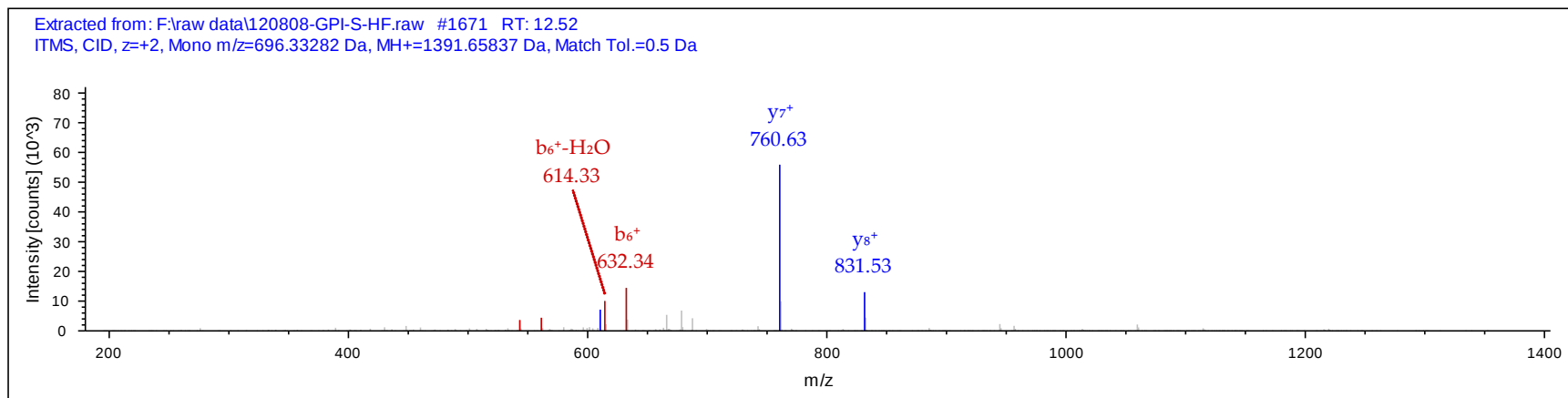


Sequence: TACDLAPRAGTTD, C3-Carbamidomethyl (57.02146 Da), D13-GPI-HF (43.04220 Da)
 Charge: +2, Monoisotopic m/z: 696.33282 Da (-0.03 mmu/-0.04 ppm), MH+: 1391.65837 Da, RT: 12.52 min,
 Identified with: Mascot (v1.27); IonScore:63, Exp Value:1.3E-004, Ions matched by search engine: 9/120
 Fragment match tolerance used for search: 0.5 Da
 Fragments used for search: b; b-H₂O; b-NH₃; y; y-H₂O; y-NH₃

Protein references (1):

- Alkaline phosphatase, placental-like OS=Homo sapiens GN=ALPPL2 PE=1 SV=4 - [PPBN_HUMAN]

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	102.05496	51.53112	T			13
2	173.09208	87.04968	A	1290.61074	645.80901	12
3	333.12273	167.06500	C-Carbamidomethyl	1219.57362	610.29045	11
4	448.14968	224.57848	D	1059.54297	530.27512	10
5	561.23375	281.12051	L	944.51602	472.76165	9
6	632.27087	316.63907	A	831.43195	416.21961	8
7	729.32364	365.16546	P	760.39483	380.70105	7
8	885.42476	443.21602	R	663.34206	332.17467	6
9	956.46188	478.73458	A	507.24094	254.12411	5
10	1013.48335	507.24531	G	436.20382	218.60555	4
11	1114.53103	557.76915	T	379.18235	190.09481	3
12	1215.57871	608.29299	T	278.13467	139.57097	2
13			D-GPI-H	177.08699	89.04713	1



Sequence: IADKKYYPS, S9-GPI-HF (43.04220 Da)

Charge: +2, Monoisotopic m/z: 564.30792 Da (-0.5 mmu/-0.88 ppm), MH+: 1127.60857 Da, RT: 11.00 min,

Identified with: Mascot (v1.27); IonScore:42, Exp Value:2.0E-002, Ions matched by search engine: 12/78

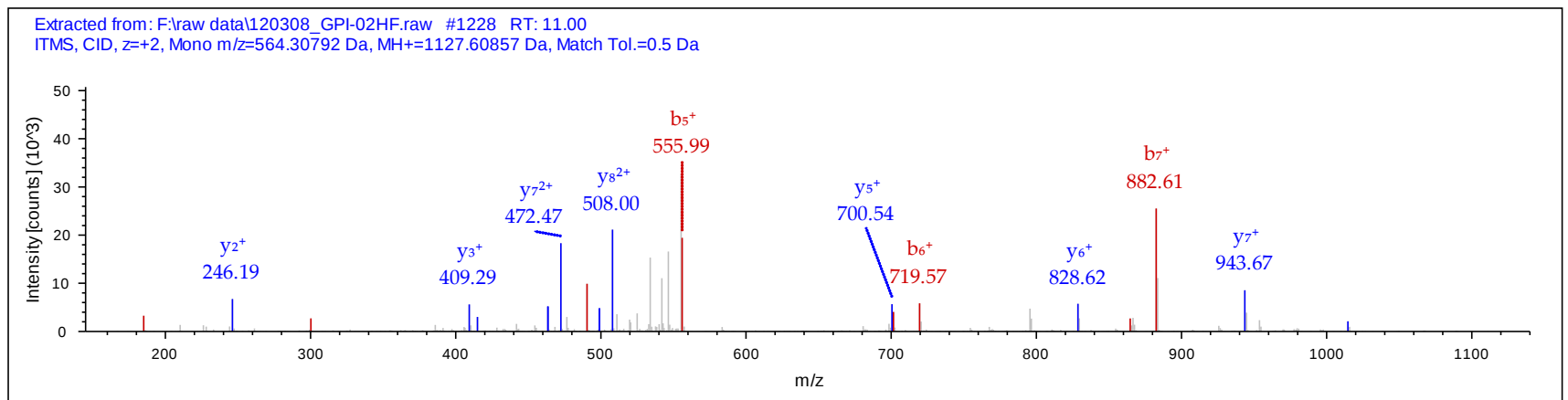
Fragment match tolerance used for search: 0.5 Da

Fragments used for search: b; b-H₂O; b-NH₃; y; y-H₂O; y-NH₃

Protein references (1):

- Bone marrow stromal antigen 2 OS=Homo sapiens GN=BST2 PE=1 SV=1 - [BST2_HUMAN]

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	114.09135	57.54931	I			9
2	185.12847	93.06787	A	1014.52549	507.76638	8
3	300.15542	150.58135	D	943.48837	472.24782	7
4	428.25039	214.62883	K	828.46142	414.73435	6
5	556.34536	278.67632	K	700.36645	350.68686	5
6	719.40868	360.20798	Y	572.27148	286.63938	4
7	882.47200	441.73964	Y	409.20816	205.10772	3
8	979.52477	490.26602	P	246.14484	123.57606	2
9			S-GPI-H	149.09207	75.04967	1



Sequence: SVRIADKKYYPS, S12-GPI-HF (43.04220 Da)

Charge: +2, Monoisotopic m/z: 735.40894 Da (-0.27 mmu/-0.36 ppm), MH+: 1469.81059 Da, RT: 12.01 min,

Identified with: Mascot (v1.27); IonScore:42, Exp Value:1.8E-002, Ions matched by search engine: 9/120

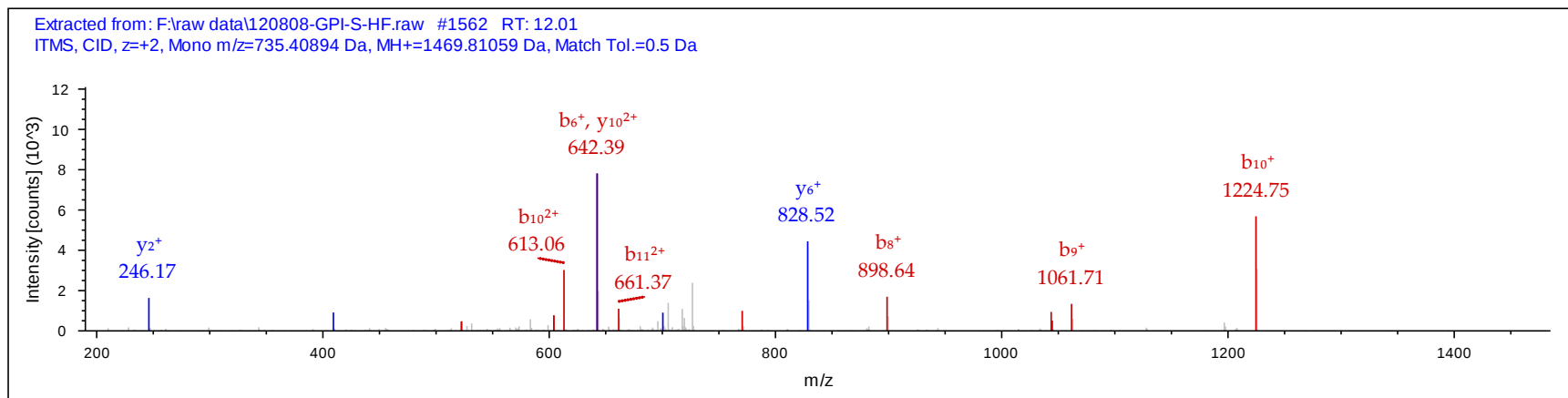
Fragment match tolerance used for search: 0.5 Da

