

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **SYELPDGQVITIGNER**

Found in **ACTA_HUMAN**, Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1

Match to Query 51981: 2101.049532 from(701.357120,3+) rtinseconds(2622) index(59395)

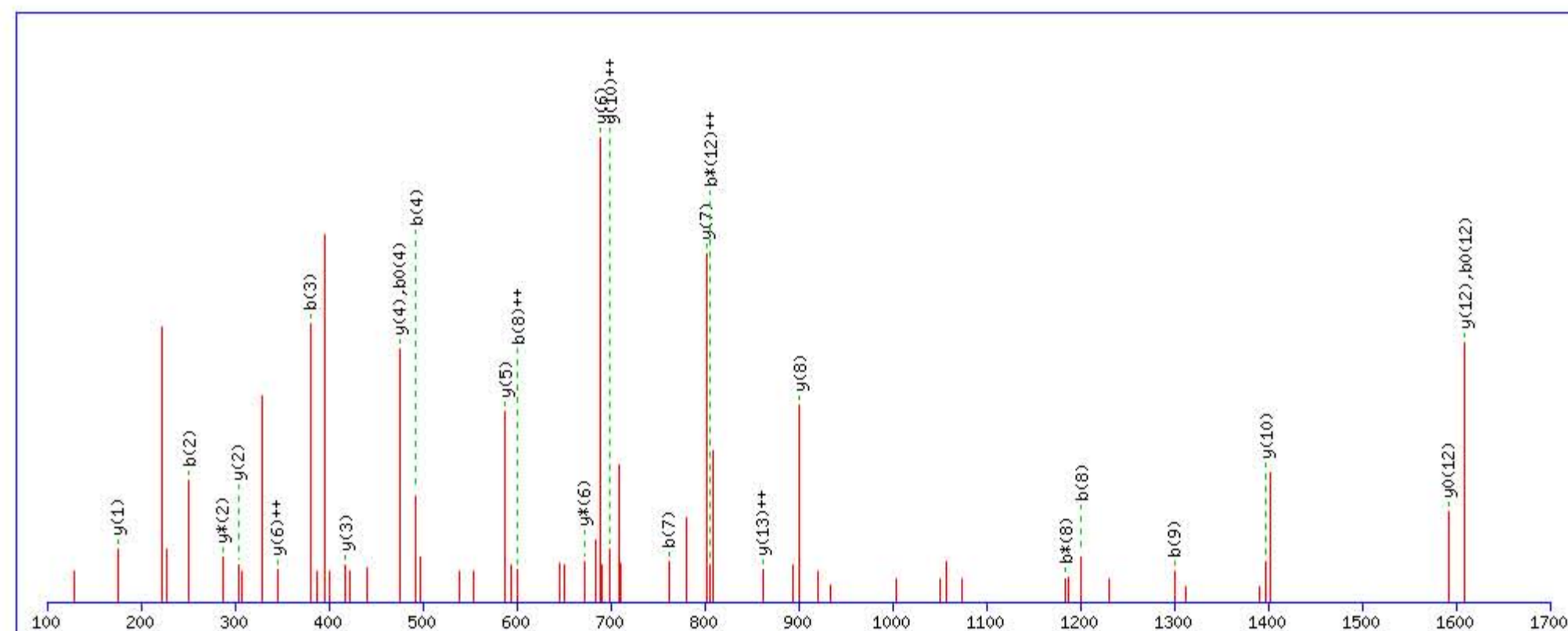
Title: Locus:1.1.1.3398.11 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2101.051376

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

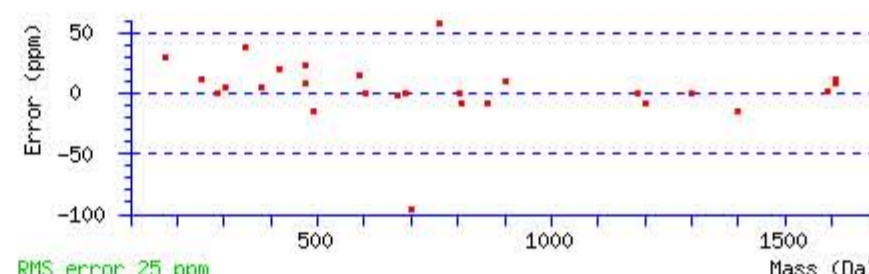
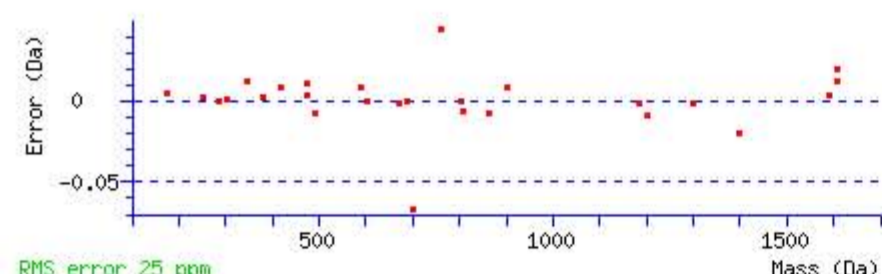
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 50 Expect: 7.2e-005

Matches : 27/164 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	88.039304	44.523290			70.028739	35.518008	S							16
2	251.102633	126.054954			233.092068	117.049672	Y	2015.026640	1008.016958	1998.000091	999.503683	1997.016075	999.011675	15
3	380.145226	190.576251			362.134661	181.570969	E	1851.963311	926.485294	1834.936762	917.972019	1833.952746	917.480011	14
4	493.229290	247.118283			475.218725	238.113001	L	1722.920718	861.963997	1705.894169	853.450722	1704.910153	852.958714	13
5	590.282054	295.644665			572.271489	286.639383	P	1609.836654	805.421965	1592.810105	796.908691	1591.826089	796.416682	12
6	705.308997	353.158137			687.298432	344.152854	D	1512.783890	756.895583	1495.757341	748.382309	1494.773325	747.890300	11
7	762.330461	381.668869			744.319896	372.663586	G	1397.756947	699.382111	1380.730398	690.868837	1379.746382	690.376829	10
8	1201.555787	601.281532	1184.529238	592.768257	1183.545222	592.276249	Q	1340.735483	670.871379	1323.708934	662.358105	1322.724918	661.866097	9
9	1300.624201	650.815739	1283.597652	642.302464	1282.613636	641.810456	V	901.510157	451.258716	884.483608	442.745442	883.499592	442.253434	8
10	1413.708265	707.357771	1396.681716	698.844496	1395.697700	698.352488	I	802.441743	401.724509	785.415194	393.211235	784.431178	392.719227	7
11	1514.755944	757.881610	1497.729395	749.368336	1496.745379	748.876328	T	689.357679	345.182478	672.331130	336.669203	671.347114	336.177195	6
12	1627.840008	814.423642	1610.813459	805.910368	1609.829443	805.418359	I	588.310000	294.658638	571.283451	286.145363	570.299435	285.653355	5
13	1684.861472	842.934374	1667.834923	834.421099	1666.850907	833.929091	G	475.225936	238.116606	458.199387	229.603331	457.215371	229.111323	4
14	1798.904399	899.955837	1781.877850	891.442563	1780.893834	890.950555	N	418.204472	209.605874	401.177923	201.092600	400.193907	200.600592	3
15	1927.946992	964.477134	1910.920443	955.963860	1909.936427	955.471851	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
16							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [SYELPDGQVITIGNER](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.7	2101.051376	-0.001844	SYELPDGQVITIGNER
5.3	2101.055237	-0.005705	VSGEQSLTWGLGGPSQSQKR
3.9	2101.029602	0.019930	MGKLISATVHEDGCEVSIR
1.7	2101.022842	0.026690	SDGSKITYIDYRQQHK

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

MASCOT SCIENCE 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 25252: 1200.611708 from(601.313130,2+) rtinseconds(1498) index(2856)

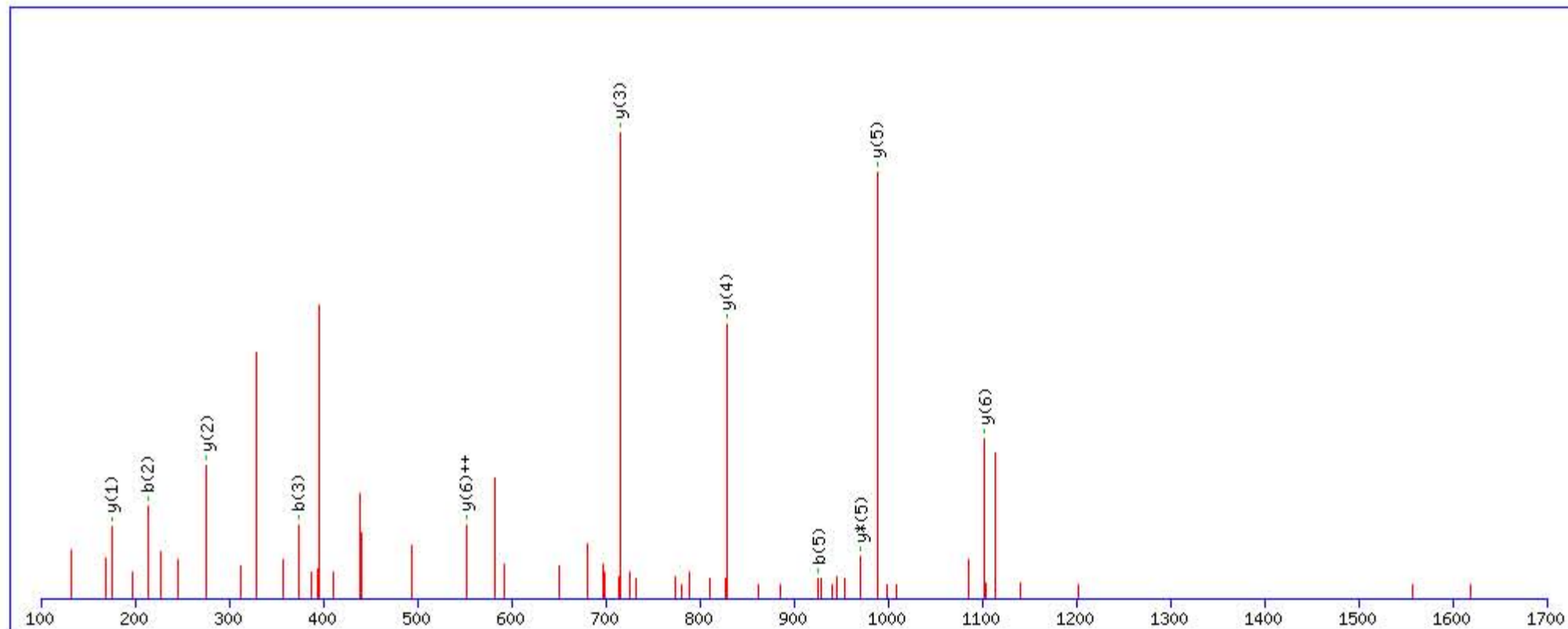
Title: Locus:1.1.1.2957.15 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

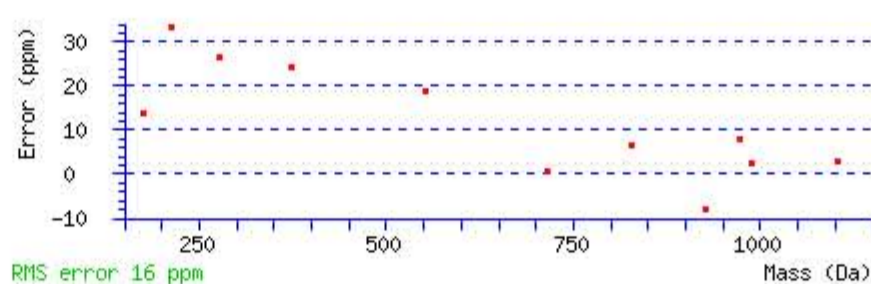
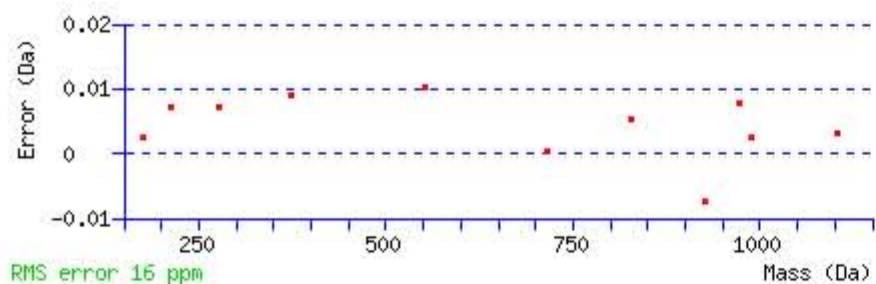
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 36 Expect: 0.0015

Matches : 11/58 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							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
35.9	1200.610733	0.000975	VNCLQTR
5.8	1200.598618	0.013090	VNPKGLDDESK
3.4	1200.621948	-0.010240	VNMLKHCKR
3.0	1200.603333	0.008375	GRIAEPSVCGR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **GQCIINSNKDDRPK**

Found in **AFAM_HUMAN**, Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

Match to Query 48069: 1954.965402 from(652.662410,3+) rtinseconds(1358) index(1831)

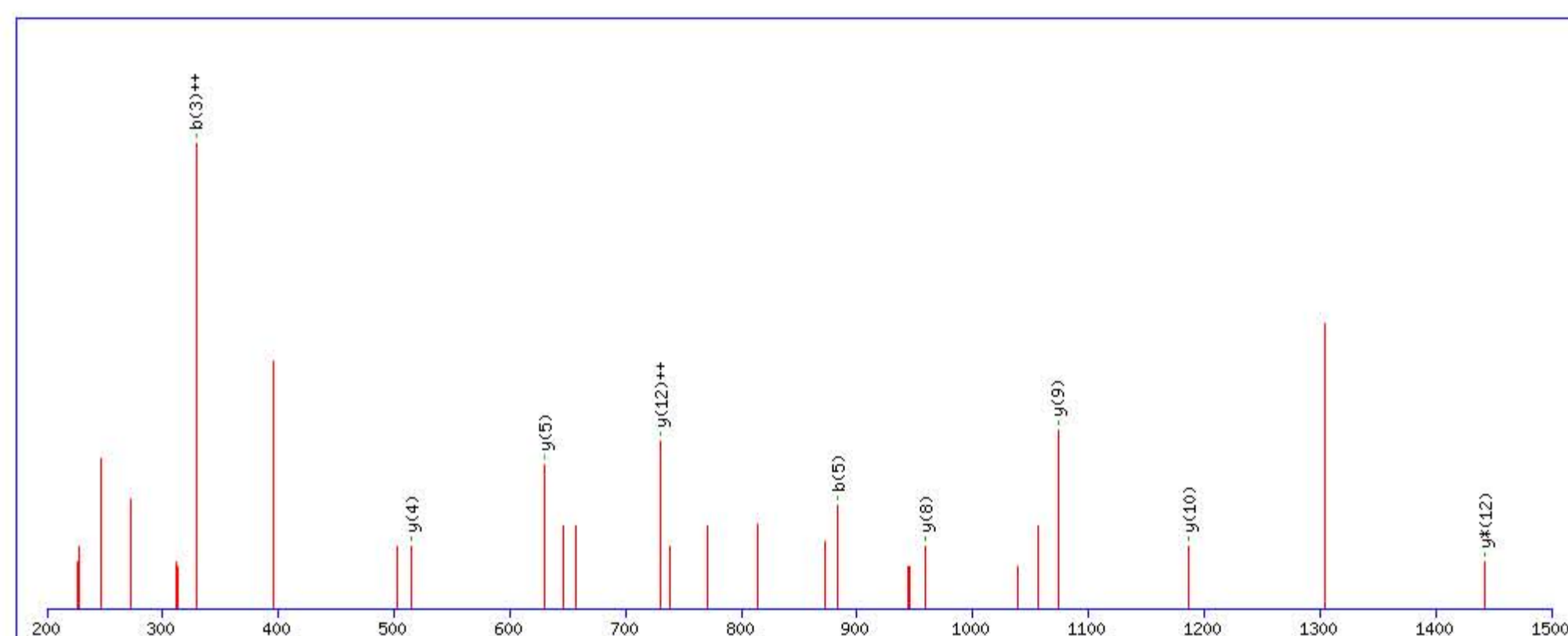
Title: Locus:1.1.1.2908.26 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1954.971680

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

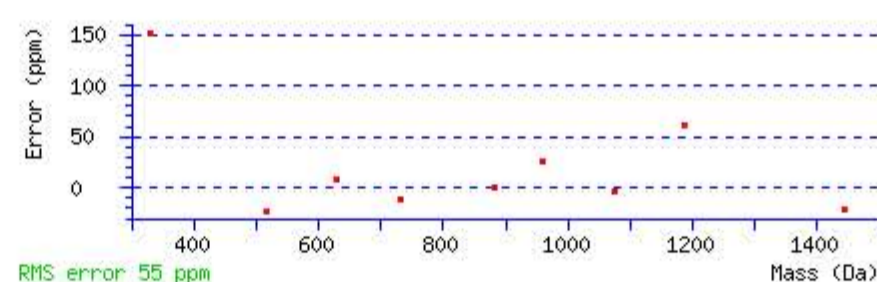
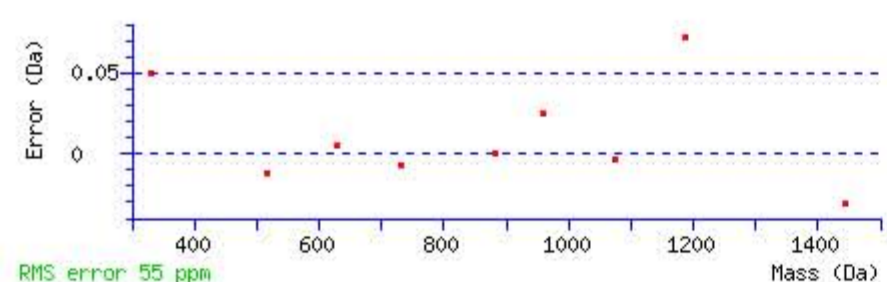
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 35 Expect: 0.0081

Matches : 9/136 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	58.028740	29.518008					G							14
2	497.254066	249.130671	480.227517	240.617397			Q	1898.957513	949.982395	1881.930964	941.469120	1880.946948	940.977112	13
3	657.284715	329.145996	640.258166	320.632721			C	1459.732187	730.369732	1442.705638	721.856457	1441.721622	721.364449	12
4	770.368779	385.688028	753.342230	377.174753			I	1299.701538	650.354407	1282.674989	641.841133	1281.690973	641.349125	11
5	883.452843	442.230060	866.426294	433.716785			I	1186.617474	593.812375	1169.590925	585.299101	1168.606909	584.807093	10
6	997.495770	499.251523	980.469221	490.738249			N	1073.533410	537.270343	1056.506861	528.757069	1055.522845	528.265061	9
7	1084.527798	542.767537	1067.501249	534.254263	1066.517233	533.762255	S	959.490483	480.248880	942.463934	471.735605	941.479918	471.243597	8
8	1198.570725	599.789001	1181.544176	591.275726	1180.560160	590.783718	N	872.458455	436.732866	855.431906	428.219591	854.447890	427.727583	7
9	1326.665688	663.836482	1309.639139	655.323208	1308.655123	654.831200	K	758.415528	379.711402	741.388979	371.198128	740.404963	370.706120	6
10	1441.692631	721.349954	1424.666082	712.836679	1423.682066	712.344671	D	630.320565	315.663921	613.294016	307.150646	612.310000	306.658638	5
11	1556.719574	778.863425	1539.693025	770.350151	1538.709009	769.858143	D	515.293622	258.150449	498.267073	249.637175	497.283057	249.145167	4
12	1712.820685	856.913981	1695.794136	848.400706	1694.810120	847.908698	R	400.266679	200.636977	383.240130	192.123703			3
13	1809.873449	905.440363	1792.846900	896.927088	1791.862884	896.435080	P	244.165568	122.586422	227.139019	114.073148			2
14							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of [GQCIINSNKDDRPK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.8	1954.971680	-0.006278	GQCIINSNKDDRPK

MASCOT 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 28706: 1312.598708 from(657.306630,2+) rtinseconds(1184) index(65968)

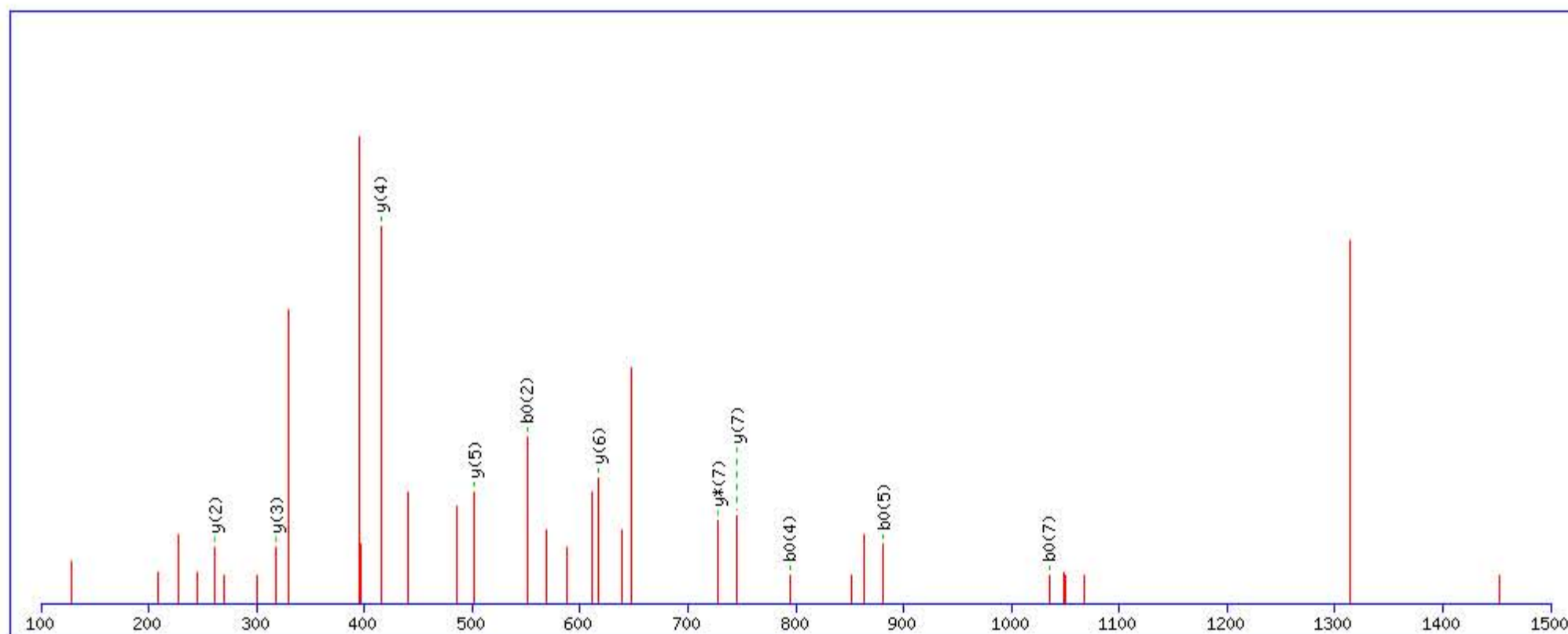
Title: Locus:1.1.1.2945.19 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1312.608139

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

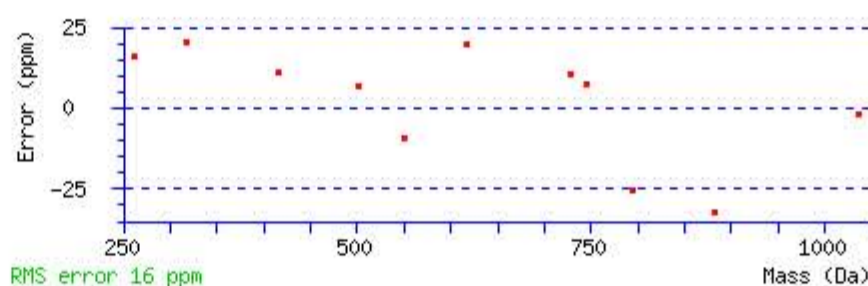
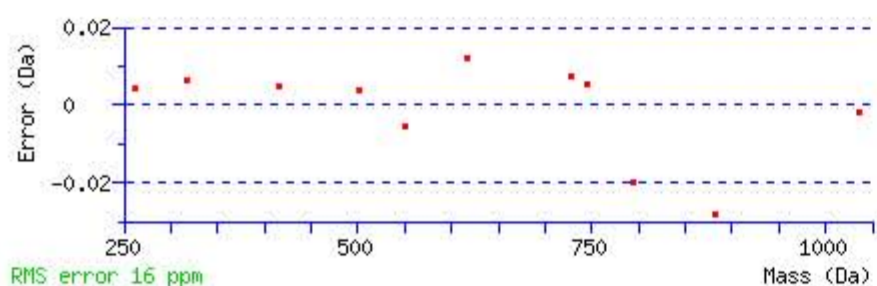
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 31 Expect: 0.0062

Matches : 11/86 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	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
31.3	1312.608139	-0.009431	EQQDSPGNK
18.3	1312.608139	-0.009431	EQQDSPGNK

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 39864: 1622.830148 from(812.422350,2+) rtinseconds(1594) index(68760)

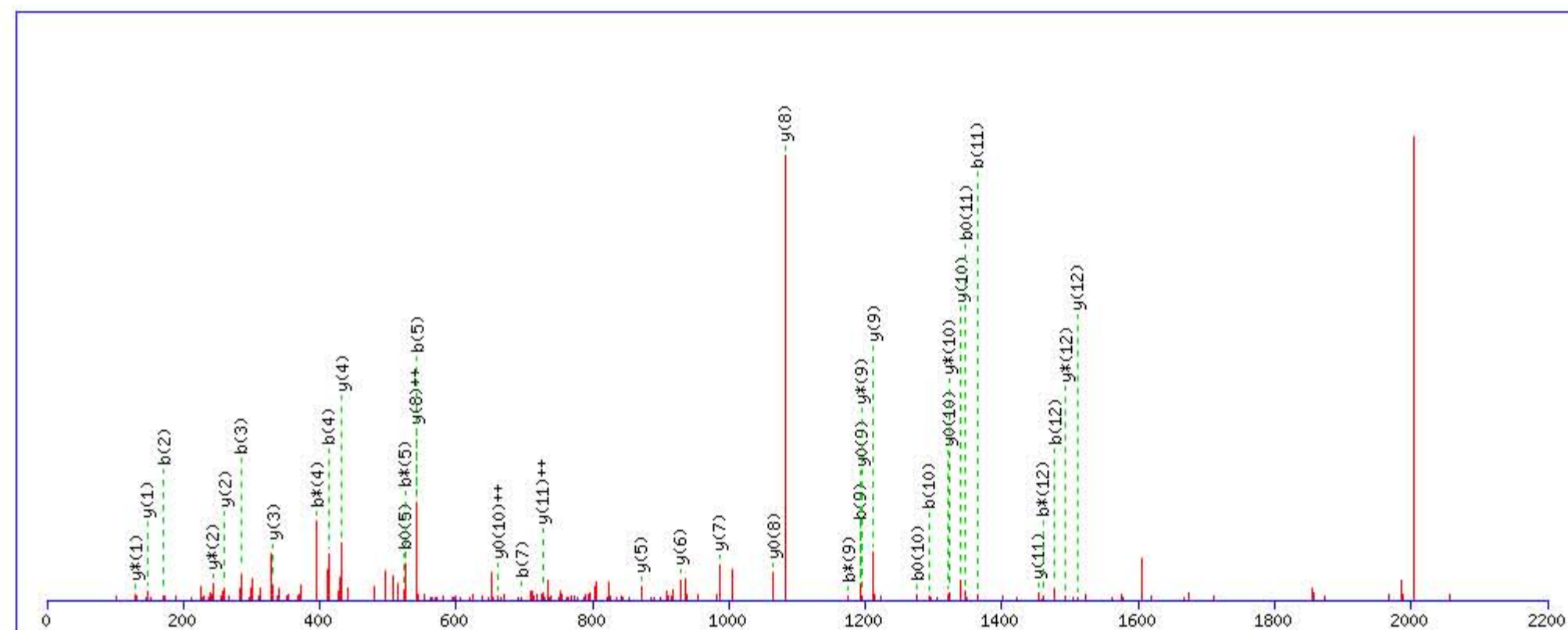
Title: Locus:1.1.1.3088.9 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

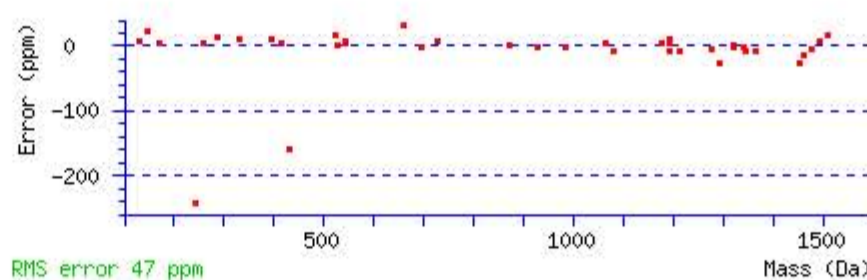
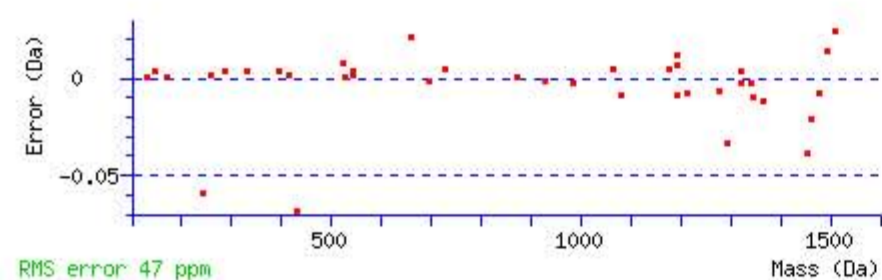
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 67 Expect: 4.4e-006

Matches : 39/126 fragment ions using 88 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					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
67.1	1622.845016	-0.014868	LGNQEPGGQTALK
17.4	1622.845016	-0.014868	LGNQEPGGQTALK
9.4	1622.813324	0.016824	NGLAQRMSHGK
3.0	1622.831085	-0.000937	GLNPNPSHQMTKRK
2.9	1622.837601	-0.007453	SQSEKQTYLEVRR
1.9	1622.820511	0.009637	FPPEASGYLHIGHAK
1.1	1622.849045	-0.018897	IPMPDFDLHLKGP
1.1	1622.819855	0.010293	NSSPRMPHLAVATDK
0.8	1622.852890	-0.022742	QFEFVGSAPTRRTK

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **QLTSGPNQEQVSPLTLK**

Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

Match to Query 55295: 2263.214382 from(755.412070,3+) rtinseconds(2529) index(74491)

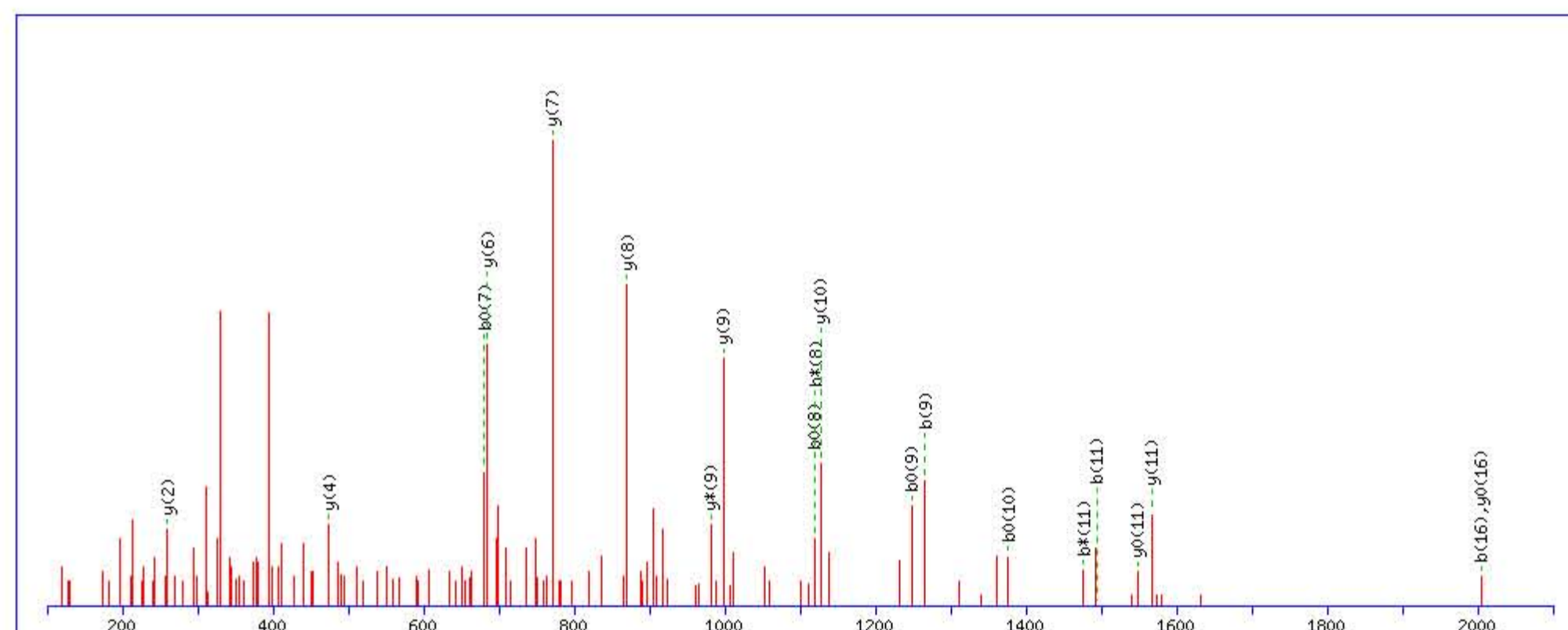
Title: Locus:1.1.1.3414.8 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2263.224594

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

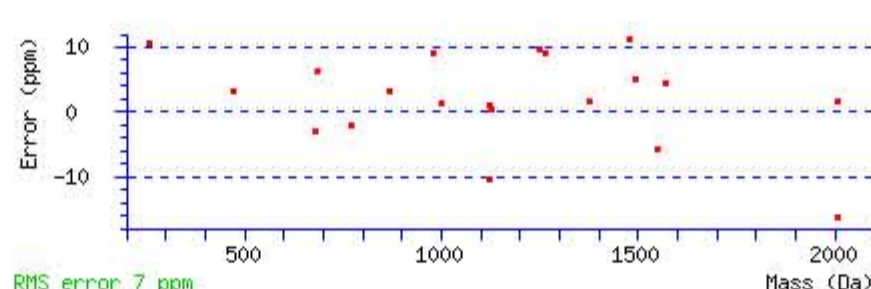
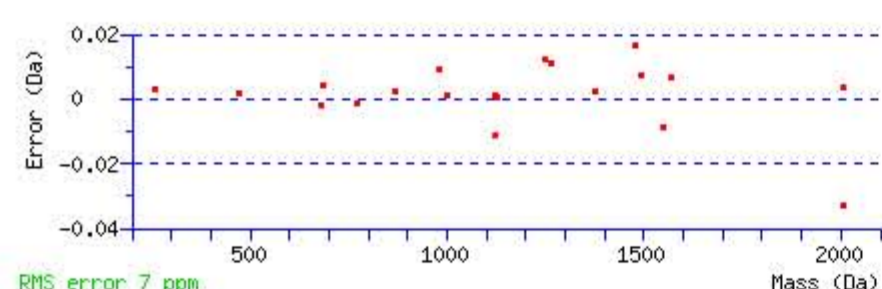
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 42 Expect: 0.00052

Matches : 20/194 fragment ions using 32 most intense peaks [\(help\)](#)

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

(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	2263.224594	-0.010212	QLTSGPNQEQVSPLTLK
30.0	2263.224594	-0.010212	QLTSGPNQEQVSPLTLK
17.9	2263.224594	-0.010212	QLTSGPNQEQVSPLTLK
6.3	2263.197586	0.016796	TCWLAAFRLFKYGVQLYK
1.3	2263.224594	-0.010212	GLALSSNKVKSVMVVDNEK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **ELKEQQDSPGNKDFLQSLK**

Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

Match to Query 60328: 2514.286016 from(629.578780,4+) rtinseconds(1897) index(5188)

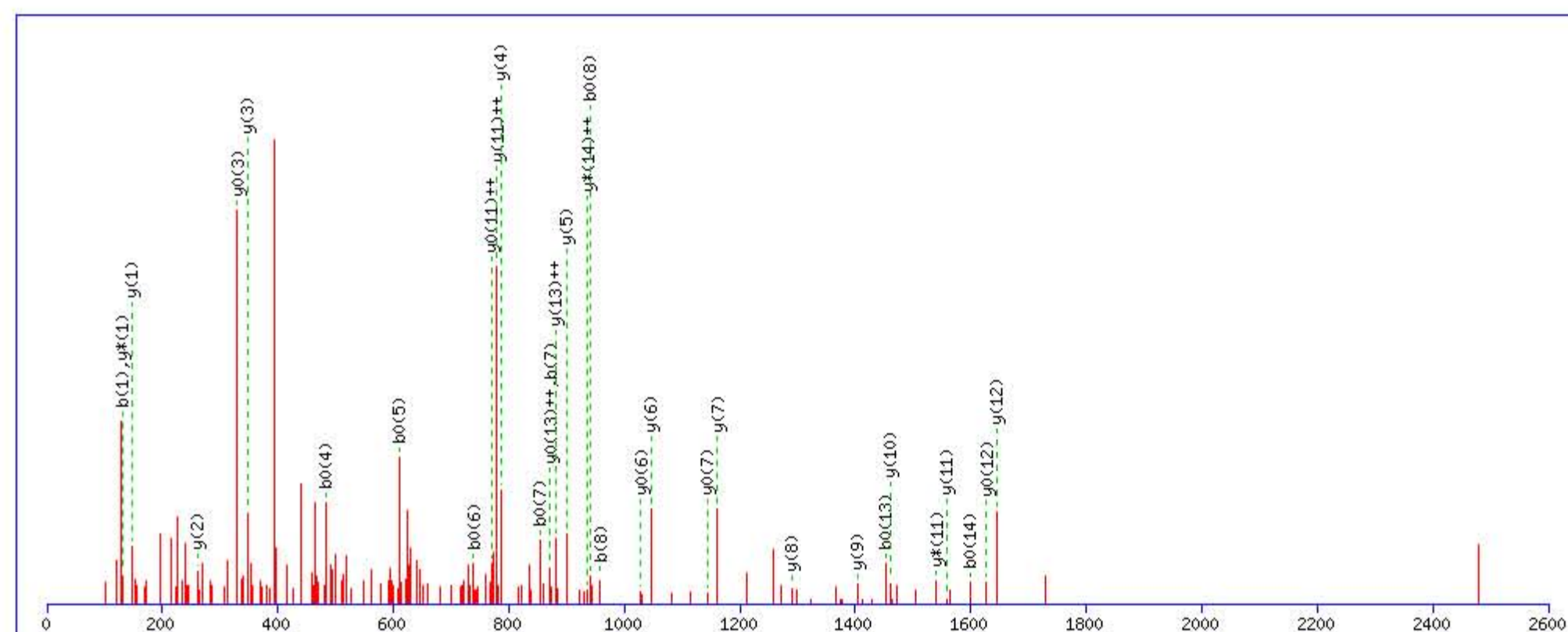
Title: Locus:1.1.1.3096.23 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2514.278793

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

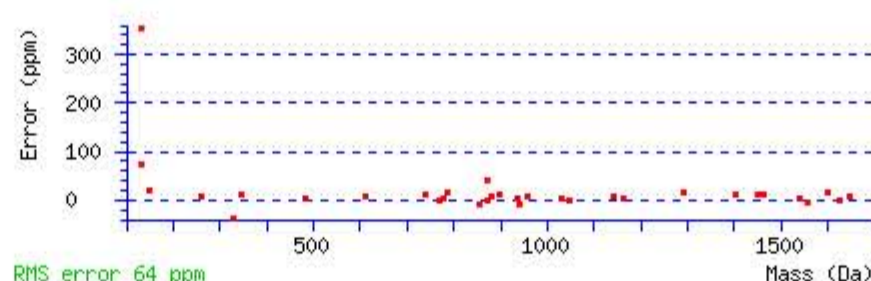
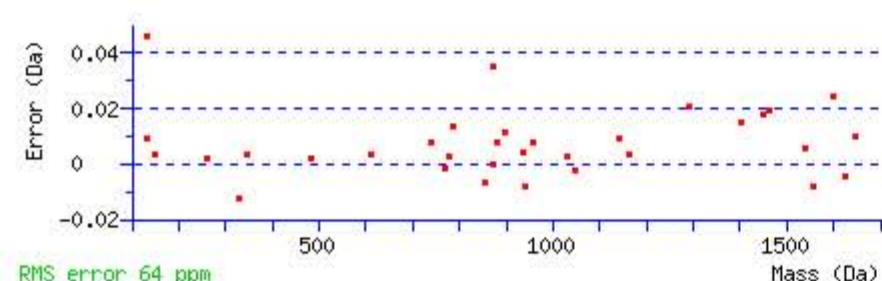
Variable modifications:

Q16 : Biotin:Thermo-21345 (Q)

Ions Score: 42 Expect: 0.00013

Matches : 33/208 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	130.049869	65.528572			112.039304	56.523290	E							19
2	243.133933	122.070605			225.123368	113.065322	L	2386.243508	1193.625392	2369.216959	1185.112117	2368.232943	1184.620109	18
3	371.228896	186.118086	354.202347	177.604812	353.218331	177.112804	K	2273.159444	1137.083360	2256.132895	1128.570085	2255.148879	1128.078077	17
4	500.271489	250.639383	483.244940	242.126108	482.260924	241.634100	E	2145.064481	1073.035878	2128.037932	1064.522604	2127.053916	1064.030596	16
5	628.330067	314.668672	611.303518	306.155397	610.319502	305.663389	Q	2016.021888	1008.514582	1998.995339	1000.001308	1998.011323	999.509300	15
6	756.388645	378.697961	739.362096	370.184686	738.378080	369.692678	Q	1887.963310	944.485293	1870.936761	935.972019	1869.952745	935.480011	14
7	871.415588	436.211432	854.389039	427.698158	853.405023	427.206150	D	1759.904732	880.456004	1742.878183	871.942730	1741.894167	871.450722	13
8	958.447616	479.727446	941.421067	471.214172	940.437051	470.722164	S	1644.877789	822.942533	1627.851240	814.429258	1626.867224	813.937250	12
9	1055.500380	528.253828	1038.473831	519.740554	1037.489815	519.248545	P	1557.845761	779.426519	1540.819212	770.913244	1539.835196	770.421236	11
10	1112.521844	556.764560	1095.495295	548.251285	1094.511279	547.759277	G	1460.792997	730.900137	1443.766448	722.386862	1442.782432	721.894854	10
11	1226.564771	613.786023	1209.538222	605.272749	1208.554206	604.780741	N	1403.771533	702.389405	1386.744984	693.876130	1385.760968	693.384122	9
12	1354.659734	677.833505	1337.633185	669.320230	1336.649169	668.828222	K	1289.728606	645.367941	1272.702057	636.854667	1271.718041	636.362659	8
13	1469.686677	735.346976	1452.660128	726.833702	1451.676112	726.341694	D	1161.633643	581.320460	1144.607094	572.807185	1143.623078	572.315177	7
14	1616.755091	808.881184	1599.728542	800.367909	1598.744526	799.875901	F	1046.606700	523.806988	1029.580151	515.293714	1028.596135	514.801706	6
15	1729.839155	865.423215	1712.812606	856.909941	1711.828590	856.417933	L	899.538286	450.272781	882.511737	441.759507	881.527721	441.267499	5
16	2169.064481	1085.035878	2152.037932	1076.522604	2151.053916	1076.030596	Q	786.454222	393.730749	769.427673	385.217475	768.443657	384.725467	4
17	2256.096509	1128.551892	2239.069960	1120.038618	2238.085944	1119.546610	S	347.228896	174.118086	330.202347	165.604812	329.218331	165.112804	3
18	2369.180573	1185.093925	2352.154024	1176.580650	2351.170008	1176.088642	L	260.196868	130.602072	243.170319	122.088798			2
19							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of [ELKEQQDSPGNKDFLQSLK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.1	2514.278793	0.007223	ELKEQQDSPGNKDFLQSLK
0.6	2514.267563	0.018453	TLADVNGVIEEEFTMARLYISK

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

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 67046: 3175.662736 from(794.922960,4+) rtinseconds(2760) index(10356)

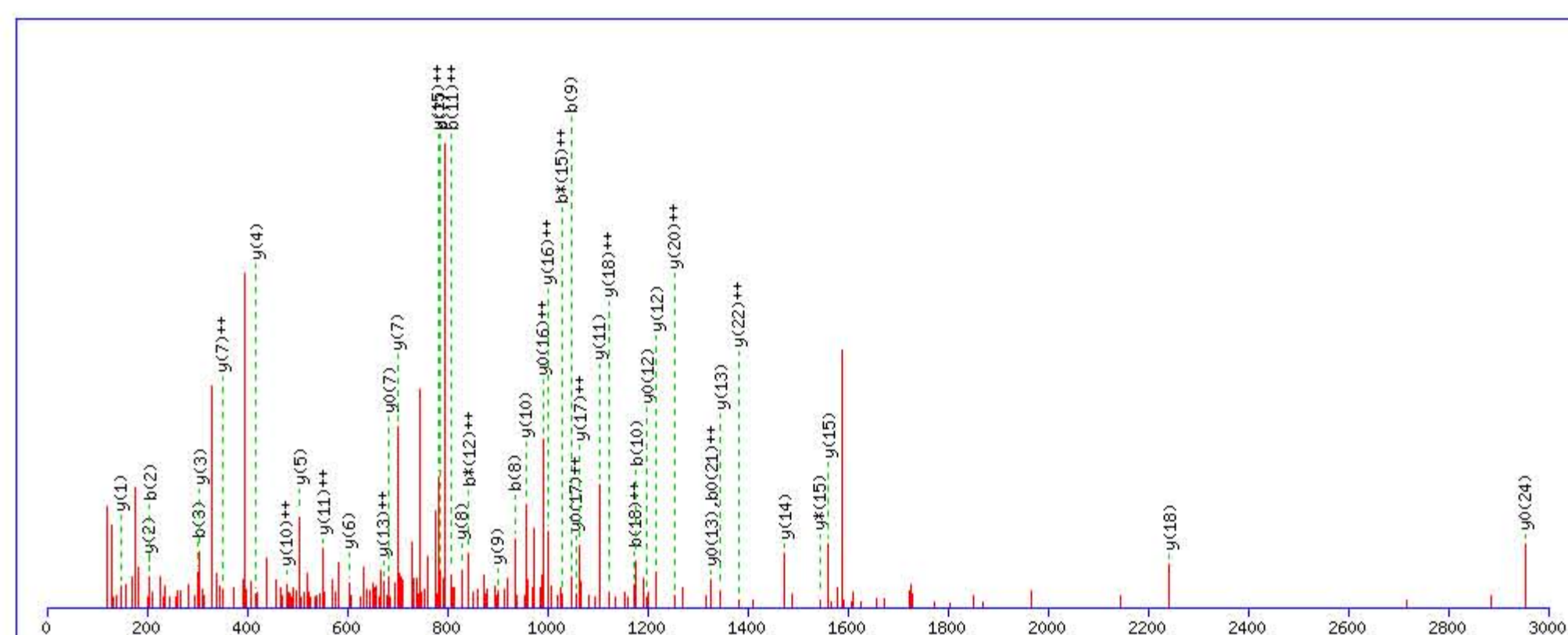
Title: Locus:1.1.1.3396.7 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

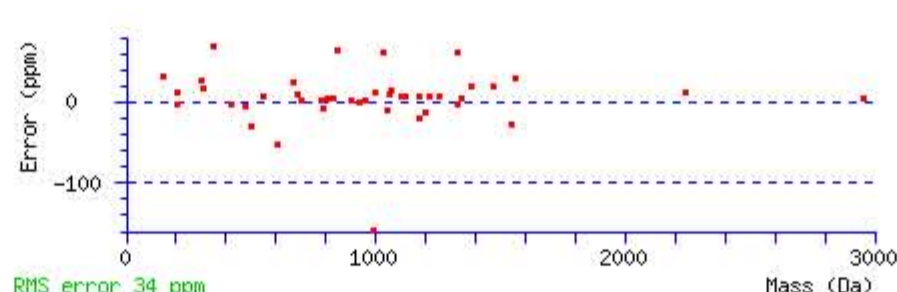
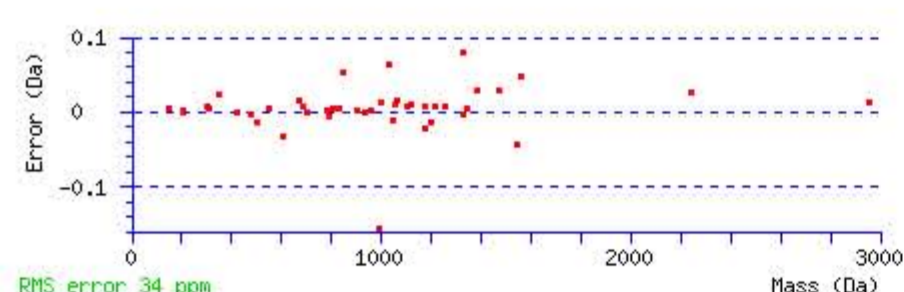
Variable modifications:

Q11 : Biotin:Thermo-21345 (Q)

Ions Score: 45 Expect: 0.00079

Matches : 44/278 fragment ions using 144 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.028740	29.518008					G							26
2	205.097154	103.052215					F	3119.648573	1560.327924	3102.622024	1551.814650	3101.638008	1551.322642	25
3	302.149918	151.578597					P	2972.580159	1486.793717	2955.553610	1478.280443	2954.569594	1477.788435	24
4	415.233982	208.120629					I	2875.527395	1438.267335	2858.500846	1429.754061	2857.516830	1429.262053	23
5	543.328945	272.168111	526.302396	263.654836			K	2762.443331	1381.725303	2745.416782	1373.212029	2744.432766	1372.720021	22
6	672.371538	336.689407	655.344989	328.176133	654.360973	327.684125	E	2634.348368	1317.677822	2617.321819	1309.164547	2616.337803	1308.672539	21
7	787.398481	394.202879	770.371932	385.689604	769.387916	385.197596	D	2505.305775	1253.156525	2488.279226	1244.643251	2487.295210	1244.151243	20
8	934.466895	467.737086	917.440346	459.223811	916.456330	458.731803	F	2390.278832	1195.643054	2373.252283	1187.129779	2372.268267	1186.637771	19
9	1047.550959	524.279117	1030.524410	515.765843	1029.540394	515.273835	L	2243.210418	1122.108847	2226.183869	1113.595572	2225.199853	1113.103564	18
10	1176.593552	588.800414	1159.567003	580.287140	1158.582987	579.795132	E	2130.126354	1065.566815	2113.099805	1057.053540	2112.115789	1056.561532	17
11	1615.818878	808.413077	1598.792329	799.899803	1597.808313	799.407795	Q	2001.083761	1001.045519	1984.057212	992.532244	1983.073196	992.040236	16
12	1702.850906	851.929091	1685.824357	843.415817	1684.840341	842.923809	S	1561.858435	781.432856	1544.831886	772.919581	1543.847870	772.427573	15
13	1831.893499	916.450388	1814.866950	907.937113	1813.882934	907.445105	E	1474.826407	737.916842	1457.799858	729.403567	1456.815842	728.911559	14
14	1959.952077	980.479677	1942.925528	971.966402	1941.941512	971.474394	Q	1345.783814	673.395545	1328.757265	664.882271	1327.773249	664.390263	13
15	2073.036141	1037.021709	2056.009592	1028.508434	2055.025576	1028.016426	L	1217.725236	609.366256	1200.698687	600.852982	1199.714671	600.360974	12
16	2220.104555	1110.555916	2203.078006	1102.042641	2202.093990	1101.550633	F	1104.641172	552.824224	1087.614623	544.310949	1086.630607	543.818941	11
17	2277.126019	1139.066648	2260.099470	1130.553373	2259.115454	1130.061365	G	957.572758	479.290017	940.546209	470.776743	939.562193	470.284735	10
18	2348.163133	1174.585205	2331.136584	1166.071930	2330.152568	1165.579922	A	900.551294	450.779285	883.524745	442.266011	882.540729	441.774003	9
19	2476.258096	1238.632686	2459.231547	1230.119412	2458.247531	1229.627404	K	829.514180	415.260728	812.487631	406.747453	811.503615	406.255445	8
20	2573.310860	1287.159068	2556.284311	1278.645794	2555.300295	1278.153786	P	701.419217	351.213246	684.392668	342.699972	683.408652	342.207964	7
21	2672.379274	1336.693275	2655.352725	1328.180001	2654.368709	1327.687993	V	604.366453	302.686864	587.339904	294.173590	586.355888	293.681582	6
22	2759.411302	1380.209289	2742.384753	1371.696015	2741.400737	1371.204007	S	505.298039	253.152657	488.271490	244.639383	487.287474	244.147375	5
23	2872.495366	1436.751321	2855.468817	1428.238047	2854.484801	1427.746039	L	418.266011	209.636643	401.239462	201.123369	400.255446	200.631361	4
24	2973.543045	1487.275161	2956.516496	1478.761886	2955.532480	1478.269878	T	305.181947	153.094611	288.155398	144.581337	287.171382	144.089329	3
25	3030.564509	1515.785893	3013.537960	1507.272618	3012.553944	1506.780610	G	204.134268	102.570772	187.107719	94.057497			2
26							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **GFPIKEDFLEQSEQLFGAKPVSLTGK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.8	3175.662750	-0.000014	GFPIKEDFLEQSEQLFGAKPVSLTGK
24.3	3175.662750	-0.000014	GFPIKEDFLEQSEQLFGAKPVSLTGK

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 48547: 1970.930142 from(657.983990,3+) rtinseconds(2078) index(39162)

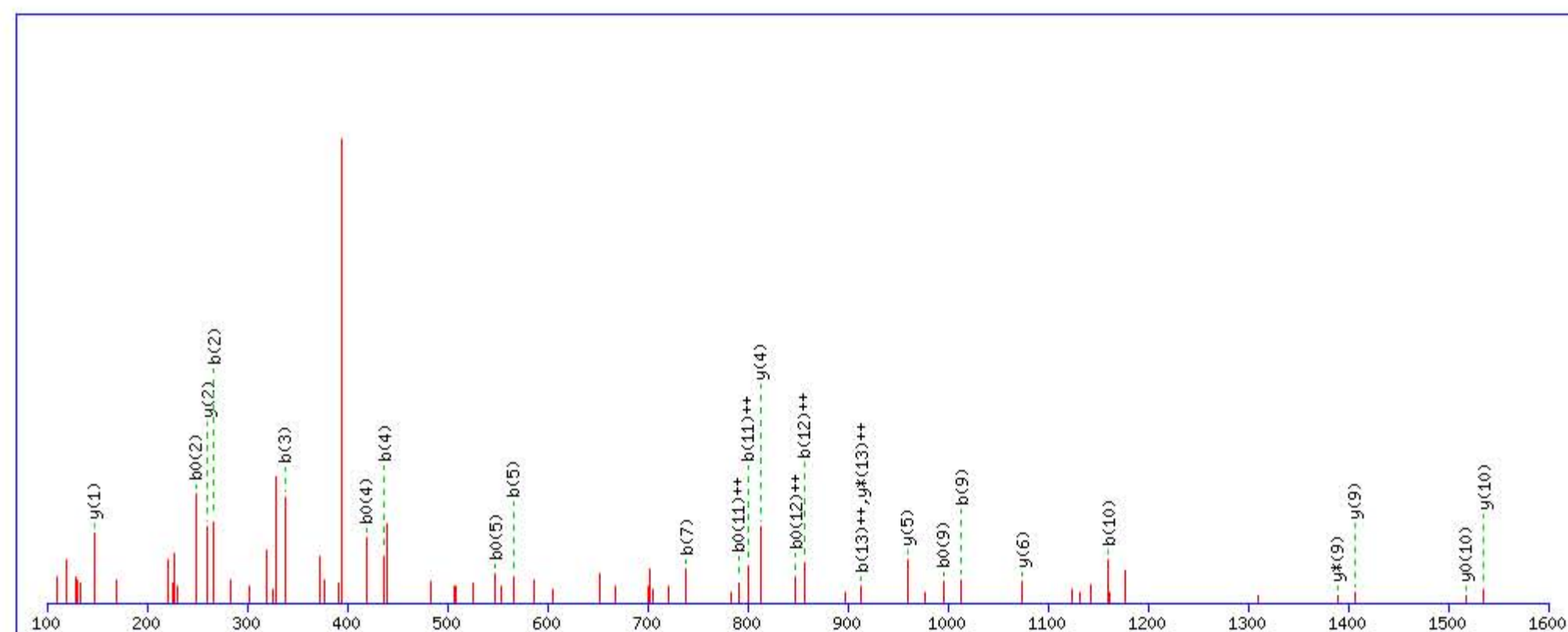
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Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

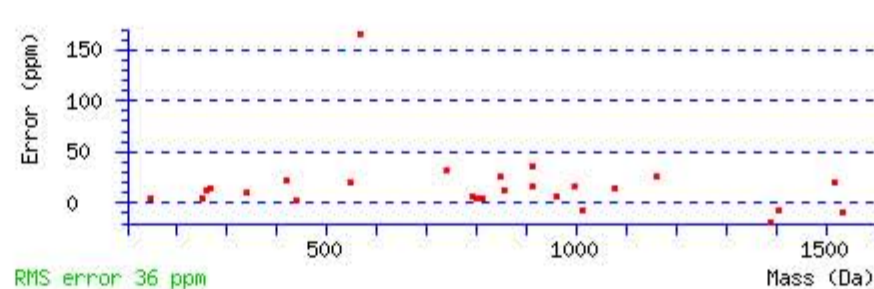
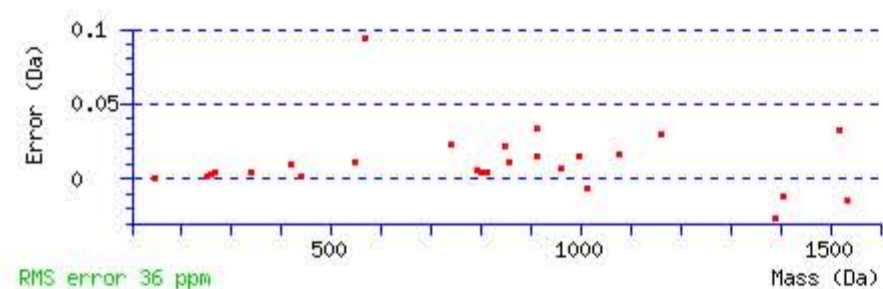
Variable modifications:

Q11 : Biotin:Thermo-21345 (Q)

Ions Score: 50 Expect: 4.4e-005

Matches : 26/126 fragment ions using 37 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.049869	65.528572			112.039304	56.523290	E							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
50.2	1970.923019	0.007123	EHAVEGDCDFQLLK
3.5	1970.959396	-0.029254	DVQSAMDRYTAFLK
1.5	1970.905258	0.024884	LDFNMTNHSFMCLIK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **VTAAPQSVCALR**

Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

Match to Query 38067: 1582.828188 from(792.421370,2+) rtinseconds(1826) index(20765)

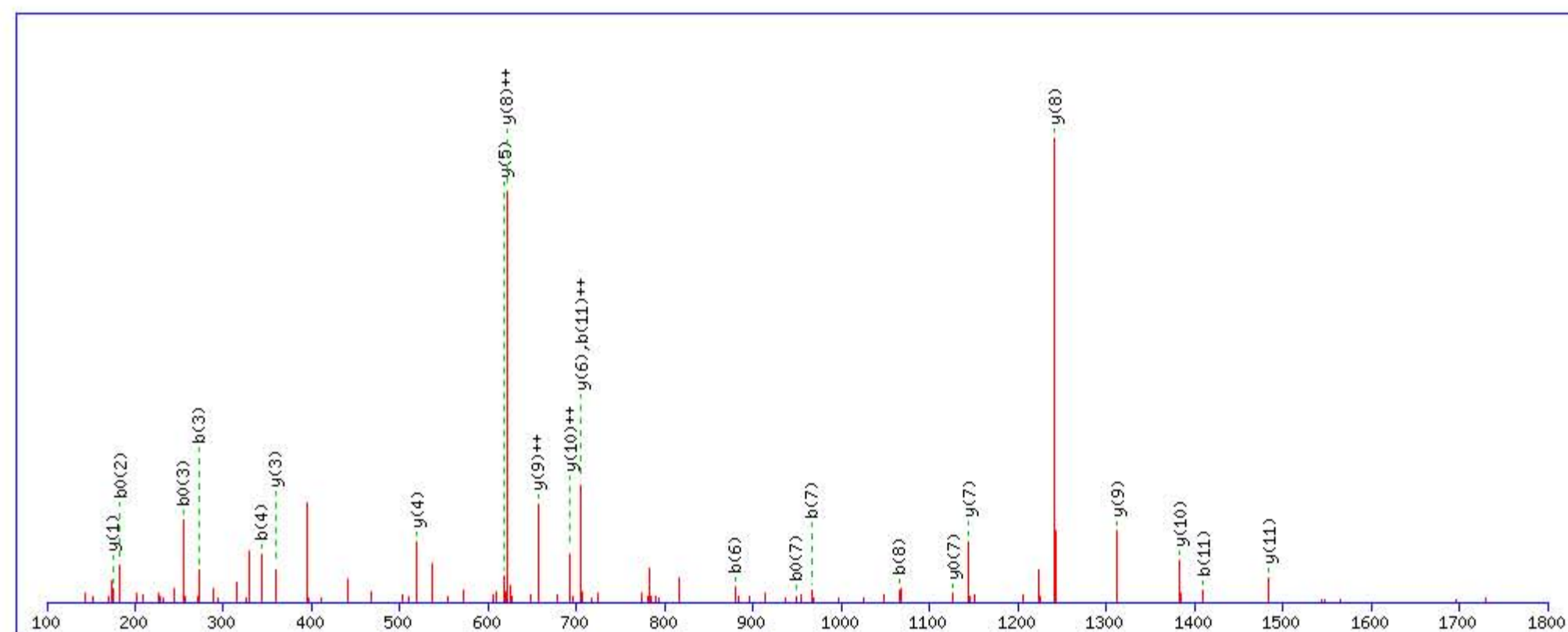
Title: Locus:1.1.1.1517.16 File:"2013-07-02 CLN FXIII 30 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

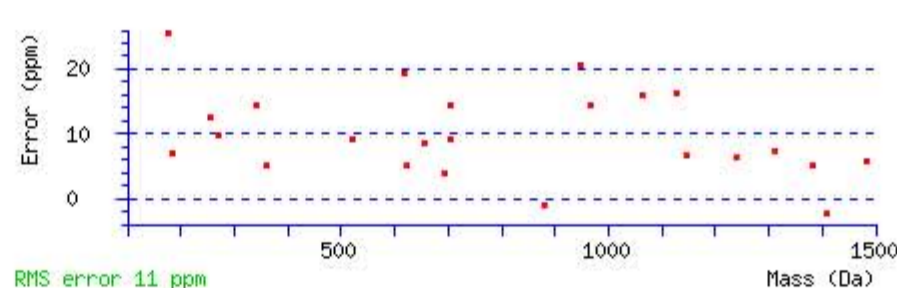
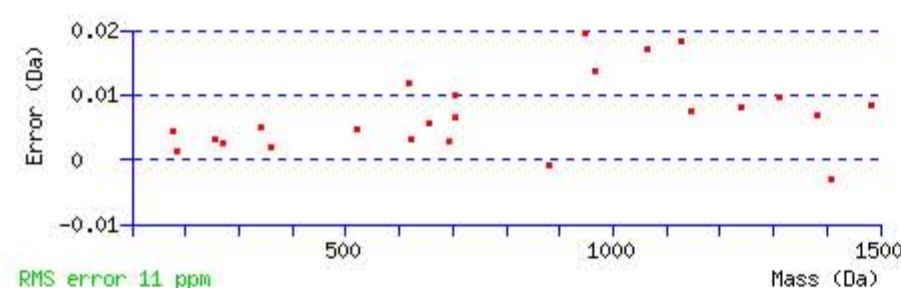
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 71 Expect: 1.1e-006

Matches : 24/110 fragment ions using 41 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.075690	50.541483					V							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
71.1	1582.832352	-0.004164	VTAAPQSVCALR
7.0	1582.844040	-0.015852	APRHGPARDPGLPSR
4.4	1582.821564	0.006624	LSKAVATWHANTER
2.1	1582.817535	0.010653	KTLSEETRQHQAR
1.3	1582.807175	0.021013	QPRMLQENTR
0.8	1582.831451	-0.003263	SAKELVEQDIQPAR
0.1	1582.850098	-0.021910	VRSSPDKDQIK

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 54072: 2210.040792 from(737.687540,3+) rtinseconds(1869) index(21006)

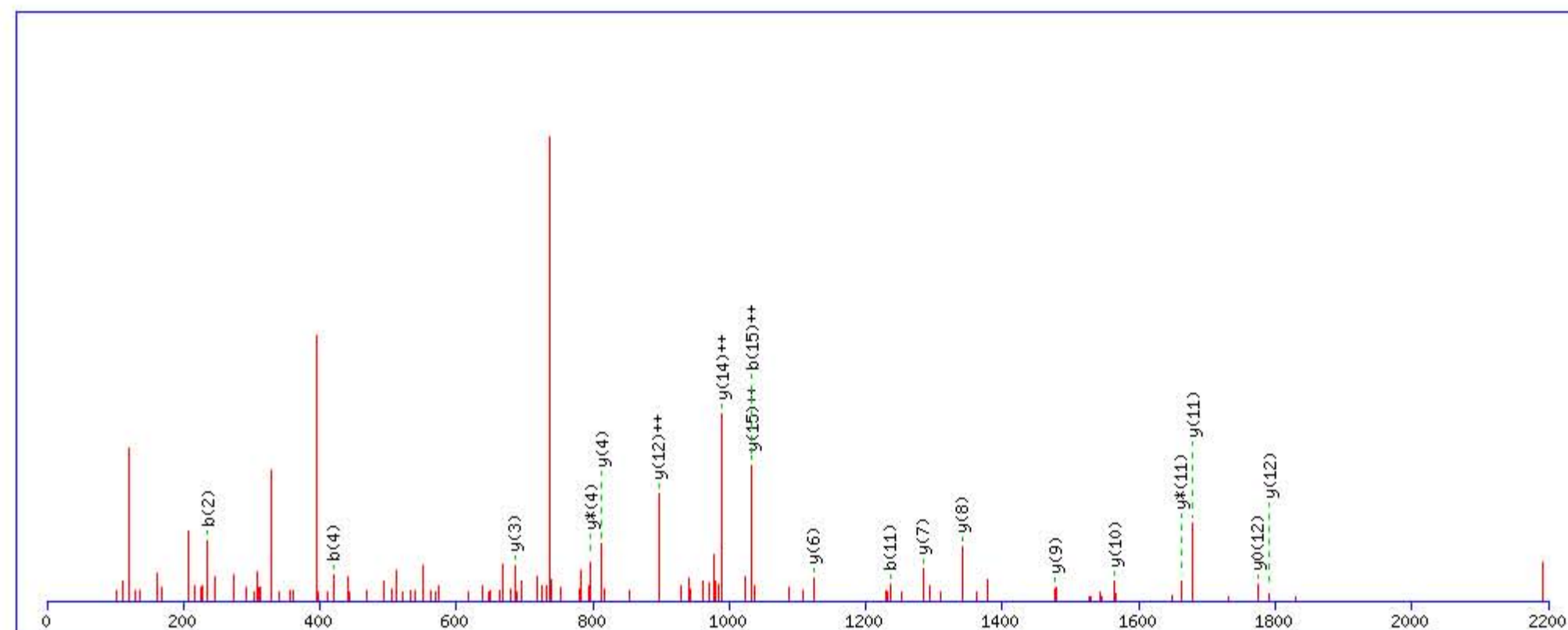
Title: Locus:1.1.1.1532.20 File:"2013-07-02 CLN FXIII 30 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

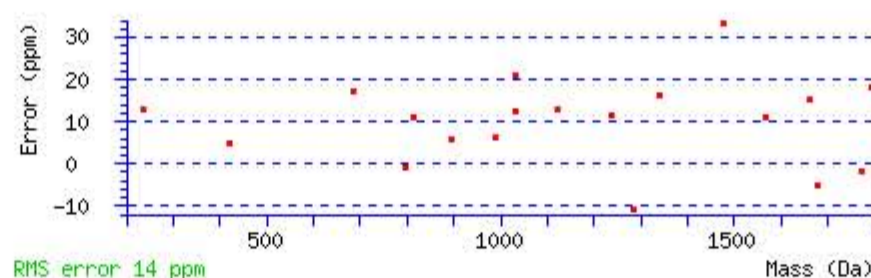
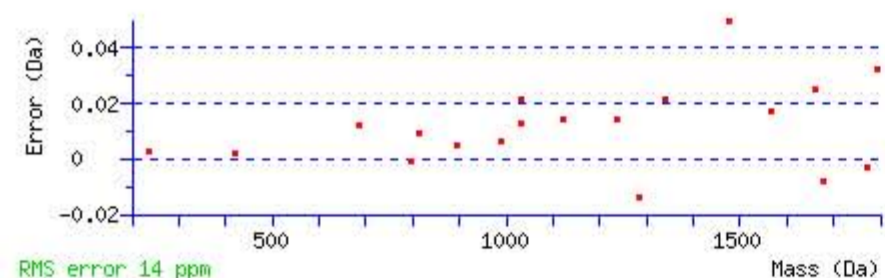
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 45 Expect: 0.00013

Matches : 19/154 fragment ions using 36 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	148.075690	74.541483					F							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
44.9	2210.040131	0.000661	FSGQLNSHGCFYQQVK
34.8	2210.040131	0.000661	FSGQLNSHGCFYQQVK
3.6	2210.045486	-0.004694	MSMKEVDEQMLAIQSK
0.0	2210.045486	-0.004694	MSMKEVDEQMLAIQSK

Mascot Search Results

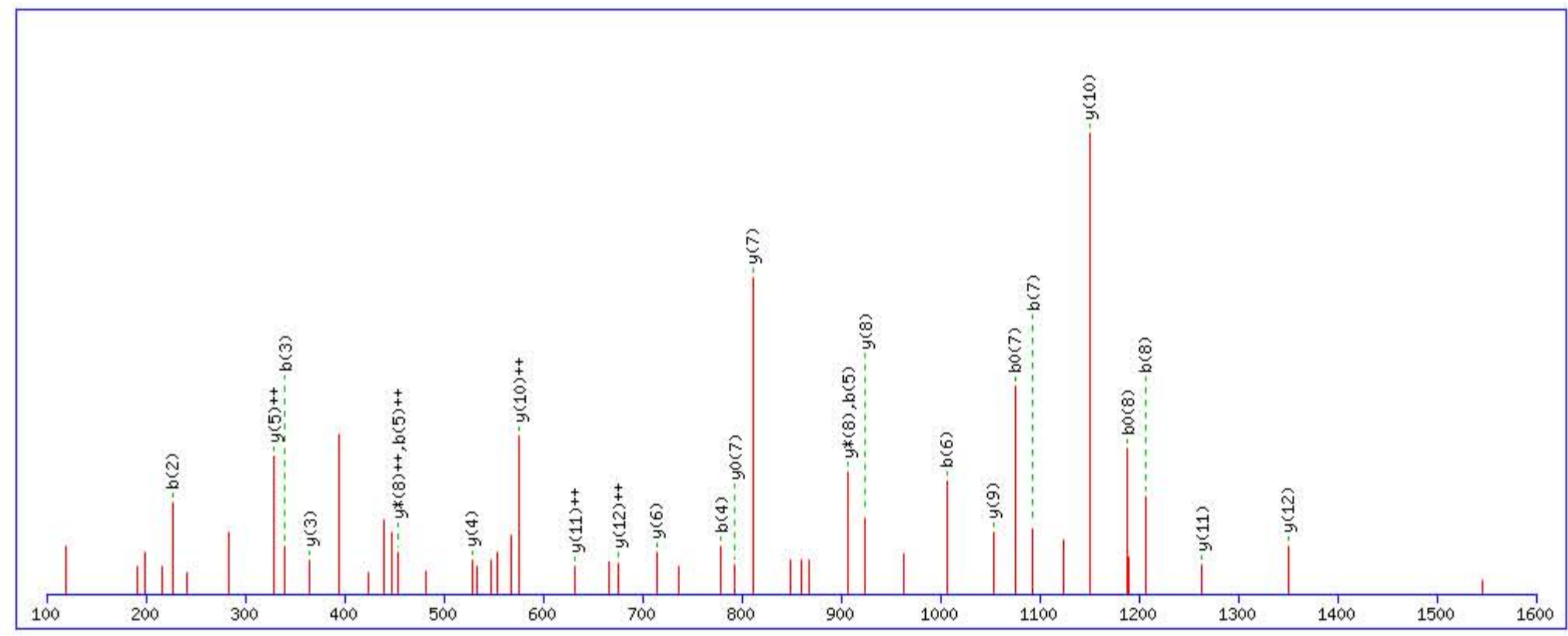
Peptide View

MS/MS Fragmentation of **LLLQVSLPELPGEYSMK**

Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

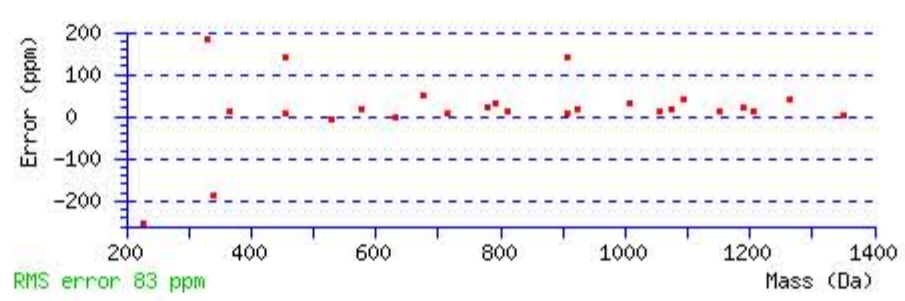
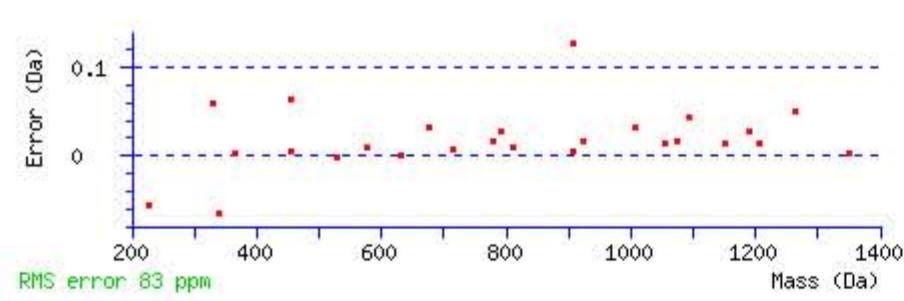
Match to Query 56964: 2355.266592 from(786.096140,3+) rtinseconds(2842) index(27061)
 Title: Locus:1.1.1.1869.14 File:"2013-07-02 CLN FXIII 30 min 2nd F 2.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 55 Expect: 1.5e-005
 Matches : 26/182 fragment ions using 44 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							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 **LLLQVSLPELPGEYSMK**
 (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	2355.258179	0.008413	LLLQVSLPELPGEYSMK
47.2	2355.258179	0.008413	LLLQVSLPELPGEYSMK
3.2	2355.288498	-0.021906	LIQQRALLNFTEWKR
2.6	2355.288498	-0.021906	LIQQRALLNFTEWKR

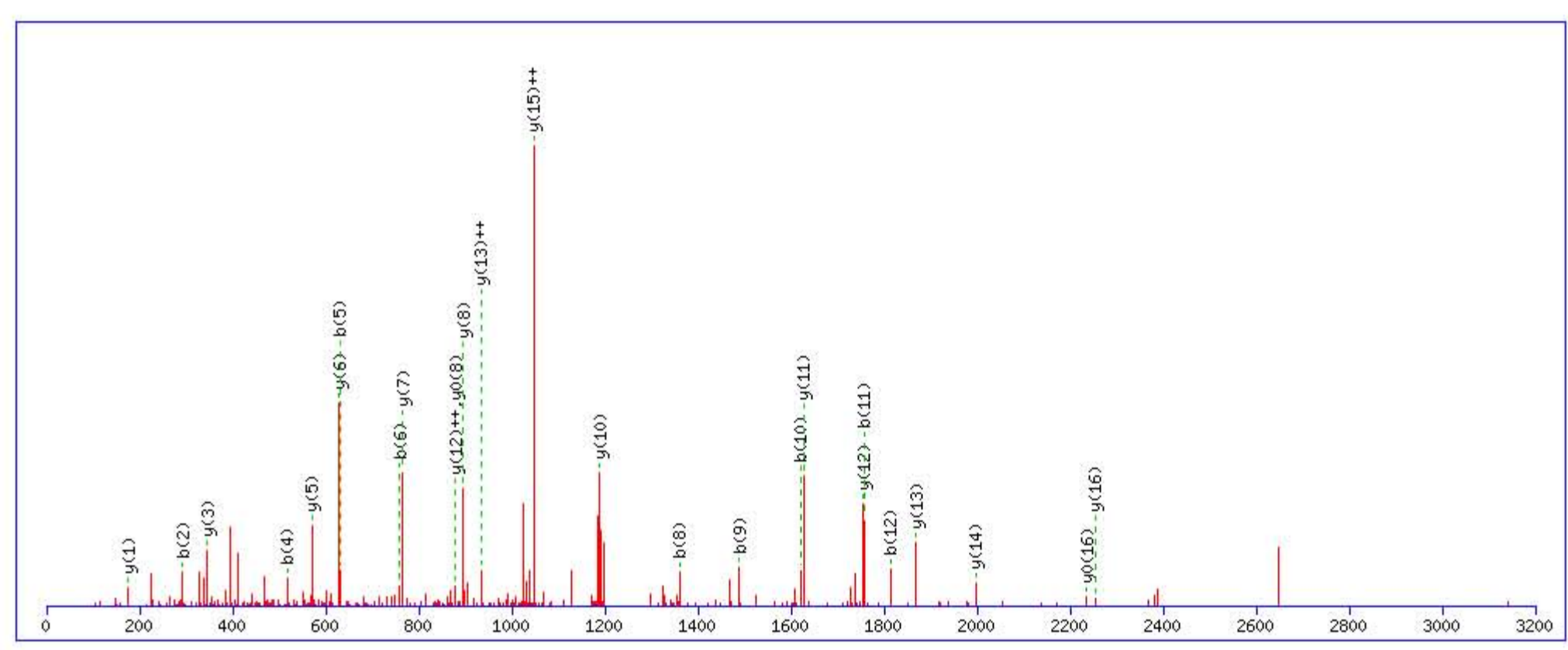
MASCOT Search Results

Peptide View

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

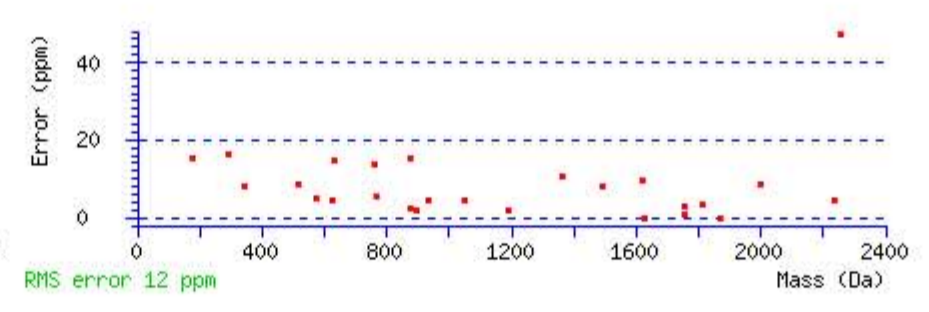
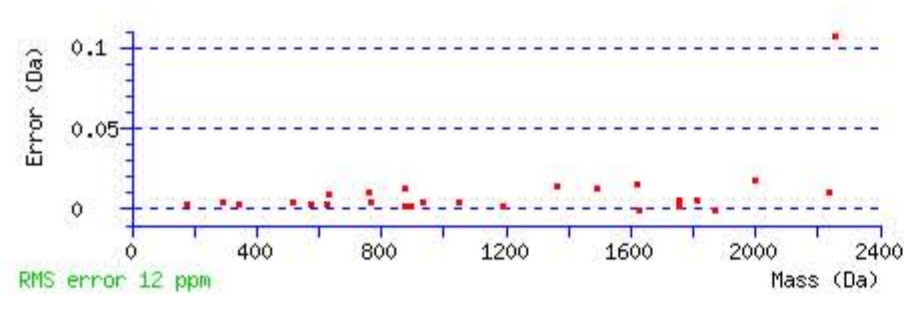
Match to Query 57237: 2384.066948 from(1193.040750,2+) rtinseconds(2025) index(21979)
 Title: Locus:1.1.1.1586.14 File:"2013-07-02 CLN FXIII 30 min 2nd F 2.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 2384.089767
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q7 : Biotin:Thermo-21345 (Q)
 Ions Score: 73 Expect: 3.8e-007
 Matches : 26/164 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	132.047761	66.527518					M							17
2	292.078410	146.542843					C	2254.056579	1127.531927	2237.030030	1119.018653	2236.046014	1118.526645	16
3	389.131174	195.069225					P	2094.025930	1047.516603	2076.999381	1039.003328	2076.015365	1038.511320	15
4	517.189752	259.098514	500.163203	250.585240			Q	1996.973166	998.990221	1979.946617	990.476947	1978.962601	989.984939	14
5	630.273816	315.640546	613.247267	307.127272			L	1868.914588	934.960932	1851.888039	926.447658	1850.904023	925.955650	13
6	758.332394	379.669835	741.305845	371.156561			Q	1755.830524	878.418900	1738.803975	869.905626	1737.819959	869.413618	12
7	1197.557720	599.282498	1180.531171	590.769224			Q	1627.771946	814.389611	1610.745397	805.876337	1609.761381	805.384329	11
8	1360.621049	680.814163	1343.594500	672.300888			Y	1188.546620	594.776948	1171.520071	586.263674	1170.536055	585.771666	10
9	1489.663642	745.335459	1472.637093	736.822185	1471.653077	736.330177	E	1025.483291	513.245284	1008.456742	504.732009	1007.472726	504.240001	9
10	1620.704127	810.855702	1603.677578	802.342427	1602.693562	801.850419	M	896.440698	448.723987	879.414149	440.210713	878.430133	439.718705	8
11	1757.763039	879.385158	1740.736490	870.871883	1739.752474	870.379875	H	765.400213	383.203745	748.373664	374.690470	747.389648	374.198462	7
12	1814.784503	907.895890	1797.757954	899.382615	1796.773938	898.890607	G	628.341301	314.674289	611.314752	306.161014	610.330736	305.669006	6
13	1911.837267	956.422272	1894.810718	947.908997	1893.826702	947.416989	P	571.319837	286.163557	554.293288	277.650282	553.309272	277.158274	5
14	2040.879860	1020.943568	2023.853311	1012.430294	2022.869295	1011.938286	E	474.267073	237.637175	457.240524	229.123900	456.256508	228.631892	4
15	2097.901324	1049.454300	2080.874775	1040.941025	2079.890759	1040.449017	G	345.224480	173.115878	328.197931	164.602603			3
16	2210.985388	1105.996332	2193.958839	1097.483057	2192.974823	1096.991049	L	288.203016	144.605146	271.176467	136.091872			2
17							R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
72.6	2384.089767	-0.022819	MCPQLQQYEMHGPEGLR
60.9	2384.089767	-0.022819	MCPQLQQYEMHGPEGLR
34.6	2384.089767	-0.022819	MCPQLQQYEMHGPEGLR

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 57256: 2384.105336 from(597.033610,4+) rtinseconds(2058) index(39040)

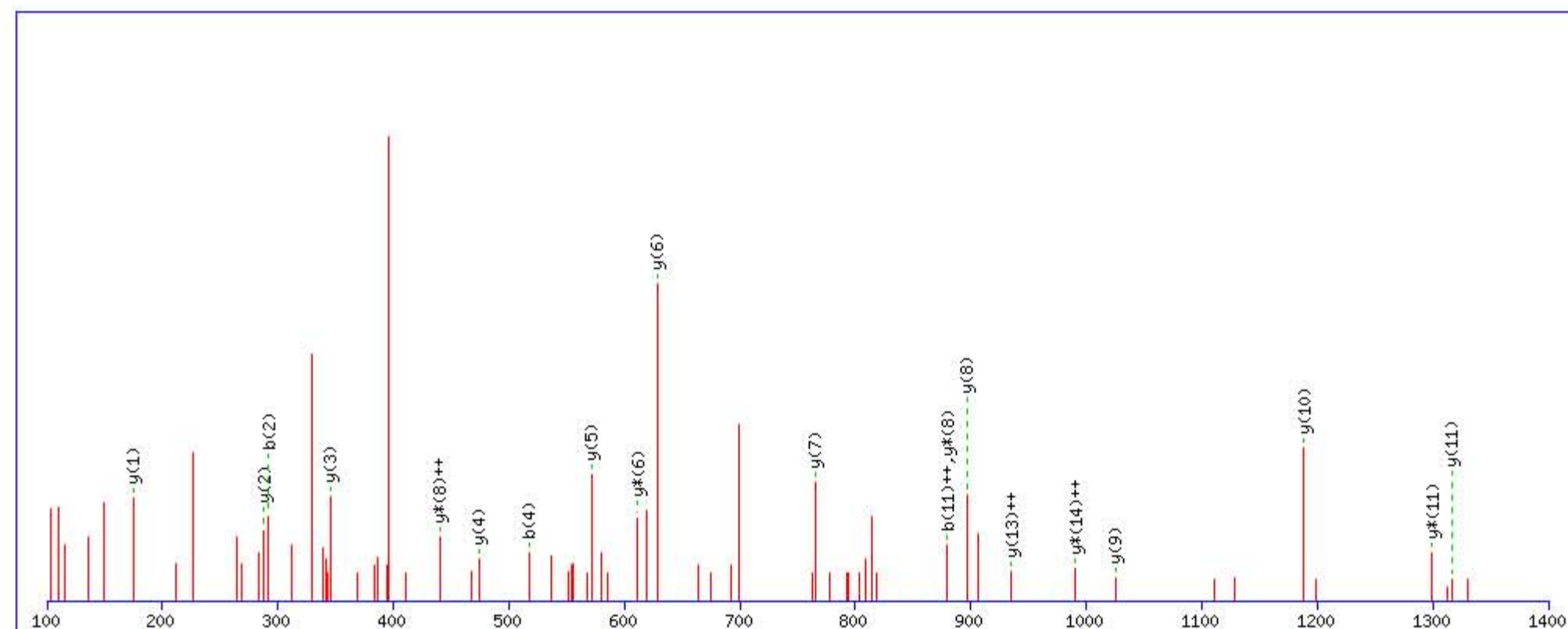
Title: Locus:1.1.1.2739.10 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

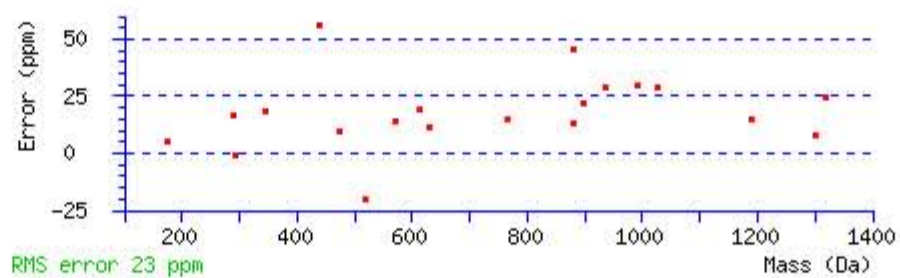
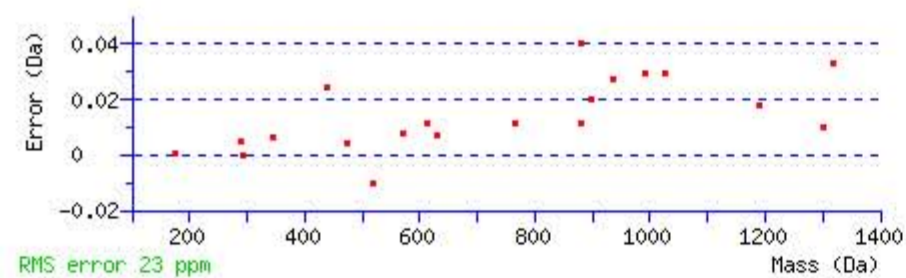
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 49 Expect: 2.6e-005

Matches : 20/164 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	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
49.2	2384.089767	0.015569	MCPQLQQYEMHGPEGLR
45.9	2384.089767	0.015569	MCPQLQQYEMHGPEGLR
41.3	2384.089767	0.015569	MCPQLQQYEMHGPEGLR
0.3	2384.118774	-0.013438	QYFRNLCSDDTMVR

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 61920: 2695.265816 from(674.823730,4+) rtinseconds(2211) index(23096)

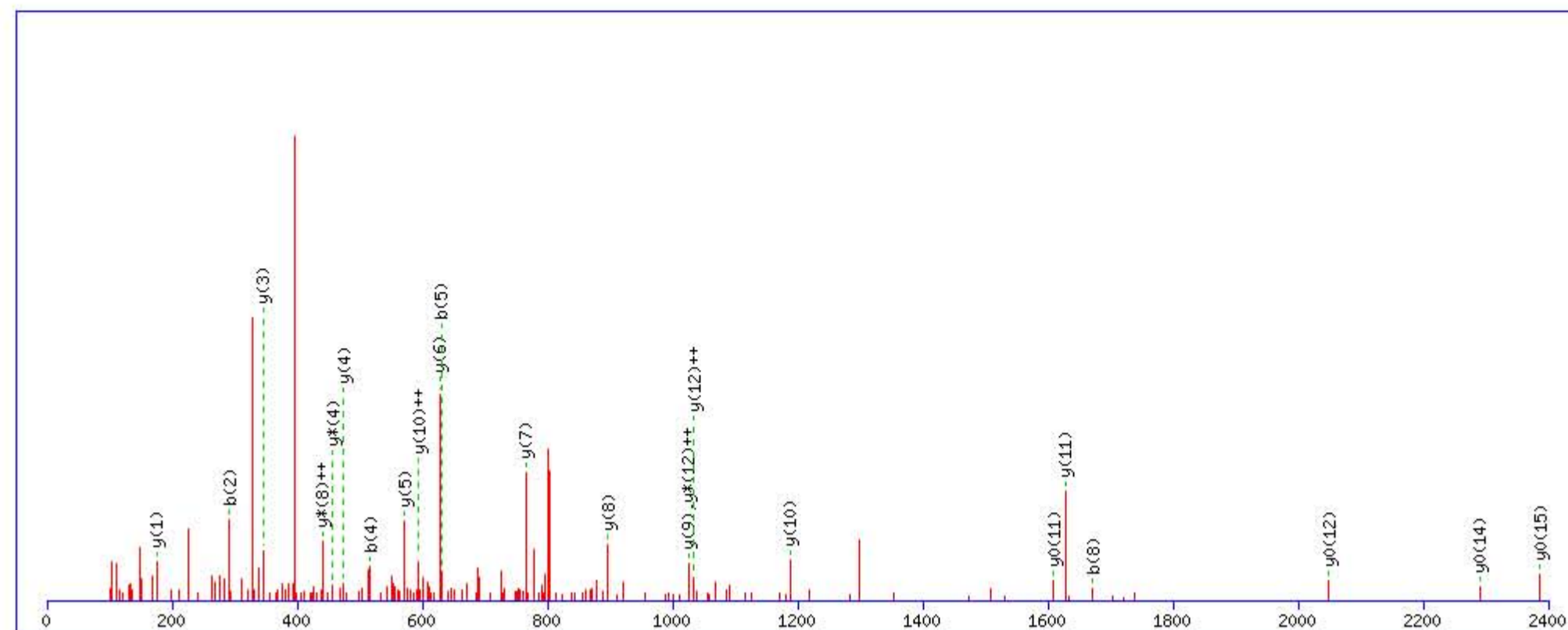
Title: Locus:1.1.1.1651.8 File:"2013-07-02 CLN FXIII 30 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2695.265816

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

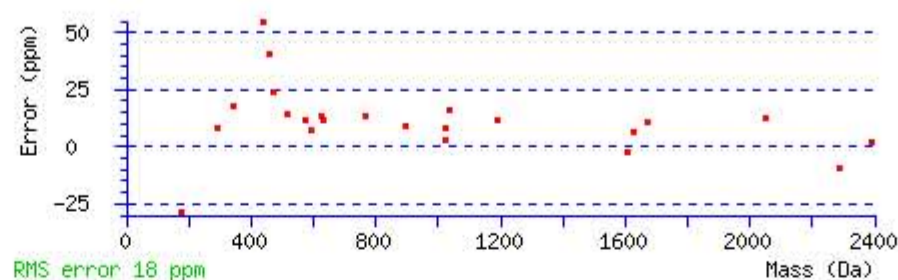
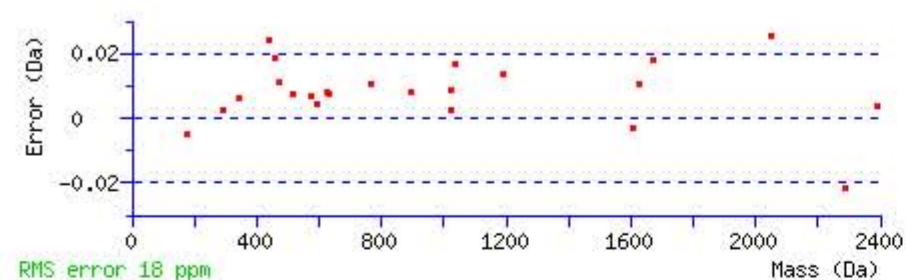
Q6 : Biotin:Thermo-21345 (Q)

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 39 Expect: 0.0022

Matches : 23/164 fragment ions using 49 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	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



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
39.0	2695.265816	0.009300	MCPQLQQYEMHGPEGLR
33.1	2695.265816	0.009300	MCPQLQQYEMHGPEGLR
25.2	2695.265816	0.009300	MCPQLQQYEMHGPEGLR

Mascot Search Results

Peptide View

MS/MS Fragmentation of **MCPQLQQYEMHGPEGLR**

Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

Match to Query 62086: 2711.259536 from(678.822160,4+) rtinseconds(2154) index(22747)

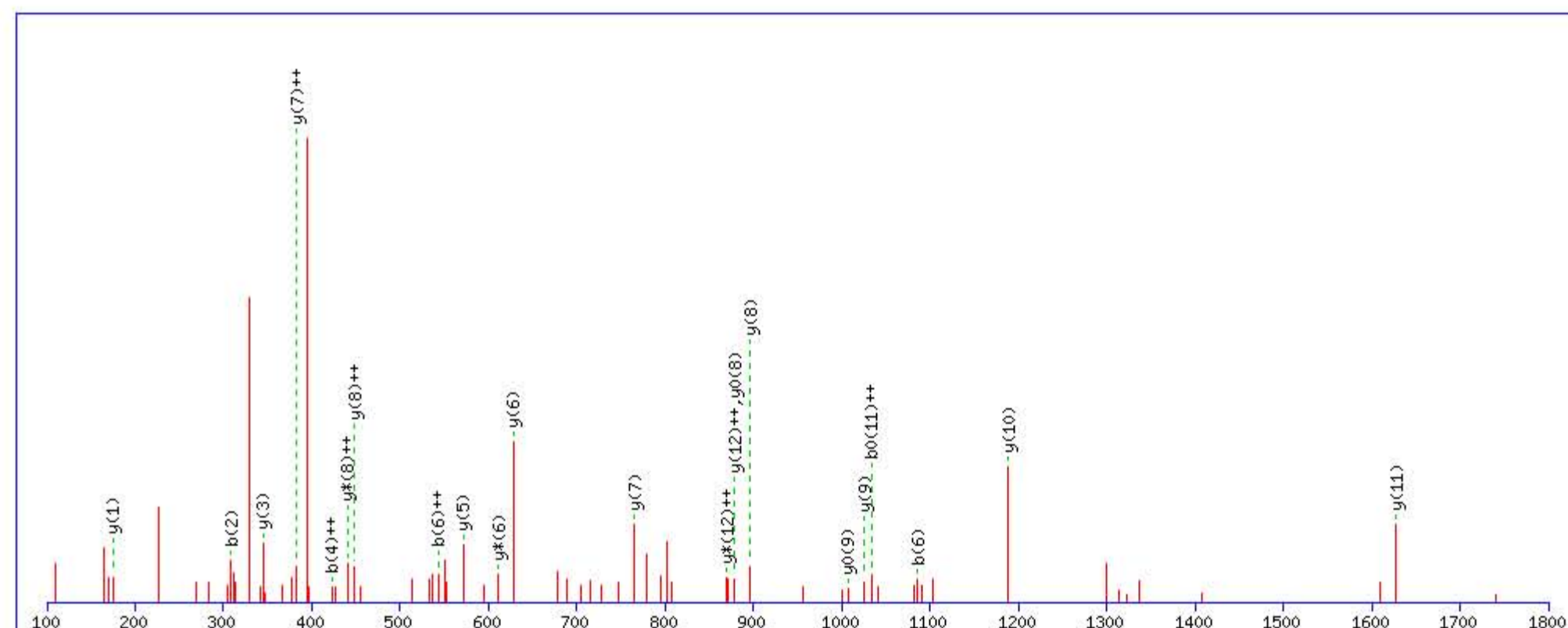
Title: Locus:1.1.1.1631.22 File:"2013-07-02 CLN FXIII 30 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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

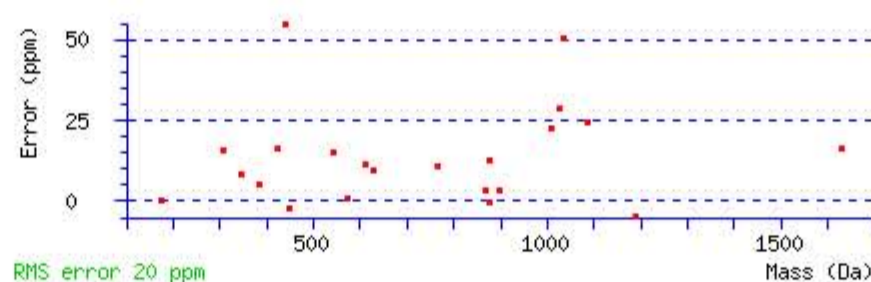
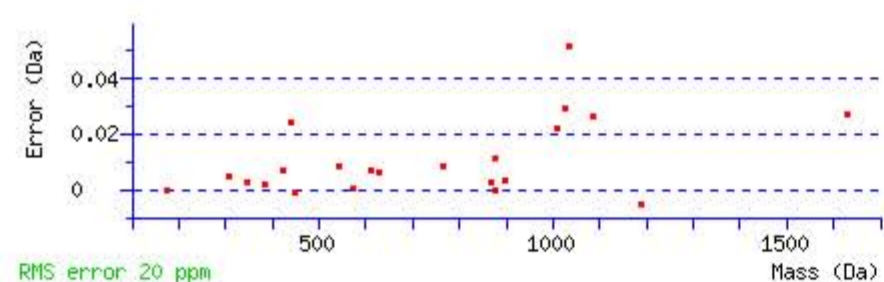
Q4 : Biotin:Thermo-21345 (Q)

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 32 Expect: 0.01

Matches : 22/238 fragment ions using 48 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	148.042676	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	1085.494057	543.250667	1068.467508	534.737392			Q	1755.830524	878.418900	1738.803975	869.905626	1737.819959	869.413618	12
7	1524.719383	762.863330	1507.692834	754.350055			Q	1627.771946	814.389611	1610.745397	805.876337	1609.761381	805.384329	11
8	1687.782712	844.394994	1670.756163	835.881720			Y	1188.546620	594.776948	1171.520071	586.263674	1170.536055	585.771666	10
9	1816.825305	908.916291	1799.798756	900.403016	1798.814740	899.911008	E	1025.483291	513.245284	1008.456742	504.732009	1007.472726	504.240001	9
10	1947.865790	974.436533	1930.839241	965.923259	1929.855225	965.431251	M	896.440698	448.723987	879.414149	440.210713	878.430133	439.718705	8
11	2084.924702	1042.965989	2067.898153	1034.452715	2066.914137	1033.960707	H	765.400213	383.203745	748.373664	374.690470	747.389648	374.198462	7
12	2141.946166	1071.476721	2124.919617	1062.963446	2123.935601	1062.471439	G	628.341301	314.674289	611.314752	306.161014	610.330736	305.669006	6
13	2238.998930	1120.003103	2221.972381	1111.489828	2220.988365	1110.997821	P	571.319837	286.163557	554.293288	277.650282	553.309272	277.158274	5
14	2368.041523	1184.524400	2351.014974	1176.011125	2350.030958	1175.519117	E	474.267073	237.637175	457.240524	229.123900	456.256508	228.631892	4
15	2425.062987	1213.035132	2408.036438	1204.521857	2407.052422	1204.029849	G	345.224480	173.115878	328.197931	164.602603			3
16	2538.147051	1269.577164	2521.120502	1261.063889	2520.136486	1260.571881	L	288.203016	144.605146	271.176467	136.091872			2
17							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [MCPQLQQYEMHGPEGLR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.8	2711.251434	0.008102	MCPQLQQYEMHGPEGLR
28.0	2711.251434	0.008102	MCPQLQQYEMHGPEGLR
19.5	2711.251434	0.008102	MCPQLQQYEMHGPEGLR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **MCPQLQQYEMHGPEGLR**

Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

Match to Query 65575: 3006.439496 from(752.617150,4+) rtinseconds(2346) index(23803)

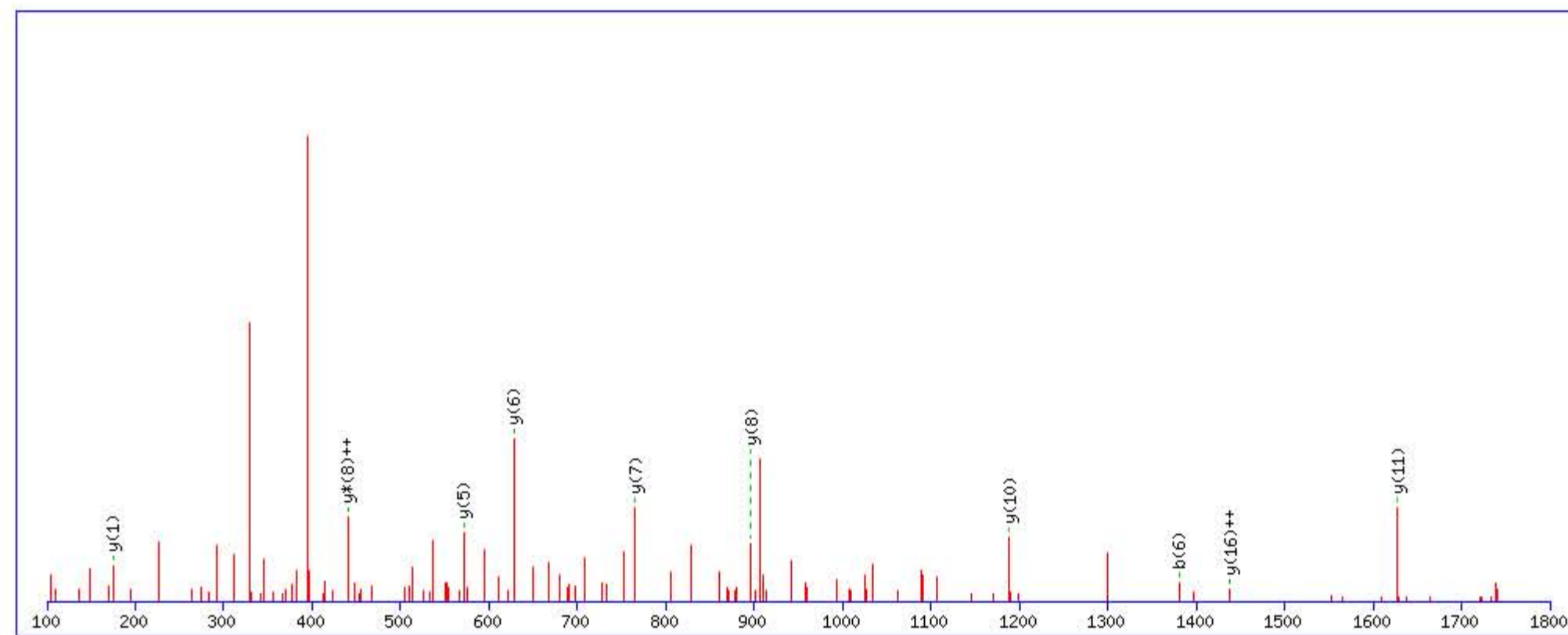
Title: Locus:1.1.1.1698.14 File:"2013-07-02 CLN FXIII 30 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

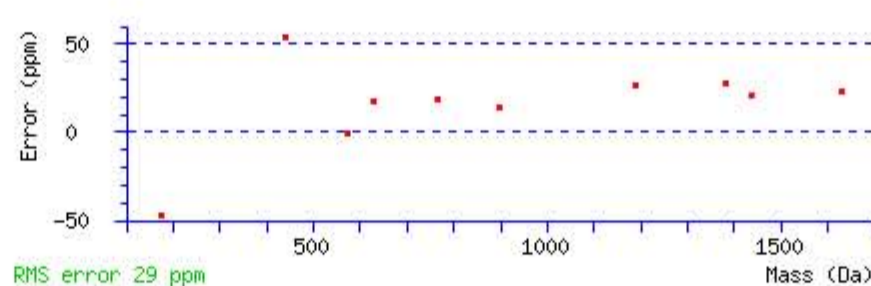
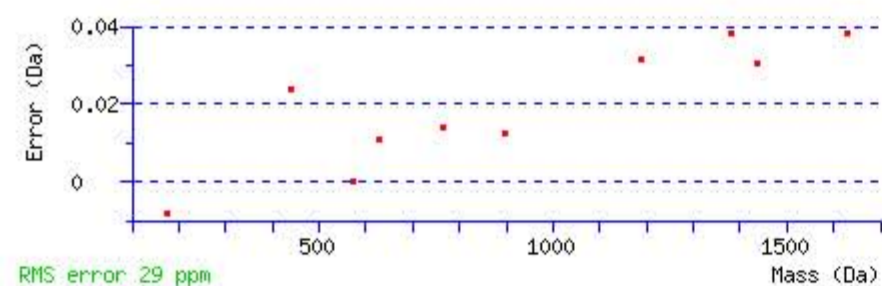
Q6 : Biotin:Thermo-21345 (Q)

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 28 Expect: 0.038

Matches : 10/164 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	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
27.9	3006.423264	0.016232	MCPQLQQYEMHGPEGLR

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

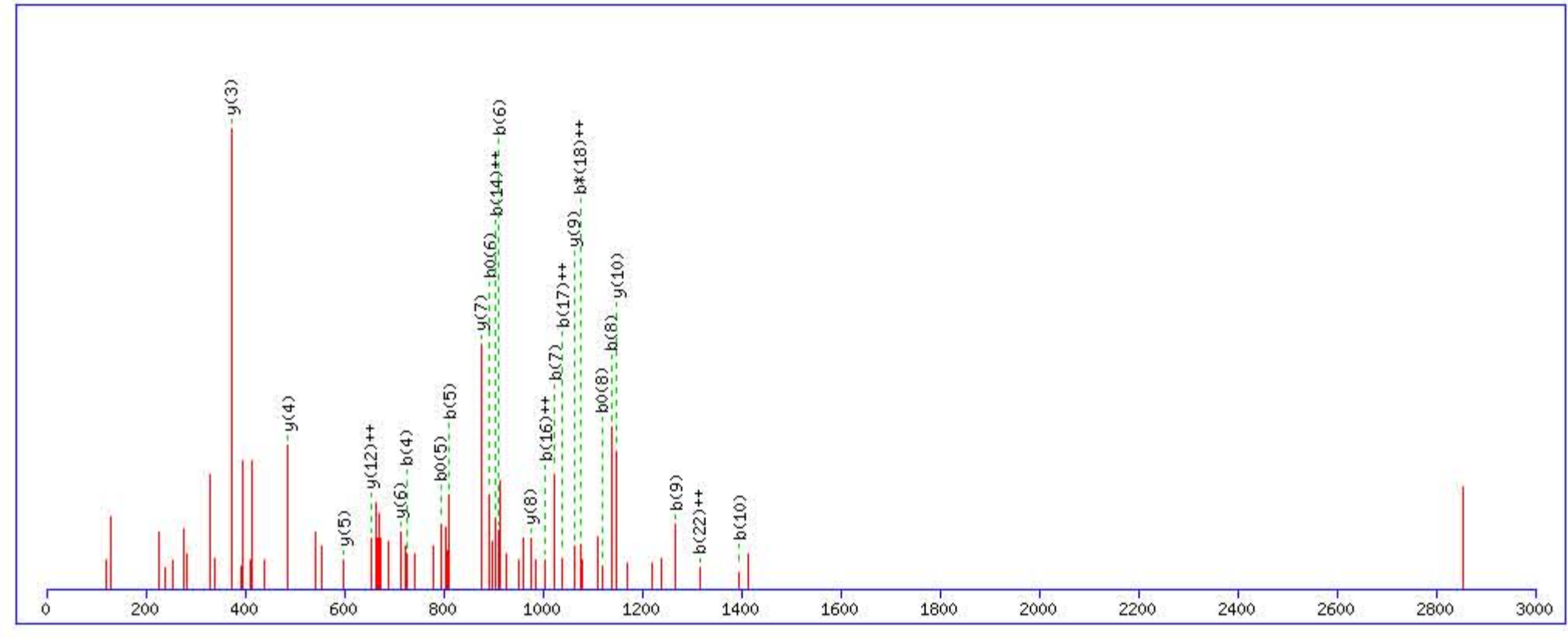
MASCOT Mascot Search Results

Peptide View

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

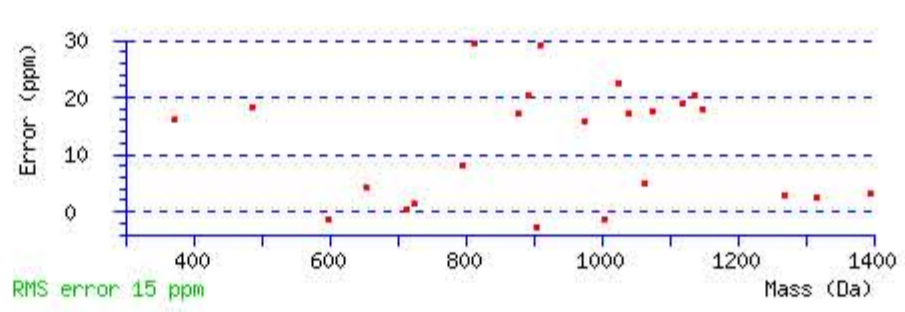
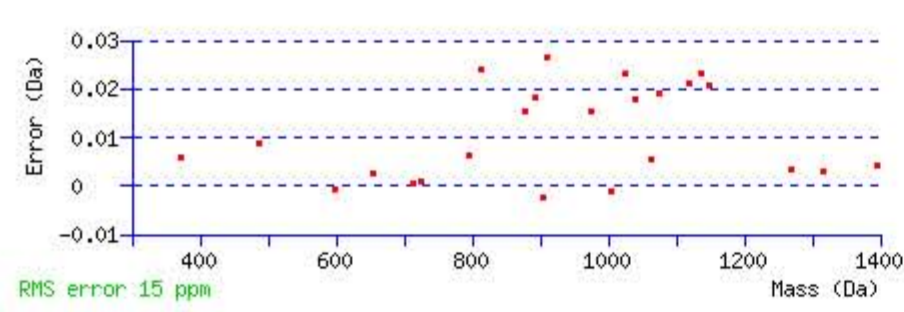
Match to Query 68036: 3227.697256 from(807.931590,4+) rtinseconds(2754) index(26477)
 Title: Locus:1.1.1.1839.14 File:"2013-07-02 CLN FXIII 30 min 2nd F 2.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 30 Expect: 0.0024
 Matches : 24/300 fragment ions using 67 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	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
29.9	3227.682129	0.015127	AVDQSVLLMKPDAELSASSVYNLLPEK
1.8	3227.668900	0.028356	SQGRGKYDFYIGLGLAMSSSIFIGGSFILK
1.3	3227.687317	0.009939	TAWPELQQSHAVNQLKDLLRQQADK
0.1	3227.673828	0.023428	LLFRCPRLLNLGLQCLSCGCLPTR

MASCOT Search Results

Peptide View

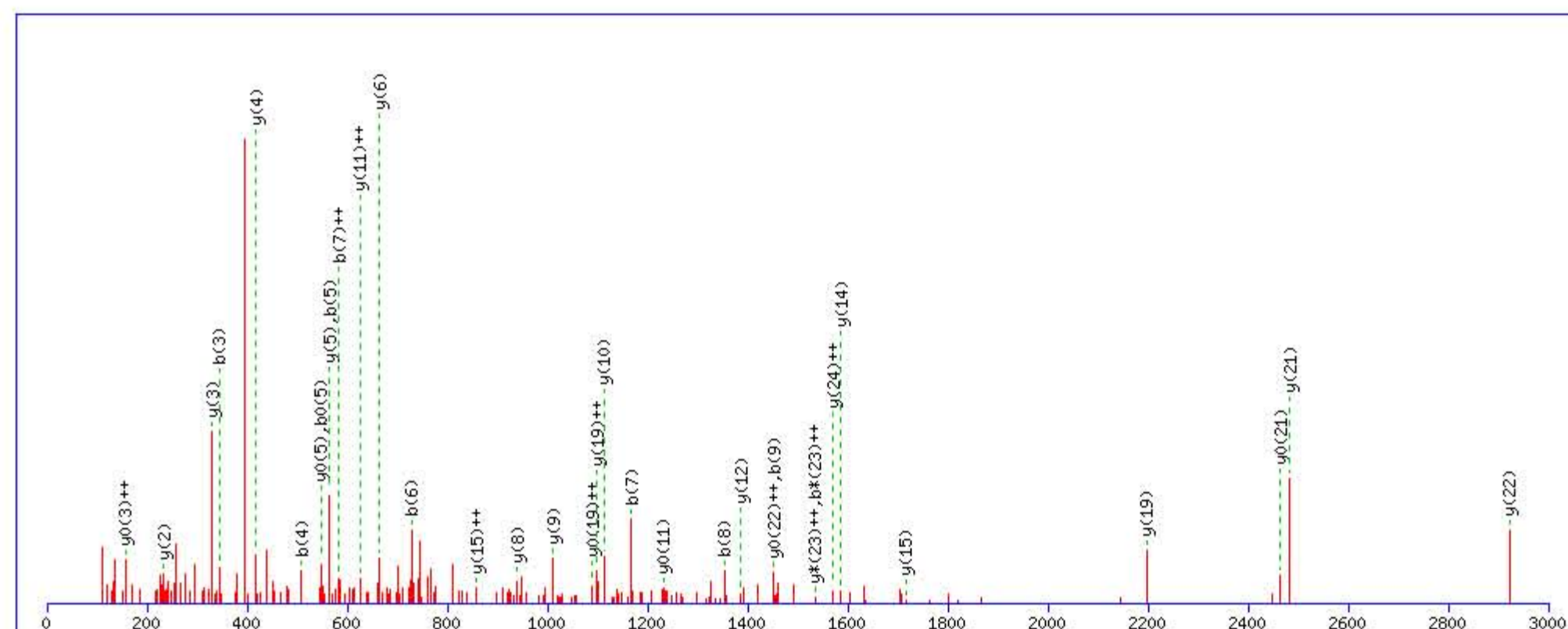
MS/MS Fragmentation of **SPCYGYQWVSEEHEEAHHTAYLVFSPSK**
 Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

Match to Query 71844: 3648.668070 from(730.740890,5+) rtinseconds(2168) index(39765)
 Title: Locus:1.1.1.2777.22 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

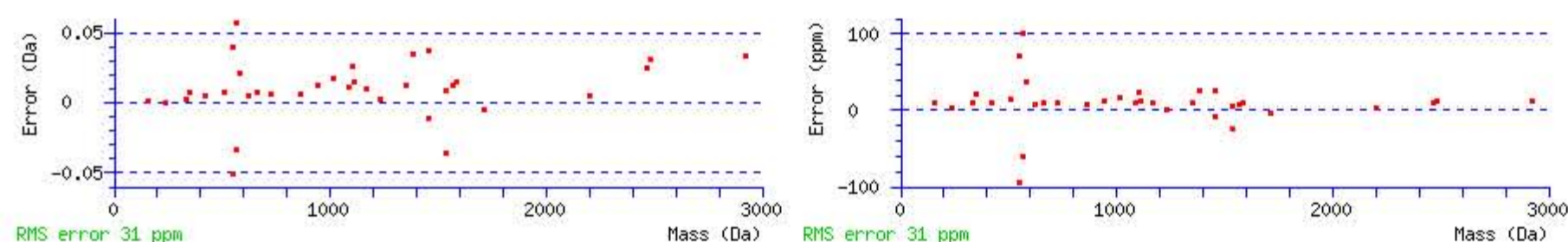
Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3648.644211
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q7 : Biotin:Thermo-21345 (Q)
 Ions Score: 50 Expect: 2.5e-005
 Matches : 35/310 fragment ions using 75 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.039304	44.523290			70.028739	35.518008	S							28
2	185.092068	93.049672			167.081503	84.044389	P	3562.619476	1781.813376	3545.592927	1773.300101	3544.608911	1772.808093	27
3	345.122717	173.064997			327.112152	164.059714	C	3465.566712	1733.286994	3448.540163	1724.773719	3447.556147	1724.281711	26
4	508.186046	254.596661			490.175481	245.591379	Y	3305.536063	1653.271669	3288.509514	1644.758395	3287.525498	1644.266387	25
5	565.207510	283.107393			547.196945	274.102111	G	3142.472734	1571.740005	3125.446185	1563.226730	3124.462169	1562.734722	24
6	728.270839	364.639058			710.260274	355.633775	Y	3085.451270	1543.229273	3068.424721	1534.715998	3067.440705	1534.223990	23
7	1167.496165	584.251721	1150.469616	575.738446	1149.485600	575.246438	Q	2922.387941	1461.697608	2905.361392	1453.184334	2904.377376	1452.692326	22
8	1353.575478	677.291377	1336.548929	668.778103	1335.564913	668.286094	W	2483.162615	1242.084945	2466.136066	1233.571671	2465.152050	1233.079663	21
9	1452.643892	726.825584	1435.617343	718.312310	1434.633327	717.820302	V	2297.083302	1149.045289	2280.056753	1140.532014	2279.072737	1140.040006	20
10	1539.675920	770.341598	1522.649371	761.828324	1521.665355	761.336316	S	2198.014888	1099.511082	2180.988339	1090.997807	2180.004323	1090.505800	19
11	1668.718513	834.862895	1651.691964	826.349620	1650.707948	825.857612	E	2110.982860	1055.995068	2093.956311	1047.481793	2092.972295	1046.989785	18
12	1797.761106	899.384191	1780.734557	890.870917	1779.750541	890.378909	E	1981.940267	991.473772	1964.913718	982.960497	1963.929702	982.468489	17
13	1934.820018	967.913647	1917.793469	959.400373	1916.809453	958.908365	H	1852.897674	926.952475	1835.871125	918.439201	1834.887109	917.947193	16
14	2063.862611	1032.434943	2046.836062	1023.921669	2045.852046	1023.429661	E	1715.838762	858.423019	1698.812213	849.909745	1697.828197	849.417737	15
15	2192.905204	1096.956240	2175.878655	1088.442965	2174.894639	1087.950958	E	1586.796169	793.901723	1569.769620	785.388448	1568.785604	784.896440	14
16	2263.942318	1132.474797	2246.915769	1123.961523	2245.931753	1123.469515	A	1457.753576	729.380426	1440.727027	720.867152	1439.743011	720.375144	13
17	2401.001230	1201.004253	2383.974681	1192.490979	2382.990665	1191.998971	H	1386.716462	693.861869	1369.689913	685.348595	1368.705897	684.856587	12
18	2538.060142	1269.533709	2521.033593	1261.020435	2520.049577	1260.528427	H	1249.657550	625.332413	1232.631001	616.819139	1231.646985	616.327131	11
19	2639.107821	1320.057548	2622.081272	1311.544274	2621.097256	1311.052266	T	1112.598638	556.802957	1095.572089	548.289683	1094.588073	547.797675	10
20	2710.144935	1355.576106	2693.118386	1347.062831	2692.134370	1346.570823	A	1011.550959	506.279118	994.524410	497.765843	993.540394	497.273835	9
21	2873.208264	1437.107770	2856.181715	1428.594496	2855.197699	1428.102488	Y	940.513845	470.760561	923.487296	462.247286	922.503280	461.755278	8
22	2986.292328	1493.649802	2969.265779	1485.136528	2968.281763	1484.644520	L	777.450516	389.228896	760.423967	380.715622	759.439951	380.223614	7
23	3085.360742	1543.184009	3068.334193	1534.670735	3067.350177	1534.178727	V	664.366452	332.686864	647.339903	324.173589	646.355887	323.681581	6
24	3232.429156	1616.718216	3215.402607	1608.204941	3214.418591	1607.712934	F	565.298038	283.152657	548.271489	274.639383	547.287473	274.147375	5
25	3319.461184	1660.234230	3302.434635	1651.720955	3301.450619	1651.228948	S	418.229624	209.618450	401.203075	201.105176	400.219059	200.613168	4
26	3416.513948	1708.760612	3399.487399	1700.247338	3398.503383	1699.755330	P	331.197596	166.102436	314.171047	157.589162	313.187031	157.097154	3
27	3503.545976	1752.276626	3486.519427	1743.763352	3485.535411	1743.271344	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
28							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **SPCYGYQWVSEEHEEAHHTAYLVFSPSK**
 (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	3648.644211	0.023859	SPCYGYQWVSEEHEEAHHTAYLVFSPSK
0.7	3648.698624	-0.030554	RTSSVVDFKMMAFDPDVWGHCPPPTTQPMLER

MASCOT 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 23159: 1143.539268 from(572.776910,2+) rtinseconds(1149) index(16753)

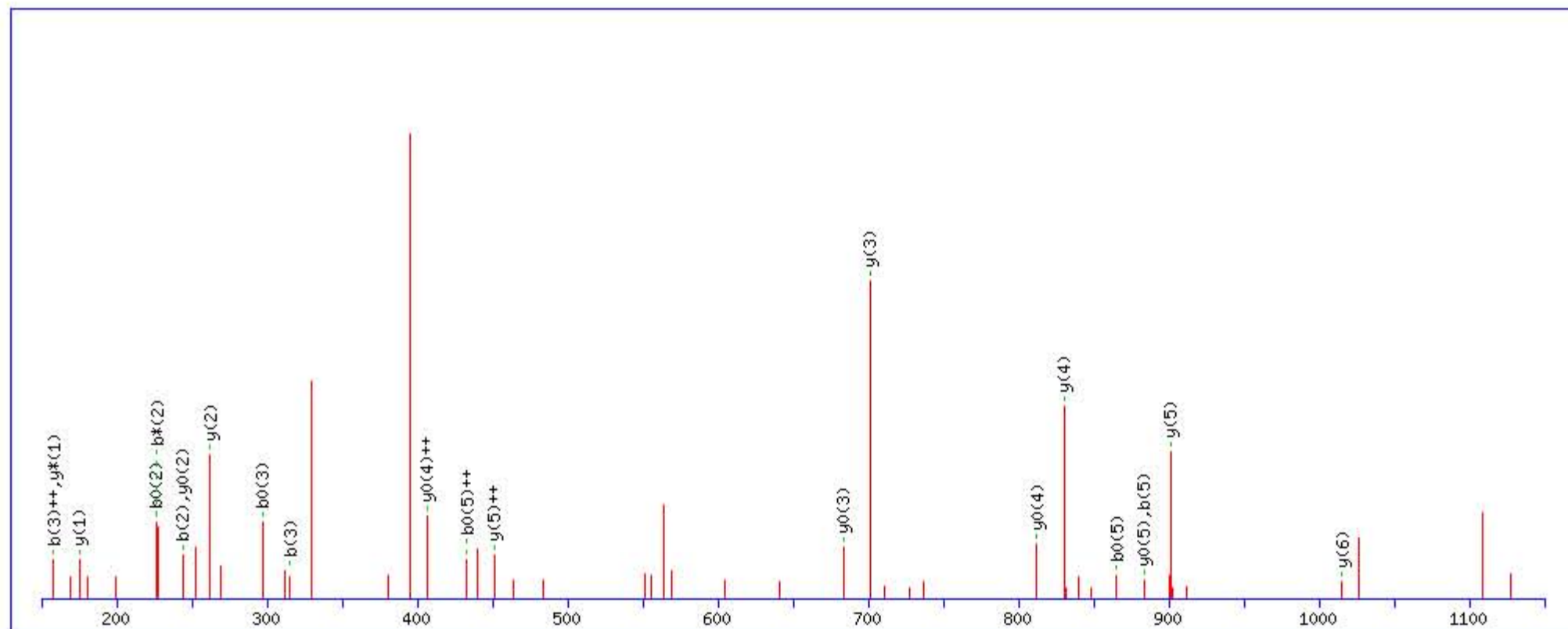
Title: Locus:1.1.1.1281.14 File:"2013-07-02 CLN FXIII 30 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

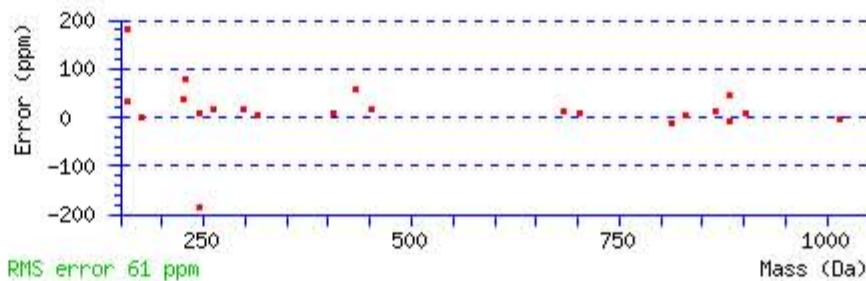
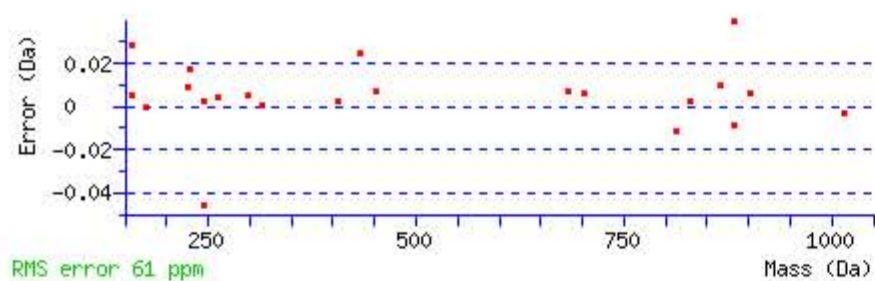
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 28 Expect: 0.02

Matches : 22/68 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	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
27.7	1143.534225	0.005043	ENAEQSR
12.6	1143.552017	-0.012749	VDDGTGREAPK
9.5	1143.549500	-0.010232	WQEQSR
7.3	1143.552002	-0.012734	SSSALDSPAGPR
0.7	1143.527710	0.011558	REFMMRSR

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 36662: 1540.860968 from(771.437760,2+) rtinseconds(2821) index(76534)

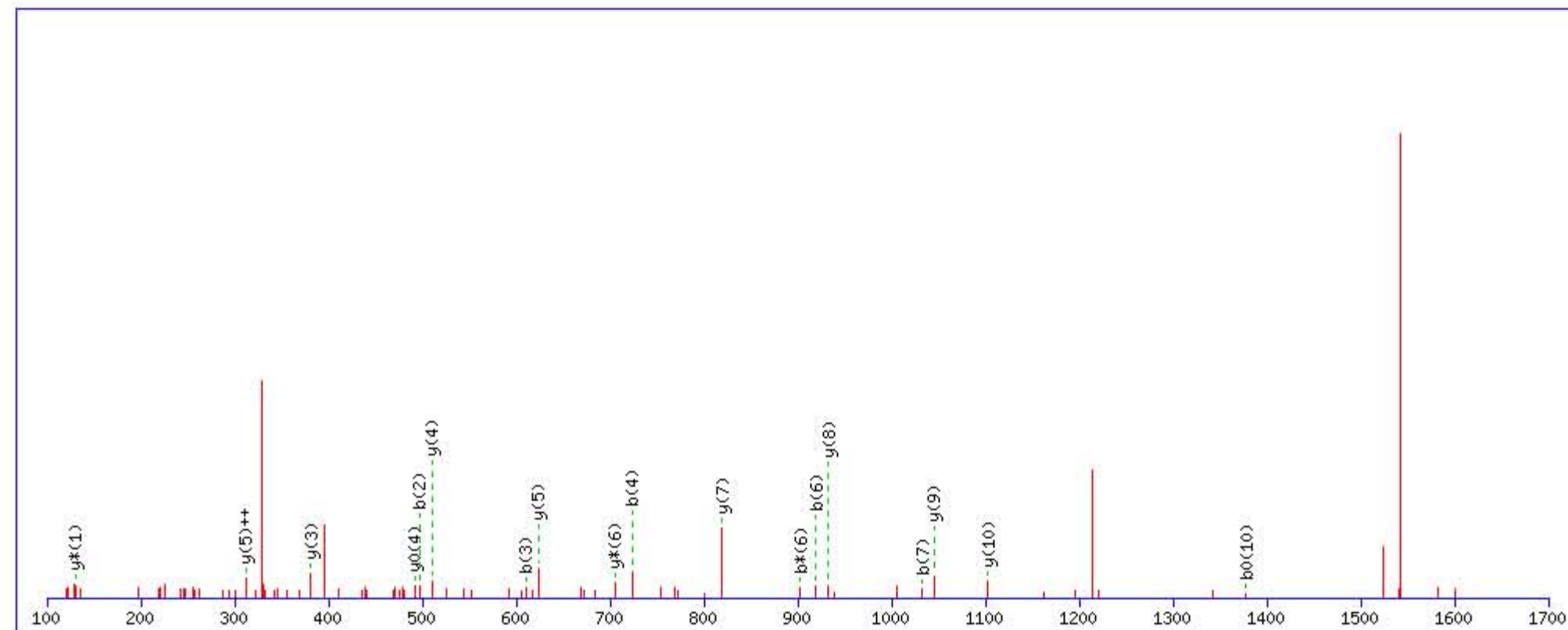
Title: Locus:1.1.1.3514.15 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1540.868713

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

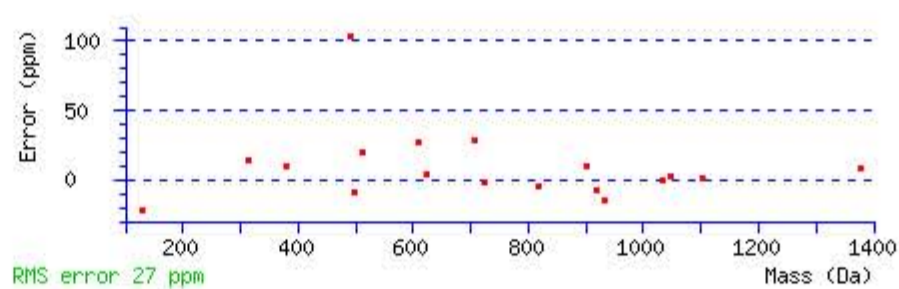
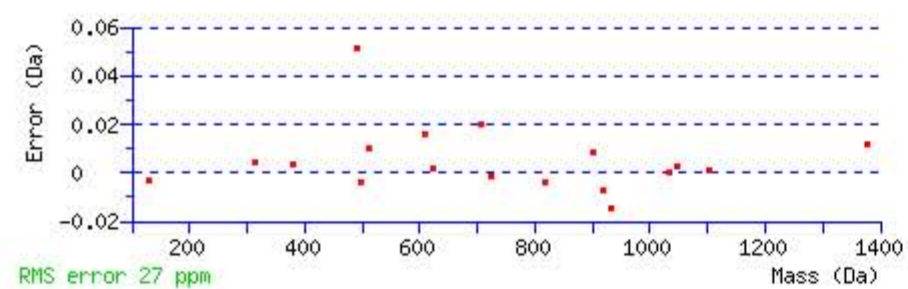
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 34 Expect: 0.0007

Matches : 18/102 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	440.232602	220.619939	423.206053	212.106664			Q							11
2	497.254066	249.130671	480.227517	240.617396			G	1102.650673	551.828975	1085.624124	543.315700	1084.640108	542.823692	10
3	610.338130	305.672703	593.311581	297.159428			L	1045.629209	523.318243	1028.602660	514.804968	1027.618644	514.312960	9
4	723.422194	362.214735	706.395645	353.701461			L	932.545145	466.776211	915.518596	458.262936	914.534580	457.770928	8
5	820.474958	410.741117	803.448409	402.227843			P	819.461081	410.234179	802.434532	401.720904	801.450516	401.228896	7
6	919.543372	460.275324	902.516823	451.762049			V	722.408317	361.707797	705.381768	353.194522	704.397752	352.702514	6
7	1032.627436	516.817356	1015.600887	508.304082			L	623.339903	312.173590	606.313354	303.660315	605.329338	303.168307	5
8	1161.670029	581.338653	1144.643480	572.825378	1143.659464	572.333370	E	510.255839	255.631558	493.229290	247.118283	492.245274	246.626275	4
9	1248.702057	624.854667	1231.675508	616.341392	1230.691492	615.849384	S	381.213246	191.110261	364.186697	182.596987	363.202681	182.104979	3
10	1395.770471	698.388874	1378.743922	689.875599	1377.759906	689.383591	F	294.181218	147.594247	277.154669	139.080973			2
11							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **QGLLPVLESFK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.4	1540.868713	-0.007745	QGLLPVLESFK
0.8	1540.850769	0.010199	KTVLGADSQRR
0.8	1540.864700	-0.003732	KVTVGKDDIQK
0.7	1540.846054	0.014914	ISQDADLKTPTKPK
0.7	1540.879761	-0.018793	TVQVLRDTANRLR

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 61573: 2660.229372 from(887.750400,3+) rtinseconds(3137) index(78721)

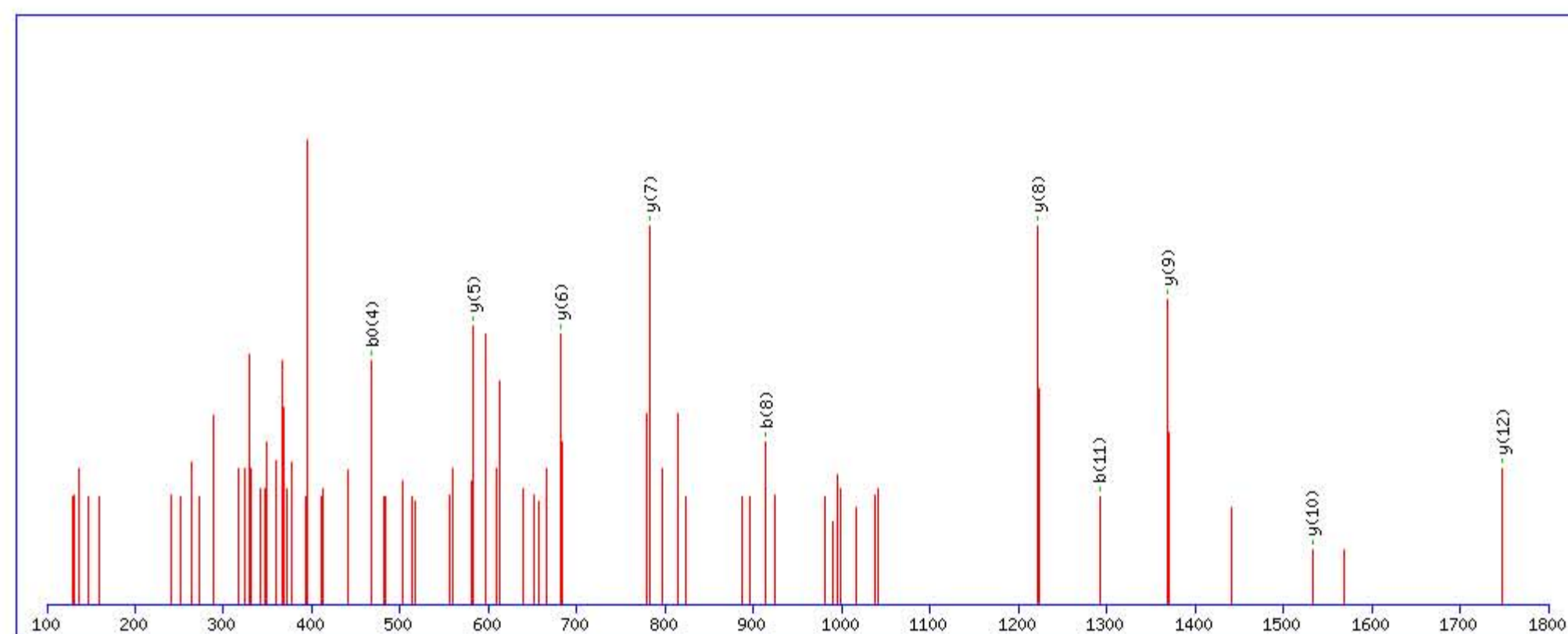
Title: Locus:1.1.1.3623.16 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\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 $M_r(\text{calc})$: 2660.250244

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

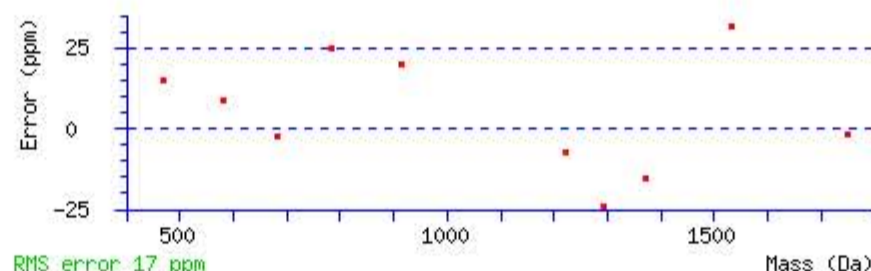
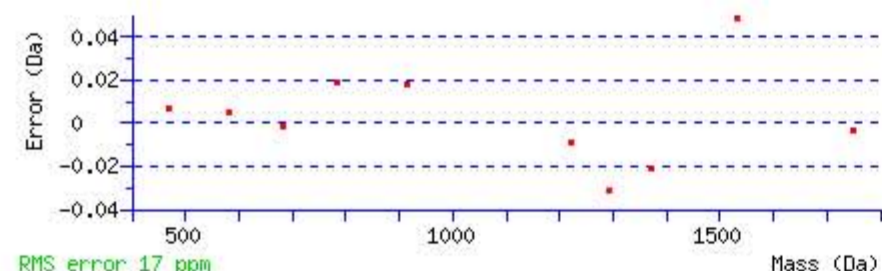
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 37 Expect: 0.0032

Matches : 10/204 fragment ions using 16 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.049869	65.528572			112.039304	56.523290	E							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	$M_r(\text{calc})$:	Delta	Sequence
37.1	2660.250244	-0.020872	EPCVESLVSQYFQTVTDYGK
11.2	2660.250244	-0.020872	EPCVESLVSQYFQTVTDYGK

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 61576: 2660.245602 from(887.755810,3+) rtinseconds(3158) index(13145)

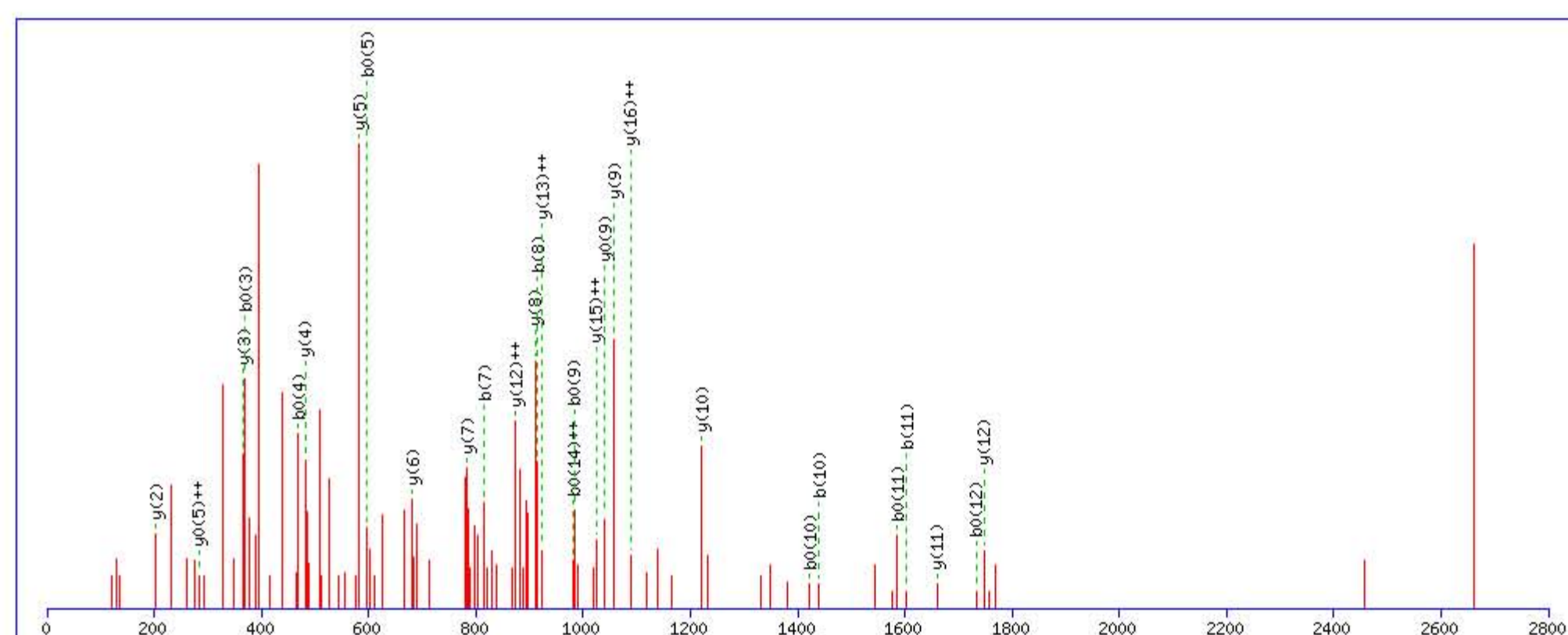
Title: Locus:1.1.1.3532.19 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

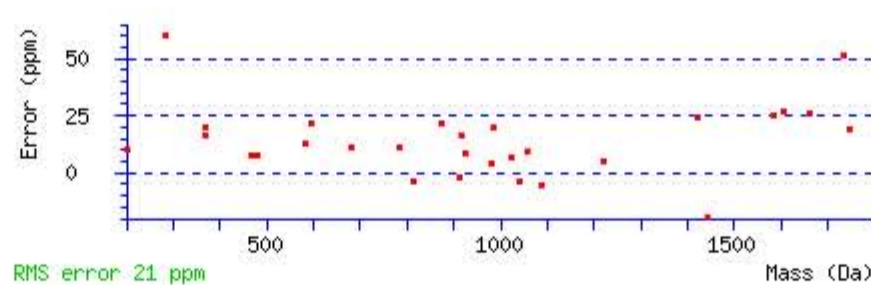
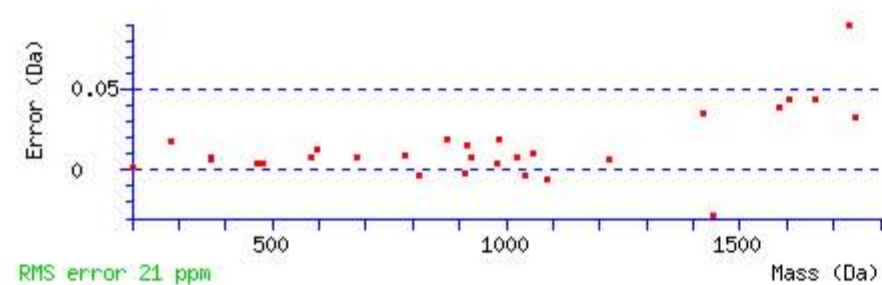
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 49 Expect: 0.00023

Matches : 29/204 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	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
49.3	2660.250244	-0.004642	EPCVESLVSQYFQTVTDYGK
21.5	2660.250244	-0.004642	EPCVESLVSQYFQTVTDYGK

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 23596: 1156.591148 from(579.302850,2+) rtinseconds(1433) index(67594)

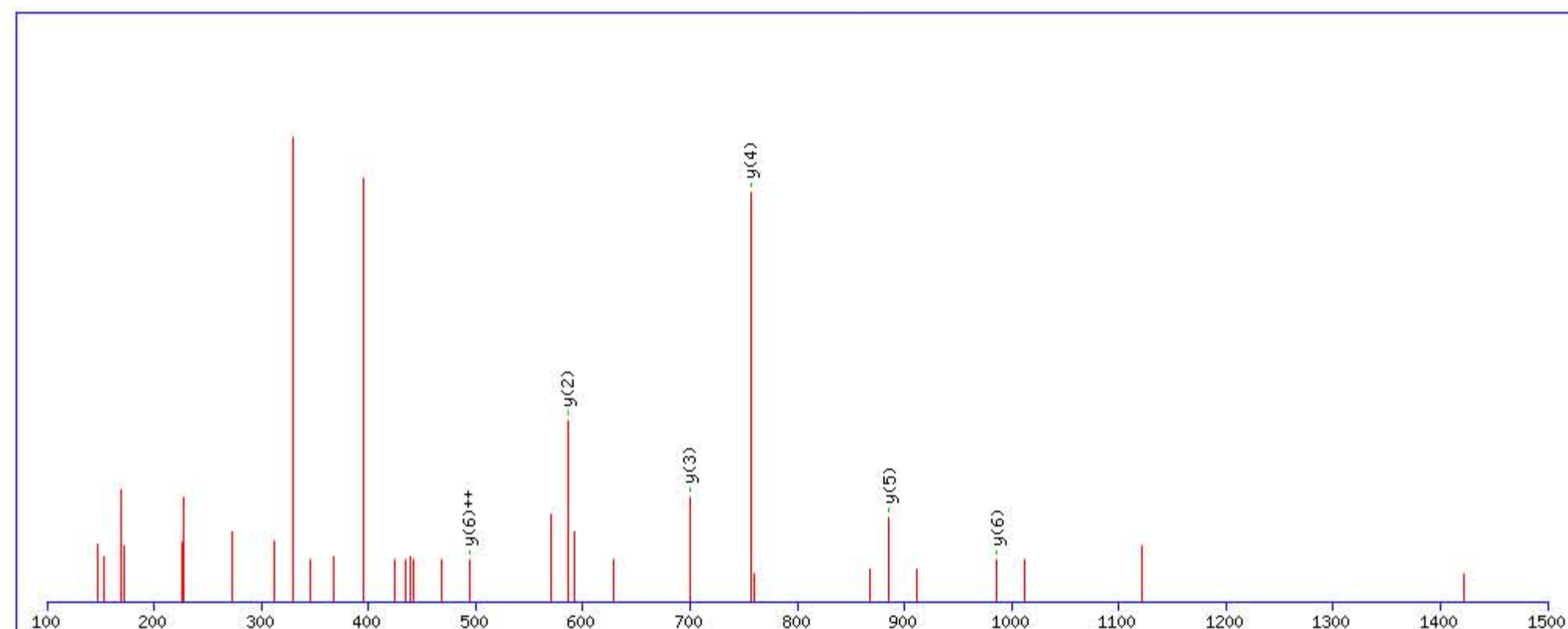
Title: Locus:1.1.1.3032.22 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1156.591034

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

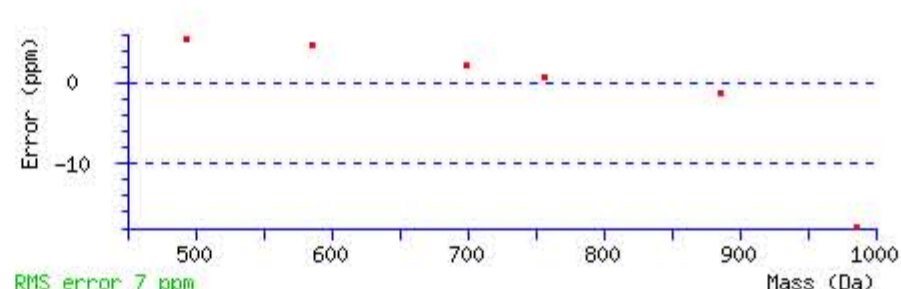
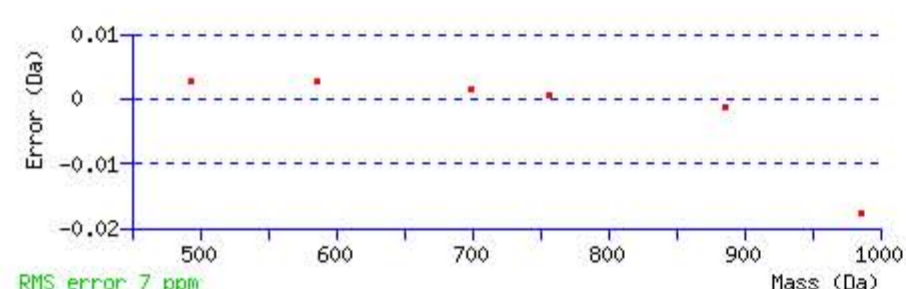
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 32 Expect: 0.0033

Matches : 6/70 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	172.071667	86.539471	155.045118	78.026197			N	1100.576857	550.792067	1083.550308	542.278792	1082.566292	541.786784	7
3	273.119346	137.063311	256.092797	128.550037	255.108781	128.058029	T	986.533930	493.770603	969.507381	485.257329	968.523365	484.765321	6
4	402.161939	201.584608	385.135390	193.071333	384.151374	192.579325	E	885.486251	443.246764	868.459702	434.733489	867.475686	434.241481	5
5	459.183403	230.095339	442.156854	221.582065	441.172838	221.090057	G	756.443658	378.725467	739.417109	370.212193			4
6	572.267467	286.637372	555.240918	278.124097	554.256902	277.632089	L	699.422194	350.214735	682.395645	341.701461			3
7	1011.492793	506.250035	994.466244	497.736760	993.482228	497.244752	Q	586.338130	293.672703	569.311581	285.159429			2
8							K	147.112804	74.060040	130.086255	65.546766			1



NCBI BLAST search of **GNTEGLQK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.0	1156.591034	0.000114	GNTEGLQK
5.3	1156.576416	0.014732	IKSQDFYEK
5.3	1156.591019	0.000129	ENTNLQK
5.1	1156.595047	-0.003899	CDYFLAKIK
4.5	1156.587662	0.003486	APGGLSLHDIK
2.7	1156.602264	-0.011116	NGMLNVSPIGR
1.3	1156.577118	0.014030	QLSTRCHQK

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 32052: 1397.715308 from(699.864930,2+) rtinseconds(1832) index(70088)

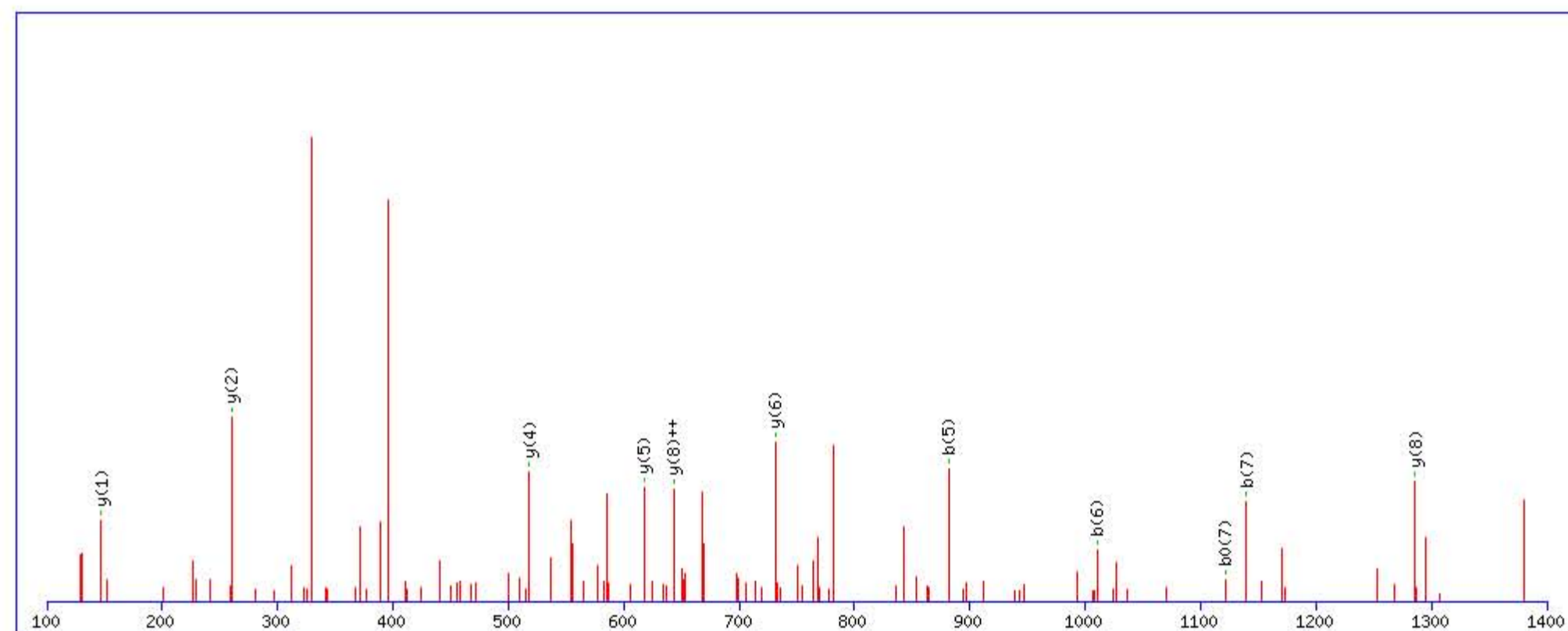
Title: Locus:1.1.1.3171.9 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

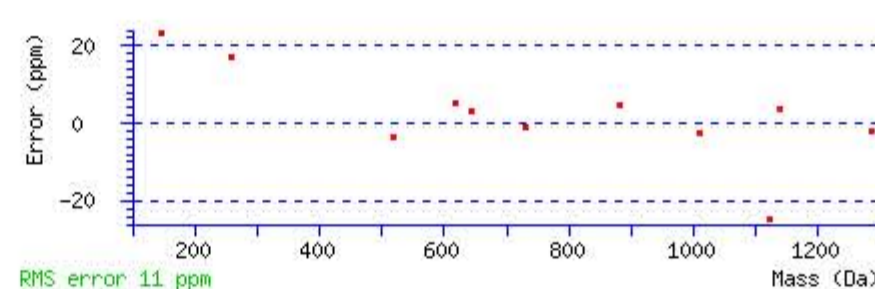
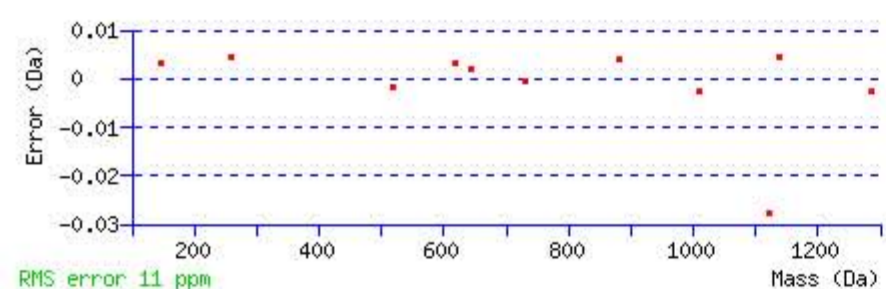
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 52 Expect: 0.00012

Matches : 11/86 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					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
52.0	1397.722427	-0.007119	IDQNVEELK
9.7	1397.734329	-0.019021	LYTHSYLGFGFK
7.7	1397.715057	0.000251	LEDGSHLTGQTLK
7.7	1397.726456	-0.011148	LEIMEFVNFLK
7.7	1397.722427	-0.007119	LENDVEQLK
7.7	1397.712540	0.002768	LMFDAFNQRLK
7.5	1397.733658	-0.018350	QNITNQLEK
5.4	1397.708496	0.006812	QMEIQKHKDNK
4.6	1397.701309	0.013999	LLFNFVEQNMK
4.5	1397.733643	-0.018335	QQKAENELK

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **IDQTV EELR**

Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

Match to Query 32978: 1412.726008 from(707.370280,2+) rtinseconds(1912) index(70555)

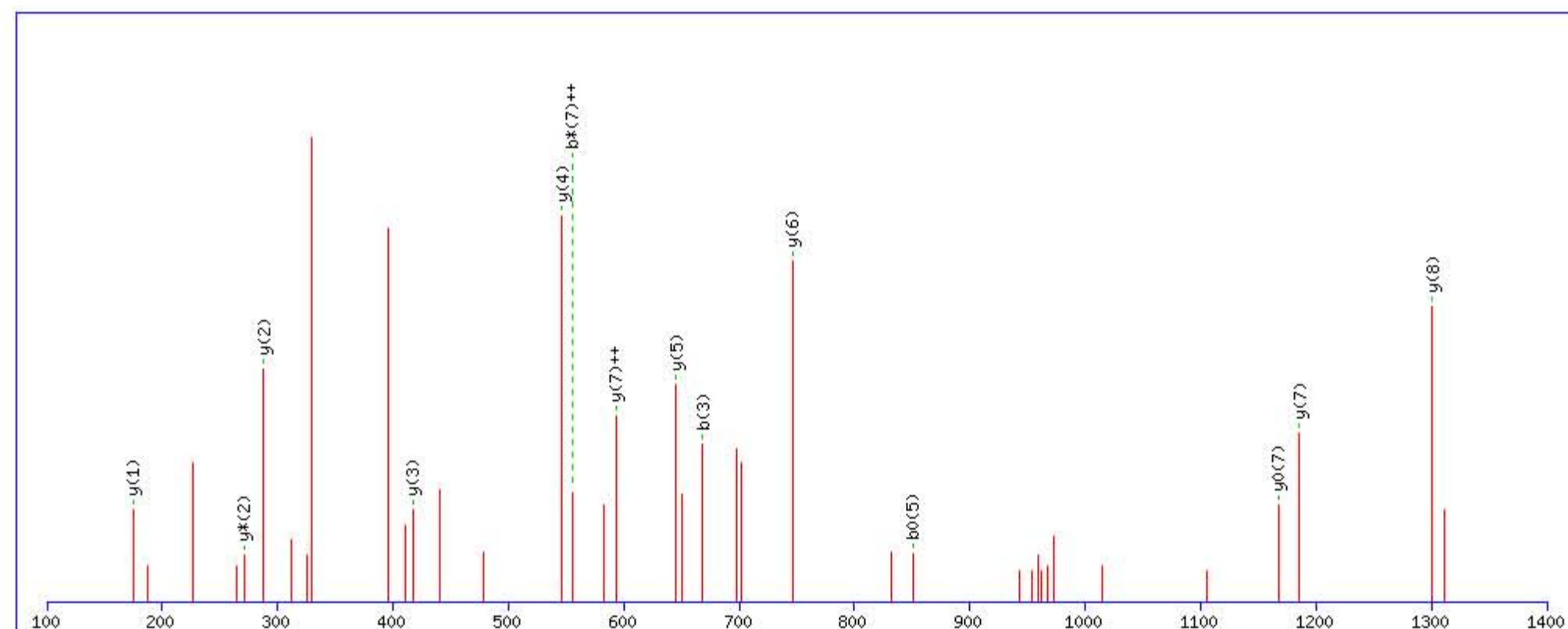
Title: Locus:1.1.1.3199.24 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

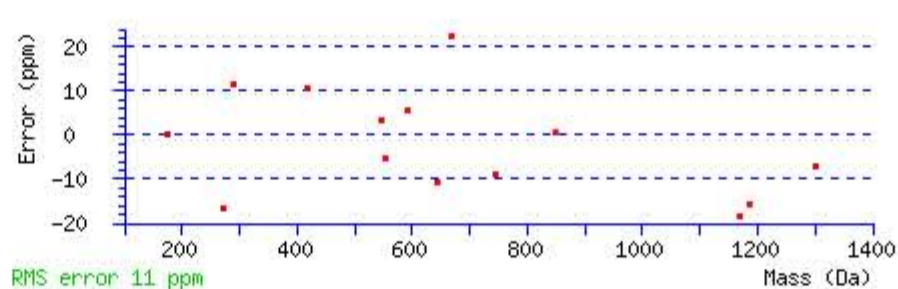
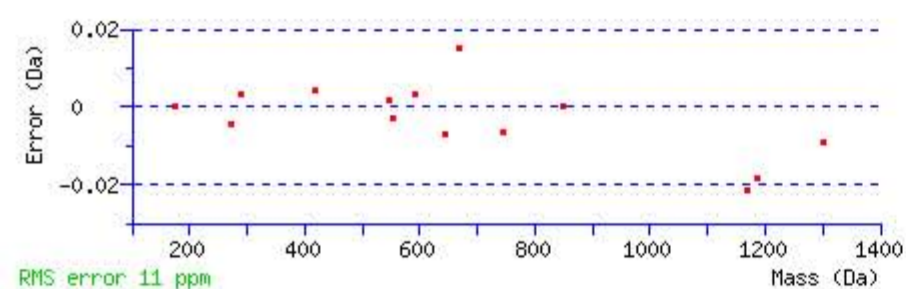
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 40 Expect: 0.0025

Matches : 14/86 fragment ions using 30 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	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 **IDQTV EELR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.9	1412.733337	-0.007329	IDQTV EELR
14.0	1412.744537	-0.018529	IPPEKMRELER
6.6	1412.708191	0.017817	LQESASGTGPR
5.0	1412.719391	0.006617	LKAEMDEHRLR
4.9	1412.734665	-0.008657	MPADWRQQLR
1.8	1412.729950	-0.003942	LDAFIEALHQEK

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 33001: 1414.721948 from(708.368250,2+) rtinseconds(1990) index(71155)

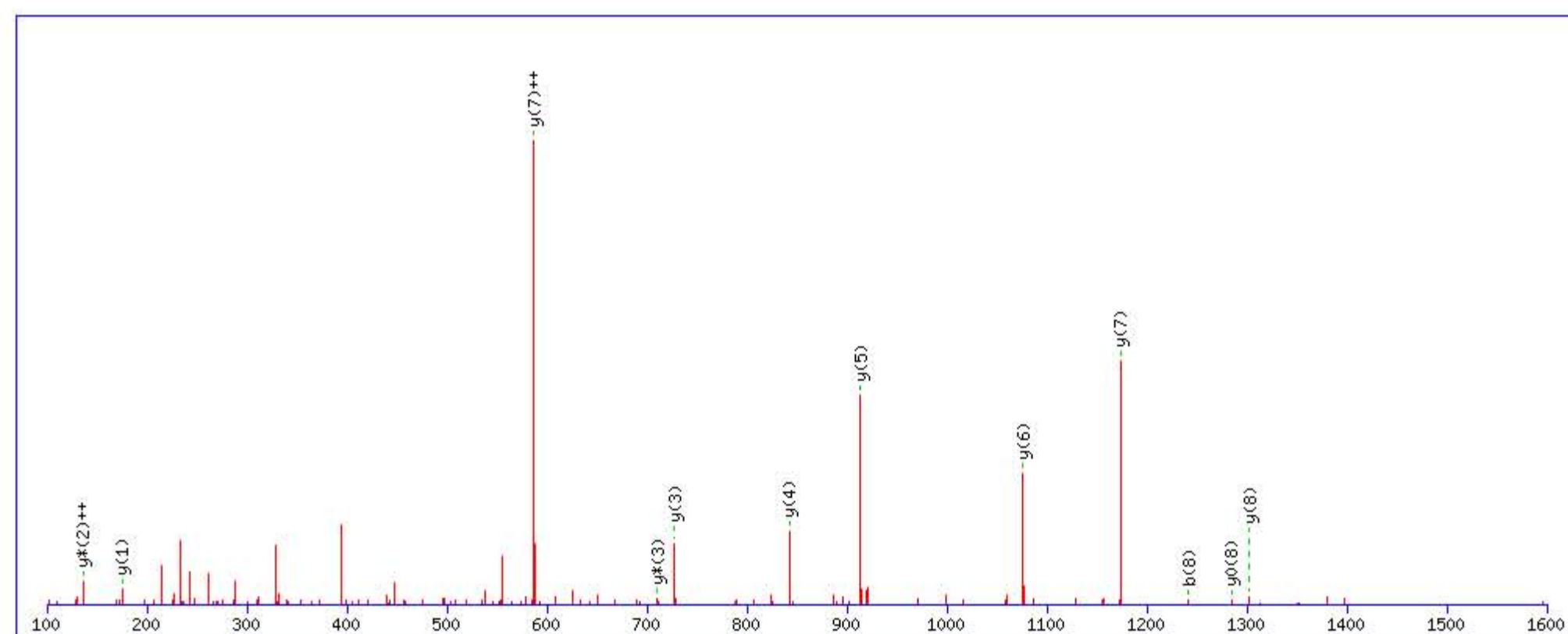
Title: Locus:1.1.1.3226.13 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

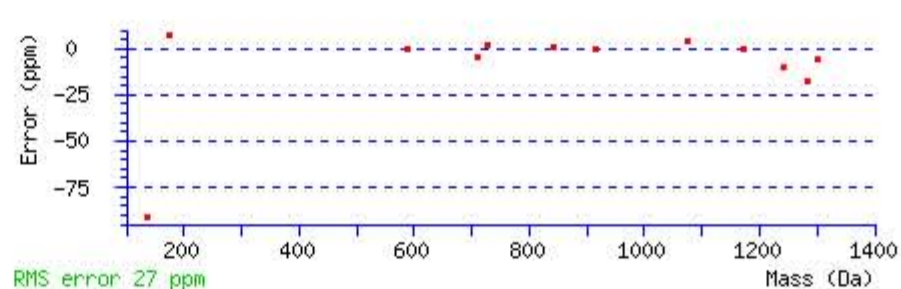
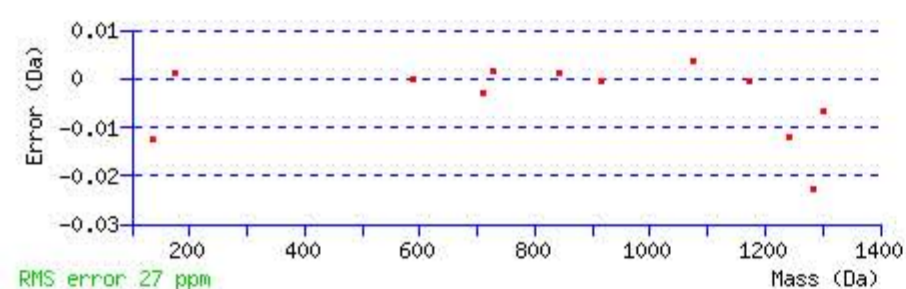
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 35 Expect: 0.0048

Matches : 12/76 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	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
34.6	1414.727844	-0.005896	LEPYADQLR
9.3	1414.712585	0.009363	EISTEEQLR
4.2	1414.735931	-0.013983	LMRGLLHCMIR
2.1	1414.713943	0.008005	KLQCIADQFHR
0.7	1414.735077	-0.013129	SSMSGHLHLVKQGR
0.6	1414.702713	0.019235	IQRDFMLSFSR
0.6	1414.716400	0.005548	LEEDARLEERR
0.6	1414.730347	-0.008399	ELSVQNQDLIEK
0.4	1414.742905	-0.020957	ERLSRNYPQPR
0.2	1414.731689	-0.009741	NKAEFHQSVISR

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 36345: 1525.802948 from(763.908750,2+) rtinseconds(2125) index(71946)

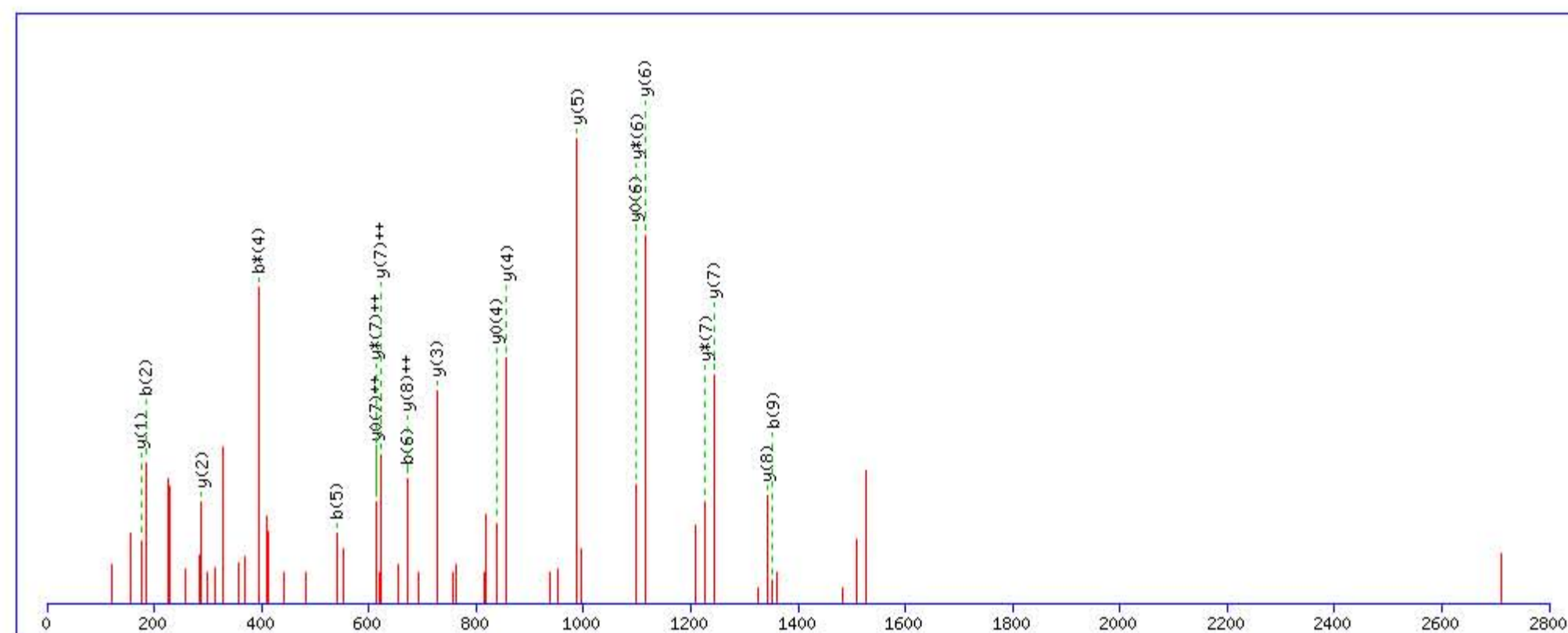
Title: Locus:1.1.1.3273.23 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

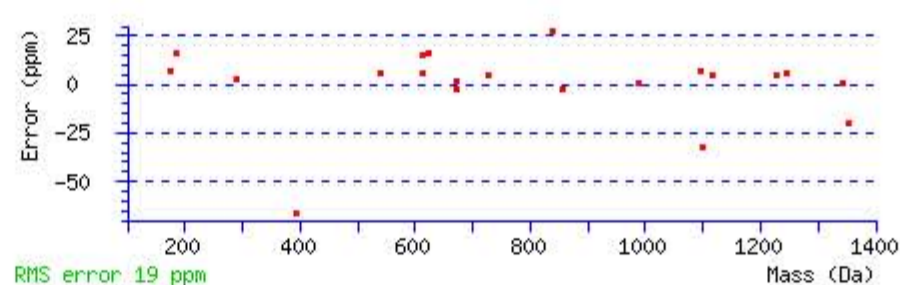
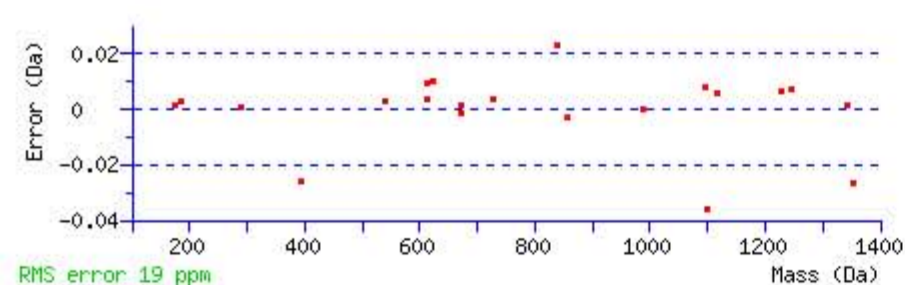
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 49 Expect: 0.00029

Matches : 21/84 fragment ions using 38 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.044390	36.525833					A							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
48.8	1525.810867	-0.007919	ALVQQMEQLR
15.8	1525.810867	-0.007919	ALVQQMEQLR
10.4	1525.798752	0.004196	SPVKEEEKPQEVK
8.1	1525.792236	0.010712	ALTEQQEQLR
5.5	1525.810867	-0.007919	ALVQQMEQLR
5.5	1525.784836	0.018112	LAQVATEEPERQR
4.2	1525.800064	0.002884	ARALQSYEAKAR
0.9	1525.807495	-0.004547	WPPQQLMLSAALR

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 36766: 1545.840282 from(516.287370,3+) rtinseconds(1530) index(68337)

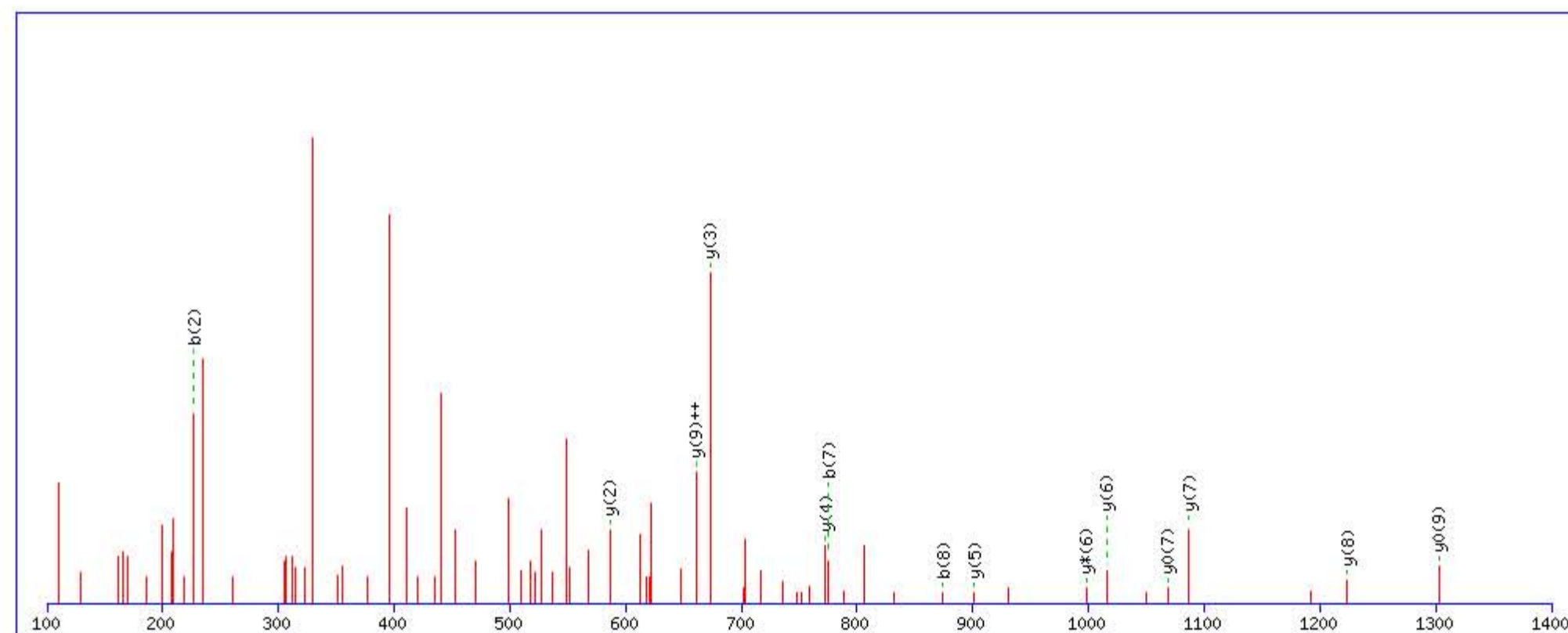
Title: Locus:1.1.1.3066.9 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

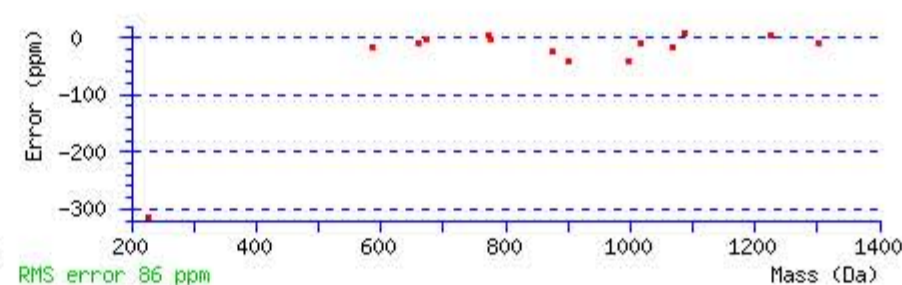
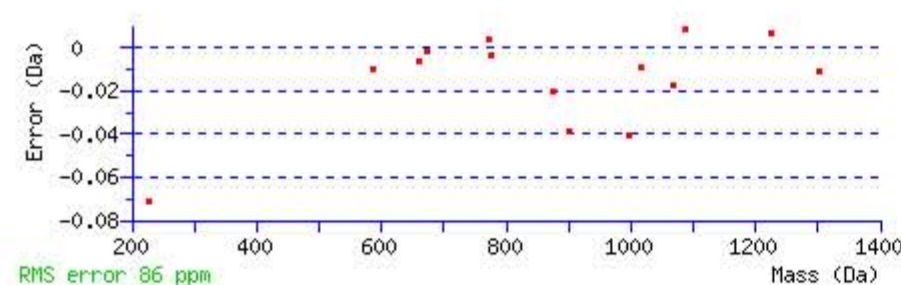
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 28 Expect: 0.003

Matches : 14/94 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					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
28.0	1545.833710	0.006572	LLPHANEVSQK
1.1	1545.826309	0.013973	AEKSRTAWTDLLR

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 41351: 1660.798128 from(831.406340,2+) rtinseconds(1734) index(69502)

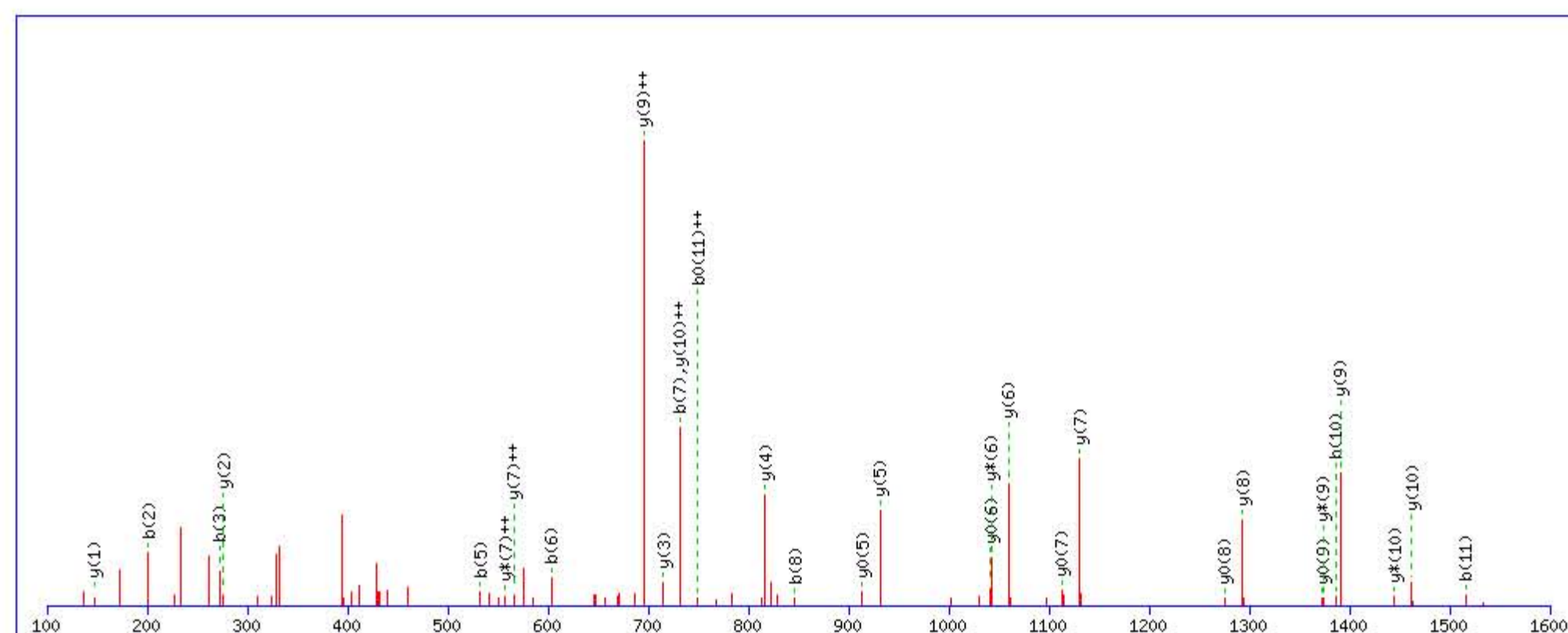
Title: Locus:1.1.1.3137.14 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

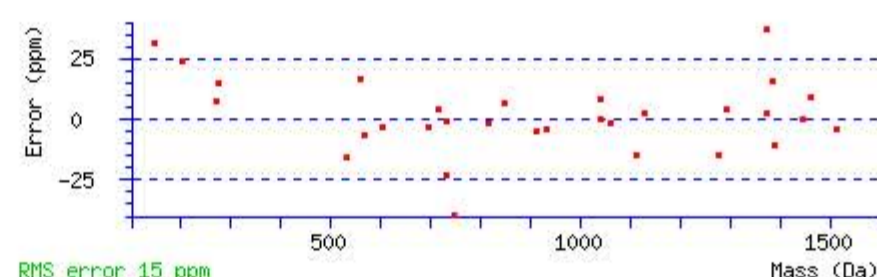
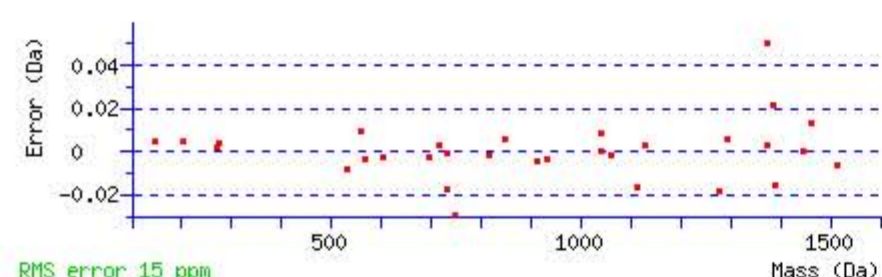
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 55 Expect: 2.7e-005

Matches : 31/118 fragment ions using 64 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	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
54.6	1660.813034	-0.014906	SLAPYAQDTQEK
27.2	1660.813034	-0.014906	SLAPYAQDTQEK
5.6	1660.777344	0.020784	QEMQSAGSQRGR
5.5	1660.820908	-0.022780	SLARAGFYITGVNDK
5.0	1660.809021	-0.010893	STEASPSRDVSPMGLK
2.6	1660.776642	0.021486	EAHVLAFTMEEEK
1.6	1660.820236	-0.022108	MALSGEGQEKGKASPR
0.9	1660.808990	-0.010862	INPDEREEMKVSAAK
0.7	1660.797791	0.000337	VSKESSVEPVSCPEK

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 42677: 1717.858028 from(859.936290,2+) rtinseconds(1989) index(5757)

