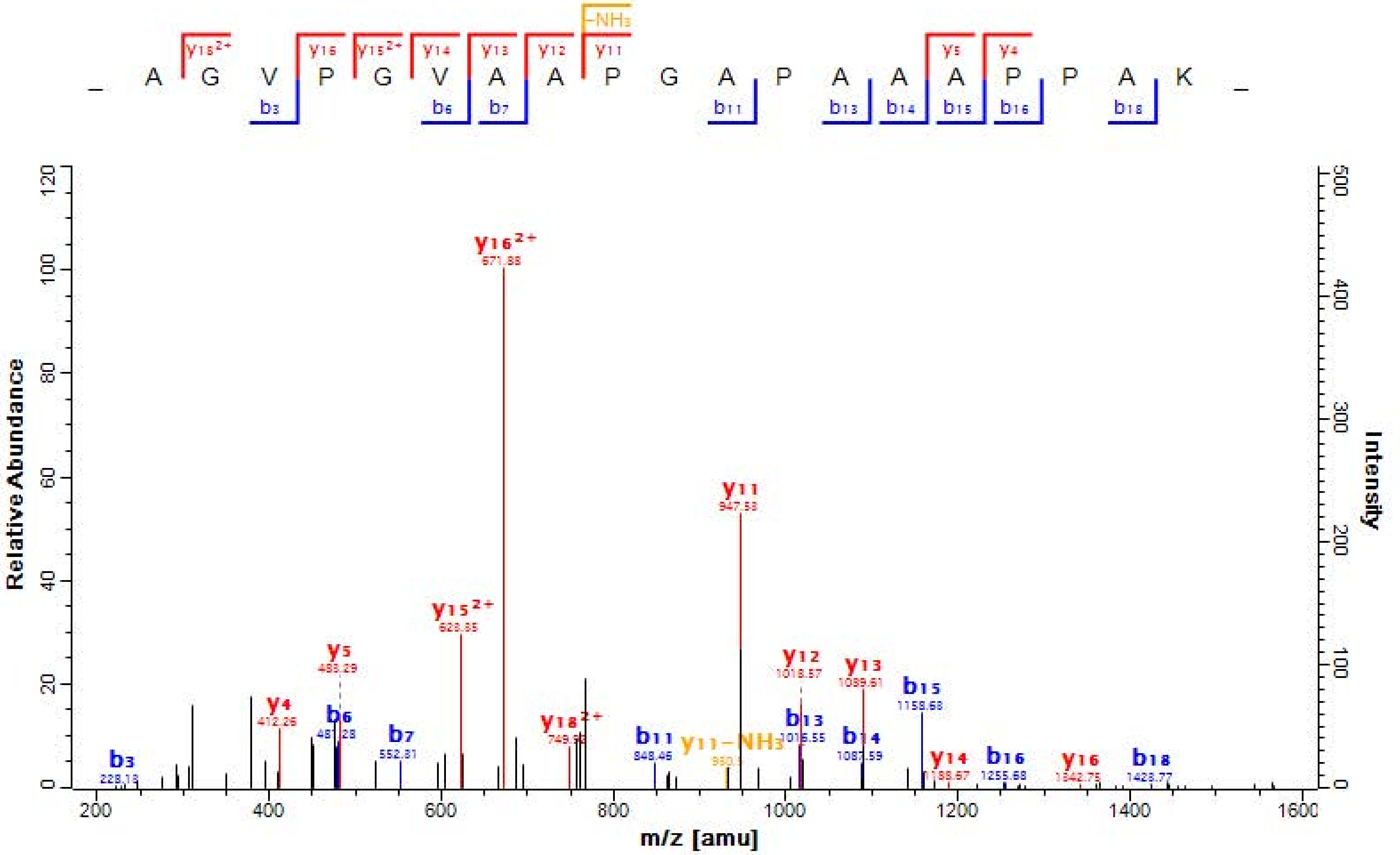
Scan number	1323	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	100.45



precursor information

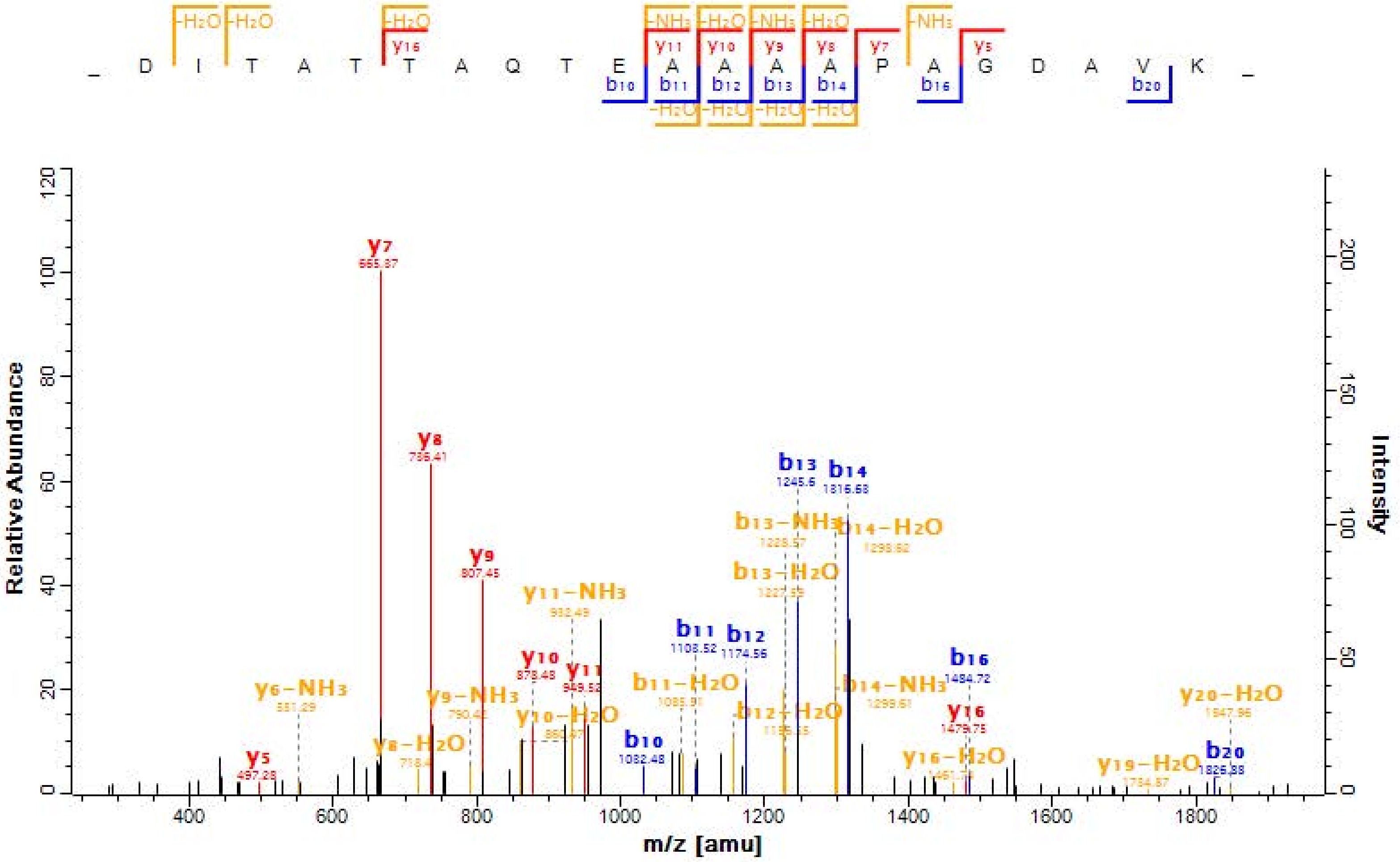
Mass:	1568.86763
m/z:	785.44109
Charge:	2+
Retentiontime:	17.471033096313
Score:	100.4537
Mass Error [ppm]:	0.10063
PEP:	0.00044045
Precursor Type:	ISO

general information

Annotation:	14 of 19
AminoAcids Coverag	74 %
Intensity Coverage:	51 %
Peak Coverage:	24 %
Protein Localisation:	20 ... 38

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	18				
	129.0659	2	G	17	1498.838		749.9225	-0.4971
+0.0189	228.1343	3	V	16	1441.816		1441.816	
	325.187	4	P	15	1342.748	+0.051677	671.8775	+0.267501
	382.2085	5	G	14	1245.695		623.3511	-0.03205
+0.024726	481.2769	6	V	13	1188.674	-0.10517	1188.674	
+0.08124	552.314	7	A	12	1089.605	-0.06178	1089.605	
	623.3511	8	A	11	1018.568	+0.00017	1018.568	
	720.4039	9	P	10	947.5309	-0.04792	947.5309	
	777.4254	10	G	9	850.4781		850.4781	
-0.09401	848.4625	11	A	8	793.4567		793.4567	
	945.5152	12	P	7	722.4196		722.4196	
-0.01427	1016.552	13	A	6	625.3668		625.3668	
-0.08495	1087.589	14	A	5	554.3297		554.3297	
-0.02978	1158.627	15	A	4	483.2926	-0.10988	483.2926	
-0.04397	1255.679	16	P	3	412.2554	+0.121813	412.2554	
	1352.732	17	P	2	315.2027		315.2027	
+0.086976	1423.769	18	A	1	218.1499		218.1499	
		19	K	0	147.1128		147.1128	

Scan number	1599	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	112.55



precursor information

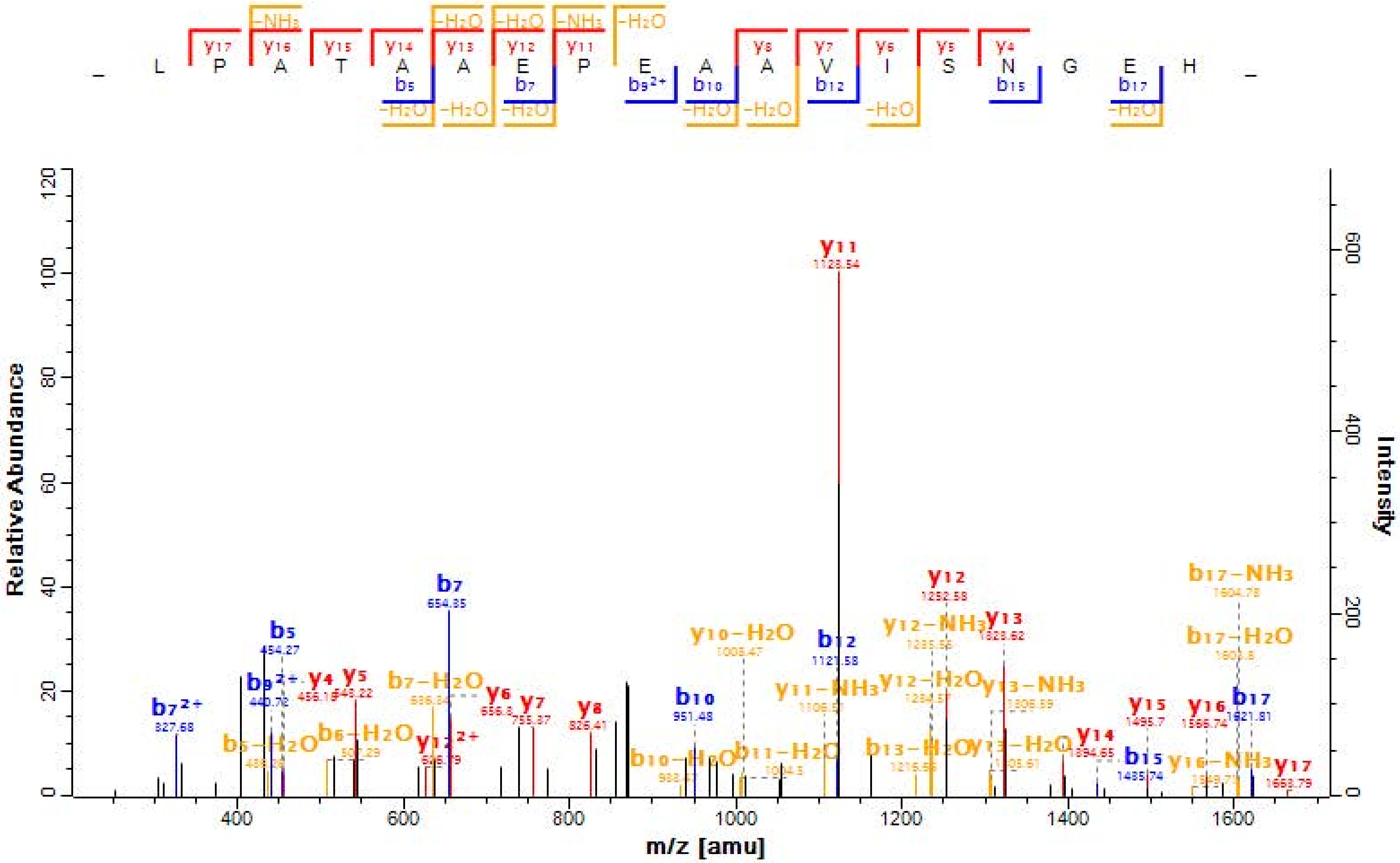
Mass:	1971.97513
m/z:	986.99484
Charge:	2+
Retentiontime:	20.175220489502
Score:	112.5493
Mass Error [ppm]:	0.10928
PEP:	3.0954E-09
Precursor Type:	MULTI

general information

Annotation:	13 of 21
AminoAcids Coverag	62 %
Intensity Coverage:	58 %
Peak Coverage:	30 %
Protein Localisation:	1011 ... 1031

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	116.034219499	1	D	20		
	229.118283479	2	I	19	1865.96944629	
	330.165961953	3	T	18	1752.88538231	
	401.203075741	4	A	17	1651.83770384	
	502.250754215	5	T	16	1580.80059005	
	603.298432689	6	T	15	1479.75291158	+0.0667906
	674.335546477	7	A	14	1378.7052331	
	802.394123988	8	Q	13	1307.66811932	
	903.441802462	9	T	12	1179.6095418	
-0.0510459	1032.48439556	10	E	11	1078.56186333	
-0.0512945	1103.52150935	11	A	10	949.519270234	-0.0836013
-0.1587208	1174.55862313	12	A	9	878.482156447	+0.1433318
-0.1550631	1245.59573692	13	A	8	807.445042659	+0.0256605
-0.1312638	1316.63285071	14	A	7	736.407928871	+0.0715633
	1413.68561456	15	P	6	665.370815083	+0.0461161
+0.4556164	1484.72272835	16	A	5	568.318051231	
	1541.74419207	17	G	4	497.280937443	+0.1931226
	1656.77113511	18	D	3	440.25947372	
	1727.80824889	19	A	2	325.232530688	
-0.142654	1826.87666281	20	V	1	254.1954169	
		21	K	0	155.127002984	

Scan number	1974	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	173.28



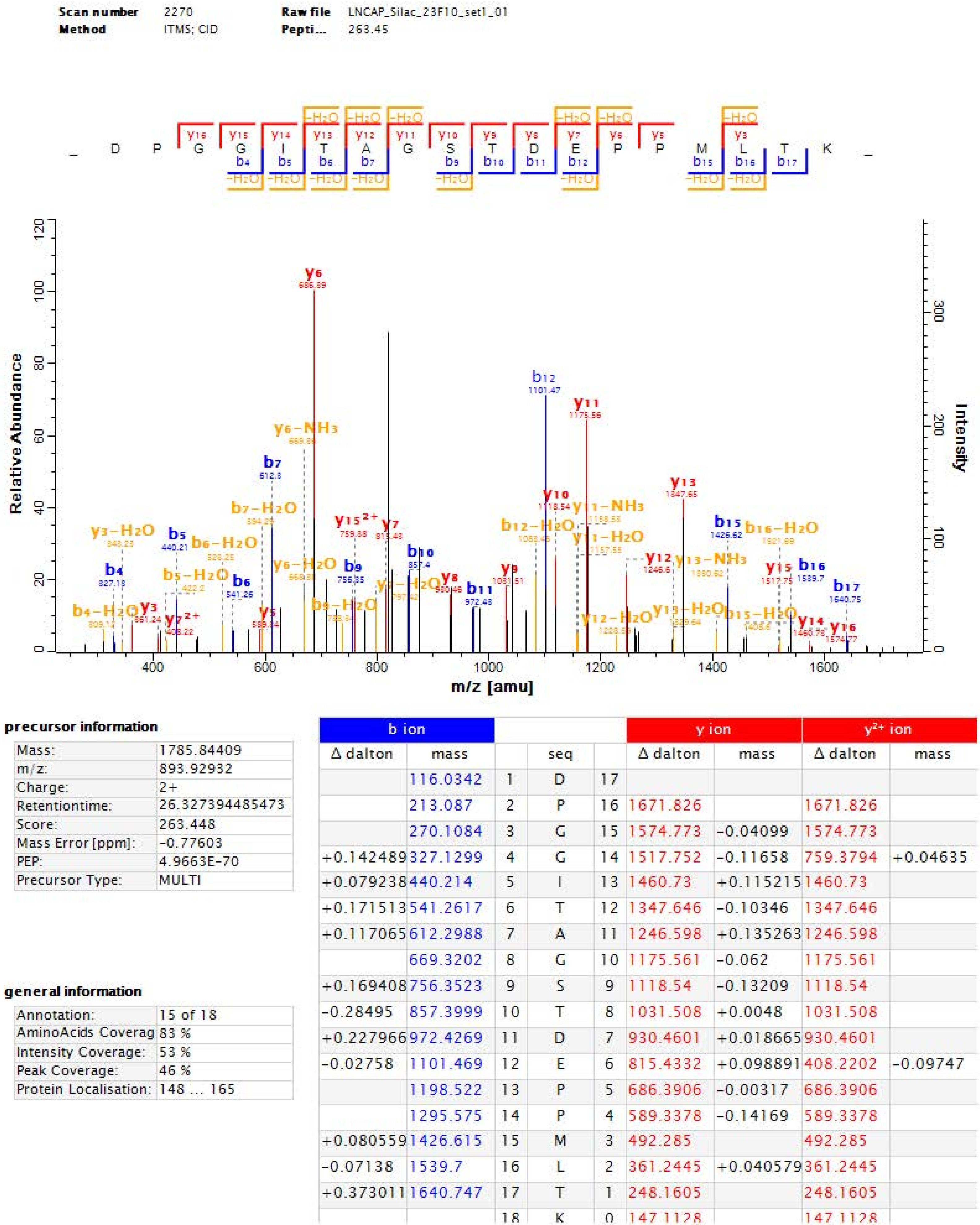
precursor information

Mass:	1775.86939
m/z:	888.94197
Charge:	2+
Retentiontime:	23.764400482177
Score:	173.2785
Mass Error [ppm]:	0.22113
PEP:	3.9844E-18
Precursor Type:	ISO

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	50 %
Peak Coverage:	44 %
Protein Localisation:	503 ... 520

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	17				
	211.14		211.14	2	P	16	1663.8	+0.0371	1663.8	
	282.18		282.18	3	A	15	1566.7	-0.027	1566.7	
	383.23		383.23	4	T	14	1495.7	+0.1138	1495.7	
	454.27	+0.0641	454.27	5	A	13	1394.7	-0.018	1394.7	
	525.3		525.3	6	A	12	1323.6	-0.132	1323.6	
-0.4	327.68	+0.0009	654.35	7	E	11	1252.6	+0.0969	626.79	-0.324
	751.4		751.4	8	P	10	1123.5	+0.0661	1123.5	
-0.384	440.72		880.44	9	E	9	1026.5		1026.5	
	951.48	-0.117	951.48	10	A	8	897.44		897.44	
	1022.5		1022.5	11	A	7	826.41	+0.0268	826.41	
	1121.6	-0.094	1121.6	12	V	6	755.37	+0.069	755.37	
	1234.7		1234.7	13	I	5	656.3	+0.1565	656.3	
	1321.7		1321.7	14	S	4	543.22	+0.1067	543.22	
	1435.7	-0.06	1435.7	15	N	3	456.18	+0.0503	456.18	
	1492.8		1492.8	16	G	2	342.14		342.14	
	1621.8	-0.132	1621.8	17	E	1	285.12		285.12	
				18	H	0	156.08		156.08	



Scan number	2270	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	263.45

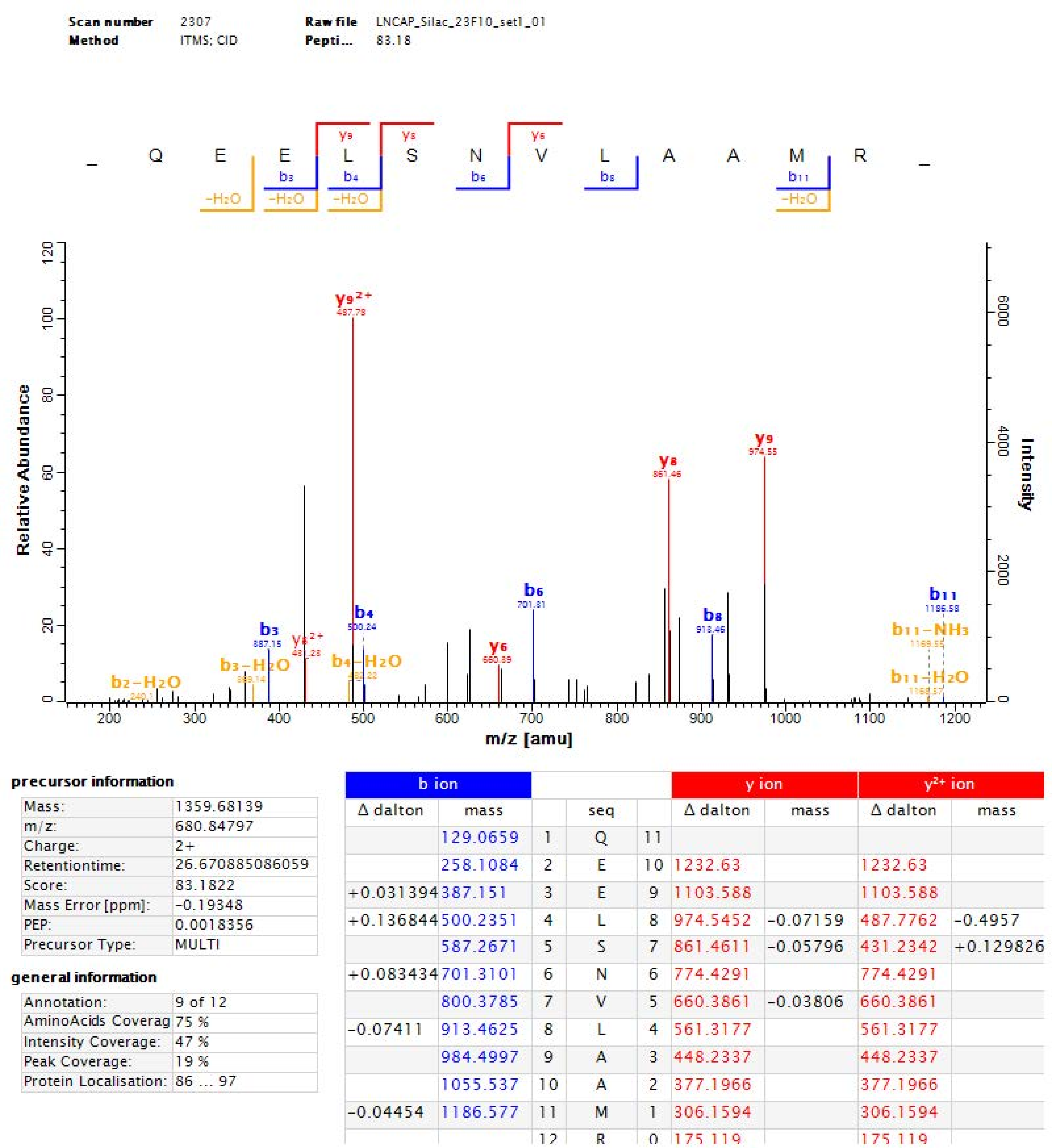
precursor information

Mass:	1785.84409
m/z:	893.92932
Charge:	2+
Retentiontime:	26.327394485473
Score:	263.448
Mass Error [ppm]:	-0.77603
PEP:	4.9663E-70
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	53 %
Peak Coverage:	46 %
Protein Localisation:	148 ... 165

