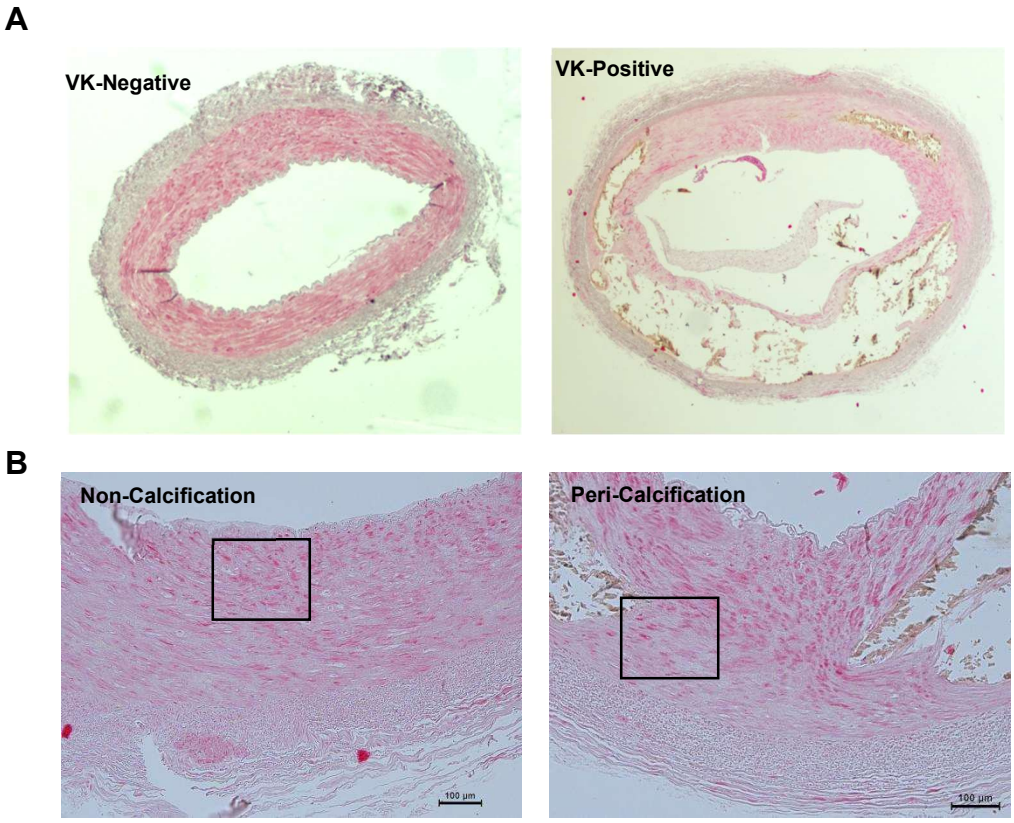
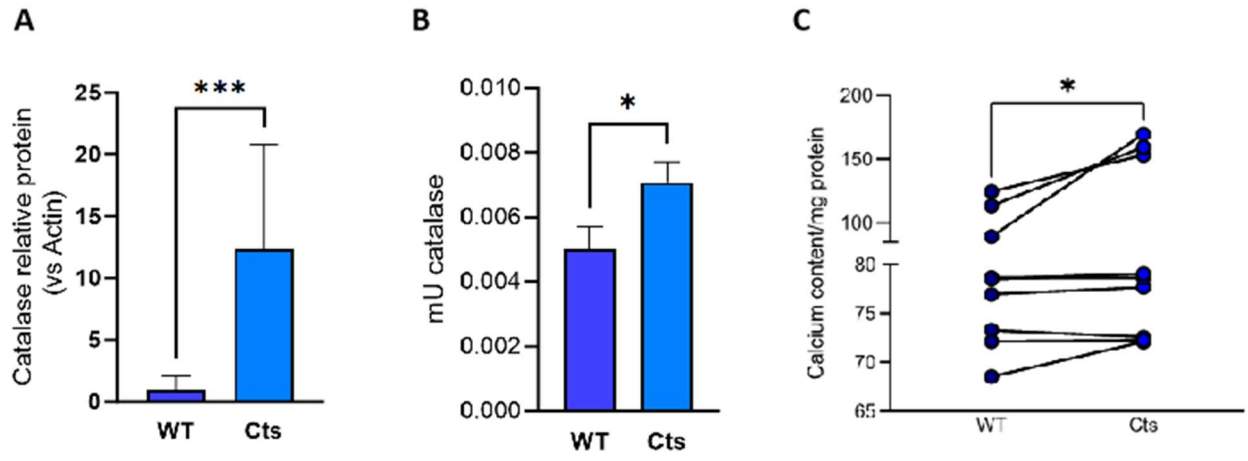
Supplementary material

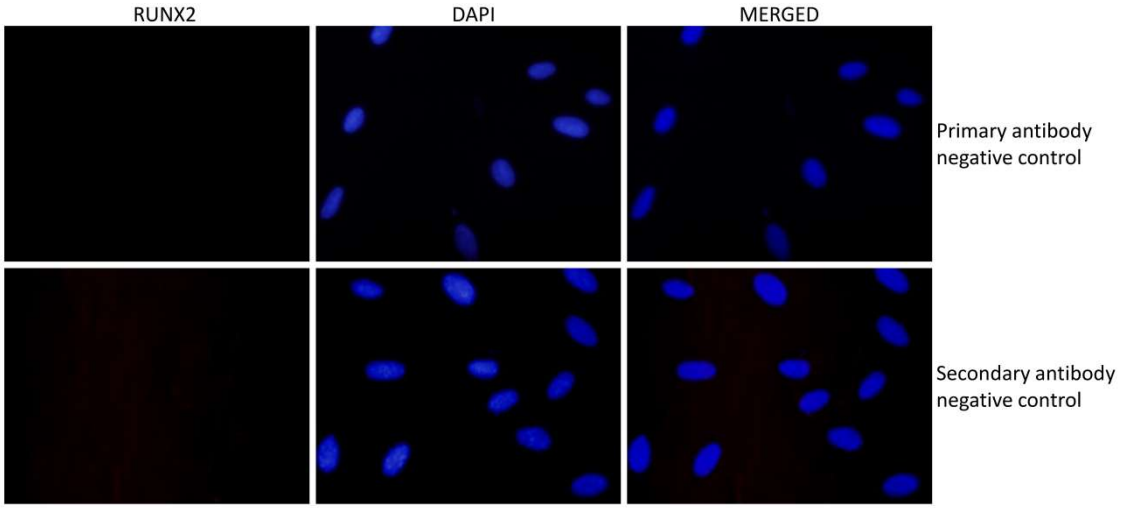
Catalase mitigates vascular calcification by non-nuclear Runx2 translocation in Chronic-Kidney Disease models



Supplementary Figure 1: Representative images of von Kossa staining. A) Epigastric arteria negative and positive for von kossa staining. B) Micrographies of distant and peri-calcification areas of the same epigastric ar-teria section for Von Kossa staining.



Supplementary Figure 2: VSMCs from Wild-type (WT) and Catalase (Cts) cell culture. A) Relative optical density of western-blot data for catalase protein expression. B) Cts activity in VSMC cell culture. C) Calcium content per mg of protein in WT cell culture and Cts overexpressing cells. Each pair correspond to one individual experiment.



Supplementary Figure 3. Immunofluorescence of RUNX2 in VSMCs. Negative controls for primary (rabbit anti-RUNX2) and secondary antibody (anti-rabbit Alexa Fluor 594). DAPI is used as nuclear counter-staining.

Supplementary Table 1: Biochemical parameters of sham-operated rats with normal renal function without vascular calcification (No-VC) and nephrectomised rats fed a high phosphorus (HPD) with vascular calcification (VC) diet at 20 weeks.

	No-VC (N= 3)			VC (N=3)			
	Mean	**SD**	**95%CI**	**Mean**	**SD**	**95%CI**	**p-value**
Creatinine (mg/dL)	0.43	0.05	0.29-0.57	3.2	0.52	1.88-4.51	0.011
Urea (mg/dL)	39	13.07	6.52-71.48	262	39.66	163.48-360-52	0.001
Albumin (mg/dL)	46.9	1.75	42.54-51.25	29.46	2.77	22.56-36.37	0.001
Phosphorus (mg/dL)	5.06	1.19	2.10-8.03	15.16	2.22	9.64-20.69	0.002
Calcium (mg/dL)	11.8	0.79	9.82-13.77	10.9	0.10	10.65-11.14	0.187

SD: standard deviation; CI: confidence interval

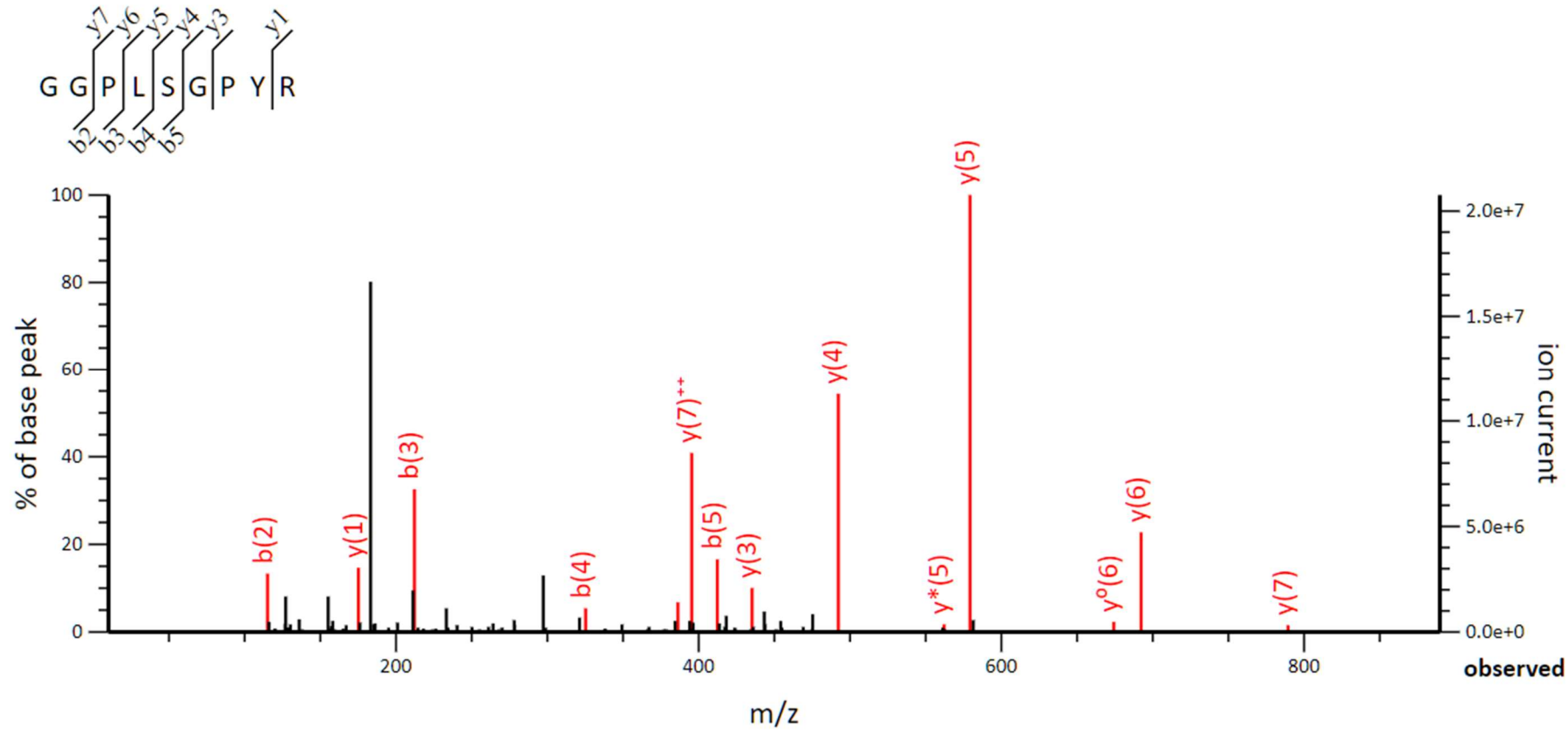
Supplementary Table 2. Summary of the peptides identified by LC-MS/MS. More detailed information can be found in the annexe.