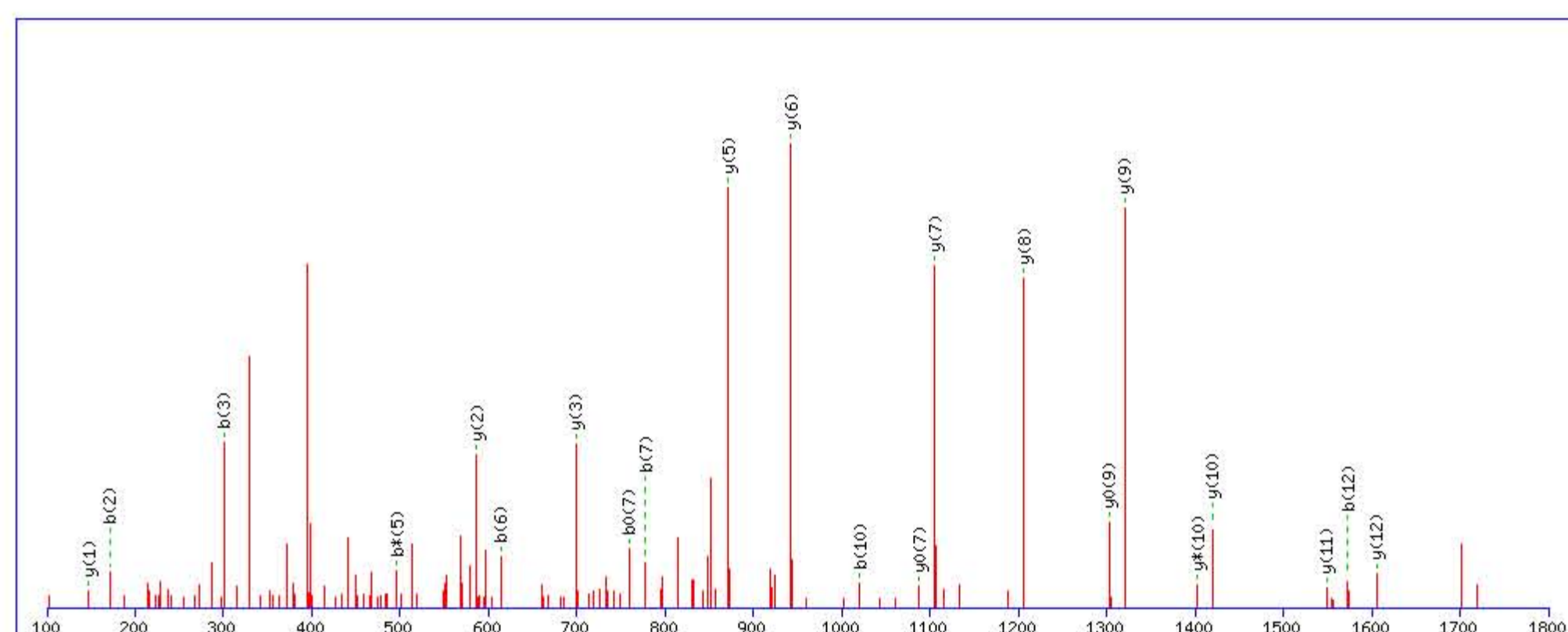
Title: Locus:1.1.1.3128.18 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

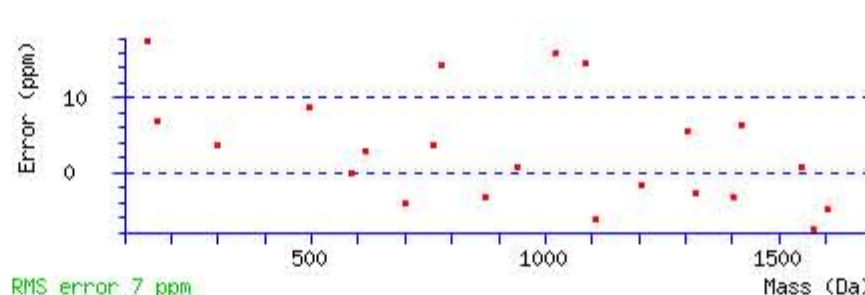
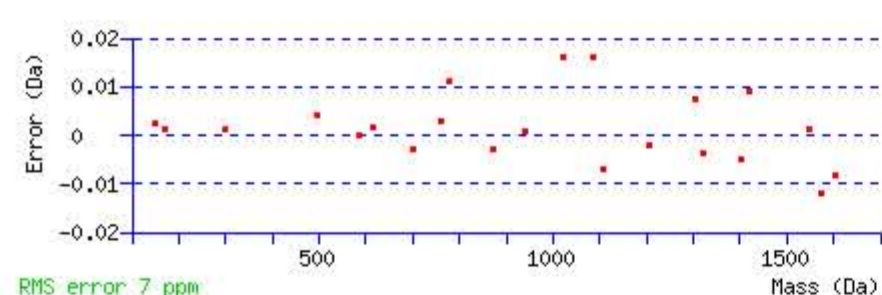
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 95 Expect: 8.2e-009

Matches : 22/126 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	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
95.0	1717.870895	-0.012867	LGEVNTYAGDLQK
14.7	1717.866867	-0.008839	IDAVNAETIREVCTK
7.2	1717.878067	-0.020039	RATEKEINNMGNTLK
4.2	1717.878754	-0.020726	IDAVAWNTTPYQLAR
3.5	1717.882126	-0.024098	NNKNFSTVDIQK
3.0	1717.863495	-0.005467	KSNISVYEVGKDHK
2.1	1717.855606	0.002422	VANAEKLMDDLK
1.9	1717.874741	-0.016713	GIEVTSWTADASRGLR
1.3	1717.837860	0.020168	MENKPTSELQK
1.2	1717.855652	0.002376	VSLVELCDGQADLTK

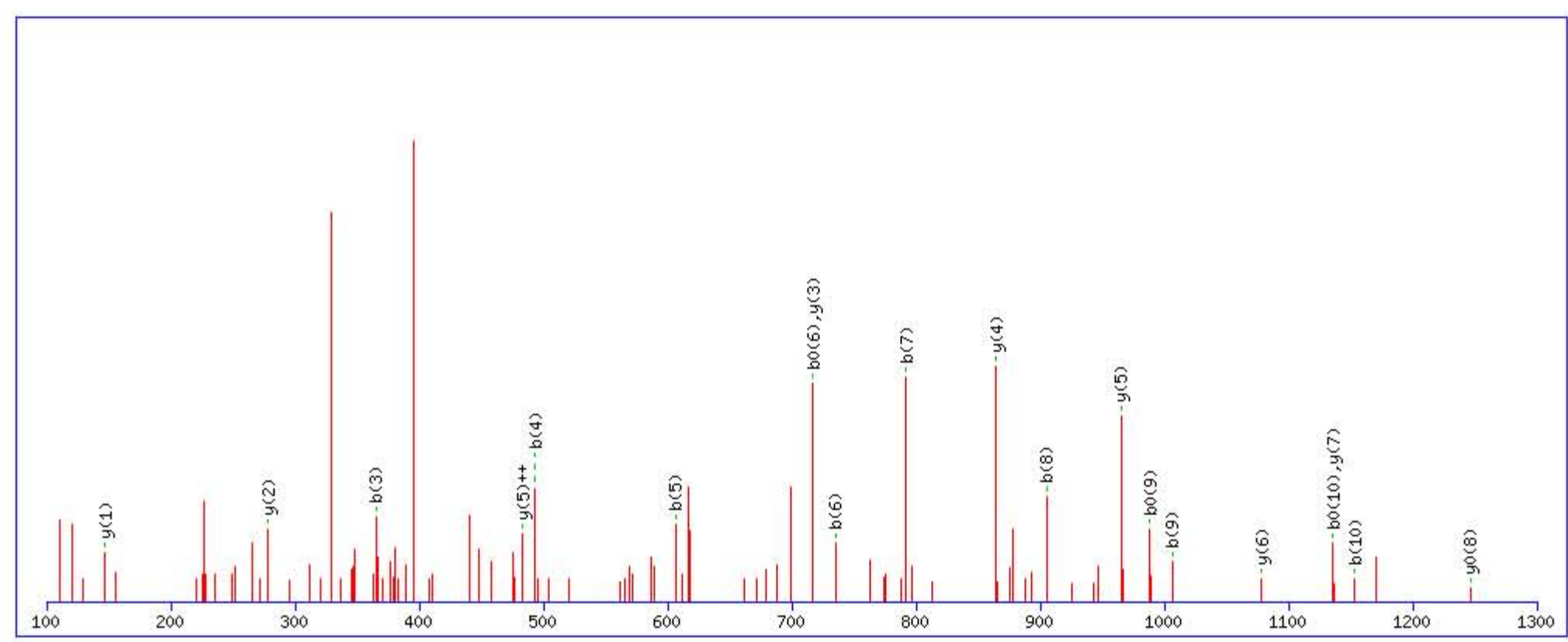
MASCOT SEARCH RESULTS

Peptide View

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

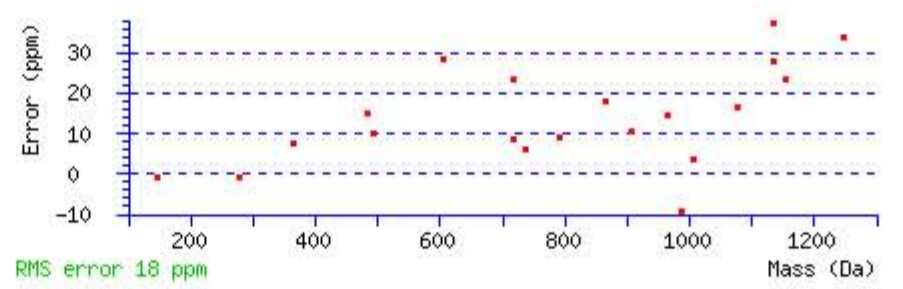
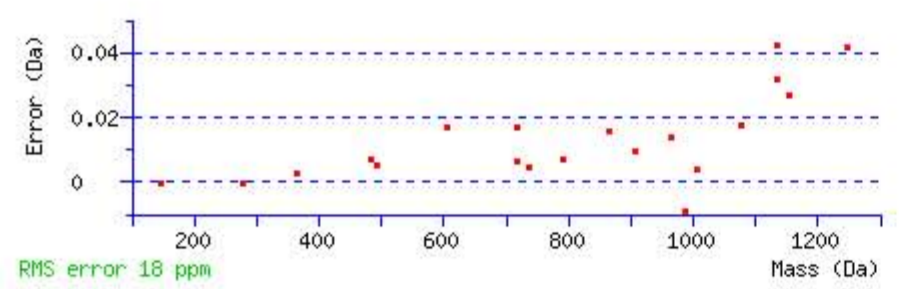
Match to Query 46306: 1868.976552 from(623.999460,3+) rtinseconds(2159) index(39683)
 Title: Locus:1.1.1.2774.15 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 1868.964081
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q11 : Biotin:Thermo-21345 (Q)
 Ions Score: 47 Expect: 0.00058
 Matches : 20/124 fragment ions using 32 most intense peaks [\(help\)](#)

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



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.1	1868.964081	0.012471	LNHQLEGLTFQMK

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 47021: 1908.986802 from(637.336210,3+) rtinseconds(1926) index(70671)

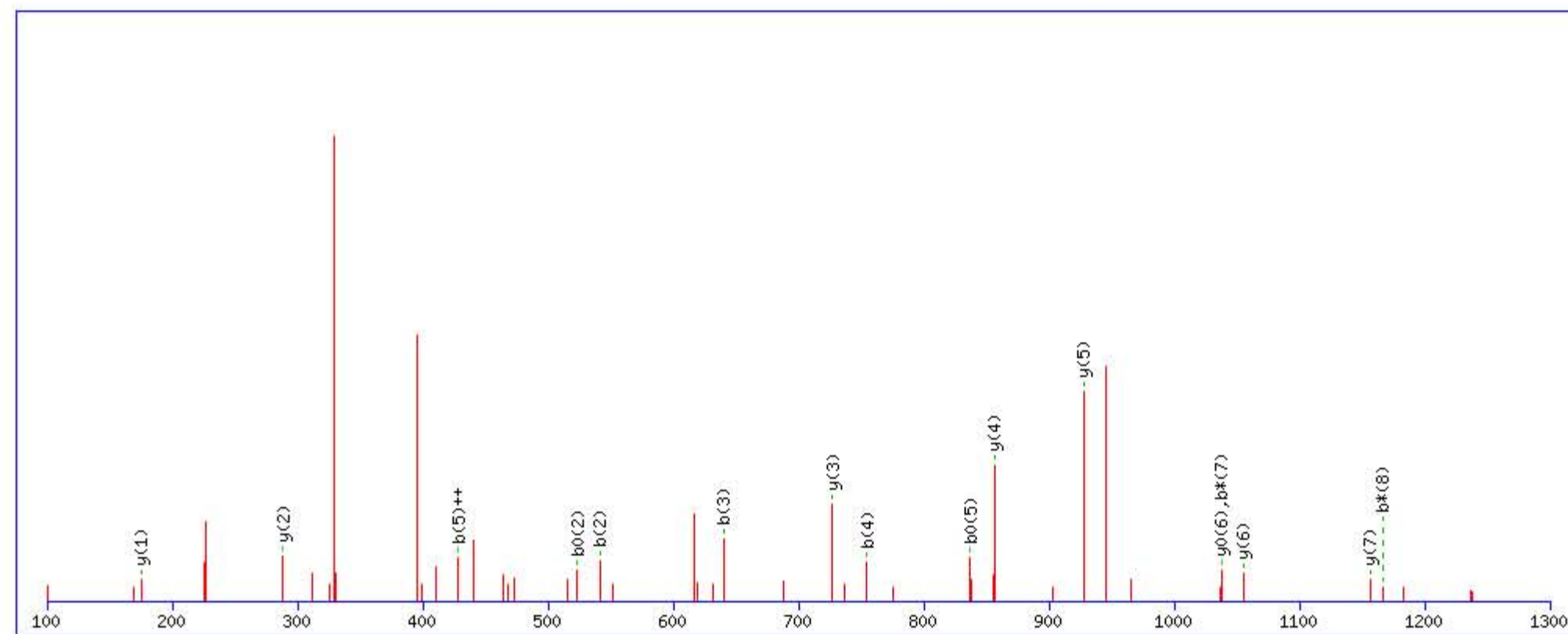
Title: Locus:1.1.1.3204.15 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1908.991364

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

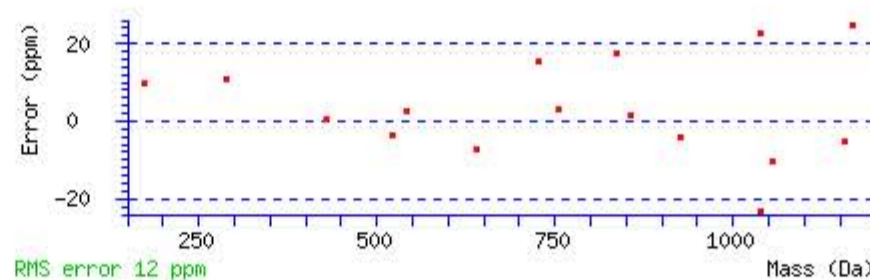
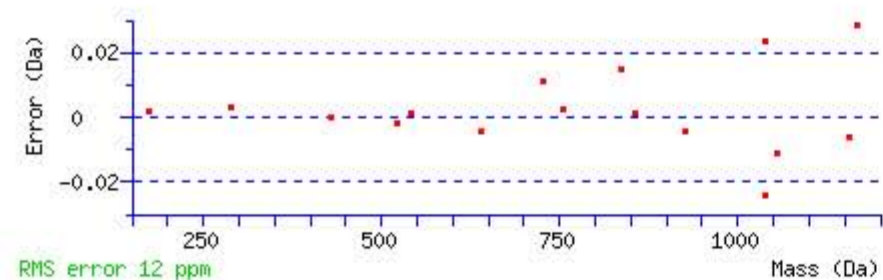
Q2 : Biotin:Thermo-21345 (Q)

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 37 Expect: 0.00041

Matches : 16/112 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	102.054955	51.531116			84.044390	42.525833	T							11
2	541.280281	271.143779	524.253732	262.630504	523.269716	262.138496	Q	1808.950973	904.979125	1791.924424	896.465850	1790.940408	895.973842	10
3	640.348695	320.677986	623.322146	312.164711	622.338130	311.672703	V	1369.725647	685.366462	1352.699098	676.853187	1351.715082	676.361179	9
4	754.391622	377.699449	737.365073	369.186174	736.381057	368.694166	N	1270.657233	635.832255	1253.630684	627.318980	1252.646668	626.826972	8
5	855.439301	428.223289	838.412752	419.710014	837.428736	419.218006	T	1156.614306	578.810791	1139.587757	570.297517	1138.603741	569.805509	7
6	983.497879	492.252578	966.471330	483.739303	965.487314	483.247295	Q	1055.566627	528.286952	1038.540078	519.773677	1037.556062	519.281669	6
7	1054.534993	527.771135	1037.508444	519.257860	1036.524428	518.765852	A	927.508049	464.257663	910.481500	455.744388	909.497484	455.252380	5
8	1183.577586	592.292431	1166.551037	583.779157	1165.567021	583.287149	E	856.470935	428.739106	839.444386	420.225831	838.460370	419.733823	4
9	1622.802912	811.905094	1605.776363	803.391820	1604.792347	802.899812	Q	727.428342	364.217809	710.401793	355.704535			3
10	1735.886976	868.447126	1718.860427	859.933852	1717.876411	859.441844	L	288.203016	144.605146	271.176467	136.091871			2
11							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **TQVNTQAEQLR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.3	1908.991364	-0.004562	TQVNTQAEQLR
11.1	1908.991364	-0.004562	TQVNTQAEQLR
9.6	1908.991364	-0.004562	TQVNTQAEQLR
1.1	1908.966202	0.020600	KASQILPQATMNR
0.5	1909.002579	-0.015777	QQLETARNATR

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

MASCOT Search Results

Peptide View

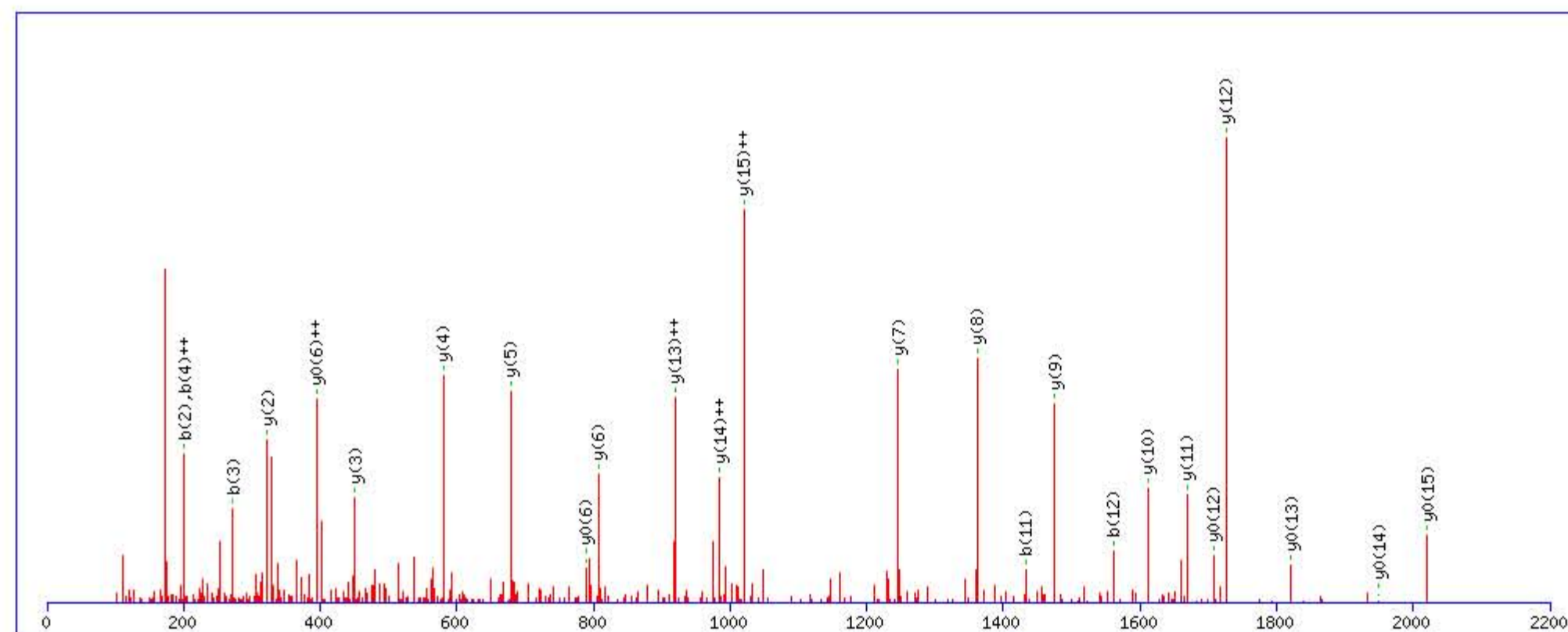
MS/MS Fragmentation of **SLAELGGHLDQQVEEFR**
 Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

Match to Query 54746: 2238.096882 from(747.039570,3+) rtinseconds(2243) index(72731)
 Title: Locus:1.1.1.3314.25 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

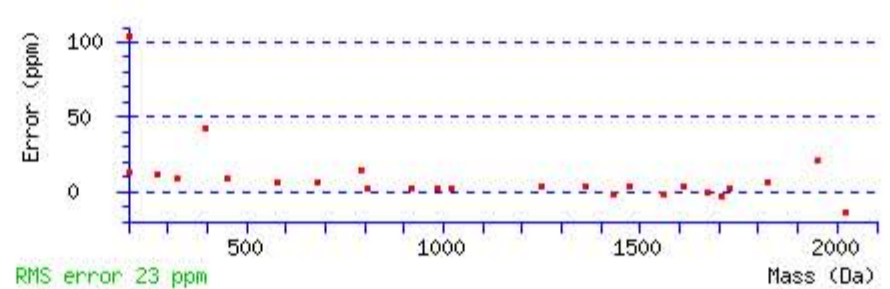
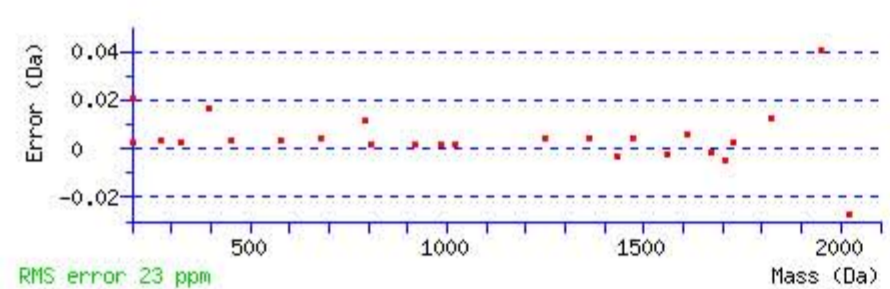
Or, Plot from to Da

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: 70 Expect: 2.6e-006
 Matches : 25/168 fragment ions using 39 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.039304	44.523290			70.028739	35.518008	S							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
69.8	2238.110291	-0.013409	SLAELGGHLDQQVEEFR
52.4	2238.110291	-0.013409	SLAELGGHLDQQVEEFR

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 60665: 2543.301912 from(848.774580,3+) rtinseconds(3213) index(63332)

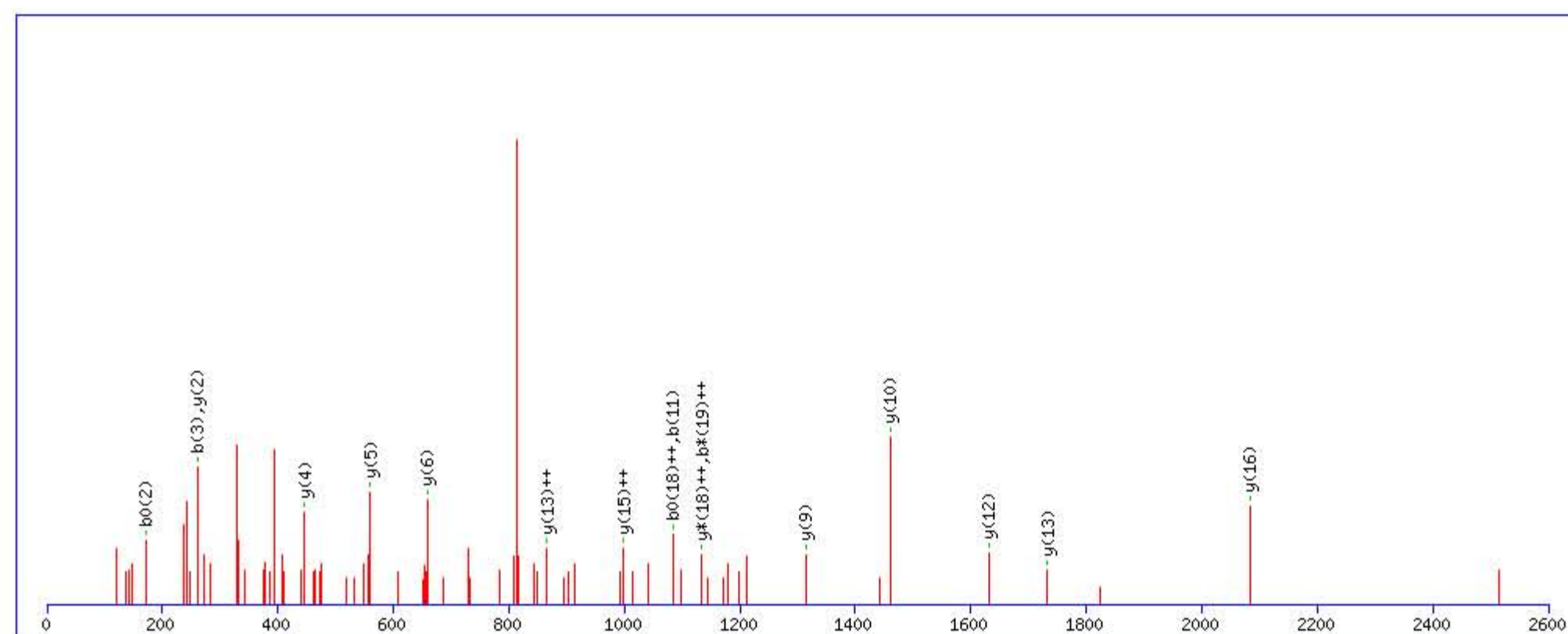
Title: Locus:1.1.1.3599.14 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

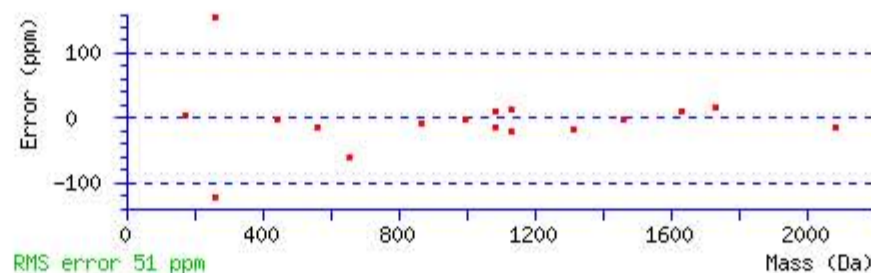
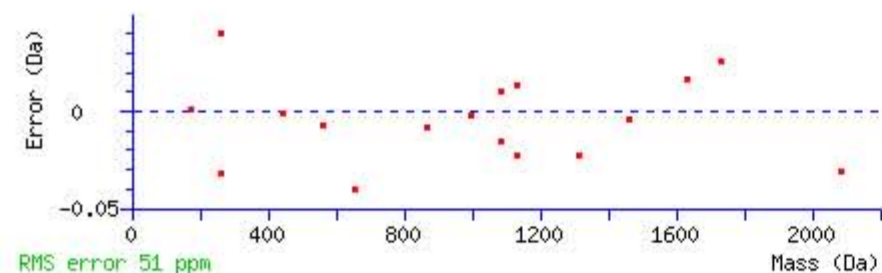
Variable modifications:

Q15 : Biotin:Thermo-21345 (Q)

Ions Score: 65 Expect: 9.1e-006

Matches : 17/206 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							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
65.1	2543.301544	0.000368	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 50483: 2027.006712 from(676.676180,3+) rtinseconds(1942) index(55380)

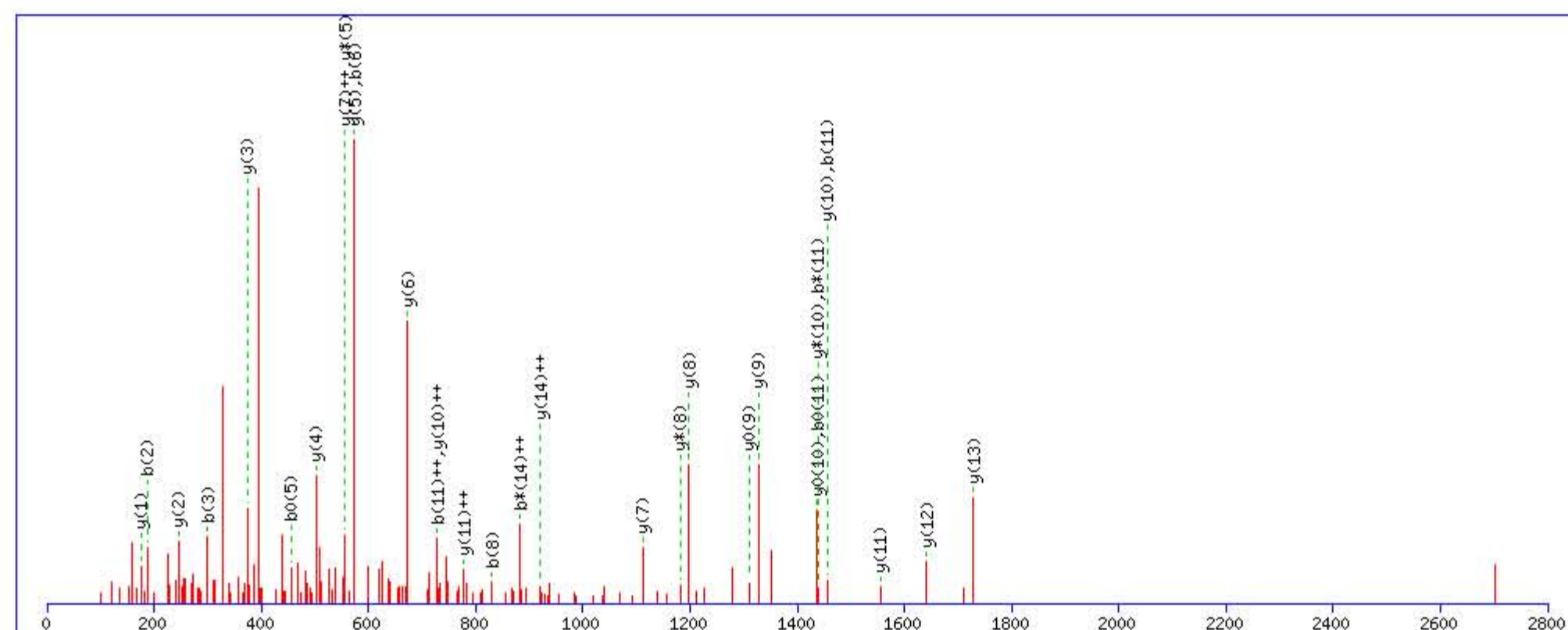
Title: Locus:1.1.1.3162.12 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\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)

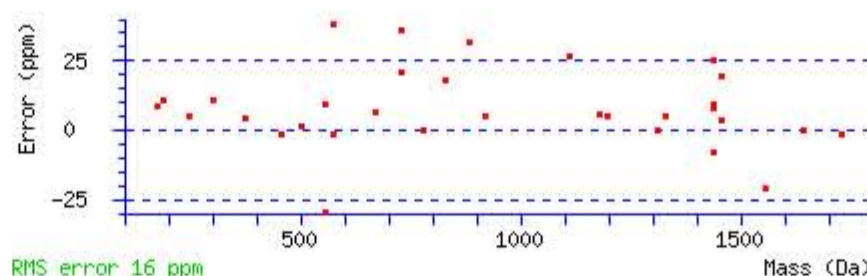
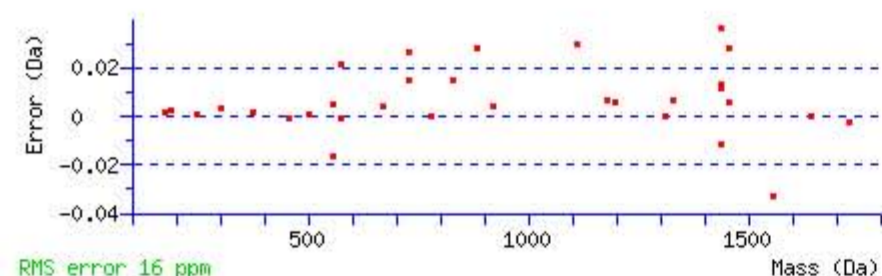
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 87 Expect: 1.4e-008

Matches : 32/154 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	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
87.1	2027.010574	-0.003862	DALSSVQESQVAQQAR
56.6	2027.010574	-0.003862	DALSSVQESQVAQQAR
47.8	2027.010574	-0.003862	DALSSVQESQVAQQAR
46.5	2027.010574	-0.003862	DALSSVQESQVAQQAR
3.1	2027.035721	-0.029009	LLLQMDSSATAYGSTVSKR
2.4	2027.029633	-0.022921	QEESHSHKHLIELRR

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 50484: 2027.006712 from(676.676180,3+) rtinseconds(1933) index(55306)

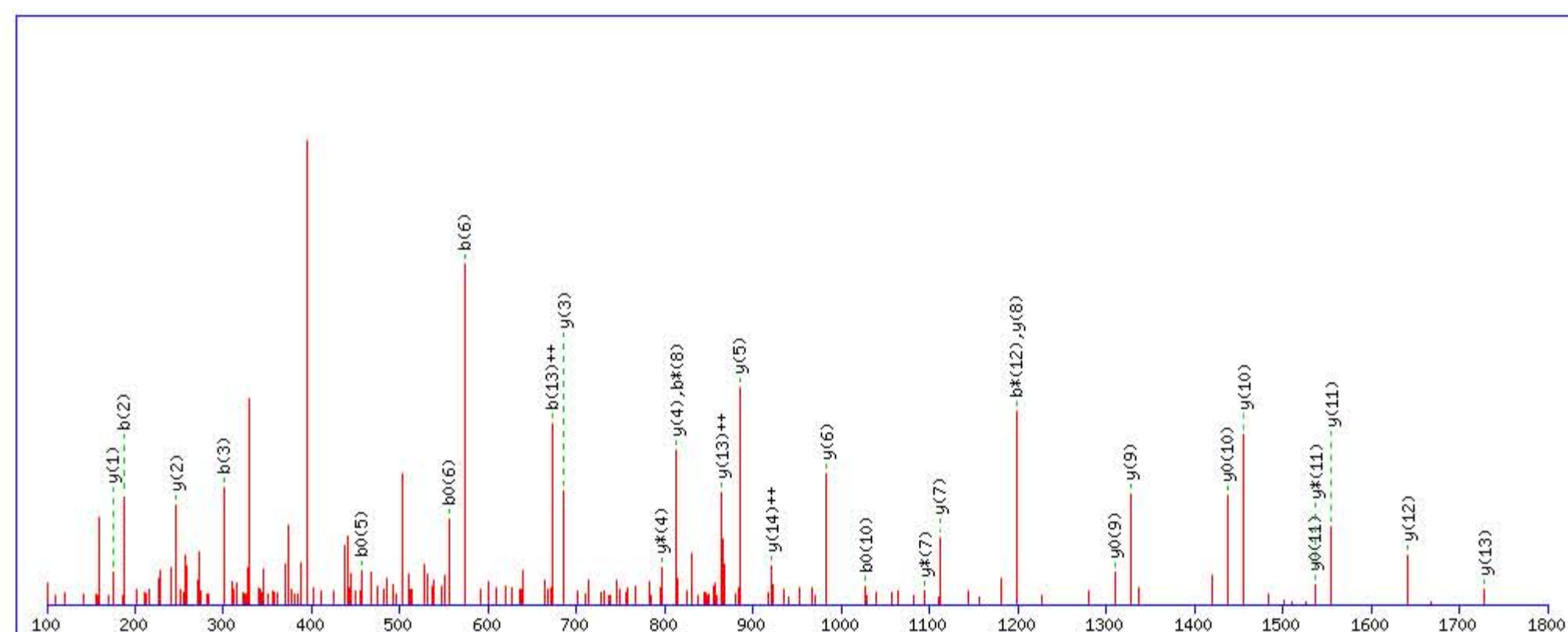
Title: Locus:1.1.1.3159.13 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

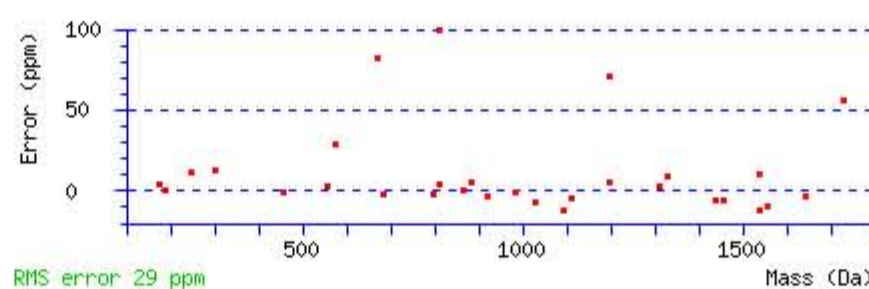
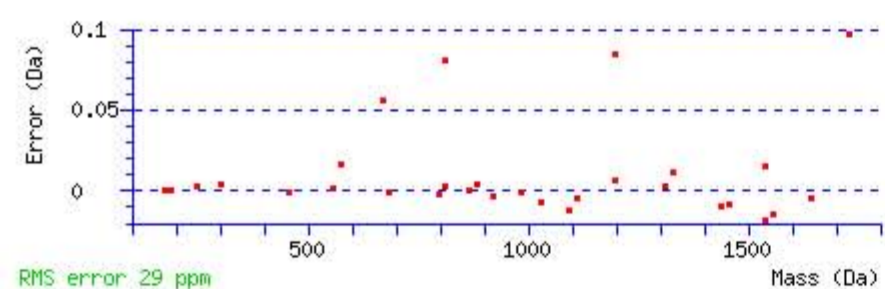
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 88 Expect: 1.4e-008

Matches : 30/154 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	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
87.5	2027.010574	-0.003862	DALSSVQESQVAQQAR
87.2	2027.010574	-0.003862	DALSSVQESQVAQQAR
83.1	2027.010574	-0.003862	DALSSVQESQVAQQAR
42.8	2027.010574	-0.003862	DALSSVQESQVAQQAR
3.7	2027.029633	-0.022921	QEESHSKHLIELRR

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 50485: 2027.007312 from(676.676380,3+) rtinseconds(1886) index(54909)

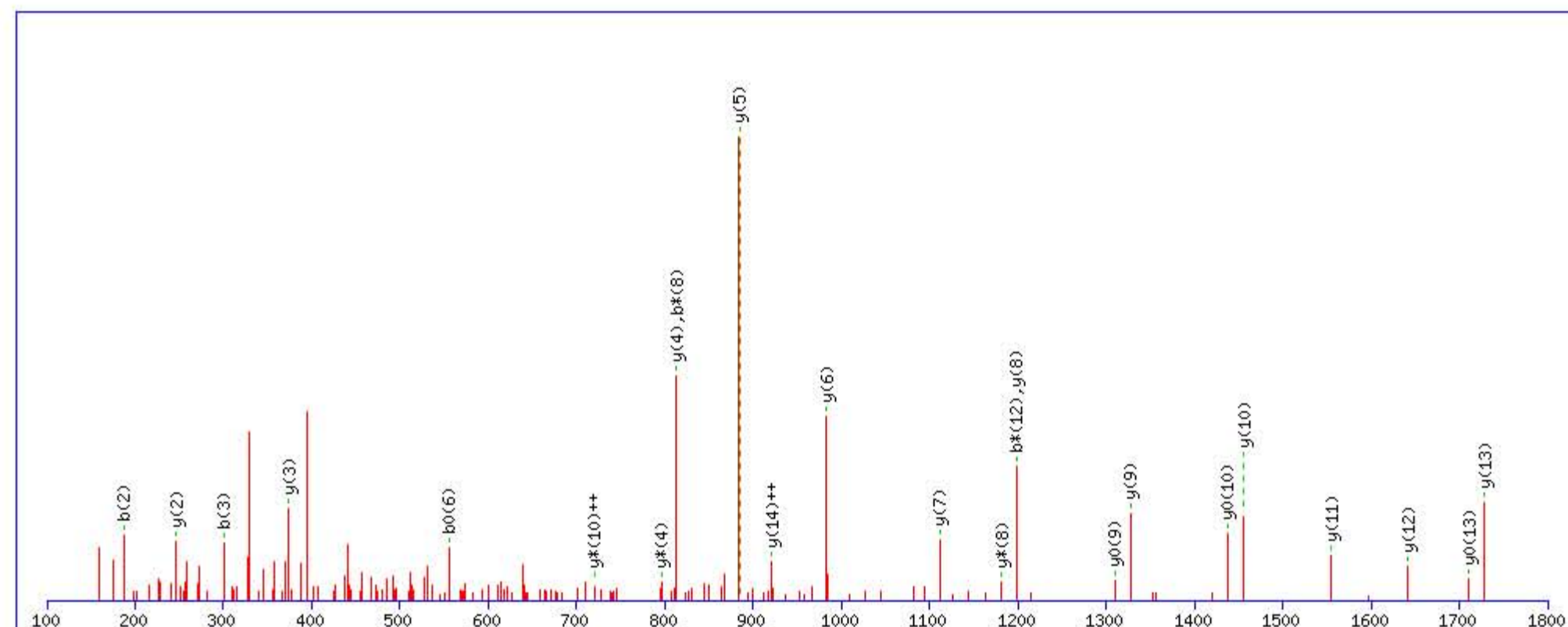
Title: Locus:1.1.1.3143.16 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

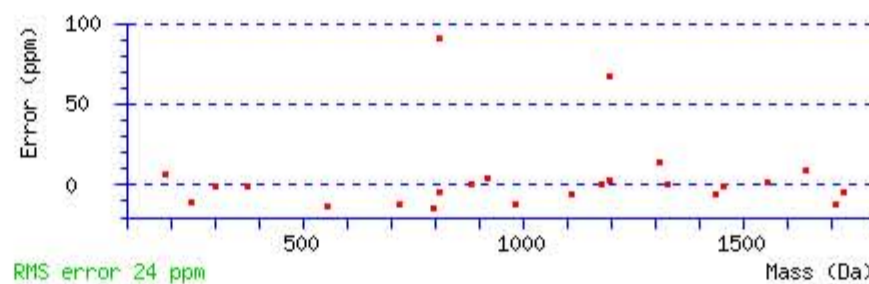
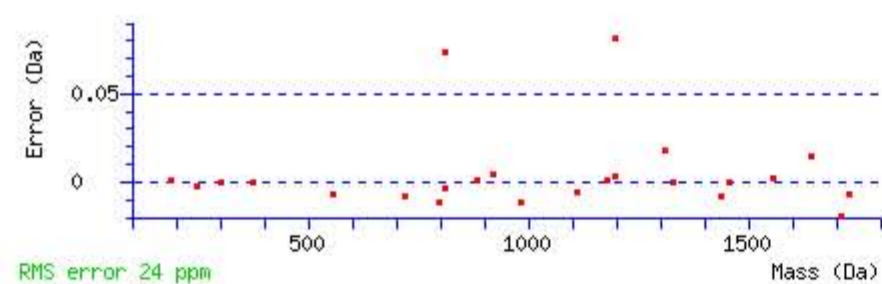
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 93 Expect: 3e-009

Matches : 24/154 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	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
92.6	2027.010574	-0.003262	DALSSVQESQVAQQAR
78.4	2027.010574	-0.003262	DALSSVQESQVAQQAR
55.3	2027.010574	-0.003262	DALSSVQESQVAQQAR
19.8	2027.010574	-0.003262	DALSSVQESQVAQQAR
1.6	2026.978012	0.029300	AEGAQNQGQKGEQAQNQGKK
0.4	2027.017960	-0.010648	MFELTLRGMSEALVDKR

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 50486: 2027.018802 from(676.680210,3+) rtinseconds(1967) index(38442)

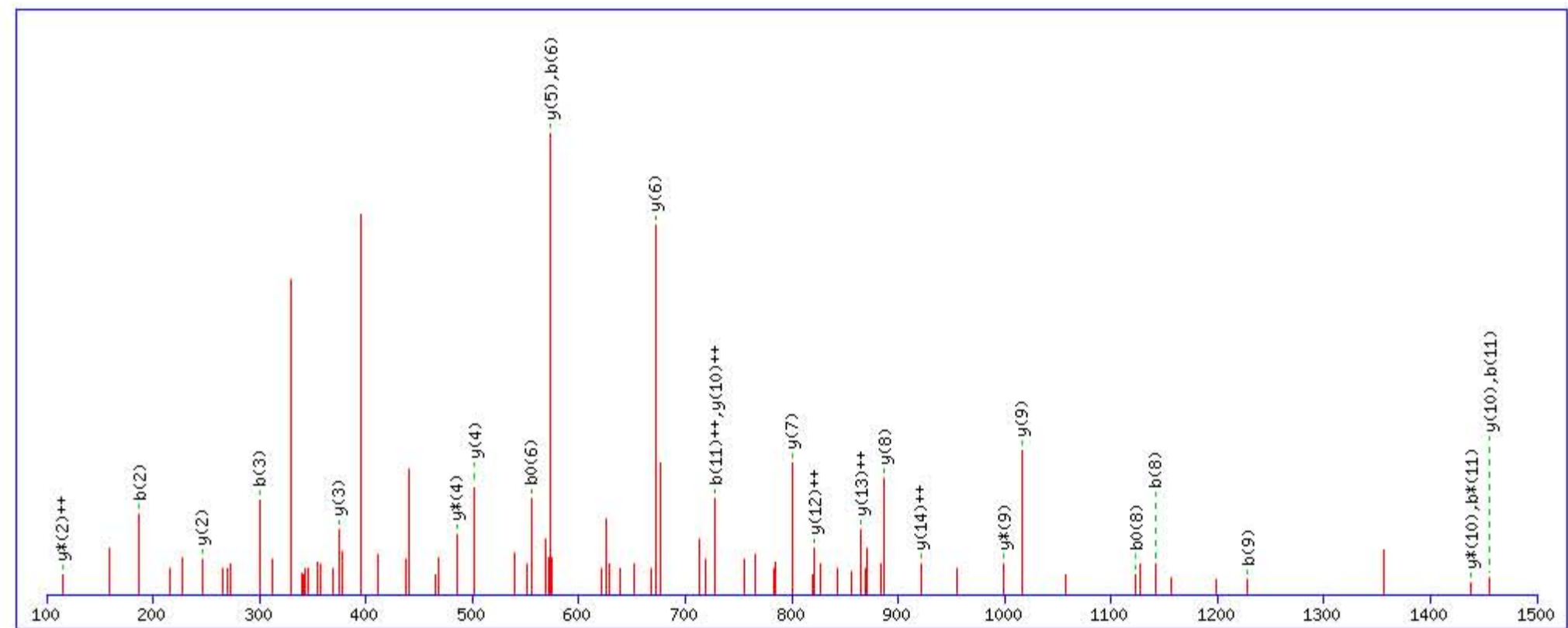
Title: Locus:1.1.1.2707.21 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\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): 2027.010574

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

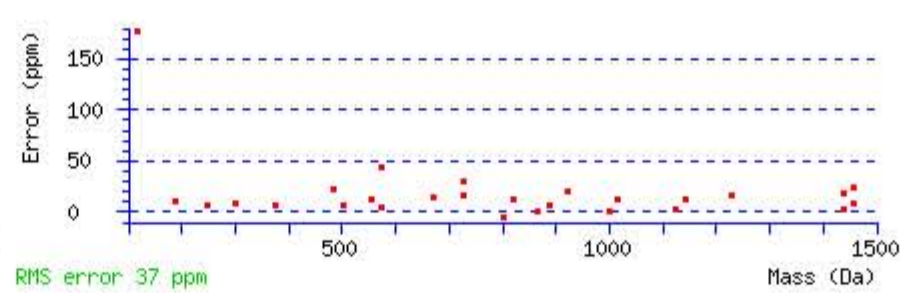
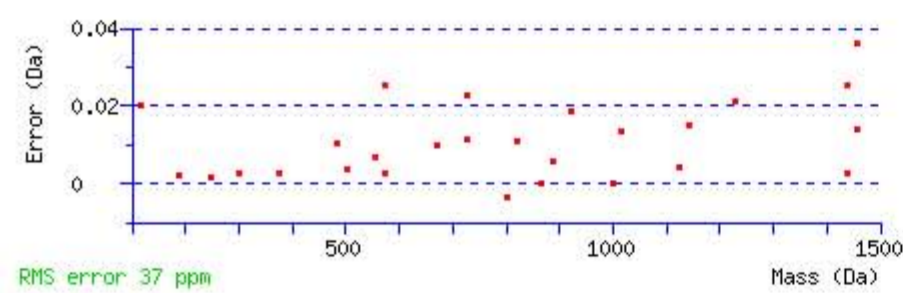
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 55 Expect: 1.5e-005

Matches : 27/154 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	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
55.0	2027.010574	0.008228	DALSSVQESQVAQQAR
21.4	2027.010574	0.008228	DALSSVQESQVAQQAR
8.0	2027.010574	0.008228	DALSSVQESQVAQQAR
6.3	2027.010574	0.008228	DALSSVQESQVAQQAR
3.6	2027.010559	0.008243	LTGRGAEDSLADQAANK
3.3	2027.000870	0.017932	QMSEPNIPFPQGFK

MASCOT 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 27711: 1278.709688 from(640.362120,2+) rtinseconds(1957) index(55509)

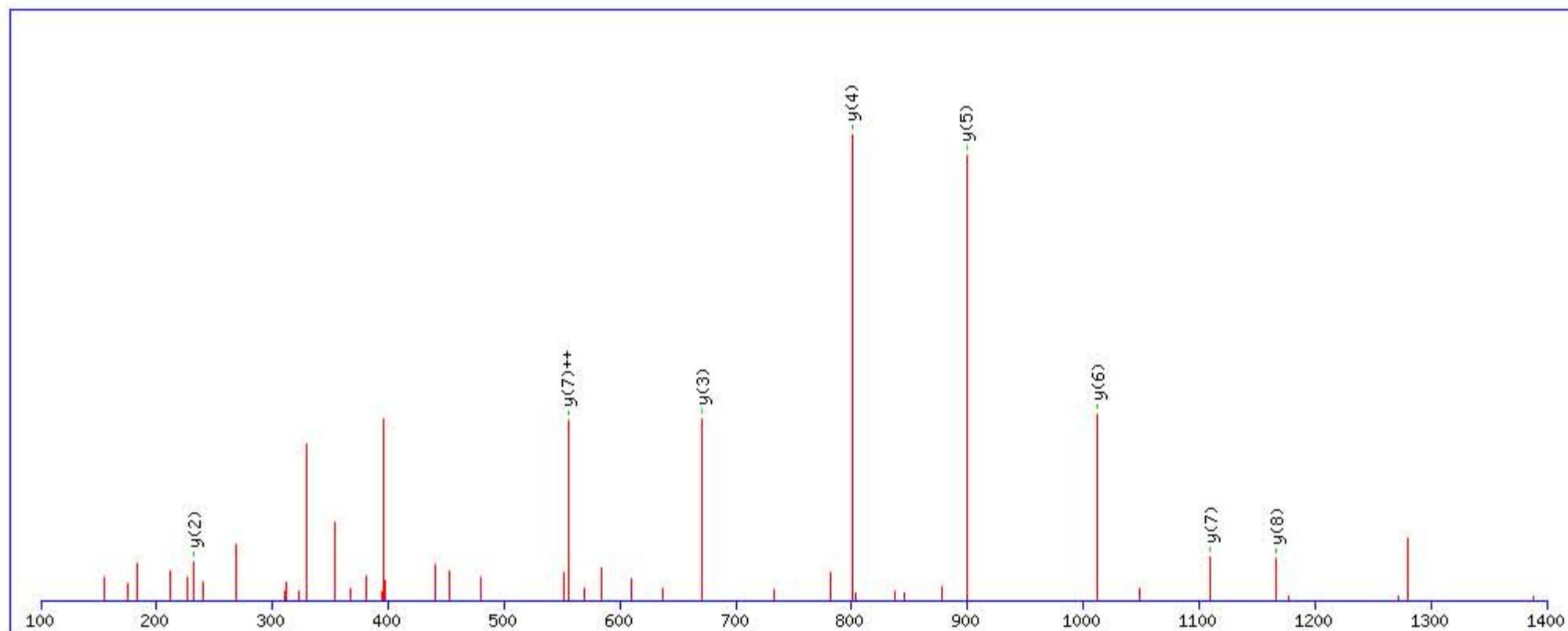
Title: Locus:1.1.1.3167.16 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

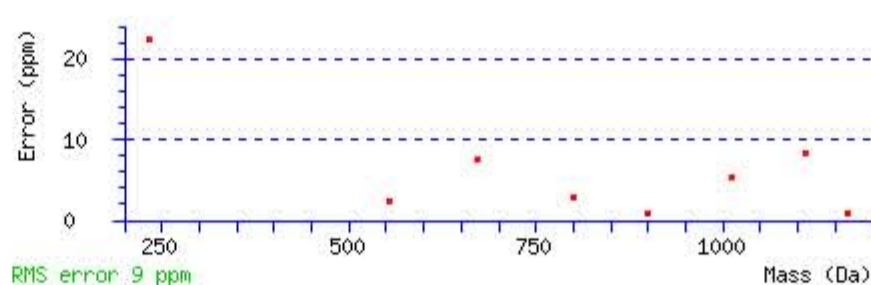
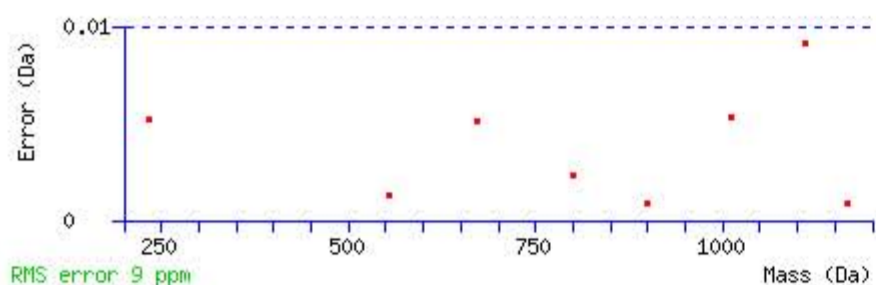
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 57 Expect: 2.8e-005

Matches : 8/68 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	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
56.9	1278.711823	-0.002135	LGPLVEQGR

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

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 33508: 1424.744888 from(713.379720,2+) rtinseconds(1566) index(35986)

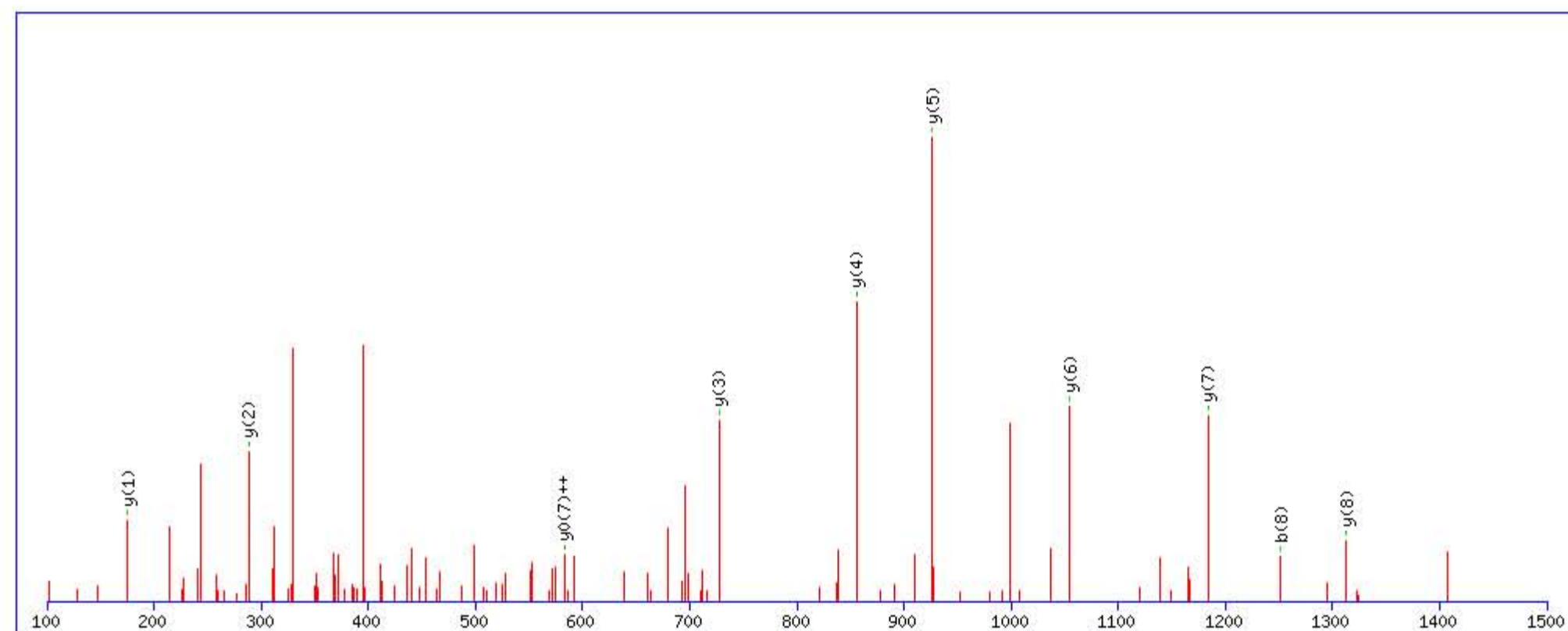
Title: Locus:1.1.1.2567.24 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

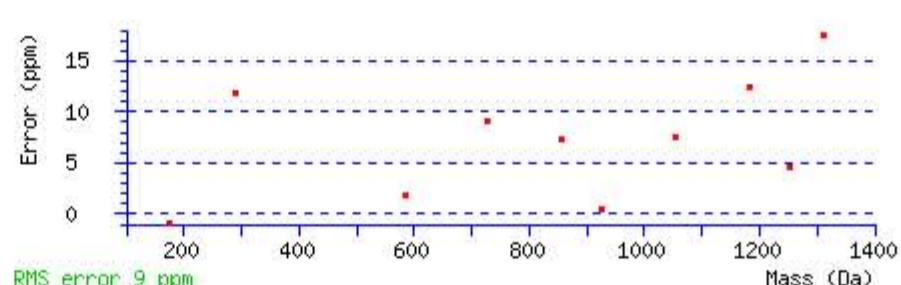
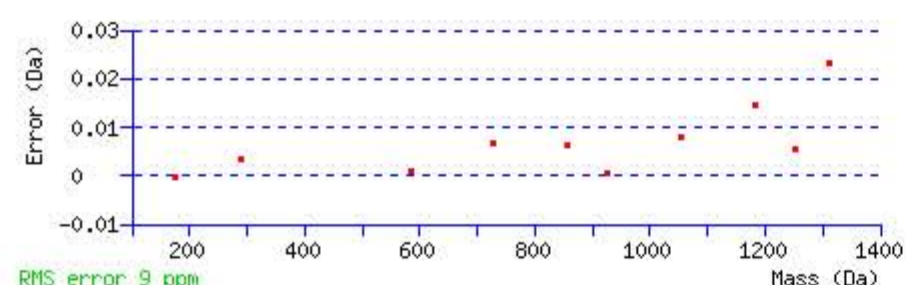
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 74 Expect: 7.8e-007

Matches : 10/76 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							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
74.5	1424.744553	0.000335	LEEQAQQIR
57.6	1424.744553	0.000335	LEEQAQQIR
27.7	1424.744553	0.000335	LEEQAQQIR
18.5	1424.733322	0.011566	LEQETEPLR
12.7	1424.745438	-0.000550	QMQQIR
8.2	1424.744583	0.000305	QLSGDQPTIR
7.3	1424.734680	0.010208	WVLTAAHCLAQR
6.0	1424.730667	0.014221	QPGCAVPOSGRRLR
5.9	1424.737183	0.007705	IEGDPQGVQQAKR
5.9	1424.744553	0.000335	IEIAHALCLTER

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 37004: 1557.730648 from(779.872600,2+) rtinseconds(1562) index(52941)

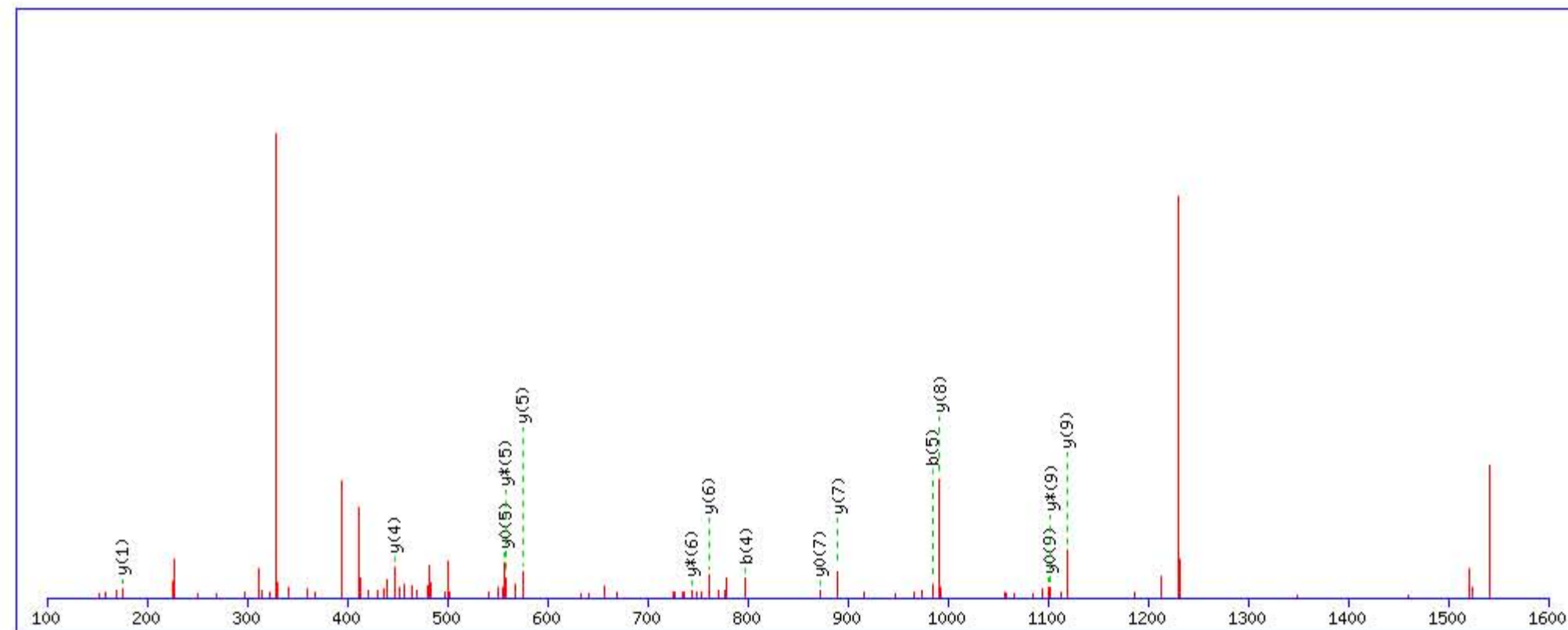
Title: Locus:1.1.1.3030.16 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

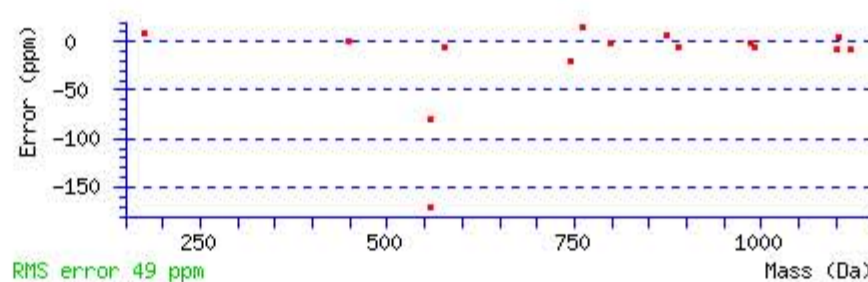
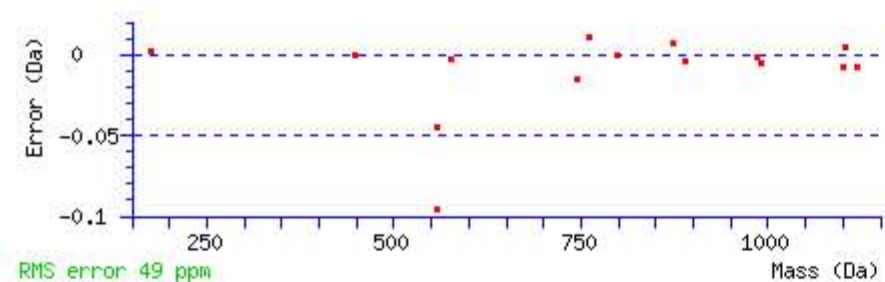
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 28 Expect: 0.02

Matches : 15/98 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							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
28.4	1557.735809	-0.005161	QQTEWQSGQR
17.0	1557.735809	-0.005161	QQTEWQSGQR
10.0	1557.720566	0.010082	QEAATGVDICTHR
1.8	1557.709274	0.021374	EAQDMLNHSEKEK
1.8	1557.749496	-0.018848	QAEATRQAAQEEER
1.7	1557.747040	-0.016392	AFSHCSSLTKHQR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **AATVGS LAGQPLQER**

Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

Match to Query 44849: 1807.950702 from(603.657510,3+) rtinseconds(1948) index(55430)

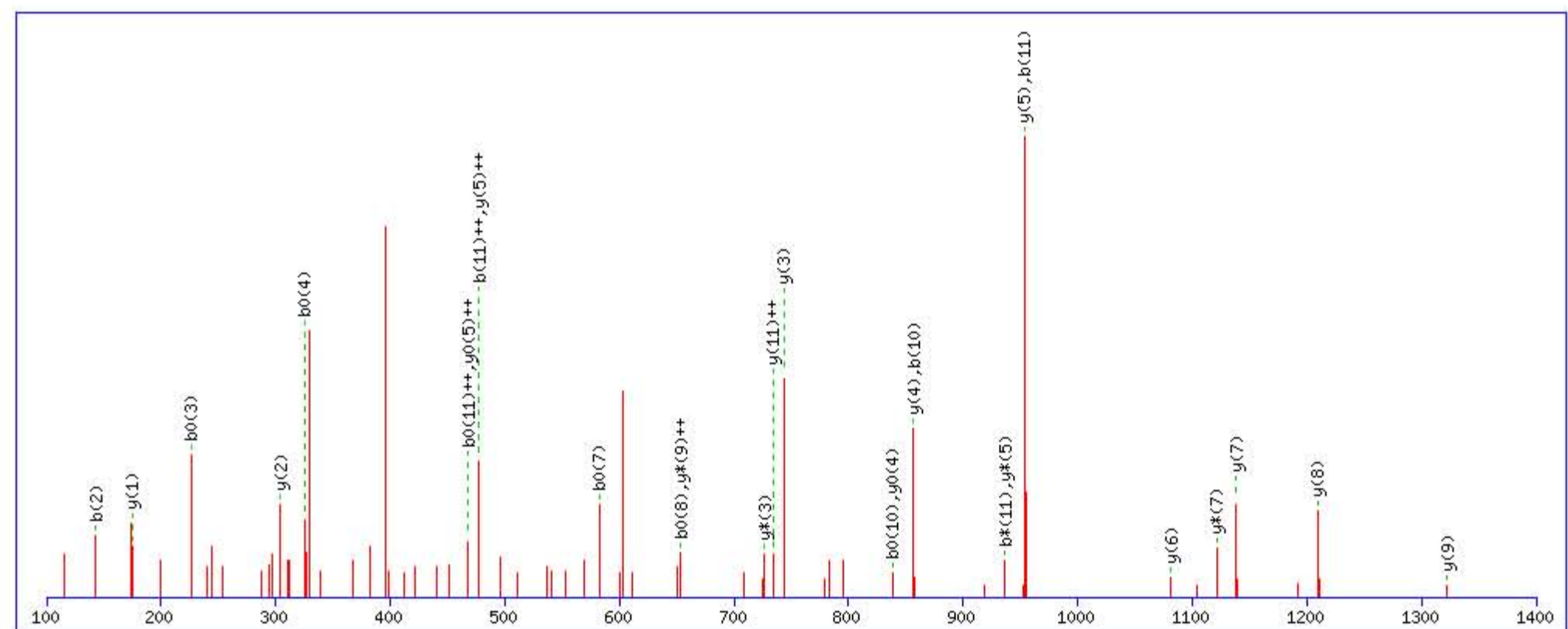
Title: Locus:1.1.1.3164.12 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

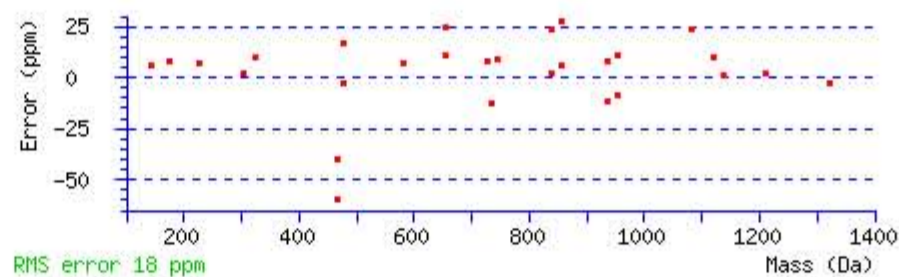
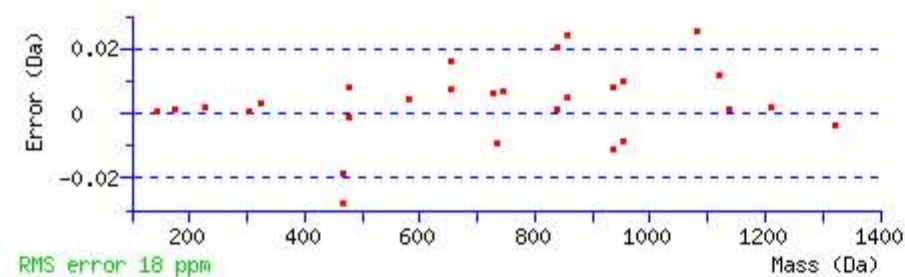
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 58 Expect: 8.1e-006

Matches : 28/144 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							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 **AATVGS LAGQPLQER**

(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	1807.961441	-0.010739	AATVGS LAGQPLQER
14.2	1807.961441	-0.010739	AATVGS LAGQPLQER
3.8	1807.942795	0.007907	ENKDQLESVLEVLHR
3.4	1807.947510	0.003192	VGLAQIAAMDISRGNHR
0.5	1807.925720	0.024982	WNWIIVLVSSDTYGR

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 45743: 1846.881868 from(924.448210,2+) rtinseconds(2814) index(43926)

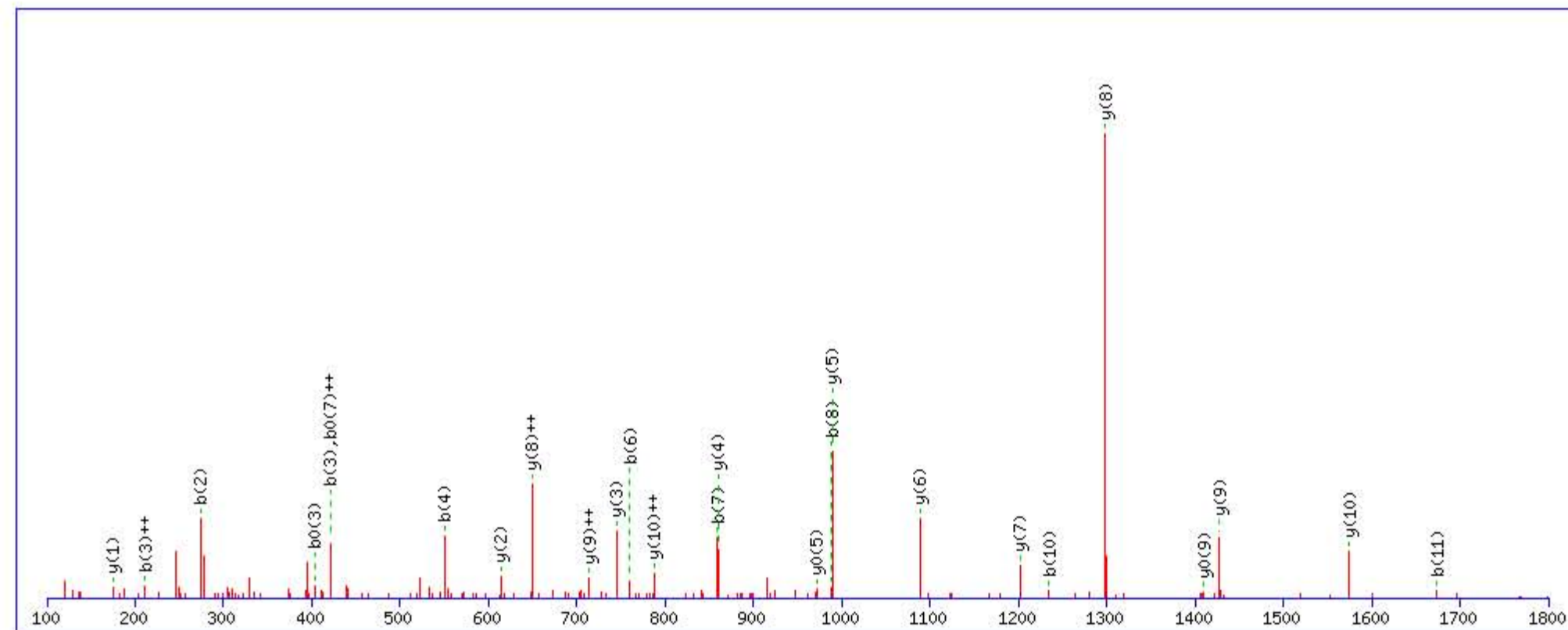
Title: Locus:1.1.1.3000.8 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

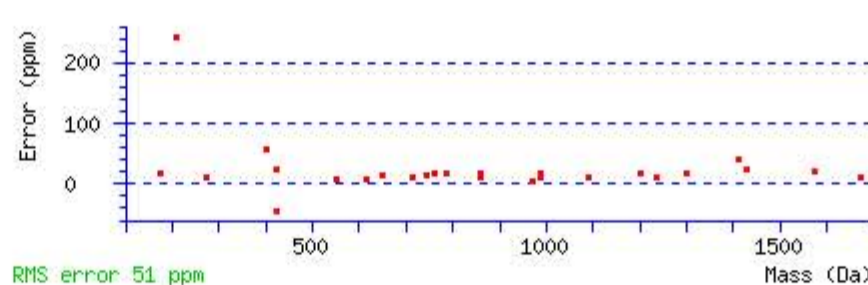
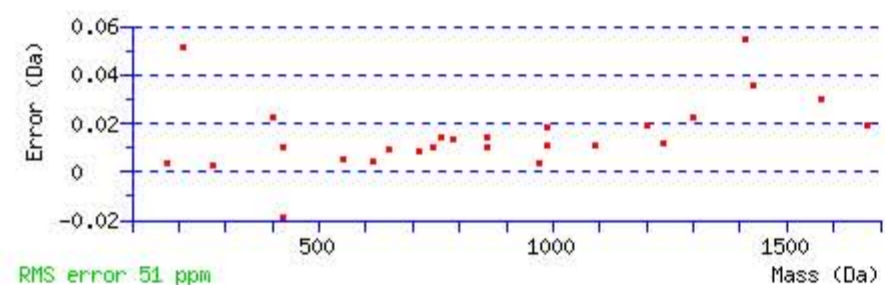
Variable modifications:

Q11 : Biotin:Thermo-21345 (Q)

Ions Score: 56 Expect: 4.5e-005

Matches : 26/106 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							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
56.0	1846.874603	0.007265	SWFEPLVEDMQR
17.6	1846.866562	0.015306	LCMAQPRTVQDVEER
7.3	1846.895706	-0.013838	CFELQALLEEER
2.2	1846.870560	0.011308	IHIGEKPYECKECKGK

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 50151: 2008.017008 from(1005.015780,2+) rtinseconds(2470) index(58436)

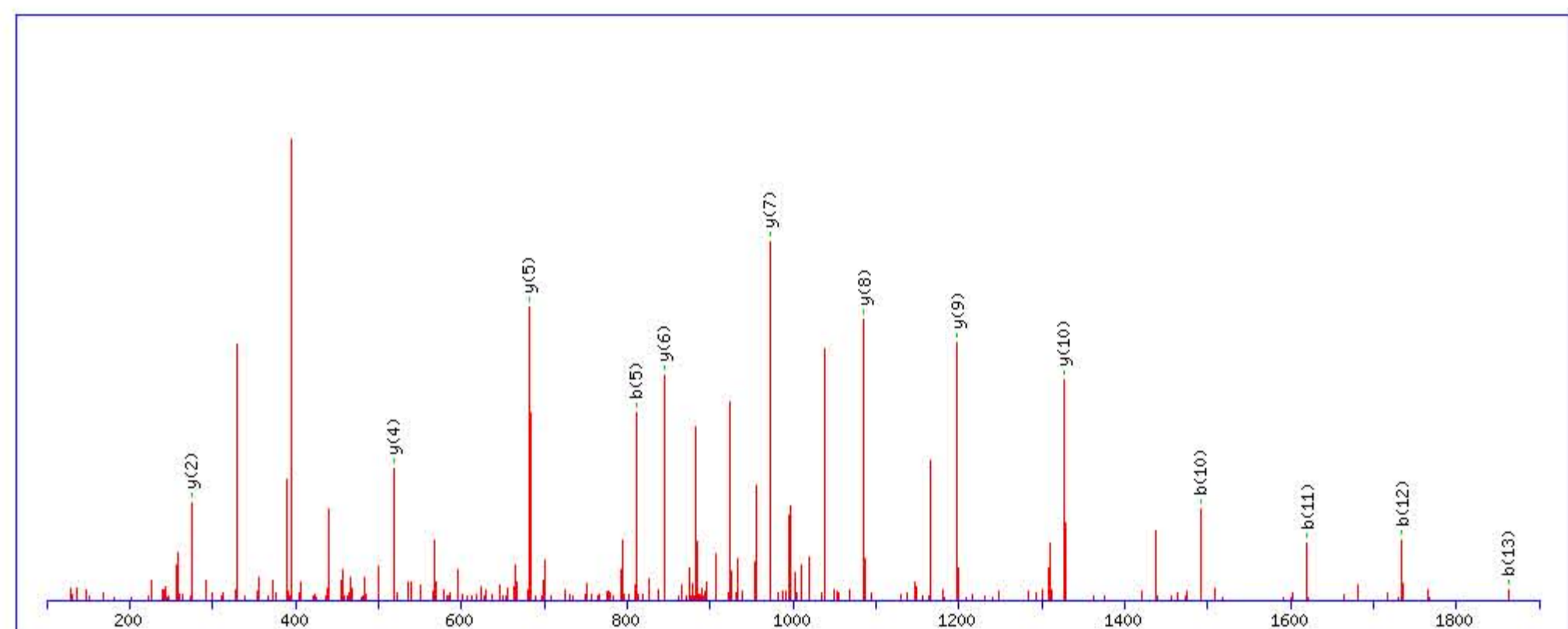
Title: Locus:1.1.1.3345.25 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

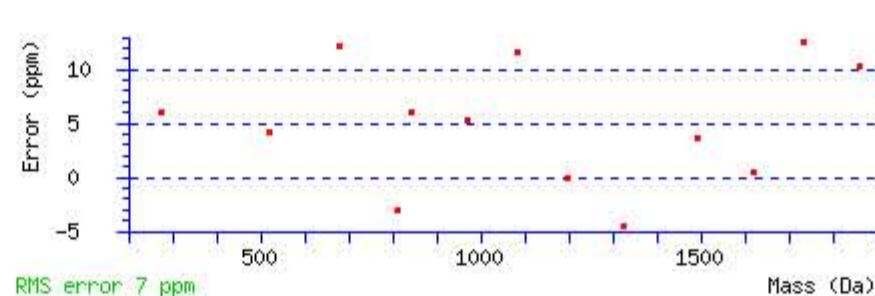
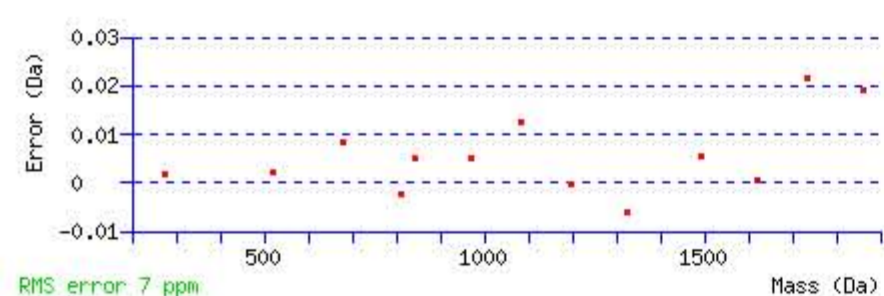
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 57 Expect: 1.9e-005

Matches : 13/146 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							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
57.0	2008.008789	0.008219	SGVQQLIQYYQDQK
49.3	2008.008789	0.008219	SGVQQLIQYYQDQK
26.8	2008.008789	0.008219	SGVQQLIQYYQDQK
6.3	2007.998215	0.018793	QQLNLRTHMADENK
6.2	2008.037308	-0.020300	VVPVLSLSELYLLQCNMK
5.9	2007.998215	0.018793	QQLNLRTHMADENK
5.6	2008.005630	0.011378	ITQRMVCAGYKEGGK
5.5	2008.008789	0.008219	SGVQQLIQYYQDQK
4.9	2008.030762	-0.013754	ASVMLFMKGKQEAQ
1.8	2008.037766	-0.020758	NYEDSVIQSVFRAKPKQ

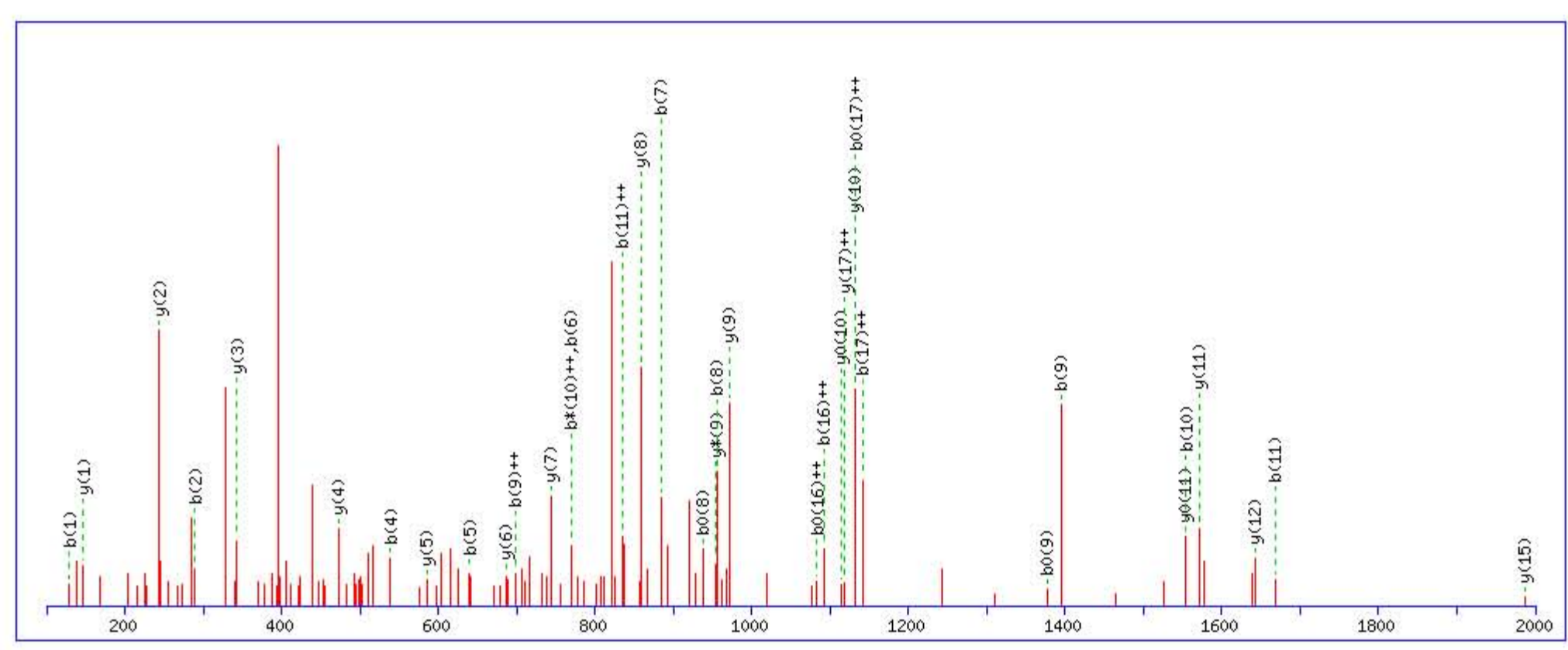
MASCOT SCIENCE Mascot Search Results

Peptide View

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

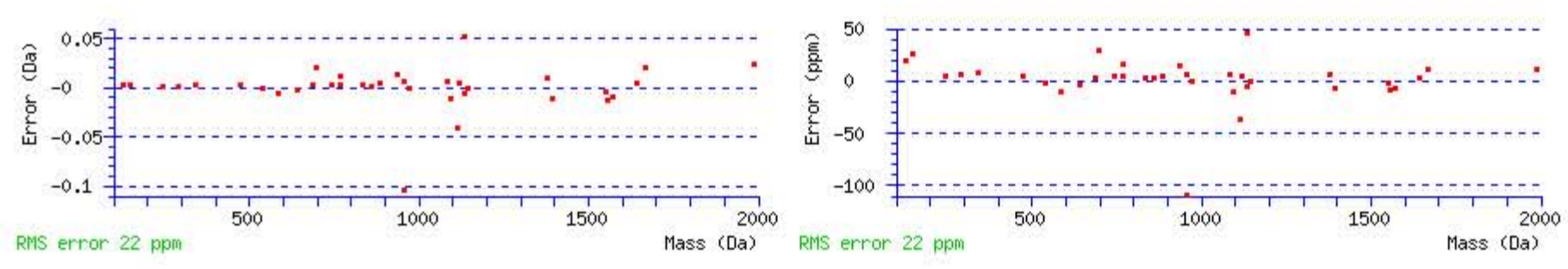
Match to Query 60442: 2524.148862 from(842.390230,3+) rtinseconds(1982) index(71118)
 Title: Locus:1.1.1.3223.13 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 63 Expect: 4.7e-006
 Matches : 36/206 fragment ions using 79 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	129.102239	65.054757	112.075690	56.541483			K							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
63.5	2524.164780	-0.015918	KCSYTEDAQCIDGTIEVPK

MASCOT SCIENCE 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 27039: 1258.704008 from(630.359280,2+) rtinseconds(2034) index(55992)

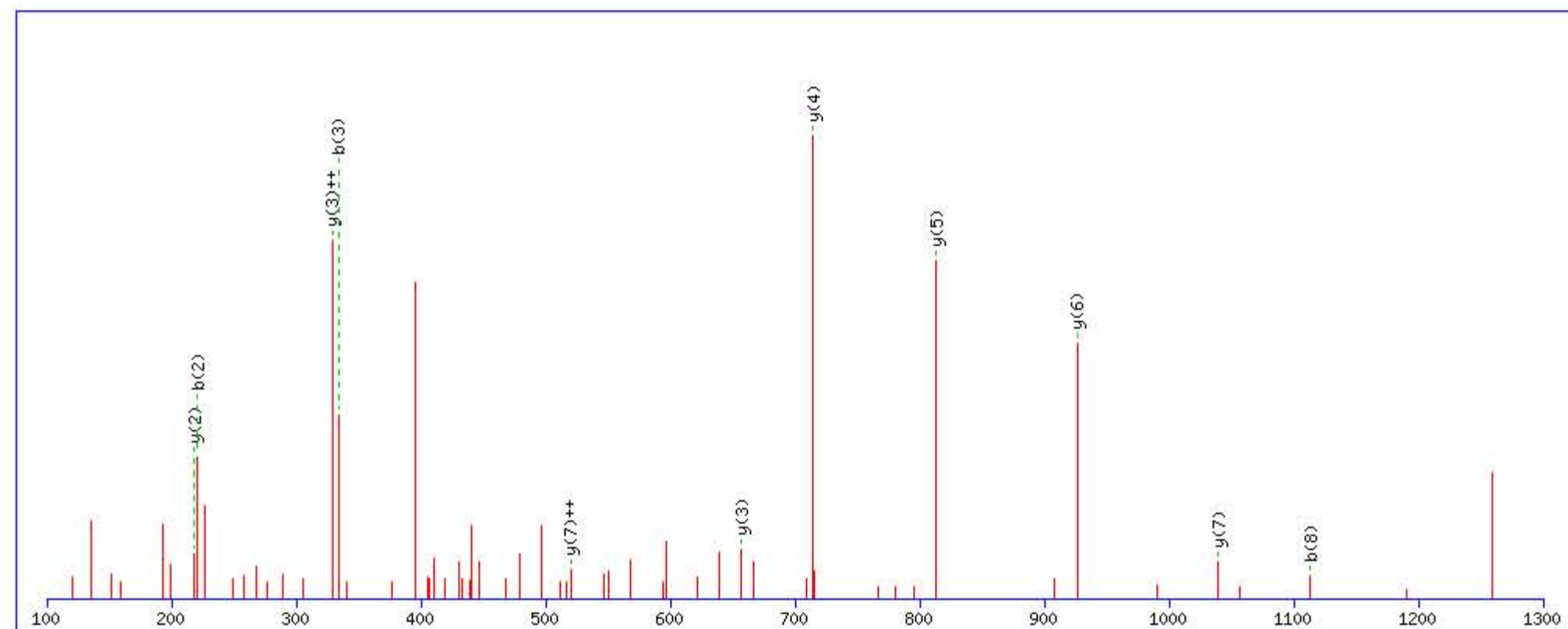
Title: Locus:1.1.1.3194.9 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

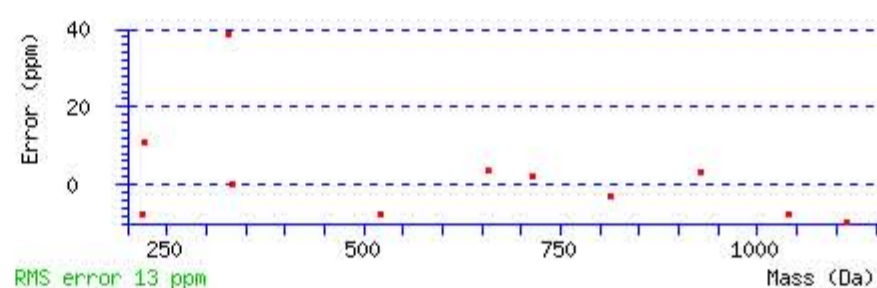
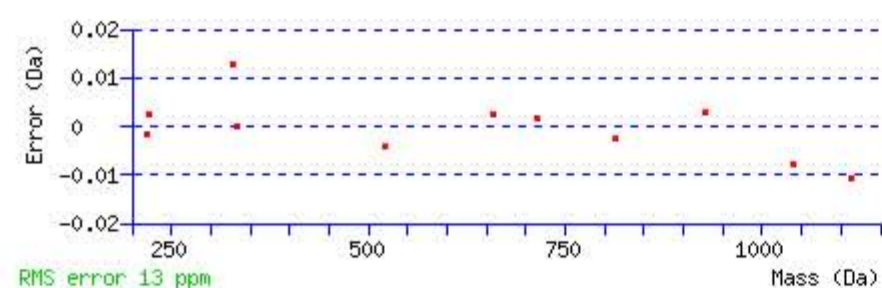
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.032

Matches : 11/52 fragment ions using 28 most intense peaks [\(help\)](#)

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



NCBI BLAST search of [GYILVGQAK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.9	1258.710754	-0.006746	GYILVGQAK
10.4	1258.717941	-0.013933	RILAKVQEMR
7.3	1258.721970	-0.017962	GYILQAKR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **QSSYSFFK**

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

Match to Query 31722: 1390.665088 from(696.339820,2+) rtinseconds(2124) index(56604)

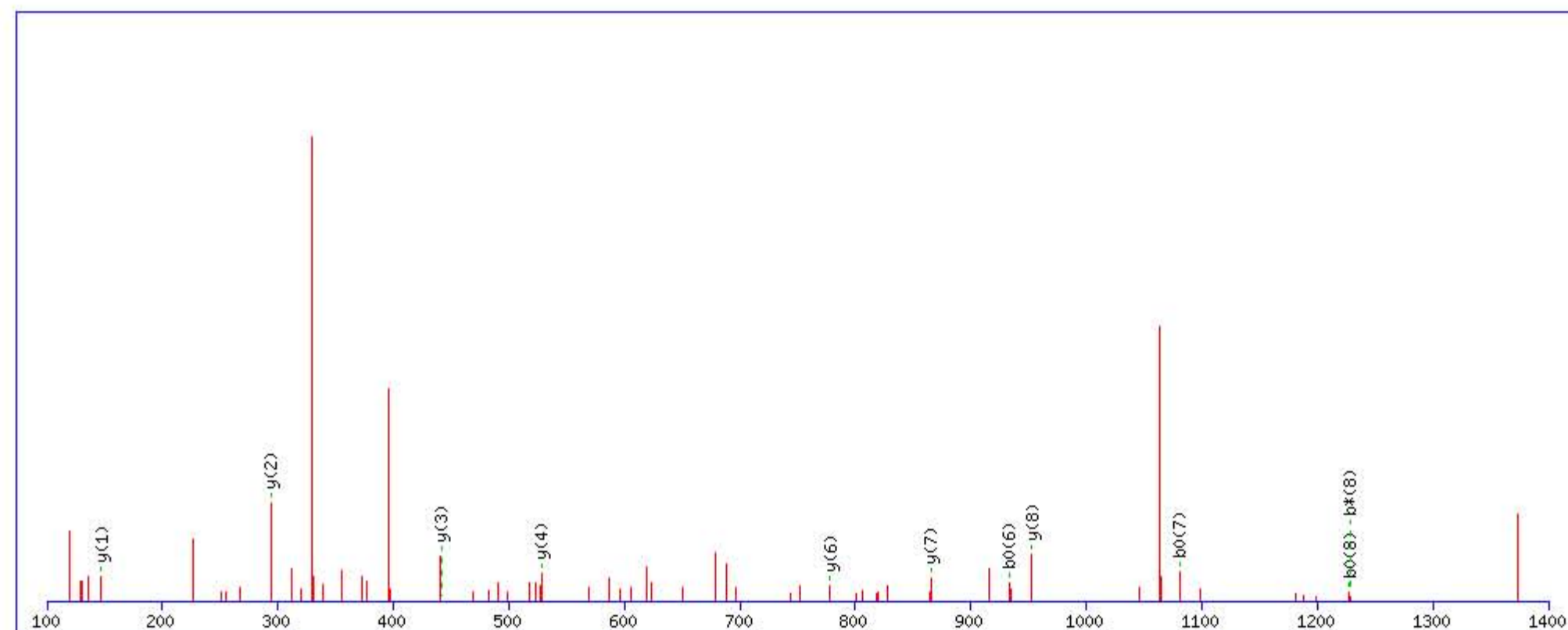
Title: Locus:1.1.1.3225.9 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1390.659119

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

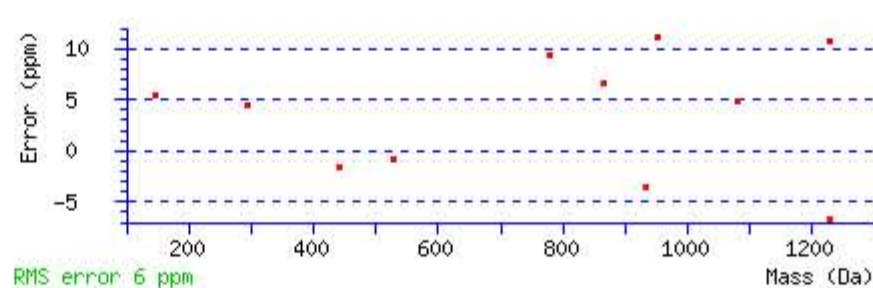
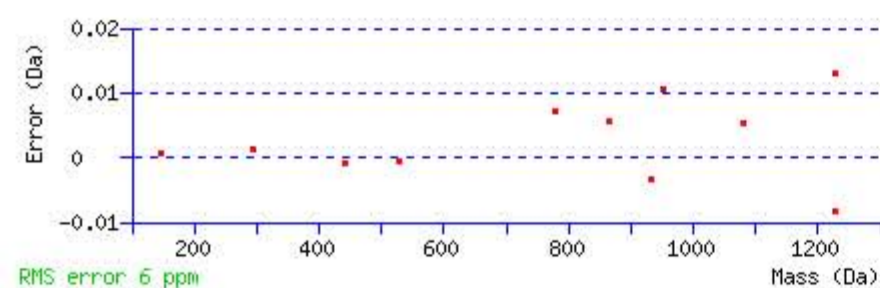
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 30 Expect: 0.0047

Matches : 11/88 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	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 **QSSYSFFK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	$M_r(\text{calc})$:	Delta	Sequence
29.5	1390.659119	0.005969	QSSYSFFK
4.5	1390.646317	0.018771	TNELEEELSAEK
2.0	1390.676208	-0.011120	LTENNSQPLMTK
1.8	1390.669678	-0.004590	CAPASIRLMDNK
0.5	1390.673706	-0.008618	TLNADLMMFAHK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **LSCSYSHWSAPAPQCK**

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

Match to Query 53707: 2188.989372 from(730.670400,3+) rtinseconds(1777) index(37193)

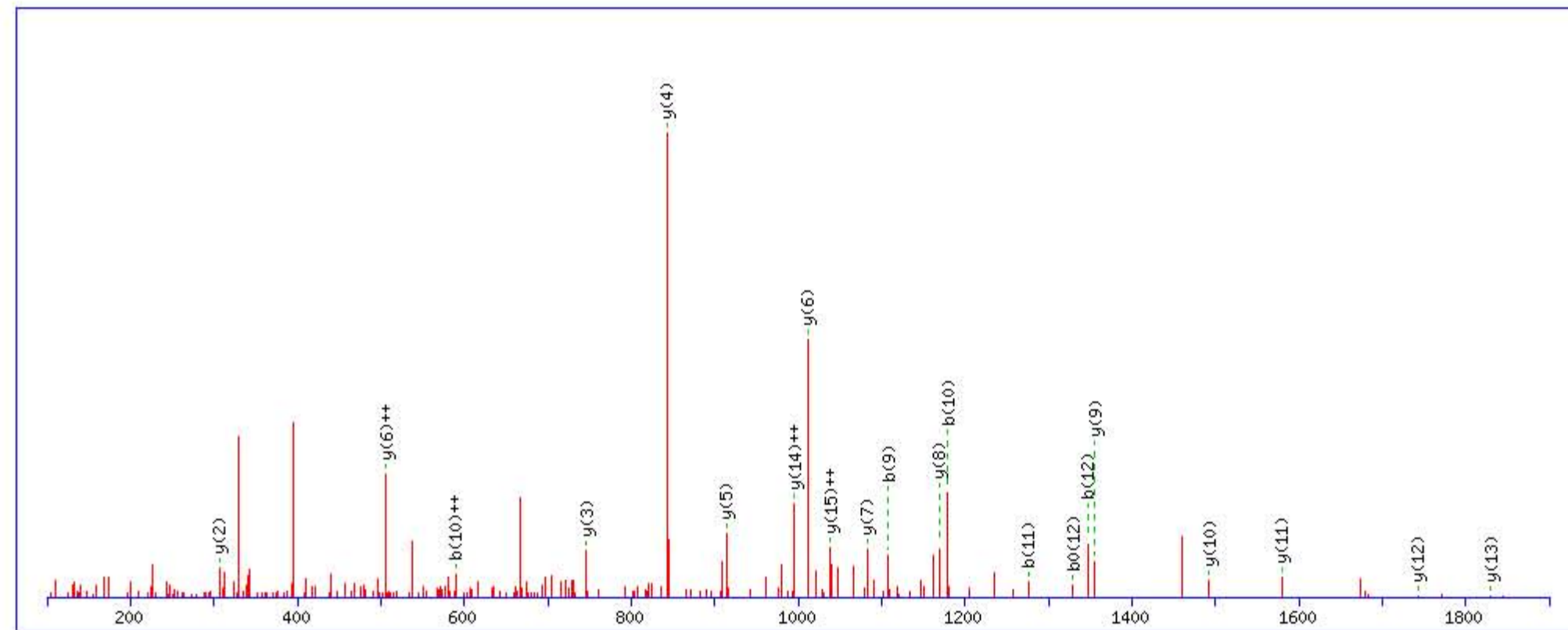
Title: Locus:1.1.1.2641.19 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\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): 2188.985626

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

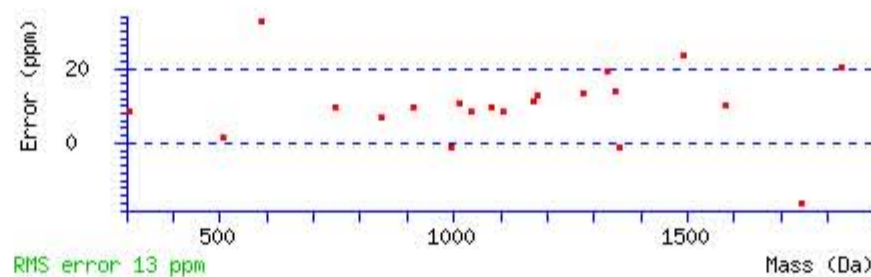
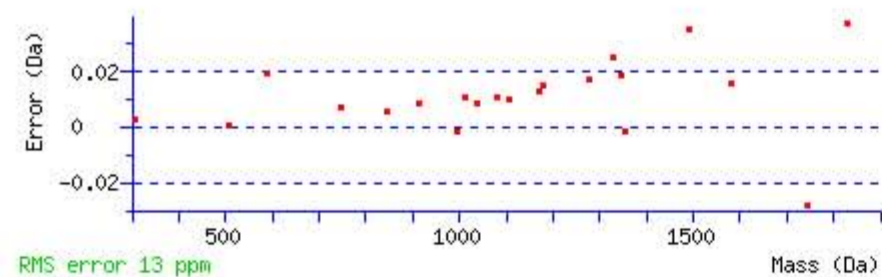
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 60 Expect: 1.1e-005

Matches : 21/138 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							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
59.5	2188.985626	0.003746	LSCSYSHWSAPAPQCK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **DHLGFQVTWPDESK**

Found in **CPN2_HUMAN**, Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3

Match to Query 48479: 1968.951702 from(657.324510,3+) rtinseconds(2317) index(40631)

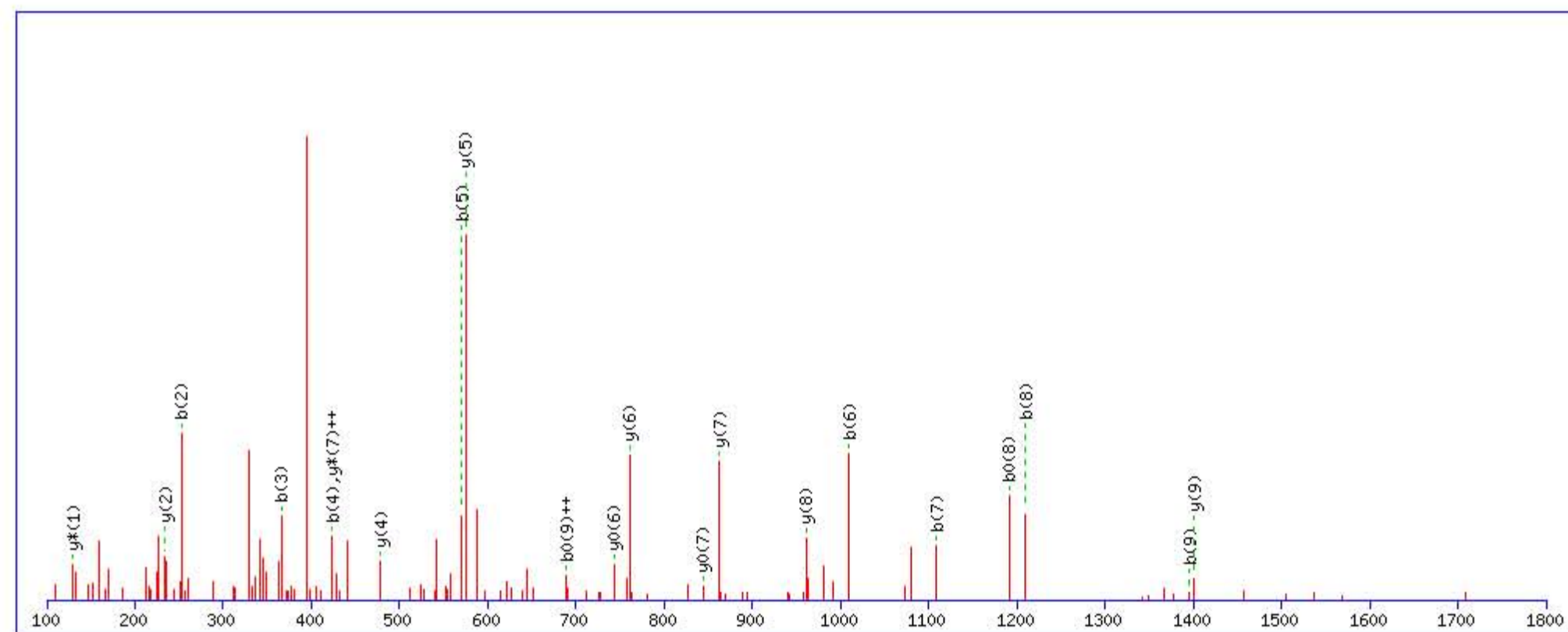
Title: Locus:1.1.1.2829.11 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

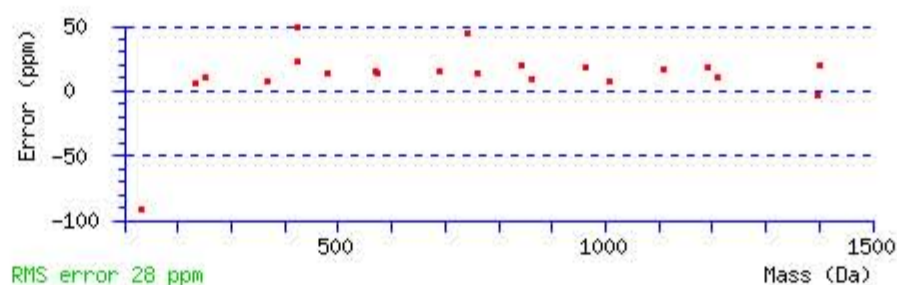
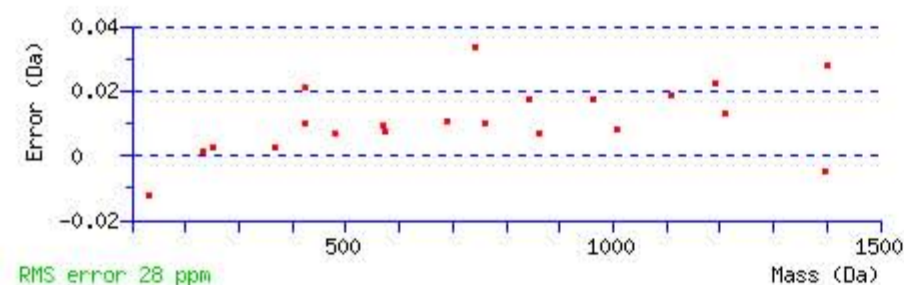
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 42 Expect: 0.0007

Matches : 21/144 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	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
42.1	1968.940399	0.011303	DHLGFQVTWPDESK
8.5	1968.949585	0.002117	EGQMESVEAAMSSKTLKK

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

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SQCTYSNPEGTVVLACDQAQCR**

Found in **CPN2_HUMAN**, Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3

Match to Query 63912: 2854.253502 from(952.425110,3+) rtinseconds(2057) index(39028)

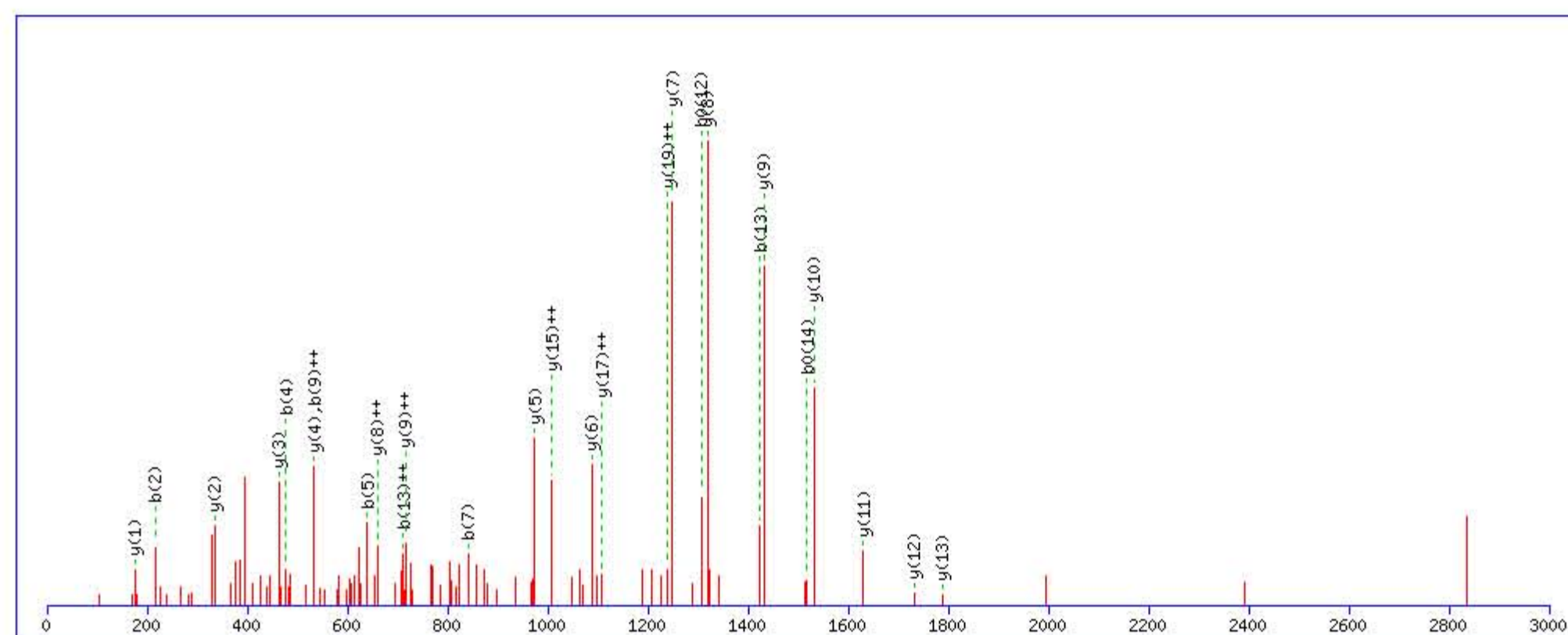
Title: Locus:1.1.1.2738.23 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

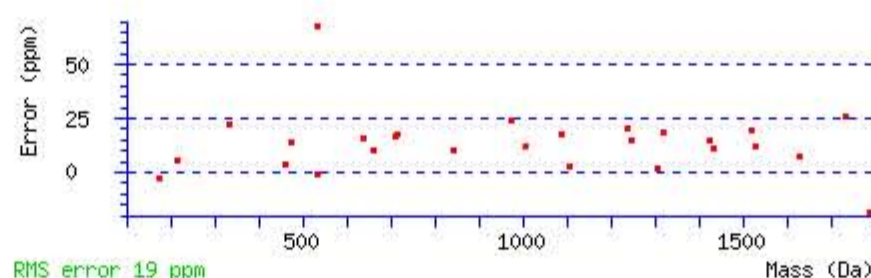
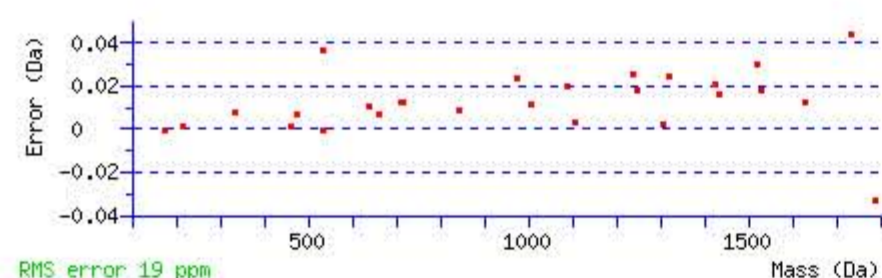
Variable modifications:

Q18 : Biotin:Thermo-21345 (Q)

Ions Score: 98 Expect: 8e-010

Matches : 27/240 fragment ions using 36 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	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
98.0	2854.250671	0.002831	SQCTYSNPEGTVVLACDQAQCR
75.8	2854.250671	0.002831	SQCTYSNPEGTVVLACDQAQCR
1.9	2854.250671	0.002831	SQCTYSNPEGTVVLACDQAQCR

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

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

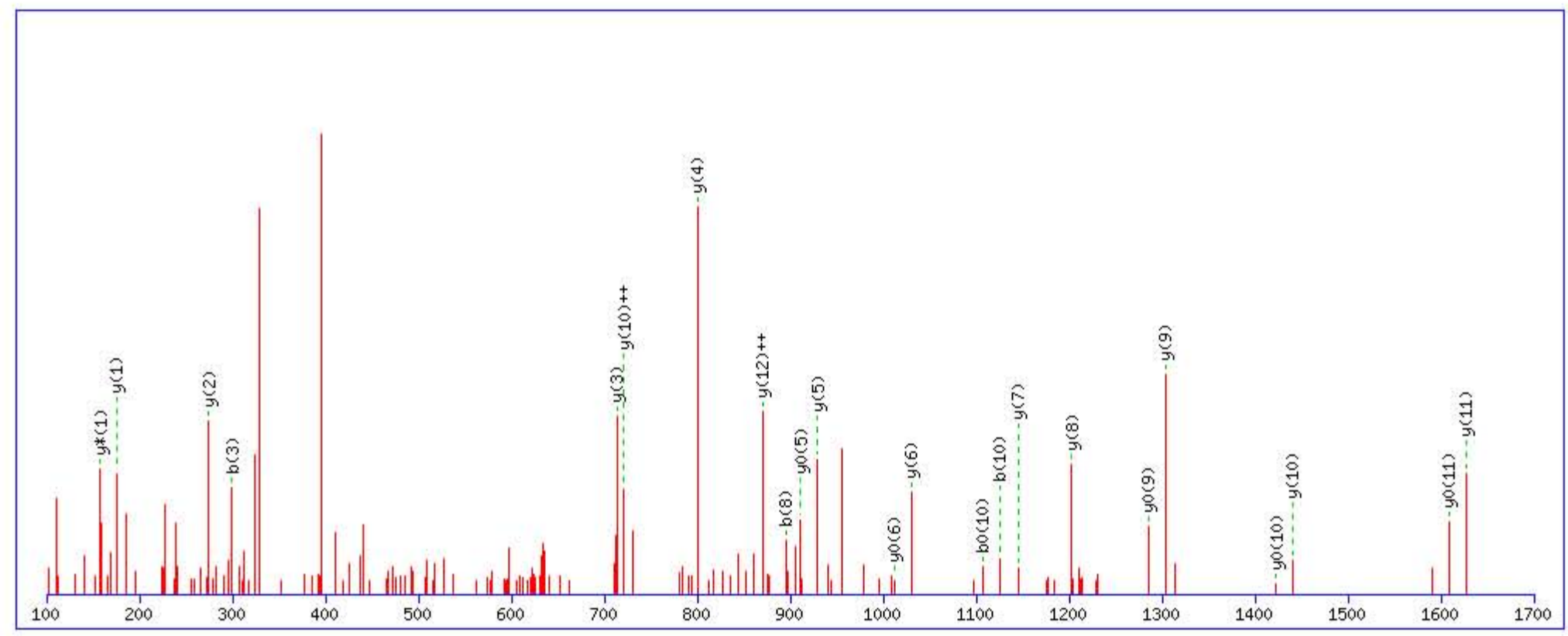
Match to Query 47367: 1923.920802 from(642.314210,3+) rtinseconds(1740) index(54079)
 Title: Locus:1.1.1.3092.13 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

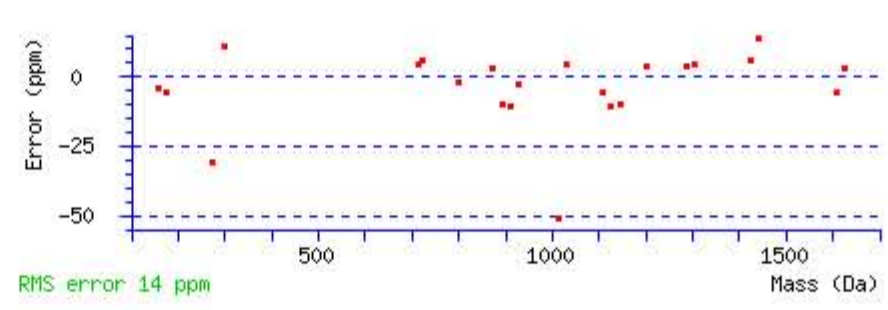
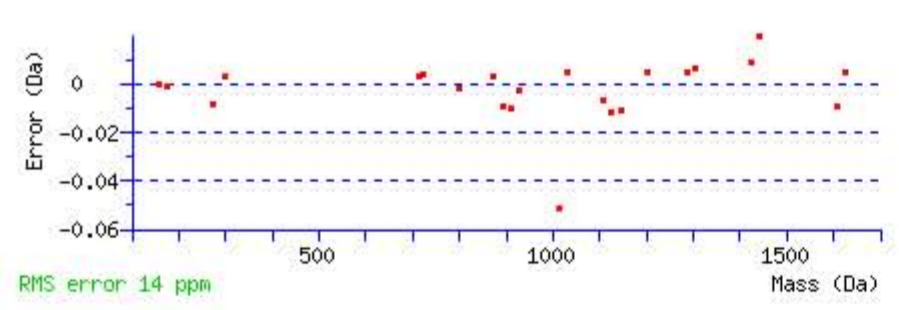
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 66 Expect: 4.9e-006

Matches : 23/140 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	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
65.5	1923.926132	-0.005330	NALWHTGDTESQVR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **ELDESLQVAER**

Found in **CLUS_HUMAN**, Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

Match to Query 38939: 1598.795868 from(800.405210,2+) rtinseconds(1949) index(55441)

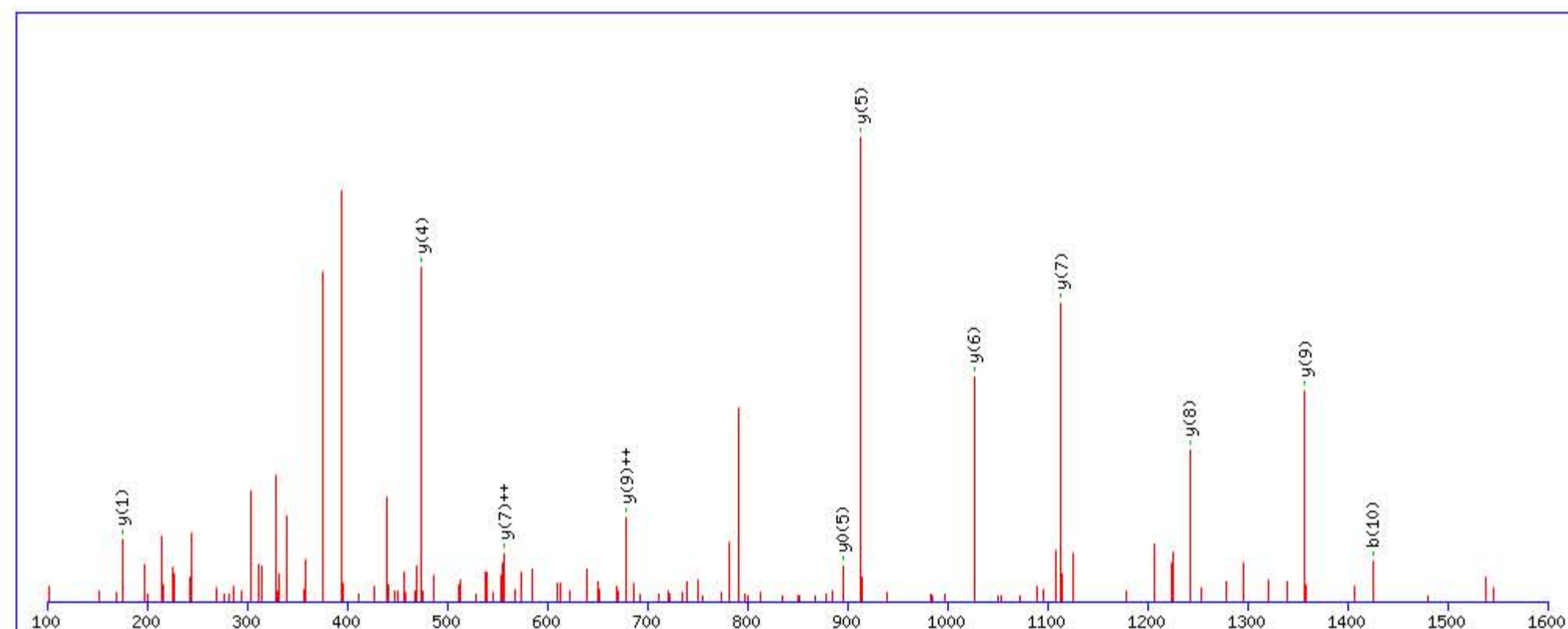
Title: Locus:1.1.1.3164.23 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

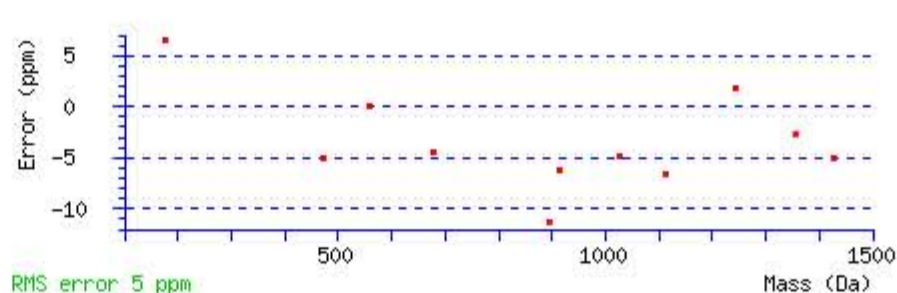
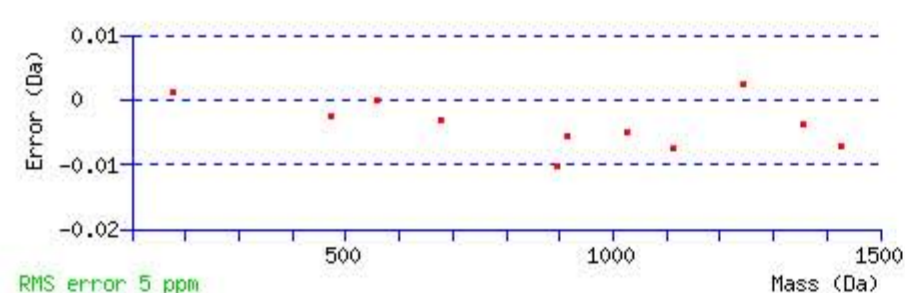
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 53 Expect: 7.3e-005

Matches : 11/106 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	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
52.5	1598.797379	-0.001511	ELDESLQVAER
7.9	1598.783478	0.012390	EDSVQRSTPNR
7.5	1598.797409	-0.001541	EDVDDLVSQLR
5.0	1598.776932	0.018936	FPIDYPYSPPTFR
4.2	1598.790024	0.005844	VTAEGDSHTEVVISR
4.2	1598.797379	-0.001511	LEESDVLQEAR
2.9	1598.808640	-0.012772	SLGAVEPICSVNTPR
1.6	1598.816025	-0.020157	LDQPMTEIVSR
1.6	1598.789993	0.005875	AGATSGELPVVEAENR
1.3	1598.787506	0.008362	AGGSWDLAVQER

MASCOT 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 42378: 1703.856372 from(568.959400,3+) rtinseconds(2806) index(60754)

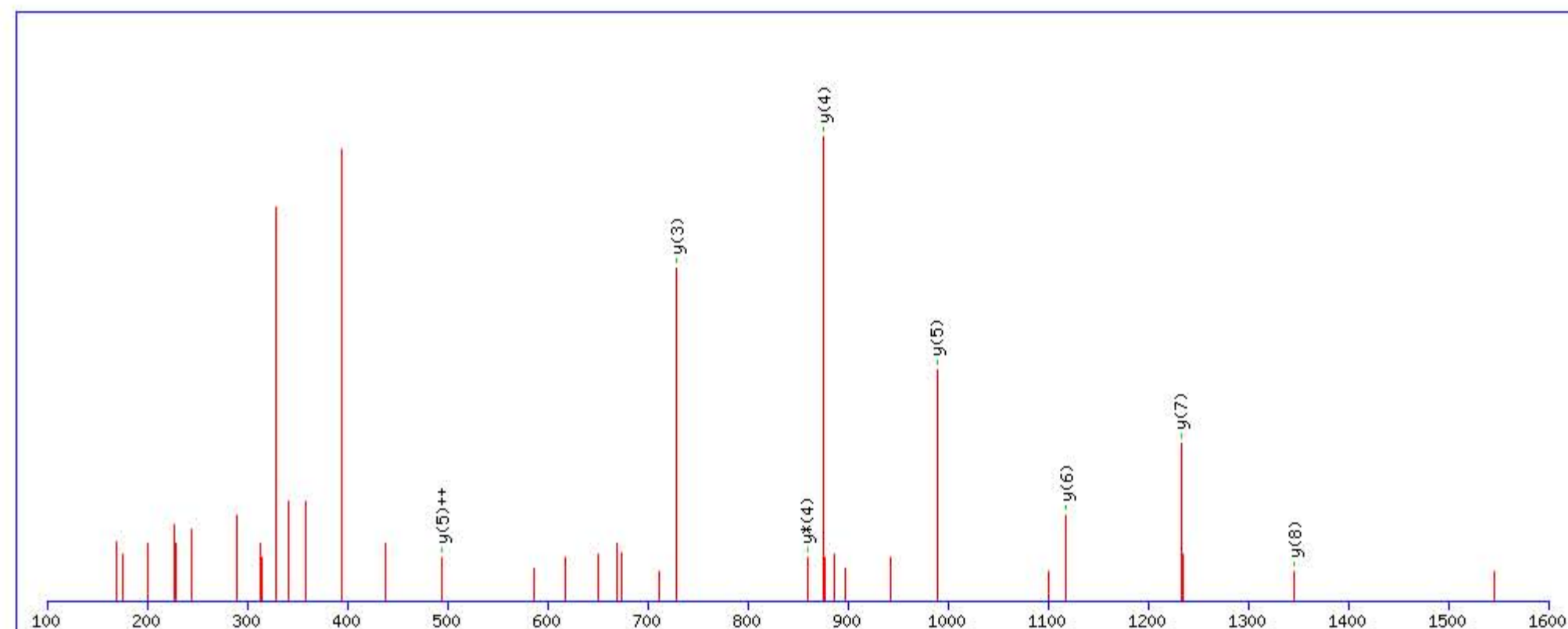
Title: Locus:1.1.1.3461.5 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

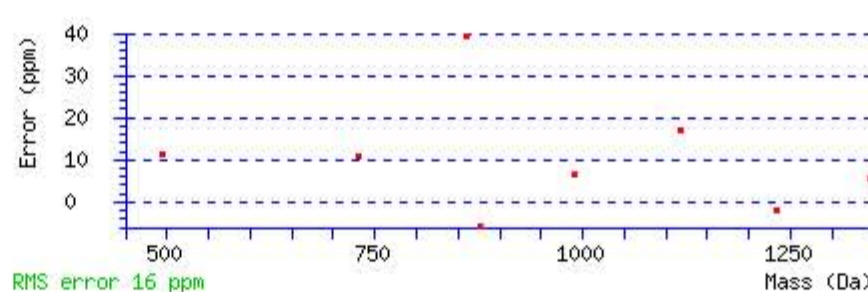
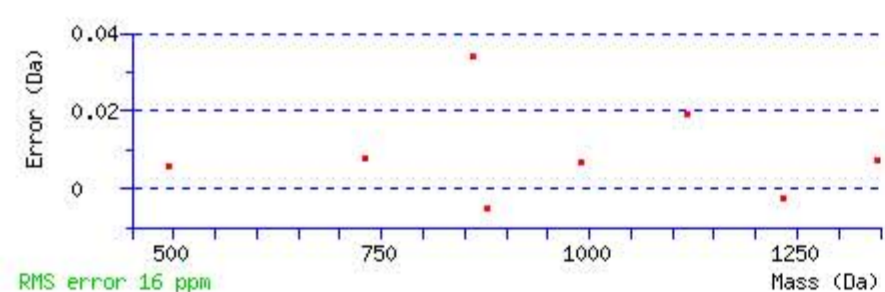
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 37 Expect: 0.00055

Matches : 8/110 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							12
2	159.076418	80.041847			141.065853	71.036564	S	1633.825419	817.416348	1616.798870	808.903073	1615.814854	808.411065	11
3	246.108446	123.557861			228.097881	114.552578	S	1546.793391	773.900333	1529.766842	765.387059	1528.782826	764.895051	10
4	359.192510	180.099893			341.181945	171.094610	I	1459.761363	730.384320	1442.734814	721.871045	1441.750798	721.379037	9
5	472.276574	236.641925			454.266009	227.636642	I	1346.677299	673.842288	1329.650750	665.329013	1328.666734	664.837005	8
6	587.303517	294.155397			569.292952	285.150114	D	1233.593235	617.300256	1216.566686	608.786981	1215.582670	608.294973	7
7	716.346110	358.676693			698.335545	349.671411	E	1118.566292	559.786784	1101.539743	551.273510	1100.555727	550.781501	6
8	829.430174	415.218725			811.419609	406.213443	L	989.523699	495.265488	972.497150	486.752213	971.513134	486.260205	5
9	976.498588	488.752932			958.488023	479.747650	F	876.439635	438.723456	859.413086	430.210181	858.429070	429.718173	4
10	1415.723914	708.365595	1398.697365	699.852321	1397.713349	699.360312	Q	729.371221	365.189249	712.344672	356.675974	711.360656	356.183966	3
11	1530.750857	765.879067	1513.724308	757.365792	1512.740292	756.873784	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
12							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [ASSIIDELFQDR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.0	1703.855240	0.001132	ASSIIDELFQDR
2.2	1703.877701	-0.021329	SSSPNSPLPMFRRTK
1.8	1703.881088	-0.024716	VQTSIAVCKLQACAR
1.0	1703.839966	0.016406	DCQDLEDLIKAKEK

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

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 51492: 2072.969868 from(1037.492210,2+) rtinseconds(1798) index(20614)

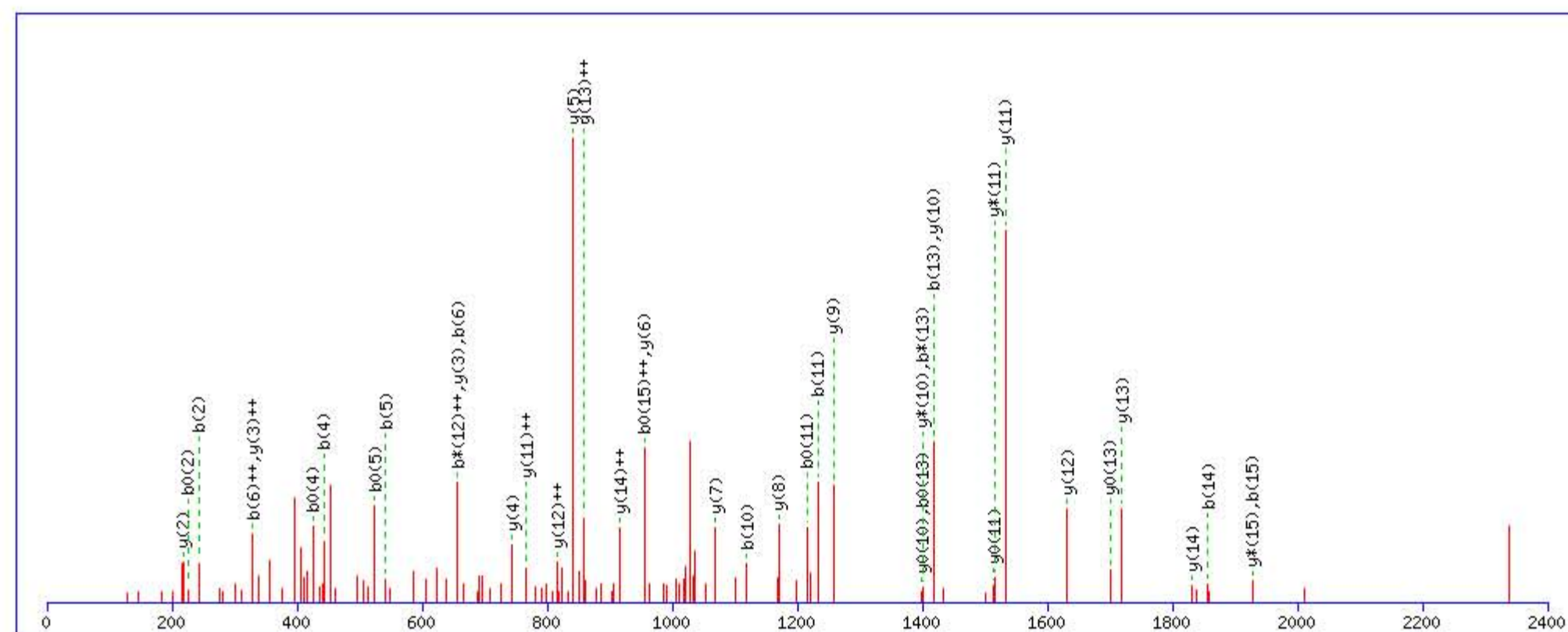
Title: Locus:1.1.1.1507.16 File:"2013-07-02 CLN FXIII 30 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\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): 2072.987061

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

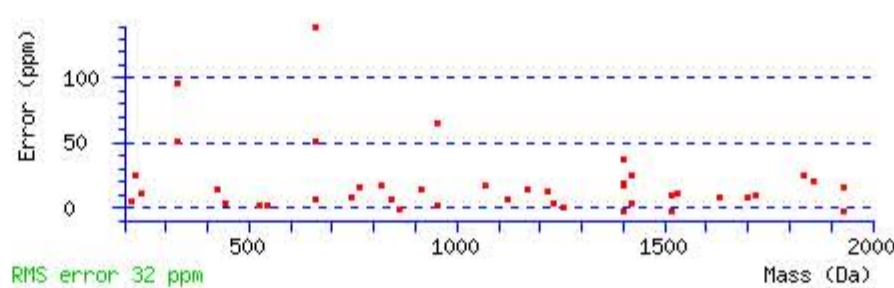
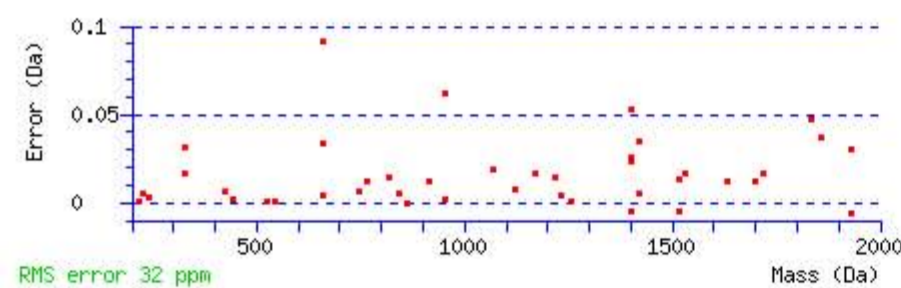
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 102 Expect: 1e-009

Matches : 42/156 fragment ions using 50 most intense peaks (help)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.049869	65.528572			112.039304	56.523290	E							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
101.7	2072.987061	-0.017193	EILSVDCSTNNPSQAK
7.8	2072.994492	-0.024624	ELVKSGLGADGVCMTFMK
1.9	2072.994904	-0.025036	MQDPNADTEWNDILRKK

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSVSQTSK**

Found in **FA9_HUMAN**, Coagulation factor IX OS=Homo sapiens GN=F9 PE=1 SV=2

Match to Query 23233: 1145.604868 from(573.809710,2+) rtinseconds(1411) index(51960)

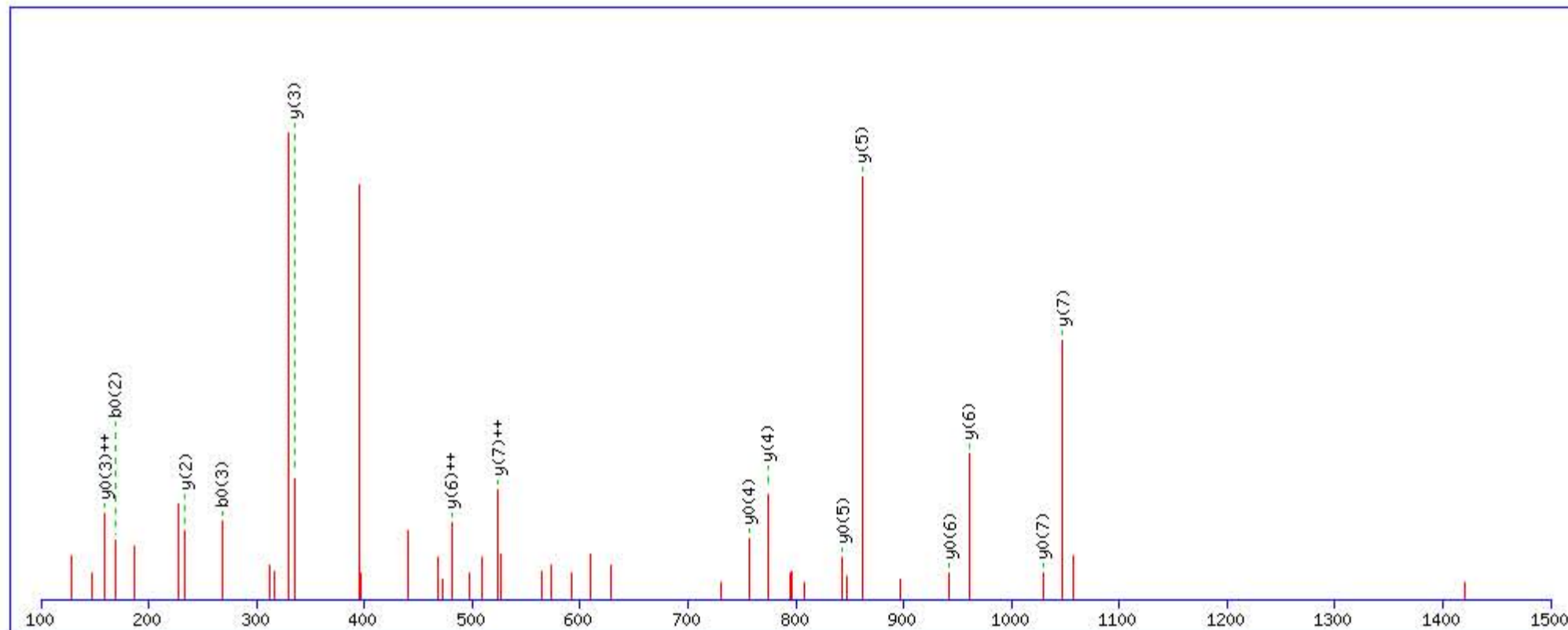
Title: Locus:1.1.1.2977.18 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

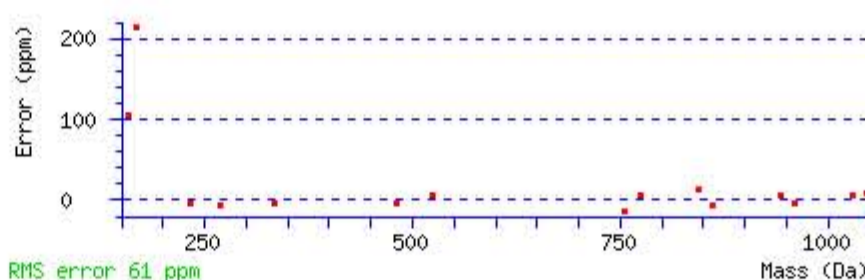
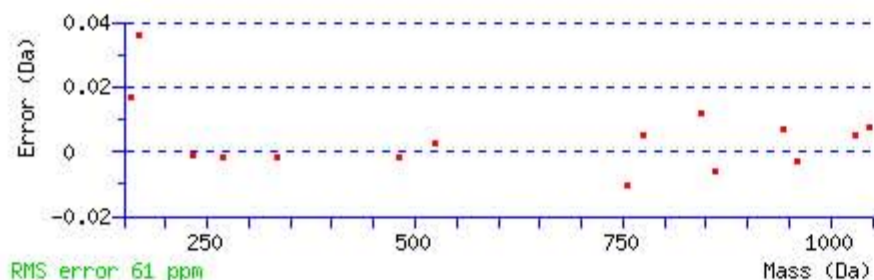
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 33 Expect: 0.0031

Matches : 15/72 fragment ions using 26 most intense peaks [\(help\)](#)

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



NCBI BLAST search of **VSVSQTSK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.6	1145.611450	-0.006582	VSVSQTSK
5.5	1145.592819	0.012049	VSDGVTKSPEK
0.6	1145.608047	-0.003179	WTKEKTEPK

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 44656: 1797.877752 from(600.299860,3+) rtinseconds(1742) index(54101)

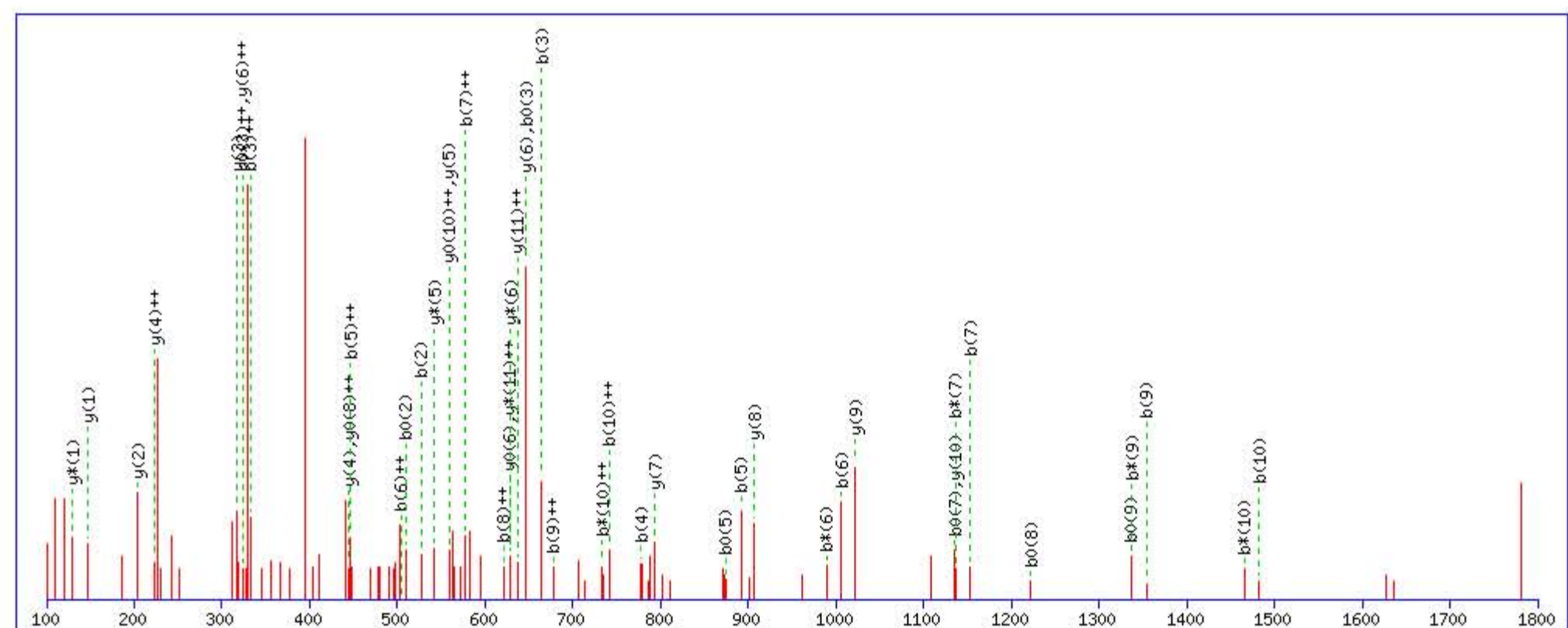
Title: Locus:1.1.1.3093.10 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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:

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **APSHQQATTAGSPLR**

Found in **FA5_HUMAN**, Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4

Match to Query 45374: 1831.929072 from(611.650300,3+) rtinseconds(1399) index(51864)

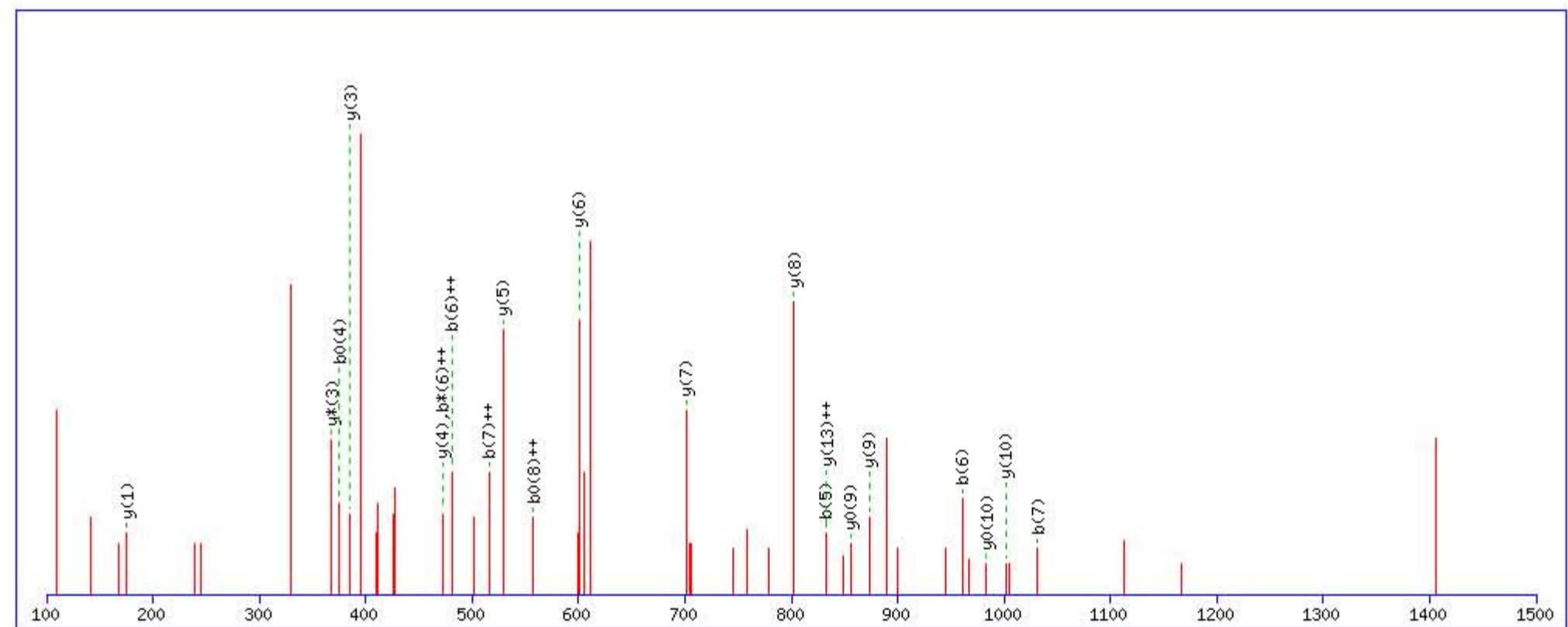
Title: Locus:1.1.1.2973.22 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1831.936295

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

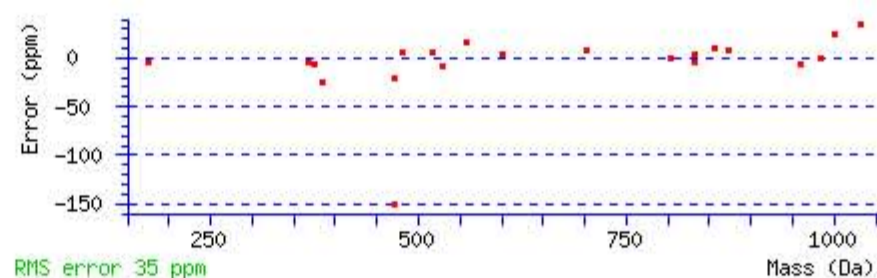
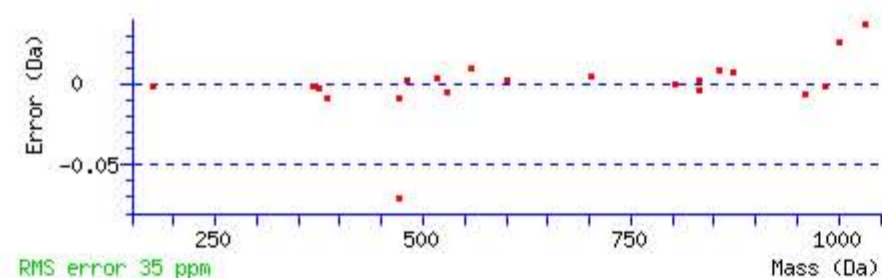
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 40 Expect: 0.00056

Matches : 21/150 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							15
2	169.097154	85.052215					P	1761.906466	881.456871	1744.879917	872.943597	1743.895901	872.451588	14
3	256.129182	128.568229			238.118617	119.562947	S	1664.853702	832.930489	1647.827153	824.417215	1646.843137	823.925206	13
4	393.188094	197.097685			375.177529	188.092402	H	1577.821674	789.414475	1560.795125	780.901200	1559.811109	780.409192	12
5	832.413420	416.710348	815.386871	408.197073	814.402855	407.705065	Q	1440.762762	720.885019	1423.736213	712.371744	1422.752197	711.879736	11
6	960.471998	480.739637	943.445449	472.226362	942.461433	471.734354	Q	1001.537436	501.272356	984.510887	492.759081	983.526871	492.267073	10
7	1031.509112	516.258194	1014.482563	507.744919	1013.498547	507.252911	A	873.478858	437.243067	856.452309	428.729792	855.468293	428.237784	9
8	1132.556791	566.782034	1115.530242	558.268759	1114.546226	557.776751	T	802.441744	401.724510	785.415195	393.211235	784.431179	392.719227	8
9	1233.604470	617.305873	1216.577921	608.792599	1215.593905	608.300591	T	701.394065	351.200671	684.367516	342.687396	683.383500	342.195388	7
10	1304.641584	652.824430	1287.615035	644.311156	1286.631019	643.819147	A	600.346386	300.676831	583.319837	292.163556	582.335821	291.671548	6
11	1361.663048	681.335162	1344.636499	672.821888	1343.652483	672.329879	G	529.309272	265.158274	512.282723	256.644999	511.298707	256.152991	5
12	1448.695076	724.851176	1431.668527	716.337902	1430.684511	715.845893	S	472.287808	236.647542	455.261259	228.134267	454.277243	227.642259	4
13	1545.747840	773.377558	1528.721291	764.864284	1527.737275	764.372276	P	385.255780	193.131528	368.229231	184.618253			3
14	1658.831904	829.919590	1641.805355	821.406316	1640.821339	820.914307	L	288.203016	144.605146	271.176467	136.091871			2
15							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **APSHQQATTAGSPLR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.0	1831.936295	-0.007223	APSHQQATTAGSPLR
29.9	1831.936295	-0.007223	APSHQQATTAGSPLR
5.4	1831.916336	0.012736	VQTTADSVSDEAELLVR

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 48821: 1988.016042 from(663.679290,3+) rtinseconds(2456) index(58354)

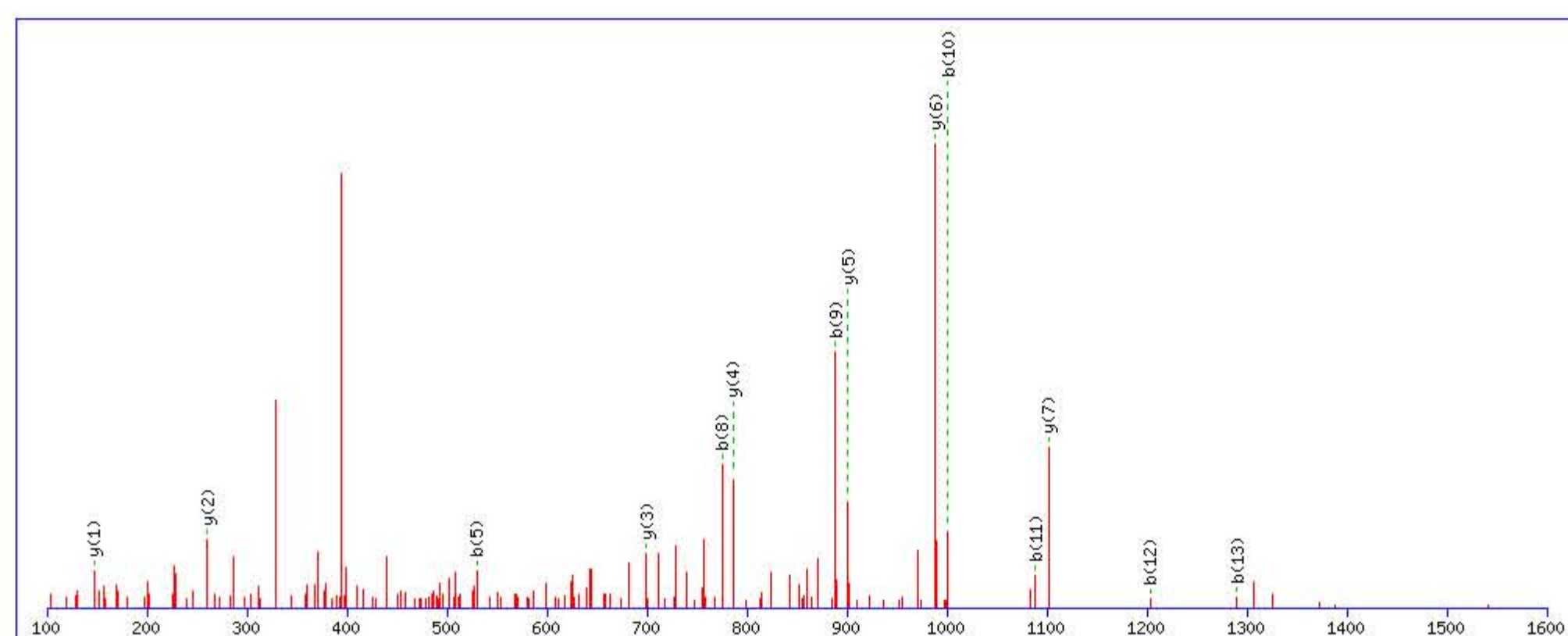
Title: Locus:1.1.1.3341.4 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

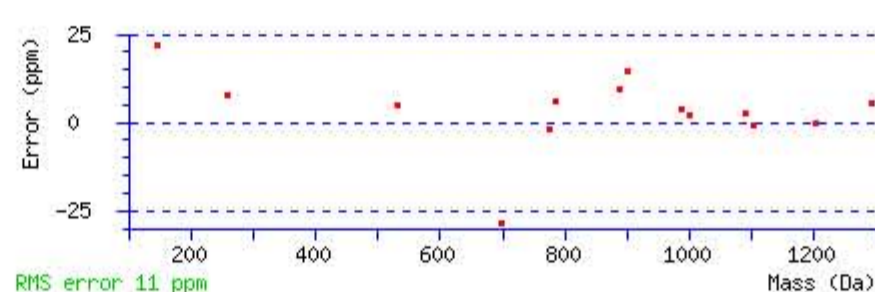
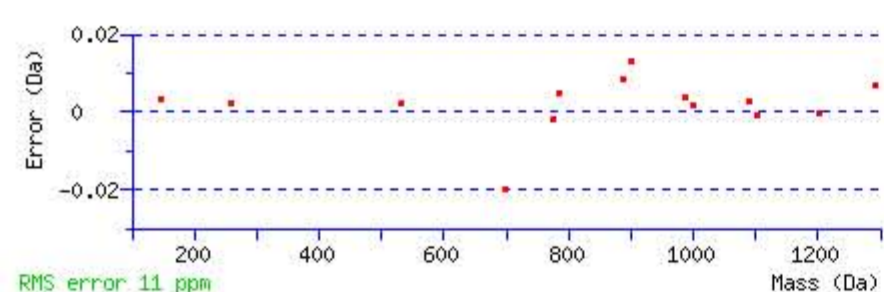
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 43 Expect: 0.00057

Matches : 14/138 fragment ions using 26 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	132.047761	66.527518					M							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
43.4	1988.014465	0.001577	MPMGLSTGIISDSQIK
8.3	1988.000519	0.015523	QQMLENQMEVRKK
4.0	1987.989319	0.026723	MQKSEGSQGTQLK
2.6	1988.004562	0.011480	QNLDKCYGQIK
0.9	1987.998535	0.017507	VCAQCRVFLRGTHAWK
0.6	1988.000519	0.015523	QQMLENQMEVRKK
0.4	1987.989273	0.026769	ENQMRMADLSELLK

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

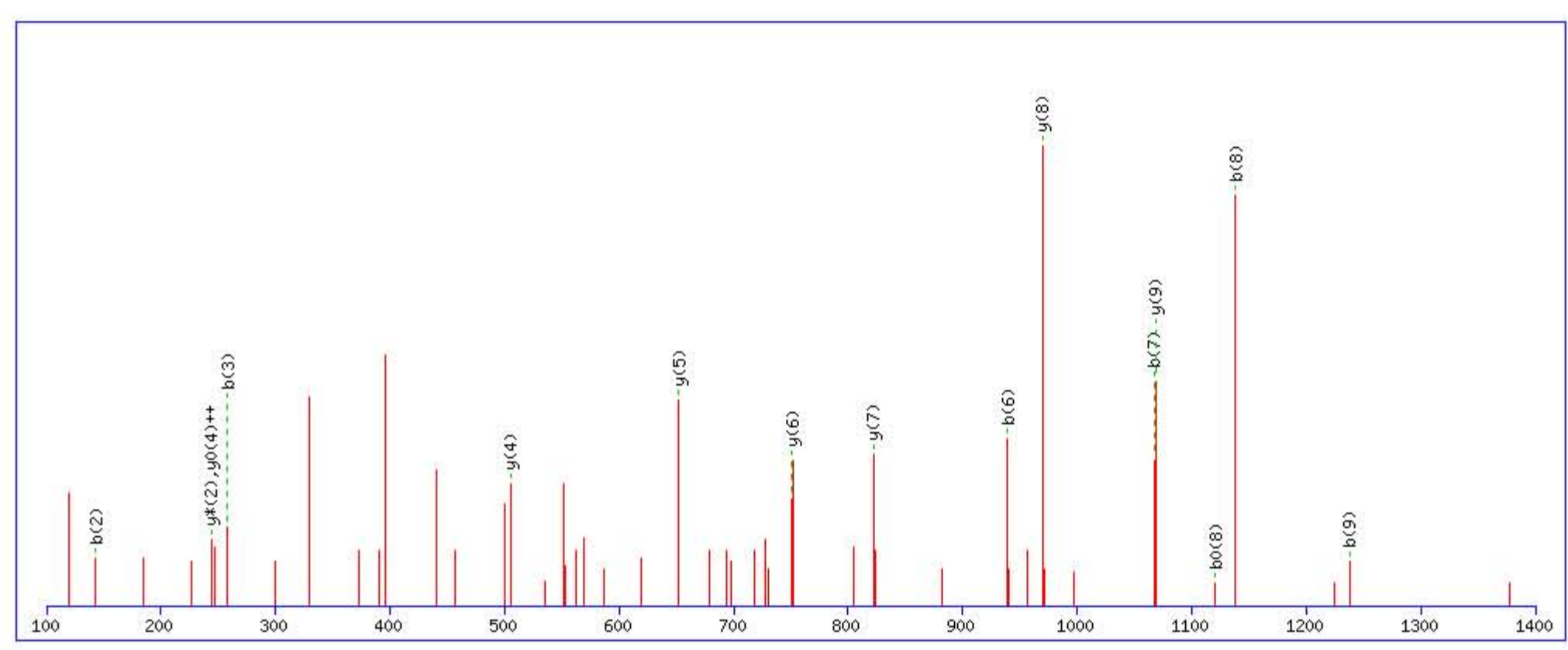
MASCOT Search Results

Peptide View

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

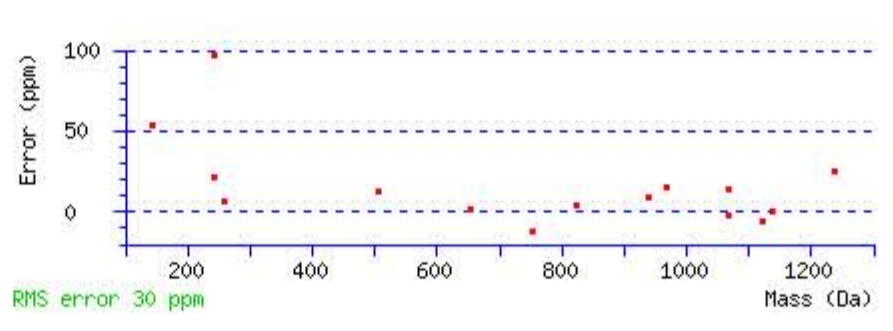
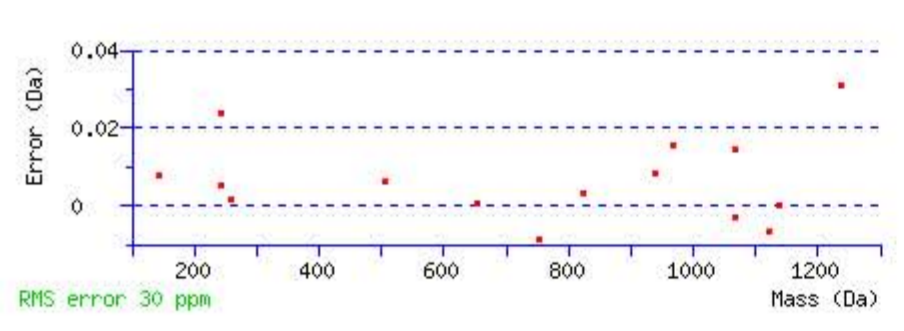
Match to Query 53990: 2205.081462 from(736.034430,3+) rtinseconds(2745) index(60259)
 Title: Locus:1.1.1.3440.9 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 0.00016
 Matches : 15/174 fragment ions using 25 most intense peaks [\(help\)](#)

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



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.7	2205.077591	0.003871	AADIEQQAVFAVFDENK
33.6	2205.077591	0.003871	AADIEQQAVFAVFDENK
1.2	2205.080063	0.001399	EKENDELDIQLKVF DENK

MASCOT 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 25249: 1200.592788 from(601.303670,2+) rtinseconds(1411) index(51961)

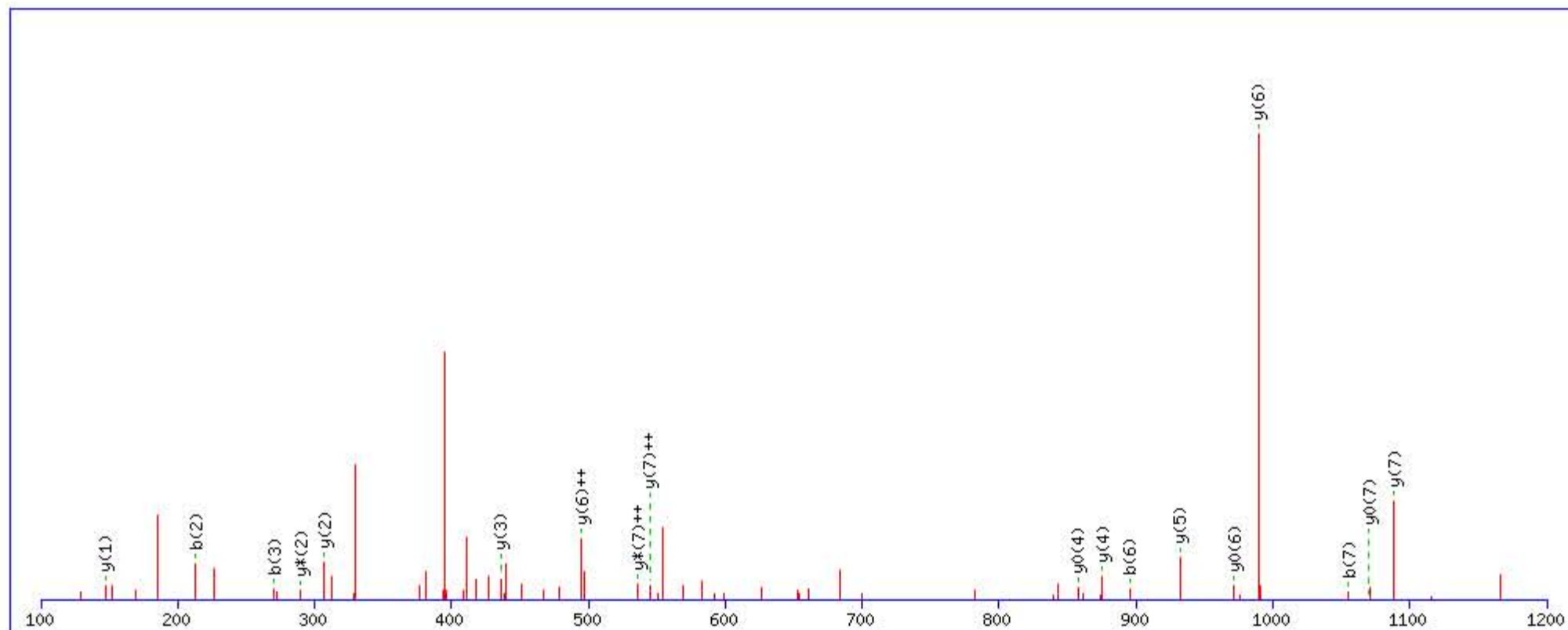
Title: Locus:1.1.1.2977.19 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

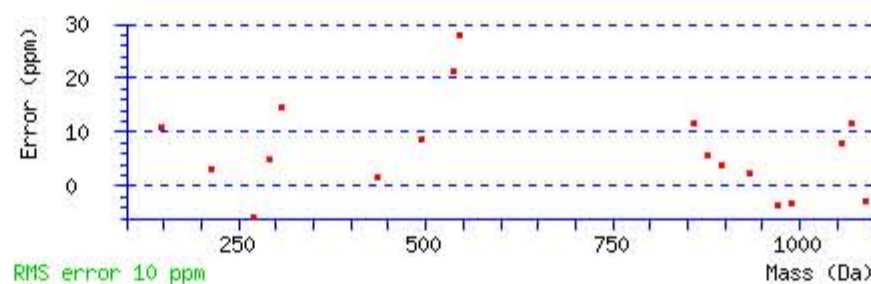
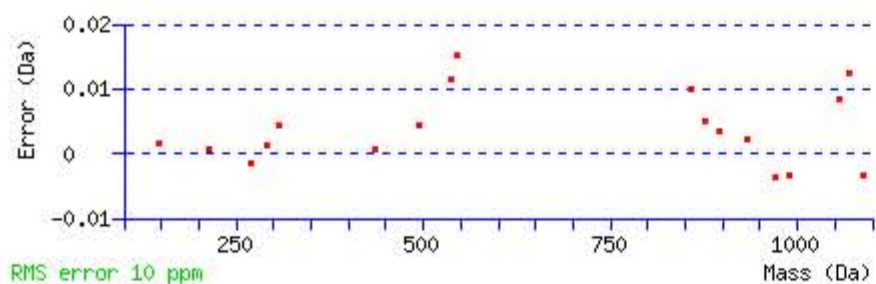
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 34 Expect: 0.0081

Matches : 18/62 fragment ions using 47 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					I							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
33.6	1200.599503	-0.006715	IVGGQECK
13.0	1200.599503	-0.006715	LIQGDGCK
8.9	1200.599487	-0.006699	LLNDQCK
3.4	1200.596100	-0.003312	LVKMYDNR

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **DWAESTLMTQK**

Found in **FA10_HUMAN**, Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2

Match to Query 39637: 1619.768848 from(810.891700,2+) rtinseconds(2271) index(57475)

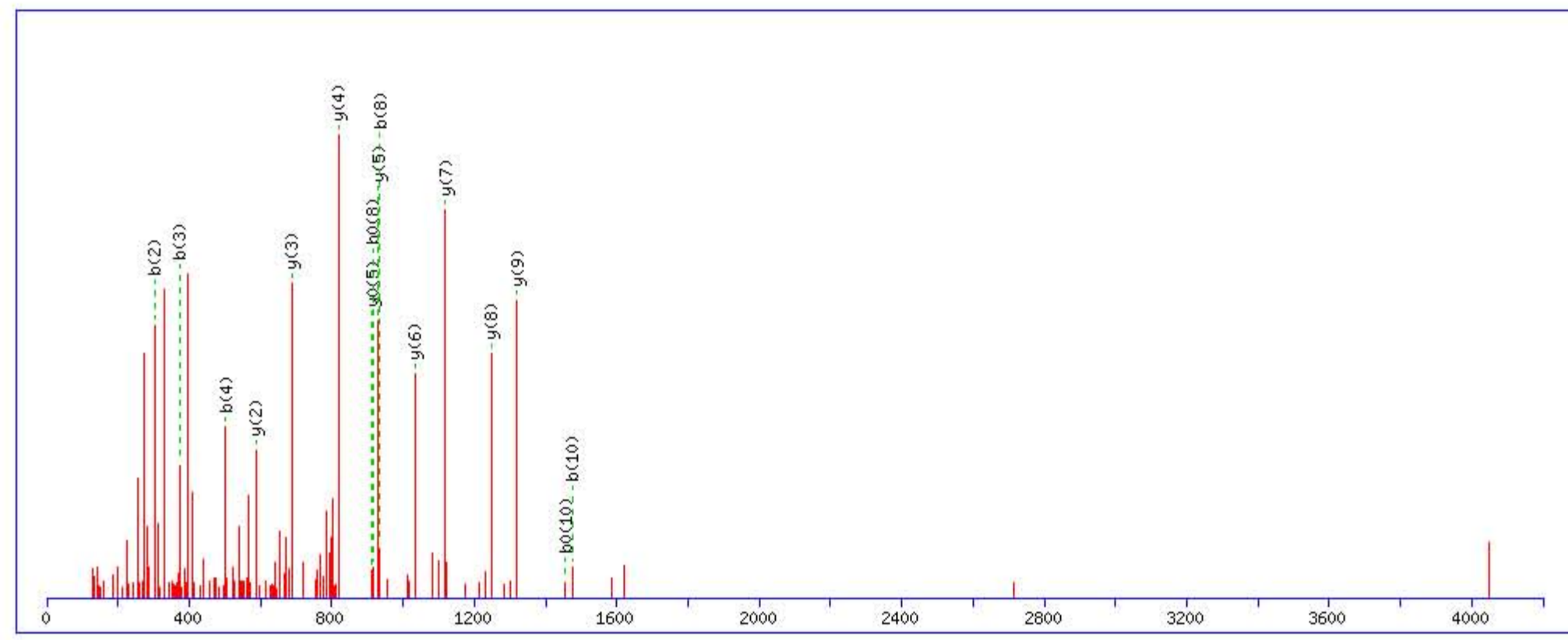
Title: Locus:1.1.1.3276.10 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1619.768738

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

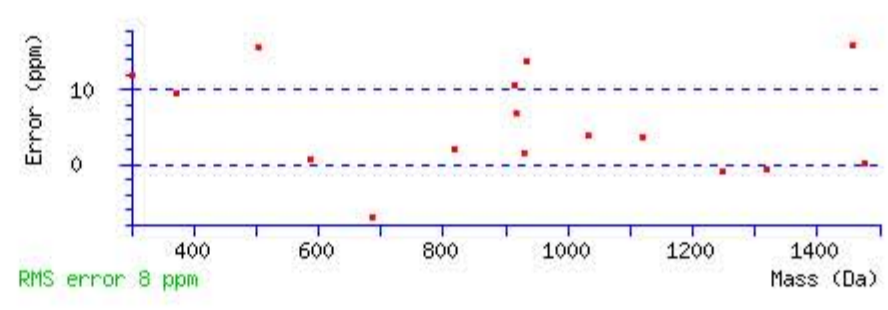
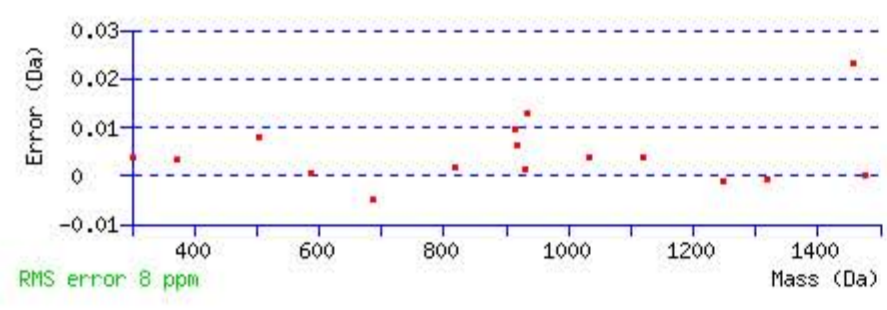
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 53 Expect: 2.5e-005

Matches : 16/98 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	302.113532	151.560404			284.102967	142.555122	W	1505.749085	753.378180	1488.722536	744.864906	1487.738520	744.372898	10
3	373.150646	187.078961			355.140081	178.073679	A	1319.669772	660.338524	1302.643223	651.825250	1301.659207	651.333241	9
4	502.193239	251.600258			484.182674	242.594975	E	1248.632658	624.819967	1231.606109	616.306693	1230.622093	615.814685	8
5	589.225267	295.116272			571.214702	286.110989	S	1119.590065	560.298671	1102.563516	551.785396	1101.579500	551.293388	7
6	690.272946	345.640111			672.262381	336.634829	T	1032.558037	516.782657	1015.531488	508.269382	1014.547472	507.777374	6
7	803.357010	402.182143			785.346445	393.176861	L	931.510358	466.258817	914.483809	457.745543	913.499793	457.253535	5
8	934.397495	467.702386			916.386930	458.697103	M	818.426294	409.716785	801.399745	401.203510	800.415729	400.711502	4
9	1035.445174	518.226225			1017.434609	509.220942	T	687.385809	344.196543	670.359260	335.683268	669.375244	335.191260	3
10	1474.670500	737.838888	1457.643951	729.325614	1456.659935	728.833605	Q	586.338130	293.672703	569.311581	285.159429			2
11							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **DWAESTLMTQK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.0	1619.768738	0.000110	DWAESTLMTQK
3.7	1619.747437	0.021411	MAPADSGPHRDPPTTR
3.3	1619.783340	-0.014492	MLGNEICLCIVGNK
1.7	1619.750107	0.018741	DCPWKISDEEITK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **QEDACQGDSSGGPHVTR**

Found in **FA10_HUMAN**, Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2

Match to Query 50412: 2023.875762 from(675.632530,3+) rtinseconds(1296) index(51202)

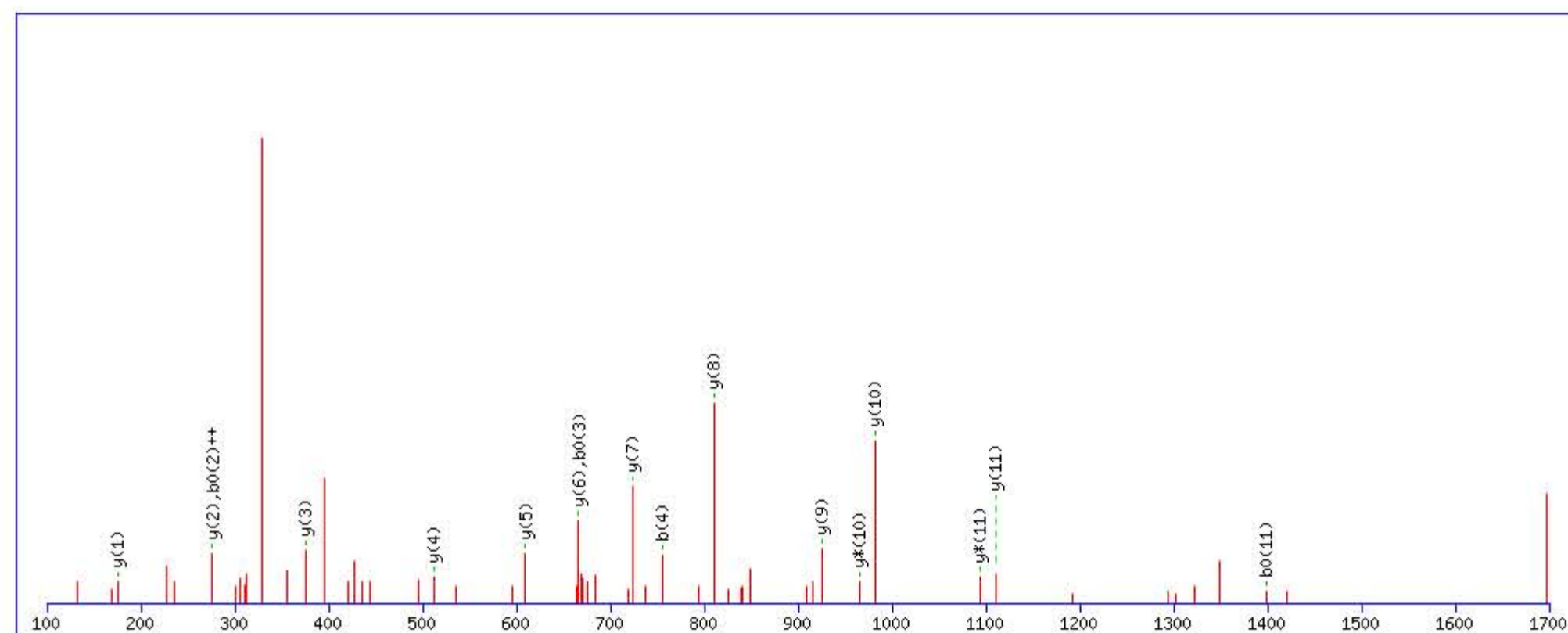
Title: Locus:1.1.1.2937.26 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

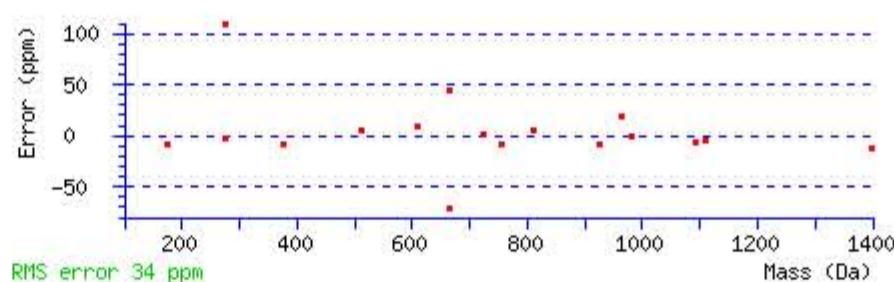
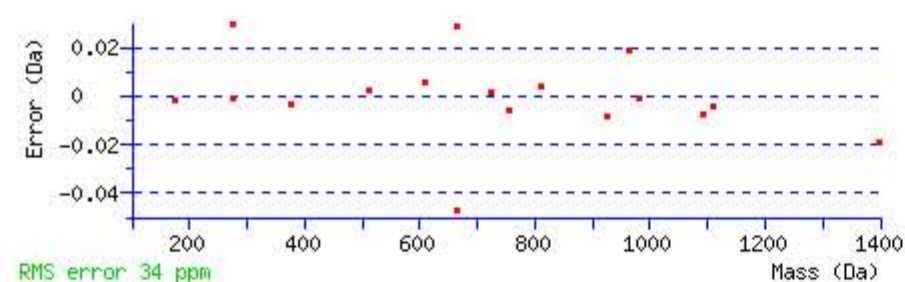
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 69 Expect: 5.1e-007

Matches : 17/176 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							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 **QEDACQGDSSGGPHVTR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.3	2023.884033	-0.008271	QEDACQGDSSGGPHVTR
55.1	2023.884033	-0.008271	QEDACQGDSSGGPHVTR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **YKDGQCETSPCQNQGK**

Found in **FA10_HUMAN**, Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2

Match to Query 56529: 2324.981202 from(776.001010,3+) rtinseconds(1262) index(51000)

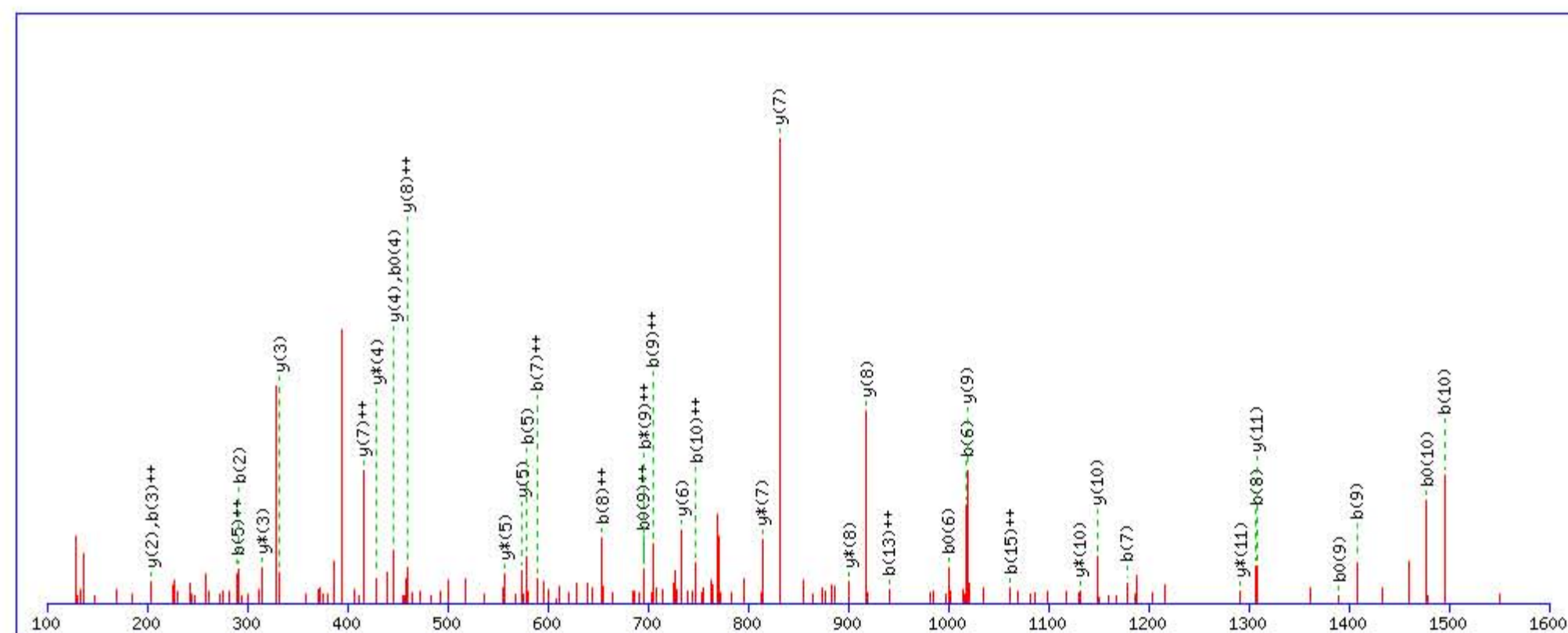
Title: Locus:1.1.1.2925.11 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2324.982407

