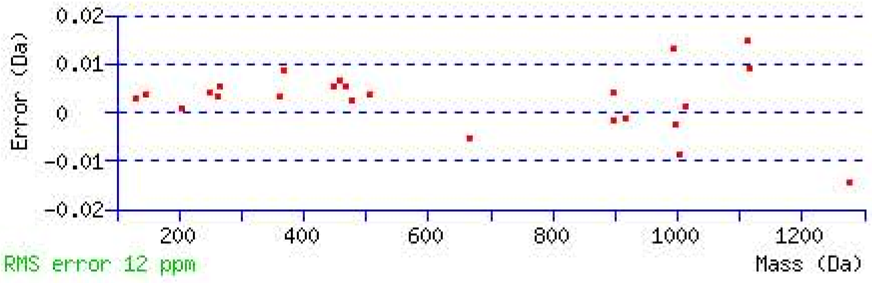
Match to Query 29355: 1476.752742 from(493.258190,3+) rtinseconds(1201) index(58459)
Title: Locus:1.1.1.3044.6 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

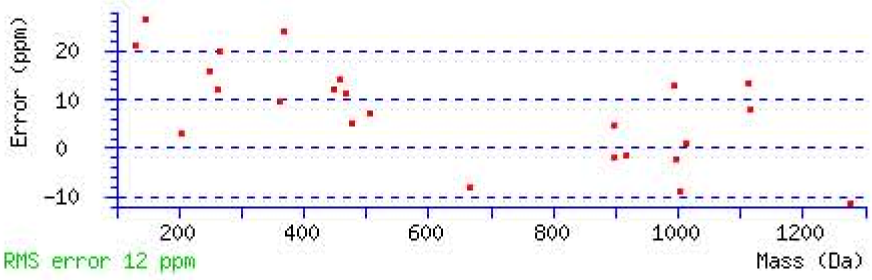
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1476.750748
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.029
Matches : 24/108 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							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
27.2	1476.750748	0.001994	HQTVPQNTGGK
10.2	1476.736115	0.016627	HQEALIGQSFYGK
1.9	1476.750748	0.001994	HQTVPQNTGGK
1.3	1476.750687	0.002055	NKMEIQGNPKYR

Mascot: http://www.matrixscience.com/

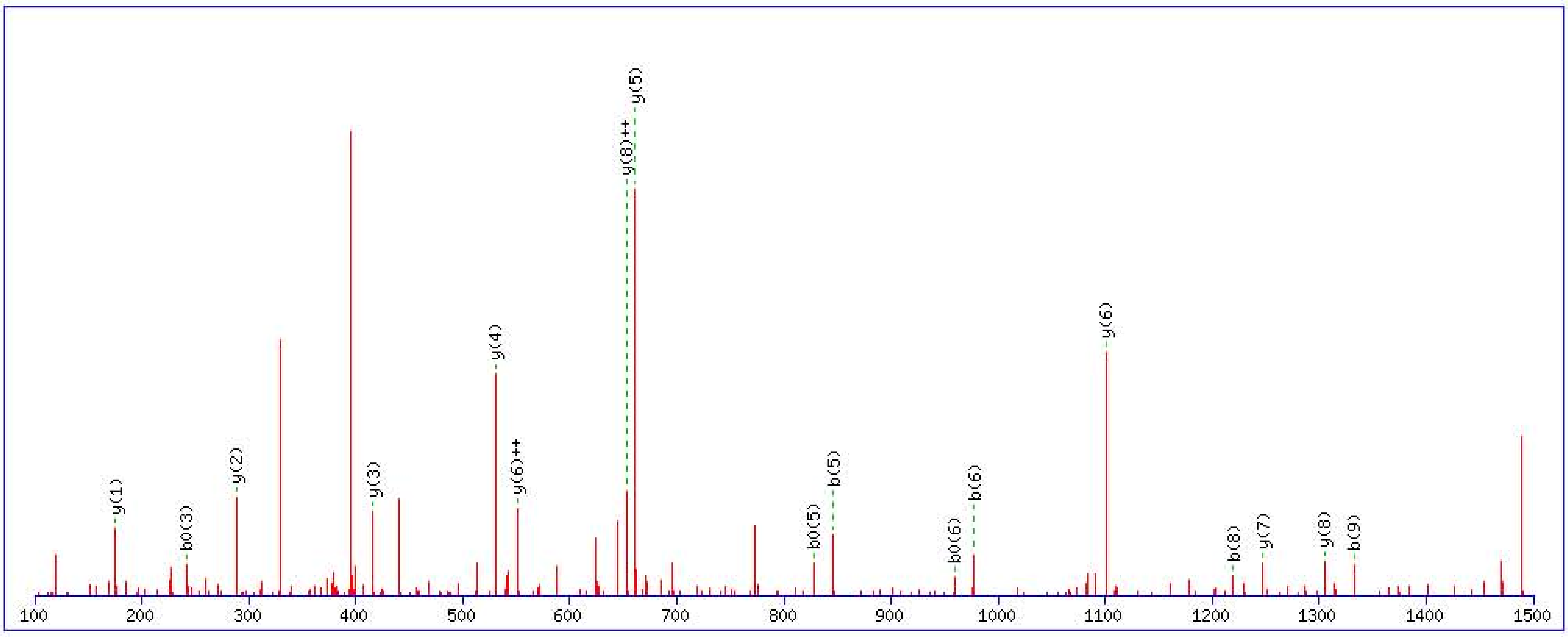
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DSGFQMNQLR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

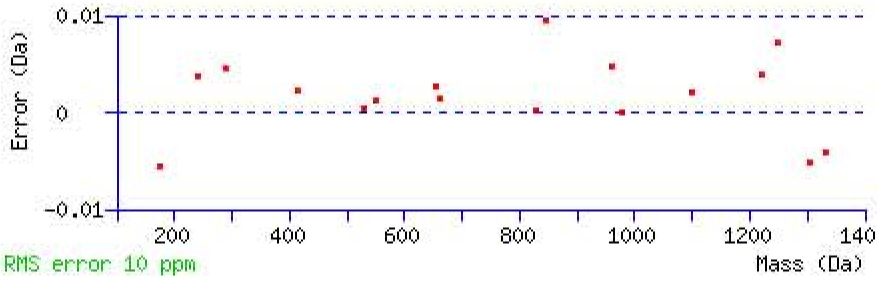
Match to Query 30077: 1505.712868 from(753.863710,2+) rtinseconds(2077) index(62967)
Title: Locus:1.1.1.3349.11 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

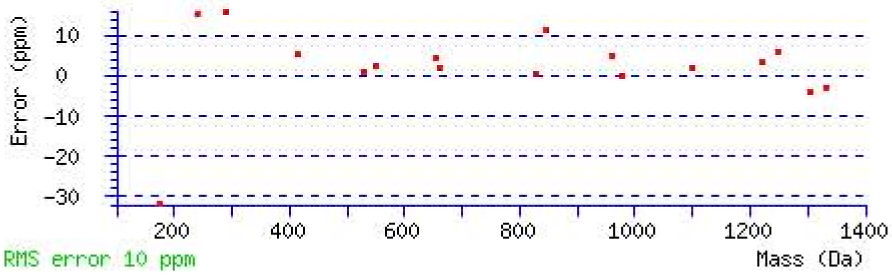


Monoisotopic mass of neutral peptide Mr(calc): 1505.711899
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 57 **Expect:** 3.3e-005
Matches : 17/84 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							10
2	203.066247	102.036761			185.055682	93.031479	S	1391.692238	696.349757	1374.665689	687.836482	1373.681673	687.344474	9
3	260.087711	130.547493			242.077146	121.542211	G	***1304.660210***	652.833743	1287.633661	644.320469			8
4	407.156125	204.081700			389.145560	195.076418	F	***1247.638746***	624.323011	1230.612197	615.809736			7
5	**846.381451**	423.694364	829.354902	415.181089	828.370886	414.689081	Q	***1100.570332***	550.788804	1083.543783	542.275530			6
6	**977.421936**	489.214606	960.395387	480.701331	959.411371	480.209323	M	***661.345006***	331.176141	644.318457	322.662867			5
7	1091.464863	546.236069	1074.438314	537.722795	1073.454298	537.230787	N	***530.304521***	265.655899	513.277972	257.142624			4
8	**1219.523441**	610.265359	1202.496892	601.752084	1201.512876	601.260076	Q	***416.261594***	208.634435	399.235045	200.121160			3
9	**1332.607505**	666.807391	1315.580956	658.294116	1314.596940	657.802108	L	***288.203016***	144.605146	271.176467	136.091871			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 10 ppm



RMS error 10 ppm

NCBI **BLAST** search of DSGFQMNQLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.5	1505.711899	0.000969	DSGFQMNQLR
19.1	1505.711899	0.000969	DSGFQMNQLR
16.7	1505.703140	0.009728	DETMEEQDIKLR
7.3	1505.704025	0.008843	MQMEIDQLR
5.4	1505.691910	0.020958	MEDLLDLDEELR

Mascot: http://www.matrixscience.com/

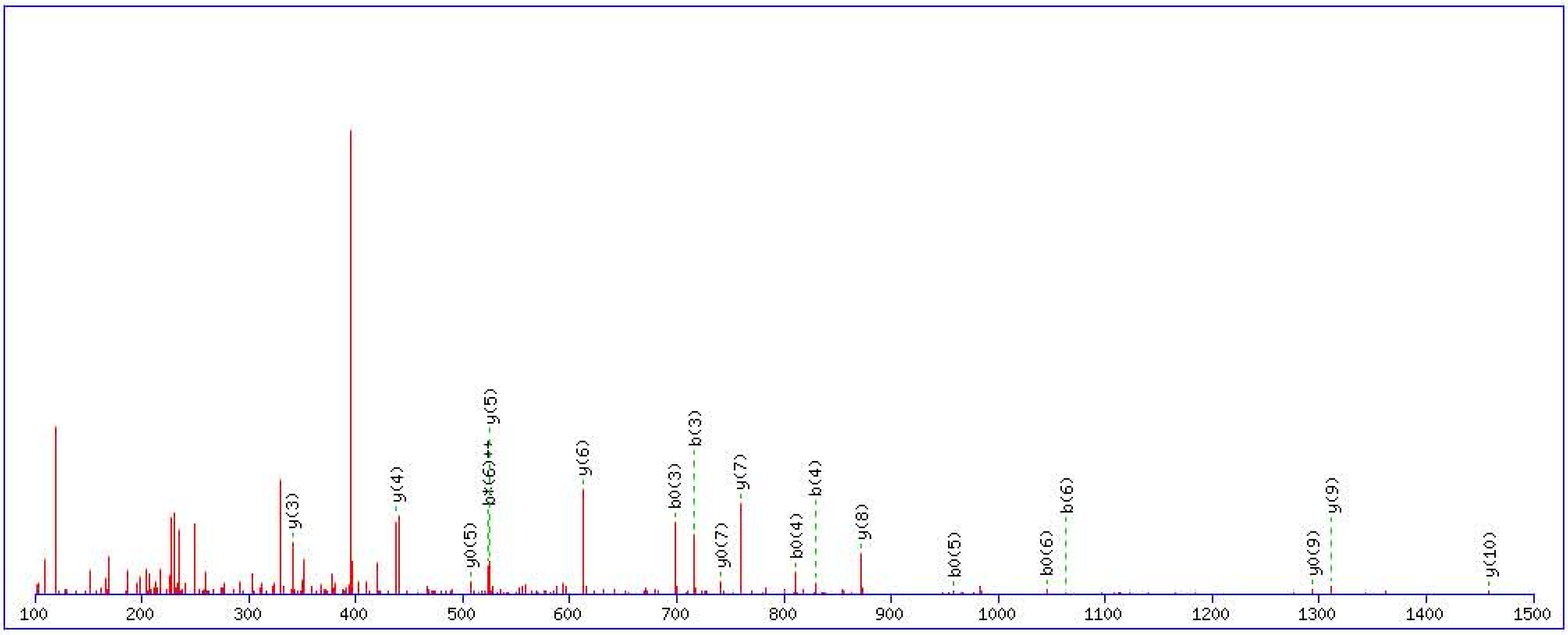
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EFQLFSSPHGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

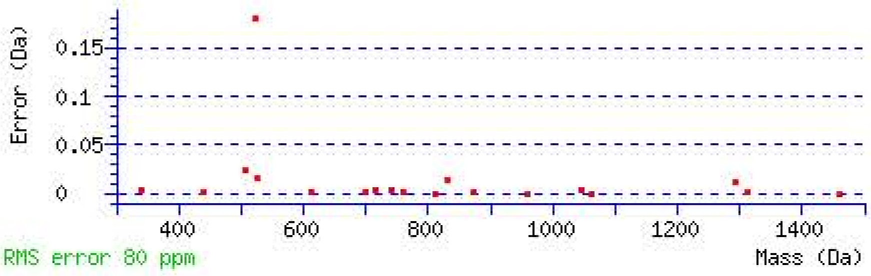
Match to Query 32646: 1586.792262 from(529.938030,3+) rtinseconds(2121) index(63262)
Title: Locus:1.1.1.3365.6 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

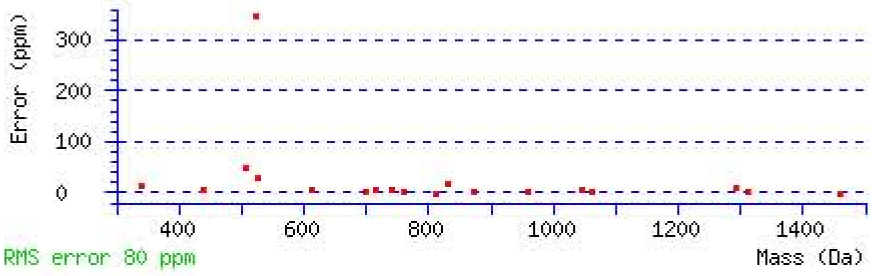
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1586.791534
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 38 **Expect:** 0.0041
Matches : 19/108 fragment ions using 39 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
37.9	1586.791534	0.000728	EFQLFSSPHGK

Mascot: http://www.matrixscience.com/

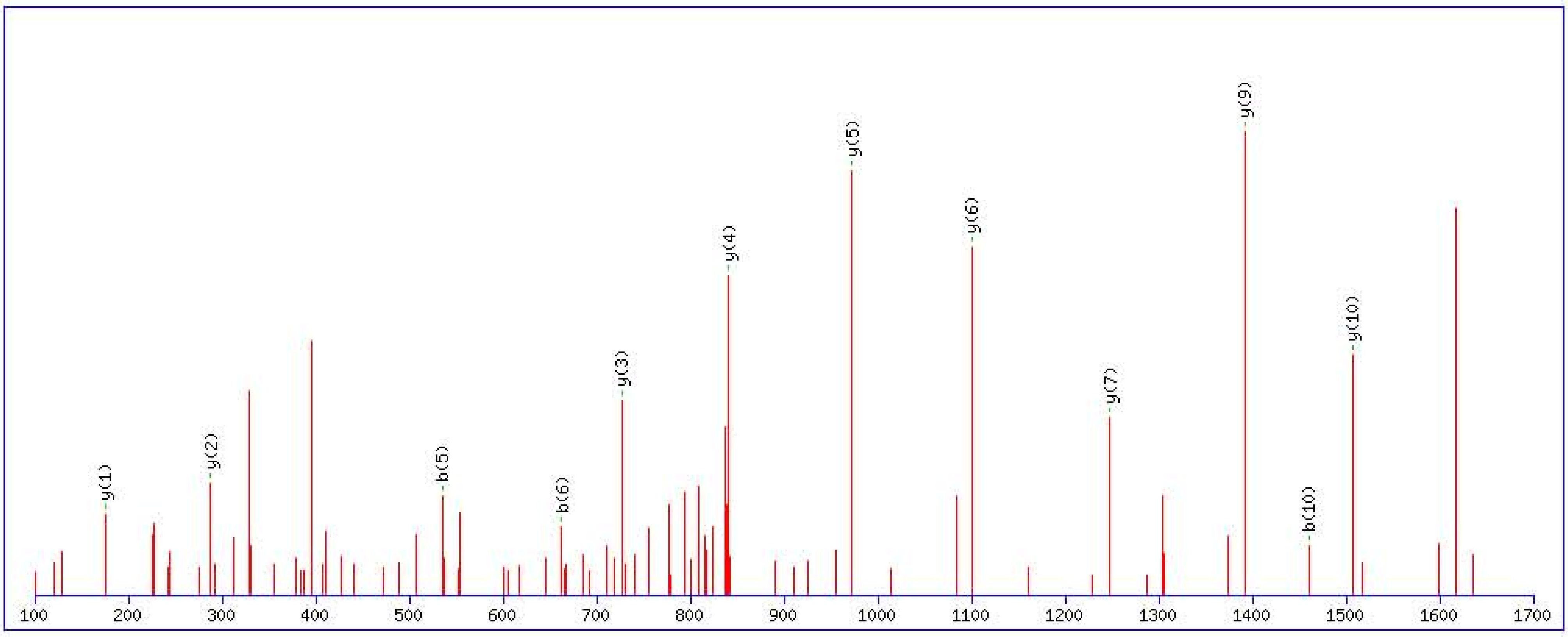
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KDSGFQMNQLR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

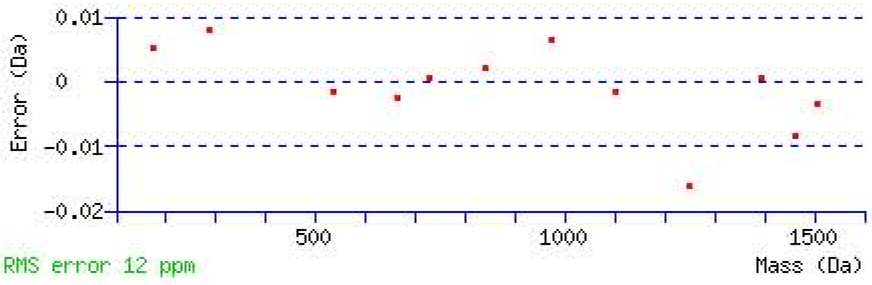
Match to Query 35061: 1633.810228 from(817.912390,2+) rtinseconds(1870) index(61695)
Title: Locus:1.1.1.3277.15 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

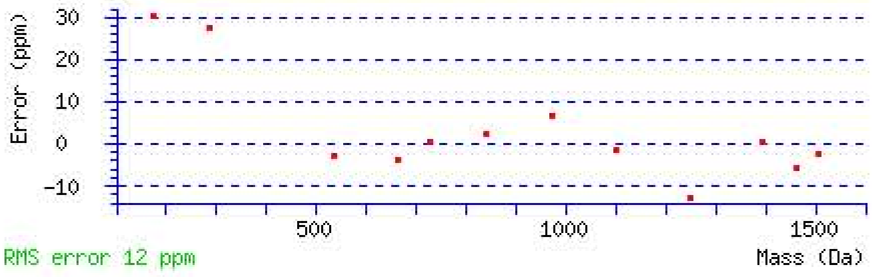
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1633.806854
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 81  Expect: 2e-007
Matches : 12/102 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	**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
80.5	1633.806854	0.003374	KDSGFQMNQLR
33.8	1633.806854	0.003374	KDSGFQMNQLR
14.3	1633.799454	0.010774	DANSFKSRDQR
9.4	1633.834518	-0.024290	KADIGVAMGIAGSDVSK
9.2	1633.832016	-0.021788	MSIFTPTNQIR
8.1	1633.795609	0.014619	KFMEDEQQLR
5.9	1633.822128	-0.011900	QFMKGQVSWGR
5.6	1633.810699	-0.000471	DQTIRIWSCSRGR
5.5	1633.798096	0.012132	QDQEKDNMIEKLK
2.2	1633.817184	-0.006956	HLHEGAKSASAEELR

Mascot: http://www.matrixscience.com/

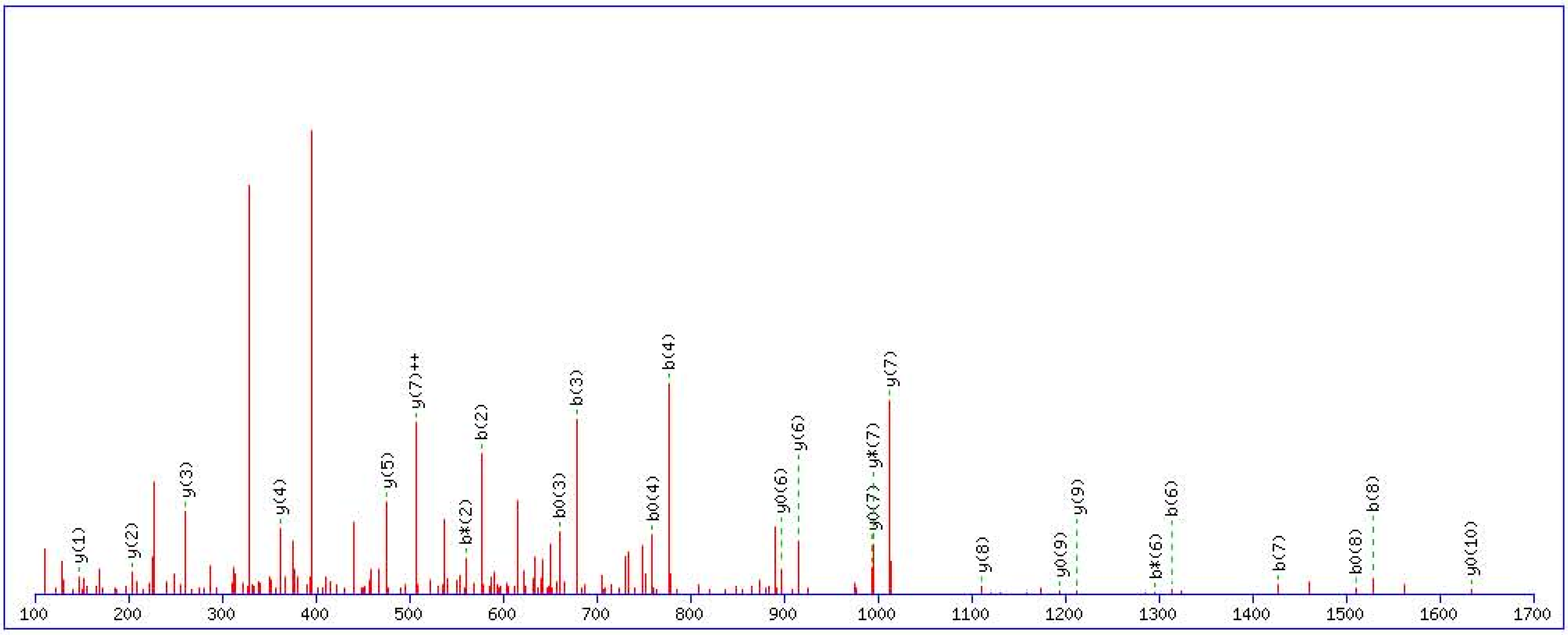
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQTVPQNTGGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

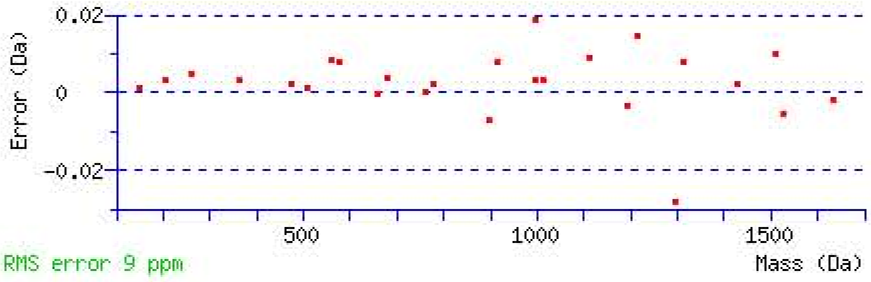
Match to Query 38264: 1787.915832 from(596.979220,3+) rtinseconds(1612) index(60507)
Title: Locus:1.1.1.3187.9 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

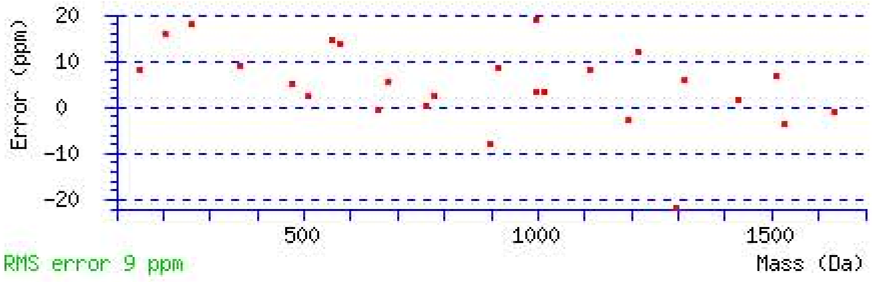


Monoisotopic mass of neutral peptide Mr(calc): 1787.917496
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 33 **Expect:** 0.015
Matches : 26/108 fragment ions using 64 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	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



RMS error 9 ppm



RMS error 9 ppm

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
33.0	1787.917496	-0.001664	HQTVPQNTGGK

Mascot: http://www.matrixscience.com/

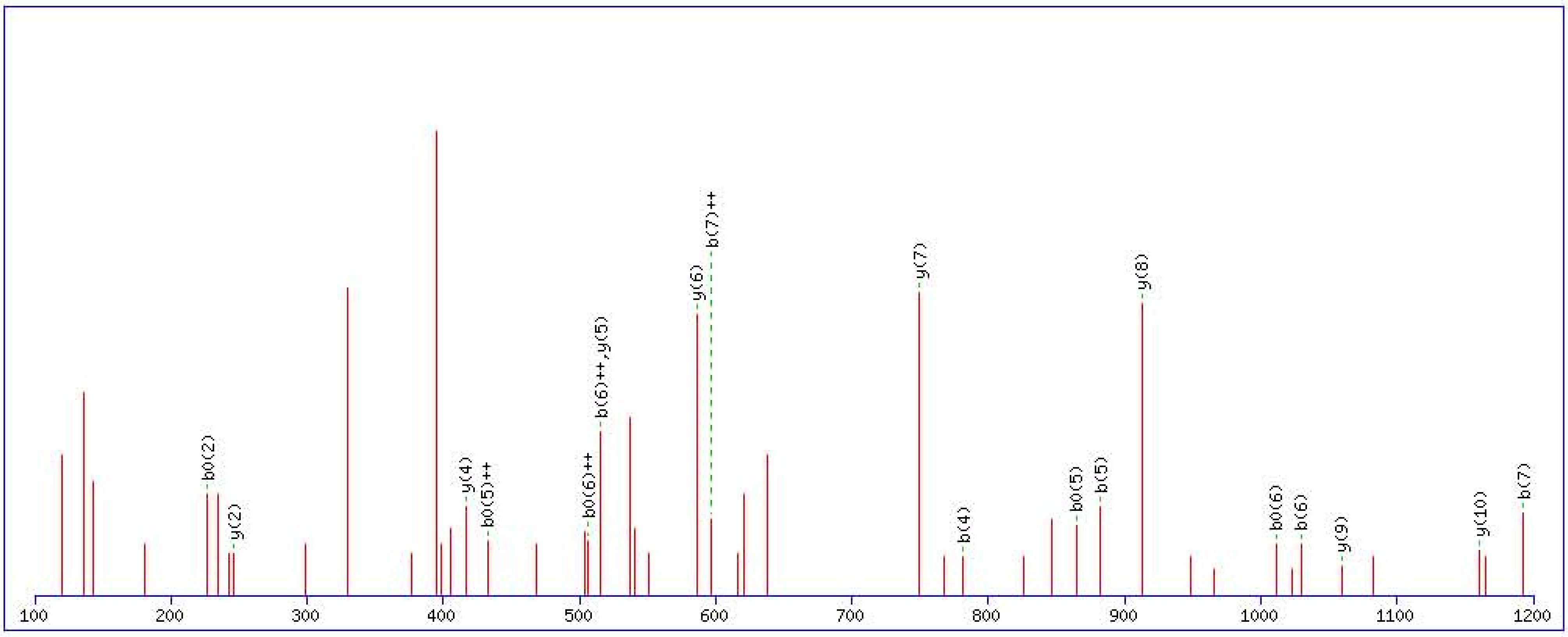
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EDPQTFYYAVAVVK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

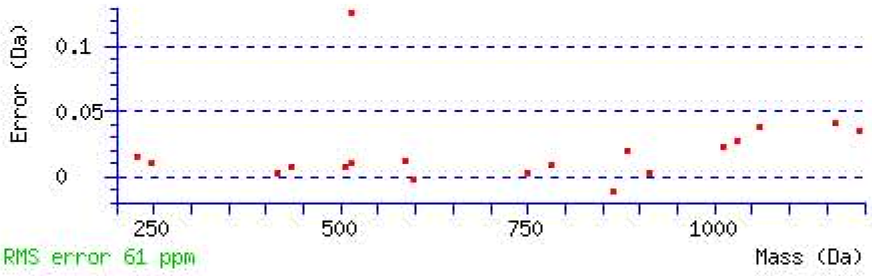
Match to Query 40919: 1939.983702 from(647.668510,3+) rtinseconds(2574) index(65537)
Title: Locus:1.1.1.3523.6 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

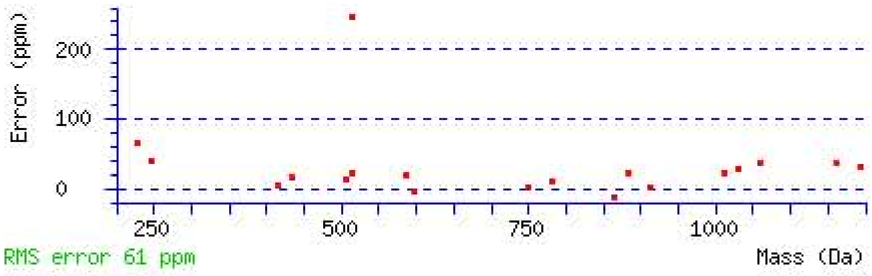
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1939.975372
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.012
Matches : 19/132 fragment ions using 40 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							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
34.2	1939.975372	0.008330	EDPQTFYYAVAVVK