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342	1	D	17				
	213.087	2	P	16	1671.826		1671.826	
	270.1084	3	G	15	1574.773	-0.04099	1574.773	
+0.142489	327.1299	4	G	14	1517.752	-0.11658	759.3794	+0.04635
+0.079238	440.214	5	I	13	1460.73	+0.115215	1460.73	
+0.171513	541.2617	6	T	12	1347.646	-0.10346	1347.646	
+0.117065	612.2988	7	A	11	1246.598	+0.135263	1246.598	
	669.3202	8	G	10	1175.561	-0.062	1175.561	
+0.169408	756.3523	9	S	9	1118.54	-0.13209	1118.54	
-0.28495	857.3999	10	T	8	1031.508	+0.0048	1031.508	
+0.227966	972.4269	11	D	7	930.4601	+0.018665	930.4601	
-0.02758	1101.469	12	E	6	815.4332	+0.098891	408.2202	-0.09747
	1198.522	13	P	5	686.3906	-0.00317	686.3906	
	1295.575	14	P	4	589.3378	-0.14169	589.3378	
+0.080559	1426.615	15	M	3	492.285		492.285	
-0.07138	1539.7	16	L	2	361.2445	+0.040579	361.2445	
+0.373011	1640.747	17	T	1	248.1605		248.1605	
		18	K	0	147.1128		147.1128	



Scan number	2307	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	83.18

precursor information

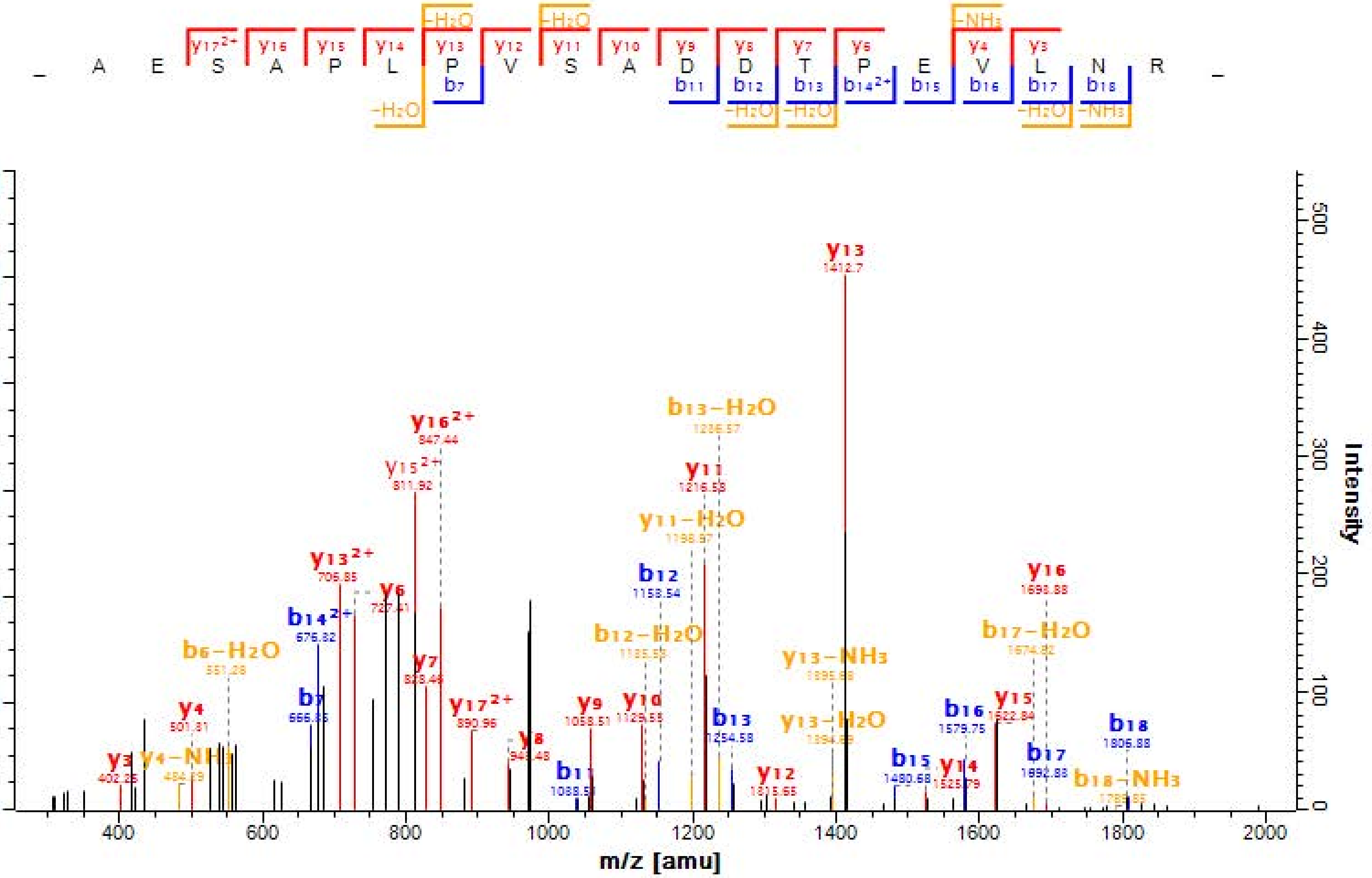
Mass:	1359.68139
m/z:	680.84797
Charge:	2+
Retentiontime:	26.670885086059
Score:	83.1822
Mass Error [ppm]:	-0.19348
PEP:	0.0018356
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	47 %
Peak Coverage:	19 %
Protein Localisation:	86 ... 97

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.0659	1	Q	11				
	258.1084	2	E	10	1232.63		1232.63	
+0.031394	387.151	3	E	9	1103.588		1103.588	
+0.136844	500.2351	4	L	8	974.5452	-0.07159	487.7762	-0.4957
	587.2671	5	S	7	861.4611	-0.05796	431.2342	+0.129826
+0.083434	701.3101	6	N	6	774.4291		774.4291	
	800.3785	7	V	5	660.3861	-0.03806	660.3861	
-0.07411	913.4625	8	L	4	561.3177		561.3177	
	984.4997	9	A	3	448.2337		448.2337	
	1055.537	10	A	2	377.1966		377.1966	
-0.04454	1186.577	11	M	1	306.1594		306.1594	
		12	R	0	175.119		175.119	

Scan number	3013	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	176.94



precursor information

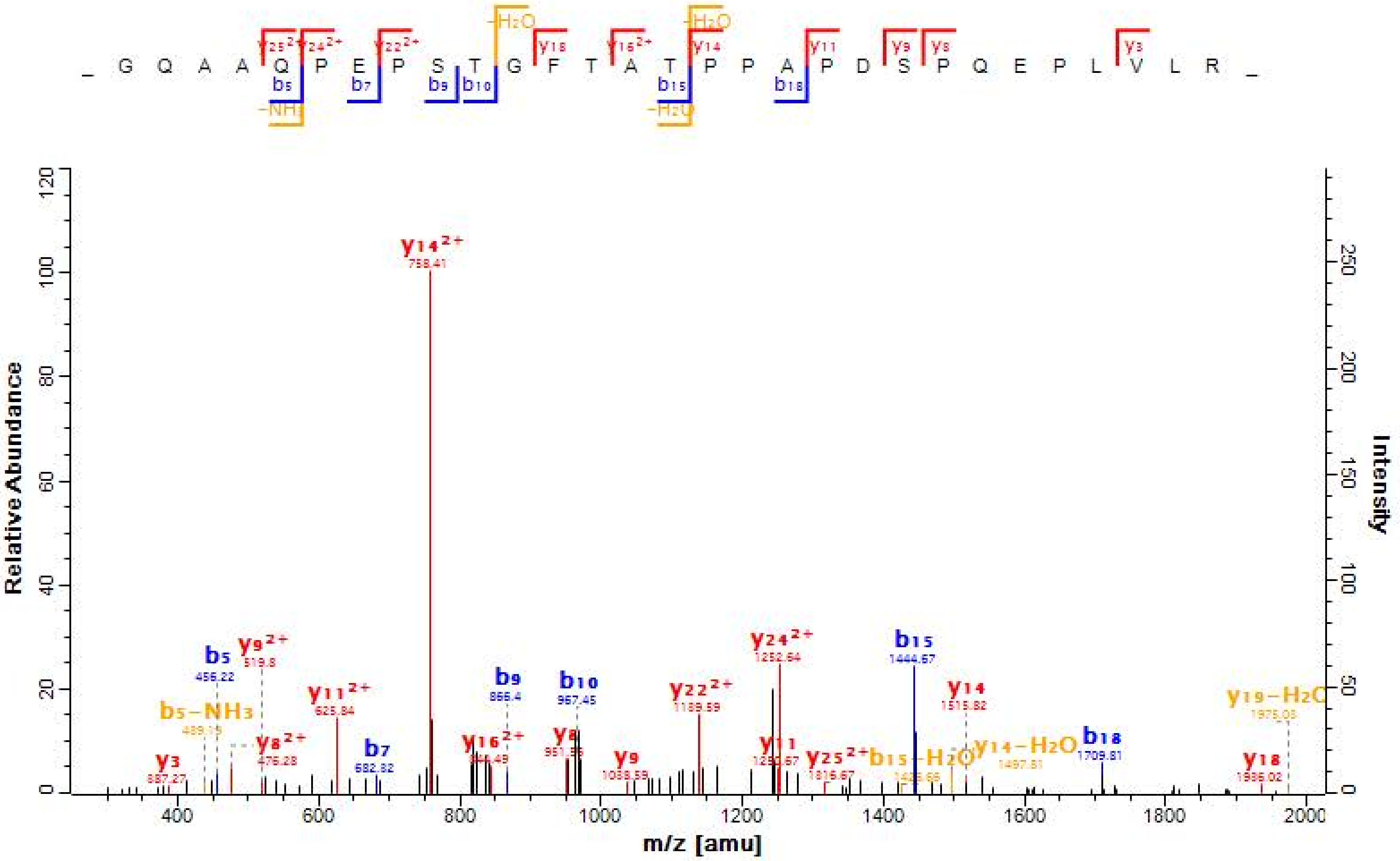
Mass:	1979.97982
m/z:	990.99719
Charge:	2+
Retentiontime:	33.027172088623
Score:	176.9393
Mass Error [ppm]:	-0.091309
PEP:	2.1483E-34
Precursor Type:	MULTI

general information

Annotation:	16 of 19
AminoAcids Coverag	84 %
Intensity Coverage:	48 %
Peak Coverage:	34 %
Protein Localisation:	39 ... 57

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	18				
	201.09		201.09	2	E	17	1910		1910	
	288.12		288.12	3	S	16	1780.9		890.96	+0.2546
	359.16		359.16	4	A	15	1693.9	-0.382	847.44	+0.1747
	456.21		456.21	5	P	14	1622.8	-0.133	811.92	+0.0018
	569.29		569.29	6	L	13	1525.8	+0.2004	1525.8	
	666.35	+0.0989	666.35	7	P	12	1412.7	-0.054	706.85	+0.3018
	765.41		765.41	8	V	11	1315.6	-0.031	1315.6	
	852.45		852.45	9	S	10	1216.6	+0.0073	1216.6	
	923.48		923.48	10	A	9	1129.5	-0.005	1129.5	
	1038.5	+0.001	1038.5	11	D	8	1058.5	+0.0178	1058.5	
	1153.5	-0.149	1153.5	12	D	7	943.48	+0.0682	943.48	
	1254.6	-0.049	1254.6	13	T	6	828.46	+0.0707	828.46	
+0.0158	676.32		1351.6	14	P	5	727.41	-0.004	727.41	
	1480.7	-0.18	1480.7	15	E	4	630.36		630.36	
	1579.7	-0.16	1579.7	16	V	3	501.31	+0.006	501.31	
	1692.8	-0.197	1692.8	17	L	2	402.25	+0.1684	402.25	
	1806.9	+0.2824	1806.9	18	N	1	289.16		289.16	
				19	R	0	175.12		175.12	

Scan number	3686	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	58.92



precursor information

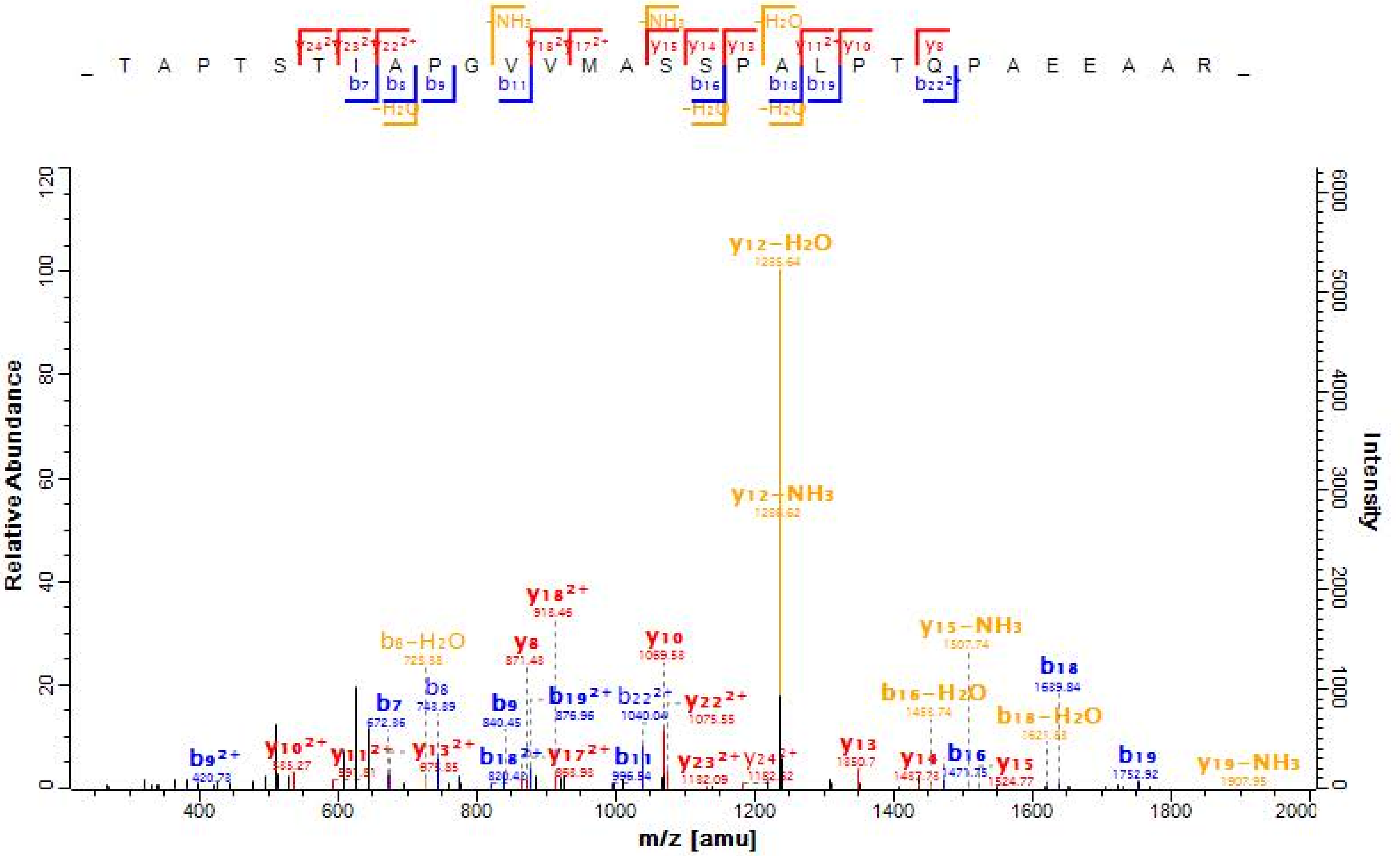
Mass:	2958.47259
m/z:	987.16481
Charge:	3+
Retentiontime:	38.791988372802
Score:	58.92403
Mass Error [ppm]:	0.093055
PEP:	1.6924E-05
Precursor Type:	MULTI

general information

Annotation:	16 of 29
AminoAcids Coverag	55 %
Intensity Coverage:	48 %
Peak Coverage:	24 %
Protein Localisation:	78 ... 106

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	28				
	186.0873	2	Q	27	2902.458		2902.458	
	257.1244	3	A	26	2774.4		2774.4	
	328.1615	4	A	25	2703.362		2703.362	
+0.179871	456.2201	5	Q	24	2632.325		1316.666	+0.206869
	553.2729	6	P	23	2504.267		1252.637	+0.288282
+0.08076	682.3155	7	E	22	2407.214		2407.214	
	779.3682	8	P	21	2278.171		1139.589	+0.310692
+0.27258	866.4003	9	S	20	2181.119		2181.119	
+0.215135	967.448	10	T	19	2094.087		2094.087	
	1024.469	11	G	18	1993.039		1993.039	
	1171.538	12	F	17	1936.017	-0.16858	1936.017	
	1272.586	13	T	16	1788.949		1788.949	
	1343.623	14	A	15	1687.901		844.4543	-0.23105
-0.11634	1444.67	15	T	14	1616.864		1616.864	
	1541.723	16	P	13	1515.817	+0.027059	758.4119	+0.165104
	1638.776	17	P	12	1418.764		1418.764	
-0.06868	1709.813	18	A	11	1321.711		1321.711	
	1806.866	19	P	10	1250.674	+0.09951	625.8406	+0.103978
	1921.893	20	D	9	1153.621		1153.621	
	2008.925	21	S	8	1038.594	-0.19786	519.8007	+0.114779
	2105.977	22	P	7	951.5622	-0.08172	476.2847	+0.142725
	2234.036	23	Q	6	854.5094		854.5094	
	2363.079	24	E	5	726.4509		726.4509	
	2460.131	25	P	4	597.4083		597.4083	
	2573.215	26	L	3	500.3555		500.3555	
	2672.284	27	V	2	387.2714	-0.12104	387.2714	
	2785.368	28	L	1	288.203		288.203	
		29	R	0	175.119		175.119	

Scan number	3706	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	90.78



precursor information

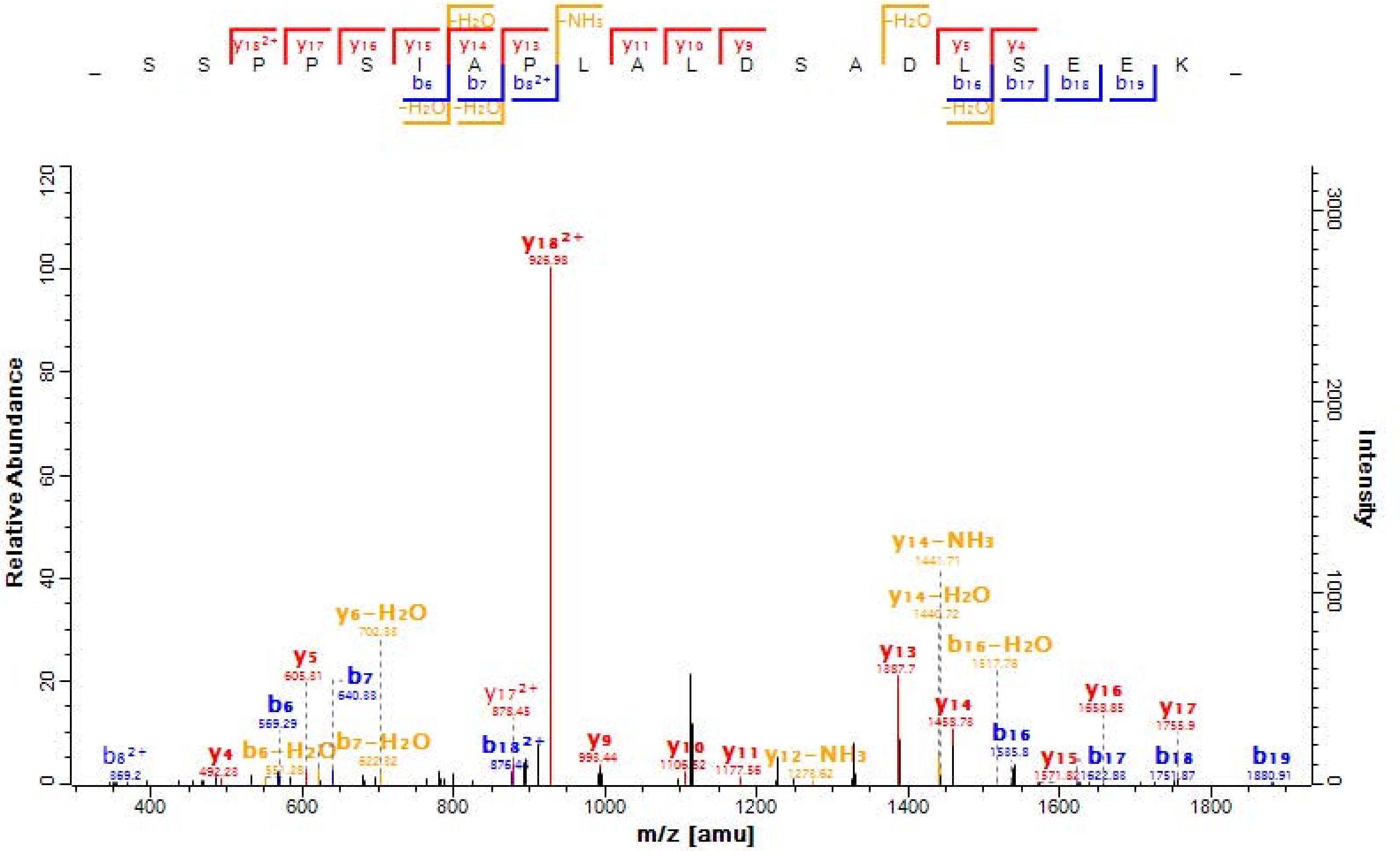
Mass:	2820.43368
m/z:	941.15184
Charge:	3+
Retentiontime:	38.950019836425
Score:	90.77802
Mass Error [ppm]:	0.32827
PEP:	1.2094E-13
Precursor Type:	MULTI

general information

Annotation:	15 of 29
AminoAcids Coverag	52 %
Intensity Coverage:	58 %
Peak Coverage:	32 %
Protein Localisation:	256 ... 284

