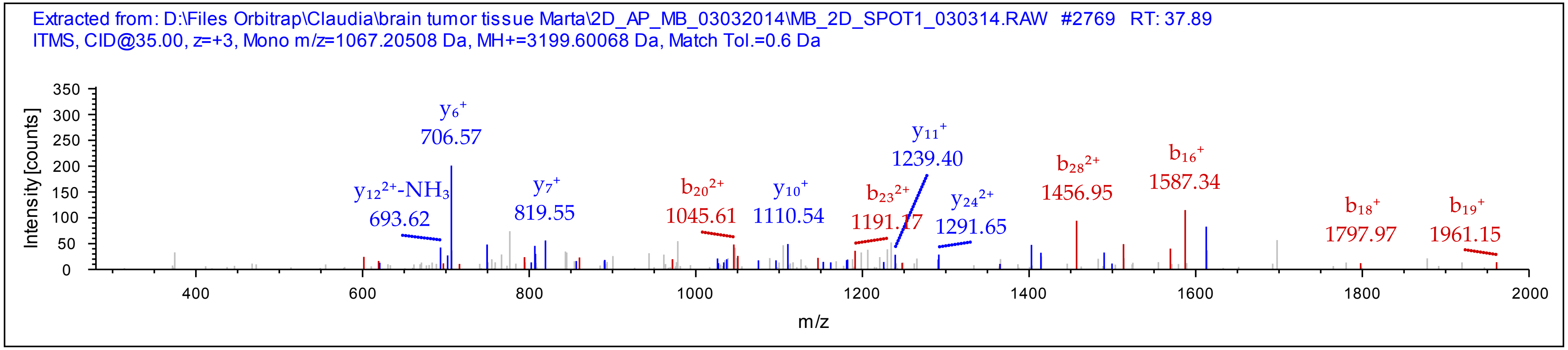
Spot #	Uniprot Accession Number	Description	MW^{a} [kDa]	pI ^{a}	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*
1	P60709	Actin, cytoplasmic 1	41.7	5.3	491.70	55.47 %	7	20	MB, PA	NS	NS

Sequence: TTGIVMDSGDGVTHTVPIYEGYALPHAILR, M6-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 1067.20508 Da (-2.89 mmu/-2.71 ppm), MH+: 3199.60068 Da, RT: 37.89 min,
Identified with: Sequest HT (v1.3); XCorr:4.94, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (2):
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]

#1	b^{+}	b^{2+}	b^{3+}	Seq.	y^{+}	y^{2+}	y^{3+}	#2
1	102.05496	51.53112	34.68984	T				30
2	203.10264	102.05496	68.37240	T	3098.56168	1549.78448	1033.52541	29
3	260.12411	130.56569	87.37955	G	2997.51400	1499.26064	999.84285	28
4	373.20818	187.10773	125.07424	I	2940.49253	1470.74990	980.83569	27
5	472.27660	236.64194	158.09705	V	2827.40846	1414.20787	943.14100	26
6	619.31201	310.15964	207.10885	M-Oxidation	2728.34004	1364.67366	910.11820	25
7	734.33896	367.67312	245.45117	D	2581.30462	1291.15595	861.10639	24
8	821.37099	411.18913	274.46185	S	2466.27767	1233.64247	822.76407	23
9	878.39246	439.69987	293.46900	G	2379.24564	1190.12646	793.75340	22
10	993.41941	497.21334	331.81132	D	2322.22417	1161.61572	774.74624	21
11	1050.44088	525.72408	350.81848	G	2207.19722	1104.10225	736.40392	20
12	1149.50930	575.25829	383.84128	V	2150.17575	1075.59151	717.39677	19
13	1250.55698	625.78213	417.52384	T	2051.10733	1026.05730	684.37396	18
14	1387.61589	694.31158	463.21015	H	1950.05965	975.53346	650.69140	17
15	1488.66357	744.83542	496.89271	T	1813.00074	907.00401	605.00510	16
16	1587.73199	794.36963	529.91551	V	1711.95306	856.48017	571.32254	15
17	1684.78476	842.89602	562.26644	P	1612.88464	806.94596	538.29973	14
18	1797.86883	899.43805	599.96113	I	1515.83187	758.41957	505.94881	13
19	1960.93215	980.96971	654.31557	Y	1402.74780	701.87754	468.25412	12
20	2089.97475	1045.49101	697.32977	E	1239.68448	620.34588	413.89968	11
21	2146.99622	1074.00175	716.33692	G	1110.64188	555.82458	370.88548	10
22	2310.05954	1155.53341	770.69136	Y	1053.62041	527.31384	351.87832	9
23	2381.09666	1191.05197	794.37040	A	890.55709	445.78218	297.52388	8
24	2494.18073	1247.59400	832.06509	L	819.51997	410.26362	273.84484	7

25	2591.23350	1296.12039	864.41602	P	706.43590	353.72159	236.15015	6
26	2728.29241	1364.64984	910.10232	H	609.38313	305.19520	203.79923	5
27	2799.32953	1400.16840	933.78136	A	472.32422	236.66575	158.11292	4
28	2912.41360	1456.71044	971.47605	I	401.28710	201.14719	134.43388	3
29	3025.49767	1513.25247	1009.17074	L	288.20303	144.60515	96.73919	2
30				R	175.11896	88.06312	59.04450	1

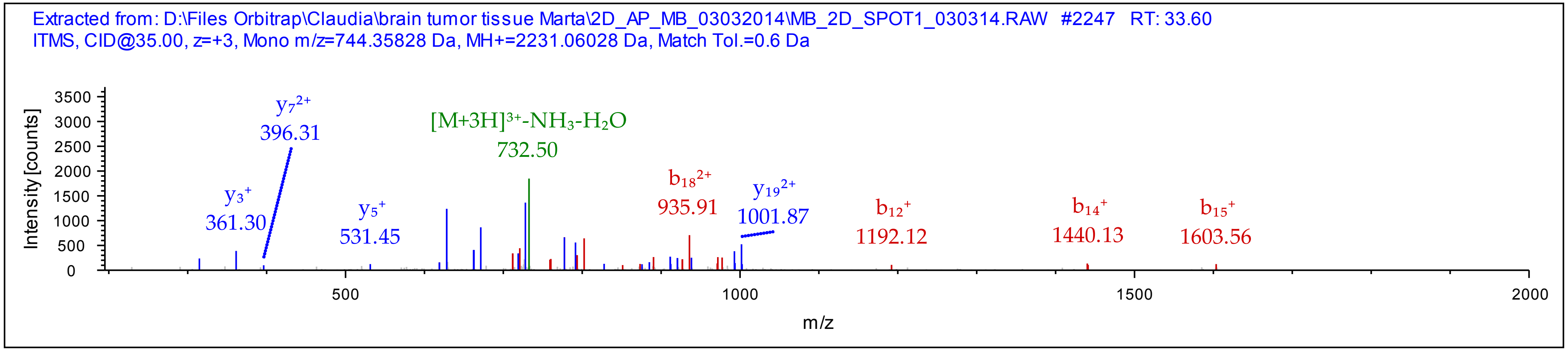

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT1_030314.RAW #2769 RT: 37.89
ITMS, CID@35.00, z=+3, Mono m/z=1067.20508 Da, MH+=3199.60068 Da, Match Tol.=0.6 Da

Sequence: DLYANTVLSGGTTMYPGIADR, M14-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 744.35828 Da (-1.56 mmu/-2.1 ppm), MH+: 2231.06028 Da, RT: 33.60 min,
Identified with: Sequest HT (v1.3); XCorr:4.85, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H$_2$O; b-NH$_3$; y; y-H$_2$O; y-NH$_3$

Protein references (2):
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]

#1	**b^{+}**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^{+}**	**y^{2+}**	**y^{3+}**
1	116.03423	58.52075	39.34959	D			
2	229.11830	115.06279	77.04428	L	2116.03802	1058.52265	706.01752
3	392.18162	196.59445	131.39872	Y	2002.95395	1001.98061	668.32283
4	463.21874	232.11301	155.07776	A	1839.89063	920.44895	613.96839
5	577.26167	289.13447	193.09207	N	1768.85351	884.93039	590.28935
6	678.30935	339.65831	226.77463	T	1654.81058	827.90893	552.27504
7	777.37777	389.19252	259.79744	V	1553.76290	777.38509	518.59248
8	890.46184	445.73456	297.49213	L	1454.69448	727.85088	485.56968
9	977.49387	489.25057	326.50281	S	1341.61041	671.30884	447.87499

10	1034.51534	517.76131	345.50996	G	1254.57838	627.79283	418.86431
11	1091.53681	546.27204	364.51712	G	1197.55691	599.28209	399.85715
12	1192.58449	596.79588	398.19968	T	1140.53544	570.77136	380.85000
13	1293.63217	647.31972	431.88224	T	1039.48776	520.24752	347.16744
14	1440.66758	720.83743	480.89404	M-Oxidation	938.44008	469.72368	313.48488
15	1603.73090	802.36909	535.24848	Y	791.40466	396.20597	264.47307
16	1700.78367	850.89547	567.59941	P	628.34134	314.67431	210.11863
17	1757.80514	879.40621	586.60656	G	531.28857	266.14792	177.76771
18	1870.88921	935.94824	624.30125	I	474.26710	237.63719	158.76055
19	1941.92633	971.46680	647.98029	A	361.18303	181.09515	121.06586
20	2056.95328	1028.98028	686.32261	D	290.14591	145.57659	97.38682
21				R	175.11896	88.06312	59.04450

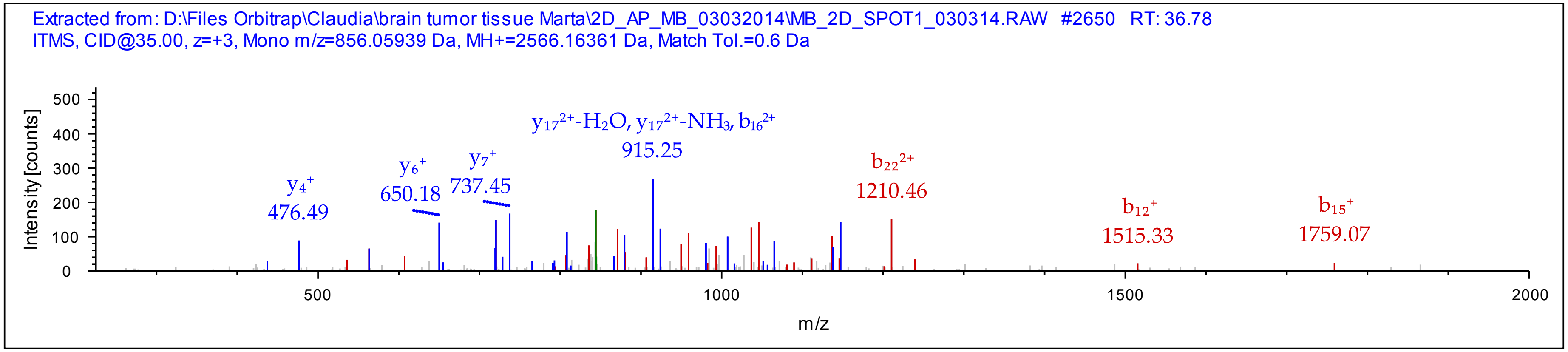


Sequence: LCYVALDFEQEMATAASSSSLEK, C2-Carbamidomethyl (57.02146 Da), M12-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 856.05939 Da (-1.75 mmu/-2.05 ppm), MH+: 2566.16361 Da, RT: 36.78 min,
Identified with: Sequest HT (v1.3); XCorr:4.43, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 - [POTEE_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**
1	114.09135	57.54931	38.70197	L			
2	274.12200	137.56464	92.04552	C-Carbamidomethyl	2453.08479	1227.04603	818.36645

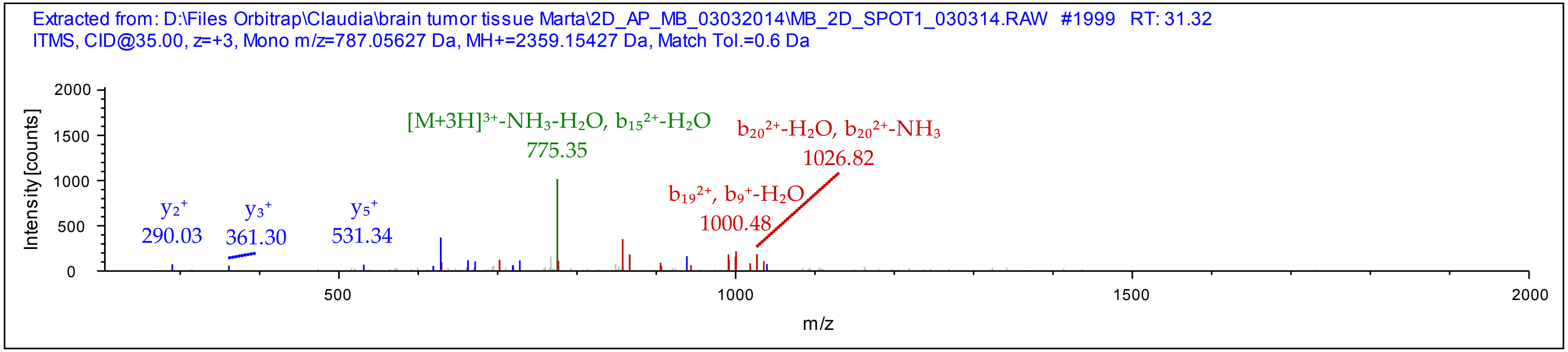
3	437.18532	219.09630	146.39996	Y	2293.05414	1147.03071	765.02290
4	536.25374	268.63051	179.42276	V	2129.99082	1065.49905	710.66846
5	607.29086	304.14907	203.10180	A	2030.92240	1015.96484	677.64565
6	720.37493	360.69110	240.79649	L	1959.88528	980.44628	653.96661
7	835.40188	418.20458	279.13881	D	1846.80121	923.90424	616.27192
8	982.47030	491.73879	328.16162	F	1731.77426	866.39077	577.92960
9	1111.51290	556.26009	371.17582	E	1584.70584	792.85656	528.90680
10	1239.57148	620.28938	413.86201	Q	1455.66324	728.33526	485.89260
11	1368.61408	684.81068	456.87621	E	1327.60466	664.30597	443.20640
12	1515.64950	758.32839	505.88802	M-Oxidation	1198.56206	599.78467	400.19220
13	1586.68662	793.84695	529.56706	A	1051.52664	526.26696	351.18040
14	1687.73430	844.37079	563.24962	T	980.48952	490.74840	327.50136
15	1758.77142	879.88935	586.92866	A	879.44184	440.22456	293.81880
16	1829.80854	915.40791	610.60770	A	808.40472	404.70600	270.13976
17	1916.84057	958.92392	639.61837	S	737.36760	369.18744	246.46072
18	2003.87260	1002.43994	668.62905	S	650.33557	325.67142	217.45004
19	2090.90463	1045.95595	697.63973	S	563.30354	282.15541	188.43936
20	2177.93666	1089.47197	726.65040	S	476.27151	238.63939	159.42869
21	2291.02073	1146.01400	764.34509	L	389.23948	195.12338	130.41801
22	2420.06333	1210.53530	807.35929	E	276.15541	138.58134	92.72332
23				K	147.11281	74.06004	49.70912


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT1_030314.RAW #2650 RT: 36.78
ITMS, CID@35.00, z=+3, Mono m/z=856.05939 Da, MH+=2566.16361 Da, Match Tol.=0.6 Da

Sequence: KDLYANTVLSGGTTMYPGIADR, M15-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 787.05627 Da (-1.89 mmu/-2.4 ppm), MH+: 2359.15427 Da, RT: 31.32 min,
Identified with: Sequest HT (v1.3); XCorr:4.09, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]

#1	**b^{+}**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^{+}**	**y^{2+}**	**y^{3+}**	**#2**
1	129.10225	65.05476	43.70560	K				22
2	244.12920	122.56824	82.04792	D	2231.06497	1116.03612	744.35984	21
3	357.21327	179.11027	119.74261	L	2116.03802	1058.52265	706.01752	20
4	520.27659	260.64193	174.09705	Y	2002.95395	1001.98061	668.32283	19
5	591.31371	296.16049	197.77609	A	1839.89063	920.44895	613.96839	18
6	705.35664	353.18196	235.79040	N	1768.85351	884.93039	590.28935	17
7	806.40432	403.70580	269.47296	T	1654.81058	827.90893	552.27504	16
8	905.47274	453.24001	302.49576	V	1553.76290	777.38509	518.59248	15
9	1018.55681	509.78204	340.19045	L	1454.69448	727.85088	485.56968	14
10	1105.58884	553.29806	369.20113	S	1341.61041	671.30884	447.87499	13
11	1162.61031	581.80879	388.20829	G	1254.57838	627.79283	418.86431	12
12	1219.63178	610.31953	407.21544	G	1197.55691	599.28209	399.85715	11
13	1320.67946	660.84337	440.89800	T	1140.53544	570.77136	380.85000	10
14	1421.72714	711.36721	474.58056	T	1039.48776	520.24752	347.16744	9
15	1568.76255	784.88491	523.59237	M-Oxidation	938.44008	469.72368	313.48488	8
16	1731.82587	866.41657	577.94681	Y	791.40466	396.20597	264.47307	7
17	1828.87864	914.94296	610.29773	P	628.34134	314.67431	210.11863	6
18	1885.90011	943.45369	629.30489	G	531.28857	266.14792	177.76771	5
19	1998.98418	999.99573	666.99958	I	474.26710	237.63719	158.76055	4
20	2070.02130	1035.51429	690.67862	A	361.18303	181.09515	121.06586	3
21	2185.04825	1093.02776	729.02093	D	290.14591	145.57659	97.38682	2
22				R	175.11896	88.06312	59.04450	1

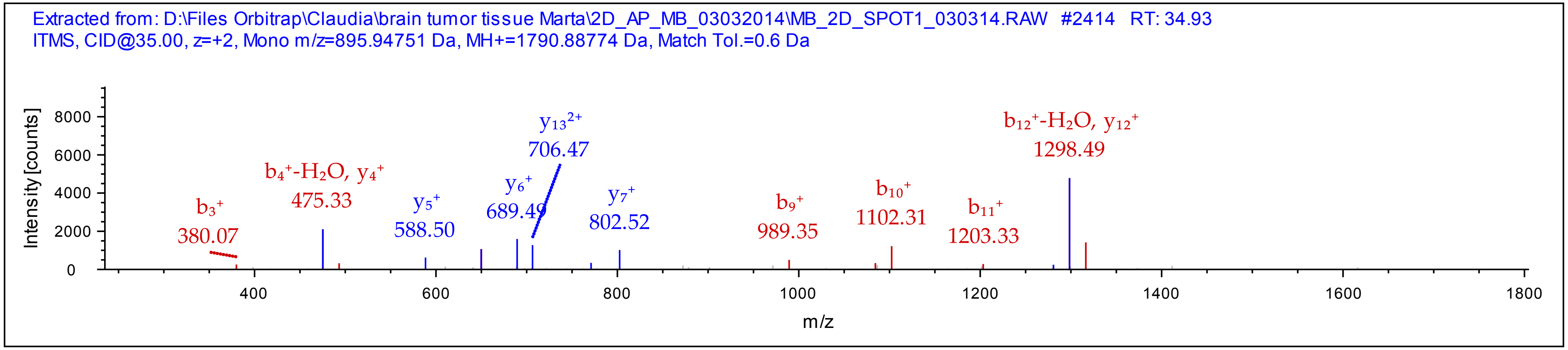


Sequence: SYELPDGQVITIGNER, Charge: +2, Monoisotopic m/z: 895.94751 Da (-2.13 mmu/-2.37 ppm), MH+: 1790.88774 Da, RT: 34.93 min,
Identified with: Sequest HT (v1.3); XCorr:3.75, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (10):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 - [ACTBL_HUMAN]
- Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1 - [ACTBM_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]
- POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 - [POTEE_HUMAN]
- POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2 - [POTEF_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	88.03931	44.52329	S			16
2	251.10263	126.05495	Y	1703.85996	852.43362	15
3	380.14523	190.57625	E	1540.79664	770.90196	14
4	493.22930	247.11829	L	1411.75404	706.38066	13
5	590.28207	295.64467	P	1298.66997	649.83862	12
6	705.30902	353.15815	D	1201.61720	601.31224	11
7	762.33049	381.66888	G	1086.59025	543.79876	10
8	890.38907	445.69817	Q	1029.56878	515.28803	9
9	989.45749	495.23238	V	901.51020	451.25874	8
10	1102.54156	551.77442	I	802.44178	401.72453	7

11	1203.58924	602.29826	T	689.35771	345.18249	6
12	1316.67331	658.84029	I	588.31003	294.65865	5
13	1373.69478	687.35103	G	475.22596	238.11662	4
14	1487.73771	744.37249	N	418.20449	209.60588	3
15	1616.78031	808.89379	E	304.16156	152.58442	2
16			R	175.11896	88.06312	1

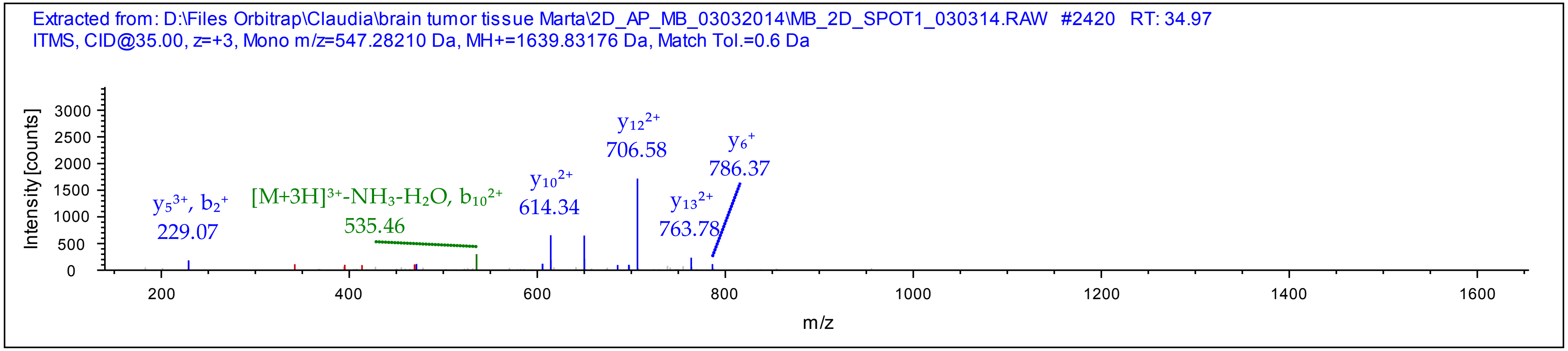


Sequence: LDLAGRDLTDYLMK, M13-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 547.28210 Da (-1.44 mmu/-2.63 ppm), MH+: 1639.83176 Da, RT: 34.97 min,
Identified with: Sequest HT (v1.3); XCorr:3.30, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 - [ACTBL_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**
1	114.09135	57.54931	38.70197	L			
2	229.11830	115.06279	77.04428	D	1526.75200	763.87964	509.58885
3	342.20237	171.60482	114.73897	L	1411.72505	706.36616	471.24653
4	413.23949	207.12338	138.41801	A	1298.64098	649.82413	433.55184

5	470.26096	235.63412	157.42517	G	1227.60386	614.30557	409.87280
6	626.36208	313.68468	209.45888	R	1170.58239	585.79483	390.86565
7	741.38903	371.19815	247.80119	D	1014.48127	507.74427	338.83194
8	854.47310	427.74019	285.49588	L	899.45432	450.23080	300.48962
9	955.52078	478.26403	319.17844	T	786.37025	393.68876	262.79493
10	1070.54773	535.77750	357.52076	D	685.32257	343.16492	229.11237
11	1233.61105	617.30916	411.87520	Y	570.29562	285.65145	190.77006
12	1346.69512	673.85120	449.56989	L	407.23230	204.11979	136.41562
13	1493.73053	747.36890	498.58169	M-Oxidation	294.14823	147.57775	98.72093
14				K	147.11281	74.06004	49.70912

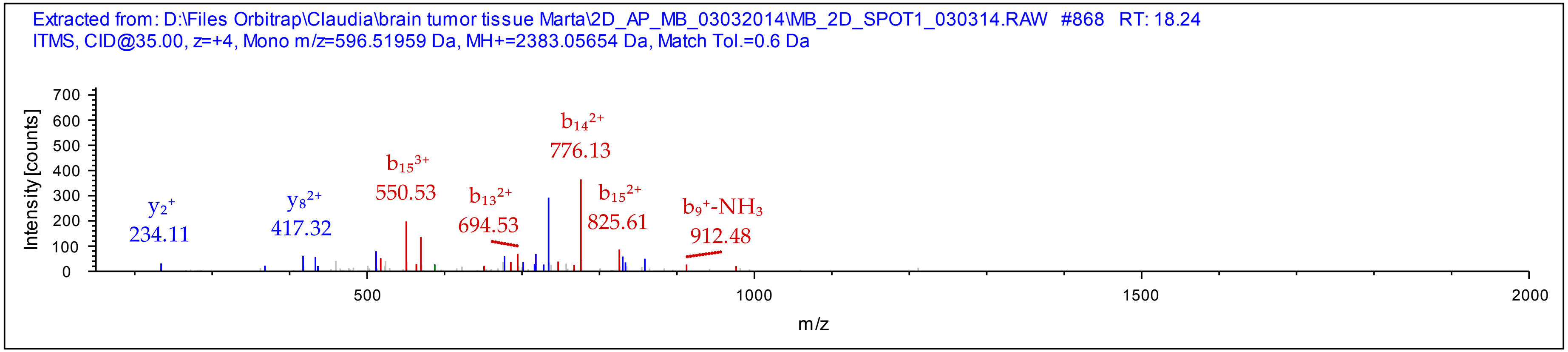


Sequence: HQGVMVGMGQKDSYVGDEAQSK, M5-Oxidation (15.99492 Da), M8-Oxidation (15.99492 Da)
Charge: +4, Monoisotopic m/z: 596.51959 Da (-2.22 mmu/-3.72 ppm), MH+: 2383.05654 Da, RT: 18.24 min,
Identified with: Sequest HT (v1.3); XCorr:3.22, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]

#1	**b^{+}**	**b^{2+}**	**b^{3+}**	**b^{4+}**	**Seq.**	**y^{+}**	**y^{2+}**	**y^{3+}**	**y^{4+}**
1	138.06619	69.53673	46.69358	35.27200	H				
2	266.12477	133.56602	89.37977	67.28665	Q	2246.00649	1123.50688	749.34035	562.25708

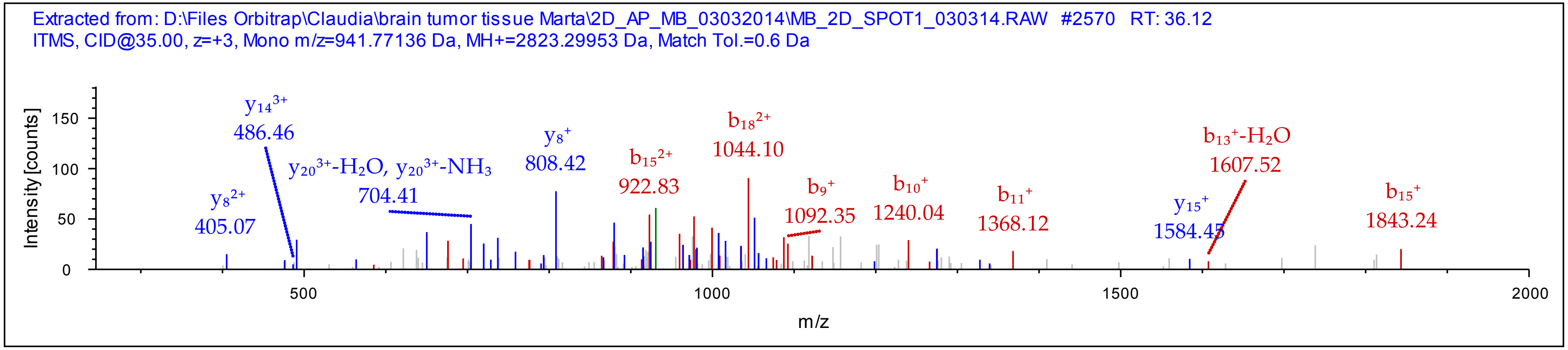
3	323.14624	162.07676	108.38693	81.54202	G	2117.94791	1059.47759	706.65415	530.24244
4	422.21466	211.61097	141.40974	106.30912	V	2060.92644	1030.96686	687.64700	515.98707
5	569.25007	285.12867	190.42154	143.06798	M-Oxidation	1961.85802	981.43265	654.62419	491.21996
6	668.31849	334.66288	223.44435	167.83508	V	1814.82261	907.91494	605.61239	454.46111
7	725.33996	363.17362	242.45150	182.09045	G	1715.75419	858.38073	572.58958	429.69400
8	872.37538	436.69133	291.46331	218.84930	M-Oxidation	1658.73272	829.87000	553.58242	415.43864
9	929.39685	465.20206	310.47047	233.10467	G	1511.69730	756.35229	504.57062	378.67978
10	1057.45543	529.23135	353.15666	265.11931	Q	1454.67583	727.84155	485.56346	364.42442
11	1185.55040	593.27884	395.85498	297.14306	K	1326.61725	663.81226	442.87727	332.40977
12	1300.57735	650.79231	434.19730	325.89979	D	1198.52228	599.76478	400.17894	300.38603
13	1387.60938	694.30833	463.20798	347.65780	S	1083.49533	542.25130	361.83663	271.62929
14	1550.67270	775.83999	517.56242	388.42363	Y	996.46330	498.73529	332.82595	249.87128
15	1649.74112	825.37420	550.58522	413.19074	V	833.39998	417.20363	278.47151	209.10545
16	1706.76259	853.88493	569.59238	427.44610	G	734.33156	367.66942	245.44870	184.33835
17	1821.78954	911.39841	607.93470	456.20284	D	677.31009	339.15868	226.44155	170.08298
18	1950.83214	975.91971	650.94890	488.46349	E	562.28314	281.64521	188.09923	141.32624
19	2021.86926	1011.43827	674.62794	506.22277	A	433.24054	217.12391	145.08503	109.06559
20	2149.92784	1075.46756	717.31413	538.23742	Q	362.20342	181.60535	121.40599	91.30631
21	2236.95987	1118.98357	746.32481	559.99542	S	234.14484	117.57606	78.71980	59.29167
22					K	147.11281	74.06004	49.70912	37.53366



Sequence: EKLCYVALDFEQEMATAASSSSLEK, C4-Carbamidomethyl (57.02146 Da), M14-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 941.77136 Da (-2.3 mmu/-2.44 ppm), MH+: 2823.29953 Da, RT: 36.12 min,
Identified with: Sequest HT (v1.3); XCorr:3.01, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 - [POTEE_HUMAN]

#1	**b^{+}**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^{+}**	**y^{2+}**	**y^{3+}**	
1	130.04988	65.52858	44.02148	E				25
2	258.14485	129.57606	86.71980	K	2694.26383	1347.63555	898.75946	24
3	371.22892	186.11810	124.41449	L	2566.16886	1283.58807	856.06114	23
4	531.25957	266.13342	177.75804	C-Carbamidomethyl	2453.08479	1227.04603	818.36645	22
5	694.32289	347.66508	232.11248	Y	2293.05414	1147.03071	765.02290	21
6	793.39131	397.19929	265.13529	V	2129.99082	1065.49905	710.66846	20
7	864.42843	432.71785	288.81433	A	2030.92240	1015.96484	677.64565	19
8	977.51250	489.25989	326.50902	L	1959.88528	980.44628	653.96661	18
9	1092.53945	546.77336	364.85133	D	1846.80121	923.90424	616.27192	17
10	1239.60787	620.30757	413.87414	F	1731.77426	866.39077	577.92960	16
11	1368.65047	684.82887	456.88834	E	1584.70584	792.85656	528.90680	15
12	1496.70905	748.85816	499.57453	Q	1455.66324	728.33526	485.89260	14
13	1625.75165	813.37946	542.58873	E	1327.60466	664.30597	443.20640	13
14	1772.78707	886.89717	591.60054	M-Oxidation	1198.56206	599.78467	400.19220	12
15	1843.82419	922.41573	615.27958	A	1051.52664	526.26696	351.18040	11
16	1944.87187	972.93957	648.96214	T	980.48952	490.74840	327.50136	10
17	2015.90899	1008.45813	672.64118	A	879.44184	440.22456	293.81880	9
18	2086.94611	1043.97669	696.32022	A	808.40472	404.70600	270.13976	8
19	2173.97814	1087.49271	725.33090	S	737.36760	369.18744	246.46072	7
20	2261.01017	1131.00872	754.34157	S	650.33557	325.67142	217.45004	6
21	2348.04220	1174.52474	783.35225	S	563.30354	282.15541	188.43936	5
22	2435.07423	1218.04075	812.36293	S	476.27151	238.63939	159.42869	4
23	2548.15830	1274.58279	850.05762	L	389.23948	195.12338	130.41801	3
24	2677.20090	1339.10409	893.07182	E	276.15541	138.58134	92.72332	2
25				K	147.11281	74.06004	49.70912	1

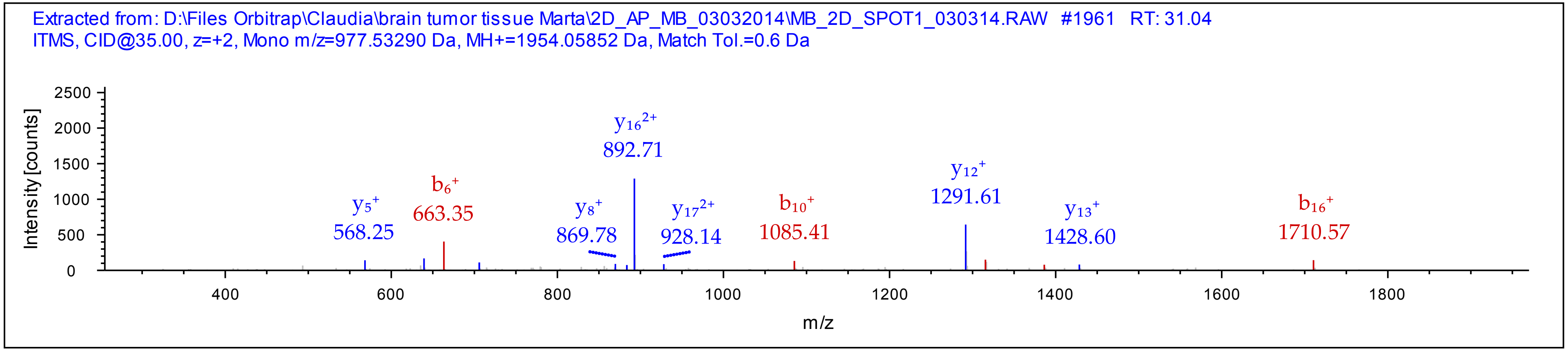

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT1_030314.RAW #2570 RT: 36.12
ITMS, CID@35.00, z=+3, Mono m/z=941.77136 Da, MH+=2823.29953 Da, Match Tol.=0.6 Da

Sequence: VAPEEHPVLLTEAPLNPK, Charge: +2, Monoisotopic m/z: 977.53290 Da (-2.99 mmu/-3.06 ppm),
MH+: 1954.05852 Da, RT: 31.04 min,
Identified with: Sequest HT (v1.3); XCorr:2.84, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	100.07570	50.54149	V			18
2	171.11282	86.06005	A	1854.99608	928.00168	17
3	268.16559	134.58643	P	1783.95896	892.48312	16
4	397.20819	199.10773	E	1686.90619	843.95673	15
5	526.25079	263.62903	E	1557.86359	779.43543	14
6	663.30970	332.15849	H	1428.82099	714.91413	13
7	760.36247	380.68487	P	1291.76208	646.38468	12
8	859.43089	430.21908	V	1194.70931	597.85829	11
9	972.51496	486.76112	L	1095.64089	548.32408	10
10	1085.59903	543.30315	L	982.55682	491.78205	9
11	1186.64671	593.82699	T	869.47275	435.24001	8
12	1315.68931	658.34829	E	768.42507	384.71617	7
13	1386.72643	693.86685	A	639.38247	320.19487	6

14	1483.77920	742.39324	P	568.34535	284.67631	5
15	1596.86327	798.93527	L	471.29258	236.14993	4
16	1710.90620	855.95674	N	358.20851	179.60789	3
17	1807.95897	904.48312	P	244.16558	122.58643	2
18			K	147.11281	74.06004	1

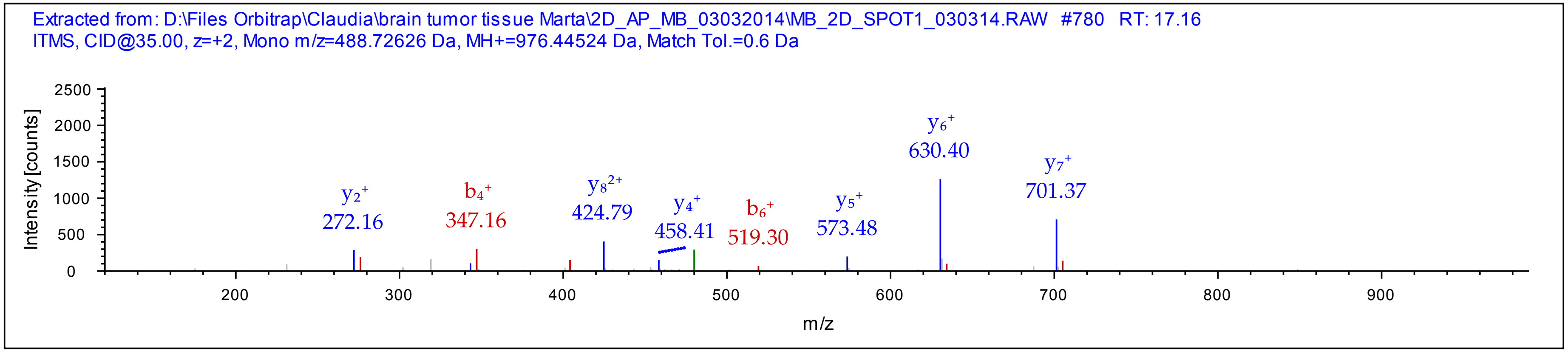

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT1_030314.RAW #1961 RT: 31.04
ITMS, CID@35.00, z=+2, Mono m/z=977.53290 Da, MH+=1954.05852 Da, Match Tol.=0.6 Da

Sequence: AGFAGDDAPR, Charge: +2, Monoisotopic m/z: 488.72626 Da (-1.56 mmu/-3.19 ppm), MH+: 976.44524 Da, RT: 17.16 min,
Identified with: Sequest HT (v1.3); XCorr:2.81, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (10):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]
- POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 - [POTEE_HUMAN]
- POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2 - [POTEF_HUMAN]
- POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=3 SV=1 - [POTEI_HUMAN]
- POTE ankyrin domain family member J OS=Homo sapiens GN=POTEJ PE=3 SV=1 - [POTEJ_HUMAN]

#1	**b^{+}**	**b^{2+}**	**Seq.**	**y^{+}**	**y^{2+}**	**#2**
1	72.04440	36.52584	A			10
2	129.06587	65.03657	G	905.41123	453.20925	9
3	276.13429	138.57078	F	848.38976	424.69852	8

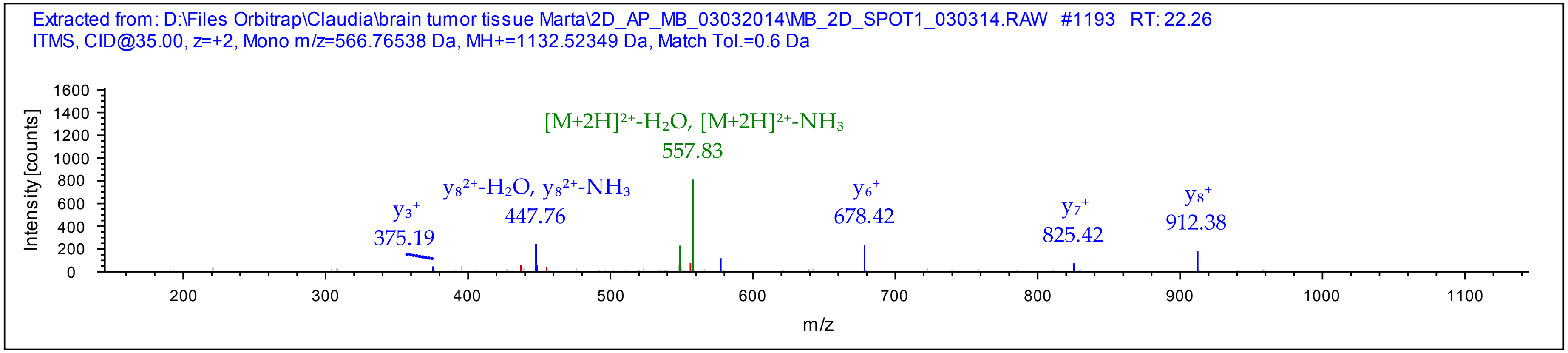
4	347.17141	174.08934	A	701.32134	351.16431	7
5	404.19288	202.60008	G	630.28422	315.64575	6
6	519.21983	260.11355	D	573.26275	287.13501	5
7	634.24678	317.62703	D	458.23580	229.62154	4
8	705.28390	353.14559	A	343.20885	172.10806	3
9	802.33667	401.67197	P	272.17173	136.58950	2
10			R	175.11896	88.06312	1



Sequence: GYSFTTTAER, Charge: +2, Monoisotopic m/z: 566.76538 Da (-1.74 mmu/-3.07 ppm), MH+: 1132.52349 Da, RT: 22.26 min,
Identified with: Sequest HT (v1.3); XCorr:2.77, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3
Protein references (2):
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]

#1	**b$^+$**	**b^{2+}**	**Seq.**	**y$^+$**	**y^{2+}**	**#2**
1	58.02875	29.51801	G			10
2	221.09207	111.04967	Y	1075.50549	538.25638	9
3	308.12410	154.56569	S	912.44217	456.72472	8
4	455.19252	228.09990	F	825.41014	413.20871	7
5	556.24020	278.62374	T	678.34172	339.67450	6
6	657.28788	329.14758	T	577.29404	289.15066	5
7	758.33556	379.67142	T	476.24636	238.62682	4
8	829.37268	415.18998	A	375.19868	188.10298	3
9	958.41528	479.71128	E	304.16156	152.58442	2

10 R 175.11896 88.06312 1

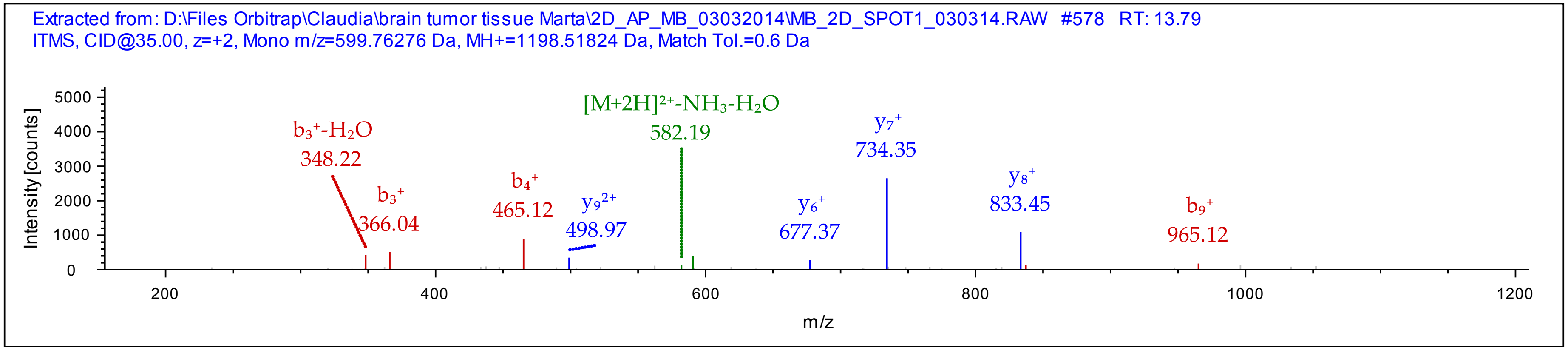


Sequence: DSYVGDEAQSK, Charge: +2, Monoisotopic m/z: 599.76276 Da (-2.02 mmu/-3.38 ppm), MH+: 1198.51824 Da, RT: 13.79 min,
Identified with: Sequest HT (v1.3); XCorr:2.67, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]

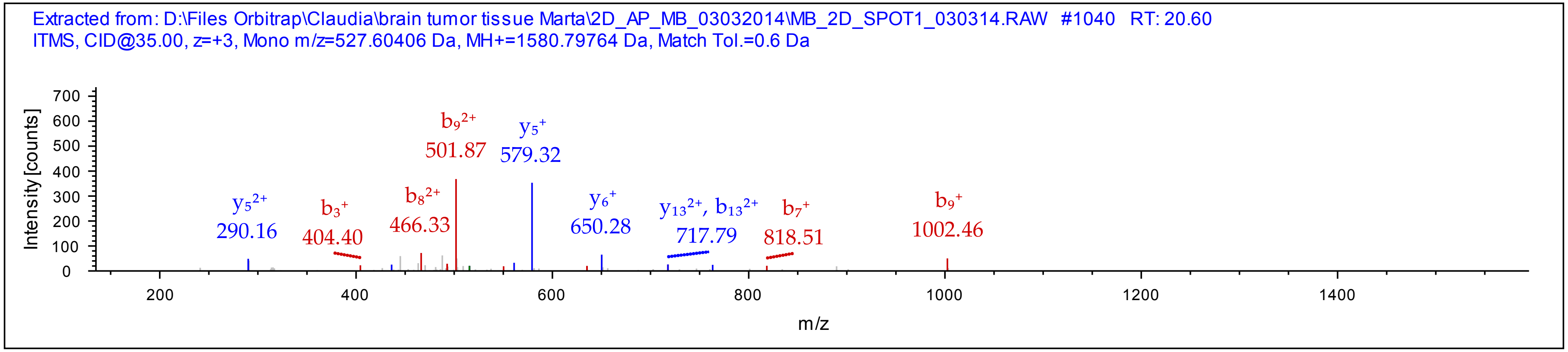
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**
1	116.03423	58.52075	D		
2	203.06626	102.03677	S	1083.49533	542.25130
3	366.12958	183.56843	Y	996.46330	498.73529
4	465.19800	233.10264	V	833.39998	417.20363
5	522.21947	261.61337	G	734.33156	367.66942
6	637.24642	319.12685	D	677.31009	339.15868
7	766.28902	383.64815	E	562.28314	281.64521
8	837.32614	419.16671	A	433.24054	217.12391
9	965.38472	483.19600	Q	362.20342	181.60535
10	1052.41675	526.71201	S	234.14484	117.57606
11			K	147.11281	74.06004



Sequence: MQKEITALAPSTMK, M1-Oxidation (15.99492 Da), M13-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 527.60406 Da (-1.57 mmu/-2.97 ppm), MH+: 1580.79764 Da, RT: 20.60 min,
Identified with: Sequest HT (v1.3); XCorr:2.50, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

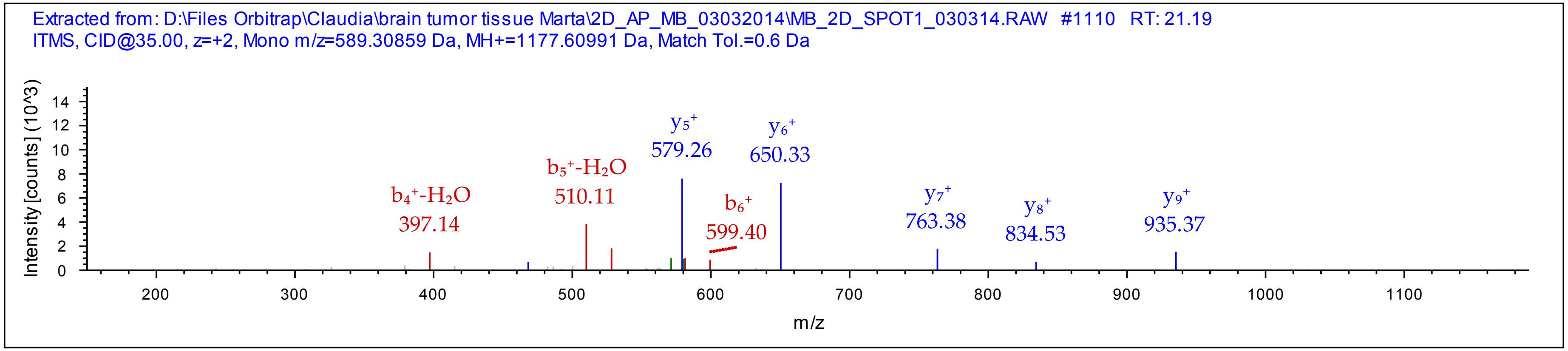
Protein references (6):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	148.04269	74.52498	50.01908	M-Oxidation				14
2	276.10127	138.55427	92.70527	Q	1433.76692	717.38710	478.59382	13
3	404.19624	202.60176	135.40360	K	1305.70834	653.35781	435.90763	12
4	533.23884	267.12306	178.41780	E	1177.61337	589.31032	393.20931	11
5	646.32291	323.66509	216.11249	I	1048.57077	524.78902	350.19511	10
6	747.37059	374.18893	249.79505	T	935.48670	468.24699	312.50042	9
7	818.40771	409.70749	273.47409	A	834.43902	417.72315	278.81786	8
8	931.49178	466.24953	311.16878	L	763.40190	382.20459	255.13882	7
9	1002.52890	501.76809	334.84782	A	650.31783	325.66255	217.44413	6
10	1099.58167	550.29447	367.19874	P	579.28071	290.14399	193.76509	5
11	1186.61370	593.81049	396.20942	S	482.22794	241.61761	161.41416	4
12	1287.66138	644.33433	429.89198	T	395.19591	198.10159	132.40349	3
13	1434.69680	717.85204	478.90378	M-Oxidation	294.14823	147.57775	98.72093	2
14				K	147.11281	74.06004	49.70912	1



Sequence: EITALAPSTMK, M10-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 589.30859 Da (-1.73 mmu/-2.93 ppm), MH+: 1177.60991 Da, RT: 21.19 min,
Identified with: Sequest HT (v1.3); XCorr:2.47, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3
Protein references (6):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]

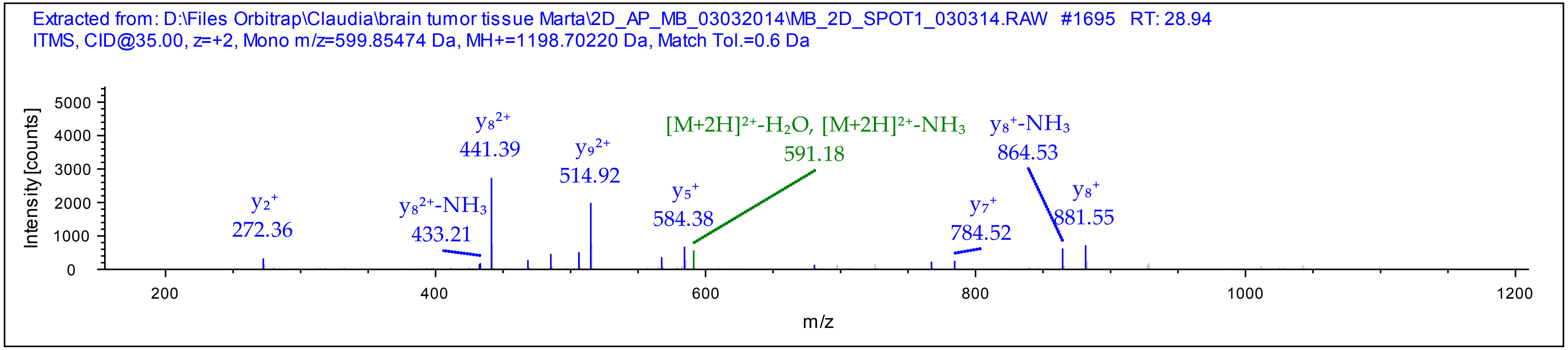
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	130.04988	65.52858	E			11
2	243.13395	122.07061	I	1048.57077	524.78902	10
3	344.18163	172.59445	T	935.48670	468.24699	9
4	415.21875	208.11301	A	834.43902	417.72315	8
5	528.30282	264.65505	L	763.40190	382.20459	7
6	599.33994	300.17361	A	650.31783	325.66255	6
7	696.39271	348.69999	P	579.28071	290.14399	5
8	783.42474	392.21601	S	482.22794	241.61761	4
9	884.47242	442.73985	T	395.19591	198.10159	3
10	1031.50783	516.25755	M-Oxidation	294.14823	147.57775	2
11			K	147.11281	74.06004	1



Sequence: AVFPSIVGRPR, Charge: +2, Monoisotopic m/z: 599.85474 Da (-1.69 mmu/-2.82 ppm), MH+: 1198.70220 Da, RT: 28.94 min,
Identified with: Sequest HT (v1.3); XCorr:2.20, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H$_2$O; b-NH$_3$; y; y-H$_2$O; y-NH$_3$
Protein references (9):

- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]
- POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 - [POTEE_HUMAN]
- POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2 - [POTEF_HUMAN]
- POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=3 SV=1 - [POTEI_HUMAN]

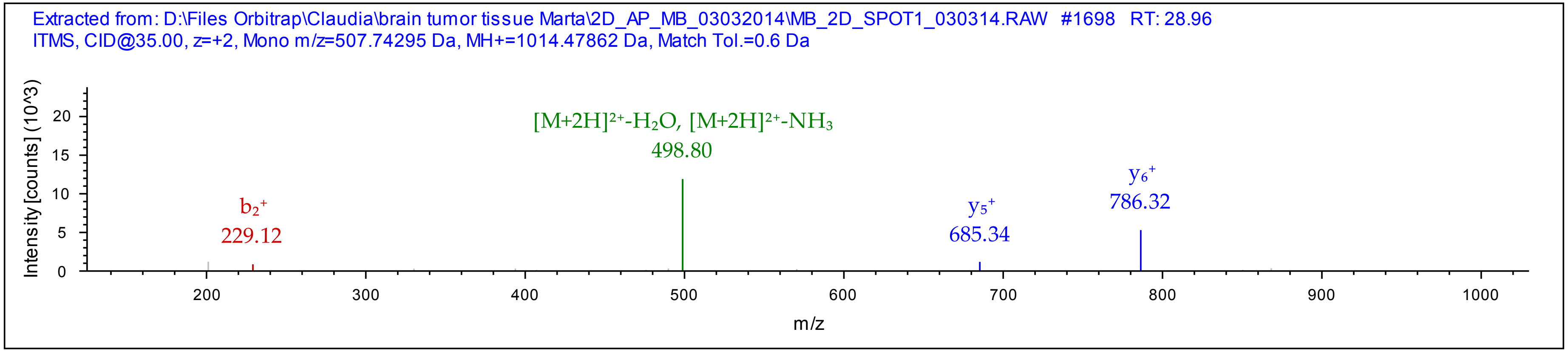
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	72.04440	36.52584	A			11
2	171.11282	86.06005	V	1127.66845	564.33786	10
3	318.18124	159.59426	F	1028.60003	514.80365	9
4	415.23401	208.12064	P	881.53161	441.26944	8
5	502.26604	251.63666	S	784.47884	392.74306	7
6	615.35011	308.17869	I	697.44681	349.22704	6
7	714.41853	357.71290	V	584.36274	292.68501	5
8	771.44000	386.22364	G	485.29432	243.15080	4
9	927.54112	464.27420	R	428.27285	214.64006	3
10	1024.59389	512.80058	P	272.17173	136.58950	2
11			R	175.11896	88.06312	1



Sequence: DLTDYLMK, M7-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 507.74295 Da (-1.32 mmu/-2.6 ppm), MH+: 1014.47862 Da, RT: 28.96 min,
Identified with: Sequest HT (v1.3); XCorr:2.05, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

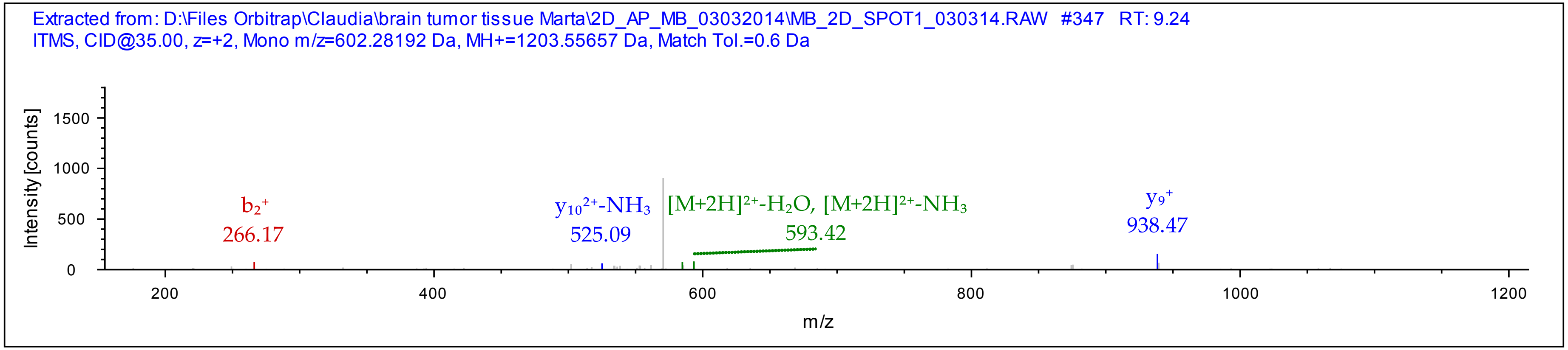
Protein references (7):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 - [ACTBL_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	116.03423	58.52075	D			8
2	229.11830	115.06279	L	899.45432	450.23080	7
3	330.16598	165.58663	T	786.37025	393.68876	6
4	445.19293	223.10010	D	685.32257	343.16492	5
5	608.25625	304.63176	Y	570.29562	285.65145	4
6	721.34032	361.17380	L	407.23230	204.11979	3
7	868.37573	434.69150	M-Oxidation	294.14823	147.57775	2
8			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT1_030314.RAW #1698 RT: 28.96
ITMS, CID@35.00, z=+2, Mono m/z=507.74295 Da, MH+=1014.47862 Da, Match Tol.=0.6 Da

Sequence: HQGVMVGMGQK, M5-Oxidation (15.99492 Da), M8-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 602.28192 Da (-2.2 mmu/-3.65 ppm), MH+: 1203.55657 Da, RT: 9.24 min,
Identified with: Sequest HT (v1.3); XCorr:1.93, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; $b\text{-}NH_3$; y; $y\text{-}NH_3$
Protein references (7):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 - [ACTBL_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]

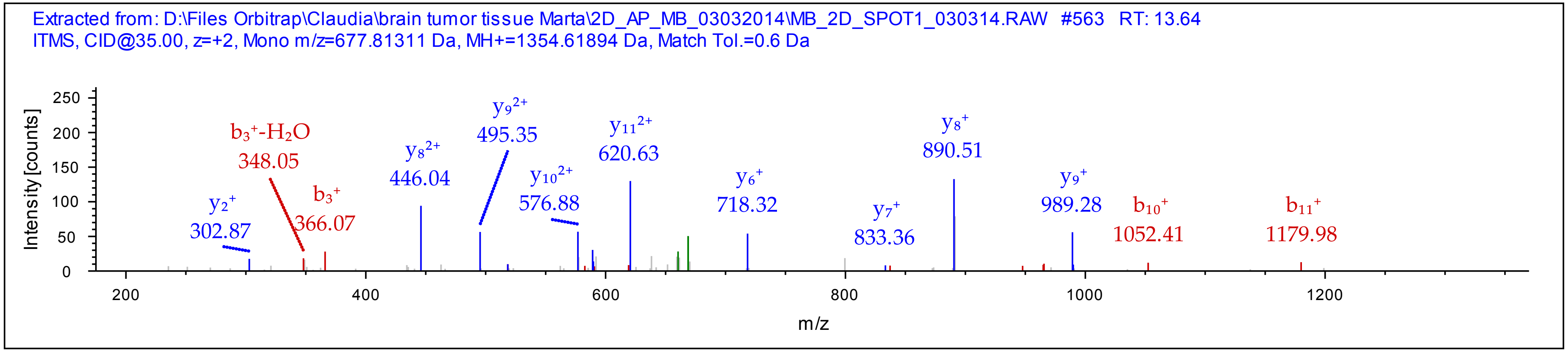
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	138.06619	69.53673	H			11
2	266.12477	133.56602	Q	1066.50205	533.75466	10
3	323.14624	162.07676	G	938.44347	469.72537	9
4	422.21466	211.61097	V	881.42200	441.21464	8
5	569.25007	285.12867	M-Oxidation	782.35358	391.68043	7
6	668.31849	334.66288	V	635.31817	318.16272	6
7	725.33996	363.17362	G	536.24975	268.62851	5
8	872.37538	436.69133	M-Oxidation	479.22828	240.11778	4
9	929.39685	465.20206	G	332.19286	166.60007	3
10	1057.45543	529.23135	Q	275.17139	138.08933	2
11			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT1_030314.RAW #347 RT: 9.24
ITMS, CID@35.00, z=+2, Mono m/z=602.28192 Da, MH+=1203.55657 Da, Match Tol.=0.6 Da

Sequence: DSYVGDEAQSKR, Charge: +2, Monoisotopic m/z: 677.81311 Da (-2.23 mmu/-3.29 ppm), MH+: 1354.61894 Da, RT: 13.64 min,
Identified with: Sequest HT (v1.3); XCorr:1.88, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (6):

- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]

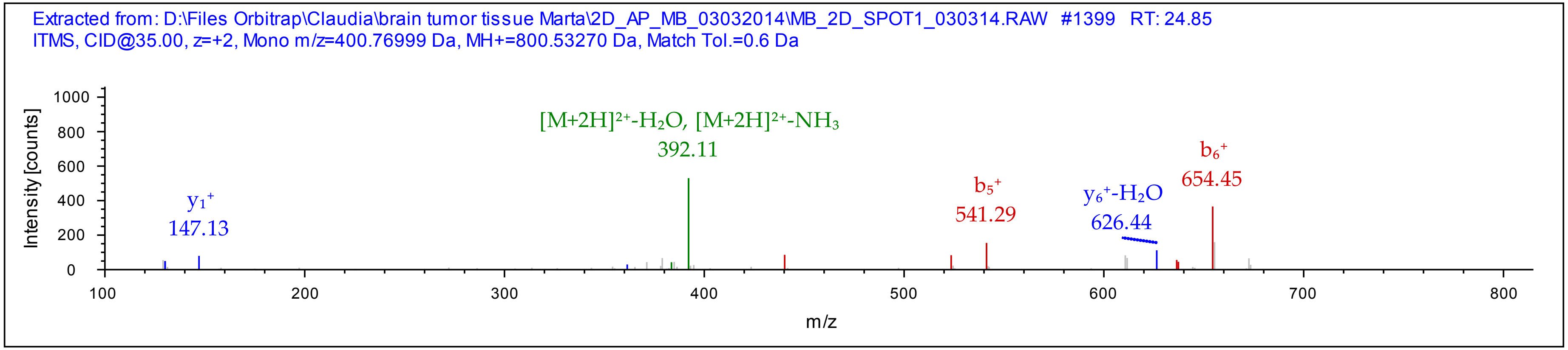
#1	**b^{+}**	**b^{2+}**	**Seq.**	**y^{+}**	**y^{2+}**	**#2**
1	116.03423	58.52075	D			12
2	203.06626	102.03677	S	1239.59645	620.30186	11
3	366.12958	183.56843	Y	1152.56442	576.78585	10
4	465.19800	233.10264	V	989.50110	495.25419	9
5	522.21947	261.61337	G	890.43268	445.71998	8
6	637.24642	319.12685	D	833.41121	417.20924	7
7	766.28902	383.64815	E	718.38426	359.69577	6
8	837.32614	419.16671	A	589.34166	295.17447	5
9	965.38472	483.19600	Q	518.30454	259.65591	4
10	1052.41675	526.71201	S	390.24596	195.62662	3
11	1180.51172	590.75950	K	303.21393	152.11060	2
12			R	175.11896	88.06312	1



Sequence: RGILTLK, Charge: +2, Monoisotopic m/z: 400.76999 Da (-1.3 mmu/-3.24 ppm), MH+: 800.53270 Da, RT: 24.85 min,
Identified with: Sequest HT (v1.3); XCorr:1.75, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (10):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]
- POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 - [POTEE_HUMAN]
- POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2 - [POTEF_HUMAN]
- POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=3 SV=1 - [POTEI_HUMAN]
- POTE ankyrin domain family member J OS=Homo sapiens GN=POTEJ PE=3 SV=1 - [POTEJ_HUMAN]

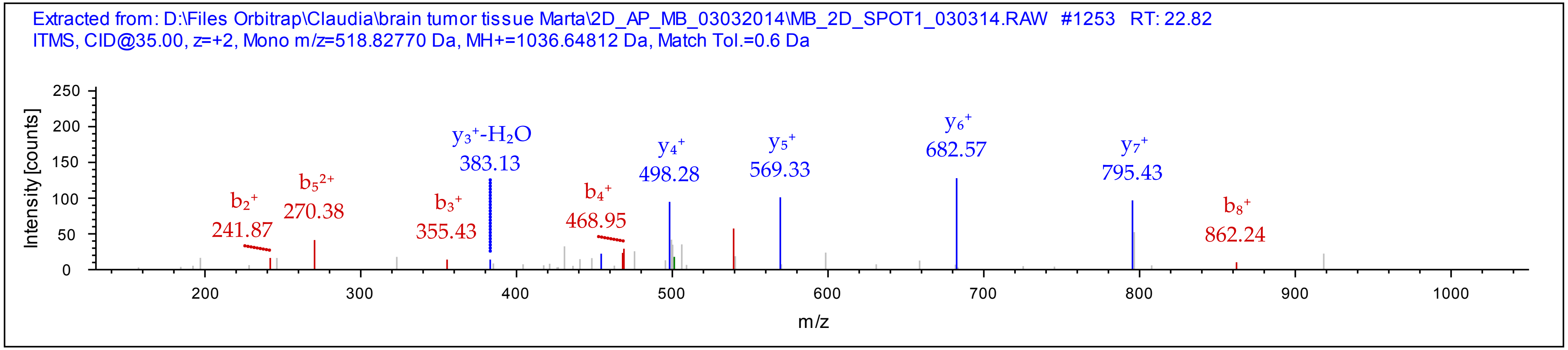
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	157.10840	79.05784	R			7
2	214.12987	107.56857	G	644.43417	322.72072	6
3	327.21394	164.11061	I	587.41270	294.20999	5
4	440.29801	220.65264	L	474.32863	237.66795	4
5	541.34569	271.17648	T	361.24456	181.12592	3
6	654.42976	327.71852	L	260.19688	130.60208	2
7			K	147.11281	74.06004	1



Sequence: IKIIAPPER, Charge: +2, Monoisotopic m/z: 518.82770 Da (-1.64 mmu/-3.17 ppm), MH+: 1036.64812 Da, RT: 22.82 min,
Identified with: Sequest HT (v1.3); XCorr:1.63, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 - [ACTBL_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	114.09135	57.54931	I			9
2	242.18632	121.59680	K	923.56733	462.28730	8
3	355.27039	178.13883	I	795.47236	398.23982	7
4	468.35446	234.68087	I	682.38829	341.69778	6
5	539.39158	270.19943	A	569.30422	285.15575	5
6	636.44435	318.72581	P	498.26710	249.63719	4
7	733.49712	367.25220	P	401.21433	201.11080	3
8	862.53972	431.77350	E	304.16156	152.58442	2
9			R	175.11896	88.06312	1



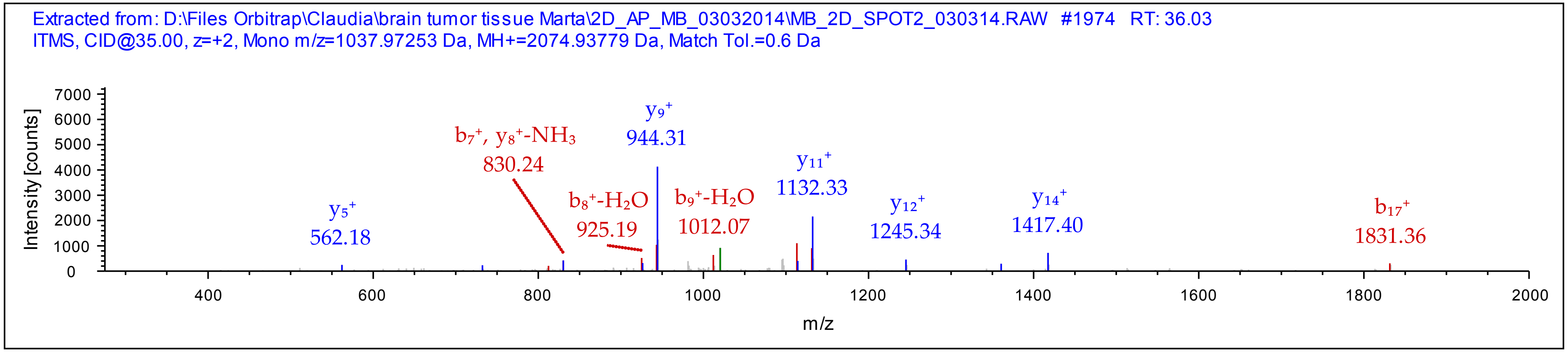
Spot #	Uniprot Accession Number	Description	MW[a] [kDa]	pI [a]	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*
2	P68871	Hemoglobin subunit beta	15.9	6.8	127.53	54.42%	7	7	MB, PA	NS	NS

Sequence: FFESFGDLSTPDAVMGNPK, M15-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 1037.97253 Da (-2.48 mmu/-2.39 ppm), MH+: 2074.93779 Da, RT: 36.03 min,
Identified with: Sequest HT (v1.3); XCorr:3.46, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	148.07570	74.54149	F			19
2	295.14412	148.07570	F	1927.87433	964.44080	18
3	424.18672	212.59700	E	1780.80591	890.90659	17
4	511.21875	256.11301	S	1651.76331	826.38529	16
5	658.28717	329.64722	F	1564.73128	782.86928	15
6	715.30864	358.15796	G	1417.66286	709.33507	14
7	830.33559	415.67143	D	1360.64139	680.82433	13
8	943.41966	472.21347	L	1245.61444	623.31086	12
9	1030.45169	515.72948	S	1132.53037	566.76882	11
10	1131.49937	566.25332	T	1045.49834	523.25281	10
11	1228.55214	614.77971	P	944.45066	472.72897	9

12	1343.57909	672.29318	D	847.39789	424.20258	8
13	1414.61621	707.81174	A	732.37094	366.68911	7
14	1513.68463	757.34595	V	661.33382	331.17055	6
15	1660.72004	830.86366	M-Oxidation	562.26540	281.63634	5
16	1717.74151	859.37439	G	415.22998	208.11863	4
17	1831.78444	916.39586	N	358.20851	179.60789	3
18	1928.83721	964.92224	P	244.16558	122.58643	2
19			K	147.11281	74.06004	1

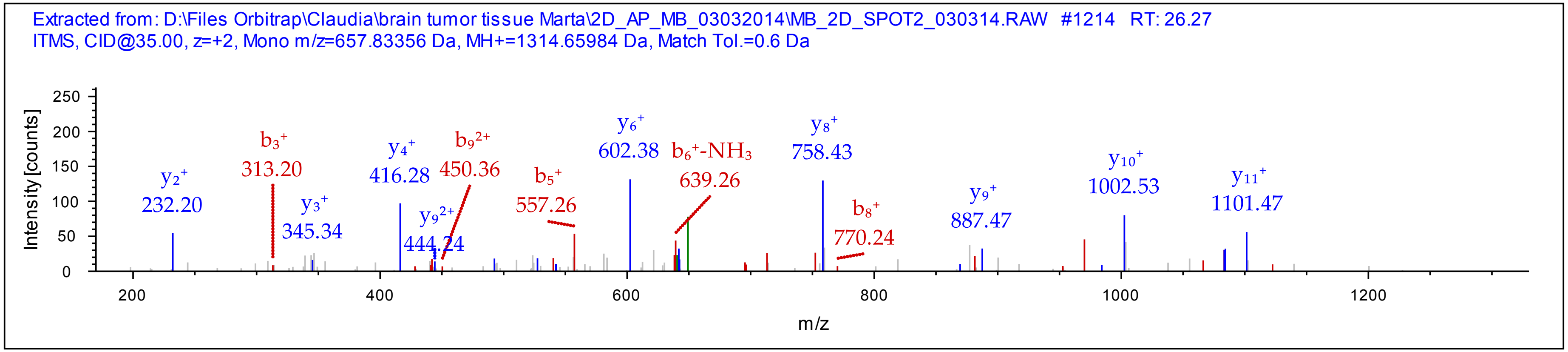


Sequence: VNVDEVGGEALGR, Charge: +2, Monoisotopic m/z: 657.83356 Da (-2.53 mmu/-3.85 ppm), MH+: 1314.65984 Da, RT: 26.27 min,
Identified with: Sequest HT (v1.3); XCorr:3.39, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	100.07570	50.54149	V			13
2	214.11863	107.56295	N	1215.59648	608.30188	12
3	313.18705	157.09716	V	1101.55355	551.28041	11
4	428.21400	214.61064	D	1002.48513	501.74620	10
5	557.25660	279.13194	E	887.45818	444.23273	9
6	656.32502	328.66615	V	758.41558	379.71143	8
7	713.34649	357.17688	G	659.34716	330.17722	7
8	770.36796	385.68762	G	602.32569	301.66648	6
9	899.41056	450.20892	E	545.30422	273.15575	5
10	970.44768	485.72748	A	416.26162	208.63445	4

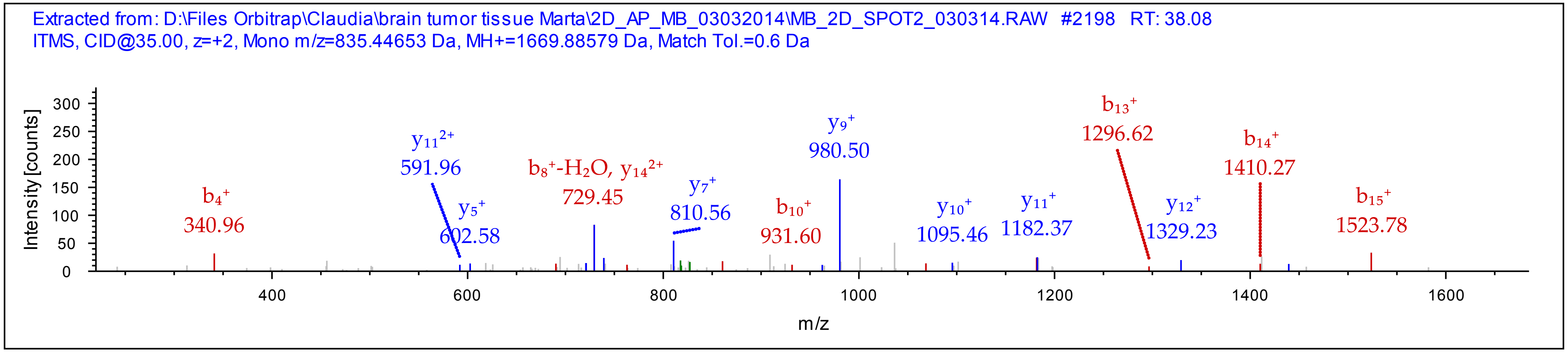
11	1083.53175	542.26951	L	345.22450	173.11589	3
12	1140.55322	570.78025	G	232.14043	116.57385	2
13			R	175.11896	88.06312	1



Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT2_030314.RAW #1214 RT: 26.27
ITMS, CID@35.00, z=+2, Mono m/z=657.83356 Da, MH+=1314.65984 Da, Match Tol.=0.6 Da

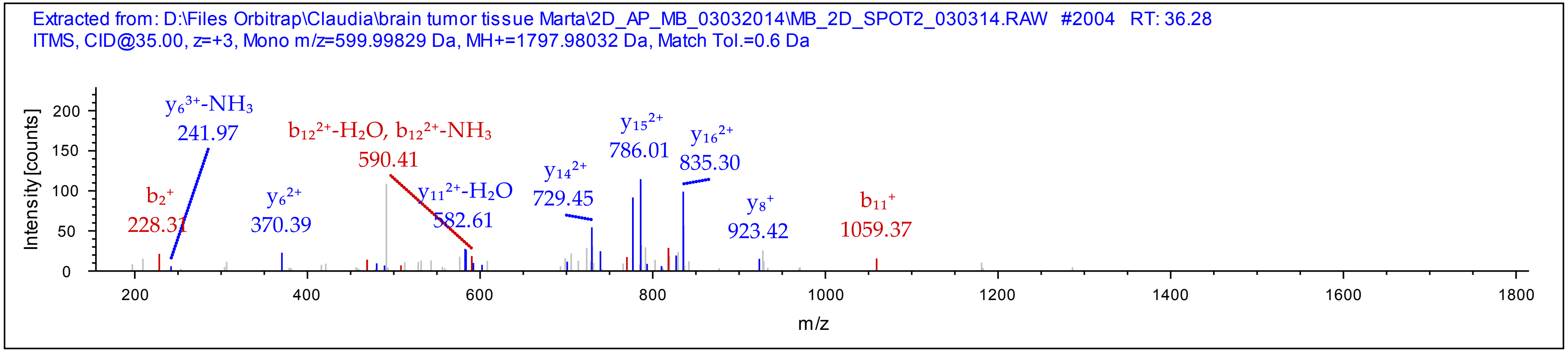
Sequence: VLGAFSDGLAHLDNLK, Charge: +2, Monoisotopic m/z: 835.44653 Da (-2.55 mmu/-3.05 ppm), MH+: 1669.88579 Da, RT: 38.08 min,
Identified with: Sequest HT (v1.3); XCorr:2.56, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H$_2$O; b-NH$_3$; y; y-H$_2$O; y-NH$_3$
Protein references (2):
- Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]
- Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2 - [HBD_HUMAN]

#1	**b$^+$**	**b^{2+}**	**Seq.**	**y$^+$**	**y^{2+}**	**#2**
1	100.07570	50.54149	V			16
2	213.15977	107.08352	L	1570.82246	785.91487	15
3	270.18124	135.59426	G	1457.73839	729.37283	14
4	341.21836	171.11282	A	1400.71692	700.86210	13
5	488.28678	244.64703	F	1329.67980	665.34354	12
6	575.31881	288.16304	S	1182.61138	591.80933	11
7	690.34576	345.67652	D	1095.57935	548.29331	10
8	747.36723	374.18725	G	980.55240	490.77984	9
9	860.45130	430.72929	L	923.53093	462.26910	8
10	931.48842	466.24785	A	810.44686	405.72707	7
11	1068.54733	534.77730	H	739.40974	370.20851	6
12	1181.63140	591.31934	L	602.35083	301.67905	5
13	1296.65835	648.83281	D	489.26676	245.13702	4
14	1410.70128	705.85428	N	374.23981	187.62354	3
15	1523.78535	762.39631	L	260.19688	130.60208	2
16			K	147.11281	74.06004	1



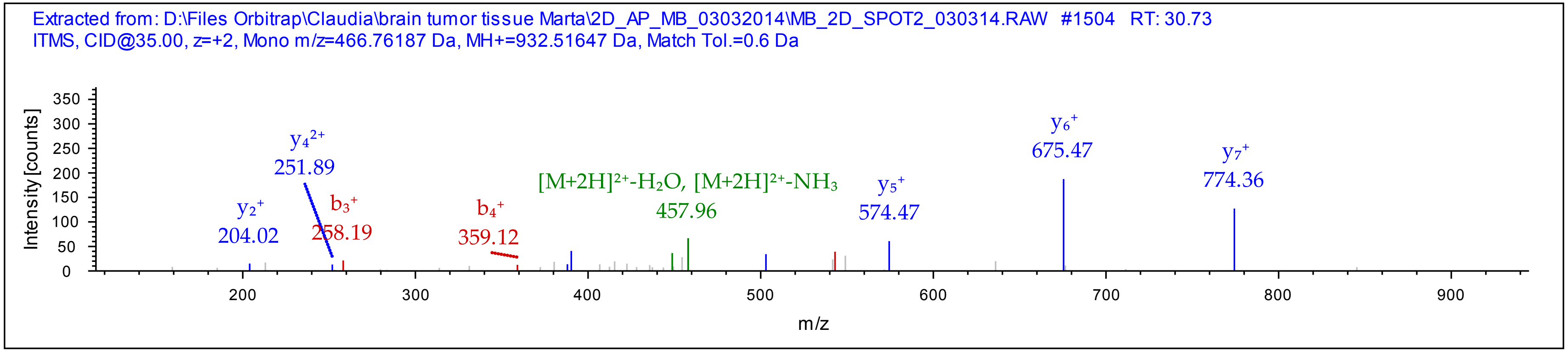
Sequence: KVLGAFSDGLAHLDNLK, Charge: +3, Monoisotopic m/z: 599.99829 Da (-1.85 mmu/-3.08 ppm), MH+: 1797.98032 Da, RT: 36.28 min,
Identified with: Sequest HT (v1.3); XCorr:2.34, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H$_2$O; b-NH$_3$; y; y-H$_2$O; y-NH$_3$
Protein references (2):
- Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]
- Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2 - [HBD_HUMAN]

#1	**b$^+$**	**b^{2+}**	**b^{3+}**	**Seq.**	**y$^+$**	**y^{2+}**	**y^{3+}**	**#2**
1	129.10225	65.05476	43.70560	K				17
2	228.17067	114.58897	76.72841	V	1669.89088	835.44908	557.30181	16
3	341.25474	171.13101	114.42310	L	1570.82246	785.91487	524.27900	15
4	398.27621	199.64174	133.43025	G	1457.73839	729.37283	486.58431	14
5	469.31333	235.16030	157.10929	A	1400.71692	700.86210	467.57716	13
6	616.38175	308.69451	206.13210	F	1329.67980	665.34354	443.89812	12
7	703.41378	352.21053	235.14278	S	1182.61138	591.80933	394.87531	11
8	818.44073	409.72400	273.48509	D	1095.57935	548.29331	365.86463	10
9	875.46220	438.23474	292.49225	G	980.55240	490.77984	327.52232	9
10	988.54627	494.77677	330.18694	L	923.53093	462.26910	308.51516	8
11	1059.58339	530.29533	353.86598	A	810.44686	405.72707	270.82047	7
12	1196.64230	598.82479	399.55228	H	739.40974	370.20851	247.14143	6
13	1309.72637	655.36682	437.24697	L	602.35083	301.67905	201.45513	5
14	1424.75332	712.88030	475.58929	D	489.26676	245.13702	163.76044	4
15	1538.79625	769.90176	513.60360	N	374.23981	187.62354	125.41812	3
16	1651.88032	826.44380	551.29829	L	260.19688	130.60208	87.40381	2
17				K	147.11281	74.06004	49.70912	1



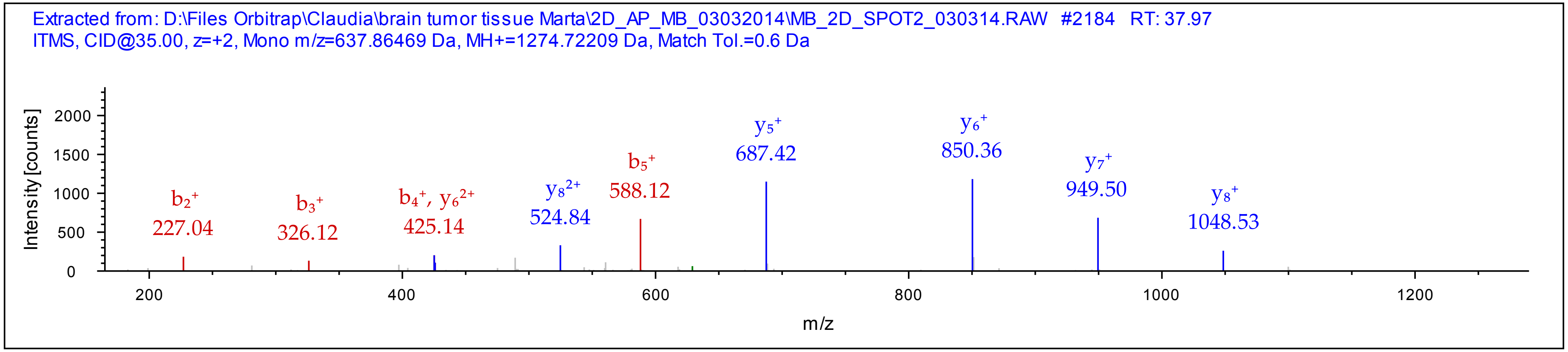
Sequence: SAVTALWGK, Charge: +2, Monoisotopic m/z: 466.76187 Da (-1.79 mmu/-3.83 ppm), MH+: 932.51647 Da, RT: 30.73 min,
Identified with: Sequest HT (v1.3); XCorr:2.19, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3
Protein references (1):
Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	88.03931	44.52329	S			9
2	159.07643	80.04185	A	845.48801	423.24764	8
3	258.14485	129.57606	V	774.45089	387.72908	7
4	359.19253	180.09990	T	675.38247	338.19487	6
5	430.22965	215.61846	A	574.33479	287.67103	5
6	543.31372	272.16050	L	503.29767	252.15247	4
7	729.39304	365.20016	W	390.21360	195.61044	3
8	786.41451	393.71089	G	204.13428	102.57078	2
9			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT2_030314.RAW #1504 RT: 30.73
ITMS, CID@35.00, z=+2, Mono m/z=466.76187 Da, MH+=932.51647 Da, Match Tol.=0.6 Da

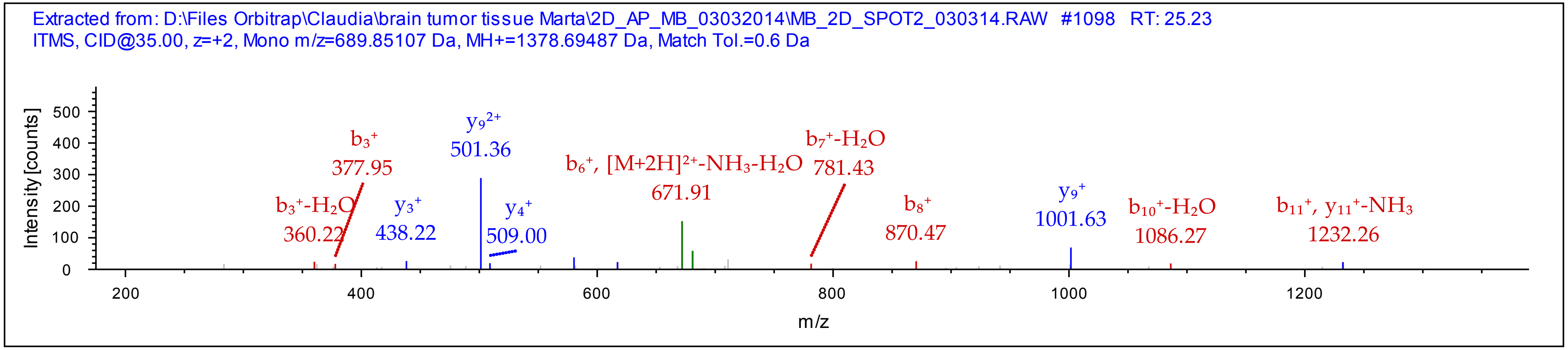
Sequence: LLVVYPWTQR, Charge: +2, Monoisotopic m/z: 637.86469 Da (-1.76 mmu/-2.76 ppm), MH+: 1274.72209 Da, RT: 37.97 min,
Identified with: Sequest HT (v1.3); XCorr:2.19, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (5):
- Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]
- Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2 - [HBD_HUMAN]
- Hemoglobin subunit epsilon OS=Homo sapiens GN=HBE1 PE=1 SV=2 - [HBE_HUMAN]
- Hemoglobin subunit gamma-1 OS=Homo sapiens GN=HBG1 PE=1 SV=2 - [HBG1_HUMAN]
- Hemoglobin subunit gamma-2 OS=Homo sapiens GN=HBG2 PE=1 SV=2 - [HBG2_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	114.09135	57.54931	L			10
2	227.17542	114.09135	L	1161.64154	581.32441	9
3	326.24384	163.62556	V	1048.55747	524.78237	8
4	425.31226	213.15977	V	949.48905	475.24816	7
5	588.37558	294.69143	Y	850.42063	425.71395	6
6	685.42835	343.21781	P	687.35731	344.18229	5
7	871.50767	436.25747	W	590.30454	295.65591	4
8	972.55535	486.78131	T	404.22522	202.61625	3
9	1100.61393	550.81060	Q	303.17754	152.09241	2
10			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT2_030314.RAW #2184 RT: 37.97
ITMS, CID@35.00, z=+2, Mono m/z=637.86469 Da, MH+=1274.72209 Da, Match Tol.=0.6 Da

Sequence: EFTPPVQAAYQK, Charge: +2, Monoisotopic m/z: 689.85107 Da (-2.66 mmu/-3.86 ppm), MH+: 1378.69487 Da, RT: 25.23 min,
Identified with: Sequest HT (v1.3); XCorr:1.68, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]

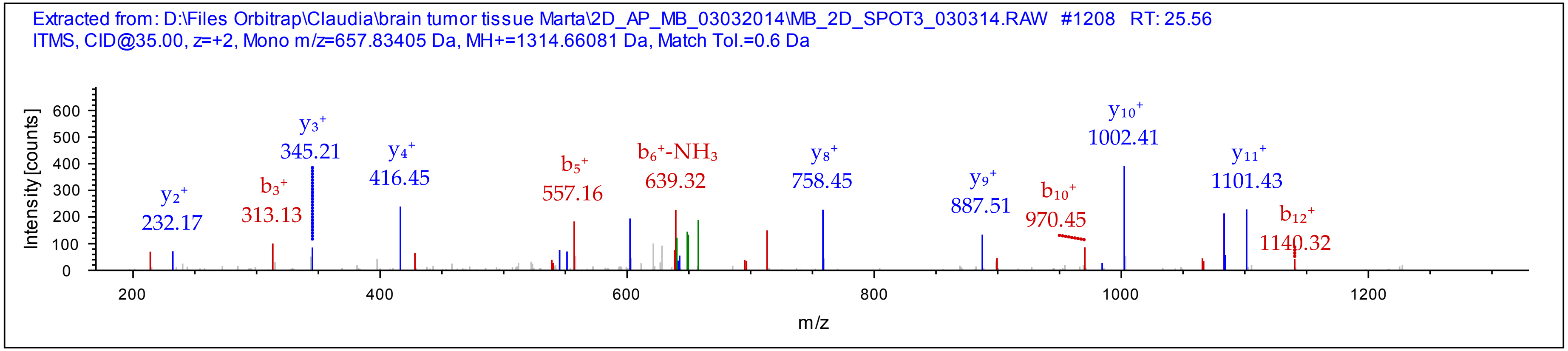
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	130.04988	65.52858	E			12
2	277.11830	139.06279	F	1249.65759	625.33243	11
3	378.16598	189.58663	T	1102.58917	551.79822	10
4	475.21875	238.11301	P	1001.54149	501.27438	9
5	572.27152	286.63940	P	904.48872	452.74800	8
6	671.33994	336.17361	V	807.43595	404.22161	7
7	799.39852	400.20290	Q	708.36753	354.68740	6
8	870.43564	435.72146	A	580.30895	290.65811	5
9	941.47276	471.24002	A	509.27183	255.13955	4
10	1104.53608	552.77168	Y	438.23471	219.62099	3
11	1232.59466	616.80097	Q	275.17139	138.08933	2
12			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT2_030314.RAW #1098 RT: 25.23
ITMS, CID@35.00, z=+2, Mono m/z=689.85107 Da, MH+=1378.69487 Da, Match Tol.=0.6 Da
Intensity [counts]
0
100
200
300
400
500
200
400
600
800
1000
1200
m/z
b3+-H2O
360.22
b3+
377.95
y3+
438.22
y92+
501.36
y4+
509.00
b6+, [M+2H]2+-NH3-H2O
671.91
b7+-H2O
781.43
b8+
870.47
y9+
1001.63
b10+-H2O
1086.27
b11+, y11+-NH3
1232.26

Spot #	Uniprot Accession Number	Description	MW[a] [kDa]	pI [a]	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*
3	P68871	Hemoglobin subunit beta	15.9	6.8	305.4	62.59%	9	9	MB, PA	NS	NS

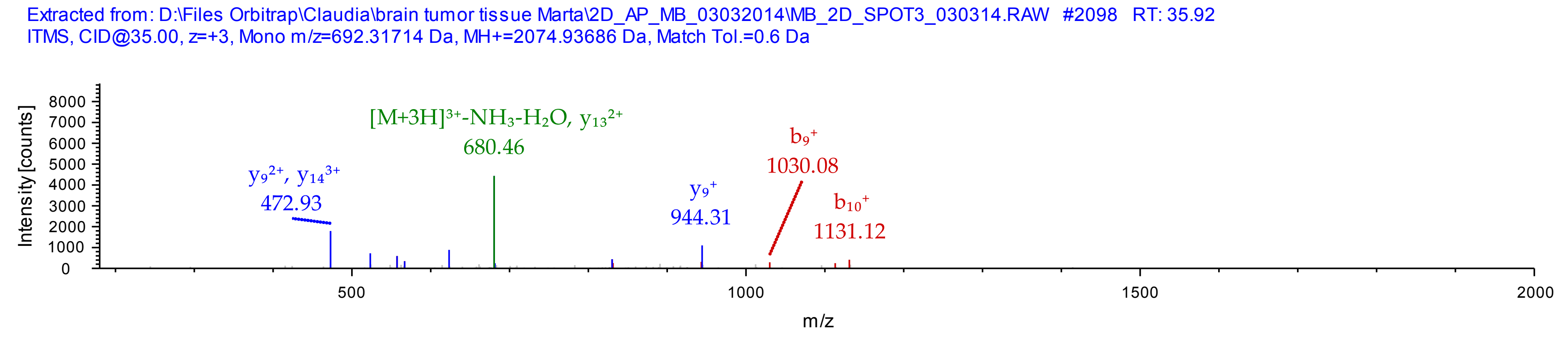
Sequence: VNVDEVGGEALGR, Charge: +2, Monoisotopic m/z: 657.83405 Da (-2.05 mmu/-3.11 ppm), MH+: 1314.66081 Da, RT: 25.56 min,
Identified with: Sequest HT (v1.3); XCorr:4.12, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	100.07570	50.54149	V			13
2	214.11863	107.56295	N	1215.59648	608.30188	12
3	313.18705	157.09716	V	1101.55355	551.28041	11
4	428.21400	214.61064	D	1002.48513	501.74620	10
5	557.25660	279.13194	E	887.45818	444.23273	9
6	656.32502	328.66615	V	758.41558	379.71143	8
7	713.34649	357.17688	G	659.34716	330.17722	7
8	770.36796	385.68762	G	602.32569	301.66648	6
9	899.41056	450.20892	E	545.30422	273.15575	5
10	970.44768	485.72748	A	416.26162	208.63445	4
11	1083.53175	542.26951	L	345.22450	173.11589	3
12	1140.55322	570.78025	G	232.14043	116.57385	2
13			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT3_030314.RAW #1208 RT: 25.56
ITMS, CID@35.00, z=+2, Mono m/z=657.83405 Da, MH+=1314.66081 Da, Match Tol.=0.6 Da

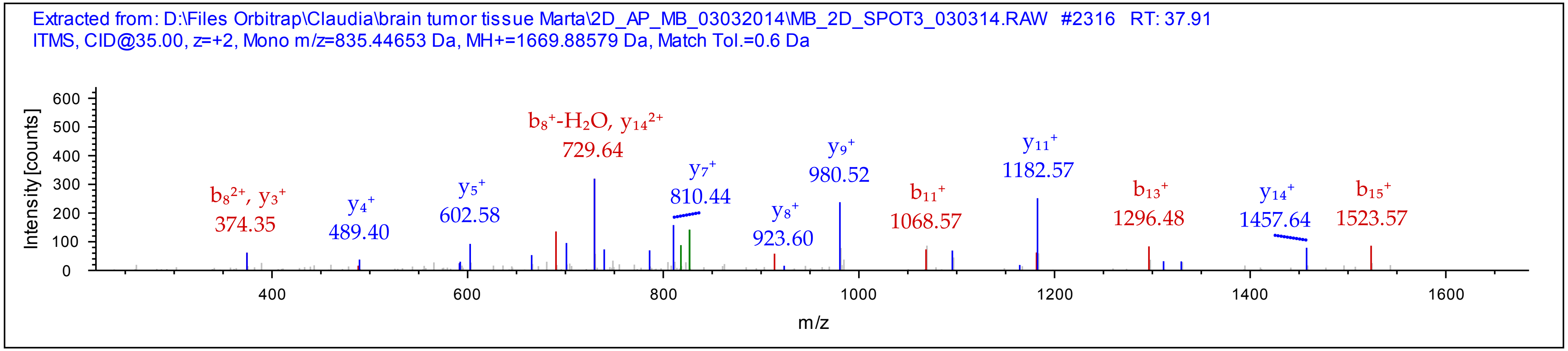
Sequence: FFESFGDLSTPDAVMGNPK, M15-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 692.31714 Da (-1.96 mmu/-2.84 ppm), MH+: 2074.93686 Da, RT: 35.92 min,
Identified with: Sequest HT (v1.3); XCorr:3.99, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	148.07570	74.54149	50.03008	F				19
2	295.14412	148.07570	99.05289	F	1927.87433	964.44080	643.29629	18
3	424.18672	212.59700	142.06709	E	1780.80591	890.90659	594.27349	17
4	511.21875	256.11301	171.07777	S	1651.76331	826.38529	551.25929	16
5	658.28717	329.64722	220.10057	F	1564.73128	782.86928	522.24861	15
6	715.30864	358.15796	239.10773	G	1417.66286	709.33507	473.22580	14
7	830.33559	415.67143	277.45005	D	1360.64139	680.82433	454.21865	13
8	943.41966	472.21347	315.14474	L	1245.61444	623.31086	415.87633	12
9	1030.45169	515.72948	344.15541	S	1132.53037	566.76882	378.18164	11
10	1131.49937	566.25332	377.83797	T	1045.49834	523.25281	349.17096	10
11	1228.55214	614.77971	410.18890	P	944.45066	472.72897	315.48840	9
12	1343.57909	672.29318	448.53121	D	847.39789	424.20258	283.13748	8
13	1414.61621	707.81174	472.21025	A	732.37094	366.68911	244.79516	7
14	1513.68463	757.34595	505.23306	V	661.33382	331.17055	221.11612	6
15	1660.72004	830.86366	554.24486	M-Oxidation	562.26540	281.63634	188.09332	5
16	1717.74151	859.37439	573.25202	G	415.22998	208.11863	139.08151	4
17	1831.78444	916.39586	611.26633	N	358.20851	179.60789	120.07435	3
18	1928.83721	964.92224	643.61725	P	244.16558	122.58643	82.06004	2
19				K	147.11281	74.06004	49.70912	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT3_030314.RAW #2098 RT: 35.92
ITMS, CID@35.00, z=+3, Mono m/z=692.31714 Da, MH+=2074.93686 Da, Match Tol.=0.6 Da

Sequence: VLGAFSDGLAHLDNLK, Charge: +2, Monoisotopic m/z: 835.44653 Da (-2.55 mmu/-3.05 ppm), MH+: 1669.88579 Da, RT: 37.91 min,
Identified with: Sequest HT (v1.3); XCorr:3.70, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (2):
- Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]
- Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2 - [HBD_HUMAN]

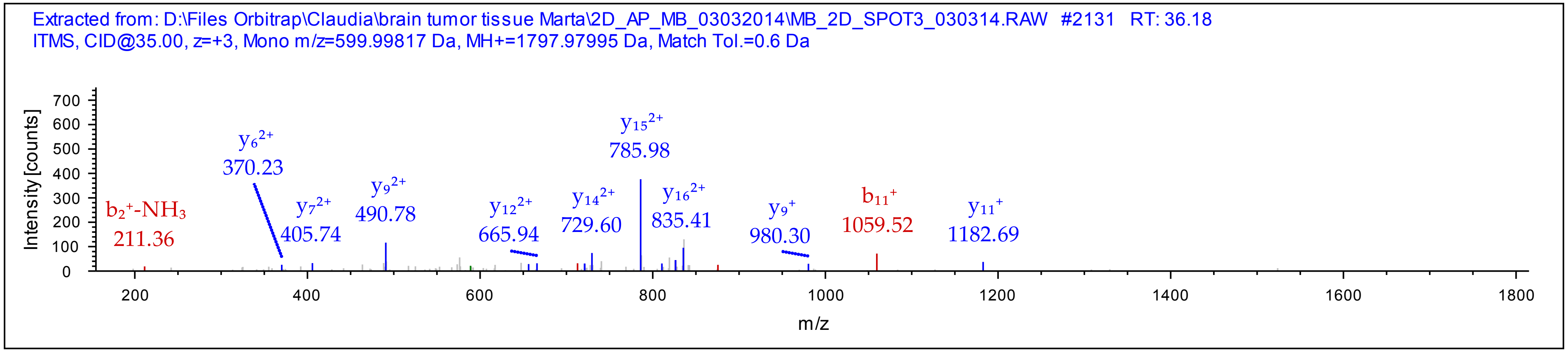
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	100.07570	50.54149	V			16
2	213.15977	107.08352	L	1570.82246	785.91487	15
3	270.18124	135.59426	G	1457.73839	729.37283	14
4	341.21836	171.11282	A	1400.71692	700.86210	13
5	488.28678	244.64703	F	1329.67980	665.34354	12
6	575.31881	288.16304	S	1182.61138	591.80933	11
7	690.34576	345.67652	D	1095.57935	548.29331	10
8	747.36723	374.18725	G	980.55240	490.77984	9
9	860.45130	430.72929	L	923.53093	462.26910	8
10	931.48842	466.24785	A	810.44686	405.72707	7
11	1068.54733	534.77730	H	739.40974	370.20851	6
12	1181.63140	591.31934	L	602.35083	301.67905	5
13	1296.65835	648.83281	D	489.26676	245.13702	4
14	1410.70128	705.85428	N	374.23981	187.62354	3
15	1523.78535	762.39631	L	260.19688	130.60208	2
16			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT3_030314.RAW #2316 RT: 37.91
ITMS, CID@35.00, z=+2, Mono m/z=835.44653 Da, MH+=1669.88579 Da, Match Tol.=0.6 Da

Sequence: KVLGAFSDGLAHLDNLK, Charge: +3, Monoisotopic m/z: 599.99817 Da (-1.97 mmu/-3.28 ppm), MH+: 1797.97995 Da, RT: 36.18 min,
Identified with: Sequest HT (v1.3); XCorr:3.70, Ions matched by search engine: 0/0

Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (2):
- Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]
- Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2 - [HBD_HUMAN]

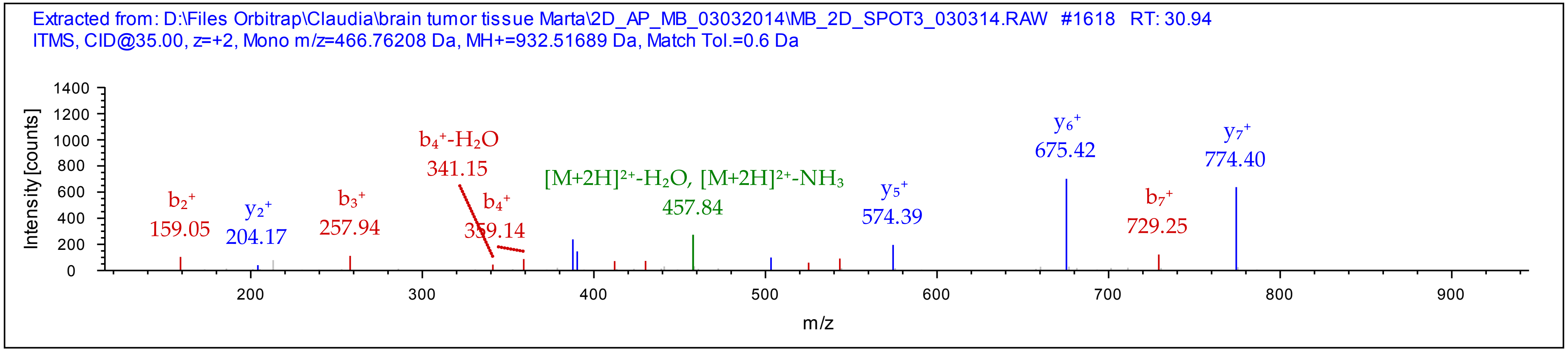
#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	129.10225	65.05476	43.70560	K				17
2	228.17067	114.58897	76.72841	V	1669.89088	835.44908	557.30181	16
3	341.25474	171.13101	114.42310	L	1570.82246	785.91487	524.27900	15
4	398.27621	199.64174	133.43025	G	1457.73839	729.37283	486.58431	14
5	469.31333	235.16030	157.10929	A	1400.71692	700.86210	467.57716	13
6	616.38175	308.69451	206.13210	F	1329.67980	665.34354	443.89812	12
7	703.41378	352.21053	235.14278	S	1182.61138	591.80933	394.87531	11
8	818.44073	409.72400	273.48509	D	1095.57935	548.29331	365.86463	10
9	875.46220	438.23474	292.49225	G	980.55240	490.77984	327.52232	9
10	988.54627	494.77677	330.18694	L	923.53093	462.26910	308.51516	8
11	1059.58339	530.29533	353.86598	A	810.44686	405.72707	270.82047	7
12	1196.64230	598.82479	399.55228	H	739.40974	370.20851	247.14143	6
13	1309.72637	655.36682	437.24697	L	602.35083	301.67905	201.45513	5
14	1424.75332	712.88030	475.58929	D	489.26676	245.13702	163.76044	4
15	1538.79625	769.90176	513.60360	N	374.23981	187.62354	125.41812	3
16	1651.88032	826.44380	551.29829	L	260.19688	130.60208	87.40381	2
17				K	147.11281	74.06004	49.70912	1



Sequence: SAVTALWGK, Charge: +2, Monoisotopic m/z: 466.76208 Da (-1.58 mmu/-3.38 ppm), MH+: 932.51689 Da, RT: 30.94 min,
Identified with: Sequest HT (v1.3); XCorr:2.85, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da

Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3
Protein references (1):
Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]

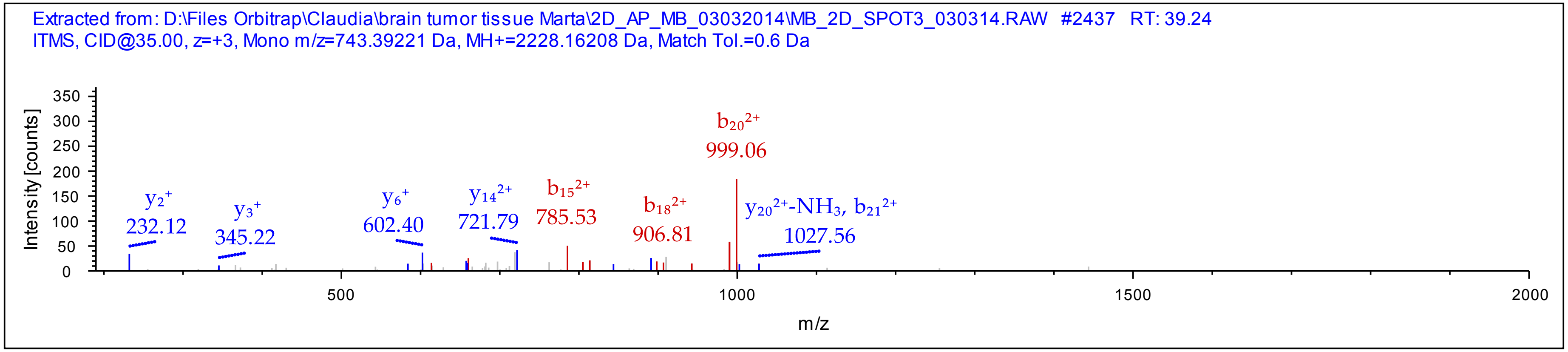
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	88.03931	44.52329	S			9
2	159.07643	80.04185	A	845.48801	423.24764	8
3	258.14485	129.57606	V	774.45089	387.72908	7
4	359.19253	180.09990	T	675.38247	338.19487	6
5	430.22965	215.61846	A	574.33479	287.67103	5
6	543.31372	272.16050	L	503.29767	252.15247	4
7	729.39304	365.20016	W	390.21360	195.61044	3
8	786.41451	393.71089	G	204.13428	102.57078	2
9			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT3_030314.RAW #1618 RT: 30.94
ITMS, CID@35.00, z=+2, Mono m/z=466.76208 Da, MH+=932.51689 Da, Match Tol.=0.6 Da

Sequence: SAVTALWGKVNVDEVGGEALGR, Charge: +3, Monoisotopic m/z: 743.39221 Da (-1.67 mmu/-2.25 ppm), MH+: 2228.16208 Da, RT: 39.24 min,
Identified with: Sequest HT (v1.3); XCorr:2.62, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	88.03931	44.52329	30.01795	S				22
2	159.07643	80.04185	53.69699	A	2141.13507	1071.07117	714.38321	21
3	258.14485	129.57606	86.71980	V	2070.09795	1035.55261	690.70417	20
4	359.19253	180.09990	120.40236	T	1971.02953	986.01840	657.68136	19
5	430.22965	215.61846	144.08140	A	1869.98185	935.49456	623.99880	18
6	543.31372	272.16050	181.77609	L	1798.94473	899.97600	600.31976	17

7	729.39304	365.20016	243.80253	W	1685.86066	843.43397	562.62507	16
8	786.41451	393.71089	262.80969	G	1499.78134	750.39431	500.59863	15
9	914.50948	457.75838	305.50801	K	1442.75987	721.88357	481.59147	14
10	1013.57790	507.29259	338.53082	V	1314.66490	657.83609	438.89315	13
11	1127.62083	564.31405	376.54513	N	1215.59648	608.30188	405.87034	12
12	1226.68925	613.84826	409.56793	V	1101.55355	551.28041	367.85603	11
13	1341.71620	671.36174	447.91025	D	1002.48513	501.74620	334.83323	10
14	1470.75880	735.88304	490.92445	E	887.45818	444.23273	296.49091	9
15	1569.82722	785.41725	523.94726	V	758.41558	379.71143	253.47671	8
16	1626.84869	813.92798	542.95441	G	659.34716	330.17722	220.45390	7
17	1683.87016	842.43872	561.96157	G	602.32569	301.66648	201.44675	6
18	1812.91276	906.96002	604.97577	E	545.30422	273.15575	182.43959	5
19	1883.94988	942.47858	628.65481	A	416.26162	208.63445	139.42539	4
20	1997.03395	999.02061	666.34950	L	345.22450	173.11589	115.74635	3
21	2054.05542	1027.53135	685.35666	G	232.14043	116.57385	78.05166	2
22				R	175.11896	88.06312	59.04450	1

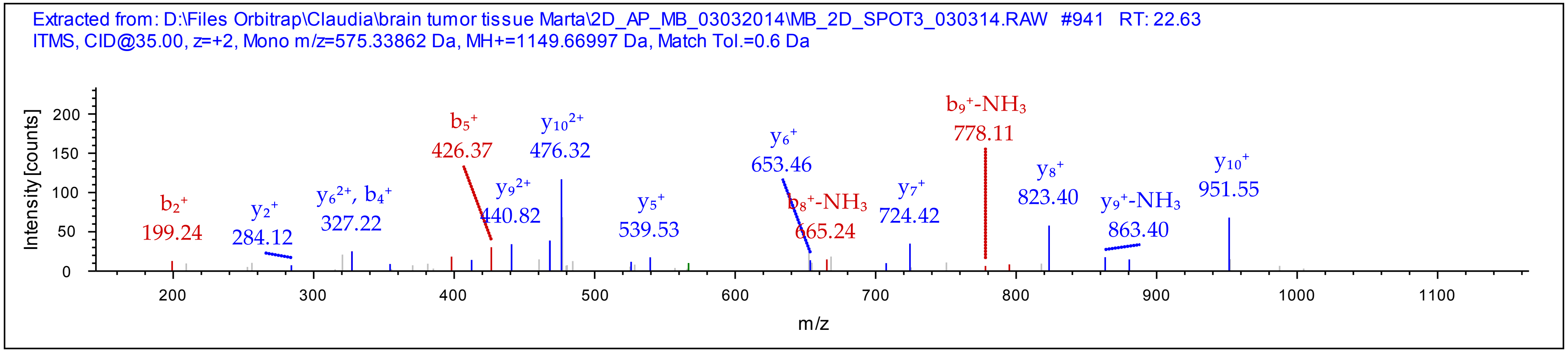


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT3_030314.RAW #2437 RT: 39.24
ITMS, CID@35.00, z=+3, Mono m/z=743.39221 Da, MH+=2228.16208 Da, Match Tol.=0.6 Da

Sequence: VVAGVANALAHK, Charge: +2, Monoisotopic m/z: 575.33862 Da (-1.98 mmu/-3.45 ppm), MH+: 1149.66997 Da, RT: 22.63 min,
Identified with: Sequest HT (v1.3); XCorr:2.30, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-NH_3; y; y-NH_3
Protein references (2):
- Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]
- Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2 - [HBD_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	100.07570	50.54149	V			12
2	199.14412	100.07570	V	1050.60551	525.80639	11
3	270.18124	135.59426	A	951.53709	476.27218	10

4	327.20271	164.10499	G	880.49997	440.75362	9
5	426.27113	213.63920	V	823.47850	412.24289	8
6	497.30825	249.15776	A	724.41008	362.70868	7
7	611.35118	306.17923	N	653.37296	327.19012	6
8	682.38830	341.69779	A	539.33003	270.16865	5
9	795.47237	398.23982	L	468.29291	234.65009	4
10	866.50949	433.75838	A	355.20884	178.10806	3
11	1003.56840	502.28784	H	284.17172	142.58950	2
12			K	147.11281	74.06004	1

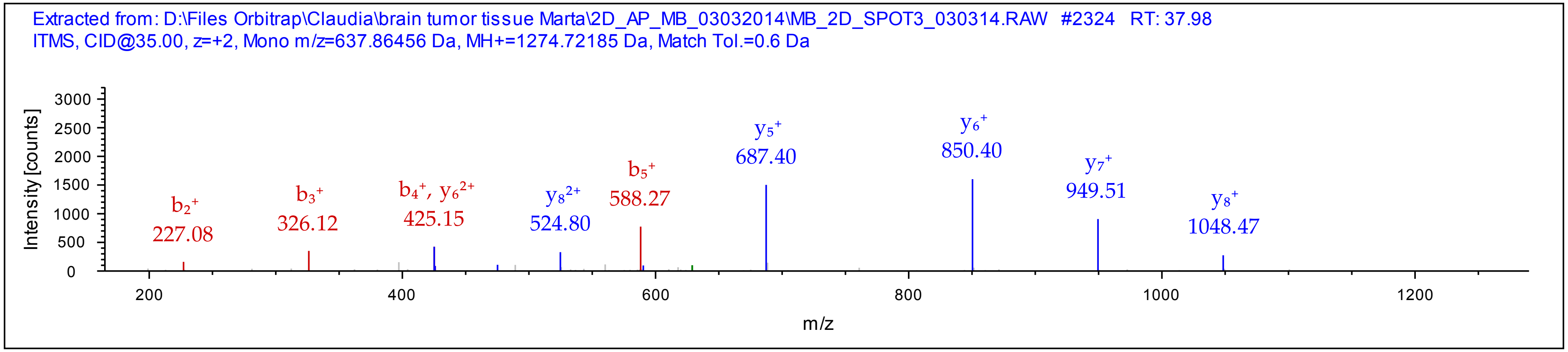


Sequence: LLVVYPWTQR, Charge: +2, Monoisotopic m/z: 637.86456 Da (-1.88 mmu/-2.95 ppm), MH+: 1274.72185 Da, RT: 37.98 min,
Identified with: Sequest HT (v1.3); XCorr:2.29, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (5):

- Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]
- Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2 - [HBD_HUMAN]
- Hemoglobin subunit epsilon OS=Homo sapiens GN=HBE1 PE=1 SV=2 - [HBE_HUMAN]
- Hemoglobin subunit gamma-1 OS=Homo sapiens GN=HBG1 PE=1 SV=2 - [HBG1_HUMAN]
- Hemoglobin subunit gamma-2 OS=Homo sapiens GN=HBG2 PE=1 SV=2 - [HBG2_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	114.09135	57.54931	L			10
2	227.17542	114.09135	L	1161.64154	581.32441	9
3	326.24384	163.62556	V	1048.55747	524.78237	8
4	425.31226	213.15977	V	949.48905	475.24816	7
5	588.37558	294.69143	Y	850.42063	425.71395	6
6	685.42835	343.21781	P	687.35731	344.18229	5
7	871.50767	436.25747	W	590.30454	295.65591	4

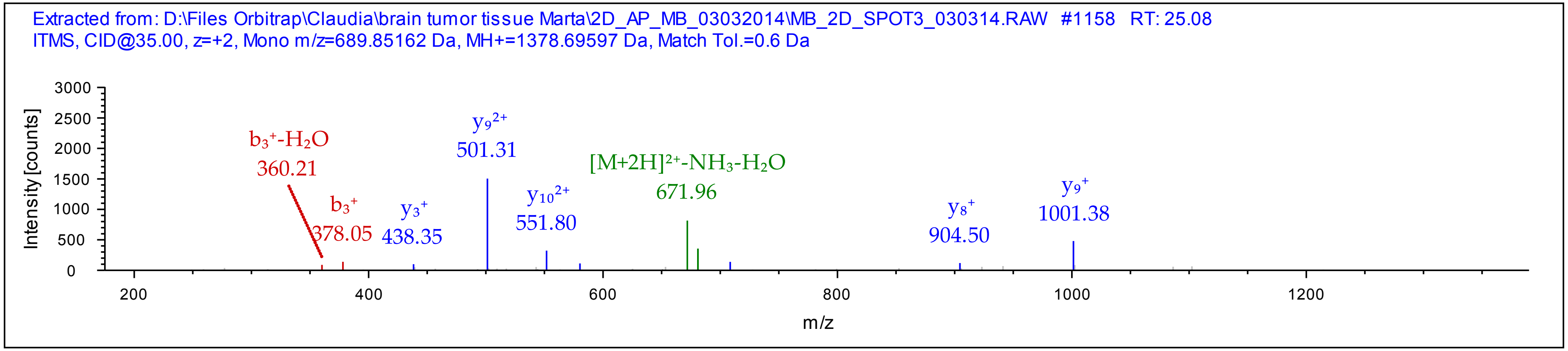
8	972.55535	486.78131	T	404.22522	202.61625	3
9	1100.61393	550.81060	Q	303.17754	152.09241	2
10			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT3_030314.RAW #2324 RT: 37.98
ITMS, CID@35.00, z=+2, Mono m/z=637.86456 Da, MH+=1274.72185 Da, Match Tol.=0.6 Da

Sequence: EFTPPVQAAYQK, Charge: +2, Monoisotopic m/z: 689.85162 Da (-2.11 mmu/-3.06 ppm), MH+: 1378.69597 Da, RT: 25.08 min,
Identified with: Sequest HT (v1.3); XCorr:2.07, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):

- Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	130.04988	65.52858	E			12
2	277.11830	139.06279	F	1249.65759	625.33243	11
3	378.16598	189.58663	T	1102.58917	551.79822	10
4	475.21875	238.11301	P	1001.54149	501.27438	9
5	572.27152	286.63940	P	904.48872	452.74800	8
6	671.33994	336.17361	V	807.43595	404.22161	7
7	799.39852	400.20290	Q	708.36753	354.68740	6
8	870.43564	435.72146	A	580.30895	290.65811	5
9	941.47276	471.24002	A	509.27183	255.13955	4
10	1104.53608	552.77168	Y	438.23471	219.62099	3
11	1232.59466	616.80097	Q	275.17139	138.08933	2
12			K	147.11281	74.06004	1

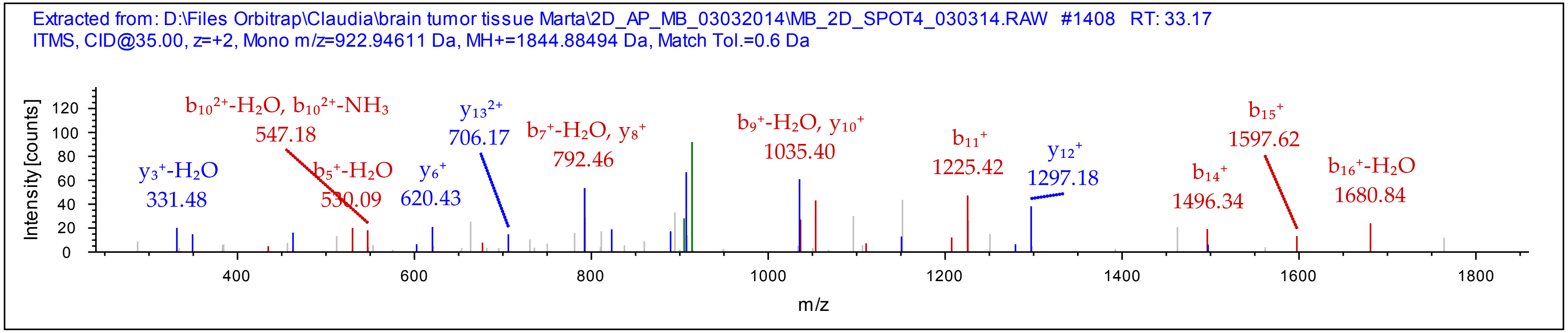


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT3_030314.RAW #1158 RT: 25.08
ITMS, CID@35.00, z=+2, Mono m/z=689.85162 Da, MH+=1378.69597 Da, Match Tol.=0.6 Da

Spot #	Uniprot Accession Number	Description	MW^a [kDa]	pI ^{a}	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*
4	P62158	Calmodulin	16.7	4.1	41.2	75.17%	4	6	MB, PA	2.89E-02	1.7 ↑ MB

Sequence: EAFSLFDKDGDGTITTK, Charge: +2, Monoisotopic m/z: 922.94611 Da (-3.2 mmu/-3.47 ppm), MH+: 1844.88494 Da, RT: 33.17 min,
Identified with: Sequest HT (v1.3); XCorr:1.96, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H$_2$O; b-NH$_3$; y; y-H$_2$O; y-NH$_3$
Protein references (1):
Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2 - [CALM_HUMAN]

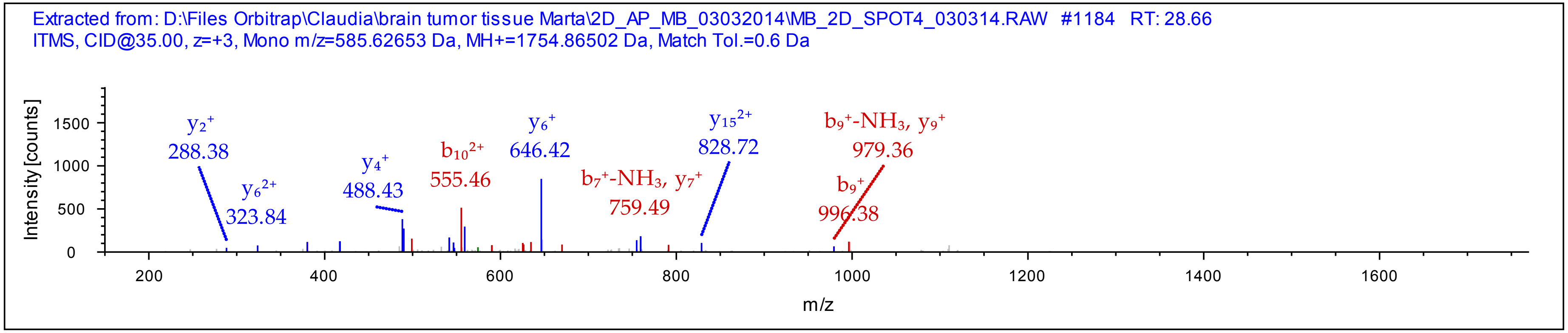
#1	b$^+$	b^{2+}	Seq.	y$^+$	y^{2+}	#2
1	130.04988	65.52858	E			17
2	201.08700	101.04714	A	1715.84874	858.42801	16
3	348.15542	174.58135	F	1644.81162	822.90945	15
4	435.18745	218.09736	S	1497.74320	749.37524	14
5	548.27152	274.63940	L	1410.71117	705.85922	13
6	695.33994	348.17361	F	1297.62710	649.31719	12
7	810.36689	405.68708	D	1150.55868	575.78298	11
8	938.46186	469.73457	K	1035.53173	518.26950	10
9	1053.48881	527.24804	D	907.43676	454.22202	9
10	1110.51028	555.75878	G	792.40981	396.70854	8
11	1225.53723	613.27225	D	735.38834	368.19781	7
12	1282.55870	641.78299	G	620.36139	310.68433	6
13	1383.60638	692.30683	T	563.33992	282.17360	5
14	1496.69045	748.84886	I	462.29224	231.64976	4
15	1597.73813	799.37270	T	349.20817	175.10772	3
16	1698.78581	849.89654	T	248.16049	124.58388	2
17			K	147.11281	74.06004	1



Sequence: VFDKDGNGYISAAELR, Charge: +3, Monoisotopic m/z: 585.62640 Da (-2.07 mmu/-3.54 ppm), MH+: 1754.86466 Da, RT: 28.43 min,
Identified with: Sequest HT (v1.3); XCorr:2.45, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):

- Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2 - [CALM_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	100.07570	50.54149	34.03008	V				16
2	247.14412	124.07570	83.05289	F	1655.80245	828.40486	552.60567	15
3	362.17107	181.58917	121.39521	D	1508.73403	754.87065	503.58286	14
4	490.26604	245.63666	164.09353	K	1393.70708	697.35718	465.24054	13
5	605.29299	303.15013	202.43585	D	1265.61211	633.30969	422.54222	12
6	662.31446	331.66087	221.44300	G	1150.58516	575.79622	384.19990	11
7	776.35739	388.68233	259.45731	N	1093.56369	547.28548	365.19275	10
8	833.37886	417.19307	278.46447	G	979.52076	490.26402	327.17844	9
9	996.44218	498.72473	332.81891	Y	922.49929	461.75328	308.17128	8
10	1109.52625	555.26676	370.51360	I	759.43597	380.22162	253.81684	7
11	1196.55828	598.78278	399.52428	S	646.35190	323.67959	216.12215	6
12	1267.59540	634.30134	423.20332	A	559.31987	280.16357	187.11147	5
13	1338.63252	669.81990	446.88236	A	488.28275	244.64501	163.43243	4
14	1467.67512	734.34120	489.89656	E	417.24563	209.12645	139.75339	3
15	1580.75919	790.88323	527.59125	L	288.20303	144.60515	96.73919	2
16				R	175.11896	88.06312	59.04450	1

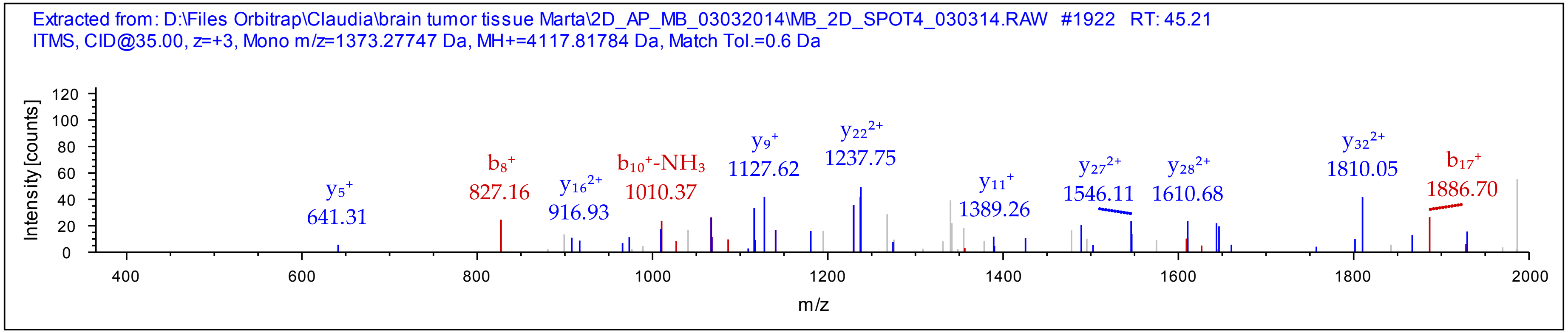


Sequence: SLGQNPTEAELQDMINEVDADGNGTIDFPEFLTMMAR, M14-Oxidation (15.99492 Da), M34-Oxidation (15.99492 Da), M35-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 1373.27747 Da (-4.5 mmu/-3.28 ppm), MH+: 4117.81784 Da, RT: 45.18 min,
Identified with: Sequest HT (v1.3); XCorr:2.30, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):

- Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2 - [CALM_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	88.03931	44.52329	30.01795	S				37
2	201.12338	101.06533	67.71264	L	4030.79932	2015.90330	1344.27129	36
3	258.14485	129.57606	86.71980	G	3917.71525	1959.36126	1306.57660	35
4	386.20343	193.60535	129.40599	Q	3860.69378	1930.85053	1287.56944	34
5	500.24636	250.62682	167.42030	N	3732.63520	1866.82124	1244.88325	33
6	597.29913	299.15320	199.77123	P	3618.59227	1809.79977	1206.86894	32
7	698.34681	349.67704	233.45379	T	3521.53950	1761.27339	1174.51802	31
8	827.38941	414.19834	276.46799	E	3420.49182	1710.74955	1140.83546	30
9	898.42653	449.71690	300.14703	A	3291.44922	1646.22825	1097.82126	29
10	1027.46913	514.23820	343.16123	E	3220.41210	1610.70969	1074.14222	28
11	1140.55320	570.78024	380.85592	L	3091.36950	1546.18839	1031.12802	27
12	1268.61178	634.80953	423.54211	Q	2978.28543	1489.64635	993.43333	26
13	1383.63873	692.32300	461.88443	D	2850.22685	1425.61706	950.74713	25
14	1530.67414	765.84071	510.89623	M-Oxidation	2735.19990	1368.10359	912.40482	24
15	1643.75821	822.38274	548.59092	I	2588.16448	1294.58588	863.39301	23
16	1757.80114	879.40421	586.60523	N	2475.08041	1238.04384	825.69832	22
17	1886.84374	943.92551	629.61943	E	2361.03748	1181.02238	787.68401	21
18	1985.91216	993.45972	662.64224	V	2231.99488	1116.50108	744.66981	20
19	2100.93911	1050.97319	700.98455	D	2132.92646	1066.96687	711.64700	19

20	2171.97623	1086.49175	724.66359	A	2017.89951	1009.45339	673.30469	18
21	2287.00318	1144.00523	763.00591	D	1946.86239	973.93483	649.62565	17
22	2344.02465	1172.51596	782.01307	G	1831.83544	916.42136	611.28333	16
23	2458.06758	1229.53743	820.02738	N	1774.81397	887.91062	592.27617	15
24	2515.08905	1258.04816	839.03453	G	1660.77104	830.88916	554.26186	14
25	2616.13673	1308.57200	872.71709	T	1603.74957	802.37842	535.25471	13
26	2729.22080	1365.11404	910.41178	I	1502.70189	751.85458	501.57215	12
27	2844.24775	1422.62751	948.75410	D	1389.61782	695.31255	463.87746	11
28	2991.31617	1496.16172	997.77691	F	1274.59087	637.79907	425.53514	10
29	3088.36894	1544.68811	1030.12783	P	1127.52245	564.26486	376.51233	9
30	3217.41154	1609.20941	1073.14203	E	1030.46968	515.73848	344.16141	8
31	3364.47996	1682.74362	1122.16484	F	901.42708	451.21718	301.14721	7
32	3477.56403	1739.28565	1159.85953	L	754.35866	377.68297	252.12440	6
33	3578.61171	1789.80949	1193.54209	T	641.27459	321.14093	214.42971	5
34	3725.64713	1863.32720	1242.55389	M-Oxidation	540.22691	270.61709	180.74715	4
35	3872.68254	1936.84491	1291.56570	M-Oxidation	393.19150	197.09939	131.73535	3
36	3943.71966	1972.36347	1315.24474	A	246.15608	123.58168	82.72354	2
37				R	175.11896	88.06312	59.04450	1



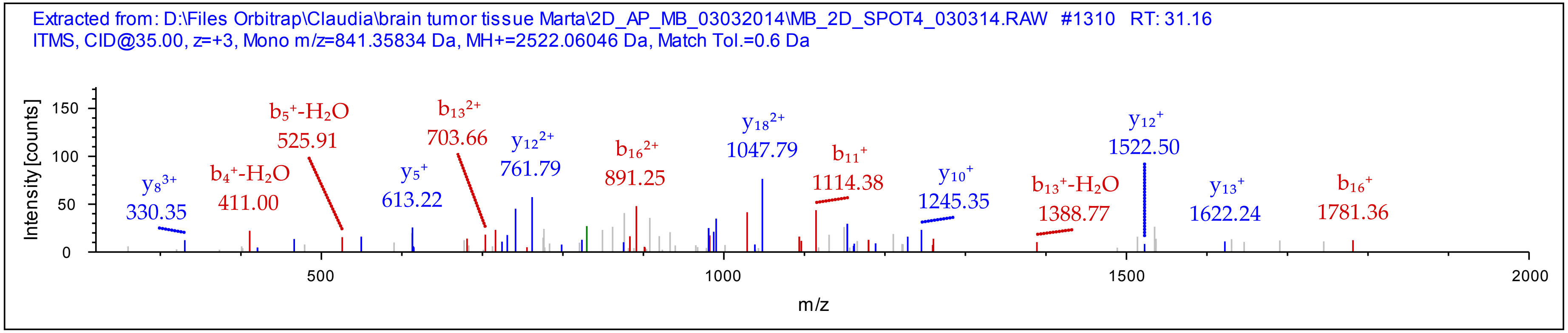
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT4_030314.RAW #1922 RT: 45.21
ITMS, CID@35.00, z=+3, Mono m/z=1373.27747 Da, MH+=4117.81784 Da, Match Tol.=0.6 Da

Sequence: EADIDGDGQVNYEEFVQMMTAK, M18-Oxidation (15.99492 Da), M19-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 841.35834 Da (-3.15 mmu/-3.74 ppm), MH+: 2522.06046 Da, RT: 31.16 min,
Identified with: Sequest HT (v1.3); XCorr:3.80, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2 - [CALM_HUMAN]

#1	b^{+}	b^{2+}	b^{3+}	Seq.	y^{+}	y^{2+}	y^{3+}	#2
1	130.04988	65.52858	44.02148	E				22
2	201.08700	101.04714	67.70052	A	2393.02729	1197.01728	798.34728	21
3	316.11395	158.56061	106.04283	D	2321.99017	1161.49872	774.66824	20
4	429.19802	215.10265	143.73752	I	2206.96322	1103.98525	736.32592	19
5	544.22497	272.61612	182.07984	D	2093.87915	1047.44321	698.63123	18
6	601.24644	301.12686	201.08700	G	1978.85220	989.92974	660.28892	17
7	716.27339	358.64033	239.42931	D	1921.83073	961.41900	641.28176	16
8	773.29486	387.15107	258.43647	G	1806.80378	903.90553	602.93944	15
9	901.35344	451.18036	301.12266	Q	1749.78231	875.39479	583.93229	14
10	1000.42186	500.71457	334.14547	V	1621.72373	811.36550	541.24609	13
11	1114.46479	557.73603	372.15978	N	1522.65531	761.83129	508.22329	12
12	1277.52811	639.26769	426.51422	Y	1408.61238	704.80983	470.20898	11
13	1406.57071	703.78899	469.52842	E	1245.54906	623.27817	415.85454	10
14	1535.61331	768.31029	512.54262	E	1116.50646	558.75687	372.84034	9
15	1682.68173	841.84450	561.56543	F	987.46386	494.23557	329.82614	8
16	1781.75015	891.37871	594.58823	V	840.39544	420.70136	280.80333	7
17	1909.80873	955.40800	637.27443	Q	741.32702	371.16715	247.78052	6
18	2056.84414	1028.92571	686.28623	M-Oxidation	613.26844	307.13786	205.09433	5
19	2203.87956	1102.44342	735.29804	M-Oxidation	466.23303	233.62015	156.08253	4
20	2304.92724	1152.96726	768.98060	T	319.19761	160.10244	107.07072	3
21	2375.96436	1188.48582	792.65964	A	218.14993	109.57860	73.38816	2
22				K	147.11281	74.06004	49.70912	1

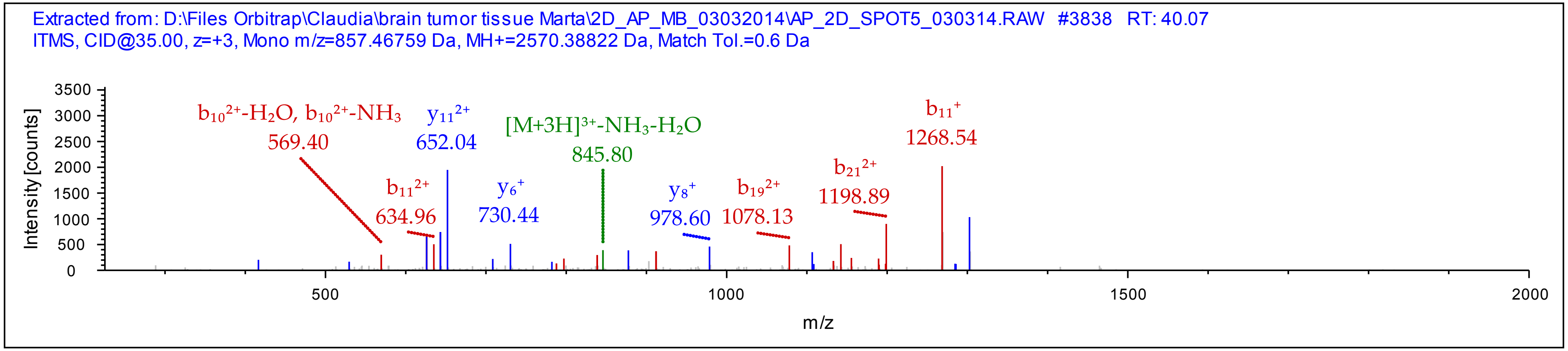

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT4_030314.RAW #1310 RT: 31.16
ITMS, CID@35.00, z=+3, Mono m/z=841.35834 Da, MH+=2522.06046 Da, Match Tol.=0.6 Da
Intensity [counts]
150
100
50
0
y_8^{3+} 330.35
b_4^+-H_2O 411.00
b_5^+-H_2O 525.91
y_5^+ 613.22
b_{13}^{2+} 703.66
y_{12}^{2+} 761.79
b_{16}^{2+} 891.25
y_{18}^{2+} 1047.79
b_{11}^+ 1114.38
y_{10}^+ 1245.35
b_{13}^+-H_2O 1388.77
y_{12}^+ 1522.50
y_{13}^+ 1622.24
b_{16}^+ 1781.36
500
1000
1500
2000
m/z

Spot #	Uniprot Accession Number	Description	MWa [kDa]	pI a	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*
5a	P14136	Glial fibrillary acidic protein	49.9	5.4	146.6	28.47%	10	10	PA	4.57E-04	7.1 ↑ in PA
5b	P14136	Glial fibrillary acidic protein	49.9	5.4	146.6	28.47%	10	10	PA	1.79E-04	9.4 ↑ in PA
5c	P14136	Glial fibrillary acidic protein	49.9	5.4	146.6	28.47%	10	10	PA	9.49E-04	8.4 ↑ in PA
5d	P14136	Glial fibrillary acidic protein	49.9	5.4	146.6	28.47%	10	10	PA	7.00E-03	3.0 ↑ in PA

Sequence: LLEGEENRITIPVQTFSNLQIR, Charge: +3, Monoisotopic m/z: 857.46759 Da (-1.86 mmu/-2.17 ppm), MH+: 2570.38822 Da, RT: 40.07 min,
Identified with: Sequest HT (v1.3); XCorr:5.26, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H$_2$O; b-NH$_3$; y; y-H$_2$O; y-NH$_3$
Protein references (1):

- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

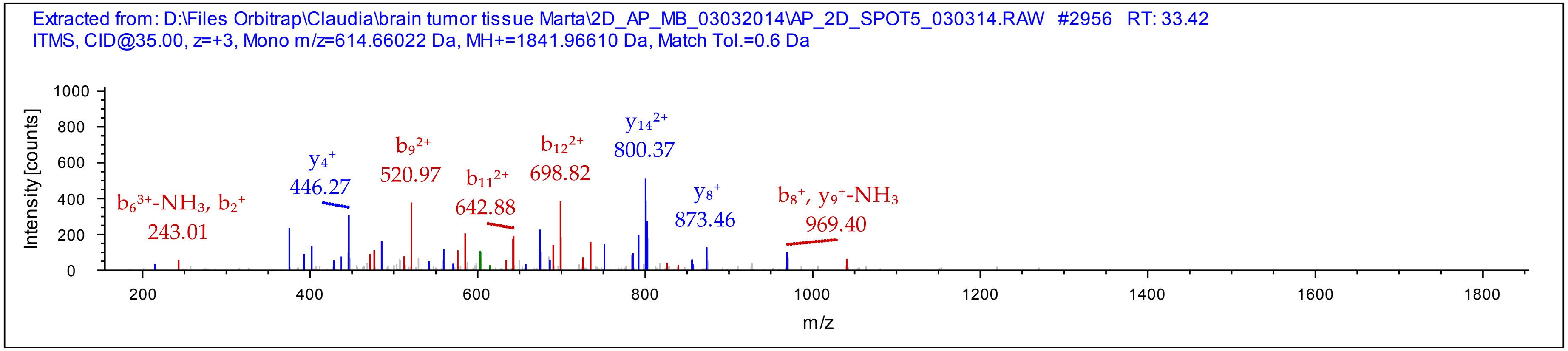
#1	b$^+$	b^{2+}	b^{3+}	Seq.	y$^+$	y^{2+}	y^{3+}	#2
1	114.09135	57.54931	38.70197	L				22
2	227.17542	114.09135	76.39666	L	2457.30972	1229.15850	819.77476	21
3	356.21802	178.61265	119.41086	E	2344.22565	1172.61646	782.08007	20
4	413.23949	207.12338	138.41801	G	2215.18305	1108.09516	739.06587	19
5	542.28209	271.64468	181.43221	E	2158.16158	1079.58443	720.05871	18
6	671.32469	336.16598	224.44641	E	2029.11898	1015.06313	677.04451	17
7	785.36762	393.18745	262.46072	N	1900.07638	950.54183	634.03031	16
8	941.46874	471.23801	314.49443	R	1786.03345	893.52036	596.01600	15
9	1054.55281	527.78004	352.18912	I	1629.93233	815.46980	543.98229	14
10	1155.60049	578.30388	385.87168	T	1516.84826	758.92777	506.28760	13
11	1268.68456	634.84592	423.56637	I	1415.80058	708.40393	472.60504	12
12	1365.73733	683.37230	455.91729	P	1302.71651	651.86189	434.91035	11
13	1464.80575	732.90651	488.94010	V	1205.66374	603.33551	402.55943	10
14	1592.86433	796.93580	531.62629	Q	1106.59532	553.80130	369.53662	9
15	1693.91201	847.45964	565.30885	T	978.53674	489.77201	326.85043	8
16	1840.98043	920.99385	614.33166	F	877.48906	439.24817	293.16787	7
17	1928.01246	964.50987	643.34234	S	730.42064	365.71396	244.14506	6
18	2042.05539	1021.53133	681.35665	N	643.38861	322.19794	215.13439	5
19	2155.13946	1078.07337	719.05134	L	529.34568	265.17648	177.12008	4
20	2283.19804	1142.10266	761.73753	Q	416.26161	208.63444	139.42539	3
21	2396.28211	1198.64469	799.43222	I	288.20303	144.60515	96.73919	2
22				R	175.11896	88.06312	59.04450	1