Mascot: http://www.matrixscience.com/

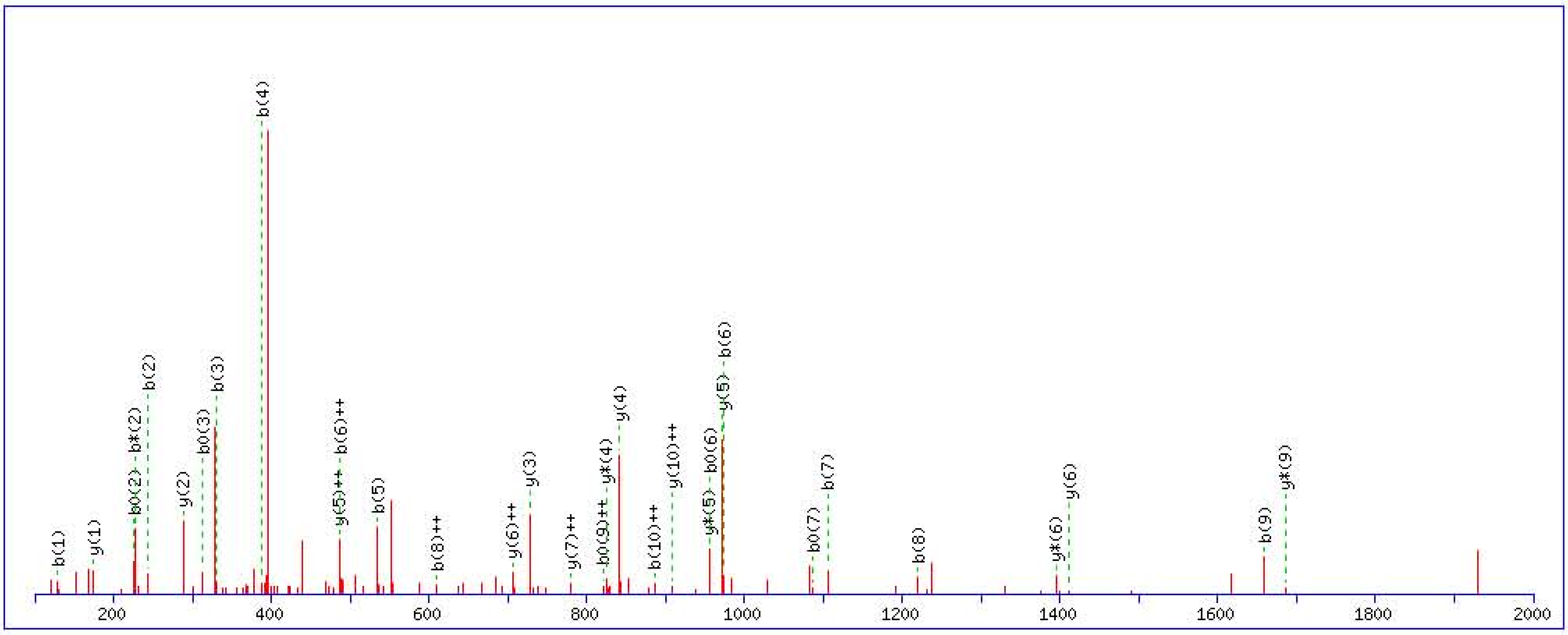
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KDSGFQMNQLR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

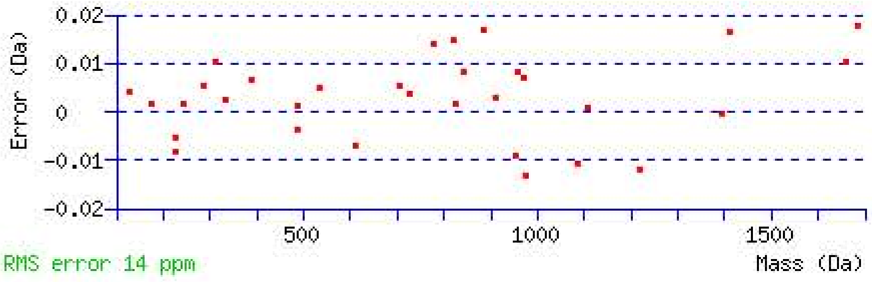
Match to Query 40999: 1944.976152 from(649.332660,3+) rtinseconds(2106) index(63129)
Title: Locus:1.1.1.3359.21 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

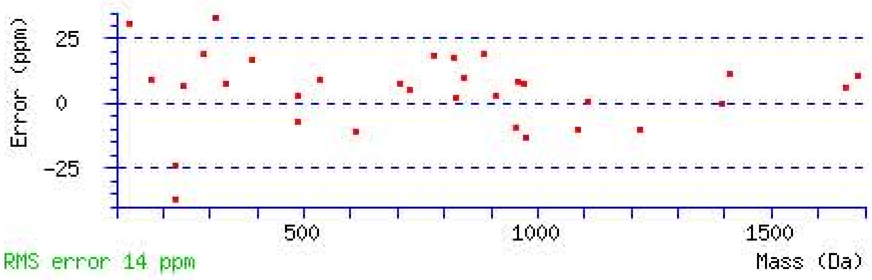
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 30  Expect: 0.0018
Matches : 32/102 fragment ions using 85 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	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
29.5	1944.973602	0.002550	KDSGFQMNQLR
0.3	1944.965729	0.010423	QQITMEMSALR

Mascot: http://www.matrixscience.com/

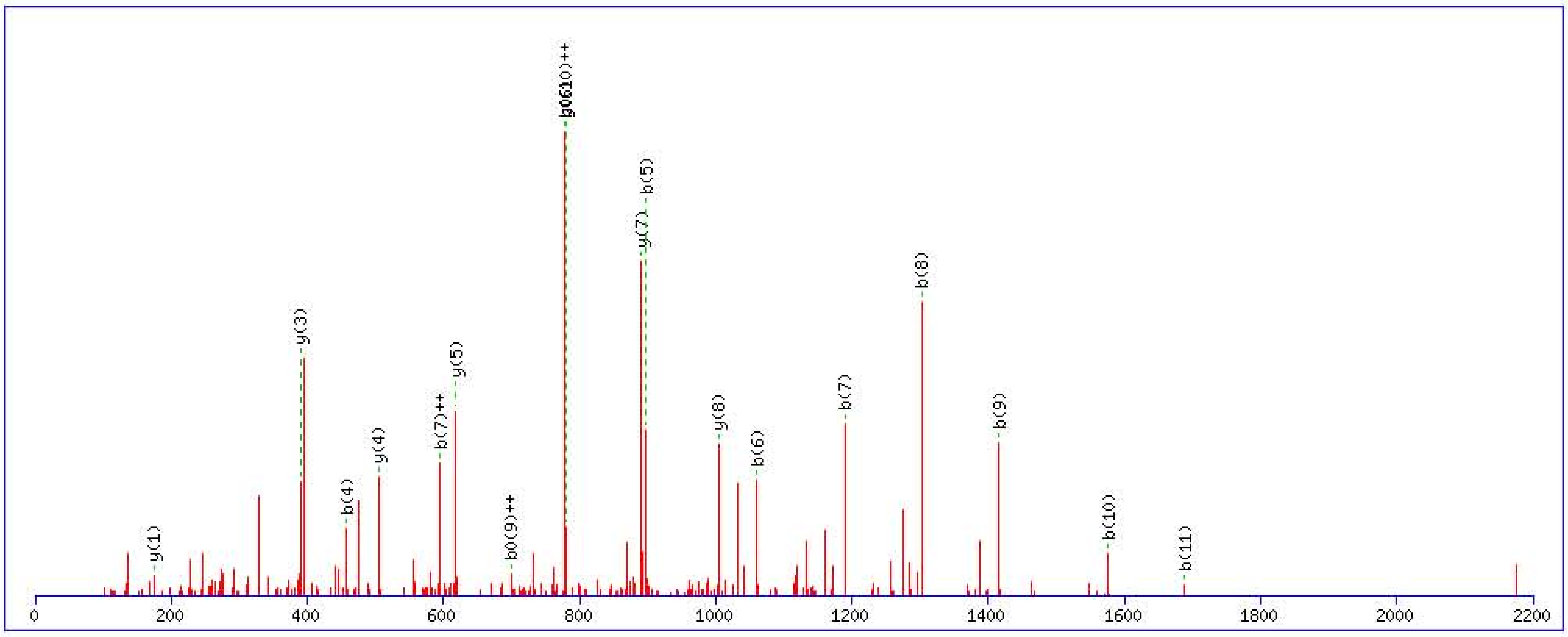
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADRDQYELLCLDNTR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

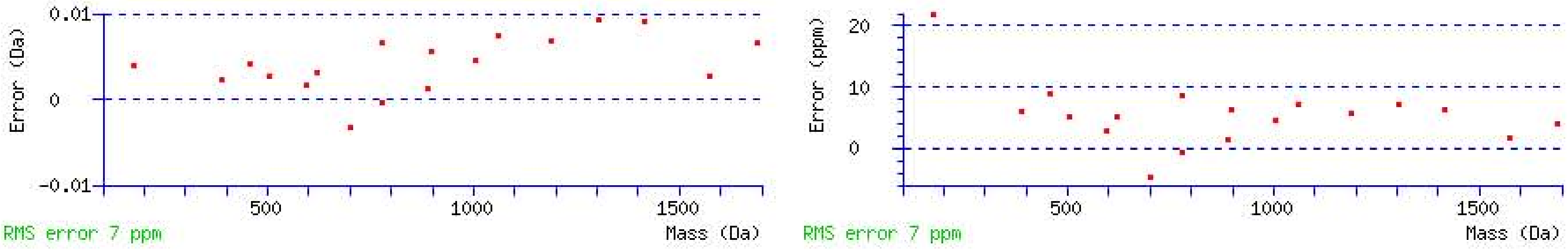
Match to Query 45912: 2192.042352 from(731.688060,3+) rtinseconds(2215) index(63750)
Title: Locus:1.1.1.3397.7 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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): 2192.035400
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00032
Matches : 18/160 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							15
2	187.071333	94.039304			169.060768	85.034022	D	2122.005587	1061.506431	2104.979038	1052.993157	2103.995022	1052.501149	14
3	343.172444	172.089860	326.145895	163.576585	325.161879	163.084577	R	2006.978644	1003.992960	1989.952095	995.479685	1988.968079	994.987677	13
4	***458.199387***	229.603332	441.172838	221.090057	440.188822	220.598049	D	1850.877533	925.942404	1833.850984	917.429130	1832.866968	916.937122	12
5	***897.424713***	449.215995	880.398164	440.702720	879.414148	440.210712	Q	1735.850590	868.428933	1718.824041	859.915658	1717.840025	859.423650	11
6	***1060.488042***	530.747659	1043.461493	522.234385	1042.477477	521.742376	Y	1296.625264	648.816270	1279.598715	640.302995	1278.614699	639.810987	10
7	***1189.530635***	595.268955	1172.504086	586.755681	1171.520070	586.263673	E	1133.561935	567.284605	1116.535386	558.771331	1115.551370	558.279323	9
8	***1302.614699***	651.810987	1285.588150	643.297713	1284.604134	642.805705	L	***1004.519342***	502.763309	987.492793	494.250034	986.508777	493.758026	8
9	***1415.698763***	708.353019	1398.672214	699.839745	1397.688198	699.347737	L	***891.435278***	446.221277	874.408729	437.708002	873.424713	437.215994	7
10	***1575.729412***	788.368344	1558.702863	779.855069	1557.718847	779.363061	C	***778.351214***	389.679245	761.324665	381.165971	760.340649	380.673963	6
11	***1688.813476***	844.910376	1671.786927	836.397101	1670.802911	835.905093	L	***618.320565***	309.663921	601.294016	301.150646	600.310000	300.658638	5
12	1803.840419	902.423847	1786.813870	893.910573	1785.829854	893.418565	D	***505.236501***	253.121888	488.209952	244.608614	487.225936	244.116606	4
13	1917.883346	959.445311	1900.856797	950.932036	1899.872781	950.440028	N	***390.209558***	195.608417	373.183009	187.095142	372.198993	186.603134	3
14	2018.931025	1009.969150	2001.904476	1001.455876	2000.920460	1000.963868	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
15							R	***175.118952***	88.063114	158.092403	79.549839			1



NCBI **BLAST** search of ADRDQYELLCLDNTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.8	2192.035400	0.006952	ADRDQYELLCLDNTR

Mascot: http://www.matrixscience.com/

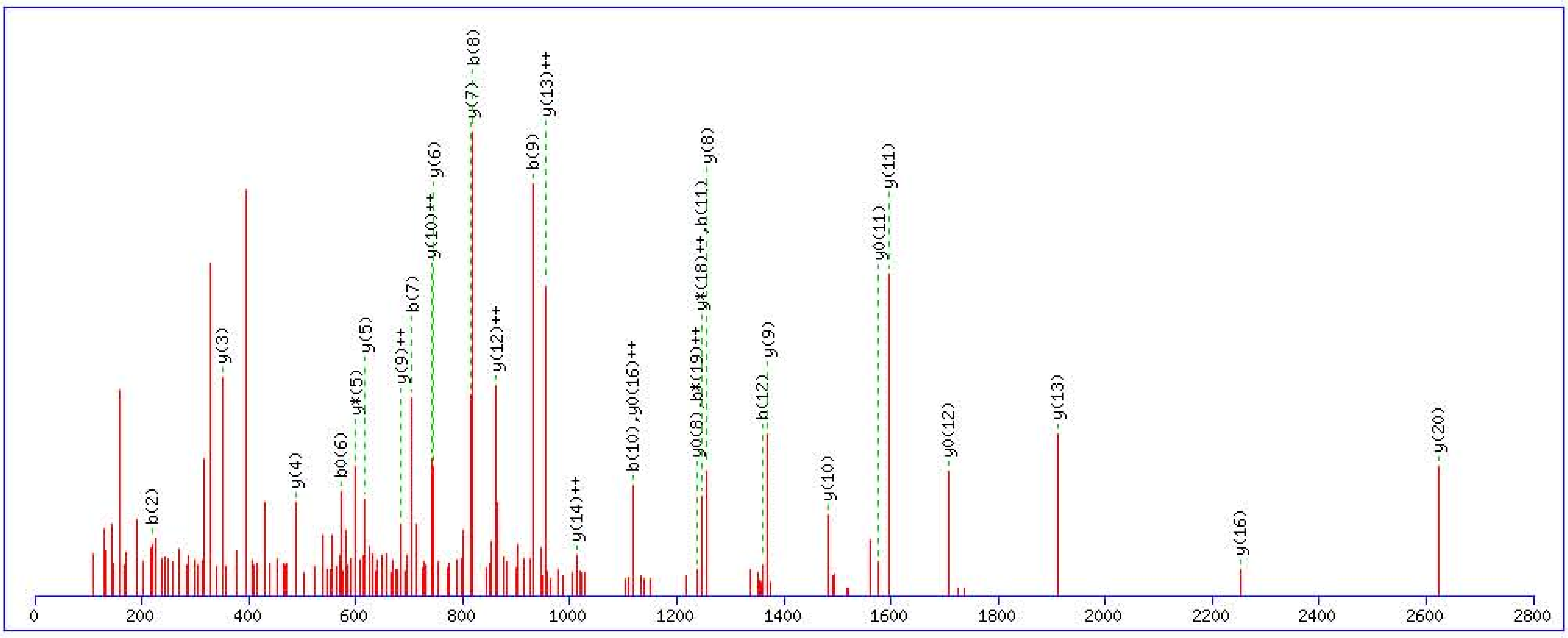
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SMGGKEDLIWELLNQAQEHFGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

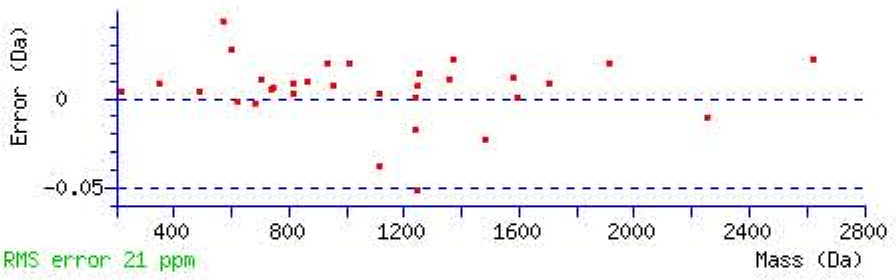
Match to Query 54313: 2840.412696 from(711.110450,4+) rtinseconds(3013) index(68637)
Title: Locus:1.1.1.3672.3 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

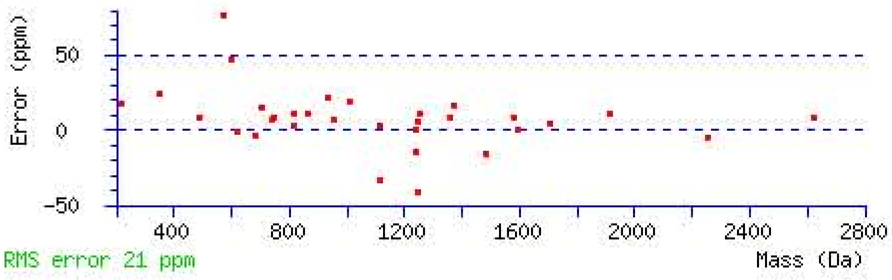
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from [0] to [2800] Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2840.398926
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15     : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 9.2e-007
Matches : 32/236 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	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





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
64.6	2840.398926	0.013770	SMGGKEDLIWELLNQAQEHFGK
49.9	2840.398926	0.013770	SMGGKEDLIWELLNQAQEHFGK
0.2	2840.380539	0.032157	SLGTIQQCCDAIDHLCRIIEK

Mascot: http://www.matrixscience.com/

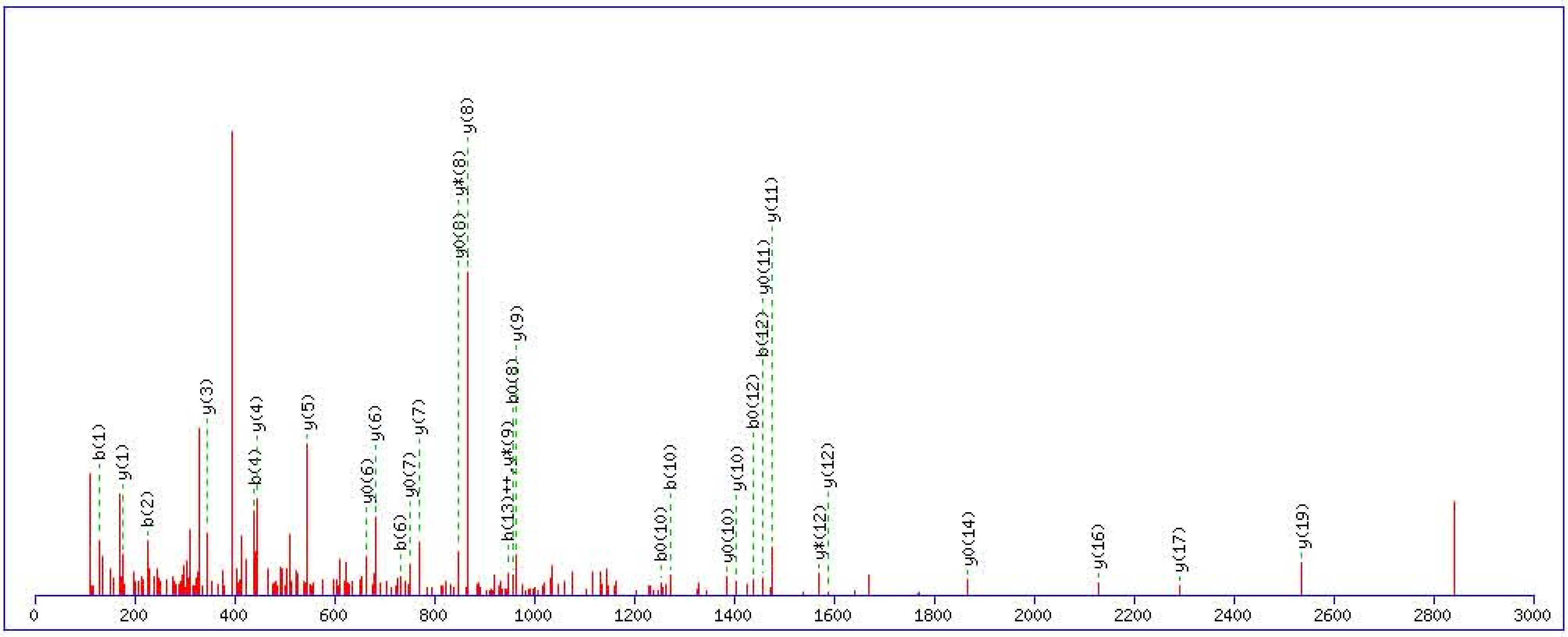
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPVDEYKDCHLAQVPSHTVVAR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

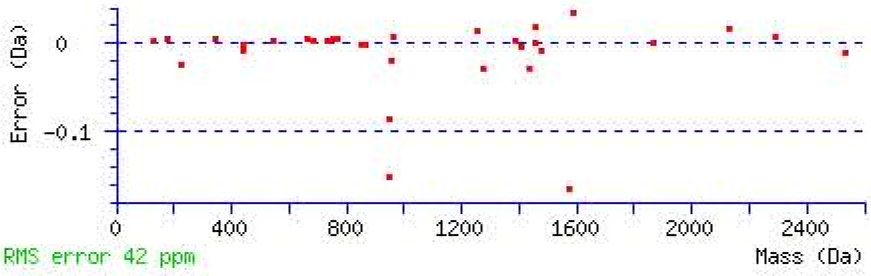
Match to Query 54768: 2859.448020 from(572.896880,5+) rtinseconds(1561) index(60177)
Title: Locus:1.1.1.3169.20 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

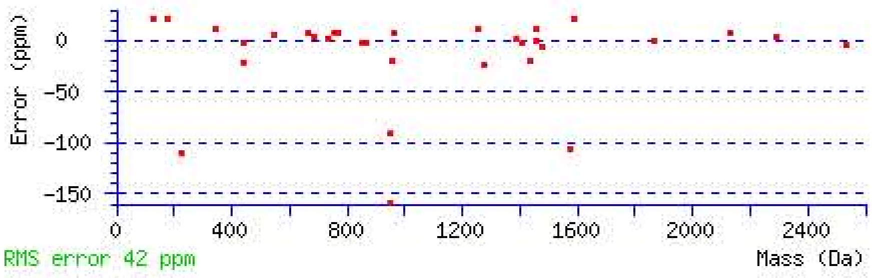
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2859.452393
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 66  Expect: 7e-006
Matches : 33/238 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	**129.102239**	65.054757	112.075690	56.541483			K							22
2	**226.155003**	113.581139	209.128454	105.067865			P	2732.364705	1366.685990	2715.338156	1358.172716	2714.354140	1357.680708	21
3	325.223417	163.115346	308.196868	154.602072			V	2635.311941	1318.159608	2618.285392	1309.646334	2617.301376	1309.154326	20
4	**440.250360**	220.628818	423.223811	212.115544	422.239795	211.623536	D	***2536.243527***	1268.625401	2519.216978	1260.112127	2518.232962	1259.620119	19
5	569.292953	285.150115	552.266404	276.636840	551.282388	276.144832	E	2421.216584	1211.111930	2404.190035	1202.598655	2403.206019	1202.106647	18
6	**732.356282**	366.681779	715.329733	358.168505	714.345717	357.676497	Y	***2292.173991***	1146.590633	2275.147442	1138.077359	2274.163426	1137.585351	17
7	860.451245	430.729261	843.424696	422.215986	842.440680	421.723978	K	***2129.110662***	1065.058969	2112.084113	1056.545694	2111.100097	1056.053686	16
8	975.478188	488.242732	958.451639	479.729458	957.467623	479.237450	D	2001.015699	1001.011487	1983.989150	992.498213	1983.005134	992.006205	15
9	1135.508837	568.258057	1118.482288	559.744782	1117.498272	559.252774	C	1885.988756	943.498016	1868.962207	934.984741	1867.978191	934.492733	14
10	**1272.567749**	636.787513	1255.541200	628.274238	1254.557184	627.782230	H	1725.958107	863.482691	1708.931558	854.969417	1707.947542	854.477409	13
11	1385.651813	693.329545	1368.625264	684.816270	1367.641248	684.324262	L	***1588.899195***	794.953235	1571.872646	786.439961	1570.888630	785.947953	12
12	**1456.688927**	728.848101	1439.662378	720.334827	1438.678362	719.842819	A	***1475.815131***	738.411203	1458.788582	729.897929	1457.804566	729.405921	11
13	1895.914253	948.460765	1878.887704	939.947490	1877.903688	939.455482	Q	***1404.778017***	702.892646	1387.751468	694.379372	1386.767452	693.887364	10
14	1994.982667	997.994972	1977.956118	989.481697	1976.972102	988.989689	V	***965.552691***	483.279983	948.526142	474.766709	947.542126	474.274701	9
15	2092.035431	1046.521353	2075.008882	1038.008079	2074.024866	1037.516071	P	***866.484277***	433.745776	849.457728	425.232502	848.473712	424.740494	8
16	2179.067459	1090.037367	2162.040910	1081.524093	2161.056894	1081.032085	S	***769.431513***	385.219394	752.404964	376.706120	751.420948	376.214112	7
17	2316.126371	1158.566823	2299.099822	1150.053549	2298.115806	1149.561541	H	***682.399485***	341.703380	665.372936	333.190106	664.388920	332.698098	6
18	2417.174050	1209.090663	2400.147501	1200.577388	2399.163485	1200.085380	T	***545.340573***	273.173924	528.314024	264.660650	527.330008	264.168642	5
19	2516.242464	1258.624870	2499.215915	1250.111595	2498.231899	1249.619587	V	***444.292894***	222.650085	427.266345	214.136810			4
20	2615.310878	1308.159077	2598.284329	1299.645802	2597.300313	1299.153794	V	***345.224480***	173.115878	328.197931	164.602603			3
21	2686.347992	1343.677634	2669.321443	1335.164359	2668.337427	1334.672351	A	246.156066	123.581671	229.129517	115.068397			2
22							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of KPVDEYKDCHLAQVPSHTVVAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.2	2859.452393	-0.004373	KPVDEYKDCHLAQVPSHTVVAR

Mascot: http://www.matrixscience.com/

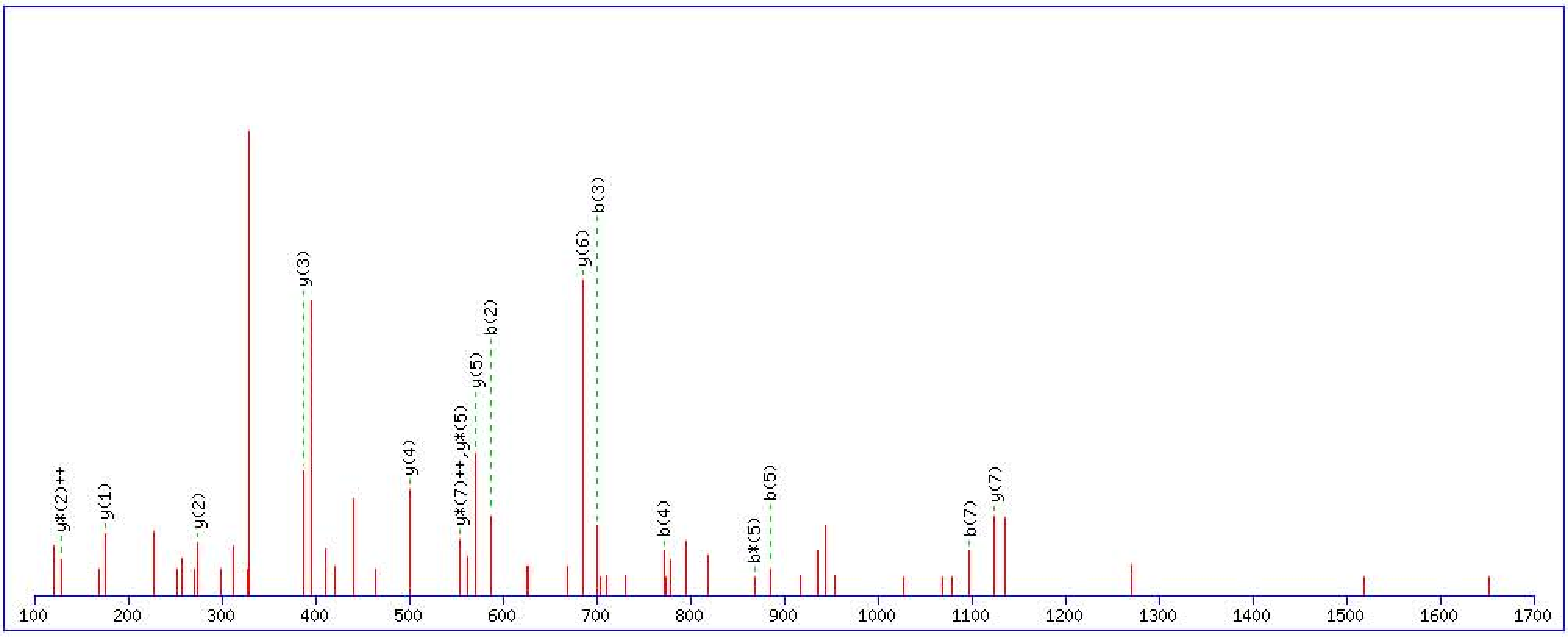
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FQNALLVR**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

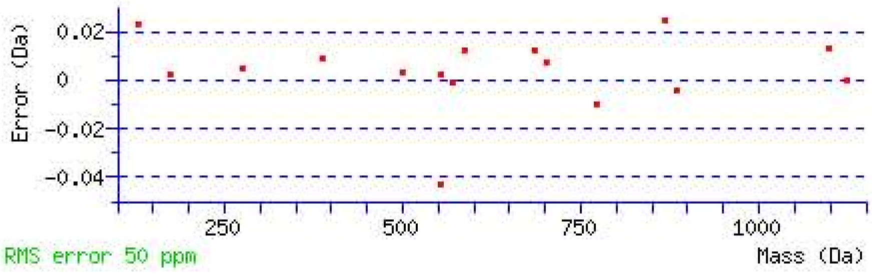
Match to Query 22229: 1270.719388 from(636.366970,2+) rtinseconds(2140) index(5725)
Title: Locus:1.1.1.3297.18 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