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	28				
	173.09		173.09	2	A	27	2720.4		2720.4	
	270.14		270.14	3	P	26	2649.4		2649.4	
	371.19		371.19	4	T	25	2552.3		2552.3	
	458.22		458.22	5	S	24	2451.3		2451.3	
	559.27		559.27	6	T	23	2364.2		1182.6	+0.1031
	672.36	+0.0459	672.36	7	I	22	2263.2		1132.1	+0.4386
	743.39	+0.0095	743.39	8	A	21	2150.1		1075.5	+0.066
-0.363	420.73	-0.477	840.45	9	P	20	2079.1		2079.1	
	897.47		897.47	10	G	19	1982		1982	
	996.54	+0.0456	996.54	11	V	18	1925		1925	
	1095.6		1095.6	12	V	17	1825.9		913.46	+0.0844
	1226.6		1226.6	13	M	16	1726.8		863.93	-0.028
	1297.7		1297.7	14	A	15	1595.8		1595.8	
	1384.7		1384.7	15	S	14	1524.8	+0.114	1524.8	
	1471.7	-0.077	1471.7	16	S	13	1437.7	-0.221	1437.7	
	1568.8		1568.8	17	P	12	1350.7	-0.26	675.85	+0.0217
+0.1713	820.42	-0.339	1639.8	18	A	11	1253.6		1253.6	
+0.1269	876.96	-0.165	1752.9	19	L	10	1182.6		591.81	-0.021
	1850		1850	20	P	9	1069.5	+0.0191	535.27	+0.1647
	1951		1951	21	T	8	972.47		972.47	
+0.1919	1040		2079.1	22	Q	7	871.43	+0.3664	871.43	
	2176.1		2176.1	23	P	6	743.37		743.37	
	2247.2		2247.2	24	A	5	646.32		646.32	
	2376.2		2376.2	25	E	4	575.28		575.28	
	2505.3		2505.3	26	E	3	446.24		446.24	
	2576.3		2576.3	27	A	2	317.19		317.19	
	2647.3		2647.3	28	A	1	246.16		246.16	
				29	R	0	175.12		175.12	

Scan number	4124	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	96.01



precursor information

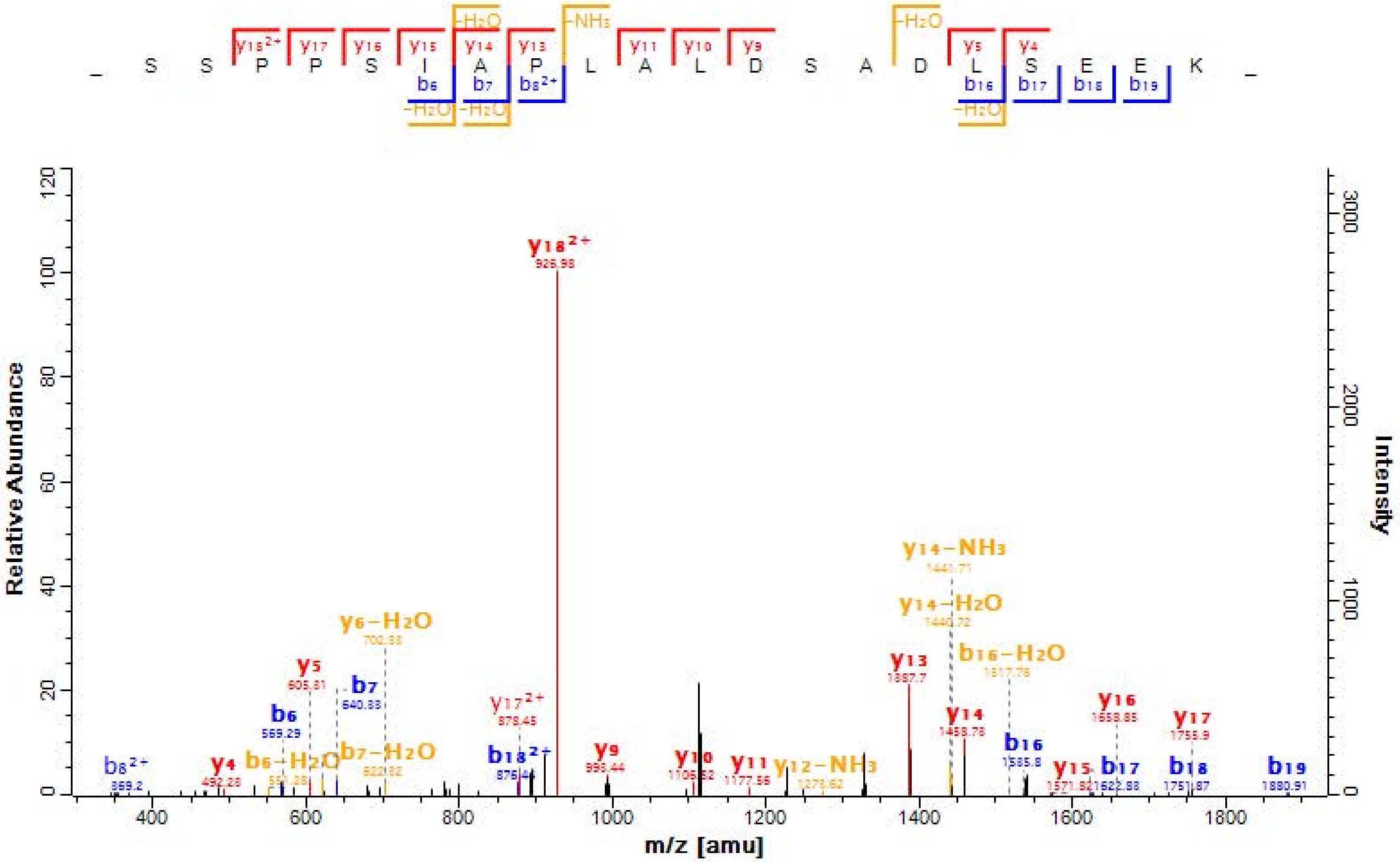
Mass:	2026.01008
m/z:	1014.01231
Charge:	2+
Retentiontime:	42.572048187255
Score:	96.01244
Mass Error [ppm]:	-0.27354
PEP:	3.4867E-06
Precursor Type:	MULTI

general information

Annotation:	16 of 20
AminoAcids Coverag	80 %
Intensity Coverage:	52 %
Peak Coverage:	28 %
Protein Localisation:	183 ... 202

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	19				
	175.07		175.07	2	S	18	1940		1940	
	272.12		272.12	3	P	17	1853		926.98	+0.2414
	369.18		369.18	4	P	16	1755.9	-0.06	878.45	+0.065
	456.21		456.21	5	S	15	1658.8	+0.1086	1658.8	
	569.29	+0.1221	569.29	6	I	14	1571.8	+0.0692	1571.8	
	640.33	+0.1483	640.33	7	A	13	1458.7	-0.071	1458.7	
+0.042	369.2		737.38	8	P	12	1387.7	-0.035	1387.7	
	850.47		850.47	9	L	11	1290.6		1290.6	
	921.5		921.5	10	A	10	1177.6	+0.0059	1177.6	
	1034.6		1034.6	11	L	9	1106.5	+0.0508	1106.5	
	1149.6		1149.6	12	D	8	993.44	-0.05	993.44	
	1236.6		1236.6	13	S	7	878.41		878.41	
	1307.7		1307.7	14	A	6	791.38		791.38	
	1422.7		1422.7	15	D	5	720.34		720.34	
	1535.8	-0.025	1535.8	16	L	4	605.31	+0.1176	605.31	
	1622.8	+0.1534	1622.8	17	S	3	492.23	+0.0943	492.23	
-0.045	876.44	-0.076	1751.9	18	E	2	405.2		405.2	
	1880.9	+0.0328	1880.9	19	E	1	276.16		276.16	
				20	K	0	147.11		147.11	

Scan number	4124	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	96.01



precursor information

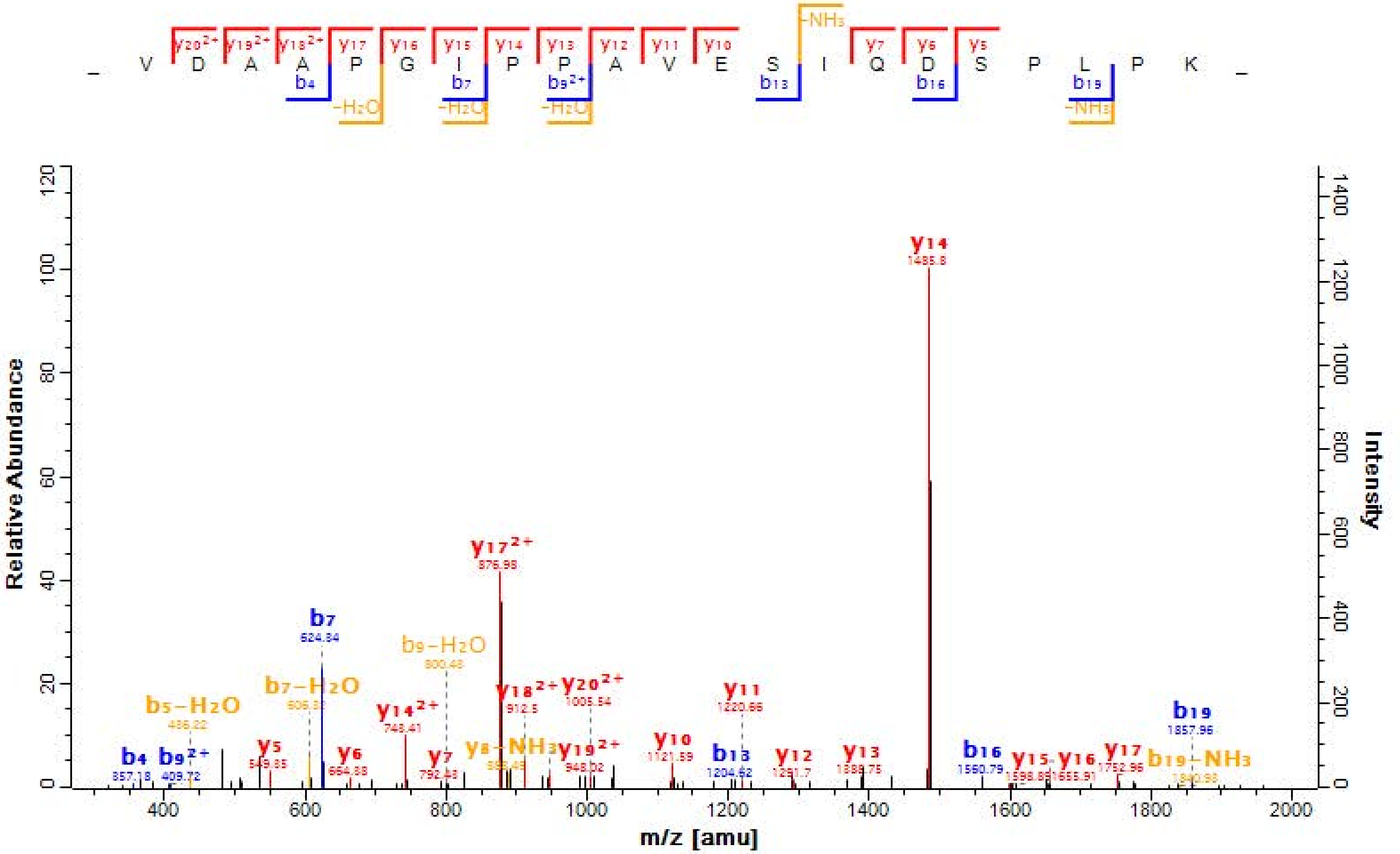
Mass:	2026.01008
m/z:	1014.01231
Charge:	2+
Retentiontime:	42.572048187255
Score:	96.01244
Mass Error [ppm]:	-0.27354
PEP:	3.4867E-06
Precursor Type:	MULTI

general information

Annotation:	16 of 20
AminoAcids Coverag	80 %
Intensity Coverage:	52 %
Peak Coverage:	28 %
Protein Localisation:	183 ... 202

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	19				
	175.07		175.07	2	S	18	1940		1940	
	272.12		272.12	3	P	17	1853		926.98	+0.2414
	369.18		369.18	4	P	16	1755.9	-0.06	878.45	+0.065
	456.21		456.21	5	S	15	1658.8	+0.1086	1658.8	
	569.29	+0.1221	569.29	6	I	14	1571.8	+0.0692	1571.8	
	640.33	+0.1483	640.33	7	A	13	1458.7	-0.071	1458.7	
+0.042	369.2		737.38	8	P	12	1387.7	-0.035	1387.7	
	850.47		850.47	9	L	11	1290.6		1290.6	
	921.5		921.5	10	A	10	1177.6	+0.0059	1177.6	
	1034.6		1034.6	11	L	9	1106.5	+0.0508	1106.5	
	1149.6		1149.6	12	D	8	993.44	-0.05	993.44	
	1236.6		1236.6	13	S	7	878.41		878.41	
	1307.7		1307.7	14	A	6	791.38		791.38	
	1422.7		1422.7	15	D	5	720.34		720.34	
	1535.8	-0.025	1535.8	16	L	4	605.31	+0.1176	605.31	
	1622.8	+0.1534	1622.8	17	S	3	492.23	+0.0943	492.23	
-0.045	876.44	-0.076	1751.9	18	E	2	405.2		405.2	
	1880.9	+0.0328	1880.9	19	E	1	276.16		276.16	
				20	K	0	147.11		147.11	

Scan number	4138	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	111.57



precursor information

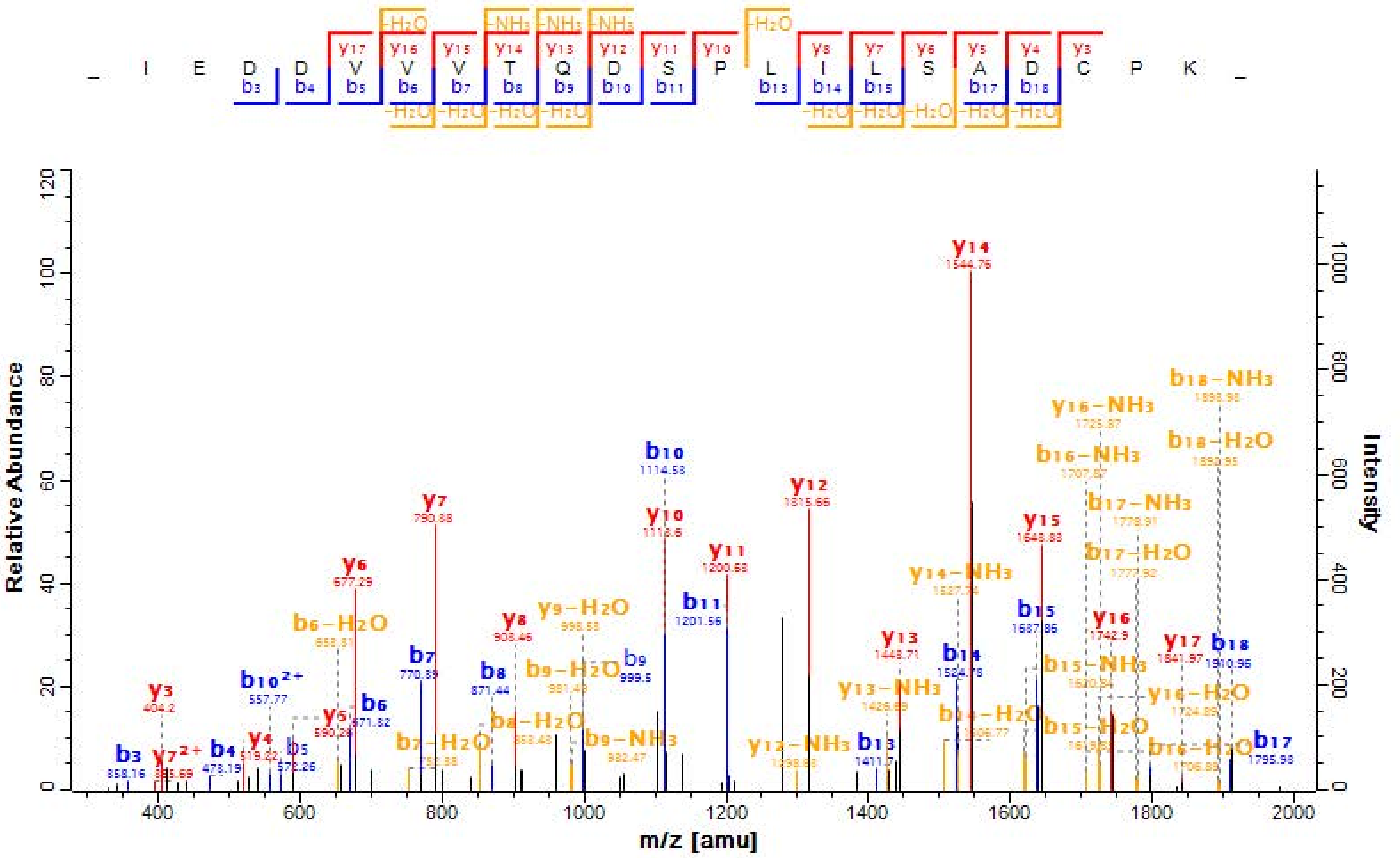
Mass:	2100.11134
m/z:	1051.06295
Charge:	2+
Retentiontime:	42.698543548584
Score:	111.5698
Mass Error [ppm]:	0.49921
PEP:	3.543E-09
Precursor Type:	MULTI

general information

Annotation:	17 of 21
AminoAcids Coverag	81 %
Intensity Coverage:	49 %
Peak Coverage:	26 %
Protein Localisation:	152 ... 172

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	20				
	215.1		215.1	2	D	19	2010.1		1005.5	-0.143
	286.14		286.14	3	A	18	1895		948.02	+0.1361
	357.18	+0.048	357.18	4	A	17	1824		912.5	+0.0523
	454.23		454.23	5	P	16	1753	+0.3052	876.98	-0.035
	511.25		511.25	6	G	15	1655.9	+0.1791	1655.9	
	624.34	-0.049	624.34	7	I	14	1598.9	-0.375	1598.9	
	721.39		721.39	8	P	13	1485.8	-0.012	743.41	+0.2023
+0.4439	409.72		818.44	9	P	12	1388.8	+0.3225	1388.8	
	889.48		889.48	10	A	11	1291.7	+0.2896	1291.7	
	988.55		988.55	11	V	10	1220.7	+0.1008	1220.7	
	1117.6		1117.6	12	E	9	1121.6	-0.108	1121.6	
	1204.6	-0.143	1204.6	13	S	8	992.55		992.55	
	1317.7		1317.7	14	I	7	905.52		905.52	
	1445.8		1445.8	15	Q	6	792.43	+0.1943	792.43	
	1560.8	-0.17	1560.8	16	D	5	664.38	-0.02	664.38	
	1647.8		1647.8	17	S	4	549.35	+0.0809	549.35	
	1744.9		1744.9	18	P	3	462.32		462.32	
	1858	+0.1568	1858	19	L	2	365.26		365.26	
	1955		1955	20	P	1	252.18		252.18	
				21	K	0	155.13		155.13	

Scan number 4181 **Raw file** LNCAP_Silac_23F10_set1_01
Method ITMS; CID **Pepti...** 270.35



precursor information

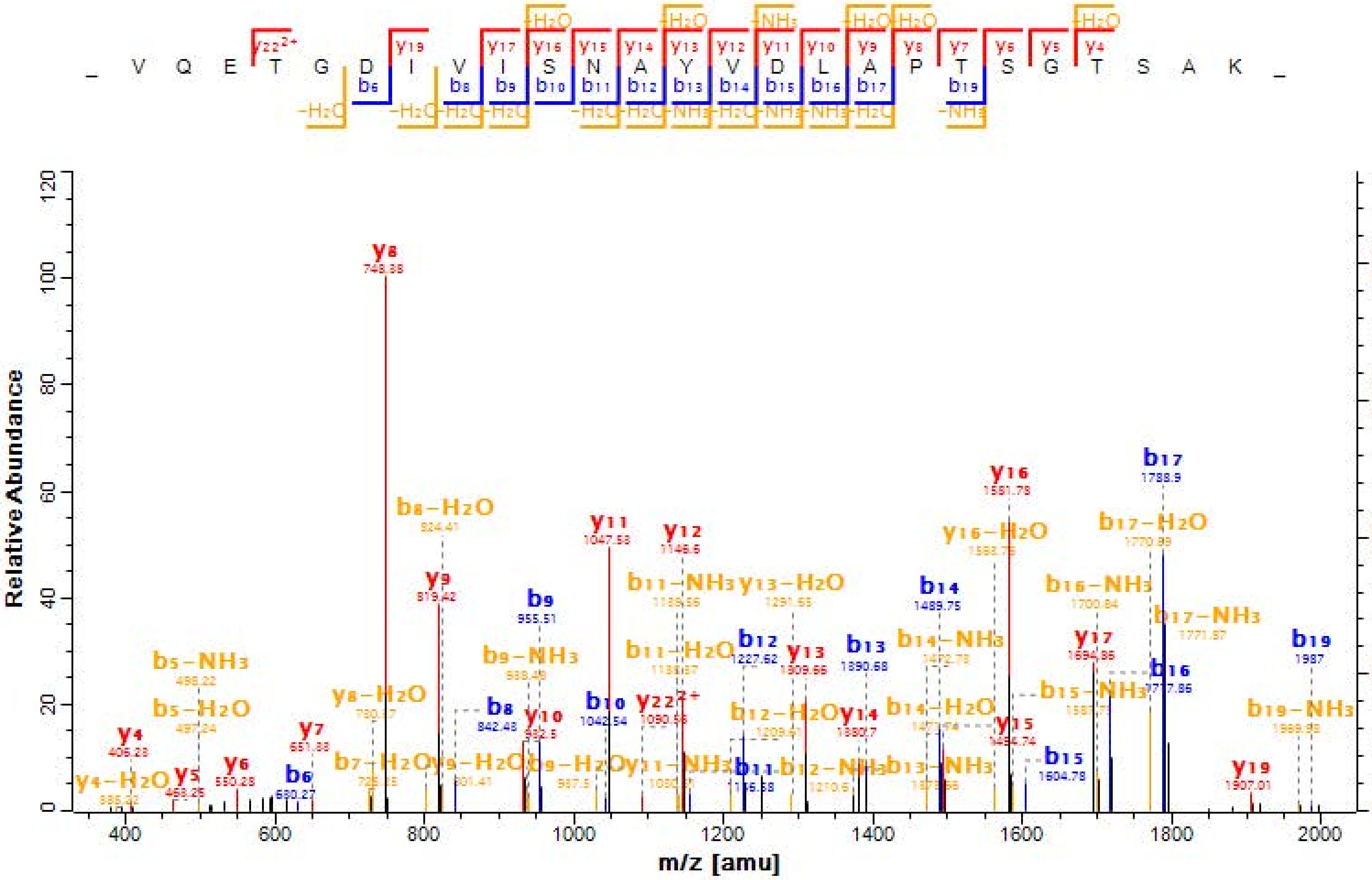
Mass:	2313.14136
m/z:	1157.57796
Charge:	2+
Retentiontime:	43.043979644775
Score:	270.354
Mass Error [ppm]:	0.15749
PEP:	4.9617E-99
Precursor Type:	MULTI

general information

Annotation:	17 of 21
AminoAcids Coverag	81 %
Intensity Coverage:	66 %
Peak Coverage:	50 %
Protein Localisation:	474 ... 494

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	I	20				
	243.13		243.13	2	E	19	2201.1		2201.1	
	358.16	+0.1892	358.16	3	D	18	2072		2072	
	473.19	+0.0966	473.19	4	D	17	1957		1957	
	572.26	+0.1132	572.26	5	V	16	1842	-0.262	1842	
	671.32	-0.025	671.32	6	V	15	1742.9	-0.106	1742.9	
	770.39	-0.069	770.39	7	V	14	1643.8	-0.125	1643.8	
	871.44	-0.077	871.44	8	T	13	1544.8	-0.067	1544.8	
	999.5	-0.006	999.5	9	Q	12	1443.7	-0.045	1443.7	
+0.4715	557.77	+0.0285	1114.5	10	D	11	1315.7	-0.08	1315.7	
	1201.6	+0.0696	1201.6	11	S	10	1200.6	-0.052	1200.6	
	1298.6		1298.6	12	P	9	1113.6	-0.042	1113.6	
	1411.7	-0.047	1411.7	13	L	8	1016.5		1016.5	
	1524.8	-0.158	1524.8	14	I	7	903.46	+0.0326	903.46	
	1637.9	-0.268	1637.9	15	L	6	790.38	+0.0138	395.69	-0.436
	1724.9		1724.9	16	S	5	677.29	+0.0063	677.29	
	1795.9	-0.182	1795.9	17	A	4	590.26	+0.0543	590.26	
	1911	-0.278	1911	18	D	3	519.22	+0.11	519.22	
	2071		2071	19	C	2	404.2	+0.0862	404.2	
	2168		2168	20	P	1	244.17		244.17	
				21	K	0	147.11		147.11	