Fragments used for search: b; b-H₂O; b-NH₃; y; y-H₂O; y-NH₃

Protein references (1):

- Bone marrow stromal antigen 2 OS=Homo sapiens GN=BST2 PE=1 SV=1 - [BST2_HUMAN]

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	88.03931	44.52329	S			12
2	187.10773	94.05750	V	1382.77910	691.89319	11
3	343.20885	172.10806	R	1283.71068	642.35898	10
4	456.29292	228.65010	I	1127.60956	564.30842	9
5	527.33004	264.16866	A	1014.52549	507.76638	8
6	642.35699	321.68213	D	943.48837	472.24782	7
7	770.45196	385.72962	K	828.46142	414.73435	6
8	898.54693	449.77710	K	700.36645	350.68686	5
9	1061.61025	531.30876	Y	572.27148	286.63938	4
10	1224.67357	612.84042	Y	409.20816	205.10772	3
11	1321.72634	661.36681	P	246.14484	123.57606	2
12			S-GPI-H	149.09207	75.04967	1



Sequence: IADKKYYPSS, S10-GPI-HF (43.04220 Da)

Charge: +2, Monoisotopic m/z: 607.82440 Da (-0.03 mmu/-0.05 ppm), MH+: 1214.64153 Da, RT: 10.94 min,

Identified with: Mascot (v1.27); IonScore:35, Exp Value:6.9E-002, Ions matched by search engine: 8/88

Fragment match tolerance used for search: 0.5 Da

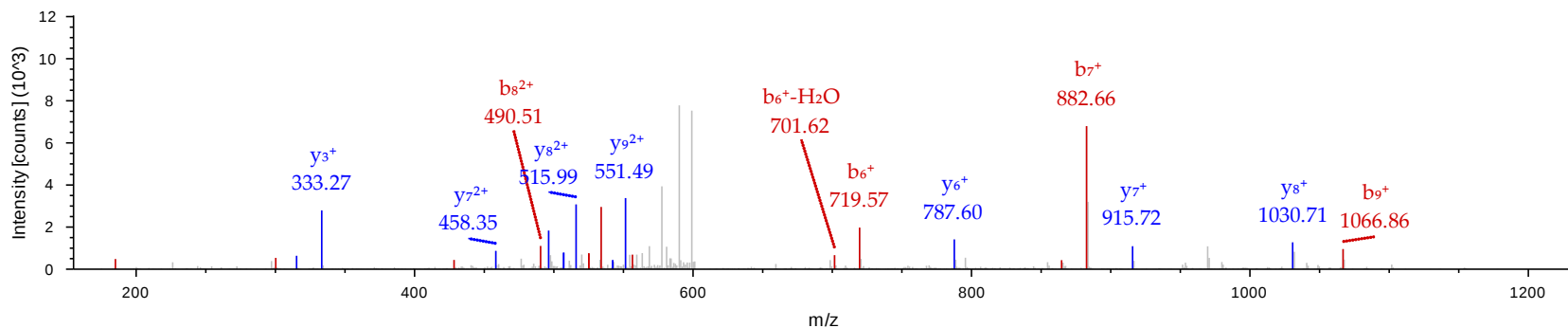
Fragments used for search: b; b-H₂O; b-NH₃; y; y-H₂O; y-NH₃

Protein references (1):

- Bone marrow stromal antigen 2 OS=Homo sapiens GN=BST2 PE=1 SV=1 - [BST2_HUMAN]

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	114.09135	57.54931	I			10
2	185.12847	93.06787	A	1101.55752	551.28240	9
3	300.15542	150.58135	D	1030.52040	515.76384	8
4	428.25039	214.62883	K	915.49345	458.25036	7
5	556.34536	278.67632	K	787.39848	394.20288	6
6	719.40868	360.20798	Y	659.30351	330.15539	5
7	882.47200	441.73964	Y	496.24019	248.62373	4
8	979.52477	490.26602	P	333.17687	167.09207	3
9	1066.55680	533.78204	S	236.12410	118.56569	2
10			S-GPI-H	149.09207	75.04967	1

Extracted from: F:\raw data\120308_GPI-02HF.raw #1213 RT: 10.94
ITMS, CID, z=+2, Mono m/z=607.82440 Da, MH+=1214.64153 Da, Match Tol.=0.5 Da



Sequence: IADKKYYPSSQD, D12-GPI-HF (43.04220 Da)

Charge: +2, Monoisotopic m/z: 729.36707 Da (-0.13 mmu/-0.18 ppm), MH+: 1457.72685 Da, RT: 11.07 min,

Identified with: Mascot (v1.27); IonScore:65, Exp Value:1.0E-004, Ions matched by search engine: 17/120

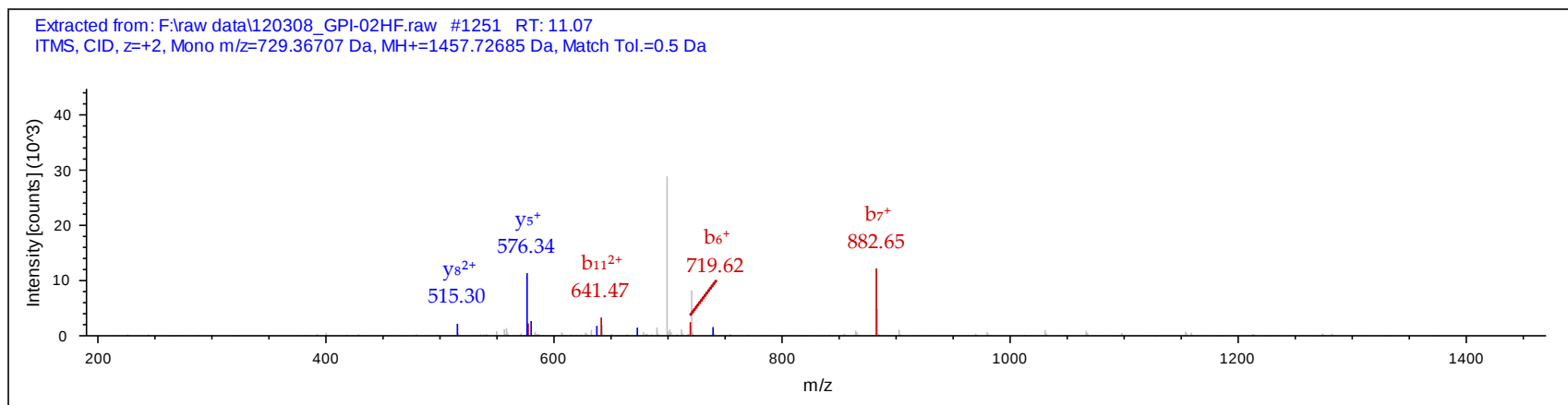
Fragment match tolerance used for search: 0.5 Da

Fragments used for search: b; b-H₂O; b-NH₃; y; y-H₂O; y-NH₃

Protein references (1):

- Bone marrow stromal antigen 2 OS=Homo sapiens GN=BST2 PE=1 SV=1 - [BST2_HUMAN]

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	114.09135	57.54931	I			12
2	185.12847	93.06787	A	1344.64305	672.82516	11
3	300.15542	150.58135	D	1273.60593	637.30660	10
4	428.25039	214.62883	K	1158.57898	579.79313	9
5	556.34536	278.67632	K	1030.48401	515.74564	8
6	719.40868	360.20798	Y	902.38904	451.69816	7
7	882.47200	441.73964	Y	739.32572	370.16650	6
8	979.52477	490.26602	P	576.26240	288.63484	5
9	1066.55680	533.78204	S	479.20963	240.10845	4
10	1153.58883	577.29805	S	392.17760	196.59244	3
11	1281.64741	641.32734	Q	305.14557	153.07642	2
12			D-GPI-H	177.08699	89.04713	1



Sequence: KYYPSSQD, D8-GPI-HF (43.04220 Da)

Charge: +2, Monoisotopic m/z: 515.74561 Da (-0.04 mmu/-0.07 ppm), MH+: 1030.48393 Da, RT: 11.43 min,

Identified with: Mascot (v1.27); IonScore:37, Exp Value:2.1E-002, Ions matched by search engine: 12/74