Sequence: LEVERDNLAQDLATVR, Charge: +3, Monoisotopic m/z: 614.66022 Da (-1.86 mmu/-3.02 ppm), MH+: 1841.96610 Da, RT: 33.42 min,
Identified with: Sequest HT (v1.3); XCorr:4.86, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):

- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

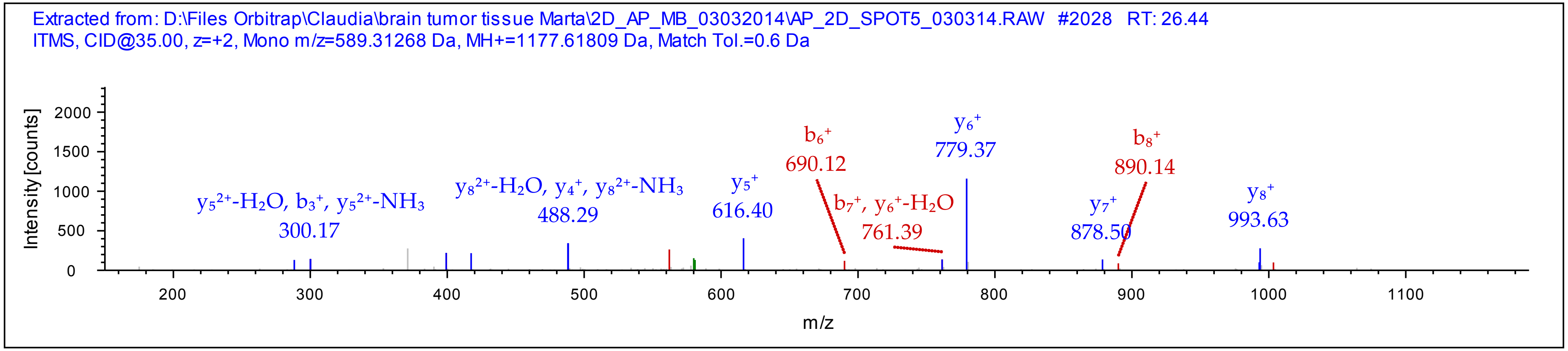
#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	114.09135	57.54931	38.70197	L				16
2	243.13395	122.07061	81.71617	E	1728.88759	864.94743	576.96738	15
3	342.20237	171.60482	114.73897	V	1599.84499	800.42613	533.95318	14
4	471.24497	236.12612	157.75317	E	1500.77657	750.89192	500.93037	13
5	627.34609	314.17668	209.78688	R	1371.73397	686.37062	457.91617	12
6	742.37304	371.69016	248.12920	D	1215.63285	608.32006	405.88247	11
7	856.41597	428.71162	286.14351	N	1100.60590	550.80659	367.54015	10
8	969.50004	485.25366	323.83820	L	986.56297	493.78512	329.52584	9
9	1040.53716	520.77222	347.51724	A	873.47890	437.24309	291.83115	8
10	1168.59574	584.80151	390.20343	Q	802.44178	401.72453	268.15211	7
11	1283.62269	642.31498	428.54575	D	674.38320	337.69524	225.46592	6
12	1396.70676	698.85702	466.24044	L	559.35625	280.18176	187.12360	5
13	1467.74388	734.37558	489.91948	A	446.27218	223.63973	149.42891	4
14	1568.79156	784.89942	523.60204	T	375.23506	188.12117	125.74987	3
15	1667.85998	834.43363	556.62484	V	274.18738	137.59733	92.06731	2
16				R	175.11896	88.06312	59.04450	1



Sequence: LADVYQAELR, Charge: +2, Monoisotopic m/z: 589.31268 Da (-1.56 mmu/-2.65 ppm), MH+: 1177.61809 Da, RT: 26.44 min,
Identified with: Sequest HT (v1.3); XCorr:3.94, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):

- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			10
2	185.12847	93.06787	A	1064.53714	532.77221	9
3	300.15542	150.58135	D	993.50002	497.25365	8
4	399.22384	200.11556	V	878.47307	439.74017	7
5	562.28716	281.64722	Y	779.40465	390.20596	6
6	690.34574	345.67651	Q	616.34133	308.67430	5
7	761.38286	381.19507	A	488.28275	244.64501	4
8	890.42546	445.71637	E	417.24563	209.12645	3
9	1003.50953	502.25840	L	288.20303	144.60515	2
10			R	175.11896	88.06312	1

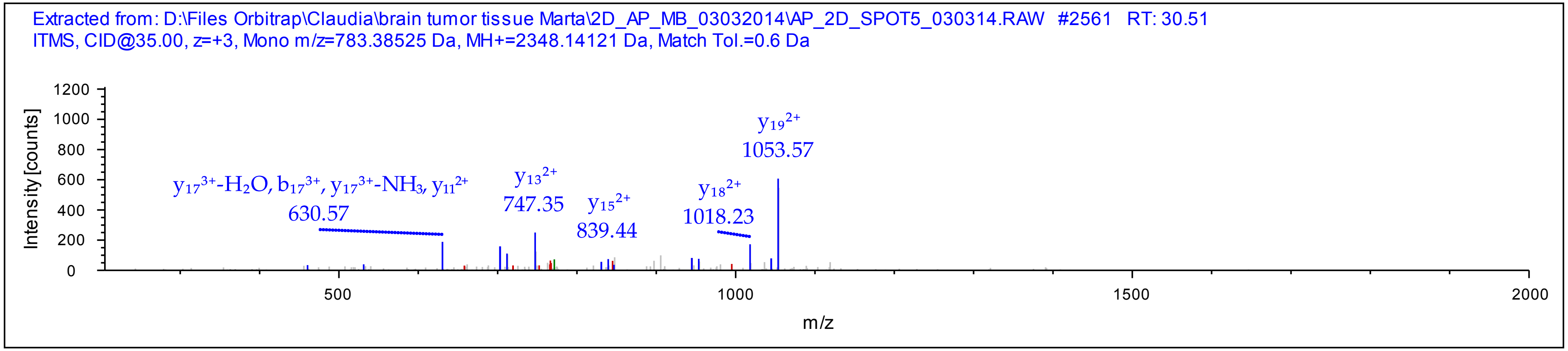

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\AP_2D_SPOT5_030314.RAW #2028 RT: 26.44
ITMS, CID@35.00, z=+2, Mono m/z=589.31268 Da, MH+=1177.61809 Da, Match Tol.=0.6 Da

Sequence: LEAENNLAAYRQEADEATLAR, Charge: +3, Monoisotopic m/z: 783.38525 Da (-2.2 mmu/-2.81 ppm), MH+: 2348.14121 Da, RT: 30.51 min,
Identified with: Sequest HT (v1.3); XCorr:3.54, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):

- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	114.09135	57.54931	38.70197	L				21
2	243.13395	122.07061	81.71617	E	2235.06373	1118.03550	745.69276	20
3	314.17107	157.58917	105.39521	A	2106.02113	1053.51420	702.67856	19
4	443.21367	222.11047	148.40941	E	2034.98401	1017.99564	678.99952	18
5	557.25660	279.13194	186.42372	N	1905.94141	953.47434	635.98532	17
6	671.29953	336.15340	224.43803	N	1791.89848	896.45288	597.97101	16
7	784.38360	392.69544	262.13272	L	1677.85555	839.43141	559.95670	15
8	855.42072	428.21400	285.81176	A	1564.77148	782.88938	522.26201	14
9	926.45784	463.73256	309.49080	A	1493.73436	747.37082	498.58297	13
10	1089.52116	545.26422	363.84524	Y	1422.69724	711.85226	474.90393	12
11	1245.62228	623.31478	415.87894	R	1259.63392	630.32060	420.54949	11
12	1373.68086	687.34407	458.56514	Q	1103.53280	552.27004	368.51578	10
13	1502.72346	751.86537	501.57934	E	975.47422	488.24075	325.82959	9
14	1573.76058	787.38393	525.25838	A	846.43162	423.71945	282.81539	8
15	1688.78753	844.89740	563.60069	D	775.39450	388.20089	259.13635	7
16	1817.83013	909.41870	606.61489	E	660.36755	330.68741	220.79403	6
17	1888.86725	944.93726	630.29393	A	531.32495	266.16611	177.77983	5
18	1989.91493	995.46110	663.97649	T	460.28783	230.64755	154.10079	4
19	2102.99900	1052.00314	701.67118	L	359.24015	180.12371	120.41823	3

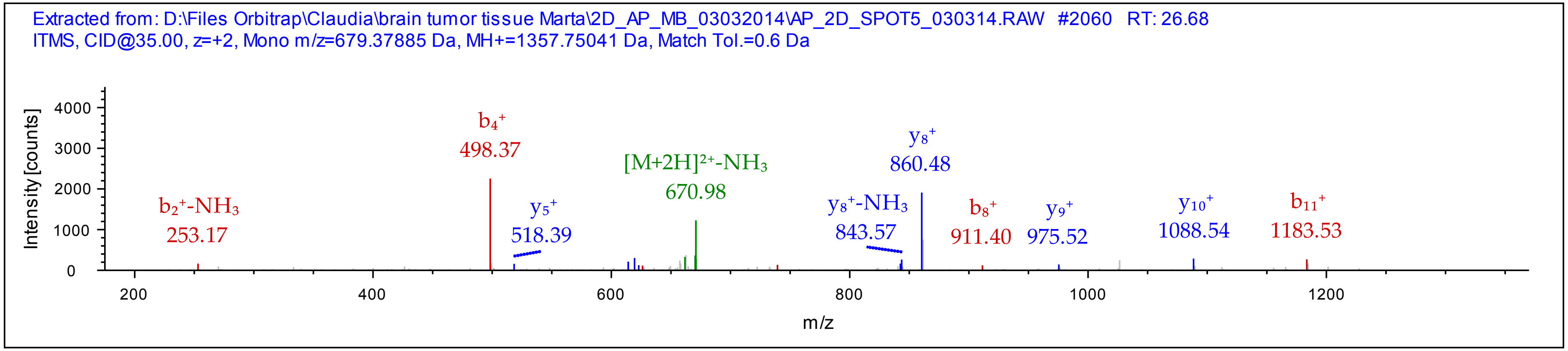
20	2174.03612	1087.52170	725.35022	A	246.15608	123.58168	82.72354	2
21				R	175.11896	88.06312	59.04450	1



Sequence: LRLDQLTANSAR, Charge: +2, Monoisotopic m/z: 679.37885 Da (-2.15 mmu/-3.16 ppm), MH+: 1357.75041 Da, RT: 26.68 min,
Identified with: Sequest HT (v1.3); XCorr:3.51, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):

- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

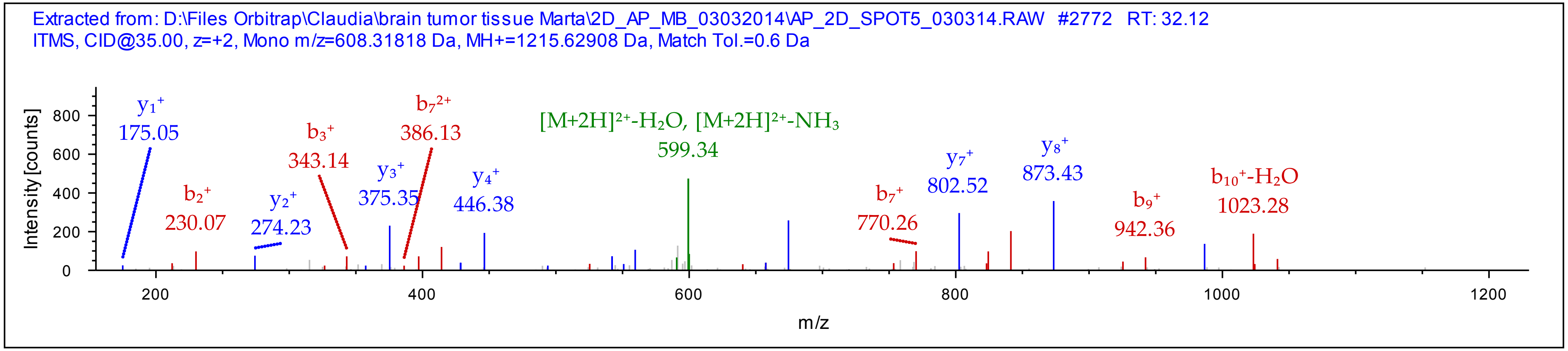
#1	**b^{+}**	**b^{2+}**	**Seq.**	**y^{+}**	**y^{2+}**	**#2**
1	114.09135	57.54931	L			12
2	270.19247	135.59987	R	1244.67063	622.83895	11
3	383.27654	192.14191	L	1088.56951	544.78839	10
4	498.30349	249.65538	D	975.48544	488.24636	9
5	626.36207	313.68467	Q	860.45849	430.73288	8
6	739.44614	370.22671	L	732.39991	366.70359	7
7	840.49382	420.75055	T	619.31584	310.16156	6
8	911.53094	456.26911	A	518.26816	259.63772	5
9	1025.57387	513.29057	N	447.23104	224.11916	4
10	1112.60590	556.80659	S	333.18811	167.09769	3
11	1183.64302	592.32515	A	246.15608	123.58168	2
12			R	175.11896	88.06312	1



Sequence: DNLAQDLATVR, Charge: +2, Monoisotopic m/z: 608.31818 Da (-1.89 mmu/-3.11 ppm), MH+: 1215.62908 Da, RT: 32.12 min,
Identified with: Sequest HT (v1.3); XCorr:3.43, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):

- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	116.03423	58.52075	D			11
2	230.07716	115.54222	N	1100.60590	550.80659	10
3	343.16123	172.08425	L	986.56297	493.78512	9
4	414.19835	207.60281	A	873.47890	437.24309	8
5	542.25693	271.63210	Q	802.44178	401.72453	7
6	657.28388	329.14558	D	674.38320	337.69524	6
7	770.36795	385.68761	L	559.35625	280.18176	5
8	841.40507	421.20617	A	446.27218	223.63973	4
9	942.45275	471.73001	T	375.23506	188.12117	3
10	1041.52117	521.26422	V	274.18738	137.59733	2
11			R	175.11896	88.06312	1

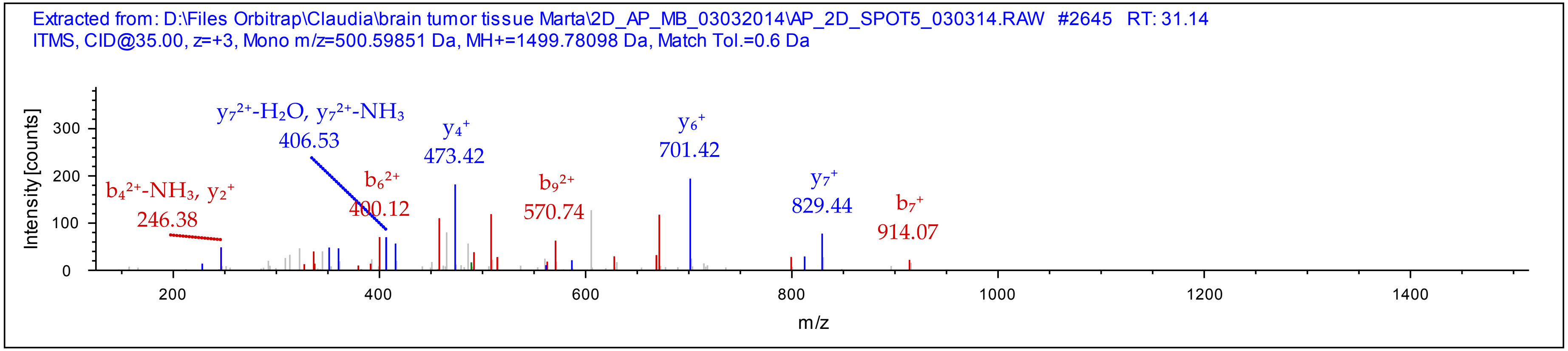


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\AP_2D_SPOT5_030314.RAW #2772 RT: 32.12
ITMS, CID@35.00, z=+2, Mono m/z=608.31818 Da, MH+=1215.62908 Da, Match Tol.=0.6 Da

Sequence: HLQEYQDLLNVK, Charge: +3, Monoisotopic m/z: 500.59851 Da (-1.45 mmu/-2.89 ppm), MH+: 1499.78098 Da, RT: 31.14 min,
Identified with: Sequest HT (v1.3); XCorr:3.42, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):

- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

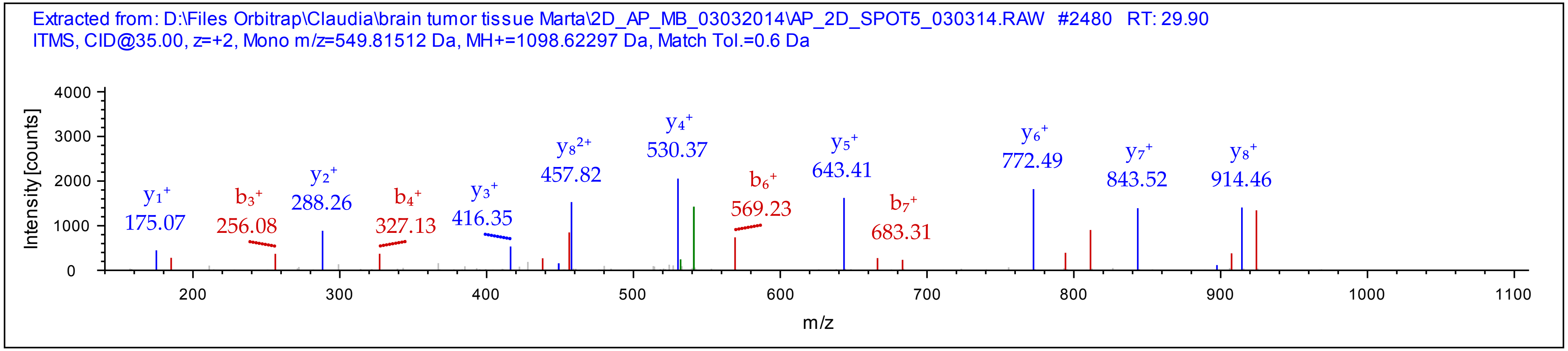
#1	b⁺	b²⁺	b³⁺	Seq.	y⁺	y²⁺	y³⁺	#2
1	138.06619	69.53673	46.69358	H				12
2	251.15026	126.07877	84.38827	L	1362.72640	681.86684	454.91365	11
3	379.20884	190.10806	127.07446	Q	1249.64233	625.32480	417.21896	10
4	508.25144	254.62936	170.08866	E	1121.58375	561.29551	374.53277	9
5	671.31476	336.16102	224.44310	Y	992.54115	496.77421	331.51857	8
6	799.37334	400.19031	267.12930	Q	829.47783	415.24255	277.16413	7
7	914.40029	457.70378	305.47161	D	701.41925	351.21326	234.47793	6
8	1027.48436	514.24582	343.16630	L	586.39230	293.69979	196.13562	5
9	1140.56843	570.78785	380.86099	L	473.30823	237.15775	158.44093	4
10	1254.61136	627.80932	418.87530	N	360.22416	180.61572	120.74624	3
11	1353.67978	677.34353	451.89811	V	246.18123	123.59425	82.73193	2
12				K	147.11281	74.06004	49.70912	1



Sequence: ALAAELNQLR, Charge: +2, Monoisotopic m/z: 549.81512 Da (-1.84 mmu/-3.34 ppm), MH+: 1098.62297 Da, RT: 29.90 min,
Identified with: Sequest HT (v1.3); XCorr:3.36, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):

- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

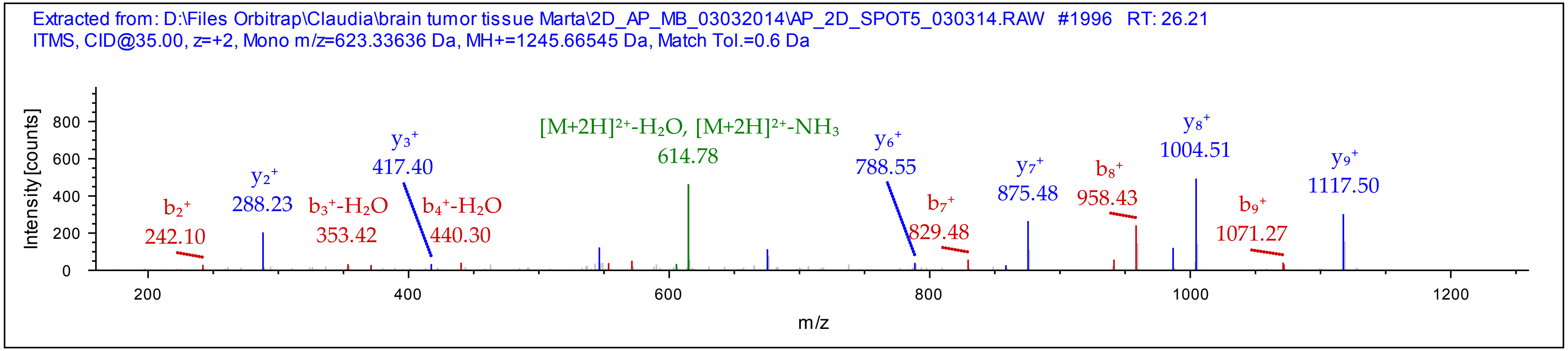
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	72.04440	36.52584	A			10
2	185.12847	93.06787	L	1027.58952	514.29840	9
3	256.16559	128.58643	A	914.50545	457.75636	8
4	327.20271	164.10499	A	843.46833	422.23780	7
5	456.24531	228.62629	E	772.43121	386.71924	6
6	569.32938	285.16833	L	643.38861	322.19794	5
7	683.37231	342.18979	N	530.30454	265.65591	4
8	811.43089	406.21908	Q	416.26161	208.63444	3
9	924.51496	462.76112	L	288.20303	144.60515	2
10			R	175.11896	88.06312	1



Sequence: KIESLEEEIR, Charge: +2, Monoisotopic m/z: 623.33636 Da (-1.56 mmu/-2.5 ppm), MH+: 1245.66545 Da, RT: 26.21 min,
Identified with: Sequest HT (v1.3); XCorr:3.27, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):

- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

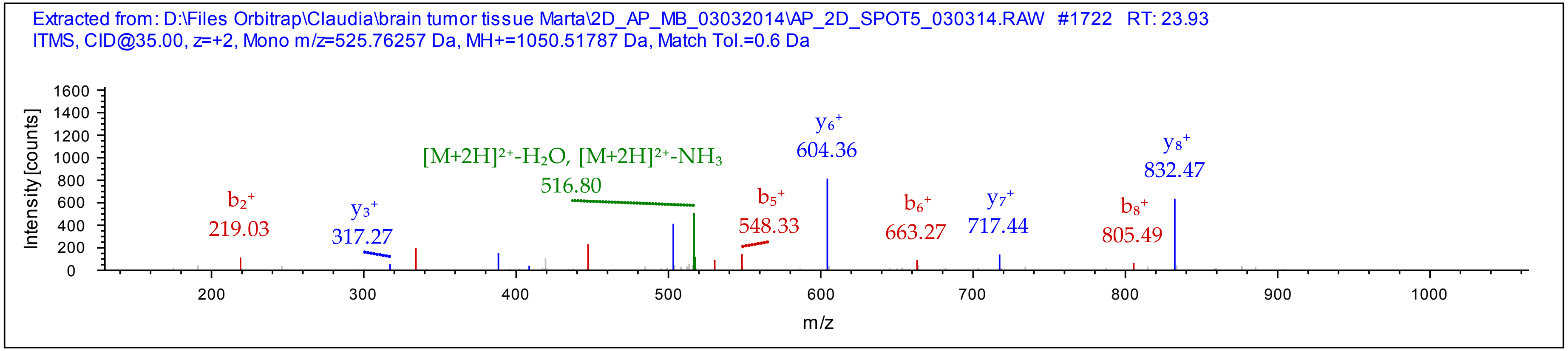
#1	b$^+$	b^{2+}	Seq.	y$^+$	y^{2+}	#2
1	129.10225	65.05476	K			10
2	242.18632	121.59680	I	1117.57360	559.29044	9
3	371.22892	186.11810	E	1004.48953	502.74840	8
4	458.26095	229.63411	S	875.44693	438.22710	7
5	571.34502	286.17615	L	788.41490	394.71109	6
6	700.38762	350.69745	E	675.33083	338.16905	5
7	829.43022	415.21875	E	546.28823	273.64775	4
8	958.47282	479.74005	E	417.24563	209.12645	3
9	1071.55689	536.28208	I	288.20303	144.60515	2
10			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\AP_2D_SPOT5_030314.RAW #1996 RT: 26.21
ITMS, CID@35.00, z=+2, Mono m/z=623.33636 Da, MH+=1245.66545 Da, Match Tol.=0.6 Da

Sequence: FADLTDAAAR, Charge: +2, Monoisotopic m/z: 525.76257 Da (-1.82 mmu/-3.47 ppm), MH+: 1050.51787 Da, RT: 23.93 min,
Identified with: Sequest HT (v1.3); XCorr:3.27, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3
Protein references (1):

- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

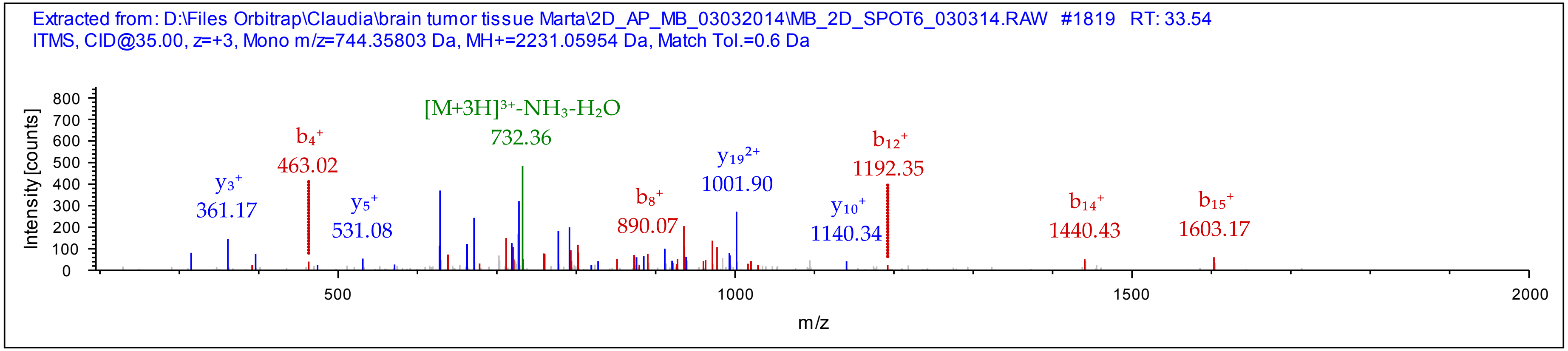
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	148.07570	74.54149	F			10
2	219.11282	110.06005	A	903.45309	452.23018	9
3	334.13977	167.57352	D	832.41597	416.71162	8
4	447.22384	224.11556	L	717.38902	359.19815	7
5	548.27152	274.63940	T	604.30495	302.65611	6
6	663.29847	332.15287	D	503.25727	252.13227	5
7	734.33559	367.67143	A	388.23032	194.61880	4
8	805.37271	403.18999	A	317.19320	159.10024	3
9	876.40983	438.70855	A	246.15608	123.58168	2
10			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\AP_2D_SPOT5_030314.RAW #1722 RT: 23.93
ITMS, CID@35.00, z=+2, Mono m/z=525.76257 Da, MH+=1050.51787 Da, Match Tol.=0.6 Da
Intensity [counts]
1600
1400
1200
1000
800
600
400
200
0
m/z
200
300
400
500
600
700
800
900
1000
b_2^+
219.03
y_3^+
317.27
$[M+2H]^{2+}-H_2O, [M+2H]^{2+}-NH_3$
516.80
b_5^+
548.33
y_6^+
604.36
b_6^+
663.27
y_7^+
717.44
b_8^+
805.49
y_8^+
832.47

Spot #	Uniprot Accession Number	Description	MW[a] [kDa]	pI [a]	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*
6	P60709	Actin, cytoplasmic 1	41.7	5.3	185.9	44.00%	6	11	MB	NS	1.4 ↑ in PA

Sequence: DLYANTVLSGGTTMYPGIADR, M14-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 744.35803 Da (-1.81 mmu/-2.43 ppm), MH+: 2231.05954 Da, RT: 33.54 min,
Identified with: Sequest HT (v1.3); XCorr:4.77, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (2):
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]

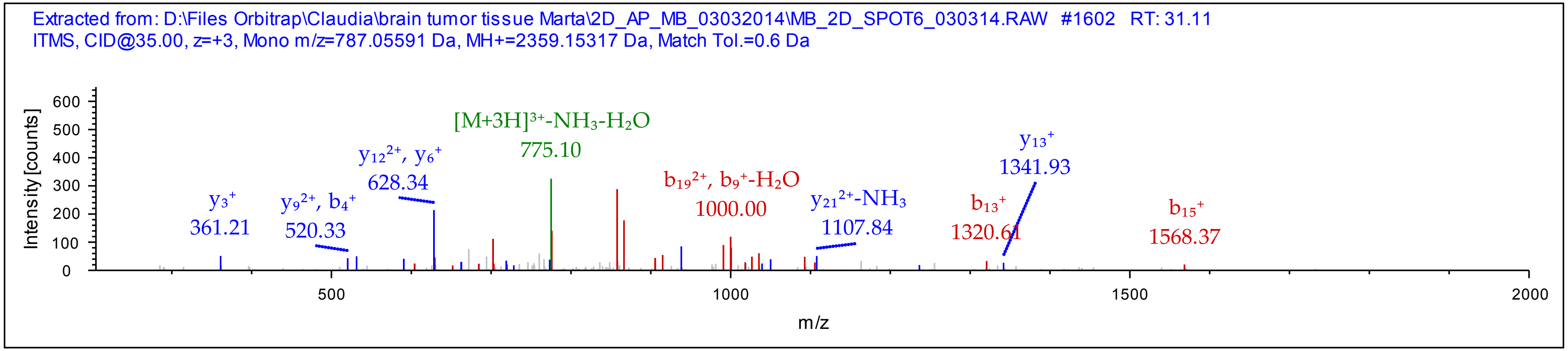
#1	**b^{+}**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^{+}**	**y^{2+}**	**y^{3+}**	**#2**
1	116.03423	58.52075	39.34959	D				21
2	229.11830	115.06279	77.04428	L	2116.03802	1058.52265	706.01752	20
3	392.18162	196.59445	131.39872	Y	2002.95395	1001.98061	668.32283	19
4	463.21874	232.11301	155.07776	A	1839.89063	920.44895	613.96839	18
5	577.26167	289.13447	193.09207	N	1768.85351	884.93039	590.28935	17
6	678.30935	339.65831	226.77463	T	1654.81058	827.90893	552.27504	16
7	777.37777	389.19252	259.79744	V	1553.76290	777.38509	518.59248	15
8	890.46184	445.73456	297.49213	L	1454.69448	727.85088	485.56968	14
9	977.49387	489.25057	326.50281	S	1341.61041	671.30884	447.87499	13
10	1034.51534	517.76131	345.50996	G	1254.57838	627.79283	418.86431	12
11	1091.53681	546.27204	364.51712	G	1197.55691	599.28209	399.85715	11
12	1192.58449	596.79588	398.19968	T	1140.53544	570.77136	380.85000	10
13	1293.63217	647.31972	431.88224	T	1039.48776	520.24752	347.16744	9
14	1440.66758	720.83743	480.89404	M-Oxidation	938.44008	469.72368	313.48488	8
15	1603.73090	802.36909	535.24848	Y	791.40466	396.20597	264.47307	7
16	1700.78367	850.89547	567.59941	P	628.34134	314.67431	210.11863	6
17	1757.80514	879.40621	586.60656	G	531.28857	266.14792	177.76771	5
18	1870.88921	935.94824	624.30125	I	474.26710	237.63719	158.76055	4
19	1941.92633	971.46680	647.98029	A	361.18303	181.09515	121.06586	3
20	2056.95328	1028.98028	686.32261	D	290.14591	145.57659	97.38682	2
21				R	175.11896	88.06312	59.04450	1



Sequence: KDLYANTVLSGGTTMYPGIADR, M15-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 787.05591 Da (-2.26 mmu/-2.87 ppm), MH+: 2359.15317 Da, RT: 31.11 min,
Identified with: Sequest HT (v1.3); XCorr:3.94, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (2):
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	129.10225	65.05476	43.70560	K				22
2	244.12920	122.56824	82.04792	D	2231.06497	1116.03612	744.35984	21
3	357.21327	179.11027	119.74261	L	2116.03802	1058.52265	706.01752	20
4	520.27659	260.64193	174.09705	Y	2002.95395	1001.98061	668.32283	19
5	591.31371	296.16049	197.77609	A	1839.89063	920.44895	613.96839	18
6	705.35664	353.18196	235.79040	N	1768.85351	884.93039	590.28935	17
7	806.40432	403.70580	269.47296	T	1654.81058	827.90893	552.27504	16
8	905.47274	453.24001	302.49576	V	1553.76290	777.38509	518.59248	15
9	1018.55681	509.78204	340.19045	L	1454.69448	727.85088	485.56968	14
10	1105.58884	553.29806	369.20113	S	1341.61041	671.30884	447.87499	13
11	1162.61031	581.80879	388.20829	G	1254.57838	627.79283	418.86431	12
12	1219.63178	610.31953	407.21544	G	1197.55691	599.28209	399.85715	11
13	1320.67946	660.84337	440.89800	T	1140.53544	570.77136	380.85000	10
14	1421.72714	711.36721	474.58056	T	1039.48776	520.24752	347.16744	9
15	1568.76255	784.88491	523.59237	M-Oxidation	938.44008	469.72368	313.48488	8
16	1731.82587	866.41657	577.94681	Y	791.40466	396.20597	264.47307	7
17	1828.87864	914.94296	610.29773	P	628.34134	314.67431	210.11863	6
18	1885.90011	943.45369	629.30489	G	531.28857	266.14792	177.76771	5

19	1998.98418	999.99573	666.99958	I	474.26710	237.63719	158.76055	4
20	2070.02130	1035.51429	690.67862	A	361.18303	181.09515	121.06586	3
21	2185.04825	1093.02776	729.02093	D	290.14591	145.57659	97.38682	2
22				R	175.11896	88.06312	59.04450	1

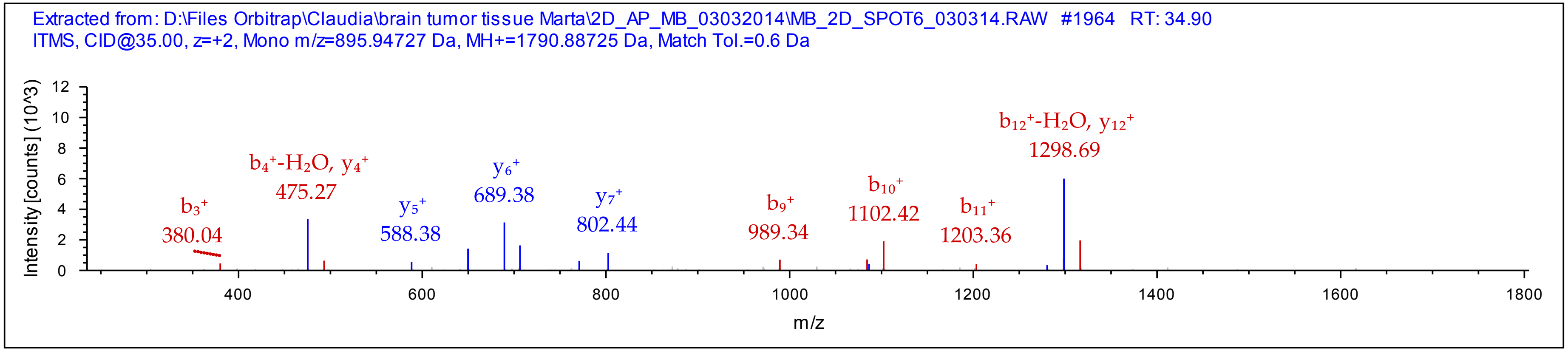


Sequence: SYELPDGQVITIGNER, Charge: +2, Monoisotopic m/z: 895.94727 Da (-2.37 mmu/-2.64 ppm), MH+: 1790.88725 Da, RT: 34.90 min,
Identified with: Sequest HT (v1.3); XCorr:3.90, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (10):

- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 - [ACTBL_HUMAN]
- Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1 - [ACTBM_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]
- POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 - [POTEE_HUMAN]
- POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2 - [POTEF_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	88.03931	44.52329	S			16
2	251.10263	126.05495	Y	1703.85996	852.43362	15
3	380.14523	190.57625	E	1540.79664	770.90196	14
4	493.22930	247.11829	L	1411.75404	706.38066	13
5	590.28207	295.64467	P	1298.66997	649.83862	12
6	705.30902	353.15815	D	1201.61720	601.31224	11
7	762.33049	381.66888	G	1086.59025	543.79876	10

8	890.38907	445.69817	Q	1029.56878	515.28803	9
9	989.45749	495.23238	V	901.51020	451.25874	8
10	1102.54156	551.77442	I	802.44178	401.72453	7
11	1203.58924	602.29826	T	689.35771	345.18249	6
12	1316.67331	658.84029	I	588.31003	294.65865	5
13	1373.69478	687.35103	G	475.22596	238.11662	4
14	1487.73771	744.37249	N	418.20449	209.60588	3
15	1616.78031	808.89379	E	304.16156	152.58442	2
16			R	175.11896	88.06312	1

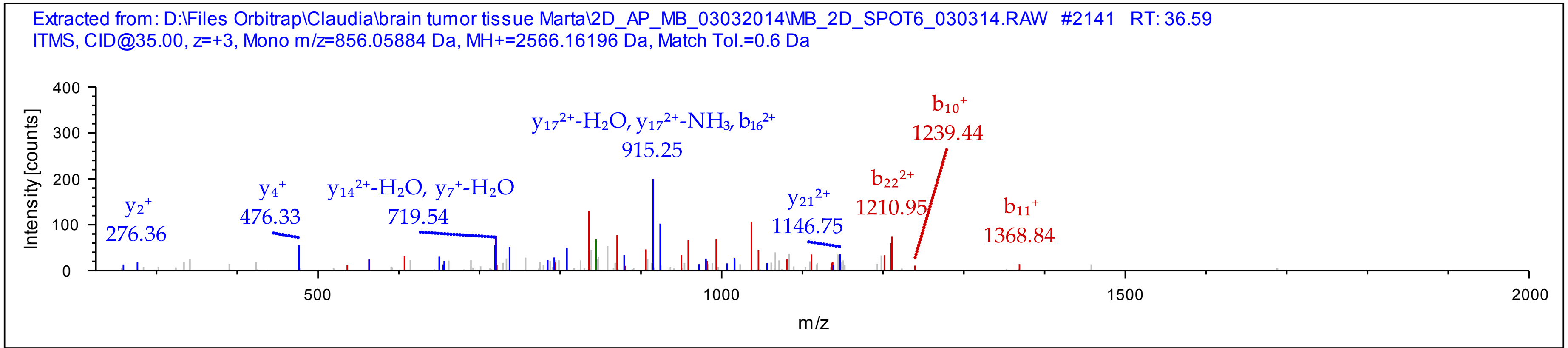

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT6_030314.RAW #1964 RT: 34.90
ITMS, CID@35.00, z=+2, Mono m/z=895.94727 Da, MH+=1790.88725 Da, Match Tol.=0.6 Da

Sequence: LCYVALDFEQEMATAASSSSLEK, C2-Carbamidomethyl (57.02146 Da), M12-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 856.05884 Da (-2.3 mmu/-2.69 ppm), MH+: 2566.16196 Da, RT: 36.59 min,
Identified with: Sequest HT (v1.3); XCorr:3.79, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 - [POTEE_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	114.09135	57.54931	38.70197	L				23
2	274.12200	137.56464	92.04552	C-Carbamidomethyl	2453.08479	1227.04603	818.36645	22
3	437.18532	219.09630	146.39996	Y	2293.05414	1147.03071	765.02290	21
4	536.25374	268.63051	179.42276	V	2129.99082	1065.49905	710.66846	20

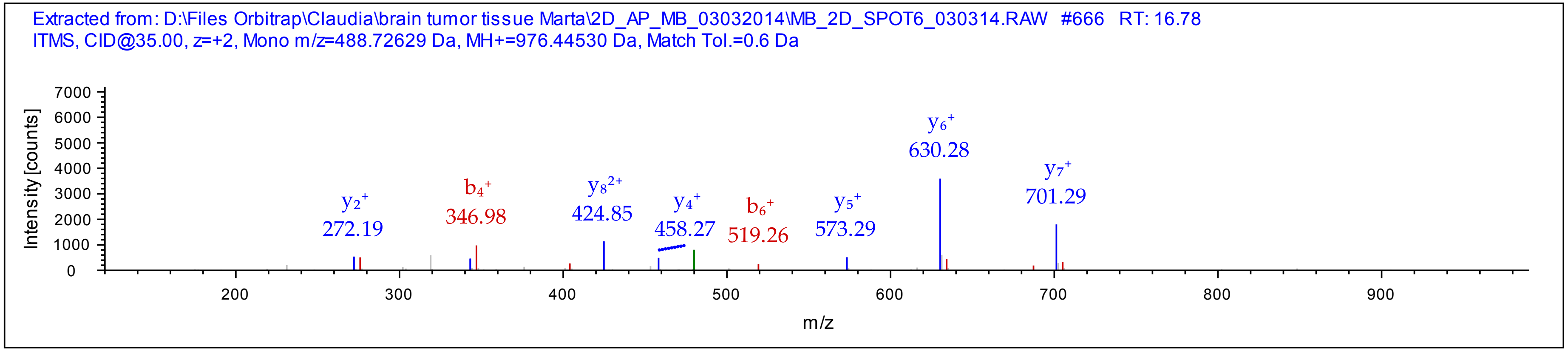
5	607.29086	304.14907	203.10180	A	2030.92240	1015.96484	677.64565	19
6	720.37493	360.69110	240.79649	L	1959.88528	980.44628	653.96661	18
7	835.40188	418.20458	279.13881	D	1846.80121	923.90424	616.27192	17
8	982.47030	491.73879	328.16162	F	1731.77426	866.39077	577.92960	16
9	1111.51290	556.26009	371.17582	E	1584.70584	792.85656	528.90680	15
10	1239.57148	620.28938	413.86201	Q	1455.66324	728.33526	485.89260	14
11	1368.61408	684.81068	456.87621	E	1327.60466	664.30597	443.20640	13
12	1515.64950	758.32839	505.88802	M-Oxidation	1198.56206	599.78467	400.19220	12
13	1586.68662	793.84695	529.56706	A	1051.52664	526.26696	351.18040	11
14	1687.73430	844.37079	563.24962	T	980.48952	490.74840	327.50136	10
15	1758.77142	879.88935	586.92866	A	879.44184	440.22456	293.81880	9
16	1829.80854	915.40791	610.60770	A	808.40472	404.70600	270.13976	8
17	1916.84057	958.92392	639.61837	S	737.36760	369.18744	246.46072	7
18	2003.87260	1002.43994	668.62905	S	650.33557	325.67142	217.45004	6
19	2090.90463	1045.95595	697.63973	S	563.30354	282.15541	188.43936	5
20	2177.93666	1089.47197	726.65040	S	476.27151	238.63939	159.42869	4
21	2291.02073	1146.01400	764.34509	L	389.23948	195.12338	130.41801	3
22	2420.06333	1210.53530	807.35929	E	276.15541	138.58134	92.72332	2
23				K	147.11281	74.06004	49.70912	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT6_030314.RAW #2141 RT: 36.59
ITMS, CID@35.00, z=+3, Mono m/z=856.05884 Da, MH+=2566.16196 Da, Match Tol.=0.6 Da

Sequence: AGFAGDDAPR, Charge: +2, Monoisotopic m/z: 488.72629 Da (-1.53 mmu/-3.13 ppm), MH+: 976.44530 Da, RT: 16.78 min,
Identified with: Sequest HT (v1.3); XCorr:2.90, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3
Protein references (10):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]

- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]
- POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 - [POTEE_HUMAN]
- POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2 - [POTEF_HUMAN]
- POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=3 SV=1 - [POTEI_HUMAN]
- POTE ankyrin domain family member J OS=Homo sapiens GN=POTEJ PE=3 SV=1 - [POTEJ_HUMAN]

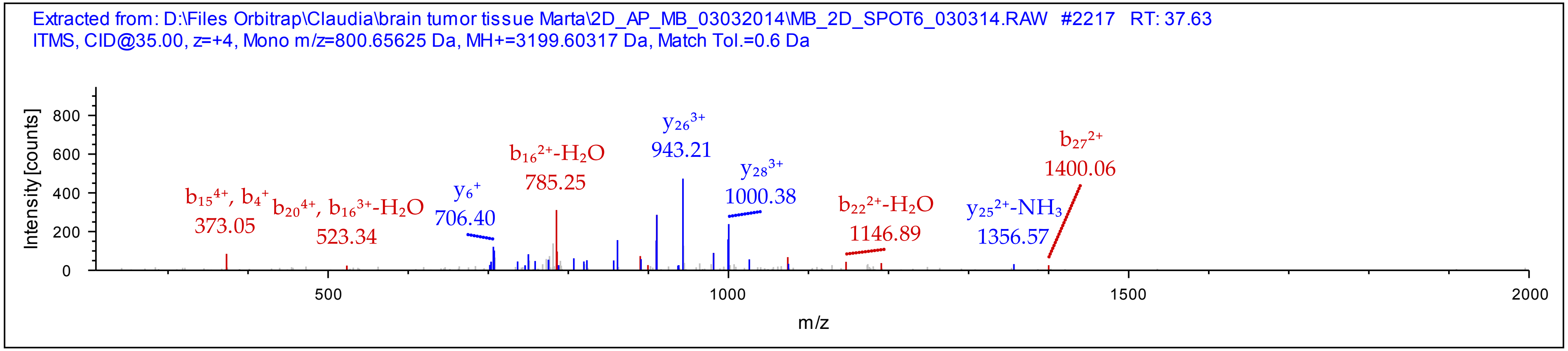
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	72.04440	36.52584	A			10
2	129.06587	65.03657	G	905.41123	453.20925	9
3	276.13429	138.57078	F	848.38976	424.69852	8
4	347.17141	174.08934	A	701.32134	351.16431	7
5	404.19288	202.60008	G	630.28422	315.64575	6
6	519.21983	260.11355	D	573.26275	287.13501	5
7	634.24678	317.62703	D	458.23580	229.62154	4
8	705.28390	353.14559	A	343.20885	172.10806	3
9	802.33667	401.67197	P	272.17173	136.58950	2
10			R	175.11896	88.06312	1



Sequence: TTGIVMDSGDGVTHTVPIYEGYALPHAILR, M6-Oxidation (15.99492 Da)
Charge: +4, Monoisotopic m/z: 800.65625 Da (-1.55 mmu/-1.93 ppm), MH+: 3199.60317 Da, RT: 37.63 min,
Identified with: Sequest HT (v1.3); XCorr:2.86, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3
Protein references (2):
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**b^{4+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**y^{4+}**	**#2**

1	102.05496	51.53112	34.68984	26.26920	T					30
2	203.10264	102.05496	68.37240	51.53112	T	3098.56168	1549.78448	1033.52541	775.39588	29
3	260.12411	130.56569	87.37955	65.78648	G	2997.51400	1499.26064	999.84285	750.13396	28
4	373.20818	187.10773	125.07424	94.05750	I	2940.49253	1470.74990	980.83569	735.87859	27
5	472.27660	236.64194	158.09705	118.82461	V	2827.40846	1414.20787	943.14100	707.60757	26
6	619.31201	310.15964	207.10885	155.58346	M-Oxidation	2728.34004	1364.67366	910.11820	682.84047	25
7	734.33896	367.67312	245.45117	184.34020	D	2581.30462	1291.15595	861.10639	646.08161	24
8	821.37099	411.18913	274.46185	206.09821	S	2466.27767	1233.64247	822.76407	617.32488	23
9	878.39246	439.69987	293.46900	220.35357	G	2379.24564	1190.12646	793.75340	595.56687	22
10	993.41941	497.21334	331.81132	249.11031	D	2322.22417	1161.61572	774.74624	581.31150	21
11	1050.44088	525.72408	350.81848	263.36568	G	2207.19722	1104.10225	736.40392	552.55476	20
12	1149.50930	575.25829	383.84128	288.13278	V	2150.17575	1075.59151	717.39677	538.29940	19
13	1250.55698	625.78213	417.52384	313.39470	T	2051.10733	1026.05730	684.37396	513.53229	18
14	1387.61589	694.31158	463.21015	347.65943	H	1950.05965	975.53346	650.69140	488.27037	17
15	1488.66357	744.83542	496.89271	372.92135	T	1813.00074	907.00401	605.00510	454.00564	16
16	1587.73199	794.36963	529.91551	397.68846	V	1711.95306	856.48017	571.32254	428.74372	15
17	1684.78476	842.89602	562.26644	421.95165	P	1612.88464	806.94596	538.29973	403.97662	14
18	1797.86883	899.43805	599.96113	450.22267	I	1515.83187	758.41957	505.94881	379.71343	13
19	1960.93215	980.96971	654.31557	490.98850	Y	1402.74780	701.87754	468.25412	351.44241	12
20	2089.97475	1045.49101	697.32977	523.24915	E	1239.68448	620.34588	413.89968	310.67658	11
21	2146.99622	1074.00175	716.33692	537.50451	G	1110.64188	555.82458	370.88548	278.41593	10
22	2310.05954	1155.53341	770.69136	578.27034	Y	1053.62041	527.31384	351.87832	264.16056	9
23	2381.09666	1191.05197	794.37040	596.02962	A	890.55709	445.78218	297.52388	223.39473	8
24	2494.18073	1247.59400	832.06509	624.30064	L	819.51997	410.26362	273.84484	205.63545	7
25	2591.23350	1296.12039	864.41602	648.56383	P	706.43590	353.72159	236.15015	177.36443	6
26	2728.29241	1364.64984	910.10232	682.82856	H	609.38313	305.19520	203.79923	153.10124	5
27	2799.32953	1400.16840	933.78136	700.58784	A	472.32422	236.66575	158.11292	118.83651	4
28	2912.41360	1456.71044	971.47605	728.85886	I	401.28710	201.14719	134.43388	101.07723	3
29	3025.49767	1513.25247	1009.17074	757.12988	L	288.20303	144.60515	96.73919	72.80622	2
30					R	175.11896	88.06312	59.04450	44.53520	1

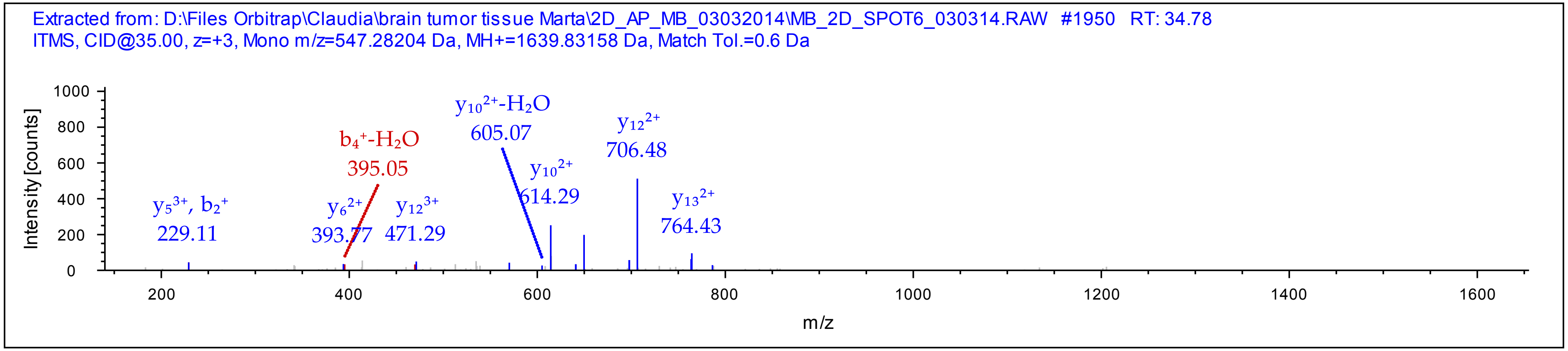


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT6_030314.RAW #2217 RT: 37.63
ITMS, CID@35.00, z=+4, Mono m/z=800.65625 Da, MH+=3199.60317 Da, Match Tol.=0.6 Da

Sequence: LDLAGRDLTDYLMK, M13-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 547.28204 Da (-1.5 mmu/-2.74 ppm), MH+: 1639.83158 Da, RT: 34.78 min,
Identified with: Sequest HT (v1.3); XCorr:2.84, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (7):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 - [ACTBL_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]

#1	b^{+}	b^{2+}	b^{3+}	Seq.	y^{+}	y^{2+}	y^{3+}	#2
1	114.09135	57.54931	38.70197	L				14
2	229.11830	115.06279	77.04428	D	1526.75200	763.87964	509.58885	13
3	342.20237	171.60482	114.73897	L	1411.72505	706.36616	471.24653	12
4	413.23949	207.12338	138.41801	A	1298.64098	649.82413	433.55184	11
5	470.26096	235.63412	157.42517	G	1227.60386	614.30557	409.87280	10
6	626.36208	313.68468	209.45888	R	1170.58239	585.79483	390.86565	9
7	741.38903	371.19815	247.80119	D	1014.48127	507.74427	338.83194	8
8	854.47310	427.74019	285.49588	L	899.45432	450.23080	300.48962	7
9	955.52078	478.26403	319.17844	T	786.37025	393.68876	262.79493	6
10	1070.54773	535.77750	357.52076	D	685.32257	343.16492	229.11237	5
11	1233.61105	617.30916	411.87520	Y	570.29562	285.65145	190.77006	4
12	1346.69512	673.85120	449.56989	L	407.23230	204.11979	136.41562	3
13	1493.73053	747.36890	498.58169	M-Oxidation	294.14823	147.57775	98.72093	2

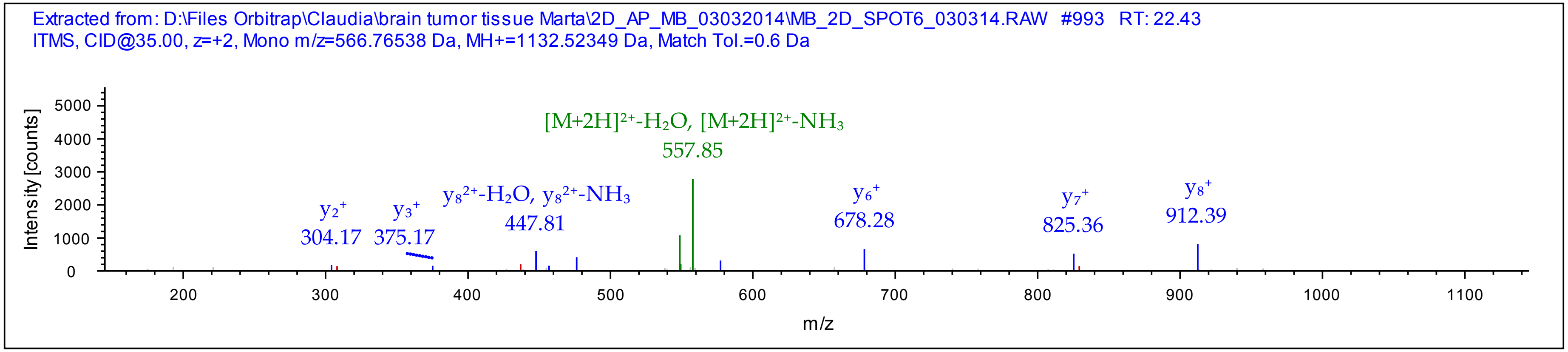
14				K	147.11281	74.06004	49.70912	1



Sequence: GYSFTTTAER, Charge: +2, Monoisotopic m/z: 566.76538 Da (-1.74 mmu/-3.07 ppm), MH+: 1132.52349 Da, RT: 22.43 min,
Identified with: Sequest HT (v1.3); XCorr:2.82, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (2):
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	58.02875	29.51801	G			10
2	221.09207	111.04967	Y	1075.50549	538.25638	9
3	308.12410	154.56569	S	912.44217	456.72472	8
4	455.19252	228.09990	F	825.41014	413.20871	7
5	556.24020	278.62374	T	678.34172	339.67450	6
6	657.28788	329.14758	T	577.29404	289.15066	5
7	758.33556	379.67142	T	476.24636	238.62682	4
8	829.37268	415.18998	A	375.19868	188.10298	3
9	958.41528	479.71128	E	304.16156	152.58442	2
10			R	175.11896	88.06312	1



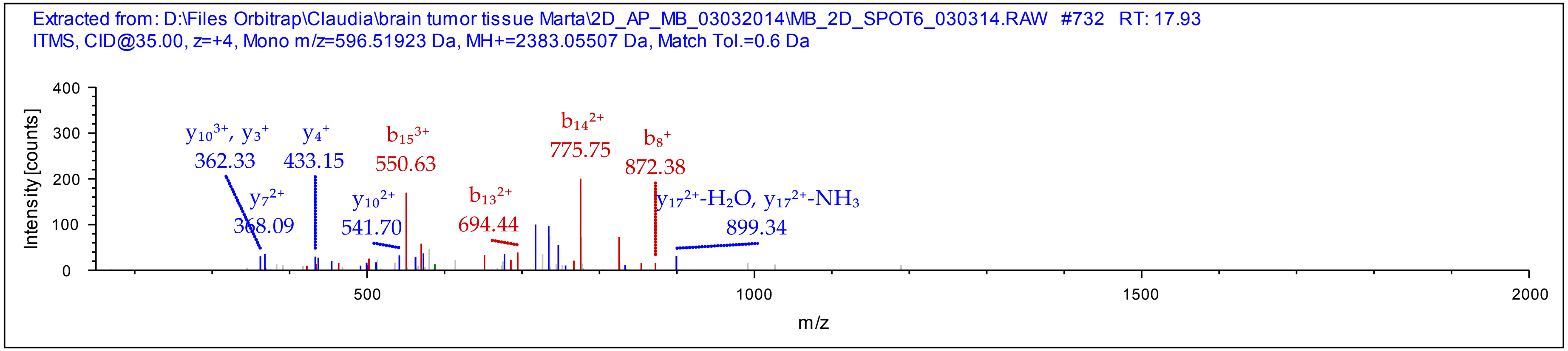
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT6_030314.RAW #993 RT: 22.43
ITMS, CID@35.00, z=+2, Mono m/z=566.76538 Da, MH+=1132.52349 Da, Match Tol.=0.6 Da

Sequence: HQGVMVGMGQKDSYVGDEAQSK, M5-Oxidation (15.99492 Da), M8-Oxidation (15.99492 Da)
Charge: +4, Monoisotopic m/z: 596.51923 Da (-2.58 mmu/-4.33 ppm), MH+: 2383.05507 Da, RT: 17.93 min,
Identified with: Sequest HT (v1.3); XCorr:2.73, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (6):

- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]

#1	b^+	b^{2+}	b^{3+}	b^{4+}	Seq.	y^+	y^{2+}	y^{3+}	y^{4+}	#2
1	138.06619	69.53673	46.69358	35.27200	H					22
2	266.12477	133.56602	89.37977	67.28665	Q	2246.00649	1123.50688	749.34035	562.25708	21
3	323.14624	162.07676	108.38693	81.54202	G	2117.94791	1059.47759	706.65415	530.24244	20
4	422.21466	211.61097	141.40974	106.30912	V	2060.92644	1030.96686	687.64700	515.98707	19
5	569.25007	285.12867	190.42154	143.06798	M-Oxidation	1961.85802	981.43265	654.62419	491.21996	18
6	668.31849	334.66288	223.44435	167.83508	V	1814.82261	907.91494	605.61239	454.46111	17
7	725.33996	363.17362	242.45150	182.09045	G	1715.75419	858.38073	572.58958	429.69400	16
8	872.37538	436.69133	291.46331	218.84930	M-Oxidation	1658.73272	829.87000	553.58242	415.43864	15
9	929.39685	465.20206	310.47047	233.10467	G	1511.69730	756.35229	504.57062	378.67978	14
10	1057.45543	529.23135	353.15666	265.11931	Q	1454.67583	727.84155	485.56346	364.42442	13
11	1185.55040	593.27884	395.85498	297.14306	K	1326.61725	663.81226	442.87727	332.40977	12
12	1300.57735	650.79231	434.19730	325.89979	D	1198.52228	599.76478	400.17894	300.38603	11
13	1387.60938	694.30833	463.20798	347.65780	S	1083.49533	542.25130	361.83663	271.62929	10

14	1550.67270	775.83999	517.56242	388.42363	Y	996.46330	498.73529	332.82595	249.87128	9
15	1649.74112	825.37420	550.58522	413.19074	V	833.39998	417.20363	278.47151	209.10545	8
16	1706.76259	853.88493	569.59238	427.44610	G	734.33156	367.66942	245.44870	184.33835	7
17	1821.78954	911.39841	607.93470	456.20284	D	677.31009	339.15868	226.44155	170.08298	6
18	1950.83214	975.91971	650.94890	488.46349	E	562.28314	281.64521	188.09923	141.32624	5
19	2021.86926	1011.43827	674.62794	506.22277	A	433.24054	217.12391	145.08503	109.06559	4
20	2149.92784	1075.46756	717.31413	538.23742	Q	362.20342	181.60535	121.40599	91.30631	3
21	2236.95987	1118.98357	746.32481	559.99542	S	234.14484	117.57606	78.71980	59.29167	2
22					K	147.11281	74.06004	49.70912	37.53366	1

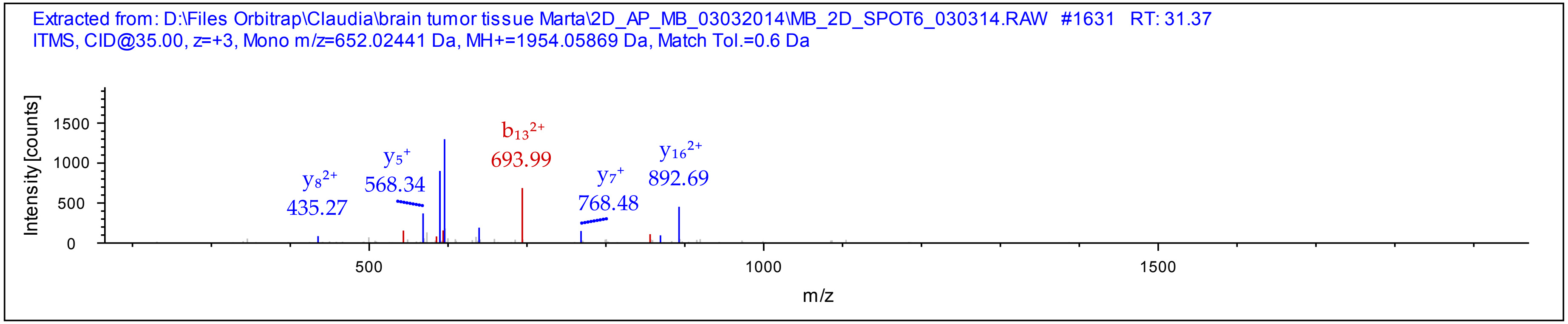


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT6_030314.RAW #732 RT: 17.93
ITMS, CID@35.00, z=+4, Mono m/z=596.51923 Da, MH+=2383.05507 Da, Match Tol.=0.6 Da

Sequence: VAPEEHPVLLTEAPLNPK, Charge: +3, Monoisotopic m/z: 652.02441 Da (-1.94 mmu/-2.97 ppm), MH+: 1954.05869 Da, RT: 31.37 min,
Identified with: Sequest HT (v1.3); XCorr:2.84, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (2):
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]

#1	b^{+}	b^{2+}	b^{3+}	Seq.	y^{+}	y^{2+}	y^{3+}	#2
1	100.07570	50.54149	34.03008	V				18
2	171.11282	86.06005	57.70912	A	1854.99608	928.00168	619.00354	17
3	268.16559	134.58643	90.06005	P	1783.95896	892.48312	595.32450	16
4	397.20819	199.10773	133.07425	E	1686.90619	843.95673	562.97358	15
5	526.25079	263.62903	176.08845	E	1557.86359	779.43543	519.95938	14
6	663.30970	332.15849	221.77475	H	1428.82099	714.91413	476.94518	13
7	760.36247	380.68487	254.12567	P	1291.76208	646.38468	431.25888	12
8	859.43089	430.21908	287.14848	V	1194.70931	597.85829	398.90795	11
9	972.51496	486.76112	324.84317	L	1095.64089	548.32408	365.88515	10
10	1085.59903	543.30315	362.53786	L	982.55682	491.78205	328.19046	9
11	1186.64671	593.82699	396.22042	T	869.47275	435.24001	290.49577	8

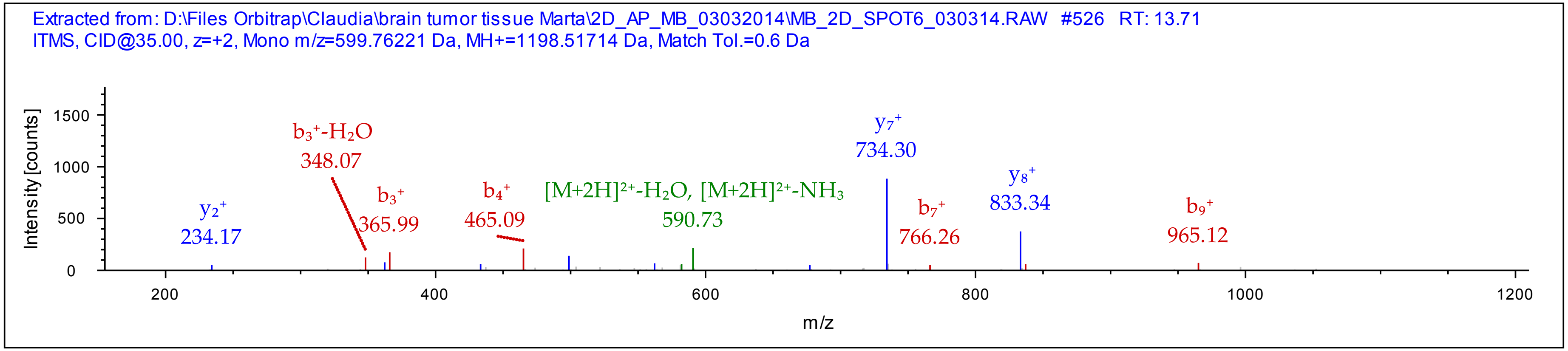
12	1315.68931	658.34829	439.23462	E	768.42507	384.71617	256.81321	7
13	1386.72643	693.86685	462.91366	A	639.38247	320.19487	213.79901	6
14	1483.77920	742.39324	495.26458	P	568.34535	284.67631	190.11997	5
15	1596.86327	798.93527	532.95927	L	471.29258	236.14993	157.76904	4
16	1710.90620	855.95674	570.97358	N	358.20851	179.60789	120.07435	3
17	1807.95897	904.48312	603.32451	P	244.16558	122.58643	82.06004	2
18				K	147.11281	74.06004	49.70912	1



Sequence: DSYVGDEAQSK, Charge: +2, Monoisotopic m/z: 599.76221 Da (-2.57 mmu/-4.29 ppm), MH+: 1198.51714 Da, RT: 13.71 min,
Identified with: Sequest HT (v1.3); XCorr:2.59, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (6):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	116.03423	58.52075	D			11
2	203.06626	102.03677	S	1083.49533	542.25130	10
3	366.12958	183.56843	Y	996.46330	498.73529	9
4	465.19800	233.10264	V	833.39998	417.20363	8
5	522.21947	261.61337	G	734.33156	367.66942	7
6	637.24642	319.12685	D	677.31009	339.15868	6
7	766.28902	383.64815	E	562.28314	281.64521	5

8	837.32614	419.16671	A	433.24054	217.12391	4
9	965.38472	483.19600	Q	362.20342	181.60535	3
10	1052.41675	526.71201	S	234.14484	117.57606	2
11			K	147.11281	74.06004	1

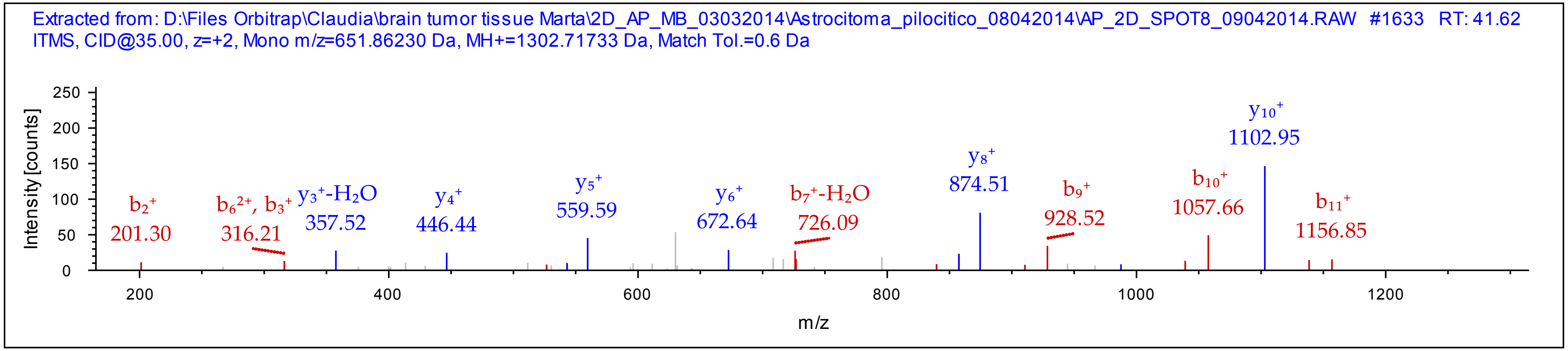

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT6_030314.RAW #526 RT: 13.71
ITMS, CID@35.00, z=+2, Mono m/z=599.76221 Da, MH+=1198.51714 Da, Match Tol.=0.6 Da

Spot #	Uniprot Accession Number	Description	MW^a [kDa]	pI ^{a}	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
8	P04264	Keratin, type II cytoskeletal 1	65.9	8.2	18.6	6.99%	3	4	PA	NS	1.9	↑ MB

Sequence: SLDLDSIIAEVK, Charge: +2, Monoisotopic m/z: 651.86230 Da (+1.07 mmu/+1.64 ppm), MH+: 1302.71733 Da, RT: 41.62 min,
Identified with: Sequest HT (v1.3); XCorr:2.51, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3
Protein references (1):

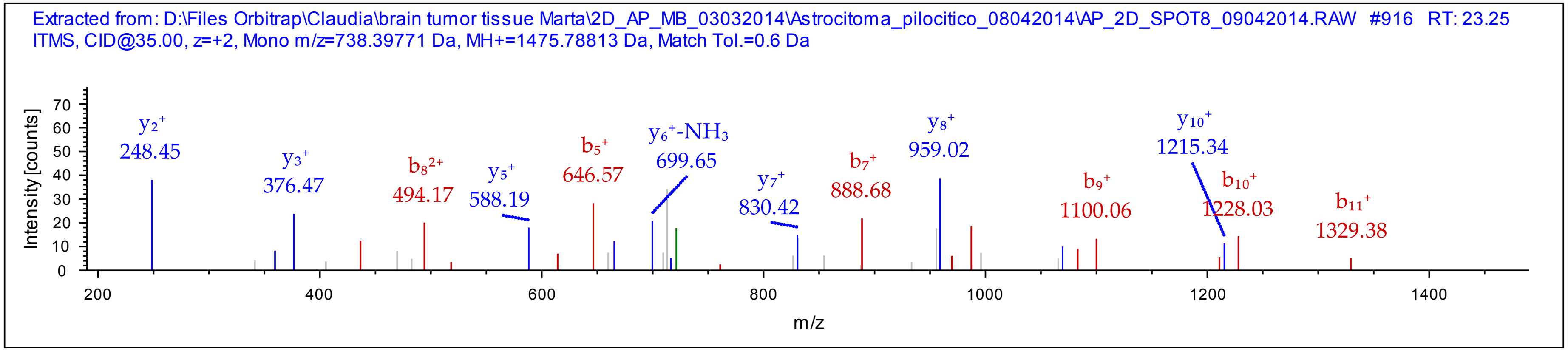
- Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	88.03931	44.52329	S			12
2	201.12338	101.06533	L	1215.68316	608.34522	11
3	316.15033	158.57880	D	1102.59909	551.80318	10
4	429.23440	215.12084	L	987.57214	494.28971	9
5	544.26135	272.63431	D	874.48807	437.74767	8
6	631.29338	316.15033	S	759.46112	380.23420	7
7	744.37745	372.69236	I	672.42909	336.71818	6
8	857.46152	429.23440	I	559.34502	280.17615	5
9	928.49864	464.75296	A	446.26095	223.63411	4
10	1057.54124	529.27426	E	375.22383	188.11555	3
11	1156.60966	578.80847	V	246.18123	123.59425	2
12			K	147.11281	74.06004	1



Sequence: FLEQQNQVLQTK, Charge: +2, Monoisotopic m/z: 738.39771 Da (+1.41 mmu/+1.91 ppm), MH+: 1475.78813 Da, RT: 23.25 min,
Identified with: Sequest HT (v1.3); XCorr:2.19, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (3):
- Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN]
- Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3 - [K2C1B_HUMAN]
- Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN]

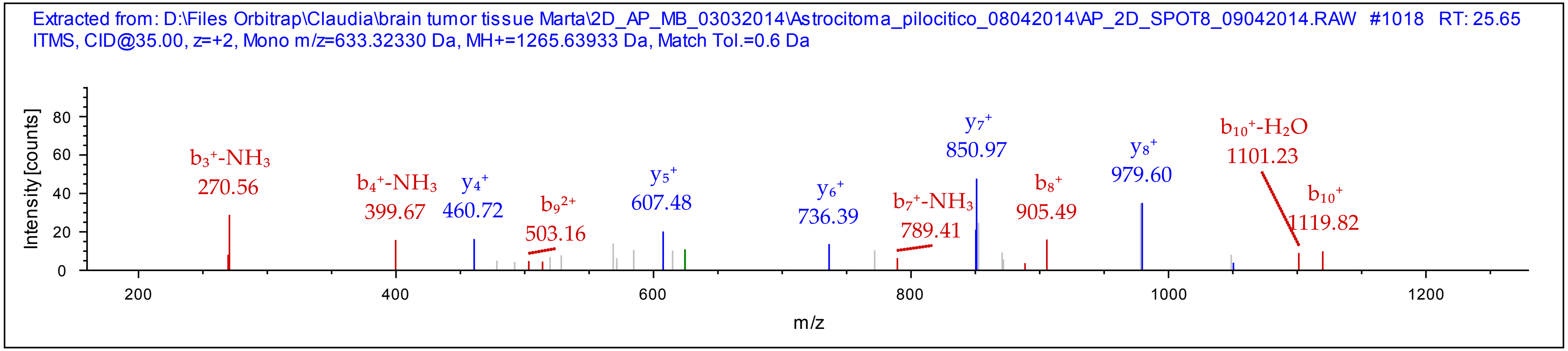
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	148.07570	74.54149	F			12
2	261.15977	131.08352	L	1328.71690	664.86209	11
3	390.20237	195.60482	E	1215.63283	608.32005	10
4	518.26095	259.63411	Q	1086.59023	543.79875	9
5	646.31953	323.66340	Q	958.53165	479.76946	8
6	760.36246	380.68487	N	830.47307	415.74017	7
7	888.42104	444.71416	Q	716.43014	358.71871	6
8	987.48946	494.24837	V	588.37156	294.68942	5
9	1100.57353	550.79040	L	489.30314	245.15521	4
10	1228.63211	614.81969	Q	376.21907	188.61317	3
11	1329.67979	665.34353	T	248.16049	124.58388	2
12			K	147.11281	74.06004	1



Sequence: TNAENEFVTIK, Charge: +2, Monoisotopic m/z: 633.32330 Da (+1.04 mmu/+1.63 ppm), MH+: 1265.63933 Da, RT: 25.65 min,
Identified with: Sequest HT (v1.3); XCorr:1.65, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):

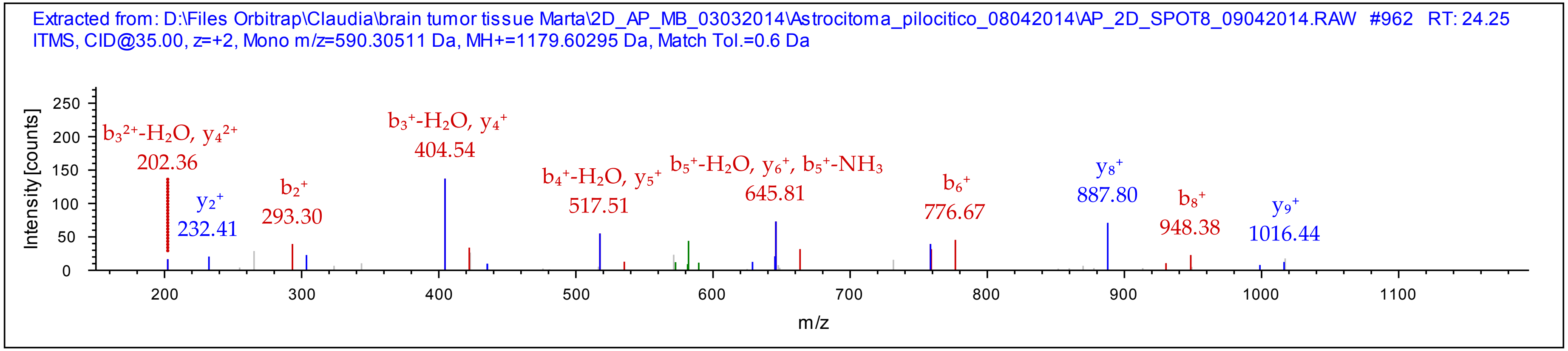
- Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	102.05496	51.53112	T			11
2	216.09789	108.55258	N	1164.58958	582.79843	10
3	287.13501	144.07114	A	1050.54665	525.77696	9
4	416.17761	208.59244	E	979.50953	490.25840	8
5	530.22054	265.61391	N	850.46693	425.73710	7
6	659.26314	330.13521	E	736.42400	368.71564	6
7	806.33156	403.66942	F	607.38140	304.19434	5
8	905.39998	453.20363	V	460.31298	230.66013	4
9	1006.44766	503.72747	T	361.24456	181.12592	3
10	1119.53173	560.26950	I	260.19688	130.60208	2
11			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\Astrocitoma_pilocitico_08042014\AP_2D_SPOT8_09042014.RAW #1018 RT: 25.65
ITMS, CID@35.00, z=+2, Mono m/z=633.32330 Da, MH+=1265.63933 Da, Match Tol.=0.6 Da

Sequence: YEELQITAGR, Charge: +2, Monoisotopic m/z: 590.30511 Da (+1.24 mmu/+2.1 ppm), MH+: 1179.60295 Da, RT: 24.25 min,
Identified with: Sequest HT (v1.3); XCorr:1.50, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (2):
- Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN]
- Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5 - [K2C6B_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	164.07060	82.53894	Y			10
2	293.11320	147.06024	E	1016.53715	508.77221	9
3	422.15580	211.58154	E	887.49455	444.25091	8
4	535.23987	268.12357	L	758.45195	379.72961	7
5	663.29845	332.15286	Q	645.36788	323.18758	6
6	776.38252	388.69490	I	517.30930	259.15829	5
7	877.43020	439.21874	T	404.22523	202.61625	4
8	948.46732	474.73730	A	303.17755	152.09241	3
9	1005.48879	503.24803	G	232.14043	116.57385	2
10			R	175.11896	88.06312	1

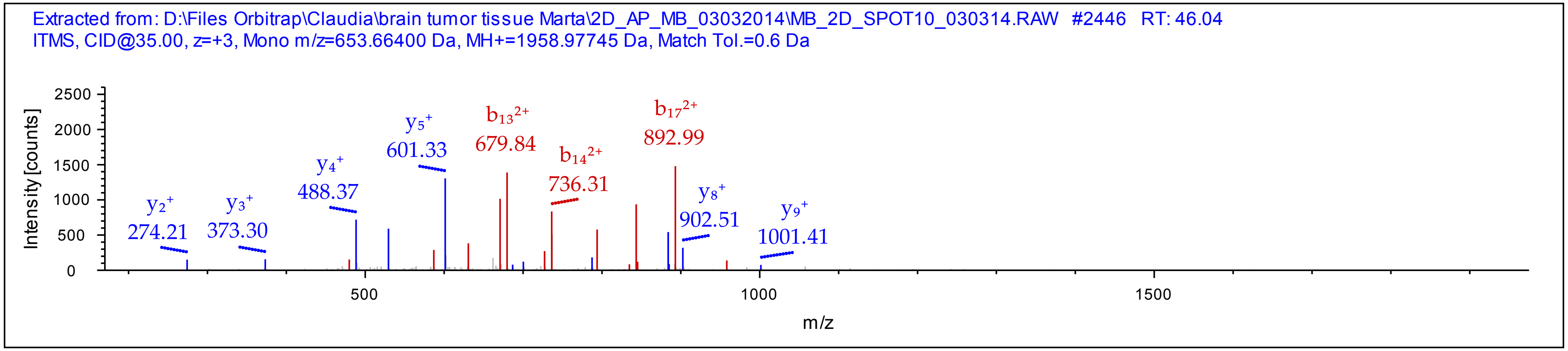


Spot #	Uniprot Accession Number	Description	MW^a [kDa]	pI ^{a}	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*
10	Q9BVA1	Tubulin beta	49.9	4.8	331.9	50.34%	4	19	MB	NS	1.9 ↑ in MB

Sequence: GHYTEGAELVDSVLDVVR, Charge: +3, Monoisotopic m/z: 653.66400 Da (-1.48 mmu/-2.26 ppm), MH+: 1958.97745 Da, RT: 46.04 min,
Identified with: Sequest HT (v1.3); XCorr:3.97, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3
Protein references (5):
- Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]
- Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]
- Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]
- Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]
- Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	58.02875	29.51801	20.01443	G				18
2	195.08766	98.04747	65.70074	H	1901.96041	951.48384	634.65832	17
3	358.15098	179.57913	120.05518	Y	1764.90150	882.95439	588.97202	16
4	459.19866	230.10297	153.73774	T	1601.83818	801.42273	534.61758	15
5	588.24126	294.62427	196.75194	E	1500.79050	750.89889	500.93502	14

6	645.26273	323.13500	215.75909	G	1371.74790	686.37759	457.92082	13
7	716.29985	358.65356	239.43813	A	1314.72643	657.86685	438.91366	12
8	845.34245	423.17486	282.45233	E	1243.68931	622.34829	415.23462	11
9	958.42652	479.71690	320.14702	L	1114.64671	557.82699	372.22042	10
10	1057.49494	529.25111	353.16983	V	1001.56264	501.28496	334.52573	9
11	1172.52189	586.76458	391.51215	D	902.49422	451.75075	301.50292	8
12	1259.55392	630.28060	420.52282	S	787.46727	394.23727	263.16061	7
13	1358.62234	679.81481	453.54563	V	700.43524	350.72126	234.14993	6
14	1471.70641	736.35684	491.24032	L	601.36682	301.18705	201.12712	5
15	1586.73336	793.87032	529.58264	D	488.28275	244.64501	163.43243	4
16	1685.80178	843.40453	562.60544	V	373.25580	187.13154	125.09012	3
17	1784.87020	892.93874	595.62825	V	274.18738	137.59733	92.06731	2
18				R	175.11896	88.06312	59.04450	1

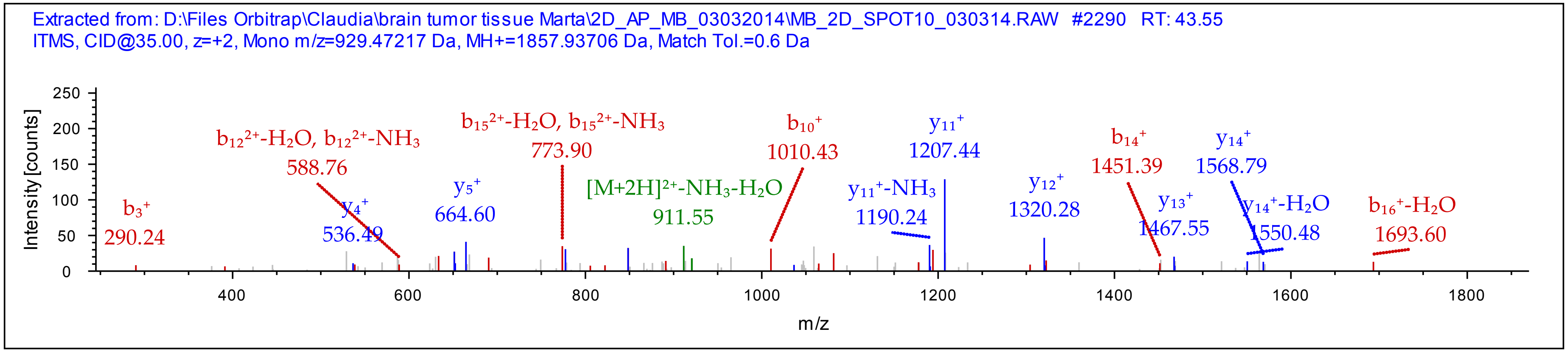


Sequence: MSATFIGNSTAIQELFK, Charge: +2, Monoisotopic m/z: 929.47217 Da (-2.27 mmu/-2.44 ppm), MH+: 1857.93706 Da, RT: 43.55 min,
Identified with: Sequest HT (v1.3); XCorr:3.55, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (3):

- Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]
- Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]
- Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]

#1	**b^{+}**	**b^{2+}**	**Seq.**	**y^{+}**	**y^{2+}**	**#2**
1	132.04778	66.52753	M			17
2	219.07981	110.04354	S	1726.90110	863.95419	16
3	290.11693	145.56210	A	1639.86907	820.43817	15
4	391.16461	196.08594	T	1568.83195	784.91961	14
5	538.23303	269.62015	F	1467.78427	734.39577	13
6	651.31710	326.16219	I	1320.71585	660.86156	12

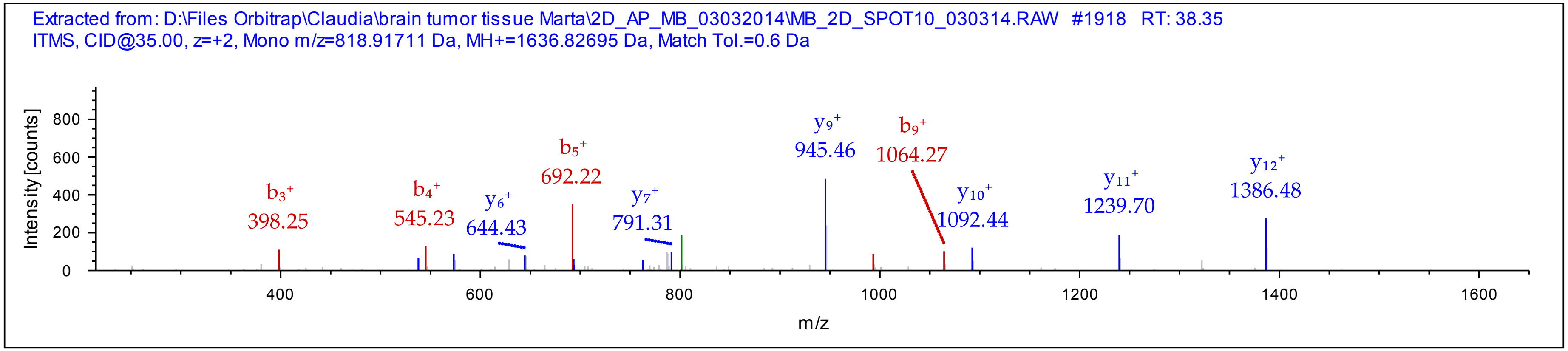
7	708.33857	354.67292	G	1207.63178	604.31953	11
8	822.38150	411.69439	N	1150.61031	575.80879	10
9	909.41353	455.21040	S	1036.56738	518.78733	9
10	1010.46121	505.73424	T	949.53535	475.27131	8
11	1081.49833	541.25280	A	848.48767	424.74747	7
12	1194.58240	597.79484	I	777.45055	389.22891	6
13	1322.64098	661.82413	Q	664.36648	332.68688	5
14	1451.68358	726.34543	E	536.30790	268.65759	4
15	1564.76765	782.88746	L	407.26530	204.13629	3
16	1711.83607	856.42167	F	294.18123	147.59425	2
17			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT10_030314.RAW #2290 RT: 43.55
ITMS, CID@35.00, z=+2, Mono m/z=929.47217 Da, MH+=1857.93706 Da, Match Tol.=0.6 Da

Sequence: LHFFMPGFAPLTSR, M5-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 818.91711 Da (-1.79 mmu/-2.18 ppm), MH+: 1636.82695 Da, RT: 38.35 min,
Identified with: Sequest HT (v1.3); XCorr:3.44, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3
Protein references (9):
- Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]
- Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]
- Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 - [TBB4A_HUMAN]
- Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]
- Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]
- Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 - [TBB6_HUMAN]
- Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens PE=1 SV=1 - [TBB8L_HUMAN]
- Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2 - [TBB8_HUMAN]
- Putative tubulin beta chain-like protein ENSP00000290377 OS=Homo sapiens PE=5 SV=2 - [YI016_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**

1	114.09135	57.54931	L			14
2	251.15026	126.07877	H	1523.74646	762.37687	13
3	398.21868	199.61298	F	1386.68755	693.84741	12
4	545.28710	273.14719	F	1239.61913	620.31320	11
5	692.32251	346.66489	M-Oxidation	1092.55071	546.77899	10
6	789.37528	395.19128	P	945.51529	473.26128	9
7	846.39675	423.70201	G	848.46252	424.73490	8
8	993.46517	497.23622	F	791.44105	396.22416	7
9	1064.50229	532.75478	A	644.37263	322.68995	6
10	1161.55506	581.28117	P	573.33551	287.17139	5
11	1274.63913	637.82320	L	476.28274	238.64501	4
12	1375.68681	688.34704	T	363.19867	182.10297	3
13	1462.71884	731.86306	S	262.15099	131.57913	2
14			R	175.11896	88.06312	1

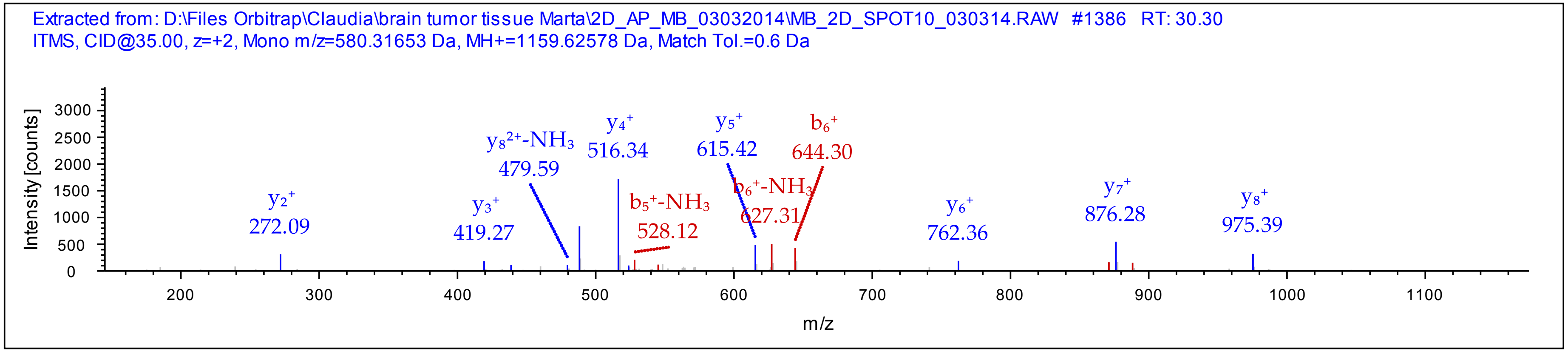

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT10_030314.RAW #1918 RT: 38.35
ITMS, CID@35.00, z=+2, Mono m/z=818.91711 Da, MH+=1636.82695 Da, Match Tol.=0.6 Da

Sequence: LAVNMVPFPR, M5-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 580.31653 Da (-1.76 mmu/-3.03 ppm), MH+: 1159.62578 Da, RT: 30.30 min,
Identified with: Sequest HT (v1.3); XCorr:3.42, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-NH_3; y; y-NH_3

Protein references (11):
- Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1 - [TBB1_HUMAN]
- Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]
- Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]
- Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]
- Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 - [TBB4A_HUMAN]
- Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]

- Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]
- Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 - [TBB6_HUMAN]
- Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens PE=1 SV=1 - [TBB8L_HUMAN]
- Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2 - [TBB8_HUMAN]
- Putative tubulin beta chain-like protein ENSP00000290377 OS=Homo sapiens PE=5 SV=2 - [YI016_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			10
2	185.12847	93.06787	A	1046.54523	523.77625	9
3	284.19689	142.60208	V	975.50811	488.25769	8
4	398.23982	199.62355	N	876.43969	438.72348	7
5	545.27523	273.14125	M-Oxidation	762.39676	381.70202	6
6	644.34365	322.67546	V	615.36134	308.18431	5
7	741.39642	371.20185	P	516.29292	258.65010	4
8	888.46484	444.73606	F	419.24015	210.12371	3
9	985.51761	493.26244	P	272.17173	136.58950	2
10			R	175.11896	88.06312	1



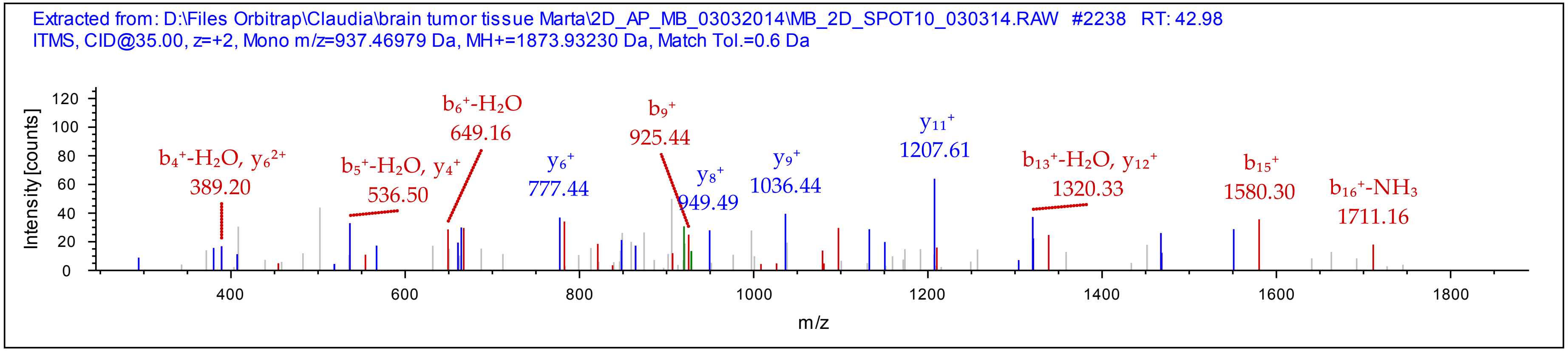
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT10_030314.RAW #1386 RT: 30.30
ITMS, CID@35.00, z=+2, Mono m/z=580.31653 Da, MH+=1159.62578 Da, Match Tol.=0.6 Da

Sequence: MSATFIGNSTAIQELFK, M1-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 937.46979 Da (-2.11 mmu/-2.25 ppm), MH+: 1873.93230 Da, RT: 42.98 min,
Identified with: Sequest HT (v1.3); XCorr:3.26, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):
- Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]

- Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]
- Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]

#1	**b^{+}**	**b^{2+}**	**Seq.**	**y^{+}**	**y^{2+}**	**#2**
1	148.04269	74.52498	M-Oxidation			17
2	235.07472	118.04100	S	1726.90110	863.95419	16
3	306.11184	153.55956	A	1639.86907	820.43817	15
4	407.15952	204.08340	T	1568.83195	784.91961	14
5	554.22794	277.61761	F	1467.78427	734.39577	13
6	667.31201	334.15964	I	1320.71585	660.86156	12
7	724.33348	362.67038	G	1207.63178	604.31953	11
8	838.37641	419.69184	N	1150.61031	575.80879	10
9	925.40844	463.20786	S	1036.56738	518.78733	9
10	1026.45612	513.73170	T	949.53535	475.27131	8
11	1097.49324	549.25026	A	848.48767	424.74747	7
12	1210.57731	605.79229	I	777.45055	389.22891	6
13	1338.63589	669.82158	Q	664.36648	332.68688	5
14	1467.67849	734.34288	E	536.30790	268.65759	4
15	1580.76256	790.88492	L	407.26530	204.13629	3
16	1727.83098	864.41913	F	294.18123	147.59425	2
17			K	147.11281	74.06004	1

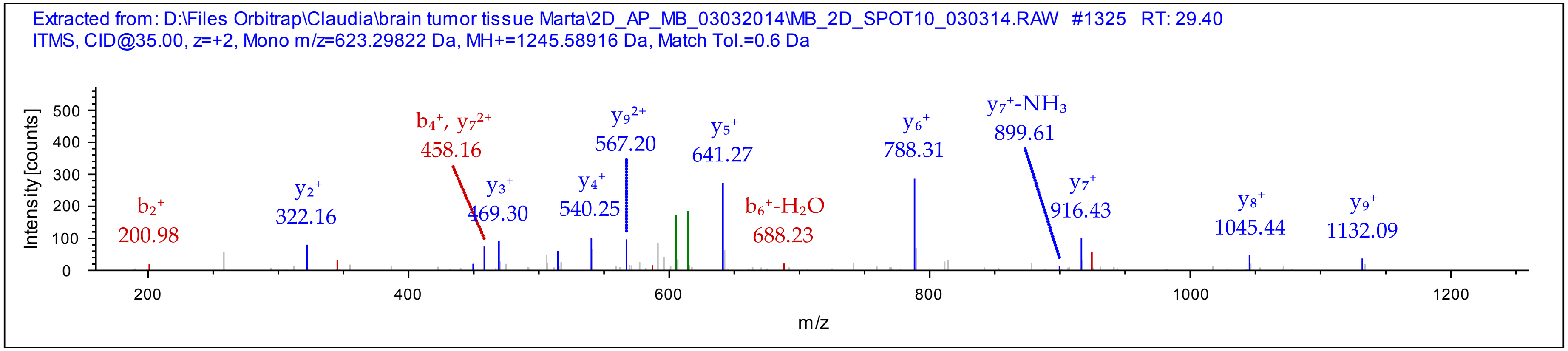

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT10_030314.RAW #2238 RT: 42.98
ITMS, CID@35.00, z=+2, Mono m/z=937.46979 Da, MH+=1873.93230 Da, Match Tol.=0.6 Da

Sequence: ISEQFTAMFR, M8-Oxidation (15.99492 Da)

Charge: +2,   Monoisotopic m/z: 623.29822 Da (-2.07 mmu/-3.32 ppm),   MH+: 1245.58916 Da,   RT: 29.40 min,
Identified with: Sequest HT (v1.3); XCorr:3.08, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):
- Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]
- Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]
- Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]
- Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 - [TBB4A_HUMAN]
- Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]
- Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]

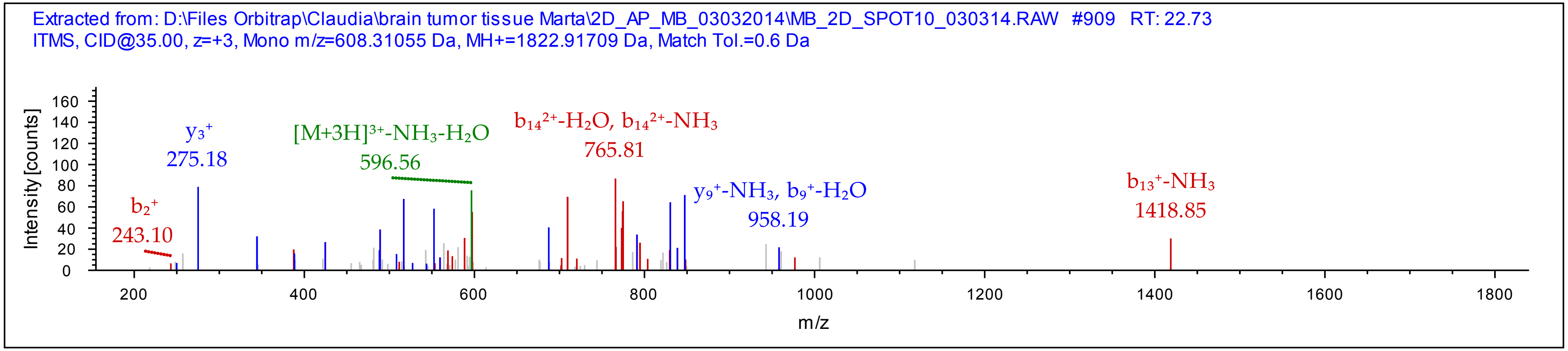
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	114.09135	57.54931	I			10
2	201.12338	101.06533	S	1132.50923	566.75825	9
3	330.16598	165.58663	E	1045.47720	523.24224	8
4	458.22456	229.61592	Q	916.43460	458.72094	7
5	605.29298	303.15013	F	788.37602	394.69165	6
6	706.34066	353.67397	T	641.30760	321.15744	5
7	777.37778	389.19253	A	540.25992	270.63360	4
8	924.41319	462.71023	M-Oxidation	469.22280	235.11504	3
9	1071.48161	536.24444	F	322.18738	161.59733	2
10			R	175.11896	88.06312	1



Sequence: EIVHIQAGQCGNQIGAK, C10-Carbamidomethyl (57.02146 Da)
Charge: +3,   Monoisotopic m/z: 608.31055 Da (-1.95 mmu/-3.2 ppm),   MH+: 1822.91709 Da,   RT: 22.73 min,
Identified with: Sequest HT (v1.3); XCorr:3.02, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-NH_3

Protein references (4):
- Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]
- Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]
- Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]
- Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]

#1	**b^{+}**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^{+}**	**y^{2+}**	**y^{3+}**	**#2**
1	130.04988	65.52858	44.02148	E				17
2	243.13395	122.07061	81.71617	I	1693.88033	847.44380	565.29829	16
3	342.20237	171.60482	114.73897	V	1580.79626	790.90177	527.60360	15
4	479.26128	240.13428	160.42528	H	1481.72784	741.36756	494.58080	14
5	592.34535	296.67631	198.11997	I	1344.66893	672.83810	448.89449	13
6	720.40393	360.70560	240.80616	Q	1231.58486	616.29607	411.19980	12
7	791.44105	396.22416	264.48520	A	1103.52628	552.26678	368.51361	11
8	848.46252	424.73490	283.49236	G	1032.48916	516.74822	344.83457	10
9	976.52110	488.76419	326.17855	Q	975.46769	488.23748	325.82741	9
10	1136.55175	568.77951	379.52210	C-Carbamidomethyl	847.40911	424.20819	283.14122	8
11	1193.57322	597.29025	398.52926	G	687.37845	344.19286	229.79767	7
12	1307.61615	654.31171	436.54357	N	630.35698	315.68213	210.79051	6
13	1435.67473	718.34100	479.22976	Q	516.31405	258.66066	172.77620	5
14	1548.75880	774.88304	516.92445	I	388.25547	194.63137	130.09001	4
15	1605.78027	803.39377	535.93161	G	275.17140	138.08934	92.39532	3
16	1676.81739	838.91233	559.61065	A	218.14993	109.57860	73.38816	2
17				K	147.11281	74.06004	49.70912	1



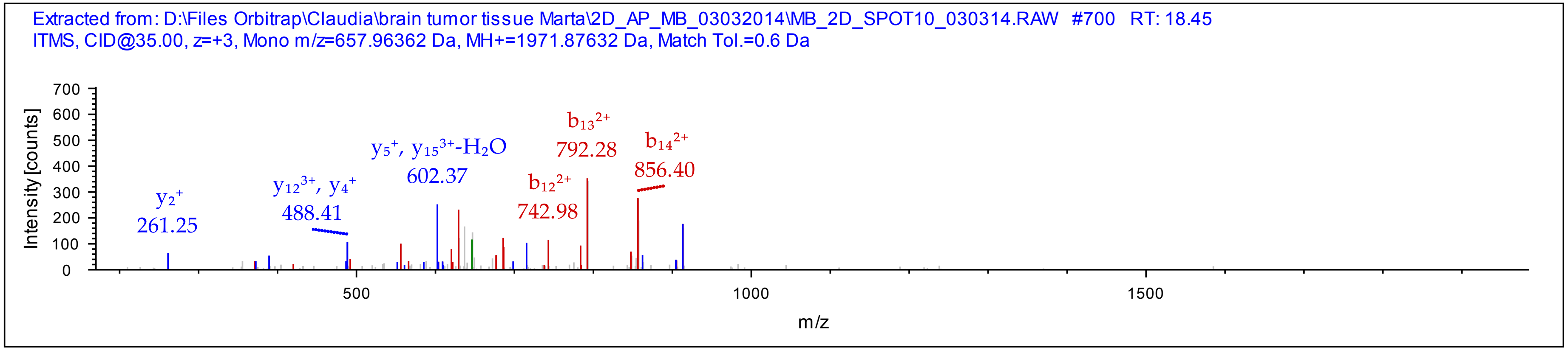
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT10_030314.RAW #909 RT: 22.73
ITMS, CID@35.00, z=+3, Mono m/z=608.31055 Da, MH+=1822.91709 Da, Match Tol.=0.6 Da

Sequence: MSMKEVDEQMLNVQNK, M1-Oxidation (15.99492 Da), M3-Oxidation (15.99492 Da), M10-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 657.96362 Da (-1.94 mmu/-2.95 ppm), MH+: 1971.87632 Da, RT: 18.45 min,
Identified with: Sequest HT (v1.3); XCorr:2.97, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):
- Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]
- Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]
- Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]
- Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	148.04269	74.52498	50.01908	M-Oxidation				16
2	235.07472	118.04100	79.02976	S	1824.84672	912.92700	608.95376	15
3	382.11014	191.55871	128.04156	M-Oxidation	1737.81469	869.41098	579.94308	14
4	510.20511	255.60619	170.73989	K	1590.77928	795.89328	530.93128	13
5	639.24771	320.12749	213.75409	E	1462.68431	731.84579	488.23295	12
6	738.31613	369.66170	246.77689	V	1333.64171	667.32449	445.21875	11
7	853.34308	427.17518	285.11921	D	1234.57329	617.79028	412.19595	10
8	982.38568	491.69648	328.13341	E	1119.54634	560.27681	373.85363	9
9	1110.44426	555.72577	370.81960	Q	990.50374	495.75551	330.83943	8
10	1257.47967	629.24347	419.83141	M-Oxidation	862.44516	431.72622	288.15324	7
11	1370.56374	685.78551	457.52610	L	715.40974	358.20851	239.14143	6
12	1484.60667	742.80697	495.54041	N	602.32567	301.66647	201.44674	5
13	1583.67509	792.34118	528.56321	V	488.28274	244.64501	163.43243	4

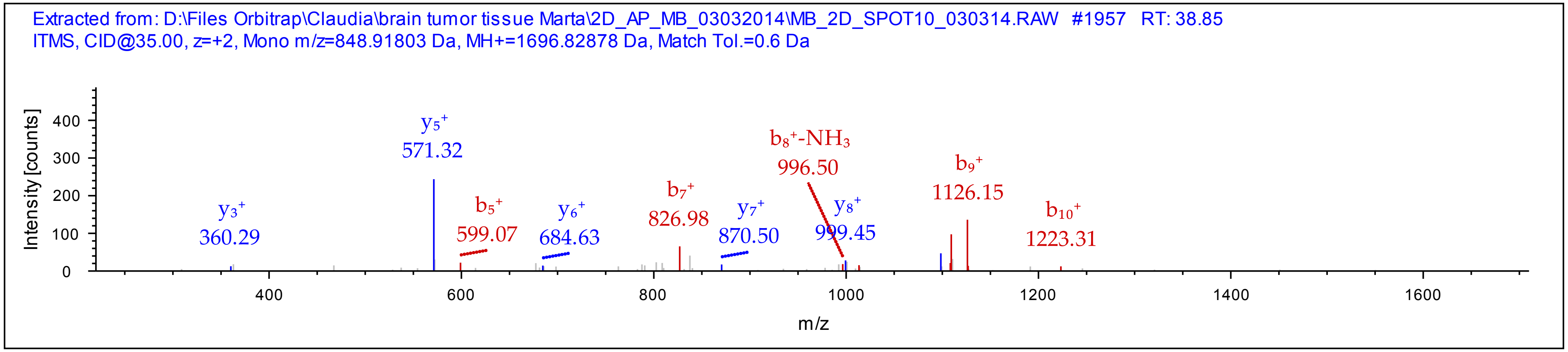
14	1711.73367	856.37047	571.24941	Q	389.21432	195.11080	130.40962	3
15	1825.77660	913.39194	609.26372	N	261.15574	131.08151	87.72343	2
16				K	147.11281	74.06004	49.70912	1



Sequence: NSSYFVEWIPNNVK, Charge: +2, Monoisotopic m/z: 848.91803 Da (-2.11 mmu/-2.49 ppm), MH+: 1696.82878 Da, RT: 38.85 min,
Identified with: Sequest HT (v1.3); XCorr:2.79, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (7):
- Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]
- Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]
- Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]
- Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 - [TBB4A_HUMAN]
- Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]
- Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]
- Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 - [TBB6_HUMAN]

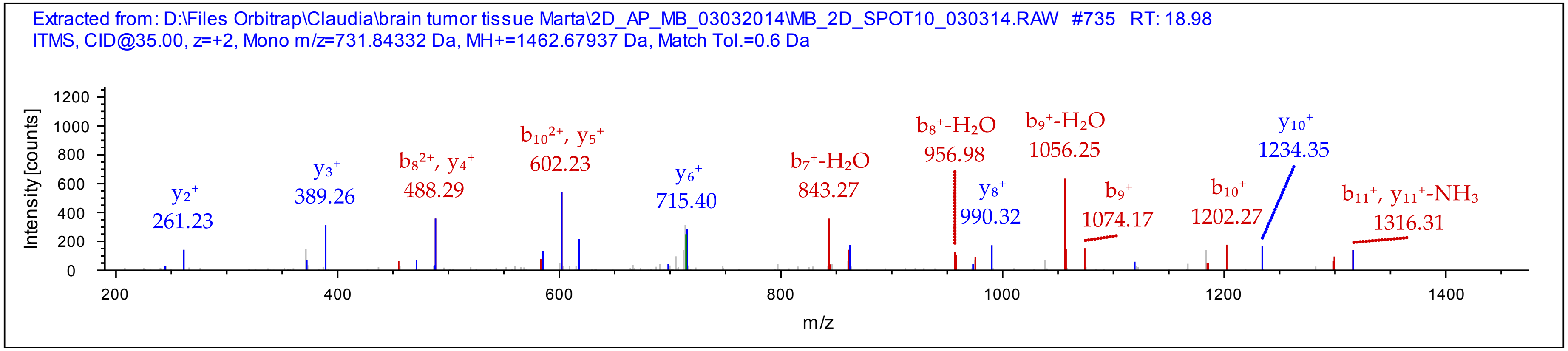
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	115.05021	58.02874	N			14
2	202.08224	101.54476	S	1582.79007	791.89867	13
3	289.11427	145.06077	S	1495.75804	748.38266	12
4	452.17759	226.59243	Y	1408.72601	704.86664	11
5	599.24601	300.12664	F	1245.66269	623.33498	10
6	698.31443	349.66085	V	1098.59427	549.80077	9
7	827.35703	414.18215	E	999.52585	500.26656	8
8	1013.43635	507.22181	W	870.48325	435.74526	7
9	1126.52042	563.76385	I	684.40393	342.70560	6
10	1223.57319	612.29023	P	571.31986	286.16357	5
11	1337.61612	669.31170	N	474.26709	237.63718	4

12	1451.65905	726.33316	N	360.22416	180.61572	3
13	1550.72747	775.86737	V	246.18123	123.59425	2
14			K	147.11281	74.06004	1



Sequence: EVDEQMLNVQNK, M6-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 731.84332 Da (-2.47 mmu/-3.38 ppm), MH+: 1462.67937 Da, RT: 18.98 min,
Identified with: Sequest HT (v1.3); XCorr:2.78, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (4):
- Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]
- Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]
- Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]
- Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]

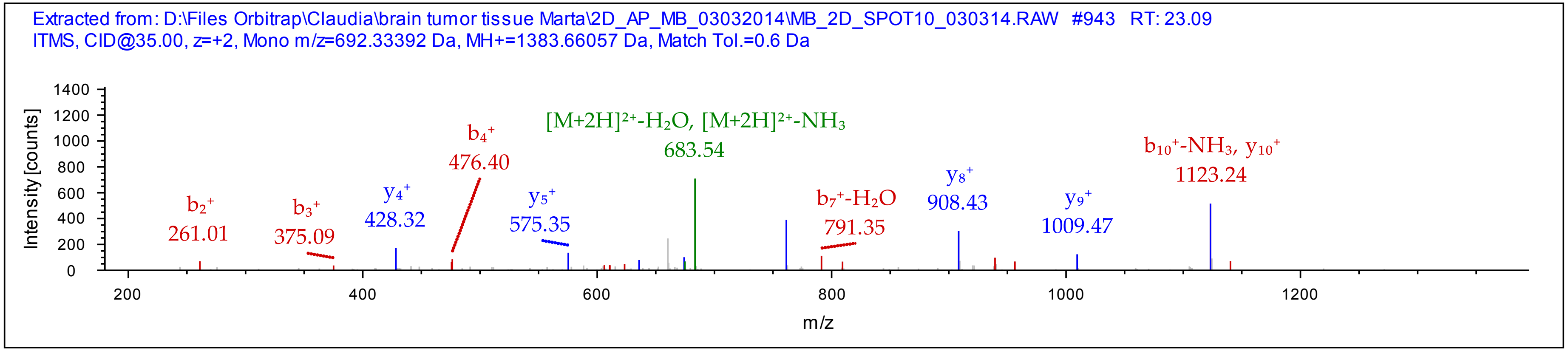
#1	**b⁺**	**b²⁺**	**Seq.**	**y⁺**	**y²⁺**	**#2**
1	130.04988	65.52858	E			12
2	229.11830	115.06279	V	1333.64171	667.32449	11
3	344.14525	172.57626	D	1234.57329	617.79028	10
4	473.18785	237.09756	E	1119.54634	560.27681	9
5	601.24643	301.12685	Q	990.50374	495.75551	8
6	748.28184	374.64456	M-Oxidation	862.44516	431.72622	7
7	861.36591	431.18659	L	715.40974	358.20851	6
8	975.40884	488.20806	N	602.32567	301.66647	5
9	1074.47726	537.74227	V	488.28274	244.64501	4
10	1202.53584	601.77156	Q	389.21432	195.11080	3
11	1316.57877	658.79302	N	261.15574	131.08151	2
12			K	147.11281	74.06004	1



Sequence: IMNTFSVMPSPK, M2-Oxidation (15.99492 Da), M8-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 692.33392 Da (-2.1 mmu/-3.03 ppm), MH+: 1383.66057 Da, RT: 23.09 min,
Identified with: Sequest HT (v1.3); XCorr:2.75, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):
- Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]
- Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]
- Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 - [TBB6_HUMAN]

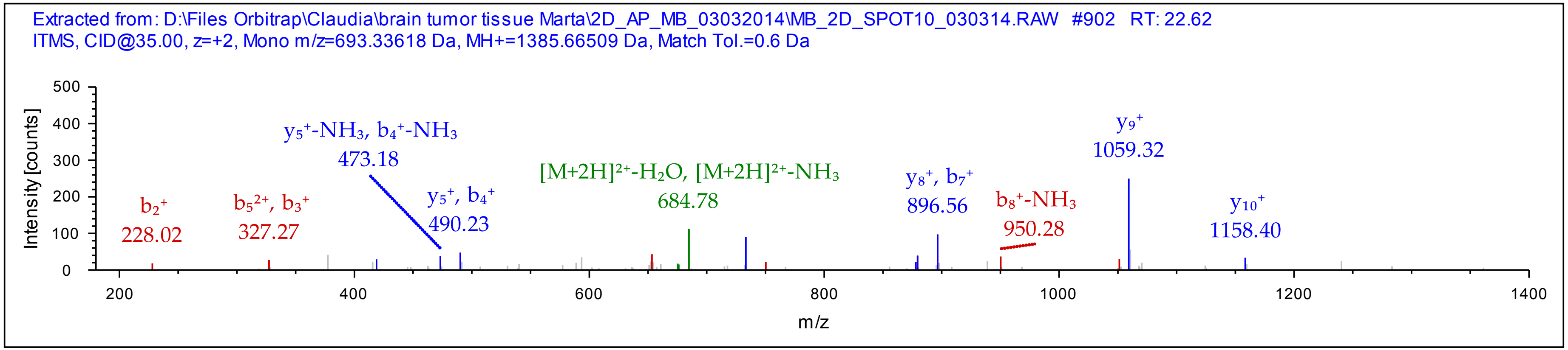
#1	**b^{+}**	**b^{2+}**	**Seq.**	**y^{+}**	**y^{2+}**	**#2**
1	114.09135	57.54931	I			12
2	261.12676	131.06702	M-Oxidation	1270.58069	635.79398	11
3	375.16969	188.08848	N	1123.54528	562.27628	10
4	476.21737	238.61232	T	1009.50235	505.25481	9
5	623.28579	312.14653	F	908.45467	454.73097	8
6	710.31782	355.66255	S	761.38625	381.19676	7
7	809.38624	405.19676	V	674.35422	337.68075	6
8	956.42166	478.71447	M-Oxidation	575.28580	288.14654	5
9	1053.47443	527.24085	P	428.25038	214.62883	4
10	1140.50646	570.75687	S	331.19761	166.10244	3
11	1237.55923	619.28325	P	244.16558	122.58643	2
12			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT10_030314.RAW #943 RT: 23.09
ITMS, CID@35.00, z=+2, Mono m/z=692.33392 Da, MH+=1383.66057 Da, Match Tol.=0.6 Da

Sequence: INVYYNEATGNK, Charge: +2, Monoisotopic m/z: 693.33618 Da (-2.26 mmu/-3.26 ppm), MH+: 1385.66509 Da, RT: 22.62 min,
Identified with: Sequest HT (v1.3); XCorr:2.62, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; $b-H_2O$; $b-NH_3$; y; $y-H_2O$; $y-NH_3$
Protein references (1):

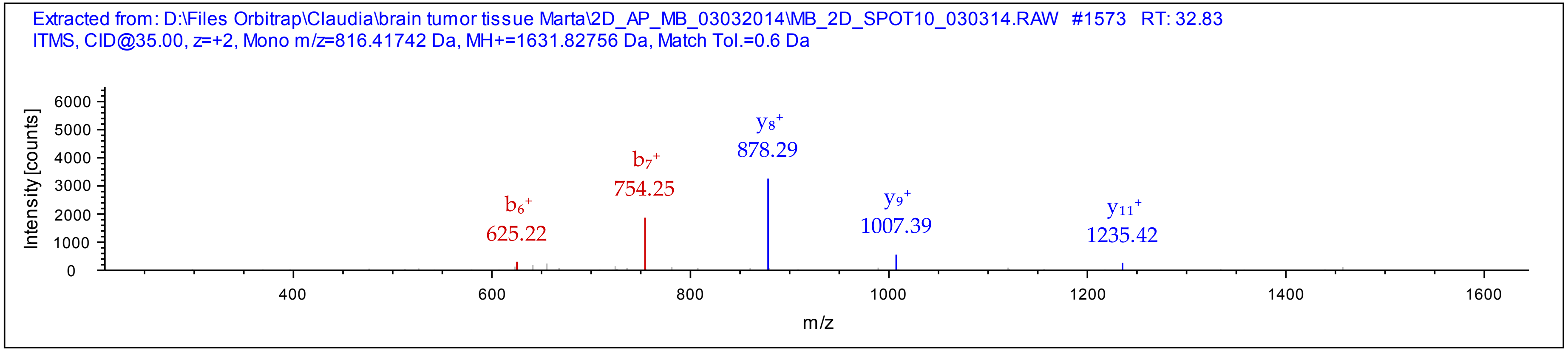
- Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]

#1	**b^{+}**	**b^{2+}**	**Seq.**	**y^{+}**	**y^{2+}**	**#2**
1	114.09135	57.54931	I			12
2	228.13428	114.57078	N	1272.58553	636.79640	11
3	327.20270	164.10499	V	1158.54260	579.77494	10
4	490.26602	245.63665	Y	1059.47418	530.24073	9
5	653.32934	327.16831	Y	896.41086	448.70907	8
6	767.37227	384.18977	N	733.34754	367.17741	7
7	896.41487	448.71107	E	619.30461	310.15594	6
8	967.45199	484.22963	A	490.26201	245.63464	5
9	1068.49967	534.75347	T	419.22489	210.11608	4
10	1125.52114	563.26421	G	318.17721	159.59224	3
11	1239.56407	620.28567	N	261.15574	131.08151	2
12			K	147.11281	74.06004	1



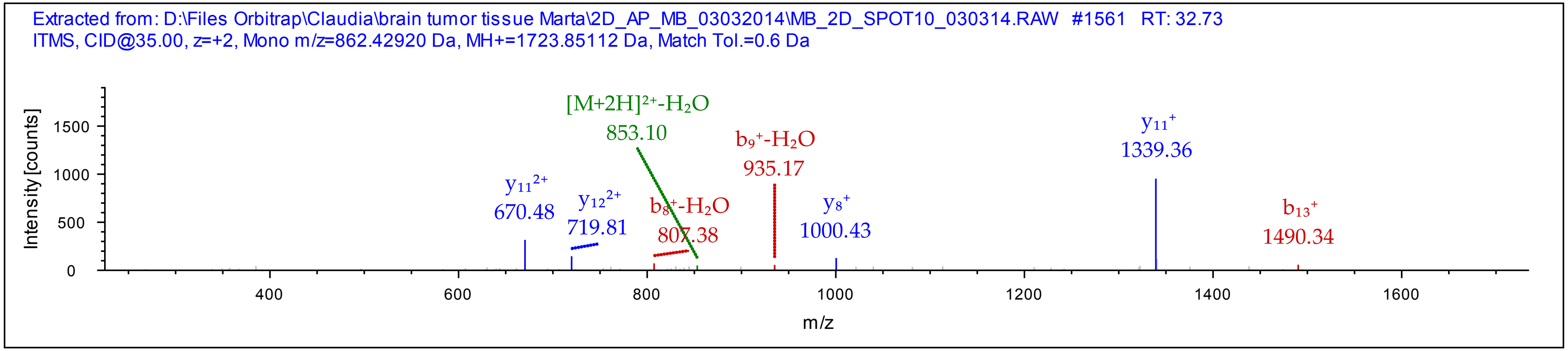
Sequence: AILVDLEPGTMDSVR, M11-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 816.41742 Da (-1.72 mmu/-2.1 ppm), MH+: 1631.82756 Da, RT: 32.83 min,
Identified with: Sequest HT (v1.3); XCorr:2.57, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3
Protein references (4):
- Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]
- Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]
- Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]
- Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	72.04440	36.52584	A			15
2	185.12847	93.06787	I	1560.79388	780.90058	14
3	298.21254	149.60991	L	1447.70981	724.35854	13
4	397.28096	199.14412	V	1334.62574	667.81651	12
5	512.30791	256.65759	D	1235.55732	618.28230	11
6	625.39198	313.19963	L	1120.53037	560.76882	10
7	754.43458	377.72093	E	1007.44630	504.22679	9
8	851.48735	426.24731	P	878.40370	439.70549	8
9	908.50882	454.75805	G	781.35093	391.17910	7
10	1009.55650	505.28189	T	724.32946	362.66837	6
11	1156.59191	578.79959	M-Oxidation	623.28178	312.14453	5
12	1271.61886	636.31307	D	476.24636	238.62682	4
13	1358.65089	679.82908	S	361.21941	181.11334	3
14	1457.71931	729.36329	V	274.18738	137.59733	2
15			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT10_030314.RAW #1573 RT: 32.83
ITMS, CID@35.00, z=+2, Mono m/z=816.41742 Da, MH+=1631.82756 Da, Match Tol.=0.6 Da

Sequence: ALTVPELTQQMFDSK, M11-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 862.42920 Da (-3.04 mmu/-3.52 ppm), MH+: 1723.85112 Da, RT: 32.73 min,
Identified with: Sequest HT (v1.3); XCorr:2.55, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (2):
- Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]
- Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]

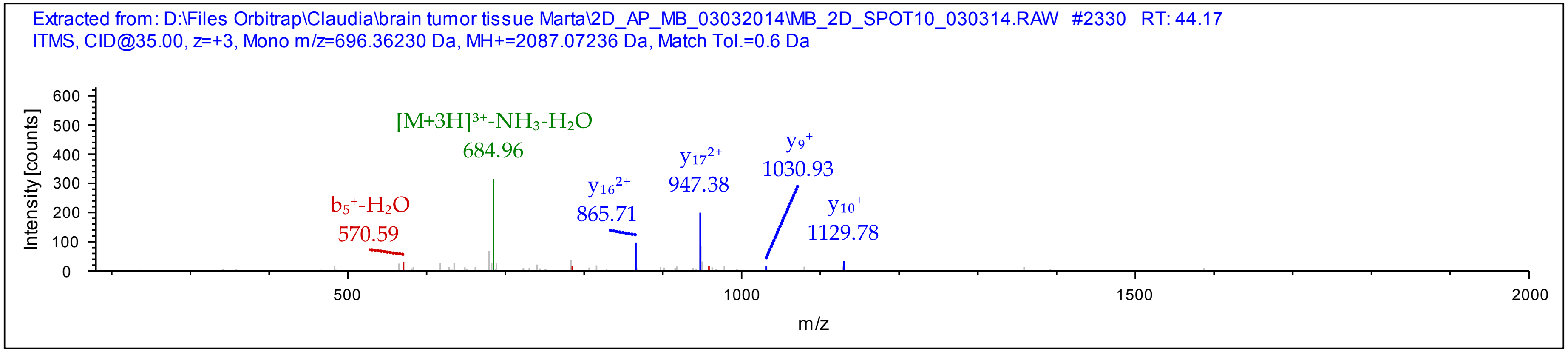
#1	**b$^+$**	**b^{2+}**	**Seq.**	**y$^+$**	**y^{2+}**	**#2**
1	72.04440	36.52584	A			15
2	185.12847	93.06787	L	1652.82008	826.91368	14
3	286.17615	143.59171	T	1539.73601	770.37164	13
4	385.24457	193.12592	V	1438.68833	719.84780	12
5	482.29734	241.65231	P	1339.61991	670.31359	11
6	611.33994	306.17361	E	1242.56714	621.78721	10
7	724.42401	362.71564	L	1113.52454	557.26591	9
8	825.47169	413.23948	T	1000.44047	500.72387	8
9	953.53027	477.26877	Q	899.39279	450.20003	7
10	1081.58885	541.29806	Q	771.33421	386.17074	6
11	1228.62426	614.81577	M-Oxidation	643.27563	322.14145	5
12	1375.69268	688.34998	F	496.24021	248.62374	4
13	1490.71963	745.86345	D	349.17179	175.08953	3
14	1577.75166	789.37947	S	234.14484	117.57606	2
15			K	147.11281	74.06004	1



Sequence: GHYTEGAELVDSVLDVVRK, Charge: +3, Monoisotopic m/z: 696.36230 Da (-1.5 mmu/-2.15 ppm), MH+: 2087.07236 Da, RT: 44.17 min,
Identified with: Sequest HT (v1.3); XCorr:2.50, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (5):
- Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]
- Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]
- Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]
- Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]
- Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	58.02875	29.51801	20.01443	G				19
2	195.08766	98.04747	65.70074	H	2030.05538	1015.53133	677.35664	18
3	358.15098	179.57913	120.05518	Y	1892.99647	947.00187	631.67034	17
4	459.19866	230.10297	153.73774	T	1729.93315	865.47021	577.31590	16
5	588.24126	294.62427	196.75194	E	1628.88547	814.94637	543.63334	15
6	645.26273	323.13500	215.75909	G	1499.84287	750.42507	500.61914	14
7	716.29985	358.65356	239.43813	A	1442.82140	721.91434	481.61198	13
8	845.34245	423.17486	282.45233	E	1371.78428	686.39578	457.93294	12
9	958.42652	479.71690	320.14702	L	1242.74168	621.87448	414.91874	11
10	1057.49494	529.25111	353.16983	V	1129.65761	565.33244	377.22405	10
11	1172.52189	586.76458	391.51215	D	1030.58919	515.79823	344.20125	9
12	1259.55392	630.28060	420.52282	S	915.56224	458.28476	305.85893	8
13	1358.62234	679.81481	453.54563	V	828.53021	414.76874	276.84825	7
14	1471.70641	736.35684	491.24032	L	729.46179	365.23453	243.82545	6
15	1586.73336	793.87032	529.58264	D	616.37772	308.69250	206.13076	5
16	1685.80178	843.40453	562.60544	V	501.35077	251.17902	167.78844	4

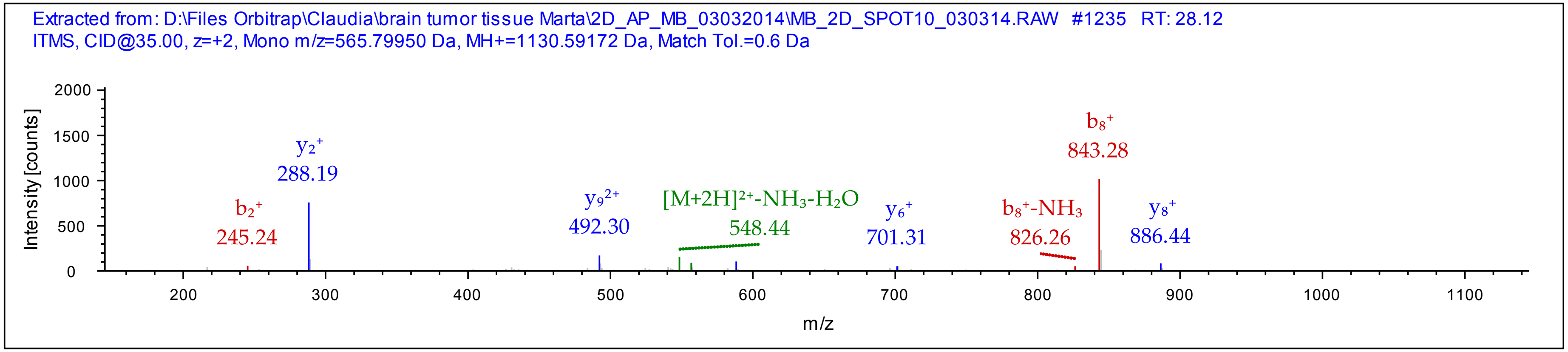
17	1784.87020	892.93874	595.62825	V	402.28235	201.64481	134.76563	3
18	1940.97132	970.98930	647.66196	R	303.21393	152.11060	101.74283	2
19				K	147.11281	74.06004	49.70912	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT10_030314.RAW #2330 RT: 44.17
ITMS, CID@35.00, z=+3, Mono m/z=696.36230 Da, MH+=2087.07236 Da, Match Tol.=0.6 Da

Sequence: FPGQLNADLR, Charge: +2, Monoisotopic m/z: 565.79950 Da (-1.81 mmu/-3.2 ppm), MH+: 1130.59172 Da, RT: 28.12 min,
Identified with: Sequest HT (v1.3); XCorr:2.49, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (11):
- Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1 - [TBB1_HUMAN]
- Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]
- Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]
- Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]
- Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 - [TBB4A_HUMAN]
- Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]
- Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]
- Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 - [TBB6_HUMAN]
- Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens PE=1 SV=1 - [TBB8L_HUMAN]
- Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2 - [TBB8_HUMAN]
- Putative tubulin beta chain-like protein ENSP00000290377 OS=Homo sapiens PE=5 SV=2 - [YI016_HUMAN]

#1	**b^{+}**	**b^{2+}**	**Seq.**	**y^{+}**	**y^{2+}**	**#2**
1	148.07570	74.54149	F			10
2	245.12847	123.06787	P	983.52692	492.26710	9
3	302.14994	151.57861	G	886.47415	443.74071	8
4	430.20852	215.60790	Q	829.45268	415.22998	7
5	543.29259	272.14993	L	701.39410	351.20069	6
6	657.33552	329.17140	N	588.31003	294.65865	5
7	728.37264	364.68996	A	474.26710	237.63719	4

8	843.39959	422.20343	D	403.22998	202.11863	3
9	956.48366	478.74547	L	288.20303	144.60515	2
10			R	175.11896	88.06312	1

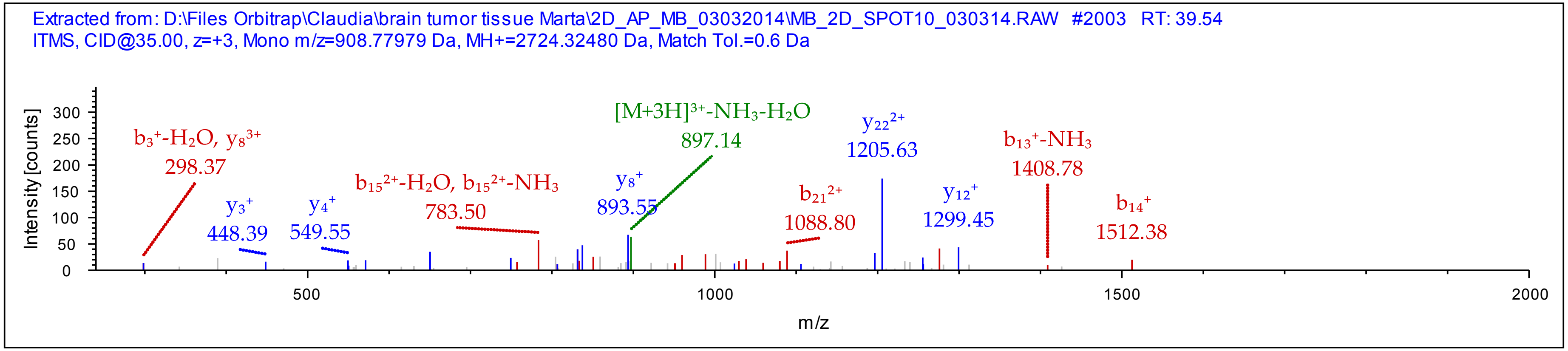


Sequence: LTTPTYGDLNHLVSATMSGVTTCLR, M17-Oxidation (15.99492 Da), C23-Carbamidomethyl (57.02146 Da)
Charge: +3, Monoisotopic m/z: 908.77979 Da (-2.81 mmu/-3.09 ppm), MH+: 2724.32480 Da, RT: 39.54 min,
Identified with: Sequest HT (v1.3); XCorr:2.31, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):
- Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]
- Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]
- Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 - [TBB4A_HUMAN]
- Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]
- Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]

#1	**b^{+}**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^{+}**	**y^{2+}**	**y^{3+}**	**#2**
1	114.09135	57.54931	38.70197	L				25
2	215.13903	108.07315	72.38453	T	2611.24916	1306.12822	871.08790	24
3	316.18671	158.59699	106.06709	T	2510.20148	1255.60438	837.40534	23
4	413.23948	207.12338	138.41801	P	2409.15380	1205.08054	803.72278	22
5	514.28716	257.64722	172.10057	T	2312.10103	1156.55415	771.37186	21
6	677.35048	339.17888	226.45501	Y	2211.05335	1106.03031	737.68930	20
7	734.37195	367.68961	245.46217	G	2047.99003	1024.49865	683.33486	19
8	849.39890	425.20309	283.80448	D	1990.96856	995.98792	664.32770	18
9	962.48297	481.74512	321.49917	L	1875.94161	938.47444	625.98539	17
10	1076.52590	538.76659	359.51348	N	1762.85754	881.93241	588.29070	16

11	1213.58481	607.29604	405.19979	H	1648.81461	824.91094	550.27639	15
12	1326.66888	663.83808	442.89448	L	1511.75570	756.38149	504.59008	14
13	1425.73730	713.37229	475.91728	V	1398.67163	699.83945	466.89539	13
14	1512.76933	756.88830	504.92796	S	1299.60321	650.30524	433.87259	12
15	1583.80645	792.40686	528.60700	A	1212.57118	606.78923	404.86191	11
16	1684.85413	842.93070	562.28956	T	1141.53406	571.27067	381.18287	10
17	1831.88954	916.44841	611.30136	M-Oxidation	1040.48638	520.74683	347.50031	9
18	1918.92157	959.96442	640.31204	S	893.45097	447.22912	298.48851	8
19	1975.94304	988.47516	659.31920	G	806.41894	403.71311	269.47783	7
20	2075.01146	1038.00937	692.34200	V	749.39747	375.20237	250.47067	6
21	2176.05914	1088.53321	726.02456	T	650.32905	325.66816	217.44787	5
22	2277.10682	1139.05705	759.70712	T	549.28137	275.14432	183.76531	4
23	2437.13748	1219.07238	813.05068	C-Carbamidomethyl	448.23369	224.62048	150.08275	3
24	2550.22155	1275.61441	850.74537	L	288.20303	144.60515	96.73919	2
25				R	175.11896	88.06312	59.04450	1

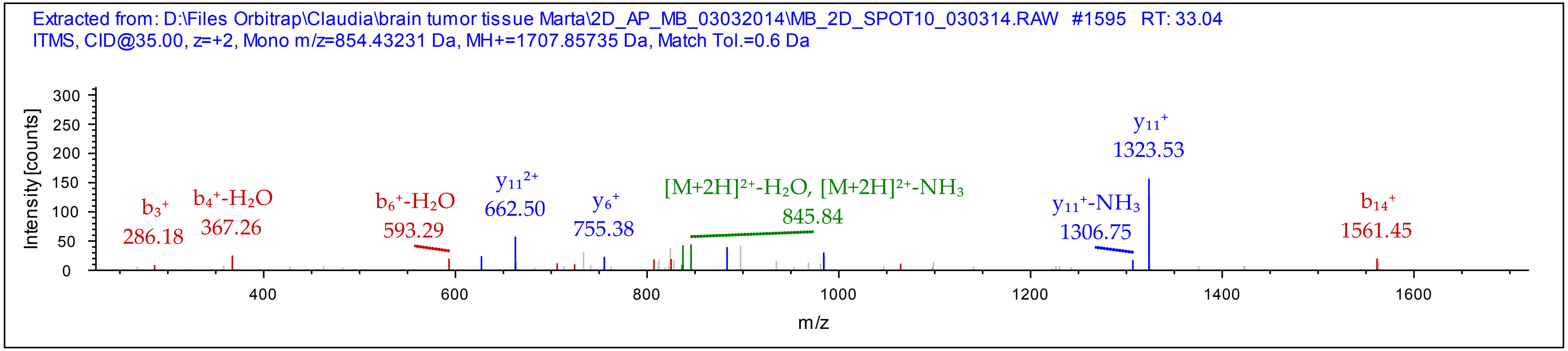


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT10_030314.RAW #2003 RT: 39.54
ITMS, CID@35.00, z=+3, Mono m/z=908.77979 Da, MH+=2724.32480 Da, Match Tol.=0.6 Da

Sequence: ALTVPELTQQMFDSK, Charge: +2, Monoisotopic m/z: 854.43231 Da (-2.47 mmu/-2.89 ppm), MH+: 1707.85735 Da, RT: 33.04 min,
Identified with: Sequest HT (v1.3); XCorr:2.29, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (2):
- Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]
- Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**

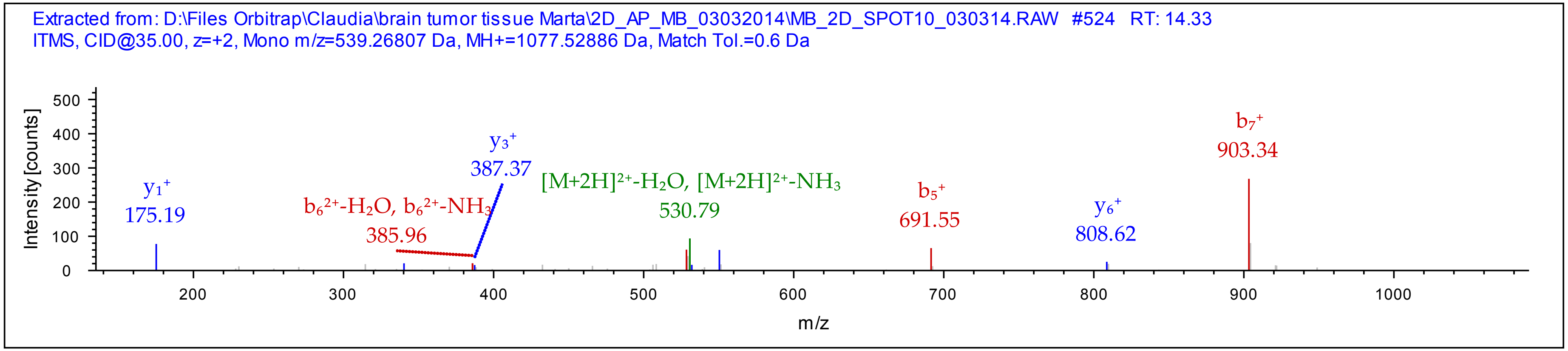
1	72.04440	36.52584	A			15
2	185.12847	93.06787	L	1636.82516	818.91622	14
3	286.17615	143.59171	T	1523.74109	762.37418	13
4	385.24457	193.12592	V	1422.69341	711.85034	12
5	482.29734	241.65231	P	1323.62499	662.31613	11
6	611.33994	306.17361	E	1226.57222	613.78975	10
7	724.42401	362.71564	L	1097.52962	549.26845	9
8	825.47169	413.23948	T	984.44555	492.72641	8
9	953.53027	477.26877	Q	883.39787	442.20257	7
10	1081.58885	541.29806	Q	755.33929	378.17328	6
11	1212.62935	606.81831	M	627.28071	314.14399	5
12	1359.69777	680.35252	F	496.24021	248.62374	4
13	1474.72472	737.86600	D	349.17179	175.08953	3
14	1561.75675	781.38201	S	234.14484	117.57606	2
15			K	147.11281	74.06004	1



Sequence: IREEYPDR, Charge: +2, Monoisotopic m/z: 539.26807 Da (-1.77 mmu/-3.28 ppm), MH+: 1077.52886 Da, RT: 14.33 min,
Identified with: Sequest HT (v1.3); XCorr:2.27, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (8):
- Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1 - [TBB1_HUMAN]
- Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]
- Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]
- Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]
- Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]

- Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens PE=1 SV=1 - [TBB8L_HUMAN]
- Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2 - [TBB8_HUMAN]
- Putative tubulin beta chain-like protein ENSP00000290377 OS=Homo sapiens PE=5 SV=2 - [YI016_HUMAN]

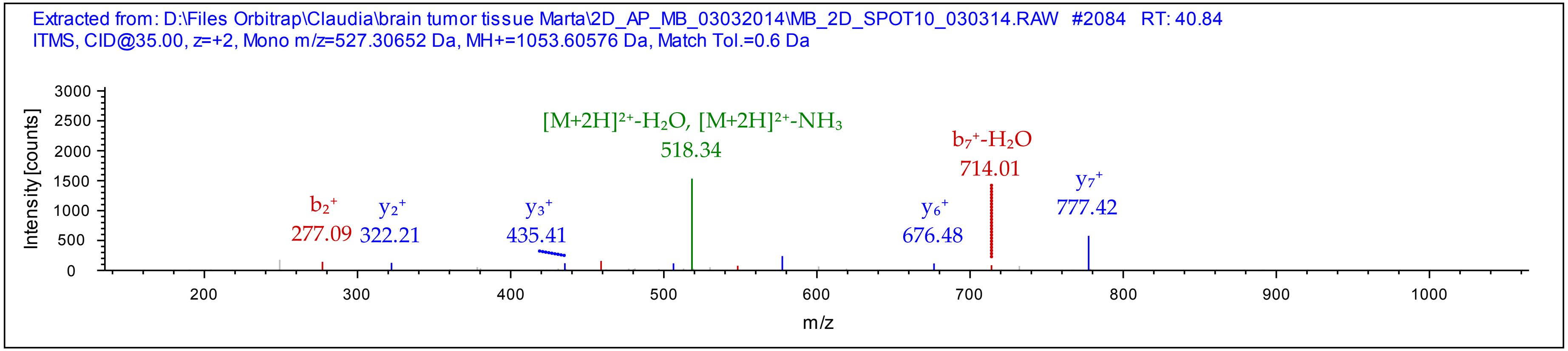
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	114.09135	57.54931	I			8
2	270.19247	135.59987	R	964.44832	482.72780	7
3	399.23507	200.12117	E	808.34720	404.67724	6
4	528.27767	264.64247	E	679.30460	340.15594	5
5	691.34099	346.17413	Y	550.26200	275.63464	4
6	788.39376	394.70052	P	387.19868	194.10298	3
7	903.42071	452.21399	D	290.14591	145.57659	2
8			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT10_030314.RAW #524 RT: 14.33
ITMS, CID@35.00, z=+2, Mono m/z=539.26807 Da, MH+=1077.52886 Da, Match Tol.=0.6 Da

Sequence: YLTVAAIFR, Charge: +2, Monoisotopic m/z: 527.30652 Da (-1.71 mmu/-3.25 ppm), MH+: 1053.60576 Da, RT: 40.84 min,
Identified with: Sequest HT (v1.3); XCorr:2.22, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3
Protein references (2):
- Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]
- Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	164.07060	82.53894	Y			9
2	277.15467	139.08097	L	890.54586	445.77657	8

3	378.20235	189.60481	T	777.46179	389.23453	7
4	477.27077	239.13902	V	676.41411	338.71069	6
5	548.30789	274.65758	A	577.34569	289.17648	5
6	619.34501	310.17614	A	506.30857	253.65792	4
7	732.42908	366.71818	I	435.27145	218.13936	3
8	879.49750	440.25239	F	322.18738	161.59733	2
9			R	175.11896	88.06312	1

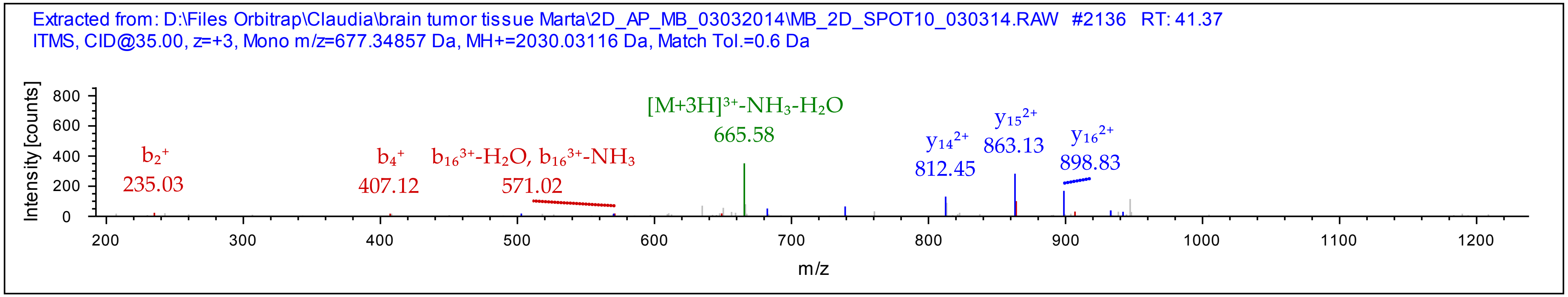


Sequence: MSATFIGNSTAIQELFKR, M1-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 677.34875 Da (-1.98 mmu/-2.92 ppm), MH+: 2030.03171 Da, RT: 41.05 min,
Identified with: Sequest HT (v1.3); XCorr:2.08, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):
- Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]
- Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]
- Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	148.04269	74.52498	50.01908	M-Oxidation				18
2	235.07472	118.04100	79.02976	S	1883.00222	942.00475	628.33892	17
3	306.11184	153.55956	102.70880	A	1795.97019	898.48873	599.32825	16
4	407.15952	204.08340	136.39136	T	1724.93307	862.97017	575.64921	15
5	554.22794	277.61761	185.41416	F	1623.88539	812.44633	541.96665	14
6	667.31201	334.15964	223.10885	I	1476.81697	738.91212	492.94384	13

7	724.33348	362.67038	242.11601	G	1363.73290	682.37009	455.24915	12
8	838.37641	419.69184	280.13032	N	1306.71143	653.85935	436.24199	11
9	925.40844	463.20786	309.14100	S	1192.66850	596.83789	398.22768	10
10	1026.45612	513.73170	342.82356	T	1105.63647	553.32187	369.21701	9
11	1097.49324	549.25026	366.50260	A	1004.58879	502.79803	335.53445	8
12	1210.57731	605.79229	404.19729	I	933.55167	467.27947	311.85541	7
13	1338.63589	669.82158	446.88348	Q	820.46760	410.73744	274.16072	6
14	1467.67849	734.34288	489.89768	E	692.40902	346.70815	231.47452	5
15	1580.76256	790.88492	527.59237	L	563.36642	282.18685	188.46032	4
16	1727.83098	864.41913	576.61518	F	450.28235	225.64481	150.76563	3
17	1855.92595	928.46661	619.31350	K	303.21393	152.11060	101.74283	2
18				R	175.11896	88.06312	59.04450	1



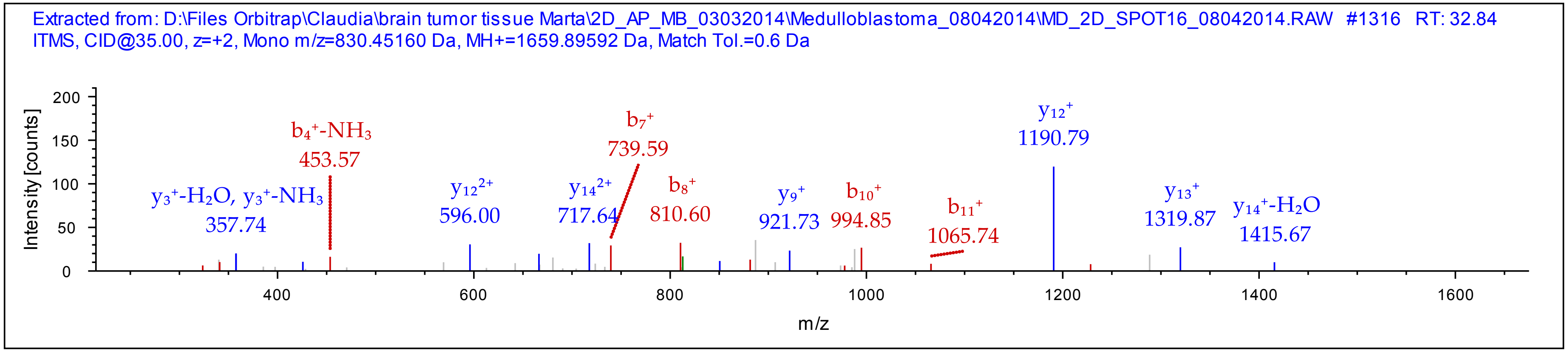
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT10_030314.RAW #2136 RT: 41.37
ITMS, CID@35.00, z=+3, Mono m/z=677.34857 Da, MH+=2030.03116 Da, Match Tol.=0.6 Da

Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
16	P11142	Heat shock cognate 71 kDa protein	70.7	5.4	12.9	22.29%	9	15	MB	NS	1.4	↑ in MB

Sequence: IINEPTAAAIAYGLDK, Charge: +2, Monoisotopic m/z: 830.45160 Da (+0.32 mmu/+0.38 ppm), MH+: 1659.89592 Da, RT: 32.84 min,
Identified with: Sequest HT (v1.3); XCorr:1.78, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (4):
- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]
- Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2 - [HS71L_HUMAN]
- Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1 - [HSP72_HUMAN]
- Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**

1	114.09135	57.54931	I			16
2	227.17542	114.09135	I	1546.81122	773.90925	15
3	341.21835	171.11281	N	1433.72715	717.36721	14
4	470.26095	235.63411	E	1319.68422	660.34575	13
5	567.31372	284.16050	P	1190.64162	595.82445	12
6	668.36140	334.68434	T	1093.58885	547.29806	11
7	739.39852	370.20290	A	992.54117	496.77422	10
8	810.43564	405.72146	A	921.50405	461.25566	9
9	881.47276	441.24002	A	850.46693	425.73710	8
10	994.55683	497.78205	I	779.42981	390.21854	7
11	1065.59395	533.30061	A	666.34574	333.67651	6
12	1228.65727	614.83227	Y	595.30862	298.15795	5
13	1285.67874	643.34301	G	432.24530	216.62629	4
14	1398.76281	699.88504	L	375.22383	188.11555	3
15	1513.78976	757.39852	D	262.13976	131.57352	2
16			K	147.11281	74.06004	1

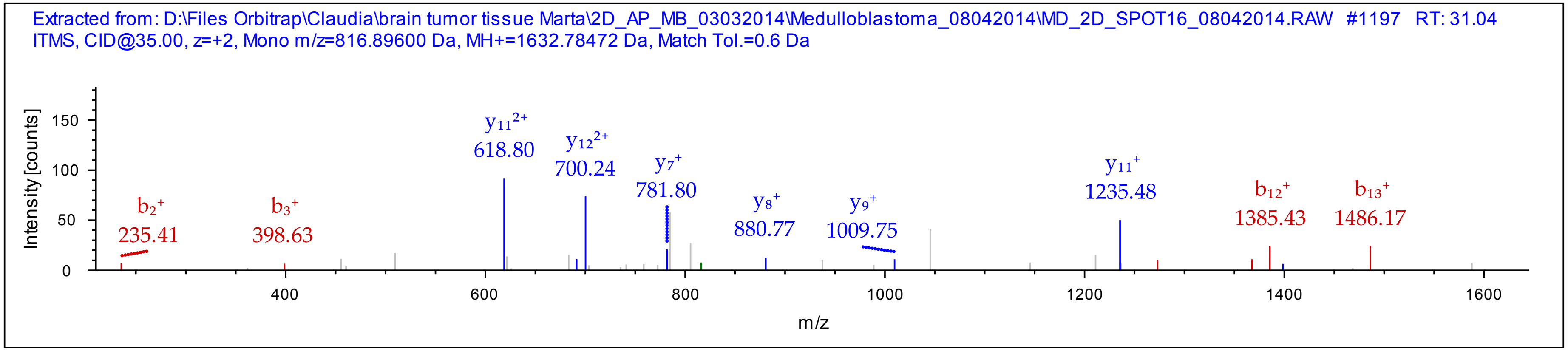


Sequence: SFYPEEVSSMVLTK, M10-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 816.89600 Da (+1.05 mmu/+1.29 ppm), MH+: 1632.78472 Da, RT: 31.04 min,
Identified with: Sequest HT (v1.3); XCorr:1.66, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3
Protein references (1):

- Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	88.03931	44.52329	S			14

2	235.10773	118.05750	F	1545.75059	773.37893	13
3	398.17105	199.58916	Y	1398.68217	699.84472	12
4	495.22382	248.11555	P	1235.61885	618.31306	11
5	624.26642	312.63685	E	1138.56608	569.78668	10
6	753.30902	377.15815	E	1009.52348	505.26538	9
7	852.37744	426.69236	V	880.48088	440.74408	8
8	939.40947	470.20837	S	781.41246	391.20987	7
9	1026.44150	513.72439	S	694.38043	347.69385	6
10	1173.47691	587.24209	M-Oxidation	607.34840	304.17784	5
11	1272.54533	636.77630	V	460.31298	230.66013	4
12	1385.62940	693.31834	L	361.24456	181.12592	3
13	1486.67708	743.84218	T	248.16049	124.58388	2
14			K	147.11281	74.06004	1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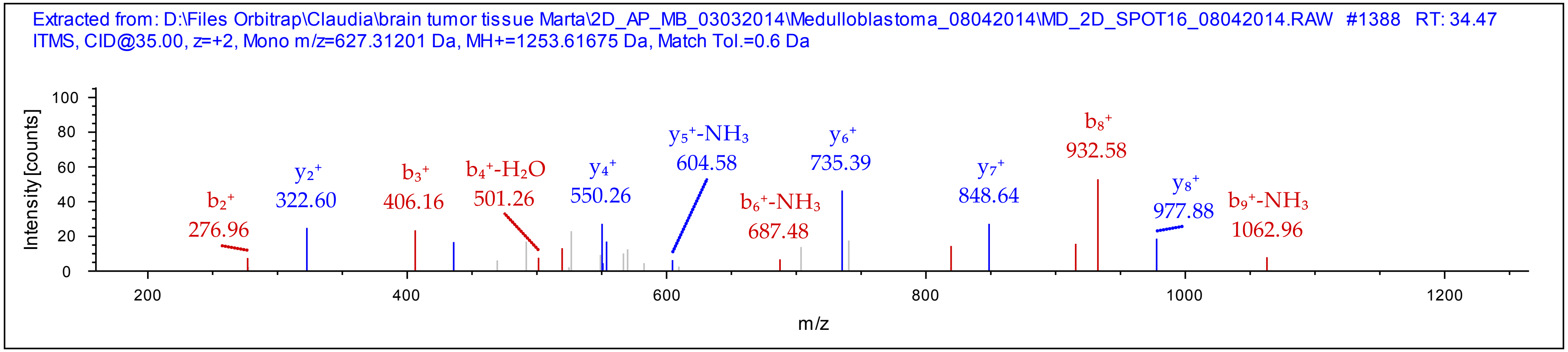
ITMS, CID@35.00, z=+2, Mono m/z=816.89600 Da, MH+=1632.78472 Da, Match Tol.=0.6 Da

Sequence: FEELNADLFR, Charge: +2, Monoisotopic m/z: 627.31201 Da (+0.3 mmu/+0.48 ppm), MH+: 1253.61675 Da, RT: 34.47 min,
Identified with: Sequest HT (v1.3); XCorr:1.61, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (2):
- Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1 - [HSP72_HUMAN]
- Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	148.07570	74.54149	F			10
2	277.11830	139.06279	E	1106.54772	553.77750	9
3	406.16090	203.58409	E	977.50512	489.25620	8

4	519.24497	260.12612	L	848.46252	424.73490	7
5	633.28790	317.14759	N	735.37845	368.19286	6
6	704.32502	352.66615	A	621.33552	311.17140	5
7	819.35197	410.17962	D	550.29840	275.65284	4
8	932.43604	466.72166	L	435.27145	218.13936	3
9	1079.50446	540.25587	F	322.18738	161.59733	2
10			R	175.11896	88.06312	1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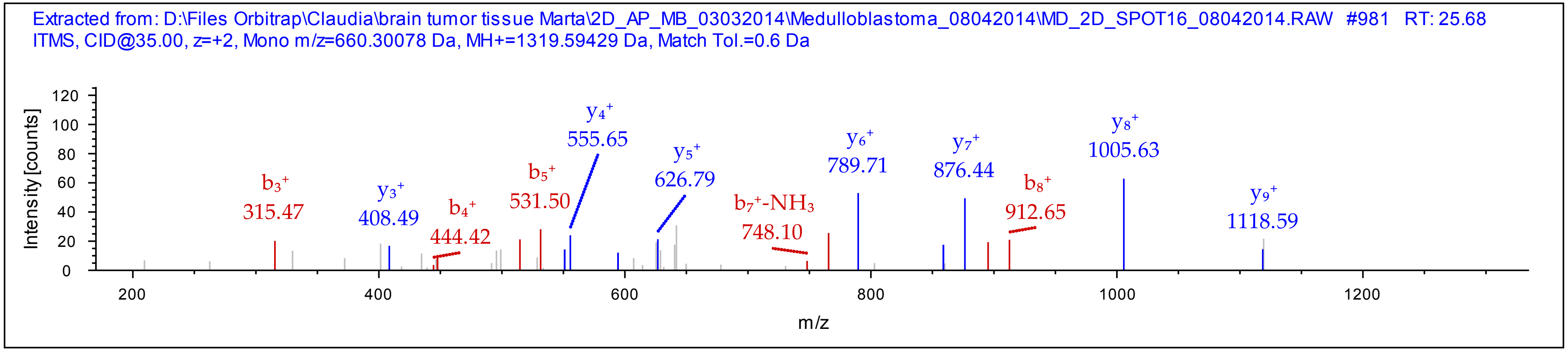
ITMS, CID@35.00, z=+2, Mono m/z=627.31201 Da, MH+=1253.61675 Da, Match Tol.=0.6 Da

Sequence: NSLESYAFNMK, M10-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 660.30078 Da (+0.31 mmu/+0.46 ppm), MH+: 1319.59429 Da, RT: 25.68 min,
Identified with: Sequest HT (v1.3); XCorr:1.55, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):

- Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]

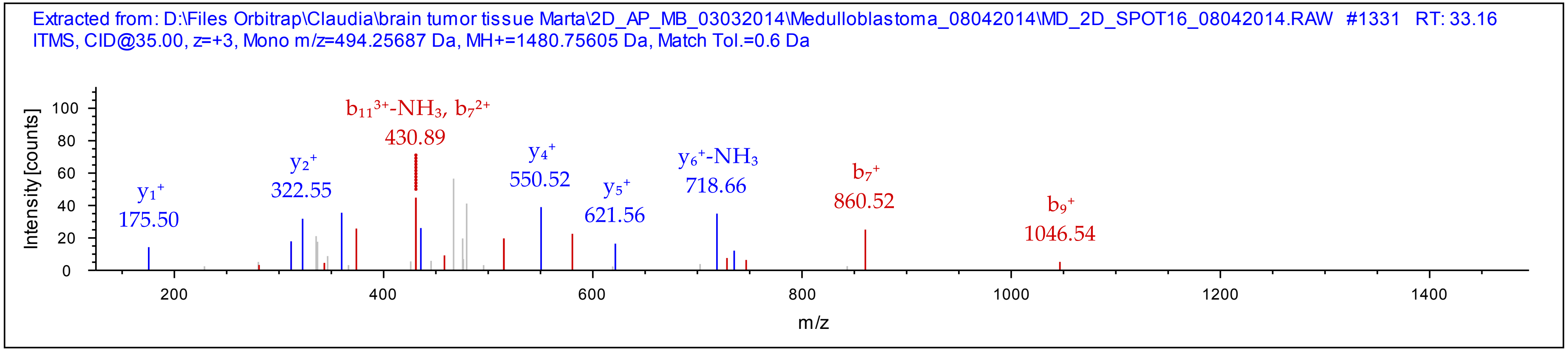
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	115.05021	58.02874	N			11
2	202.08224	101.54476	S	1205.55075	603.27901	10
3	315.16631	158.08679	L	1118.51872	559.76300	9
4	444.20891	222.60809	E	1005.43465	503.22096	8
5	531.24094	266.12411	S	876.39205	438.69966	7
6	694.30426	347.65577	Y	789.36002	395.18365	6
7	765.34138	383.17433	A	626.29670	313.65199	5
8	912.40980	456.70854	F	555.25958	278.13343	4
9	1026.45273	513.73000	N	408.19116	204.59922	3

10	1173.48814	587.24771	M-Oxidation	294.14823	147.57775	2
11			K	147.11281	74.06004	1



Sequence: ARFEELNADLFR, Charge: +3, Monoisotopic m/z: 494.25687 Da (+0.56 mmu/+1.12 ppm), MH+: 1480.75605 Da, RT: 33.16 min,
Identified with: Sequest HT (v1.3); XCorr:1.52, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (2):
- Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1 - [HSP72_HUMAN]
- Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]

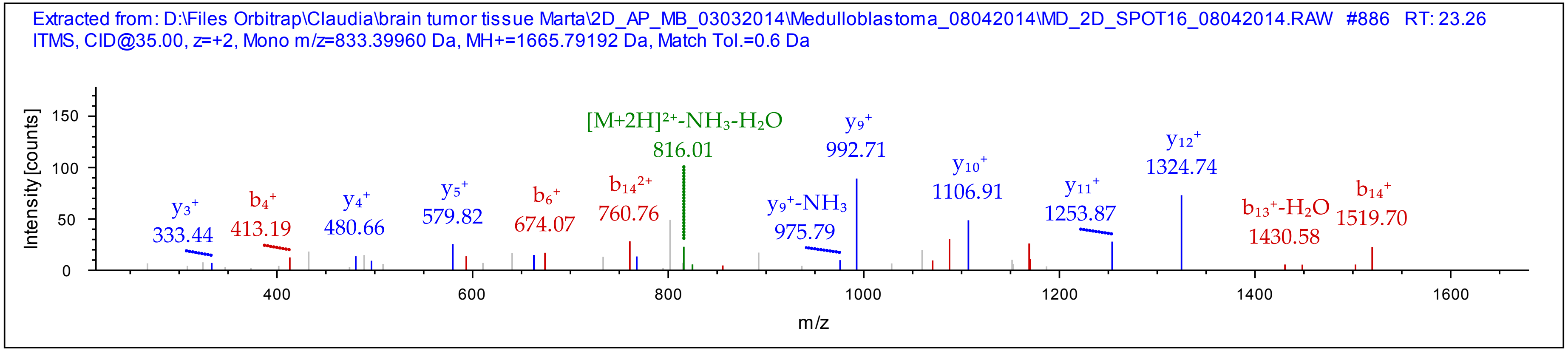
#1	b^{+}	b^{2+}	b^{3+}	Seq.	y^{+}	y^{2+}	y^{3+}	#2
1	72.04440	36.52584	24.68632	A				12
2	228.14552	114.57640	76.72002	R	1409.71726	705.36227	470.57727	11
3	375.21394	188.11061	125.74283	F	1253.61614	627.31171	418.54356	10
4	504.25654	252.63191	168.75703	E	1106.54772	553.77750	369.52076	9
5	633.29914	317.15321	211.77123	E	977.50512	489.25620	326.50656	8
6	746.38321	373.69524	249.46592	L	848.46252	424.73490	283.49236	7
7	860.42614	430.71671	287.48023	N	735.37845	368.19286	245.79767	6
8	931.46326	466.23527	311.15927	A	621.33552	311.17140	207.78336	5
9	1046.49021	523.74874	349.50159	D	550.29840	275.65284	184.10432	4
10	1159.57428	580.29078	387.19628	L	435.27145	218.13936	145.76200	3
11	1306.64270	653.82499	436.21908	F	322.18738	161.59733	108.06731	2
12				R	175.11896	88.06312	59.04450	1



Sequence: NQVAMNPTNTVFDAK, M5-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 833.39960 Da (+0.87 mmu/+1.05 ppm), MH+: 1665.79192 Da, RT: 23.26 min,
Identified with: Sequest HT (v1.3); XCorr:1.42, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H$_2$O; b-NH$_3$; y; y-H$_2$O; y-NH$_3$

Protein references (1):
- Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]

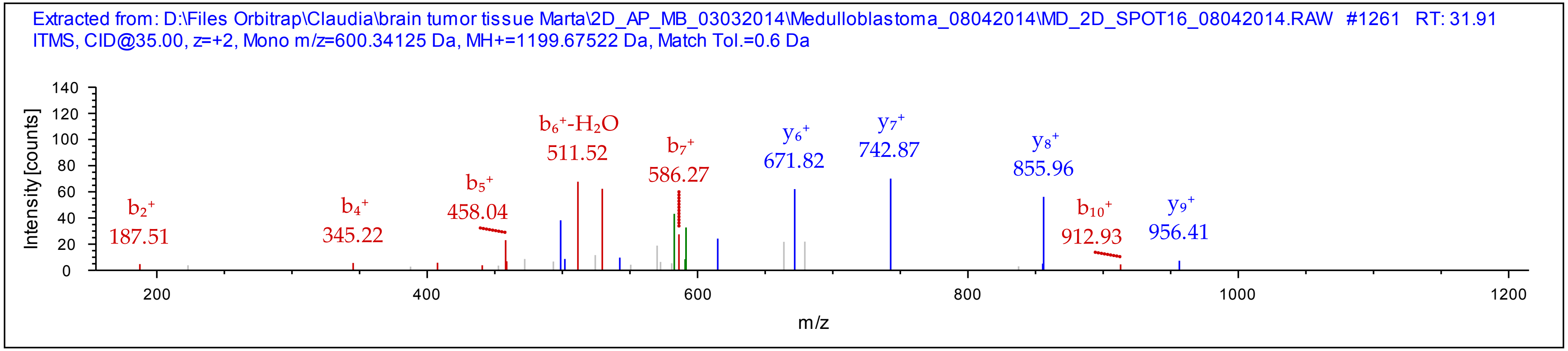
#1	**b$^+$**	**b^{2+}**	**Seq.**	**y$^+$**	**y^{2+}**	**#2**
1	115.05021	58.02874	N			15
2	243.10879	122.05803	Q	1551.74725	776.37726	14
3	342.17721	171.59224	V	1423.68867	712.34797	13
4	413.21433	207.11080	A	1324.62025	662.81376	12
5	560.24974	280.62851	M-Oxidation	1253.58313	627.29520	11
6	674.29267	337.64997	N	1106.54771	553.77749	10
7	771.34544	386.17636	P	992.50478	496.75603	9
8	872.39312	436.70020	T	895.45201	448.22964	8
9	986.43605	493.72166	N	794.40433	397.70580	7
10	1087.48373	544.24550	T	680.36140	340.68434	6
11	1186.55215	593.77971	V	579.31372	290.16050	5
12	1333.62057	667.31392	F	480.24530	240.62629	4
13	1448.64752	724.82740	D	333.17688	167.09208	3
14	1519.68464	760.34596	A	218.14993	109.57860	2
15			K	147.11281	74.06004	1



Sequence: DAGTIAGLNVLR, Charge: +2, Monoisotopic m/z: 600.34125 Da (+0.44 mmu/+0.74 ppm), MH+: 1199.67522 Da, RT: 31.91 min,
Identified with: Sequest HT (v1.3); XCorr:1.40, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):

- Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]

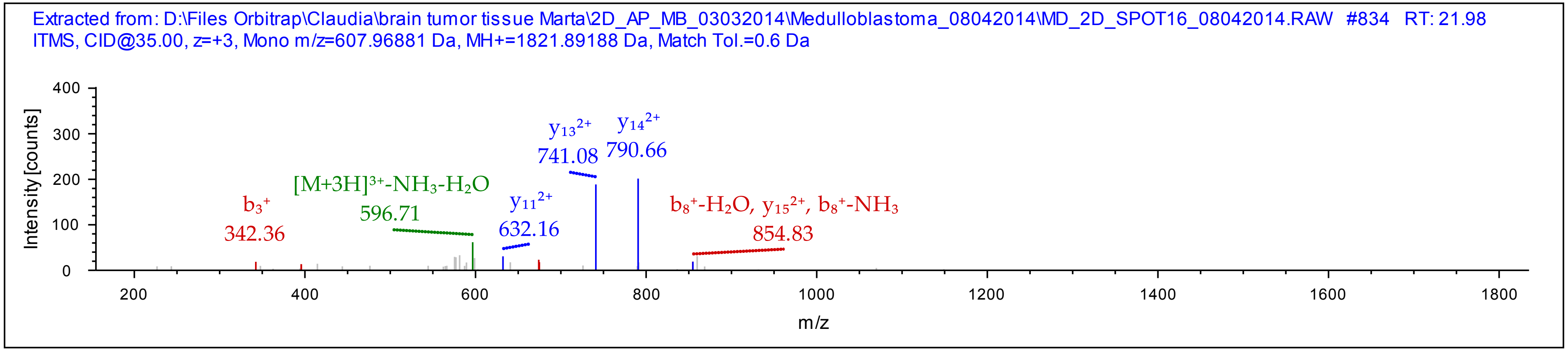
#1	b⁺	b²⁺	Seq.	y⁺	y²⁺	#2
1	116.03423	58.52075	D			12
2	187.07135	94.03931	A	1084.64738	542.82733	11
3	244.09282	122.55005	G	1013.61026	507.30877	10
4	345.14050	173.07389	T	956.58879	478.79803	9
5	458.22457	229.61592	I	855.54111	428.27419	8
6	529.26169	265.13448	A	742.45704	371.73216	7
7	586.28316	293.64522	G	671.41992	336.21360	6
8	699.36723	350.18725	L	614.39845	307.70286	5
9	813.41016	407.20872	N	501.31438	251.16083	4
10	912.47858	456.74293	V	387.27145	194.13936	3
11	1025.56265	513.28496	L	288.20303	144.60515	2
12			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\Medulloblastoma_08042014\MD_2D_SPOT16_08042014.RAW #1261 RT: 31.91
ITMS, CID@35.00, z=+2, Mono m/z=600.34125 Da, MH+=1199.67522 Da, Match Tol.=0.6 Da

Sequence: NQVAMNPTNTVFDAKR, M5-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 607.96881 Da (+0.19 mmu/+0.32 ppm), MH+: 1821.89188 Da, RT: 21.98 min,
Identified with: Sequest HT (v1.3); XCorr:1.39, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):

- Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]

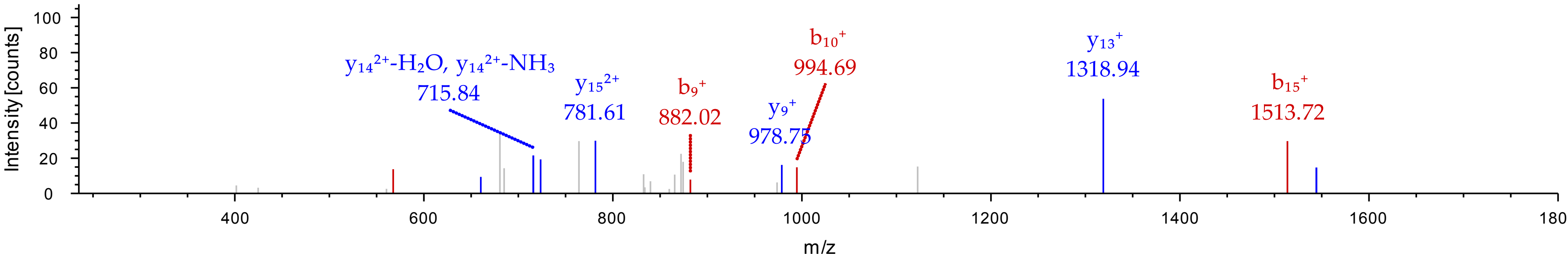
#1	**b⁺**	**b²⁺**	**b³⁺**	**Seq.**	**y⁺**	**y²⁺**	**y³⁺**	**#2**
1	115.05021	58.02874	39.02159	N				16
2	243.10879	122.05803	81.70778	Q	1707.84837	854.42782	569.95431	15
3	342.17721	171.59224	114.73059	V	1579.78979	790.39853	527.26811	14
4	413.21433	207.11080	138.40963	A	1480.72137	740.86432	494.24531	13
5	560.24974	280.62851	187.42143	M-Oxidation	1409.68425	705.34576	470.56627	12
6	674.29267	337.64997	225.43574	N	1262.64883	631.82805	421.55446	11
7	771.34544	386.17636	257.78666	P	1148.60590	574.80659	383.54015	10
8	872.39312	436.70020	291.46922	T	1051.55313	526.28020	351.18923	9
9	986.43605	493.72166	329.48353	N	950.50545	475.75636	317.50667	8
10	1087.48373	544.24550	363.16609	T	836.46252	418.73490	279.49236	7
11	1186.55215	593.77971	396.18890	V	735.41484	368.21106	245.80980	6
12	1333.62057	667.31392	445.21171	F	636.34642	318.67685	212.78699	5
13	1448.64752	724.82740	483.55402	D	489.27800	245.14264	163.76418	4
14	1519.68464	760.34596	507.23306	A	374.25105	187.62916	125.42187	3
15	1647.77961	824.39344	549.93139	K	303.21393	152.11060	101.74283	2
16				R	175.11896	88.06312	59.04450	1



Sequence: IINEPTAAAIAYGLDKK, Charge: +2, Monoisotopic m/z: 894.49988 Da (+1.11 mmu/+1.24 ppm), MH+: 1787.99248 Da, RT: 30.96 min,
Identified with: Sequest HT (v1.3); XCorr:1.29, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (2):
- Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1 - [HSP72_HUMAN]
- Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	114.09135	57.54931	I			17
2	227.17542	114.09135	I	1674.90619	837.95673	16
3	341.21835	171.11281	N	1561.82212	781.41470	15
4	470.26095	235.63411	E	1447.77919	724.39323	14
5	567.31372	284.16050	P	1318.73659	659.87193	13
6	668.36140	334.68434	T	1221.68382	611.34555	12
7	739.39852	370.20290	A	1120.63614	560.82171	11
8	810.43564	405.72146	A	1049.59902	525.30315	10
9	881.47276	441.24002	A	978.56190	489.78459	9
10	994.55683	497.78205	I	907.52478	454.26603	8
11	1065.59395	533.30061	A	794.44071	397.72399	7
12	1228.65727	614.83227	Y	723.40359	362.20543	6
13	1285.67874	643.34301	G	560.34027	280.67377	5
14	1398.76281	699.88504	L	503.31880	252.16304	4
15	1513.78976	757.39852	D	390.23473	195.62100	3
16	1641.88473	821.44600	K	275.20778	138.10753	2
17			K	147.11281	74.06004	1

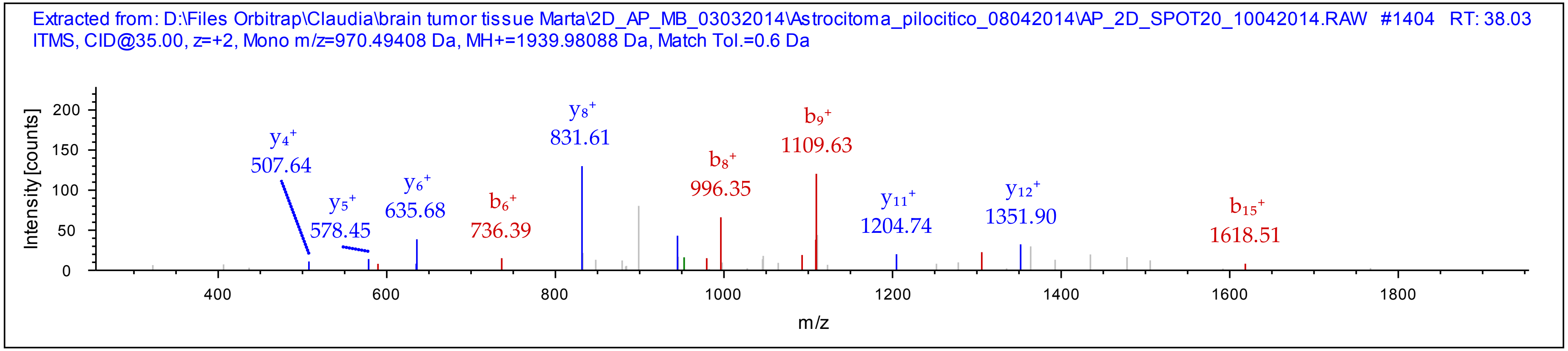
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\Medulloblastoma_08042014\MD_2D_SPOT16_08042014.RAW #1190 RT: 30.96
ITMS, CID@35.00, z=+2, Mono m/z=894.49988 Da, MH+=1787.99248 Da, Match Tol.=0.6 Da



Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
20	P06733	Alpha-enolase	47.0	7.0	9.9	19.12%	5	5	PA	8.35E-03	1.4	↑ in MB

Sequence: LAMQEFMILPVGAANFR, M3-Oxidation (15.99492 Da), M7-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 970.49408 Da (+1.96 mmu/+2.02 ppm), MH+: 1939.98088 Da, RT: 38.03 min,
Identified with: Sequest HT (v1.3); XCorr:2.59, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	114.09135	57.54931	L			17
2	185.12847	93.06787	A	1826.89290	913.95009	16
3	332.16388	166.58558	M-Oxidation	1755.85578	878.43153	15
4	460.22246	230.61487	Q	1608.82037	804.91382	14
5	589.26506	295.13617	E	1480.76179	740.88453	13
6	736.33348	368.67038	F	1351.71919	676.36323	12
7	883.36890	442.18809	M-Oxidation	1204.65077	602.82902	11
8	996.45297	498.73012	I	1057.61535	529.31131	10
9	1109.53704	555.27216	L	944.53128	472.76928	9
10	1206.58981	603.79854	P	831.44721	416.22724	8
11	1305.65823	653.33275	V	734.39444	367.70086	7
12	1362.67970	681.84349	G	635.32602	318.16665	6
13	1433.71682	717.36205	A	578.30455	289.65591	5
14	1504.75394	752.88061	A	507.26743	254.13735	4
15	1618.79687	809.90207	N	436.23031	218.61879	3
16	1765.86529	883.43628	F	322.18738	161.59733	2
17			R	175.11896	88.06312	1

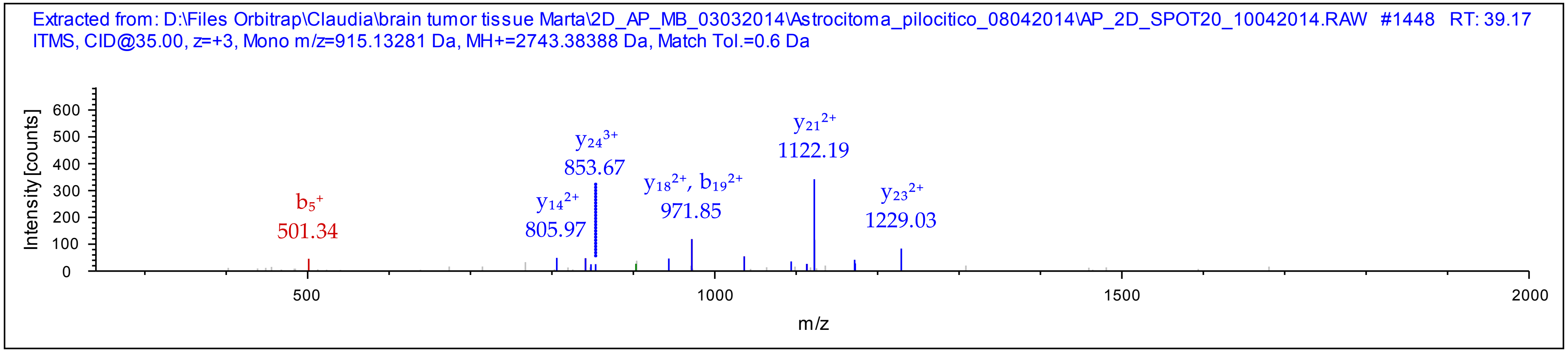


Sequence: DATNVGDEGGFAPNILENKEGLELLK, Charge: +3, Monoisotopic m/z: 915.13281 Da (+1.75 mmu/+1.91 ppm), MH+: 2743.38388 Da, RT: 39.17 min,
Identified with: Sequest HT (v1.3); XCorr:1.84, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]

#1	b+	b2+	b3+	Seq.	y+	y2+	y3+	#2
1	116.03423	58.52075	39.34959	D				26
2	187.07135	94.03931	63.02863	A	2628.35168	1314.67948	876.78874	25
3	288.11903	144.56315	96.71119	T	2557.31456	1279.16092	853.10970	24
4	402.16196	201.58462	134.72550	N	2456.26688	1228.63708	819.42714	23
5	501.23038	251.11883	167.74831	V	2342.22395	1171.61561	781.41283	22
6	558.25185	279.62956	186.75547	G	2243.15553	1122.08140	748.39003	21
7	673.27880	337.14304	225.09778	D	2186.13406	1093.57067	729.38287	20
8	802.32140	401.66434	268.11198	E	2071.10711	1036.05719	691.04055	19
9	859.34287	430.17507	287.11914	G	1942.06451	971.53589	648.02635	18
10	916.36434	458.68581	306.12630	G	1885.04304	943.02516	629.01920	17
11	1063.43276	532.22002	355.14910	F	1828.02157	914.51442	610.01204	16
12	1134.46988	567.73858	378.82814	A	1680.95315	840.98021	560.98923	15
13	1231.52265	616.26496	411.17907	P	1609.91603	805.46165	537.31019	14
14	1345.56558	673.28643	449.19338	N	1512.86326	756.93527	504.95927	13
15	1458.64965	729.82846	486.88807	I	1398.82033	699.91380	466.94496	12
16	1571.73372	786.37050	524.58276	L	1285.73626	643.37177	429.25027	11
17	1700.77632	850.89180	567.59696	E	1172.65219	586.82973	391.55558	10
18	1814.81925	907.91326	605.61127	N	1043.60959	522.30843	348.54138	9
19	1942.91422	971.96075	648.30959	K	929.56666	465.28697	310.52707	8

20	2071.95682	1036.48205	691.32379	E	801.47169	401.23948	267.82875	7
21	2128.97829	1064.99278	710.33095	G	672.42909	336.71818	224.81455	6
22	2242.06236	1121.53482	748.02564	L	615.40762	308.20745	205.80739	5
23	2371.10496	1186.05612	791.03984	E	502.32355	251.66541	168.11270	4
24	2484.18903	1242.59815	828.73453	L	373.28095	187.14411	125.09850	3
25	2597.27310	1299.14019	866.42922	L	260.19688	130.60208	87.40381	2
26				K	147.11281	74.06004	49.70912	1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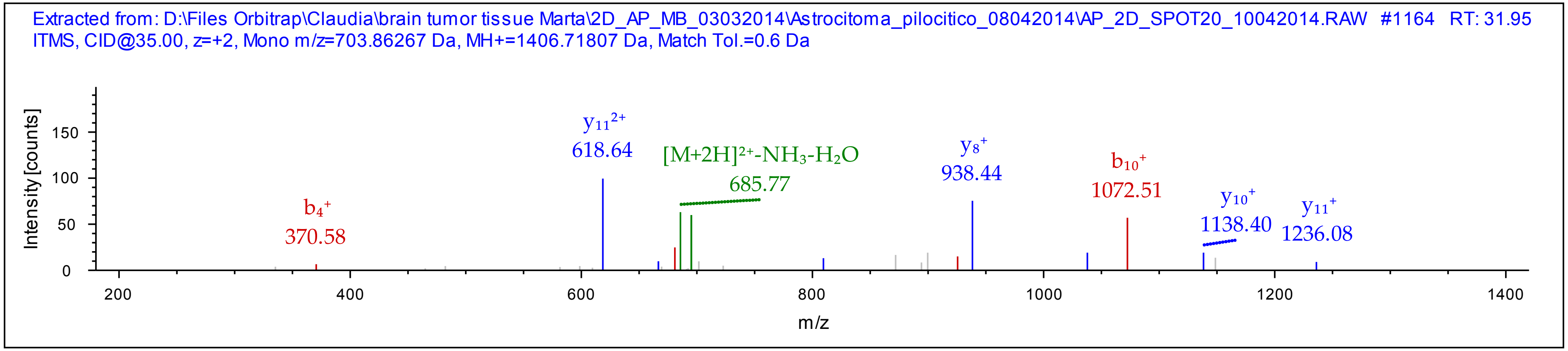
ITMS, CID@35.00, z=+3, Mono m/z=915.13281 Da, MH+=2743.38388 Da, Match Tol.=0.6 Da

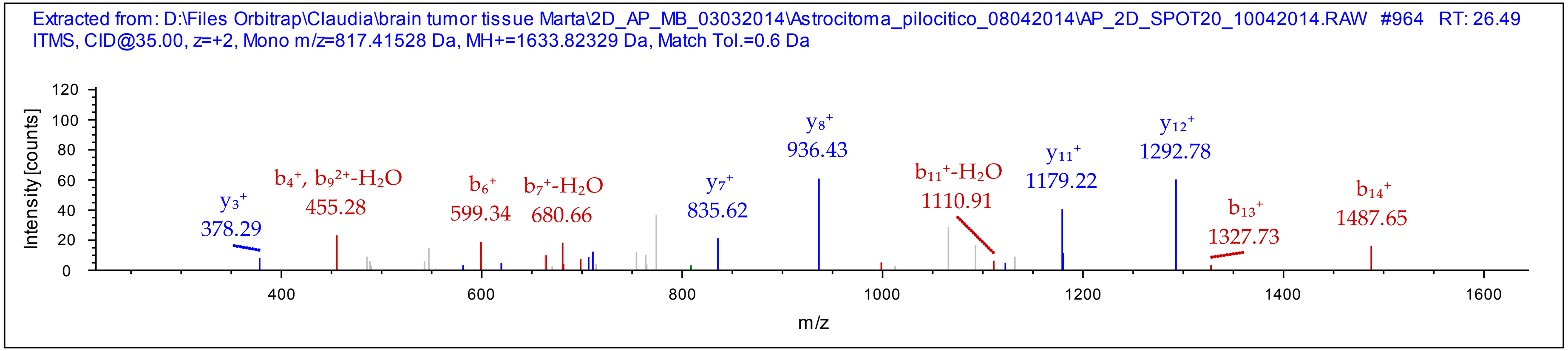
Sequence: GNPTVEVDLFTSK, Charge: +2, Monoisotopic m/z: 703.86267 Da (+0.91 mmu/+1.29 ppm), MH+: 1406.71807 Da, RT: 31.95 min,
Identified with: Sequest HT (v1.3); XCorr:1.71, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]

#1	**b$^+$**	**b^{2+}**	**Seq.**	**y$^+$**	**y^{2+}**	**#2**
1	58.02875	29.51801	G			13
2	172.07168	86.53948	N	1349.69478	675.35103	12
3	269.12445	135.06586	P	1235.65185	618.32956	11
4	370.17213	185.58970	T	1138.59908	569.80318	10
5	469.24055	235.12391	V	1037.55140	519.27934	9
6	598.28315	299.64521	E	938.48298	469.74513	8
7	697.35157	349.17942	V	809.44038	405.22383	7
8	812.37852	406.69290	D	710.37196	355.68962	6
9	925.46259	463.23493	L	595.34501	298.17614	5
10	1072.53101	536.76914	F	482.26094	241.63411	4
11	1173.57869	587.29298	T	335.19252	168.09990	3
12	1260.61072	630.80900	S	234.14484	117.57606	2
13			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\Astrocitoma_pilocitico_08042014\AP_2D_SPOT20_10042014.RAW #1164 RT: 31.95
ITMS, CID@35.00, z=+2, Mono m/z=703.86267 Da, MH+=1406.71807 Da, Match Tol.=0.6 Da

Sequence: VNQIGSVTESLQACK, C14-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 817.41528 Da (+0.91 mmu/+1.12 ppm), MH+: 1633.82329 Da, RT: 26.49 min,
Identified with: Sequest HT (v1.3); XCorr:1.43, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]

#1	b+	b2+	Seq.	y+	y2+	#2
1	100.07570	50.54149	V			15
2	214.11863	107.56295	N	1534.75305	767.88016	14
3	342.17721	171.59224	Q	1420.71012	710.85870	13
4	455.26128	228.13428	I	1292.65154	646.82941	12
5	512.28275	256.64501	G	1179.56747	590.28737	11
6	599.31478	300.16103	S	1122.54600	561.77664	10
7	698.38320	349.69524	V	1035.51397	518.26062	9
8	799.43088	400.21908	T	936.44555	468.72641	8
9	928.47348	464.74038	E	835.39787	418.20257	7
10	1015.50551	508.25639	S	706.35527	353.68127	6
11	1128.58958	564.79843	L	619.32324	310.16526	5
12	1256.64816	628.82772	Q	506.23917	253.62322	4
13	1327.68528	664.34628	A	378.18059	189.59393	3
14	1487.71593	744.36160	C-Carbamidomethyl	307.14347	154.07537	2
15			K	147.11281	74.06004	1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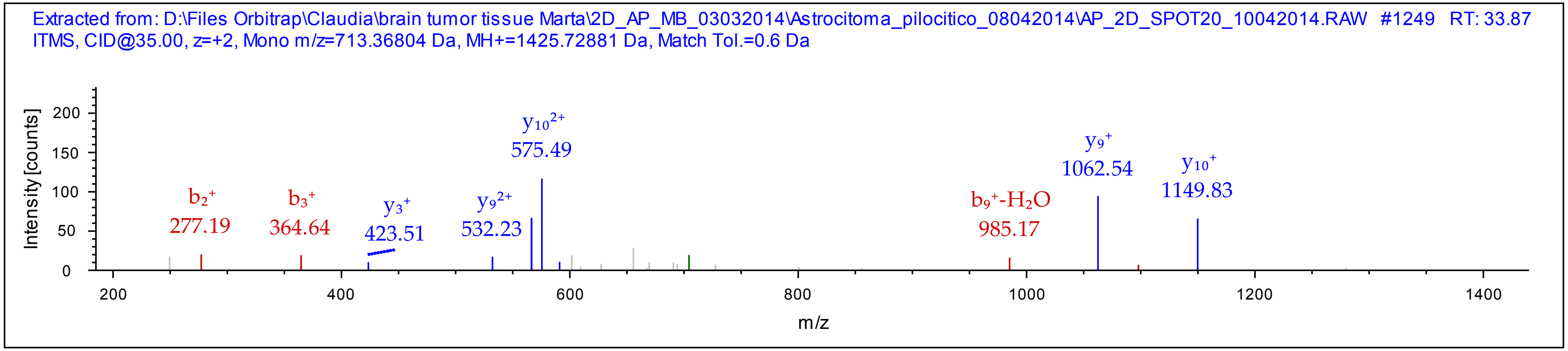
ITMS, CID@35.00, z=+2, Mono m/z=817.41528 Da, MH+=1633.82329 Da, Match Tol.=0.6 Da

Sequence: YISPDQLADLYK, Charge: +2, Monoisotopic m/z: 713.36804 Da (+1.37 mmu/+1.93 ppm), MH+: 1425.72881 Da, RT: 33.87 min,
Identified with: Sequest HT (v1.3); XCorr:1.15, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	164.07060	82.53894	Y			12
2	277.15467	139.08097	I	1262.66274	631.83501	11
3	364.18670	182.59699	S	1149.57867	575.29297	10
4	461.23947	231.12337	P	1062.54664	531.77696	9
5	576.26642	288.63685	D	965.49387	483.25057	8
6	704.32500	352.66614	Q	850.46692	425.73710	7
7	817.40907	409.20817	L	722.40834	361.70781	6
8	888.44619	444.72673	A	609.32427	305.16577	5
9	1003.47314	502.24021	D	538.28715	269.64721	4
10	1116.55721	558.78224	L	423.26020	212.13374	3
11	1279.62053	640.31390	Y	310.17613	155.59170	2
12			K	147.11281	74.06004	1

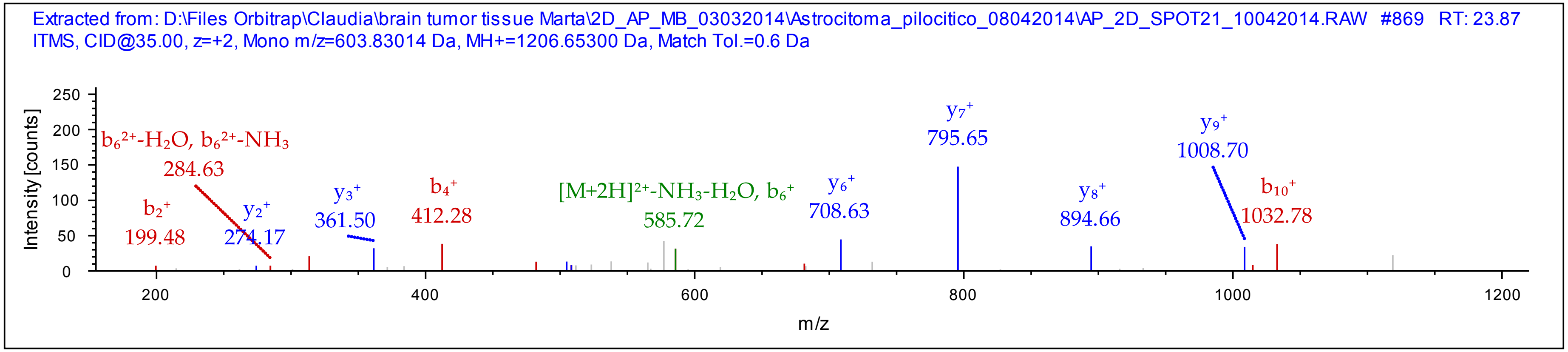


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\Astrocitoma_pilocitico_08042014\AP_2D_SPOT20_10042014.RAW #1249 RT: 33.87
ITMS, CID@35.00, z=+2, Mono m/z=713.36804 Da, MH+=1425.72881 Da, Match Tol.=0.6 Da

Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
21	P16152	Carbonyl reductase [NADPH] 1	30.2	8.6	6.5	9.75%	2	2	PA	8.64E-04	1.6	↑ in MB

Sequence: VVNVSSIMSVR, M8-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 603.83014 Da (+0.93 mmu/+1.54 ppm), MH+: 1206.65300 Da, RT: 23.87 min,
Identified with: Sequest HT (v1.3); XCorr:2.39, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3 - [CBR1_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	100.07570	50.54149	V			11
2	199.14412	100.07570	V	1107.58273	554.29500	10
3	313.18705	157.09716	N	1008.51431	504.76079	9
4	412.25547	206.63137	V	894.47138	447.73933	8
5	499.28750	250.14739	S	795.40296	398.20512	7
6	586.31953	293.66340	S	708.37093	354.68910	6
7	699.40360	350.20544	I	621.33890	311.17309	5
8	846.43901	423.72314	M-Oxidation	508.25483	254.63105	4
9	933.47104	467.23916	S	361.21941	181.11334	3
10	1032.53946	516.77337	V	274.18738	137.59733	2
11			R	175.11896	88.06312	1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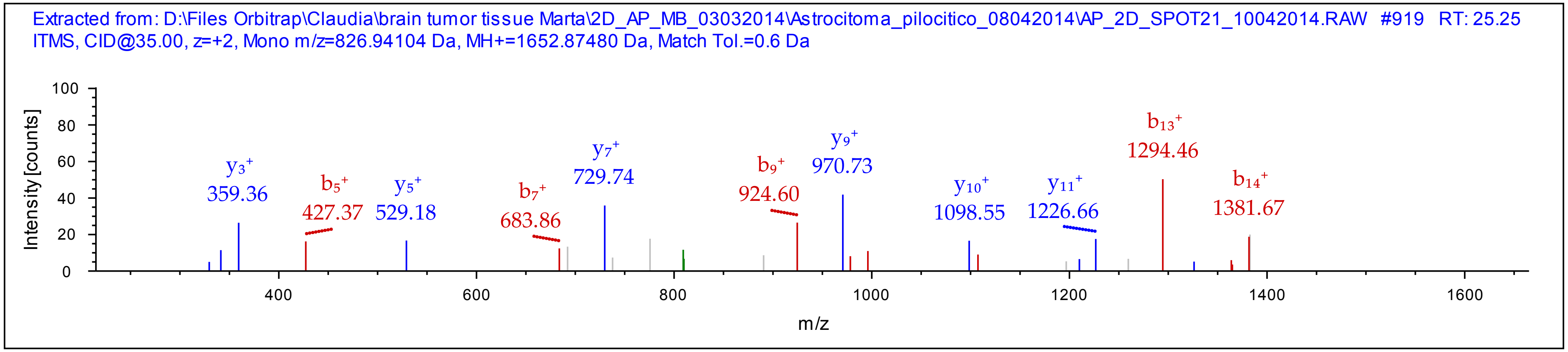
ITMS, CID@35.00, z=+2, Mono m/z=603.83014 Da, MH+=1206.65300 Da, Match Tol.=0.6 Da

Sequence: GQAAVQQLQAEGLSPR, Charge: +2, Monoisotopic m/z: 826.94104 Da (+1.63 mmu/+1.97 ppm), MH+: 1652.87480 Da, RT: 25.25 min,
Identified with: Sequest HT (v1.3); XCorr:1.36, Ions matched by search engine: 0/0

Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (2):
- Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3 - [CBR1_HUMAN]
- Carbonyl reductase [NADPH] 3 OS=Homo sapiens GN=CBR3 PE=1 SV=3 - [CBR3_HUMAN]

#1	**b$^+$**	**b^{2+}**	**Seq.**	**y$^+$**	**y^{2+}**	**#2**
1	58.02875	29.51801	G			16
2	186.08733	93.54730	Q	1595.85007	798.42867	15
3	257.12445	129.06586	A	1467.79149	734.39938	14
4	328.16157	164.58442	A	1396.75437	698.88082	13
5	427.22999	214.11863	V	1325.71725	663.36226	12
6	555.28857	278.14792	Q	1226.64883	613.82805	11
7	683.34715	342.17721	Q	1098.59025	549.79876	10
8	796.43122	398.71925	L	970.53167	485.76947	9
9	924.48980	462.74854	Q	857.44760	429.22744	8
10	995.52692	498.26710	A	729.38902	365.19815	7
11	1124.56952	562.78840	E	658.35190	329.67959	6
12	1181.59099	591.29913	G	529.30930	265.15829	5
13	1294.67506	647.84117	L	472.28783	236.64755	4
14	1381.70709	691.35718	S	359.20376	180.10552	3
15	1478.75986	739.88357	P	272.17173	136.58950	2
16			R	175.11896	88.06312	1

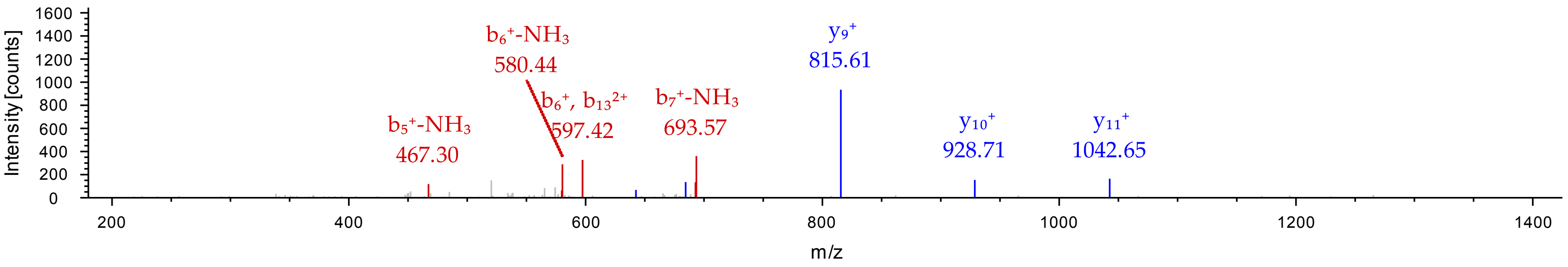

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\Astrocitoma_pilocitico_08042014\AP_2D_SPOT21_10042014.RAW #919 RT: 25.25
ITMS, CID@35.00, z=+2, Mono m/z=826.94104 Da, MH+=1652.87480 Da, Match Tol.=0.6 Da

Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
23	P04406	Glyceraldehyde-3-phosphate dehydrogenase	35.9	8.6	7.4	19.70%	2	3	PA	NS	1.5	↑ in MB

Sequence: GALQNIIPASTGAAK, Charge: +2, Monoisotopic m/z: 706.39990 Da (+1.05 mmu/+1.49 ppm), MH+: 1411.79253 Da, RT: 28.48 min,
Identified with: Sequest HT (v1.3); XCorr:1.71, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]

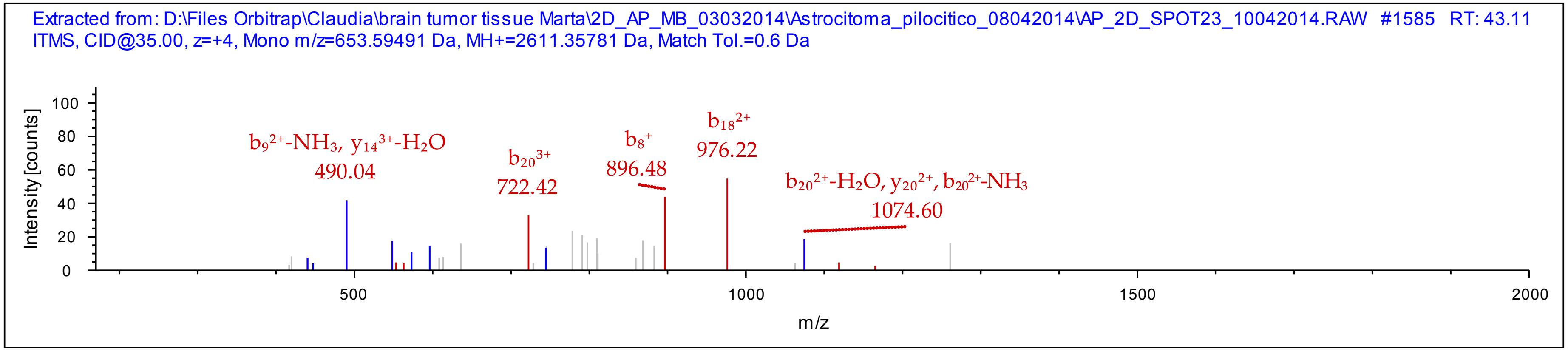
#1	**b$^+$**	**b^{2+}**	**Seq.**	**y$^+$**	**y^{2+}**	**#2**
1	58.02875	29.51801	G			15
2	129.06587	65.03657	A	1354.76896	677.88812	14
3	242.14994	121.57861	L	1283.73184	642.36956	13
4	370.20852	185.60790	Q	1170.64777	585.82752	12
5	484.25145	242.62936	N	1042.58919	521.79823	11
6	597.33552	299.17140	I	928.54626	464.77677	10
7	710.41959	355.71343	I	815.46219	408.23473	9
8	807.47236	404.23982	P	702.37812	351.69270	8
9	878.50948	439.75838	A	605.32535	303.16631	7
10	965.54151	483.27439	S	534.28823	267.64775	6
11	1066.58919	533.79823	T	447.25620	224.13174	5
12	1123.61066	562.30897	G	346.20852	173.60790	4
13	1194.64778	597.82753	A	289.18705	145.09716	3
14	1265.68490	633.34609	A	218.14993	109.57860	2
15			K	147.11281	74.06004	1

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\Astrocitoma_pilocitico_08042014\AP_2D_SPOT23_10042014.RAW #1037 RT: 28.48
ITMS, CID@35.00, z=+2, Mono m/z=706.39990 Da, MH+=1411.79253 Da, Match Tol.=0.6 Da



Sequence: VIHDNFGIVEGLMTTVHAITATQK, M13-Oxidation (15.99492 Da)
Charge: +4, Monoisotopic m/z: 653.59491 Da (+0.71 mmu/+1.09 ppm), MH+: 2611.35781 Da, RT: 43.11 min,
Identified with: Sequest HT (v1.3); XCorr:1.38, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]

#1	**b^{+}**	**b^{2+}**	**b^{3+}**	**b^{4+}**	**Seq.**	**y^{+}**	**y^{2+}**	**y^{3+}**	**y^{4+}**	**#2**
1	100.07570	50.54149	34.03008	25.77438	V					24
2	213.15977	107.08352	71.72477	54.04540	I	2512.28655	1256.64691	838.10037	628.82709	23
3	350.21868	175.61298	117.41108	88.31013	H	2399.20248	1200.10488	800.40568	600.55608	22
4	465.24563	233.12645	155.75339	117.06686	D	2262.14357	1131.57542	754.71937	566.29135	21
5	579.28856	290.14792	193.76770	145.57760	N	2147.11662	1074.06195	716.37706	537.53461	20
6	726.35698	363.68213	242.79051	182.34470	F	2033.07369	1017.04048	678.36275	509.02388	19
7	783.37845	392.19286	261.79767	196.60007	G	1886.00527	943.50627	629.33994	472.25677	18
8	896.46252	448.73490	299.49236	224.87109	I	1828.98380	914.99554	610.33278	458.00141	17
9	995.53094	498.26911	332.51516	249.63819	V	1715.89973	858.45350	572.63809	429.73039	16
10	1124.57354	562.79041	375.52936	281.89884	E	1616.83131	808.91929	539.61529	404.96328	15
11	1181.59501	591.30114	394.53652	296.15421	G	1487.78871	744.39799	496.60109	372.70263	14
12	1294.67908	647.84318	432.23121	324.42523	L	1430.76724	715.88726	477.59393	358.44727	13
13	1441.71449	721.36088	481.24301	361.18408	M-Oxidation	1317.68317	659.34522	439.89924	330.17625	12
14	1542.76217	771.88472	514.92557	386.44600	T	1170.64775	585.82751	390.88743	293.41740	11
15	1643.80985	822.40856	548.60813	411.70792	T	1069.60007	535.30367	357.20487	268.15548	10
16	1742.87827	871.94277	581.63094	436.47503	V	968.55239	484.77983	323.52231	242.89356	9
17	1879.93718	940.47223	627.31724	470.73975	H	869.48397	435.24562	290.49951	218.12645	8
18	1950.97430	975.99079	650.99628	488.49903	A	732.42506	366.71617	244.81320	183.86172	7
19	2064.05837	1032.53282	688.69097	516.77005	I	661.38794	331.19761	221.13416	166.10244	6
20	2165.10605	1083.05666	722.37353	542.03197	T	548.30387	274.65557	183.43947	137.83143	5
21	2236.14317	1118.57522	746.05257	559.79125	A	447.25619	224.13173	149.75691	112.56951	4
22	2337.19085	1169.09906	779.73513	585.05317	T	376.21907	188.61317	126.07787	94.81023	3
23	2465.24943	1233.12835	822.42133	617.06782	Q	275.17139	138.08933	92.39531	69.54831	2
24					K	147.11281	74.06004	49.70912	37.53366	1



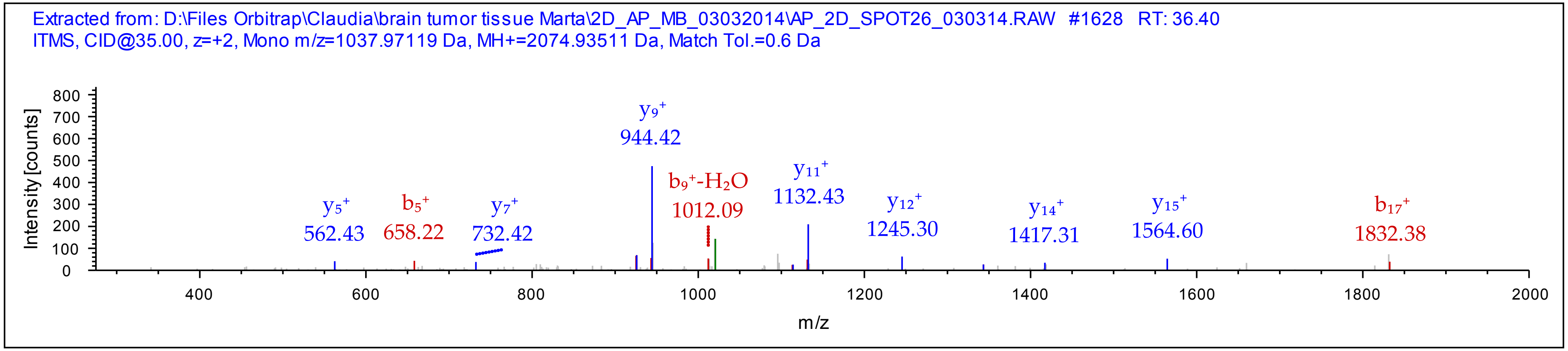
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\Astrocitoma_pilocitico_08042014\AP_2D_SPOT23_10042014.RAW #1585 RT: 43.11
ITMS, CID@35.00, z=+4, Mono m/z=653.59491 Da, MH+=2611.35781 Da, Match Tol.=0.6 Da

Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*
26	P68871	Hemoglobin subunit beta	15.9	6.8	50.86	34.69%	4	4	MB, PA	NS	NS

Sequence: FFESFGDLSTPDAVMGNPK, M15-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 1037.97119 Da (-3.82 mmu/-3.68 ppm), MH+: 2074.93511 Da, RT: 36.40 min,
Identified with: Sequest HT (v1.3); XCorr:2.41, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]

#1	**b$^+$**	**b^{2+}**	**Seq.**	**y$^+$**	**y^{2+}**	**#2**
1	148.07570	74.54149	F			19
2	295.14412	148.07570	F	1927.87433	964.44080	18
3	424.18672	212.59700	E	1780.80591	890.90659	17
4	511.21875	256.11301	S	1651.76331	826.38529	16
5	658.28717	329.64722	F	1564.73128	782.86928	15
6	715.30864	358.15796	G	1417.66286	709.33507	14
7	830.33559	415.67143	D	1360.64139	680.82433	13
8	943.41966	472.21347	L	1245.61444	623.31086	12
9	1030.45169	515.72948	S	1132.53037	566.76882	11
10	1131.49937	566.25332	T	1045.49834	523.25281	10
11	1228.55214	614.77971	P	944.45066	472.72897	9
12	1343.57909	672.29318	D	847.39789	424.20258	8
13	1414.61621	707.81174	A	732.37094	366.68911	7
14	1513.68463	757.34595	V	661.33382	331.17055	6
15	1660.72004	830.86366	M-Oxidation	562.26540	281.63634	5
16	1717.74151	859.37439	G	415.22998	208.11863	4
17	1831.78444	916.39586	N	358.20851	179.60789	3
18	1928.83721	964.92224	P	244.16558	122.58643	2
19			K	147.11281	74.06004	1

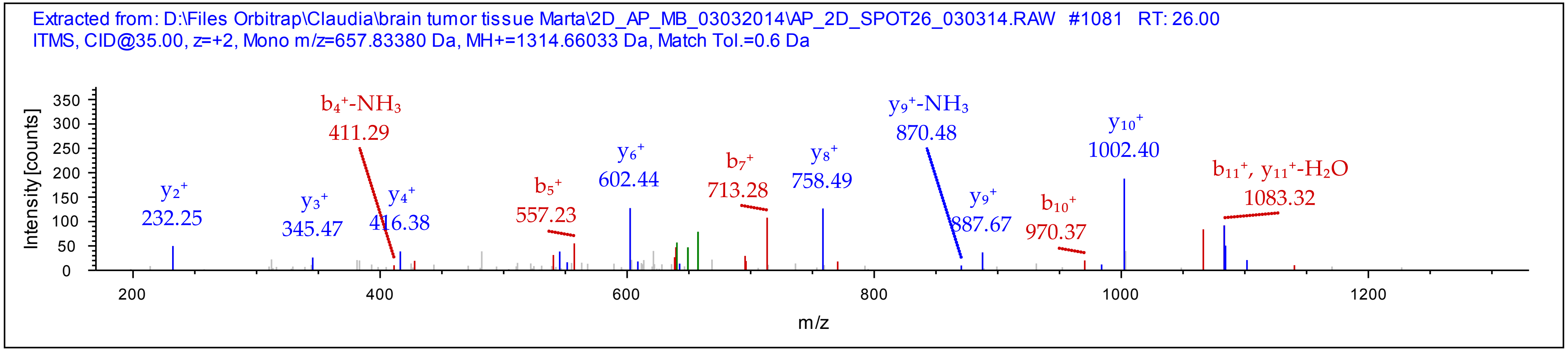


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\AP_2D_SPOT26_030314.RAW #1628 RT: 36.40
ITMS, CID@35.00, z=+2, Mono m/z=1037.97119 Da, MH+=2074.93511 Da, Match Tol.=0.6 Da

Sequence: VNVDEVGGEALGR, Charge: +2, Monoisotopic m/z: 657.83380 Da (-2.29 mmu/-3.48 ppm), MH+: 1314.66033 Da, RT: 26.00 min,
Identified with: Sequest HT (v1.3); XCorr:2.37, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]

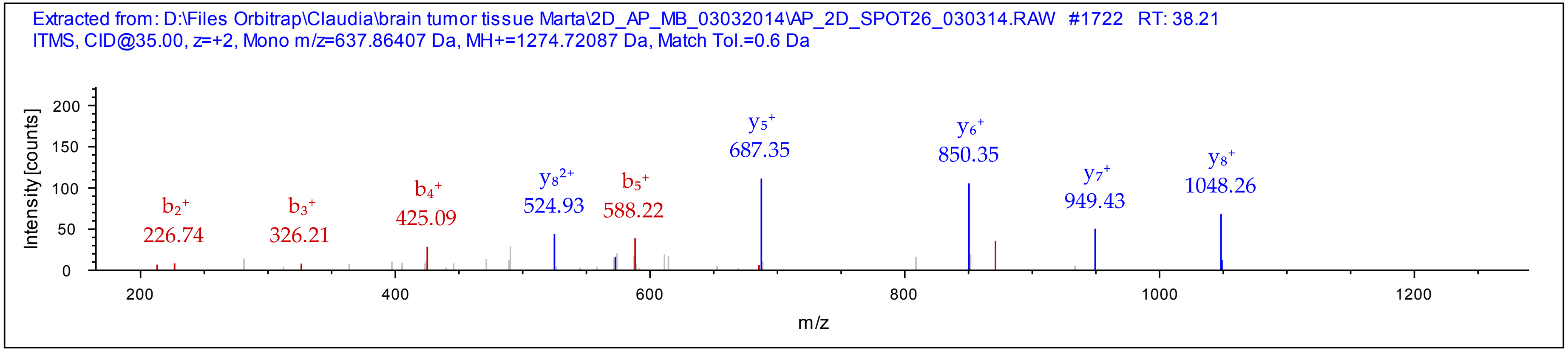
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	100.07570	50.54149	V			13
2	214.11863	107.56295	N	1215.59648	608.30188	12
3	313.18705	157.09716	V	1101.55355	551.28041	11
4	428.21400	214.61064	D	1002.48513	501.74620	10
5	557.25660	279.13194	E	887.45818	444.23273	9
6	656.32502	328.66615	V	758.41558	379.71143	8
7	713.34649	357.17688	G	659.34716	330.17722	7
8	770.36796	385.68762	G	602.32569	301.66648	6
9	899.41056	450.20892	E	545.30422	273.15575	5
10	970.44768	485.72748	A	416.26162	208.63445	4
11	1083.53175	542.26951	L	345.22450	173.11589	3
12	1140.55322	570.78025	G	232.14043	116.57385	2
13			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\AP_2D_SPOT26_030314.RAW #1081 RT: 26.00
ITMS, CID@35.00, z=+2, Mono m/z=657.83380 Da, MH+=1314.66033 Da, Match Tol.=0.6 Da

Sequence: LLVVYPWTQR, Charge: +2, Monoisotopic m/z: 637.86407 Da (-2.37 mmu/-3.72 ppm), MH+: 1274.72087 Da, RT: 38.21 min,
Identified with: Sequest HT (v1.3); XCorr:1.72, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):
- Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]
- Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2 - [HBD_HUMAN]
- Hemoglobin subunit epsilon OS=Homo sapiens GN=HBE1 PE=1 SV=2 - [HBE_HUMAN]
- Hemoglobin subunit gamma-1 OS=Homo sapiens GN=HBG1 PE=1 SV=2 - [HBG1_HUMAN]
- Hemoglobin subunit gamma-2 OS=Homo sapiens GN=HBG2 PE=1 SV=2 - [HBG2_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			10
2	227.17542	114.09135	L	1161.64154	581.32441	9
3	326.24384	163.62556	V	1048.55747	524.78237	8
4	425.31226	213.15977	V	949.48905	475.24816	7
5	588.37558	294.69143	Y	850.42063	425.71395	6
6	685.42835	343.21781	P	687.35731	344.18229	5
7	871.50767	436.25747	W	590.30454	295.65591	4
8	972.55535	486.78131	T	404.22522	202.61625	3
9	1100.61393	550.81060	Q	303.17754	152.09241	2
10			R	175.11896	88.06312	1

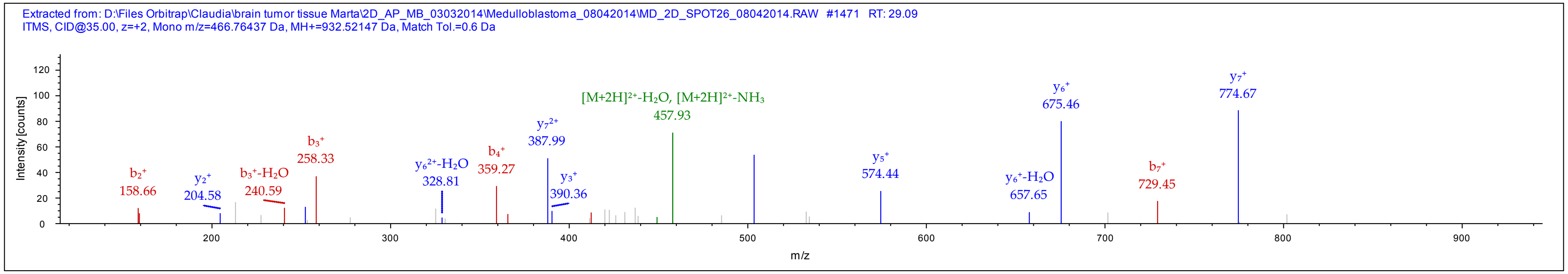


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\AP_2D_SPOT26_030314.RAW #1722 RT: 38.21
ITMS, CID@35.00, z=+2, Mono m/z=637.86407 Da, MH+=1274.72087 Da, Match Tol.=0.6 Da

Sequence: SAVTALWGK, Charge: +2, Monoisotopic m/z: 466.76437 Da (+0.72 mmu/+1.53 ppm), MH+: 932.52147 Da, RT: 29.09 min,
Identified with: Sequest HT (v1.3); XCorr:1.54, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	88.03931	44.52329	S			9
2	159.07643	80.04185	A	845.48801	423.24764	8
3	258.14485	129.57606	V	774.45089	387.72908	7
4	359.19253	180.09990	T	675.38247	338.19487	6
5	430.22965	215.61846	A	574.33479	287.67103	5
6	543.31372	272.16050	L	503.29767	252.15247	4
7	729.39304	365.20016	W	390.21360	195.61044	3
8	786.41451	393.71089	G	204.13428	102.57078	2
9			K	147.11281	74.06004	1

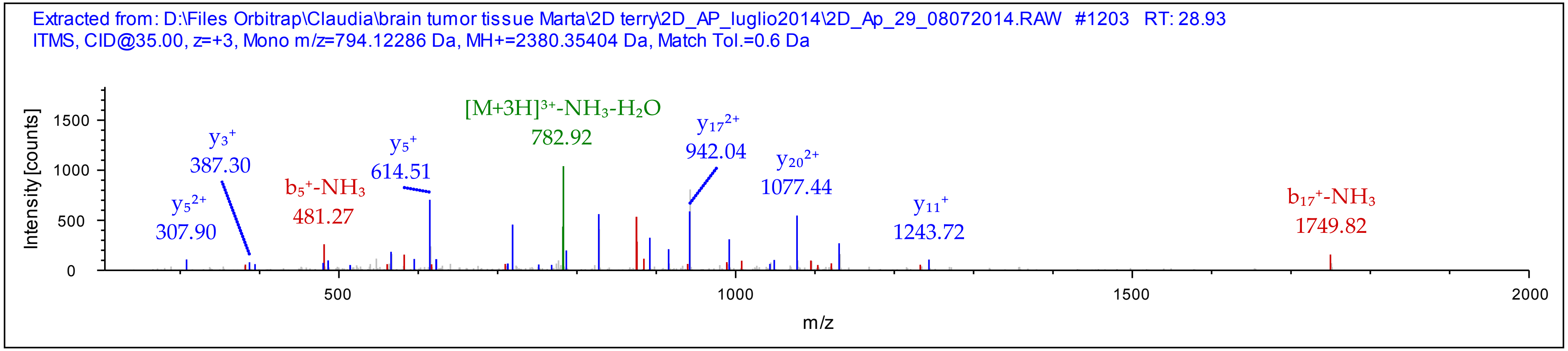

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\Medulloblastoma_08042014\MD_2D_SPOT26_08042014.RAW #1471 RT: 29.09
ITMS, CID@35.00, z=+2, Mono m/z=466.76437 Da, MH+=932.52147 Da, Match Tol.=0.6 Da

Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
29	O15540	Fatty acid-binding protein, brain	14.8	5.4	87.3	72.73%	7	7	PA	2.80E-02	2.0	↑ in PA

Sequence: QVGNVTKPTVIISQEGDKVVIR, Charge: +3, Monoisotopic m/z: 794.12286 Da (-0.64 mmu/-0.8 ppm), MH+: 2380.35404 Da, RT: 28.93 min,
Identified with: Sequest HT (v1.3); XCorr:4.17, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Fatty acid-binding protein, brain OS=Homo sapiens GN=FABP7 PE=1 SV=3 - [FABP7_HUMAN]

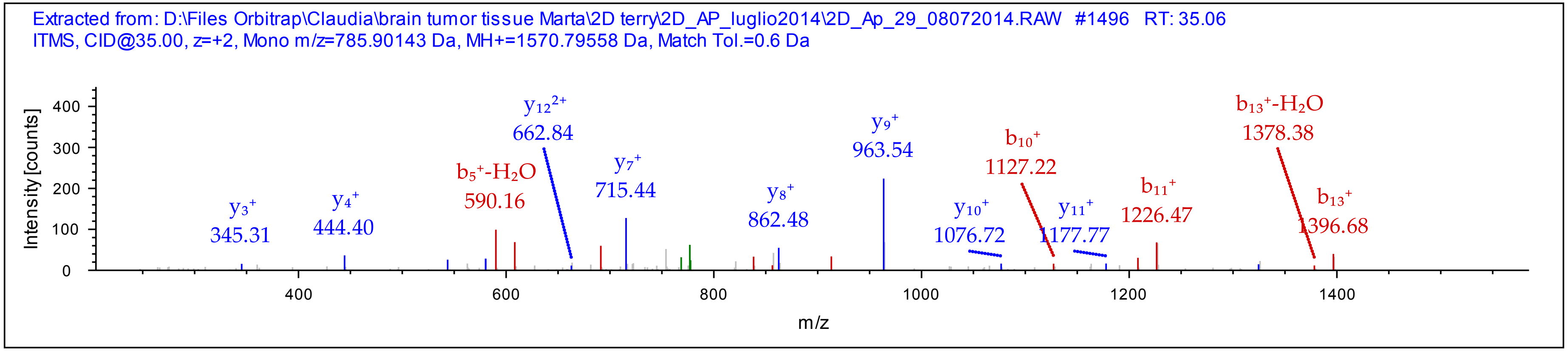
#1	b^{+}	b^{2+}	b^{3+}	Seq.	y^{+}	y^{2+}	y^{3+}	#2
1	129.06586	65.03657	43.69347	Q				22
2	228.13428	114.57078	76.71628	V	2252.29737	1126.65232	751.43731	21
3	285.15575	143.08151	95.72343	G	2153.22895	1077.11811	718.41450	20
4	399.19868	200.10298	133.73774	N	2096.20748	1048.60738	699.40734	19
5	498.26710	249.63719	166.76055	V	1982.16455	991.58591	661.39303	18
6	599.31478	300.16103	200.44311	T	1883.09613	942.05170	628.37023	17
7	727.40975	364.20851	243.14143	K	1782.04845	891.52786	594.68767	16
8	824.46252	412.73490	275.49236	P	1653.95348	827.48038	551.98934	15
9	925.51020	463.25874	309.17492	T	1556.90071	778.95399	519.63842	14
10	1024.57862	512.79295	342.19772	V	1455.85303	728.43015	485.95586	13
11	1137.66269	569.33498	379.89241	I	1356.78461	678.89594	452.93305	12
12	1250.74676	625.87702	417.58710	I	1243.70054	622.35391	415.23836	11
13	1337.77879	669.39303	446.59778	S	1130.61647	565.81187	377.54367	10
14	1465.83737	733.42232	489.28397	Q	1043.58444	522.29586	348.53300	9
15	1594.87997	797.94362	532.29817	E	915.52586	458.26657	305.84680	8
16	1651.90144	826.45436	551.30533	G	786.48326	393.74527	262.83260	7
17	1766.92839	883.96783	589.64765	D	729.46179	365.23453	243.82545	6
18	1895.02336	948.01532	632.34597	K	614.43484	307.72106	205.48313	5
19	1994.09178	997.54953	665.36878	V	486.33987	243.67357	162.78481	4
20	2093.16020	1047.08374	698.39158	V	387.27145	194.13936	129.76200	3
21	2206.24427	1103.62577	736.08627	I	288.20303	144.60515	96.73919	2
22				R	175.11896	88.06312	59.04450	1



Sequence: MVMTLTFGDVVAVR, M1-Oxidation (15.99492 Da), M3-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 785.90143 Da (-0.64 mmu/-0.82 ppm), MH+: 1570.79558 Da, RT: 35.06 min,
Identified with: Sequest HT (v1.3); XCorr:3.48, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Fatty acid-binding protein, brain OS=Homo sapiens GN=FABP7 PE=1 SV=3 - [FABP7_HUMAN]

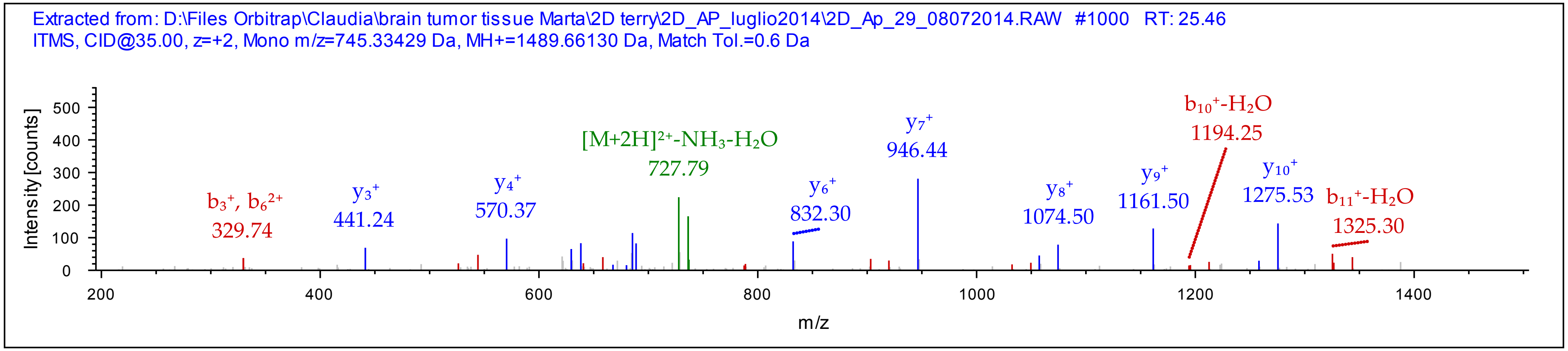
#1	b$^+$	b^{2+}	Seq.	y$^+$	y^{2+}	#2
1	148.04269	74.52498	M-Oxidation			14
2	247.11111	124.05919	V	1423.76145	712.38436	13
3	394.14653	197.57690	M-Oxidation	1324.69303	662.85015	12
4	495.19421	248.10074	T	1177.65761	589.33244	11
5	608.27828	304.64278	L	1076.60993	538.80860	10
6	709.32596	355.16662	T	963.52586	482.26657	9
7	856.39438	428.70083	F	862.47818	431.74273	8
8	913.41585	457.21156	G	715.40976	358.20852	7
9	1028.44280	514.72504	D	658.38829	329.69778	6
10	1127.51122	564.25925	V	543.36134	272.18431	5
11	1226.57964	613.79346	V	444.29292	222.65010	4
12	1297.61676	649.31202	A	345.22450	173.11589	3
13	1396.68518	698.84623	V	274.18738	137.59733	2
14			R	175.11896	88.06312	1



Sequence: LTNSQNFDEYMK, Charge: +2, Monoisotopic m/z: 745.33429 Da (-0.76 mmu/-1.02 ppm), MH+: 1489.66130 Da, RT: 25.46 min,
Identified with: Sequest HT (v1.3); XCorr:2.91, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

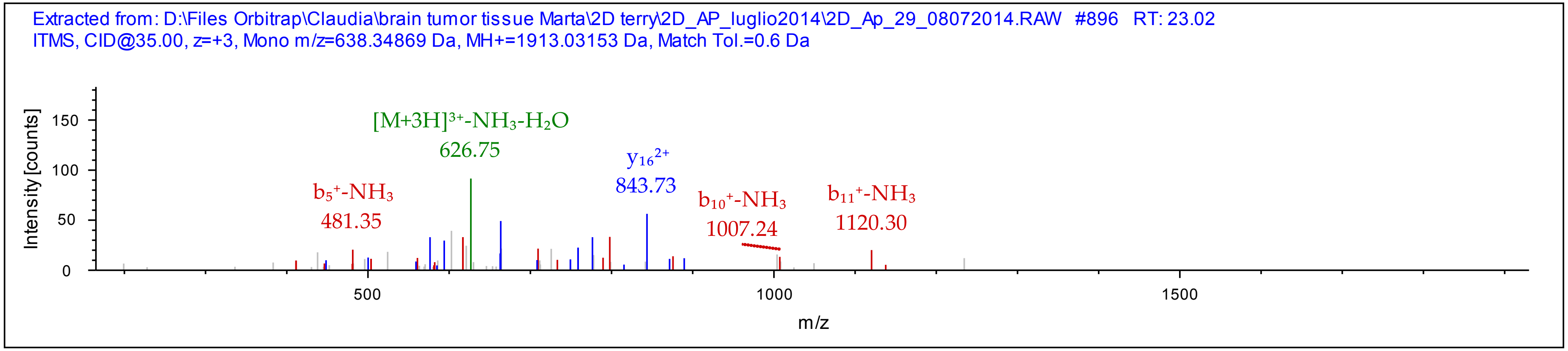
Protein references (1):
- Fatty acid-binding protein, brain OS=Homo sapiens GN=FABP7 PE=1 SV=3 - [FABP7_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			12
2	215.13903	108.07315	T	1376.57875	688.79301	11
3	329.18196	165.09462	N	1275.53107	638.26917	10
4	416.21399	208.61063	S	1161.48814	581.24771	9
5	544.27257	272.63992	Q	1074.45611	537.73169	8
6	658.31550	329.66139	N	946.39753	473.70240	7
7	805.38392	403.19560	F	832.35460	416.68094	6
8	920.41087	460.70907	D	685.28618	343.14673	5
9	1049.45347	525.23037	E	570.25923	285.63325	4
10	1212.51679	606.76203	Y	441.21663	221.11195	3
11	1343.55729	672.28228	M	278.15331	139.58029	2
12			K	147.11281	74.06004	1



Sequence: QVGNVTKPTVIISQEGDK, Charge: +3, Monoisotopic m/z: 638.34869 Da (-0.8 mmu/-1.25 ppm), MH+: 1913.03153 Da, RT: 23.02 min,
Identified with: Sequest HT (v1.3); XCorr:2.61, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Fatty acid-binding protein, brain OS=Homo sapiens GN=FABP7 PE=1 SV=3 - [FABP7_HUMAN]

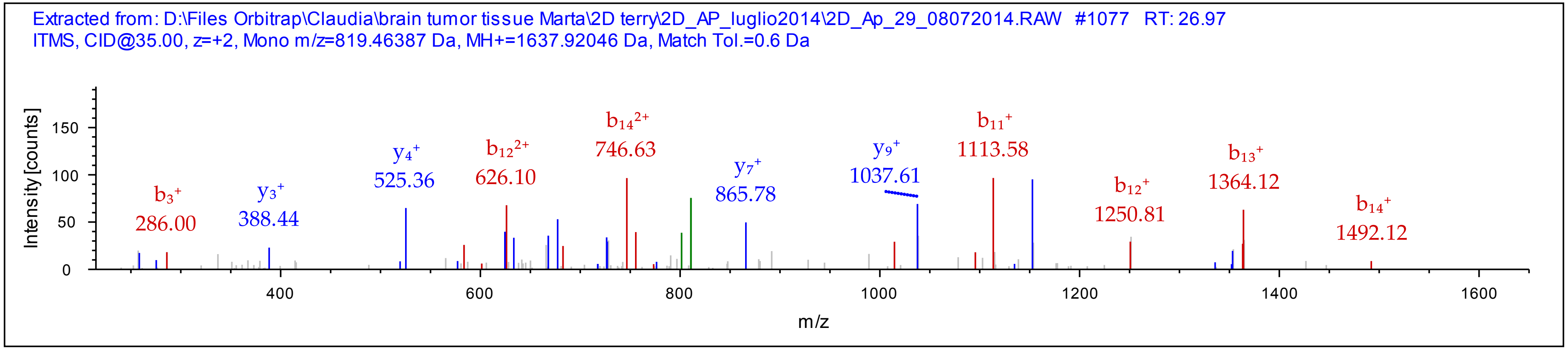
#1	b$^+$	b^{2+}	b^{3+}	Seq.	y$^+$	y^{2+}	y^{3+}	#2
1	129.06586	65.03657	43.69347	Q				18
2	228.13428	114.57078	76.71628	V	1784.97534	892.99131	595.66330	17
3	285.15575	143.08151	95.72343	G	1685.90692	843.45710	562.64049	16
4	399.19868	200.10298	133.73774	N	1628.88545	814.94636	543.63333	15
5	498.26710	249.63719	166.76055	V	1514.84252	757.92490	505.61902	14
6	599.31478	300.16103	200.44311	T	1415.77410	708.39069	472.59622	13
7	727.40975	364.20851	243.14143	K	1314.72642	657.86685	438.91366	12
8	824.46252	412.73490	275.49236	P	1186.63145	593.81936	396.21533	11
9	925.51020	463.25874	309.17492	T	1089.57868	545.29298	363.86441	10
10	1024.57862	512.79295	342.19772	V	988.53100	494.76914	330.18185	9
11	1137.66269	569.33498	379.89241	I	889.46258	445.23493	297.15904	8
12	1250.74676	625.87702	417.58710	I	776.37851	388.69289	259.46435	7
13	1337.77879	669.39303	446.59778	S	663.29444	332.15086	221.76966	6
14	1465.83737	733.42232	489.28397	Q	576.26241	288.63484	192.75899	5
15	1594.87997	797.94362	532.29817	E	448.20383	224.60555	150.07279	4
16	1651.90144	826.45436	551.30533	G	319.16123	160.08425	107.05859	3
17	1766.92839	883.96783	589.64765	D	262.13976	131.57352	88.05144	2
18				K	147.11281	74.06004	49.70912	1



Sequence: SVVSLDGDKLVHIQK, Charge: +2, Monoisotopic m/z: 819.46387 Da (-0.86 mmu/-1.05 ppm), MH+: 1637.92046 Da, RT: 26.97 min,
Identified with: Sequest HT (v1.3); XCorr:2.60, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Fatty acid-binding protein, brain OS=Homo sapiens GN=FABP7 PE=1 SV=3 - [FABP7_HUMAN]

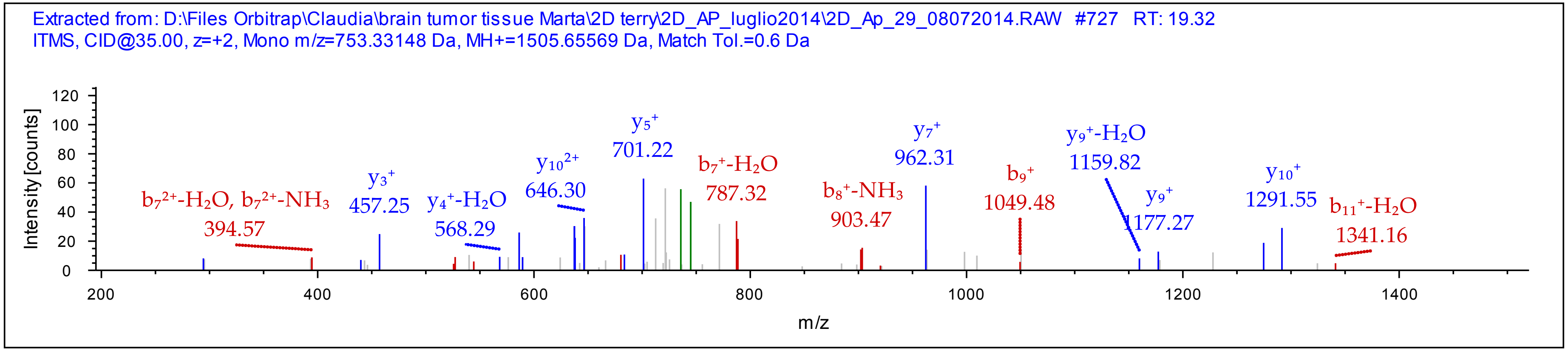
#1	**b⁺**	**b²⁺**	**Seq.**	**y⁺**	**y²⁺**	**#2**
1	88.03931	44.52329	S			15
2	187.10773	94.05750	V	1550.89014	775.94871	14
3	286.17615	143.59171	V	1451.82172	726.41450	13
4	373.20818	187.10773	S	1352.75330	676.88029	12
5	486.29225	243.64976	L	1265.72127	633.36427	11
6	601.31920	301.16324	D	1152.63720	576.82224	10
7	658.34067	329.67397	G	1037.61025	519.30876	9
8	773.36762	387.18745	D	980.58878	490.79803	8
9	901.46259	451.23493	K	865.56183	433.28455	7
10	1014.54666	507.77697	L	737.46686	369.23707	6
11	1113.61508	557.31118	V	624.38279	312.69503	5
12	1250.67399	625.84063	H	525.31437	263.16082	4
13	1363.75806	682.38267	I	388.25546	194.63137	3
14	1491.81664	746.41196	Q	275.17139	138.08933	2
15			K	147.11281	74.06004	1



Sequence: LTNSQNFDEYMK, M11-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 753.33148 Da (-1.03 mmu/-1.36 ppm), MH+: 1505.65569 Da, RT: 19.32 min,
Identified with: Sequest HT (v1.3); XCorr:2.56, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Fatty acid-binding protein, brain OS=Homo sapiens GN=FABP7 PE=1 SV=3 - [FABP7_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			12
2	215.13903	108.07315	T	1392.57367	696.79047	11
3	329.18196	165.09462	N	1291.52599	646.26663	10
4	416.21399	208.61063	S	1177.48306	589.24517	9
5	544.27257	272.63992	Q	1090.45103	545.72915	8
6	658.31550	329.66139	N	962.39245	481.69986	7
7	805.38392	403.19560	F	848.34952	424.67840	6
8	920.41087	460.70907	D	701.28110	351.14419	5
9	1049.45347	525.23037	E	586.25415	293.63071	4
10	1212.51679	606.76203	Y	457.21155	229.10941	3
11	1359.55220	680.27974	M-Oxidation	294.14823	147.57775	2
12			K	147.11281	74.06004	1

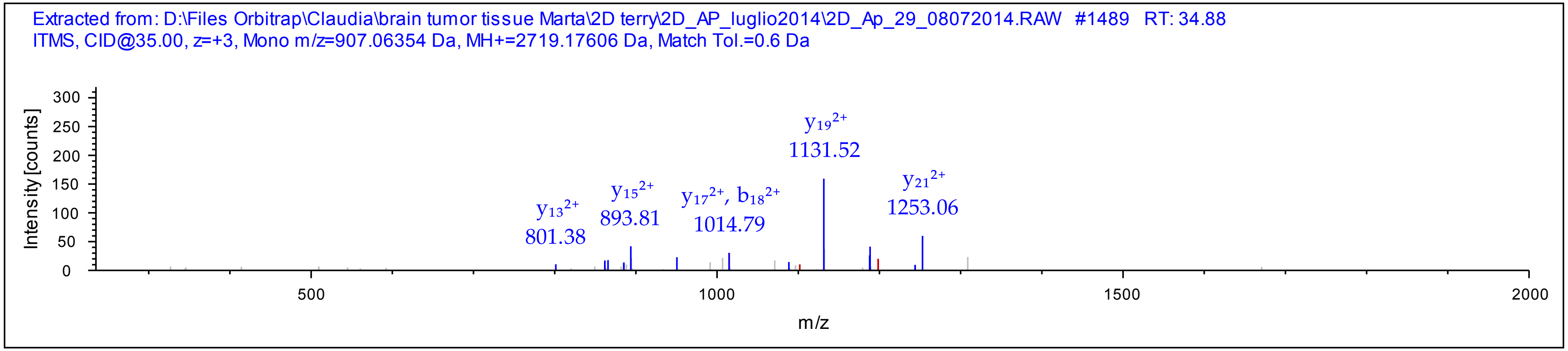

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_AP_luglio2014\2D_Ap_29_08072014.RAW #727 RT: 19.32
ITMS, CID@35.00, z=+2, Mono m/z=753.33148 Da, MH+=1505.65569 Da, Match Tol.=0.6 Da

Sequence: NTEISFQLGEEFDETTADDRNCK, C22-Carbamidomethyl (57.02146 Da)
Charge: +3, Monoisotopic m/z: 907.06354 Da (-0.95 mmu/-1.05 ppm), MH+: 2719.17606 Da, RT: 34.88 min,
Identified with: Sequest HT (v1.3); XCorr:1.78, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Fatty acid-binding protein, brain OS=Homo sapiens GN=FABP7 PE=1 SV=3 - [FABP7_HUMAN]

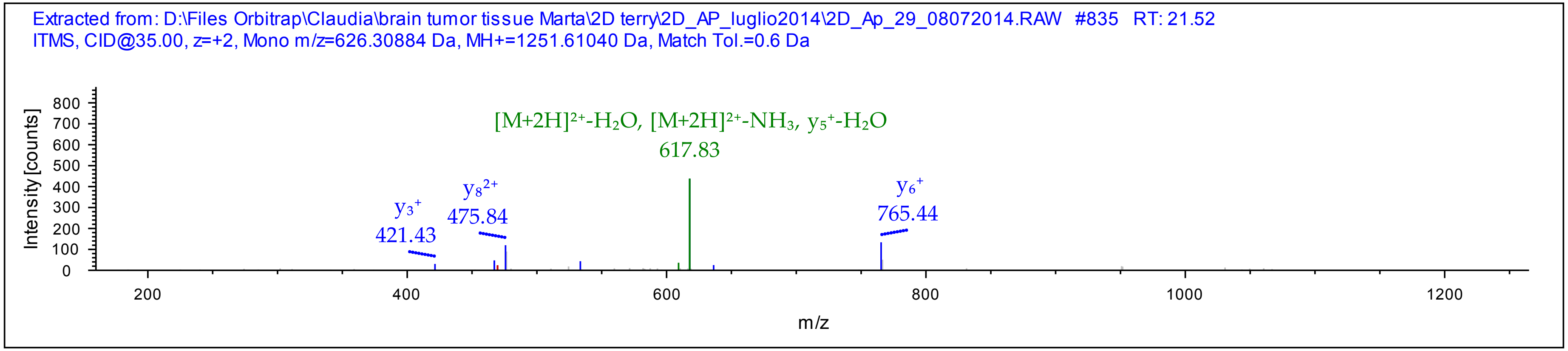
#1	b⁺	b²⁺	b³⁺	Seq.	y⁺	y²⁺	y³⁺	#2
1	115.05021	58.02874	39.02159	N				23
2	216.09789	108.55258	72.70415	T	2605.13599	1303.07163	869.05018	22
3	345.14049	173.07388	115.71835	E	2504.08831	1252.54779	835.36762	21
4	458.22456	229.61592	153.41304	I	2375.04571	1188.02649	792.35342	20
5	545.25659	273.13193	182.42371	S	2261.96164	1131.48446	754.65873	19
6	692.32501	346.66614	231.44652	F	2174.92961	1087.96844	725.64805	18
7	820.38359	410.69543	274.13271	Q	2027.86119	1014.43423	676.62525	17
8	933.46766	467.23747	311.82740	L	1899.80261	950.40494	633.93905	16
9	990.48913	495.74820	330.83456	G	1786.71854	893.86291	596.24436	15
10	1119.53173	560.26950	373.84876	E	1729.69707	865.35217	577.23721	14
11	1248.57433	624.79080	416.86296	E	1600.65447	800.83087	534.22301	13
12	1395.64275	698.32501	465.88577	F	1471.61187	736.30957	491.20881	12
13	1510.66970	755.83849	504.22808	D	1324.54345	662.77536	442.18600	11
14	1639.71230	820.35979	547.24228	E	1209.51650	605.26189	403.84368	10
15	1740.75998	870.88363	580.92484	T	1080.47390	540.74059	360.82948	9
16	1841.80766	921.40747	614.60740	T	979.42622	490.21675	327.14692	8
17	1912.84478	956.92603	638.28644	A	878.37854	439.69291	293.46436	7

18	2027.87173	1014.43950	676.62876	D	807.34142	404.17435	269.78532	6
19	2142.89868	1071.95298	714.97108	D	692.31447	346.66087	231.44301	5
20	2298.99980	1150.00354	767.00478	R	577.28752	289.14740	193.10069	4
21	2413.04273	1207.02500	805.01909	N	421.18640	211.09684	141.06698	3
22	2573.07338	1287.04033	858.36264	C-Carbamidomethyl	307.14347	154.07537	103.05267	2
23				K	147.11281	74.06004	49.70912	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_AP_luglio2014\2D_Ap_29_08072014.RAW #1489 RT: 34.88
ITMS, CID@35.00, z=+3, Mono m/z=907.06354 Da, MH+=2719.17606 Da, Match Tol.=0.6 Da

Sequence: WDGKETNFVR, Charge: +2, Monoisotopic m/z: 626.30884 Da (-0.66 mmu/-1.06 ppm), MH+: 1251.61040 Da, RT: 21.52 min,
Identified with: Sequest HT (v1.3); XCorr:1.63, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	187.08660	94.04694	W			10
2	302.11355	151.56041	D	1065.53240	533.26984	9
3	359.13502	180.07115	G	950.50545	475.75636	8
4	487.22999	244.11863	K	893.48398	447.24563	7
5	616.27259	308.63993	E	765.38901	383.19814	6
6	717.32027	359.16377	T	636.34641	318.67684	5
7	831.36320	416.18524	N	535.29873	268.15300	4
8	978.43162	489.71945	F	421.25580	211.13154	3
9	1077.50004	539.25366	V	274.18738	137.59733	2
10			R	175.11896	88.06312	1



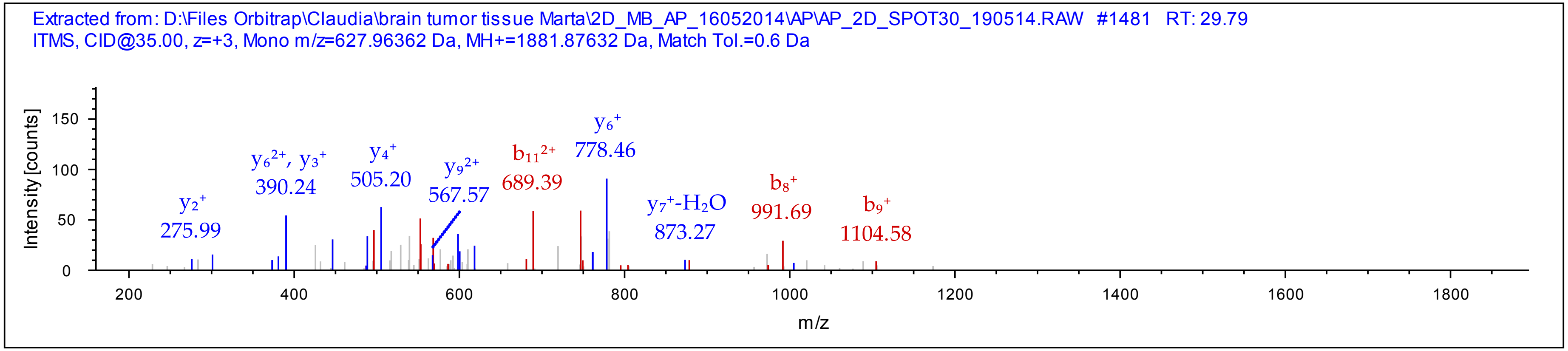
Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*

30	P02787	Serotransferrin	75.1	6.7	72.14	24.93%	13	13	PA	8.02E-04	5.1	↑ in PA

Sequence: ADRDQYELLCLDNTR, C10-Carbamidomethyl (57.02146 Da)
Charge: +3, Monoisotopic m/z: 627.96362 Da (+0.1 mmu/+0.15 ppm), MH+: 1881.87632 Da, RT: 29.79 min,
Identified with: Sequest HT (v1.3); XCorr:3.16, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]

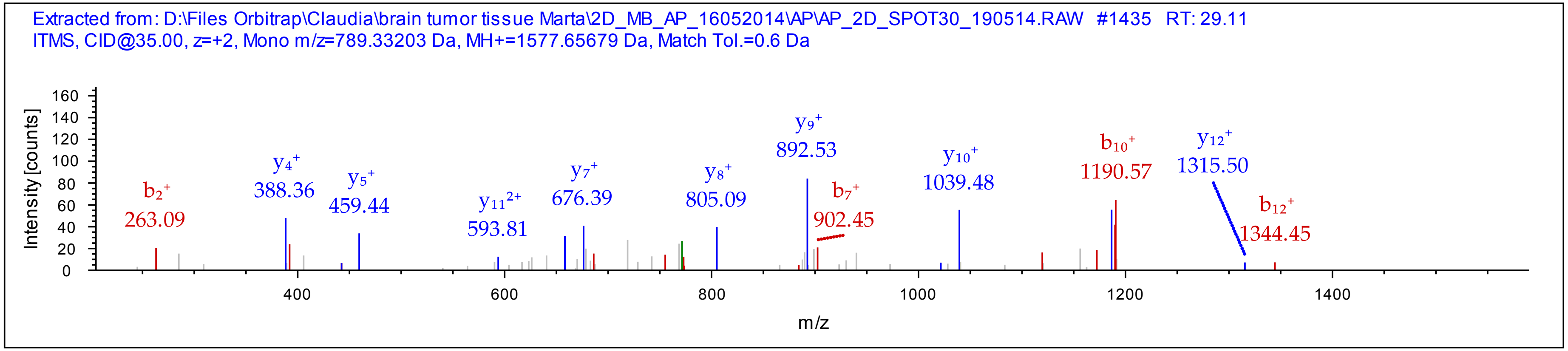
#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	72.04440	36.52584	24.68632	A				15
2	187.07135	94.03931	63.02863	D	1810.83891	905.92309	604.28449	14
3	343.17247	172.08987	115.06234	R	1695.81196	848.40962	565.94217	13
4	458.19942	229.60335	153.40466	D	1539.71084	770.35906	513.90846	12
5	586.25800	293.63264	196.09085	Q	1424.68389	712.84558	475.56615	11
6	749.32132	375.16430	250.44529	Y	1296.62531	648.81629	432.87995	10
7	878.36392	439.68560	293.45949	E	1133.56199	567.28463	378.52551	9
8	991.44799	496.22763	331.15418	L	1004.51939	502.76333	335.51131	8
9	1104.53206	552.76967	368.84887	L	891.43532	446.22130	297.81662	7
10	1264.56271	632.78499	422.19242	C-Carbamidomethyl	778.35125	389.67926	260.12193	6
11	1377.64678	689.32703	459.88711	L	618.32059	309.66393	206.77838	5
12	1492.67373	746.84050	498.22943	D	505.23652	253.12190	169.08369	4
13	1606.71666	803.86197	536.24374	N	390.20957	195.60842	130.74137	3
14	1707.76434	854.38581	569.92630	T	276.16664	138.58696	92.72706	2
15				R	175.11896	88.06312	59.04450	1



Sequence: FDEFFSEGCAPGSK, C9-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 789.33203 Da (-0.49 mmu/-0.62 ppm), MH+: 1577.65679 Da, RT: 29.11 min,
Identified with: Sequest HT (v1.3); XCorr:3.15, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]

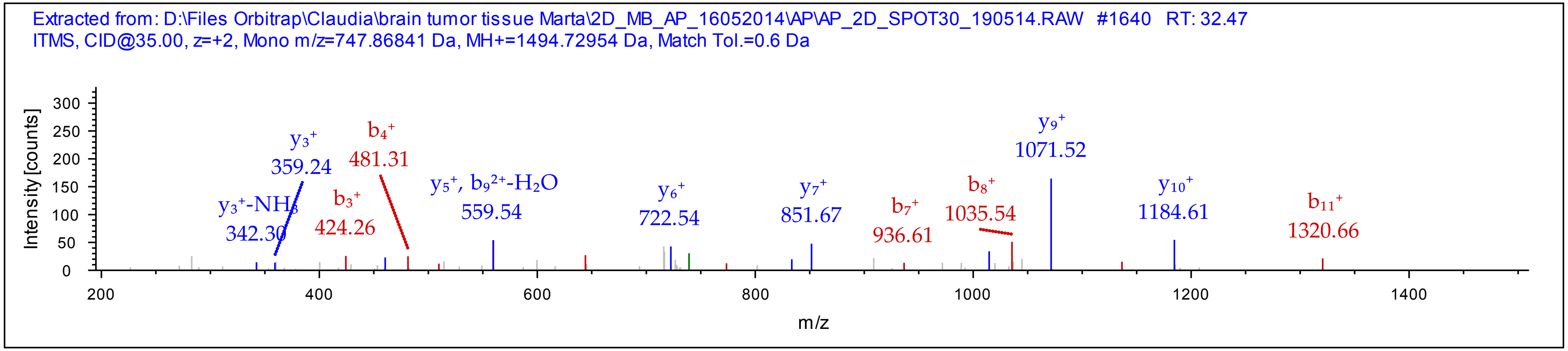
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	148.07570	74.54149	F			14
2	263.10265	132.05496	D	1430.58935	715.79831	13
3	392.14525	196.57626	E	1315.56240	658.28484	12
4	539.21367	270.11047	F	1186.51980	593.76354	11
5	686.28209	343.64468	F	1039.45138	520.22933	10
6	773.31412	387.16070	S	892.38296	446.69512	9
7	902.35672	451.68200	E	805.35093	403.17910	8
8	959.37819	480.19273	G	676.30833	338.65780	7
9	1119.40884	560.20806	C-Carbamidomethyl	619.28686	310.14707	6
10	1190.44596	595.72662	A	459.25620	230.13174	5
11	1287.49873	644.25300	P	388.21908	194.61318	4
12	1344.52020	672.76374	G	291.16631	146.08679	3
13	1431.55223	716.27975	S	234.14484	117.57606	2
14			K	147.11281	74.06004	1



Sequence: MYLGYEYVTAIR, M1-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 747.86841 Da (-0.11 mmu/-0.15 ppm), MH+: 1494.72954 Da, RT: 32.47 min,
Identified with: Sequest HT (v1.3); XCorr:2.90, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

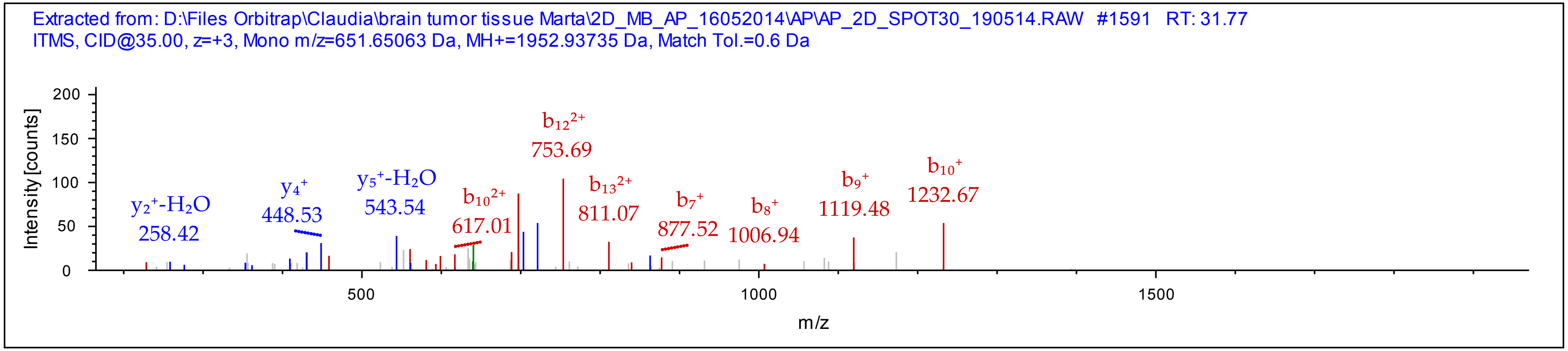
Protein references (1):
- Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]

#1	**b$^+$**	**b^{2+}**	**Seq.**	**y$^+$**	**y^{2+}**	**#2**
1	148.04269	74.52498	M-Oxidation			12
2	311.10601	156.05664	Y	1347.69435	674.35081	11
3	424.19008	212.59868	L	1184.63103	592.81915	10
4	481.21155	241.10941	G	1071.54696	536.27712	9
5	644.27487	322.64107	Y	1014.52549	507.76638	8
6	773.31747	387.16237	E	851.46217	426.23472	7
7	936.38079	468.69403	Y	722.41957	361.71342	6
8	1035.44921	518.22824	V	559.35625	280.18176	5
9	1136.49689	568.75208	T	460.28783	230.64755	4
10	1207.53401	604.27064	A	359.24015	180.12371	3
11	1320.61808	660.81268	I	288.20303	144.60515	2
12			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT30_190514.RAW #1640 RT: 32.47
ITMS, CID@35.00, z=+2, Mono m/z=747.86841 Da, MH+=1494.72954 Da, Match Tol.=0.6 Da

Sequence: NLNEKDYELLCLDGTR, C11-Carbamidomethyl (57.02146 Da)
Charge: +3, Monoisotopic m/z: 651.65063 Da (-0.32 mmu/-0.48 ppm), MH+: 1952.93735 Da, RT: 31.77 min,
Identified with: Sequest HT (v1.3); XCorr:2.80, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	115.05021	58.02874	39.02159	N				16
2	228.13428	114.57078	76.71628	L	1838.89537	919.95132	613.63664	15
3	342.17721	171.59224	114.73059	N	1725.81130	863.40929	575.94195	14
4	471.21981	236.11354	157.74479	E	1611.76837	806.38782	537.92764	13
5	599.31478	300.16103	200.44311	K	1482.72577	741.86652	494.91344	12
6	714.34173	357.67450	238.78543	D	1354.63080	677.81904	452.21512	11
7	877.40505	439.20616	293.13987	Y	1239.60385	620.30556	413.87280	10
8	1006.44765	503.72746	336.15407	E	1076.54053	538.77390	359.51836	9
9	1119.53172	560.26950	373.84876	L	947.49793	474.25260	316.50416	8
10	1232.61579	616.81153	411.54345	L	834.41386	417.71057	278.80947	7
11	1392.64644	696.82686	464.88700	C-Carbamidomethyl	721.32979	361.16853	241.11478	6
12	1505.73051	753.36889	502.58169	L	561.29913	281.15320	187.77123	5
13	1620.75746	810.88237	540.92400	D	448.21506	224.61117	150.07654	4
14	1677.77893	839.39310	559.93116	G	333.18811	167.09769	111.73422	3
15	1778.82661	889.91694	593.61372	T	276.16664	138.58696	92.72706	2
16				R	175.11896	88.06312	59.04450	1

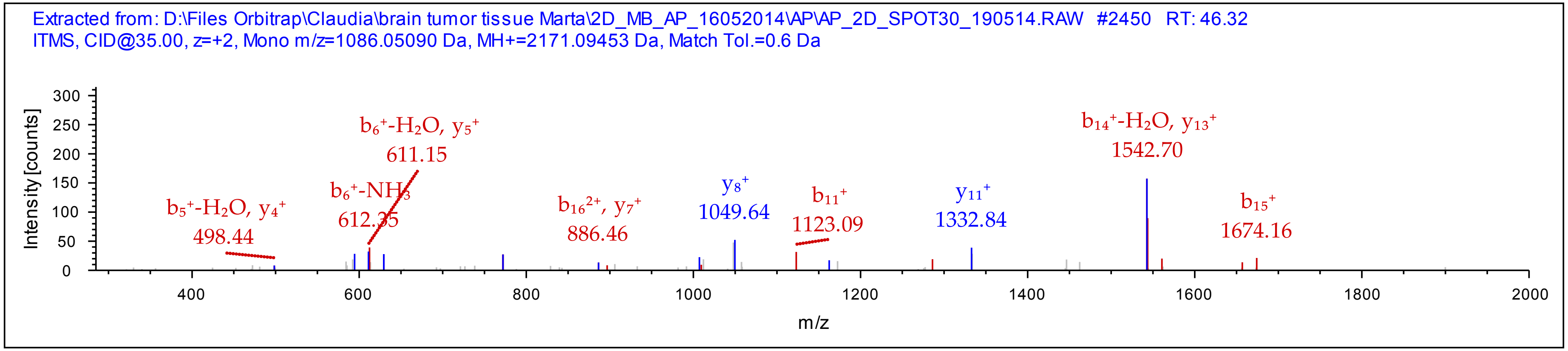

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT30_190514.RAW #1591 RT: 31.77
ITMS, CID@35.00, z=+3, Mono m/z=651.65063 Da, MH+=1952.93735 Da, Match Tol.=0.6 Da

Sequence: SAGWNIPIGLLYCDLPEPR, C13-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 1086.05090 Da (-0.48 mmu/-0.44 ppm), MH+: 2171.09453 Da, RT: 46.32 min,
Identified with: Sequest HT (v1.3); XCorr:2.78, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	88.03931	44.52329	S			19
2	159.07643	80.04185	A	2084.06346	1042.53537	18
3	216.09790	108.55259	G	2013.02634	1007.01681	17
4	402.17722	201.59225	W	1956.00487	978.50607	16
5	516.22015	258.61371	N	1769.92555	885.46641	15
6	629.30422	315.15575	I	1655.88262	828.44495	14
7	726.35699	363.68213	P	1542.79855	771.90291	13
8	839.44106	420.22417	I	1445.74578	723.37653	12
9	896.46253	448.73490	G	1332.66171	666.83449	11
10	1009.54660	505.27694	L	1275.64024	638.32376	10
11	1122.63067	561.81897	L	1162.55617	581.78172	9
12	1285.69399	643.35063	Y	1049.47210	525.23969	8
13	1445.72464	723.36596	C-Carbamidomethyl	886.40878	443.70803	7
14	1560.75159	780.87943	D	726.37812	363.69270	6
15	1673.83566	837.42147	L	611.35117	306.17922	5
16	1770.88843	885.94785	P	498.26710	249.63719	4
17	1899.93103	950.46915	E	401.21433	201.11080	3

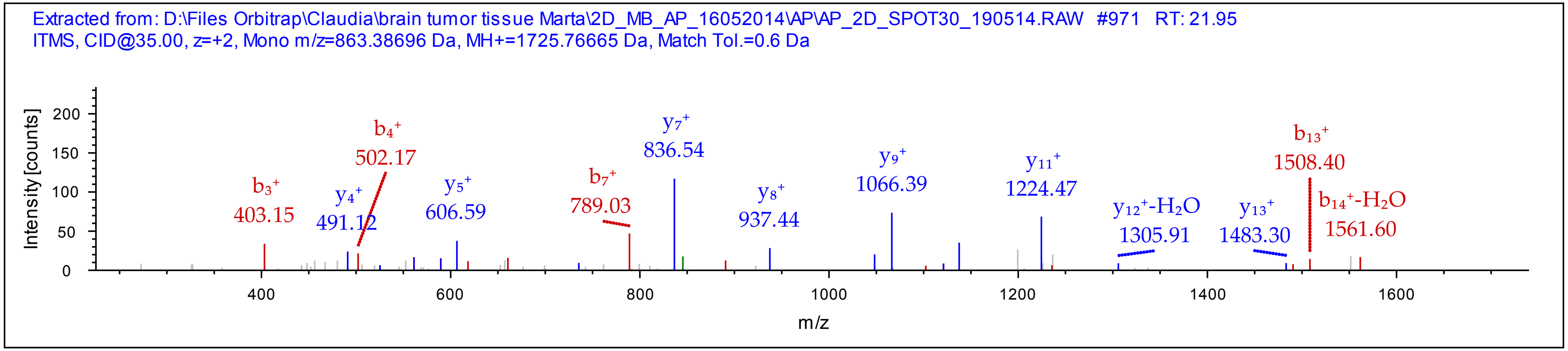
18	1996.98380	998.99554	P	272.17173	136.58950	2
19			R	175.11896	88.06312	1



Sequence: IECVSAETTEDCIAK, C3-Carbamidomethyl (57.02146 Da), C12-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 863.38696 Da (-0.21 mmu/-0.24 ppm), MH+: 1725.76665 Da, RT: 21.95 min,
Identified with: Sequest HT (v1.3); XCorr:2.64, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

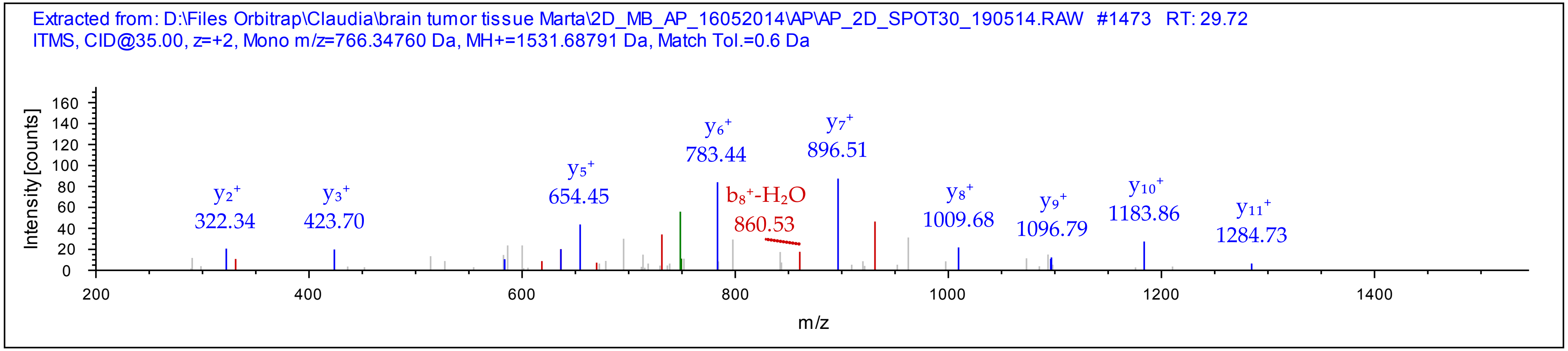
Protein references (1):
- Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	I			15
2	243.13395	122.07061	E	1612.68299	806.84513	14
3	403.16460	202.08594	C-Carbamidomethyl	1483.64039	742.32383	13
4	502.23302	251.62015	V	1323.60974	662.30851	12
5	589.26505	295.13616	S	1224.54132	612.77430	11
6	660.30217	330.65472	A	1137.50929	569.25828	10
7	789.34477	395.17602	E	1066.47217	533.73972	9
8	890.39245	445.69986	T	937.42957	469.21842	8
9	991.44013	496.22370	T	836.38189	418.69458	7
10	1120.48273	560.74500	E	735.33421	368.17074	6
11	1235.50968	618.25848	D	606.29161	303.64944	5
12	1395.54033	698.27381	C-Carbamidomethyl	491.26466	246.13597	4
13	1508.62440	754.81584	I	331.23400	166.12064	3
14	1579.66152	790.33440	A	218.14993	109.57860	2
15			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT30_190514.RAW #971 RT: 21.95
ITMS, CID@35.00, z=+2, Mono m/z=863.38696 Da, MH+=1725.76665 Da, Match Tol.=0.6 Da

Sequence: CSTSSLLEACTFR, C1-Carbamidomethyl (57.02146 Da), C10-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 766.34760 Da (-0.04 mmu/-0.06 ppm), MH+: 1531.68791 Da, RT: 29.72 min,
Identified with: Sequest HT (v1.3); XCorr:2.38, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3
Protein references (1):
- Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]

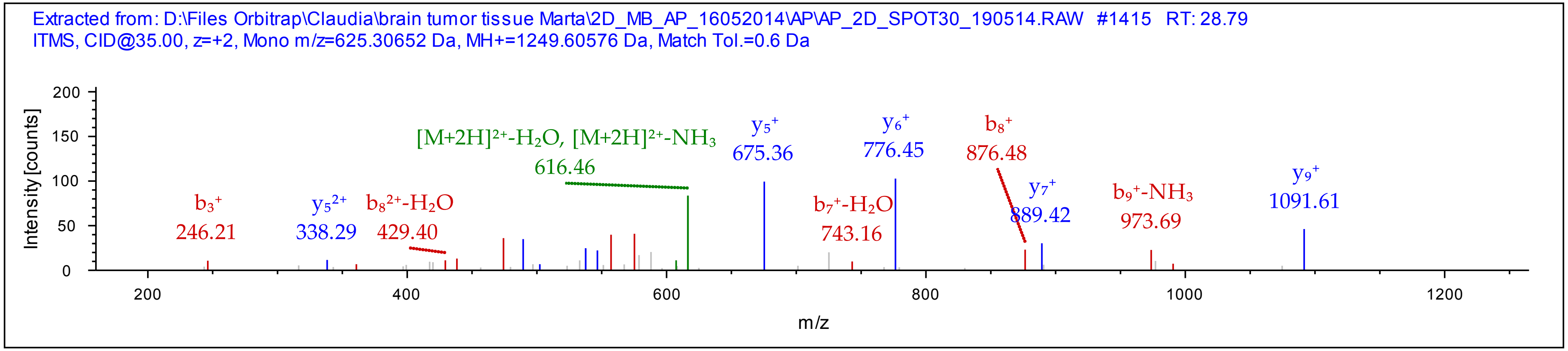
#1	b+	b2+	Seq.	y+	y2+	#2
1	161.03793	81.02260	C-Carbamidomethyl			13
2	248.06996	124.53862	S	1371.65735	686.33231	12
3	349.11764	175.06246	T	1284.62532	642.81630	11
4	436.14967	218.57847	S	1183.57764	592.29246	10
5	523.18170	262.09449	S	1096.54561	548.77644	9
6	636.26577	318.63652	L	1009.51358	505.26043	8
7	749.34984	375.17856	L	896.42951	448.71839	7
8	878.39244	439.69986	E	783.34544	392.17636	6
9	949.42956	475.21842	A	654.30284	327.65506	5
10	1109.46021	555.23375	C-Carbamidomethyl	583.26572	292.13650	4
11	1210.50789	605.75759	T	423.23506	212.12117	3
12	1357.57631	679.29180	F	322.18738	161.59733	2
13			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT30_190514.RAW #1473 RT: 29.72
ITMS, CID@35.00, z=+2, Mono m/z=766.34760 Da, MH+=1531.68791 Da, Match Tol.=0.6 Da

Sequence: SASDLTWDNLK, Charge: +2, Monoisotopic m/z: 625.30652 Da (-0.1 mmu/-0.16 ppm), MH+: 1249.60576 Da, RT: 28.79 min,
Identified with: Sequest HT (v1.3); XCorr:2.07, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H$_2$O; b-NH$_3$; y; y-H$_2$O; y-NH$_3$

Protein references (1):
- Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]

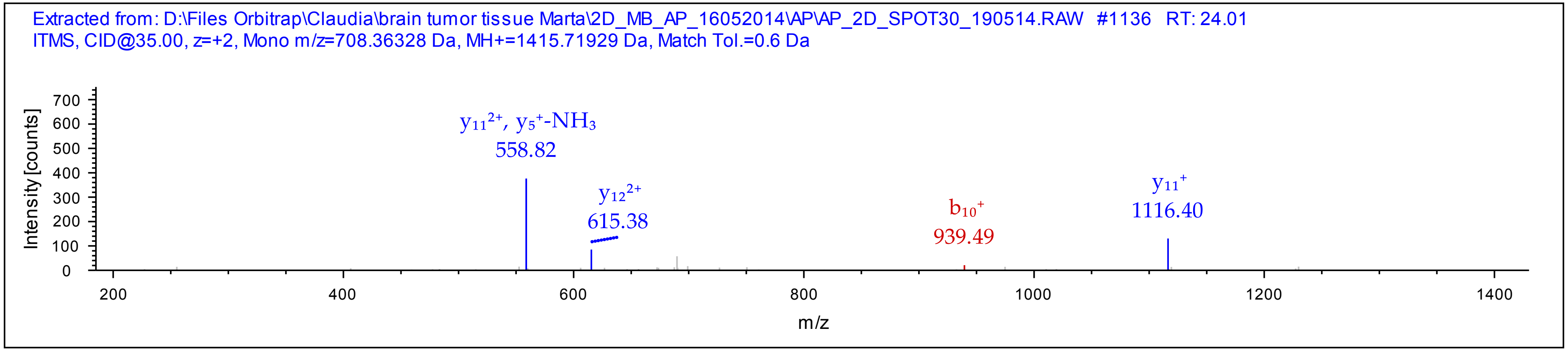
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	88.03931	44.52329	S			11
2	159.07643	80.04185	A	1162.57393	581.79060	10
3	246.10846	123.55787	S	1091.53681	546.27204	9
4	361.13541	181.07134	D	1004.50478	502.75603	8
5	474.21948	237.61338	L	889.47783	445.24255	7
6	575.26716	288.13722	T	776.39376	388.70052	6
7	761.34648	381.17688	W	675.34608	338.17668	5
8	876.37343	438.69035	D	489.26676	245.13702	4
9	990.41636	495.71182	N	374.23981	187.62354	3
10	1103.50043	552.25385	L	260.19688	130.60208	2
11			K	147.11281	74.06004	1



Sequence: SVIPSDGPSVACVK, C12-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 708.36328 Da (-0.34 mmu/-0.48 ppm), MH+: 1415.71929 Da, RT: 24.01 min,
Identified with: Sequest HT (v1.3); XCorr:1.91, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]

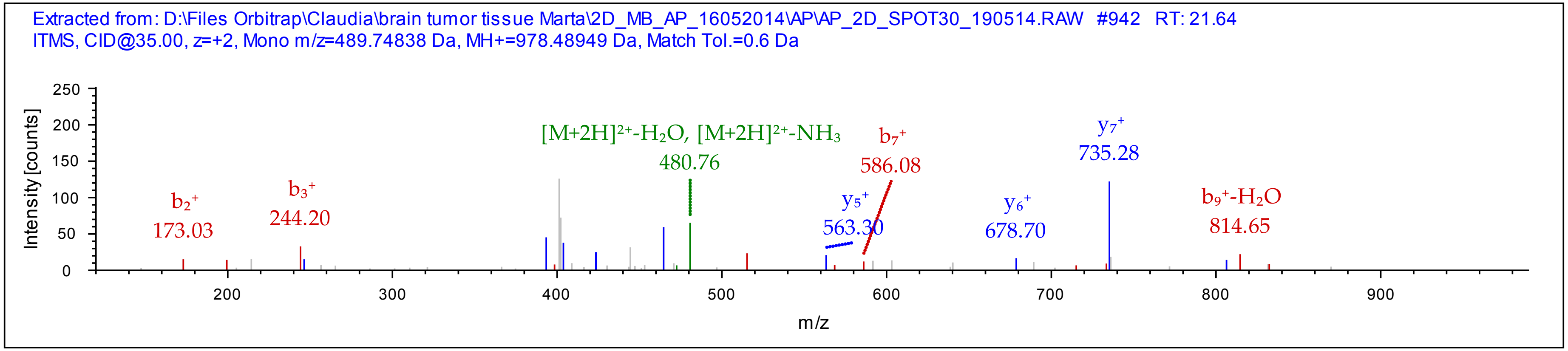
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	88.03931	44.52329	S			14
2	187.10773	94.05750	V	1328.68794	664.84761	13
3	300.19180	150.59954	I	1229.61952	615.31340	12
4	397.24457	199.12592	P	1116.53545	558.77136	11
5	484.27660	242.64194	S	1019.48268	510.24498	10
6	599.30355	300.15541	D	932.45065	466.72896	9
7	656.32502	328.66615	G	817.42370	409.21549	8
8	753.37779	377.19253	P	760.40223	380.70475	7
9	840.40982	420.70855	S	663.34946	332.17837	6
10	939.47824	470.24276	V	576.31743	288.66235	5
11	1010.51536	505.76132	A	477.24901	239.12814	4
12	1170.54601	585.77664	C-Carbamidomethyl	406.21189	203.60958	3
13	1269.61443	635.31085	V	246.18123	123.59425	2
14			K	147.11281	74.06004	1



Sequence: DGAGDVAFVK, Charge: +2, Monoisotopic m/z: 489.74838 Da (+0.17 mmu/+0.34 ppm), MH+: 978.48949 Da, RT: 21.64 min,
Identified with: Sequest HT (v1.3); XCorr:1.83, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

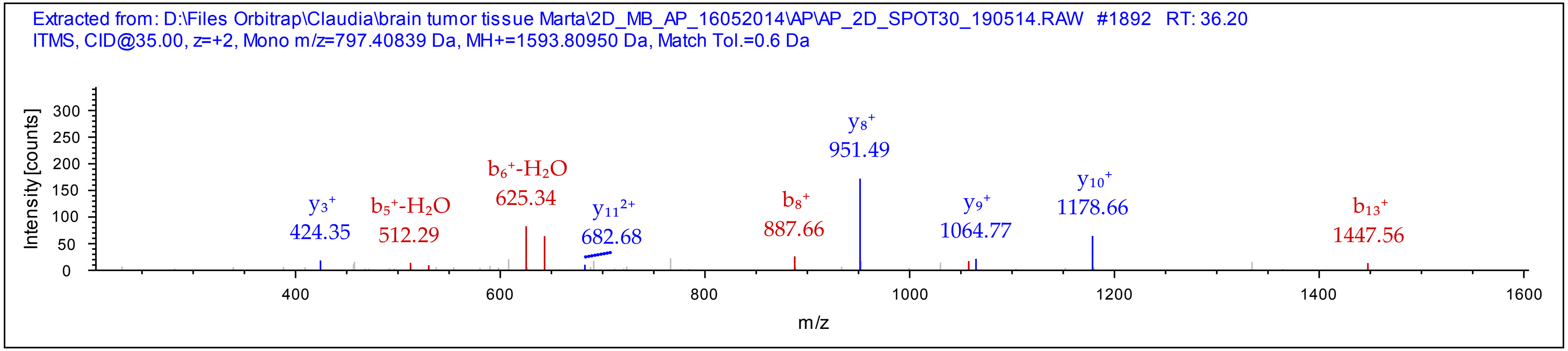
Protein references (1):
- Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	116.03423	58.52075	D			10
2	173.05570	87.03149	G	863.46220	432.23474	9
3	244.09282	122.55005	A	806.44073	403.72400	8
4	301.11429	151.06078	G	735.40361	368.20544	7
5	416.14124	208.57426	D	678.38214	339.69471	6
6	515.20966	258.10847	V	563.35519	282.18123	5
7	586.24678	293.62703	A	464.28677	232.64702	4
8	733.31520	367.16124	F	393.24965	197.12846	3
9	832.38362	416.69545	V	246.18123	123.59425	2
10			K	147.11281	74.06004	1



Sequence: TAGWNIPMGLLYNK, M8-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 797.40839 Da (+0.02 mmu/+0.03 ppm), MH+: 1593.80950 Da, RT: 36.20 min,
Identified with: Sequest HT (v1.3); XCorr:1.82, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-NH_3
Protein references (1):
- Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]

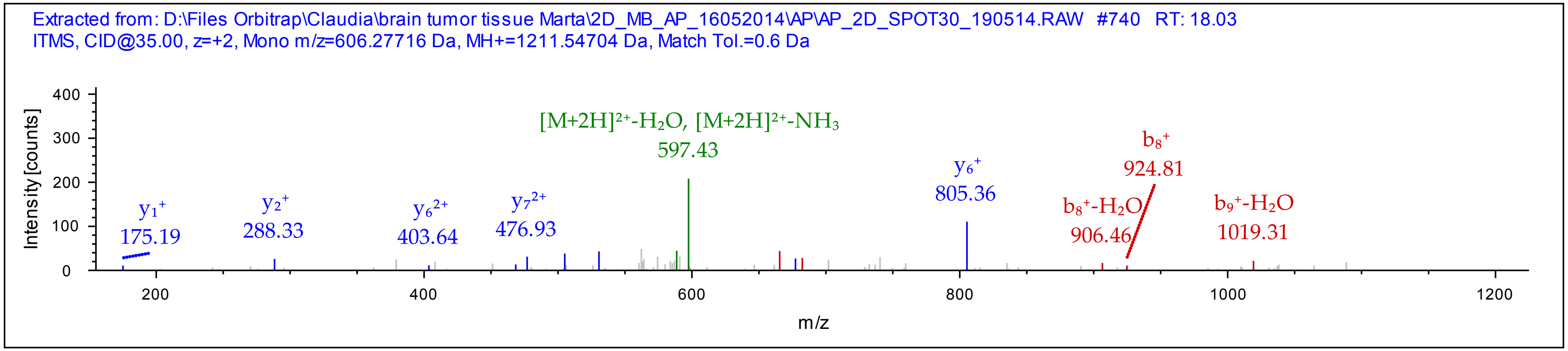
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	102.05496	51.53112	T			14
2	173.09208	87.04968	A	1492.76177	746.88452	13
3	230.11355	115.56041	G	1421.72465	711.36596	12
4	416.19287	208.60007	W	1364.70318	682.85523	11
5	530.23580	265.62154	N	1178.62386	589.81557	10
6	643.31987	322.16357	I	1064.58093	532.79410	9
7	740.37264	370.68996	P	951.49686	476.25207	8
8	887.40805	444.20766	M-Oxidation	854.44409	427.72568	7
9	944.42952	472.71840	G	707.40867	354.20797	6
10	1057.51359	529.26043	L	650.38720	325.69724	5
11	1170.59766	585.80247	L	537.30313	269.15520	4
12	1333.66098	667.33413	Y	424.21906	212.61317	3
13	1447.70391	724.35559	N	261.15574	131.08151	2
14			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT30_190514.RAW #1892 RT: 36.20
ITMS, CID@35.00, z=+2, Mono m/z=797.40839 Da, MH+=1593.80950 Da, Match Tol.=0.6 Da

Sequence: DSGFQMNQLR, M6-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 606.27716 Da (-0.18 mmu/-0.3 ppm), MH+: 1211.54704 Da, RT: 18.03 min,
Identified with: Sequest HT (v1.3); XCorr:1.78, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]