Scan number	4200	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	240.49



precursor information

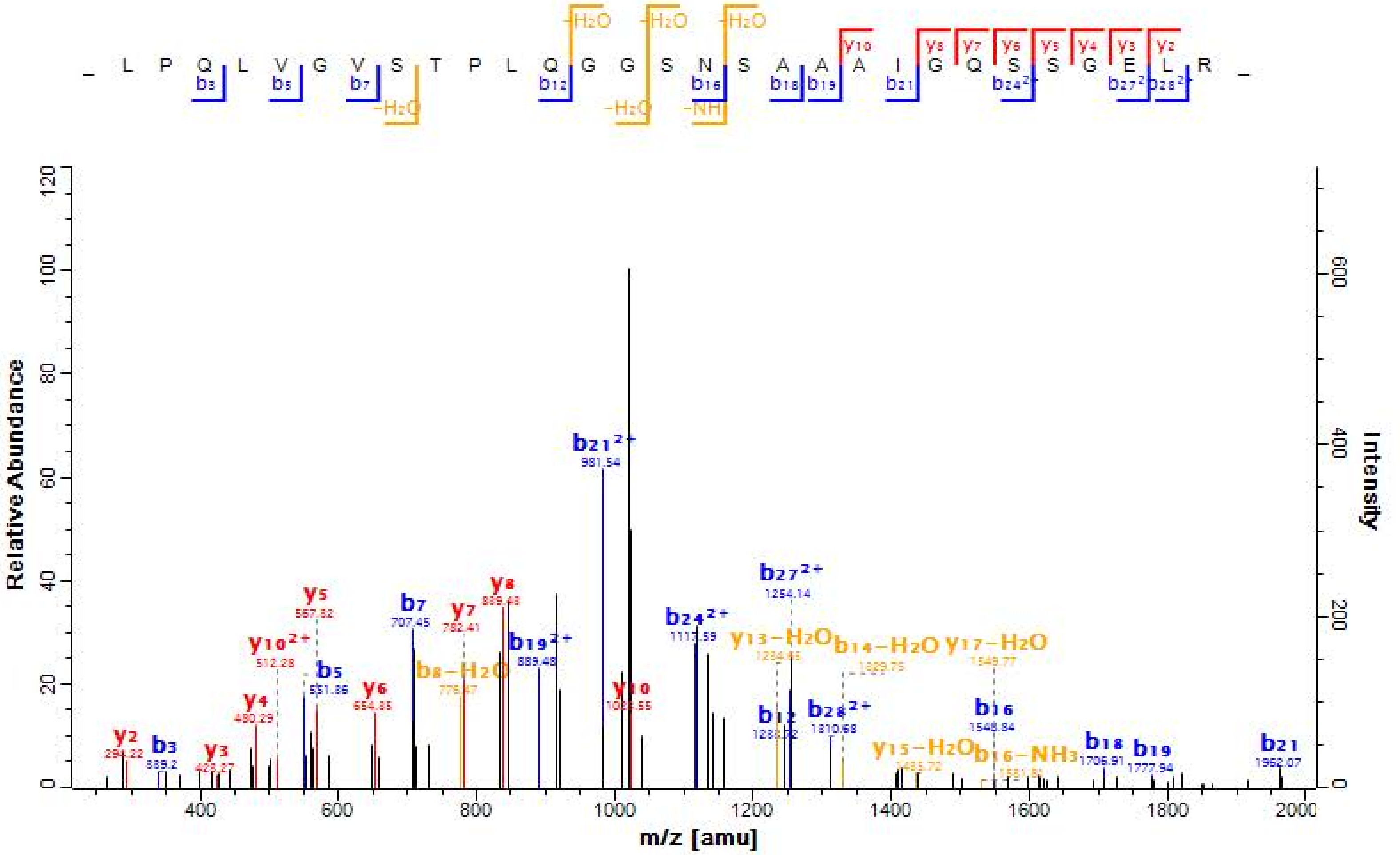
Mass:	2535.27082
m/z:	1268.64269
Charge:	2+
Retentiontime:	43.217903137207
Score:	240.4852
Mass Error [ppm]:	0.15568
PEP:	1.1008E-92
Precursor Type:	MULTI

general information

Annotation:	19 of 25
AminoAcids Coverag	76 %
Intensity Coverage:	67 %
Peak Coverage:	53 %
Protein Localisation:	590 ... 614

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	24				
	228.1343	2	Q	23	2437.209		2437.209	
	357.1769	3	E	22	2309.151		2309.151	
	458.2245	4	T	21	2180.108		1090.558	+0.222453
	515.246	5	G	20	2079.06		2079.06	
+0.308108	630.2729	6	D	19	2022.039		2022.039	
	743.357	7	I	18	1907.012	-0.1208	1907.012	
-0.16175	842.4254	8	V	17	1793.928		1793.928	
-0.07248	955.5095	9	I	16	1694.86	-0.15484	1694.86	
+0.035388	1042.542	10	S	15	1581.775	-0.07286	1581.775	
+0.003691	1156.584	11	N	14	1494.743	-0.06414	1494.743	
-0.04099	1227.622	12	A	13	1380.701	-0.14963	1380.701	
+0.021046	1390.685	13	Y	12	1309.663	-0.05185	1309.663	
-0.11622	1489.753	14	V	11	1146.6	-0.04394	1146.6	
-0.27451	1604.78	15	D	10	1047.532	+0.031552	1047.532	
-0.26873	1717.864	16	L	9	932.5047	+2.37E-05	932.5047	
-0.1668	1788.901	17	A	8	819.4207	+0.010174	819.4207	
	1885.954	18	P	7	748.3836	+0.041062	748.3836	
-0.00662	1987.002	19	T	6	651.3308	-0.09239	651.3308	
	2074.034	20	S	5	550.2831	+0.094569	550.2831	
	2131.055	21	G	4	463.2511	+0.139536	463.2511	
	2232.103	22	T	3	406.2296	+0.219106	406.2296	
	2319.135	23	S	2	305.1819		305.1819	
	2390.172	24	A	1	218.1499		218.1499	
		25	K	0	147.1128		147.1128	

Scan number	4301	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	80.36



precursor information

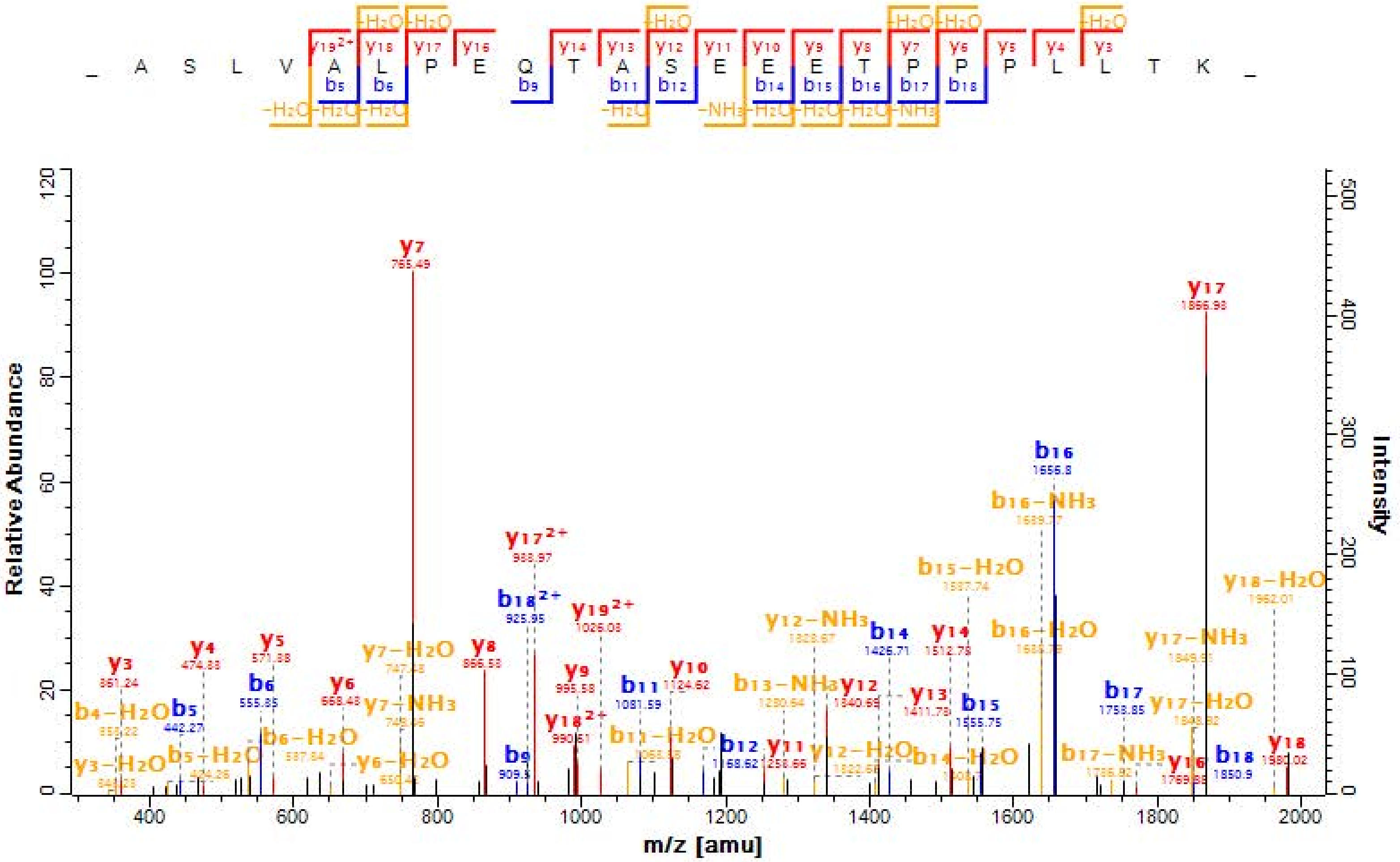
Mass:	2793.462
m/z:	932.16128
Charge:	3+
Retentiontime:	44.104724884033
Score:	80.3587
Mass Error [ppm]:	-0.028645
PEP:	3.1862E-09
Precursor Type:	MULTI

general information

Annotation:	21 of 29
AminoAcids Coverag	72 %
Intensity Coverage:	33 %
Peak Coverage:	27 %
Protein Localisation:	50 ... 78

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	28				
	211.14		211.14	2	P	27	2687.4		2687.4	
	339.2	+0.0427	339.2	3	Q	26	2590.4		2590.4	
	452.29		452.29	4	L	25	2462.3		2462.3	
	551.36	-0.019	551.36	5	V	24	2349.2		2349.2	
	608.38		608.38	6	G	23	2250.1		2250.1	
	707.45	-0.076	707.45	7	V	22	2193.1		2193.1	
	794.48		794.48	8	S	21	2094.1		2094.1	
	895.52		895.52	9	T	20	2007		2007	
	992.58		992.58	10	P	19	1906		1906	
	1105.7		1105.7	11	L	18	1808.9		1808.9	
	1233.7	-0.133	1233.7	12	Q	17	1695.8		1695.8	
	1290.7		1290.7	13	G	16	1567.8		1567.8	
	1347.8		1347.8	14	G	15	1510.8		1510.8	
	1434.8		1434.8	15	S	14	1453.7		1453.7	
	1548.8	-0.423	1548.8	16	N	13	1366.7		1366.7	
	1635.9		1635.9	17	S	12	1252.7		1252.7	
	1706.9	+0.0159	1706.9	18	A	11	1165.6		1165.6	
+0.0896	889.48	+0.035	1777.9	19	A	10	1094.6		1094.6	
	1849		1849	20	A	9	1023.6	+0.0806	512.28	-0.018
+0.1443	981.54	+0.1561	1962.1	21	I	8	952.52		952.52	
	2019.1		2019.1	22	G	7	839.43	-0.029	839.43	
	2147.1		2147.1	23	Q	6	782.41	-0.093	782.41	
+0.1107	1117.6		2234.2	24	S	5	654.35	+0.1656	654.35	
	2321.2		2321.2	25	S	4	567.32	+0.0391	567.32	
	2378.2		2378.2	26	G	3	480.29	+0.1221	480.29	
-0.186	1254.1		2507.3	27	E	2	423.27	-0.004	423.27	
+0.397	1310.7		2620.4	28	L	1	294.22	+0.0975	294.22	
				29	R	0	181.14		181.14	

Scan number	4372	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	235.25



precursor information

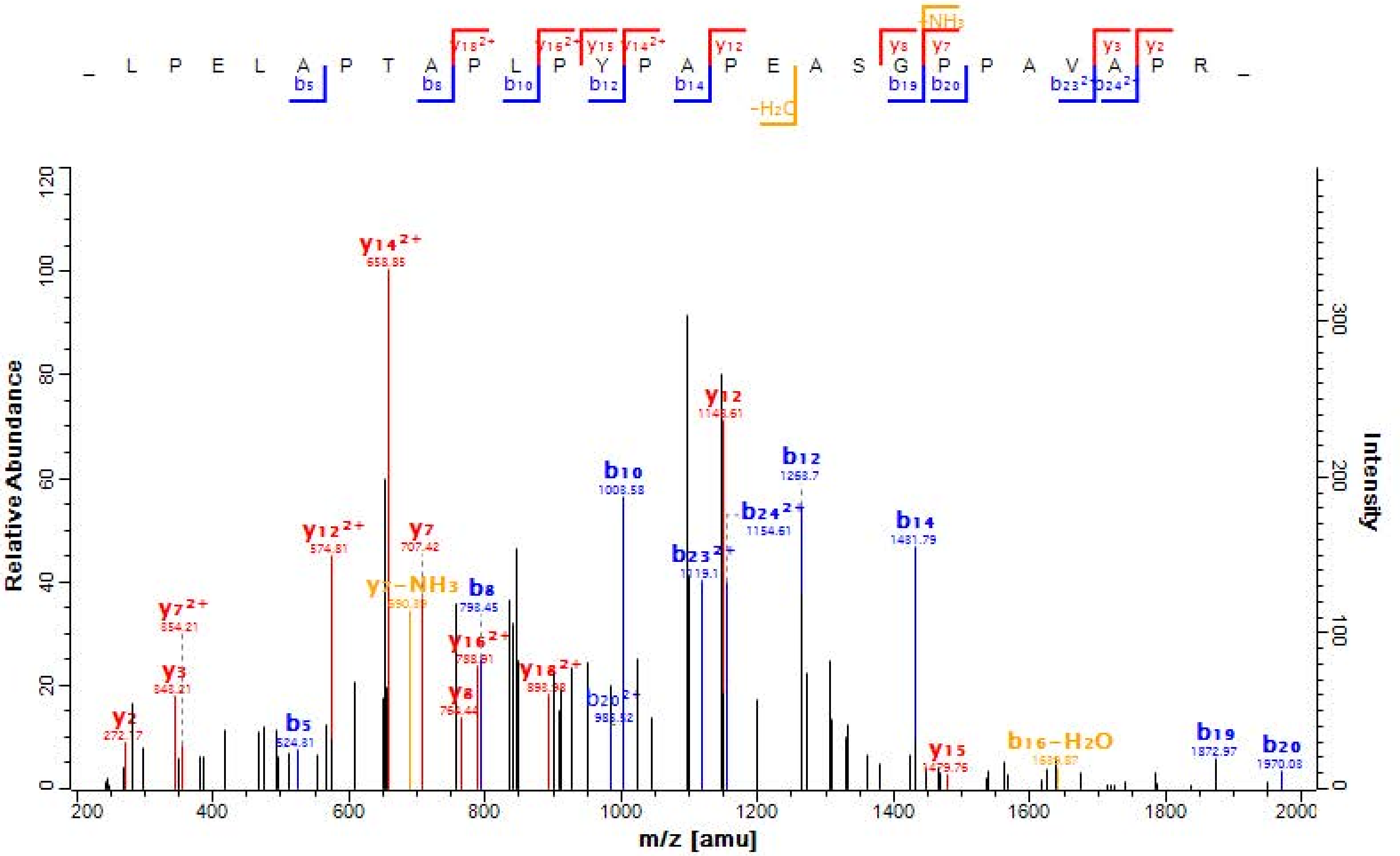
Mass:	2420.2682
m/z:	1211.14138
Charge:	2+
Retentiontime:	44.765167236328
Score:	235.2523
Mass Error [ppm]:	-0.18142
PEP:	3.0669E-87
Precursor Type:	MULTI

general information

Annotation:	18 of 23
AminoAcids Coverag	78 %
Intensity Coverage:	60 %
Peak Coverage:	48 %
Protein Localisation:	301 ... 323

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	22				
	159.08		159.08	2	S	21	2350.2		2350.2	
	272.16		272.16	3	L	20	2263.2		2263.2	
	371.23		371.23	4	V	19	2150.1		2150.1	
	442.27	+0.2055	442.27	5	A	18	2051.1		1026	+0.3536
	555.35	+0.1416	555.35	6	L	17	1980	-0.195	990.51	-0.073
	652.4		652.4	7	P	16	1866.9	-0.083	933.97	+0.2223
	781.45		781.45	8	E	15	1769.9	+0.12	1769.9	
	909.5	+0.0261	909.5	9	Q	14	1640.8		1640.8	
	1010.6		1010.6	10	T	13	1512.8	-0.192	1512.8	
	1081.6	-0.25	1081.6	11	A	12	1411.7	-0.181	1411.7	
	1168.6	+0.0801	1168.6	12	S	11	1340.7	-0.084	1340.7	
	1297.7		1297.7	13	E	10	1253.7	-0.057	1253.7	
	1426.7	-0.249	1426.7	14	E	9	1124.6	-0.086	1124.6	
	1555.7	-0.159	1555.7	15	E	8	995.58	+0.0725	995.58	
	1656.8	-0.16	1656.8	16	T	7	866.53	+0.0202	866.53	
	1753.8	-0.451	1753.8	17	P	6	765.49	+0.0044	765.49	
+0.1199	925.95	-0.054	1850.9	18	P	5	668.43	+0.0143	668.43	
	1948		1948	19	P	4	571.38	+0.1061	571.38	
	2061		2061	20	L	3	474.33	+0.0562	474.33	
	2174.1		2174.1	21	L	2	361.24	-0.001	361.24	
	2275.2		2275.2	22	T	1	248.16		248.16	
				23	K	0	147.11		147.11	

Scan number	4408	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	67.11



precursor information

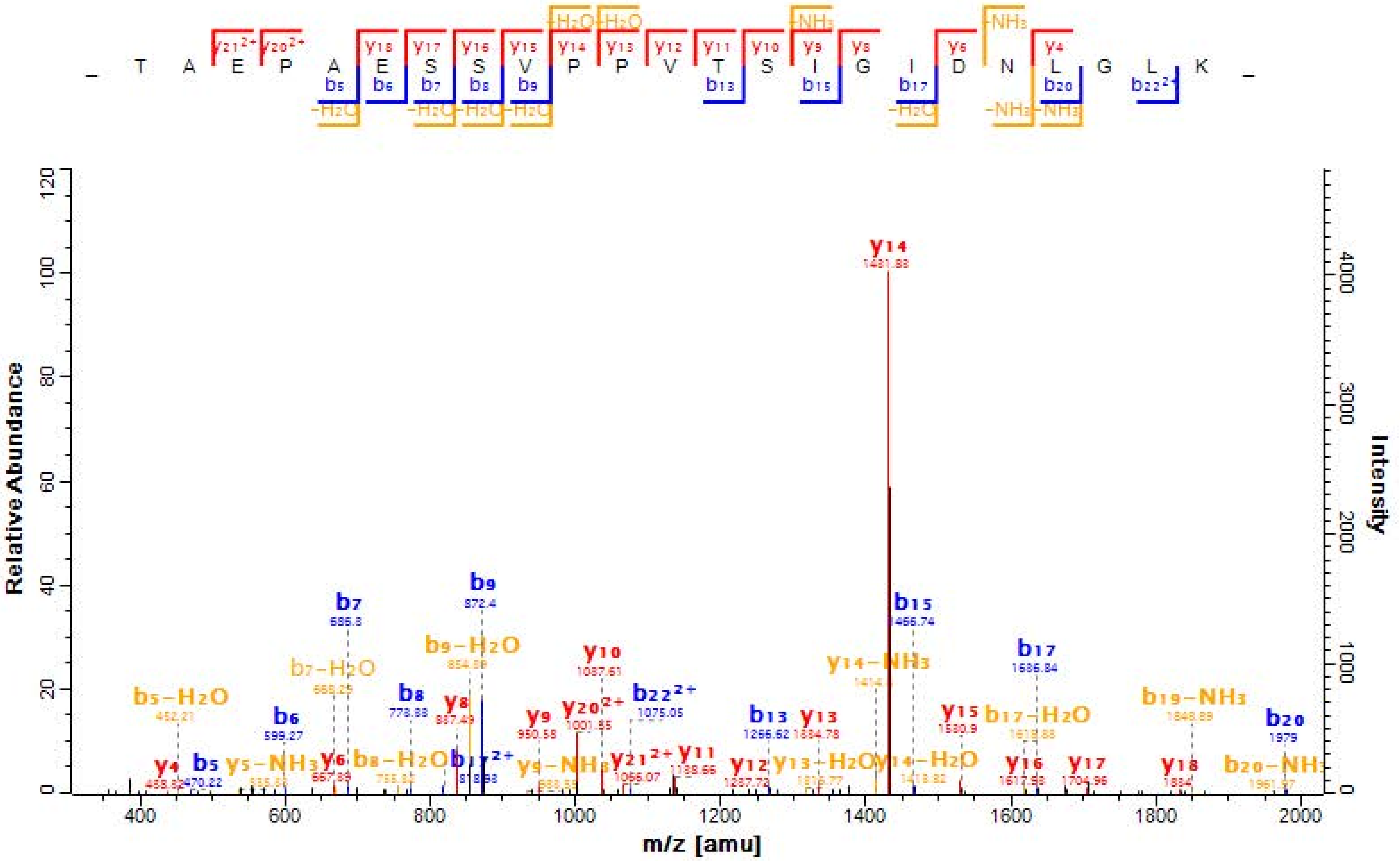
Mass:	2578.37943
m/z:	860.46709
Charge:	3+
Retentiontime:	45.078979492187
Score:	67.10954
Mass Error [ppm]:	-0.035382
PEP:	2.647E-05
Precursor Type:	MULTI

general information

Annotation:	15 of 26
AminoAcids Coverag	58 %
Intensity Coverage:	38 %
Peak Coverage:	23 %
Protein Localisation:	180 ... 205