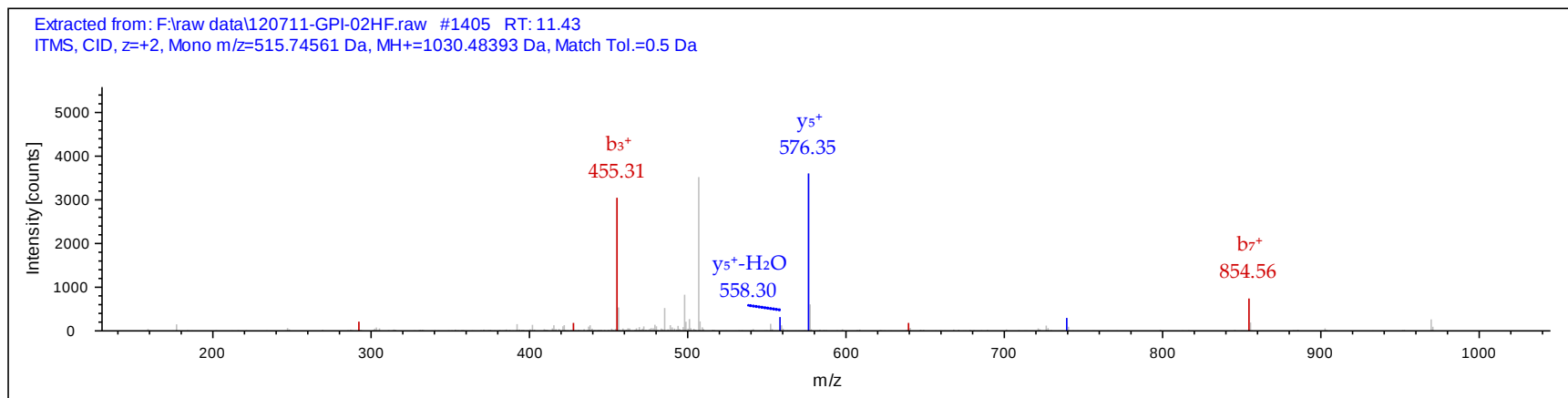
Fragment match tolerance used for search: 0.5 Da

Fragments used for search: b; b-H₂O; b-NH₃; y; y-H₂O; y-NH₃

Protein references (1):

- Bone marrow stromal antigen 2 OS=Homo sapiens GN=BST2 PE=1 SV=1 - [BST2_HUMAN]

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	129.10225	65.05476	K			8
2	292.16557	146.58642	Y	902.38904	451.69816	7
3	455.22889	228.11808	Y	739.32572	370.16650	6
4	552.28166	276.64447	P	576.26240	288.63484	5
5	639.31369	320.16048	S	479.20963	240.10845	4
6	726.34572	363.67650	S	392.17760	196.59244	3
7	854.40430	427.70579	Q	305.14557	153.07642	2
8			D-GPI-H	177.08699	89.04713	1



Sequence: SVRIADKKYYPSSQD, D15-GPI-HF (43.04220 Da)

Charge: +2, Monoisotopic m/z: 900.46838 Da (+0.4 mmu/+0.44 ppm), MH+: 1799.92949 Da, RT: 12.16 min,

Identified with: Mascot (v1.27); IonScore:58, Exp Value:5.9E-004, Ions matched by search engine: 10/162

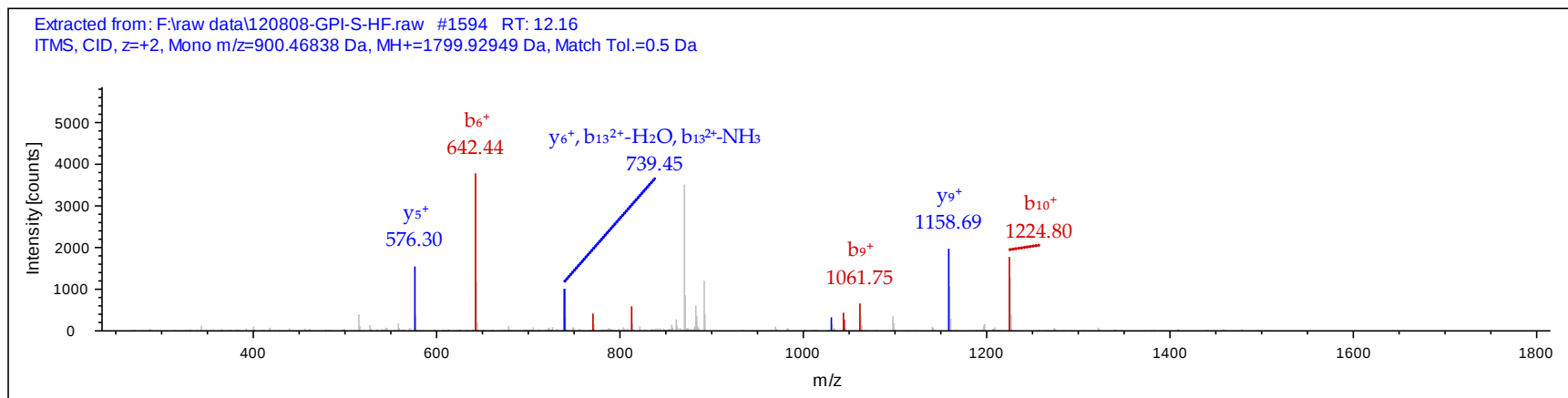
Fragment match tolerance used for search: 0.5 Da

Fragments used for search: b; b-H₂O; b-NH₃; y; y-H₂O; y-NH₃

Protein references (1):

- Bone marrow stromal antigen 2 OS=Homo sapiens GN=BST2 PE=1 SV=1 - [BST2_HUMAN]

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	88.03931	44.52329	S			15
2	187.10773	94.05750	V	1712.89666	856.95197	14
3	343.20885	172.10806	R	1613.82824	807.41776	13
4	456.29292	228.65010	I	1457.72712	729.36720	12
5	527.33004	264.16866	A	1344.64305	672.82516	11
6	642.35699	321.68213	D	1273.60593	637.30660	10
7	770.45196	385.72962	K	1158.57898	579.79313	9
8	898.54693	449.77710	K	1030.48401	515.74564	8
9	1061.61025	531.30876	Y	902.38904	451.69816	7
10	1224.67357	612.84042	Y	739.32572	370.16650	6
11	1321.72634	661.36681	P	576.26240	288.63484	5
12	1408.75837	704.88282	S	479.20963	240.10845	4
13	1495.79040	748.39884	S	392.17760	196.59244	3
14	1623.84898	812.42813	Q	305.14557	153.07642	2
15			D-GPI-H	177.08699	89.04713	1



Sequence: QQLGQRTVIKS, S11-GPI-HF (43.04220 Da)

Charge: +2, Monoisotopic m/z: 650.88831 Da (-0.14 mmu/-0.21 ppm), MH+: 1300.76933 Da, RT: 11.21 min,

Identified with: Mascot (v1.27); IonScore:43, Exp Value:8.0E-003, Ions matched by search engine: 13/106

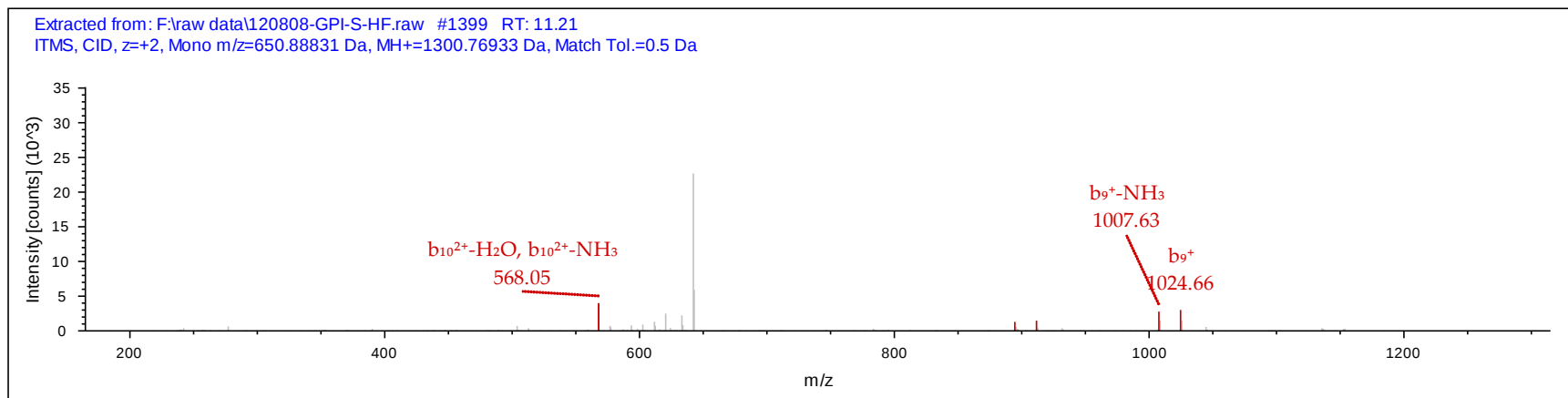
Fragment match tolerance used for search: 0.5 Da

Fragments used for search: b; b-H₂O; b-NH₃; y; y-H₂O; y-NH₃

Protein references (1):

- Carbonic anhydrase 4 OS=Homo sapiens GN=CA4 PE=1 SV=2 - [CAH4_HUMAN]

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	129.06586	65.03657	Q			11
2	257.12444	129.06586	Q	1172.71103	586.85915	10
3	370.20851	185.60789	L	1044.65245	522.82986	9
4	427.22998	214.11863	G	931.56838	466.28783	8
5	555.28856	278.14792	Q	874.54691	437.77709	7
6	711.38968	356.19848	R	746.48833	373.74780	6
7	812.43736	406.72232	T	590.38721	295.69724	5
8	911.50578	456.25653	V	489.33953	245.17340	4
9	1024.58985	512.79856	I	390.27111	195.63919	3
10	1152.68482	576.84605	K	277.18704	139.09716	2
11			S-GPI-H	149.09207	75.04967	1