Spot Nº	MASCOT Symbol	Peptide sequence	Observed m/z	Ion charge	Mr(expt)	Mr(calc)	Delta	Score	Matches	RMS error (ppm)
1	CAH3	GGPLSGPYR	452.4518	2+	902.8890	902.4610	0.4279	50	15/64	399
		VVFDDTFDR	557.5192	2+	1113.0239	1112.5139	0.5100	43	20/72	216
		EPMTVSSDQMAK	678.4788	2+	1354.9431	1354.5745	0.3686	53	53/200	472
2	GPX3	QEPGENSEILPSLK	770.9166	2+	1539.8186	1540.7620	-0.9434	57	31/150	1123
		NSCPPTAELLGSPGR	778.4015	2+	1554.7885	1554.7460	0.0424	68	21/160	1341
3	GSTM2	LYSEFLGK	478.9332	2+	955.8518	955.5015	0.3503	32	10/58	794
		ITQSNAILR	508.4895	2+	1014.9644	1014.5822	0.3822	65	22/80	570
		CLDAFPNLK	539.4450	2+	1076.8755	1076.5325	0.3430	37	22/68	950
		YSMGDAPDYDR	653.3469	2+	1304.6793	1304.4979	0.1814	58	17/140	1019
		VDVLENQAMDTR	703.9233	2+	1405.8321	1405.6507	0.1814	78	41/184	558
		LFLEYTDTSYEDK	812.3617	2+	1622.7088	1622.7352	-0.0264	63	13/112	305
		LFLEYTDTSYEDKK	876.3865	2+	1750.7584	1750.8301	-0.0717	68	21/122	780
4	SODM	GELLEAIKR	514.9566	2+	1027.8986	1027.6026	0.2961	51	20/72	1109
		GDVTTQVALQPALK	720.9116	2+	1439.8087	1439.7984	0.0103	93	20/126	936
5	TKT	LAVSQVPR	435.4305	2+	868.8465	868.5130	0.3335	40	12/62	291
		HQPTAIIAK	489.9728	2+	977.9310	977.5658	0.3652	29	17/78	1219

MASCOT search parameters; Database: SwissProt 2022_04 (accessed 12/14/2022), Taxonomy: Rattus (8,180 sequences), Enzyme: Trypsin, Max missed cleavages: 1, Fixed modifications: Carbamidomethyl (C), Variable modifications: Deaminated (NQ) and Oxidation (M), Peptide mass tolerance: 1.2 Da, Fragment mass tolerance: 0.6 Da, Instrument: ESI-TRAP.

ANNEXE

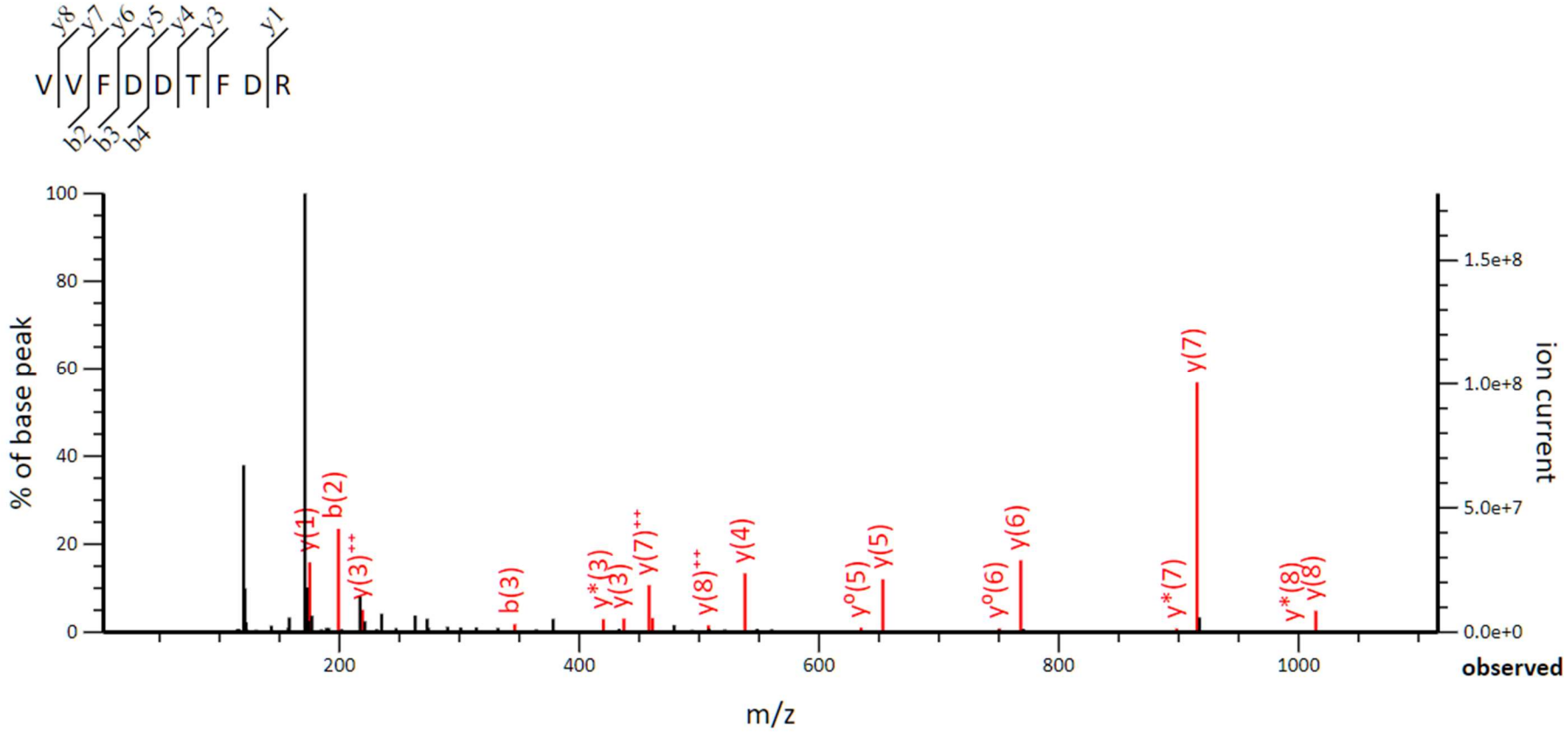
MS/MS Fragmentation of **GGPLSGPYR** found in **CAH3**



Monoisotopic mass of neutral peptide Mr(calc): 902.4610
Ions Score: 50 **Expect:** 0.00024
Matches: 15/64 fragment ions using 19 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							9
2	115.0502	58.0287			G	846.4468	423.7271	829.4203	415.2138	828.4363	414.7218	8
3	212.1030	106.5551			P	*789.4254*	395.2163	772.3988	386.7030	771.4148	386.2110	7
4	325.1870	163.0972			L	*692.3726*	346.6899	675.3461	338.1767	674.3620	337.6847	6
5	412.2191	206.6132	394.2085	197.6079	S	*579.2885*	290.1479	562.2620	281.6346	561.2780	281.1426	5
6	469.2405	235.1239	451.2300	226.1186	G	*492.2565*	246.6319	475.2300	238.1186			4
7	566.2933	283.6503	548.2827	274.6450	P	*435.2350*	218.1212	418.2085	209.6079			3
8	729.3566	365.1819	711.3461	356.1767	Y	338.1823	169.5948	321.1557	161.0815			2
9					R	*175.1190*	88.0631	158.0924	79.5498			1

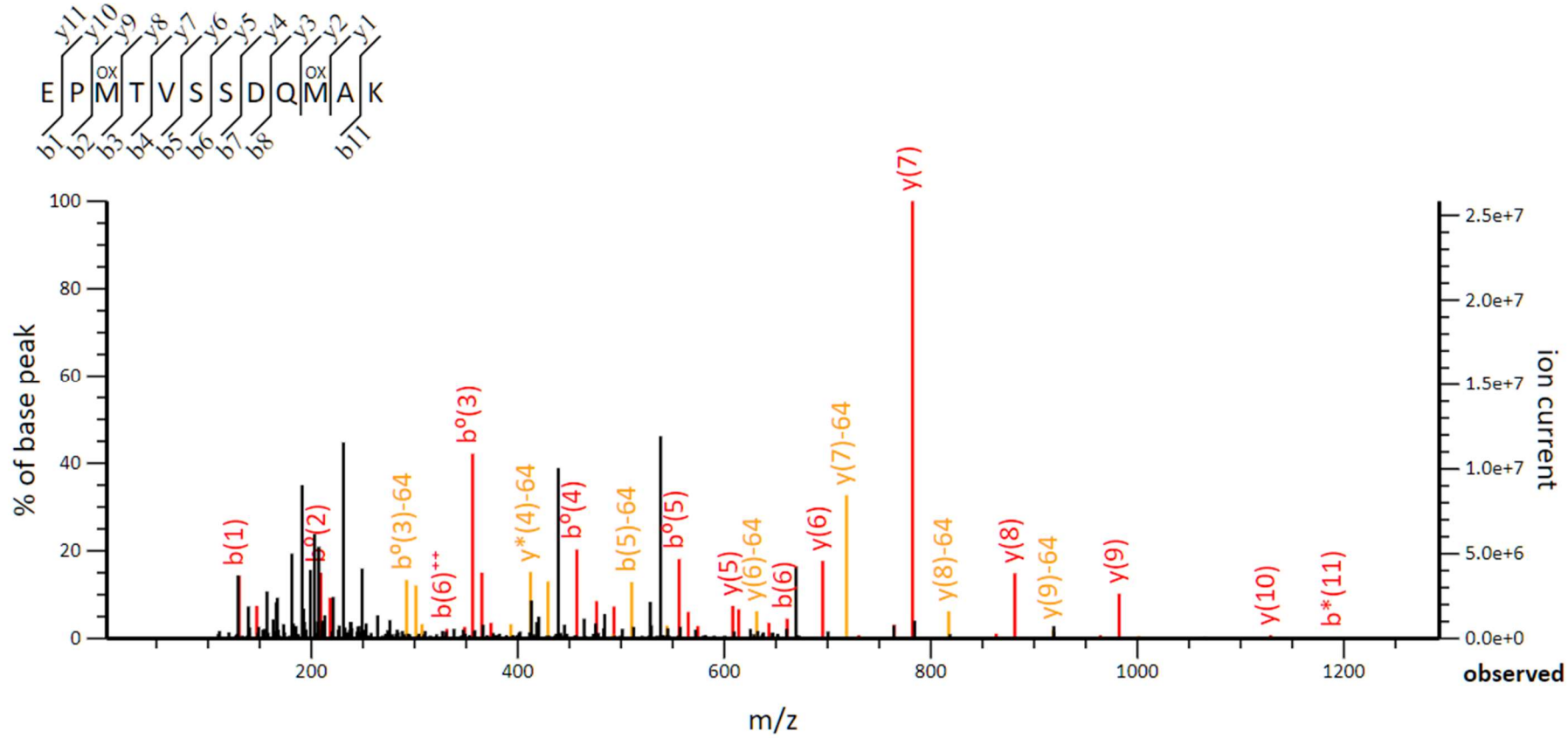
MS/MS Fragmentation of **VVFDDTFDR** found in **CAH3**



Monoisotopic mass of neutral peptide Mr(calc): 1112.5139
Ions Score: 43 **Expect:** 0.0017
Matches: 20/72 fragment ions using 38 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415			V							9
2	**199.1441**	100.0757			V	***1014.4527***	**507.7300**	997.4262	499.2167	996.4421	498.7247	8
3	**346.2125**	173.6099			F	***915.3843***	**458.1958**	898.3577	449.6825	897.3737	449.1905	7
4	**461.2395**	231.1234	443.2289	222.1181	D	***768.3159***	384.6616	751.2893	376.1483	750.3053	375.6563	6
5	576.2664	288.6368	558.2558	279.6316	D	***653.2889***	327.1481	636.2624	318.6348	635.2784	318.1428	5
6	677.3141	339.1607	659.3035	330.1554	T	***538.2620***	269.6346	521.2354	261.1214	520.2514	260.6293	4
7	824.3825	412.6949	806.3719	403.6896	F	***437.2143***	**219.1108**	420.1878	210.5975	419.2037	210.1055	3
8	939.4094	470.2084	921.3989	461.2031	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
9					R	***175.1190***	88.0631	158.0924	79.5498			1