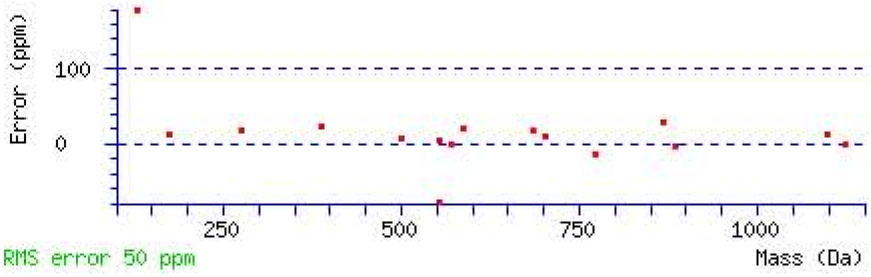
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1270.721985
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.005
Matches : 16/54 fragment ions using 32 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
38.0	1270.721985	-0.002597	FQNALLVR
14.1	1270.733215	-0.013827	MFHIRAVILR
11.3	1270.735687	-0.016299	KEAELRSGIIR
10.6	1270.706711	0.012677	NMPAKTELIVR
7.6	1270.706696	0.012692	LPALLEKNAMR
7.1	1270.722000	-0.002612	FQIAQVVR
6.0	1270.733215	-0.013827	FQRQILR
4.5	1270.710541	0.008847	AVNSKAEVARAR
1.9	1270.724457	-0.005069	EKELLIDKQR
1.8	1270.725357	-0.005969	QKVMAIVR

Mascot: http://www.matrixscience.com/

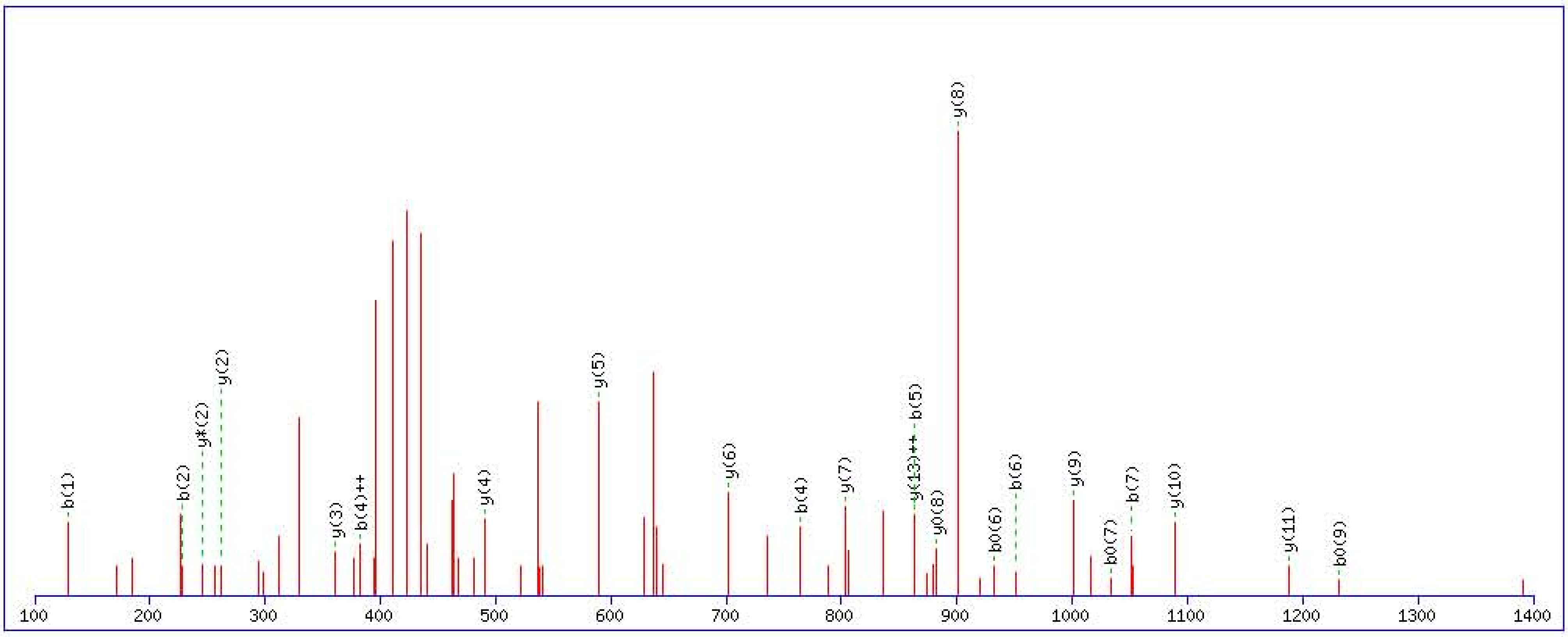
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KVPQVSTPTLVEVSR**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

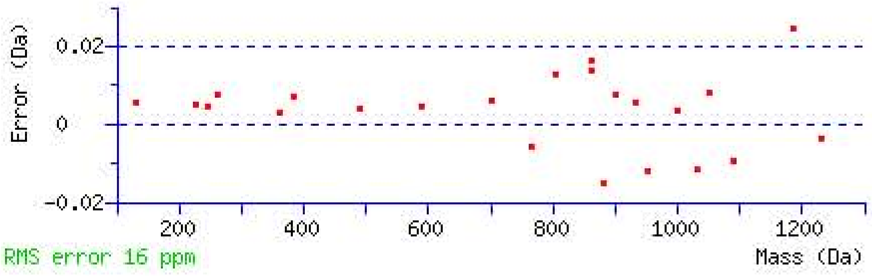
Match to Query 41093: 1950.104562 from(651.042130,3+) rtinseconds(2011) index(62654)
Title: Locus:1.1.1.3326.15 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

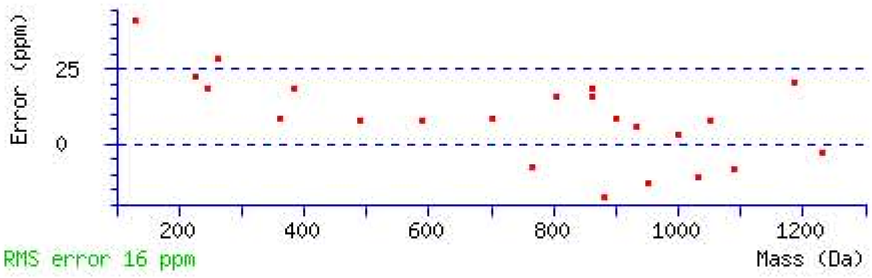
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1950.097229
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.0011
Matches : 23/156 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	**129.102239**	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
39.7	1950.097229	0.007333	KVPQVSTPTLVEVSR

Mascot: http://www.matrixscience.com/

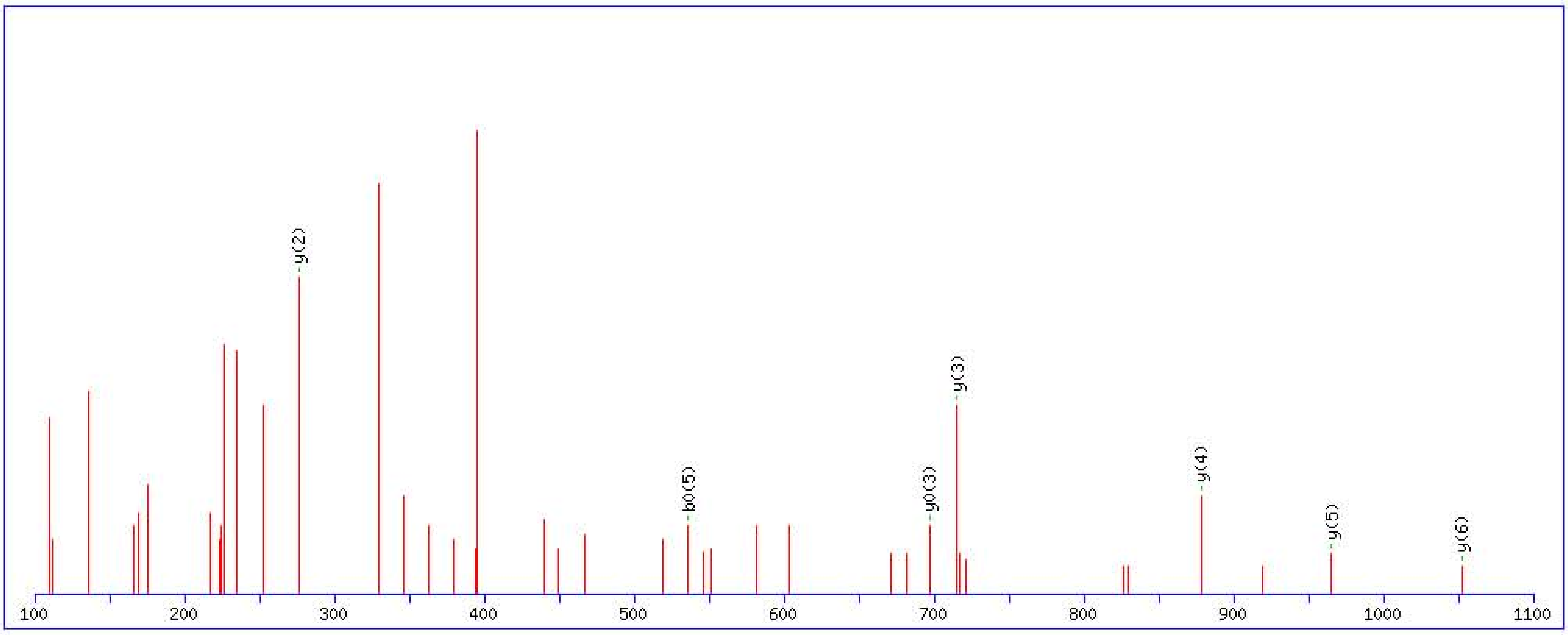
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NHQSSYQTR**
Found in **PON1_HUMAN**, Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3

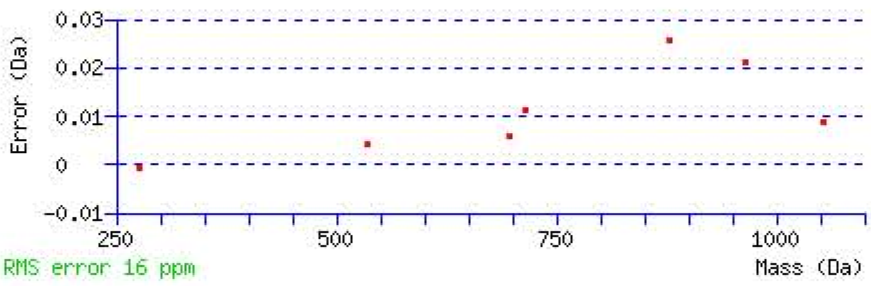
Match to Query 28031: 1430.671002 from(477.897610,3+) rtinseconds(1185) index(42651)
Title: Locus:1.1.1.2461.6 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

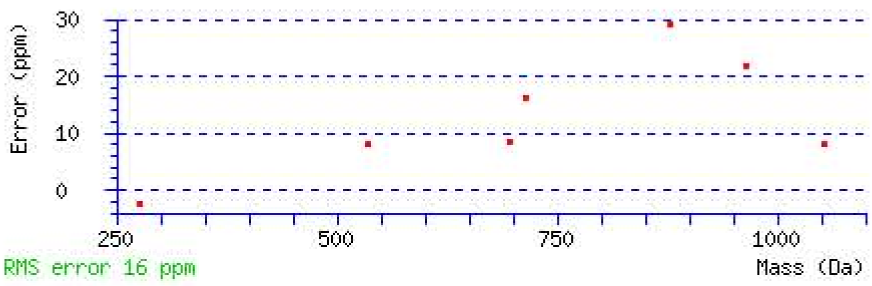
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1430.672470
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.022
Matches : 7/88 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	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





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
28.1	1430.672470	-0.001468	NHQSSYQTR

Mascot: http://www.matrixscience.com/

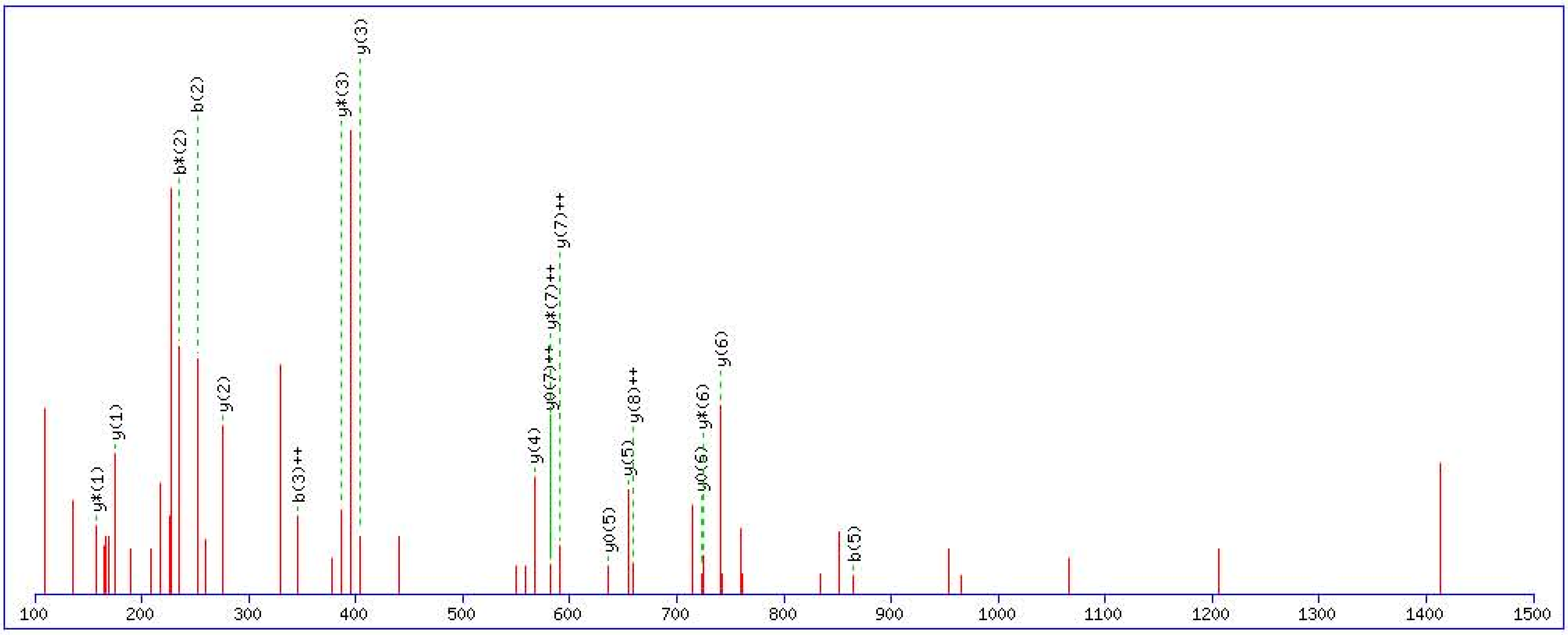
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NHQSSYQTR**
Found in **PON1_HUMAN**, Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3

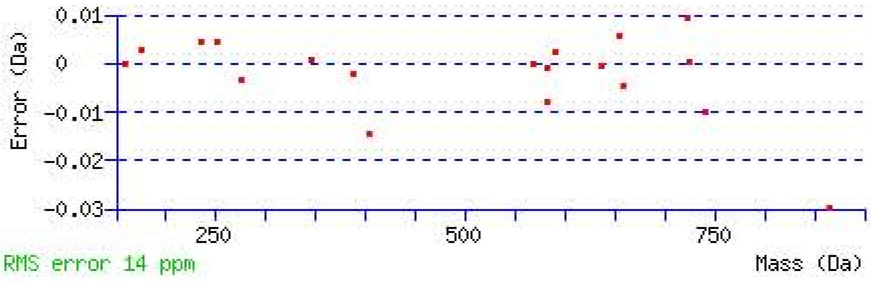
Match to Query 28034: 1430.672292 from(477.898040,3+) rtinseconds(1151) index(28617)
Title: Locus:1.1.1.2949.7 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

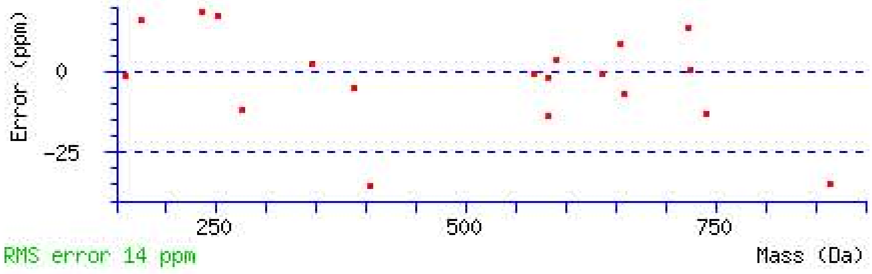
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1430.672470
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 27 **Expect:** 0.0073
Matches : 19/88 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	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	691.334441	346.170859	674.307892	337.657584			Q	1180.577920	590.792598	1163.551371	582.279324	1162.567355	581.787316	7
4	778.366469	389.686872	761.339920	381.173598	760.355904	380.681590	S	***741.352594***	371.179935	724.326045	362.666661	723.342029	362.174653	6
5	**865.398497**	433.202886	848.371948	424.689612	847.387932	424.197604	S	***654.320566***	327.663921	637.294017	319.150647	636.310001	318.658639	5
6	1028.461826	514.734551	1011.435277	506.221276	1010.451261	505.729268	Y	***567.288538***	284.147907	550.261989	275.634633	549.277973	275.142625	4
7	1156.520404	578.763840	1139.493855	570.250566	1138.509839	569.758558	Q	***404.225209***	202.616243	387.198660	194.102968	386.214644	193.610960	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





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
27.4	1430.672470	-0.000178	NHQSSYQTR
6.2	1430.672470	-0.000178	NHQSSYQTR
4.4	1430.689743	-0.017451	QLGMAAAESDK
0.9	1430.686371	-0.014079	LICESLYASGYR

Mascot: http://www.matrixscience.com/

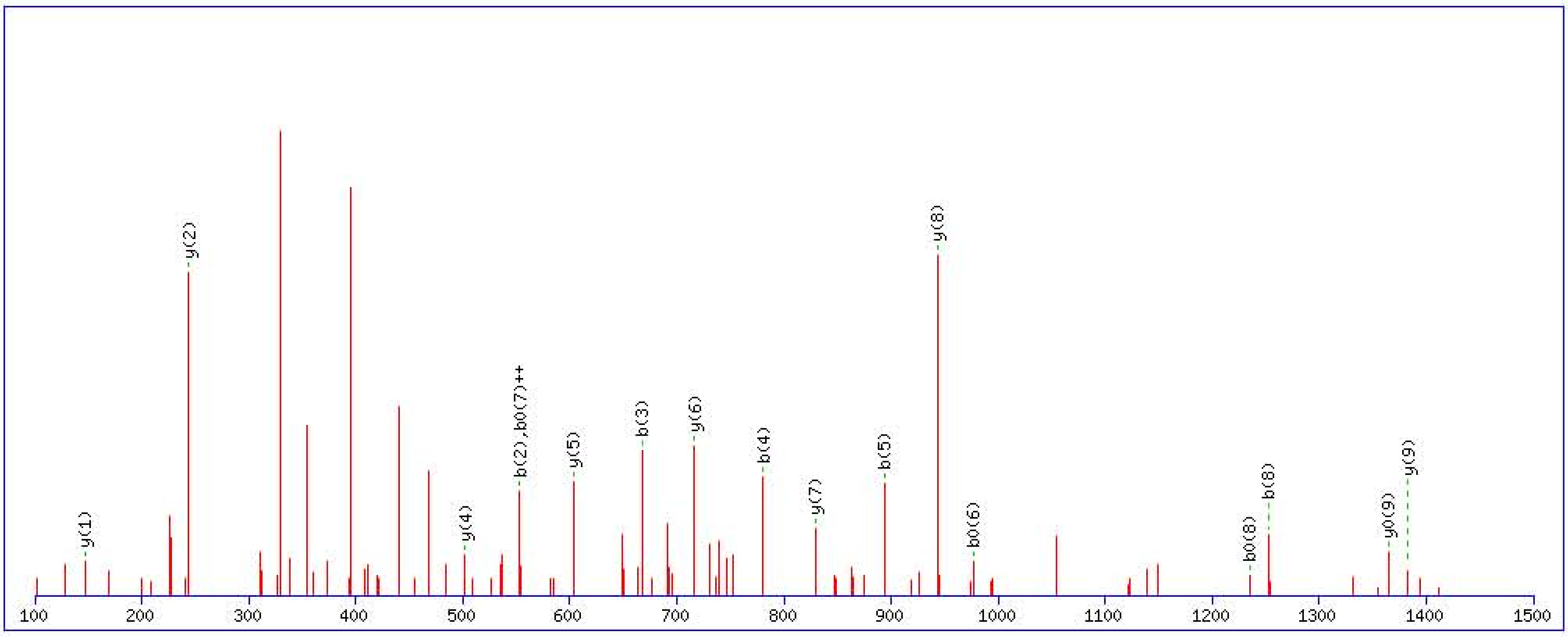
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQNILTEEPK**
Found in **PON1_HUMAN**, Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3

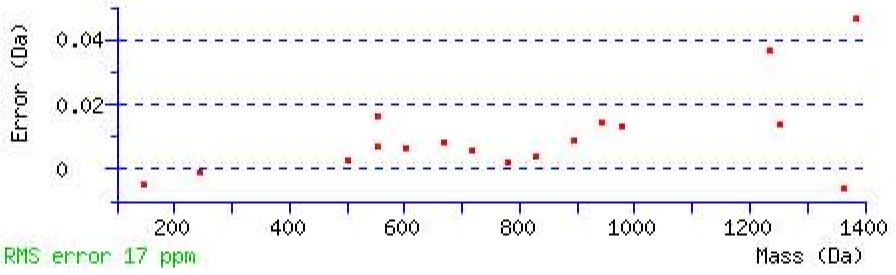
Match to Query 29813: 1494.821508 from(748.418030,2+) rtinseconds(2024) index(47569)
Title: Locus:1.1.1.2753.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

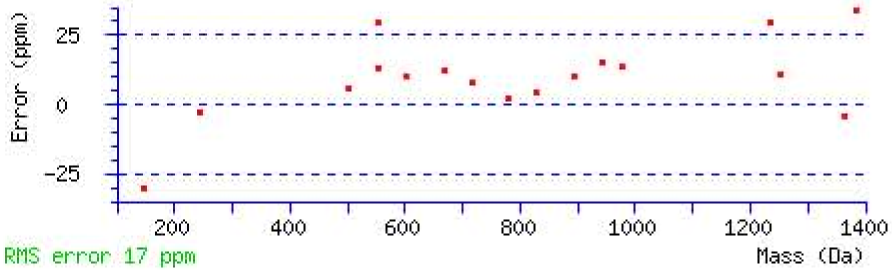
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1494.811569
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 9.7e-005
Matches : 17/92 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	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	355.197596	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
52.7	1494.811569	0.009939	IQNILTEEPK
9.5	1494.815430	0.006078	KGSTKDSGHLQIPK
6.3	1494.834030	-0.012522	QLLRALEEGR
5.2	1494.834030	-0.012522	QLNAIRDNIK
1.5	1494.841446	-0.019938	QLTKQQK
0.7	1494.819427	0.002081	NKFGRDYLLEIK
0.3	1494.824142	-0.002634	QIRSYPHRK

Mascot: http://www.matrixscience.com/

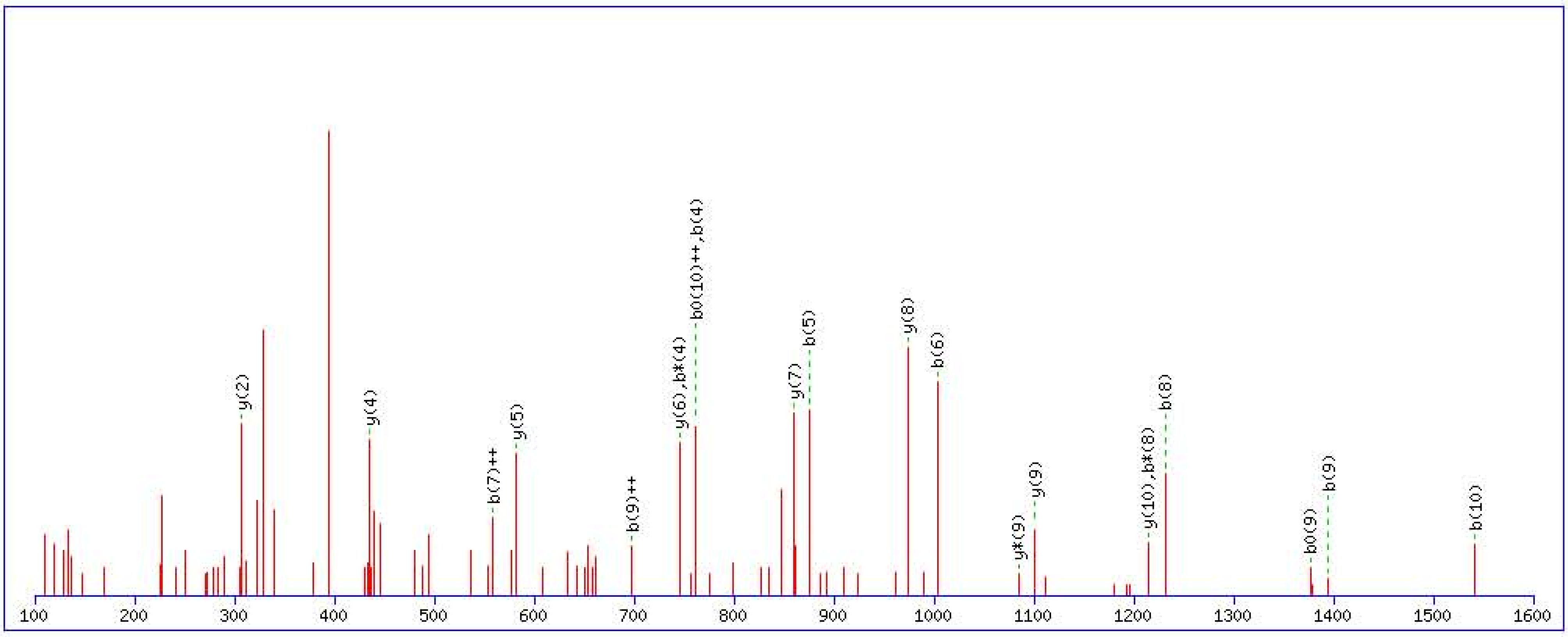
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KGHQLQLDYFGACK**
Found in **SPRL1_HUMAN**, SPARC-like protein 1 OS=Homo sapiens GN=SPARCL1 PE=1 SV=2

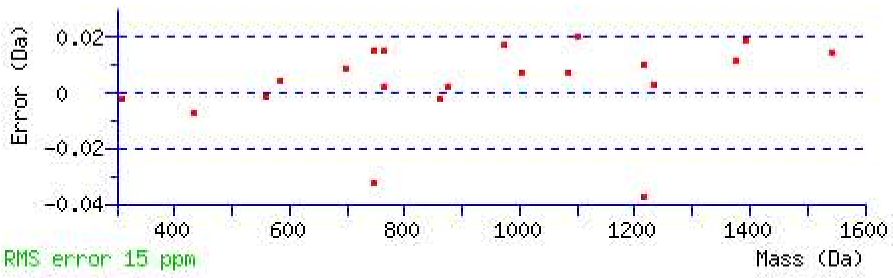
Match to Query 41600: 1974.993102 from(659.338310,3+) rtinseconds(1949) index(47058)
Title: Locus:1.1.1.2727.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

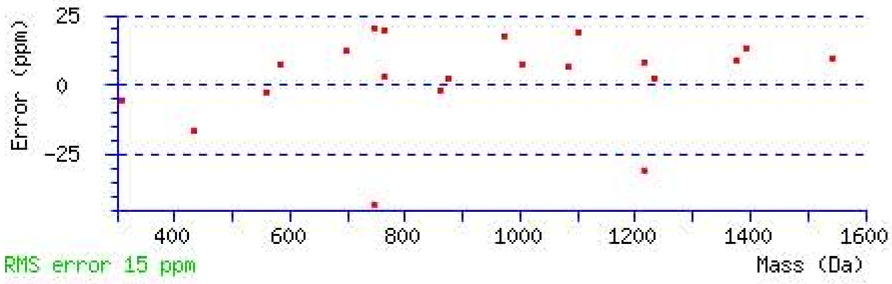
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1974.980804
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 0.00011
Matches : 21/130 fragment ions using 27 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							14
2	186.123703	93.565489	169.097154	85.052215			G	1847.893125	924.450201	1830.866576	915.936926	1829.882560	915.444918	13
3	323.182615	162.094945	306.156066	153.581671			H	1790.871661	895.939469	1773.845112	887.426194	1772.861096	886.934186	12
4	**762.407941**	381.707609	745.381392	373.194334			Q	1653.812749	827.410013	1636.786200	818.896738	1635.802184	818.404730	11
5	**875.492005**	438.249641	858.465456	429.736366			L	***1214.587423***	607.797350	1197.560874	599.284075	1196.576858	598.792067	10
6	**1003.550583**	502.278930	986.524034	493.765655			Q	***1101.503359***	551.255318	1084.476810	542.742043	1083.492794	542.250035	9
7	1116.634647	**558.820962**	1099.608098	550.307687			L	***973.444781***	487.226029	956.418232	478.712754	955.434216	478.220746	8
8	**1231.661590**	616.334433	1214.635041	607.821159	1213.651025	607.329151	D	***860.360717***	430.683997	843.334168	422.170722	842.350152	421.678714	7
9	**1394.724919**	**697.866098**	1377.698370	689.352823	1376.714354	688.860815	Y	***745.333774***	373.170525	728.307225	364.657251			6
10	**1541.793333**	771.400305	1524.766784	762.887030	1523.782768	762.395022	F	***582.270445***	291.638861	565.243896	283.125586			5
11	1598.814797	799.911037	1581.788248	791.397762	1580.804232	790.905754	G	***435.202031***	218.104653	418.175482	209.591379			4
12	1669.851911	835.429594	1652.825362	826.916319	1651.841346	826.424311	A	378.180567	189.593921	361.154018	181.080647			3
13	1829.882560	915.444918	1812.856011	906.931644	1811.871995	906.439636	C	***307.143453***	154.075365	290.116904	145.562090			2
14							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of KGHQLQLDYFGACK
(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	1974.980804	0.012298	KGHQLQLDYFGACK
27.0	1974.980804	0.012298	KGHQLQLDYFGACK
8.6	1974.966888	0.026214	HMHIHISTVNHAFKCK