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

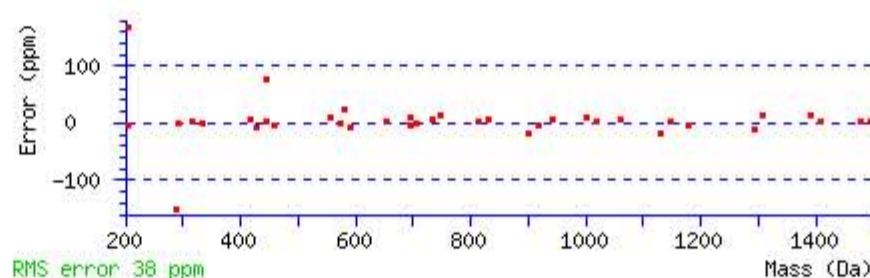
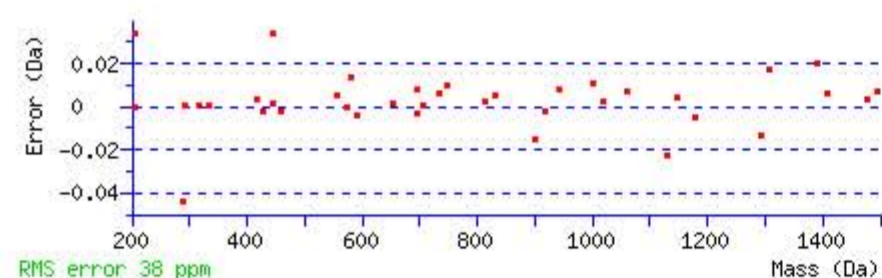
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 50 Expect: 2.5e-005

Matches : 40/172 fragment ions using 67 most intense peaks [\(help\)](#)

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



NCBI BLAST search of **YKDGQCETSPCQNQGK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.0	2324.982407	-0.001205	YKDGQCETSPCQNQGK

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 23577: 1155.605688 from(578.810120,2+) rtinseconds(1399) index(67296)

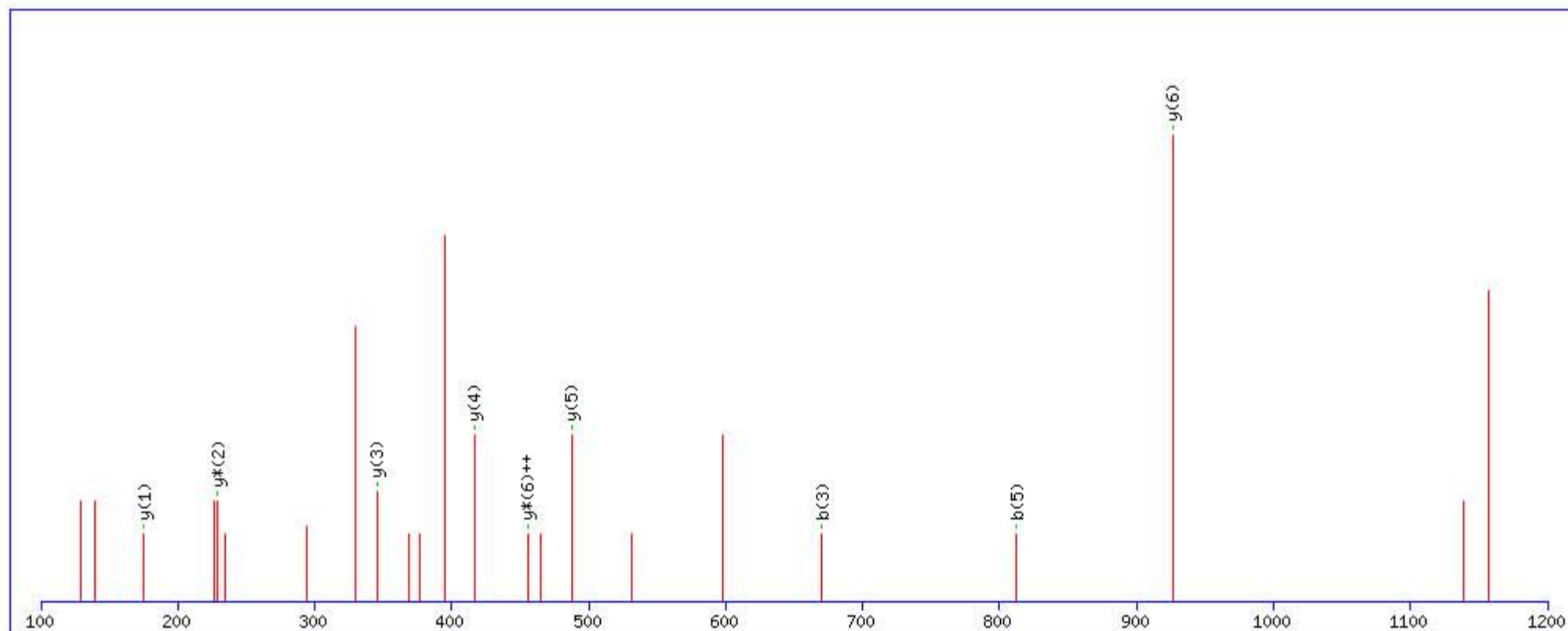
Title: Locus:1.1.1.3020.22 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

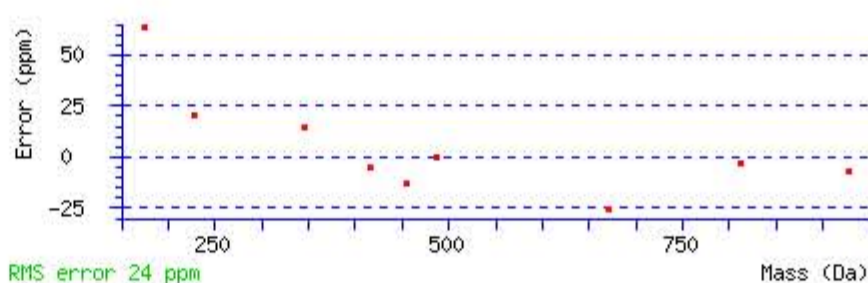
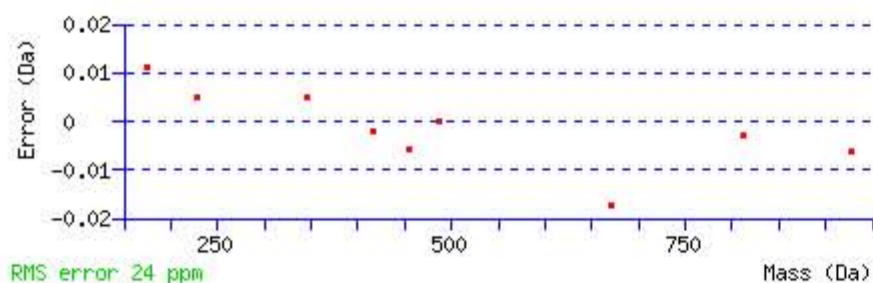
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 26 Expect: 0.016

Matches : 9/68 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	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
26.0	1155.607010	-0.001322	TEQAAVAR
6.9	1155.588394	0.017294	VEQIEAGTPGR

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

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 24866: 1187.581248 from(594.797900,2+) rtinseconds(1736) index(20205)

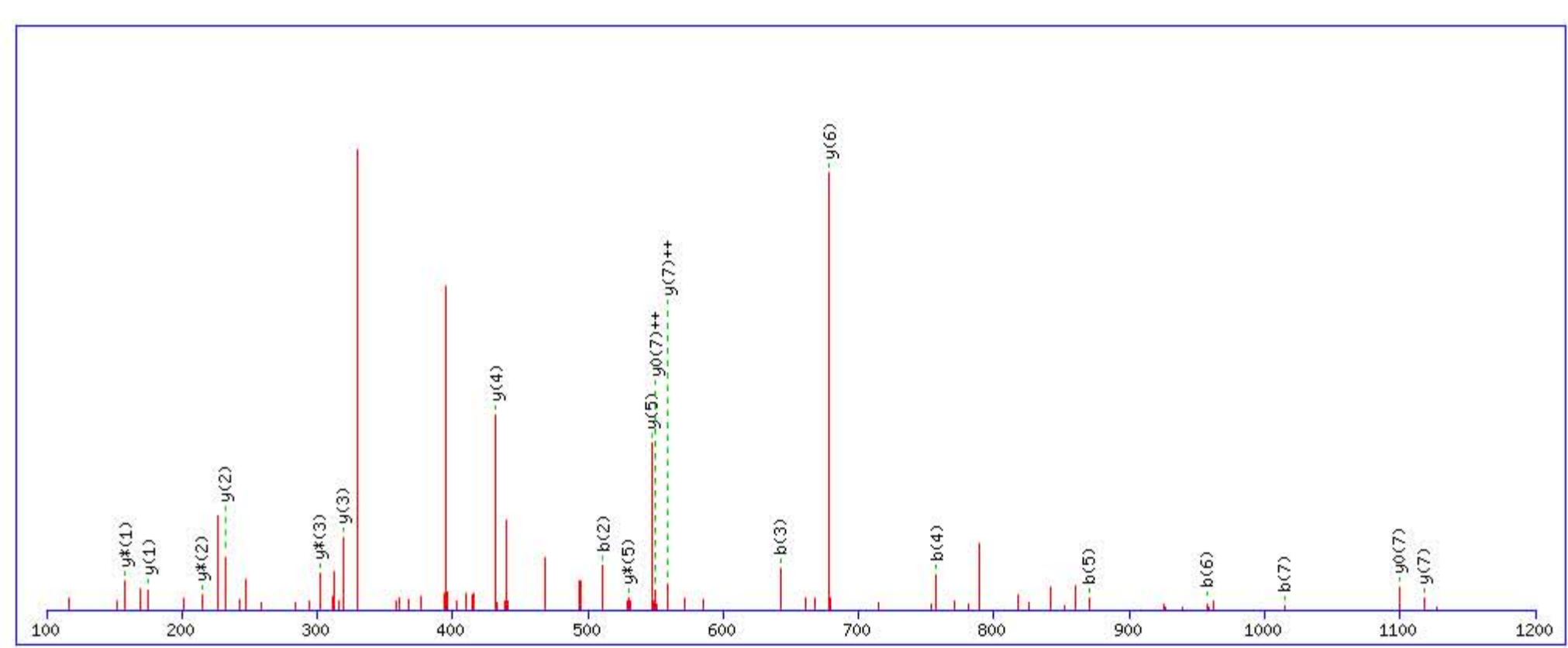
Title: Locus:1.1.1.1486.9 File:"2013-07-02 CLN FXIII 30 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

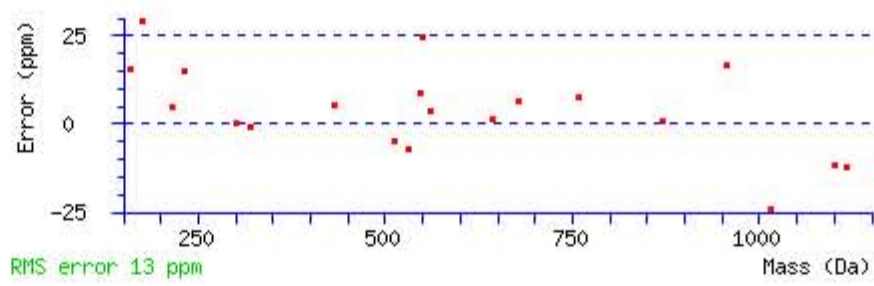
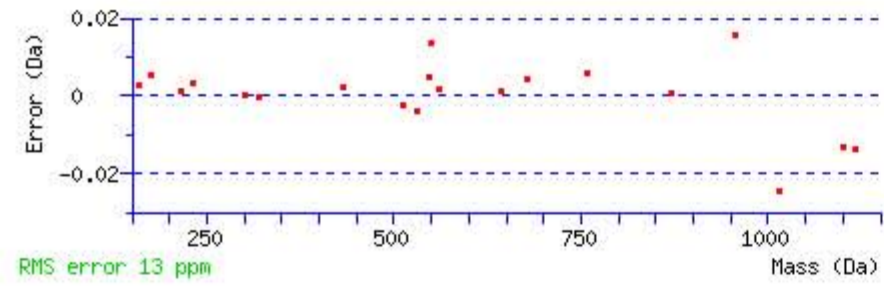
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 37 Expect: 0.0023

Matches : 20/72 fragment ions using 39 most intense peaks [\(help\)](#)

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



NCBI BLAST search of **AQMDLSGR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.2	1187.579086	0.002162	AQMDLSGR
8.5	1187.578201	0.003047	SSLENEPSLGR
8.0	1187.568344	0.012904	DHGFKVSADGR
4.1	1187.579086	0.002162	QAAEVMGR
4.0	1187.568314	0.012934	QREDIWEGR
3.6	1187.564270	0.016978	REERAEQDR
3.4	1187.575714	0.005534	YQDAAGPR
2.0	1187.596832	-0.015584	TLNGAEMAPIR
1.7	1187.593475	-0.012227	AESFPNTPLGR
0.3	1187.564255	0.016993	ARREEENR

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 34549: 1461.650308 from(731.832430,2+) rtinseconds(1450) index(52214)

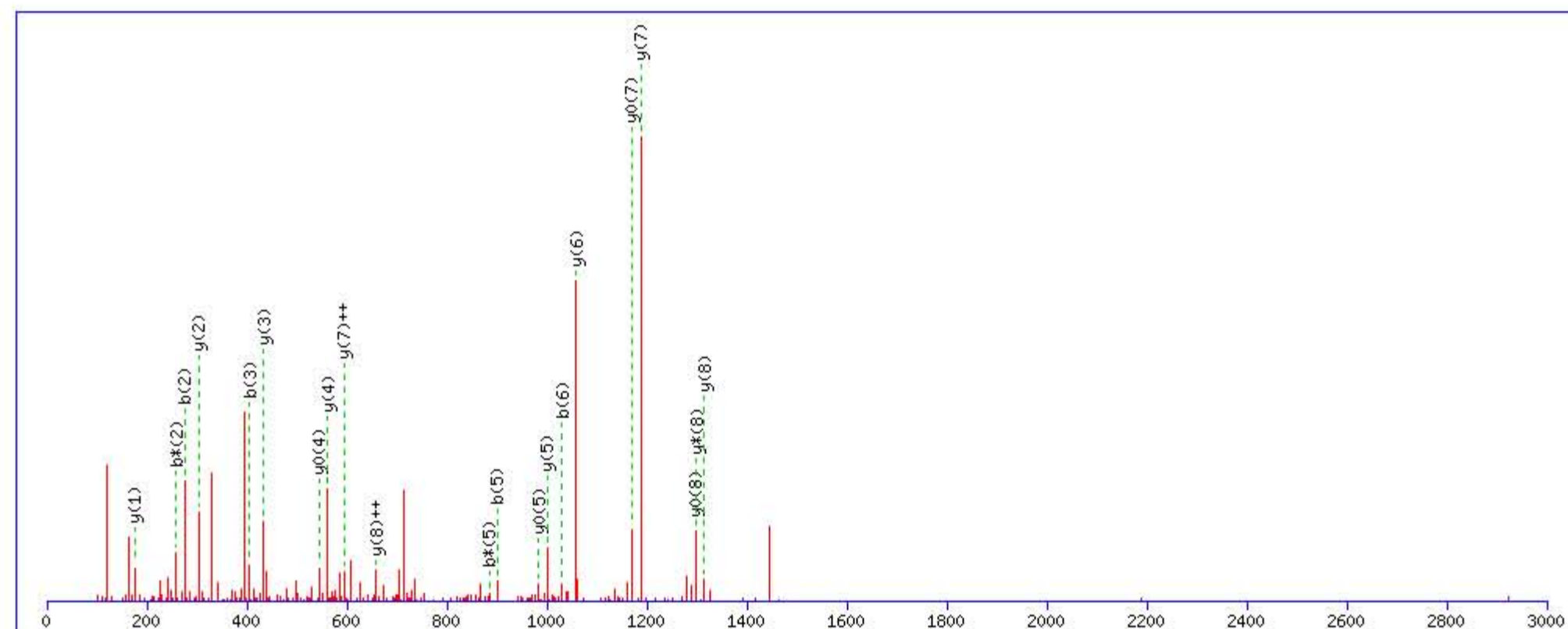
Title: Locus:1.1.1.2991.13 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1461.655807

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

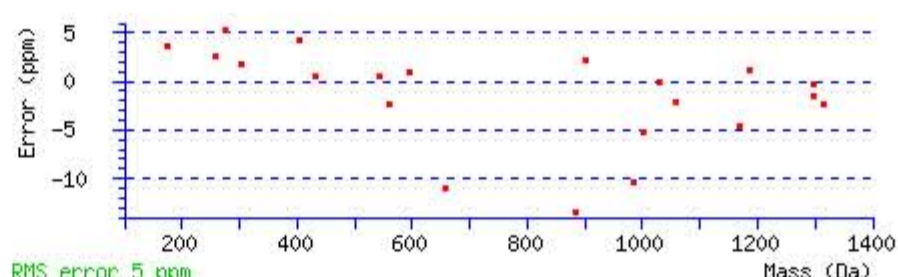
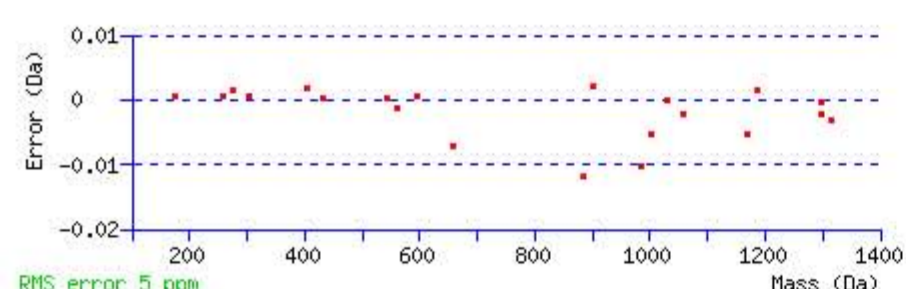
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 46 Expect: 0.00014

Matches : 21/88 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	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
46.4	1461.655807	-0.005499	FQEGQEEER
11.0	1461.640564	0.009744	NSGTQSDGEEK
9.1	1461.655807	-0.005499	FQEGQEEER
8.1	1461.648392	0.001916	HREELSDYEER
7.5	1461.640564	0.009744	VMTDVAGNPEEER
3.4	1461.637161	0.013147	ESELQWQEEER
0.1	1461.657166	-0.006858	CSFSPWTEHRR

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 43990: 1766.908092 from(589.976640,3+) rtinseconds(1960) index(55531)

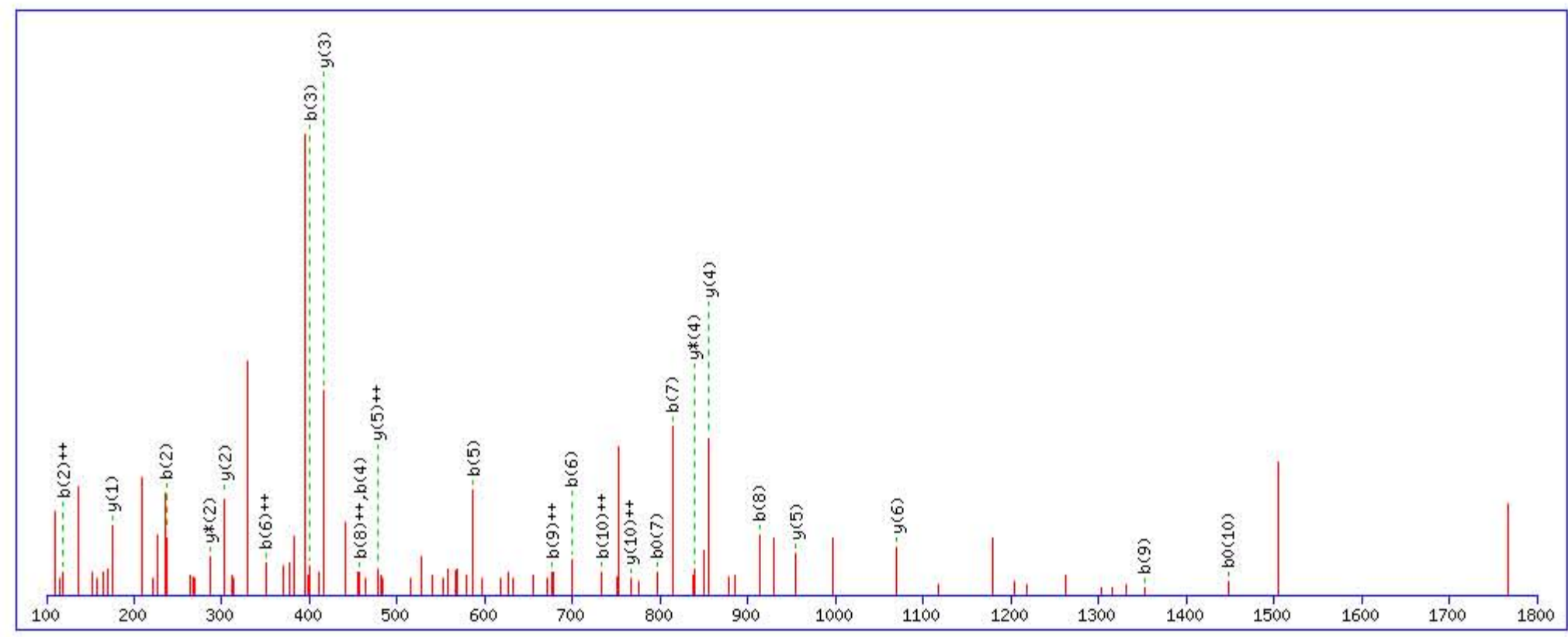
Title: Locus:1.1.1.3168.13 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1766.913773

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

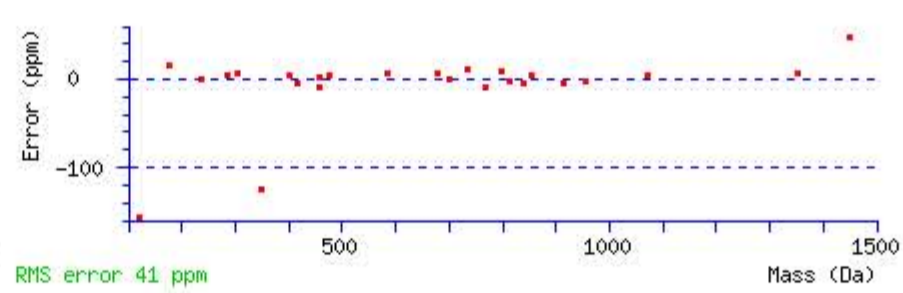
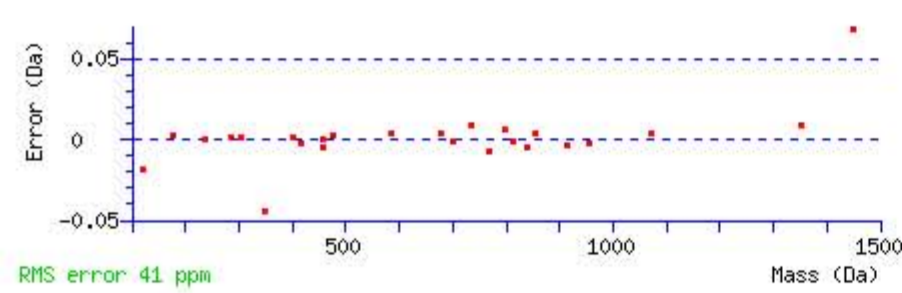
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.0071

Matches : 25/98 fragment ions using 65 most intense peaks [\(help\)](#)

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



NCBI BLAST search of **HVYGELDVQIQR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.8	1766.913773	-0.005681	HVYGELDVQIQR
11.9	1766.913773	-0.005681	HVYGELDVQIQR
3.9	1766.924988	-0.016896	GNFPVEAVKMQHALAR

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

MASCOT 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 44166: 1772.815812 from(591.945880,3+) rtinseconds(1840) index(54599)

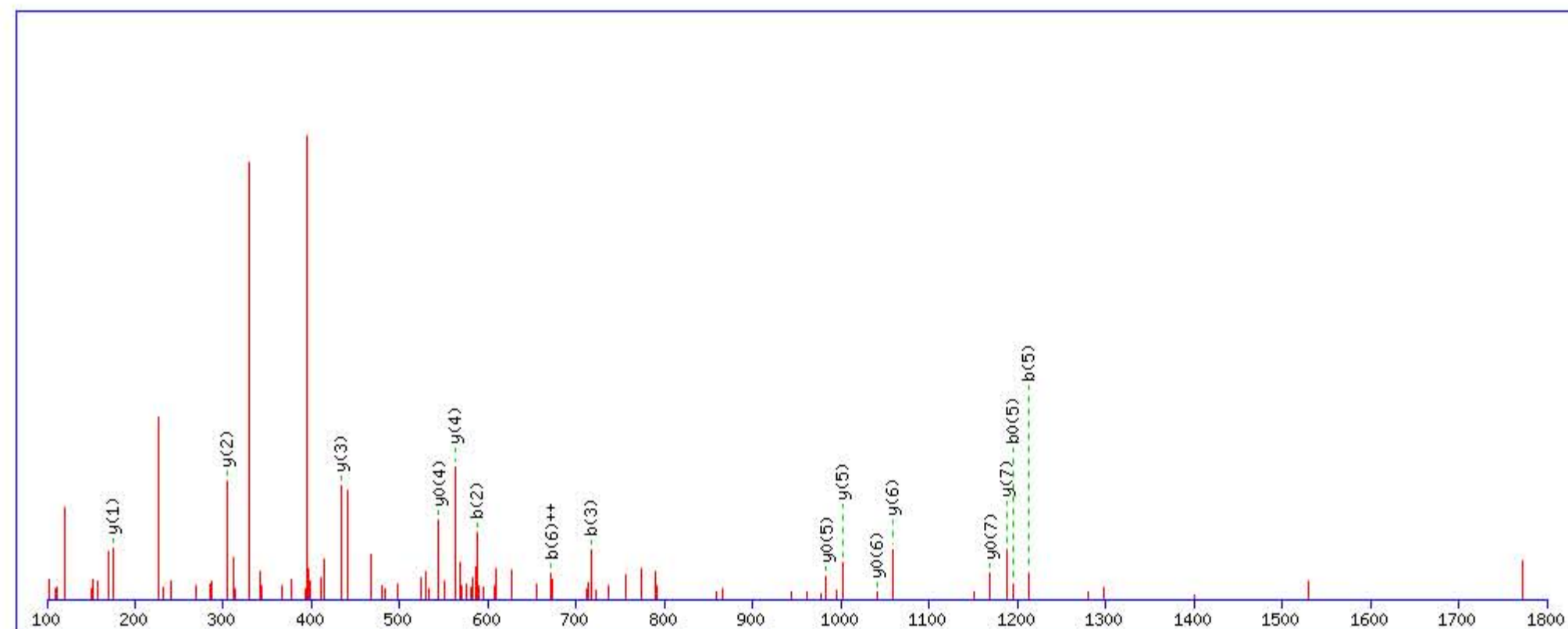
Title: Locus:1.1.1.3127.7 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1772.822556

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

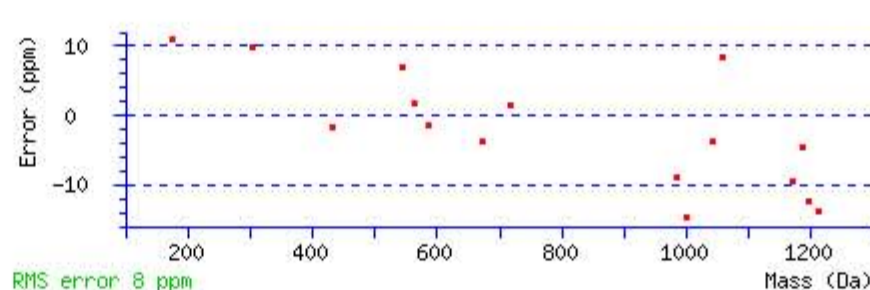
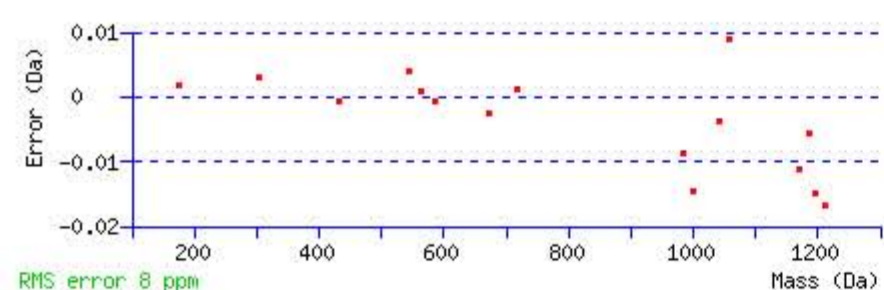
Q2 : Biotin:Thermo-21345 (Q)

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 26 Expect: 0.029

Matches : 16/88 fragment ions using 36 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	148.075690	74.541483					F							9
2	587.301016	294.154146	570.274467	285.640872			Q	1626.761440	813.884358	1609.734891	805.371084	1608.750875	804.879076	8
3	716.343609	358.675443	699.317060	350.162168	698.333044	349.670160	E	1187.536114	594.271695	1170.509565	585.758421	1169.525549	585.266413	7
4	773.365073	387.186175	756.338524	378.672900	755.354508	378.180892	G	1058.493521	529.750399	1041.466972	521.237124	1040.482956	520.745116	6
5	1212.590399	606.798837	1195.563850	598.285563	1194.579834	597.793555	Q	1001.472057	501.239667	984.445508	492.726392	983.461492	492.234384	5
6	1341.632992	671.320134	1324.606443	662.806860	1323.622427	662.314852	E	562.246731	281.627004	545.220182	273.113729	544.236166	272.621721	4
7	1470.675585	735.841431	1453.649036	727.328156	1452.665020	726.836148	E	433.204138	217.105707	416.177589	208.592433	415.193573	208.100425	3
8	1599.718178	800.362727	1582.691629	791.849453	1581.707613	791.357445	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
9							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **FQEGQEEER**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.1	1772.822556	-0.006744	FQEGQEEER
16.3	1772.803909	0.011903	ESELQWQEEER
2.8	1772.798752	0.017060	HISSCMRWPGHYSR
0.7	1772.811127	0.004685	QHELSESCSASALQAR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **GTYPVPIVSELQSGK**

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

Match to Query 49031: 1998.084522 from(667.035450,3+) rtinseconds(2759) index(76009)

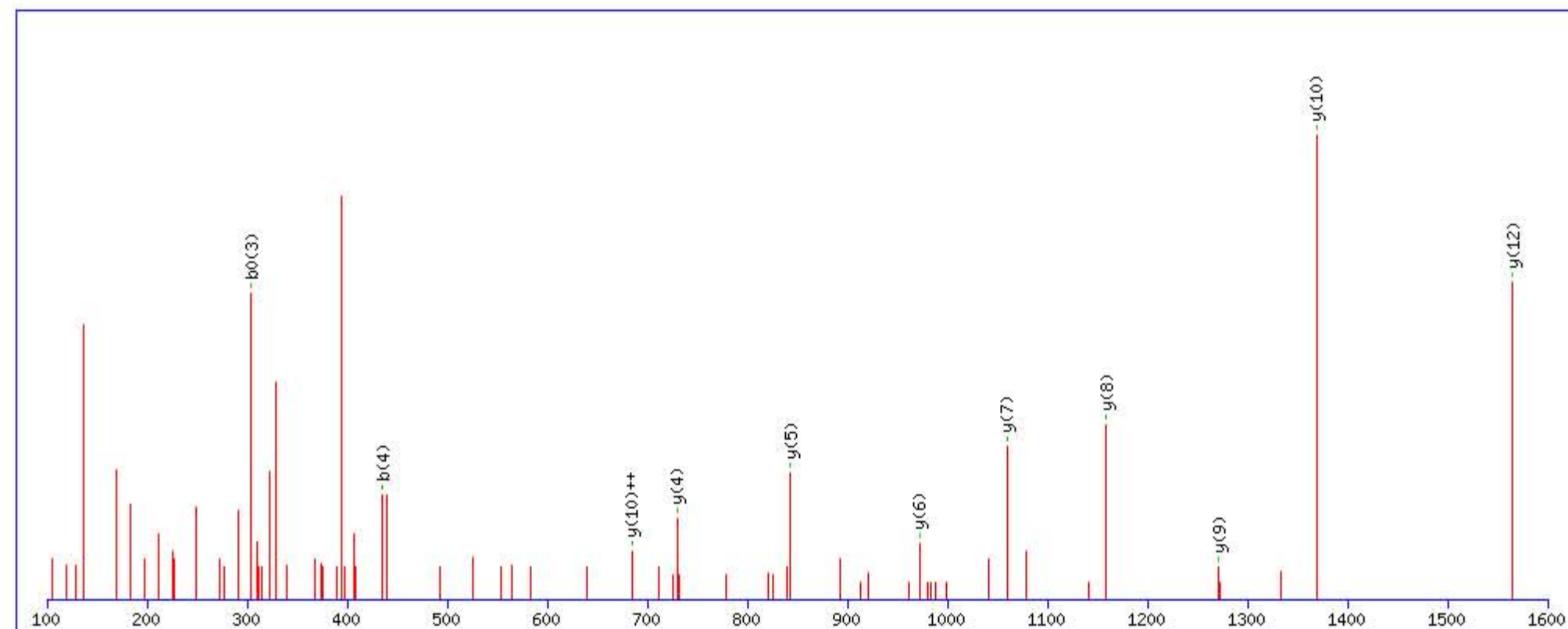
Title: Locus:1.1.1.3493.15 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

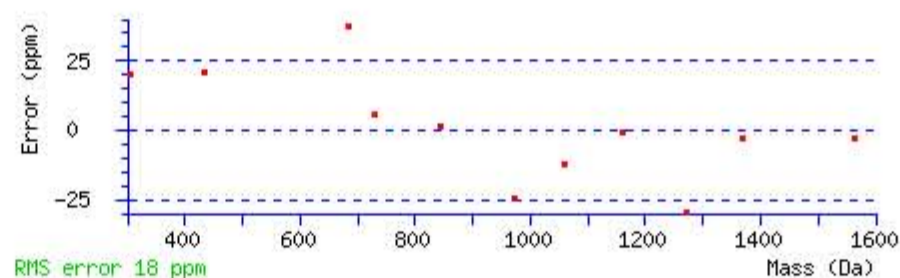
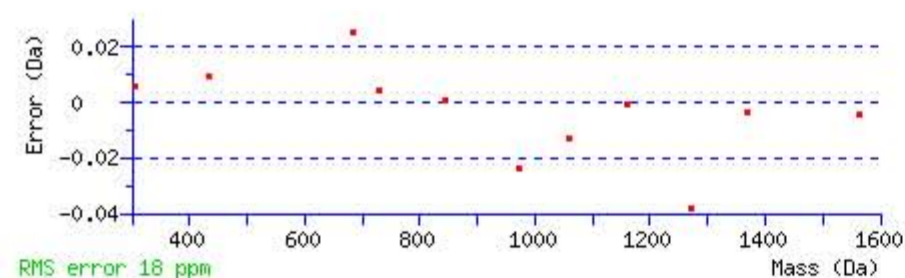
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 62 Expect: 2.4e-006

Matches : 11/150 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 **GTYPVPIVSELQSGK**

(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	1998.085983	-0.001461	GTYPVPIVSELQSGK
1.9	1998.099731	-0.015209	GDEVVVELVENGKKVTVGK

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 55079: 2255.203932 from(752.741920,3+) rtinseconds(3007) index(77876)

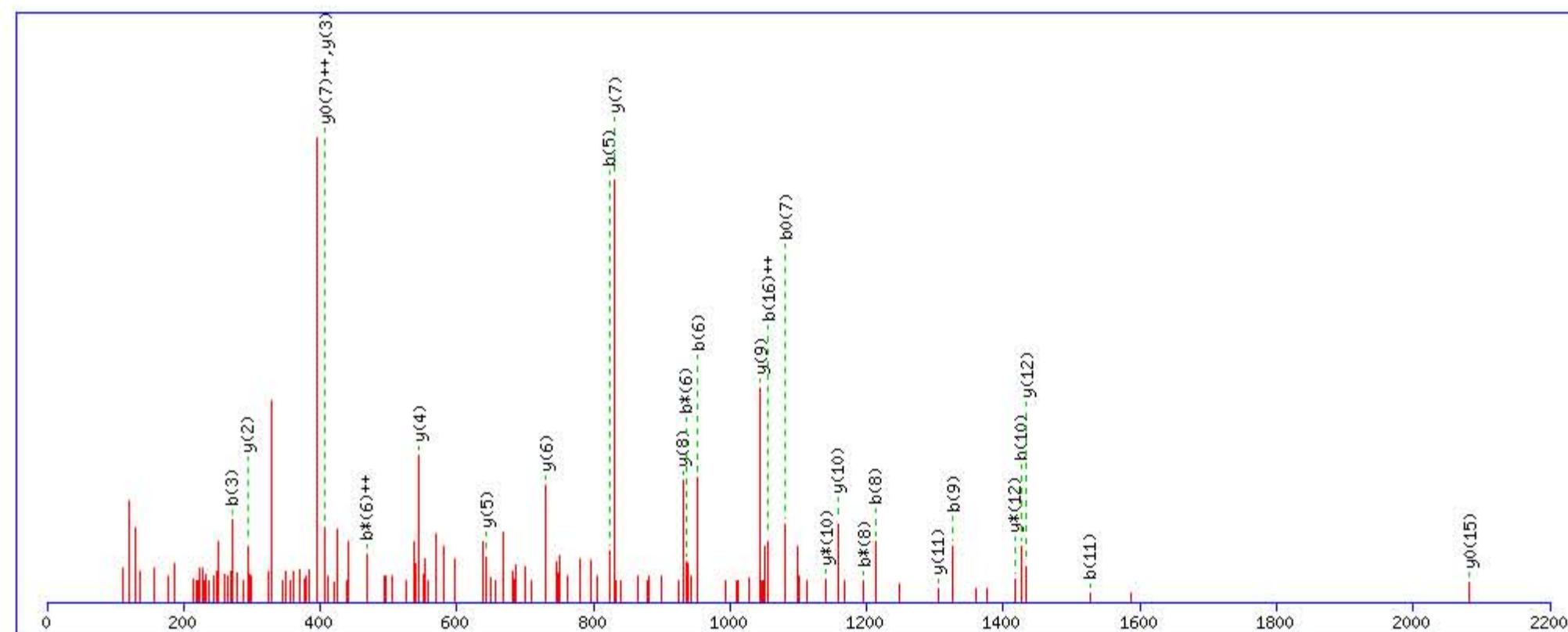
Title: Locus:1.1.1.3578.10 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

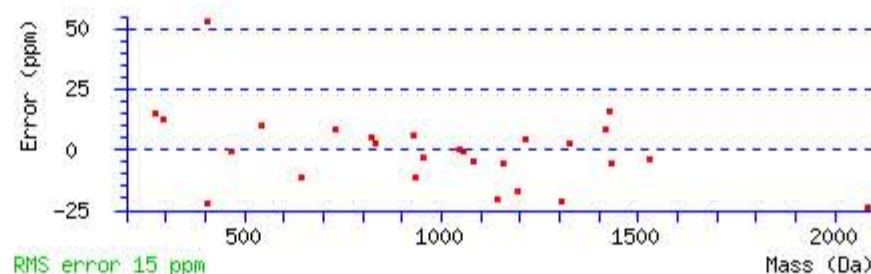
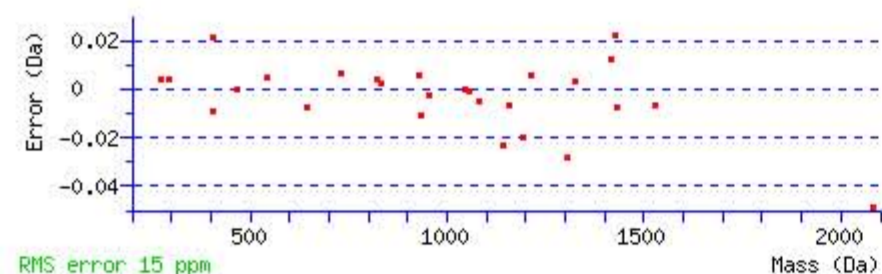
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 62 Expect: 3.2e-006

Matches : 27/168 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							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
61.6	2255.213654	-0.009722	GVNLQEFLNVTSVHLFK
3.0	2255.177032	0.026900	RPEYRHLSTGDISAQKELR

MASCOT Search Results

Peptide View

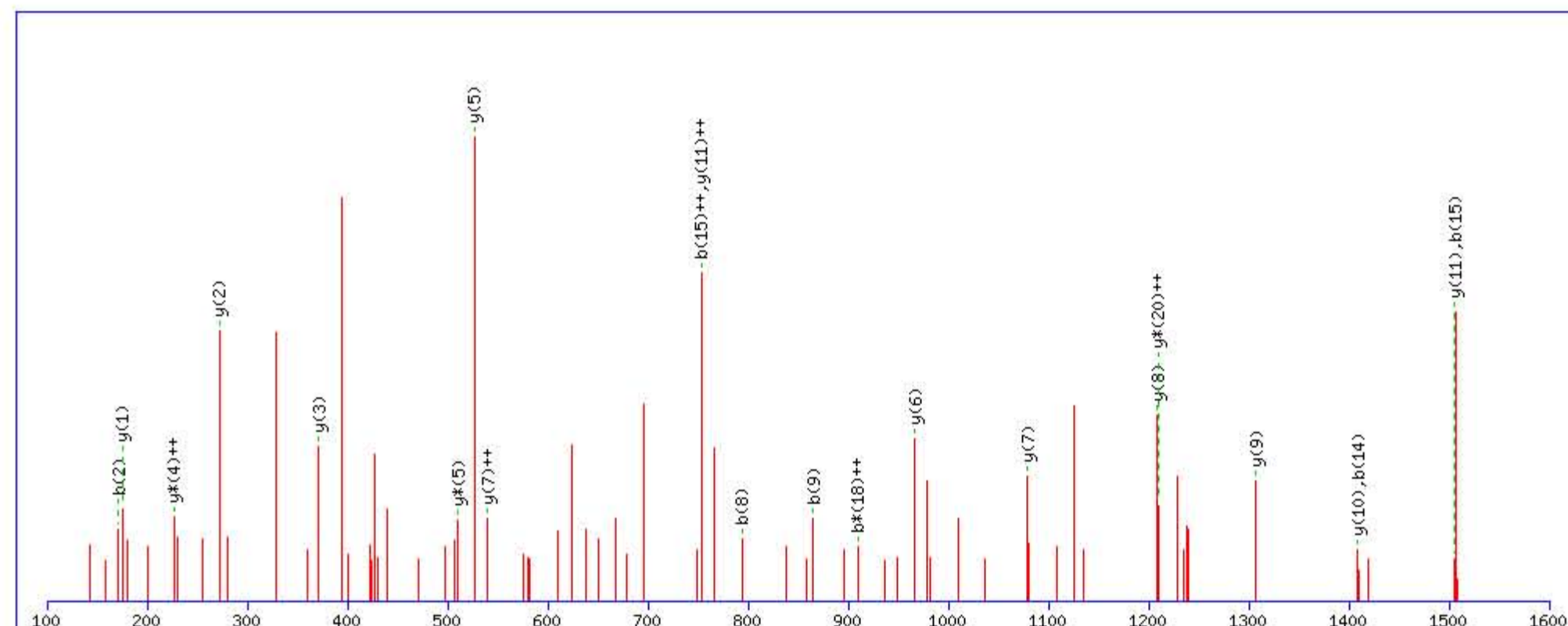
MS/MS Fragmentation of **AVPPNNSNAEEDDLPTVELQGVVPR**
 Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

Match to Query 64647: 2912.463456 from(729.123140,4+) rtinseconds(2488) index(74148)
 Title: Locus:1.1.1.3400.14 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

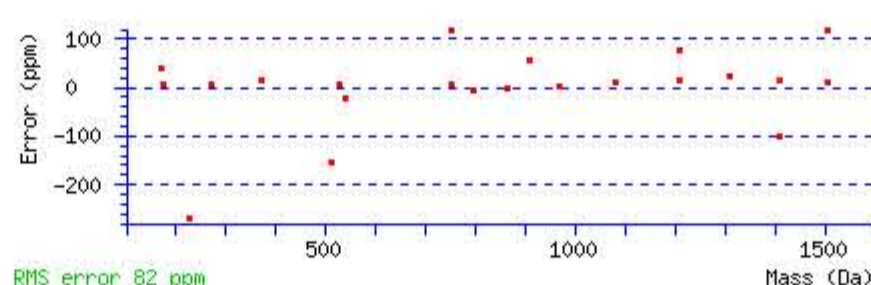
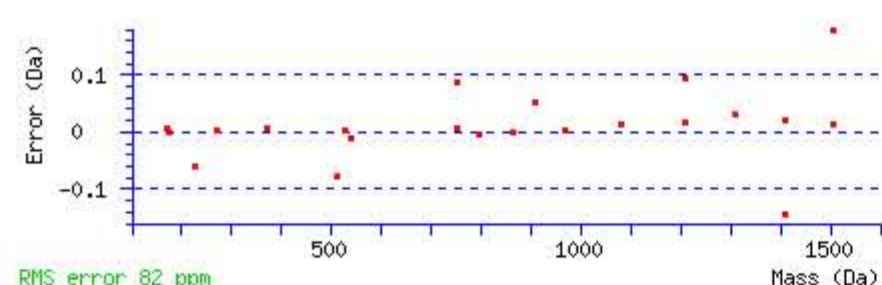
Or, Plot from to Da

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: 43 Expect: 0.00033
 Matches : 22/254 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							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 **AVPPNNSNAEEDDLPTVELQGVVPR**
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.0	2912.470200	-0.006744	AVPPNNSNAEEDDLPTVELQGVVPR
5.5	2912.492661	-0.029205	TNHSSPEAQSKQTGRVLEPPVPSR
4.1	2912.492661	-0.029205	TNHSSPEAQSKQTGRVLEPPVPSR
0.3	2912.506577	-0.043121	VQQNMFSGSEDIAVERVISVEPLLPR
0.0	2912.482285	-0.018829	YTQDHKQMKGRPSLILDTPAMR
0.0	2912.482285	-0.018829	YTQDHKQMKGRPSLILDTPAMR

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 28711: 1312.707848 from(657.361200,2+) rtinseconds(1822) index(37453)

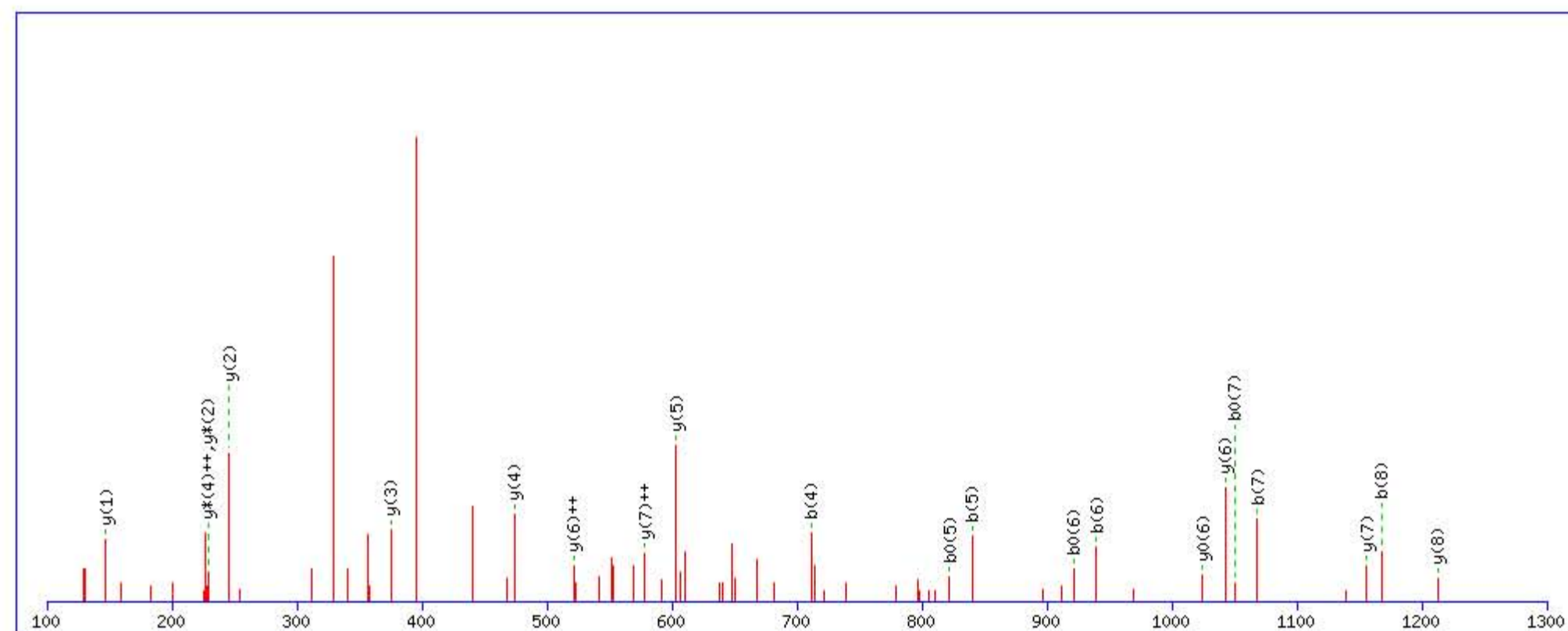
Title: Locus:1.1.1.2657.12 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

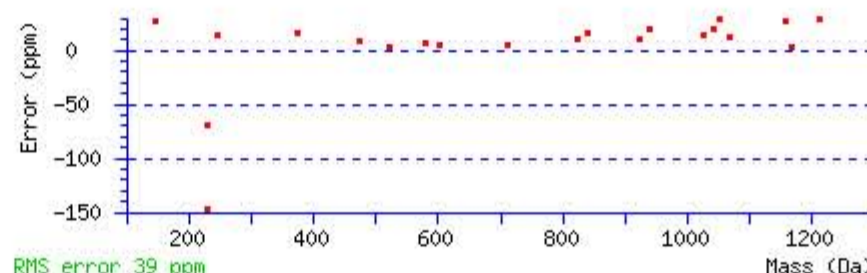
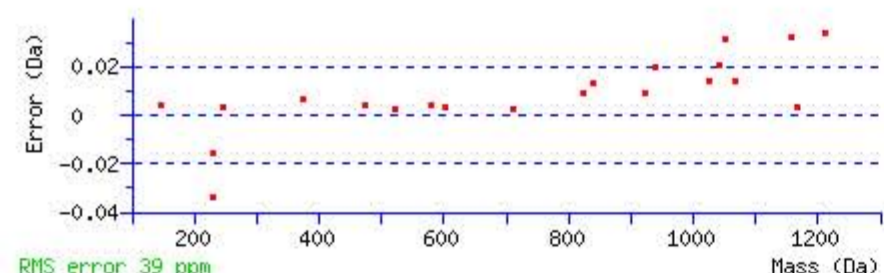
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 55 Expect: 0.00019

Matches : 21/86 fragment ions using 33 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	102.054955	51.531116			84.044390	42.525833	T							9
2	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
55.3	1312.706070	0.001778	TGLQEVEVK
15.0	1312.713913	-0.006065	KVFEKYTTAAR
7.6	1312.699524	0.008324	TIMHLMINNVK
5.1	1312.721130	-0.013282	QVEVLTNQRR
3.3	1312.691422	0.016426	YKELYLEEVEK
2.9	1312.717300	-0.009452	ASLQTVDIR
2.5	1312.692139	0.015709	DRQSQIQK
2.5	1312.706055	0.001793	LQSELGVEK
2.4	1312.702682	0.005166	IQYSLGKYDVK
2.4	1312.721115	-0.013267	KKPQRDSQAQK

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 38964: 1599.779472 from(534.267100,3+) rtinseconds(1533) index(35784)

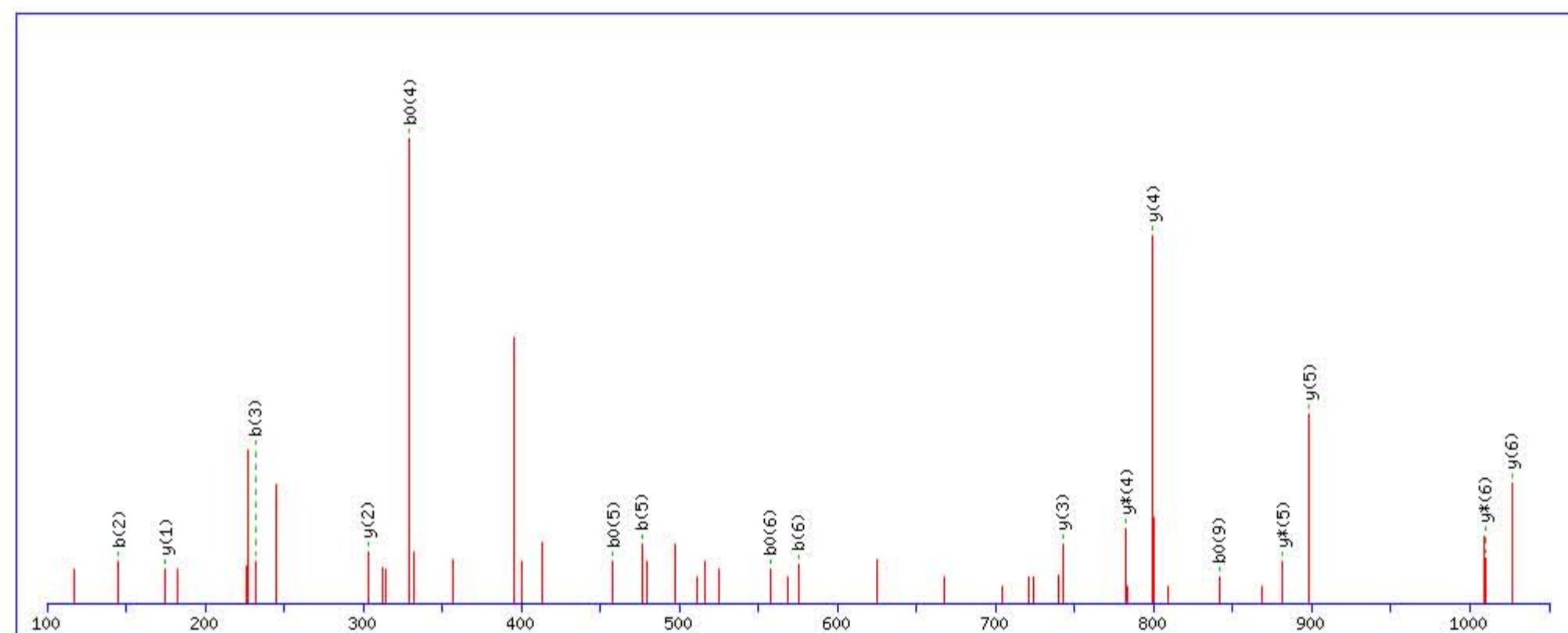
Title: Locus:1.1.1.2556.9 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

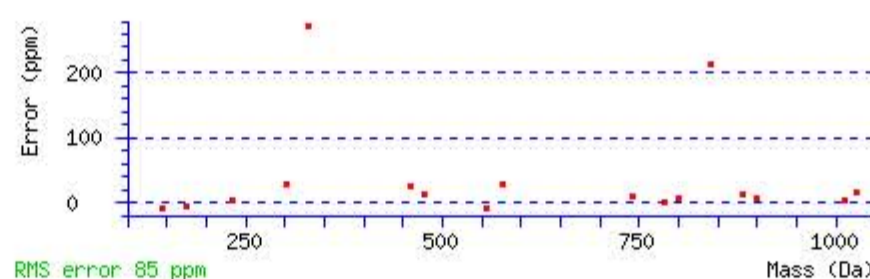
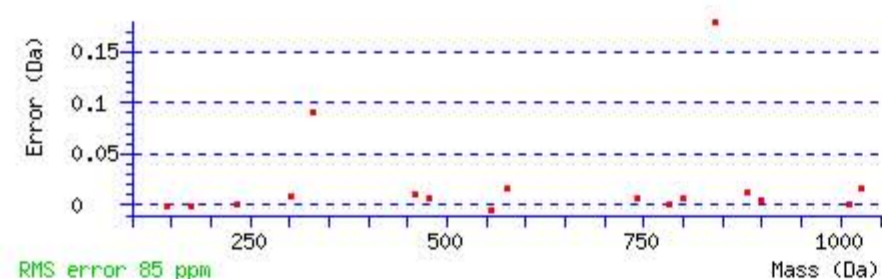
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 32 Expect: 0.0011

Matches : 17/106 fragment ions using 34 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	88.039304	44.523290			70.028739	35.518008	S							12
2	145.060768	73.034022			127.050203	64.028740	G	1513.742754	757.375015	1496.716205	748.861741	1495.732189	748.369733	11
3	232.092796	116.550036			214.082231	107.544753	S	1456.721290	728.864283	1439.694741	720.351009	1438.710725	719.859001	10
4	347.119739	174.063507			329.109174	165.058225	D	1369.689262	685.348269	1352.662713	676.834995	1351.678697	676.342987	9
5	476.162332	238.584804			458.151767	229.579522	E	1254.662319	627.834798	1237.635770	619.321523	1236.651754	618.829515	8
6	575.230746	288.119011			557.220181	279.113729	V	1125.619726	563.313501	1108.593177	554.800227			7
7	703.289324	352.148300	686.262775	343.635026	685.278759	343.143018	Q	1026.551312	513.779294	1009.524763	505.266020			6
8	802.357738	401.682507	785.331189	393.169233	784.347173	392.677225	V	898.492734	449.750005	881.466185	441.236731			5
9	859.379202	430.193239	842.352653	421.679965	841.368637	421.187957	G	799.424320	400.215798	782.397771	391.702524			4
10	1298.604528	649.805902	1281.577979	641.292628	1280.593963	640.800620	Q	742.402856	371.705066	725.376307	363.191792			3
11	1426.663106	713.835191	1409.636557	705.321917	1408.652541	704.829909	Q	303.177530	152.092403	286.150981	143.579129			2
12							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **SGSDEVQVGQQR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.4	1599.767517	0.011955	SGSDEVQVGQQR
25.3	1599.767517	0.011955	SGSDEVQVGQQR
9.3	1599.767517	0.011955	SGSDEVQVGQQR
0.8	1599.771515	0.007957	YVTSAPMPEPQAPGR
0.6	1599.793961	-0.014489	VGAPAWREAAQAMAR
0.2	1599.763641	0.015831	MLCGNSLLGYLSEK

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 42274: 1699.848432 from(567.623420,3+) rtinseconds(1385) index(51739)

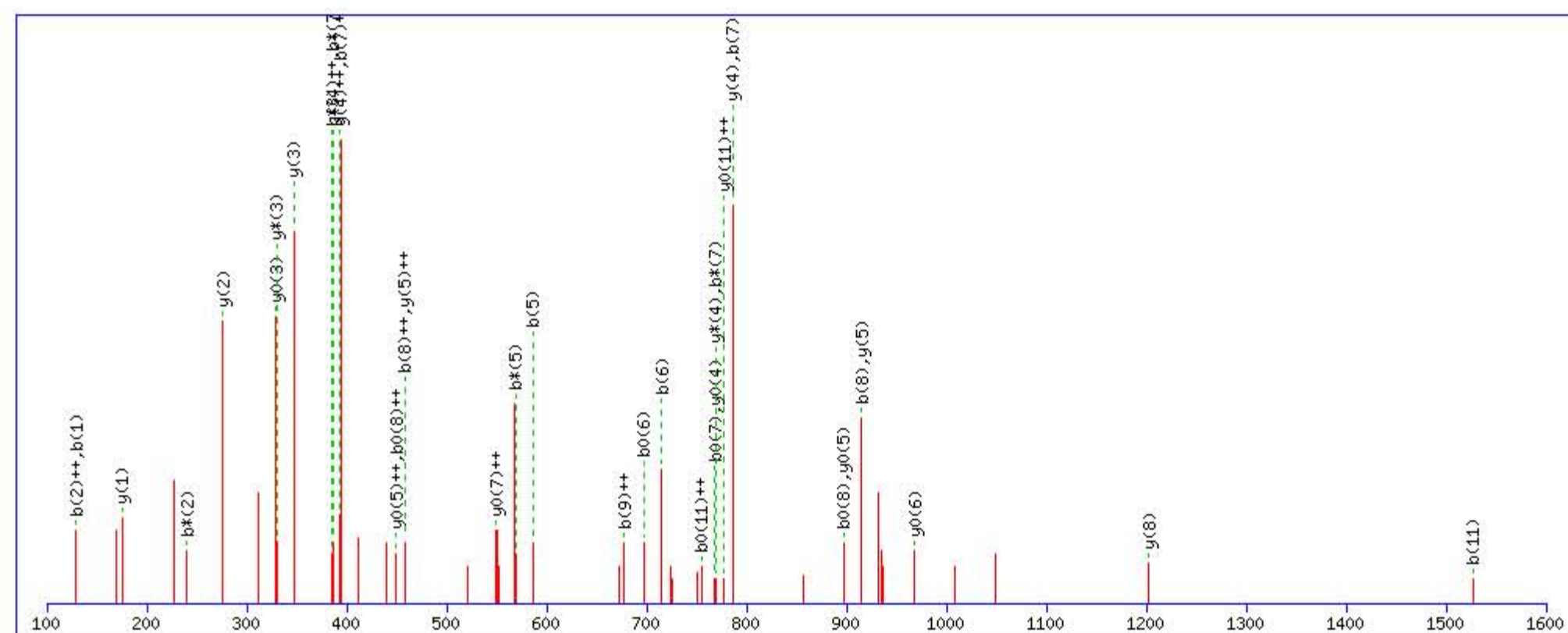
Title: Locus:1.1.1.2968.22 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

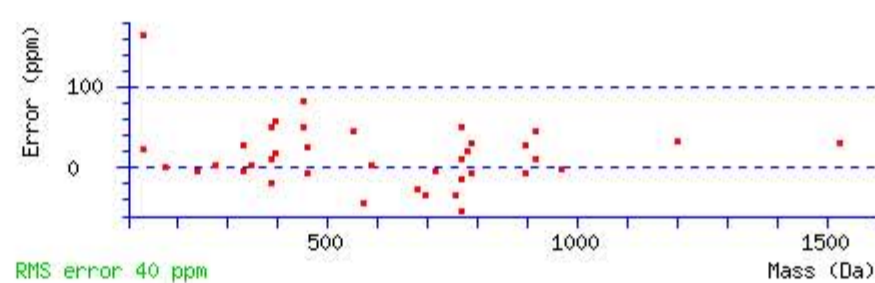
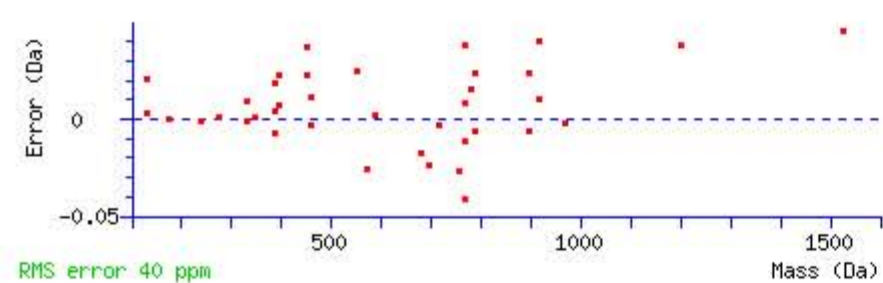
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 37 Expect: 0.0039

Matches : 38/126 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	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
37.1	1699.856277	-0.007845	KQELSEAEQATR
17.6	1699.856277	-0.007845	KQELSEAEQATR
10.8	1699.845932	0.002500	QAMQEQLSK
5.9	1699.849792	-0.001360	QEMRTTQLGPGR
5.8	1699.845932	0.002500	QAMQEQLSK
5.4	1699.839874	0.008558	QKMFQHRENK
1.7	1699.843063	0.005369	GKVSEGIDFVHHYGR
1.6	1699.832016	0.016416	EPQRGMGSMGPKR
1.6	1699.832016	0.016416	EPQRGMGSMGPKR
1.2	1699.846405	0.002027	HQEVKMQAPAFRDK

MASCOT 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 44102: 1769.980452 from(591.000760,3+) rtinseconds(1894) index(37845)

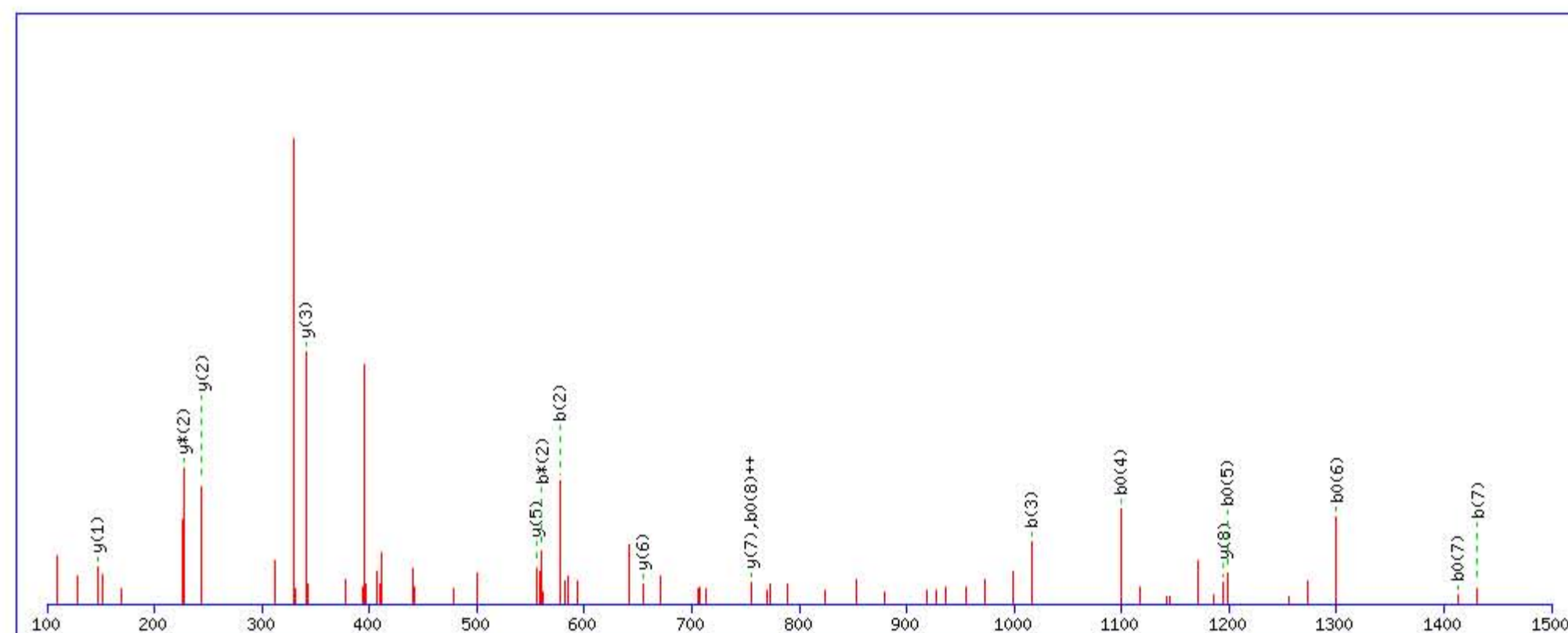
Title: Locus:1.1.1.2682.18 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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:

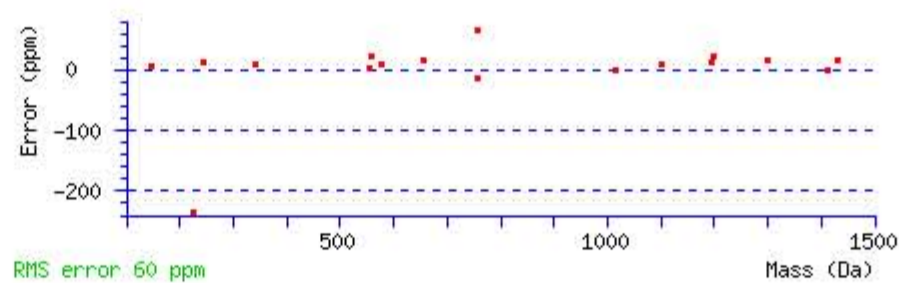
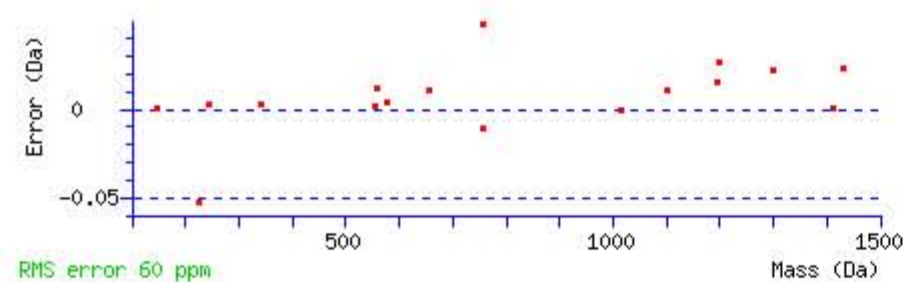
Q2 : Biotin:Thermo-21345 (Q)

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 28 Expect: 0.018

Matches : 17/92 fragment ions using 37 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	138.066188	69.536732					H							10
2	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
28.1	1769.968460	0.011992	HQQTVTIPPK
9.0	1769.997437	-0.016985	AVPPRMPAVNLGQVPPK
0.9	1769.961029	0.019423	WMLSRDRASTLPLPK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **GQGTLSSVVTMYHAK**

Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

Match to Query 44743: 1801.918842 from(601.646890,3+) rtinseconds(1988) index(55746)

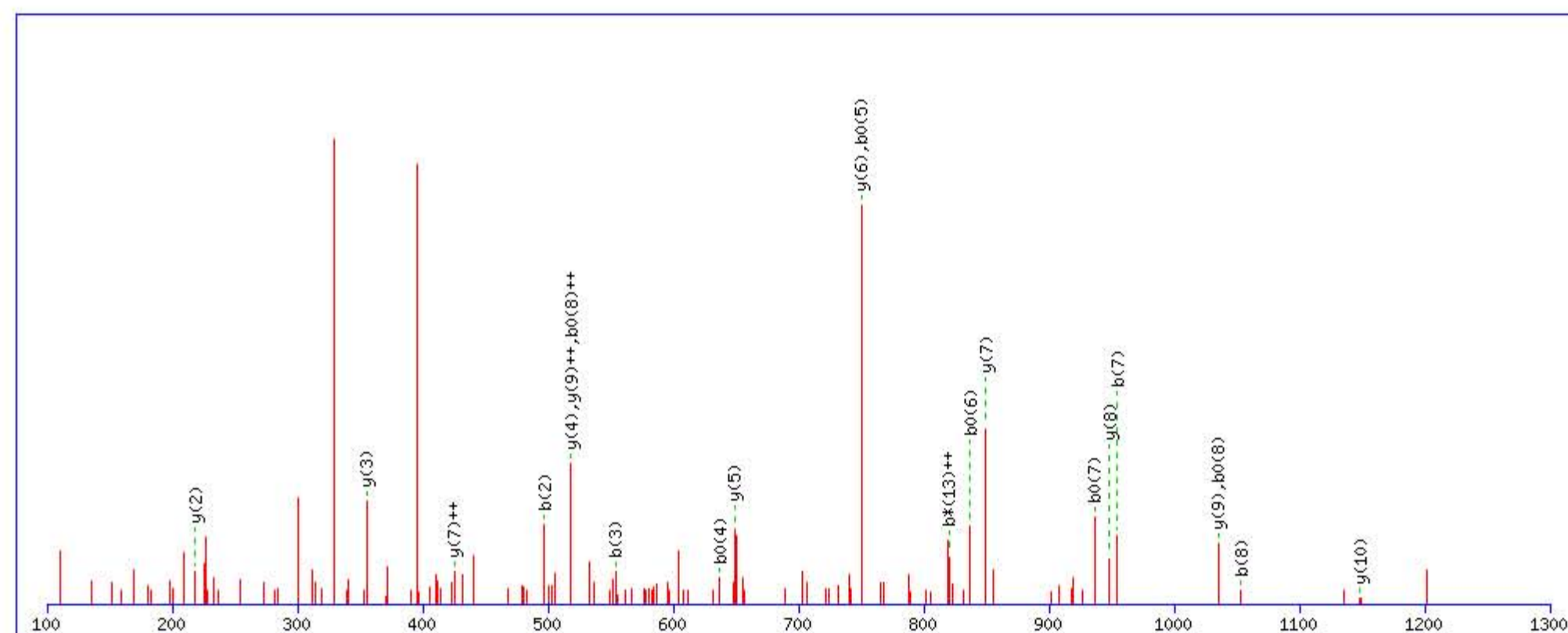
Title: Locus:1.1.1.3178.8 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1801.921906

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

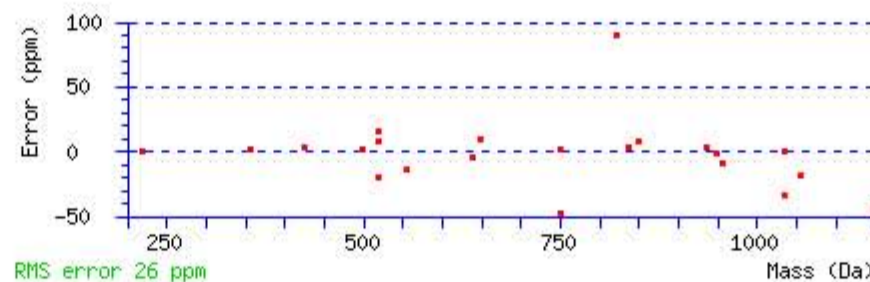
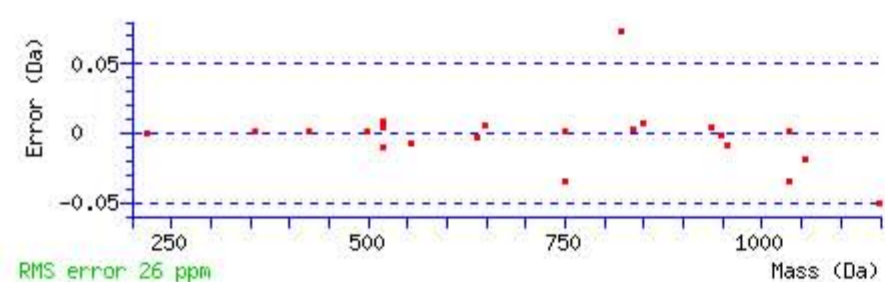
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 41 Expect: 0.00056

Matches : 22/138 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	58.028740	29.518008					G							14
2	497.254066	249.130671	480.227517	240.617397			Q	1745.907712	873.457494	1728.881163	864.944220	1727.897147	864.452212	13
3	554.275530	277.641403	537.248981	269.128129			G	1306.682386	653.844831	1289.655837	645.331557	1288.671821	644.839549	12
4	655.323209	328.165243	638.296660	319.651968	637.312644	319.159960	T	1249.660922	625.334099	1232.634373	616.820825	1231.650357	616.328817	11
5	768.407273	384.707275	751.380724	376.194000	750.396708	375.701992	L	1148.613243	574.810260	1131.586694	566.296985	1130.602678	565.804977	10
6	855.439301	428.223289	838.412752	419.710014	837.428736	419.218006	S	1035.529179	518.268228	1018.502630	509.754953	1017.518614	509.262945	9
7	954.507715	477.757496	937.481166	469.244221	936.497150	468.752213	V	948.497151	474.752214	931.470602	466.238939	930.486586	465.746931	8
8	1053.576129	527.291703	1036.549580	518.778428	1035.565564	518.286420	V	849.428737	425.218007	832.402188	416.704732	831.418172	416.212724	7
9	1154.623808	577.815542	1137.597259	569.302268	1136.613243	568.810260	T	750.360323	375.683800	733.333774	367.170525	732.349758	366.678517	6
10	1285.664293	643.335785	1268.637744	634.822510	1267.653728	634.330502	M	649.312644	325.159960	632.286095	316.646686			5
11	1448.727622	724.867449	1431.701073	716.354175	1430.717057	715.862167	Y	518.272159	259.639718	501.245610	251.126443			4
12	1585.786534	793.396905	1568.759985	784.883631	1567.775969	784.391623	H	355.208830	178.108053	338.182281	169.594778			3
13	1656.823648	828.915462	1639.797099	820.402188	1638.813083	819.910180	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 **GQGTLSSVVTMYHAK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.9	1801.921906	-0.003064	GQGTLSSVVTMYHAK
6.0	1801.928421	-0.009579	KFMTLDPVSDALPPK
2.9	1801.896729	0.022113	QDNERVLFAPMR

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

MASCOT SCIENCE 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 51933: 2098.138962 from(700.386930,3+) rtinseconds(2334) index(40717)

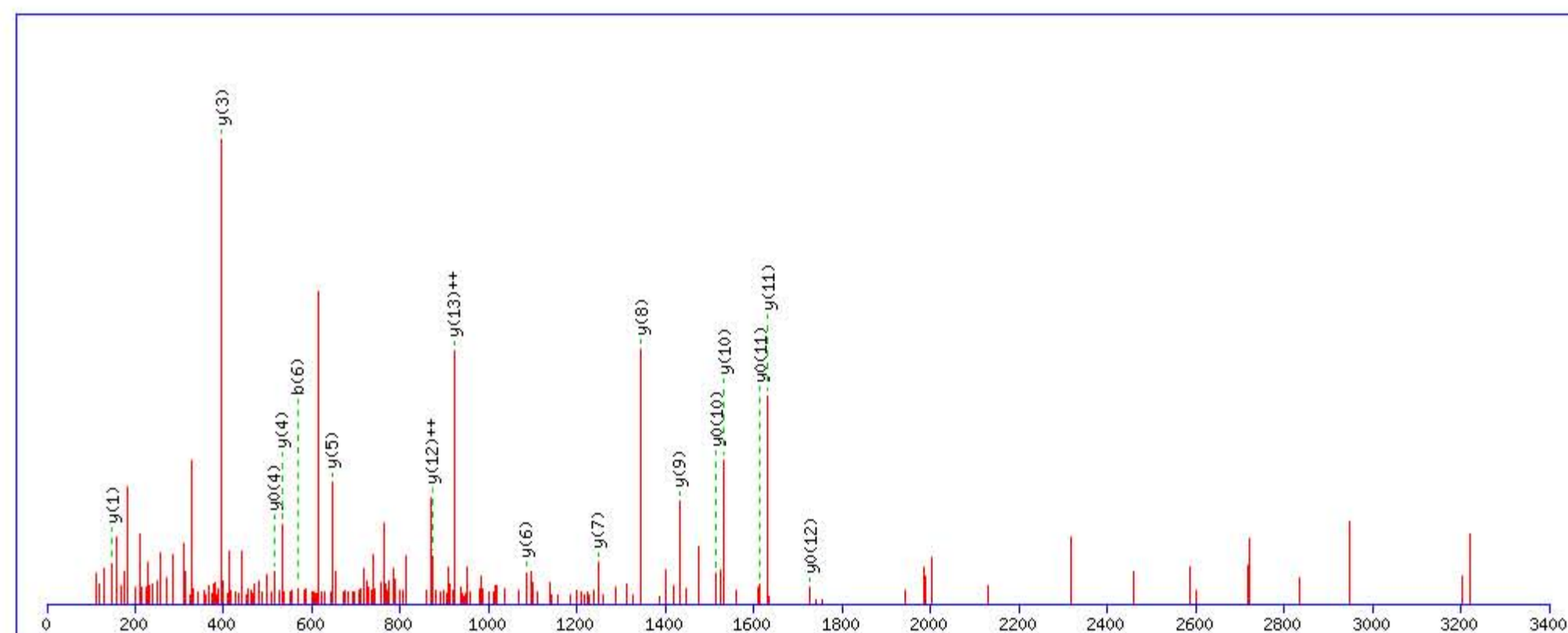
Title: Locus:1.1.1.2835.10 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

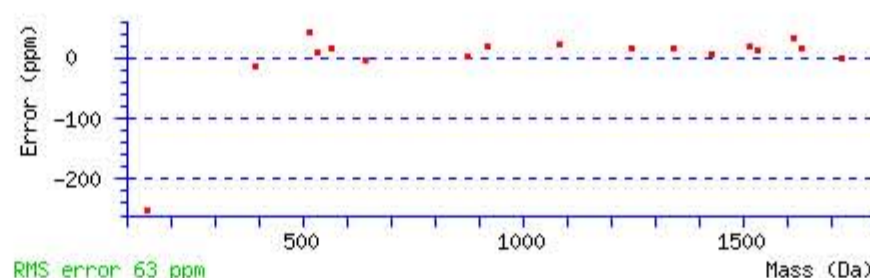
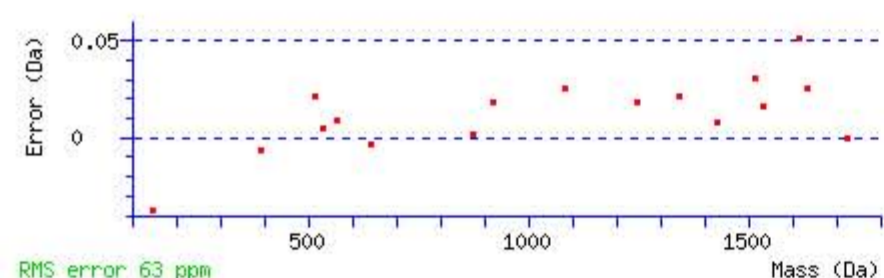
Variable modifications:

Q11 : Biotin:Thermo-21345 (Q)

Ions Score: 33 Expect: 0.0096

Matches : 17/158 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	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
32.8	2098.128525	0.010437	SGIPIVTSPYQIHFTK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **LSINTHPSQKPLSITVR**

Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

Match to Query 53934: 2201.228896 from(551.314500,4+) rtinseconds(1880) index(54855)

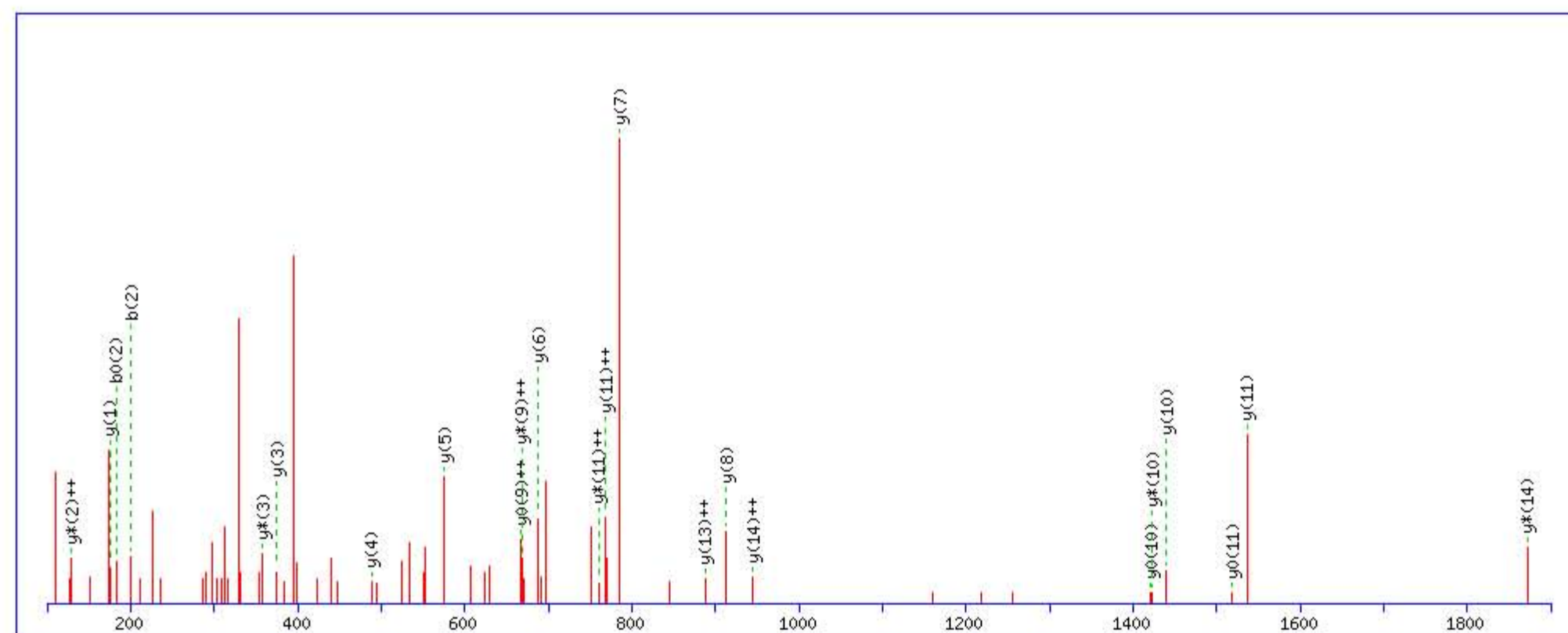
Title: Locus:1.1.1.3141.12 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 2201.235428

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

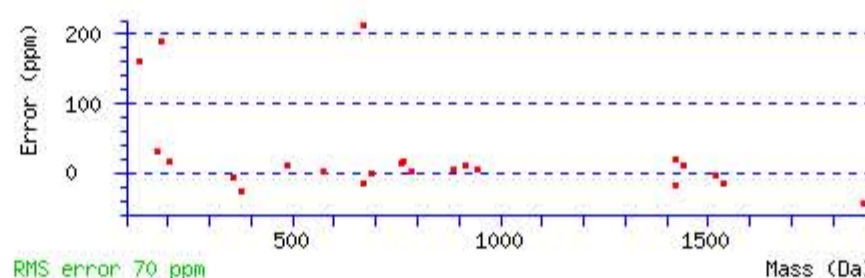
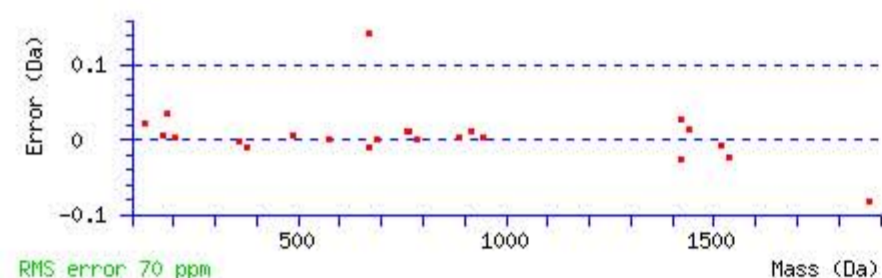
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 28 Expect: 0.016

Matches : 23/180 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					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	$M_r(\text{calc})$:	Delta	Sequence
27.6	2201.235428	-0.006532	LSINTHPSQKPLSITVR

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

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 58644: 2457.239472 from(820.087100,3+) rtinseconds(2493) index(41648)

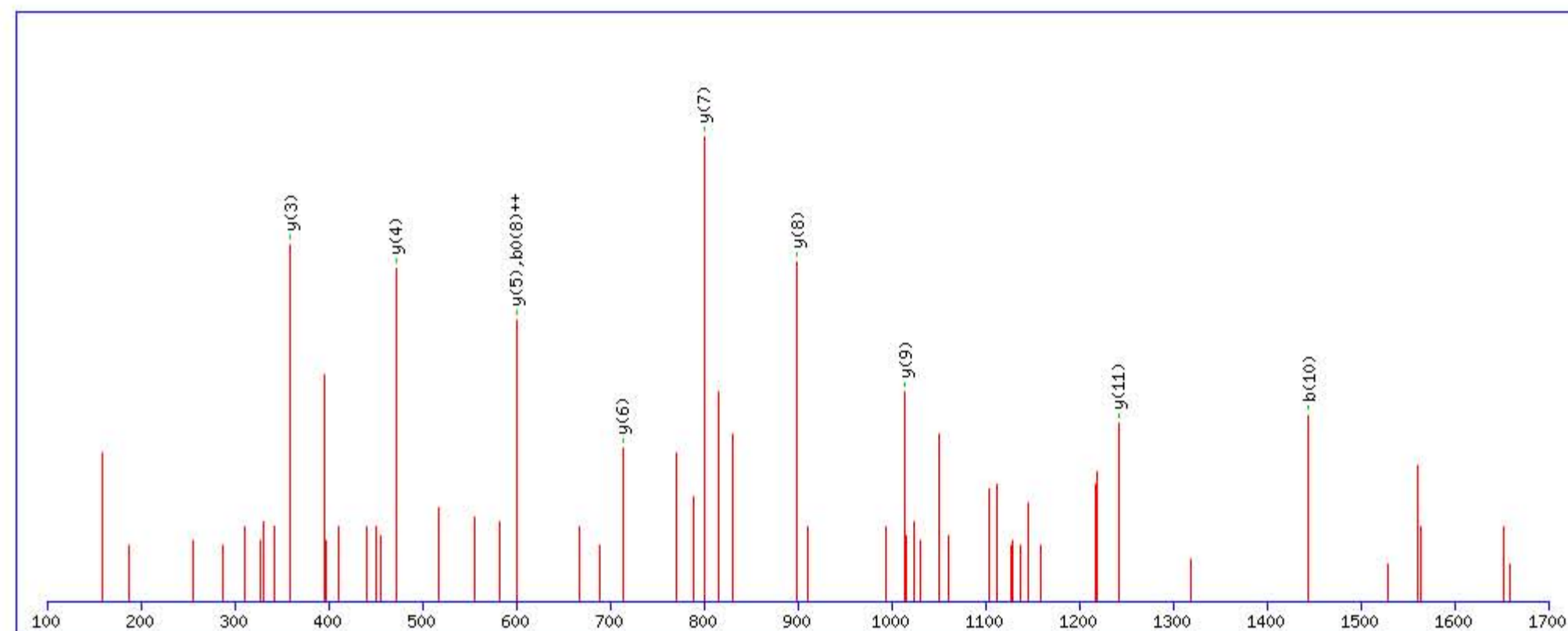
Title: Locus:1.1.1.2890.21 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

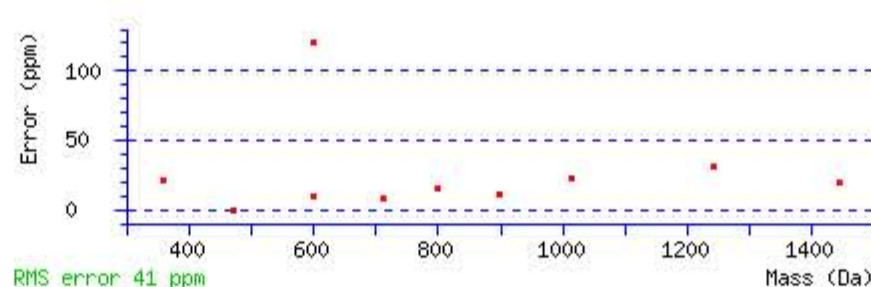
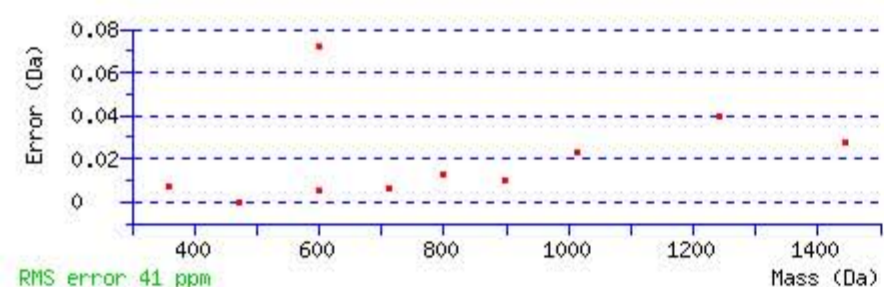
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 43 Expect: 0.0016

Matches : 10/204 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							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
42.9	2457.232193	0.007279	DAPDHQELNLDVSLQLPSR
13.7	2457.243423	-0.003951	TGLSDAFMILNPSDPVPESTR
0.6	2457.236221	0.003251	QDPELAYISSNFITGHGIGK

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

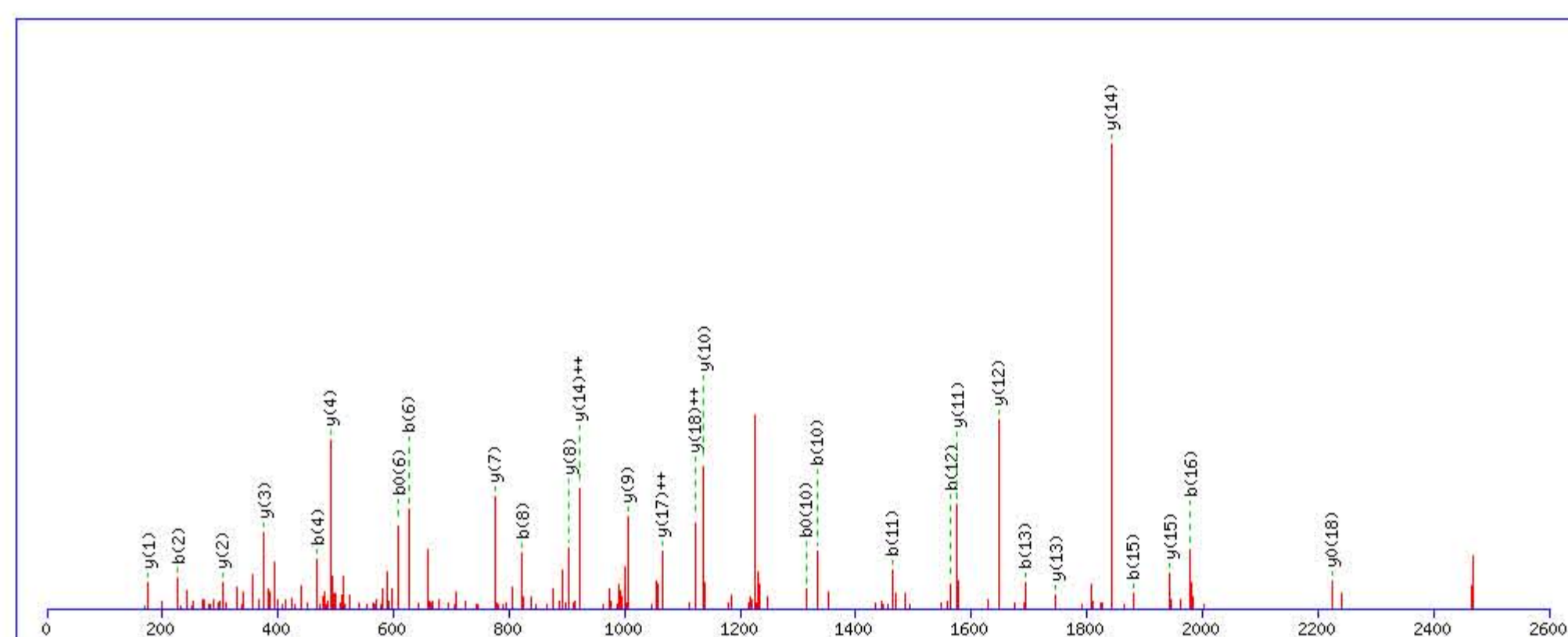
Mascot Search Results

Peptide View

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

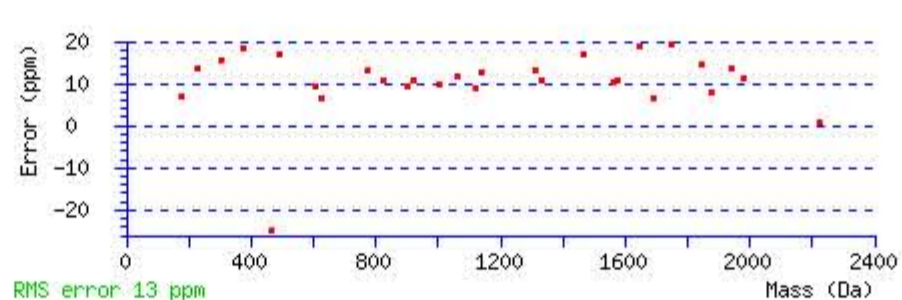
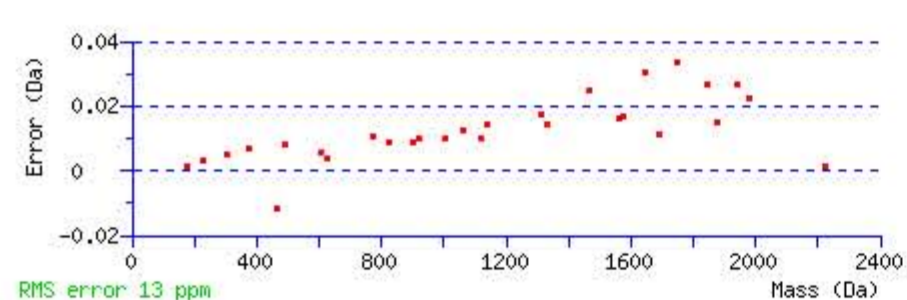
Match to Query 58919: 2467.237848 from(1234.626200,2+) rtinseconds(2642) index(42611)
 Title: Locus:1.1.1.2941.9 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 2467.245071
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q10 : Biotin:Thermo-21345 (Q)
 Ions Score: 107 Expect: 1.1e-010
 Matches : 29/210 fragment ions using 41 most intense peaks [\(help\)](#)

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



NCBI BLAST search of [ILLQGPVAQMTEDAVER](#)
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
106.8	2467.245071	-0.007223	ILLQGPVAQMTEDAVER
38.5	2467.245071	-0.007223	ILLQGPVAQMTEDAVER
0.5	2467.257614	-0.019766	DQAIATREELHAQHR

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 58924: 2467.251342 from(823.424390,3+) rtinseconds(2664) index(42752)

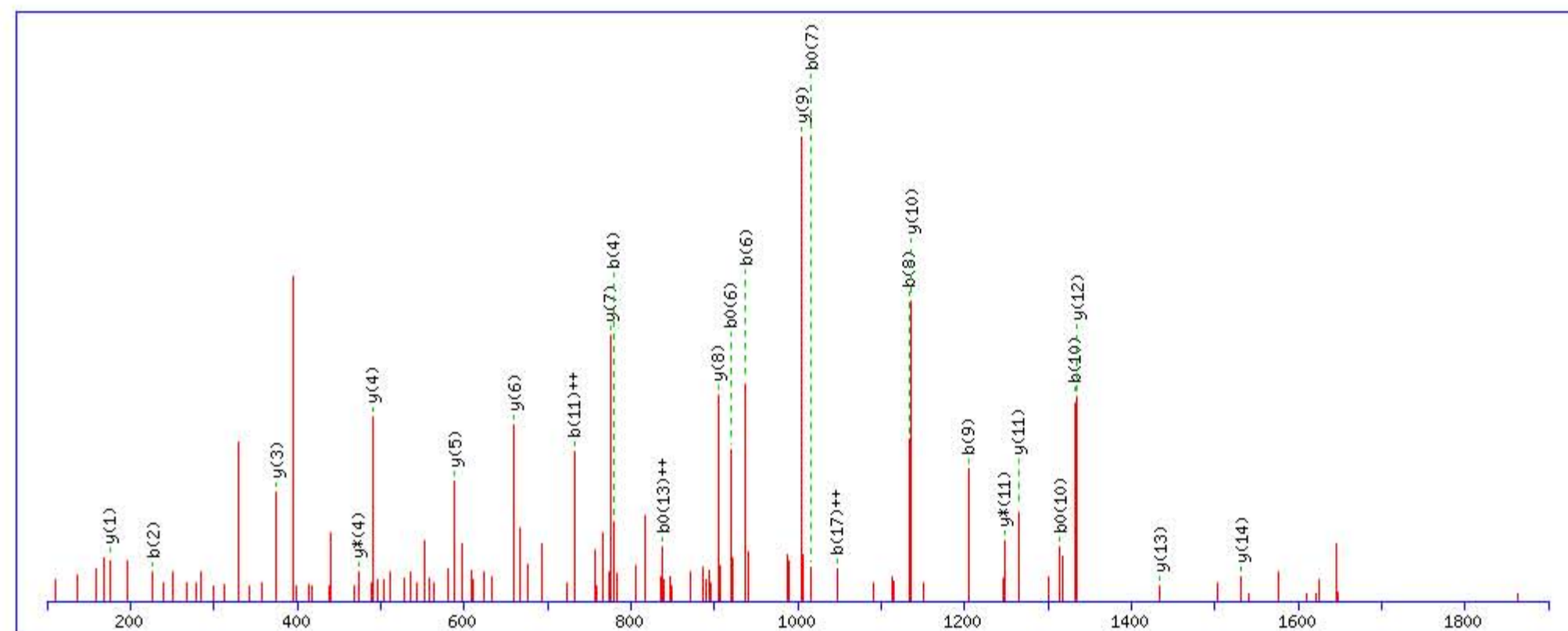
Title: Locus:1.1.1.2949.19 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

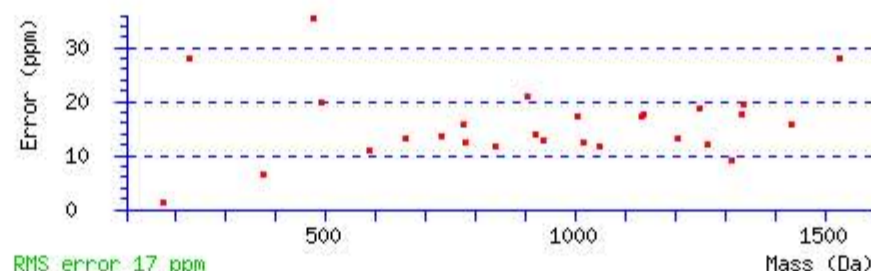
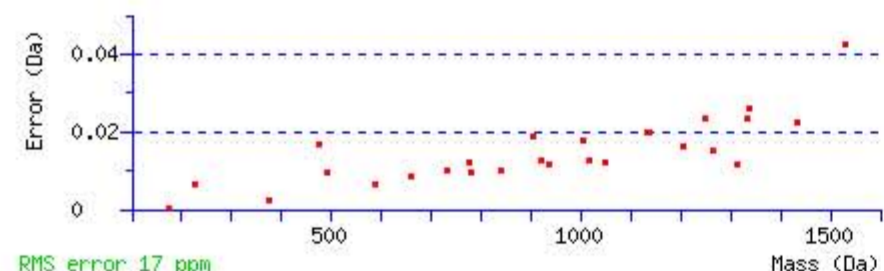
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 80 Expect: 3.5e-007

Matches : 27/210 fragment ions using 48 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	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
79.5	2467.245071	0.006271	ILLQGTPVAQMTEDAVDAER
51.5	2467.245071	0.006271	ILLQGTPVAQMTEDAVDAER

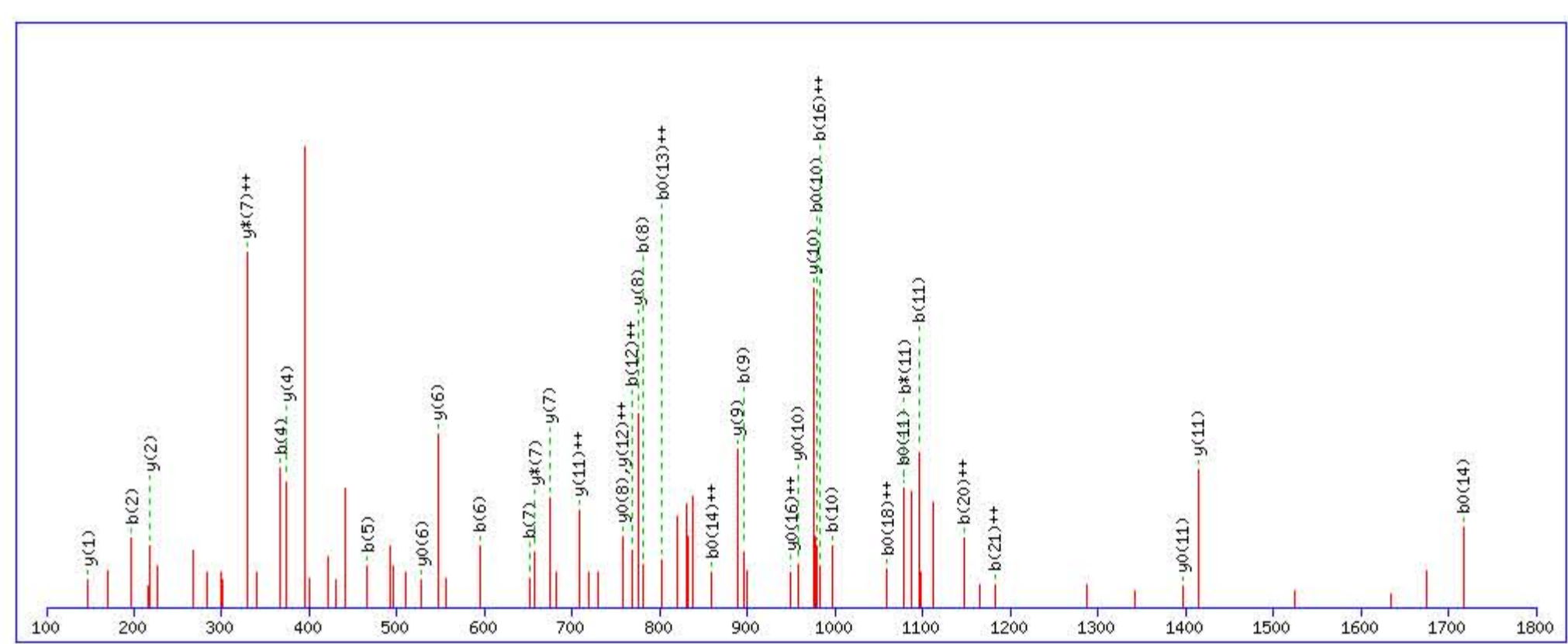
Mascot Search Results

Peptide View

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

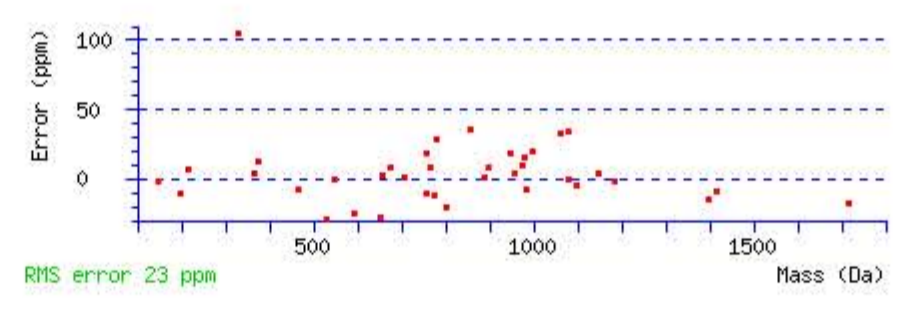
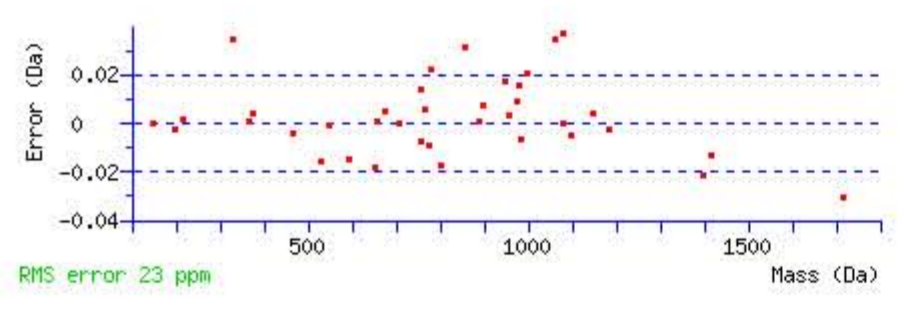
Match to Query 60226: 2508.289122 from(837.103650,3+) rtinseconds(2226) index(57211)
 Title: Locus:1.1.1.3260.24 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 2508.289429
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications: Q12 : Biotin:Thermo-21345 (Q)
 Ions Score: 61 Expect: 2.1e-005
 Matches : 38/220 fragment ions using 75 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	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	$M_r(\text{calc})$:	Delta	Sequence
61.0	2508.289429	-0.000307	VPVAVQGEDTVQSLTQGDGVAK
44.3	2508.289429	-0.000307	VPVAVQGEDTVQSLTQGDGVAK
22.4	2508.289429	-0.000307	VPVAVQGEDTVQSLTQGDGVAK

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 64220: 2874.463776 from(719.623220,4+) rtinseconds(2231) index(40143)

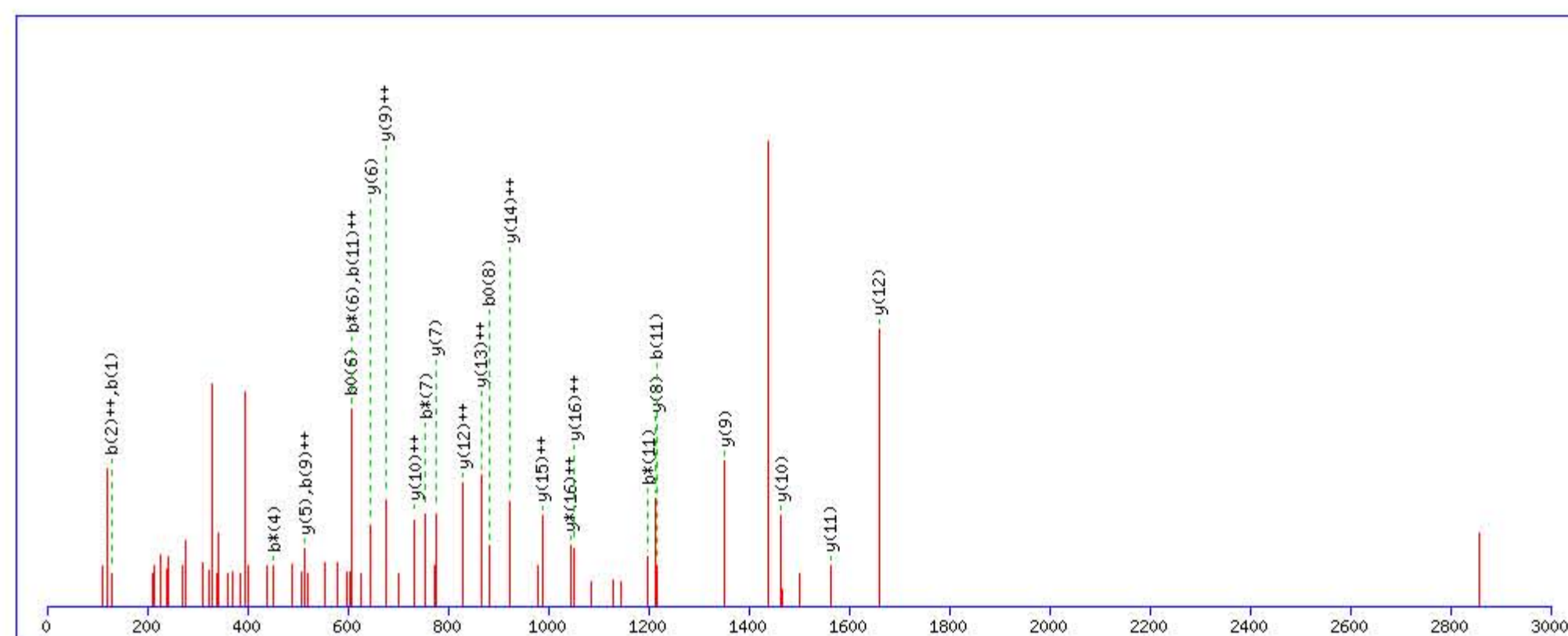
Title: Locus:1.1.1.2799.16 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2874.452057

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

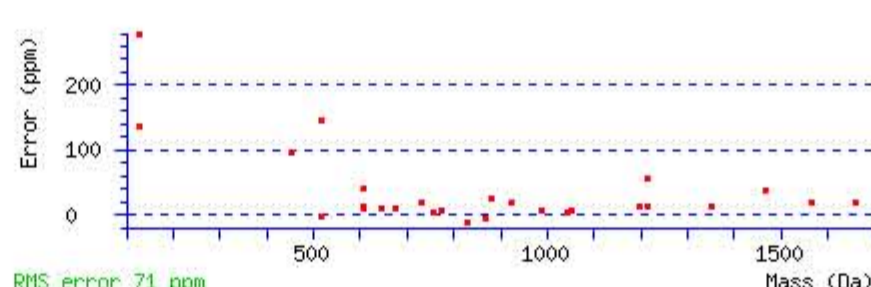
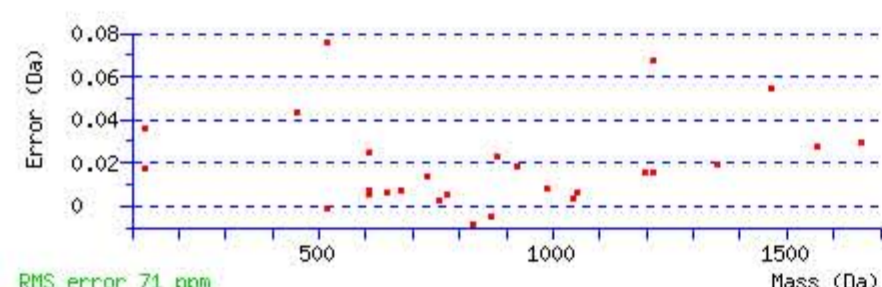
Variable modifications:

Q16 : Biotin:Thermo-21345 (Q)

Ions Score: 43 Expect: 0.0015

Matches : 27/246 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	129.065854	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
42.8	2874.452057	0.011719	QKPDGVFQEDAPVIHQEMIGGLR

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 64659: 2913.189792 from(972.070540,3+) rtinseconds(2120) index(39406)

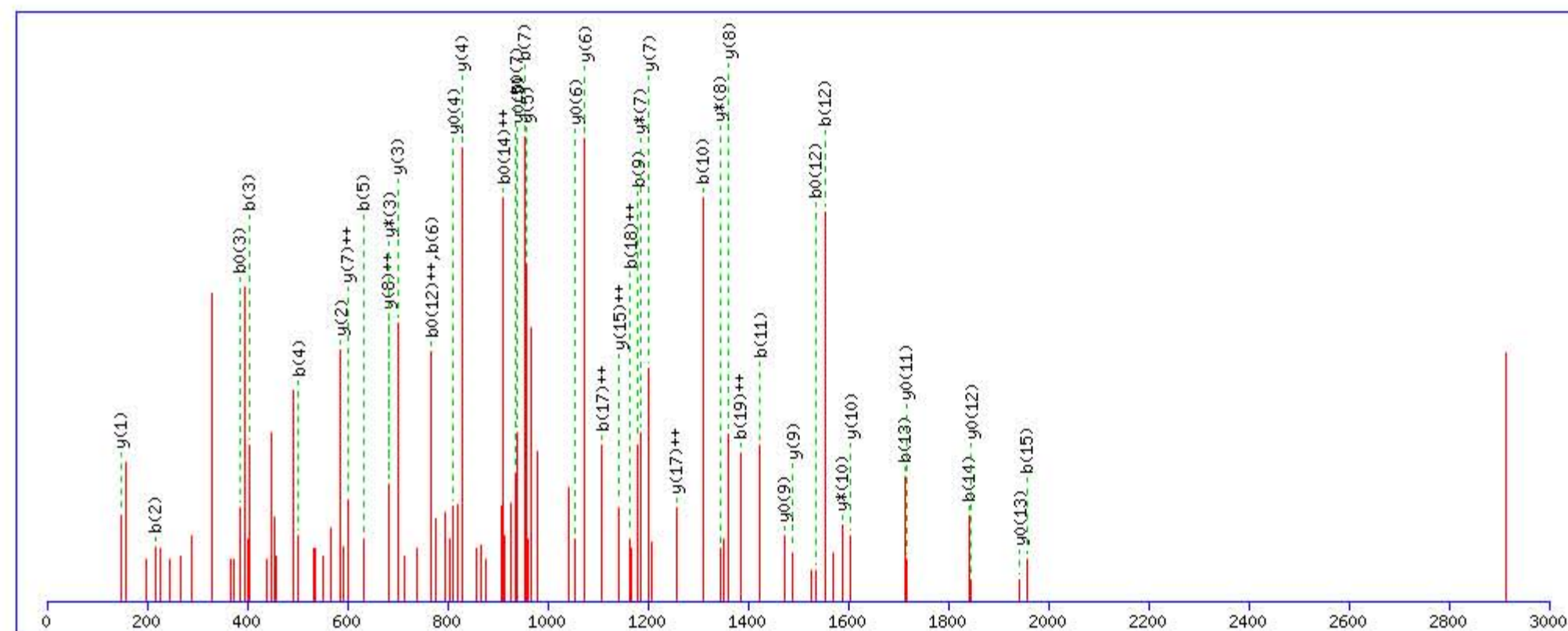
Title: Locus:1.1.1.2760.25 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

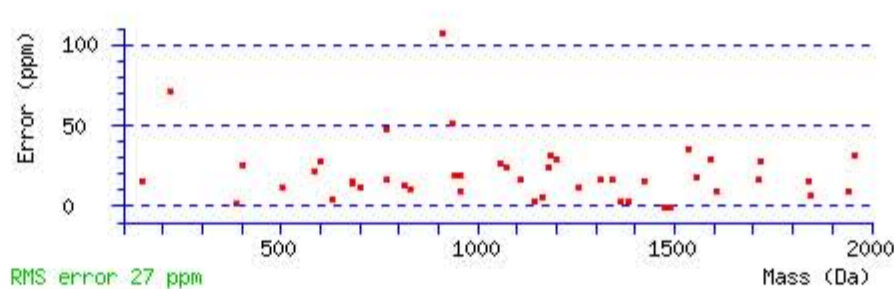
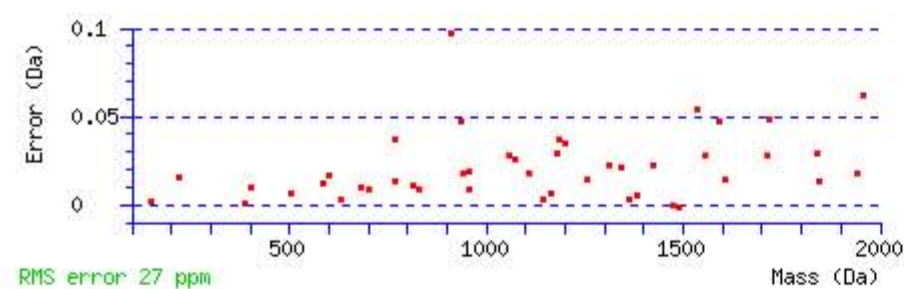
Variable modifications:

Q19 : Biotin:Thermo-21345 (Q)

Ions Score: 88 Expect: 1.9e-009

Matches : 46/196 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	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
87.5	2913.185776	0.004016	DTWVEHWPEEDECQDEENQK
41.0	2913.185776	0.004016	DTWVEHWPEEDECQDEENQK

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

MASCOT Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQAGLQR**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 18516: 1039.549508 from(520.782030,2+) rtinseconds(1408) index(51939)

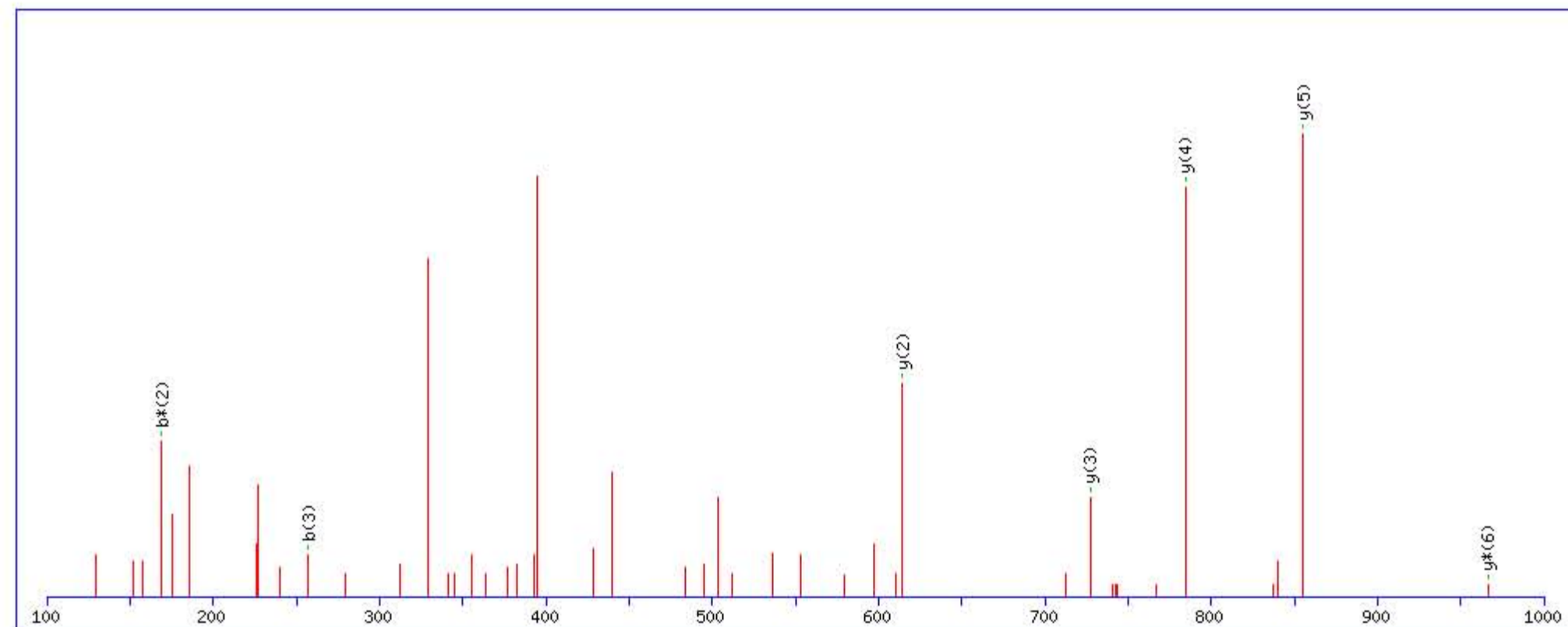
Title: Locus:1.1.1.2976.22 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1039.559677

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

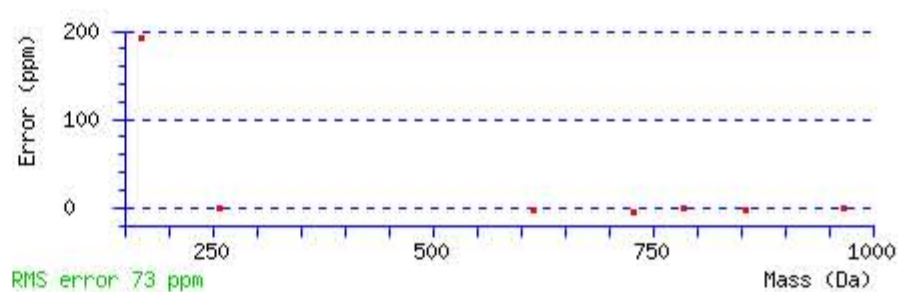
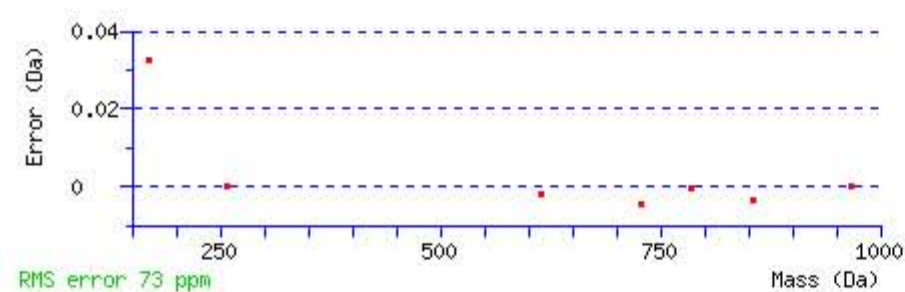
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 29 Expect: 0.017

Matches : 7/46 fragment ions using 9 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	#
1	58.028740	29.518008			G					7
2	186.087318	93.547297	169.060769	85.034023	Q	983.545498	492.276387	966.518949	483.763113	6
3	257.124432	129.065854	240.097883	120.552580	A	855.486920	428.247098	838.460371	419.733824	5
4	314.145896	157.576586	297.119347	149.063312	G	784.449806	392.728541	767.423257	384.215267	4
5	427.229960	214.118618	410.203411	205.605344	L	727.428342	364.217809	710.401793	355.704535	3
6	866.455286	433.731281	849.428737	425.218007	Q	614.344278	307.675777	597.317729	299.162503	2
7					R	175.118952	88.063114	158.092403	79.549840	1



NCBI BLAST search of **GQAGLQR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.3	1039.559677	-0.010169	GQAGLQR
10.4	1039.559677	-0.010169	GQQIQR
8.9	1039.541061	0.008447	GQGDLLQPGR
4.7	1039.563492	-0.013984	AEGARARGPR
4.6	1039.559677	-0.010169	KGGPSQR
2.1	1039.552277	-0.002769	QRAALDGGPR
1.6	1039.541046	0.008462	GSELTLHQR
0.8	1039.548431	0.001077	LSPEQR

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 25568: 1212.570008 from(607.292280,2+) rtinseconds(1273) index(51047)

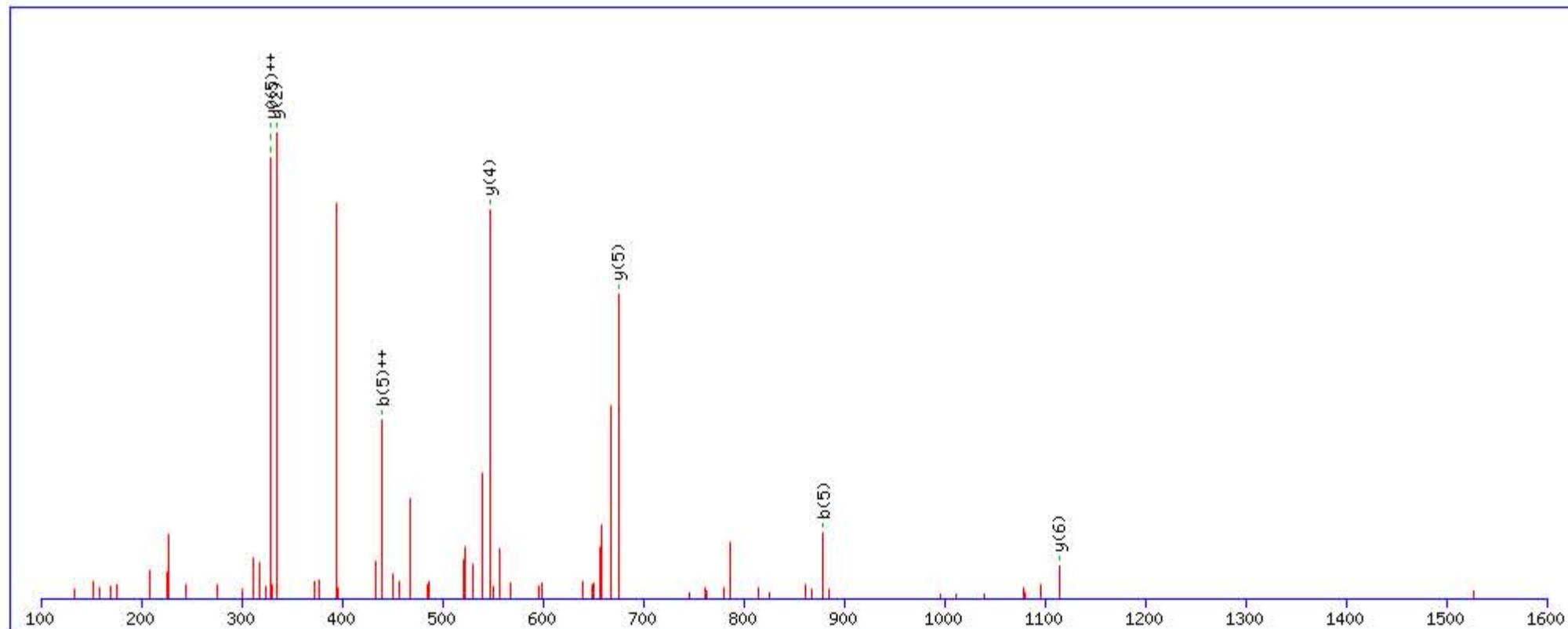
Title: Locus:1.1.1.2929.18 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1212.574356

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

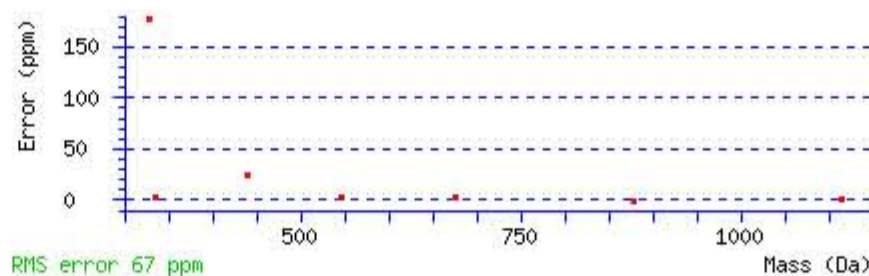
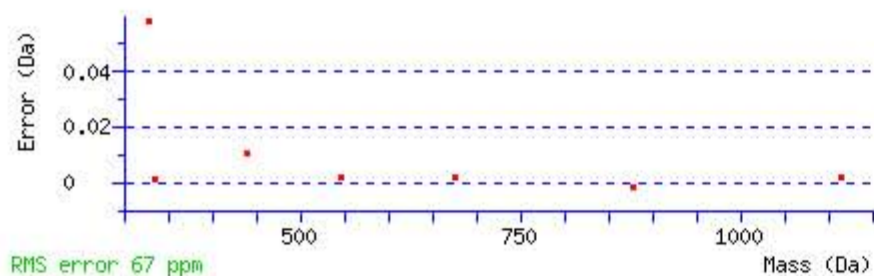
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.0089

Matches : 7/58 fragment ions using 10 most intense peaks ([help](#))

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



NCBI BLAST search of **VQQPDCR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.0	1212.574356	-0.004348	VQQPDCR
11.8	1212.574356	-0.004348	VQQPDCR
4.9	1212.555725	0.014283	QSPGPEPSVCR
1.6	1212.562241	0.007767	TTAQYDQASTK

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 27774: 1279.659228 from(640.836890,2+) rtinseconds(1975) index(55660)

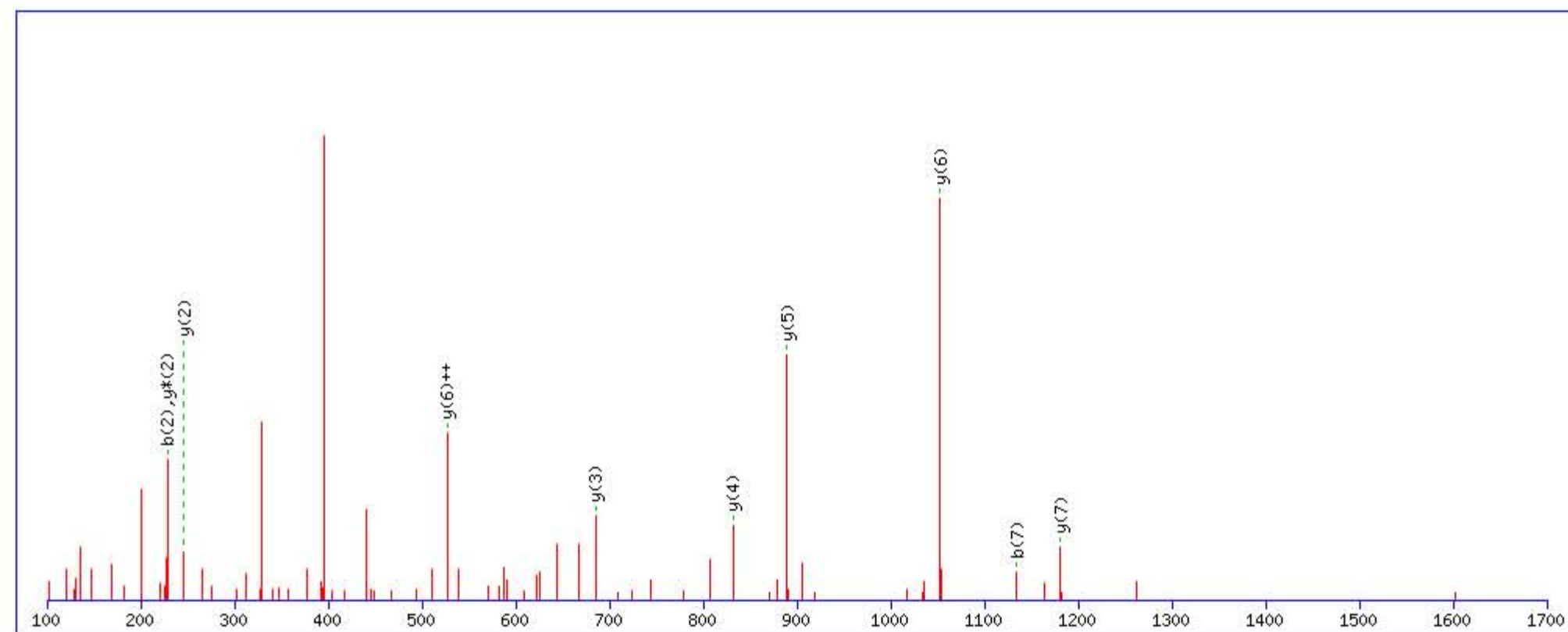
Title: Locus:1.1.1.3173.17 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

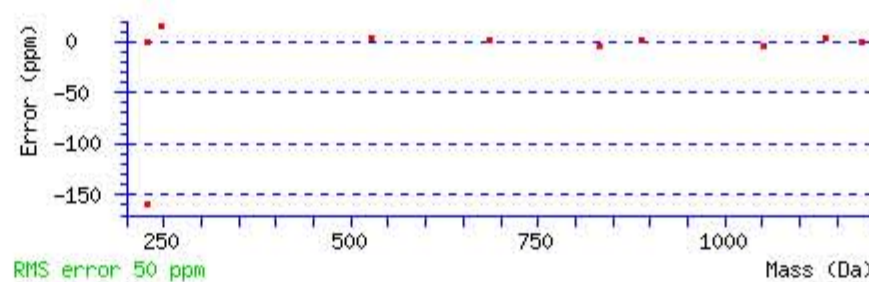
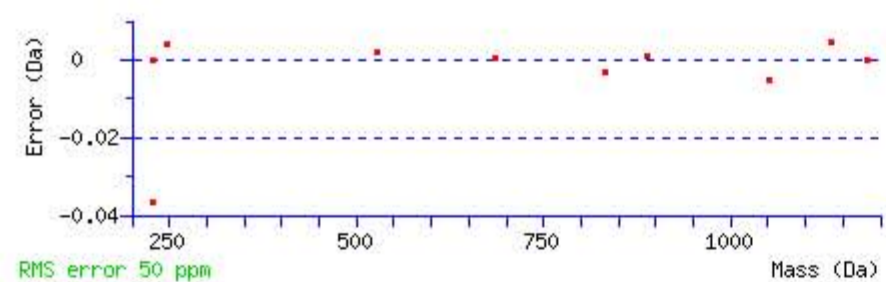
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.037

Matches : 10/60 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	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
27.3	1279.663483	-0.004255	VEYGFQVK
12.2	1279.663483	-0.004255	QFVG YLDK
10.1	1279.659470	-0.000242	VCSFGKQVVEK
3.7	1279.670670	-0.011442	VEHKS NQK
2.5	1279.677216	-0.017988	VFKTEDTQGKK
1.0	1279.652039	0.007189	QAVRSYNSEVK
0.8	1279.677185	-0.017957	EARSLS TELFK
0.5	1279.677246	-0.018018	TGGFTGNVSIIVK
0.2	1279.677200	-0.017972	EYVGK TSLVER

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVEEQESR**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 28087: 1285.630888 from(643.822720,2+) rtinseconds(1347) index(51504)

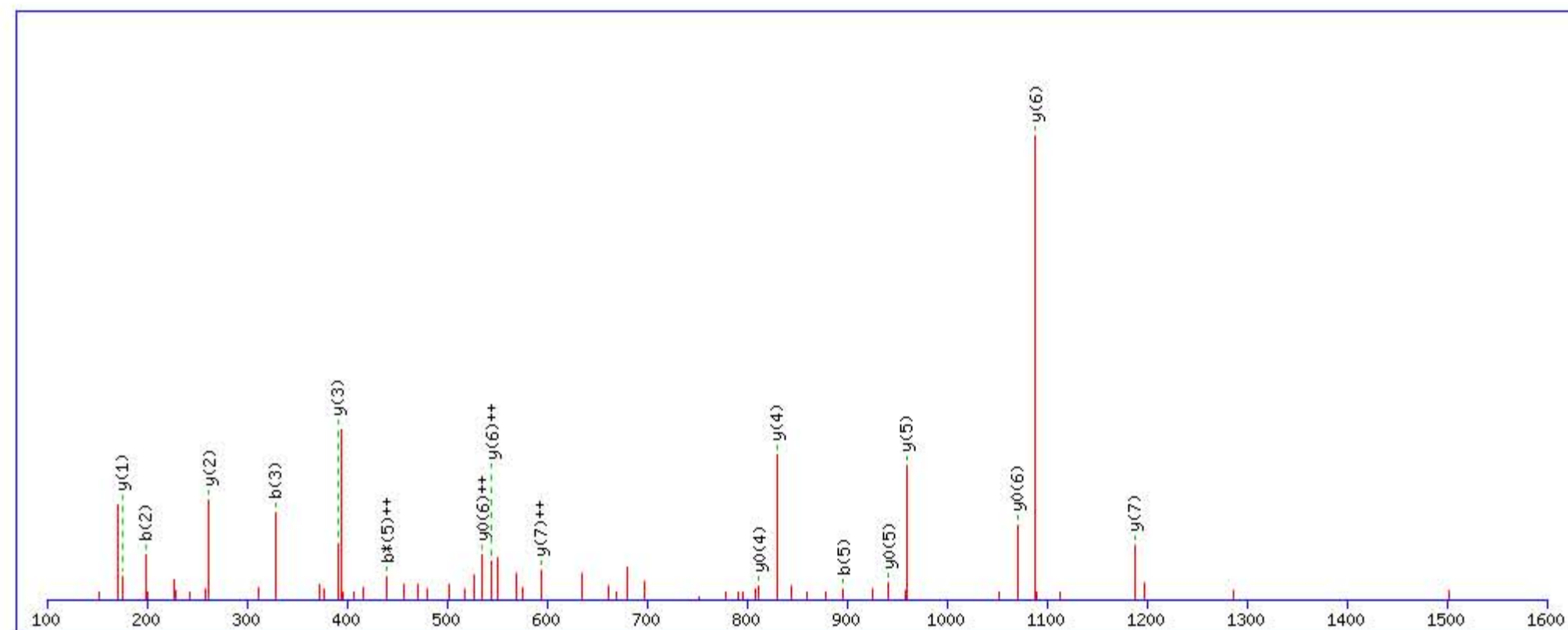
Title: Locus:1.1.1.2955.14 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

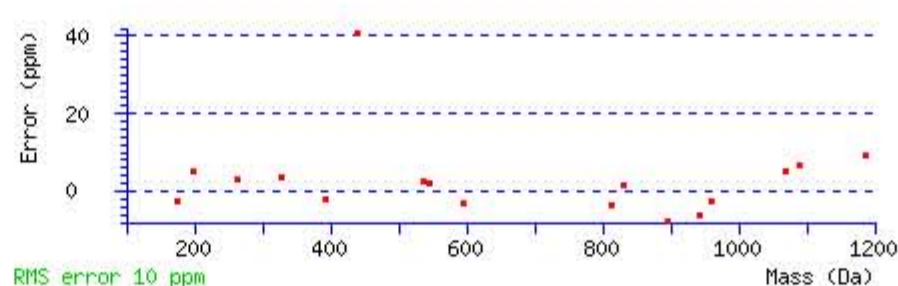
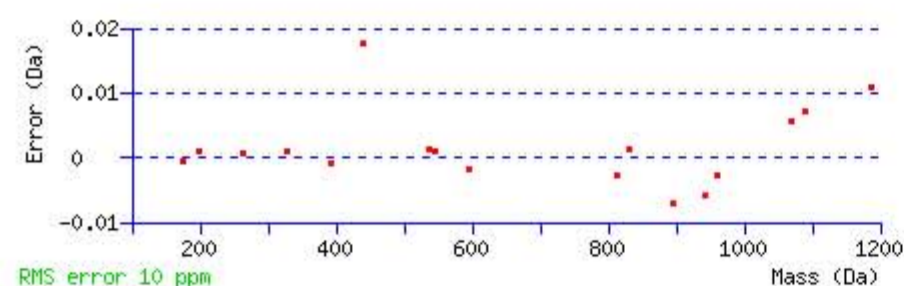
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 43 Expect: 0.00016

Matches : 17/70 fragment ions using 32 most intense peaks ([help](#))

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



NCBI BLAST search of **VVEEQESR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.9	1285.633621	-0.002733	VVEEQESR
2.2	1285.644867	-0.013979	DTLHSAMAVVSR
1.4	1285.637451	-0.006563	TAPASGSAPRESR

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

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **LGQYASPTAK**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 29459: 1345.701308 from(673.857930,2+) rtinseconds(1582) index(53084)

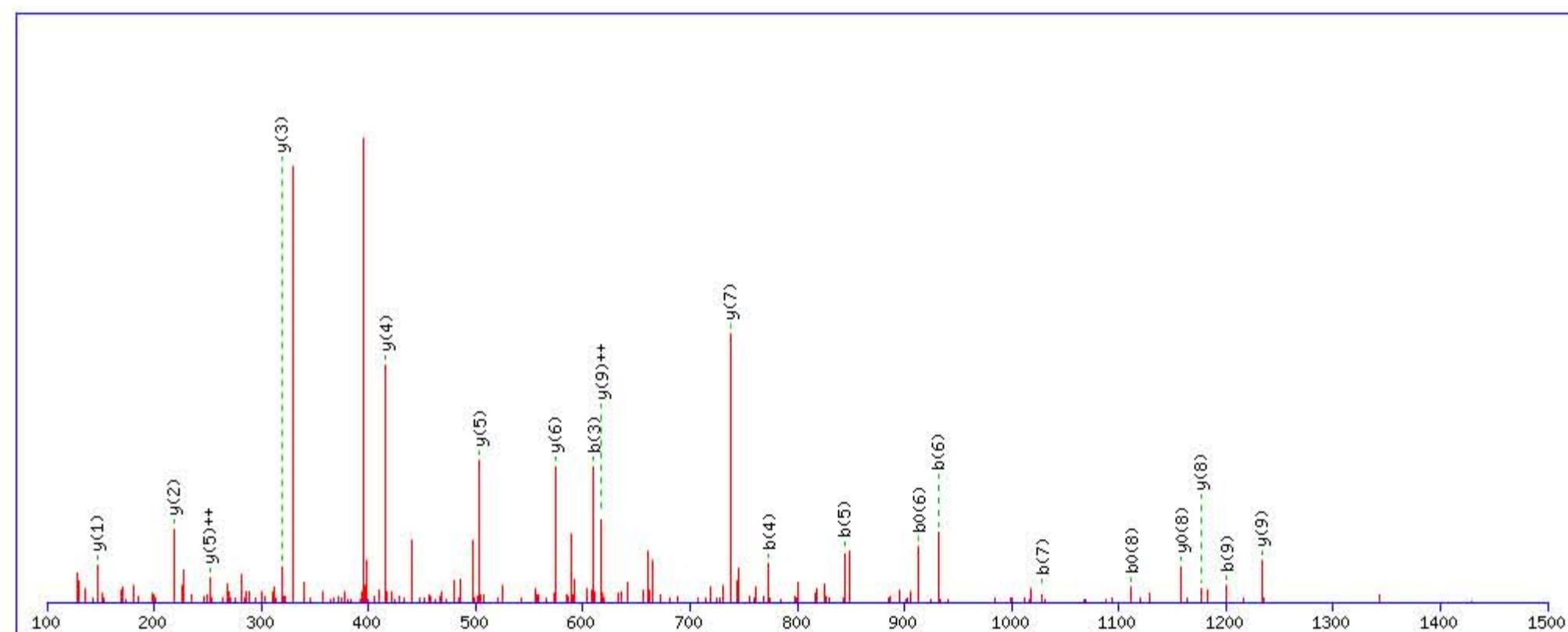
Title: Locus:1.1.1.3037.12 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

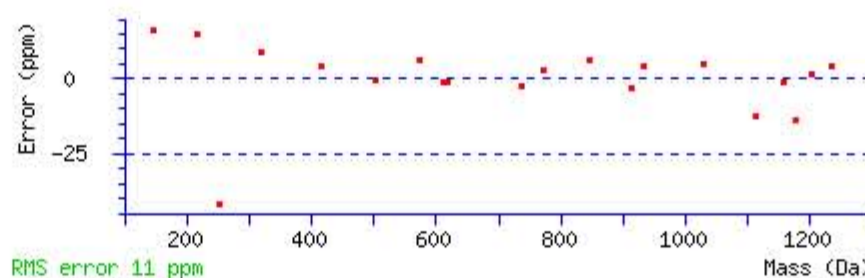
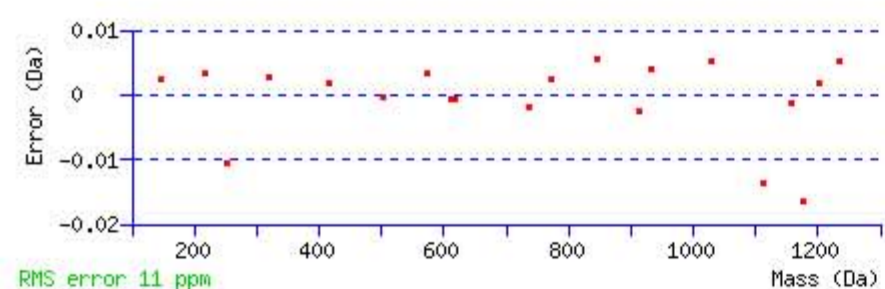
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 60 Expect: 2e-005

Matches : 20/90 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							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
60.3	1345.706390	-0.005082	LGQYASPTAK
9.4	1345.706390	-0.005082	LGQYDQALK
8.1	1345.706406	-0.005098	QGLYTPQTK
5.4	1345.692474	0.008834	VASCRYPALGPR
3.0	1345.717636	-0.016328	QMPQPTFILRK
1.3	1345.691116	0.010192	LIEAVDNMLSNK
0.5	1345.717606	-0.016298	EKVKNIHGVMK
0.1	1345.708893	-0.007585	IIVGDATEKDASK
0.1	1345.717606	-0.016298	QLKKCWENIK

MASCOT SCIENCE 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 42871: 1726.857928 from(864.436240,2+) rtinseconds(1989) index(55749)

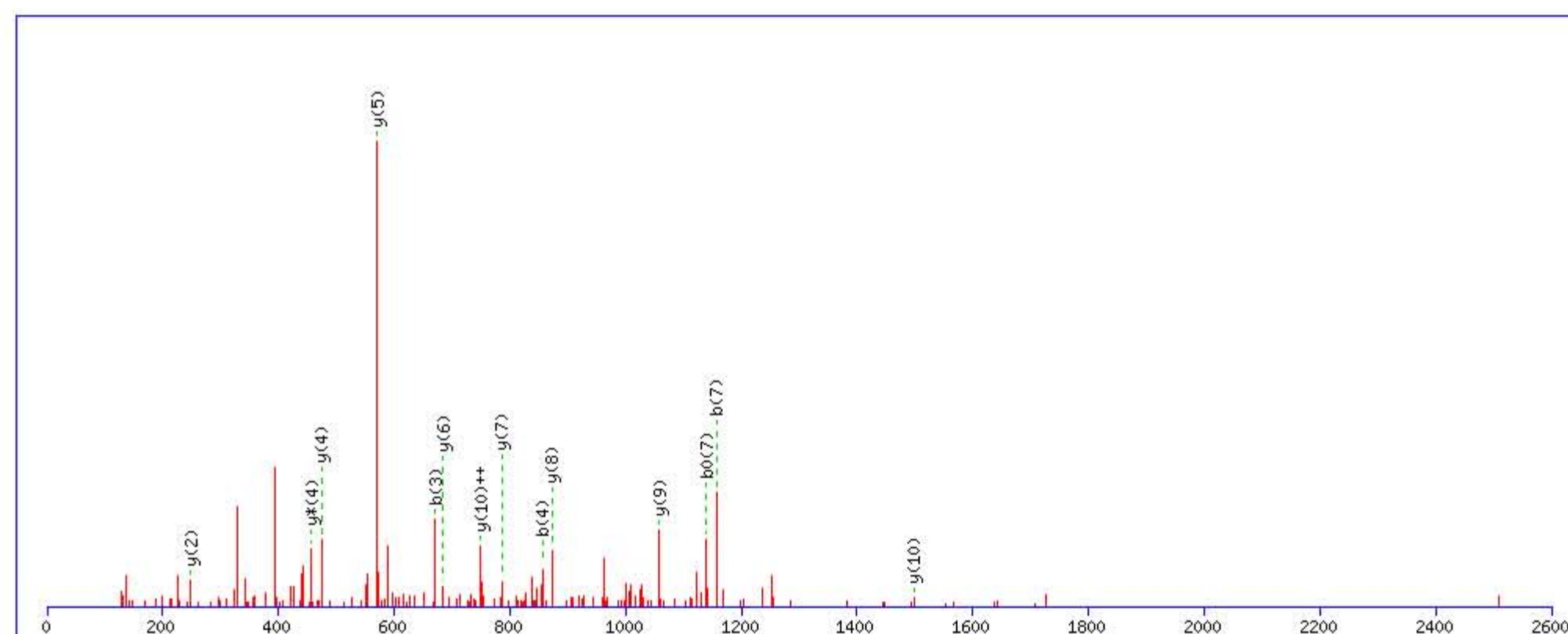
Title: Locus:1.1.1.3178.11 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

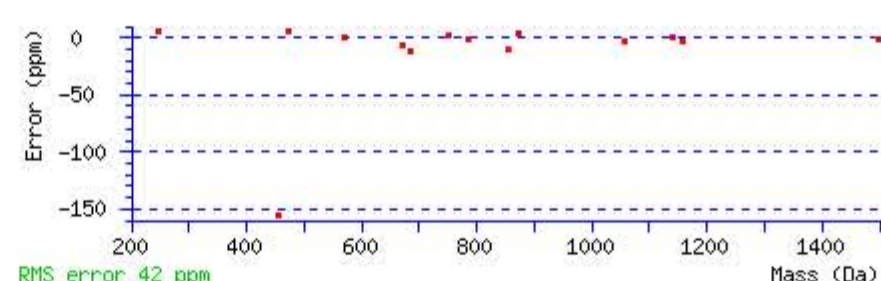
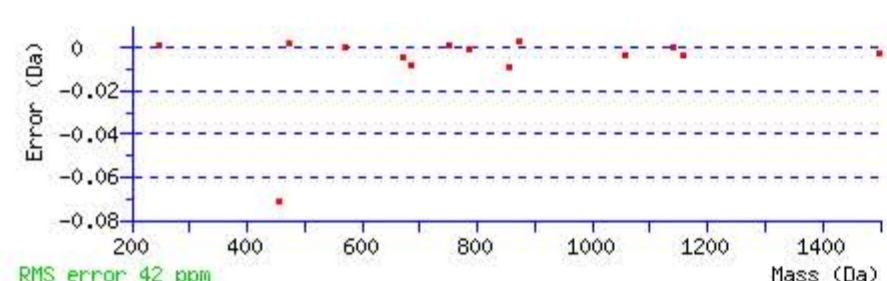
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 37 Expect: 0.0048

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
36.6	1726.860001	-0.002073	TEQWSTLPPETK
11.2	1726.849960	0.007968	TERFGQGGAGPVGGQGPR
1.3	1726.853485	0.004443	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 43500: 1746.883392 from(583.301740,3+) rtinseconds(2546) index(58902)

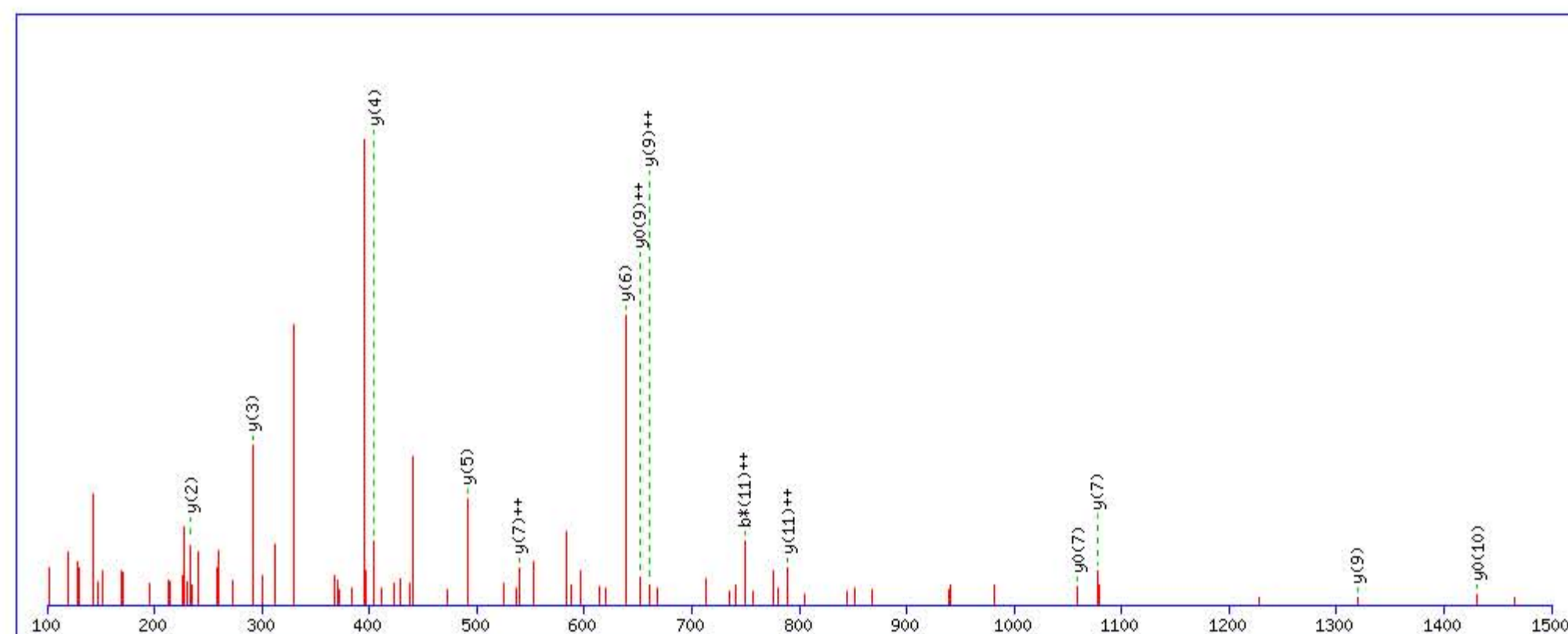
Title: Locus:1.1.1.3372.6 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

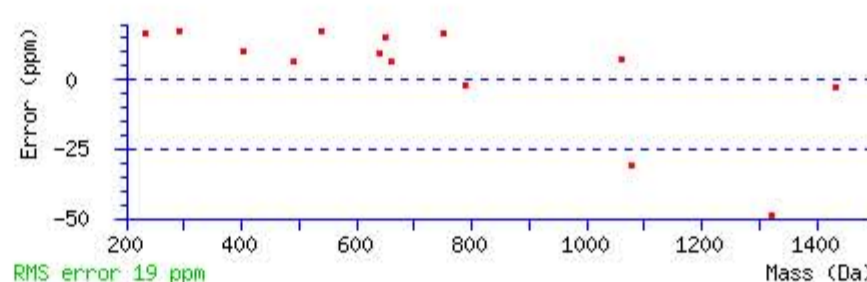
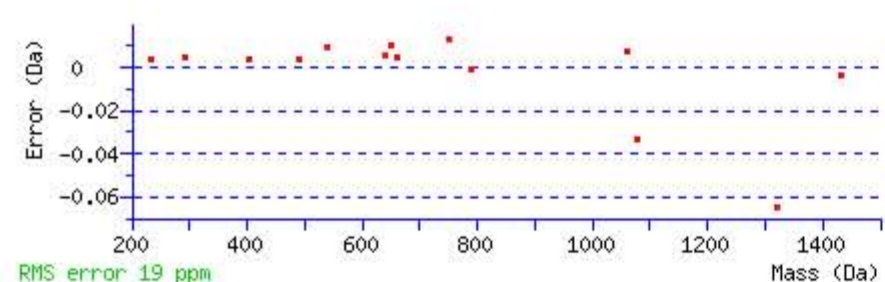
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 25 Expect: 0.081

Matches : 14/126 fragment ions using 34 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	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
25.2	1746.886200	-0.002808	GLEEELQFSLGSK

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

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPFLSCCQFAESLR**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 51142: 2053.944852 from(685.655560,3+) rtinseconds(2474) index(58474)

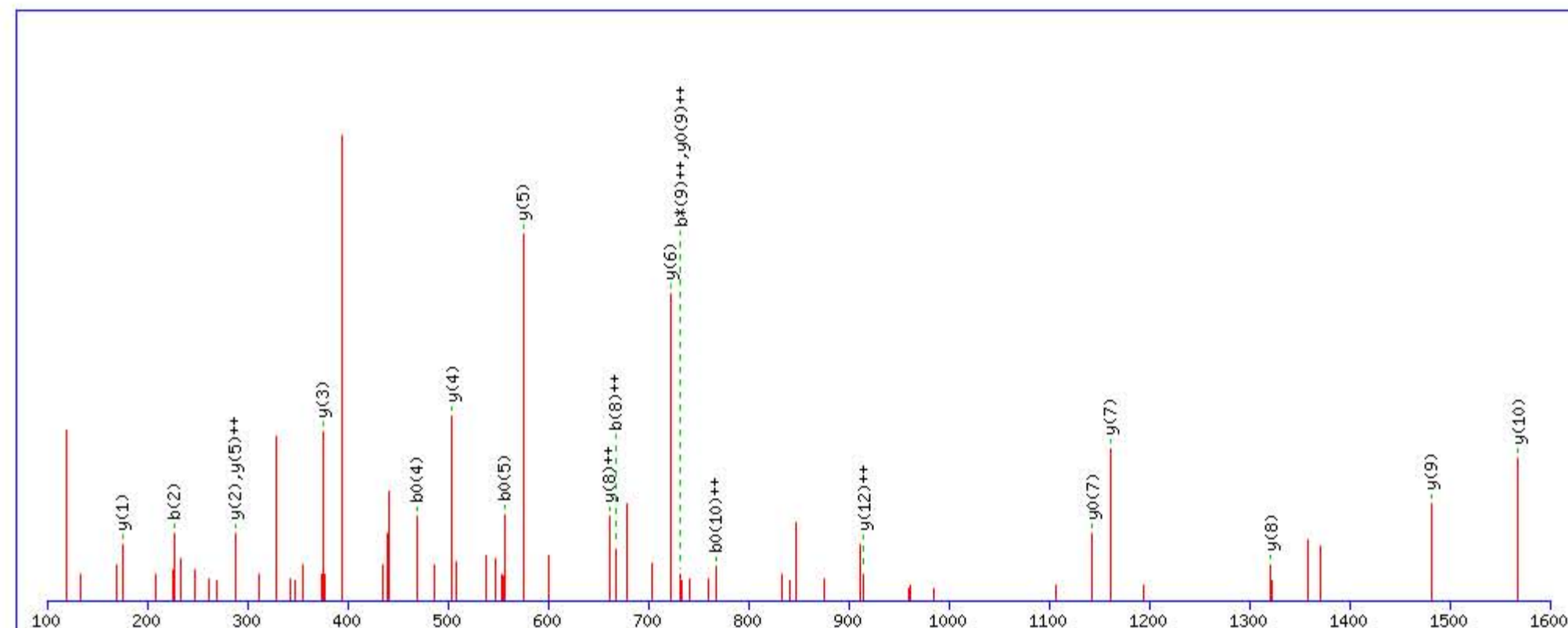
Title: Locus:1.1.1.3347.14 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

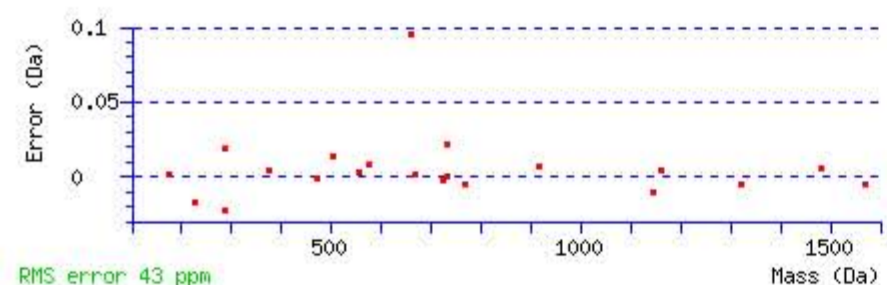
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

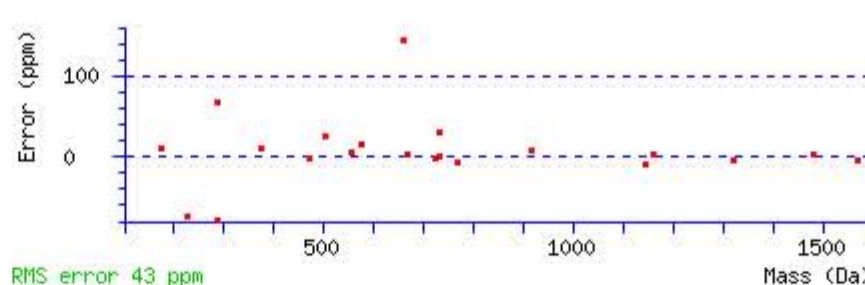
Ions Score: 48 Expect: 0.00022

Matches : 21/138 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							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



RMS error 43 ppm



RMS error 43 ppm

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
47.5	2053.942368	0.002484	EPFLSCCQFAESLR

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 54392: 2220.035352 from(741.019060,3+) rtinseconds(2119) index(71902)

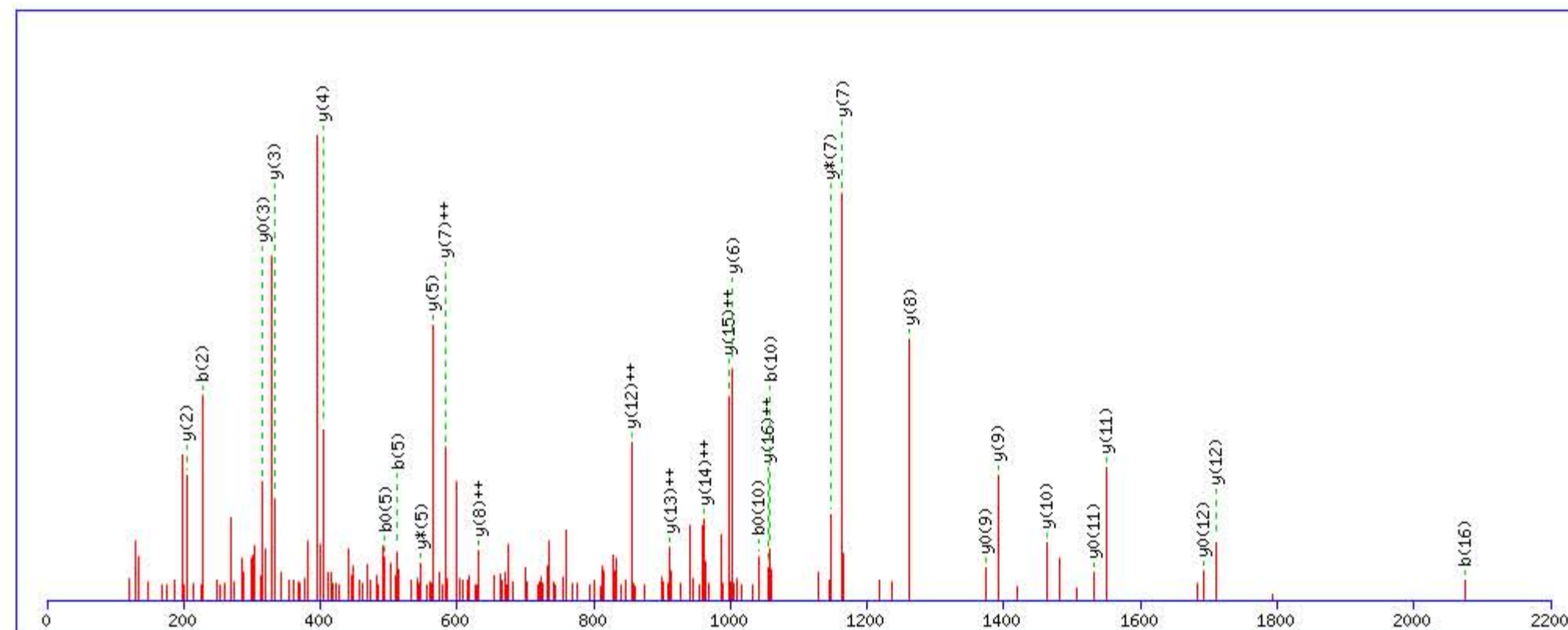
Title: Locus:1.1.1.3271.14 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 2220.041092

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

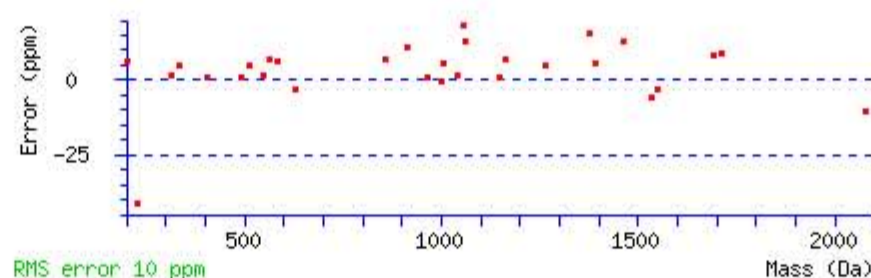
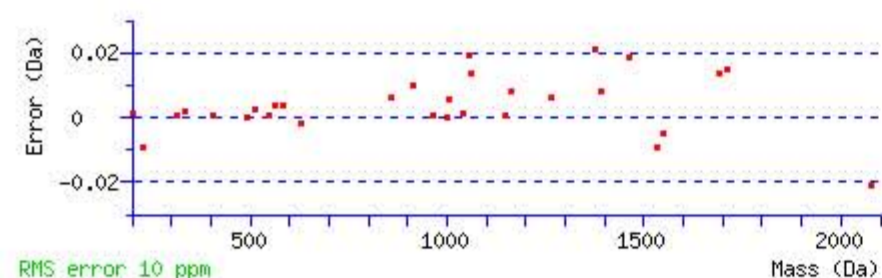
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 57 Expect: 2.7e-005

Matches : 30/160 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							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	$M_r(\text{calc})$:	Delta	Sequence
57.3	2220.041092	-0.005740	LLATLCSAEVCQCAEGK

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 60952: 2583.160902 from(862.060910,3+) rtinseconds(2728) index(60118)

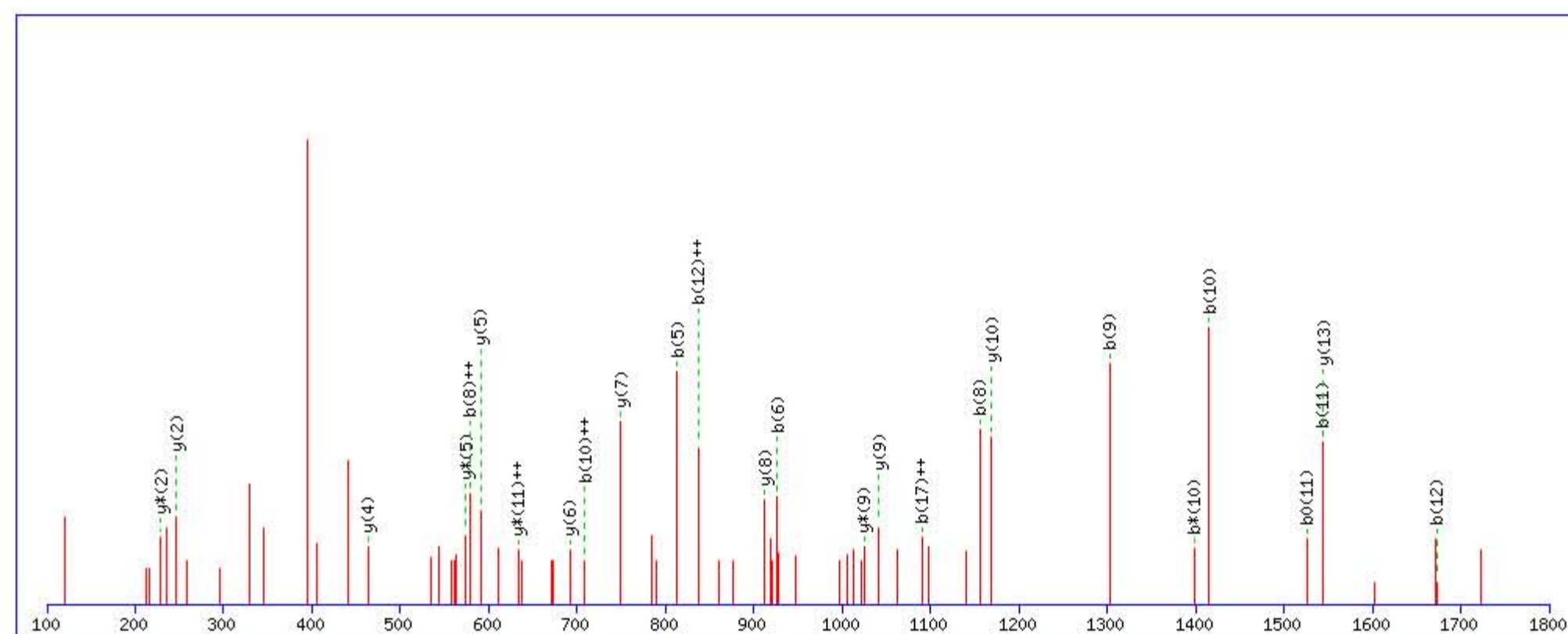
Title: Locus:1.1.1.3434.18 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

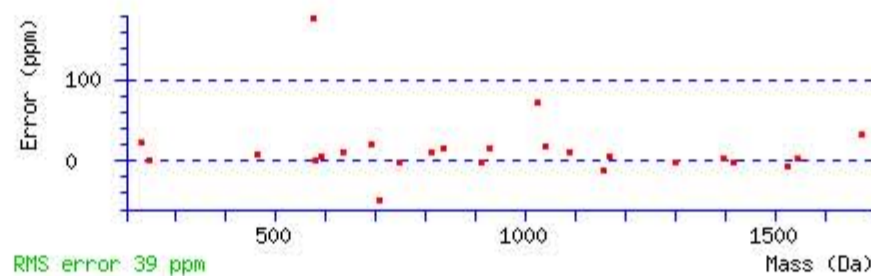
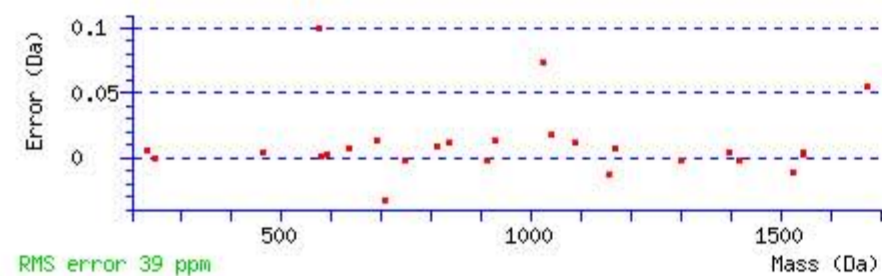
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 56 Expect: 2.2e-005

Matches : 26/194 fragment ions using 43 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.044390	36.525833					A							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
55.6	2583.155624	0.005278	AACAQLNDFLQEYGTQGCQV
18.2	2583.155624	0.005278	AACAQLNDFLQEYGTQGCQV

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 32025: 1396.631028 from(699.322790,2+) rtinseconds(1633) index(3606)

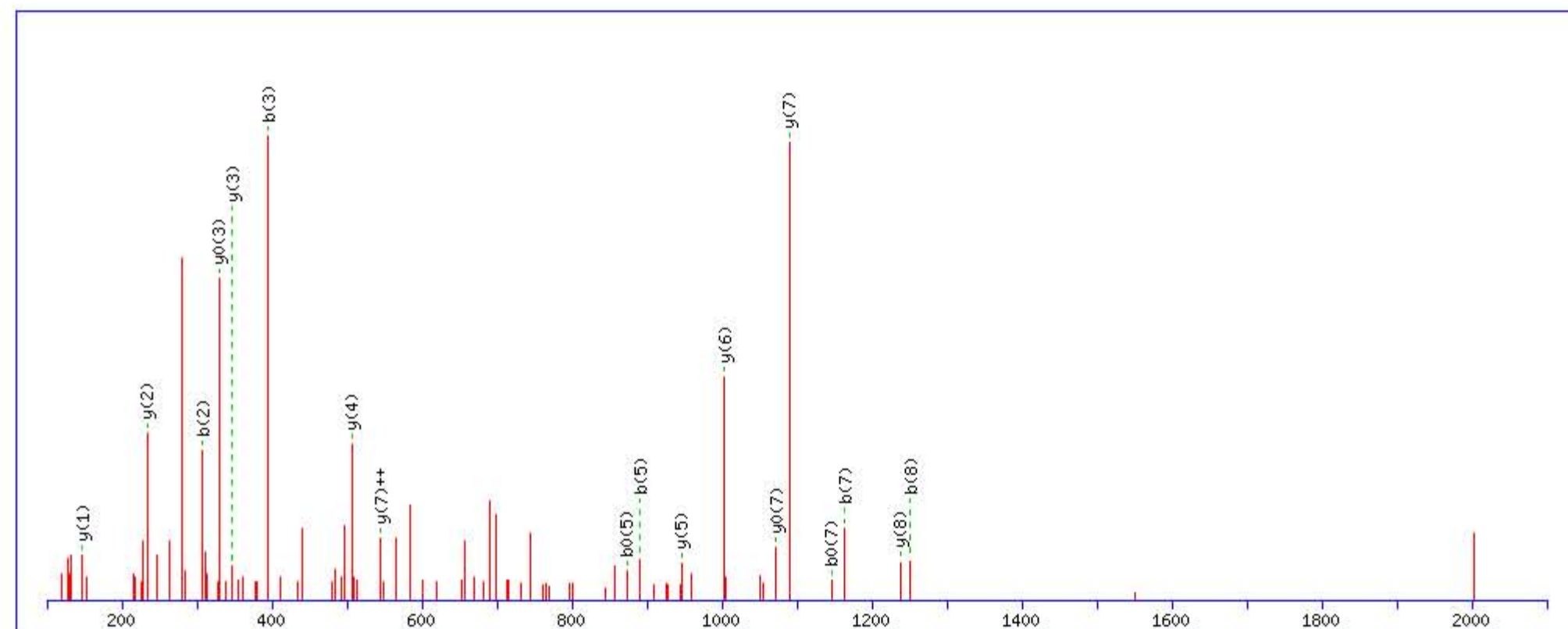
Title: Locus:1.1.1.3004.14 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

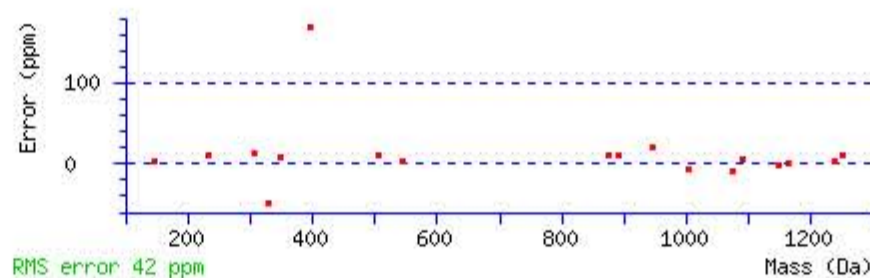
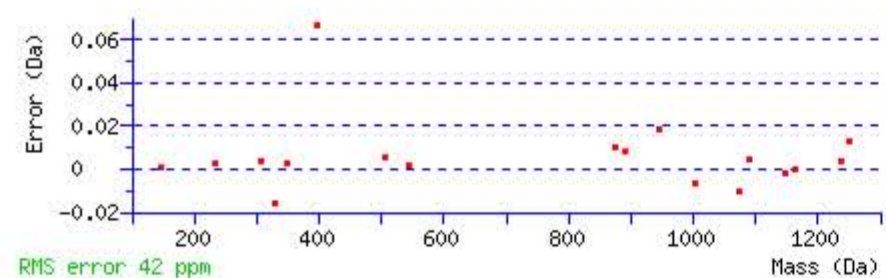
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 48 Expect: 8.7e-005

Matches : 18/82 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							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
48.2	1396.630157	0.000871	CFSGQCISK
4.6	1396.629272	0.001756	QLSQAQATDFCK
2.4	1396.629257	0.001771	CPSSYNILDNSK
0.7	1396.629303	0.001725	GQTDTSLPGCFKSK
0.2	1396.644516	-0.013488	NAPYFPCDKASK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **WLVGEMHCQK**

Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

Match to Query 38906: 1597.766202 from(533.596010,3+) rtinseconds(1882) index(5055)

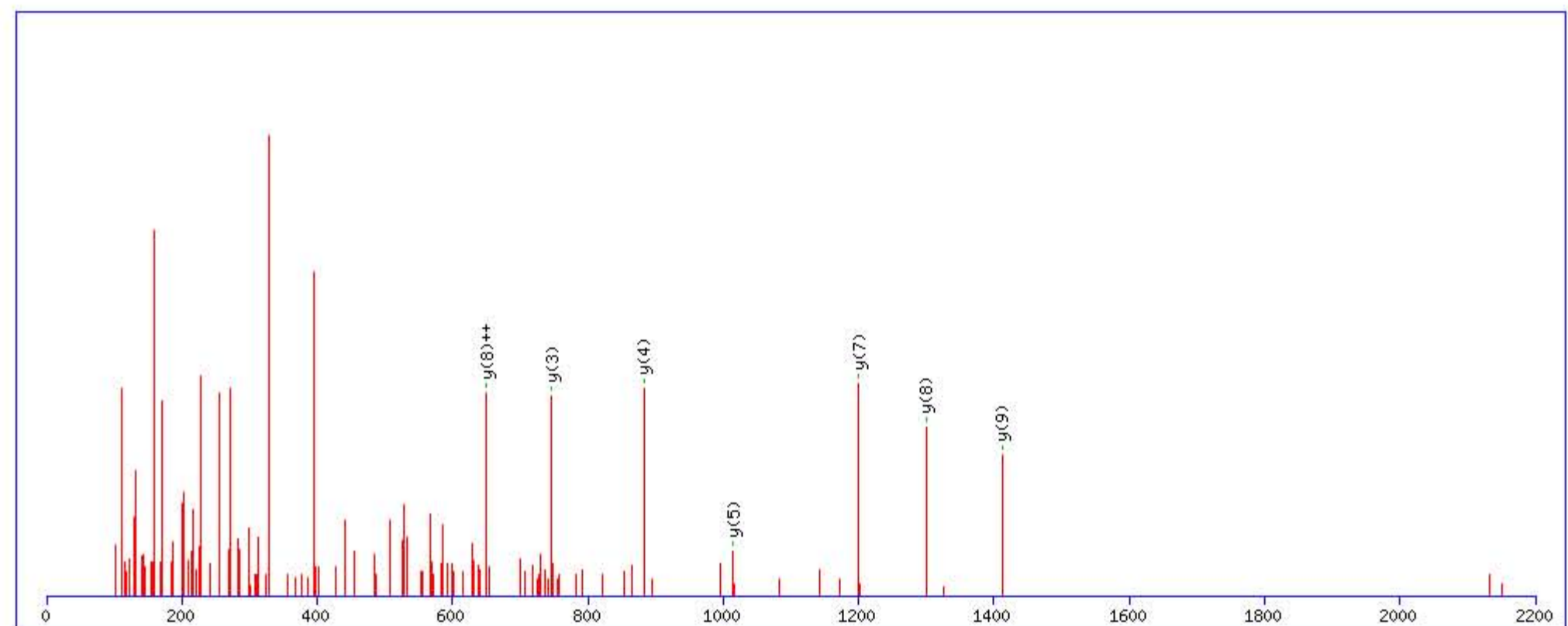
Title: Locus:1.1.1.3091.15 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1597.756744

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

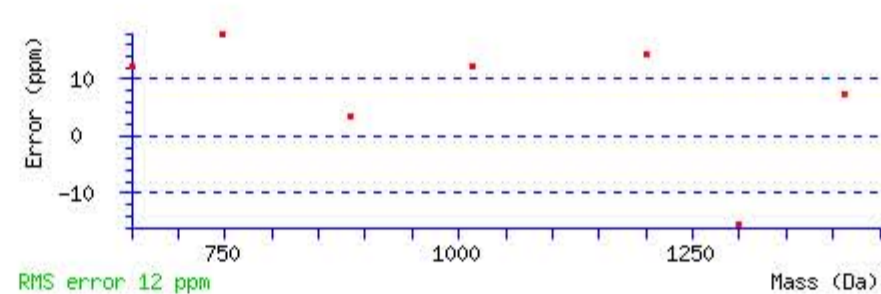
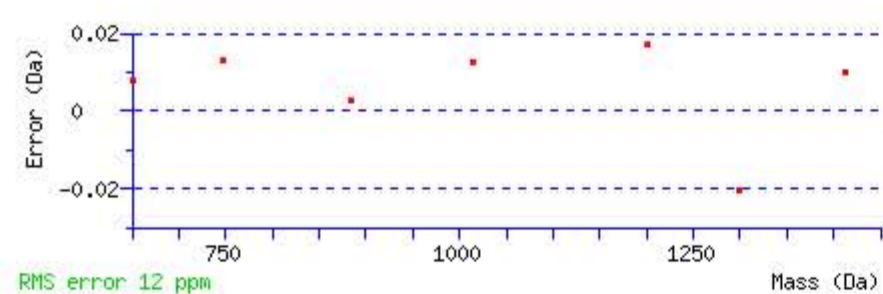
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 30 Expect: 0.0046

Matches : 7/74 fragment ions using 14 most intense peaks [\(help\)](#)

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



NCBI BLAST search of [WLVGEMHCQK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.0	1597.756744	0.009458	WLVGEMHCQK
5.0	1597.751846	0.014356	NPEDDGCLLKQGPR

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 43928: 1765.937888 from(883.976220,2+) rtinseconds(2468) index(8571)