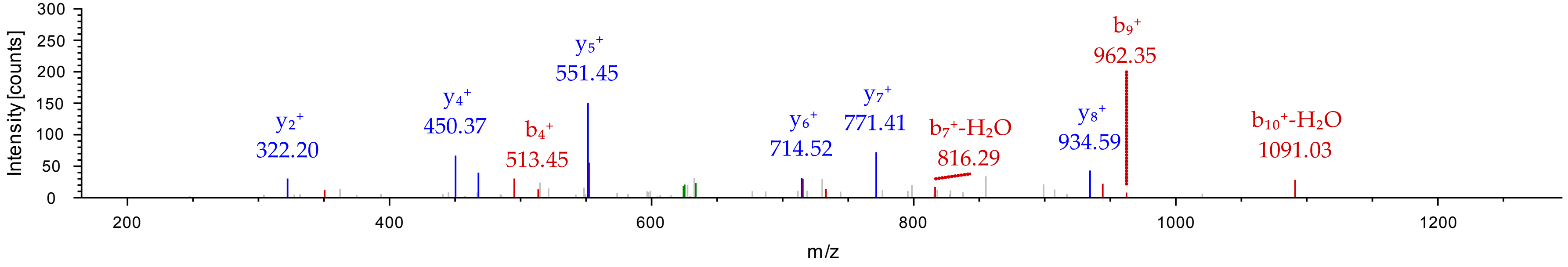
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	116.03423	58.52075	D			10
2	203.06626	102.03677	S	1096.52046	548.76387	9
3	260.08773	130.54750	G	1009.48843	505.24785	8
4	407.15615	204.08171	F	952.46696	476.73712	7
5	535.21473	268.11100	Q	805.39854	403.20291	6
6	682.25014	341.62871	M-Oxidation	677.33996	339.17362	5
7	796.29307	398.65017	N	530.30454	265.65591	4
8	924.35165	462.67946	Q	416.26161	208.63444	3
9	1037.43572	519.22150	L	288.20303	144.60515	2
10			R	175.11896	88.06312	1



Sequence: EGYYGYTGAFR, Charge: +2, Monoisotopic m/z: 642.28802 Da (-0.19 mmu/-0.29 ppm), MH+: 1283.56877 Da, RT: 26.77 min,
Identified with: Sequest HT (v1.3); XCorr:1.76, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3
Protein references (1):
- Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	130.04988	65.52858	E			11
2	187.07135	94.03931	G	1154.52655	577.76691	10
3	350.13467	175.57097	Y	1097.50508	549.25618	9
4	513.19799	257.10263	Y	934.44176	467.72452	8
5	570.21946	285.61337	G	771.37844	386.19286	7
6	733.28278	367.14503	Y	714.35697	357.68212	6
7	834.33046	417.66887	T	551.29365	276.15046	5
8	891.35193	446.17960	G	450.24597	225.62662	4
9	962.38905	481.69816	A	393.22450	197.11589	3
10	1109.45747	555.23237	F	322.18738	161.59733	2
11			R	175.11896	88.06312	1

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT30_190514.RAW #1297 RT: 26.77
ITMS, CID@35.00, z=+2, Mono m/z=642.28802 Da, MH+=1283.56877 Da, Match Tol.=0.6 Da

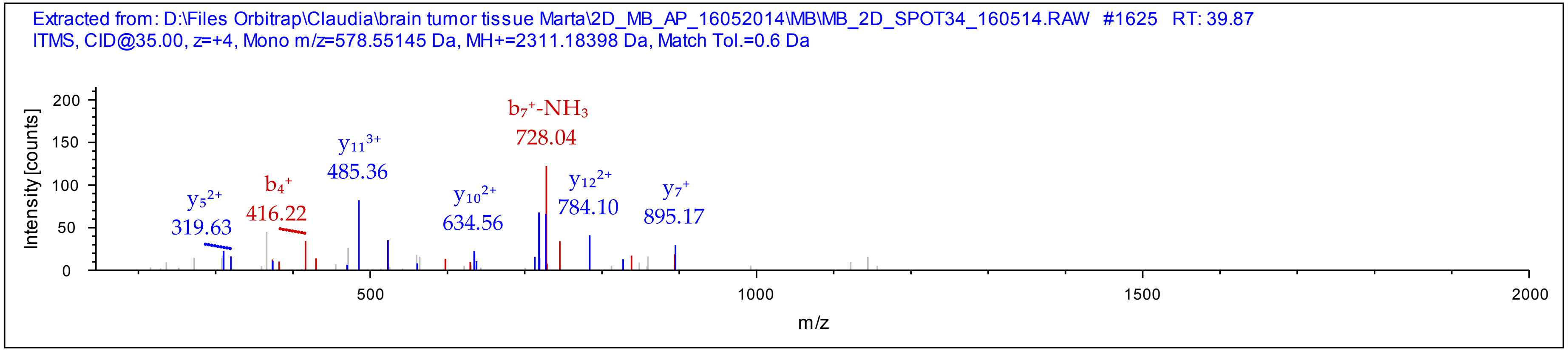


Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
34	P22392	Nucleoside diphosphate kinase B	17.2	8.6	43.43	44.08%	5	5	MB	2.00E-02	1.8	↑ in MB

Sequence: SAEKEISLWFKPEELVDYK, Charge: +4, Monoisotopic m/z: 578.55145 Da (-0.44 mmu/-0.76 ppm), MH+: 2311.18398 Da, RT: 39.87 min,
Identified with: Sequest HT (v1.3); XCorr:2.94, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H$_2$O; b-NH$_3$; y; y-H$_2$O; y-NH$_3$

Protein references (1):
- Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1 - [NDKB_HUMAN]

#1	**b$^+$**	**b^{2+}**	**b^{3+}**	**b^{4+}**	**Seq.**	**y$^+$**	**y^{2+}**	**y^{3+}**	**y^{4+}**	**#2**
1	88.03931	44.52329	30.01795	22.76528	S					19
2	159.07643	80.04185	53.69699	40.52456	A	2224.15371	1112.58049	742.05609	556.79389	18
3	288.11903	144.56315	96.71119	72.78521	E	2153.11659	1077.06193	718.37705	539.03461	17
4	416.21400	208.61064	139.40952	104.80896	K	2024.07399	1012.54063	675.36285	506.77396	16
5	545.25660	273.13194	182.42372	137.06961	E	1895.97902	948.49315	632.66452	474.75021	15
6	658.34067	329.67397	220.11841	165.34062	I	1766.93642	883.97185	589.65032	442.48956	14
7	745.37270	373.18999	249.12908	187.09863	S	1653.85235	827.42981	551.95563	414.21855	13
8	858.45677	429.73202	286.82377	215.36965	L	1566.82032	783.91380	522.94496	392.46054	12
9	1044.53609	522.77168	348.85021	261.88948	W	1453.73625	727.37176	485.25027	364.18952	11
10	1191.60451	596.30589	397.87302	298.65658	F	1267.65693	634.33210	423.22383	317.66969	10
11	1319.69948	660.35338	440.57134	330.68033	K	1120.58851	560.79789	374.20102	280.90259	9
12	1416.75225	708.87976	472.92227	354.94352	P	992.49354	496.75041	331.50270	248.87884	8
13	1545.79485	773.40106	515.93647	387.20417	E	895.44077	448.22402	299.15177	224.61565	7
14	1674.83745	837.92236	558.95067	419.46482	E	766.39817	383.70272	256.13757	192.35500	6
15	1787.92152	894.46440	596.64536	447.73584	L	637.35557	319.18142	213.12337	160.09435	5
16	1886.98994	943.99861	629.66816	472.50294	V	524.27150	262.63939	175.42868	131.82333	4
17	2002.01689	1001.51208	668.01048	501.25968	D	425.20308	213.10518	142.40588	107.05623	3
18	2165.08021	1083.04374	722.36492	542.02551	Y	310.17613	155.59170	104.06356	78.29949	2
19					K	147.11281	74.06004	49.70912	37.53366	1

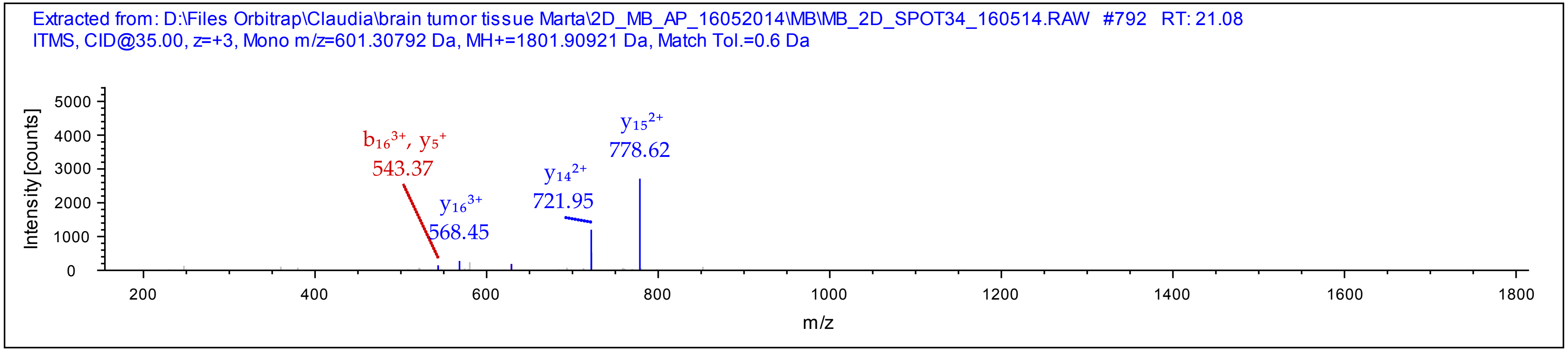


Sequence: VMLGETNPADSKPGTIR, M2-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 601.30792 Da (-0.72 mmu/-1.2 ppm), MH+: 1801.90921 Da, RT: 21.08 min,
Identified with: Sequest HT (v1.3); XCorr:2.73, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H$_2$O; b-NH$_3$; y; y-H$_2$O; y-NH$_3$

Protein references (3):
- Putative nucleoside diphosphate kinase OS=Homo sapiens GN=NME2P1 PE=5 SV=1 - [NDK8_HUMAN]
- Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 - [NDKA_HUMAN]
- Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1 - [NDKB_HUMAN]

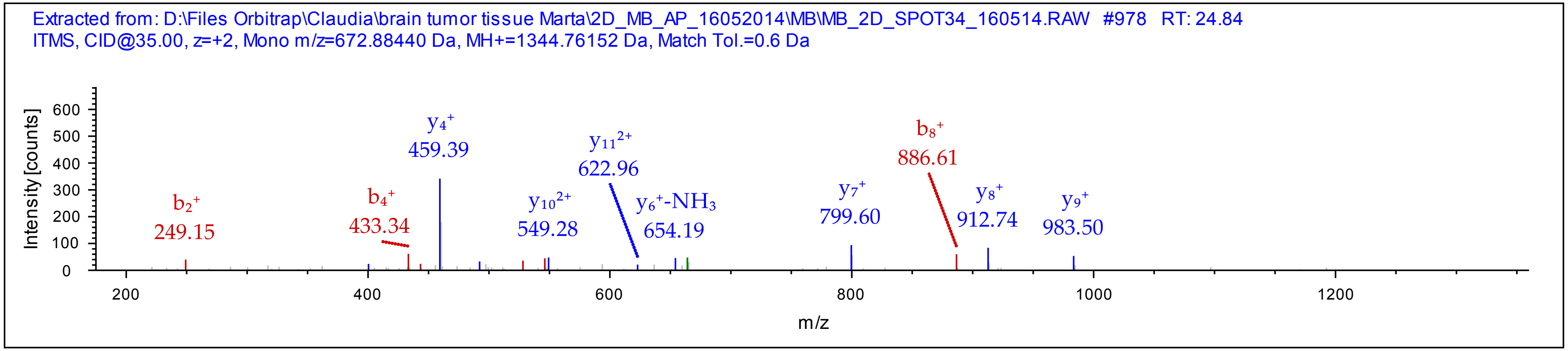
#1	b$^+$	b^{2+}	b^{3+}	Seq.	y$^+$	y^{2+}	y^{3+}	#2
1	100.07570	50.54149	34.03008	V				17
2	247.11111	124.05919	83.04189	M-Oxidation	1702.84296	851.92512	568.28584	16
3	360.19518	180.60123	120.73658	L	1555.80754	778.40741	519.27403	15
4	417.21665	209.11196	139.74373	G	1442.72347	721.86537	481.57934	14
5	546.25925	273.63326	182.75793	E	1385.70200	693.35464	462.57218	13
6	647.30693	324.15710	216.44049	T	1256.65940	628.83334	419.55798	12
7	761.34986	381.17857	254.45480	N	1155.61172	578.30950	385.87542	11
8	858.40263	429.70495	286.80573	P	1041.56879	521.28803	347.86111	10
9	929.43975	465.22351	310.48477	A	944.51602	472.76165	315.51019	9
10	1044.46670	522.73699	348.82708	D	873.47890	437.24309	291.83115	8
11	1131.49873	566.25300	377.83776	S	758.45195	379.72961	253.48883	7
12	1259.59370	630.30049	420.53608	K	671.41992	336.21360	224.47816	6
13	1356.64647	678.82687	452.88701	P	543.32495	272.16611	181.77983	5
14	1413.66794	707.33761	471.89416	G	446.27218	223.63973	149.42891	4
15	1514.71562	757.86145	505.57672	T	389.25071	195.12899	130.42175	3

16	1627.79969	814.40348	543.27141	I	288.20303	144.60515	96.73919	2
17				R	175.11896	88.06312	59.04450	1



Sequence: TFIAIKPDGVQR, Charge: +2, Monoisotopic m/z: 672.88440 Da (-0.98 mmu/-1.46 ppm), MH+: 1344.76152 Da, RT: 24.84 min,
Identified with: Sequest HT (v1.3); XCorr:2.65, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (2):
- Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 - [NDKA_HUMAN]
- Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1 - [NDKB_HUMAN]

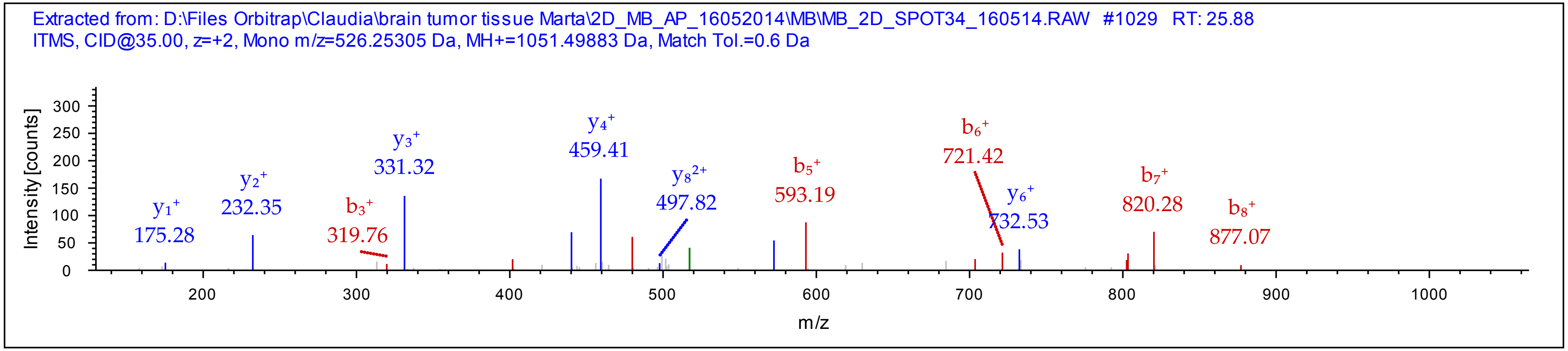
#1	**b^{+}**	**b^{2+}**	**Seq.**	**y^{+}**	**y^{2+}**	**#2**
1	102.05496	51.53112	T			12
2	249.12338	125.06533	F	1243.71580	622.36154	11
3	362.20745	181.60736	I	1096.64738	548.82733	10
4	433.24457	217.12592	A	983.56331	492.28529	9
5	546.32864	273.66796	I	912.52619	456.76673	8
6	674.42361	337.71544	K	799.44212	400.22470	7
7	771.47638	386.24183	P	671.34715	336.17721	6
8	886.50333	443.75530	D	574.29438	287.65083	5
9	943.52480	472.26604	G	459.26743	230.13735	4
10	1042.59322	521.80025	V	402.24596	201.62662	3
11	1170.65180	585.82954	Q	303.17754	152.09241	2
12			R	175.11896	88.06312	1



Sequence: GDFCIQVGR, C4-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 526.25305 Da (-0.08 mmu/-0.16 ppm), MH+: 1051.49883 Da, RT: 25.88 min,
Identified with: Sequest HT (v1.3); XCorr:2.43, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):
- Putative nucleoside diphosphate kinase OS=Homo sapiens GN=NME2P1 PE=5 SV=1 - [NDK8_HUMAN]
- Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 - [NDKA_HUMAN]
- Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1 - [NDKB_HUMAN]

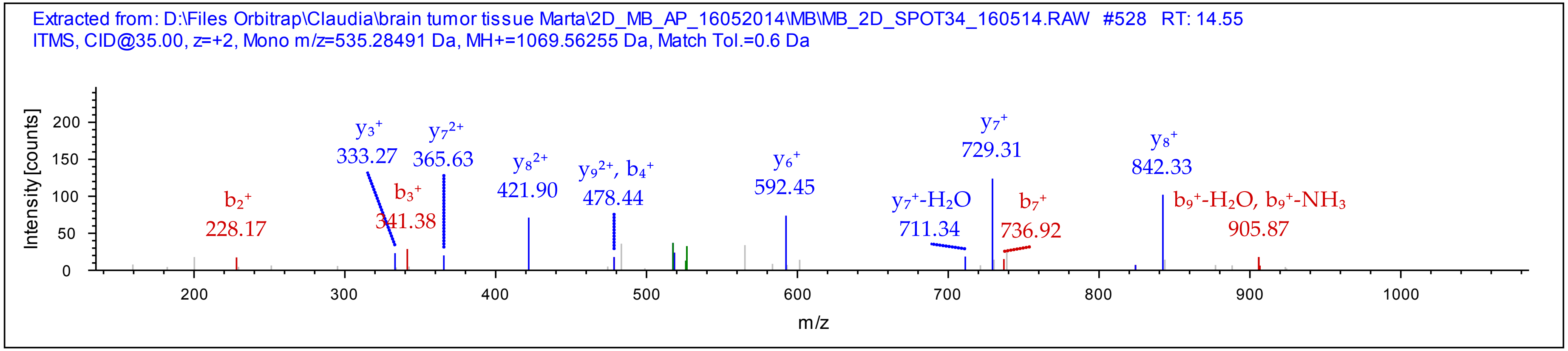
#1	**b⁺**	**b²⁺**	**Seq.**	**y⁺**	**y²⁺**	**#2**
1	58.02875	29.51801	G			9
2	173.05570	87.03149	D	994.47753	497.74240	8
3	320.12412	160.56570	F	879.45058	440.22893	7
4	480.15477	240.58102	C-Carbamidomethyl	732.38216	366.69472	6
5	593.23884	297.12306	I	572.35150	286.67939	5
6	721.29742	361.15235	Q	459.26743	230.13735	4
7	820.36584	410.68656	V	331.20885	166.10806	3
8	877.38731	439.19729	G	232.14043	116.57385	2
9			R	175.11896	88.06312	1



Sequence: NIIHGSDSVK, Charge: +2, Monoisotopic m/z: 535.28491 Da (-0.57 mmu/-1.07 ppm), MH+: 1069.56255 Da, RT: 14.55 min,
Identified with: Sequest HT (v1.3); XCorr:1.83, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):
- Putative nucleoside diphosphate kinase OS=Homo sapiens GN=NME2P1 PE=5 SV=1 - [NDK8_HUMAN]
- Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1 - [NDKB_HUMAN]

#1	b^{+}	b^{2+}	Seq.	y^{+}	y^{2+}	#2
1	115.05021	58.02874	N			10
2	228.13428	114.57078	I	955.52076	478.26402	9
3	341.21835	171.11281	I	842.43669	421.72198	8
4	478.27726	239.64227	H	729.35262	365.17995	7
5	535.29873	268.15300	G	592.29371	296.65049	6
6	622.33076	311.66902	S	535.27224	268.13976	5
7	737.35771	369.18249	D	448.24021	224.62374	4
8	824.38974	412.69851	S	333.21326	167.11027	3
9	923.45816	462.23272	V	246.18123	123.59425	2
10			K	147.11281	74.06004	1

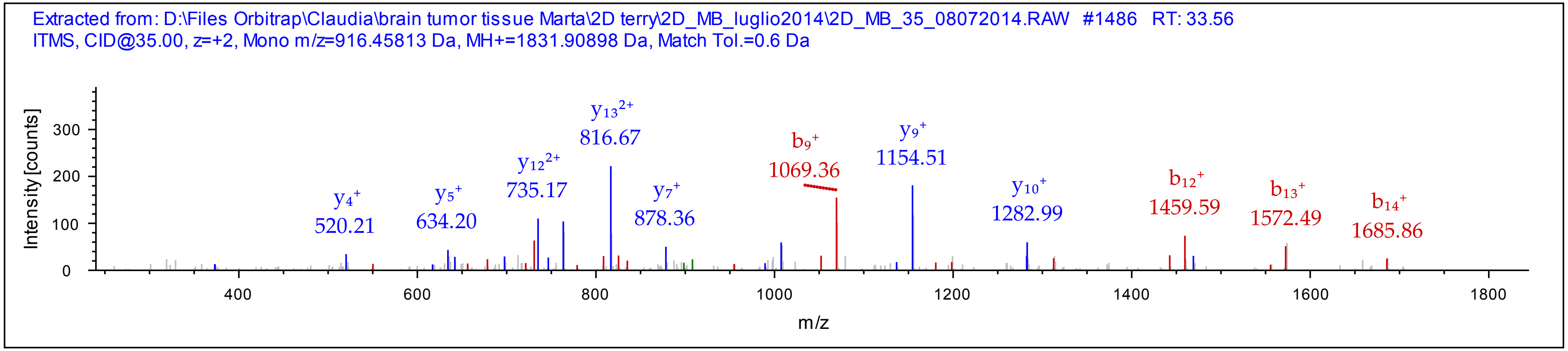

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT34_160514.RAW #528 RT: 14.55
ITMS, CID@35.00, z=+2, Mono m/z=535.28491 Da, MH+=1069.56255 Da, Match Tol.=0.6 Da

Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
35	P62937	Peptidyl-prolyl cis-trans isomerase A	18.0	7.7	60.58	47.27%	6	6	MB	2.59E-05	2.3	↑ in MB

Sequence: SIYGEKFEDENFILK, Charge: +2, Monoisotopic m/z: 916.45813 Da (-1.17 mmu/-1.28 ppm), MH+: 1831.90898 Da, RT: 33.56 min,
Identified with: Sequest HT (v1.3); XCorr:3.95, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H$_2$O; b-NH$_3$; y; y-H$_2$O; y-NH$_3$

Protein references (1):
- Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA_HUMAN]

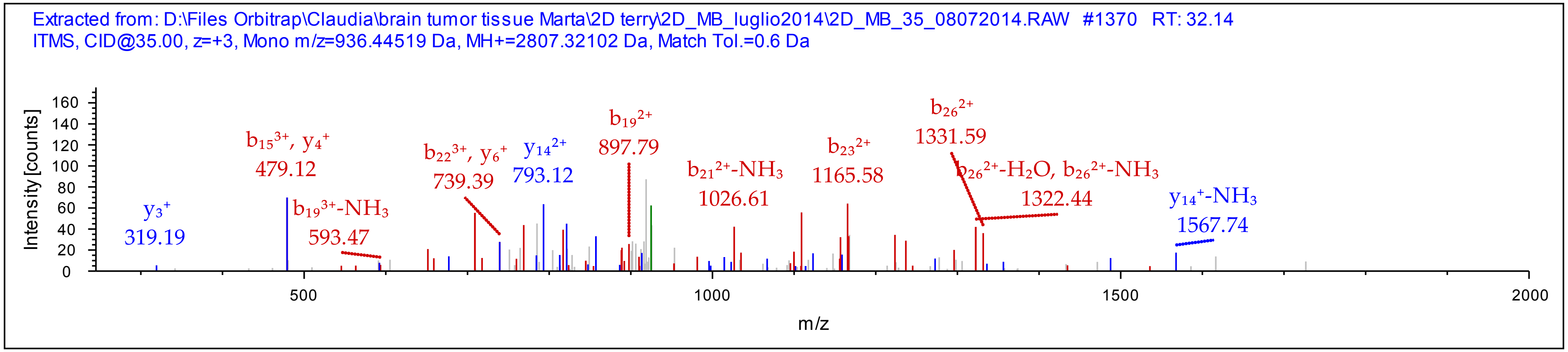
#1	**b$^+$**	**b^{2+}**	**Seq.**	**y$^+$**	**y^{2+}**	**#2**
1	88.03931	44.52329	S			15
2	201.12338	101.06533	I	1744.87930	872.94329	14
3	364.18670	182.59699	Y	1631.79523	816.40125	13
4	421.20817	211.10772	G	1468.73191	734.86959	12
5	550.25077	275.62902	E	1411.71044	706.35886	11
6	678.34574	339.67651	K	1282.66784	641.83756	10
7	825.41416	413.21072	F	1154.57287	577.79007	9
8	954.45676	477.73202	E	1007.50445	504.25586	8
9	1069.48371	535.24549	D	878.46185	439.73456	7
10	1198.52631	599.76679	E	763.43490	382.22109	6
11	1312.56924	656.78826	N	634.39230	317.69979	5
12	1459.63766	730.32247	F	520.34937	260.67832	4
13	1572.72173	786.86450	I	373.28095	187.14411	3
14	1685.80580	843.40654	L	260.19688	130.60208	2
15			K	147.11281	74.06004	1



Sequence: HTGPGILSMANAGPNTNGSQFFICTAK, M9-Oxidation (15.99492 Da), C24-Carbamidomethyl (57.02146 Da)
Charge: +3, Monoisotopic m/z: 936.44519 Da (-1.02 mmu/-1.09 ppm), MH+: 2807.32102 Da, RT: 32.14 min,
Identified with: Sequest HT (v1.3); XCorr:3.85, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA_HUMAN]

#1	b^{+}	b^{2+}	b^{3+}	Seq.	y^{+}	y^{2+}	y^{3+}	#2
1	138.06619	69.53673	46.69358	H				27
2	239.11387	120.06057	80.37614	T	2670.26518	1335.63623	890.75991	26
3	296.13534	148.57131	99.38330	G	2569.21750	1285.11239	857.07735	25
4	393.18811	197.09769	131.73422	P	2512.19603	1256.60165	838.07019	24
5	450.20958	225.60843	150.74138	G	2415.14326	1208.07527	805.71927	23
6	563.29365	282.15046	188.43607	I	2358.12179	1179.56453	786.71211	22
7	676.37772	338.69250	226.13076	L	2245.03772	1123.02250	749.01742	21
8	763.40975	382.20851	255.14143	S	2131.95365	1066.48046	711.32273	20
9	910.44516	455.72622	304.15324	M-Oxidation	2044.92162	1022.96445	682.31206	19
10	981.48228	491.24478	327.83228	A	1897.88621	949.44674	633.30025	18
11	1095.52521	548.26624	365.84659	N	1826.84909	913.92818	609.62121	17
12	1166.56233	583.78480	389.52563	A	1712.80616	856.90672	571.60690	16
13	1223.58380	612.29554	408.53278	G	1641.76904	821.38816	547.92786	15
14	1320.63657	660.82192	440.88371	P	1584.74757	792.87742	528.92071	14
15	1434.67950	717.84339	478.89802	N	1487.69480	744.35104	496.56978	13
16	1535.72718	768.36723	512.58058	T	1373.65187	687.32957	458.55547	12
17	1649.77011	825.38869	550.59489	N	1272.60419	636.80573	424.87291	11
18	1706.79158	853.89943	569.60204	G	1158.56126	579.78427	386.85860	10

19	1793.82361	897.41544	598.61272	S	1101.53979	551.27353	367.85145	9
20	1921.88219	961.44473	641.29891	Q	1014.50776	507.75752	338.84077	8
21	2068.95061	1034.97894	690.32172	F	886.44918	443.72823	296.15458	7
22	2216.01903	1108.51315	739.34453	F	739.38076	370.19402	247.13177	6
23	2329.10310	1165.05519	777.03922	I	592.31234	296.65981	198.10896	5
24	2489.13376	1245.07052	830.38277	C-Carbamidomethyl	479.22827	240.11777	160.41427	4
25	2590.18144	1295.59436	864.06533	T	319.19761	160.10244	107.07072	3
26	2661.21856	1331.11292	887.74437	A	218.14993	109.57860	73.38816	2
27				K	147.11281	74.06004	49.70912	1

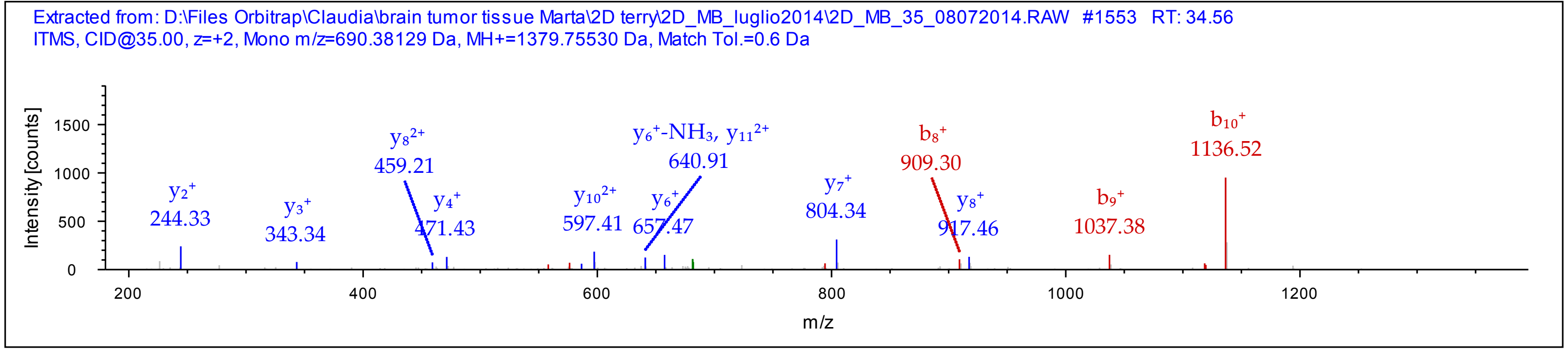

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_MB_luglio2014\2D_MB_35_08072014.RAW #1370 RT: 32.14
ITMS, CID@35.00, z=+3, Mono m/z=936.44519 Da, MH+=2807.32102 Da, Match Tol.=0.6 Da

Sequence: VSFELFADKVPK, Charge: +2, Monoisotopic m/z: 690.38129 Da (-0.85 mmu/-1.24 ppm), MH+: 1379.75530 Da, RT: 34.56 min,
Identified with: Sequest HT (v1.3); XCorr:3.63, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	100.07570	50.54149	V			12
2	187.10773	94.05750	S	1280.68858	640.84793	11
3	334.17615	167.59171	F	1193.65655	597.33191	10
4	463.21875	232.11301	E	1046.58813	523.79770	9
5	576.30282	288.65505	L	917.54553	459.27640	8
6	723.37124	362.18926	F	804.46146	402.73437	7
7	794.40836	397.70782	A	657.39304	329.20016	6
8	909.43531	455.22129	D	586.35592	293.68160	5
9	1037.53028	519.26878	K	471.32897	236.16812	4

10	1136.59870	568.80299	V	343.23400	172.12064	3
11	1233.65147	617.32937	P	244.16558	122.58643	2
12			K	147.11281	74.06004	1

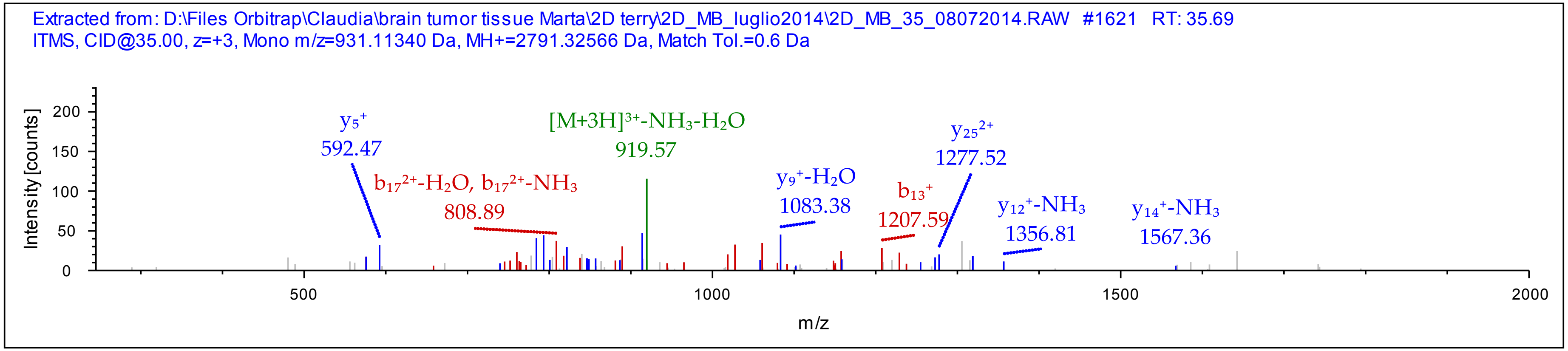


Sequence: HTGPGILSMANAGPNTNGSQFFICTAK, C24-Carbamidomethyl (57.02146 Da)
Charge: +3, Monoisotopic m/z: 931.11340 Da (-1.17 mmu/-1.26 ppm), MH+: 2791.32566 Da, RT: 35.69 min,
Identified with: Sequest HT (v1.3); XCorr:2.96, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA_HUMAN]

#1	b$^+$	b^{2+}	b^{3+}	Seq.	y$^+$	y^{2+}	y^{3+}	#2
1	138.06619	69.53673	46.69358	H				27
2	239.11387	120.06057	80.37614	T	2654.27027	1327.63877	885.42827	26
3	296.13534	148.57131	99.38330	G	2553.22259	1277.11493	851.74571	25
4	393.18811	197.09769	131.73422	P	2496.20112	1248.60420	832.73856	24
5	450.20958	225.60843	150.74138	G	2399.14835	1200.07781	800.38763	23
6	563.29365	282.15046	188.43607	I	2342.12688	1171.56708	781.38048	22
7	676.37772	338.69250	226.13076	L	2229.04281	1115.02504	743.68579	21
8	763.40975	382.20851	255.14143	S	2115.95874	1058.48301	705.99110	20
9	894.45025	447.72876	298.82160	M	2028.92671	1014.96699	676.98042	19
10	965.48737	483.24732	322.50064	A	1897.88621	949.44674	633.30025	18
11	1079.53030	540.26879	360.51495	N	1826.84909	913.92818	609.62121	17
12	1150.56742	575.78735	384.19399	A	1712.80616	856.90672	571.60690	16
13	1207.58889	604.29808	403.20115	G	1641.76904	821.38816	547.92786	15
14	1304.64166	652.82447	435.55207	P	1584.74757	792.87742	528.92071	14
15	1418.68459	709.84593	473.56638	N	1487.69480	744.35104	496.56978	13
16	1519.73227	760.36977	507.24894	T	1373.65187	687.32957	458.55547	12

17	1633.77520	817.39124	545.26325	N	1272.60419	636.80573	424.87291	11
18	1690.79667	845.90197	564.27041	G	1158.56126	579.78427	386.85860	10
19	1777.82870	889.41799	593.28108	S	1101.53979	551.27353	367.85145	9
20	1905.88728	953.44728	635.96728	Q	1014.50776	507.75752	338.84077	8
21	2052.95570	1026.98149	684.99008	F	886.44918	443.72823	296.15458	7
22	2200.02412	1100.51570	734.01289	F	739.38076	370.19402	247.13177	6
23	2313.10819	1157.05773	771.70758	I	592.31234	296.65981	198.10896	5
24	2473.13884	1237.07306	825.05113	C-Carbamidomethyl	479.22827	240.11777	160.41427	4
25	2574.18652	1287.59690	858.73369	T	319.19761	160.10244	107.07072	3
26	2645.22364	1323.11546	882.41273	A	218.14993	109.57860	73.38816	2
27				K	147.11281	74.06004	49.70912	1

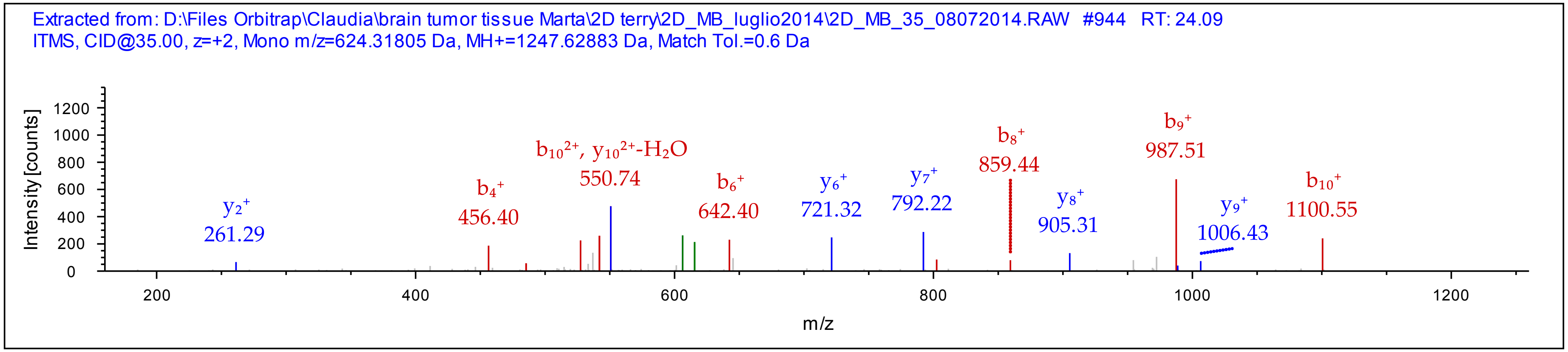

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_MB_luglio2014\2D_MB_35_08072014.RAW #1621 RT: 35.69
ITMS, CID@35.00, z=+3, Mono m/z=931.11340 Da, MH+=2791.32566 Da, Match Tol.=0.6 Da

Sequence: KITIADCGQLE, C7-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 624.31805 Da (-0.62 mmu/-1 ppm), MH+: 1247.62883 Da, RT: 24.09 min,
Identified with: Sequest HT (v1.3); XCorr:2.88, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	129.10225	65.05476	K			11
2	242.18632	121.59680	I	1119.53511	560.27119	10
3	343.23400	172.12064	T	1006.45104	503.72916	9
4	456.31807	228.66267	I	905.40336	453.20532	8

5	527.35519	264.18123	A	792.31929	396.66328	7
6	642.38214	321.69471	D	721.28217	361.14472	6
7	802.41279	401.71003	C-Carbamidomethyl	606.25522	303.63125	5
8	859.43426	430.22077	G	446.22456	223.61592	4
9	987.49284	494.25006	Q	389.20309	195.10518	3
10	1100.57691	550.79209	L	261.14451	131.07589	2
11			E	148.06044	74.53386	1

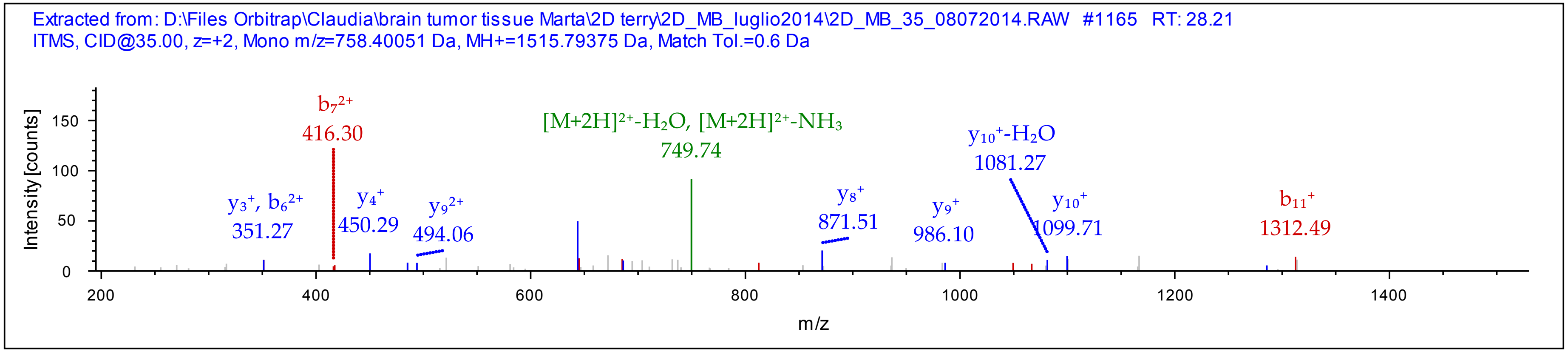

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_MB_luglio2014\2D_MB_35_08072014.RAW #944 RT: 24.09
ITMS, CID@35.00, z=+2, Mono m/z=624.31805 Da, MH+=1247.62883 Da, Match Tol.=0.6 Da

Sequence: TEWLDGKHVVFGK, Charge: +2, Monoisotopic m/z: 758.40051 Da (-0.88 mmu/-1.16 ppm), MH+: 1515.79375 Da, RT: 28.21 min,
Identified with: Sequest HT (v1.3); XCorr:2.64, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	102.05496	51.53112	T			13
2	231.09756	116.05242	E	1414.74783	707.87755	12
3	417.17688	209.09208	W	1285.70523	643.35625	11
4	530.26095	265.63411	L	1099.62591	550.31659	10
5	645.28790	323.14759	D	986.54184	493.77456	9
6	702.30937	351.65832	G	871.51489	436.26108	8
7	830.40434	415.70581	K	814.49342	407.75035	7
8	967.46325	484.23526	H	686.39845	343.70286	6

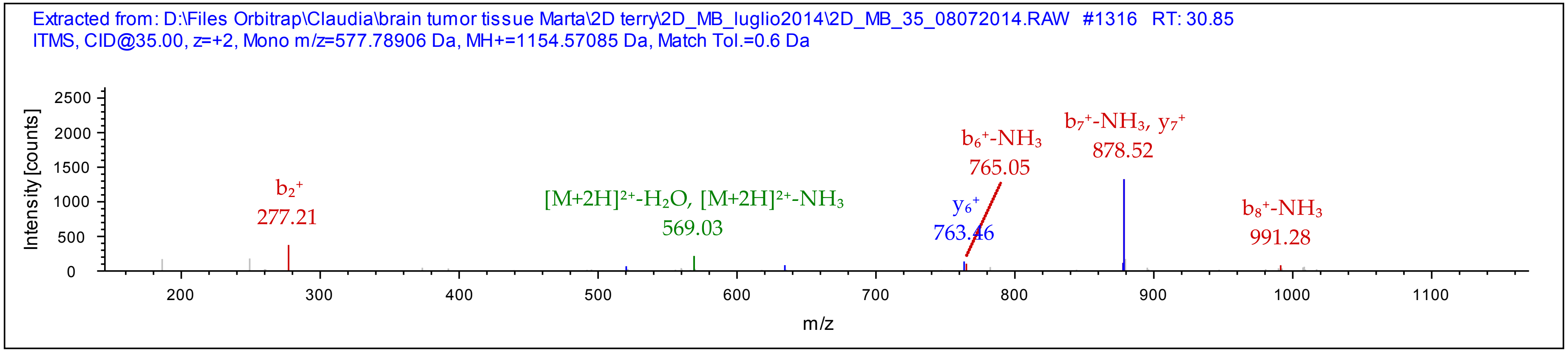
9	1066.53167	533.76947	V	549.33954	275.17341	5
10	1165.60009	583.30368	V	450.27112	225.63920	4
11	1312.66851	656.83789	F	351.20270	176.10499	3
12	1369.68998	685.34863	G	204.13428	102.57078	2
13			K	147.11281	74.06004	1



Sequence: FEDENFILK, Charge: +2, Monoisotopic m/z: 577.78906 Da (-1.01 mmu/-1.75 ppm), MH+: 1154.57085 Da, RT: 30.85 min,
Identified with: Sequest HT (v1.3); XCorr:2.40, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	148.07570	74.54149	F			9
2	277.11830	139.06279	E	1007.50445	504.25586	8
3	392.14525	196.57626	D	878.46185	439.73456	7
4	521.18785	261.09756	E	763.43490	382.22109	6
5	635.23078	318.11903	N	634.39230	317.69979	5
6	782.29920	391.65324	F	520.34937	260.67832	4
7	895.38327	448.19527	I	373.28095	187.14411	3
8	1008.46734	504.73731	L	260.19688	130.60208	2
9			K	147.11281	74.06004	1

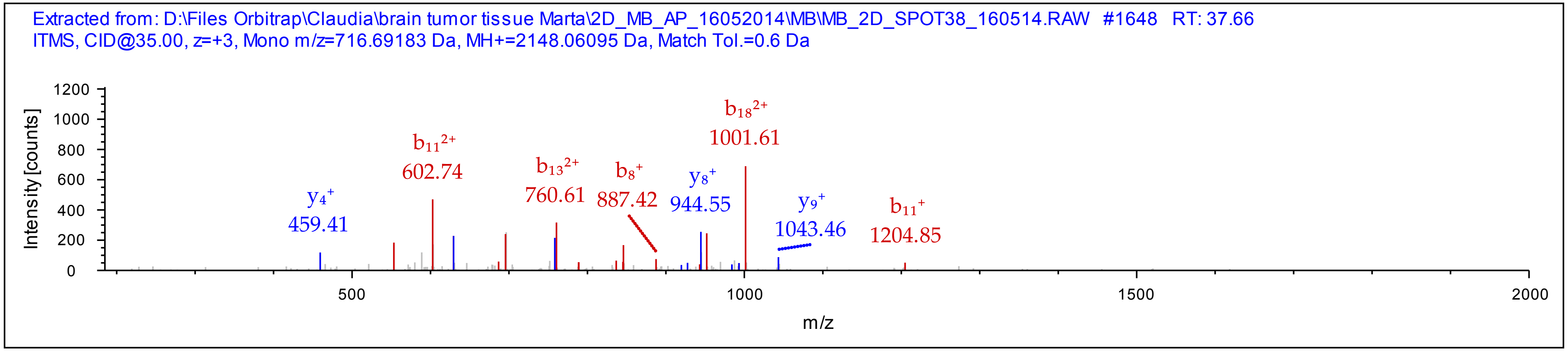


Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
38	P15531	Nucleoside diphosphate kinase A	17.0	5.8	98.4	81.58%	10	10	MB	3.38E-05	3.0	↑ in MB

Sequence: YMHSGPVVAMVWEGLNVVK, M2-Oxidation (15.99492 Da), M10-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 716.69183 Da (-0.27 mmu/-0.37 ppm), MH+: 2148.06095 Da, RT: 37.66 min,
Identified with: Sequest HT (v1.3); XCorr:4.52, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H$_2$O; b-NH$_3$; y; y-H$_2$O; y-NH$_3$

Protein references (1):
- Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 - [NDKA_HUMAN]

#1	**b^{+}**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^{+}**	**y^{2+}**	**y^{3+}**	**#2**
1	164.07060	82.53894	55.36172	Y				19
2	311.10601	156.05664	104.37352	M-Oxidation	1984.99843	993.00285	662.33766	18
3	448.16492	224.58610	150.05982	H	1837.96302	919.48515	613.32586	17
4	535.19695	268.10211	179.07050	S	1700.90411	850.95569	567.63955	16
5	592.21842	296.61285	198.07766	G	1613.87208	807.43968	538.62888	15
6	689.27119	345.13923	230.42858	P	1556.85061	778.92894	519.62172	14
7	788.33961	394.67344	263.45139	V	1459.79784	730.40256	487.27080	13
8	887.40803	444.20765	296.47419	V	1360.72942	680.86835	454.24799	12
9	958.44515	479.72621	320.15323	A	1261.66100	631.33414	421.22518	11
10	1105.48057	553.24392	369.16504	M-Oxidation	1190.62388	595.81558	397.54614	10
11	1204.54899	602.77813	402.18785	V	1043.58846	522.29787	348.53434	9
12	1390.62831	695.81779	464.21429	W	944.52004	472.76366	315.51153	8
13	1519.67091	760.33909	507.22849	E	758.44072	379.72400	253.48509	7
14	1576.69238	788.84983	526.23564	G	629.39812	315.20270	210.47089	6
15	1689.77645	845.39186	563.93033	L	572.37665	286.69196	191.46373	5
16	1803.81938	902.41333	601.94464	N	459.29258	230.14993	153.76904	4
17	1902.88780	951.94754	634.96745	V	345.24965	173.12846	115.75473	3
18	2001.95622	1001.48175	667.99026	V	246.18123	123.59425	82.73193	2
19				K	147.11281	74.06004	49.70912	1



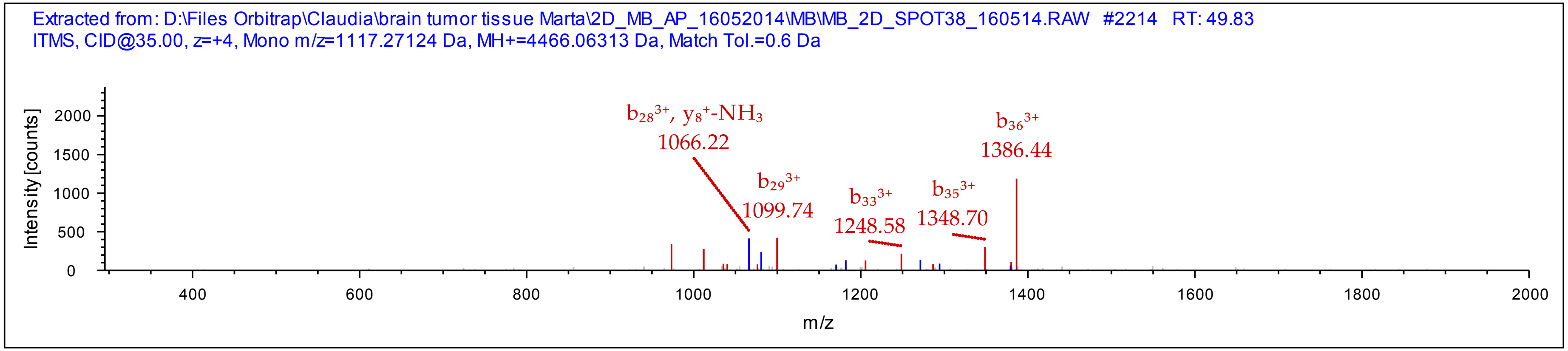
Sequence: NIIHGSDSVESAEKEIGLWFHPEELVDYTSCAQNWIYE, C31-Carbamidomethyl (57.02146 Da)
Charge: +4, Monoisotopic m/z: 1117.27124 Da (+1.8 mmu/+1.61 ppm), MH+: 4466.06313 Da, RT: 49.83 min,

Identified with: Sequest HT (v1.3); XCorr:3.70, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 - [NDKA_HUMAN]

#1	**b^{+}**	**b^{2+}**	**b^{3+}**	**b^{4+}**	**Seq.**	**y^{+}**	**y^{2+}**	**y^{3+}**	**y^{4+}**	**#2**
1	115.05021	58.02874	39.02159	29.51801	N					38
2	228.13428	114.57078	76.71628	57.78903	I	4352.01301	2176.51014	1451.34252	1088.75871	37
3	341.21835	171.11281	114.41097	86.06004	I	4238.92894	2119.96811	1413.64783	1060.48769	36
4	478.27726	239.64227	160.09727	120.32477	H	4125.84487	2063.42607	1375.95314	1032.21667	35
5	535.29873	268.15300	179.10443	134.58014	G	3988.78596	1994.89662	1330.26684	997.95195	34
6	622.33076	311.66902	208.11510	156.33815	S	3931.76449	1966.38588	1311.25968	983.69658	33
7	737.35771	369.18249	246.45742	185.09488	D	3844.73246	1922.86987	1282.24900	961.93857	32
8	824.38974	412.69851	275.46810	206.85289	S	3729.70551	1865.35639	1243.90669	933.18183	31
9	923.45816	462.23272	308.49090	231.62000	V	3642.67348	1821.84038	1214.89601	911.42383	30
10	1052.50076	526.75402	351.50510	263.88065	E	3543.60506	1772.30617	1181.87320	886.65672	29
11	1139.53279	570.27003	380.51578	285.63865	S	3414.56246	1707.78487	1138.85900	854.39607	28
12	1210.56991	605.78859	404.19482	303.39793	A	3327.53043	1664.26885	1109.84833	832.63806	27
13	1339.61251	670.30989	447.20902	335.65858	E	3256.49331	1628.75029	1086.16929	814.87878	26
14	1467.70748	734.35738	489.90734	367.68233	K	3127.45071	1564.22899	1043.15509	782.61813	25
15	1596.75008	798.87868	532.92154	399.94298	E	2999.35574	1500.18151	1000.45676	750.59439	24
16	1709.83415	855.42071	570.61623	428.21399	I	2870.31314	1435.66021	957.44256	718.33374	23
17	1766.85562	883.93145	589.62339	442.46936	G	2757.22907	1379.11817	919.74787	690.06272	22
18	1879.93969	940.47348	627.31808	470.74038	L	2700.20760	1350.60744	900.74072	675.80736	21
19	2066.01901	1033.51314	689.34452	517.26021	W	2587.12353	1294.06540	863.04603	647.53634	20
20	2213.08743	1107.04735	738.36733	554.02731	F	2401.04421	1201.02574	801.01959	601.01651	19
21	2350.14634	1175.57681	784.05363	588.29204	H	2253.97579	1127.49153	751.99678	564.24940	18
22	2447.19911	1224.10319	816.40455	612.55523	P	2116.91688	1058.96208	706.31048	529.98468	17
23	2576.24171	1288.62449	859.41875	644.81588	E	2019.86411	1010.43569	673.95955	505.72148	16
24	2705.28431	1353.14579	902.43295	677.07653	E	1890.82151	945.91439	630.94535	473.46083	15
25	2818.36838	1409.68783	940.12764	705.34755	L	1761.77891	881.39309	587.93115	441.20018	14
26	2917.43680	1459.22204	973.15045	730.11466	V	1648.69484	824.85106	550.23646	412.92917	13
27	3032.46375	1516.73551	1011.49277	758.87139	D	1549.62642	775.31685	517.21366	388.16206	12
28	3195.52707	1598.26717	1065.84721	799.63722	Y	1434.59947	717.80337	478.87134	359.40532	11
29	3296.57475	1648.79101	1099.52977	824.89914	T	1271.53615	636.27171	424.51690	318.63949	10
30	3383.60678	1692.30703	1128.54044	846.65715	S	1170.48847	585.74787	390.83434	293.37757	9
31	3543.63743	1772.32235	1181.88399	886.66482	C-Carbamidomethyl	1083.45644	542.23186	361.82366	271.61957	8
32	3614.67455	1807.84091	1205.56303	904.42410	A	923.42578	462.21653	308.48011	231.61190	7

33	3742.73313	1871.87020	1248.24923	936.43874	Q	852.38866	426.69797	284.80107	213.85262	6
34	3856.77606	1928.89167	1286.26354	964.94947	N	724.33008	362.66868	242.11488	181.83798	5
35	4042.85538	2021.93133	1348.28998	1011.46930	W	610.28715	305.64721	204.10057	153.32725	4
36	4155.93945	2078.47336	1385.98467	1039.74032	I	424.20783	212.60755	142.07413	106.80742	3
37	4319.00277	2160.00502	1440.33911	1080.50615	Y	311.12376	156.06552	104.37944	78.53640	2
38					E	148.06044	74.53386	50.02500	37.77057	1

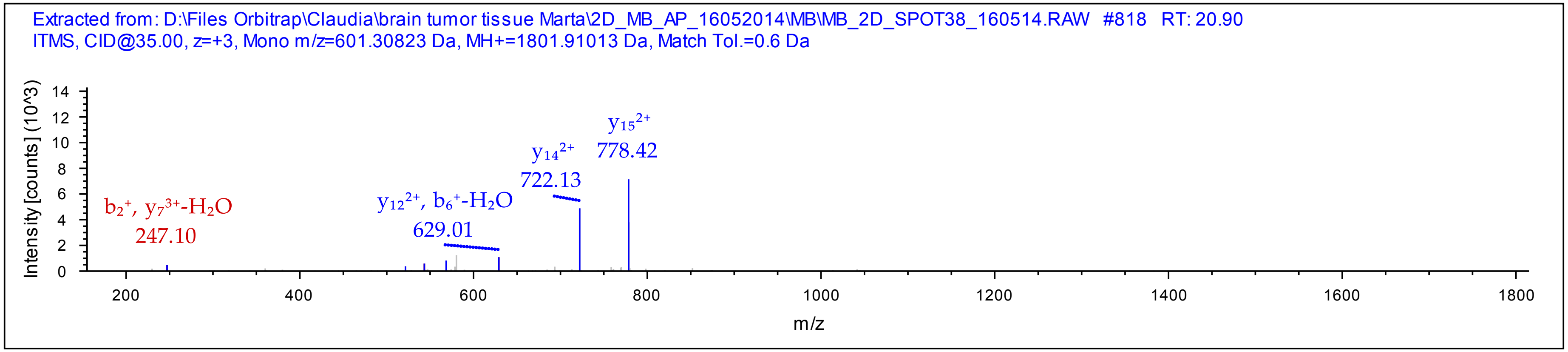

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT38_160514.RAW #2214 RT: 49.83
ITMS, CID@35.00, z=+4, Mono m/z=1117.27124 Da, MH+=4466.06313 Da, Match Tol.=0.6 Da

Sequence: VMLGETNPADSKPGTIR, M2-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 601.30823 Da (-0.42 mmu/-0.69 ppm), MH+: 1801.91013 Da, RT: 20.90 min,
Identified with: Sequest HT (v1.3); XCorr:3.09, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):
- Putative nucleoside diphosphate kinase OS=Homo sapiens GN=NME2P1 PE=5 SV=1 - [NDK8_HUMAN]
- Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 - [NDKA_HUMAN]
- Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1 - [NDKB_HUMAN]

#1	**b^{+}**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^{+}**	**y^{2+}**	**y^{3+}**	**#2**
1	100.07570	50.54149	34.03008	V				17
2	247.11111	124.05919	83.04189	M-Oxidation	1702.84296	851.92512	568.28584	16
3	360.19518	180.60123	120.73658	L	1555.80754	778.40741	519.27403	15
4	417.21665	209.11196	139.74373	G	1442.72347	721.86537	481.57934	14
5	546.25925	273.63326	182.75793	E	1385.70200	693.35464	462.57218	13
6	647.30693	324.15710	216.44049	T	1256.65940	628.83334	419.55798	12
7	761.34986	381.17857	254.45480	N	1155.61172	578.30950	385.87542	11
8	858.40263	429.70495	286.80573	P	1041.56879	521.28803	347.86111	10

9	929.43975	465.22351	310.48477	A	944.51602	472.76165	315.51019	9
10	1044.46670	522.73699	348.82708	D	873.47890	437.24309	291.83115	8
11	1131.49873	566.25300	377.83776	S	758.45195	379.72961	253.48883	7
12	1259.59370	630.30049	420.53608	K	671.41992	336.21360	224.47816	6
13	1356.64647	678.82687	452.88701	P	543.32495	272.16611	181.77983	5
14	1413.66794	707.33761	471.89416	G	446.27218	223.63973	149.42891	4
15	1514.71562	757.86145	505.57672	T	389.25071	195.12899	130.42175	3
16	1627.79969	814.40348	543.27141	I	288.20303	144.60515	96.73919	2
17				R	175.11896	88.06312	59.04450	1

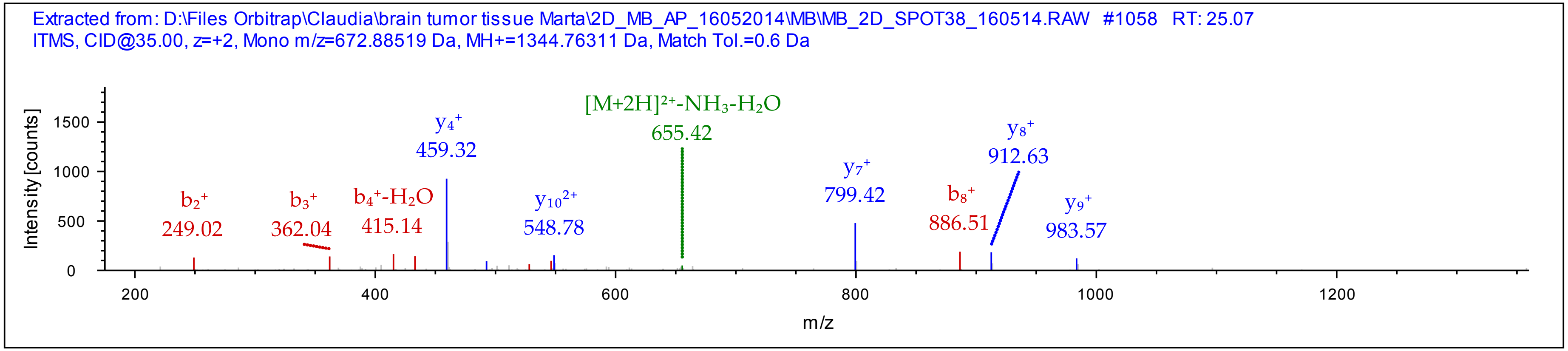


Sequence: TFIAIKPDGVQR, Charge: +2, Monoisotopic m/z: 672.88519 Da (-0.19 mmu/-0.28 ppm), MH+: 1344.76311 Da, RT: 25.07 min,
Identified with: Sequest HT (v1.3); XCorr:2.75, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):
- Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 - [NDKA_HUMAN]
- Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1 - [NDKB_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	102.05496	51.53112	T			12
2	249.12338	125.06533	F	1243.71580	622.36154	11
3	362.20745	181.60736	I	1096.64738	548.82733	10
4	433.24457	217.12592	A	983.56331	492.28529	9
5	546.32864	273.66796	I	912.52619	456.76673	8
6	674.42361	337.71544	K	799.44212	400.22470	7

7	771.47638	386.24183	P	671.34715	336.17721	6
8	886.50333	443.75530	D	574.29438	287.65083	5
9	943.52480	472.26604	G	459.26743	230.13735	4
10	1042.59322	521.80025	V	402.24596	201.62662	3
11	1170.65180	585.82954	Q	303.17754	152.09241	2
12			R	175.11896	88.06312	1

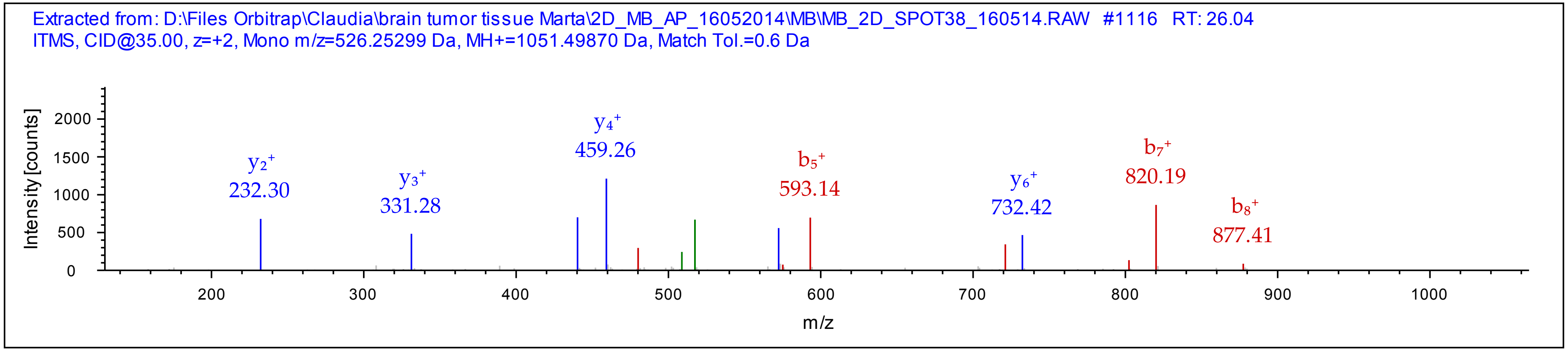


Sequence: GDFCIQVGR, C4-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 526.25299 Da (-0.15 mmu/-0.28 ppm), MH+: 1051.49870 Da, RT: 26.04 min,
Identified with: Sequest HT (v1.3); XCorr:2.47, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):
- Putative nucleoside diphosphate kinase OS=Homo sapiens GN=NME2P1 PE=5 SV=1 - [NDK8_HUMAN]
- Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 - [NDKA_HUMAN]
- Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1 - [NDKB_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	58.02875	29.51801	G			9
2	173.05570	87.03149	D	994.47753	497.74240	8
3	320.12412	160.56570	F	879.45058	440.22893	7
4	480.15477	240.58102	C-Carbamidomethyl	732.38216	366.69472	6
5	593.23884	297.12306	I	572.35150	286.67939	5
6	721.29742	361.15235	Q	459.26743	230.13735	4
7	820.36584	410.68656	V	331.20885	166.10806	3

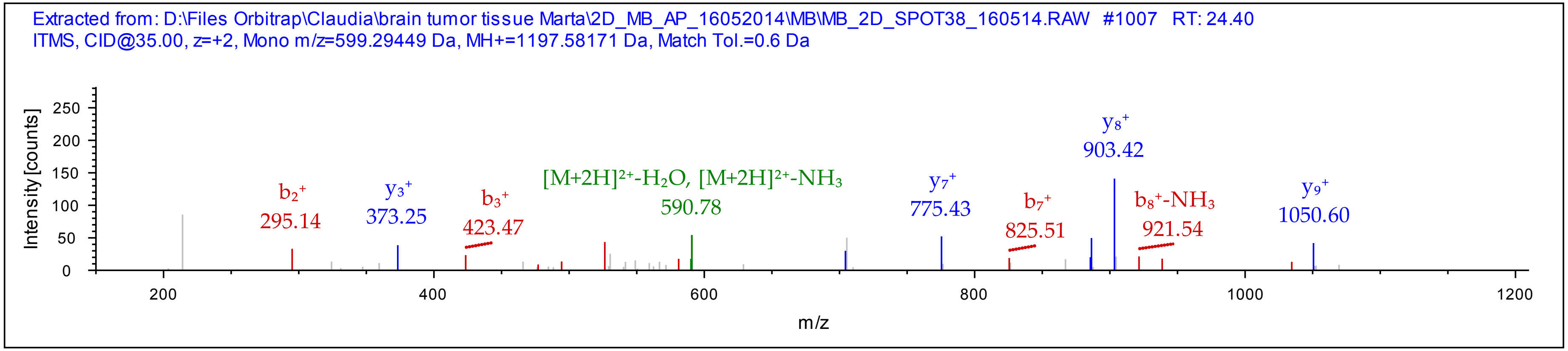
8	877.38731	439.19729	G	232.14043	116.57385	2
9			R	175.11896	88.06312	1



Sequence: FMQASEDLLK, M2-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 599.29449 Da (-0.18 mmu/-0.3 ppm), MH+: 1197.58171 Da, RT: 24.40 min,
Identified with: Sequest HT (v1.3); XCorr:2.24, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 - [NDKA_HUMAN]

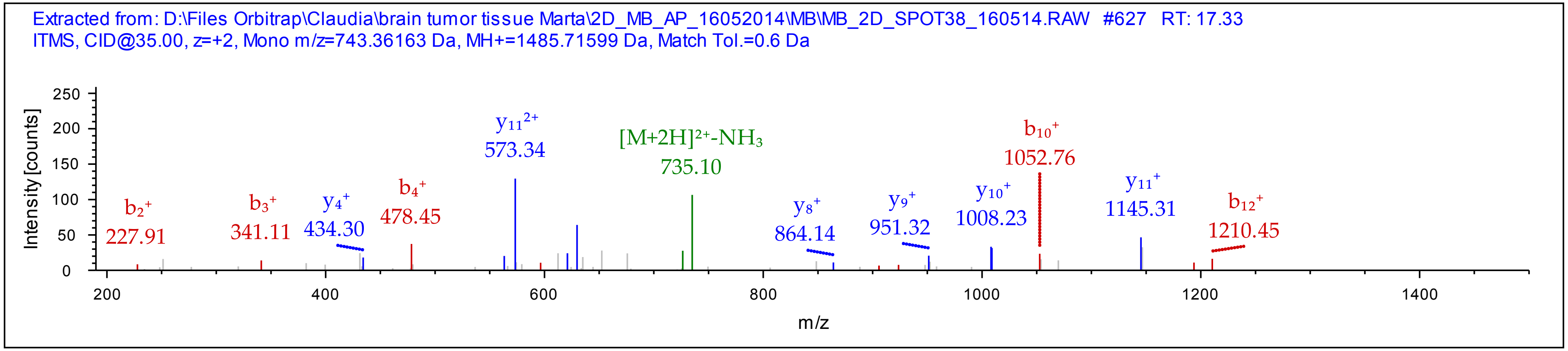
#1	**b$^+$**	**b^{2+}**	**Seq.**	**y$^+$**	**y^{2+}**	**#2**
1	148.07570	74.54149	F			10
2	295.11111	148.05919	M-Oxidation	1050.51365	525.76046	9
3	423.16969	212.08848	Q	903.47823	452.24275	8
4	494.20681	247.60704	A	775.41965	388.21346	7
5	581.23884	291.12306	S	704.38253	352.69490	6
6	710.28144	355.64436	E	617.35050	309.17889	5
7	825.30839	413.15783	D	488.30790	244.65759	4
8	938.39246	469.69987	L	373.28095	187.14411	3
9	1051.47653	526.24190	L	260.19688	130.60208	2
10			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT38_160514.RAW #1007 RT: 24.40
ITMS, CID@35.00, z=+2, Mono m/z=599.29449 Da, MH+=1197.58171 Da, Match Tol.=0.6 Da

Sequence: NIIHGSDSVESAEK, Charge: +2, Monoisotopic m/z: 743.36163 Da (-1.03 mmu/-1.38 ppm), MH+: 1485.71599 Da, RT: 17.33 min,
Identified with: Sequest HT (v1.3); XCorr:2.01, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 - [NDKA_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	115.05021	58.02874	N			14
2	228.13428	114.57078	I	1371.67511	686.34119	13
3	341.21835	171.11281	I	1258.59104	629.79916	12
4	478.27726	239.64227	H	1145.50697	573.25712	11
5	535.29873	268.15300	G	1008.44806	504.72767	10
6	622.33076	311.66902	S	951.42659	476.21693	9
7	737.35771	369.18249	D	864.39456	432.70092	8
8	824.38974	412.69851	S	749.36761	375.18744	7
9	923.45816	462.23272	V	662.33558	331.67143	6
10	1052.50076	526.75402	E	563.26716	282.13722	5
11	1139.53279	570.27003	S	434.22456	217.61592	4
12	1210.56991	605.78859	A	347.19253	174.09990	3
13	1339.61251	670.30989	E	276.15541	138.58134	2
14			K	147.11281	74.06004	1

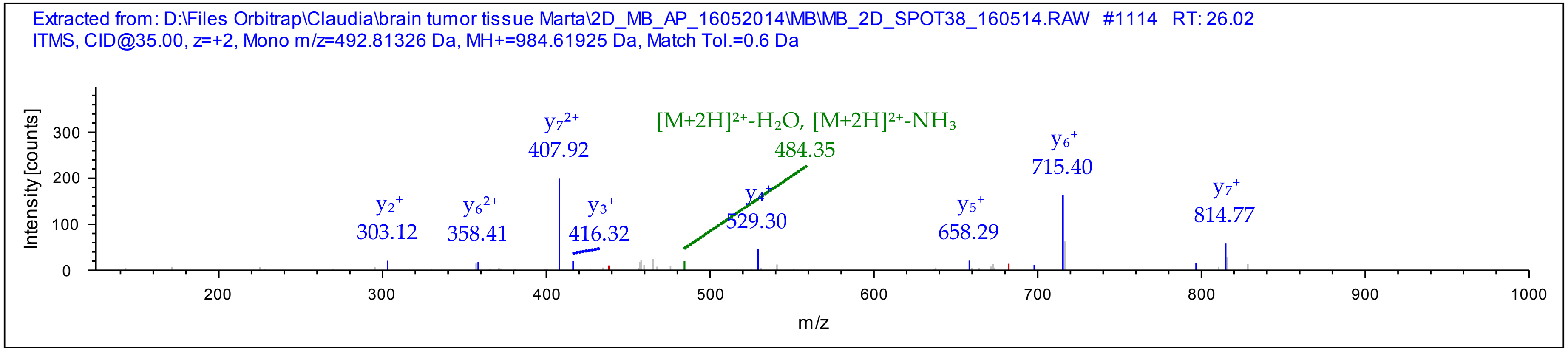


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT38_160514.RAW #627 RT: 17.33
ITMS, CID@35.00, z=+2, Mono m/z=743.36163 Da, MH+=1485.71599 Da, Match Tol.=0.6 Da

Sequence: GLVGEIIKR, Charge: +2, Monoisotopic m/z: 492.81326 Da (-0.43 mmu/-0.87 ppm), MH+: 984.61925 Da, RT: 26.02 min,
Identified with: Sequest HT (v1.3); XCorr:1.82, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):
- Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 - [NDKA_HUMAN]
- Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1 - [NDKB_HUMAN]

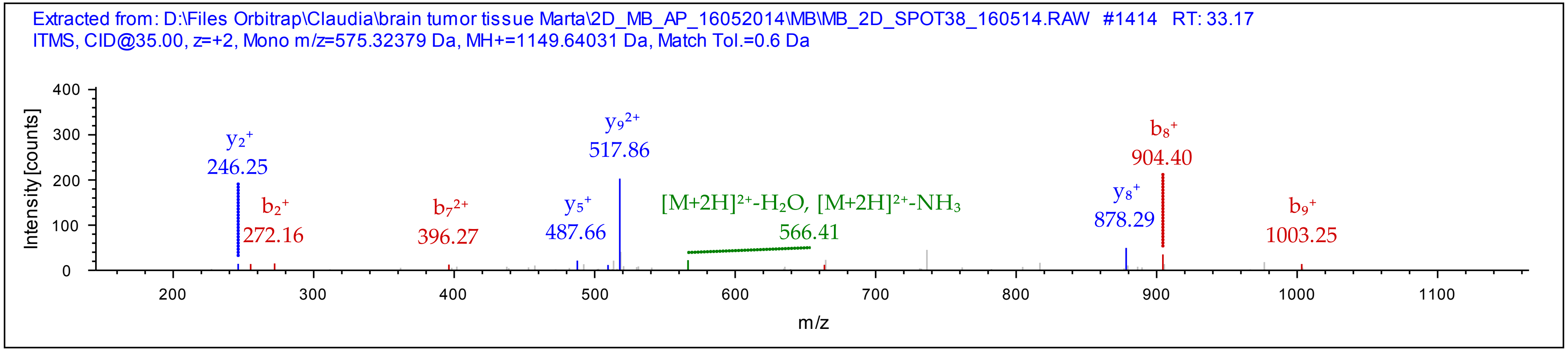
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	58.02875	29.51801	G			9
2	171.11282	86.06005	L	927.59863	464.30295	8
3	270.18124	135.59426	V	814.51456	407.76092	7
4	327.20271	164.10499	G	715.44614	358.22671	6
5	456.24531	228.62629	E	658.42467	329.71597	5
6	569.32938	285.16833	I	529.38207	265.19467	4
7	682.41345	341.71036	I	416.29800	208.65264	3
8	810.50842	405.75785	K	303.21393	152.11060	2
9			R	175.11896	88.06312	1



Sequence: DRPFFAGLVK, Charge: +2, Monoisotopic m/z: 575.32379 Da (-0.63 mmu/-1.1 ppm), MH+: 1149.64031 Da, RT: 33.17 min,
Identified with: Sequest HT (v1.3); XCorr:1.77, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-NH_3

Protein references (1):
- Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 - [NDKA_HUMAN]

#1	b^{+}	b^{2+}	Seq.	y^{+}	y^{2+}	#2
1	116.03423	58.52075	D			10
2	272.13535	136.57131	R	1034.61462	517.81095	9
3	369.18812	185.09770	P	878.51350	439.76039	8
4	516.25654	258.63191	F	781.46073	391.23400	7
5	663.32496	332.16612	F	634.39231	317.69979	6
6	734.36208	367.68468	A	487.32389	244.16558	5
7	791.38355	396.19541	G	416.28677	208.64702	4
8	904.46762	452.73745	L	359.26530	180.13629	3
9	1003.53604	502.27166	V	246.18123	123.59425	2
10			K	147.11281	74.06004	1

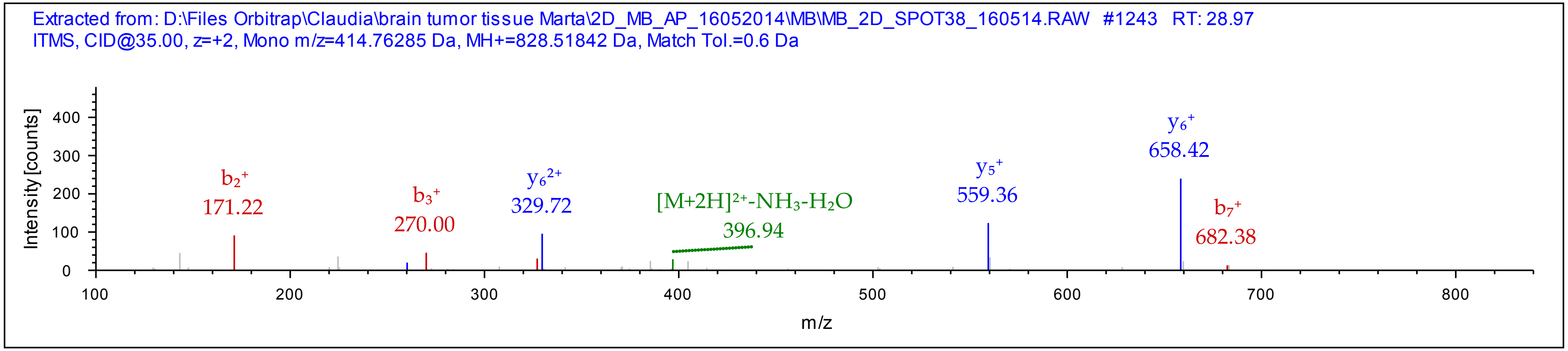


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT38_160514.RAW #1414 RT: 33.17
ITMS, CID@35.00, z=+2, Mono m/z=575.32379 Da, MH+=1149.64031 Da, Match Tol.=0.6 Da

Sequence: GLVGEIIK, Charge: +2, Monoisotopic m/z: 414.76285 Da (-0.28 mmu/-0.68 ppm), MH+: 828.51842 Da, RT: 28.97 min,
Identified with: Sequest HT (v1.3); XCorr:1.77, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (2):
- Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 - [NDKA_HUMAN]
- Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1 - [NDKB_HUMAN]

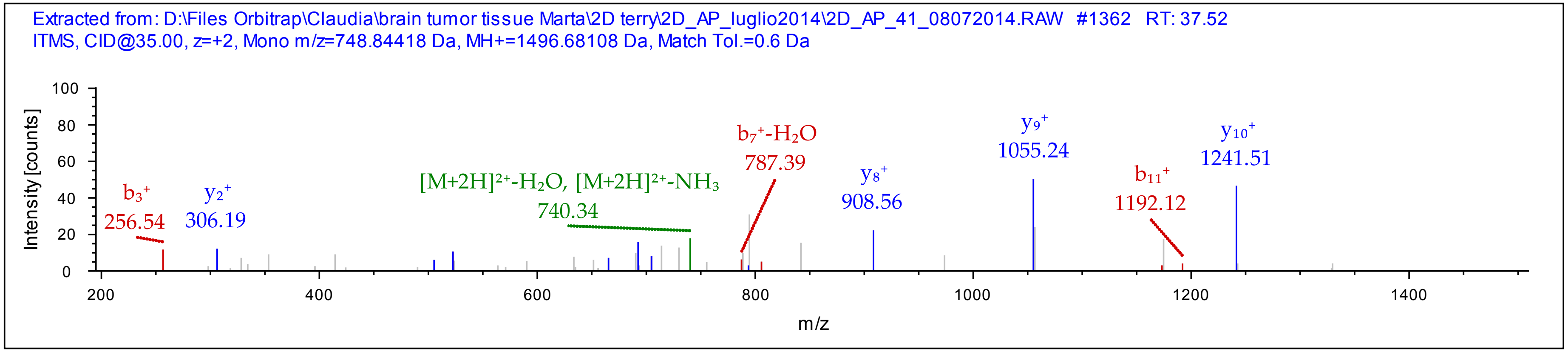
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	58.02875	29.51801	G			8
2	171.11282	86.06005	L	771.49751	386.25239	7
3	270.18124	135.59426	V	658.41344	329.71036	6
4	327.20271	164.10499	G	559.34502	280.17615	5
5	456.24531	228.62629	E	502.32355	251.66541	4
6	569.32938	285.16833	I	373.28095	187.14411	3
7	682.41345	341.71036	I	260.19688	130.60208	2
8			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT38_160514.RAW #1243 RT: 28.97
ITMS, CID@35.00, z=+2, Mono m/z=414.76285 Da, MH+=828.51842 Da, Match Tol.=0.6 Da
Intensity [counts]
400
300
200
100
0
b_2^+
171.22
b_3^+
270.00
y_6^{2+}
329.72
$[M+2H]^{2+}$-NH_3-H_2O
396.94
y_5^+
559.36
y_6^+
658.42
b_7^+
682.38
100
200
300
400
500
600
700
800
m/z

Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*
41	P02511	Alpha-crystallin B chain	20.2	6.8	12.1	17.71%	3	3	PA	4.43E-04	3.2 ↑ in PA

Sequence: APSWFDTGLSEMR, Charge: +2, Monoisotopic m/z: 748.84418 Da (-1.42 mmu/-1.9 ppm), MH+: 1496.68108 Da, RT: 37.52 min,
Identified with: Sequest HT (v1.3); XCorr:1.92, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3
Protein references (1):
- Alpha-crystallin B chain OS=Homo sapiens GN=CRYAB PE=1 SV=2 - [CRYAB_HUMAN]

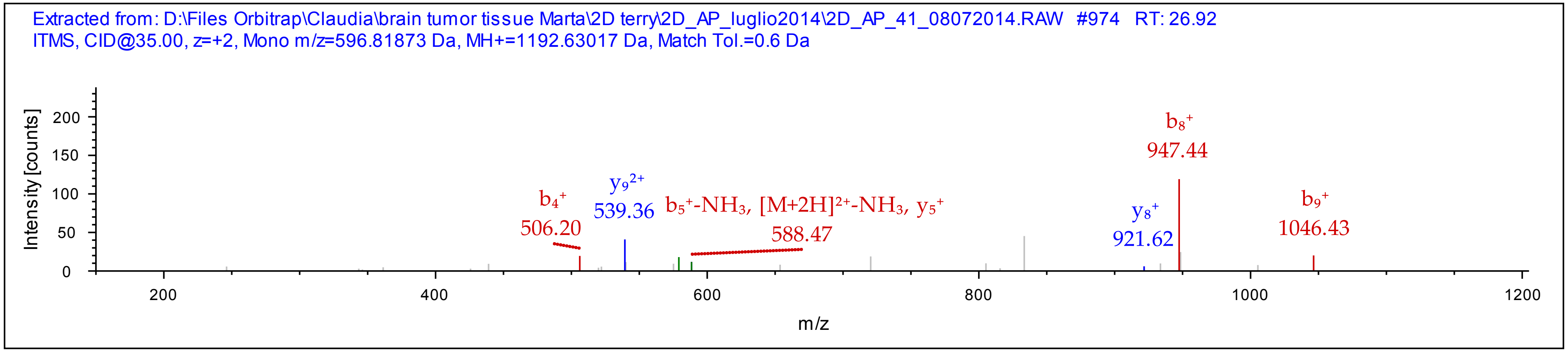
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			13
2	169.09717	85.05222	P	1425.64680	713.32704	12
3	256.12920	128.56824	S	1328.59403	664.80065	11
4	442.20852	221.60790	W	1241.56200	621.28464	10
5	589.27694	295.14211	F	1055.48268	528.24498	9
6	704.30389	352.65558	D	908.41426	454.71077	8
7	805.35157	403.17942	T	793.38731	397.19729	7
8	862.37304	431.69016	G	692.33963	346.67345	6
9	975.45711	488.23219	L	635.31816	318.16272	5
10	1062.48914	531.74821	S	522.23409	261.62068	4
11	1191.53174	596.26951	E	435.20206	218.10467	3
12	1322.57224	661.78976	M	306.15946	153.58337	2
13			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_AP_luglio2014\2D_AP_41_08072014.RAW #1362 RT: 37.52
ITMS, CID@35.00, z=+2, Mono m/z=748.84418 Da, MH+=1496.68108 Da, Match Tol.=0.6 Da

Sequence: DRFSVNLDVK, Charge: +2, Monoisotopic m/z: 596.81873 Da (-0.97 mmu/-1.63 ppm), MH+: 1192.63017 Da, RT: 26.92 min,

Identified with: Sequest HT (v1.3); XCorr:1.54, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Alpha-crystallin B chain OS=Homo sapiens GN=CRYAB PE=1 SV=2 - [CRYAB_HUMAN]

#1	**b$^+$**	**b^{2+}**	**Seq.**	**y$^+$**	**y^{2+}**	**#2**
1	116.03423	58.52075	D			10
2	272.13535	136.57131	R	1077.60517	539.30622	9
3	419.20377	210.10552	F	921.50405	461.25566	8
4	506.23580	253.62154	S	774.43563	387.72145	7
5	605.30422	303.15575	V	687.40360	344.20544	6
6	719.34715	360.17721	N	588.33518	294.67123	5
7	832.43122	416.71925	L	474.29225	237.64976	4
8	947.45817	474.23272	D	361.20818	181.10773	3
9	1046.52659	523.76693	V	246.18123	123.59425	2
10			K	147.11281	74.06004	1

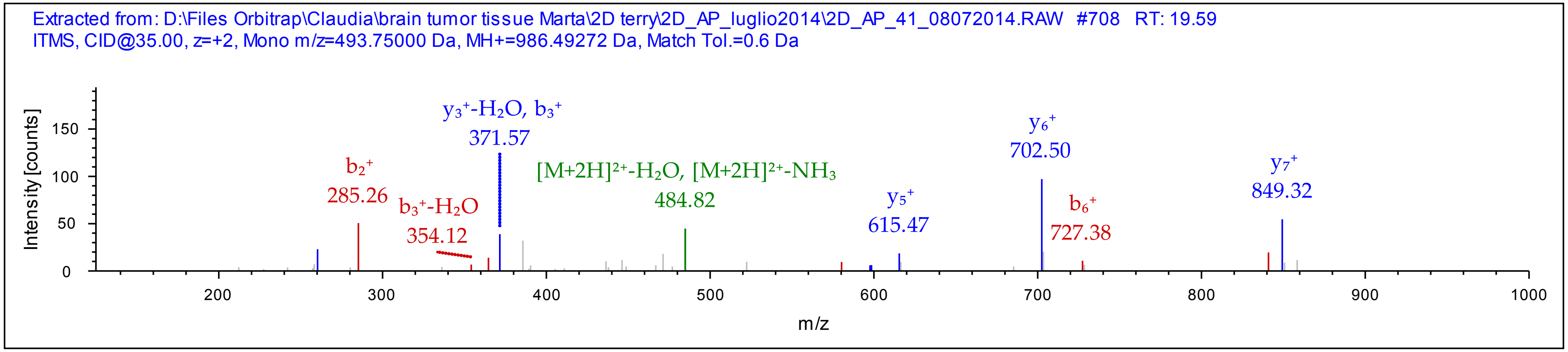

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_AP_luglio2014\2D_AP_41_08072014.RAW #974 RT: 26.92
ITMS, CID@35.00, z=+2, Mono m/z=596.81873 Da, MH+=1192.63017 Da, Match Tol.=0.6 Da

Sequence: HFSPEELK, Charge: +2, Monoisotopic m/z: 493.75000 Da (-0.74 mmu/-1.51 ppm), MH+: 986.49272 Da, RT: 19.59 min,
Identified with: Sequest HT (v1.3); XCorr:1.46, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da

Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Alpha-crystallin B chain OS=Homo sapiens GN=CRYAB PE=1 SV=2 - [CRYAB_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	138.06619	69.53673	H			8
2	285.13461	143.07094	F	849.43530	425.22129	7
3	372.16664	186.58696	S	702.36688	351.68708	6
4	469.21941	235.11334	P	615.33485	308.17106	5
5	598.26201	299.63464	E	518.28208	259.64468	4
6	727.30461	364.15594	E	389.23948	195.12338	3
7	840.38868	420.69798	L	260.19688	130.60208	2
8			K	147.11281	74.06004	1

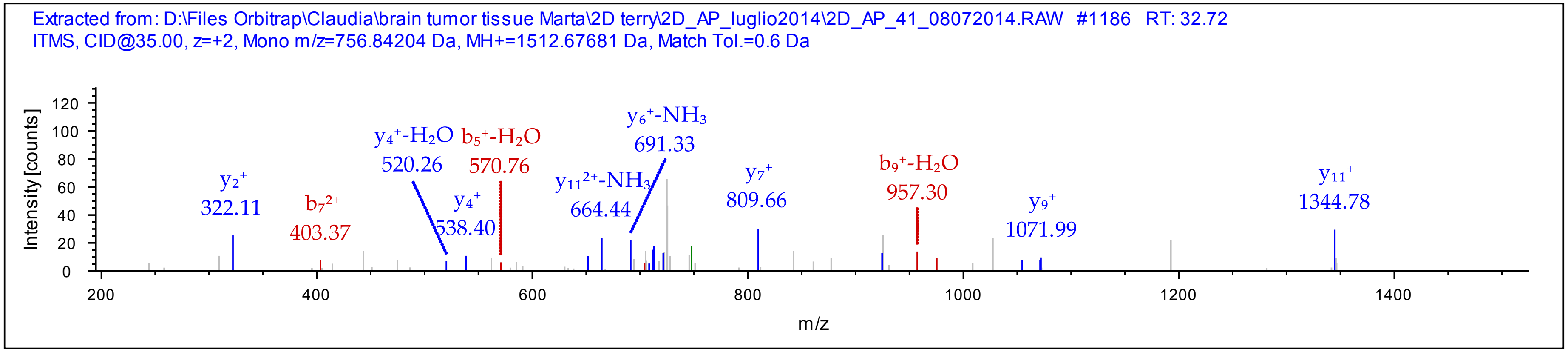

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_AP_luglio2014\2D_AP_41_08072014.RAW #708 RT: 19.59
ITMS, CID@35.00, z=+2, Mono m/z=493.75000 Da, MH+=986.49272 Da, Match Tol.=0.6 Da

Sequence: APSWFDTGLSEMR, M12-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 756.84204 Da (-1.02 mmu/-1.34 ppm), MH+: 1512.67681 Da, RT: 32.72 min,
Identified with: Sequest HT (v1.3); XCorr:1.43, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da

Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Alpha-crystallin B chain OS=Homo sapiens GN=CRYAB PE=1 SV=2 - [CRYAB_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			13
2	169.09717	85.05222	P	1441.64172	721.32450	12
3	256.12920	128.56824	S	1344.58895	672.79811	11
4	442.20852	221.60790	W	1257.55692	629.28210	10
5	589.27694	295.14211	F	1071.47760	536.24244	9
6	704.30389	352.65558	D	924.40918	462.70823	8
7	805.35157	403.17942	T	809.38223	405.19475	7
8	862.37304	431.69016	G	708.33455	354.67091	6
9	975.45711	488.23219	L	651.31308	326.16018	5
10	1062.48914	531.74821	S	538.22901	269.61814	4
11	1191.53174	596.26951	E	451.19698	226.10213	3
12	1338.56715	669.78721	M-Oxidation	322.15438	161.58083	2
13			R	175.11896	88.06312	1

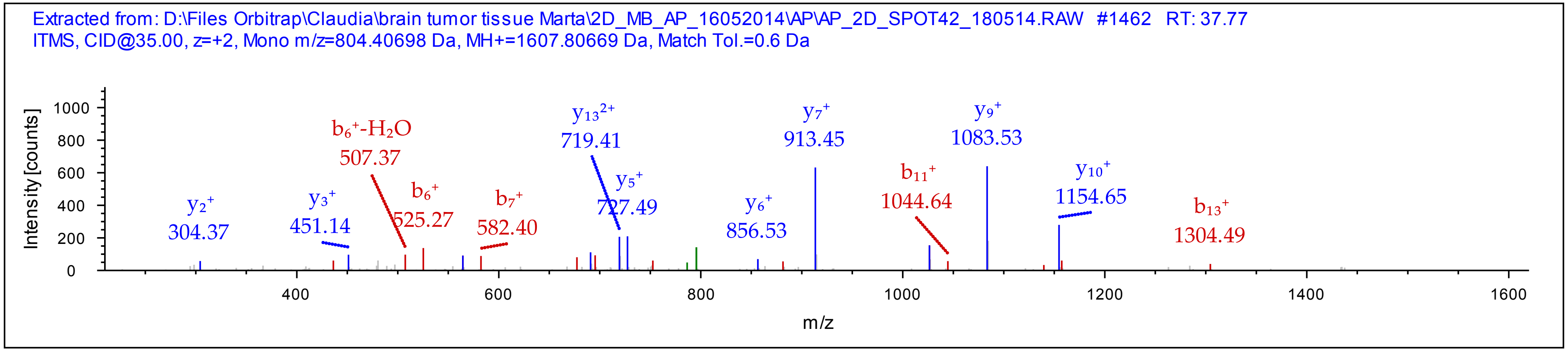

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_AP_luglio2014\2D_AP_41_08072014.RAW #1186 RT: 32.72
ITMS, CID@35.00, z=+2, Mono m/z=756.84204 Da, MH+=1512.67681 Da, Match Tol.=0.6 Da

Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
42	P02792	Ferritin light chain	19.9	5.5	29.9	28.57%	3	3	PA	1.19E-04	3.4	↑ in PA

Sequence: LGGPEAGLGEYLFER, Charge: +2, Monoisotopic m/z: 804.40698 Da (+0.1 mmu/+0.13 ppm), MH+: 1607.80669 Da, RT: 37.77 min,
Identified with: Sequest HT (v1.3); XCorr:3.72, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

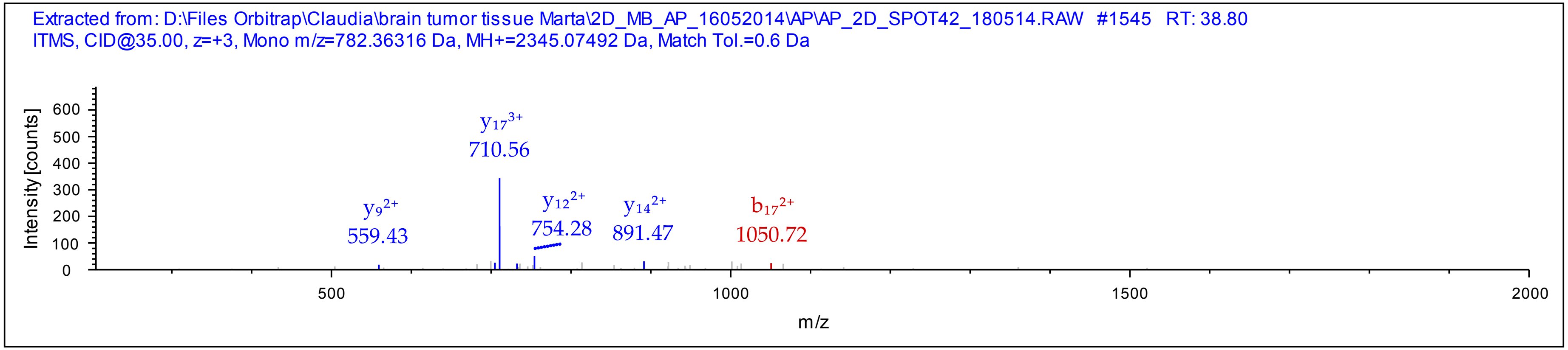
Protein references (1):
- Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 - [FRIL_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	114.09135	57.54931	L			15
2	171.11282	86.06005	G	1494.72241	747.86484	14
3	228.13429	114.57078	G	1437.70094	719.35411	13
4	325.18706	163.09717	P	1380.67947	690.84337	12
5	454.22966	227.61847	E	1283.62670	642.31699	11
6	525.26678	263.13703	A	1154.58410	577.79569	10
7	582.28825	291.64776	G	1083.54698	542.27713	9
8	695.37232	348.18980	L	1026.52551	513.76639	8
9	752.39379	376.70053	G	913.44144	457.22436	7
10	881.43639	441.22183	E	856.41997	428.71362	6
11	1044.49971	522.75349	Y	727.37737	364.19232	5
12	1157.58378	579.29553	L	564.31405	282.66066	4
13	1304.65220	652.82974	F	451.22998	226.11863	3
14	1433.69480	717.35104	E	304.16156	152.58442	2
15			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT42_180514.RAW #1462 RT: 37.77
ITMS, CID@35.00, z=+2, Mono m/z=804.40698 Da, MH+=1607.80669 Da, Match Tol.=0.6 Da

Sequence: TDPHLCDFLETHFLDEEVK, C6-Carbamidomethyl (57.02146 Da)
Charge: +3, Monoisotopic m/z: 782.36316 Da (-0.2 mmu/-0.26 ppm), MH+: 2345.07492 Da, RT: 38.80 min,
Identified with: Sequest HT (v1.3); XCorr:2.11, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3
Protein references (1):
- Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 - [FRIL_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	102.05496	51.53112	34.68984	T				19
2	217.08191	109.04459	73.03215	D	2244.02786	1122.51757	748.68080	18
3	314.13468	157.57098	105.38308	P	2129.00091	1065.00409	710.33849	17
4	451.19359	226.10043	151.06938	H	2031.94814	1016.47771	677.98756	16
5	564.27766	282.64247	188.76407	L	1894.88923	947.94825	632.30126	15
6	724.30831	362.65779	242.10762	C-Carbamidomethyl	1781.80516	891.40622	594.60657	14
7	839.33526	420.17127	280.44994	D	1621.77450	811.39089	541.26302	13
8	986.40368	493.70548	329.47274	F	1506.74755	753.87741	502.92070	12
9	1099.48775	550.24751	367.16743	L	1359.67913	680.34320	453.89789	11
10	1228.53035	614.76881	410.18163	E	1246.59506	623.80117	416.20320	10
11	1329.57803	665.29265	443.86419	T	1117.55246	559.27987	373.18900	9
12	1466.63694	733.82211	489.55050	H	1016.50478	508.75603	339.50644	8
13	1613.70536	807.35632	538.57330	F	879.44587	440.22657	293.82014	7
14	1726.78943	863.89835	576.26799	L	732.37745	366.69236	244.79733	6
15	1841.81638	921.41183	614.61031	D	619.29338	310.15033	207.10264	5
16	1970.85898	985.93313	657.62451	E	504.26643	252.63685	168.76033	4
17	2099.90158	1050.45443	700.63871	E	375.22383	188.11555	125.74613	3
18	2198.97000	1099.98864	733.66152	V	246.18123	123.59425	82.73193	2
19				K	147.11281	74.06004	49.70912	1



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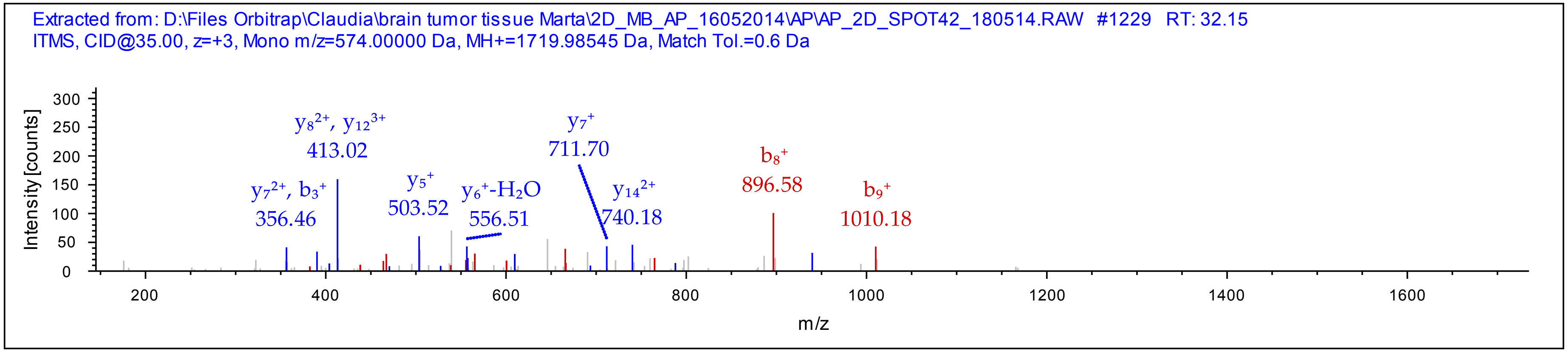
ITMS, CID@35.00, z=+3, Mono m/z=782.36316 Da, MH+=2345.07492 Da, Match Tol.=0.6 Da

Sequence: KLNQALLDLHALGSAR, Charge: +3, Monoisotopic m/z: 574.00000 Da (-0.36 mmu/-0.62 ppm), MH+: 1719.98545 Da, RT: 32.15 min,
Identified with: Sequest HT (v1.3); XCorr:1.52, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 - [FRIL_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	129.10225	65.05476	43.70560	K				16
2	242.18632	121.59680	81.40029	L	1591.89154	796.44941	531.30203	15
3	356.22925	178.61826	119.41460	N	1478.80747	739.90737	493.60734	14
4	484.28783	242.64755	162.10079	Q	1364.76454	682.88591	455.59303	13
5	555.32495	278.16611	185.77983	A	1236.70596	618.85662	412.90684	12
6	668.40902	334.70815	223.47452	L	1165.66884	583.33806	389.22780	11
7	781.49309	391.25018	261.16921	L	1052.58477	526.79602	351.53311	10
8	896.52004	448.76366	299.51153	D	939.50070	470.25399	313.83842	9
9	1009.60411	505.30569	337.20622	L	824.47375	412.74051	275.49610	8
10	1146.66302	573.83515	382.89252	H	711.38968	356.19848	237.80141	7
11	1217.70014	609.35371	406.57156	A	574.33077	287.66902	192.11511	6
12	1330.78421	665.89574	444.26625	L	503.29365	252.15046	168.43607	5
13	1387.80568	694.40648	463.27341	G	390.20958	195.60843	130.74138	4
14	1474.83771	737.92249	492.28409	S	333.18811	167.09769	111.73422	3
15	1545.87483	773.44105	515.96313	A	246.15608	123.58168	82.72354	2
16				R	175.11896	88.06312	59.04450	1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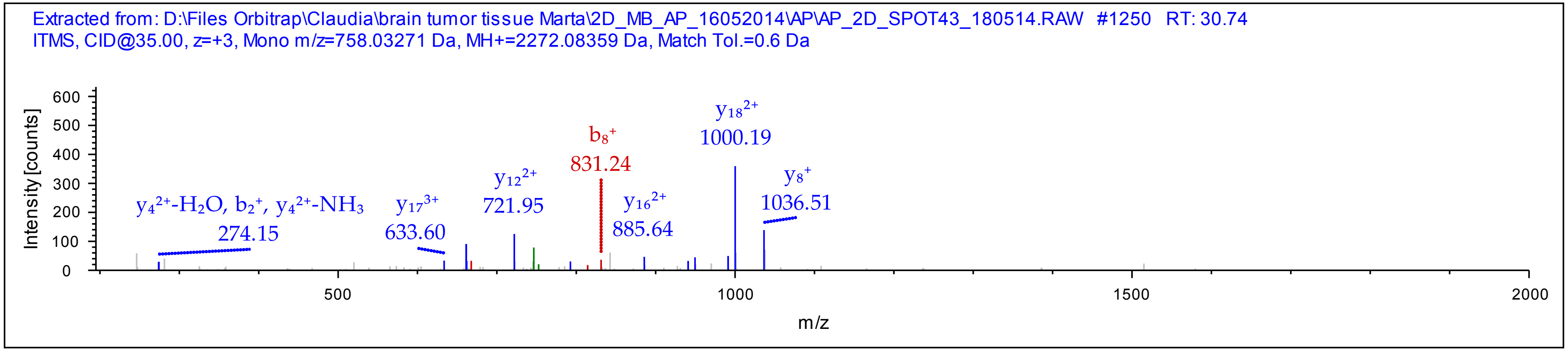
ITMS, CID@35.00, z=+3, Mono m/z=574.00000 Da, MH+=1719.98545 Da, Match Tol.=0.6 Da

Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
43	P30626	Sorcin	21.7	5.3	30.2	43.43%	6	6	PA	4.60E-04	2.3	↑ in PA

Sequence: CLTQSGIAGGYKPFNLETCR, C1-Carbamidomethyl (57.02146 Da), C19-Carbamidomethyl (57.02146 Da)
Charge: +3, Monoisotopic m/z: 758.03271 Da (-0.47 mmu/-0.62 ppm), MH+: 2272.08359 Da, RT: 30.74 min,
Identified with: Sequest HT (v1.3); XCorr:2.97, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Sorcin OS=Homo sapiens GN=SRI PE=1 SV=1 - [SORCN_HUMAN]

#1	b^{+}	b^{2+}	b^{3+}	Seq.	y^{+}	y^{2+}	y^{3+}	#2
1	161.03793	81.02260	54.35083	C-Carbamidomethyl				20
2	274.12200	137.56464	92.04552	L	2112.05434	1056.53081	704.68963	19
3	375.16968	188.08848	125.72808	T	1998.97027	999.98877	666.99494	18
4	503.22826	252.11777	168.41427	Q	1897.92259	949.46493	633.31238	17
5	590.26029	295.63378	197.42495	S	1769.86401	885.43564	590.62619	16
6	647.28176	324.14452	216.43210	G	1682.83198	841.91963	561.61551	15
7	760.36583	380.68655	254.12679	I	1625.81051	813.40889	542.60835	14
8	831.40295	416.20511	277.80583	A	1512.72644	756.86686	504.91366	13
9	888.42442	444.71585	296.81299	G	1441.68932	721.34830	481.23462	12
10	945.44589	473.22658	315.82015	G	1384.66785	692.83756	462.22747	11
11	1108.50921	554.75824	370.17459	Y	1327.64638	664.32683	443.22031	10
12	1236.60418	618.80573	412.87291	K	1164.58306	582.79517	388.86587	9
13	1333.65695	667.33211	445.22383	P	1036.48809	518.74768	346.16755	8
14	1480.72537	740.86632	494.24664	F	939.43532	470.22130	313.81662	7
15	1594.76830	797.88779	532.26095	N	792.36690	396.68709	264.79382	6
16	1707.85237	854.42982	569.95564	L	678.32397	339.66562	226.77951	5
17	1836.89497	918.95112	612.96984	E	565.23990	283.12359	189.08482	4
18	1937.94265	969.47496	646.65240	T	436.19730	218.60229	146.07062	3
19	2097.97330	1049.49029	699.99595	C-Carbamidomethyl	335.14962	168.07845	112.38806	2
20				R	175.11896	88.06312	59.04450	1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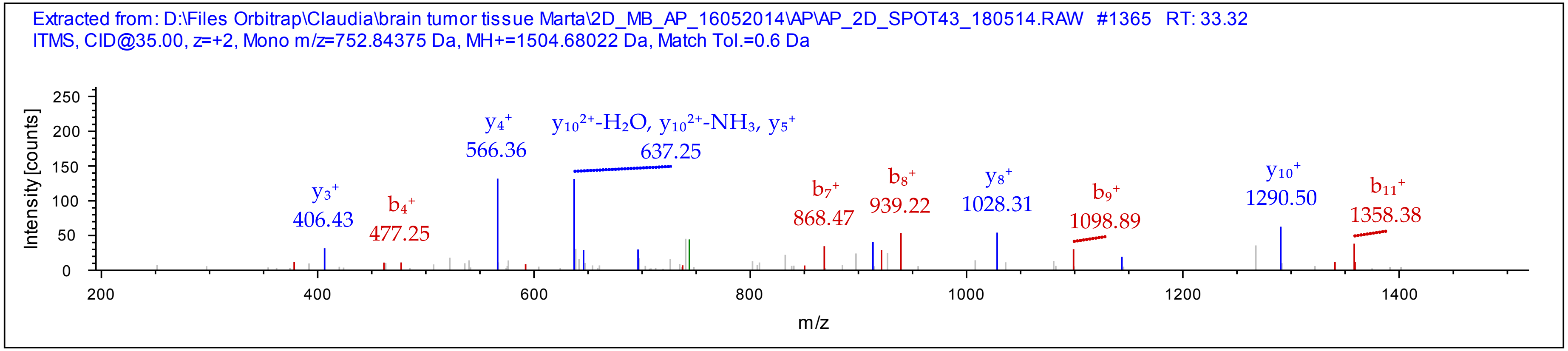
ITMS, CID@35.00, z=+3, Mono m/z=758.03271 Da, MH+=2272.08359 Da, Match Tol.=0.6 Da

Sequence: ITFDDYIACCVK, C9-Carbamidomethyl (57.02146 Da), C10-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 752.84375 Da (-0.45 mmu/-0.6 ppm), MH+: 1504.68022 Da, RT: 33.32 min,
Identified with: Sequest HT (v1.3); XCorr:2.85, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Sorcin OS=Homo sapiens GN=SRI PE=1 SV=1 - [SORCN_HUMAN]

#1	**b⁺**	**b²⁺**	**Seq.**	**y⁺**	**y²⁺**	**#2**
1	114.09135	57.54931	I			12
2	215.13903	108.07315	T	1391.59705	696.30216	11
3	362.20745	181.60736	F	1290.54937	645.77832	10
4	477.23440	239.12084	D	1143.48095	572.24411	9
5	592.26135	296.63431	D	1028.45400	514.73064	8
6	755.32467	378.16597	Y	913.42705	457.21716	7
7	868.40874	434.70801	I	750.36373	375.68550	6
8	939.44586	470.22657	A	637.27966	319.14347	5
9	1099.47651	550.24189	C-Carbamidomethyl	566.24254	283.62491	4
10	1259.50716	630.25722	C-Carbamidomethyl	406.21189	203.60958	3
11	1358.57558	679.79143	V	246.18123	123.59425	2
12			K	147.11281	74.06004	1

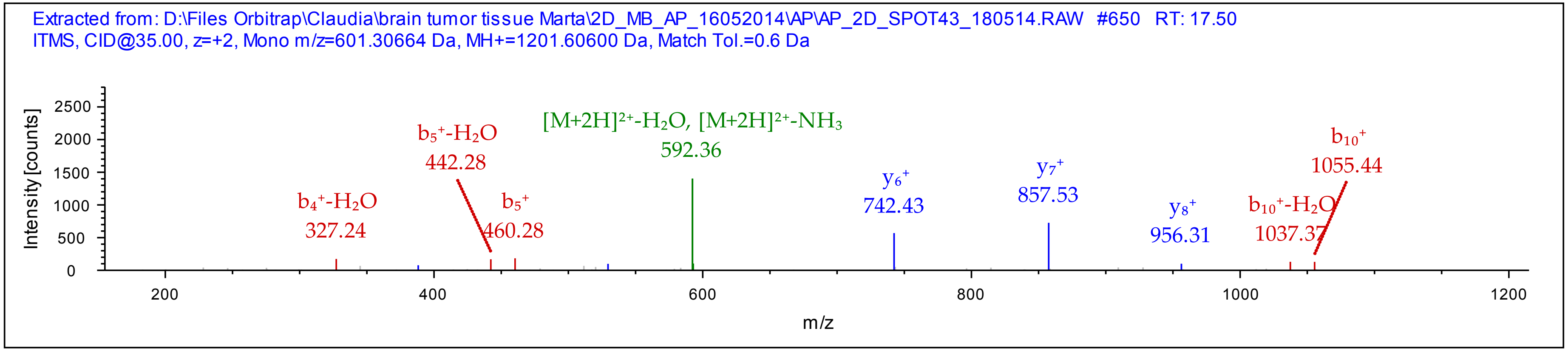


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT43_180514.RAW #1365 RT: 33.32
ITMS, CID@35.00, z=+2, Mono m/z=752.84375 Da, MH+=1504.68022 Da, Match Tol.=0.6 Da

Sequence: SGTVDPQELQK, Charge: +2, Monoisotopic m/z: 601.30664 Da (+0.02 mmu/+0.04 ppm), MH+: 1201.60600 Da, RT: 17.50 min,
Identified with: Sequest HT (v1.3); XCorr:2.58, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Sorcin OS=Homo sapiens GN=SRI PE=1 SV=1 - [SORCN_HUMAN]

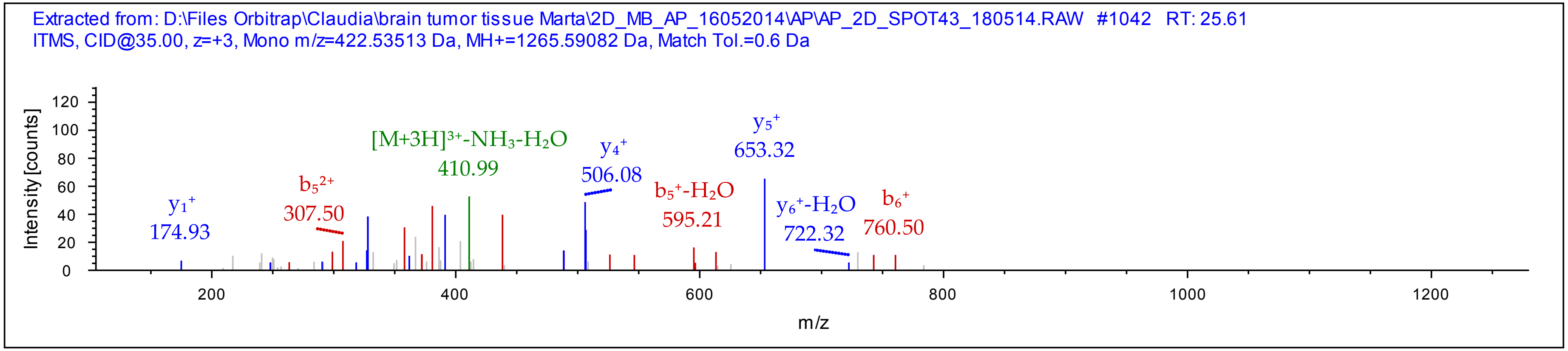
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	88.03931	44.52329	S			11
2	145.06078	73.03403	G	1114.57393	557.79060	10
3	246.10846	123.55787	T	1057.55246	529.27987	9
4	345.17688	173.09208	V	956.50478	478.75603	8
5	460.20383	230.60555	D	857.43636	429.22182	7
6	557.25660	279.13194	P	742.40941	371.70834	6
7	685.31518	343.16123	Q	645.35664	323.18196	5
8	814.35778	407.68253	E	517.29806	259.15267	4
9	927.44185	464.22456	L	388.25546	194.63137	3
10	1055.50043	528.25385	Q	275.17139	138.08933	2
11			K	147.11281	74.06004	1



Sequence: QHFISFDTDR, Charge: +3, Monoisotopic m/z: 422.53513 Da (-0.05 mmu/-0.12 ppm), MH+: 1265.59082 Da, RT: 25.61 min,
Identified with: Sequest HT (v1.3); XCorr:2.23, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Sorcin OS=Homo sapiens GN=SRI PE=1 SV=1 - [SORCN_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	129.06586	65.03657	43.69347	Q				10
2	266.12477	133.56602	89.37977	H	1137.53239	569.26983	379.84898	9
3	413.19319	207.10023	138.40258	F	1000.47348	500.74038	334.16268	8
4	526.27726	263.64227	176.09727	I	853.40506	427.20617	285.13987	7
5	613.30929	307.15828	205.10795	S	740.32099	370.66413	247.44518	6
6	760.37771	380.69249	254.13075	F	653.28896	327.14812	218.43450	5
7	875.40466	438.20597	292.47307	D	506.22054	253.61391	169.41170	4
8	976.45234	488.72981	326.15563	T	391.19359	196.10043	131.06938	3
9	1091.47929	546.24328	364.49795	D	290.14591	145.57659	97.38682	2
10				R	175.11896	88.06312	59.04450	1

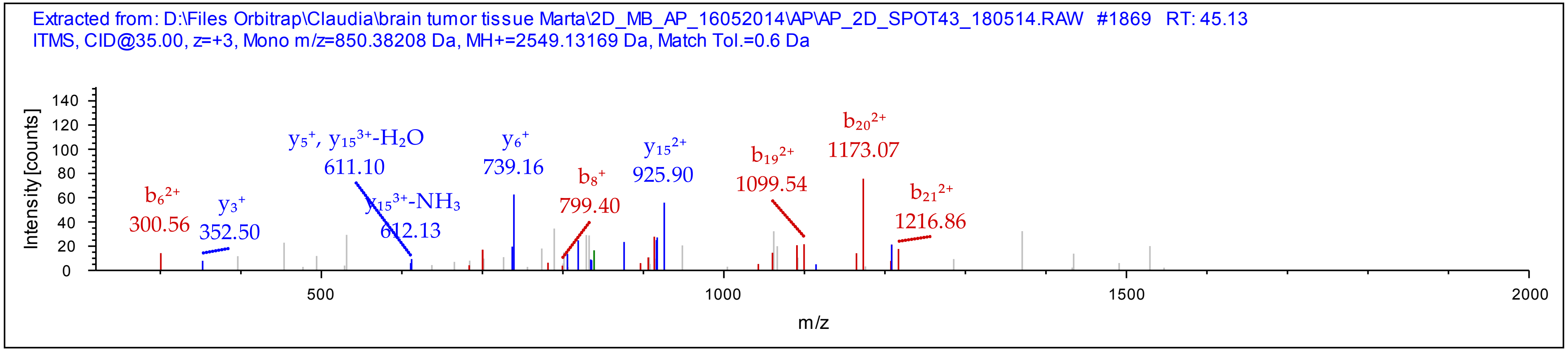

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT43_180514.RAW #1042 RT: 25.61
ITMS, CID@35.00, z=+3, Mono m/z=422.53513 Da, MH+=1265.59082 Da, Match Tol.=0.6 Da

Sequence: DTAQQGVVNFPYDDFIQCVMSV, C18-Carbamidomethyl (57.02146 Da), M20-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 850.38208 Da (-0.24 mmu/-0.28 ppm), MH+: 2549.13169 Da, RT: 45.13 min,
Identified with: Sequest HT (v1.3); XCorr:1.81, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Sorcin OS=Homo sapiens GN=SRI PE=1 SV=1 - [SORCN_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	116.03423	58.52075	39.34959	D				22
2	217.08191	109.04459	73.03215	T	2434.10546	1217.55637	812.04000	21
3	288.11903	144.56315	96.71119	A	2333.05778	1167.03253	778.35744	20
4	416.17761	208.59244	139.39739	Q	2262.02066	1131.51397	754.67840	19
5	544.23619	272.62173	182.08358	Q	2133.96208	1067.48468	711.99221	18
6	601.25766	301.13247	201.09074	G	2005.90350	1003.45539	669.30602	17
7	700.32608	350.66668	234.11354	V	1948.88203	974.94465	650.29886	16
8	799.39450	400.20089	267.13635	V	1849.81361	925.41044	617.27605	15
9	913.43743	457.22235	305.15066	N	1750.74519	875.87623	584.25325	14
10	1060.50585	530.75656	354.17347	F	1636.70226	818.85477	546.23894	13
11	1157.55862	579.28295	386.52439	P	1489.63384	745.32056	497.21613	12
12	1320.62194	660.81461	440.87883	Y	1392.58107	696.79417	464.86521	11
13	1435.64889	718.32808	479.22115	D	1229.51775	615.26251	410.51077	10
14	1550.67584	775.84156	517.56346	D	1114.49080	557.74904	372.16845	9
15	1697.74426	849.37577	566.58627	F	999.46385	500.23556	333.82613	8
16	1810.82833	905.91780	604.28096	I	852.39543	426.70135	284.80333	7
17	1938.88691	969.94709	646.96715	Q	739.31136	370.15932	247.10864	6

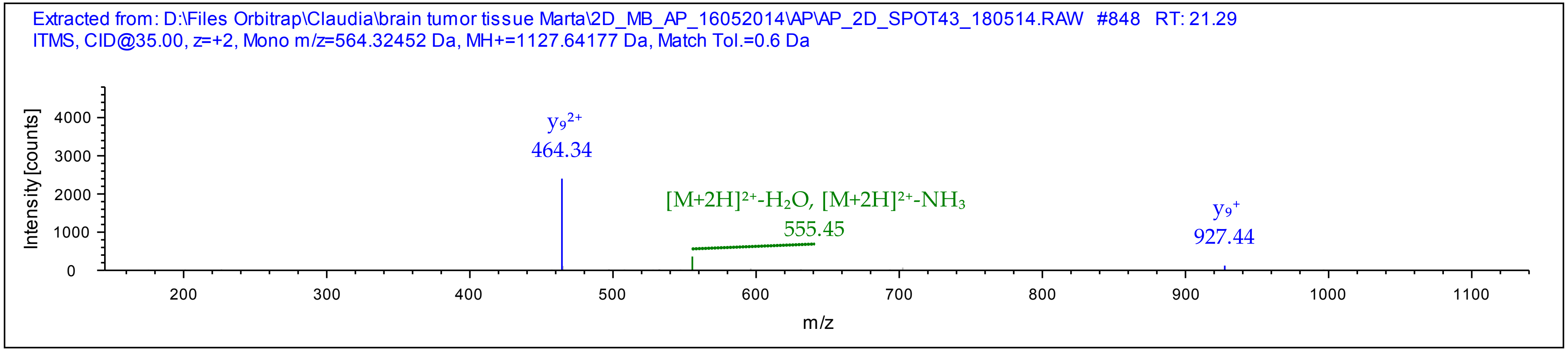
18	2098.91756	1049.96242	700.31070	C-Carbamidomethyl	611.25278	306.13003	204.42244	5
19	2197.98598	1099.49663	733.33351	V	451.22213	226.11470	151.07889	4
20	2345.02140	1173.01434	782.34532	M-Oxidation	352.15371	176.58049	118.05609	3
21	2432.05343	1216.53035	811.35599	S	205.11829	103.06278	69.04428	2
22				V	118.08626	59.54677	40.03360	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT43_180514.RAW #1869 RT: 45.13
ITMS, CID@35.00, z=+3, Mono m/z=850.38208 Da, MH+=2549.13169 Da, Match Tol.=0.6 Da

Sequence: LSPQAVNSIAK, Charge: +2, Monoisotopic m/z: 564.32452 Da (-0.09 mmu/-0.16 ppm), MH+: 1127.64177 Da, RT: 21.29 min,
Identified with: Sequest HT (v1.3); XCorr:1.49, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Sorcin OS=Homo sapiens GN=SRI PE=1 SV=1 - [SORCN_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			11
2	201.12338	101.06533	S	1014.55788	507.78258	10
3	298.17615	149.59171	P	927.52585	464.26656	9
4	426.23473	213.62100	Q	830.47308	415.74018	8
5	497.27185	249.13956	A	702.41450	351.71089	7
6	596.34027	298.67377	V	631.37738	316.19233	6
7	710.38320	355.69524	N	532.30896	266.65812	5
8	797.41523	399.21125	S	418.26603	209.63665	4
9	910.49930	455.75329	I	331.23400	166.12064	3
10	981.53642	491.27185	A	218.14993	109.57860	2
11			K	147.11281	74.06004	1

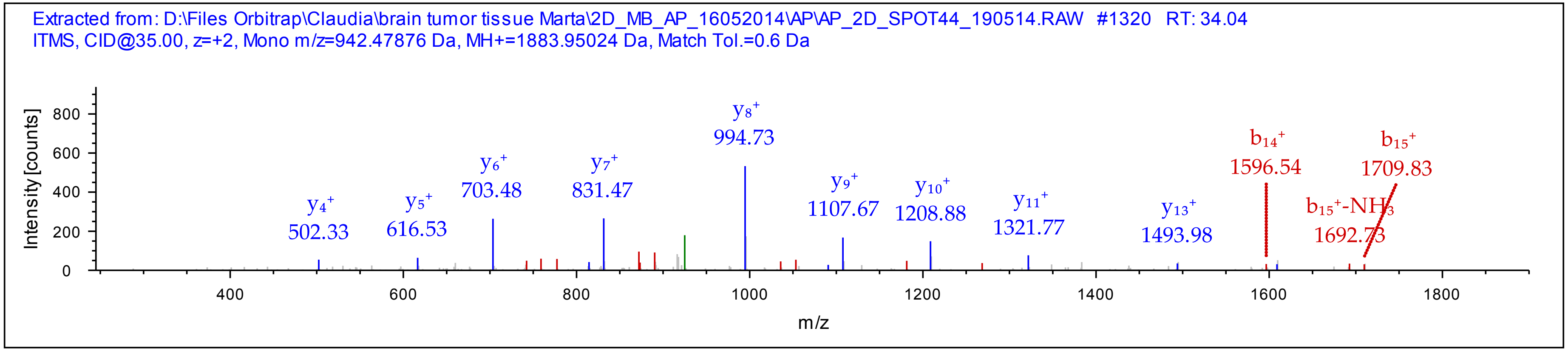

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT43_180514.RAW #848 RT: 21.29
ITMS, CID@35.00, z=+2, Mono m/z=564.32452 Da, MH+=1127.64177 Da, Match Tol.=0.6 Da
Intensity [counts]
0
1000
2000
3000
4000
y_9^{2+}
464.34
$[M+2H]^{2+}$-H_2O, $[M+2H]^{2+}$-NH_3
555.45
y_9^{+}
927.44
200
300
400
500
600
700
800
900
1000
1100
m/z

Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
44	P09211	Glutathione S-transferase P	23.2	5.4	39.4	37.14%	4	4	MB, PA	8.09E-04	2.4	↑ in MB

Sequence: FQDGDLTLYQSNTILR, Charge: +2, Monoisotopic m/z: 942.47876 Da (+0.21 mmu/+0.22 ppm), MH+: 1883.95024 Da, RT: 34.04 min,
Identified with: Sequest HT (v1.3); XCorr:4.46, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]

#1	**b^{+}**	**b^{2+}**	**Seq.**	**y^{+}**	**y^{2+}**	**#2**
1	148.07570	74.54149	F			16
2	276.13428	138.57078	Q	1736.88141	868.94434	15
3	391.16123	196.08425	D	1608.82283	804.91505	14
4	448.18270	224.59499	G	1493.79588	747.40158	13
5	563.20965	282.10846	D	1436.77441	718.89084	12
6	676.29372	338.65050	L	1321.74746	661.37737	11
7	777.34140	389.17434	T	1208.66339	604.83533	10
8	890.42547	445.71637	L	1107.61571	554.31149	9
9	1053.48879	527.24803	Y	994.53164	497.76946	8
10	1181.54737	591.27732	Q	831.46832	416.23780	7
11	1268.57940	634.79334	S	703.40974	352.20851	6
12	1382.62233	691.81480	N	616.37771	308.69249	5
13	1483.67001	742.33864	T	502.33478	251.67103	4
14	1596.75408	798.88068	I	401.28710	201.14719	3
15	1709.83815	855.42271	L	288.20303	144.60515	2
16			R	175.11896	88.06312	1

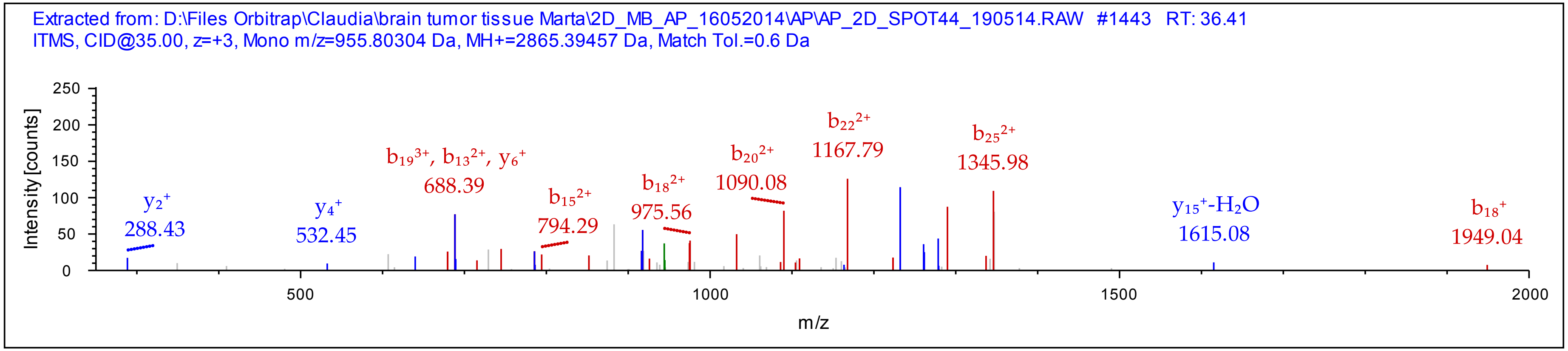


Sequence: TLGLYGKDQQEAALVDMVNDGVEDLR, M17-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 955.80304 Da (+0.31 mmu/+0.33 ppm), MH+: 2865.39457 Da, RT: 36.41 min,
Identified with: Sequest HT (v1.3); XCorr:3.57, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	102.05496	51.53112	34.68984	T				26
2	215.13903	108.07315	72.38453	L	2764.34595	1382.67661	922.12017	25
3	272.16050	136.58389	91.39168	G	2651.26188	1326.13458	884.42548	24
4	385.24457	193.12592	129.08637	L	2594.24041	1297.62384	865.41832	23
5	548.30789	274.65758	183.44081	Y	2481.15634	1241.08181	827.72363	22
6	605.32936	303.16832	202.44797	G	2318.09302	1159.55015	773.36919	21
7	733.42433	367.21580	245.14629	K	2261.07155	1131.03941	754.36203	20
8	848.45128	424.72928	283.48861	D	2132.97658	1066.99193	711.66371	19
9	976.50986	488.75857	326.17480	Q	2017.94963	1009.47845	673.32139	18
10	1104.56844	552.78786	368.86100	Q	1889.89105	945.44916	630.63520	17
11	1233.61104	617.30916	411.87520	E	1761.83247	881.41987	587.94901	16
12	1304.64816	652.82772	435.55424	A	1632.78987	816.89857	544.93481	15
13	1375.68528	688.34628	459.23328	A	1561.75275	781.38001	521.25577	14
14	1488.76935	744.88831	496.92797	L	1490.71563	745.86145	497.57673	13
15	1587.83777	794.42252	529.95077	V	1377.63156	689.31942	459.88204	12
16	1702.86472	851.93600	568.29309	D	1278.56314	639.78521	426.85923	11

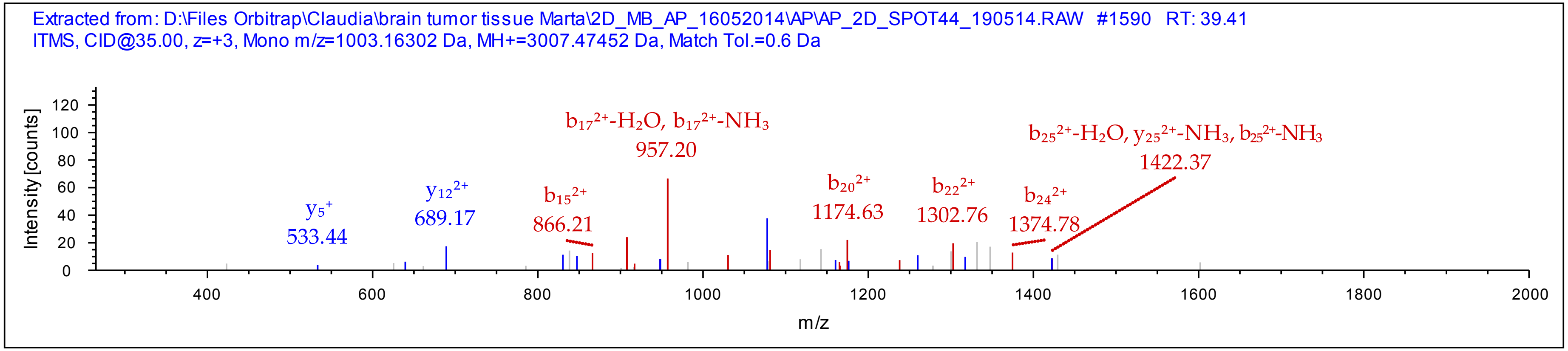
17	1849.90013	925.45370	617.30489	M-Oxidation	1163.53619	582.27173	388.51691	10
18	1948.96855	974.98791	650.32770	V	1016.50077	508.75402	339.50511	9
19	2063.01148	1032.00938	688.34201	N	917.43235	459.21981	306.48230	8
20	2178.03843	1089.52285	726.68433	D	803.38942	402.19835	268.46799	7
21	2235.05990	1118.03359	745.69148	G	688.36247	344.68487	230.12567	6
22	2334.12832	1167.56780	778.71429	V	631.34100	316.17414	211.11852	5
23	2463.17092	1232.08910	821.72849	E	532.27258	266.63993	178.09571	4
24	2578.19787	1289.60257	860.07081	D	403.22998	202.11863	135.08151	3
25	2691.28194	1346.14461	897.76550	L	288.20303	144.60515	96.73919	2
26				R	175.11896	88.06312	59.04450	1



Sequence: MLLADQGQSWKEEVVTVETWQEGSLK, M1-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 1003.16302 Da (+0.88 mmu/+0.88 ppm), MH+: 3007.47452 Da, RT: 39.41 min,
Identified with: Sequest HT (v1.3); XCorr:2.38, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]

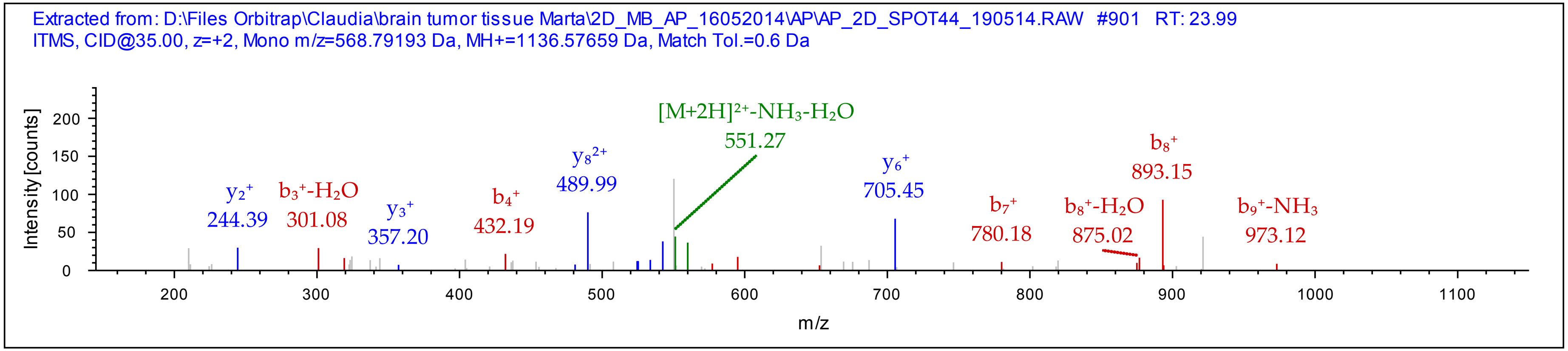
#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	148.04269	74.52498	50.01908	M-Oxidation				26
2	261.12676	131.06702	87.71377	L	2860.43646	1430.72187	954.15034	25
3	374.21083	187.60905	125.40846	L	2747.35239	1374.17983	916.45565	24
4	445.24795	223.12761	149.08750	A	2634.26832	1317.63780	878.76096	23
5	560.27490	280.64109	187.42982	D	2563.23120	1282.11924	855.08192	22
6	688.33348	344.67038	230.11601	Q	2448.20425	1224.60576	816.73960	21
7	745.35495	373.18111	249.12317	G	2320.14567	1160.57647	774.05341	20
8	873.41353	437.21040	291.80936	Q	2263.12420	1132.06574	755.04625	19
9	960.44556	480.72642	320.82004	S	2135.06562	1068.03645	712.36006	18

10	1146.52488	573.76608	382.84648	W	2048.03359	1024.52043	683.34938	17
11	1274.61985	637.81356	425.54480	K	1861.95427	931.48077	621.32294	16
12	1403.66245	702.33486	468.55900	E	1733.85930	867.43329	578.62462	15
13	1532.70505	766.85616	511.57320	E	1604.81670	802.91199	535.61042	14
14	1631.77347	816.39037	544.59601	V	1475.77410	738.39069	492.59622	13
15	1730.84189	865.92458	577.61881	V	1376.70568	688.85648	459.57341	12
16	1831.88957	916.44842	611.30137	T	1277.63726	639.32227	426.55060	11
17	1930.95799	965.98263	644.32418	V	1176.58958	588.79843	392.86804	10
18	2060.00059	1030.50393	687.33838	E	1077.52116	539.26422	359.84524	9
19	2161.04827	1081.02777	721.02094	T	948.47856	474.74292	316.83104	8
20	2347.12759	1174.06743	783.04738	W	847.43088	424.21908	283.14848	7
21	2475.18617	1238.09672	825.73357	Q	661.35156	331.17942	221.12204	6
22	2604.22877	1302.61802	868.74777	E	533.29298	267.15013	178.43584	5
23	2661.25024	1331.12876	887.75493	G	404.25038	202.62883	135.42164	4
24	2748.28227	1374.64477	916.76561	S	347.22891	174.11809	116.41449	3
25	2861.36634	1431.18681	954.46030	L	260.19688	130.60208	87.40381	2
26				K	147.11281	74.06004	49.70912	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT44_190514.RAW #1590 RT: 39.41
ITMS, CID@35.00, z=+3, Mono m/z=1003.16302 Da, MH+=3007.47452 Da, Match Tol.=0.6 Da

Sequence: ASCLYGQLPK, C3-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 568.79193 Da (-0.15 mmu/-0.27 ppm), MH+: 1136.57659 Da, RT: 23.99 min,
Identified with: Sequest HT (v1.3); XCorr:1.85, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			10
2	159.07643	80.04185	S	1065.53978	533.27353	9
3	319.10708	160.05718	C-Carbamidomethyl	978.50775	489.75751	8
4	432.19115	216.59921	L	818.47709	409.74218	7
5	595.25447	298.13087	Y	705.39302	353.20015	6
6	652.27594	326.64161	G	542.32970	271.66849	5
7	780.33452	390.67090	Q	485.30823	243.15775	4
8	893.41859	447.21293	L	357.24965	179.12846	3
9	990.47136	495.73932	P	244.16558	122.58643	2
10			K	147.11281	74.06004	1

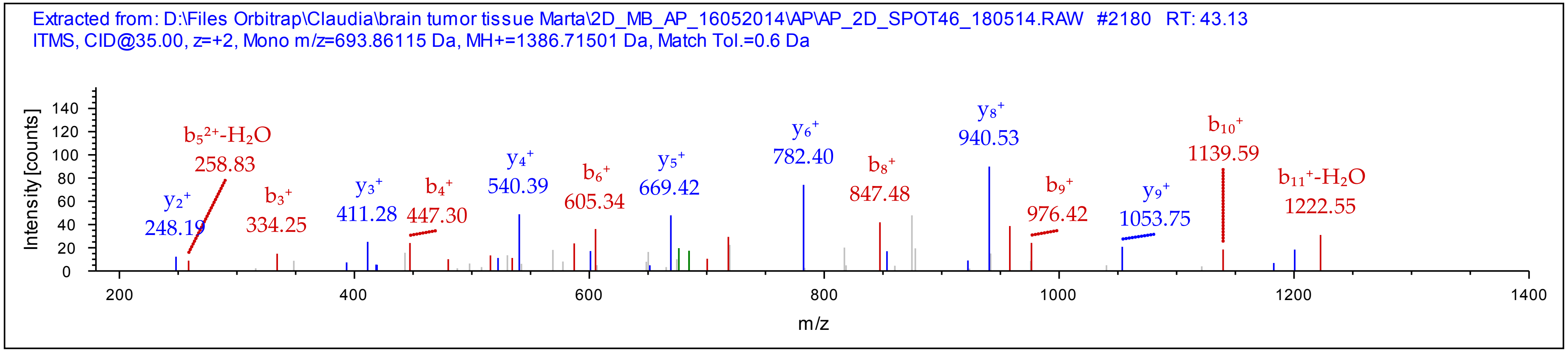


Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
46	P02647	Apolipoprotein A-I	28.1	5.3	73.22	31.84	7	7	PA	5.00E-03	2.8	↑ in MB

Sequence: VSFLSALEEYTK, Charge: +2, Monoisotopic m/z: 693.86115 Da (-0.08 mmu/-0.11 ppm), MH+: 1386.71501 Da, RT: 43.13 min,
Identified with: Sequest HT (v1.3); XCorr:3.59, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1 - [APOA1_HUMAN]

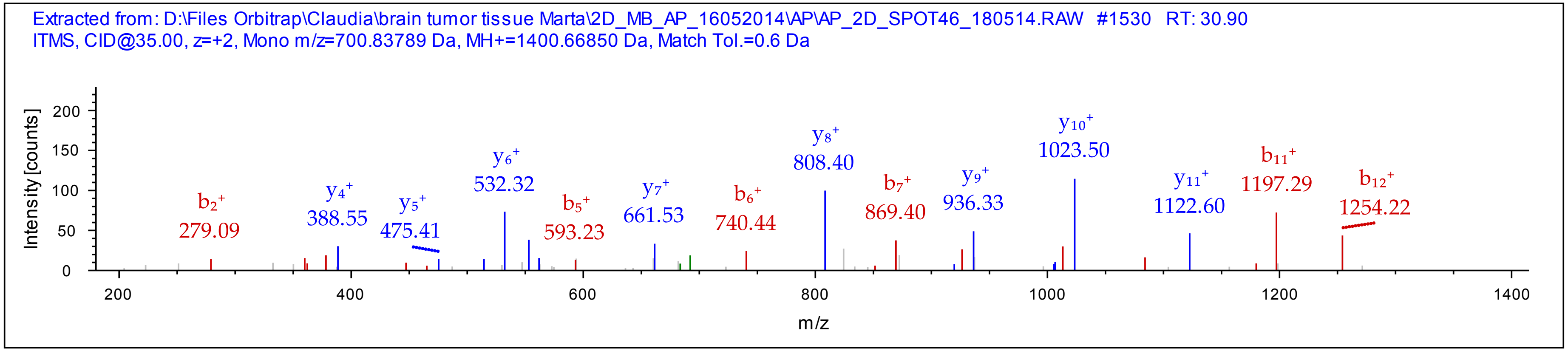
#1	**b⁺**	**b²⁺**	**Seq.**	**y⁺**	**y²⁺**	**#2**
1	100.07570	50.54149	V			12
2	187.10773	94.05750	S	1287.64675	644.32701	11
3	334.17615	167.59171	F	1200.61472	600.81100	10
4	447.26022	224.13375	L	1053.54630	527.27679	9
5	534.29225	267.64976	S	940.46223	470.73475	8
6	605.32937	303.16832	A	853.43020	427.21874	7
7	718.41344	359.71036	L	782.39308	391.70018	6
8	847.45604	424.23166	E	669.30901	335.15814	5
9	976.49864	488.75296	E	540.26641	270.63684	4
10	1139.56196	570.28462	Y	411.22381	206.11554	3
11	1240.60964	620.80846	T	248.16049	124.58388	2
12			K	147.11281	74.06004	1



