

Supplementary information

Title: Differential oxidation of protein-tyrosine phosphatases during zebrafish caudal fin regeneration

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Fig. S1. Sequence alignments and logos of all predicted PTP motif peptides in the zebrafish Uniprot+trEMBL database. (a) Sequence alignment of 52 predicted catalytic sites ± 20 flanking residues, representing 44 distinct PTPs, in the zebrafish Uniprot+trEMBL database (release Feb 2017). PTPs containing two catalytic sites are aligned as separate entries. Alignment generated with Boxshade 3.21, shading indicates sequence conservation $>80\%$. **(b)** Sequence logo visualized with WebLogo, overall height of stack at each position indicates sequence conservation; height of symbols within the stack indicates relative frequency of each amino acid in the position.



Fig. S2. Representative raw spectrum for each zebrafish PTP catalytic site detected.

Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
B3DJL5_site1 (C7U129)	Ptptra protein	ptpra	Receptor	QQQQSGNHPITVHcSAGAGR	C14(hyper)	76

Peptide Summary
 Sequence: QQQQSGNHPITVHCSAGAGR, C14-hyperoxidation (47.98474 Da)
 Charge: +2, Monoisotopic m/z: 1062.48486 Da (-0.58 mmu/-0.55 ppm), MH+: 2123.96245 Da, RT: 12.88 min,
 Identified with: Mascot (v1.30); IonScore:113, Exp Value:6.1E-010, Ions matched by search engine: 14/210
 Fragment match tolerance used for search: 0.05 Da

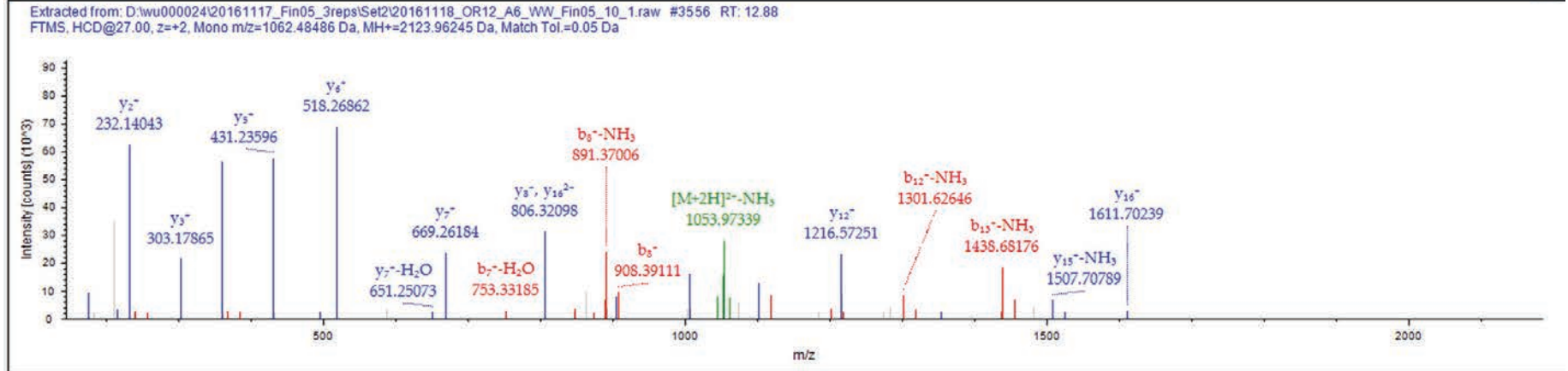
Fragment Matches

Value Type: Theo. Mass [Da]

Ion Series: Neutral Losses | Precursor Ions

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	129.06586	65.03657	Q			20
2	257.12444	129.06586	Q	1995.90504	998.45616	19
3	385.18302	193.09515	Q	1867.84646	934.42687	18
4	513.24160	257.12444	Q	1739.78788	870.39758	17
5	600.27363	300.64045	S	1611.72930	806.36829	16
6	657.29510	329.15119	G	1524.69727	762.85227	15
7	771.33803	386.17265	N	1467.67580	734.34154	14
8	908.39694	454.70211	H	1353.63287	677.32007	13
9	1005.44971	503.22849	P	1216.57396	608.79062	12
10	1118.53378	559.77053	I	1119.52119	560.26423	11
11	1219.58146	610.29437	T	1006.43712	503.72220	10
12	1318.64988	659.82858	V	905.38944	453.19836	9
13	1455.70879	728.35803	H	806.32102	403.66415	8
14	1606.70272	803.85500	C-hyper	669.26211	335.13469	7
15	1693.73475	847.37101	S	518.26817	259.63772	6
16	1764.77187	882.88957	A	431.23614	216.12171	5
17	1821.79334	911.40031	G	360.19902	180.60315	4
18	1892.83046	946.91887	A	303.17755	152.09241	3
19	1949.85193	975.42960	G	232.14043	116.57385	2
20			R	175.11896	88.06312	1

Fragment Spectrum



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
B3DJL5_site2 (C7U129)	Ptptra protein	ptpra	Receptor	NcNPQYAGPIV VHcSAGVGR	C14(hyper)	33

Peptide Summary
 Sequence: NcNPQYAGPIVHCSAGVGR, C2-hydroxylation (47.98474 Da), C14-hydroxylation (47.98474 Da)
 Charge: +2, Monoisotopic m/z: 1069.47363 Da (+0.47 mmu/+0.44 ppm), MH+: 2137.93999 Da, RT: 19.30 min,
 Identified with: Mascot (v1.30); IonScore:108, Exp Value:1.3E-009, Ions matched by search engine: 11/190
 Fragment match tolerance used for search: 0.05 Da

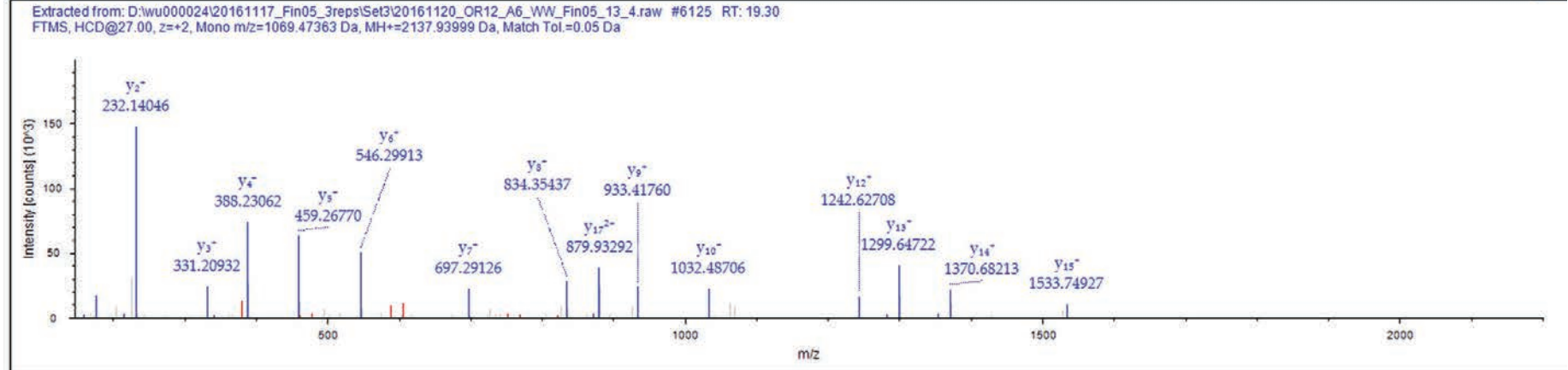
Fragment Matches

Value Type: Theo. Mass [Da]

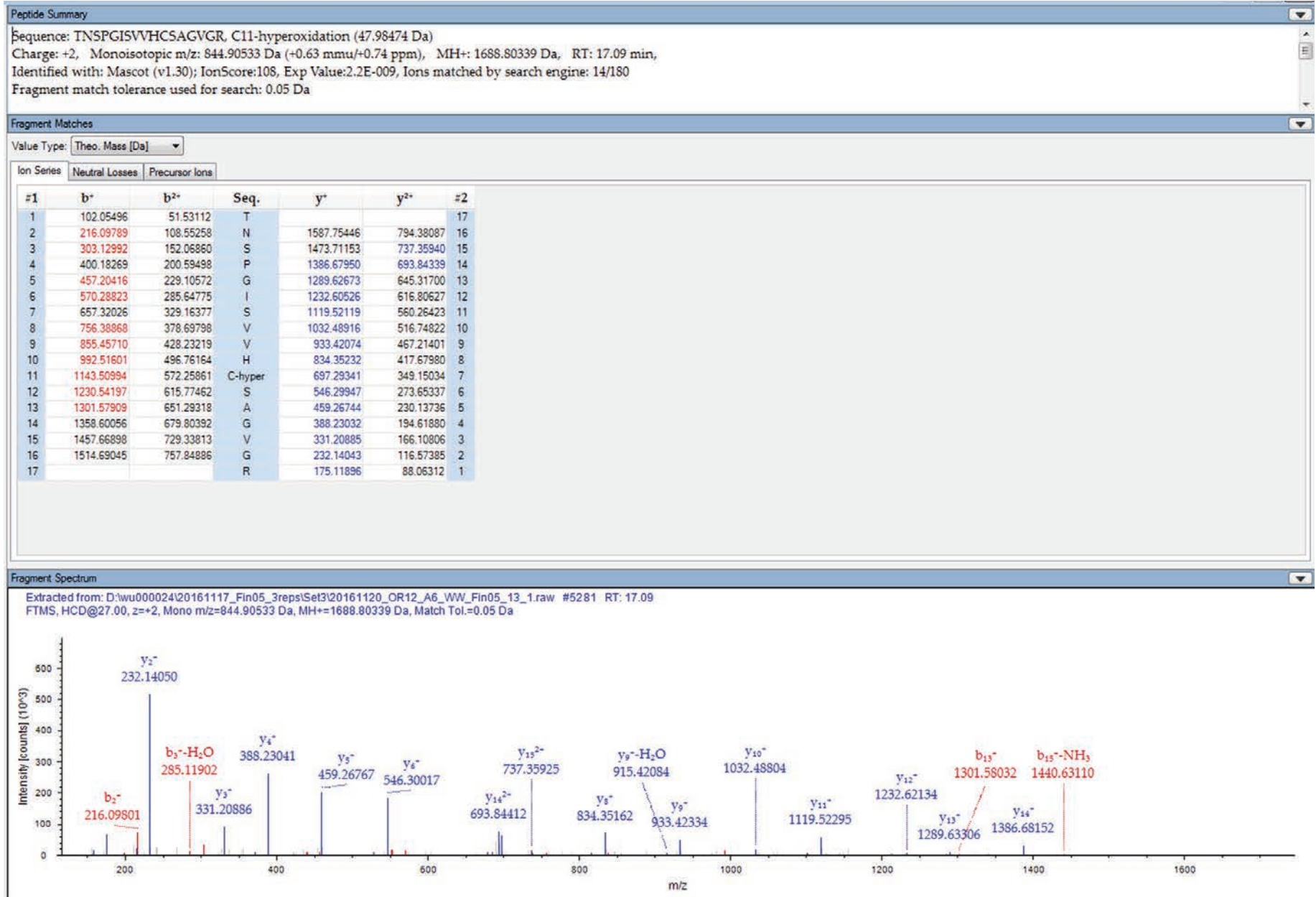
Ion Series: Neutral Losses | Precursor Ions

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	115.05021	58.02874	N			20
2	266.04414	133.52571	C-hyper	2023.89612	1012.45170	19
3	380.08707	190.54717	N	1872.90219	936.95473	18
4	477.13984	239.07356	P	1758.85926	879.93327	17
5	605.19842	303.10285	Q	1661.80649	831.40688	16
6	768.26174	384.63451	Y	1533.74791	767.37759	15
7	839.29886	420.15307	A	1370.68459	685.84593	14
8	896.32033	448.66380	G	1299.64747	650.32737	13
9	993.37310	497.19019	P	1242.62600	621.81664	12
10	1106.45717	553.73222	I	1145.57323	573.29025	11
11	1205.52559	603.26643	V	1032.48916	516.74822	10
12	1304.59401	652.80064	V	933.42074	467.21401	9
13	1441.65292	721.33010	H	834.35232	417.67980	8
14	1592.64685	796.82707	C-hyper	697.29341	349.15034	7
15	1679.67888	840.34308	S	546.29947	273.65337	6
16	1750.71600	875.86164	A	459.26744	230.13736	5
17	1807.73747	904.37238	G	388.23032	194.61880	4
18	1906.80589	953.90659	V	331.20885	166.10806	3
19	1963.82736	982.41732	G	232.14043	116.57385	2
20			R	175.11896	88.06312	1

Fragment Spectrum



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
AOA0R4ITJ9 (C7U135)	Uncharacterized protein	ptprb	Receptor	TNSPGISV VHcSAGVGR	C11(hyper)	51



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
C7U126	CD45 antigen (Fragment)	ptprc	Receptor	NFFSGPIV VHcSAGVGR	C11(hyper)	93

Peptide Summary

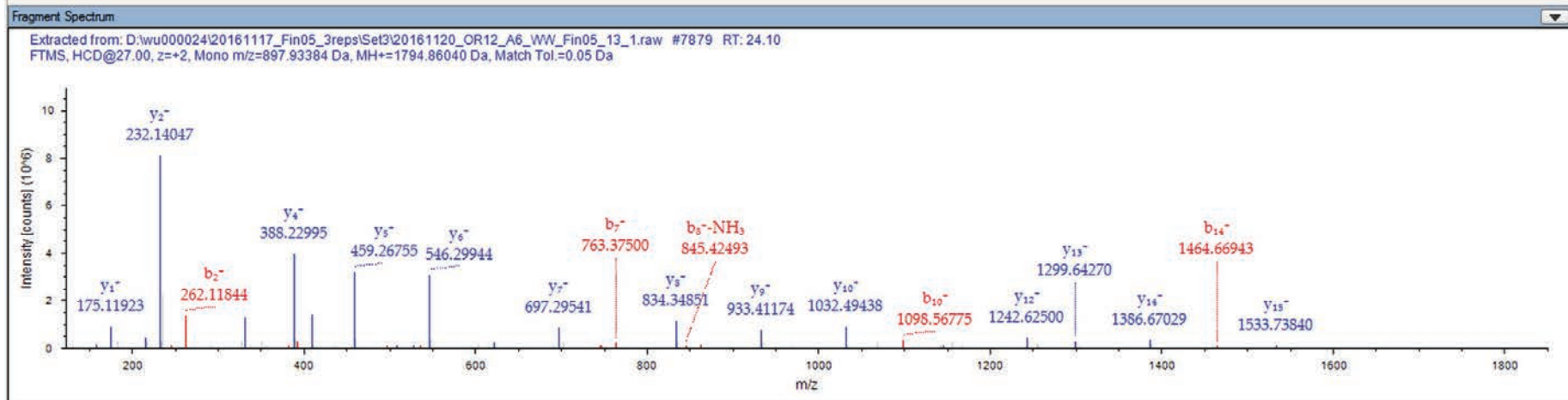
Sequence: NFFSGPIV**VHcSAGVGR**, C11-hyperoxidation (47.98474 Da)
 Charge: +2, Monoisotopic m/z: 897.93384 Da (+0.57 mmu/+0.63 ppm), MH+: 1794.86040 Da, RT: 24.10 min,
 Identified with: Mascot (v1.30); IonScore:129, Exp Value:1.8E-011, Ions matched by search engine: 15/176
 Fragment match tolerance used for search: 0.05 Da

Fragment Matches

Value Type: Theo. Mass [Da]

Ion Series: Neutral Losses | Precursor Ions

#1	b ⁺	b ²⁺	Seq.	y ⁻	y ²⁺	#2
1	115.05021	58.02874	N			17
2	262.11863	131.56295	F	1680.81634	840.91181	16
3	409.18705	205.09716	F	1533.74792	767.37760	15
4	496.21908	248.61318	S	1386.67950	693.84339	14
5	553.24055	277.12391	G	1299.64747	650.32737	13
6	650.29332	325.65030	P	1242.62600	621.81664	12
7	763.37739	382.19233	I	1145.57323	573.29025	11
8	862.44581	431.72654	V	1032.48916	516.74822	10
9	961.51423	481.26075	V	933.42074	467.21401	9
10	1098.57314	549.79021	H	834.35232	417.67980	8
11	1249.56707	625.28717	C-hyper	697.29341	349.15034	7
12	1336.59910	668.80319	S	546.29947	273.65337	6
13	1407.63622	704.32175	A	459.26744	230.13736	5
14	1464.65769	732.83248	G	388.23032	194.61880	4
15	1563.72611	782.36669	V	331.20885	166.10806	3
16	1620.74758	810.87743	G	232.14043	116.57385	2
17			R	175.11896	88.06312	1



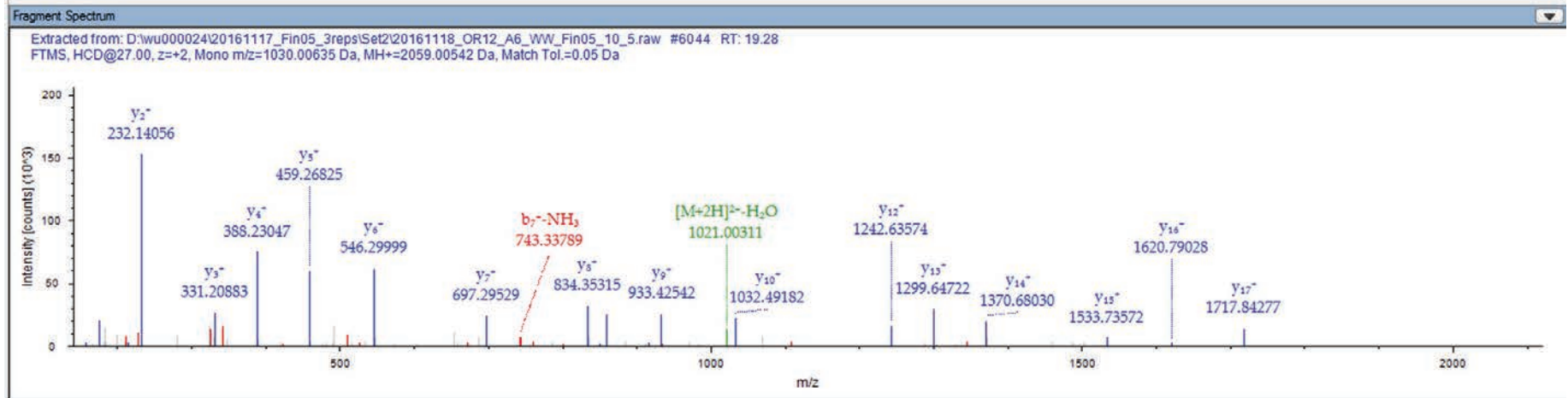
Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
E7EZG7_site1	Receptor-type tyrosine-protein phosphatase	ptprea	Receptor	QVNPSYAGPIV VHcSAGVGR	C14(hyper)	35

Peptide Summary
 Sequence: QVNPSYAGPIVVHCSAGVGR, C14-hydroxylation (47.98474 Da)
 Charge: +2, Monoisotopic m/z: 1030.00635 Da (+1.39 mmu/+1.35 ppm), MH+: 2059.00542 Da, RT: 19.28 min,
 Identified with: Mascot (v1.30); IonScore:143, Exp Value:7.5E-013, Ions matched by search engine: 14/210
 Fragment match tolerance used for search: 0.05 Da

Fragment Matches
 Value Type: Theo. Mass [Da]

Ion Series: Neutral Losses | Precursor Ions

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	129.06586	65.03657	Q			20
2	228.13428	114.57078	V	1930.94406	965.97567	19
3	342.17721	171.59224	N	1831.87564	916.44146	18
4	439.22998	220.11863	P	1717.83271	859.41999	17
5	526.26201	263.63464	S	1620.77994	810.89361	16
6	689.32533	345.16630	Y	1533.74791	767.37759	15
7	760.36245	380.68486	A	1370.68459	685.84593	14
8	817.38392	409.19560	G	1299.64747	650.32737	13
9	914.43669	457.72198	P	1242.62600	621.81664	12
10	1027.52076	514.26402	I	1145.57323	573.29025	11
11	1126.58918	563.79823	V	1032.48916	516.74822	10
12	1225.65760	613.33244	V	933.42074	467.21401	9
13	1362.71651	681.86189	H	834.35232	417.67980	8
14	1513.71044	757.35886	C-hyper	697.29341	349.15034	7
15	1600.74247	800.87487	S	546.29947	273.65337	6
16	1671.77959	836.39343	A	459.26744	230.13736	5
17	1728.80106	864.90417	G	388.23032	194.61880	4
18	1827.86948	914.43838	V	331.20885	166.10806	3
19	1884.89095	942.94911	G	232.14043	116.57385	2
20			R	175.11896	88.06312	1