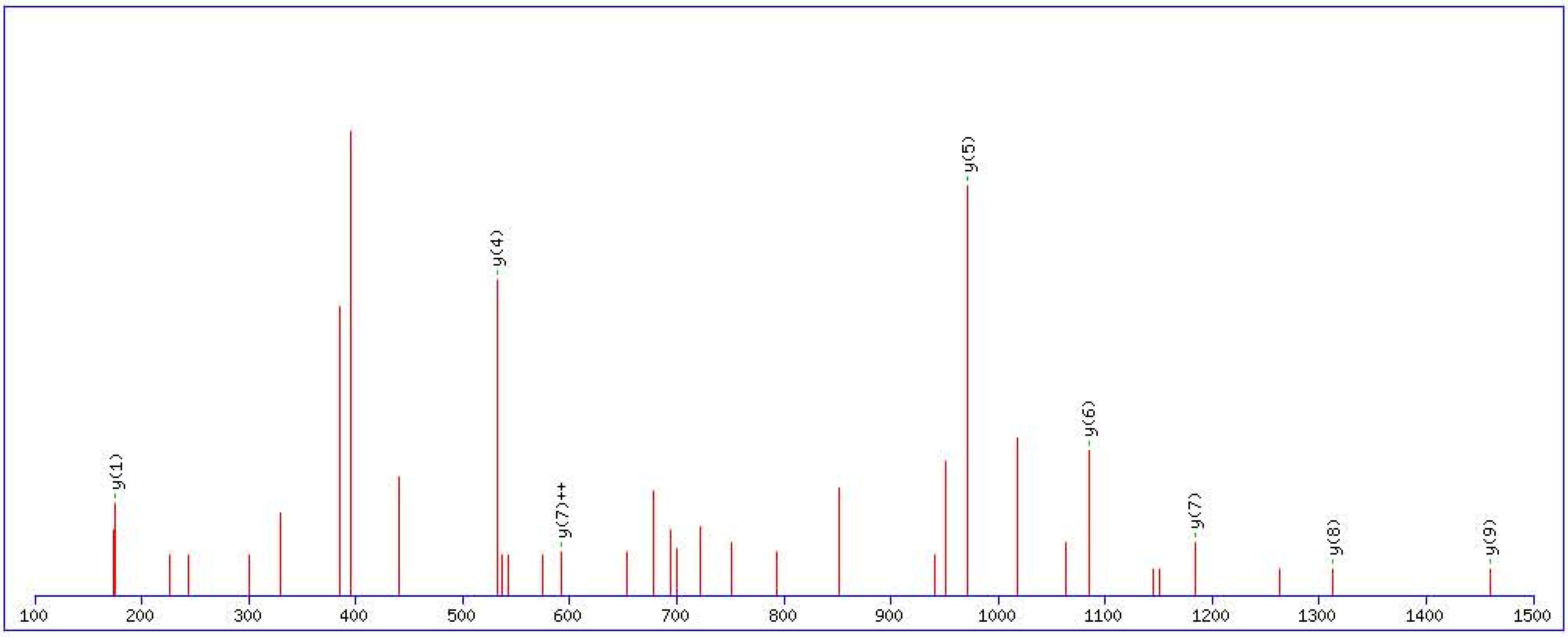
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SIPTCTDFEVIQFPLR**
Found in **SPRL1_HUMAN**, SPARC-like protein 1 OS=Homo sapiens GN=SPARCL1 PE=1 SV=2

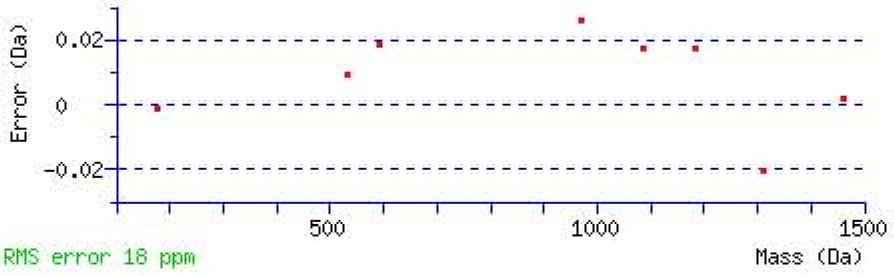
Match to Query 46624: 2233.151802 from(745.391210,3+) rtinseconds(2822) index(52614)
Title: Locus:1.1.1.3029.13 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

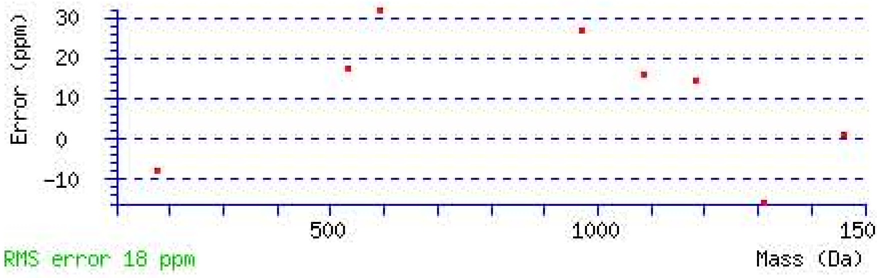
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2233.127548
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12    : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.00056
Matches : 8/144 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**							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
41.9	2233.127548	0.024254	SIPTCTDFEVIQFPLR
6.8	2233.141861	0.009941	FELPLDIPEEEARYWAKK
1.1	2233.142090	0.009712	EMAMLIAQALQTINYGR

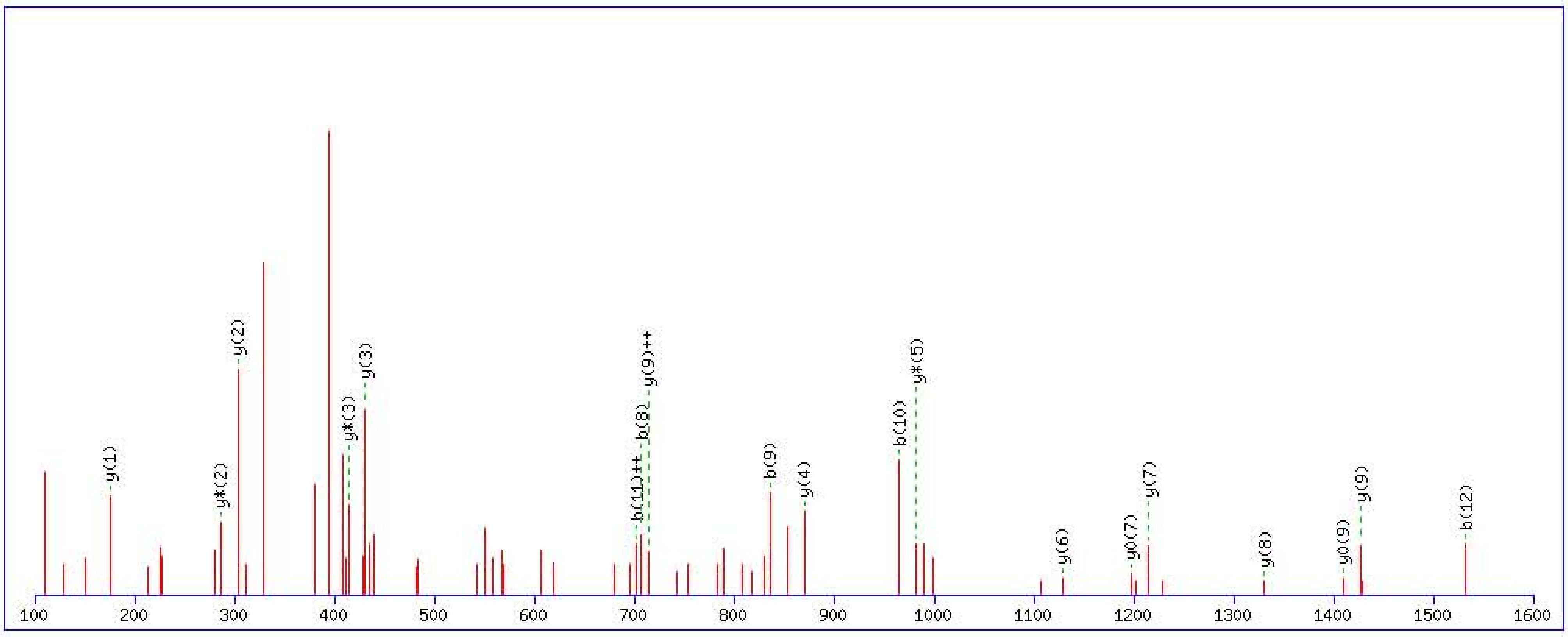
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GAAAHPDSEEQQQR**
Found in **TLN1_HUMAN**, Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3

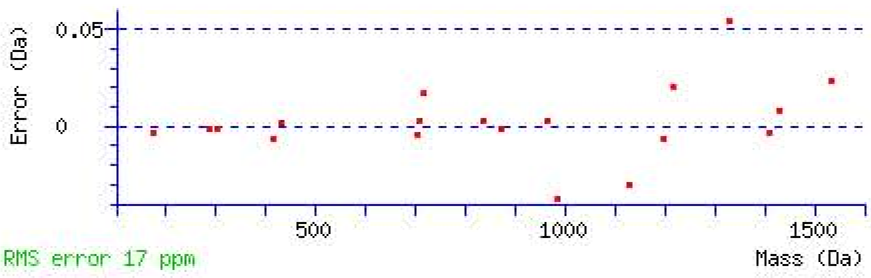
Match to Query 39104: 1833.842142 from(612.287990,3+) rtinseconds(1143) index(42495)
Title: Locus:1.1.1.2446.11 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

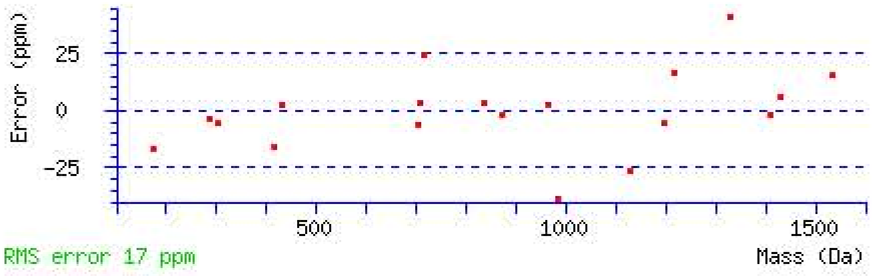
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1833.842773
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 48 **Expect:** 0.00019
Matches : 19/116 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							14
2	129.065854	65.036565					A	1777.828609	889.417943	1760.802060	880.904668	1759.818044	880.412660	13
3	200.102968	100.555122					A	1706.791495	853.899386	1689.764946	845.386111	1688.780930	844.894103	12
4	271.140082	136.073679					A	1635.754381	818.380829	1618.727832	809.867554	1617.743816	809.375546	11
5	408.198994	204.603135					H	1564.717267	782.862272	1547.690718	774.348997	1546.706702	773.856989	10
6	505.251758	253.129517					P	***1427.658355***	714.332816	1410.631806	705.819541	1409.647790	705.327533	9
7	620.278701	310.642989			602.268136	301.637706	D	***1330.605591***	665.806434	1313.579042	657.293159	1312.595026	656.801151	8
8	**707.310729**	354.159003			689.300164	345.153720	S	***1215.578648***	608.292962	1198.552099	599.779688	1197.568083	599.287680	7
9	**836.353322**	418.680299			818.342757	409.675017	E	***1128.546620***	564.776948	1111.520071	556.263674	1110.536055	555.771666	6
10	**965.395915**	483.201596			947.385350	474.196313	E	999.504027	500.255652	982.477478	491.742377	981.493462	491.250369	5
11	1404.621241	702.814259	1387.594692	694.300984	1386.610676	693.808976	Q	***870.461434***	435.734355	853.434885	427.221081			4
12	**1532.679819**	766.843548	1515.653270	758.330273	1514.669254	757.838265	Q	***431.236108***	216.121692	414.209559	207.608418			3
13	1660.738397	830.872837	1643.711848	822.359562	1642.727832	821.867554	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 GAAAHPDSEEQQQR
(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	1833.842773	-0.000631	GAAAHPDSEEQQQR
34.2	1833.842773	-0.000631	GAAAHPDSEEQQQR
24.7	1833.842773	-0.000631	GAAAHPDSEEQQQR
7.5	1833.864761	-0.022619	QREQMEQMKQR
6.8	1833.864761	-0.022619	QREQMEQMKQR
4.9	1833.864761	-0.022619	QREQMEQMKQR
1.0	1833.820297	0.021845	YYKLSEMTEQDQQR

Mascot: http://www.matrixscience.com/

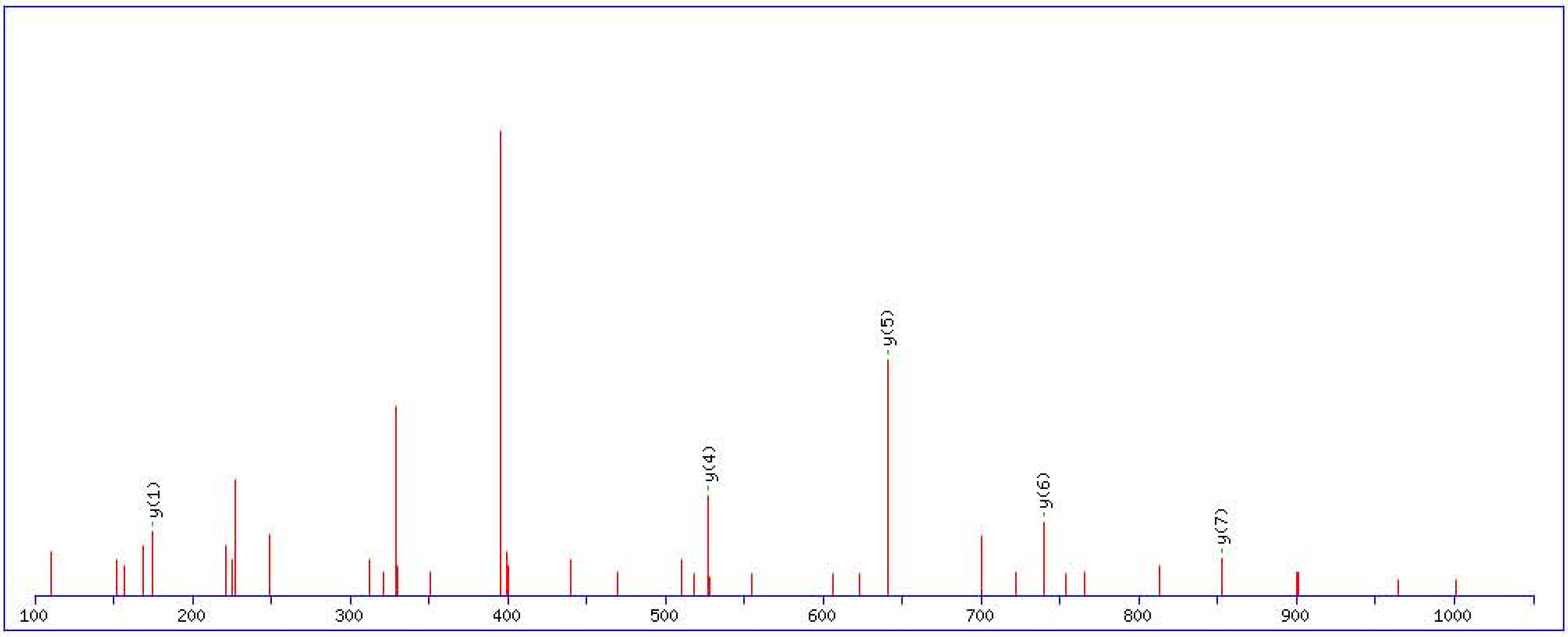
{MATRIX SCIENCE} Mascot Search Results

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

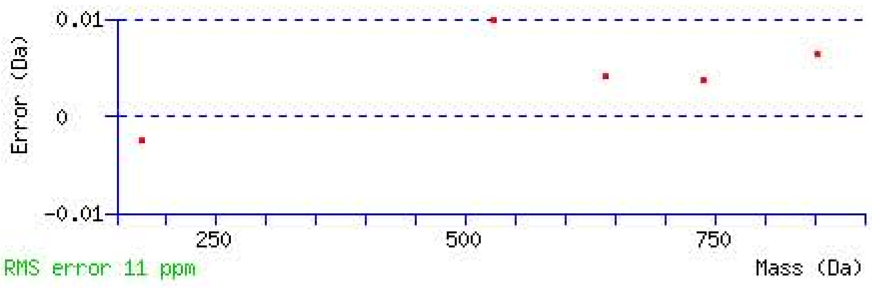
Match to Query 35171: 1637.873172 from(546.965000,3+) rtinseconds(1902) index(46656)
Title: Locus:1.1.1.2711.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

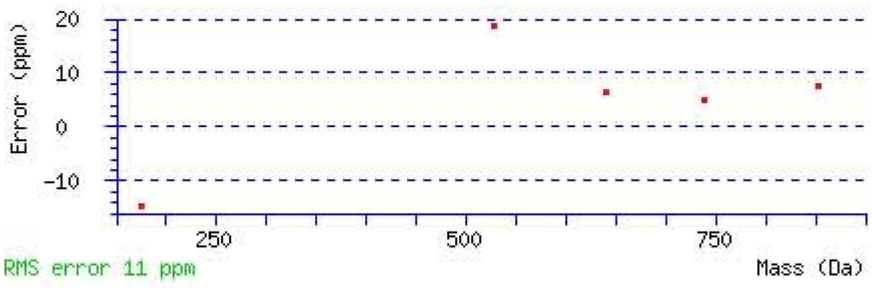
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1637.871170
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.0057
Matches : 5/112 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	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
26.9	1637.871170	0.002002	SPYQLVLQHSR
2.9	1637.857254	0.015918	RSQQHAKVVPWMR
1.0	1637.888916	-0.015744	APAPPPAGALLPEPGQR

Mascot: http://www.matrixscience.com/

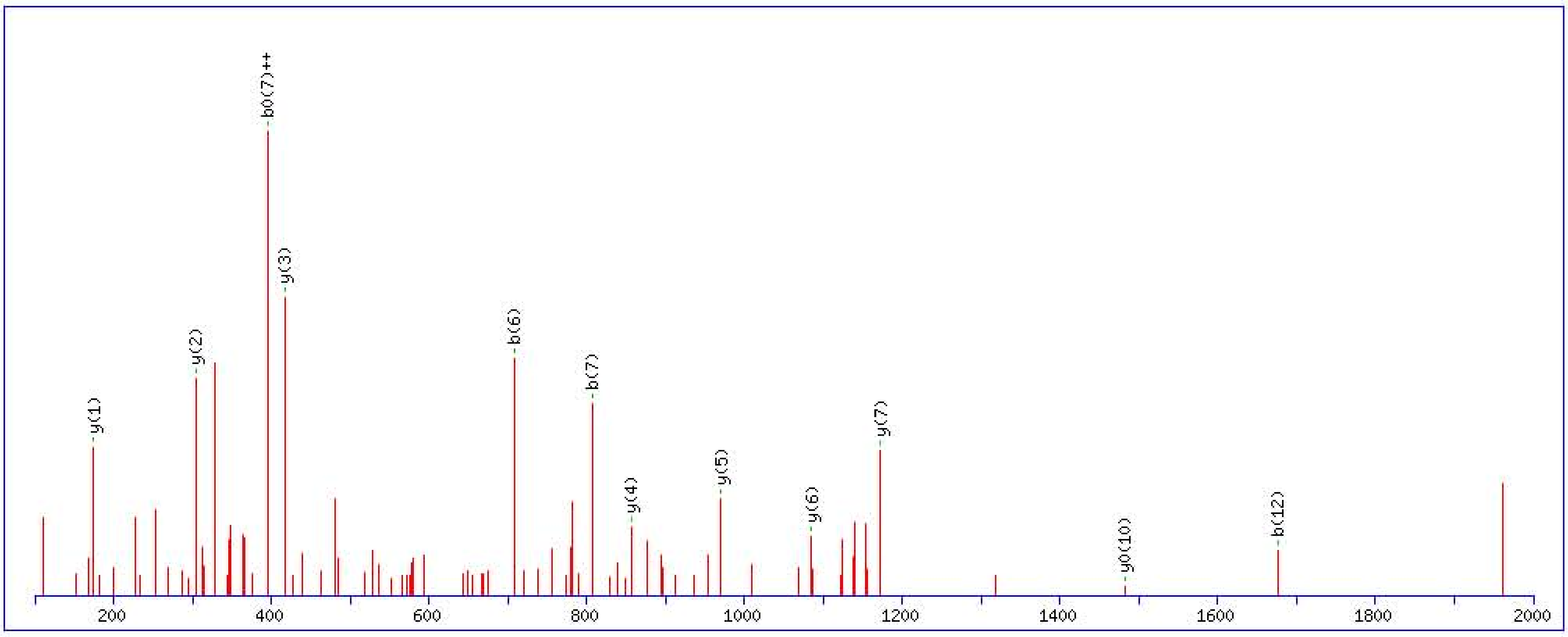
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLHDLDVSDNQLER**
Found in **VASN_HUMAN**, Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1

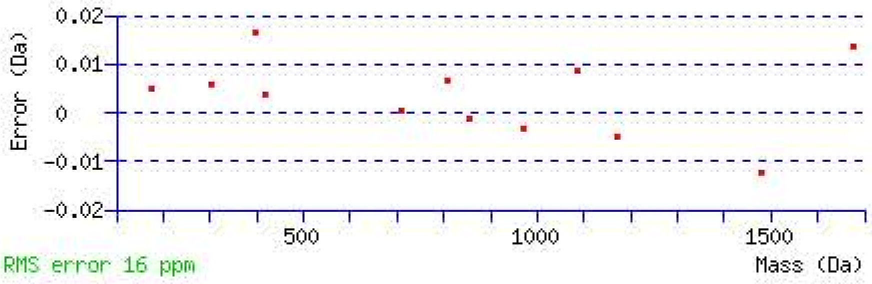
Match to Query 41615: 1977.955392 from(660.325740,3+) rtinseconds(1951) index(4638)
Title: Locus:1.1.1.3231.20 File:"2013-07-02 CLN FXIII 60 min 3rd F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

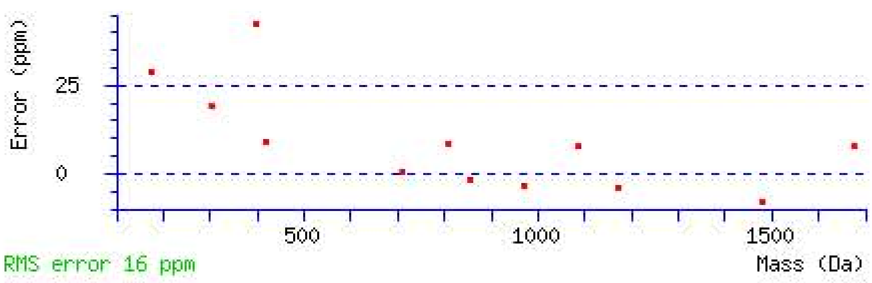
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1977.957809
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 5.2e-006
Matches : 12/148 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							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





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
56.5	1977.957809	-0.002417	NLHDLDVSDNQLER
0.2	1977.979813	-0.024421	TMPRTVPGSTMKMGSLER

Mascot: http://www.matrixscience.com/

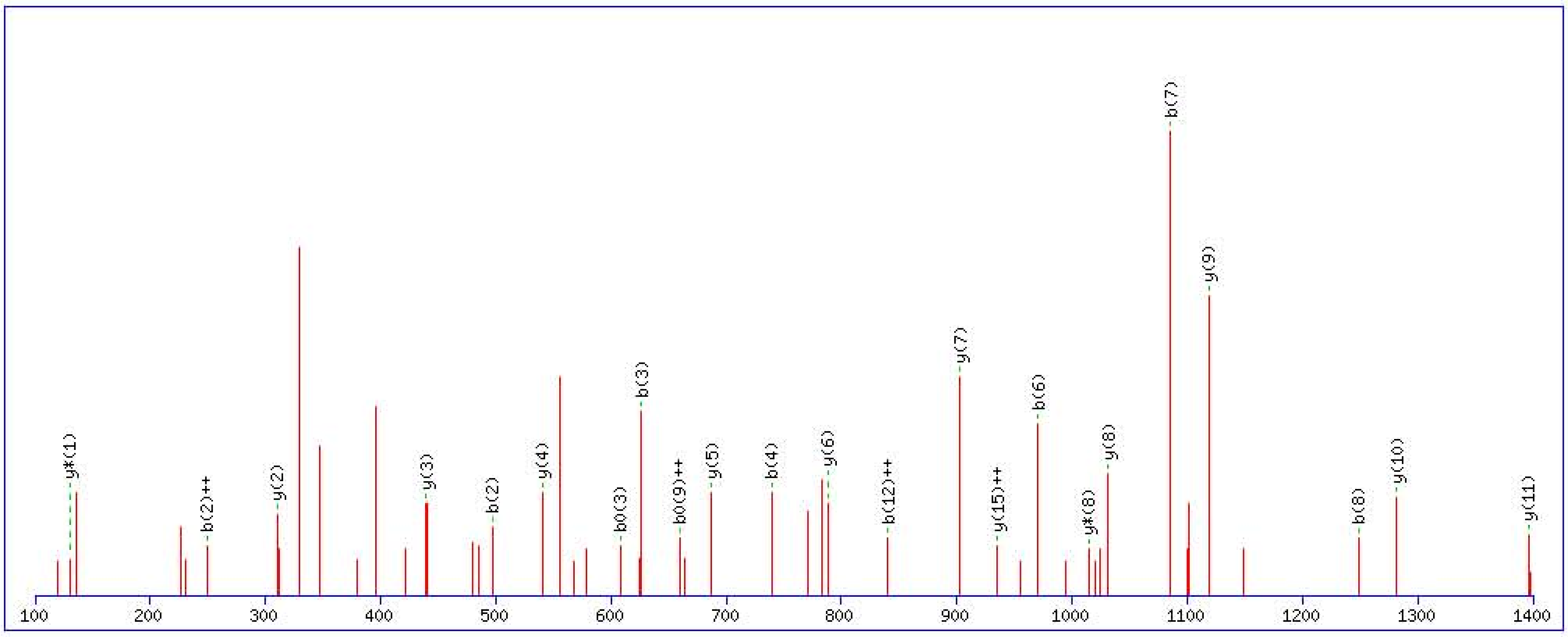
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQELCADYSENTFTEYK**
Found in **VTDB_HUMAN**, Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

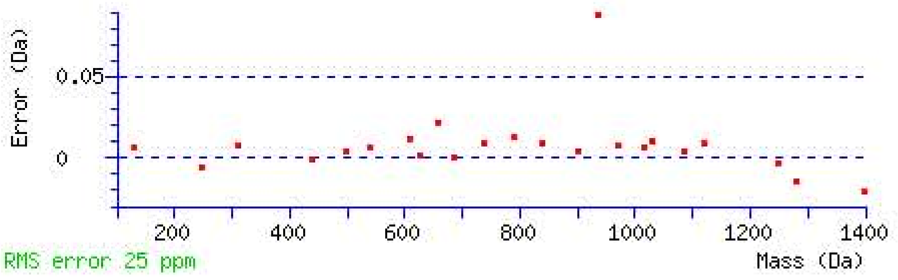
Match to Query 48664: 2365.030932 from(789.350920,3+) rtinseconds(2174) index(63561)
Title: Locus:1.1.1.3383.16 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

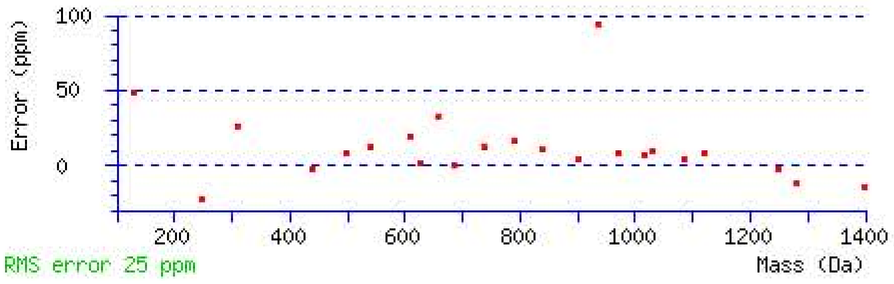
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2365.024231
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2     : Biotin:Thermo-21345 (Q)
Ions Score: 63  Expect: 2e-006
Matches : 23/182 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	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
63.2	2365.024231	0.006701	GQELCADYSENTFTEYK