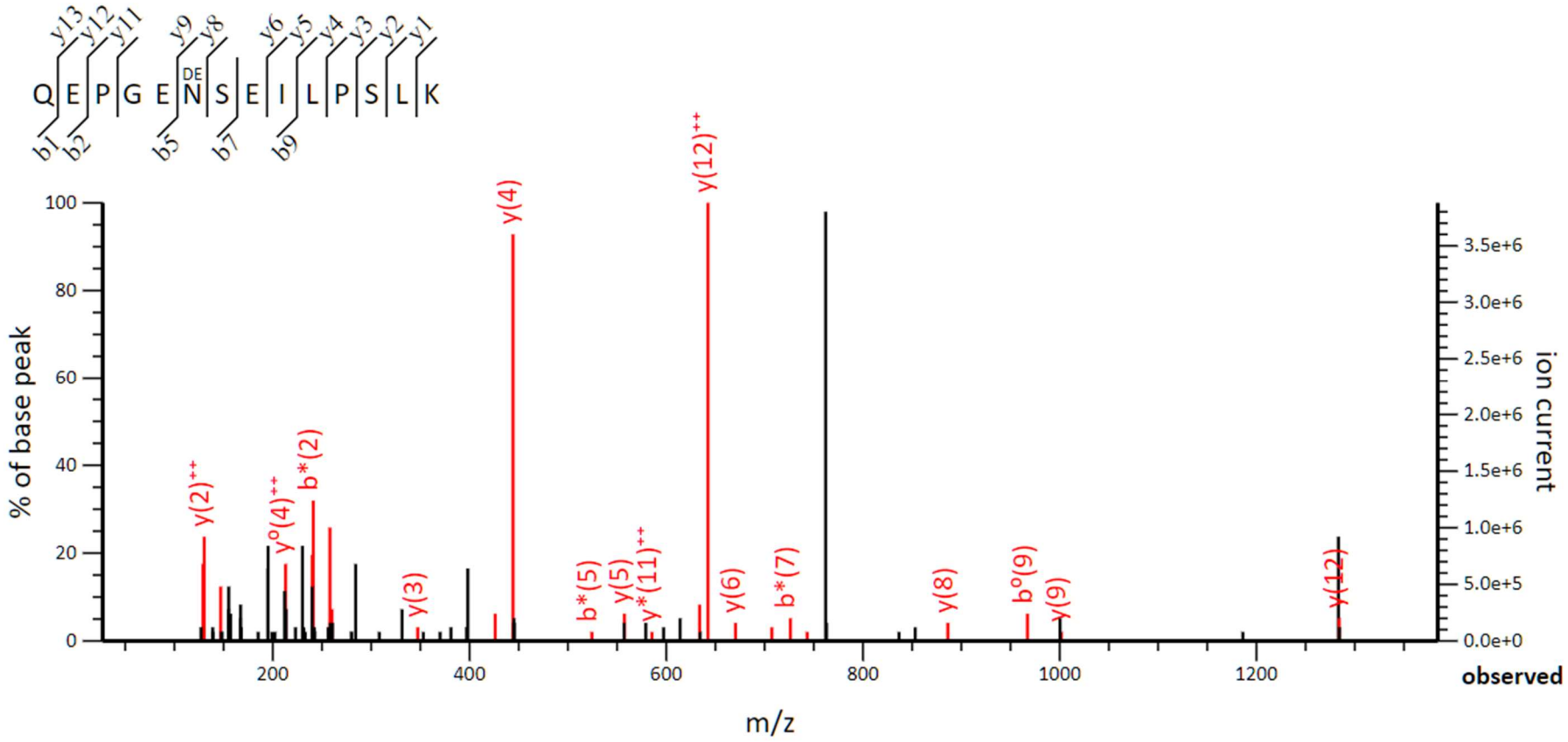
MS/MS Fragmentation of **EPMTVSSDQMAK** found in **CAH3**



Monoisotopic mass of neutral peptide Mr(calc): 1354.5745
Ions Score: 53 **Expect:** 4.1e-05
Matches : 53/200 fragment ions using 84 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**130.0499**	65.5286			112.0393	56.5233	E							12
2	227.1026	114.0550			209.0921	105.0497	P	1226.5392	**613.7732**	1209.5126	605.2599	1208.5286	604.7679	11
3	**374.1380**	187.5727			356.1275	178.5674	M	***1129.4864***	**565.2468**	1112.4598	556.7336	1111.4758	556.2415	10
4	475.1857	238.0965			457.1751	229.0912	T	***982.4510***	491.7291	965.4244	483.2159	964.4404	482.7238	9
5	**574.2541**	287.6307			556.2436	278.6254	V	***881.4033***	441.2053	864.3768	432.6920	863.3927	432.2000	8
6	**661.2862**	331.1467			643.2756	322.1414	S	***782.3349***	391.6711	765.3083	383.1578	764.3243	382.6658	7
7	748.3182	374.6627			730.3076	365.6574	S	***695.3029***	**348.1551**	678.2763	339.6418	677.2923	339.1498	6
8	**863.3451**	432.1762			845.3346	423.1709	D	***608.2708***	304.6391	591.2443	296.1258	590.2603	295.6338	5
9	991.4037	496.2055	974.3772	487.6922	973.3931	487.2002	Q	***493.2439***	247.1256	476.2173	238.6123			4
10	1138.4391	569.7232	1121.4126	561.2099	1120.4285	560.7179	M	***365.1853***	183.0963	348.1588	174.5830			3
11	1209.4762	605.2417	1192.4497	596.7285	1191.4657	596.2365	A	***218.1499***	109.5786	201.1234	101.0653			2
12							K	***147.1128***	74.0600	130.0863	65.5468			1

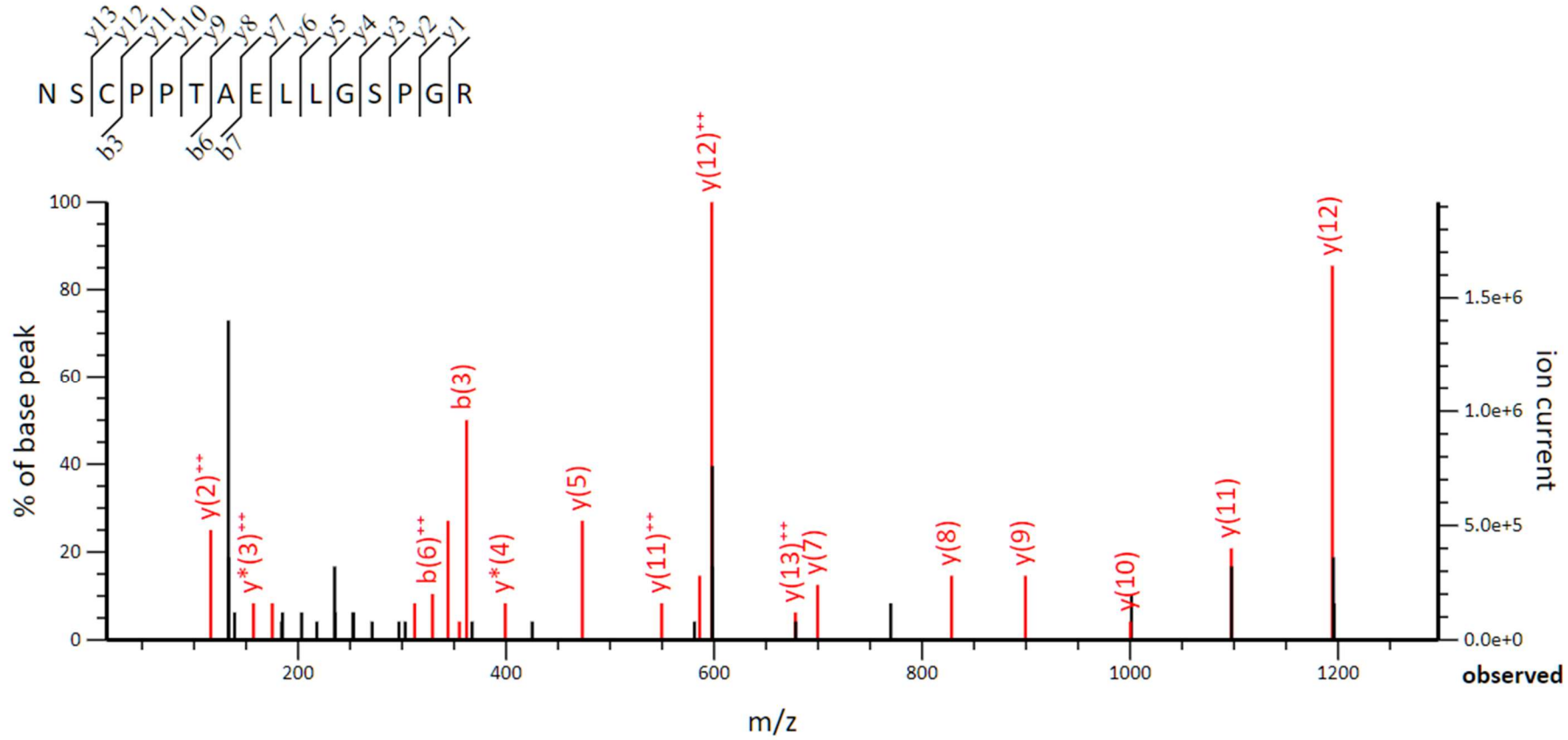
MS/MS Fragmentation of **QEPGENSEILPSLK** found in **GPX3**



Monoisotopic mass of neutral peptide Mr(calc): 1540.7620
Ions Score: 57 **Expect:** 0.00014
Matches : 31/150 fragment ions using 51 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**129.0659**	65.0366	112.0393	56.5233			Q							14
2	**258.1084**	129.5579	241.0819	121.0446	240.0979	120.5526	E	1413.7108	**707.3590**	1396.6842	698.8457	1395.7002	698.3537	13
3	355.1612	178.0842	338.1347	169.5710	337.1506	169.0790	P	***1284.6682***	**642.8377**	1267.6416	634.3244	1266.6576	633.8324	12
4	412.1827	206.5950	395.1561	198.0817	394.1721	197.5897	G	1187.6154	594.3113	1170.5889	585.7981	1169.6048	585.3061	11
5	541.2253	271.1163	524.1987	262.6030	523.2147	262.1110	E	1130.5939	565.8006	1113.5674	557.2873	1112.5834	556.7953	10
6	656.2522	328.6297	639.2257	320.1165	638.2416	319.6245	N	***1001.5514***	501.2793	984.5248	492.7660	983.5408	492.2740	9
7	**743.2842**	372.1458	726.2577	363.6325	725.2737	363.1405	S	***886.5244***	**443.7658**	869.4979	435.2526	868.5138	434.7606	8
8	872.3268	436.6671	855.3003	428.1538	854.3163	427.6618	E	799.4924	400.2498	782.4658	391.7366	781.4818	391.2445	7
9	985.4109	493.2091	968.3843	484.6958	967.4003	484.2038	I	***670.4498***	335.7285	653.4232	327.2153	652.4392	326.7232	6
10	1098.4950	549.7511	1081.4684	541.2378	1080.4844	540.7458	L	***557.3657***	279.1865	540.3392	270.6732	539.3552	270.1812	5
11	1195.5477	598.2775	1178.5212	589.7642	1177.5372	589.2722	P	***444.2817***	222.6445	427.2551	214.1312	426.2711	213.6392	4
12	1282.5798	641.7935	1265.5532	633.2802	1264.5692	632.7882	S	***347.2289***	174.1181	330.2023	165.6048	329.2183	165.1128	3
13	1395.6638	698.3355	1378.6373	689.8223	1377.6533	689.3303	L	***260.1969***	**130.6021**	243.1703	122.0888			2
14							K	***147.1128***	74.0600	130.0863	65.5468			1