Sequence: DYVSQFEGSALGK, Charge: +2, Monoisotopic m/z: 700.83789 Da (-0.39 mmu/-0.56 ppm), MH+: 1400.66850 Da, RT: 30.90 min,
Identified with: Sequest HT (v1.3); XCorr:3.51, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1 - [APOA1_HUMAN]

#1	**b⁺**	**b²⁺**	**Seq.**	**y⁺**	**y²⁺**	**#2**
1	116.03423	58.52075	D			13
2	279.09755	140.05241	Y	1285.64234	643.32481	12

3	378.16597	189.58662	V	1122.57902	561.79315	11
4	465.19800	233.10264	S	1023.51060	512.25894	10
5	593.25658	297.13193	Q	936.47857	468.74292	9
6	740.32500	370.66614	F	808.41999	404.71363	8
7	869.36760	435.18744	E	661.35157	331.17942	7
8	926.38907	463.69817	G	532.30897	266.65812	6
9	1013.42110	507.21419	S	475.28750	238.14739	5
10	1084.45822	542.73275	A	388.25547	194.63137	4
11	1197.54229	599.27478	L	317.21835	159.11281	3
12	1254.56376	627.78552	G	204.13428	102.57078	2
13			K	147.11281	74.06004	1

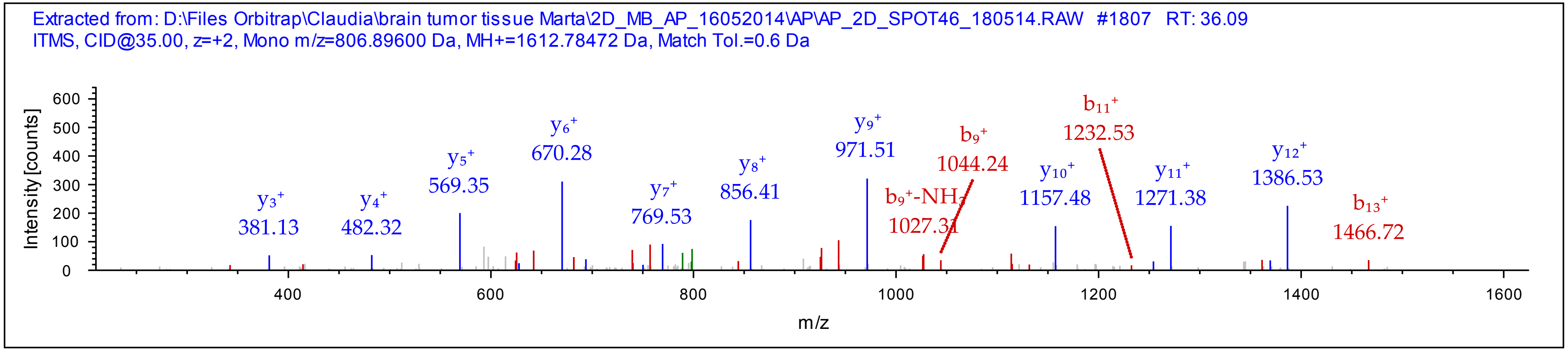

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT46_180514.RAW #1530 RT: 30.90
ITMS, CID@35.00, z=+2, Mono m/z=700.83789 Da, MH+=1400.66850 Da, Match Tol.=0.6 Da

Sequence: LLDNWDSVTSTFSK, Charge: +2, Monoisotopic m/z: 806.89600 Da (-0.34 mmu/-0.42 ppm), MH+: 1612.78472 Da, RT: 36.09 min,
Identified with: Sequest HT (v1.3); XCorr:3.33, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H$_2$O; b-NH$_3$; y; y-H$_2$O; y-NH$_3$

Protein references (1):
- Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1 - [APOA1_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			14
2	227.17542	114.09135	L	1499.70132	750.35430	13
3	342.20237	171.60482	D	1386.61725	693.81226	12

4	456.24530	228.62629	N	1271.59030	636.29879	11
5	642.32462	321.66595	W	1157.54737	579.27732	10
6	757.35157	379.17942	D	971.46805	486.23766	9
7	844.38360	422.69544	S	856.44110	428.72419	8
8	943.45202	472.22965	V	769.40907	385.20817	7
9	1044.49970	522.75349	T	670.34065	335.67396	6
10	1131.53173	566.26950	S	569.29297	285.15012	5
11	1232.57941	616.79334	T	482.26094	241.63411	4
12	1379.64783	690.32755	F	381.21326	191.11027	3
13	1466.67986	733.84357	S	234.14484	117.57606	2
14			K	147.11281	74.06004	1

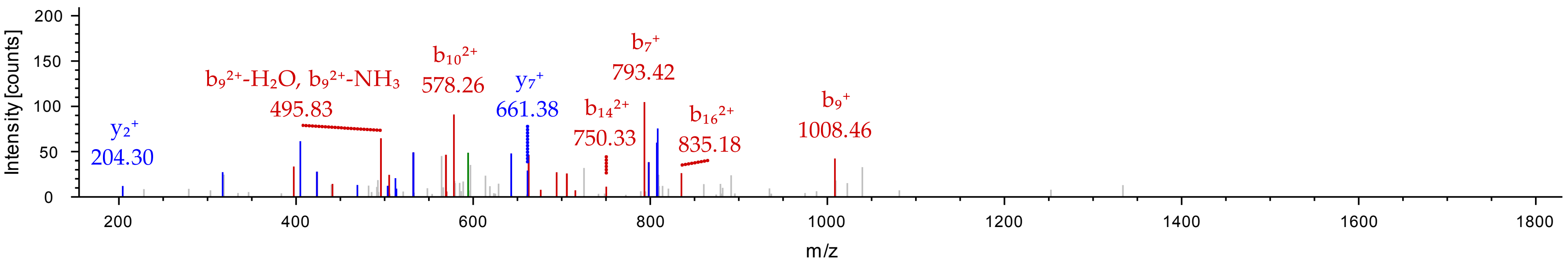

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT46_180514.RAW #1807 RT: 36.09
ITMS, CID@35.00, z=+2, Mono m/z=806.89600 Da, MH+=1612.78472 Da, Match Tol.=0.6 Da

Sequence: DSGRDYVSQFEGSALGK, Charge: +3, Monoisotopic m/z: 605.95477 Da (-0.37 mmu/-0.6 ppm), MH+: 1815.84977 Da, RT: 29.54 min,
Identified with: Sequest HT (v1.3); XCorr:3.32, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1 - [APOA1_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	116.03423	58.52075	39.34959	D				17
2	203.06626	102.03677	68.36027	S	1700.82391	850.91559	567.61282	16
3	260.08773	130.54750	87.36743	G	1613.79188	807.39958	538.60214	15
4	416.18885	208.59806	139.40113	R	1556.77041	778.88884	519.59499	14
5	531.21580	266.11154	177.74345	D	1400.66929	700.83828	467.56128	13
6	694.27912	347.64320	232.09789	Y	1285.64234	643.32481	429.21896	12

7	793.34754	397.17741	265.12070	V	1122.57902	561.79315	374.86452	11
8	880.37957	440.69342	294.13137	S	1023.51060	512.25894	341.84172	10
9	1008.43815	504.72271	336.81757	Q	936.47857	468.74292	312.83104	9
10	1155.50657	578.25692	385.84037	F	808.41999	404.71363	270.14485	8
11	1284.54917	642.77822	428.85457	E	661.35157	331.17942	221.12204	7
12	1341.57064	671.28896	447.86173	G	532.30897	266.65812	178.10784	6
13	1428.60267	714.80497	476.87241	S	475.28750	238.14739	159.10068	5
14	1499.63979	750.32353	500.55145	A	388.25547	194.63137	130.09001	4
15	1612.72386	806.86557	538.24614	L	317.21835	159.11281	106.41097	3
16	1669.74533	835.37630	557.25329	G	204.13428	102.57078	68.71628	2
17				K	147.11281	74.06004	49.70912	1

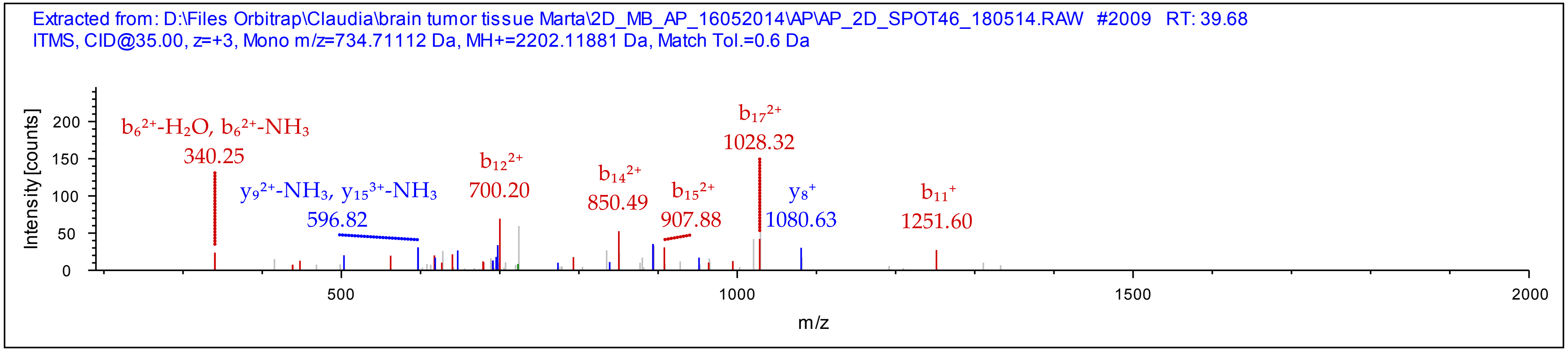
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT46_180514.RAW #1443 RT: 29.54
ITMS, CID@35.00, z=+3, Mono m/z=605.95477 Da, MH+=1815.84977 Da, Match Tol.=0.6 Da



Sequence: LREQLGPVTQEFWDNLEK, Charge: +3, Monoisotopic m/z: 734.71112 Da (-0.08 mmu/-0.11 ppm), MH+: 2202.11881 Da, RT: 39.68 min,
Identified with: Sequest HT (v1.3); XCorr:2.73, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1): - Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1 - [APOA1_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	114.09135	57.54931	38.70197	L				18
2	270.19247	135.59987	90.73567	R	2089.03499	1045.02113	697.01651	17
3	399.23507	200.12117	133.74987	E	1932.93387	966.97057	644.98281	16
4	527.29365	264.15046	176.43607	Q	1803.89127	902.44927	601.96861	15
5	640.37772	320.69250	214.13076	L	1675.83269	838.41998	559.28241	14
6	697.39919	349.20323	233.13791	G	1562.74862	781.87795	521.58772	13
7	794.45196	397.72962	265.48884	P	1505.72715	753.36721	502.58057	12
8	893.52038	447.26383	298.51164	V	1408.67438	704.84083	470.22964	11
9	994.56806	497.78767	332.19420	T	1309.60596	655.30662	437.20684	10

10	1122.62664	561.81696	374.88040	Q	1208.55828	604.78278	403.52428	9
11	1251.66924	626.33826	417.89460	E	1080.49970	540.75349	360.83808	8
12	1398.73766	699.87247	466.91740	F	951.45710	476.23219	317.82388	7
13	1584.81698	792.91213	528.94384	W	804.38868	402.69798	268.80108	6
14	1699.84393	850.42560	567.28616	D	618.30936	309.65832	206.77464	5
15	1813.88686	907.44707	605.30047	N	503.28241	252.14484	168.43232	4
16	1926.97093	963.98910	642.99516	L	389.23948	195.12338	130.41801	3
17	2056.01353	1028.51040	686.00936	E	276.15541	138.58134	92.72332	2
18				K	147.11281	74.06004	49.70912	1



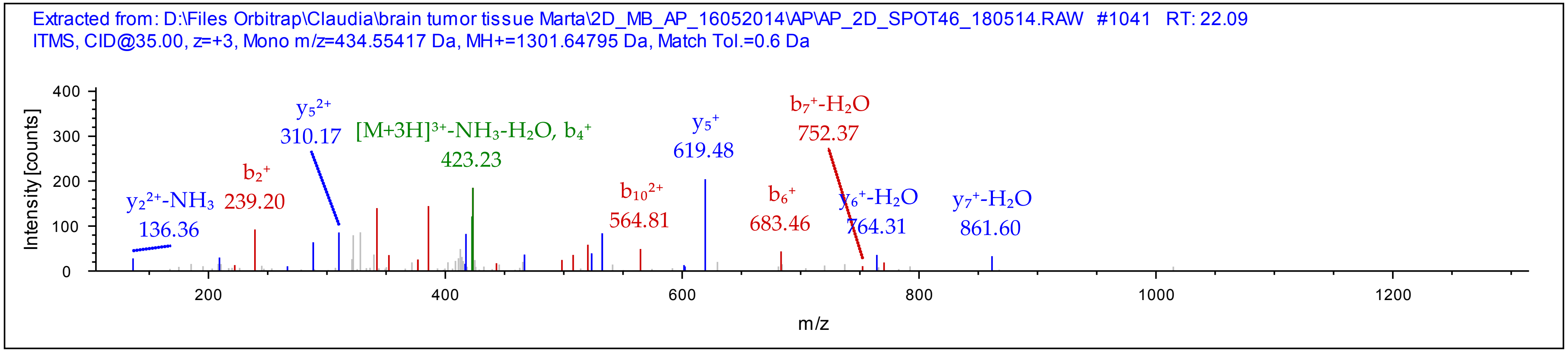
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT46_180514.RAW #2009 RT: 39.68
ITMS, CID@35.00, z=+3, Mono m/z=734.71112 Da, MH+=2202.11881 Da, Match Tol.=0.6 Da

Sequence: THLAPYSDELR, Charge: +3, Monoisotopic m/z: 434.55417 Da (-0.18 mmu/-0.41 ppm), MH+: 1301.64795 Da, RT: 22.09 min,
Identified with: Sequest HT (v1.3); XCorr:2.63, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1 - [APOA1_HUMAN]

#1	**b$^+$**	**b^{2+}**	**b^{3+}**	**Seq.**	**y$^+$**	**y^{2+}**	**y^{3+}**	**#2**
1	102.05496	51.53112	34.68984	T				11
2	239.11387	120.06057	80.37614	H	1200.60080	600.80404	400.87178	10
3	352.19794	176.60261	118.07083	L	1063.54189	532.27458	355.18548	9
4	423.23506	212.12117	141.74987	A	950.45782	475.73255	317.49079	8
5	520.28783	260.64755	174.10079	P	879.42070	440.21399	293.81175	7
6	683.35115	342.17921	228.45523	Y	782.36793	391.68760	261.46083	6
7	770.38318	385.69523	257.46591	S	619.30461	310.15594	207.10639	5
8	885.41013	443.20870	295.80823	D	532.27258	266.63993	178.09571	4
9	1014.45273	507.73000	338.82243	E	417.24563	209.12645	139.75339	3

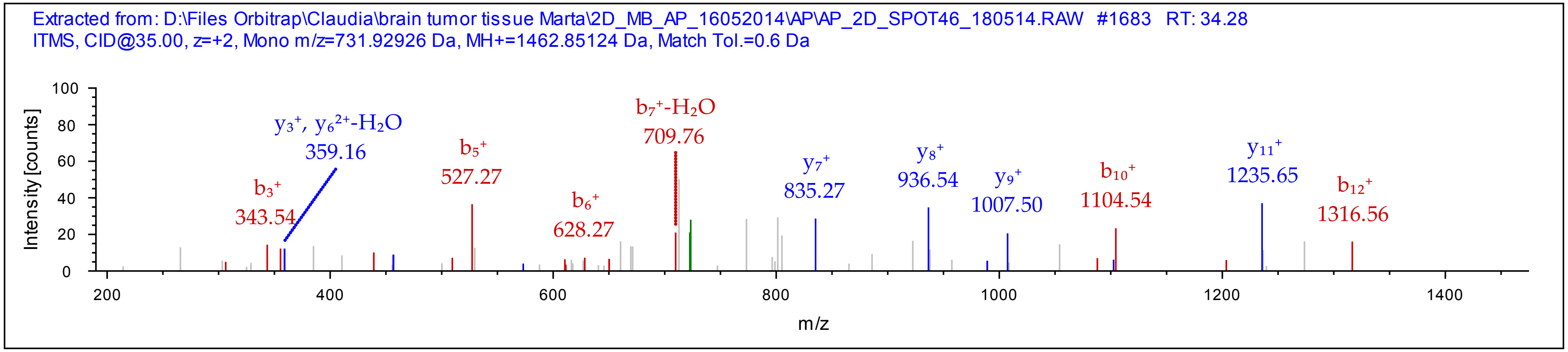
10	1127.53680	564.27204	376.51712	L	288.20303	144.60515	96.73919	2
11				R	175.11896	88.06312	59.04450	1



Sequence: VKDLATVYVDVLK, Charge: +2, Monoisotopic m/z: 731.92926 Da (-0.19 mmu/-0.26 ppm), MH+: 1462.85124 Da, RT: 34.28 min,
Identified with: Sequest HT (v1.3); XCorr:2.12, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1 - [APOA1_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	100.07570	50.54149	V			13
2	228.17067	114.58897	K	1363.78320	682.39524	12
3	343.19762	172.10245	D	1235.68823	618.34775	11
4	456.28169	228.64448	L	1120.66128	560.83428	10
5	527.31881	264.16304	A	1007.57721	504.29224	9
6	628.36649	314.68688	T	936.54009	468.77368	8
7	727.43491	364.22109	V	835.49241	418.24984	7
8	890.49823	445.75275	Y	736.42399	368.71563	6
9	989.56665	495.28696	V	573.36067	287.18397	5
10	1104.59360	552.80044	D	474.29225	237.64976	4
11	1203.66202	602.33465	V	359.26530	180.13629	3
12	1316.74609	658.87668	L	260.19688	130.60208	2
13			K	147.11281	74.06004	1



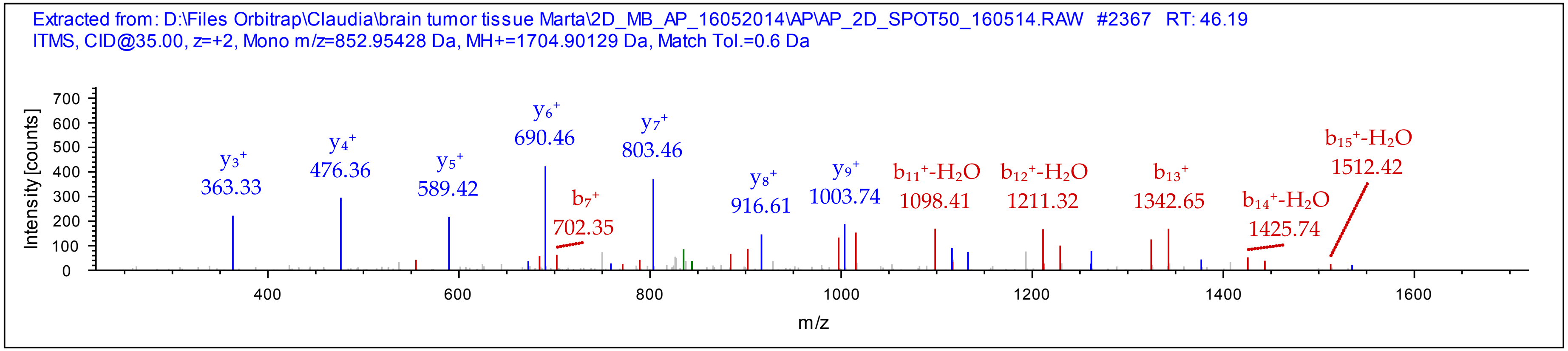
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT46_180514.RAW #1683 RT: 34.28
ITMS, CID@35.00, z=+2, Mono m/z=731.92926 Da, MH+=1462.85124 Da, Match Tol.=0.6 Da

Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
50	P08758	Annexin A5	35.8	4.9	103.11	45.63%	10	10	PA	4.30E-04	2.4	↑ in PA

Sequence: GLGTDEESILTLLTSR, Charge: +2, Monoisotopic m/z: 852.95428 Da (-0.1 mmu/-0.12 ppm), MH+: 1704.90129 Da, RT: 46.19 min,
Identified with: Sequest HT (v1.3); XCorr:3.71, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3
Protein references (1):
- Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	58.02875	29.51801	G			16
2	171.11282	86.06005	L	1647.88003	824.44365	15
3	228.13429	114.57078	G	1534.79596	767.90162	14
4	329.18197	165.09462	T	1477.77449	739.39088	13
5	444.20892	222.60810	D	1376.72681	688.86704	12
6	573.25152	287.12940	E	1261.69986	631.35357	11
7	702.29412	351.65070	E	1132.65726	566.83227	10
8	789.32615	395.16671	S	1003.61466	502.31097	9
9	902.41022	451.70875	I	916.58263	458.79495	8
10	1015.49429	508.25078	L	803.49856	402.25292	7

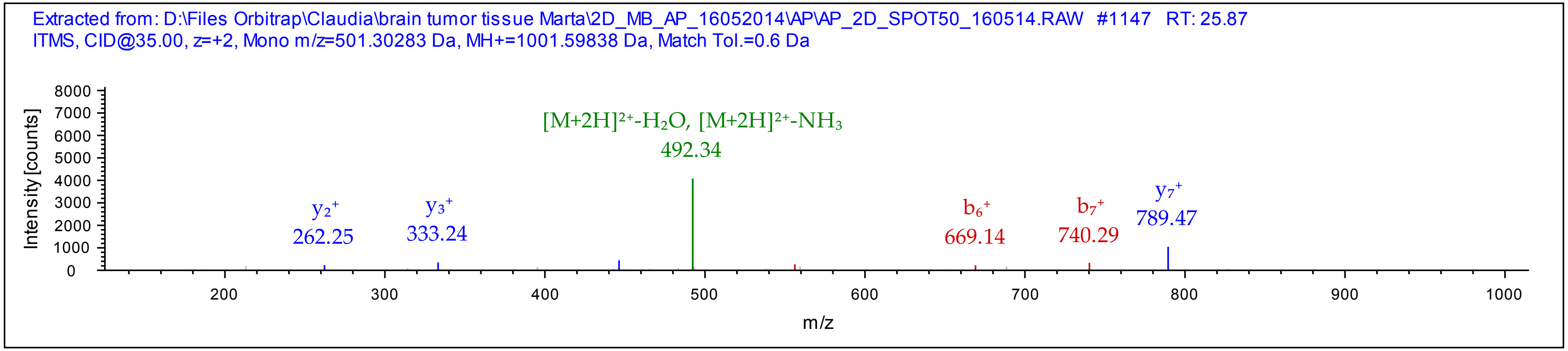
11	1116.54197	558.77462	T	690.41449	345.71088	6
12	1229.62604	615.31666	L	589.36681	295.18704	5
13	1342.71011	671.85869	L	476.28274	238.64501	4
14	1443.75779	722.38253	T	363.19867	182.10297	3
15	1530.78982	765.89855	S	262.15099	131.57913	2
16			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT50_160514.RAW #2367 RT: 46.19
ITMS, CID@35.00, z=+2, Mono m/z=852.95428 Da, MH+=1704.90129 Da, Match Tol.=0.6 Da

Sequence: VLTEIIASR, Charge: +2, Monoisotopic m/z: 501.30283 Da (-0.32 mmu/-0.65 ppm), MH+: 1001.59838 Da, RT: 25.87 min,
Identified with: Sequest HT (v1.3); XCorr:3.05, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	100.07570	50.54149	V			9
2	213.15977	107.08352	L	902.53060	451.76894	8
3	314.20745	157.60736	T	789.44653	395.22690	7
4	443.25005	222.12866	E	688.39885	344.70306	6
5	556.33412	278.67070	I	559.35625	280.18176	5
6	669.41819	335.21273	I	446.27218	223.63973	4
7	740.45531	370.73129	A	333.18811	167.09769	3
8	827.48734	414.24731	S	262.15099	131.57913	2
9			R	175.11896	88.06312	1

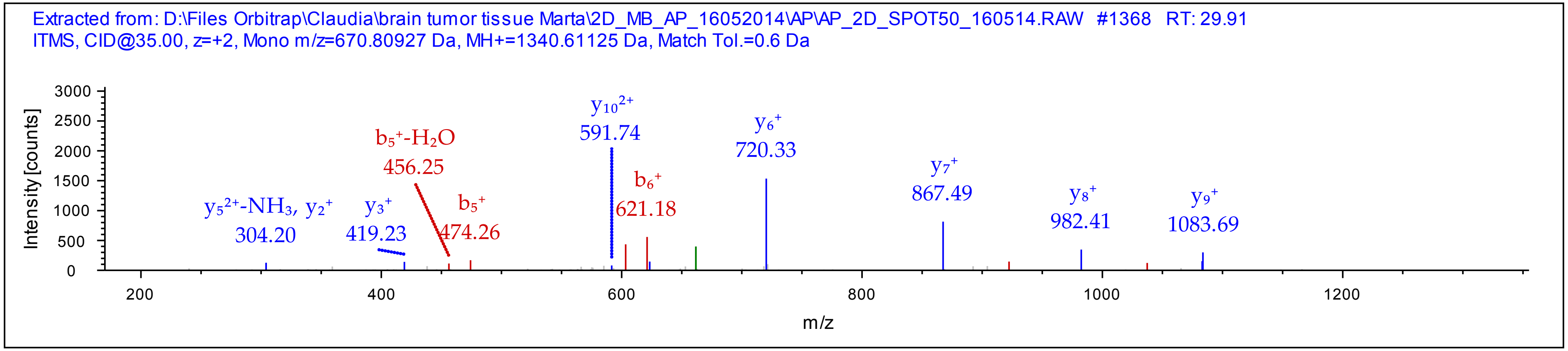


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT50_160514.RAW #1147 RT: 25.87
ITMS, CID@35.00, z=+2, Mono m/z=501.30283 Da, MH+=1001.59838 Da, Match Tol.=0.6 Da

Sequence: GTVTDFPGFDER, Charge: +2, Monoisotopic m/z: 670.80927 Da (-0.27 mmu/-0.4 ppm), MH+: 1340.61125 Da, RT: 29.91 min,
Identified with: Sequest HT (v1.3); XCorr:3.00, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_HUMAN]

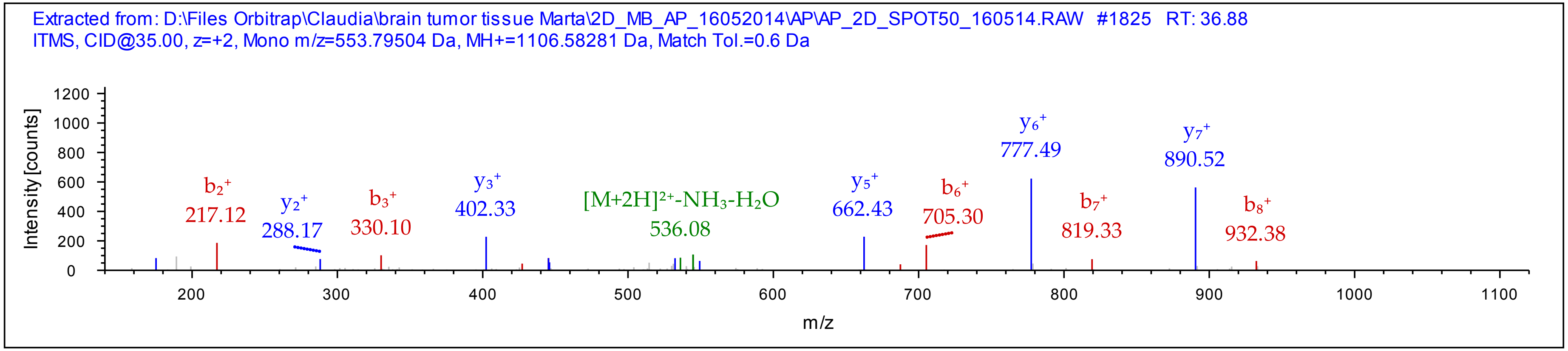
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	58.02875	29.51801	G			12
2	159.07643	80.04185	T	1283.59032	642.29880	11
3	258.14485	129.57606	V	1182.54264	591.77496	10
4	359.19253	180.09990	T	1083.47422	542.24075	9
5	474.21948	237.61338	D	982.42654	491.71691	8
6	621.28790	311.14759	F	867.39959	434.20343	7
7	718.34067	359.67397	P	720.33117	360.66922	6
8	775.36214	388.18471	G	623.27840	312.14284	5
9	922.43056	461.71892	F	566.25693	283.63210	4
10	1037.45751	519.23239	D	419.18851	210.09789	3
11	1166.50011	583.75369	E	304.16156	152.58442	2
12			R	175.11896	88.06312	1



Sequence: SEIDLFNIR, Charge: +2, Monoisotopic m/z: 553.79504 Da (-0.65 mmu/-1.17 ppm), MH+: 1106.58281 Da, RT: 36.88 min,
Identified with: Sequest HT (v1.3); XCorr:2.92, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H$_2$O; b-NH$_3$; y; y-H$_2$O; y-NH$_3$

Protein references (1):
- Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_HUMAN]

#1	b$^+$	b^{2+}	Seq.	y$^+$	y^{2+}	#2
1	88.03931	44.52329	S			9
2	217.08191	109.04459	E	1019.55207	510.27967	8
3	330.16598	165.58663	I	890.50947	445.75837	7
4	445.19293	223.10010	D	777.42540	389.21634	6
5	558.27700	279.64214	L	662.39845	331.70286	5
6	705.34542	353.17635	F	549.31438	275.16083	4
7	819.38835	410.19781	N	402.24596	201.62662	3
8	932.47242	466.73985	I	288.20303	144.60515	2
9			R	175.11896	88.06312	1

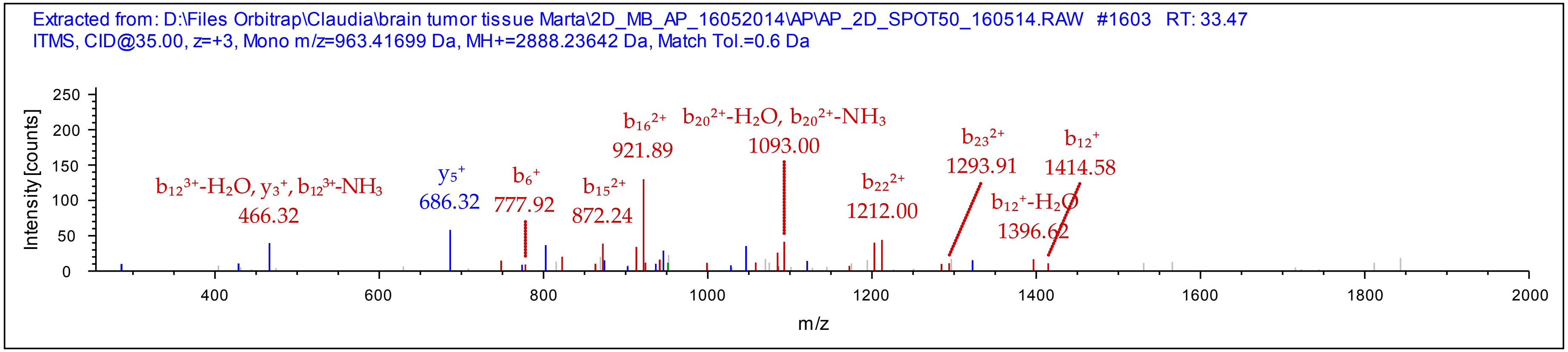


Sequence: QVYEEEYGSSLEDDVVGDTSGYYQR, Charge: +3, Monoisotopic m/z: 963.41699 Da (-0.58 mmu/-0.6 ppm), MH+: 2888.23642 Da, RT: 33.47 min,
Identified with: Sequest HT (v1.3); XCorr:2.77, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_HUMAN]

#1	b+	b2+	b3+	Seq.	y+	y2+	y3+	#2
1	129.06586	65.03657	43.69347	Q				25
2	228.13428	114.57078	76.71628	V	2760.17958	1380.59343	920.73138	24
3	391.19760	196.10244	131.07072	Y	2661.11116	1331.05922	887.70857	23
4	520.24020	260.62374	174.08492	E	2498.04784	1249.52756	833.35413	22
5	649.28280	325.14504	217.09912	E	2369.00524	1185.00626	790.33993	21
6	778.32540	389.66634	260.11332	E	2239.96264	1120.48496	747.32573	20
7	941.38872	471.19800	314.46776	Y	2110.92004	1055.96366	704.31153	19
8	998.41019	499.70873	333.47491	G	1947.85672	974.43200	649.95709	18
9	1085.44222	543.22475	362.48559	S	1890.83525	945.92126	630.94993	17
10	1172.47425	586.74076	391.49627	S	1803.80322	902.40525	601.93926	16
11	1285.55832	643.28280	429.19096	L	1716.77119	858.88923	572.92858	15
12	1414.60092	707.80410	472.20516	E	1603.68712	802.34720	535.23389	14
13	1529.62787	765.31757	510.54747	D	1474.64452	737.82590	492.21969	13
14	1644.65482	822.83105	548.88979	D	1359.61757	680.31242	453.87737	12
15	1743.72324	872.36526	581.91260	V	1244.59062	622.79895	415.53506	11
16	1842.79166	921.89947	614.93540	V	1145.52220	573.26474	382.51225	10
17	1899.81313	950.41020	633.94256	G	1046.45378	523.73053	349.48944	9
18	2014.84008	1007.92368	672.28488	D	989.43231	495.21979	330.48229	8

19	2115.88776	1058.44752	705.96744	T	874.40536	437.70632	292.13997	7
20	2202.91979	1101.96353	734.97811	S	773.35768	387.18248	258.45741	6
21	2259.94126	1130.47427	753.98527	G	686.32565	343.66646	229.44673	5
22	2423.00458	1212.00593	808.33971	Y	629.30418	315.15573	210.43958	4
23	2586.06790	1293.53759	862.69415	Y	466.24086	233.62407	156.08514	3
24	2714.12648	1357.56688	905.38034	Q	303.17754	152.09241	101.73070	2
25				R	175.11896	88.06312	59.04450	1



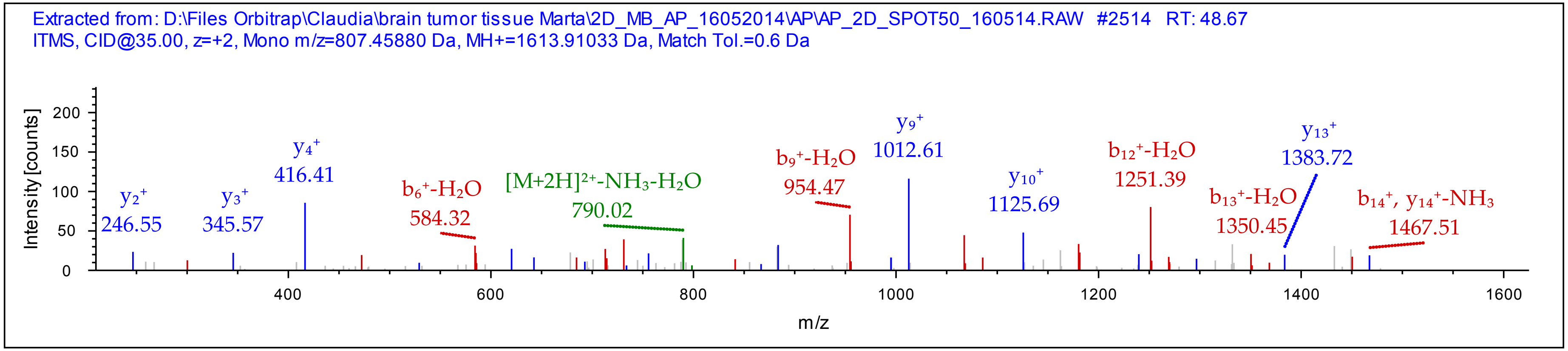
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT50_160514.RAW #1603 RT: 33.47
ITMS, CID@35.00, z=+3, Mono m/z=963.41699 Da, MH+=2888.23642 Da, Match Tol.=0.6 Da

Sequence: ETSGNLEQLLLAVVK, Charge: +2, Monoisotopic m/z: 807.45880 Da (-0.31 mmu/-0.38 ppm), MH+: 1613.91033 Da, RT: 48.67 min,
Identified with: Sequest HT (v1.3); XCorr:2.53, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	130.04988	65.52858	E			15
2	231.09756	116.05242	T	1484.86834	742.93781	14
3	318.12959	159.56843	S	1383.82066	692.41397	13
4	375.15106	188.07917	G	1296.78863	648.89795	12
5	489.19399	245.10063	N	1239.76716	620.38722	11
6	602.27806	301.64267	L	1125.72423	563.36575	10
7	731.32066	366.16397	E	1012.64016	506.82372	9
8	859.37924	430.19326	Q	883.59756	442.30242	8
9	972.46331	486.73529	L	755.53898	378.27313	7
10	1085.54738	543.27733	L	642.45491	321.73109	6
11	1198.63145	599.81936	L	529.37084	265.18906	5

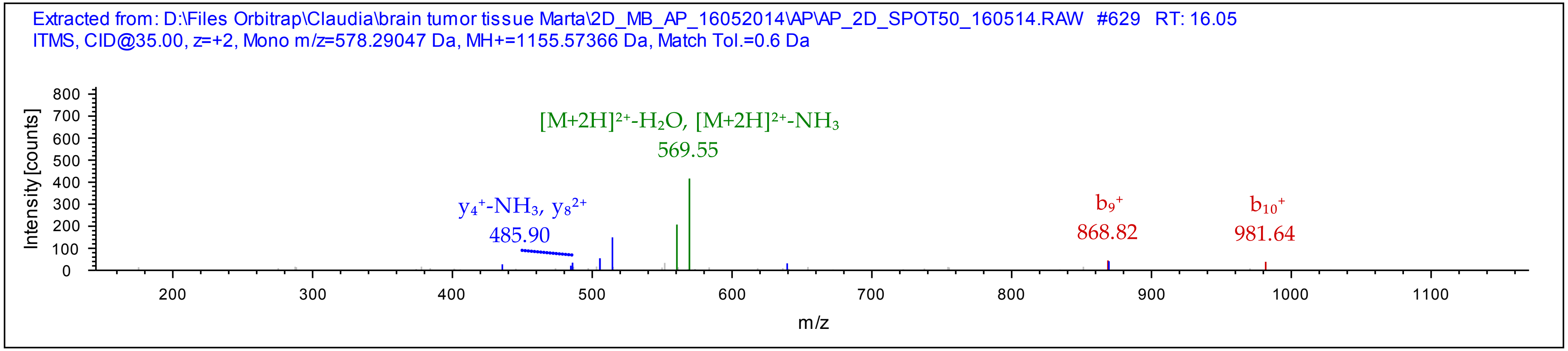
12	1269.66857	635.33792	A	416.28677	208.64702	4
13	1368.73699	684.87213	V	345.24965	173.12846	3
14	1467.80541	734.40634	V	246.18123	123.59425	2
15			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT50_160514.RAW #2514 RT: 48.67
ITMS, CID@35.00, z=+2, Mono m/z=807.45880 Da, MH+=1613.91033 Da, Match Tol.=0.6 Da

Sequence: GAGTDDHTLIR, Charge: +2, Monoisotopic m/z: 578.29047 Da (-0.84 mmu/-1.45 ppm), MH+: 1155.57366 Da, RT: 16.05 min,
Identified with: Sequest HT (v1.3); XCorr:2.45, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_HUMAN]

#1	b$^+$	b^{2+}	Seq.	y$^+$	y^{2+}	#2
1	58.02875	29.51801	G			11
2	129.06587	65.03657	A	1098.55386	549.78057	10
3	186.08734	93.54731	G	1027.51674	514.26201	9
4	287.13502	144.07115	T	970.49527	485.75127	8
5	402.16197	201.58462	D	869.44759	435.22743	7
6	517.18892	259.09810	D	754.42064	377.71396	6
7	654.24783	327.62755	H	639.39369	320.20048	5
8	755.29551	378.15139	T	502.33478	251.67103	4
9	868.37958	434.69343	L	401.28710	201.14719	3
10	981.46365	491.23546	I	288.20303	144.60515	2
11			R	175.11896	88.06312	1

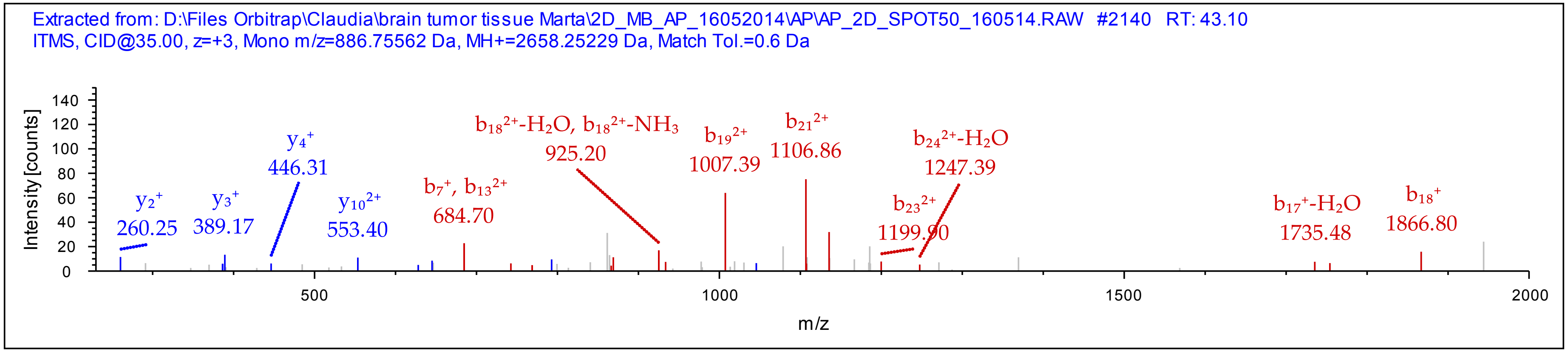

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT50_160514.RAW #629 RT: 16.05
ITMS, CID@35.00, z=+2, Mono m/z=578.29047 Da, MH+=1155.57366 Da, Match Tol.=0.6 Da

Sequence: DPDAGIDEAQVEQDAQALFQAGELK, Charge: +3, Monoisotopic m/z: 886.75562 Da (-0.27 mmu/-0.3 ppm), MH+: 2658.25229 Da, RT: 43.10 min,
Identified with: Sequest HT (v1.3); XCorr:2.38, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	116.03423	58.52075	39.34959	D				25
2	213.08700	107.04714	71.70052	P	2543.22614	1272.11671	848.41356	24
3	328.11395	164.56061	110.04283	D	2446.17337	1223.59032	816.06264	23
4	399.15107	200.07917	133.72187	A	2331.14642	1166.07685	777.72032	22
5	456.17254	228.58991	152.72903	G	2260.10930	1130.55829	754.04128	21
6	569.25661	285.13194	190.42372	I	2203.08783	1102.04755	735.03413	20
7	684.28356	342.64542	228.76604	D	2090.00376	1045.50552	697.33944	19
8	813.32616	407.16672	271.78024	E	1974.97681	987.99204	658.99712	18
9	884.36328	442.68528	295.45928	A	1845.93421	923.47074	615.98292	17
10	1012.42186	506.71457	338.14547	Q	1774.89709	887.95218	592.30388	16
11	1111.49028	556.24878	371.16828	V	1646.83851	823.92289	549.61769	15
12	1240.53288	620.77008	414.18248	E	1547.77009	774.38868	516.59488	14
13	1368.59146	684.79937	456.86867	Q	1418.72749	709.86738	473.58068	13
14	1483.61841	742.31284	495.21099	D	1290.66891	645.83809	430.89449	12
15	1554.65553	777.83140	518.89003	A	1175.64196	588.32462	392.55217	11
16	1682.71411	841.86069	561.57622	Q	1104.60484	552.80606	368.87313	10
17	1753.75123	877.37925	585.25526	A	976.54626	488.77677	326.18694	9
18	1866.83530	933.92129	622.94995	L	905.50914	453.25821	302.50790	8

19	2013.90372	1007.45550	671.97276	F	792.42507	396.71617	264.81321	7
20	2141.96230	1071.48479	714.65895	Q	645.35665	323.18196	215.79040	6
21	2212.99942	1107.00335	738.33799	A	517.29807	259.15267	173.10421	5
22	2270.02089	1135.51408	757.34515	G	446.26095	223.63411	149.42517	4
23	2399.06349	1200.03538	800.35935	E	389.23948	195.12338	130.41801	3
24	2512.14756	1256.57742	838.05404	L	260.19688	130.60208	87.40381	2
25				K	147.11281	74.06004	49.70912	1

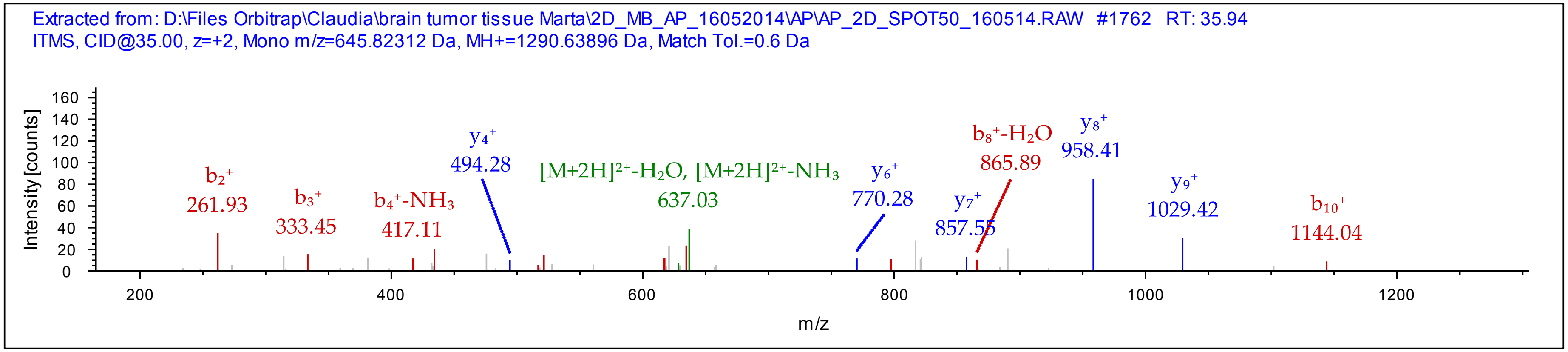


Sequence: NFATSLYSMIK, M9-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 645.82312 Da (-0.47 mmu/-0.72 ppm), MH+: 1290.63896 Da, RT: 35.94 min,
Identified with: Sequest HT (v1.3); XCorr:2.19, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	115.05021	58.02874	N			11
2	262.11863	131.56295	F	1176.59697	588.80212	10
3	333.15575	167.08151	A	1029.52855	515.26791	9
4	434.20343	217.60535	T	958.49143	479.74935	8
5	521.23546	261.12137	S	857.44375	429.22551	7
6	634.31953	317.66340	L	770.41172	385.70950	6

7	797.38285	399.19506	Y	657.32765	329.16746	5
8	884.41488	442.71108	S	494.26433	247.63580	4
9	1031.45029	516.22878	M-Oxidation	407.23230	204.11979	3
10	1144.53436	572.77082	I	260.19688	130.60208	2
11			K	147.11281	74.06004	1

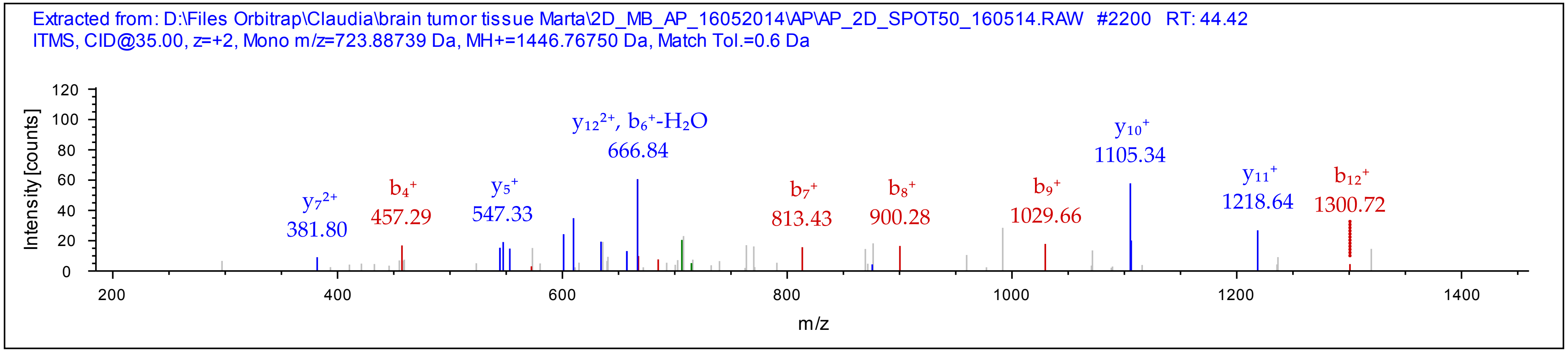


Sequence: DLLDDLKSELTGK, Charge: +2, Monoisotopic m/z: 723.88739 Da (-0.59 mmu/-0.82 ppm), MH+: 1446.76750 Da, RT: 44.42 min,
Identified with: Sequest HT (v1.3); XCorr:2.10, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	116.03423	58.52075	D			13
2	229.11830	115.06279	L	1331.74174	666.37451	12
3	342.20237	171.60482	L	1218.65767	609.83247	11
4	457.22932	229.11830	D	1105.57360	553.29044	10
5	572.25627	286.63177	D	990.54665	495.77696	9
6	685.34034	343.17381	L	875.51970	438.26349	8
7	813.43531	407.22129	K	762.43563	381.72145	7
8	900.46734	450.73731	S	634.34066	317.67397	6
9	1029.50994	515.25861	E	547.30863	274.15795	5
10	1142.59401	571.80064	L	418.26603	209.63665	4
11	1243.64169	622.32448	T	305.18196	153.09462	3
12	1300.66316	650.83522	G	204.13428	102.57078	2

13 K 147.11281 74.06004 1

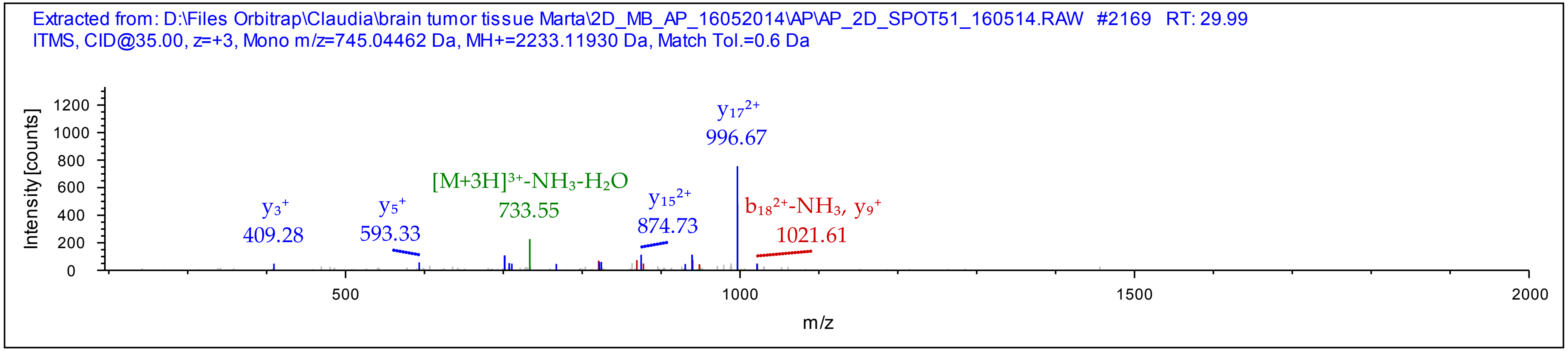


Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
51	P14136	Glial fibrillary acidic protein	49.9	5.4	103.4	22.45%	8	8	PA	5.00E-03	4.3	↑ in PA

Sequence: LQDETNLRLEAENNLAAYR, Charge: +3, Monoisotopic m/z: 745.04462 Da (-0.52 mmu/-0.69 ppm), MH+: 2233.11930 Da, RT: 29.99 min,
Identified with: Sequest HT (v1.3); XCorr:4.52, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

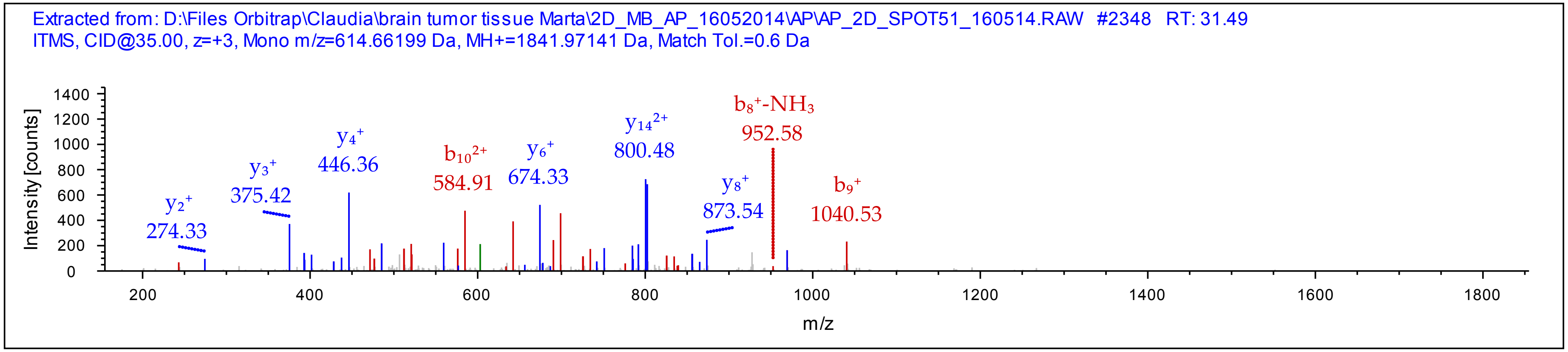
#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	114.09135	57.54931	38.70197	L				19
2	242.14993	121.57860	81.38816	Q	2120.03677	1060.52202	707.35044	18
3	357.17688	179.09208	119.73048	D	1991.97819	996.49273	664.66425	17
4	486.21948	243.61338	162.74468	E	1876.95124	938.97926	626.32193	16
5	587.26716	294.13722	196.42724	T	1747.90864	874.45796	583.30773	15
6	701.31009	351.15868	234.44155	N	1646.86096	823.93412	549.62517	14
7	814.39416	407.70072	272.13624	L	1532.81803	766.91265	511.61086	13
8	970.49528	485.75128	324.16994	R	1419.73396	710.37062	473.91617	12
9	1083.57935	542.29331	361.86463	L	1263.63284	632.32006	421.88246	11
10	1212.62195	606.81461	404.87883	E	1150.54877	575.77802	384.18777	10
11	1283.65907	642.33317	428.55787	A	1021.50617	511.25672	341.17357	9
12	1412.70167	706.85447	471.57207	E	950.46905	475.73816	317.49453	8
13	1526.74460	763.87594	509.58638	N	821.42645	411.21686	274.48033	7
14	1640.78753	820.89740	547.60069	N	707.38352	354.19540	236.46602	6
15	1753.87160	877.43944	585.29538	L	593.34059	297.17393	198.45171	5
16	1824.90872	912.95800	608.97442	A	480.25652	240.63190	160.75702	4
17	1895.94584	948.47656	632.65346	A	409.21940	205.11334	137.07798	3
18	2059.00916	1030.00822	687.00790	Y	338.18228	169.59478	113.39894	2
19				R	175.11896	88.06312	59.04450	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT51_160514.RAW #2169 RT: 29.99
ITMS, CID@35.00, z=+3, Mono m/z=745.04462 Da, MH+=2233.11930 Da, Match Tol.=0.6 Da

Sequence: LEVERDNLAQDLATVR, Charge: +3, Monoisotopic m/z: 614.66199 Da (-0.08 mmu/-0.14 ppm), MH+: 1841.97141 Da, RT: 31.49 min,
Identified with: Sequest HT (v1.3); XCorr:4.49, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	114.09135	57.54931	38.70197	L				16
2	243.13395	122.07061	81.71617	E	1728.88759	864.94743	576.96738	15
3	342.20237	171.60482	114.73897	V	1599.84499	800.42613	533.95318	14
4	471.24497	236.12612	157.75317	E	1500.77657	750.89192	500.93037	13
5	627.34609	314.17668	209.78688	R	1371.73397	686.37062	457.91617	12
6	742.37304	371.69016	248.12920	D	1215.63285	608.32006	405.88247	11
7	856.41597	428.71162	286.14351	N	1100.60590	550.80659	367.54015	10
8	969.50004	485.25366	323.83820	L	986.56297	493.78512	329.52584	9
9	1040.53716	520.77222	347.51724	A	873.47890	437.24309	291.83115	8
10	1168.59574	584.80151	390.20343	Q	802.44178	401.72453	268.15211	7
11	1283.62269	642.31498	428.54575	D	674.38320	337.69524	225.46592	6
12	1396.70676	698.85702	466.24044	L	559.35625	280.18176	187.12360	5
13	1467.74388	734.37558	489.91948	A	446.27218	223.63973	149.42891	4
14	1568.79156	784.89942	523.60204	T	375.23506	188.12117	125.74987	3
15	1667.85998	834.43363	556.62484	V	274.18738	137.59733	92.06731	2
16				R	175.11896	88.06312	59.04450	1

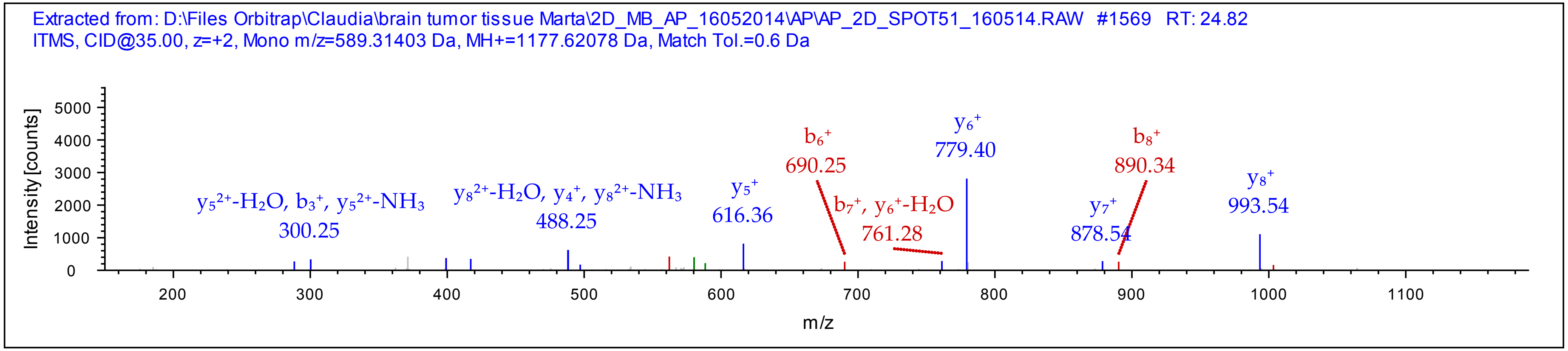


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT51_160514.RAW #2348 RT: 31.49
ITMS, CID@35.00, z=+3, Mono m/z=614.66199 Da, MH+=1841.97141 Da, Match Tol.=0.6 Da

Sequence: LADVYQAELR, Charge: +2, Monoisotopic m/z: 589.31403 Da (-0.22 mmu/-0.37 ppm), MH+: 1177.62078 Da, RT: 24.82 min,
Identified with: Sequest HT (v1.3); XCorr:3.67, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

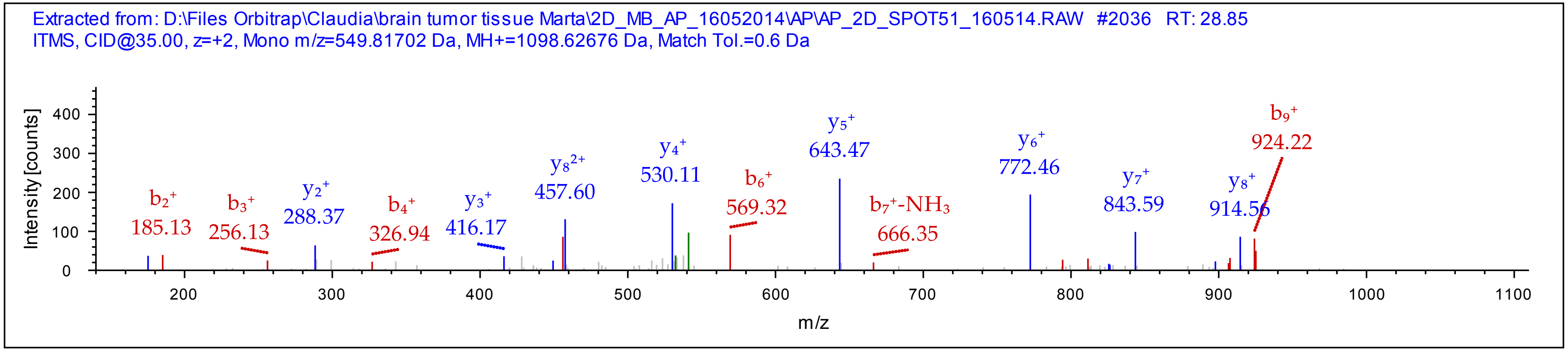
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			10
2	185.12847	93.06787	A	1064.53714	532.77221	9
3	300.15542	150.58135	D	993.50002	497.25365	8
4	399.22384	200.11556	V	878.47307	439.74017	7
5	562.28716	281.64722	Y	779.40465	390.20596	6
6	690.34574	345.67651	Q	616.34133	308.67430	5
7	761.38286	381.19507	A	488.28275	244.64501	4
8	890.42546	445.71637	E	417.24563	209.12645	3
9	1003.50953	502.25840	L	288.20303	144.60515	2
10			R	175.11896	88.06312	1



Sequence: ALAAELNQLR, Charge: +2, Monoisotopic m/z: 549.81702 Da (+0.06 mmu/+0.1 ppm), MH+: 1098.62676 Da, RT: 28.85 min,
Identified with: Sequest HT (v1.3); XCorr:3.65, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

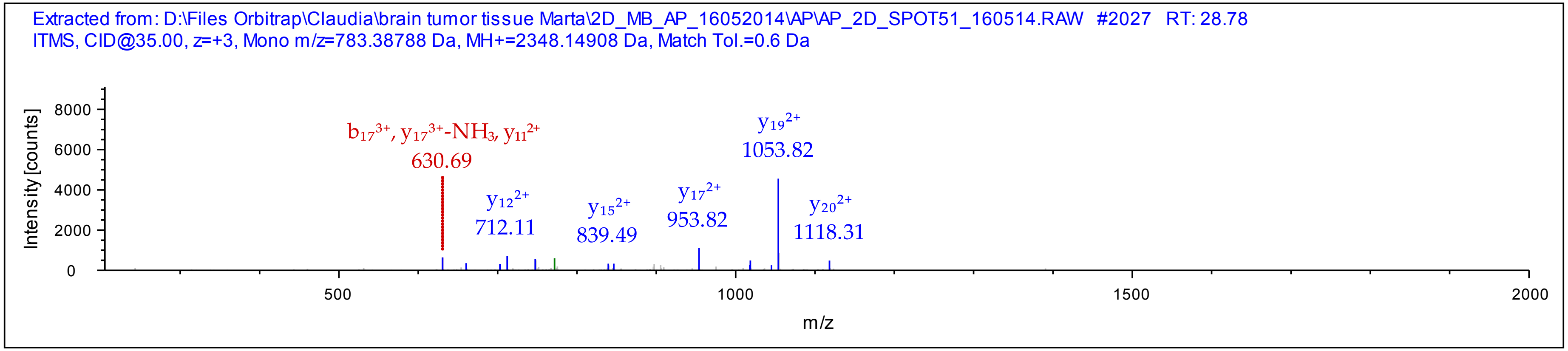
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	72.04440	36.52584	A			10
2	185.12847	93.06787	L	1027.58952	514.29840	9
3	256.16559	128.58643	A	914.50545	457.75636	8
4	327.20271	164.10499	A	843.46833	422.23780	7
5	456.24531	228.62629	E	772.43121	386.71924	6
6	569.32938	285.16833	L	643.38861	322.19794	5
7	683.37231	342.18979	N	530.30454	265.65591	4
8	811.43089	406.21908	Q	416.26161	208.63444	3
9	924.51496	462.76112	L	288.20303	144.60515	2
10			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT51_160514.RAW #2036 RT: 28.85
ITMS, CID@35.00, z=+2, Mono m/z=549.81702 Da, MH+=1098.62676 Da, Match Tol.=0.6 Da

Sequence: LEAENNLAAYRQEADEATLAR, Charge: +3, Monoisotopic m/z: 783.38788 Da (+0.43 mmu/+0.55 ppm), MH+: 2348.14908 Da, RT: 28.78 min,
Identified with: Sequest HT (v1.3); XCorr:3.60, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	114.09135	57.54931	38.70197	L				21
2	243.13395	122.07061	81.71617	E	2235.06373	1118.03550	745.69276	20
3	314.17107	157.58917	105.39521	A	2106.02113	1053.51420	702.67856	19
4	443.21367	222.11047	148.40941	E	2034.98401	1017.99564	678.99952	18
5	557.25660	279.13194	186.42372	N	1905.94141	953.47434	635.98532	17
6	671.29953	336.15340	224.43803	N	1791.89848	896.45288	597.97101	16
7	784.38360	392.69544	262.13272	L	1677.85555	839.43141	559.95670	15
8	855.42072	428.21400	285.81176	A	1564.77148	782.88938	522.26201	14
9	926.45784	463.73256	309.49080	A	1493.73436	747.37082	498.58297	13
10	1089.52116	545.26422	363.84524	Y	1422.69724	711.85226	474.90393	12
11	1245.62228	623.31478	415.87894	R	1259.63392	630.32060	420.54949	11
12	1373.68086	687.34407	458.56514	Q	1103.53280	552.27004	368.51578	10
13	1502.72346	751.86537	501.57934	E	975.47422	488.24075	325.82959	9
14	1573.76058	787.38393	525.25838	A	846.43162	423.71945	282.81539	8
15	1688.78753	844.89740	563.60069	D	775.39450	388.20089	259.13635	7
16	1817.83013	909.41870	606.61489	E	660.36755	330.68741	220.79403	6
17	1888.86725	944.93726	630.29393	A	531.32495	266.16611	177.77983	5
18	1989.91493	995.46110	663.97649	T	460.28783	230.64755	154.10079	4
19	2102.99900	1052.00314	701.67118	L	359.24015	180.12371	120.41823	3

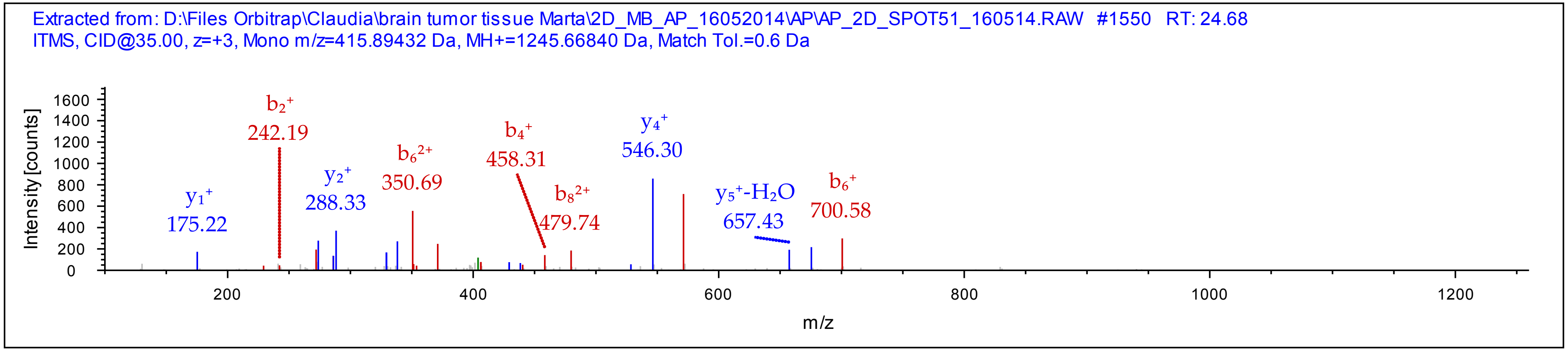
20	2174.03612	1087.52170	725.35022	A	246.15608	123.58168	82.72354	2
21				R	175.11896	88.06312	59.04450	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT51_160514.RAW #2027 RT: 28.78
ITMS, CID@35.00, z=+3, Mono m/z=783.38788 Da, MH+=2348.14908 Da, Match Tol.=0.6 Da

Sequence: KIESLEEEIR, Charge: +3, Monoisotopic m/z: 415.89432 Da (-0.06 mmu/-0.14 ppm), MH+: 1245.66840 Da, RT: 24.68 min,
Identified with: Sequest HT (v1.3); XCorr:3.52, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	129.10225	65.05476	43.70560	K				10
2	242.18632	121.59680	81.40029	I	1117.57360	559.29044	373.19605	9
3	371.22892	186.11810	124.41449	E	1004.48953	502.74840	335.50136	8
4	458.26095	229.63411	153.42517	S	875.44693	438.22710	292.48716	7
5	571.34502	286.17615	191.11986	L	788.41490	394.71109	263.47648	6
6	700.38762	350.69745	234.13406	E	675.33083	338.16905	225.78179	5
7	829.43022	415.21875	277.14826	E	546.28823	273.64775	182.76759	4
8	958.47282	479.74005	320.16246	E	417.24563	209.12645	139.75339	3
9	1071.55689	536.28208	357.85715	I	288.20303	144.60515	96.73919	2
10				R	175.11896	88.06312	59.04450	1

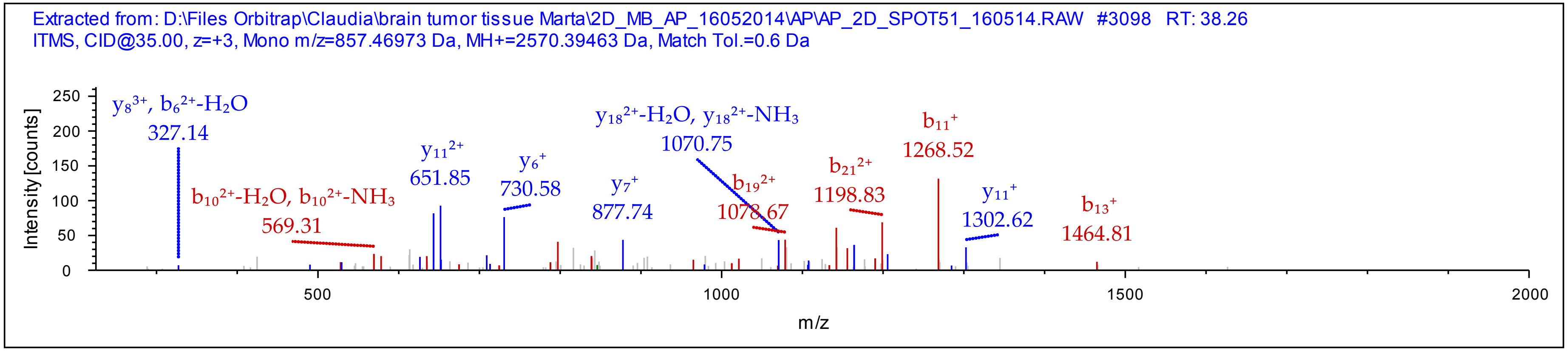

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT51_160514.RAW #1550 RT: 24.68
ITMS, CID@35.00, z=+3, Mono m/z=415.89432 Da, MH+=1245.66840 Da, Match Tol.=0.6 Da

Sequence: LLEGEENRITIPVQTFSNLQIR, Charge: +3, Monoisotopic m/z: 857.46973 Da (+0.28 mmu/+0.32 ppm), MH+: 2570.39463 Da, RT: 38.26 min,
Identified with: Sequest HT (v1.3); XCorr:3.51, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	114.09135	57.54931	38.70197	L				22
2	227.17542	114.09135	76.39666	L	2457.30972	1229.15850	819.77476	21
3	356.21802	178.61265	119.41086	E	2344.22565	1172.61646	782.08007	20
4	413.23949	207.12338	138.41801	G	2215.18305	1108.09516	739.06587	19
5	542.28209	271.64468	181.43221	E	2158.16158	1079.58443	720.05871	18
6	671.32469	336.16598	224.44641	E	2029.11898	1015.06313	677.04451	17
7	785.36762	393.18745	262.46072	N	1900.07638	950.54183	634.03031	16
8	941.46874	471.23801	314.49443	R	1786.03345	893.52036	596.01600	15
9	1054.55281	527.78004	352.18912	I	1629.93233	815.46980	543.98229	14
10	1155.60049	578.30388	385.87168	T	1516.84826	758.92777	506.28760	13
11	1268.68456	634.84592	423.56637	I	1415.80058	708.40393	472.60504	12
12	1365.73733	683.37230	455.91729	P	1302.71651	651.86189	434.91035	11
13	1464.80575	732.90651	488.94010	V	1205.66374	603.33551	402.55943	10
14	1592.86433	796.93580	531.62629	Q	1106.59532	553.80130	369.53662	9
15	1693.91201	847.45964	565.30885	T	978.53674	489.77201	326.85043	8
16	1840.98043	920.99385	614.33166	F	877.48906	439.24817	293.16787	7
17	1928.01246	964.50987	643.34234	S	730.42064	365.71396	244.14506	6
18	2042.05539	1021.53133	681.35665	N	643.38861	322.19794	215.13439	5

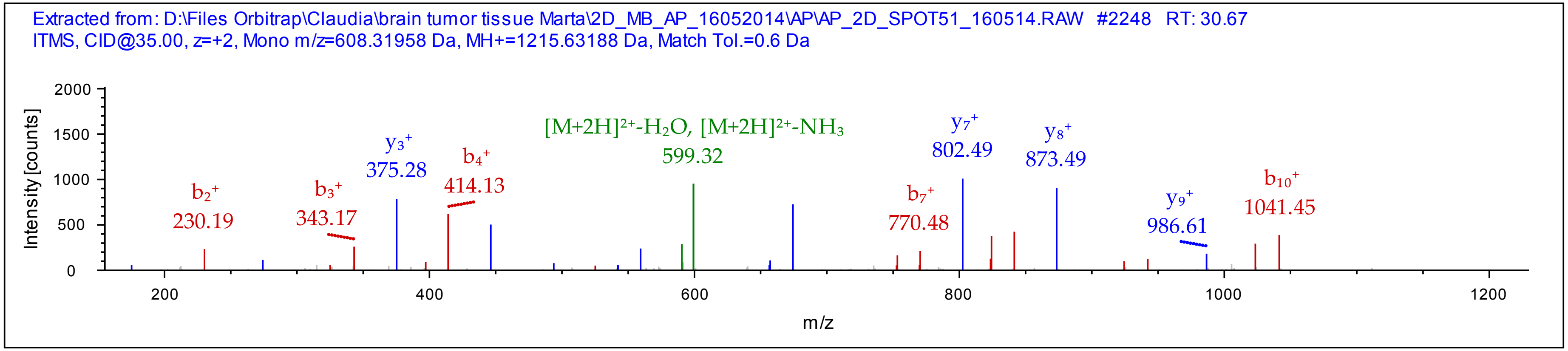
19	2155.13946	1078.07337	719.05134	L	529.34568	265.17648	177.12008	4
20	2283.19804	1142.10266	761.73753	Q	416.26161	208.63444	139.42539	3
21	2396.28211	1198.64469	799.43222	I	288.20303	144.60515	96.73919	2
22				R	175.11896	88.06312	59.04450	1



Sequence: DNLAQDLATVR, Charge: +2, Monoisotopic m/z: 608.31958 Da (-0.48 mmu/-0.8 ppm), MH+: 1215.63188 Da, RT: 30.67 min,
Identified with: Sequest HT (v1.3); XCorr:3.39, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

#1	**b⁺**	**b²⁺**	**Seq.**	**y⁺**	**y²⁺**	**#2**
1	116.03423	58.52075	D			11
2	230.07716	115.54222	N	1100.60590	550.80659	10
3	343.16123	172.08425	L	986.56297	493.78512	9
4	414.19835	207.60281	A	873.47890	437.24309	8
5	542.25693	271.63210	Q	802.44178	401.72453	7
6	657.28388	329.14558	D	674.38320	337.69524	6
7	770.36795	385.68761	L	559.35625	280.18176	5
8	841.40507	421.20617	A	446.27218	223.63973	4
9	942.45275	471.73001	T	375.23506	188.12117	3
10	1041.52117	521.26422	V	274.18738	137.59733	2
11			R	175.11896	88.06312	1

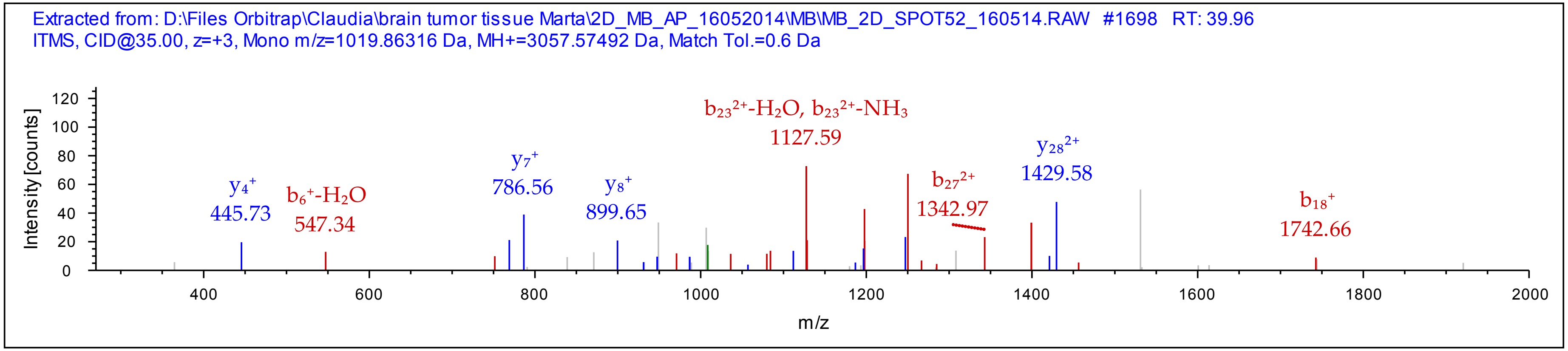

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT51_160514.RAW #2248 RT: 30.67
ITMS, CID@35.00, z=+2, Mono m/z=608.31958 Da, MH+=1215.63188 Da, Match Tol.=0.6 Da
Intensity [counts]
2000
1500
1000
500
0
m/z
200
400
600
800
1000
1200
b2+
230.19
b3+
343.17
y3+
375.28
b4+
414.13
[M+2H]2+-H2O, [M+2H]2+-NH3
599.32
b7+
770.48
y7+
802.49
y8+
873.49
y9+
986.61
b10+
1041.45

Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
52	P04075	Fructose-bisphosphate aldolase A	39.3	8.4	16.2	25.00%	5	5	MB	5.77E-04	2.2	↑ in MB

Sequence: TVPPAVTGITFLSGGQSEEEASINLNAINK, Charge: +3, Monoisotopic m/z: 1019.86316 Da (+0.3 mmu/+0.29 ppm), MH+: 3057.57492 Da, RT: 39.96 min,
Identified with: Sequest HT (v1.3); XCorr:2.52, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 - [ALDOA_HUMAN]

#1	**b$^+$**	**b^{2+}**	**b^{3+}**	**Seq.**	**y$^+$**	**y^{2+}**	**y^{3+}**	**#2**
1	102.05496	51.53112	34.68984	T				30
2	201.12338	101.06533	67.71264	V	2956.52635	1478.76681	986.18030	29
3	298.17615	149.59171	100.06357	P	2857.45793	1429.23260	953.15749	28
4	395.22892	198.11810	132.41449	P	2760.40516	1380.70622	920.80657	27
5	466.26604	233.63666	156.09353	A	2663.35239	1332.17983	888.45565	26
6	565.33446	283.17087	189.11634	V	2592.31527	1296.66127	864.77661	25
7	666.38214	333.69471	222.79890	T	2493.24685	1247.12706	831.75380	24
8	723.40361	362.20544	241.80605	G	2392.19917	1196.60322	798.07124	23
9	836.48768	418.74748	279.50074	I	2335.17770	1168.09249	779.06408	22
10	937.53536	469.27132	313.18330	T	2222.09363	1111.55045	741.36939	21
11	1084.60378	542.80553	362.20611	F	2121.04595	1061.02661	707.68683	20
12	1197.68785	599.34756	399.90080	L	1973.97753	987.49240	658.66403	19
13	1284.71988	642.86358	428.91148	S	1860.89346	930.95037	620.96934	18
14	1341.74135	671.37431	447.91863	G	1773.86143	887.43435	591.95866	17
15	1398.76282	699.88505	466.92579	G	1716.83996	858.92362	572.95150	16
16	1526.82140	763.91434	509.61198	Q	1659.81849	830.41288	553.94435	15
17	1613.85343	807.43035	538.62266	S	1531.75991	766.38359	511.25815	14
18	1742.89603	871.95165	581.63686	E	1444.72788	722.86758	482.24748	13
19	1871.93863	936.47295	624.65106	E	1315.68528	658.34628	439.23328	12
20	2000.98123	1000.99425	667.66526	E	1186.64268	593.82498	396.21908	11
21	2072.01835	1036.51281	691.34430	A	1057.60008	529.30368	353.20488	10
22	2159.05038	1080.02883	720.35498	S	986.56296	493.78512	329.52584	9
23	2272.13445	1136.57086	758.04967	I	899.53093	450.26910	300.51516	8
24	2386.17738	1193.59233	796.06398	N	786.44686	393.72707	262.82047	7
25	2499.26145	1250.13436	833.75867	L	672.40393	336.70560	224.80616	6
26	2613.30438	1307.15583	871.77298	N	559.31986	280.16357	187.11147	5

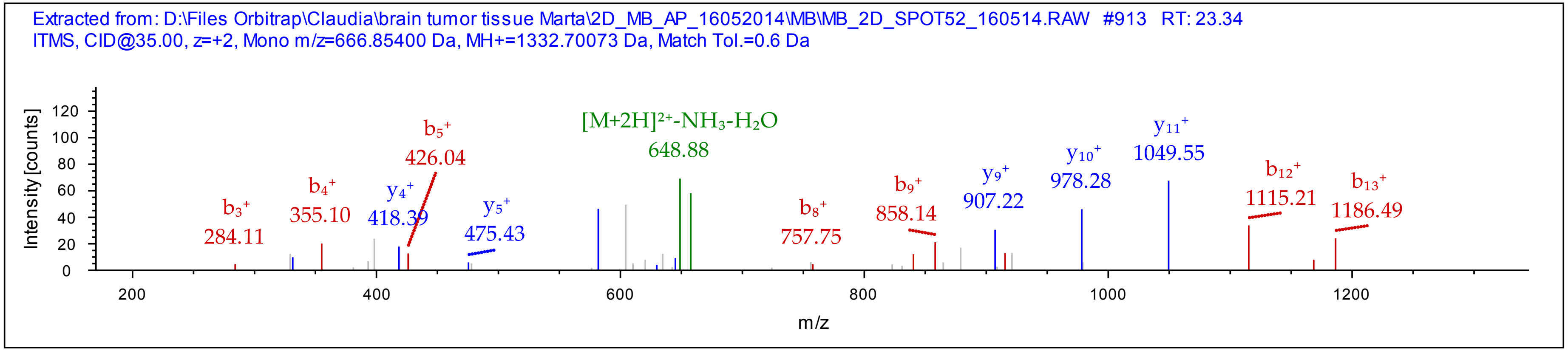
27	2684.34150	1342.67439	895.45202	A	445.27693	223.14210	149.09716	4
28	2797.42557	1399.21642	933.14671	I	374.23981	187.62354	125.41812	3
29	2911.46850	1456.23789	971.16102	N	261.15574	131.08151	87.72343	2
30				K	147.11281	74.06004	49.70912	1



Sequence: GILAADESTGSIAK, Charge: +2, Monoisotopic m/z: 666.85400 Da (+0.06 mmu/+0.09 ppm), MH+: 1332.70073 Da, RT: 23.34 min,
Identified with: Sequest HT (v1.3); XCorr:2.47, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 - [ALDOA_HUMAN]

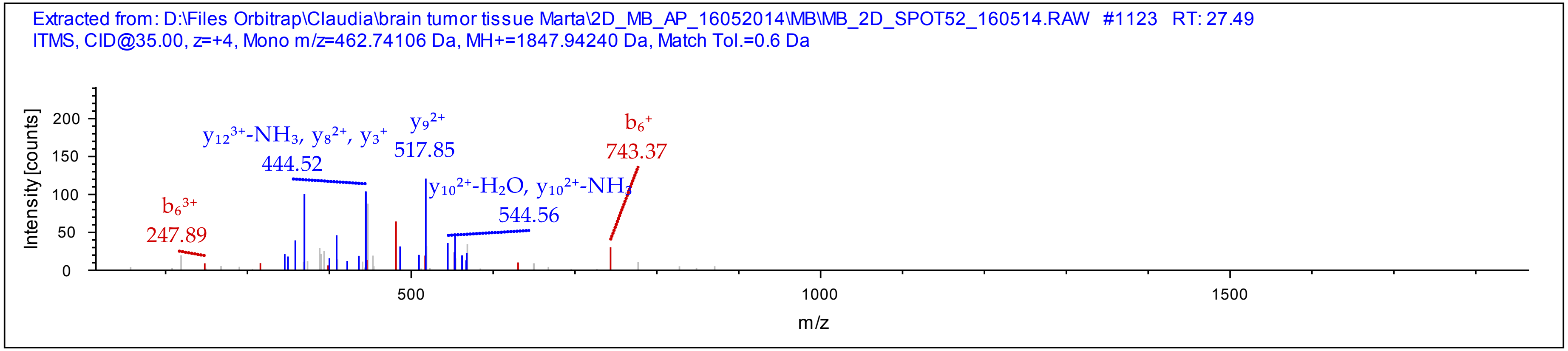
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	58.02875	29.51801	G			14
2	171.11282	86.06005	I	1275.67914	638.34321	13
3	284.19689	142.60208	L	1162.59507	581.80117	12
4	355.23401	178.12064	A	1049.51100	525.25914	11
5	426.27113	213.63920	A	978.47388	489.74058	10
6	541.29808	271.15268	D	907.43676	454.22202	9
7	670.34068	335.67398	E	792.40981	396.70854	8
8	757.37271	379.18999	S	663.36721	332.18724	7
9	858.42039	429.71383	T	576.33518	288.67123	6
10	915.44186	458.22457	G	475.28750	238.14739	5
11	1002.47389	501.74058	S	418.26603	209.63665	4
12	1115.55796	558.28262	I	331.23400	166.12064	3
13	1186.59508	593.80118	A	218.14993	109.57860	2
14			K	147.11281	74.06004	1



Sequence: FSHEEIAMATVTALRR, M8-Oxidation (15.99492 Da)
Charge: +4, Monoisotopic m/z: 462.74106 Da (-0.23 mmu/-0.5 ppm), MH+: 1847.94240 Da, RT: 27.49 min,
Identified with: Sequest HT (v1.3); XCorr:2.32, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 - [ALDOA_HUMAN]

#1	b^+	b^{2+}	b^{3+}	b^{4+}	Seq.	y^+	y^{2+}	y^{3+}	y^{4+}	#2
1	148.07570	74.54149	50.03008	37.77438	F					16
2	235.10773	118.05750	79.04076	59.53239	S	1700.87492	850.94110	567.62982	425.97419	15
3	372.16664	186.58696	124.72706	93.79712	H	1613.84289	807.42508	538.61915	404.21618	14
4	501.20924	251.10826	167.74126	126.05777	E	1476.78398	738.89563	492.93284	369.95145	13
5	630.25184	315.62956	210.75546	158.31842	E	1347.74138	674.37433	449.91864	337.69080	12
6	743.33591	372.17159	248.45015	186.58943	I	1218.69878	609.85303	406.90444	305.43015	11
7	814.37303	407.69015	272.12919	204.34871	A	1105.61471	553.31099	369.20975	277.15913	10
8	961.40844	481.20786	321.14100	241.10757	M-Oxidation	1034.57759	517.79243	345.53071	259.39985	9
9	1032.44556	516.72642	344.82004	258.86685	A	887.54217	444.27472	296.51891	222.64100	8
10	1133.49324	567.25026	378.50260	284.12877	T	816.50505	408.75616	272.83987	204.88172	7
11	1232.56166	616.78447	411.52540	308.89587	V	715.45737	358.23232	239.15731	179.61980	6
12	1333.60934	667.30831	445.20796	334.15779	T	616.38895	308.69811	206.13450	154.85270	5
13	1404.64646	702.82687	468.88700	351.91707	A	515.34127	258.17427	172.45194	129.59078	4
14	1517.73053	759.36890	506.58169	380.18809	L	444.30415	222.65571	148.77290	111.83150	3
15	1673.83165	837.41946	558.61540	419.21337	R	331.22008	166.11368	111.07821	83.56048	2
16					R	175.11896	88.06312	59.04450	44.53520	1

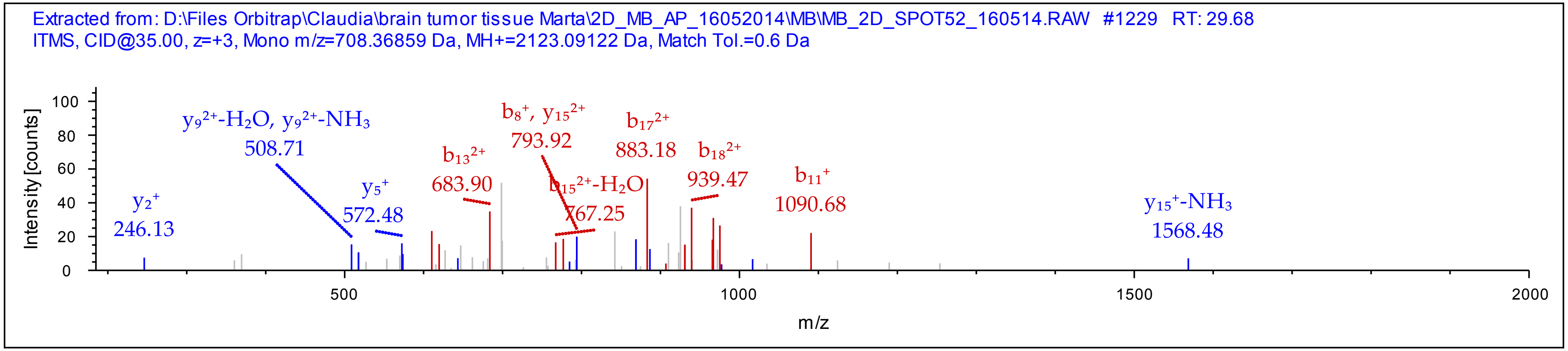

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT52_160514.RAW #1123 RT: 27.49
ITMS, CID@35.00, z=+4, Mono m/z=462.74106 Da, MH+=1847.94240 Da, Match Tol.=0.6 Da

Sequence: IGEHTPSALAIMENANVLAR, M12-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 708.36859 Da (-0.09 mmu/-0.12 ppm), MH+: 2123.09122 Da, RT: 29.68 min,
Identified with: Sequest HT (v1.3); XCorr:2.09, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 - [ALDOA_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	114.09135	57.54931	38.70197	I				20
2	171.11282	86.06005	57.70912	G	2010.00741	1005.50734	670.67399	19
3	300.15542	150.58135	100.72332	E	1952.98594	976.99661	651.66683	18
4	437.21433	219.11080	146.40963	H	1823.94334	912.47531	608.65263	17
5	538.26201	269.63464	180.09219	T	1686.88443	843.94585	562.96633	16
6	635.31478	318.16103	212.44311	P	1585.83675	793.42201	529.28377	15
7	722.34681	361.67704	241.45379	S	1488.78398	744.89563	496.93284	14
8	793.38393	397.19560	265.13283	A	1401.75195	701.37961	467.92217	13
9	906.46800	453.73764	302.82752	L	1330.71483	665.86105	444.24313	12
10	977.50512	489.25620	326.50656	A	1217.63076	609.31902	406.54844	11
11	1090.58919	545.79823	364.20125	I	1146.59364	573.80046	382.86940	10
12	1237.62460	619.31594	413.21305	M-Oxidation	1033.50957	517.25842	345.17471	9
13	1366.66720	683.83724	456.22725	E	886.47415	443.74071	296.16290	8
14	1480.71013	740.85870	494.24156	N	757.43155	379.21941	253.14870	7
15	1551.74725	776.37726	517.92060	A	643.38862	322.19795	215.13439	6
16	1665.79018	833.39873	555.93491	N	572.35150	286.67939	191.45535	5
17	1764.85860	882.93294	588.95772	V	458.30857	229.65792	153.44104	4

18	1877.94267	939.47497	626.65241	L	359.24015	180.12371	120.41823	3
19	1948.97979	974.99353	650.33145	A	246.15608	123.58168	82.72354	2
20				R	175.11896	88.06312	59.04450	1

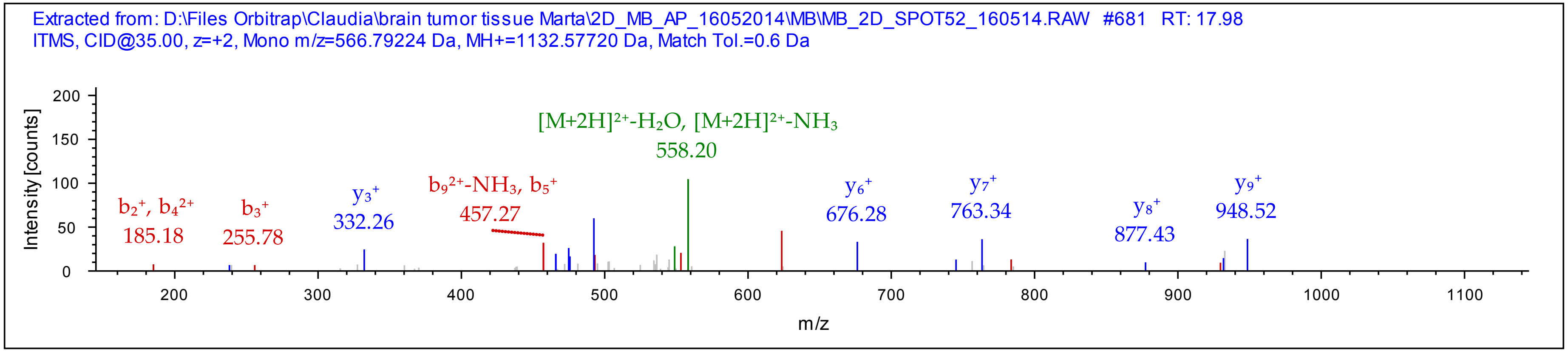


Sequence: ALANSLACQGK, C8-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 566.79224 Da (-0.39 mmu/-0.69 ppm), MH+: 1132.57720 Da, RT: 17.98 min,
Identified with: Sequest HT (v1.3); XCorr:1.80, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 - [ALDOA_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			11
2	185.12847	93.06787	L	1061.54086	531.27407	10
3	256.16559	128.58643	A	948.45679	474.73203	9
4	370.20852	185.60790	N	877.41967	439.21347	8
5	457.24055	229.12391	S	763.37674	382.19201	7
6	570.32462	285.66595	L	676.34471	338.67599	6
7	641.36174	321.18451	A	563.26064	282.13396	5
8	801.39239	401.19983	C-Carbamidomethyl	492.22352	246.61540	4
9	929.45097	465.22912	Q	332.19286	166.60007	3
10	986.47244	493.73986	G	204.13428	102.57078	2

11			K	147.11281	74.06004	1



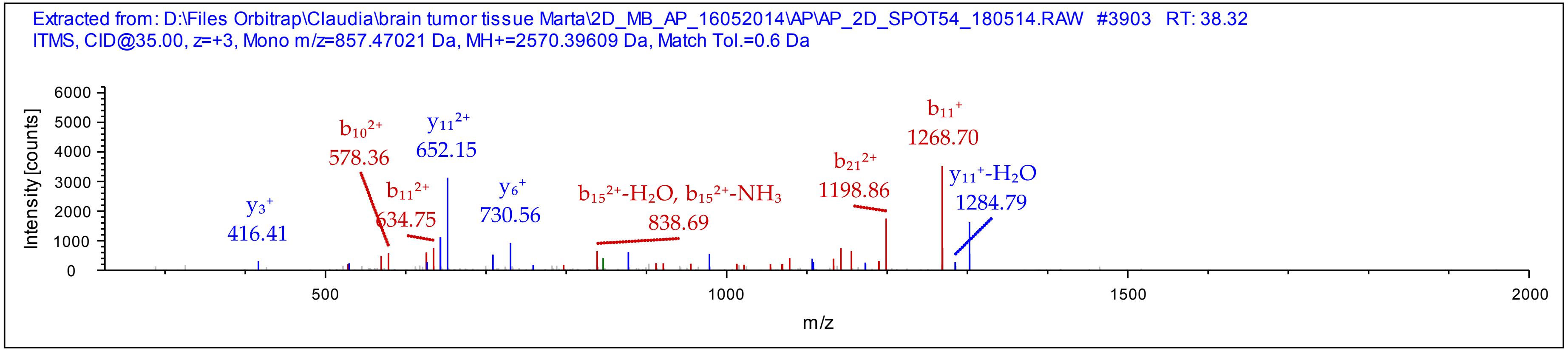
Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
54	P14136	Glial fibrillary acidic protein	49.9	5.4	295.2	41.67%	18	18	PA	2.00E-03	5.7	↑ in PA

Sequence: LLEGEENRITIPVQTFSNLQIR, Charge: +3, Monoisotopic m/z: 857.47021 Da (+0.77 mmu/+0.89 ppm), MH+: 2570.39609 Da, RT: 38.32 min,
Identified with: Sequest HT (v1.3); XCorr:5.59, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

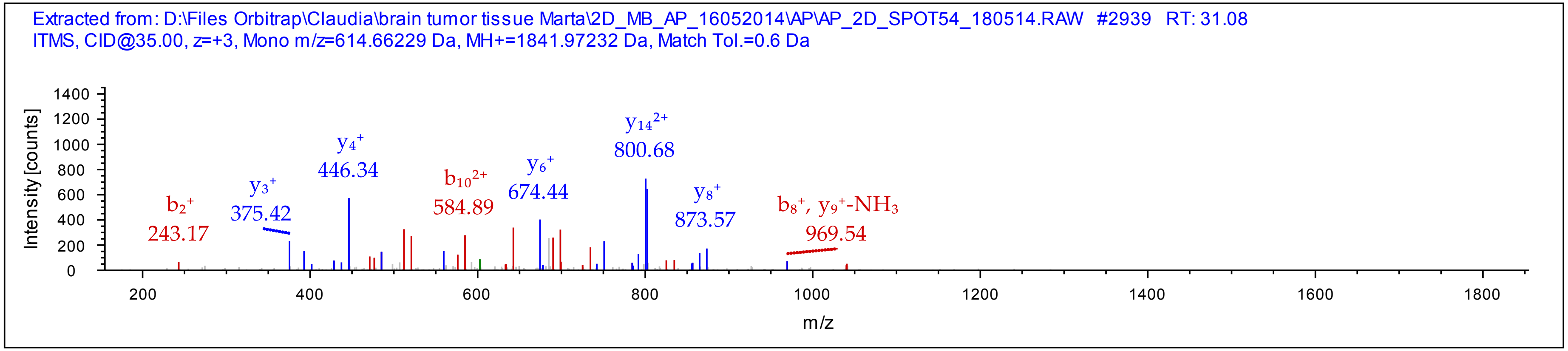
#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	114.09135	57.54931	38.70197	L				22
2	227.17542	114.09135	76.39666	L	2457.30972	1229.15850	819.77476	21
3	356.21802	178.61265	119.41086	E	2344.22565	1172.61646	782.08007	20
4	413.23949	207.12338	138.41801	G	2215.18305	1108.09516	739.06587	19
5	542.28209	271.64468	181.43221	E	2158.16158	1079.58443	720.05871	18
6	671.32469	336.16598	224.44641	E	2029.11898	1015.06313	677.04451	17
7	785.36762	393.18745	262.46072	N	1900.07638	950.54183	634.03031	16
8	941.46874	471.23801	314.49443	R	1786.03345	893.52036	596.01600	15
9	1054.55281	527.78004	352.18912	I	1629.93233	815.46980	543.98229	14
10	1155.60049	578.30388	385.87168	T	1516.84826	758.92777	506.28760	13
11	1268.68456	634.84592	423.56637	I	1415.80058	708.40393	472.60504	12
12	1365.73733	683.37230	455.91729	P	1302.71651	651.86189	434.91035	11
13	1464.80575	732.90651	488.94010	V	1205.66374	603.33551	402.55943	10
14	1592.86433	796.93580	531.62629	Q	1106.59532	553.80130	369.53662	9
15	1693.91201	847.45964	565.30885	T	978.53674	489.77201	326.85043	8
16	1840.98043	920.99385	614.33166	F	877.48906	439.24817	293.16787	7
17	1928.01246	964.50987	643.34234	S	730.42064	365.71396	244.14506	6
18	2042.05539	1021.53133	681.35665	N	643.38861	322.19794	215.13439	5
19	2155.13946	1078.07337	719.05134	L	529.34568	265.17648	177.12008	4
20	2283.19804	1142.10266	761.73753	Q	416.26161	208.63444	139.42539	3
21	2396.28211	1198.64469	799.43222	I	288.20303	144.60515	96.73919	2
22				R	175.11896	88.06312	59.04450	1



Sequence: LEVERDNLAQDLATVR, Charge: +3, Monoisotopic m/z: 614.66229 Da (+0.22 mmu/+0.36 ppm), MH+: 1841.97232 Da, RT: 31.08 min,
Identified with: Sequest HT (v1.3); XCorr:4.28, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

#1	b^{+}	b^{2+}	b^{3+}	Seq.	y^{+}	y^{2+}	y^{3+}	#2
1	114.09135	57.54931	38.70197	L				16
2	243.13395	122.07061	81.71617	E	1728.88759	864.94743	576.96738	15
3	342.20237	171.60482	114.73897	V	1599.84499	800.42613	533.95318	14
4	471.24497	236.12612	157.75317	E	1500.77657	750.89192	500.93037	13
5	627.34609	314.17668	209.78688	R	1371.73397	686.37062	457.91617	12
6	742.37304	371.69016	248.12920	D	1215.63285	608.32006	405.88247	11
7	856.41597	428.71162	286.14351	N	1100.60590	550.80659	367.54015	10
8	969.50004	485.25366	323.83820	L	986.56297	493.78512	329.52584	9
9	1040.53716	520.77222	347.51724	A	873.47890	437.24309	291.83115	8
10	1168.59574	584.80151	390.20343	Q	802.44178	401.72453	268.15211	7
11	1283.62269	642.31498	428.54575	D	674.38320	337.69524	225.46592	6
12	1396.70676	698.85702	466.24044	L	559.35625	280.18176	187.12360	5
13	1467.74388	734.37558	489.91948	A	446.27218	223.63973	149.42891	4
14	1568.79156	784.89942	523.60204	T	375.23506	188.12117	125.74987	3
15	1667.85998	834.43363	556.62484	V	274.18738	137.59733	92.06731	2
16				R	175.11896	88.06312	59.04450	1



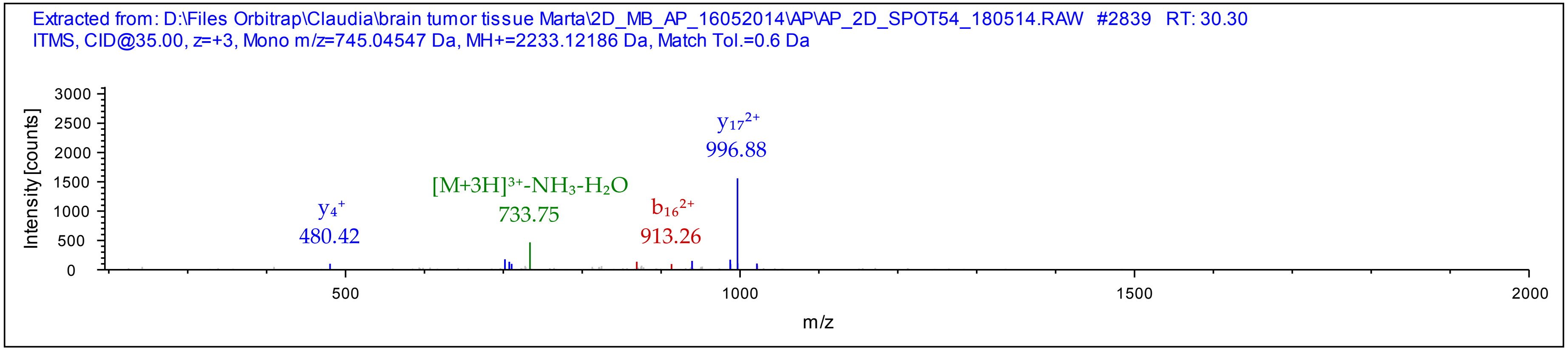
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT54_180514.RAW #2939 RT: 31.08
ITMS, CID@35.00, z=+3, Mono m/z=614.66229 Da, MH+=1841.97232 Da, Match Tol.=0.6 Da

Sequence: LQDETNLRLEAENNLAAYR, Charge: +3, Monoisotopic m/z: 745.04547 Da (+0.34 mmu/+0.46 ppm), MH+: 2233.12186 Da, RT: 30.30 min,
Identified with: Sequest HT (v1.3); XCorr:3.77, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	114.09135	57.54931	38.70197	L				19
2	242.14993	121.57860	81.38816	Q	2120.03677	1060.52202	707.35044	18
3	357.17688	179.09208	119.73048	D	1991.97819	996.49273	664.66425	17
4	486.21948	243.61338	162.74468	E	1876.95124	938.97926	626.32193	16
5	587.26716	294.13722	196.42724	T	1747.90864	874.45796	583.30773	15
6	701.31009	351.15868	234.44155	N	1646.86096	823.93412	549.62517	14
7	814.39416	407.70072	272.13624	L	1532.81803	766.91265	511.61086	13
8	970.49528	485.75128	324.16994	R	1419.73396	710.37062	473.91617	12
9	1083.57935	542.29331	361.86463	L	1263.63284	632.32006	421.88246	11
10	1212.62195	606.81461	404.87883	E	1150.54877	575.77802	384.18777	10
11	1283.65907	642.33317	428.55787	A	1021.50617	511.25672	341.17357	9
12	1412.70167	706.85447	471.57207	E	950.46905	475.73816	317.49453	8
13	1526.74460	763.87594	509.58638	N	821.42645	411.21686	274.48033	7
14	1640.78753	820.89740	547.60069	N	707.38352	354.19540	236.46602	6
15	1753.87160	877.43944	585.29538	L	593.34059	297.17393	198.45171	5
16	1824.90872	912.95800	608.97442	A	480.25652	240.63190	160.75702	4
17	1895.94584	948.47656	632.65346	A	409.21940	205.11334	137.07798	3
18	2059.00916	1030.00822	687.00790	Y	338.18228	169.59478	113.39894	2

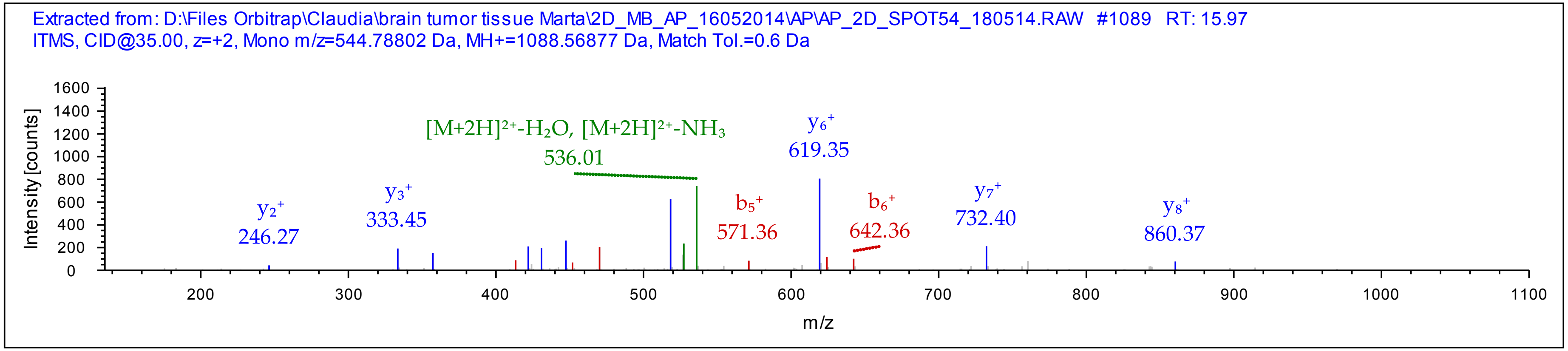
19	R	175.11896	88.06312	59.04450	1	



Sequence: LDQLTANSAR, Charge: +2, Monoisotopic m/z: 544.78802 Da (-0.37 mmu/-0.68 ppm), MH+: 1088.56877 Da, RT: 15.97 min,
Identified with: Sequest HT (v1.3); XCorr:3.58, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

#1	**b⁺**	**b²⁺**	**Seq.**	**y⁺**	**y²⁺**	**#2**
1	114.09135	57.54931	L			10
2	229.11830	115.06279	D	975.48544	488.24636	9
3	357.17688	179.09208	Q	860.45849	430.73288	8
4	470.26095	235.63411	L	732.39991	366.70359	7
5	571.30863	286.15795	T	619.31584	310.16156	6
6	642.34575	321.67651	A	518.26816	259.63772	5
7	756.38868	378.69798	N	447.23104	224.11916	4
8	843.42071	422.21399	S	333.18811	167.09769	3
9	914.45783	457.73255	A	246.15608	123.58168	2
10			R	175.11896	88.06312	1

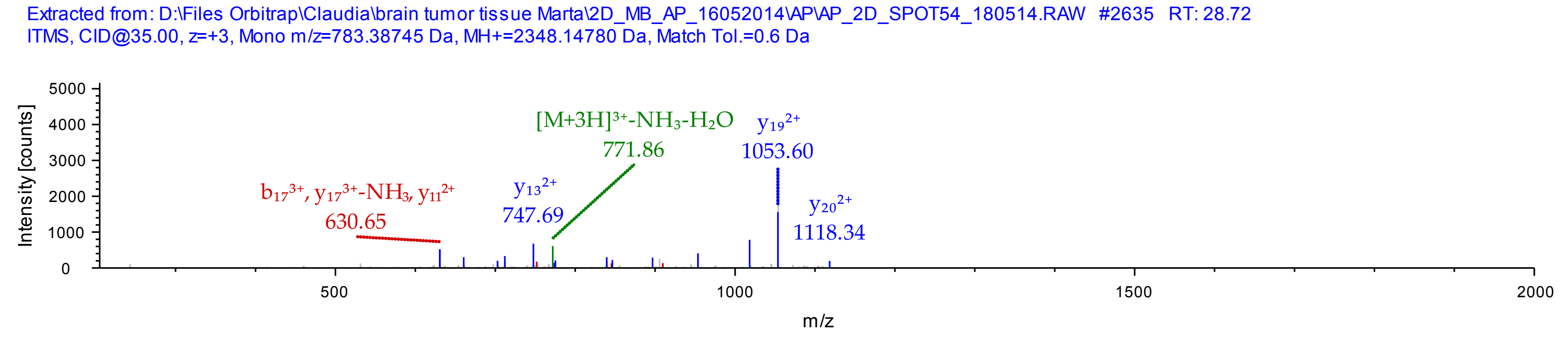


Sequence: LEAENNLAAYRQEADEATLAR, Charge: +3, Monoisotopic m/z: 783.38745 Da (0 mmu/0 ppm), MH+: 2348.14780 Da, RT: 28.72 min,
Identified with: Sequest HT (v1.3); XCorr:3.53, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

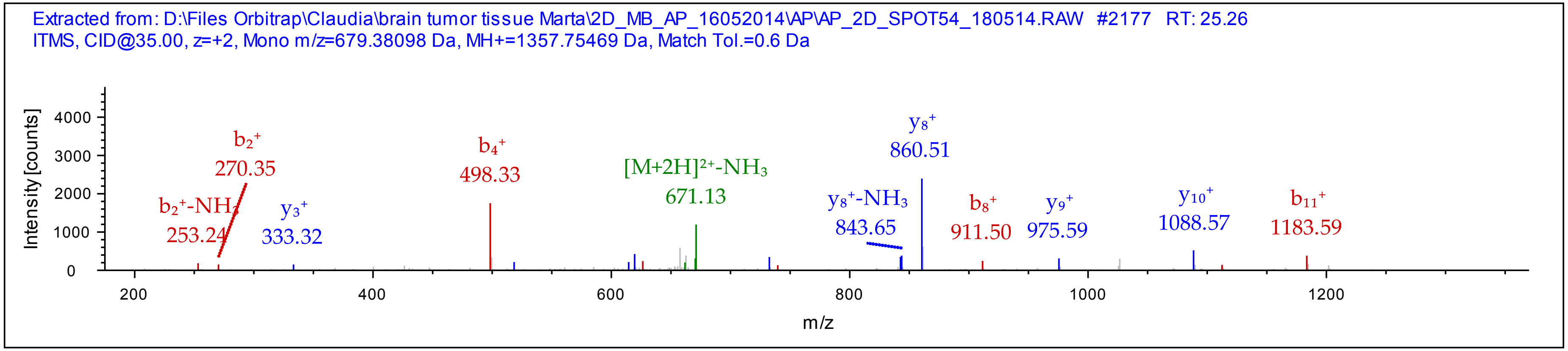
#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	114.09135	57.54931	38.70197	L				21
2	243.13395	122.07061	81.71617	E	2235.06373	1118.03550	745.69276	20
3	314.17107	157.58917	105.39521	A	2106.02113	1053.51420	702.67856	19
4	443.21367	222.11047	148.40941	E	2034.98401	1017.99564	678.99952	18
5	557.25660	279.13194	186.42372	N	1905.94141	953.47434	635.98532	17
6	671.29953	336.15340	224.43803	N	1791.89848	896.45288	597.97101	16
7	784.38360	392.69544	262.13272	L	1677.85555	839.43141	559.95670	15
8	855.42072	428.21400	285.81176	A	1564.77148	782.88938	522.26201	14
9	926.45784	463.73256	309.49080	A	1493.73436	747.37082	498.58297	13
10	1089.52116	545.26422	363.84524	Y	1422.69724	711.85226	474.90393	12
11	1245.62228	623.31478	415.87894	R	1259.63392	630.32060	420.54949	11
12	1373.68086	687.34407	458.56514	Q	1103.53280	552.27004	368.51578	10
13	1502.72346	751.86537	501.57934	E	975.47422	488.24075	325.82959	9
14	1573.76058	787.38393	525.25838	A	846.43162	423.71945	282.81539	8
15	1688.78753	844.89740	563.60069	D	775.39450	388.20089	259.13635	7
16	1817.83013	909.41870	606.61489	E	660.36755	330.68741	220.79403	6
17	1888.86725	944.93726	630.29393	A	531.32495	266.16611	177.77983	5
18	1989.91493	995.46110	663.97649	T	460.28783	230.64755	154.10079	4

19	2102.99900	1052.00314	701.67118	L	359.24015	180.12371	120.41823	3
20	2174.03612	1087.52170	725.35022	A	246.15608	123.58168	82.72354	2
21				R	175.11896	88.06312	59.04450	1



Sequence: LRLDQLTANSAR, Charge: +2, Monoisotopic m/z: 679.38098 Da (-0.01 mmu/-0.01 ppm), MH+: 1357.75469 Da, RT: 25.26 min,
Identified with: Sequest HT (v1.3); XCorr:3.52, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

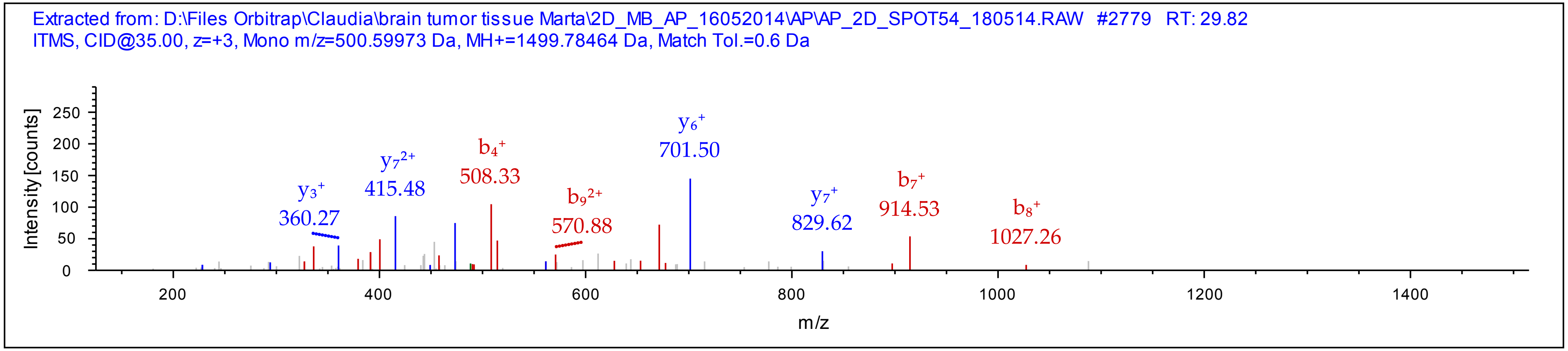
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	114.09135	57.54931	L			12
2	270.19247	135.59987	R	1244.67063	622.83895	11
3	383.27654	192.14191	L	1088.56951	544.78839	10
4	498.30349	249.65538	D	975.48544	488.24636	9
5	626.36207	313.68467	Q	860.45849	430.73288	8
6	739.44614	370.22671	L	732.39991	366.70359	7
7	840.49382	420.75055	T	619.31584	310.16156	6
8	911.53094	456.26911	A	518.26816	259.63772	5
9	1025.57387	513.29057	N	447.23104	224.11916	4
10	1112.60590	556.80659	S	333.18811	167.09769	3
11	1183.64302	592.32515	A	246.15608	123.58168	2
12			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT54_180514.RAW #2177 RT: 25.26
ITMS, CID@35.00, z=+2, Mono m/z=679.38098 Da, MH+=1357.75469 Da, Match Tol.=0.6 Da

Sequence: HLQEYQDLLNVK, Charge: +3, Monoisotopic m/z: 500.59973 Da (-0.22 mmu/-0.45 ppm), MH+: 1499.78464 Da, RT: 29.82 min,
Identified with: Sequest HT (v1.3); XCorr:3.49, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

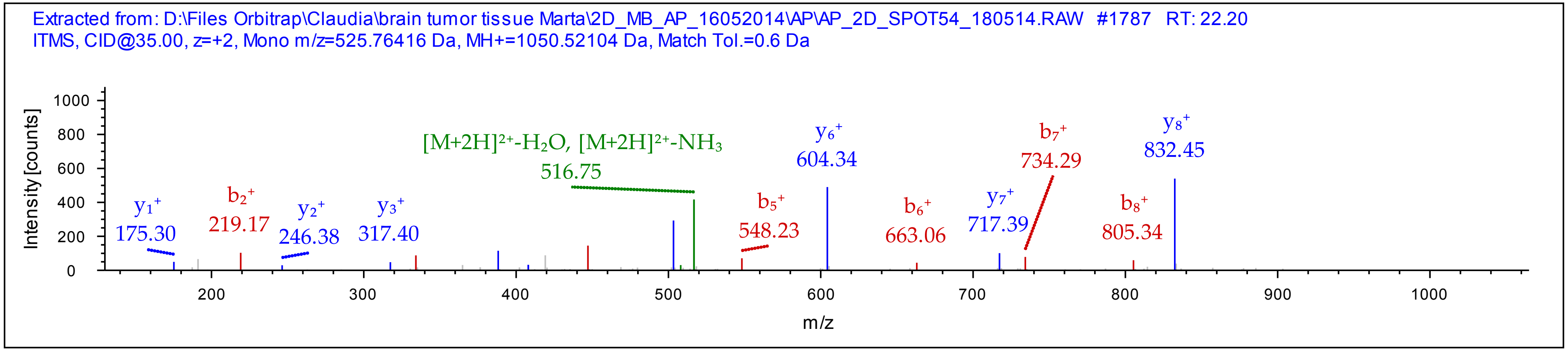
#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	138.06619	69.53673	46.69358	H				12
2	251.15026	126.07877	84.38827	L	1362.72640	681.86684	454.91365	11
3	379.20884	190.10806	127.07446	Q	1249.64233	625.32480	417.21896	10
4	508.25144	254.62936	170.08866	E	1121.58375	561.29551	374.53277	9
5	671.31476	336.16102	224.44310	Y	992.54115	496.77421	331.51857	8
6	799.37334	400.19031	267.12930	Q	829.47783	415.24255	277.16413	7
7	914.40029	457.70378	305.47161	D	701.41925	351.21326	234.47793	6
8	1027.48436	514.24582	343.16630	L	586.39230	293.69979	196.13562	5
9	1140.56843	570.78785	380.86099	L	473.30823	237.15775	158.44093	4
10	1254.61136	627.80932	418.87530	N	360.22416	180.61572	120.74624	3
11	1353.67978	677.34353	451.89811	V	246.18123	123.59425	82.73193	2
12				K	147.11281	74.06004	49.70912	1



Sequence: FADLTDAAAR, Charge: +2, Monoisotopic m/z: 525.76416 Da (-0.23 mmu/-0.45 ppm), MH+: 1050.52104 Da, RT: 22.20 min,
Identified with: Sequest HT (v1.3); XCorr:3.36, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	148.07570	74.54149	F			10
2	219.11282	110.06005	A	903.45309	452.23018	9
3	334.13977	167.57352	D	832.41597	416.71162	8
4	447.22384	224.11556	L	717.38902	359.19815	7
5	548.27152	274.63940	T	604.30495	302.65611	6
6	663.29847	332.15287	D	503.25727	252.13227	5
7	734.33559	367.67143	A	388.23032	194.61880	4
8	805.37271	403.18999	A	317.19320	159.10024	3
9	876.40983	438.70855	A	246.15608	123.58168	2
10			R	175.11896	88.06312	1

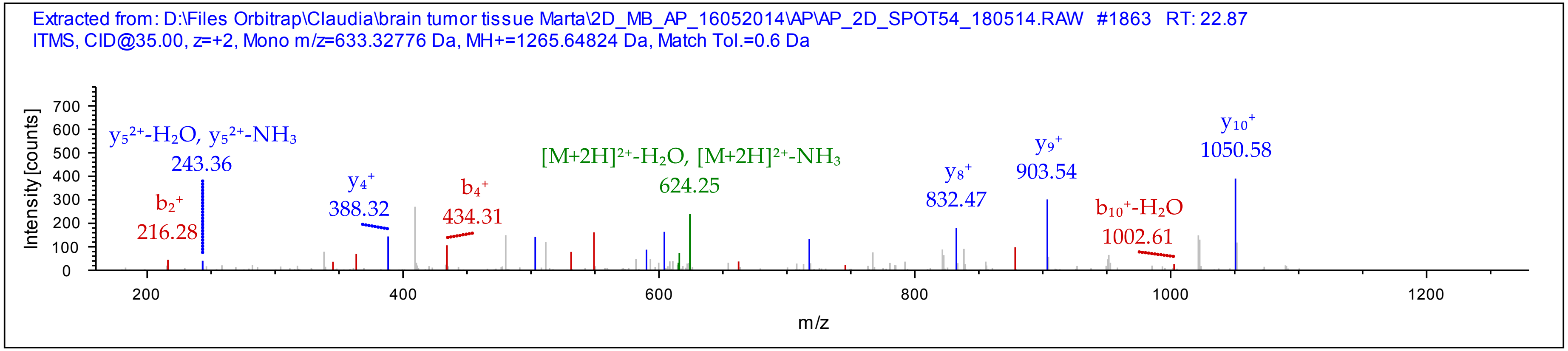


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT54_180514.RAW #1787 RT: 22.20
ITMS, CID@35.00, z=+2, Mono m/z=525.76416 Da, MH+=1050.52104 Da, Match Tol.=0.6 Da

Sequence: SKFADLTDAAAR, Charge: +2, Monoisotopic m/z: 633.32776 Da (-0.14 mmu/-0.21 ppm), MH+: 1265.64824 Da, RT: 22.87 min,
Identified with: Sequest HT (v1.3); XCorr:3.31, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	88.03931	44.52329	S			12
2	216.13428	108.57078	K	1178.61648	589.81188	11
3	363.20270	182.10499	F	1050.52151	525.76439	10
4	434.23982	217.62355	A	903.45309	452.23018	9
5	549.26677	275.13702	D	832.41597	416.71162	8
6	662.35084	331.67906	L	717.38902	359.19815	7
7	763.39852	382.20290	T	604.30495	302.65611	6
8	878.42547	439.71637	D	503.25727	252.13227	5
9	949.46259	475.23493	A	388.23032	194.61880	4
10	1020.49971	510.75349	A	317.19320	159.10024	3
11	1091.53683	546.27205	A	246.15608	123.58168	2
12			R	175.11896	88.06312	1

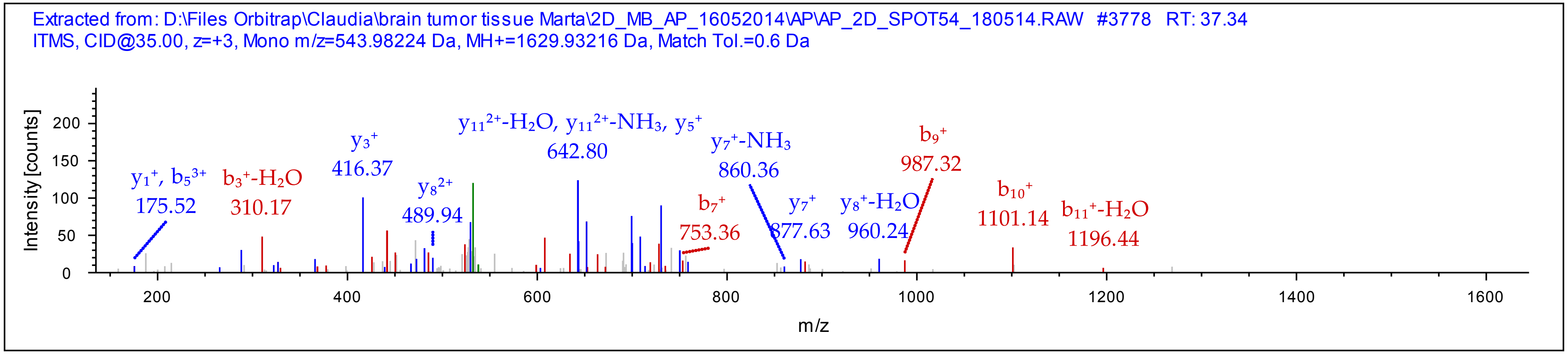


Sequence: ITIPVQTFSNLQIR, Charge: +3, Monoisotopic m/z: 543.98224 Da (-0.06 mmu/-0.1 ppm), MH+: 1629.93216 Da, RT: 37.34 min,
Identified with: Sequest HT (v1.3); XCorr:3.27, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

#1	b^{+}	b^{2+}	b^{3+}	Seq.	y^{+}	y^{2+}	y^{3+}	#2
1	114.09135	57.54931	38.70197	I				14
2	215.13903	108.07315	72.38453	T	1516.84826	758.92777	506.28760	13
3	328.22310	164.61519	110.07922	I	1415.80058	708.40393	472.60504	12
4	425.27587	213.14157	142.43014	P	1302.71651	651.86189	434.91035	11
5	524.34429	262.67578	175.45295	V	1205.66374	603.33551	402.55943	10
6	652.40287	326.70507	218.13914	Q	1106.59532	553.80130	369.53662	9
7	753.45055	377.22891	251.82170	T	978.53674	489.77201	326.85043	8
8	900.51897	450.76312	300.84451	F	877.48906	439.24817	293.16787	7
9	987.55100	494.27914	329.85518	S	730.42064	365.71396	244.14506	6
10	1101.59393	551.30060	367.86949	N	643.38861	322.19794	215.13439	5
11	1214.67800	607.84264	405.56418	L	529.34568	265.17648	177.12008	4
12	1342.73658	671.87193	448.25038	Q	416.26161	208.63444	139.42539	3
13	1455.82065	728.41396	485.94507	I	288.20303	144.60515	96.73919	2
14				R	175.11896	88.06312	59.04450	1

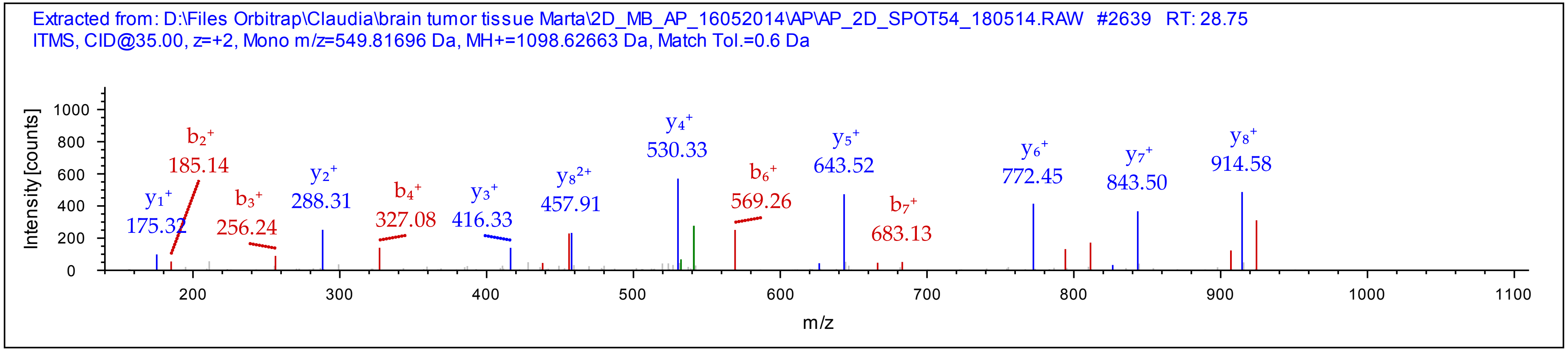


Sequence: ALAAELNQLR, Charge: +2, Monoisotopic m/z: 549.81696 Da (0 mmu/-0.01 ppm), MH+: 1098.62663 Da, RT: 28.75 min,
Identified with: Sequest HT (v1.3); XCorr:3.27, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	72.04440	36.52584	A			10
2	185.12847	93.06787	L	1027.58952	514.29840	9
3	256.16559	128.58643	A	914.50545	457.75636	8
4	327.20271	164.10499	A	843.46833	422.23780	7
5	456.24531	228.62629	E	772.43121	386.71924	6
6	569.32938	285.16833	L	643.38861	322.19794	5
7	683.37231	342.18979	N	530.30454	265.65591	4
8	811.43089	406.21908	Q	416.26161	208.63444	3
9	924.51496	462.76112	L	288.20303	144.60515	2
10			R	175.11896	88.06312	1

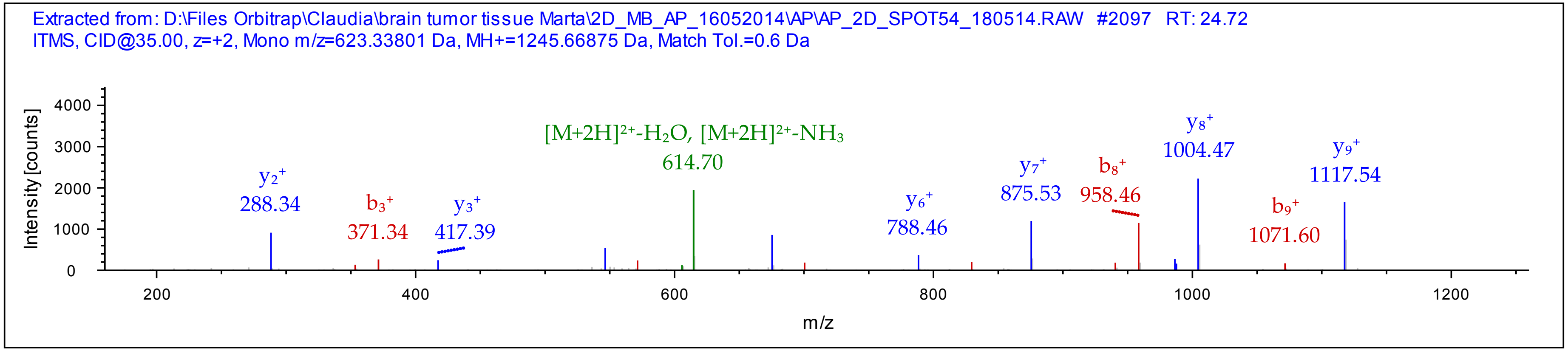


Sequence: KIESLEEEIR, Charge: +2, Monoisotopic m/z: 623.33801 Da (+0.09 mmu/+0.14 ppm), MH+: 1245.66875 Da, RT: 24.72 min,
Identified with: Sequest HT (v1.3); XCorr:3.24, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	129.10225	65.05476	K			10
2	242.18632	121.59680	I	1117.57360	559.29044	9
3	371.22892	186.11810	E	1004.48953	502.74840	8
4	458.26095	229.63411	S	875.44693	438.22710	7
5	571.34502	286.17615	L	788.41490	394.71109	6
6	700.38762	350.69745	E	675.33083	338.16905	5
7	829.43022	415.21875	E	546.28823	273.64775	4
8	958.47282	479.74005	E	417.24563	209.12645	3
9	1071.55689	536.28208	I	288.20303	144.60515	2
10			R	175.11896	88.06312	1

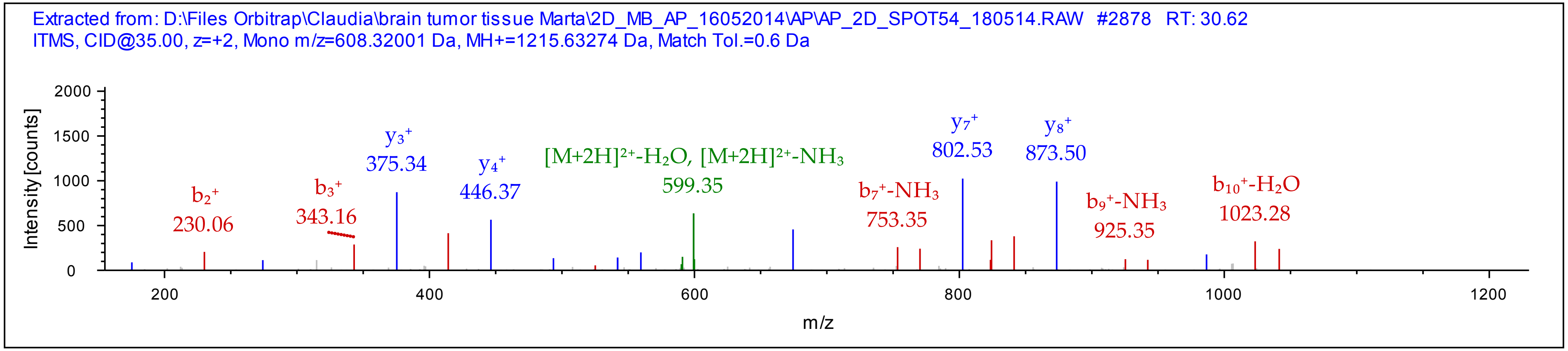


Sequence: DNLAQDLATVR, Charge: +2, Monoisotopic m/z: 608.32001 Da (-0.06 mmu/-0.09 ppm), MH+: 1215.63274 Da, RT: 30.62 min,
Identified with: Sequest HT (v1.3); XCorr:3.16, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	116.03423	58.52075	D			11
2	230.07716	115.54222	N	1100.60590	550.80659	10
3	343.16123	172.08425	L	986.56297	493.78512	9
4	414.19835	207.60281	A	873.47890	437.24309	8
5	542.25693	271.63210	Q	802.44178	401.72453	7
6	657.28388	329.14558	D	674.38320	337.69524	6
7	770.36795	385.68761	L	559.35625	280.18176	5
8	841.40507	421.20617	A	446.27218	223.63973	4
9	942.45275	471.73001	T	375.23506	188.12117	3
10	1041.52117	521.26422	V	274.18738	137.59733	2
11			R	175.11896	88.06312	1

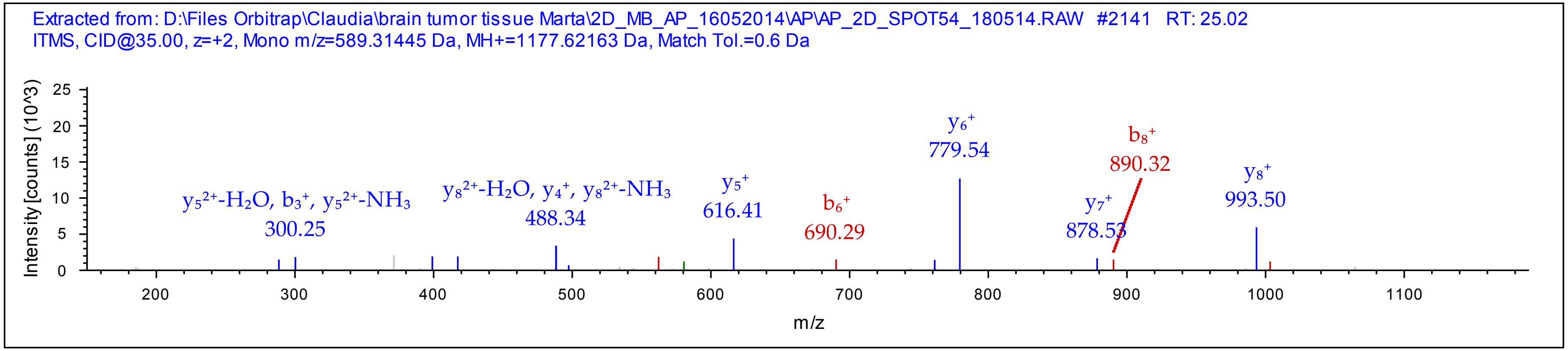


Sequence: LADVYQAELR, Charge: +2, Monoisotopic m/z: 589.31445 Da (+0.21 mmu/+0.36 ppm), MH+: 1177.62163 Da, RT: 25.02 min,
Identified with: Sequest HT (v1.3); XCorr:3.14, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

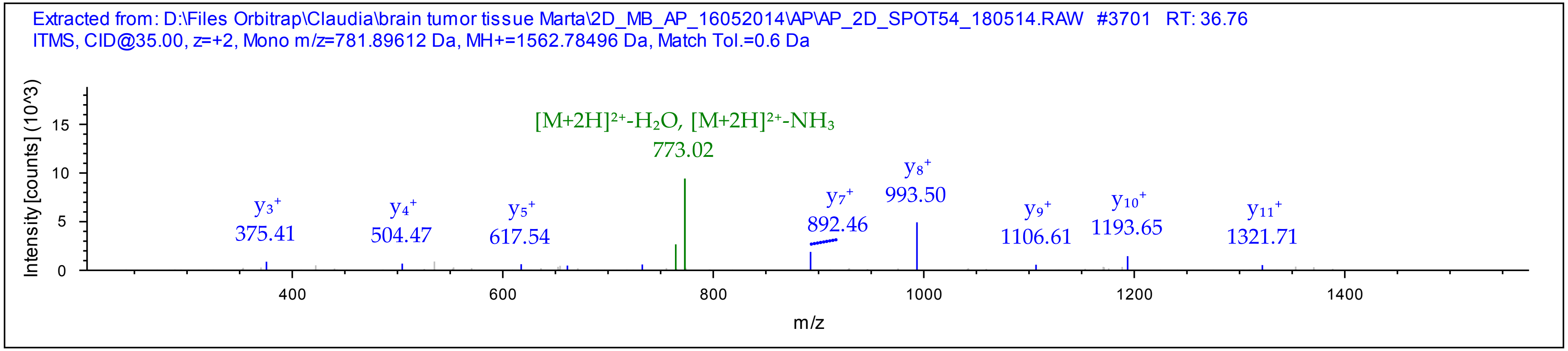
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			10
2	185.12847	93.06787	A	1064.53714	532.77221	9
3	300.15542	150.58135	D	993.50002	497.25365	8
4	399.22384	200.11556	V	878.47307	439.74017	7
5	562.28716	281.64722	Y	779.40465	390.20596	6
6	690.34574	345.67651	Q	616.34133	308.67430	5
7	761.38286	381.19507	A	488.28275	244.64501	4
8	890.42546	445.71637	E	417.24563	209.12645	3
9	1003.50953	502.25840	L	288.20303	144.60515	2
10			R	175.11896	88.06312	1



Sequence: QLQSLTCDLESLR, C7-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 781.89612 Da (+0.31 mmu/+0.39 ppm), MH+: 1562.78496 Da, RT: 36.76 min,
Identified with: Sequest HT (v1.3); XCorr:3.08, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	129.06586	65.03657	Q			13
2	242.14993	121.57860	L	1434.72577	717.86652	12
3	370.20851	185.60789	Q	1321.64170	661.32449	11
4	457.24054	229.12391	S	1193.58312	597.29520	10
5	570.32461	285.66594	L	1106.55109	553.77918	9
6	671.37229	336.18978	T	993.46702	497.23715	8
7	831.40294	416.20511	C-Carbamidomethyl	892.41934	446.71331	7
8	946.42989	473.71858	D	732.38868	366.69798	6
9	1059.51396	530.26062	L	617.36173	309.18450	5
10	1188.55656	594.78192	E	504.27766	252.64247	4
11	1275.58859	638.29793	S	375.23506	188.12117	3
12	1388.67266	694.83997	L	288.20303	144.60515	2
13			R	175.11896	88.06312	1



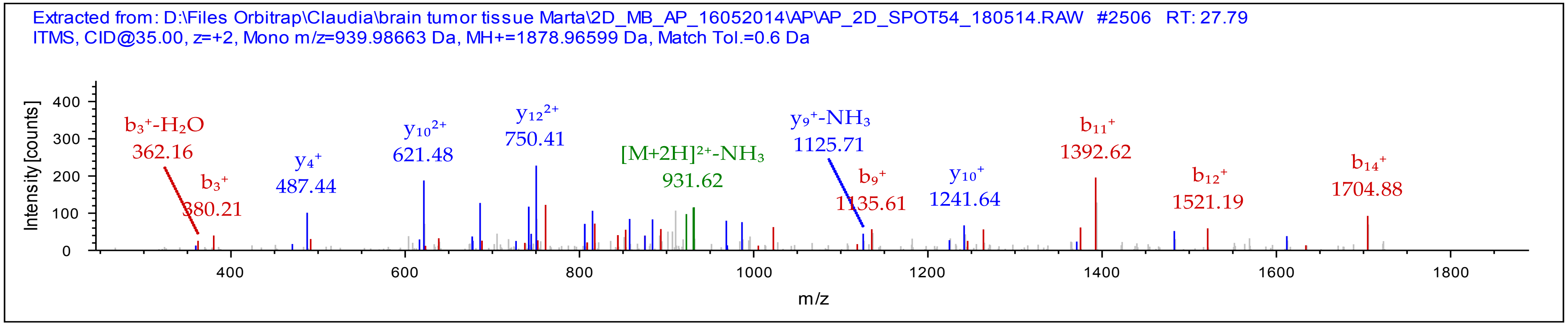
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT54_180514.RAW #3701 RT: 36.76
ITMS, CID@35.00, z=+2, Mono m/z=781.89612 Da, MH+=1562.78496 Da, Match Tol.=0.6 Da