Mascot: http://www.matrixscience.com/

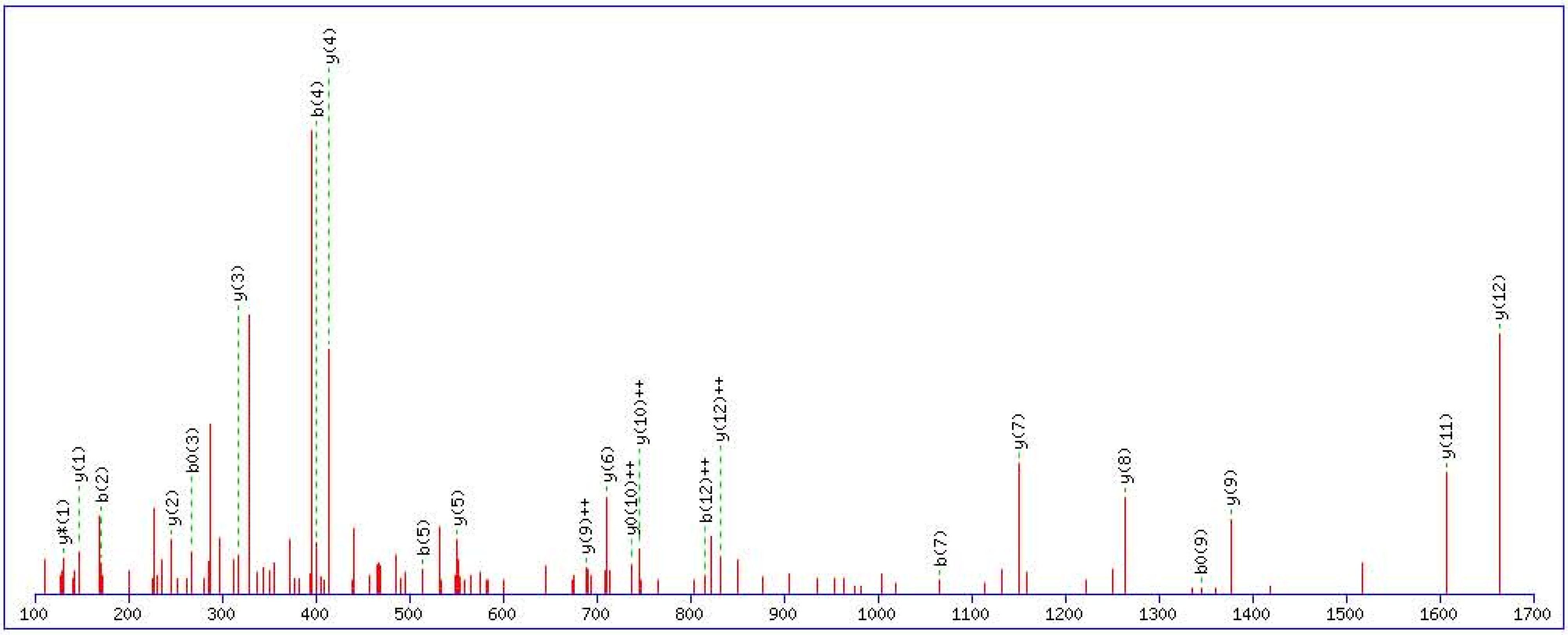
{MATRIX} {SCIENCE} Mascot Search Results

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

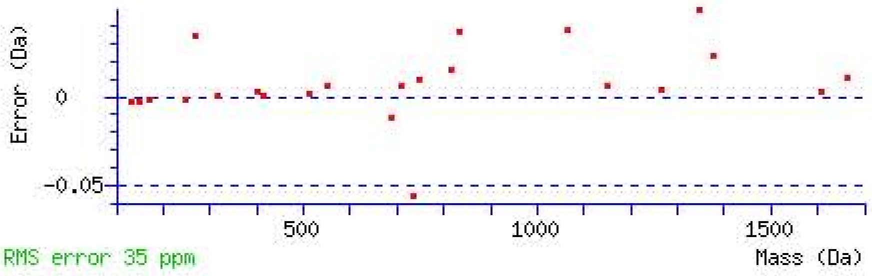
Match to Query 38081: 1775.914602 from(592.978810,3+) rtinseconds(1963) index(47167)
Title: Locus:1.1.1.2732.8 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

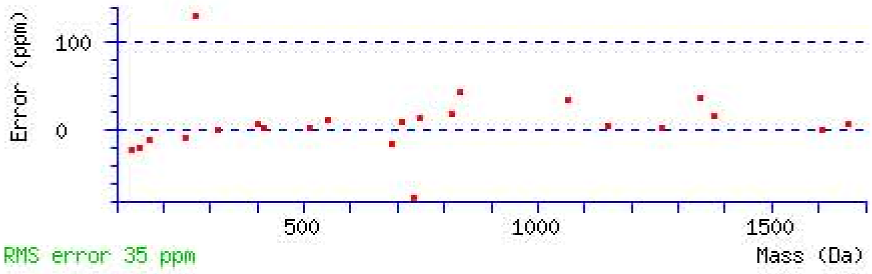
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 49  Expect: 0.00036
Matches : 23/110 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	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
48.5	1775.906250	0.008352	LGDDLLQCHPAVK

Mascot: http://www.matrixscience.com/

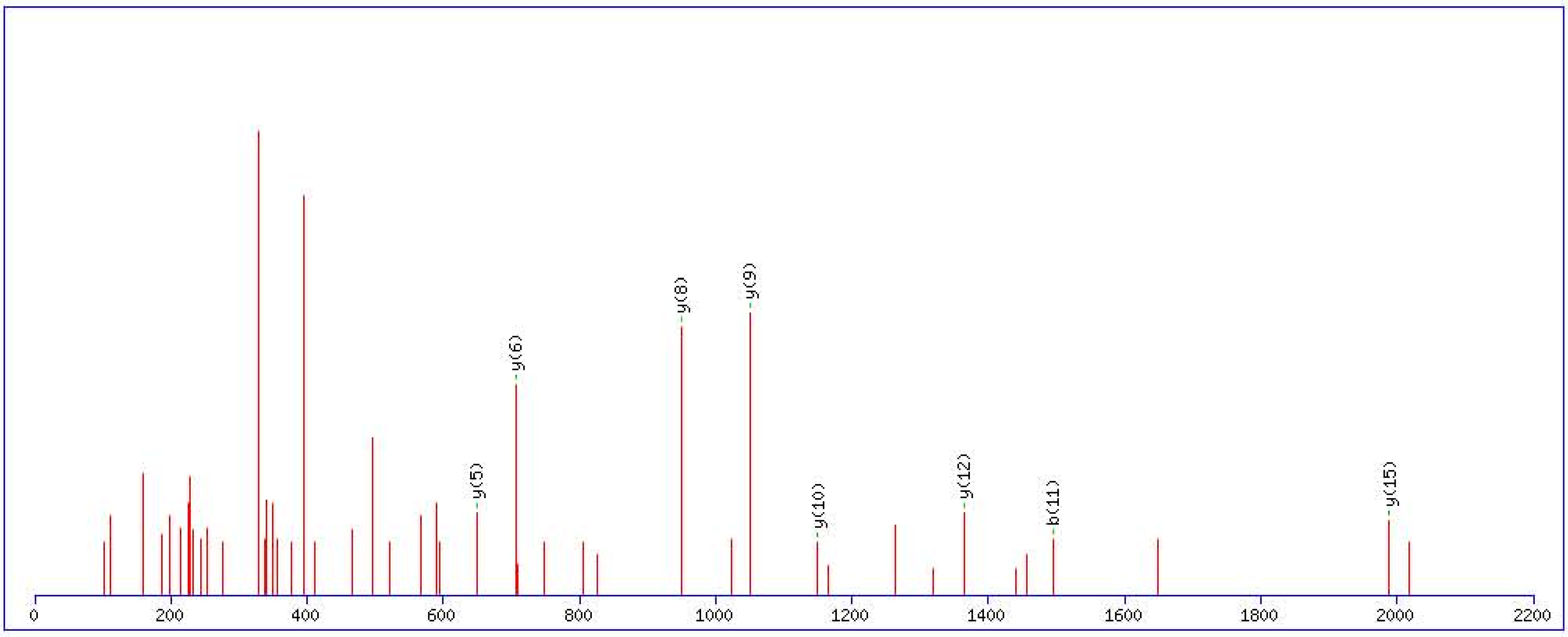
{MATRIX}{SCIENCE} Mascot Search Results

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

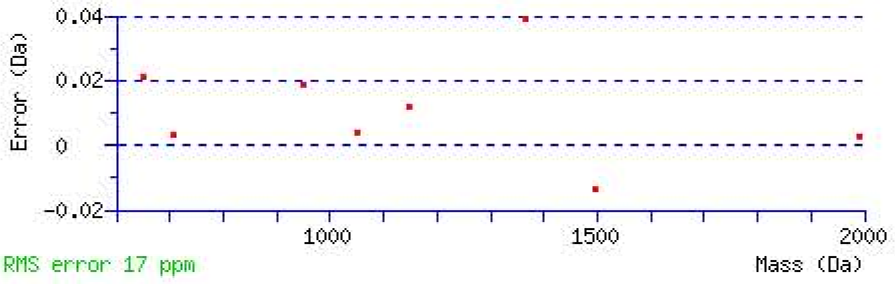
Match to Query 51648: 2543.237936 from(636.816760,4+) rtinseconds(2156) index(48375)
Title: Locus:1.1.1.2799.13 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

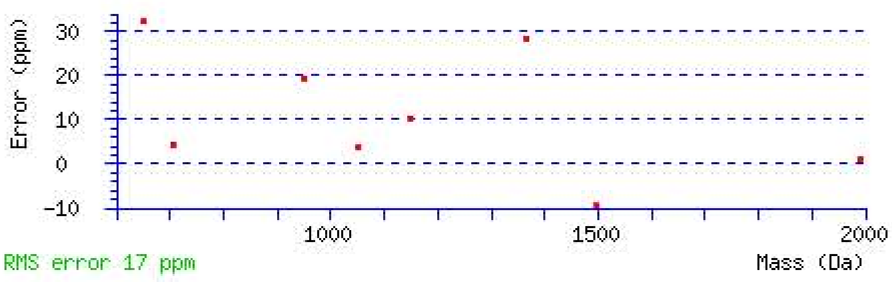
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2543.222702
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.021
Matches : 8/222 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	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
30.8	2543.222702	0.015234	ELNQAGQETLVTGWGYHSSR
21.1	2543.222702	0.015234	ELNQAGQETLVTGWGYHSSR

Mascot: http://www.matrixscience.com/

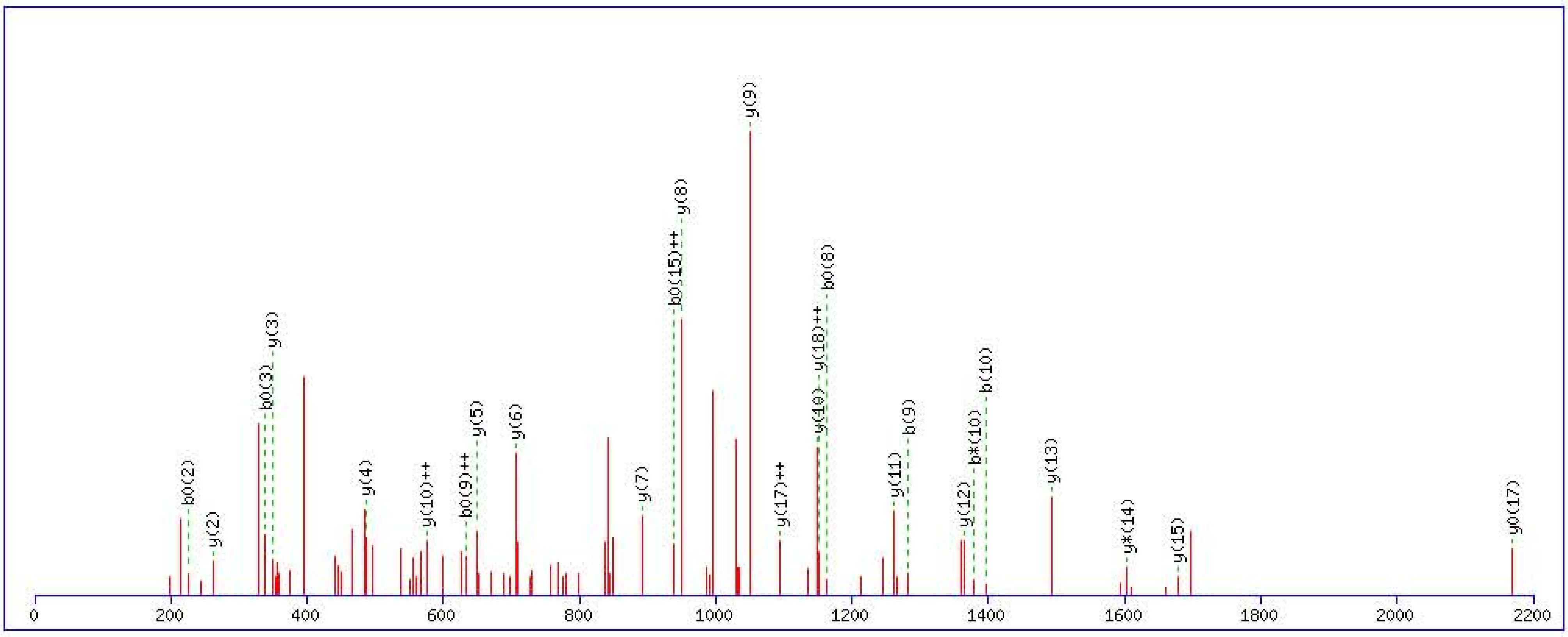
{MATRIX}{SCIENCE} Mascot Search Results

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

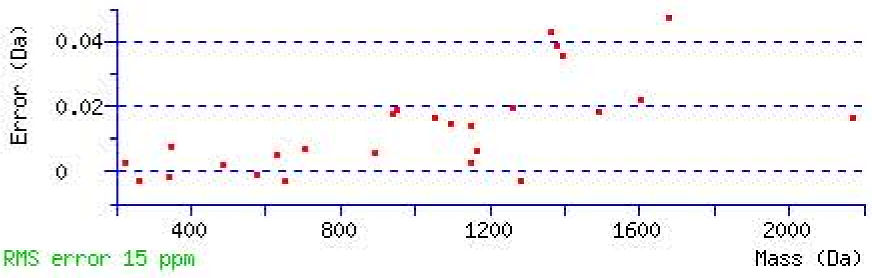
Match to Query 51649: 2543.254002 from(848.758610,3+) rtinseconds(2157) index(48385)
Title: Locus:1.1.1.2799.23 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

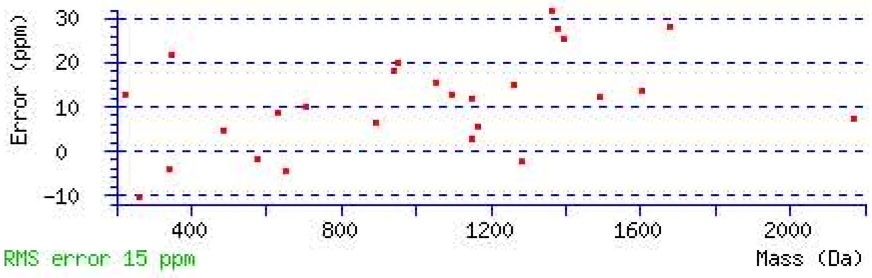
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2543.222702
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 67  Expect: 5.3e-006
Matches : 26/222 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							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	796.402186	398.704731	779.375637	390.191457	778.391621	389.699449	Q	2188.060401	1094.533838	2171.033852	1086.020564	2170.049836	1085.528556	17
5	867.439300	434.223288	850.412751	425.710014	849.428735	425.218006	A	1748.835075	874.921175	1731.808526	866.407901	1730.824510	865.915893	16
6	924.460764	462.734020	907.434215	454.220746	906.450199	453.728738	G	***1677.797961***	839.402618	1660.771412	830.889344	1659.787396	830.397336	15
7	1052.519342	526.763309	1035.492793	518.250035	1034.508777	517.758027	Q	1620.776497	810.891886	1603.749948	802.378612	1602.765932	801.886604	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	632.803162	T	***1363.675326***	682.341301	1346.648777	673.828026	1345.664761	673.336018	12
10	**1395.693678**	698.350477	1378.667129	689.837202	1377.683113	689.345194	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	738.879401	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	826.919255	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	911.445637	1820.899983	910.953629	W	***892.406026***	446.706651	875.379477	438.193376	874.395461	437.701368	7
15	1895.932012	948.469644	1878.905463	939.956369	1877.921447	939.464361	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
67.1	2543.222702	0.031300	ELNQAGQETLVTGWGYHSSR
63.7	2543.222702	0.031300	ELNQAGQETLVTGWGYHSSR

Mascot: http://www.matrixscience.com/

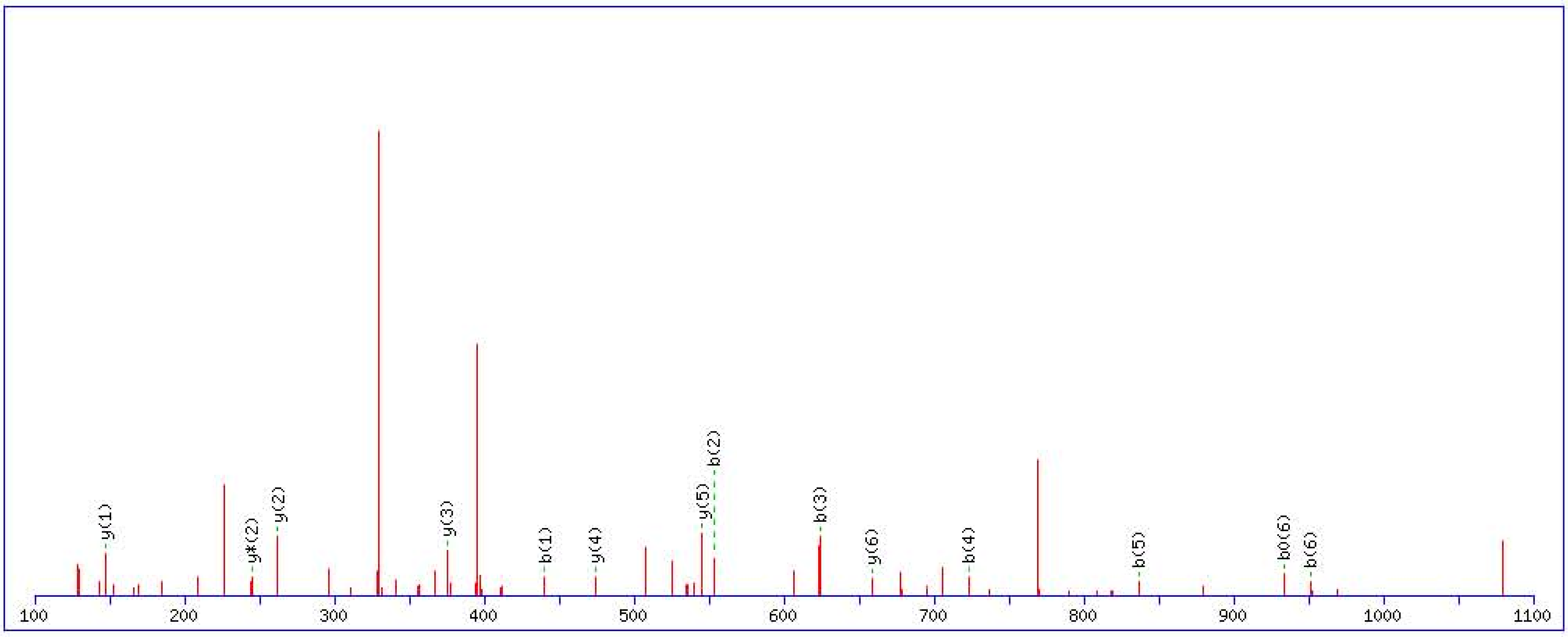
{MATRIX SCIENCE} Mascot Search Results

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

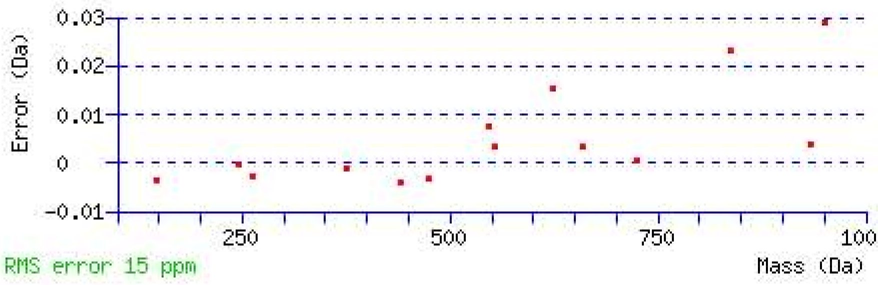
Match to Query 16121: 1096.634888 from(549.324720,2+) rtinseconds(1963) index(47165)
Title: Locus:1.1.1.2732.6 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

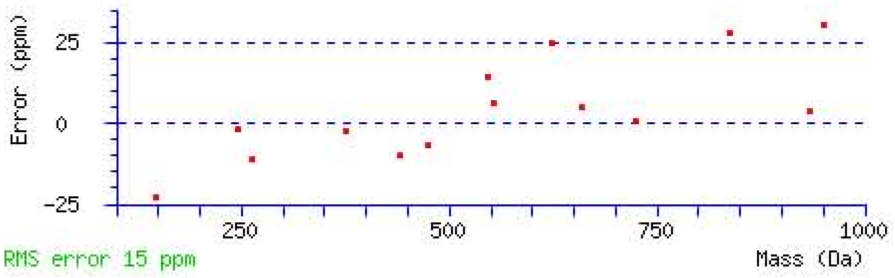
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1096.631439
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 26 **Expect:** 0.041
Matches : 14/60 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**							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
25.5	1096.631439	0.003449	QLAVLDK
17.4	1096.624054	0.010834	KPVDSVPLSR
8.7	1096.646500	-0.011612	KPDQARVRK
6.8	1096.639297	-0.004409	AHVSPLFKAK
6.6	1096.624023	0.010865	IPRENLLDK
3.6	1096.649200	-0.014312	KSPVPVETLK
1.2	1096.631439	0.003449	GILQLDK
1.2	1096.642654	-0.007766	NITMHLLKK
0.1	1096.631439	0.003449	QIDVAIK

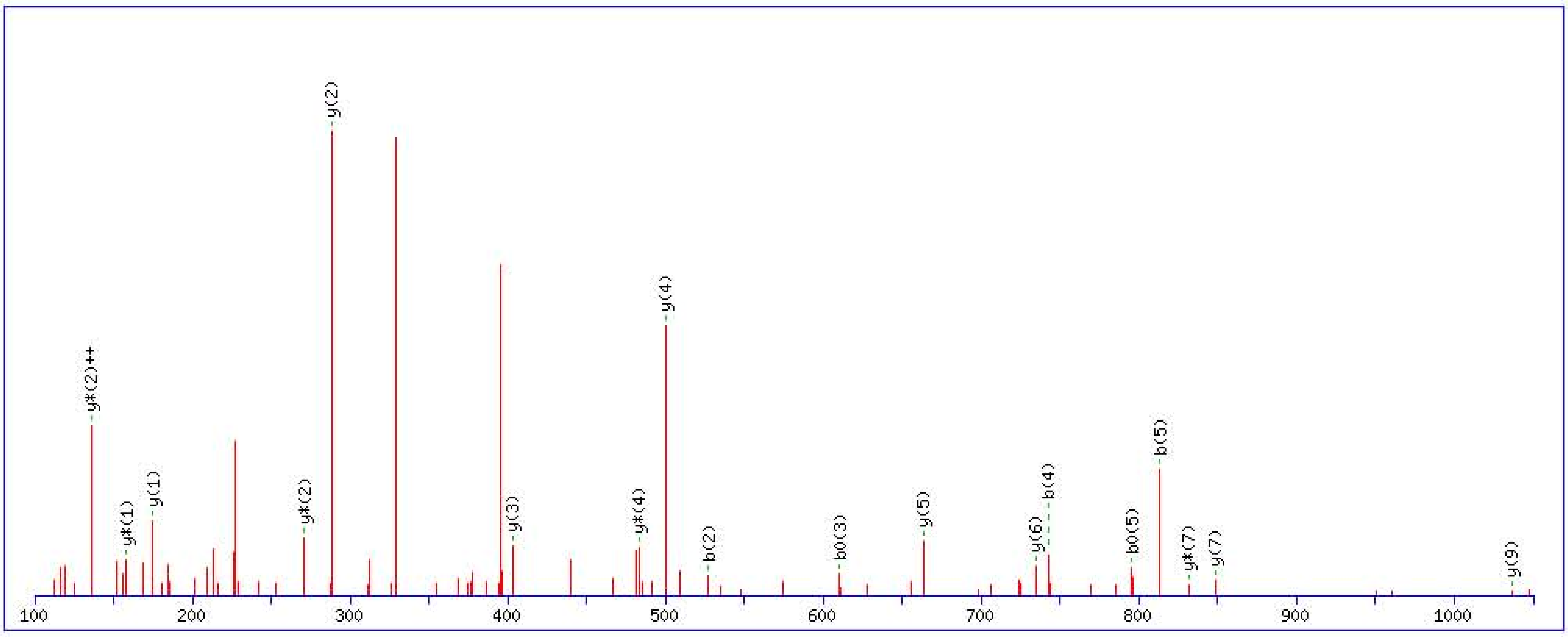
Mascot Search Results

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

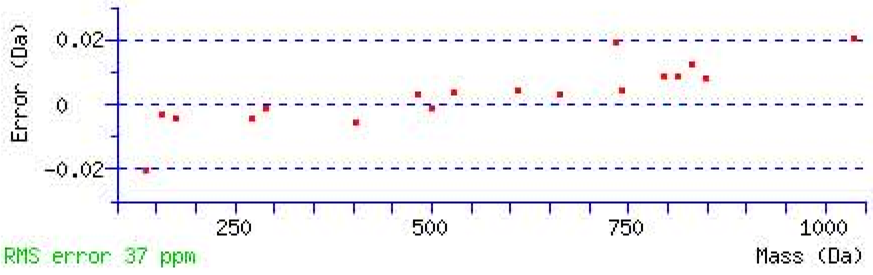
Match to Query 29282: 1474.722522 from(492.581450,3+) rtinseconds(1759) index(45839)
Title: Locus:1.1.1.2661.9 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

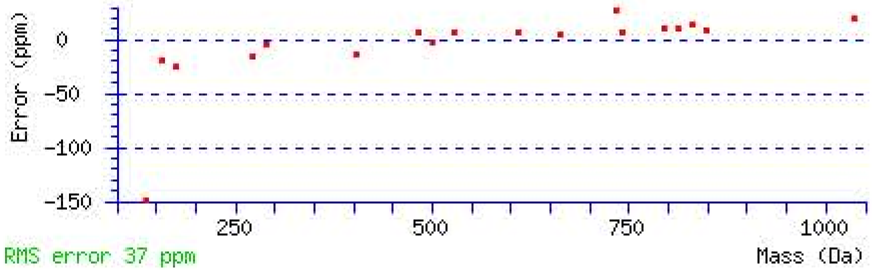
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1474.723831
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 55 **Expect:** 5.6e-005
Matches : 18/102 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	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
54.6	1474.723831	-0.001309	QSTNAYPDLR
8.7	1474.741592	-0.019070	SSLEHGSDVYLLR
8.3	1474.719788	0.002734	QQEELEQMRLR
6.0	1474.719803	0.002719	ALPNSGDETLMRR
3.1	1474.721161	0.001361	QSTHGERGHR
1.7	1474.719788	0.002734	QRLQEQEEMLR
1.5	1474.725159	-0.002637	HEEFRWMRLR

Mascot: http://www.matrixscience.com/

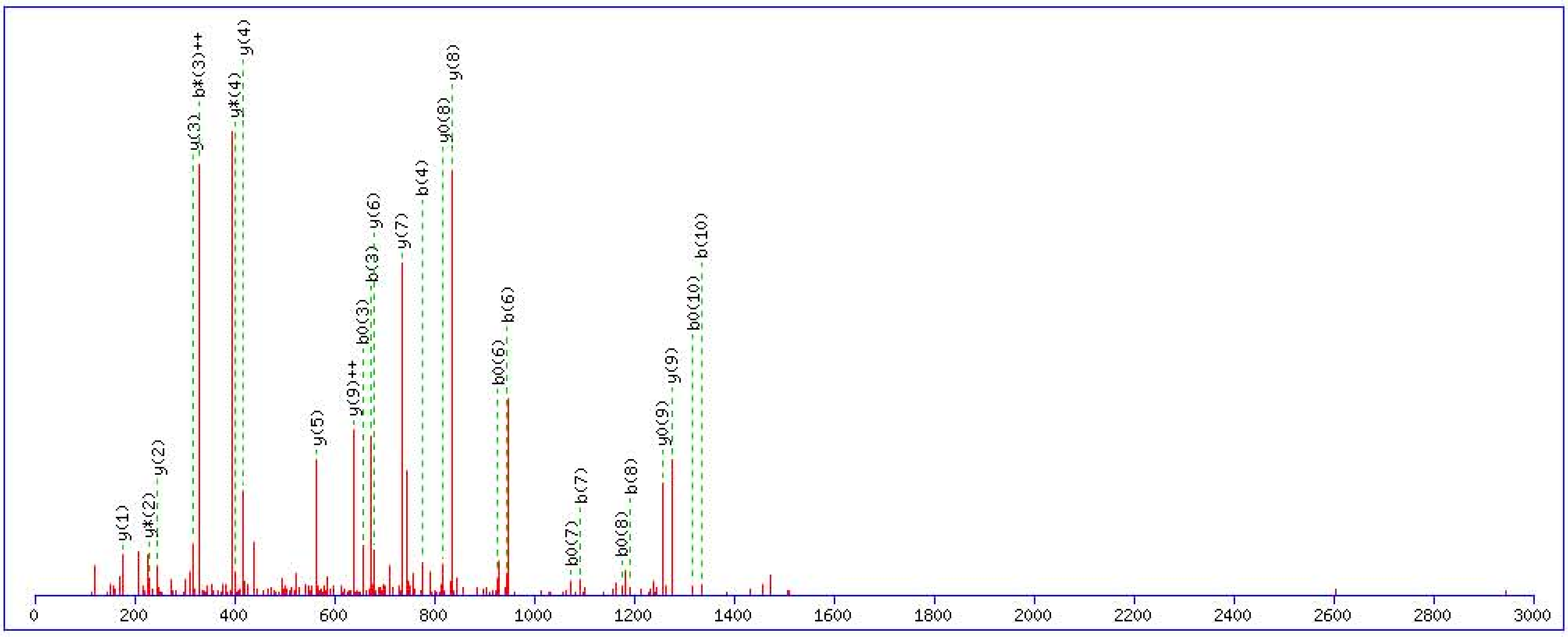
{MATRIX SCIENCE} Mascot Search Results

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

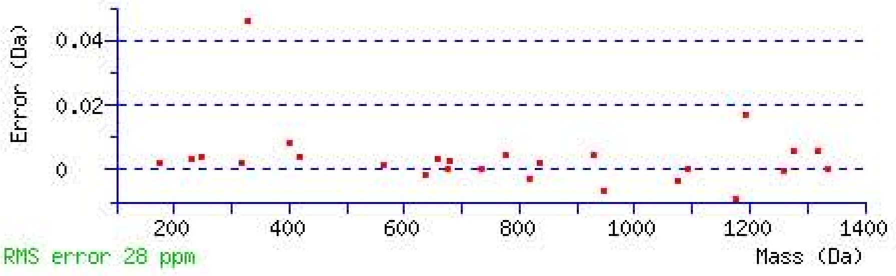
Match to Query 30243: 1508.787888 from(755.401220,2+) rtinseconds(2315) index(34898)
Title: Locus:1.1.1.3355.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