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
E7EZG7_site2	Receptor-type tyrosine-protein phosphatase	ptprea	Receptor	QQQQSGNHPIIVHcSAGAGR	C14(hyper)	119

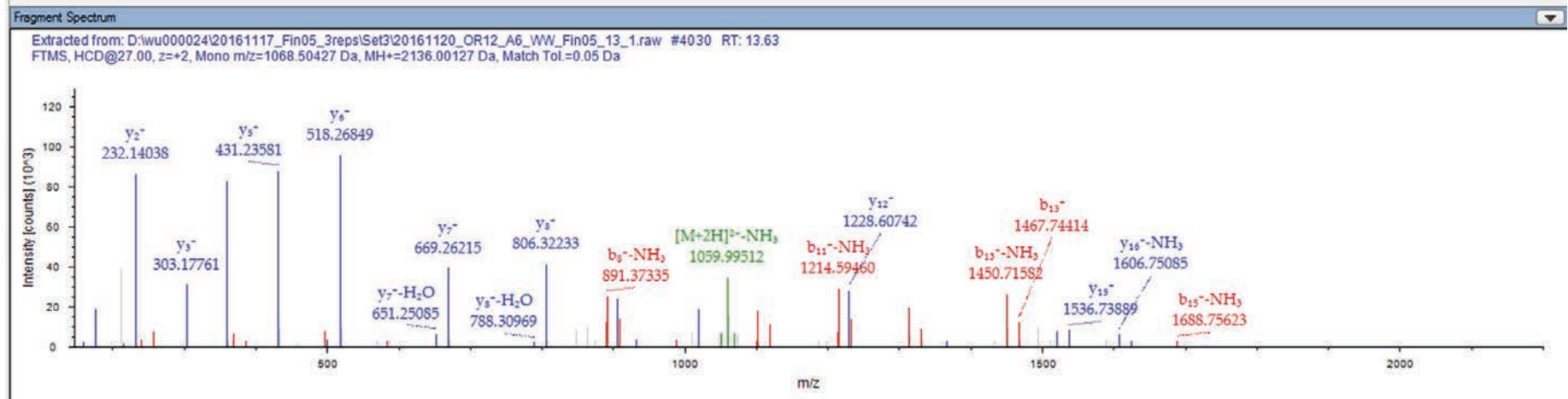
Peptide Summary

Sequence: QQQQSGNHPIIVHcSAGAGR, C14-hyperoxidation (47.98474 Da)
 Charge: +2, Monoisotopic m/z: 1068.50427 Da (+0.63 mmu/+0.59 ppm), MH+: 2136.00127 Da, RT: 13.63 min,
 Identified with: Mascot (v1.30); IonScore:103, Exp Value:7.1E-009, Ions matched by search engine: 13/210
 Fragment match tolerance used for search: 0.05 Da

Fragment Matches

Value Type: [Theo. Mass [Da]]

Ion Series	Neutral Losses	Precursor Ions				
#1	b*	b**	Seq.	y*	y**	#2
1	129.06586	65.03657	Q			20
2	257.12444	129.06586	Q	2007.94143	1004.47435	19
3	385.18302	193.09515	Q	1879.88285	940.44506	18
4	513.24160	257.12444	Q	1751.82427	876.41577	17
5	600.27363	300.64045	S	1623.76569	812.38648	16
6	657.29510	329.15119	G	1536.73366	768.87047	15
7	771.33803	386.17265	N	1479.71219	740.35973	14
8	908.39694	454.70211	H	1365.66926	683.33827	13
9	1005.44971	503.22849	P	1228.61035	614.80881	12
10	1118.53378	559.77053	I	1131.55758	566.28243	11
11	1231.61785	616.31256	I	1018.47351	509.74039	10
12	1330.69627	665.84677	V	905.38944	453.19836	9
13	1467.74518	734.37623	H	806.32102	403.66415	8
14	1618.73911	809.87319	C-hyper	669.26211	335.13469	7
15	1705.77114	853.38921	S	518.26817	259.63772	6
16	1776.80826	888.90777	A	431.23614	216.12171	5
17	1833.82973	917.41850	G	360.19902	180.60315	4
18	1904.86685	952.93706	A	303.17755	152.09241	3
19	1961.88832	981.44780	G	232.14043	116.57385	2
20			R	175.11896	88.06312	1



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
Q90YJ5_site1	Receptor protein-tyrosine phosphatase LAR (Fragment)	ptprfa	Receptor	AcNPPDAGPMV VHcSAGVGR	C14(hyper)	100

Peptide Summary

Sequence: ACNPPDAGPMV**VHcSAGVGR**, C2-hyperoxidation (47.98474 Da), C14-hyperoxidation (47.98474 Da)
 Charge: +2, Monoisotopic m/z: 1017.42896 Da (+1.57 mmu/+1.55 ppm), MH+: 2033.85063 Da, RT: 17.82 min,
 Identified with: Mascot (v1.30); IonScore:88, Exp Value:9.7E-008, Ions matched by search engine: 14/204
 Fragment match tolerance used for search: 0.05 Da

Fragment Matches

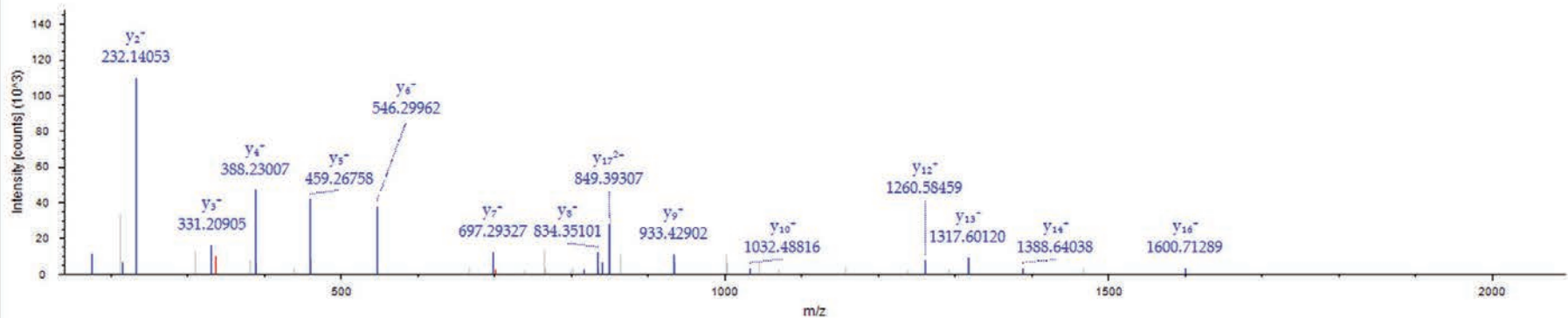
Value Type: Theo. Mass [Da]

Ion Series: Neutral Losses Precursor Ions

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	72.04440	36.52584	A			20
2	223.03833	112.02280	C-hyper	1962.81037	981.90882	19
3	337.08126	169.04427	N	1811.81644	906.41186	18
4	434.13403	217.57065	P	1697.77351	849.39039	17
5	531.18680	266.09704	P	1600.72074	800.86401	16
6	646.21375	323.61051	D	1503.66797	752.33762	15
7	717.25087	359.12907	A	1388.64102	694.82415	14
8	774.27234	387.63981	G	1317.60390	659.30559	13
9	871.32511	436.16619	P	1260.58243	630.79485	12
10	1002.36561	501.68644	M	1163.52966	582.26847	11
11	1101.43403	551.22065	V	1032.48916	516.74822	10
12	1200.50245	600.75486	V	933.42074	467.21401	9
13	1337.56136	669.28432	H	834.35232	417.67980	8
14	1488.55529	744.78129	C-hyper	697.29341	349.15034	7
15	1575.58732	788.29730	S	546.29947	273.65337	6
16	1646.62444	823.81586	A	459.26744	230.13736	5
17	1703.64591	852.32660	G	388.23032	194.61880	4
18	1802.71433	901.86081	V	331.20885	166.10806	3
19	1859.73580	930.37154	G	232.14043	116.57385	2
20			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: D:\wu000024\20161117_Fin05_3reps\Set2\20161118_OR12_A6_WW_Fin05_10_1.raw #5339 RT: 17.82
 FTMS, HCD@27.00, z=+2, Mono m/z=1017.42896 Da, MH+=2033.85063 Da, Match Tol.=0.05 Da



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
Q90YJ5_site2	Receptor protein-tyrosine phosphatase LAR (Fragment)	ptprfa	Receptor	EQFGQDGPITVHcSAGVGR	C13(hyper)	72

Peptide Summary

Sequence: EQFGQDGPITVHCSAGVGR, C13-hyperoxidation (47.98474 Da)
 Charge: +2, Monoisotopic m/z: 1003.45660 Da (+1.3 mmu/+1.3 ppm), MH+: 2005.90593 Da, RT: 18.24 min,
 Identified with: Mascot (v1.30); IonScore:124, Exp Value:4.3E-011, Ions matched by search engine: 15/204
 Fragment match tolerance used for search: 0.05 Da

Fragment Matches

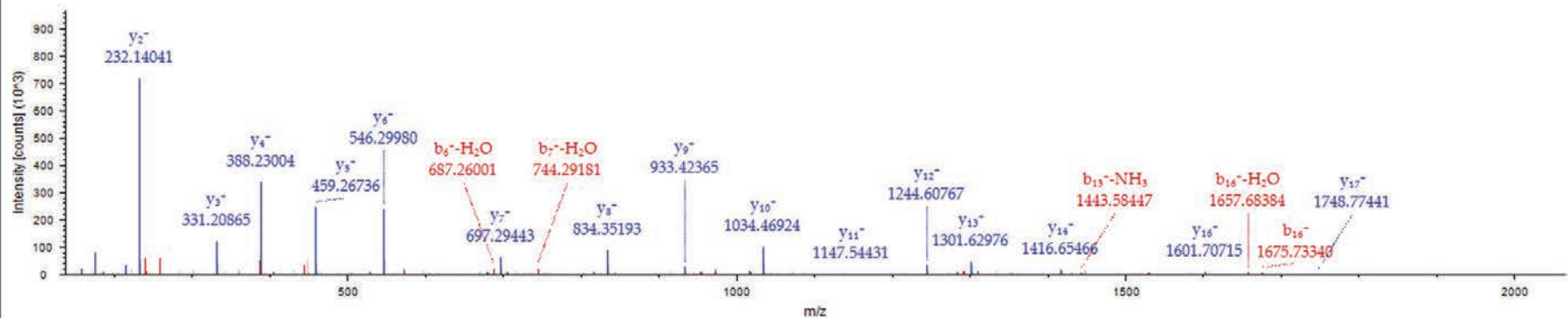
Value Type: Theo. Mass [Da]

Ion Series: Neutral Losses, Precursor Ions

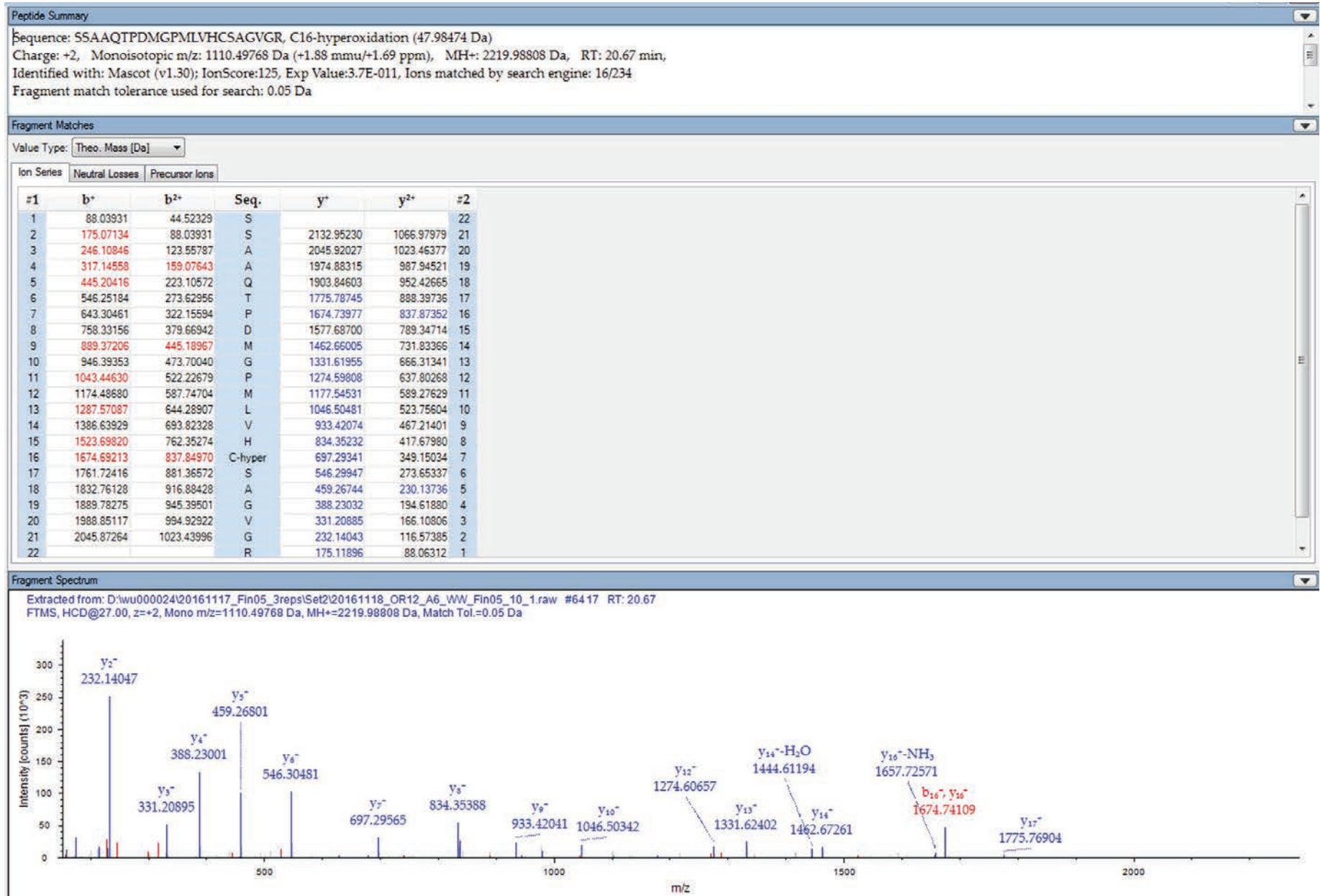
#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	130.04988	65.52858	E			19
2	258.10846	129.55787	Q	1876.86073	938.93400	18
3	405.17688	203.09208	F	1748.80215	874.90471	17
4	462.19835	231.60281	G	1601.73373	801.37050	16
5	590.25693	295.63210	Q	1544.71226	772.85977	15
6	705.28388	353.14558	D	1416.65368	708.83048	14
7	762.30535	381.65631	G	1301.62673	651.31700	13
8	859.35812	430.18270	P	1244.60526	622.80627	12
9	972.44219	486.72473	I	1147.55249	574.27988	11
10	1073.48987	537.24857	T	1034.46842	517.73785	10
11	1172.55829	586.78278	V	933.42074	467.21401	9
12	1309.61720	655.31224	H	834.35232	417.67980	8
13	1460.61113	730.80920	C-hyper	697.29341	349.15034	7
14	1547.64316	774.32522	S	546.29947	273.65337	6
15	1618.68028	809.84378	A	459.26744	230.13736	5
16	1675.70175	838.35451	G	388.23032	194.61880	4
17	1774.77017	887.88872	V	331.20885	166.10806	3
18	1831.79164	916.39946	G	232.14043	116.57385	2
19			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: D:\wu000024\20161117_Fin05_3reps\Set2\20161118_OR12_A6_WW_Fin05_7_1.raw #5734 RT: 18.24
 FTMS, HCD@27.00, z=+2, Mono m/z=1003.45660 Da, MH+=2005.90593 Da, Match Tol.=0.05 Da



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
F1Q4V8	Uncharacterized protein (Fragment)	ptprga	Receptor	SSAAQTPDMGPMLVHCSAGVGR	C16(hyper)	42



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
E7F9R2	Uncharacterized protein	ptprh	Receptor	QHIESHFSTGPTVVHcSAGVGR	C16(hyper)	159

Peptide Summary

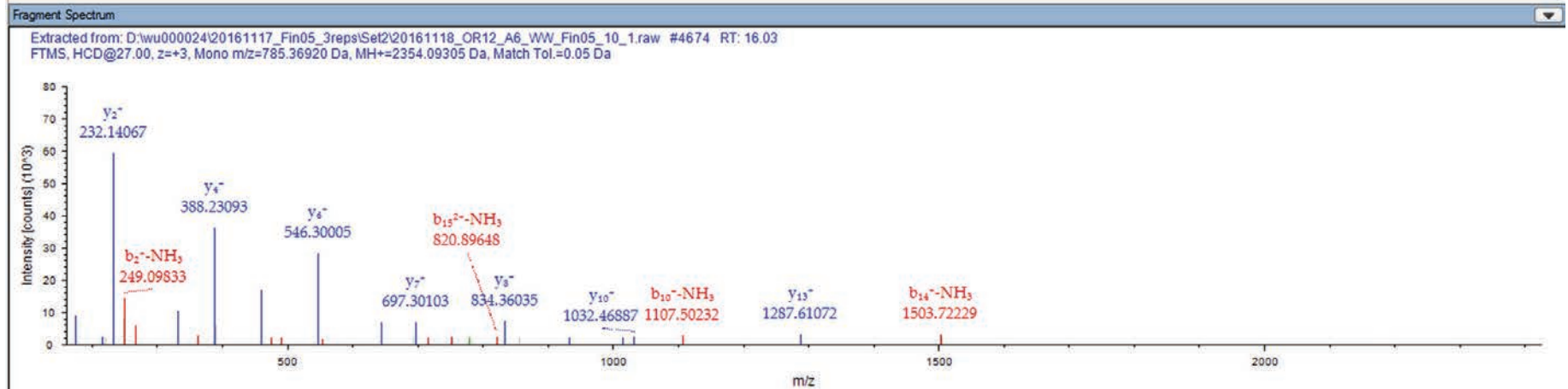
Sequence: QHIESHFSTGPTVVHCSAGVGR, C16-hyperoxidation (47.98474 Da)
 Charge: +3, Monoisotopic m/z: 785.36920 Da (-0.42 mmu/-0.53 ppm), MH+: 2354.09305 Da, RT: 16.03 min,
 Identified with: Mascot (v1.30); IonScore:76, Exp Value:3.4E-006, Ions matched by search engine: 11/236
 Fragment match tolerance used for search: 0.05 Da

Fragment Matches

Value Type: Theo. Mass [Da]

Ion Series: Neutral Losses | Precursor Ions

#1	b ⁺	b ²⁺	b ³⁺	Seq.	y ⁺	y ²⁺	y ³⁺	#2
1	129.06586	65.03657	43.69347	Q				22
2	266.12477	133.56602	89.37977	H	2226.03573	1113.52150	742.68343	21
3	379.20884	190.10806	127.07446	I	2088.97682	1044.99205	696.99712	20
4	508.25144	254.62936	170.08866	E	1975.89275	988.45001	659.30243	19
5	595.28347	298.14537	199.09934	S	1846.85015	923.92871	616.28823	18
6	732.34238	366.67483	244.78564	H	1759.81812	880.41270	587.27756	17
7	879.41080	440.20904	293.80845	F	1622.75921	811.88324	541.59125	16
8	966.44283	483.72505	322.81913	S	1475.69079	738.34903	492.56845	15
9	1067.49051	534.24889	356.50169	T	1388.65876	694.83302	463.55777	14
10	1124.51198	562.75963	375.50884	G	1287.61108	644.30918	429.87521	13
11	1221.56475	611.28601	407.85977	P	1230.58961	615.79844	410.86805	12
12	1322.61243	661.80985	441.54233	T	1133.53684	567.27206	378.51713	11
13	1421.68085	711.34406	474.56513	V	1032.48916	516.74822	344.83457	10
14	1520.74927	760.87827	507.58794	V	933.42074	467.21401	311.81176	9
15	1657.80818	829.40773	553.27424	H	834.35232	417.67980	278.78896	8
16	1808.80211	904.90469	603.60555	C-hyper	697.29341	349.15034	233.10265	7
17	1895.83414	948.42071	632.61623	S	546.29947	273.65337	182.77134	6
18	1966.87126	983.93927	656.29527	A	459.26744	230.13736	153.76066	5
19	2023.89273	1012.45000	675.30243	G	388.23032	194.61880	130.08162	4
20	2122.96115	1061.98421	708.32523	V	331.20885	166.10806	111.07447	3
21	2179.98262	1090.49495	727.33239	G	232.14043	116.57385	78.05166	2
22				R	175.11896	88.06312	59.04450	1