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	25				
	211.14		211.14	2	P	24	2466.3		2466.3	
	340.19		340.19	3	E	23	2369.2		2369.2	
	453.27		453.27	4	L	22	2240.2		2240.2	
	524.31	-0.051	524.31	5	A	21	2127.1		2127.1	
	621.36		621.36	6	P	20	2056.1		2056.1	
	722.41		722.41	7	T	19	1959		1959	
	793.45	+0.0347	793.45	8	A	18	1858		1858	
	890.5		890.5	9	P	17	1786.9		893.98	+0.410
	1003.6	+0.069	1003.6	10	L	16	1689.9		1689.9	
	1100.6		1100.6	11	P	15	1576.8		788.91	+0.342
	1263.7	-0.198	1263.7	12	Y	14	1479.8	+0.2444	1479.8	
	1360.8		1360.8	13	P	13	1316.7		658.85	+0.2001
	1431.8	+0.0174	1431.8	14	A	12	1219.6		1219.6	
	1528.8		1528.8	15	P	11	1148.6	+0.0248	574.81	-0.039
	1657.9		1657.9	16	E	10	1051.6		1051.6	
	1728.9		1728.9	17	A	9	922.51		922.51	
	1816		1816	18	S	8	851.47		851.47	
	1873	-0.084	1873	19	G	7	764.44	+0.0505	764.44	
-0.2	985.52	-0.301	1970	20	P	6	707.42	+0.054	354.21	+0.280
	2067.1		2067.1	21	P	5	610.37		610.37	
	2138.1		2138.1	22	A	4	513.31		513.31	
-0.032	1119.1		2237.2	23	V	3	442.28		442.28	
+0.0767	1154.6		2308.2	24	A	2	343.21	+0.094	343.21	
	2405.3		2405.3	25	P	1	272.17	+0.169	272.17	
				26	R	0	175.12		175.12	

Scan number	4824	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	178.32



precursor information

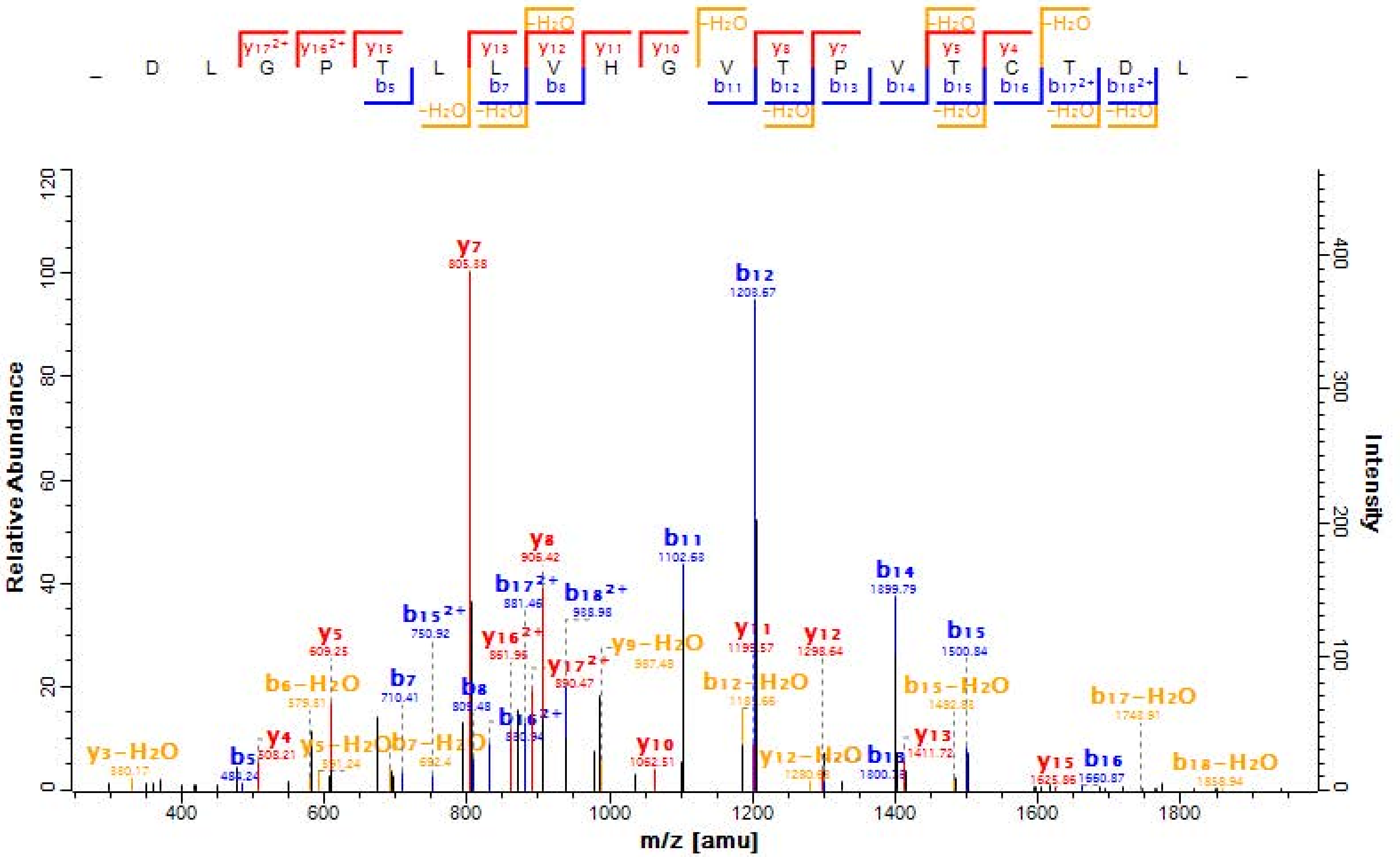
Mass:	2294.2012
m/z:	1148.10788
Charge:	2+
Retentiontime:	48.491416931152
Score:	178.3236
Mass Error [ppm]:	0.27871
PEP:	1.7587E-38
Precursor Type:	MULTI

general information

Annotation:	19 of 23
AminoAcids Coverag	83 %
Intensity Coverage:	59 %
Peak Coverage:	37 %
Protein Localisation:	339 ... 361

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	22				
	173.09		173.09	2	A	21	2202.2		2202.2	
	302.13		302.13	3	E	20	2131.1		1066.1	+0.1503
	399.19		399.19	4	P	19	2002.1		1001.6	+0.3506
	470.22	-0.291	470.22	5	A	18	1905		1905	
	599.27	+0.1597	599.27	6	E	17	1834	-0.091	1834	
	686.3	+0.1175	686.3	7	S	16	1705	-0.237	1705	
	773.33	-0.071	773.33	8	S	15	1617.9	+0.0005	1617.9	
	872.4	-0.006	872.4	9	V	14	1530.9	-0.069	1530.9	
	969.45		969.45	10	P	13	1431.8	-0.074	1431.8	
	1066.5		1066.5	11	P	12	1334.8	+0.1094	1334.8	
	1165.6		1165.6	12	V	11	1237.7	+0.2418	1237.7	
	1266.6	+0.088	1266.6	13	T	10	1138.7	+0.0853	1138.7	
	1353.7		1353.7	14	S	9	1037.6	+0.0814	1037.6	
	1466.7	-0.013	1466.7	15	I	8	950.58	+0.0151	950.58	
	1523.8		1523.8	16	G	7	837.49	+0.0035	837.49	
-0.351	818.93	-0.053	1636.8	17	I	6	780.47		780.47	
	1751.9		1751.9	18	D	5	667.39	-0.025	667.39	
	1865.9		1865.9	19	N	4	552.36		552.36	
	1979	-0.095	1979	20	L	3	438.32	-0.051	438.32	
	2036		2036	21	G	2	325.23		325.23	
+0.1814	1075.1		2149.1	22	L	1	268.21		268.21	
				23	K	0	155.13		155.13	

Scan number	5345	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	150.37



precursor information

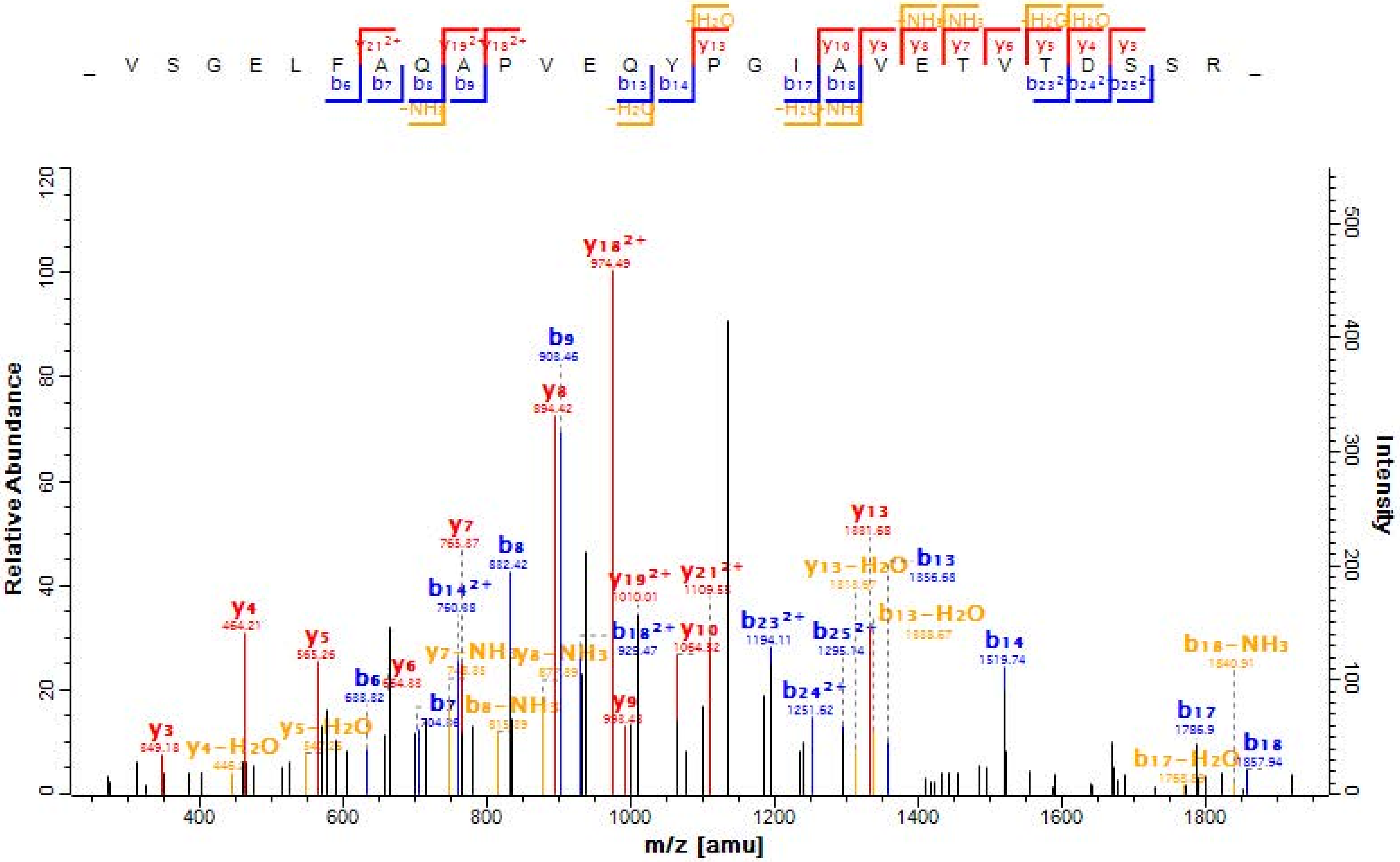
Mass:	2007.0345
m/z:	1004.52453
Charge:	2+
Retentiontime:	53.022960662841
Score:	150.3699
Mass Error [ppm]:	-0.088893
PEP:	4.5866E-13
Precursor Type:	ISO

general information

Annotation:	16 of 19
AminoAcids Coverag	84 %
Intensity Coverage:	57 %
Peak Coverage:	37 %
Protein Localisation:	896 ... 914

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	18				
	229.12		229.12	2	L	17	1893		1893	
	286.14		286.14	3	G	16	1779.9		890.47	+0.1862
	383.19		383.19	4	P	15	1722.9		861.96	+0.312
	484.24	+0.334	484.24	5	T	14	1625.9	-0.458	1625.9	
	597.32		597.32	6	L	13	1524.8		1524.8	
	710.41	+0.1437	710.41	7	L	12	1411.7	+0.057	1411.7	
	809.48	-0.066	809.48	8	V	11	1298.6	+0.0007	1298.6	
	946.54		946.54	9	H	10	1199.6	+0.0625	1199.6	
	1003.6		1003.6	10	G	9	1062.5	-0.087	1062.5	
	1102.6	-0.035	1102.6	11	V	8	1005.5		1005.5	
	1203.7	-0.023	1203.7	12	T	7	906.42	-0.014	906.42	
	1300.7	-0.175	1300.7	13	P	6	805.38	-0.036	805.38	
	1399.8	+0.0036	1399.8	14	V	5	708.32		708.32	
-0.112	750.92	-0.189	1500.8	15	T	4	609.25	+0.033	609.25	
+0.2224	830.94	-0.234	1660.9	16	C	3	508.21	+0.1303	508.21	
+0.3147	881.46		1761.9	17	T	2	348.18		348.18	
-0.034	938.98		1876.9	18	D	1	247.13		247.13	
				19	L	0	132.1		132.1	

Scan number	5514	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	131.26



precursor information

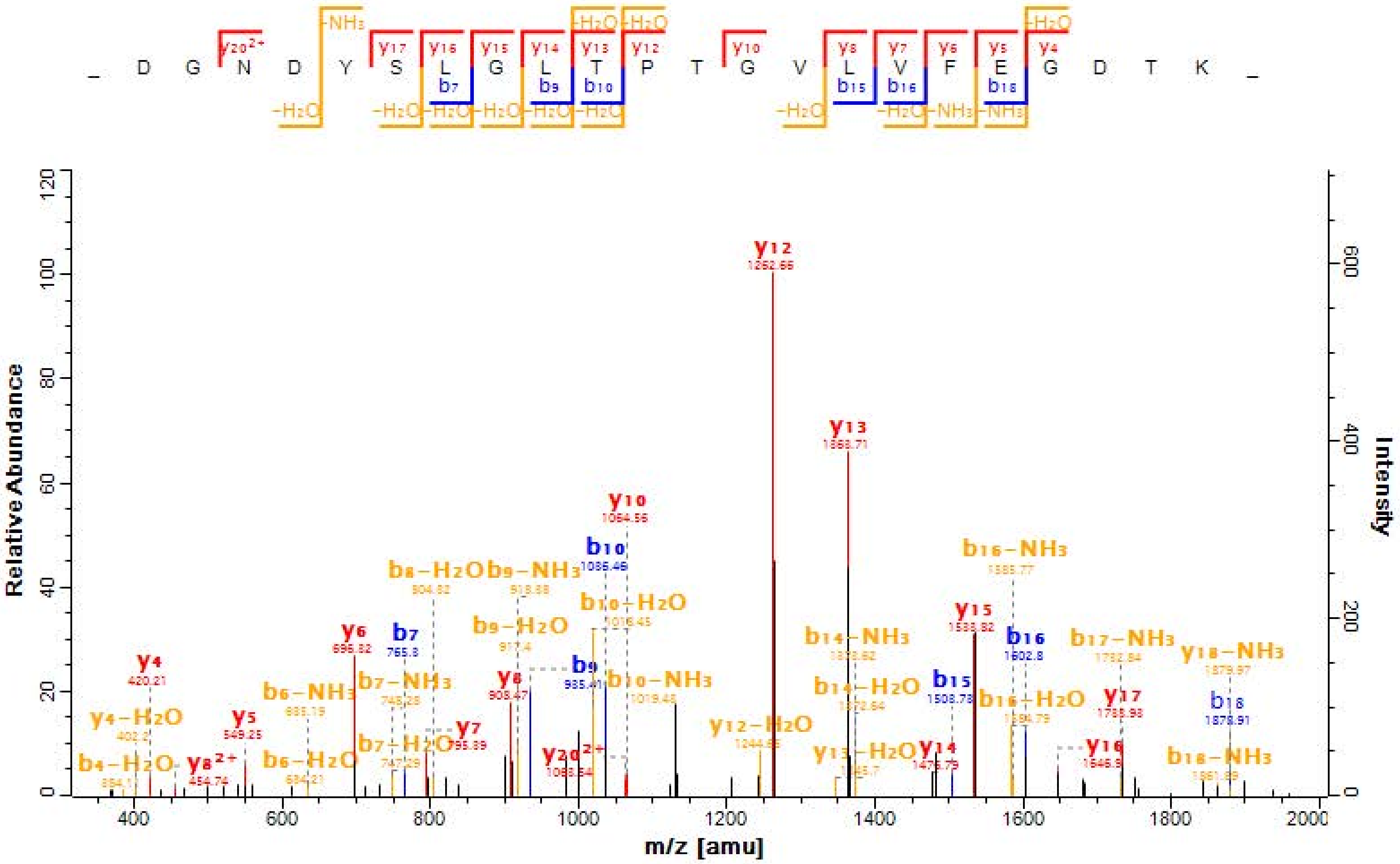
Mass:	2849.40866
m/z:	950.81016
Charge:	3+
Retentiontime:	54.445831298828
Score:	131.2577
Mass Error [ppm]:	0.11944
PEP:	1.648E-18
Precursor Type:	MULTI

general information

Annotation:	18 of 27
AminoAcids Coverag	67 %
Intensity Coverage:	52 %
Peak Coverage:	33 %
Protein Localisation:	64 ... 90

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	26				
	187.11		187.11	2	S	25	2751.3		2751.3	
	244.13		244.13	3	G	24	2664.3		2664.3	
	373.17		373.17	4	E	23	2607.3		2607.3	
	486.26		486.26	5	L	22	2478.3		2478.3	
	633.32	+0.0331	633.32	6	F	21	2365.2		2365.2	
	704.36	+0.1273	704.36	7	A	20	2218.1		1109.6	-0.25
	832.42	+0.1151	832.42	8	Q	19	2147.1		2147.1	
	903.46	-0.018	903.46	9	A	18	2019		1010	+0.0135
	1000.5		1000.5	10	P	17	1948		974.49	+0.2564
	1099.6		1099.6	11	V	16	1850.9		1850.9	
	1228.6		1228.6	12	E	15	1751.8		1751.8	
	1356.7	-0.091	1356.7	13	Q	14	1622.8		1622.8	
+0.2571	760.38	-0.041	1519.7	14	Y	13	1494.7		1494.7	
	1616.8		1616.8	15	P	12	1331.7	+0.0907	1331.7	
	1673.8		1673.8	16	G	11	1234.6		1234.6	
	1786.9	+0.3844	1786.9	17	I	10	1177.6		1177.6	
-0.015	929.47	+0.2946	1857.9	18	A	9	1064.5	-0.042	1064.5	
	1957		1957	19	V	8	993.48	+0.1046	993.48	
	2086		2086	20	E	7	894.42	-0.041	894.42	
	2187.1		2187.1	21	T	6	765.37	+0.1071	765.37	
	2286.2		2286.2	22	V	5	664.33	+0.1474	664.33	
+0.1755	1194.1		2387.2	23	T	4	565.26	+0.0484	565.26	
+0.2739	1251.6		2502.2	24	D	3	464.21	+0.0715	464.21	
-0.166	1295.1		2589.3	25	S	2	349.18	+0.1103	349.18	
	2676.3		2676.3	26	S	1	262.15		262.15	
				27	R	0	175.12		175.12	

Scan number	5645	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	152.06



precursor information

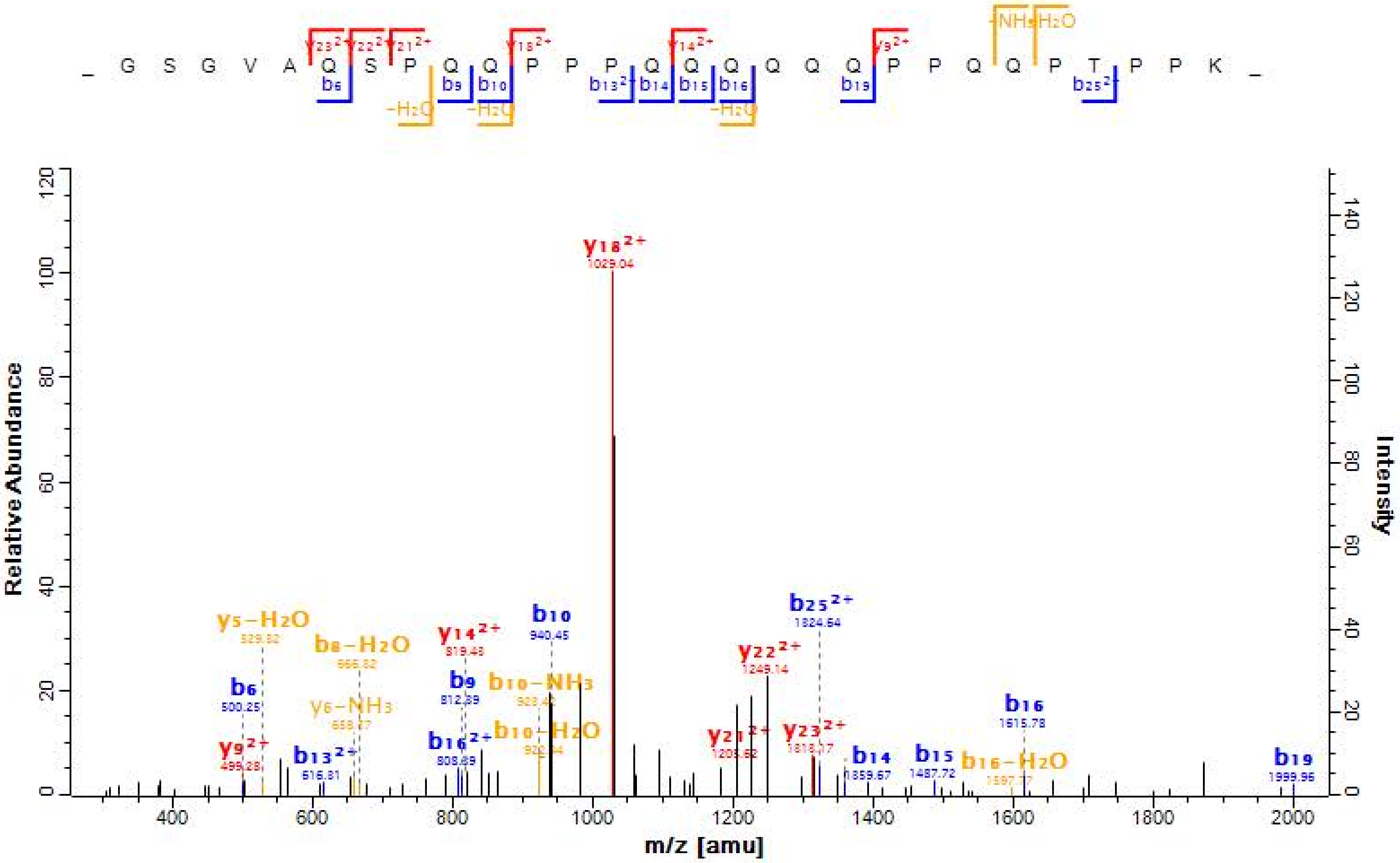
Mass:	2297.10646
m/z:	1149.56051
Charge:	2+
Retentiontime:	55.608203887939
Score:	152.0606
Mass Error [ppm]:	0.058839
PEP:	3.9594E-28
Precursor Type:	MULTI

general information

Annotation:	16 of 22
AminoAcids Coverag	73 %
Intensity Coverage:	62 %
Peak Coverage:	44 %
Protein Localisation:	241 ... 262