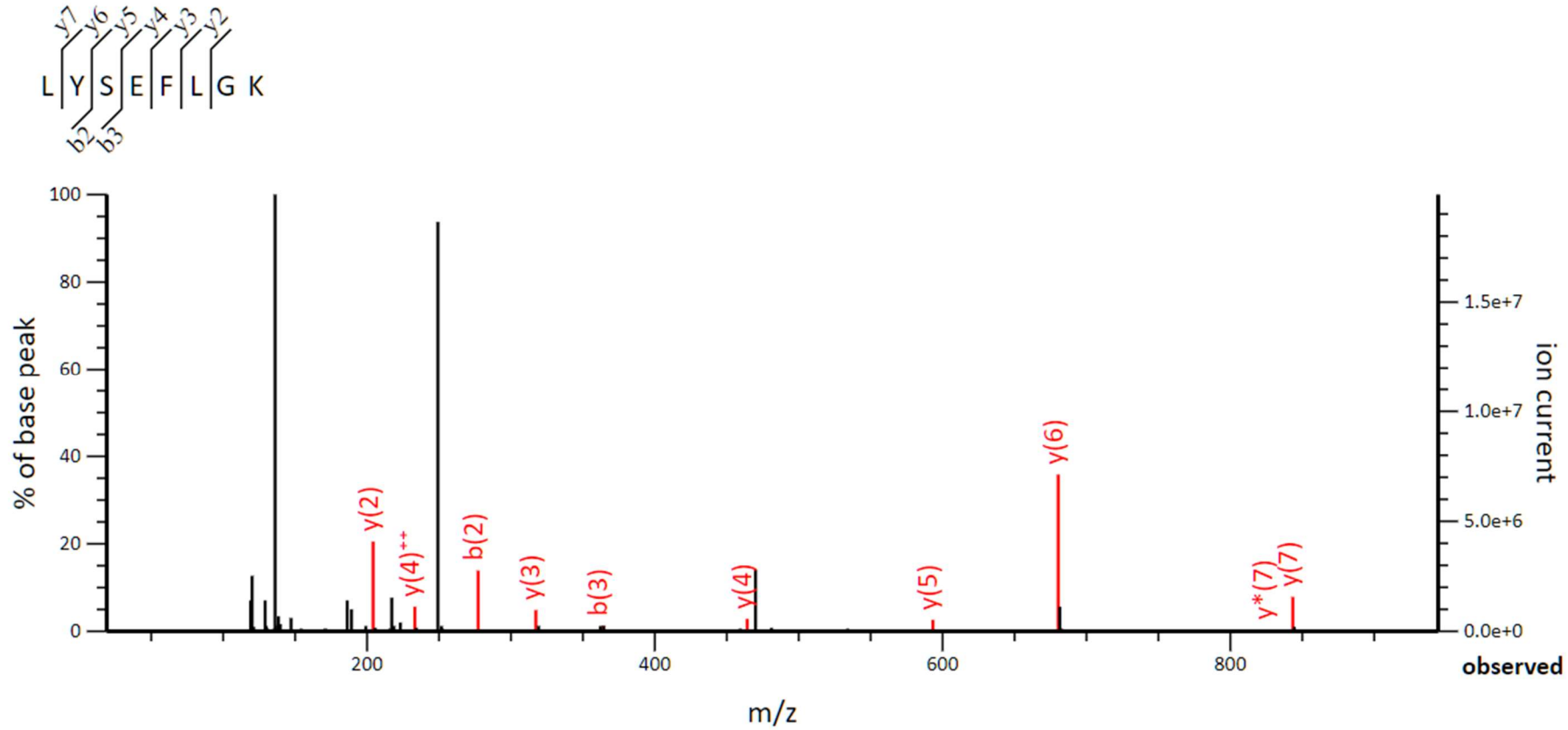
MS/MS Fragmentation of **NSCPPTAELLGSPGR** found in **GPX3**



Monoisotopic mass of neutral peptide Mr(calc): 1554.7460
Ions Score: 68 **Expect:** 2.2e-06
Matches : 21/160 fragment ions using 35 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							15
2	202.0822	101.5448	185.0557	93.0315	184.0717	92.5395	S	1441.7104	721.3588	1424.6838	712.8456	1423.6998	712.3536	14
3	362.1129	181.5601	345.0863	173.0468	344.1023	172.5548	C	1354.6784	**677.8428**	1337.6518	669.3295	1336.6678	668.8375	13
4	459.1656	230.0865	442.1391	221.5732	441.1551	221.0812	P	***1194.6477***	**597.8275**	1177.6212	589.3142	1176.6371	588.8222	12
5	556.2184	278.6128	539.1919	270.0996	538.2078	269.6076	P	***1097.5949***	**549.3011**	1080.5684	540.7878	1079.5844	540.2958	11
6	657.2661	329.1367	640.2395	320.6234	639.2555	320.1314	T	***1000.5422***	500.7747	983.5156	492.2615	982.5316	491.7694	10
7	728.3032	364.6552	711.2767	356.1420	710.2926	355.6500	A	***899.4945***	450.2509	882.4680	441.7376	881.4839	441.2456	9
8	857.3458	429.1765	840.3192	420.6633	839.3352	420.1713	E	***828.4574***	414.7323	811.4308	406.2191	810.4468	405.7271	8
9	970.4299	485.7186	953.4033	477.2053	952.4193	476.7133	L	***699.4148***	350.2110	682.3883	341.6978	681.4042	341.2058	7
10	1083.5139	542.2606	1066.4874	533.7473	1065.5034	533.2553	L	***586.3307***	293.6690	569.3042	285.1557	568.3202	284.6637	6
11	1140.5354	570.7713	1123.5088	562.2581	1122.5248	561.7660	G	***473.2467***	237.1270	456.2201	228.6137	455.2361	228.1217	5
12	1227.5674	614.2873	1210.5409	605.7741	1209.5568	605.2821	S	416.2252	208.6162	399.1987	200.1030	398.2146	199.6110	4
13	1324.6202	662.8137	1307.5936	654.3005	1306.6096	653.8084	P	***329.1932***	165.1002	312.1666	156.5870			3
14	1381.6416	691.3245	1364.6151	682.8112	1363.6311	682.3192	G	232.1404	**116.5738**	215.1139	108.0606			2
15							R	***175.1190***	88.0631	158.0924	79.5498			1

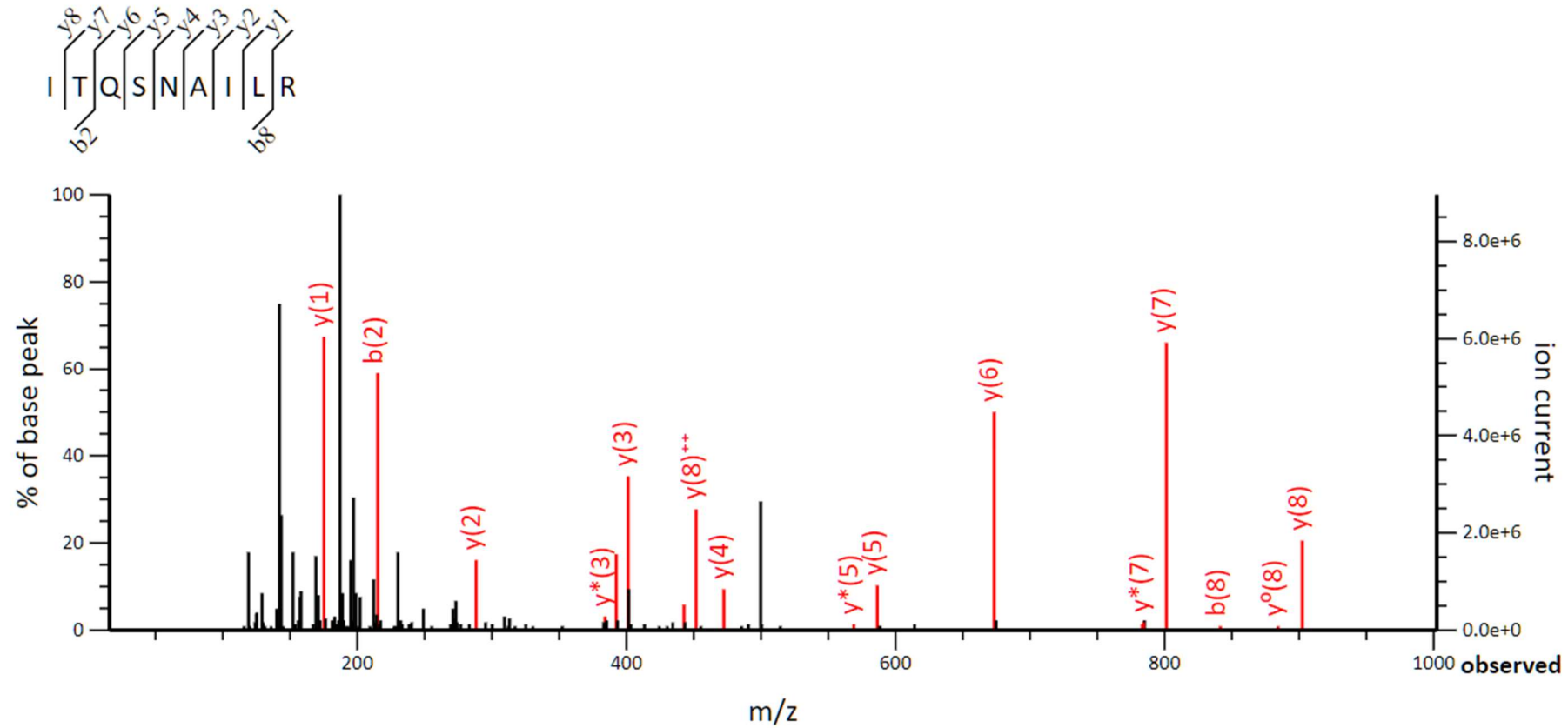
MS/MS Fragmentation of **LYSEFLGK** found in **GSTM2**



Monoisotopic mass of neutral peptide Mr(calc): 955.5015
Ions Score: 32 **Expect:** 0.0063
Matches : 10/58 fragment ions using 24 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							8
2	**277.1547**	139.0810			Y	***843.4247***	422.2160	826.3981	413.7027	825.4141	413.2107	7
3	**364.1867**	182.5970	346.1761	173.5917	S	***680.3614***	340.6843	663.3348	332.1710	662.3508	331.6790	6
4	493.2293	247.1183	475.2187	238.1130	E	***593.3293***	297.1683	576.3028	288.6550	575.3188	288.1630	5
5	640.2977	320.6525	622.2871	311.6472	F	***464.2867***	232.6470	447.2602	224.1337			4
6	753.3818	377.1945	735.3712	368.1892	L	***317.2183***	159.1128	300.1918	150.5995			3
7	810.4032	405.7053	792.3927	396.7000	G	***204.1343***	102.5708	187.1077	94.0575			2
8					K	147.1128	74.0600	130.0863	65.5468			1