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
B6HY54	Protein-tyrosine phosphatase	ptprja	Receptor	HSPTLVHcSAGVGR	C8(hyper)	52

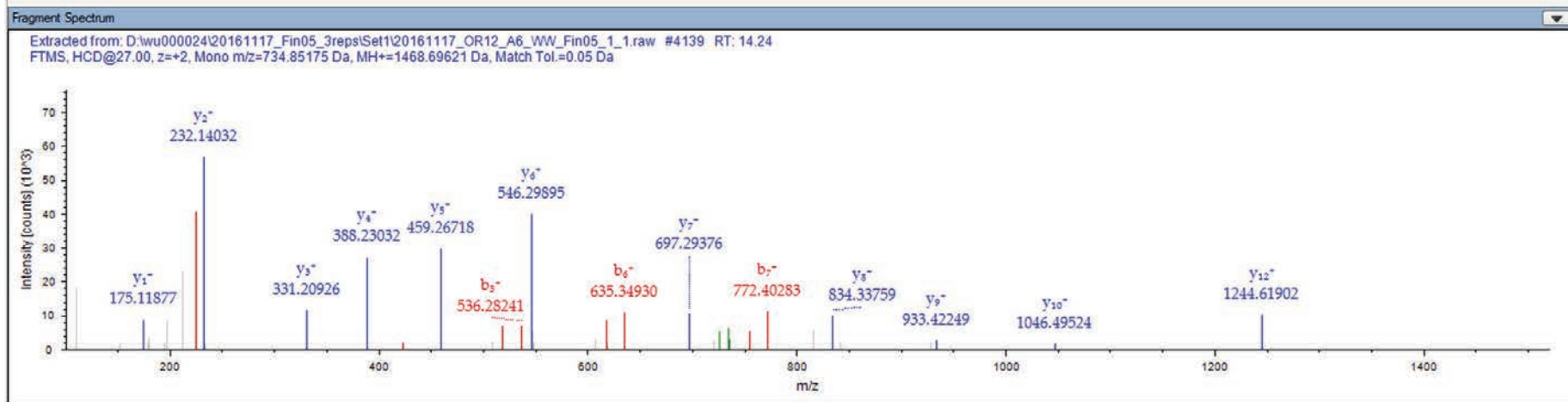
Peptide Summary
 Sequence: HSPTLVHCSAGVGR, C8-hyperoxidation (47.98474 Da)
 Charge: +2, Monoisotopic m/z: 734.85175 Da (+0.01 mmu/+0.01 ppm), MH+: 1468.69621 Da, RT: 14.24 min,
 Identified with: Mascot (v1.30); IonScore:109, Exp Value:1.6E-009, Ions matched by search engine: 11/118
 Fragment match tolerance used for search: 0.05 Da

Fragment Matches

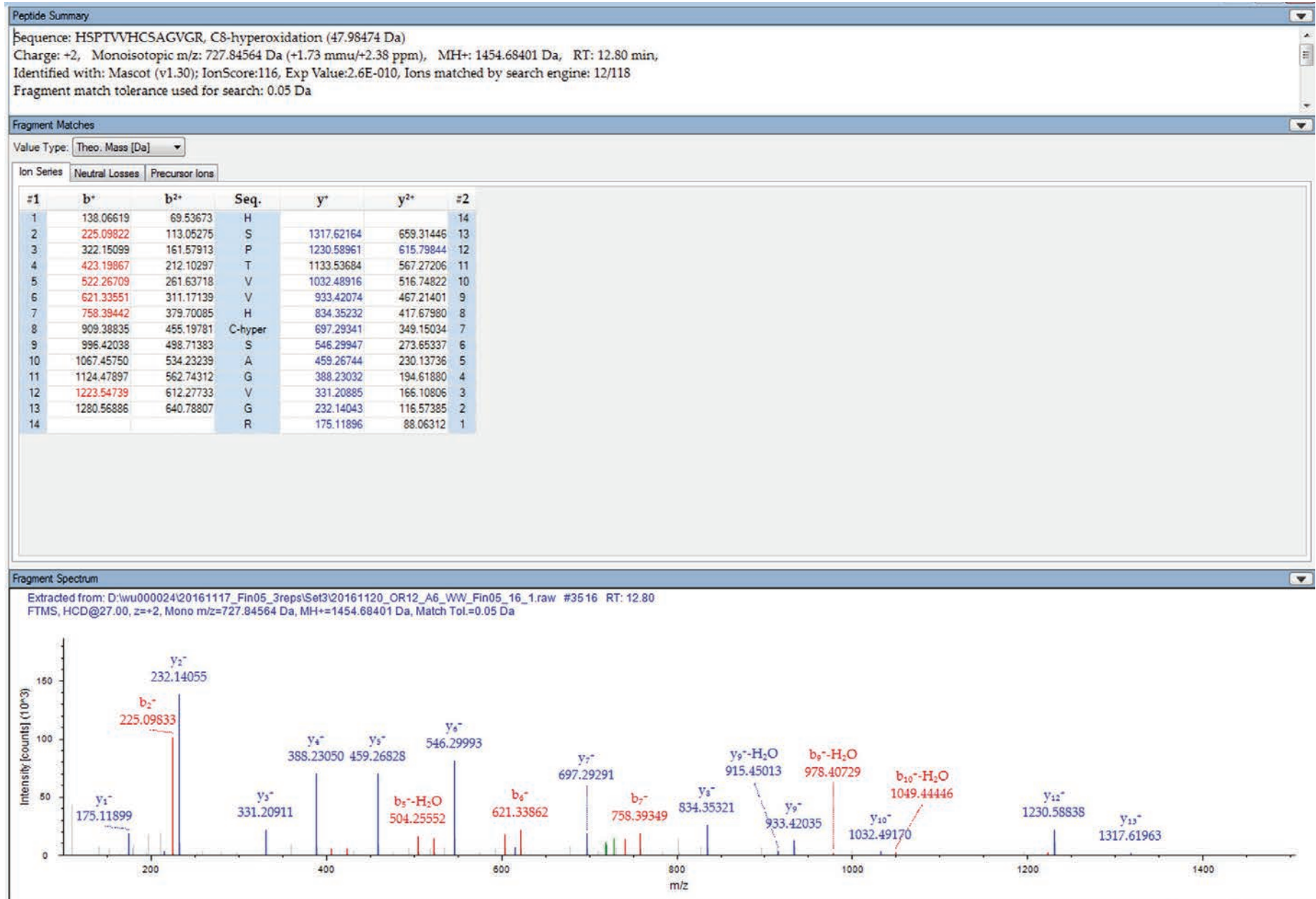
Value Type: Theo. Mass [Da]

Ion Series: Neutral Losses | Precursor Ions

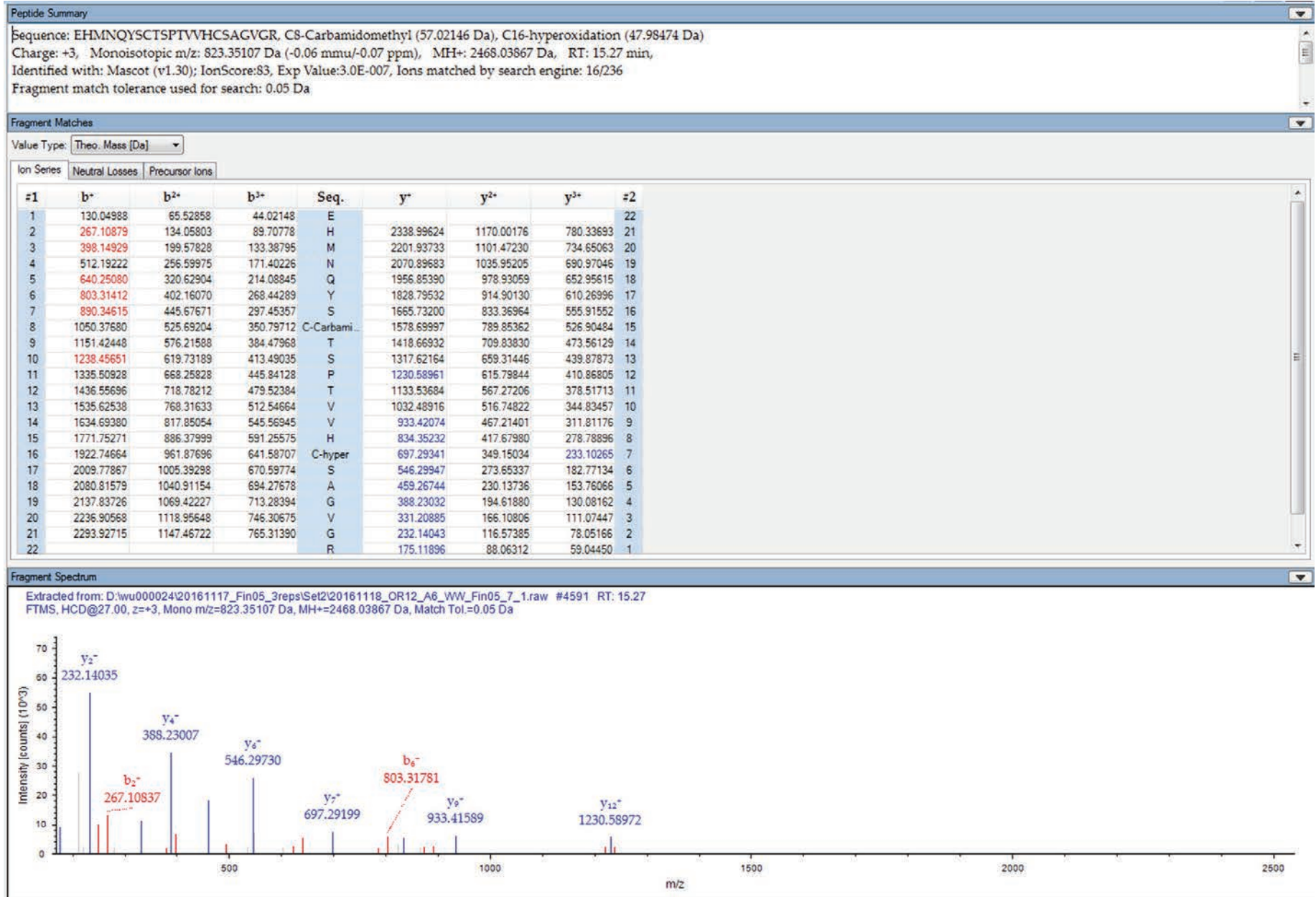
#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	138.06619	69.53673	H			14
2	225.09822	113.05275	S	1331.63729	666.32228	13
3	322.15099	161.57913	P	1244.60526	622.80627	12
4	423.19867	212.10297	T	1147.55249	574.27988	11
5	536.28274	268.64501	L	1046.50481	523.75604	10
6	635.35116	318.17922	V	933.42074	467.21401	9
7	772.41007	386.70867	H	834.35232	417.67980	8
8	923.40400	462.20564	C-hyper	697.29341	349.15034	7
9	1010.43603	505.72165	S	546.29947	273.65337	6
10	1081.47315	541.24021	A	459.26744	230.13736	5
11	1138.49462	569.75095	G	388.23032	194.61880	4
12	1237.56304	619.28516	V	331.20885	166.10806	3
13	1294.58451	647.79589	G	232.14043	116.57385	2
14			R	175.11896	88.06312	1



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
X1WCM2	Uncharacterized protein (Fragment)	ptrjrb.1	Receptor	HSPTV VHcSAGVGR	C8(hyper)	21



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
X1WF45	Uncharacterized protein (Fragment)	ptprjb.2	Receptor	EHMNQYScTSPTV VHcSAGVGR	C16(hyper)	6



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
X1WD65	Uncharacterized protein	ptprk	Receptor	MSNPPTAGPIV VHcSAGAGR	C14(hyper)	90

Peptide Summary

Sequence: MSNPPTAGPIVVHCSAGAGR, C14-hyperoxidation (47.98474 Da)
 Charge: +2, Monoisotopic m/z: 985.46545 Da (+0.83 mmu/+0.85 ppm), MH+: 1969.92363 Da, RT: 17.46 min,
 Identified with: Mascot (v1.30); IonScore:124, Exp Value:5.1E-011, Ions matched by search engine: 16/212
 Fragment match tolerance used for search: 0.05 Da

Fragment Matches

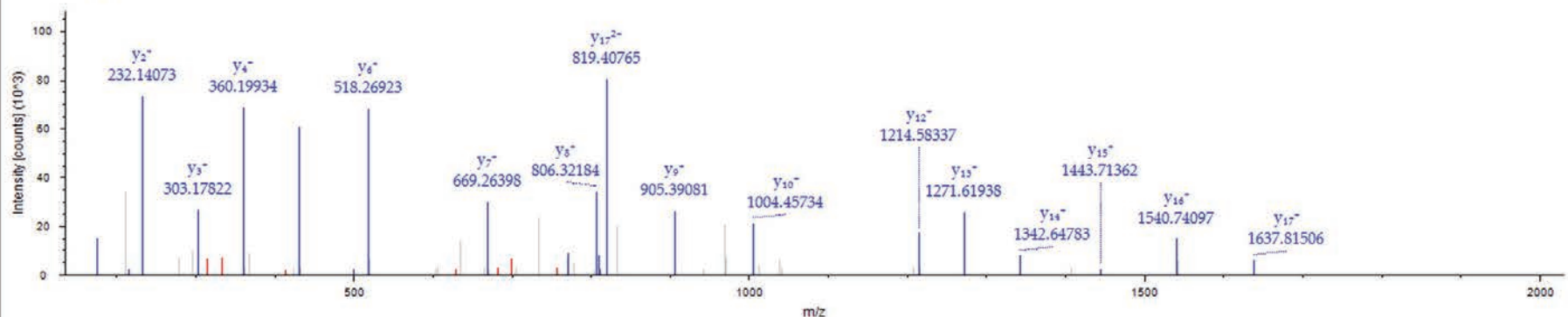
Value Type: Theo. Mass [Da]

Ion Series: Neutral Losses Precursor Ions

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	132.04778	66.52753	M			20
2	219.07981	110.04354	S	1838.88147	919.94437	19
3	333.12274	167.06501	N	1751.84944	876.42836	18
4	430.17551	215.59139	P	1637.80651	819.40689	17
5	527.22828	264.11778	P	1540.75374	770.88051	16
6	628.27596	314.64162	T	1443.70097	722.35412	15
7	699.31308	350.16018	A	1342.65329	671.83028	14
8	756.33455	378.67091	G	1271.61617	636.31172	13
9	853.38732	427.19730	P	1214.59470	607.80099	12
10	966.47139	483.73933	I	1117.54193	559.27460	11
11	1065.53981	533.27354	V	1004.45786	502.73257	10
12	1164.60823	582.80775	V	905.38944	453.19836	9
13	1301.66714	651.33721	H	806.32102	403.66415	8
14	1452.66107	726.83417	C-hyper	669.26211	335.13469	7
15	1539.69310	770.35019	S	518.26817	259.63772	6
16	1610.73022	805.86875	A	431.23614	216.12171	5
17	1667.75169	834.37948	G	360.19902	180.60315	4
18	1738.78881	869.89804	A	303.17755	152.09241	3
19	1795.81028	898.40878	G	232.14043	116.57385	2
20			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: D:\wu000024\20161117_Fin05_3reps\Set1\20161117_OR12_A6_WW_Fin05_1_5_raw #5230 RT: 17.46
 FTMS, HCD@27.00, z=+2, Mono m/z=985.46545 Da, MH+=1969.92363 Da, Match Tol.=0.05 Da



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
A0A0R4IA95	Uncharacterized protein (Fragment)	ptpro	Receptor	GPIV VHCSAGVGR	C7(hyper)	52

Peptide Summary
 Sequence: GPIVVHCSAGVGR, C7-hydroxylation (47.98474 Da)
 Charge: +2, Monoisotopic m/z: 650.32776 Da (+0.39 mmu/+0.6 ppm), MH+: 1299.64824 Da, RT: 15.37 min.
 Identified with: Mascot (v1.30); IonScore:116, Exp Value:3.1E-010, Ions matched by search engine: 11/96
 Fragment match tolerance used for search: 0.05 Da

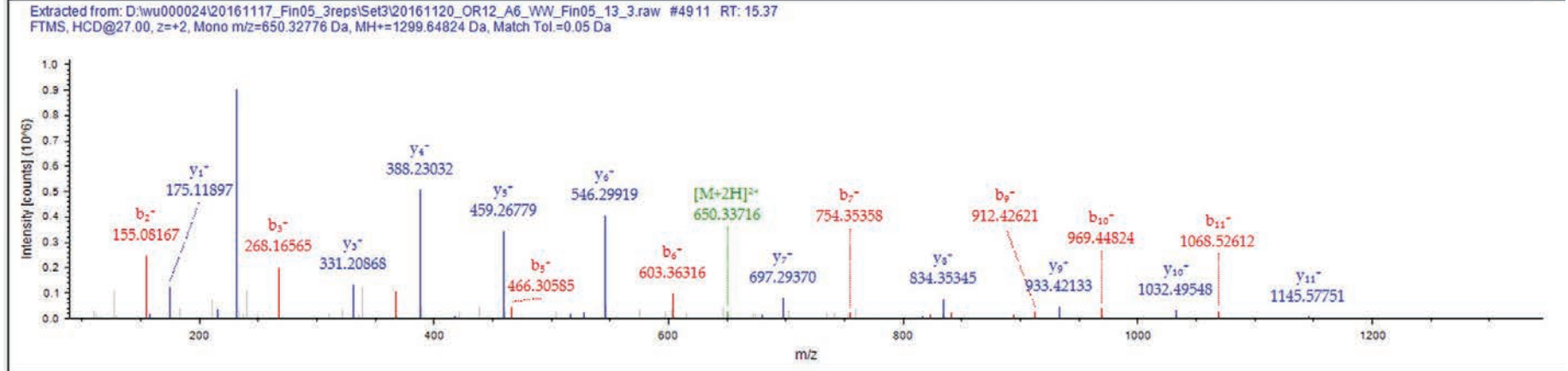
Fragment Matches

Value Type: Theo. Mass [Da]