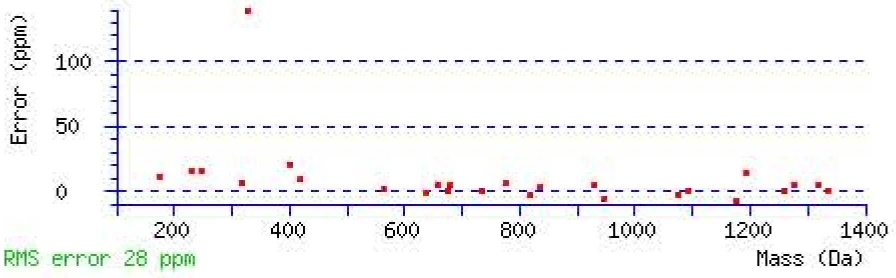
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1508.780975
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00023
Matches : 26/110 fragment ions using 55 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	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
48.2	1508.780975	0.006913	SFQTGLFTAAR
8.8	1508.805893	-0.018005	RLELPRASDAEPR
5.3	1508.776917	0.010971	MYLDLLSQSQRR
5.2	1508.798721	-0.010833	SSYGVAAPVDFLRK
4.3	1508.765701	0.022187	TKPLSMLYVDNGR
3.8	1508.776932	0.010956	LMGADSLQLFRSR
2.9	1508.780960	0.006928	TQPPPENLFR
0.3	1508.765686	0.022202	TKAFQIMQEELR
0.3	1508.765701	0.022187	LATNMAVITDFSAR

Mascot: http://www.matrixscience.com/

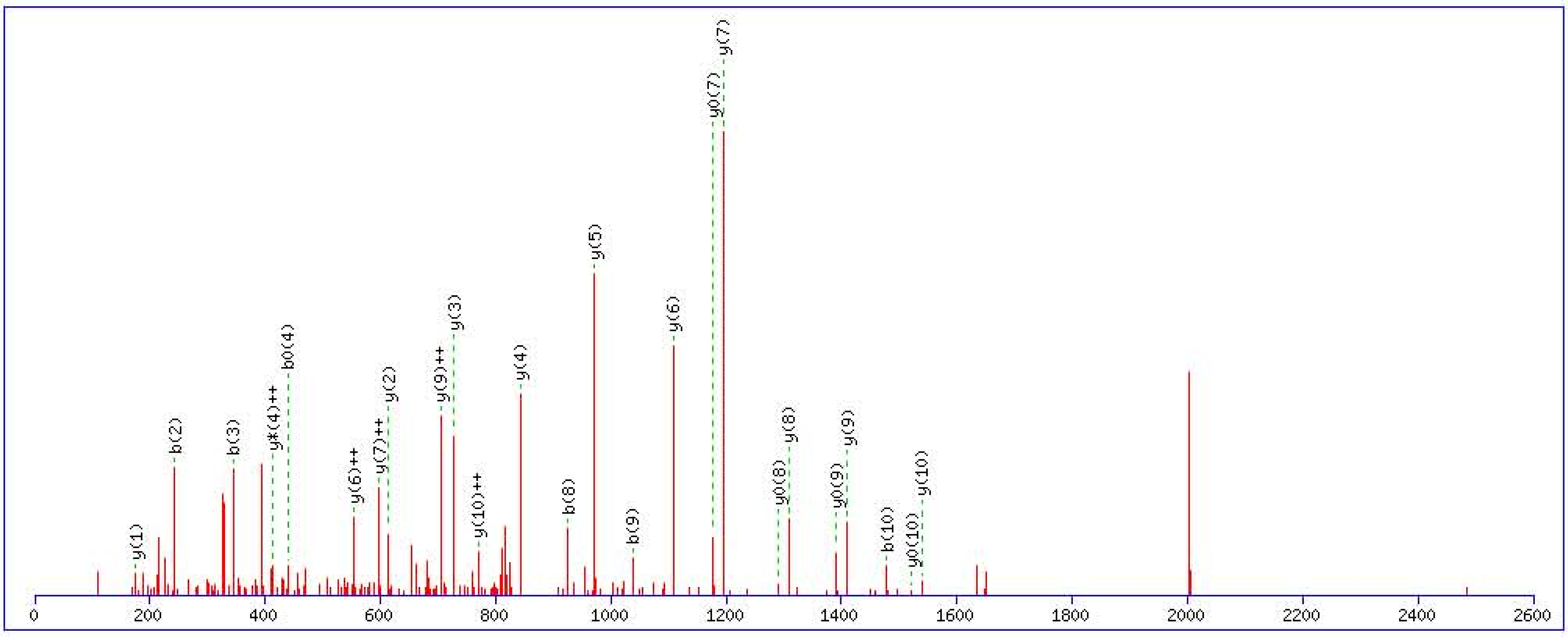
Mascot Search Results

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

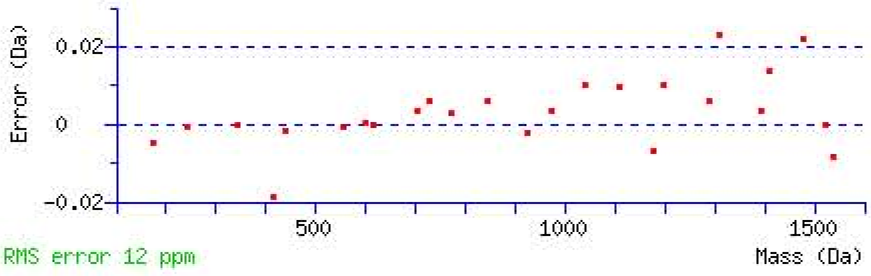
Match to Query 35456: 1650.852068 from(826.433310,2+) rtinseconds(1622) index(45007)
Title: Locus:1.1.1.2613.14 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

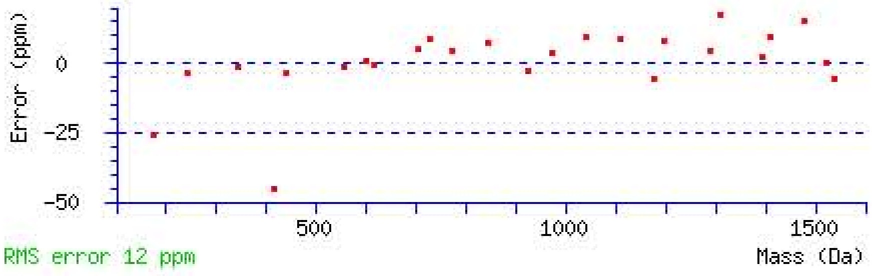
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1650.839920
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 91  Expect: 2.1e-008
Matches : 25/94 fragment ions using 32 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					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
90.6	1650.839920	0.012148	IETISHEDLQR
15.8	1650.870239	-0.018171	LFRSNSHLKEHQR
9.8	1650.855881	-0.003813	MQRTGGGAPRPGR
8.2	1650.858551	-0.006483	LQQEQDLR
7.7	1650.833389	0.018679	QQLEHIMATNR
7.3	1650.839935	0.012133	MQLLKDVVGNDTYR
4.5	1650.843765	0.008303	TLQPSSQNTKAHPSR
3.4	1650.868896	-0.016828	LELLELDHEQTRR
2.6	1650.847305	0.004763	LLFQELMSMSIAPR
2.3	1650.858536	-0.006468	QLNEELQR

Mascot: http://www.matrixscience.com/

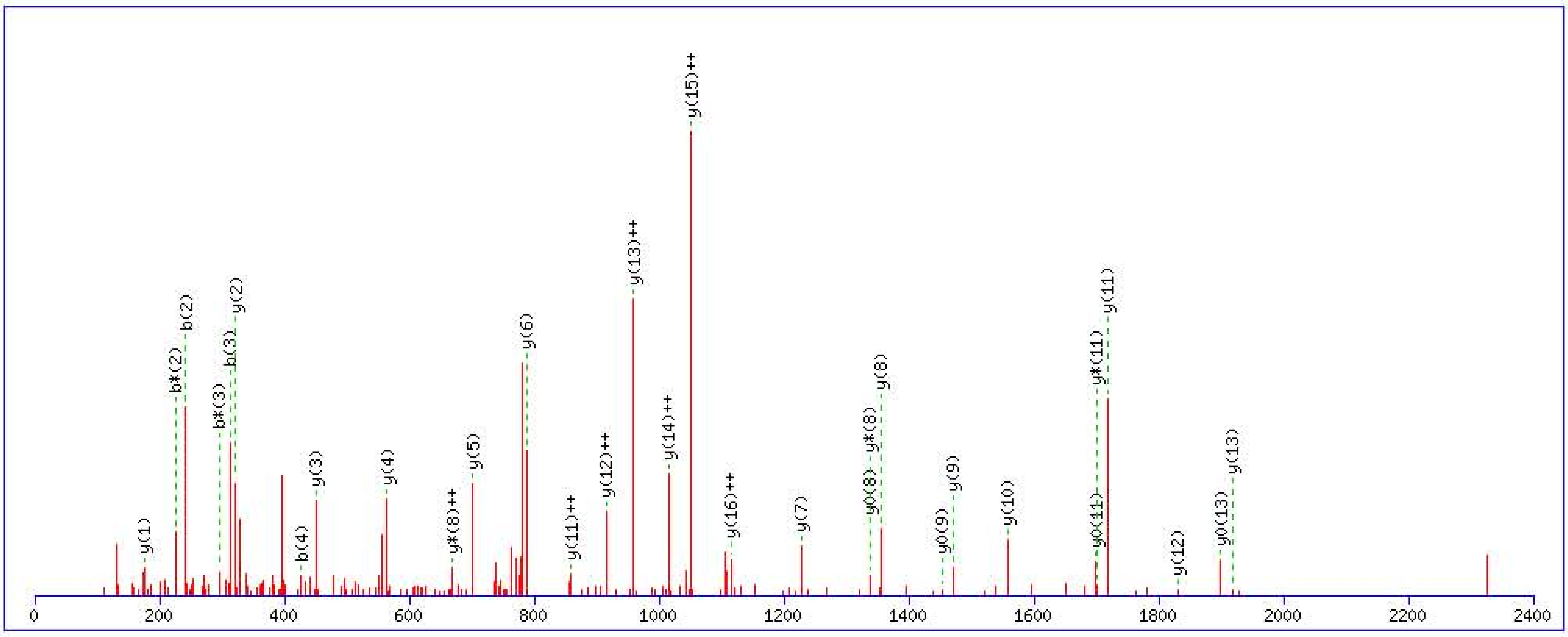
{MATRIX SCIENCE} Mascot Search Results

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

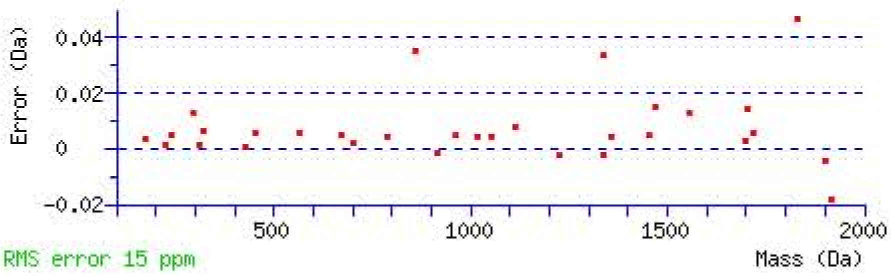
Match to Query 48440: 2342.156262 from(781.726030,3+) rtinseconds(2202) index(63702)
Title: Locus:1.1.1.3393.6 File:"2013-07-02 CLN FXIII 60 min 3rd FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

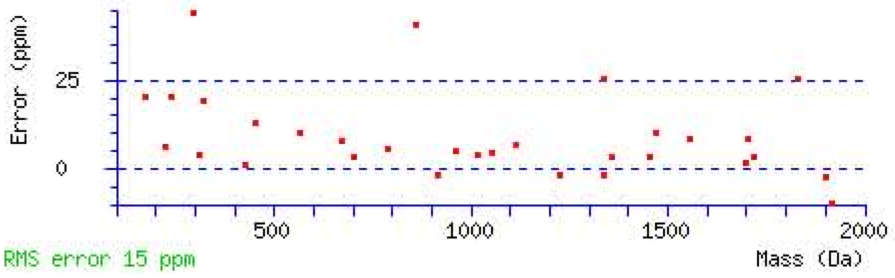
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2342.151108
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 79  Expect: 3.7e-007
Matches : 31/178 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	114.091340	57.549308					I							17
2	**242.149918**	121.578597	225.123369	113.065323			Q	2230.074335	1115.540805	2213.047786	1107.027531	2212.063770	1106.535523	16
3	**313.187032**	157.097154	296.160483	148.583879			A	2102.015757	1051.511516	2084.989208	1042.998242	2084.005192	1042.506234	15
4	**426.271096**	213.639186	409.244547	205.125912			L	2030.978643	1015.992959	2013.952094	1007.479685	2012.968078	1006.987677	14
5	513.303124	257.155200	496.276575	248.641926	495.292559	248.149918	S	***1917.894579***	959.450927	1900.868030	950.937653	1899.884014	950.445645	13
6	626.387188	313.697232	609.360639	305.183958	608.376623	304.691950	L	***1830.862551***	915.934913	1813.836002	907.421639	1812.851986	906.929631	12
7	786.417837	393.712557	769.391288	385.199282	768.407272	384.707274	C	***1717.778487***	859.392881	1700.751938	850.879607	1699.767922	850.387599	11
8	873.449865	437.228571	856.423316	428.715296	855.439300	428.223288	S	***1557.747838***	779.377557	1540.721289	770.864282	1539.737273	770.372274	10
9	988.476808	494.742042	971.450259	486.228768	970.466243	485.736760	D	***1470.715810***	735.861543	1453.689261	727.348268	1452.705245	726.856260	9
10	1116.535386	558.771331	1099.508837	550.258057	1098.524821	549.766049	Q	***1355.688867***	678.348071	1338.662318	669.834797	1337.678302	669.342789	8
11	1555.760712	778.383994	1538.734163	769.870720	1537.750147	769.378712	Q	***1227.630289***	614.318782	1210.603740	605.805508	1209.619724	605.313500	7
12	1642.792740	821.900008	1625.766191	813.386734	1624.782175	812.894726	S	***788.404963***	394.706119	771.378414	386.192845	770.394398	385.700837	6
13	1779.851652	890.429464	1762.825103	881.916190	1761.841087	881.424182	H	***701.372935***	351.190105	684.346386	342.676831	683.362370	342.184823	5
14	1892.935716	946.971496	1875.909167	938.458222	1874.925151	937.966213	L	***564.314023***	282.660649	547.287474	274.147375	546.303458	273.655367	4
15	2021.978309	1011.492793	2004.951760	1002.979518	2003.967744	1002.487510	E	***451.229959***	226.118617	434.203410	217.605343	433.219394	217.113335	3
16	2169.046723	1085.026999	2152.020174	1076.513725	2151.036158	1076.021717	F	***322.187366***	161.597321	305.160817	153.084046			2
17							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IQALSLCSDQQSHLEFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
79.0	2342.151108	0.005154	IQALSLCSDQQSHLEFR
67.6	2342.151108	0.005154	IQALSLCSDQQSHLEFR

Mascot: http://www.matrixscience.com/

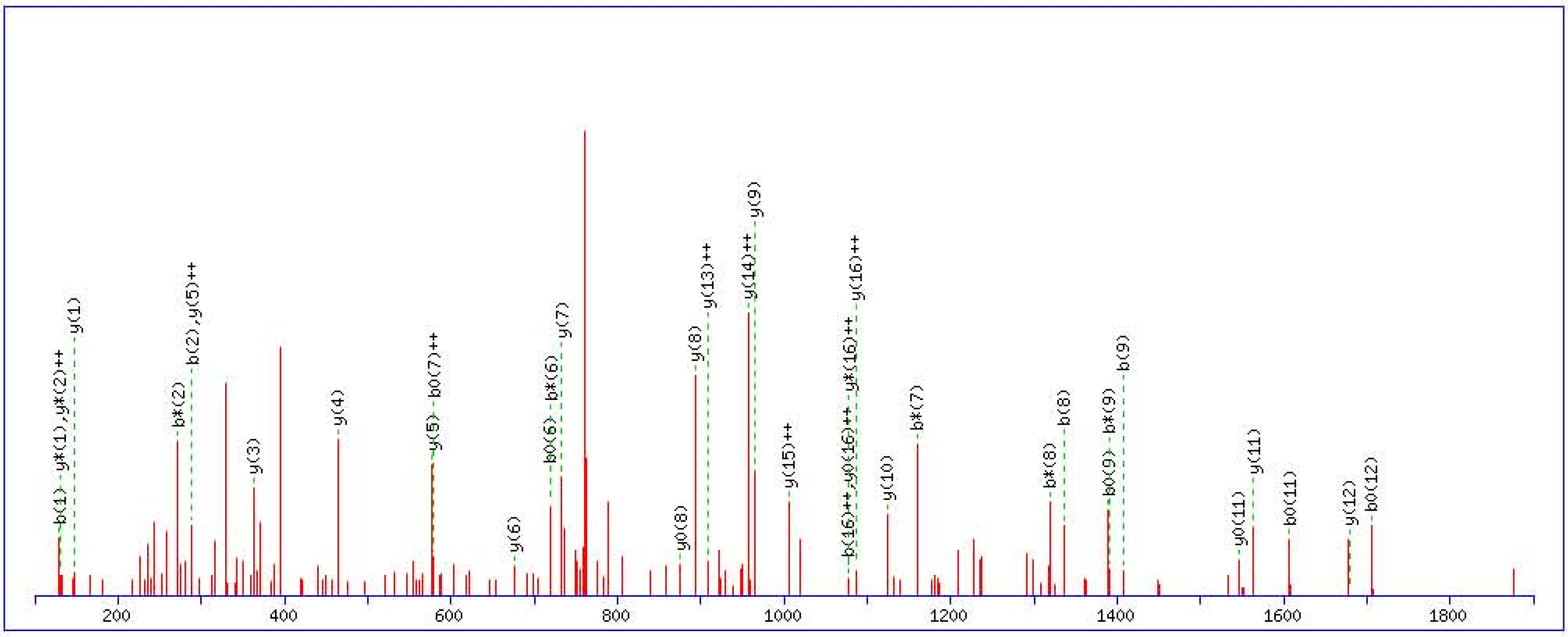
{MATRIX SCIENCE} Mascot Search Results

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

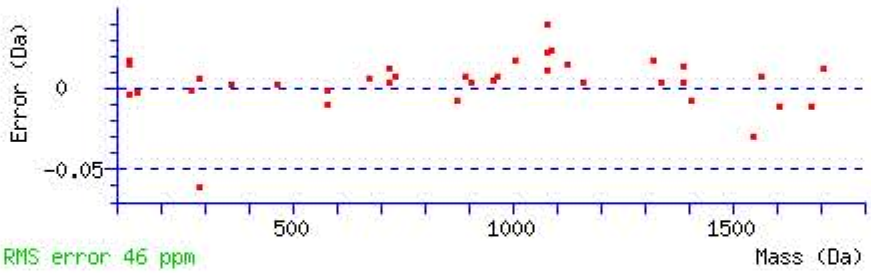
Match to Query 47800: 2299.031532 from(767.351120,3+) rtinseconds(1610) index(44930)
Title: Locus:1.1.1.2609.14 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

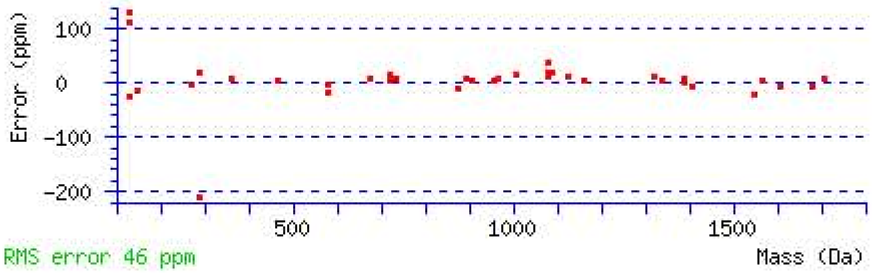
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2299.021790
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 57 **Expect:** 2.1e-005
Matches : 37/180 fragment ions using 63 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	**129.065854**	65.036565	112.039305	56.523291			Q							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
56.9	2299.021790	0.009742	QCVPHDQCACGVLTSEK
23.9	2299.021790	0.009742	QCVPHDQCACGVLTSEK

Mascot: http://www.matrixscience.com/

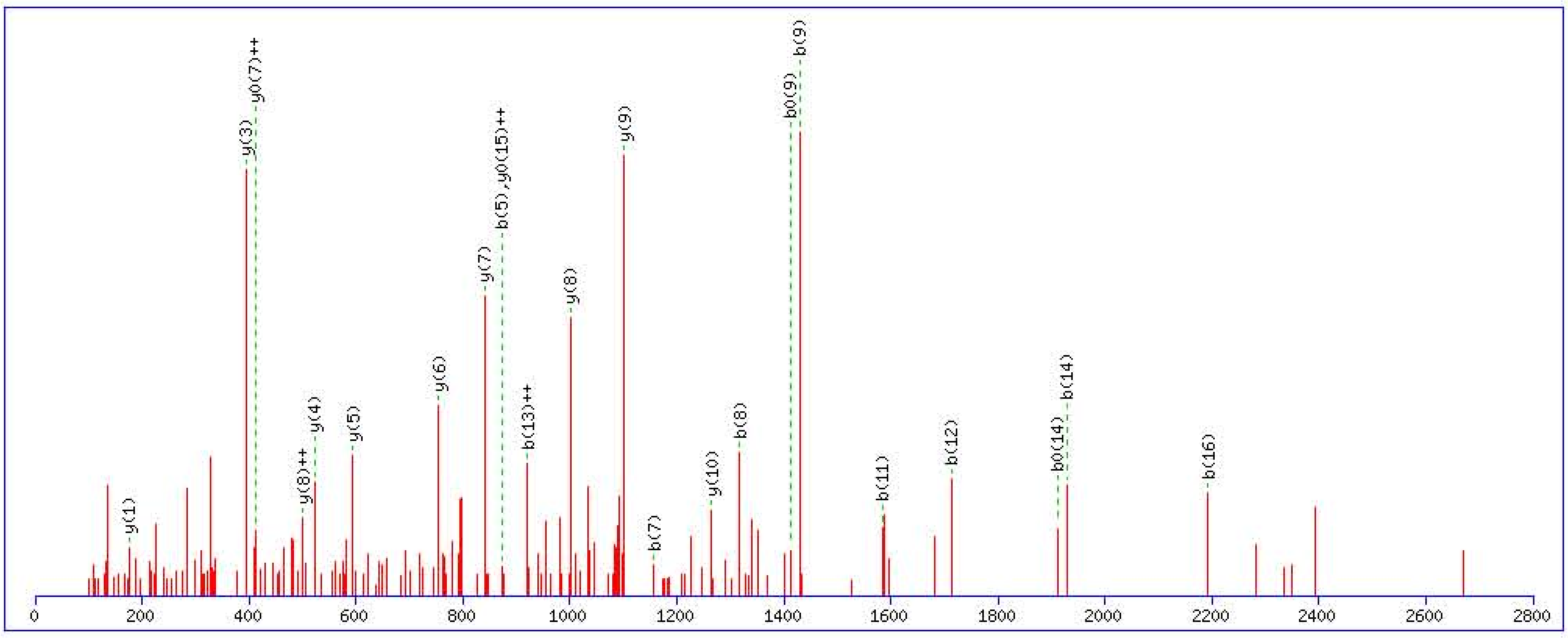
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TDGCQHFCLPGQESYTCSCAQGYR**
Found in **PROZ_HUMAN**, Vitamin K-dependent protein Z OS=Homo sapiens GN=PROZ PE=1 SV=2

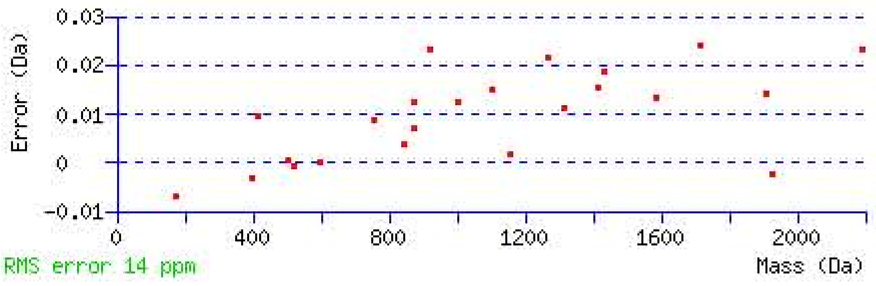
Match to Query 57532: 3192.325696 from(799.088700,4+) rtinseconds(2050) index(47700)
Title: Locus:1.1.1.2762.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

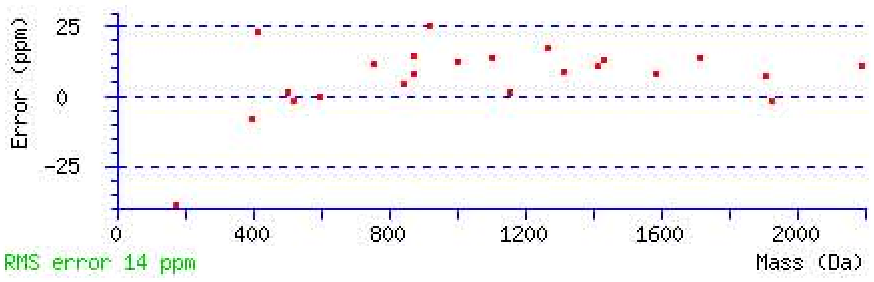
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3192.298050
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 57 **Expect:** 3.6e-006
Matches : 23/256 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	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
57.1	3192.298050	0.027646	TDGCQHFCLPGQESYTCSCAQGYR
29.5	3192.298050	0.027646	TDGCQHFCLPGQESYTCSCAQGYR

Mascot: http://www.matrixscience.com/

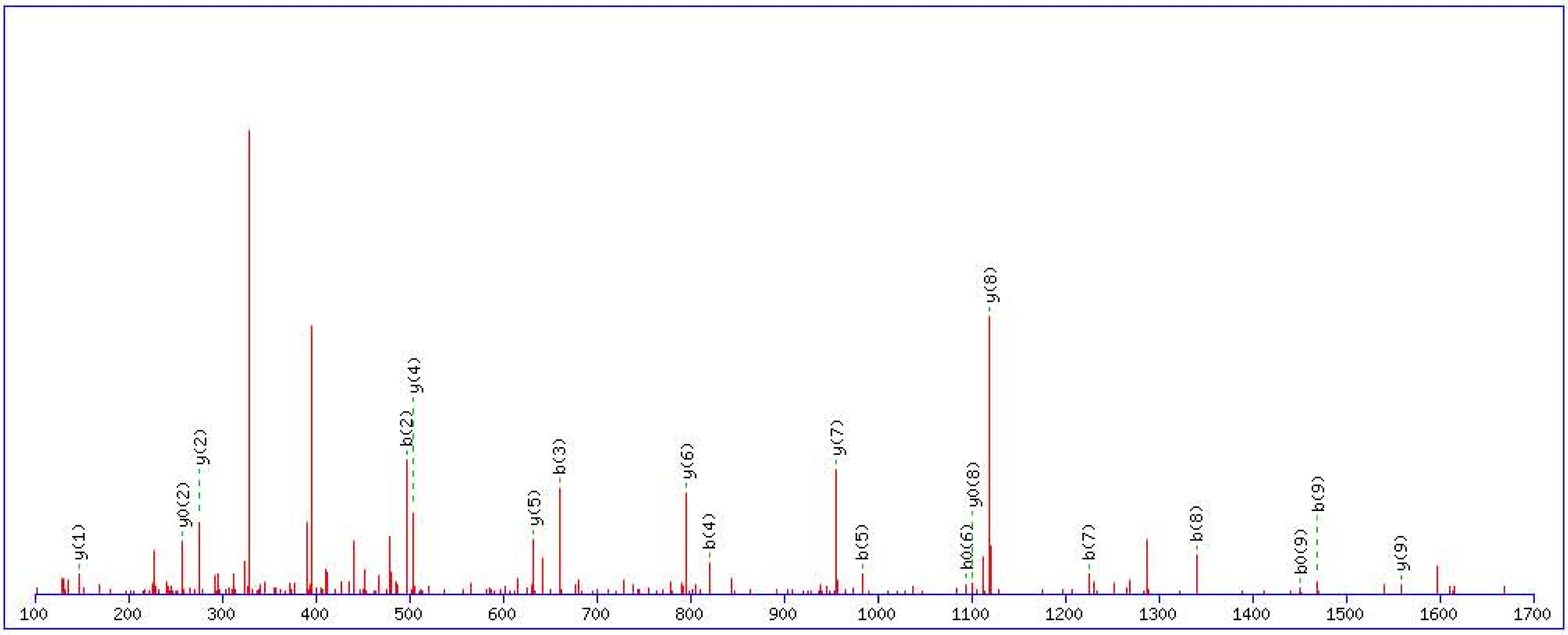
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQYCYELDEK**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

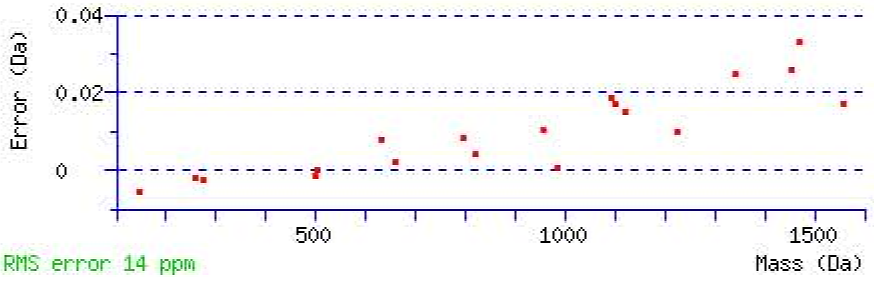
Match to Query 33812: 1614.722828 from(808.368690,2+) rtinseconds(1865) index(46397)
Title: Locus:1.1.1.2698.10 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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 ●