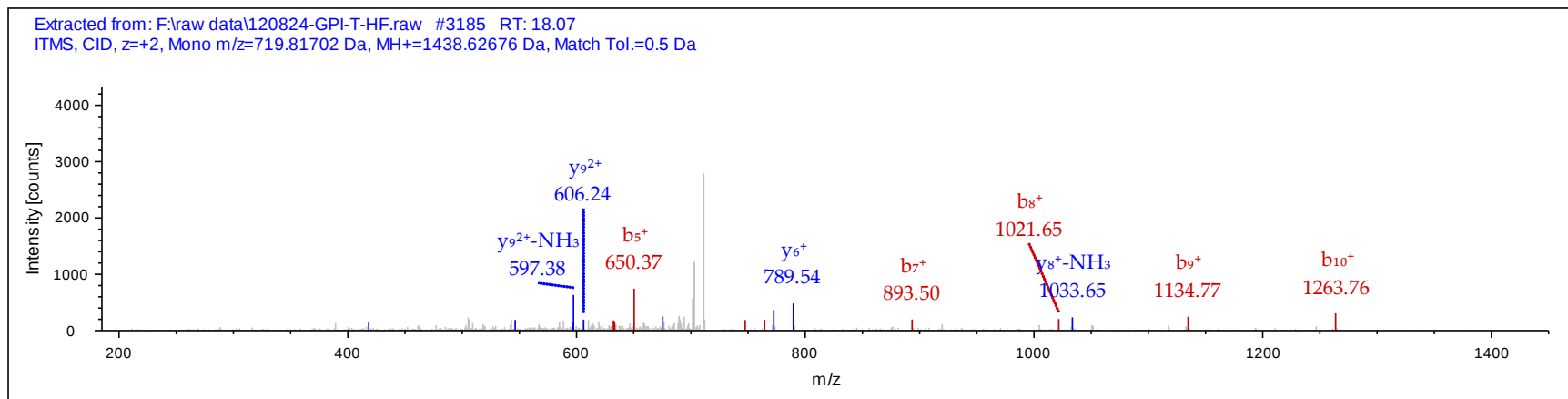


Sequence: DLCNFNEQLEN, C3-Carbamidomethyl (57.02146 Da), N11-GPI-HF (43.04220 Da)
Charge: +2, Monoisotopic m/z: 719.81702 Da (-0.01 mmu/-0.01 ppm), MH+: 1438.62676 Da, RT: 18.07 min,
Identified with: Mascot (v1.27); IonScore:38, Exp Value:2.6E-002, Ions matched by search engine: 8/112
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H₂O; b-NH₃; y; y-H₂O; y-NH₃

Protein references (1):

- CD59 glycoprotein OS=Homo sapiens GN=CD59 PE=1 SV=1 - [CD59_HUMAN]

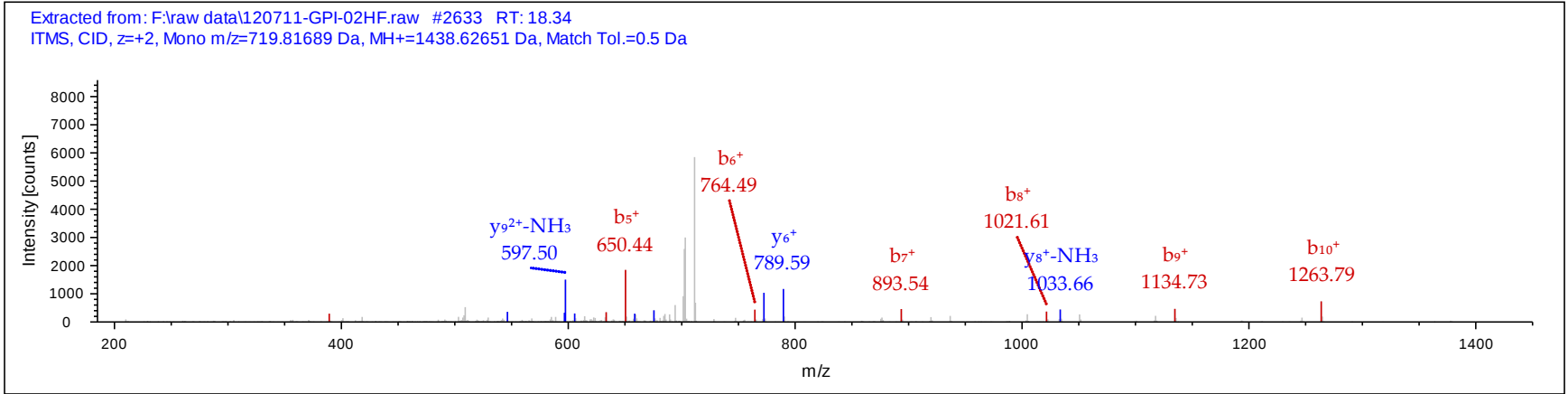
#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	116.03423	58.52075	D			11
2	229.11830	115.06279	L	1323.59982	662.30355	10
3	389.14895	195.07811	C-Carbamidomethyl	1210.51575	605.76152	9
4	503.19188	252.09958	N	1050.48510	525.74619	8
5	650.26030	325.63379	F	936.44217	468.72472	7
6	764.30323	382.65525	N	789.37375	395.19051	6
7	893.34583	447.17655	E	675.33082	338.16905	5
8	1021.40441	511.20584	Q	546.28822	273.64775	4
9	1134.48848	567.74788	L	418.22964	209.61846	3
10	1263.53108	632.26918	E	305.14557	153.07642	2
11			N-GPI-H	176.10297	88.55512	1



Sequence: DLCNFNEQLEN, C3-Carbamidomethyl (57.02146 Da), N11-GPI-HF (43.04220 Da)
 Charge: +2, Monoisotopic m/z: 719.81689 Da (-0.13 mmu/-0.18 ppm), MH+: 1438.62651 Da, RT: 18.34 min,
 Identified with: Mascot (v1.27); IonScore:41, Exp Value:1.1E-002, Ions matched by search engine: 8/112
 Fragment match tolerance used for search: 0.5 Da
 Fragments used for search: b; b-H₂O; b-NH₃; y; y-H₂O; y-NH₃

Protein references (1):
 - CD59 glycoprotein OS=Homo sapiens GN=CD59 PE=1 SV=1 - [CD59_HUMAN]

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	116.03423	58.52075	D			11
2	229.11830	115.06279	L	1323.59982	662.30355	10
3	389.14895	195.07811	C-Carbamidomethyl	1210.51575	605.76152	9
4	503.19188	252.09958	N	1050.48510	525.74619	8
5	650.26030	325.63379	F	936.44217	468.72472	7
6	764.30323	382.65525	N	789.37375	395.19051	6
7	893.34583	447.17655	E	675.33082	338.16905	5
8	1021.40441	511.20584	Q	546.28822	273.64775	4
9	1134.48848	567.74788	L	418.22964	209.61846	3
10	1263.53108	632.26918	E	305.14557	153.07642	2
11			N-GPI-H	176.10297	88.55512	1

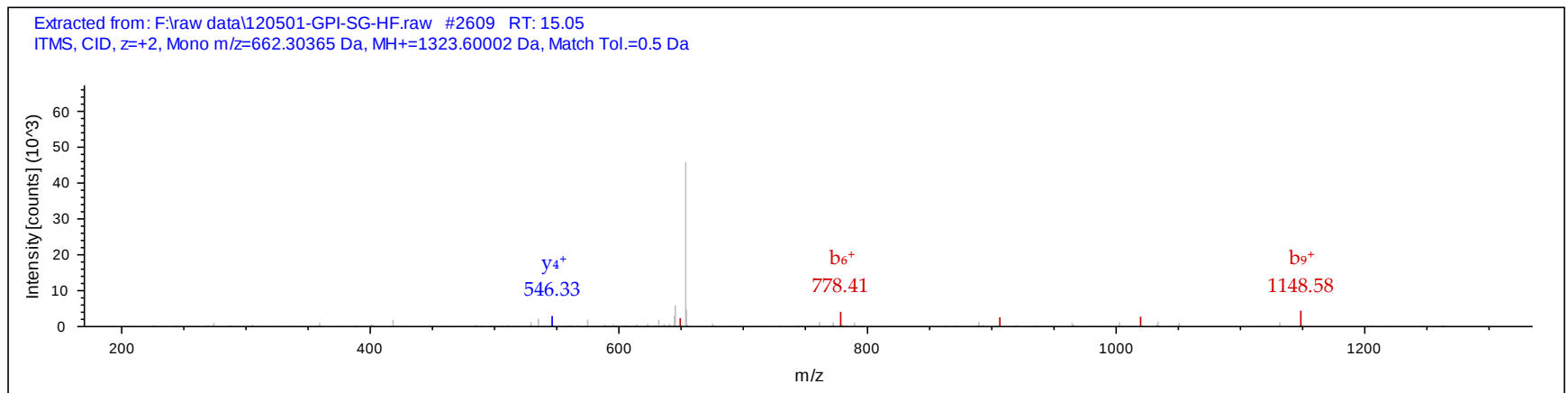


Sequence: LCNFNEQLEN, C2-Carbamidomethyl (57.02146 Da), N10-GPI-HF (43.04220 Da)
 Charge: +2, Monoisotopic m/z: 662.30365 Da (+0.1 mmu/+0.15 ppm), MH+: 1323.60002 Da, RT: 15.05 min,
 Identified with: Mascot (v1.27); IonScore:46, Exp Value:5.4E-003, Ions matched by search engine: 8/92
 Fragment match tolerance used for search: 0.5 Da
 Fragments used for search: b; b-H₂O; b-NH₃; y; y-H₂O; y-NH₃