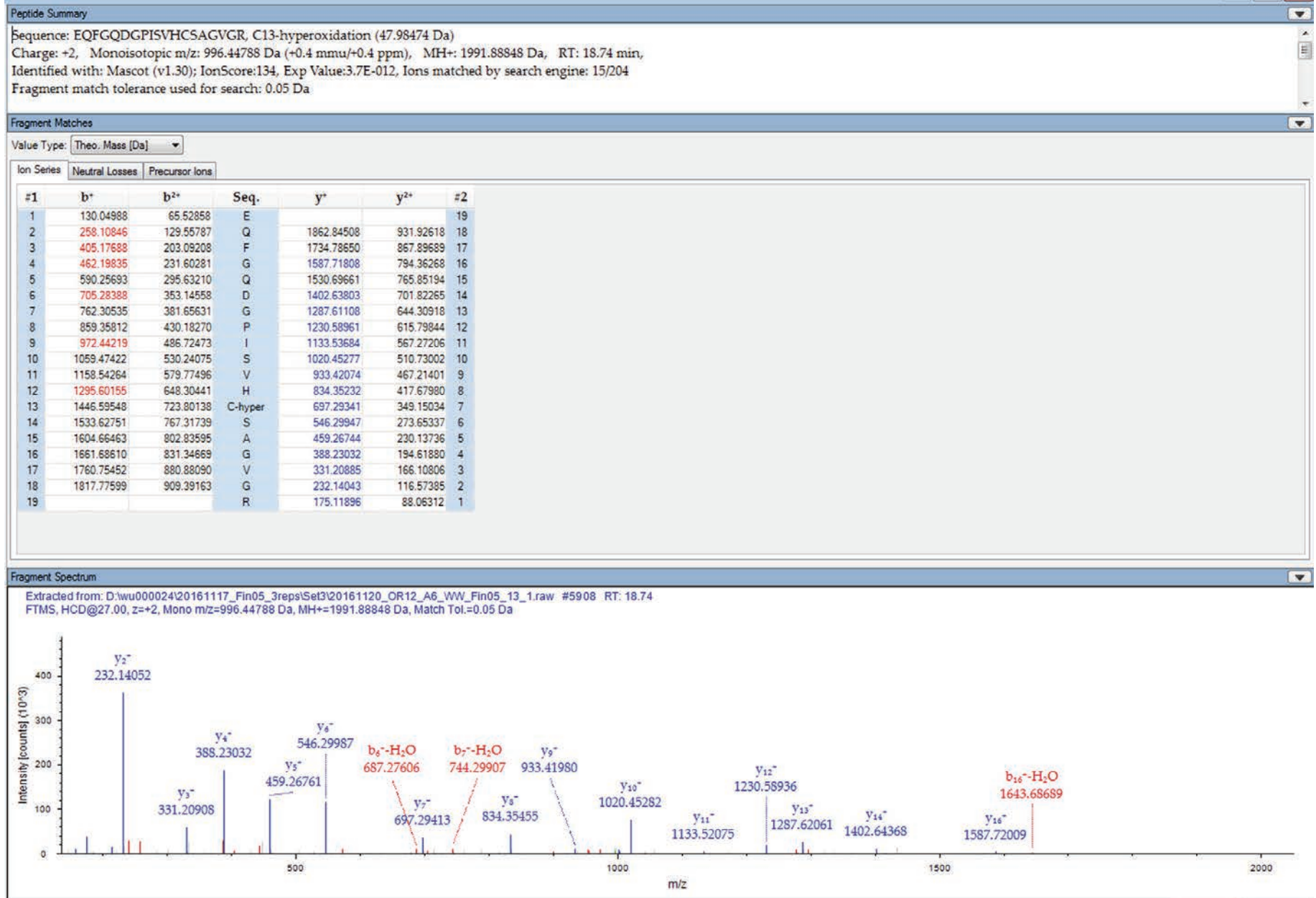
Ion Series: Neutral Losses | Precursor Ions

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	58.02875	29.51801	G			13
2	155.08152	78.04440	P	1242.62600	621.81664	12
3	268.16559	134.58643	I	1145.57323	573.29025	11
4	367.23401	184.12064	V	1032.48916	516.74822	10
5	466.30243	233.65485	V	933.42074	467.21401	9
6	603.36134	302.18431	H	834.35232	417.67980	8
7	754.35527	377.68127	C-hyper	697.29341	349.15034	7
8	841.38730	421.19729	S	546.29947	273.65337	6
9	912.42442	456.71585	A	459.26744	230.13736	5
10	969.44589	485.22658	G	388.23032	194.61880	4
11	1068.51431	534.76079	V	331.20885	166.10806	3
12	1125.53578	563.27153	G	232.14043	116.57385	2
13			R	175.11896	88.06312	1

Fragment Spectrum



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
Q90YJ4_site1	Receptor protein-tyrosine phosphatase sigma (Fragment)	ptprsa	Receptor	EQFGQDGPIS VHcSAGVGR	C13(hyper)	21



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
Q90YJ4_site2	Receptor protein-tyrosine phosphatase sigma (Fragment)	ptprsa	Receptor	TcNPPDAGPIIAHcSAGVGR	C14(hyper)	45

Peptide Summary
 Sequence: TCNPPDAGPIIAHcSAGVGR, C2-Carbamidomethyl (57.02146 Da), C14-hyperoxidation (47.98474 Da)
 Charge: +2, Monoisotopic m/z: 1020.96613 Da (+1.14 mmu/+1.12 ppm), MH+: 2040.92497 Da, RT: 17.33 min,
 Identified with: Mascot (v1.30); IonScore:123, Exp Value:6.1E-011, Ions matched by search engine: 15/214
 Fragment match tolerance used for search: 0.05 Da

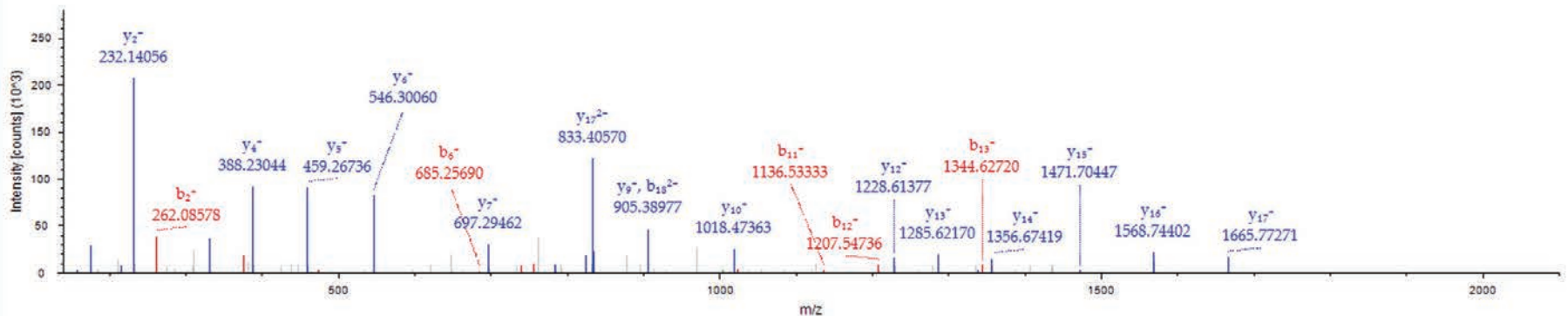
Fragment Matches

Value Type: Theo. Mass [Da]

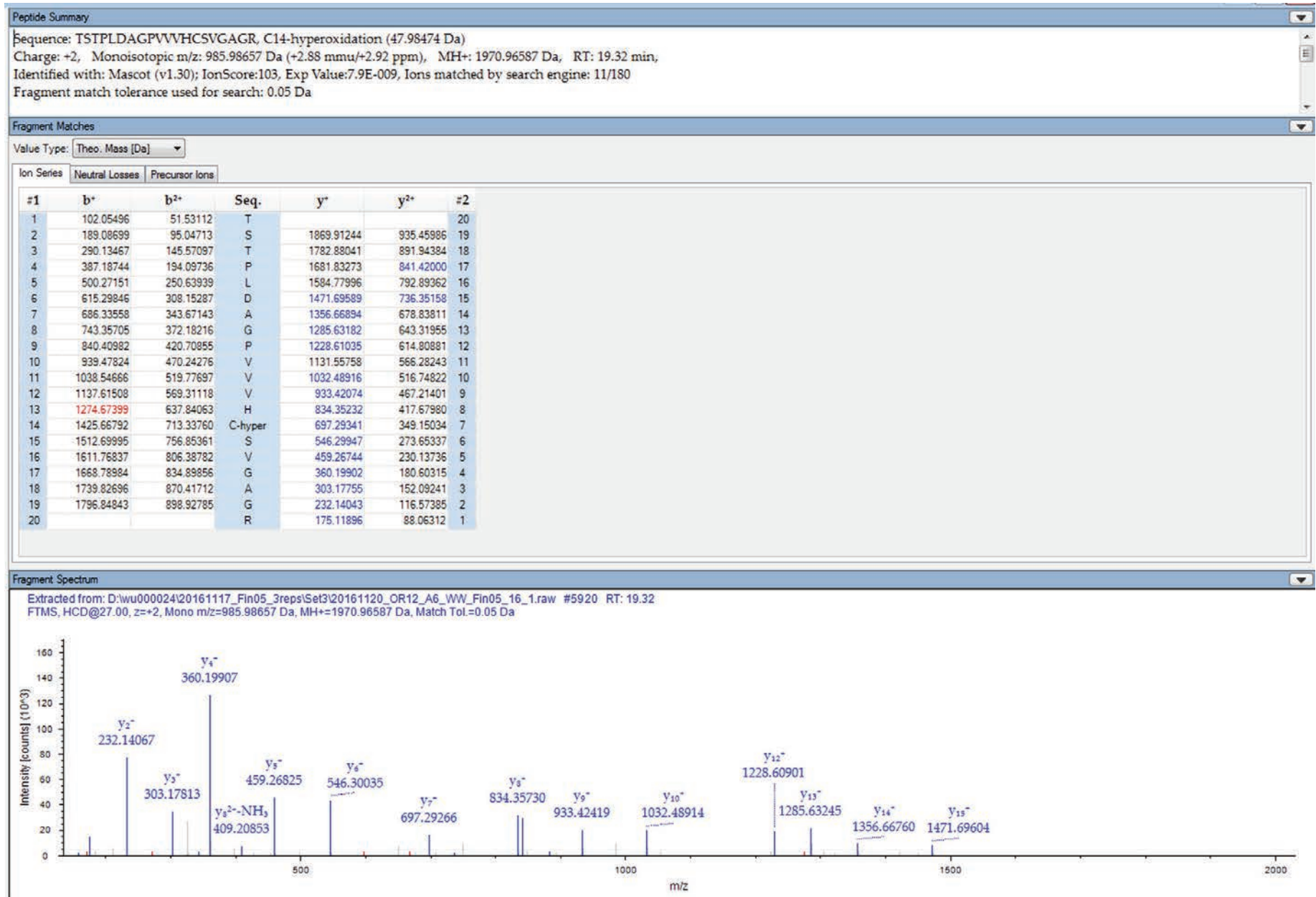
#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	102.05496	51.53112	T			20
2	262.08561	131.54644	C-Carbami...	1939.87501	970.44114	19
3	376.12854	188.56791	N	1779.84436	890.42582	18
4	473.18131	237.09429	P	1665.80143	833.40435	17
5	570.23408	285.62068	P	1568.74866	784.87797	16
6	685.26103	343.13415	D	1471.69589	736.35158	15
7	756.29815	378.65271	A	1356.66894	678.83811	14
8	813.31962	407.16345	G	1285.63182	643.31955	13
9	910.37239	455.68983	P	1228.61035	614.80881	12
10	1023.45646	512.23187	I	1131.55758	566.28243	11
11	1136.54053	568.77390	I	1018.47351	509.74039	10
12	1207.57765	604.29246	A	905.38944	453.19836	9
13	1344.63656	672.82192	H	834.35232	417.67980	8
14	1495.63049	748.31889	C-hyper	697.29341	349.15034	7
15	1582.66252	791.83490	S	546.29947	273.65337	6
16	1653.69964	827.35346	A	459.26744	230.13736	5
17	1710.72111	855.86420	G	388.23032	194.61880	4
18	1809.78953	905.39841	V	331.20885	166.10806	3
19	1866.81100	933.90914	G	232.14043	116.57385	2
20			R	175.11896	88.06312	1

Fragment Spectrum

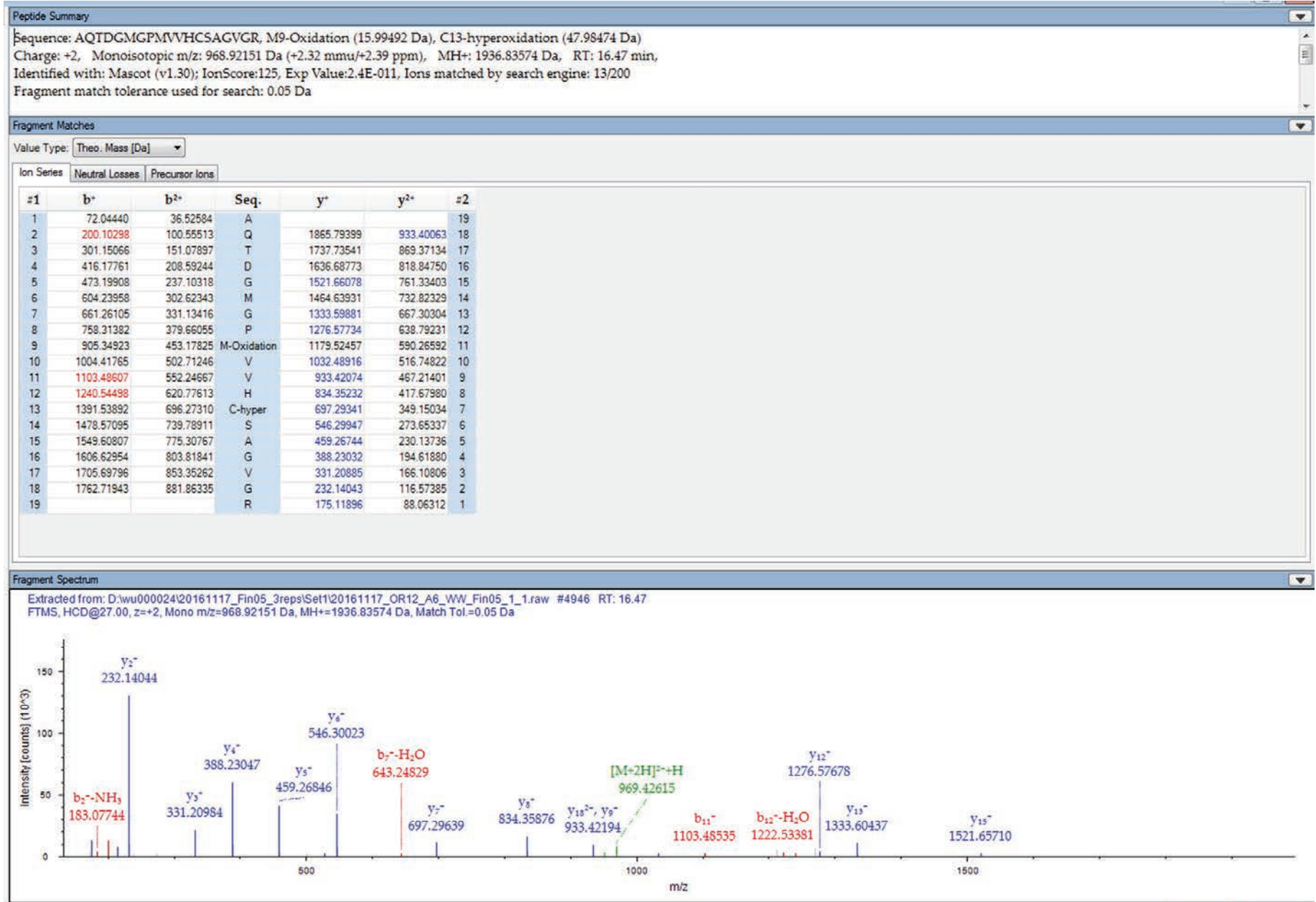
Extracted from: D:\wu000024\20161117_Fin05_3reps\Set3\20161120_OR12_A6_VW_Fin05_16_1.raw #5147 RT: 17.33
 FTMS, HCD@27.00, z=+2, Mono m/z=1020.96613 Da, MH+=2040.92497 Da, Match Tol.=0.05 Da



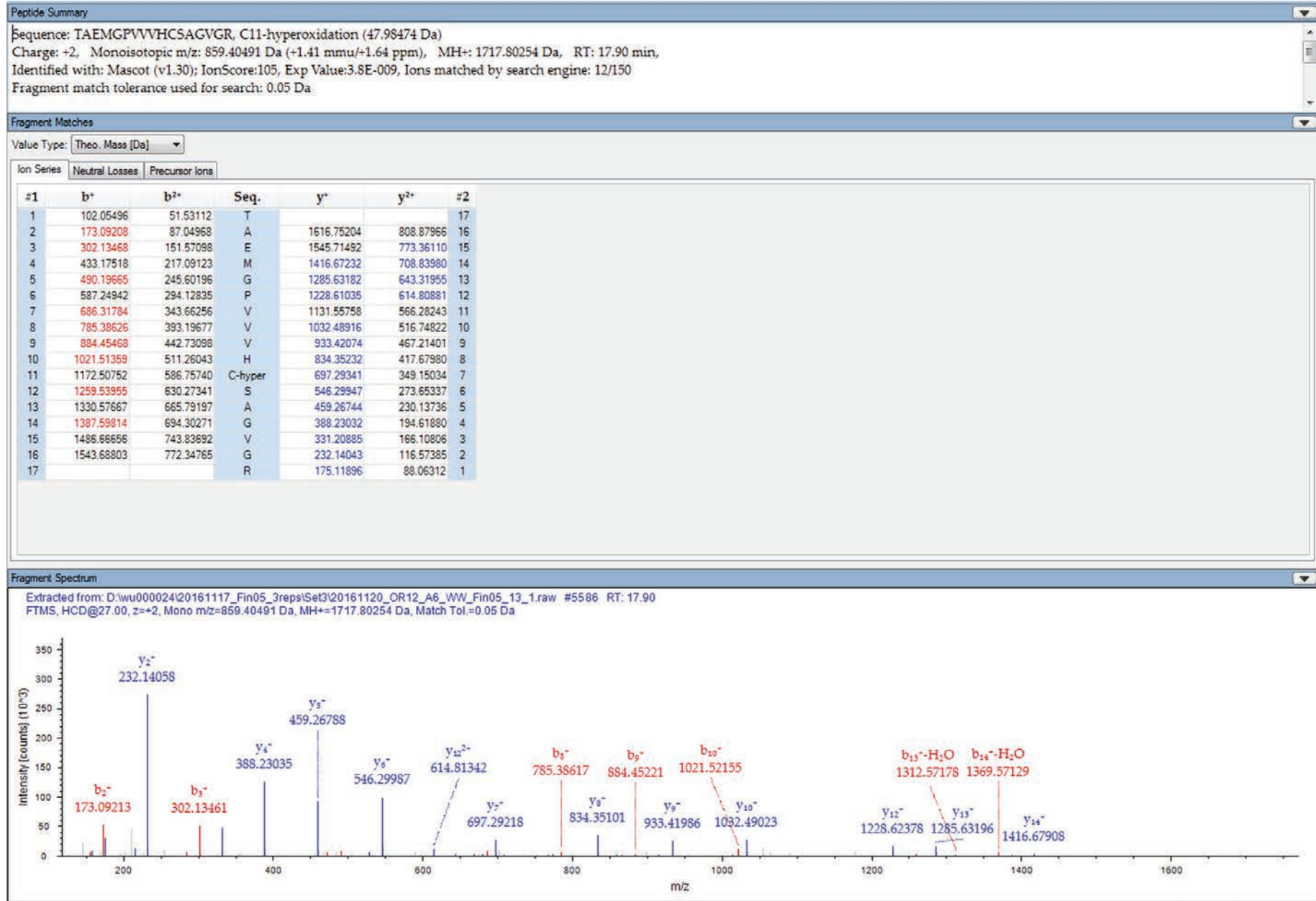
Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
A0A0R4ITF5 (C7U125)	Uncharacterized protein	ptprub	Receptor	TSTPLDAGPVV VHcSVGAGR	C14(hyper)	13