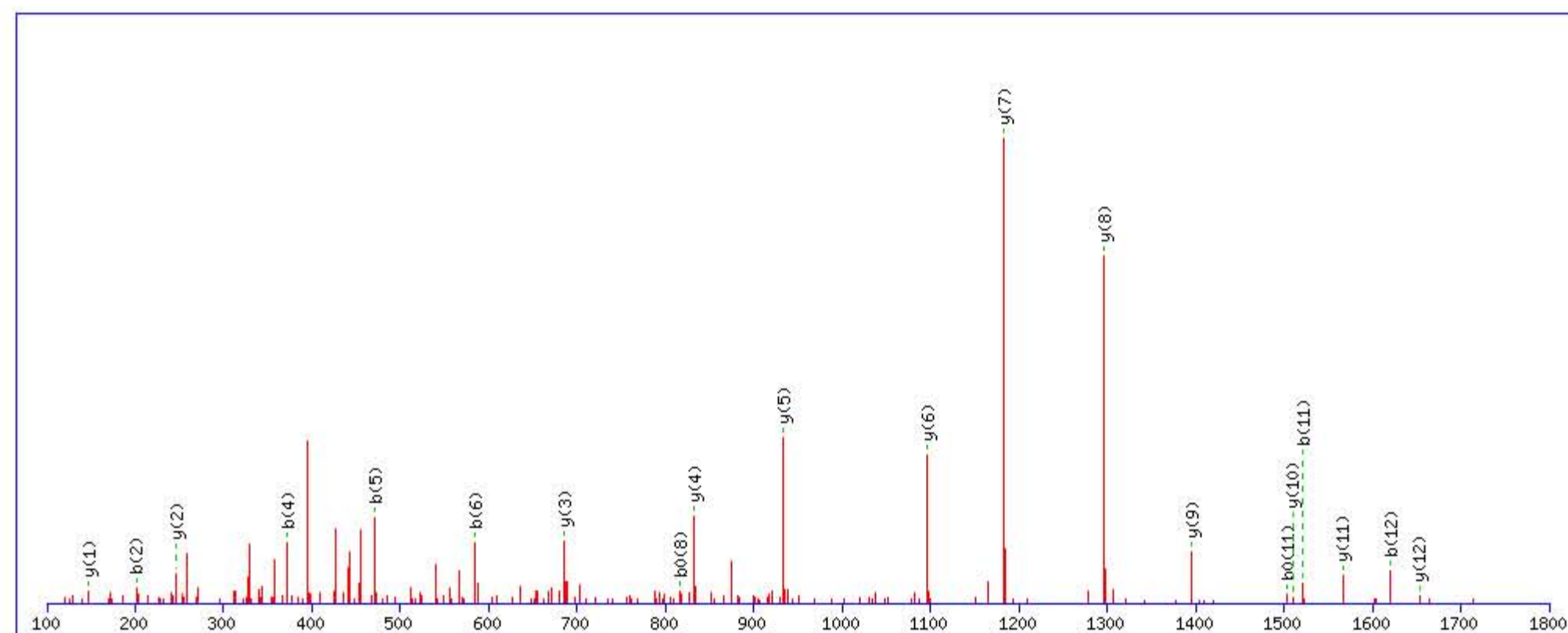
Title: Locus:1.1.1.3295.13 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

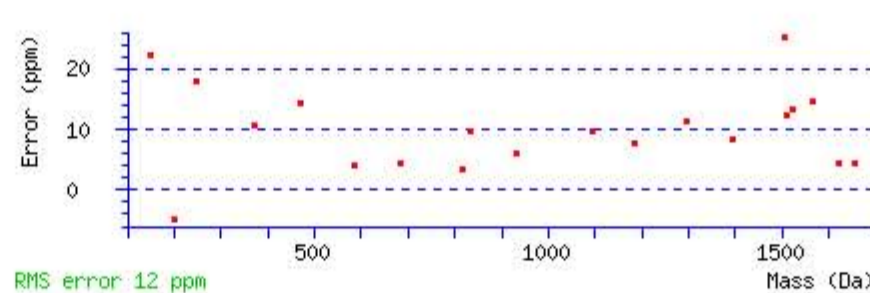
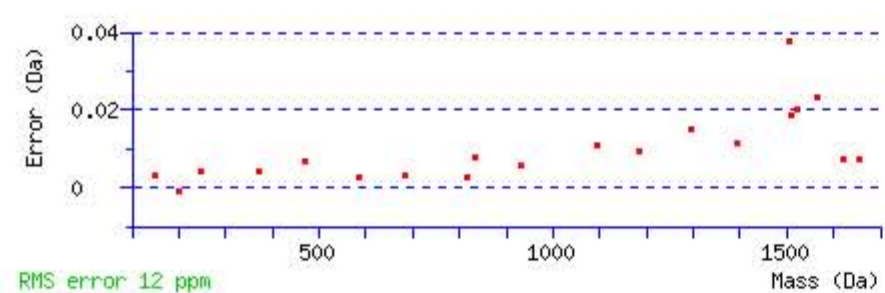
Variable modifications:

Q11 : Biotin:Thermo-21345 (Q)

Ions Score: 97 Expect: 4.5e-009

Matches : 20/128 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	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
97.1	1765.943680	-0.005792	LSGNVLSYTFQVK
7.7	1765.931763	0.006125	NMIEVVTSEMKTLLK
3.6	1765.950882	-0.012994	VTGNVSKKTNLYVMGR
2.5	1765.921005	0.016883	VENTLNIHEDLDKVK
1.4	1765.914490	0.023398	KQLTLQSMRVFDER

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **IACVLPVLM DGIQSH P QKPFYTVG EK**

Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

Match to Query 68285: 3237.665496 from(810.423650,4+) rtinseconds(2571) index(9150)

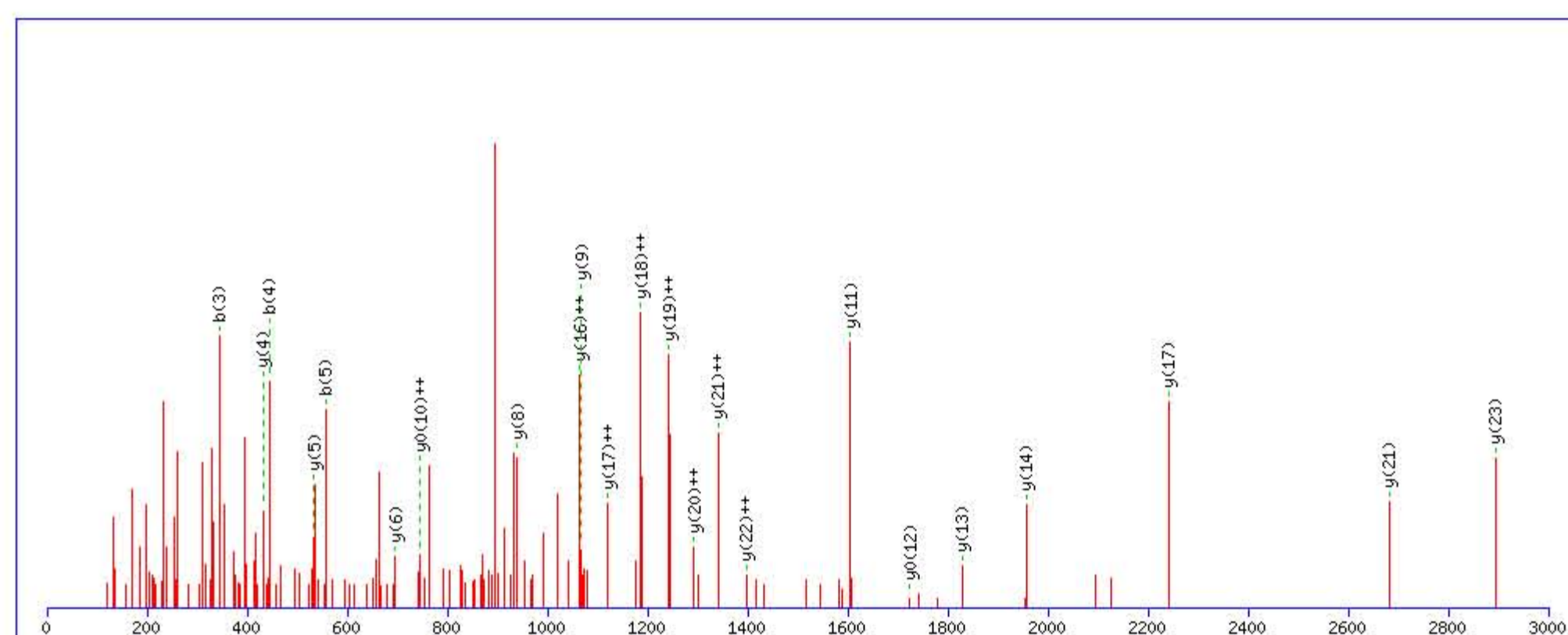
Title: Locus:1.1.1.3331.20 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

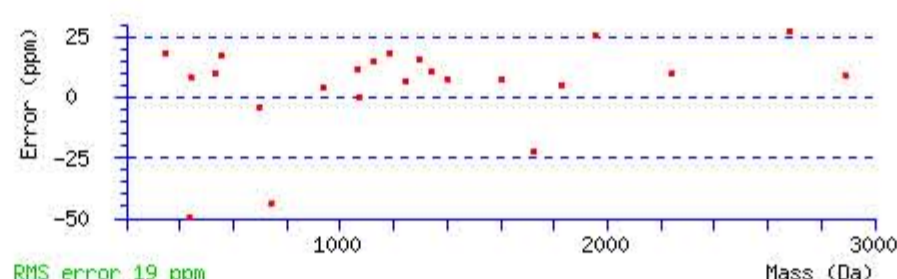
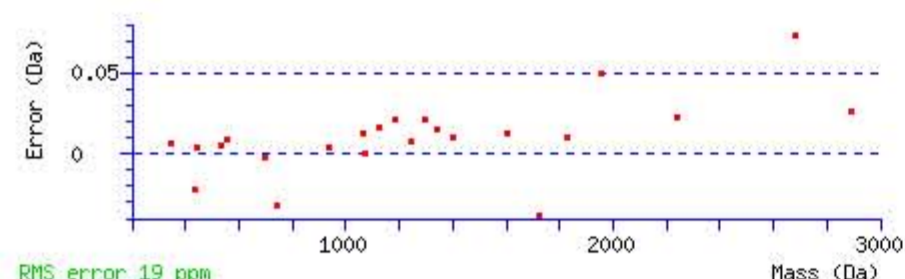
Variable modifications:

Q17 : Biotin:Thermo-21345 (Q)

Ions Score: 45 Expect: 0.00085

Matches : 23/256 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					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 **IACVLPVLM DGIQSH P QKPFYTVG EK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.0	3237.675262	-0.009766	IACVLPVLM DGIQSH P QKPFYTVG EK
35.2	3237.675262	-0.009766	IACVLPVLM DGIQSH P QKPFYTVG EK

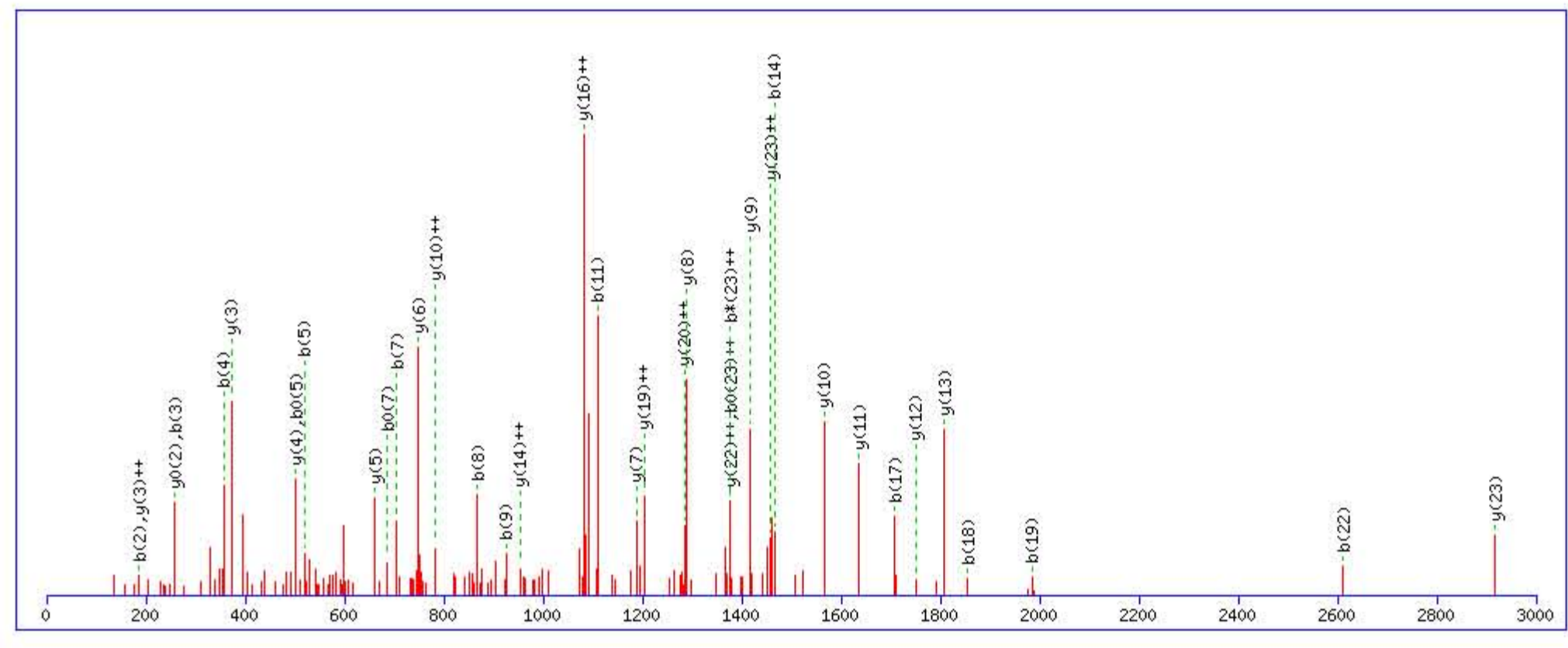
MASCOT Mascot Search Results

Peptide View

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

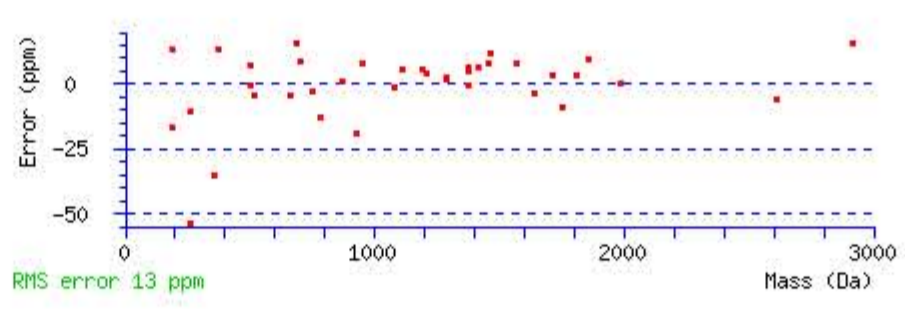
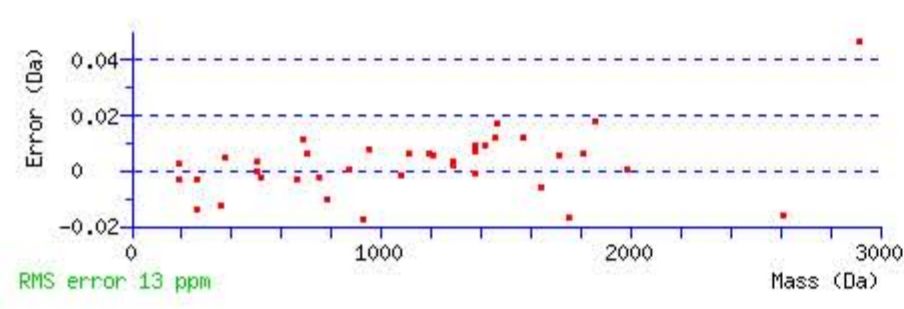
Match to Query 69156: 3272.435772 from(1091.819200,3+) rtinseconds(2161) index(6791)
 Title: Locus:1.1.1.3188.22 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 3272.468933
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q21 : Biotin:Thermo-21345 (Q)
 Ions Score: 95 Expect: 1.6e-009
 Matches : 38/298 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							27
2	187.107718	94.057497			169.097153	85.052214	V	3186.444157	1593.725716	3169.417608	1585.212442	3168.433592	1584.720434	26
3	258.144832	129.576054			240.134267	120.570772	A	3087.375743	1544.191509	3070.349194	1535.678235	3069.365178	1535.186227	25
4	357.213246	179.110261			339.202681	170.104979	V	3016.338629	1508.672952	2999.312080	1500.159678	2998.328064	1499.667670	24
5	520.276575	260.641926			502.266010	251.636643	Y	2917.270215	1459.138745	2900.243666	1450.625471	2899.259650	1450.133463	23
6	577.298039	289.152658			559.287474	280.147375	G	2754.206886	1377.607081	2737.180337	1369.093806	2736.196321	1368.601798	22
7	705.356617	353.181947	688.330068	344.668672	687.346052	344.176664	Q	2697.185422	1349.096349	2680.158873	1340.583074	2679.174857	1340.091066	21
8	868.419946	434.713611	851.393397	426.200337	850.409381	425.708329	Y	2569.126844	1285.067060	2552.100295	1276.553785	2551.116279	1276.061777	20
9	925.441410	463.224343	908.414861	454.711069	907.430845	454.219061	G	2406.063515	1203.535395	2389.036966	1195.022121	2388.052950	1194.530113	19
10	982.462874	491.735075	965.436325	483.221801	964.452309	482.729793	G	2349.042051	1175.024663	2332.015502	1166.511389	2331.031486	1166.019381	18
11	1110.521452	555.764364	1093.494903	547.251090	1092.510887	546.759082	Q	2292.020587	1146.513931	2274.994038	1138.000657	2274.010022	1137.508649	17
12	1207.574216	604.290746	1190.547667	595.777472	1189.563651	595.285464	P	2163.962009	1082.484642	2146.935460	1073.971368	2145.951444	1073.479360	16
13	1367.604865	684.306071	1350.578316	675.792796	1349.594300	675.300788	C	2066.909245	1033.958260	2049.882696	1025.444986	2048.898680	1024.952978	15
14	1466.673279	733.840278	1449.646730	725.327003	1448.662714	724.834995	V	1906.878596	953.942936	1889.852047	945.429662	1888.868031	944.937654	14
15	1523.694743	762.351010	1506.668194	753.837735	1505.684178	753.345727	G	1807.810182	904.408729	1790.783633	895.895455	1789.799617	895.403446	13
16	1637.737670	819.372473	1620.711121	810.859199	1619.727105	810.367191	N	1750.788718	875.897997	1733.762169	867.384723	1732.778153	866.892715	12
17	1708.774784	854.891030	1691.748235	846.377756	1690.764219	845.885748	A	1636.745791	818.876534	1619.719242	810.363259	1618.735226	809.871251	11
18	1855.843198	928.425237	1838.816649	919.911963	1837.832633	919.419955	F	1565.708677	783.357977	1548.682128	774.844702	1547.698112	774.352694	10
19	1984.885791	992.946534	1967.859242	984.433259	1966.875226	983.941251	E	1418.640263	709.823770	1401.613714	701.310495	1400.629698	700.818487	9
20	2085.933470	1043.470373	2068.906921	1034.957098	2067.922905	1034.465090	T	1289.597670	645.302473	1272.571121	636.789199	1271.587105	636.297190	8
21	2525.158796	1263.083036	2508.132247	1254.569761	2507.148231	1254.077754	Q	1188.549991	594.778634	1171.523442	586.265359	1170.539426	585.773351	7
22	2612.190824	1306.599050	2595.164275	1298.085776	2594.180259	1297.593768	S	749.324665	375.165970	732.298116	366.652696	731.314100	366.160688	6
23	2772.221473	1386.614374	2755.194924	1378.101100	2754.210908	1377.609092	C	662.292637	331.649956	645.266088	323.136682	644.282072	322.644674	5
24	2901.264066	1451.135671	2884.237517	1442.622396	2883.253501	1442.130389	E	502.261988	251.634632	485.235439	243.121357	484.251423	242.629349	4
25	2998.316830	1499.662053	2981.290281	1491.148778	2980.306265	1490.656771	P	373.219395	187.113335	356.192846	178.600061	355.208830	178.108053	3
26	3099.364509	1550.185892	3082.337960	1541.672618	3081.353944	1541.180610	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
27							R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
94.9	3272.468933	-0.033161	SVAVYGQYGGQPCVGNAFETQSCEPTR
30.3	3272.468933	-0.033161	SVAVYGQYGGQPCVGNAFETQSCEPTR
10.3	3272.468933	-0.033161	SVAVYGQYGGQPCVGNAFETQSCEPTR

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 16495: 983.530228 from(492.772390,2+) rtinseconds(1410) index(18100)

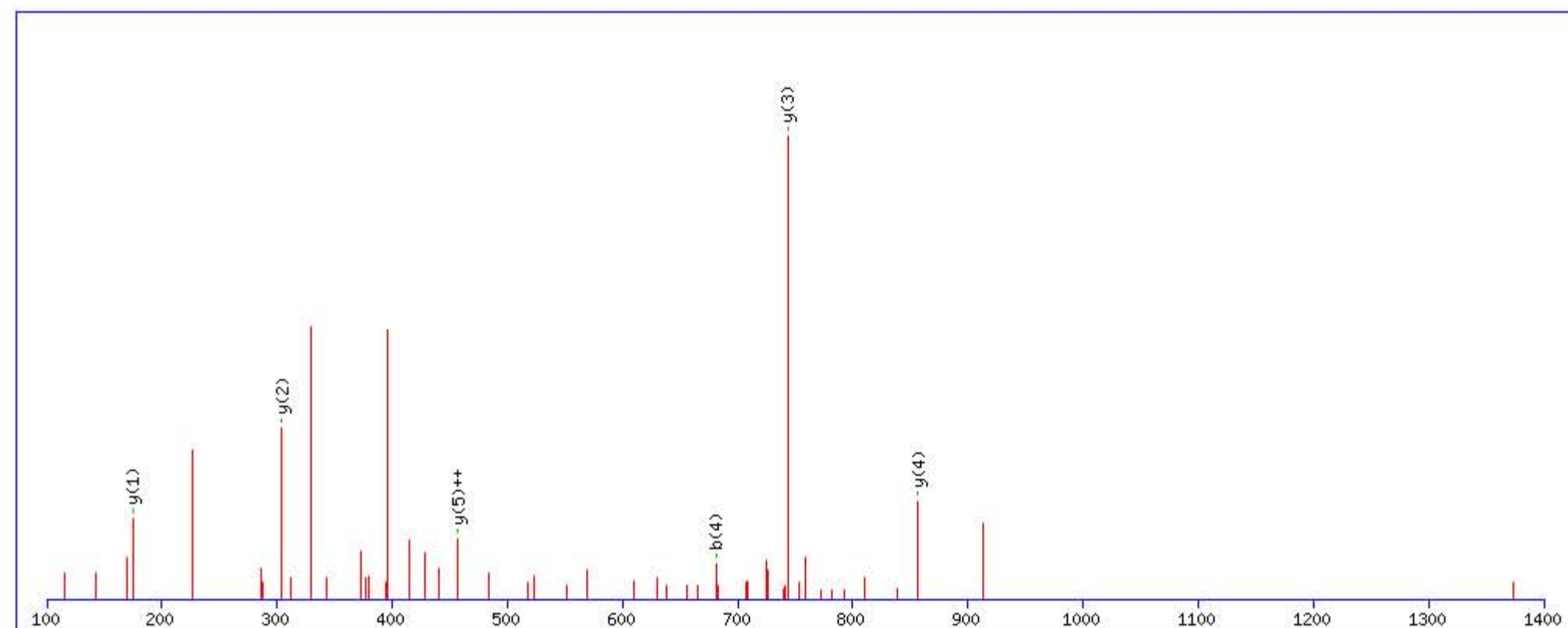
Title: Locus:1.1.1.1372.16 File:"2013-07-02 CLN FXIII 30 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

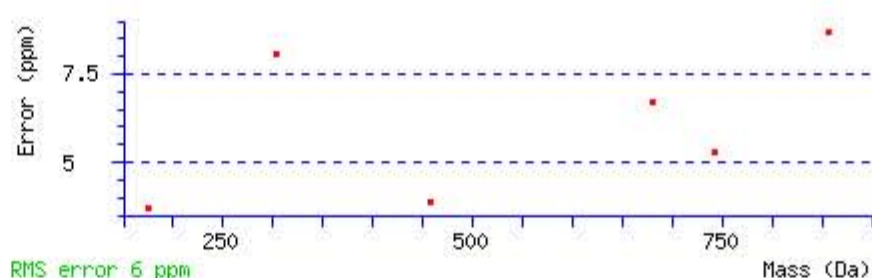
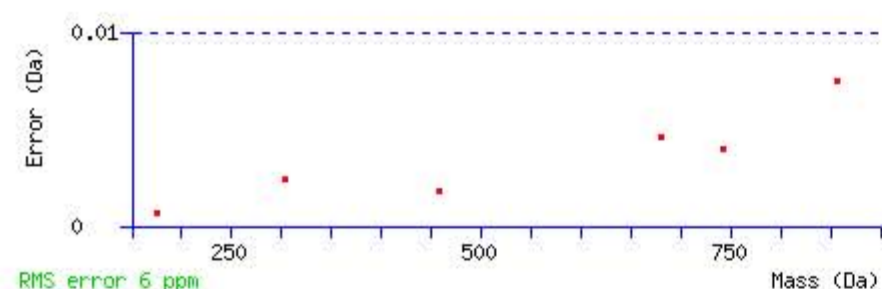
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 30 Expect: 0.022

Matches : 6/44 fragment ions using 8 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
29.5	983.522217	0.008011	AGIQER
26.1	983.522217	0.008011	QIQER
26.1	983.522217	0.008011	QLQER
15.7	983.522217	0.008011	AGLEQR
13.6	983.522217	0.008011	IQQER
13.6	983.522217	0.008011	LQQER
11.8	983.530090	0.000138	QLLNHFGR
10.7	983.522217	0.008011	QQLER
10.6	983.522202	0.008026	KLMENPPR
10.6	983.522217	0.008011	QLEQR

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

MASCOT SCIENCE Mascot Search Results

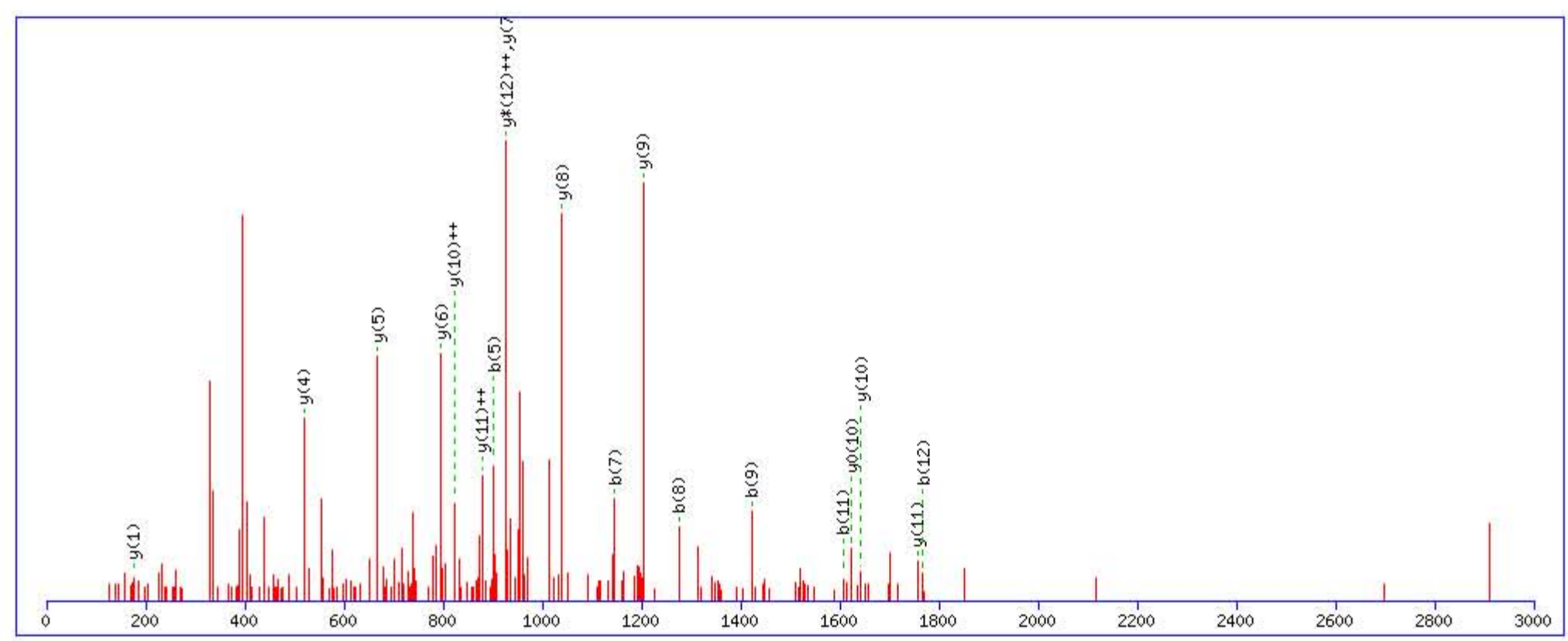
Peptide View

MS/MS Fragmentation of **ALDQYLMEFNACR**

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

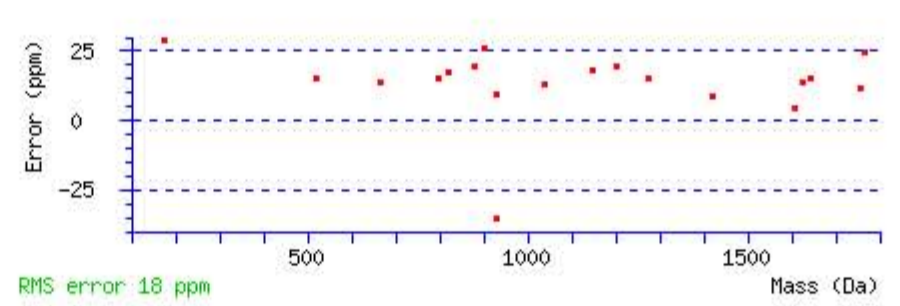
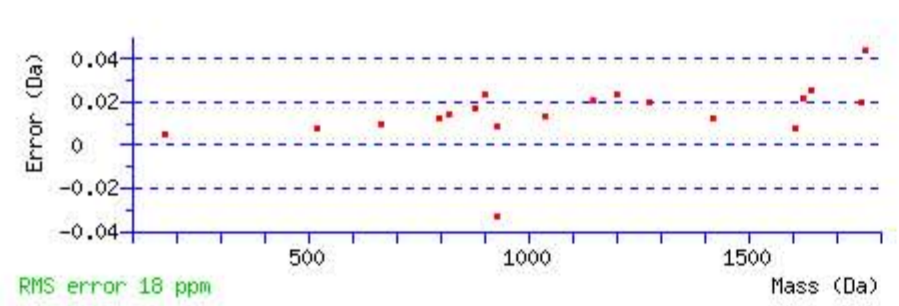
Match to Query 47785: 1940.895288 from(971.454920,2+) rtinseconds(2554) index(42002)
 Title: Locus:1.1.1.2911.9 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 47 Expect: 0.00073
 Matches : 19/124 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	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
47.4	1940.894669	0.000619	ALDQYLMEFNACR

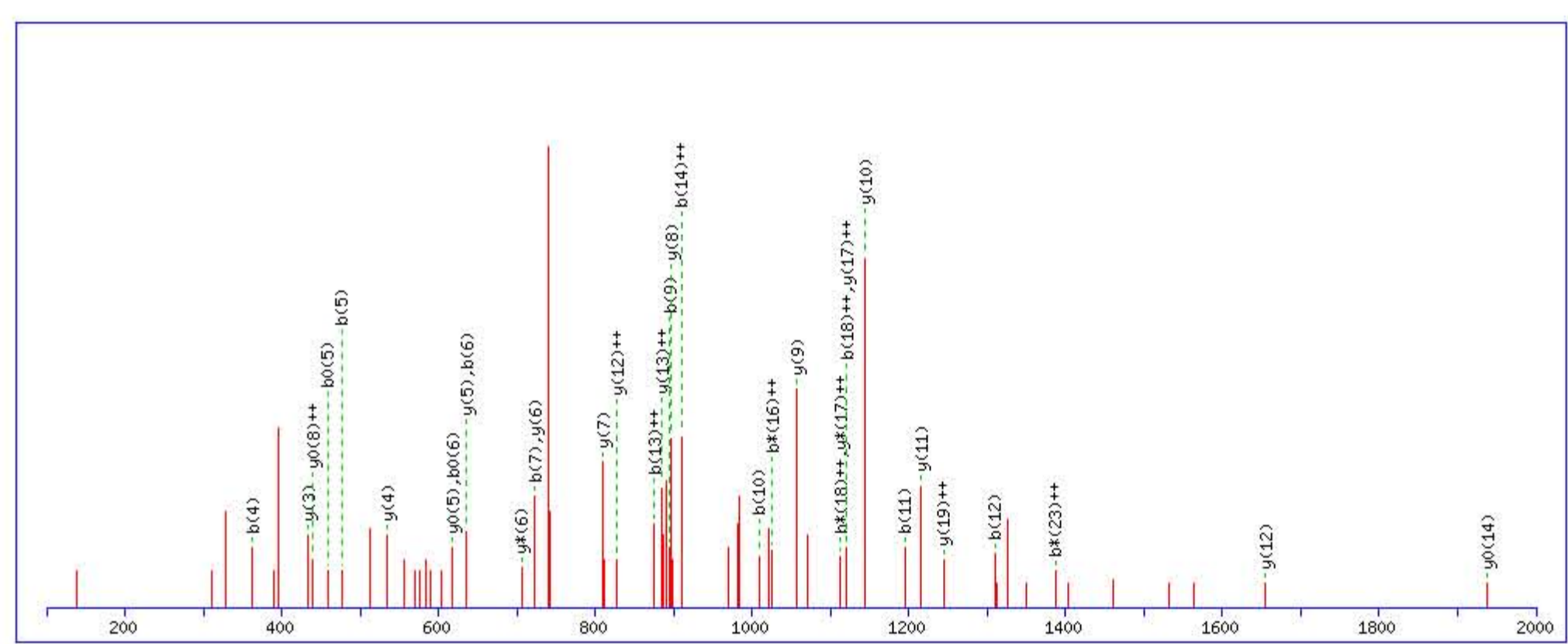
Mascot Search Results

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

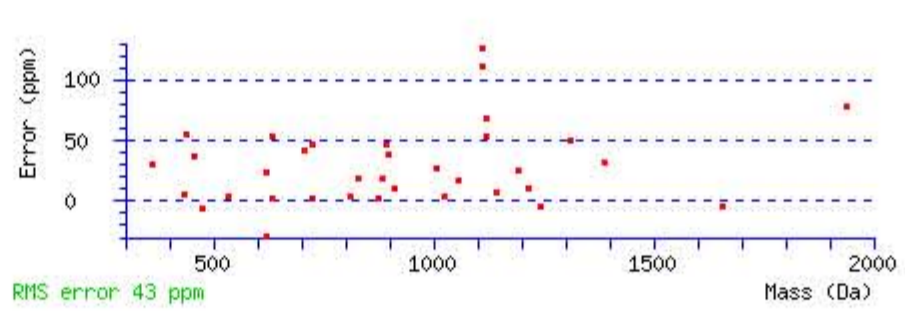
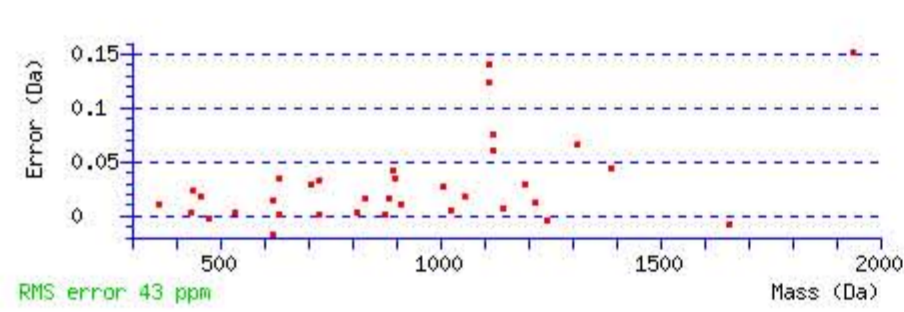
Match to Query 48600: 2962.244802 from(988.422210,3+) rtinseconds(2390) index(41098)
 Title: Locus:1.1.1.2854.26 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 47 Expect: 9e-005
 Matches : 35/240 fragment ions using 65 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	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	1025.968082	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	2310.96417	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
47.3	2962.271835	-0.027033	FGGTICSGDIWDQASCSSSTTCVR

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 50560: 2030.973768 from(1016.494160,2+) rtinseconds(1717) index(36774)

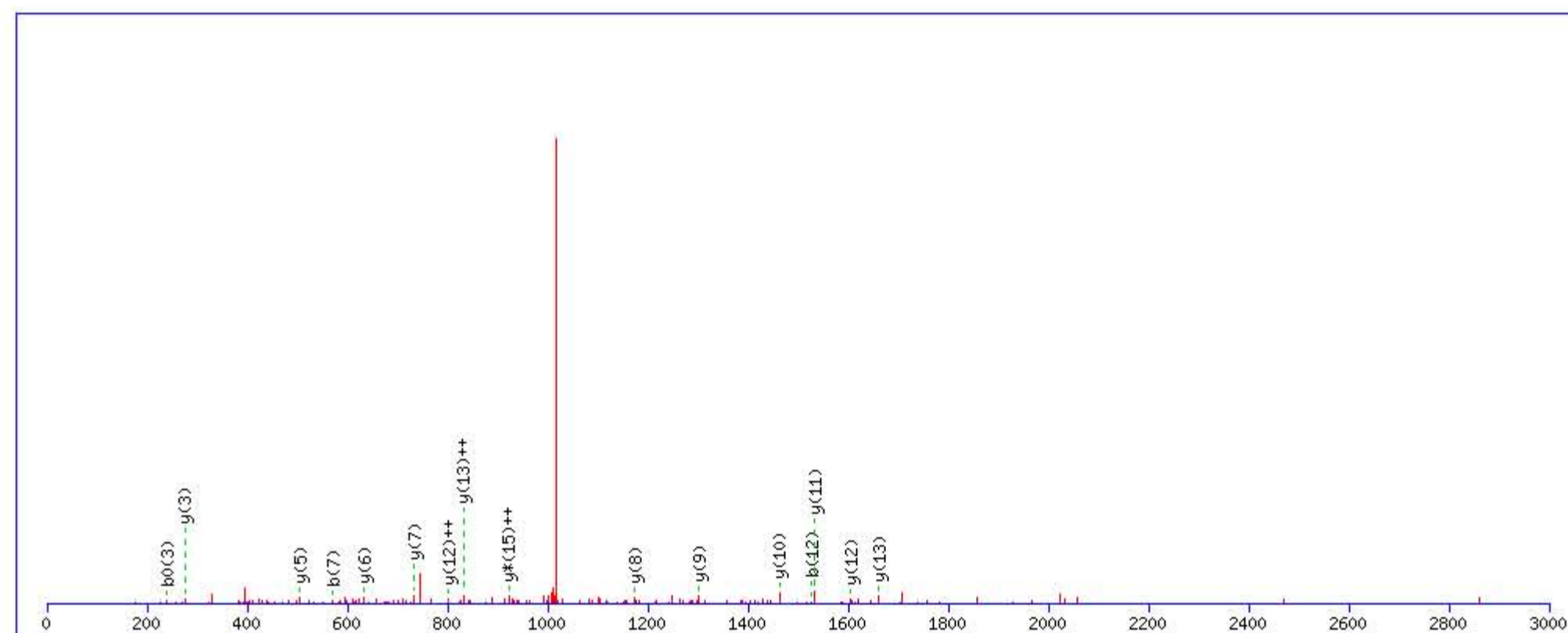
Title: Locus:1.1.1.2620.12 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

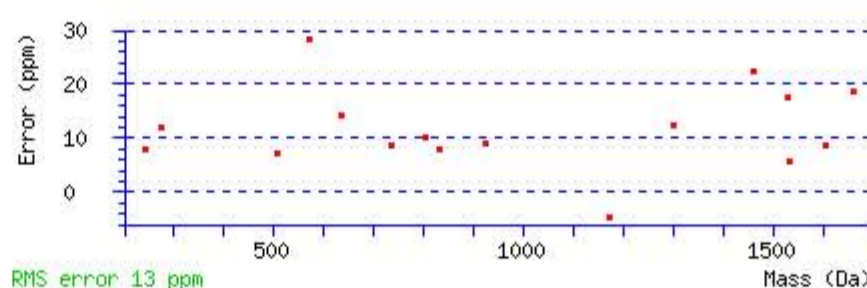
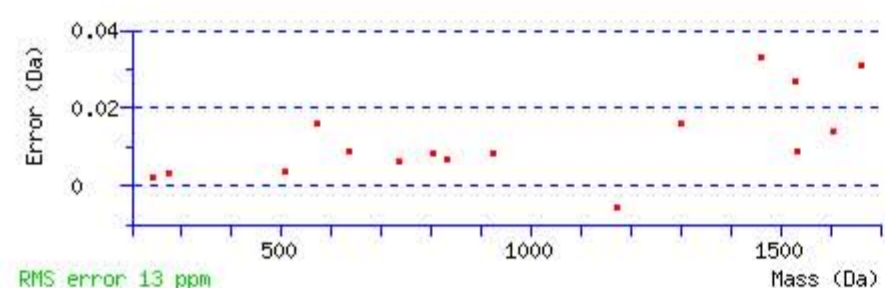
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 43 Expect: 0.0011

Matches : 16/164 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
42.7	2030.976501	-0.002733	LGSLGAACEQTQTEGAK
22.7	2030.976501	-0.002733	LGSLGAACEQTQTEGAK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **AIDEDCSQYEPGPSQK**

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

Match to Query 54925: 2247.007928 from(1124.511240,2+) rtinseconds(1904) index(37923)

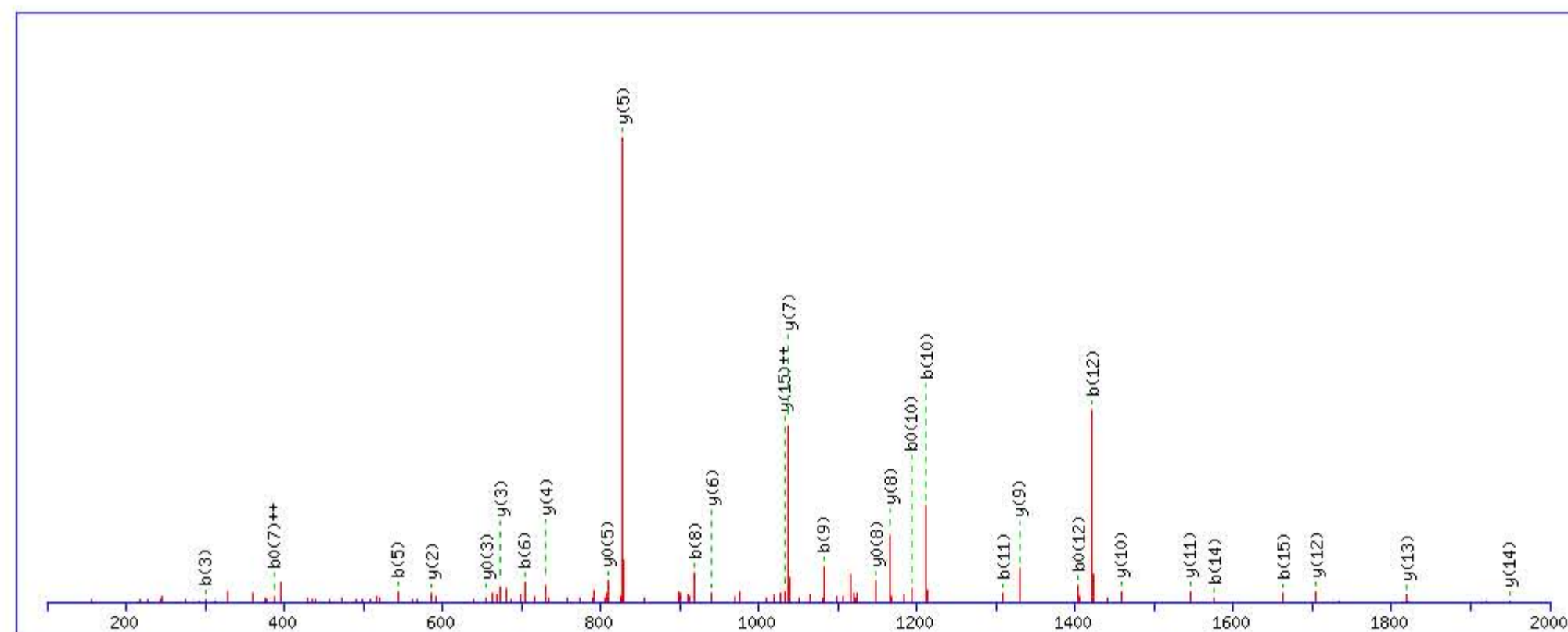
Title: Locus:1.1.1.2685.26 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

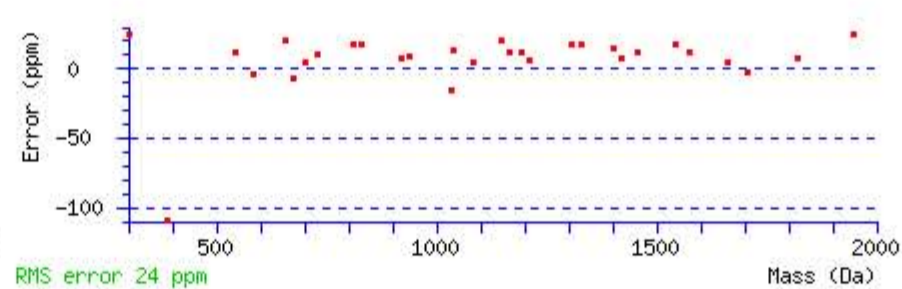
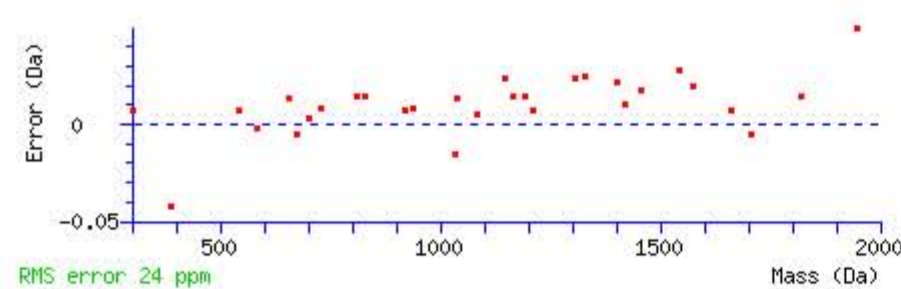
Variable modifications:

Q16 : Biotin:Thermo-21345 (Q)

Ions Score: 87 Expect: 2.1e-008

Matches : 30/170 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							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 **AIDEDCSQYEPGPSQK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

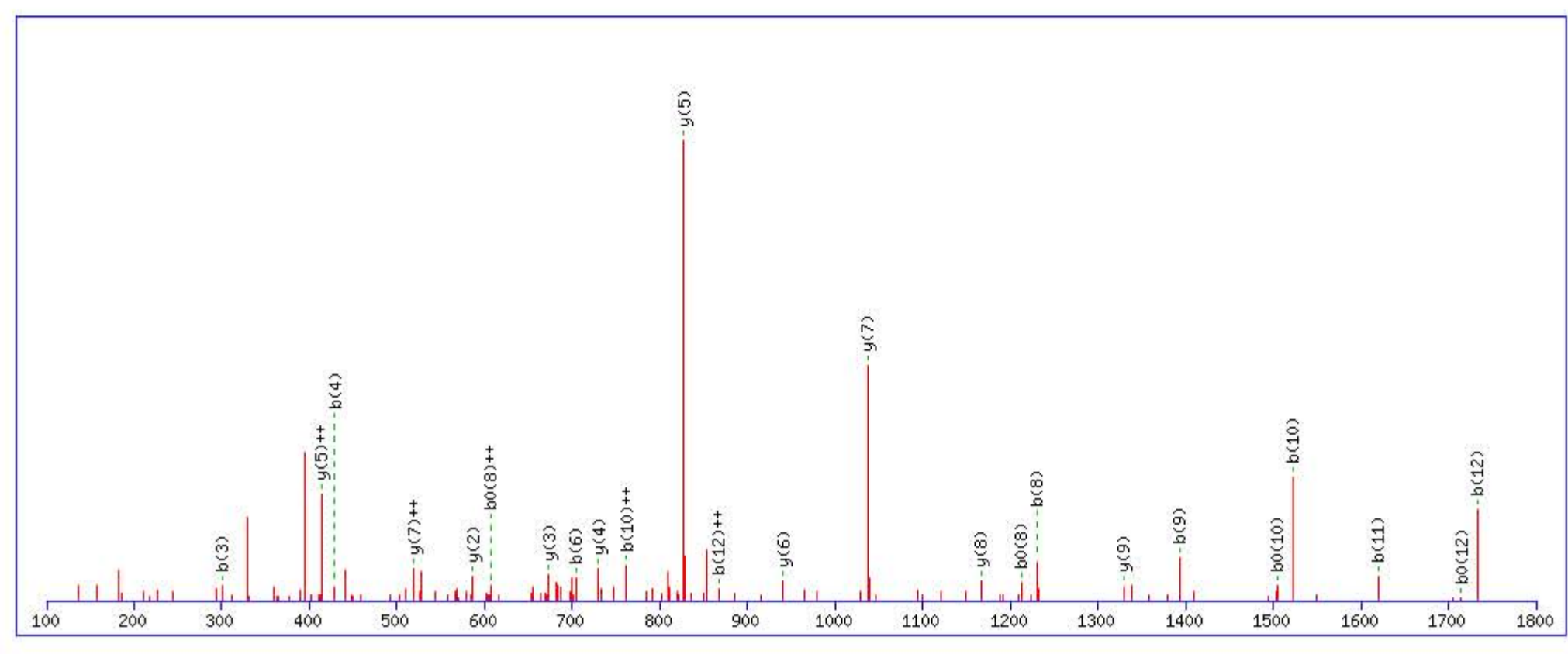
Score	Mr(calc):	Delta	Sequence
86.7	2247.018753	-0.010825	AIDEDCSQYEPGPSQK
5.3	2247.018753	-0.010825	AIDEDCSQYEPGPSQK

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

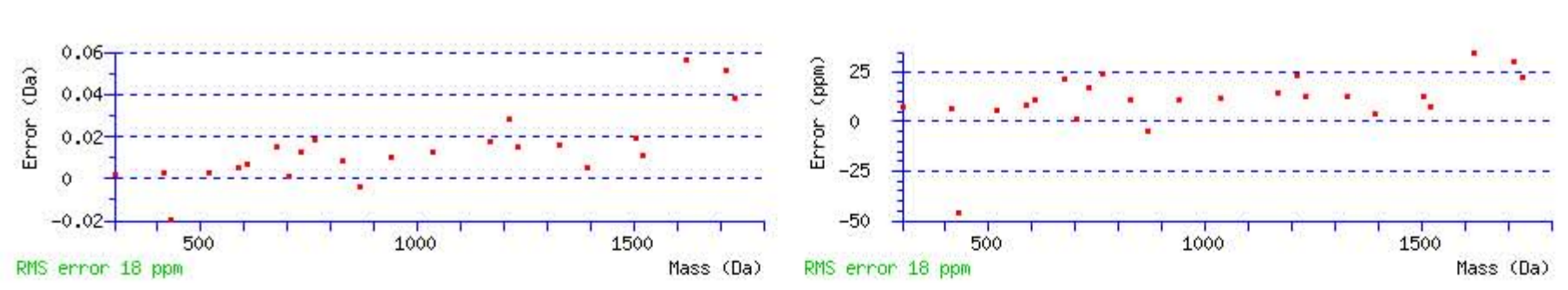
Match to Query 60761: 2558.191482 from(853.737770,3+) rtinseconds(2151) index(39616)
 Title: Locus:1.1.1.2771.11 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 2558.185501
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q8 : Biotin:Thermo-21345 (Q)
 Q16 : Biotin:Thermo-21345 (Q)
 Ions Score: 44 Expect: 0.00012
 Matches : 24/170 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	72.044390	36.525833					A							17
2	185.128454	93.067865					I	2488.155682	1244.581479	2471.129133	1236.068204	2470.145117	1235.576196	16
3	300.155397	150.581336			282.144832	141.576054	D	2375.071618	1188.039447	2358.045069	1179.526172	2357.061053	1179.034164	15
4	429.197990	215.102633			411.187425	206.097351	E	2260.044675	1130.525975	2243.018126	1122.012701	2242.034110	1121.520693	14
5	544.224933	272.616105			526.214368	263.610822	D	2131.002082	1066.004679	2113.975533	1057.491404	2112.991517	1056.999396	13
6	704.255582	352.631429			686.245017	343.626147	C	2015.975139	1008.491208	1998.948590	999.977933	1997.964574	999.485925	12
7	791.287610	396.147443			773.277045	387.142161	S	1855.944490	928.475883	1838.917941	919.962609	1837.933925	919.470601	11
8	1230.512936	615.760106	1213.486387	607.246832	1212.502371	606.754824	Q	1768.912462	884.959869	1751.885913	876.446595	1750.901897	875.954587	10
9	1393.576265	697.291771	1376.549716	688.778496	1375.565700	688.286488	Y	1329.687136	665.347206	1312.660587	656.833932	1311.676571	656.341924	9
10	1522.618858	761.813067	1505.592309	753.299793	1504.608293	752.807785	E	1166.623807	583.815541	1149.597258	575.302267	1148.613242	574.810259	8
11	1619.671622	810.339449	1602.645073	801.826175	1601.661057	801.334167	P	1037.581214	519.294245	1020.554665	510.780971	1019.570649	510.288963	7
12	1732.755686	866.881481	1715.729137	858.368207	1714.745121	857.876198	I	940.528450	470.767863	923.501901	462.254589	922.517885	461.762581	6
13	1829.808450	915.407863	1812.781901	906.894589	1811.797885	906.402581	P	827.444386	414.225831	810.417837	405.712557	809.433821	405.220549	5
14	1886.829914	943.918595	1869.803365	935.405321	1868.819349	934.913312	G	730.391622	365.699449	713.365073	357.186175	712.381057	356.694167	4
15	1973.861942	987.434609	1956.835393	978.921335	1955.851377	978.429327	S	673.370158	337.188717	656.343609	328.675443	655.359593	328.183435	3
16	2413.087268	1207.047272	2396.060719	1198.533997	2395.076703	1198.041989	Q	586.338130	293.672703	569.311581	285.159429			2
17							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.0	2558.185501	0.005981	AIDEDCSQYEPIPGSQK
2.3	2558.214981	-0.023499	TSPQSAPPSSPLSPNWWVSPDHQR
1.0	2558.171906	0.019576	QGSQSGQSPGHGQRGSGSRQSPSYGR

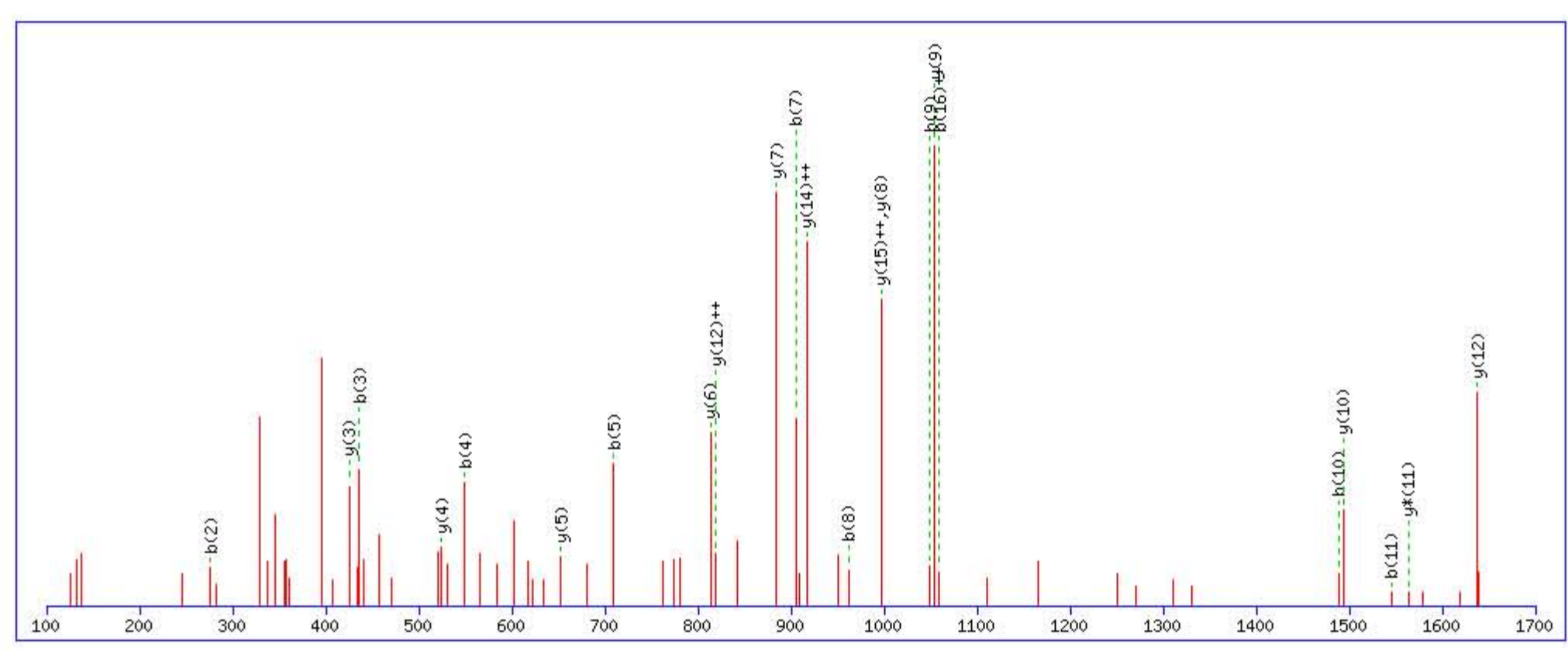
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **CDCICPVGSQGLACEVS^YR**
 Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

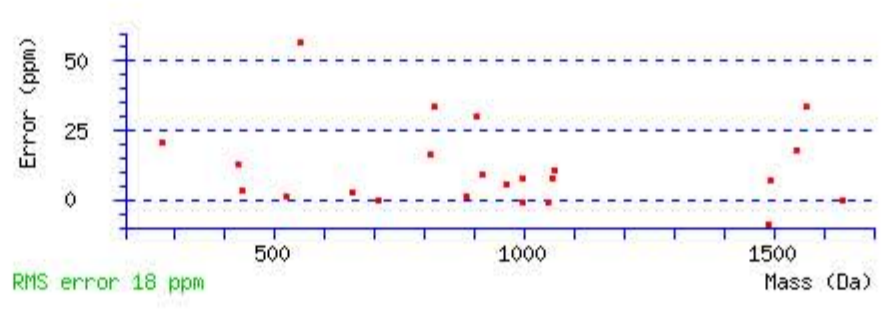
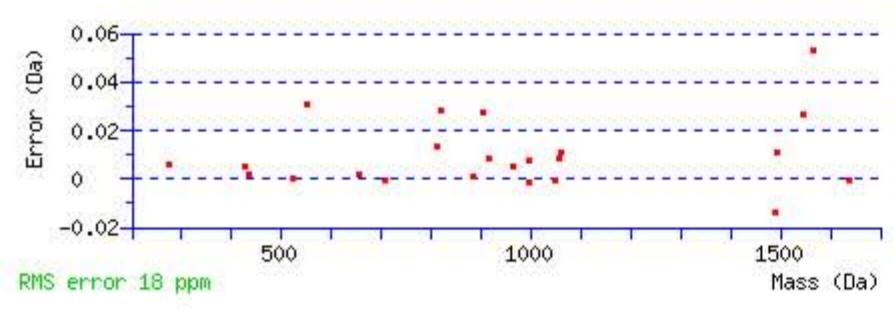
Match to Query 60639: 2541.095112 from(848.038980,3+) rtinseconds(2163) index(22823)
 Title: Locus:1.1.1.1634.23 File:"2013-07-02 CLN FXIII 30 min 2nd F 2.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 59 Expect: 4.5e-006
 Matches : 23/192 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	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 **CDCICPVGSQGLACEVS^YR**
 (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	2541.094299	0.000813	CDCICPVGSQGLACEVS^YR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **SLPVSDSVLSGFQQR**

Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

Match to Query 47515: 1930.969968 from(966.492260,2+) rtinseconds(2508) index(41778)

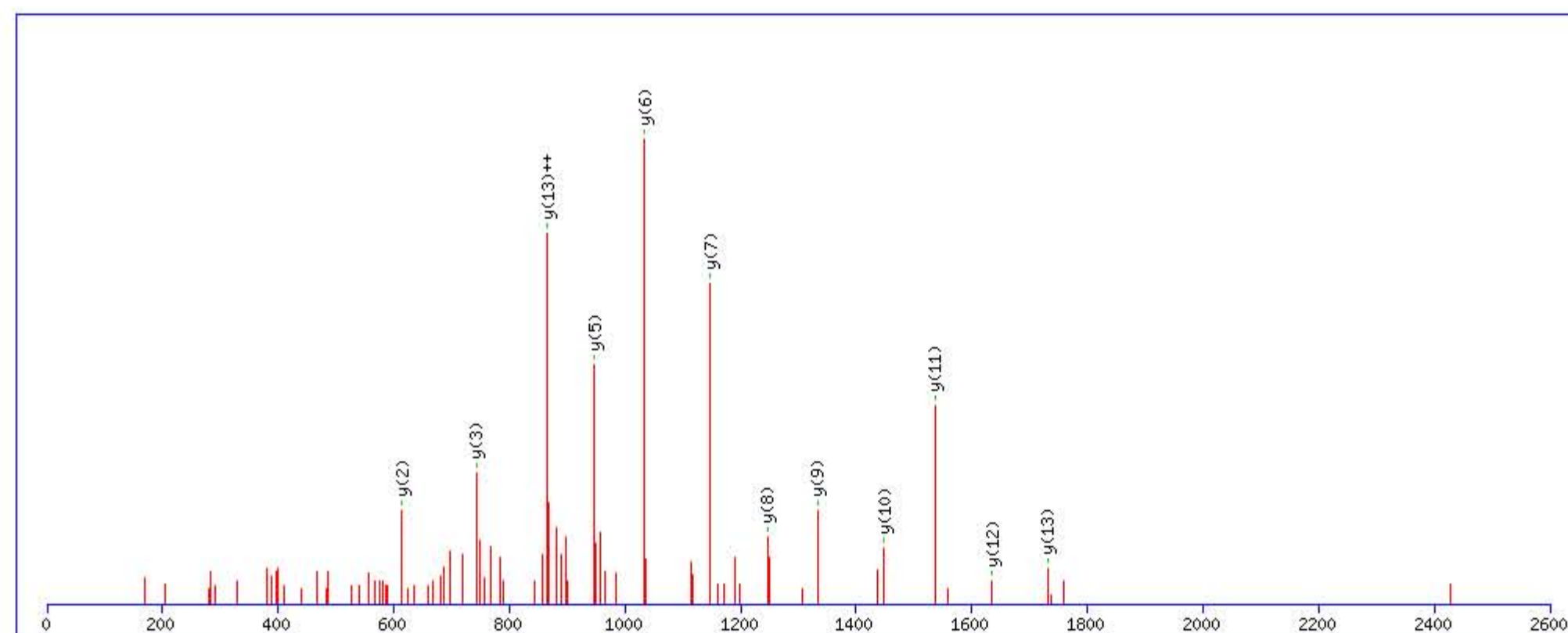
Title: Locus:1.1.1.2895.26 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

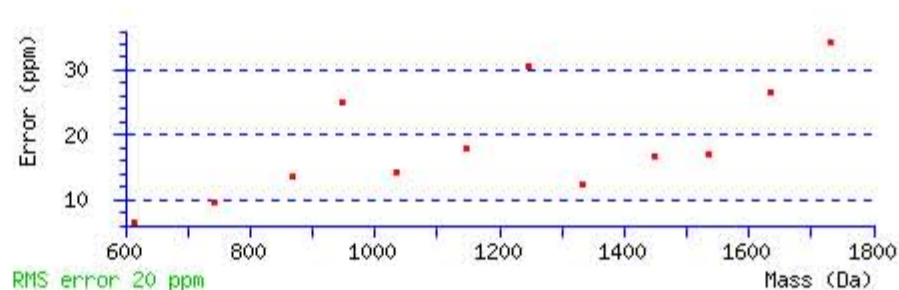
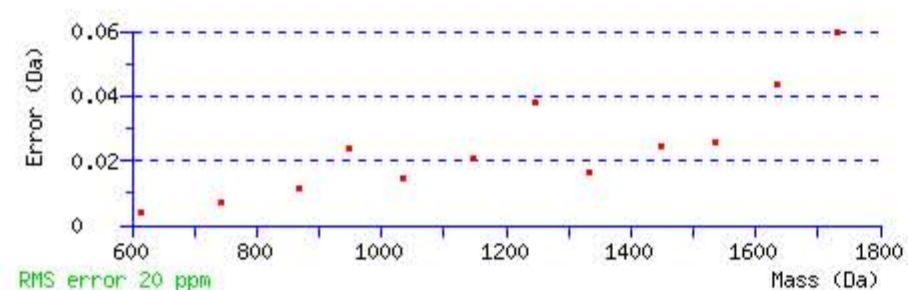
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 92 Expect: 4.6e-009

Matches : 12/138 fragment ions using 16 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.039304	44.523290			70.028739	35.518008	S							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 [SLPVSDSVLSGFQQR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
91.9	1930.982254	-0.012286	SLPVSDSVLSGFQQR
3.0	1930.989410	-0.019442	EAQSQLIKSDEMQLRLR

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

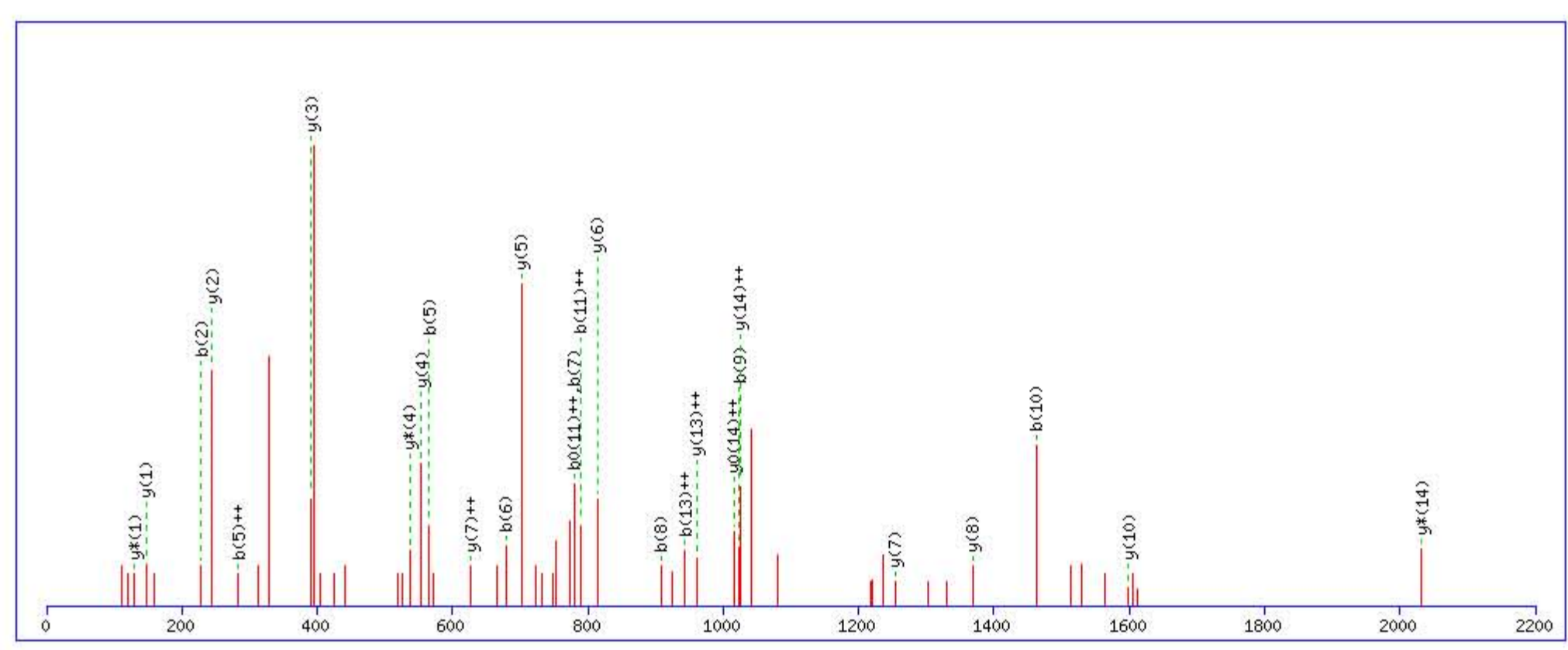
MASCOT Search Results

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

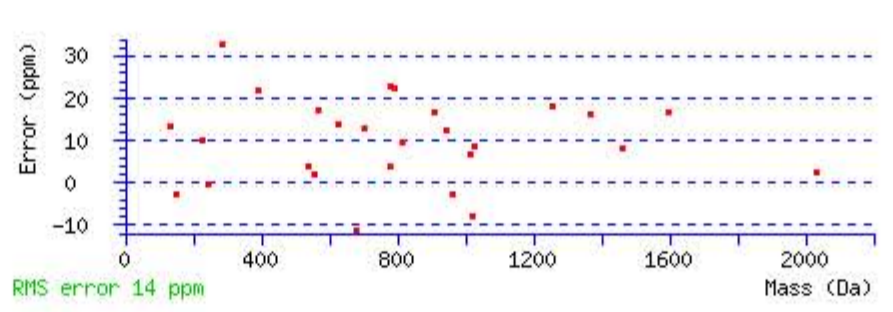
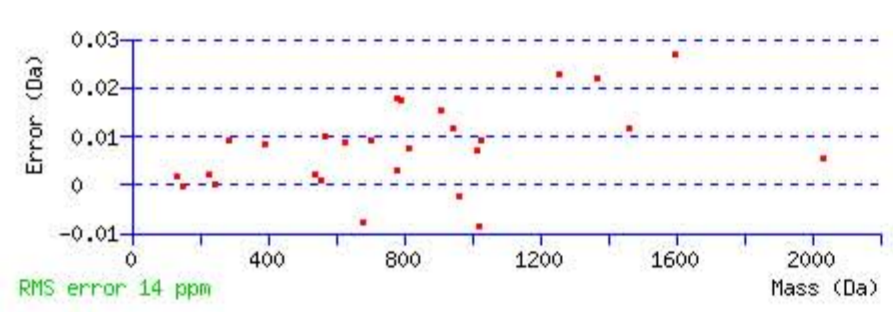
Match to Query 55595: 2275.144632 from(759.388820,3+) rtinseconds(2370) index(23979)
 Title: Locus:1.1.1.1706.25 File:"2013-07-02 CLN FXIII 30 min 2nd F 2.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 42 Expect: 0.00039
 Matches : 27/160 fragment ions using 55 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.075690	50.541483					V							16
2	228.134268	114.570772	211.107719	106.057498			Q	2177.073591	1089.040433	2160.047042	1080.527159	2159.063026	1080.035151	15
3	357.176861	179.092069	340.150312	170.578794	339.166296	170.086786	E	2049.015013	1025.011144	2031.988464	1016.497870	2031.004448	1016.005862	14
4	428.213975	214.610626	411.187426	206.097351	410.203410	205.605343	A	1919.972420	960.489848	1902.945871	951.976573	1901.961855	951.484565	13
5	565.272887	283.140082	548.246338	274.626807	547.262322	274.134799	H	1848.935306	924.971291	1831.908757	916.458016	1830.924741	915.966008	12
6	678.356951	339.682114	661.330402	331.168839	660.346386	330.676831	L	1711.876394	856.441835	1694.849845	847.928561	1693.865829	847.436552	11
7	779.404630	390.205953	762.378081	381.692679	761.394065	381.200671	T	1598.792330	799.899803	1581.765781	791.386529	1580.781765	790.894521	10
8	908.447223	454.727250	891.420674	446.213975	890.436658	445.721967	E	1497.744651	749.375963	1480.718102	740.862689	1479.734086	740.370681	9
9	1023.474166	512.240721	1006.447617	503.727447	1005.463601	503.235439	D	1368.702058	684.854667	1351.675509	676.341392	1350.691493	675.849384	8
10	1462.699492	731.853384	1445.672943	723.340110	1444.688927	722.848101	Q	1253.675115	627.341195	1236.648566	618.827921			7
11	1575.783556	788.395416	1558.757007	779.882141	1557.772991	779.390133	I	814.449789	407.728533	797.423240	399.215258			6
12	1722.851970	861.929623	1705.825421	853.416349	1704.841405	852.924340	F	701.365725	351.186501	684.339176	342.673226			5
13	1885.915299	943.461288	1868.888750	934.948013	1867.904734	934.456005	Y	554.297311	277.652294	537.270762	269.139019			4
14	2032.983713	1016.995495	2015.957164	1008.482220	2014.973148	1007.990212	F	391.233982	196.120629	374.207433	187.607354			3
15	2130.036477	1065.521876	2113.009928	1057.008602	2112.025912	1056.516594	P	244.165568	122.586422	227.139019	114.073147			2
16							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.5	2275.134720	0.009912	VQEAHLTEDQIFYFPK
16.5	2275.134720	0.009912	VQEAHLTEDQIFYFPK
5.9	2275.166412	-0.021780	AMEKLV RVIDQEMQAIGGQK
3.6	2275.160538	-0.015906	VLPYCWKGMTPEQQAIRK

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 57085: 2366.084472 from(789.702100,3+) rtinseconds(2552) index(58916)

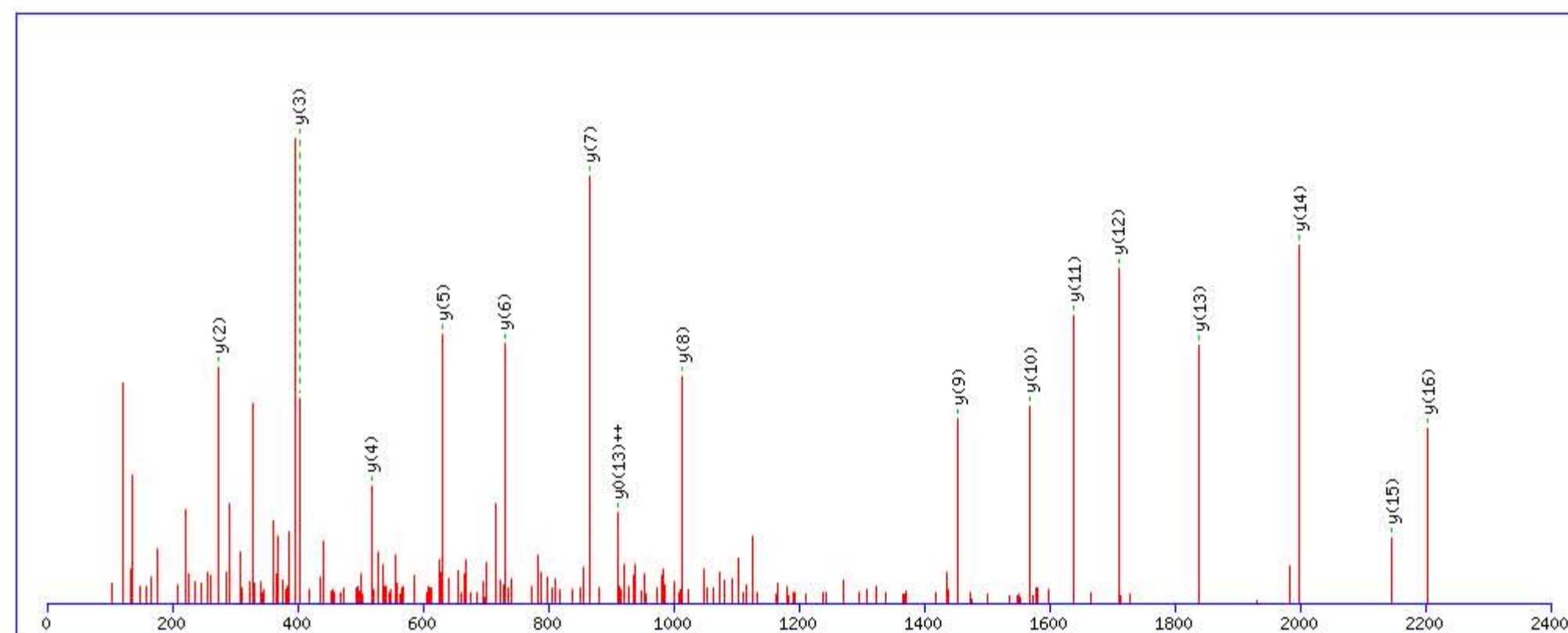
Title: Locus:1.1.1.3374.6 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

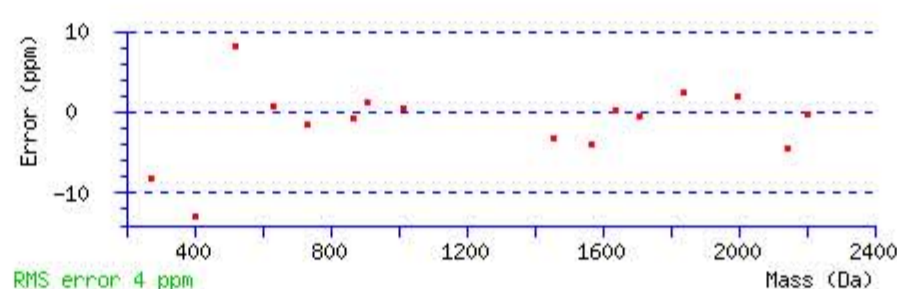
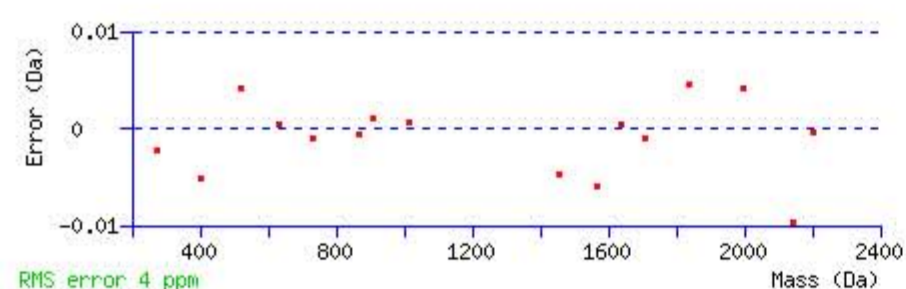
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 137 Expect: 2.4e-013

Matches : 16/164 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	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
137.2	2366.082382	0.002090	YGFCEAADQFHVLDEVR

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

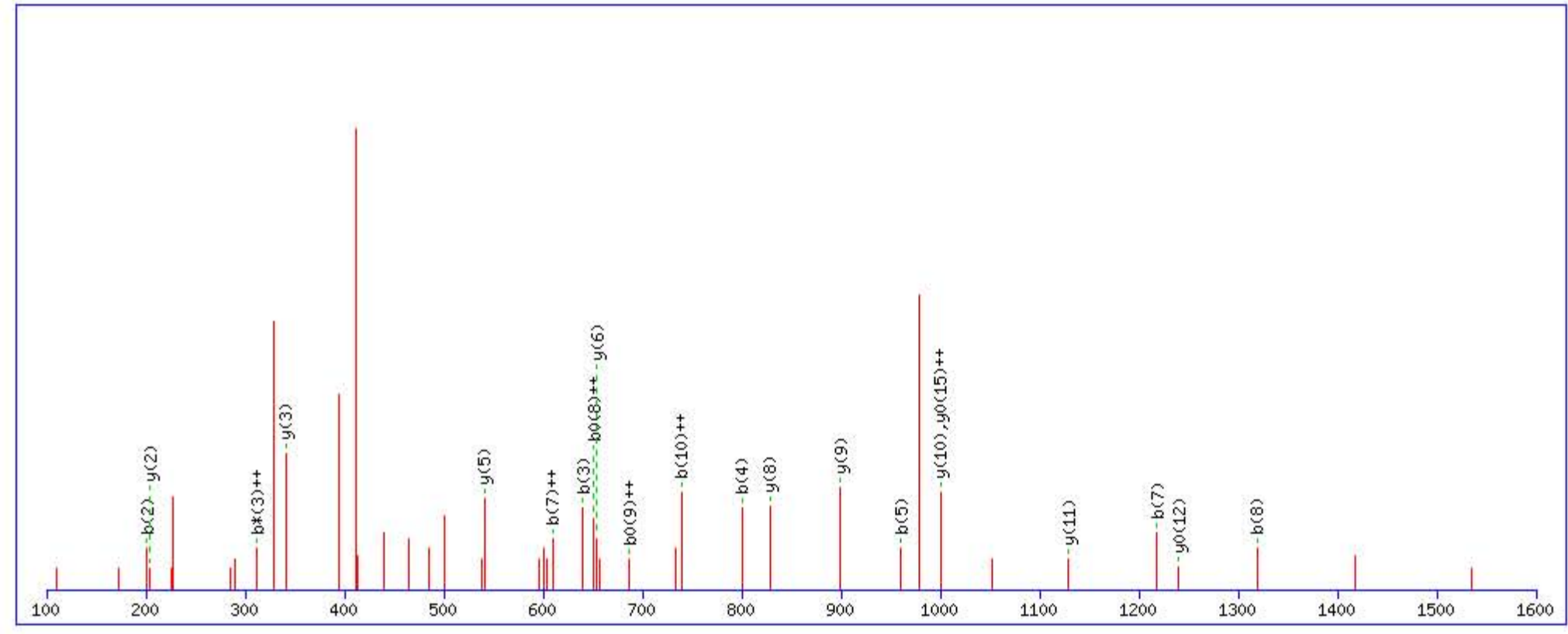
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **AEQCCEETASSISLHGK**
 Found in **CO9_HUMAN**, Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2

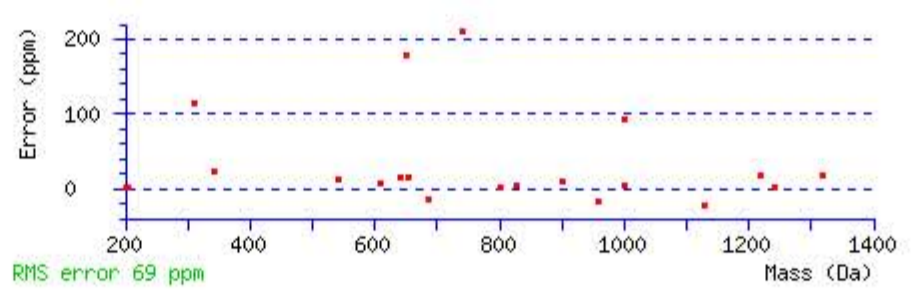
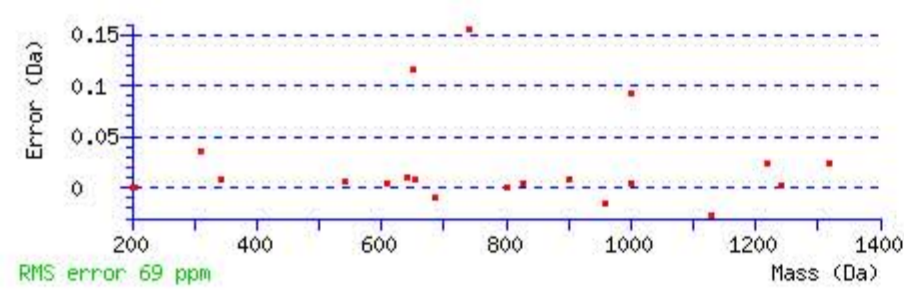
Match to Query 54318: 2216.987862 from(740.003230,3+) rtinseconds(1571) index(36020)
 Title: Locus:1.1.1.2569.18 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 44 Expect: 0.00032
 Matches : 21/178 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							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
44.2	2216.986404	0.001458	AEQCCEETASSISLHGK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **RPDSLQHVLLPVLDR**

Found in **CFAD_HUMAN**, Complement factor D OS=Homo sapiens GN=CFD PE=1 SV=5

Match to Query 51408: 2068.186016 from(518.053780,4+) rtinseconds(2371) index(40971)

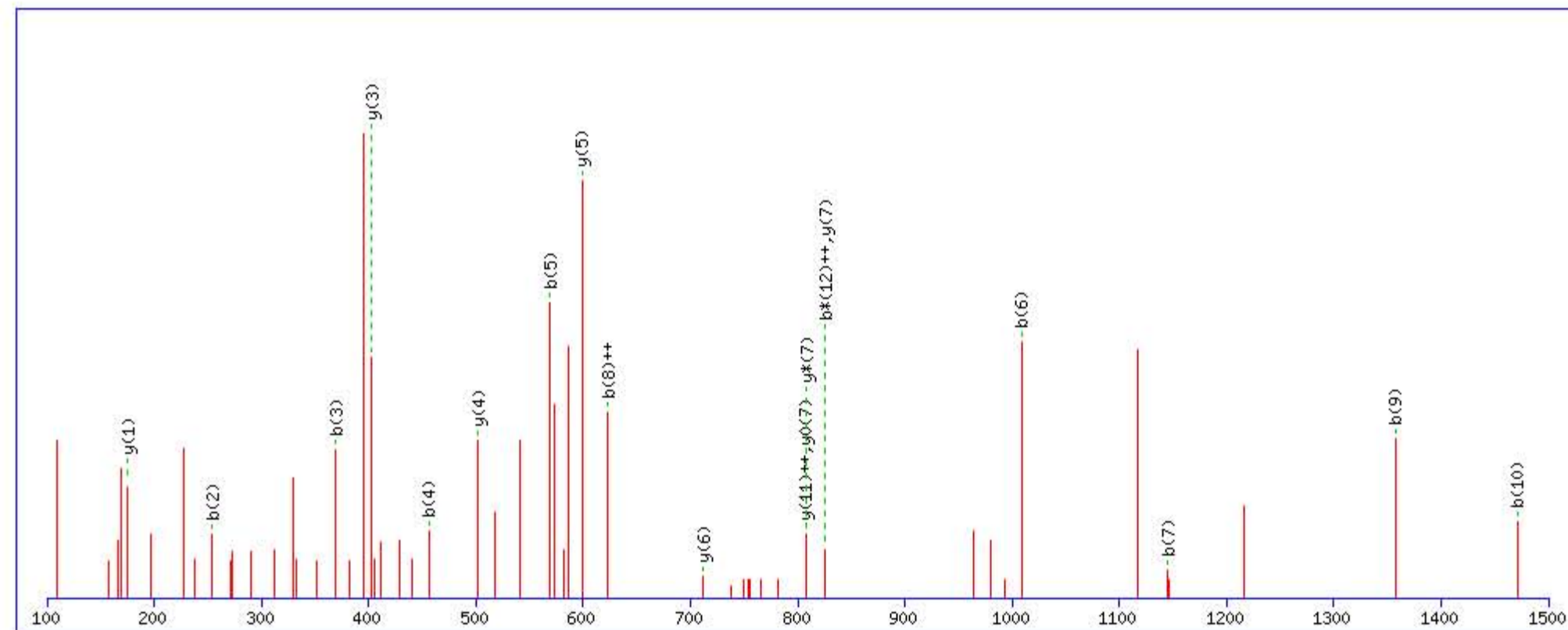
Title: Locus:1.1.1.2848.6 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2068.161545

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

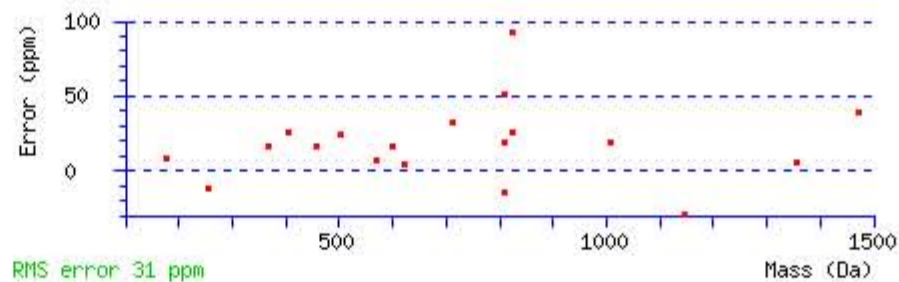
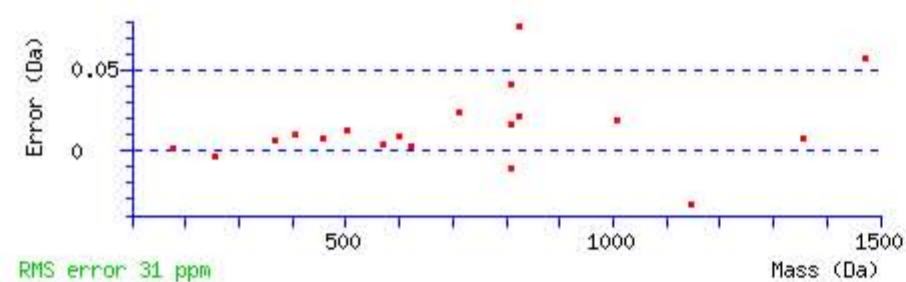
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 53 Expect: 2.8e-005

Matches : 19/162 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	157.108387	79.057831	140.081838	70.544557			R							15
2	254.161151	127.584213	237.134602	119.070939			P	1913.067716	957.037496	1896.041167	948.524222	1895.057151	948.032214	14
3	369.188094	185.097685	352.161545	176.584410	351.177529	176.092402	D	1816.014952	908.511114	1798.988403	899.997840	1798.004387	899.505832	13
4	456.220122	228.613699	439.193573	220.100425	438.209557	219.608417	S	1700.988009	850.997643	1683.961460	842.484368	1682.977444	841.992360	12
5	569.304186	285.155731	552.277637	276.642457	551.293621	276.150449	L	1613.955981	807.481629	1596.929432	798.968354	1595.945416	798.476346	11
6	1008.529512	504.768394	991.502963	496.255120	990.518947	495.763112	Q	1500.871917	750.939597	1483.845368	742.426322	1482.861352	741.934314	10
7	1145.588424	573.297850	1128.561875	564.784576	1127.577859	564.292568	H	1061.646591	531.326934	1044.620042	522.813659	1043.636026	522.321651	9
8	1244.656838	622.832057	1227.630289	614.318783	1226.646273	613.826775	V	924.587679	462.797478	907.561130	454.284203	906.577114	453.792195	8
9	1357.740902	679.374089	1340.714353	670.860815	1339.730337	670.368807	L	825.519265	413.263271	808.492716	404.749996	807.508700	404.257988	7
10	1470.824966	735.916121	1453.798417	727.402847	1452.814401	726.910838	L	712.435201	356.721239	695.408652	348.207964	694.424636	347.715956	6
11	1567.877730	784.442503	1550.851181	775.929229	1549.867165	775.437220	P	599.351137	300.179207	582.324588	291.665932	581.340572	291.173924	5
12	1666.946144	833.976710	1649.919595	825.463436	1648.935579	824.971428	V	502.298373	251.652825	485.271824	243.139550	484.287808	242.647542	4
13	1780.030208	890.518742	1763.003659	882.005468	1762.019643	881.513459	L	403.229959	202.118618	386.203410	193.605343	385.219394	193.113335	3
14	1895.057151	948.032214	1878.030602	939.518939	1877.046586	939.026931	D	290.145895	145.576586	273.119346	137.063311	272.135330	136.571303	2
15							R	175.118952	88.063114	158.092403	79.549840			1



NCBI BLAST search of [RPDSLQHVLLPVLDR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.4	2068.161545	0.024471	RPDSLQHVLLPVLDR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **AGEQVITYTCATYYK**

Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

Match to Query 48357: 1964.892488 from(983.453520,2+) rtinseconds(1873) index(21033)

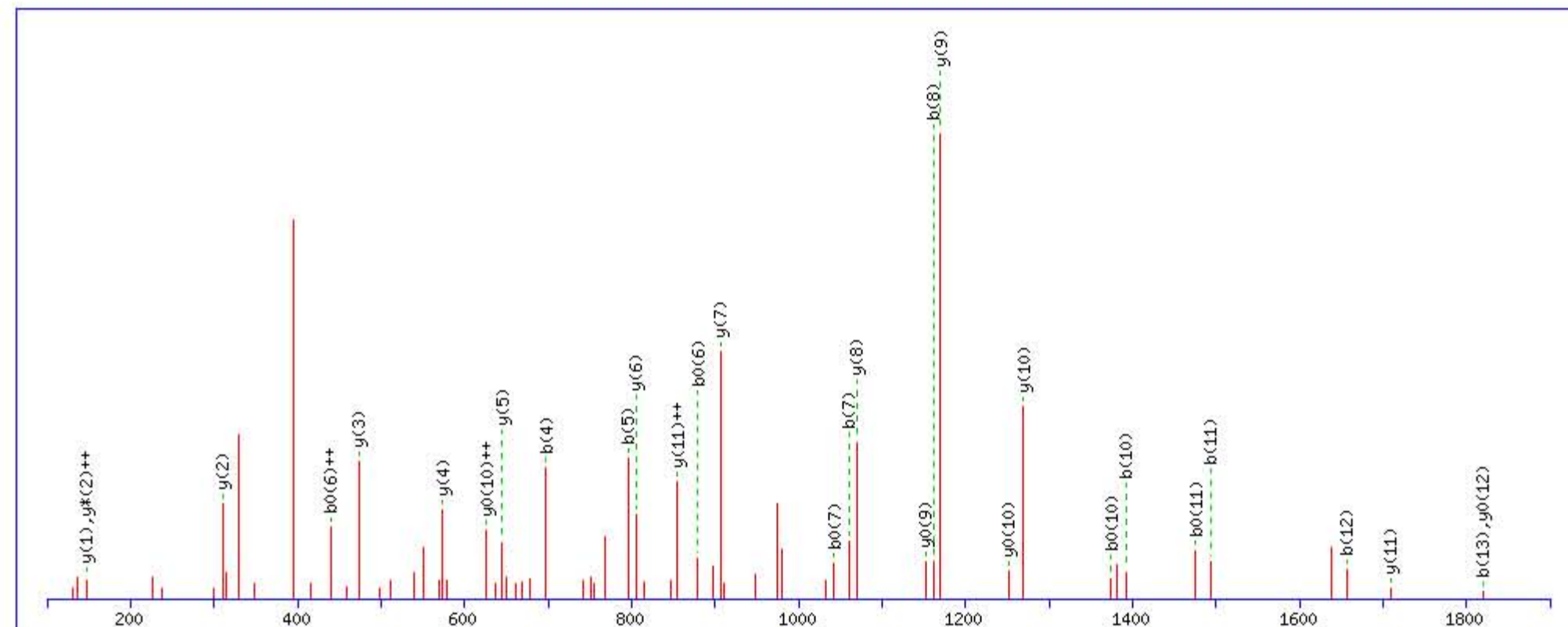
Title: Locus:1.1.1.1533.24 File:"2013-07-02 CLN FXIII 30 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

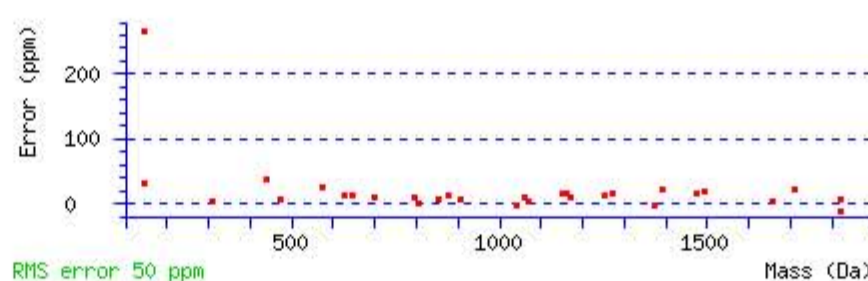
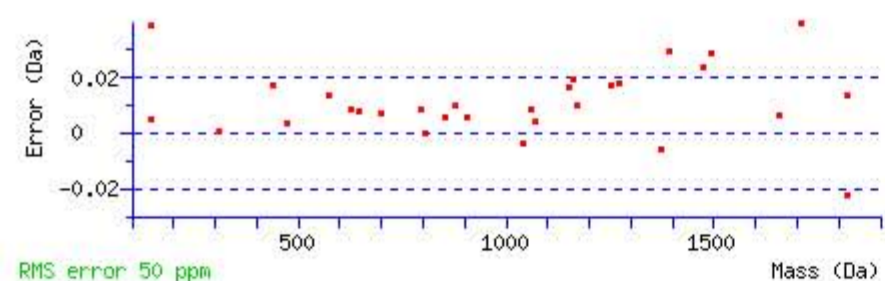
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 77 Expect: 1.9e-007

Matches : 30/140 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							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 **AGEQVITYTCATYYK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
77.2	1964.901215	-0.008727	AGEQVITYTCATYYK
6.6	1964.883255	0.009233	RTHSGEKPYECKCGK

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

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 34759: 1468.673108 from(735.343830,2+) rtinseconds(1824) index(70054)

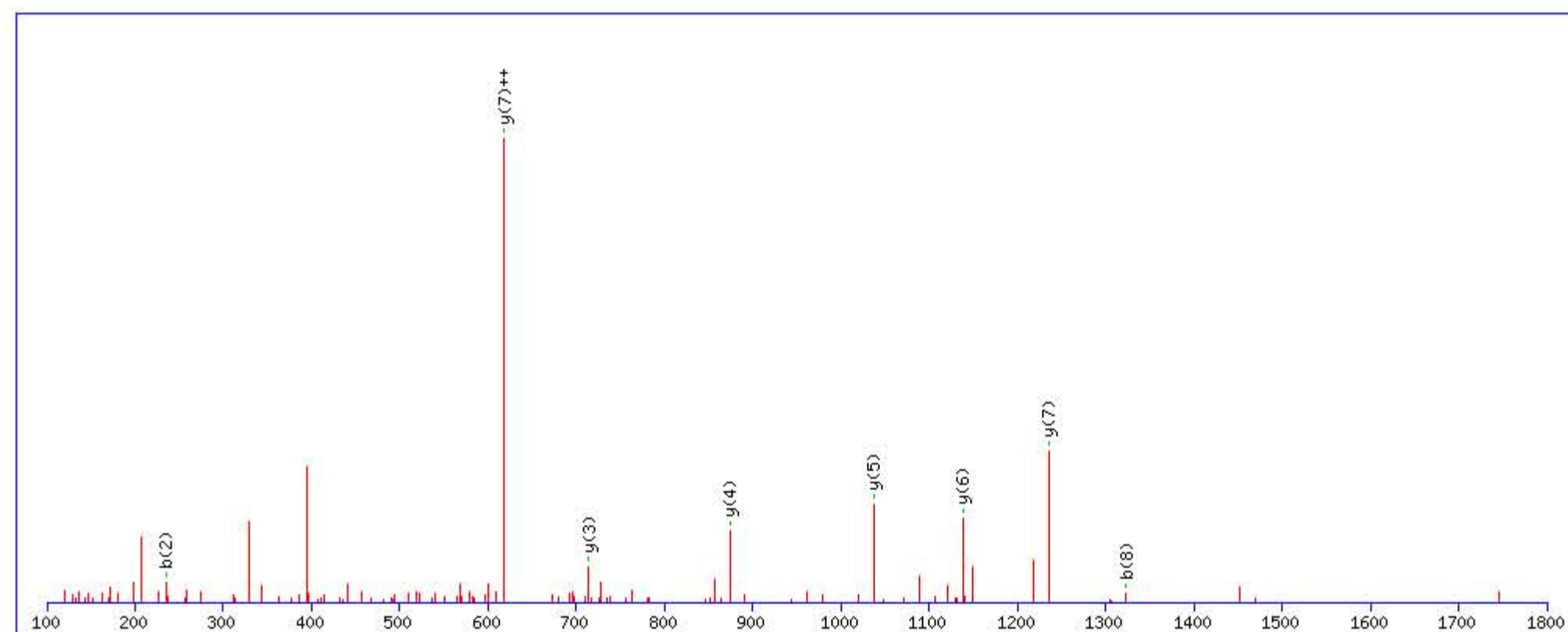
Title: Locus:1.1.1.3168.11 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

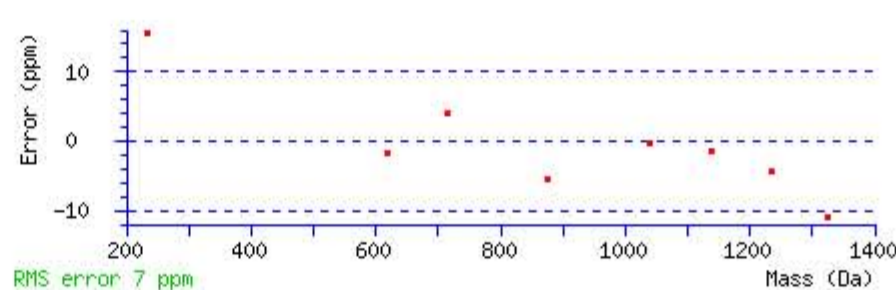
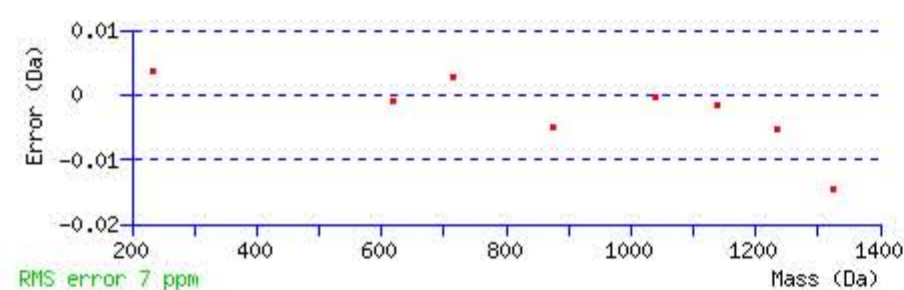
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 31 Expect: 0.0055

Matches : 8/74 fragment ions using 14 most intense peaks [\(help\)](#)

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



NCBI BLAST search of **SFPTYCQQK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.6	1468.684296	-0.011188	SFPTYCQQK
30.6	1468.684296	-0.011188	SFPTYCQQK
6.0	1468.691498	-0.018390	ESDCLVCRKFR
5.5	1468.680252	-0.007144	YAKGNGDCALLCK
4.7	1468.671524	0.001584	MEAETGSSVETGKK
3.6	1468.657593	0.015515	NSCASDKRTSSEK
1.6	1468.688126	-0.015018	FSIPSMTEHHAGR
0.9	1468.658966	0.014142	MSPHGDGRGQAQGR
0.2	1468.666336	0.006772	SMAQHVHNDKQR

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

MASCOT 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 42756: 1721.837288 from(861.925920,2+) rtinseconds(1892) index(70395)

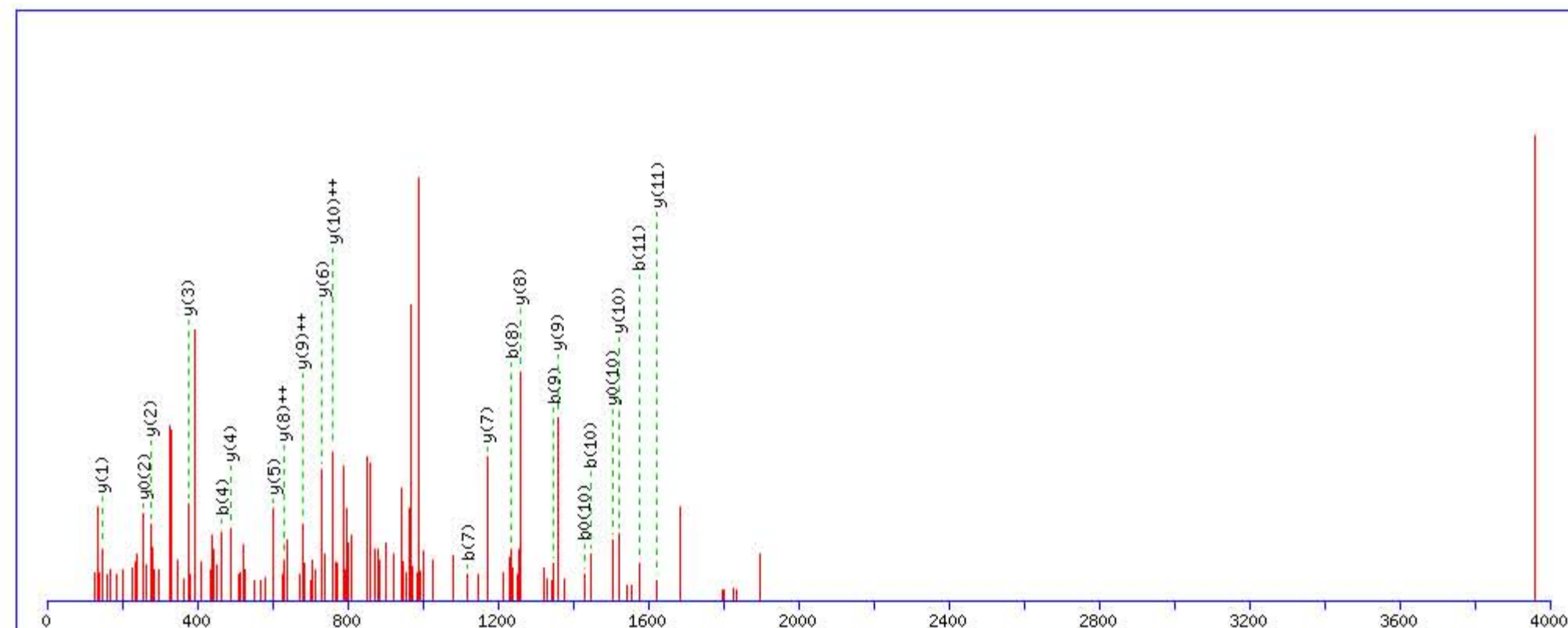
Title: Locus:1.1.1.3192.21 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

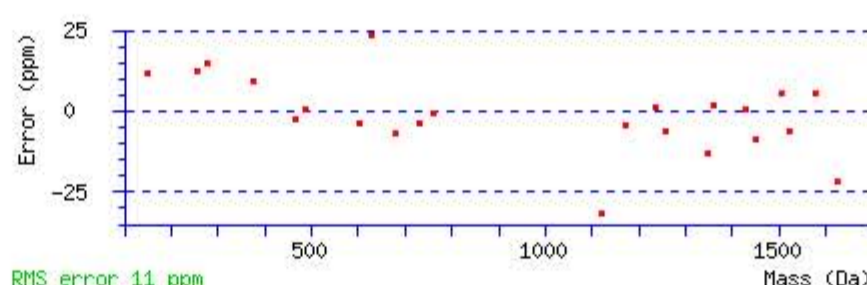
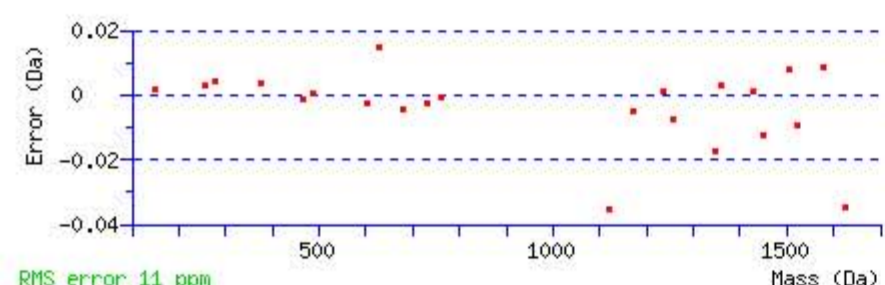
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 52 Expect: 2.8e-005

Matches : 23/118 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							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
51.6	1721.854584	-0.017296	VTYTSQEDLVEK
2.9	1721.830292	0.006996	MQNICNFLVEK
0.5	1721.840637	-0.003349	MQFEQREIDAALQK

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

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **LLPAQLPAEK**

Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

Match to Query 31712: 1389.804468 from(695.909510,2+) rtinseconds(2009) index(5856)

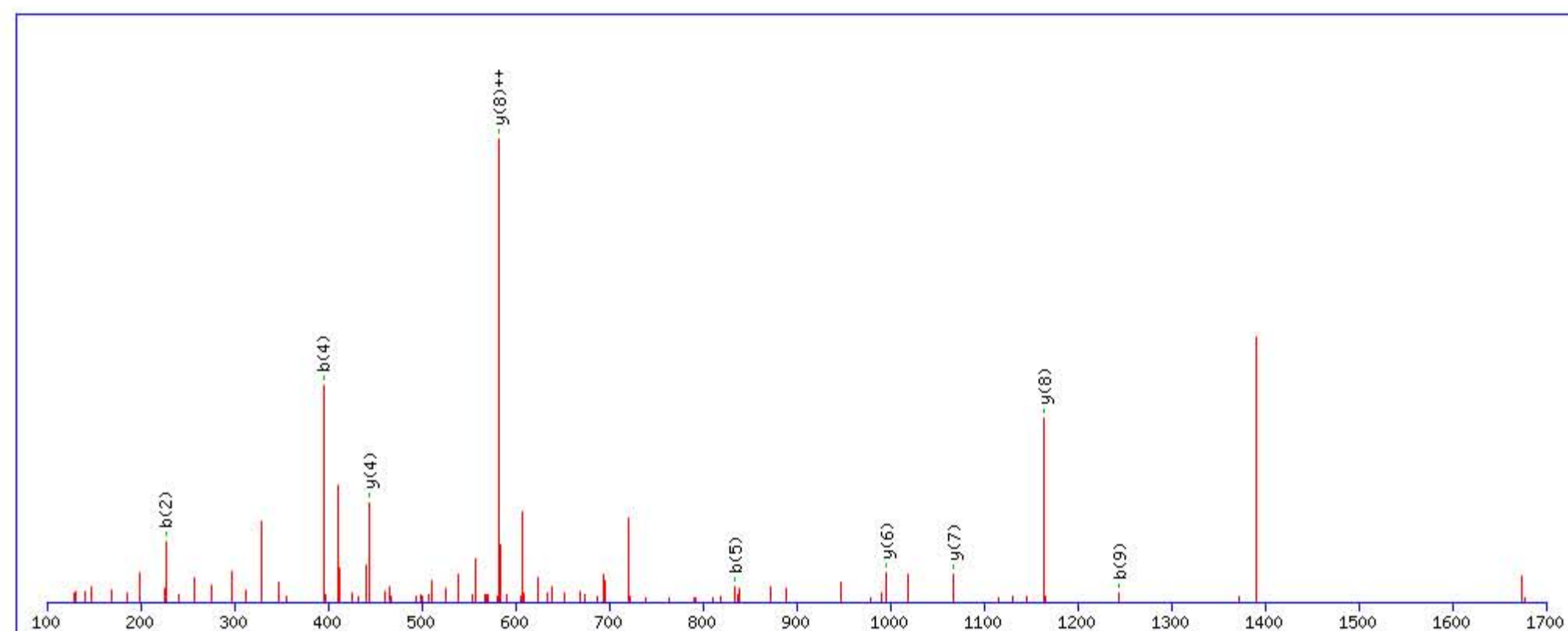
Title: Locus:1.1.1.3135.16 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1389.805359

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

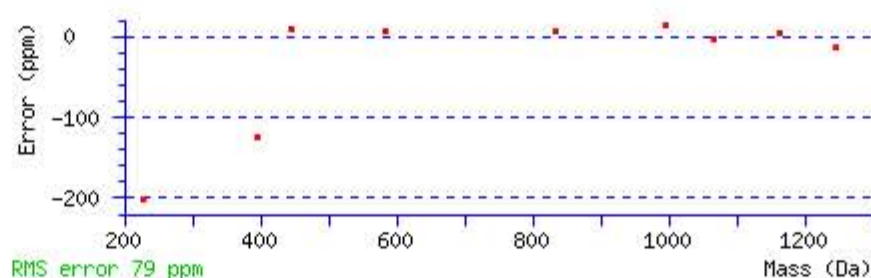
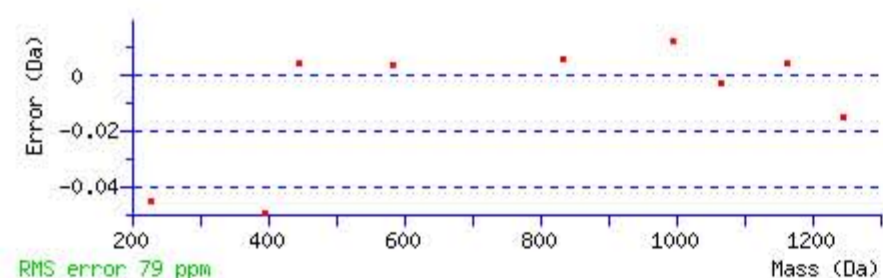
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 35 Expect: 0.0018

Matches : 9/82 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	114.091340	57.549308					L							10
2	227.175404	114.091340					L	1277.728607	639.367942	1260.702058	630.854667	1259.718042	630.362659	9
3	324.228168	162.617722					P	1164.644543	582.825909	1147.617994	574.312635	1146.633978	573.820627	8
4	395.265282	198.136279					A	1067.591779	534.299527	1050.565230	525.786253	1049.581214	525.294245	7
5	834.490608	417.748942	817.464059	409.235668			Q	996.554665	498.780970	979.528116	490.267696	978.544100	489.775688	6
6	947.574672	474.290974	930.548123	465.777700			L	557.329339	279.168307	540.302790	270.655033	539.318774	270.163025	5
7	1044.627436	522.817356	1027.600887	514.304082			P	444.245275	222.626275	427.218726	214.113001	426.234710	213.620993	4
8	1115.664550	558.335913	1098.638001	549.822639			A	347.192511	174.099893	330.165962	165.586619	329.181946	165.094611	3
9	1244.707143	622.857209	1227.680594	614.343935	1226.696578	613.851927	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
10							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **LLPAQLPAEK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	$M_r(\text{calc})$:	Delta	Sequence
35.2	1389.805359	-0.000891	LLPAQLPAEK
5.5	1389.809189	-0.004721	LIKRLDLSYNR
4.1	1389.809204	-0.004736	IARVPRLPPEDEK
1.3	1389.823135	-0.018667	ILIVITDGQKYK
0.5	1389.816605	-0.012137	ILGPLPKHMIQK
0.5	1389.797974	0.006494	ILLYRGADKDVK
0.5	1389.805359	-0.000891	LLSSYLQKK

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 46968: 1906.934682 from(636.652170,3+) rtinseconds(1888) index(5109)

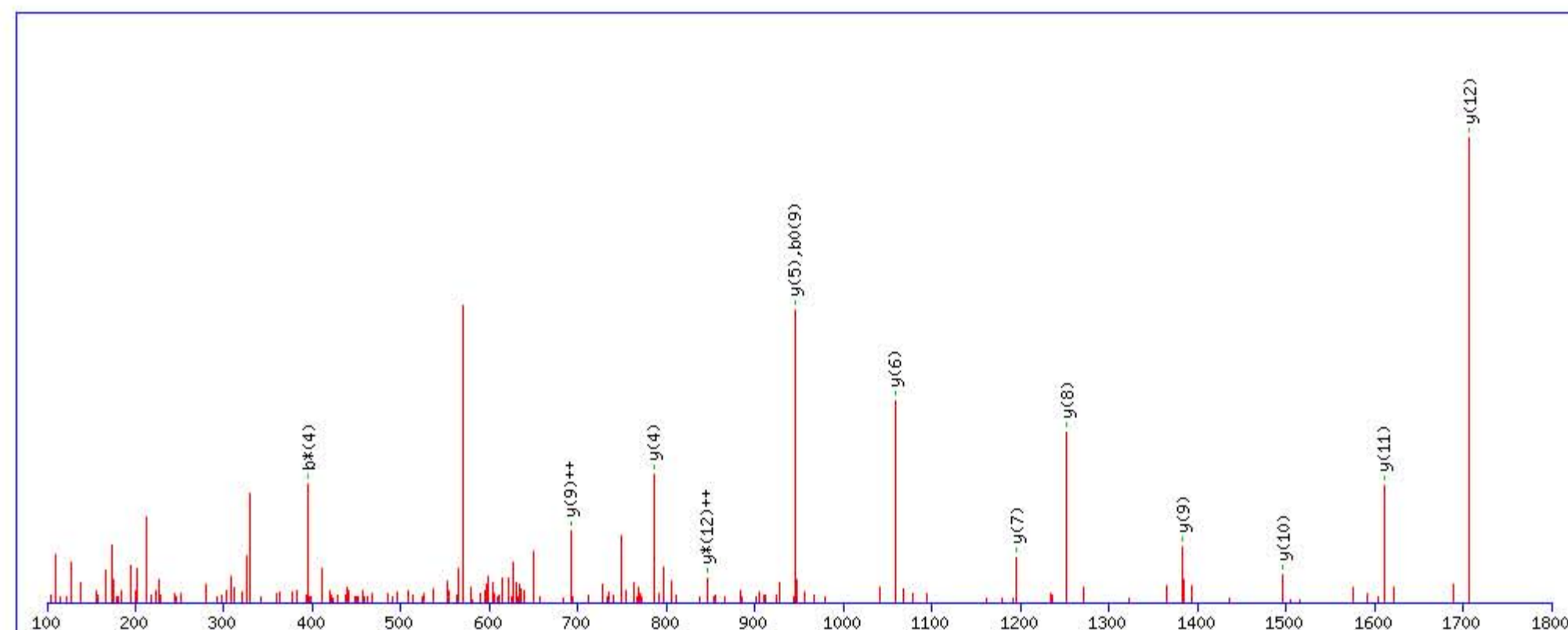
Title: Locus:1.1.1.3093.19 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

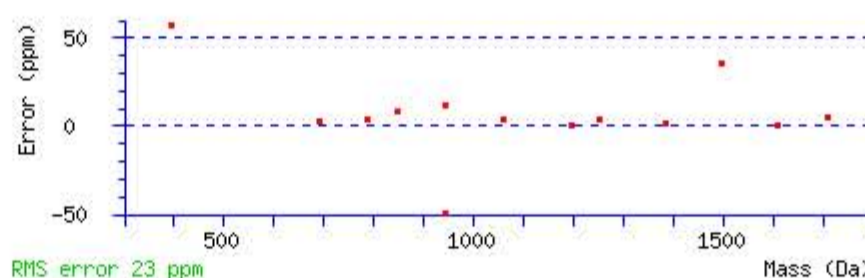
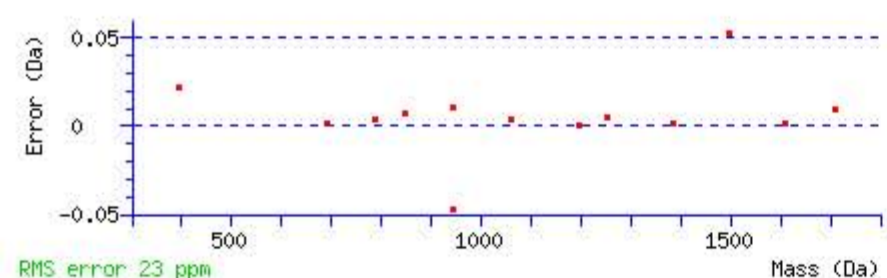
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 62 Expect: 1.6e-005

Matches : 13/124 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							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
61.5	1906.932816	0.001866	VTPNLMGHLCGNQR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **FSCFQEEAPQPHYQLR**

Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

Match to Query 56846: 2347.074492 from(783.365440,3+) rtinseconds(1935) index(5479)

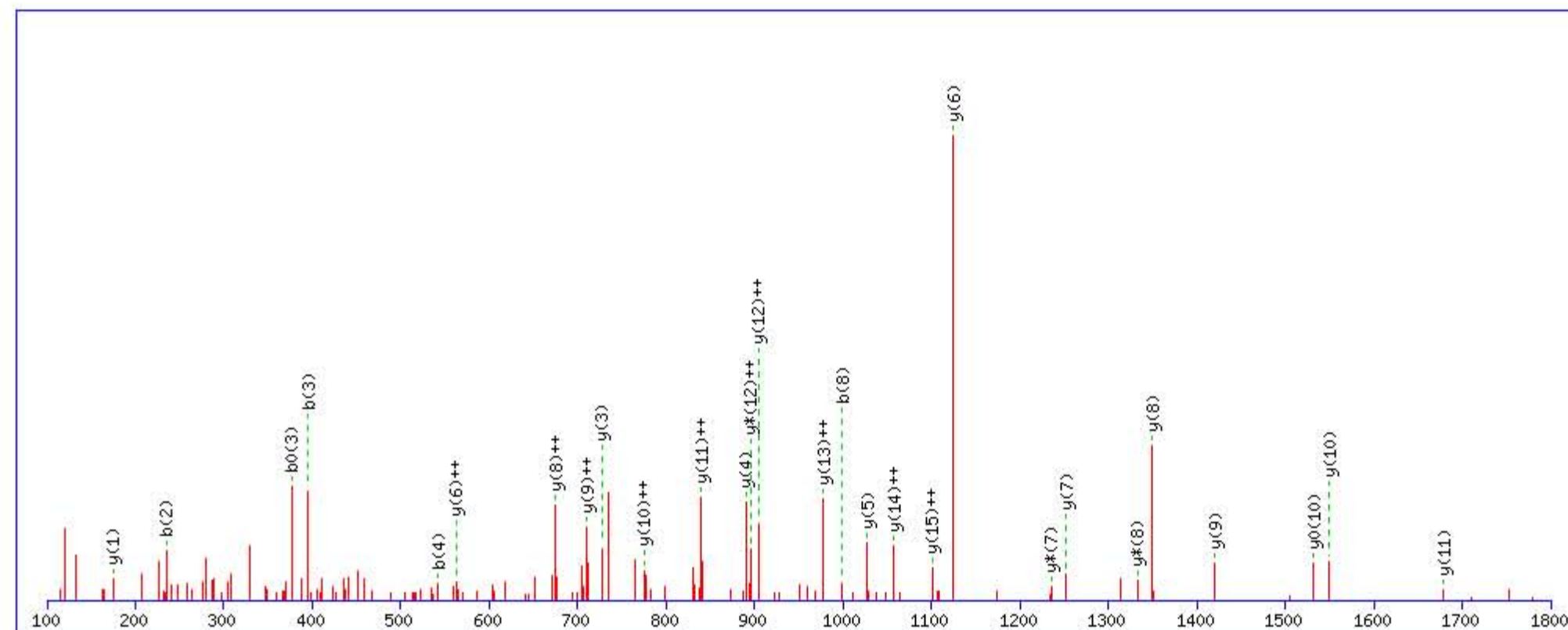
Title: Locus:1.1.1.3109.14 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 2347.087784

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

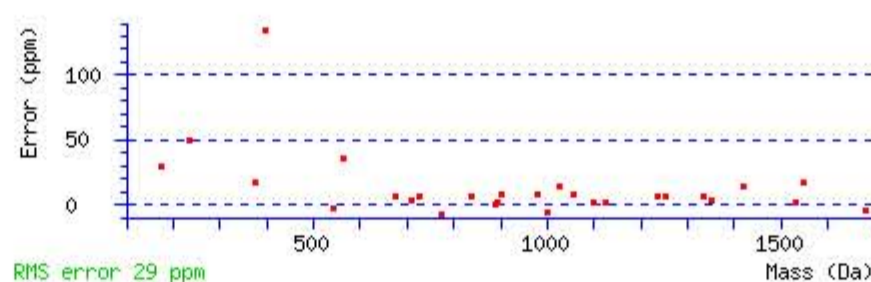
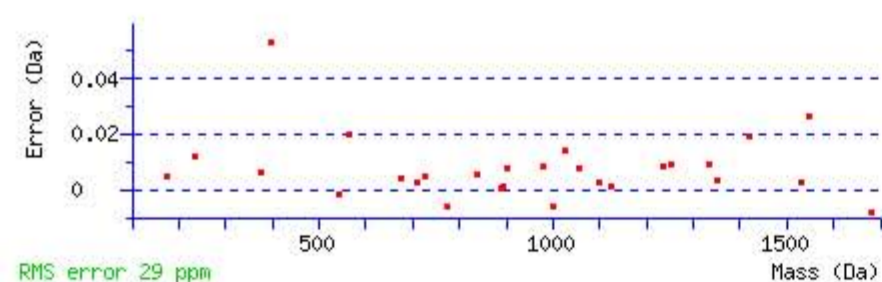
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 58 Expect: 2.1e-005

Matches : 28/152 fragment ions using 57 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	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	$M_r(\text{calc})$:	Delta	Sequence
57.8	2347.087784	-0.013292	FSCFQEEAPQPHYQLR
27.0	2347.087784	-0.013292	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 26386: 1238.699928 from(620.357240,2+) rtinseconds(1751) index(54157)

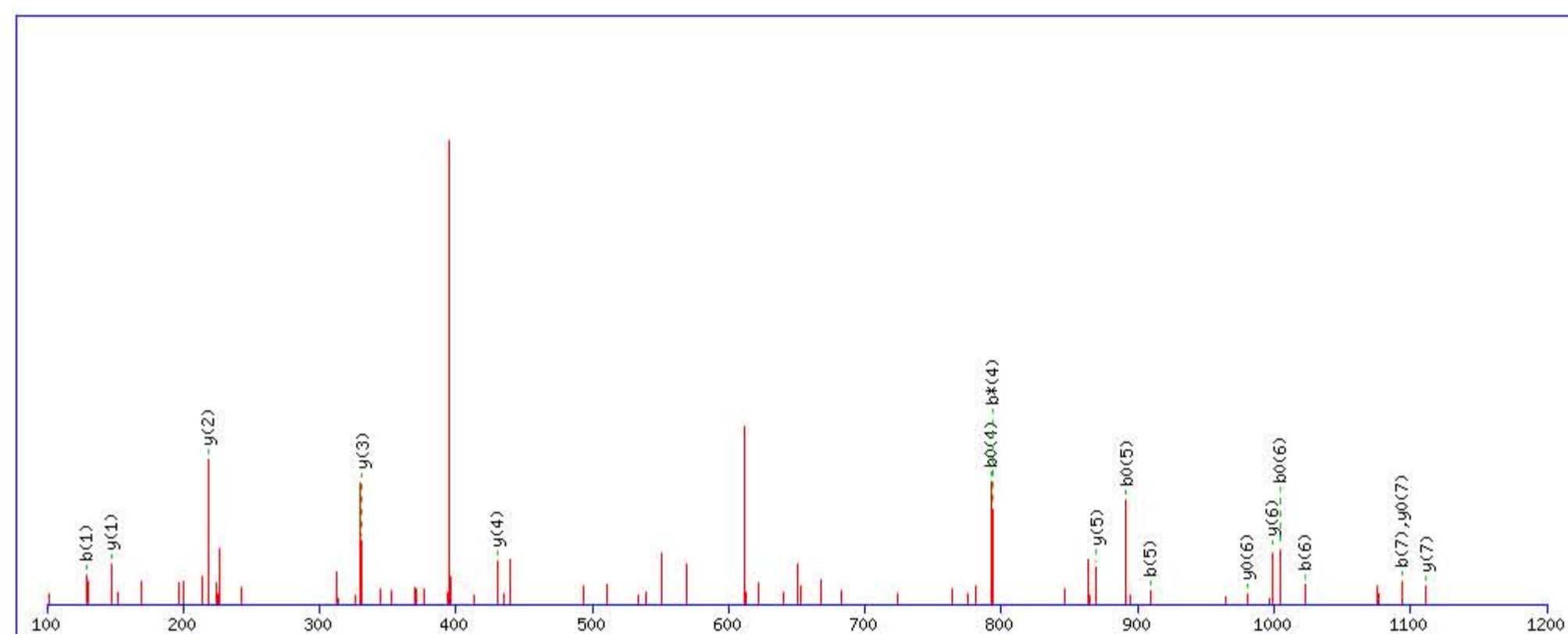
Title: Locus:1.1.1.3096.9 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

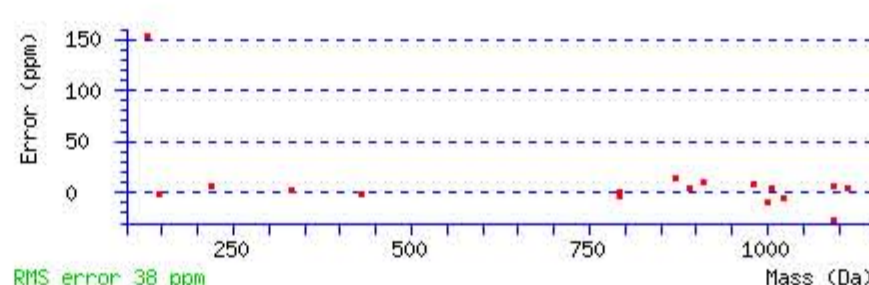
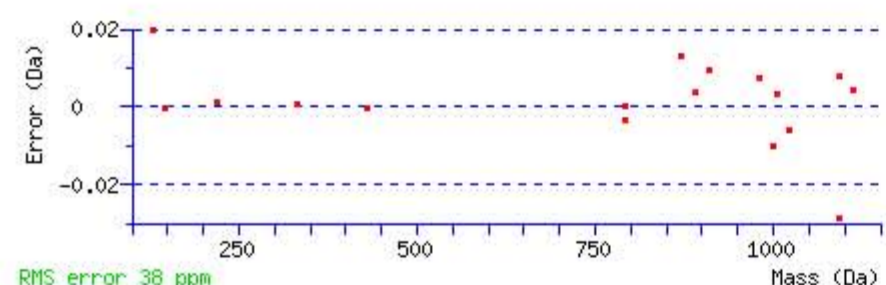
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 43 Expect: 0.00088

Matches : 17/70 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	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
42.6	1238.705658	-0.005730	QLEQVIAK
16.3	1238.705658	-0.005730	QLEQVIAK
13.7	1238.687027	0.012901	KEETQPPVALK
11.7	1238.698257	0.001671	IHADASSKVLAK
10.9	1238.716904	-0.016976	DRVQVAIK
9.9	1238.709473	-0.009545	NDLRPANKLAK
5.9	1238.702301	-0.002373	DVFKKGFSLAK
5.4	1238.716888	-0.016960	KRILCPLDPK
5.1	1238.705658	-0.005730	QIAQEIVK
4.7	1238.691742	0.008186	KAVIHERVCK

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 31546: 1388.655308 from(695.334930,2+) rtinseconds(1656) index(53458)

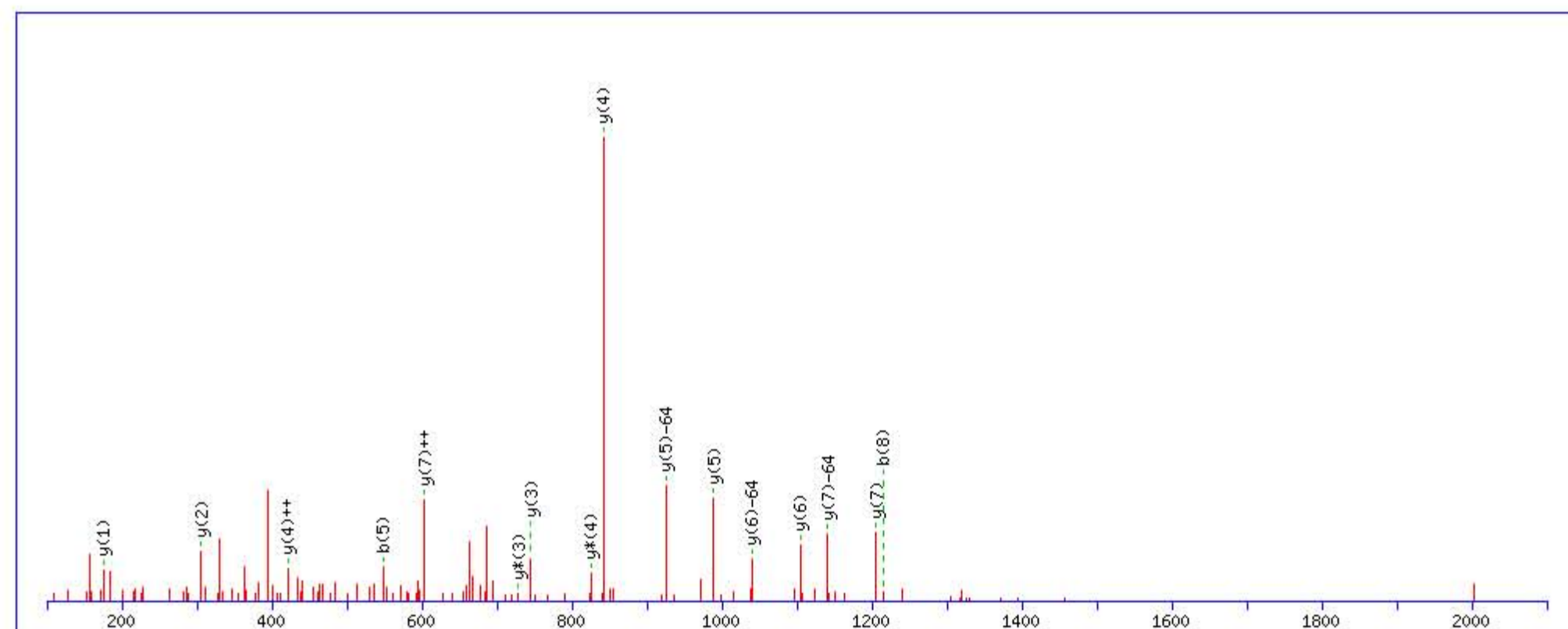
Title: Locus:1.1.1.3063.6 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1388.661438

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

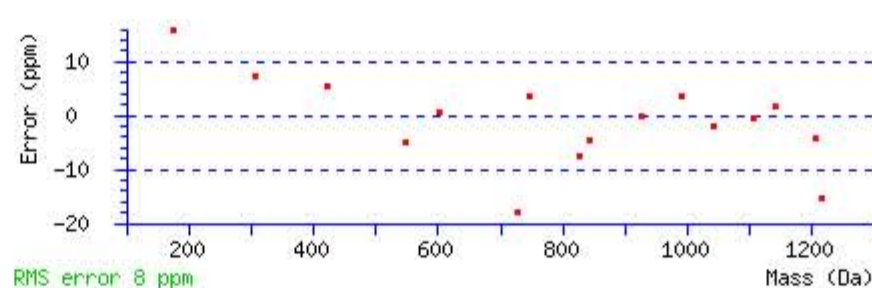
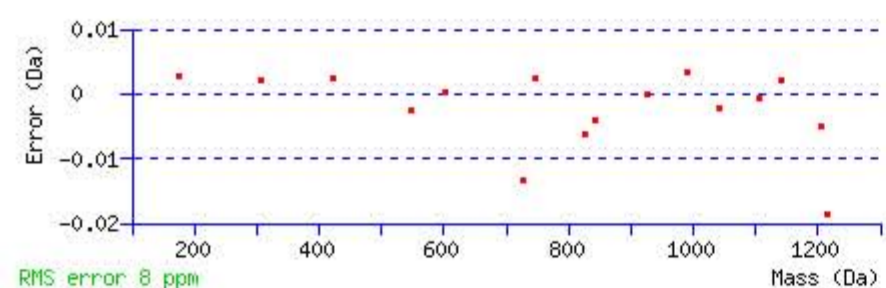
M5 : Oxidation (M), with neutral losses 0.000000 (shown in table), 63.998285

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 52 Expect: 4.9e-005

Matches : 16/112 fragment ions using 26 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.044390	36.525833					A							9
2	185.128454	93.067865					L	1318.631613	659.819445	1301.605064	651.306170	1300.621048	650.814162	8
3	286.176133	143.591704			268.165568	134.586422	T	1205.547549	603.277413	1188.521000	594.764138	1187.536984	594.272130	7
4	401.203076	201.105176			383.192511	192.099894	D	1104.499870	552.753573	1087.473321	544.240298	1086.489305	543.748290	6
5	548.238476	274.622876			530.227911	265.617594	M	989.472927	495.240102	972.446378	486.726827			5
6	645.291240	323.149258			627.280675	314.143976	P	842.437527	421.722402	825.410978	413.209127			4
7	1084.516566	542.761921	1067.490017	534.248647	1066.506001	533.756639	Q	745.384763	373.196020	728.358214	364.682745			3
8	1215.557051	608.282164	1198.530502	599.768889	1197.546486	599.276881	M	306.159437	153.583356	289.132888	145.070082			2
9							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **ALTDMPQMR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.5	1388.661438	-0.006130	ALTDMPQMR
14.9	1388.661438	-0.006130	ALTDMPQMR
5.5	1388.654053	0.001255	SMDTIVGMLHNR
4.4	1388.660568	-0.005260	SEMTASPLVGPER
3.8	1388.669296	-0.013988	DREPFQMR

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

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 35634: 1500.696068 from(751.355310,2+) rtinseconds(1561) index(3232)

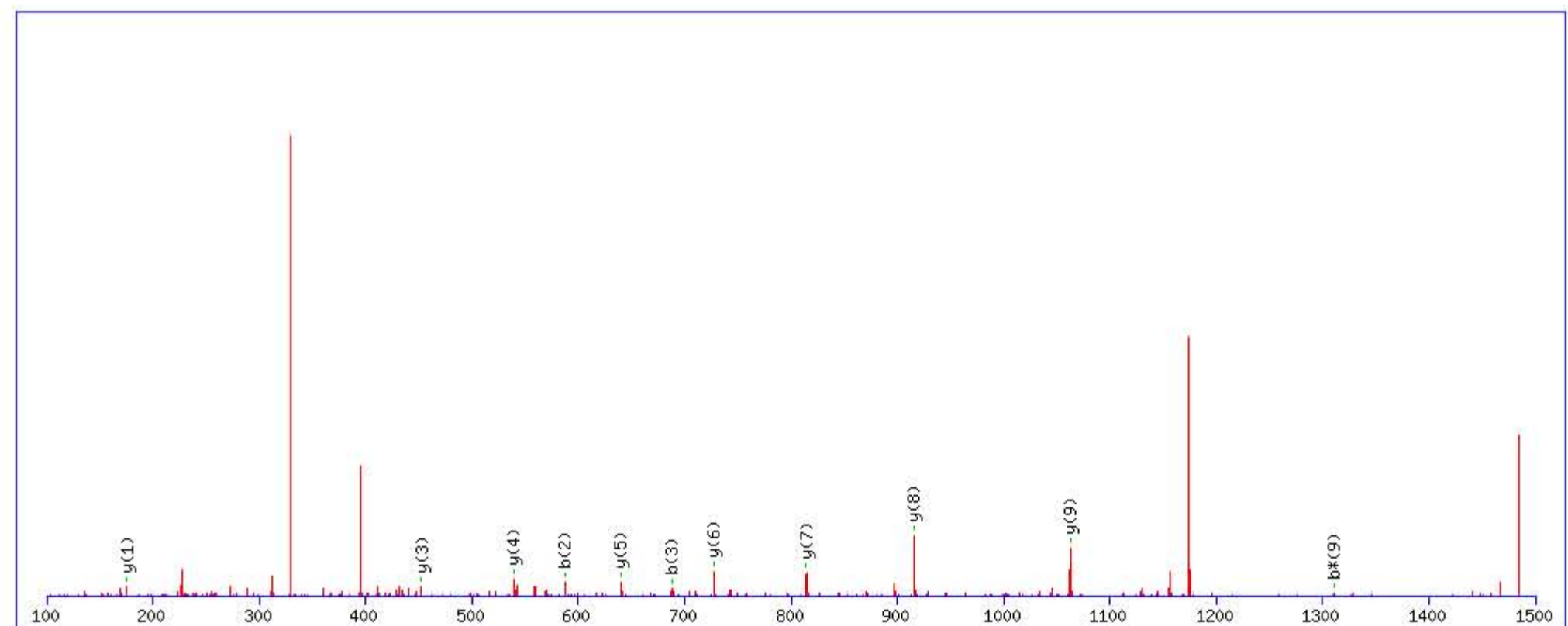
Title: Locus:1.1.1.2979.16 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

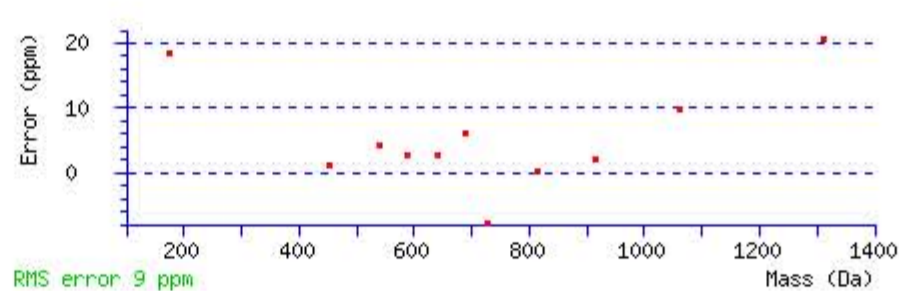
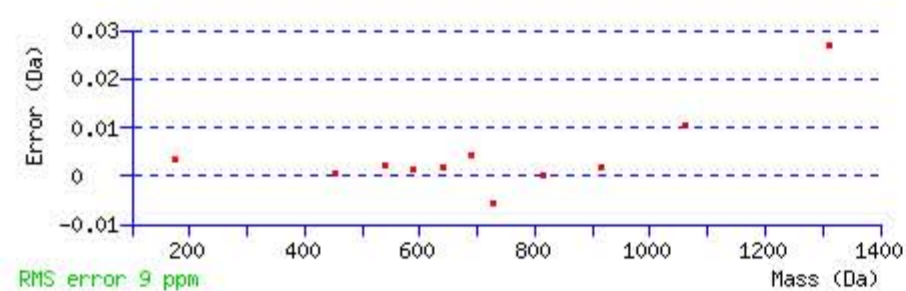
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 41 Expect: 0.00019

Matches : 11/98 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	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
40.8	1500.703110	-0.007042	QFTSSTSYNR
1.0	1500.714355	-0.018287	EEIALGGGGFCVHR

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 36868: 1549.871048 from(775.942800,2+) rtinseconds(2113) index(56543)

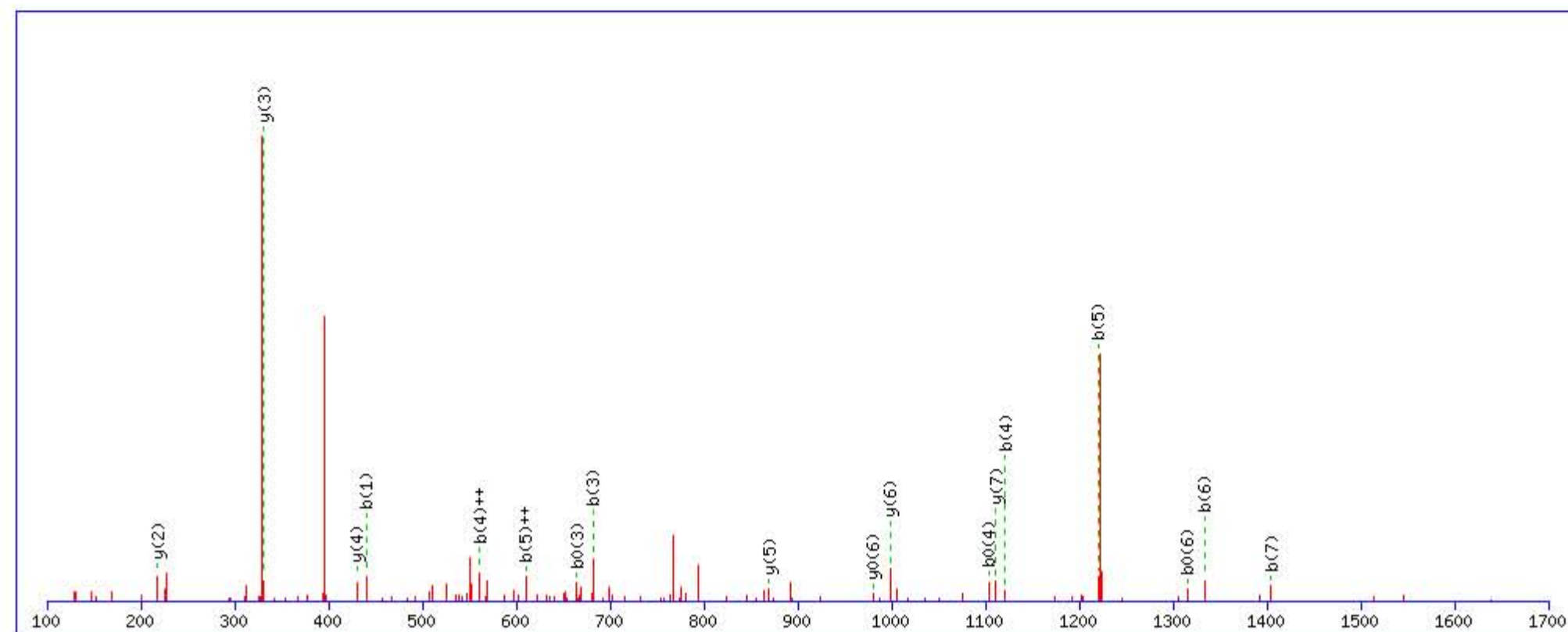
Title: Locus:1.1.1.3221.20 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1549.872406

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

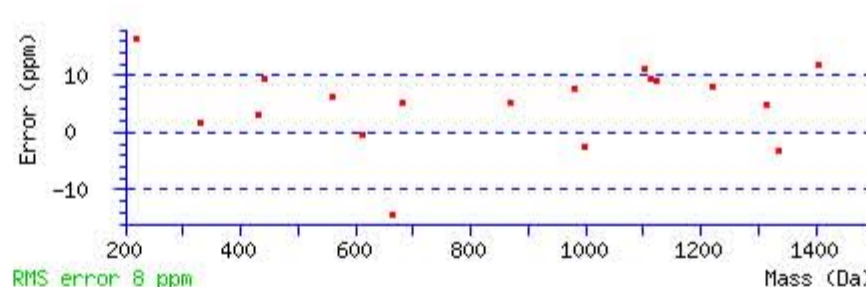
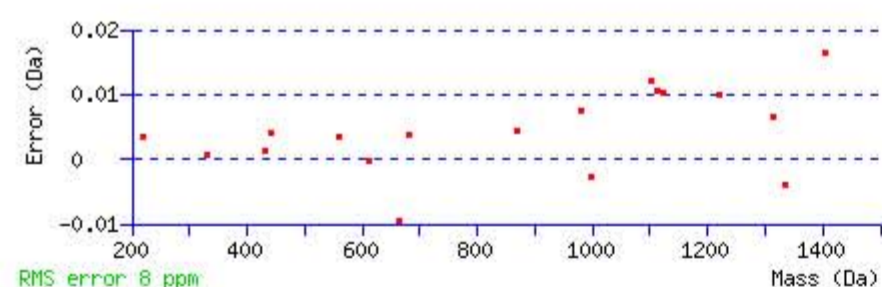
Q1 : Biotin:Thermo-21345 (Q)

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 26 Expect: 0.037

Matches : 18/70 fragment ions using 41 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	440.232602	220.619939	423.206053	212.106664			Q							8
2	553.316666	277.161971	536.290117	268.648697			L	1111.654379	556.330828	1094.627830	547.817553	1093.643814	547.325545	7
3	682.359259	341.683268	665.332710	333.169993	664.348694	332.677985	E	998.570315	499.788796	981.543766	491.275521	980.559750	490.783513	6
4	1121.584585	561.295931	1104.558036	552.782656	1103.574020	552.290648	Q	869.527722	435.267499	852.501173	426.754225			5
5	1220.652999	610.830138	1203.626450	602.316863	1202.642434	601.824855	V	430.302396	215.654836	413.275847	207.141561			4
6	1333.737063	667.372170	1316.710514	658.858895	1315.726498	658.366887	I	331.233982	166.120629	314.207433	157.607354			3
7	1404.774177	702.890727	1387.747628	694.377452	1386.763612	693.885444	A	218.149918	109.578597	201.123369	101.065322			2
8							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **QLEQVIAK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.6	1549.872406	-0.001358	QLEQVIAK
10.0	1549.886810	-0.015762	YVIGIGVGAGAYVLAK
6.4	1549.861633	0.009415	KLSRPFQSEIFAK
4.1	1549.876251	-0.005203	LVDINLVRCHALK
3.7	1549.893967	-0.022919	LIRENHELKSAIK
3.5	1549.855148	0.015900	QSFVVPVRPGPR
3.2	1549.861618	0.009430	TAEKLYRTAWIAK
3.1	1549.886795	-0.015747	KGNLVYIIDFGLAK
1.8	1549.862991	0.008057	AAWLRVFQHLGPR
0.2	1549.880264	-0.009216	LLNLMWLPKPPGR

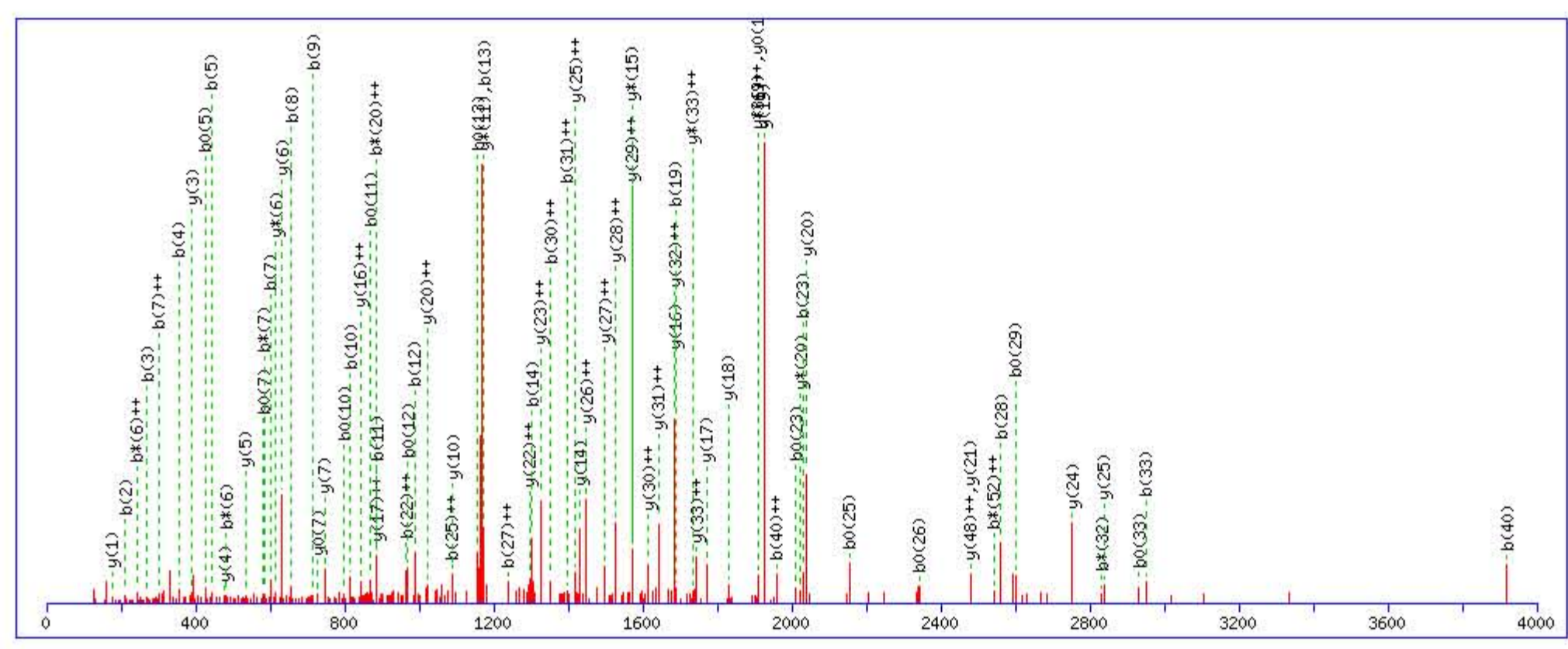
MASCOT Search Results

Peptide View

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

Match to Query 80995: 5844.555970 from(1169.918470,5+) rtinseconds(1764) index(20416)
 Title: Locus:1.1.1.1495.26 File:"2013-07-02 CLN FXIII 30 min 2nd F 2.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 107 Expect: 4.8e-011
 Matches : 81/688 fragment ions using 142 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	365.161			

Mascot Search Results

Peptide View

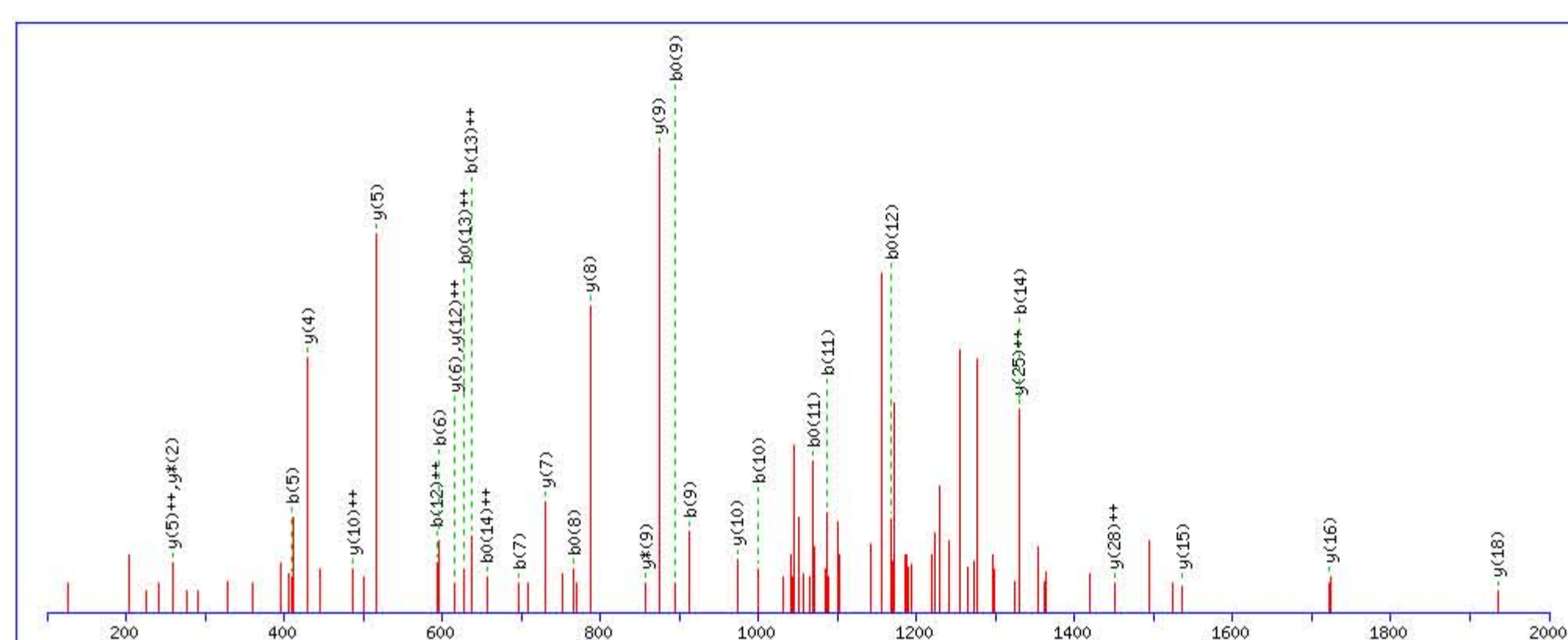
MS/MS Fragmentation of **GSAGHWTSESSVSGSTGQWHSESGSFRPDSPGSGNARPNPDWGTFFEEVSGNVSPGTR**
 Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

Match to Query 81461: 6284.705664 from(1048.458220,6+) rtinseconds(2065) index(71565)
 Title: Locus:1.1.1.3252.26 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 6284.792847
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q18 : Biotin:Thermo-21345 (Q)
 Ions Score: 39 Expect: 0.00019
 Matches : 32/646 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	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	2242.019550	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										

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 46093: 1855.981542 from(619.667790,3+) rtinseconds(1503) index(35602)

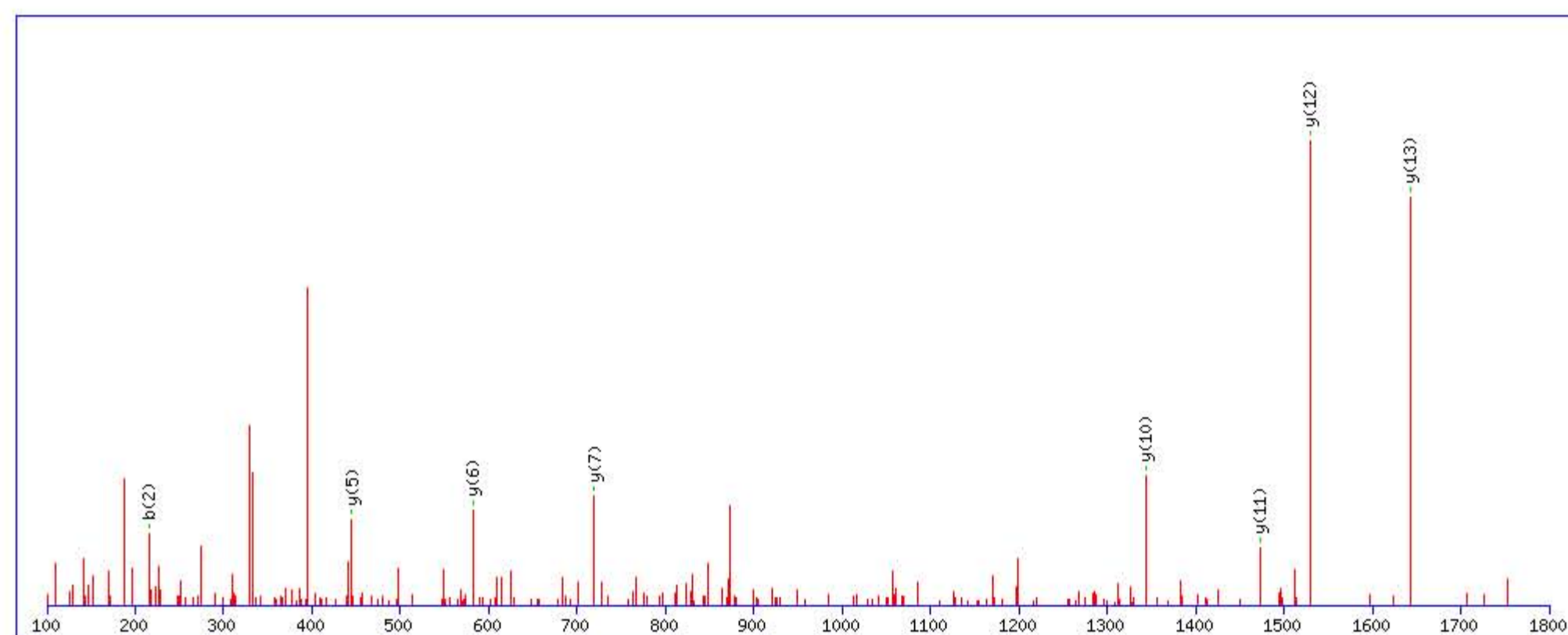
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Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

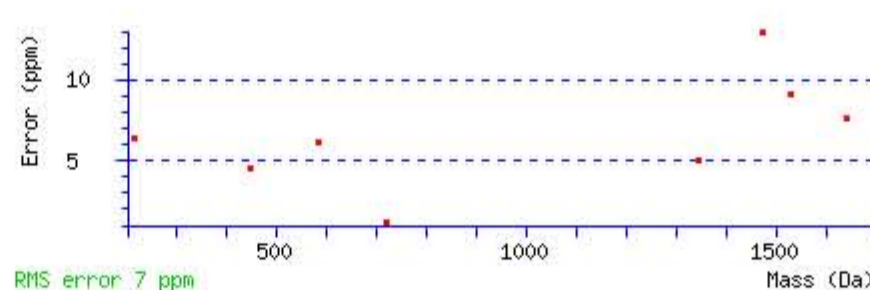
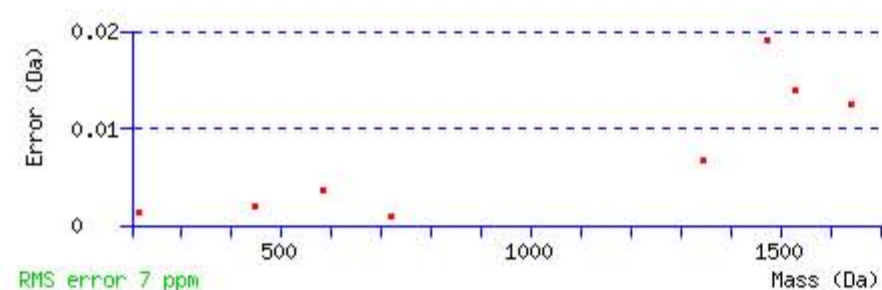
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 36 Expect: 0.00059

Matches : 8/134 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
36.3	1855.972687	0.008855	LTIGEGQQHHLGGAK
36.3	1855.972687	0.008855	LTIGEGQQHHLGGAK
1.8	1856.000519	-0.018977	TIVVTILESPYVMYK
0.2	1855.989944	-0.008402	MLSITPSQLENGKK

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 46097: 1855.989456 from(465.004640,4+) rtinseconds(1510) index(18880)

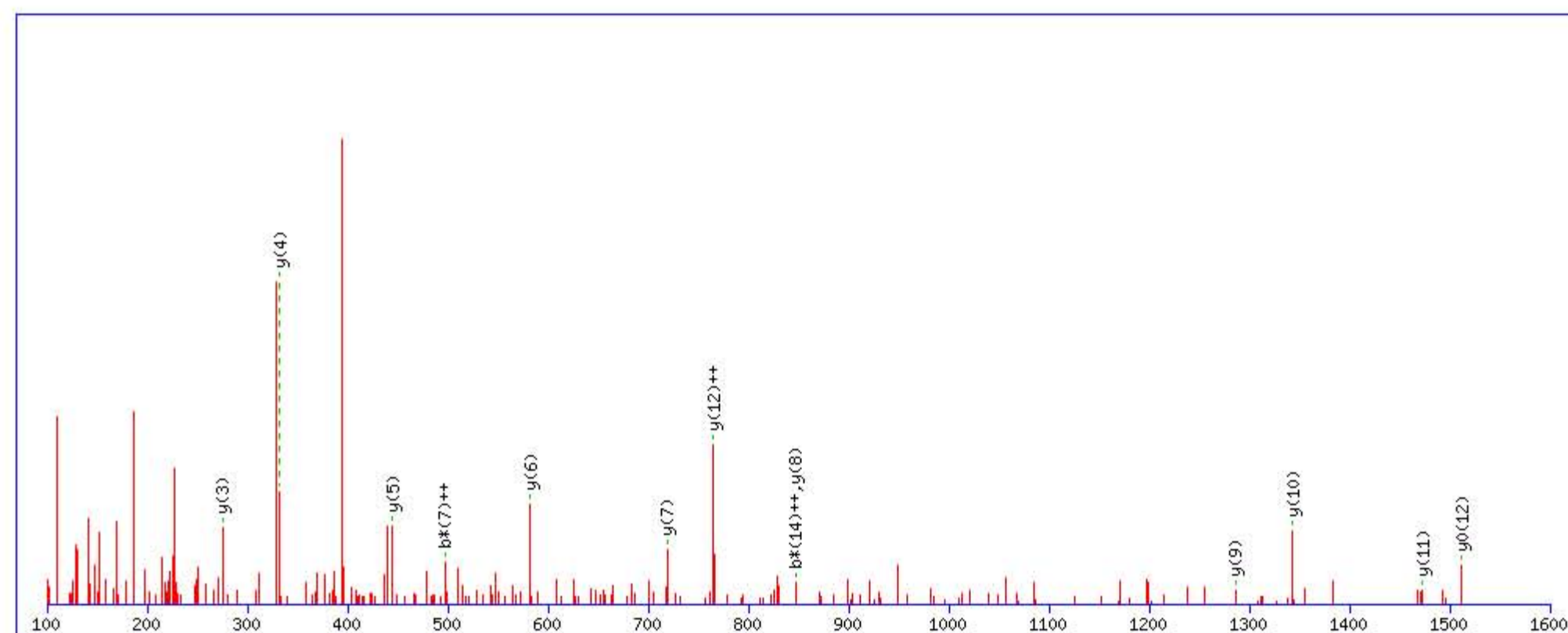
Title: Locus:1.1.1.1407.8 File:"2013-07-02 CLN FXIII 30 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

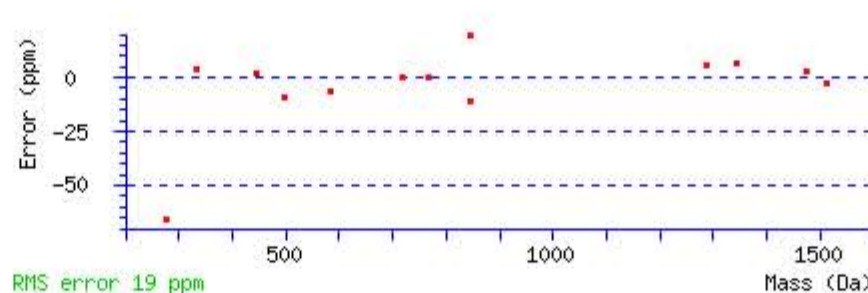
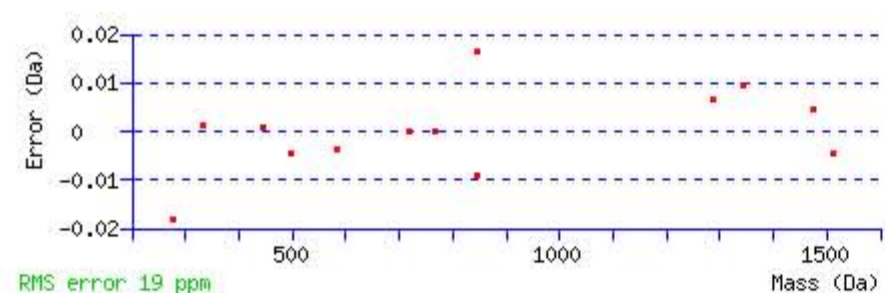
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 26 Expect: 0.064

Matches : 13/134 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	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
25.8	1855.972687	0.016769	LTIGEGQQHHLGGAK
17.8	1855.972687	0.016769	LTIGEGQQHHLGGAK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **LTIGEGQQHHLGGAK**

Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

Match to Query 53232: 2167.131896 from(542.790250,4+) rtinseconds(1748) index(54141)

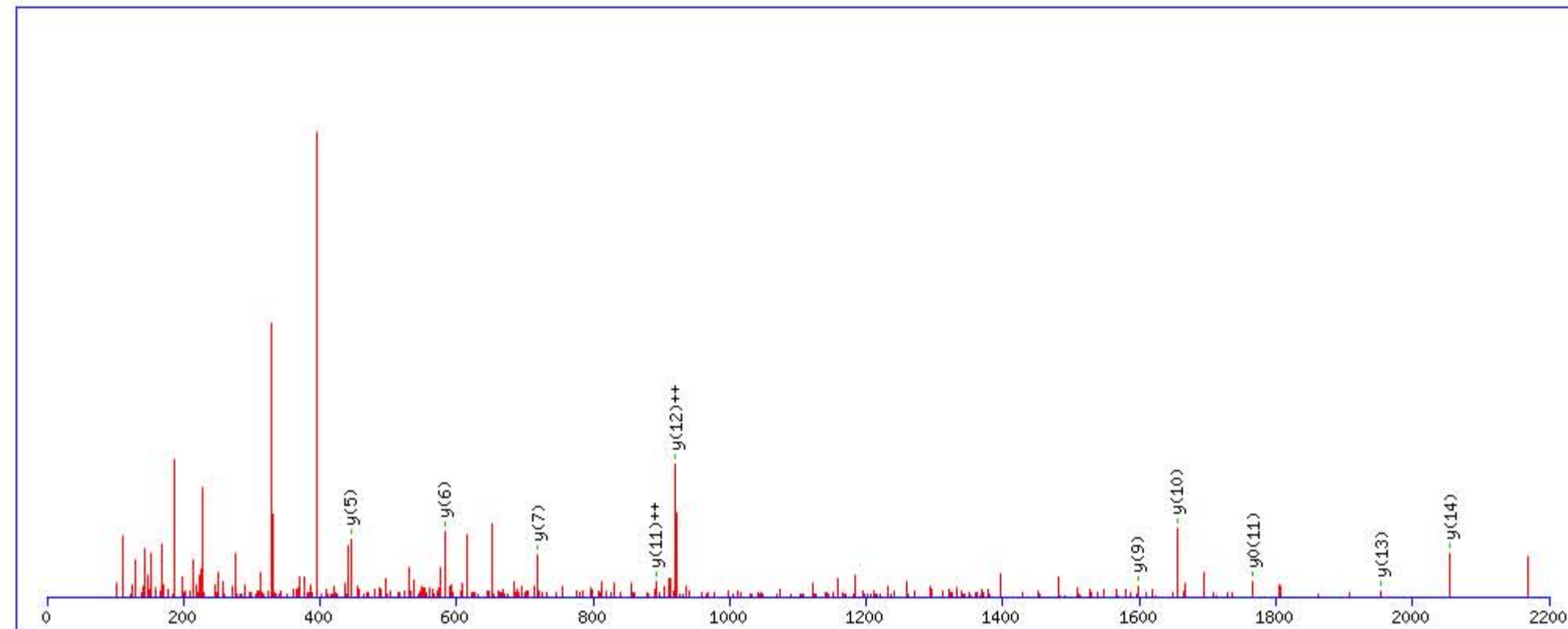
Title: Locus:1.1.1.3095.7 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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:

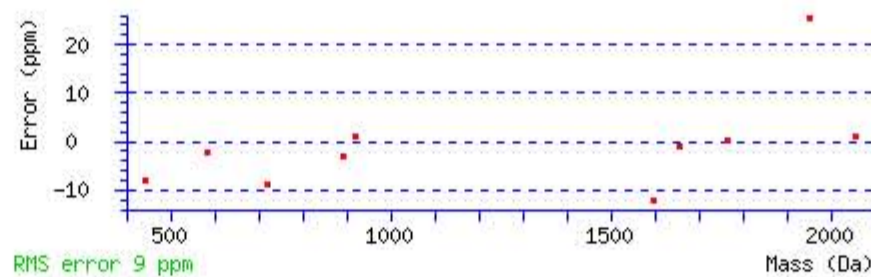
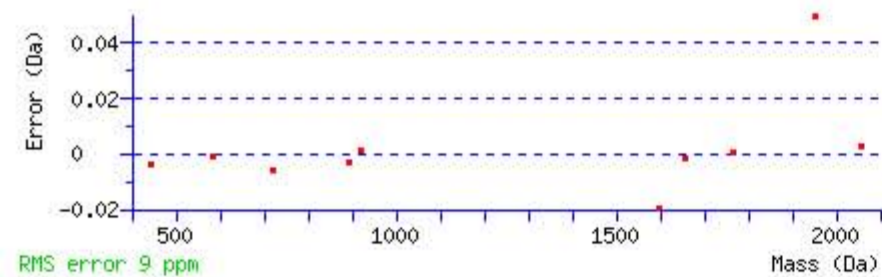
Q7 : Biotin:Thermo-21345 (Q)

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 30 Expect: 0.026

Matches : 10/134 fragment ions using 20 most intense peaks [\(help\)](#)

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



NCBI BLAST search of **LTIGEGQQHHLGGAK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.9	2167.139435	-0.007539	LTIGEGQQHHLGGAK

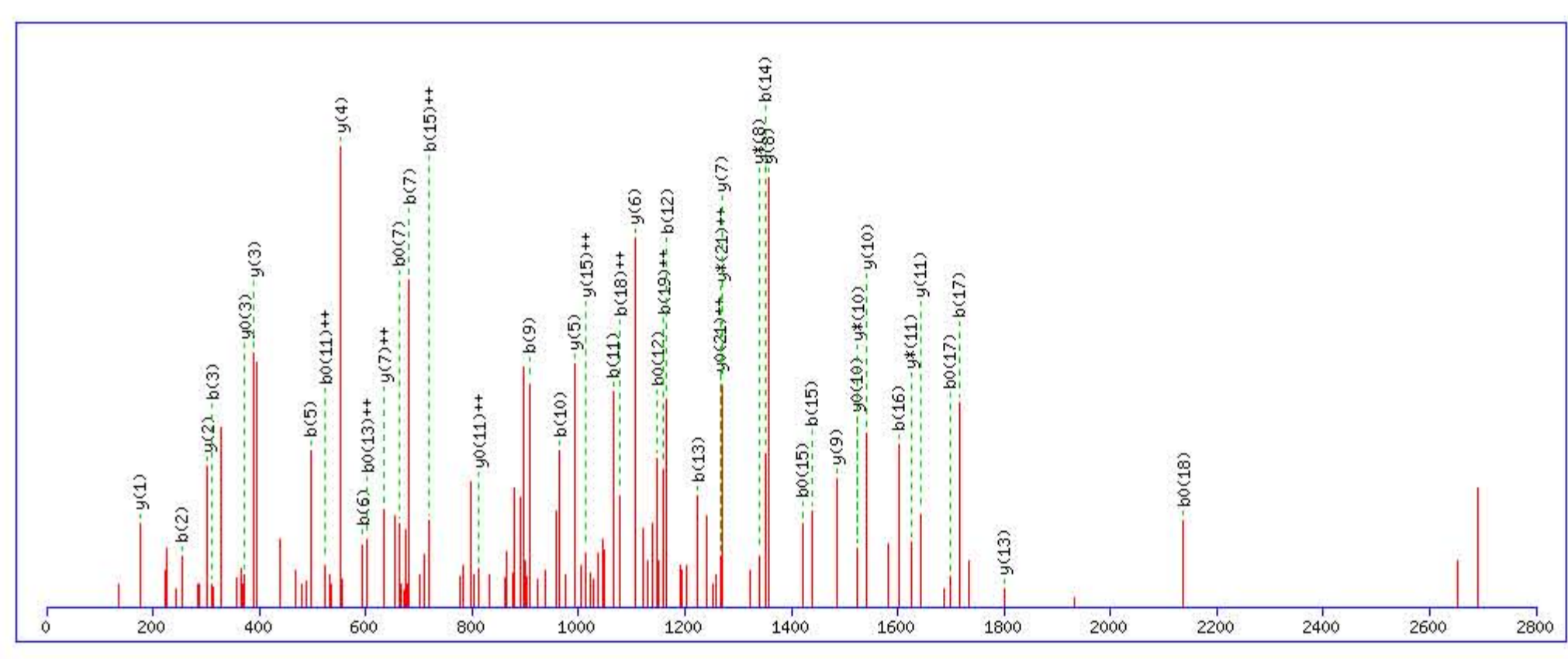
MASCOT Mascot Search Results

Peptide View

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

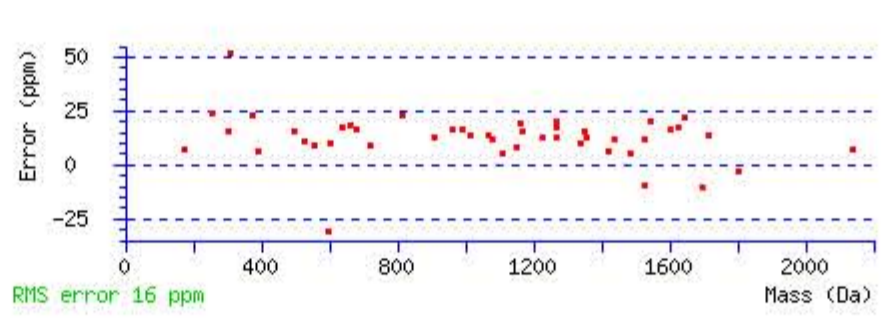
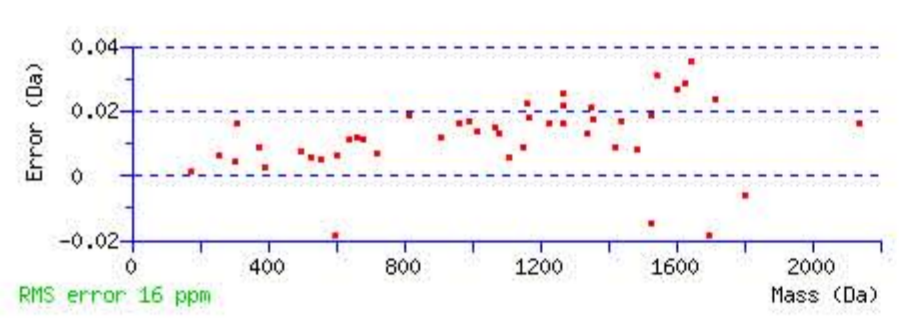
Match to Query 61985: 2706.237702 from(903.086510,3+) rtinseconds(1497) index(35580)
 Title: Locus:1.1.1.2543.26 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 102 Expect: 6.8e-010
 Matches : 47/240 fragment ions using 69 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	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 **RPGGEPSPGTTGQSYNQYSQR**
 (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	2706.245621	-0.007919	RPGGEPSPGTTGQSYNQYSQR
81.9	2706.245621	-0.007919	RPGGEPSPGTTGQSYNQYSQR
50.4	2706.245621	-0.007919	RPGGEPSPGTTGQSYNQYSQR

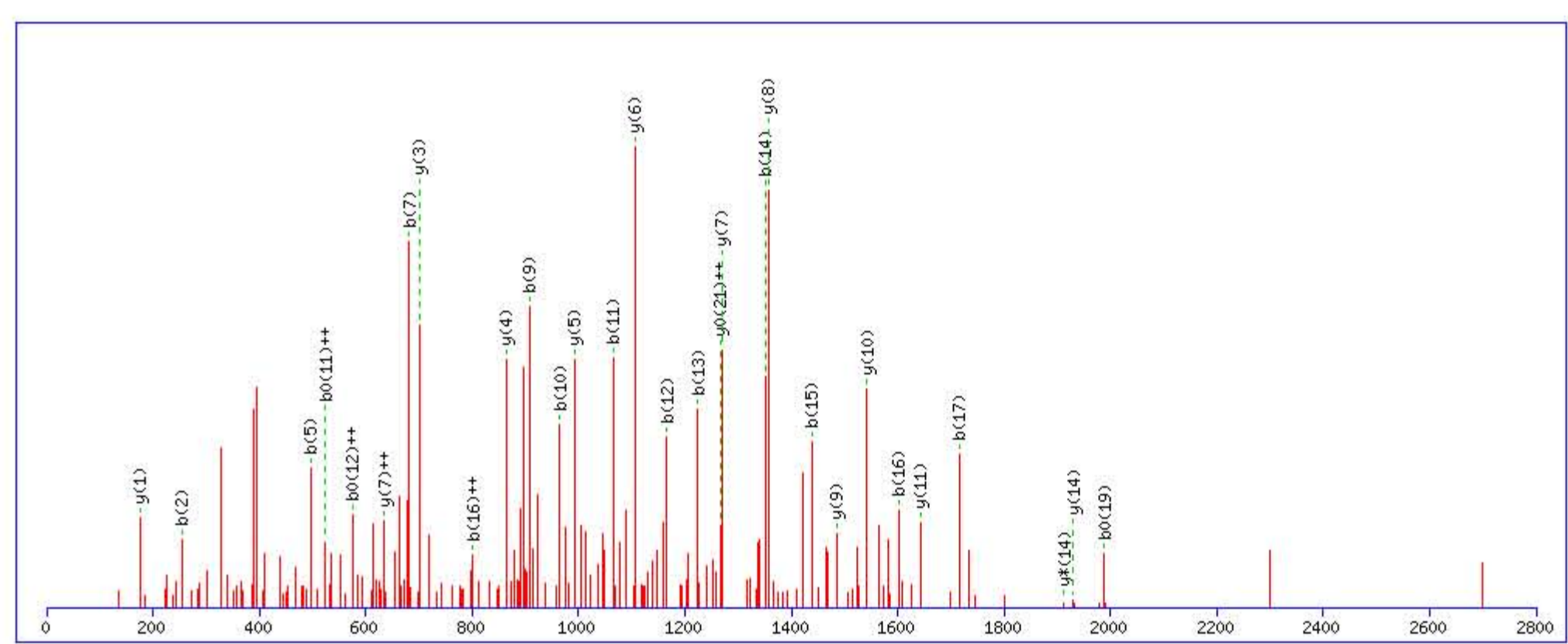
MASCOT Search Results

Peptide View

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

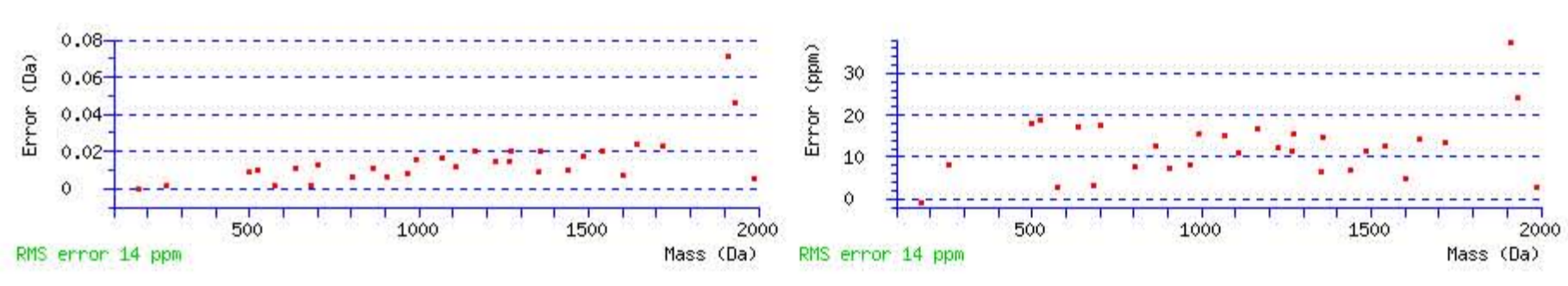
Match to Query 61986: 2706.237702 from(903.086510,3+) rtinseconds(1506) index(35619)
 Title: Locus:1.1.1.2546.15 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 2706.245621
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q21 : Biotin:Thermo-21345 (Q)
 Ions Score: 100 Expect: 1.3e-009
 Matches : 31/240 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	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	1843.820547	922.413912	1826.793998	913.900637	1825.809982	913.408629	Q	992.498213	496.752745	975.471664	488.239470	974.487648	487.747462	5
19	2006.883876	1003.945576	1989.857327	995.432302	1988.873311	994.940294	Y	864.439635	432.723456	847.413086	424.210181	846.429070	423.718173	4
20	2093.915904	1047.461590	2076.889355	1038.948315	2075.905339	1038.456307	S	701.376306	351.191791	684.349757	342.678517	683.365741	342.186509	3
21	2533.141230	1267.074253	2516.114681	1258.560978	2515.130665	1258.068971	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 [RPGGEPSPGTTGQSYNQYSQR](#)
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	$M_r(\text{calc})$:	Delta	Sequence
99.8	2706.245621	-0.007919	RPGGEPSPGTTGQSYNQYSQR
89.3	2706.245621	-0.007919	RPGGEPSPGTTGQSYNQYSQR
40.9	2706.245621	-0.007919	RPGGEPSPGTTGQSYNQYSQR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **RPGGEPSPGTTGQSYNQYSQR**

Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

Match to Query 61987: 2706.240372 from(903.087400,3+) rtinseconds(1522) index(35729)

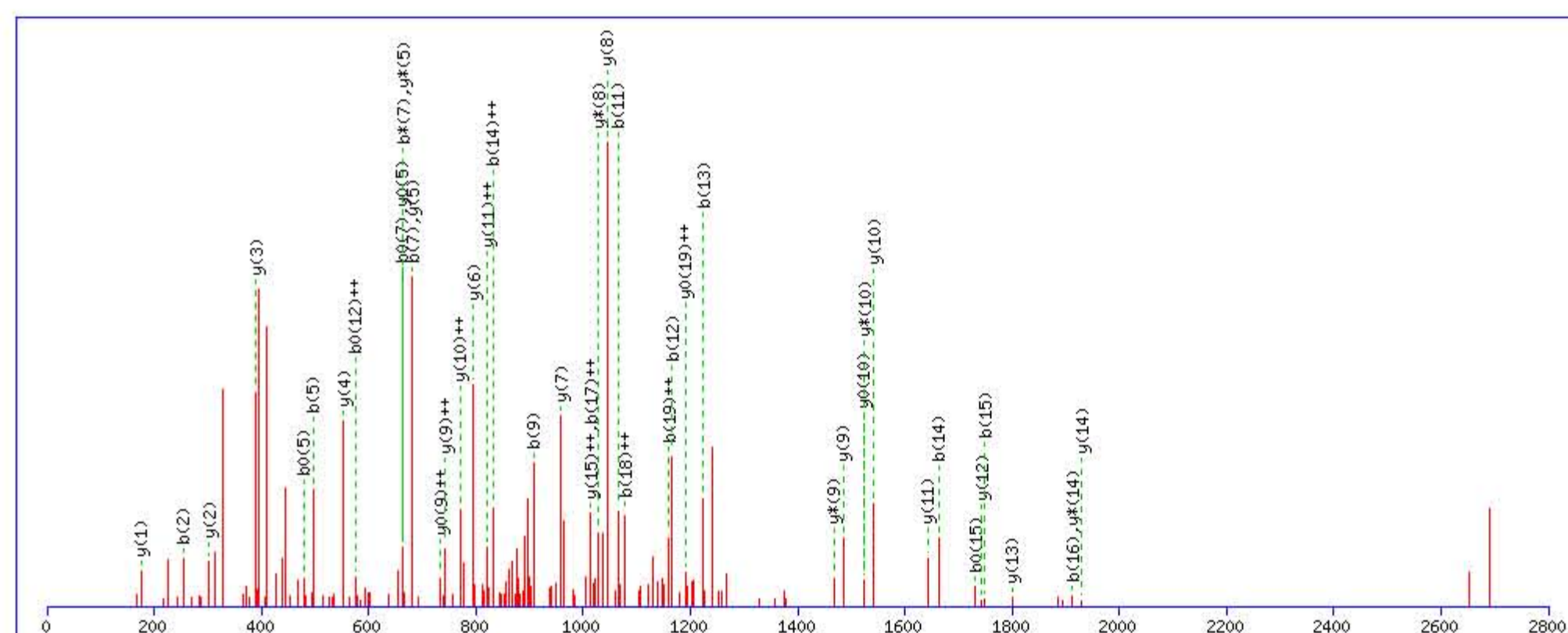
Title: Locus:1.1.1.2552.17 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2706.245621