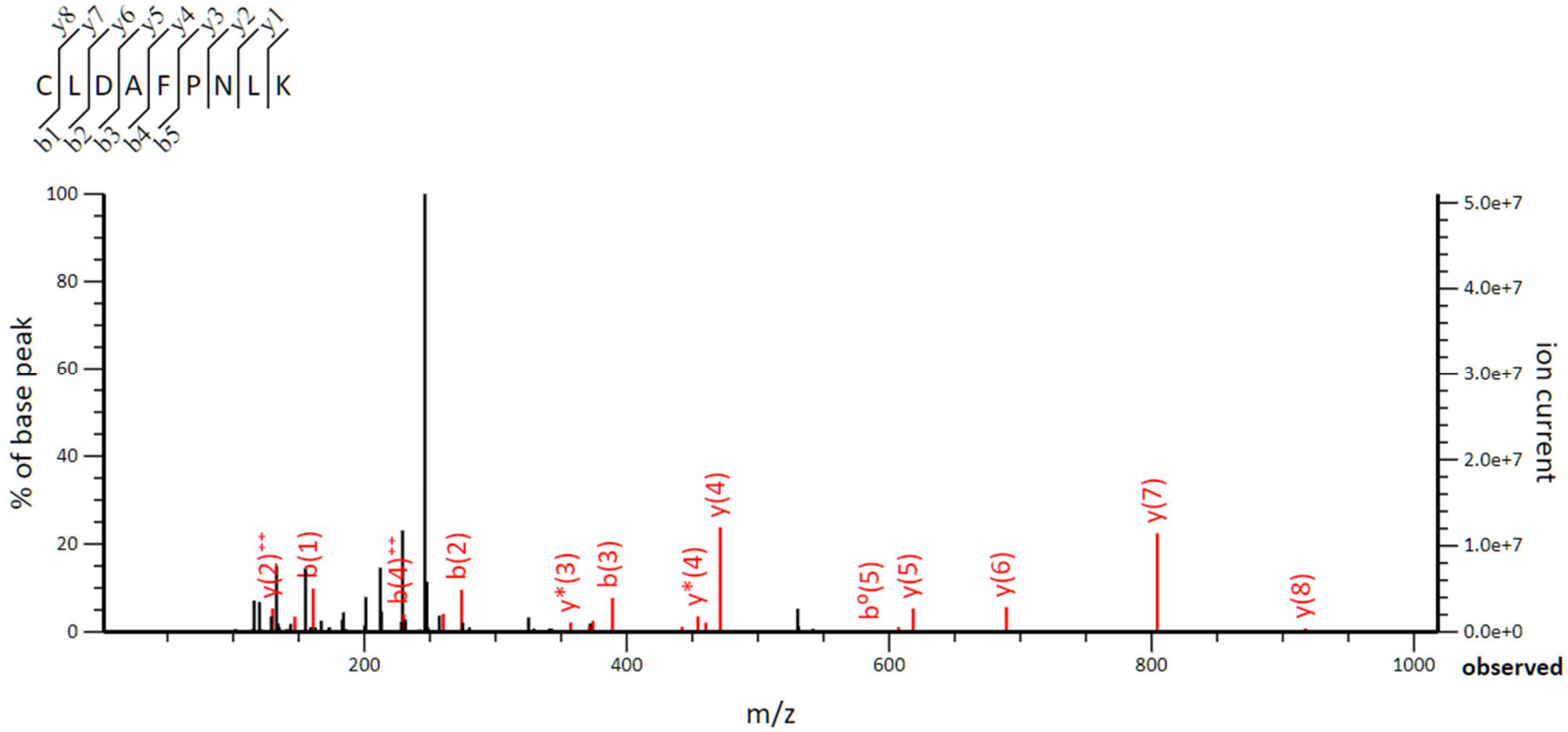
MS/MS Fragmentation of **ITQSNAILR** found in **GSTM2**



Monoisotopic mass of neutral peptide Mr(calc): 1014.5822
Ions Score: 65 **Expect:** 2.3e-05
Matches : 22/80 fragment ions using 29 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							9
2	**215.1390**	108.0731			197.1285	99.0679	T	***902.5054***	**451.7563**	885.4789	443.2431	884.4948	442.7511	8
3	343.1976	172.1024	326.1710	163.5892	325.1870	163.0972	Q	***801.4577***	**401.2325**	784.4312	392.7192	783.4472	392.2272	7
4	430.2296	215.6185	413.2031	207.1052	412.2191	206.6132	S	***673.3991***	337.2032	656.3726	328.6899	655.3886	328.1979	6
5	544.2726	272.6399	527.2460	264.1266	526.2620	263.6346	N	***586.3671***	293.6872	569.3406	285.1739			5
6	615.3097	308.1585	598.2831	299.6452	597.2991	299.1532	A	***472.3242***	236.6657	455.2976	228.1525			4
7	728.3937	364.7005	711.3672	356.1872	710.3832	355.6952	I	***401.2871***	201.1472	384.2605	192.6339			3
8	**841.4778**	421.2425	824.4512	412.7293	823.4672	412.2373	L	***288.2030***	144.6051	271.1765	136.0919			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1

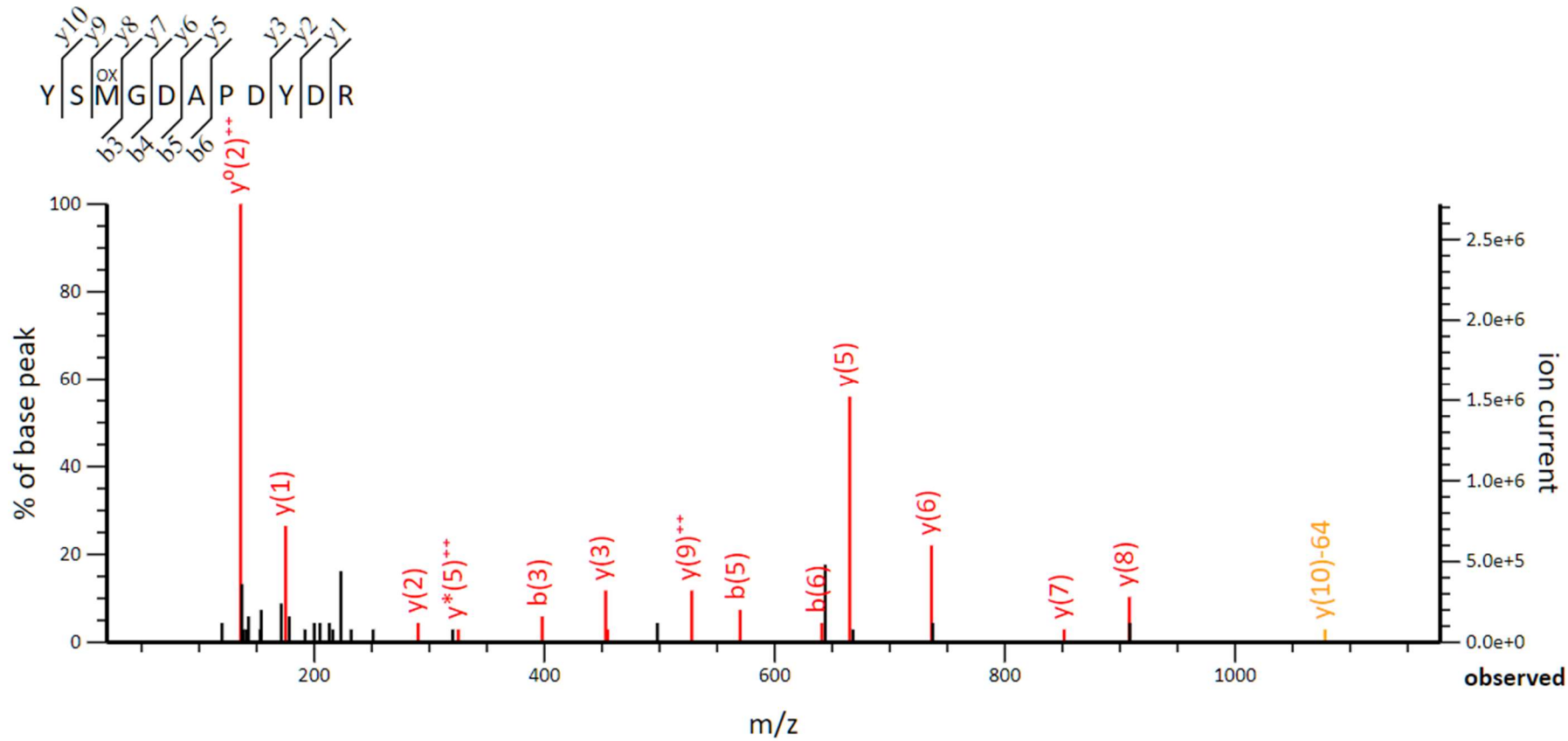
MS/MS Fragmentation of **CLDAFPNLK** found in **GSTM2**



Monoisotopic mass of neutral peptide Mr(calc): 1076.5325
Ions Score: 37 **Expect:** 0.0037
Matches : 22/68 fragment ions using 62 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**161.0379**	81.0226					C							9
2	**274.1220**	137.5646					L	***917.5091***	459.2582	900.4825	450.7449	899.4985	450.2529	8
3	**389.1489**	195.0781			371.1384	186.0728	D	***804.4250***	402.7162	787.3985	394.2029	786.4145	393.7109	7
4	**460.1860**	230.5967			442.1755	221.5914	A	***689.3981***	345.2027	672.3715	336.6894			6
5	**607.2545**	304.1309			589.2439	295.1256	F	***618.3610***	309.6841	601.3344	301.1708			5
6	704.3072	352.6573			686.2967	343.6520	P	***471.2926***	236.1499	454.2660	227.6366			4
7	818.3502	409.6787	801.3236	401.1654	800.3396	400.6734	N	***374.2398***	187.6235	357.2132	179.1103			3
8	931.4342	466.2207	914.4077	457.7075	913.4237	457.2155	L	***260.1969***	130.6021	243.1703	122.0888			2
9							K	***147.1128***	74.0600	130.0863	65.5468			1

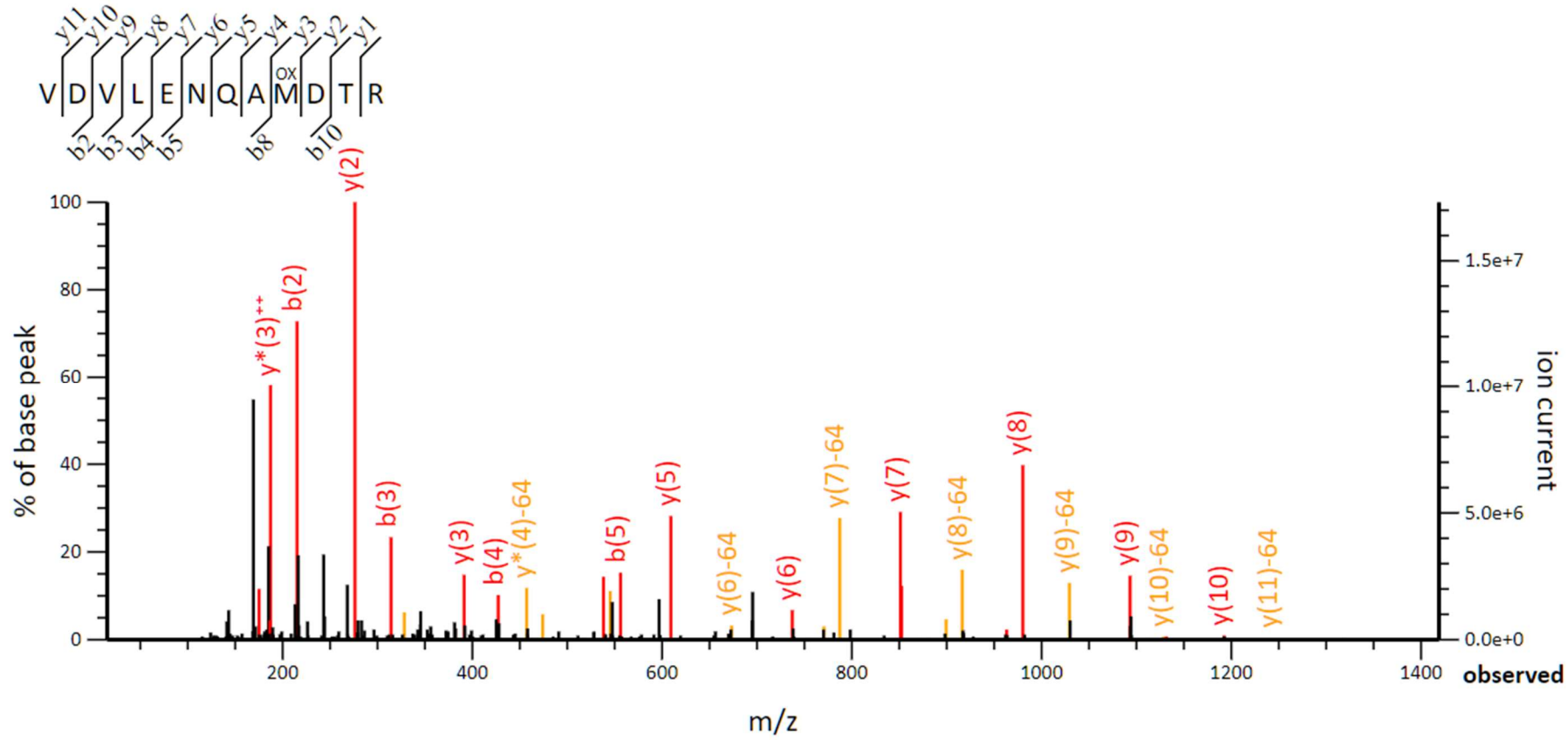
MS/MS Fragmentation of **YSMGDAPDYDR** found in **GSTM2**