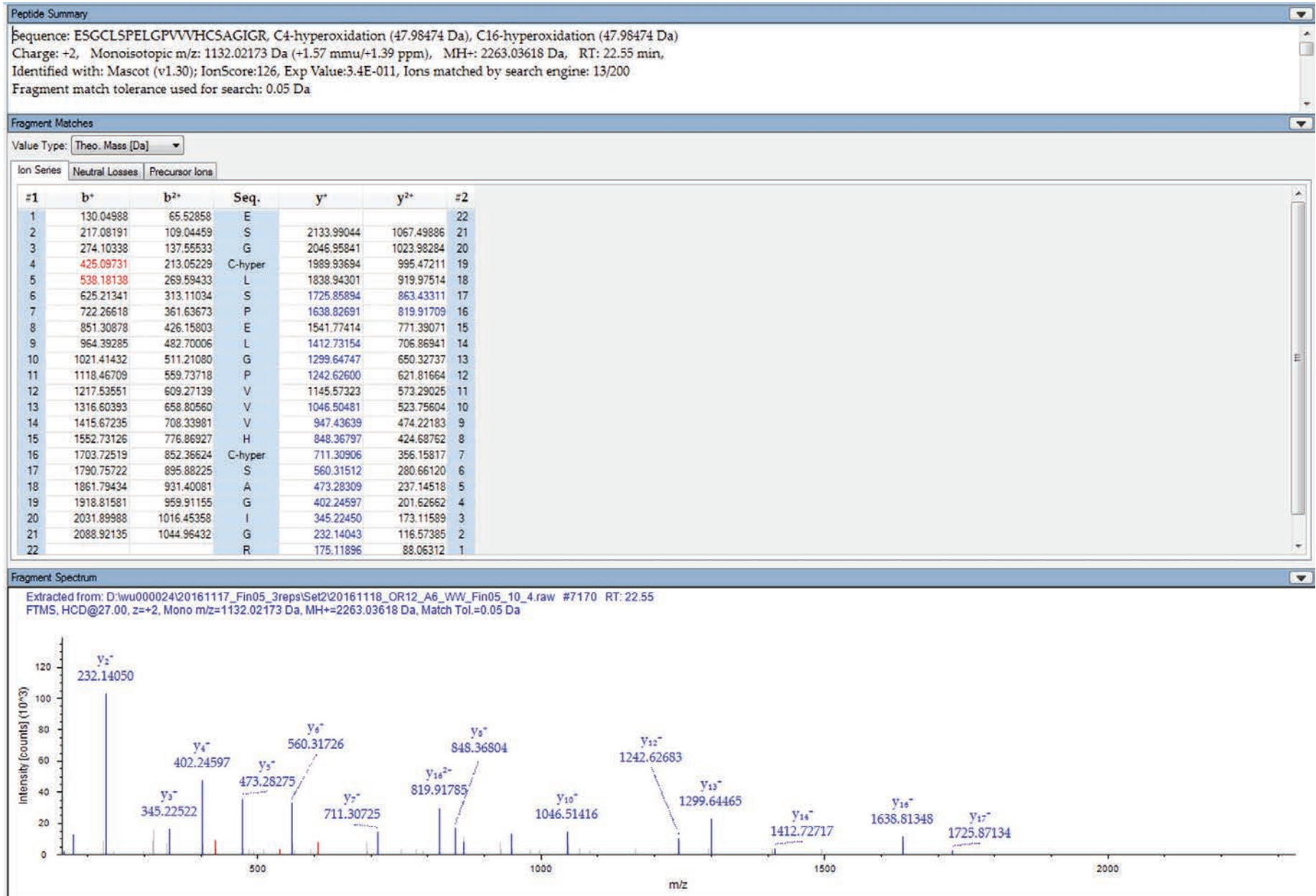
Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
X1WET2	Uncharacterized protein (Fragment)	ptprz1a	Receptor	AQTDGMGPMV VHcSAGVGR	C13(hyper)	16



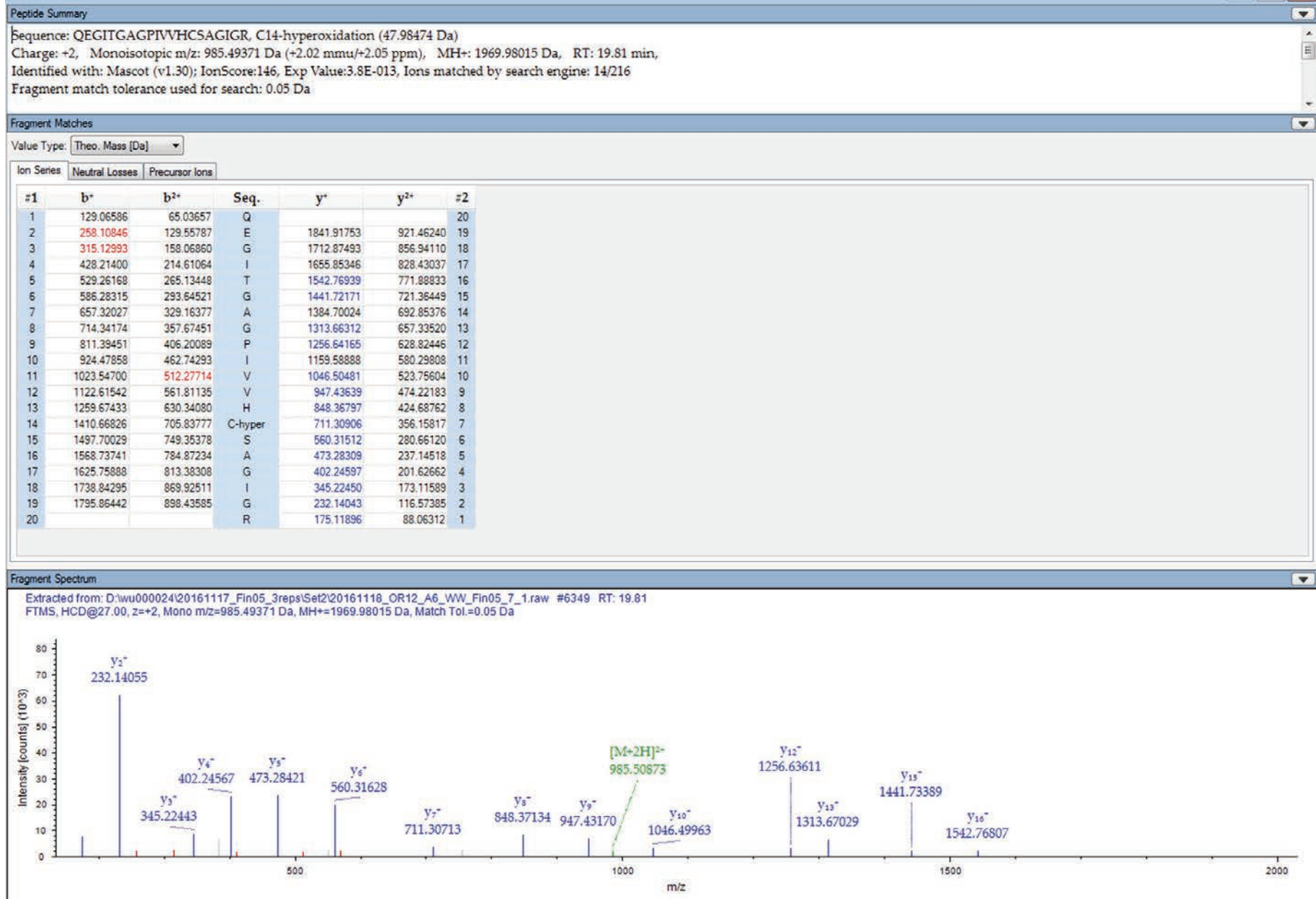
Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
B8A5J4	Uncharacterized protein	ptprz1b	Receptor	TAEMGPVVVHcSAGVGR	C11(hyper)	104



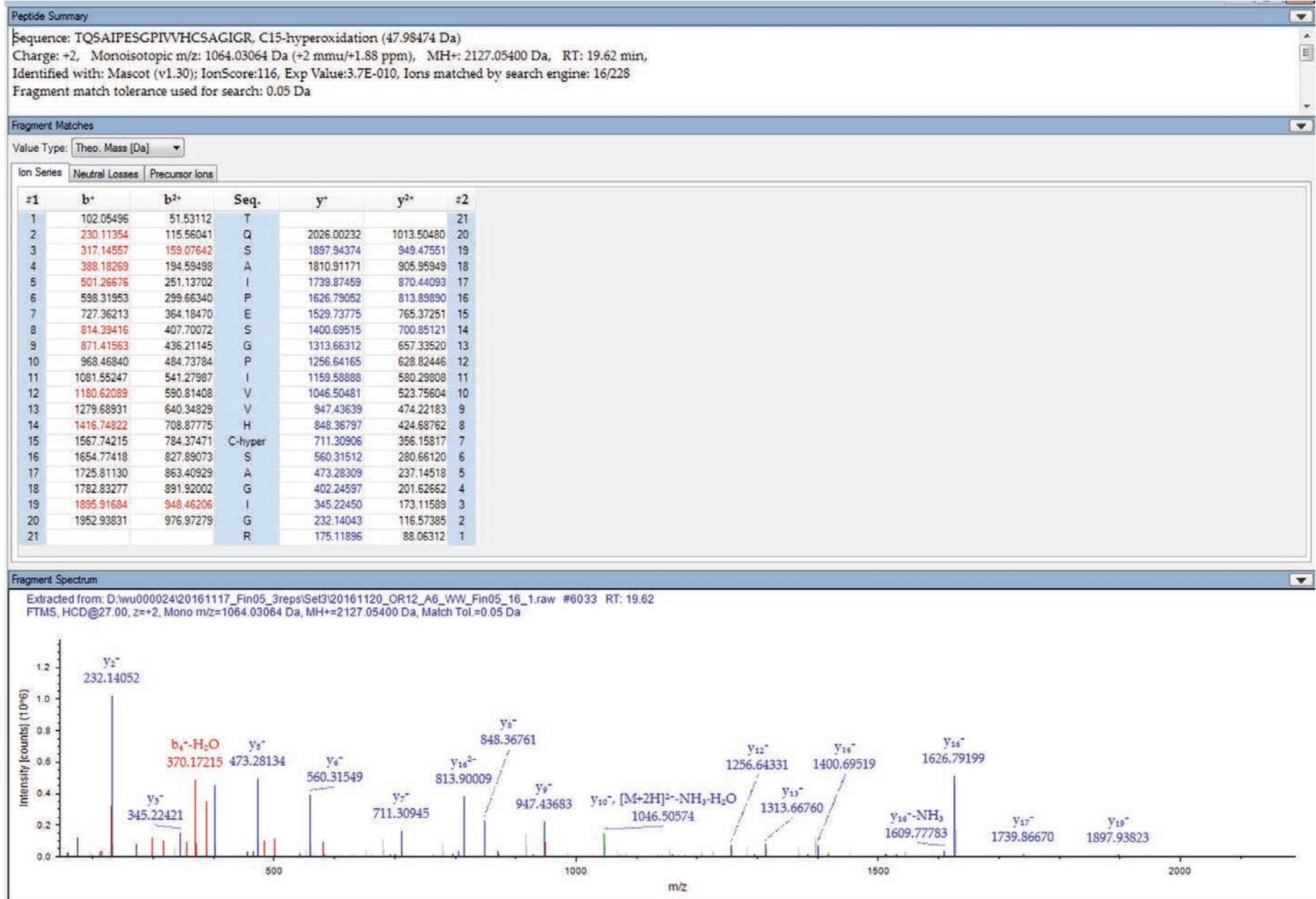
Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
C7U142	Protein-tyrosine phosphatase 1B (Fragment)	ptpn1	Non-receptor	ESGcLSPELGPVV VHcSAGIGR	C16(hyper)	142



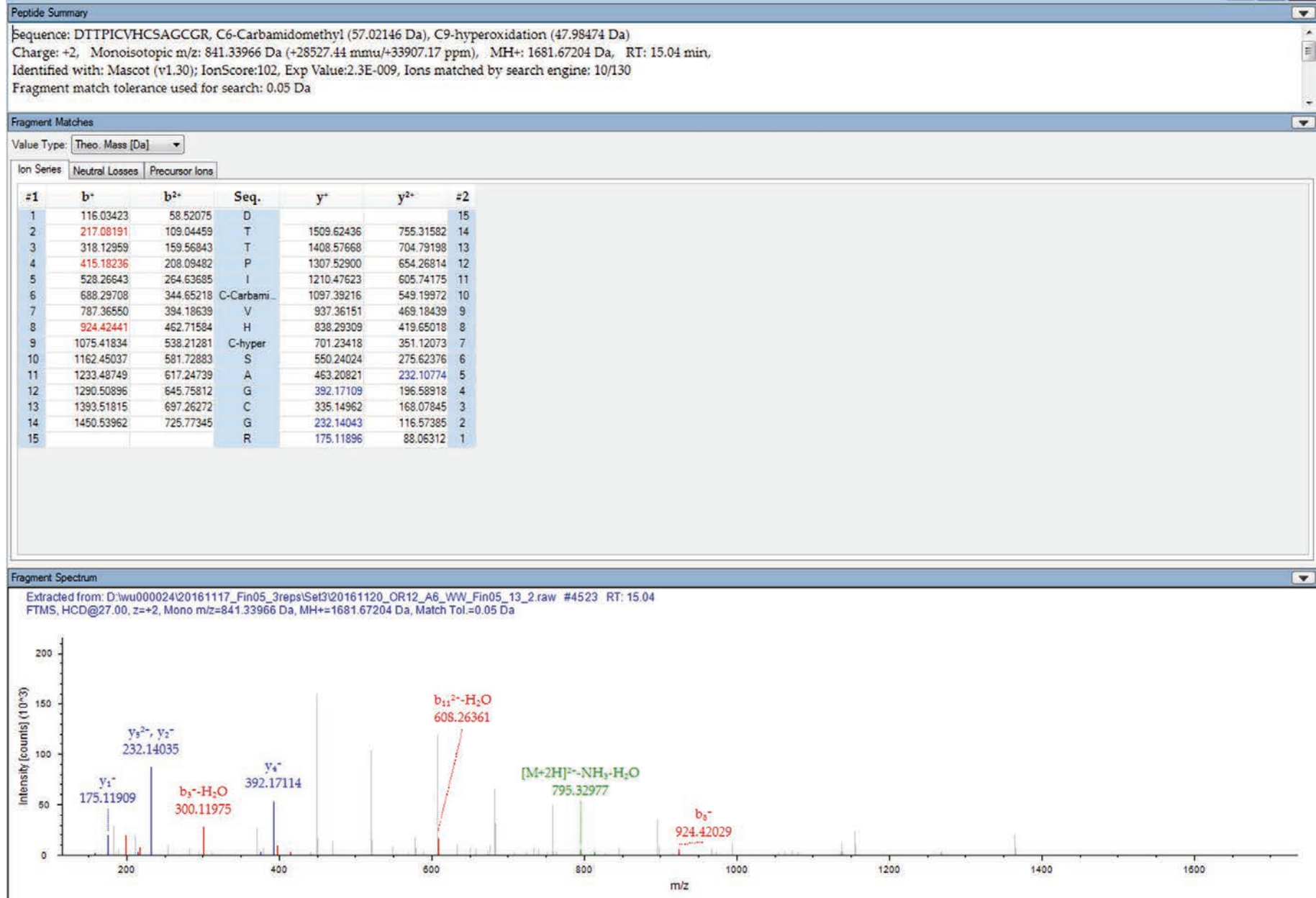
Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
C7U151	Protein-tyrosine phosphatase SHP-2a (Fragment)	ptpn11a	Non-receptor	QEGITGAGPIV VHcSAGIGR	C14(hyper)	112



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
C7U120	Protein-tyrosine phosphatase SHP-2b (Fragment)	ptpn11b	Non-receptor	TQSAIPESGPIV VHcSAGIGR	C15(hyper)	59



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
Q6PEI4	Protein tyrosine phosphatase, non-receptor type 12	ptpn12	Non-receptor	DTTPICVHcSAGcGR	C13(hyper)	71



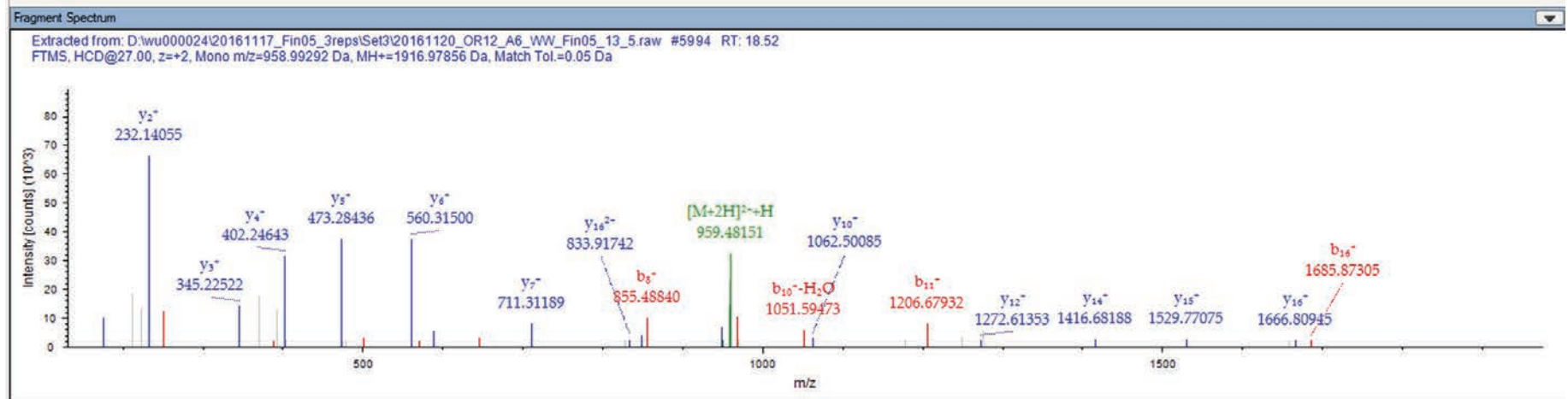
Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
C7U124	Protein-tyrosine phosphatase BAS (Fragment)	ptpn13	Non-receptor	HIHLSGPIITHCSAGIGR	C12(hyper)	64

Peptide Summary
 Sequence: HIHLSGPIITHCSAGIGR, C12-hydroxylation (47.98474 Da)
 Charge: +2, Monoisotopic m/z: 958.99292 Da (+1.27 mmu/+1.33 ppm), MH+: 1916.97856 Da, RT: 18.52 min,
 Identified with: Mascot (v1.30); IonScore:111, Exp Value:1.0E-009, Ions matched by search engine: 13/152
 Fragment match tolerance used for search: 0.05 Da

Fragment Matches
 Value Type: Theo. Mass [Da]

Ion Series: Neutral Losses | Precursor Ions

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	138.06619	69.53673	H			18
2	251.15026	126.07877	I	1779.91711	890.46219	17
3	388.20917	194.60822	H	1666.83304	833.92016	16
4	501.29324	251.15026	L	1529.77413	765.39070	15
5	588.32527	294.66627	S	1416.69006	708.84867	14
6	645.34674	323.17701	G	1329.65803	665.33265	13
7	742.39951	371.70339	P	1272.63656	636.82192	12
8	855.48358	428.24543	I	1175.58379	588.29553	11
9	968.56765	484.78746	I	1062.49972	531.75350	10
10	1069.61533	535.31130	T	949.41565	475.21146	9
11	1206.67424	603.84076	H	848.36797	424.68762	8
12	1357.66817	679.33772	C-hyper	711.30906	356.15817	7
13	1444.70020	722.85374	S	560.31512	280.66120	6
14	1515.73732	758.37230	A	473.28309	237.14518	5
15	1572.75879	786.88303	G	402.24597	201.62662	4
16	1685.84286	843.42507	I	345.22450	173.11589	3
17	1742.86433	871.93580	G	232.14043	116.57385	2
18			R	175.11896	88.06312	1



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
F1QIX3	Uncharacterized protein	ptpn20	Non-receptor	GPITVHcSAGIGR	C7(hyper)	38

Peptide Summary

Sequence: GPITVHCSAGIGR, C7-hyperoxidation (47.98474 Da)
 Charge: +2, Monoisotopic m/z: 658.32465 Da (-0.18 mmu/-0.27 ppm), MH+: 1315.64202 Da, RT: 16.51 min,
 Identified with: Mascot (v1.30); IonScore:97, Exp Value:2.3E-008, Ions matched by search engine: 10/104
 Fragment match tolerance used for search: 0.05 Da

Fragment Matches

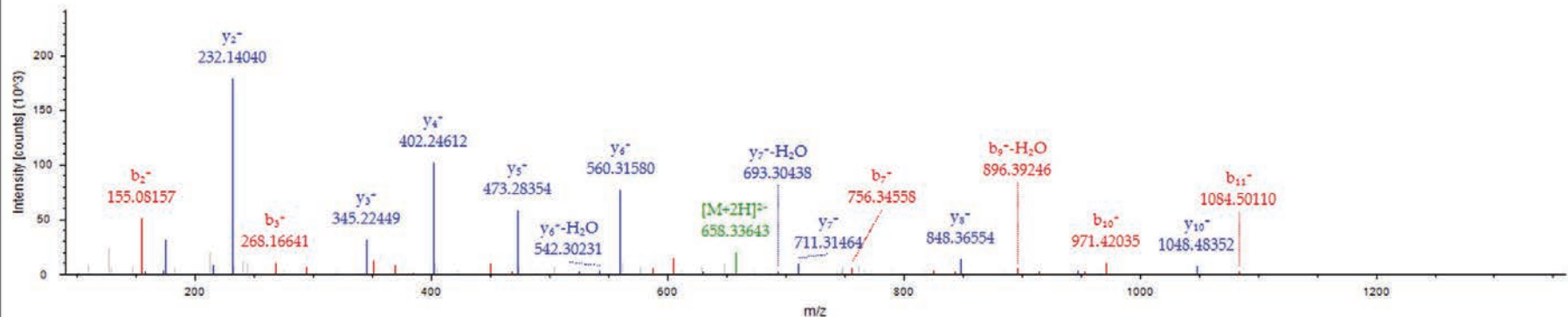
Value Type: Theo. Mass [Da]