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

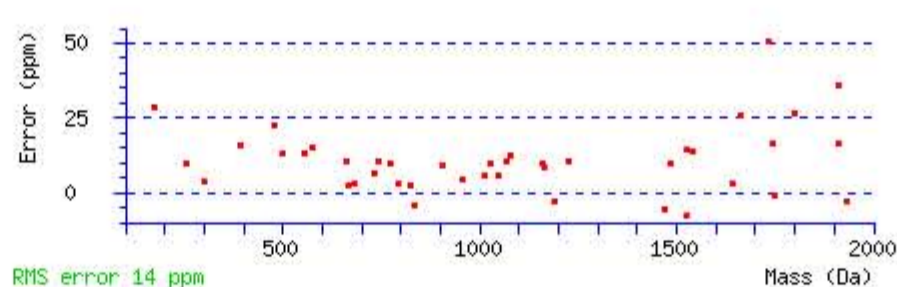
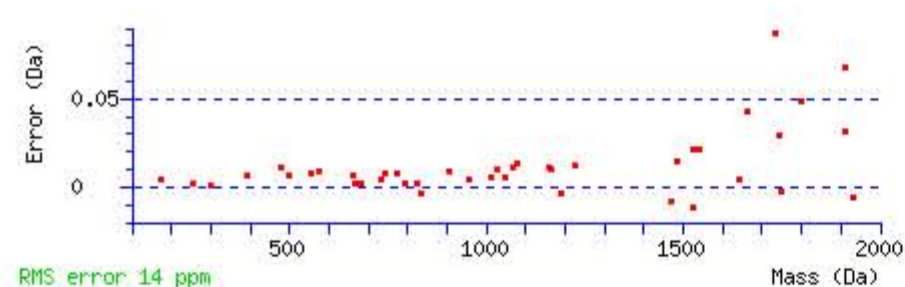
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 87 Expect: 7.4e-009

Matches : 46/240 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	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 [RPGGEPSPGTTGQSYNQYSQR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
87.0	2706.245621	-0.005249	RPGGEPSPGTTGQSYNQYSQR
44.5	2706.245621	-0.005249	RPGGEPSPGTTGQSYNQYSQR
26.7	2706.245621	-0.005249	RPGGEPSPGTTGQSYNQYSQR
0.3	2706.246658	-0.006286	MAQKMSFGFYKYSNMEFVR

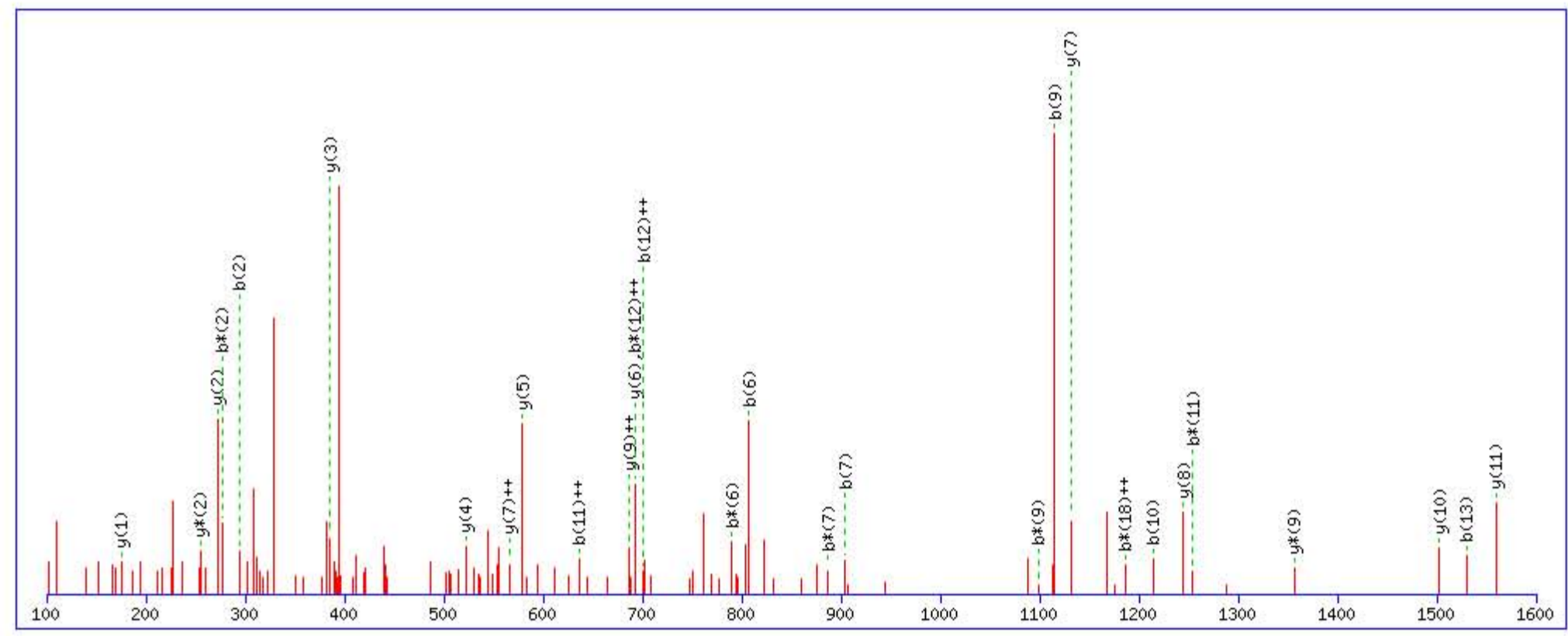
Mascot Search Results

Peptide View

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

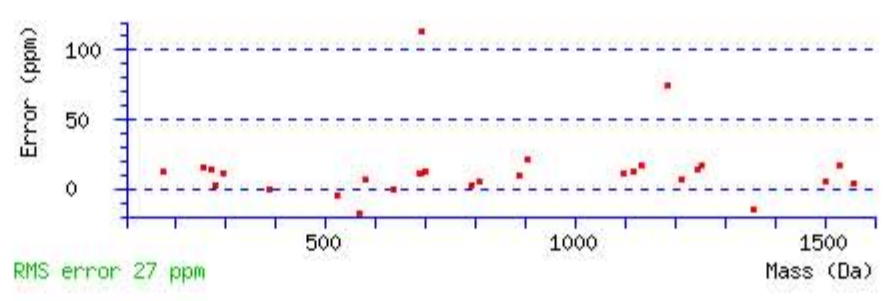
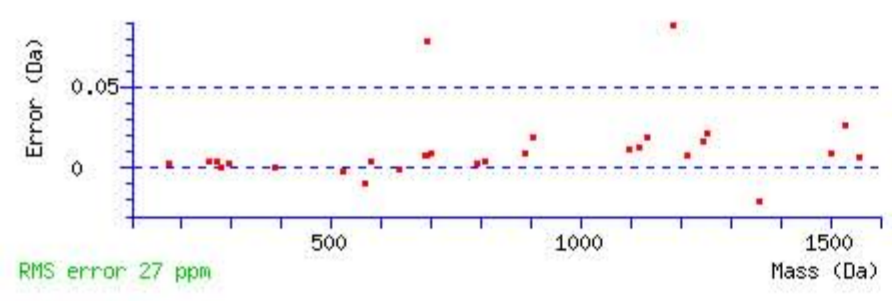
Match to Query 62791: 2772.496370 from(555.506550,5+) rtinseconds(1776) index(37185)
 Title: Locus:1.1.1.2641.11 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 2772.475815
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q15 : Biotin:Thermo-21345 (Q)
 Ions Score: 45 Expect: 0.00052
 Matches : 29/200 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							21
2	294.167299	147.587288	277.140750	139.074013			R	2636.424208	1318.715742	2619.397659	1310.202467	2618.413643	1309.710459	20
3	391.220063	196.113670	374.193514	187.600395			P	2480.323097	1240.665186	2463.296548	1232.151912	2462.312532	1231.659904	19
4	547.321174	274.164225	530.294625	265.650951			R	2383.270333	1192.138804	2366.243784	1183.625530	2365.259768	1183.133522	18
5	644.373938	322.690607	627.347389	314.177333			P	2227.169222	1114.088249	2210.142673	1105.574974	2209.158657	1105.082966	17
6	807.437267	404.222272	790.410718	395.708997			Y	2130.116458	1065.561867	2113.089909	1057.048592	2112.105893	1056.556584	16
7	904.490031	452.748654	887.463482	444.235379			P	1967.053129	984.030203	1950.026580	975.516928	1949.042564	975.024920	15
8	1001.542795	501.275036	984.516246	492.761761			P	1870.000365	935.503821	1852.973816	926.990546	1851.989800	926.498538	14
9	1115.585722	558.296499	1098.559173	549.783225			N	1772.947601	886.977439	1755.921052	878.464164	1754.937036	877.972156	13
10	1214.654136	607.830706	1197.627587	599.317432			V	1658.904674	829.955975	1641.878125	821.442701	1640.894109	820.950693	12
11	1271.675600	636.341438	1254.649051	627.828164			G	1559.836260	780.421768	1542.809711	771.908494	1541.825695	771.416486	11
12	1400.718193	700.862735	1383.691644	692.349460	1382.707628	691.857452	E	1502.814796	751.911036	1485.788247	743.397762	1484.804231	742.905754	10
13	1529.760786	765.384031	1512.734237	756.870757	1511.750221	756.378749	E	1373.772203	687.389740	1356.745654	678.876465	1355.761638	678.384457	9
14	1642.844850	821.926063	1625.818301	813.412789	1624.834285	812.920781	I	1244.729610	622.868443	1227.703061	614.355169			8
15	2082.070176	1041.538726	2065.043627	1033.025451	2064.059611	1032.533444	Q	1131.645546	566.326411	1114.618997	557.813137			7
16	2195.154240	1098.080758	2178.127691	1089.567484	2177.143675	1089.075476	I	692.420220	346.713748	675.393671	338.200474			6
17	2252.175704	1126.591490	2235.149155	1118.078215	2234.165139	1117.586208	G	579.336156	290.171716	562.309607	281.658442			5
18	2389.234616	1195.120946	2372.208067	1186.607671	2371.224051	1186.115664	H	522.314692	261.660984	505.288143	253.147710			4
19	2502.318680	1251.662978	2485.292131	1243.149704	2484.308115	1242.657696	I	385.255780	193.131528	368.229231	184.618254			3
20	2599.371444	1300.189360	2582.344895	1291.676086	2581.360879	1291.184078	P	272.171716	136.589496	255.145167	128.076221			2
21							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [HRPRPYPPNVGEEIQIGHIPR](#)
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

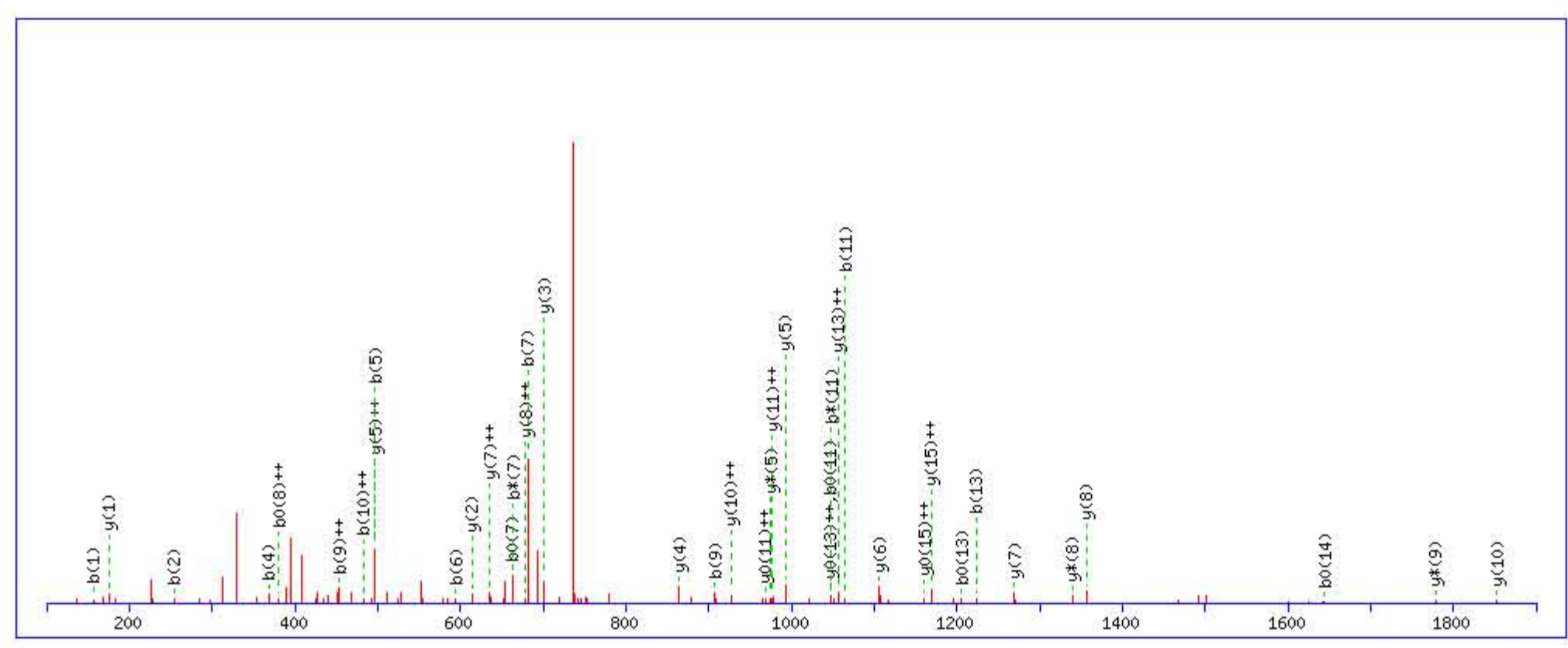
Score	Mr(calc):	Delta	Sequence
45.0	2772.475815	0.020555	HRPRPYPPNVGEEIQIGHIPR

Peptide View

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

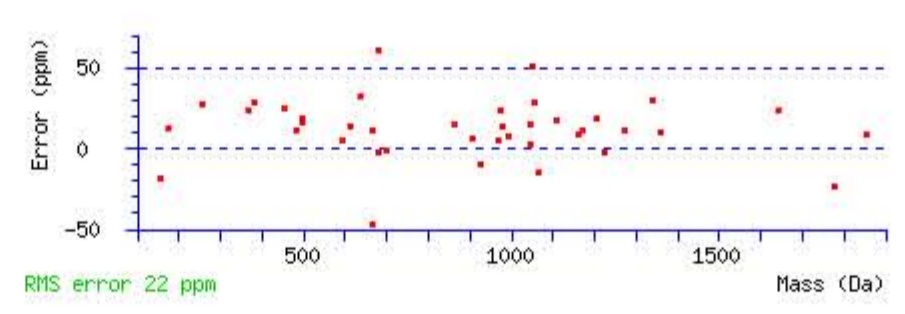
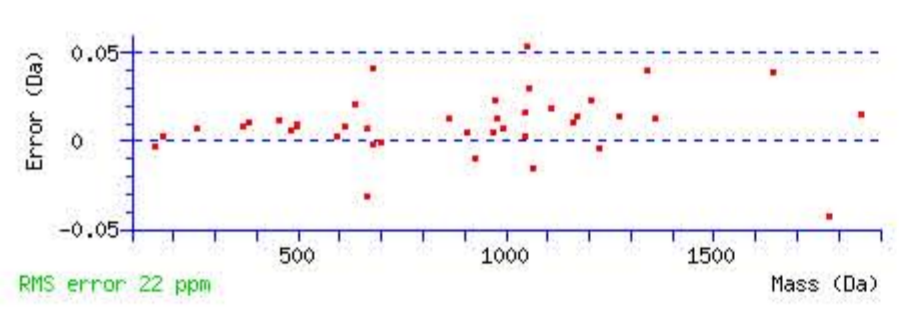
Match to Query 65636: 3017.416296 from(755.361350,4+) rtinseconds(1803) index(37363)
 Title: Locus:1.1.1.2650.13 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 43 Expect: 0.0009
 Matches : 40/240 fragment ions using 101 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 **RPGGEPSPGTTGQSYNQYSQR**
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.9	3017.412369	0.003927	RPGGEPSPGTTGQSYNQYSQR
37.1	3017.412369	0.003927	RPGGEPSPGTTGQSYNQYSQR
18.6	3017.412369	0.003927	RPGGEPSPGTTGQSYNQYSQR

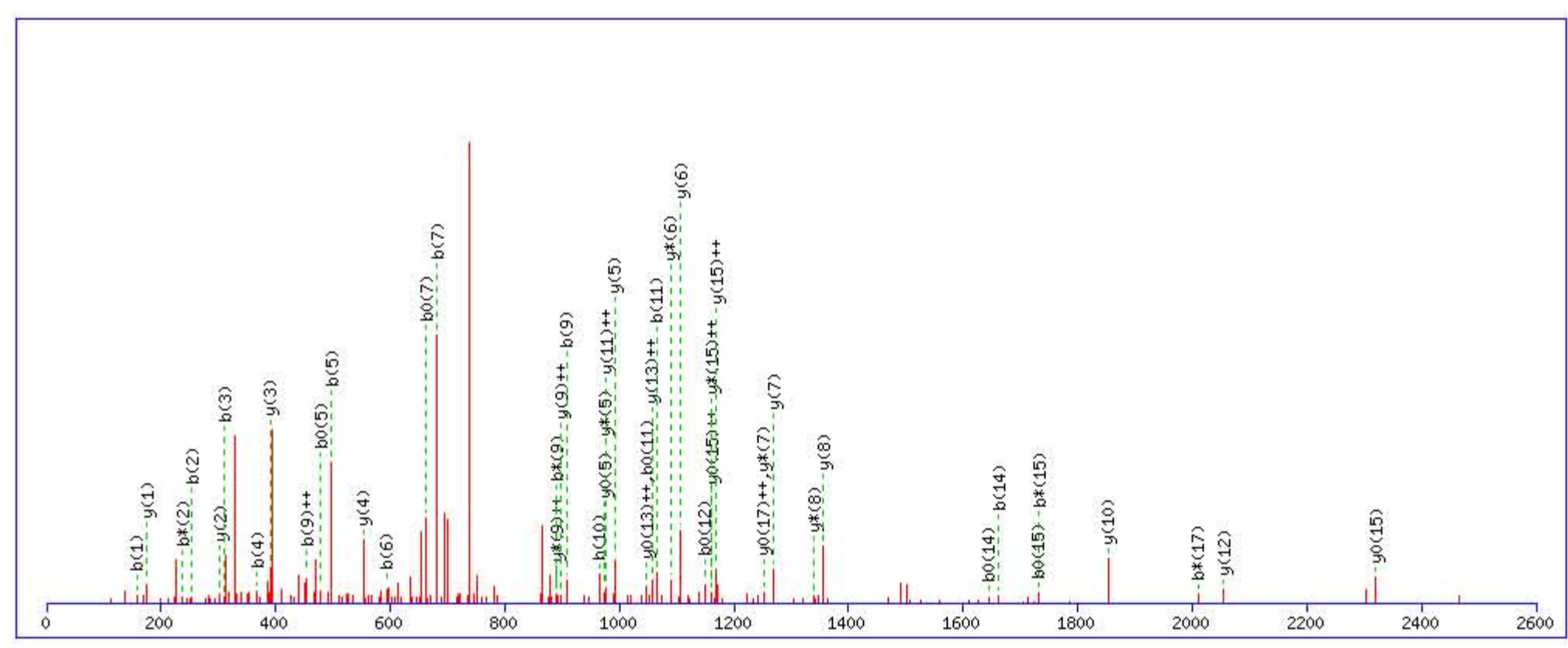
MASCOT Search Results

Peptide View

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

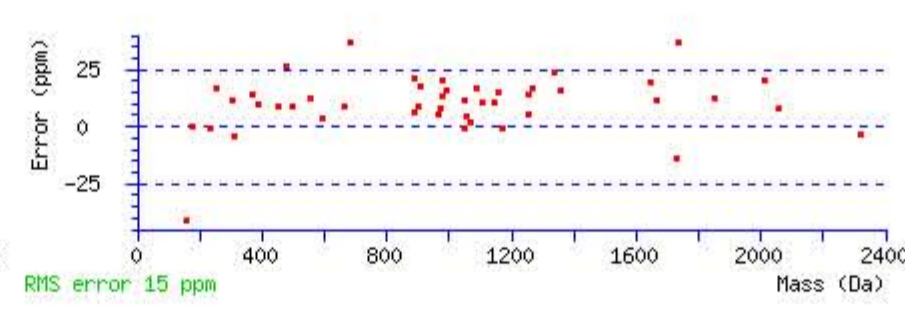
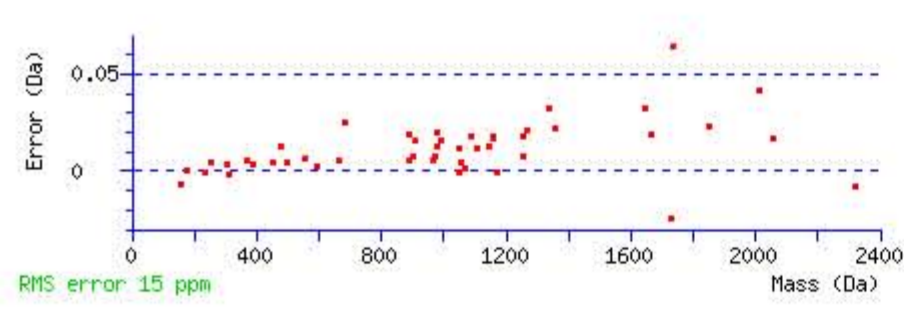
Match to Query 65637: 3017.416296 from(755.361350,4+) rtinseconds(1794) index(37307)
 Title: Locus:1.1.1.2647.20 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 51 Expect: 0.00012
 Matches : 47/240 fragment ions using 111 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 **RPGGEPSPGTTGQSYNQYSQR**
 (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	3017.412369	0.003927	RPGGEPSPGTTGQSYNQYSQR
49.4	3017.412369	0.003927	RPGGEPSPGTTGQSYNQYSQR
25.9	3017.412369	0.003927	RPGGEPSPGTTGQSYNQYSQR

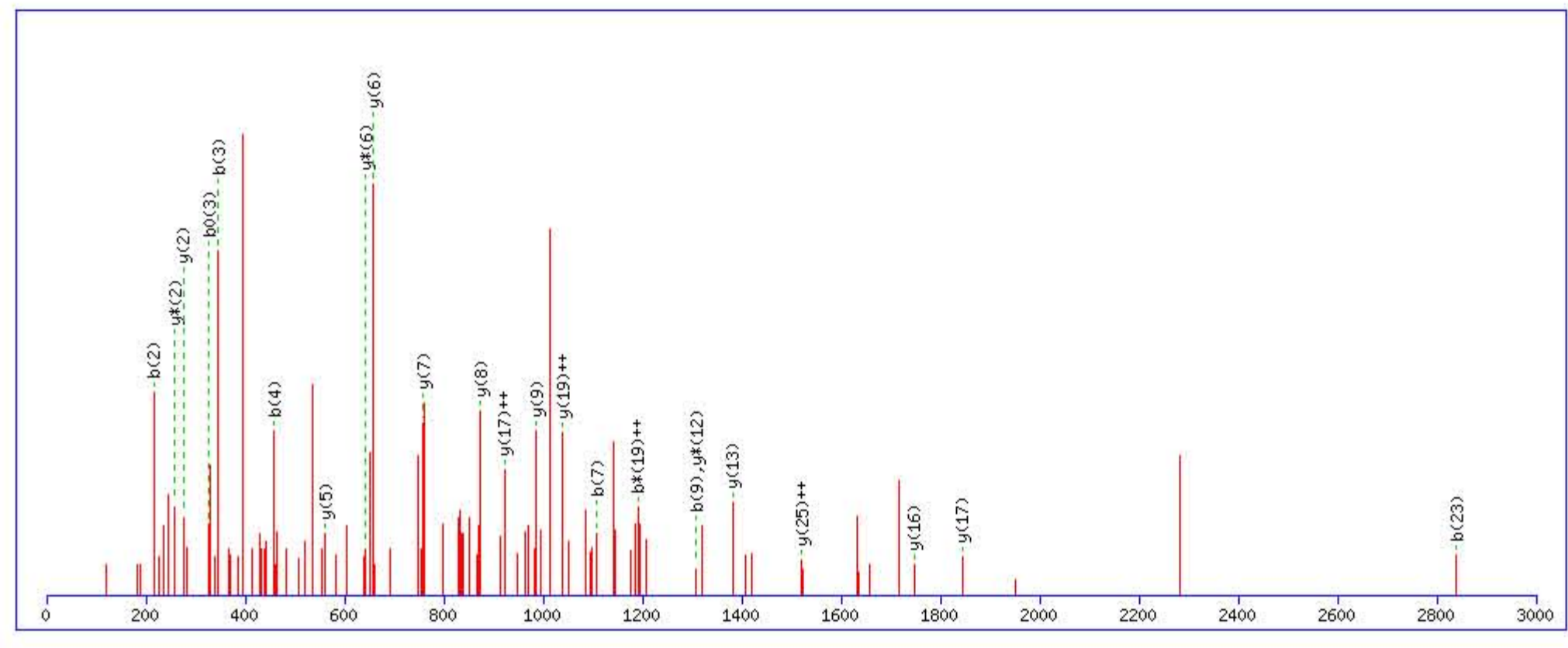
MASCOT Mascot Search Results

Peptide View

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

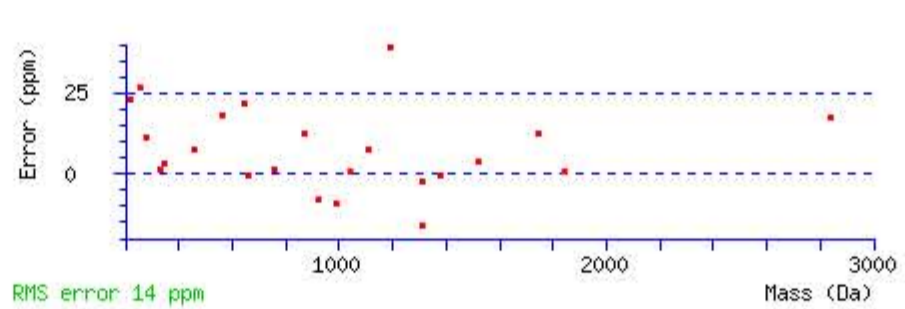
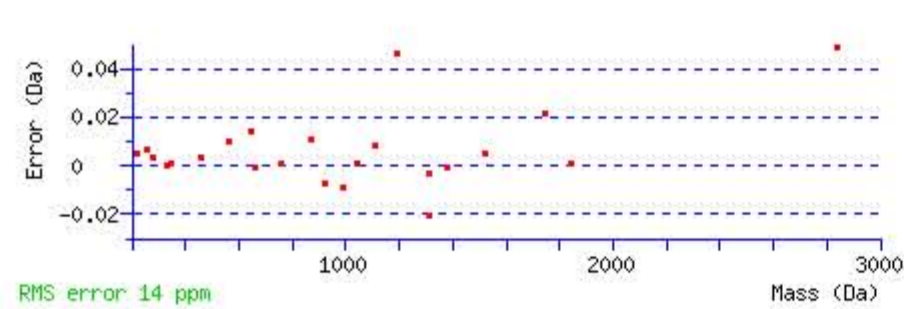
Match to Query 70849: 3497.862216 from(875.472830,4+) rtinseconds(2602) index(59233)
 Title: Locus:1.1.1.3391.24 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 27 Expect: 0.031
 Matches : 23/320 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	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
27.4	3497.859238	0.002978	TDELPQLVTLPHPNLHGPEILDVPSTVQK

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 28088: 1285.664288 from(643.839420,2+) rtinseconds(1480) index(52439)

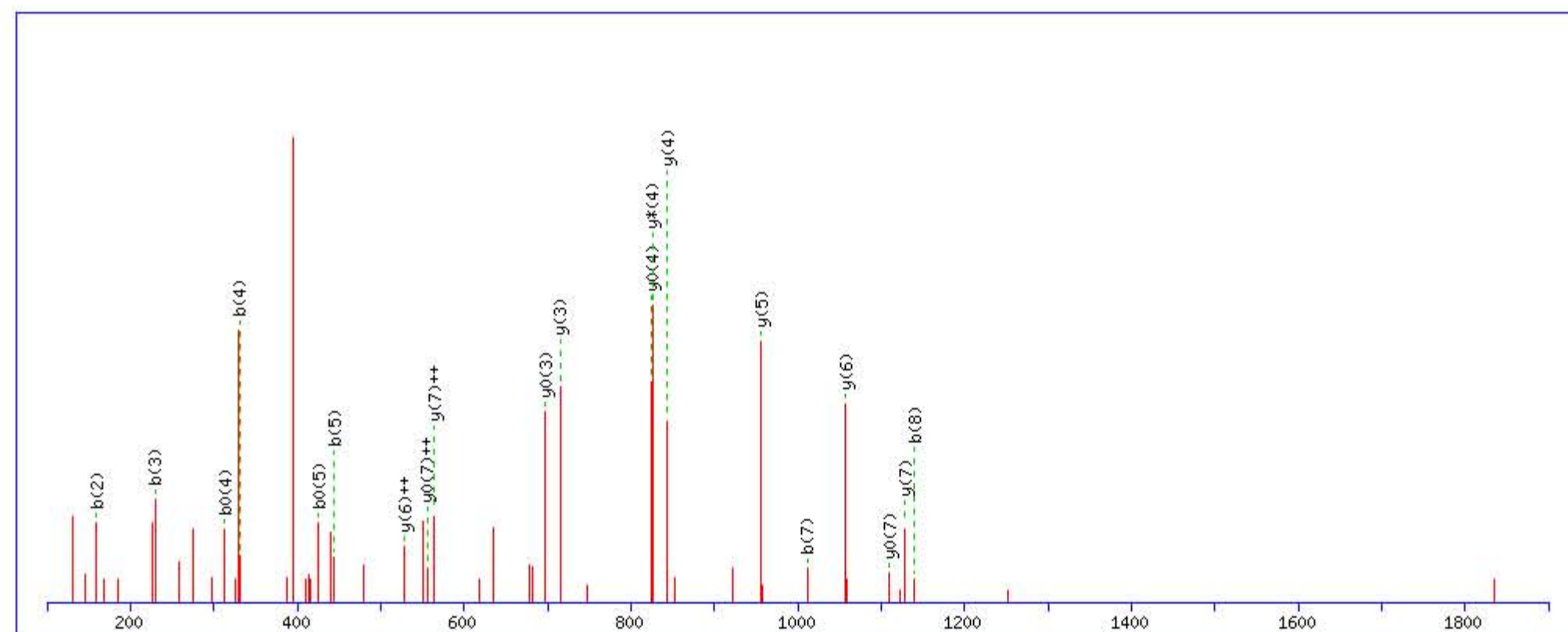
Title: Locus:1.1.1.3001.20 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

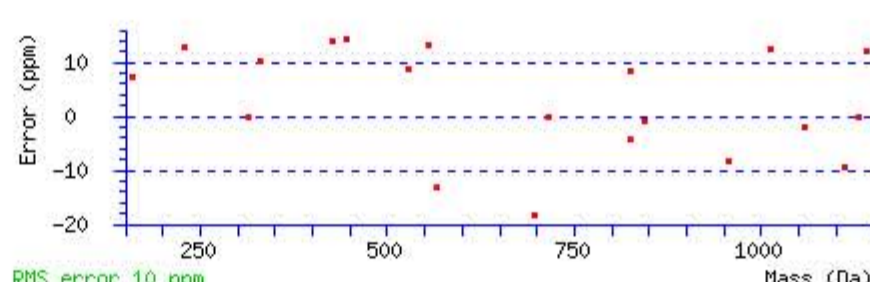
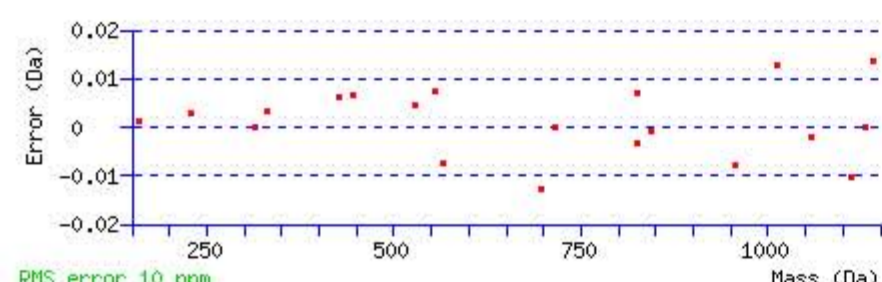
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 38 Expect: 0.0027

Matches : 20/84 fragment ions using 32 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.039304	44.523290			70.028739	35.518008	S							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
38.1	1285.669998	-0.005710	SAATLQQEK
33.6	1285.669998	-0.005710	SAATLQQEK
10.2	1285.669998	-0.005710	ASLDQGKEK
8.2	1285.651367	0.012921	LLQAVENGDAEK
8.2	1285.652237	0.012051	AMQIQEQK
5.6	1285.662598	0.001690	EARSQVVKPEK
4.3	1285.673859	-0.009571	NDVGGQRSLVNK
3.2	1285.652252	0.012036	VCALEQQK
2.7	1285.652237	0.012051	AMQIQEQK
0.8	1285.681213	-0.016925	EKQRSEAK

MASCOT Search Results

Peptide View

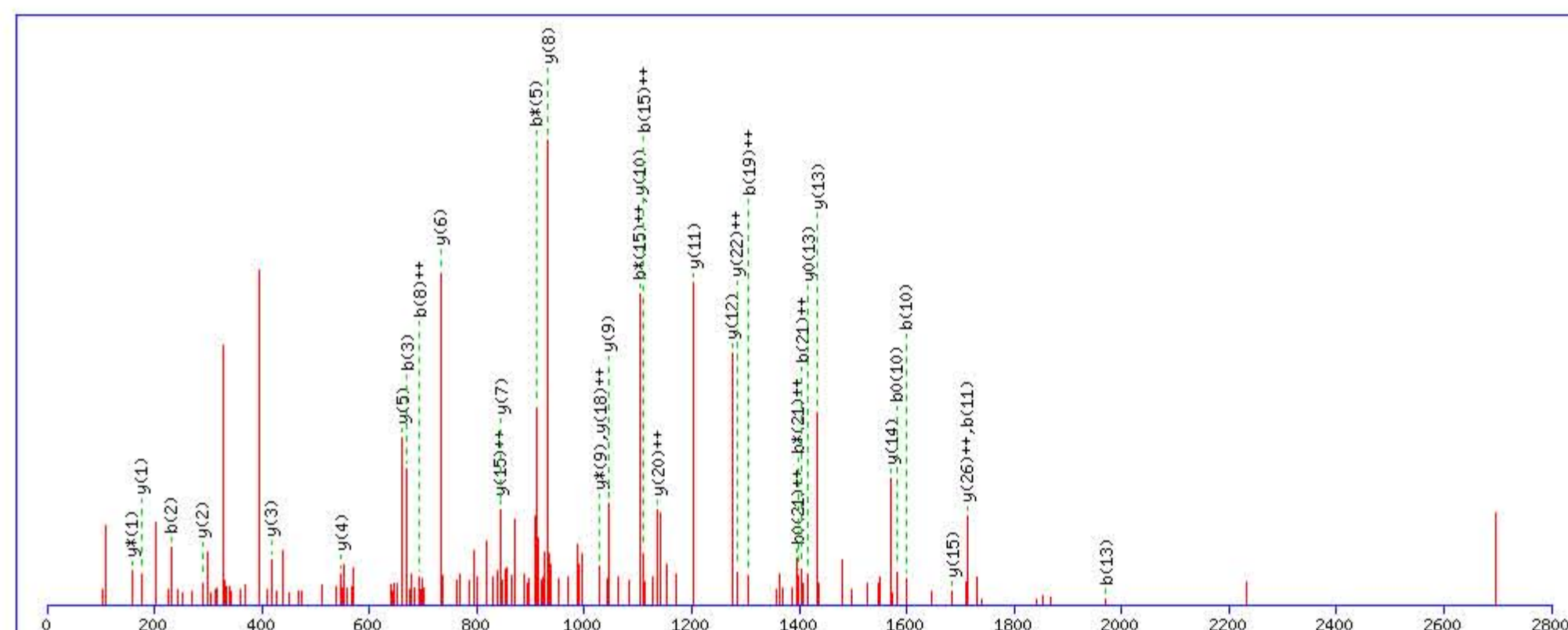
MS/MS Fragmentation of **MVQEQCCHSQLEELHCATGISLANEQDR**
 Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

Match to Query 71857: 3653.614656 from(914.410940,4+) rtinseconds(1985) index(38595)
 Title: Locus:1.1.1.2713.24 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

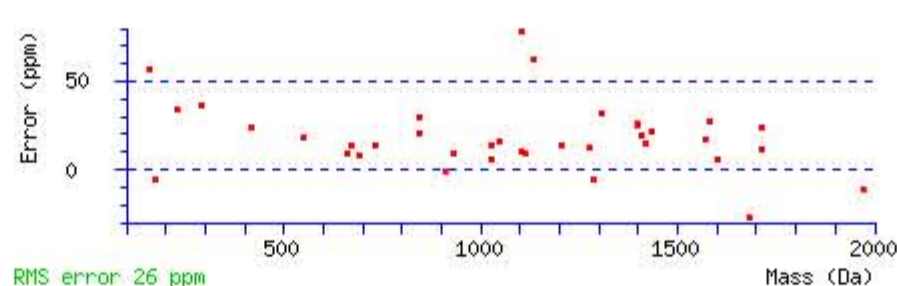
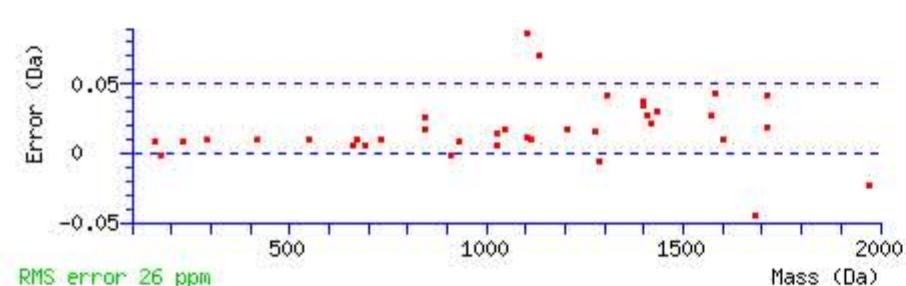
Or, Plot from to Da

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: 68 Expect: 1.1e-006
 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
67.9	3653.615311	-0.000655	MVQEQCCHSQLEELHCATGISLANEQDR
66.3	3653.615311	-0.000655	MVQEQCCHSQLEELHCATGISLANEQDR
61.7	3653.615311	-0.000655	MVQEQCCHSQLEELHCATGISLANEQDR

MASCOT Search Results

Peptide View

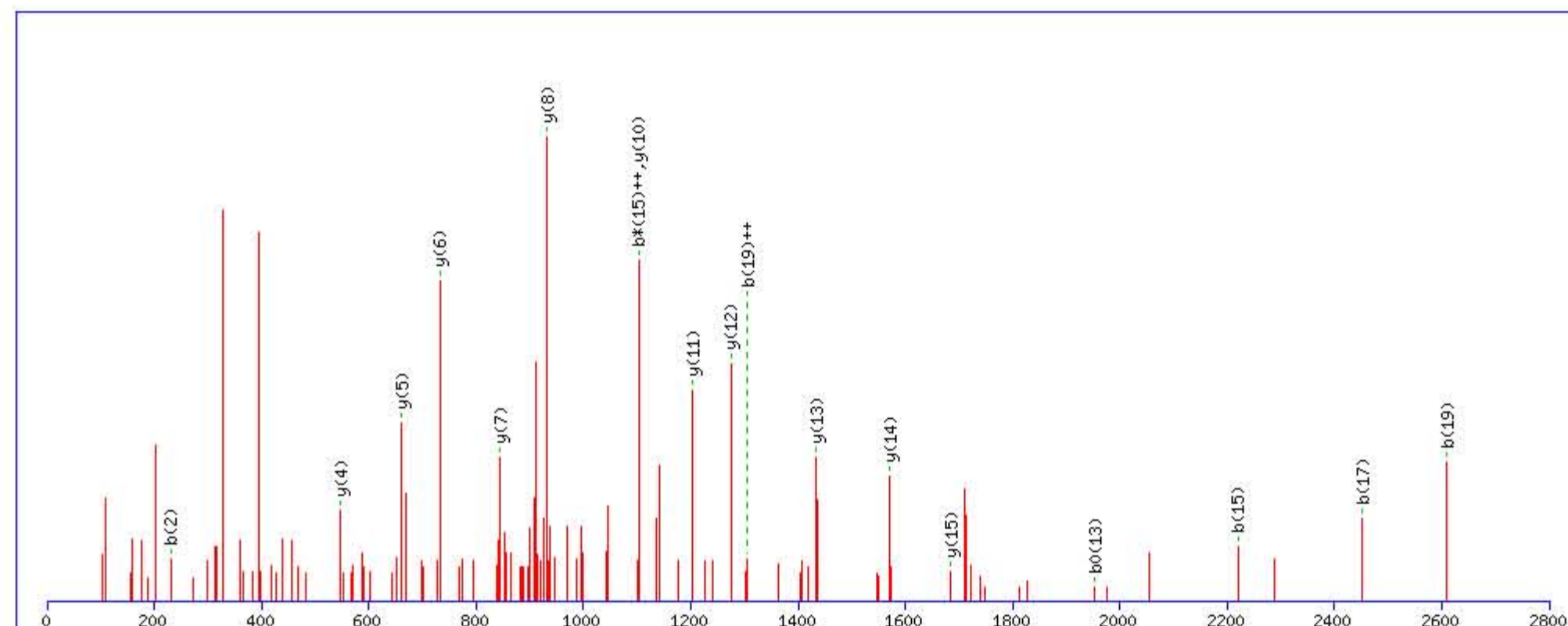
MS/MS Fragmentation of **MVQEQCCHSQLEELHLCATGISLANEQDR**
 Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

Match to Query 71858: 3653.622856 from(914.412990,4+) rtinseconds(1975) index(55667)
 Title: Locus:1.1.1.3173.24 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

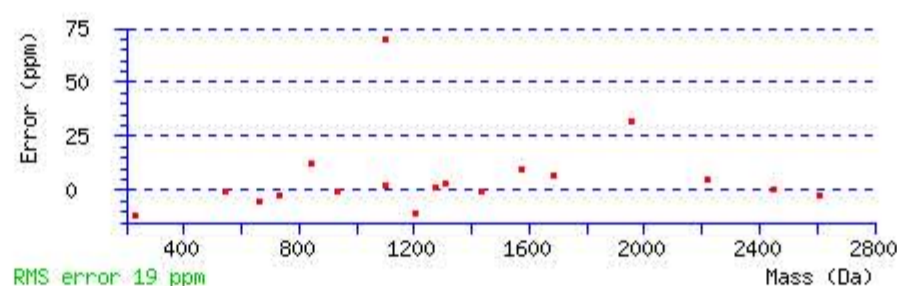
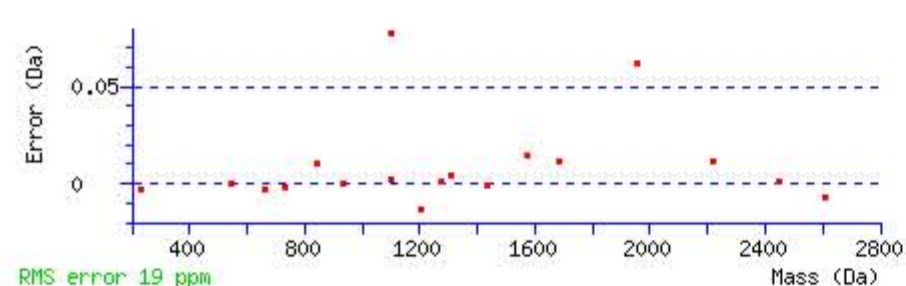
Or, Plot from to Da

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: 70 Expect: 7.7e-007
 Matches : 18/312 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	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 **MVQEQCCHSQLEELHLCATGISLANEQDR**
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.9	3653.615311	0.007545	MVQEQCCHSQLEELHLCATGISLANEQDR
69.9	3653.615311	0.007545	MVQEQCCHSQLEELHLCATGISLANEQDR
69.9	3653.615311	0.007545	MVQEQCCHSQLEELHLCATGISLANEQDR

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 33129: 1418.766108 from(710.390330,2+) rtinseconds(1482) index(52454)

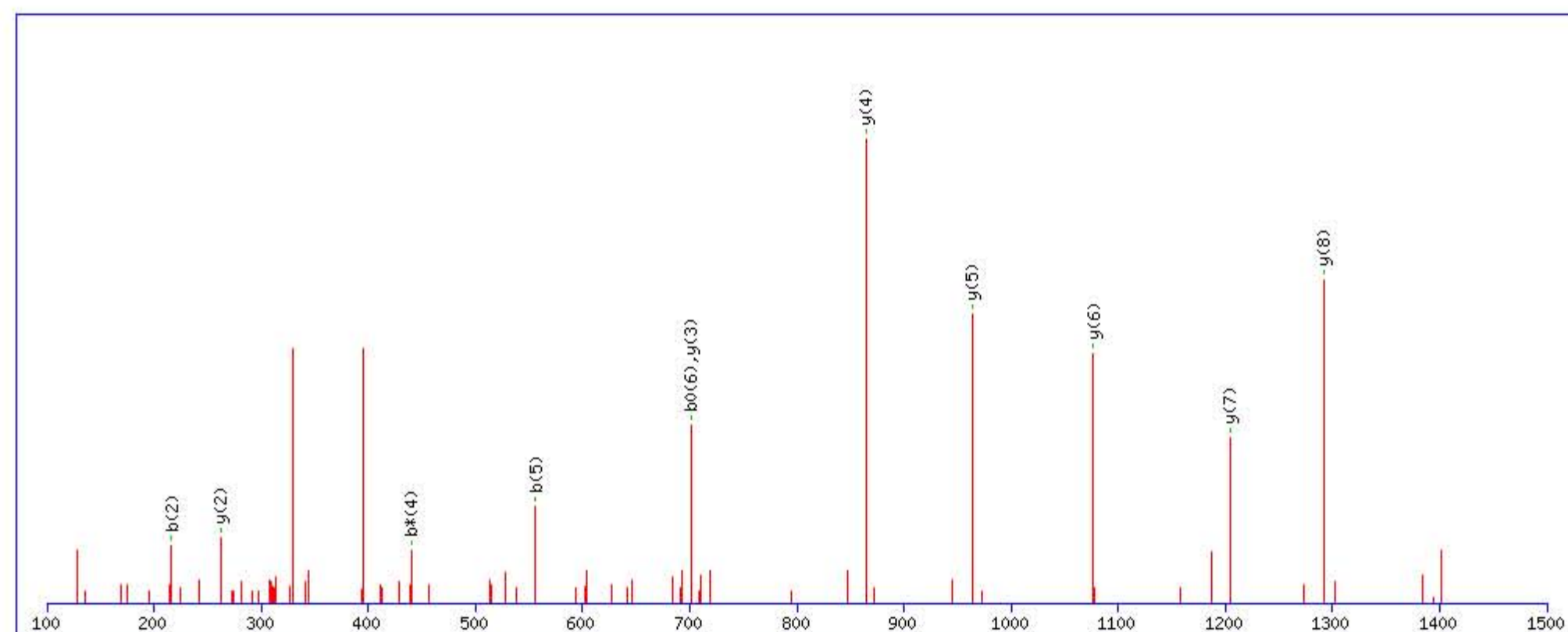
Title: Locus:1.1.1.3002.10 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

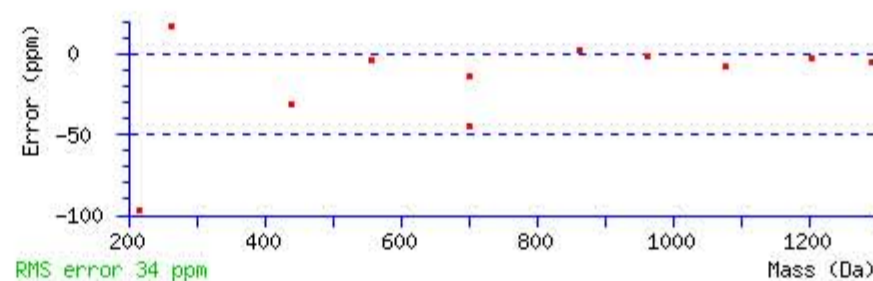
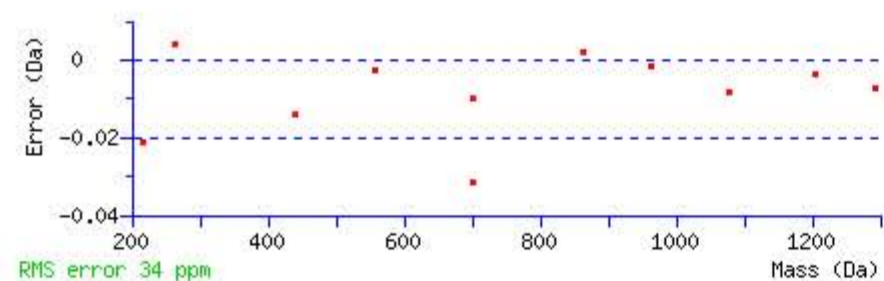
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 63 Expect: 1e-005

Matches : 11/92 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	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
62.9	1418.770386	-0.004278	KSQLVYQSR
10.4	1418.780273	-0.014165	TNQLMETLTKTIK
8.2	1418.770386	-0.004278	KSQLVYQSR
7.0	1418.763000	0.003108	IKGEQGAPGLQGHK
5.9	1418.767044	-0.000936	SQGLAGLFAGVFPR

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

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 42951: 1729.953252 from(577.658360,3+) rtinseconds(1845) index(37561)

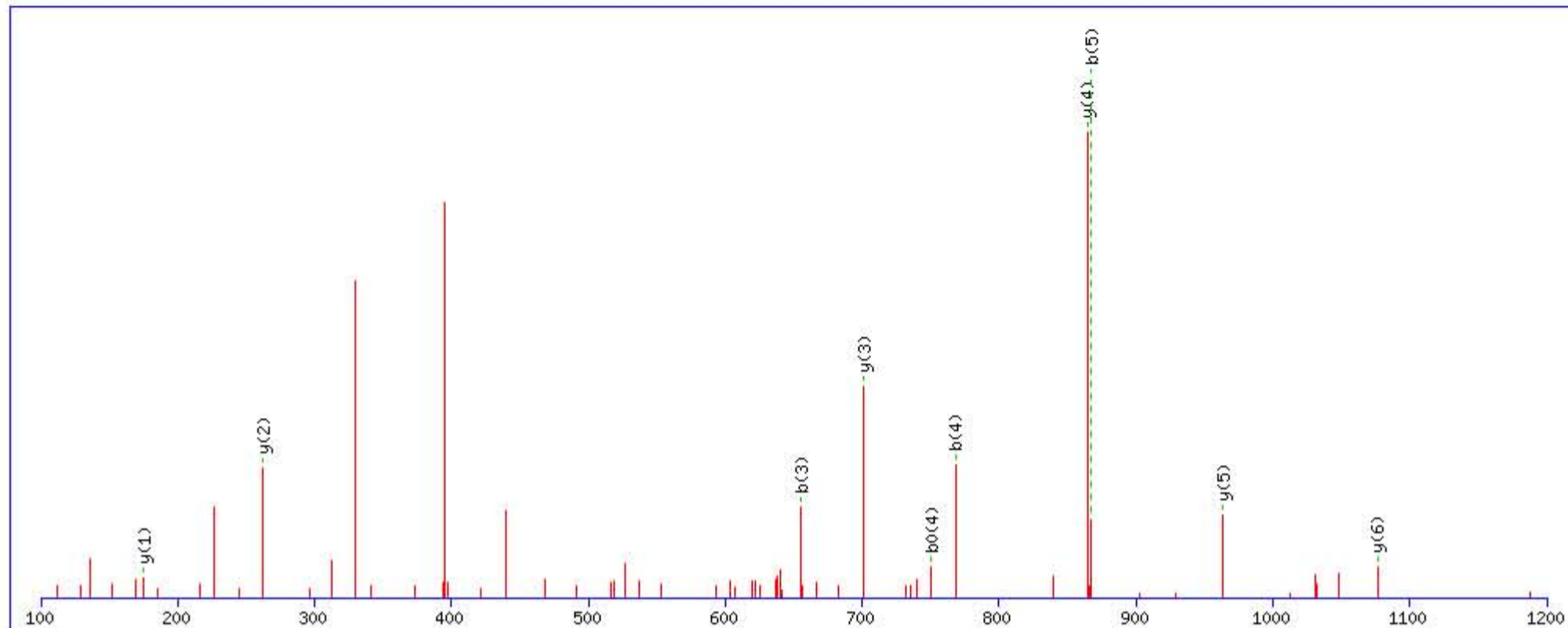
Title: Locus:1.1.1.2665.12 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1729.937134

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

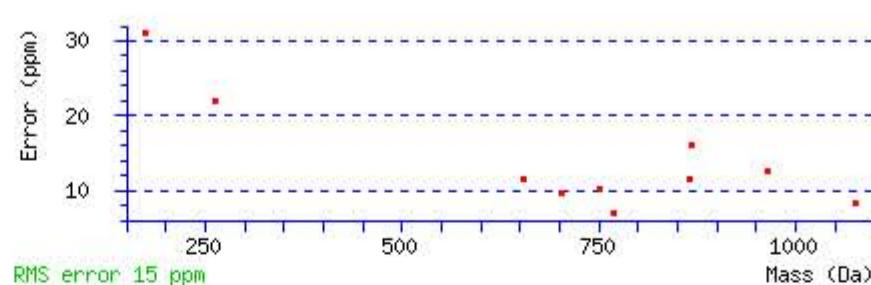
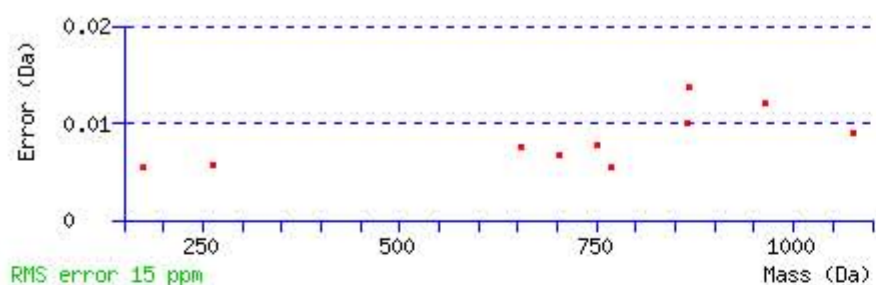
Q3 : Biotin:Thermo-21345 (Q)

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 28 Expect: 0.026

Matches : 10/92 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	129.102239	65.054757	112.075690	56.541483			K							9
2	216.134267	108.570771	199.107718	100.057497	198.123702	99.565489	S	1602.849467	801.928372	1585.822918	793.415097	1584.838902	792.923089	8
3	655.359593	328.183435	638.333044	319.670160	637.349028	319.178152	Q	1515.817439	758.412358	1498.790890	749.899083	1497.806874	749.407075	7
4	768.443657	384.725467	751.417108	376.212192	750.433092	375.720184	L	1076.592113	538.799695	1059.565564	530.286420	1058.581548	529.794412	6
5	867.512071	434.259674	850.485522	425.746399	849.501506	425.254391	V	963.508049	482.257663	946.481500	473.744388	945.497484	473.252380	5
6	1030.575400	515.791338	1013.548851	507.278063	1012.564835	506.786055	Y	864.439635	432.723456	847.413086	424.210181	846.429070	423.718173	4
7	1469.800726	735.404001	1452.774177	726.890727	1451.790161	726.398719	Q	701.376306	351.191791	684.349757	342.678517	683.365741	342.186509	3
8	1556.832754	778.920015	1539.806205	770.406741	1538.822189	769.914733	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
28.5	1729.937134	0.016118	KSQLVYQSR

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 47007: 1908.834072 from(637.285300,3+) rtinseconds(2077) index(56285)

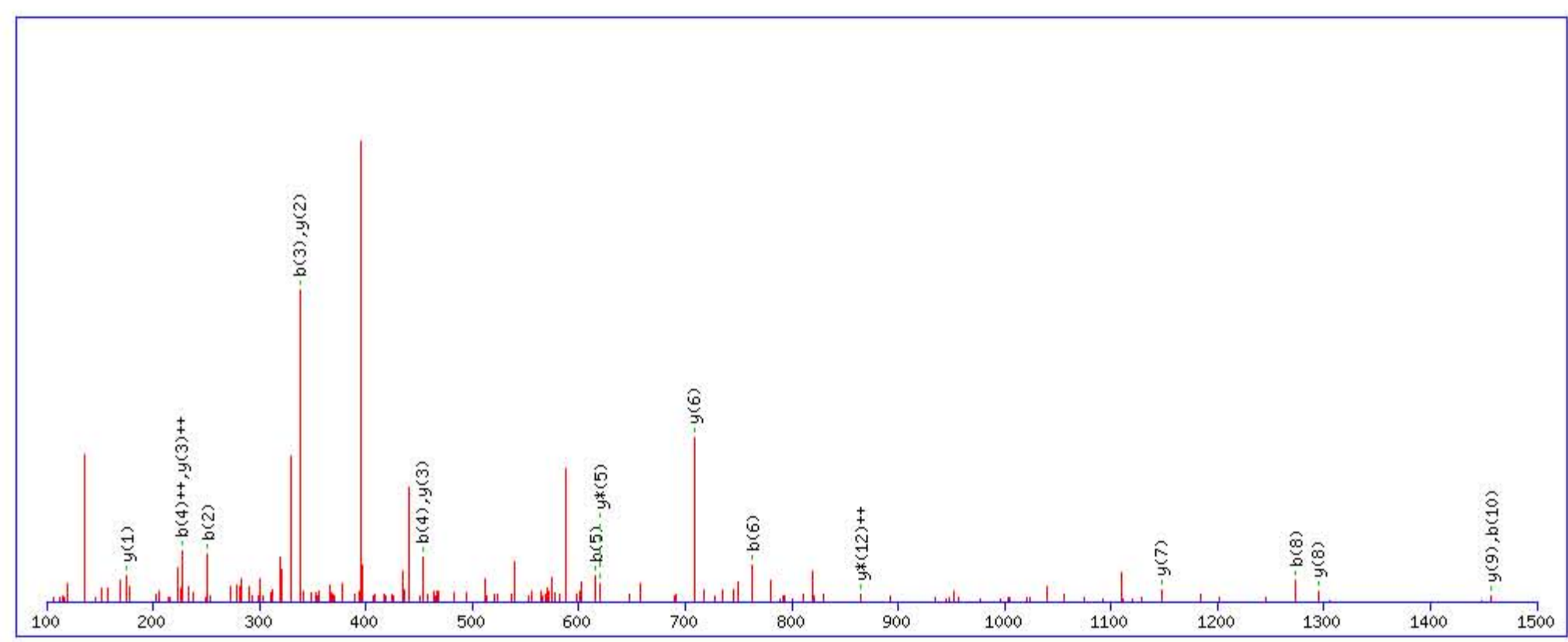
Title: Locus:1.1.1.3209.8 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

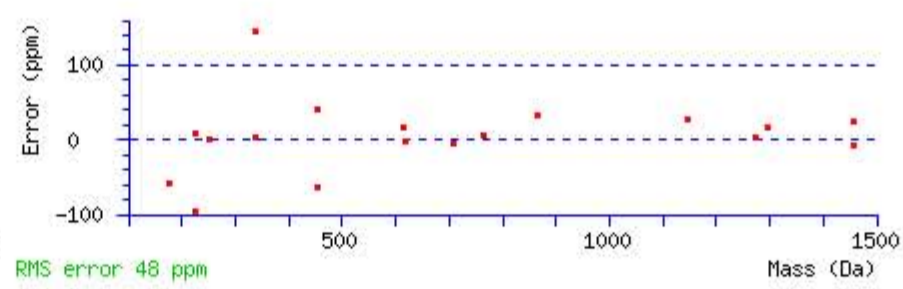
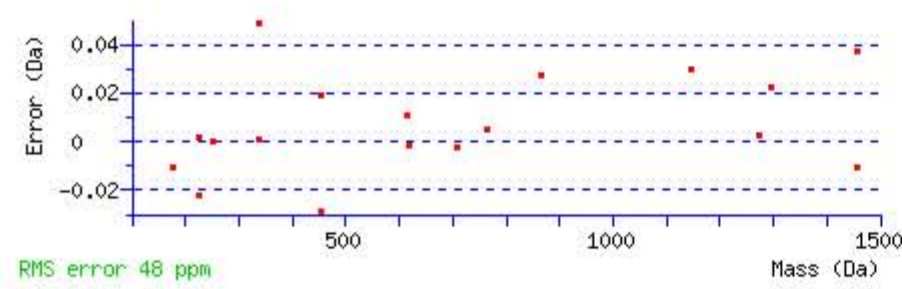
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 40 Expect: 0.0005

Matches : 18/126 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	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
40.1	1908.835236	-0.001164	YSSDYFQAPSDYR

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 28660: 1309.671372 from(437.564400,3+) rtinseconds(1253) index(1195)

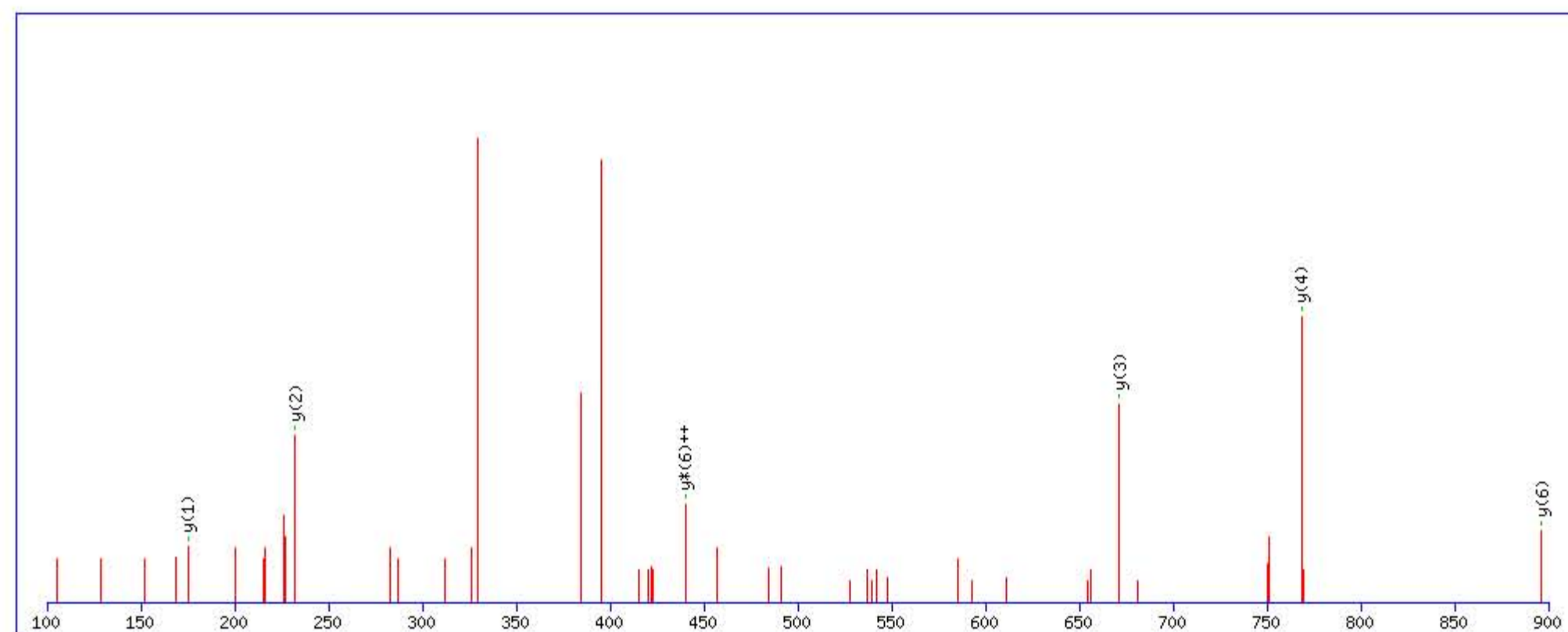
Title: Locus:1.1.1.2872.5 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

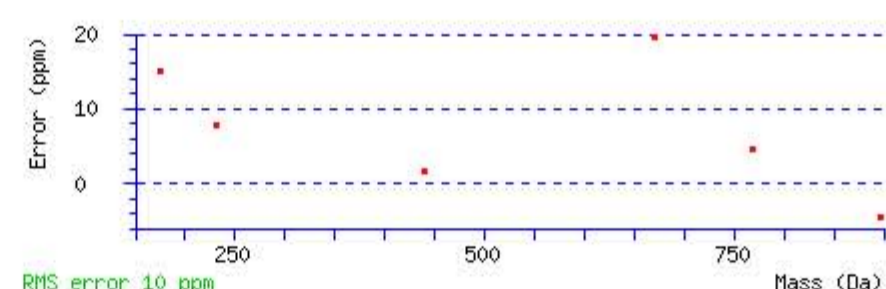
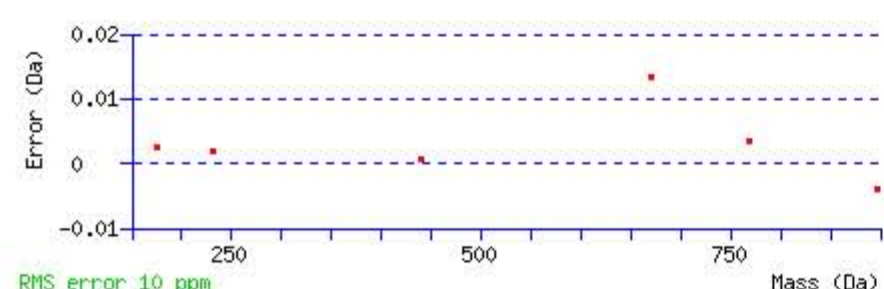
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 36 Expect: 0.0048

Matches : 6/94 fragment ions using 8 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
36.2	1309.656097	0.015275	GASQAGAPQGR
18.4	1309.656097	0.015275	GASQAGAPQGR
10.8	1309.656082	0.015290	EKNPGNQGR
8.6	1309.677887	-0.006515	HPEIVGYVPGR
8.6	1309.681259	-0.009887	LVGSDQAPGR
6.5	1309.663483	0.007889	AEQQGR
0.1	1309.685272	-0.013900	MLKPAFIFDGR
0.1	1309.689102	-0.017730	SQLFVAYRNGR

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 39663: 1620.833592 from(541.285140,3+) rtinseconds(1666) index(3749)

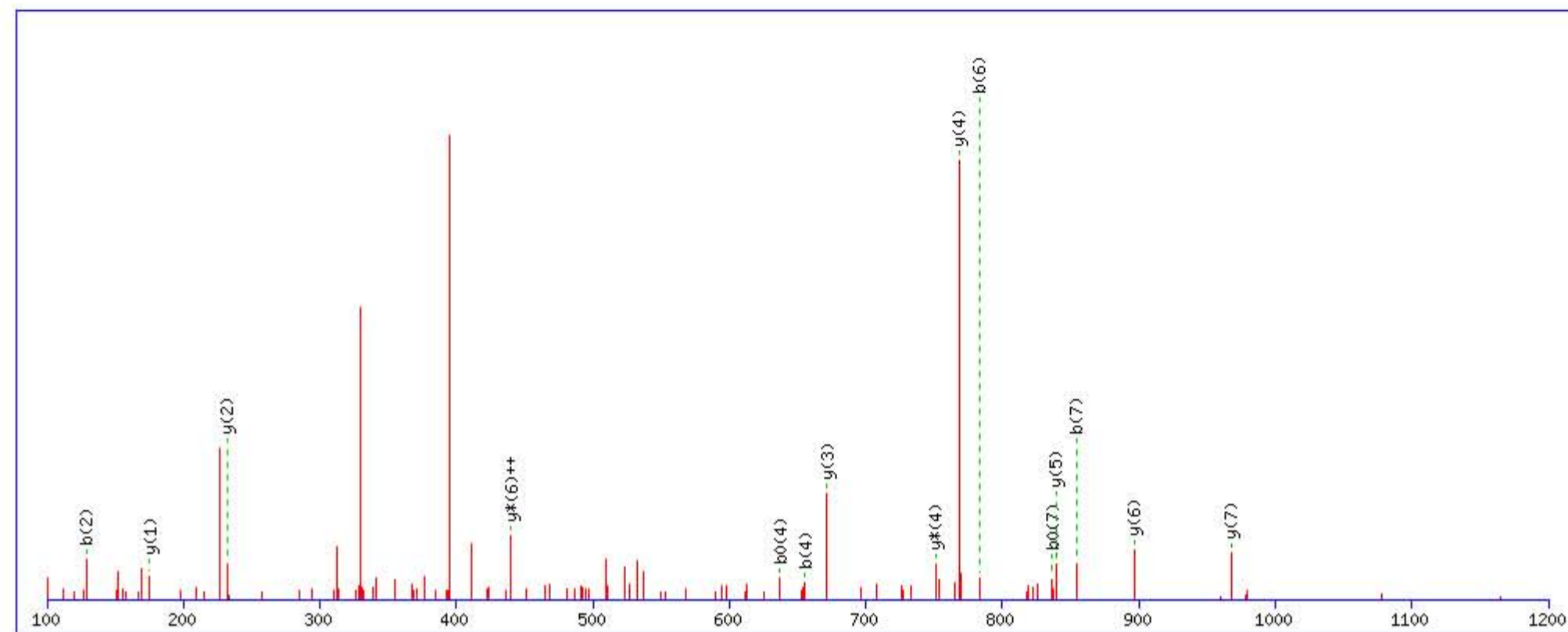
Title: Locus:1.1.1.3016.6 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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:

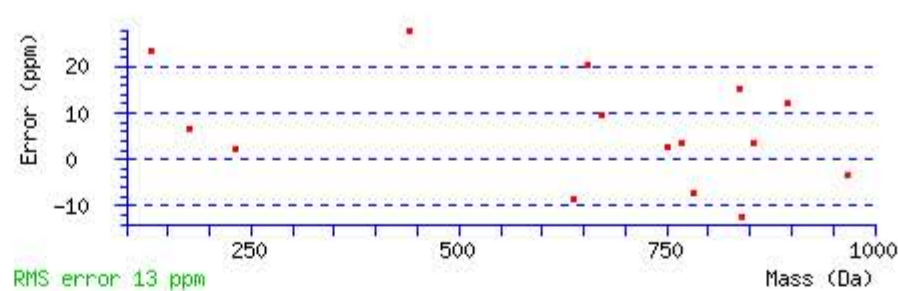
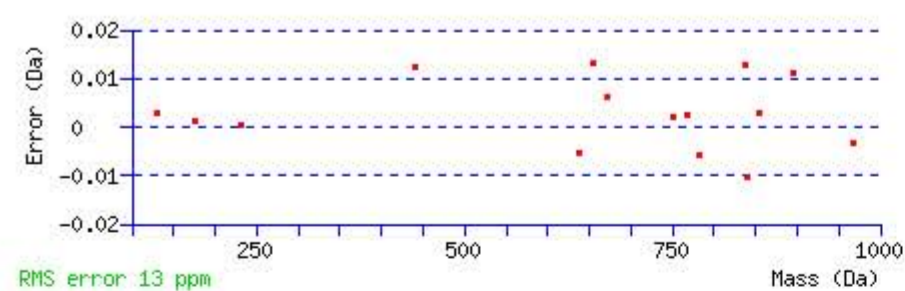
Q4 : Biotin:Thermo-21345 (Q)

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 26 Expect: 0.022

Matches : 15/94 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	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
26.5	1620.822845	0.010747	GASQAGAPQGR
8.6	1620.841248	-0.007656	SRVTNPINPWYFK
4.3	1620.815430	0.018162	SLQAQEDARHR
4.0	1620.841232	-0.007640	YYFAVRAKDIYGR

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

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **QTQVSVLPEGGETPLFK**

Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

Match to Query 58502: 2451.284472 from(818.102100,3+) rtinseconds(2610) index(59300)

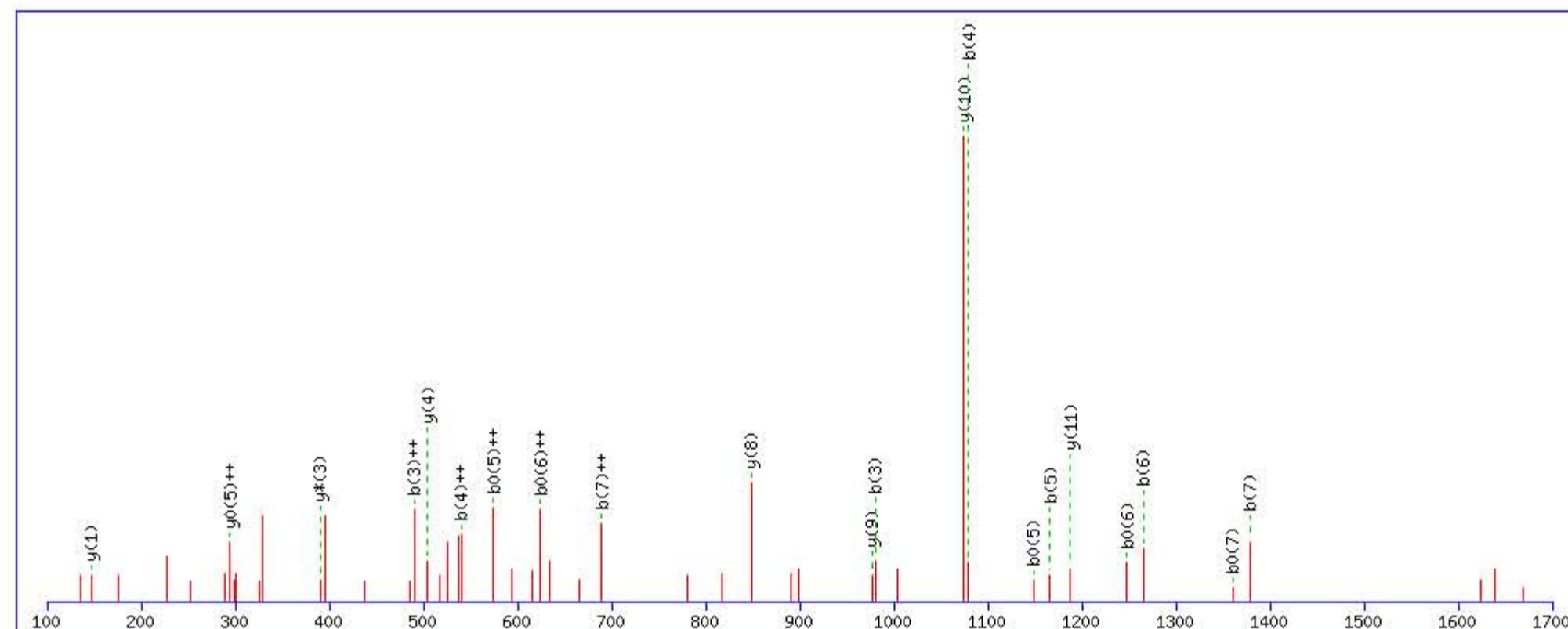
Title: Locus:1.1.1.3394.16 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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:

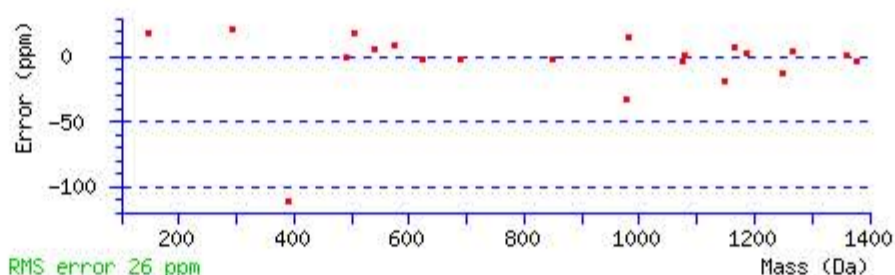
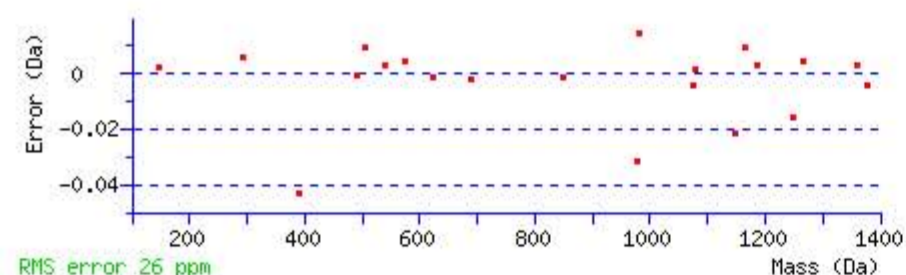
Q1 : Biotin:Thermo-21345 (Q)

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 35 Expect: 0.00067

Matches : 22/182 fragment ions using 38 most intense peaks [\(help\)](#)

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



NCBI BLAST search of **QTQVSVLPEGGETPLFK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.5	2451.290588	-0.006116	QTQVSVLPEGGETPLFK
1.5	2451.277130	0.007342	GFPSDTQLLDLRRNHFPSVPR
0.1	2451.279114	0.005358	KIQTQISSGMTNNASLLQNYLK
0.0	2451.256516	0.027956	SGSKSTQTVAKTTTAAAVASTGPSSR

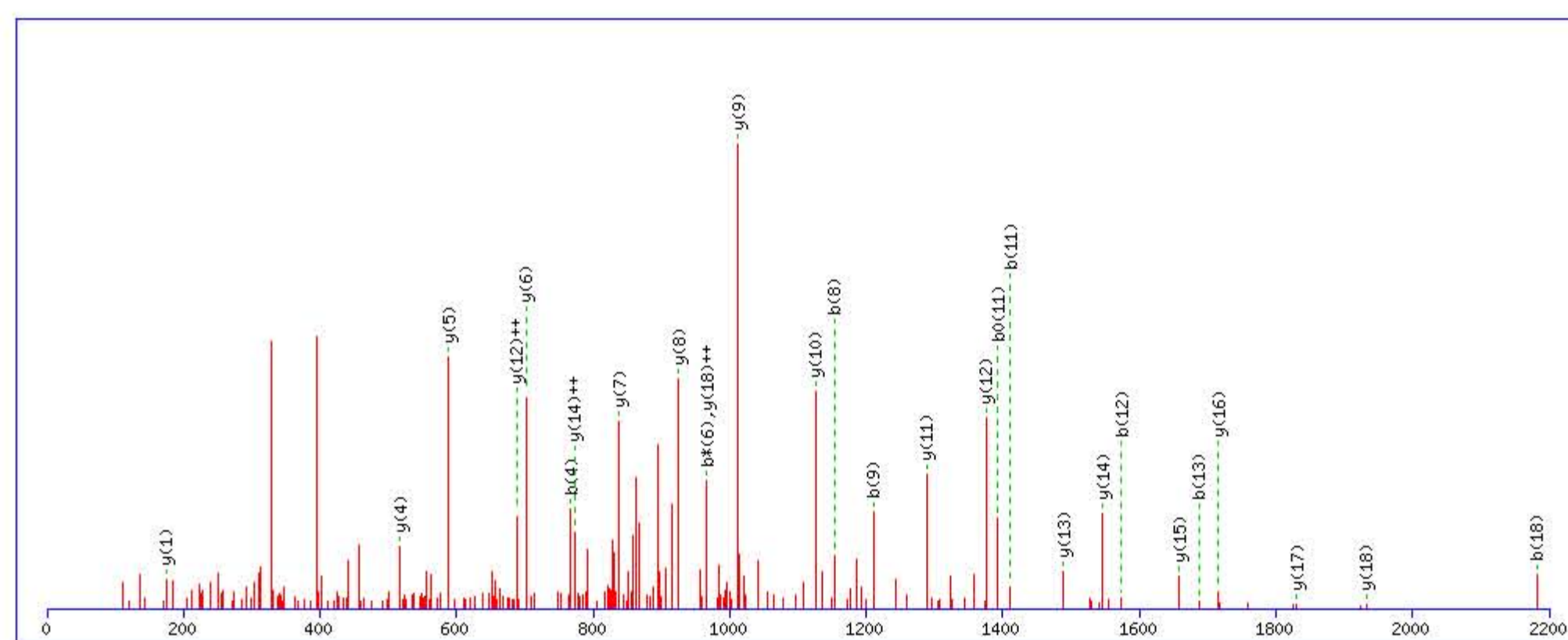
Mascot Search Results

Peptide View

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

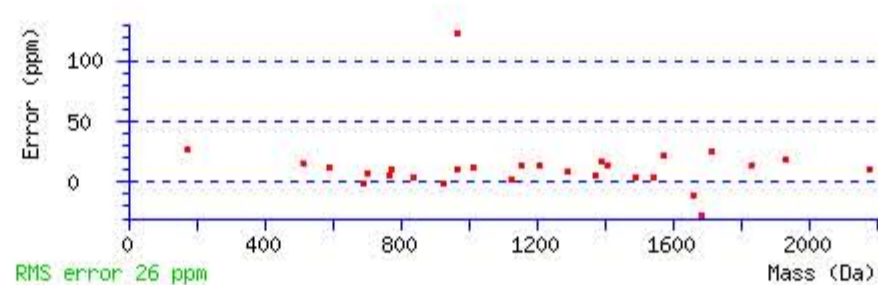
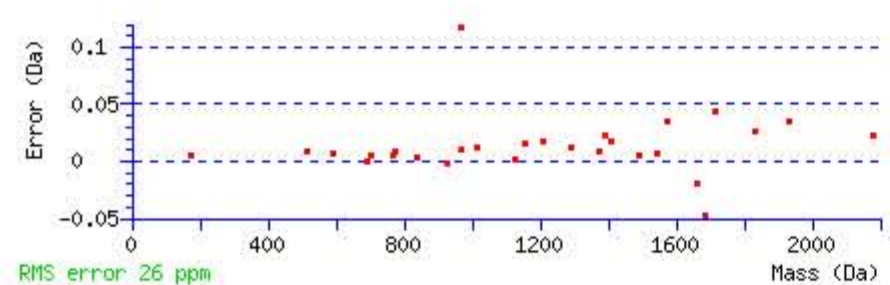
Match to Query 61944: 2697.296112 from(900.105980,3+) rtinseconds(2557) index(9029)
 Title: Locus:1.1.1.3326.11 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 125 Expect: 6.7e-012
 Matches : 28/244 fragment ions using 39 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.034219	58.520748			98.023654	49.515465	D							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
125.5	2697.306824	-0.010712	DPDQTDGLGLSYLSSHIANVER

MASCOT Search Results

Peptide View

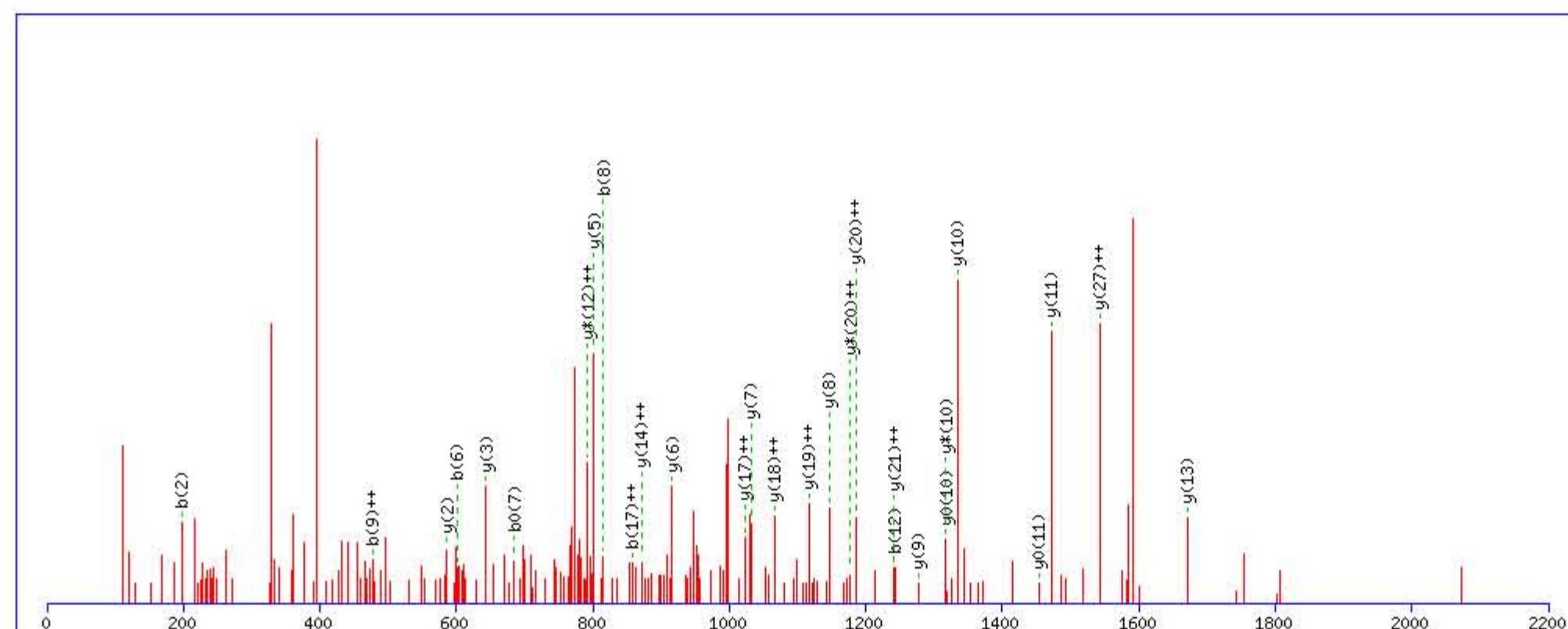
MS/MS Fragmentation of **VPFDAATLHTSTAMAAQHGMDDDDGTGQK**
 Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

Match to Query 67110: 3183.427736 from(796.864210,4+) rtinseconds(1960) index(5617)
 Title: Locus:1.1.1.3118.10 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

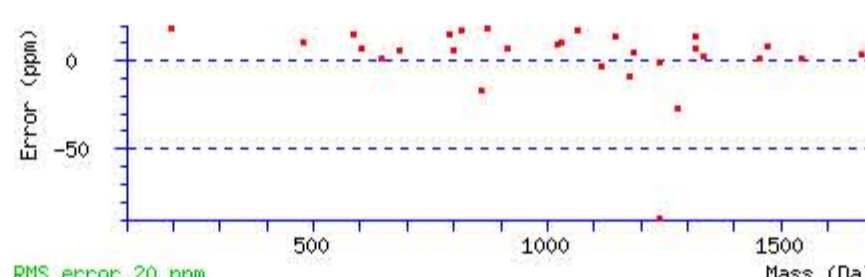
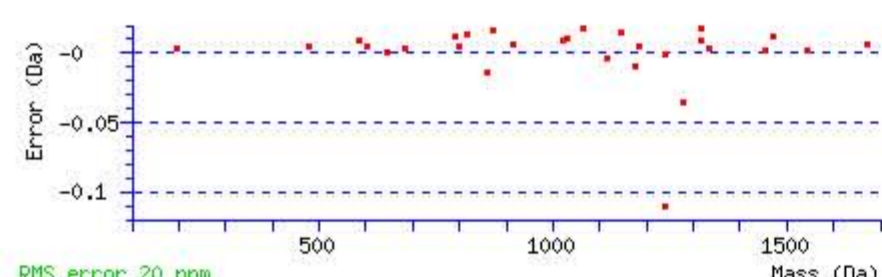
Or, Plot from to Da

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: 33 Expect: 0.0043
 Matches : 29/280 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	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 **VPFDAATLHTSTAMAAQHGMDDDDGTGQK**
 (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	3183.442383	-0.014647	VPFDAATLHTSTAMAAQHGMDDDDGTGQK
3.9	3183.442383	-0.014647	VPFDAATLHTSTAMAAQHGMDDDDGTGQK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **TYFPHFDSLHGSAQVK**

Found in **HBA_HUMAN**, Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2

Match to Query 52723: 2144.040492 from(715.687440,3+) rtinseconds(2074) index(6251)

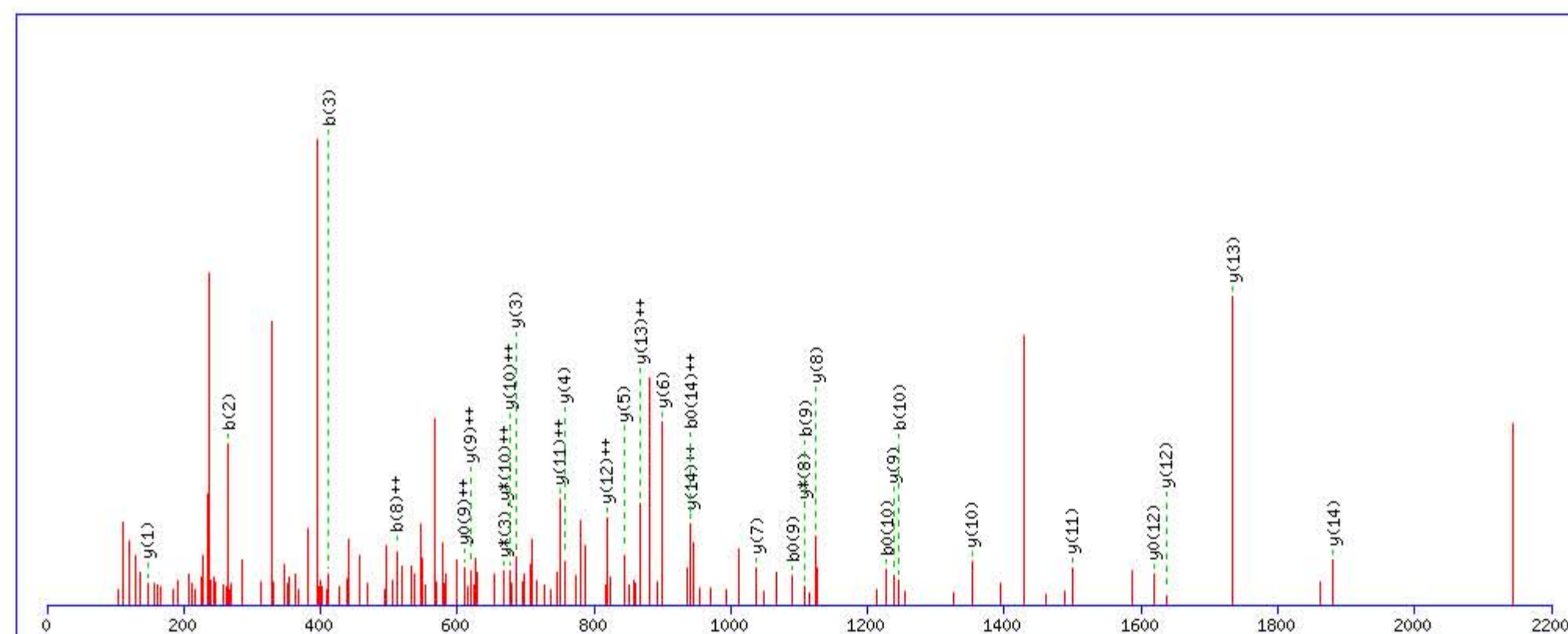
Title: Locus:1.1.1.3158.9 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2144.051346

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

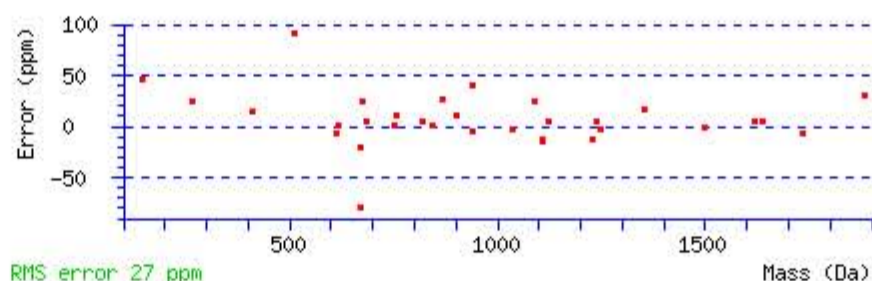
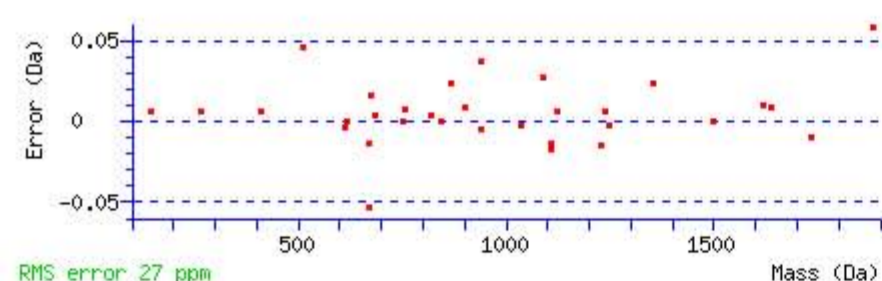
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 51 Expect: 0.00016

Matches : 32/146 fragment ions using 84 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	102.054955	51.531116			84.044390	42.525833	T							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 [TYFPHFDSLHGSAQVK](#)

(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	2144.051346	-0.010854	TYFPHFDSLHGSAQVK

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 61700: 2674.300122 from(892.440650,3+) rtinseconds(2669) index(75280)

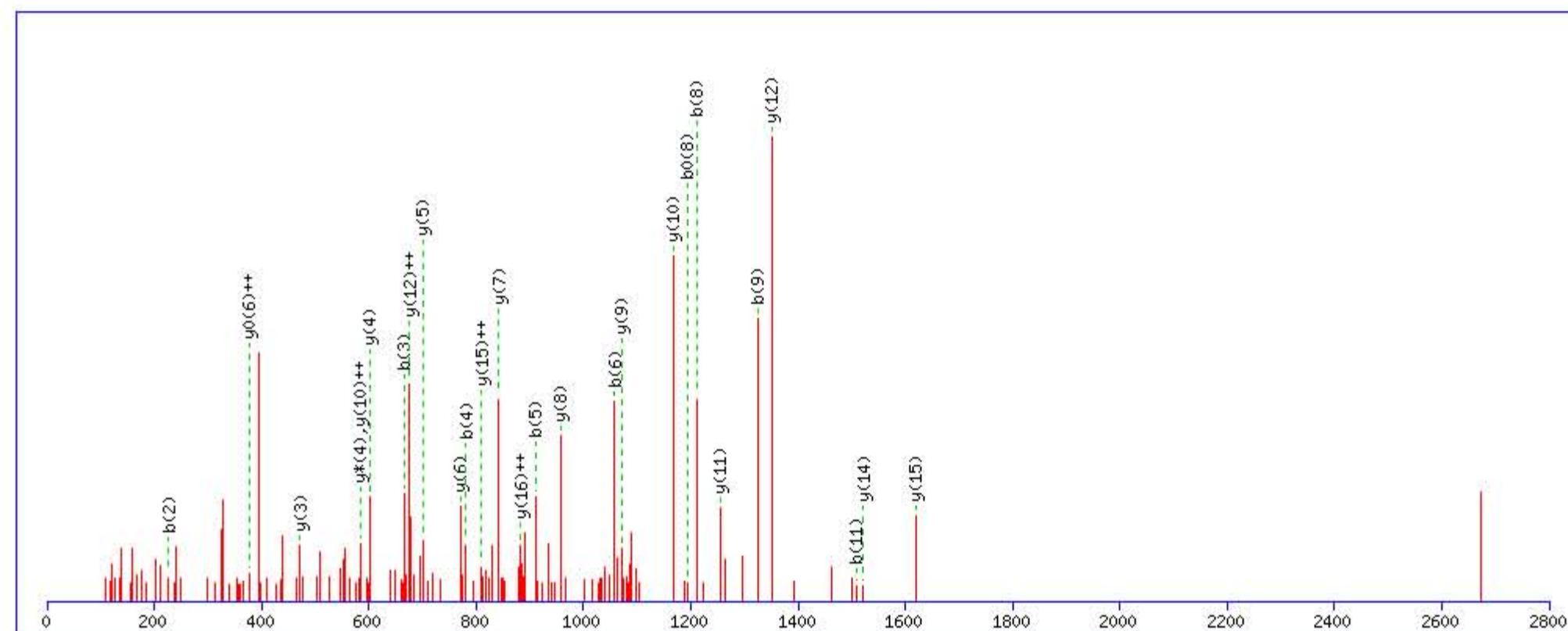
Title: Locus:1.1.1.3462.13 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

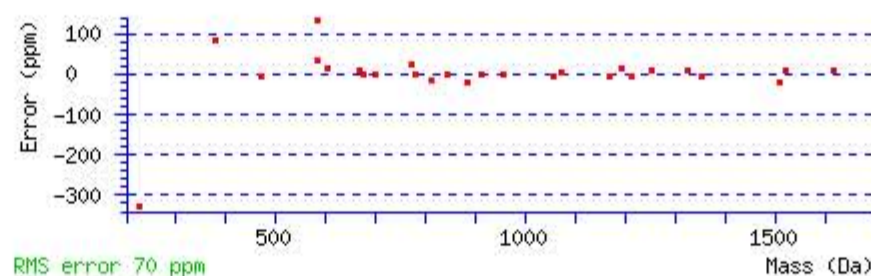
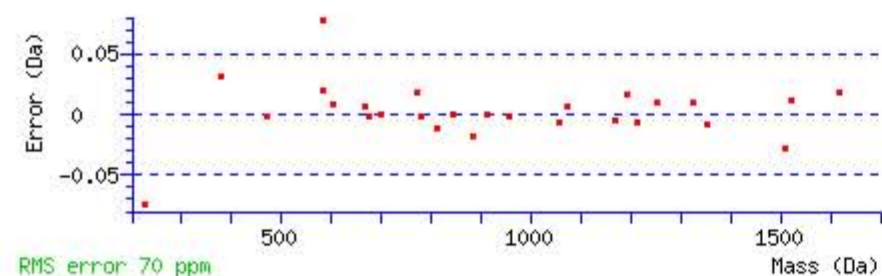
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 65 Expect: 7.6e-006

Matches : 27/224 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							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
65.1	2674.324722	-0.024600	LLQDEFPGIPSPLDAAVECHR

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

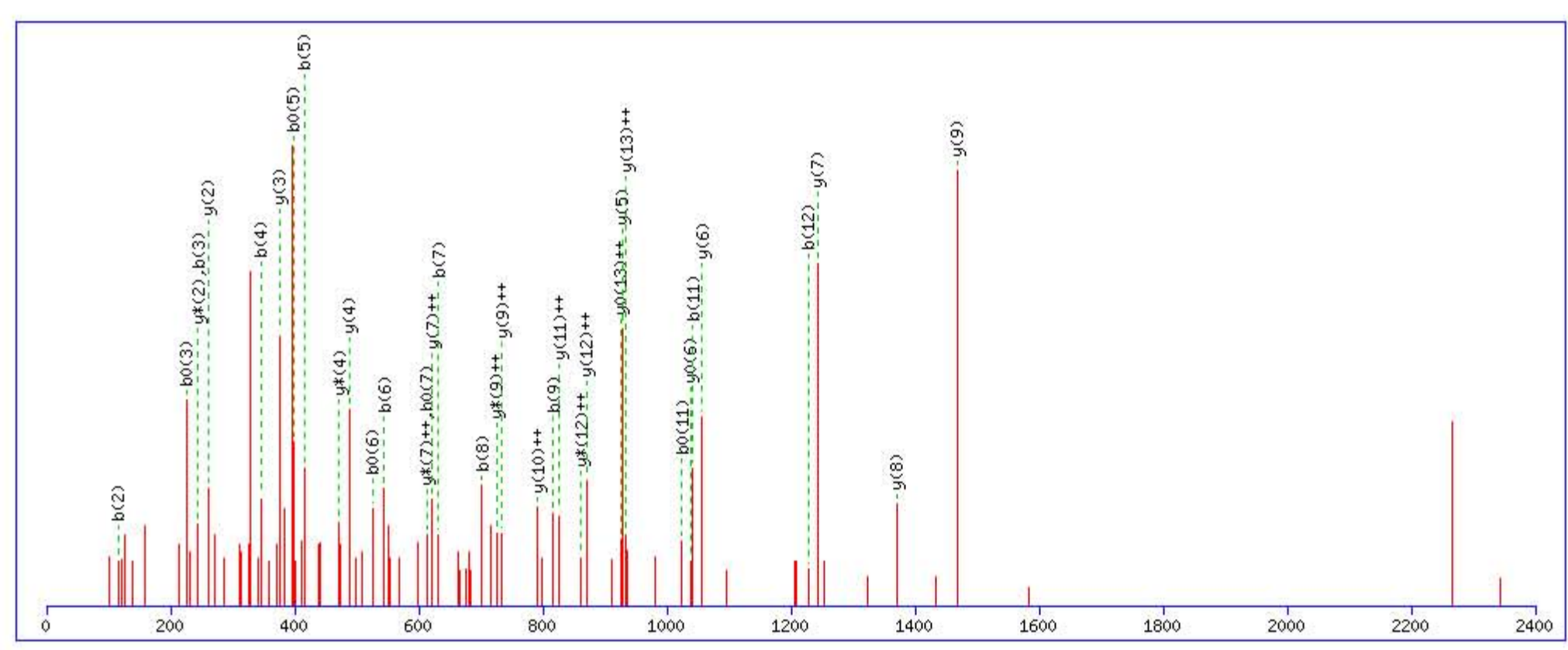
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **GGETAQSADPQWEQLNKK**
 Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

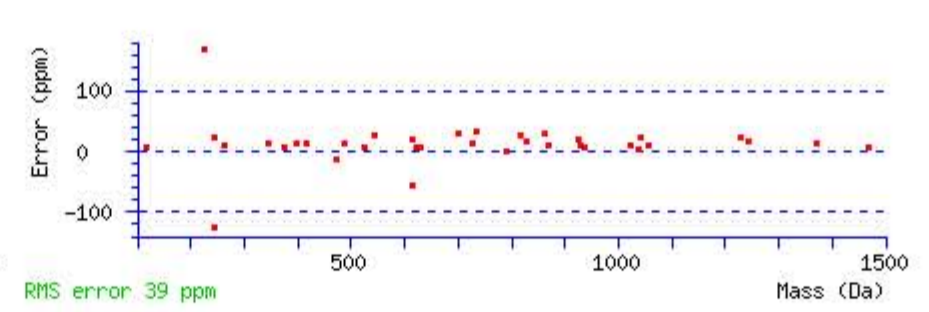
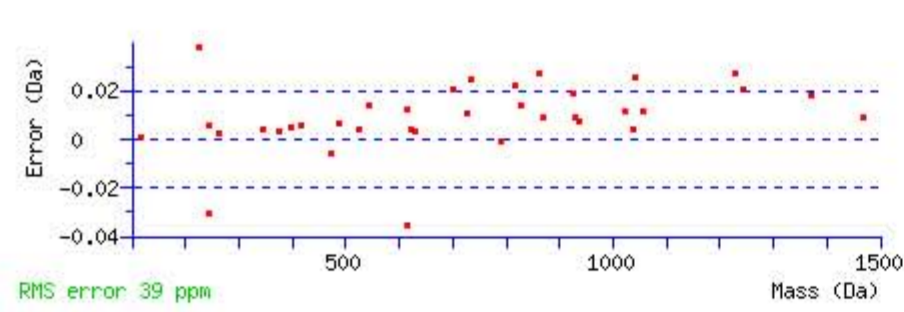
Match to Query 55748: 2283.060882 from(762.027570,3+) rtinseconds(1930) index(38121)
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 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 65 Expect: 4e-006
 Matches : 36/180 fragment ions using 61 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.028740	29.518008					G							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 **GGETAQSADPQWEQLNKK**
 (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	2283.058975	0.001907	GGETAQSADPQWEQLNKK
33.8	2283.058975	0.001907	GGETAQSADPQWEQLNKK

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 55749: 2283.065952 from(762.029260,3+) rtinseconds(1912) index(37980)

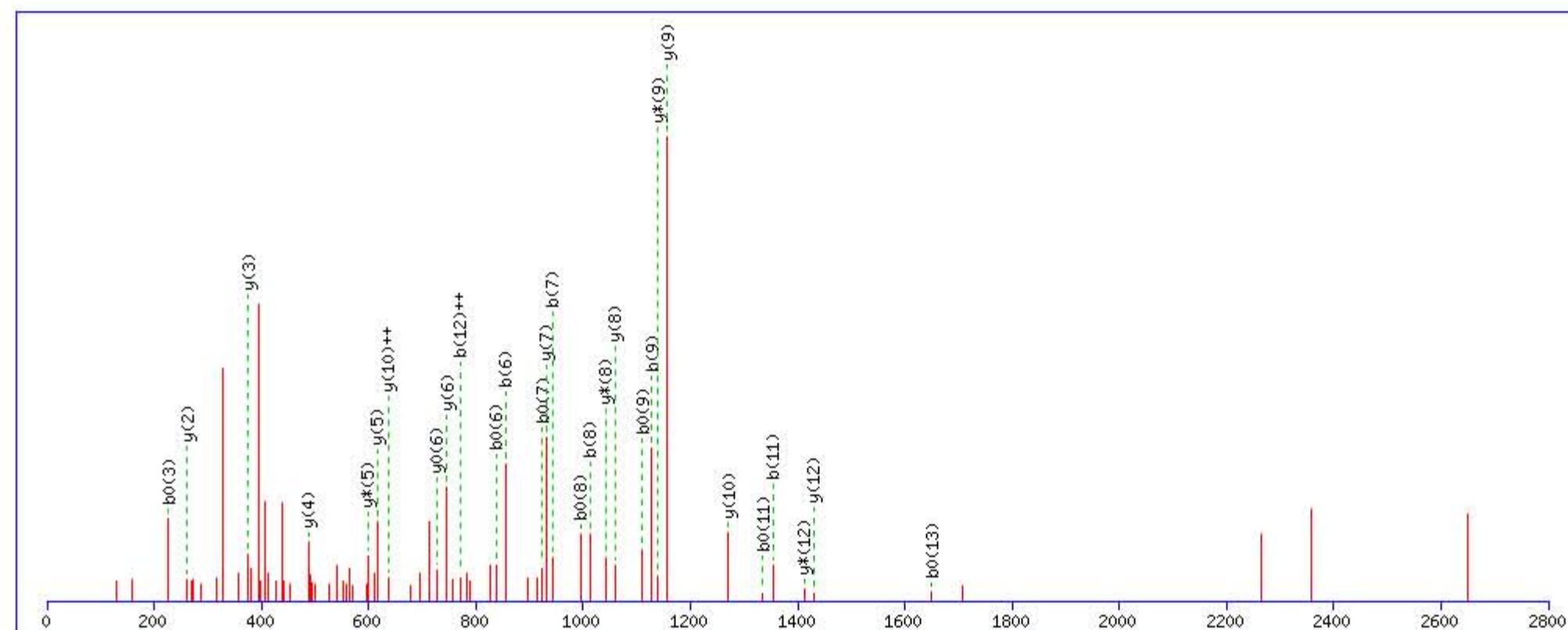
Title: Locus:1.1.1.2688.24 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

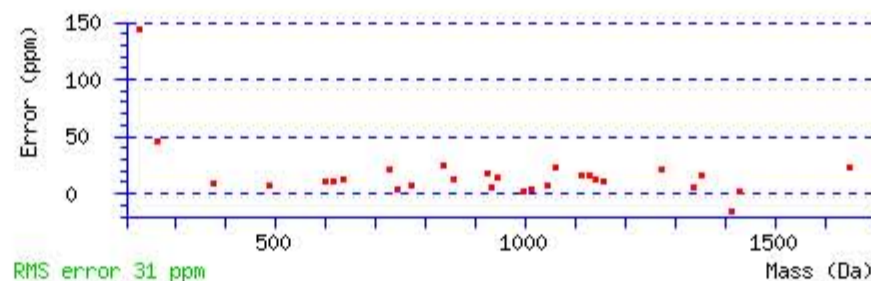
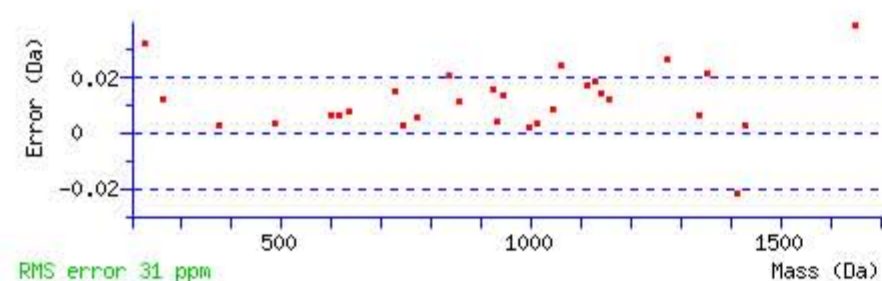
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 53 Expect: 7.6e-005

Matches : 29/180 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	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
52.8	2283.058975	0.006977	GGETAQSADPQWEQLNNK
8.3	2283.058975	0.006977	GGETAQSADPQWEQLNNK

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

MASCOT Search Results

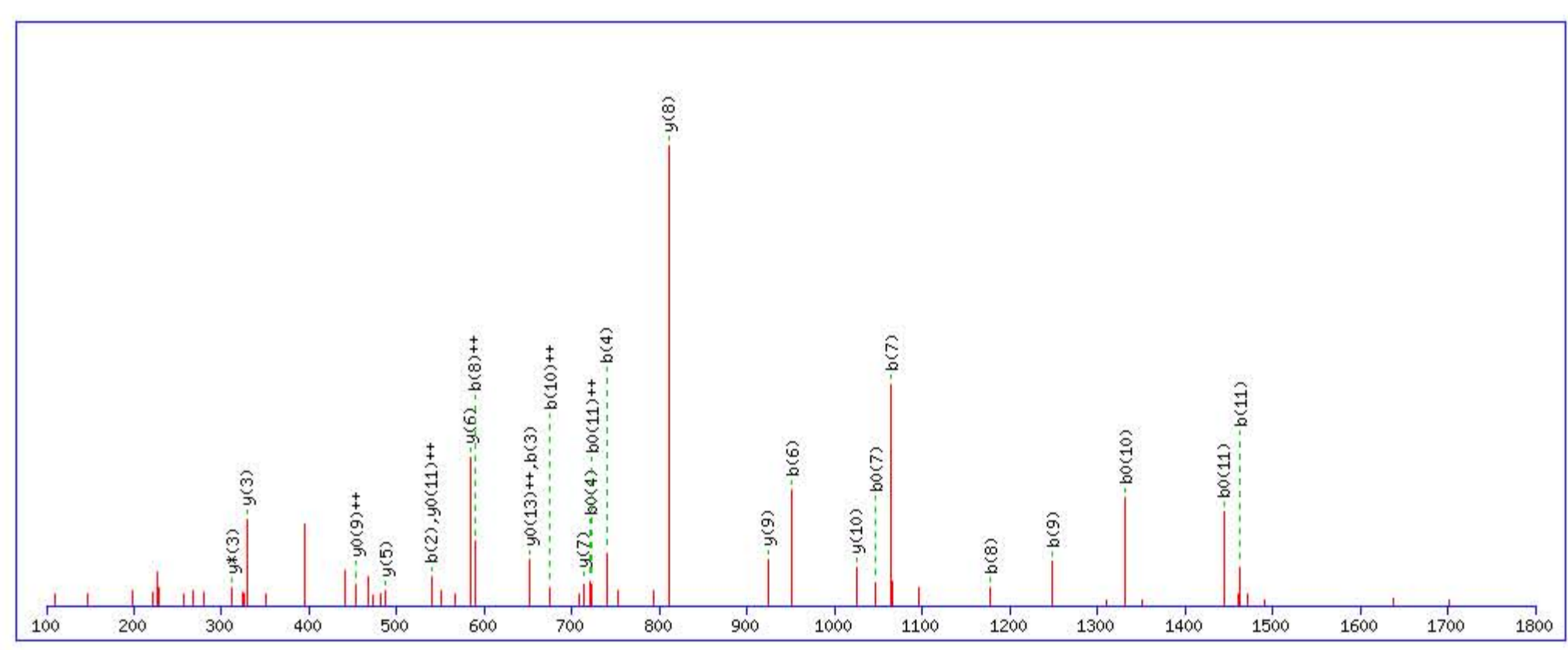
Peptide View

MS/MS Fragmentation of **VQLSPDLLATLPEPASPGR**

Found in **HGFA_HUMAN**, Hepatocyte growth factor activator OS=Homo sapiens GN=HGFA PE=1 SV=1

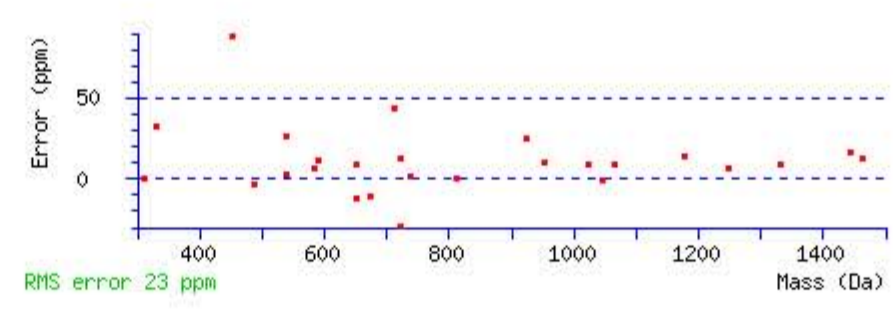
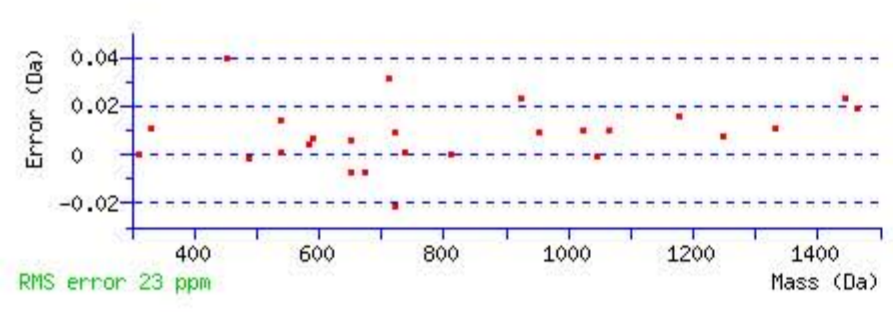
Match to Query 55504: 2271.228792 from(758.083540,3+) rtinseconds(2659) index(9658)
 Title: Locus:1.1.1.3361.24 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 53 Expect: 0.00011
 Matches : 26/202 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	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
52.5	2271.229675	-0.000883	VQLSPDLLATLPEPASPGR

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 35962: 1508.702588 from(755.358570,2+) rtinseconds(1754) index(69629)

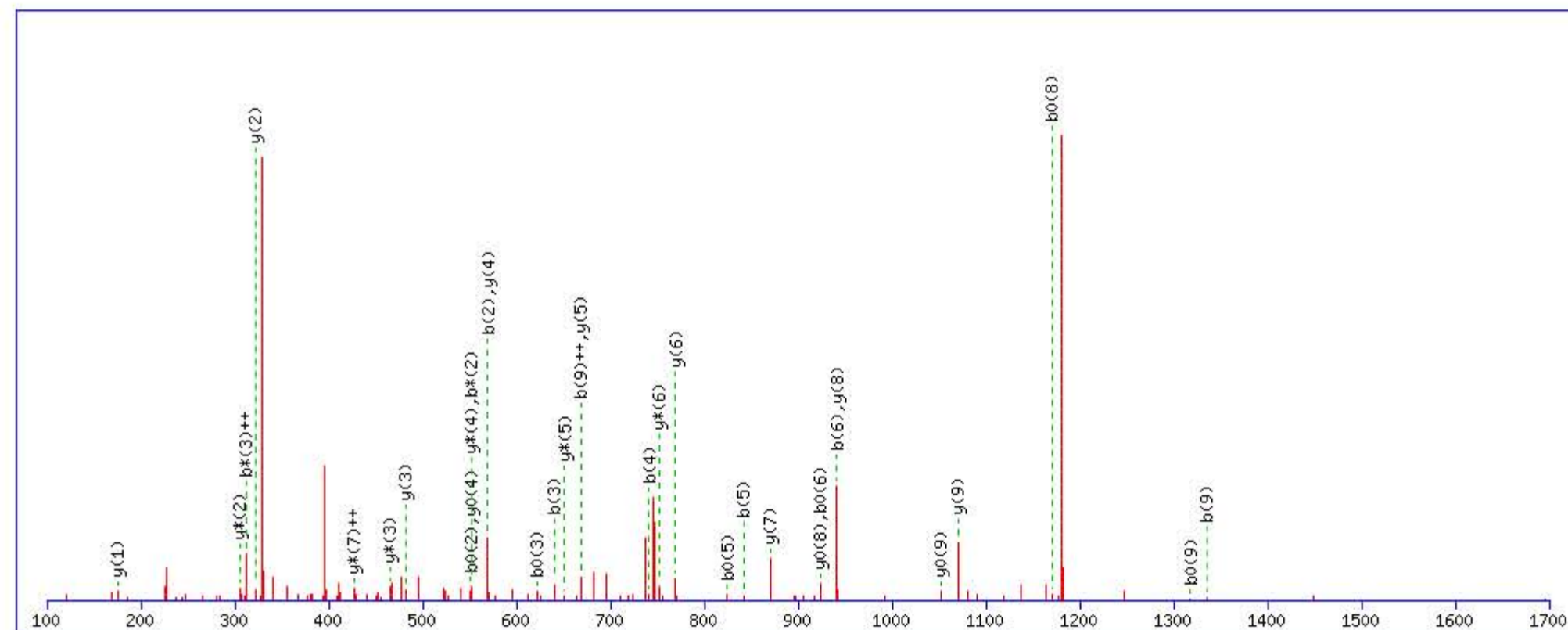
Title: Locus:1.1.1.3144.12 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

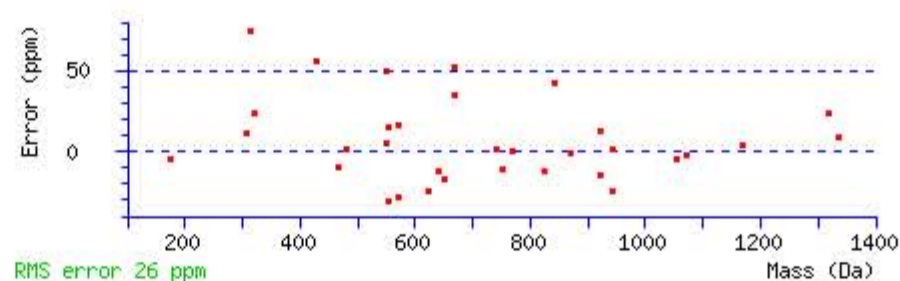
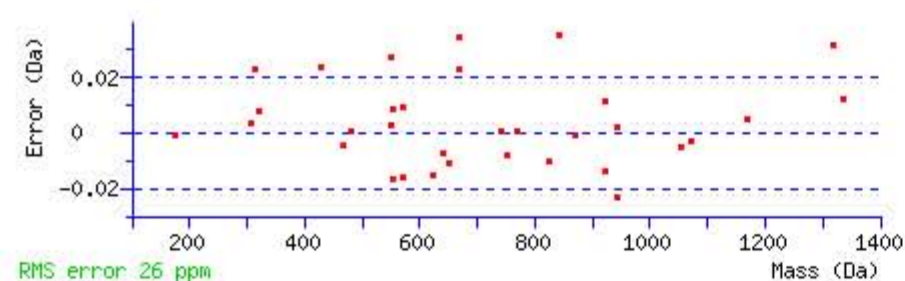
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 33 Expect: 0.0032

Matches : 33/100 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	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
32.6	1508.711578	-0.008990	QEATTVSCFR
5.7	1508.711380	-0.008792	RTASGGRTEQGMSR
4.6	1508.715408	-0.012820	DHKSVDECKVHR
4.6	1508.708191	-0.005603	EYGSMYTVHLGPR
3.4	1508.683044	0.019544	AFGHSSSLTYHMR
2.7	1508.703461	-0.000873	LKSFTYEYEDSK
0.3	1508.711548	-0.008960	QMSKYPSEGER
0.1	1508.719437	-0.016849	TFSWKSSLTCHR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **WSAETPHKQFTFTSEPHAQLEENFCR**

Found in **HGFL_HUMAN**, Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=2

Match to Query 71592: 3584.629016 from(897.164530,4+) rtinseconds(2039) index(71408)

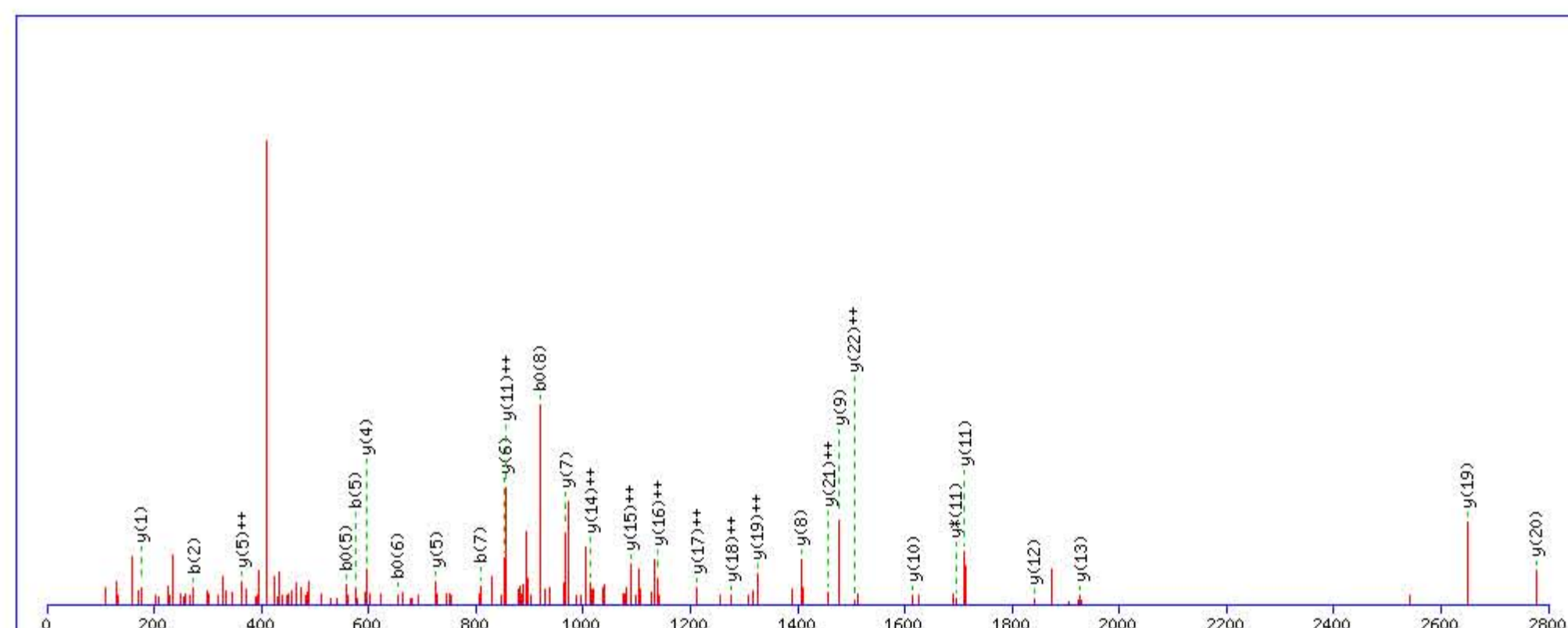
Title: Locus:1.1.1.3243.15 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

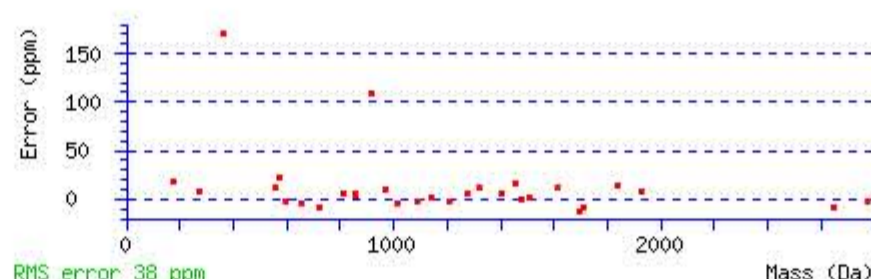
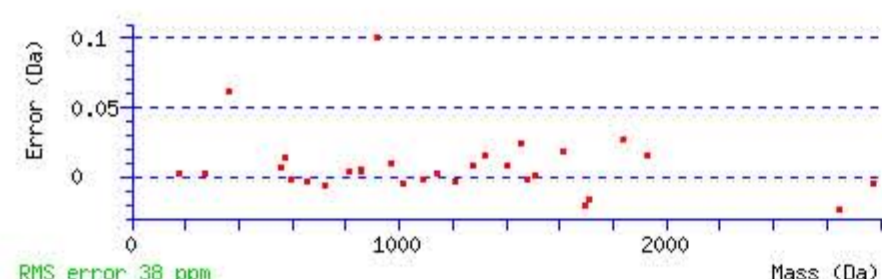
Variable modifications:

Q20 : Biotin:Thermo-21345 (Q)

Ions Score: 62 Expect: 7.3e-006

Matches : 30/288 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	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 [WSAETPHKQFTFTSEPHAQLEENFCR](#)

(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	3584.660538	-0.031522	WSAETPHKQFTFTSEPHAQLEENFCR
8.0	3584.660538	-0.031522	WSAETPHKQFTFTSEPHAQLEENFCR

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 38217: 1583.691428 from(792.852990,2+) rtinseconds(1858) index(54709)

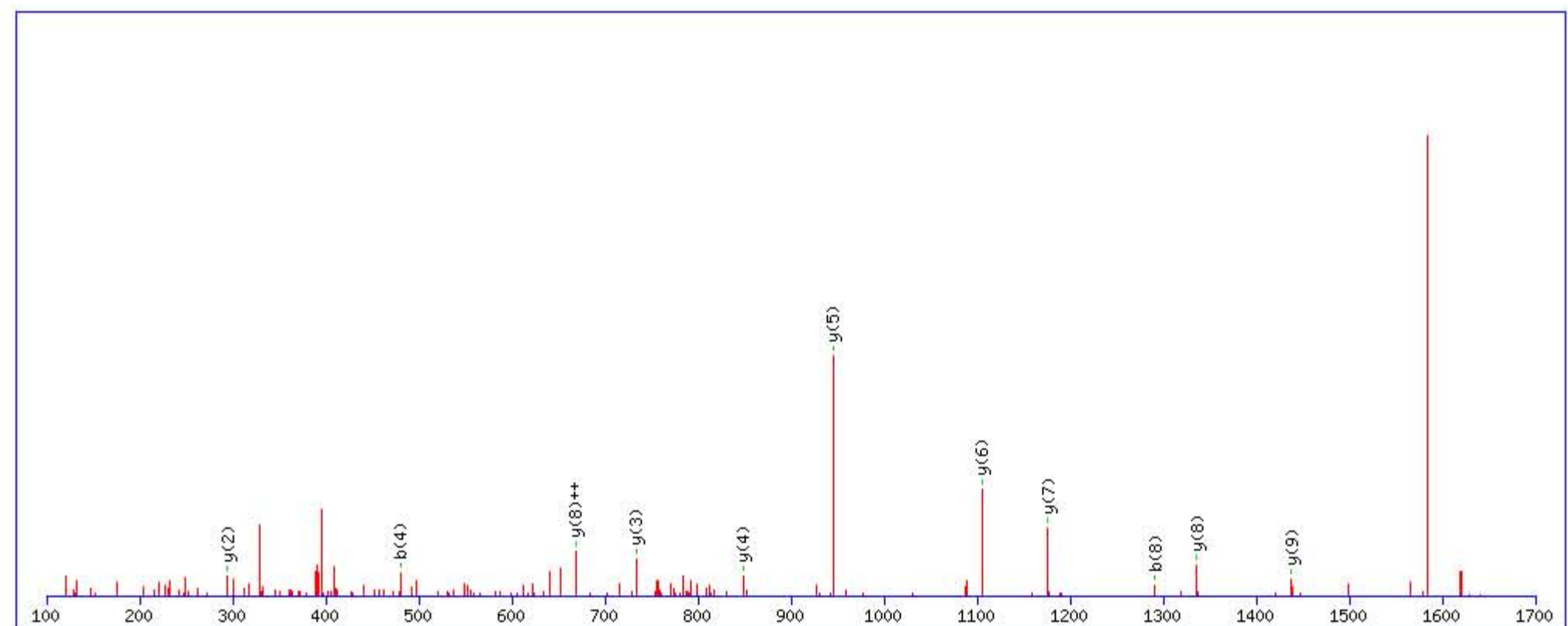
Title: Locus:1.1.1.3133.19 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1583.693497

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

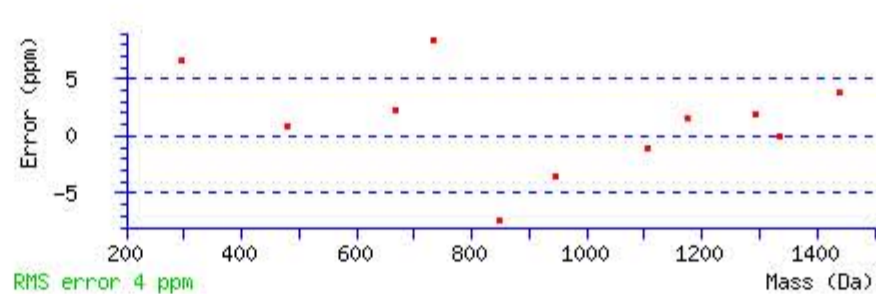
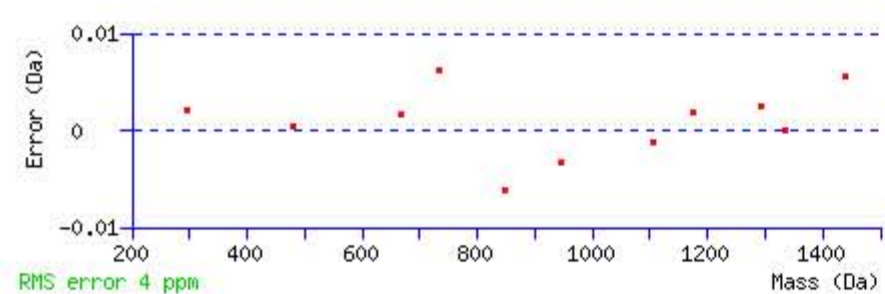
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 64 Expect: 2.6e-006

Matches : 11/86 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							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	$M_r(\text{calc})$:	Delta	Sequence
63.6	1583.693497	-0.002069	FTCACPDQFK
4.5	1583.703827	-0.012399	FKDACGKSEDWNK

MASCOT Search Results

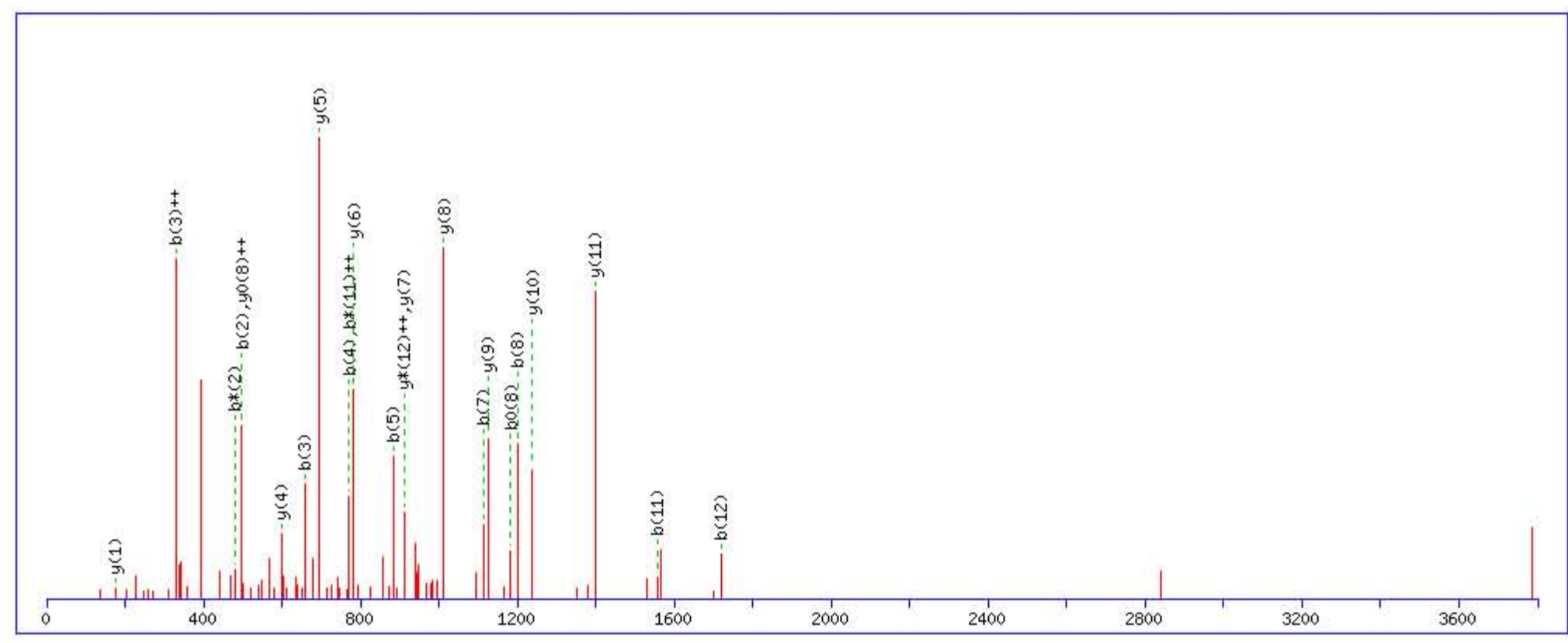
Peptide View

MS/MS Fragmentation of **GQCLITQSPYYR**

Found in **HABP2_HUMAN**, Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1

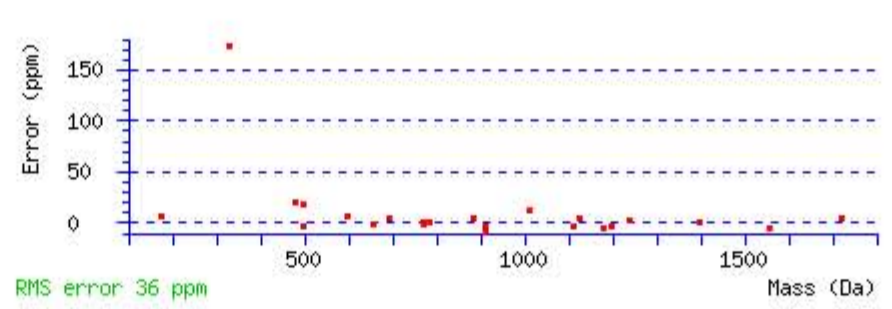
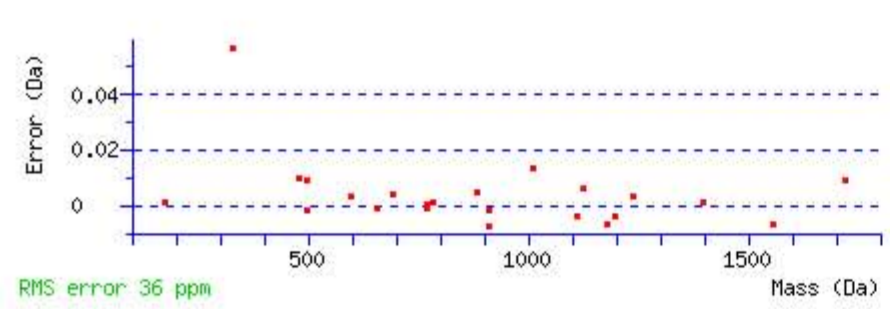
Match to Query 46666: 1892.931188 from(947.472870,2+) rtinseconds(2084) index(56322)
 Title: Locus:1.1.1.3211.12 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 64 Expect: 3.5e-006
 Matches : 23/122 fragment ions using 30 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.028740	29.518008					G							13
2	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 **GQCLITQSPYYR**
 (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	1892.927704	0.003484	GQCLITQSPYYR
13.4	1892.927704	0.003484	GQCLITQSPYYR
5.7	1892.934921	-0.003733	QGSQAGPGPQLAQQMR
1.4	1892.910400	0.020788	SSRNYFGAQPBYR
0.8	1892.909073	0.022115	LSYCGGGEALAVPFEPAR
0.2	1892.938065	-0.006877	AQESVGFDPAPAANPGPR

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 61485: 2647.306016 from(662.833780,4+) rtinseconds(2341) index(7842)

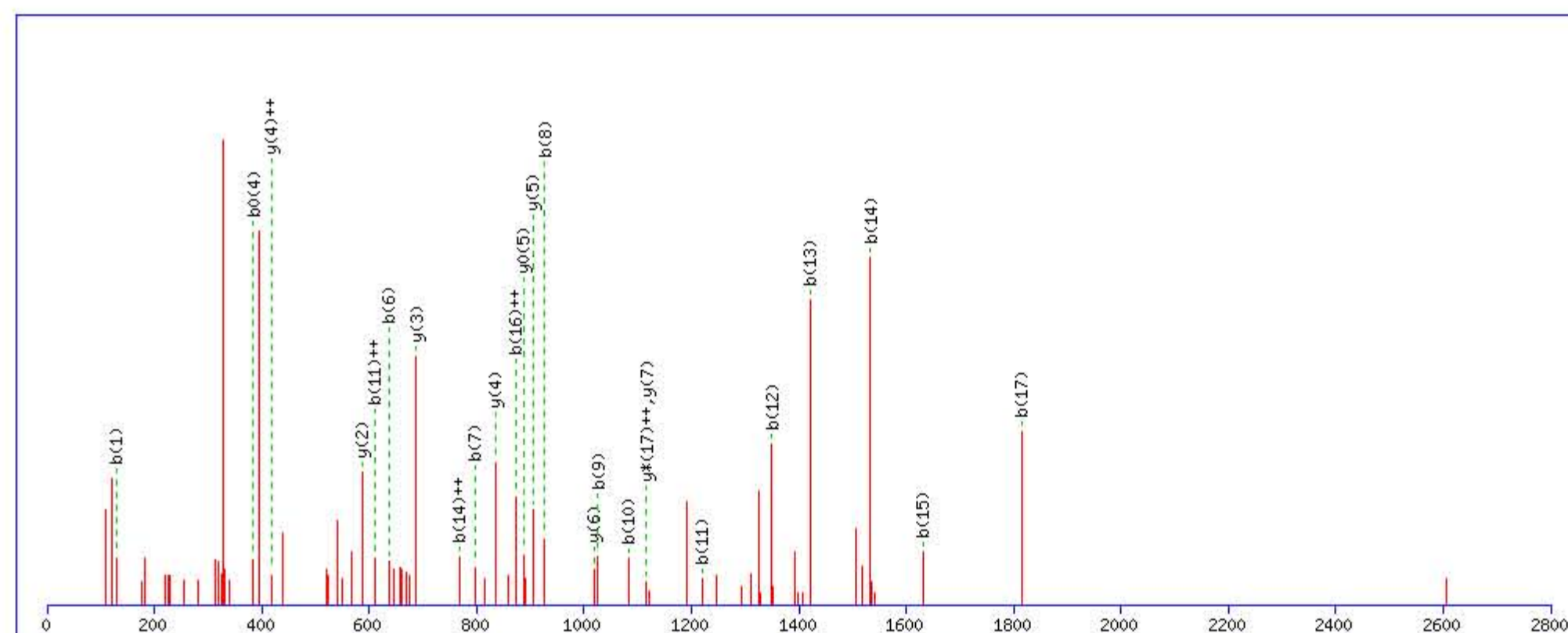
Title: Locus:1.1.1.3251.17 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

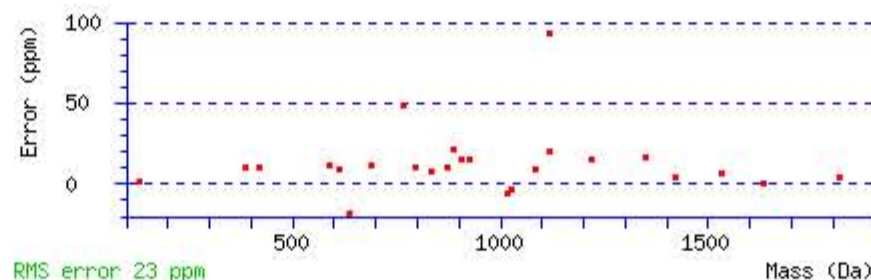
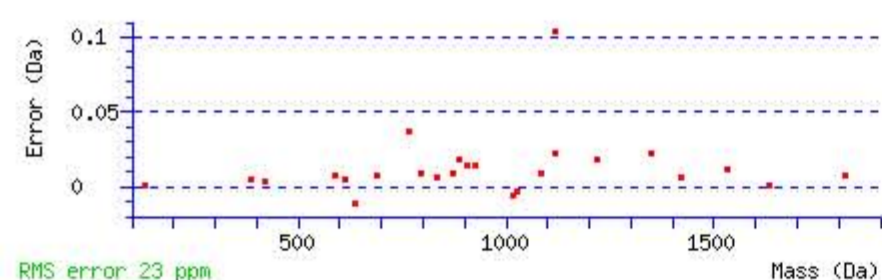
Variable modifications:

Q20 : Biotin:Thermo-21345 (Q)

Ions Score: 56 Expect: 1e-005

Matches : 25/232 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	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
56.3	2647.296082	0.009934	KGDTFSCMVGHEALPLAFTQK
3.0	2647.281662	0.024354	AAVLACQACMLAIFLSMLVSYR

MASCOT 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 25758: 1220.652568 from(611.333560,2+) rtinseconds(1448) index(67710)

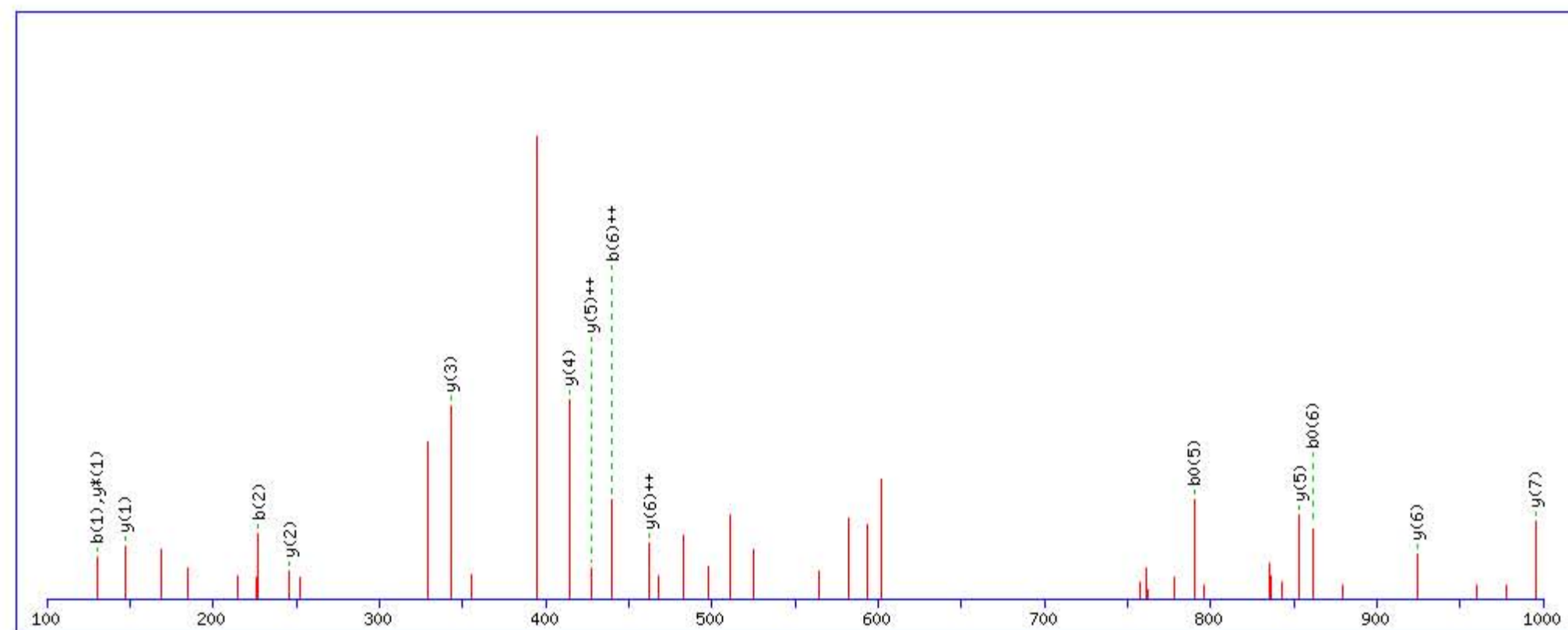
Title: Locus:1.1.1.3037.23 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

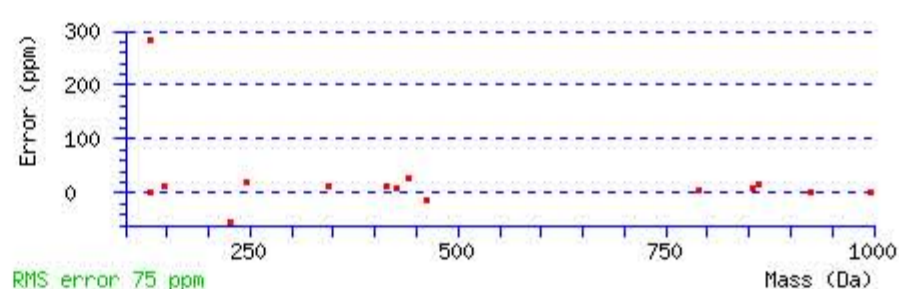
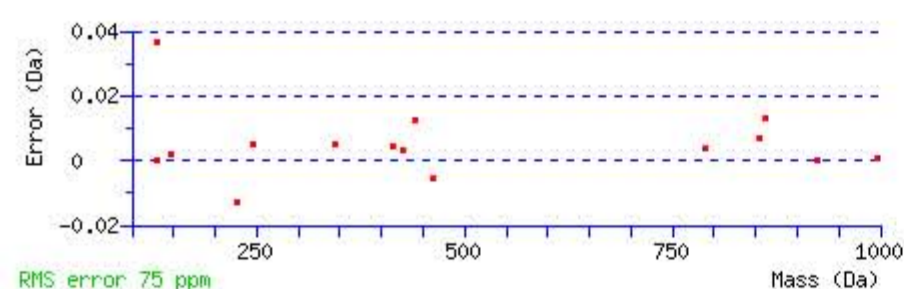
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 41 Expect: 0.00048

Matches : 15/72 fragment ions using 30 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
41.3	1220.658707	-0.006139	EPAAQAPVK
5.5	1220.655350	-0.002782	LLFSTVEWAR
4.2	1220.644119	0.008449	SFPEISFLGPK
3.0	1220.640076	0.012492	LLAEYTGAQQK
2.4	1220.658722	-0.006154	QPNLPDVK
1.1	1220.666580	-0.014012	EPAIVRFFSR
0.4	1220.667267	-0.014699	LLRGHPGRCR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **SLWNAGTSVTCTLNHPSLPPQR**

Found in **IGHD_HUMAN**, Ig delta chain C region OS=Homo sapiens GN=IGHD PE=1 SV=2

Match to Query 62442: 2746.352652 from(916.458160,3+) rtinseconds(2250) index(7374)

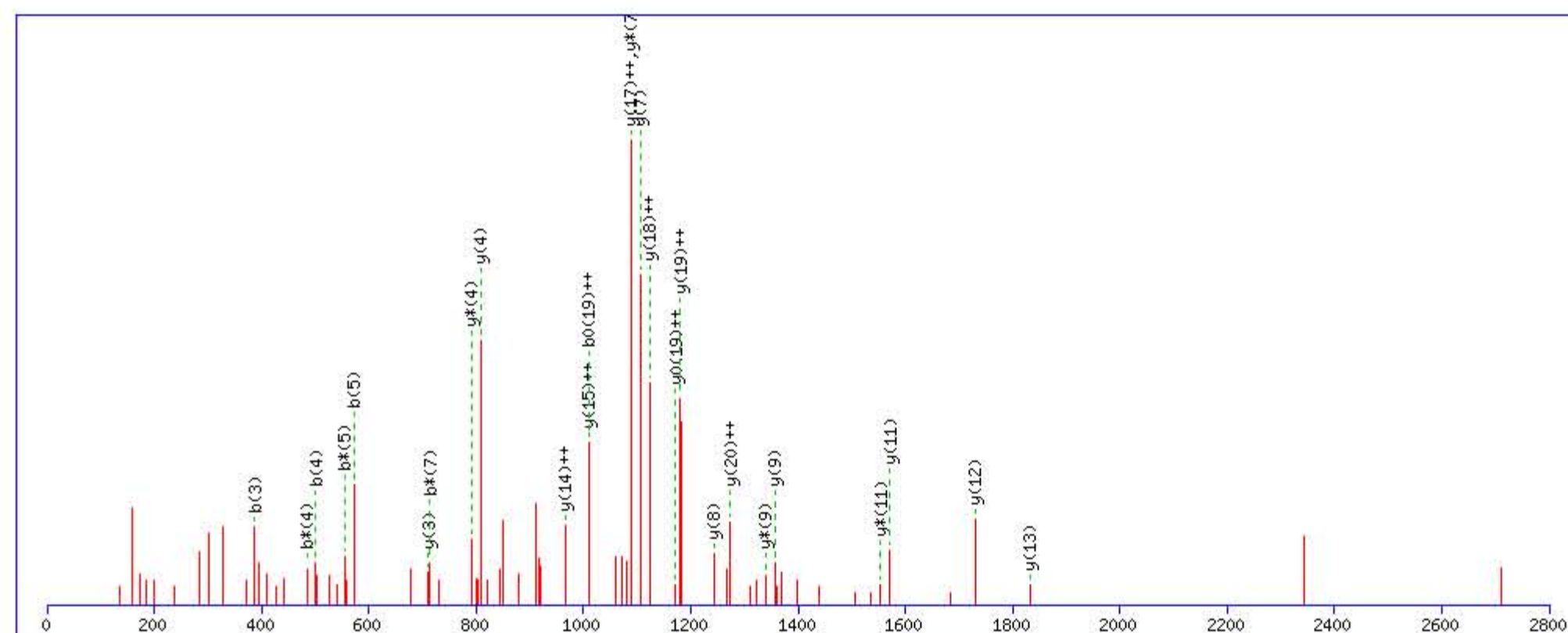
Title: Locus:1.1.1.3219.25 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2746.368332

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

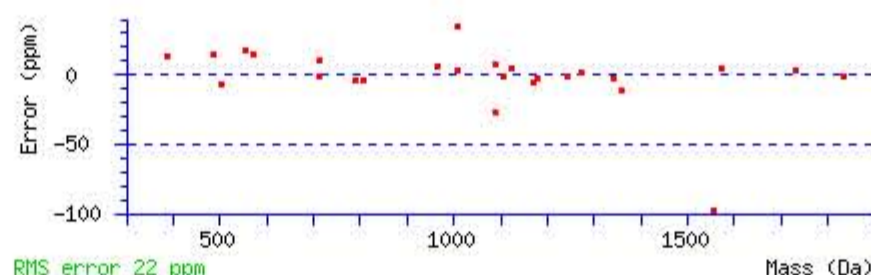
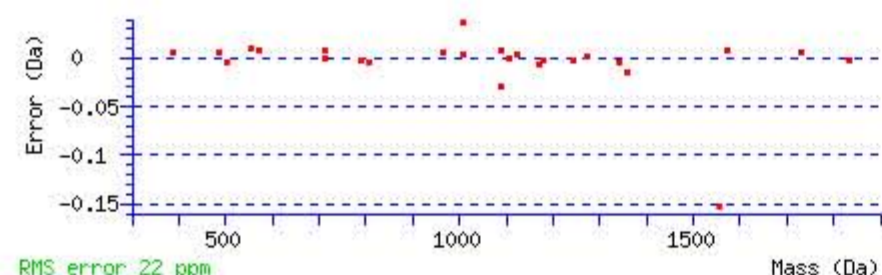
Variable modifications:

Q21 : Biotin:Thermo-21345 (Q)

Ions Score: 47 Expect: 0.00061

Matches : 26/236 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							22
2	201.123368	101.065322			183.112803	92.060039	L	2660.343575	1330.675425	2643.317026	1322.162151	2642.333010	1321.670143	21
3	387.202681	194.104978			369.192116	185.099696	W	2547.259511	1274.133393	2530.232962	1265.620119	2529.248946	1265.128111	20
4	501.245608	251.126442	484.219059	242.613168	483.235043	242.121160	N	2361.180198	1181.093737	2344.153649	1172.580462	2343.169633	1172.088454	19
5	572.282722	286.644999	555.256173	278.131725	554.272157	277.639717	A	2247.137271	1124.072273	2230.110722	1115.558999	2229.126706	1115.066991	18
6	629.304186	315.155731	612.277637	306.642457	611.293621	306.150449	G	2176.100157	1088.553716	2159.073608	1080.040442	2158.089592	1079.548434	17
7	730.351865	365.679571	713.325316	357.166296	712.341300	356.674288	T	2119.078693	1060.042984	2102.052144	1051.529710	2101.068128	1051.037702	16
8	817.383893	409.195585	800.357344	400.682310	799.373328	400.190302	S	2018.031014	1009.519145	2001.004465	1001.005871	2000.020449	1000.513863	15
9	916.452307	458.729792	899.425758	450.216517	898.441742	449.724509	V	1930.998986	966.003131	1913.972437	957.489857	1912.988421	956.997849	14
10	1017.499986	509.253631	1000.473437	500.740357	999.489421	500.248349	T	1831.930572	916.468924	1814.904023	907.955650	1813.920007	907.463642	13
11	1177.530635	589.268956	1160.504086	580.755681	1159.520070	580.263673	C	1730.882893	865.945085	1713.856344	857.431810	1712.872328	856.939802	12
12	1278.578314	639.792795	1261.551765	631.279521	1260.567749	630.787513	T	1570.852244	785.929760	1553.825695	777.416486	1552.841679	776.924478	11
13	1391.662378	696.334827	1374.635829	687.821553	1373.651813	687.329545	L	1469.804565	735.405921	1452.778016	726.892646	1451.794000	726.400638	10
14	1505.705305	753.356291	1488.678756	744.843016	1487.694740	744.351008	N	1356.720501	678.863889	1339.693952	670.350614	1338.709936	669.858606	9
15	1642.764217	821.885746	1625.737668	813.372472	1624.753652	812.880464	H	1242.677574	621.842425	1225.651025	613.329151	1224.667009	612.837143	8
16	1739.816981	870.412128	1722.790432	861.898854	1721.806416	861.406846	P	1105.618662	553.312969	1088.592113	544.799695	1087.608097	544.307687	7
17	1826.849009	913.928143	1809.822460	905.414868	1808.838444	904.922860	S	1008.565898	504.786587	991.539349	496.273313	990.555333	495.781305	6
18	1939.933073	970.470174	1922.906524	961.956900	1921.922508	961.464892	L	921.533870	461.270573	904.507321	452.757299			5
19	2036.985837	1018.996557	2019.959288	1010.483282	2018.975272	1009.991274	P	808.449806	404.728541	791.423257	396.215267			4
20	2134.038601	1067.522938	2117.012052	1059.009664	2116.028036	1058.517656	P	711.397042	356.202159	694.370493	347.688885			3
21	2573.263927	1287.135601	2556.237378	1278.622327	2555.253362	1278.130319	Q	614.344278	307.675777	597.317729	299.162503			2
22							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **SLWNAGTSVTCTLNHPSLPPQR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.7	2746.368332	-0.015680	SLWNAGTSVTCTLNHPSLPPQR

MASCOT 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 34873: 1471.781848 from(736.898200,2+) rtinseconds(2230) index(72630)

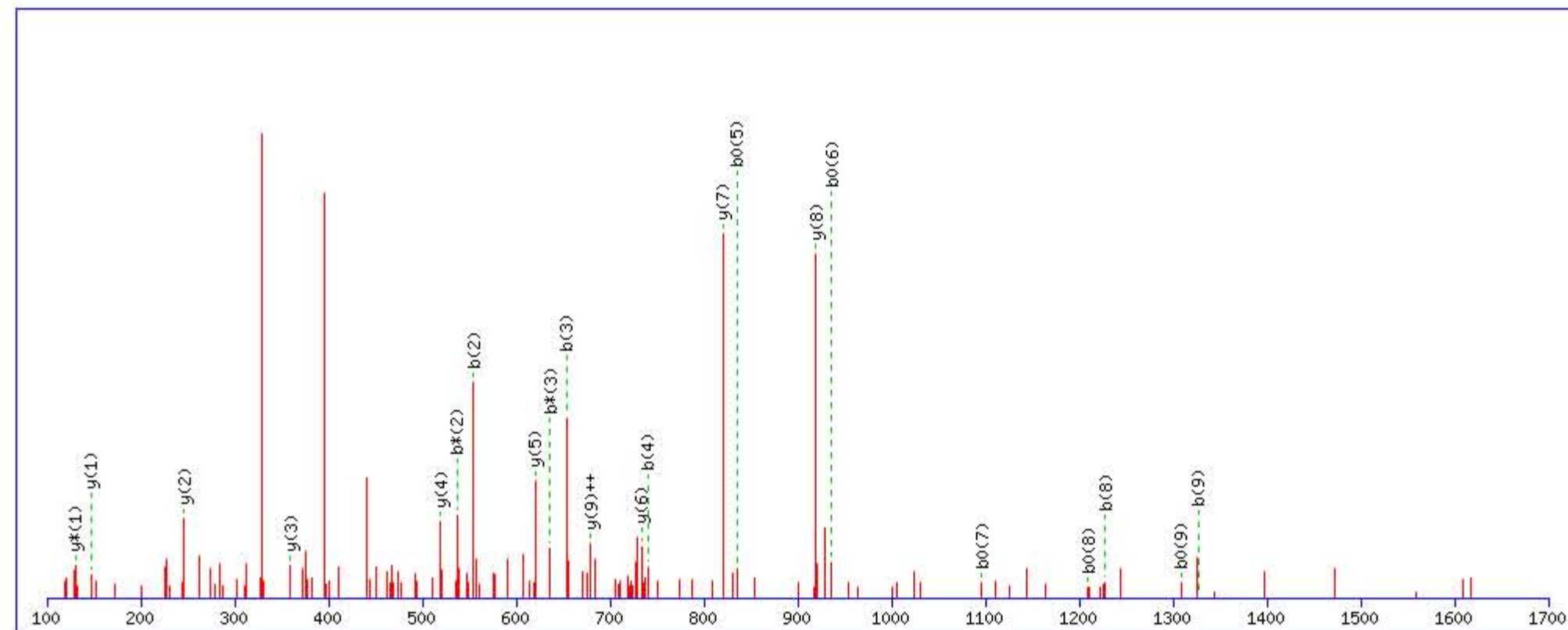
Title: Locus:1.1.1.3310.19 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

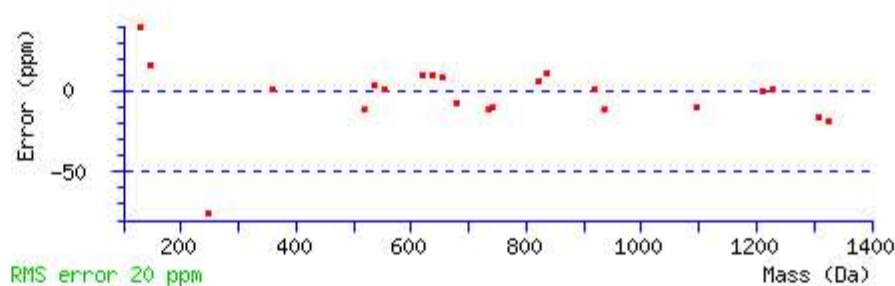
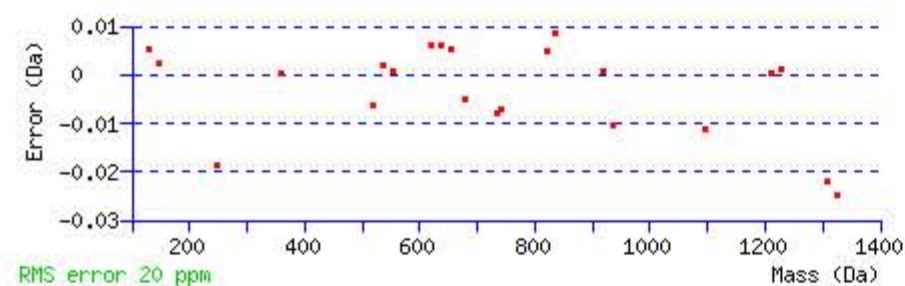
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 36 Expect: 0.0022

Matches : 22/94 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	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
36.2	1471.789093	-0.007245	NQVSLTCLVK
7.5	1471.797592	-0.015744	KYFWDR AFLVK
4.6	1471.803467	-0.021619	EKQG PLLDLFGQK
3.6	1471.799438	-0.017590	EVELDRLRDTVK
2.0	1471.770447	0.011401	QPTTAEKSATK
0.1	1471.770432	0.011416	KDKAEQLDSK

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 38884: 1596.829782 from(533.283870,3+) rtinseconds(1961) index(70968)

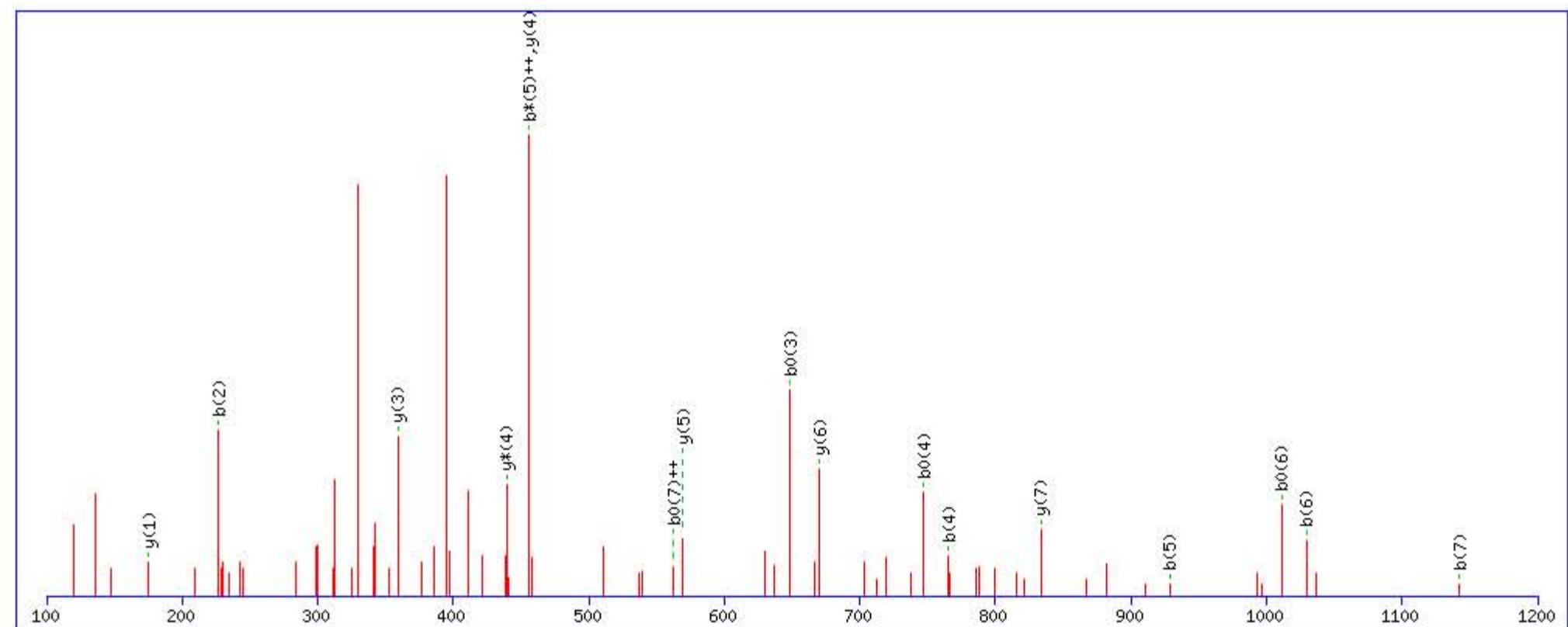
Title: Locus:1.1.1.3216.18 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

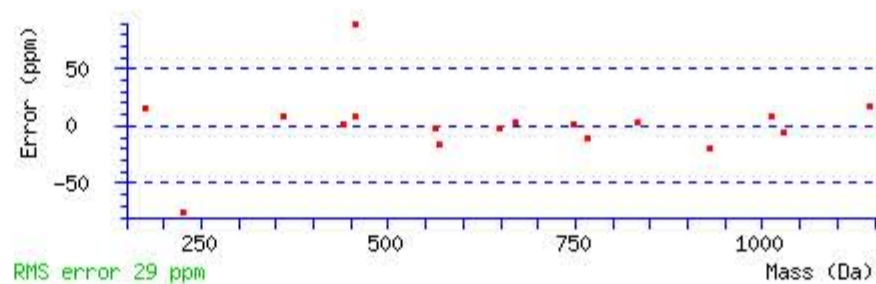
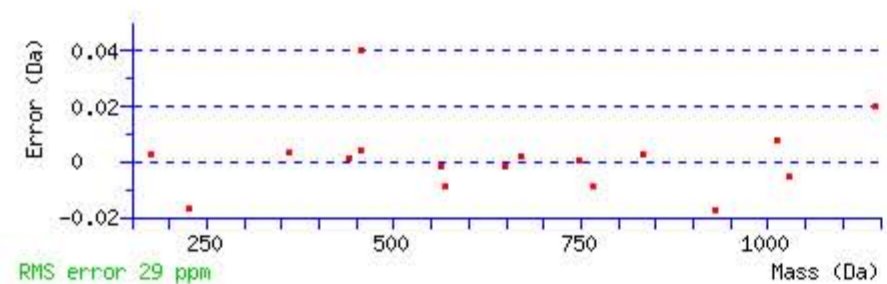
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 29 Expect: 0.0096

Matches : 17/114 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	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
29.2	1596.833389	-0.003607	EPQVYTLPPSR
7.3	1596.847122	-0.017340	ATPSSSPGTATALPALR
1.0	1596.825974	0.003808	KLSLDLEAQWAPSPR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **WQQGNVFSCSVMEALHNHYTQK**

Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

Match to Query 66351: 3111.425020 from(623.292280,5+) rtinseconds(2058) index(71511)

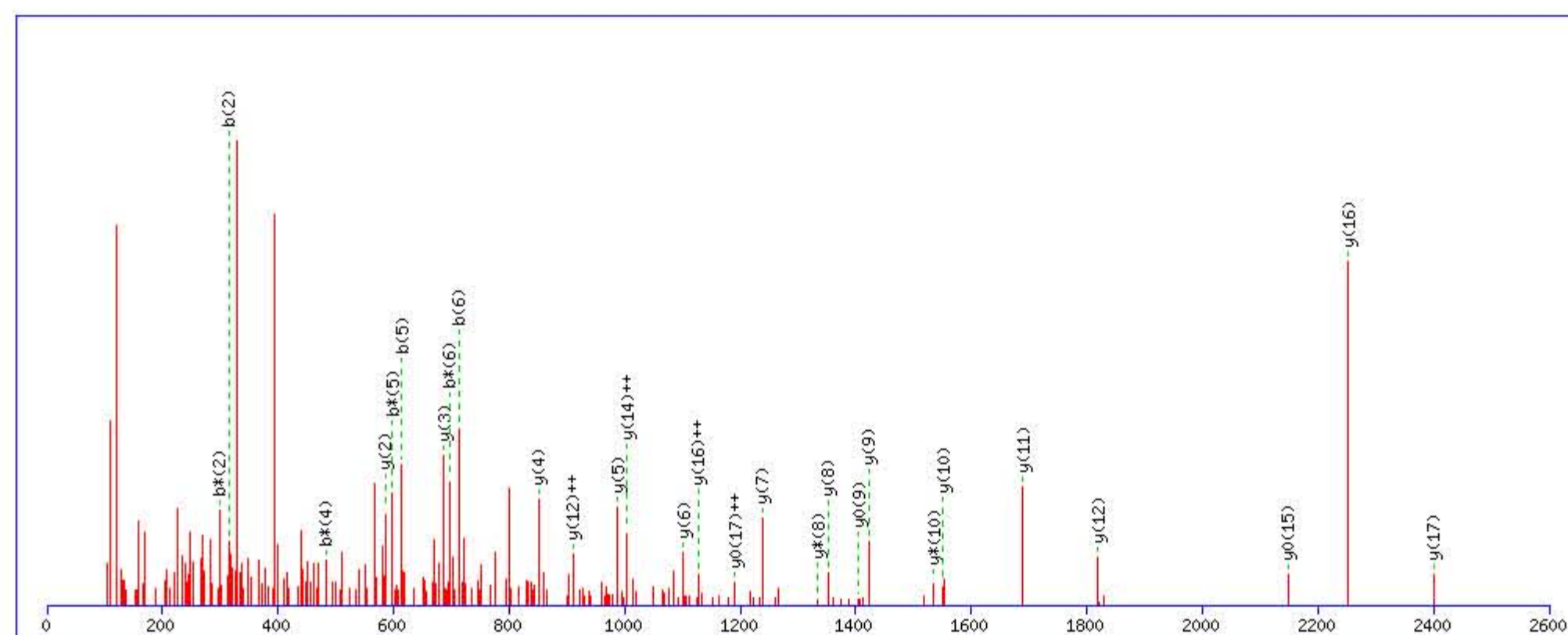
Title: Locus:1.1.1.3250.11 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

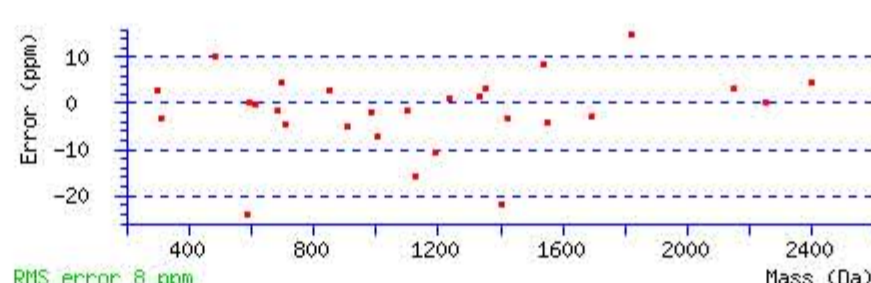
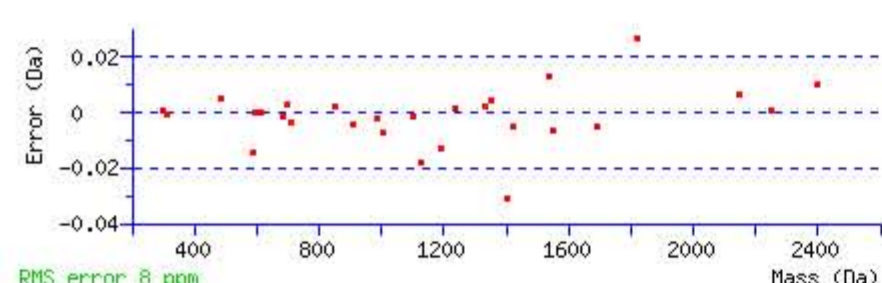
Variable modifications:

Q22 : Biotin:Thermo-21345 (Q)

Ions Score: 66 Expect: 3.7e-006

Matches : 28/244 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	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 **WQQGNVFSCSVMEALHNHYTQK**

(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	3111.426590	-0.001570	WQQGNVFSCSVMEALHNHYTQK

MASCOT 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 34873: 1471.781848 from(736.898200,2+) rtinseconds(2230) index(72630)

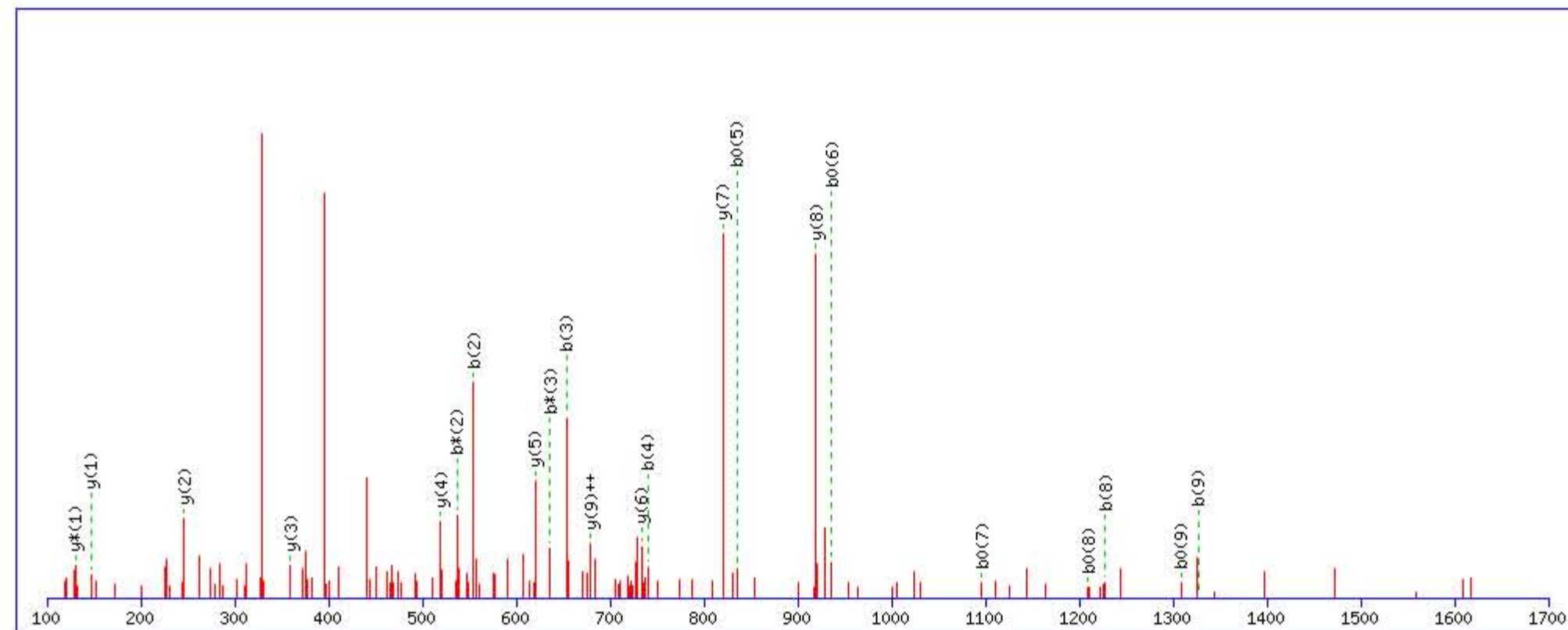
Title: Locus:1.1.1.3310.19 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

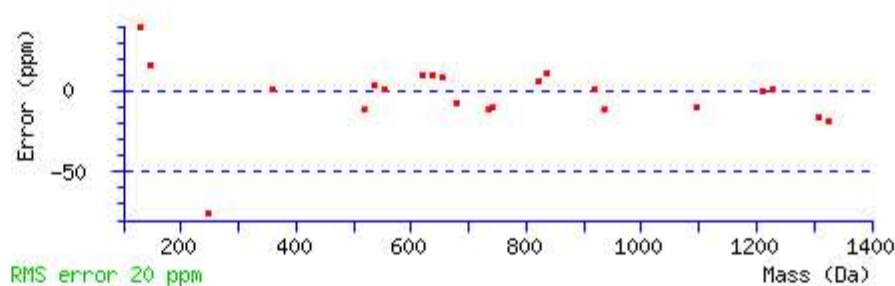
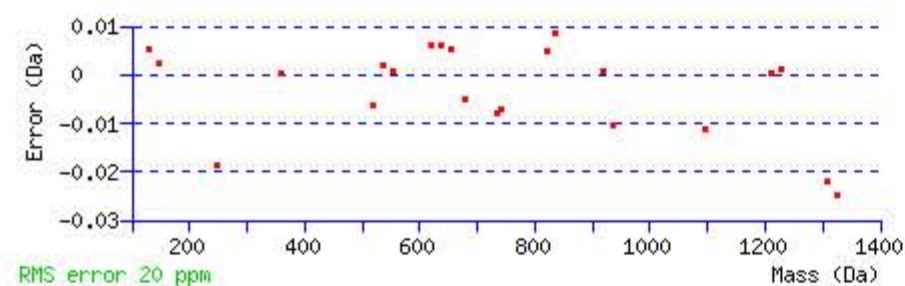
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 36 Expect: 0.0022

Matches : 22/94 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	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
36.2	1471.789093	-0.007245	NQVSLTCLVK
7.5	1471.797592	-0.015744	KYFWDRAFLVK
4.6	1471.803467	-0.021619	EKQGPLLDLFGQK
3.6	1471.799438	-0.017590	EVELDRLRDTVK
2.0	1471.770447	0.011401	QPTTAEKSATK
0.1	1471.770432	0.011416	KDKAEQLDSK

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 38884: 1596.829782 from(533.283870,3+) rtinseconds(1961) index(70968)

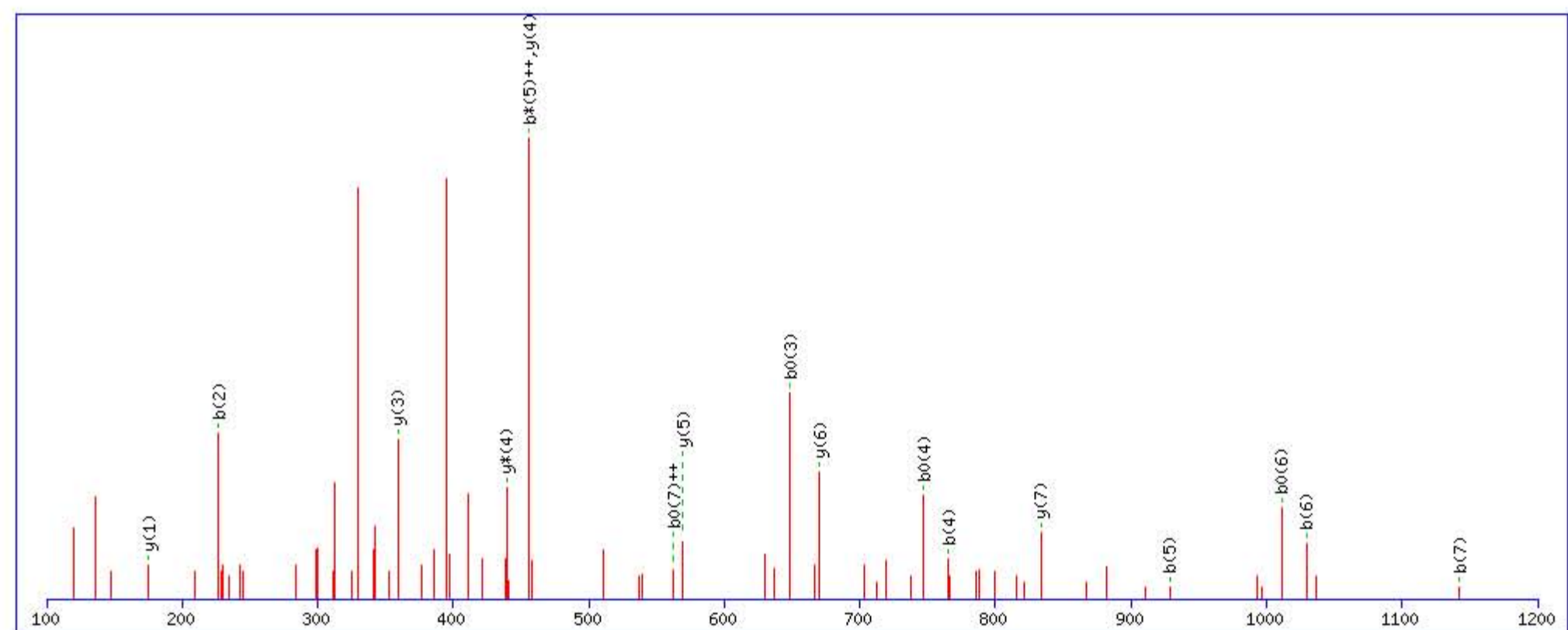
Title: Locus:1.1.1.3216.18 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

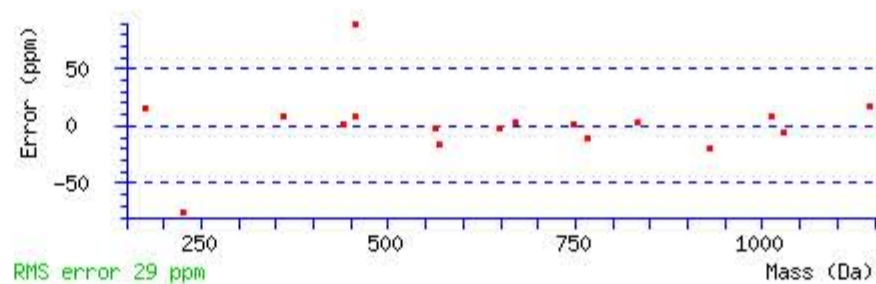
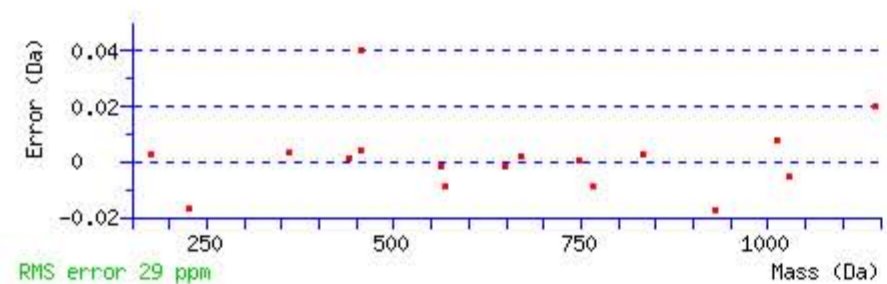
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 29 Expect: 0.0096

Matches : 17/114 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	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
29.2	1596.833389	-0.003607	EPQVYTLPPSR
7.3	1596.847122	-0.017340	ATPSSSPGTATALPALR
1.0	1596.825974	0.003808	KLSLDLEAQWAPSPR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **WQQGNVFSCSVMEALHNHYTQK**

Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

Match to Query 66351: 3111.425020 from(623.292280,5+) rtinseconds(2058) index(71511)