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342	1	D	21				
	173.0557	2	G	20	2183.087		2183.087	
	287.0986	3	N	19	2126.065		1063.536	+0.382589
	402.1256	4	D	18	2012.022		2012.022	
	565.1889	5	Y	17	1896.995		1896.995	
	652.2209	6	S	16	1733.932	-0.09544	1733.932	
-0.15403	765.305	7	L	15	1646.9	-0.01862	1646.9	
	822.3264	8	G	14	1533.816	-0.09752	1533.816	
+0.006856	935.4105	9	L	13	1476.794	+0.02551	1476.794	
-0.00139	1036.458	10	T	12	1363.71	-0.03911	1363.71	
	1133.511	11	P	11	1262.663	-0.0383	1262.663	
	1234.559	12	T	10	1165.61		1165.61	
	1291.58	13	G	9	1064.562	+0.108402	1064.562	
	1390.649	14	V	8	1007.541		1007.541	
-0.1885	1503.733	15	L	7	908.4724	+0.078041	454.7398	-0.45064
-0.17634	1602.801	16	V	6	795.3883	-0.08905	795.3883	
	1749.869	17	F	5	696.3199	+0.089894	696.3199	
-0.00256	1878.912	18	E	4	549.2515	+0.087018	549.2515	
	1935.933	19	G	3	420.2089	-0.02575	420.2089	
	2050.96	20	D	2	363.1874		363.1874	
	2152.008	21	T	1	248.1605		248.1605	
		22	K	0	147.1128		147.1128	

Scan number	569	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	44.18



precursor information

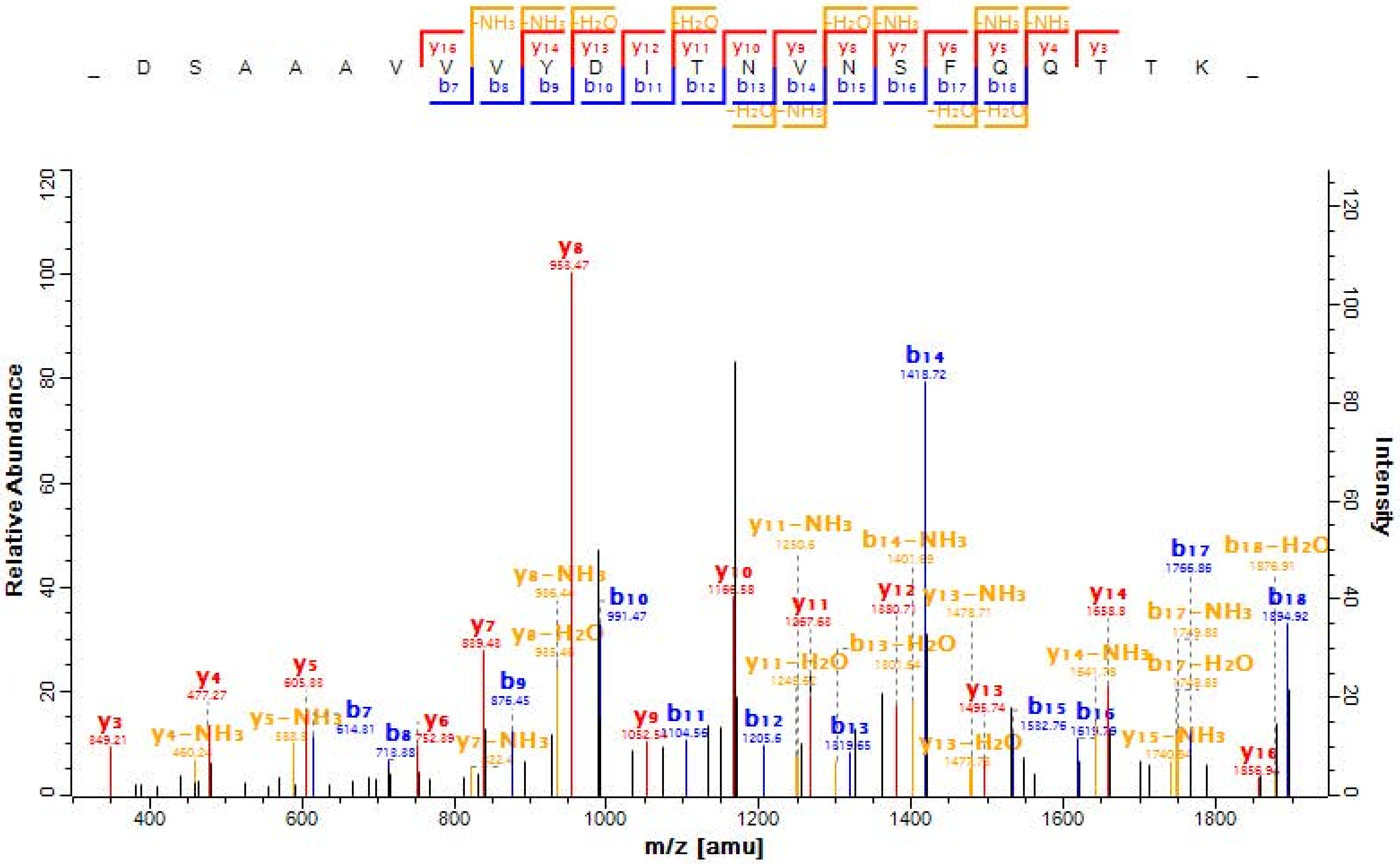
Mass:	2980.10243
m/z:	994.37475
Charge:	3+
Retentiontime:	9.9029130935668
Score:	44.18253
Mass Error [ppm]:	0.13213
PEP:	0.0011718
Precursor Type:	MULTI

general information

Annotation:	15 of 28
AminoAcids Coverag	54 %
Intensity Coverage:	36 %
Peak Coverage:	24 %
Protein Localisation:	22 ... 49

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	27				
	145.06		145.06	2	S	26	2939.5		2939.5	
	202.08		202.08	3	G	25	2852.5		2852.5	
	301.15		301.15	4	V	24	2795.4		2795.4	
	372.19		372.19	5	A	23	2696.4		2696.4	
	500.25	+0.1125	500.25	6	Q	22	2625.3		1313.2	+0.006
	587.28		587.28	7	S	21	2497.3		1249.1	+0.1301
	684.33		684.33	8	P	20	2410.2		1205.6	-0.098
	812.39	+0.1057	812.39	9	Q	19	2313.2		2313.2	
	940.45	+0.364	940.45	10	Q	18	2185.1		2185.1	
	1037.5		1037.5	11	P	17	2057.1		1029	+0.2781
	1134.6		1134.6	12	P	16	1960		1960	
+0.0247	616.31		1231.6	13	P	15	1863		1863	
	1359.7	-0.086	1359.7	14	Q	14	1765.9		1765.9	
	1487.7	-0.499	1487.7	15	Q	13	1637.8		819.43	+0.32
-0.412	808.39	-0.029	1615.8	16	Q	12	1509.8		1509.8	
	1743.8		1743.8	17	Q	11	1381.7		1381.7	
	1871.9		1871.9	18	Q	10	1253.7		1253.7	
	2000	+0.0204	2000	19	Q	9	1125.6		1125.6	
	2097		2097	20	P	8	997.56		499.28	+0.3634
	2194.1		2194.1	21	P	7	900.5		900.5	
	2322.1		2322.1	22	Q	6	803.45		803.45	
	2450.2		2450.2	23	Q	5	675.39		675.39	
	2547.2		2547.2	24	P	4	547.33		547.33	
-0.124	1324.6		2648.3	25	T	3	450.28		450.28	
	2745.3		2745.3	26	P	2	349.23		349.23	
	2842.4		2842.4	27	P	1	252.18		252.18	
				28	K	0	155.13		155.13	

Scan number	5690	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	192.09



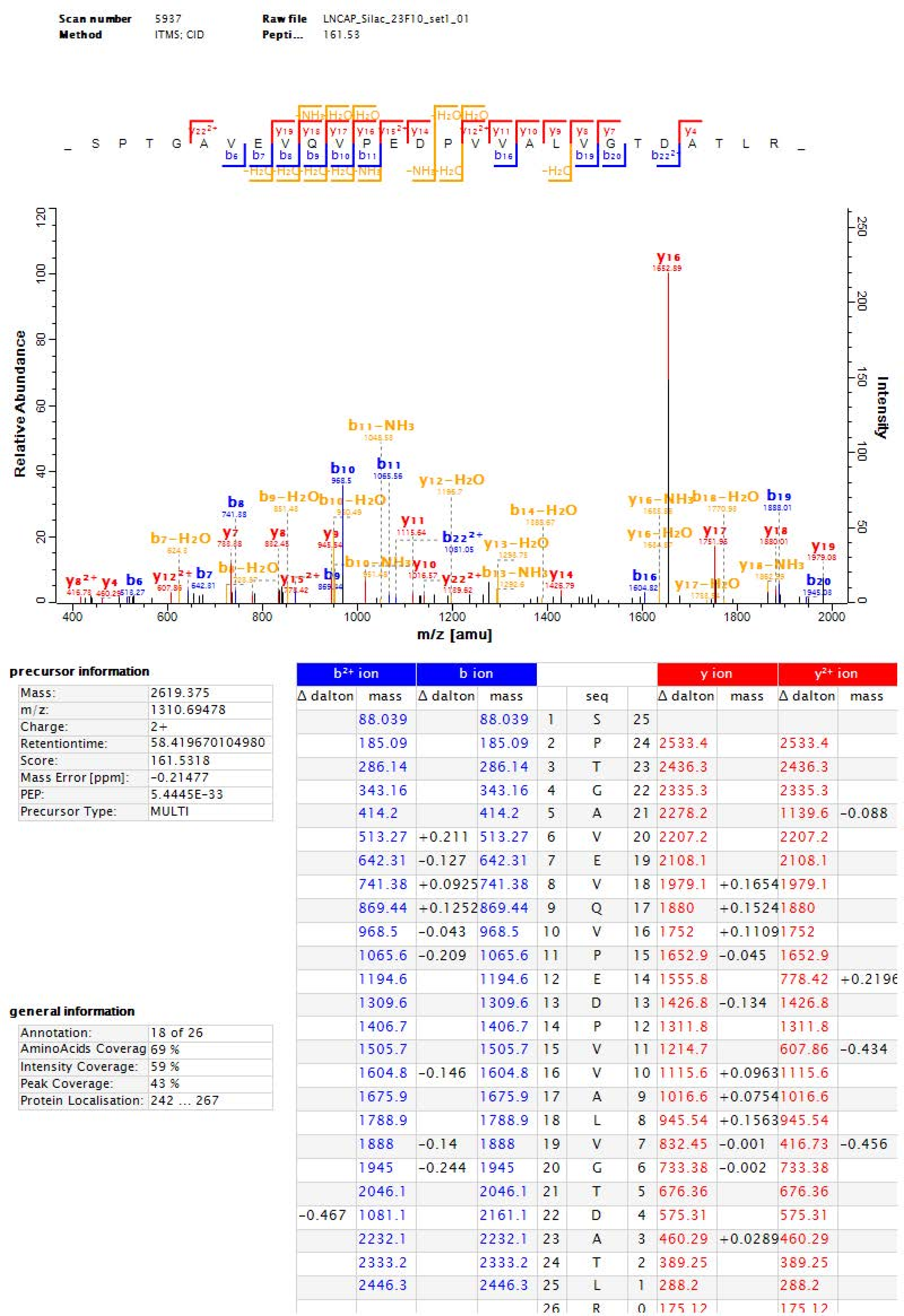
precursor information

Mass:	2370.17004
m/z:	1186.0923
Charge:	2+
Retentiontime:	56.032505035400
Score:	192.0904
Mass Error [ppm]:	-0.11693
PEP:	9.2171E-49
Precursor Type:	MULTI

general information

Annotation:	14 of 22
AminoAcids Coverag	64 %
Intensity Coverage:	55 %
Peak Coverage:	44 %
Protein Localisation:	85 ... 106

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	116.034219499	1	D	21		
	203.066247908	2	S	20	2256.15065282	
	274.103361696	3	A	19	2169.11862442	
	345.140475484	4	A	18	2098.08151063	
	416.177589272	5	A	17	2027.04439684	
	515.246003188	6	V	16	1956.00728305	
-0.1007941	614.314417104	7	V	15	1856.93886914	-0.0938984
+0.0376402	713.38283102	8	V	14	1757.87045522	
-0.1741869	876.446159559	9	Y	13	1658.8020413	+0.0125339
-0.0094795	991.473102591	10	D	12	1495.73871276	-0.2583661
+0.1133657	1104.55716657	11	I	11	1380.71176973	-0.1398703
-0.1253529	1205.60484505	12	T	10	1267.62770575	+0.2964886
+0.1791318	1319.64777249	13	N	9	1166.58002728	-0.0281474
-0.0651854	1418.71618641	14	V	8	1052.53709983	+0.4201756
+0.2600512	1532.75911386	15	N	7	953.468685915	+0.0581696
-0.2761276	1619.79114227	16	S	6	839.425758468	-0.0337907
-0.4022808	1766.85955618	17	F	5	752.393730058	+0.0727616
+0.0186339	1894.91813369	18	Q	4	605.325316142	-0.0736682
	2022.9767112	19	Q	3	477.26673863	+0.1768954
	2124.02438968	20	T	2	349.208161119	+0.2408745
	2225.07206815	21	T	1	248.160482645	
		22	K	0	147.112804171	



Scan number	5937	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	161.53

precursor information

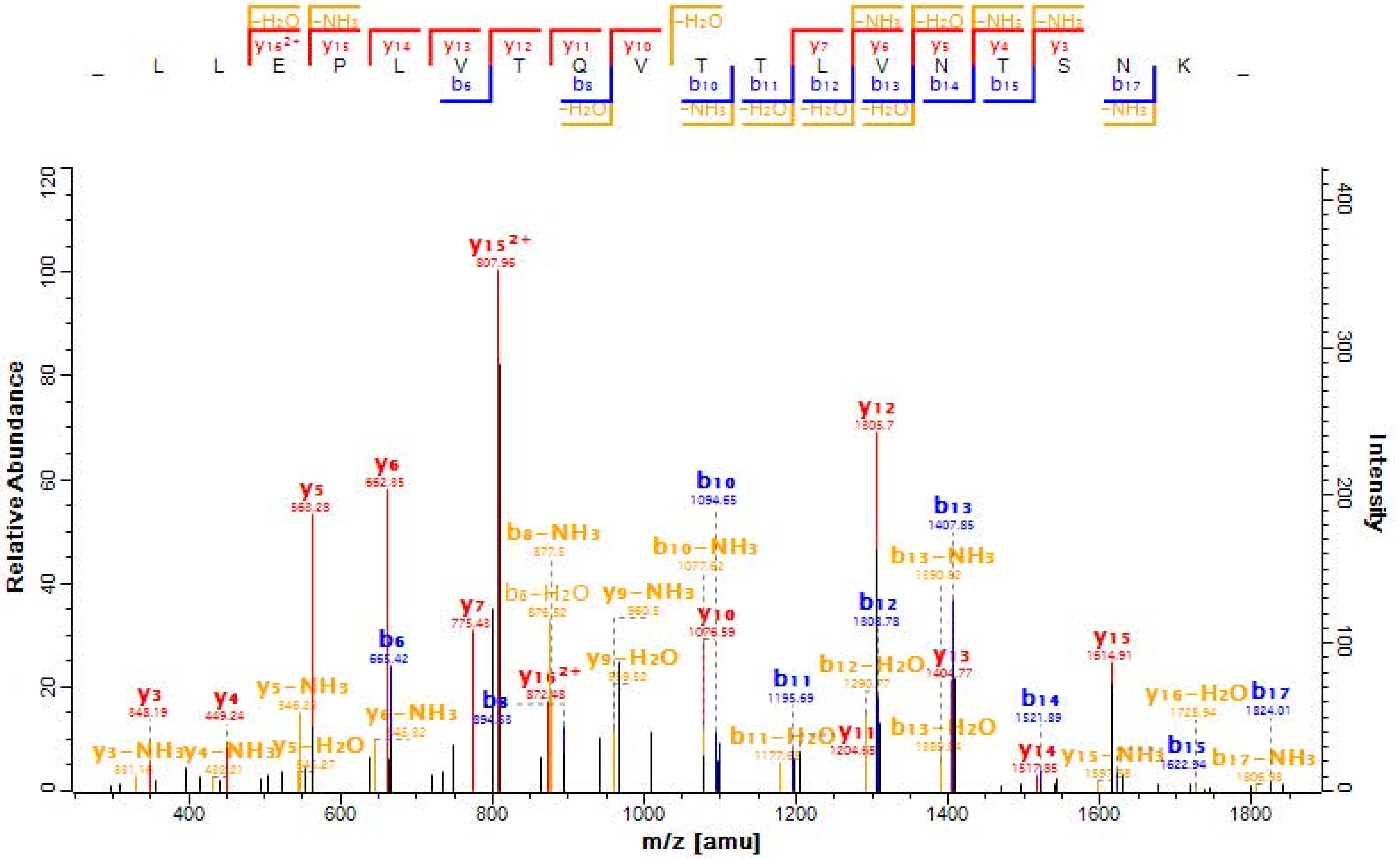
Mass:	2619.375
m/z:	1310.69478
Charge:	2+
Retentiontime:	58.419670104980
Score:	161.5318
Mass Error [ppm]:	-0.21477
PEP:	5.4445E-33
Precursor Type:	MULTI

general information

Annotation:	18 of 26
AminoAcids Coverag	69 %
Intensity Coverage:	59 %
Peak Coverage:	43 %
Protein Localisation:	242 ... 267

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	25				
	185.09		185.09	2	P	24	2533.4		2533.4	
	286.14		286.14	3	T	23	2436.3		2436.3	
	343.16		343.16	4	G	22	2335.3		2335.3	
	414.2		414.2	5	A	21	2278.2		1139.6	-0.088
	513.27	+0.211	513.27	6	V	20	2207.2		2207.2	
	642.31	-0.127	642.31	7	E	19	2108.1		2108.1	
	741.38	+0.0925	741.38	8	V	18	1979.1	+0.1654	1979.1	
	869.44	+0.1252	869.44	9	Q	17	1880	+0.1524	1880	
	968.5	-0.043	968.5	10	V	16	1752	+0.1109	1752	
	1065.6	-0.209	1065.6	11	P	15	1652.9	-0.045	1652.9	
	1194.6		1194.6	12	E	14	1555.8		778.42	+0.2196
	1309.6		1309.6	13	D	13	1426.8	-0.134	1426.8	
	1406.7		1406.7	14	P	12	1311.8		1311.8	
	1505.7		1505.7	15	V	11	1214.7		607.86	-0.434
	1604.8	-0.146	1604.8	16	V	10	1115.6	+0.0963	1115.6	
	1675.9		1675.9	17	A	9	1016.6	+0.0754	1016.6	
	1788.9		1788.9	18	L	8	945.54	+0.1563	945.54	
	1888	-0.14	1888	19	V	7	832.45	-0.001	416.73	-0.456
	1945	-0.244	1945	20	G	6	733.38	-0.002	733.38	
	2046.1		2046.1	21	T	5	676.36		676.36	
-0.467	1081.1		2161.1	22	D	4	575.31		575.31	
	2232.1		2232.1	23	A	3	460.29	+0.0289	460.29	
	2333.2		2333.2	24	T	2	389.25		389.25	
	2446.3		2446.3	25	L	1	288.2		288.2	
				26	R	0	175.12		175.12	

Scan number	5999	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	190.55



precursor information

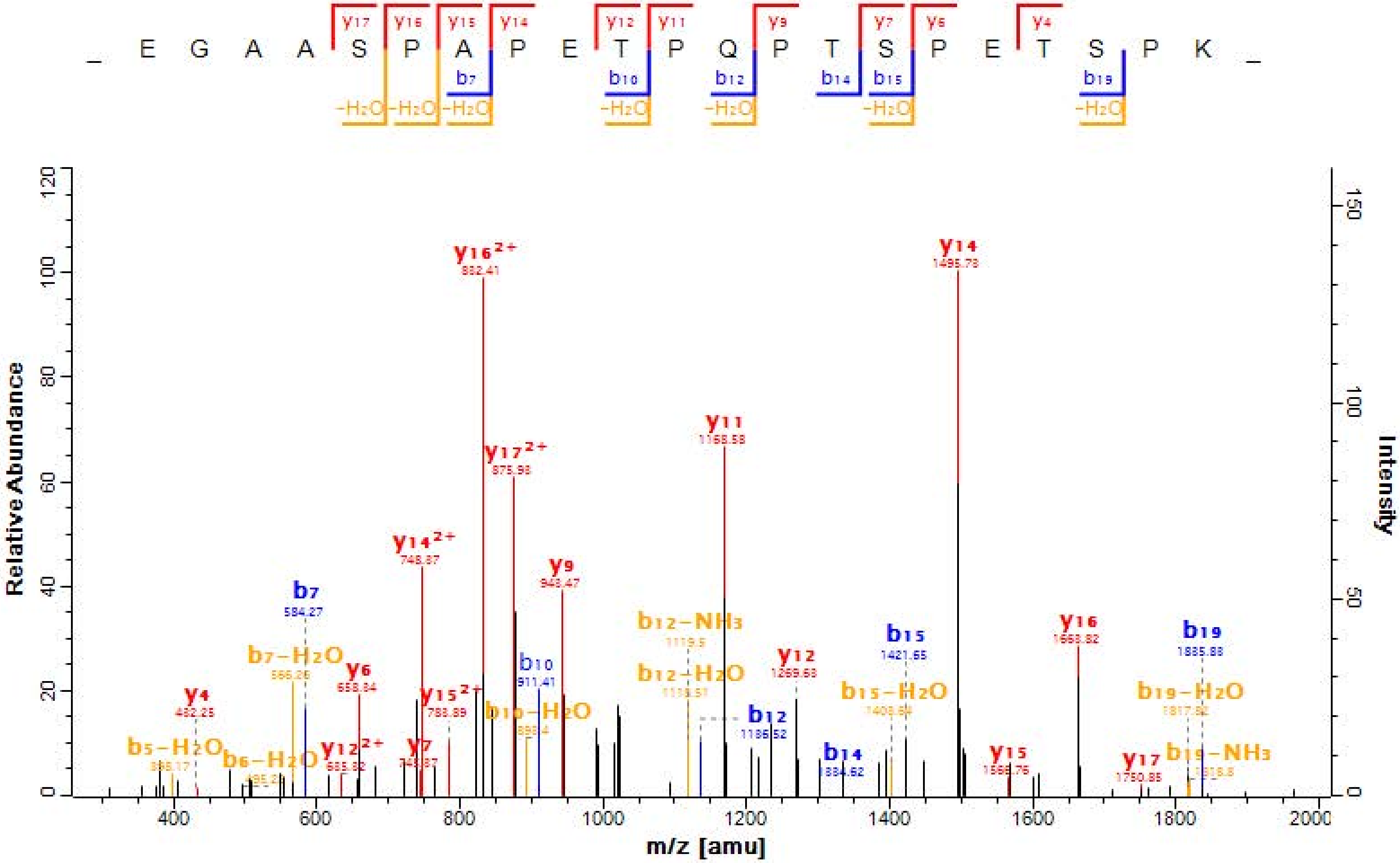
Mass:	1969.10992
m/z:	985.56224
Charge:	2+
Retentiontime:	59.009738922119
Score:	190.5502
Mass Error [ppm]:	0.18553
PEP:	1.0163E-34
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	59 %
Peak Coverage:	42 %
Protein Localisation:	61 ... 78