Ion Series: Neutral Losses | Precursor Ions

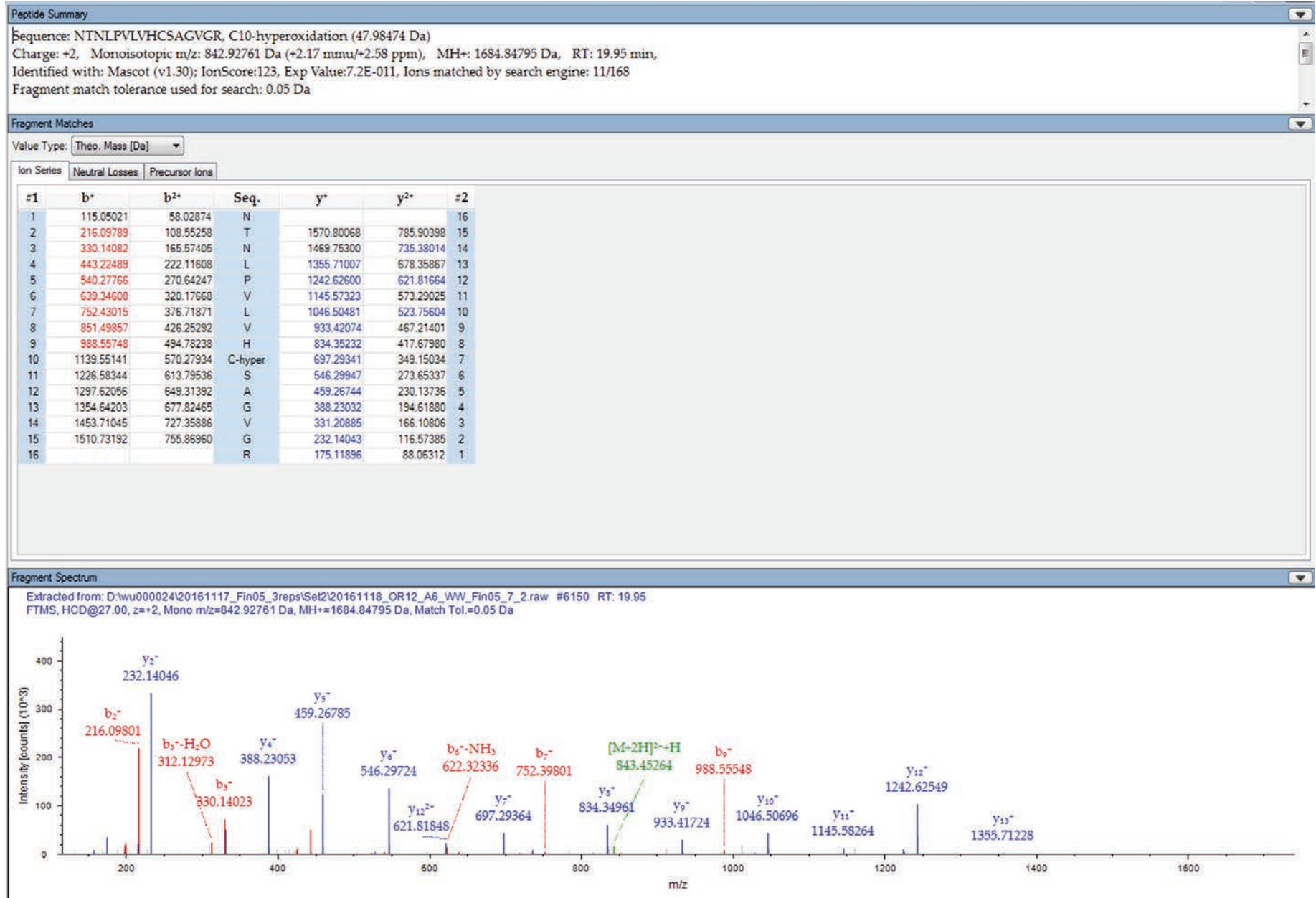
#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	58.02875	29.51801	G			13
2	155.08152	78.04440	P	1258.62091	629.81409	12
3	268.16559	134.58643	I	1161.56814	581.28771	11
4	369.21327	185.11027	T	1048.48407	524.74567	10
5	468.28169	234.64448	V	947.43639	474.22183	9
6	605.34060	303.17394	H	848.36797	424.68762	8
7	756.33453	378.67090	C-hyper	711.30906	356.15817	7
8	843.36656	422.18692	S	560.31512	280.66120	6
9	914.40368	457.70548	A	473.28309	237.14518	5
10	971.42515	486.21621	G	402.24597	201.62662	4
11	1084.50922	542.75825	I	345.22450	173.11589	3
12	1141.53069	571.26898	G	232.14043	116.57385	2
13			R	175.11896	88.06312	1

Fragment Spectrum

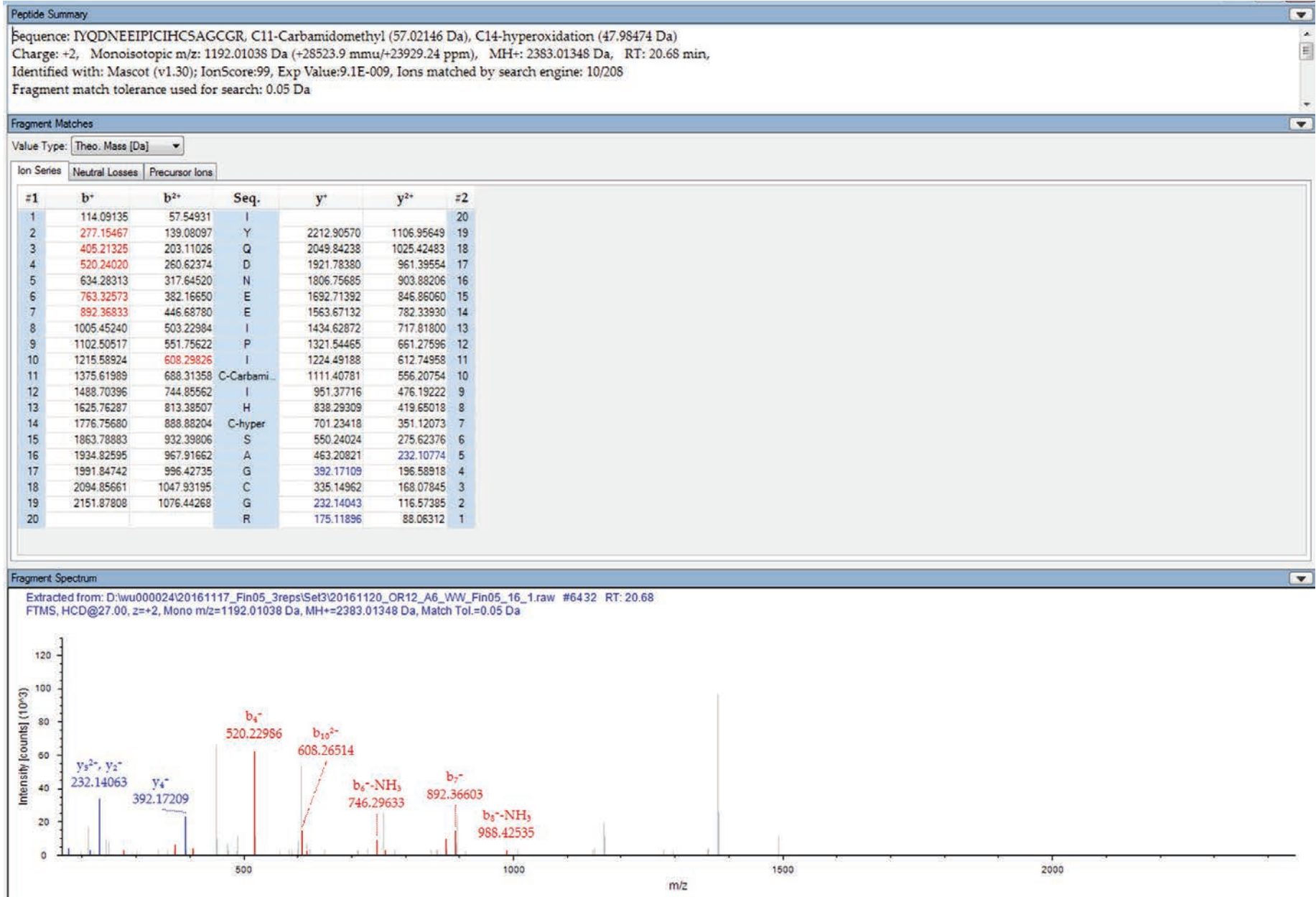
Extracted from: D:\wu000024\20161117_Fin05_3reps\Set1\20161117_OR12_A6_VW_Fin05_1_1.raw #4960 RT: 16.51
 FTMS, HCD@27.00, z=+2, Mono m/z=658.32465 Da, MH+=1315.64202 Da, Match Tol.=0.05 Da



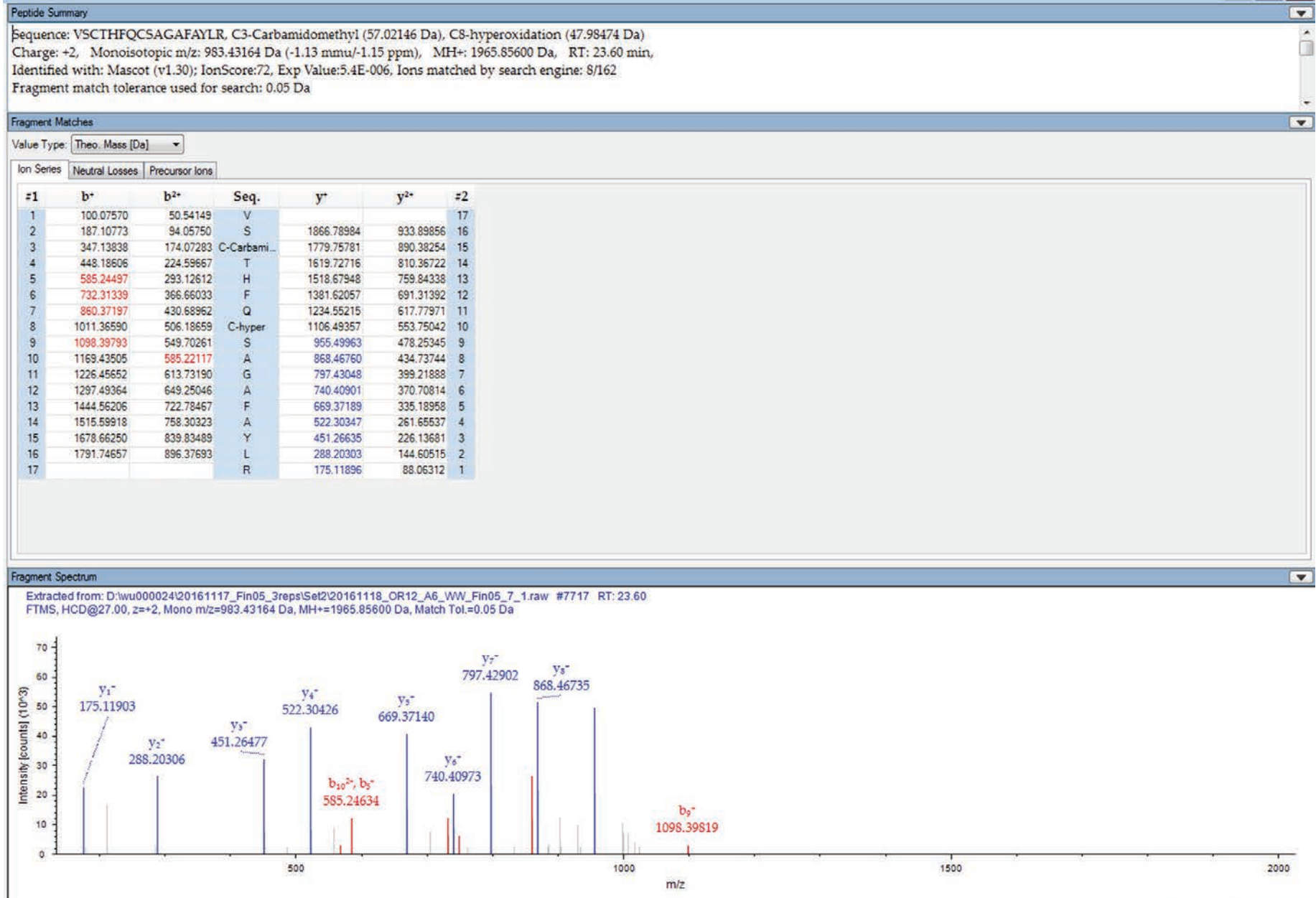
Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
F1Q6T9	Uncharacterized protein	ptpn21	Non-receptor	NTNLPVLVHcSAGVGR	C10(hyper)	29



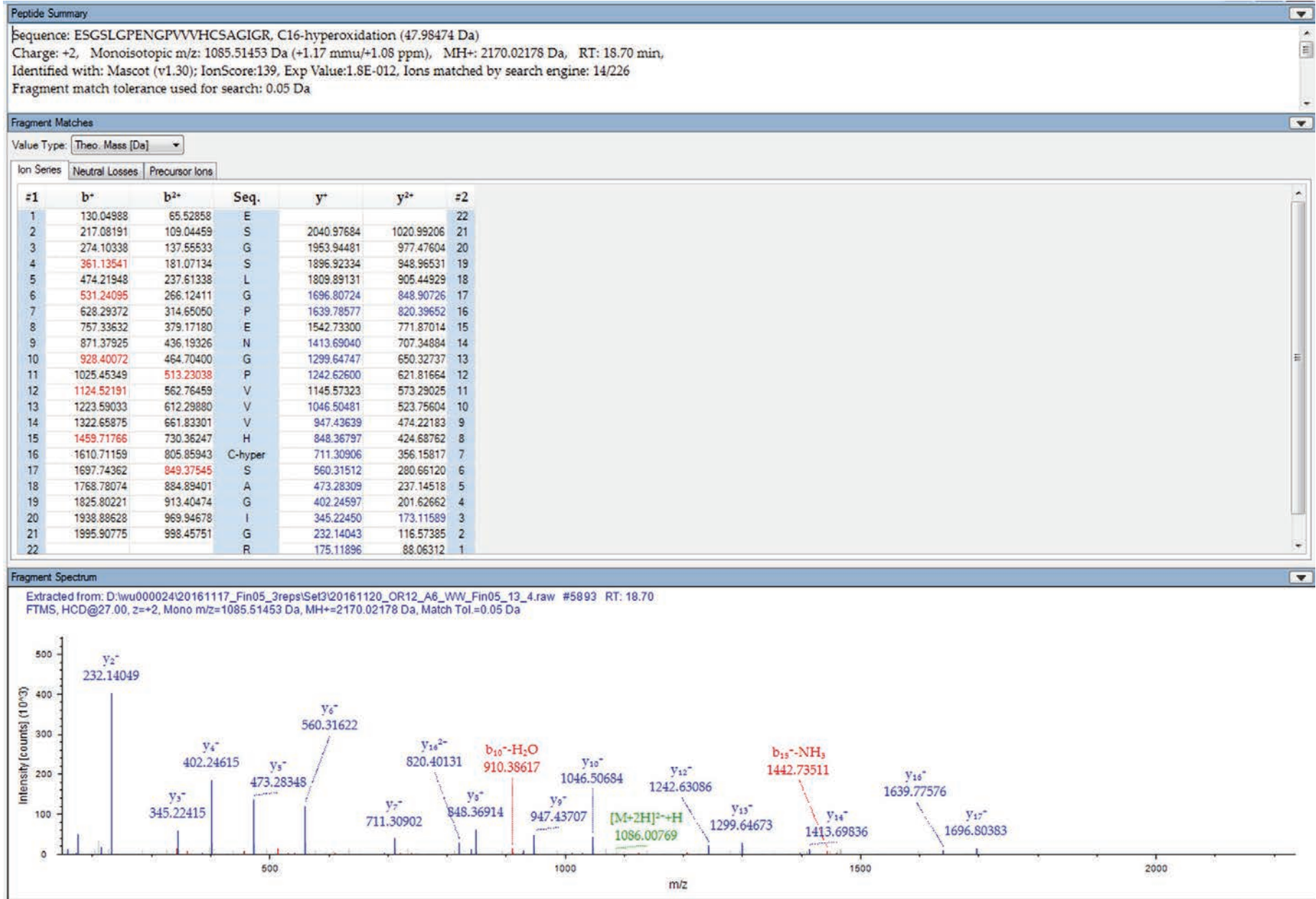
Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
C7U128	Protein-tyrosine phosphatase LyPTP (Fragment)	ptpn22	Non-receptor	IYQDNEEIPIC IHC SAGcGR	C18(hyper)	13



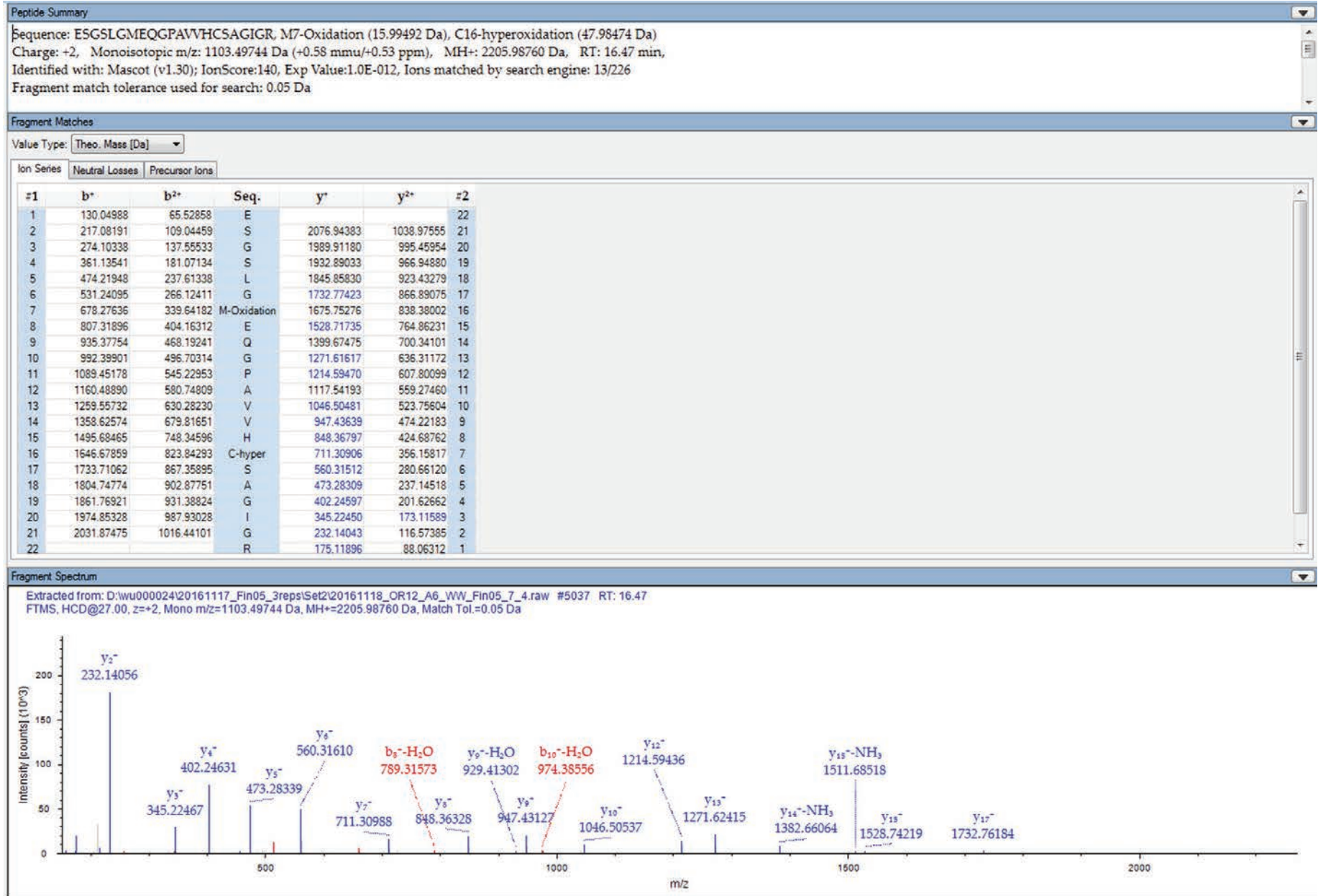
Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
F1R1D1	Uncharacterized protein	ptpn23a	Non-receptor	VScTHFQcSAGAFAYLR	C8(hyper)	138