Monoisotopic mass of neutral peptide Mr(calc): 1304.4979
Ions Score: 58 **Expect:** 0.00016
Matches : 17/140 fragment ions using 23 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389			Y							11
2	251.1026	126.0550	233.0921	117.0497	S	1142.4419	571.7246	1125.4153	563.2113	1124.4313	562.7193	10
3	398.1380	199.5727	380.1275	190.5674	M	1055.4099	528.2086	1038.3833	519.6953	1037.3993	519.2033	9
4	455.1595	228.0834	437.1489	219.0781	G	908.3745	454.6909	891.3479	446.1776	890.3639	445.6856	8
5	570.1864	285.5969	552.1759	276.5916	D	851.3530	426.1801	834.3264	417.6669	833.3424	417.1748	7
6	641.2236	321.1154	623.2130	312.1101	A	736.3260	368.6667	719.2995	360.1534	718.3155	359.6614	6
7	738.2763	369.6418	720.2658	360.6365	P	665.2889	333.1481	648.2624	324.6348	647.2784	324.1428	5
8	853.3033	427.1553	835.2927	418.1500	D	568.2362	284.6217	551.2096	276.1084	550.2256	275.6164	4
9	1016.3666	508.6869	998.3560	499.6817	Y	453.2092	227.1082	436.1827	218.5950	435.1987	218.1030	3
10	1131.3935	566.2004	1113.3830	557.1951	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
11					R	175.1190	88.0631	158.0924	79.5498			1

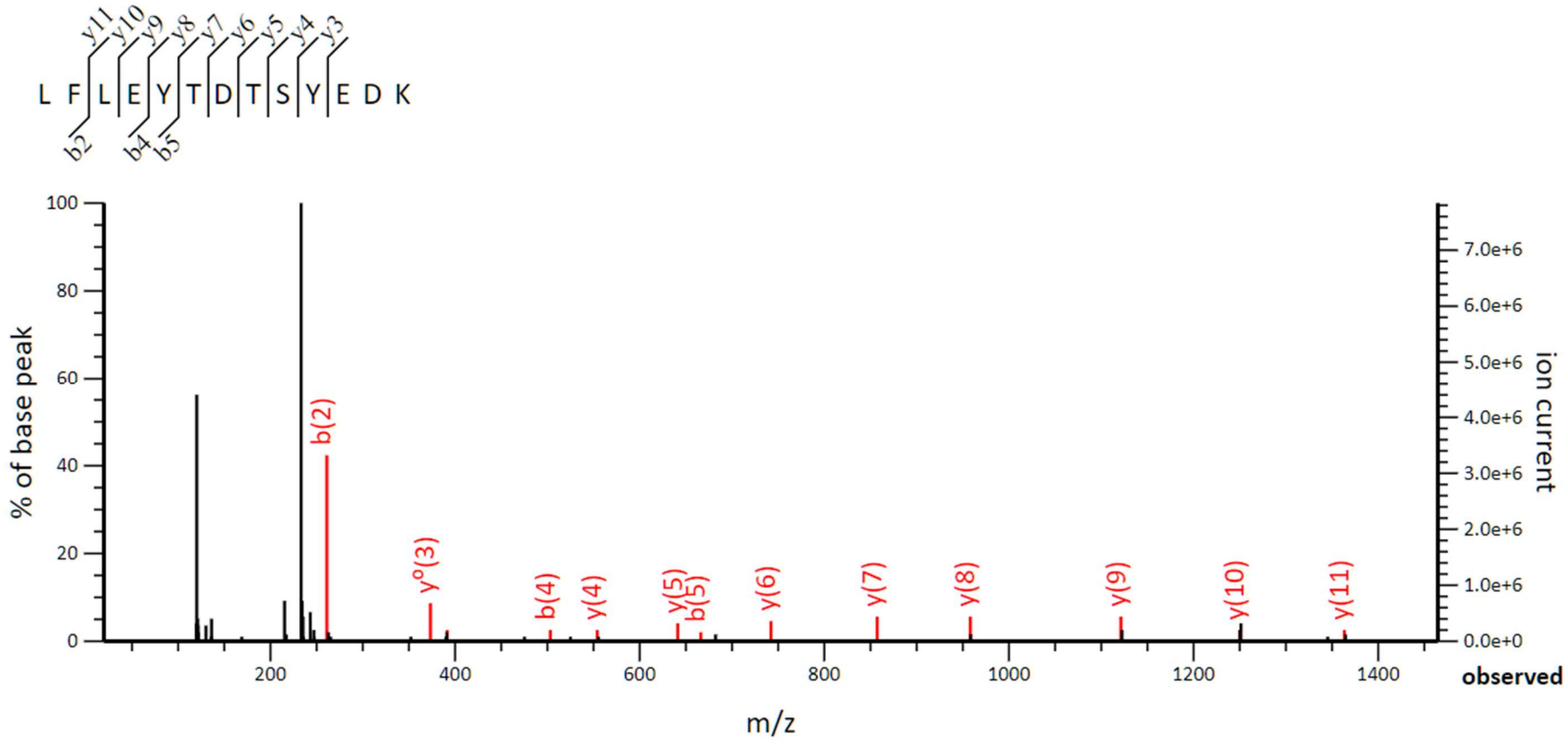
MS/MS Fragmentation of **VDVLENQAMDTR** found in **GSTM2**



Monoisotopic mass of neutral peptide Mr(calc): 1405.6507
Ions Score: 78 **Expect:** 1.7e-06
Matches : 41/184 fragment ions using 46 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							12
2	**215.1026**	108.0550			197.0921	99.0497	D	***1243.5913***	622.2993	1226.5648	613.7860	1225.5808	613.2940	11
3	**314.1710**	157.5892			296.1605	148.5839	V	***1128.5644***	564.7858	1111.5378	556.2726	1110.5538	555.7805	10
4	**427.2551**	214.1312			409.2445	205.1259	L	***1029.4960***	515.2516	1012.4694	506.7383	1011.4854	506.2463	9
5	**556.2977**	278.6525			538.2871	269.6472	E	***916.4119***	458.7096	899.3854	450.1963	898.4013	449.7043	8
6	670.3406	335.6740	653.3141	327.1607	652.3301	326.6687	N	***787.3693***	394.1883	770.3428	385.6750	769.3587	385.1830	7
7	798.3992	399.7032	781.3727	391.1900	780.3886	390.6980	Q	***673.3264***	337.1668	656.2998	328.6536	655.3158	328.1615	6
8	869.4363	435.2218	852.4098	426.7085	851.4258	426.2165	A	***545.2678***	273.1375	528.2413	264.6243	527.2572	264.1323	5
9	952.4734	476.7404	935.4469	468.2271	934.4629	467.7351	M	***474.2307***	237.6190	457.2041	229.1057	456.2201	228.6137	4
10	1067.5004	534.2538	1050.4738	525.7406	1049.4898	525.2485	D	***391.1936***	196.1004	374.1670	187.5872	373.1830	187.0951	3
11	1168.5481	584.7777	1151.5215	576.2644	1150.5375	575.7724	T	***276.1666***	138.5870	259.1401	130.0737	258.1561	129.5817	2
12							R	***175.1190***	88.0631	158.0924	79.5498			1

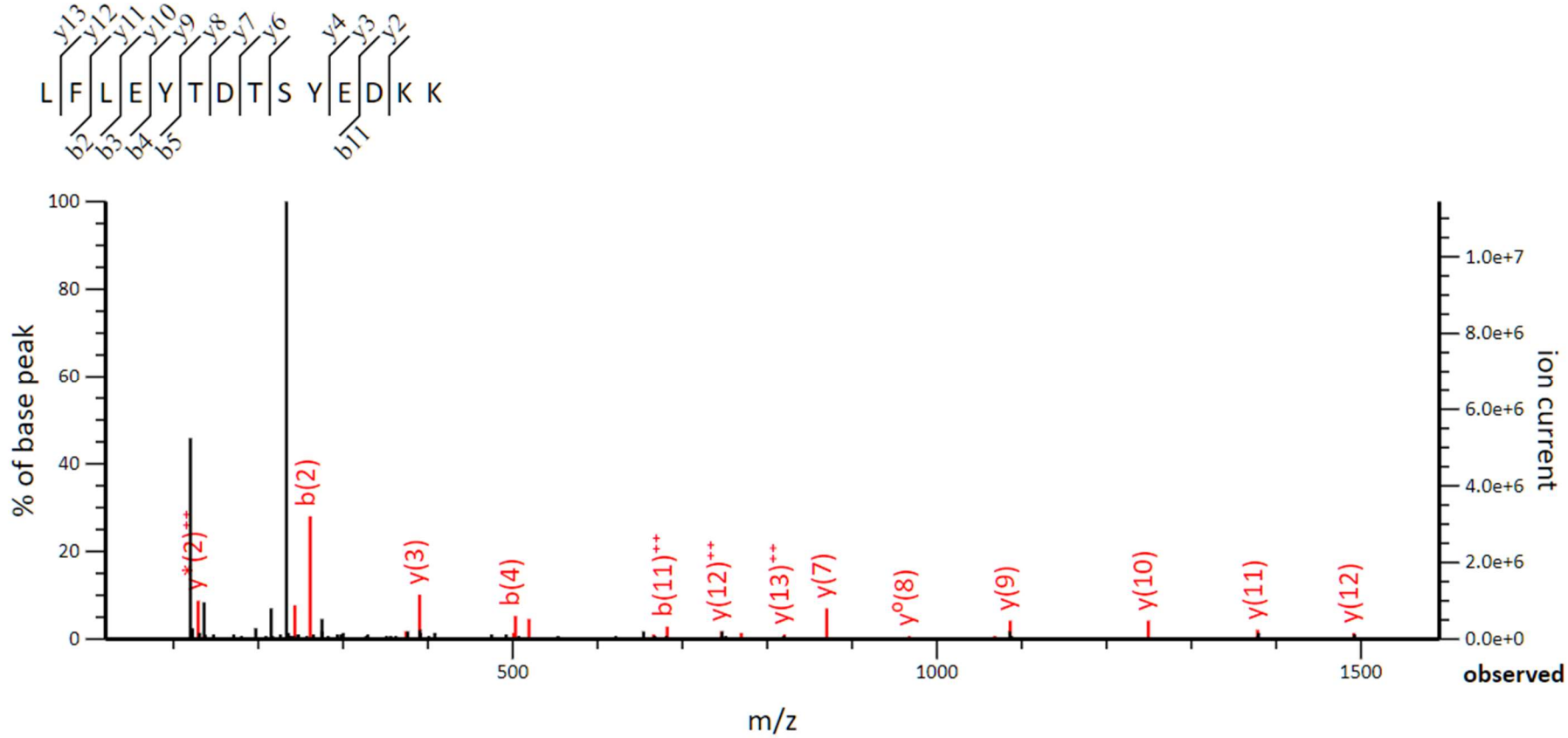
MS/MS Fragmentation of **LFLEYTDTSYEDK** found in **GSTM2**