Protein references (1):

- CD59 glycoprotein OS=Homo sapiens GN=CD59 PE=1 SV=1 - [CD59_HUMAN]

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	114.09135	57.54931	L			10
2	274.12200	137.56464	C-Carbamidomethyl	1210.51575	605.76152	9
3	388.16493	194.58610	N	1050.48510	525.74619	8
4	535.23335	268.12031	F	936.44217	468.72472	7
5	649.27628	325.14178	N	789.37375	395.19051	6
6	778.31888	389.66308	E	675.33082	338.16905	5
7	906.37746	453.69237	Q	546.28822	273.64775	4
8	1019.46153	510.23440	L	418.22964	209.61846	3
9	1148.50413	574.75570	E	305.14557	153.07642	2
10			N-GPI-H	176.10297	88.55512	1

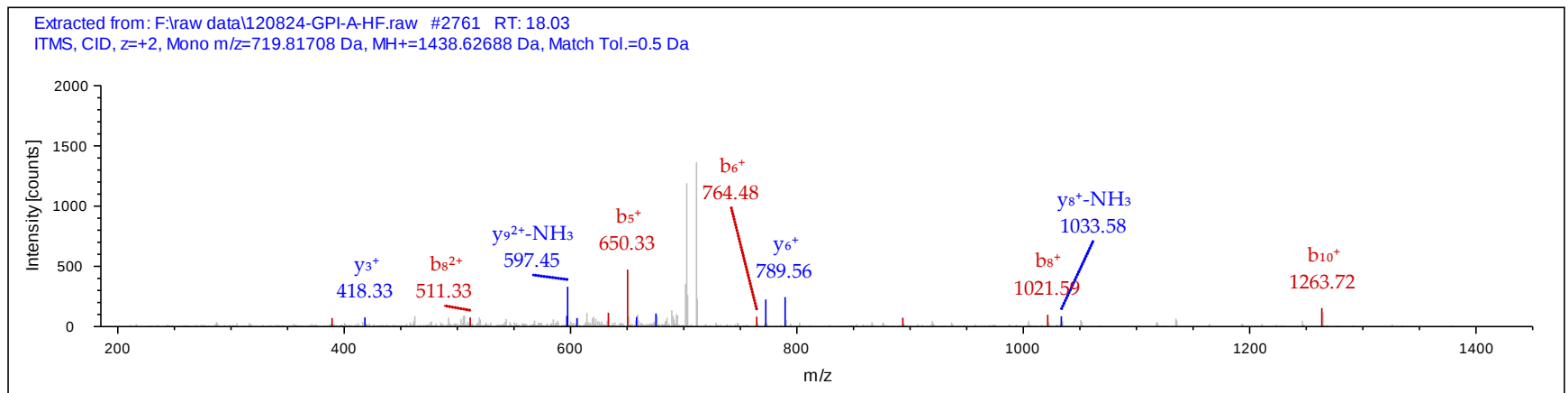


Sequence: DLCNFNEQLEN, C3-Carbamidomethyl (57.02146 Da), N11-GPI-HF (43.04220 Da)
Charge: +2, Monoisotopic m/z: 719.81708 Da (+0.05 mmu/+0.07 ppm), MH+: 1438.62688 Da, RT: 18.03 min,
Identified with: Mascot (v1.27); IonScore:34, Exp Value:5.6E-002, Ions matched by search engine: 6/112
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H₂O; b-NH₃; y; y-H₂O; y-NH₃

Protein references (1):

- CD59 glycoprotein OS=Homo sapiens GN=CD59 PE=1 SV=1 - [CD59_HUMAN]

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	116.03423	58.52075	D			11
2	229.11830	115.06279	L	1323.59982	662.30355	10
3	389.14895	195.07811	C-Carbamidomethyl	1210.51575	605.76152	9
4	503.19188	252.09958	N	1050.48510	525.74619	8
5	650.26030	325.63379	F	936.44217	468.72472	7
6	764.30323	382.65525	N	789.37375	395.19051	6
7	893.34583	447.17655	E	675.33082	338.16905	5
8	1021.40441	511.20584	Q	546.28822	273.64775	4
9	1134.48848	567.74788	L	418.22964	209.61846	3
10	1263.53108	632.26918	E	305.14557	153.07642	2
11			N-GPI-H	176.10297	88.55512	1



Sequence: YRNLPD, D6-GPI-HF (43.04220 Da)

Charge: +2, Monoisotopic m/z: 410.71893 Da (-0.31 mmu/-0.74 ppm), MH+: 820.43059 Da, RT: 11.67 min,

Identified with: Mascot (v1.27); IonScore:35, Exp Value:5.5E-002, Ions matched by search engine: 7/42

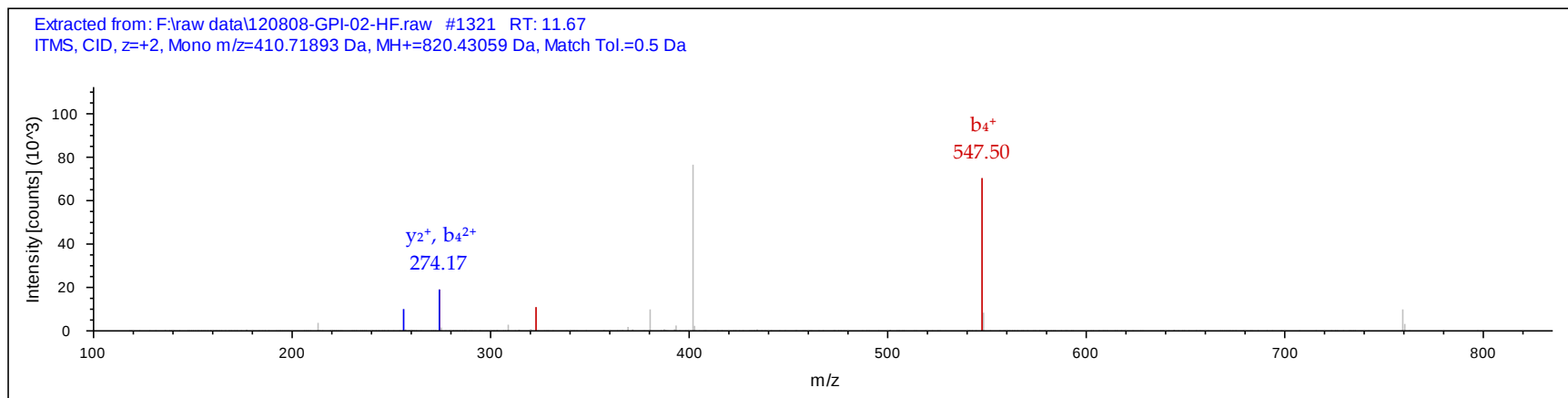
Fragment match tolerance used for search: 0.5 Da

Fragments used for search: b; b-NH₃; y; y-H₂O; y-NH₃

Protein references (1):

- Carboxypeptidase M OS=Homo sapiens GN=CPM PE=1 SV=2 - [CBPM_HUMAN]

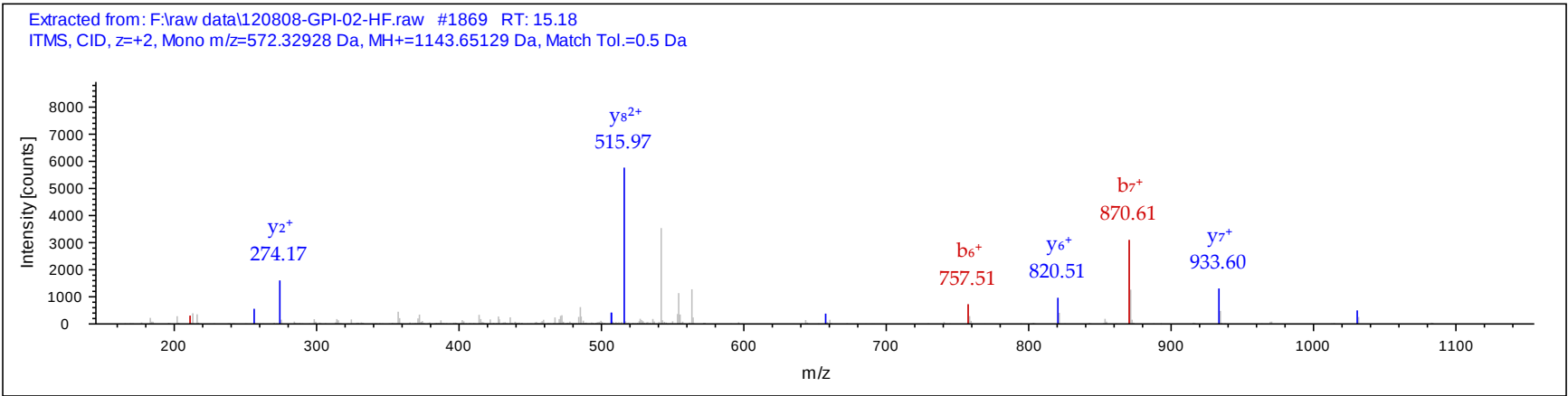
#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	164.07060	82.53894	Y			6
2	320.17172	160.58950	R	657.36788	329.18758	5
3	434.21465	217.61096	N	501.26676	251.13702	4
4	547.29872	274.15300	L	387.22383	194.11555	3
5	644.35149	322.67938	P	274.13976	137.57352	2
6			D-GPI-H	177.08699	89.04713	1