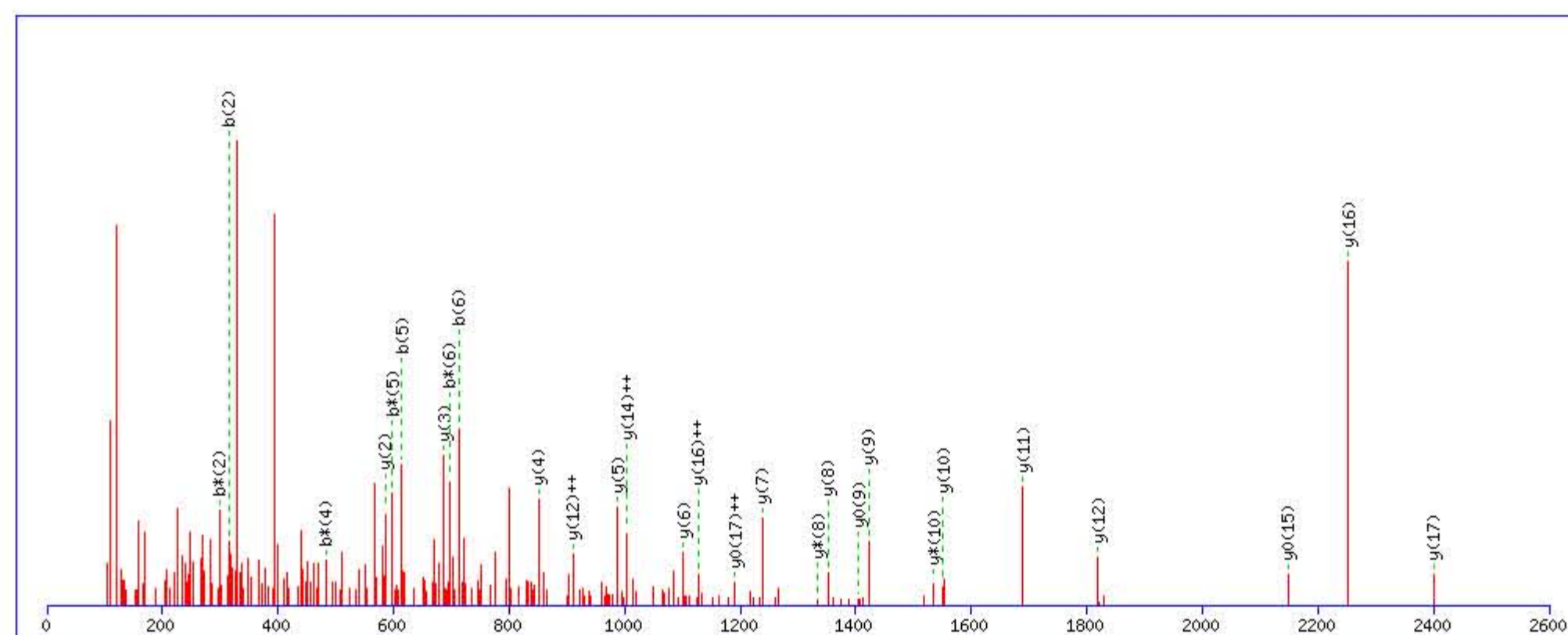
Title: Locus:1.1.1.3250.11 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

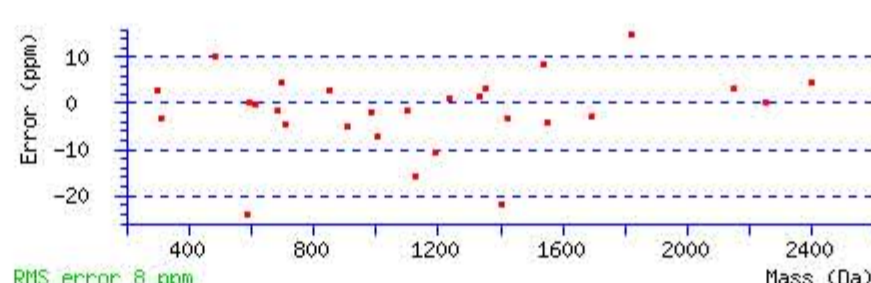
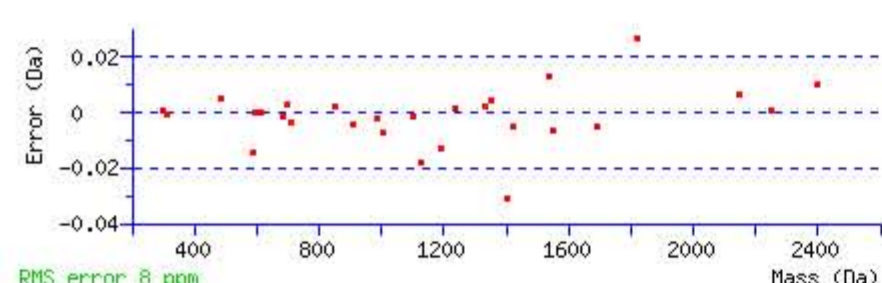
Variable modifications:

Q22 : Biotin:Thermo-21345 (Q)

Ions Score: 66 Expect: 3.7e-006

Matches : 28/244 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	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 **WQQGNVFSCSVMEALHNHYTQK**

(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	3111.426590	-0.001570	WQQGNVFSCSVMEALHNHYTQK

MASCOT 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 34873: 1471.781848 from(736.898200,2+) rtinseconds(2230) index(72630)

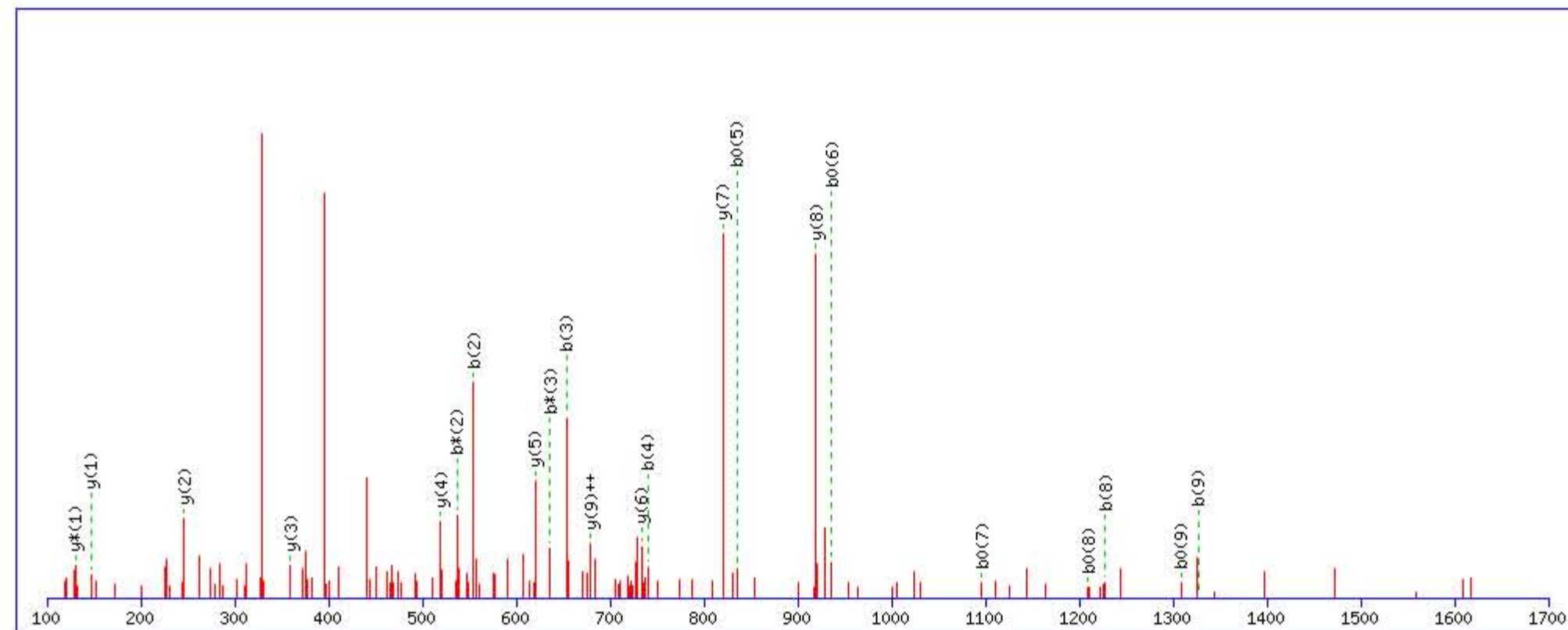
Title: Locus:1.1.1.3310.19 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

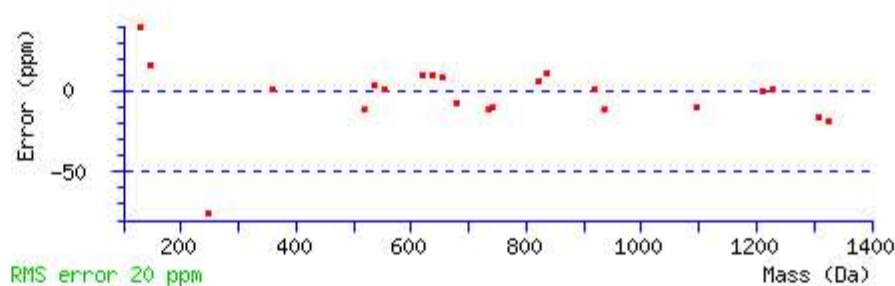
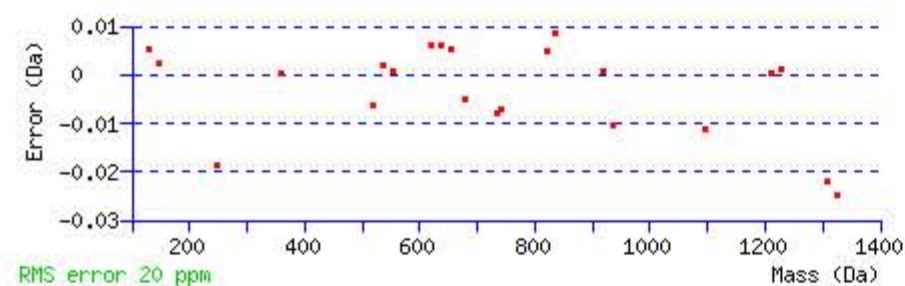
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 36 Expect: 0.0022

Matches : 22/94 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	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
36.2	1471.789093	-0.007245	NQVSLTCLVK
7.5	1471.797592	-0.015744	KYFWDRAFLVK
4.6	1471.803467	-0.021619	EKQGPLLDLFGQK
3.6	1471.799438	-0.017590	EVELDRLRDTVK
2.0	1471.770447	0.011401	QPTTAEKSATK
0.1	1471.770432	0.011416	KDKAEQLDSK

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 38884: 1596.829782 from(533.283870,3+) rtinseconds(1961) index(70968)

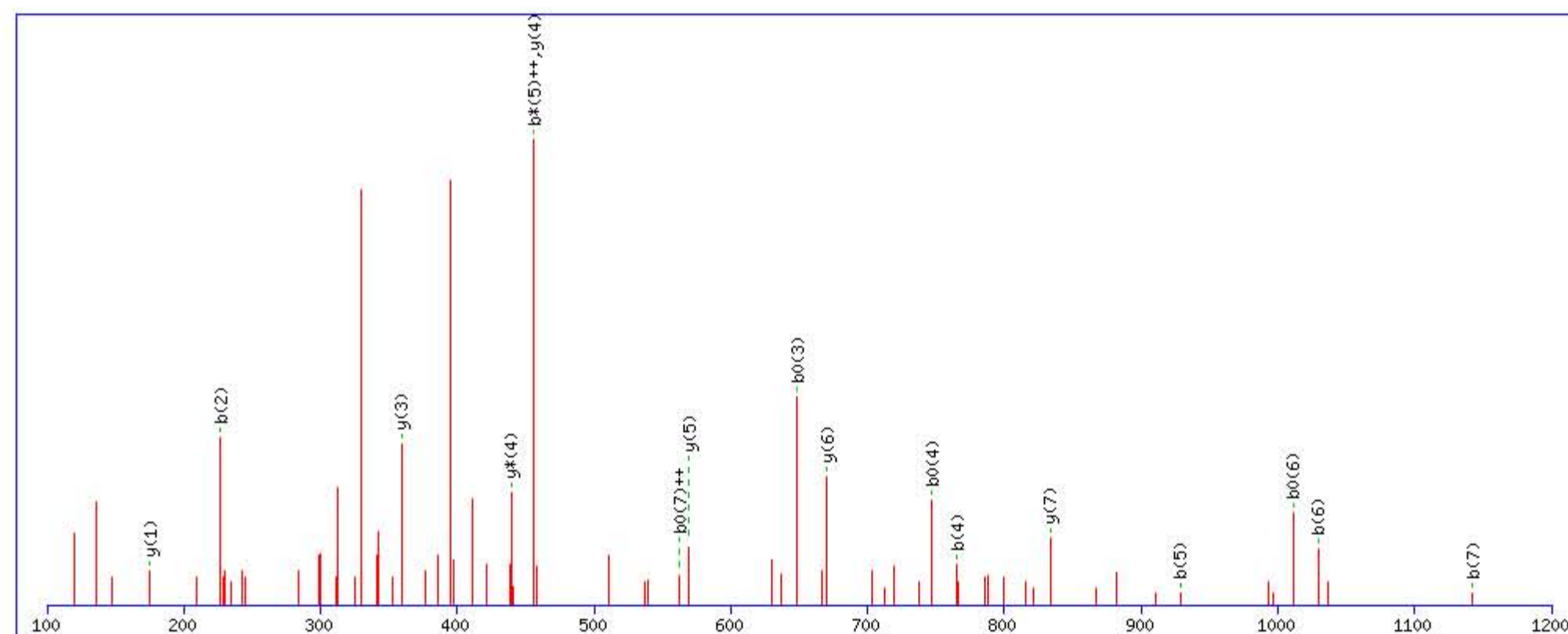
Title: Locus:1.1.1.3216.18 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

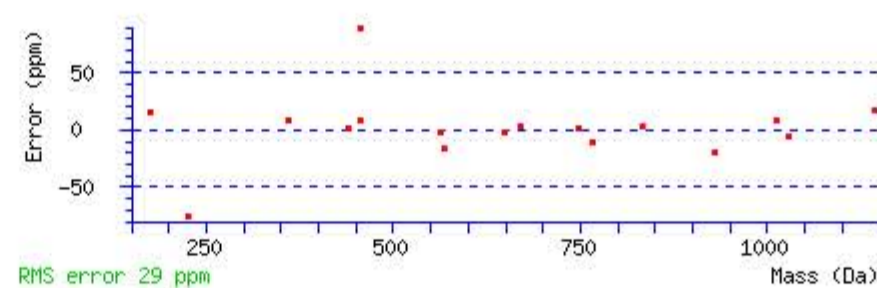
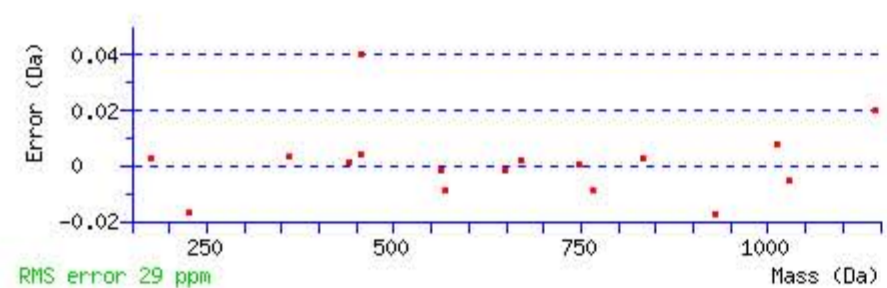
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 29 Expect: 0.0096

Matches : 17/114 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	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
29.2	1596.833389	-0.003607	EPQVYTLPPSR
7.3	1596.847122	-0.017340	ATPSSSPGTATALPALR
1.0	1596.825974	0.003808	KLSLDLEAQWAPSPR

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

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **VYACEVTHQGLSSPVTK**

Found in **IGKC_HUMAN**, Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1

Match to Query 53676: 2186.079492 from(729.700440,3+) rtinseconds(1780) index(69819)

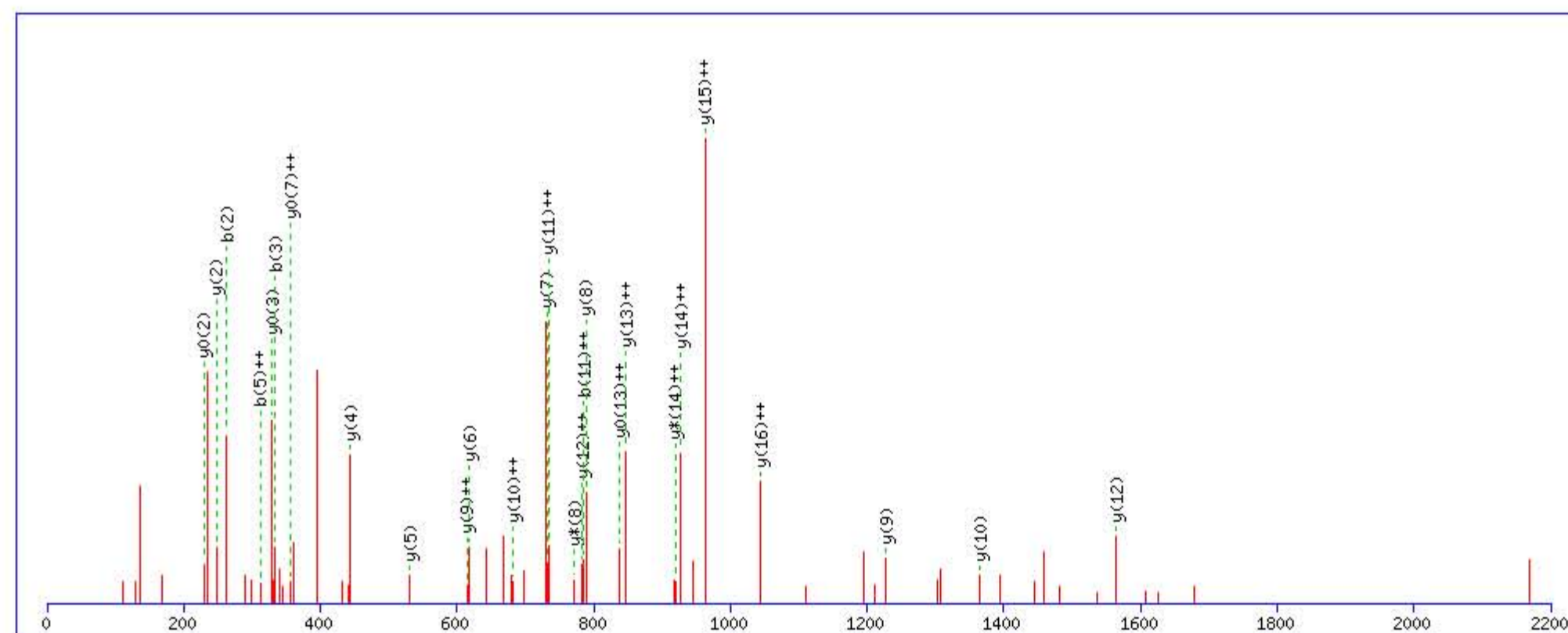
Title: Locus:1.1.1.3153.22 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 2186.086411

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

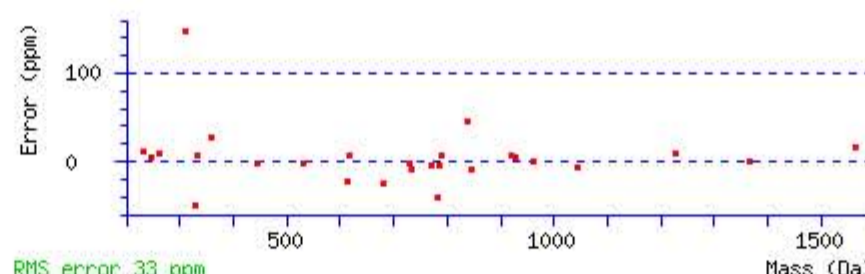
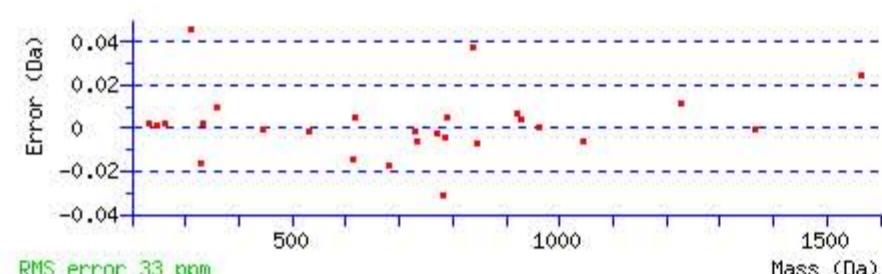
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 45 Expect: 0.00085

Matches : 27/166 fragment ions using 69 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.075690	50.541483					V							17
2	263.139019	132.073148					Y	2088.025261	1044.516268	2070.998712	1036.002994	2070.014696	1035.510986	16
3	334.176133	167.591704					A	1924.961932	962.984604	1907.935383	954.471330	1906.951367	953.979322	15
4	494.206782	247.607029					C	1853.924818	927.466047	1836.898269	918.952773	1835.914253	918.460765	14
5	623.249375	312.128326			605.238810	303.123043	E	1693.894169	847.450723	1676.867620	838.937448	1675.883604	838.445440	13
6	722.317789	361.662533			704.307224	352.657250	V	1564.851576	782.929426	1547.825027	774.416152	1546.841011	773.924144	12
7	823.365468	412.186372			805.354903	403.181090	T	1465.783162	733.395219	1448.756613	724.881945	1447.772597	724.389937	11
8	960.424380	480.715828			942.413815	471.710546	H	1364.735483	682.871380	1347.708934	674.358105	1346.724918	673.866097	10
9	1399.649706	700.328491	1382.623157	691.815217	1381.639141	691.323208	Q	1227.676571	614.341924	1210.650022	605.828649	1209.666006	605.336641	9
10	1456.671170	728.839223	1439.644621	720.325948	1438.660605	719.833940	G	788.451245	394.729261	771.424696	386.215986	770.440680	385.723978	8
11	1569.755234	785.381255	1552.728685	776.867980	1551.744669	776.375972	L	731.429781	366.218529	714.403232	357.705254	713.419216	357.213246	7
12	1656.787262	828.897269	1639.760713	820.383994	1638.776697	819.891986	S	618.345717	309.676497	601.319168	301.163222	600.335152	300.671214	6
13	1743.819290	872.413283	1726.792741	863.900009	1725.808725	863.408000	S	531.313689	266.160483	514.287140	257.647208	513.303124	257.155200	5
14	1840.872054	920.939665	1823.845505	912.426391	1822.861489	911.934382	P	444.281661	222.644469	427.255112	214.131194	426.271096	213.639186	4
15	1939.940468	970.473872	1922.913919	961.960598	1921.929903	961.468590	V	347.228897	174.118087	330.202348	165.604812	329.218332	165.112804	3
16	2040.988147	1020.997712	2023.961598	1012.484437	2022.977582	1011.992429	T	248.160483	124.583880	231.133934	116.070605	230.149918	115.578597	2
17							K	147.112804	74.060040	130.086255	65.546766			1



NCBI BLAST search of **VYACEVTHQGLSSPVTK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	$M_r(\text{calc})$:	Delta	Sequence
45.0	2186.086411	-0.006919	VYACEVTHQGLSSPVTK

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

MASCOT SEARCH RESULTS

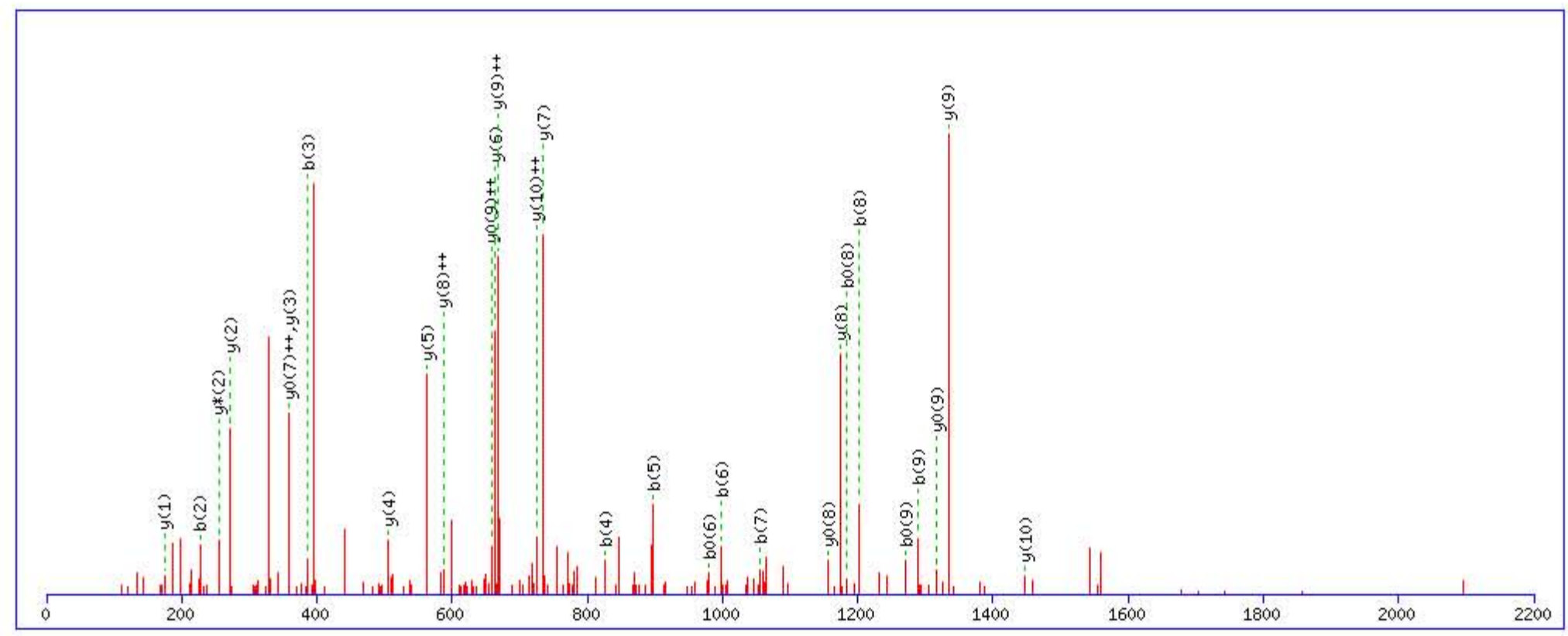
Peptide View

MS/MS Fragmentation of **LICQATGFSPR**

Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

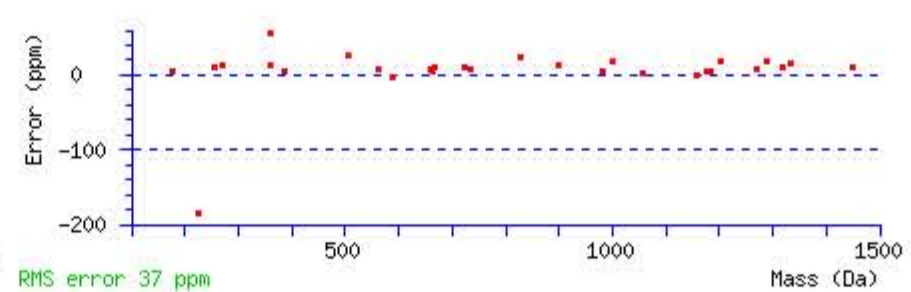
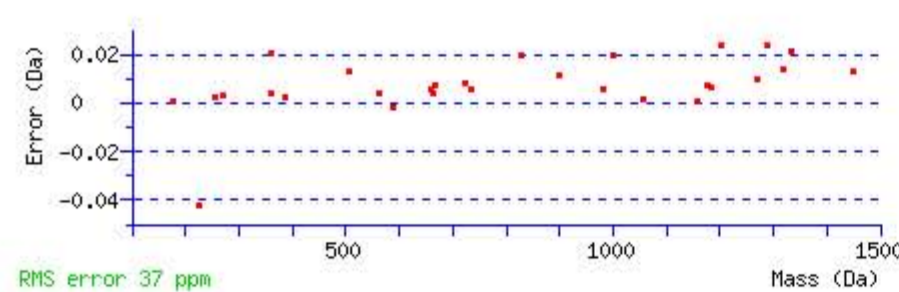
Match to Query 37081: 1559.798648 from(780.906600,2+) rtinseconds(1982) index(38568)
 Title: Locus:1.1.1.2712.22 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 59 Expect: 1.2e-005
 Matches : 29/100 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							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
58.6	1559.795242	0.003406	LICQATGFSPR
5.8	1559.820190	-0.021542	MTRSATQAAKQVPR
5.2	1559.808960	-0.010312	LDRLSGLADQMVAR
0.1	1559.808975	-0.010327	LLDRDACDITVRVK

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 38354: 1587.875208 from(794.944880,2+) rtinseconds(2054) index(39004)

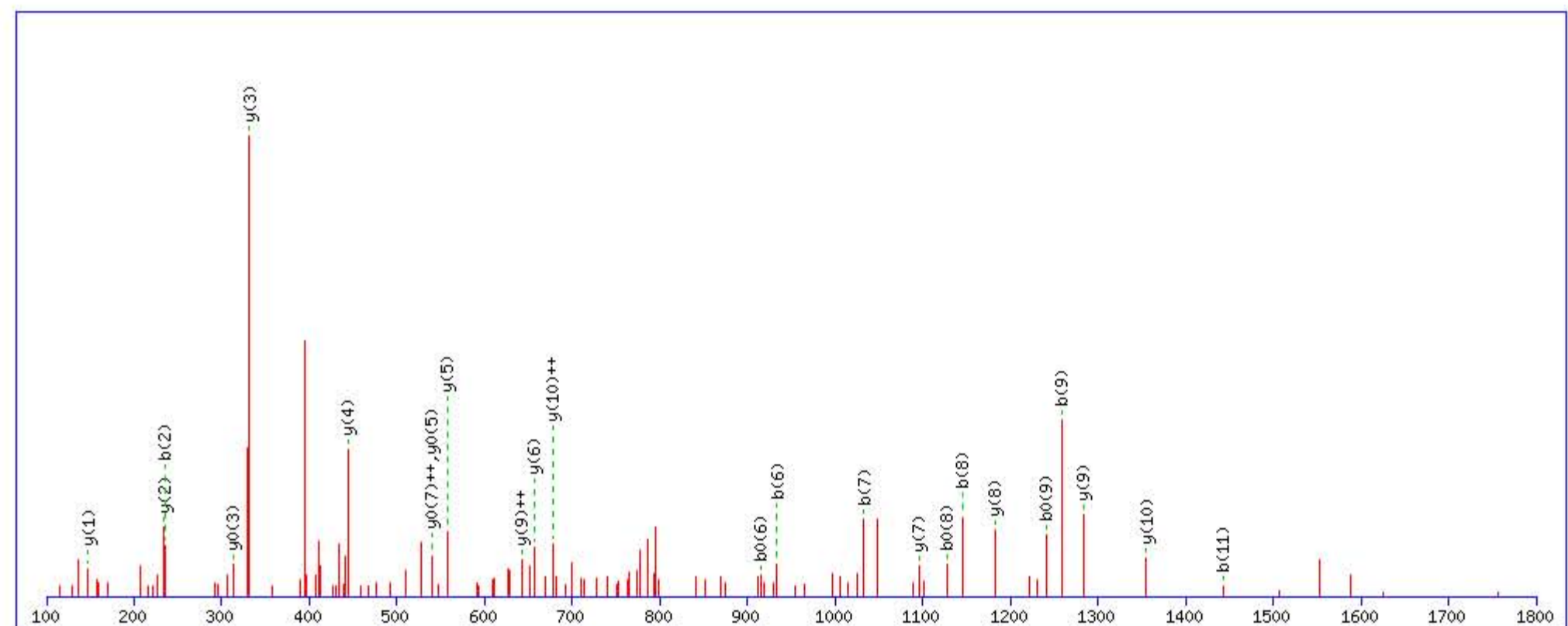
Title: Locus:1.1.1.2737.16 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1587.869431

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

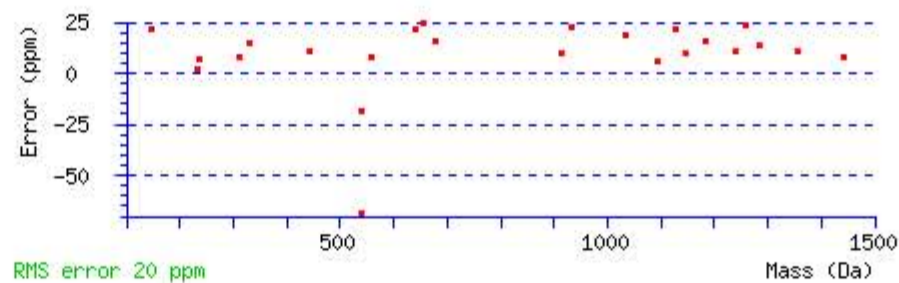
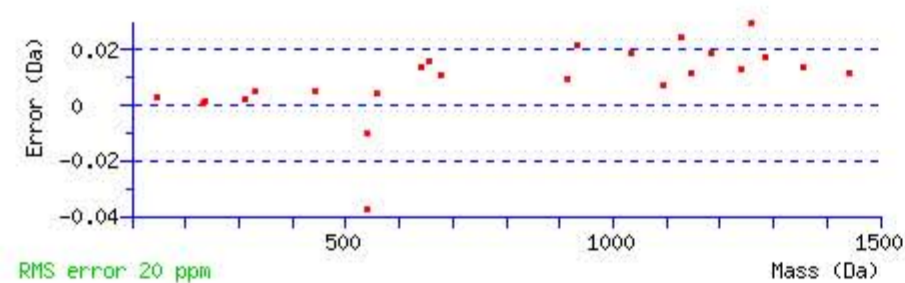
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 71 Expect: 1.5e-006

Matches : 24/114 fragment ions using 40 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	164.070605	82.538940					Y							12
2	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	$M_r(\text{calc})$:	Delta	Sequence
71.2	1587.869431	0.005777	YAATSQVLLPSK
19.5	1587.862045	0.013163	VTGQNQEQLLLAK
7.4	1587.891220	-0.016012	TIQTIVFLYSLYK
6.4	1587.862045	0.013163	SKDLTAADVVKQWK
2.9	1587.862030	0.013178	EDAKLSFKHVSSLK
2.7	1587.888062	-0.012854	AMAAFQIVVLAK
1.9	1587.884018	-0.008810	TKTKMSAAQALK
1.0	1587.862045	0.013163	DGASLSPATLFIQIR
0.5	1587.873276	0.001932	DLLTGEQFIQLRR
0.5	1587.855499	0.019709	LCGLRILQPYAER

MASCOT Search Results

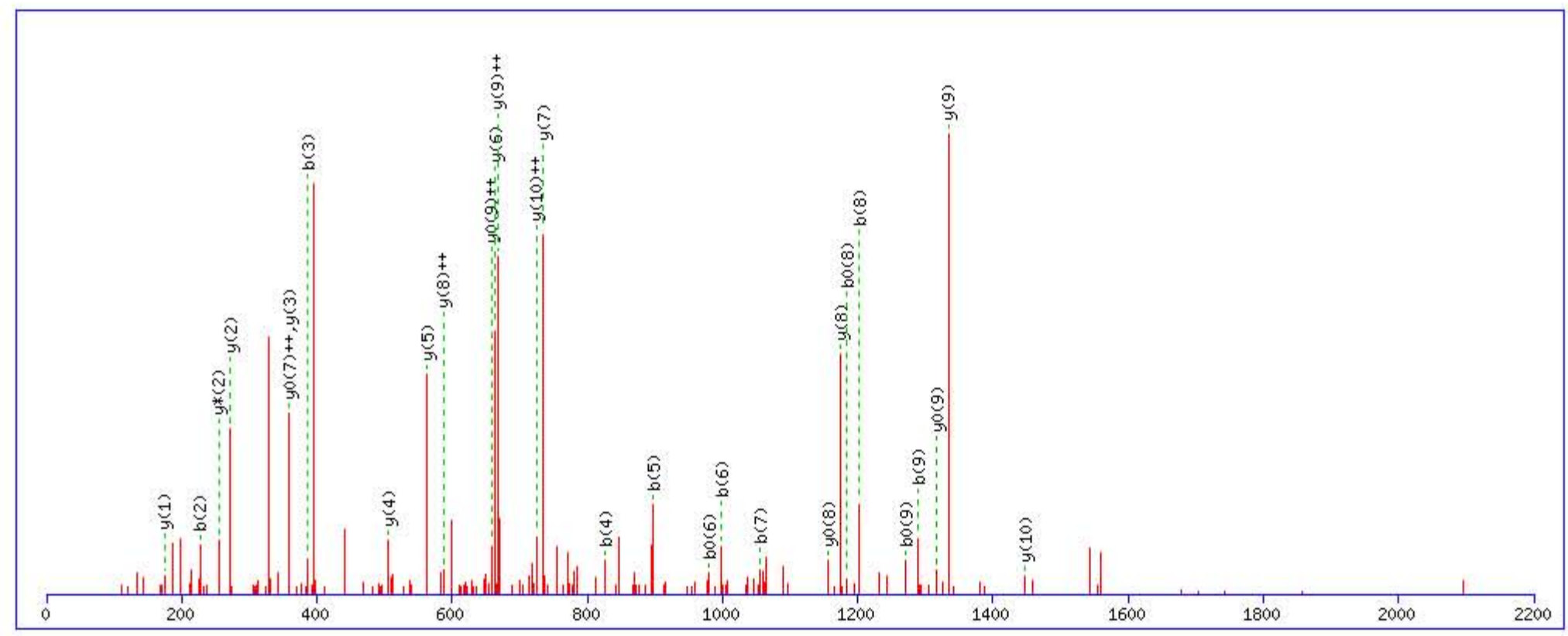
Peptide View

MS/MS Fragmentation of **LICQATGFSPR**

Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

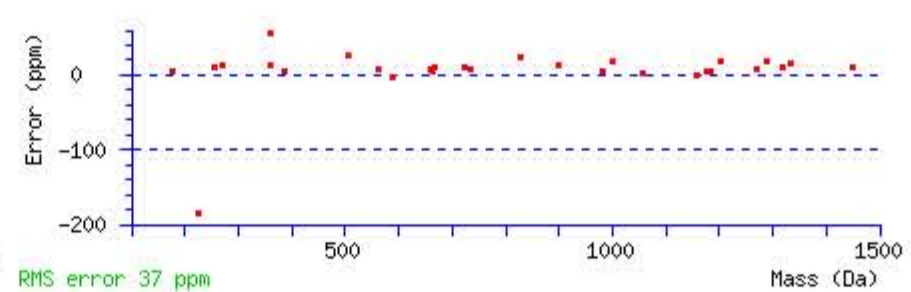
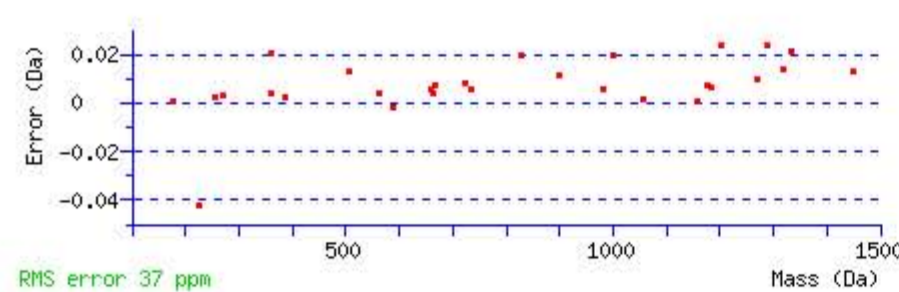
Match to Query 37081: 1559.798648 from(780.906600,2+) rtinseconds(1982) index(38568)
 Title: Locus:1.1.1.2712.22 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 59 Expect: 1.2e-005
 Matches : 29/100 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							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
58.6	1559.795242	0.003406	LICQATGFSPR
5.8	1559.820190	-0.021542	MTRSATQAAKQVPR
5.2	1559.808960	-0.010312	LDRLSGLADQMVAR
0.1	1559.808975	-0.010327	LLDRDACDITVRVK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **SFEGLGQLEVLTLTDHNLQLEVK**

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 46389: 2807.457222 from(936.826350,3+) rtinseconds(2700) index(43052)

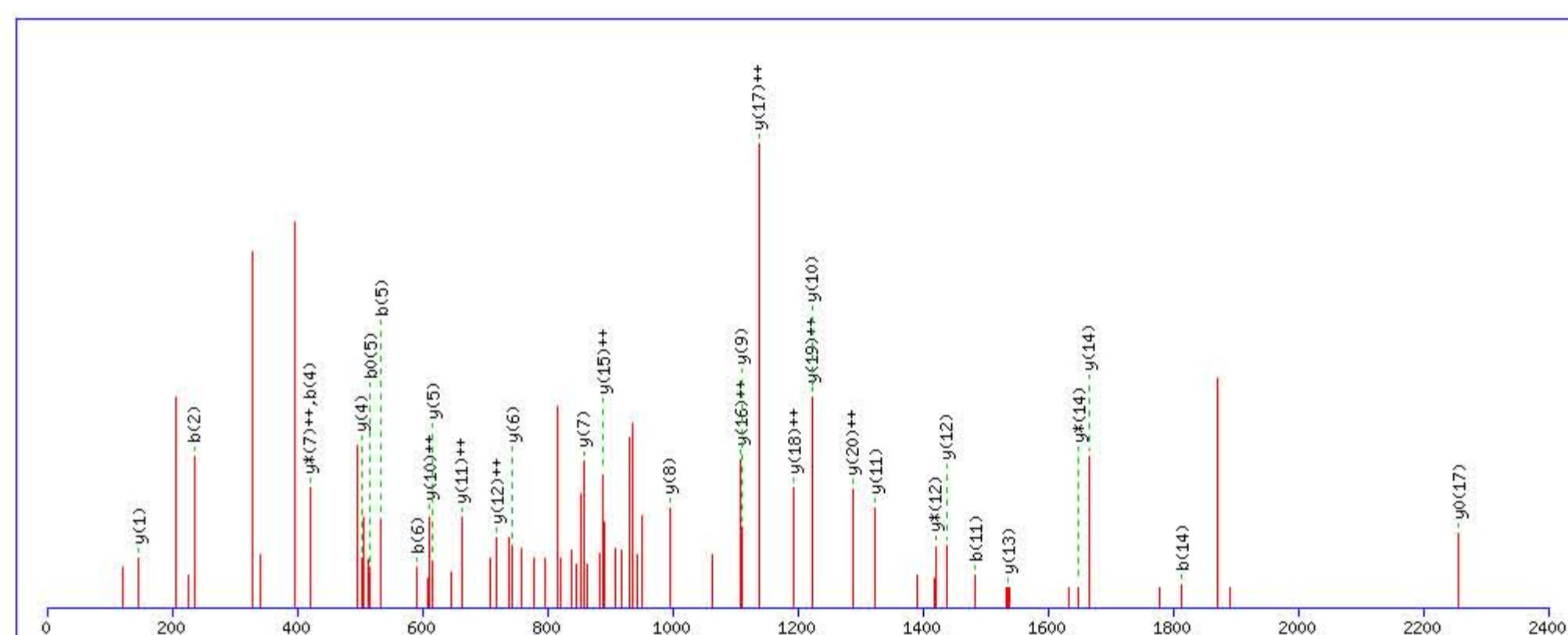
Title: Locus:1.1.1.2961.19 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

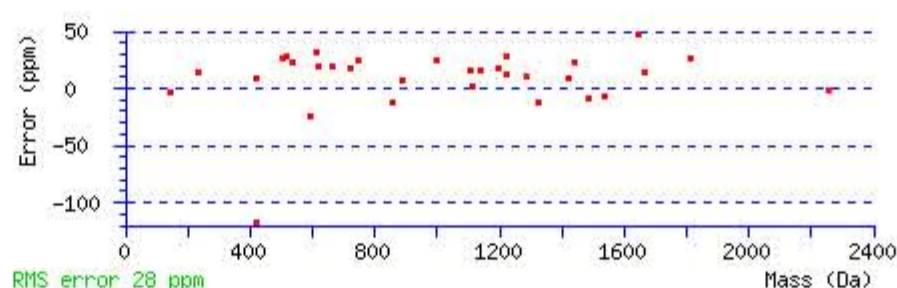
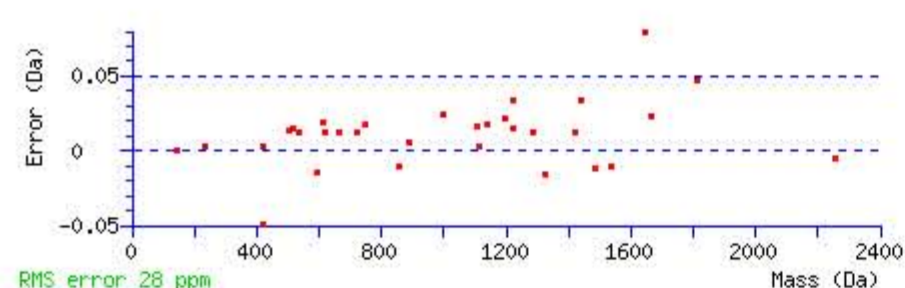
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 59 Expect: 3.1e-005

Matches : 32/236 fragment ions using 74 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	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 [SFEGLGQLEVLTLTDHNLQLEVK](#)

(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	2807.452759	0.004463	SFEGLGQLEVLTLTDHNLQLEVK
1.6	2807.452759	0.004463	SFEGLGQLEVLTLTDHNLQLEVK
0.6	2807.452759	0.004463	SFEGLGQLEVLTLTDHNLQLEVK

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

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **ELAAQTIK**

Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

Match to Query 24753: 1183.659888 from(592.837220,2+) rtinseconds(1708) index(53837)

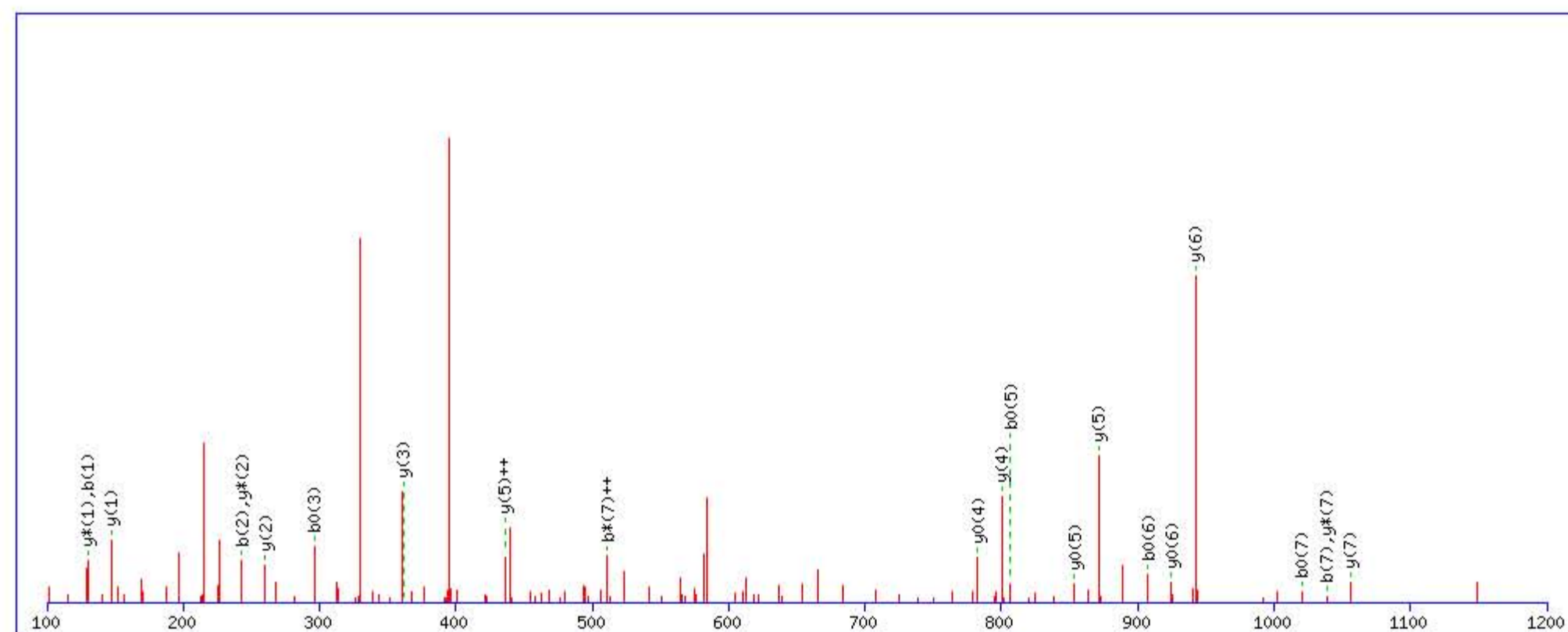
Title: Locus:1.1.1.3081.7 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

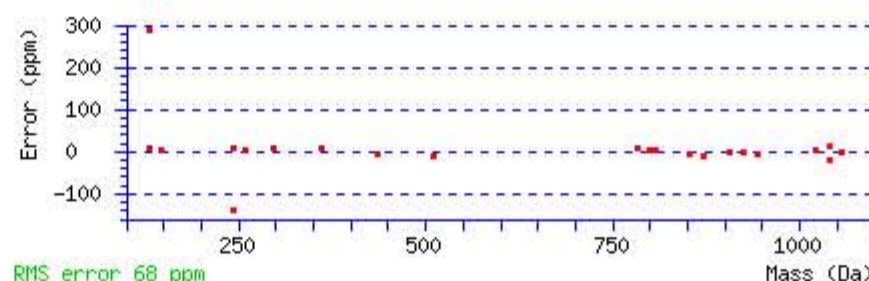
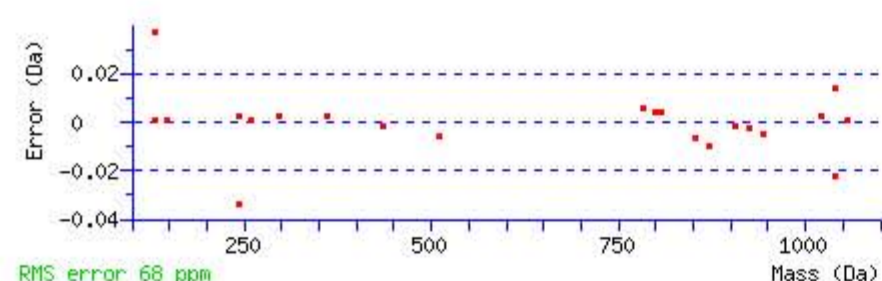
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 30 Expect: 0.023

Matches : 22/72 fragment ions using 50 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	130.049869	65.528572			112.039304	56.523290	E							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
29.8	1183.663452	-0.003564	ELAAQTIK
28.6	1183.663452	-0.003564	ELAAQTIK
13.2	1183.663467	-0.003579	TQLSPSIK
7.4	1183.667282	-0.007394	ELAERQGLLR
6.8	1183.649551	0.010337	KVCGHKQSLK
6.3	1183.674683	-0.014795	ELIQRK
6.3	1183.674683	-0.014795	ELLSRQK
6.3	1183.667282	-0.007394	ELQRLQAAQK
6.3	1183.674683	-0.014795	ELRQLSK
5.5	1183.660080	-0.000192	AIEAVAISPWK

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 32091: 1399.753548 from(700.884050,2+) rtinseconds(2216) index(57131)

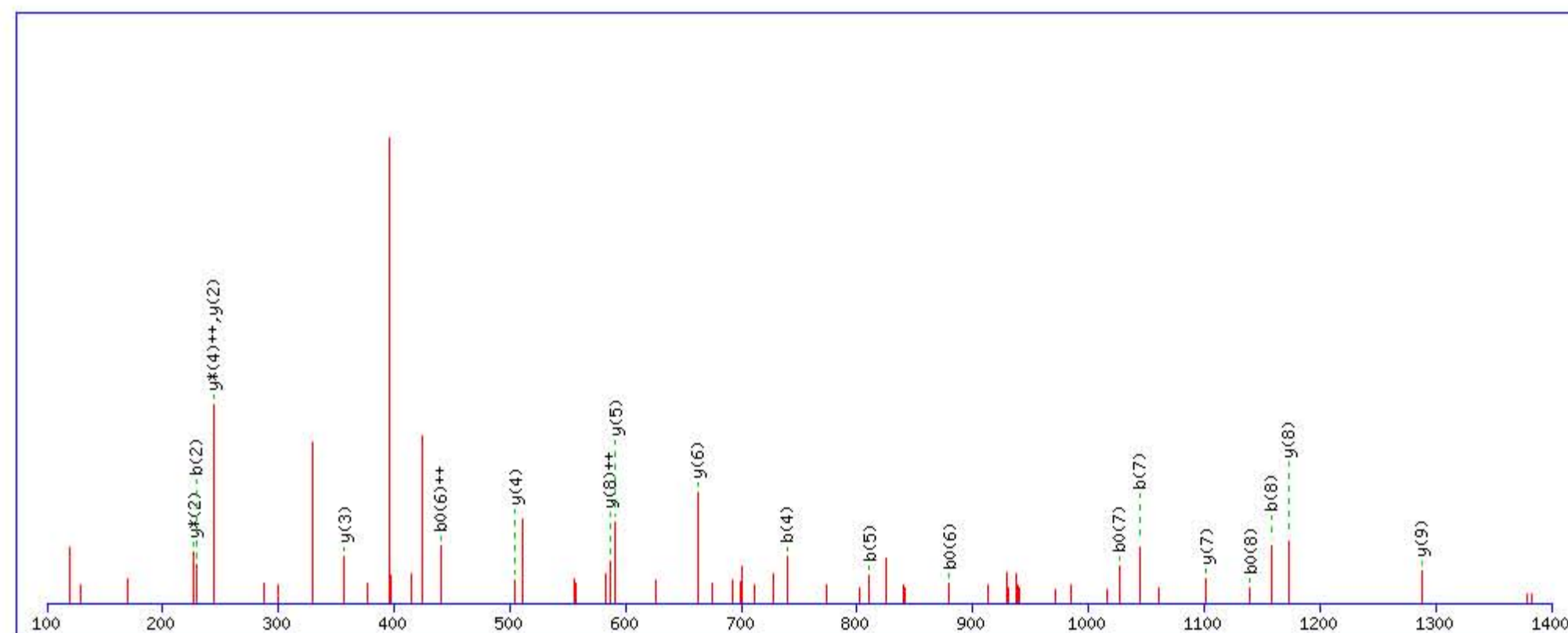
Title: Locus:1.1.1.3257.14 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1399.753342

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

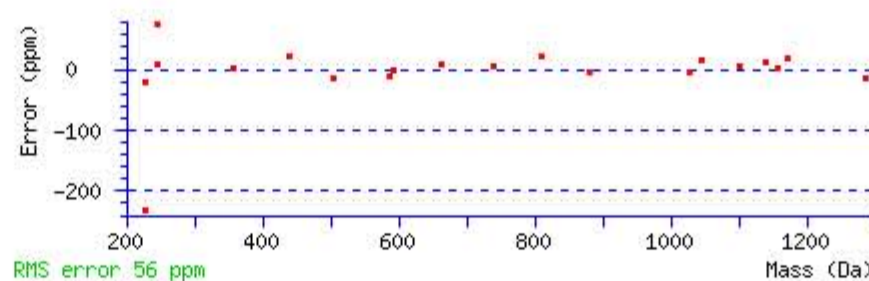
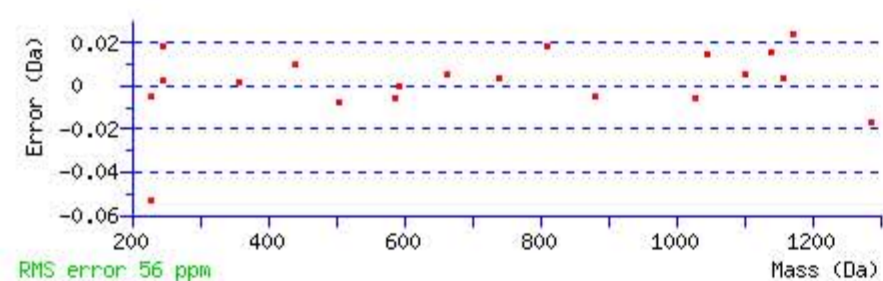
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 39 Expect: 0.0022

Matches : 20/92 fragment ions using 45 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							10
2	229.118283	115.062779			211.107718	106.057497	D	1287.676571	644.341924	1270.650022	635.828649	1269.666006	635.336641	9
3	300.155397	150.581336			282.144832	141.576054	A	1172.649628	586.828452	1155.623079	578.315178	1154.639063	577.823169	8
4	739.380723	370.194000	722.354174	361.680725	721.370158	361.188717	Q	1101.612514	551.309895	1084.585965	542.796621	1083.601949	542.304612	7
5	810.417837	405.712557	793.391288	397.199282	792.407272	396.707274	A	662.387188	331.697232	645.360639	323.183957	644.376623	322.691949	6
6	897.449865	449.228570	880.423316	440.715296	879.439300	440.223288	S	591.350074	296.178675	574.323525	287.665400	573.339509	287.173392	5
7	1044.518279	522.762777	1027.491730	514.249503	1026.507714	513.757495	F	504.318046	252.662661	487.291497	244.149386			4
8	1157.602343	579.304809	1140.575794	570.791535	1139.591778	570.299527	L	357.249632	179.128454	340.223083	170.615179			3
9	1254.655107	627.831191	1237.628558	619.317917	1236.644542	618.825909	P	244.165568	122.586422	227.139019	114.073148			2
10							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **LDAQASFLPK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	$M_r(\text{calc})$:	Delta	Sequence
38.5	1399.753342	0.000206	LDAQASFLPK
9.6	1399.745972	0.007576	IDAATGIPVTTWR
1.8	1399.738083	0.015465	QASDLSLIDK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **GSLVQASEANLQAAQDFVR**

Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

Match to Query 56358: 2314.177452 from(772.399760,3+) rtinseconds(2484) index(58542)

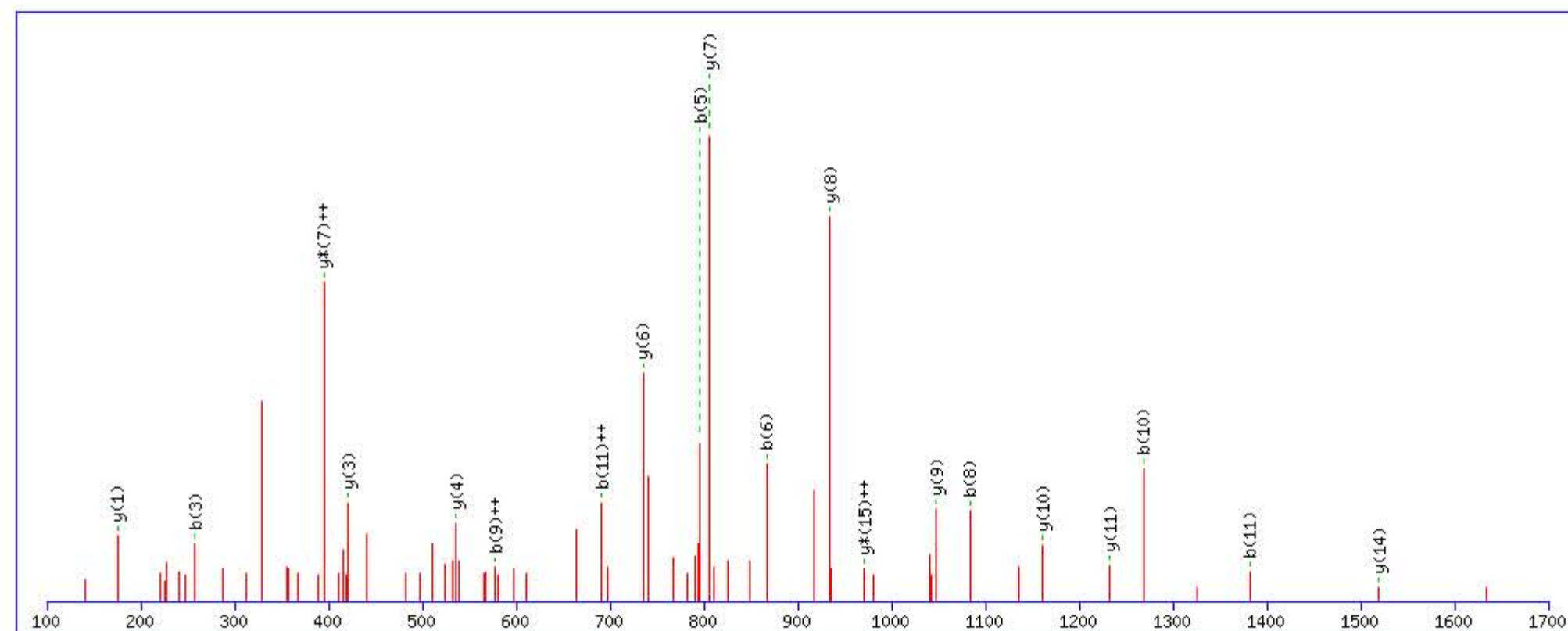
Title: Locus:1.1.1.3350.20 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

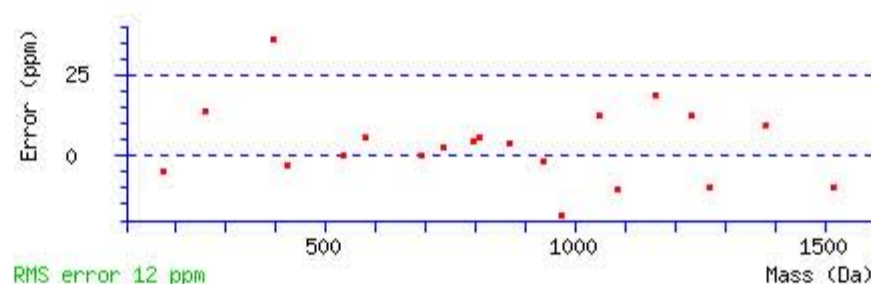
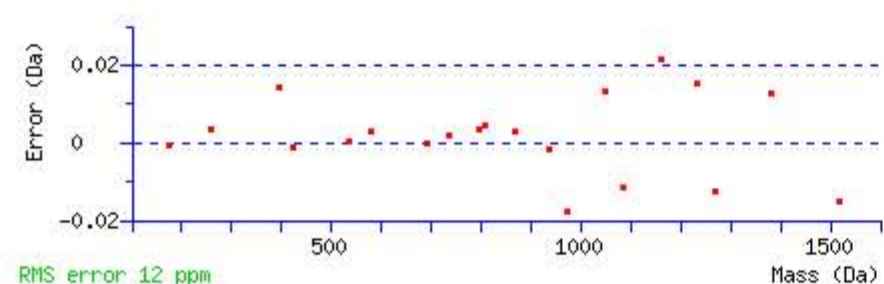
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 74 Expect: 1.8e-007

Matches : 20/200 fragment ions using 27 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.028740	29.518008					G							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
74.3	2314.173950	0.003502	GSLVQASEANLQAAQDFVR
10.2	2314.173950	0.003502	GSLVQASEANLQAAQDFVR
2.5	2314.178635	-0.001183	NKDRPAMQLYQPGARSR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **GSLVQASEANLQAAQDFVR**

Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

Match to Query 56359: 2314.179548 from(1158.097050,2+) rtinseconds(2530) index(58858)

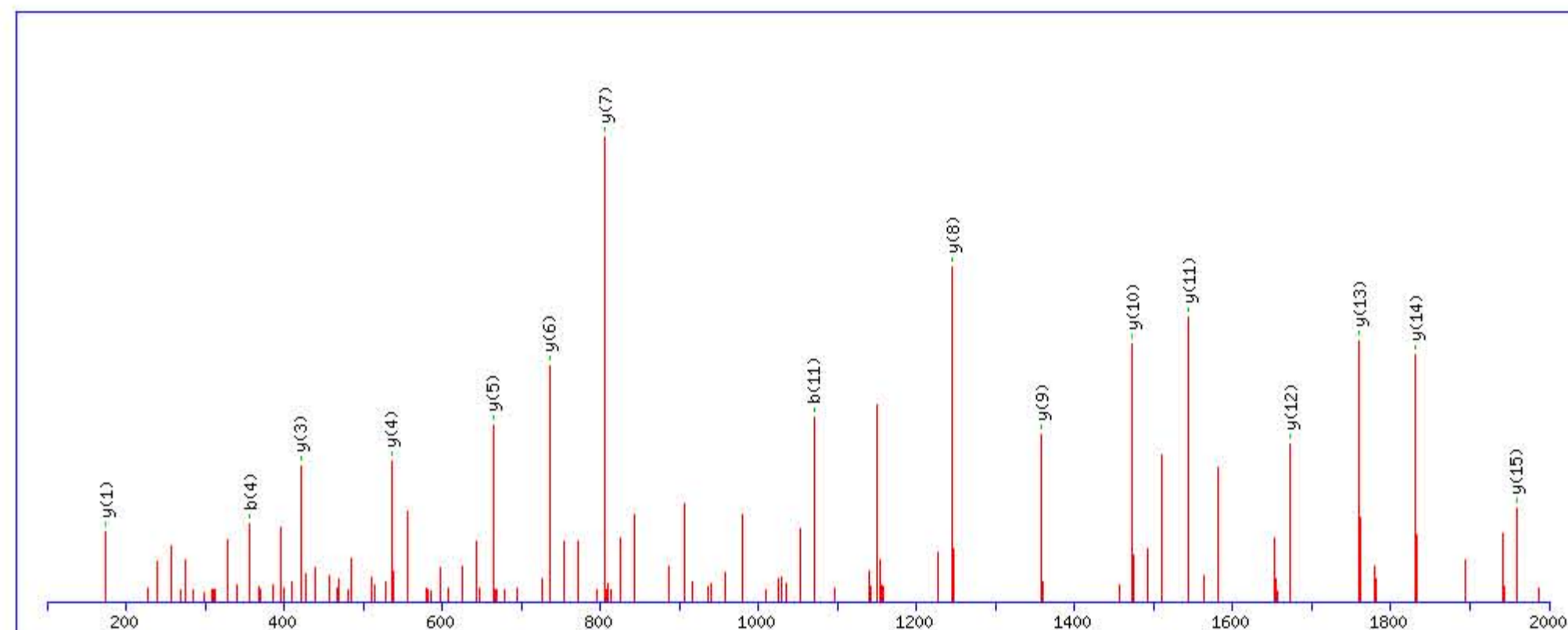
Title: Locus:1.1.1.3366.19 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

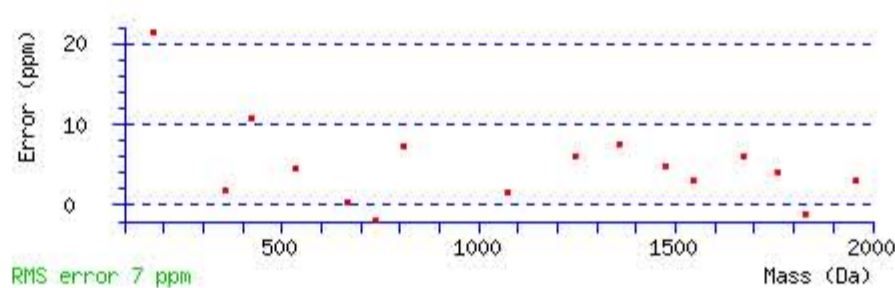
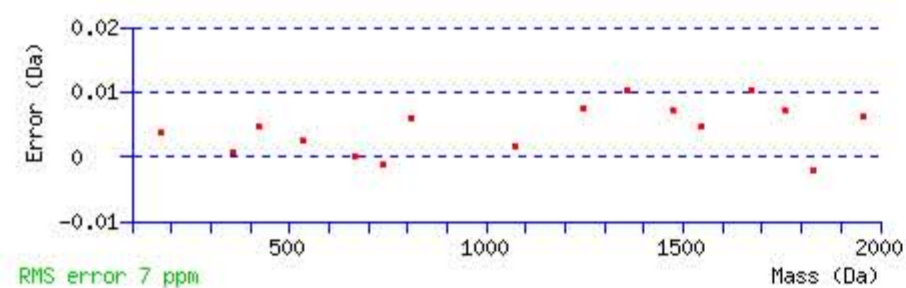
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 141 Expect: 1.7e-013

Matches : 16/200 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							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
140.9	2314.173950	0.005598	GSLVQASEANLQAAQDFVR
87.5	2314.173950	0.005598	GSLVQASEANLQAAQDFVR
28.6	2314.173950	0.005598	GSLVQASEANLQAAQDFVR
4.7	2314.178635	0.000913	NKDRPAMQLYQPGARSR

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 56384: 2316.164562 from(773.062130,3+) rtinseconds(1937) index(55340)

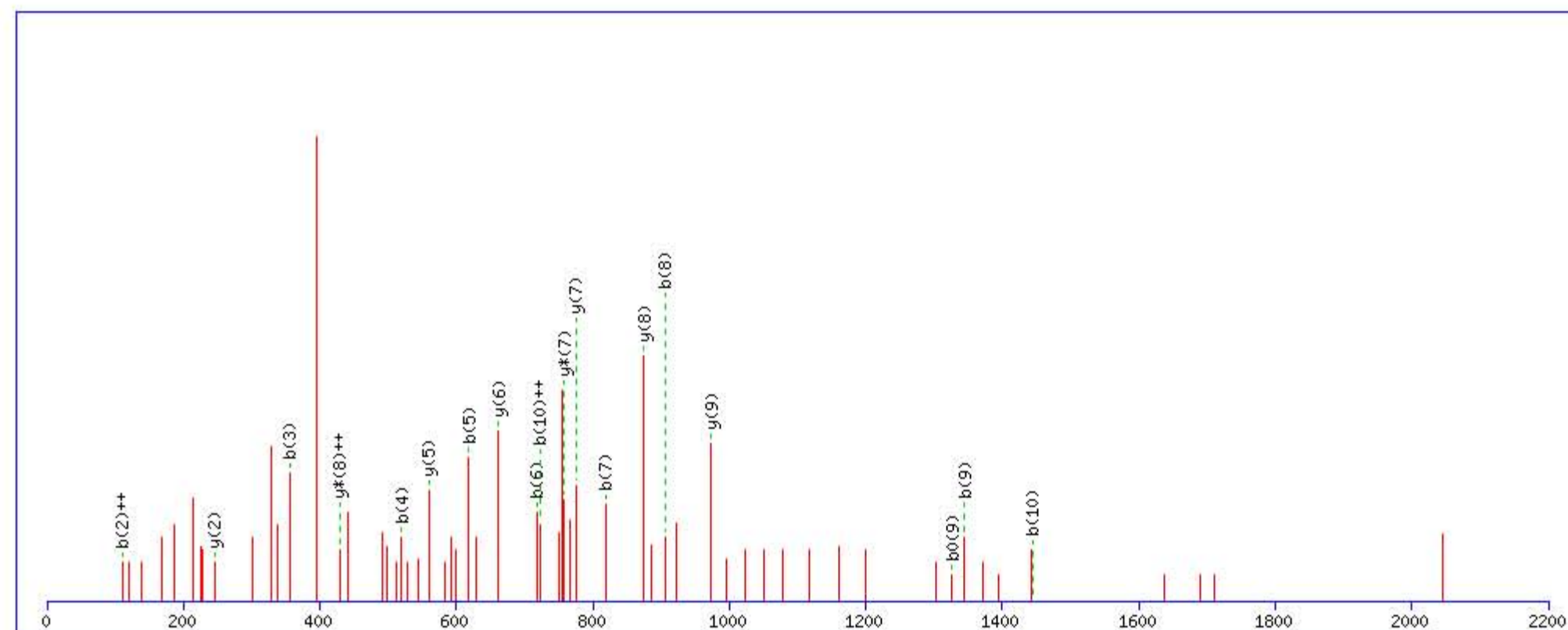
Title: Locus:1.1.1.3160.22 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

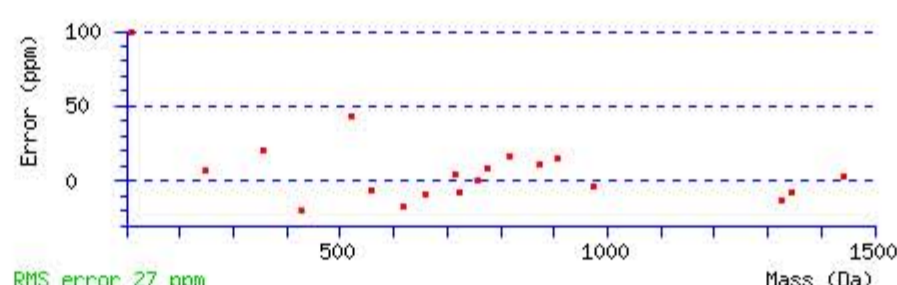
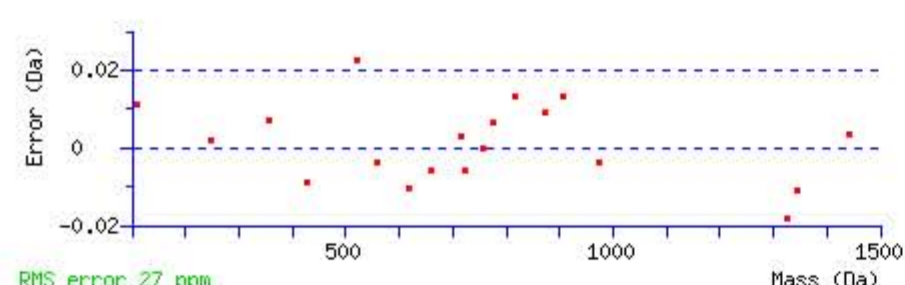
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 29 Expect: 0.0069

Matches : 19/172 fragment ions using 56 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	148.075690	74.541483					F							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
28.7	2316.168488	-0.003926	FAHYVVTSQVVNTANEAR
5.7	2316.168442	-0.003880	KPWSQQDPYANLMTRKEK

MASCOT Search Results

Peptide View

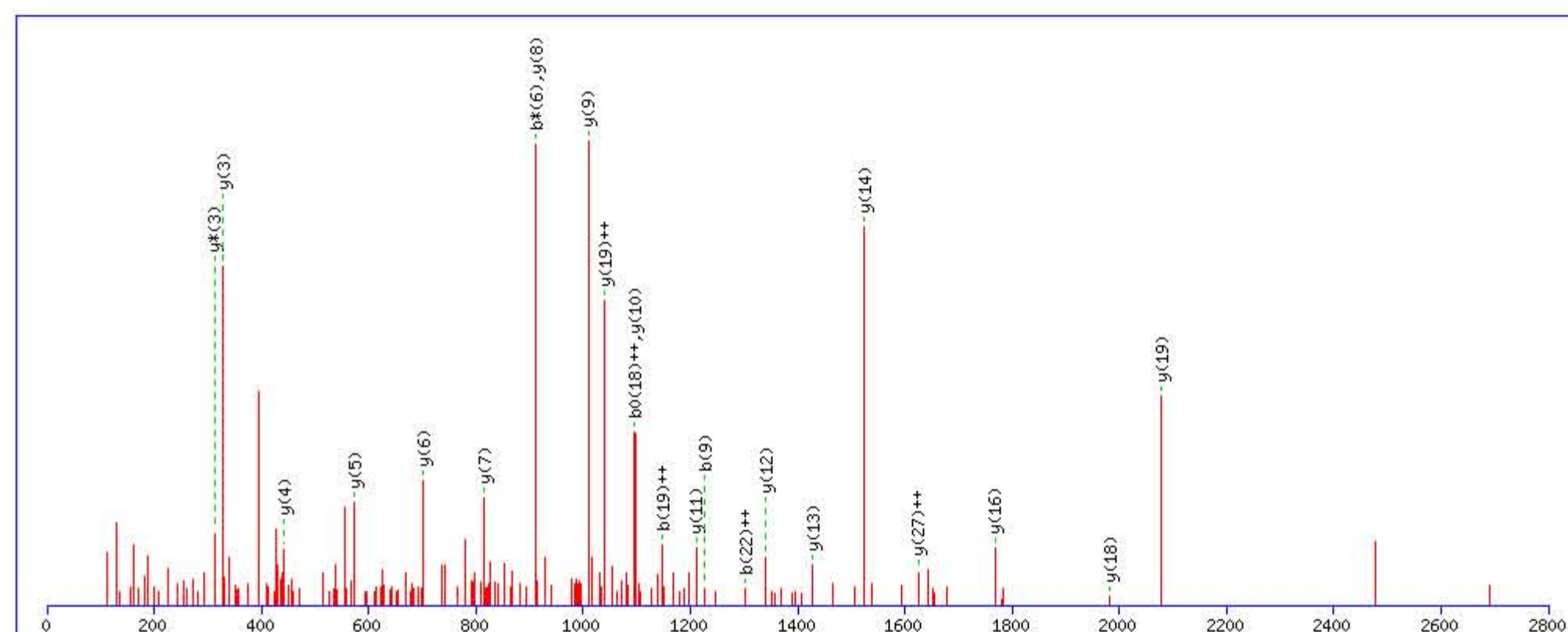
MS/MS Fragmentation of **GMADQDGLKPTIDKPSEDSPPLEMLGPR**
 Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

Match to Query 69452: 3304.617776 from(827.161720,4+) rtinseconds(2232) index(57233)
 Title: Locus:1.1.1.3262.15 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

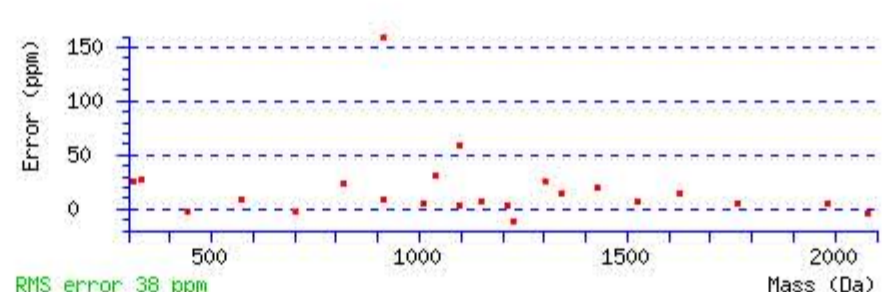
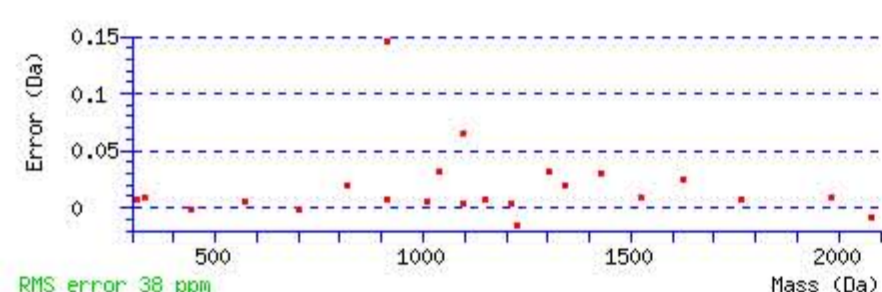
Or, Plot from to Da

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: 93 Expect: 1.4e-008
 Matches : 23/300 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	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
92.7	3304.614151	0.003625	GMADQDGLKPTIDKPSEDSPPLEMLGPR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **TQVADAK**

Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

Match to Query 18588: 1042.542028 from(522.278290,2+) rtinseconds(1281) index(51095)

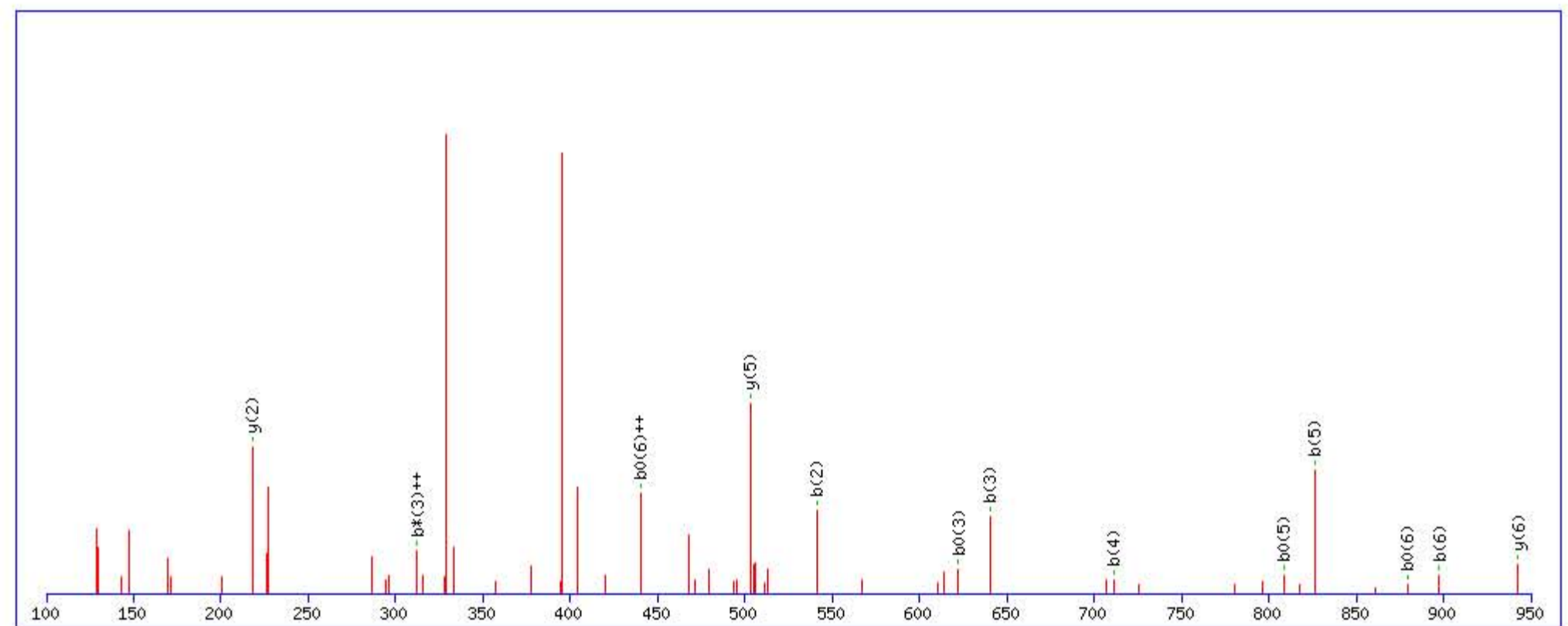
Title: Locus:1.1.1.2932.20 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

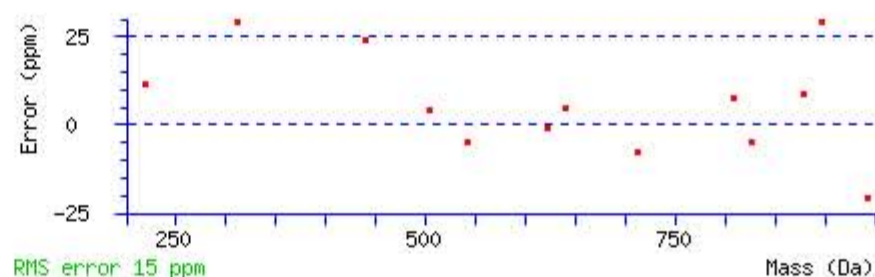
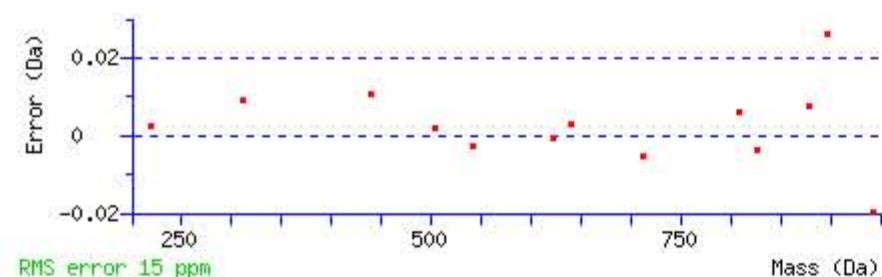
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 36 Expect: 0.0067

Matches : 13/66 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
35.7	1042.548111	-0.006083	TQVADAK
16.7	1042.548096	-0.006068	SLQADAK
10.2	1042.540726	0.001302	KPVSEVGDGR
6.7	1042.548096	-0.006068	QEAGLSK
6.1	1042.548080	-0.006052	EKEQAK
6.1	1042.544724	-0.002696	WKGIEPGEK
5.1	1042.529465	0.012563	TEAGAALPEGK
5.1	1042.540680	0.001348	EAEKRPADK
4.4	1042.529480	0.012548	TSPQPESGIK
4.4	1042.548096	-0.006068	ISAQDAK

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

MASCOT 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 20365: 1102.589708 from(552.302130,2+) rtinseconds(1642) index(53390)

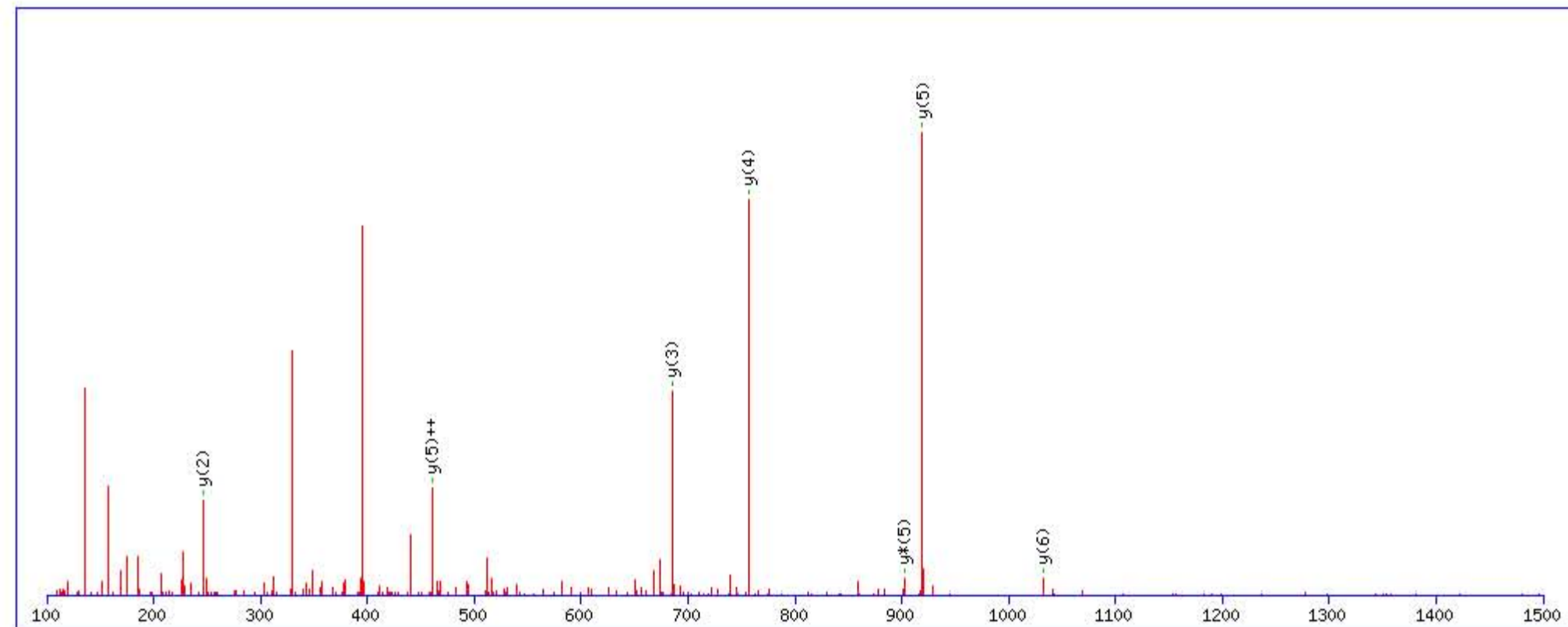
Title: Locus:1.1.1.3058.6 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

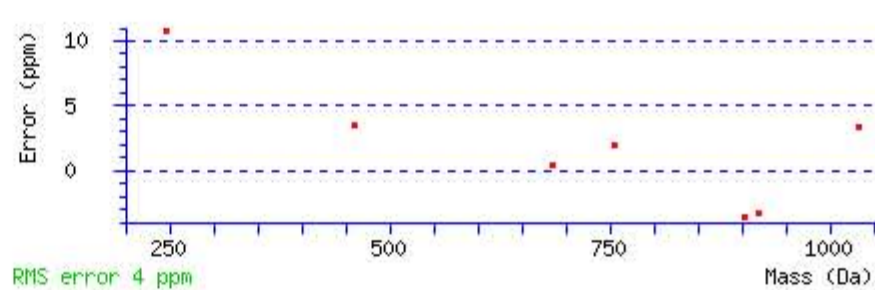
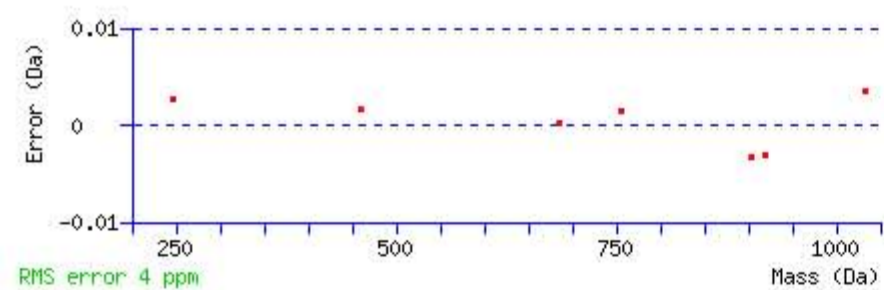
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 38 Expect: 0.0036

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
37.6	1102.595703	-0.005995	ALYAQAR
10.9	1102.602234	-0.012526	AIELGYNPVK
5.2	1102.580460	0.009248	AMVENVTLAR
4.7	1102.588333	0.001375	SPYGLTPRGR
3.6	1102.580475	0.009233	SPQMVSAIVR
3.4	1102.591660	-0.001952	AMKRLEEAR
2.8	1102.598221	-0.008513	LAGSLATDLSR
1.0	1102.598221	-0.008513	DDLKATLTAR
1.0	1102.584305	0.005403	QSSQRGLTAR
0.5	1102.602921	-0.013213	LLRQRMDR

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 25265: 1201.642988 from(601.828770,2+) rtinseconds(1473) index(52384)

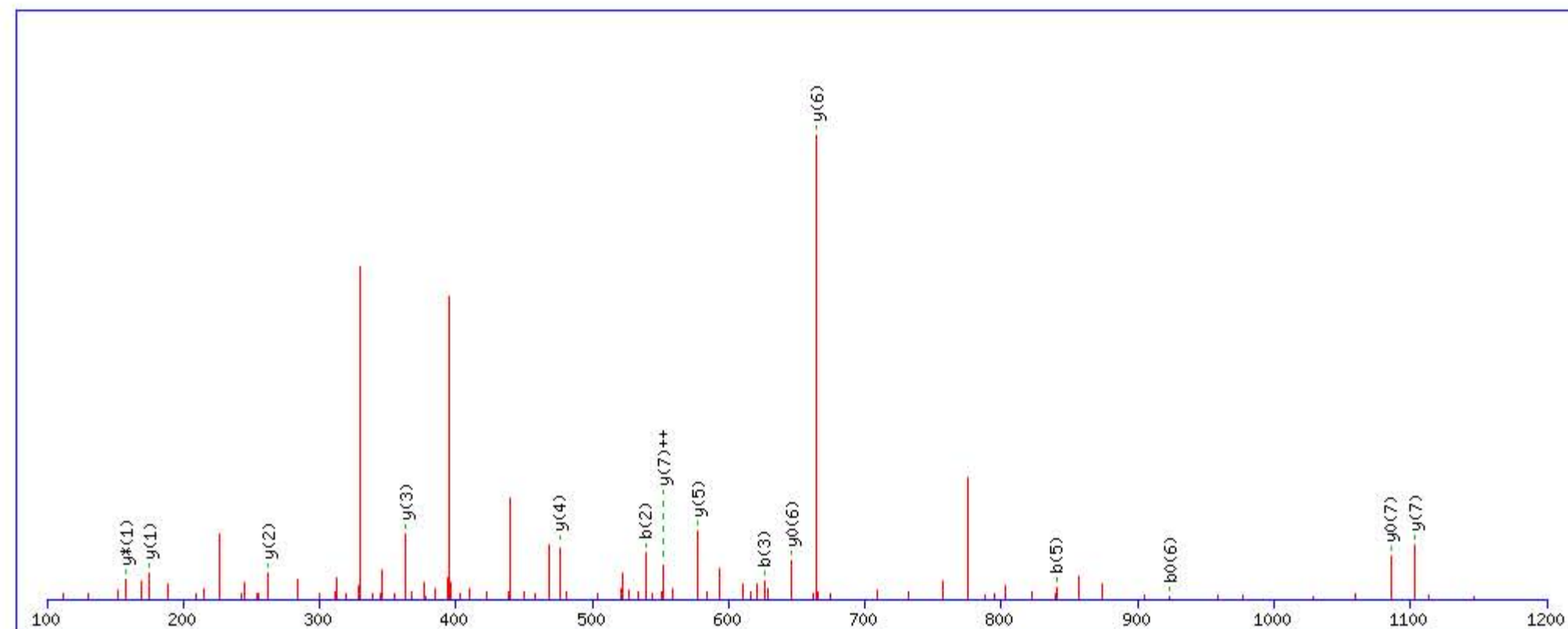
Title: Locus:1.1.1.2999.15 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

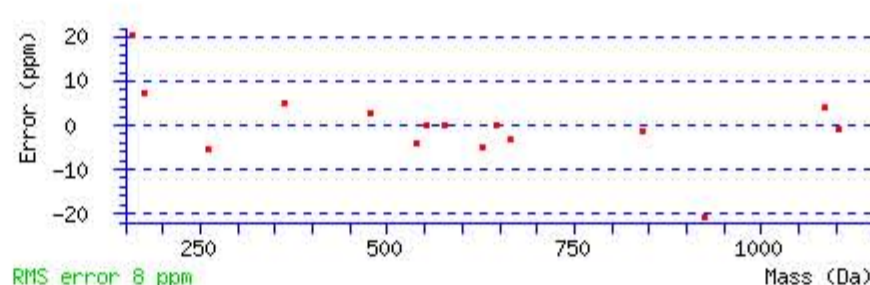
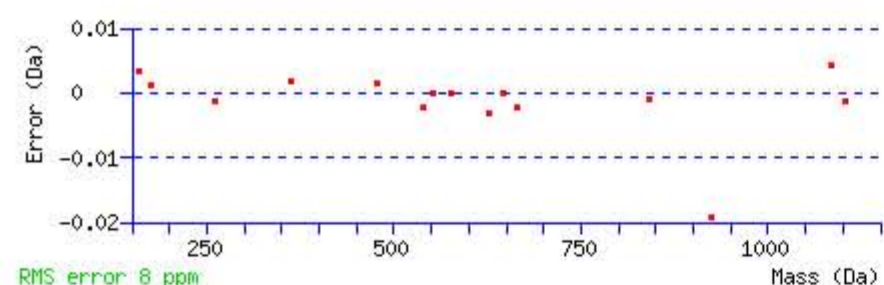
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 36 Expect: 0.0024

Matches : 15/76 fragment ions using 32 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.075690	50.541483					V							8
2	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
36.3	1201.648895	-0.005907	VQSTITSR
8.1	1201.638992	0.003996	VQPPSHAR
7.5	1201.641479	0.001509	VSIKDNQKDR
5.2	1201.630249	0.012739	KLDAEDVIGSR
2.6	1201.638992	0.003996	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 28828: 1320.663328 from(661.338940,2+) rtinseconds(1714) index(53889)

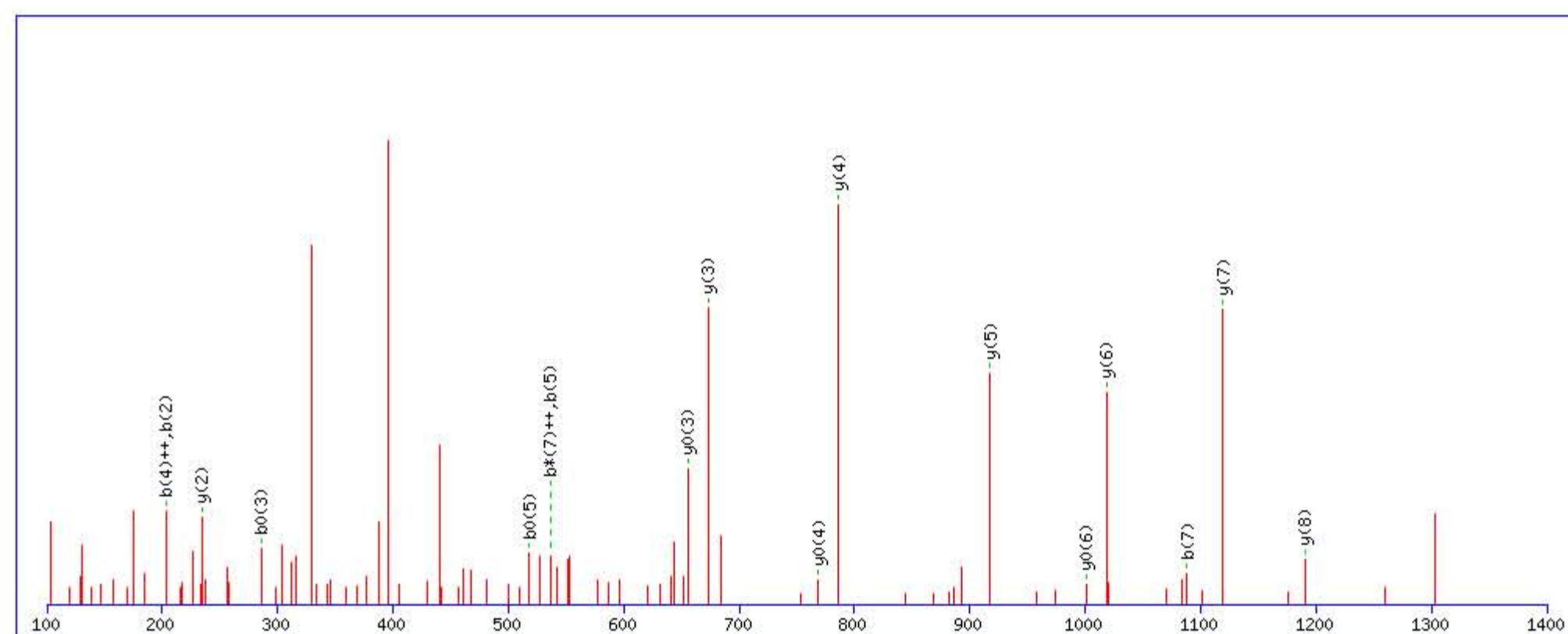
Title: Locus:1.1.1.3083.9 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1320.660370

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

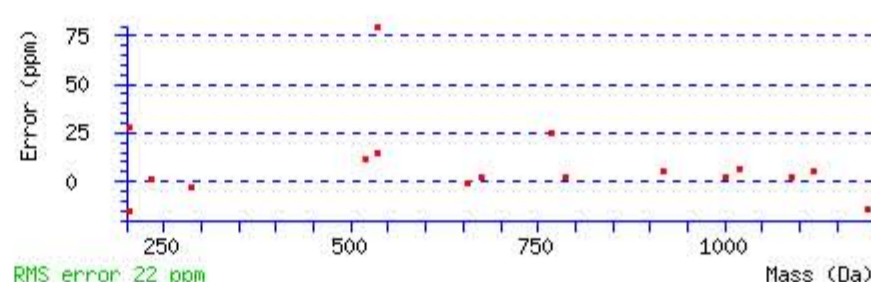
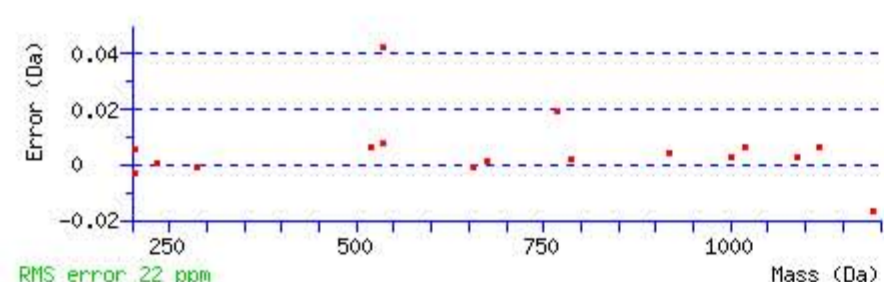
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 49 Expect: 0.00017

Matches : 17/78 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	132.047761	66.527518					M							9
2	203.084875	102.046075					A	1190.627179	595.817228	1173.600630	587.303953	1172.616614	586.811945	8
3	304.132554	152.569915			286.121989	143.564632	T	1119.590065	560.298671	1102.563516	551.785396	1101.579500	551.293388	7
4	405.180233	203.093754			387.169668	194.088472	T	1018.542386	509.774831	1001.515837	501.261557	1000.531821	500.769549	6
5	536.220718	268.613997			518.210153	259.608715	M	917.494707	459.250992	900.468158	450.737717	899.484142	450.245709	5
6	649.304782	325.156029			631.294217	316.150747	I	786.454222	393.730749	769.427673	385.217475	768.443657	384.725467	4
7	1088.530108	544.768692	1071.503559	536.255418	1070.519543	535.763410	Q	673.370158	337.188717	656.343609	328.675443	655.359593	328.183435	3
8	1175.562136	588.284706	1158.535587	579.771432	1157.551571	579.279424	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
9							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **MATTMIQSK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.3	1320.660370	0.002958	MATTMIQSK
8.5	1320.670715	-0.007387	IAPKASMAGASSSK
3.9	1320.654785	0.008543	HNLGHGHKHER
2.7	1320.663330	-0.000002	QSGNTEQKSKSK
2.3	1320.675461	-0.012133	RMRLVVDGMGR
1.3	1320.678604	-0.015276	TERHPPVSPSSK
1.1	1320.660858	0.002470	FLDCVVRAGER
0.9	1320.678574	-0.015246	EKQLRSEFER
0.6	1320.678574	-0.015246	SFRAAAAETLER

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 36816: 1548.772962 from(517.264930,3+) rtinseconds(1375) index(67098)

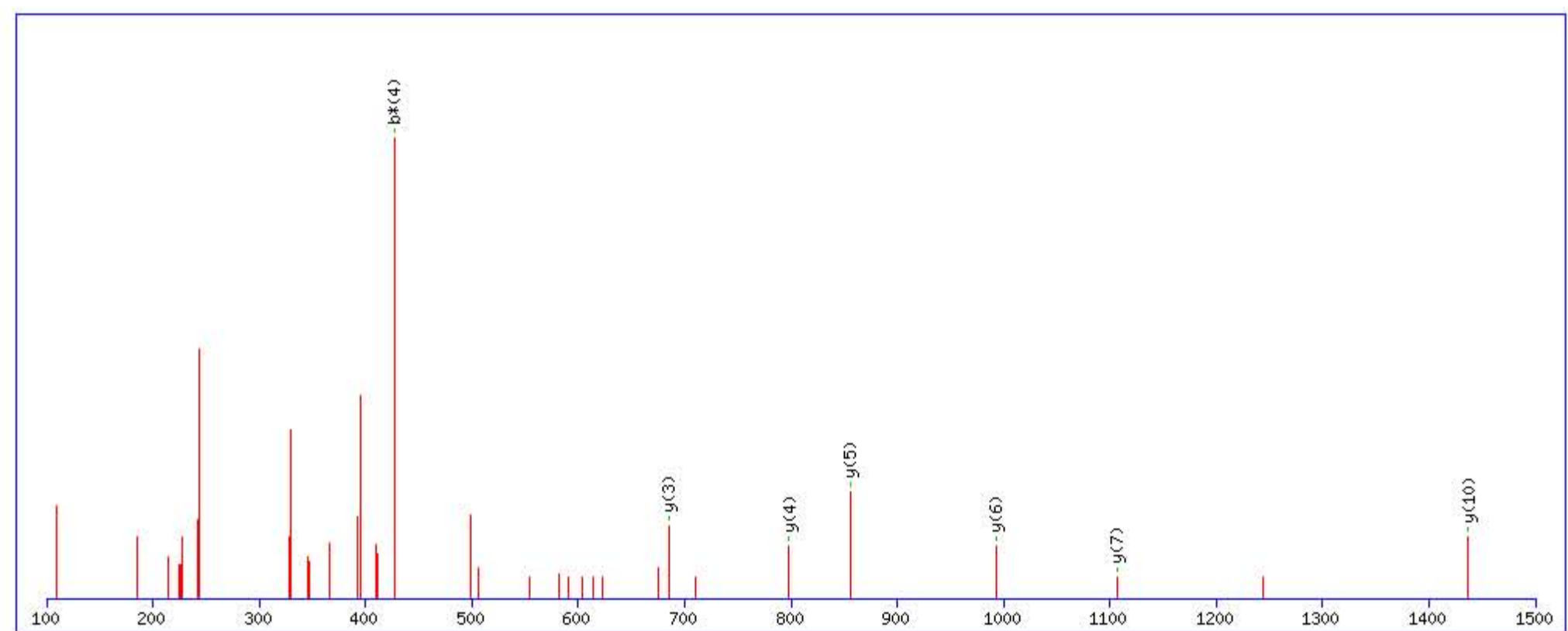
Title: Locus:1.1.1.3012.20 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1548.783066

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

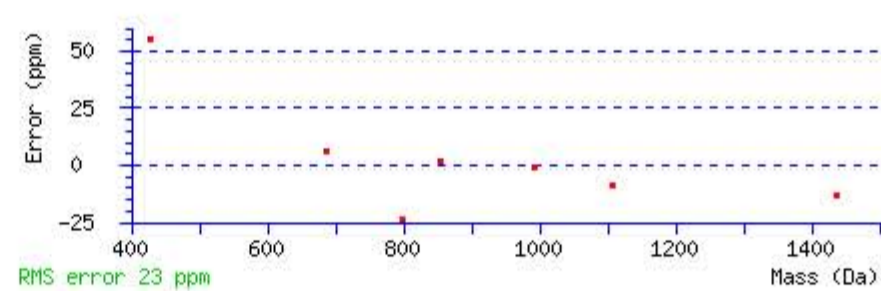
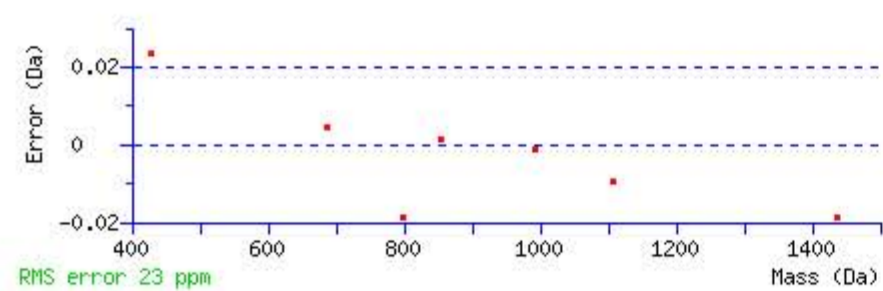
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 31 Expect: 0.019

Matches : 7/100 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							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	$M_r(\text{calc})$:	Delta	Sequence
30.8	1548.783066	-0.010104	LSNENHGIAQR

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 41095: 1647.869908 from(824.942230,2+) rtinseconds(2288) index(40473)

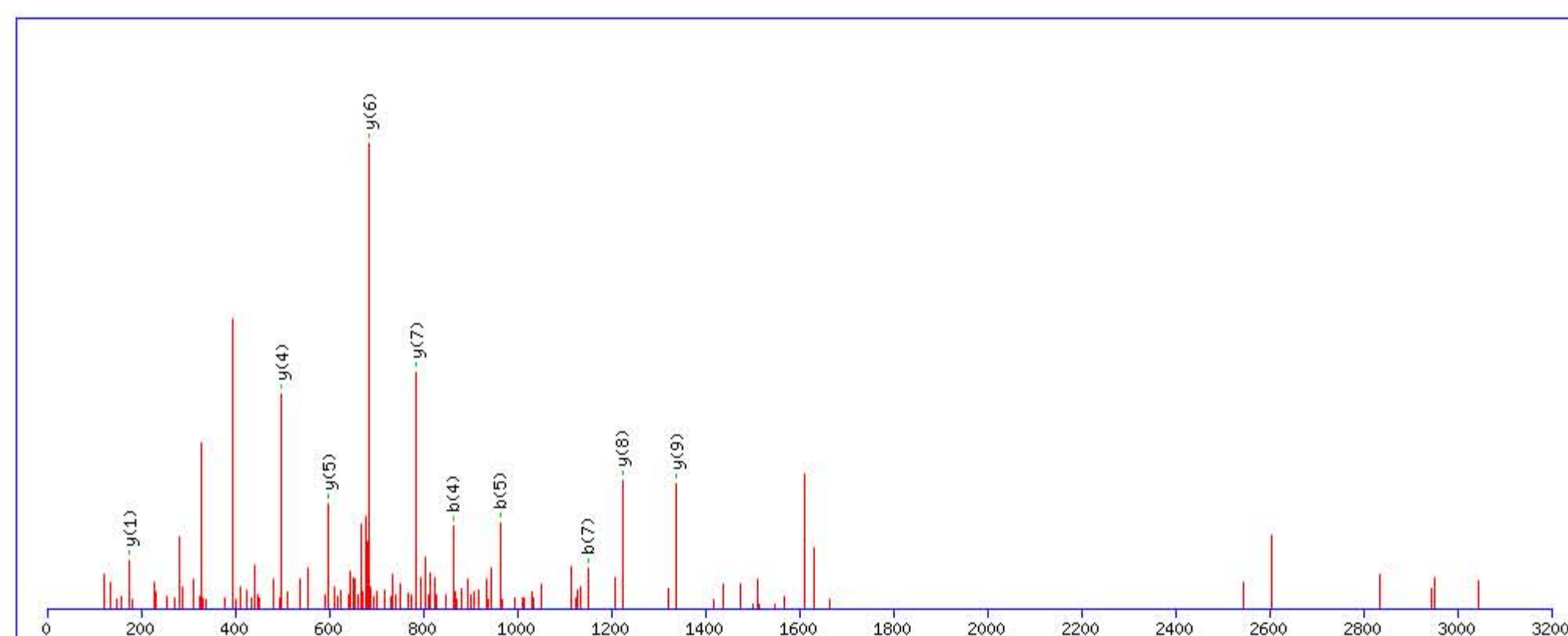
Title: Locus:1.1.1.2819.12 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

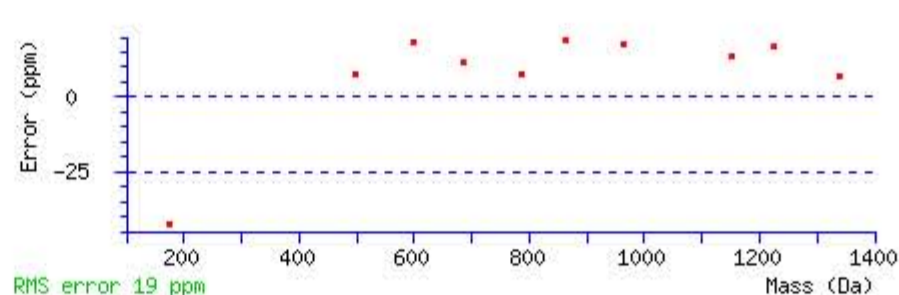
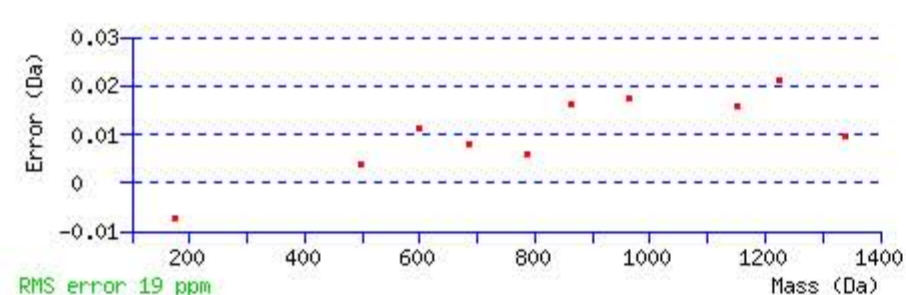
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 49 Expect: 0.00013

Matches : 10/98 fragment ions using 16 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	148.075690	74.541483					F							11
2	311.139019	156.073148					Y	1501.819547	751.413411	1484.792998	742.900137	1483.808982	742.408129	10
3	425.181946	213.094611	408.155397	204.581337			N	1338.756218	669.881747	1321.729669	661.368472	1320.745653	660.876464	9
4	864.407272	432.707274	847.380723	424.194000			Q	1224.713291	612.860283	1207.686742	604.347009	1206.702726	603.855001	8
5	963.475686	482.241481	946.449137	473.728207			V	785.487965	393.247620	768.461416	384.734346	767.477400	384.242338	7
6	1050.507714	525.757495	1033.481165	517.244221	1032.497149	516.752213	S	686.419551	343.713414	669.393002	335.200139	668.408986	334.708131	6
7	1151.555393	576.281335	1134.528844	567.768060	1133.544828	567.276052	T	599.387523	300.197399	582.360974	291.684125	581.376958	291.192117	5
8	1248.608157	624.807717	1231.581608	616.294442	1230.597592	615.802434	P	498.339844	249.673560	481.313295	241.160285			4
9	1361.692221	681.349749	1344.665672	672.836474	1343.681656	672.344466	L	401.287080	201.147178	384.260531	192.633903			3
10	1474.776285	737.891780	1457.749736	729.378506	1456.765720	728.886498	L	288.203016	144.605146	271.176467	136.091871			2
11							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **FYNQVSTPLLR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.3	1647.880676	-0.010768	FYNQVSTPLLR
7.8	1647.887878	-0.017970	TLNQQLTNHIR
5.5	1647.873260	-0.003352	AFKELPVNAQNYVR
3.1	1647.887878	-0.017970	TLNQQLTNHIR

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

MASCOT 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 41411: 1663.815792 from(555.612540,3+) rtinseconds(1629) index(53332)

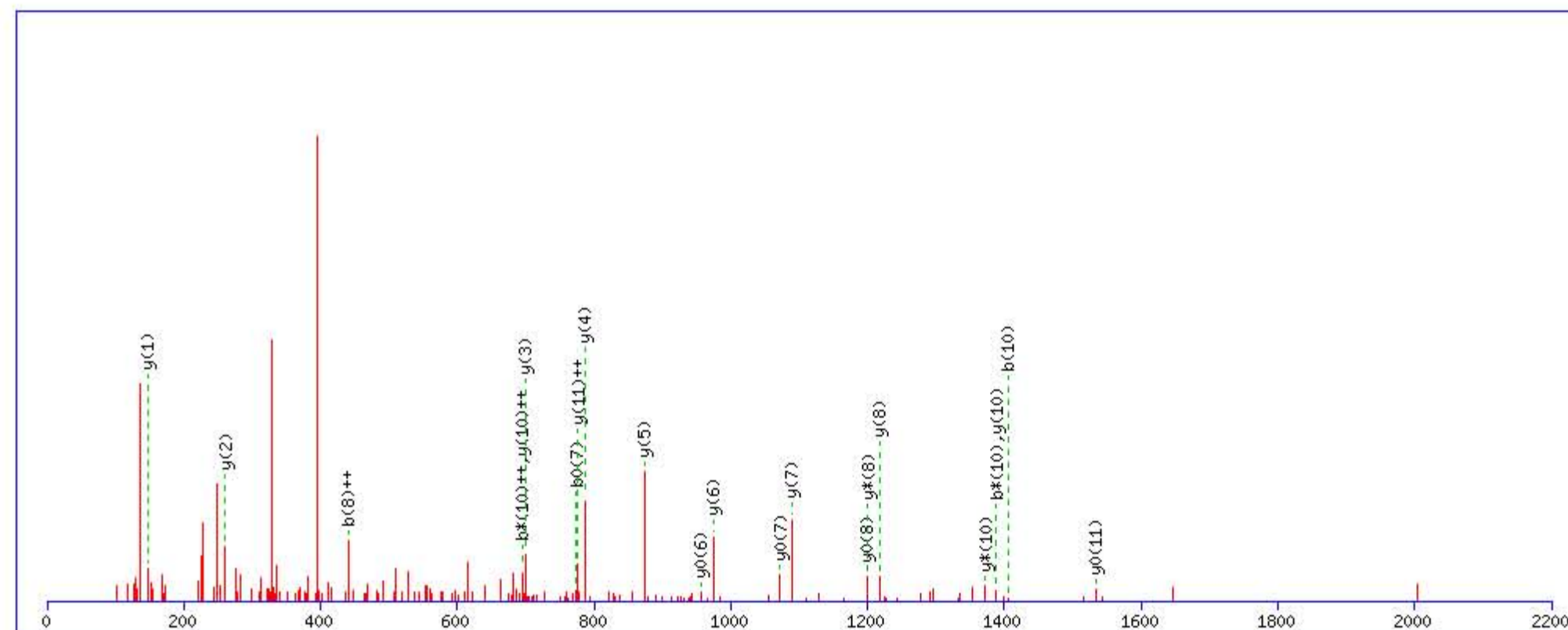
Title: Locus:1.1.1.3053.8 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

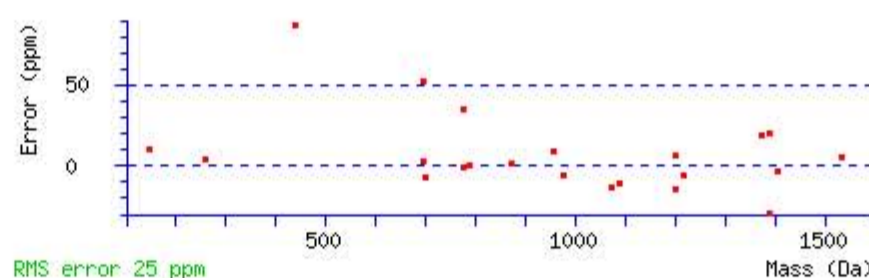
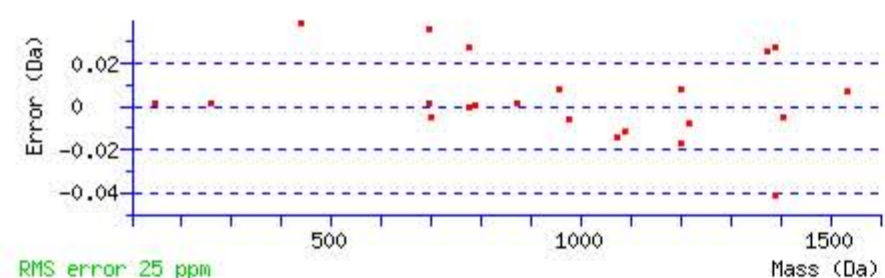
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 41 Expect: 0.0019

Matches : 22/110 fragment ions using 44 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					I							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
40.5	1663.823944	-0.008152	IYGNQDTSSQLK
2.5	1663.823944	-0.008152	IYGNQDTSSQLK

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 44315: 1778.952096 from(445.745300,4+) rtinseconds(1484) index(52465)

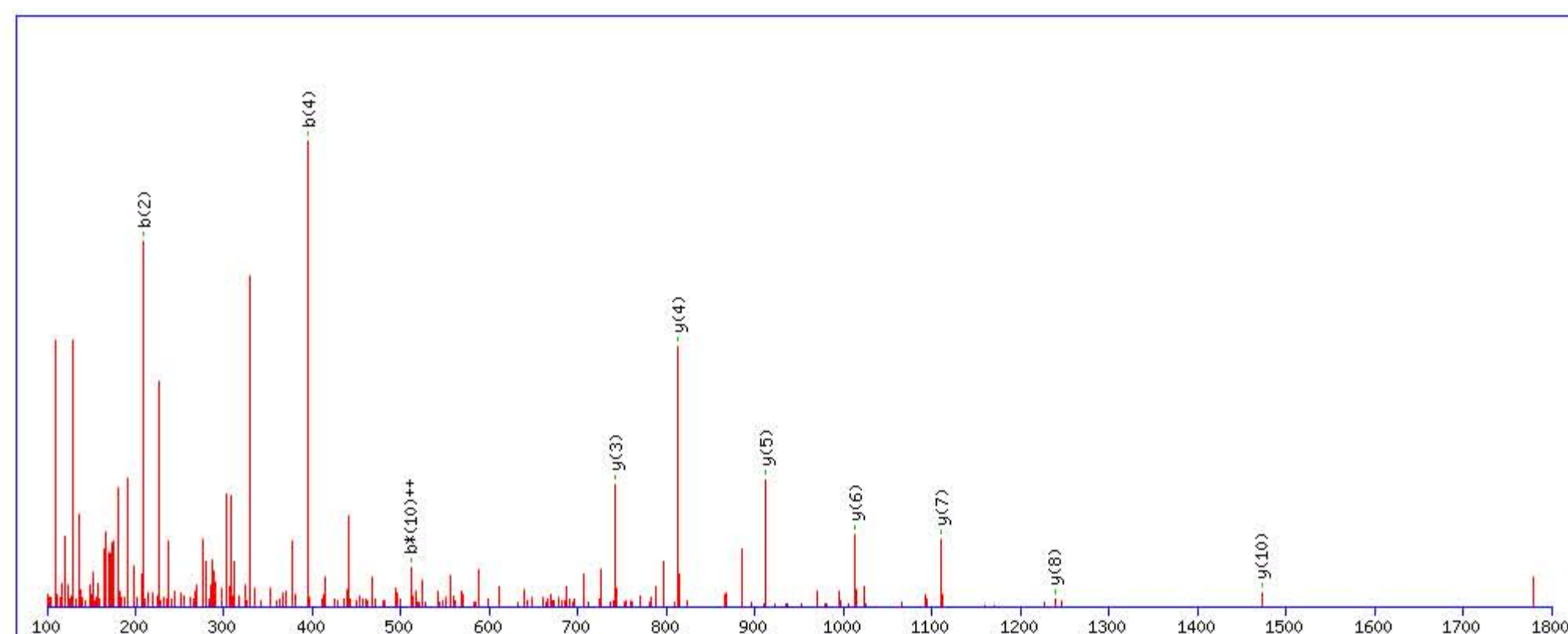
Title: Locus:1.1.1.3003.5 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

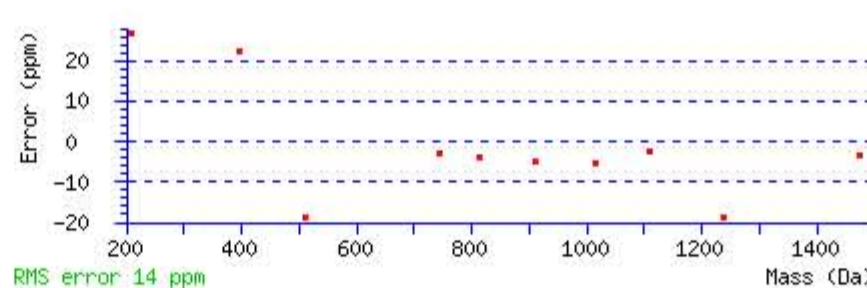
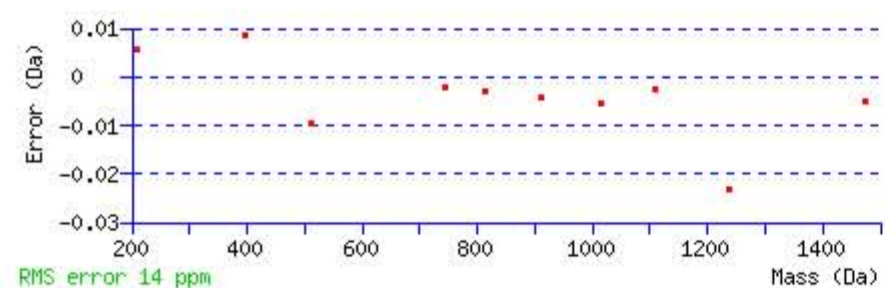
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 52 Expect: 0.00014

Matches : 10/118 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							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
51.8	1778.961395	-0.009299	AHVSFKPTVAQQR
51.8	1778.961395	-0.009299	AHVSFKPTVAQQR

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

MASCOT 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 48610: 1974.981608 from(988.498080,2+) rtinseconds(1989) index(55752)

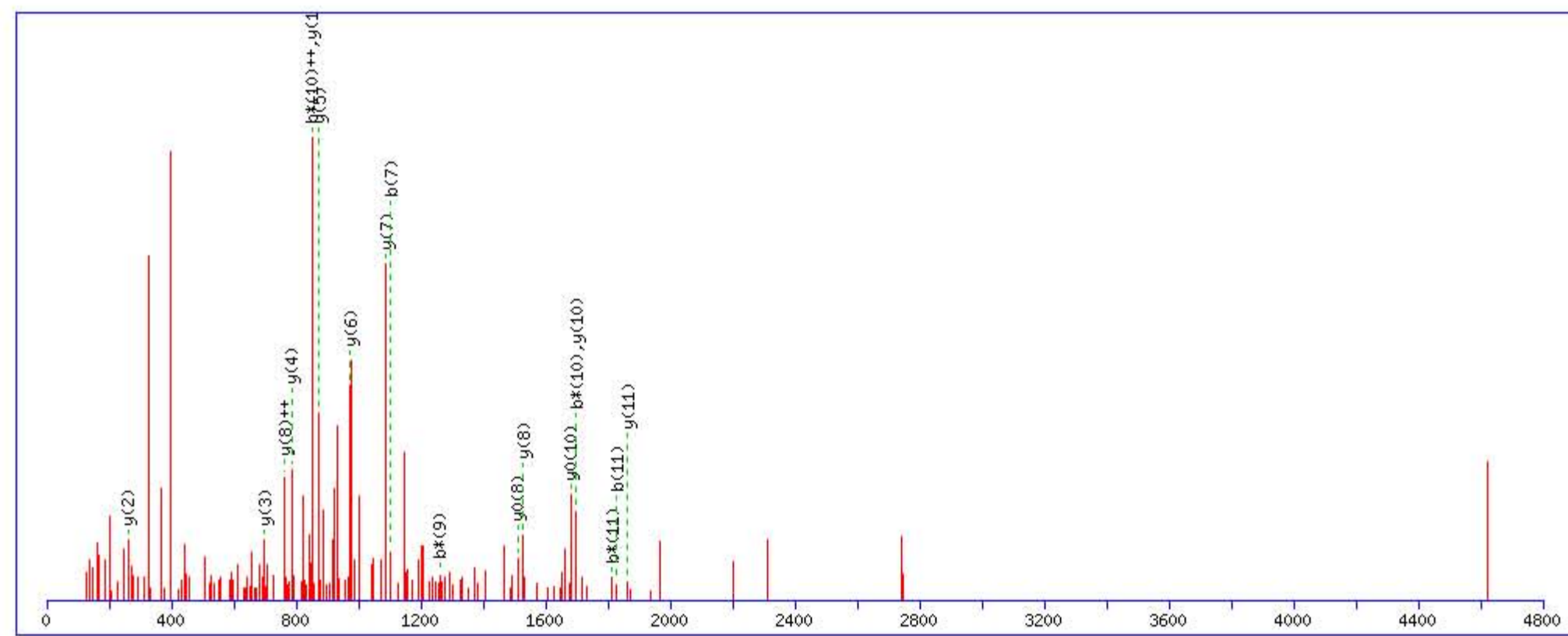
Title: Locus:1.1.1.3178.14 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1974.990692

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

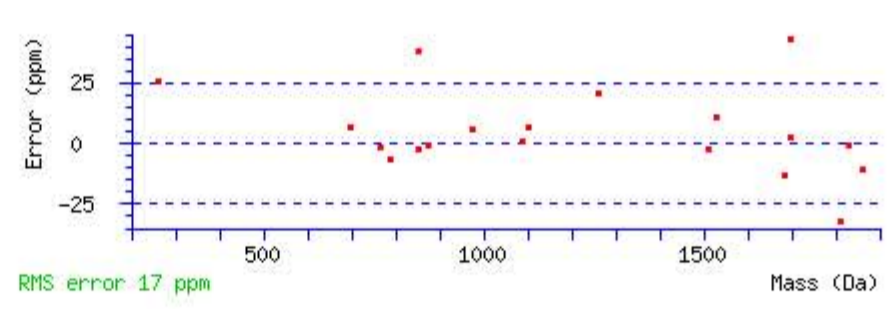
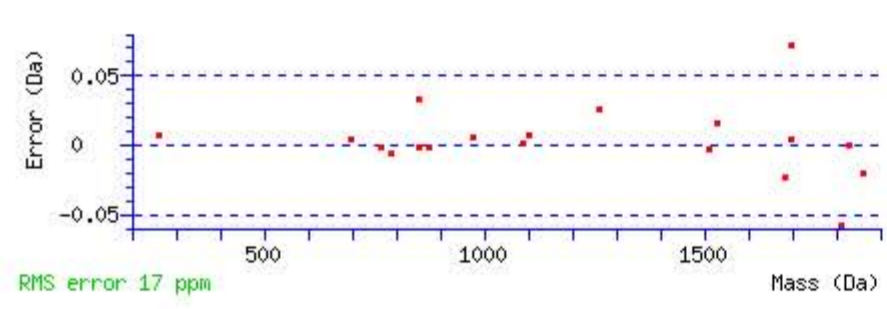
Q5 : Biotin:Thermo-21345 (Q)

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 45 Expect: 0.00026

Matches : 19/110 fragment ions using 38 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					I							12
2	277.154669	139.080973					Y	1862.913918	931.960597	1845.887369	923.447323	1844.903353	922.955315	11
3	334.176133	167.591704					G	1699.850589	850.428933	1682.824040	841.915658	1681.840024	841.423650	10
4	448.219060	224.613168	431.192511	216.099894			N	1642.829125	821.918201	1625.802576	813.404926	1624.818560	812.912918	9
5	887.444386	444.225831	870.417837	435.712557			Q	1528.786198	764.896737	1511.759649	756.383463	1510.775633	755.891455	8
6	1002.471329	501.739303	985.444780	493.226028	984.460764	492.734020	D	1089.560872	545.284074	1072.534323	536.770800	1071.550307	536.278792	7
7	1103.519008	552.263142	1086.492459	543.749868	1085.508443	543.257860	T	974.533929	487.770603	957.507380	479.257328	956.523364	478.765320	6
8	1190.551036	595.779156	1173.524487	587.265882	1172.540471	586.773874	S	873.486250	437.246763	856.459701	428.733489	855.475685	428.241481	5
9	1277.583064	639.295170	1260.556515	630.781896	1259.572499	630.289888	S	786.454222	393.730749	769.427673	385.217475	768.443657	384.725467	4
10	1716.808390	858.907833	1699.781841	850.394559	1698.797825	849.902551	Q	699.422194	350.214735	682.395645	341.701461			3
11	1829.892454	915.449865	1812.865905	906.936591	1811.881889	906.444583	L	260.196868	130.602072	243.170319	122.088797			2
12							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **IYGNQDTSSQLK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.8	1974.990692	-0.009084	IYGNQDTSSQLK
6.6	1974.993820	-0.012212	VVQYNINTEELYSYLK

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 51803: 2090.117736 from(523.536710,4+) rtinseconds(1745) index(54118)

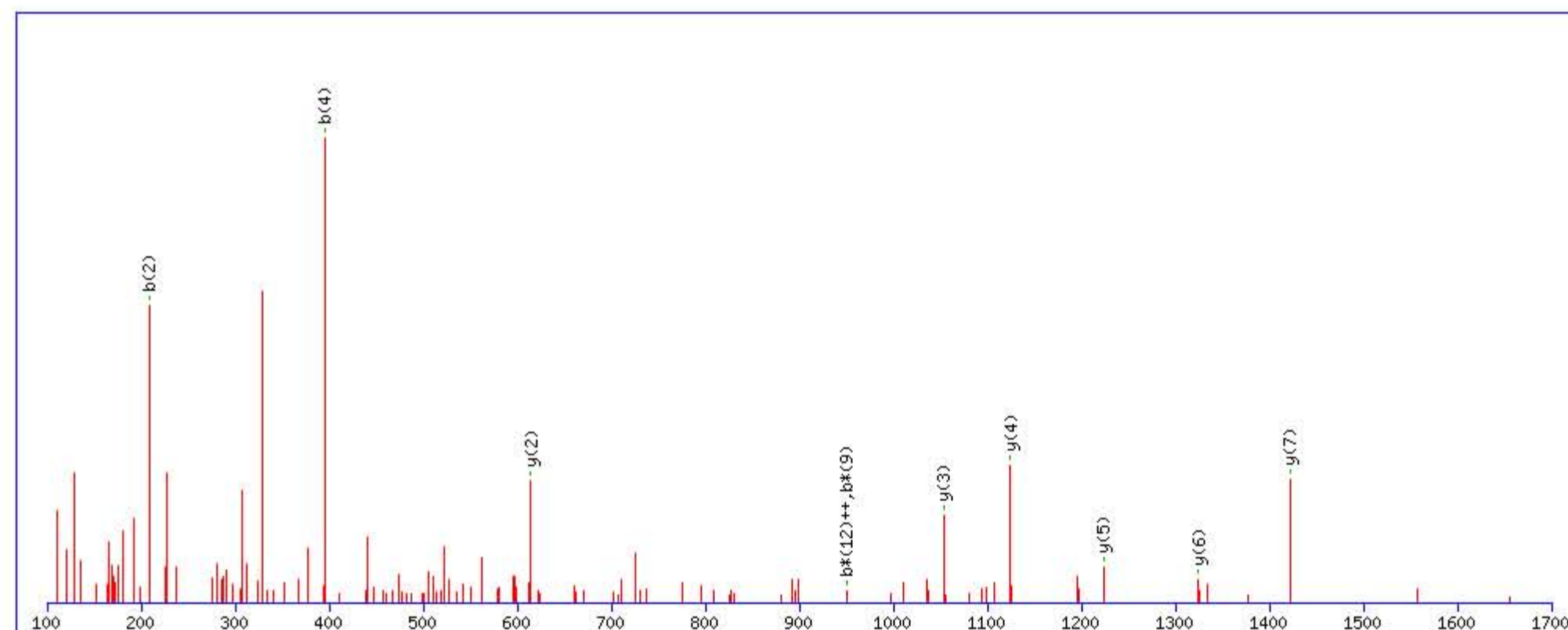
Title: Locus:1.1.1.3094.8 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2090.128143

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

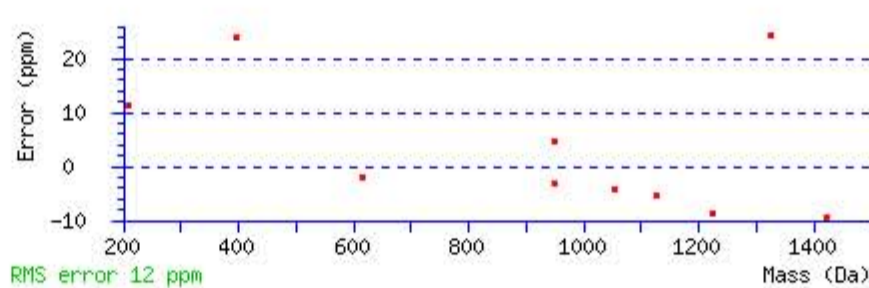
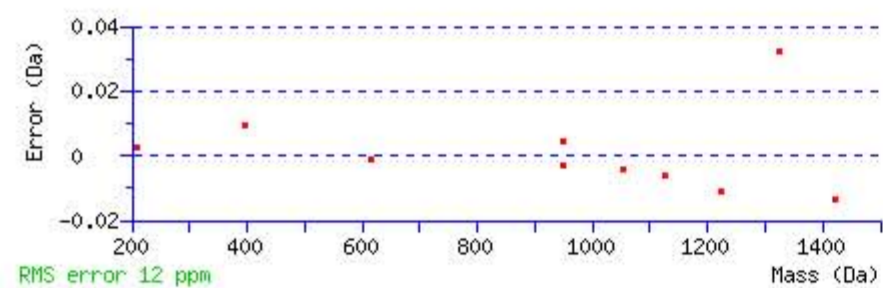
Q11 : Biotin:Thermo-21345 (Q)

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 31 Expect: 0.02

Matches : 10/118 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	2020.098306	1010.552791	2003.071757	1002.039517	2002.087741	1001.547509	12
3	308.171716	154.589496					V	1883.039394	942.023335	1866.012845	933.510061	1865.028829	933.018053	11
4	395.203744	198.105510			377.193179	189.100227	S	1783.970980	892.489128	1766.944431	883.975854	1765.960415	883.483846	10
5	542.272158	271.639717			524.261593	262.634435	F	1696.938952	848.973114	1679.912403	840.459840	1678.928387	839.967832	9
6	670.367121	335.687199	653.340572	327.173924	652.356556	326.681916	K	1549.870538	775.438907	1532.843989	766.925633	1531.859973	766.433625	8
7	767.419885	384.213581	750.393336	375.700306	749.409320	375.208298	P	1421.775575	711.391426	1404.749026	702.878151	1403.765010	702.386143	7
8	868.467564	434.737420	851.441015	426.224146	850.456999	425.732138	T	1324.722811	662.865044	1307.696262	654.351769	1306.712246	653.859761	6
9	967.535978	484.271627	950.509429	475.758353	949.525413	475.266345	V	1223.675132	612.341204	1206.648583	603.827930			5
10	1038.573092	519.790184	1021.546543	511.276910	1020.562527	510.784902	A	1124.606718	562.806997	1107.580169	554.293723			4
11	1477.798418	739.402847	1460.771869	730.889573	1459.787853	730.397565	Q	1053.569604	527.288440	1036.543055	518.775166			3
12	1917.023744	959.015510	1899.997195	950.502236	1899.013179	950.010228	Q	614.344278	307.675777	597.317729	299.162503			2
13							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **AHVSFKPTVAQQR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.8	2090.128143	-0.010407	AHVSFKPTVAQQR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **AEDHFSVIDFNQNR**

Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

Match to Query 52228: 2115.029388 from(1058.521970,2+) rtinseconds(2274) index(57484)

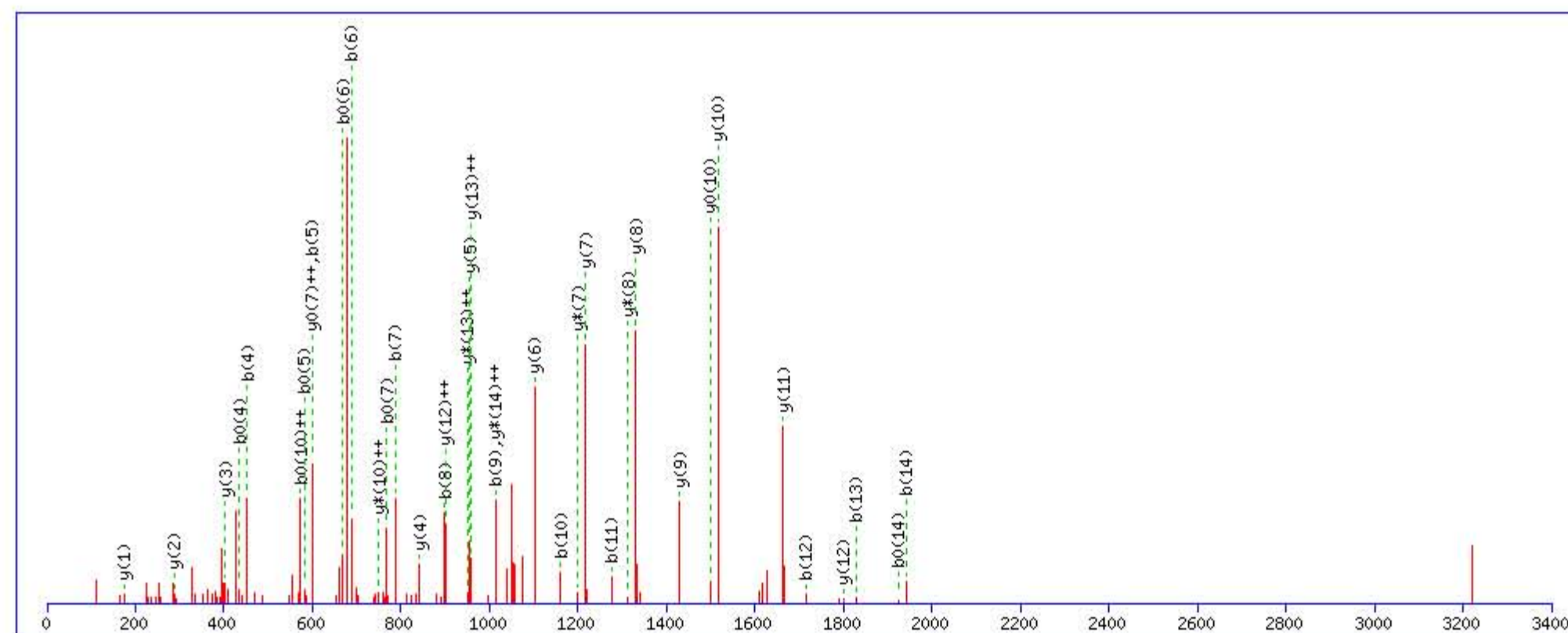
Title: Locus:1.1.1.3277.7 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

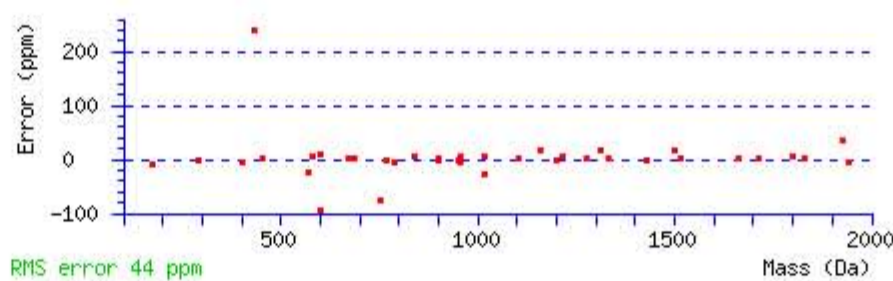
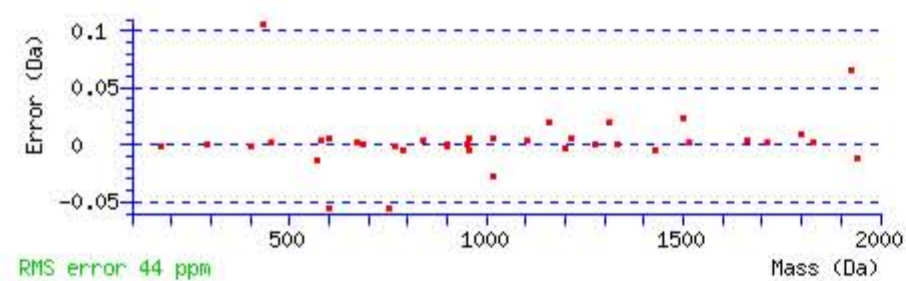
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 69 Expect: 2.2e-006

Matches : 38/134 fragment ions using 67 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	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 [AEDHFSVIDFNQNR](#)

(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	2115.020752	0.008636	AEDHFSVIDFNQNR
8.3	2115.033981	-0.004593	ESADRQVLMQEEIHK
5.1	2115.060501	-0.031113	NNKVNVLQNFMYTMLR
2.1	2115.027237	0.002151	KYSDYIKGSNLDAPEPYR

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

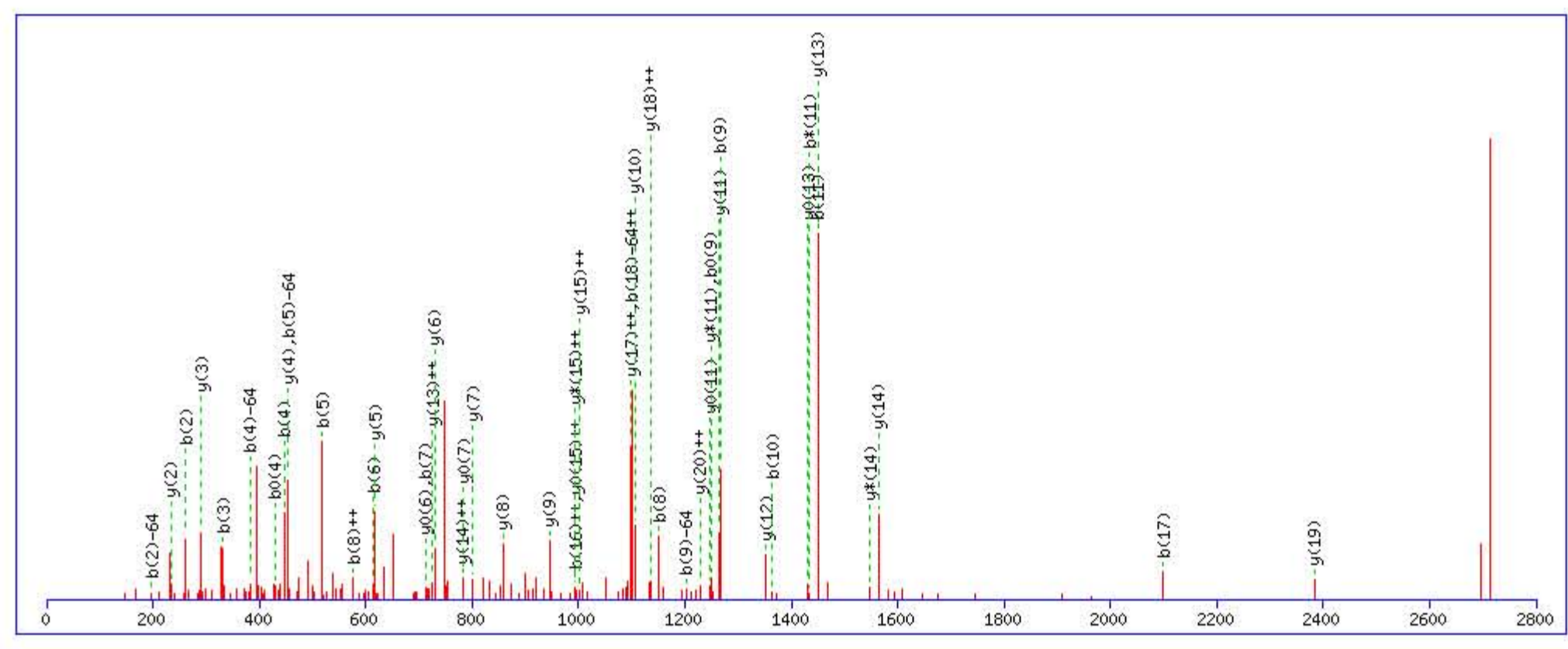
MASCOT Search Results

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

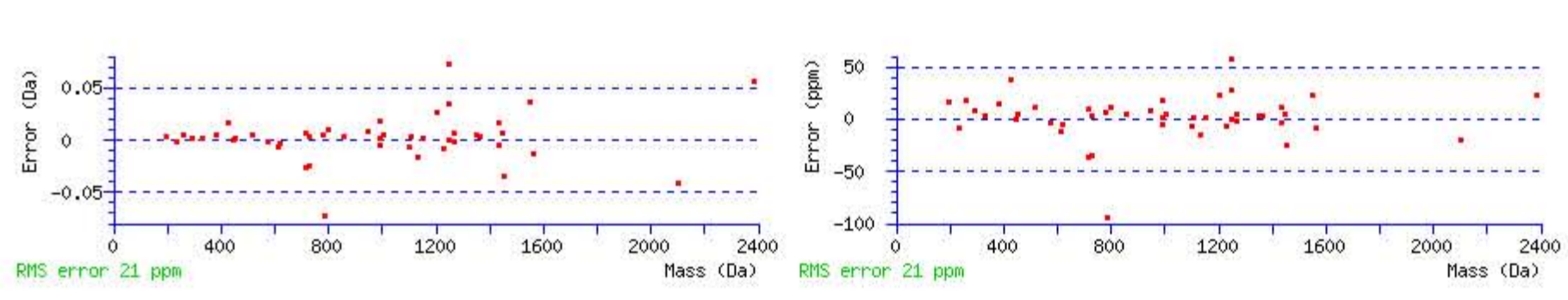
Match to Query 62124: 2714.188002 from(905.736610,3+) rtinseconds(1994) index(55781)
 Title: Locus:1.1.1.3180.10 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 2714.184860
 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
 Q8 : Biotin:Thermo-21345 (Q)
 Ions Score: 83 Expect: 2.9e-008
 Matches : 49/336 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	148.042676	74.524976					M							22
2	261.126740	131.067008					L	2568.156746	1284.582011	2551.130197	1276.068736	2550.146181	1275.576728	21
3	332.163854	166.585565					A	2455.072682	1228.039979	2438.046133	1219.526704	2437.062117	1219.034696	20
4	447.190797	224.099036			429.180232	215.093754	D	2384.035568	1192.521422	2367.009019	1184.008147	2366.025003	1183.516139	19
5	518.227911	259.617594			500.217346	250.612311	A	2269.008625	1135.007950	2251.982076	1126.494676	2250.998060	1126.002668	18
6	615.280675	308.143976			597.270110	299.138693	P	2197.971511	1099.489393	2180.944962	1090.976119	2179.960946	1090.484111	17
7	712.333439	356.670358			694.322874	347.665075	P	2100.918747	1050.963011	2083.892198	1042.449737	2082.908182	1041.957729	16
8	1151.558765	576.283021	1134.532216	567.769746	1133.548200	567.277738	Q	2003.865983	1002.436630	1986.839434	993.923355	1985.855418	993.431347	15
9	1266.585708	633.796492	1249.559159	625.283218	1248.575143	624.791210	D	1564.640657	782.823967	1547.614108	774.310692	1546.630092	773.818684	14
10	1363.638472	682.322874	1346.611923	673.809600	1345.627907	673.317592	P	1449.613714	725.310495	1432.587165	716.797221	1431.603149	716.305213	13
11	1450.670500	725.838888	1433.643951	717.325614	1432.659935	716.833606	S	1352.560950	676.784113	1335.534401	668.270839	1334.550385	667.778831	12
12	1610.701149	805.854213	1593.674600	797.340938	1592.690584	796.848930	C	1265.528922	633.268099	1248.502373	624.754825	1247.518357	624.262817	11
13	1770.731798	885.869537	1753.705249	877.356263	1752.721233	876.864255	C	1105.498273	553.252775	1088.471724	544.739500	1087.487708	544.247492	10
14	1857.763826	929.385551	1840.737277	920.872277	1839.753261	920.380269	S	945.467624	473.237450	928.441075	464.724176	927.457059	464.232168	9
15	1914.785290	957.896283	1897.758741	949.383009	1896.774725	948.891001	G	858.435596	429.721436	841.409047	421.208162	840.425031	420.716154	8
16	1985.822404	993.414840	1968.795855	984.901566	1967.811839	984.409558	A	801.414132	401.210704	784.387583	392.697430	783.403567	392.205422	7
17	2098.906468	1049.956872	2081.879919	1041.443597	2080.895903	1040.951590	L	730.377018	365.692147	713.350469	357.178873	712.366453	356.686865	6
18	2261.969797	1131.488537	2244.943248	1122.975262	2243.959232	1122.483254	Y	617.292954	309.150115	600.266405	300.636841	599.282389	300.144833	5
19	2425.033126	1213.020201	2408.006577	1204.506927	2407.022561	1204.014919	Y	454.229625	227.618451	437.203076	219.105176	436.219060	218.613168	4
20	2482.054590	1241.530933	2465.028041	1233.017658	2464.044025	1232.525651	G	291.166296	146.086786	274.139747	137.573512	273.155731	137.081504	3
21	2569.086618	1285.046947	2552.060069	1276.533673	2551.076053	1276.041665	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
22							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
82.7	2714.184860	0.003142	MLADAPPQDPSCCSGALYYGSK

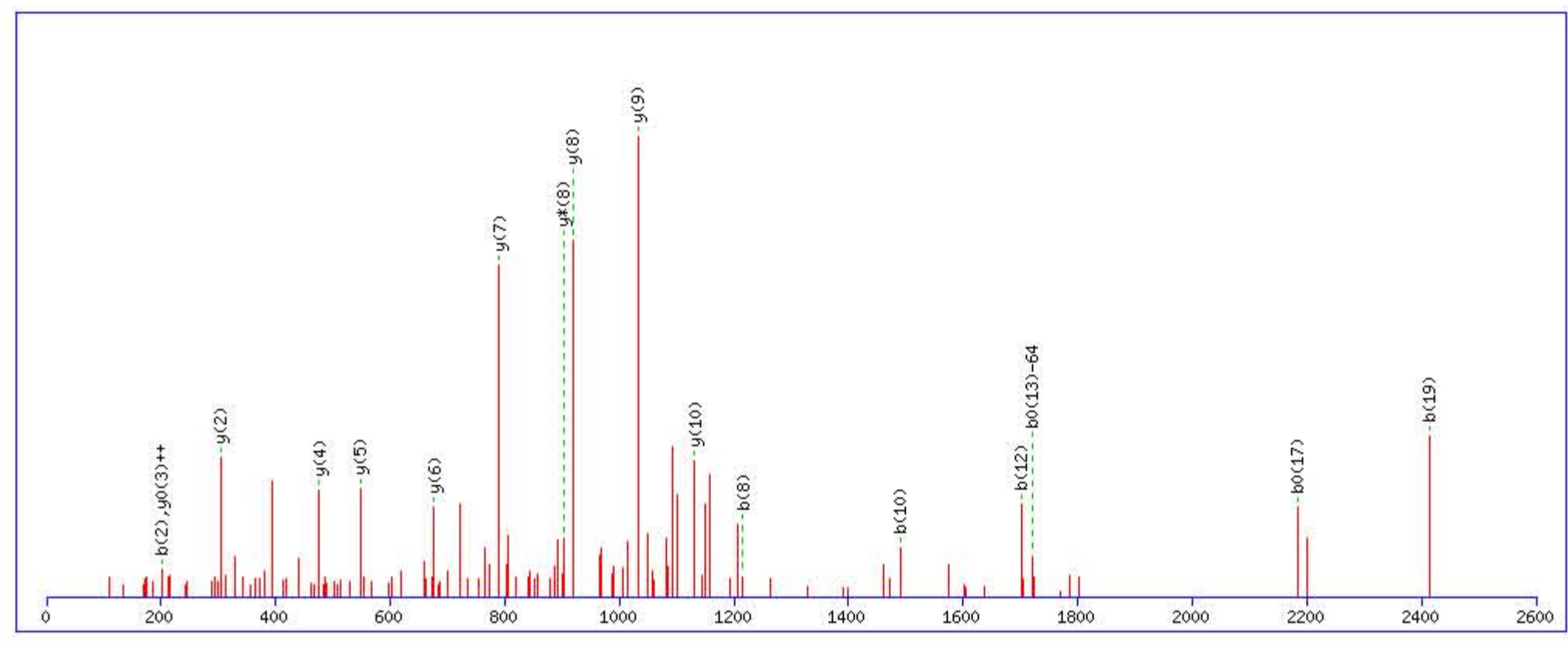
MASCOT Mascot Search Results

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

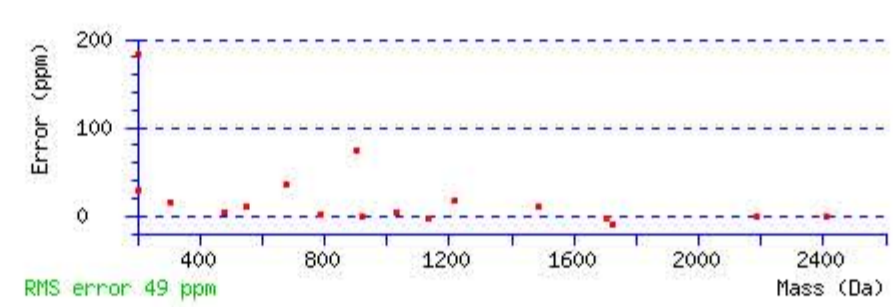
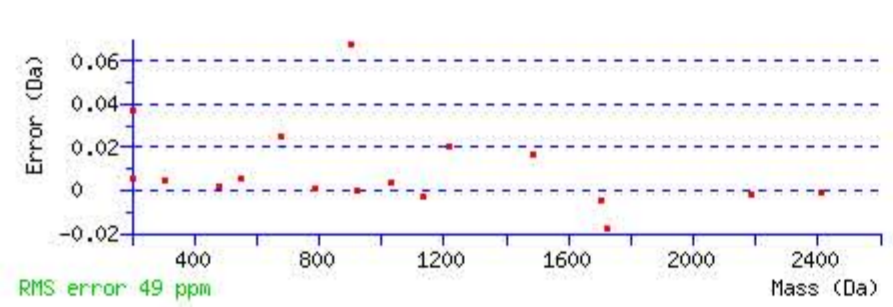
Match to Query 70424: 3443.751976 from(861.945270,4+) rtinseconds(2654) index(59508)
 Title: Locus:1.1.1.3409.12 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 59 Expect: 3.5e-005
 Matches : 17/478 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	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
58.9	3443.742859	0.009117	SILQMSLDHHIVTPLTSLVIENEAGDER

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **NVQFNYPHTSVTDVDTQNNFHNHYFGGSEIVVAGK**

Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

Match to Query 73518: 3993.916776 from(999.486470,4+) rtinseconds(2378) index(58030)

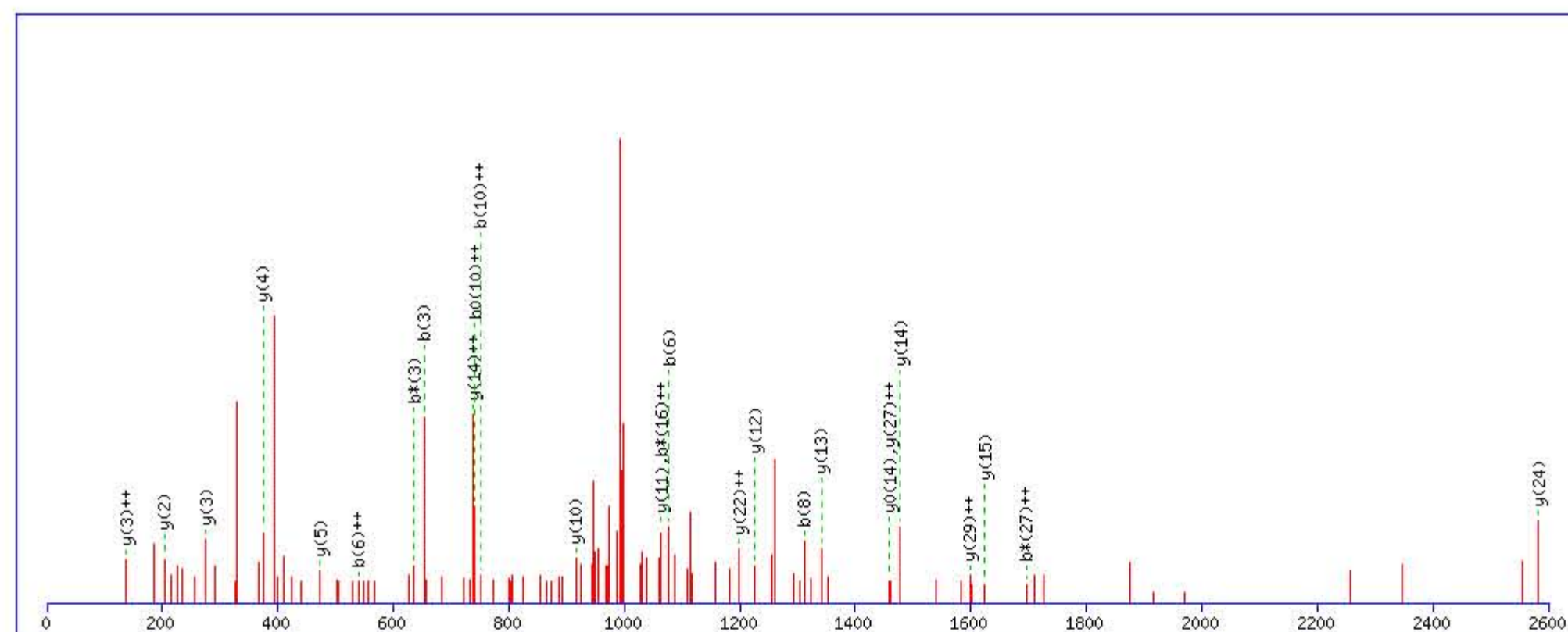
Title: Locus:1.1.1.3313.18 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

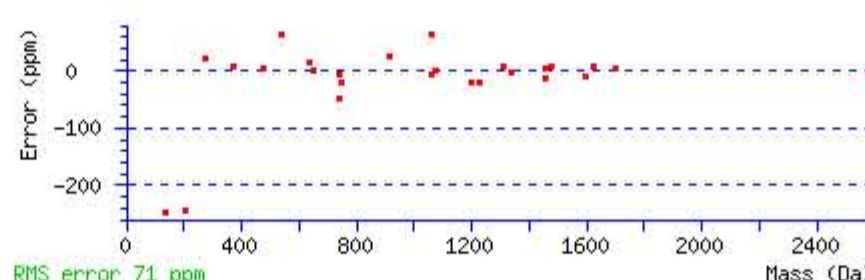
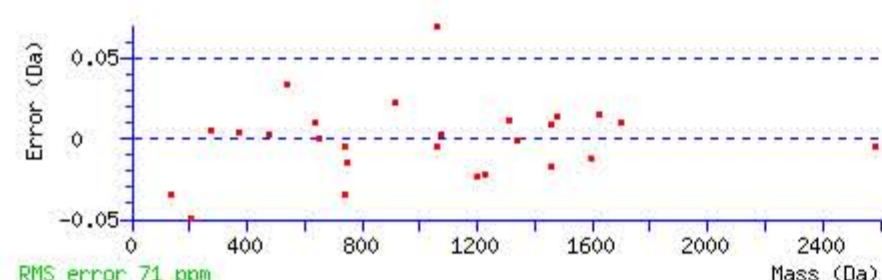
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 25 Expect: 0.061

Matches : 26/356 fragment ions using 69 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	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 [NVQFNYPHTSVTDVDTQNNFHNHYFGGSEIVVAGK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.3	3993.910858	0.005918	NVQFNYPHTSVTDVDTQNNFHNHYFGGSEIVVAGK
10.6	3993.910858	0.005918	NVQFNYPHTSVTDVDTQNNFHNHYFGGSEIVVAGK

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **GHVSFKPSLDQQR**

Found in **ITIH3_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2

Match to Query 44911: 1808.928042 from(603.983290,3+) rtinseconds(1584) index(53098)

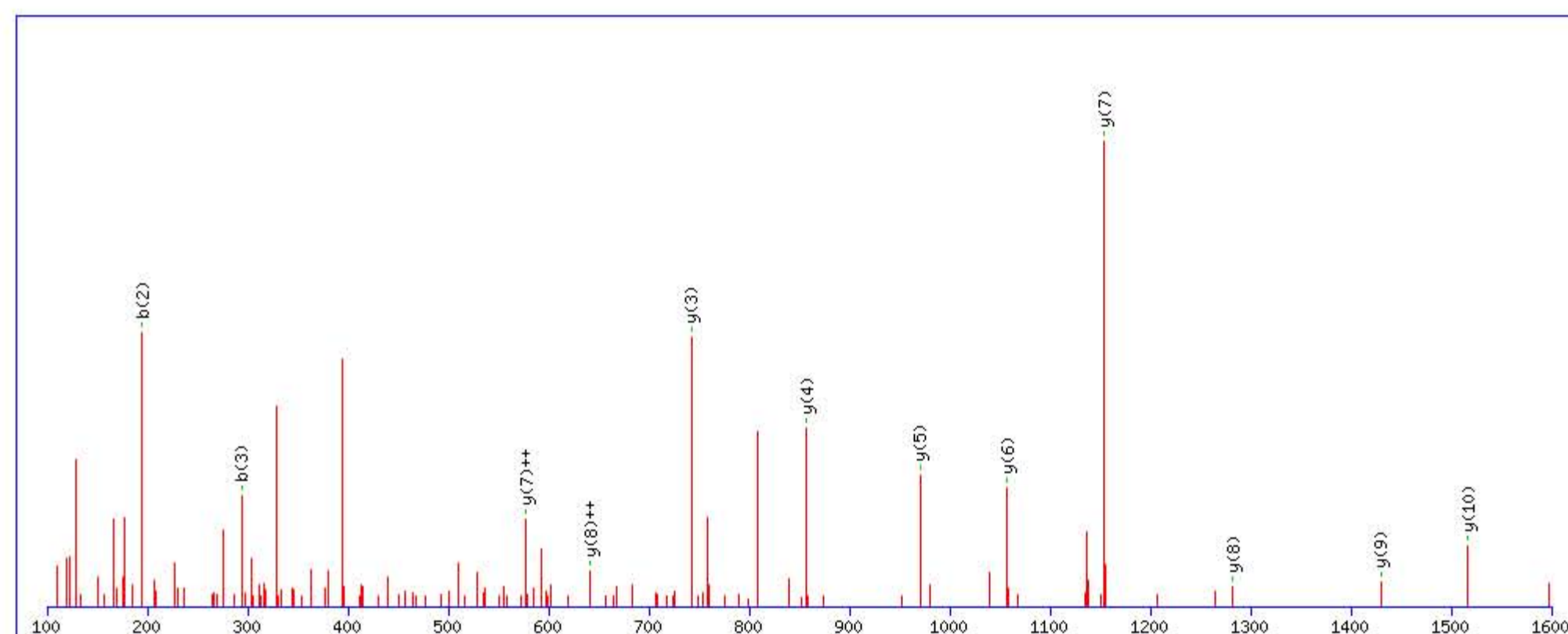
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Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1808.935577

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

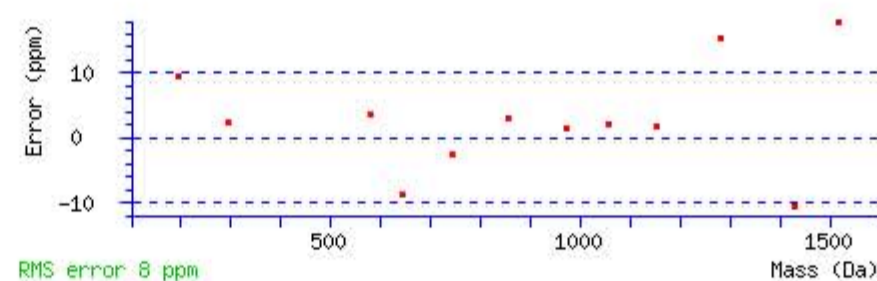
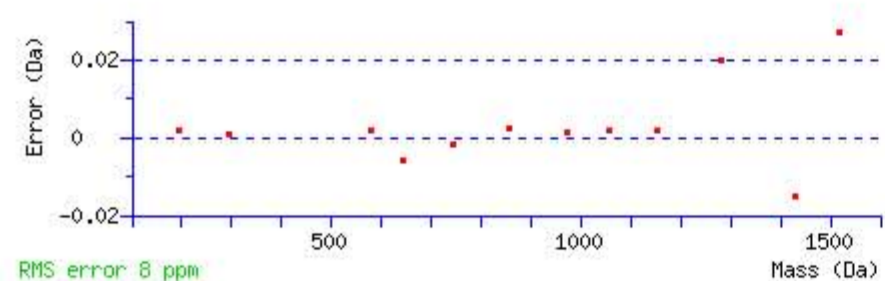
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 69 Expect: 3.5e-006

Matches : 12/122 fragment ions using 14 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.028740	29.518008					G							13
2	195.087652	98.047464					H	1752.921386	876.964331	1735.894837	868.451057	1734.910821	867.959049	12
3	294.156066	147.581671					V	1615.862474	808.434875	1598.835925	799.921601	1597.851909	799.429593	11
4	381.188094	191.097685			363.177529	182.092403	S	1516.794060	758.900668	1499.767511	750.387394	1498.783495	749.895386	10
5	528.256508	264.631892			510.245943	255.626610	F	1429.762032	715.384654	1412.735483	706.871380	1411.751467	706.379372	9
6	656.351471	328.679374	639.324922	320.166099	638.340906	319.674091	K	1282.693618	641.850447	1265.667069	633.337173	1264.683053	632.845165	8
7	753.404235	377.205756	736.377686	368.692481	735.393670	368.200473	P	1154.598655	577.802966	1137.572106	569.289691	1136.588090	568.797683	7
8	840.436263	420.721770	823.409714	412.208495	822.425698	411.716487	S	1057.545891	529.276584	1040.519342	520.763309	1039.535326	520.271301	6
9	953.520327	477.263802	936.493778	468.750527	935.509762	468.258519	L	970.513863	485.760570	953.487314	477.247295	952.503298	476.755287	5
10	1068.547270	534.777273	1051.520721	526.263999	1050.536705	525.771991	D	857.429799	429.218538	840.403250	420.705263	839.419234	420.213255	4
11	1196.605848	598.806562	1179.579299	590.293288	1178.595283	589.801279	Q	742.402856	371.705066	725.376307	363.191792			3
12	1635.831174	818.419225	1618.804625	809.905951	1617.820609	809.413943	Q	614.344278	307.675777	597.317729	299.162503			2
13							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **GHVSFKPSLDQQR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.5	1808.935577	-0.007535	GHVSFKPSLDQQR
68.5	1808.935577	-0.007535	GHVSFKPSLDQQR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **QLGLPGPPDVPDHAAYHPFR**

Found in **ITIH4_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4

Match to Query 59865: 2494.256296 from(624.571350,4+) rtinseconds(2160) index(6787)

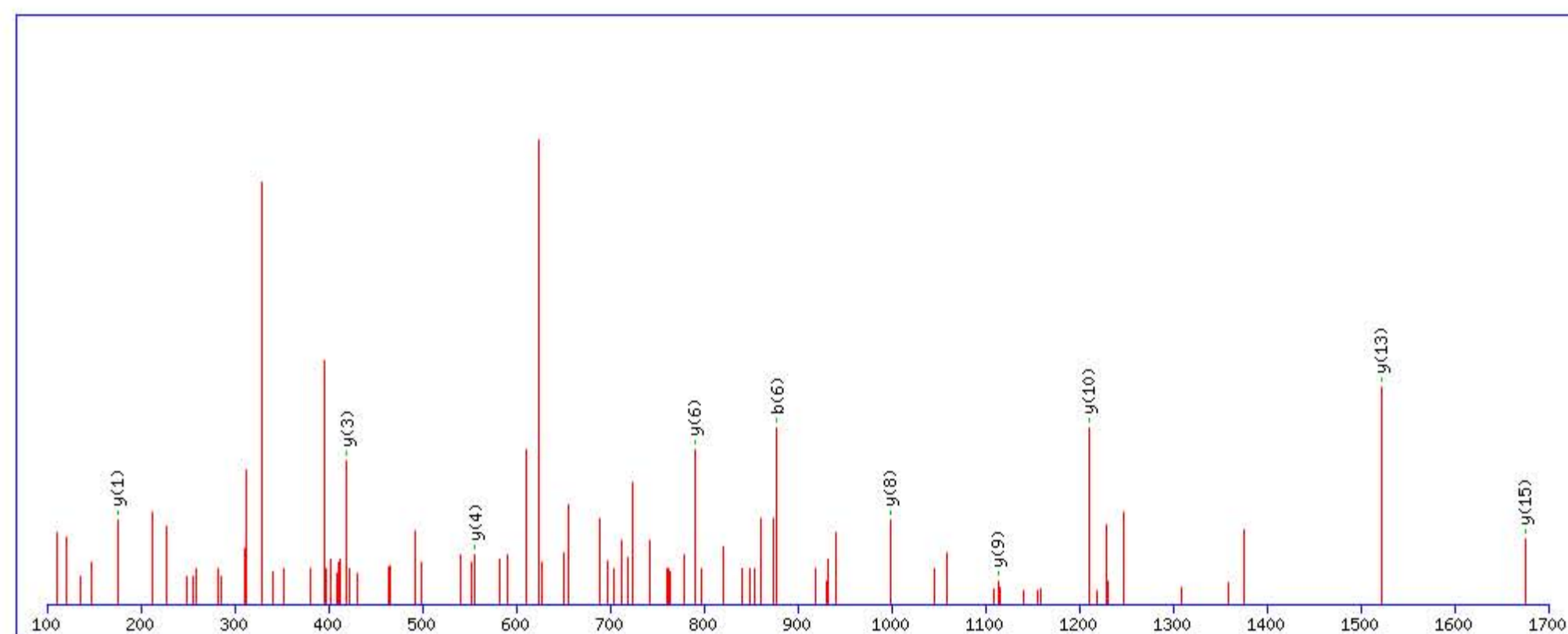
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Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2494.257980

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

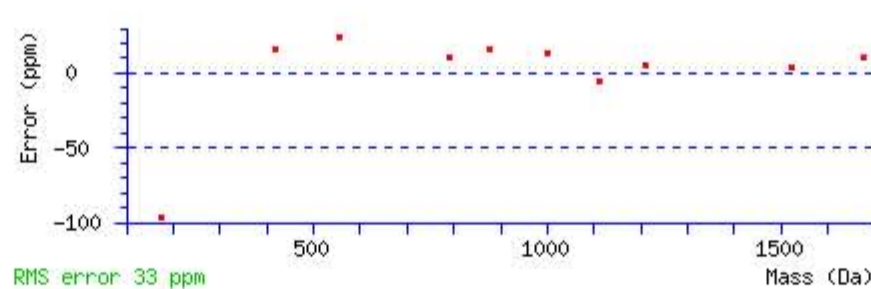
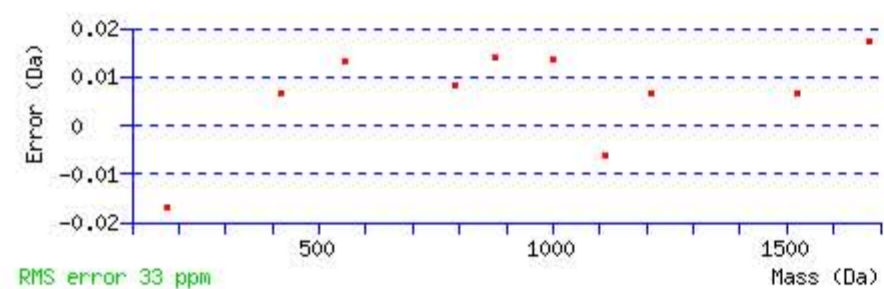
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 55 Expect: 2.9e-005

Matches : 10/196 fragment ions using 15 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	440.232602	220.619939	423.206053	212.106664			Q							20
2	553.316666	277.161971	536.290117	268.648697			L	2056.039923	1028.523599	2039.013374	1020.010325	2038.029358	1019.518317	19
3	610.338130	305.672703	593.311581	297.159429			G	1942.955859	971.981568	1925.929310	963.468293	1924.945294	962.976285	18
4	723.422194	362.214735	706.395645	353.701461			L	1885.934395	943.470836	1868.907846	934.957561	1867.923830	934.465553	17
5	820.474958	410.741117	803.448409	402.227843			P	1772.850331	886.928804	1755.823782	878.415529	1754.839766	877.923521	16
6	877.496422	439.251849	860.469873	430.738575			G	1675.797567	838.402422	1658.771018	829.889147	1657.787002	829.397139	15
7	974.549186	487.778231	957.522637	479.264957			P	1618.776103	809.891690	1601.749554	801.378415	1600.765538	800.886407	14
8	1071.601950	536.304613	1054.575401	527.791339			P	1521.723339	761.365308	1504.696790	752.852033	1503.712774	752.360025	13
9	1186.628893	593.818085	1169.602344	585.304810	1168.618328	584.812802	D	1424.670575	712.838926	1407.644026	704.325651	1406.660010	703.833643	12
10	1285.697307	643.352292	1268.670758	634.839017	1267.686742	634.347009	V	1309.643632	655.325454	1292.617083	646.812180	1291.633067	646.320172	11
11	1382.750071	691.878674	1365.723522	683.365399	1364.739506	682.873391	P	1210.575218	605.791247	1193.548669	597.277973	1192.564653	596.785964	10
12	1497.777014	749.392145	1480.750465	740.878871	1479.766449	740.386863	D	1113.522454	557.264865	1096.495905	548.751591	1095.511889	548.259582	9
13	1634.835926	817.921601	1617.809377	809.408327	1616.825361	808.916319	H	998.495511	499.751393	981.468962	491.238119			8
14	1705.873040	853.440158	1688.846491	844.926884	1687.862475	844.434876	A	861.436599	431.221937	844.410050	422.708663			7
15	1776.910154	888.958715	1759.883605	880.445441	1758.899589	879.953433	A	790.399485	395.703380	773.372936	387.190106			6
16	1939.973483	970.490380	1922.946934	961.977105	1921.962918	961.485097	Y	719.362371	360.184823	702.335822	351.671549			5
17	2077.032395	1039.019836	2060.005846	1030.506561	2059.021830	1030.014553	H	556.299042	278.653159	539.272493	270.139884			4
18	2174.085159	1087.546218	2157.058610	1079.032943	2156.074594	1078.540935	P	419.240130	210.123703	402.213581	201.610428			3
19	2321.153573	1161.080424	2304.127024	1152.567150	2303.143008	1152.075142	F	322.187366	161.597321	305.160817	153.084046			2
20							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **QLGLPGPPDVPDHAAYHPFR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.3	2494.257980	-0.001684	QLGLPGPPDVPDHAAYHPFR
7.0	2494.256424	-0.000128	SPHRESLPGLSSTATPGNPALYSR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **YNSQNQSNNQFVLYR**

Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

Match to Query 53636: 2185.040228 from(1093.527390,2+) rtinseconds(2134) index(39516)

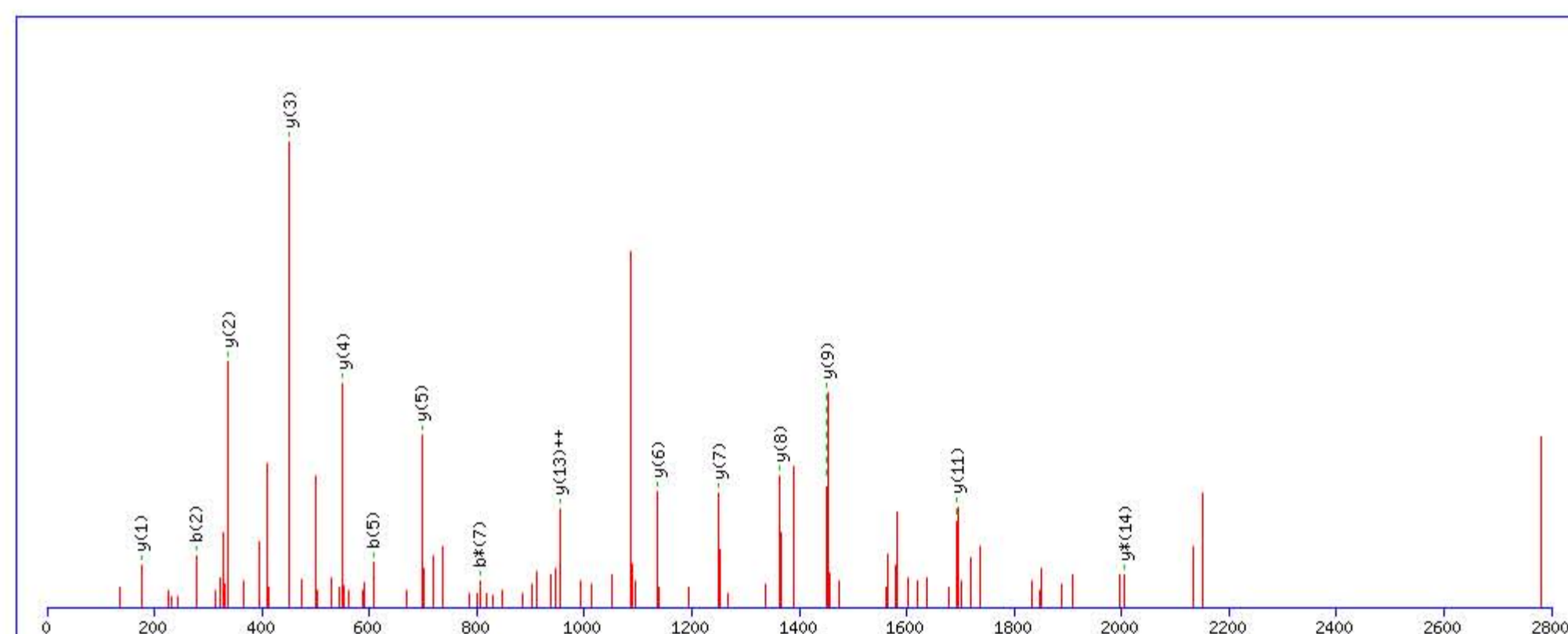
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Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2185.037445

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

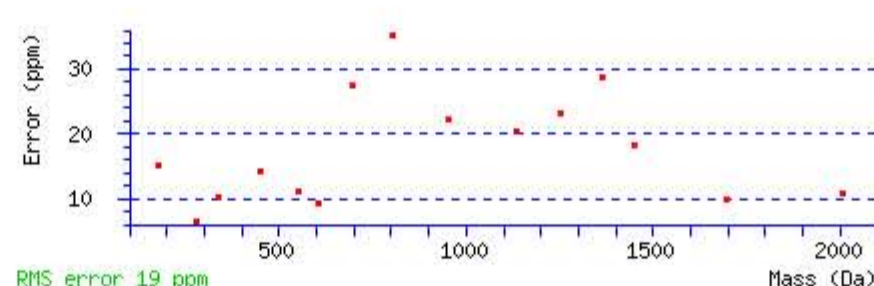
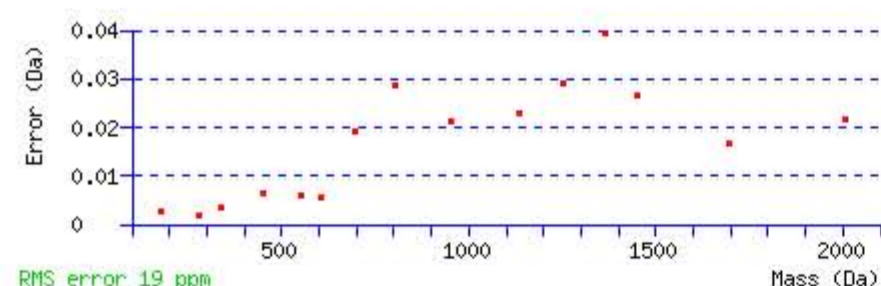
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 42 Expect: 0.0011

Matches : 15/146 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
42.4	2185.037445	0.002783	YNSQNQSNNQFVLYR
12.1	2185.037445	0.002783	YNSQNQSNNQFVLYR
10.6	2185.037445	0.002783	YNSQNQSNNQFVLYR

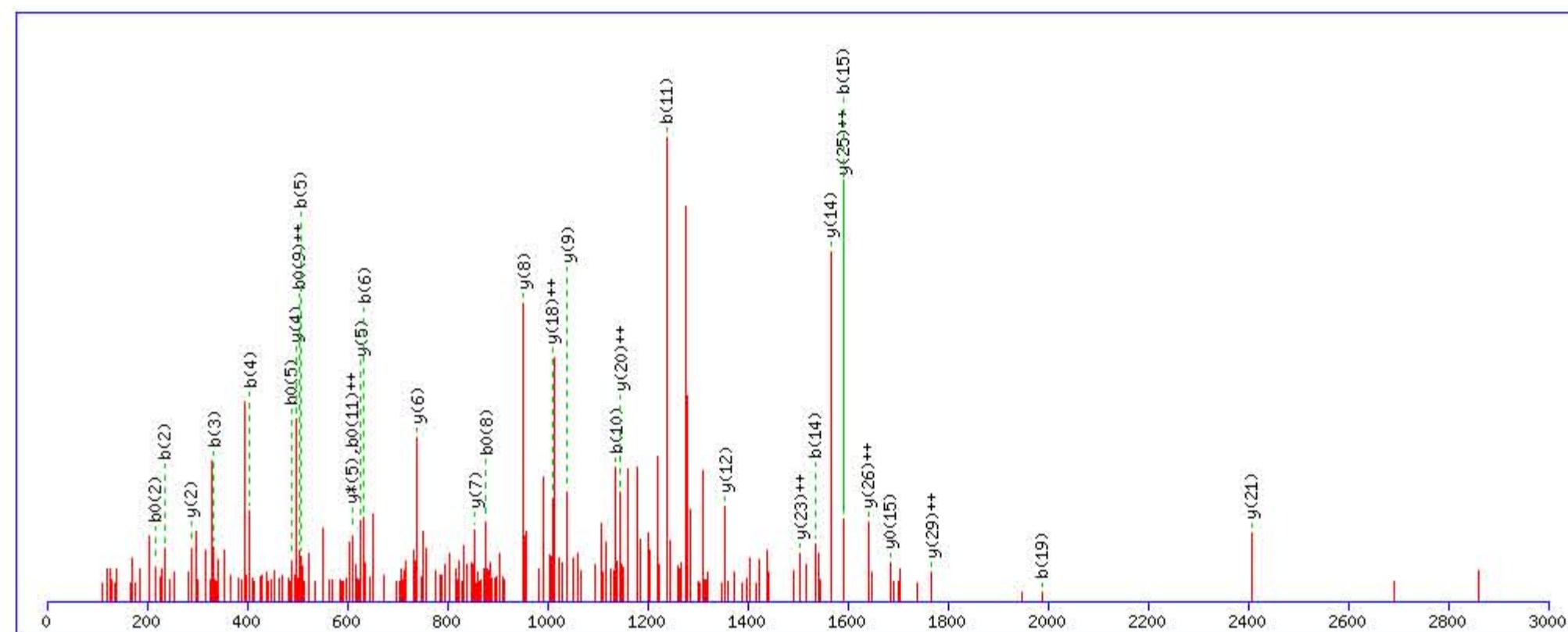
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR**
 Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