Monoisotopic mass of neutral peptide Mr(calc): 1622.7352
Ions Score: 63 **Expect:** 1.3e-05
Matches : 13/112 fragment ions using 22 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							13
2	261.1598	131.0835			F	1510.6584	755.8328	1493.6318	747.3196	1492.6478	746.8276	12
3	374.2438	187.6255			L	1363.5900	682.2986	1346.5634	673.7854	1345.5794	673.2933	11
4	503.2864	252.1468	485.2758	243.1416	E	1250.5059	625.7566	1233.4794	617.2433	1232.4954	616.7513	10
5	666.3497	333.6785	648.3392	324.6732	Y	1121.4633	561.2353	1104.4368	552.7220	1103.4528	552.2300	9
6	767.3974	384.2023	749.3869	375.1971	T	958.4000	479.7036	941.3734	471.1904	940.3894	470.6984	8
7	882.4244	441.7158	864.4138	432.7105	D	857.3523	429.1798	840.3258	420.6665	839.3418	420.1745	7
8	983.4720	492.2397	965.4615	483.2344	T	742.3254	371.6663	725.2988	363.1531	724.3148	362.6610	6
9	1070.5041	535.7557	1052.4935	526.7504	S	641.2777	321.1425	624.2511	312.6292	623.2671	312.1372	5
10	1233.5674	617.2873	1215.5568	608.2821	Y	554.2457	277.6265	537.2191	269.1132	536.2351	268.6212	4
11	1362.6100	681.8086	1344.5994	672.8034	E	391.1823	196.0948	374.1558	187.5815	373.1718	187.0895	3
12	1477.6369	739.3221	1459.6264	730.3168	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
13					K	147.1128	74.0600	130.0863	65.5468			1

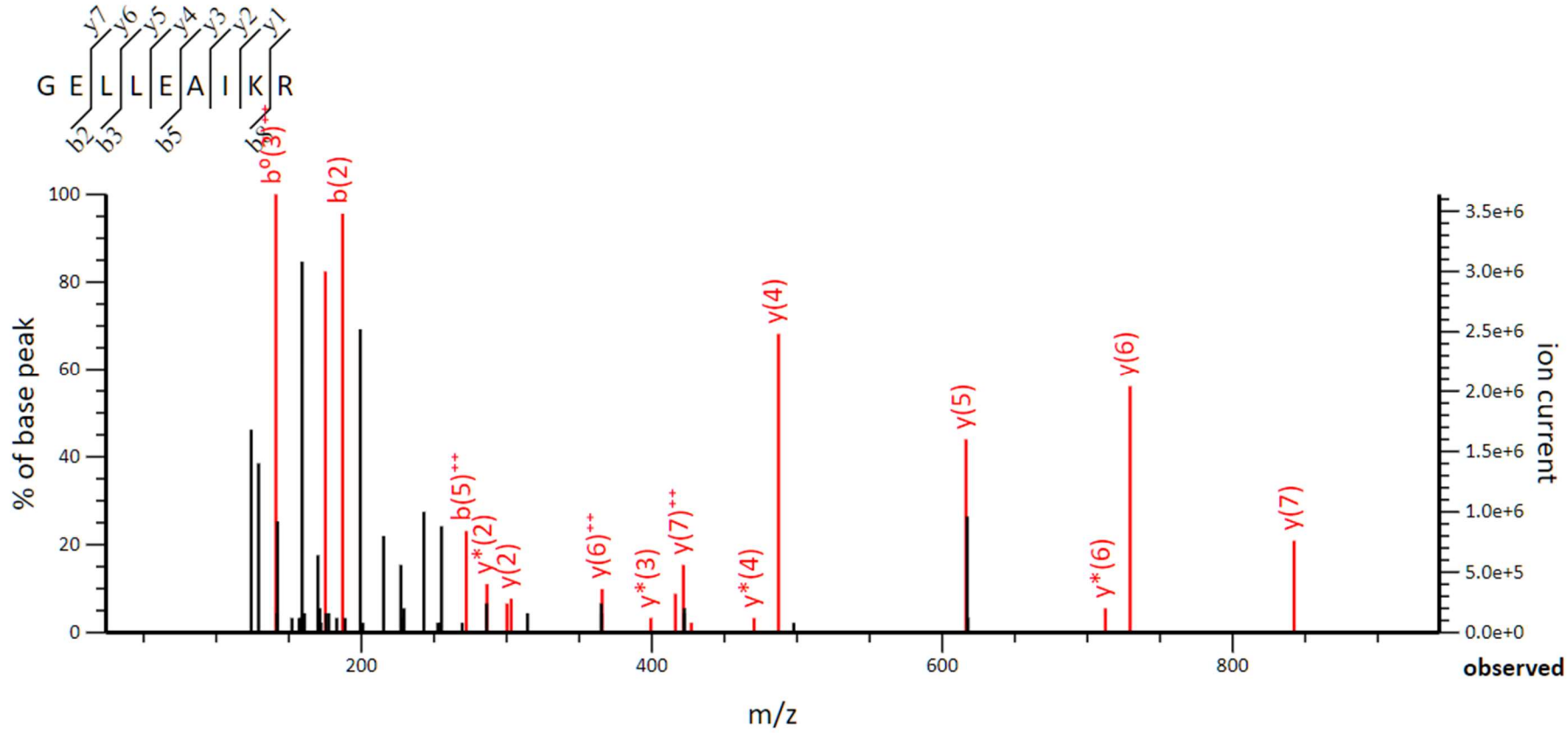
MS/MS Fragmentation of **LFLEYTDTSYEDKK** found in **GSTM2**



Monoisotopic mass of neutral peptide Mr(calc): 1750.8301
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 68 **Expect:** 2.9e-06
Matches : 21/122 fragment ions using 31 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							14
2	**261.1598**	131.0835					F	1638.7534	**819.8803**	1621.7268	811.3670	1620.7428	810.8750	13
3	**374.2438**	187.6255					L	***1491.6849***	**746.3461**	1474.6584	737.8328	1473.6744	737.3408	12
4	**503.2864**	252.1468			485.2758	243.1416	E	***1378.6009***	689.8041	1361.5743	681.2908	1360.5903	680.7988	11
5	**666.3497**	333.6785			648.3392	324.6732	Y	***1249.5583***	625.2828	1232.5317	616.7695	1231.5477	616.2775	10
6	767.3974	384.2023			749.3869	375.1971	T	***1086.4950***	543.7511	1069.4684	535.2378	1068.4844	534.7458	9
7	882.4244	441.7158			864.4138	432.7105	D	985.4473	493.2273	968.4207	484.7140	967.4367	484.2220	8
8	983.4720	492.2397			965.4615	483.2344	T	***870.4203***	435.7138	853.3938	427.2005	852.4098	426.7085	7
9	1070.5041	535.7557			1052.4935	526.7504	S	***769.3727***	385.1900	752.3461	376.6767	751.3621	376.1847	6
10	1233.5674	617.2873			1215.5568	608.2821	Y	***682.3406***	341.6740	665.3141	333.1607	664.3301	332.6687	5
11	1362.6100	681.8086			1344.5994	672.8034	E	***519.2773***	260.1423	502.2508	251.6290	501.2667	251.1370	4
12	1477.6369	739.3221			1459.6264	730.3168	D	***390.2347***	195.6210	373.2082	187.1077	372.2241	186.6157	3
13	1605.7319	803.3696	1588.7053	794.8563	1587.7213	794.3643	K	275.2078	138.1075	258.1812	129.5942			2
14							K	147.1128	74.0600	130.0863	65.5468			1

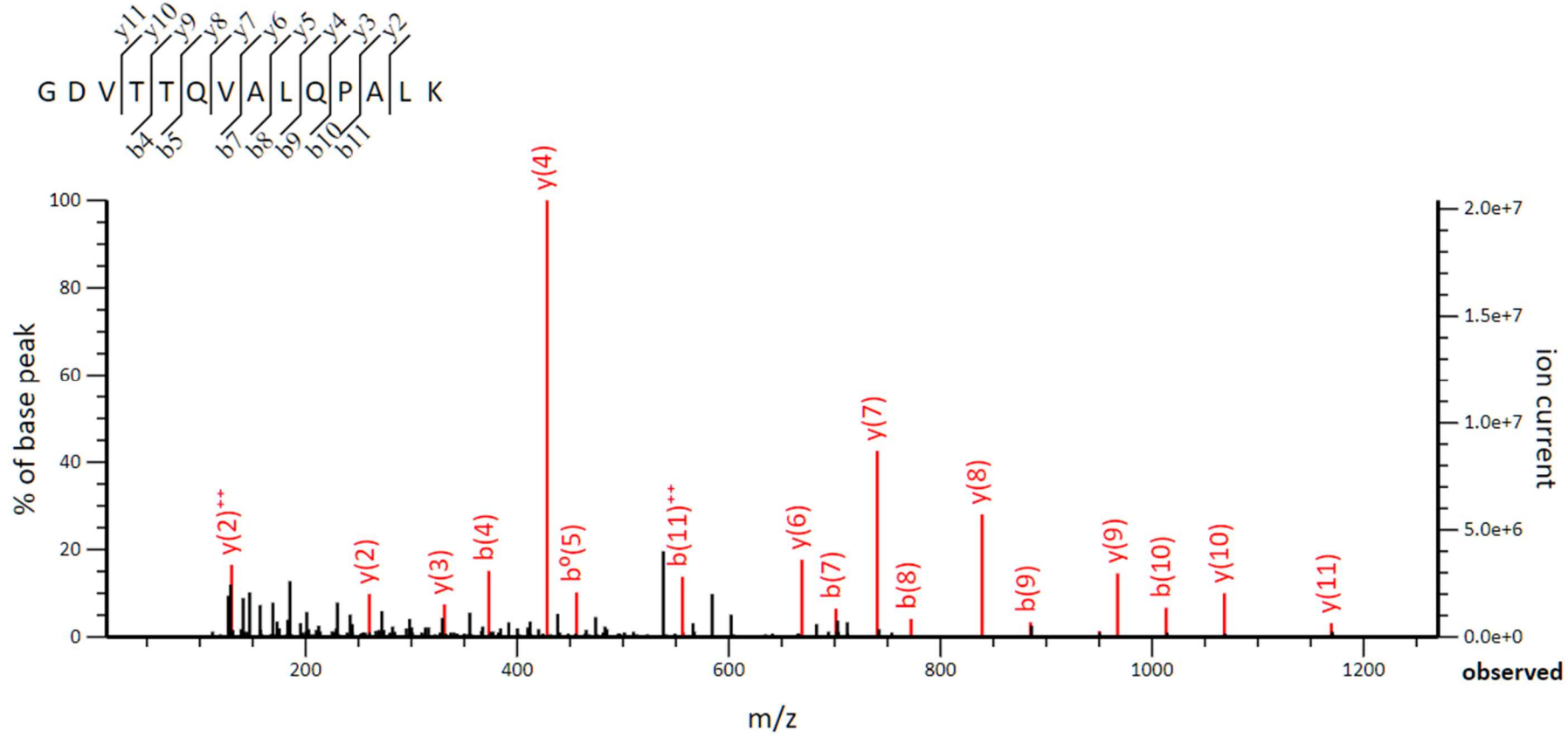
MS/MS Fragmentation of **GELLEAIKR** found in **SODM**



Monoisotopic mass of neutral peptide Mr(calc): 1027.6026
Ions Score: 51 **Expect:** 0.00055
Matches : 20/72 fragment ions using 34 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							9
2	**187.0713**	94.0393			169.0608	85.0340	E	971.5884	486.2978	954.5619	477.7846	953.5778	477.2926	8
3	**300.1554**	150.5813			282.1448	141.5761	L	***842.5458***	**421.7765**	825.5193	413.2633	824.5352	412.7713	7
4	413.2395	207.1234			395.2289	198.1181	L	***729.4617***	**365.2345**	712.4352	356.7212	711.4512	356.2292	6
5	542.2821	**271.6447**			524.2715	262.6394	E	***616.3777***	308.6925	599.3511	300.1792	598.3671	299.6872	5
6	613.3192	307.1632			595.3086	298.1579	A	***487.3351***	244.1712	470.3085	235.6579			4
7	726.4032	363.7053			708.3927	354.7000	I	***416.2980***	208.6526	399.2714	200.1394			3
8	854.4982	**427.7527**	837.4716	419.2395	836.4876	418.7475	K	***303.2139***	152.1106	286.1874	143.5973			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1