Sequence: IPLYRNLPD, D9-GPI-HF (43.04220 Da)
Charge: +2, Monoisotopic m/z: 572.32928 Da (-0.41 mmu/-0.71 ppm), MH+: 1143.65129 Da, RT: 15.18 min,
Identified with: Mascot (v1.27); IonScore:27, Exp Value:6.8E-001, Ions matched by search engine: 5/66
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-NH₃; y; y-H₂O; y-NH₃

Protein references (1):
- Carboxypeptidase M OS=Homo sapiens GN=CPM PE=1 SV=2 - [CBPM_HUMAN]

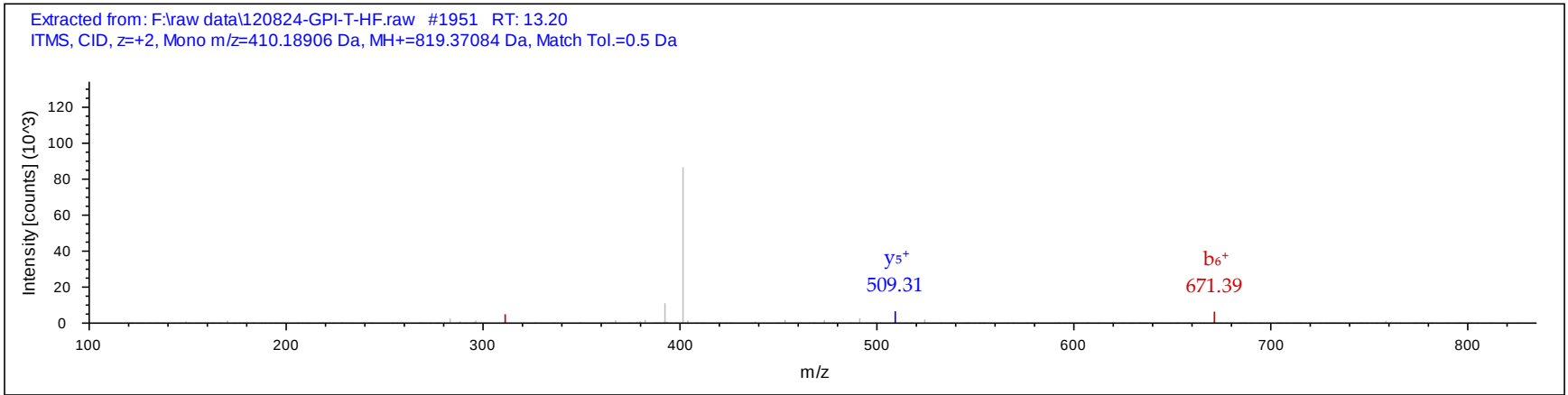
#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	114.09135	57.54931	I			9
2	211.14412	106.07570	P	1030.56804	515.78766	8
3	324.22819	162.61773	L	933.51527	467.26127	7
4	487.29151	244.14939	Y	820.43120	410.71924	6
5	643.39263	322.19995	R	657.36788	329.18758	5
6	757.43556	379.22142	N	501.26676	251.13702	4
7	870.51963	435.76345	L	387.22383	194.11555	3
8	967.57240	484.28984	P	274.13976	137.57352	2
9			D-GPI-H	177.08699	89.04713	1



Sequence: FYAAAMS, M6-Oxidation (15.99492 Da), S7-GPI-HF (43.04220 Da)
 Charge: +2, Monoisotopic m/z: 410.18906 Da (+0.13 mmu/+0.31 ppm), MH+: 819.37084 Da, RT: 13.20 min,
 Identified with: Mascot (v1.27); IonScore:40, Exp Value:1.2E-002, Ions matched by search engine: 9/50
 Fragment match tolerance used for search: 0.5 Da
 Fragments used for search: b; y; y-H₂O

Protein references (1):
 - Folate receptor alpha OS=Homo sapiens GN=FOLR1 PE=1 SV=3 - [FOLR1_HUMAN]

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	148.07570	74.54149	F			7
2	311.13902	156.07315	Y	672.30217	336.65472	6
3	382.17614	191.59171	A	509.23885	255.12306	5
4	453.21326	227.11027	A	438.20173	219.60450	4
5	524.25038	262.62883	A	367.16461	184.08594	3
6	671.28579	336.14653	M-Oxidation	296.12749	148.56738	2
7			S-GPI-H	149.09207	75.04967	1



Sequence: VARFYAAAMS, S10-GPI-HF (43.04220 Da)

Charge: +2, Monoisotopic m/z: 565.29449 Da (-0.31 mmu/-0.55 ppm), MH+: 1129.58171 Da, RT: 14.45 min,

Identified with: Mascot (v1.27); IonScore:26, Exp Value:5.9E-001, Ions matched by search engine: 5/72

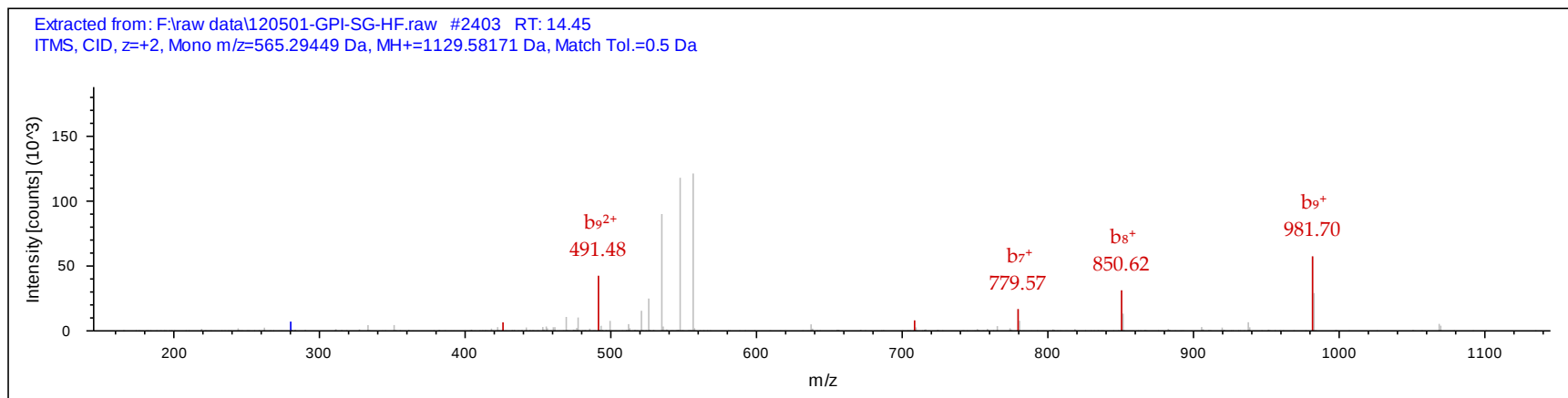
Fragment match tolerance used for search: 0.5 Da

Fragments used for search: b; b-NH₃; y; y-H₂O; y-NH₃

Protein references (1):

- Folate receptor alpha OS=Homo sapiens GN=FOLR1 PE=1 SV=3 - [FOLR1_HUMAN]

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	100.07570	50.54149	V			10
2	171.11282	86.06005	A	1030.51391	515.76059	9
3	327.21394	164.11061	R	959.47679	480.24203	8
4	474.28236	237.64482	F	803.37567	402.19147	7
5	637.34568	319.17648	Y	656.30725	328.65726	6
6	708.38280	354.69504	A	493.24393	247.12560	5
7	779.41992	390.21360	A	422.20681	211.60704	4
8	850.45704	425.73216	A	351.16969	176.08848	3
9	981.49754	491.25241	M	280.13257	140.56992	2
10			S-GPI-H	149.09207	75.04967	1



Sequence: VARFYAAAMS, M9-Oxidation (15.99492 Da), S10-GPI-HF (43.04220 Da)

Charge: +2, Monoisotopic m/z: 573.29230 Da (+0.04 mmu/+0.06 ppm), MH+: 1145.57732 Da, RT: 12.92 min,

Identified with: Mascot (v1.27); IonScore:34, Exp Value:1.1E-001, Ions matched by search engine: 7/72