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	17				
	227.1754	2	L	16	1857.033		1857.033	
	356.218	3	E	15	1743.949		872.478	+0.152258
	453.2708	4	P	14	1614.906	-0.14915	807.9567	+0.061982
	566.3548	5	L	13	1517.853	+0.236251	1517.853	
+0.028177	665.4232	6	V	12	1404.769	-0.0299	1404.769	
	766.4709	7	T	11	1305.701	-0.06501	1305.701	
-0.07906	894.5295	8	Q	10	1204.653	-0.04492	1204.653	
	993.5979	9	V	9	1076.595	+0.010976	1076.595	
-0.06234	1094.646	10	T	8	977.5262		977.5262	
-0.05997	1195.693	11	T	7	876.4785		876.4785	
-0.09325	1308.777	12	L	6	775.4308	+0.061588	775.4308	
-0.05778	1407.846	13	V	5	662.3468	-0.00242	662.3468	
+0.026368	1521.889	14	N	4	563.2784	+0.140701	563.2784	
+0.102835	1622.936	15	T	3	449.2354	+0.0752	449.2354	
	1709.968	16	S	2	348.1878	+0.100814	348.1878	
+0.260057	1824.011	17	N	1	261.1557		261.1557	
		18	K	0	147.1128		147.1128	

Scan number 659 **Raw file** LNCAP_Silac_23F10_set1_01
Method ITMS; CID **Pepti...** 113.73



precursor information

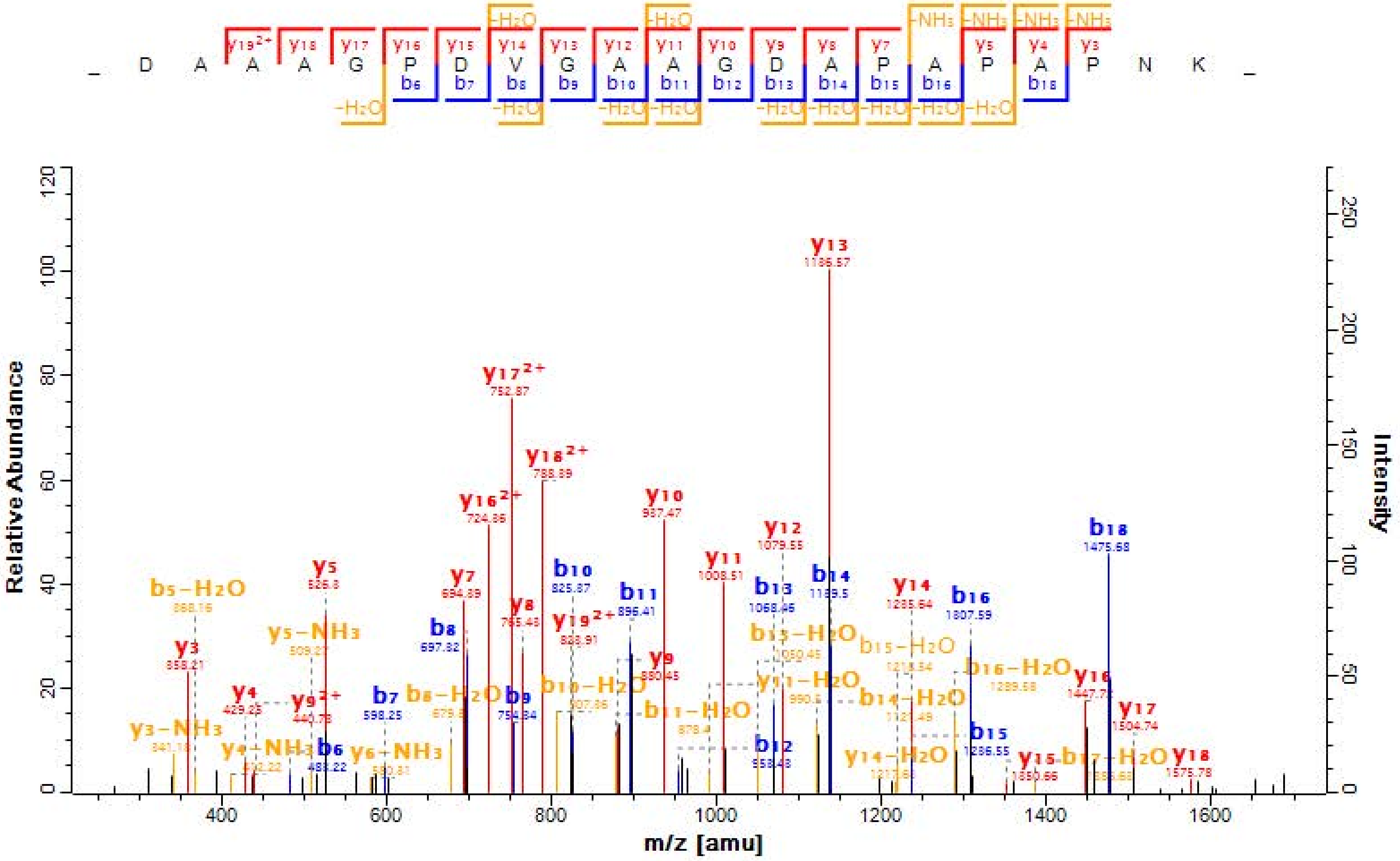
Mass:	2077.98073
m/z:	1039.99764
Charge:	2+
Retentiontime:	10.844576835632
Score:	113.7346
Mass Error [ppm]:	0.16335
PEP:	2.5537E-09
Precursor Type:	MULTI

general information

Annotation:	14 of 21
AminoAcids Coverag	67 %
Intensity Coverage:	52 %
Peak Coverage:	31 %
Protein Localisation:	372 ... 392

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	20				
	187.0713	2	G	19	1949.945		1949.945	
	258.1084	3	A	18	1892.924		1892.924	
	329.1456	4	A	17	1821.886		1821.886	
	416.1776	5	S	16	1750.849	-0.23549	875.9283	-0.07787
	513.2304	6	P	15	1663.817	-0.03342	832.4123	+0.316443
-1.1E-05	584.2675	7	A	14	1566.765	+0.069147	783.8859	+0.185476
	681.3202	8	P	13	1495.727	+0.023985	748.3674	+0.272637
	810.3628	9	E	12	1398.675		1398.675	
-0.11875	911.4105	10	T	11	1269.632	-0.31987	635.3197	+0.08948
	1008.463	11	P	10	1168.584	+0.051787	1168.584	
-0.07665	1136.522	12	Q	9	1071.532		1071.532	
	1233.575	13	P	8	943.4731	-0.09481	943.4731	
-0.21213	1334.622	14	T	7	846.4203		846.4203	
+0.136579	1421.654	15	S	6	745.3727	+0.161153	745.3727	
	1518.707	16	P	5	658.3406	+0.112554	658.3406	
	1647.75	17	E	4	561.2879		561.2879	
	1748.797	18	T	3	432.2453	+0.28982	432.2453	
-0.08402	1835.829	19	S	2	331.1976		331.1976	
	1932.882	20	P	1	244.1656		244.1656	
		21	K	0	147.1128		147.1128	

Scan number	705	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	282.49



precursor information

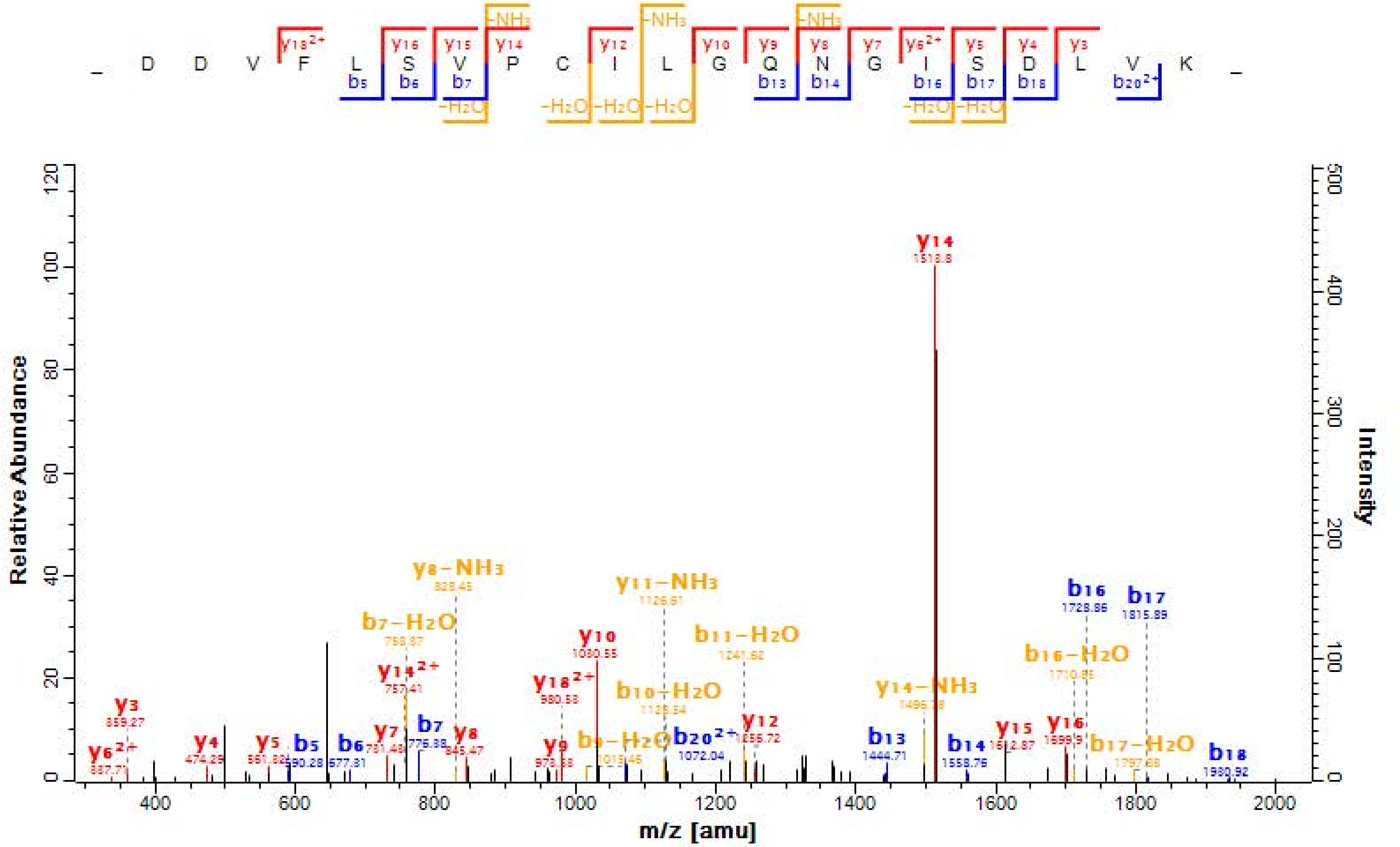
Mass:	1831.8704
m/z:	916.94247
Charge:	2+
Retentiontime:	11.308469772338
Score:	282.4875
Mass Error [ppm]:	0.1866
PEP:	1.9525E-112
Precursor Type:	MULTI

general information

Annotation:	17 of 21
AminoAcids Coverag	81 %
Intensity Coverage:	74 %
Peak Coverage:	52 %
Protein Localisation:	33 ... 53

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342	1	D	20				
	187.0713	2	A	19	1717.85		1717.85	
	258.1084	3	A	18	1646.813		823.9103	-0.07898
	329.1456	4	A	17	1575.776	-0.01066	788.3917	+0.114873
	386.167	5	G	16	1504.739	-0.16458	752.8732	+0.229927
+0.169311	483.2198	6	P	15	1447.718	-0.00115	724.3624	+0.2337
+0.044589	598.2467	7	D	14	1350.665	+0.09458	1350.665	
+0.031962	697.3151	8	V	13	1235.638	-0.02594	1235.638	
-0.07318	754.3366	9	G	12	1136.569	-0.05262	1136.569	
+0.089473	825.3737	10	A	11	1079.548	-0.08767	1079.548	
-0.01618	896.4108	11	A	10	1008.511	-0.25435	1008.511	
-0.0111	953.4323	12	G	9	937.4738	-0.04994	937.4738	
-0.20399	1068.459	13	D	8	880.4523	+0.097436	440.7298	-0.43011
-0.00734	1139.496	14	A	7	765.4254	+0.148976	765.4254	
+0.060254	1236.549	15	P	6	694.3883	+0.040887	694.3883	
-0.04705	1307.586	16	A	5	597.3355		597.3355	
	1404.639	17	P	4	526.2984	+0.006192	526.2984	
-0.06491	1475.676	18	A	3	429.2456	+0.063473	429.2456	
	1572.729	19	P	2	358.2085	+0.049561	358.2085	
	1686.772	20	N	1	261.1557		261.1557	
		21	K	0	147.1128		147.1128	

Scan number	7163	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	109.22



precursor information

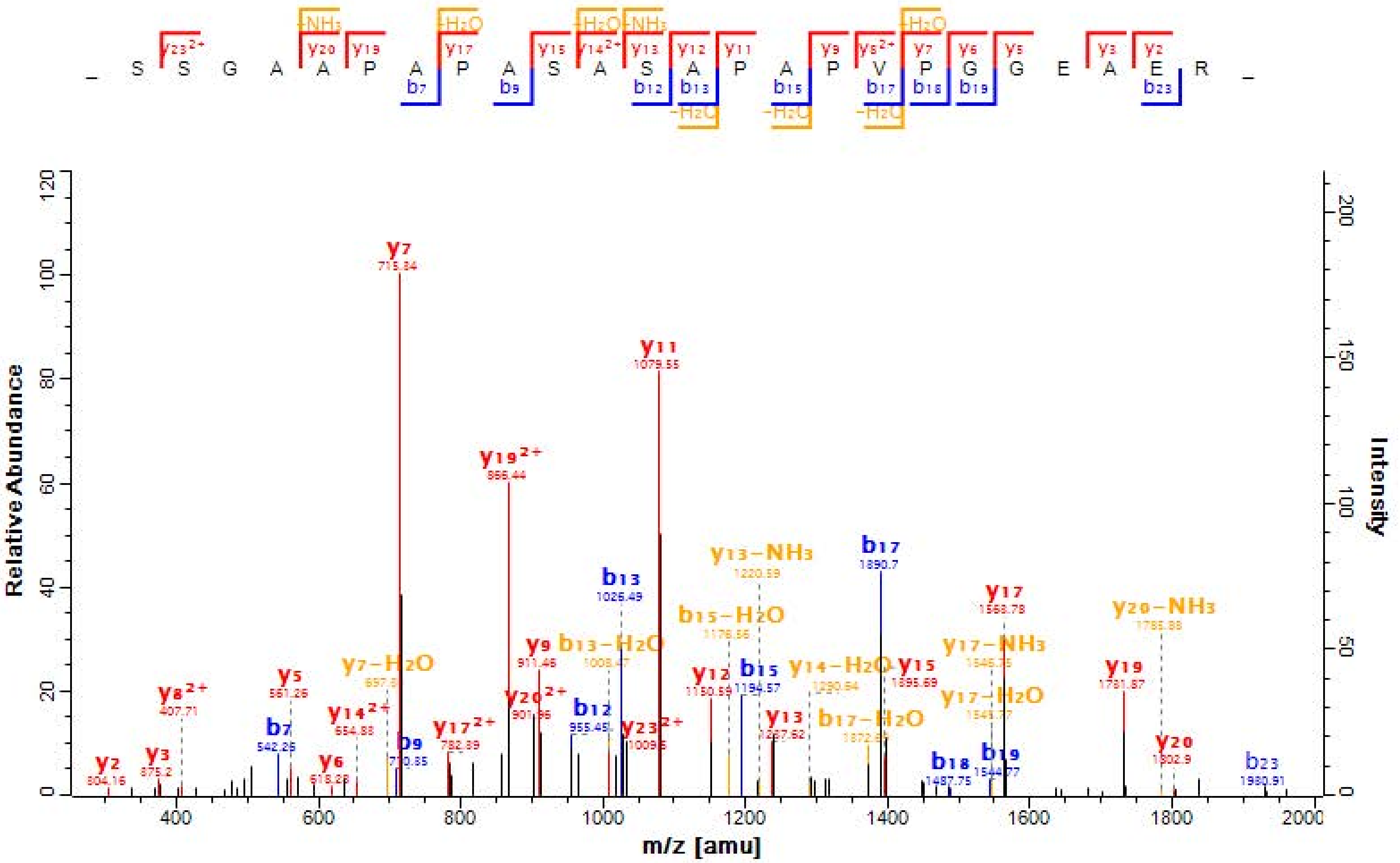
Mass:	2288.17084
m/z:	1145.09269
Charge:	2+
Retentiontime:	71.462028503418
Score:	109.221
Mass Error [ppm]:	-0.61112
PEP:	4.6165E-09
Precursor Type:	MULTI

general information

Annotation:	18 of 21
AminoAcids Coverag	86 %
Intensity Coverage:	43 %
Peak Coverage:	32 %
Protein Localisation:	314 ... 334

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	20				
	231.06		231.06	2	D	19	2174.2		2174.2	
	330.13		330.13	3	V	18	2059.1		2059.1	
	477.2		477.2	4	F	17	1960.1		980.53	+0.392
	590.28	+0.065	590.28	5	L	16	1813		1813	
	677.31	-0.161	677.31	6	S	15	1699.9	-0.119	1699.9	
	776.38	+0.0875	776.38	7	V	14	1612.9	-0.209	1612.9	
	873.44		873.44	8	P	13	1513.8	+0.0071	757.41	+0.2357
	1033.5		1033.5	9	C	12	1416.8		1416.8	
	1146.5		1146.5	10	I	11	1256.7	+0.0332	1256.7	
	1259.6		1259.6	11	L	10	1143.6		1143.6	
	1316.7		1316.7	12	G	9	1030.6	-0.039	1030.6	
	1444.7	+0.3625	1444.7	13	Q	8	973.53	+0.2695	973.53	
	1558.8	+0.2832	1558.8	14	N	7	845.47	+0.0112	845.47	
	1615.8		1615.8	15	G	6	731.43	+0.0019	731.43	
	1728.9	-0.083	1728.9	16	I	5	674.41		337.71	-0.364
	1815.9	-0.099	1815.9	17	S	4	561.32	+0.1499	561.32	
	1930.9	-0.425	1930.9	18	D	3	474.29	-0.026	474.29	
	2044		2044	19	L	2	359.27	+0.4154	359.27	
+0.3577	1072		2143.1	20	V	1	246.18		246.18	
				21	K	0	147.11		147.11	

Scan number	887	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	155.71



precursor information

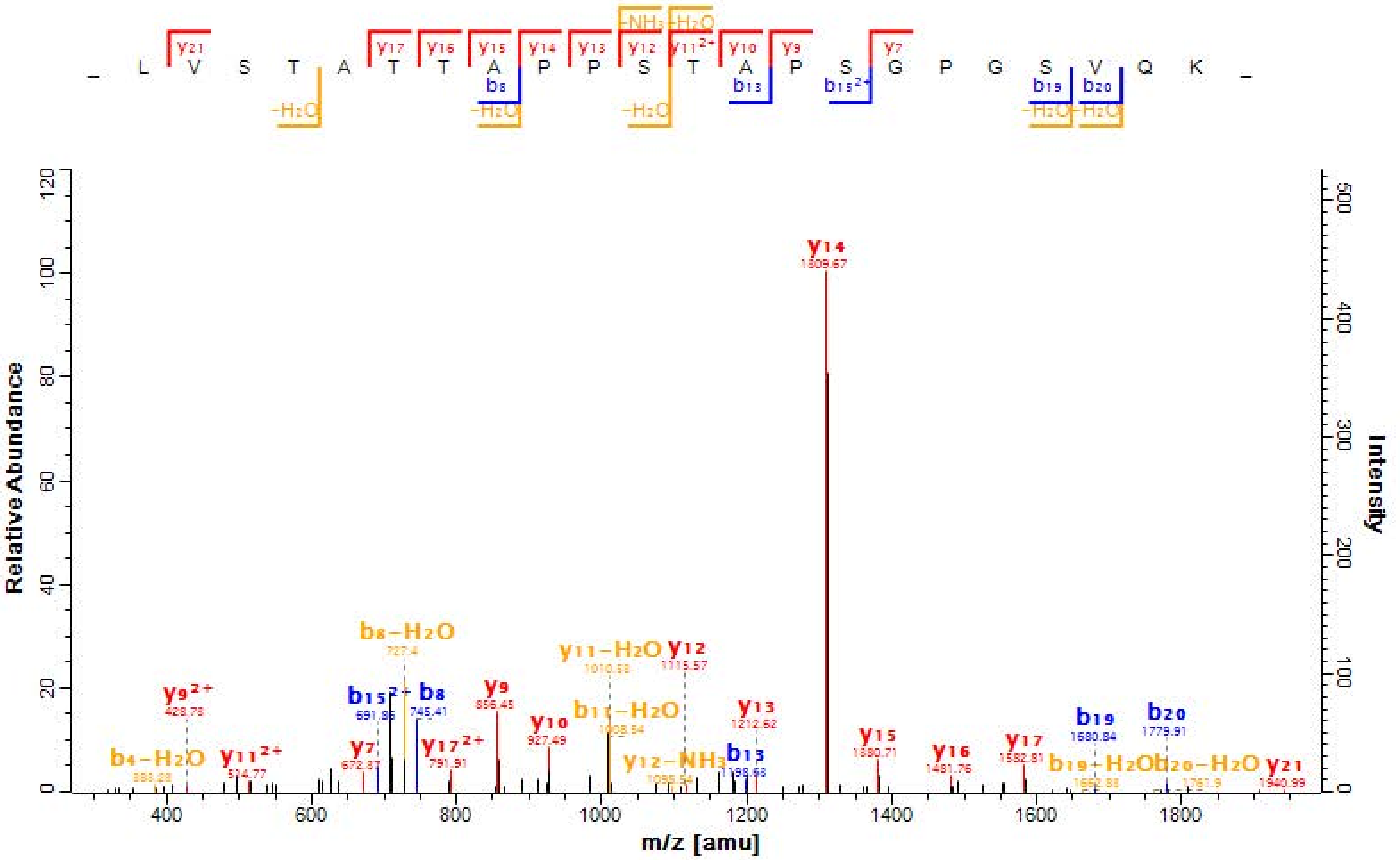
Mass:	2104.01877
m/z:	1053.01666
Charge:	2+
Retentiontime:	13.157961845397
Score:	155.7071
Mass Error [ppm]:	0.12388
PEP:	5.6525E-31
Precursor Type:	MULTI

general information

Annotation:	20 of 24
AminoAcids Coverag	83 %
Intensity Coverage:	58 %
Peak Coverage:	37 %
Protein Localisation:	92 ... 115

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	23				
	175.0713	2	S	22	2017.994		1009.501	+0.015596
	232.0928	3	G	21	1930.962		1930.962	
	303.1299	4	A	20	1873.94		1873.94	
	374.167	5	A	19	1802.903	+0.3582	901.9552	+0.102281
	471.2198	6	P	18	1731.866	-0.30183	866.4367	+0.20409
+0.14007	542.2569	7	A	17	1634.813		1634.813	
	639.3097	8	P	16	1563.776	-0.12406	782.3917	+0.497197
+0.089133	710.3468	9	A	15	1466.723		1466.723	
	797.3788	10	S	14	1395.686	-0.03516	1395.686	
	868.4159	11	A	13	1308.654		654.8308	-0.1758
+0.064623	955.448	12	S	12	1237.617	-0.09932	1237.617	
+0.052045	1026.485	13	A	11	1150.585	+0.080415	1150.585	
	1123.538	14	P	10	1079.548	-0.02053	1079.548	
-0.09496	1194.575	15	A	9	982.4952		982.4952	
	1291.628	16	P	8	911.4581	+0.107919	911.4581	
-0.15108	1390.696	17	V	7	814.4054		407.7063	+0.100934
-0.12278	1487.749	18	P	6	715.3369	+0.06302	715.3369	
-0.00838	1544.77	19	G	5	618.2842	+0.085083	618.2842	
	1601.792	20	G	4	561.2627	-0.02529	561.2627	
	1730.834	21	E	3	504.2413		504.2413	
	1801.872	22	A	2	375.1987	+0.259349	375.1987	
-0.31023	1930.914	23	E	1	304.1615	+0.2397	304.1615	
		24	R	0	175.119		175.119	