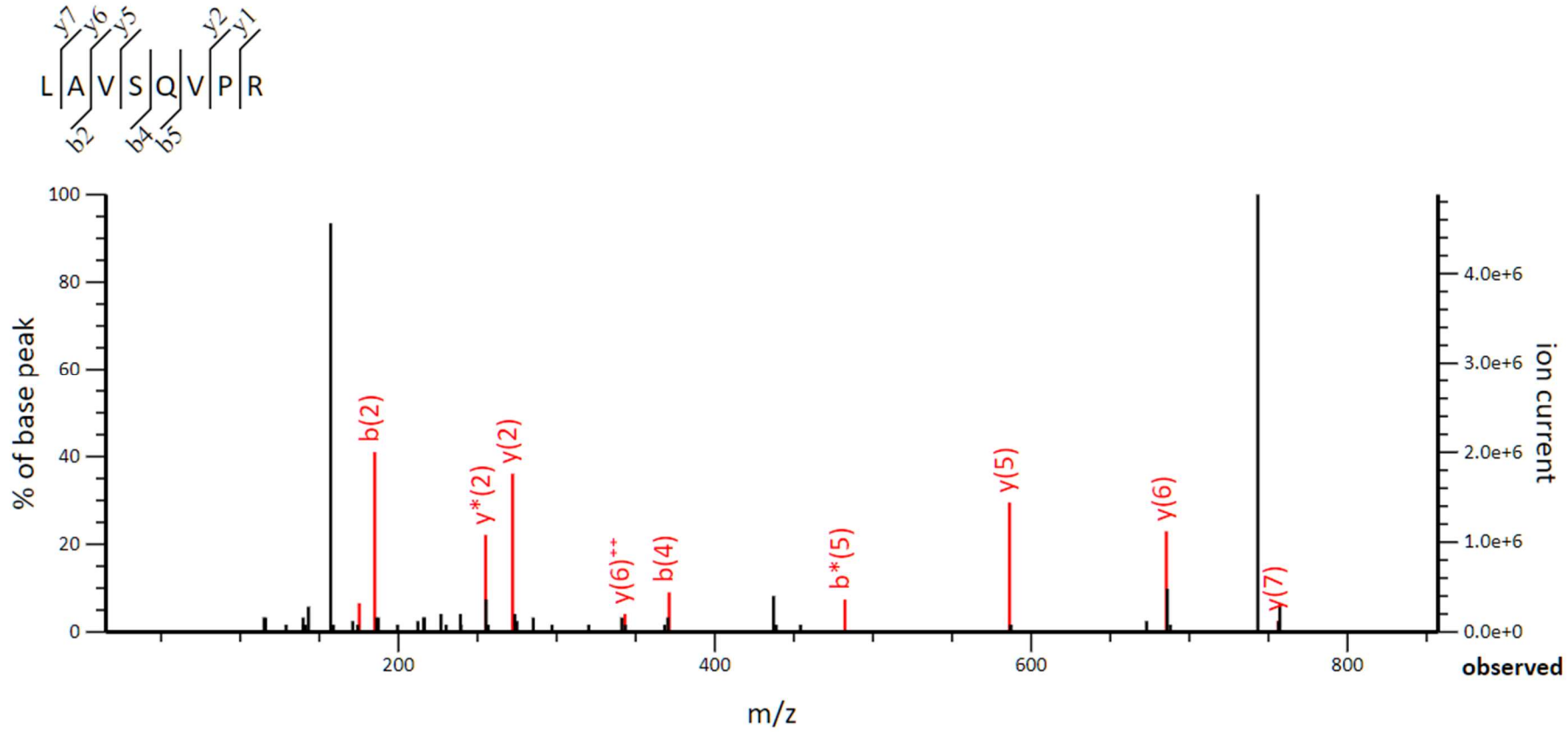
MS/MS Fragmentation of **GDVTTQVALQPALK** found in **SODM**



Monoisotopic mass of neutral peptide Mr(calc): 1439.7984
Ions Score: 93 **Expect:** 4.3e-08
Matches : 20/126 fragment ions using 22 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							14
2	173.0557	87.0315			155.0451	78.0262	D	1383.7842	692.3957	1366.7577	683.8825	1365.7736	683.3905	13
3	272.1241	136.5657			254.1135	127.5604	V	1268.7573	634.8823	1251.7307	626.3690	1250.7467	625.8770	12
4	**373.1718**	187.0895			355.1612	178.0842	T	***1169.6889***	585.3481	1152.6623	576.8348	1151.6783	576.3428	11
5	474.2195	237.6134			456.2089	228.6081	T	***1068.6412***	534.8242	1051.6146	526.3109	1050.6306	525.8189	10
6	602.2780	301.6427	585.2515	293.1294	584.2675	292.6374	Q	***967.5935***	484.3004	950.5669	475.7871			9
7	**701.3464**	351.1769	684.3199	342.6636	683.3359	342.1716	V	***839.5349***	420.2711	822.5084	411.7578			8
8	**772.3836**	386.6954	755.3570	378.1821	754.3730	377.6901	A	***740.4665***	370.7369	723.4400	362.2236			7
9	**885.4676**	443.2375	868.4411	434.7242	867.4571	434.2322	L	***669.4294***	335.2183	652.4028	326.7051			6
10	**1013.5262**	507.2667	996.4997	498.7535	995.5156	498.2615	Q	***556.3453***	278.6763	539.3188	270.1630			5
11	1110.5790	555.7931	1093.5524	547.2798	1092.5684	546.7878	P	***428.2867***	214.6470	411.2602	206.1337			4
12	1181.6161	591.3117	1164.5895	582.7984	1163.6055	582.3064	A	***331.2340***	166.1206	314.2074	157.6074			3
13	1294.7001	647.8537	1277.6736	639.3404	1276.6896	638.8484	L	***260.1969***	130.6021	243.1703	122.0888			2
14							K	147.1128	74.0600	130.0863	65.5468			1

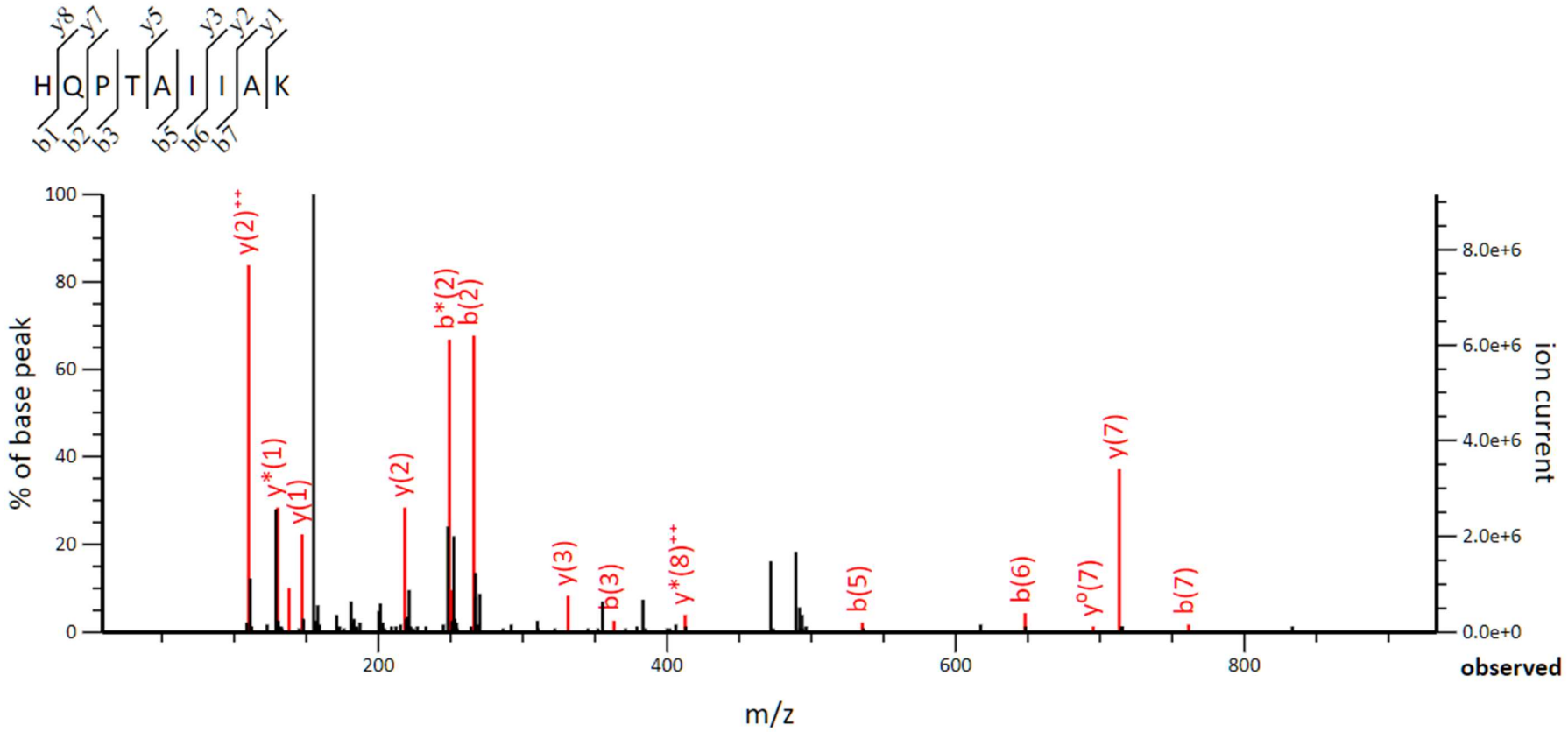
MS/MS Fragmentation of **LAVSQVPR** found in **TKT**



Monoisotopic mass of neutral peptide Mr(calc): 868.5130
Ions Score: 40 **Expect:** 0.0022
Matches : 12/62 fragment ions using 21 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							8
2	**185.1285**	93.0679					A	***756.4363***	378.7218	739.4097	370.2085	738.4257	369.7165	7
3	284.1969	142.6021					V	***685.3991***	343.2032	668.3726	334.6899	667.3886	334.1979	6
4	**371.2289**	186.1181			353.2183	177.1128	S	***586.3307***	293.6690	569.3042	285.1557	568.3202	284.6637	5
5	499.2875	250.1474	482.2609	241.6341	481.2769	241.1421	Q	499.2987	250.1530	482.2722	241.6397			4
6	598.3559	299.6816	581.3293	291.1683	580.3453	290.6763	V	***371.2401***	186.1237	354.2136	177.6104			3
7	695.4087	348.2080	678.3821	339.6947	677.3981	339.2027	P	***272.1717***	136.5895	255.1452	128.0762			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **HQPTAIIAK** found in **TKT**



Monoisotopic mass of neutral peptide Mr(calc): 977.5658
Ions Score: 29 **Expect:** 0.028
Matches : 17/78 fragment ions using 40 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	***138.0662***	69.5367					H							9
2	***266.1248***	133.5660	249.0982	125.0527			Q	841.5142	421.2607	824.4876	412.7475	823.5036	412.2554	8
3	***363.1775***	182.0924	346.1510	173.5791			P	**713.4556**	357.2314	696.4291	348.7182	695.4450	348.2262	7
4	464.2252	232.6162	447.1987	224.1030	446.2146	223.6110	T	616.4028	308.7051	599.3763	300.1918	598.3923	299.6998	6
5	***535.2623***	268.1348	518.2358	259.6215	517.2518	259.1295	A	515.3552	258.1812	498.3286	249.6679			5
6	***648.3464***	324.6768	631.3198	316.1636	630.3358	315.6715	I	444.3180	222.6627	427.2915	214.1494			4
7	***761.4305***	381.2189	744.4039	372.7056	743.4199	372.2136	I	**331.2340**	166.1206	314.2074	157.6074			3
8	832.4676	416.7374	815.4410	408.2241	814.4570	407.7321	A	**218.1499**	109.5786	201.1234	101.0653			2
9							K	**147.1128**	74.0600	130.0863	65.5468			1