Sequence: IHEEEVRELQEQLAR, Charge: +2, Monoisotopic m/z: 939.98663 Da (-0.46 mmu/-0.49 ppm), MH+: 1878.96599 Da, RT: 27.79 min,
Identified with: Sequest HT (v1.3); XCorr:3.07, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

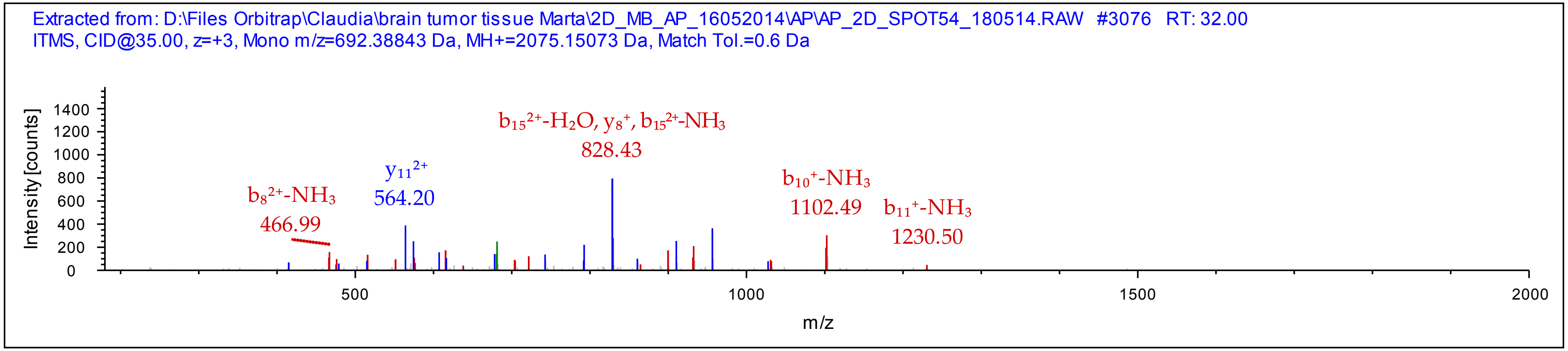
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	114.09135	57.54931	I			15
2	251.15026	126.07877	H	1765.88283	883.44505	14
3	380.19286	190.60007	E	1628.82392	814.91560	13
4	509.23546	255.12137	E	1499.78132	750.39430	12
5	638.27806	319.64267	E	1370.73872	685.87300	11
6	737.34648	369.17688	V	1241.69612	621.35170	10
7	893.44760	447.22744	R	1142.62770	571.81749	9
8	1022.49020	511.74874	E	986.52658	493.76693	8
9	1135.57427	568.29077	L	857.48398	429.24563	7
10	1263.63285	632.32006	Q	744.39991	372.70359	6
11	1392.67545	696.84136	E	616.34133	308.67430	5
12	1520.73403	760.87065	Q	487.29873	244.15300	4
13	1633.81810	817.41269	L	359.24015	180.12371	3
14	1704.85522	852.93125	A	246.15608	123.58168	2
15			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT54_180514.RAW #2506 RT: 27.79
ITMS, CID@35.00, z=+2, Mono m/z=939.98663 Da, MH+=1878.96599 Da, Match Tol.=0.6 Da

Sequence: QQVHVELDVAKPDLTAALK, Charge: +3, Monoisotopic m/z: 692.38843 Da (+0.37 mmu/+0.53 ppm), MH+: 2075.15073 Da, RT: 32.00 min,
Identified with: Sequest HT (v1.3); XCorr:3.01, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):

- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	129.06586	65.03657	43.69347	Q				19
2	257.12444	129.06586	86.37966	Q	1947.09105	974.04916	649.70187	18
3	356.19286	178.60007	119.40247	V	1819.03247	910.01987	607.01567	17
4	493.25177	247.12952	165.08877	H	1719.96405	860.48566	573.99287	16
5	592.32019	296.66373	198.11158	V	1582.90514	791.95621	528.30656	15
6	721.36279	361.18503	241.12578	E	1483.83672	742.42200	495.28376	14
7	834.44686	417.72707	278.82047	L	1354.79412	677.90070	452.26956	13
8	949.47381	475.24054	317.16279	D	1241.71005	621.35866	414.57487	12
9	1048.54223	524.77475	350.18559	V	1126.68310	563.84519	376.23255	11
10	1119.57935	560.29331	373.86463	A	1027.61468	514.31098	343.20974	10
11	1247.67432	624.34080	416.56296	K	956.57756	478.79242	319.53070	9
12	1344.72709	672.86718	448.91388	P	828.48259	414.74493	276.83238	8
13	1459.75404	730.38066	487.25620	D	731.42982	366.21855	244.48146	7
14	1572.83811	786.92269	524.95089	L	616.40287	308.70507	206.13914	6
15	1673.88579	837.44653	558.63345	T	503.31880	252.16304	168.44445	5
16	1744.92291	872.96509	582.31249	A	402.27112	201.63920	134.76189	4
17	1815.96003	908.48365	605.99153	A	331.23400	166.12064	111.08285	3
18	1929.04410	965.02569	643.68622	L	260.19688	130.60208	87.40381	2
19				K	147.11281	74.06004	49.70912	1



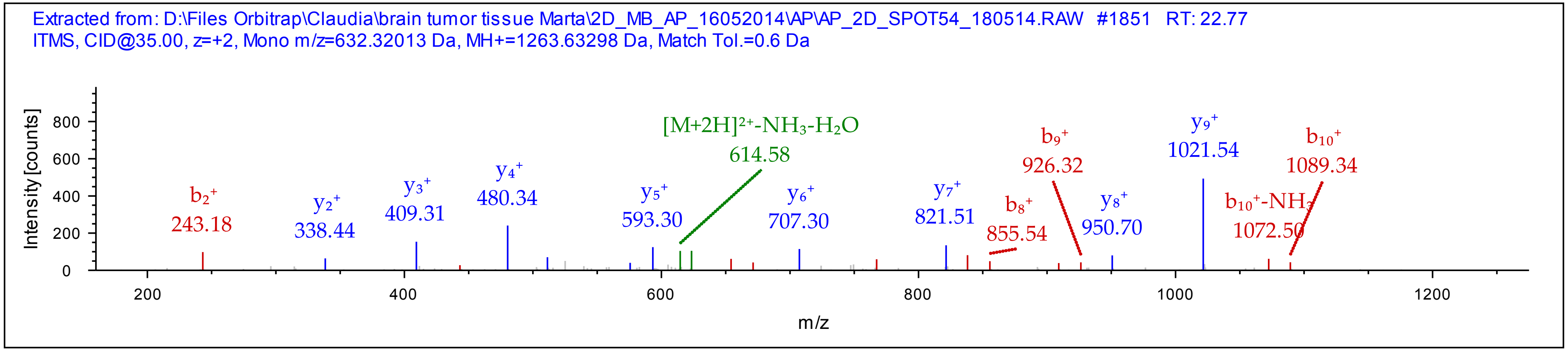
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT54_180514.RAW #3076 RT: 32.00
ITMS, CID@35.00, z=+3, Mono m/z=692.38843 Da, MH+=2075.15073 Da, Match Tol.=0.6 Da

Sequence: LEAENNLAAYR, Charge: +2, Monoisotopic m/z: 632.32013 Da (+0.07 mmu/+0.11 ppm), MH+: 1263.63298 Da, RT: 22.77 min,
Identified with: Sequest HT (v1.3); XCorr:2.89, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	114.09135	57.54931	L			11
2	243.13395	122.07061	E	1150.54877	575.77802	10
3	314.17107	157.58917	A	1021.50617	511.25672	9
4	443.21367	222.11047	E	950.46905	475.73816	8
5	557.25660	279.13194	N	821.42645	411.21686	7
6	671.29953	336.15340	N	707.38352	354.19540	6
7	784.38360	392.69544	L	593.34059	297.17393	5
8	855.42072	428.21400	A	480.25652	240.63190	4
9	926.45784	463.73256	A	409.21940	205.11334	3
10	1089.52116	545.26422	Y	338.18228	169.59478	2
11			R	175.11896	88.06312	1

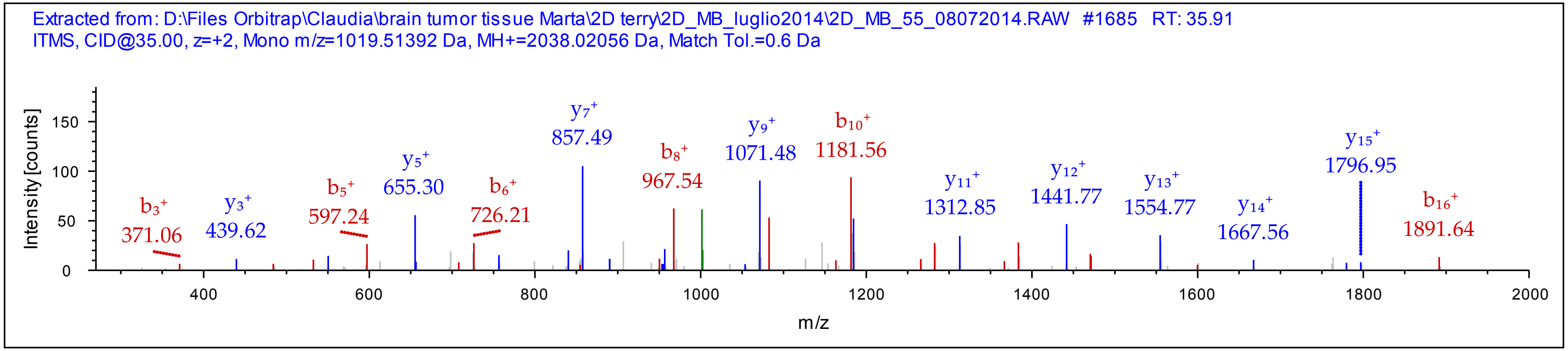

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\AP\AP_2D_SPOT54_180514.RAW #1851 RT: 22.77
ITMS, CID@35.00, z=+2, Mono m/z=632.32013 Da, MH+=1263.63298 Da, Match Tol.=0.6 Da
Intensity [counts]
0
200
400
600
800
m/z
200
400
600
800
1000
1200
b₂⁺ 243.18
y₂⁺ 338.44
y₃⁺ 409.31
y₄⁺ 480.34
y₅⁺ 593.30
[M+2H]²⁺-NH₃-H₂O 614.58
y₆⁺ 707.30
y₇⁺ 821.51
b₈⁺ 855.54
b₉⁺ 926.32
y₈⁺ 950.70
y₉⁺ 1021.54
b₁₀⁺-NH₃ 1072.50
b₁₀⁺ 1089.34

Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
55	P10809	60 kDa heat shock protein, mitochondrial	57.9	5.2	350.0	53.23%	27	27	MB	NS	1.5	↑ in PA

Sequence: IQEIIEQLDVTTSEYEK, Charge: +2, Monoisotopic m/z: 1019.51392 Da (-1.09 mmu/-1.07 ppm), MH+: 2038.02056 Da, RT: 35.91 min,
Identified with: Sequest HT (v1.3); XCorr:5.14, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	b$^+$	b^{2+}	Seq.	y$^+$	y^{2+}	#2
1	114.09135	57.54931	I			17
2	242.14993	121.57860	Q	1924.93866	962.97297	16
3	371.19253	186.09990	E	1796.88008	898.94368	15
4	484.27660	242.64194	I	1667.83748	834.42238	14
5	597.36067	299.18397	I	1554.75341	777.88034	13
6	726.40327	363.70527	E	1441.66934	721.33831	12
7	854.46185	427.73456	Q	1312.62674	656.81701	11
8	967.54592	484.27660	L	1184.56816	592.78772	10
9	1082.57287	541.79007	D	1071.48409	536.24568	9
10	1181.64129	591.32428	V	956.45714	478.73221	8
11	1282.68897	641.84812	T	857.38872	429.19800	7
12	1383.73665	692.37196	T	756.34104	378.67416	6
13	1470.76868	735.88798	S	655.29336	328.15032	5
14	1599.81128	800.40928	E	568.26133	284.63430	4
15	1762.87460	881.94094	Y	439.21873	220.11300	3
16	1891.91720	946.46224	E	276.15541	138.58134	2
17			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_MB_luglio2014\2D_MB_55_08072014.RAW #1685 RT: 35.91
ITMS, CID@35.00, z=+2, Mono m/z=1019.51392 Da, MH+=2038.02056 Da, Match Tol.=0.6 Da

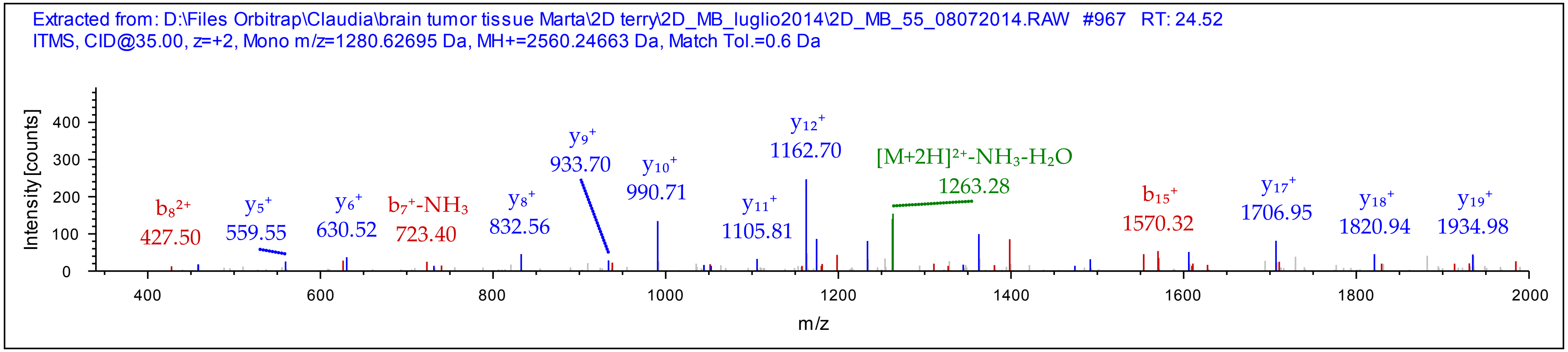
Sequence: LVQDVANNTNEEAGDGTTTATVLAR, Charge: +2, Monoisotopic m/z: 1280.62695 Da (-1.01 mmu/-0.79 ppm), MH+: 2560.24663 Da, RT: 24.52 min,
Identified with: Sequest HT (v1.3); XCorr:4.98, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	b$^+$	b^{2+}	Seq.	y$^+$	y^{2+}	#2
1	114.09135	57.54931	L			25
2	213.15977	107.08352	V	2447.16458	1224.08593	24
3	341.21835	171.11281	Q	2348.09616	1174.55172	23
4	456.24530	228.62629	D	2220.03758	1110.52243	22
5	555.31372	278.16050	V	2105.01063	1053.00895	21
6	626.35084	313.67906	A	2005.94221	1003.47474	20
7	740.39377	370.70052	N	1934.90509	967.95618	19
8	854.43670	427.72199	N	1820.86216	910.93472	18
9	955.48438	478.24583	T	1706.81923	853.91325	17
10	1069.52731	535.26729	N	1605.77155	803.38941	16
11	1198.56991	599.78859	E	1491.72862	746.36795	15
12	1327.61251	664.30989	E	1362.68602	681.84665	14
13	1398.64963	699.82845	A	1233.64342	617.32535	13
14	1455.67110	728.33919	G	1162.60630	581.80679	12
15	1570.69805	785.85266	D	1105.58483	553.29605	11
16	1627.71952	814.36340	G	990.55788	495.78258	10
17	1728.76720	864.88724	T	933.53641	467.27184	9
18	1829.81488	915.41108	T	832.48873	416.74800	8

19	1930.86256	965.93492	T	731.44105	366.22416	7
20	2001.89968	1001.45348	A	630.39337	315.70032	6
21	2102.94736	1051.97732	T	559.35625	280.18176	5
22	2202.01578	1101.51153	V	458.30857	229.65792	4
23	2315.09985	1158.05356	L	359.24015	180.12371	3
24	2386.13697	1193.57212	A	246.15608	123.58168	2
25			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_MB_luglio2014\2D_MB_55_08072014.RAW #967 RT: 24.52
ITMS, CID@35.00, z=+2, Mono m/z=1280.62695 Da, MH+=2560.24663 Da, Match Tol.=0.6 Da

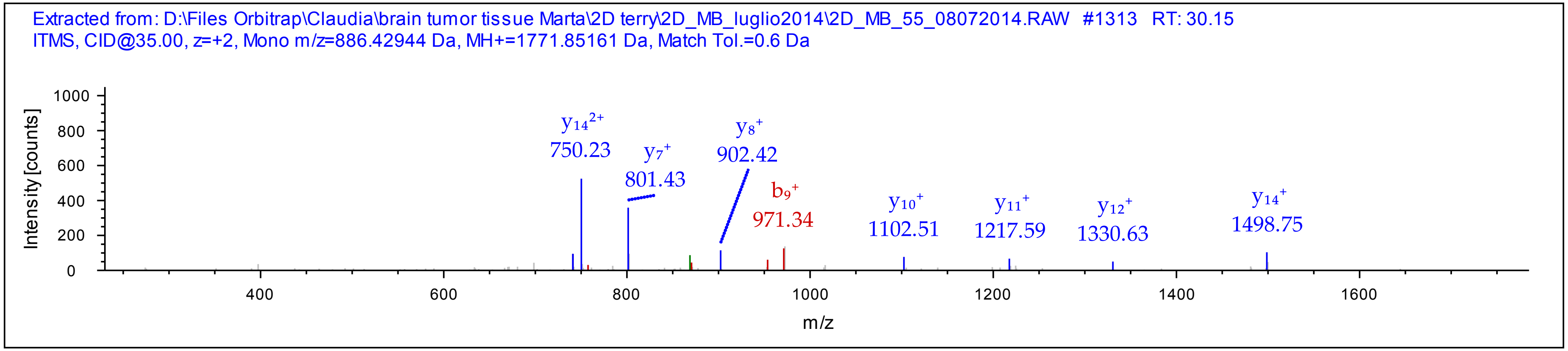
Sequence: CIPALDSLTPANEDQK, C1-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 886.42944 Da (-0.78 mmu/-0.88 ppm), MH+: 1771.85161 Da, RT: 30.15 min,
Identified with: Sequest HT (v1.3); XCorr:3.61, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	161.03793	81.02260	C-Carbamidomethyl			16
2	274.12200	137.56464	I	1611.82252	806.41490	15
3	371.17477	186.09102	P	1498.73845	749.87286	14
4	442.21189	221.60958	A	1401.68568	701.34648	13
5	555.29596	278.15162	L	1330.64856	665.82792	12
6	670.32291	335.66509	D	1217.56449	609.28588	11
7	757.35494	379.18111	S	1102.53754	551.77241	10
8	870.43901	435.72314	L	1015.50551	508.25639	9
9	971.48669	486.24698	T	902.42144	451.71436	8
10	1068.53946	534.77337	P	801.37376	401.19052	7

11	1139.57658	570.29193	A	704.32099	352.66413	6
12	1253.61951	627.31339	N	633.28387	317.14557	5
13	1382.66211	691.83469	E	519.24094	260.12411	4
14	1497.68906	749.34817	D	390.19834	195.60281	3
15	1625.74764	813.37746	Q	275.17139	138.08933	2
16			K	147.11281	74.06004	1



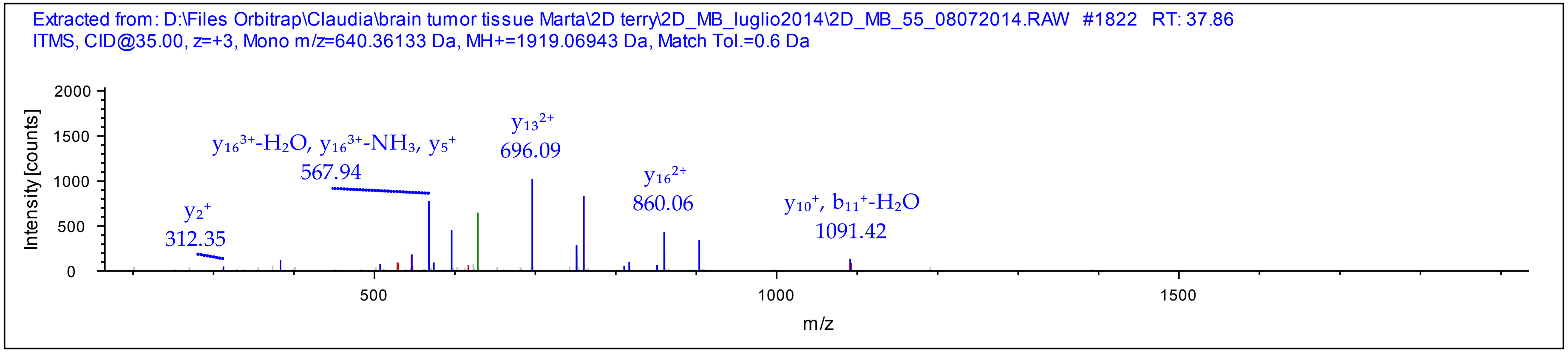
Sequence: ISSIQSIVPALEIANAHR, Charge: +3, Monoisotopic m/z: 640.36133 Da (-0.51 mmu/-0.8 ppm), MH+: 1919.06943 Da, RT: 37.86 min,
Identified with: Sequest HT (v1.3); XCorr:3.36, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	**b⁺**	**b²⁺**	**b³⁺**	**Seq.**	**y⁺**	**y²⁺**	**y³⁺**	**#2**
1	114.09135	57.54931	38.70197	I				18
2	201.12338	101.06533	67.71264	S	1805.98690	903.49709	602.66715	17
3	288.15541	144.58134	96.72332	S	1718.95487	859.98107	573.65647	16
4	401.23948	201.12338	134.41801	I	1631.92284	816.46506	544.64580	15
5	529.29806	265.15267	177.10420	Q	1518.83877	759.92302	506.95111	14
6	616.33009	308.66868	206.11488	S	1390.78019	695.89373	464.26491	13
7	729.41416	365.21072	243.80957	I	1303.74816	652.37772	435.25424	12
8	828.48258	414.74493	276.83238	V	1190.66409	595.83568	397.55955	11
9	925.53535	463.27131	309.18330	P	1091.59567	546.30147	364.53674	10
10	996.57247	498.78987	332.86234	A	994.54290	497.77509	332.18582	9
11	1109.65654	555.33191	370.55703	L	923.50578	462.25653	308.50678	8
12	1238.69914	619.85321	413.57123	E	810.42171	405.71449	270.81209	7

13	1351.78321	676.39524	451.26592	I	681.37911	341.19319	227.79789	6
14	1422.82033	711.91380	474.94496	A	568.29504	284.65116	190.10320	5
15	1536.86326	768.93527	512.95927	N	497.25792	249.13260	166.42416	4
16	1607.90038	804.45383	536.63831	A	383.21499	192.11113	128.40985	3
17	1744.95929	872.98328	582.32461	H	312.17787	156.59257	104.73081	2
18				R	175.11896	88.06312	59.04450	1



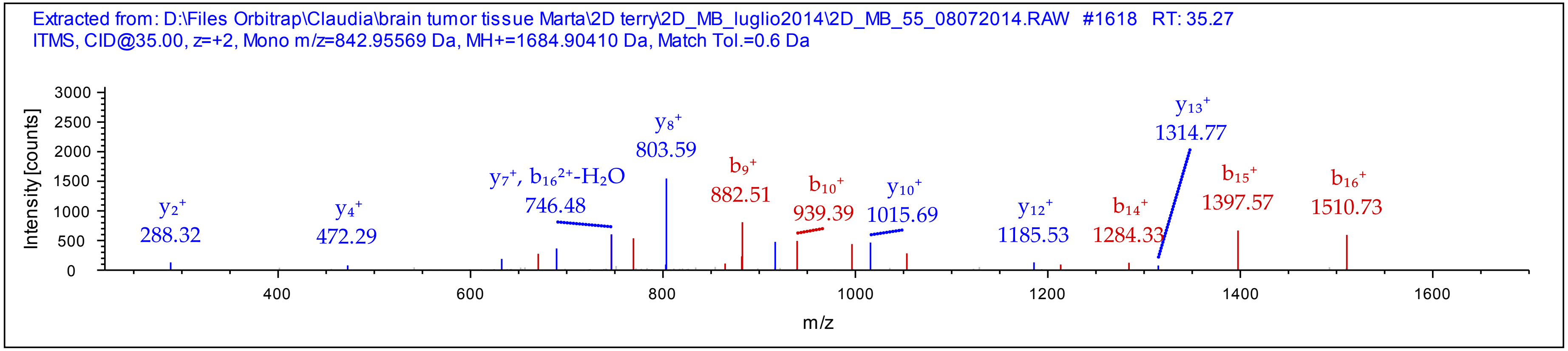
Sequence: AAVEEGIVLGGGCALLR, C13-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 842.95569 Da (-0.54 mmu/-0.64 ppm), MH+: 1684.90410 Da, RT: 35.27 min,
Identified with: Sequest HT (v1.3); XCorr:3.32, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	b^{+}	b^{2+}	Seq.	y^{+}	y^{2+}	#2
1	72.04440	36.52584	A			17
2	143.08152	72.04440	A	1613.86806	807.43767	16
3	242.14994	121.57861	V	1542.83094	771.91911	15
4	371.19254	186.09991	E	1443.76252	722.38490	14
5	500.23514	250.62121	E	1314.71992	657.86360	13
6	557.25661	279.13194	G	1185.67732	593.34230	12
7	670.34068	335.67398	I	1128.65585	564.83156	11
8	769.40910	385.20819	V	1015.57178	508.28953	10
9	882.49317	441.75022	L	916.50336	458.75532	9
10	939.51464	470.26096	G	803.41929	402.21328	8

11	996.53611	498.77169	G	746.39782	373.70255	7
12	1053.55758	527.28243	G	689.37635	345.19181	6
13	1213.58823	607.29775	C-Carbamidomethyl	632.35488	316.68108	5
14	1284.62535	642.81631	A	472.32422	236.66575	4
15	1397.70942	699.35835	L	401.28710	201.14719	3
16	1510.79349	755.90038	L	288.20303	144.60515	2
17			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_MB_luglio2014\2D_MB_55_08072014.RAW #1618 RT: 35.27
ITMS, CID@35.00, z=+2, Mono m/z=842.95569 Da, MH+=1684.90410 Da, Match Tol.=0.6 Da

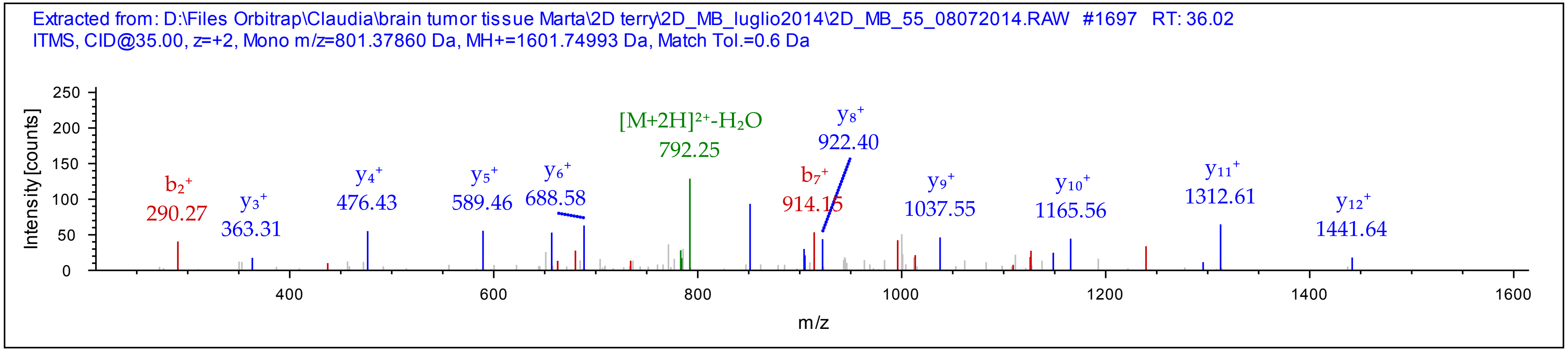
Sequence: CEFQDAYVLLSEK, C1-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 801.37860 Da (-0.86 mmu/-1.07 ppm), MH+: 1601.74993 Da, RT: 36.02 min,
Identified with: Sequest HT (v1.3); XCorr:3.28, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	**b^{+}**	**b^{2+}**	**Seq.**	**y^{+}**	**y^{2+}**	**#2**
1	161.03793	81.02260	C-Carbamidomethyl			13
2	290.08053	145.54390	E	1441.72099	721.36413	12
3	437.14895	219.07811	F	1312.67839	656.84283	11
4	565.20753	283.10740	Q	1165.60997	583.30862	10
5	680.23448	340.62088	D	1037.55139	519.27933	9
6	751.27160	376.13944	A	922.52444	461.76586	8
7	914.33492	457.67110	Y	851.48732	426.24730	7
8	1013.40334	507.20531	V	688.42400	344.71564	6
9	1126.48741	563.74734	L	589.35558	295.18143	5

10	1239.57148	620.28938	L	476.27151	238.63939	4
11	1326.60351	663.80539	S	363.18744	182.09736	3
12	1455.64611	728.32669	E	276.15541	138.58134	2
13			K	147.11281	74.06004	1



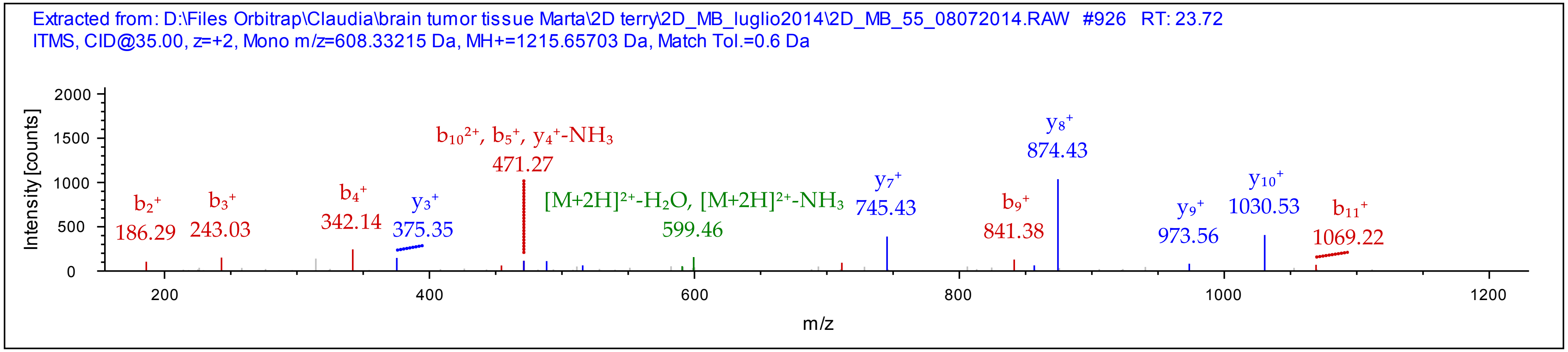
Sequence: NAGVEGSLIVEK, Charge: +2, Monoisotopic m/z: 608.33215 Da (-0.49 mmu/-0.81 ppm), MH+: 1215.65703 Da, RT: 23.72 min,
Identified with: Sequest HT (v1.3); XCorr:3.18, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	115.05021	58.02874	N			12
2	186.08733	93.54730	A	1101.61508	551.31118	11
3	243.10880	122.05804	G	1030.57796	515.79262	10
4	342.17722	171.59225	V	973.55649	487.28188	9
5	471.21982	236.11355	E	874.48807	437.74767	8
6	528.24129	264.62428	G	745.44547	373.22637	7
7	615.27332	308.14030	S	688.42400	344.71564	6
8	728.35739	364.68233	L	601.39197	301.19962	5
9	841.44146	421.22437	I	488.30790	244.65759	4

10	940.50988	470.75858	V	375.22383	188.11555	3
11	1069.55248	535.27988	E	276.15541	138.58134	2
12			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_MB_luglio2014\2D_MB_55_08072014.RAW #926 RT: 23.72
ITMS, CID@35.00, z=+2, Mono m/z=608.33215 Da, MH+=1215.65703 Da, Match Tol.=0.6 Da

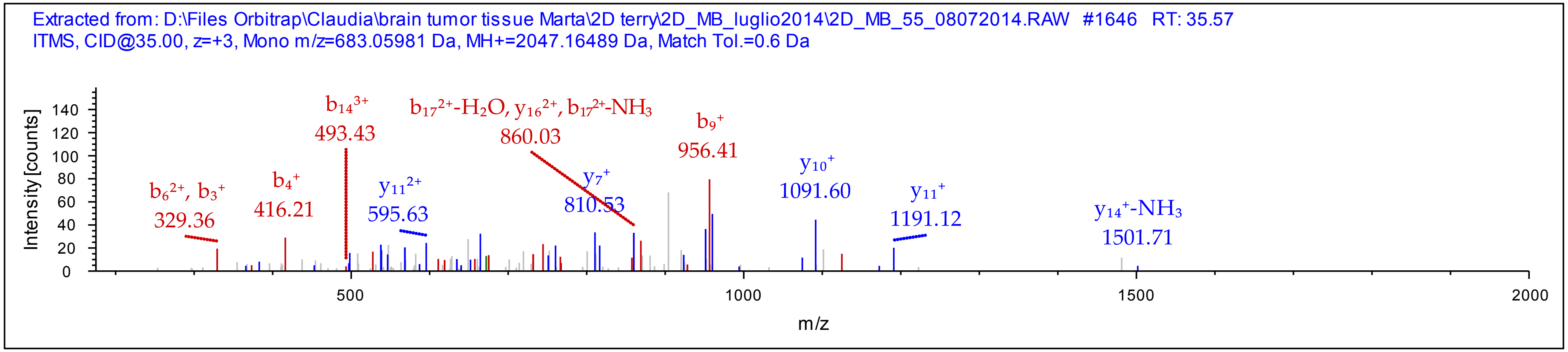
Sequence: KISSIQSIVPALEIANAHR, Charge: +3, Monoisotopic m/z: 683.05981 Da (-0.35 mmu/-0.51 ppm), MH+: 2047.16489 Da, RT: 35.57 min,
Identified with: Sequest HT (v1.3); XCorr:3.17, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	129.10225	65.05476	43.70560	K				19
2	242.18632	121.59680	81.40029	I	1919.07097	960.03912	640.36184	18
3	329.21835	165.11281	110.41097	S	1805.98690	903.49709	602.66715	17
4	416.25038	208.62883	139.42164	S	1718.95487	859.98107	573.65647	16
5	529.33445	265.17086	177.11633	I	1631.92284	816.46506	544.64580	15
6	657.39303	329.20015	219.80253	Q	1518.83877	759.92302	506.95111	14
7	744.42506	372.71617	248.81320	S	1390.78019	695.89373	464.26491	13
8	857.50913	429.25820	286.50789	I	1303.74816	652.37772	435.25424	12
9	956.57755	478.79241	319.53070	V	1190.66409	595.83568	397.55955	11
10	1053.63032	527.31880	351.88162	P	1091.59567	546.30147	364.53674	10
11	1124.66744	562.83736	375.56066	A	994.54290	497.77509	332.18582	9

12	1237.75151	619.37939	413.25535	L	923.50578	462.25653	308.50678	8
13	1366.79411	683.90069	456.26955	E	810.42171	405.71449	270.81209	7
14	1479.87818	740.44273	493.96424	I	681.37911	341.19319	227.79789	6
15	1550.91530	775.96129	517.64328	A	568.29504	284.65116	190.10320	5
16	1664.95823	832.98275	555.65759	N	497.25792	249.13260	166.42416	4
17	1735.99535	868.50131	579.33663	A	383.21499	192.11113	128.40985	3
18	1873.05426	937.03077	625.02294	H	312.17787	156.59257	104.73081	2
19				R	175.11896	88.06312	59.04450	1



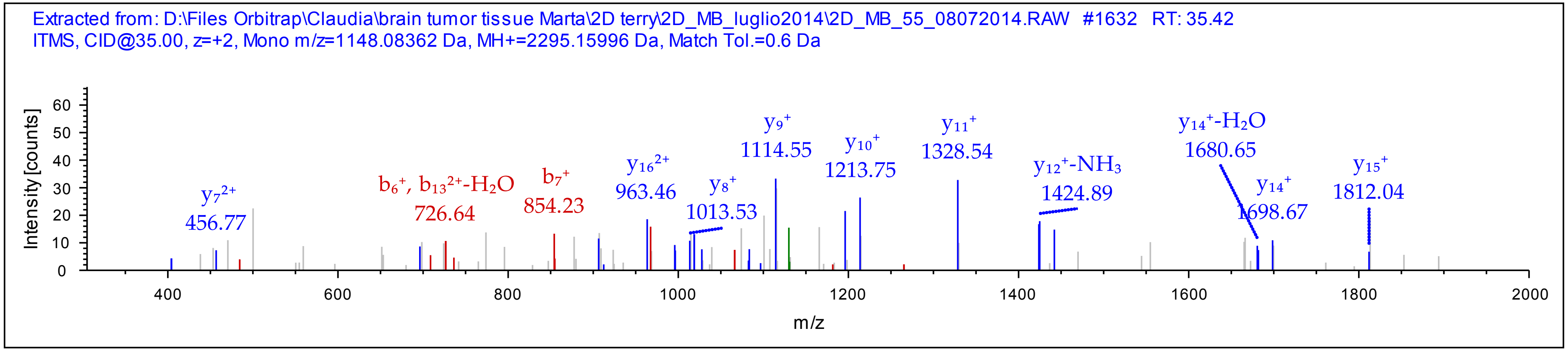
Sequence: IQEIIEQLDVTTSEYEKEK, Charge: +2, Monoisotopic m/z: 1148.08362 Da (-0.17 mmu/-0.15 ppm), MH+: 2295.15996 Da, RT: 35.42 min,
Identified with: Sequest HT (v1.3); XCorr:3.03, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	I			19
2	242.14993	121.57860	Q	2182.07623	1091.54175	18
3	371.19253	186.09990	E	2054.01765	1027.51246	17
4	484.27660	242.64194	I	1924.97505	962.99116	16
5	597.36067	299.18397	I	1811.89098	906.44913	15
6	726.40327	363.70527	E	1698.80691	849.90709	14

7	854.46185	427.73456	Q	1569.76431	785.38579	13
8	967.54592	484.27660	L	1441.70573	721.35650	12
9	1082.57287	541.79007	D	1328.62166	664.81447	11
10	1181.64129	591.32428	V	1213.59471	607.30099	10
11	1282.68897	641.84812	T	1114.52629	557.76678	9
12	1383.73665	692.37196	T	1013.47861	507.24294	8
13	1470.76868	735.88798	S	912.43093	456.71910	7
14	1599.81128	800.40928	E	825.39890	413.20309	6
15	1762.87460	881.94094	Y	696.35630	348.68179	5
16	1891.91720	946.46224	E	533.29298	267.15013	4
17	2020.01217	1010.50972	K	404.25038	202.62883	3
18	2149.05477	1075.03102	E	276.15541	138.58134	2
19			K	147.11281	74.06004	1



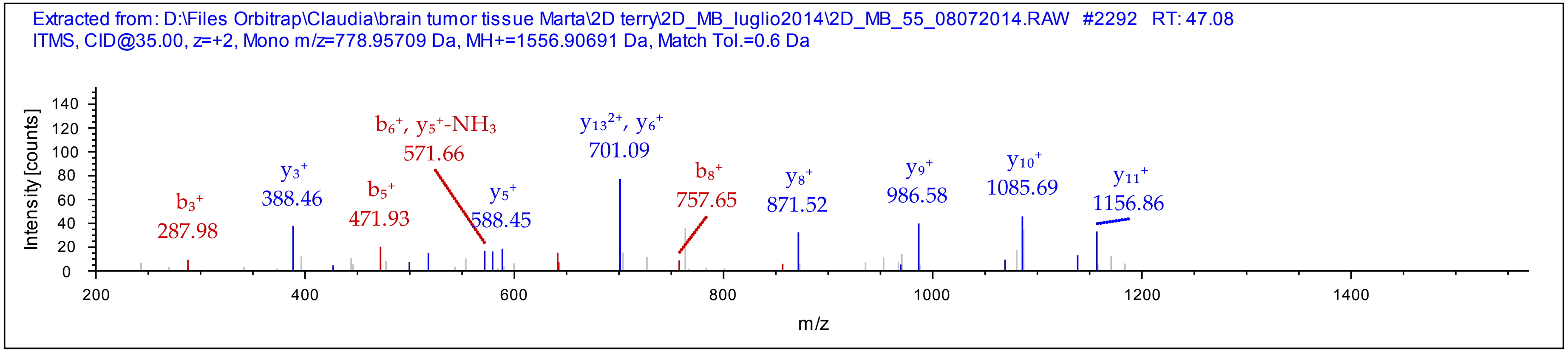
Sequence: GVMLAVDAVIAELKK, Charge: +2, Monoisotopic m/z: 778.95709 Da (-0.61 mmu/-0.79 ppm), MH+: 1556.90691 Da, RT: 47.08 min,
Identified with: Sequest HT (v1.3); XCorr:2.93, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	58.02875	29.51801	G			15

2	157.09717	79.05222	V	1499.88666	750.44697	14
3	288.13767	144.57247	M	1400.81824	700.91276	13
4	401.22174	201.11451	L	1269.77774	635.39251	12
5	472.25886	236.63307	A	1156.69367	578.85047	11
6	571.32728	286.16728	V	1085.65655	543.33191	10
7	686.35423	343.68075	D	986.58813	493.79770	9
8	757.39135	379.19931	A	871.56118	436.28423	8
9	856.45977	428.73352	V	800.52406	400.76567	7
10	969.54384	485.27556	I	701.45564	351.23146	6
11	1040.58096	520.79412	A	588.37157	294.68942	5
12	1169.62356	585.31542	E	517.33445	259.17086	4
13	1282.70763	641.85745	L	388.29185	194.64956	3
14	1410.80260	705.90494	K	275.20778	138.10753	2
15			K	147.11281	74.06004	1



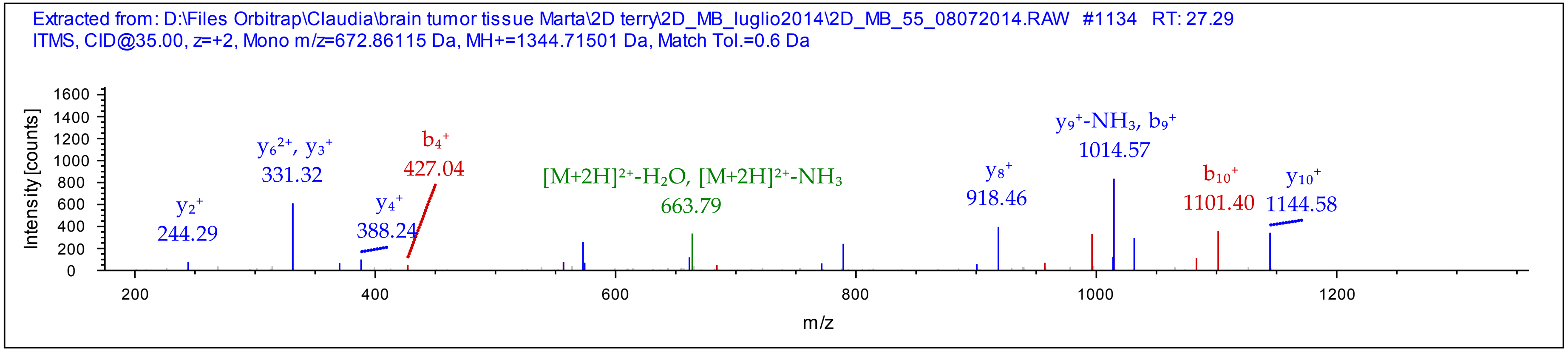
Sequence: TVIIEQSWGSPK, Charge: +2, Monoisotopic m/z: 672.86115 Da (-0.42 mmu/-0.62 ppm), MH+: 1344.71501 Da, RT: 27.29 min,
Identified with: Sequest HT (v1.3); XCorr:2.91, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	102.05496	51.53112	T			12
2	201.12338	101.06533	V	1243.66817	622.33772	11

3	314.20745	157.60736	I	1144.59975	572.80351	10
4	427.29152	214.14940	I	1031.51568	516.26148	9
5	556.33412	278.67070	E	918.43161	459.71944	8
6	684.39270	342.69999	Q	789.38901	395.19814	7
7	771.42473	386.21600	S	661.33043	331.16885	6
8	957.50405	479.25566	W	574.29840	287.65284	5
9	1014.52552	507.76640	G	388.21908	194.61318	4
10	1101.55755	551.28241	S	331.19761	166.10244	3
11	1198.61032	599.80880	P	244.16558	122.58643	2
12			K	147.11281	74.06004	1



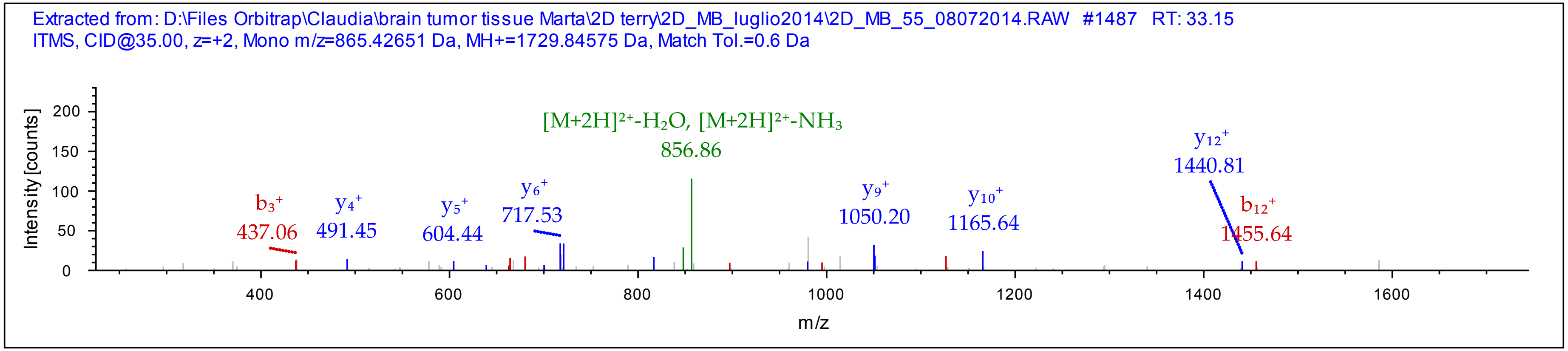
Sequence: CEFQDAYVLLSEKK, C1-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 865.42651 Da (-0.43 mmu/-0.5 ppm), MH+: 1729.84575 Da, RT: 33.15 min,
Identified with: Sequest HT (v1.3); XCorr:2.87, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	161.03793	81.02260	C-Carbamidomethyl			14
2	290.08053	145.54390	E	1569.81596	785.41162	13
3	437.14895	219.07811	F	1440.77336	720.89032	12
4	565.20753	283.10740	Q	1293.70494	647.35611	11
5	680.23448	340.62088	D	1165.64636	583.32682	10
6	751.27160	376.13944	A	1050.61941	525.81334	9
7	914.33492	457.67110	Y	979.58229	490.29478	8

8	1013.40334	507.20531	V	816.51897	408.76312	7
9	1126.48741	563.74734	L	717.45055	359.22891	6
10	1239.57148	620.28938	L	604.36648	302.68688	5
11	1326.60351	663.80539	S	491.28241	246.14484	4
12	1455.64611	728.32669	E	404.25038	202.62883	3
13	1583.74108	792.37418	K	275.20778	138.10753	2
14			K	147.11281	74.06004	1



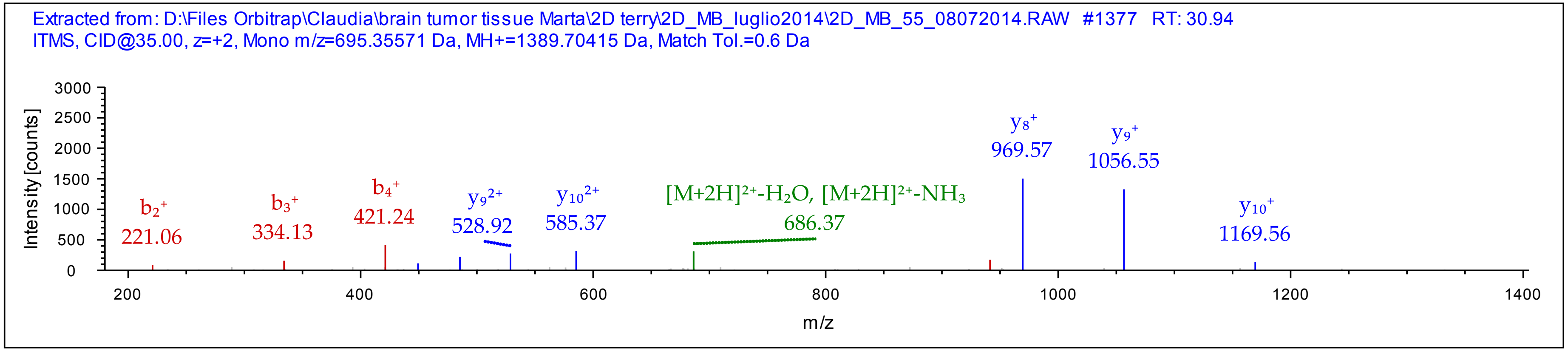
Sequence: GYISPYFINTSK, Charge: +2, Monoisotopic m/z: 695.35571 Da (-0.39 mmu/-0.56 ppm), MH+: 1389.70415 Da, RT: 30.94 min,
Identified with: Sequest HT (v1.3); XCorr:2.70, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	58.02875	29.51801	G			12
2	221.09207	111.04967	Y	1332.68345	666.84536	11
3	334.17614	167.59171	I	1169.62013	585.31370	10
4	421.20817	211.10772	S	1056.53606	528.77167	9
5	518.26094	259.63411	P	969.50403	485.25565	8
6	681.32426	341.16577	Y	872.45126	436.72927	7
7	828.39268	414.69998	F	709.38794	355.19761	6
8	941.47675	471.24201	I	562.31952	281.66340	5
9	1055.51968	528.26348	N	449.23545	225.12136	4

10	1156.56736	578.78732	T	335.19252	168.09990	3
11	1243.59939	622.30333	S	234.14484	117.57606	2
12			K	147.11281	74.06004	1

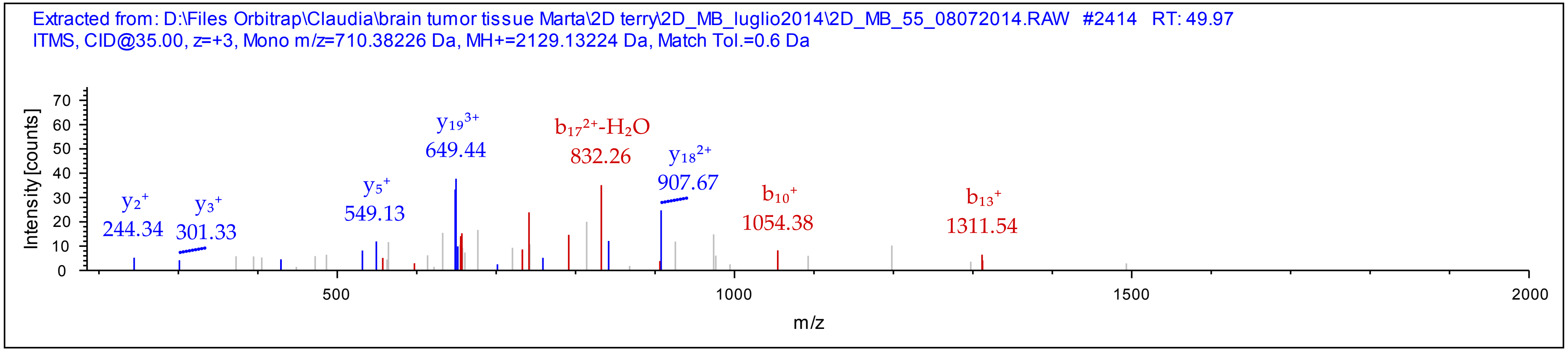


Sequence: ALMLQGVDLLADAVAVTMGPK, M18-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 710.38226 Da (-0.79 mmu/-1.12 ppm), MH+: 2129.13224 Da, RT: 49.97 min,
Identified with: Sequest HT (v1.3); XCorr:2.68, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	72.04440	36.52584	24.68632	A				21
2	185.12847	93.06787	62.38101	L	2058.09750	1029.55239	686.70402	20
3	316.16897	158.58812	106.06117	M	1945.01343	973.01035	649.00933	19
4	429.25304	215.13016	143.75586	L	1813.97293	907.49010	605.32916	18
5	557.31162	279.15945	186.44206	Q	1700.88886	850.94807	567.63447	17
6	614.33309	307.67018	205.44921	G	1572.83028	786.91878	524.94828	16
7	713.40151	357.20439	238.47202	V	1515.80881	758.40804	505.94112	15
8	828.42846	414.71787	276.81434	D	1416.74039	708.87383	472.91831	14
9	941.51253	471.25990	314.50903	L	1301.71344	651.36036	434.57600	13
10	1054.59660	527.80194	352.20372	L	1188.62937	594.81832	396.88131	12
11	1125.63372	563.32050	375.88276	A	1075.54530	538.27629	359.18662	11
12	1240.66067	620.83397	414.22507	D	1004.50818	502.75773	335.50758	10
13	1311.69779	656.35253	437.90411	A	889.48123	445.24425	297.16526	9

14	1410.76621	705.88674	470.92692	V	818.44411	409.72569	273.48622	8
15	1481.80333	741.40530	494.60596	A	719.37569	360.19148	240.46341	7
16	1580.87175	790.93951	527.62877	V	648.33857	324.67292	216.78437	6
17	1681.91943	841.46335	561.31133	T	549.27015	275.13871	183.76157	5
18	1828.95484	914.98106	610.32313	M-Oxidation	448.22247	224.61487	150.07901	4
19	1885.97631	943.49179	629.33029	G	301.18705	151.09716	101.06720	3
20	1983.02908	992.01818	661.68121	P	244.16558	122.58643	82.06004	2
21				K	147.11281	74.06004	49.70912	1

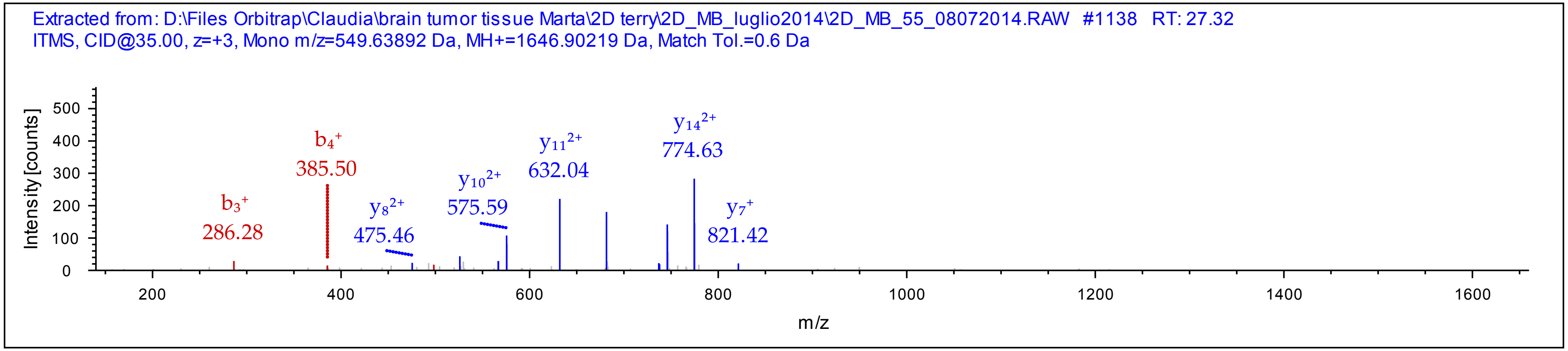

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_MB_luglio2014\2D_MB_55_08072014.RAW #2414 RT: 49.97
ITMS, CID@35.00, z=+3, Mono m/z=710.38226 Da, MH+=2129.13224 Da, Match Tol.=0.6 Da

Sequence: VGEVIVTKDDAMLLK, M12-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 549.63892 Da (-0.41 mmu/-0.75 ppm), MH+: 1646.90219 Da, RT: 27.32 min,
Identified with: Sequest HT (v1.3); XCorr:2.67, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	100.07570	50.54149	34.03008	V				15
2	157.09717	79.05222	53.03724	G	1547.83502	774.42115	516.61652	14
3	286.13977	143.57352	96.05144	E	1490.81355	745.91041	497.60937	13
4	385.20819	193.10773	129.07425	V	1361.77095	681.38911	454.59517	12
5	498.29226	249.64977	166.76894	I	1262.70253	631.85490	421.57236	11
6	597.36068	299.18398	199.79174	V	1149.61846	575.31287	383.87767	10
7	698.40836	349.70782	233.47430	T	1050.55004	525.77866	350.85486	9
8	826.50333	413.75530	276.17263	K	949.50236	475.25482	317.17230	8
9	941.53028	471.26878	314.51494	D	821.40739	411.20733	274.47398	7

10	1056.55723	528.78225	352.85726	D	706.38044	353.69386	236.13166	6
11	1127.59435	564.30081	376.53630	A	591.35349	296.18038	197.78935	5
12	1274.62976	637.81852	425.54810	M-Oxidation	520.31637	260.66182	174.11031	4
13	1387.71383	694.36055	463.24279	L	373.28095	187.14411	125.09850	3
14	1500.79790	750.90259	500.93748	L	260.19688	130.60208	87.40381	2
15				K	147.11281	74.06004	49.70912	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_MB_luglio2014\2D_MB_55_08072014.RAW #1138 RT: 27.32
ITMS, CID@35.00, z=+3, Mono m/z=549.63892 Da, MH+=1646.90219 Da, Match Tol.=0.6 Da

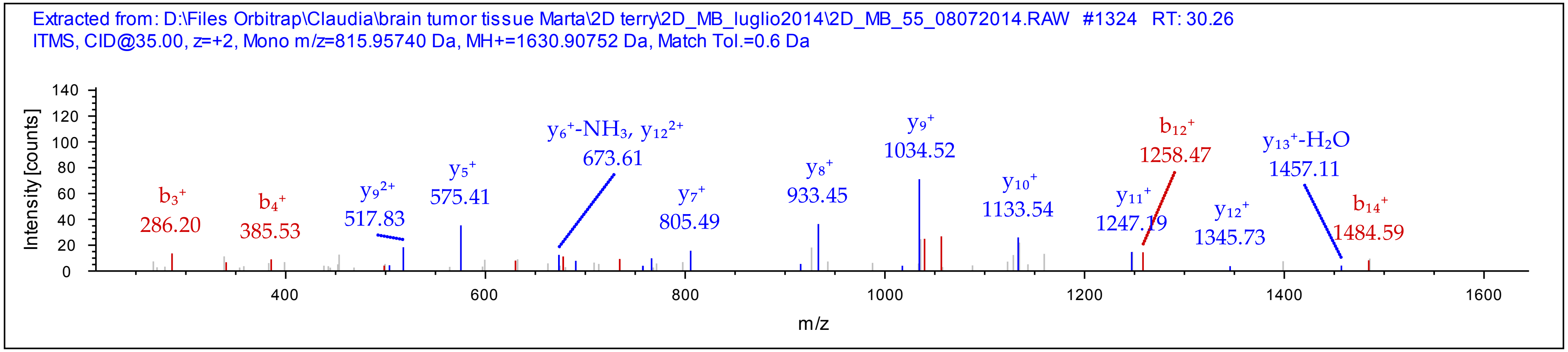
Sequence: VGEVIVTKDDAMLLK, Charge: +2, Monoisotopic m/z: 815.95740 Da (-0.5 mmu/-0.61 ppm), MH+: 1630.90752 Da, RT: 30.26 min,
Identified with: Sequest HT (v1.3); XCorr:2.56, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	100.07570	50.54149	V			15
2	157.09717	79.05222	G	1531.84010	766.42369	14
3	286.13977	143.57352	E	1474.81863	737.91295	13
4	385.20819	193.10773	V	1345.77603	673.39165	12
5	498.29226	249.64977	I	1246.70761	623.85744	11
6	597.36068	299.18398	V	1133.62354	567.31541	10
7	698.40836	349.70782	T	1034.55512	517.78120	9
8	826.50333	413.75530	K	933.50744	467.25736	8
9	941.53028	471.26878	D	805.41247	403.20987	7
10	1056.55723	528.78225	D	690.38552	345.69640	6
11	1127.59435	564.30081	A	575.35857	288.18292	5
12	1258.63485	629.82106	M	504.32145	252.66436	4

13	1371.71892	686.36310	L	373.28095	187.14411	3
14	1484.80299	742.90513	L	260.19688	130.60208	2
15			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_MB_luglio2014\2D_MB_55_08072014.RAW #1324 RT: 30.26
ITMS, CID@35.00, z=+2, Mono m/z=815.95740 Da, MH+=1630.90752 Da, Match Tol.=0.6 Da

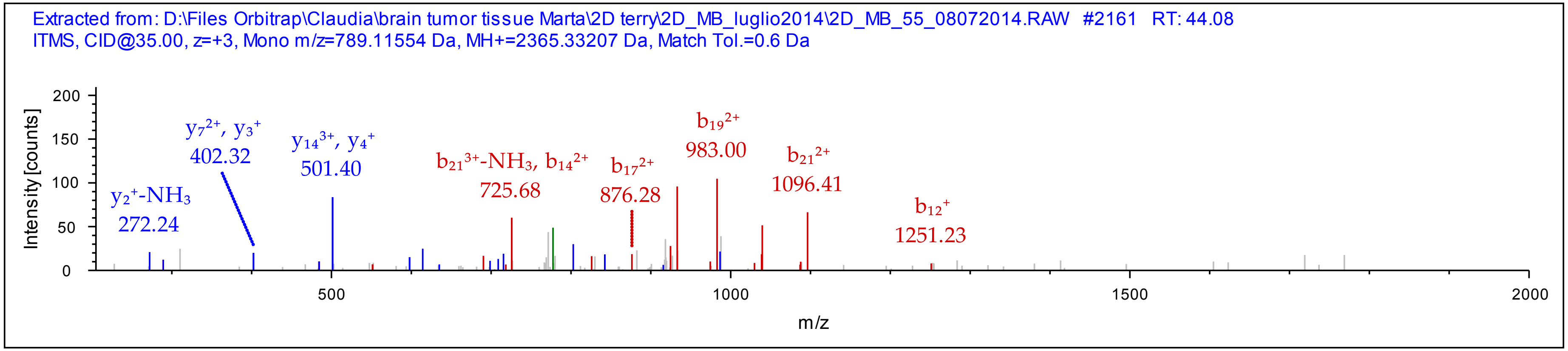
Sequence: KPLVIIAEDVDGEALSTLVLNR, Charge: +3, Monoisotopic m/z: 789.11554 Da (-0.59 mmu/-0.75 ppm), MH+: 2365.33207 Da, RT: 44.08 min,
Identified with: Sequest HT (v1.3); XCorr:2.46, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	**b⁺**	**b²⁺**	**b³⁺**	**Seq.**	**y⁺**	**y²⁺**	**y³⁺**	**#2**
1	129.10225	65.05476	43.70560	K				22
2	226.15502	113.58115	76.05652	P	2237.23886	1119.12307	746.41780	21
3	339.23909	170.12318	113.75121	L	2140.18609	1070.59668	714.06688	20
4	438.30751	219.65739	146.77402	V	2027.10202	1014.05465	676.37219	19
5	551.39158	276.19943	184.46871	I	1928.03360	964.52044	643.34938	18
6	664.47565	332.74146	222.16340	I	1814.94953	907.97840	605.65469	17
7	735.51277	368.26002	245.84244	A	1701.86546	851.43637	567.96000	16
8	864.55537	432.78132	288.85664	E	1630.82834	815.91781	544.28096	15
9	979.58232	490.29480	327.19896	D	1501.78574	751.39651	501.26676	14
10	1078.65074	539.82901	360.22176	V	1386.75879	693.88303	462.92445	13
11	1193.67769	597.34248	398.56408	D	1287.69037	644.34882	429.90164	12
12	1250.69916	625.85322	417.57124	G	1172.66342	586.83535	391.55932	11
13	1379.74176	690.37452	460.58544	E	1115.64195	558.32461	372.55217	10
14	1450.77888	725.89308	484.26448	A	986.59935	493.80331	329.53797	9
15	1563.86295	782.43511	521.95917	L	915.56223	458.28475	305.85893	8
16	1650.89498	825.95113	550.96984	S	802.47816	401.74272	268.16424	7

17	1751.94266	876.47497	584.65240	T	715.44613	358.22670	239.15356	6
18	1865.02673	933.01700	622.34709	L	614.39845	307.70286	205.47100	5
19	1964.09515	982.55121	655.36990	V	501.31438	251.16083	167.77631	4
20	2077.17922	1039.09325	693.06459	L	402.24596	201.62662	134.75350	3
21	2191.22215	1096.11471	731.07890	N	289.16189	145.08458	97.05881	2
22				R	175.11896	88.06312	59.04450	1



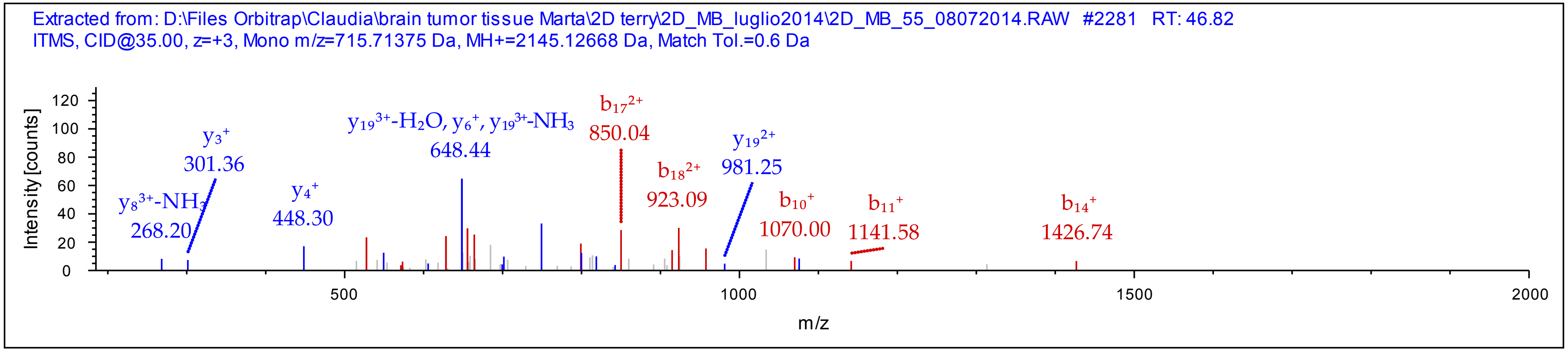
Sequence: ALMLQGVDLLADAVAVTMGPK, M3-Oxidation (15.99492 Da), M18-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 715.71375 Da (-0.95 mmu/-1.33 ppm), MH+: 2145.12668 Da, RT: 46.82 min,
Identified with: Sequest HT (v1.3); XCorr:2.37, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	b^{+}	b^{2+}	b^{3+}	Seq.	y^{+}	y^{2+}	y^{3+}	#2
1	72.04440	36.52584	24.68632	A				21
2	185.12847	93.06787	62.38101	L	2074.09241	1037.54984	692.03565	20
3	332.16388	166.58558	111.39281	M-Oxidation	1961.00834	981.00781	654.34096	19
4	445.24795	223.12761	149.08750	L	1813.97293	907.49010	605.32916	18
5	573.30653	287.15690	191.77369	Q	1700.88886	850.94807	567.63447	17
6	630.32800	315.66764	210.78085	G	1572.83028	786.91878	524.94828	16
7	729.39642	365.20185	243.80366	V	1515.80881	758.40804	505.94112	15
8	844.42337	422.71532	282.14597	D	1416.74039	708.87383	472.91831	14
9	957.50744	479.25736	319.84066	L	1301.71344	651.36036	434.57600	13

10	1070.59151	535.79939	357.53535	L	1188.62937	594.81832	396.88131	12
11	1141.62863	571.31795	381.21439	A	1075.54530	538.27629	359.18662	11
12	1256.65558	628.83143	419.55671	D	1004.50818	502.75773	335.50758	10
13	1327.69270	664.34999	443.23575	A	889.48123	445.24425	297.16526	9
14	1426.76112	713.88420	476.25856	V	818.44411	409.72569	273.48622	8
15	1497.79824	749.40276	499.93760	A	719.37569	360.19148	240.46341	7
16	1596.86666	798.93697	532.96040	V	648.33857	324.67292	216.78437	6
17	1697.91434	849.46081	566.64296	T	549.27015	275.13871	183.76157	5
18	1844.94976	922.97852	615.65477	M-Oxidation	448.22247	224.61487	150.07901	4
19	1901.97123	951.48925	634.66193	G	301.18705	151.09716	101.06720	3
20	1999.02400	1000.01564	667.01285	P	244.16558	122.58643	82.06004	2
21				K	147.11281	74.06004	49.70912	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_MB_luglio2014\2D_MB_55_08072014.RAW #2281 RT: 46.82
ITMS, CID@35.00, z=+3, Mono m/z=715.71375 Da, MH+=2145.12668 Da, Match Tol.=0.6 Da

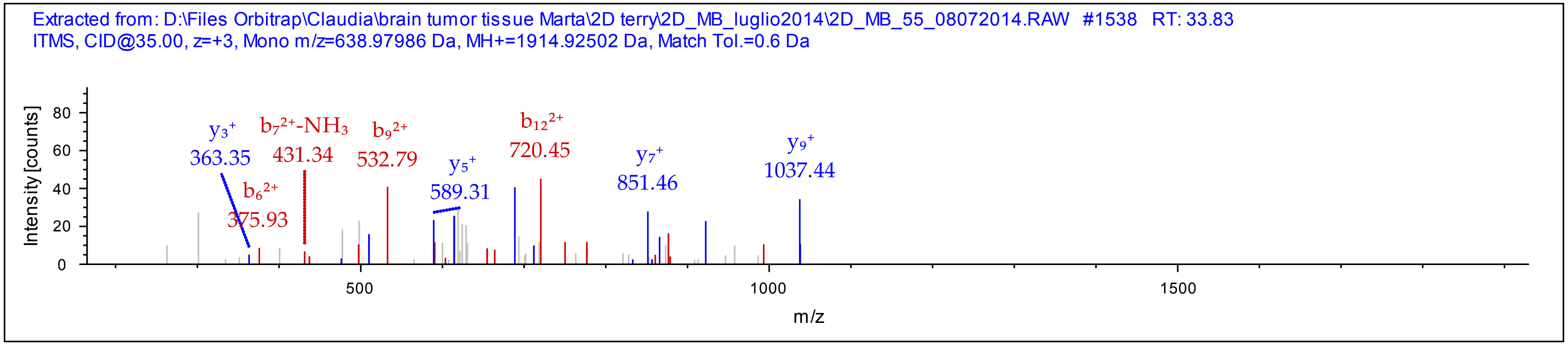
Sequence: GQKCEFQDAYVLLSEK, C4-Carbamidomethyl (57.02146 Da)
Charge: +3, Monoisotopic m/z: 638.97986 Da (-0.55 mmu/-0.86 ppm), MH+: 1914.92502 Da, RT: 33.83 min,
Identified with: Sequest HT (v1.3); XCorr:2.30, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	b^{+}	b^{2+}	b^{3+}	Seq.	y^{+}	y^{2+}	y^{3+}	#2
1	58.02875	29.51801	20.01443	G				16
2	186.08733	93.54730	62.70063	Q	1857.90520	929.45624	619.97325	15
3	314.18230	157.59479	105.39895	K	1729.84662	865.42695	577.28706	14
4	474.21295	237.61011	158.74250	C-Carbamidomethyl	1601.75165	801.37946	534.58873	13

5	603.25555	302.13141	201.75670	E	1441.72099	721.36413	481.24518	12
6	750.32397	375.66562	250.77951	F	1312.67839	656.84283	438.23098	11
7	878.38255	439.69491	293.46570	Q	1165.60997	583.30862	389.20817	10
8	993.40950	497.20839	331.80802	D	1037.55139	519.27933	346.52198	9
9	1064.44662	532.72695	355.48706	A	922.52444	461.76586	308.17966	8
10	1227.50994	614.25861	409.84150	Y	851.48732	426.24730	284.50062	7
11	1326.57836	663.79282	442.86430	V	688.42400	344.71564	230.14618	6
12	1439.66243	720.33485	480.55899	L	589.35558	295.18143	197.12338	5
13	1552.74650	776.87689	518.25368	L	476.27151	238.63939	159.42869	4
14	1639.77853	820.39290	547.26436	S	363.18744	182.09736	121.73400	3
15	1768.82113	884.91420	590.27856	E	276.15541	138.58134	92.72332	2
16				K	147.11281	74.06004	49.70912	1

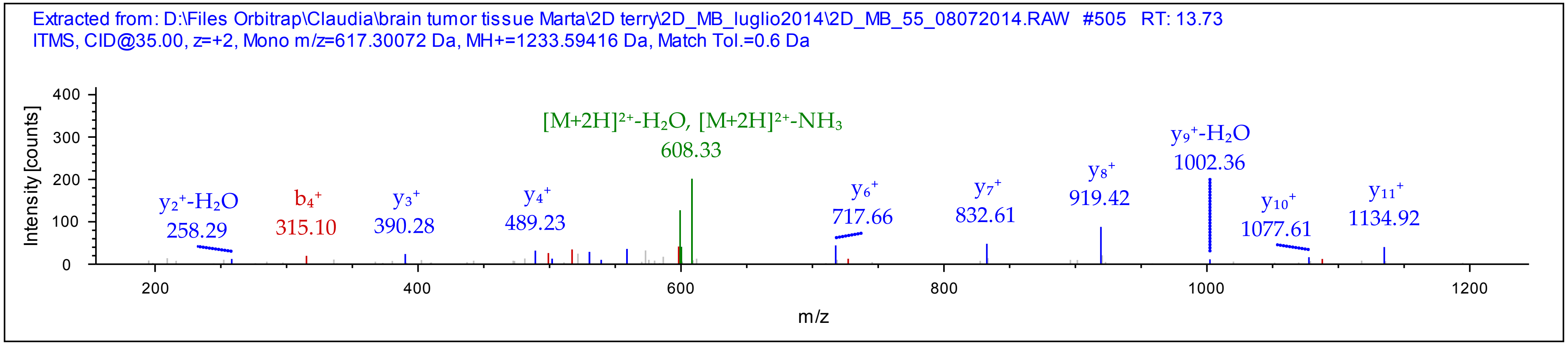


Sequence: VGGTSDVEVNEK, Charge: +2, Monoisotopic m/z: 617.30072 Da (-0.82 mmu/-1.33 ppm), MH+: 1233.59416 Da, RT: 13.73 min,
Identified with: Sequest HT (v1.3); XCorr:2.27, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	**b^{+}**	**b^{2+}**	**Seq.**	**y^{+}**	**y^{2+}**	**#2**
1	100.07570	50.54149	V			12
2	157.09717	79.05222	G	1134.52738	567.76733	11
3	214.11864	107.56296	G	1077.50591	539.25659	10
4	315.16632	158.08680	T	1020.48444	510.74586	9
5	402.19835	201.60281	S	919.43676	460.22202	8
6	517.22530	259.11629	D	832.40473	416.70600	7

7	616.29372	308.65050	V	717.37778	359.19253	6
8	745.33632	373.17180	E	618.30936	309.65832	5
9	844.40474	422.70601	V	489.26676	245.13702	4
10	958.44767	479.72747	N	390.19834	195.60281	3
11	1087.49027	544.24877	E	276.15541	138.58134	2
12			K	147.11281	74.06004	1



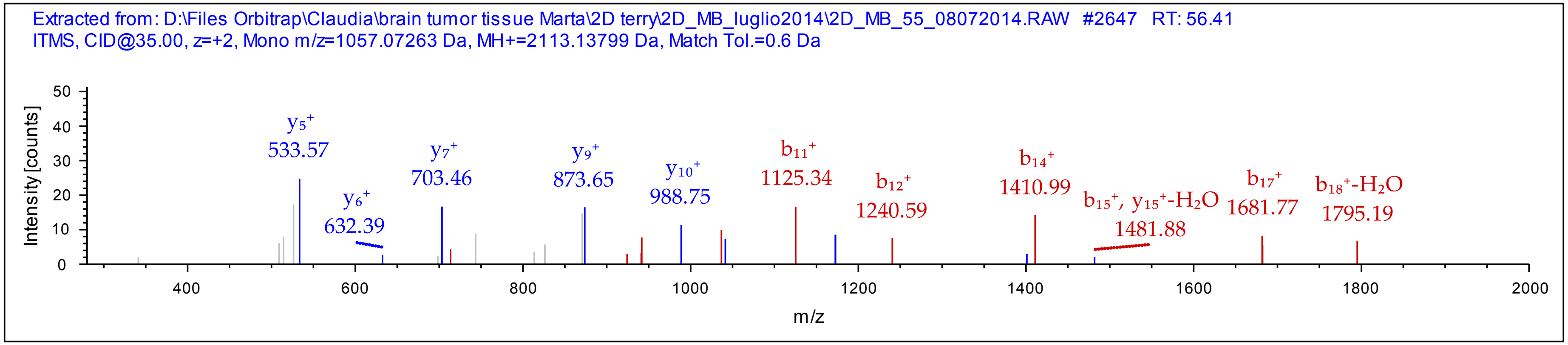
Sequence: ALMLQGVDLLADAVAVTMGPK, Charge: +2, Monoisotopic m/z: 1057.07263 Da (-0.86 mmu/-0.81 ppm), MH+: 2113.13799 Da, RT: 56.41 min,
Identified with: Sequest HT (v1.3); XCorr:2.12, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]
-

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			21
2	185.12847	93.06787	L	2042.10258	1021.55493	20
3	316.16897	158.58812	M	1929.01851	965.01289	19
4	429.25304	215.13016	L	1797.97801	899.49264	18
5	557.31162	279.15945	Q	1684.89394	842.95061	17
6	614.33309	307.67018	G	1556.83536	778.92132	16
7	713.40151	357.20439	V	1499.81389	750.41058	15
8	828.42846	414.71787	D	1400.74547	700.87637	14
9	941.51253	471.25990	L	1285.71852	643.36290	13
10	1054.59660	527.80194	L	1172.63445	586.82086	12

11	1125.63372	563.32050	A	1059.55038	530.27883	11
12	1240.66067	620.83397	D	988.51326	494.76027	10
13	1311.69779	656.35253	A	873.48631	437.24679	9
14	1410.76621	705.88674	V	802.44919	401.72823	8
15	1481.80333	741.40530	A	703.38077	352.19402	7
16	1580.87175	790.93951	V	632.34365	316.67546	6
17	1681.91943	841.46335	T	533.27523	267.14125	5
18	1812.95993	906.98360	M	432.22755	216.61741	4
19	1869.98140	935.49434	G	301.18705	151.09716	3
20	1967.03417	984.02072	P	244.16558	122.58643	2
21			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_MB_luglio2014\2D_MB_55_08072014.RAW #2647 RT: 56.41
ITMS, CID@35.00, z=+2, Mono m/z=1057.07263 Da, MH+=2113.13799 Da, Match Tol.=0.6 Da

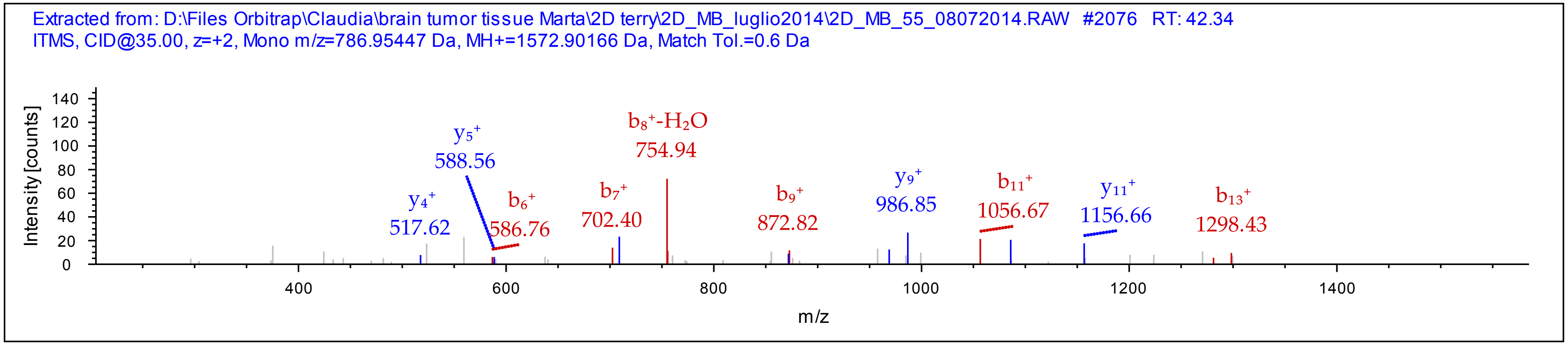
Sequence: GVMLAVDAVIAELKK, M3-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 786.95447 Da (-0.69 mmu/-0.88 ppm), MH+: 1572.90166 Da, RT: 42.34 min,
Identified with: Sequest HT (v1.3); XCorr:2.01, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	58.02875	29.51801	G			15
2	157.09717	79.05222	V	1515.88158	758.44443	14
3	304.13258	152.56993	M-Oxidation	1416.81316	708.91022	13
4	417.21665	209.11196	L	1269.77774	635.39251	12

5	488.25377	244.63052	A	1156.69367	578.85047	11
6	587.32219	294.16473	V	1085.65655	543.33191	10
7	702.34914	351.67821	D	986.58813	493.79770	9
8	773.38626	387.19677	A	871.56118	436.28423	8
9	872.45468	436.73098	V	800.52406	400.76567	7
10	985.53875	493.27301	I	701.45564	351.23146	6
11	1056.57587	528.79157	A	588.37157	294.68942	5
12	1185.61847	593.31287	E	517.33445	259.17086	4
13	1298.70254	649.85491	L	388.29185	194.64956	3
14	1426.79751	713.90239	K	275.20778	138.10753	2
15			K	147.11281	74.06004	1



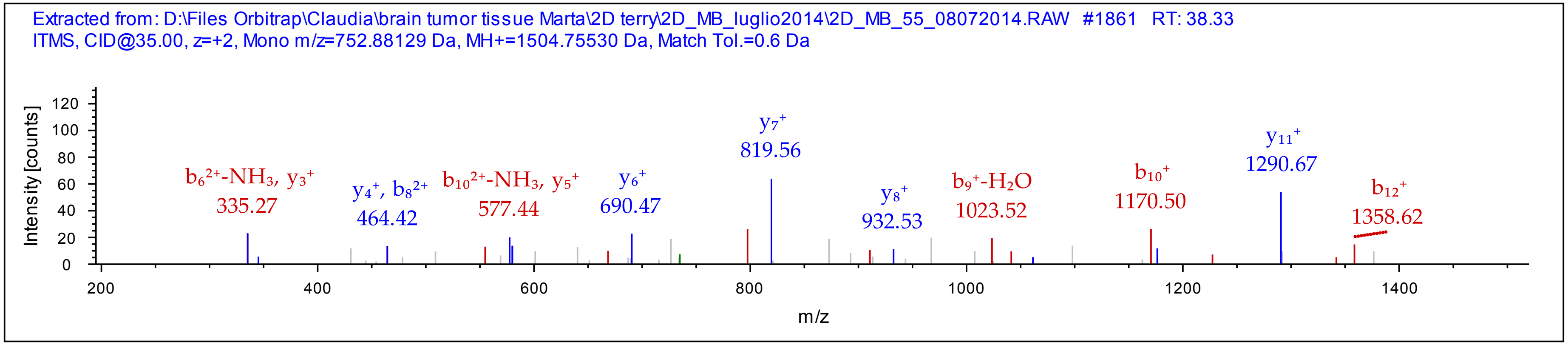
Sequence: TLNDELEIIEGMK, Charge: +2, Monoisotopic m/z: 752.88129 Da (-0.56 mmu/-0.75 ppm), MH+: 1504.75530 Da, RT: 38.33 min,
Identified with: Sequest HT (v1.3); XCorr:1.97, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	102.05496	51.53112	T			13
2	215.13903	108.07315	L	1403.70874	702.35801	12
3	329.18196	165.09462	N	1290.62467	645.81597	11
4	444.20891	222.60809	D	1176.58174	588.79451	10
5	573.25151	287.12939	E	1061.55479	531.28103	9
6	686.33558	343.67143	L	932.51219	466.75973	8

7	815.37818	408.19273	E	819.42812	410.21770	7
8	928.46225	464.73476	I	690.38552	345.69640	6
9	1041.54632	521.27680	I	577.30145	289.15436	5
10	1170.58892	585.79810	E	464.21738	232.61233	4
11	1227.61039	614.30883	G	335.17478	168.09103	3
12	1358.65089	679.82908	M	278.15331	139.58029	2
13			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_MB_luglio2014\2D_MB_55_08072014.RAW #1861 RT: 38.33
ITMS, CID@35.00, z=+2, Mono m/z=752.88129 Da, MH+=1504.75530 Da, Match Tol.=0.6 Da

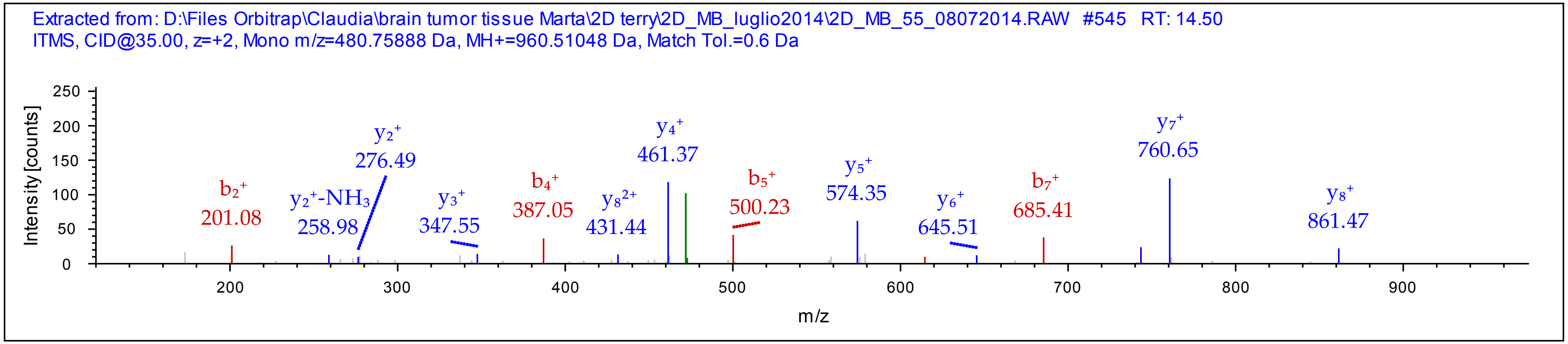
Sequence: VTDALNATR, Charge: +2, Monoisotopic m/z: 480.75888 Da (-0.22 mmu/-0.47 ppm), MH+: 960.51048 Da, RT: 14.50 min,
Identified with: Sequest HT (v1.3); XCorr:1.96, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H$_2$O; b-NH$_3$; y; y-H$_2$O; y-NH$_3$

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	100.07570	50.54149	V			9
2	201.12338	101.06533	T	861.44251	431.22489	8
3	316.15033	158.57880	D	760.39483	380.70105	7
4	387.18745	194.09736	A	645.36788	323.18758	6
5	500.27152	250.63940	L	574.33076	287.66902	5
6	614.31445	307.66086	N	461.24669	231.12698	4
7	685.35157	343.17942	A	347.20376	174.10552	3
8	786.39925	393.70326	T	276.16664	138.58696	2

9			R	175.11896	88.06312	1

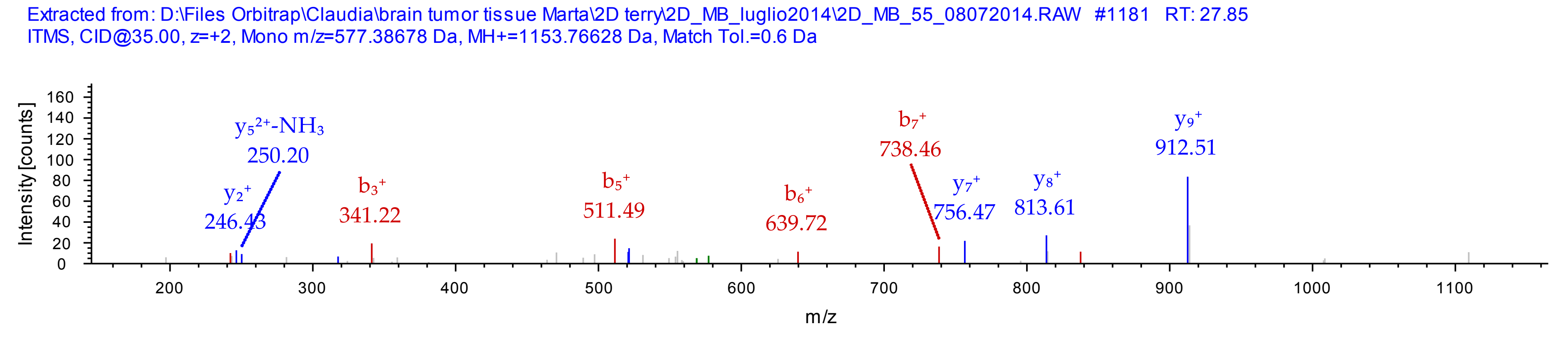


Sequence: LKVGLQVVAVK, Charge: +2, Monoisotopic m/z: 577.38678 Da (-0.24 mmu/-0.42 ppm), MH+: 1153.76628 Da, RT: 27.85 min,
Identified with: Sequest HT (v1.3); XCorr:1.93, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-NH_3; y; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			11
2	242.18632	121.59680	K	1040.68270	520.84499	10
3	341.25474	171.13101	V	912.58773	456.79750	9
4	398.27621	199.64174	G	813.51931	407.26329	8
5	511.36028	256.18378	L	756.49784	378.75256	7
6	639.41886	320.21307	Q	643.41377	322.21052	6
7	738.48728	369.74728	V	515.35519	258.18123	5
8	837.55570	419.28149	V	416.28677	208.64702	4
9	908.59282	454.80005	A	317.21835	159.11281	3
10	1007.66124	504.33426	V	246.18123	123.59425	2
11			K	147.11281	74.06004	1

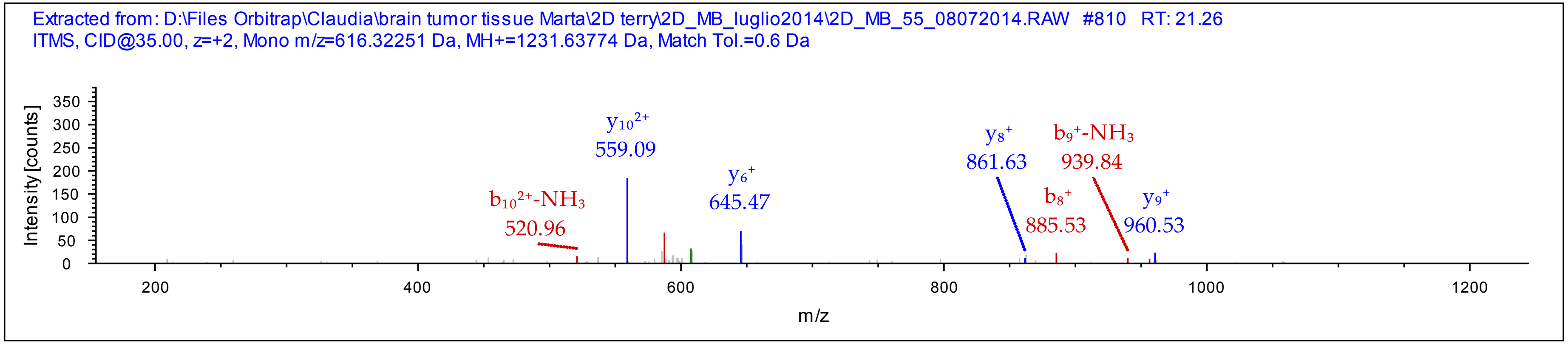


Sequence: DRVTDALNATR, Charge: +2, Monoisotopic m/z: 616.32251 Da (-0.63 mmu/-1.02 ppm), MH+: 1231.63774 Da, RT: 21.26 min,
Identified with: Sequest HT (v1.3); XCorr:1.86, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	116.03423	58.52075	D			11
2	272.13535	136.57131	R	1116.61205	558.80966	10
3	371.20377	186.10552	V	960.51093	480.75910	9
4	472.25145	236.62936	T	861.44251	431.22489	8
5	587.27840	294.14284	D	760.39483	380.70105	7
6	658.31552	329.66140	A	645.36788	323.18758	6
7	771.39959	386.20343	L	574.33076	287.66902	5
8	885.44252	443.22490	N	461.24669	231.12698	4
9	956.47964	478.74346	A	347.20376	174.10552	3
10	1057.52732	529.26730	T	276.16664	138.58696	2
11			R	175.11896	88.06312	1

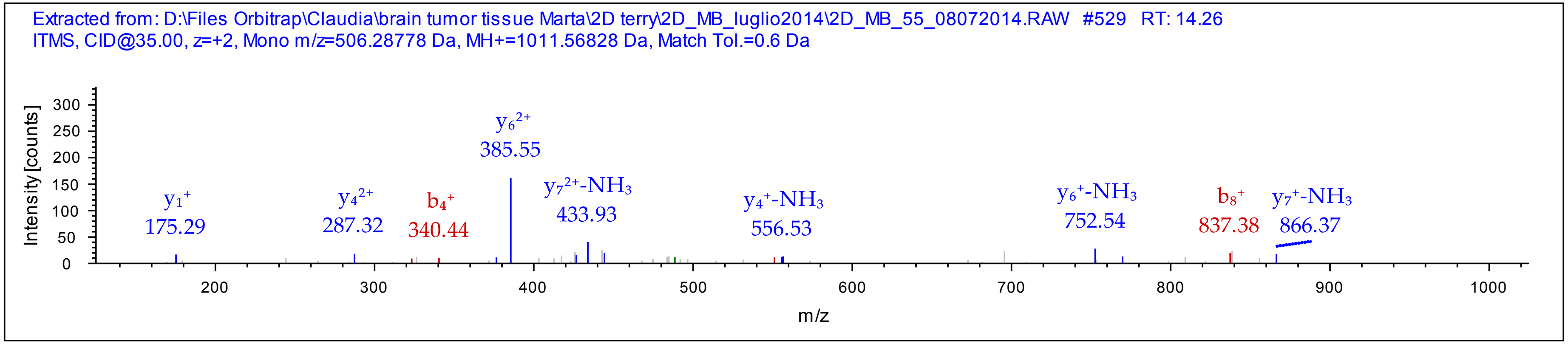


Sequence: GANPVEIRR, Charge: +2, Monoisotopic m/z: 506.28778 Da (-0.59 mmu/-1.16 ppm), MH+: 1011.56828 Da, RT: 14.26 min,
Identified with: Sequest HT (v1.3); XCorr:1.84, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	58.02875	29.51801	G			9
2	129.06587	65.03657	A	954.54799	477.77763	8
3	243.10880	122.05804	N	883.51087	442.25907	7
4	340.16157	170.58442	P	769.46794	385.23761	6
5	439.22999	220.11863	V	672.41517	336.71122	5
6	568.27259	284.63993	E	573.34675	287.17701	4
7	681.35666	341.18197	I	444.30415	222.65571	3
8	837.45778	419.23253	R	331.22008	166.11368	2
9			R	175.11896	88.06312	1



Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_MB_luglio2014\2D_MB_55_08072014.RAW #529 RT: 14.26
ITMS, CID@35.00, z=+2, Mono m/z=506.28778 Da, MH+=1011.56828 Da, Match Tol.=0.6 Da

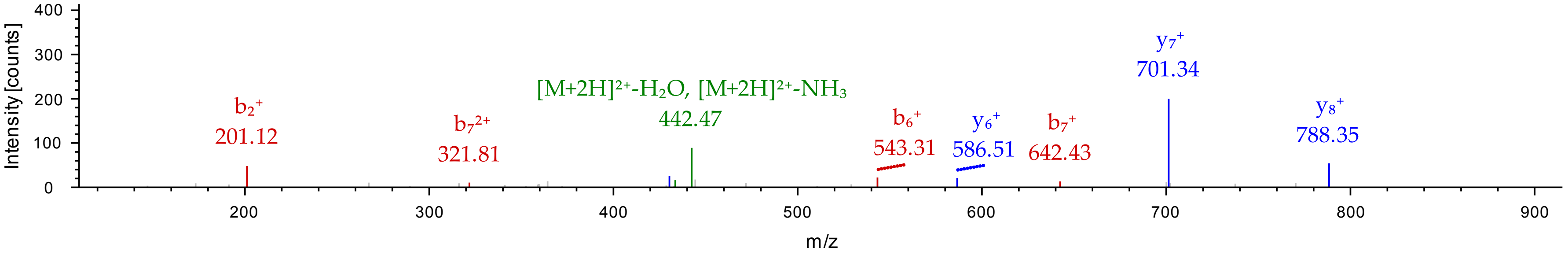
Sequence: LSDGVAVLK, Charge: +2, Monoisotopic m/z: 451.27103 Da (-0.29 mmu/-0.65 ppm), MH+: 901.53478 Da, RT: 22.85 min,
Identified with: Sequest HT (v1.3); XCorr:1.79, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):

- 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			9
2	201.12338	101.06533	S	788.45129	394.72928	8
3	316.15033	158.57880	D	701.41926	351.21327	7
4	373.17180	187.08954	G	586.39231	293.69979	6
5	472.24022	236.62375	V	529.37084	265.18906	5
6	543.27734	272.14231	A	430.30242	215.65485	4
7	642.34576	321.67652	V	359.26530	180.13629	3
8	755.42983	378.21855	L	260.19688	130.60208	2
9			K	147.11281	74.06004	1

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_MB_luglio2014\2D_MB_55_08072014.RAW #883 RT: 22.85
ITMS, CID@35.00, z=+2, Mono m/z=451.27103 Da, MH+=901.53478 Da, Match Tol.=0.6 Da



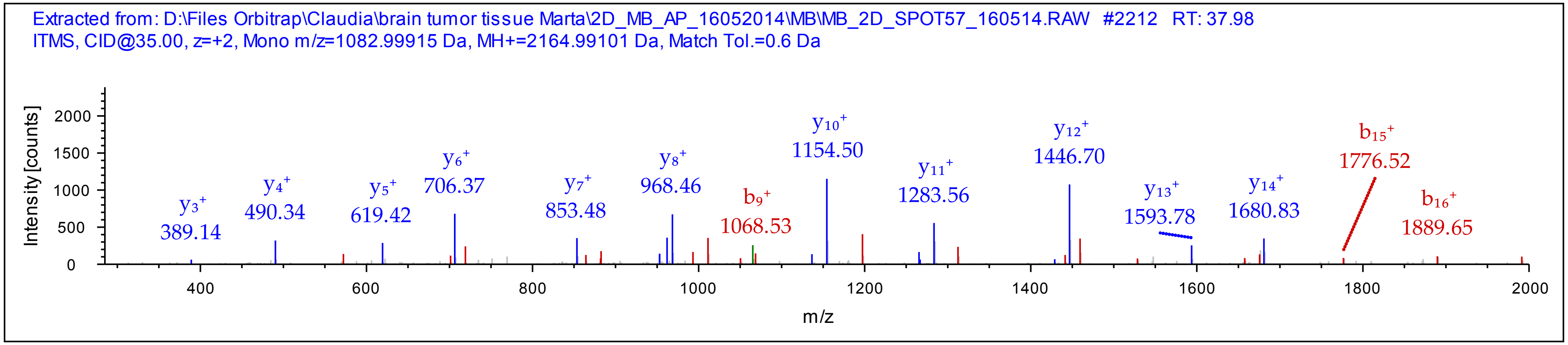
Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
57	P11021	78 kDa glucose-regulated protein	70.4	5.0	450.20	42.05 %	23	25	MB, PA	NS	1.7	↑ in PA

Sequence: IEIESFYEGEDFSETLTR, Charge: +2, Monoisotopic m/z: 1082.99915 Da (-0.58 mmu/-0.53 ppm), MH+: 2164.99101 Da, RT: 37.98 min,
Identified with: Sequest HT (v1.3); XCorr:5.38, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):

- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	114.09135	57.54931	I			18
2	243.13395	122.07061	E	2051.90810	1026.45769	17
3	356.21802	178.61265	I	1922.86550	961.93639	16
4	485.26062	243.13395	E	1809.78143	905.39435	15
5	572.29265	286.64996	S	1680.73883	840.87305	14
6	719.36107	360.18417	F	1593.70680	797.35704	13
7	882.42439	441.71583	Y	1446.63838	723.82283	12
8	1011.46699	506.23713	E	1283.57506	642.29117	11
9	1068.48846	534.74787	G	1154.53246	577.76987	10
10	1197.53106	599.26917	E	1097.51099	549.25913	9
11	1312.55801	656.78264	D	968.46839	484.73783	8
12	1459.62643	730.31685	F	853.44144	427.22436	7
13	1546.65846	773.83287	S	706.37302	353.69015	6
14	1675.70106	838.35417	E	619.34099	310.17413	5
15	1776.74874	888.87801	T	490.29839	245.65283	4
16	1889.83281	945.42004	L	389.25071	195.12899	3
17	1990.88049	995.94388	T	276.16664	138.58696	2
18			R	175.11896	88.06312	1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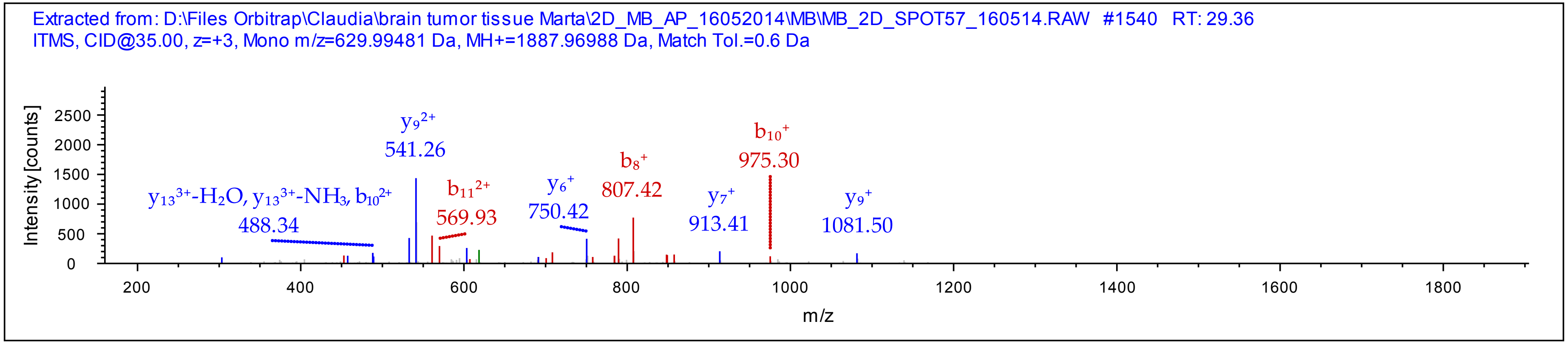
ITMS, CID@35.00, z=+2, Mono m/z=1082.99915 Da, MH+=2164.99101 Da, Match Tol.=0.6 Da

Sequence: VTHAVVTVPAYFNDAQR, Charge: +3, Monoisotopic m/z: 629.99481 Da (-0.45 mmu/-0.72 ppm), MH+: 1887.96988 Da, RT: 29.36 min,
Identified with: Sequest HT (v1.3); XCorr:4.60, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	100.07570	50.54149	34.03008	V				17
2	201.12338	101.06533	67.71264	T	1788.90282	894.95505	596.97246	16
3	338.18229	169.59478	113.39895	H	1687.85514	844.43121	563.28990	15
4	409.21941	205.11334	137.07799	A	1550.79623	775.90175	517.60359	14
5	508.28783	254.64755	170.10079	V	1479.75911	740.38319	493.92455	13
6	607.35625	304.18176	203.12360	V	1380.69069	690.84898	460.90175	12
7	708.40393	354.70560	236.80616	T	1281.62227	641.31477	427.87894	11
8	807.47235	404.23981	269.82897	V	1180.57459	590.79093	394.19638	10
9	904.52512	452.76620	302.17989	P	1081.50617	541.25672	361.17357	9
10	975.56224	488.28476	325.85893	A	984.45340	492.73034	328.82265	8
11	1138.62556	569.81642	380.21337	Y	913.41628	457.21178	305.14361	7
12	1285.69398	643.35063	429.23618	F	750.35296	375.68012	250.78917	6
13	1399.73691	700.37209	467.25049	N	603.28454	302.14591	201.76636	5
14	1514.76386	757.88557	505.59280	D	489.24161	245.12444	163.75205	4
15	1585.80098	793.40413	529.27184	A	374.21466	187.61097	125.40974	3
16	1713.85956	857.43342	571.95804	Q	303.17754	152.09241	101.73070	2
17				R	175.11896	88.06312	59.04450	1

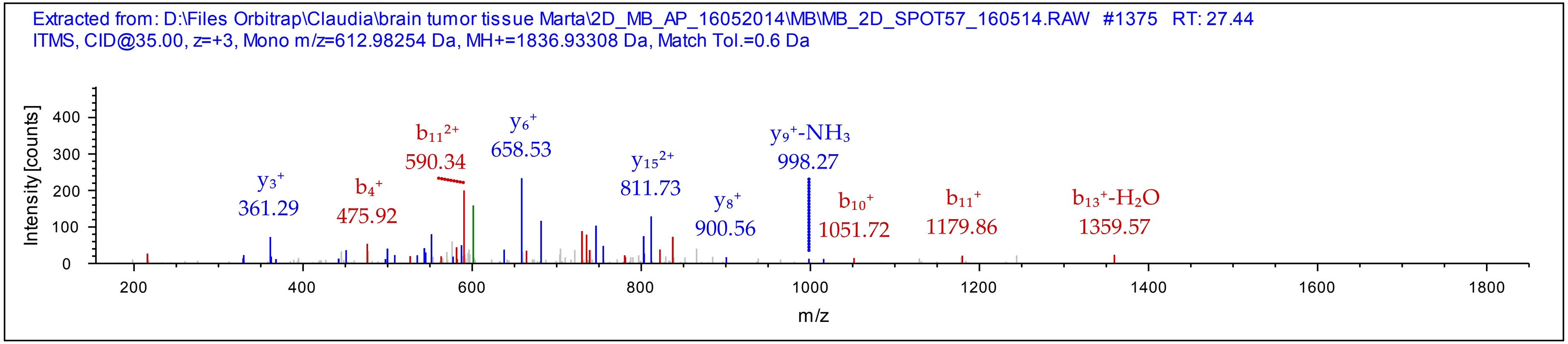

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT57_160514.RAW #1540 RT: 29.36
ITMS, CID@35.00, z=+3, Mono m/z=629.99481 Da, MH+=1887.96988 Da, Match Tol.=0.6 Da

Sequence: SQIFSTASDNQPTVTIK, Charge: +3, Monoisotopic m/z: 612.98254 Da (-0.26 mmu/-0.42 ppm), MH+: 1836.93308 Da, RT: 27.44 min,
Identified with: Sequest HT (v1.3); XCorr:4.59, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	88.03931	44.52329	30.01795	S				17
2	216.09789	108.55258	72.70415	Q	1749.90182	875.45455	583.97212	16
3	329.18196	165.09462	110.39884	I	1621.84324	811.42526	541.28593	15
4	476.25038	238.62883	159.42164	F	1508.75917	754.88322	503.59124	14
5	563.28241	282.14484	188.43232	S	1361.69075	681.34901	454.56843	13
6	664.33009	332.66868	222.11488	T	1274.65872	637.83300	425.55776	12
7	735.36721	368.18724	245.79392	A	1173.61104	587.30916	391.87520	11
8	822.39924	411.70326	274.80460	S	1102.57392	551.79060	368.19616	10
9	937.42619	469.21673	313.14691	D	1015.54189	508.27458	339.18548	9
10	1051.46912	526.23820	351.16122	N	900.51494	450.76111	300.84316	8
11	1179.52770	590.26749	393.84742	Q	786.47201	393.73964	262.82885	7
12	1276.58047	638.79387	426.19834	P	658.41343	329.71035	220.14266	6
13	1377.62815	689.31771	459.88090	T	561.36066	281.18397	187.79174	5
14	1476.69657	738.85192	492.90371	V	460.31298	230.66013	154.10918	4
15	1577.74425	789.37576	526.58627	T	361.24456	181.12592	121.08637	3
16	1690.82832	845.91780	564.28096	I	260.19688	130.60208	87.40381	2
17				K	147.11281	74.06004	49.70912	1



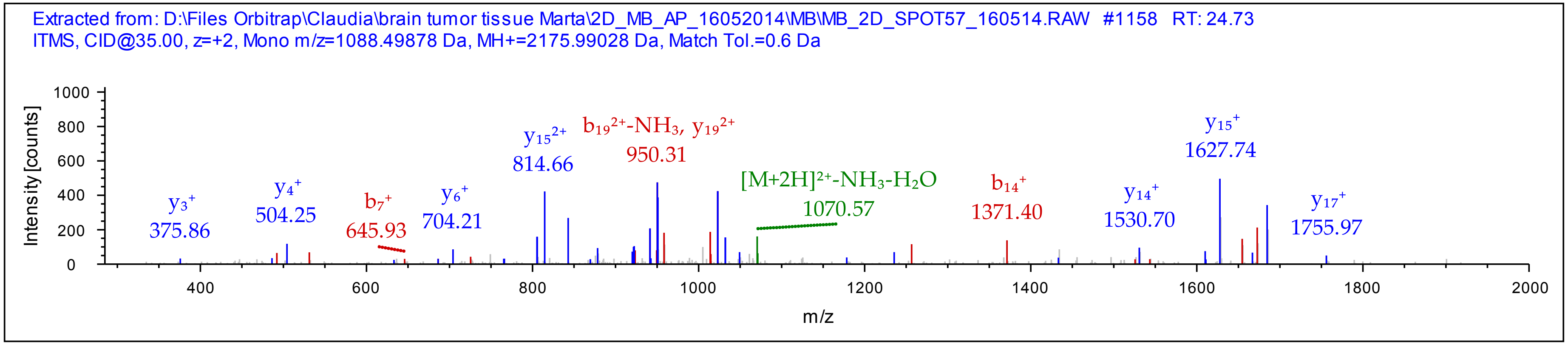
Sequence: LYGSAGPPPTGEEDTAEKDEL, Charge: +2, Monoisotopic m/z: 1088.49878 Da (-1.32 mmu/-1.21 ppm), MH+: 2175.99028 Da, RT: 24.73 min,
Identified with: Sequest HT (v1.3); XCorr:4.25, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	L			21
2	277.15467	139.08097	Y	2062.90885	1031.95806	20
3	334.17614	167.59171	G	1899.84553	950.42640	19
4	421.20817	211.10772	S	1842.82406	921.91567	18
5	492.24529	246.62628	A	1755.79203	878.39965	17
6	549.26676	275.13702	G	1684.75491	842.88109	16
7	646.31953	323.66340	P	1627.73344	814.37036	15
8	743.37230	372.18979	P	1530.68067	765.84397	14
9	840.42507	420.71617	P	1433.62790	717.31759	13
10	941.47275	471.24001	T	1336.57513	668.79120	12
11	998.49422	499.75075	G	1235.52745	618.26736	11
12	1127.53682	564.27205	E	1178.50598	589.75663	10
13	1256.57942	628.79335	E	1049.46338	525.23533	9
14	1371.60637	686.30682	D	920.42078	460.71403	8
15	1472.65405	736.83066	T	805.39383	403.20055	7
16	1543.69117	772.34922	A	704.34615	352.67671	6
17	1672.73377	836.87052	E	633.30903	317.15815	5
18	1800.82874	900.91801	K	504.26643	252.63685	4

19	1915.85569	958.43148	D	376.17146	188.58937	3
20	2044.89829	1022.95278	E	261.14451	131.07589	2
21			L	132.10191	66.55459	1

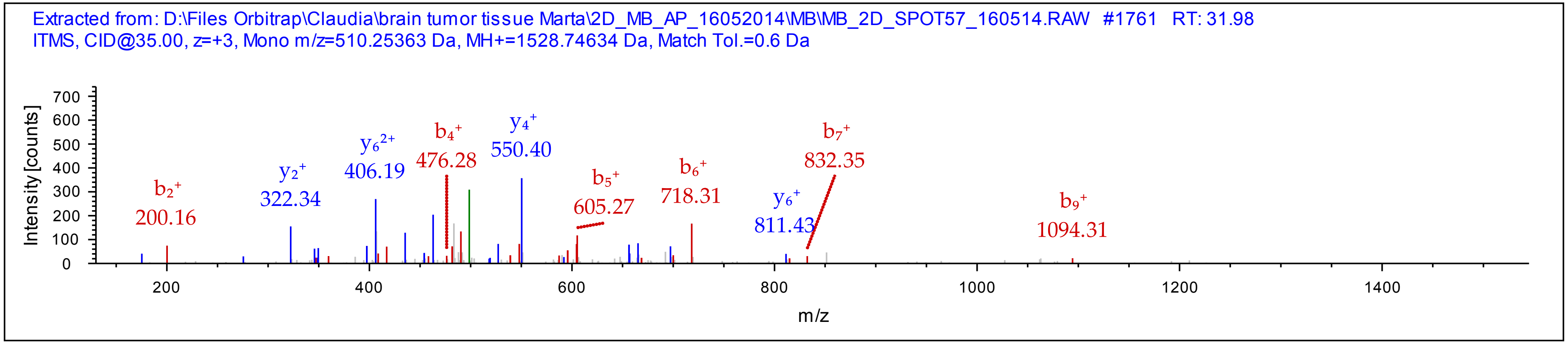


Sequence: AKFEELNMDLFR, M8-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 510.25363 Da (-0.06 mmu/-0.12 ppm), MH+: 1528.74634 Da, RT: 31.98 min,
Identified with: Sequest HT (v1.3); XCorr:4.14, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

#1	**b$^+$**	**b^{2+}**	**b^{3+}**	**Seq.**	**y$^+$**	**y^{2+}**	**y^{3+}**	**#2**
1	72.04440	36.52584	24.68632	A				12
2	200.13937	100.57332	67.38464	K	1457.70941	729.35834	486.57465	11
3	347.20779	174.10753	116.40745	F	1329.61444	665.31086	443.87633	10
4	476.25039	238.62883	159.42165	E	1182.54602	591.77665	394.85352	9
5	605.29299	303.15013	202.43585	E	1053.50342	527.25535	351.83932	8
6	718.37706	359.69217	240.13054	L	924.46082	462.73405	308.82512	7
7	832.41999	416.71363	278.14485	N	811.37675	406.19201	271.13043	6
8	979.45540	490.23134	327.15665	M-Oxidation	697.33382	349.17055	233.11612	5
9	1094.48235	547.74481	365.49897	D	550.29840	275.65284	184.10432	4
10	1207.56642	604.28685	403.19366	L	435.27145	218.13936	145.76200	3
11	1354.63484	677.82106	452.21646	F	322.18738	161.59733	108.06731	2
12				R	175.11896	88.06312	59.04450	1

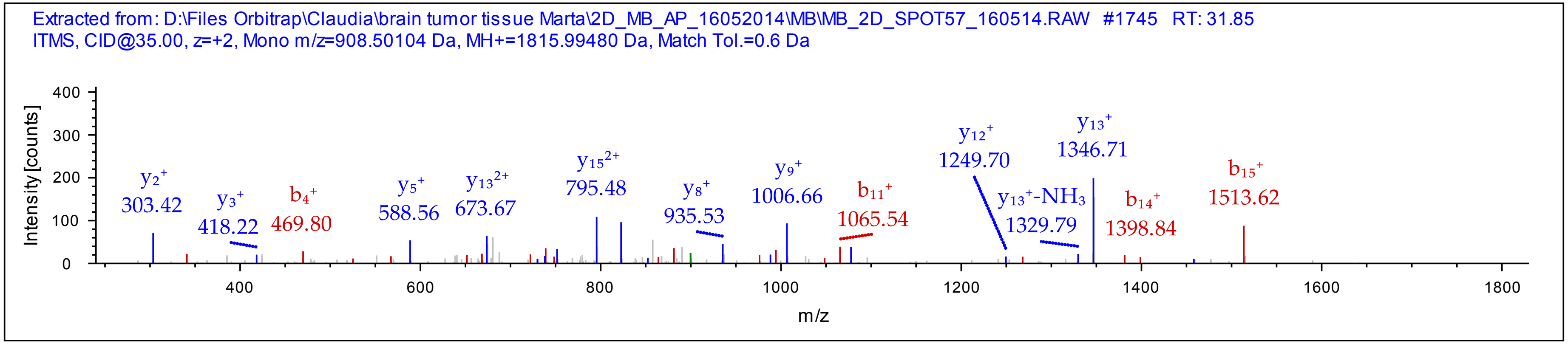


Sequence: IINEPTAAAIAYGLDKR, Charge: +2, Monoisotopic m/z: 908.50104 Da (-0.81 mmu/-0.89 ppm), MH+: 1815.99480 Da, RT: 31.85 min,
Identified with: Sequest HT (v1.3); XCorr:3.98, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

#1	b^{+}	b^{2+}	Seq.	y^{+}	y^{2+}	#2
1	114.09135	57.54931	I			17
2	227.17542	114.09135	I	1702.91234	851.95981	16
3	341.21835	171.11281	N	1589.82827	795.41777	15
4	470.26095	235.63411	E	1475.78534	738.39631	14
5	567.31372	284.16050	P	1346.74274	673.87501	13
6	668.36140	334.68434	T	1249.68997	625.34862	12
7	739.39852	370.20290	A	1148.64229	574.82478	11
8	810.43564	405.72146	A	1077.60517	539.30622	10
9	881.47276	441.24002	A	1006.56805	503.78766	9
10	994.55683	497.78205	I	935.53093	468.26910	8
11	1065.59395	533.30061	A	822.44686	411.72707	7
12	1228.65727	614.83227	Y	751.40974	376.20851	6
13	1285.67874	643.34301	G	588.34642	294.67685	5
14	1398.76281	699.88504	L	531.32495	266.16611	4
15	1513.78976	757.39852	D	418.24088	209.62408	3
16	1641.88473	821.44600	K	303.21393	152.11060	2
17			R	175.11896	88.06312	1



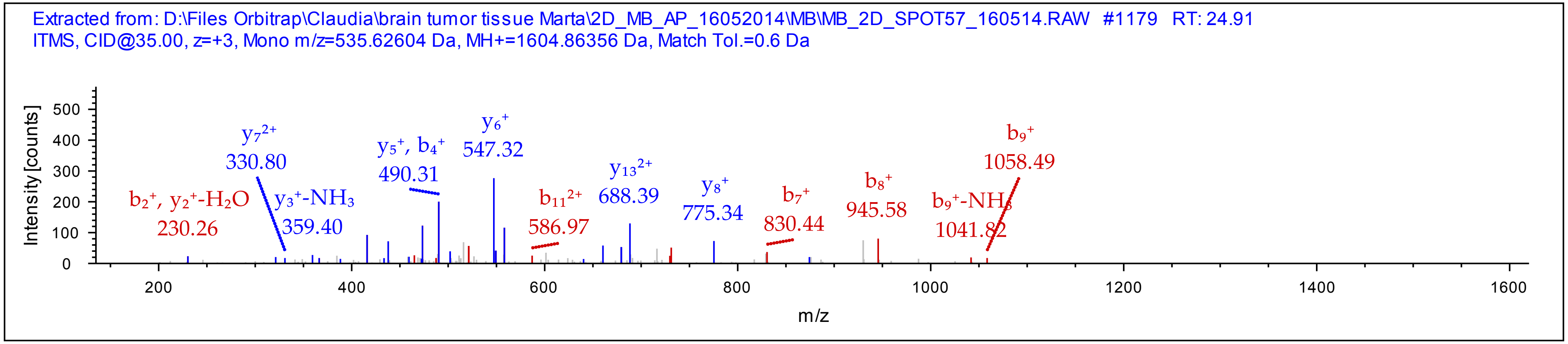
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT57_160514.RAW #1745 RT: 31.85
ITMS, CID@35.00, z=+2, Mono m/z=908.50104 Da, MH+=1815.99480 Da, Match Tol.=0.6 Da

Sequence: TKPYIQVDIGGGQTK, Charge: +3, Monoisotopic m/z: 535.62604 Da (-0.25 mmu/-0.47 ppm), MH+: 1604.86356 Da, RT: 24.91 min,
Identified with: Sequest HT (v1.3); XCorr:3.49, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	102.05496	51.53112	34.68984	T				15
2	230.14993	115.57860	77.38816	K	1503.81663	752.41195	501.94373	14
3	327.20270	164.10499	109.73908	P	1375.72166	688.36447	459.24540	13
4	490.26602	245.63665	164.09352	Y	1278.66889	639.83808	426.89448	12
5	603.35009	302.17868	201.78821	I	1115.60557	558.30642	372.54004	11
6	731.40867	366.20797	244.47441	Q	1002.52150	501.76439	334.84535	10
7	830.47709	415.74218	277.49721	V	874.46292	437.73510	292.15916	9
8	945.50404	473.25566	315.83953	D	775.39450	388.20089	259.13635	8
9	1058.58811	529.79769	353.53422	I	660.36755	330.68741	220.79403	7
10	1115.60958	558.30843	372.54138	G	547.28348	274.14538	183.09934	6
11	1172.63105	586.81916	391.54853	G	490.26201	245.63464	164.09219	5
12	1229.65252	615.32990	410.55569	G	433.24054	217.12391	145.08503	4
13	1357.71110	679.35919	453.24188	Q	376.21907	188.61317	126.07787	3
14	1458.75878	729.88303	486.92444	T	248.16049	124.58388	83.39168	2
15				K	147.11281	74.06004	49.70912	1

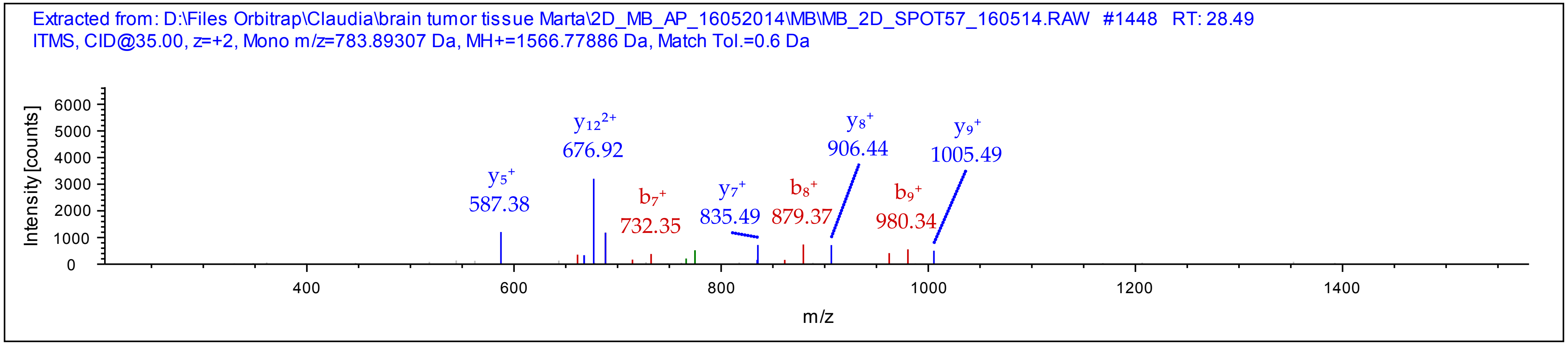

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT57_160514.RAW #1179 RT: 24.91
ITMS, CID@35.00, z=+3, Mono m/z=535.62604 Da, MH+=1604.86356 Da, Match Tol.=0.6 Da

Sequence: ITPSYVAFTPEGER, Charge: +2, Monoisotopic m/z: 783.89307 Da (-0.53 mmu/-0.67 ppm), MH+: 1566.77886 Da, RT: 28.49 min,
Identified with: Sequest HT (v1.3); XCorr:3.38, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):

- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

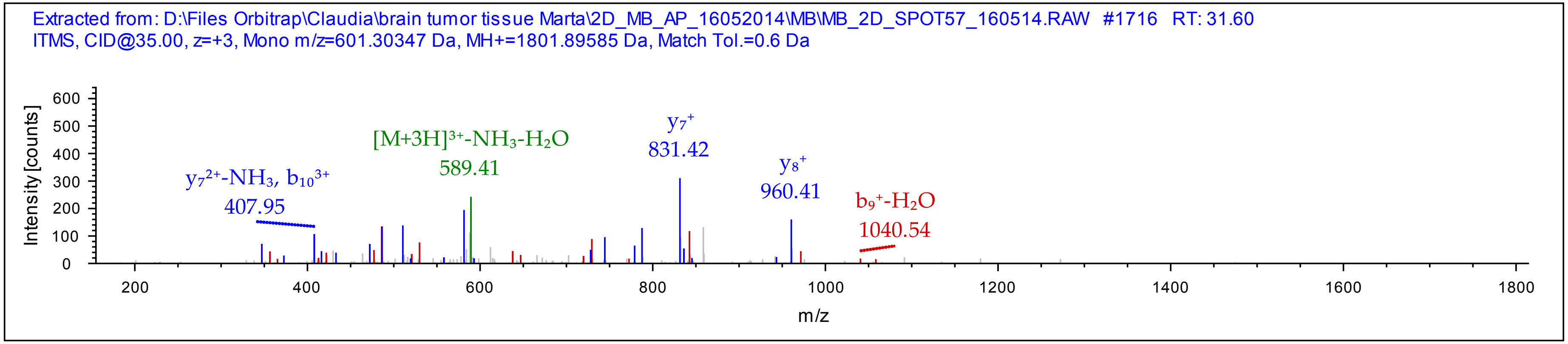
#1	b⁺	b²⁺	Seq.	y⁺	y²⁺	#2
1	114.09135	57.54931	I			14
2	215.13903	108.07315	T	1453.69584	727.35156	13
3	312.19180	156.59954	P	1352.64816	676.82772	12
4	399.22383	200.11555	S	1255.59539	628.30133	11
5	562.28715	281.64721	Y	1168.56336	584.78532	10
6	661.35557	331.18142	V	1005.50004	503.25366	9
7	732.39269	366.69998	A	906.43162	453.71945	8
8	879.46111	440.23419	F	835.39450	418.20089	7
9	980.50879	490.75803	T	688.32608	344.66668	6
10	1077.56156	539.28442	P	587.27840	294.14284	5
11	1206.60416	603.80572	E	490.22563	245.61645	4
12	1263.62563	632.31645	G	361.18303	181.09515	3
13	1392.66823	696.83775	E	304.16156	152.58442	2
14			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT57_160514.RAW #1448 RT: 28.49
ITMS, CID@35.00, z=+2, Mono m/z=783.89307 Da, MH+=1566.77886 Da, Match Tol.=0.6 Da

Sequence: IDTRNELESYAYSLK, Charge: +3, Monoisotopic m/z: 601.30347 Da (-0.29 mmu/-0.49 ppm), MH+: 1801.89585 Da, RT: 31.60 min,
Identified with: Sequest HT (v1.3); XCorr:3.35, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

#1	b^{+}	b^{2+}	b^{3+}	Seq.	y^{+}	y^{2+}	y^{3+}	#2
1	114.09135	57.54931	38.70197	I				15
2	229.11830	115.06279	77.04428	D	1688.81265	844.90996	563.60907	14
3	330.16598	165.58663	110.72684	T	1573.78570	787.39649	525.26675	13
4	486.26710	243.63719	162.76055	R	1472.73802	736.87265	491.58419	12
5	600.31003	300.65865	200.77486	N	1316.63690	658.82209	439.55048	11
6	729.35263	365.17995	243.78906	E	1202.59397	601.80062	401.53617	10
7	842.43670	421.72199	281.48375	L	1073.55137	537.27932	358.52197	9
8	971.47930	486.24329	324.49795	E	960.46730	480.73729	320.82728	8
9	1058.51133	529.75930	353.50863	S	831.42470	416.21599	277.81308	7
10	1221.57465	611.29096	407.86307	Y	744.39267	372.69997	248.80241	6
11	1292.61177	646.80952	431.54211	A	581.32935	291.16831	194.44797	5
12	1455.67509	728.34118	485.89655	Y	510.29223	255.64975	170.76893	4
13	1542.70712	771.85720	514.90722	S	347.22891	174.11809	116.41449	3
14	1655.79119	828.39923	552.60191	L	260.19688	130.60208	87.40381	2
15				K	147.11281	74.06004	49.70912	1

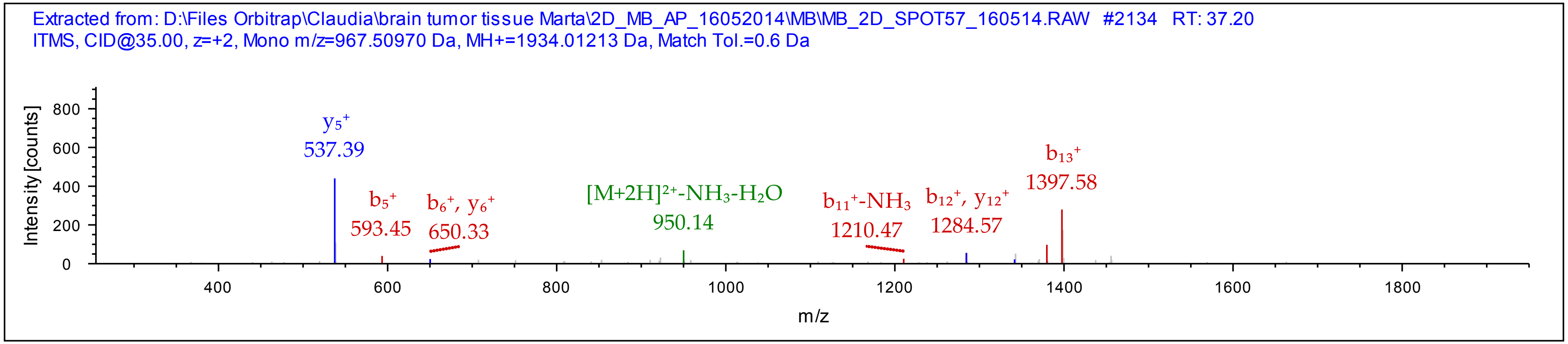

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT57_160514.RAW #1716 RT: 31.60
ITMS, CID@35.00, z=+3, Mono m/z=601.30347 Da, MH+=1801.89585 Da, Match Tol.=0.6 Da

Sequence: DNHLLGTFDLTGIPPAPR, Charge: +2, Monoisotopic m/z: 967.50970 Da (-0.5 mmu/-0.52 ppm), MH+: 1934.01213 Da, RT: 37.20 min,
Identified with: Sequest HT (v1.3); XCorr:3.27, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	116.03423	58.52075	D			18
2	230.07716	115.54222	N	1818.98618	909.99673	17
3	367.13607	184.07167	H	1704.94325	852.97526	16
4	480.22014	240.61371	L	1567.88434	784.44581	15
5	593.30421	297.15574	L	1454.80027	727.90377	14
6	650.32568	325.66648	G	1341.71620	671.36174	13
7	751.37336	376.19032	T	1284.69473	642.85100	12
8	898.44178	449.72453	F	1183.64705	592.32716	11
9	1013.46873	507.23800	D	1036.57863	518.79295	10
10	1126.55280	563.78004	L	921.55168	461.27948	9
11	1227.60048	614.30388	T	808.46761	404.73744	8
12	1284.62195	642.81461	G	707.41993	354.21360	7
13	1397.70602	699.35665	I	650.39846	325.70287	6
14	1494.75879	747.88303	P	537.31439	269.16083	5
15	1591.81156	796.40942	P	440.26162	220.63445	4
16	1662.84868	831.92798	A	343.20885	172.10806	3
17	1759.90145	880.45436	P	272.17173	136.58950	2
18			R	175.11896	88.06312	1

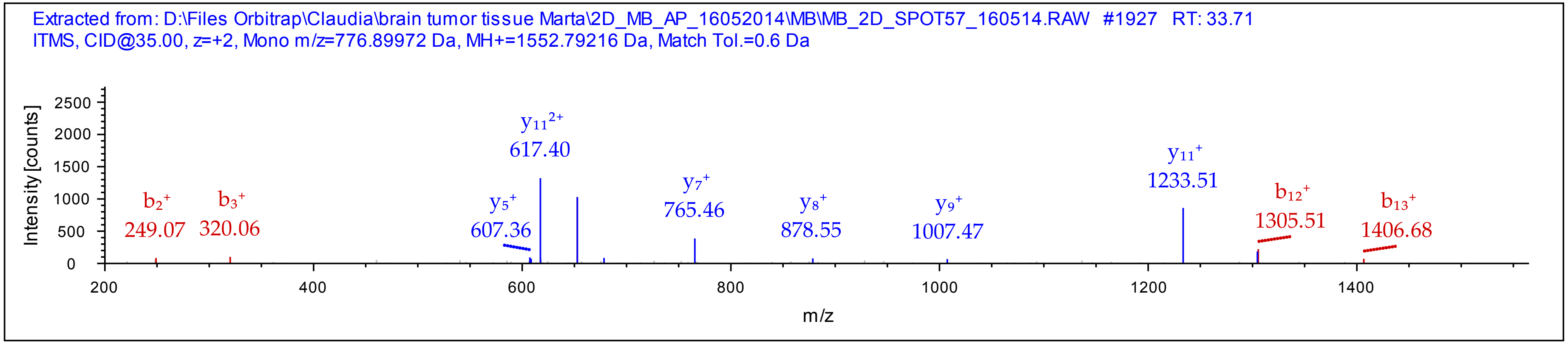


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT57_160514.RAW #2134 RT: 37.20
ITMS, CID@35.00, z=+2, Mono m/z=967.50970 Da, MH+=1934.01213 Da, Match Tol.=0.6 Da

Sequence: TFAPEEISAMVLTK, M10-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 776.89972 Da (-0.32 mmu/-0.42 ppm), MH+: 1552.79216 Da, RT: 33.71 min,
Identified with: Sequest HT (v1.3); XCorr:3.24, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	102.05496	51.53112	T			14
2	249.12338	125.06533	F	1451.74513	726.37620	13
3	320.16050	160.58389	A	1304.67671	652.84199	12
4	417.21327	209.11027	P	1233.63959	617.32343	11
5	546.25587	273.63157	E	1136.58682	568.79705	10
6	675.29847	338.15287	E	1007.54422	504.27575	9
7	788.38254	394.69491	I	878.50162	439.75445	8
8	875.41457	438.21092	S	765.41755	383.21241	7
9	946.45169	473.72948	A	678.38552	339.69640	6
10	1093.48710	547.24719	M-Oxidation	607.34840	304.17784	5
11	1192.55552	596.78140	V	460.31298	230.66013	4
12	1305.63959	653.32343	L	361.24456	181.12592	3
13	1406.68727	703.84727	T	248.16049	124.58388	2
14			K	147.11281	74.06004	1

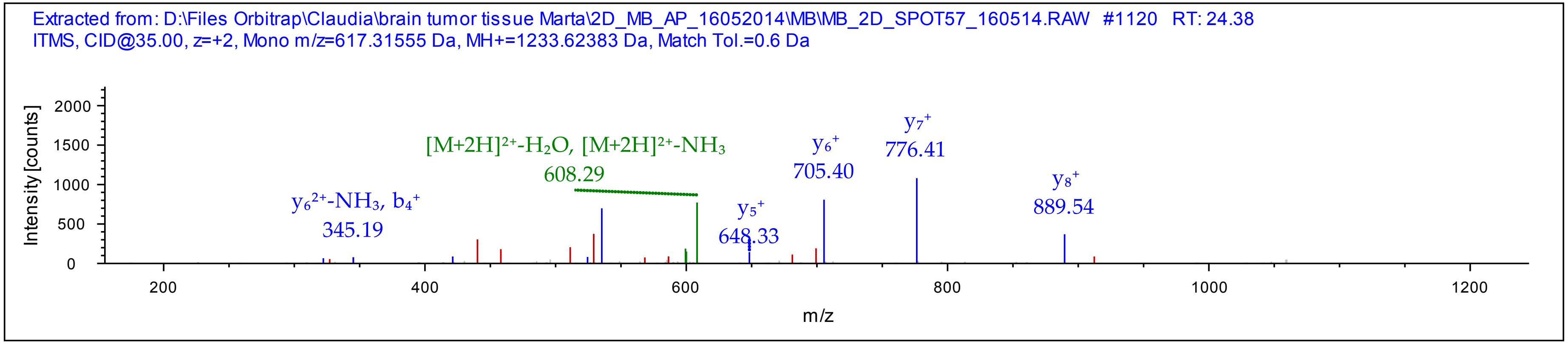


Sequence: DAGTIAGLNVMR, M11-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 617.31555 Da (-0.93 mmu/-1.5 ppm), MH+: 1233.62383 Da, RT: 24.38 min,
Identified with: Sequest HT (v1.3); XCorr:3.23, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

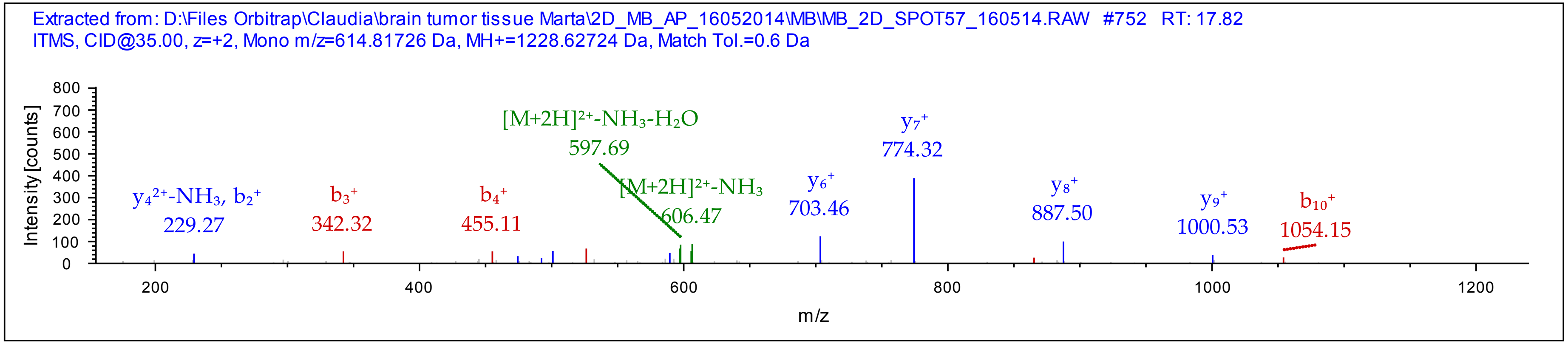
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	116.03423	58.52075	D			12
2	187.07135	94.03931	A	1118.59873	559.80300	11
3	244.09282	122.55005	G	1047.56161	524.28444	10
4	345.14050	173.07389	T	990.54014	495.77371	9
5	458.22457	229.61592	I	889.49246	445.24987	8
6	529.26169	265.13448	A	776.40839	388.70783	7
7	586.28316	293.64522	G	705.37127	353.18927	6
8	699.36723	350.18725	L	648.34980	324.67854	5
9	813.41016	407.20872	N	535.26573	268.13650	4
10	912.47858	456.74293	V	421.22280	211.11504	3
11	1059.51399	530.26063	M-Oxidation	322.15438	161.58083	2
12			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT57_160514.RAW #1120 RT: 24.38
ITMS, CID@35.00, z=+2, Mono m/z=617.31555 Da, MH+=1233.62383 Da, Match Tol.=0.6 Da

Sequence: VEIIANDQGNR, Charge: +2, Monoisotopic m/z: 614.81726 Da (-0.43 mmu/-0.7 ppm), MH+: 1228.62724 Da, RT: 17.82 min,
Identified with: Sequest HT (v1.3); XCorr:3.17, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):
- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]
- Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2 - [HS71L_HUMAN]
- Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5 - [HSP71_HUMAN]
- Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1 - [HSP72_HUMAN]
- Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]

#1	**b$^+$**	**b^{2+}**	**Seq.**	**y$^+$**	**y^{2+}**	**#2**
1	100.07570	50.54149	V			11
2	229.11830	115.06279	E	1129.55968	565.28348	10
3	342.20237	171.60482	I	1000.51708	500.76218	9
4	455.28644	228.14686	I	887.43301	444.22014	8
5	526.32356	263.66542	A	774.34894	387.67811	7
6	640.36649	320.68688	N	703.31182	352.15955	6
7	755.39344	378.20036	D	589.26889	295.13808	5
8	883.45202	442.22965	Q	474.24194	237.62461	4
9	940.47349	470.74038	G	346.18336	173.59532	3
10	1054.51642	527.76185	N	289.16189	145.08458	2
11			R	175.11896	88.06312	1