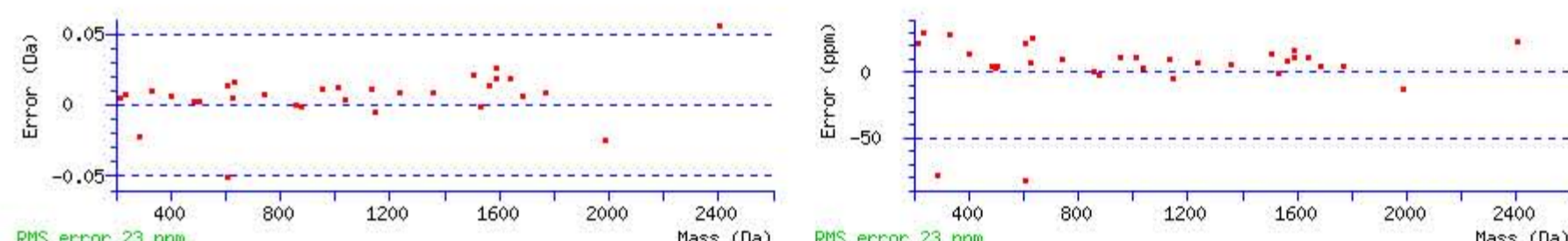
Match to Query 79777: 5066.434620 from(1014.294200,5+) rtinseconds(2647) index(9574)
 Title: Locus:1.1.1.3357.7 File:"2013-07-02 CLN FXIII 30 min 2nd F 1.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 48 Expect: 0.00027
 Matches : 33/484 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	148.075690	74.541483					F							43
2	235.107718	118.057497			217.097153	109.052214	S	4920.403881	2460.705578	4903.377332	2452.192304	4902.393316	2451.700296	42
3	334.176132	167.591704			316.165567	158.586422	V	4833.371853	2417.189565	4816.345304	2408.676290	4815.361288	2408.184282	41
4	405.213246	203.110261			387.202681	194.104978	A	4734.303439	2367.655357	4717.276890	2359.142083	4716.292874	2358.650075	40
5	506.260925	253.634100			488.250360	244.628818	T	4663.266325	2332.136800	4646.239776	2323.623526	4645.255760	2323.131518	39
6	634.319503	317.663390	617.292954	309.150115	616.308938	308.658107	Q	4562.218646	2281.612961	4545.192097	2273.099686	4544.208081	2272.607679	38
7	735.367182	368.187229	718.340633	359.673955	717.356617	359.181947	T	4434.160068	2217.583672	4417.133519	2209.070397	4416.149503	2208.578390	37
8	895.397831	448.202554	878.371282	439.689279	877.387266	439.197271	C	4333.112389	2167.059833	4316.085840	2158.546558	4315.101824	2158.054550	36
9	1023.456409	512.231843	1006.429860	503.718568	1005.445844	503.226560	Q	4173.081740	2087.044508	4156.055191	2078.531233	4155.071175	2078.039226	35
10	1136.540473	568.773875	1119.513924	560.260600	1118.529908	559.768592	I	4045.023162	2023.015219	4027.996613	2014.501944	4027.012597	2014.009936	34
11	1237.588152	619.297714	1220.561603	610.784440	1219.577587	610.292432	T	3931.939098	1966.473187	3914.912549	1957.959912	3913.928533	1957.467904	33
12	1334.640916	667.824096	1317.614367	659.310822	1316.630351	658.818814	P	3830.891419	1915.949347	3813.864870	1907.436073	3812.880854	1906.944065	32
13	1405.678030	703.342653	1388.651481	694.829379	1387.667465	694.337371	A	3733.838655	1867.422965	3716.812106	1858.909691	3715.828090	1858.417683	31
14	1534.720623	767.863949	1517.694074	759.350675	1516.710058	758.858667	E	3662.801541	1831.904408	3645.774992	1823.391134	3644.790976	1822.899126	30
15	1591.742087	796.374681	1574.715538	787.861407	1573.731522	787.369399	G	3533.758948	1767.383112	3516.732399	1758.869837	3515.748383	1758.377829	29
16	1688.794851	844.901063	1671.768302	836.387789	1670.784286	835.895781	P	3476.737484	1738.872380	3459.710935	1730.359105	3458.726919	1729.867097	28
17	1787.863265	894.435271	1770.836716	885.921996	1769.852700	885.429988	V	3379.684720	1690.345998	3362.658171	1681.832723	3361.674155	1681.340715	27
18	1886.931679	943.969478	1869.905130	935.456203	1868.921114	934.964195	V	3280.616306	1640.811791	3263.589757	1632.298516	3262.605741	1631.806508	26
19	1987.979358	994.493317	1970.952809	985.980043	1969.968793	985.488035	T	3181.547892	1591.277584	3164.521343	1582.764309	3163.537327	1582.272301	25
20	2059.016472	1030.011874	2041.989923	1021.498600	2041.005907	1021.006591	A	3080.500213	1540.753744	3063.473664	1532.240470	3062.489648	1531.748462	24
21	2498.241798	1249.624537	2481.215249	1241.111262	2480.231233	1240.619254	Q	3009.463099	1505.235187	2992.436550	1496.721913	2991.452534	1496.229905	23
22	2661.305127	1331.156202	2644.278578	1322.642927	2643.294562	1322.150919	Y	2570.237773	1285.622524	2553.211224	1277.109250	2552.227208	1276.617242	22
23	2776.332070	1388.669673	2759.305521	1380.156398	2758.321505	1379.664390	D	2407.174444	1204.090860	2390.147895	1195.577585	2389.163879	1195.085577	21
24	2936.362719	1468.684997	2919.336170	1460.171723	2918.352154	1459.679715	C	2292.147501	1146.577388	2275.120952	1138.064114	2274.136936	1137.572106	20
25	3049.446783	1525.227029	3032.420234	1516.713755	3031.436218	1516.221747	L	2132.116852	1066.562064	2115.090303	1058.048789	2114.106287	1057.556781	19
26	3106.468247	1553.737761	3089.441698	1545.224487	3088.457682	1544.732479	G	2019.032788	1010.020032	2002.006239	1001.506757	2001.022223	1001.014749	18
27	3266.498896	1633.753086	3249.472347	1625.239811	3248.488331	1624.747803	C	1962.011324	981.509300	1944.984775	972.996025	1944.000759	972.504017	17
28	3365.567310	1683.287293	3348.540761	1674.774018	3347.556745	1674.282010	V	1801.980675	901.493975	1784.954126	892.980701	1783.970110	892.488693	16
29	3502.626222	1751.816749	3485.599673	1743.303474	3484.615657	1742.811466	H	1702.912261	851.959768	1685.885712	843.446494	1684.901696	842.954486	15
30	3599.678986	1800.343131	3582.652437	1791.829856	3581.668421	1791.337848	P	1565.853349	783.430312	1548.826800	774.917038	1547.842784	774.425030	14
31	3712.763050	1856.885163	3695.736501	1848.371888	3694.752485	1847.879880	I	1468.800585	734.903930	1451.774036	726.390656	1450.790020	725.898648	13
32	3799.795078	1900.401177	3782.768529	1891.887902	3781.784513	1891.395894	S	1355.716521	678.361898	1338.689972	669.848624	1337.705956	669.356616	12
33	3900.842757	1950.925016	3883.816208	1942.411742	3882.832192	1941.919734	T	1268.684493	634.845884	1251.657944	626.332610	1250.673928	625.840602	11
34	4028.901335	2014.954305	4011.874786	2006.441031	4010.890770	2005.949023	Q	1167.636814	584.322045	1150.610265	575.808770	1149.626249	575.316762	10
35	4115.933363	2058.470320	4098.906814	2049.957045	4097.922798	2049.465037	S	1039.578236	520.292756	1022.551687	511.779481	1021.567671	511.287473	9
36	4212.986127	2106.996702	4195.959578	2098.483427	4194.975562	2097.991419	P	952.546208	476.776742	935.519659	468.263467	934.535643	467.771459	8
37	4328.013070	2164.510173	4310.986521	2155.996899	4310.002505	2155.504891	D	855.493444	428.250360	838.466895	419.737085	837.482879	419.245077	7
38	4441.097134	2221.052205	4424.070585	2212.538930	4423.086569	2212.046923	L	740.466501	370.736888	723.439952	362.223614	722.455936	361.731606	6
39	4570.139727	2285.573502	4553.113178	2277.060227	4552.129162	2276.568219	E	627.382437	314.194856	610.355888	305.681582	609.371872	305.189574	5
40	4667.192491	2334.099884	4650.165942	2325.586609	4649.181926	2325.094601	P	498.339844	249.673560	481.313295	241.160285			4
41	4780.276555	2390.641915	4763.250006	2382.128641	4762.265990	2381.636633	I	401.287080	201.147178	384.260531	192.633903			3
42	4893.360619	2447.183947	4876.334070	2438.670673	4875.350054	2438.178665	L	288.203016	144.605146	271.176467	136.091871			2
43							R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.8	5066.465057	-0.030437	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR
25.9	5066.465057	-0.030437	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR
17.0	5066.465057	-0.030437	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR
13.7	5066.465057	-0.030437	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **VECSDNLF^TQ^R**

Found in **MASP1_HUMAN**, Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3

Match to Query 41766: 1678.776402 from(560.599410,3+) rtinseconds(2083) index(56315)

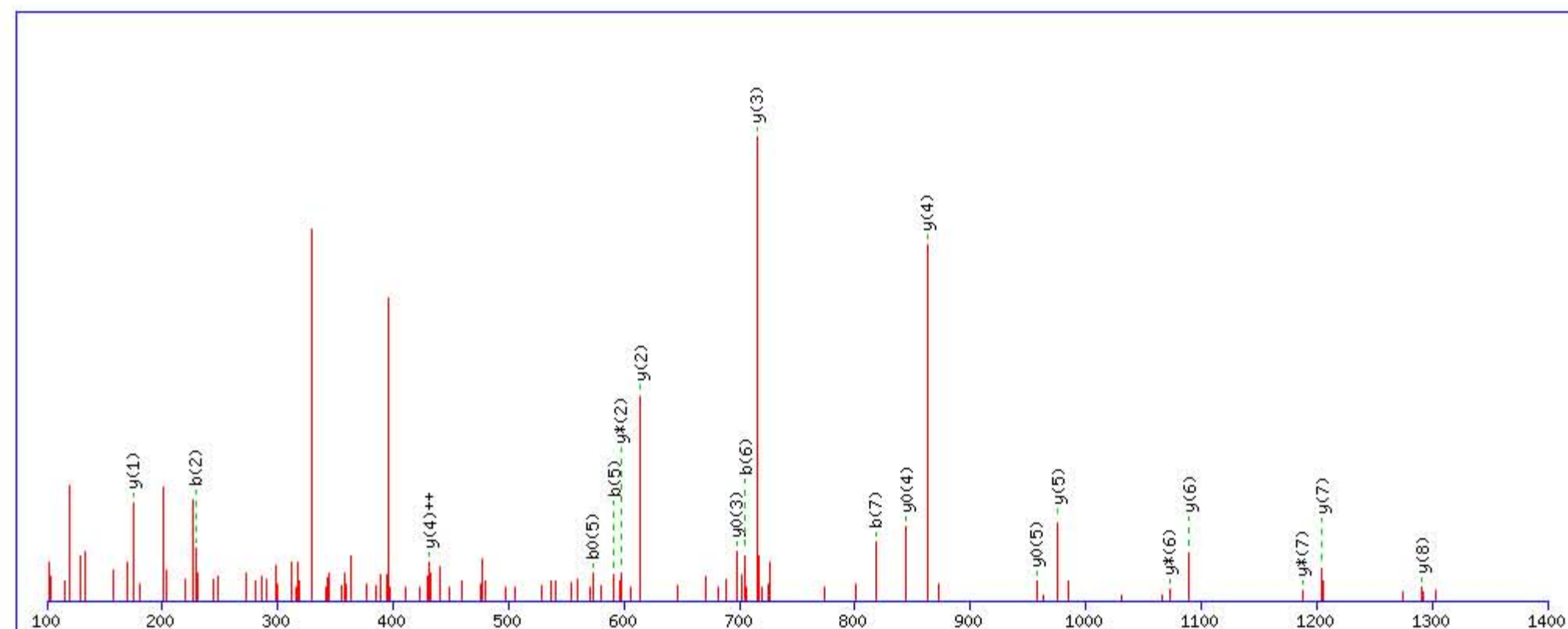
Title: Locus:1.1.1.3211.5 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

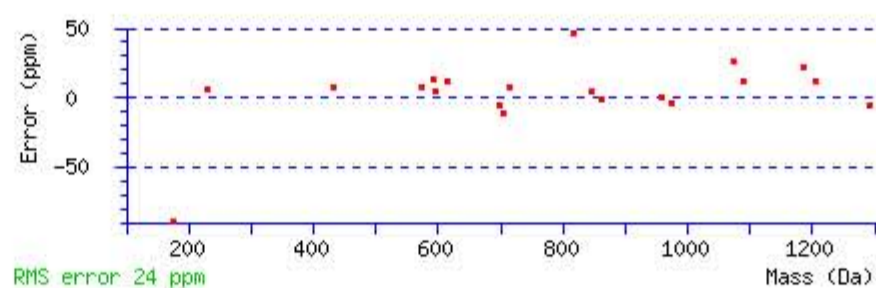
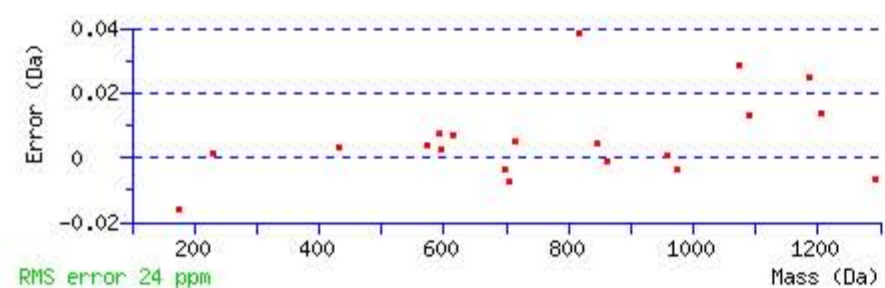
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 43 Expect: 0.00062

Matches : 20/104 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							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 [VECSDNLF^TQ^R](#)

(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	1678.780716	-0.004314	VECSDNLF^TQ^R

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

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 61950: 2697.326922 from(900.116250,3+) rtinseconds(2752) index(60321)

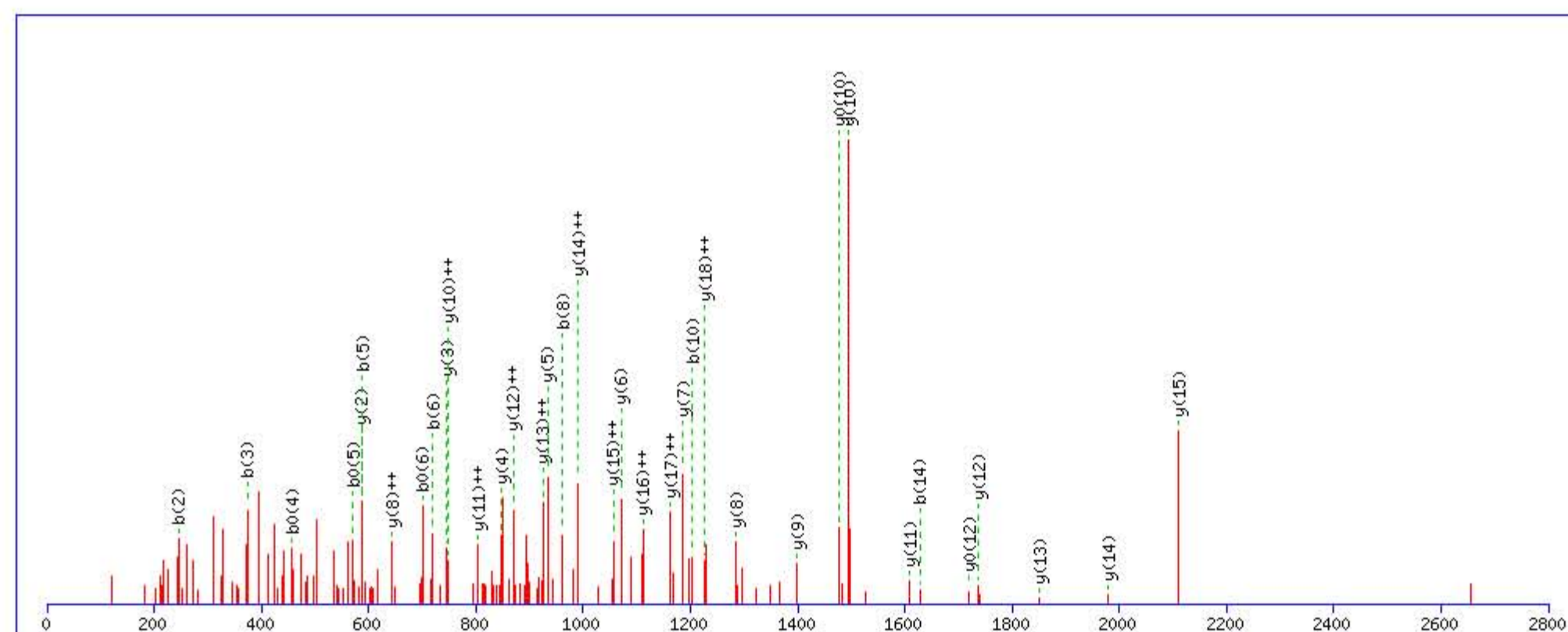
Title: Locus:1.1.1.3442.21 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

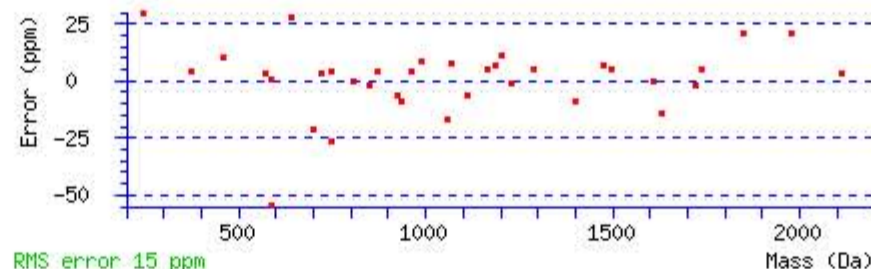
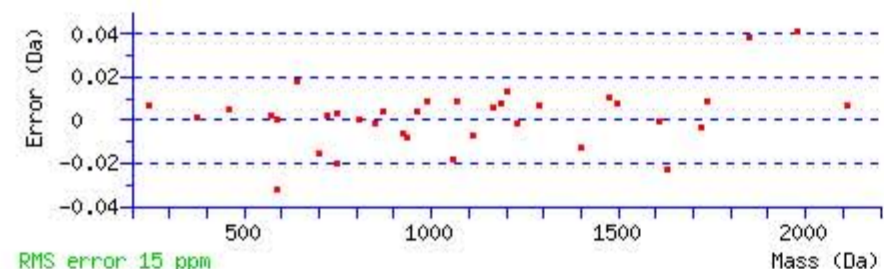
Variable modifications:

Q19 : Biotin:Thermo-21345 (Q)

Ions Score: 80 Expect: 2.9e-007

Matches : 36/182 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	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
79.9	2697.321609	0.005313	FPETLMEIEIPIVDHSTCQK

Mascot Search Results

Peptide View

MS/MS Fragmentation of **APEPISTQSHSVLILFHSDNSGENR**

Found in **MASPI_HUMAN**, Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASPI PE=1 SV=3

Match to Query 65896: 3045.494336 from(762.380860,4+) rtinseconds(2245) index(57328)

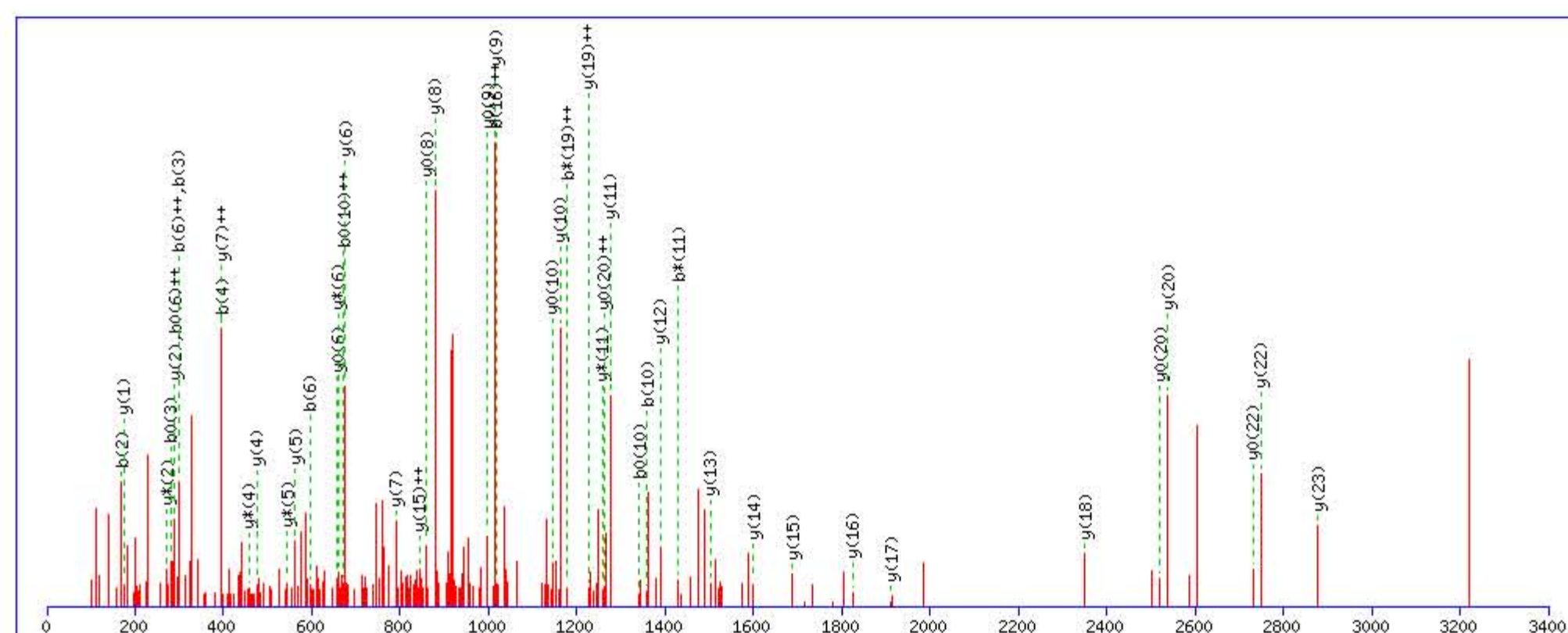
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Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

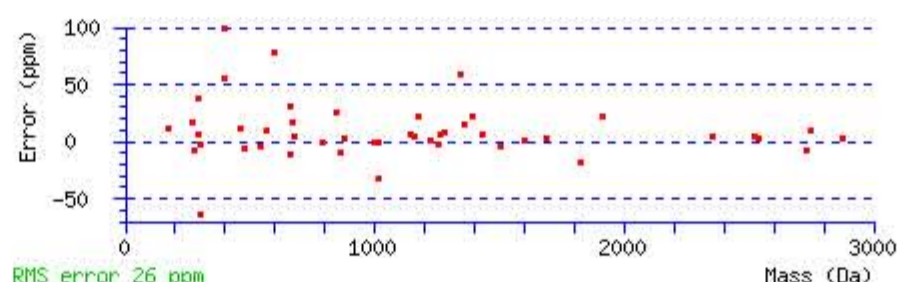
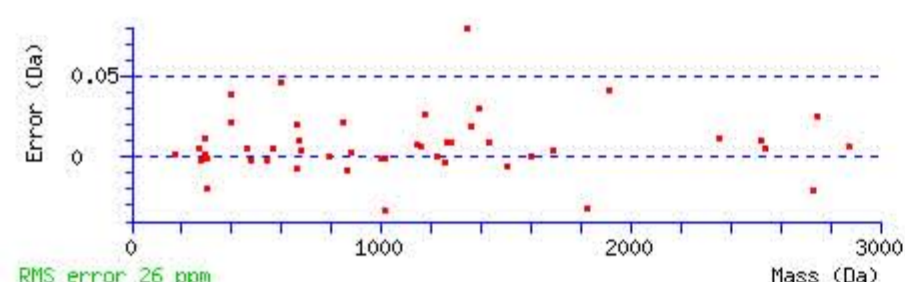
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 73 Expect: 1.3e-006

Matches : 48/266 fragment ions using 150 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.044390	36.525833					A							25
2	169.097154	85.052215					P	2975.467980	1488.237628	2958.441431	1479.724353	2957.457415	1479.232345	24
3	298.139747	149.573512			280.129182	140.568229	E	2878.415216	1439.711246	2861.388667	1431.197971	2860.404651	1430.705963	23
4	395.192511	198.099894			377.181946	189.094611	P	2749.372623	1375.189949	2732.346074	1366.676675	2731.362058	1366.184667	22
5	508.276575	254.641926			490.266010	245.636643	I	2652.319859	1326.663567	2635.293310	1318.150293	2634.309294	1317.658285	21
6	595.308603	298.157940			577.298038	289.152657	S	2539.235795	1270.121535	2522.209246	1261.608261	2521.225230	1261.116253	20
7	696.356282	348.681779			678.345717	339.676497	T	2452.203767	1226.605521	2435.177218	1218.092247	2434.193202	1217.600239	19
8	1135.581608	568.294442	1118.555059	559.781168	1117.571043	559.289160	Q	2351.156088	1176.081682	2334.129539	1167.568407	2333.145523	1167.076399	18
9	1222.613636	611.810456	1205.587087	603.297182	1204.603071	602.805174	S	1911.930762	956.469019	1894.904213	947.955745	1893.920197	947.463737	17
10	1359.672548	680.339912	1342.645999	671.826638	1341.661983	671.334630	H	1824.898734	912.953005	1807.872185	904.439731	1806.888169	903.947723	16
11	1446.704576	723.855926	1429.678027	715.342652	1428.694011	714.850644	S	1687.839822	844.423549	1670.813273	835.910275	1669.829257	835.418267	15
12	1545.772990	773.390133	1528.746441	764.876859	1527.762425	764.384851	V	1600.807794	800.907535	1583.781245	792.394261	1582.797229	791.902253	14
13	1658.857054	829.932165	1641.830505	821.418891	1640.846489	820.926883	L	1501.739380	751.373328	1484.712831	742.860054	1483.728815	742.368045	13
14	1771.941118	886.474197	1754.914569	877.960923	1753.930553	877.468915	I	1388.655316	694.831296	1371.628767	686.318022	1370.644751	685.826014	12
15	1885.025182	943.016229	1867.998633	934.502955	1867.014617	934.010947	L	1275.571252	638.289264	1258.544703	629.775990	1257.560687	629.283982	11
16	2032.093596	1016.550436	2015.067047	1008.037162	2014.083031	1007.545154	F	1162.487188	581.747232	1145.460639	573.233958	1144.476623	572.741950	10
17	2169.152508	1085.079892	2152.125959	1076.566617	2151.141943	1076.074610	H	1015.418774	508.213025	998.392225	499.699751	997.408209	499.207743	9
18	2256.184536	1128.595906	2239.157987	1120.082631	2238.173971	1119.590624	S	878.359862	439.683569	861.333313	431.170295	860.349297	430.678287	8
19	2371.211479	1186.109377	2354.184930	1177.596103	2353.200914	1177.104095	D	791.327834	396.167555	774.301285	387.654280	773.317269	387.162272	7
20	2485.254406	1243.130841	2468.227857	1234.617566	2467.243841	1234.125558	N	676.300891	338.654084	659.274342	330.140809	658.290326	329.648801	6
21	2572.286434	1286.646855	2555.259885	1278.133580	2554.275869	1277.641572	S	562.257964	281.632620	545.231415	273.119346	544.247399	272.627338	5
22	2629.307898	1315.157587	2612.281349	1306.644312	2611.297333	1306.152304	G	475.225936	238.116606	458.199387	229.603331	457.215371	229.111323	4
23	2758.350491	1379.678884	2741.323942	1371.165609	2740.339926	1370.673601	E	418.204472	209.605874	401.177923	201.092600	400.193907	200.600592	3
24	2872.393418	1436.700347	2855.366869	1428.187072	2854.382853	1427.695064	N	289.161879	145.084577	272.135330	136.571303			2
25							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [APEPISTQSHSVLILFHSDNSGENR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
73.2	3045.497803	-0.003467	APEPISTQSHSVLILFHSDNSGENR

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

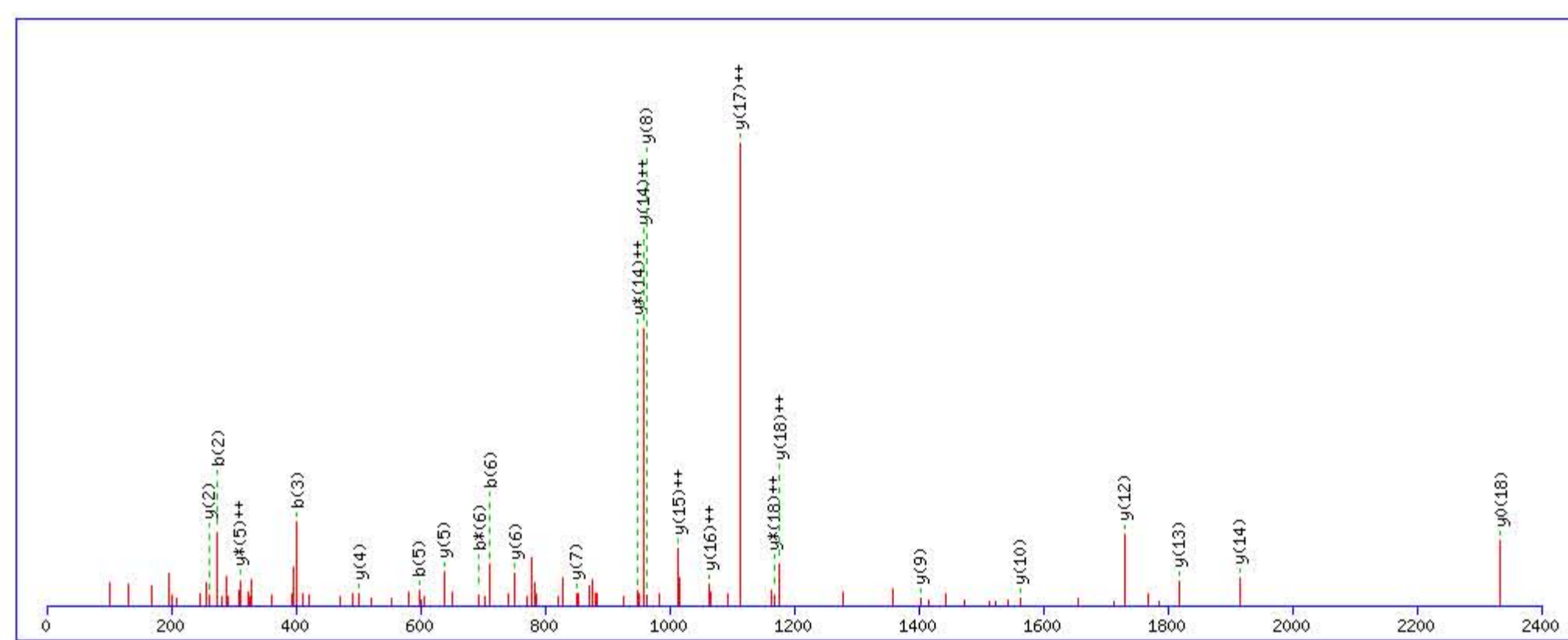
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **LCQPVLSPACQLVLHQILK**
 Found in **PMEL_HUMAN**, Melanocyte protein PMEL OS=Homo sapiens GN=PMEL PE=1 SV=2

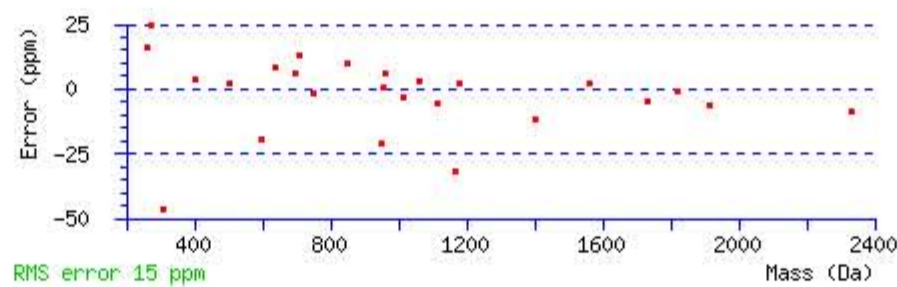
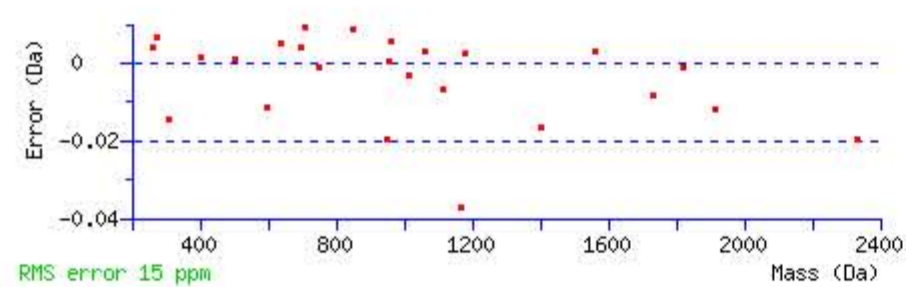
Match to Query 61326: 2624.436462 from(875.819430,3+) rtinseconds(2660) index(59545)
 Title: Locus:1.1.1.3411.20 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 2624.436859
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q12 : Biotin:Thermo-21345 (Q)
 Ions Score: 32 Expect: 0.0019
 Matches : 25/186 fragment ions using 83 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							20
2	274.121989	137.564632					C	2512.360078	1256.683677	2495.333529	1248.170402	2494.349513	1247.678394	19
3	402.180567	201.593921	385.154018	193.080647			Q	2352.329429	1176.668352	2335.302880	1168.155078	2334.318864	1167.663070	18
4	499.233331	250.120303	482.206782	241.607029			P	2224.270851	1112.639063	2207.244302	1104.125789	2206.260286	1103.633781	17
5	598.301745	299.654511	581.275196	291.141236			V	2127.218087	1064.112681	2110.191538	1055.599407	2109.207522	1055.107399	16
6	711.385809	356.196543	694.359260	347.683268			L	2028.149673	1014.578475	2011.123124	1006.065200	2010.139108	1005.573192	15
7	808.438573	404.722925	791.412024	396.209650			P	1915.065609	958.036443	1898.039060	949.523168	1897.055044	949.031160	14
8	895.470601	448.238939	878.444052	439.725664	877.460036	439.233656	S	1818.012845	909.510061	1800.986296	900.996786	1800.002280	900.504778	13
9	992.523365	496.765321	975.496816	488.252046	974.512800	487.760038	P	1730.980817	865.994047	1713.954268	857.480772			12
10	1063.560479	532.283878	1046.533930	523.770603	1045.549914	523.278595	A	1633.928053	817.467665	1616.901504	808.954390			11
11	1223.591128	612.299202	1206.564579	603.785928	1205.580563	603.293920	C	1562.890939	781.949108	1545.864390	773.435833			10
12	1662.816454	831.911865	1645.789905	823.398591	1644.805889	822.906583	Q	1402.860290	701.933783	1385.833741	693.420509			9
13	1775.900518	888.453897	1758.873969	879.940623	1757.889953	879.448614	L	963.634964	482.321120	946.608415	473.807846			8
14	1874.968932	937.988104	1857.942383	929.474830	1856.958367	928.982822	V	850.550900	425.779088	833.524351	417.265814			7
15	1988.052996	994.530136	1971.026447	986.016862	1970.042431	985.524853	L	751.482486	376.244881	734.455937	367.731607			6
16	2125.111908	1063.059592	2108.085359	1054.546317	2107.101343	1054.054309	H	638.398422	319.702849	621.371873	311.189575			5
17	2253.170486	1127.088881	2236.143937	1118.575606	2235.159921	1118.083598	Q	501.339510	251.173393	484.312961	242.660119			4
18	2366.254550	1183.630913	2349.228001	1175.117638	2348.243985	1174.625630	I	373.280932	187.144104	356.254383	178.630830			3
19	2479.338614	1240.172945	2462.312065	1231.659670	2461.328049	1231.167663	L	260.196868	130.602072	243.170319	122.088798			2
20							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.3	2624.436859	-0.000397	LCQPVLSPACQLVLHQILK
18.7	2624.436859	-0.000397	LCQPVLSPACQLVLHQILK
3.3	2624.454590	-0.018128	ASQILASRGAELFQATIVK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **IIGLDQVAGMSETALPGAFK**

Found in **MYH9_HUMAN**, Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4

Match to Query 56571: 2328.207222 from(777.076350,3+) rtinseconds(2845) index(61087)

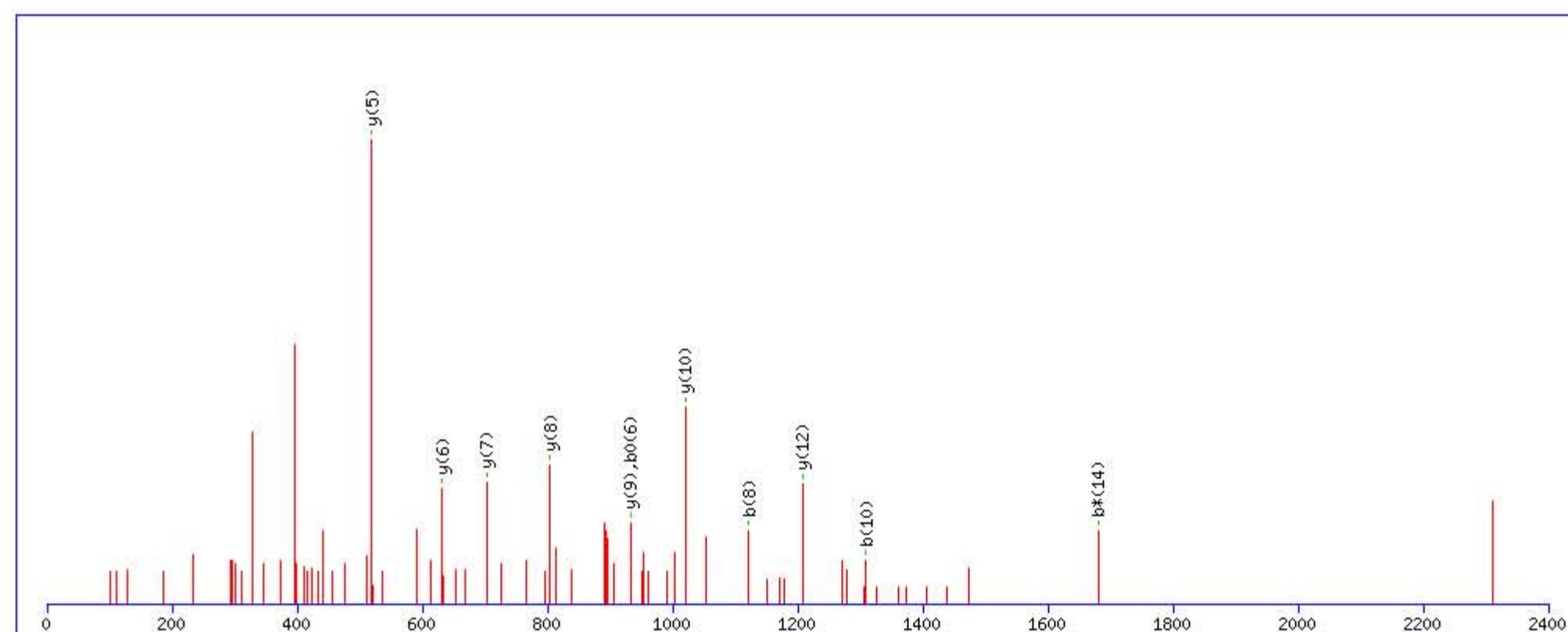
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Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2328.222153

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

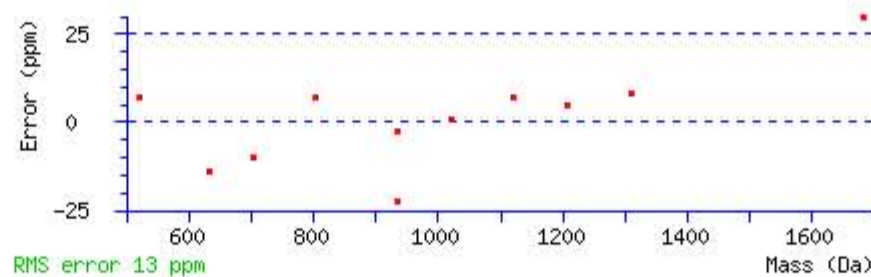
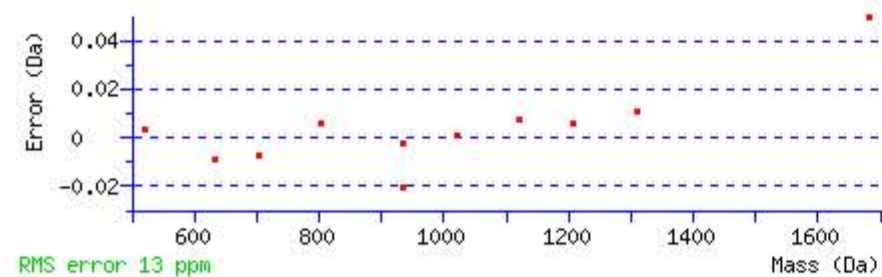
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 44 Expect: 0.0011

Matches : 11/196 fragment ions using 16 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					I							20
2	227.175404	114.091340					I	2216.145376	1108.576326	2199.118827	1100.063051	2198.134811	1099.571043	19
3	284.196868	142.602072					G	2103.061312	1052.034294	2086.034763	1043.521019	2085.050747	1043.029011	18
4	397.280932	199.144104					L	2046.039848	1023.523562	2029.013299	1015.010288	2028.029283	1014.518279	17
5	512.307875	256.657576			494.297310	247.652293	D	1932.955784	966.981530	1915.929235	958.468255	1914.945219	957.976247	16
6	951.533201	476.270239	934.506652	467.756964	933.522636	467.264956	Q	1817.928841	909.468058	1800.902292	900.954784	1799.918276	900.462776	15
7	1050.601615	525.804446	1033.575066	517.291171	1032.591050	516.799163	V	1378.703515	689.855395	1361.676966	681.342121	1360.692950	680.850113	14
8	1121.638729	561.323003	1104.612180	552.809728	1103.628164	552.317720	A	1279.635101	640.321188	1262.608552	631.807914	1261.624536	631.315906	13
9	1178.660193	589.833734	1161.633644	581.320460	1160.649628	580.828452	G	1208.597987	604.802631	1191.571438	596.289357	1190.587422	595.797349	12
10	1309.700678	655.353977	1292.674129	646.840703	1291.690113	646.348694	M	1151.576523	576.291900	1134.549974	567.778625	1133.565958	567.286617	11
11	1396.732706	698.869991	1379.706157	690.356717	1378.722141	689.864709	S	1020.536038	510.771657	1003.509489	502.258382	1002.525473	501.766374	10
12	1525.775299	763.391288	1508.748750	754.878013	1507.764734	754.386005	E	933.504010	467.255643	916.477461	458.742368	915.493445	458.250360	9
13	1626.822978	813.915127	1609.796429	805.401853	1608.812413	804.909845	T	804.461417	402.734346	787.434868	394.221072	786.450852	393.729064	8
14	1697.860092	849.433684	1680.833543	840.920410	1679.849527	840.428402	A	703.413738	352.210507	686.387189	343.697232			7
15	1810.944156	905.975716	1793.917607	897.462442	1792.933591	896.970434	L	632.376624	316.691950	615.350075	308.178675			6
16	1907.996920	954.502098	1890.970371	945.988824	1889.986355	945.496816	P	519.292560	260.149918	502.266011	251.636643			5
17	1965.018384	983.012830	1947.991835	974.499556	1947.007819	974.007547	G	422.239796	211.623536	405.213247	203.110261			4
18	2036.055498	1018.531387	2019.028949	1010.018113	2018.044933	1009.526105	A	365.218332	183.112804	348.191783	174.599529			3
19	2183.123912	1092.065594	2166.097363	1083.552319	2165.113347	1083.060311	F	294.181218	147.594247	277.154669	139.080972			2
20							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **IIGLDQVAGMSETALPGAFK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.0	2328.222153	-0.014931	IIGLDQVAGMSETALPGAFK

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

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 47167: 1915.008348 from(958.511450,2+) rtinseconds(2303) index(57616)

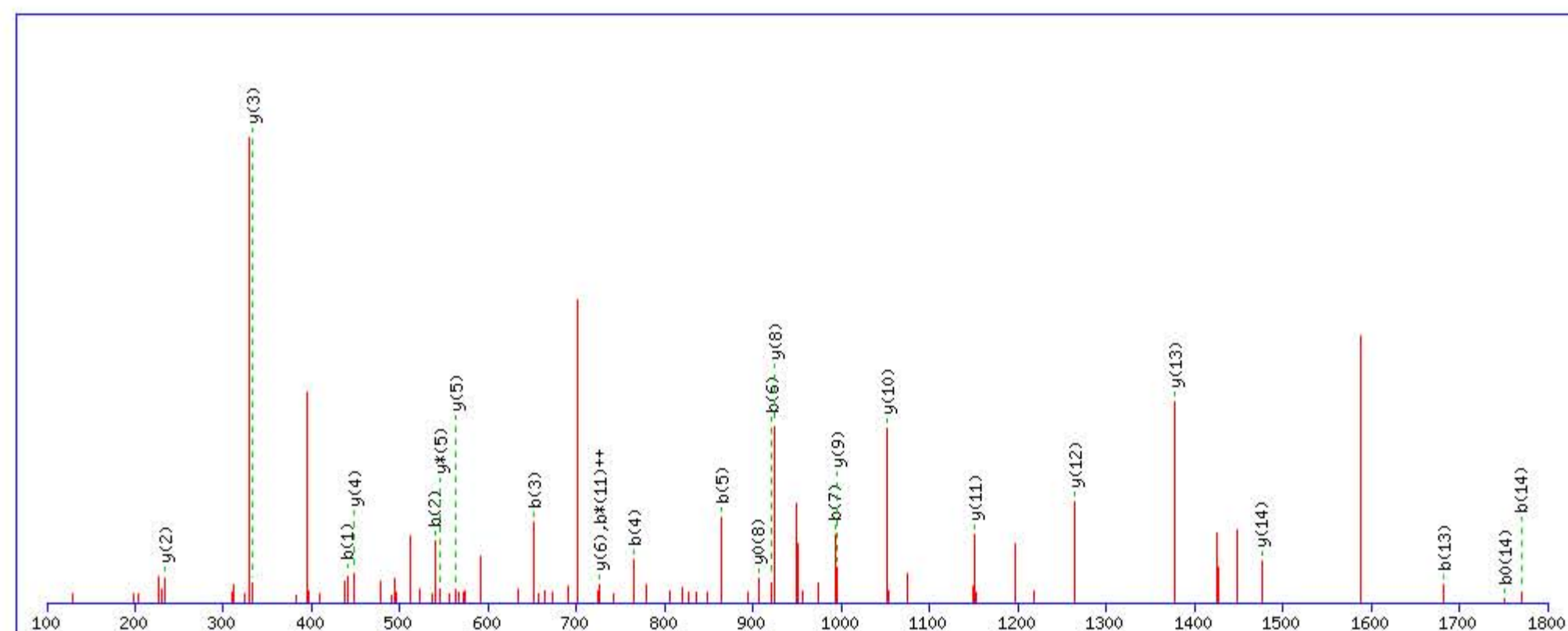
Title: Locus:1.1.1.3287.12 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

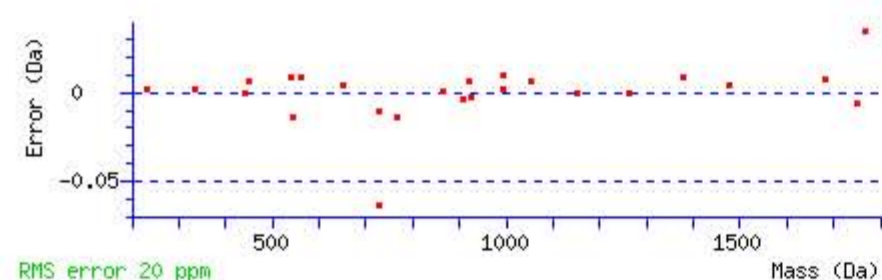
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

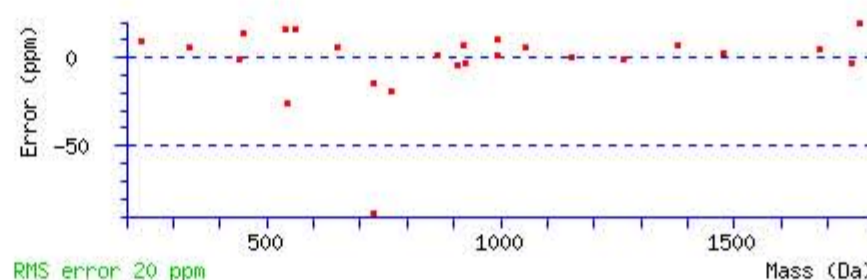
Ions Score: 66 Expect: 6.2e-006

Matches : 25/150 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	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



RMS error 20 ppm



RMS error 20 ppm

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
66.3	1915.012497	-0.004149	QVLLVGAPTYDDVSK
10.1	1915.027710	-0.019362	DYPIYLLKFKQCLSK
8.7	1915.008438	-0.000090	VIQKNQEETTSISK
8.5	1915.008438	-0.000090	VIQKNQEETTSISK
4.6	1915.009323	-0.000975	MTQLVLPGMVERSK

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 31276: 1375.655802 from(459.559210,3+) rtinseconds(1395) index(67266)

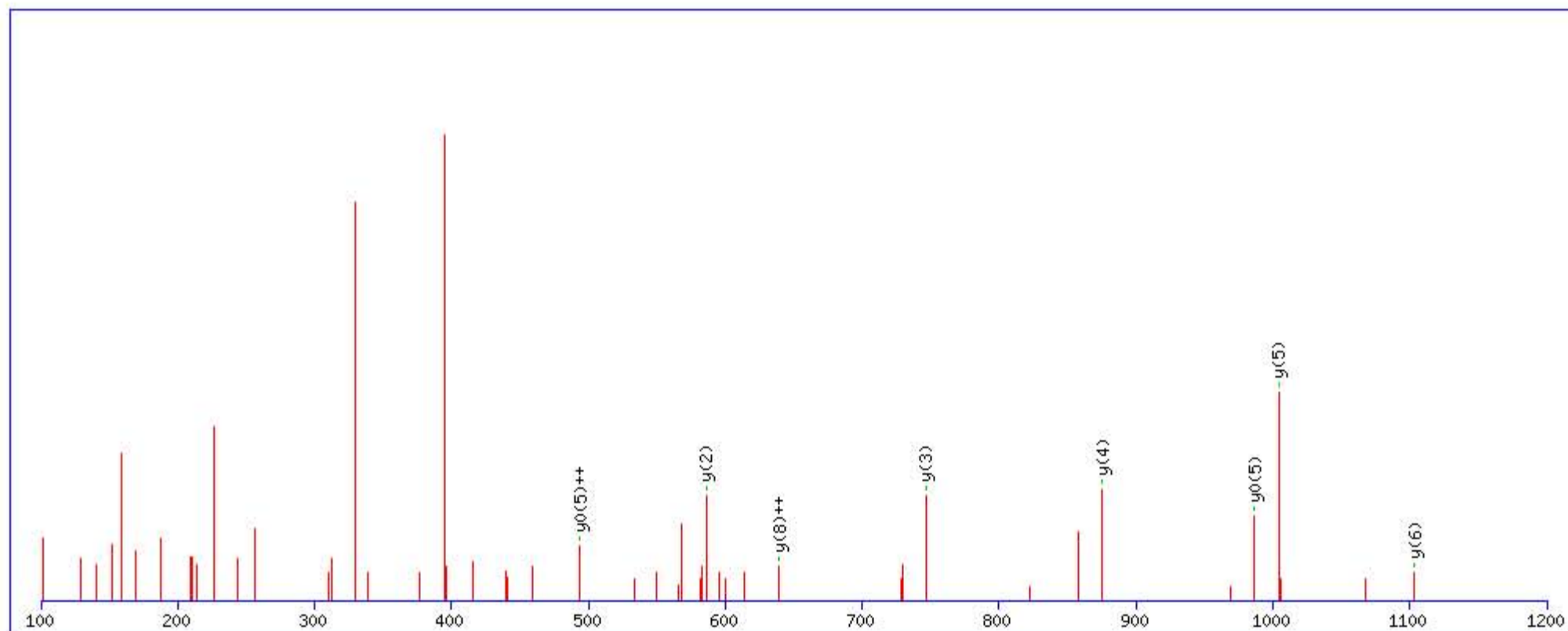
Title: Locus:1.1.1.3019.13 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

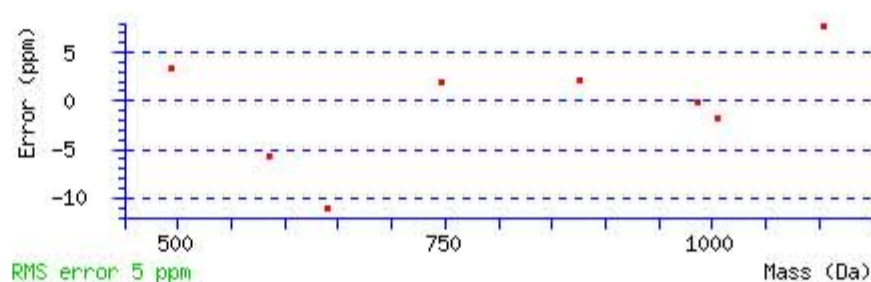
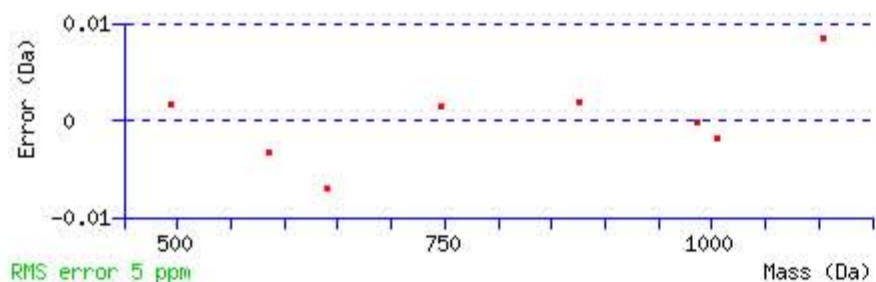
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 32 Expect: 0.0085

Matches : 8/74 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							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
32.3	1375.647568	0.008234	VSSVEECQK

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

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 45962: 1853.942742 from(618.988190,3+) rtinseconds(2147) index(72071)

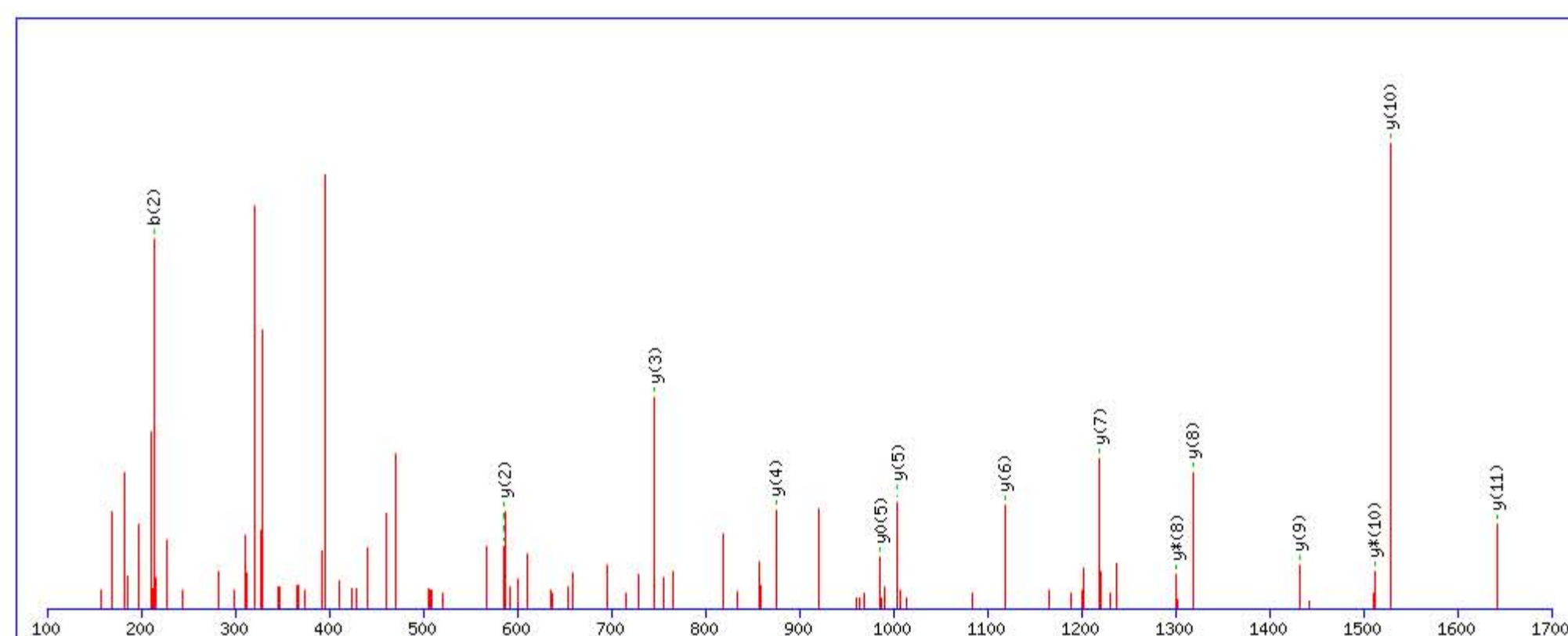
Title: Locus:1.1.1.3281.13 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1853.937927

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

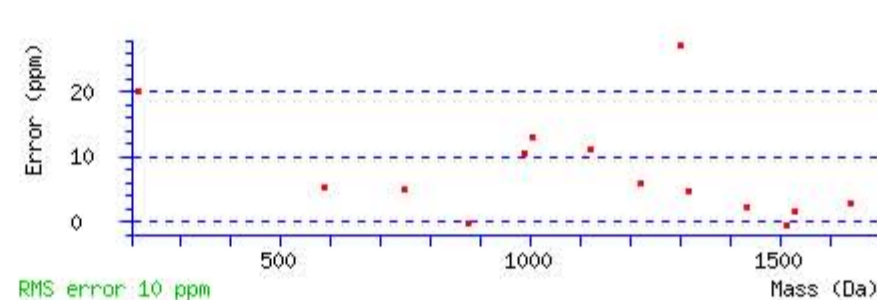
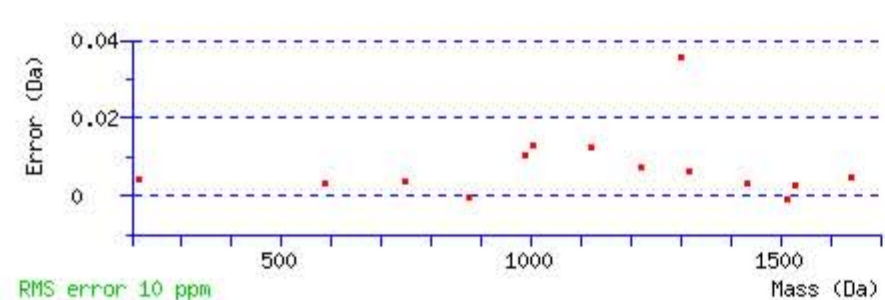
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 56 Expect: 1.4e-005

Matches : 14/124 fragment ions using 29 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.075690	50.541483					V							13
2	214.118617	107.562947	197.092068	99.049672			N	1755.876804	878.442040	1738.850255	869.928766	1737.866239	869.436758	12
3	327.202681	164.104978	310.176132	155.591704			I	1641.833877	821.420577	1624.807328	812.907302	1623.823312	812.415294	11
4	424.255445	212.631360	407.228896	204.118086			P	1528.749813	764.878545	1511.723264	756.365270	1510.739248	755.873262	10
5	537.339509	269.173393	520.312960	260.660118			L	1431.697049	716.352163	1414.670500	707.838888	1413.686484	707.346880	9
6	636.407923	318.707600	619.381374	310.194325			V	1318.612985	659.810131	1301.586436	651.296856	1300.602420	650.804848	8
7	737.455602	369.231439	720.429053	360.718165	719.445037	360.226157	T	1219.544571	610.275924	1202.518022	601.762649	1201.534006	601.270641	7
8	851.498529	426.252903	834.471980	417.739628	833.487964	417.247620	N	1118.496892	559.752084	1101.470343	551.238810	1100.486327	550.746802	6
9	980.541122	490.774199	963.514573	482.260924	962.530557	481.768916	E	1004.453965	502.730621	987.427416	494.217346	986.443400	493.725338	5
10	1109.583715	555.295496	1092.557166	546.782221	1091.573150	546.290213	E	875.411372	438.209324	858.384823	429.696050	857.400807	429.204042	4
11	1269.614364	635.310820	1252.587815	626.797546	1251.603799	626.305538	C	746.368779	373.688028	729.342230	365.174753			3
12	1708.839690	854.923483	1691.813141	846.410209	1690.829125	845.918201	Q	586.338130	293.672703	569.311581	285.159429			2
13							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **VNIPLVTNEECQK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.4	1853.937927	0.004815	VNIPLVTNEECQK
4.8	1853.934341	0.008401	RGLSNPNELQAIDSNR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **QCGHQISACHR**

Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

Match to Query 48606: 1974.935056 from(494.741040,4+) rtinseconds(1456) index(18490)

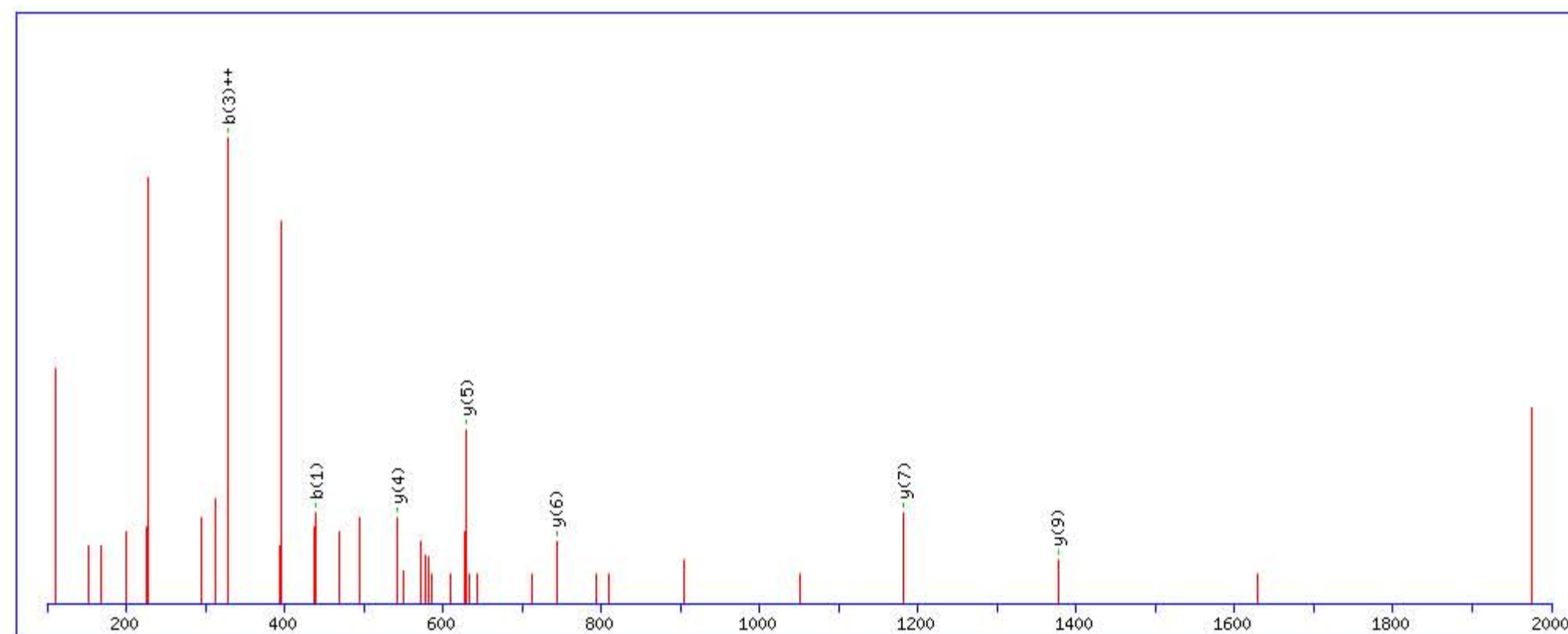
Title: Locus:1.1.1.1388.18 File:"2013-07-02 CLN FXIII 30 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1974.916122

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

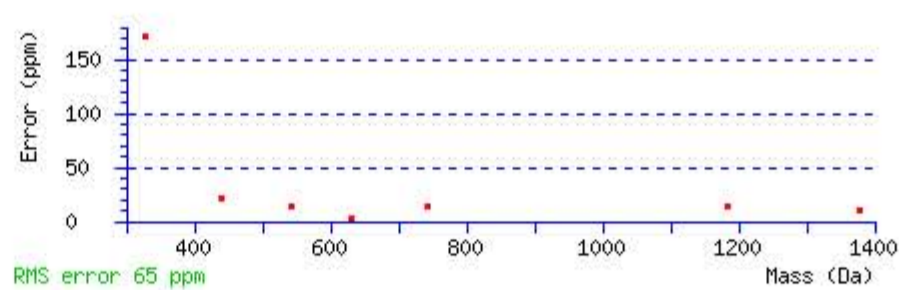
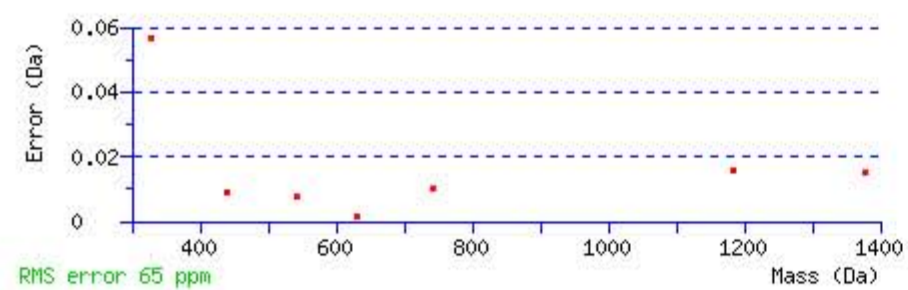
Q1 : Biotin:Thermo-21345 (Q)

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 25 Expect: 0.049

Matches : 7/100 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	440.232602	220.619939	423.206053	212.106664			Q							11
2	600.263251	300.635264	583.236702	292.121989			C	1536.698070	768.852673	1519.671521	760.339399	1518.687505	759.847391	10
3	657.284715	329.145996	640.258166	320.632721			G	1376.667421	688.837349	1359.640872	680.324074	1358.656856	679.832066	9
4	794.343627	397.675452	777.317078	389.162177			H	1319.645957	660.326617	1302.619408	651.813342	1301.635392	651.321334	8
5	1233.568953	617.288115	1216.542404	608.774840			Q	1182.587045	591.797161	1165.560496	583.283886	1164.576480	582.791878	7
6	1346.653017	673.830147	1329.626468	665.316872			I	743.361719	372.184498	726.335170	363.671223	725.351154	363.179215	6
7	1433.685045	717.346161	1416.658496	708.832886	1415.674480	708.340878	S	630.277655	315.642466	613.251106	307.129191	612.267090	306.637183	5
8	1504.722159	752.864718	1487.695610	744.351443	1486.711594	743.859435	A	543.245627	272.126452	526.219078	263.613177			4
9	1664.752808	832.880042	1647.726259	824.366768	1646.742243	823.874760	C	472.208513	236.607894	455.181964	228.094620			3
10	1801.811720	901.409498	1784.785171	892.896224	1783.801155	892.404216	H	312.177864	156.592570	295.151315	148.079295			2
11							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **QCGHQISACHR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	$M_r(\text{calc})$:	Delta	Sequence
25.3	1974.916122	0.018934	QCGHQISACHR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **EAQLPVIENK**

Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

Match to Query 34309: 1450.778448 from(726.396500,2+) rtinseconds(1979) index(71105)

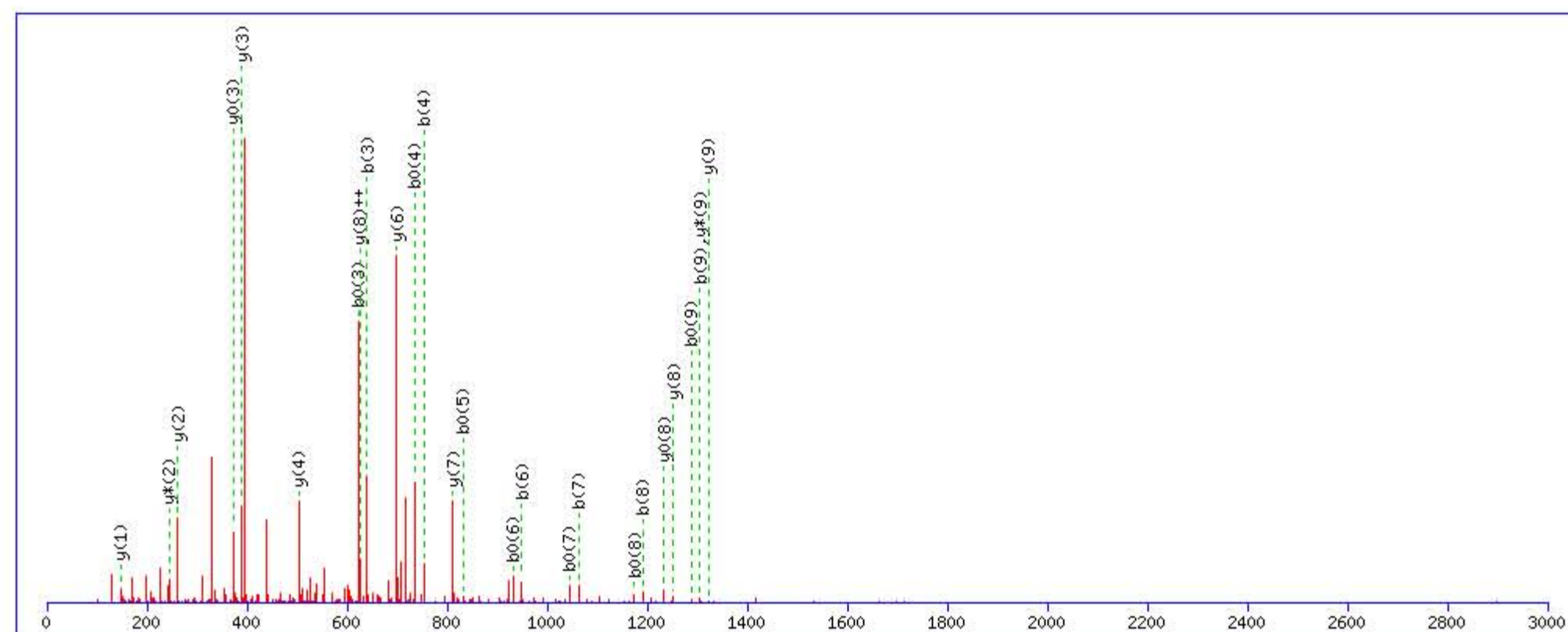
Title: Locus:1.1.1.3222.13 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

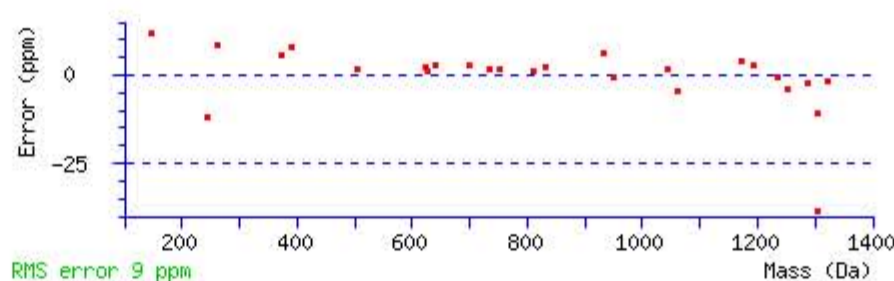
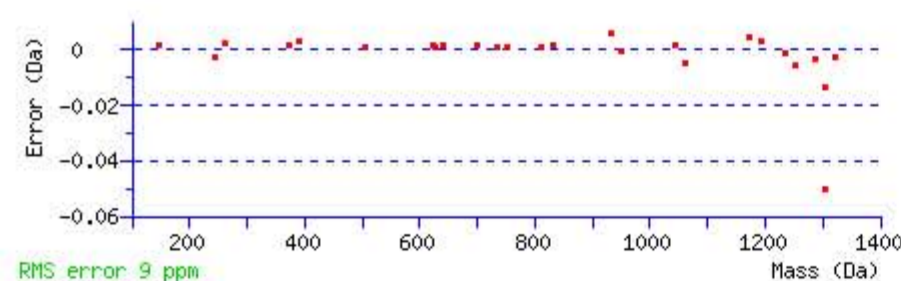
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 39 Expect: 0.00085

Matches : 26/100 fragment ions using 53 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.049869	65.528572			112.039304	56.523290	E							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
39.0	1450.785355	-0.006907	EAQLPVIENK
5.9	1450.764236	0.014212	EIFHPEIQK
4.0	1450.777985	0.000463	TVKGGFSETRIEK
4.0	1450.790527	-0.012079	QNIWRHNRLSK
3.0	1450.775467	0.002981	QAPAPTKWNK
2.5	1450.785355	-0.006907	TLQIFNIEMKSK
0.9	1450.789429	-0.010981	VIIAFGFMVPDVK
0.4	1450.764252	0.014196	QKFSEQVFK
0.3	1450.764236	0.014212	AEPPTWAQLK

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 41983: 1687.785372 from(563.602400,3+) rtinseconds(1802) index(69946)

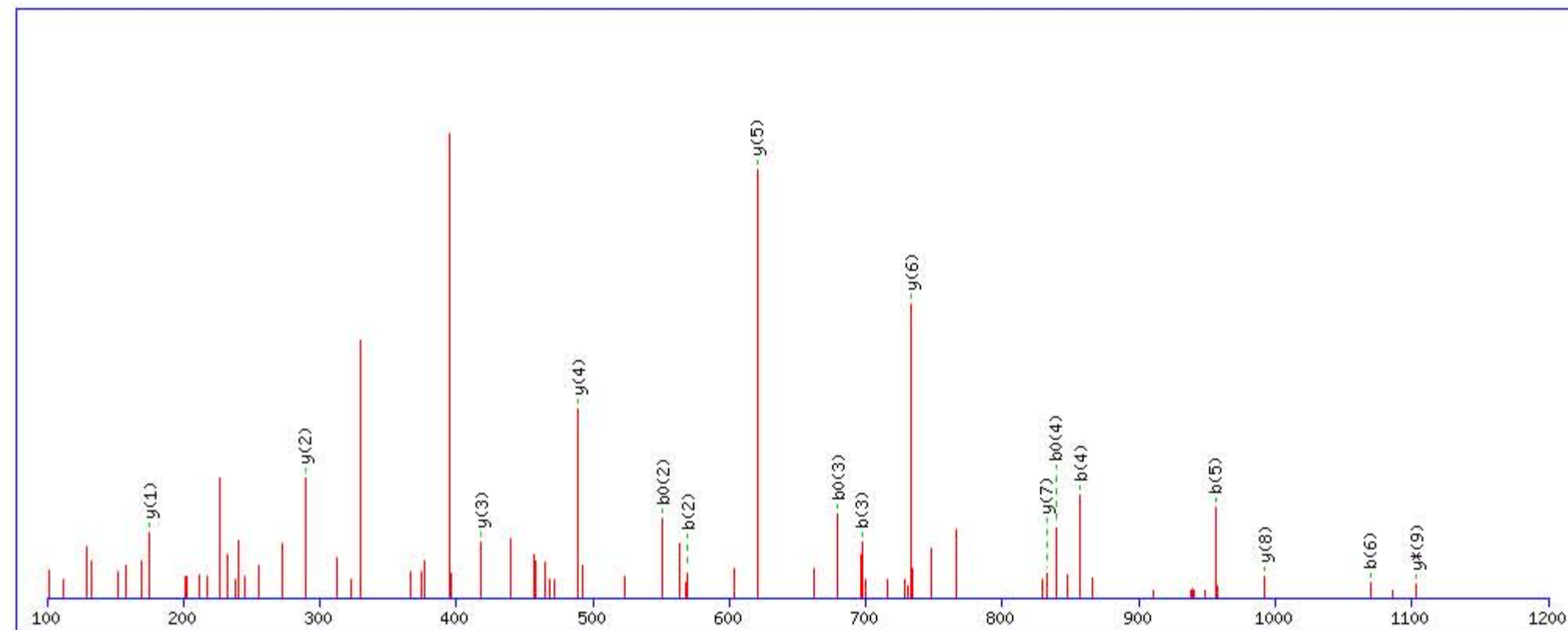
Title: Locus:1.1.1.3161.10 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

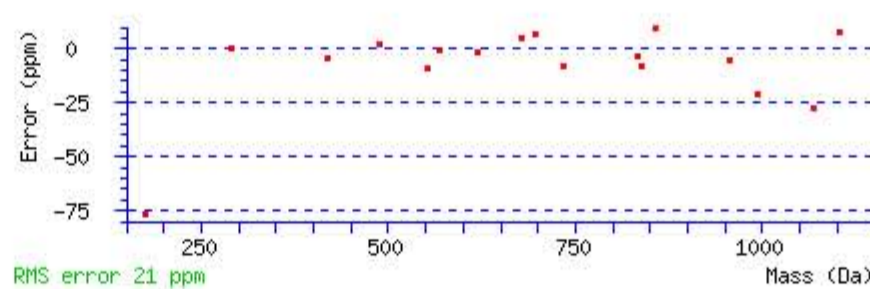
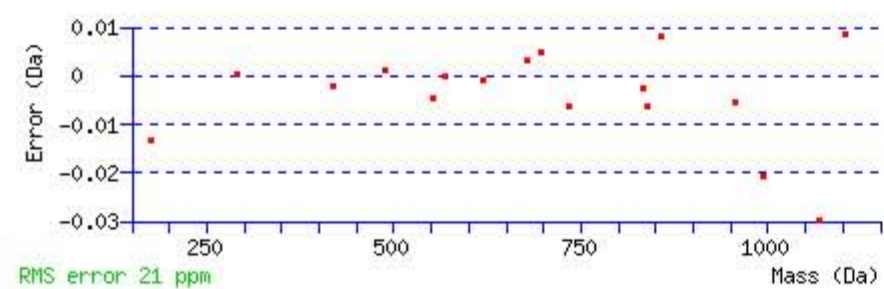
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 45 Expect: 0.00015

Matches : 17/114 fragment ions using 31 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	569.275195	285.141236	552.248646	276.627961	551.264630	276.135953	Q	1559.749102	780.378189	1542.722553	771.864915	1541.738537	771.372907	10
3	697.333773	349.170525	680.307224	340.657250	679.323208	340.165242	Q	1120.523776	560.765526	1103.497227	552.252252	1102.513211	551.760244	9
4	857.364422	429.185849	840.337873	420.672575	839.353857	420.180567	C	992.465198	496.736237	975.438649	488.222963	974.454633	487.730955	8
5	956.432836	478.720056	939.406287	470.206782	938.422271	469.714774	V	832.434549	416.720913	815.408000	408.207638	814.423984	407.715630	7
6	1069.516900	535.262088	1052.490351	526.748814	1051.506335	526.256806	I	733.366135	367.186706	716.339586	358.673431	715.355570	358.181423	6
7	1200.557385	600.782331	1183.530836	592.269056	1182.546820	591.777048	M	620.282071	310.644674	603.255522	302.131399	602.271506	301.639391	5
8	1271.594499	636.300888	1254.567950	627.787613	1253.583934	627.295605	A	489.241586	245.124431	472.215037	236.611156	471.231021	236.119148	4
9	1400.637092	700.822184	1383.610543	692.308910	1382.626527	691.816902	E	418.204472	209.605874	401.177923	201.092600	400.193907	200.600592	3
10	1514.680019	757.843648	1497.653470	749.330373	1496.669454	748.838365	N	289.161879	145.084577	272.135330	136.571303			2
11							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [EQQCVIMAENR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.0	1687.784393	0.000979	EQQCVIMAENR
41.3	1687.784393	0.000979	EQQCVIMAENR
4.1	1687.773666	0.011706	TTGPPSGQMPDNPPHR
1.5	1687.776093	0.009279	QQEEAQAASAAESAER
1.0	1687.787552	-0.002180	GASEDGEYFLMIRGK

MASCOT 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 43981: 1766.830392 from(589.950740,3+) rtinseconds(1528) index(68317)

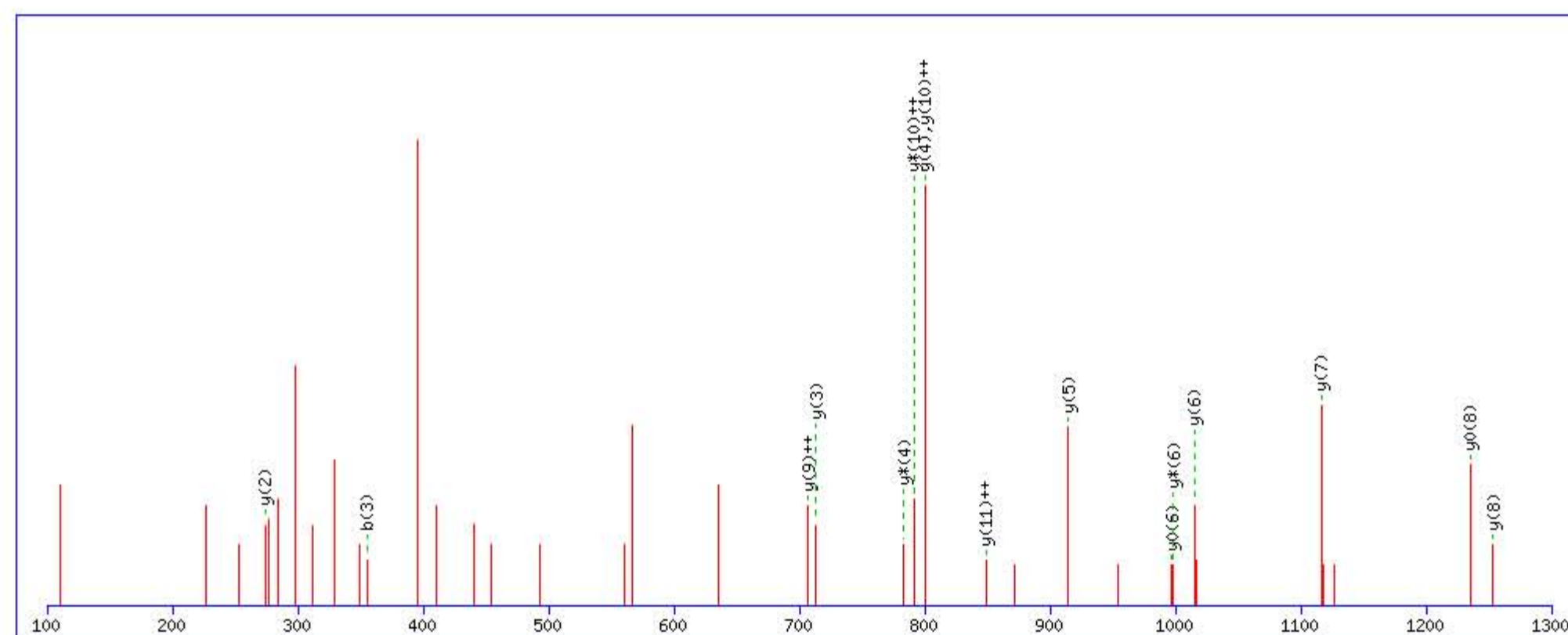
Title: Locus:1.1.1.3065.14 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

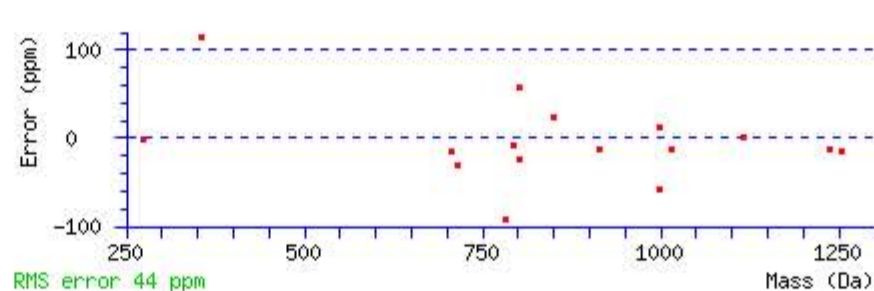
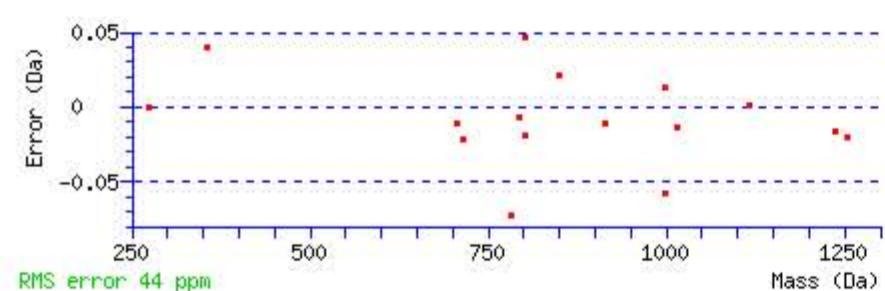
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 26 Expect: 0.042

Matches : 16/102 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							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
25.8	1766.834488	-0.004096	APWCHTTNSQVR

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

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **EQQCIVMAENR**

Found in **PLGB_HUMAN**, Plasminogen-like protein B OS=Homo sapiens GN=PLGLB1 PE=1 SV=1

Match to Query 49050: 1998.946152 from(667.322660,3+) rtinseconds(2118) index(71897)

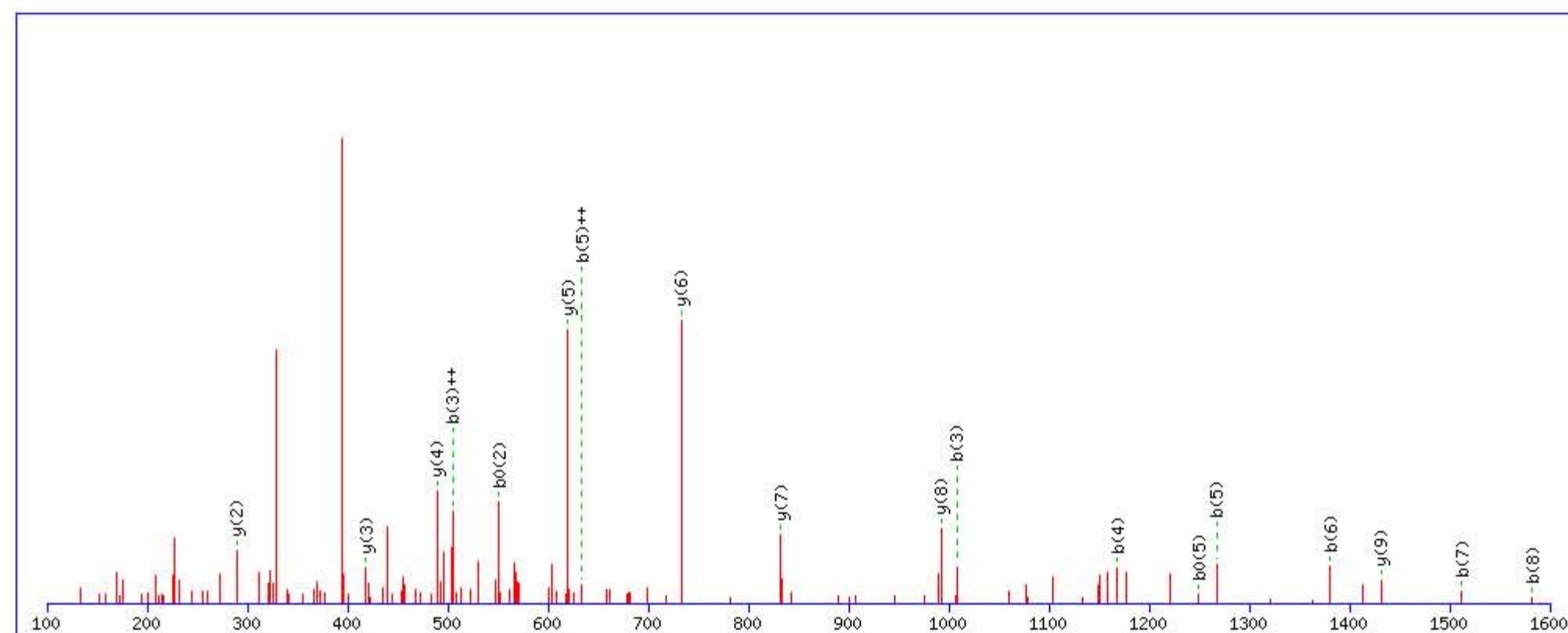
Title: Locus:1.1.1.3271.9 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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:

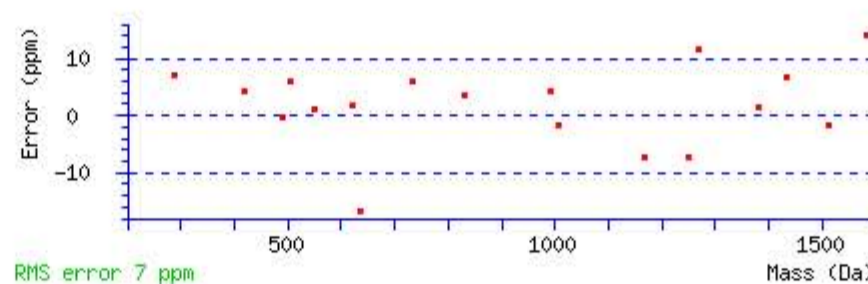
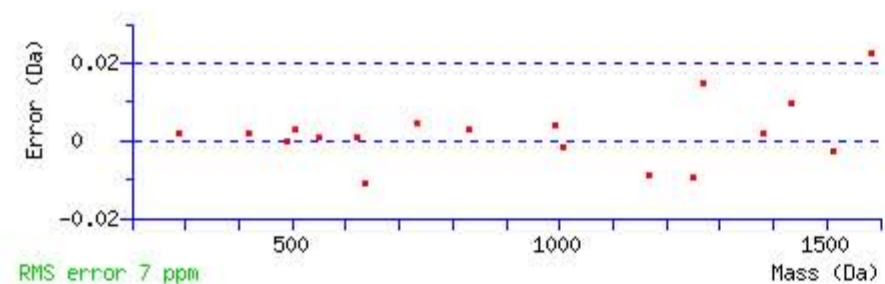
Q2 : Biotin:Thermo-21345 (Q)

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 47 Expect: 8.6e-005

Matches : 18/114 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	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 [EQQCIVMAENR](#)

(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	1998.951141	-0.004989	EQQCIVMAENR
3.8	1998.942841	0.003311	QQEEAQAAAAAASAESR
3.8	1998.942841	0.003311	QQEEAQAAAAAASAESR
3.0	1998.921280	0.024872	LSQMCLNTEWVEMKSK
0.3	1998.950912	-0.004760	YEAQQLRTFYQMYDK

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 52058: 2103.966852 from(702.329560,3+) rtinseconds(1757) index(69654)

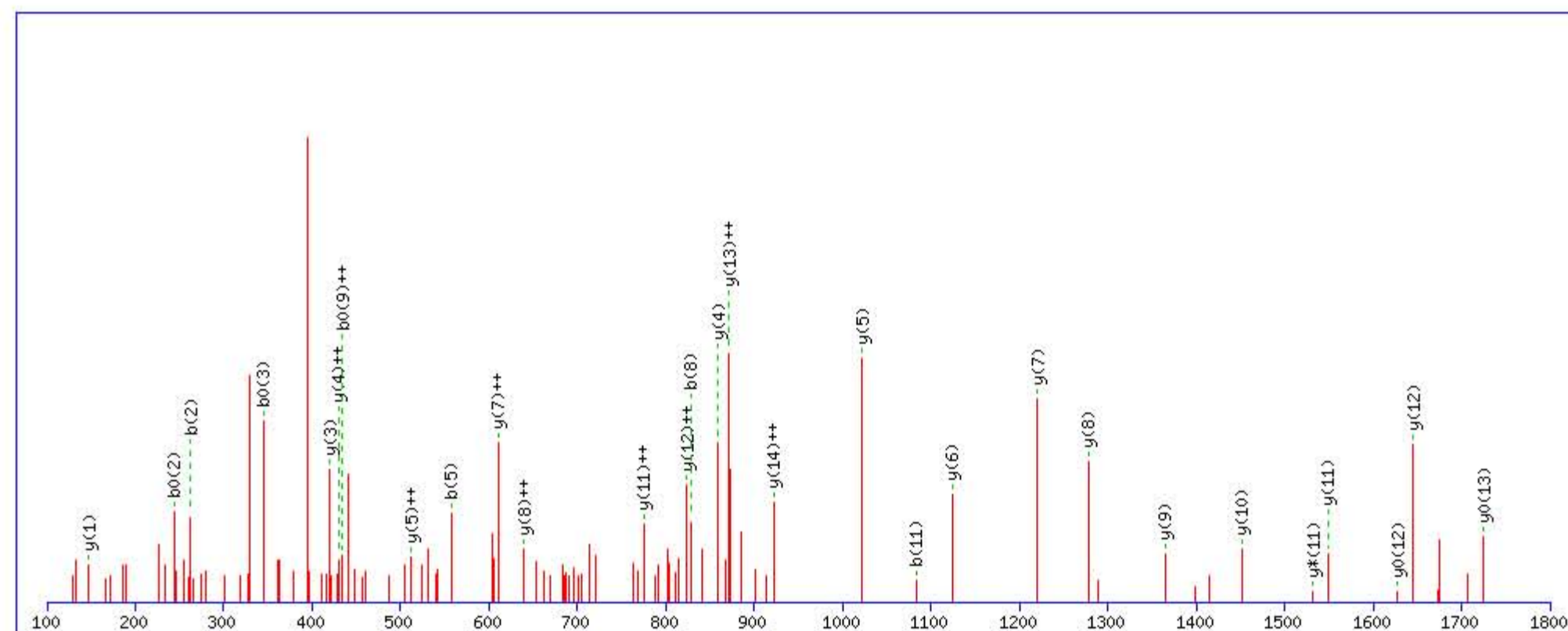
Title: Locus:1.1.1.3145.20 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

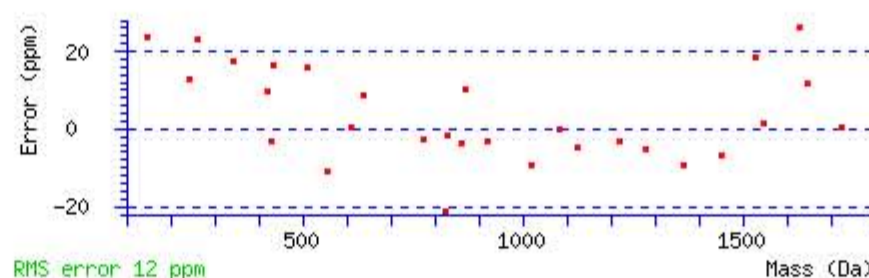
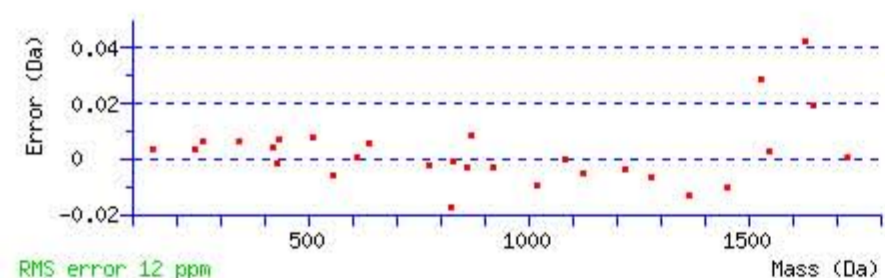
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 66 Expect: 3.6e-006

Matches : 29/144 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	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
65.7	2103.979172	-0.012320	CTTPPPSSGPTYQCLK
7.6	2103.964554	0.002298	TAADTPAIMNWDLFFTMK
3.3	2103.937866	0.028986	ASSVSKQSSCESITDEFSR
1.8	2103.975754	-0.008902	AEVEQMHSYQELK

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 58272: 2436.110682 from(813.044170,3+) rtinseconds(1858) index(70203)

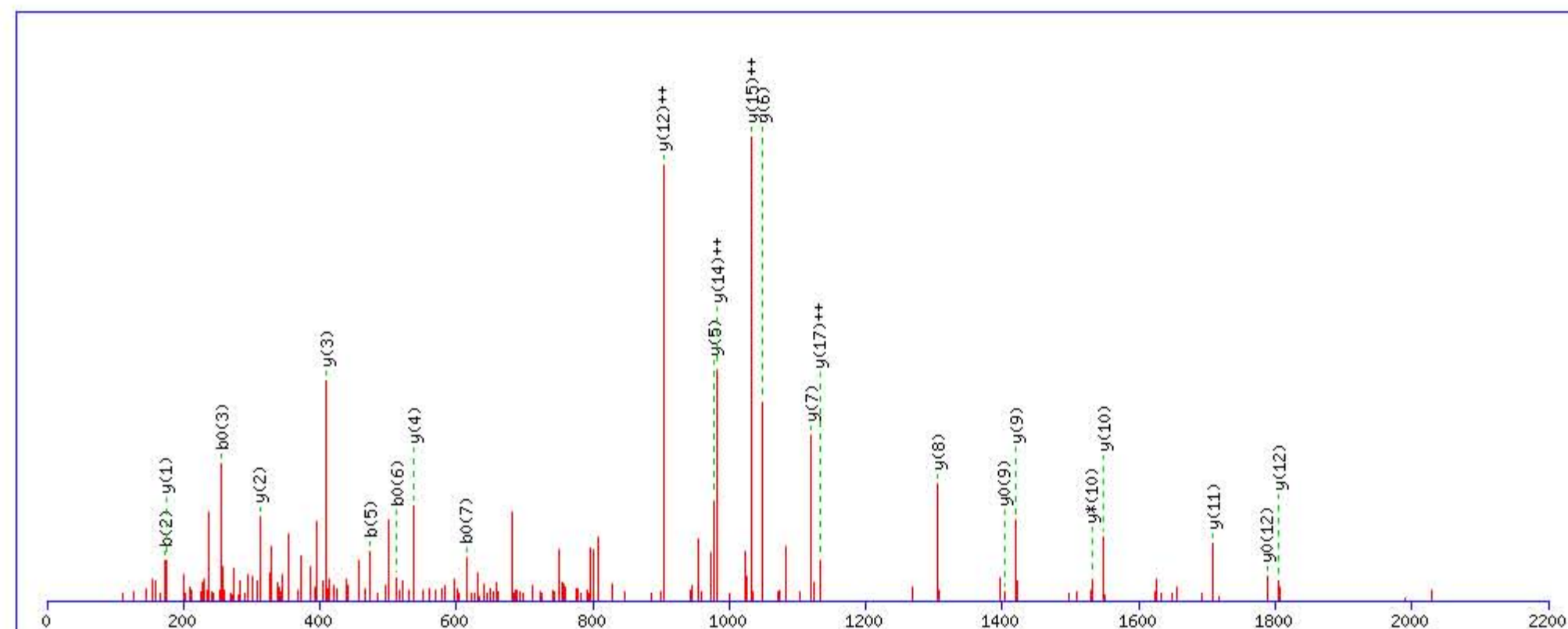
Title: Locus:1.1.1.3180.12 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

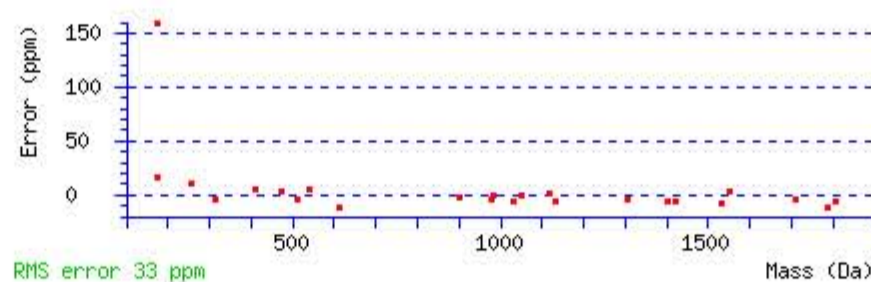
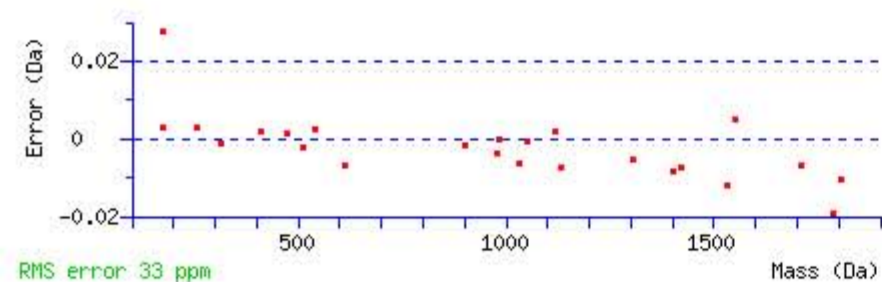
Variable modifications:

Q15 : Biotin:Thermo-21345 (Q)

Ions Score: 84 Expect: 4.4e-008

Matches : 24/190 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	72.044390	36.525833					A							19
2	173.092069	87.049672			155.081504	78.044390	T	2366.101616	1183.554446	2349.075067	1175.041171	2348.091051	1174.549163	18
3	274.139748	137.573512			256.129183	128.568230	T	2265.053937	1133.030606	2248.027388	1124.517332	2247.043372	1124.025324	17
4	373.208162	187.107719			355.197597	178.102437	V	2164.006258	1082.506767	2146.979709	1073.993492	2145.995693	1073.501484	16
5	474.255841	237.631559			456.245276	228.626276	T	2064.937844	1032.972560	2047.911295	1024.459285	2046.927279	1023.967277	15
6	531.277305	266.142291			513.266740	257.137008	G	1963.890165	982.448721	1946.863616	973.935446	1945.879600	973.443438	14
7	632.324984	316.666130			614.314419	307.660848	T	1906.868701	953.937989	1889.842152	945.424714	1888.858136	944.932706	13
8	729.377748	365.192512			711.367183	356.187230	P	1805.821022	903.414149	1788.794473	894.900875	1787.810457	894.408867	12
9	889.408397	445.207837			871.397832	436.202554	C	1708.768258	854.887767	1691.741709	846.374493	1690.757693	845.882485	11
10	1017.466975	509.237126	1000.440426	500.723851	999.456410	500.231843	Q	1548.737609	774.872443	1531.711060	766.359168	1530.727044	765.867160	10
11	1132.493918	566.750597	1115.467369	558.237323	1114.483353	557.745315	D	1420.679031	710.843154	1403.652482	702.329879	1402.668466	701.837871	9
12	1318.573231	659.790254	1301.546682	651.276979	1300.562666	650.784971	W	1305.652088	653.329682	1288.625539	644.816408	1287.641523	644.324400	8
13	1389.610345	695.308811	1372.583796	686.795536	1371.599780	686.303528	A	1119.572775	560.290026	1102.546226	551.776751	1101.562210	551.284743	7
14	1460.647459	730.827368	1443.620910	722.314093	1442.636894	721.822085	A	1048.535661	524.771469	1031.509112	516.258194	1030.525096	515.766186	6
15	1899.872785	950.440031	1882.846236	941.926756	1881.862220	941.434748	Q	977.498547	489.252912	960.471998	480.739637	959.487982	480.247629	5
16	2028.915378	1014.961327	2011.888829	1006.448053	2010.904813	1005.956045	E	538.273221	269.640249	521.246672	261.126974	520.262656	260.634966	4
17	2125.968142	1063.487709	2108.941593	1054.974434	2107.957577	1054.482427	P	409.230628	205.118952	392.204079	196.605677			3
18	2263.027054	1132.017165	2246.000505	1123.503890	2245.016489	1123.011883	H	312.177864	156.592570	295.151315	148.079295			2
19							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [ATTVTGTPCQDWAAQEPHR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
84.2	2436.131470	-0.020788	ATTVTGTPCQDWAAQEPHR
32.9	2436.131470	-0.020788	ATTVTGTPCQDWAAQEPHR

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 59350: 2482.232742 from(828.418190,3+) rtinseconds(2207) index(72489)

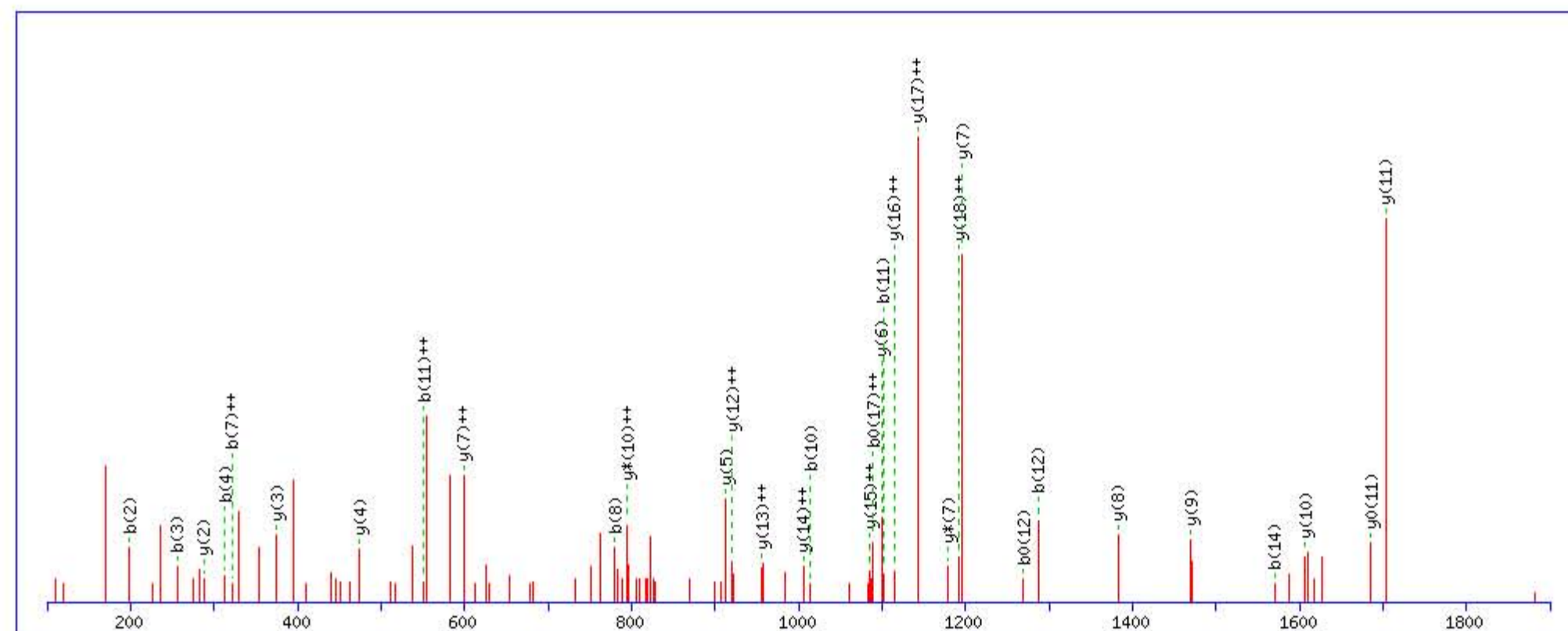
Title: Locus:1.1.1.3302.15 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

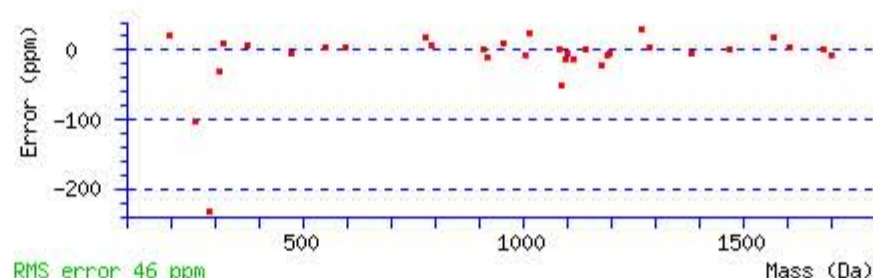
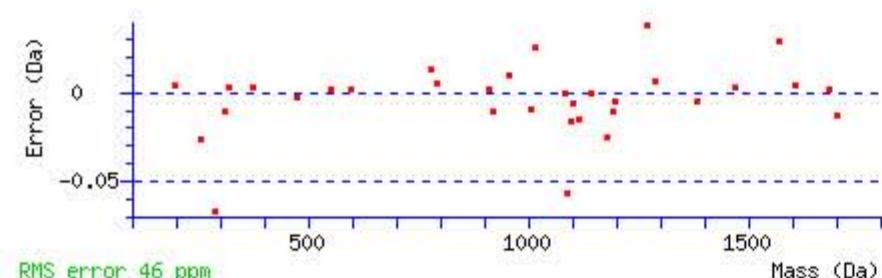
Variable modifications:

Q15 : Biotin:Thermo-21345 (Q)

Ions Score: 49 Expect: 0.00039

Matches : 33/164 fragment ions using 86 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.075690	50.541483					V							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
48.8	2482.251480	-0.018738	VVGGCVAHPHSWPWQVSLR

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

MASCOT Search Results

Peptide View

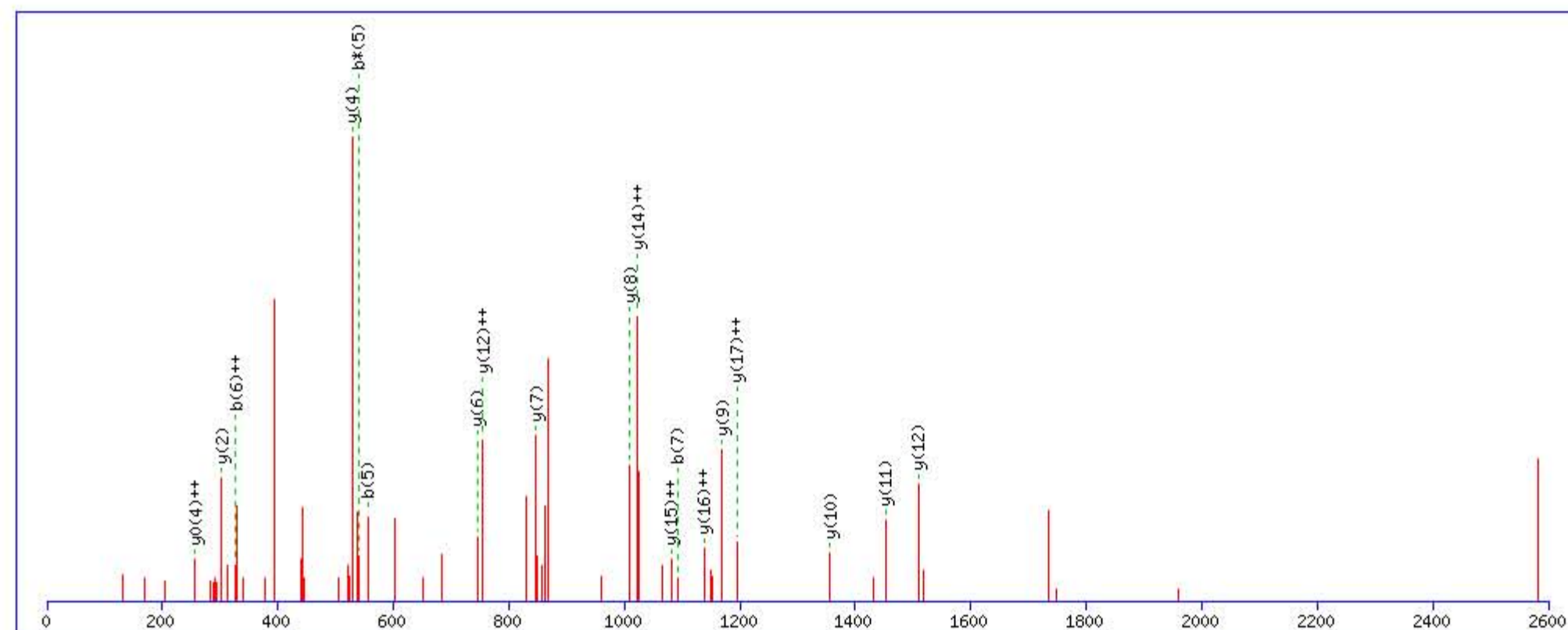
MS/MS Fragmentation of **NPDNDPQGPWCYTIDPEKR**
 Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

Match to Query 61164: 2600.115822 from(867.712550,3+) rtinseconds(1956) index(70925)
 Title: Locus:1.1.1.3214.25 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

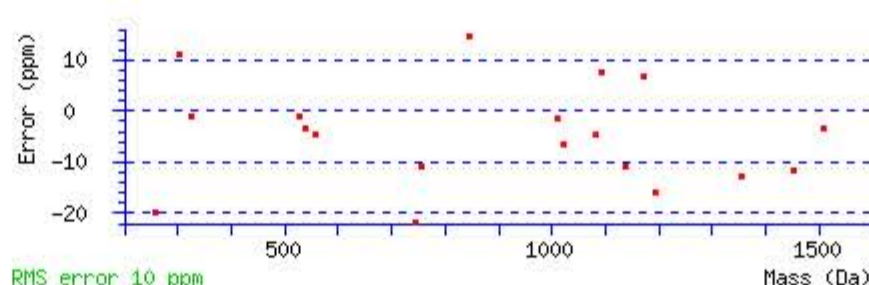
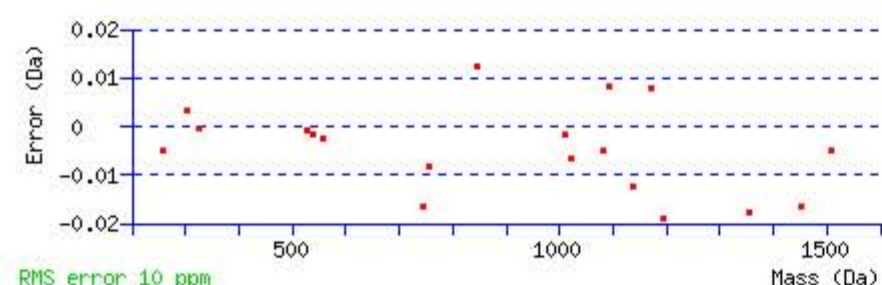
Or, Plot from to Da

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: 37 Expect: 0.00065
 Matches : 20/208 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	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 [NPDNDPQGPWCYTIDPEKR](#)
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.4	2600.142410	-0.026588	NPDNDPQGPWCYTIDPEKR

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 63164: 2806.463576 from(702.623170,4+) rtinseconds(2093) index(71740)

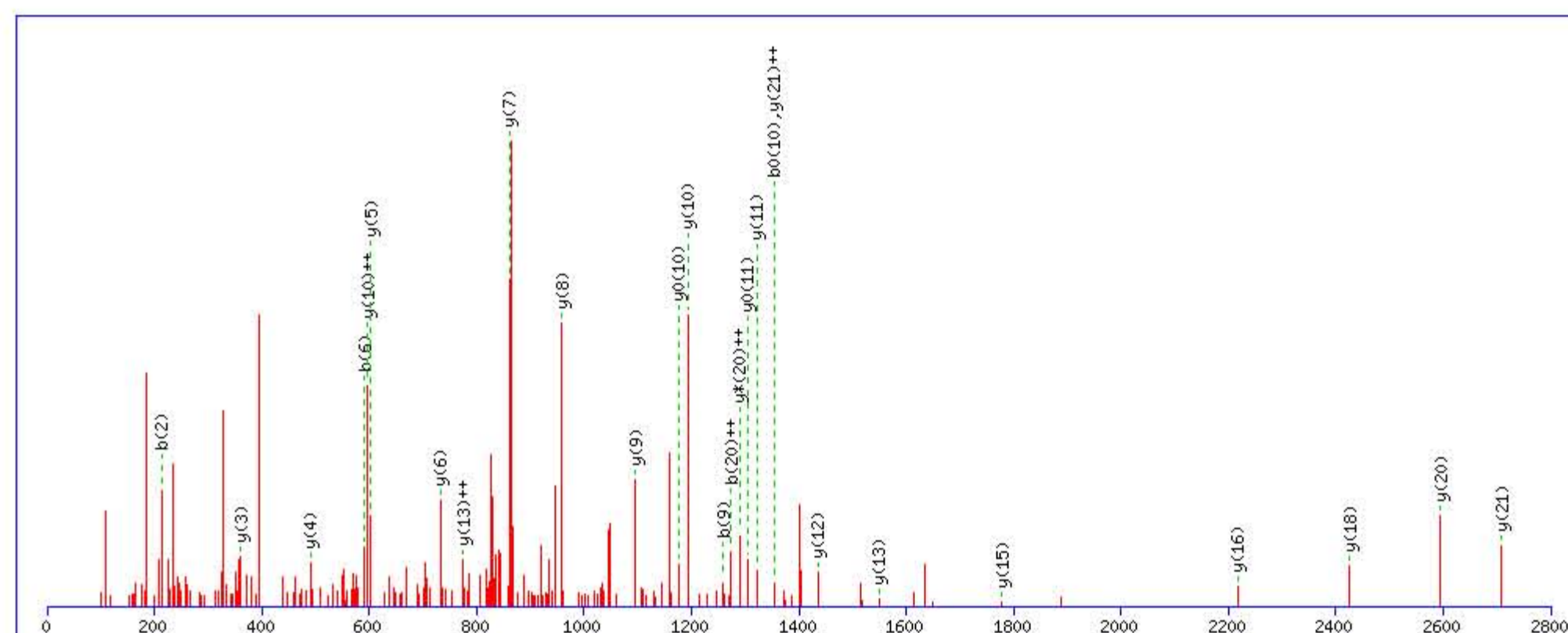
Title: Locus:1.1.1.3262.17 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

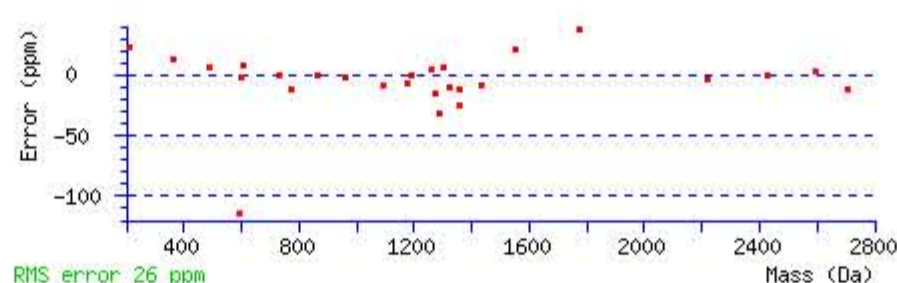
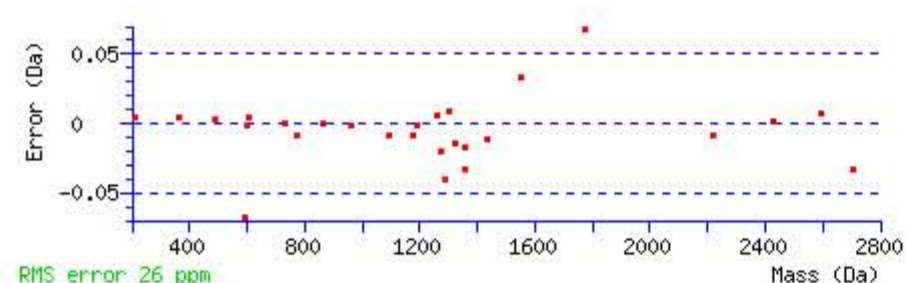
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 88 Expect: 6.4e-009

Matches : 27/224 fragment ions using 55 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.075690	50.541483					V							22
2	213.159754	107.083515					I	2708.418847	1354.713061	2691.392298	1346.199787	2690.408282	1345.707779	21
3	326.243818	163.625547					L	2595.334783	1298.171029	2578.308234	1289.657755	2577.324218	1289.165747	20
4	383.265282	192.136279					G	2482.250719	1241.628997	2465.224170	1233.115723	2464.240154	1232.623715	19
5	454.302396	227.654836					A	2425.229255	1213.118265	2408.202706	1204.604991	2407.218690	1204.112983	18
6	591.361308	296.184292					H	2354.192141	1177.599708	2337.165592	1169.086434	2336.181576	1168.594426	17
7	1030.586634	515.796955	1013.560085	507.283681			Q	2217.133229	1109.070252	2200.106680	1100.556978	2199.122664	1100.064970	16
8	1159.629227	580.318252	1142.602678	571.804977	1141.618662	571.312969	E	1777.907903	889.457590	1760.881354	880.944315	1759.897338	880.452307	15
9	1258.697641	629.852459	1241.671092	621.339184	1240.687076	620.847176	V	1648.865310	824.936293	1631.838761	816.423019	1630.854745	815.931011	14
10	1372.740568	686.873922	1355.714019	678.360648	1354.730003	677.868640	N	1549.796896	775.402086	1532.770347	766.888812	1531.786331	766.396804	13
11	1485.824632	743.415954	1468.798083	734.902680	1467.814067	734.410672	L	1435.753969	718.380623	1418.727420	709.867348	1417.743404	709.375340	12
12	1614.867225	807.937251	1597.840676	799.423976	1596.856660	798.931968	E	1322.669905	661.838591	1305.643356	653.325316	1304.659340	652.833308	11
13	1711.919989	856.463633	1694.893440	847.950358	1693.909424	847.458350	P	1193.627312	597.317294	1176.600763	588.804020	1175.616747	588.312012	10
14	1848.978901	924.993089	1831.952352	916.479814	1830.968336	915.987806	H	1096.574548	548.790912	1079.547999	540.277638	1078.563983	539.785630	9
15	1948.047315	974.527296	1931.020766	966.014021	1930.036750	965.522013	V	959.515636	480.261456	942.489087	471.748182	941.505071	471.256174	8
16	2076.105893	1038.556584	2059.079344	1030.043310	2058.095328	1029.551302	Q	860.447222	430.727249	843.420673	422.213975	842.436657	421.721967	7
17	2205.148486	1103.077881	2188.121937	1094.564606	2187.137921	1094.072598	E	732.388644	366.697960	715.362095	358.184686	714.378079	357.692678	6
18	2318.232550	1159.619913	2301.206001	1151.106638	2300.221985	1150.614631	I	603.346051	302.176664	586.319502	293.663389	585.335486	293.171381	5
19	2447.275143	1224.141210	2430.248594	1215.627935	2429.264578	1215.135927	E	490.261987	245.634631	473.235438	237.121357	472.251422	236.629349	4
20	2546.343557	1273.675417	2529.317008	1265.162142	2528.332992	1264.670134	V	361.219394	181.113335	344.192845	172.600060	343.208829	172.108052	3
21	2633.375585	1317.191431	2616.349036	1308.678156	2615.365020	1308.186148	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
22							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [VILGAHQEVNLEPHVQEIEVSR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
87.9	2806.479965	-0.016389	VILGAHQEVNLEPHVQEIEVSR
17.4	2806.479965	-0.016389	VILGAHQEVNLEPHVQEIEVSR
0.6	2806.424484	0.039092	VAQGIMKLCLEELFADVTISVEGR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **VILGAHQEVNLEPHVQEIIVSR**

Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

Match to Query 63165: 2806.466856 from(702.623990,4+) rtinseconds(2067) index(71584)

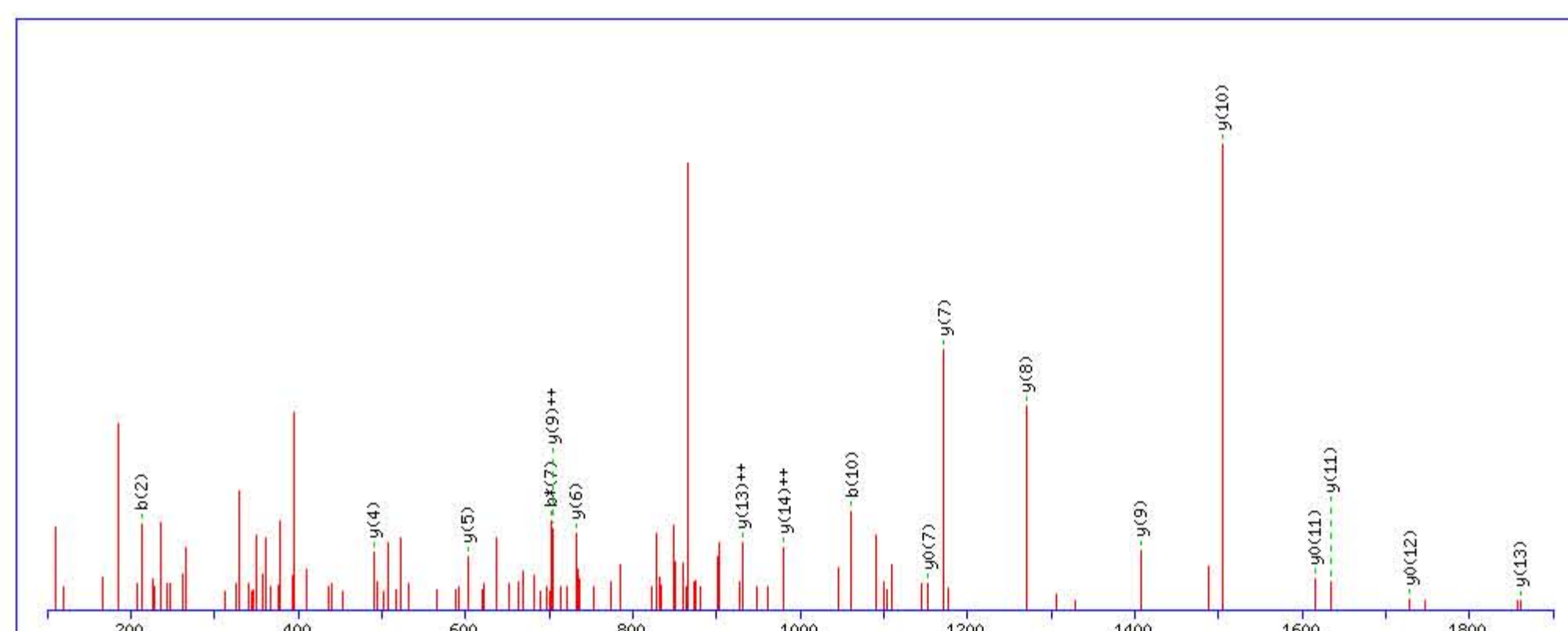
Title: Locus:1.1.1.3253.20 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

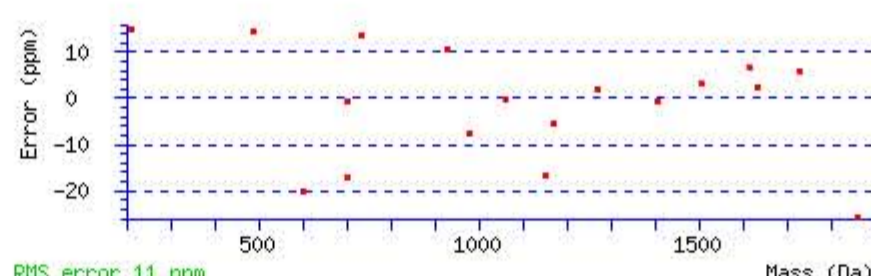
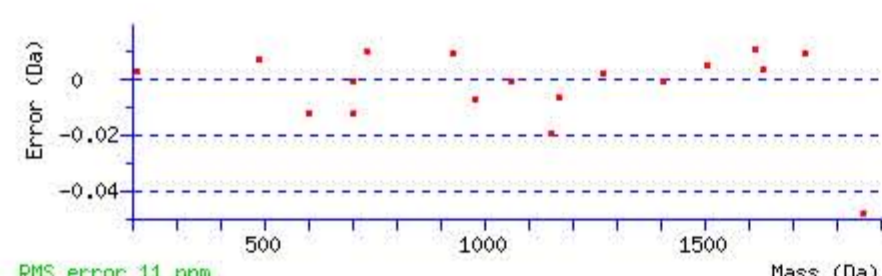
Variable modifications:

Q16 : Biotin:Thermo-21345 (Q)

Ions Score: 41 Expect: 0.0021

Matches : 18/224 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	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 [VILGAHQEVNLEPHVQEIIVSR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.8	2806.479965	-0.013109	VILGAHQEVNLEPHVQEIIVSR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **TMSGLECAWDSQSPHAHGYIPSK**

Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

Match to Query 65483: 2997.335416 from(750.341130,4+) rtinseconds(1931) index(70719)

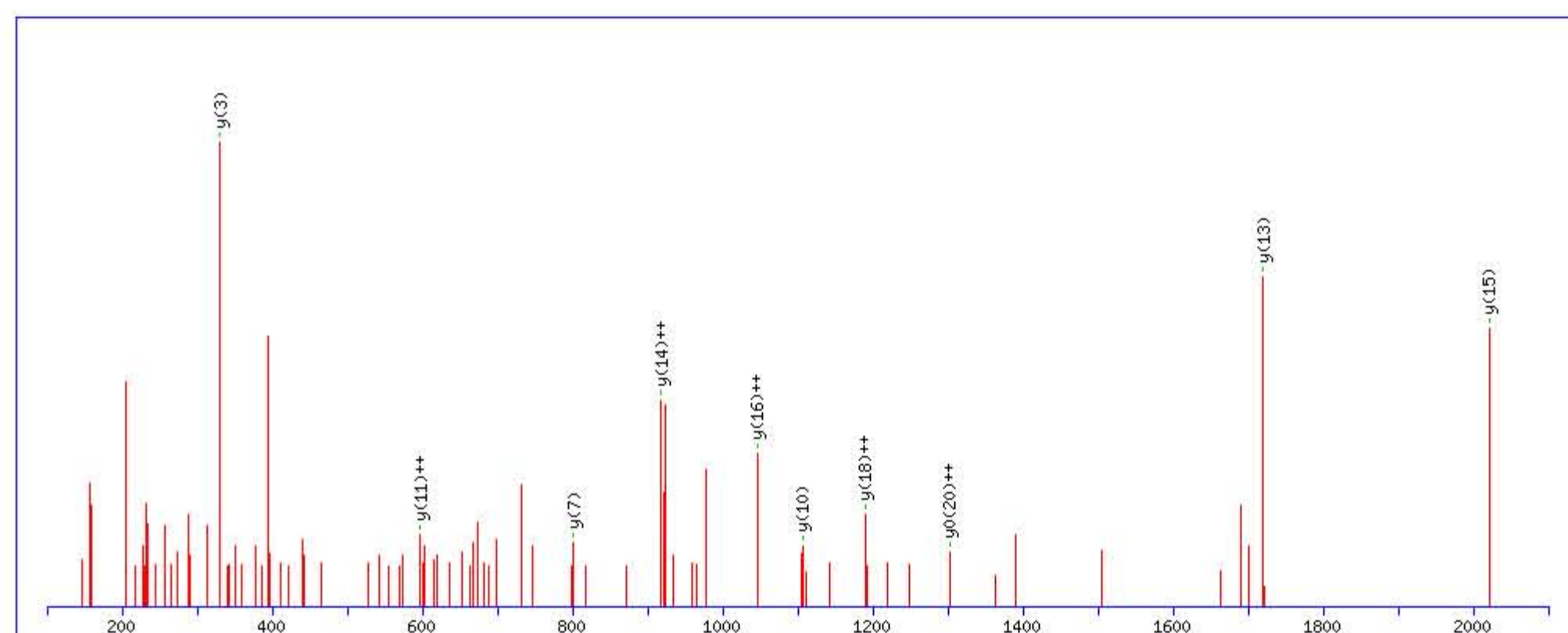
Title: Locus:1.1.1.3206.13 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

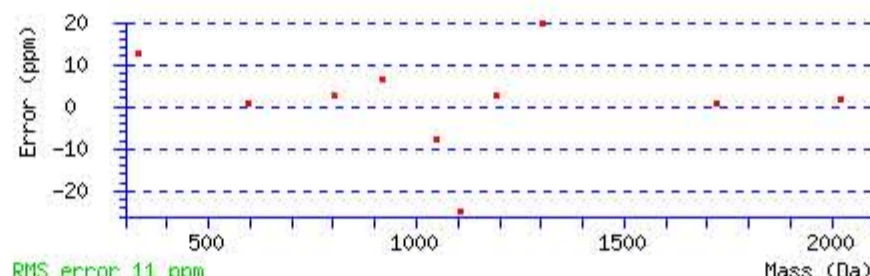
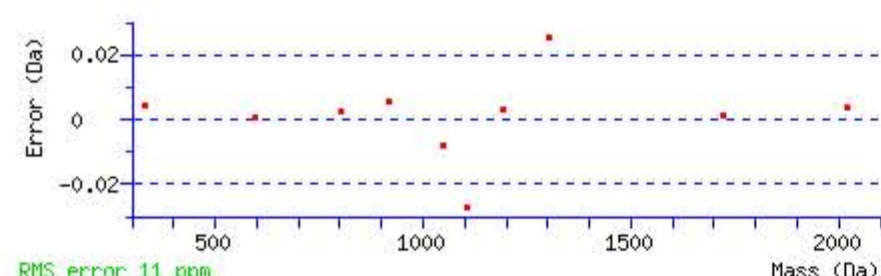
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 30 Expect: 0.0076

Matches : 10/260 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	102.054955	51.531116			84.044390	42.525833	T							24
2	233.095440	117.051358			215.084875	108.046076	M	2897.316768	1449.162022	2880.290219	1440.648748	2879.306203	1440.156740	23
3	320.127468	160.567372			302.116903	151.562089	S	2766.276283	1383.641780	2749.249734	1375.128505	2748.265718	1374.636497	22
4	377.148932	189.078104			359.138367	180.072821	G	2679.244255	1340.125766	2662.217706	1331.612491	2661.233690	1331.120483	21
5	490.232996	245.620136			472.222431	236.614853	L	2622.222791	1311.615034	2605.196242	1303.101759	2604.212226	1302.609751	20
6	619.275589	310.141433			601.265024	301.136150	E	2509.138727	1255.073002	2492.112178	1246.559727	2491.128162	1246.067719	19
7	779.306238	390.156757			761.295673	381.151475	C	2380.096134	1190.551705	2363.069585	1182.038431	2362.085569	1181.546423	18
8	907.364816	454.186046	890.338267	445.672772	889.354251	445.180764	Q	2220.065485	1110.536381	2203.038936	1102.023106	2202.054920	1101.531098	17
9	978.401930	489.704603	961.375381	481.191329	960.391365	480.699321	A	2092.006907	1046.507092	2074.980358	1037.993817	2073.996342	1037.501809	16
10	1164.481243	582.744260	1147.454694	574.230985	1146.470678	573.738977	W	2020.969793	1010.988535	2003.943244	1002.475260	2002.959228	1001.983252	15
11	1279.508186	640.257731	1262.481637	631.744457	1261.497621	631.252449	D	1834.890480	917.948878	1817.863931	909.435604	1816.879915	908.943596	14
12	1366.540214	683.773745	1349.513665	675.260471	1348.529649	674.768463	S	1719.863537	860.435407	1702.836988	851.922132	1701.852972	851.430124	13
13	1805.765540	903.386408	1788.738991	894.873134	1787.754975	894.381126	Q	1632.831509	816.919393	1615.804960	808.406118	1614.820944	807.914110	12
14	1892.797568	946.902422	1875.771019	938.389148	1874.787003	937.897140	S	1193.606183	597.306730	1176.579634	588.793455	1175.595618	588.301447	11
15	1989.850332	995.428804	1972.823783	986.915530	1971.839767	986.423522	P	1106.574155	553.790716	1089.547606	545.277441	1088.563590	544.785433	10
16	2126.909244	1063.958260	2109.882695	1055.444986	2108.898679	1054.952978	H	1009.521391	505.264334	992.494842	496.751059	991.510826	496.259051	9
17	2197.946358	1099.476817	2180.919809	1090.963543	2179.935793	1090.471535	A	872.462479	436.734878	855.435930	428.221603	854.451914	427.729595	8
18	2335.005270	1168.006273	2317.978721	1159.492999	2316.994705	1159.000991	H	801.425365	401.216321	784.398816	392.703046	783.414800	392.211038	7
19	2392.026734	1196.517005	2375.000185	1188.003731	2374.016169	1187.511723	G	664.366453	332.686865	647.339904	324.173590	646.355888	323.681582	6
20	2555.090063	1278.048670	2538.063514	1269.535395	2537.079498	1269.043387	Y	607.344989	304.176133	590.318440	295.662858	589.334424	295.170850	5
21	2668.174127	1334.590702	2651.147578	1326.077427	2650.163562	1325.585419	I	444.281660	222.644468	427.255111	214.131194	426.271095	213.639186	4
22	2765.226891	1383.117084	2748.200342	1374.603809	2747.216326	1374.111801	P	331.197596	166.102436	314.171047	157.589162	313.187031	157.097154	3
23	2852.258919	1426.633098	2835.232370	1418.119823	2834.248354	1417.627815	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
24							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **TMSGLECAWDSQSPHAHGYIPSK**

(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	2997.357162	-0.021746	TMSGLECAWDSQSPHAHGYIPSK
2.3	2997.357162	-0.021746	TMSGLECAWDSQSPHAHGYIPSK

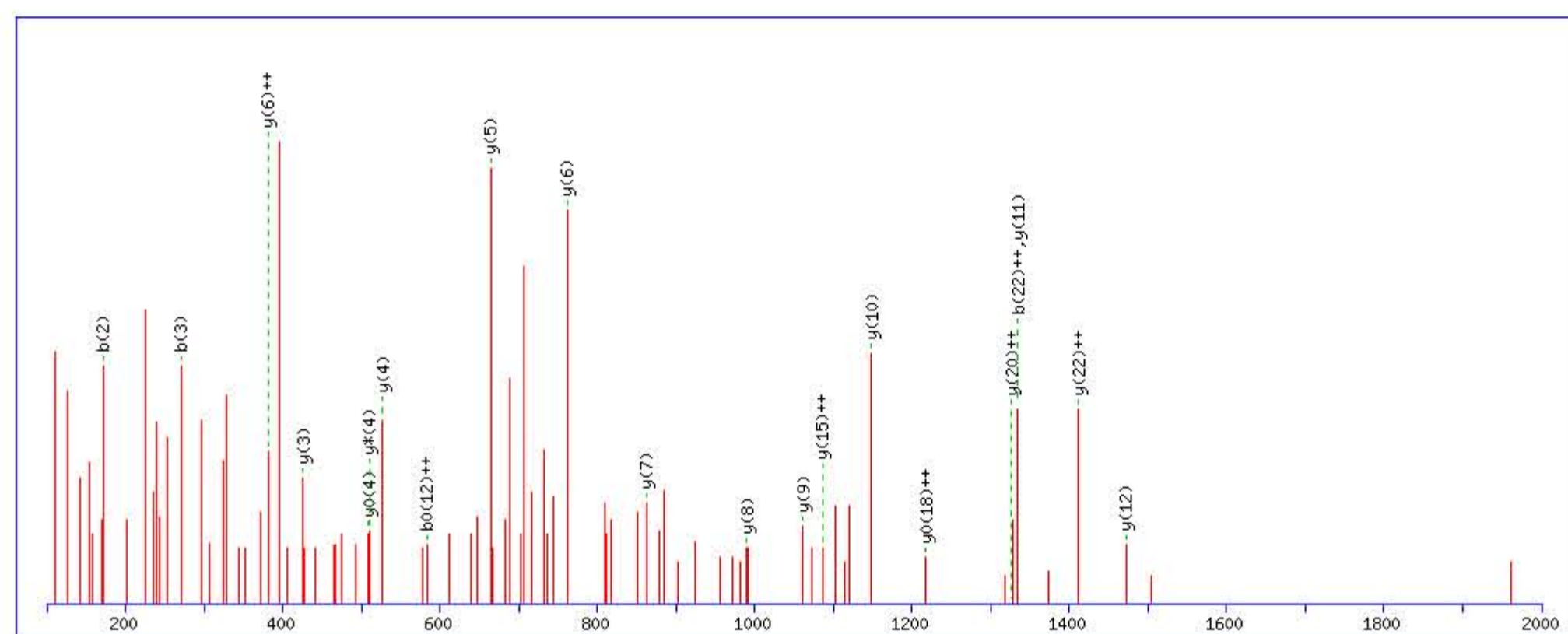
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNVAVTVSGHTCQHWSAQTPHTHNR**
 Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

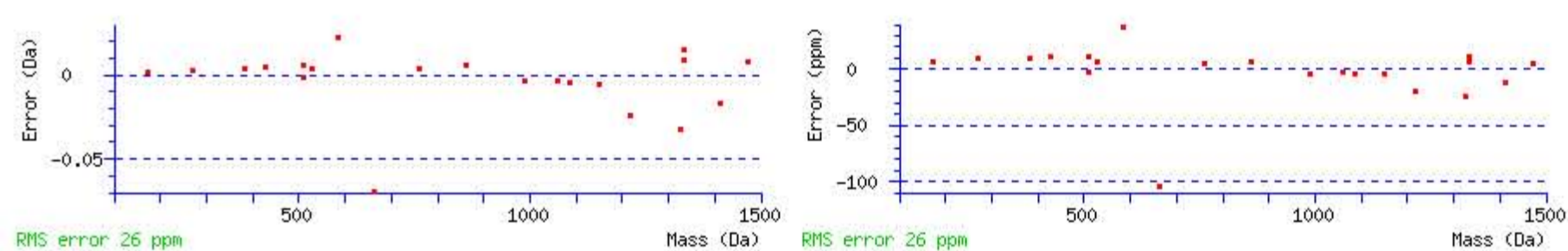
Match to Query 66223: 3092.444820 from(619.496240,5+) rtinseconds(1451) index(67735)
 Title: Locus:1.1.1.3038.23 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 42 Expect: 0.0011
 Matches : 21/270 fragment ions using 41 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.028740	29.518008					G							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
42.0	3092.457016	-0.012196	GNVAVTVSGHTCQHWSAQTPHTHNR
10.4	3092.457016	-0.012196	GNVAVTVSGHTCQHWSAQTPHTHNR

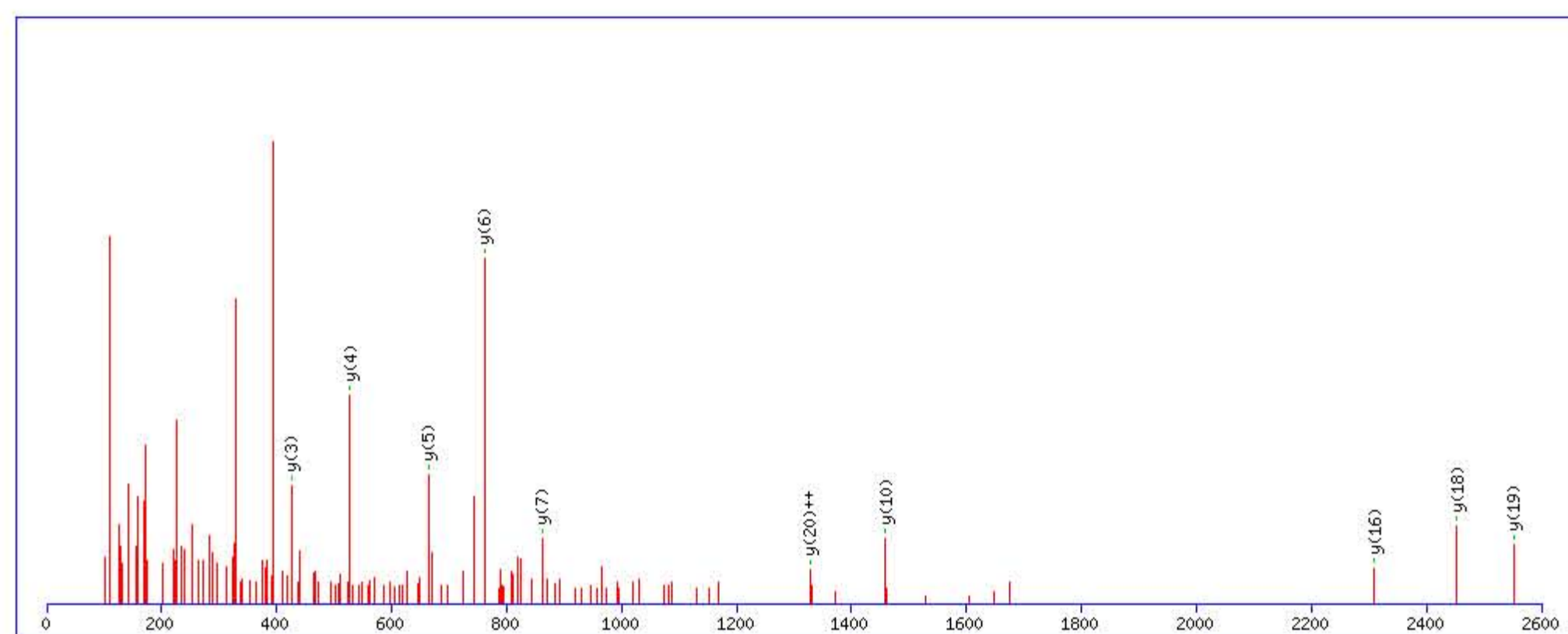
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNVAVTVSGHTCQHWSAQTPHTHNR**
 Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

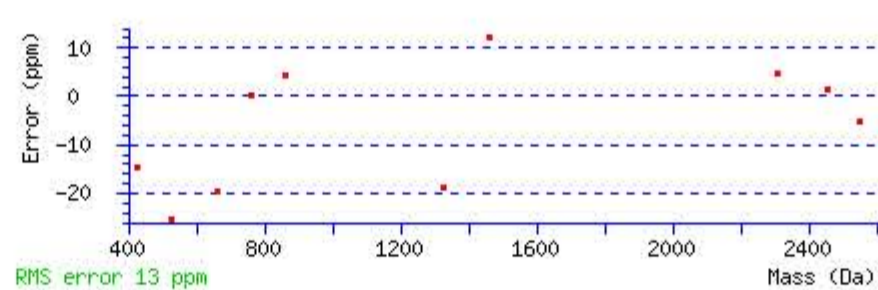
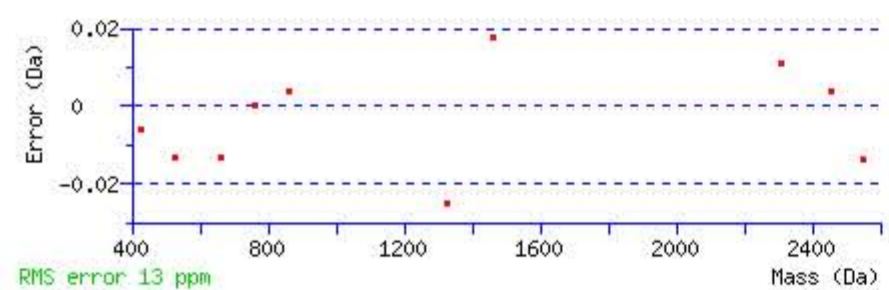
Match to Query 66229: 3092.465244 from(516.418150,6+) rtinseconds(1412) index(67412)
 Title: Locus:1.1.1.3025.15 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 44 Expect: 0.0008
 Matches : 10/270 fragment ions using 18 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.028740	29.518008					G							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
44.1	3092.457016	0.008228	GNVAVTVSGHTCQHWSAQTPHTHNR
33.2	3092.457016	0.008228	GNVAVTVSGHTCQHWSAQTPHTHNR

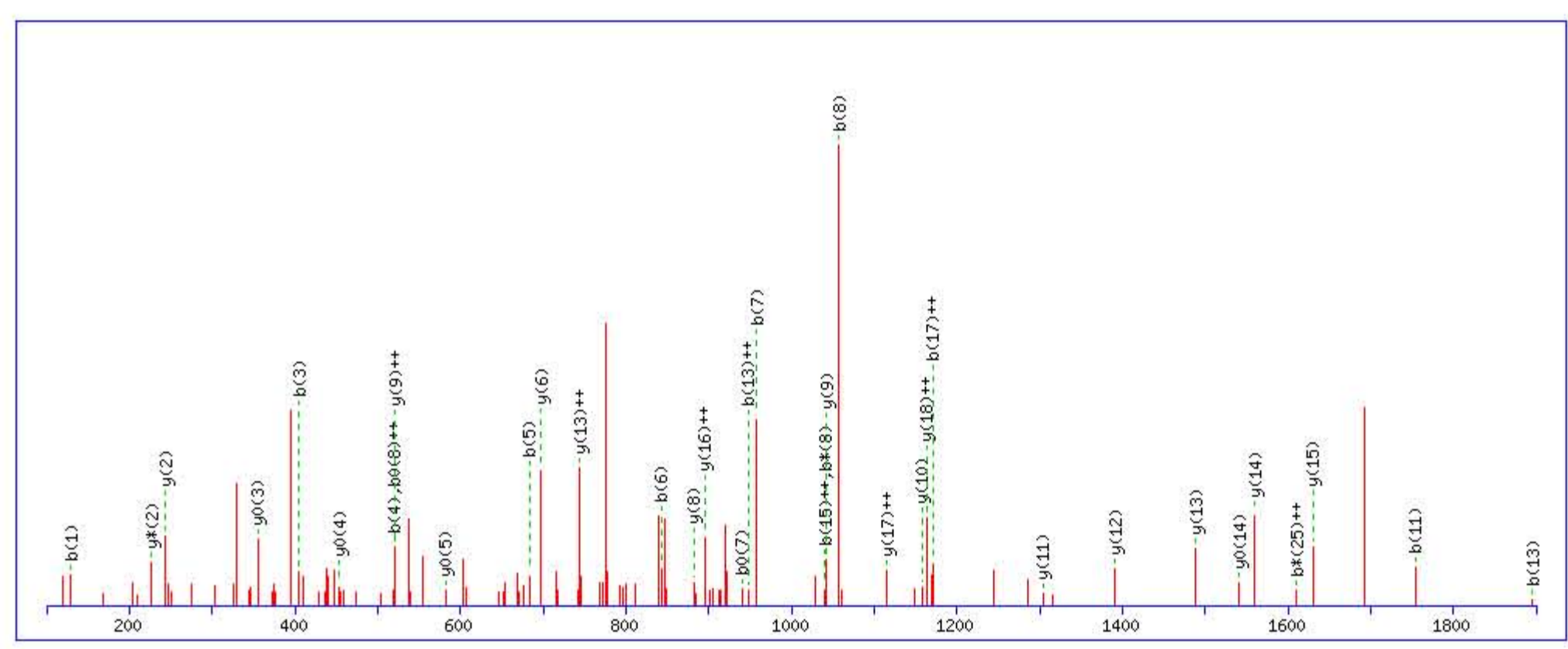
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **KLYDYCDVPQCAAPSFDCGKQVEPK**
 Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

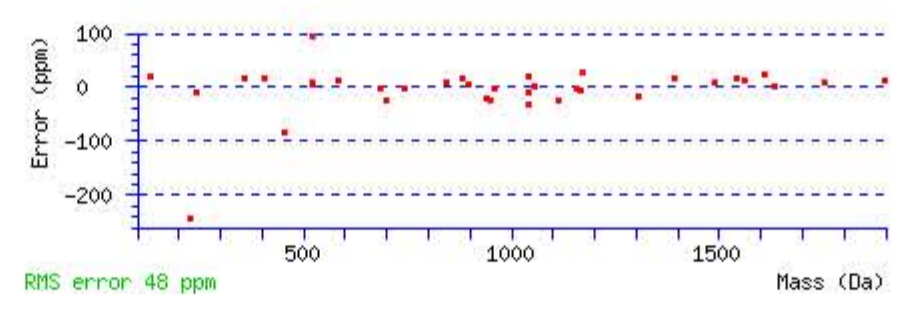
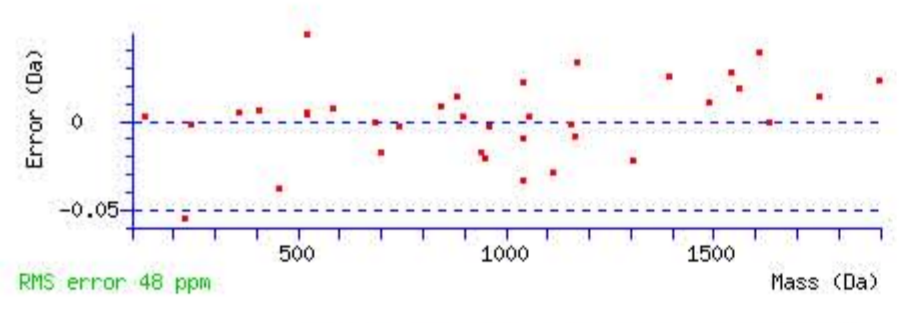
Match to Query 69888: 3382.520736 from(846.637460,4+) rtinseconds(1982) index(71119)
 Title: Locus:1.1.1.3223.14 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 3382.549469
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q10 : Biotin:Thermo-21345 (Q)
 Ions Score: 44 Expect: 0.00034
 Matches : 36/290 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	129.102239	65.054757	112.075690	56.541483			K							26
2	242.186303	121.596790	225.159754	113.083515			L	3255.461780	1628.234528	3238.435231	1619.721253	3237.451215	1619.229245	25
3	405.249632	203.128454	388.223083	194.615180			Y	3142.377716	1571.692496	3125.351167	1563.179221	3124.367151	1562.687213	24
4	520.276575	260.641926	503.250026	252.128651	502.266010	251.636643	D	2979.314387	1490.160831	2962.287838	1481.647557	2961.303822	1481.155549	23
5	683.339904	342.173590	666.313355	333.660316	665.329339	333.168308	Y	2864.287444	1432.647360	2847.260895	1424.134085	2846.276879	1423.642077	22
6	843.370553	422.188915	826.344004	413.675640	825.359988	413.183632	C	2701.224115	1351.115695	2684.197566	1342.602421	2683.213550	1342.110413	21
7	958.397496	479.702386	941.370947	471.189112	940.386931	470.697104	D	2541.193466	1271.100371	2524.166917	1262.587096	2523.182901	1262.095088	20
8	1057.465910	529.236593	1040.439361	520.723319	1039.455345	520.231311	V	2426.166523	1213.586899	2409.139974	1205.073625	2408.155958	1204.581617	19
9	1154.518674	577.762975	1137.492125	569.249701	1136.508109	568.757693	P	2327.098109	1164.052692	2310.071560	1155.539418	2309.087544	1155.047410	18
10	1593.744000	797.375638	1576.717451	788.862364	1575.733435	788.370356	Q	2230.045345	1115.526310	2213.018796	1107.013036	2212.034780	1106.521028	17
11	1753.774649	877.390963	1736.748100	868.877688	1735.764084	868.385680	C	1790.820019	895.913647	1773.793470	887.400373	1772.809454	886.908365	16
12	1824.811763	912.909520	1807.785214	904.396245	1806.801198	903.904237	A	1630.789370	815.898323	1613.762821	807.385048	1612.778805	806.893040	15
13	1895.848877	948.428077	1878.822328	939.914802	1877.838312	939.422794	A	1559.752256	780.379766	1542.725707	771.866491	1541.741691	771.374483	14
14	1992.901641	996.954459	1975.875092	988.441184	1974.891076	987.949176	P	1488.715142	744.861209	1471.688593	736.347934	1470.704577	735.855926	13
15	2079.933669	1040.470472	2062.907120	1031.957198	2061.923104	1031.465190	S	1391.662378	696.334827	1374.635829	687.821552	1373.651813	687.329544	12
16	2227.002083	1114.004679	2209.975534	1105.491405	2208.991518	1104.999397	F	1304.630350	652.818813	1287.603801	644.305538	1286.619785	643.813530	11
17	2342.029026	1171.518151	2325.002477	1163.004876	2324.018461	1162.512868	D	1157.561936	579.284606	1140.535387	570.771331	1139.551371	570.279323	10
18	2502.059675	1251.533475	2485.033126	1243.020201	2484.049110	1242.528193	C	1042.534993	521.771135	1025.508444	513.257860	1024.524428	512.765852	9
19	2559.081139	1280.044207	2542.054590	1271.530933	2541.070574	1271.038925	G	882.504344	441.755810	865.477795	433.242536	864.493779	432.750528	8
20	2687.176102	1344.091689	2670.149553	1335.578414	2669.165537	1335.086406	K	825.482880	413.245078	808.456331	404.731804	807.472315	404.239796	7
21	2784.228866	1392.618071	2767.202317	1384.104796	2766.218301	1383.612788	P	697.387917	349.197597	680.361368	340.684322	679.377352	340.192314	6
22	2912.287444	1456.647360	2895.260895	1448.134085	2894.276879	1447.642077	Q	600.335153	300.671215	583.308604	292.157940	582.324588	291.665932	5
23	3011.355858	1506.181567	2994.329309	1497.668292	2993.345293	1497.176284	V	472.276575	236.641925	455.250026	228.128651	454.266010	227.636643	4
24	3140.398451	1570.702863	3123.371902	1562.189589	3122.387886	1561.697581	E	373.208161	187.107719	356.181612	178.594444	355.197596	178.102436	3
25	3237.451215	1619.229245	3220.424666	1610.715971	3219.440650	1610.223963	P	244.165568	122.586422	227.139019	114.073148			2
26							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.5	3382.549469	-0.028733	KLYDYCDVPQCAAPSFDCGKQVEPK
1.7	3382.549469	-0.028733	KLYDYCDVPQCAAPSFDCGKQVEPK

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 70131: 3403.606320 from(681.728540,5+) rtinseconds(1663) index(69050)

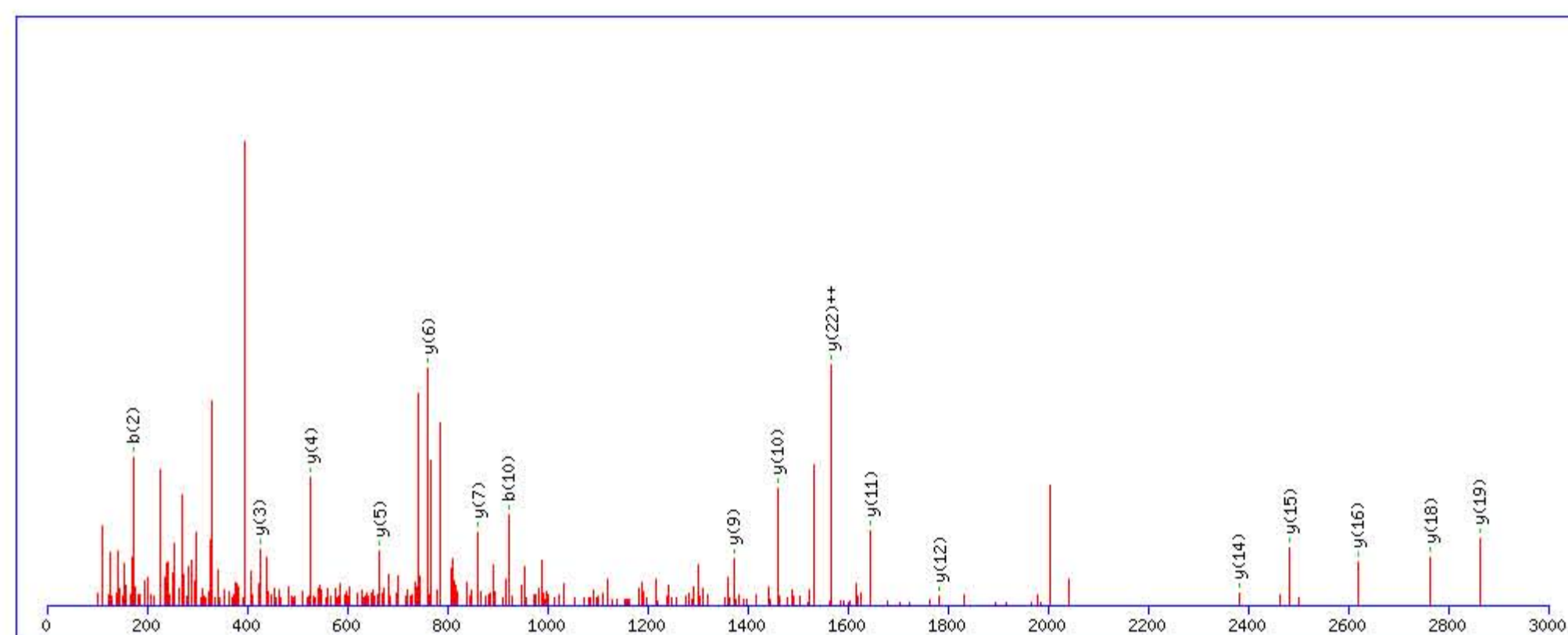
Title: Locus:1.1.1.3112.9 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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:

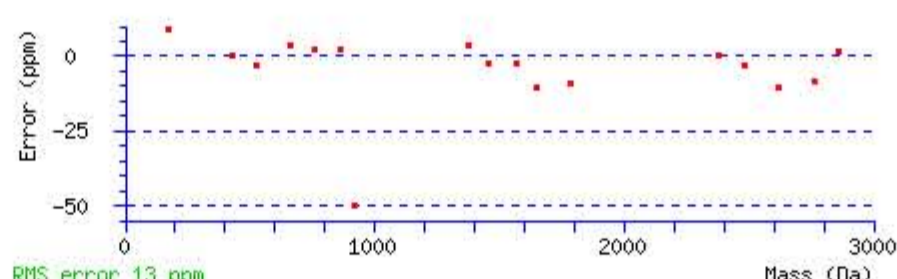
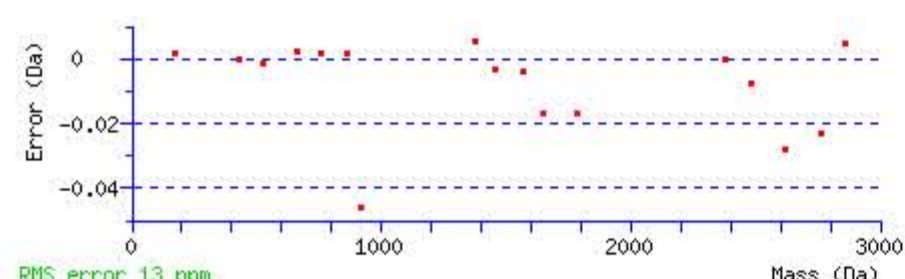
Q13 : Biotin:Thermo-21345 (Q)

Q18 : Biotin:Thermo-21345 (Q)

Ions Score: 92 Expect: 1.5e-008

Matches : 17/270 fragment ions using 26 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.028740	29.518008					G							25
2	172.071667	86.539471	155.045118	78.026197			N	3347.609538	1674.308407	3330.582989	1665.795132	3329.598973	1665.303124	24
3	271.140081	136.073679	254.113532	127.560404			V	3233.566611	1617.286943	3216.540062	1608.773669	3215.556046	1608.281661	23
4	342.177195	171.592236	325.150646	163.078961			A	3134.498197	1567.752736	3117.471648	1559.239462	3116.487632	1558.747454	22
5	441.245609	221.126443	424.219060	212.613168			V	3063.461083	1532.234179	3046.434534	1523.720905	3045.450518	1523.228897	21
6	542.293288	271.650282	525.266739	263.137008	524.282723	262.645000	T	2964.392669	1482.699972	2947.366120	1474.186698	2946.382104	1473.694690	20
7	641.361702	321.184489	624.335153	312.671215	623.351137	312.179207	V	2863.344990	1432.176133	2846.318441	1423.662858	2845.334425	1423.170850	19
8	728.393730	364.700503	711.367181	356.187229	710.383165	355.695221	S	2764.276576	1382.641926	2747.250027	1374.128651	2746.266011	1373.636643	18
9	785.415194	393.211235	768.388645	384.697961	767.404629	384.205953	G	2677.244548	1339.125912	2660.217999	1330.612637	2659.233983	1330.120629	17
10	922.474106	461.740691	905.447557	453.227417	904.463541	452.735409	H	2620.223084	1310.615180	2603.196535	1302.101905	2602.212519	1301.609897	16
11	1023.521785	512.264530	1006.495236	503.751256	1005.511220	503.259248	T	2483.164172	1242.085724	2466.137623	1233.572449	2465.153607	1233.080441	15
12	1183.552434	592.279855	1166.525885	583.766581	1165.541869	583.274572	C	2382.116493	1191.561884	2365.089944	1183.048610	2364.105928	1182.556602	14
13	1622.777760	811.892518	1605.751211	803.379244	1604.767195	802.887236	Q	2222.085844	1111.546560	2205.059295	1103.033285	2204.075279	1102.541277	13
14	1759.836672	880.421974	1742.810123	871.908700	1741.826107	871.416692	H	1782.860518	891.933897	1765.833969	883.420622	1764.849953	882.928614	12
15	1945.915985	973.461631	1928.889436	964.948356	1927.905420	964.456348	W	1645.801606	823.404441	1628.775057	814.891166	1627.791041	814.399158	11
16	2032.948013	1016.977645	2015.921464	1008.464370	2014.937448	1007.972362	S	1459.722293	730.364784	1442.695744	721.851510	1441.711728	721.359502	10
17	2103.985127	1052.496201	2086.958578	1043.982927	2085.974562	1043.490919	A	1372.690265	686.848770	1355.663716	678.335496	1354.679700	677.843488	9
18	2543.210453	1272.108865	2526.183904	1263.595590	2525.199888	1263.103582	Q	1301.653151	651.330213	1284.626602	642.816939	1283.642586	642.324931	8
19	2644.258132	1322.632704	2627.231583	1314.119429	2626.247567	1313.627421	T	862.427825	431.717550	845.401276	423.204276	844.417260	422.712268	7
20	2741.310896	1371.159086	2724.284347	1362.645811	2723.300331	1362.153803	P	761.380146	381.193711	744.353597	372.680436	743.369581	372.188428	6
21	2878.369808	1439.688542	2861.343259	1431.175267	2860.359243	1430.683259	H	664.327382	332.667329	647.300833	324.154054	646.316817	323.662046	5
22	2979.417487	1490.212381	2962.390938	1481.699107	2961.406922	1481.207099	T	527.268470	264.137873	510.241921	255.624598	509.257905	255.132590	4
23	3116.476399	1558.741837	3099.449850	1550.228563	3098.465834	1549.736555	H	426.220791	213.614033	409.194242	205.100759			3
24	3230.519326	1615.763301	3213.492777	1607.250026	3212.508761	1606.758018	N	289.161879	145.084577	272.135330	136.571303			2
25							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **GNVAVTVSGHTCQHWSAQTPHTHNR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
91.7	3403.623764	-0.017444	GNVAVTVSGHTCQHWSAQTPHTHNR

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

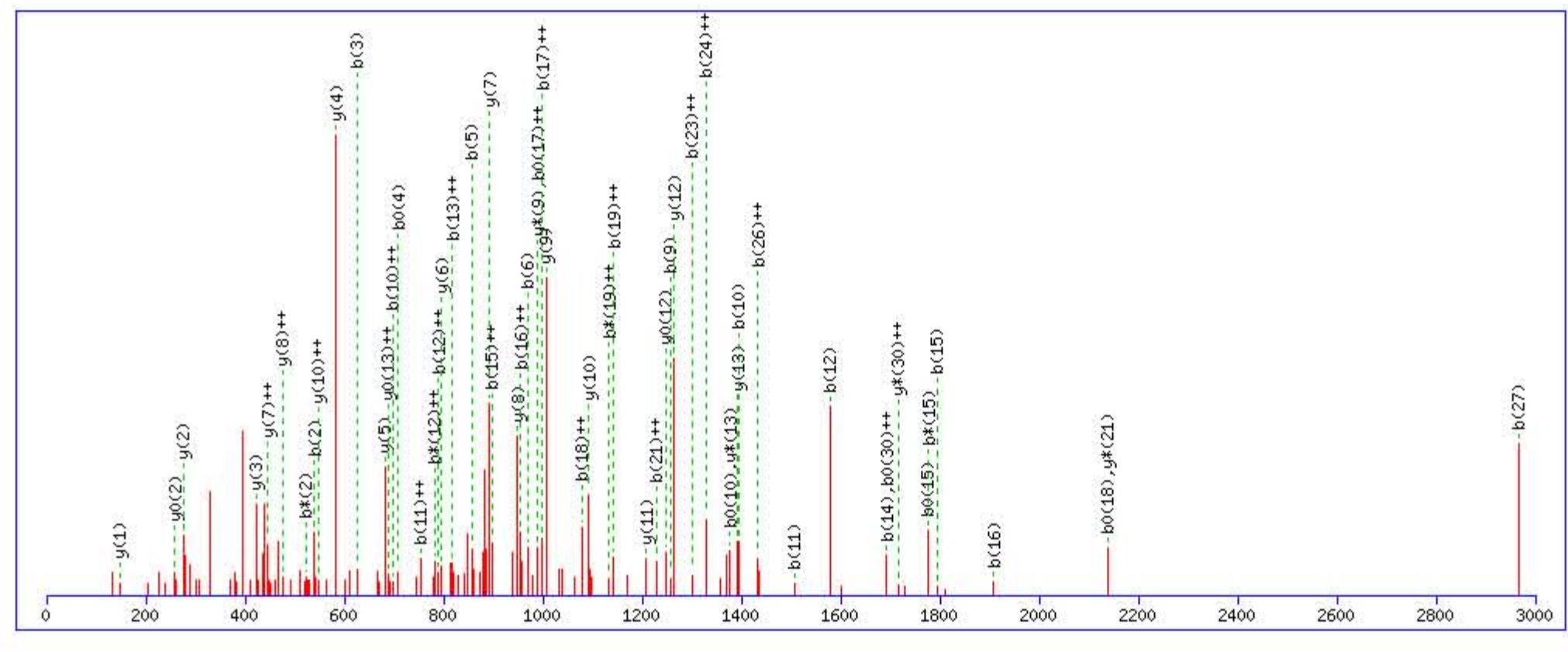
MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **VQSTELCAGHLAGGTDSCQGDSGGPLVCFEK**
 Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

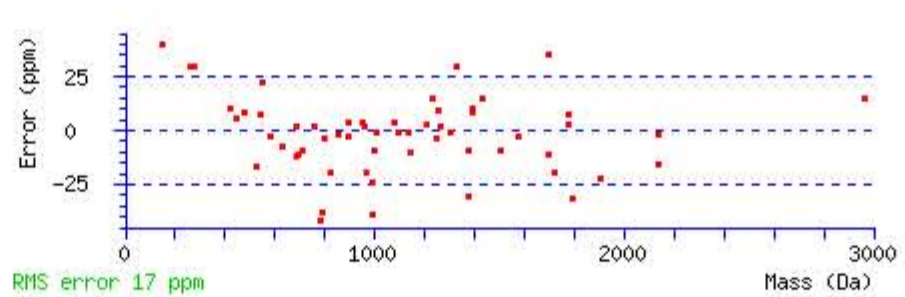
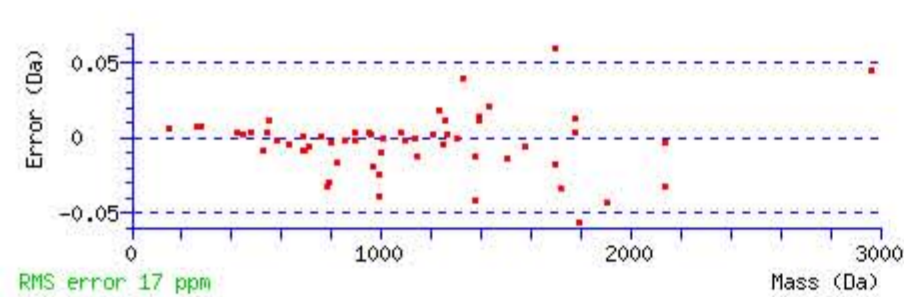
Match to Query 71182: 3547.553096 from(887.895550,4+) rtinseconds(2168) index(72223)
 Title: Locus:1.1.1.3288.25 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 3547.584061
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q2 : Biotin:Thermo-21345 (Q)
 Ions Score: 88 Expect: 5.7e-009
 Matches : 58/352 fragment ions using 104 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.075690	50.541483					V							31
2	539.301016	270.154146	522.274467	261.640872			Q	3449.522877	1725.265076	3432.496328	1716.751802	3431.512312	1716.259794	30
3	626.333044	313.670160	609.306495	305.156886	608.322479	304.664878	S	3010.297551	1505.652413	2993.271002	1497.139139	2992.286986	1496.647131	29
4	727.380723	364.194000	710.354174	355.680725	709.370158	355.188717	T	2923.265523	1462.136399	2906.238974	1453.623125	2905.254958	1453.131117	28
5	856.423316	428.715296	839.396767	420.202022	838.412751	419.710014	E	2822.217844	1411.612560	2805.191295	1403.099285	2804.207279	1402.607277	27
6	969.507380	485.257328	952.480831	476.744054	951.496815	476.252046	L	2693.175251	1347.091263	2676.148702	1338.577989	2675.164686	1338.085981	26
7	1129.538029	565.272653	1112.511480	556.759378	1111.527464	556.267370	C	2580.091187	1290.549231	2563.064638	1282.035957	2562.080622	1281.543949	25
8	1200.575143	600.791210	1183.548594	592.277935	1182.564578	591.785927	A	2420.060538	1210.533907	2403.033989	1202.020632	2402.049973	1201.528624	24
9	1257.596607	629.301942	1240.570058	620.788667	1239.586042	620.296659	G	2349.023424	1175.015350	2331.996875	1166.502075	2331.012859	1166.010067	23
10	1394.655519	697.831397	1377.628970	689.318123	1376.644954	688.826115	H	2292.001960	1146.504618	2274.975411	1137.991343	2273.991395	1137.499335	22
11	1507.739583	754.373429	1490.713034	745.860155	1489.729018	745.368147	L	2154.943048	1077.975162	2137.916499	1069.461887	2136.932483	1068.969879	21
12	1578.776697	789.891986	1561.750148	781.378712	1560.766132	780.886704	A	2041.858984	1021.433130	2024.832435	1012.919855	2023.848419	1012.427847	20
13	1635.798161	818.402718	1618.771612	809.889444	1617.787596	809.397436	G	1970.821870	985.914573	1953.795321	977.401298	1952.811305	976.909290	19
14	1692.819625	846.913450	1675.793076	838.400176	1674.809060	837.908168	G	1913.800406	957.403841	1896.773857	948.890566	1895.789841	948.398558	18
15	1793.867304	897.437290	1776.840755	888.924015	1775.856739	888.432007	T	1856.778942	928.893109	1839.752393	920.379835	1838.768377	919.887826	17
16	1908.894247	954.950761	1891.867698	946.437487	1890.883682	945.945479	D	1755.731263	878.369269	1738.704714	869.855995	1737.720698	869.363987	16
17	1995.926275	998.466775	1978.899726	989.953501	1977.915710	989.461493	S	1640.704320	820.855798	1623.677771	812.342523	1622.693755	811.850515	15
18	2155.956924	1078.482100	2138.930375	1069.968825	2137.946359	1069.476817	C	1553.672292	777.339784	1536.645743	768.826509	1535.661727	768.334501	14
19	2284.015502	1142.511389	2266.988953	1133.998114	2266.004937	1133.506106	Q	1393.641643	697.324459	1376.615094	688.811185	1375.631078	688.319177	13
20	2341.036966	1171.022121	2324.010417	1162.508846	2323.026401	1162.016838	G	1265.583065	633.295170	1248.556516	624.781896	1247.572500	624.289888	12
21	2456.063909	1228.535592	2439.037360	1220.022318	2438.053344	1219.530310	D	1208.561601	604.784438	1191.535052	596.271164	1190.551036	595.779156	11
22	2543.095937	1272.051606	2526.069388	1263.538332	2525.085372	1263.046324	S	1093.534658	547.270967	1076.508109	538.757692	1075.524093	538.265684	10
23	2600.117401	1300.562338	2583.090852	1292.049064	2582.106836	1291.557056	G	1006.502630	503.754953	989.476081	495.241678	988.492065	494.749670	9
24	2657.138865	1329.073070	2640.112316	1320.559796	2639.128300	1320.067788	G	949.481166	475.244221	932.454617	466.730946	931.470601	466.238938	8
25	2754.191629	1377.599452	2737.165080	1369.086178	2736.181064	1368.594170	P	892.459702	446.733489	875.433153	438.220214	874.449137	437.728206	7
26	2867.275693	1434.141484	2850.249144	1425.628210	2849.265128	1425.136202	L	795.406938	398.207107	778.380389	389.693832	777.396373	389.201824	6
27	2966.344107	1483.675691	2949.317558	1475.162417	2948.333542	1474.670409	V	682.322874	341.665075	665.296325	333.151800	664.312309	332.659792	5
28	3126.374756	1563.691016	3109.348207	1555.177741	3108.364191	1554.685733	C	583.254460	292.130868	566.227911	283.617593	565.243895	283.125585	4
29	3273.443170	1637.225223	3256.416621	1628.711948	3255.432605	1628.219940	F	423.223811	212.115543	406.197262	203.602269	405.213246	203.110261	3
30	3402.485763	1701.746519	3385.459214	1693.233245	3384.475198	1692.741237	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
31							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
88.2	3547.584061	-0.030965	VQSTELCAGHLAGGTDSCQGDSGGPLVCFEK
33.3	3547.584061	-0.030965	VQSTELCAGHLAGGTDSCQGDSGGPLVCFEK

MASCOT 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 27657: 1276.565848 from(639.290200,2+) rtinseconds(1474) index(52388)

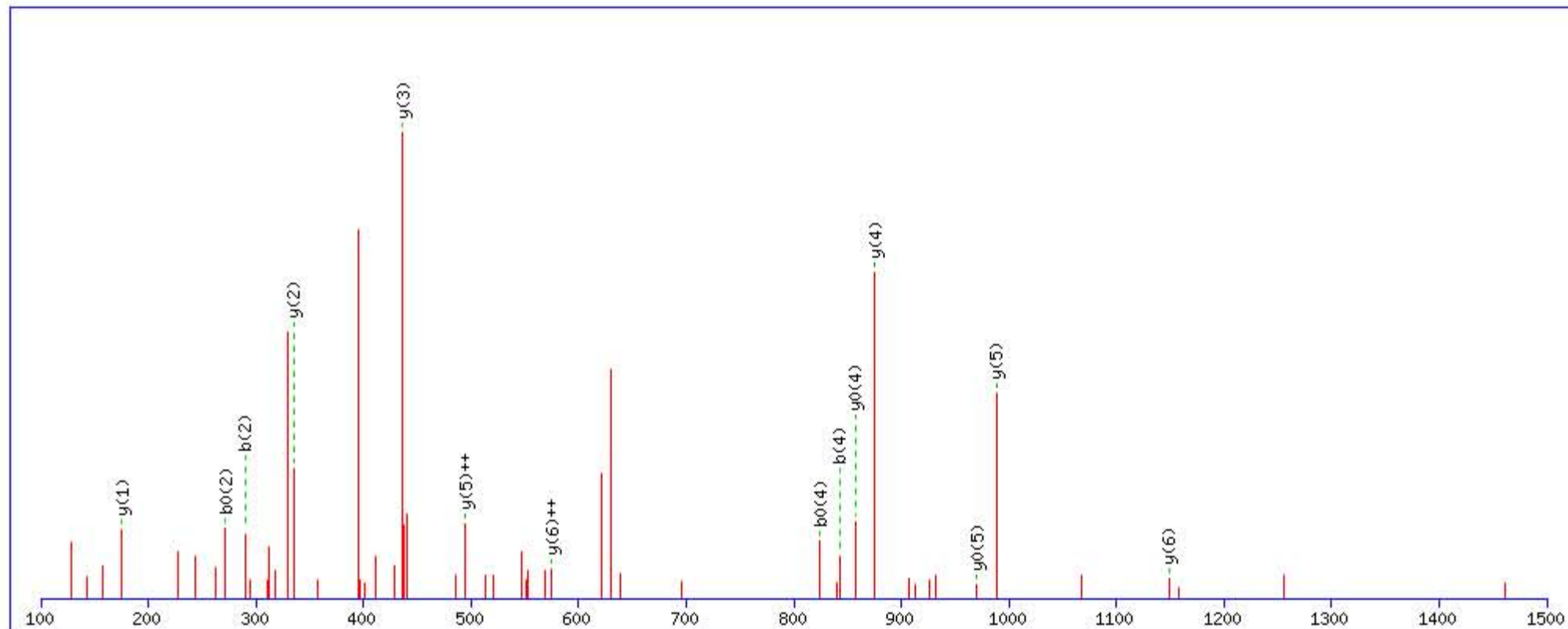
Title: Locus:1.1.1.2999.19 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

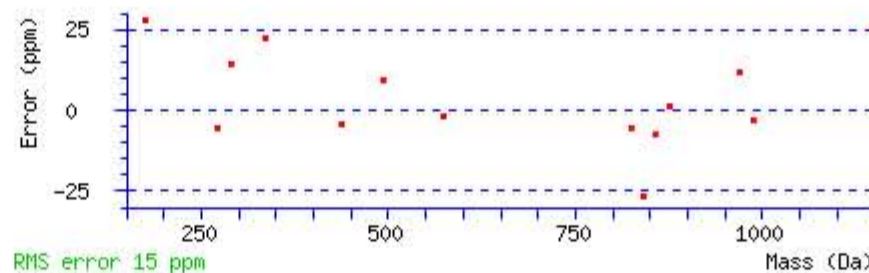
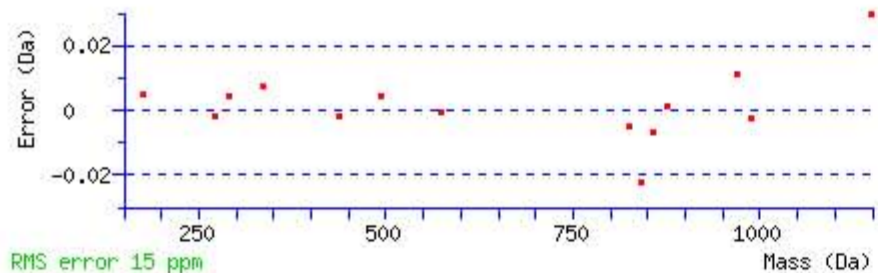
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 33 Expect: 0.0024

Matches : 14/62 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	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
33.4	1276.572632	-0.006784	ECLQTCR
7.1	1276.579605	-0.013757	EEQRSPFNDR
2.9	1276.583862	-0.018014	KMSLSCHVCR
1.2	1276.560516	0.005332	QQVPSSEDSMEK

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 60688: 2545.113702 from(849.378510,3+) rtinseconds(1872) index(54791)