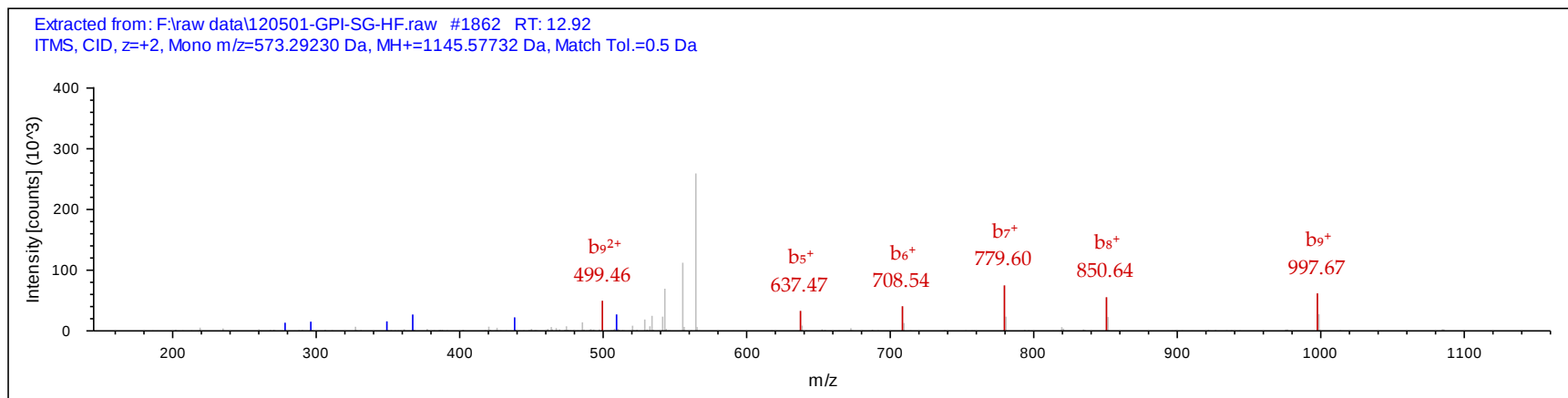
Fragment match tolerance used for search: 0.5 Da

Fragments used for search: b; b-NH₃; y; y-H₂O; y-NH₃

Protein references (1):

- Folate receptor alpha OS=Homo sapiens GN=FOLR1 PE=1 SV=3 - [FOLR1_HUMAN]

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	100.07570	50.54149	V			10
2	171.11282	86.06005	A	1046.50883	523.75805	9
3	327.21394	164.11061	R	975.47171	488.23949	8
4	474.28236	237.64482	F	819.37059	410.18893	7
5	637.34568	319.17648	Y	672.30217	336.65472	6
6	708.38280	354.69504	A	509.23885	255.12306	5
7	779.41992	390.21360	A	438.20173	219.60450	4
8	850.45704	425.73216	A	367.16461	184.08594	3
9	997.49245	499.24986	M-Oxidation	296.12749	148.56738	2
10			S-GPI-H	149.09207	75.04967	1



Sequence: GLGASSHITTKS, S12-GPI-HF (43.04220 Da)

Charge: +2, Monoisotopic m/z: 601.33063 Da (+0.2 mmu/+0.34 ppm), MH+: 1201.65398 Da, RT: 10.42 min,

Identified with: Mascot (v1.27); IonScore:53, Exp Value:1.8E-003, Ions matched by search engine: 13/102

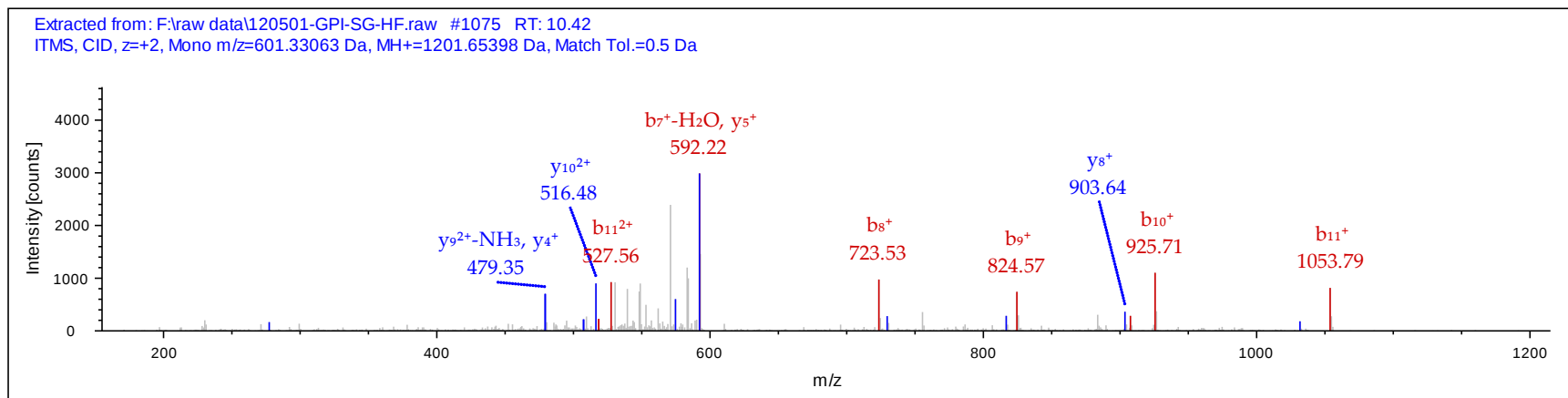
Fragment match tolerance used for search: 0.5 Da

Fragments used for search: b; b-H₂O; b-NH₃; y; y-H₂O; y-NH₃

Protein references (1):

- GDNF family receptor alpha-1 OS=Homo sapiens GN=GFRA1 PE=2 SV=2 - [GFRA1_HUMAN]

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	58.02875	29.51801	G			12
2	171.11282	86.06005	L	1144.63210	572.81969	11
3	228.13429	114.57078	G	1031.54803	516.27765	10
4	299.17141	150.08934	A	974.52656	487.76692	9
5	386.20344	193.60536	S	903.48944	452.24836	8
6	473.23547	237.12137	S	816.45741	408.73234	7
7	610.29438	305.65083	H	729.42538	365.21633	6
8	723.37845	362.19286	I	592.36647	296.68687	5
9	824.42613	412.71670	T	479.28240	240.14484	4
10	925.47381	463.24054	T	378.23472	189.62100	3
11	1053.56878	527.28803	K	277.18704	139.09716	2
12			S-GPI-H	149.09207	75.04967	1



Sequence: KVIYPAVEGRIKFS, S14-GPI-HF (43.04220 Da)

Charge: +3, Monoisotopic m/z: 550.66235 Da (-0.43 mmu/-0.79 ppm), MH+: 1649.97251 Da, RT: 14.24 min,

Identified with: Mascot (v1.27); IonScore:39, Exp Value:1.3E-002, Ions matched by search engine: 8/138

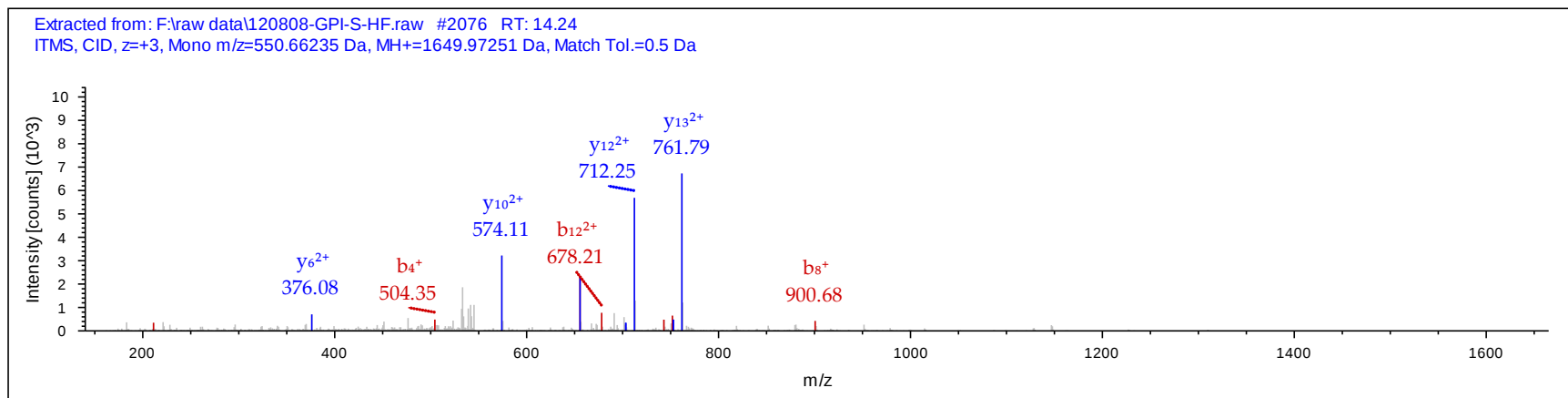
Fragment match tolerance used for search: 0.5 Da

Fragments used for search: b; b-H₂O; b-NH₃; y; y-H₂O; y-NH₃

Protein references (1):

- 5'-nucleotidase OS=Homo sapiens GN=NT5E PE=1 SV=1 - [5NTD_HUMAN]