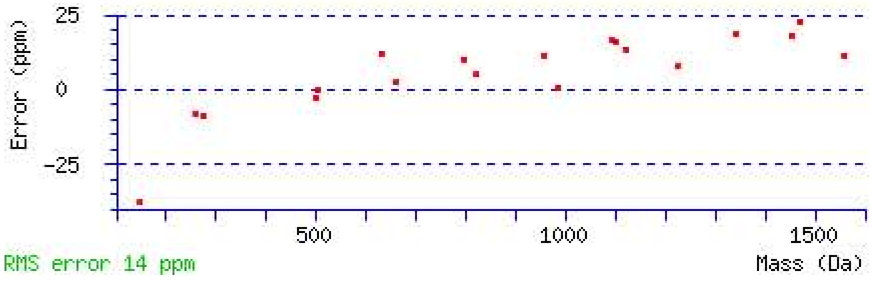


Monoisotopic mass of neutral peptide Mr(calc): 1614.705795
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 51 **Expect:** 4.2e-005
Matches : 19/94 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							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



RMS error 14 ppm



RMS error 14 ppm

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
51.2	1614.705795	0.017033	GQYCYELDEK
6.8	1614.717010	0.005818	EYFRMELMHAEK
3.7	1614.738129	-0.015301	EKAKADAECYTAMK

Mascot: http://www.matrixscience.com/

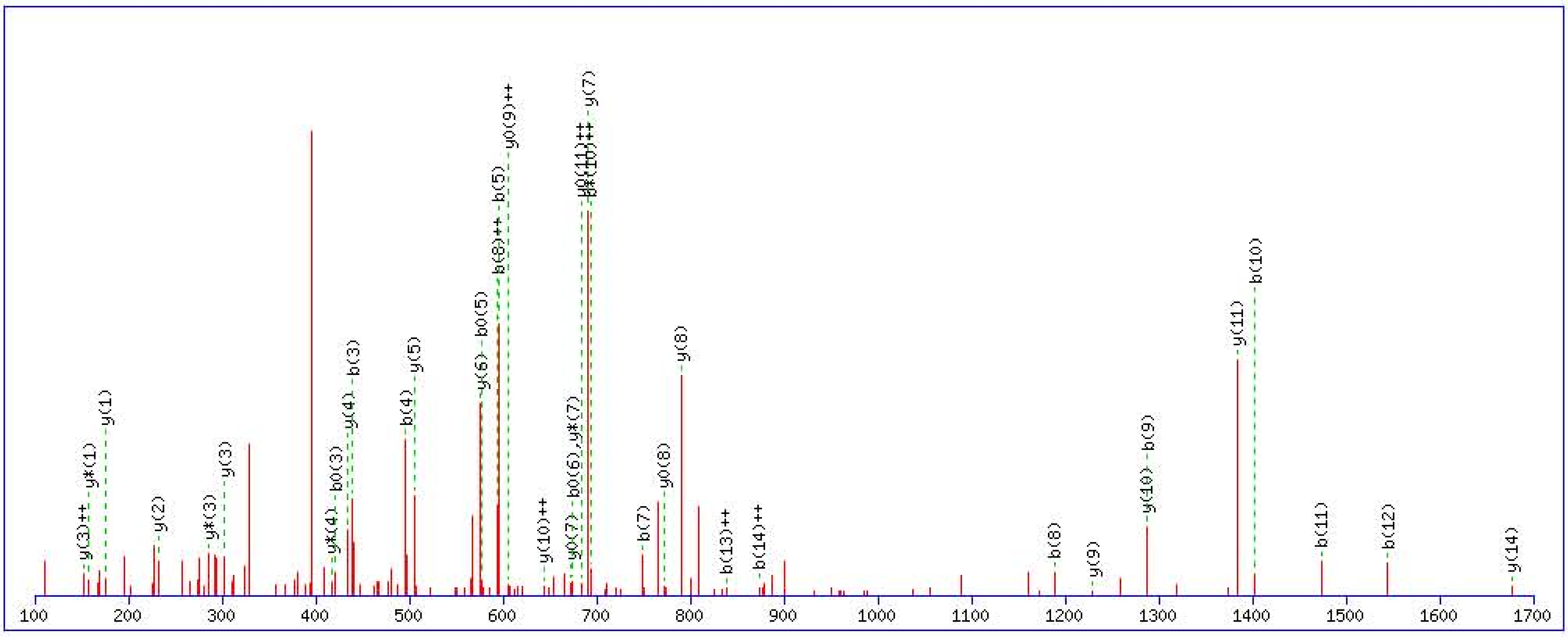
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DWHGVPGQVDAAMAGR**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

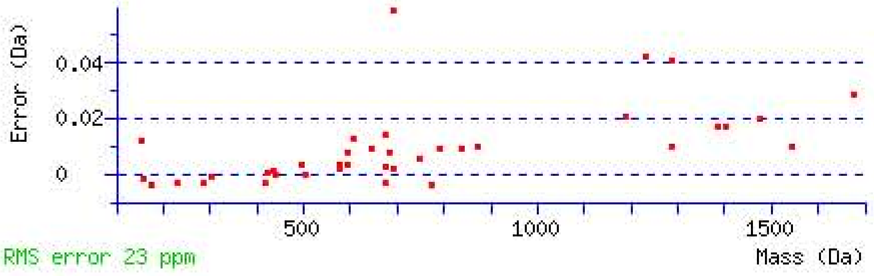
Match to Query 41611: 1976.947692 from(659.989840,3+) rtinseconds(2162) index(48425)
Title: Locus:1.1.1.2801.13 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

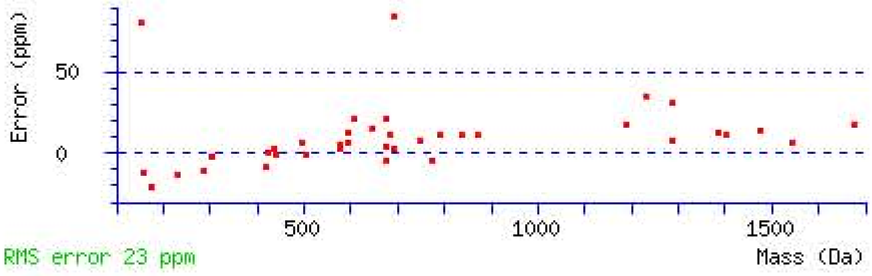
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1976.934937
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 4.6e-005
Matches : 38/154 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	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
52.0	1976.934937	0.012755	DWHGVPGQVDAAMAGR
5.8	1976.918793	0.028899	DDGLQYRPDVKDASDQR

Mascot: http://www.matrixscience.com/

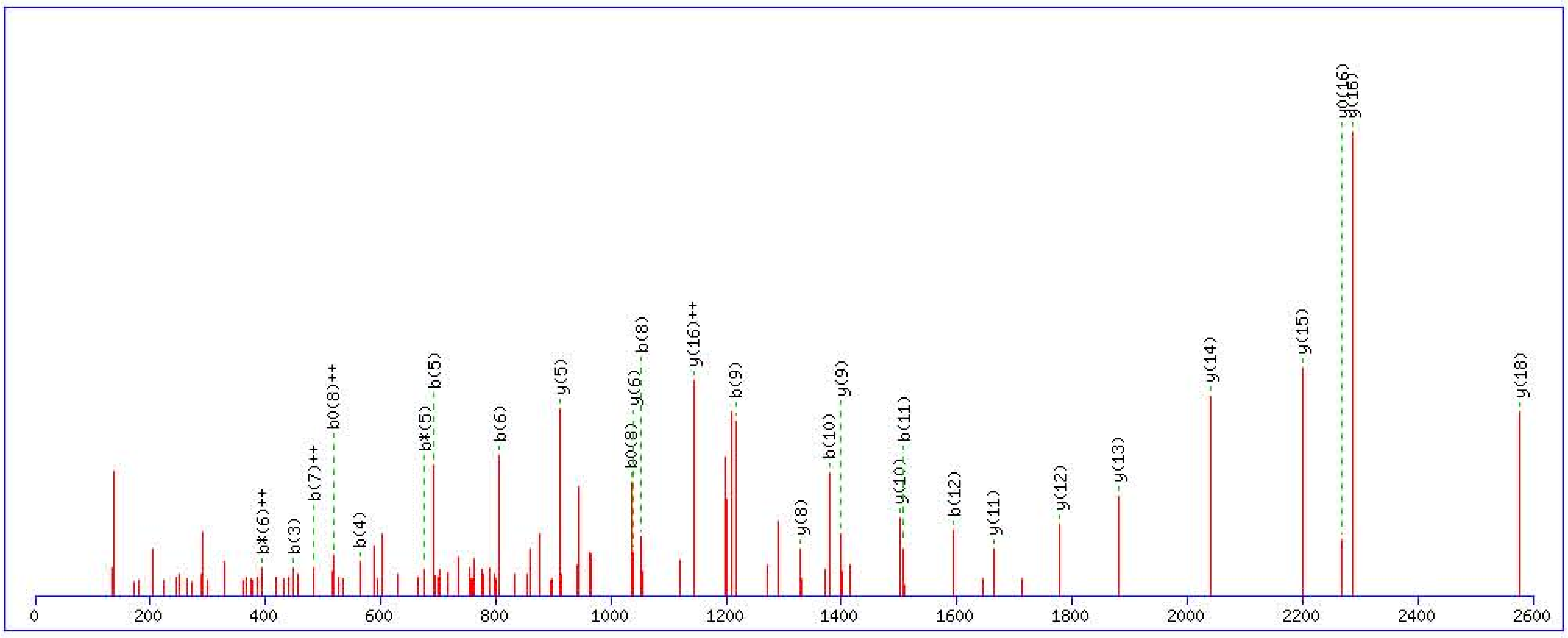
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CQCDELCSYYQSCCTDYTAECKPQVTR**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

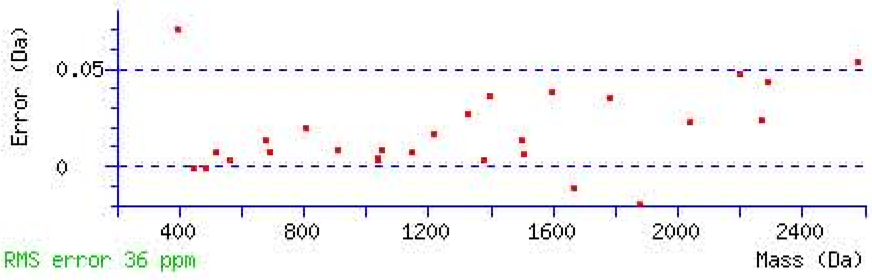
Match to Query 62956: 3792.552456 from(949.145390,4+) rtinseconds(1944) index(47018)
Title: Locus:1.1.1.2725.21 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

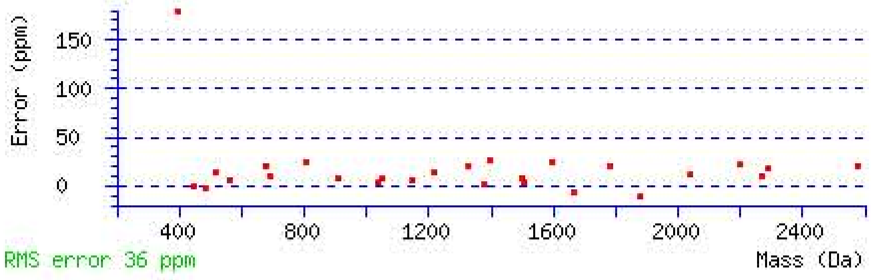
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3792.511536
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q24     : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 6.3e-007
Matches : 28/302 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	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
62.0	3792.511536	0.040920	CQCDELCSYYQSCCTDYTAECKPQVTR
9.9	3792.511536	0.040920	CQCDELCSYYQSCCTDYTAECKPQVTR

Mascot: http://www.matrixscience.com/

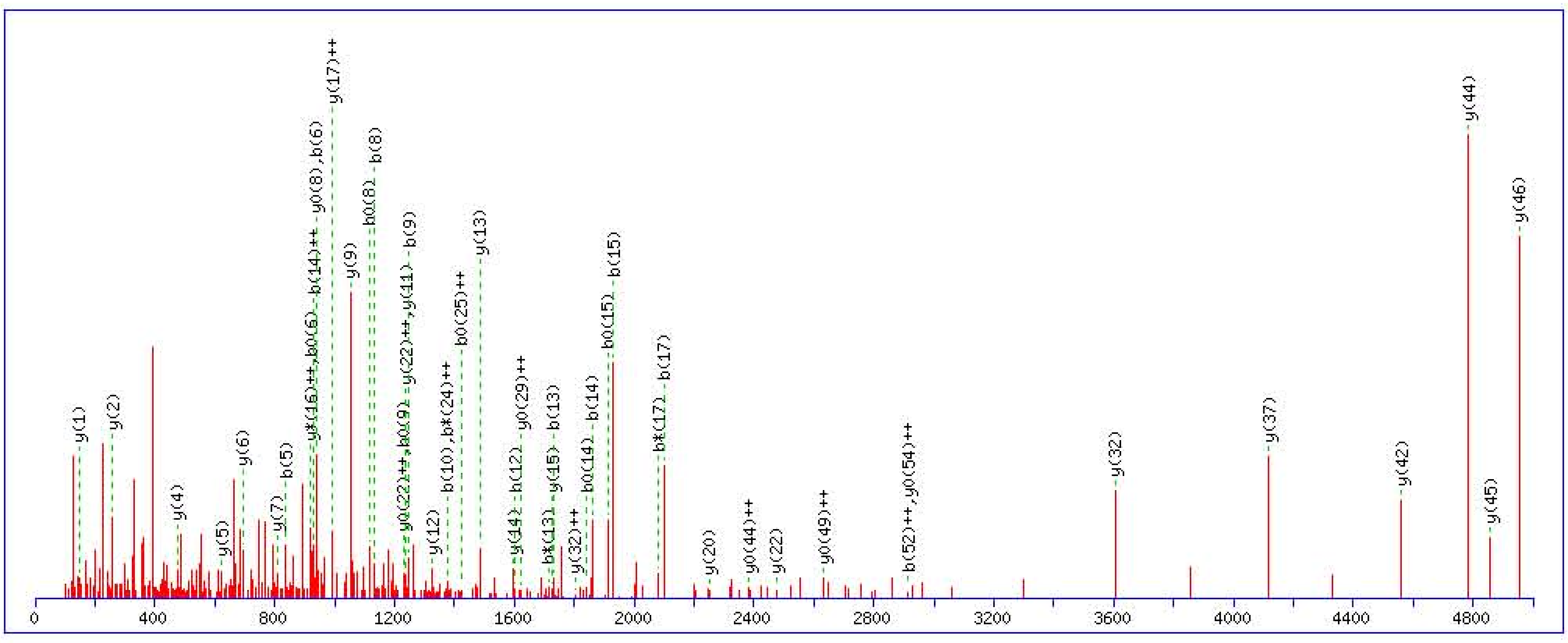
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNPEQTPVLKPEEEAPAPEVGASKPEGIDSRPETLHPGRPQPPAEEELCSGKPFDAFTDLK**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