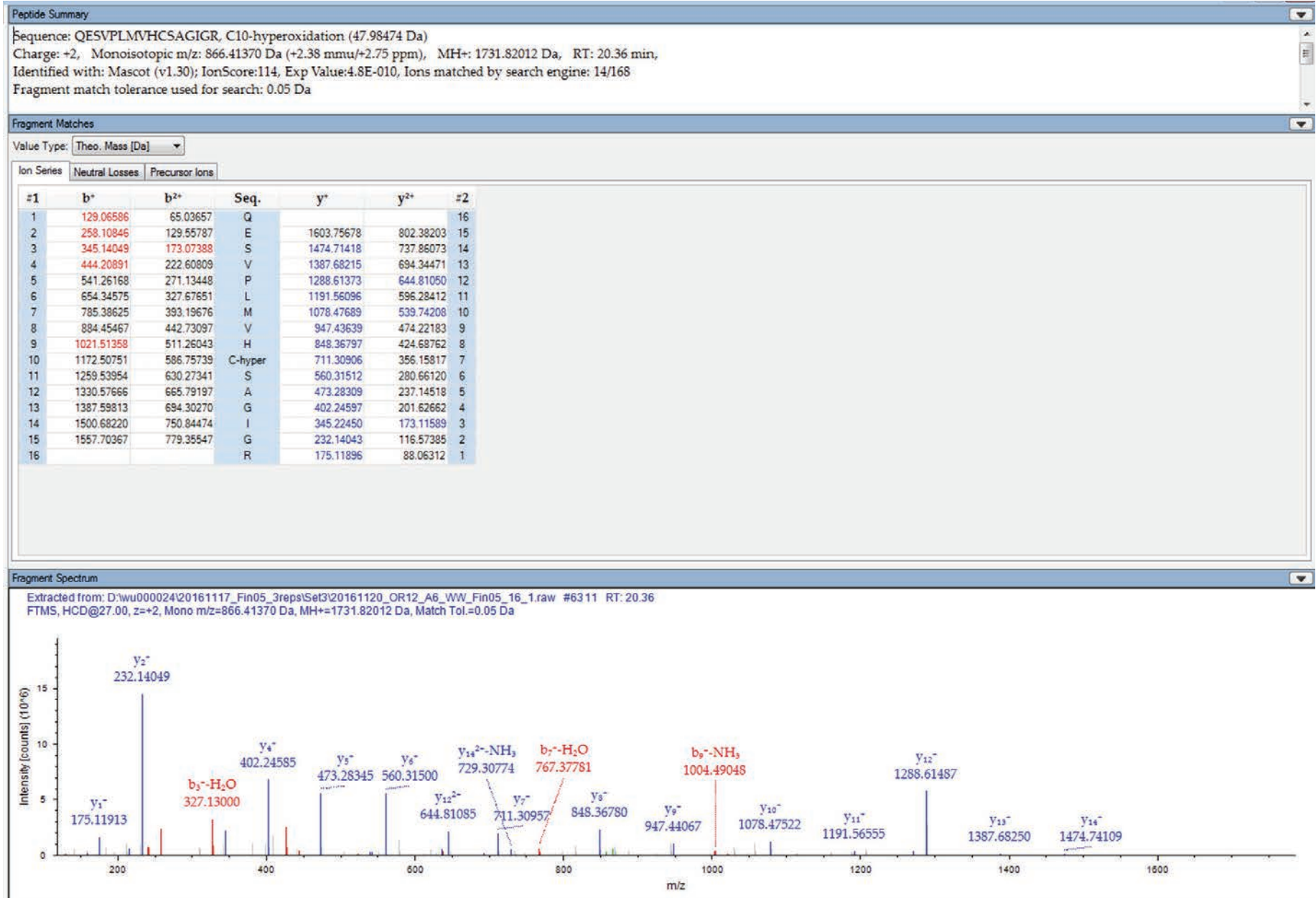
Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
F1QXQ5 (F1QGX6)	Tyrosine-protein phosphatase non-receptor type	ptpn2a	Non-receptor	ESGSLGPENGPVV VHcSAGIGR	C16(hyper)	86



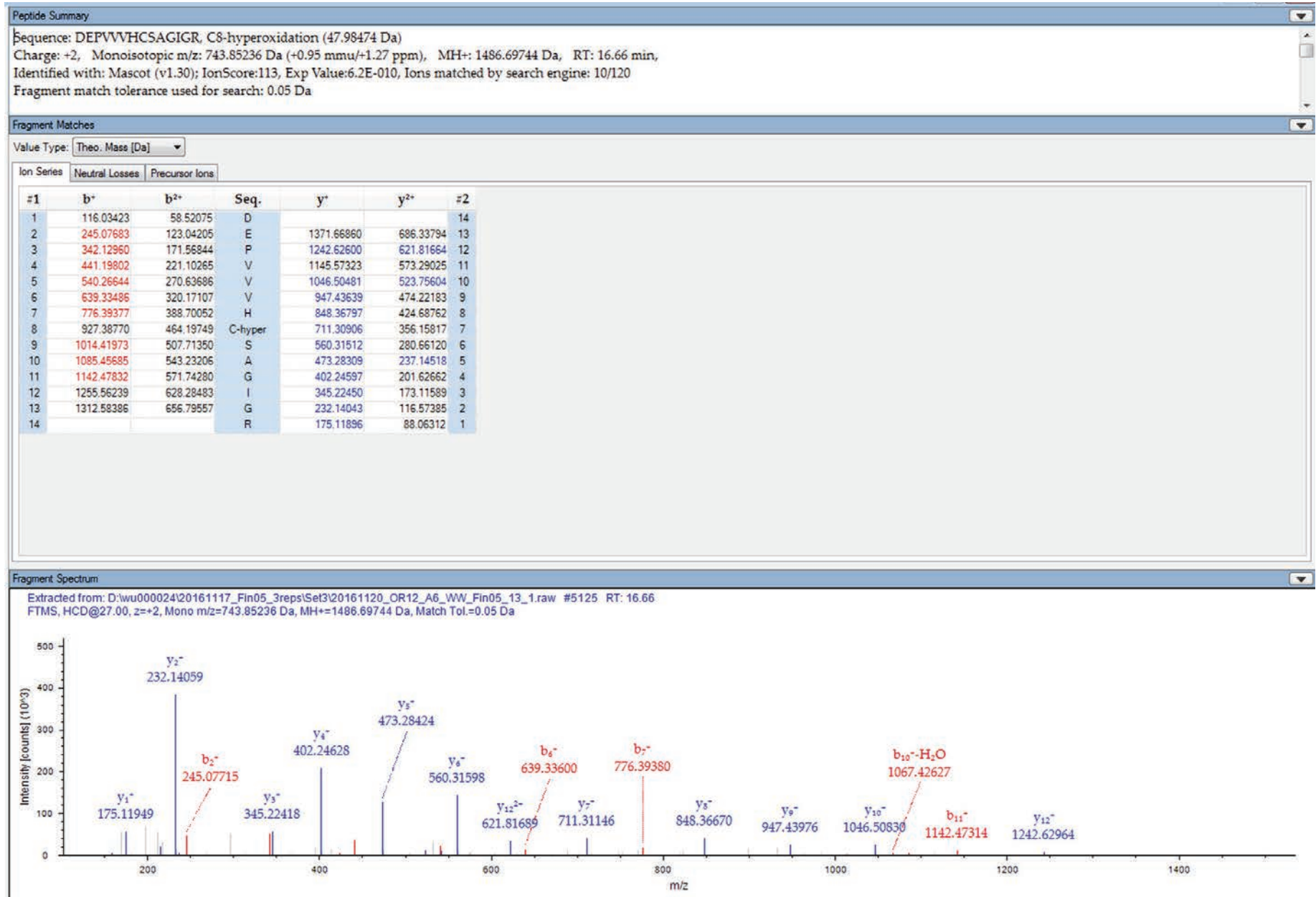
Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
Q6NY86	Tyrosine-protein phosphatase non-receptor type	ptpn2b	Non-receptor	ESGSLGMEQGPAAV VHcSAGIGR	C16(hyper)	159



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
F1QLN8	Uncharacterized protein	ptpn3	Non-receptor	QESVPLMVHCSAGIGR	C10(hyper)	97



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
C7U127	Protein-tyrosine phosphatase MEG1a (Fragment)	ptpn4a	Non-receptor	DEPVV VHcSAGIGR	C8(hyper)	19



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
C7U113	Protein-tyrosine phosphatase MEG1a (Fragment)	ptpn4b	Non-receptor	ADGPEPVV VHCSAGIGR	C11(hyper)	156

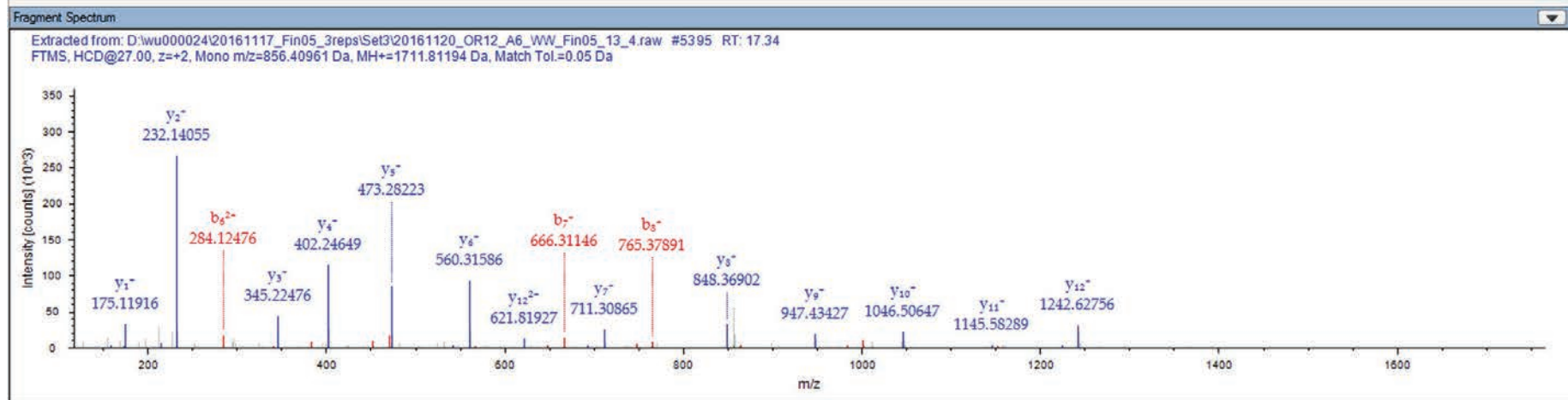
Peptide Summary
 Sequence: ADGPEPVV**VHCSAGIGR**, C11-hyperoxidation (47.98474 Da)
 Charge: +2, Monoisotopic m/z: 856.40961 Da (+2.52 mmu/+2.94 ppm), MH+: 1711.81194 Da, RT: 17.34 min,
 Identified with: Mascot (v1.30); IonScore:98, Exp Value:2.4E-008, Ions matched by search engine: 12/148
 Fragment match tolerance used for search: 0.05 Da

Fragment Matches

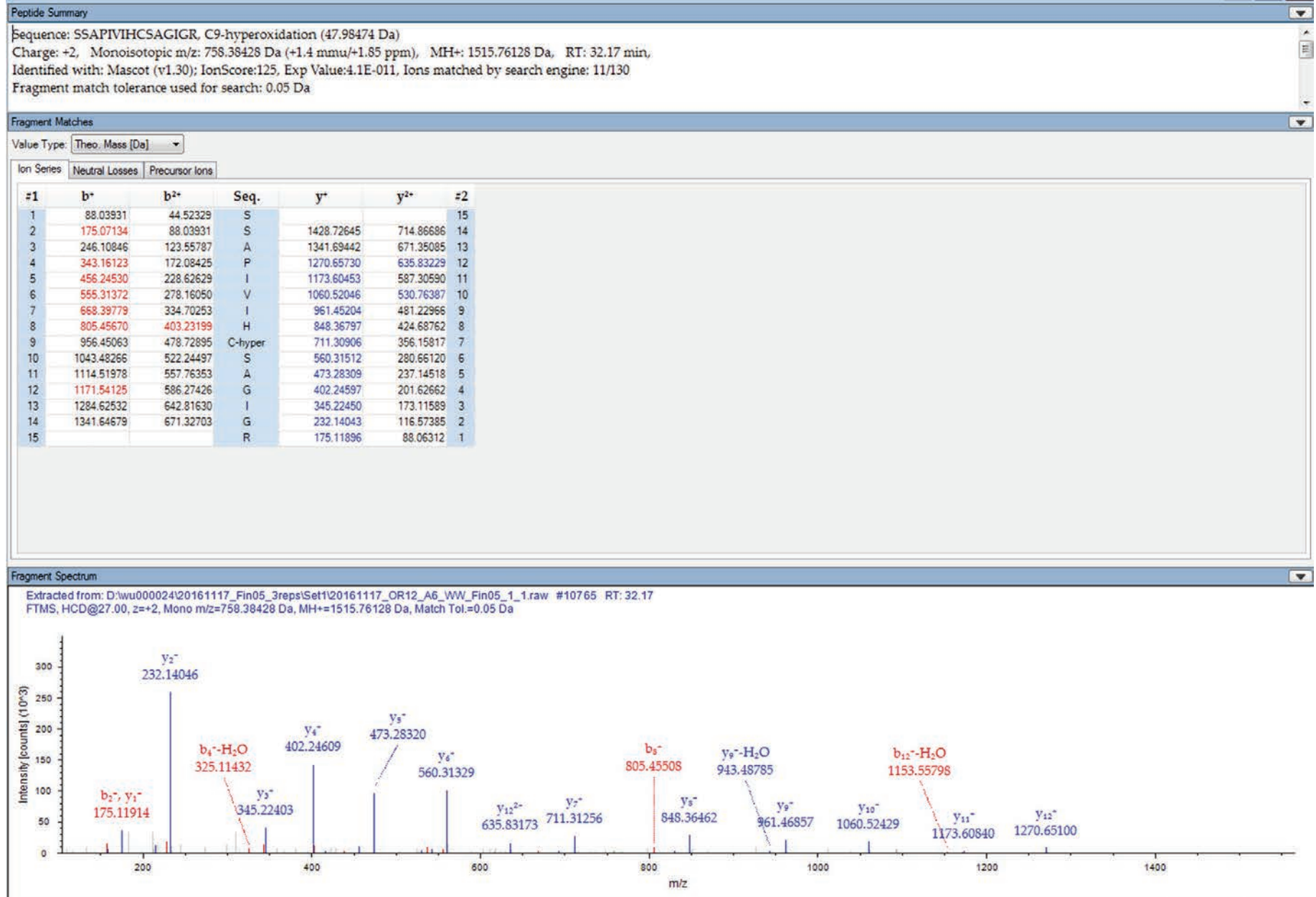
Value Type:

Ion Series	Neutral Losses	Precursor Ions
#1	b*	b2*
#2		y*
#1		y2*
#2		
#1		Seq.
#2		

#1	b*	b2*	Seq.	y*	y2*	#2
1	72.04440	36.52584	A			17
2	187.07135	94.03931	D	1640.76979	820.88853	16
3	244.09282	122.55005	G	1525.74284	763.37506	15
4	341.14559	171.07643	P	1468.72137	734.86432	14
5	470.18819	235.59773	E	1371.66860	686.33794	13
6	567.24096	284.12412	P	1242.62600	621.81664	12
7	666.30938	333.65833	V	1145.57323	573.29025	11
8	765.37780	383.19254	V	1046.50481	523.75604	10
9	864.44622	432.72675	V	947.43639	474.22183	9
10	1001.50513	501.25620	H	848.36797	424.68762	8
11	1152.49906	576.75317	C-hyper	711.30906	356.15817	7
12	1239.53109	620.26918	S	560.31512	280.66120	6
13	1310.56821	655.78774	A	473.28309	237.14518	5
14	1367.58968	684.29848	G	402.24597	201.62662	4
15	1480.67375	740.84051	I	345.22450	173.11589	3
16	1537.69522	769.35125	G	232.14043	116.57385	2
17			R	175.11896	88.06312	1



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
C7U118	Protein-tyrosine phosphatase SHP-1 (Fragment)	ptpn6	Non-receptor	SSAPIVHCSAGIGR	C9(hyper)	82



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
X1WVF4	Uncharacterized protein (Fragment)	ptpn9a	Non-receptor	GHPLGPPMV VHcSAGIGR	C12(hyper)	170

Peptide Summary

Sequence: GHPLGPPMV**VHcSAGIGR**, MS-Oxidation (15.99492 Da), C12-hyperoxidation (47.98474 Da)
 Charge: +2, Monoisotopic m/z: 924.94702 Da (+1.16 mmu/+1.25 ppm), MH+: 1848.88677 Da, RT: 17.30 min,
 Identified with: Mascot (v1.30); IonScore:123, Exp Value:7.6E-011, Ions matched by search engine: 12/136
 Fragment match tolerance used for search: 0.05 Da

Fragment Matches

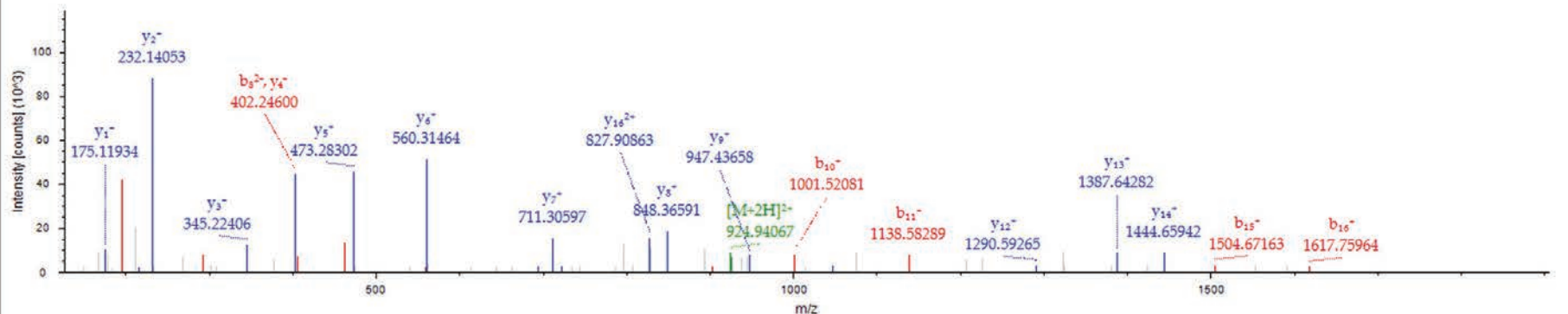
Value Type: Theo. Mass [Da]

Ion Series: Neutral Losses Precursor Ions

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	58.02875	29.51801	G			18
2	195.08766	98.04747	H	1791.86298	896.43513	17
3	292.14043	146.57385	P	1654.80407	827.90567	16
4	405.22450	203.11589	L	1557.75130	779.37929	15
5	462.24597	231.62662	G	1444.66723	722.83725	14
6	559.29874	280.15301	P	1387.64576	694.32652	13
7	656.35151	328.67939	P	1290.59299	645.80013	12
8	803.38692	402.19710	M-Oxidation	1193.54022	597.27375	11
9	902.45534	451.73131	V	1046.50481	523.75604	10
10	1001.52376	501.26552	V	947.43639	474.22183	9
11	1138.58267	569.79497	H	848.36797	424.68762	8
12	1289.57661	645.29194	C-hyper	711.30906	356.15817	7
13	1376.60864	688.80796	S	560.31512	280.66120	6
14	1447.64576	724.32652	A	473.28309	237.14518	5
15	1504.66723	752.83725	G	402.24597	201.62662	4
16	1617.75130	809.37929	I	345.22450	173.11589	3
17	1674.77277	837.89002	G	232.14043	116.57385	2
18			R	175.11896	88.06312	1