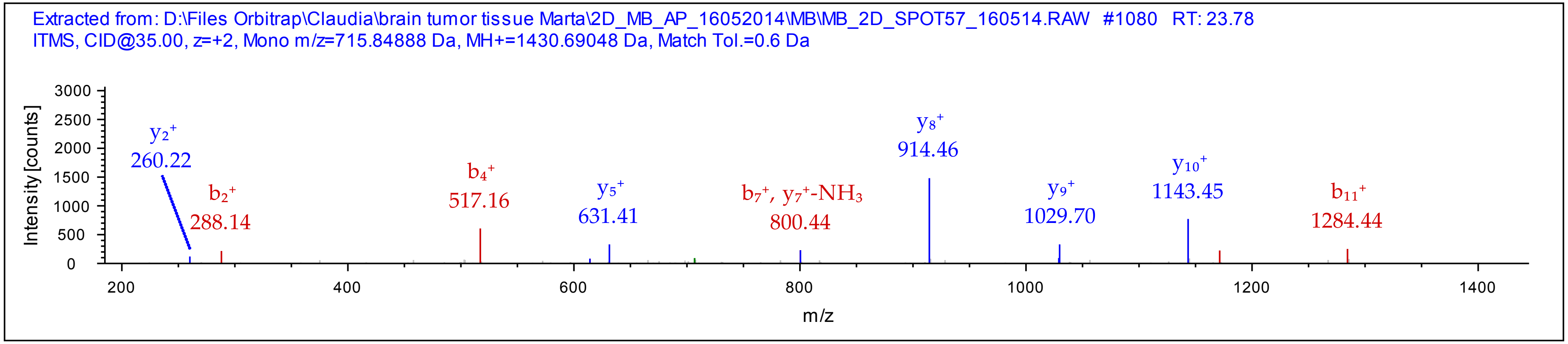


Sequence: TWNDPSVQQDIK, Charge: +2, Monoisotopic m/z: 715.84888 Da (-0.31 mmu/-0.43 ppm), MH+: 1430.69048 Da, RT: 23.78 min,
Identified with: Sequest HT (v1.3); XCorr:3.12, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	102.05496	51.53112	T			12
2	288.13428	144.57078	W	1329.64341	665.32534	11
3	402.17721	201.59224	N	1143.56409	572.28568	10
4	517.20416	259.10572	D	1029.52116	515.26422	9
5	614.25693	307.63210	P	914.49421	457.75074	8
6	701.28896	351.14812	S	817.44144	409.22436	7
7	800.35738	400.68233	V	730.40941	365.70834	6
8	928.41596	464.71162	Q	631.34099	316.17413	5
9	1056.47454	528.74091	Q	503.28241	252.14484	4
10	1171.50149	586.25438	D	375.22383	188.11555	3
11	1284.58556	642.79642	I	260.19688	130.60208	2
12			K	147.11281	74.06004	1

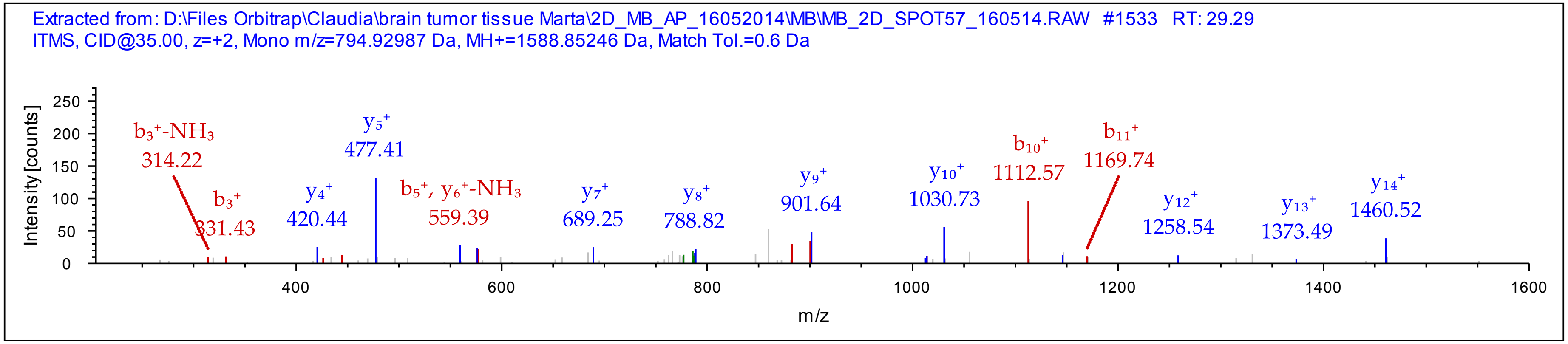


Sequence: KSDIDEIVLVGGSTR, Charge: +2, Monoisotopic m/z: 794.92987 Da (-0.85 mmu/-1.07 ppm), MH+: 1588.85246 Da, RT: 29.29 min,
Identified with: Sequest HT (v1.3); XCorr:3.07, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	129.10225	65.05476	K			15
2	216.13428	108.57078	S	1460.75919	730.88323	14
3	331.16123	166.08425	D	1373.72716	687.36722	13
4	444.24530	222.62629	I	1258.70021	629.85374	12
5	559.27225	280.13976	D	1145.61614	573.31171	11
6	688.31485	344.66106	E	1030.58919	515.79823	10
7	801.39892	401.20310	I	901.54659	451.27693	9
8	900.46734	450.73731	V	788.46252	394.73490	8
9	1013.55141	507.27934	L	689.39410	345.20069	7
10	1112.61983	556.81355	V	576.31003	288.65865	6
11	1169.64130	585.32429	G	477.24161	239.12444	5
12	1226.66277	613.83502	G	420.22014	210.61371	4
13	1313.69480	657.35104	S	363.19867	182.10297	3
14	1414.74248	707.87488	T	276.16664	138.58696	2
15			R	175.11896	88.06312	1

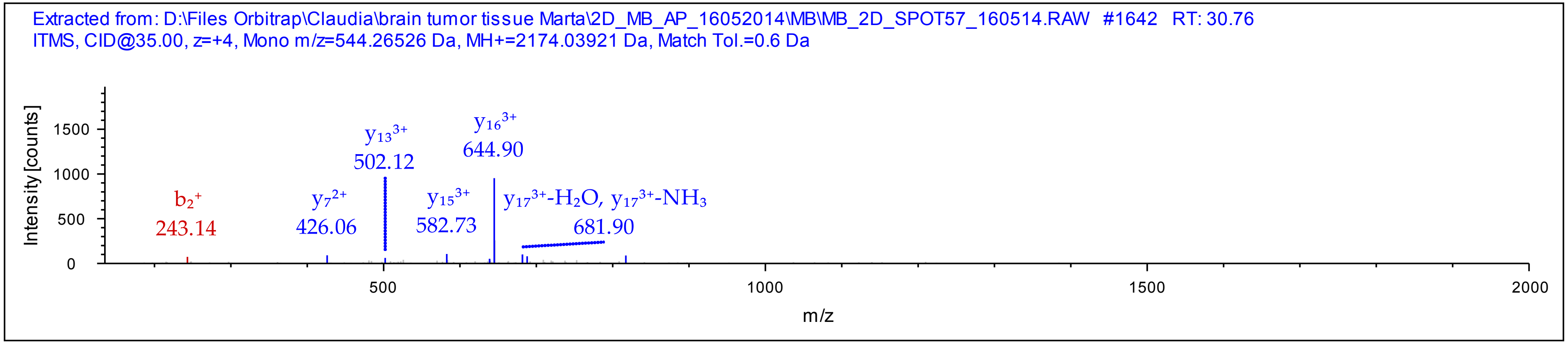


Sequence: IEWLESHQDADIEDFKAK, Charge: +4, Monoisotopic m/z: 544.26526 Da (-0.23 mmu/-0.43 ppm), MH+: 2174.03921 Da, RT: 30.76 min,
Identified with: Sequest HT (v1.3); XCorr:3.03, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

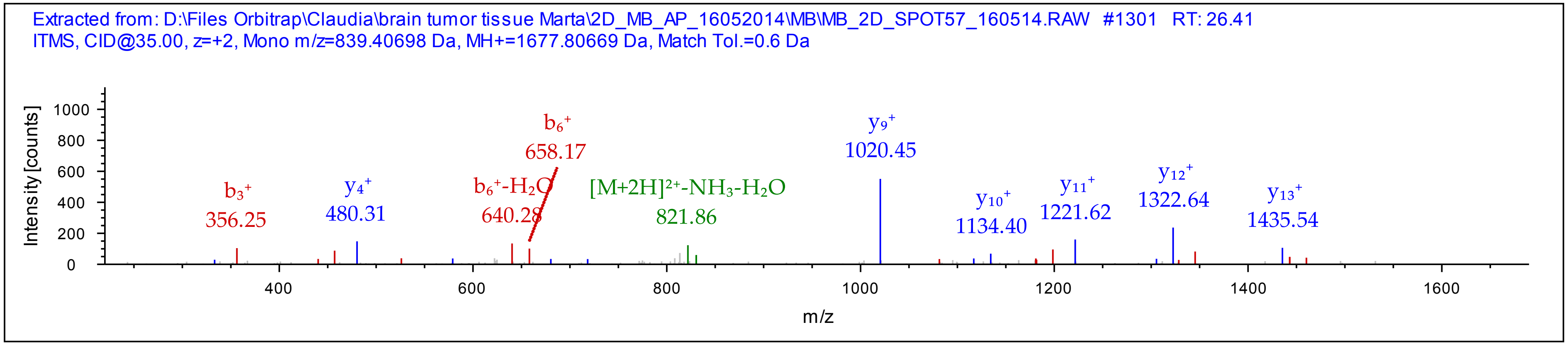
#1	**b^+**	**b^{2+}**	**b^{3+}**	**b^{4+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**y^{4+}**	**#2**
1	114.09135	57.54931	38.70197	29.27829	I					18
2	243.13395	122.07061	81.71617	61.53894	E	2060.95607	1030.98167	687.65687	515.99448	17
3	429.21327	215.11027	143.74261	108.05877	W	1931.91347	966.46037	644.64267	483.73383	16
4	542.29734	271.65231	181.43730	136.32979	L	1745.83415	873.42071	582.61623	437.21400	15
5	671.33994	336.17361	224.45150	168.59044	E	1632.75008	816.87868	544.92154	408.94298	14
6	758.37197	379.68962	253.46217	190.34845	S	1503.70748	752.35738	501.90734	376.68233	13
7	895.43088	448.21908	299.14848	224.61318	H	1416.67545	708.84136	472.89667	354.92432	12
8	1023.48946	512.24837	341.83467	256.62782	Q	1279.61654	640.31191	427.21036	320.65959	11
9	1138.51641	569.76184	380.17699	285.38456	D	1151.55796	576.28262	384.52417	288.64495	10
10	1209.55353	605.28040	403.85603	303.14384	A	1036.53101	518.76914	346.18185	259.88821	9
11	1324.58048	662.79388	442.19834	331.90058	D	965.49389	483.25058	322.50281	242.12893	8
12	1437.66455	719.33591	479.89303	360.17159	I	850.46694	425.73711	284.16050	213.37219	7
13	1566.70715	783.85721	522.90723	392.43224	E	737.38287	369.19507	246.46581	185.10118	6
14	1681.73410	841.37069	561.24955	421.18898	D	608.34027	304.67377	203.45161	152.84053	5
15	1828.80252	914.90490	610.27236	457.95609	F	493.31332	247.16030	165.10929	124.08379	4
16	1956.89749	978.95238	652.97068	489.97983	K	346.24490	173.62609	116.08648	87.31668	3
17	2027.93461	1014.47094	676.64972	507.73911	A	218.14993	109.57860	73.38816	55.29294	2
18					K	147.11281	74.06004	49.70912	37.53366	1



Sequence: NQLTSNPENTVFDAK, Charge: +2, Monoisotopic m/z: 839.40698 Da (-0.62 mmu/-0.73 ppm), MH+: 1677.80669 Da, RT: 26.41 min,
Identified with: Sequest HT (v1.3); XCorr:2.99, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

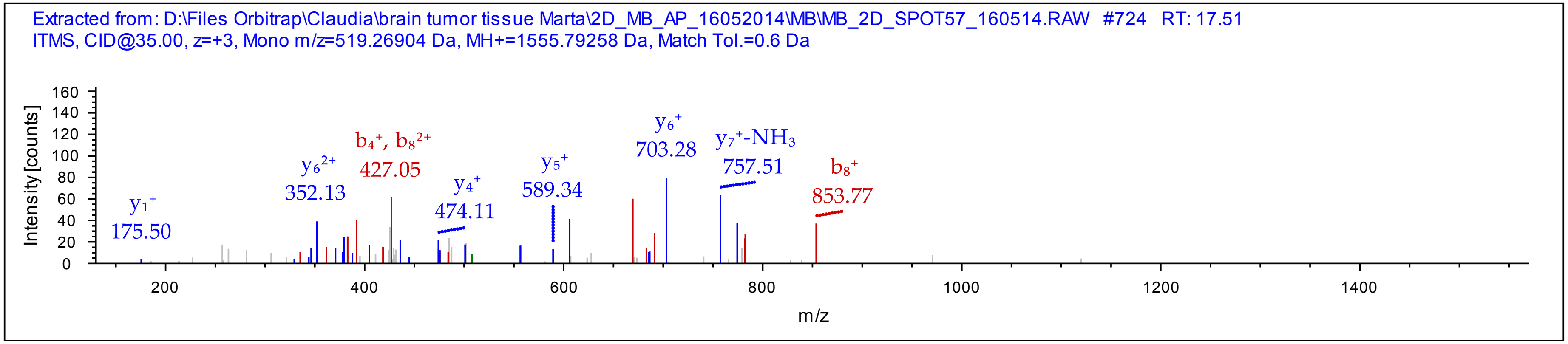
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	115.05021	58.02874	N			15
2	243.10879	122.05803	Q	1563.76499	782.38613	14
3	356.19286	178.60007	L	1435.70641	718.35684	13
4	457.24054	229.12391	T	1322.62234	661.81481	12
5	544.27257	272.63992	S	1221.57466	611.29097	11
6	658.31550	329.66139	N	1134.54263	567.77495	10
7	755.36827	378.18777	P	1020.49970	510.75349	9
8	884.41087	442.70907	E	923.44693	462.22710	8
9	998.45380	499.73054	N	794.40433	397.70580	7
10	1099.50148	550.25438	T	680.36140	340.68434	6
11	1198.56990	599.78859	V	579.31372	290.16050	5
12	1345.63832	673.32280	F	480.24530	240.62629	4
13	1460.66527	730.83627	D	333.17688	167.09208	3
14	1531.70239	766.35483	A	218.14993	109.57860	2
15			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT57_160514.RAW #1301 RT: 26.41
ITMS, CID@35.00, z=+2, Mono m/z=839.40698 Da, MH+=1677.80669 Da, Match Tol.=0.6 Da

Sequence: NGRVEIIANDQGNR, Charge: +3, Monoisotopic m/z: 519.26904 Da (-0.35 mmu/-0.67 ppm), MH+: 1555.79258 Da, RT: 17.51 min,
Identified with: Sequest HT (v1.3); XCorr:2.91, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):

- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	115.05021	58.02874	39.02159	N				14
2	172.07168	86.53948	58.02874	G	1441.75069	721.37898	481.25508	13
3	328.17280	164.59004	110.06245	R	1384.72922	692.86825	462.24792	12
4	427.24122	214.12425	143.08526	V	1228.62810	614.81769	410.21422	11
5	556.28382	278.64555	186.09946	E	1129.55968	565.28348	377.19141	10
6	669.36789	335.18758	223.79415	I	1000.51708	500.76218	334.17721	9
7	782.45196	391.72962	261.48884	I	887.43301	444.22014	296.48252	8
8	853.48908	427.24818	285.16788	A	774.34894	387.67811	258.78783	7
9	967.53201	484.26964	323.18219	N	703.31182	352.15955	235.10879	6
10	1082.55896	541.78312	361.52450	D	589.26889	295.13808	197.09448	5
11	1210.61754	605.81241	404.21070	Q	474.24194	237.62461	158.75216	4
12	1267.63901	634.32314	423.21785	G	346.18336	173.59532	116.06597	3
13	1381.68194	691.34461	461.23216	N	289.16189	145.08458	97.05881	2
14				R	175.11896	88.06312	59.04450	1

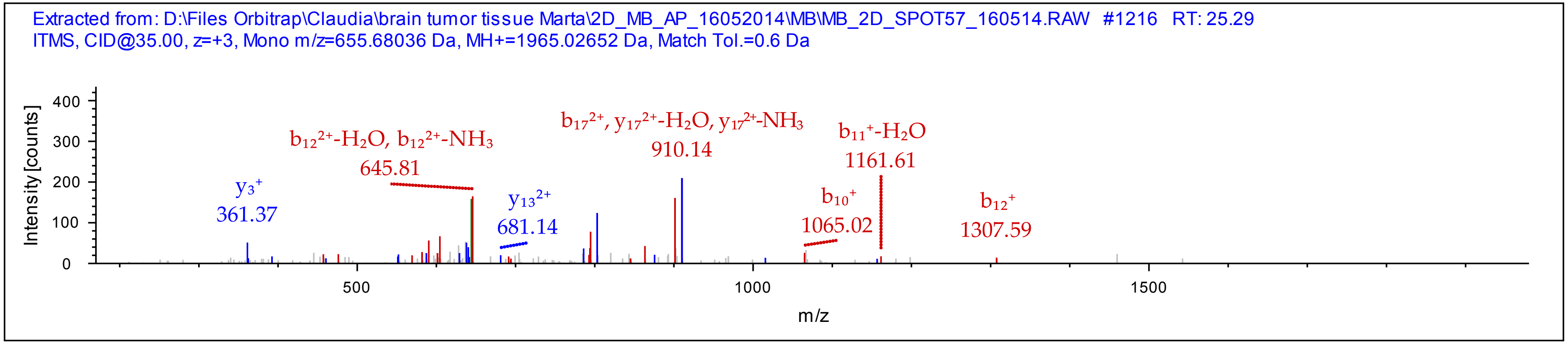


Sequence: KSQIFSTASDNQPTVTIK, Charge: +3, Monoisotopic m/z: 655.68036 Da (-0.77 mmu/-1.17 ppm), MH+: 1965.02652 Da, RT: 25.29 min,
Identified with: Sequest HT (v1.3); XCorr:2.87, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

#1	b^{+}	b^{2+}	b^{3+}	Seq.	y^{+}	y^{2+}	y^{3+}	#2
1	129.10225	65.05476	43.70560	K				18
2	216.13428	108.57078	72.71628	S	1836.93385	918.97056	612.98280	17
3	344.19286	172.60007	115.40247	Q	1749.90182	875.45455	583.97212	16
4	457.27693	229.14210	153.09716	I	1621.84324	811.42526	541.28593	15
5	604.34535	302.67631	202.11997	F	1508.75917	754.88322	503.59124	14
6	691.37738	346.19233	231.13064	S	1361.69075	681.34901	454.56843	13
7	792.42506	396.71617	264.81320	T	1274.65872	637.83300	425.55776	12
8	863.46218	432.23473	288.49224	A	1173.61104	587.30916	391.87520	11
9	950.49421	475.75074	317.50292	S	1102.57392	551.79060	368.19616	10
10	1065.52116	533.26422	355.84524	D	1015.54189	508.27458	339.18548	9
11	1179.56409	590.28568	393.85955	N	900.51494	450.76111	300.84316	8
12	1307.62267	654.31497	436.54574	Q	786.47201	393.73964	262.82885	7
13	1404.67544	702.84136	468.89666	P	658.41343	329.71035	220.14266	6
14	1505.72312	753.36520	502.57922	T	561.36066	281.18397	187.79174	5
15	1604.79154	802.89941	535.60203	V	460.31298	230.66013	154.10918	4
16	1705.83922	853.42325	569.28459	T	361.24456	181.12592	121.08637	3
17	1818.92329	909.96528	606.97928	I	260.19688	130.60208	87.40381	2
18				K	147.11281	74.06004	49.70912	1

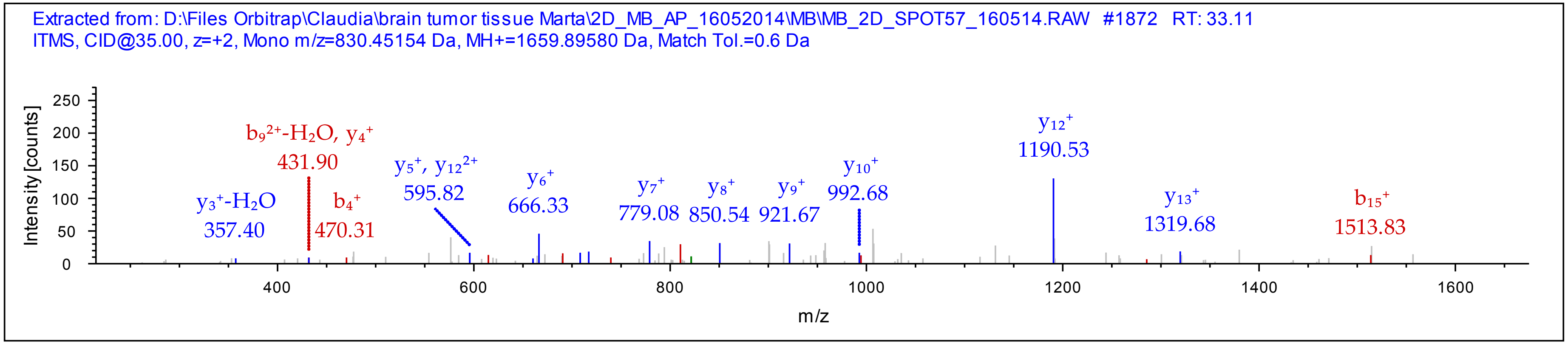

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT57_160514.RAW #1216 RT: 25.29
ITMS, CID@35.00, z=+3, Mono m/z=655.68036 Da, MH+=1965.02652 Da, Match Tol.=0.6 Da

Sequence: IINEPTAAAIAYGLDK, Charge: +2, Monoisotopic m/z: 830.45154 Da (+0.25 mmu/+0.31 ppm), MH+: 1659.89580 Da, RT: 33.11 min,
Identified with: Sequest HT (v1.3); XCorr:2.66, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):
- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]
- Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2 - [HS71L_HUMAN]
- Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1 - [HSP72_HUMAN]
- Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	I			16
2	227.17542	114.09135	I	1546.81122	773.90925	15
3	341.21835	171.11281	N	1433.72715	717.36721	14
4	470.26095	235.63411	E	1319.68422	660.34575	13
5	567.31372	284.16050	P	1190.64162	595.82445	12
6	668.36140	334.68434	T	1093.58885	547.29806	11
7	739.39852	370.20290	A	992.54117	496.77422	10
8	810.43564	405.72146	A	921.50405	461.25566	9
9	881.47276	441.24002	A	850.46693	425.73710	8
10	994.55683	497.78205	I	779.42981	390.21854	7
11	1065.59395	533.30061	A	666.34574	333.67651	6
12	1228.65727	614.83227	Y	595.30862	298.15795	5
13	1285.67874	643.34301	G	432.24530	216.62629	4
14	1398.76281	699.88504	L	375.22383	188.11555	3
15	1513.78976	757.39852	D	262.13976	131.57352	2

16			K	147.11281	74.06004	1

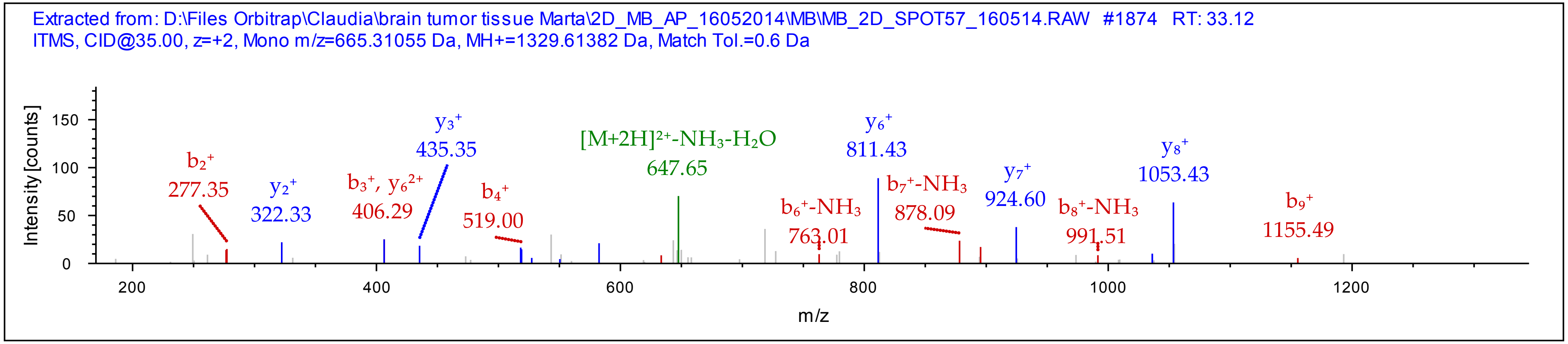


Sequence: FEELNMDLFR, M6-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 665.31055 Da (-0.31 mmu/-0.47 ppm), MH+: 1329.61382 Da, RT: 33.12 min,
Identified with: Sequest HT (v1.3); XCorr:2.62, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	148.07570	74.54149	F			10
2	277.11830	139.06279	E	1182.54602	591.77665	9
3	406.16090	203.58409	E	1053.50342	527.25535	8
4	519.24497	260.12612	L	924.46082	462.73405	7
5	633.28790	317.14759	N	811.37675	406.19201	6
6	780.32331	390.66529	M-Oxidation	697.33382	349.17055	5
7	895.35026	448.17877	D	550.29840	275.65284	4
8	1008.43433	504.72080	L	435.27145	218.13936	3
9	1155.50275	578.25501	F	322.18738	161.59733	2
10			R	175.11896	88.06312	1

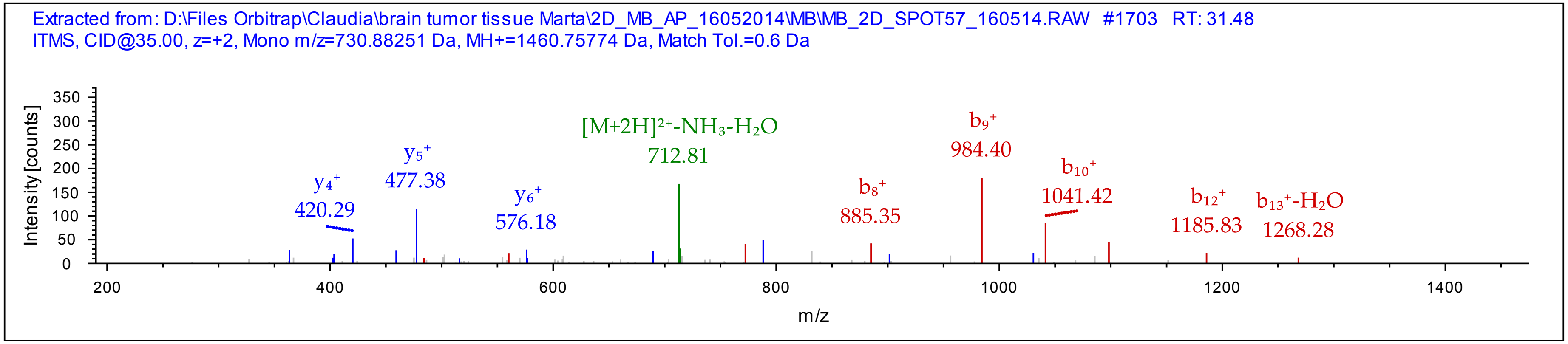


Sequence: SDIDEIVLVGGSTR, Charge: +2, Monoisotopic m/z: 730.88251 Da (-0.73 mmu/-0.99 ppm), MH+: 1460.75774 Da, RT: 31.48 min,
Identified with: Sequest HT (v1.3); XCorr:2.45, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):

- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	88.03931	44.52329	S			14
2	203.06626	102.03677	D	1373.72716	687.36722	13
3	316.15033	158.57880	I	1258.70021	629.85374	12
4	431.17728	216.09228	D	1145.61614	573.31171	11
5	560.21988	280.61358	E	1030.58919	515.79823	10
6	673.30395	337.15561	I	901.54659	451.27693	9
7	772.37237	386.68982	V	788.46252	394.73490	8
8	885.45644	443.23186	L	689.39410	345.20069	7
9	984.52486	492.76607	V	576.31003	288.65865	6
10	1041.54633	521.27680	G	477.24161	239.12444	5
11	1098.56780	549.78754	G	420.22014	210.61371	4
12	1185.59983	593.30355	S	363.19867	182.10297	3
13	1286.64751	643.82739	T	276.16664	138.58696	2
14			R	175.11896	88.06312	1

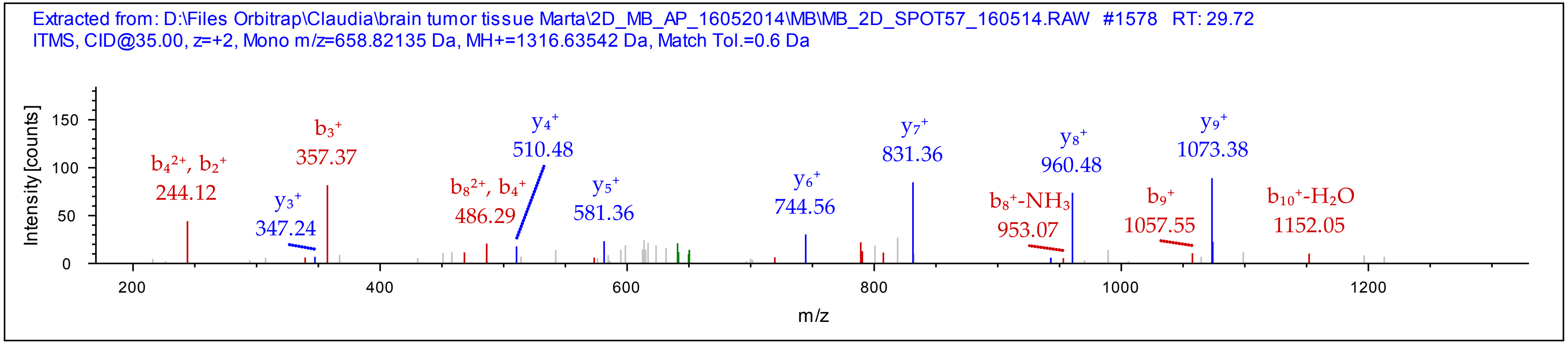

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT57_160514.RAW #1703 RT: 31.48
ITMS, CID@35.00, z=+2, Mono m/z=730.88251 Da, MH+=1460.75774 Da, Match Tol.=0.6 Da

Sequence: NELESYAYSLK, Charge: +2, Monoisotopic m/z: 658.82135 Da (-0.74 mmu/-1.12 ppm), MH+: 1316.63542 Da, RT: 29.72 min,
Identified with: Sequest HT (v1.3); XCorr:2.42, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	115.05021	58.02874	N			11
2	244.09281	122.55004	E	1202.59397	601.80062	10
3	357.17688	179.09208	L	1073.55137	537.27932	9
4	486.21948	243.61338	E	960.46730	480.73729	8
5	573.25151	287.12939	S	831.42470	416.21599	7
6	736.31483	368.66105	Y	744.39267	372.69997	6
7	807.35195	404.17961	A	581.32935	291.16831	5
8	970.41527	485.71127	Y	510.29223	255.64975	4
9	1057.44730	529.22729	S	347.22891	174.11809	3
10	1170.53137	585.76932	L	260.19688	130.60208	2
11			K	147.11281	74.06004	1

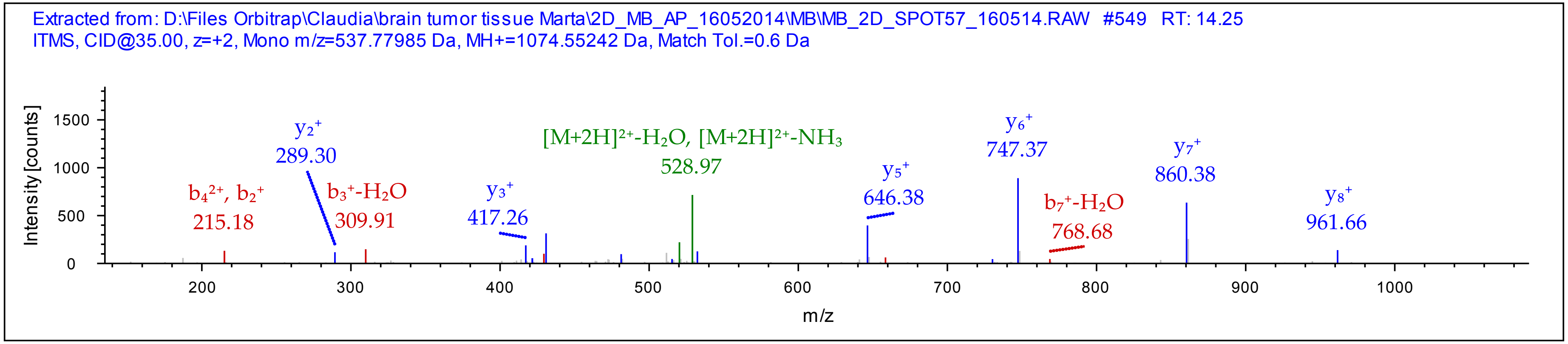


Sequence: ITITNDQNR, Charge: +2, Monoisotopic m/z: 537.77985 Da (-0.72 mmu/-1.34 ppm), MH+: 1074.55242 Da, RT: 14.25 min,
Identified with: Sequest HT (v1.3); XCorr:2.42, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	114.09135	57.54931	I			9
2	215.13903	108.07315	T	961.46978	481.23853	8
3	328.22310	164.61519	I	860.42210	430.71469	7
4	429.27078	215.13903	T	747.33803	374.17265	6
5	543.31371	272.16049	N	646.29035	323.64881	5
6	658.34066	329.67397	D	532.24742	266.62735	4
7	786.39924	393.70326	Q	417.22047	209.11387	3
8	900.44217	450.72472	N	289.16189	145.08458	2
9			R	175.11896	88.06312	1



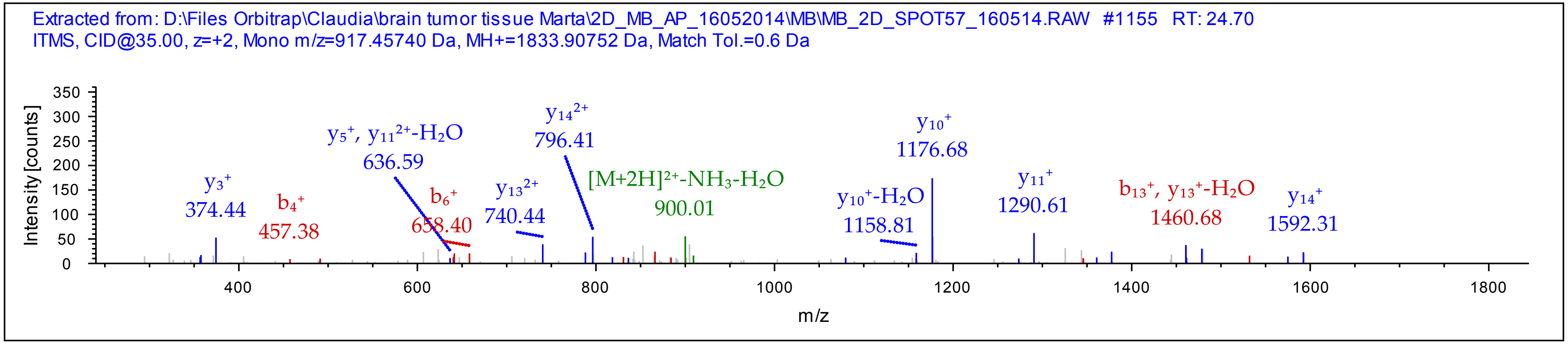
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT57_160514.RAW #549 RT: 14.25
ITMS, CID@35.00, z=+2, Mono m/z=537.77985 Da, MH+=1074.55242 Da, Match Tol.=0.6 Da

Sequence: NQLTSNPENTVFDAKR, Charge: +2, Monoisotopic m/z: 917.45740 Da (-0.76 mmu/-0.83 ppm), MH+: 1833.90752 Da, RT: 24.70 min,
Identified with: Sequest HT (v1.3); XCorr:2.40, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	115.05021	58.02874	N			16
2	243.10879	122.05803	Q	1719.86611	860.43669	15
3	356.19286	178.60007	L	1591.80753	796.40740	14
4	457.24054	229.12391	T	1478.72346	739.86537	13
5	544.27257	272.63992	S	1377.67578	689.34153	12
6	658.31550	329.66139	N	1290.64375	645.82551	11
7	755.36827	378.18777	P	1176.60082	588.80405	10
8	884.41087	442.70907	E	1079.54805	540.27766	9
9	998.45380	499.73054	N	950.50545	475.75636	8
10	1099.50148	550.25438	T	836.46252	418.73490	7
11	1198.56990	599.78859	V	735.41484	368.21106	6
12	1345.63832	673.32280	F	636.34642	318.67685	5
13	1460.66527	730.83627	D	489.27800	245.14264	4
14	1531.70239	766.35483	A	374.25105	187.62916	3
15	1659.79736	830.40232	K	303.21393	152.11060	2
16			R	175.11896	88.06312	1



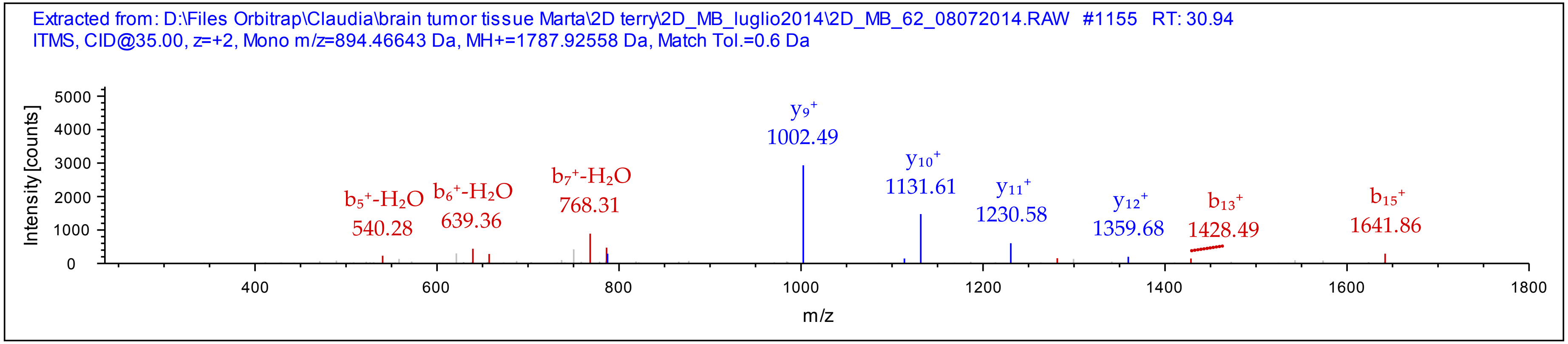
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT57_160514.RAW #1155 RT: 24.70
ITMS, CID@35.00, z=+2, Mono m/z=917.45740 Da, MH+=1833.90752 Da, Match Tol.=0.6 Da

Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
62	P0CG48	Ubiquitin	8.6	6.6	36.4	64.38%	5	5	MB	NS	2.1	↑ in MB

Sequence: TITLEVEPSDTIENVK, Charge: +2, Monoisotopic m/z: 894.46643 Da (-0.9 mmu/-1 ppm), MH+: 1787.92558 Da, RT: 30.94 min,
Identified with: Sequest HT (v1.3); XCorr:3.64, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):
- Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2 - [RL40_HUMAN]
- Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 - [RS27A_HUMAN]
- Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1 - [UBB_HUMAN]
- Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=3 - [UBC_HUMAN]

#1	**b^{+}**	**b^{2+}**	**Seq.**	**y^{+}**	**y^{2+}**	**#2**
1	102.05496	51.53112	T			16
2	215.13903	108.07315	I	1686.87970	843.94349	15
3	316.18671	158.59699	T	1573.79563	787.40145	14
4	429.27078	215.13903	L	1472.74795	736.87761	13
5	558.31338	279.66033	E	1359.66388	680.33558	12
6	657.38180	329.19454	V	1230.62128	615.81428	11
7	786.42440	393.71584	E	1131.55286	566.28007	10
8	883.47717	442.24222	P	1002.51026	501.75877	9
9	970.50920	485.75824	S	905.45749	453.23238	8
10	1085.53615	543.27171	D	818.42546	409.71637	7
11	1186.58383	593.79555	T	703.39851	352.20289	6
12	1299.66790	650.33759	I	602.35083	301.67905	5
13	1428.71050	714.85889	E	489.26676	245.13702	4
14	1542.75343	771.88035	N	360.22416	180.61572	3
15	1641.82185	821.41456	V	246.18123	123.59425	2
16			K	147.11281	74.06004	1

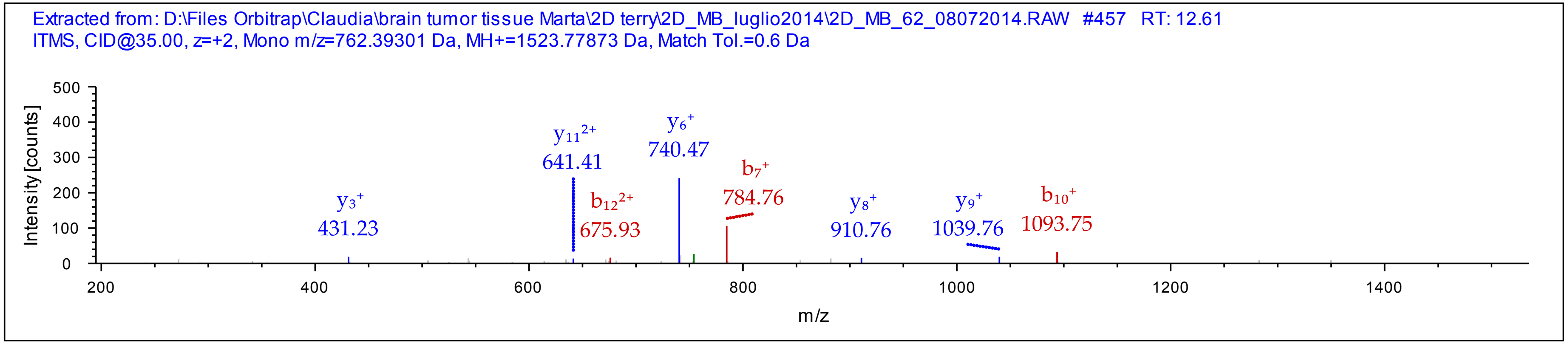


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_MB_luglio2014\2D_MB_62_08072014.RAW #1155 RT: 30.94
ITMS, CID@35.00, z=+2, Mono m/z=894.46643 Da, MH+=1787.92558 Da, Match Tol.=0.6 Da

Sequence: IQDKEGIPPDQQR, Charge: +2, Monoisotopic m/z: 762.39301 Da (-1.29 mmu/-1.7 ppm), MH+: 1523.77873 Da, RT: 12.61 min,
Identified with: Sequest HT (v1.3); XCorr:2.18, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):
- Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2 - [RL40_HUMAN]
- Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 - [RS27A_HUMAN]
- Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1 - [UBB_HUMAN]
- Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=3 - [UBC_HUMAN]

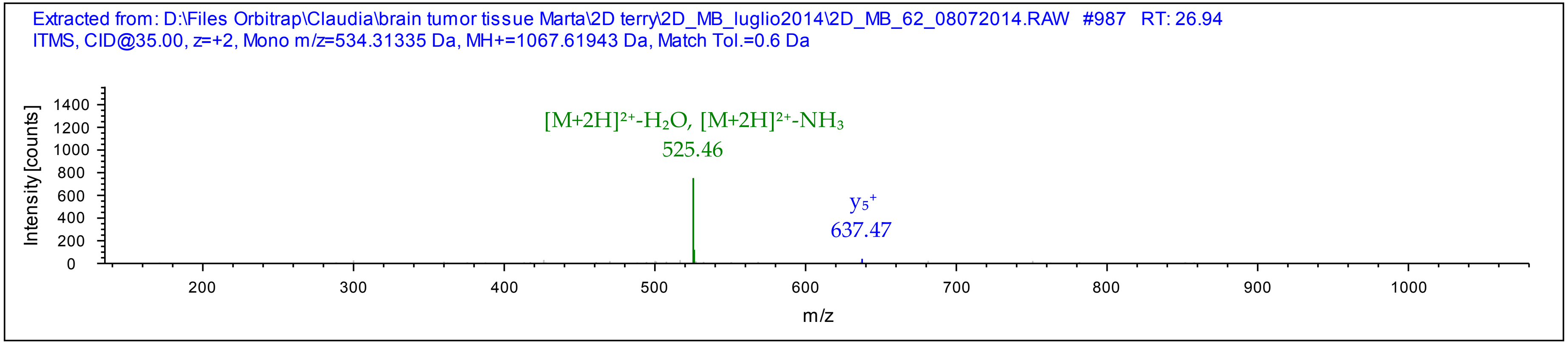
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	114.09135	57.54931	I			13
2	242.14993	121.57860	Q	1410.69725	705.85226	12
3	357.17688	179.09208	D	1282.63867	641.82297	11
4	485.27185	243.13956	K	1167.61172	584.30950	10
5	614.31445	307.66086	E	1039.51675	520.26201	9
6	671.33592	336.17160	G	910.47415	455.74071	8
7	784.41999	392.71363	I	853.45268	427.22998	7
8	881.47276	441.24002	P	740.36861	370.68794	6
9	978.52553	489.76640	P	643.31584	322.16156	5
10	1093.55248	547.27988	D	546.26307	273.63517	4
11	1221.61106	611.30917	Q	431.23612	216.12170	3
12	1349.66964	675.33846	Q	303.17754	152.09241	2
13			R	175.11896	88.06312	1



Sequence: ESTLHLVLR, Charge: +2, Monoisotopic m/z: 534.31335 Da (-0.69 mmu/-1.29 ppm), MH+: 1067.61943 Da, RT: 26.94 min,
Identified with: Sequest HT (v1.3); XCorr:1.83, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (4):
- Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2 - [RL40_HUMAN]
- Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 - [RS27A_HUMAN]
- Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1 - [UBB_HUMAN]
- Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=3 - [UBC_HUMAN]

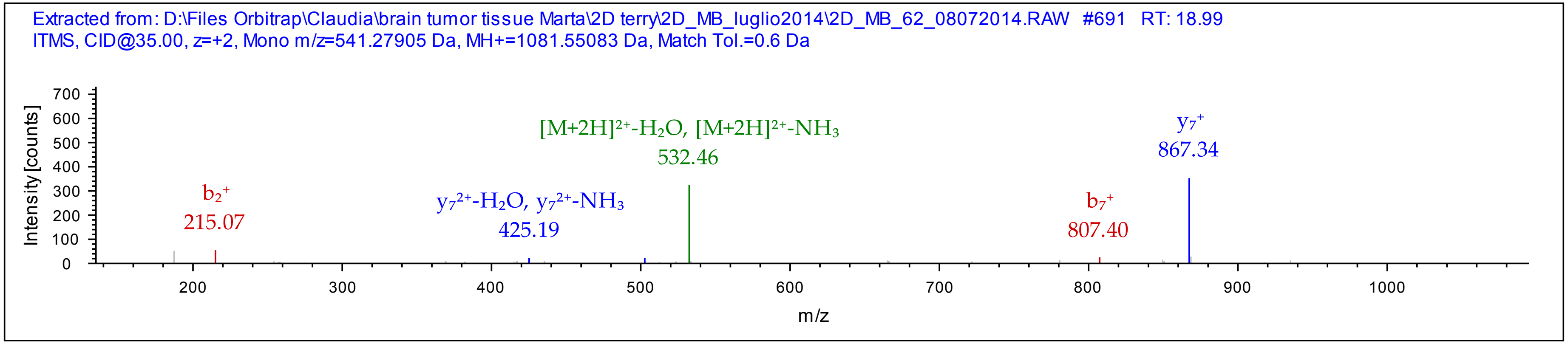
#1	**b$^+$**	**b^{2+}**	**Seq.**	**y$^+$**	**y^{2+}**	**#2**
1	130.04988	65.52858	E			9
2	217.08191	109.04459	S	938.57821	469.79274	8
3	318.12959	159.56843	T	851.54618	426.27673	7
4	431.21366	216.11047	L	750.49850	375.75289	6
5	568.27257	284.63992	H	637.41443	319.21085	5
6	681.35664	341.18196	L	500.35552	250.68140	4
7	780.42506	390.71617	V	387.27145	194.13936	3
8	893.50913	447.25820	L	288.20303	144.60515	2
9			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_MB_luglio2014\2D_MB_62_08072014.RAW #987 RT: 26.94
ITMS, CID@35.00, z=+2, Mono m/z=534.31335 Da, MH+=1067.61943 Da, Match Tol.=0.6 Da

Sequence: TLSDYNIQK, Charge: +2, Monoisotopic m/z: 541.27905 Da (-0.81 mmu/-1.49 ppm), MH+: 1081.55083 Da, RT: 18.99 min,
Identified with: Sequest HT (v1.3); XCorr:1.71, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):
- Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2 - [RL40_HUMAN]
- Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 - [RS27A_HUMAN]
- Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1 - [UBB_HUMAN]
- Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=3 - [UBC_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	102.05496	51.53112	T			9
2	215.13903	108.07315	L	980.50476	490.75602	8
3	302.17106	151.58917	S	867.42069	434.21398	7
4	417.19801	209.10264	D	780.38866	390.69797	6
5	580.26133	290.63430	Y	665.36171	333.18449	5
6	694.30426	347.65577	N	502.29839	251.65283	4
7	807.38833	404.19780	I	388.25546	194.63137	3
8	935.44691	468.22709	Q	275.17139	138.08933	2
9			K	147.11281	74.06004	1

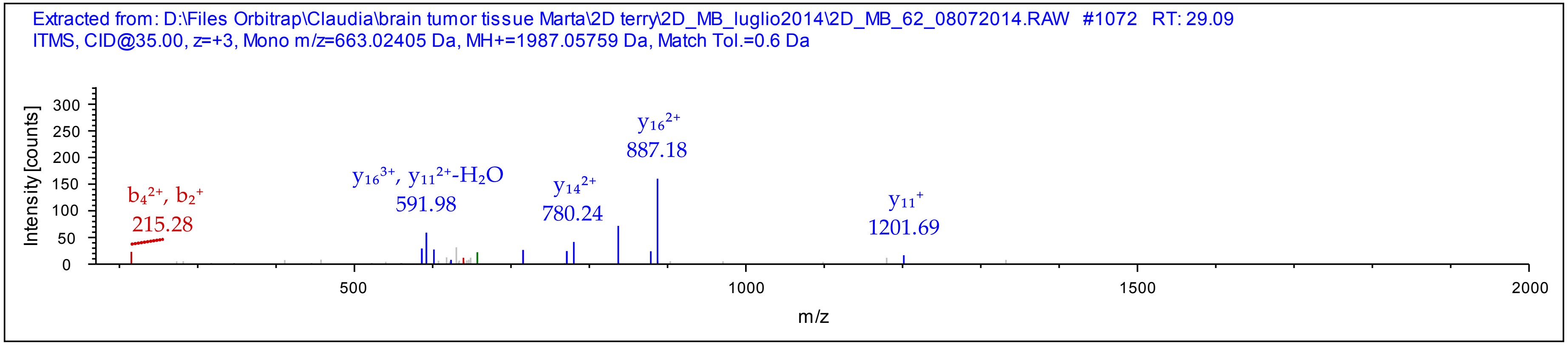


Sequence: TITLEVEPSDTIENVKAK, Charge: +3, Monoisotopic m/z: 663.02405 Da (-0.63 mmu/-0.95 ppm), MH+: 1987.05759 Da, RT: 29.09 min,
Identified with: Sequest HT (v1.3); XCorr:1.29, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):
- Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2 - [RL40_HUMAN]
- Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 - [RS27A_HUMAN]
- Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1 - [UBB_HUMAN]
- Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=3 - [UBC_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	102.05496	51.53112	34.68984	T				18
2	215.13903	108.07315	72.38453	I	1886.01179	943.50953	629.34211	17
3	316.18671	158.59699	106.06709	T	1772.92772	886.96750	591.64742	16
4	429.27078	215.13903	143.76178	L	1671.88004	836.44366	557.96486	15
5	558.31338	279.66033	186.77598	E	1558.79597	779.90162	520.27017	14
6	657.38180	329.19454	219.79878	V	1429.75337	715.38032	477.25597	13
7	786.42440	393.71584	262.81298	E	1330.68495	665.84611	444.23317	12
8	883.47717	442.24222	295.16391	P	1201.64235	601.32481	401.21897	11
9	970.50920	485.75824	324.17458	S	1104.58958	552.79843	368.86804	10
10	1085.53615	543.27171	362.51690	D	1017.55755	509.28241	339.85737	9
11	1186.58383	593.79555	396.19946	T	902.53060	451.76894	301.51505	8
12	1299.66790	650.33759	433.89415	I	801.48292	401.24510	267.83249	7
13	1428.71050	714.85889	476.90835	E	688.39885	344.70306	230.13780	6
14	1542.75343	771.88035	514.92266	N	559.35625	280.18176	187.12360	5
15	1641.82185	821.41456	547.94547	V	445.31332	223.16030	149.10929	4

16	1769.91682	885.46205	590.64379	K	346.24490	173.62609	116.08648	3
17	1840.95394	920.98061	614.32283	A	218.14993	109.57860	73.38816	2
18				K	147.11281	74.06004	49.70912	1



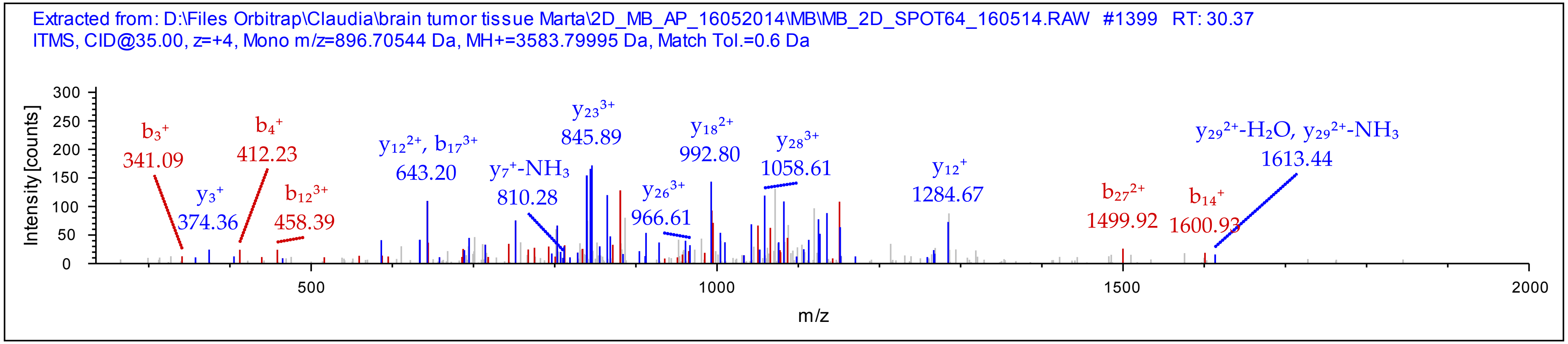
Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
64	Q06830	Peroxiredoxin-1	21.9	8.3	122.50	57.79%	11	11	MB	2.00E-03	3.8	↑ in MB

Sequence: LVQAFQFTDKHGEVCPAGWKPGSDTIKPDVQK, C15-Carbamidomethyl (57.02146 Da)
Charge: +4, Monoisotopic m/z: 896.70544 Da (-0.11 mmu/-0.12 ppm), MH+: 3583.79995 Da, RT: 30.37 min,
Identified with: Sequest HT (v1.3); XCorr:4.06, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]

#1	b^+	b^{2+}	b^{3+}	b^{4+}	Seq.	y^+	y^{2+}	y^{3+}	y^{4+}	#2
1	114.09135	57.54931	38.70197	29.27829	L					32
2	213.15977	107.08352	71.72477	54.04540	V	3470.71632	1735.86180	1157.57696	868.43454	31
3	341.21835	171.11281	114.41097	86.06004	Q	3371.64790	1686.32759	1124.55415	843.66743	30
4	412.25547	206.63137	138.09001	103.81932	A	3243.58932	1622.29830	1081.86796	811.65279	29
5	559.32389	280.16558	187.11281	140.58643	F	3172.55220	1586.77974	1058.18892	793.89351	28
6	687.38247	344.19487	229.79901	172.60107	Q	3025.48378	1513.24553	1009.16611	757.12640	27
7	834.45089	417.72908	278.82181	209.36818	F	2897.42520	1449.21624	966.47992	725.11176	26
8	935.49857	468.25292	312.50437	234.63010	T	2750.35678	1375.68203	917.45711	688.34465	25
9	1050.52552	525.76640	350.84669	263.38684	D	2649.30910	1325.15819	883.77455	663.08273	24
10	1178.62049	589.81388	393.54501	295.41058	K	2534.28215	1267.64471	845.43223	634.32599	23
11	1315.67940	658.34334	439.23132	329.67531	H	2406.18718	1203.59723	802.73391	602.30225	22
12	1372.70087	686.85407	458.23847	343.93067	G	2269.12827	1135.06777	757.04761	568.03752	21
13	1501.74347	751.37537	501.25267	376.19132	E	2212.10680	1106.55704	738.04045	553.78216	20
14	1600.81189	800.90958	534.27548	400.95843	V	2083.06420	1042.03574	695.02625	521.52151	19
15	1760.84254	880.92491	587.61903	440.96609	C-Carbamidomethyl	1983.99578	992.50153	662.00344	496.75440	18
16	1857.89531	929.45129	619.96995	465.22929	P	1823.96512	912.48620	608.65989	456.74674	17
17	1928.93243	964.96985	643.64899	482.98857	A	1726.91235	863.95981	576.30897	432.48355	16
18	1985.95390	993.48059	662.65615	497.24393	G	1655.87523	828.44125	552.62993	414.72427	15
19	2172.03322	1086.52025	724.68259	543.76376	W	1598.85376	799.93052	533.62277	400.46890	14
20	2300.12819	1150.56773	767.38091	575.78751	K	1412.77444	706.89086	471.59633	353.94907	13
21	2397.18096	1199.09412	799.73184	600.05070	P	1284.67947	642.84337	428.89801	321.92533	12
22	2454.20243	1227.60485	818.73899	614.30607	G	1187.62670	594.31699	396.54708	297.66213	11
23	2541.23446	1271.12087	847.74967	636.06407	S	1130.60523	565.80625	377.53993	283.40677	10
24	2656.26141	1328.63434	886.09199	664.82081	D	1043.57320	522.29024	348.52925	261.64876	9

25	2757.30909	1379.15818	919.77455	690.08273	T	928.54625	464.77676	310.18693	232.89202	8
26	2870.39316	1435.70022	957.46924	718.35375	I	827.49857	414.25292	276.50437	207.63010	7
27	2998.48813	1499.74770	1000.16756	750.37749	K	714.41450	357.71089	238.80968	179.35908	6
28	3095.54090	1548.27409	1032.51848	774.64068	P	586.31953	293.66340	196.11136	147.33534	5
29	3210.56785	1605.78756	1070.86080	803.39742	D	489.26676	245.13702	163.76044	123.07215	4
30	3309.63627	1655.32177	1103.88361	828.16453	V	374.23981	187.62354	125.41812	94.31541	3
31	3437.69485	1719.35106	1146.56980	860.17917	Q	275.17139	138.08933	92.39531	69.54831	2
32					K	147.11281	74.06004	49.70912	37.53366	1

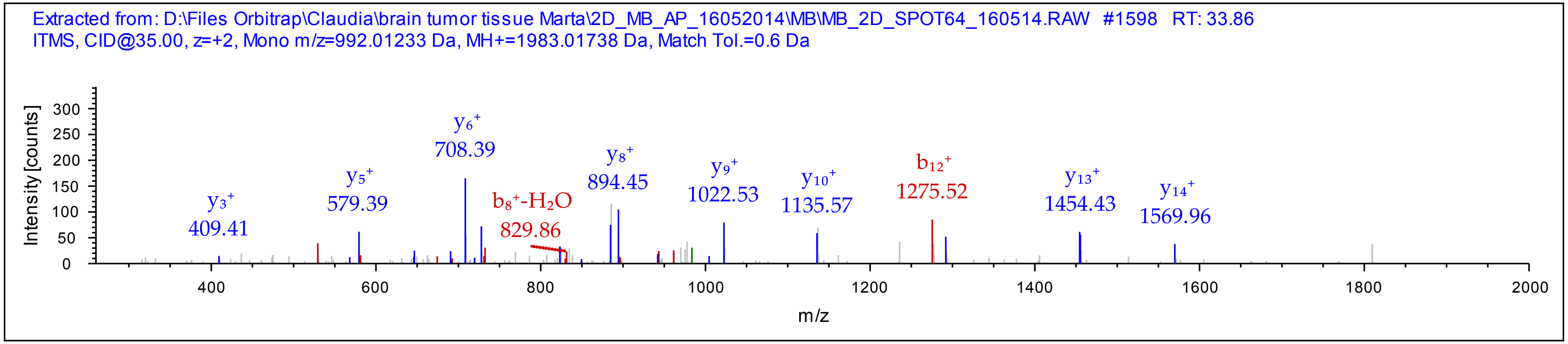


Sequence: TIAQDYGVLKADEGISFR, Charge: +2, Monoisotopic m/z: 992.01233 Da (-0.45 mmu/-0.45 ppm), MH+: 1983.01738 Da, RT: 33.86 min,
Identified with: Sequest HT (v1.3); XCorr:3.72, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]

#1	b+	b2+	Seq.	y+	y2+	#2
1	102.05496	51.53112	T			18
2	215.13903	108.07315	I	1881.97059	941.48893	17
3	286.17615	143.59171	A	1768.88652	884.94690	16
4	414.23473	207.62100	Q	1697.84940	849.42834	15
5	529.26168	265.13448	D	1569.79082	785.39905	14
6	692.32500	346.66614	Y	1454.76387	727.88557	13
7	749.34647	375.17687	G	1291.70055	646.35391	12
8	848.41489	424.71108	V	1234.67908	617.84318	11
9	961.49896	481.25312	L	1135.61066	568.30897	10
10	1089.59393	545.30060	K	1022.52659	511.76693	9

11	1160.63105	580.81916	A	894.43162	447.71945	8
12	1275.65800	638.33264	D	823.39450	412.20089	7
13	1404.70060	702.85394	E	708.36755	354.68741	6
14	1461.72207	731.36467	G	579.32495	290.16611	5
15	1574.80614	787.90671	I	522.30348	261.65538	4
16	1661.83817	831.42272	S	409.21941	205.11334	3
17	1808.90659	904.95693	F	322.18738	161.59733	2
18			R	175.11896	88.06312	1

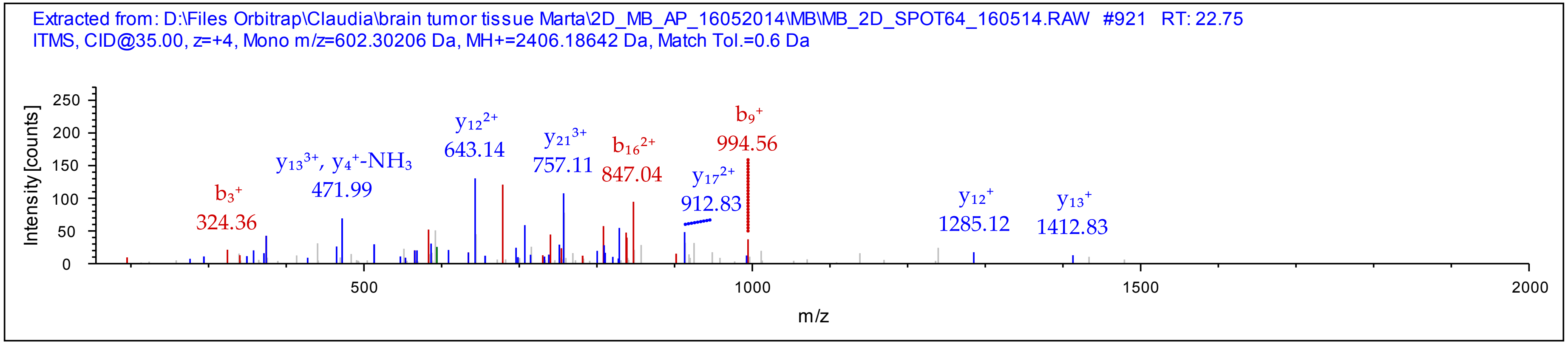


Sequence: HGEVCPAGWKPGSDTIKPDVQK, C5-Carbamidomethyl (57.02146 Da)
Charge: +4, Monoisotopic m/z: 602.30206 Da (-0.19 mmu/-0.31 ppm), MH+: 2406.18642 Da, RT: 22.75 min,
Identified with: Sequest HT (v1.3); XCorr:3.39, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]

#1	b^+	b^{2+}	b^{3+}	b^{4+}	Seq.	y^+	y^{2+}	y^{3+}	y^{4+}	#2
1	138.06619	69.53673	46.69358	35.27200	H					22
2	195.08766	98.04747	65.70074	49.52737	G	2269.12827	1135.06777	757.04761	568.03752	21
3	324.13026	162.56877	108.71494	81.78802	E	2212.10680	1106.55704	738.04045	553.78216	20
4	423.19868	212.10298	141.73774	106.55513	V	2083.06420	1042.03574	695.02625	521.52151	19
5	583.22933	292.11830	195.08129	146.56279	C-Carbamidomethyl	1983.99578	992.50153	662.00344	496.75440	18
6	680.28210	340.64469	227.43222	170.82598	P	1823.96512	912.48620	608.65989	456.74674	17
7	751.31922	376.16325	251.11126	188.58526	A	1726.91235	863.95981	576.30897	432.48355	16
8	808.34069	404.67398	270.11841	202.84063	G	1655.87523	828.44125	552.62993	414.72427	15
9	994.42001	497.71364	332.14485	249.36046	W	1598.85376	799.93052	533.62277	400.46890	14

10	1122.51498	561.76113	374.84318	281.38420	K	1412.77444	706.89086	471.59633	353.94907	13
11	1219.56775	610.28751	407.19410	305.64740	P	1284.67947	642.84337	428.89801	321.92533	12
12	1276.58922	638.79825	426.20126	319.90276	G	1187.62670	594.31699	396.54708	297.66213	11
13	1363.62125	682.31426	455.21193	341.66077	S	1130.60523	565.80625	377.53993	283.40677	10
14	1478.64820	739.82774	493.55425	370.41751	D	1043.57320	522.29024	348.52925	261.64876	9
15	1579.69588	790.35158	527.23681	395.67943	T	928.54625	464.77676	310.18693	232.89202	8
16	1692.77995	846.89361	564.93150	423.95045	I	827.49857	414.25292	276.50437	207.63010	7
17	1820.87492	910.94110	607.62982	455.97419	K	714.41450	357.71089	238.80968	179.35908	6
18	1917.92769	959.46748	639.98075	480.23738	P	586.31953	293.66340	196.11136	147.33534	5
19	2032.95464	1016.98096	678.32306	508.99412	D	489.26676	245.13702	163.76044	123.07215	4
20	2132.02306	1066.51517	711.34587	533.76122	V	374.23981	187.62354	125.41812	94.31541	3
21	2260.08164	1130.54446	754.03206	565.77587	Q	275.17139	138.08933	92.39531	69.54831	2
22					K	147.11281	74.06004	49.70912	37.53366	1

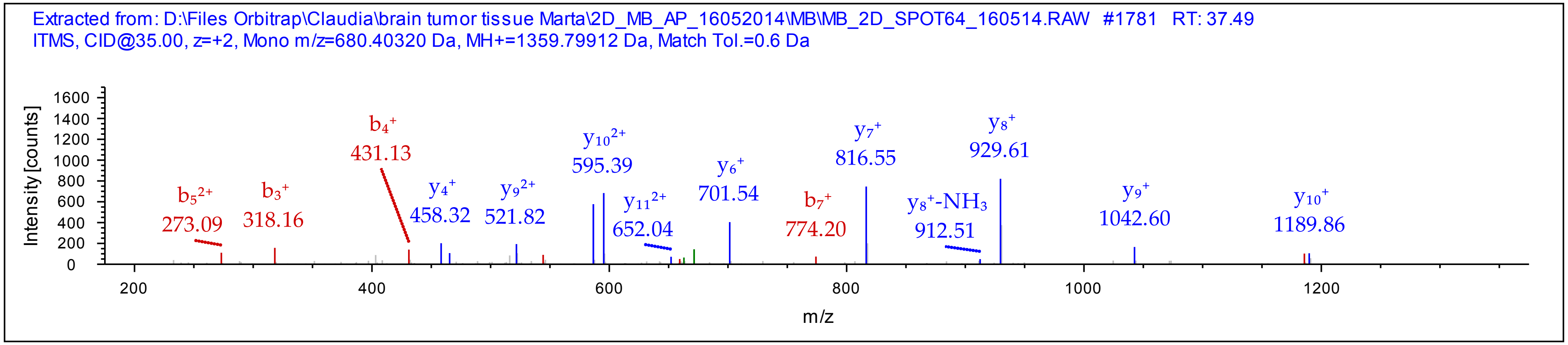

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT64_160514.RAW #921 RT: 22.75
ITMS, CID@35.00, z=+4, Mono m/z=602.30206 Da, MH+=2406.18642 Da, Match Tol.=0.6 Da

Sequence: GLFIIDDKGILR, Charge: +2, Monoisotopic m/z: 680.40320 Da (-0.21 mmu/-0.31 ppm), MH+: 1359.79912 Da, RT: 37.49 min,
Identified with: Sequest HT (v1.3); XCorr:2.73, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]
- Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 - [PRDX4_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	58.02875	29.51801	G			12

2	171.11282	86.06005	L	1302.77807	651.89267	11
3	318.18124	159.59426	F	1189.69400	595.35064	10
4	431.26531	216.13629	I	1042.62558	521.81643	9
5	544.34938	272.67833	I	929.54151	465.27439	8
6	659.37633	330.19180	D	816.45744	408.73236	7
7	774.40328	387.70528	D	701.43049	351.21888	6
8	902.49825	451.75276	K	586.40354	293.70541	5
9	959.51972	480.26350	G	458.30857	229.65792	4
10	1072.60379	536.80553	I	401.28710	201.14719	3
11	1185.68786	593.34757	L	288.20303	144.60515	2
12			R	175.11896	88.06312	1

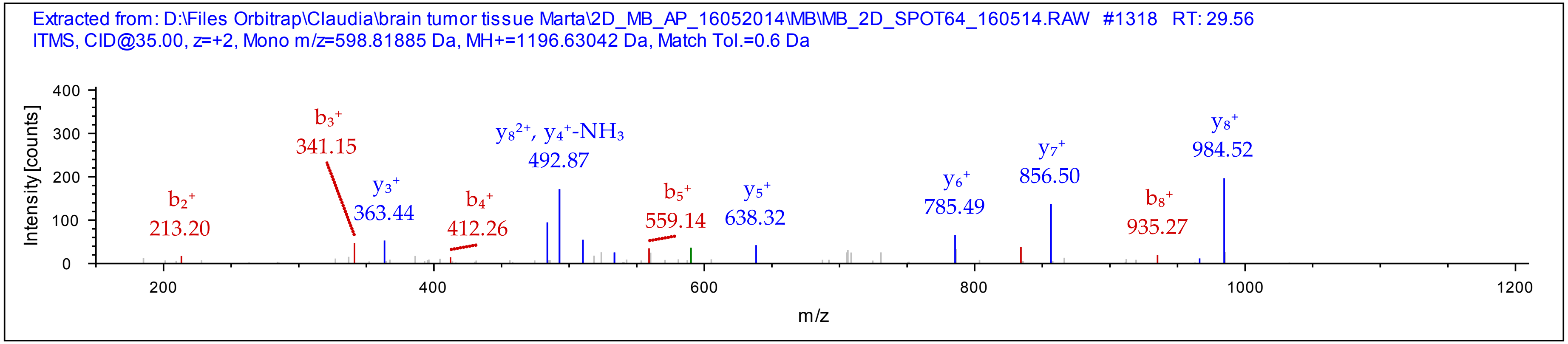

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT64_160514.RAW #1781 RT: 37.49
ITMS, CID@35.00, z=+2, Mono m/z=680.40320 Da, MH+=1359.79912 Da, Match Tol.=0.6 Da

Sequence: LVQAFQFTDK, Charge: +2, Monoisotopic m/z: 598.81885 Da (-0.32 mmu/-0.53 ppm), MH+: 1196.63042 Da, RT: 29.56 min,
Identified with: Sequest HT (v1.3); XCorr:2.47, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	114.09135	57.54931	L			10
2	213.15977	107.08352	V	1083.54698	542.27713	9
3	341.21835	171.11281	Q	984.47856	492.74292	8
4	412.25547	206.63137	A	856.41998	428.71363	7

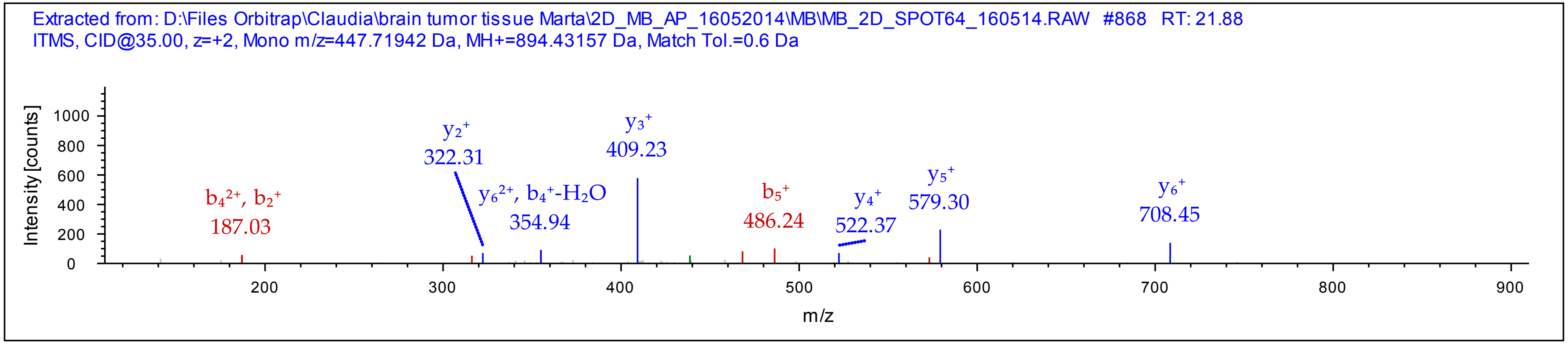
5	559.32389	280.16558	F	785.38286	393.19507	6
6	687.38247	344.19487	Q	638.31444	319.66086	5
7	834.45089	417.72908	F	510.25586	255.63157	4
8	935.49857	468.25292	T	363.18744	182.09736	3
9	1050.52552	525.76640	D	262.13976	131.57352	2
10			K	147.11281	74.06004	1



Sequence: ADEGISFR, Charge: +2, Monoisotopic m/z: 447.71942 Da (-0.03 mmu/-0.06 ppm), MH+: 894.43157 Da, RT: 21.88 min,
Identified with: Sequest HT (v1.3); XCorr:2.31, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]

#1	**b⁺**	**b²⁺**	**Seq.**	**y⁺**	**y²⁺**	**#2**
1	72.04440	36.52584	A			8
2	187.07135	94.03931	D	823.39450	412.20089	7
3	316.11395	158.56061	E	708.36755	354.68741	6
4	373.13542	187.07135	G	579.32495	290.16611	5
5	486.21949	243.61338	I	522.30348	261.65538	4
6	573.25152	287.12940	S	409.21941	205.11334	3
7	720.31994	360.66361	F	322.18738	161.59733	2
8			R	175.11896	88.06312	1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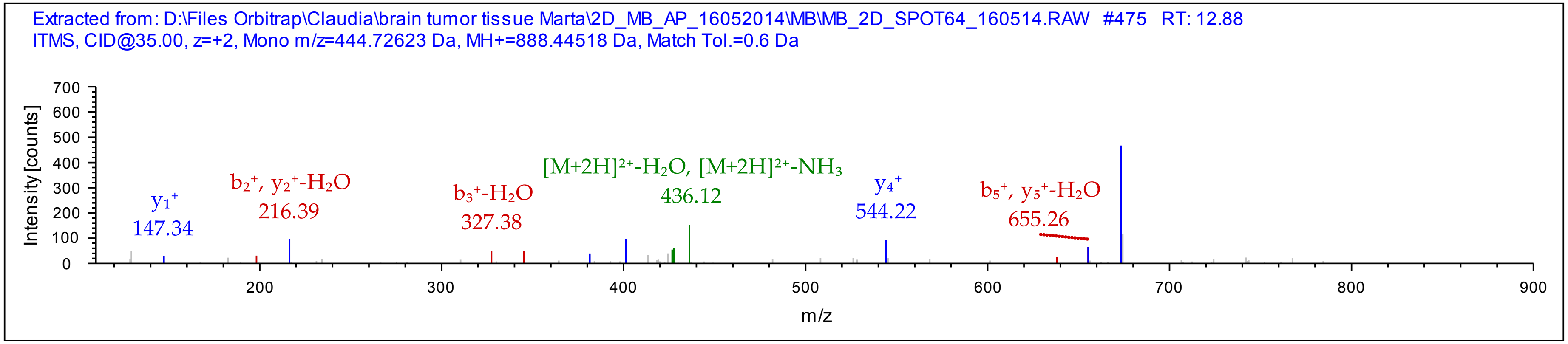
ITMS, CID@35.00, z=+2, Mono m/z=447.71942 Da, MH+=894.43157 Da, Match Tol.=0.6 Da

Sequence: SKEYFSK, Charge: +2, Monoisotopic m/z: 444.72623 Da (-0.5 mmu/-1.13 ppm), MH+: 888.44518 Da, RT: 12.88 min,
Identified with: Sequest HT (v1.3); XCorr:2.20, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]

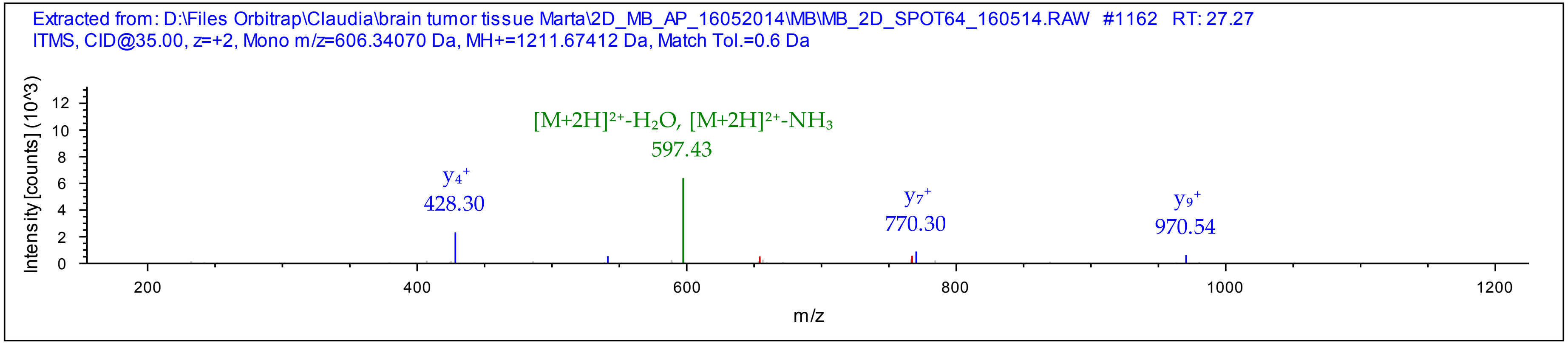
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	88.03931	44.52329	S			7
2	216.13428	108.57078	K	801.41415	401.21071	6
3	345.17688	173.09208	E	673.31918	337.16323	5
4	508.24020	254.62374	Y	544.27658	272.64193	4
5	655.30862	328.15795	F	381.21326	191.11027	3
6	742.34065	371.67396	S	234.14484	117.57606	2
7			K	147.11281	74.06004	1



Sequence: QITVNDLPVGR, Charge: +2, Monoisotopic m/z: 606.34070 Da (-0.1 mmu/-0.17 ppm), MH+: 1211.67412 Da, RT: 27.27 min,
Identified with: Sequest HT (v1.3); XCorr:2.18, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]
- Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5 - [PRDX2_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	129.06586	65.03657	Q			11
2	242.14993	121.57860	I	1083.61574	542.31151	10
3	343.19761	172.10244	T	970.53167	485.76947	9
4	442.26603	221.63665	V	869.48399	435.24563	8
5	556.30896	278.65812	N	770.41557	385.71142	7
6	671.33591	336.17159	D	656.37264	328.68996	6
7	784.41998	392.71363	L	541.34569	271.17648	5
8	881.47275	441.24001	P	428.26162	214.63445	4
9	980.54117	490.77422	V	331.20885	166.10806	3
10	1037.56264	519.28496	G	232.14043	116.57385	2
11			R	175.11896	88.06312	1

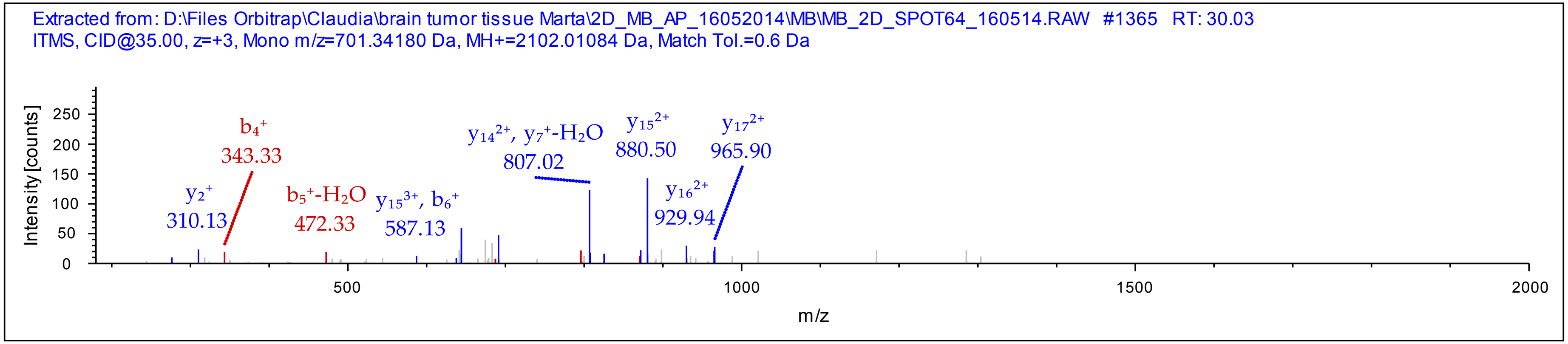

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT64_160514.RAW #1162 RT: 27.27
ITMS, CID@35.00, z=+2, Mono m/z=606.34070 Da, MH+=1211.67412 Da, Match Tol.=0.6 Da

Sequence: ATAVMPDGQFKDISLSDYK, M5-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 701.34180 Da (-0.1 mmu/-0.15 ppm), MH+: 2102.01084 Da, RT: 30.03 min,
Identified with: Sequest HT (v1.3); XCorr:2.09, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	72.04440	36.52584	24.68632	A				19
2	173.09208	87.04968	58.36888	T	2030.97403	1015.99065	677.66286	18
3	244.12920	122.56824	82.04792	A	1929.92635	965.46681	643.98030	17
4	343.19762	172.10245	115.07072	V	1858.88923	929.94825	620.30126	16
5	490.23303	245.62015	164.08253	M-Oxidation	1759.82081	880.41404	587.27845	15
6	587.28580	294.14654	196.43345	P	1612.78539	806.89633	538.26665	14
7	702.31275	351.66001	234.77577	D	1515.73262	758.36995	505.91572	13
8	759.33422	380.17075	253.78292	G	1400.70567	700.85647	467.57341	12
9	887.39280	444.20004	296.46912	Q	1343.68420	672.34574	448.56625	11
10	1034.46122	517.73425	345.49192	F	1215.62562	608.31645	405.88006	10
11	1162.55619	581.78173	388.19025	K	1068.55720	534.78224	356.85725	9
12	1277.58314	639.29521	426.53256	D	940.46223	470.73475	314.15893	8
13	1390.66721	695.83724	464.22725	I	825.43528	413.22128	275.81661	7
14	1477.69924	739.35326	493.23793	S	712.35121	356.67924	238.12192	6
15	1590.78331	795.89529	530.93262	L	625.31918	313.16323	209.11124	5
16	1677.81534	839.41131	559.94330	S	512.23511	256.62119	171.41655	4
17	1792.84229	896.92478	598.28561	D	425.20308	213.10518	142.40588	3

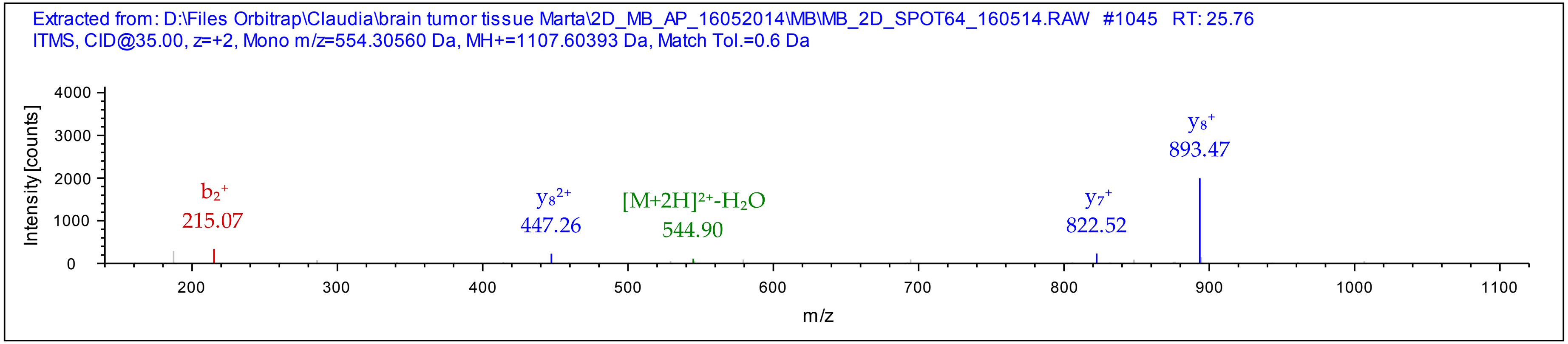
18	1955.90561	978.45644	652.64005	Y	310.17613	155.59170	104.06356	2
19				K	147.11281	74.06004	49.70912	1



Sequence: TIAQDYGVLK, Charge: +2, Monoisotopic m/z: 554.30560 Da (-0.28 mmu/-0.51 ppm), MH+: 1107.60393 Da, RT: 25.76 min,
Identified with: Sequest HT (v1.3); XCorr:2.05, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

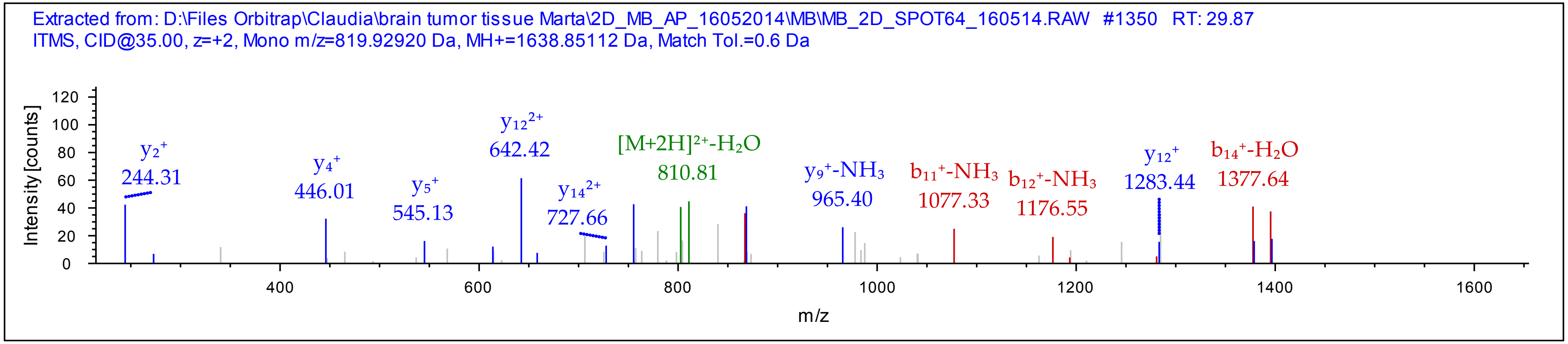
Protein references (1):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	102.05496	51.53112	T			10
2	215.13903	108.07315	I	1006.55681	503.78204	9
3	286.17615	143.59171	A	893.47274	447.24001	8
4	414.23473	207.62100	Q	822.43562	411.72145	7
5	529.26168	265.13448	D	694.37704	347.69216	6
6	692.32500	346.66614	Y	579.35009	290.17868	5
7	749.34647	375.17687	G	416.28677	208.64702	4
8	848.41489	424.71108	V	359.26530	180.13629	3
9	961.49896	481.25312	L	260.19688	130.60208	2
10			K	147.11281	74.06004	1



Sequence: QGGLGPMNIPLVSDPK, M7-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 819.92920 Da (-0.47 mmu/-0.58 ppm), MH+: 1638.85112 Da, RT: 29.87 min,
Identified with: Sequest HT (v1.3); XCorr:2.00, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]

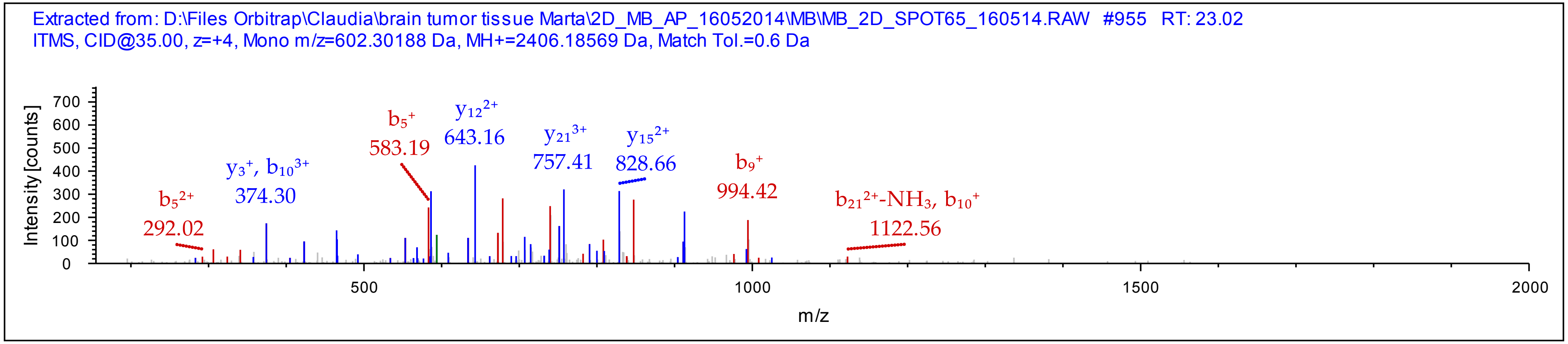
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	129.06586	65.03657	Q			16
2	186.08733	93.54730	G	1510.79349	755.90038	15
3	243.10880	122.05804	G	1453.77202	727.38965	14
4	356.19287	178.60007	L	1396.75055	698.87891	13
5	413.21434	207.11081	G	1283.66648	642.33688	12
6	510.26711	255.63719	P	1226.64501	613.82614	11
7	657.30252	329.15490	M-Oxidation	1129.59224	565.29976	10
8	771.34545	386.17636	N	982.55682	491.78205	9
9	884.42952	442.71840	I	868.51389	434.76058	8
10	981.48229	491.24478	P	755.42982	378.21855	7
11	1094.56636	547.78682	L	658.37705	329.69216	6
12	1193.63478	597.32103	V	545.29298	è	5
13	1280.66681	640.83704	S	446.22456	223.61592	4
14	1395.69376	698.35052	D	359.19253	180.09990	3
15	1492.74653	746.87690	P	244.16558	122.58643	2
16			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT64_160514.RAW #1350 RT: 29.87
ITMS, CID@35.00, z=+2, Mono m/z=819.92920 Da, MH+=1638.85112 Da, Match Tol.=0.6 Da

Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
65	Q06830	Peroxiredoxin-1	21.9	8.3	166.11	54.77	14	14	MB	3.59E-04	2.8	↑ in MB

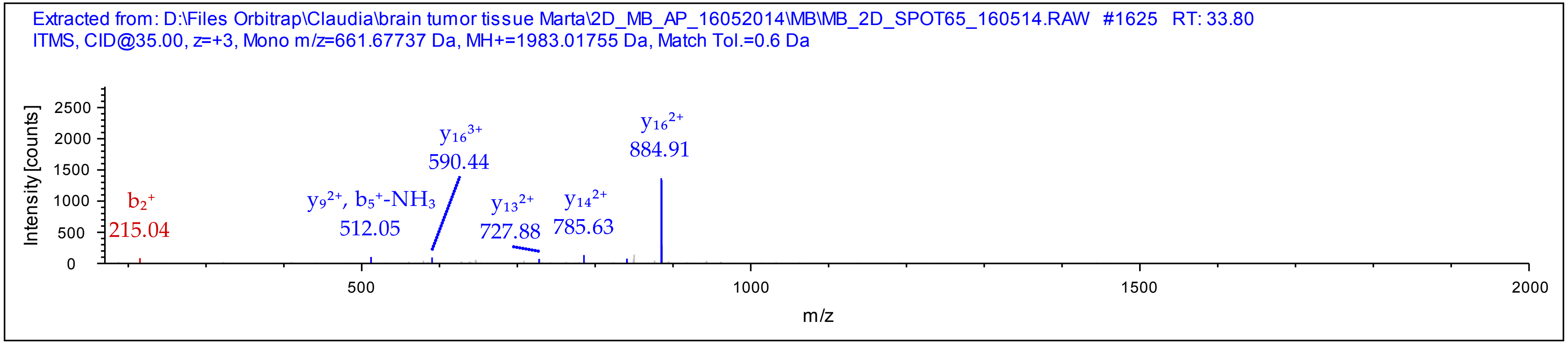
Sequence: HGEVCPAGWKPGSDTIKPDVQK, C5-Carbamidomethyl (57.02146 Da)
Charge: +4, Monoisotopic m/z: 602.30188 Da (-0.37 mmu/-0.62 ppm), MH+: 2406.18569 Da, RT: 23.02 min,
Identified with: Sequest HT (v1.3); XCorr:4.68, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]

#1	**b^{+}**	**b^{2+}**	**b^{3+}**	**b^{4+}**	**Seq.**	**y^{+}**	**y^{2+}**	**y^{3+}**	**y^{4+}**	**#2**
1	138.06619	69.53673	46.69358	35.27200	H					22
2	195.08766	98.04747	65.70074	49.52737	G	2269.12827	1135.06777	757.04761	568.03752	21
3	324.13026	162.56877	108.71494	81.78802	E	2212.10680	1106.55704	738.04045	553.78216	20
4	423.19868	212.10298	141.73774	106.55513	V	2083.06420	1042.03574	695.02625	521.52151	19
5	583.22933	292.11830	195.08129	146.56279	C-Carbamidomethyl	1983.99578	992.50153	662.00344	496.75440	18
6	680.28210	340.64469	227.43222	170.82598	P	1823.96512	912.48620	608.65989	456.74674	17
7	751.31922	376.16325	251.11126	188.58526	A	1726.91235	863.95981	576.30897	432.48355	16
8	808.34069	404.67398	270.11841	202.84063	G	1655.87523	828.44125	552.62993	414.72427	15
9	994.42001	497.71364	332.14485	249.36046	W	1598.85376	799.93052	533.62277	400.46890	14
10	1122.51498	561.76113	374.84318	281.38420	K	1412.77444	706.89086	471.59633	353.94907	13
11	1219.56775	610.28751	407.19410	305.64740	P	1284.67947	642.84337	428.89801	321.92533	12
12	1276.58922	638.79825	426.20126	319.90276	G	1187.62670	594.31699	396.54708	297.66213	11
13	1363.62125	682.31426	455.21193	341.66077	S	1130.60523	565.80625	377.53993	283.40677	10
14	1478.64820	739.82774	493.55425	370.41751	D	1043.57320	522.29024	348.52925	261.64876	9
15	1579.69588	790.35158	527.23681	395.67943	T	928.54625	464.77676	310.18693	232.89202	8
16	1692.77995	846.89361	564.93150	423.95045	I	827.49857	414.25292	276.50437	207.63010	7
17	1820.87492	910.94110	607.62982	455.97419	K	714.41450	357.71089	238.80968	179.35908	6
18	1917.92769	959.46748	639.98075	480.23738	P	586.31953	293.66340	196.11136	147.33534	5
19	2032.95464	1016.98096	678.32306	508.99412	D	489.26676	245.13702	163.76044	123.07215	4
20	2132.02306	1066.51517	711.34587	533.76122	V	374.23981	187.62354	125.41812	94.31541	3
21	2260.08164	1130.54446	754.03206	565.77587	Q	275.17139	138.08933	92.39531	69.54831	2
22					K	147.11281	74.06004	49.70912	37.53366	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT65_160514.RAW #955 RT: 23.02
ITMS, CID@35.00, z=+4, Mono m/z=602.30188 Da, MH+=2406.18569 Da, Match Tol.=0.6 Da

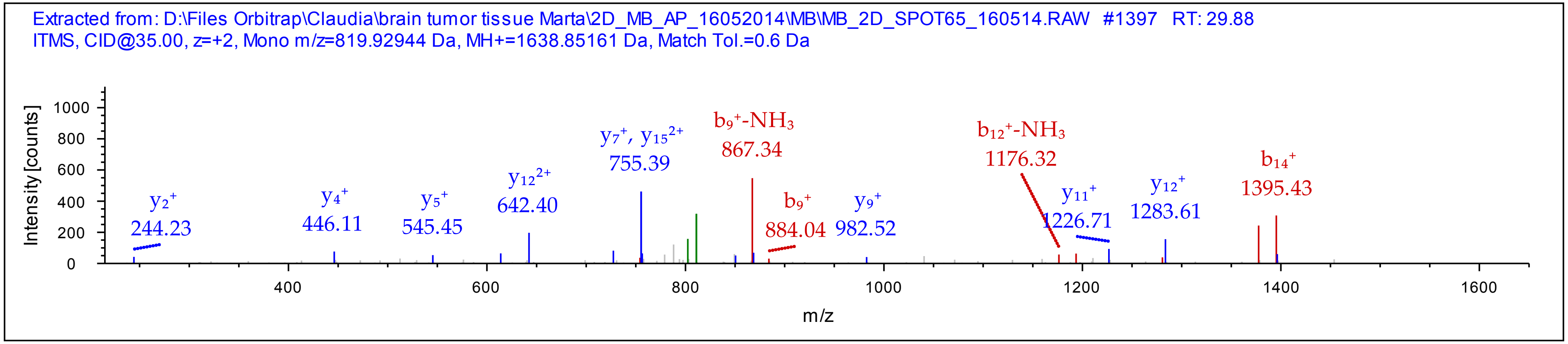
Sequence: TIAQDYGVLKADEGISFR, Charge: +3, Monoisotopic m/z: 661.67737 Da (-0.24 mmu/-0.36 ppm), MH+: 1983.01755 Da, RT: 33.80 min,
Identified with: Sequest HT (v1.3); XCorr:3.16, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]

#1	b$^+$	b^{2+}	b^{3+}	Seq.	y$^+$	y^{2+}	y^{3+}	#2
1	102.05496	51.53112	34.68984	T				18
2	215.13903	108.07315	72.38453	I	1881.97059	941.48893	627.99505	17
3	286.17615	143.59171	96.06357	A	1768.88652	884.94690	590.30036	16
4	414.23473	207.62100	138.74976	Q	1697.84940	849.42834	566.62132	15
5	529.26168	265.13448	177.09208	D	1569.79082	785.39905	523.93512	14
6	692.32500	346.66614	231.44652	Y	1454.76387	727.88557	485.59281	13
7	749.34647	375.17687	250.45367	G	1291.70055	646.35391	431.23837	12
8	848.41489	424.71108	283.47648	V	1234.67908	617.84318	412.23121	11
9	961.49896	481.25312	321.17117	L	1135.61066	568.30897	379.20840	10
10	1089.59393	545.30060	363.86949	K	1022.52659	511.76693	341.51371	9
11	1160.63105	580.81916	387.54853	A	894.43162	447.71945	298.81539	8
12	1275.65800	638.33264	425.89085	D	823.39450	412.20089	275.13635	7
13	1404.70060	702.85394	468.90505	E	708.36755	354.68741	236.79403	6
14	1461.72207	731.36467	487.91221	G	579.32495	290.16611	193.77983	5
15	1574.80614	787.90671	525.60690	I	522.30348	261.65538	174.77268	4
16	1661.83817	831.42272	554.61757	S	409.21941	205.11334	137.07799	3
17	1808.90659	904.95693	603.64038	F	322.18738	161.59733	108.06731	2
18				R	175.11896	88.06312	59.04450	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT65_160514.RAW #1625 RT: 33.80
ITMS, CID@35.00, z=+3, Mono m/z=661.67737 Da, MH+=1983.01755 Da, Match Tol.=0.6 Da

Sequence: QGGLGPMNIPLVSDPK, M7-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 819.92944 Da (-0.23 mmu/-0.28 ppm), MH+: 1638.85161 Da, RT: 29.88 min,
Identified with: Sequest HT (v1.3); XCorr:3.08, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]

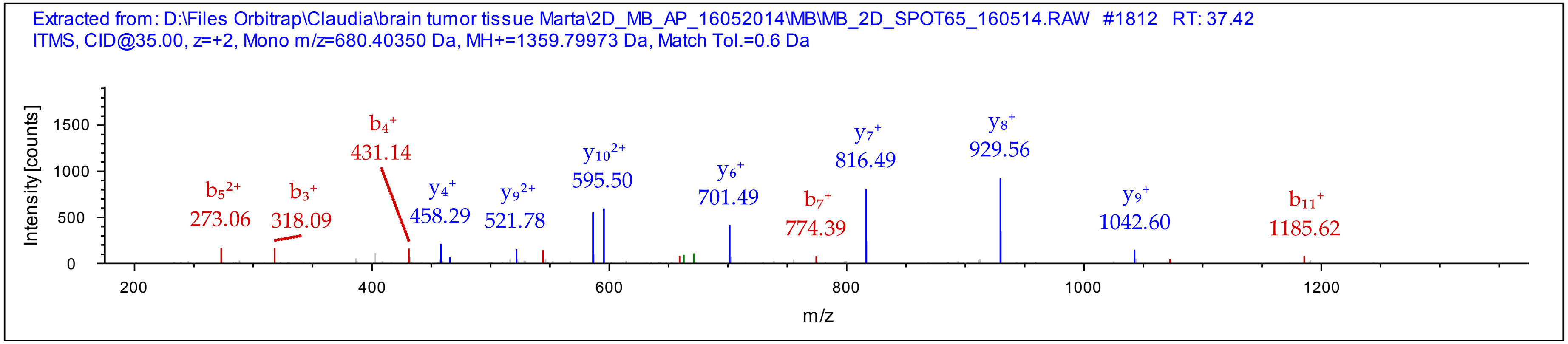
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	129.06586	65.03657	Q			16
2	186.08733	93.54730	G	1510.79349	755.90038	15
3	243.10880	122.05804	G	1453.77202	727.38965	14
4	356.19287	178.60007	L	1396.75055	698.87891	13
5	413.21434	207.11081	G	1283.66648	642.33688	12
6	510.26711	255.63719	P	1226.64501	613.82614	11
7	657.30252	329.15490	M-Oxidation	1129.59224	565.29976	10
8	771.34545	386.17636	N	982.55682	491.78205	9
9	884.42952	442.71840	I	868.51389	434.76058	8
10	981.48229	491.24478	P	755.42982	378.21855	7
11	1094.56636	547.78682	L	658.37705	329.69216	6
12	1193.63478	597.32103	V	545.29298	273.15013	5
13	1280.66681	640.83704	S	446.22456	223.61592	4
14	1395.69376	698.35052	D	359.19253	180.09990	3
15	1492.74653	746.87690	P	244.16558	122.58643	2
16			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT65_160514.RAW #1397 RT: 29.88
ITMS, CID@35.00, z=+2, Mono m/z=819.92944 Da, MH+=1638.85161 Da, Match Tol.=0.6 Da

Sequence: GLFIIDDKGILR, Charge: +2, Monoisotopic m/z: 680.40350 Da (+0.09 mmu/+0.14 ppm), MH+: 1359.79973 Da, RT: 37.42 min,
Identified with: Sequest HT (v1.3); XCorr:2.97, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]
- Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 - [PRDX4_HUMAN]

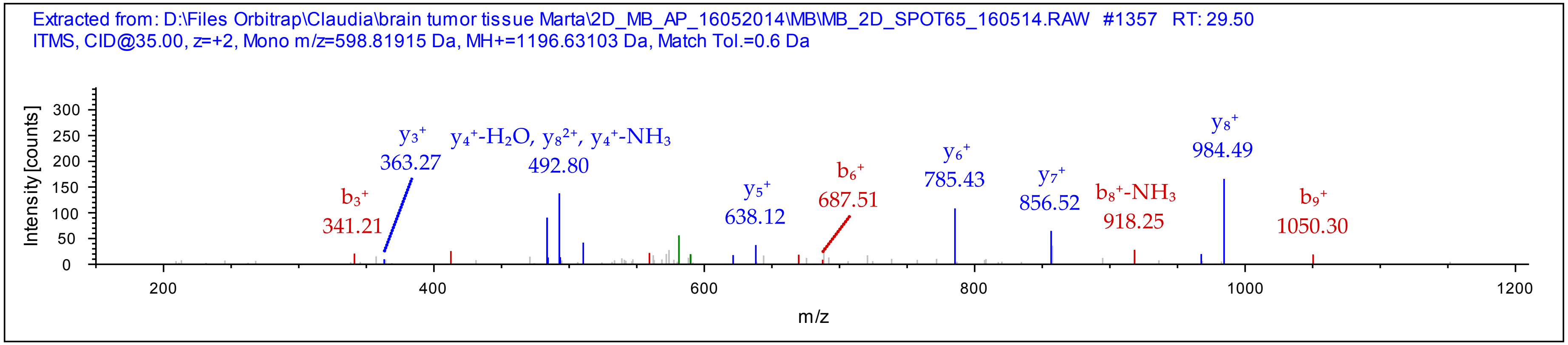
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	58.02875	29.51801	G			12
2	171.11282	86.06005	L	1302.77807	651.89267	11
3	318.18124	159.59426	F	1189.69400	595.35064	10
4	431.26531	216.13629	I	1042.62558	521.81643	9
5	544.34938	272.67833	I	929.54151	465.27439	8
6	659.37633	330.19180	D	816.45744	408.73236	7
7	774.40328	387.70528	D	701.43049	351.21888	6
8	902.49825	451.75276	K	586.40354	293.70541	5
9	959.51972	480.26350	G	458.30857	229.65792	4
10	1072.60379	536.80553	I	401.28710	201.14719	3
11	1185.68786	593.34757	L	288.20303	144.60515	2
12			R	175.11896	88.06312	1



Sequence: LVQAFQFTDK, Charge: +2, Monoisotopic m/z: 598.81915 Da (-0.01 mmu/-0.02 ppm), MH+: 1196.63103 Da, RT: 29.50 min,
Identified with: Sequest HT (v1.3); XCorr:2.82, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

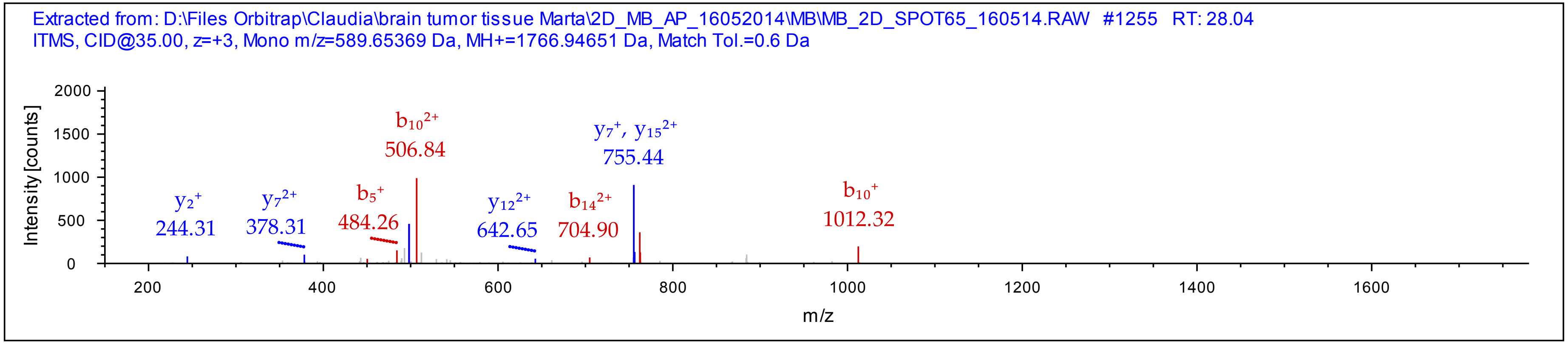
Protein references (1):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	114.09135	57.54931	L			10
2	213.15977	107.08352	V	1083.54698	542.27713	9
3	341.21835	171.11281	Q	984.47856	492.74292	8
4	412.25547	206.63137	A	856.41998	428.71363	7
5	559.32389	280.16558	F	785.38286	393.19507	6
6	687.38247	344.19487	Q	638.31444	319.66086	5
7	834.45089	417.72908	F	510.25586	255.63157	4
8	935.49857	468.25292	T	363.18744	182.09736	3
9	1050.52552	525.76640	D	262.13976	131.57352	2
10			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT65_160514.RAW #1357 RT: 29.50
ITMS, CID@35.00, z=+2, Mono m/z=598.81915 Da, MH+=1196.63103 Da, Match Tol.=0.6 Da

Sequence: KQGGLGPMNIPLVSDPK, M8-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 589.65369 Da (-0.18 mmu/-0.3 ppm), MH+: 1766.94651 Da, RT: 28.04 min,
Identified with: Sequest HT (v1.3); XCorr:2.65, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]

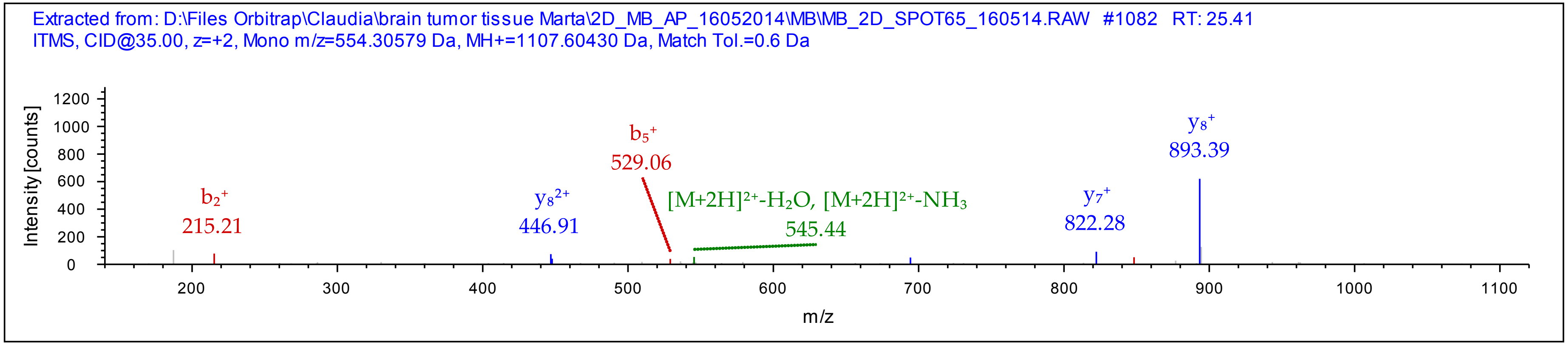
#1	**b^{+}**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^{+}**	**y^{2+}**	**y^{3+}**	**#2**
1	129.10225	65.05476	43.70560	K				17
2	257.16083	129.08405	86.39179	Q	1638.85207	819.92967	546.95554	16
3	314.18230	157.59479	105.39895	G	1510.79349	755.90038	504.26935	15
4	371.20377	186.10552	124.40611	G	1453.77202	727.38965	485.26219	14
5	484.28784	242.64756	162.10080	L	1396.75055	698.87891	466.25503	13
6	541.30931	271.15829	181.10795	G	1283.66648	642.33688	428.56034	12
7	638.36208	319.68468	213.45888	P	1226.64501	613.82614	409.55319	11
8	785.39749	393.20238	262.47068	M-Oxidation	1129.59224	565.29976	377.20226	10
9	899.44042	450.22385	300.48499	N	982.55682	491.78205	328.19046	9
10	1012.52449	506.76588	338.17968	I	868.51389	434.76058	290.17615	8
11	1109.57726	555.29227	370.53060	P	755.42982	378.21855	252.48146	7
12	1222.66133	611.83430	408.22529	L	658.37705	329.69216	220.13053	6
13	1321.72975	661.36851	441.24810	V	545.29298	273.15013	182.43584	5
14	1408.76178	704.88453	470.25878	S	446.22456	223.61592	149.41304	4
15	1523.78873	762.39800	508.60109	D	359.19253	180.09990	120.40236	3
16	1620.84150	810.92439	540.95202	P	244.16558	122.58643	82.06004	2
17				K	147.11281	74.06004	49.70912	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT65_160514.RAW #1255 RT: 28.04
ITMS, CID@35.00, z=+3, Mono m/z=589.65369 Da, MH+=1766.94651 Da, Match Tol.=0.6 Da

Sequence: TIAQDYGVLK, Charge: +2, Monoisotopic m/z: 554.30579 Da (-0.1 mmu/-0.18 ppm), MH+: 1107.60430 Da, RT: 25.41 min,
Identified with: Sequest HT (v1.3); XCorr:2.40, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H$_2$O; b-NH$_3$; y; y-H$_2$O; y-NH$_3$

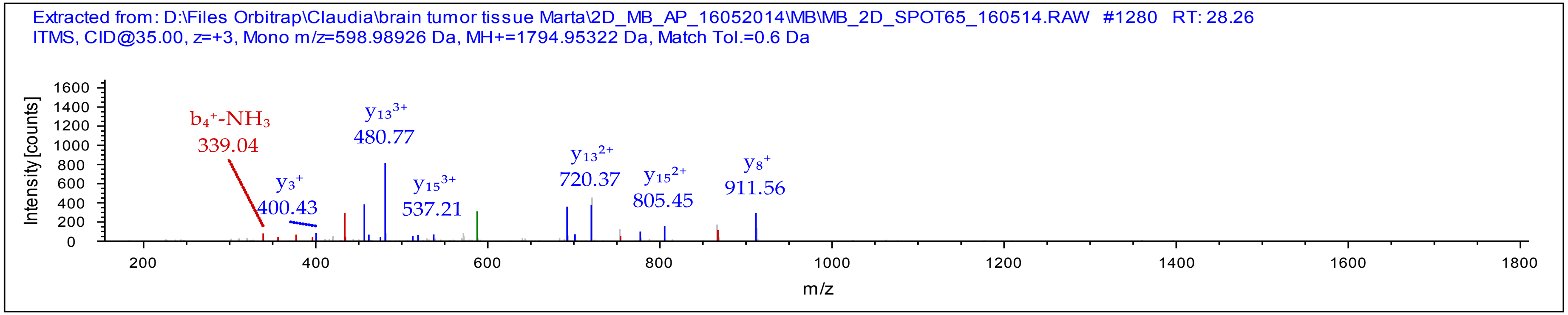
Protein references (1):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]

#1	**b^{+}**	**b^{2+}**	**Seq.**	**y^{+}**	**y^{2+}**	**#2**
1	102.05496	51.53112	T			10
2	215.13903	108.07315	I	1006.55681	503.78204	9
3	286.17615	143.59171	A	893.47274	447.24001	8
4	414.23473	207.62100	Q	822.43562	411.72145	7
5	529.26168	265.13448	D	694.37704	347.69216	6
6	692.32500	346.66614	Y	579.35009	290.17868	5
7	749.34647	375.17687	G	416.28677	208.64702	4
8	848.41489	424.71108	V	359.26530	180.13629	3
9	961.49896	481.25312	L	260.19688	130.60208	2
10			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT65_160514.RAW #1082 RT: 25.41
ITMS, CID@35.00, z=+2, Mono m/z=554.30579 Da, MH+=1107.60430 Da, Match Tol.=0.6 Da

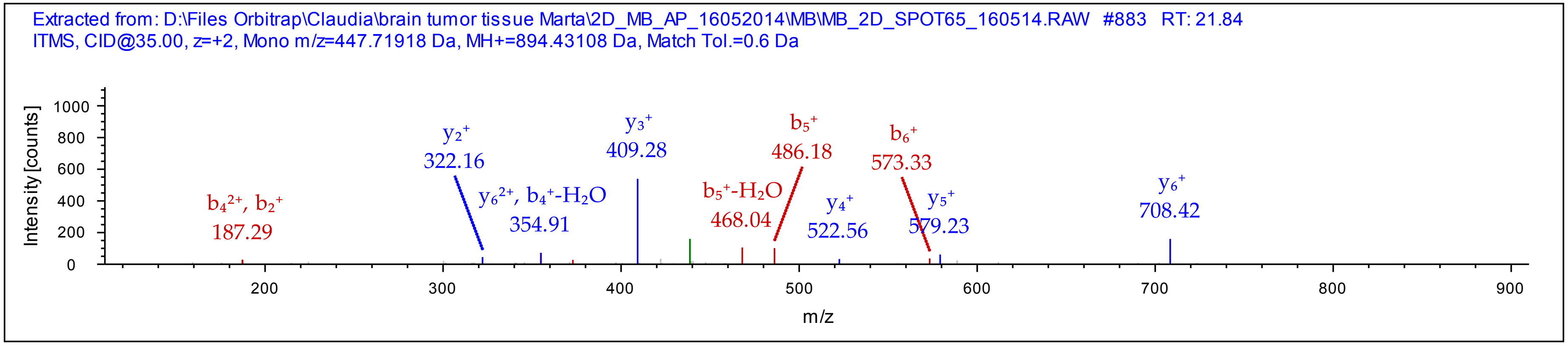
Sequence: QGGLGPMNIPLVSDPKR, M7-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 598.98926 Da (+0.01 mmu/+0.02 ppm), MH+: 1794.95322 Da, RT: 28.26 min,
Identified with: Sequest HT (v1.3); XCorr:2.39, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	129.06586	65.03657	43.69347	Q				17
2	186.08733	93.54730	62.70063	G	1666.89461	833.95094	556.30305	16
3	243.10880	122.05804	81.70778	G	1609.87314	805.44021	537.29590	15
4	356.19287	178.60007	119.40247	L	1552.85167	776.92947	518.28874	14
5	413.21434	207.11081	138.40963	G	1439.76760	720.38744	480.59405	13
6	510.26711	255.63719	170.76055	P	1382.74613	691.87670	461.58689	12
7	657.30252	329.15490	219.77236	M-Oxidation	1285.69336	643.35032	429.23597	11
8	771.34545	386.17636	257.78667	N	1138.65794	569.83261	380.22416	10
9	884.42952	442.71840	295.48136	I	1024.61501	512.81114	342.20985	9
10	981.48229	491.24478	327.83228	P	911.53094	456.26911	304.51516	8
11	1094.56636	547.78682	365.52697	L	814.47817	407.74272	272.16424	7
12	1193.63478	597.32103	398.54978	V	701.39410	351.20069	234.46955	6
13	1280.66681	640.83704	427.56045	S	602.32568	301.66648	201.44674	5
14	1395.69376	698.35052	465.90277	D	515.29365	258.15046	172.43607	4
15	1492.74653	746.87690	498.25369	P	400.26670	200.63699	134.09375	3
16	1620.84150	810.92439	540.95202	K	303.21393	152.11060	101.74283	2
17				R	175.11896	88.06312	59.04450	1



Sequence: ADEGISFR, Charge: +2, Monoisotopic m/z: 447.71918 Da (-0.27 mmu/-0.61 ppm), MH+: 894.43108 Da, RT: 21.84 min,
Identified with: Sequest HT (v1.3); XCorr:2.16, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3
Protein references (1):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	72.04440	36.52584	A			8
2	187.07135	94.03931	D	823.39450	412.20089	7
3	316.11395	158.56061	E	708.36755	354.68741	6
4	373.13542	187.07135	G	579.32495	290.16611	5
5	486.21949	243.61338	I	522.30348	261.65538	4
6	573.25152	287.12940	S	409.21941	205.11334	3
7	720.31994	360.66361	F	322.18738	161.59733	2
8			R	175.11896	88.06312	1

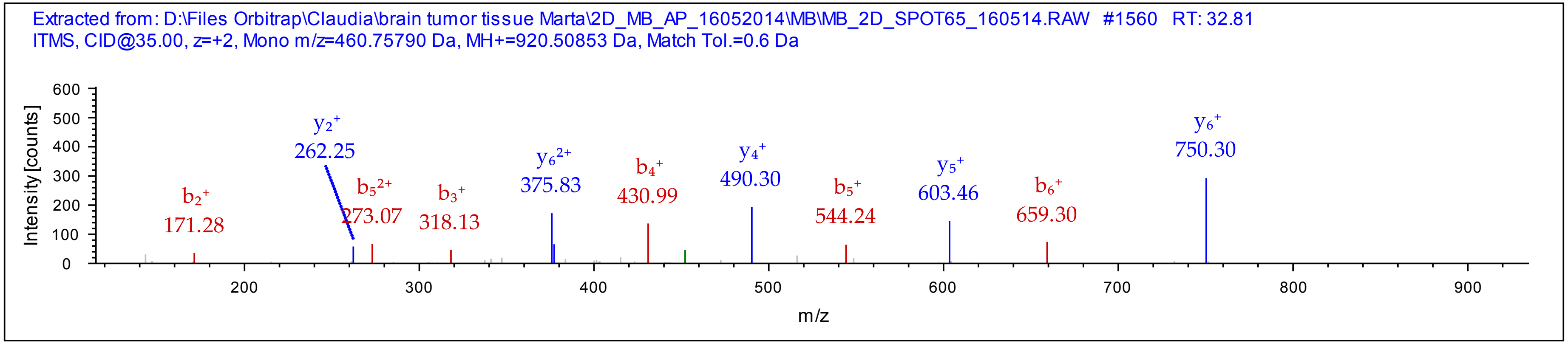


Sequence: GLFIIDDK, Charge: +2, Monoisotopic m/z: 460.75790 Da (-0.14 mmu/-0.3 ppm), MH+: 920.50853 Da, RT: 32.81 min,

Identified with: Sequest HT (v1.3); XCorr:2.15, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (2):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]
- Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 - [PRDX4_HUMAN]

#1	**b$^+$**	**b^{2+}**	**Seq.**	**y$^+$**	**y^{2+}**	**#2**
1	58.02875	29.51801	G			8
2	171.11282	86.06005	L	863.48734	432.24731	7
3	318.18124	159.59426	F	750.40327	375.70527	6
4	431.26531	216.13629	I	603.33485	302.17106	5
5	544.34938	272.67833	I	490.25078	245.62903	4
6	659.37633	330.19180	D	377.16671	189.08699	3
7	774.40328	387.70528	D	262.13976	131.57352	2
8			K	147.11281	74.06004	1

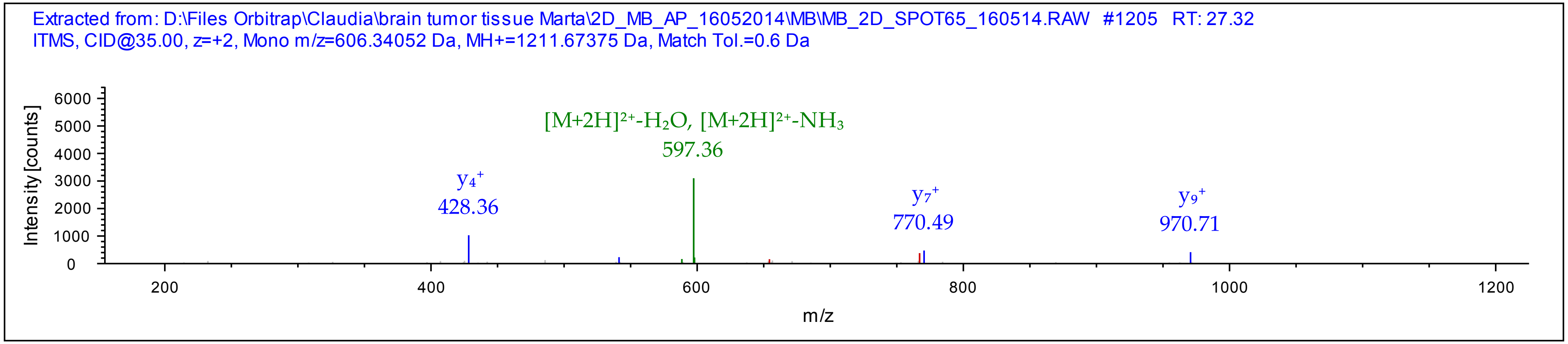

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT65_160514.RAW #1560 RT: 32.81
ITMS, CID@35.00, z=+2, Mono m/z=460.75790 Da, MH+=920.50853 Da, Match Tol.=0.6 Da

Sequence: QITVNDLPVGR, Charge: +2, Monoisotopic m/z: 606.34052 Da (-0.28 mmu/-0.47 ppm), MH+: 1211.67375 Da, RT: 27.32 min,
Identified with: Sequest HT (v1.3); XCorr:2.11, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]
- Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5 - [PRDX2_HUMAN]

#1	**b$^+$**	**b^{2+}**	**Seq.**	**y$^+$**	**y^{2+}**	**#2**
1	129.06586	65.03657	Q			11

2	242.14993	121.57860	I	1083.61574	542.31151	10
3	343.19761	172.10244	T	970.53167	485.76947	9
4	442.26603	221.63665	V	869.48399	435.24563	8
5	556.30896	278.65812	N	770.41557	385.71142	7
6	671.33591	336.17159	D	656.37264	328.68996	6
7	784.41998	392.71363	L	541.34569	271.17648	5
8	881.47275	441.24001	P	428.26162	214.63445	4
9	980.54117	490.77422	V	331.20885	166.10806	3
10	1037.56264	519.28496	G	232.14043	116.57385	2
11			R	175.11896	88.06312	1



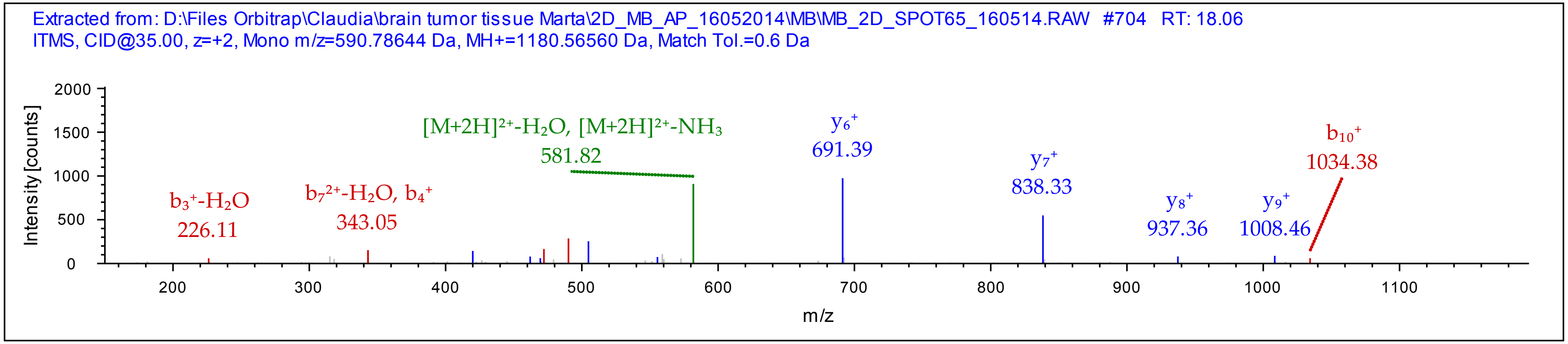
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT65_160514.RAW #1205 RT: 27.32
ITMS, CID@35.00, z=+2, Mono m/z=606.34052 Da, MH+=1211.67375 Da, Match Tol.=0.6 Da

Sequence: ATAVMPDGQFK, M5-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 590.78644 Da (-0.58 mmu/-0.98 ppm), MH+: 1180.56560 Da, RT: 18.06 min,
Identified with: Sequest HT (v1.3); XCorr:2.09, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]

#1	b⁺	b²⁺	Seq.	y⁺	y²⁺	#2
1	72.04440	36.52584	A			11
2	173.09208	87.04968	T	1109.52964	555.26846	10
3	244.12920	122.56824	A	1008.48196	504.74462	9
4	343.19762	172.10245	V	937.44484	469.22606	8
5	490.23303	245.62015	M-Oxidation	838.37642	419.69185	7
6	587.28580	294.14654	P	691.34100	346.17414	6
7	702.31275	351.66001	D	594.28823	297.64775	5

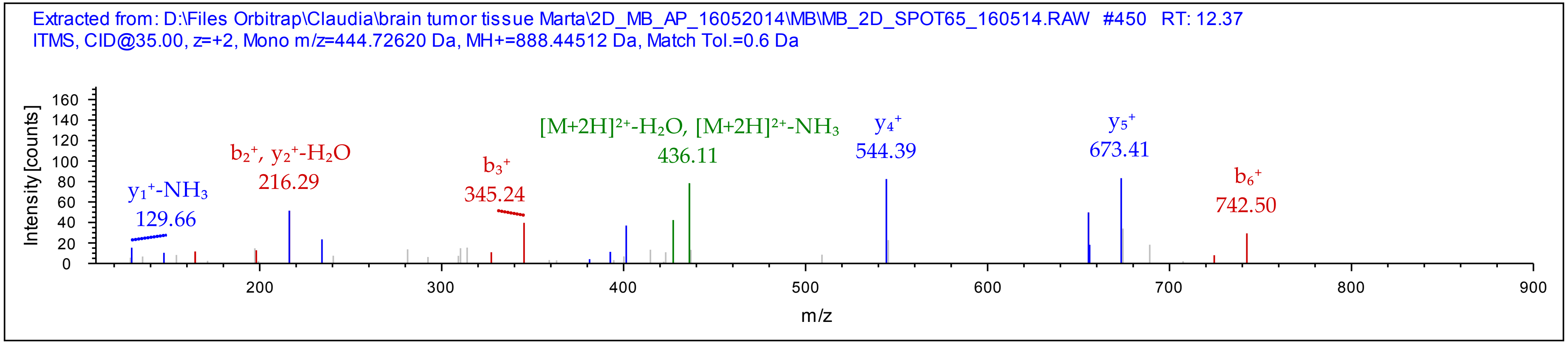
8	759.33422	380.17075	G	479.26128	240.13428	4
9	887.39280	444.20004	Q	422.23981	211.62354	3
10	1034.46122	517.73425	F	294.18123	147.59425	2
11			K	147.11281	74.06004	1



Sequence: SKEYFSK, Charge: +2, Monoisotopic m/z: 444.72620 Da (-0.53 mmu/-1.2 ppm), MH+: 888.44512 Da, RT: 12.37 min,
Identified with: Sequest HT (v1.3); XCorr:1.99, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]

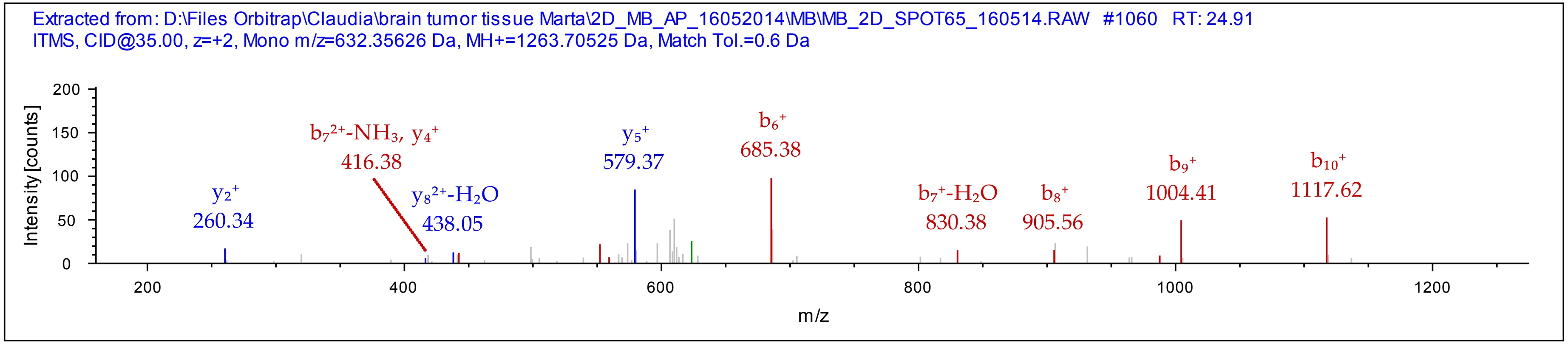
#1	b$^+$	b^{2+}	Seq.	y$^+$	y^{2+}	#2
1	88.03931	44.52329	S			7
2	216.13428	108.57078	K	801.41415	401.21071	6
3	345.17688	173.09208	E	673.31918	337.16323	5
4	508.24020	254.62374	Y	544.27658	272.64193	4
5	655.30862	328.15795	F	381.21326	191.11027	3
6	742.34065	371.67396	S	234.14484	117.57606	2
7			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT65_160514.RAW #450 RT: 12.37
ITMS, CID@35.00, z=+2, Mono m/z=444.72620 Da, MH+=888.44512 Da, Match Tol.=0.6 Da

Sequence: RTIAQDYGVLK, Charge: +2, Monoisotopic m/z: 632.35626 Da (-0.18 mmu/-0.29 ppm), MH+: 1263.70525 Da, RT: 24.91 min,
Identified with: Sequest HT (v1.3); XCorr:1.81, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	157.10840	79.05784	R			11
2	258.15608	129.58168	T	1107.60449	554.30588	10
3	371.24015	186.12371	I	1006.55681	503.78204	9
4	442.27727	221.64227	A	893.47274	447.24001	8
5	570.33585	285.67156	Q	822.43562	411.72145	7
6	685.36280	343.18504	D	694.37704	347.69216	6
7	848.42612	424.71670	Y	579.35009	290.17868	5
8	905.44759	453.22743	G	416.28677	208.64702	4
9	1004.51601	502.76164	V	359.26530	180.13629	3
10	1117.60008	559.30368	L	260.19688	130.60208	2
11			K	147.11281	74.06004	1



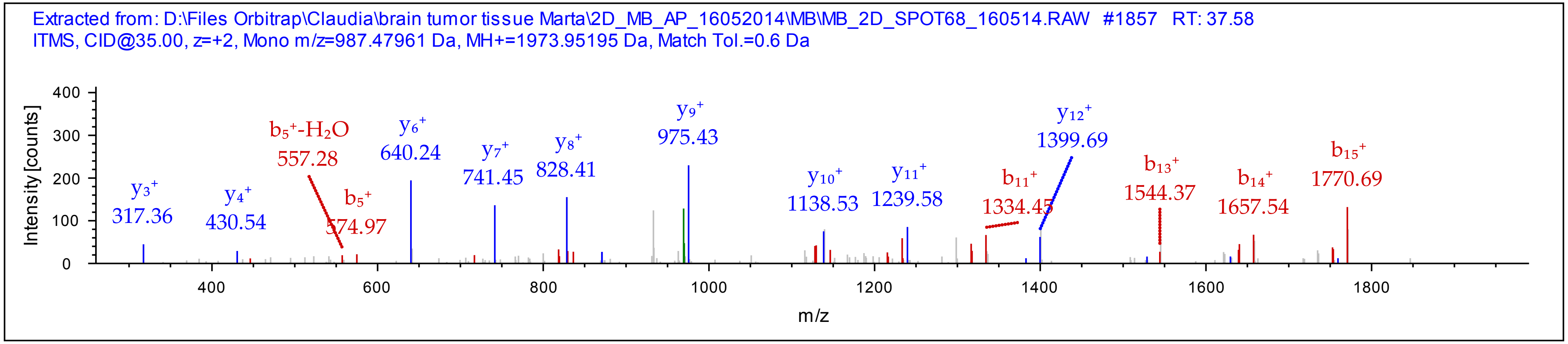
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT65_160514.RAW #1060 RT: 24.91
ITMS, CID@35.00, z=+2, Mono m/z=632.35626 Da, MH+=1263.70525 Da, Match Tol.=0.6 Da

Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
68	P40926	Malate dehydrogenase, mitochondrial	32.9	8.5	125.33	46.45%	12	12	MB	2.00E-03	3.2	↑ in MB

Sequence: SQETECTYFSTPLLLGK, C6-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 987.47961 Da (-0.29 mmu/-0.3 ppm), MH+: 1973.95195 Da, RT: 37.58 min,
Identified with: Sequest HT (v1.3); XCorr:4.23, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	88.03931	44.52329	S			17
2	216.09789	108.55258	Q	1886.92051	943.96389	16
3	345.14049	173.07388	E	1758.86193	879.93460	15
4	446.18817	223.59772	T	1629.81933	815.41330	14
5	575.23077	288.11902	E	1528.77165	764.88946	13
6	735.26142	368.13435	C-Carbamidomethyl	1399.72905	700.36816	12
7	836.30910	418.65819	T	1239.69839	620.35283	11
8	999.37242	500.18985	Y	1138.65071	569.82899	10
9	1146.44084	573.72406	F	975.58739	488.29733	9
10	1233.47287	617.24007	S	828.51897	414.76312	8
11	1334.52055	667.76391	T	741.48694	371.24711	7
12	1431.57332	716.29030	P	640.43926	320.72327	6
13	1544.65739	772.83233	L	543.38649	272.19688	5
14	1657.74146	829.37437	L	430.30242	215.65485	4
15	1770.82553	885.91640	L	317.21835	159.11281	3
16	1827.84700	914.42714	G	204.13428	102.57078	2
17			K	147.11281	74.06004	1

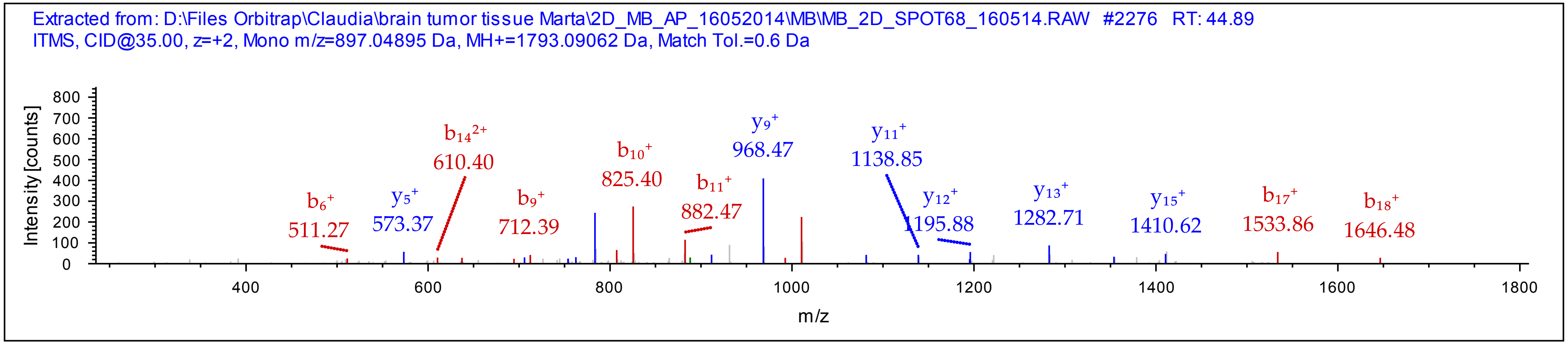


Sequence: VAVLGASGGIGQPLSLLLK, Charge: +2, Monoisotopic m/z: 897.04895 Da (+0.51 mmu/+0.57 ppm), MH+: 1793.09062 Da, RT: 44.89 min,
Identified with: Sequest HT (v1.3); XCorr:4.02, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	100.07570	50.54149	V			19
2	171.11282	86.06005	A	1694.02118	847.51423	18
3	270.18124	135.59426	V	1622.98406	811.99567	17
4	383.26531	192.13629	L	1523.91564	762.46146	16
5	440.28678	220.64703	G	1410.83157	705.91942	15
6	511.32390	256.16559	A	1353.81010	677.40869	14
7	598.35593	299.68160	S	1282.77298	641.89013	13
8	655.37740	328.19234	G	1195.74095	598.37411	12
9	712.39887	356.70307	G	1138.71948	569.86338	11
10	825.48294	413.24511	I	1081.69801	541.35264	10
11	882.50441	441.75584	G	968.61394	484.81061	9
12	1010.56299	505.78513	Q	911.59247	456.29987	8
13	1107.61576	554.31152	P	783.53389	392.27058	7
14	1220.69983	610.85355	L	686.48112	343.74420	6
15	1307.73186	654.36957	S	573.39705	287.20216	5
16	1420.81593	710.91160	L	486.36502	243.68615	4
17	1533.90000	767.45364	L	373.28095	187.14411	3
18	1646.98407	823.99567	L	260.19688	130.60208	2

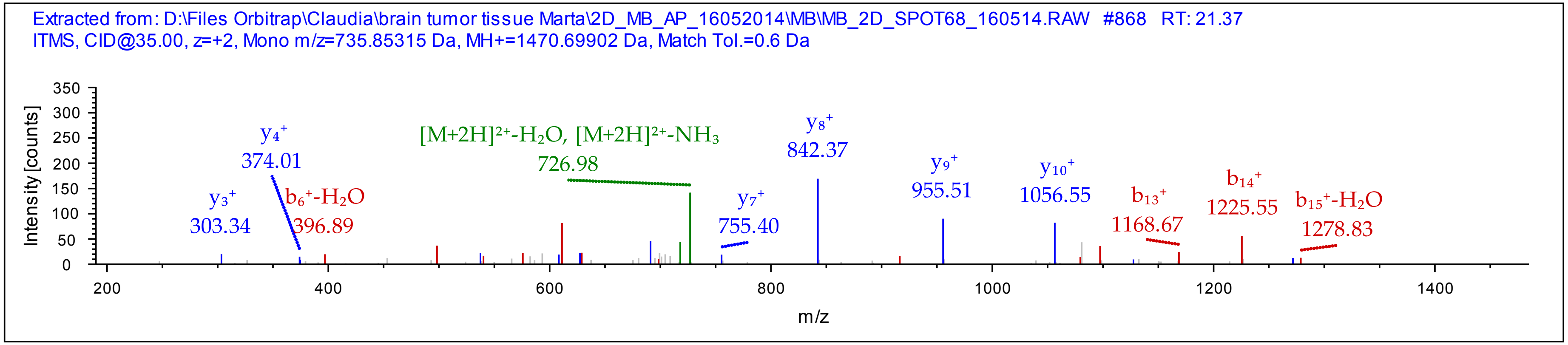
19			K	147.11281	74.06004	1



Sequence: AGAGSATLSMAYAGAR, M10-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 735.85315 Da (-0.81 mmu/-1.1 ppm), MH+: 1470.69902 Da, RT: 21.37 min,
Identified with: Sequest HT (v1.3); XCorr:2.84, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]

#1	**b^{+}**	**b^{2+}**	**Seq.**	**y^{+}**	**y^{2+}**	**#2**
1	72.04440	36.52584	A			16
2	129.06587	65.03657	G	1399.66352	700.33540	15
3	200.10299	100.55513	A	1342.64205	671.82466	14
4	257.12446	129.06587	G	1271.60493	636.30610	13
5	344.15649	172.58188	S	1214.58346	607.79537	12
6	415.19361	208.10044	A	1127.55143	564.27935	11
7	516.24129	258.62428	T	1056.51431	528.76079	10
8	629.32536	315.16632	L	955.46663	478.23695	9
9	716.35739	358.68233	S	842.38256	421.69492	8
10	863.39280	432.20004	M-Oxidation	755.35053	378.17890	7
11	934.42992	467.71860	A	608.31511	304.66119	6
12	1097.49324	549.25026	Y	537.27799	269.14263	5
13	1168.53036	584.76882	A	374.21467	187.61097	4
14	1225.55183	613.27955	G	303.17755	152.09241	3
15	1296.58895	648.79811	A	246.15608	123.58168	2
16			R	175.11896	88.06312	1