Match to Query 70831: 6883.397632 from(861.431980,8+) rtinseconds(2086) index(33617)
Title: Locus:1.1.1.3275.17 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 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 5000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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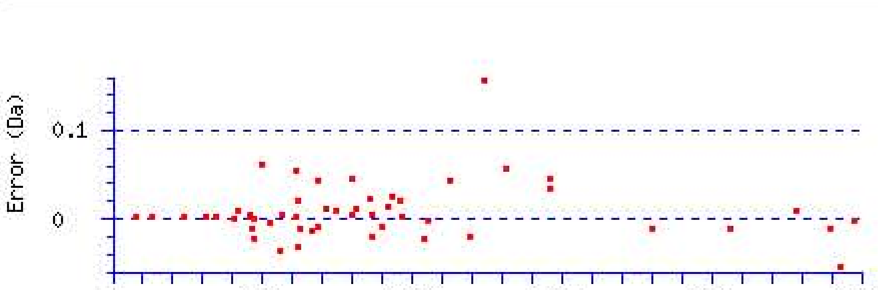
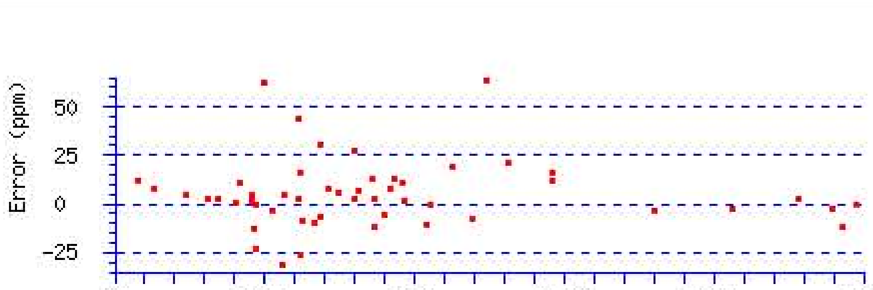
Monoisotopic mass of neutral peptide Mr(calc): 6883.374893
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.0031
Matches : 51/708 fragment ions using 157 most intense peaks   (help)
```

#	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
35.9	6883.374893	0.022739	GNPEQTPVLKPEEEAPAPEVGASKPEGIDSRPETLHPGRPQPPAEEELCSGKPFDAFTDLK
0.1	6883.374893	0.022739	GNPEQTPVLKPEEEAPAPEVGASKPEGIDSRPETLHPGRPQPPAEEELCSGKPFDAFTDLK

Mascot: http://www.matrixscience.com/

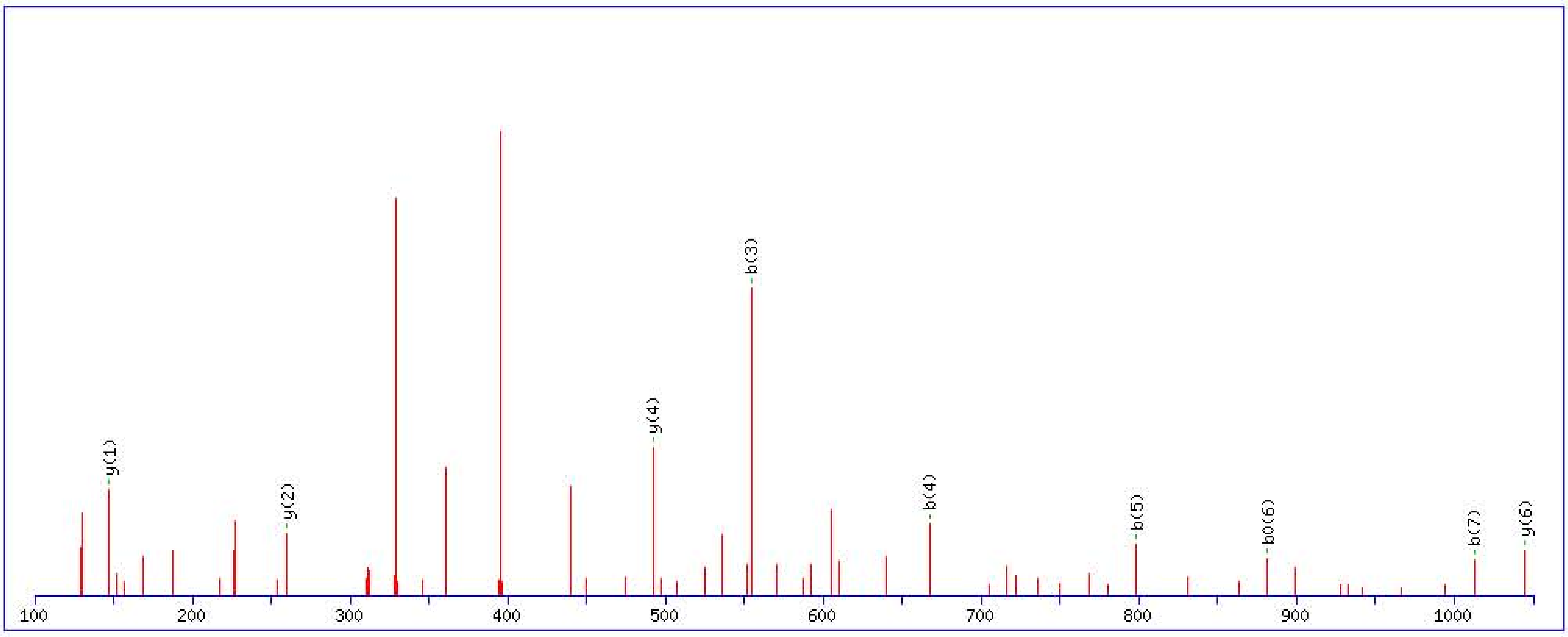
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGQIMTLK**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

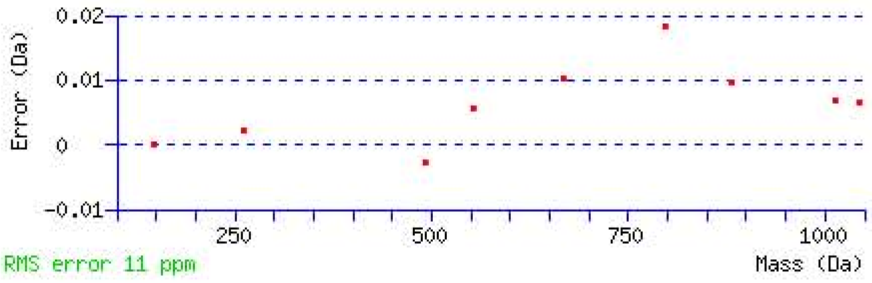
Match to Query 19020: 1157.628388 from(579.821470,2+) rtinseconds(1919) index(32561)
Title: Locus:1.1.1.3217.18 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

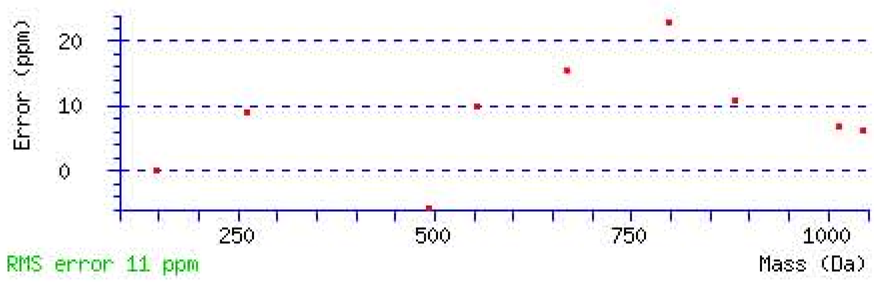
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1157.630066
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.0022
Matches : 9/66 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
41.1	1157.630066	-0.001678	GGQIMTLK
16.2	1157.630051	-0.001663	QLSQMLK
12.7	1157.630051	-0.001663	QIKSMLQ
12.7	1157.630051	-0.001663	QLSQMLK
10.8	1157.640411	-0.012023	AQQLLSSGNLK
10.5	1157.619293	0.009095	TNFEGPPRLK
10.2	1157.630035	-0.001647	EAQKMLK
9.6	1157.630051	-0.001663	QAGAMLLK
8.2	1157.622665	0.005723	QRTDSLK
6.9	1157.640411	-0.012023	SPGKNSSIQLK

Mascot: http://www.matrixscience.com/

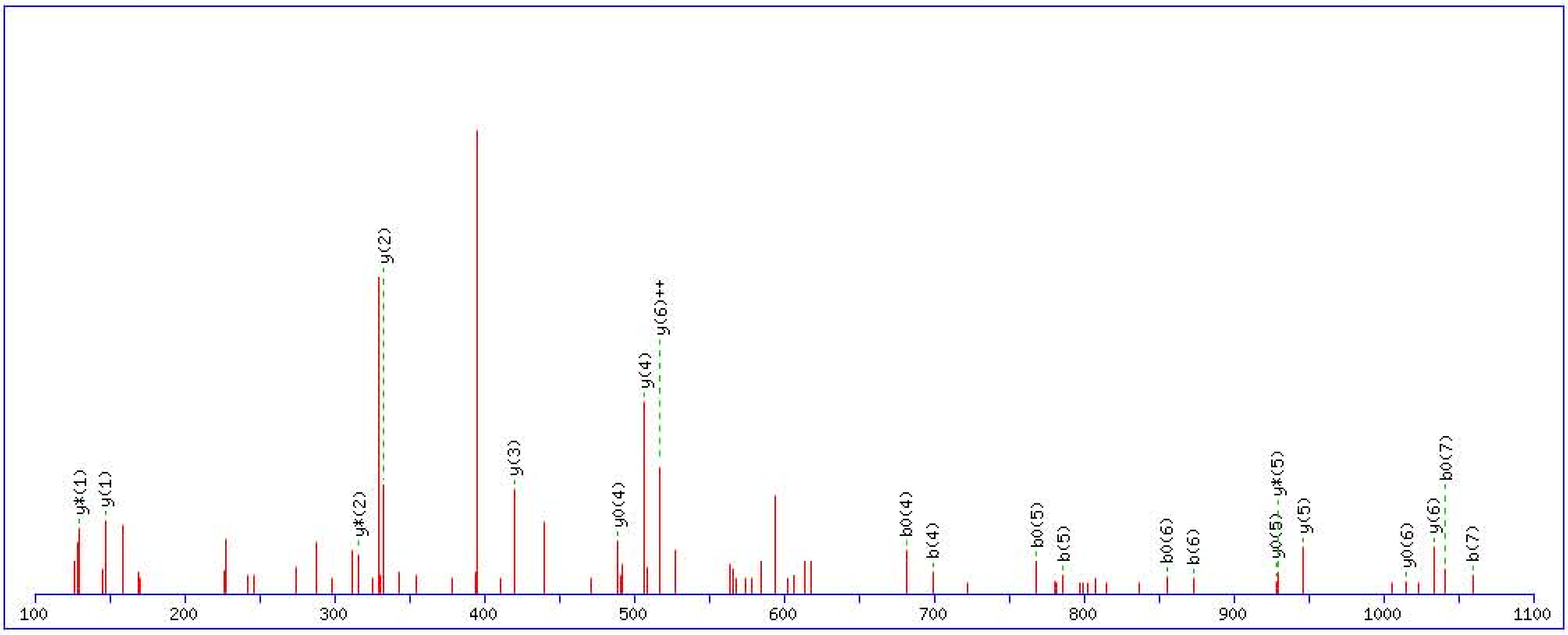
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GDSQSSWK**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

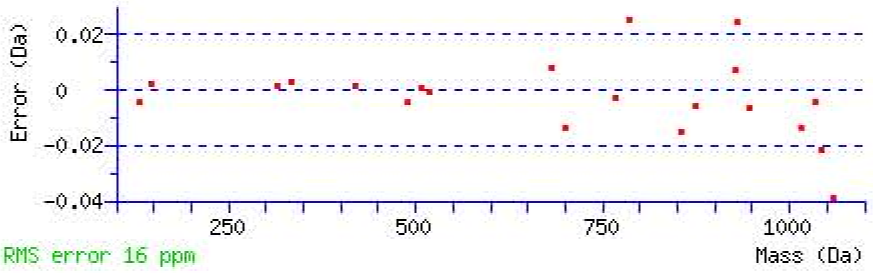
Match to Query 20409: 1204.554508 from(603.284530,2+) rtinseconds(1584) index(30774)
Title: Locus:1.1.1.3100.23 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

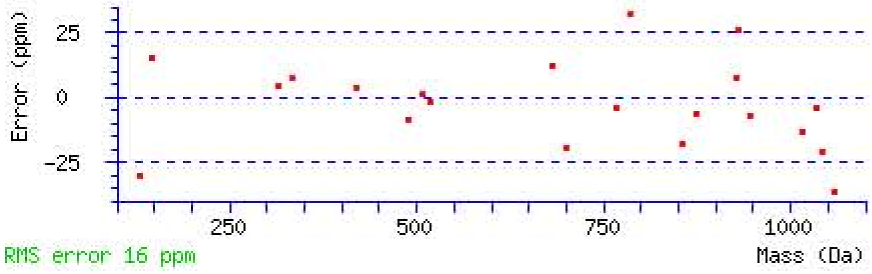
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1204.554657
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.0049
Matches : 21/72 fragment ions using 37 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							8
2	173.055683	87.031479			155.045118	78.026197	D	1148.540470	574.773873	1131.513921	566.260599	1130.529905	565.768591	7
3	260.087711	130.547493			242.077146	121.542211	S	***1033.513527***	517.260402	1016.486978	508.747127	1015.502962	508.255119	6
4	**699.313037**	350.160157	682.286488	341.646882	681.302472	341.154874	Q	***946.481499***	473.744388	929.454950	465.231113	928.470934	464.739105	5
5	**786.345065**	393.676171	769.318516	385.162896	768.334500	384.670888	S	***507.256173***	254.131724	490.229624	245.618450	489.245608	245.126442	4
6	**873.377093**	437.192185	856.350544	428.678910	855.366528	428.186902	S	***420.224145***	210.615711	403.197596	202.102436	402.213580	201.610428	3
7	**1059.456406**	530.231841	1042.429857	521.718567	1041.445841	521.226559	W	***333.192117***	167.099697	316.165568	158.586422			2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of GDSQSSWK
(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	1204.554657	-0.000149	GDSQSSWK
6.6	1204.540253	0.014255	QMQECAK
4.9	1204.565872	-0.011364	QAKQACDAWK
0.9	1204.545883	0.008625	EDLKEEEEGK

Mascot: http://www.matrixscience.com/

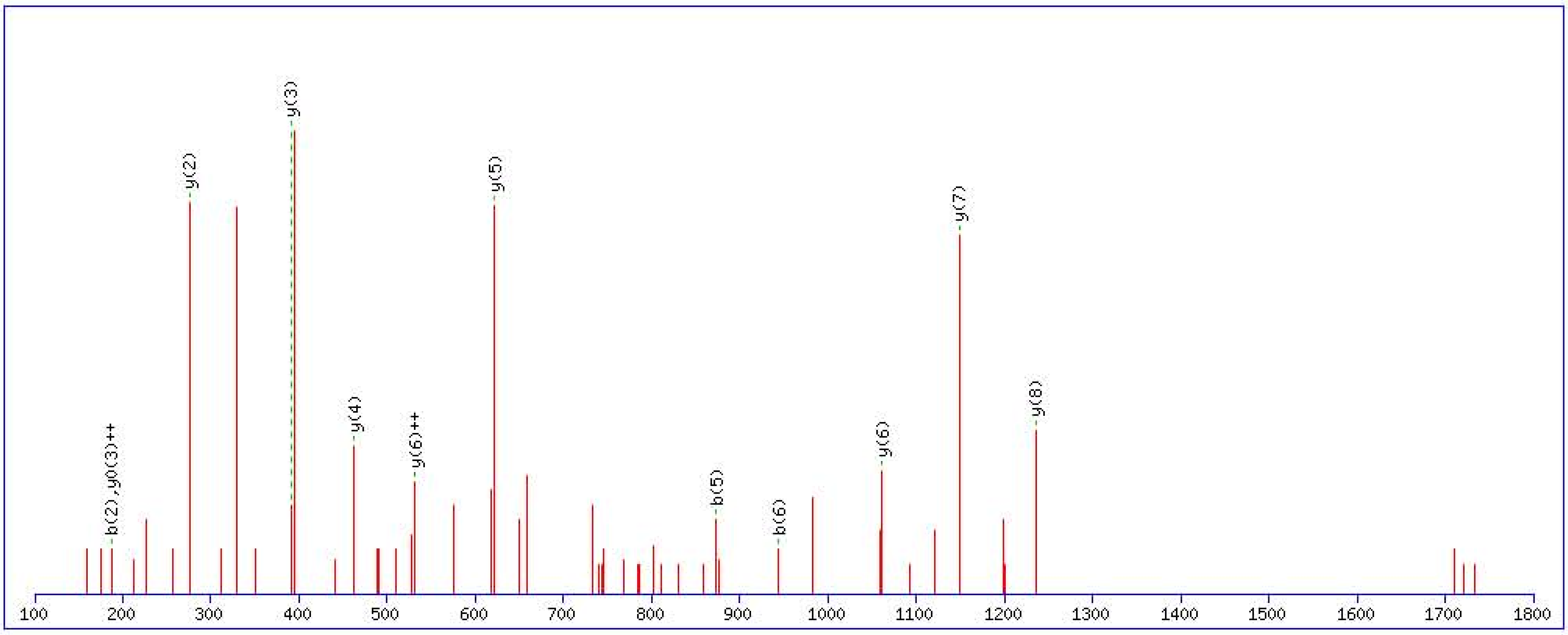
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSSQCADTR**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

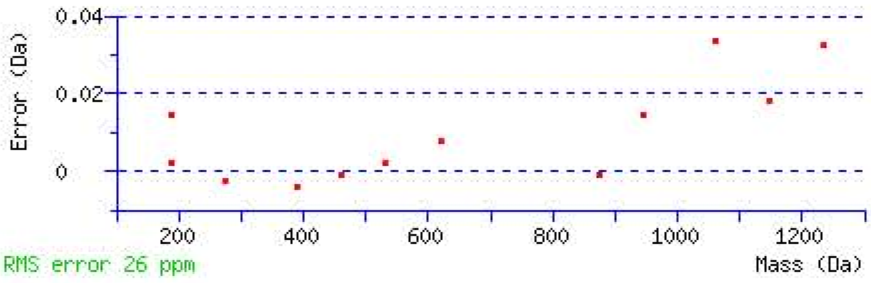
Match to Query 23629: 1333.607108 from(667.810830,2+) rtinseconds(1273) index(42936)
Title: Locus:1.1.1.2491.14 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

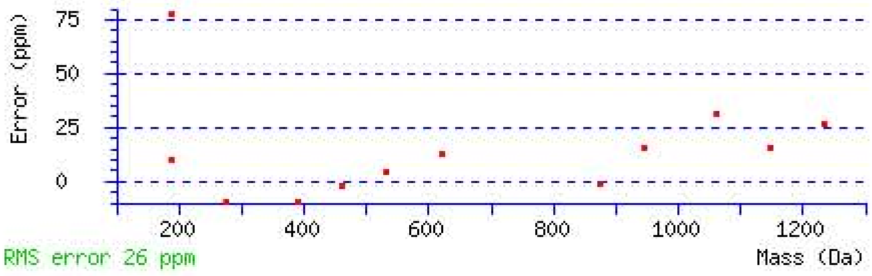
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1333.611862
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.00027
Matches : 12/86 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	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
42.5	1333.611862	-0.004754	VSSQCADTR
4.4	1333.607117	-0.000009	GEIEIESDAPMK

Mascot: http://www.matrixscience.com/

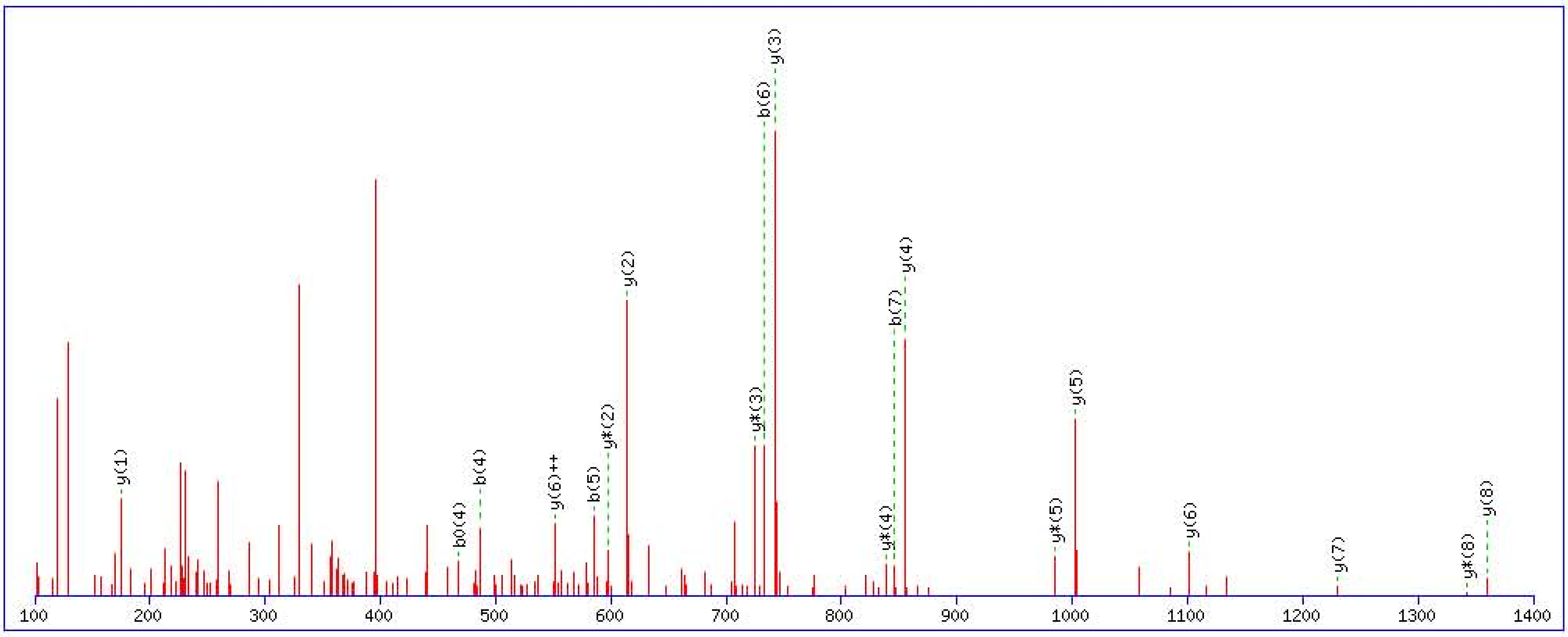
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VKEEVFIQQR**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

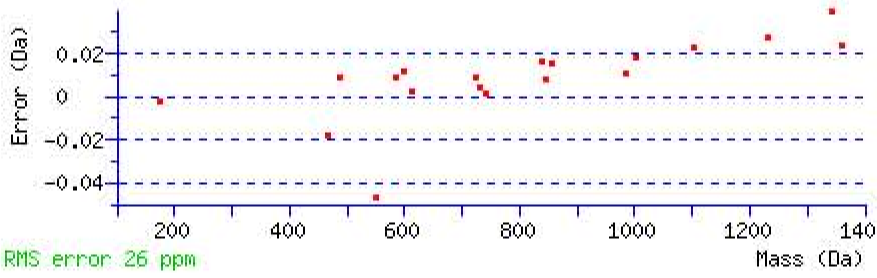
Match to Query 32626: 1585.866132 from(529.629320,3+) rtinseconds(1776) index(45937)
Title: Locus:1.1.1.2667.6 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

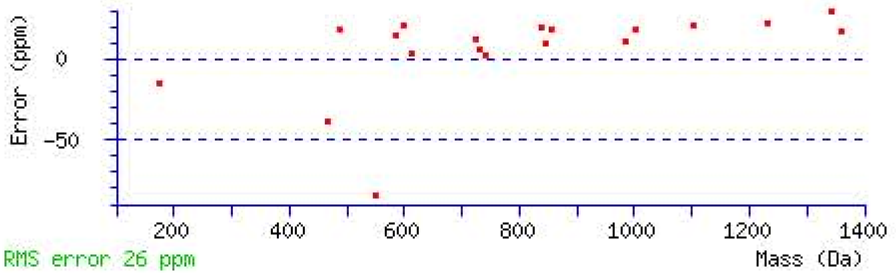
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1585.865021
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.0013
Matches : 19/90 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	100.075690	50.541483					V							10
2	228.170653	114.588965	211.144104	106.075690			K	1487.803897	744.405587	1470.777348	735.892312	1469.793332	735.400304	9
3	357.213246	179.110261	340.186697	170.596987	339.202681	170.104979	E	***1359.708934***	680.358105	1342.682385	671.844831	1341.698369	671.352823	8
4	**486.255839**	243.631558	469.229290	235.118283	468.245274	234.626275	E	***1230.666341***	615.836809	1213.639792	607.323534	1212.655776	606.831526	7
5	**585.324253**	293.165765	568.297704	284.652490	567.313688	284.160482	V	***1101.623748***	551.315512	1084.597199	542.802238			6
6	**732.392667**	366.699972	715.366118	358.186697	714.382102	357.694689	F	***1002.555334***	501.781305	985.528785	493.268031			5
7	**845.476731**	423.242004	828.450182	414.728729	827.466166	414.236721	I	***855.486920***	428.247098	838.460371	419.733824			4
8	973.535309	487.271293	956.508760	478.758018	955.524744	478.266010	Q	***742.402856***	371.705066	725.376307	363.191792			3
9	1412.760635	706.883956	1395.734086	698.370681	1394.750070	697.878673	Q	***614.344278***	307.675777	597.317729	299.162503			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VKEEVFIQQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.5	1585.865021	0.001111	VKEEVFIQQR
30.1	1585.865021	0.001111	VKEEVFIQQR
11.4	1585.842392	0.023740	EIQTTTGNQQVLVR
7.6	1585.857605	0.008527	QEEVAGIRAKFPNK
3.0	1585.842407	0.023725	QLQTGGIIDTVTGQR
0.2	1585.842361	0.023771	QSVLVKSNEEGIQR

Mascot: http://www.matrixscience.com/

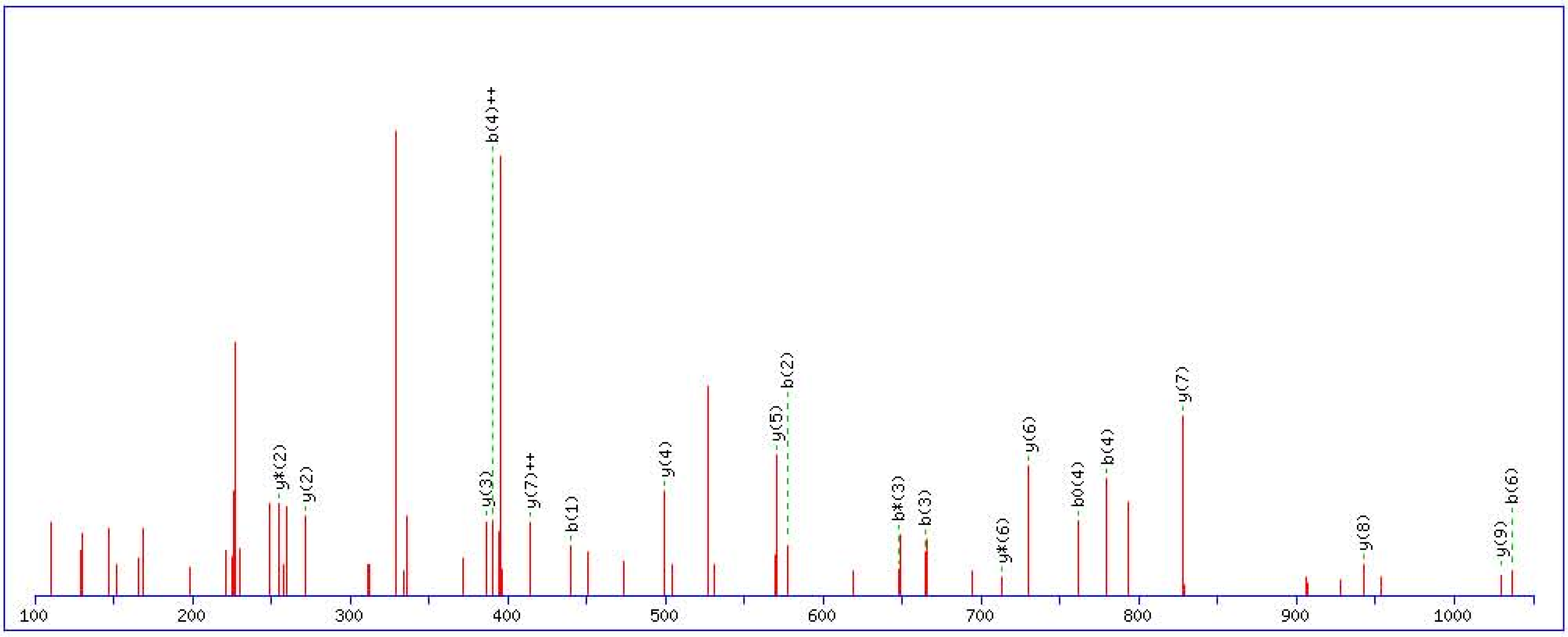
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QHSDPCALNPR**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

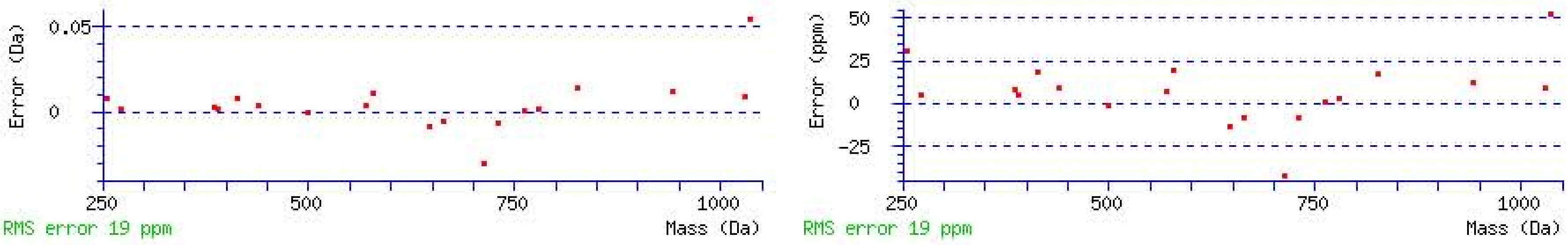
Match to Query 33387: 1604.750442 from(535.924090,3+) rtinseconds(1429) index(29761)
Title: Locus:1.1.1.3046.17 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

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): 1604.755157
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.014
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	**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
27.3	1604.755157	-0.004715	QHSDPCALNPR
7.5	1604.736725	0.013717	EGMGWSYLVFCLK
7.0	1604.743912	0.006530	QMIMKDKNWHDK
5.8	1604.772247	-0.021805	TDDIPVWDQEFLK

Mascot: http://www.matrixscience.com/

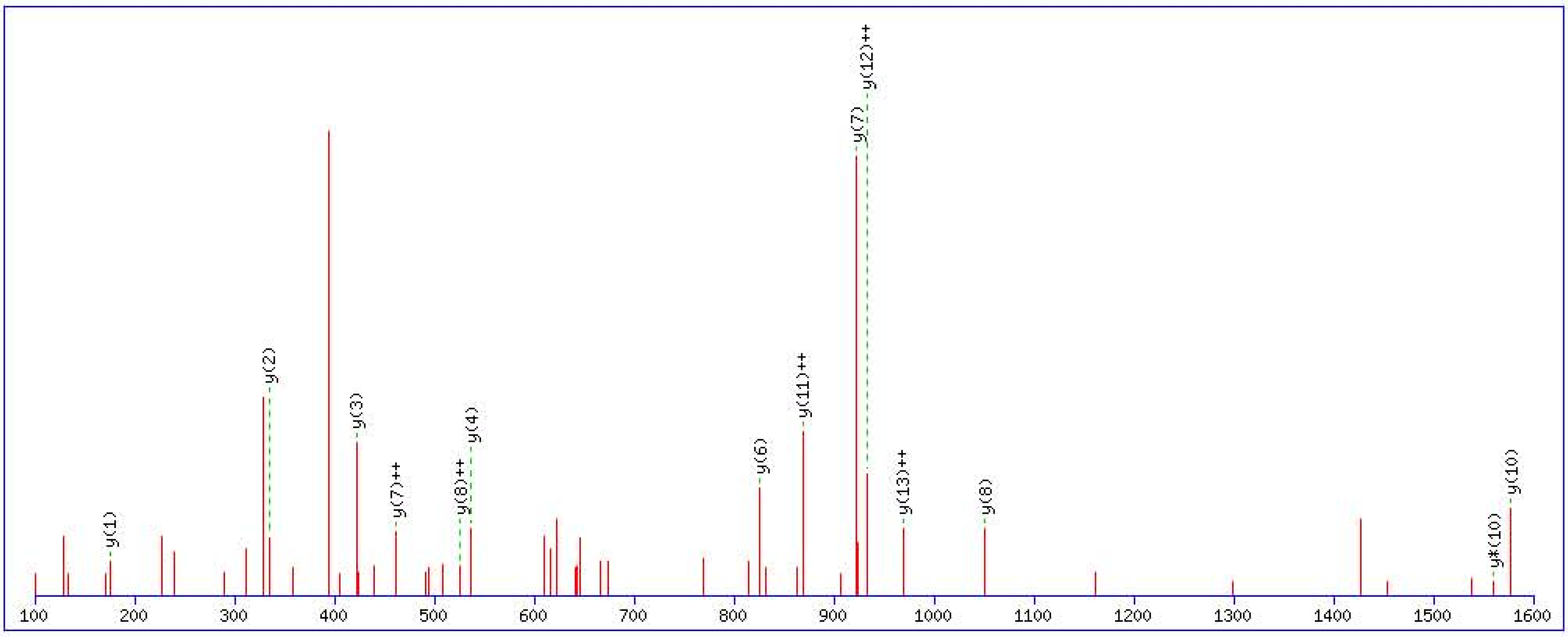
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VAQCSQKPCEDSCR**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

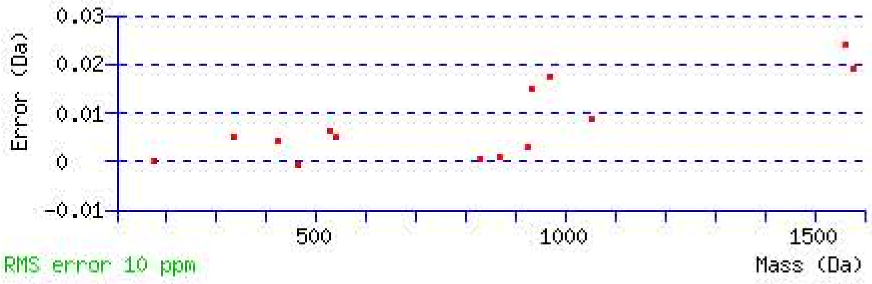
Match to Query 43294: 2034.879702 from(679.300510,3+) rtinseconds(1186) index(42657)
Title: Locus:1.1.1.2461.12 File:"2013-07-02 CLN FXIII 60 min 3rd F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

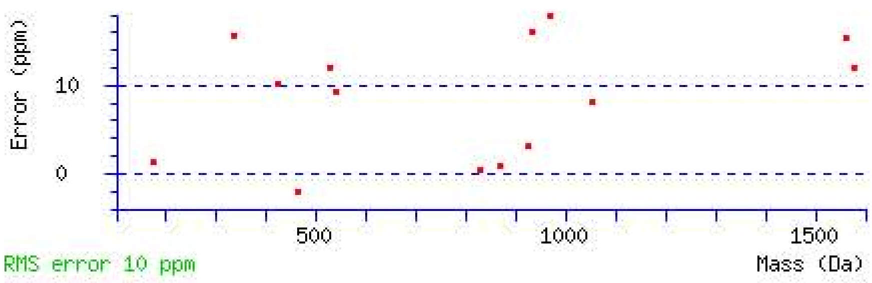
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2034.874374
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.00069
Matches : 14/140 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	100.075690	50.541483					V							14
2	171.112804	86.060040					A	1936.813236	968.910256	1919.786687	960.396982	1918.802671	959.904973	13
3	299.171382	150.089329	282.144833	141.576055			Q	1865.776122	933.391699	1848.749573	924.878425	1847.765557	924.386417	12
4	459.202031	230.104653	442.175482	221.591379			C	1737.717544	869.362410	1720.690995	860.849136	1719.706979	860.357128	11
5	546.234059	273.620668	529.207510	265.107393	528.223494	264.615385	S	***1577.686895***	789.347086	1560.660346	780.833811	1559.676330	780.341803	10
6	985.459385	493.233331	968.432836	484.720056	967.448820	484.228048	Q	1490.654867	745.831072	1473.628318	737.317797	1472.644302	736.825789	9
7	1113.554348	557.280812	1096.527799	548.767538	1095.543783	548.275529	K	***1051.429541***	526.218409	1034.402992	517.705134	1033.418976	517.213126	8
8	1210.607112	605.807194	1193.580563	597.293920	1192.596547	596.801911	P	***923.334578***	462.170927	906.308029	453.657653	905.324013	453.165645	7
9	1370.637761	685.822519	1353.611212	677.309244	1352.627196	676.817236	C	***826.281814***	413.644545	809.255265	405.131271	808.271249	404.639263	6
10	1499.680354	750.343815	1482.653805	741.830540	1481.669789	741.338532	E	666.251165	333.629221	649.224616	325.115946	648.240600	324.623938	5
11	1614.707297	807.857286	1597.680748	799.344012	1596.696732	798.852004	D	***537.208572***	269.107924	520.182023	260.594650	519.198007	260.102642	4
12	1701.739325	851.373301	1684.712776	842.860026	1683.728760	842.368018	S	***422.181629***	211.594453	405.155080	203.081178	404.171064	202.589170	3
13	1861.769974	931.388625	1844.743425	922.875351	1843.759409	922.383343	C	***335.149601***	168.078438	318.123052	159.565164			2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VAQCSQKPCEDSCR
(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	2034.874374	0.005328	VAQCSQKPCEDSCR
32.5	2034.874374	0.005328	VAQCSQKPCEDSCR

Mascot: http://www.matrixscience.com/

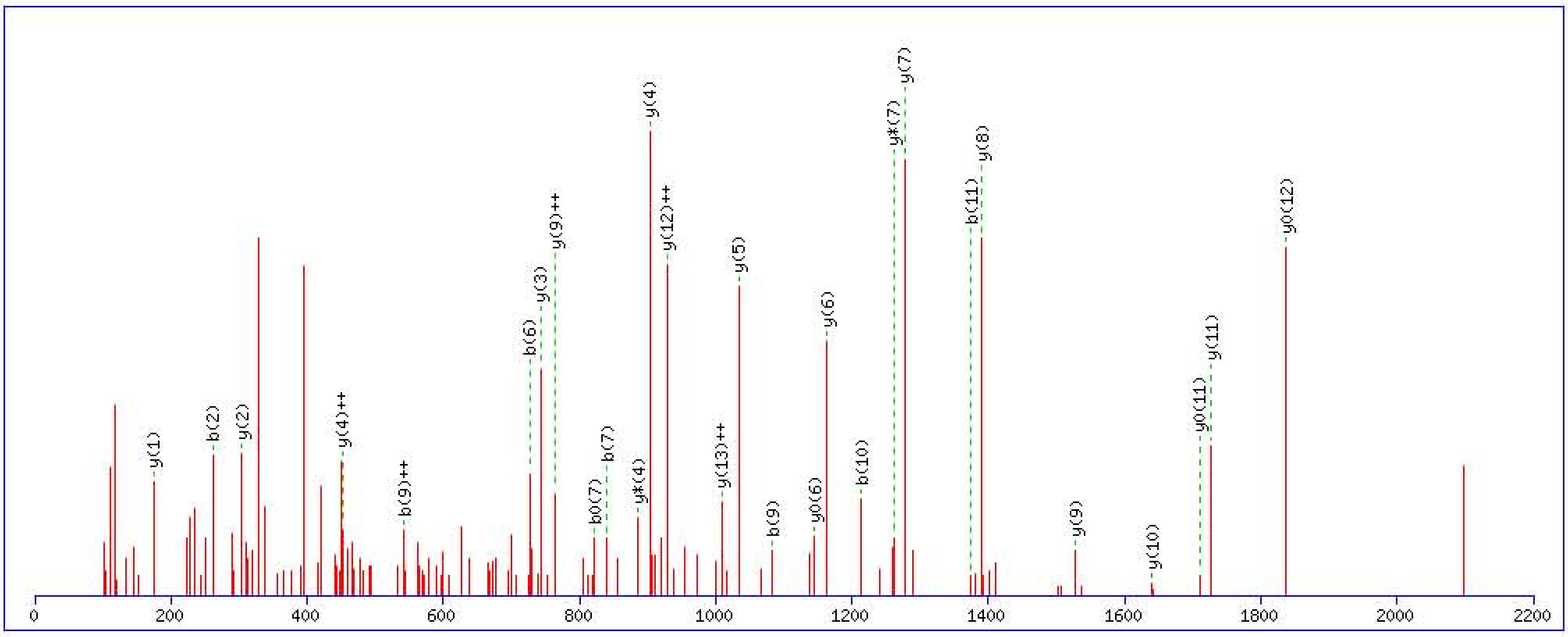
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TCQSLHINEMCQER**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

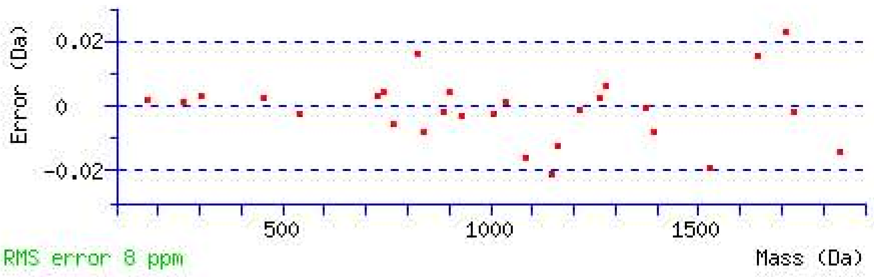
Match to Query 44688: 2115.932562 from(706.318130,3+) rtinseconds(1738) index(31600)
Title: Locus:1.1.1.3154.13 File:"2013-07-02 CLN FXIII 60 min 3rd F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\6 FXIII 60 min 3rd\mascot_daemon_merge.mgf

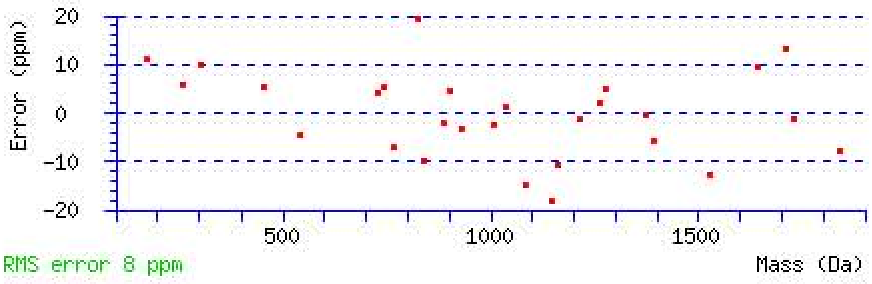
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2115.932205
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 63 **Expect:** 3e-006
Matches : 28/150 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							14
2	**262.085604**	131.546440			244.075039	122.541158	C	2015.891820	1008.449548	1998.865271	999.936274	1997.881255	999.444266	13
3	390.144182	195.575729	373.117633	187.062455	372.133617	186.570447	Q	1855.861171	928.434224	1838.834622	919.920949	1837.850606	919.428941	12
4	477.176210	239.091743	460.149661	230.578469	459.165645	230.086461	S	***1727.802593***	864.404935	1710.776044	855.891660	1709.792028	855.399652	11
5	590.260274	295.633775	573.233725	287.120501	572.249709	286.628493	L	***1640.770565***	820.888921	1623.744016	812.375646	1622.760000	811.883638	10
6	**727.319186**	364.163231	710.292637	355.649957	709.308621	355.157949	H	***1527.686501***	764.346889	1510.659952	755.833614	1509.675936	755.341606	9
7	**840.403250**	420.705263	823.376701	412.191989	822.392685	411.699981	I	***1390.627589***	695.817433	1373.601040	687.304158	1372.617024	686.812150	8
8	954.446177	477.726727	937.419628	469.213452	936.435612	468.721444	N	***1277.543525***	639.275401	1260.516976	630.762126	1259.532960	630.270118	7
9	**1083.488770**	542.248023	1066.462221	533.734749	1065.478205	533.242741	E	***1163.500598***	582.253937	1146.474049	573.740663	1145.490033	573.248655	6
10	**1214.529255**	607.768266	1197.502706	599.254991	1196.518690	598.762983	M	***1034.458005***	517.732641	1017.431456	509.219366	1016.447440	508.727358	5
11	**1374.559904**	687.783590	1357.533355	679.270316	1356.549339	678.778308	C	***903.417520***	452.212398	886.390971	443.699124	885.406955	443.207116	4
12	1813.785230	907.396253	1796.758681	898.882979	1795.774665	898.390971	Q	***743.386871***	372.197074	726.360322	363.683799	725.376306	363.191791	3
13	1942.827823	971.917550	1925.801274	963.404275	1924.817258	962.912267	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TCQSLHINEMCQER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.9	2115.932205	0.000357	TCQSLHINEMCQER

Mascot: http://www.matrixscience.com/