Fragment Spectrum

Extracted from: D:\wu000024\20161117_Fin05_3reps\Set3\20161120_OR12_A6_VW_Fin05_13_1.raw #5357 RT: 17.30
 FTMS, HCD@27.00, z=+2, Mono m/z=924.94702 Da, MH+=1848.88677 Da, Match Tol.=0.05 Da



Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidised cysteine	Total MS/MS count
F1QTI4	Uncharacterized protein	ptpn9b	Non-receptor	TLYPDWTGPPGGPPVV VHcSAGIGR	C19(hyper)	86

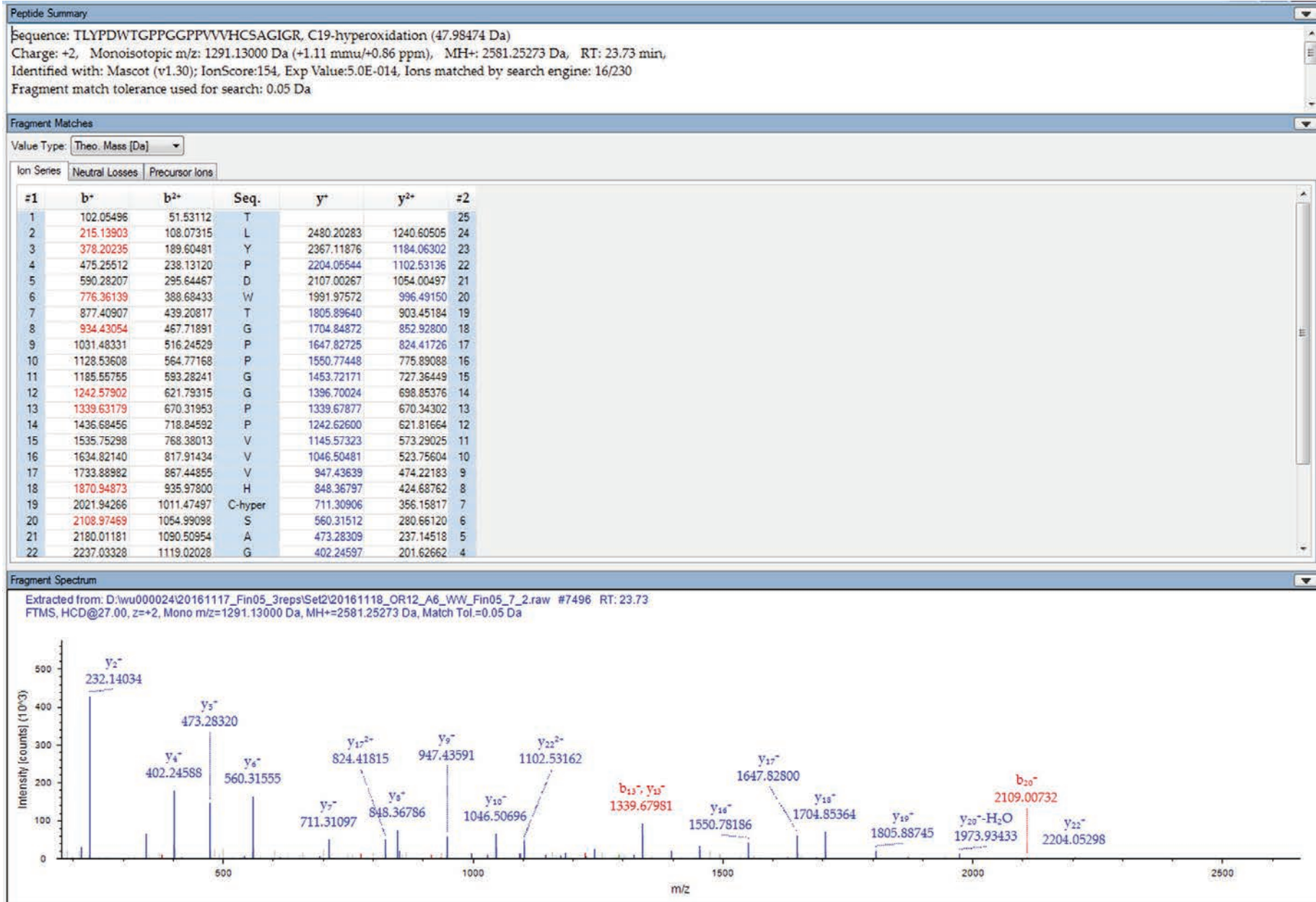


Fig. S3. Zebrafish *ptpra* knock-out embryos (*ptpra*^{-/-}) lack RPTP α protein. Adult zebrafish heterozygous for *ptpra* (*ptpra*^{+/-}) were in-crossed to generate *ptpra* knock-out embryos (*ptpra*^{-/-}). At 4 dpf, individual embryos were cut in half: one half lysed for protein, and the other half lysed for DNA extraction. Following genotyping, protein lysates of *ptpra*^{+/+}, *ptpra*^{+/-}, and *ptpra*^{-/-} embryos were pooled, and 5 embryo equivalents per condition were run on an SDS-PAGE gel, immunoblotted and probed with an Rptp α -specific antibody and with tubulin to monitor equal loading. Control lane represents wild-type TL zebrafish embryos at 3 dpf.

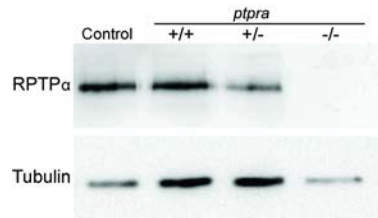


Table S1. PTP motif peptides detected. Conserved catalytic site sequence in blue. Position of hyperoxidized cysteine refers to residue number within a properly cleaved tryptic peptide, without missed cleavage. Total MS/MS count is the sum of all spectra obtained from each biological replicate of PV-treated sample. Peptides oxidized in the second fin clip are highlighted in grey.

Uniprot Accession	Description	Gene name	PTP type	Sequence	Hyperoxidized cysteine	Total MS/MS count
B3DJL5_site1 (C7U129)	Ptpra protein	ptpra	Receptor	QQQQSGNHPIV VHcSAGAGR	C14(hyper)	76
B3DJL5_site2 (C7U129)	Ptpra protein	ptpra	Receptor	NcNPQYAGPIVV VHcSAGVGR	C14(hyper)	33
A0A0R4ITJ9 (C7U135)	Uncharacterized protein	ptprb	Receptor	TNSPGISV VHcSAGVGR	C11(hyper)	51
C7U126	CD45 antigen (Fragment)	ptprc	Receptor	NFFSGPIVV VHcSAGVGR	C11(hyper)	93
E7EZG7_site1	Receptor-type tyrosine-protein phosphatase	ptprea	Receptor	QVNPYSYAGPIVV VHcSAGVGR	C14(hyper)	35
E7EZG7_site2	Receptor-type tyrosine-protein phosphatase	ptprea	Receptor	QQQQSGNHPII VHcSAGAGR	C14(hyper)	119
Q90YJ5_site1	Receptor protein-tyrosine phosphatase LAR (Fragment)	ptprfa	Receptor	AcNPPDAGPMVV VHcSAGVGR	C14(hyper)	100
Q90YJ5_site2	Receptor protein-tyrosine phosphatase LAR (Fragment)	ptprfa	Receptor	EQFGQDGPITV VHcSAGVGR	C13(hyper)	72
F1Q4V8	Uncharacterized protein (Fragment)	ptprga	Receptor	SSAAQTPDMGPMVLV VHcSAGVGR	C16(hyper)	42
E7F9R2	Uncharacterized protein	ptprh	Receptor	QHIESHFSTGPTV VHcSAGVGR	C16(hyper)	159
B6HY54	Protein-tyrosine phosphatase	ptprja	Receptor	HSPTLV VHcSAGVGR	C8(hyper)	52
X1WCM2	Uncharacterized protein (Fragment)	ptprjb.1	Receptor	HSPTV VHcSAGVGR	C8(hyper)	21
X1WF45	Uncharacterized protein (Fragment)	ptprjb.2	Receptor	EHMNQYScTSPVV VHcSAGVGR	C16(hyper)	6
X1WD65	Uncharacterized protein	ptprk	Receptor	MSNPPTAGPIVV VHcSAGAGR	C14(hyper)	90
A0A0R4IA95	Uncharacterized protein (Fragment)	ptpro	Receptor	GPIVV VHcSAGVGR	C7(hyper)	52
Q90YJ4_site1	Receptor protein-tyrosine phosphatase sigma (Fragment)	ptprsa	Receptor	EQFGQDGPISV VHcSAGVGR	C13(hyper)	21
Q90YJ4_site2	Receptor protein-tyrosine phosphatase sigma (Fragment)	ptprsa	Receptor	TcNPPDAGPII AHcSAGVGR	C14(hyper)	45
A0A0R4ITF5 (C7U125)	Uncharacterized protein	ptprub	Receptor	TSTPLDAGPVVV VHcSVGAGR	C14(hyper)	13
X1WET2	Uncharacterized protein (Fragment)	ptprz1a	Receptor	AQTDGMGPMVV VHcSAGVGR	C13(hyper)	16
B8A5J4	Uncharacterized protein	ptprz1b	Receptor	TAEMGPVVV VHcSAGVGR	C11(hyper)	104
C7U142	Protein-tyrosine phosphatase 1B (Fragment)	ptpn1	Non-receptor	ESGcLSPELGPVV VHcSAGIGR	C16(hyper)	142
C7U151	Protein-tyrosine phosphatase SHP-2a (Fragment)	ptpn11a	Non-receptor	QEGITGAGPIV VHcSAGIGR	C14(hyper)	112
C7U120	Protein-tyrosine phosphatase SHP-2b (Fragment)	ptpn11b	Non-receptor	TQSAIPESGPIV VHcSAGIGR	C15(hyper)	59
Q6PEI4	Protein tyrosine phosphatase, non-receptor type 12	ptpn12	Non-receptor	DTTPIC VHcSAGcGR	C13(hyper)	71
C7U124	Protein-tyrosine phosphatase BAS (Fragment)	ptpn13	Non-receptor	HIHLSGPII THcSAGIGR	C12(hyper)	64
F1QIX3	Uncharacterized protein	ptpn20	Non-receptor	GPIT VHcSAGIGR	C7(hyper)	38
F1Q6T9	Uncharacterized protein	ptpn21	Non-receptor	NTNLPVLV VHcSAGVGR	C10(hyper)	29
C7U128	Protein-tyrosine phosphatase LyPTP (Fragment)	ptpn22	Non-receptor	IYQDNEEIPId HcSAGcGR	C18(hyper)	13
F1R1D1	Uncharacterized protein	ptpn23a	Non-receptor	VScTHFQc SAGAFAYLR	C8(hyper)	138
F1QXQ5 (F1QG6)	Tyrosine-protein phosphatase non-receptor type	ptpn2a	Non-receptor	ESGSLGPENGPVV VHcSAGIGR	C16(hyper)	86
Q6NY86	Tyrosine-protein phosphatase non-receptor type	ptpn2b	Non-receptor	ESGSLGMEQGPVV VHcSAGIGR	C16(hyper)	159
F1QLN8	Uncharacterized protein	ptpn3	Non-receptor	QESVPLM VHcSAGIGR	C10(hyper)	97
C7U127	Protein-tyrosine phosphatase MEG1a (Fragment)	ptpn4a	Non-receptor	DEPVV VHcSAGIGR	C8(hyper)	19
C7U113	Protein-tyrosine phosphatase MEG1a (Fragment)	ptpn4b	Non-receptor	ADGPEPVV VHcSAGIGR	C11(hyper)	156
C7U118	Protein-tyrosine phosphatase SHP-1 (Fragment)	ptpn6	Non-receptor	SSAPIV VHcSAGIGR	C9(hyper)	82
X1WV4	Uncharacterized protein (Fragment)	ptpn9a	Non-receptor	GHPPLGPPMV VHcSAGIGR	C12(hyper)	170
F1QTI4	Uncharacterized protein	ptpn9b	Non-receptor	TLYPDWTGPPGPPVV VHcSAGIGR	C19(hyper)	86

Table S2. PTP motif peptide oxidation in response to caudal fin amputation. Mean spectra count and standard error obtained from 3 biological replicates. Peptides oxidized in second fin clip highlighted in grey. Student *t*-test statistics for difference between first and second fin clip reported as exact two-tailed *p*-value.

Uniprot Accession	Gene name	PTP type	Total MS/MS count	First fin clip						Second fin clip						T.test (PV 1st clip: PV 2nd clip)	T.test (NEM 2nd clip : NEM 1st clip)
				Mean spectra count PV	SEM PV	Mean spectra count NEM	SEM NEM	Mean spectra count Control	SEM Control	Mean spectra count PV	SEM PV	Mean spectra count NEM	SEM NEM	Mean spectra count Control	SEM Control		
B3DJL5_site1 (C7U129)	ptpra	Receptor	76	13,0	2,1	0,7	0,3	0,0	0,0	11,3	1,2	0,3	0,3	0,0	0,0	0,62	0,21
B3DJL5_site2 (C7U129)	ptpra	Receptor	33	6,7	0,9	0,7	0,7	0,0	0,0	3,3	0,9	0,3	0,3	0,0	0,0	0,20	0,42
AOAOR4ITJ9 (C7U135)	ptprb	Receptor	51	9,0	0,6	0,0	0,0	0,0	0,0	8,0	1,7	0,0	0,0	0,0	0,0	0,48	Not detected
C7U126	ptprc	Receptor	93	18,0	1,7	0,3	0,3	0,0	0,0	12,3	0,9	0,3	0,3	0,0	0,0	0,14	Not detected
E7EZG7_site1	ptprea	Receptor	35	6,3	0,9	0,7	0,7	0,0	0,0	4,0	1,2	0,7	0,3	0,0	0,0	0,12	1,00
E7EZG7_site2	ptprea	Receptor	119	18,0	1,5	0,3	0,3	0,0	0,0	15,3	0,9	6,0	1,2	0,0	0,0	0,37	0,04
Q90YJ5_site1	ptprfa	Receptor	100	22,0	2,3	0,0	0,0	0,0	0,0	11,3	0,7	0,0	0,0	0,0	0,0	0,07	Not detected
Q90YJ5_site2	ptprfa	Receptor	72	12,3	1,8	0,3	0,3	0,0	0,0	11,0	1,5	0,3	0,3	0,0	0,0	0,63	Not detected
F1Q4V8	ptprga	Receptor	42	8,7	1,5	0,0	0,0	0,0	0,0	5,3	0,3	0,0	0,0	0,0	0,0	0,20	Not detected
E7F9R2	ptprh	Receptor	159	22,0	1,5	0,0	0,0	0,0	0,0	19,3	2,0	11,7	1,5	0,0	0,0	0,38	0,02
B6HY54	ptprja	Receptor	52	8,0	0,6	1,0	0,0	0,0	0,0	8,3	0,9	0,0	0,0	0,0	0,0	0,83	Not detected
X1WCM2	ptprjb.1	Receptor	21	4,0	1,2	0,0	0,0	0,0	0,0	3,0	1,0	0,0	0,0	0,0	0,0	0,68	Not detected
X1WF45	ptprjb.2	Receptor	6	1,0	0,0	0,0	0,0	0,0	0,0	0,7	0,3	0,3	0,3	0,0	0,0	0,42	0,42
X1WD65	ptprk	Receptor	90	16,7	0,9	0,0	0,0	0,0	0,0	13,0	0,6	0,3	0,3	0,0	0,0	0,05	0,42
AOAOR4IA95	ptpro	Receptor	52	8,3	0,9	0,3	0,3	0,0	0,0	8,3	1,2	0,3	0,3	0,0	0,0	1,00	Not detected
Q90YJ4_site1	ptprsa	Receptor	21	4,0	0,6	0,0	0,0	0,0	0,0	2,7	0,3	0,3	0,3	0,0	0,0	0,06	0,42
Q90YJ4_site2	ptprsa	Receptor	45	8,0	1,0	0,0	0,0	0,0	0,0	7,0	1,7	0,0	0,0	0,0	0,0	0,42	Not detected
AOAOR4ITF5 (C7U125)	ptprub	Receptor	13	2,3	0,3	0,0	0,0	0,0	0,0	2,0	0,0	0,0	0,0	0,0	0,0	0,42	Not detected
X1WET2	ptprz1a	Receptor	16	3,7	0,3	0,0	0,0	0,0	0,0	1,3	0,3	0,3	0,3	0,0	0,0	0,07	0,42
B8A514	ptprz1b	Receptor	104	21,7	2,4	0,0	0,0	0,0	0,0	12,7	1,5	0,3	0,3	0,0	0,0	0,12	0,42
C7U142	ptpn1	Non-receptor	142	22,0	2,1	0,7	0,7	0,3	0,3	20,7	1,5	3,7	0,7	0,0	0,0	0,73	0,04
C7U151	ptpn11a	Non-receptor	112	14,7	1,5	0,7	0,3	0,3	0,3	11,3	0,9	10,3	0,9	0,0	0,0	0,27	0,00
C7U120	ptpn11b	Non-receptor	59	7,3	0,3	0,0	0,0	0,0	0,0	5,0	0,6	7,3	0,7	0,0	0,0	0,07	0,01
Q6PEI4	ptpn12	Non-receptor	71	13,0	1,2	0,0	0,0	0,0	0,0	10,7	1,5	0,0	0,0	0,0	0,0	0,46	Not detected
C7U124	ptpn13	Non-receptor	64	13,3	2,0	1,0	0,6	0,0	0,0	6,7	0,7	0,3	0,3	0,0	0,0	0,12	0,53
F1QIX3	ptpn20	Non-receptor	38	7,0	1,0	0,0	0,0	0,0	0,0	5,7	1,2	0,0	0,0	0,0	0,0	0,06	Not detected
F1Q6T9	ptpn21	Non-receptor	29	4,0	0,6	1,0	0,6	0,0	0,0	4,3	1,2	0,3	0,3	0,0	0,0	0,67	0,42
C7U128	ptpn22	Non-receptor	13	3,0	0,0	0,0	0,0	0,0	0,0	1,0	0,6	0,3	0,3	0,0	0,0	0,07	0,42
F1R1D1	ptpn23a	Non-receptor	138	24,7	2,0	0,0	0,0	0,0	0,0	21,0	1,5	0,3	0,3	0,0	0,0	0,39	0,42
F1QXQ5 (F1QGX6)	ptpn2a	Non-receptor	86	15,7	0,7	0,3	0,3	0,0	0,0	9,7	0,9	3,0	0,6	0,0	0,0	0,06	0,04
Q6NY86	ptpn2b	Non-receptor	159	32,7	2,8	0,3	0,3	0,0	0,0	19,7	3,3	0,0	0,0	0,3	0,3	0,16	0,42
F1QLN8	ptpn3	Non-receptor	97	17,0	1,5	0,7	0,3	0,0	0,0	14,3	2,3	0,3	0,3	0,0	0,0	0,37	0,42
C7U127	ptpn4a	Non-receptor	19	3,3	0,3	0,0	0,0	0,0	0,0	3,0	1,2	0,0	0,0	0,0	0,0	0,81	Not detected
C7U113	ptpn4b	Non-receptor	156	27,7	1,5	0,0	0,0	0,0	0,0	22,3	0,7	5,7	0,3	0,0	0,0	0,09	0,00
C7U118	ptpn6	Non-receptor	82	15,7	1,5	0,7	0,7	0,3	0,3	10,3	0,3	0,0	0,0	0,3	0,3	0,09	0,42
X1WV4	ptpn9a	Non-receptor	170	28,7	1,9	0,3	0,3	0,0	0,0	22,3	1,5	5,3	0,9	0,0	0,0	0,18	0,01
F1QT14	ptpn9b	Non-receptor	86	16,3	0,9	0,7	0,3	0,0	0,0	11,3	1,5	0,3	0,3	0,0	0,0	0,13	0,42