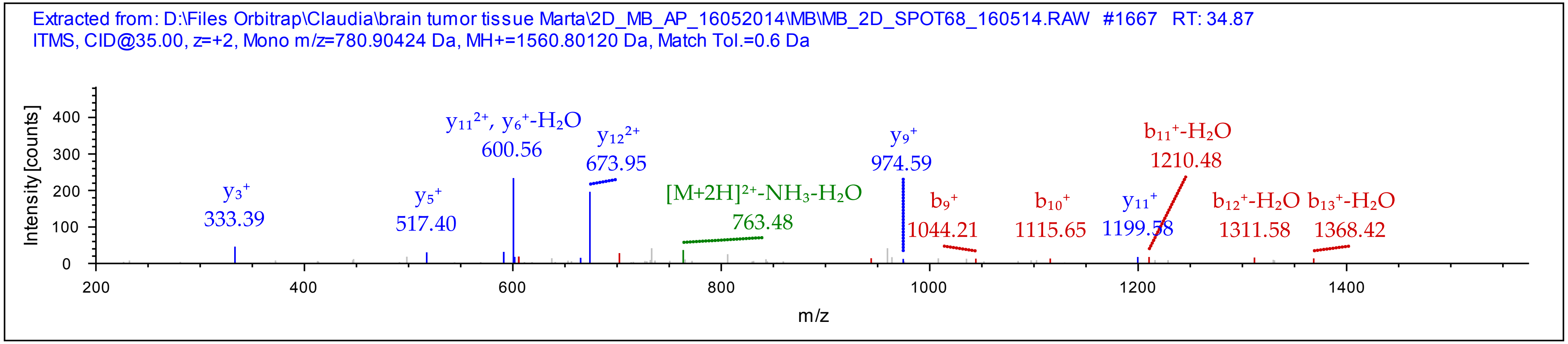


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT68_160514.RAW #868 RT: 21.37
ITMS, CID@35.00, z=+2, Mono m/z=735.85315 Da, MH+=1470.69902 Da, Match Tol.=0.6 Da

Sequence: VDFPQDQLTALTGR, Charge: +2, Monoisotopic m/z: 780.90424 Da (-0.26 mmu/-0.34 ppm), MH+: 1560.80120 Da, RT: 34.87 min,
Identified with: Sequest HT (v1.3); XCorr:2.80, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]

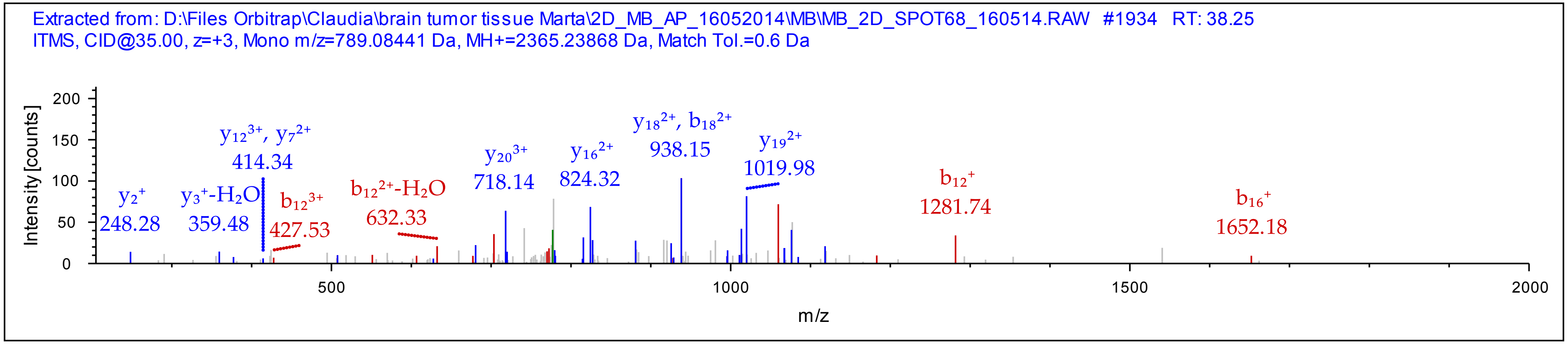
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	100.07570	50.54149	V			14
2	215.10265	108.05496	D	1461.73330	731.37029	13
3	362.17107	181.58917	F	1346.70635	673.85681	12
4	459.22384	230.11556	P	1199.63793	600.32260	11
5	587.28242	294.14485	Q	1102.58516	551.79622	10
6	702.30937	351.65832	D	974.52658	487.76693	9
7	830.36795	415.68761	Q	859.49963	430.25345	8
8	943.45202	472.22965	L	731.44105	366.22416	7
9	1044.49970	522.75349	T	618.35698	309.68213	6
10	1115.53682	558.27205	A	517.30930	259.15829	5
11	1228.62089	614.81408	L	446.27218	223.63973	4
12	1329.66857	665.33792	T	333.18811	167.09769	3
13	1386.69004	693.84866	G	232.14043	116.57385	2
14			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT68_160514.RAW #1667 RT: 34.87
ITMS, CID@35.00, z=+2, Mono m/z=780.90424 Da, MH+=1560.80120 Da, Match Tol.=0.6 Da

Sequence: LTLYDIAHTPGVAADLSHIETK, Charge: +3, Monoisotopic m/z: 789.08441 Da (-0.4 mmu/-0.51 ppm), MH+: 2365.23868 Da, RT: 38.25 min,
Identified with: Sequest HT (v1.3); XCorr:2.73, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3
Protein references (1):
- Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]

#1	b^{+}	b^{2+}	b^{3+}	Seq.	y^{+}	y^{2+}	y^{3+}	#2
1	114.09135	57.54931	38.70197	L				22
2	215.13903	108.07315	72.38453	T	2252.15582	1126.58155	751.39012	21
3	328.22310	164.61519	110.07922	L	2151.10814	1076.05771	717.70756	20
4	491.28642	246.14685	164.43366	Y	2038.02407	1019.51567	680.01287	19
5	606.31337	303.66032	202.77597	D	1874.96075	937.98401	625.65843	18
6	719.39744	360.20236	240.47066	I	1759.93380	880.47054	587.31612	17
7	790.43456	395.72092	264.14970	A	1646.84973	823.92850	549.62143	16
8	927.49347	464.25037	309.83601	H	1575.81261	788.40994	525.94239	15
9	1028.54115	514.77421	343.51857	T	1438.75370	719.88049	480.25608	14
10	1125.59392	563.30060	375.86949	P	1337.70602	669.35665	446.57352	13
11	1182.61539	591.81133	394.87665	G	1240.65325	620.83026	414.22260	12
12	1281.68381	641.34554	427.89945	V	1183.63178	592.31953	395.21544	11
13	1352.72093	676.86410	451.57849	A	1084.56336	542.78532	362.19264	10
14	1423.75805	712.38266	475.25753	A	1013.52624	507.26676	338.51360	9
15	1538.78500	769.89614	513.59985	D	942.48912	471.74820	314.83456	8
16	1651.86907	826.43817	551.29454	L	827.46217	414.23472	276.49224	7
17	1738.90110	869.95419	580.30522	S	714.37810	357.69269	238.79755	6
18	1875.96001	938.48364	625.99152	H	627.34607	314.17667	209.78687	5
19	1989.04408	995.02568	663.68621	I	490.28716	245.64722	164.10057	4

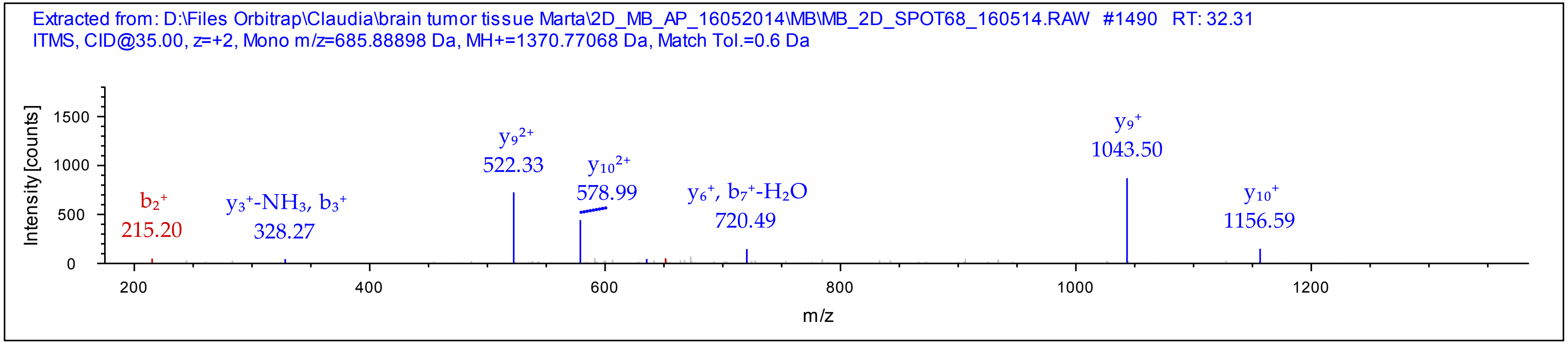
20	2118.08668	1059.54698	706.70041	E	377.20309	189.10518	126.40588	3
21	2219.13436	1110.07082	740.38297	T	248.16049	124.58388	83.39168	2
22				K	147.11281	74.06004	49.70912	1



Sequence: TIIPLISQCTPK, C9-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 685.88898 Da (-0.29 mmu/-0.42 ppm), MH+: 1370.77068 Da, RT: 32.31 min,
Identified with: Sequest HT (v1.3); XCorr:2.63, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]

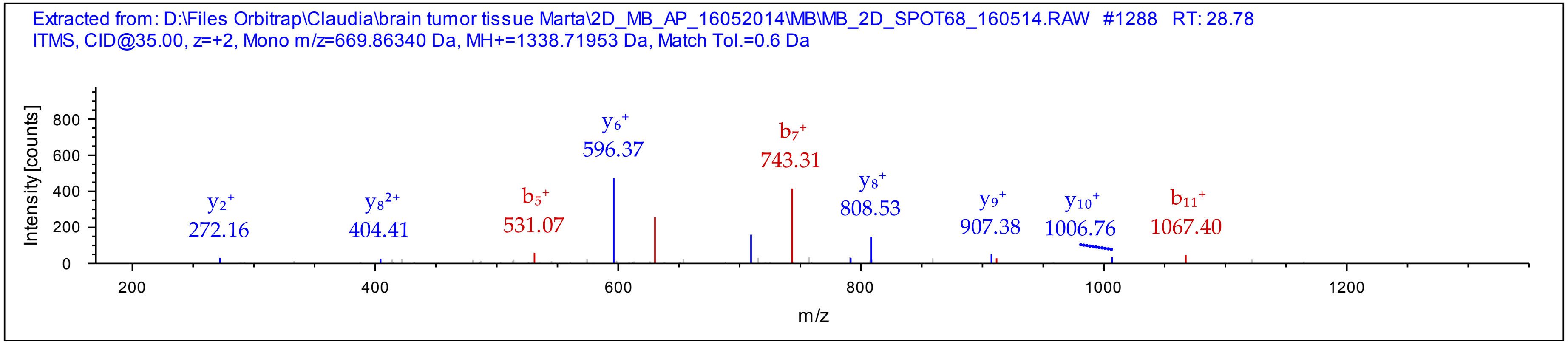
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	102.05496	51.53112	T			12
2	215.13903	108.07315	I	1269.72358	635.36543	11
3	328.22310	164.61519	I	1156.63951	578.82339	10
4	425.27587	213.14157	P	1043.55544	522.28136	9
5	538.35994	269.68361	L	946.50267	473.75497	8
6	651.44401	326.22564	I	833.41860	417.21294	7
7	738.47604	369.74166	S	720.33453	360.67090	6
8	866.53462	433.77095	Q	633.30250	317.15489	5
9	1026.56527	513.78627	C-Carbamidomethyl	505.24392	253.12560	4
10	1127.61295	564.31011	T	345.21326	173.11027	3
11	1224.66572	612.83650	P	244.16558	122.58643	2
12			K	147.11281	74.06004	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT68_160514.RAW #1490 RT: 32.31
ITMS, CID@35.00, z=+2, Mono m/z=685.88898 Da, MH+=1370.77068 Da, Match Tol.=0.6 Da

Sequence: GCDVVVIPAGVPR, C2-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 669.86340 Da (-0.19 mmu/-0.29 ppm), MH+: 1338.71953 Da, RT: 28.78 min,
Identified with: Sequest HT (v1.3); XCorr:2.56, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]

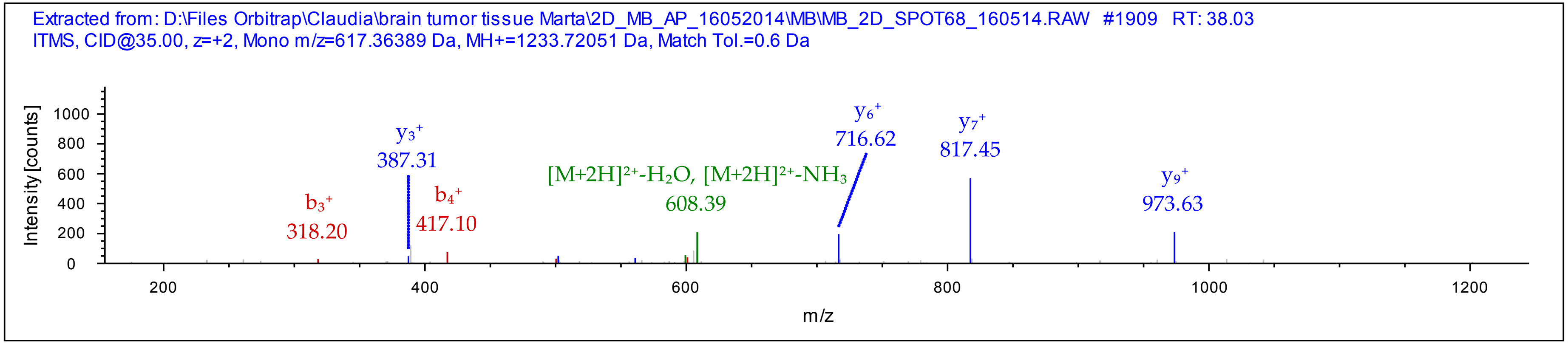
#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	58.02875	29.51801	G			13
2	218.05940	109.53334	C-Carbamidomethyl	1281.69845	641.35286	12
3	333.08635	167.04681	D	1121.66779	561.33753	11
4	432.15477	216.58102	V	1006.64084	503.82406	10
5	531.22319	266.11523	V	907.57242	454.28985	9
6	630.29161	315.64944	V	808.50400	404.75564	8
7	743.37568	372.19148	I	709.43558	355.22143	7
8	840.42845	420.71786	P	596.35151	298.67939	6
9	911.46557	456.23642	A	499.29874	250.15301	5
10	968.48704	484.74716	G	428.26162	214.63445	4
11	1067.55546	534.28137	V	371.24015	186.12371	3
12	1164.60823	582.80775	P	272.17173	136.58950	2
13			R	175.11896	88.06312	1



Sequence: IFGVTTLDIVR, Charge: +2, Monoisotopic m/z: 617.36389 Da (+0.15 mmu/+0.24 ppm), MH+: 1233.72051 Da, RT: 38.03 min,
Identified with: Sequest HT (v1.3); XCorr:2.52, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]

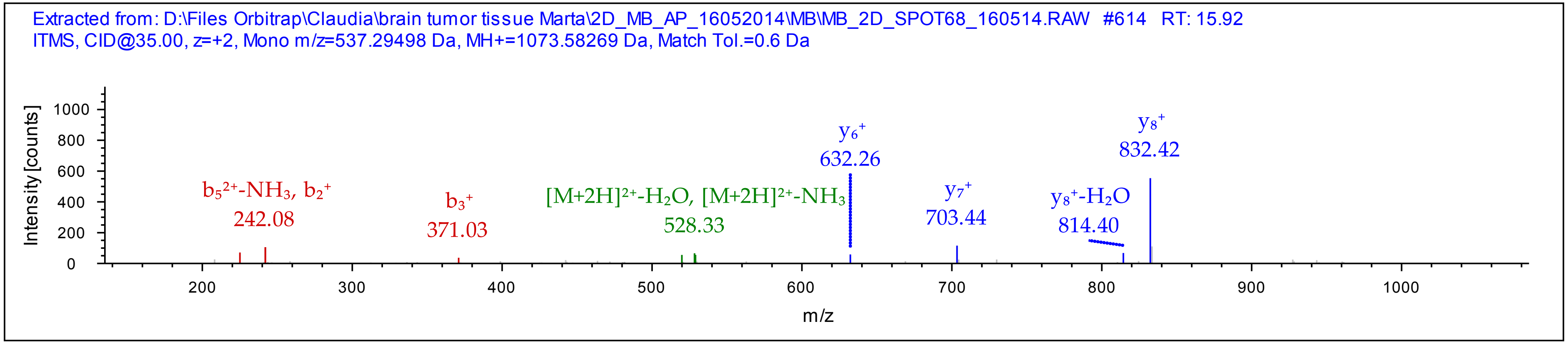
#1	**b^{+}**	**b^{2+}**	**Seq.**	**y^{+}**	**y^{2+}**	**#2**
1	114.09135	57.54931	I			11
2	261.15977	131.08352	F	1120.63614	560.82171	10
3	318.18124	159.59426	G	973.56772	487.28750	9
4	417.24966	209.12847	V	916.54625	458.77676	8
5	518.29734	259.65231	T	817.47783	409.24255	7
6	619.34502	310.17615	T	716.43015	358.71871	6
7	732.42909	366.71818	L	615.38247	308.19487	5
8	847.45604	424.23166	D	502.29840	251.65284	4
9	960.54011	480.77369	I	387.27145	194.13936	3
10	1059.60853	530.30790	V	274.18738	137.59733	2
11			R	175.11896	88.06312	1



Sequence: IQEAGTEVVK, Charge: +2, Monoisotopic m/z: 537.29498 Da (-0.54 mmu/-1.01 ppm), MH+: 1073.58269 Da, RT: 15.92 min,
Identified with: Sequest HT (v1.3); XCorr:2.15, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	114.09135	57.54931	I			10
2	242.14993	121.57860	Q	960.49970	480.75349	9
3	371.19253	186.09990	E	832.44112	416.72420	8
4	442.22965	221.61846	A	703.39852	352.20290	7
5	499.25112	250.12920	G	632.36140	316.68434	6
6	600.29880	300.65304	T	575.33993	288.17360	5
7	729.34140	365.17434	E	474.29225	237.64976	4
8	828.40982	414.70855	V	345.24965	173.12846	3
9	927.47824	464.24276	V	246.18123	123.59425	2
10			K	147.11281	74.06004	1

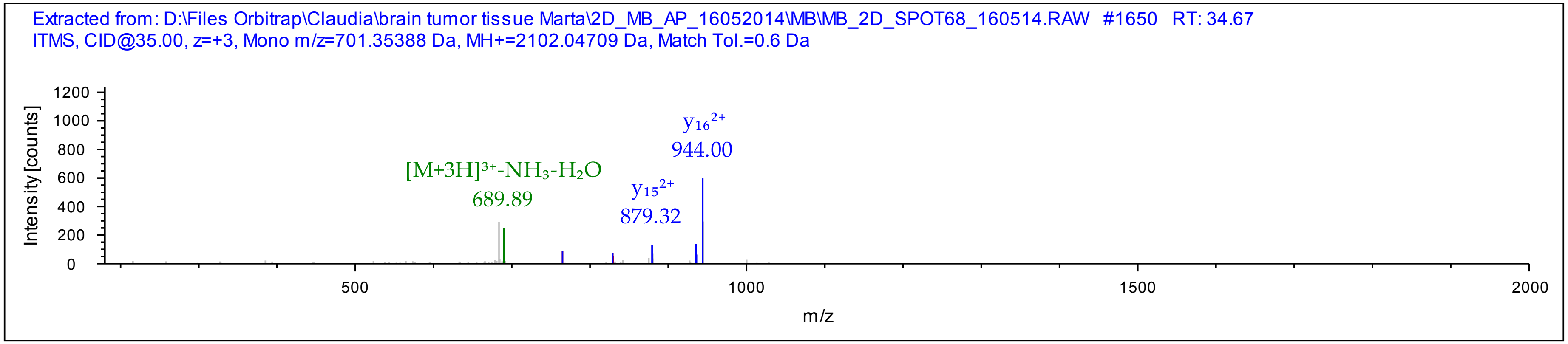


Sequence: SQETECTYFSTPLLLGKK, C6-Carbamidomethyl (57.02146 Da)
Charge: +3, Monoisotopic m/z: 701.35388 Da (-0.14 mmu/-0.2 ppm), MH+: 2102.04709 Da, RT: 34.67 min,
Identified with: Sequest HT (v1.3); XCorr:2.10, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	88.03931	44.52329	30.01795	S				18
2	216.09789	108.55258	72.70415	Q	2015.01548	1008.01138	672.34334	17
3	345.14049	173.07388	115.71835	E	1886.95690	943.98209	629.65715	16
4	446.18817	223.59772	149.40091	T	1757.91430	879.46079	586.64295	15
5	575.23077	288.11902	192.41511	E	1656.86662	828.93695	552.96039	14
6	735.26142	368.13435	245.75866	C-Carbamidomethyl	1527.82402	764.41565	509.94619	13
7	836.30910	418.65819	279.44122	T	1367.79336	684.40032	456.60264	12
8	999.37242	500.18985	333.79566	Y	1266.74568	633.87648	422.92008	11
9	1146.44084	573.72406	382.81846	F	1103.68236	552.34482	368.56564	10
10	1233.47287	617.24007	411.82914	S	956.61394	478.81061	319.54283	9
11	1334.52055	667.76391	445.51170	T	869.58191	435.29459	290.53215	8
12	1431.57332	716.29030	477.86262	P	768.53423	384.77075	256.84959	7
13	1544.65739	772.83233	515.55731	L	671.48146	336.24437	224.49867	6
14	1657.74146	829.37437	553.25200	L	558.39739	279.70233	186.80398	5
15	1770.82553	885.91640	590.94669	L	445.31332	223.16030	149.10929	4
16	1827.84700	914.42714	609.95385	G	332.22925	166.61826	111.41460	3
17	1955.94197	978.47462	652.65217	K	275.20778	138.10753	92.40744	2

18				K	147.11281	74.06004	49.70912	1

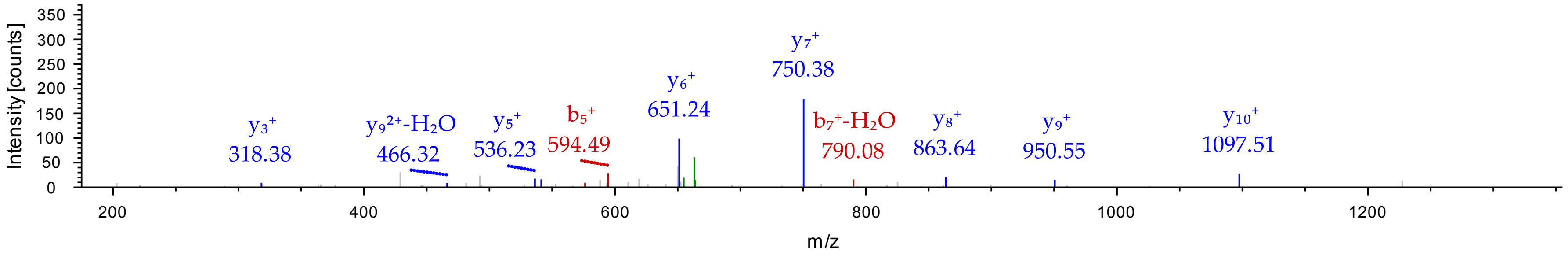


Sequence: FVFSLVDAMNGK, M9-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 672.33630 Da (-0.57 mmu/-0.85 ppm), MH+: 1343.66533 Da, RT: 34.90 min,
Identified with: Sequest HT (v1.3); XCorr:2.09, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; $b-H_2O$; $b-NH_3$; y; $y-H_2O$; $y-NH_3$

Protein references (1):
- Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	148.07570	74.54149	F			12
2	247.14412	124.07570	V	1196.59806	598.80267	11
3	394.21254	197.60991	F	1097.52964	549.26846	10
4	481.24457	241.12592	S	950.46122	475.73425	9
5	594.32864	297.66796	L	863.42919	432.21823	8
6	693.39706	347.20217	V	750.34512	375.67620	7
7	808.42401	404.71564	D	651.27670	326.14199	6
8	879.46113	440.23420	A	536.24975	268.62851	5
9	1026.49654	513.75191	M-Oxidation	465.21263	233.10995	4
10	1140.53947	570.77337	N	318.17721	159.59224	3
11	1197.56094	599.28411	G	204.13428	102.57078	2
12			K	147.11281	74.06004	1

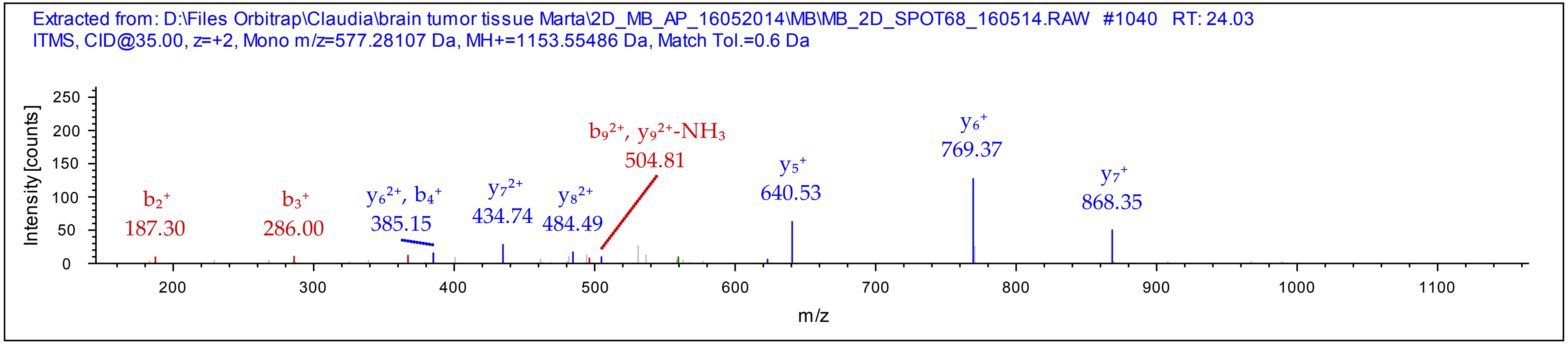
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT68_160514.RAW #1671 RT: 34.90
ITMS, CID@35.00, z=+2, Mono m/z=672.33630 Da, MH+=1343.66533 Da, Match Tol.=0.6 Da



Sequence: EGVVECSFVK, C6-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 577.28107 Da (-0.49 mmu/-0.86 ppm), MH+: 1153.55486 Da, RT: 24.03 min,
Identified with: Sequest HT (v1.3); XCorr:2.03, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	130.04988	65.52858	E			10
2	187.07135	94.03931	G	1024.51325	512.76026	9
3	286.13977	143.57352	V	967.49178	484.24953	8
4	385.20819	193.10773	V	868.42336	434.71532	7
5	514.25079	257.62903	E	769.35494	385.18111	6
6	674.28144	337.64436	C-Carbamidomethyl	640.31234	320.65981	5
7	761.31347	381.16037	S	480.28168	240.64448	4
8	908.38189	454.69458	F	393.24965	197.12846	3
9	1007.45031	504.22879	V	246.18123	123.59425	2
10			K	147.11281	74.06004	1



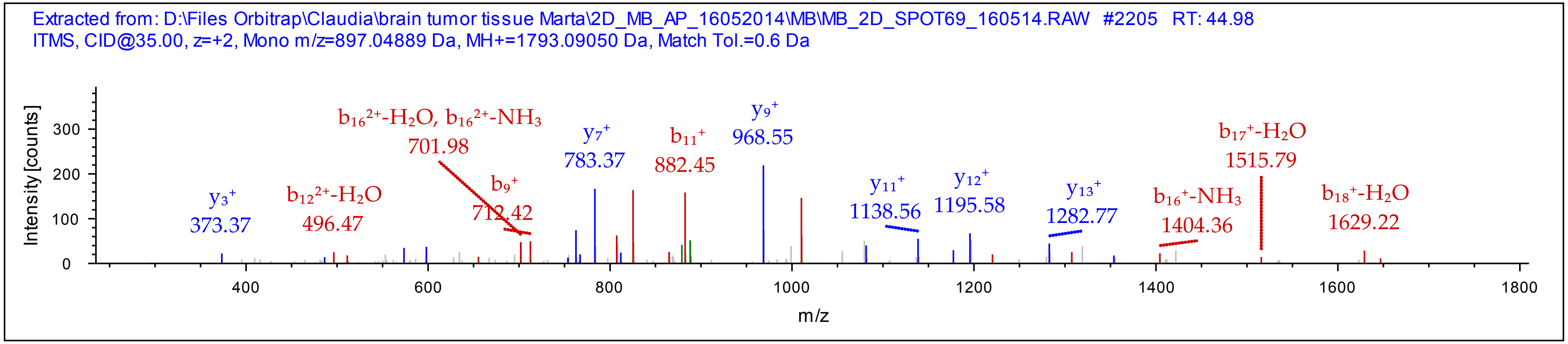
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT68_160514.RAW #1040 RT: 24.03
ITMS, CID@35.00, z=+2, Mono m/z=577.28107 Da, MH+=1153.55486 Da, Match Tol.=0.6 Da

Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
69	P40926	Malate dehydrogenase, mitochondrial	32.9	8.5	89.68	36.69%	8	8	MB	2.00E-03	2.9	↑ in MB

Sequence: VAVLGASGGIGQPLSLLLK, Charge: +2, Monoisotopic m/z: 897.04889 Da (+0.45 mmu/+0.5 ppm), MH+: 1793.09050 Da, RT: 44.98 min,
Identified with: Sequest HT (v1.3); XCorr:4.08, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	100.07570	50.54149	V			19
2	171.11282	86.06005	A	1694.02118	847.51423	18
3	270.18124	135.59426	V	1622.98406	811.99567	17
4	383.26531	192.13629	L	1523.91564	762.46146	16
5	440.28678	220.64703	G	1410.83157	705.91942	15
6	511.32390	256.16559	A	1353.81010	677.40869	14
7	598.35593	299.68160	S	1282.77298	641.89013	13
8	655.37740	328.19234	G	1195.74095	598.37411	12
9	712.39887	356.70307	G	1138.71948	569.86338	11
10	825.48294	413.24511	I	1081.69801	541.35264	10
11	882.50441	441.75584	G	968.61394	484.81061	9
12	1010.56299	505.78513	Q	911.59247	456.29987	8
13	1107.61576	554.31152	P	783.53389	392.27058	7
14	1220.69983	610.85355	L	686.48112	343.74420	6
15	1307.73186	654.36957	S	573.39705	287.20216	5
16	1420.81593	710.91160	L	486.36502	243.68615	4
17	1533.90000	767.45364	L	373.28095	187.14411	3
18	1646.98407	823.99567	L	260.19688	130.60208	2
19			K	147.11281	74.06004	1

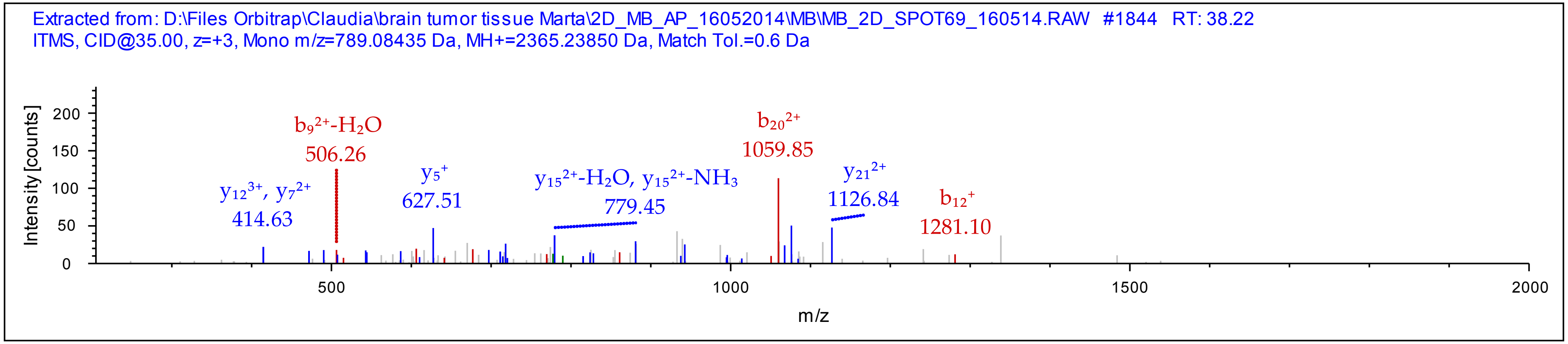


Sequence: LTLYDIAHTPGVAADLSHIETK, Charge: +3, Monoisotopic m/z: 789.08435 Da (-0.46 mmu/-0.59 ppm), MH+: 2365.23850 Da, RT: 38.22 min,
Identified with: Sequest HT (v1.3); XCorr:3.58, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	114.09135	57.54931	38.70197	L				22
2	215.13903	108.07315	72.38453	T	2252.15582	1126.58155	751.39012	21
3	328.22310	164.61519	110.07922	L	2151.10814	1076.05771	717.70756	20
4	491.28642	246.14685	164.43366	Y	2038.02407	1019.51567	680.01287	19
5	606.31337	303.66032	202.77597	D	1874.96075	937.98401	625.65843	18
6	719.39744	360.20236	240.47066	I	1759.93380	880.47054	587.31612	17
7	790.43456	395.72092	264.14970	A	1646.84973	823.92850	549.62143	16
8	927.49347	464.25037	309.83601	H	1575.81261	788.40994	525.94239	15
9	1028.54115	514.77421	343.51857	T	1438.75370	719.88049	480.25608	14
10	1125.59392	563.30060	375.86949	P	1337.70602	669.35665	446.57352	13
11	1182.61539	591.81133	394.87665	G	1240.65325	620.83026	414.22260	12
12	1281.68381	641.34554	427.89945	V	1183.63178	592.31953	395.21544	11
13	1352.72093	676.86410	451.57849	A	1084.56336	542.78532	362.19264	10
14	1423.75805	712.38266	475.25753	A	1013.52624	507.26676	338.51360	9
15	1538.78500	769.89614	513.59985	D	942.48912	471.74820	314.83456	8
16	1651.86907	826.43817	551.29454	L	827.46217	414.23472	276.49224	7
17	1738.90110	869.95419	580.30522	S	714.37810	357.69269	238.79755	6
18	1875.96001	938.48364	625.99152	H	627.34607	314.17667	209.78687	5

19	1989.04408	995.02568	663.68621	I	490.28716	245.64722	164.10057	4
20	2118.08668	1059.54698	706.70041	E	377.20309	189.10518	126.40588	3
21	2219.13436	1110.07082	740.38297	T	248.16049	124.58388	83.39168	2
22				K	147.11281	74.06004	49.70912	1

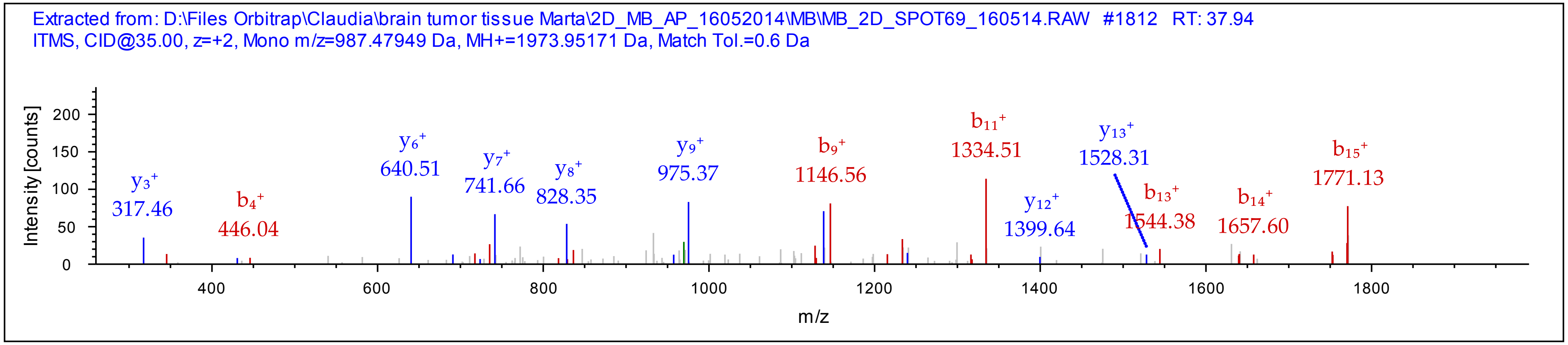


Sequence: SQETECTYFSTPLLLGK, C6-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 987.47949 Da (-0.41 mmu/-0.42 ppm), MH+: 1973.95171 Da, RT: 37.94 min,
Identified with: Sequest HT (v1.3); XCorr:3.50, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]

#1	b⁺	b²⁺	Seq.	y⁺	y²⁺	#2
1	88.03931	44.52329	S			17
2	216.09789	108.55258	Q	1886.92051	943.96389	16
3	345.14049	173.07388	E	1758.86193	879.93460	15
4	446.18817	223.59772	T	1629.81933	815.41330	14
5	575.23077	288.11902	E	1528.77165	764.88946	13
6	735.26142	368.13435	C-Carbamidomethyl	1399.72905	700.36816	12
7	836.30910	418.65819	T	1239.69839	620.35283	11
8	999.37242	500.18985	Y	1138.65071	569.82899	10
9	1146.44084	573.72406	F	975.58739	488.29733	9
10	1233.47287	617.24007	S	828.51897	414.76312	8
11	1334.52055	667.76391	T	741.48694	371.24711	7
12	1431.57332	716.29030	P	640.43926	320.72327	6
13	1544.65739	772.83233	L	543.38649	272.19688	5

14	1657.74146	829.37437	L	430.30242	215.65485	4
15	1770.82553	885.91640	L	317.21835	159.11281	3
16	1827.84700	914.42714	G	204.13428	102.57078	2
17			K	147.11281	74.06004	1

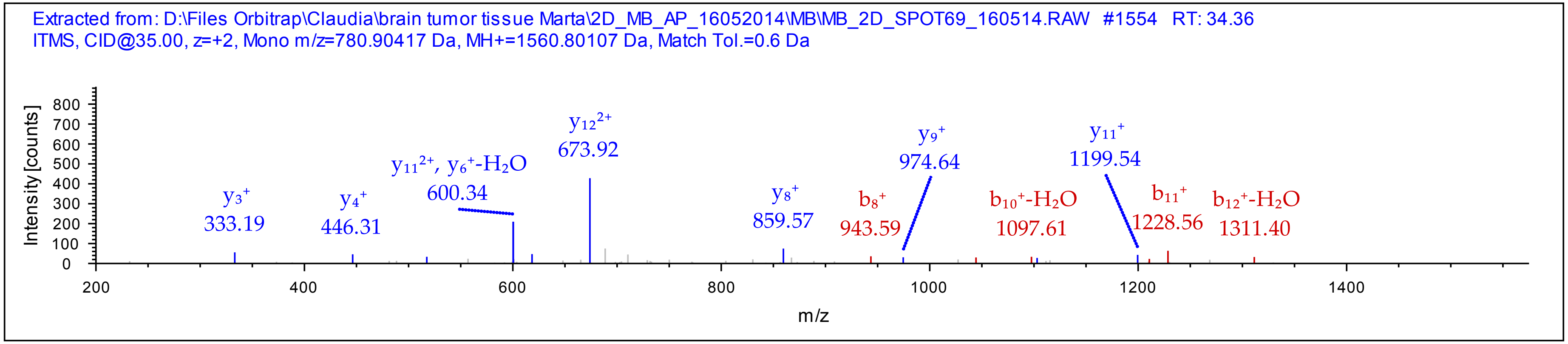


Sequence: VDFPQDQLTALTGR, Charge: +2, Monoisotopic m/z: 780.90417 Da (-0.32 mmu/-0.42 ppm), MH+: 1560.80107 Da, RT: 34.36 min,
Identified with: Sequest HT (v1.3); XCorr:2.83, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]

#1	b⁺	b²⁺	Seq.	y⁺	y²⁺	#2
1	100.07570	50.54149	V			14
2	215.10265	108.05496	D	1461.73330	731.37029	13
3	362.17107	181.58917	F	1346.70635	673.85681	12
4	459.22384	230.11556	P	1199.63793	600.32260	11
5	587.28242	294.14485	Q	1102.58516	551.79622	10
6	702.30937	351.65832	D	974.52658	487.76693	9
7	830.36795	415.68761	Q	859.49963	430.25345	8
8	943.45202	472.22965	L	731.44105	366.22416	7
9	1044.49970	522.75349	T	618.35698	309.68213	6
10	1115.53682	558.27205	A	517.30930	259.15829	5
11	1228.62089	614.81408	L	446.27218	223.63973	4
12	1329.66857	665.33792	T	333.18811	167.09769	3
13	1386.69004	693.84866	G	232.14043	116.57385	2

14			R	175.11896	88.06312	1



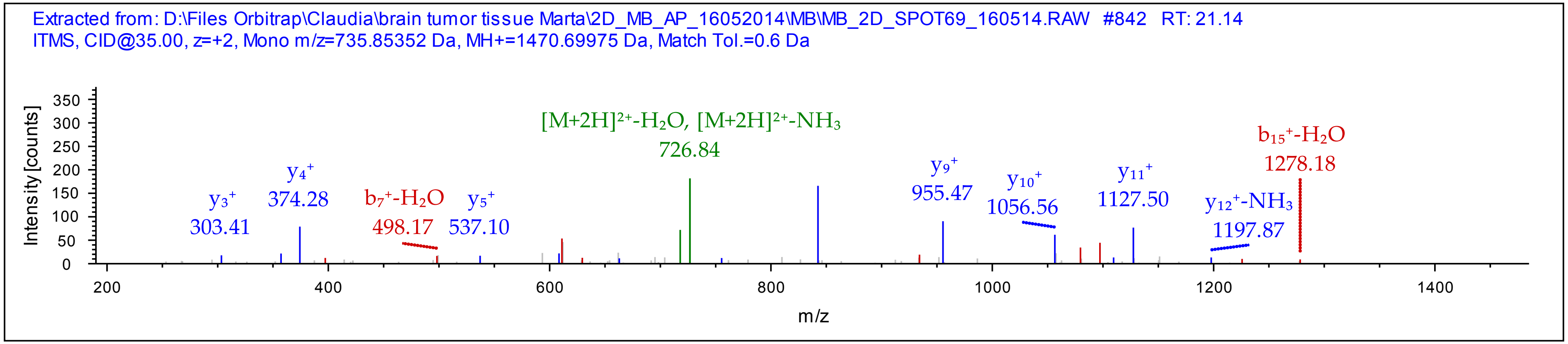
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT69_160514.RAW #1554 RT: 34.36
ITMS, CID@35.00, z=+2, Mono m/z=780.90417 Da, MH+=1560.80107 Da, Match Tol.=0.6 Da

Sequence: AGAGSATLSMAYAGAR, M10-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 735.85352 Da (-0.44 mmu/-0.6 ppm), MH+: 1470.69975 Da, RT: 21.14 min,
Identified with: Sequest HT (v1.3); XCorr:2.52, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	72.04440	36.52584	A			16
2	129.06587	65.03657	G	1399.66352	700.33540	15
3	200.10299	100.55513	A	1342.64205	671.82466	14
4	257.12446	129.06587	G	1271.60493	636.30610	13
5	344.15649	172.58188	S	1214.58346	607.79537	12
6	415.19361	208.10044	A	1127.55143	564.27935	11
7	516.24129	258.62428	T	1056.51431	528.76079	10
8	629.32536	315.16632	L	955.46663	478.23695	9
9	716.35739	358.68233	S	842.38256	421.69492	8
10	863.39280	432.20004	M-Oxidation	755.35053	378.17890	7
11	934.42992	467.71860	A	608.31511	304.66119	6
12	1097.49324	549.25026	Y	537.27799	269.14263	5
13	1168.53036	584.76882	A	374.21467	187.61097	4
14	1225.55183	613.27955	G	303.17755	152.09241	3
15	1296.58895	648.79811	A	246.15608	123.58168	2

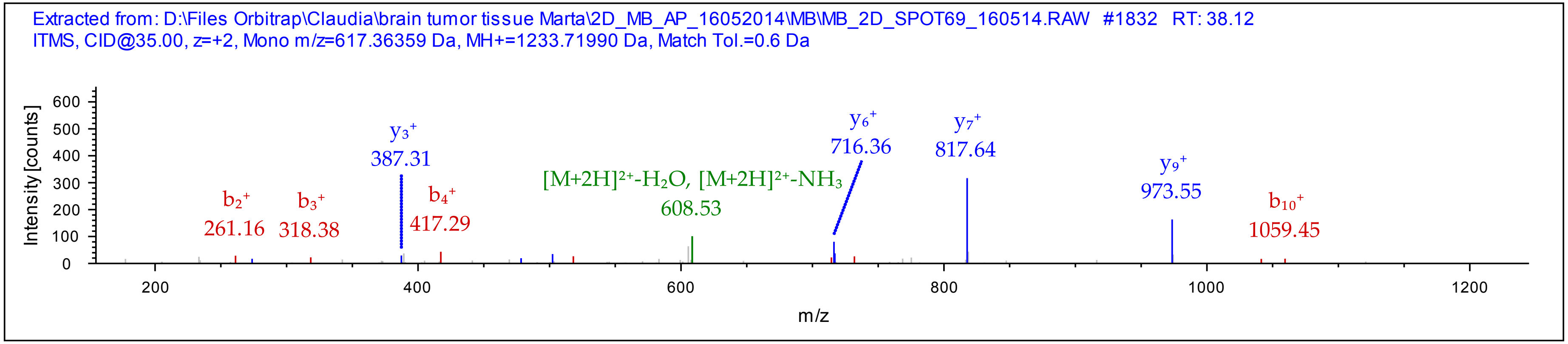
16			R	175.11896	88.06312	1



Sequence: IFGVTTLDIVR, Charge: +2, Monoisotopic m/z: 617.36359 Da (-0.16 mmu/-0.26 ppm), MH+: 1233.71990 Da, RT: 38.12 min,
Identified with: Sequest HT (v1.3); XCorr:2.49, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]

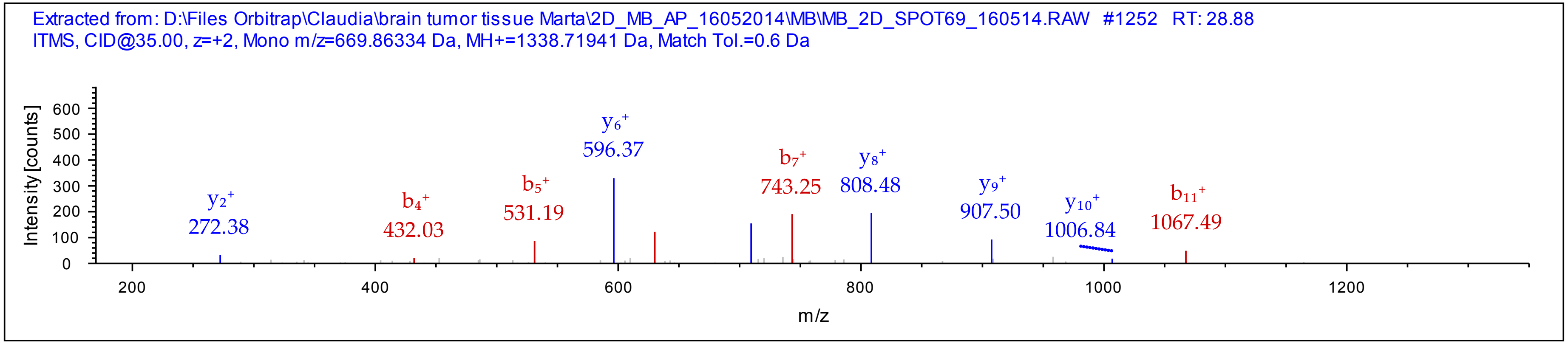
#1	b$^+$	b^{2+}	Seq.	y$^+$	y^{2+}	#2
1	114.09135	57.54931	I			11
2	261.15977	131.08352	F	1120.63614	560.82171	10
3	318.18124	159.59426	G	973.56772	487.28750	9
4	417.24966	209.12847	V	916.54625	458.77676	8
5	518.29734	259.65231	T	817.47783	409.24255	7
6	619.34502	310.17615	T	716.43015	358.71871	6
7	732.42909	366.71818	L	615.38247	308.19487	5
8	847.45604	424.23166	D	502.29840	251.65284	4
9	960.54011	480.77369	I	387.27145	194.13936	3
10	1059.60853	530.30790	V	274.18738	137.59733	2
11			R	175.11896	88.06312	1



Sequence: GCDVVVIPAGVPR, C2-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 669.86334 Da (-0.25 mmu/-0.38 ppm), MH+: 1338.71941 Da, RT: 28.88 min,
Identified with: Sequest HT (v1.3); XCorr:2.45, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]

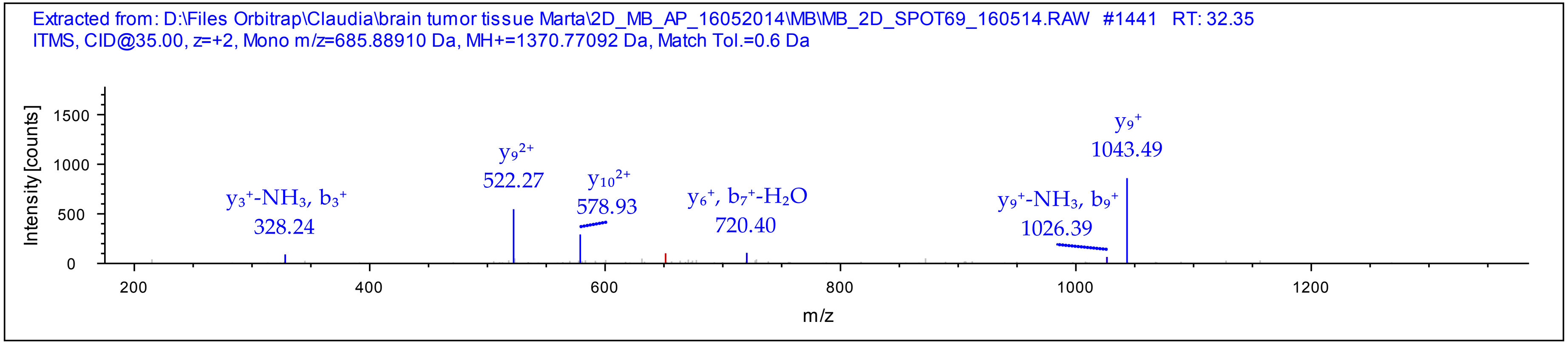
#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	58.02875	29.51801	G			13
2	218.05940	109.53334	C-Carbamidomethyl	1281.69845	641.35286	12
3	333.08635	167.04681	D	1121.66779	561.33753	11
4	432.15477	216.58102	V	1006.64084	503.82406	10
5	531.22319	266.11523	V	907.57242	454.28985	9
6	630.29161	315.64944	V	808.50400	404.75564	8
7	743.37568	372.19148	I	709.43558	355.22143	7
8	840.42845	420.71786	P	596.35151	298.67939	6
9	911.46557	456.23642	A	499.29874	250.15301	5
10	968.48704	484.74716	G	428.26162	214.63445	4
11	1067.55546	534.28137	V	371.24015	186.12371	3
12	1164.60823	582.80775	P	272.17173	136.58950	2
13			R	175.11896	88.06312	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT69_160514.RAW #1252 RT: 28.88
ITMS, CID@35.00, z=+2, Mono m/z=669.86334 Da, MH+=1338.71941 Da, Match Tol.=0.6 Da

Sequence: TIIPLISQCTPK, C9-Carbamidomethyl (57.02146 Da)
Charge: +2, Monoisotopic m/z: 685.88910 Da (-0.17 mmu/-0.24 ppm), MH+: 1370.77092 Da, RT: 32.35 min,
Identified with: Sequest HT (v1.3); XCorr:2.03, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	102.05496	51.53112	T			12
2	215.13903	108.07315	I	1269.72358	635.36543	11
3	328.22310	164.61519	I	1156.63951	578.82339	10
4	425.27587	213.14157	P	1043.55544	522.28136	9
5	538.35994	269.68361	L	946.50267	473.75497	8
6	651.44401	326.22564	I	833.41860	417.21294	7
7	738.47604	369.74166	S	720.33453	360.67090	6
8	866.53462	433.77095	Q	633.30250	317.15489	5
9	1026.56527	513.78627	C-Carbamidomethyl	505.24392	253.12560	4
10	1127.61295	564.31011	T	345.21326	173.11027	3
11	1224.66572	612.83650	P	244.16558	122.58643	2
12			K	147.11281	74.06004	1



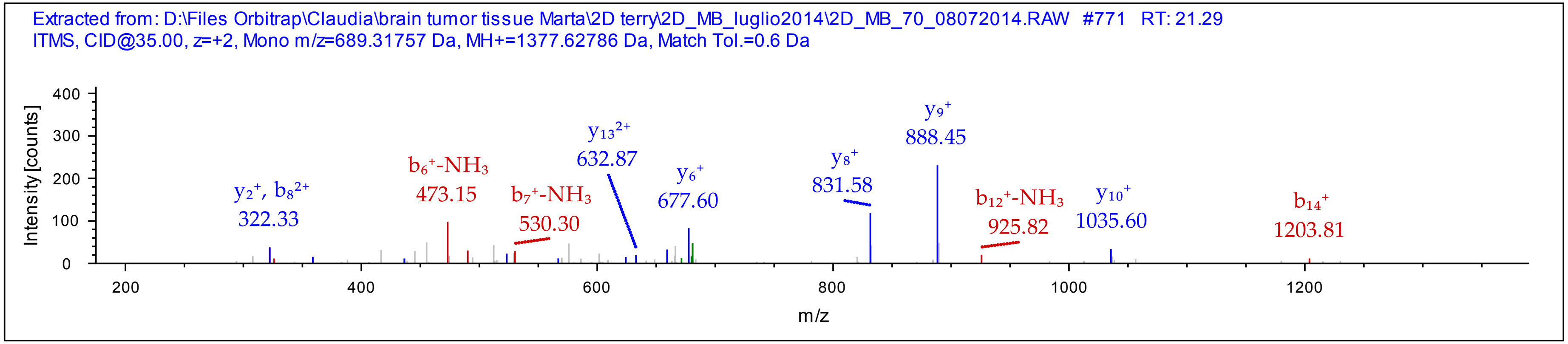
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT69_160514.RAW #1441 RT: 32.35
ITMS, CID@35.00, z=+2, Mono m/z=685.88910 Da, MH+=1370.77092 Da, Match Tol.=0.6 Da

Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
70	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	37.4	9.0	11.4	7.08%	2	2	MB	9.86E-05	6.0	↑ in MB

Sequence: GGGGNFGPGPGSNFR, Charge: +2, Monoisotopic m/z: 689.31757 Da (-0.83 mmu/-1.21 ppm), MH+: 1377.62786 Da, RT: 21.29 min,
Identified with: Sequest HT (v1.3); XCorr:2.17, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	58.02875	29.51801	G			15
2	115.05022	58.02875	G	1320.60805	660.80766	14
3	172.07169	86.53948	G	1263.58658	632.29693	13
4	229.09316	115.05022	G	1206.56511	603.78619	12
5	343.13609	172.07168	N	1149.54364	575.27546	11
6	490.20451	245.60589	F	1035.50071	518.25399	10
7	547.22598	274.11663	G	888.43229	444.71978	9
8	644.27875	322.64301	P	831.41082	416.20905	8
9	701.30022	351.15375	G	734.35805	367.68266	7
10	798.35299	399.68013	P	677.33658	339.17193	6
11	855.37446	428.19087	G	580.28381	290.64554	5
12	942.40649	471.70688	S	523.26234	262.13481	4
13	1056.44942	528.72835	N	436.23031	218.61879	3
14	1203.51784	602.26256	F	322.18738	161.59733	2
15			R	175.11896	88.06312	1

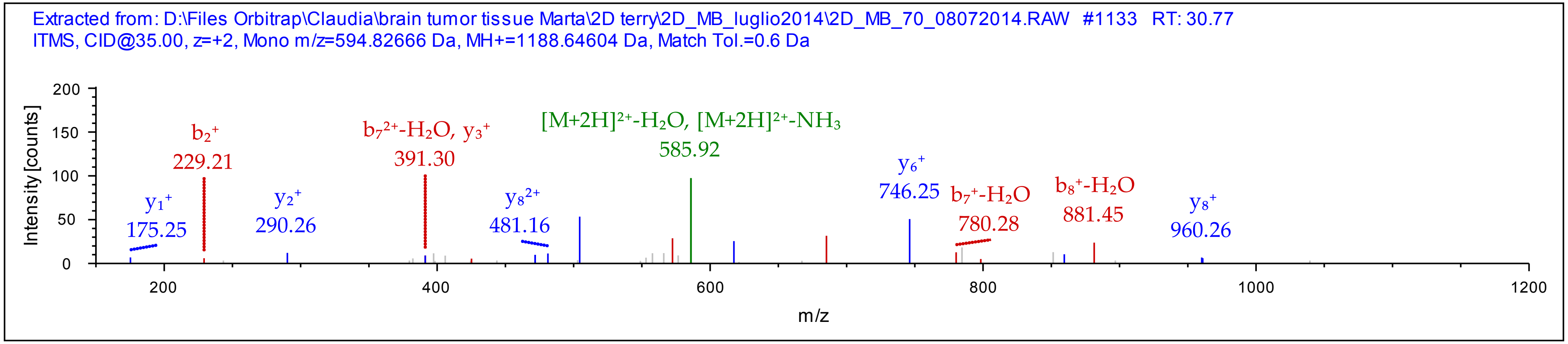


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_MB_luglio2014\2D_MB_70_08072014.RAW #771 RT: 21.29
ITMS, CID@35.00, z=+2, Mono m/z=689.31757 Da, MH+=1377.62786 Da, Match Tol.=0.6 Da

Sequence: IDTIEIITDR, Charge: +2, Monoisotopic m/z: 594.82666 Da (-0.53 mmu/-0.89 ppm), MH+: 1188.64604 Da, RT: 30.77 min,
Identified with: Sequest HT (v1.3); XCorr:1.78, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	114.09135	57.54931	I			10
2	229.11830	115.06279	D	1075.56303	538.28515	9
3	330.16598	165.58663	T	960.53608	480.77168	8
4	443.25005	222.12866	I	859.48840	430.24784	7
5	572.29265	286.64996	E	746.40433	373.70580	6
6	685.37672	343.19200	I	617.36173	309.18450	5
7	798.46079	399.73403	I	504.27766	252.64247	4
8	899.50847	450.25787	T	391.19359	196.10043	3
9	1014.53542	507.77135	D	290.14591	145.57659	2
10			R	175.11896	88.06312	1

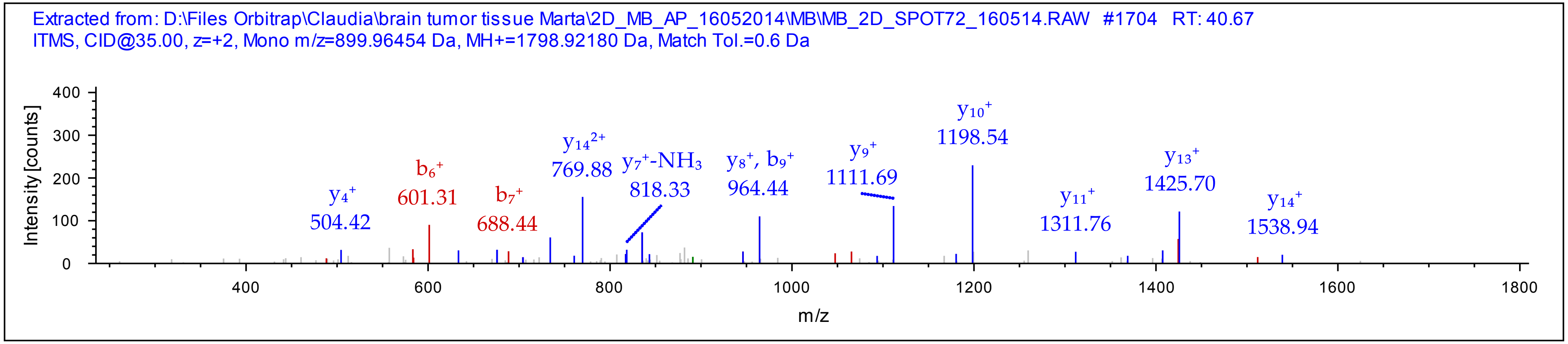

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D terry\2D_MB_luglio2014\2D_MB_70_08072014.RAW #1133 RT: 30.77
ITMS, CID@35.00, z=+2, Mono m/z=594.82666 Da, MH+=1188.64604 Da, Match Tol.=0.6 Da
Intensity [counts]
200
150
100
50
0
y_1^+
175.25
b_2^+
229.21
y_2^+
290.26
b_7^{2+}-H_2O, y_3^+
391.30
y_8^{2+}
481.16
$[M+2H]^{2+}$-H_2O, $[M+2H]^{2+}$-NH_3
585.92
y_6^+
746.25
b_7^+-H_2O
780.28
b_8^+-H_2O
881.45
y_8^+
960.26
200
400
600
800
1000
1200
m/z

Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*	
72	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	37.4	9.0	69.0	37.11%	8	8	MB	1.40E-02	2.8	↑ in MB

Sequence: LFIGGLSFETTEESLR, Charge: +2, Monoisotopic m/z: 899.96454 Da (-0.22 mmu/-0.25 ppm), MH+: 1798.92180 Da, RT: 40.67 min,
Identified with: Sequest HT (v1.3); XCorr:3.23, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	114.09135	57.54931	L			16
2	261.15977	131.08352	F	1685.83817	843.42272	15
3	374.24384	187.62556	I	1538.76975	769.88851	14
4	431.26531	216.13629	G	1425.68568	713.34648	13
5	488.28678	244.64703	G	1368.66421	684.83574	12
6	601.37085	301.18906	L	1311.64274	656.32501	11
7	688.40288	344.70508	S	1198.55867	599.78297	10
8	835.47130	418.23929	F	1111.52664	556.26696	9
9	964.51390	482.76059	E	964.45822	482.73275	8
10	1065.56158	533.28443	T	835.41562	418.21145	7
11	1166.60926	583.80827	T	734.36794	367.68761	6
12	1295.65186	648.32957	E	633.32026	317.16377	5
13	1424.69446	712.85087	E	504.27766	252.64247	4
14	1511.72649	756.36688	S	375.23506	188.12117	3
15	1624.81056	812.90892	L	288.20303	144.60515	2
16			R	175.11896	88.06312	1

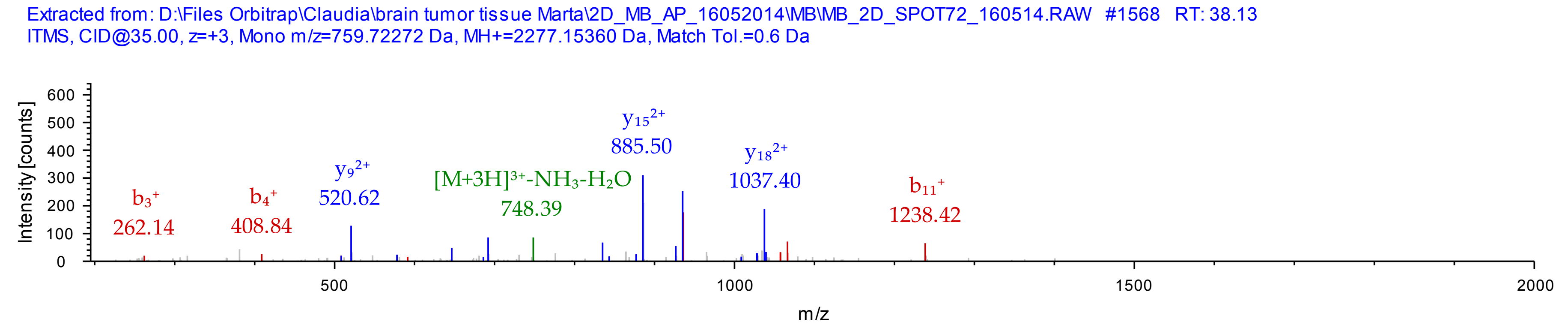


Sequence: GFGFVTFDDHDPVDKIVLQK, Charge: +3, Monoisotopic m/z: 759.72272 Da (-0.51 mmu/-0.67 ppm), MH+: 2277.15360 Da, RT: 38.13 min,
Identified with: Sequest HT (v1.3); XCorr:2.99, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	58.02875	29.51801	20.01443	G				20
2	205.09717	103.05222	69.03724	F	2220.13365	1110.57046	740.71607	19
3	262.11864	131.56296	88.04440	G	2073.06523	1037.03625	691.69326	18
4	409.18706	205.09717	137.06720	F	2016.04376	1008.52552	672.68610	17
5	508.25548	254.63138	170.09001	V	1868.97534	934.99131	623.66330	16
6	609.30316	305.15522	203.77257	T	1769.90692	885.45710	590.64049	15
7	756.37158	378.68943	252.79538	F	1668.85924	834.93326	556.95793	14
8	871.39853	436.20290	291.13769	D	1521.79082	761.39905	507.93512	13
9	986.42548	493.71638	329.48001	D	1406.76387	703.88557	469.59281	12
10	1123.48439	562.24583	375.16631	H	1291.73692	646.37210	431.25049	11
11	1238.51134	619.75931	413.50863	D	1154.67801	577.84264	385.56419	10
12	1335.56411	668.28569	445.85955	P	1039.65106	520.32917	347.22187	9
13	1434.63253	717.81990	478.88236	V	942.59829	471.80278	314.87095	8
14	1549.65948	775.33338	517.22468	D	843.52987	422.26857	281.84814	7
15	1677.75445	839.38086	559.92300	K	728.50292	364.75510	243.50582	6
16	1790.83852	895.92290	597.61769	I	600.40795	300.70761	200.80750	5
17	1889.90694	945.45711	630.64050	V	487.32388	244.16558	163.11281	4
18	2002.99101	1001.99914	668.33519	L	388.25546	194.63137	130.09000	3

19	2131.04959	1066.02843	711.02138	Q	275.17139	138.08933	92.39531	2
20				K	147.11281	74.06004	49.70912	1

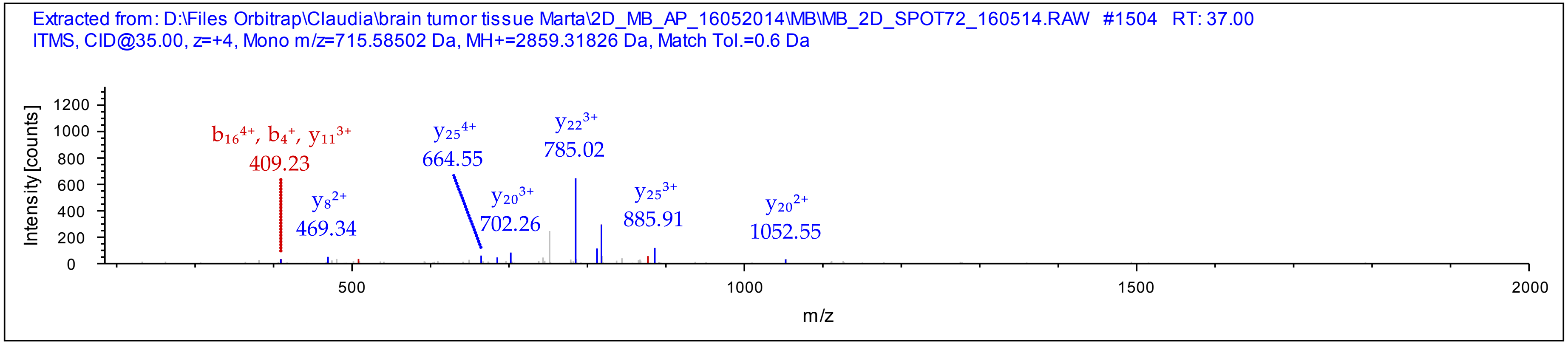


Sequence: GFGFVTFSSMAEVDAAMAARPHSIDGR, M10-Oxidation (15.99492 Da), M17-Oxidation (15.99492 Da)
Charge: +4, Monoisotopic m/z: 715.58502 Da (-0.2 mmu/-0.27 ppm), MH+: 2859.31826 Da, RT: 37.00 min,
Identified with: Sequest HT (v1.3); XCorr:2.81, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]

#1	b^+	b^{2+}	b^{3+}	b^{4+}	Seq.	y^+	y^{2+}	y^{3+}	y^{4+}	#2
1	58.02875	29.51801	20.01443	15.26264	G					27
2	205.09717	103.05222	69.03724	52.02975	F	2802.29757	1401.65242	934.77071	701.32985	26
3	262.11864	131.56296	88.04440	66.28512	G	2655.22915	1328.11821	885.74790	664.56275	25
4	409.18706	205.09717	137.06720	103.05222	F	2598.20768	1299.60748	866.74074	650.30738	24
5	508.25548	254.63138	170.09001	127.81933	V	2451.13926	1226.07327	817.71794	613.54027	23
6	609.30316	305.15522	203.77257	153.08125	T	2352.07084	1176.53906	784.69513	588.77317	22
7	756.37158	378.68943	252.79538	189.84835	F	2251.02316	1126.01522	751.01257	563.51125	21
8	843.40361	422.20544	281.80605	211.60636	S	2103.95474	1052.48101	701.98976	526.74414	20
9	930.43564	465.72146	310.81673	233.36437	S	2016.92271	1008.96499	672.97909	504.98614	19
10	1077.47105	539.23916	359.82853	270.12322	M-Oxidation	1929.89068	965.44898	643.96841	483.22813	18
11	1148.50817	574.75772	383.50757	287.88250	A	1782.85527	891.93127	594.95661	446.46927	17
12	1277.55077	639.27902	426.52177	320.14315	E	1711.81815	856.41271	571.27757	428.70999	16
13	1376.61919	688.81323	459.54458	344.91026	V	1582.77555	791.89141	528.26337	396.44934	15
14	1491.64614	746.32671	497.88690	373.66699	D	1483.70713	742.35720	495.24056	371.68224	14
15	1562.68326	781.84527	521.56594	391.42627	A	1368.68018	684.84373	456.89824	342.92550	13

16	1633.72038	817.36383	545.24498	409.18555	A	1297.64306	649.32517	433.21920	325.16622	12
17	1780.75580	890.88154	594.25678	445.94441	M-Oxidation	1226.60594	613.80661	409.54016	307.40694	11
18	1851.79292	926.40010	617.93582	463.70369	A	1079.57052	540.28890	360.52836	270.64809	10
19	1922.83004	961.91866	641.61486	481.46297	A	1008.53340	504.77034	336.84932	252.88881	9
20	2078.93116	1039.96922	693.64857	520.48825	R	937.49628	469.25178	313.17028	235.12953	8
21	2175.98393	1088.49560	725.99949	544.75144	P	781.39516	391.20122	261.13657	196.10425	7
22	2313.04284	1157.02506	771.68580	579.01617	H	684.34239	342.67483	228.78565	171.84106	6
23	2400.07487	1200.54107	800.69647	600.77417	S	547.28348	274.14538	183.09934	137.57633	5
24	2513.15894	1257.08311	838.39116	629.04519	I	460.25145	230.62936	154.08867	115.81832	4
25	2628.18589	1314.59658	876.73348	657.80193	D	347.16738	174.08733	116.39398	87.54730	3
26	2685.20736	1343.10732	895.74064	672.05730	G	232.14043	116.57385	78.05166	58.79057	2
27					R	175.11896	88.06312	59.04450	44.53520	1



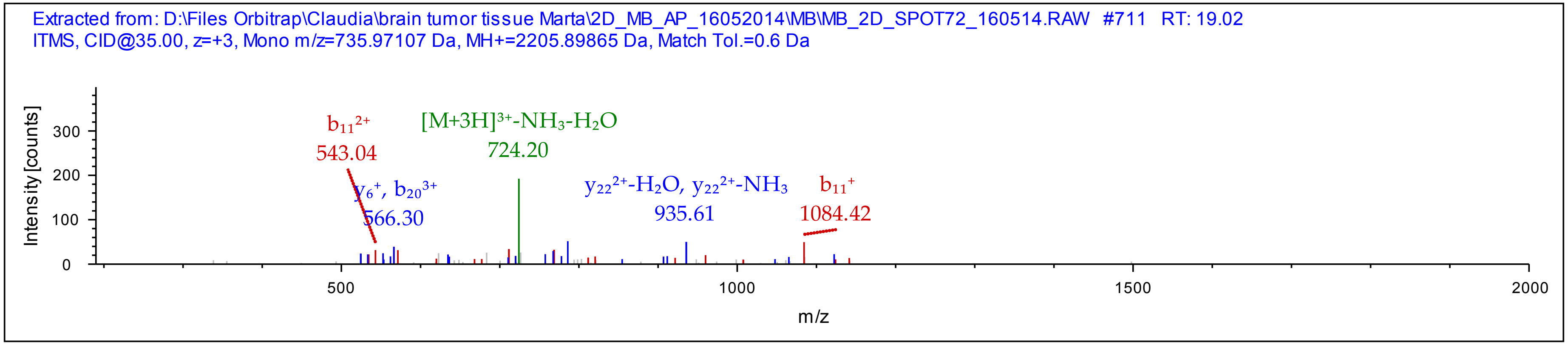
Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT72_160514.RAW #1504 RT: 37.00
ITMS, CID@35.00, z=+4, Mono m/z=715.58502 Da, MH+=2859.31826 Da, Match Tol.=0.6 Da

Sequence: NMGGPYGGGNYGPGGSGGSGGYGGR, M2-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 735.97107 Da (-0.57 mmu/-0.78 ppm), MH+: 2205.89865 Da, RT: 19.02 min,
Identified with: Sequest HT (v1.3); XCorr:2.52, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]

#1	**b^{+}**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^{+}**	**y^{2+}**	**y^{3+}**	**#2**
1	115.05021	58.02874	39.02159	N				25
2	262.08562	131.54645	88.03339	M-Oxidation	2091.85745	1046.43236	697.95733	24
3	319.10709	160.05718	107.04055	G	1944.82203	972.91465	648.94553	23
4	376.12856	188.56792	126.04770	G	1887.80056	944.40392	629.93837	22
5	473.18133	237.09430	158.39863	P	1830.77909	915.89318	610.93121	21

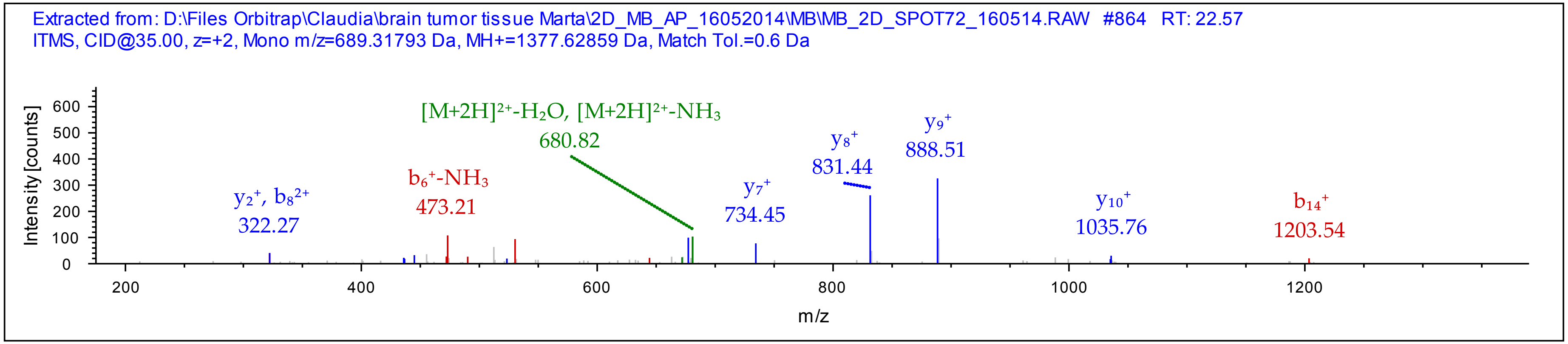
6	636.24465	318.62596	212.75307	Y	1733.72632	867.36680	578.58029	20
7	693.26612	347.13670	231.76022	G	1570.66300	785.83514	524.22585	19
8	750.28759	375.64743	250.76738	G	1513.64153	757.32440	505.21869	18
9	807.30906	404.15817	269.77454	G	1456.62006	728.81367	486.21154	17
10	921.35199	461.17963	307.78885	N	1399.59859	700.30293	467.20438	16
11	1084.41531	542.71129	362.14329	Y	1285.55566	643.28147	429.19007	15
12	1141.43678	571.22203	381.15044	G	1122.49234	561.74981	374.83563	14
13	1238.48955	619.74841	413.50137	P	1065.47087	533.23907	355.82847	13
14	1295.51102	648.25915	432.50852	G	968.41810	484.71269	323.47755	12
15	1352.53249	676.76988	451.51568	G	911.39663	456.20195	304.47039	11
16	1439.56452	720.28590	480.52636	S	854.37516	427.69122	285.46324	10
17	1496.58599	748.79663	499.53351	G	767.34313	384.17520	256.45256	9
18	1553.60746	777.30737	518.54067	G	710.32166	355.66447	237.44540	8
19	1640.63949	820.82338	547.55135	S	653.30019	327.15373	218.43825	7
20	1697.66096	849.33412	566.55850	G	566.26816	283.63772	189.42757	6
21	1754.68243	877.84485	585.56566	G	509.24669	255.12698	170.42041	5
22	1917.74575	959.37651	639.92010	Y	452.22522	226.61625	151.41326	4
23	1974.76722	987.88725	658.92726	G	289.16190	145.08459	97.05882	3
24	2031.78869	1016.39798	677.93441	G	232.14043	116.57385	78.05166	2
25				R	175.11896	88.06312	59.04450	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT72_160514.RAW #711 RT: 19.02
ITMS, CID@35.00, z=+3, Mono m/z=735.97107 Da, MH+=2205.89865 Da, Match Tol.=0.6 Da

Sequence: GGGGNFGPGPGSNFR, Charge: +2, Monoisotopic m/z: 689.31793 Da (-0.47 mmu/-0.68 ppm), MH+: 1377.62859 Da, RT: 22.57 min,
Identified with: Sequest HT (v1.3); XCorr:2.46, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	58.02875	29.51801	G			15
2	115.05022	58.02875	G	1320.60805	660.80766	14
3	172.07169	86.53948	G	1263.58658	632.29693	13
4	229.09316	115.05022	G	1206.56511	603.78619	12
5	343.13609	172.07168	N	1149.54364	575.27546	11
6	490.20451	245.60589	F	1035.50071	518.25399	10
7	547.22598	274.11663	G	888.43229	444.71978	9
8	644.27875	322.64301	P	831.41082	416.20905	8
9	701.30022	351.15375	G	734.35805	367.68266	7
10	798.35299	399.68013	P	677.33658	339.17193	6
11	855.37446	428.19087	G	580.28381	290.64554	5
12	942.40649	471.70688	S	523.26234	262.13481	4
13	1056.44942	528.72835	N	436.23031	218.61879	3
14	1203.51784	602.26256	F	322.18738	161.59733	2
15			R	175.11896	88.06312	1

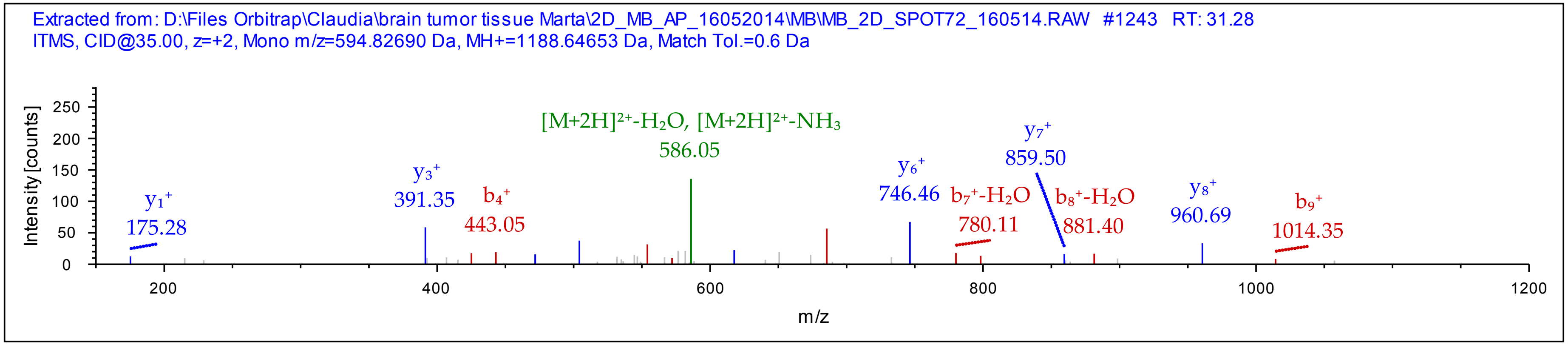


Sequence: IDTIEIITDR, Charge: +2, Monoisotopic m/z: 594.82690 Da (-0.28 mmu/-0.48 ppm), MH+: 1188.64653 Da, RT: 31.28 min,
Identified with: Sequest HT (v1.3); XCorr:2.43, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (1):
- Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2

1	114.09135	57.54931	I			10
2	229.11830	115.06279	D	1075.56303	538.28515	9
3	330.16598	165.58663	T	960.53608	480.77168	8
4	443.25005	222.12866	I	859.48840	430.24784	7
5	572.29265	286.64996	E	746.40433	373.70580	6
6	685.37672	343.19200	I	617.36173	309.18450	5
7	798.46079	399.73403	I	504.27766	252.64247	4
8	899.50847	450.25787	T	391.19359	196.10043	3
9	1014.53542	507.77135	D	290.14591	145.57659	2
10			R	175.11896	88.06312	1



Sequence: GGNFGFGDSR, Charge: +2, Monoisotopic m/z: 507.22522 Da (-0.21 mmu/-0.42 ppm), MH+: 1013.44316 Da, RT: 22.74 min,
Identified with: Sequest HT (v1.3); XCorr:2.24, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	58.02875	29.51801	G			10
2	115.05022	58.02875	G	956.42212	478.71470	9
3	229.09315	115.05021	N	899.40065	450.20396	8
4	376.16157	188.58442	F	785.35772	393.18250	7
5	433.18304	217.09516	G	638.28930	319.64829	6

6	580.25146	290.62937	F	581.26783	291.13755	5
7	637.27293	319.14010	G	434.19941	217.60334	4
8	752.29988	376.65358	D	377.17794	189.09261	3
9	839.33191	420.16959	S	262.15099	131.57913	2
10			R	175.11896	88.06312	1

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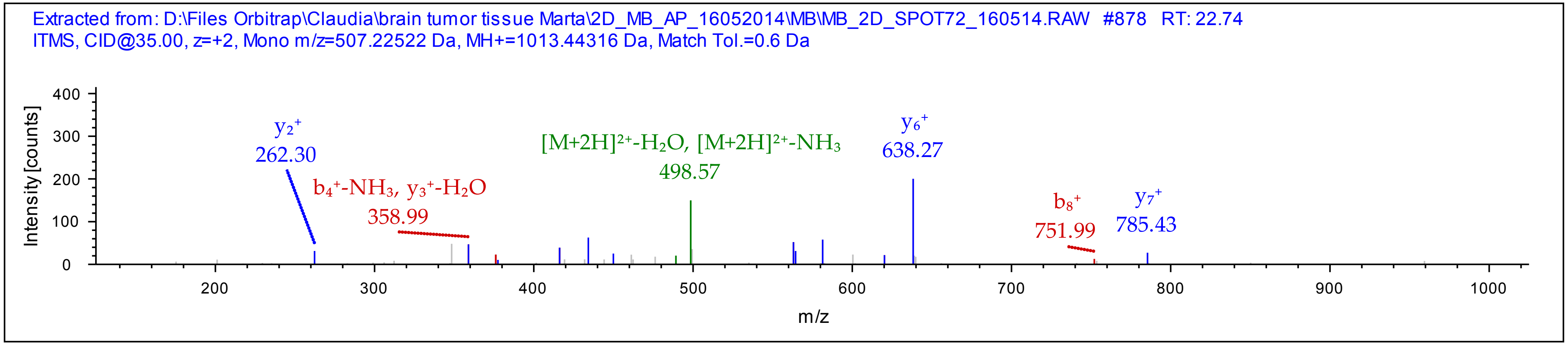
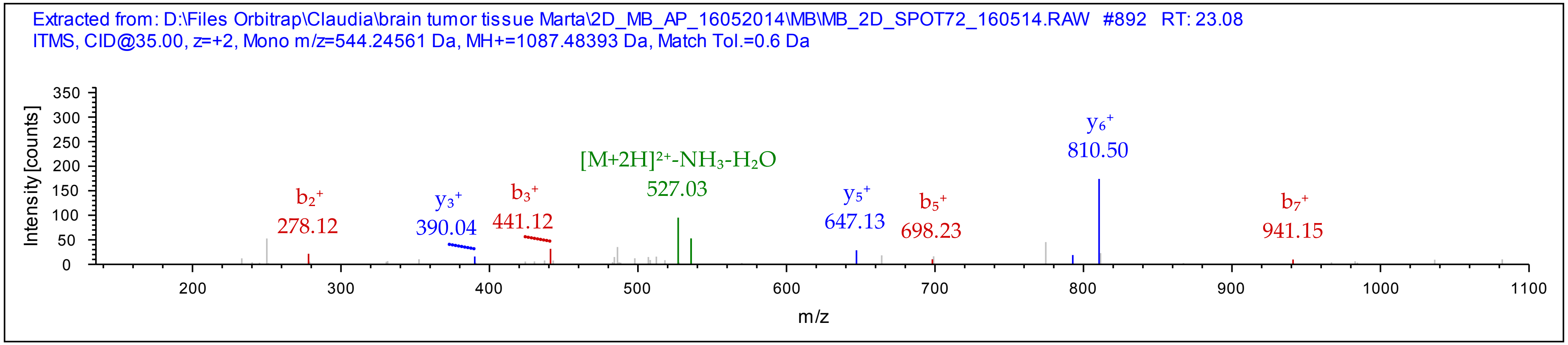


Sequence: NYYEQWGK, Charge: +2, Monoisotopic m/z: 544.24561 Da (-0.21 mmu/-0.38 ppm), MH+: 1087.48393 Da, RT: 23.08 min,
Identified with: Sequest HT (v1.3); XCorr:1.76, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (1):
- Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	115.05021	58.02874	N			8
2	278.11353	139.56040	Y	973.44142	487.22435	7
3	441.17685	221.09206	Y	810.37810	405.69269	6
4	570.21945	285.61336	E	647.31478	324.16103	5
5	698.27803	349.64265	Q	518.27218	259.63973	4
6	884.35735	442.68231	W	390.21360	195.61044	3
7	941.37882	471.19305	G	204.13428	102.57078	2
8			K	147.11281	74.06004	1

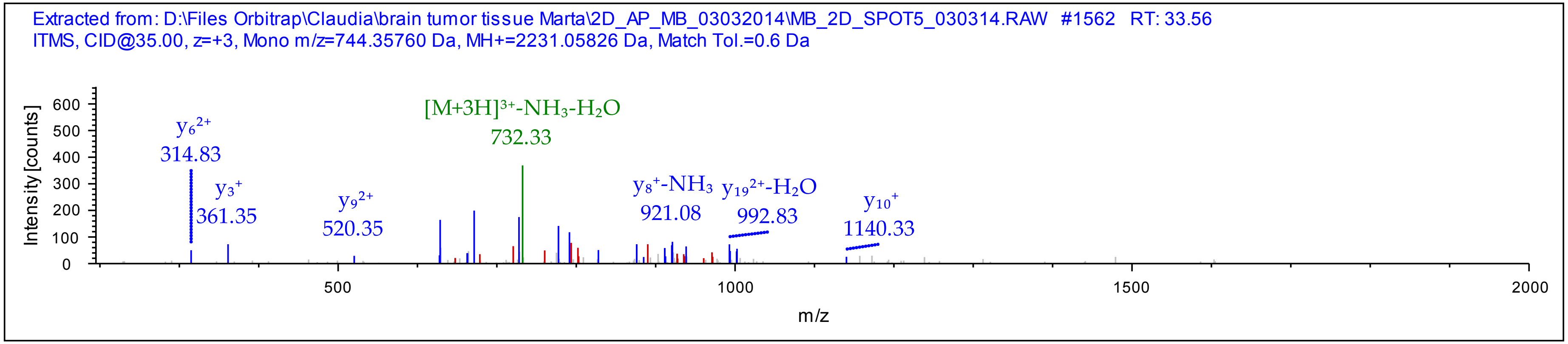

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_MB_AP_16052014\MB\MB_2D_SPOT72_160514.RAW #892 RT: 23.08
ITMS, CID@35.00, z=+2, Mono m/z=544.24561 Da, MH+=1087.48393 Da, Match Tol.=0.6 Da

Spot #	Uniprot Accession Number	Description	MWa [kDa]	pIa	Score	Coverage	# Unique Peptides	# Peptides	Identified in	Anova (p)*	Fold Variation*
80	P60709	Actin, cytoplasmic 1	41.7	5.3	250.05	54.13%	16	16	MB	NS	NS

Sequence: DLYANTVLSGGTTMYPGIADR, M14-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 744.35760 Da (-2.24 mmu/-3.01 ppm), MH+: 2231.05826 Da, RT: 33.56 min,
Identified with: Sequest HT (v1.3); XCorr:4.00, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (2):
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]

#1	b^+	b^{2+}	b^{3+}	Seq.	y^+	y^{2+}	y^{3+}	#2
1	116.03423	58.52075	39.34959	D				21
2	229.11830	115.06279	77.04428	L	2116.03802	1058.52265	706.01752	20
3	392.18162	196.59445	131.39872	Y	2002.95395	1001.98061	668.32283	19
4	463.21874	232.11301	155.07776	A	1839.89063	920.44895	613.96839	18
5	577.26167	289.13447	193.09207	N	1768.85351	884.93039	590.28935	17
6	678.30935	339.65831	226.77463	T	1654.81058	827.90893	552.27504	16
7	777.37777	389.19252	259.79744	V	1553.76290	777.38509	518.59248	15
8	890.46184	445.73456	297.49213	L	1454.69448	727.85088	485.56968	14
9	977.49387	489.25057	326.50281	S	1341.61041	671.30884	447.87499	13
10	1034.51534	517.76131	345.50996	G	1254.57838	627.79283	418.86431	12
11	1091.53681	546.27204	364.51712	G	1197.55691	599.28209	399.85715	11
12	1192.58449	596.79588	398.19968	T	1140.53544	570.77136	380.85000	10

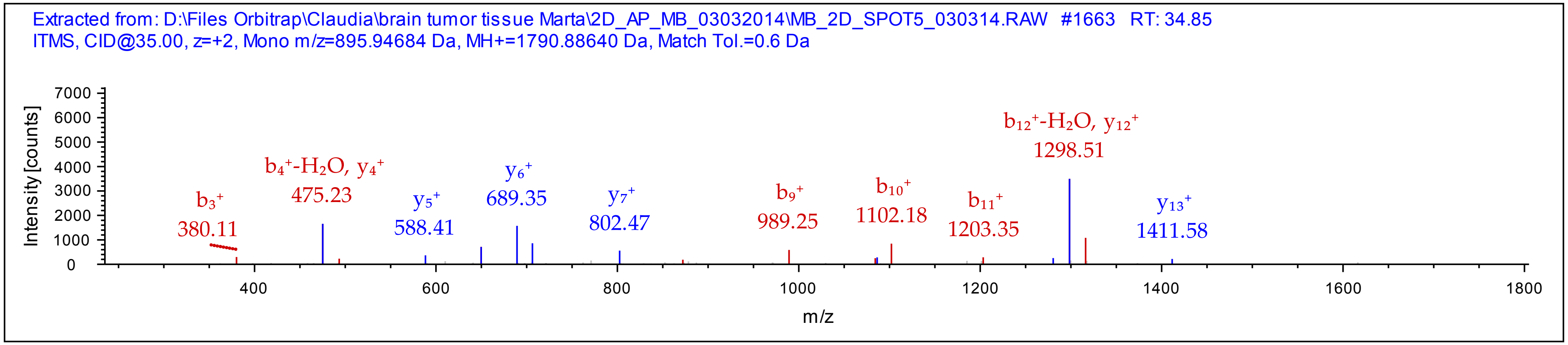
13	1293.63217	647.31972	431.88224	T	1039.48776	520.24752	347.16744	9
14	1440.66758	720.83743	480.89404	M-Oxidation	938.44008	469.72368	313.48488	8
15	1603.73090	802.36909	535.24848	Y	791.40466	396.20597	264.47307	7
16	1700.78367	850.89547	567.59941	P	628.34134	314.67431	210.11863	6
17	1757.80514	879.40621	586.60656	G	531.28857	266.14792	177.76771	5
18	1870.88921	935.94824	624.30125	I	474.26710	237.63719	158.76055	4
19	1941.92633	971.46680	647.98029	A	361.18303	181.09515	121.06586	3
20	2056.95328	1028.98028	686.32261	D	290.14591	145.57659	97.38682	2
21				R	175.11896	88.06312	59.04450	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT5_030314.RAW #1562 RT: 33.56
ITMS, CID@35.00, z=+3, Mono m/z=744.35760 Da, MH+=2231.05826 Da, Match Tol.=0.6 Da

Sequence: SYELPDGQVITIGNER, Charge: +2, Monoisotopic m/z: 895.94684 Da (-2.8 mmu/-3.12 ppm), MH+: 1790.88640 Da, RT: 34.85 min,
Identified with: Sequest HT (v1.3); XCorr:3.97, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3
Protein references (10):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 - [ACTBL_HUMAN]
- Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1 - [ACTBM_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]
- POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 - [POTEE_HUMAN]
- POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2 - [POTEF_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	88.03931	44.52329	S			16

2	251.10263	126.05495	Y	1703.85996	852.43362	15
3	380.14523	190.57625	E	1540.79664	770.90196	14
4	493.22930	247.11829	L	1411.75404	706.38066	13
5	590.28207	295.64467	P	1298.66997	649.83862	12
6	705.30902	353.15815	D	1201.61720	601.31224	11
7	762.33049	381.66888	G	1086.59025	543.79876	10
8	890.38907	445.69817	Q	1029.56878	515.28803	9
9	989.45749	495.23238	V	901.51020	451.25874	8
10	1102.54156	551.77442	I	802.44178	401.72453	7
11	1203.58924	602.29826	T	689.35771	345.18249	6
12	1316.67331	658.84029	I	588.31003	294.65865	5
13	1373.69478	687.35103	G	475.22596	238.11662	4
14	1487.73771	744.37249	N	418.20449	209.60588	3
15	1616.78031	808.89379	E	304.16156	152.58442	2
16			R	175.11896	88.06312	1

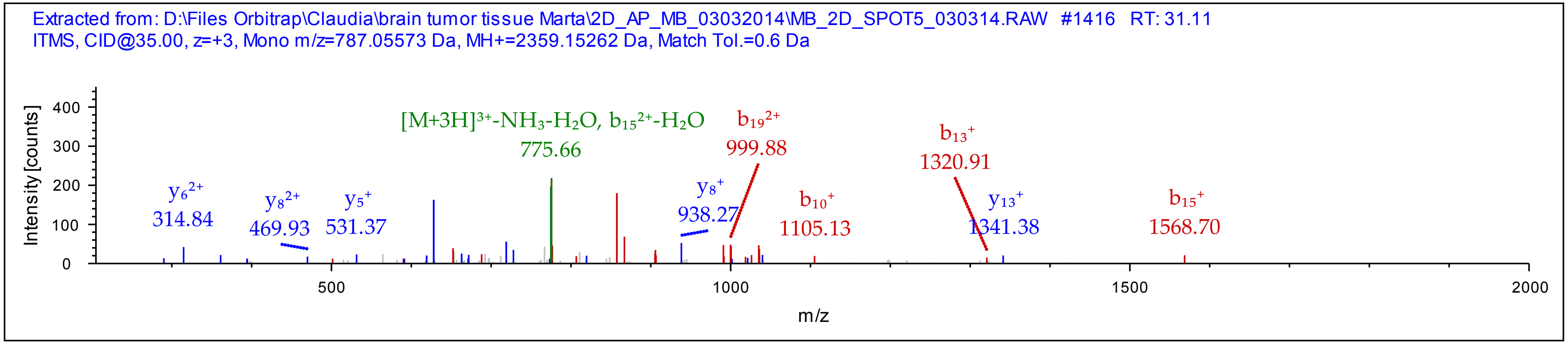


Sequence: KDLYANTVLSGGTTMYPGIADR, M15-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 787.05573 Da (-2.44 mmu/-3.1 ppm), MH+: 2359.15262 Da, RT: 31.11 min,
Identified with: Sequest HT (v1.3); XCorr:3.56, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	129.10225	65.05476	43.70560	K				22

2	244.12920	122.56824	82.04792	D	2231.06497	1116.03612	744.35984	21
3	357.21327	179.11027	119.74261	L	2116.03802	1058.52265	706.01752	20
4	520.27659	260.64193	174.09705	Y	2002.95395	1001.98061	668.32283	19
5	591.31371	296.16049	197.77609	A	1839.89063	920.44895	613.96839	18
6	705.35664	353.18196	235.79040	N	1768.85351	884.93039	590.28935	17
7	806.40432	403.70580	269.47296	T	1654.81058	827.90893	552.27504	16
8	905.47274	453.24001	302.49576	V	1553.76290	777.38509	518.59248	15
9	1018.55681	509.78204	340.19045	L	1454.69448	727.85088	485.56968	14
10	1105.58884	553.29806	369.20113	S	1341.61041	671.30884	447.87499	13
11	1162.61031	581.80879	388.20829	G	1254.57838	627.79283	418.86431	12
12	1219.63178	610.31953	407.21544	G	1197.55691	599.28209	399.85715	11
13	1320.67946	660.84337	440.89800	T	1140.53544	570.77136	380.85000	10
14	1421.72714	711.36721	474.58056	T	1039.48776	520.24752	347.16744	9
15	1568.76255	784.88491	523.59237	M-Oxidation	938.44008	469.72368	313.48488	8
16	1731.82587	866.41657	577.94681	Y	791.40466	396.20597	264.47307	7
17	1828.87864	914.94296	610.29773	P	628.34134	314.67431	210.11863	6
18	1885.90011	943.45369	629.30489	G	531.28857	266.14792	177.76771	5
19	1998.98418	999.99573	666.99958	I	474.26710	237.63719	158.76055	4
20	2070.02130	1035.51429	690.67862	A	361.18303	181.09515	121.06586	3
21	2185.04825	1093.02776	729.02093	D	290.14591	145.57659	97.38682	2
22				R	175.11896	88.06312	59.04450	1

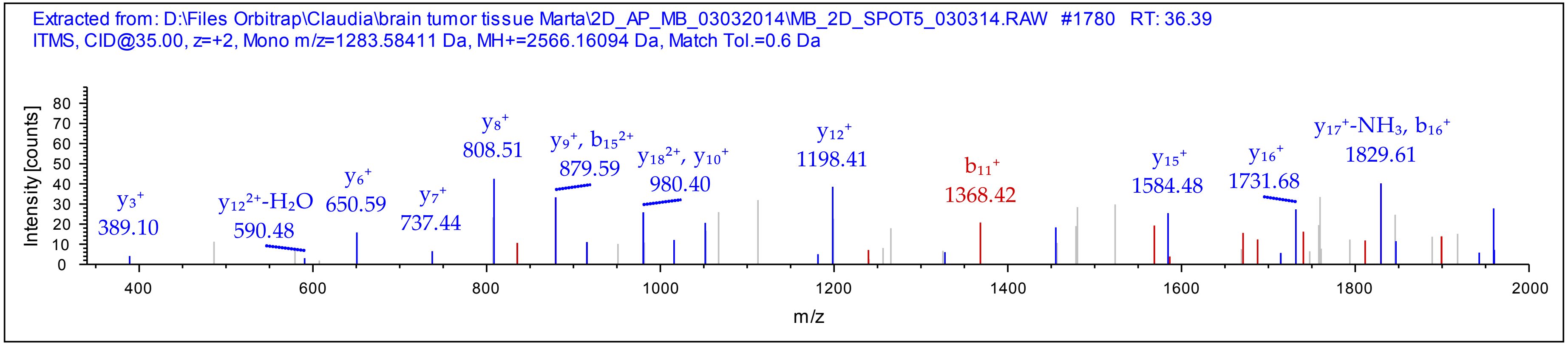


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT5_030314.RAW #1416 RT: 31.11
ITMS, CID@35.00, z=+3, Mono m/z=787.05573 Da, MH+=2359.15262 Da, Match Tol.=0.6 Da

Sequence: LCYVALDFEQEMATAASSSSLEK, C2-Carbamidomethyl (57.02146 Da), M12-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 1283.58411 Da (-3.96 mmu/-3.09 ppm), MH+: 2566.16094 Da, RT: 36.39 min,
Identified with: Sequest HT (v1.3); XCorr:3.30, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 - [POTEE_HUMAN]

#1	**b^{+}**	**b^{2+}**	**Seq.**	**y^{+}**	**y^{2+}**	**#2**
1	114.09135	57.54931	L			23
2	274.12200	137.56464	C-Carbamidomethyl	2453.08479	1227.04603	22
3	437.18532	219.09630	Y	2293.05414	1147.03071	21
4	536.25374	268.63051	V	2129.99082	1065.49905	20
5	607.29086	304.14907	A	2030.92240	1015.96484	19
6	720.37493	360.69110	L	1959.88528	980.44628	18
7	835.40188	418.20458	D	1846.80121	923.90424	17
8	982.47030	491.73879	F	1731.77426	866.39077	16
9	1111.51290	556.26009	E	1584.70584	792.85656	15
10	1239.57148	620.28938	Q	1455.66324	728.33526	14
11	1368.61408	684.81068	E	1327.60466	664.30597	13
12	1515.64950	758.32839	M-Oxidation	1198.56206	599.78467	12
13	1586.68662	793.84695	A	1051.52664	526.26696	11
14	1687.73430	844.37079	T	980.48952	490.74840	10
15	1758.77142	879.88935	A	879.44184	440.22456	9
16	1829.80854	915.40791	A	808.40472	404.70600	8
17	1916.84057	958.92392	S	737.36760	369.18744	7
18	2003.87260	1002.43994	S	650.33557	325.67142	6
19	2090.90463	1045.95595	S	563.30354	282.15541	5
20	2177.93666	1089.47197	S	476.27151	238.63939	4
21	2291.02073	1146.01400	L	389.23948	195.12338	3
22	2420.06333	1210.53530	E	276.15541	138.58134	2
23			K	147.11281	74.06004	1

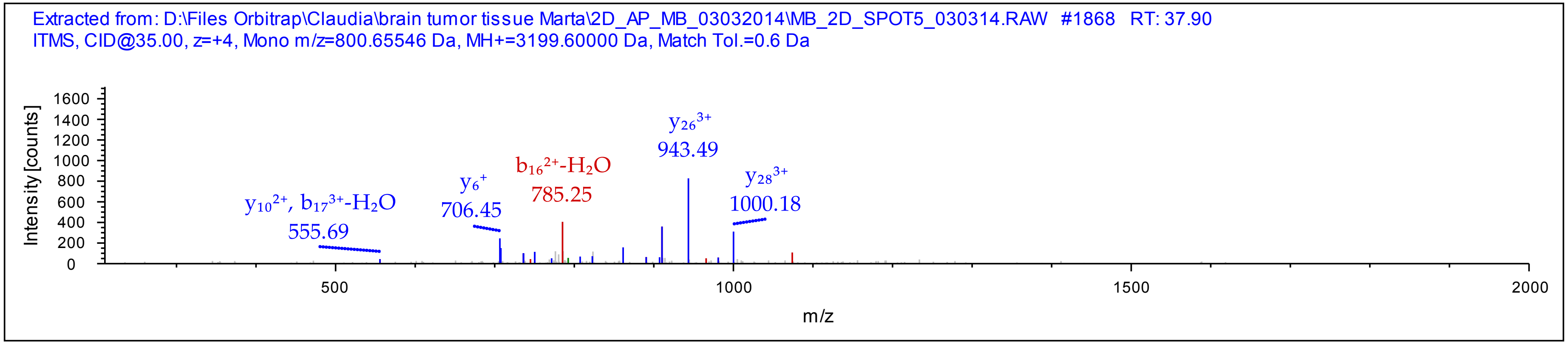


Sequence: TTGIVMDSGDGVTHTVPIYEGYALPHAILR, M6-Oxidation (15.99492 Da)
Charge: +4, Monoisotopic m/z: 800.65546 Da (-2.34 mmu/-2.93 ppm), MH+: 3199.60000 Da, RT: 37.90 min,
Identified with: Sequest HT (v1.3); XCorr:3.27, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (2):
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]

#1	b^+	b^{2+}	b^{3+}	b^{4+}	Seq.	y^+	y^{2+}	y^{3+}	y^{4+}	#2
1	102.05496	51.53112	34.68984	26.26920	T					30
2	203.10264	102.05496	68.37240	51.53112	T	3098.56168	1549.78448	1033.52541	775.39588	29
3	260.12411	130.56569	87.37955	65.78648	G	2997.51400	1499.26064	999.84285	750.13396	28
4	373.20818	187.10773	125.07424	94.05750	I	2940.49253	1470.74990	980.83569	735.87859	27
5	472.27660	236.64194	158.09705	118.82461	V	2827.40846	1414.20787	943.14100	707.60757	26
6	619.31201	310.15964	207.10885	155.58346	M-Oxidation	2728.34004	1364.67366	910.11820	682.84047	25
7	734.33896	367.67312	245.45117	184.34020	D	2581.30462	1291.15595	861.10639	646.08161	24
8	821.37099	411.18913	274.46185	206.09821	S	2466.27767	1233.64247	822.76407	617.32488	23
9	878.39246	439.69987	293.46900	220.35357	G	2379.24564	1190.12646	793.75340	595.56687	22
10	993.41941	497.21334	331.81132	249.11031	D	2322.22417	1161.61572	774.74624	581.31150	21
11	1050.44088	525.72408	350.81848	263.36568	G	2207.19722	1104.10225	736.40392	552.55476	20
12	1149.50930	575.25829	383.84128	288.13278	V	2150.17575	1075.59151	717.39677	538.29940	19
13	1250.55698	625.78213	417.52384	313.39470	T	2051.10733	1026.05730	684.37396	513.53229	18
14	1387.61589	694.31158	463.21015	347.65943	H	1950.05965	975.53346	650.69140	488.27037	17
15	1488.66357	744.83542	496.89271	372.92135	T	1813.00074	907.00401	605.00510	454.00564	16
16	1587.73199	794.36963	529.91551	397.68846	V	1711.95306	856.48017	571.32254	428.74372	15

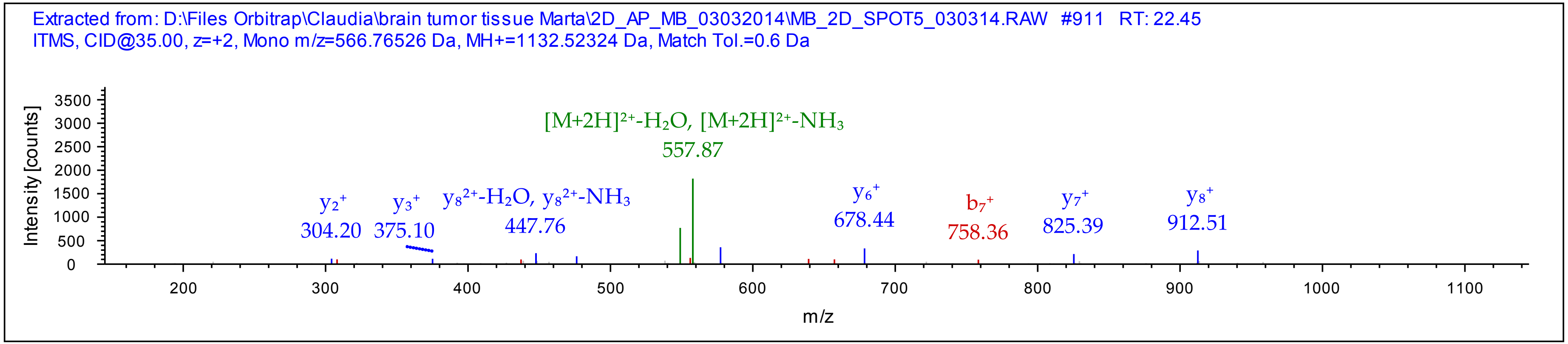
17	1684.78476	842.89602	562.26644	421.95165	P	1612.88464	806.94596	538.29973	403.97662	14
18	1797.86883	899.43805	599.96113	450.22267	I	1515.83187	758.41957	505.94881	379.71343	13
19	1960.93215	980.96971	654.31557	490.98850	Y	1402.74780	701.87754	468.25412	351.44241	12
20	2089.97475	1045.49101	697.32977	523.24915	E	1239.68448	620.34588	413.89968	310.67658	11
21	2146.99622	1074.00175	716.33692	537.50451	G	1110.64188	555.82458	370.88548	278.41593	10
22	2310.05954	1155.53341	770.69136	578.27034	Y	1053.62041	527.31384	351.87832	264.16056	9
23	2381.09666	1191.05197	794.37040	596.02962	A	890.55709	445.78218	297.52388	223.39473	8
24	2494.18073	1247.59400	832.06509	624.30064	L	819.51997	410.26362	273.84484	205.63545	7
25	2591.23350	1296.12039	864.41602	648.56383	P	706.43590	353.72159	236.15015	177.36443	6
26	2728.29241	1364.64984	910.10232	682.82856	H	609.38313	305.19520	203.79923	153.10124	5
27	2799.32953	1400.16840	933.78136	700.58784	A	472.32422	236.66575	158.11292	118.83651	4
28	2912.41360	1456.71044	971.47605	728.85886	I	401.28710	201.14719	134.43388	101.07723	3
29	3025.49767	1513.25247	1009.17074	757.12988	L	288.20303	144.60515	96.73919	72.80622	2
30					R	175.11896	88.06312	59.04450	44.53520	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT5_030314.RAW #1868 RT: 37.90
ITMS, CID@35.00, z=+4, Mono m/z=800.65546 Da, MH+=3199.60000 Da, Match Tol.=0.6 Da

Sequence: GYSFTTTAER, Charge: +2, Monoisotopic m/z: 566.76526 Da (-1.86 mmu/-3.29 ppm), MH+: 1132.52324 Da, RT: 22.45 min,
Identified with: Sequest HT (v1.3); XCorr:2.91, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3
Protein references (2):
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]

#1	**b^{+}**	**b^{2+}**	**Seq.**	**y^{+}**	**y^{2+}**	**#2**
1	58.02875	29.51801	G			10
2	221.09207	111.04967	Y	1075.50549	538.25638	9
3	308.12410	154.56569	S	912.44217	456.72472	8
4	455.19252	228.09990	F	825.41014	413.20871	7

5	556.24020	278.62374	T	678.34172	339.67450	6
6	657.28788	329.14758	T	577.29404	289.15066	5
7	758.33556	379.67142	T	476.24636	238.62682	4
8	829.37268	415.18998	A	375.19868	188.10298	3
9	958.41528	479.71128	E	304.16156	152.58442	2
10			R	175.11896	88.06312	1

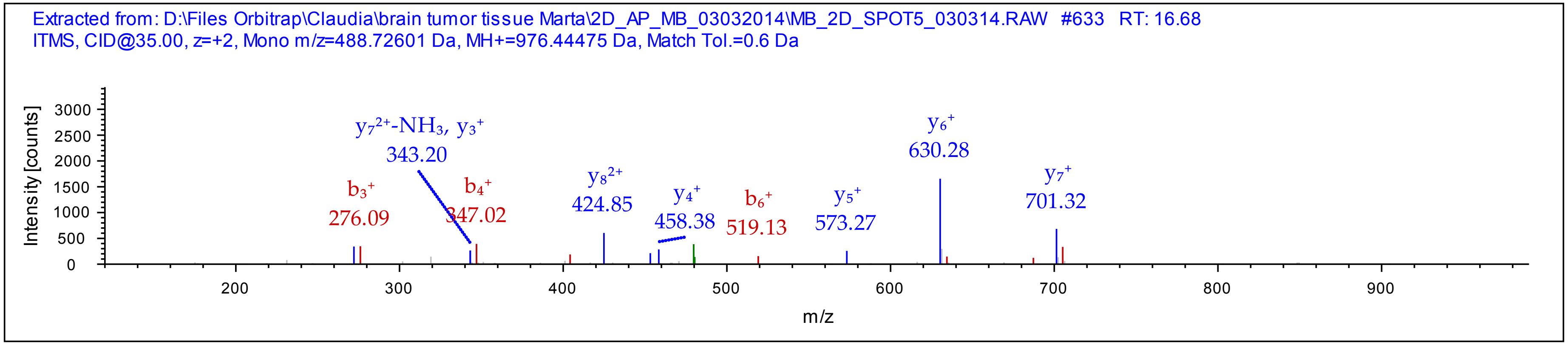


Sequence: AGFAGDDAPR, Charge: +2, Monoisotopic m/z: 488.72601 Da (-1.8 mmu/-3.69 ppm), MH+: 976.44475 Da, RT: 16.68 min,
Identified with: Sequest HT (v1.3); XCorr:2.87, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (10):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]
- POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 - [POTEE_HUMAN]
- POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2 - [POTEF_HUMAN]
- POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=3 SV=1 - [POTEI_HUMAN]
- POTE ankyrin domain family member J OS=Homo sapiens GN=POTEJ PE=3 SV=1 - [POTEJ_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	72.04440	36.52584	A			10
2	129.06587	65.03657	G	905.41123	453.20925	9
3	276.13429	138.57078	F	848.38976	424.69852	8
4	347.17141	174.08934	A	701.32134	351.16431	7
5	404.19288	202.60008	G	630.28422	315.64575	6

6	519.21983	260.11355	D	573.26275	287.13501	5
7	634.24678	317.62703	D	458.23580	229.62154	4
8	705.28390	353.14559	A	343.20885	172.10806	3
9	802.33667	401.67197	P	272.17173	136.58950	2
10			R	175.11896	88.06312	1

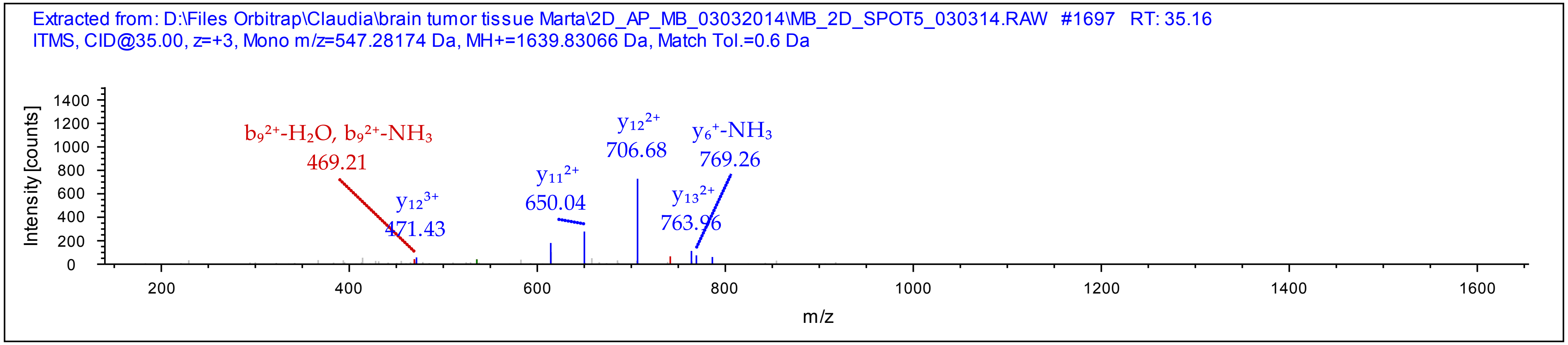


Sequence: LDLAGRDLTDYLMK, M13-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 547.28174 Da (-1.8 mmu/-3.3 ppm), MH+: 1639.83066 Da, RT: 35.16 min,
Identified with: Sequest HT (v1.3); XCorr:2.78, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 - [ACTBL_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	114.09135	57.54931	38.70197	L				14
2	229.11830	115.06279	77.04428	D	1526.75200	763.87964	509.58885	13
3	342.20237	171.60482	114.73897	L	1411.72505	706.36616	471.24653	12
4	413.23949	207.12338	138.41801	A	1298.64098	649.82413	433.55184	11
5	470.26096	235.63412	157.42517	G	1227.60386	614.30557	409.87280	10
6	626.36208	313.68468	209.45888	R	1170.58239	585.79483	390.86565	9
7	741.38903	371.19815	247.80119	D	1014.48127	507.74427	338.83194	8

8	854.47310	427.74019	285.49588	L	899.45432	450.23080	300.48962	7
9	955.52078	478.26403	319.17844	T	786.37025	393.68876	262.79493	6
10	1070.54773	535.77750	357.52076	D	685.32257	343.16492	229.11237	5
11	1233.61105	617.30916	411.87520	Y	570.29562	285.65145	190.77006	4
12	1346.69512	673.85120	449.56989	L	407.23230	204.11979	136.41562	3
13	1493.73053	747.36890	498.58169	M-Oxidation	294.14823	147.57775	98.72093	2
14				K	147.11281	74.06004	49.70912	1

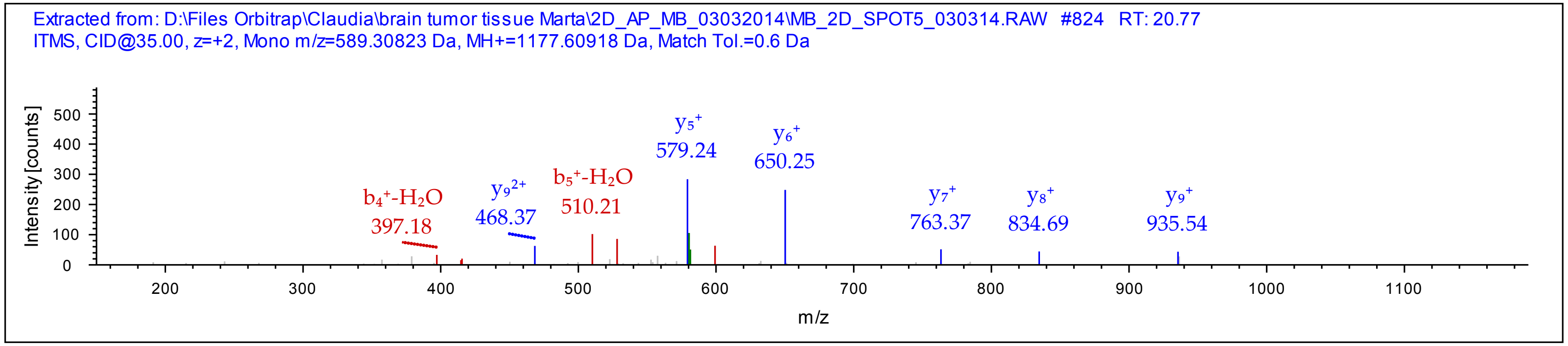

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT5_030314.RAW #1697 RT: 35.16
ITMS, CID@35.00, z=+3, Mono m/z=547.28174 Da, MH+=1639.83066 Da, Match Tol.=0.6 Da

Sequence: EITALAPSTMK, M10-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 589.30823 Da (-2.1 mmu/-3.56 ppm), MH+: 1177.60918 Da, RT: 20.77 min,
Identified with: Sequest HT (v1.3); XCorr:2.58, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (6):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	130.04988	65.52858	E			11
2	243.13395	122.07061	I	1048.57077	524.78902	10
3	344.18163	172.59445	T	935.48670	468.24699	9
4	415.21875	208.11301	A	834.43902	417.72315	8
5	528.30282	264.65505	L	763.40190	382.20459	7
6	599.33994	300.17361	A	650.31783	325.66255	6

7	696.39271	348.69999	P	579.28071	290.14399	5
8	783.42474	392.21601	S	482.22794	241.61761	4
9	884.47242	442.73985	T	395.19591	198.10159	3
10	1031.50783	516.25755	M-Oxidation	294.14823	147.57775	2
11			K	147.11281	74.06004	1

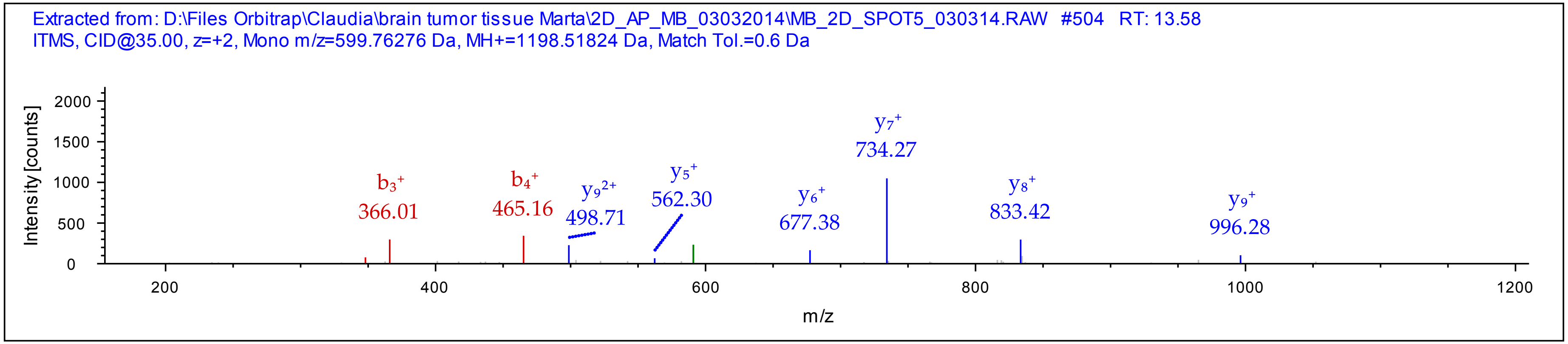


Sequence: DSYVGDEAQSK, Charge: +2, Monoisotopic m/z: 599.76276 Da (-2.02 mmu/-3.38 ppm), MH+: 1198.51824 Da, RT: 13.58 min,
Identified with: Sequest HT (v1.3); XCorr:2.56, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	116.03423	58.52075	D			11
2	203.06626	102.03677	S	1083.49533	542.25130	10
3	366.12958	183.56843	Y	996.46330	498.73529	9
4	465.19800	233.10264	V	833.39998	417.20363	8
5	522.21947	261.61337	G	734.33156	367.66942	7
6	637.24642	319.12685	D	677.31009	339.15868	6
7	766.28902	383.64815	E	562.28314	281.64521	5
8	837.32614	419.16671	A	433.24054	217.12391	4
9	965.38472	483.19600	Q	362.20342	181.60535	3
10	1052.41675	526.71201	S	234.14484	117.57606	2

11			K	147.11281	74.06004	1

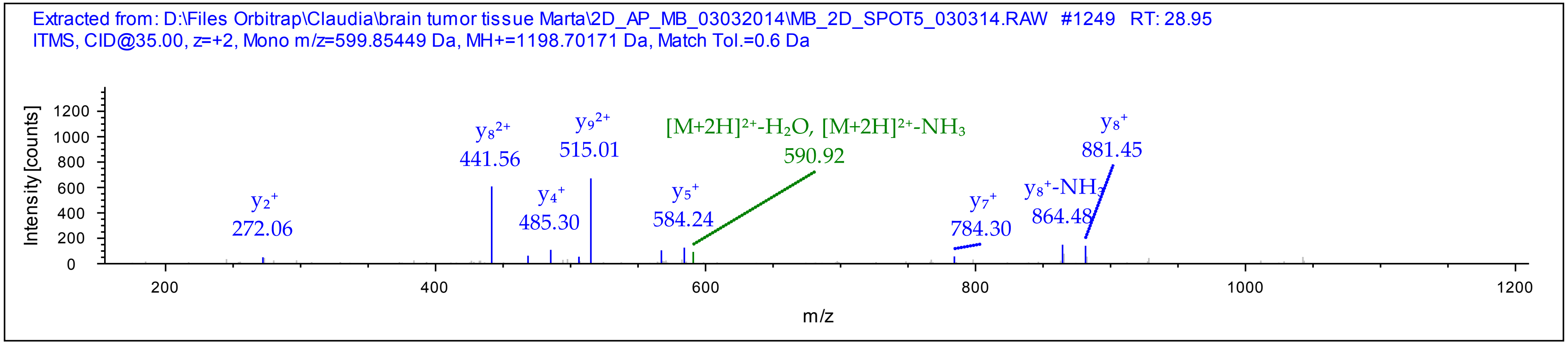

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT5_030314.RAW #504 RT: 13.58
ITMS, CID@35.00, z=+2, Mono m/z=599.76276 Da, MH+=1198.51824 Da, Match Tol.=0.6 Da

Sequence: AVFPSIVGRPR, Charge: +2, Monoisotopic m/z: 599.85449 Da (-1.93 mmu/-3.22 ppm), MH+: 1198.70171 Da, RT: 28.95 min,
Identified with: Sequest HT (v1.3); XCorr:2.46, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (9):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]
- POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 - [POTEE_HUMAN]
- POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2 - [POTEF_HUMAN]
- POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=3 SV=1 - [POTEI_HUMAN]

#1	**b^+**	**b^{2+}**	**Seq.**	**y^+**	**y^{2+}**	**#2**
1	72.04440	36.52584	A			11
2	171.11282	86.06005	V	1127.66845	564.33786	10
3	318.18124	159.59426	F	1028.60003	514.80365	9
4	415.23401	208.12064	P	881.53161	441.26944	8
5	502.26604	251.63666	S	784.47884	392.74306	7
6	615.35011	308.17869	I	697.44681	349.22704	6
7	714.41853	357.71290	V	584.36274	292.68501	5
8	771.44000	386.22364	G	485.29432	243.15080	4
9	927.54112	464.27420	R	428.27285	214.64006	3
10	1024.59389	512.80058	P	272.17173	136.58950	2

11			R	175.11896	88.06312	1

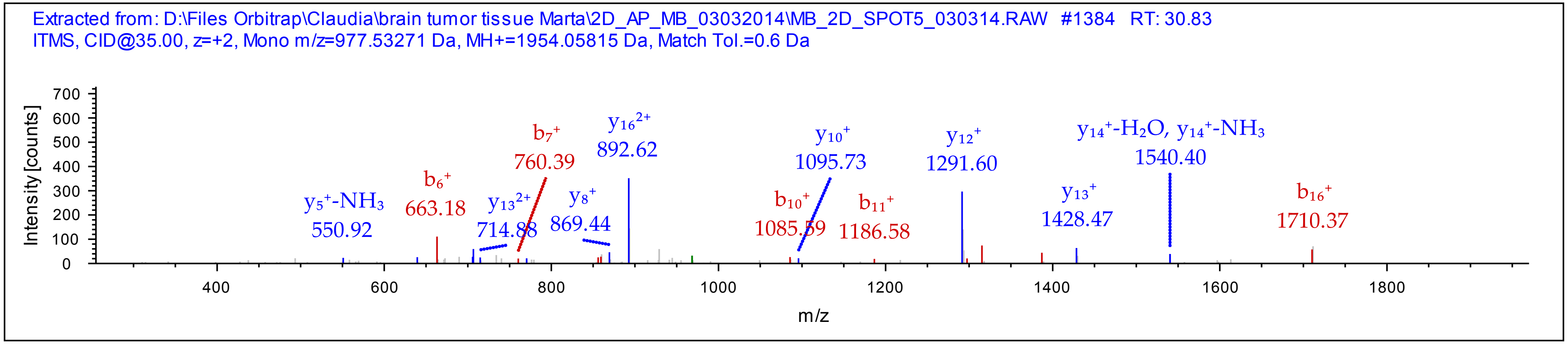


Sequence: VAPEEHPVLLTEAPLNPK, Charge: +2, Monoisotopic m/z: 977.53271 Da (-3.18 mmu/-3.25 ppm), MH+: 1954.05815 Da, RT: 30.83 min,
Identified with: Sequest HT (v1.3); XCorr:2.35, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]

#1	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	100.07570	50.54149	V			18
2	171.11282	86.06005	A	1854.99608	928.00168	17
3	268.16559	134.58643	P	1783.95896	892.48312	16
4	397.20819	199.10773	E	1686.90619	843.95673	15
5	526.25079	263.62903	E	1557.86359	779.43543	14
6	663.30970	332.15849	H	1428.82099	714.91413	13
7	760.36247	380.68487	P	1291.76208	646.38468	12
8	859.43089	430.21908	V	1194.70931	597.85829	11
9	972.51496	486.76112	L	1095.64089	548.32408	10
10	1085.59903	543.30315	L	982.55682	491.78205	9
11	1186.64671	593.82699	T	869.47275	435.24001	8
12	1315.68931	658.34829	E	768.42507	384.71617	7
13	1386.72643	693.86685	A	639.38247	320.19487	6
14	1483.77920	742.39324	P	568.34535	284.67631	5
15	1596.86327	798.93527	L	471.29258	236.14993	4
16	1710.90620	855.95674	N	358.20851	179.60789	3

17	1807.95897	904.48312	P	244.16558	122.58643	2
18			K	147.11281	74.06004	1

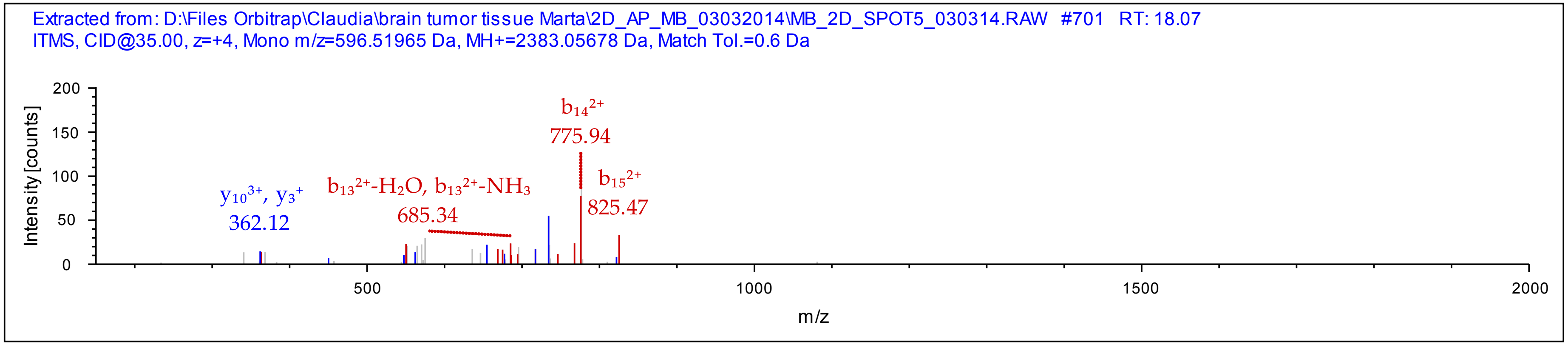


Sequence: HQGVMVGMGQKDSYVGDEAQSK, M5-Oxidation (15.99492 Da), M8-Oxidation (15.99492 Da)
Charge: +4, Monoisotopic m/z: 596.51965 Da (-2.16 mmu/-3.62 ppm), MH+: 2383.05678 Da, RT: 18.07 min,
Identified with: Sequest HT (v1.3); XCorr:2.14, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**b^{4+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**y^{4+}**	**#2**
1	138.06619	69.53673	46.69358	35.27200	H					22
2	266.12477	133.56602	89.37977	67.28665	Q	2246.00649	1123.50688	749.34035	562.25708	21
3	323.14624	162.07676	108.38693	81.54202	G	2117.94791	1059.47759	706.65415	530.24244	20
4	422.21466	211.61097	141.40974	106.30912	V	2060.92644	1030.96686	687.64700	515.98707	19
5	569.25007	285.12867	190.42154	143.06798	M-Oxidation	1961.85802	981.43265	654.62419	491.21996	18
6	668.31849	334.66288	223.44435	167.83508	V	1814.82261	907.91494	605.61239	454.46111	17
7	725.33996	363.17362	242.45150	182.09045	G	1715.75419	858.38073	572.58958	429.69400	16
8	872.37538	436.69133	291.46331	218.84930	M-Oxidation	1658.73272	829.87000	553.58242	415.43864	15
9	929.39685	465.20206	310.47047	233.10467	G	1511.69730	756.35229	504.57062	378.67978	14
10	1057.45543	529.23135	353.15666	265.11931	Q	1454.67583	727.84155	485.56346	364.42442	13
11	1185.55040	593.27884	395.85498	297.14306	K	1326.61725	663.81226	442.87727	332.40977	12

12	1300.57735	650.79231	434.19730	325.89979	D	1198.52228	599.76478	400.17894	300.38603	11
13	1387.60938	694.30833	463.20798	347.65780	S	1083.49533	542.25130	361.83663	271.62929	10
14	1550.67270	775.83999	517.56242	388.42363	Y	996.46330	498.73529	332.82595	249.87128	9
15	1649.74112	825.37420	550.58522	413.19074	V	833.39998	417.20363	278.47151	209.10545	8
16	1706.76259	853.88493	569.59238	427.44610	G	734.33156	367.66942	245.44870	184.33835	7
17	1821.78954	911.39841	607.93470	456.20284	D	677.31009	339.15868	226.44155	170.08298	6
18	1950.83214	975.91971	650.94890	488.46349	E	562.28314	281.64521	188.09923	141.32624	5
19	2021.86926	1011.43827	674.62794	506.22277	A	433.24054	217.12391	145.08503	109.06559	4
20	2149.92784	1075.46756	717.31413	538.23742	Q	362.20342	181.60535	121.40599	91.30631	3
21	2236.95987	1118.98357	746.32481	559.99542	S	234.14484	117.57606	78.71980	59.29167	2
22					K	147.11281	74.06004	49.70912	37.53366	1

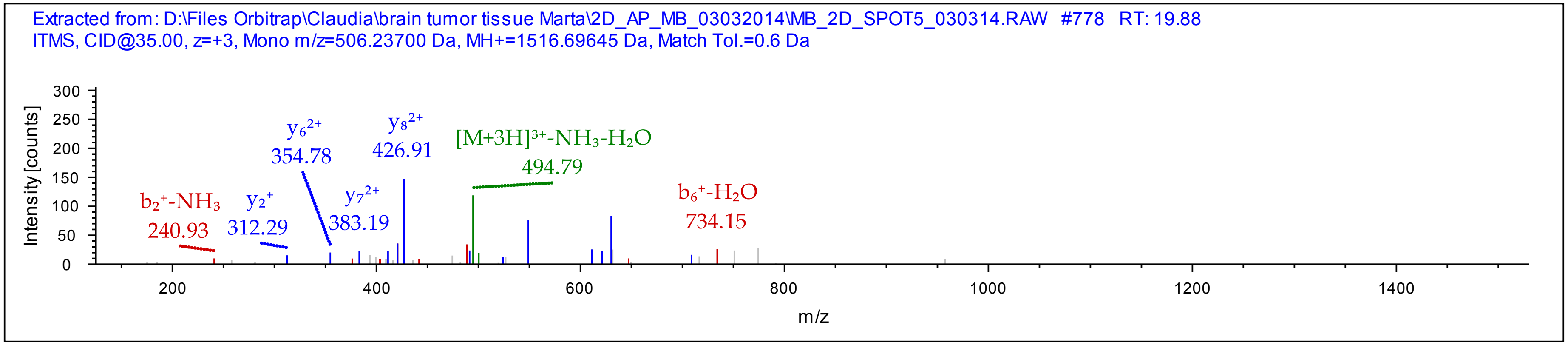

Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT5_030314.RAW #701 RT: 18.07
ITMS, CID@35.00, z=+4, Mono m/z=596.51965 Da, MH+=2383.05678 Da, Match Tol.=0.6 Da

Sequence: QEYDESGPSIVHR, Charge: +3, Monoisotopic m/z: 506.23700 Da (-2.09 mmu/-4.13 ppm), MH+: 1516.69645 Da, RT: 19.88 min,
Identified with: Sequest HT (v1.3); XCorr:2.07, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):
- Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1 - [ACTBM_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 - [POTEE_HUMAN]
- POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2 - [POTEF_HUMAN]
- POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=3 SV=1 - [POTEI_HUMAN]
- POTE ankyrin domain family member J OS=Homo sapiens GN=POTEJ PE=3 SV=1 - [POTEJ_HUMAN]

#1	**b^+**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^+**	**y^{2+}**	**y^{3+}**	**#2**
1	129.06586	65.03657	43.69347	Q				13
2	258.10846	129.55787	86.70767	E	1388.64413	694.82570	463.55289	12

3	421.17178	211.08953	141.06211	Y	1259.60153	630.30440	420.53869	11
4	536.19873	268.60300	179.40443	D	1096.53821	548.77274	366.18425	10
5	665.24133	333.12430	222.41863	E	981.51126	491.25927	327.84194	9
6	752.27336	376.64032	251.42930	S	852.46866	426.73797	284.82774	8
7	809.29483	405.15105	270.43646	G	765.43663	383.22195	255.81706	7
8	906.34760	453.67744	302.78738	P	708.41516	354.71122	236.80990	6
9	993.37963	497.19345	331.79806	S	611.36239	306.18483	204.45898	5
10	1106.46370	553.73549	369.49275	I	524.33036	262.66882	175.44830	4
11	1205.53212	603.26970	402.51556	V	411.24629	206.12678	137.75361	3
12	1342.59103	671.79915	448.20186	H	312.17787	156.59257	104.73081	2
13				R	175.11896	88.06312	59.04450	1

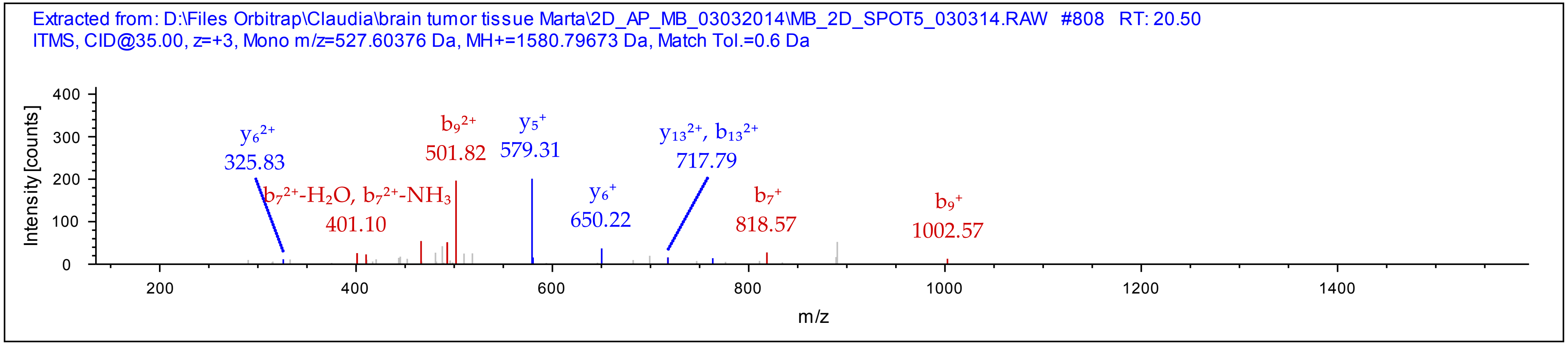


Sequence: MQKEITALAPSTMK, M1-Oxidation (15.99492 Da), M13-Oxidation (15.99492 Da)
Charge: +3, Monoisotopic m/z: 527.60376 Da (-1.87 mmu/-3.55 ppm), MH+: 1580.79673 Da, RT: 20.50 min,
Identified with: Sequest HT (v1.3); XCorr:2.00, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]
- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]

#1	**b^{+}**	**b^{2+}**	**b^{3+}**	**Seq.**	**y^{+}**	**y^{2+}**	**y^{3+}**	**#2**
1	148.04269	74.52498	50.01908	M-Oxidation				14
2	276.10127	138.55427	92.70527	Q	1433.76692	717.38710	478.59382	13

3	404.19624	202.60176	135.40360	K	1305.70834	653.35781	435.90763	12
4	533.23884	267.12306	178.41780	E	1177.61337	589.31032	393.20931	11
5	646.32291	323.66509	216.11249	I	1048.57077	524.78902	350.19511	10
6	747.37059	374.18893	249.79505	T	935.48670	468.24699	312.50042	9
7	818.40771	409.70749	273.47409	A	834.43902	417.72315	278.81786	8
8	931.49178	466.24953	311.16878	L	763.40190	382.20459	255.13882	7
9	1002.52890	501.76809	334.84782	A	650.31783	325.66255	217.44413	6
10	1099.58167	550.29447	367.19874	P	579.28071	290.14399	193.76509	5
11	1186.61370	593.81049	396.20942	S	482.22794	241.61761	161.41416	4
12	1287.66138	644.33433	429.89198	T	395.19591	198.10159	132.40349	3
13	1434.69680	717.85204	478.90378	M-Oxidation	294.14823	147.57775	98.72093	2
14				K	147.11281	74.06004	49.70912	1


Extracted from: D:\Files Orbitrap\Claudia\brain tumor tissue Marta\2D_AP_MB_03032014\MB_2D_SPOT5_030314.RAW #808 RT: 20.50
ITMS, CID@35.00, z=+3, Mono m/z=527.60376 Da, MH+=1580.79673 Da, Match Tol.=0.6 Da

Sequence: DLTDYLMK, M7-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 507.74255 Da (-1.72 mmu/-3.39 ppm), MH+: 1014.47783 Da, RT: 28.79 min,
Identified with: Sequest HT (v1.3); XCorr:1.97, Ions matched by search engine: 0/0
Fragment match tolerance used for search: 0.6 Da
Fragments used for search: b; b-H_2O; y; y-H_2O; y-NH_3

Protein references (7):
- Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]
- Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 - [ACTBL_HUMAN]
- Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
- Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]
- Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]
- Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]

- Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]

#1	**b^{+}**	**b^{2+}**	**Seq.**	**y^{+}**	**y^{2+}**	**#2**
1	116.03423	58.52075	D			8
2	229.11830	115.06279	L	899.45432	450.23080	7
3	330.16598	165.58663	T	786.37025	393.68876	6
4	445.19293	223.10010	D	685.32257	343.16492	5
5	608.25625	304.63176	Y	570.29562	285.65145	4
6	721.34032	361.17380	L	407.23230	204.11979	3
7	868.37573	434.69150	M-Oxidation	294.14823	147.57775	2
8			K	147.11281	74.06004	1