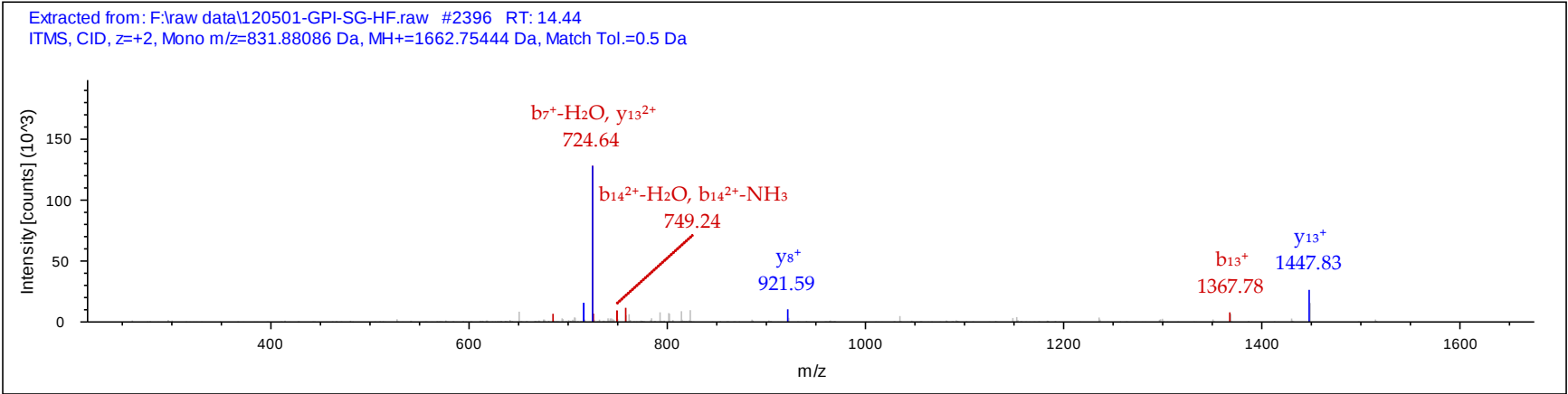
#1	b ⁺	b ²⁺	b ³⁺	Seq.	y ⁺	y ²⁺	y ³⁺	#2
1	129.10225	65.05476	43.70560	K				14
2	228.17067	114.58897	76.72841	V	1521.87884	761.44306	507.96446	13
3	341.25474	171.13101	114.42310	I	1422.81042	711.90885	474.94166	12
4	504.31806	252.66267	168.77754	Y	1309.72635	655.36681	437.24697	11
5	601.37083	301.18905	201.12846	P	1146.66303	573.83515	382.89253	10
6	672.40795	336.70761	224.80750	A	1049.61026	525.30877	350.54160	9
7	771.47637	386.24182	257.83031	V	978.57314	489.79021	326.86256	8
8	900.51897	450.76312	300.84451	E	879.50472	440.25600	293.83976	7
9	957.54044	479.27386	319.85166	G	750.46212	375.73470	250.82556	6
10	1113.64156	557.32442	371.88537	R	693.44065	347.22396	231.81840	5
11	1226.72563	613.86645	409.58006	I	537.33953	269.17340	179.78469	4
12	1354.82060	677.91394	452.27838	K	424.25546	212.63137	142.09000	3
13	1501.88902	751.44815	501.30119	F	296.16049	148.58388	99.39168	2
14				S-GPI-H	149.09207	75.04967	50.36887	1



Sequence: SQPDSNLGSHLAFS, C8-Carbamidomethyl (57.02146 Da), S15-GPI-HF (43.04220 Da)
Charge: +2, Monoisotopic m/z: 831.88086 Da (+0.17 mmu/+0.2 ppm), MH+: 1662.75444 Da, RT: 14.44 min,
Identified with: Mascot (v1.27); IonScore:46, Exp Value:5.0E-003, Ions matched by search engine: 9/148
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H₂O; b-NH₃; y; y-H₂O; y-NH₃

Protein references (1):
- Prostatic OS=Homo sapiens GN=PRSS8 PE=1 SV=1 - [PRSS8_HUMAN]

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	88.03931	44.52329	S			15
2	216.09789	108.55258	Q	1575.72207	788.36468	14
3	313.15066	157.07897	P	1447.66349	724.33539	13
4	428.17761	214.59244	D	1350.61072	675.80900	12
5	515.20964	258.10846	S	1235.58377	618.29553	11
6	629.25257	315.12992	N	1148.55174	574.77951	10
7	742.33664	371.67196	L	1034.50881	517.75805	9
8	902.36729	451.68728	C-Carbamidomethyl	921.42474	461.21601	8
9	959.38876	480.19802	G	761.39409	381.20068	7
10	1046.42079	523.71403	S	704.37262	352.68995	6
11	1183.47970	592.24349	H	617.34059	309.17393	5
12	1296.56377	648.78552	L	480.28168	240.64448	4
13	1367.60089	684.30408	A	367.19761	184.10244	3
14	1514.66931	757.83829	F	296.16049	148.58388	2
15			S-GPI-H	149.09207	75.04967	1



Sequence: DSNLCGSHLAFS, C5-Carbamidomethyl (57.02146 Da), S12-GPI-HF (43.04220 Da)

Charge: +2, Monoisotopic m/z: 675.80939 Da (+0.39 mmu/+0.57 ppm), MH+: 1350.61150 Da, RT: 15.39 min,

Identified with: Mascot (v1.27); IonScore:49, Exp Value:2.5E-003, Ions matched by search engine: 8/110

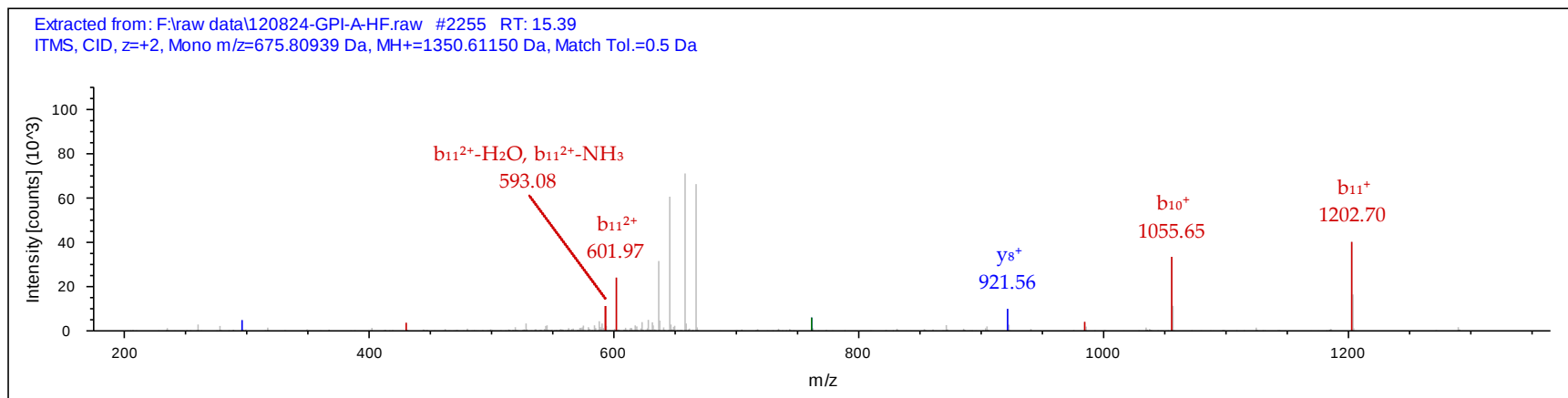
Fragment match tolerance used for search: 0.5 Da

Fragments used for search: b; b-H₂O; b-NH₃; y; y-H₂O; y-NH₃

Protein references (1):

- Prostatic OS=Homo sapiens GN=PRSS8 PE=1 SV=1 - [PRSS8_HUMAN]

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	116.03423	58.52075	D			12
2	203.06626	102.03677	S	1235.58377	618.29553	11
3	317.10919	159.05823	N	1148.55174	574.77951	10
4	430.19326	215.60027	L	1034.50881	517.75805	9
5	590.22391	295.61559	C-Carbamidomethyl	921.42474	461.21601	8
6	647.24538	324.12633	G	761.39409	381.20068	7
7	734.27741	367.64234	S	704.37262	352.68995	6
8	871.33632	436.17180	H	617.34059	309.17393	5
9	984.42039	492.71383	L	480.28168	240.64448	4
10	1055.45751	528.23239	A	367.19761	184.10244	3
11	1202.52593	601.76660	F	296.16049	148.58388	2
12			S-GPI-H	149.09207	75.04967	1



Sequence: QVDIDAYTTCLYA, C10-Carbamidomethyl (57.02146 Da), A13-GPI-HF (43.04220 Da)
Charge: +2, Monoisotopic m/z: 788.37103 Da (-0.59 mmu/-0.75 ppm), MH+: 1575.73479 Da, RT: 19.26 min,
Identified with: Mascot (v1.27); IonScore:39, Exp Value:3.0E-002, Ions matched by search engine: 14/108
Fragment match tolerance used for search: 0.5 Da
Fragments used for search: b; b-H₂O; b-NH₃; y; y-H₂O

Protein references (1):

- Acid sphingomyelinase-like phosphodiesterase 3b OS=Homo sapiens GN=SMPDL3B PE=2 SV=2 - [ASM3B_HUMAN]

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	129.06586	65.03657	Q			13
2	228.13428	114.57078	V	1447.67739	724.34234	12
3	343.16123	172.08425	D	1348.60897	674.80813	11
4	456.24530	228.62629	I	1233.58202	617.29465	10
5	571.27225	286.13976	D	1120.49795	560.75262	9
6	642.30937	321.65832	A	1005.47100	503.23914	8
7	805.37269	403.18998	Y	934.43388	467.72058	7
8	906.42037	453.71382	T	771.37056	386.18892	6
9	1007.46805	504.23766	T	670.32288	335.66508	5
10	1167.49870	584.25299	C-Carbamidomethyl	569.27520	285.14124	4
11	1280.58277	640.79502	L	409.24455	205.12591	3
12	1443.64609	722.32668	Y	296.16048	148.58388	2
13			A-GPI-H	133.09716	67.05222	1