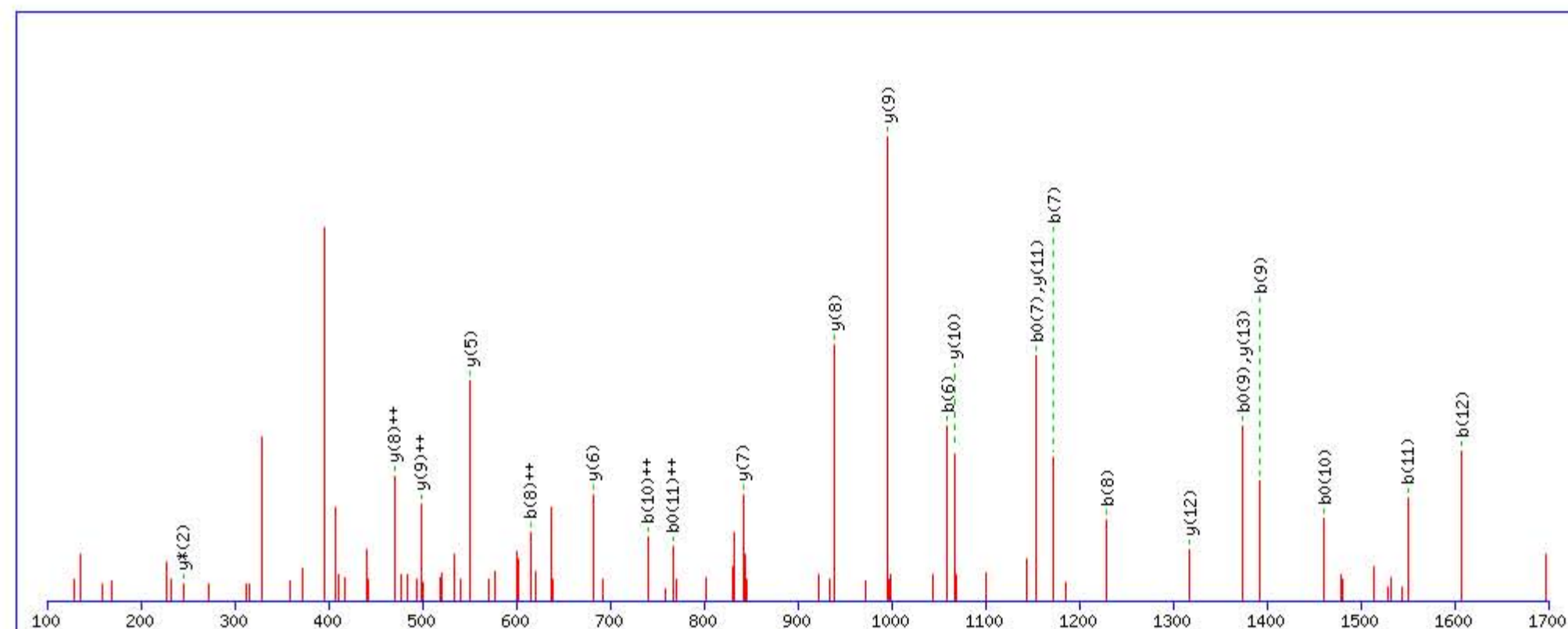
Title: Locus:1.1.1.3138.18 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

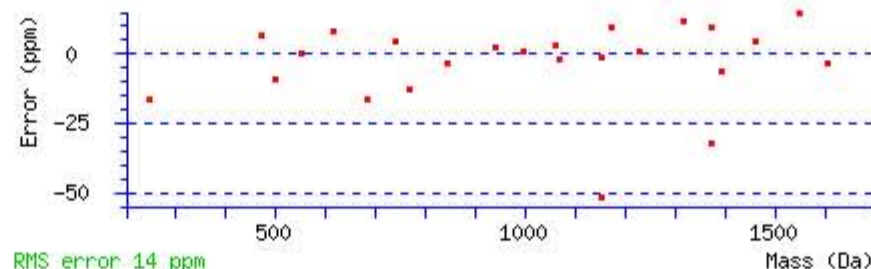
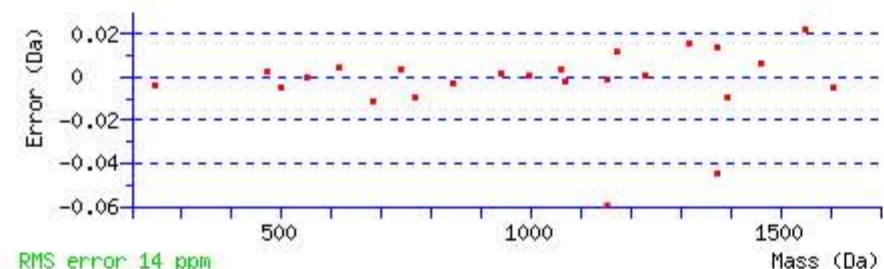
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 58 Expect: 8.2e-006

Matches : 24/224 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	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
58.1	2545.089188	0.024514	KEDSCQLGYSAGPCMGMTSR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **VGALSQLR**

Found in **MENT_HUMAN**, Protein MENT OS=Homo sapiens GN=MENT PE=2 SV=1

Match to Query 23551: 1153.657448 from(577.836000,2+) rtinseconds(1924) index(55228)

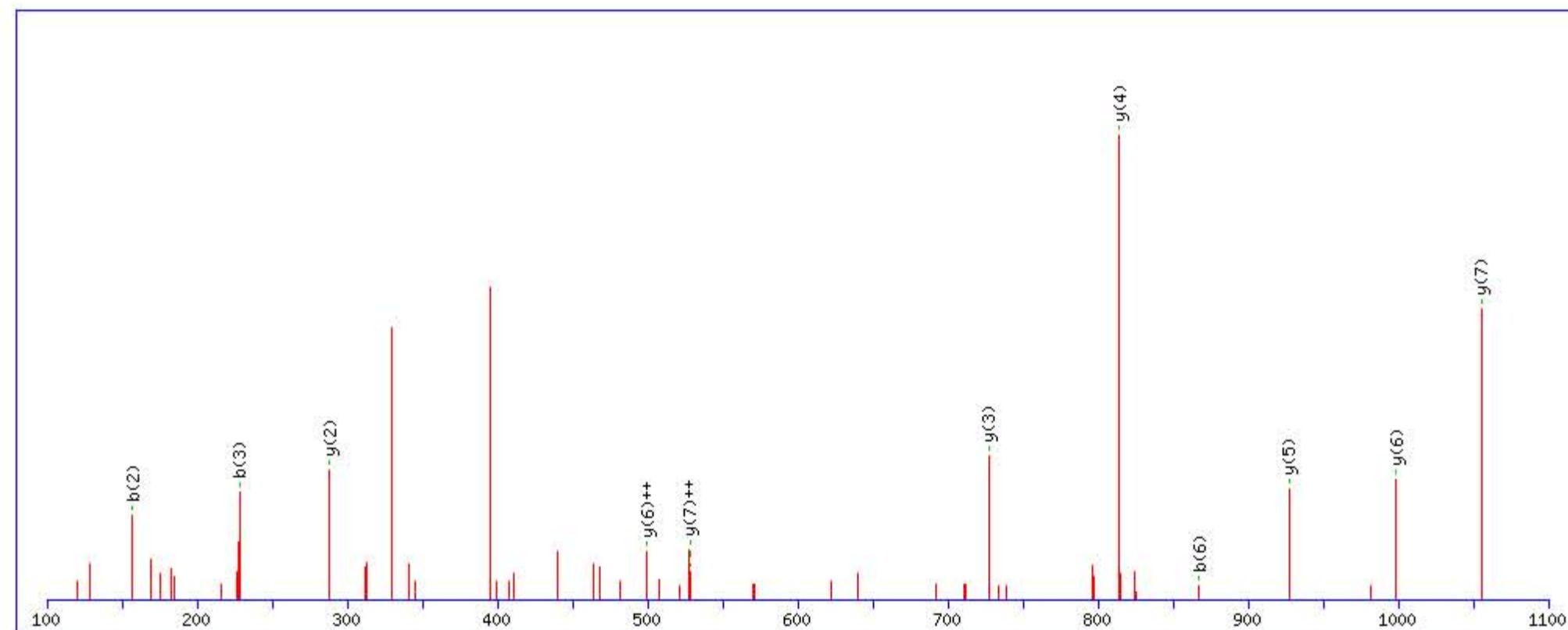
Title: Locus:1.1.1.3156.10 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

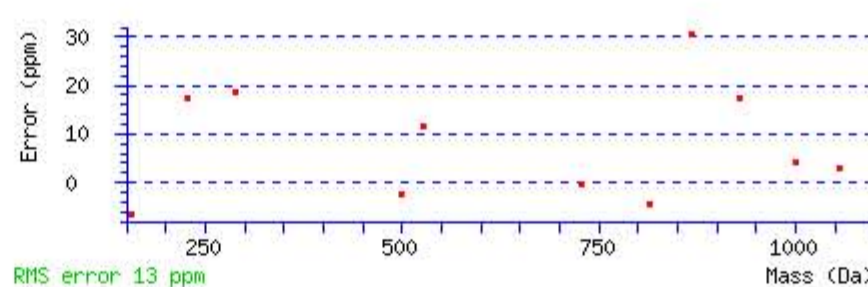
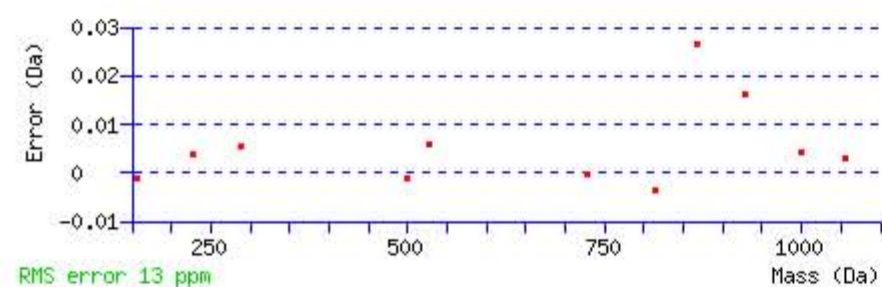
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 39 Expect: 0.0018

Matches : 11/60 fragment ions using 19 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.075690	50.541483					V							8
2	157.097154	79.052215					G	1055.603012	528.305144	1038.576463	519.791870	1037.592447	519.299862	7
3	228.134268	114.570772					A	998.581548	499.794412	981.554999	491.281138	980.570983	490.789130	6
4	341.218332	171.112804					L	927.544434	464.275855	910.517885	455.762581	909.533869	455.270573	5
5	428.250360	214.628818			410.239795	205.623535	S	814.460370	407.733823	797.433821	399.220549	796.449805	398.728541	4
6	867.475686	434.241481	850.449137	425.728207	849.465121	425.236199	Q	727.428342	364.217809	710.401793	355.704535			3
7	980.559750	490.783513	963.533201	482.270239	962.549185	481.778231	L	288.203016	144.605146	271.176467	136.091872			2
8							R	175.118952	88.063114	158.092403	79.549840			1



NCBI BLAST search of [VGALSQLR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.0	1153.664139	-0.006691	VGALSQLR
10.8	1153.645477	0.011971	RALAAPVAEEK
8.3	1153.656723	0.000725	RPSADPGKKAK
4.8	1153.664124	-0.006676	VKQEALR
3.4	1153.667953	-0.010505	RANPNSIRVK

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 37149: 1561.819488 from(781.917020,2+) rtinseconds(2122) index(56593)

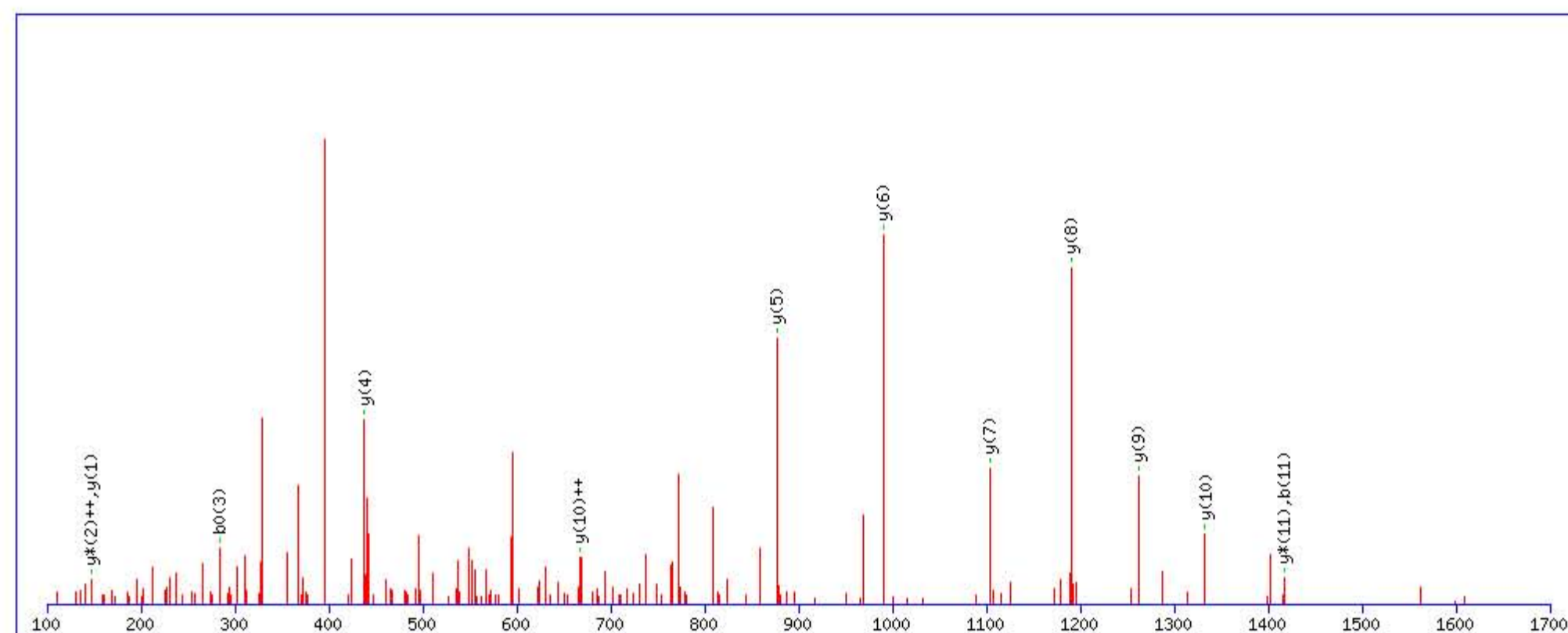
Title: Locus:1.1.1.3224.21 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

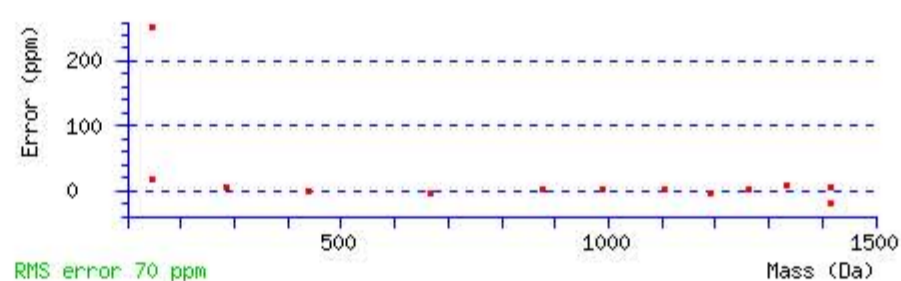
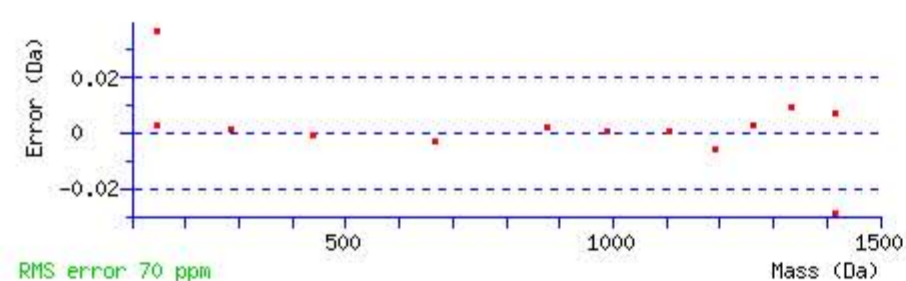
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 70 Expect: 5.7e-007

Matches : 13/104 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	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
70.5	1561.817383	0.002105	ETAASLLQAGYK
3.7	1561.817398	0.002090	VLPEVLEKQCGYK
1.0	1561.835129	-0.015641	TEEALQLYNQIIK
0.0	1561.828613	-0.009125	QLASRYASVEK
0.0	1561.809998	0.009490	SASDLTWDNLKGGK

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

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TATSEYQTFNPR**

Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

Match to Query 46392: 1871.893728 from(936.954140,2+) rtinseconds(2262) index(57432)

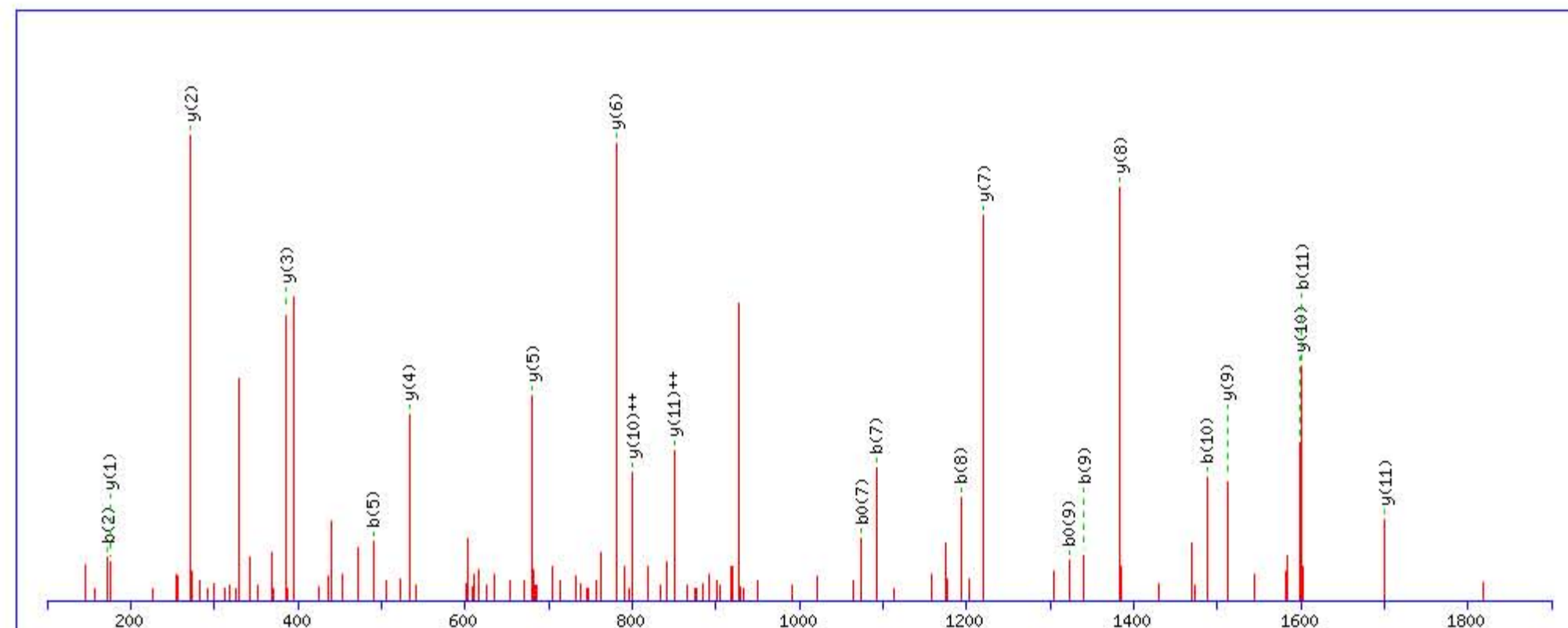
Title: Locus:1.1.1.3273.13 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1871.887619

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

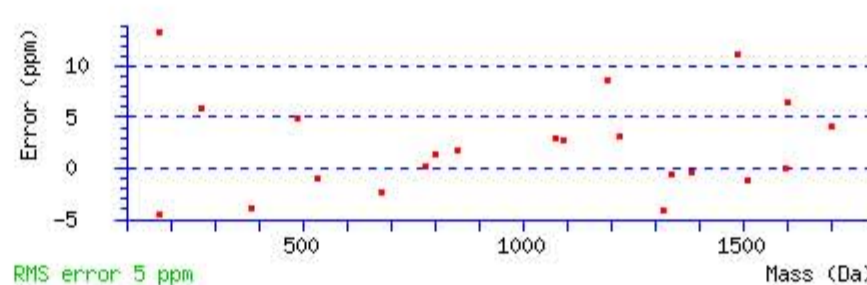
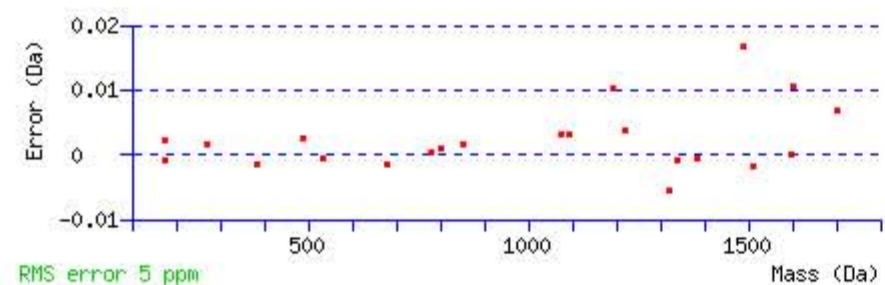
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 88 Expect: 1.4e-008

Matches : 22/122 fragment ions using 32 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	102.054955	51.531116			84.044390	42.525833	T							13
2	173.092069	87.049672			155.081504	78.044390	A	1771.847219	886.427248	1754.820670	877.913973	1753.836654	877.421965	12
3	274.139748	137.573512			256.129183	128.568230	T	1700.810105	850.908691	1683.783556	842.395416	1682.799540	841.903408	11
4	361.171776	181.089526			343.161211	172.084243	S	1599.762426	800.384851	1582.735877	791.871577	1581.751861	791.379569	10
5	490.214369	245.610822			472.203804	236.605540	E	1512.730398	756.868837	1495.703849	748.355563	1494.719833	747.863555	9
6	653.277698	327.142487			635.267133	318.137205	Y	1383.687805	692.347541	1366.661256	683.834266	1365.677240	683.342258	8
7	1092.503024	546.755150	1075.476475	538.241876	1074.492459	537.749868	Q	1220.624476	610.815876	1203.597927	602.302602	1202.613911	601.810594	7
8	1193.550703	597.278990	1176.524154	588.765715	1175.540138	588.273707	T	781.399150	391.203213	764.372601	382.689939	763.388585	382.197931	6
9	1340.619117	670.813197	1323.592568	662.299922	1322.608552	661.807914	F	680.351471	340.679374	663.324922	332.166099			5
10	1487.687531	744.347404	1470.660982	735.834129	1469.676966	735.342121	F	533.283057	267.145167	516.256508	258.631892			4
11	1601.730458	801.368867	1584.703909	792.855593	1583.719893	792.363585	N	386.214643	193.610959	369.188094	185.097685			3
12	1698.783222	849.895249	1681.756673	841.381975	1680.772657	840.889967	P	272.171716	136.589496	255.145167	128.076221			2
13							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **TATSEYQTFNPR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
88.3	1871.887619	0.006109	TATSEYQTFNPR
4.4	1871.921310	-0.027582	QHFRKLCYQDAPGPR

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 48094: 1955.992188 from(979.003370,2+) rtinseconds(2473) index(58461)

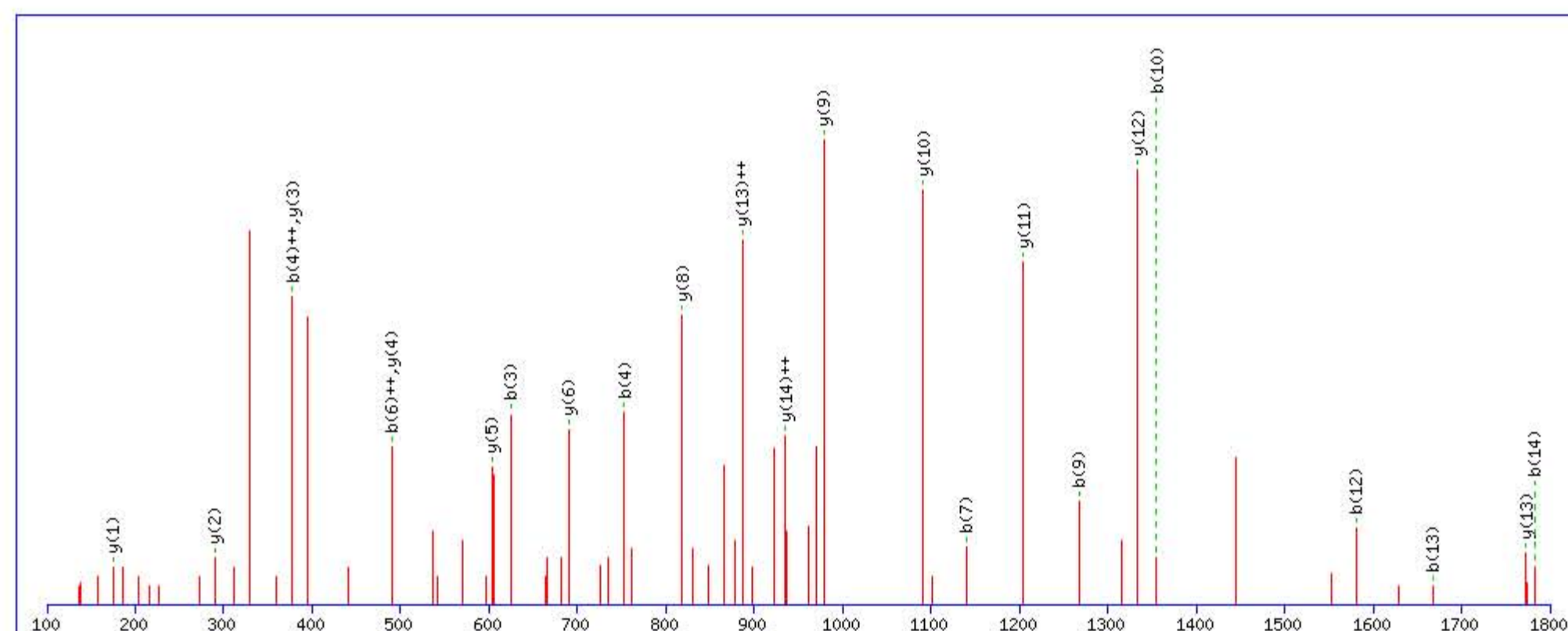
Title: Locus:1.1.1.3346.26 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

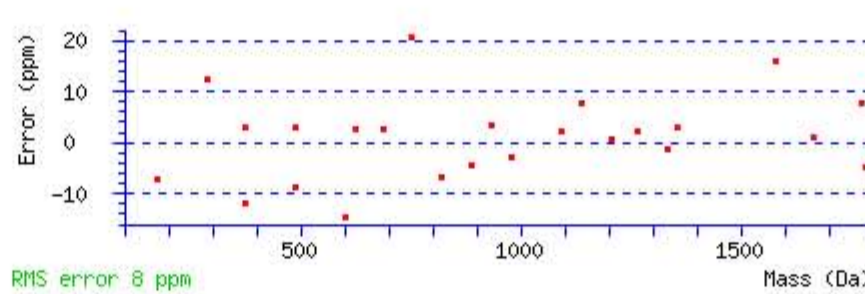
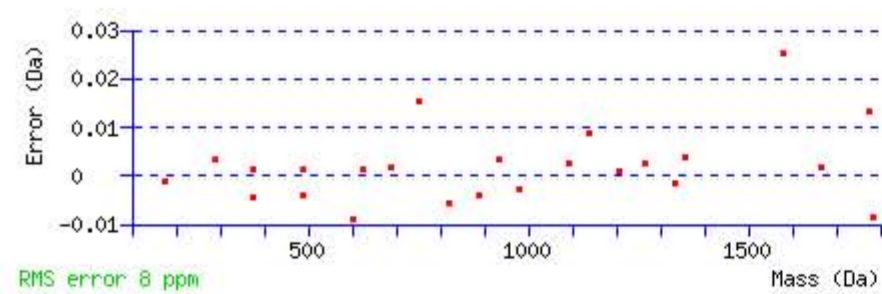
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 101 Expect: 2.2e-009

Matches : 24/162 fragment ions using 31 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.039304	44.523290			70.028739	35.518008	S							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

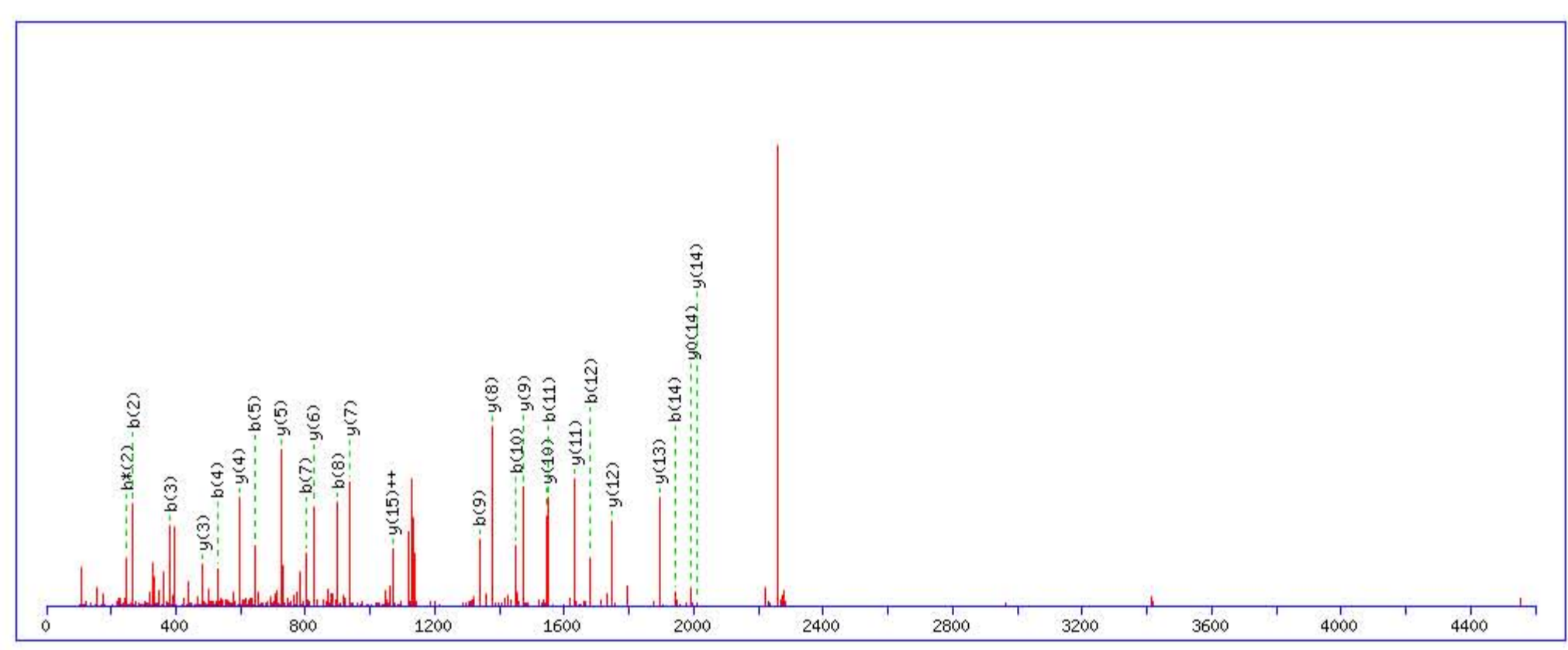
Score	Mr(calc):	Delta	Sequence
100.9	1955.980850	0.011338	SPQELLCGASLISDR
19.6	1956.006470	-0.014282	AILRVAELSSDDFHLDR
4.7	1956.003342	-0.011154	GTLPLSRICAMVTTQHR
4.2	1955.975464	0.016724	QHSLHSAQWFAGAFILR
1.4	1955.963531	0.028657	AEGPLREEFRHEAMLR
1.1	1955.985565	0.006623	RAAQLCGAGMAAVVDR
0.1	1955.974335	0.017853	LVHSMQVAKMQSDR

Peptide View

MS/MS Fragmentation of **HQDFNSAVQLVENFCR**
 Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

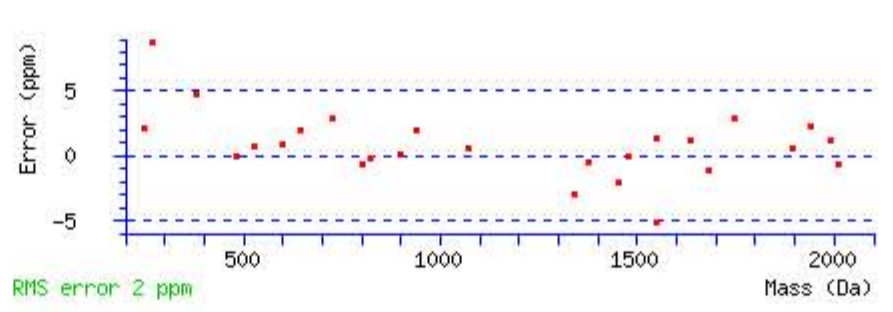
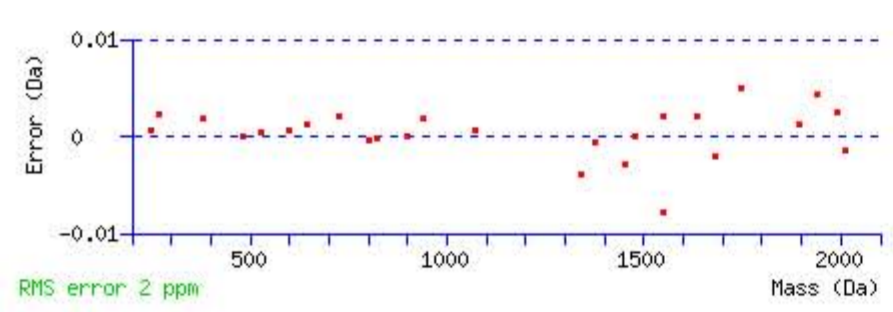
Match to Query 55553: 2274.073608 from(1138.044080,2+) rtinseconds(2450) index(58337)
 Title: Locus:1.1.1.3338.10 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 86 Expect: 2.8e-008
 Matches : 26/166 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	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
85.8	2274.067398	0.006210	HQDFNSAVQLVENFCR
11.2	2274.067398	0.006210	HQDFNSAVQLVENFCR
5.2	2274.055481	0.018127	HQDSMSKSEM QVKEQR
0.1	2274.055481	0.018127	HQDSMSKSEM QVKEQR

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 56208: 2305.209762 from(769.410530,3+) rtinseconds(2360) index(57939)

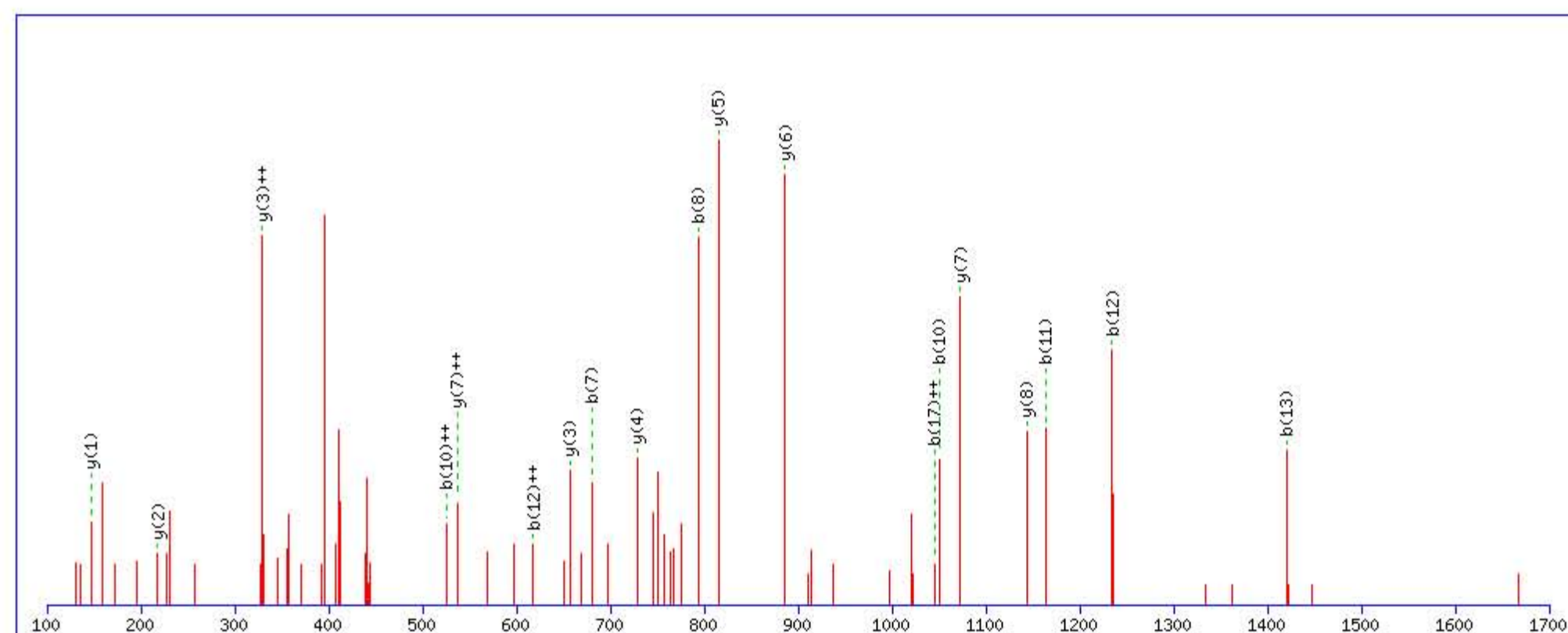
Title: Locus:1.1.1.3307.18 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

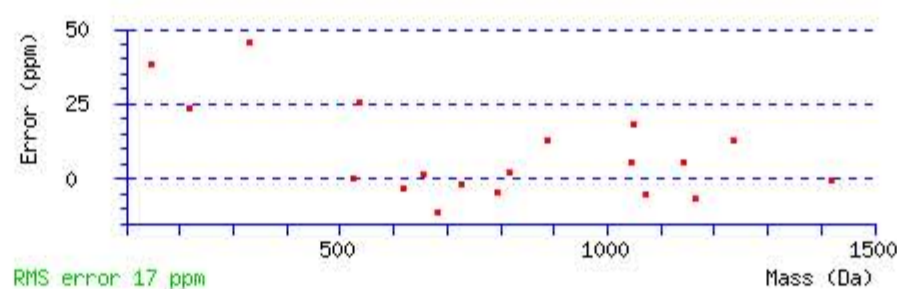
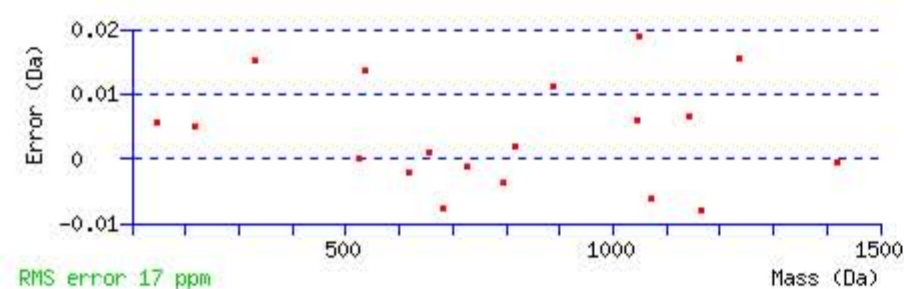
Variable modifications:

Q17 : Biotin:Thermo-21345 (Q)

Ions Score: 41 Expect: 0.00018

Matches : 19/170 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							19
2	185.128454	93.067865					A	2193.130730	1097.069003	2176.104181	1088.555728	2175.120165	1088.063720	18
3	284.196868	142.602072					V	2122.093616	1061.550446	2105.067067	1053.037171	2104.083051	1052.545163	17
4	385.244547	193.125912			367.233982	184.120629	T	2023.025202	1012.016239	2005.998653	1003.502965	2005.014637	1003.010957	16
5	486.292226	243.649751			468.281661	234.644469	T	1921.977523	961.492400	1904.950974	952.979125	1903.966958	952.487117	15
6	623.351138	312.179207			605.340573	303.173925	H	1820.929844	910.968560	1803.903295	902.455286	1802.919279	901.963278	14
7	680.372602	340.689939			662.362037	331.684657	G	1683.870932	842.439104	1666.844383	833.925830	1665.860367	833.433822	13
8	793.456666	397.231971			775.446101	388.226689	L	1626.849468	813.928372	1609.822919	805.415098	1608.838903	804.923090	12
9	890.509430	445.758353			872.498865	436.753071	P	1513.765404	757.386340	1496.738855	748.873066	1495.754839	748.381058	11
10	1050.540079	525.773678			1032.529514	516.768395	C	1416.712640	708.859958	1399.686091	700.346684	1398.702075	699.854675	10
11	1163.624143	582.315710			1145.613578	573.310427	L	1256.681991	628.844634	1239.655442	620.331359	1238.671426	619.839351	9
12	1234.661257	617.834267			1216.650692	608.828984	A	1143.597927	572.302602	1126.571378	563.789327	1125.587362	563.297319	8
13	1420.740570	710.873923			1402.730005	701.868640	W	1072.560813	536.784045	1055.534264	528.270770	1054.550248	527.778762	7
14	1491.777684	746.392480			1473.767119	737.387197	A	886.481500	443.744388	869.454951	435.231114	868.470935	434.739106	6
15	1578.809712	789.908494			1560.799147	780.903212	S	815.444386	408.225831	798.417837	399.712557	797.433821	399.220549	5
16	1649.846826	825.427051			1631.836261	816.421768	A	728.412358	364.709817	711.385809	356.196543			4
17	2089.072152	1045.039714	2072.045603	1036.526439	2071.061587	1036.034431	Q	657.375244	329.191260	640.348695	320.677986			3
18	2160.109266	1080.558271	2143.082717	1072.044996	2142.098701	1071.552988	A	218.149918	109.578597	201.123369	101.065323			2
19							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **LAVTTHGLPCLAWASAQAK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.7	2305.207504	0.002258	LAVTTHGLPCLAWASAQAK
0.8	2305.189545	0.020217	RSKSIRPPQSPQNC

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

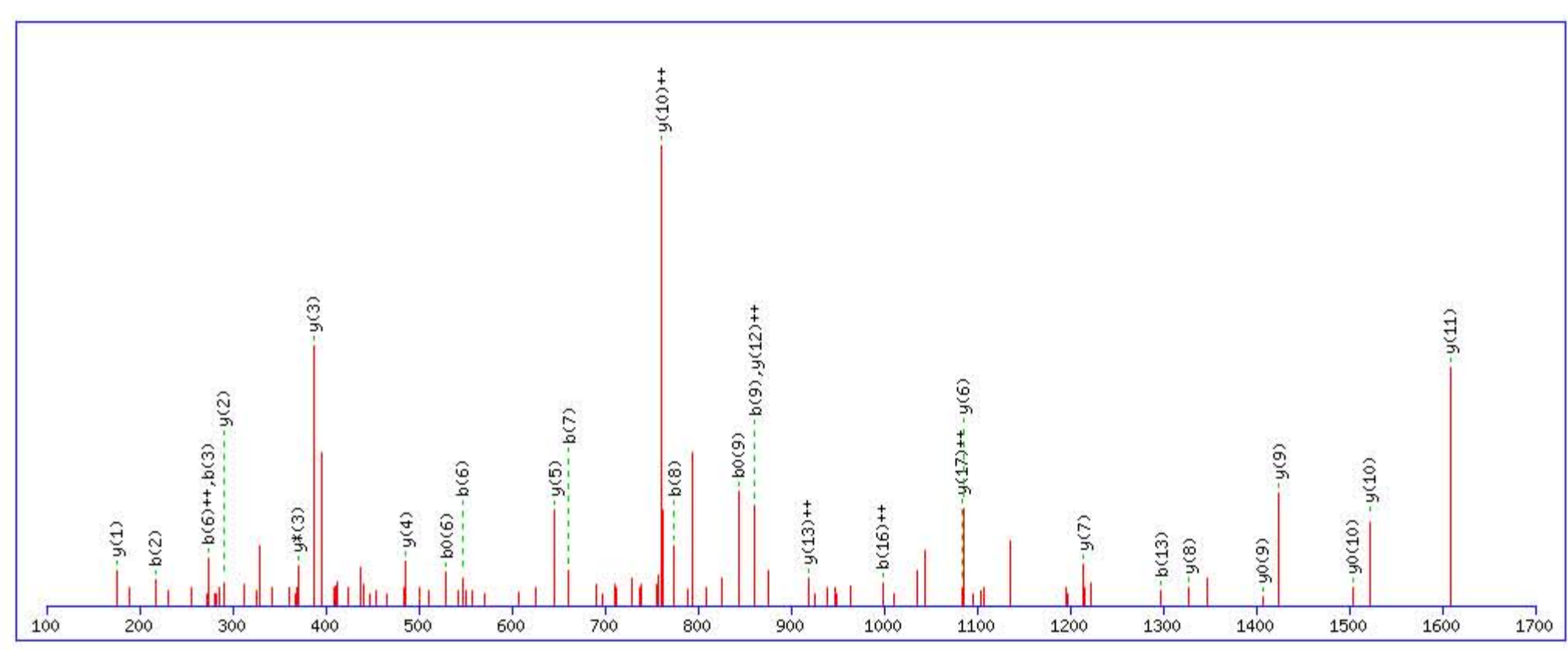
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **SEGSSVNLSPPLEQVPDR**
 Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

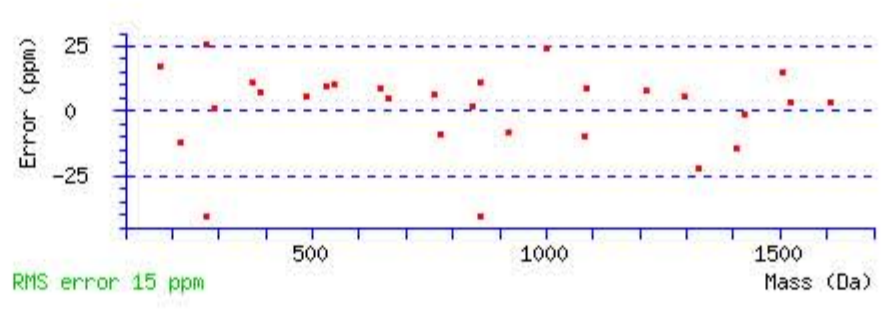
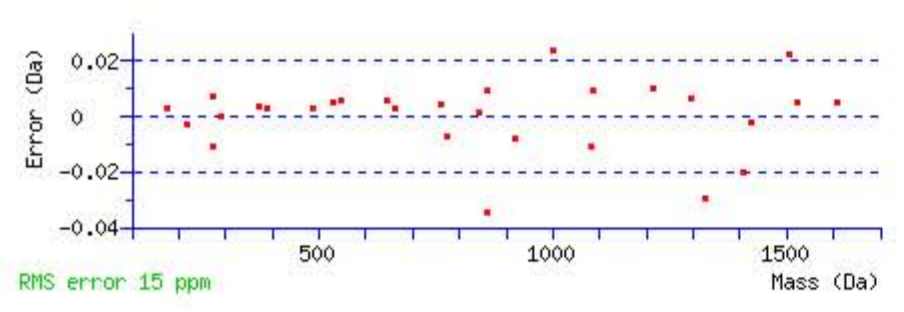
Match to Query 57208: 2381.136162 from(794.719330,3+) rtinseconds(2157) index(56817)
 Title: Locus:1.1.1.3236.25 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 78 Expect: 3.2e-007
 Matches : 29/202 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	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 [SEGSSVNLSPPLEQVPDR](#)
 (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	2381.135529	0.000633	SEGSSVNLSPPLEQVPDR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **GQPSVLQVVNLPIVERPVCK**

Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

Match to Query 60656: 2542.415742 from(848.479190,3+) rtinseconds(2501) index(58687)

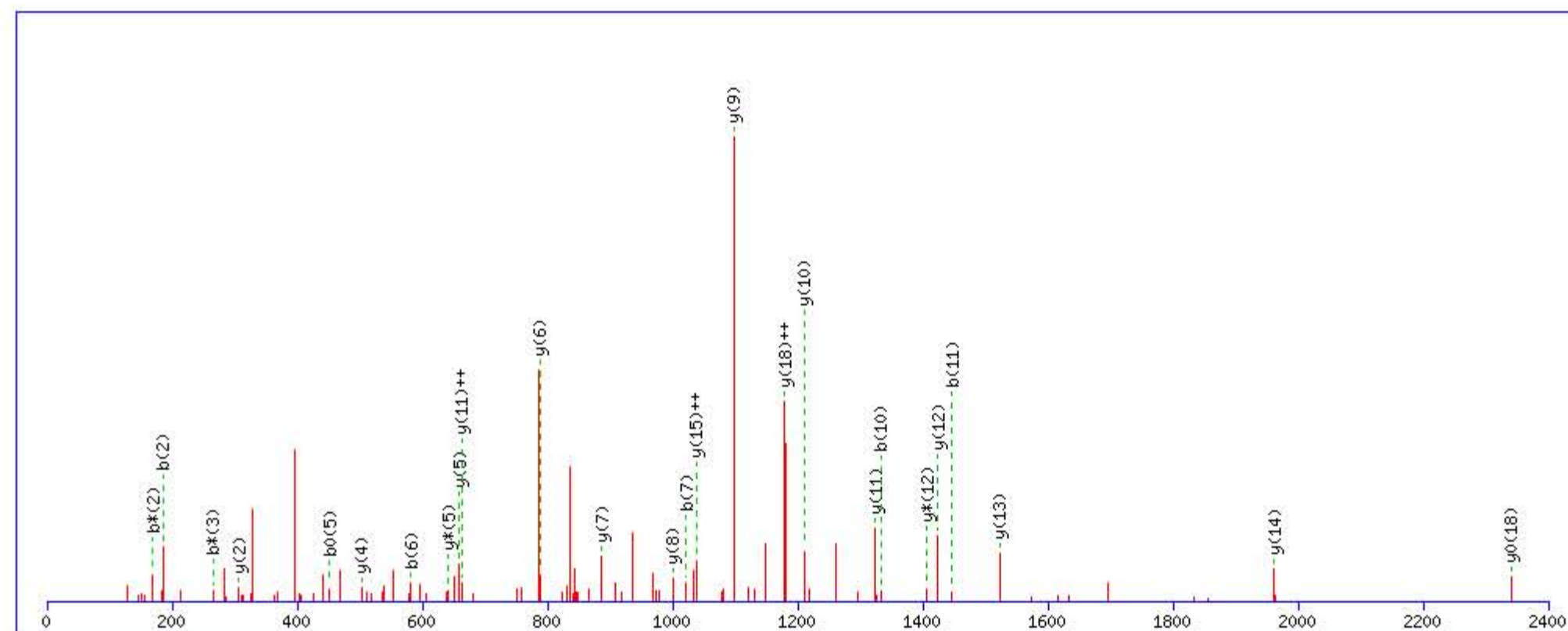
Title: Locus:1.1.1.3356.22 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2542.412766

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

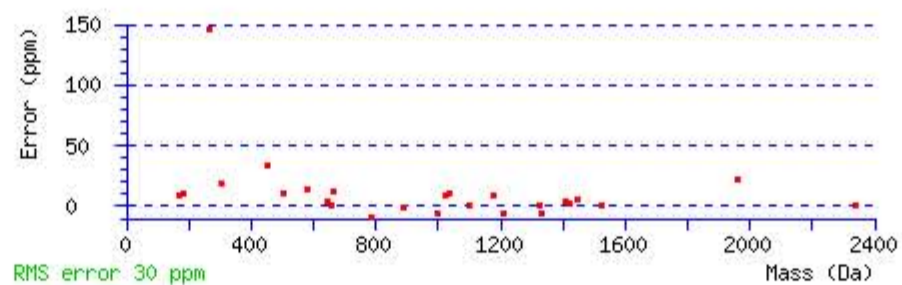
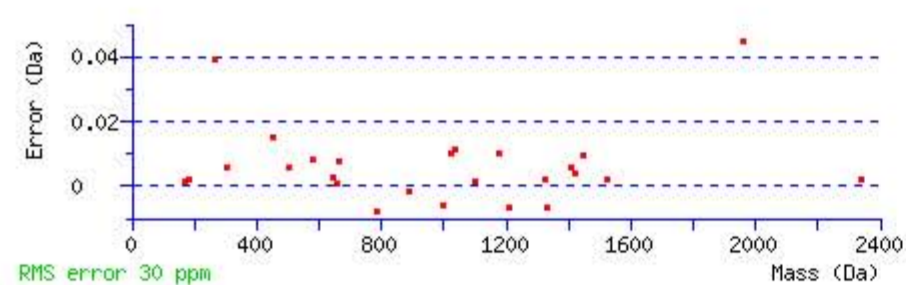
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 48 Expect: 0.00014

Matches : 26/210 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	58.028740	29.518008					G							20
2	186.087318	93.547297	169.060769	85.034023			Q	2486.398570	1243.702923	2469.372021	1235.189648	2468.388005	1234.697640	19
3	283.140082	142.073679	266.113533	133.560405			P	2358.339992	1179.673634	2341.313443	1171.160359	2340.329427	1170.668351	18
4	370.172110	185.589693	353.145561	177.076419	352.161545	176.584411	S	2261.287228	1131.147252	2244.260679	1122.633977	2243.276663	1122.141969	17
5	469.240524	235.123900	452.213975	226.610626	451.229959	226.118618	V	2174.255200	1087.631238	2157.228651	1079.117963	2156.244635	1078.625955	16
6	582.324588	291.665932	565.298039	283.152658	564.314023	282.660650	L	2075.186786	1038.097031	2058.160237	1029.583756	2057.176221	1029.091748	15
7	1021.549914	511.278595	1004.523365	502.765321	1003.539349	502.273313	Q	1962.102722	981.554999	1945.076173	973.041724	1944.092157	972.549716	14
8	1120.618328	560.812802	1103.591779	552.299528	1102.607763	551.807520	V	1522.877396	761.942336	1505.850847	753.429061	1504.866831	752.937053	13
9	1219.686742	610.347009	1202.660193	601.833735	1201.676177	601.341727	V	1423.808982	712.408129	1406.782433	703.894854	1405.798417	703.402846	12
10	1333.729669	667.368473	1316.703120	658.855198	1315.719104	658.363190	N	1324.740568	662.873922	1307.714019	654.360647	1306.730003	653.868639	11
11	1446.813733	723.910505	1429.787184	715.397230	1428.803168	714.905222	L	1210.697641	605.852458	1193.671092	597.339184	1192.687076	596.847176	10
12	1543.866497	772.436887	1526.839948	763.923612	1525.855932	763.431604	P	1097.613577	549.310426	1080.587028	540.797152	1079.603012	540.305144	9
13	1656.950561	828.978918	1639.924012	820.465644	1638.939996	819.973636	I	1000.560813	500.784044	983.534264	492.270770	982.550248	491.778762	8
14	1756.018975	878.513126	1738.992426	869.999851	1738.008410	869.507843	V	887.476749	444.242012	870.450200	435.728738	869.466184	435.236730	7
15	1885.061568	943.034422	1868.035019	934.521147	1867.051003	934.029139	E	788.408335	394.707805	771.381786	386.194531	770.397770	385.702523	6
16	2041.162679	1021.084977	2024.136130	1012.571703	2023.152114	1012.079695	R	659.365742	330.186509	642.339193	321.673234			5
17	2138.215443	1069.611359	2121.188894	1061.098085	2120.204878	1060.606077	P	503.264631	252.135953	486.238082	243.622679			4
18	2237.283857	1119.145566	2220.257308	1110.632292	2219.273292	1110.140284	V	406.211867	203.609571	389.185318	195.096297			3
19	2397.314506	1199.160891	2380.287957	1190.647616	2379.303941	1190.155608	C	307.143453	154.075364	290.116904	145.562090			2
20							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **GQPSVLQVVNLPIVERPVCK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.4	2542.412766	0.002976	GQPSVLQVVNLPIVERPVCK
27.9	2542.412766	0.002976	GQPSVLQVVNLPIVERPVCK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **RQEC SIPVCGQDQVT VAMTPR**

Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

Match to Query 62398: 2742.307662 from(915.109830,3+) rtinseconds(1963) index(55564)

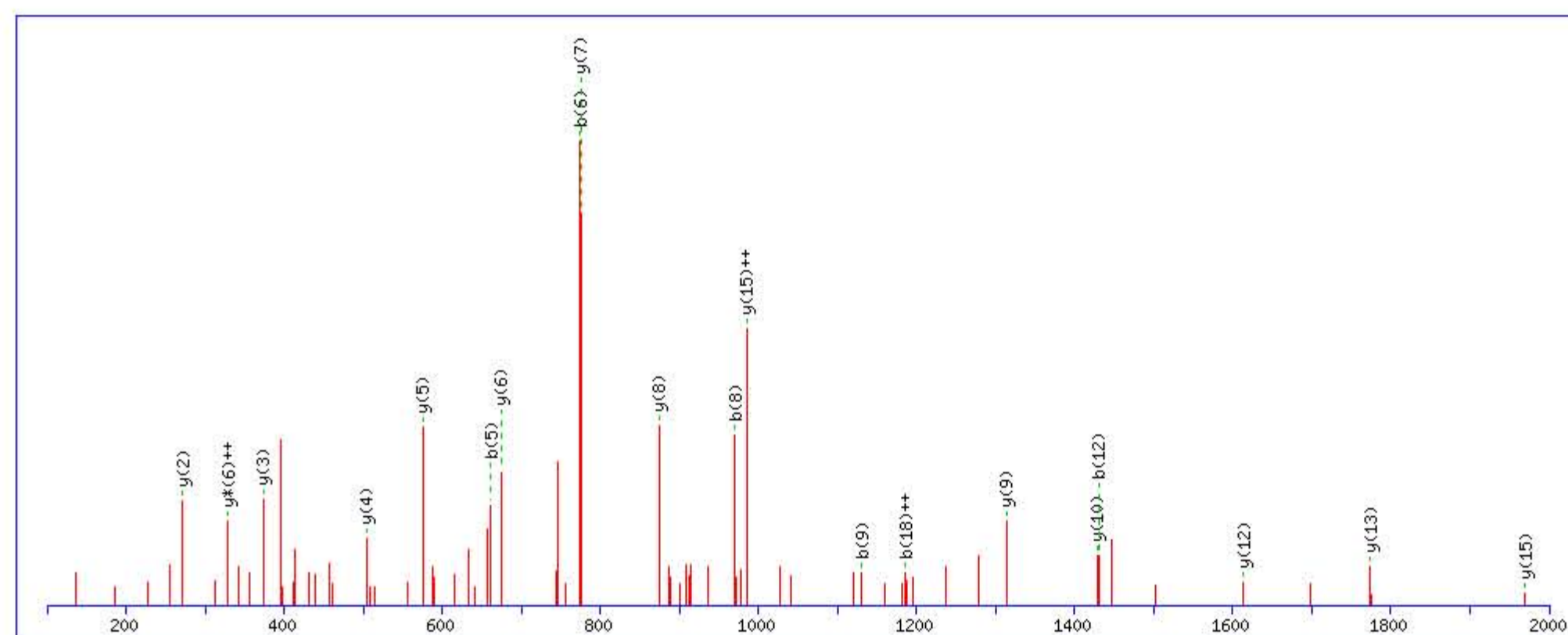
Title: Locus:1.1.1.3169.21 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

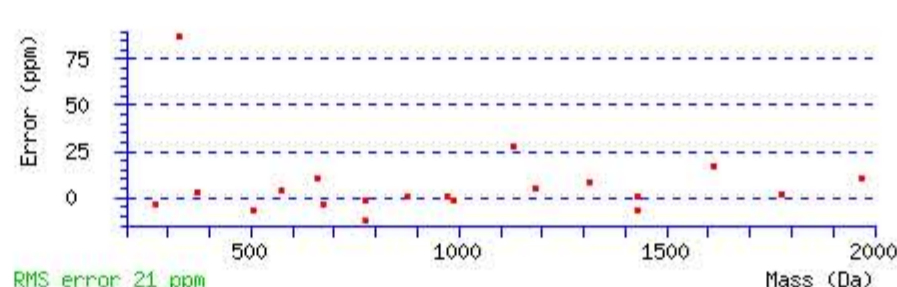
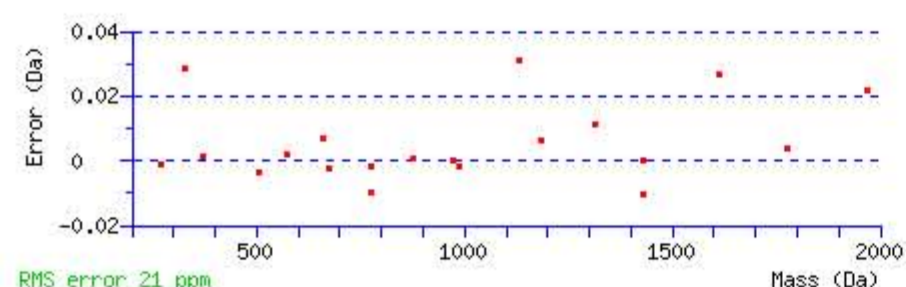
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 72 Expect: 1.4e-006

Matches : 20/232 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	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 [RQEC SIPVCGQDQVT VAMTPR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
72.2	2742.307404	0.000258	RQEC SIPVCGQDQVT VAMTPR
49.6	2742.307404	0.000258	RQEC SIPVCGQDQVT VAMTPR
16.6	2742.307404	0.000258	RQEC SIPVCGQDQVT VAMTPR

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 35026: 1476.757662 from(493.259830,3+) rtinseconds(1217) index(66179)

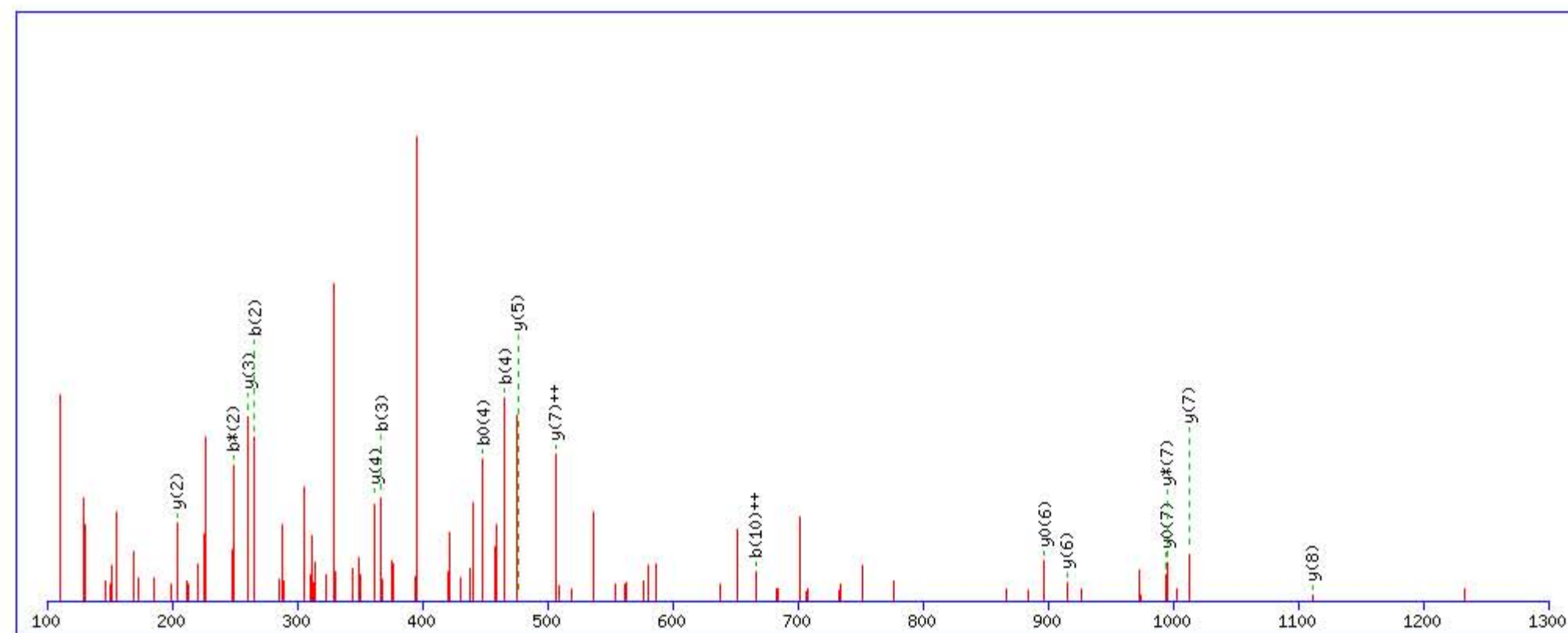
Title: Locus:1.1.1.2957.11 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

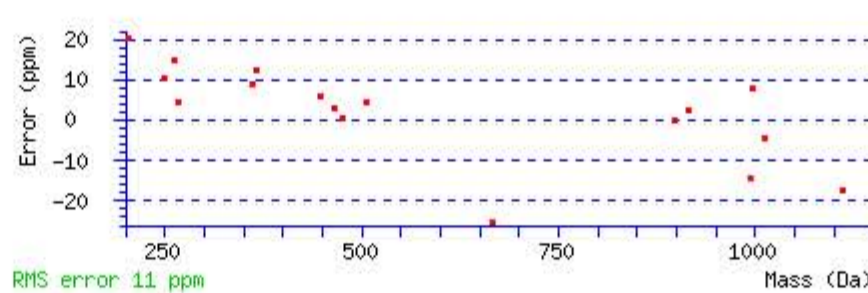
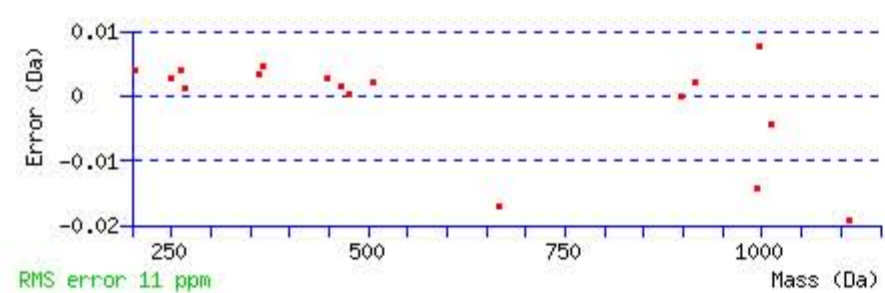
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.013

Matches : 17/108 fragment ions using 39 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	138.066188	69.536732					H							11
2	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
26.8	1476.750748	0.006914	HQTVPQNTGGK
6.9	1476.750748	0.006914	HQTVPQNTGGK
6.3	1476.736115	0.021547	HQEALIGQSFY GK
4.4	1476.739487	0.018175	GPEVMAFIEQGKR
3.5	1476.758102	-0.000440	KEAFSIGMQR

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

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 38331: 1586.795982 from(529.939270,3+) rtinseconds(2103) index(71803)

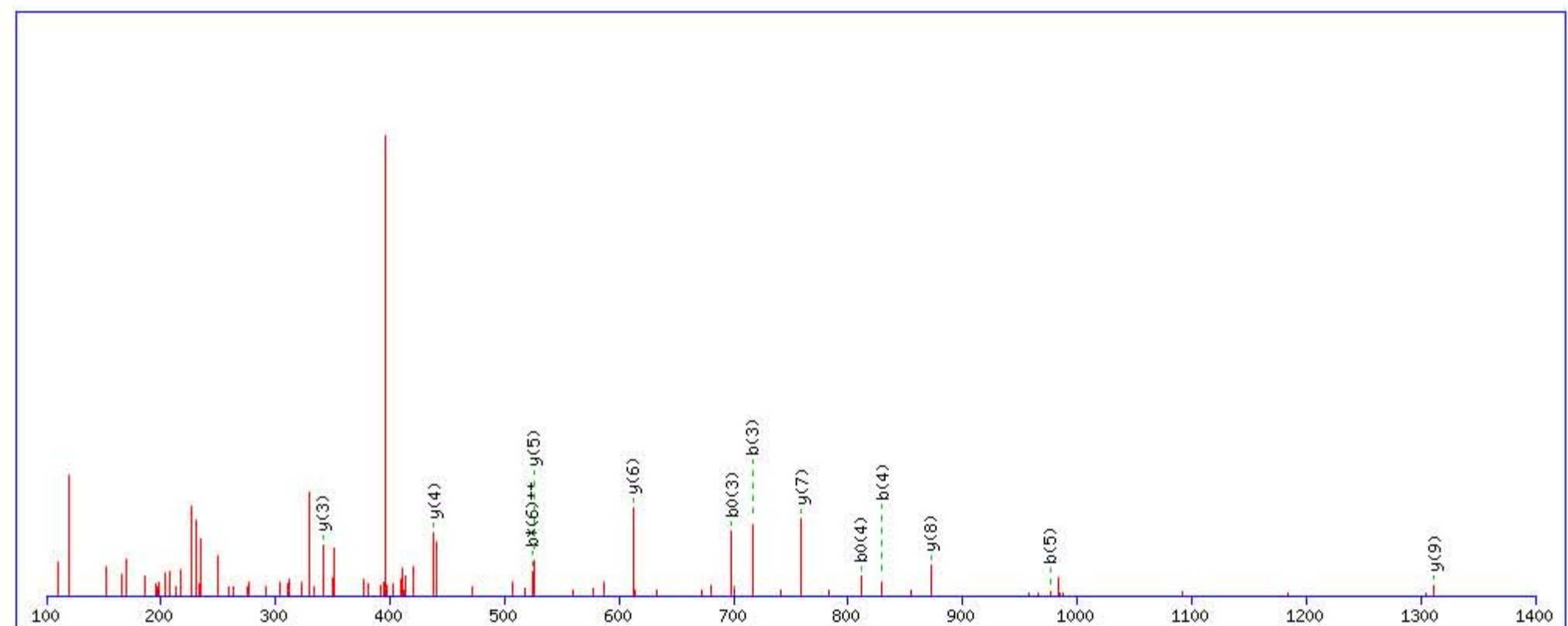
Title: Locus:1.1.1.3266.5 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1586.791534

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

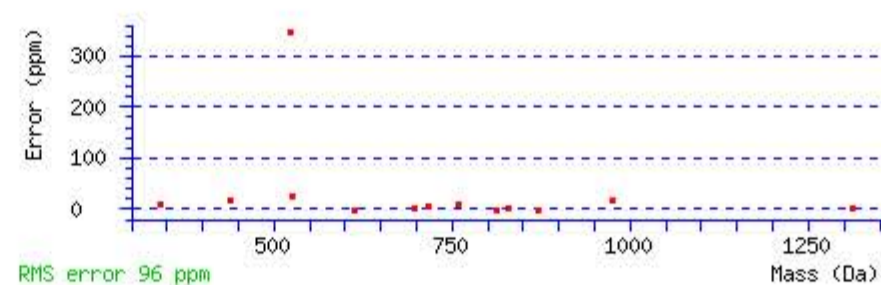
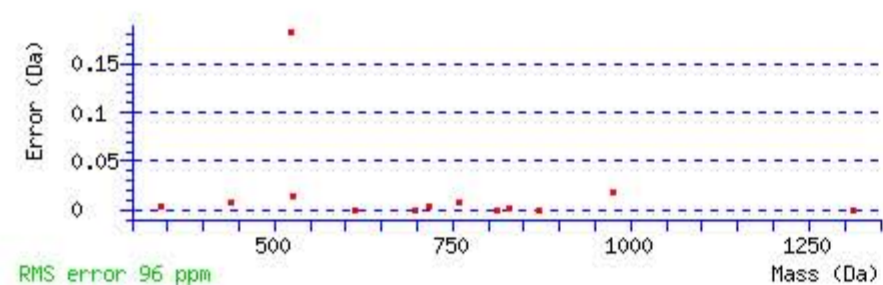
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 28 Expect: 0.037

Matches : 13/108 fragment ions using 31 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	277.118283	139.062779			259.107718	130.057497	F	1458.756218	729.881747	1441.729669	721.368473	1440.745653	720.876465	10
3	716.343609	358.675443	699.317060	350.162168	698.333044	349.670160	Q	1311.687804	656.347540	1294.661255	647.834266	1293.677239	647.342258	9
4	829.427673	415.217475	812.401124	406.704200	811.417108	406.212192	L	872.462478	436.734877	855.435929	428.221603	854.451913	427.729595	8
5	976.496087	488.751682	959.469538	480.238407	958.485522	479.746399	F	759.378414	380.192845	742.351865	371.679571	741.367849	371.187563	7
6	1063.528115	532.267696	1046.501566	523.754421	1045.517550	523.262413	S	612.310000	306.658638	595.283451	298.145364	594.299435	297.653356	6
7	1150.560143	575.783710	1133.533594	567.270435	1132.549578	566.778427	S	525.277972	263.142624	508.251423	254.629350	507.267407	254.137342	5
8	1247.612907	624.310092	1230.586358	615.796817	1229.602342	615.304809	P	438.245944	219.626610	421.219395	211.113335			4
9	1384.671819	692.839548	1367.645270	684.326273	1366.661254	683.834265	H	341.193180	171.100228	324.166631	162.586953			3
10	1441.693283	721.350280	1424.666734	712.837005	1423.682718	712.344997	G	204.134268	102.570772	187.107719	94.057497			2
11							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **EFQLFSSPHGK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.4	1586.791534	0.004448	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 40646: 1633.787448 from(817.901000,2+) rtinseconds(1754) index(69631)

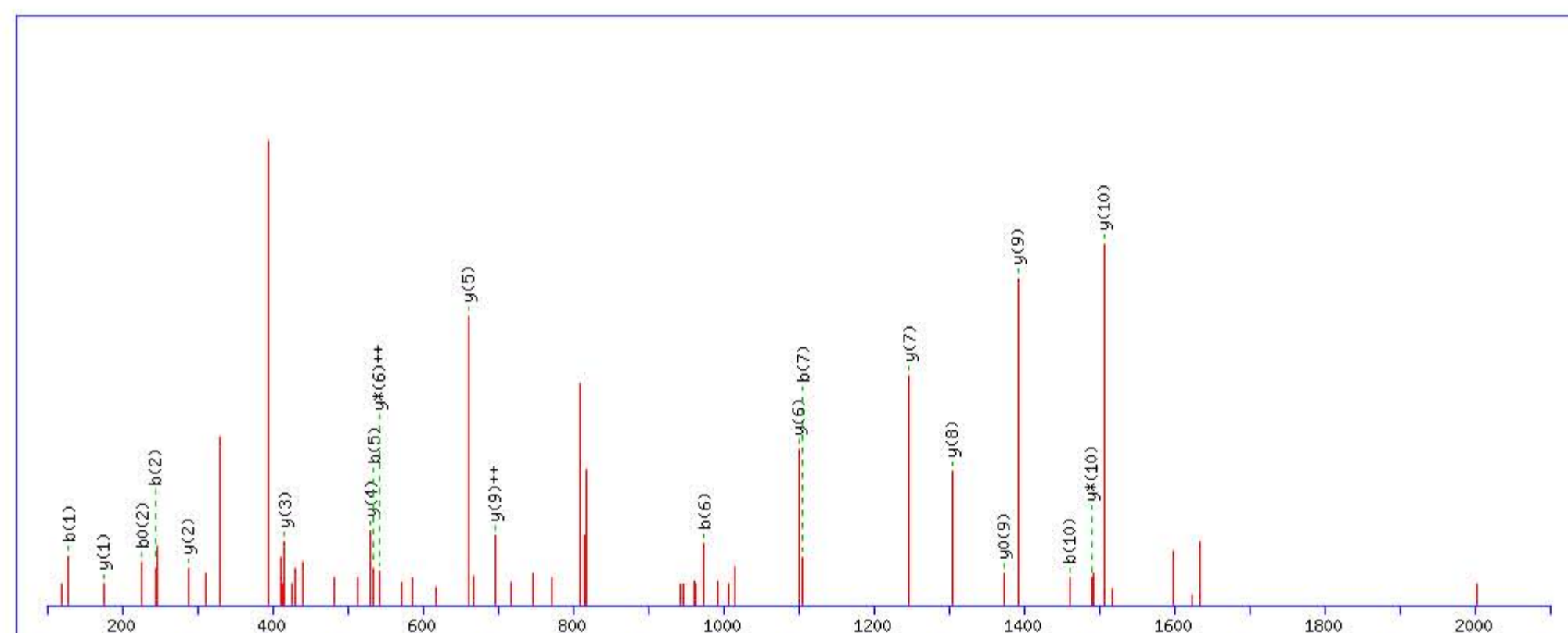
Title: Locus:1.1.1.3144.14 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1633.806854

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

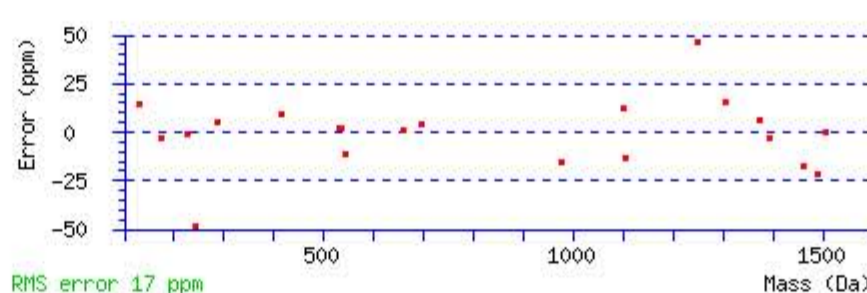
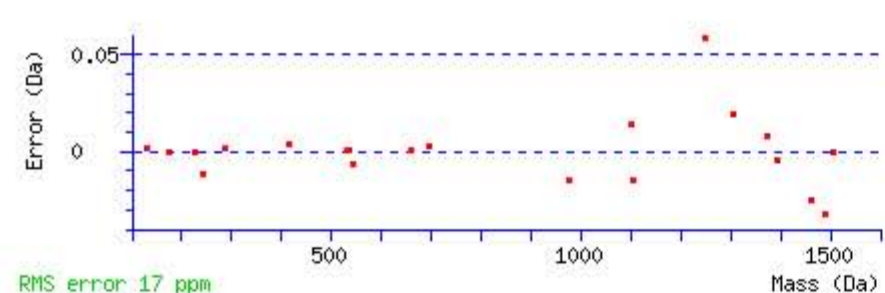
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 63 Expect: 1.3e-005

Matches : 21/102 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							11
2	244.129182	122.568229	227.102633	114.054955	226.118617	113.562947	D	1506.719181	753.863228	1489.692632	745.349954	1488.708616	744.857946	10
3	331.161210	166.084243	314.134661	157.570969	313.150645	157.078961	S	1391.692238	696.349757	1374.665689	687.836482	1373.681673	687.344474	9
4	388.182674	194.594975	371.156125	186.081701	370.172109	185.589693	G	1304.660210	652.833743	1287.633661	644.320468			8
5	535.251088	268.129182	518.224539	259.615908	517.240523	259.123900	F	1247.638746	624.323011	1230.612197	615.809736			7
6	974.476414	487.741845	957.449865	479.228571	956.465849	478.736563	Q	1100.570332	550.788804	1083.543783	542.275530			6
7	1105.516899	553.262088	1088.490350	544.748813	1087.506334	544.256805	M	661.345006	331.176141	644.318457	322.662866			5
8	1219.559826	610.283551	1202.533277	601.770277	1201.549261	601.278268	N	530.304521	265.655899	513.277972	257.142624			4
9	1347.618404	674.312840	1330.591855	665.799566	1329.607839	665.307558	Q	416.261594	208.634435	399.235045	200.121160			3
10	1460.702468	730.854872	1443.675919	722.341598	1442.691903	721.849589	L	288.203016	144.605146	271.176467	136.091871			2
11							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **KDSGFQMNQLR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.7	1633.806854	-0.019406	KDSGFQMNQLR
27.9	1633.806854	-0.019406	KDSGFQMNQLR
9.9	1633.769608	0.017840	AGDGSSVKEVETYHR
7.3	1633.774307	0.013141	DQWTSVANMRDRR
6.9	1633.803482	-0.016034	QLFERDWSSR
6.4	1633.809998	-0.022550	KQYDSFTYRAEVK
6.0	1633.798096	-0.010648	QDQEKDNMIEKLK
4.3	1633.810715	-0.023267	QPVEPHMGVGRQQR
2.0	1633.798111	-0.010663	CTTVDEAEKAIELR
1.1	1633.784180	0.003268	QEESVQKQAMRR

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 40650: 1633.807302 from(545.609710,3+) rtinseconds(1840) index(70124)

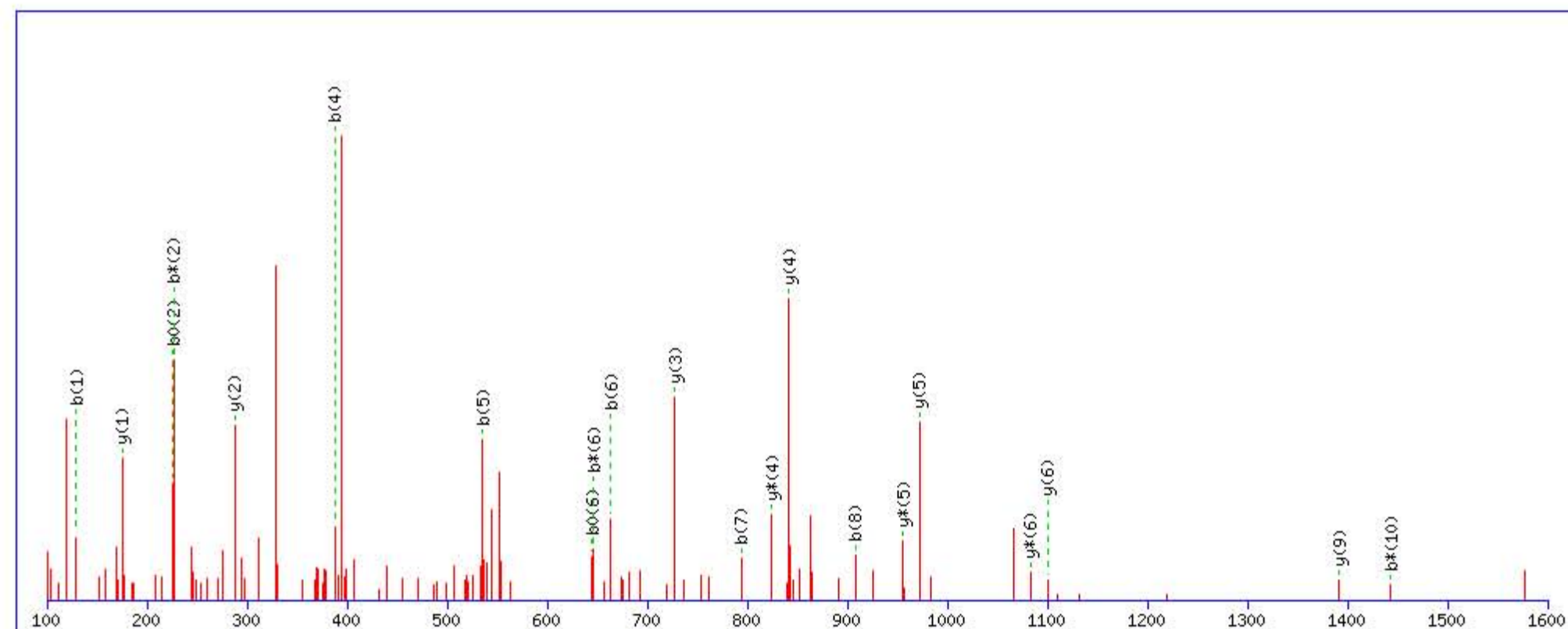
Title: Locus:1.1.1.3174.6 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

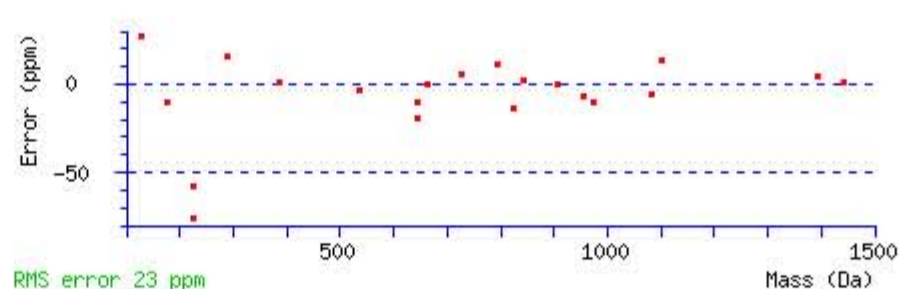
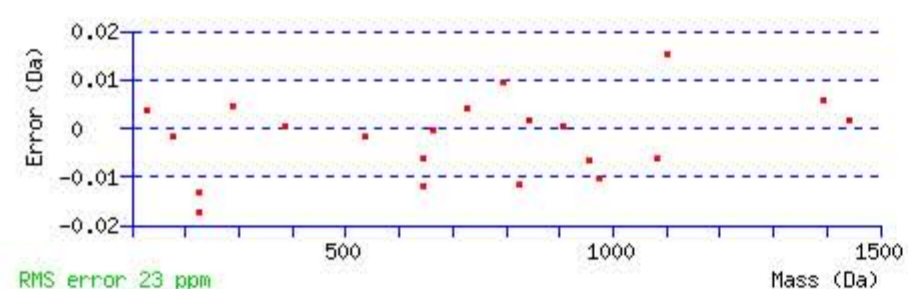
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 42 Expect: 0.00015

Matches : 21/102 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	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
42.0	1633.806854	0.000448	KDSGFQMNQLR
11.0	1633.806854	0.000448	KDSGFQMNQLR
1.4	1633.799454	0.007848	DANSFKSRDQR

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

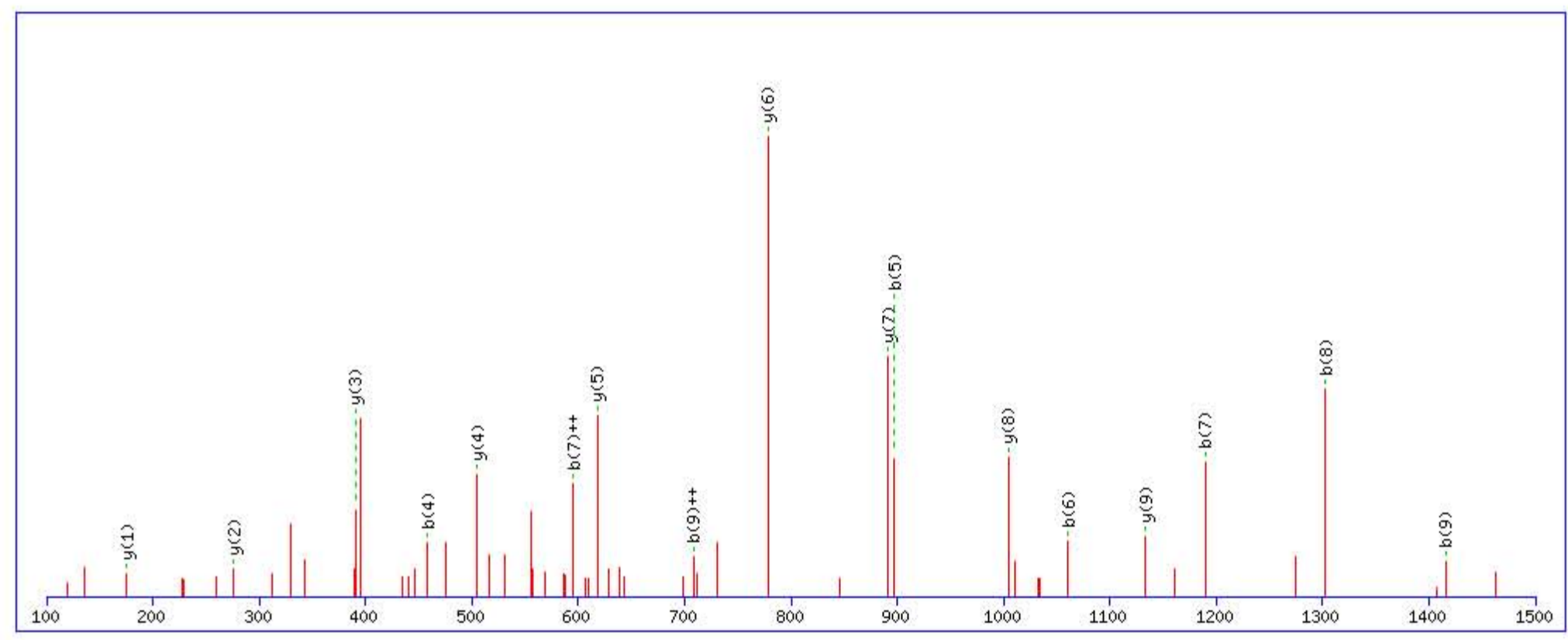
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **ADDRDQYELLCLDNTR**
 Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

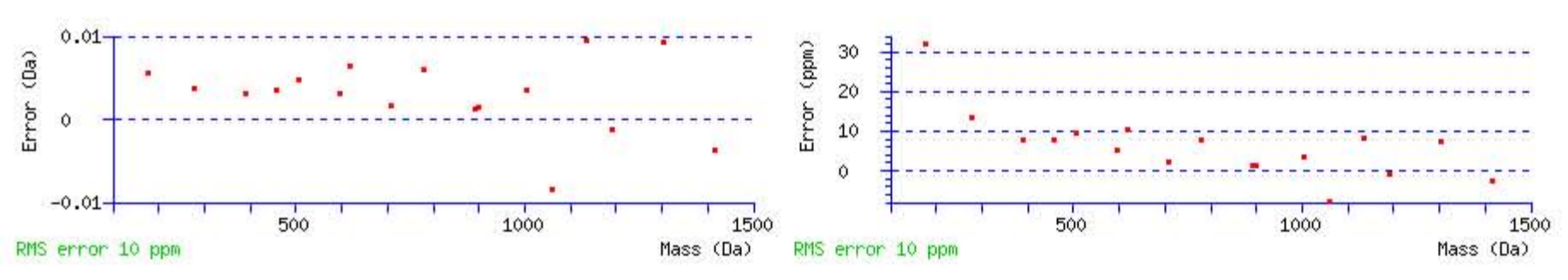
Match to Query 53778: 2192.048322 from(731.690050,3+) rtinseconds(2201) index(72449)
 Title: Locus:1.1.1.3300.11 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 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: 59 Expect: 5.1e-006
 Matches : 17/160 fragment ions using 27 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.044390	36.525833					A							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 **ADDRDQYELLCLDNTR**
 (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	2192.035400	0.012922	ADDRDQYELLCLDNTR
2.3	2192.021027	0.027295	AQRDVIEDCLMSLCR
0.8	2192.017639	0.030683	QGMMSARGDFLNYALSLMR
0.8	2192.017639	0.030683	QGMMSARGDFLNYALSLMR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **EDLIWELLNQAQEHFGK**

Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

Match to Query 57197: 2380.174512 from(794.398780,3+) rtinseconds(3238) index(79566)

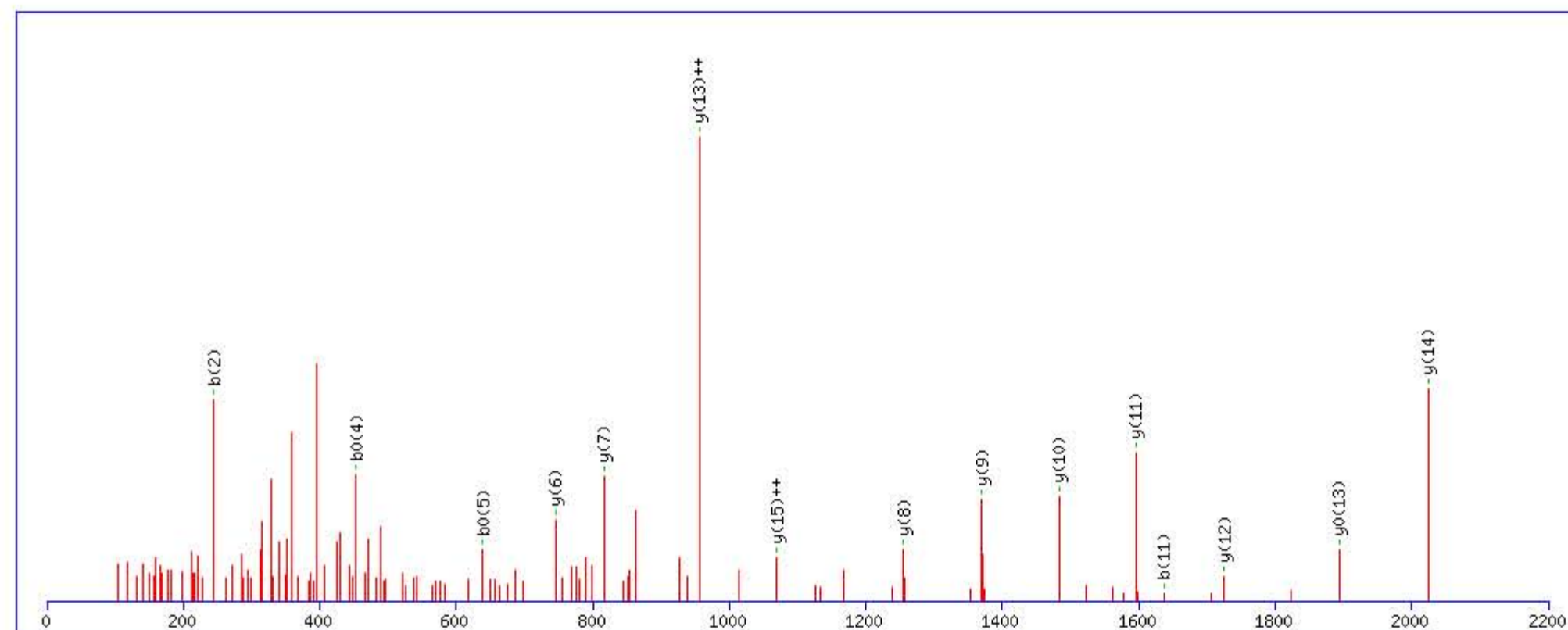
Title: Locus:1.1.1.3657.11 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2380.188522

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

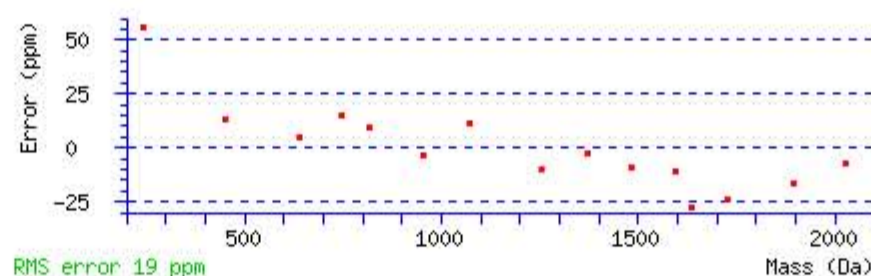
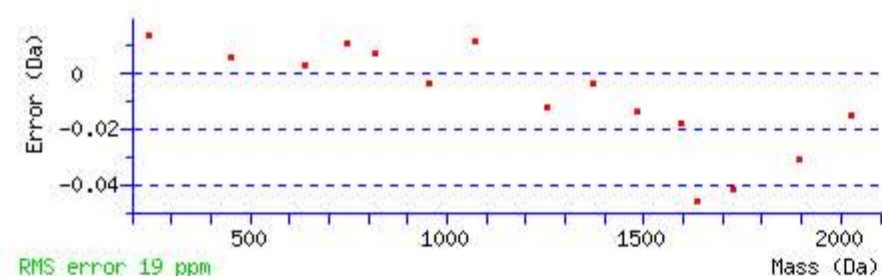
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 57 Expect: 4.9e-006

Matches : 15/168 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	130.049869	65.528572			112.039304	56.523290	E							17
2	245.076812	123.042044			227.066247	114.036762	D	2252.153237	1126.580256	2235.126688	1118.066982	2234.142672	1117.574974	16
3	358.160876	179.584076			340.150311	170.578794	L	2137.126294	1069.066785	2120.099745	1060.553510	2119.115729	1060.061502	15
4	471.244940	236.126108			453.234375	227.120826	I	2024.042230	1012.524753	2007.015681	1004.011479	2006.031665	1003.519470	14
5	657.324253	329.165765			639.313688	320.160482	W	1910.958166	955.982721	1893.931617	947.469447	1892.947601	946.977438	13
6	786.366846	393.687061			768.356281	384.681779	E	1724.878853	862.943064	1707.852304	854.429790	1706.868288	853.937782	12
7	899.450910	450.229093			881.440345	441.223811	L	1595.836260	798.421768	1578.809711	789.908493	1577.825695	789.416485	11
8	1012.534974	506.771125			994.524409	497.765843	L	1482.752196	741.879736	1465.725647	733.366461	1464.741631	732.874453	10
9	1126.577901	563.792589	1109.551352	555.279314	1108.567336	554.787306	N	1369.668132	685.337704	1352.641583	676.824429	1351.657567	676.332421	9
10	1565.803227	783.405252	1548.776678	774.891977	1547.792662	774.399969	Q	1255.625205	628.316240	1238.598656	619.802966	1237.614640	619.310958	8
11	1636.840341	818.923809	1619.813792	810.410534	1618.829776	809.918526	A	816.399879	408.703577	799.373330	400.190303	798.389314	399.698295	7
12	1764.898919	882.953098	1747.872370	874.439823	1746.888354	873.947815	Q	745.362765	373.185020	728.336216	364.671746	727.352200	364.179738	6
13	1893.941512	947.474394	1876.914963	938.961120	1875.930947	938.469112	E	617.304187	309.155732	600.277638	300.642457	599.293622	300.150449	5
14	2031.000424	1016.003850	2013.973875	1007.490576	2012.989859	1006.998568	H	488.261594	244.634435	471.235045	236.121160			4
15	2178.068838	1089.538057	2161.042289	1081.024782	2160.058273	1080.532774	F	351.202682	176.104979	334.176133	167.591704			3
16	2235.090302	1118.048789	2218.063753	1109.535514	2217.079737	1109.043506	G	204.134268	102.570772	187.107719	94.057497			2
17							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **EDLIWELLNQAQEHFGK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.7	2380.188522	-0.014010	EDLIWELLNQAQEHFGK
29.9	2380.188522	-0.014010	EDLIWELLNQAQEHFGK
0.1	2380.158020	0.016492	DELLTNQLIDHLLGENDGMPK

Peptide View

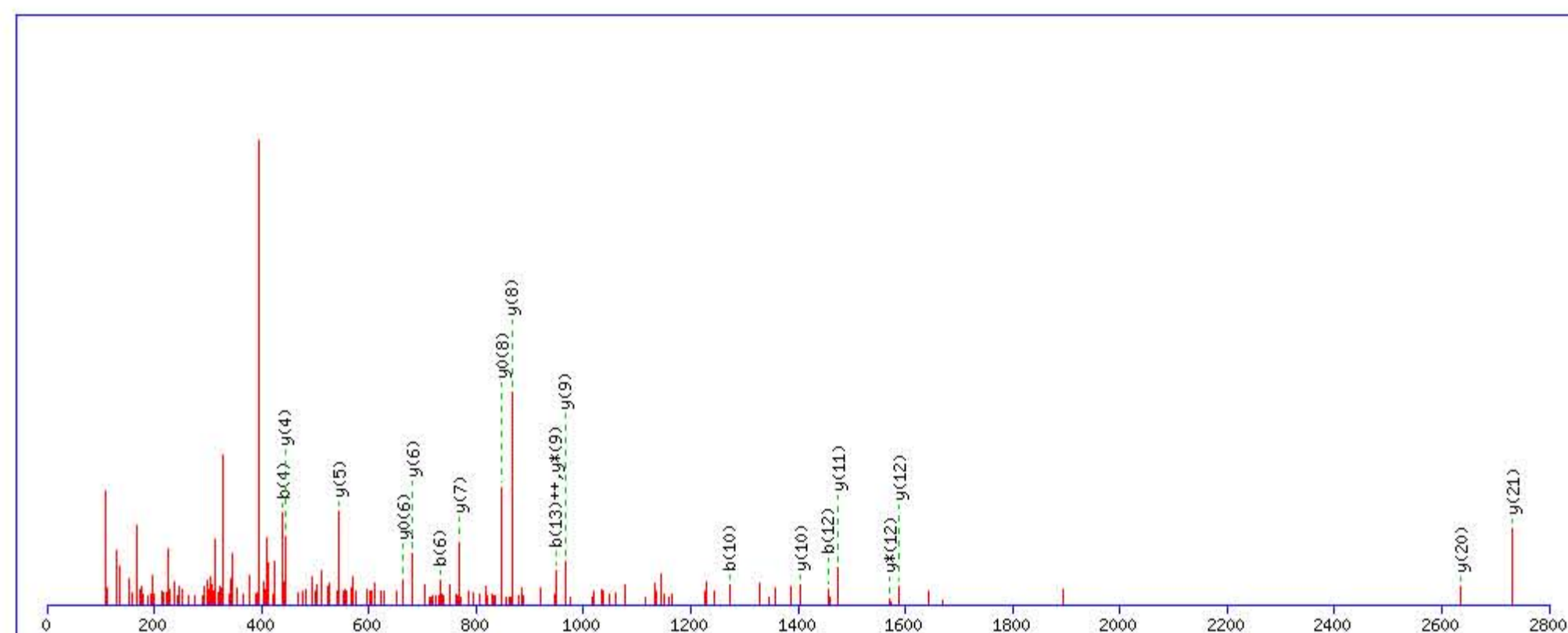
MS/MS Fragmentation of **KPVDEYKDCHLAQVPSHTVVAR**
 Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

Match to Query 64001: 2859.447220 from(572.896720,5+) rtinseconds(1527) index(68316)
 Title: Locus:1.1.1.3065.13 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

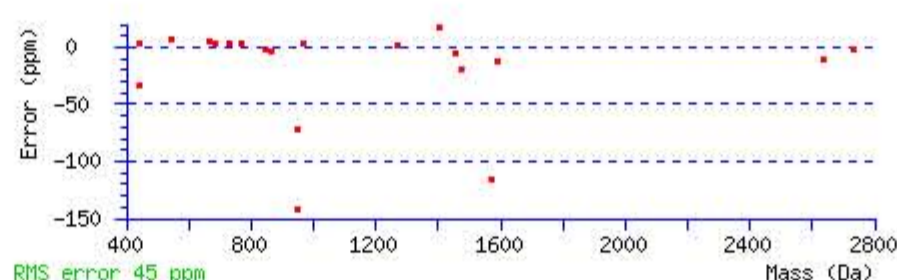
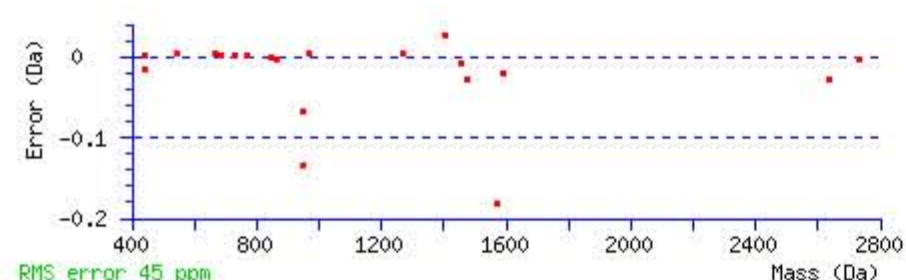
Or, Plot from to Da

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: 58 Expect: 5e-005
 Matches : 20/238 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	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
57.8	2859.452393	-0.005173	KPVDEYKDCHLAQVPSHTVVAR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **AKLIALTLLGMGLALFRNHQSSYQTR**

Found in **PON1_HUMAN**, Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3

Match to Query 67319: 3212.772016 from(804.200280,4+) rtinseconds(3183) index(63184)

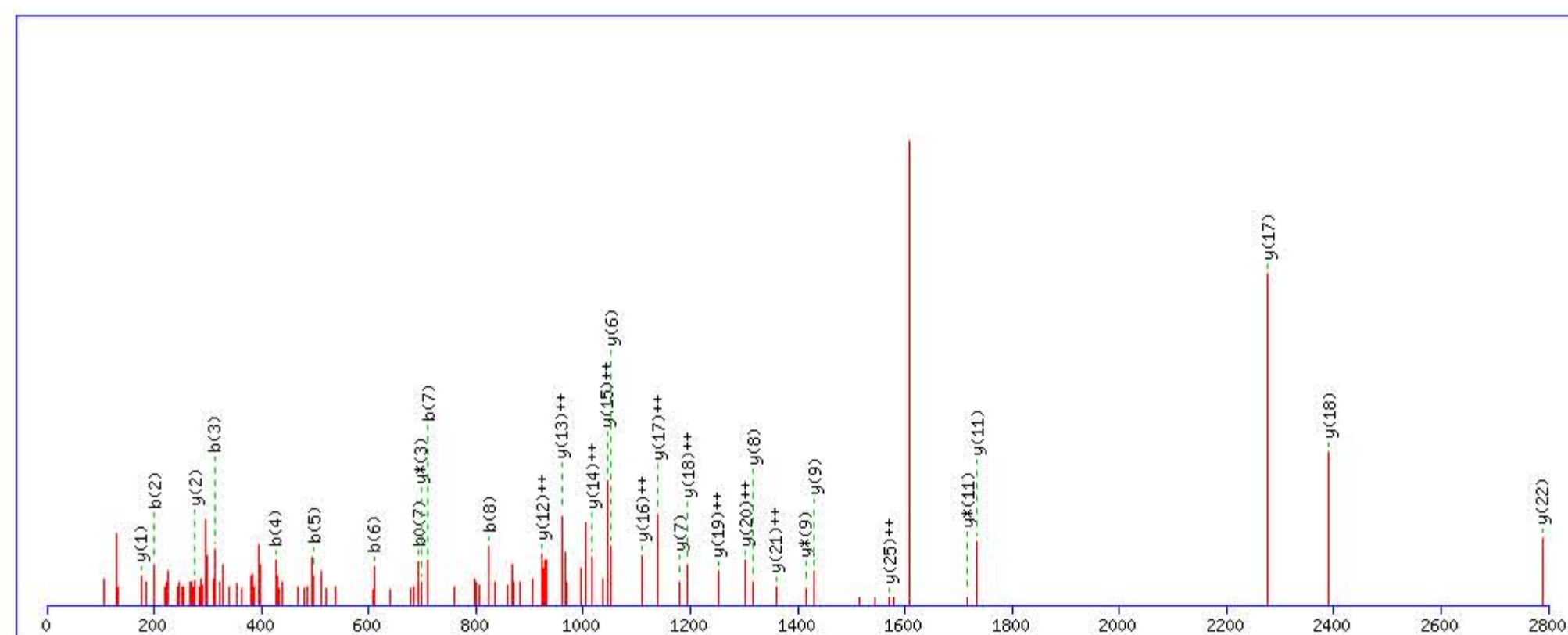
Title: Locus:1.1.1.3589.9 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GHQLQLDYFGACK**

Found in **SPRL1_HUMAN**, SPARC-like protein 1 OS=Homo sapiens GN=SPARCL1 PE=1 SV=2

Match to Query 45744: 1846.882182 from(616.634670,3+) rtinseconds(2109) index(56509)

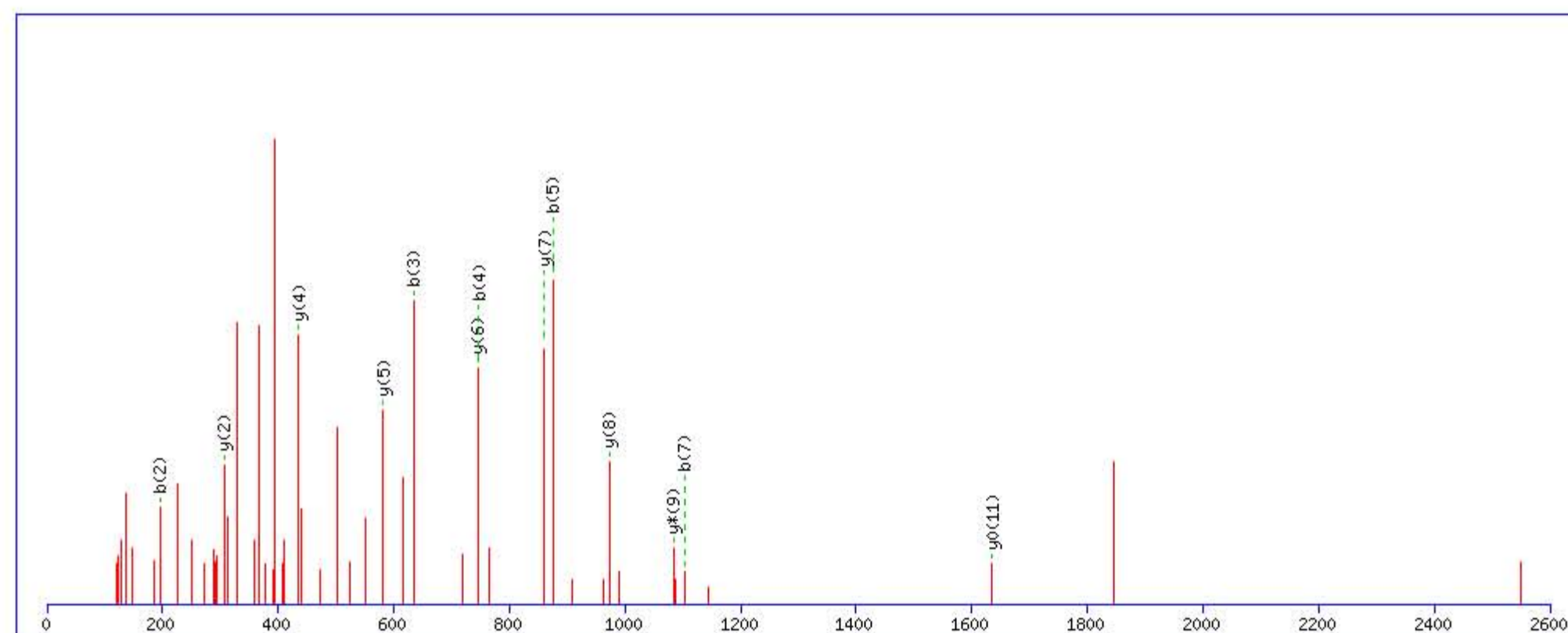
Title: Locus:1.1.1.3220.11 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\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): 1846.885849

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

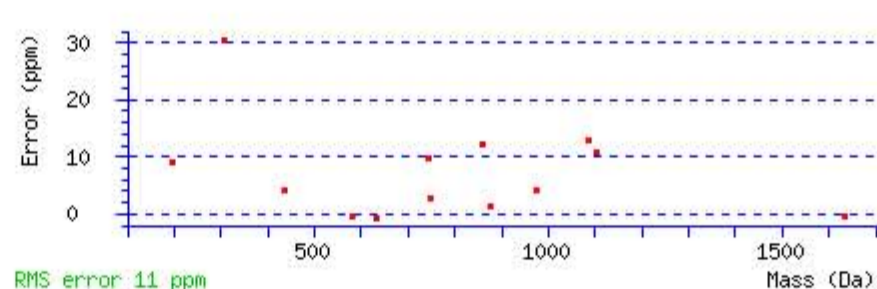
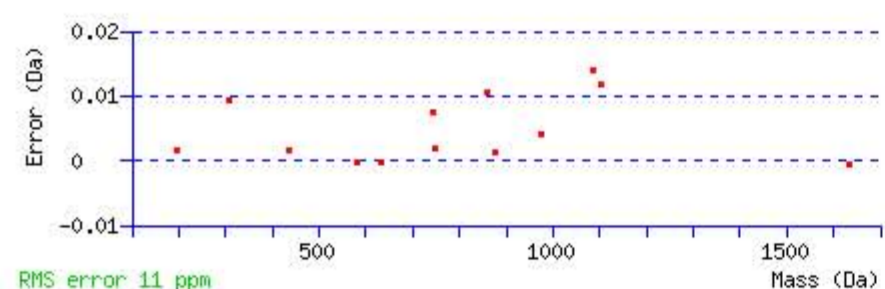
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 40 Expect: 0.00027

Matches : 13/116 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	58.028740	29.518008					G							13
2	195.087652	98.047464					H	1790.871661	895.939469	1773.845112	887.426194	1772.861096	886.934186	12
3	634.312978	317.660127	617.286429	309.146853			Q	1653.812749	827.410013	1636.786200	818.896738	1635.802184	818.404730	11
4	747.397042	374.202159	730.370493	365.688885			L	1214.587423	607.797350	1197.560874	599.284075	1196.576858	598.792067	10
5	875.455620	438.231448	858.429071	429.718174			Q	1101.503359	551.255318	1084.476810	542.742043	1083.492794	542.250035	9
6	988.539684	494.773480	971.513135	486.260206			L	973.444781	487.226029	956.418232	478.712754	955.434216	478.220746	8
7	1103.566627	552.286952	1086.540078	543.773677	1085.556062	543.281669	D	860.360717	430.683997	843.334168	422.170722	842.350152	421.678714	7
8	1266.629956	633.818616	1249.603407	625.305342	1248.619391	624.813334	Y	745.333774	373.170525	728.307225	364.657251			6
9	1413.698370	707.352823	1396.671821	698.839549	1395.687805	698.347541	F	582.270445	291.638861	565.243896	283.125586			5
10	1470.719834	735.863555	1453.693285	727.350281	1452.709269	726.858273	G	435.202031	218.104653	418.175482	209.591379			4
11	1541.756948	771.382112	1524.730399	762.868838	1523.746383	762.376830	A	378.180567	189.593921	361.154018	181.080647			3
12	1701.787597	851.397437	1684.761048	842.884162	1683.777032	842.392154	C	307.143453	154.075365	290.116904	145.562090			2
13							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **GHQLQLDYFGACK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.2	1846.885849	-0.003667	GHQLQLDYFGACK
24.9	1846.885849	-0.003667	GHQLQLDYFGACK
2.1	1846.906082	-0.023900	DLNTGVFNNQENEILK
2.0	1846.899063	-0.016881	MQLKPEINPEMLNK

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

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 40787: 1637.864502 from(546.962110,3+) rtinseconds(1895) index(54982)

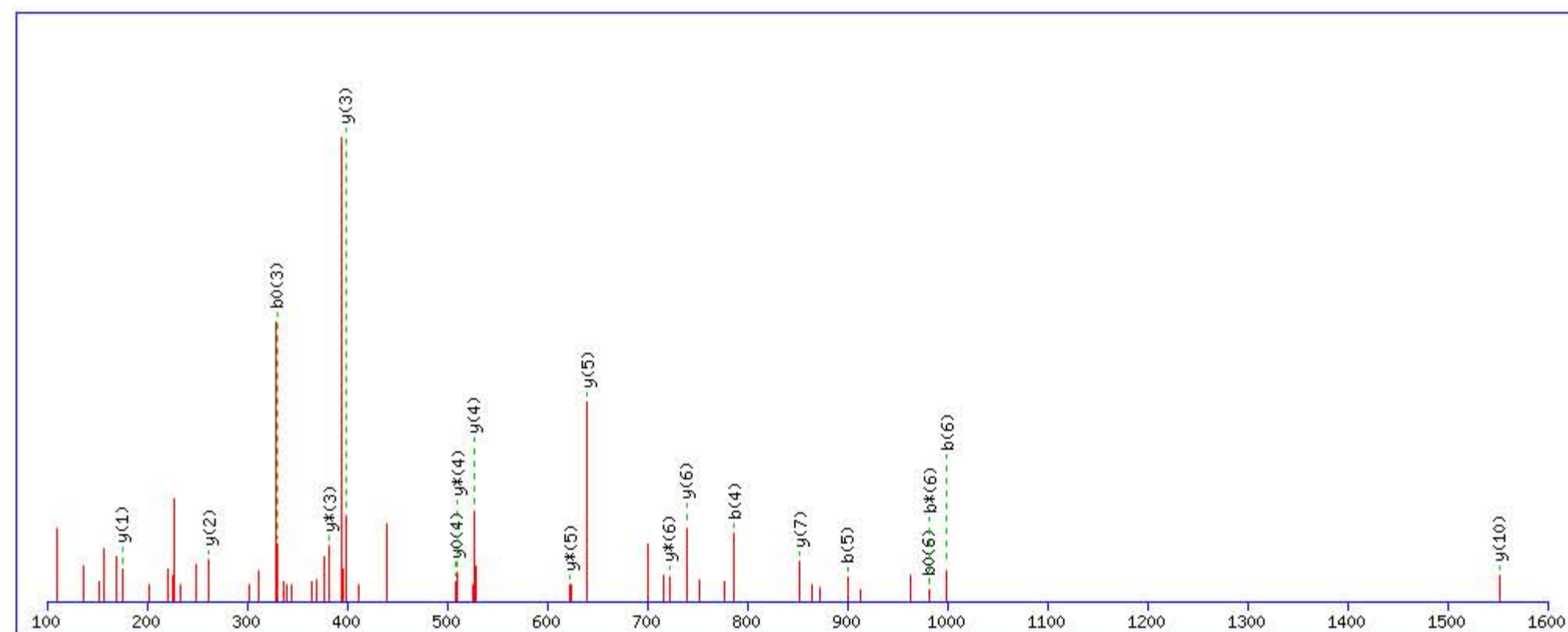
Title: Locus:1.1.1.3146.14 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1637.871170

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

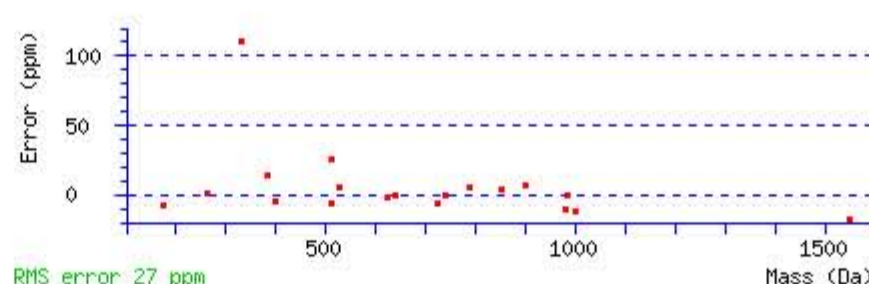
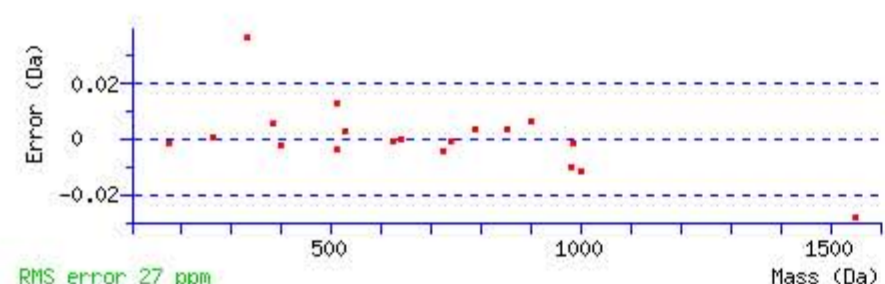
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 36 Expect: 0.00052

Matches : 19/112 fragment ions using 42 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.039304	44.523290			70.028739	35.518008	S							11
2	185.092068	93.049672			167.081503	84.044389	P	1551.846431	776.426853	1534.819882	767.913579	1533.835866	767.421571	10
3	348.155397	174.581336			330.144832	165.576054	Y	1454.793667	727.900471	1437.767118	719.387197	1436.783102	718.895189	9
4	787.380723	394.194000	770.354174	385.680725	769.370158	385.188717	Q	1291.730338	646.368807	1274.703789	637.855532	1273.719773	637.363524	8
5	900.464787	450.736032	883.438238	442.222757	882.454222	441.730749	L	852.505012	426.756144	835.478463	418.242869	834.494447	417.750861	7
6	999.533201	500.270239	982.506652	491.756964	981.522636	491.264956	V	739.420948	370.214112	722.394399	361.700837	721.410383	361.208829	6
7	1112.617265	556.812270	1095.590716	548.298996	1094.606700	547.806988	L	640.352534	320.679905	623.325985	312.166630	622.341969	311.674622	5
8	1240.675843	620.841559	1223.649294	612.328285	1222.665278	611.836277	Q	527.268470	264.137873	510.241921	255.624598	509.257905	255.132590	4
9	1377.734755	689.371015	1360.708206	680.857741	1359.724190	680.365733	H	399.209892	200.108584	382.183343	191.595309	381.199327	191.103301	3
10	1464.766783	732.887029	1447.740234	724.373755	1446.756218	723.881747	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
11							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **SPYQLVLQHSR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.4	1637.871170	-0.006668	SPYQLVLQHSR
1.4	1637.855911	0.008591	RTAYSGVPMILSSR

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 44249: 1775.900322 from(592.974050,3+) rtinseconds(1951) index(55457)

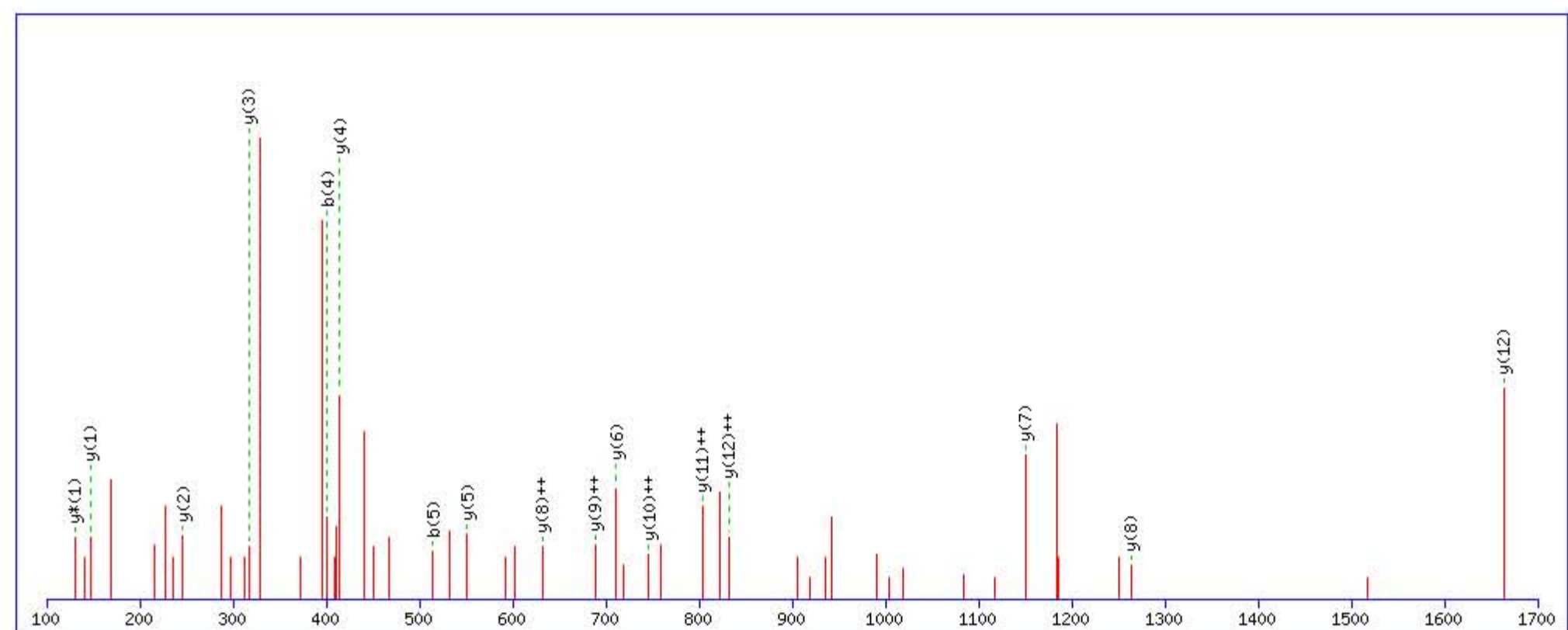
Title: Locus:1.1.1.3165.14 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

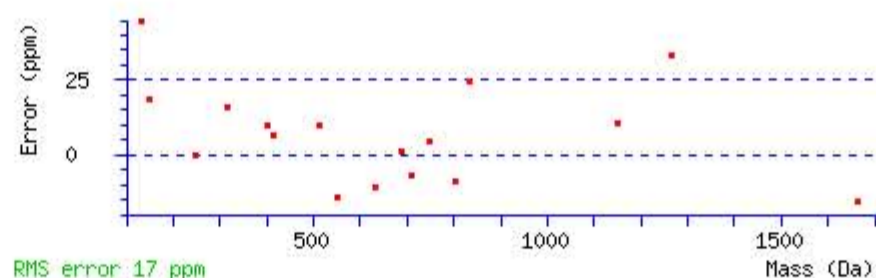
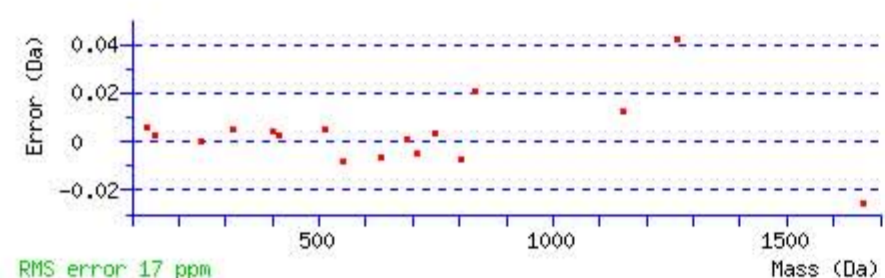
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 41 Expect: 0.002

Matches : 17/110 fragment ions using 44 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							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
41.2	1775.906250	-0.005928	LGDDLLQCHPAVK

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

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 20267: 1096.623868 from(549.319210,2+) rtinseconds(1953) index(55479)

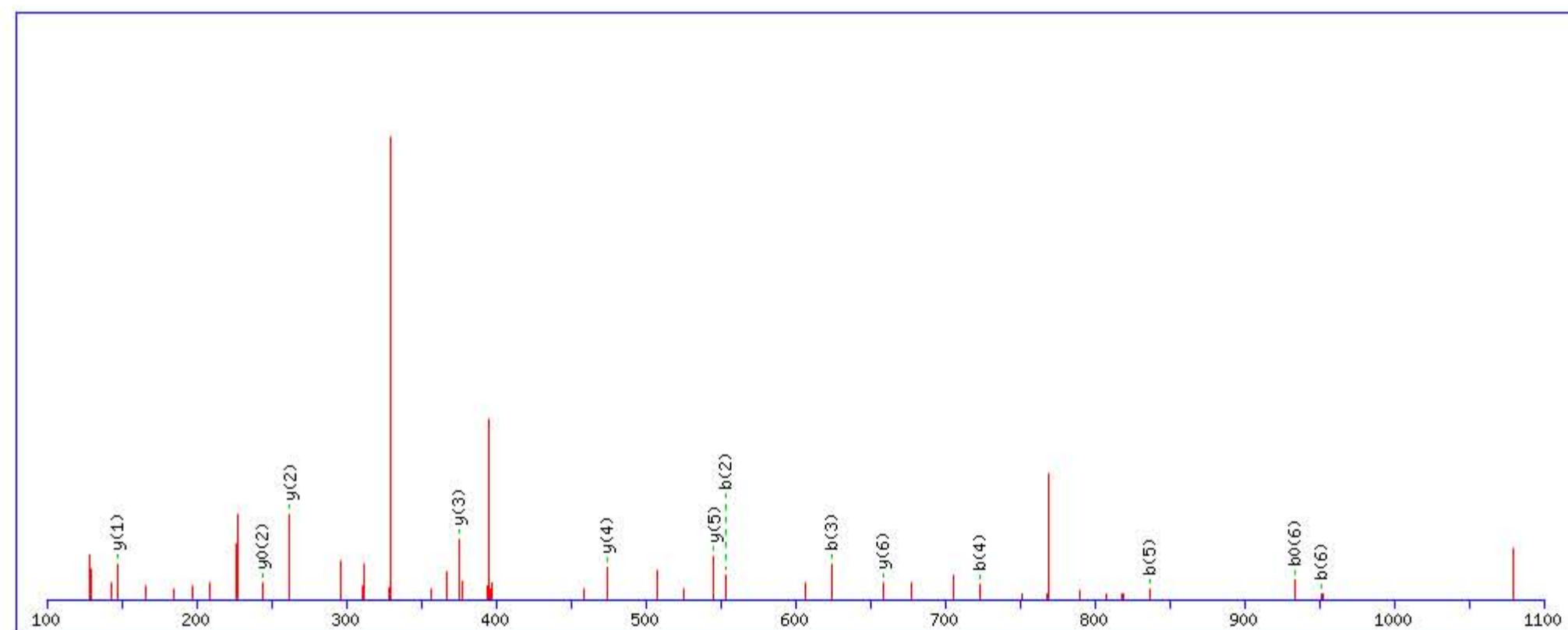
Title: Locus:1.1.1.3166.11 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

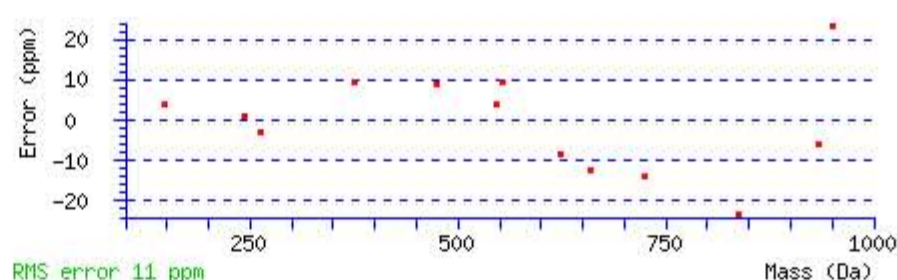
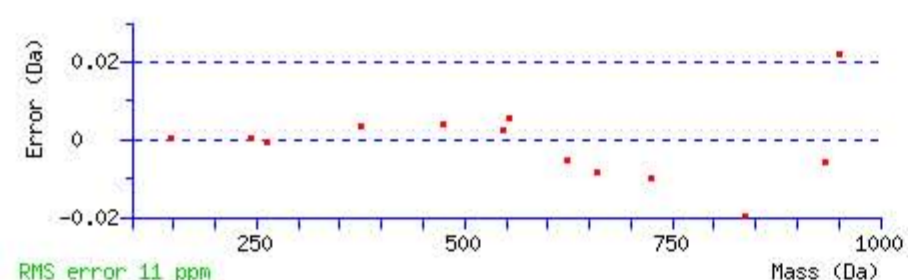
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 26 Expect: 0.03

Matches : 13/60 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	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
25.9	1096.631439	-0.007571	QLAVLDK
11.2	1096.624054	-0.000186	KPVDSVPLSR
8.1	1096.624023	-0.000155	IPRENLLDK
7.5	1096.639297	-0.015429	AHVSPLFKAK
2.8	1096.612793	0.011075	QPILDAIEAK
1.0	1096.631439	-0.007571	GILQLDK

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

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 34942: 1474.724508 from(738.369530,2+) rtinseconds(1746) index(54126)

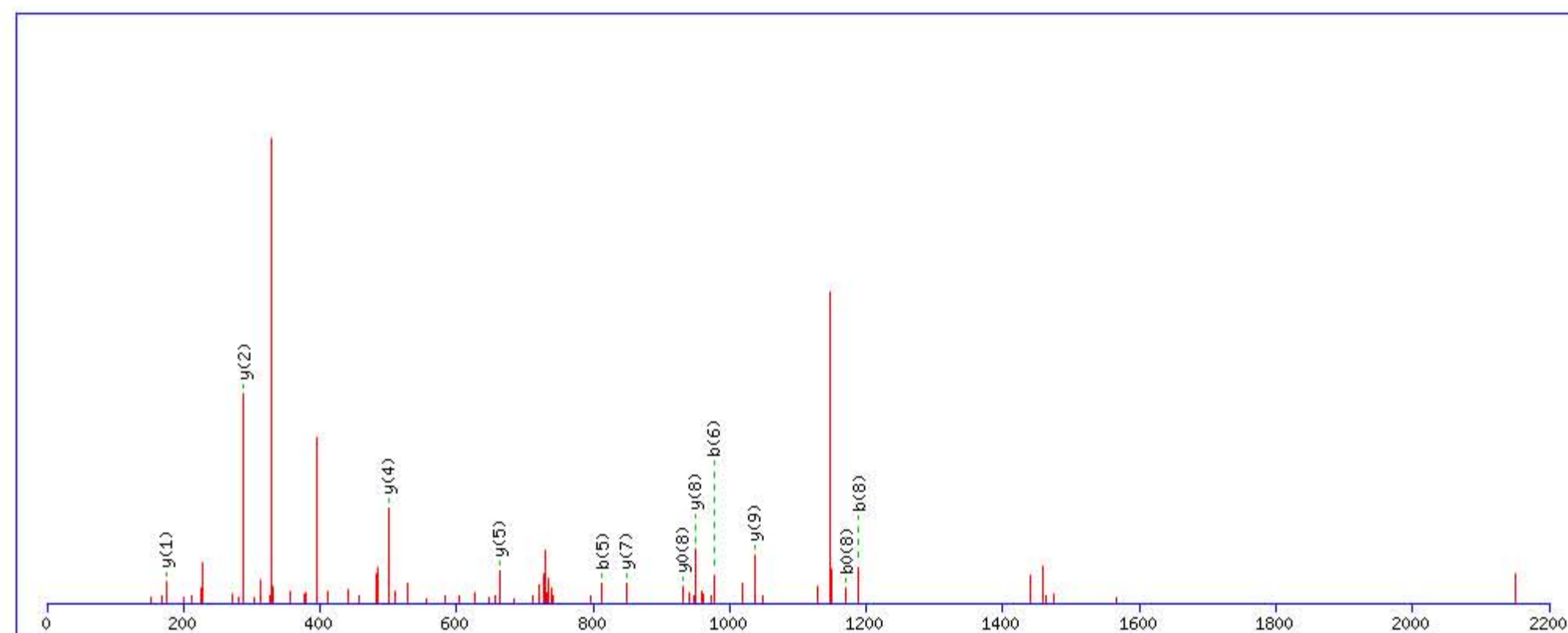
Title: Locus:1.1.1.3094.16 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1474.723831

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

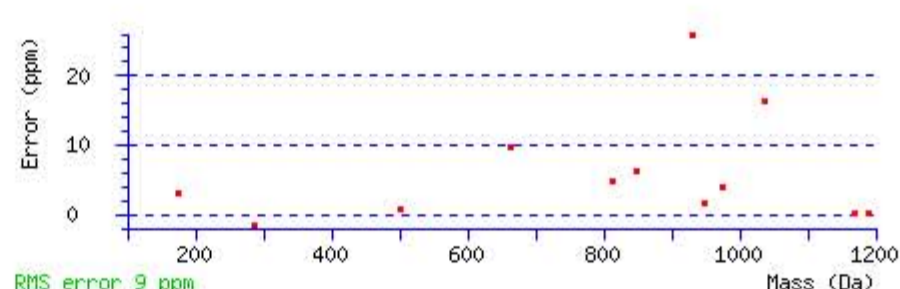
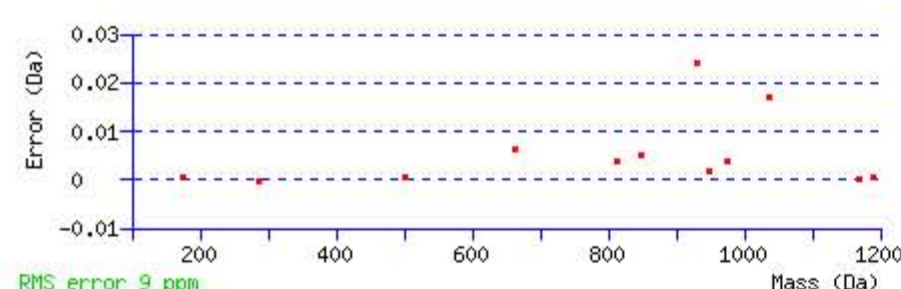
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 41 Expect: 0.0013

Matches : 12/102 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	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	$M_r(\text{calc})$:	Delta	Sequence
41.4	1474.723831	0.000677	QSTNAYPDLR
9.9	1474.741592	-0.017084	SSLEHGSDVYLLR
9.6	1474.744934	-0.020426	LSKEELIQNMDR
9.1	1474.721161	0.003347	QSTHGERGHR
6.2	1474.745605	-0.021097	EPWEELFSIGLR
1.8	1474.731033	-0.006525	RGDGGKMAAAGALER
1.6	1474.746307	-0.021799	DAVQHERGPR
0.5	1474.726303	-0.001795	VQTEKEEKEEAR

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 35997: 1508.780408 from(755.397480,2+) rtinseconds(2294) index(57570)

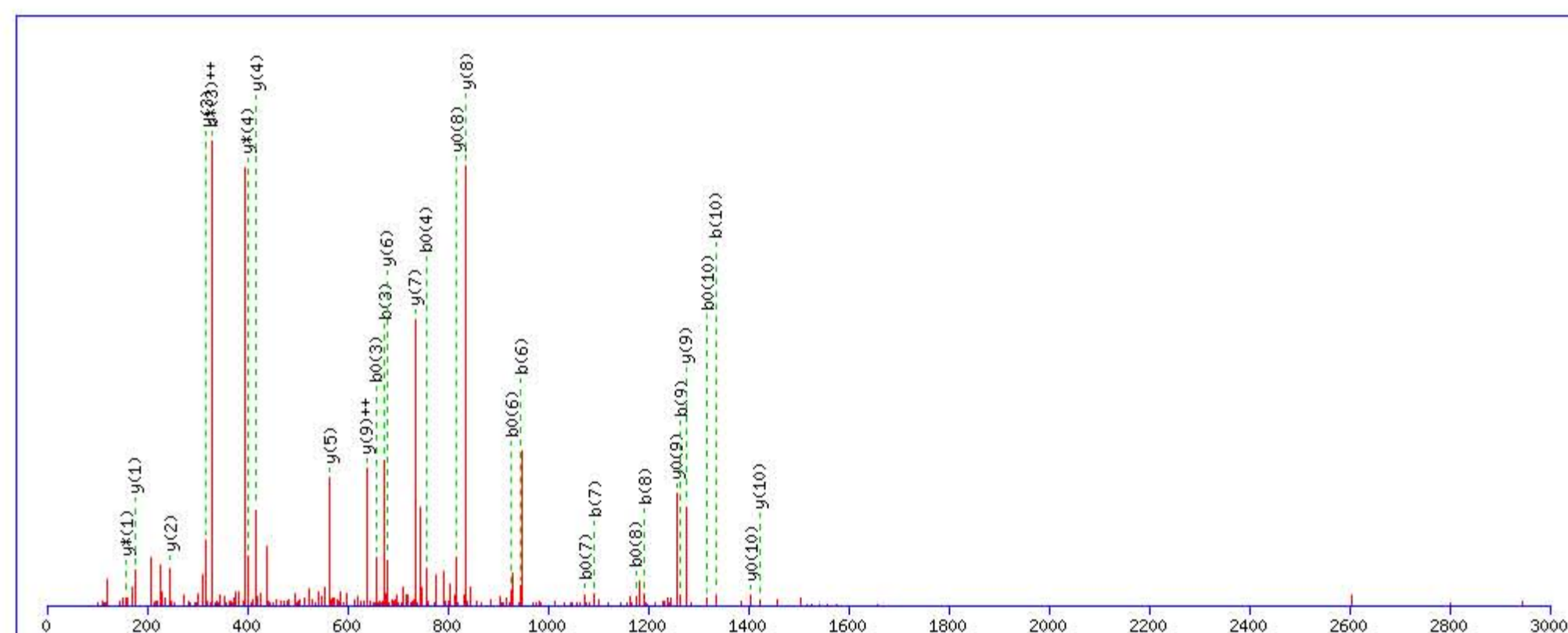
Title: Locus:1.1.1.3284.8 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

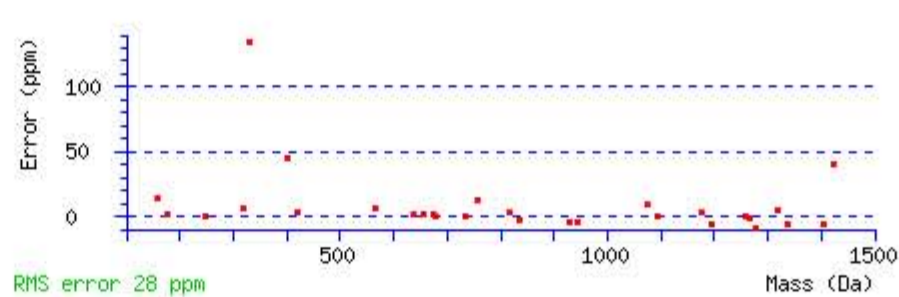
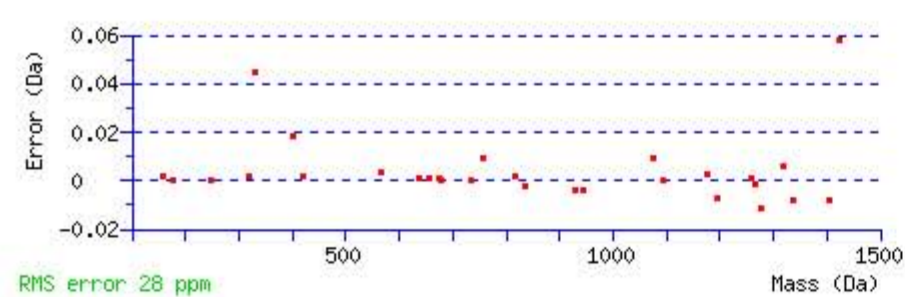
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 59 Expect: 1.9e-005

Matches : 29/110 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							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
58.7	1508.780975	-0.000567	SFQTGLFTAAR
7.9	1508.762344	0.018064	EDFVPFTGEKKGR
4.1	1508.798721	-0.018313	SSYGVAAPVDFLRK
3.2	1508.776932	0.003476	LMGADSLQLFRSR
1.8	1508.776917	0.003491	MYLDLLSQSQRR
1.8	1508.765686	0.014722	TKAFQIMQEELR
1.6	1508.759201	0.021207	HPVTTQVCIMPAR
1.3	1508.759186	0.021222	QVHCGSEILR
1.3	1508.759171	0.021237	SQMITYQRR
1.2	1508.780960	-0.000552	TQPPPENLFR

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 41153: 1650.831702 from(551.284510,3+) rtinseconds(1625) index(53318)

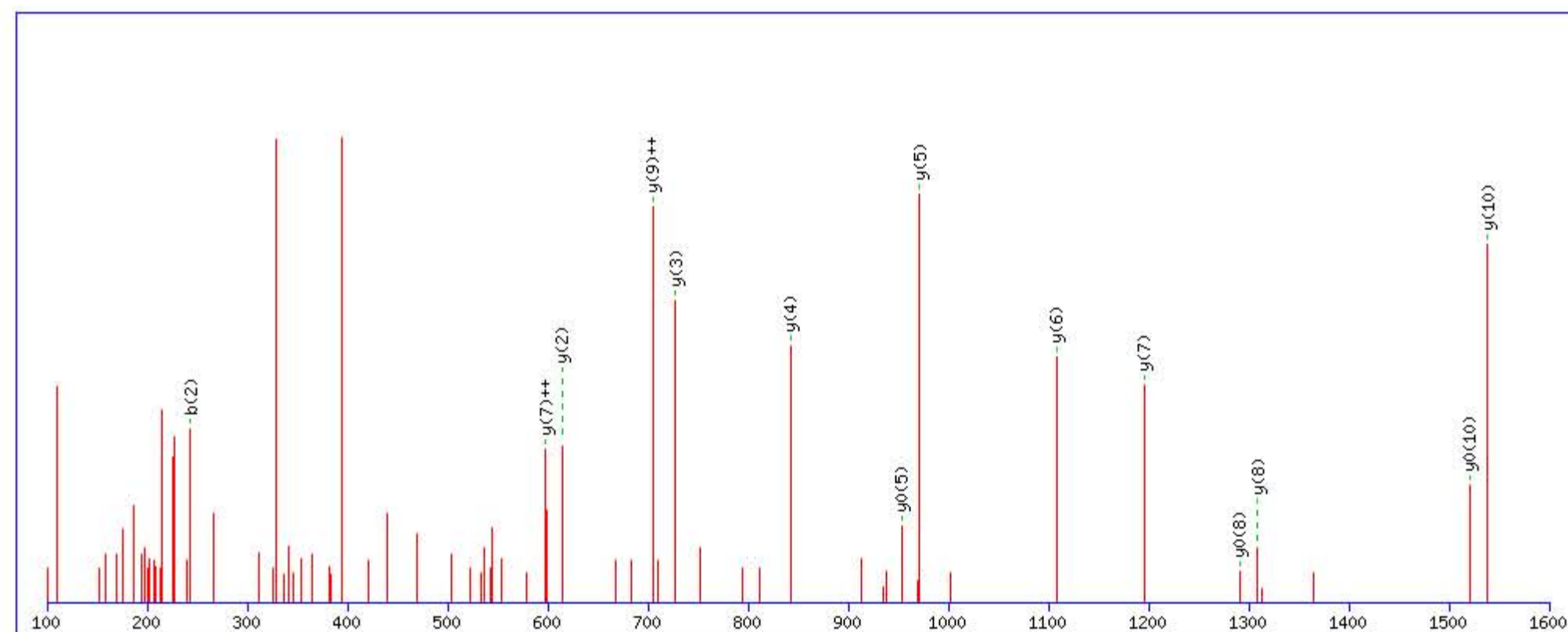
Title: Locus:1.1.1.3052.9 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

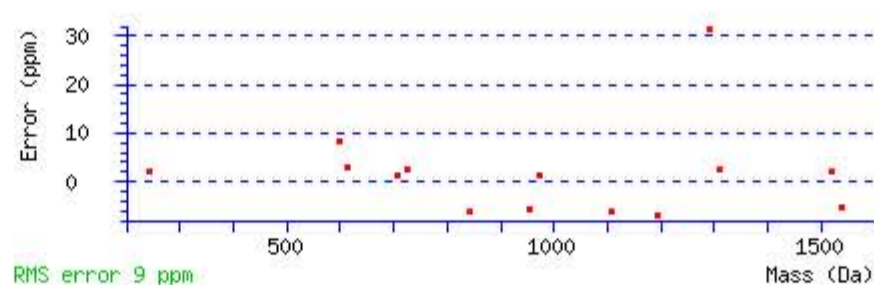
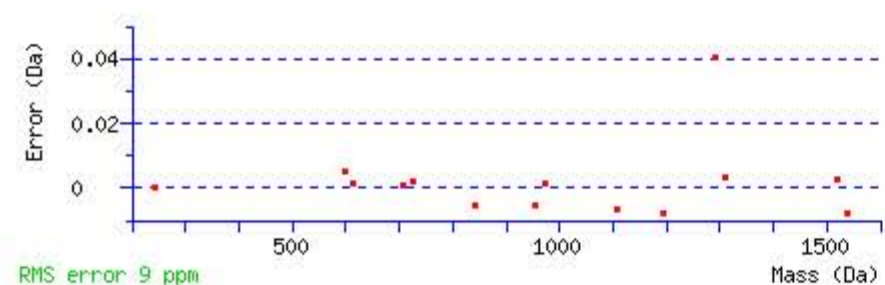
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 46 Expect: 7.2e-005

Matches : 14/94 fragment ions using 26 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	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
45.7	1650.839920	-0.008218	IETISHEDLQR
1.5	1650.833389	-0.001687	QQLEHIMATNR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **IQALSLCSDQQSHLEFR**

Found in **PROS_HUMAN**, Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1

Match to Query 56795: 2342.136942 from(781.719590,3+) rtinseconds(2174) index(72274)

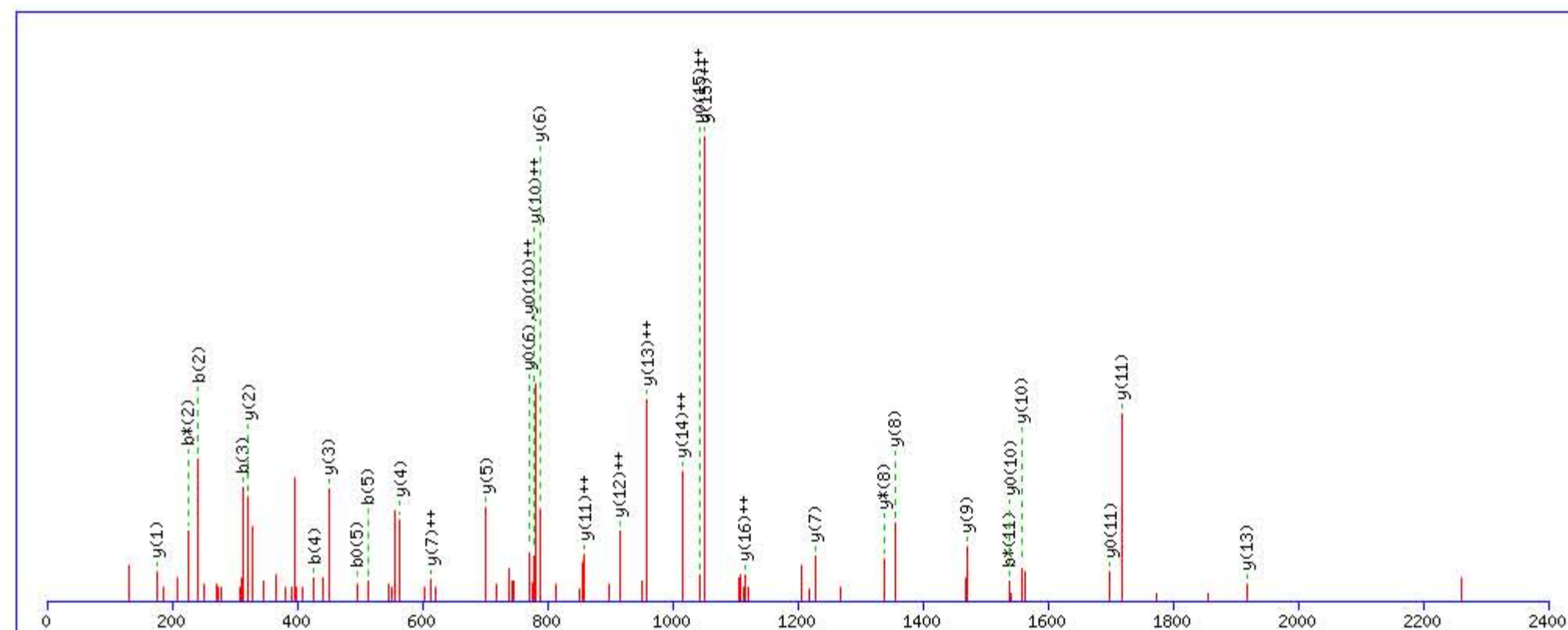
Title: Locus:1.1.1.3290.26 File:"2013-07-02 CLN FXIII 30 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

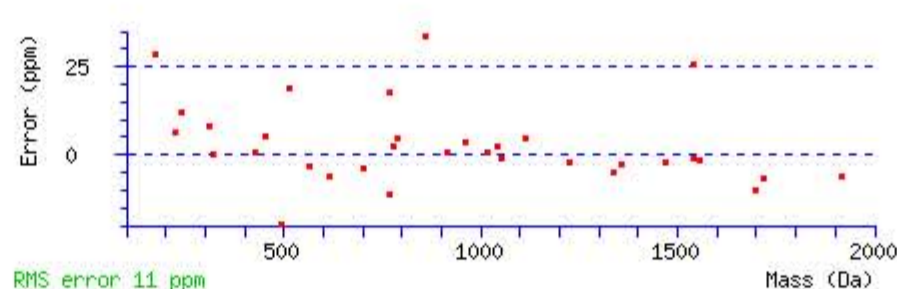
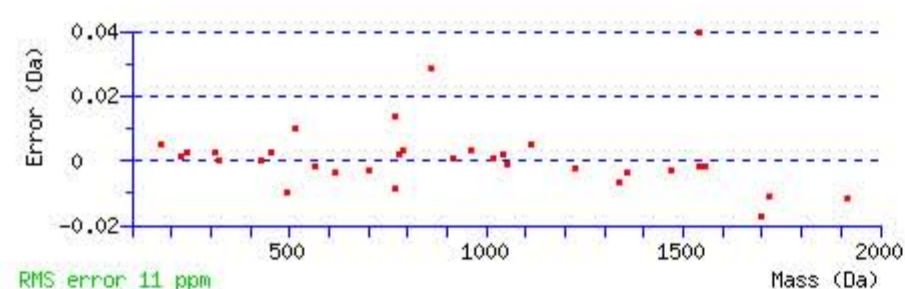
Variable modifications:

Q11 : Biotin:Thermo-21345 (Q)

Ions Score: 74 Expect: 1.1e-006

Matches : 33/178 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
73.7	2342.151108	-0.014166	IQALSLCSDQQSHLEFR
69.9	2342.151108	-0.014166	IQALSLCSDQQSHLEFR
0.7	2342.151108	-0.014166	IQALSLCSDQQSHLEFR

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

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TDGCQHFCLPGQESYTCSCAQGYR**

Found in **PROZ_HUMAN**, Vitamin K-dependent protein Z OS=Homo sapiens GN=PROZ PE=1 SV=2

Match to Query 67170: 3192.301302 from(1065.107710,3+) rtinseconds(2030) index(55972)

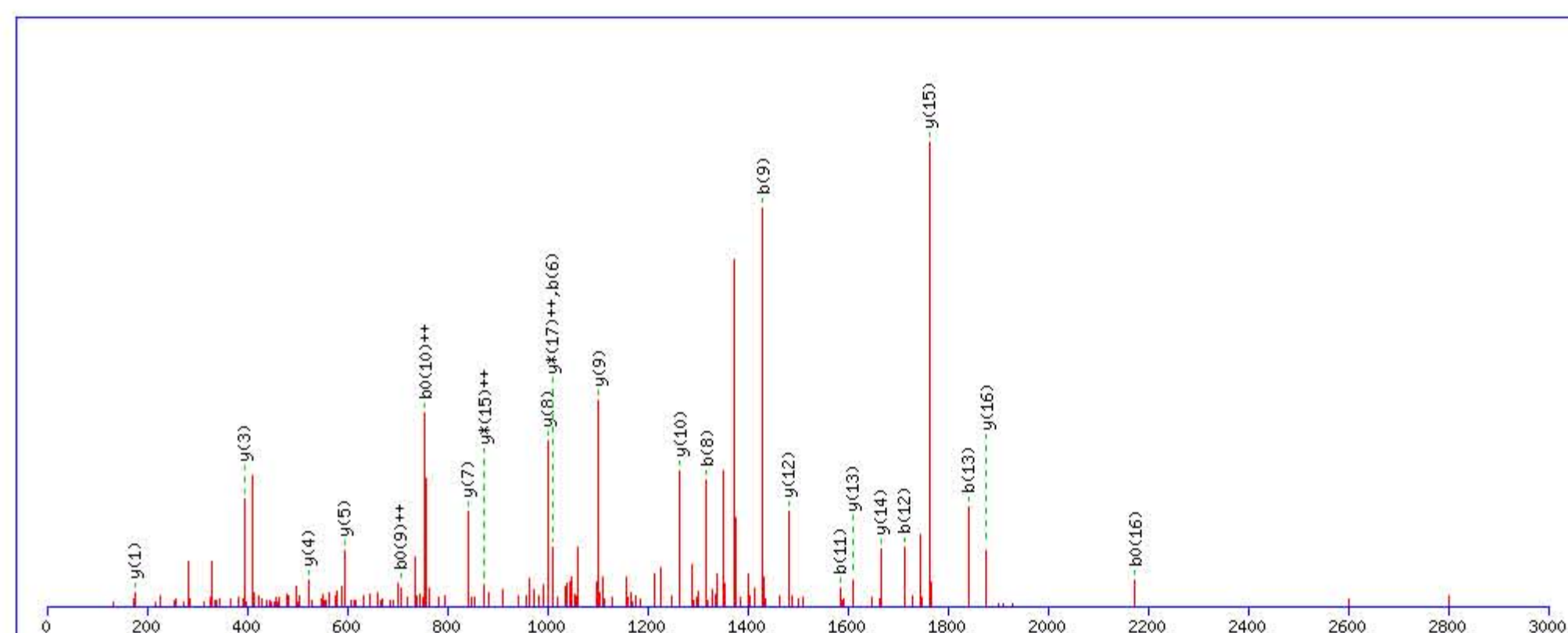
Title: Locus:1.1.1.3192.13 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

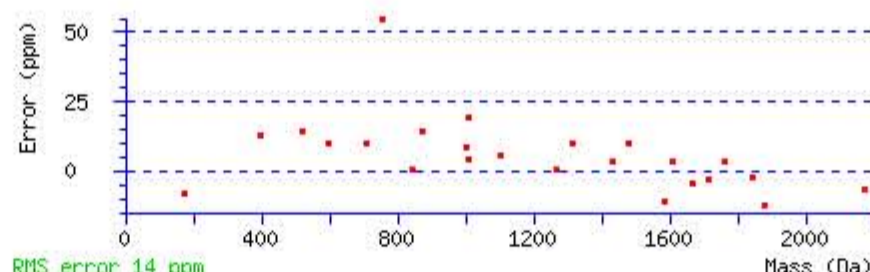
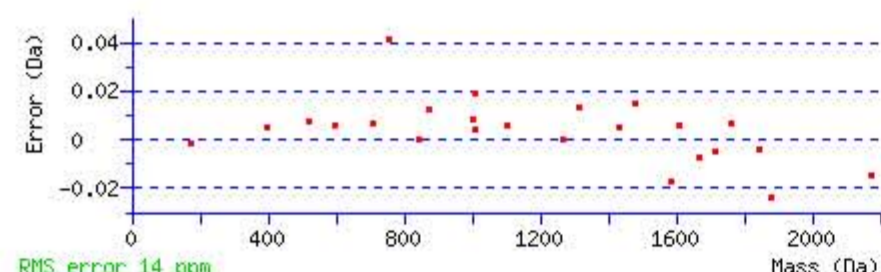
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 77 Expect: 1.9e-008

Matches : 24/256 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
77.3	3192.298050	0.003252	TDGCQHFCLPGQESYTCSCAQGYR
34.6	3192.298050	0.003252	TDGCQHFCLPGQESYTCSCAQGYR

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 39408: 1614.706308 from(808.360430,2+) rtinseconds(1861) index(54727)

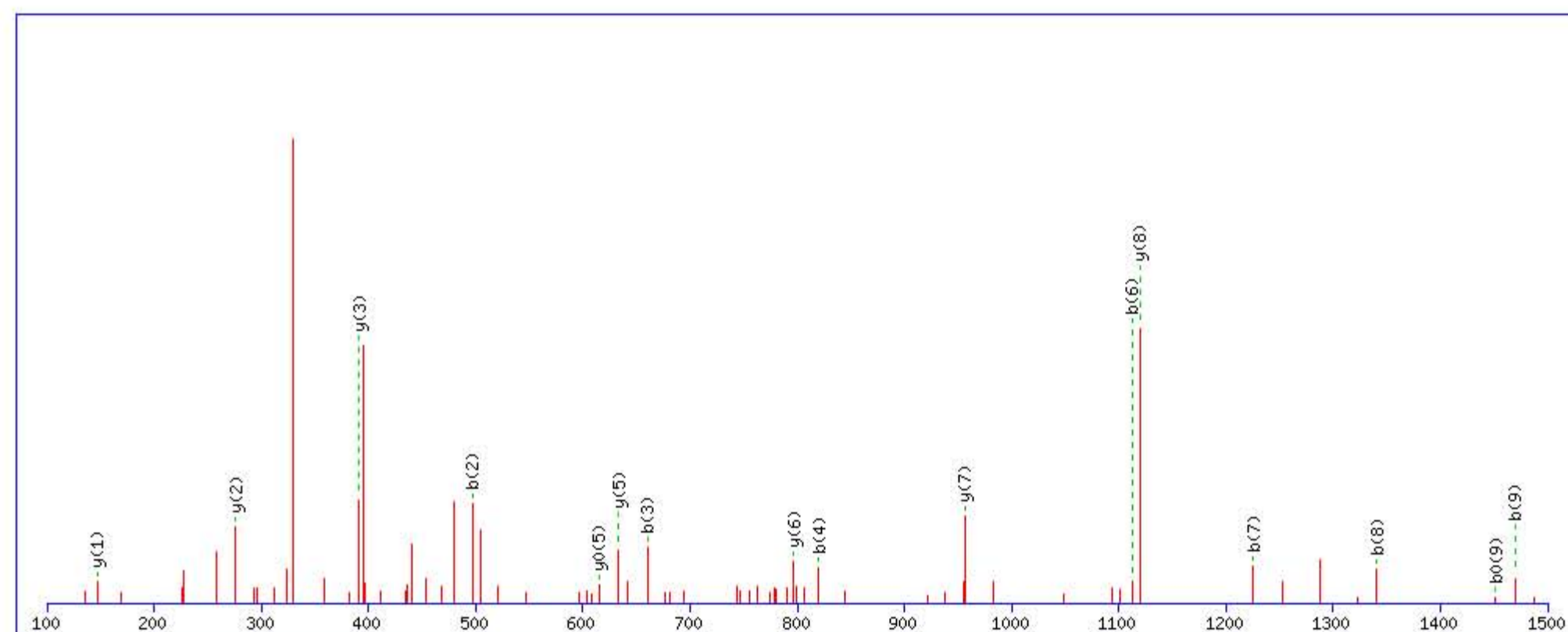
Title: Locus:1.1.1.3134.17 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

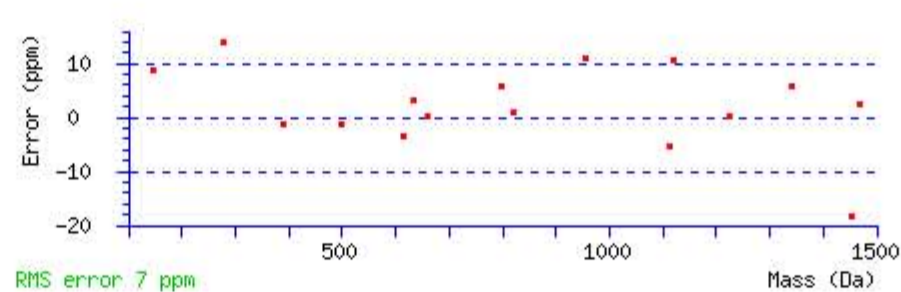
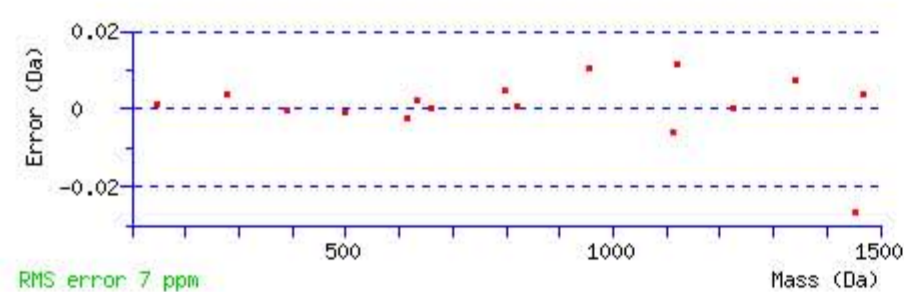
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 46 Expect: 9e-005

Matches : 16/94 fragment ions using 26 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.028740	29.518008					G							10
2	497.254066	249.130671	480.227517	240.617397			Q	1558.691630	779.849453	1541.665081	771.336179	1540.681065	770.844171	9
3	660.317395	330.662336	643.290846	322.149061			Y	1119.466304	560.236790	1102.439755	551.723516	1101.455739	551.231508	8
4	820.348044	410.677660	803.321495	402.164386			C	956.402975	478.705126	939.376426	470.191851	938.392410	469.699843	7
5	983.411373	492.209325	966.384824	483.696050			Y	796.372326	398.689801	779.345777	390.176527	778.361761	389.684519	6
6	1112.453966	556.730621	1095.427417	548.217347	1094.443401	547.725339	E	633.308997	317.158137	616.282448	308.644862	615.298432	308.152854	5
7	1225.538030	613.272653	1208.511481	604.759379	1207.527465	604.267371	L	504.266404	252.636840	487.239855	244.123566	486.255839	243.631558	4
8	1340.564973	670.786125	1323.538424	662.272850	1322.554408	661.780842	D	391.182340	196.094808	374.155791	187.581534	373.171775	187.089526	3
9	1469.607566	735.307421	1452.581017	726.794147	1451.597001	726.302139	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
10							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **GQYCYELDEK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.3	1614.705795	0.000513	GQYCYELDEK
3.5	1614.717010	-0.010702	EYFRMELMHAEK
2.7	1614.683167	0.023141	YQVSSLCGTDNEDK
1.1	1614.702667	0.003641	LWCCTGNSIMVMK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **DWHGVPGQVDAAMAGR**

Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

Match to Query 48622: 1976.931342 from(659.984390,3+) rtinseconds(2165) index(56888)

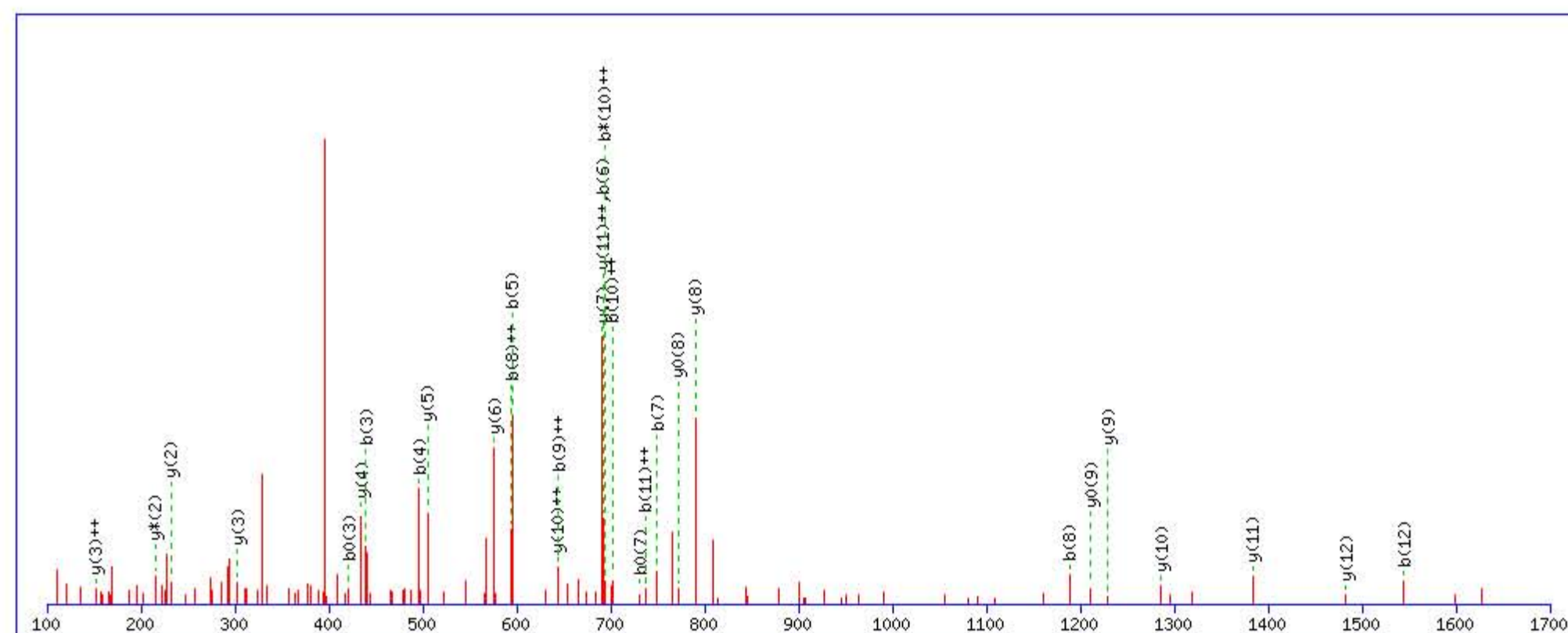
Title: Locus:1.1.1.3239.21 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

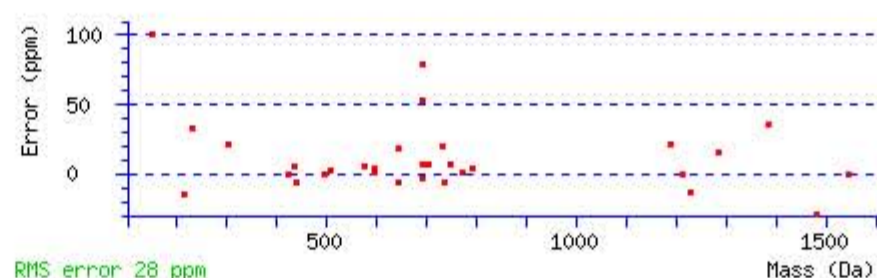
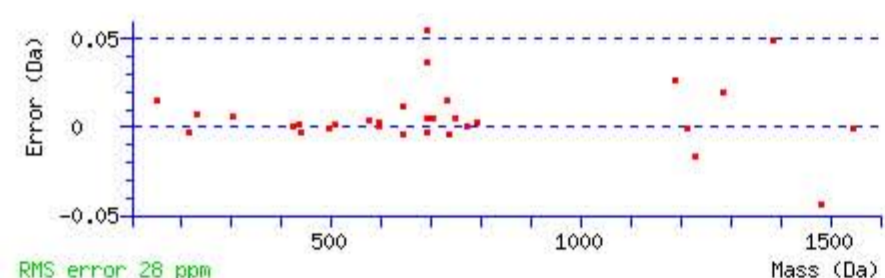
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 45 Expect: 0.00054

Matches : 31/154 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	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
45.3	1976.934937	-0.003595	DWHGVPGQVDAAMAGR

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

Mascot Search Results

Peptide View

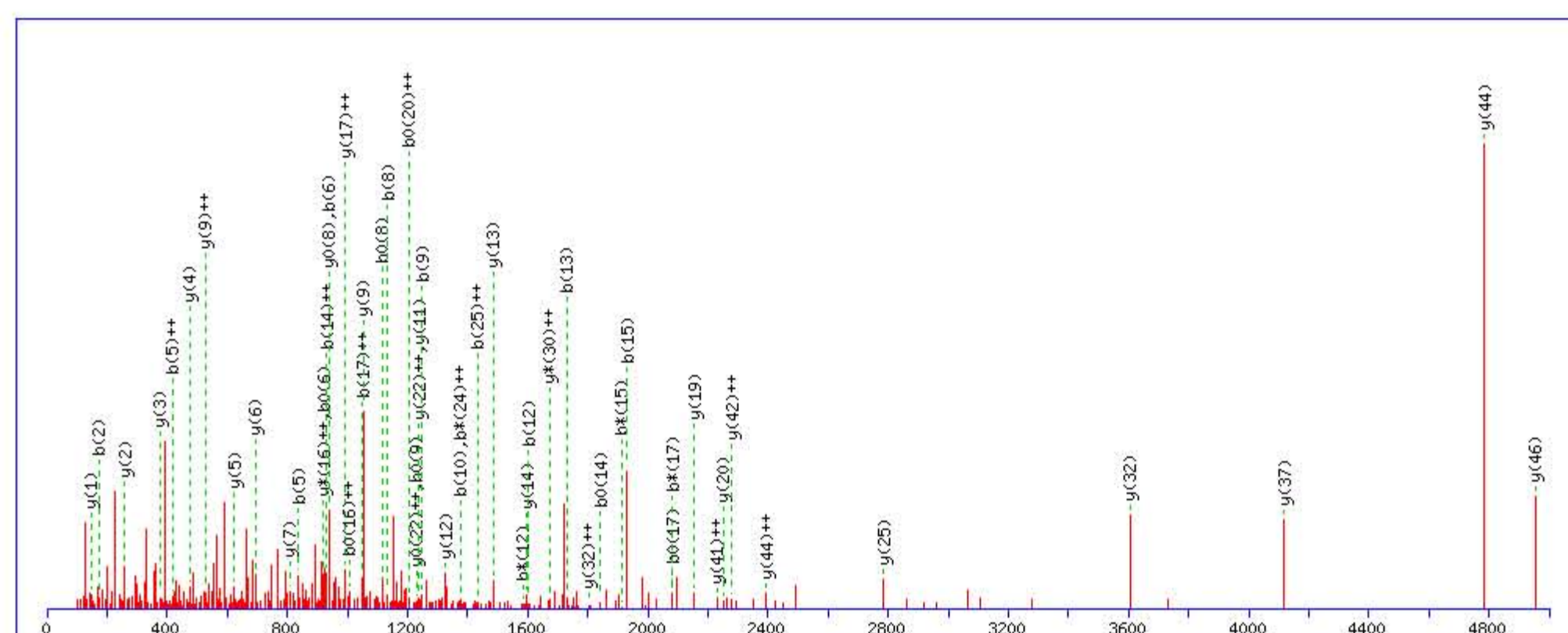
MS/MS Fragmentation of **GNPEQTPVLKPEEEAPAVEVGASKPEGIDSRPETLHPGRPQPPAEELCSGKPFDAFTDLK**
 Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

Match to Query 81986: 6883.387392 from(861.430700,8+) rtinseconds(2061) index(56185)
 Title: Locus:1.1.1.3203.8 File:"2013-07-02 CLN FXIII 30 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 6883.374893
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q5 : Biotin:Thermo-21345 (Q)
 Ions Score: 28 Expect: 0.021
 Matches : 54/708 fragment ions using 181 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			

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 23647: 1157.640348 from(579.827450,2+) rtinseconds(1920) index(38038)

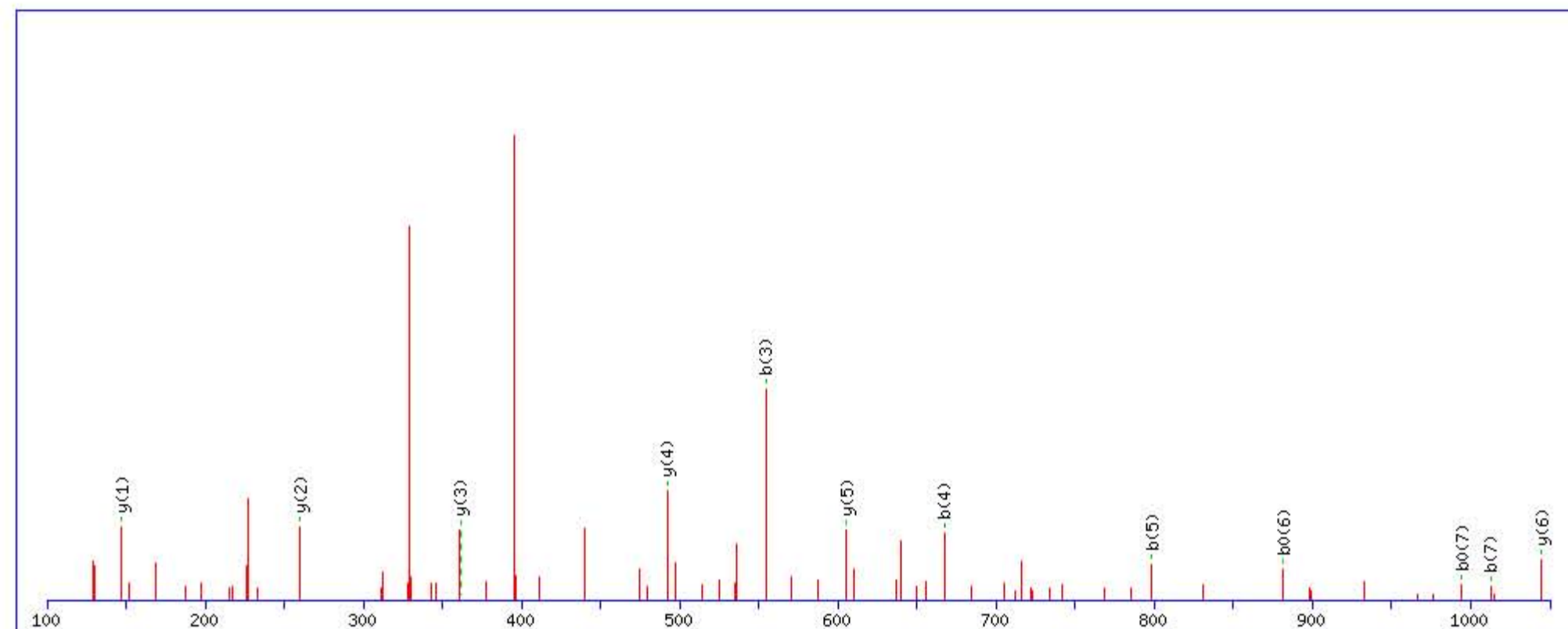
Title: Locus:1.1.1.2691.17 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

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)

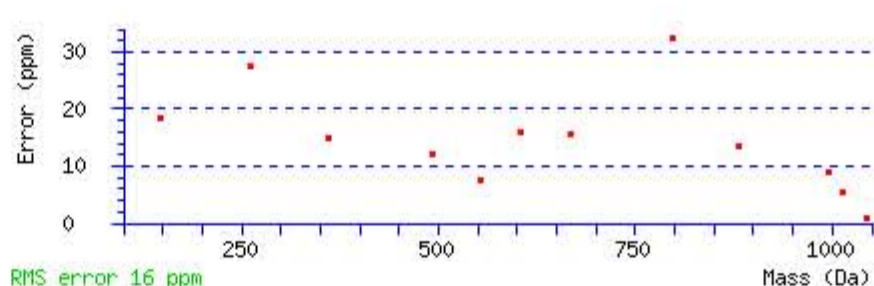
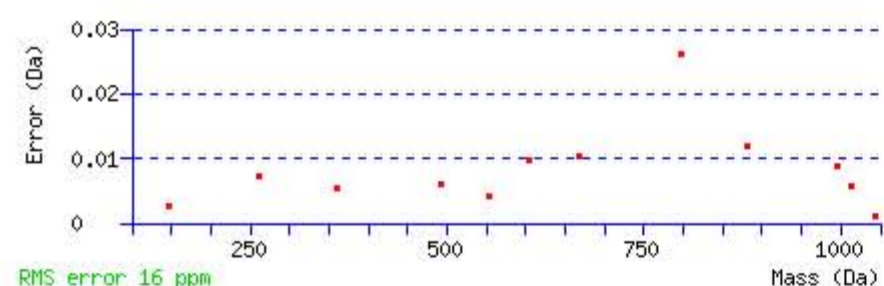
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.043

Matches : 12/66 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	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
27.0	1157.630066	0.010282	GGQIMTLK
11.7	1157.640411	-0.000063	AQQLLSSGNLK
11.2	1157.630051	0.010297	QLSQMLK
6.4	1157.647827	-0.007479	ALVGGTAPMTIK
5.3	1157.636566	0.003782	LLAIMPDELK
3.6	1157.637924	0.002424	NQLGFLR
2.6	1157.630051	0.010297	QLSQMLK
2.0	1157.630081	0.010267	CVTLVQK
1.8	1157.630051	0.010297	QIKSMLQ
1.3	1157.629196	0.011152	EPQITQLTK

MASCOT 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 38320: 1585.875102 from(529.632310,3+) rtinseconds(1791) index(37278)

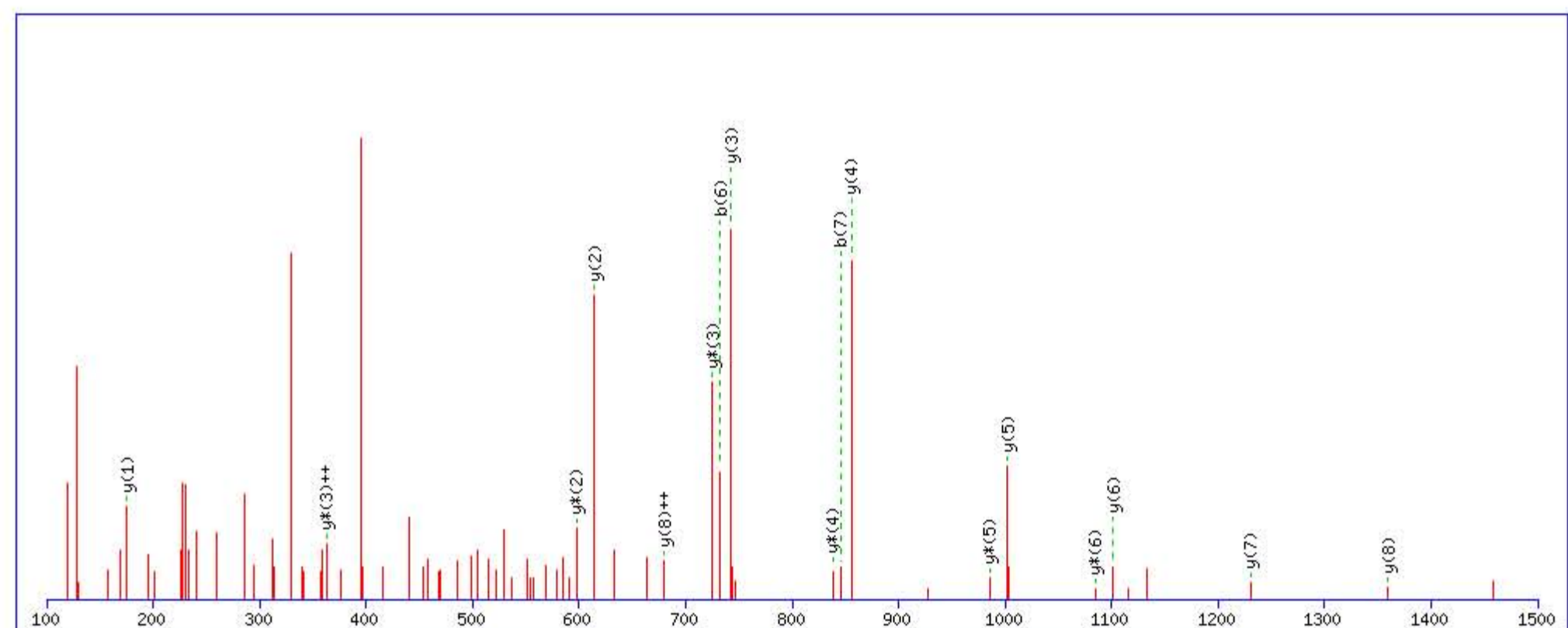
Title: Locus:1.1.1.2646.16 File:"2013-07-02 CLN FXIII 30 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf2 FXIII 30 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1585.865021

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

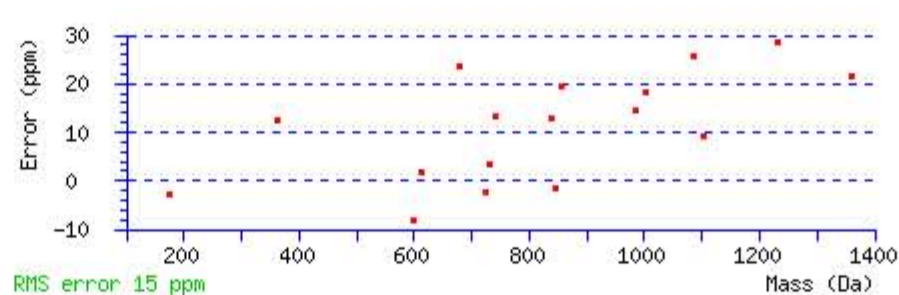
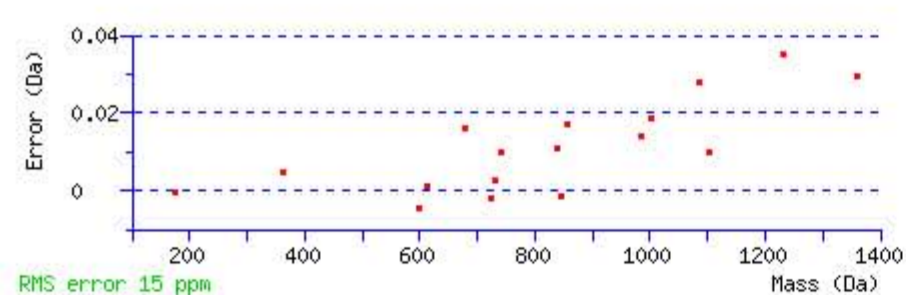
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 40 Expect: 0.00026

Matches : 17/90 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	100.075690	50.541483					V							10
2	228.170653	114.588965	211.144104	106.075690			K	1487.803897	744.405587	1470.777348	735.892312	1469.793332	735.400304	9
3	357.213246	179.110261	340.186697	170.596987	339.202681	170.104979	E	1359.708934	680.358105	1342.682385	671.844831	1341.698369	671.352823	8
4	486.255839	243.631558	469.229290	235.118283	468.245274	234.626275	E	1230.666341	615.836809	1213.639792	607.323534	1212.655776	606.831526	7
5	585.324253	293.165765	568.297704	284.652490	567.313688	284.160482	V	1101.623748	551.315512	1084.597199	542.802238			6
6	732.392667	366.699972	715.366118	358.186697	714.382102	357.694689	F	1002.555334	501.781305	985.528785	493.268031			5
7	845.476731	423.242004	828.450182	414.728729	827.466166	414.236721	I	855.486920	428.247098	838.460371	419.733824			4
8	973.535309	487.271293	956.508760	478.758018	955.524744	478.266010	Q	742.402856	371.705066	725.376307	363.191792			3
9	1412.760635	706.883956	1395.734086	698.370681	1394.750070	697.878673	Q	614.344278	307.675777	597.317729	299.162503			2
10							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **VKEEVFIQQR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.3	1585.865021	0.010081	VKEEVFIQQR
29.6	1585.865021	0.010081	VKEEVFIQQR
2.1	1585.893524	-0.018422	QDLIKSLAMLK
2.1	1585.857605	0.017497	QEEVAGIRAKFPNK

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