Scan number	906	**Raw file**	LNCAP_Silac_23F10_set1_01
Method	ITMS; CID	**Pepti...**	85.86



precursor information

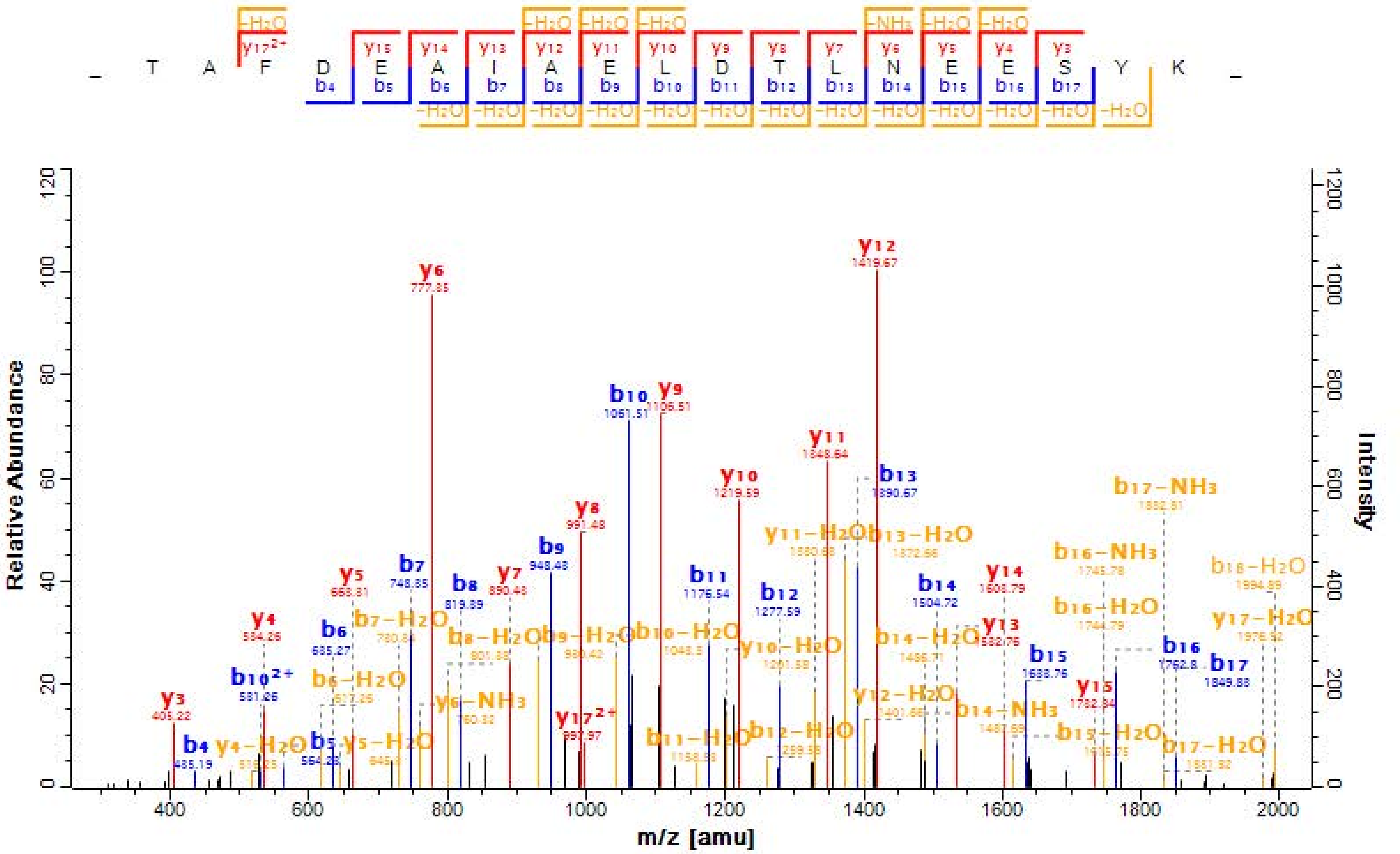
Mass:	2053.06943
m/z:	1027.54199
Charge:	2+
Retentiontime:	13.351268768310
Score:	85.85516
Mass Error [ppm]:	0.13556
PEP:	3.952E-05
Precursor Type:	MULTI

general information

Annotation:	15 of 22
AminoAcids Coverag	68 %
Intensity Coverage:	49 %
Peak Coverage:	28 %
Protein Localisation:	621 ... 642

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	21				
	213.16		213.16	2	V	20	1941	-0.085	1941	
	300.19		300.19	3	S	19	1841.9		1841.9	
	401.24		401.24	4	T	18	1754.9		1754.9	
	472.28		472.28	5	A	17	1653.8		1653.8	
	573.32		573.32	6	T	16	1582.8	+0.0415	791.91	-0.274
	674.37		674.37	7	T	15	1481.8	-0.02	1481.8	
	745.41	-0.013	745.41	8	A	14	1380.7	-0.081	1380.7	
	842.46		842.46	9	P	13	1309.7	-0.055	1309.7	
	939.51		939.51	10	P	12	1212.6	+0.0981	1212.6	
	1026.5		1026.5	11	S	11	1115.6	+0.4261	1115.6	
	1127.6		1127.6	12	T	10	1028.5		514.77	+0.041
	1198.6	-0.034	1198.6	13	A	9	927.49	-0.031	927.49	
	1295.7		1295.7	14	P	8	856.45	+0.0047	428.73	-0.458
-0.486	691.86		1382.7	15	S	7	759.4		759.4	
	1439.7		1439.7	16	G	6	672.37	-0.002	672.37	
	1536.8		1536.8	17	P	5	615.35		615.35	
	1593.8		1593.8	18	G	4	518.29		518.29	
	1680.8	-0.061	1680.8	19	S	3	461.27		461.27	
	1779.9	+0.394	1779.9	20	V	2	374.24		374.24	
	1908		1908	21	Q	1	275.17		275.17	
				22	K	0	147.11		147.11	

Scan number	10193	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	362.73



precursor information

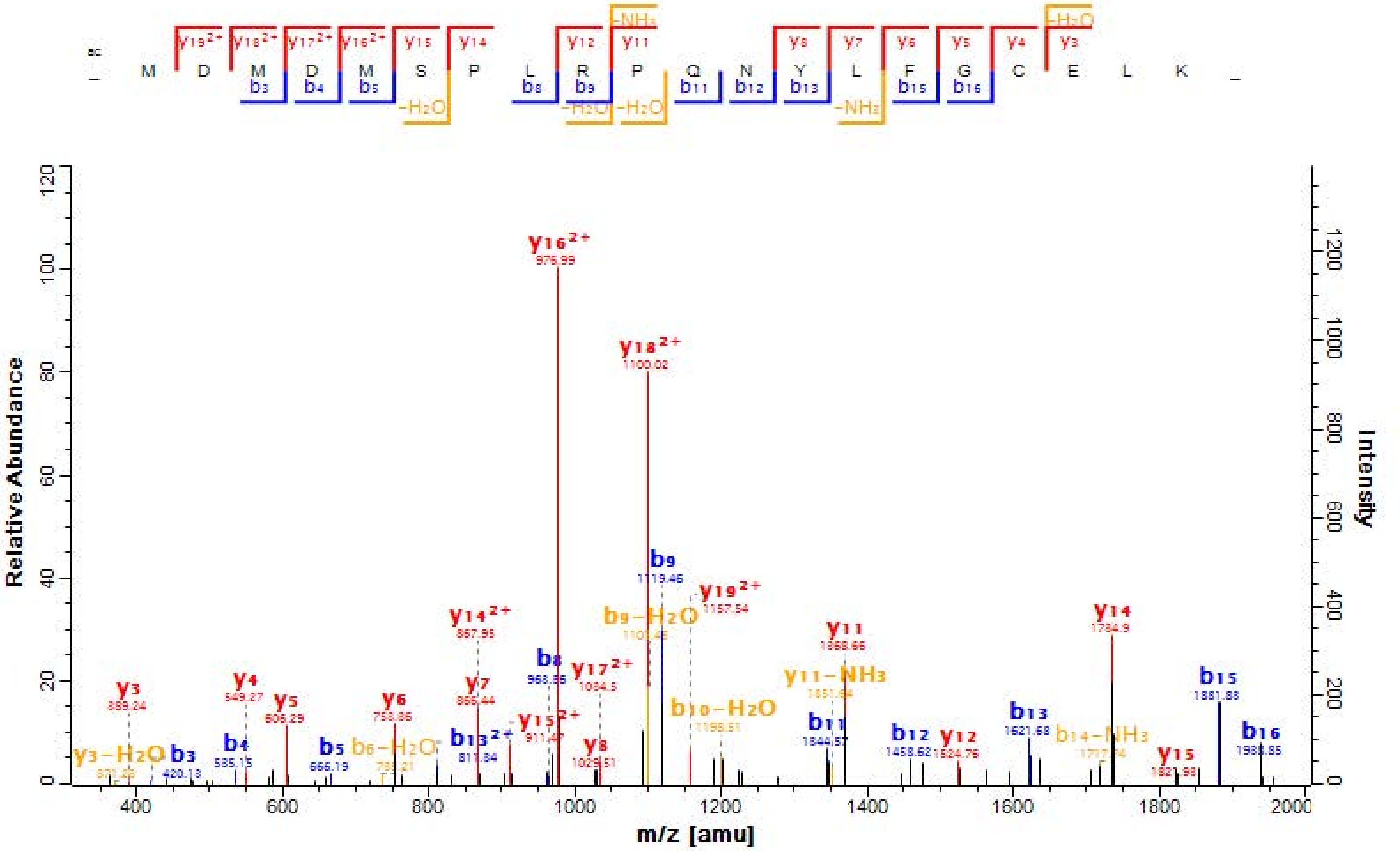
Mass:	2157.99517
m/z:	1080.00486
Charge:	2+
Retentiontime:	62.228397369384
Score:	362.7282
Mass Error [ppm]:	-0.093663
PEP:	5.5672E-189
Precursor Type:	MULTI

general information

Annotation:	16 of 19
AminoAcids Coverag	84 %
Intensity Coverage:	81 %
Peak Coverage:	52 %
Protein Localisation:	196 ... 214

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	18				
	173.09		173.09	2	A	17	2066		2066	
	320.16		320.16	3	F	16	1994.9		997.97	+0.186
	435.19	+0.0944	435.19	4	D	15	1847.9		1847.9	
	564.23	+0.0617	564.23	5	E	14	1732.8	-0.234	1732.8	
	635.27	+0.0388	635.27	6	A	13	1603.8	-0.09	1603.8	
	748.35	+0.0404	748.35	7	I	12	1532.8	+0.0376	1532.8	
	819.39	+0.0301	819.39	8	A	11	1419.7	+0.0052	1419.7	
	948.43	+0.0566	948.43	9	E	10	1348.6	+0.0289	1348.6	
+0.1135	531.26	-0.093	1061.5	10	L	9	1219.6	+0.1033	1219.6	
	1176.5	-0.128	1176.5	11	D	8	1106.5	+0.139	1106.5	
	1277.6	+0.0813	1277.6	12	T	7	991.48	+0.1027	991.48	
	1390.7	-0.082	1390.7	13	L	6	890.43	+0.2079	890.43	
	1504.7	-0.083	1504.7	14	N	5	777.35	+0.0815	777.35	
	1633.8	-0.048	1633.8	15	E	4	663.31	+0.1398	663.31	
	1762.8	-0.054	1762.8	16	E	3	534.26	+0.0677	534.26	
	1849.8	-0.1	1849.8	17	S	2	405.22	+0.1416	405.22	
	2012.9		2012.9	18	Y	1	318.19		318.19	
				19	K	0	155.13		155.13	

Scan number	10427	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	171.68



precursor information

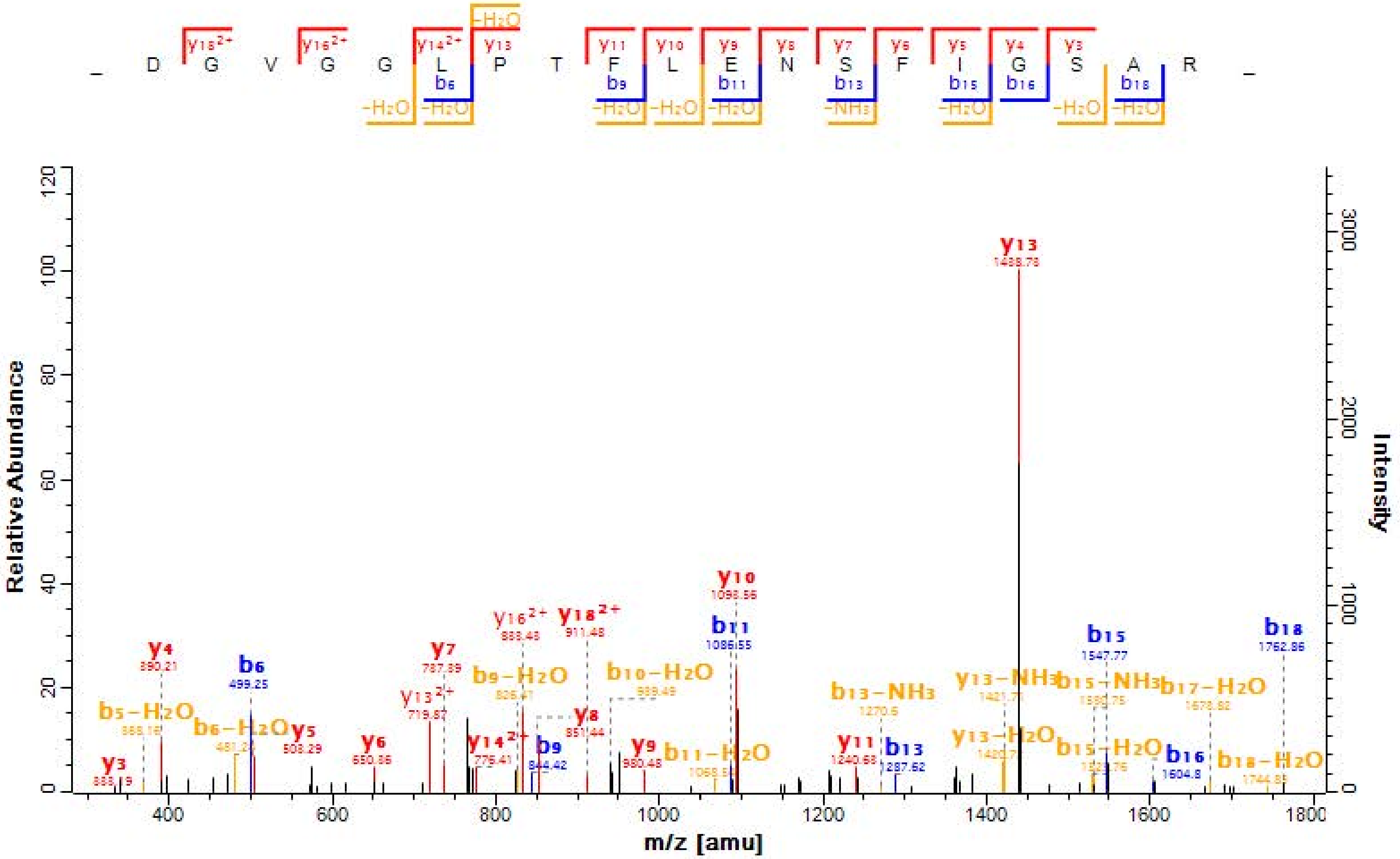
Mass:	2486.10938
m/z:	1244.06197
Charge:	2+
Retentiontime:	63.758819580078
Score:	171.6759
Mass Error [ppm]:	-0.34576
PEP:	9.487E-36
Precursor Type:	MULTI

general information

Annotation:	17 of 20
AminoAcids Coverag	85 %
Intensity Coverage:	62 %
Peak Coverage:	34 %
Protein Localisation:	1 ... 20

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	174.06		174.06	1	M	19				
	289.09		289.09	2	D	18	2314.1		1157.5	+0.1604
	420.13	-0.079	420.13	3	M	17	2199		1100	+0.3251
	535.15	+0.0571	535.15	4	D	16	2068		1034.5	+0.2727
	666.19	-0.073	666.19	5	M	15	1953		976.99	+0.2963
	753.23		753.23	6	S	14	1821.9	-0.366	911.47	+0.3203
	850.28		850.28	7	P	13	1734.9	-0.043	867.95	+0.2214
	963.36	+0.0579	963.36	8	L	12	1637.8		1637.8	
	1119.5	+0.053	1119.5	9	R	11	1524.8	+0.0259	1524.8	
	1216.5		1216.5	10	P	10	1368.7	-0.113	1368.7	
	1344.6	-0.087	1344.6	11	Q	9	1271.6		1271.6	
	1458.6	-0.065	1458.6	12	N	8	1143.6		1143.6	
+0.03	811.34	-0.101	1621.7	13	Y	7	1029.5	-0.038	1029.5	
	1734.8		1734.8	14	L	6	866.44	+0.0491	866.44	
	1881.8	-0.106	1881.8	15	F	5	753.36	+0.0941	753.36	
	1938.9	-0.001	1938.9	16	G	4	606.29	+0.134	606.29	
	2098.9		2098.9	17	C	3	549.27	+0.1096	549.27	
	2227.9		2227.9	18	E	2	389.24	+0.0423	389.24	
	2341		2341	19	L	1	260.2		260.2	
				20	K	0	147.11		147.11	

Scan number	10698	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	141.6



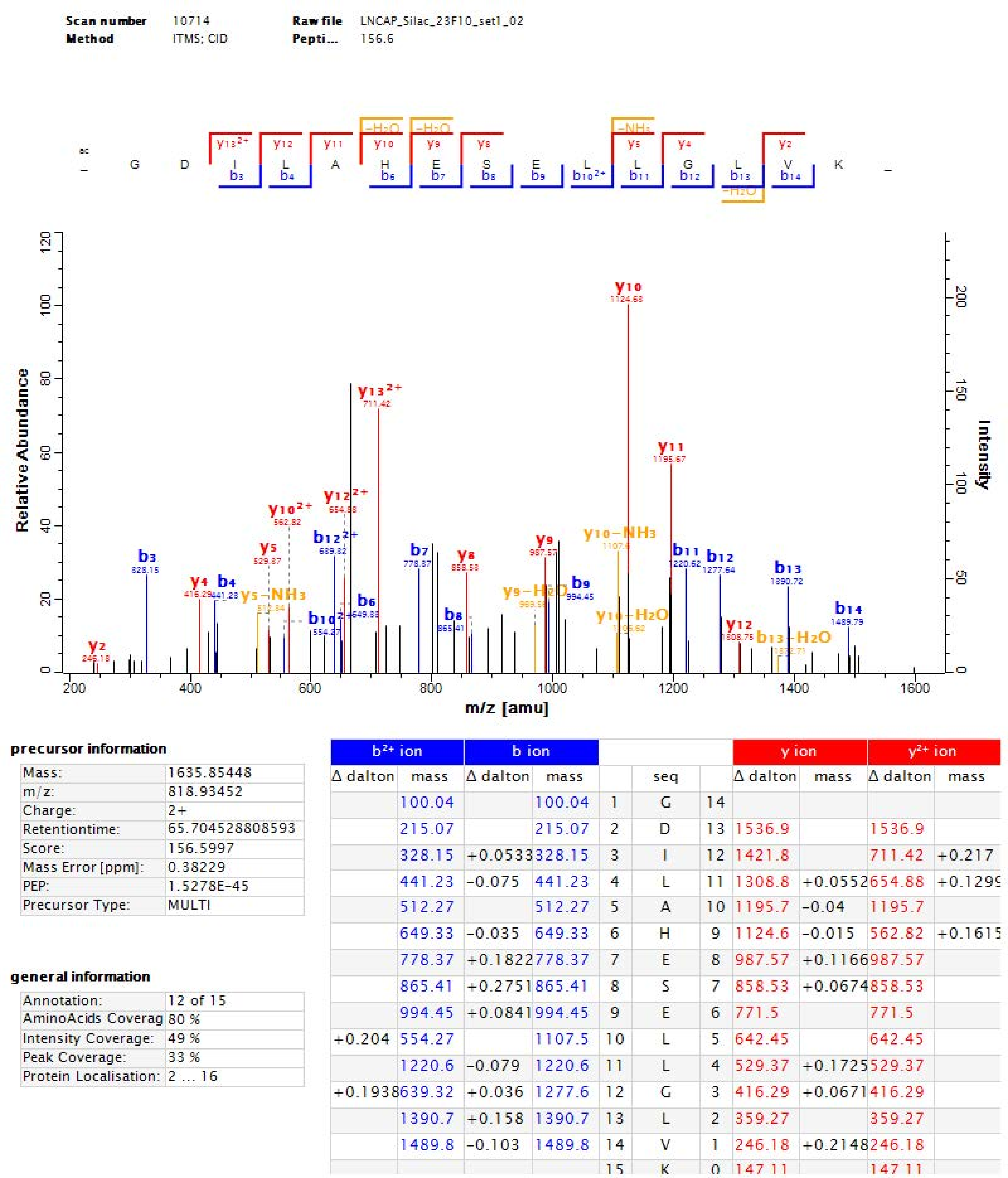
precursor information

Mass:	1935.96918
m/z:	968.99187
Charge:	2+
Retentiontime:	65.589561462402
Score:	141.5988
Mass Error [ppm]:	0.07294
PEP:	8.2978E-19
Precursor Type:	MULTI

general information

Annotation:	15 of 19
AminoAcids Coverag	79 %
Intensity Coverage:	54 %
Peak Coverage:	37 %
Protein Localisation:	150 ... 168

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342	1	D	18				
	173.0557	2	G	17	1821.949		911.4783	+0.181282
	272.1241	3	V	16	1764.928		1764.928	
	329.1456	4	G	15	1665.859		833.4334	+0.245019
	386.167	5	G	14	1608.838		1608.838	
+0.058543	499.2511	6	L	13	1551.817		776.4119	+0.191349
	596.3039	7	P	12	1438.733	+0.020302	719.8699	+0.200849
	697.3515	8	T	11	1341.68		1341.68	
+0.152382	844.4199	9	F	10	1240.632	+0.083025	1240.632	
	957.504	10	L	9	1093.564	+0.01118	1093.564	
-0.06528	1086.547	11	E	8	980.4796	+0.33322	980.4796	
	1200.59	12	N	7	851.437	+0.153035	851.437	
-0.11411	1287.622	13	S	6	737.3941	-0.00796	737.3941	
	1434.69	14	F	5	650.362	-0.05491	650.362	
-0.03661	1547.774	15	I	4	503.2936	+0.053424	503.2936	
-0.20736	1604.795	16	G	3	390.2096	-0.02377	390.2096	
	1691.828	17	S	2	333.1881	+0.037705	333.1881	
-0.20412	1762.865	18	A	1	246.1561		246.1561	
		19	R	0	175.119		175.119	



Scan number	10714	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	156.6

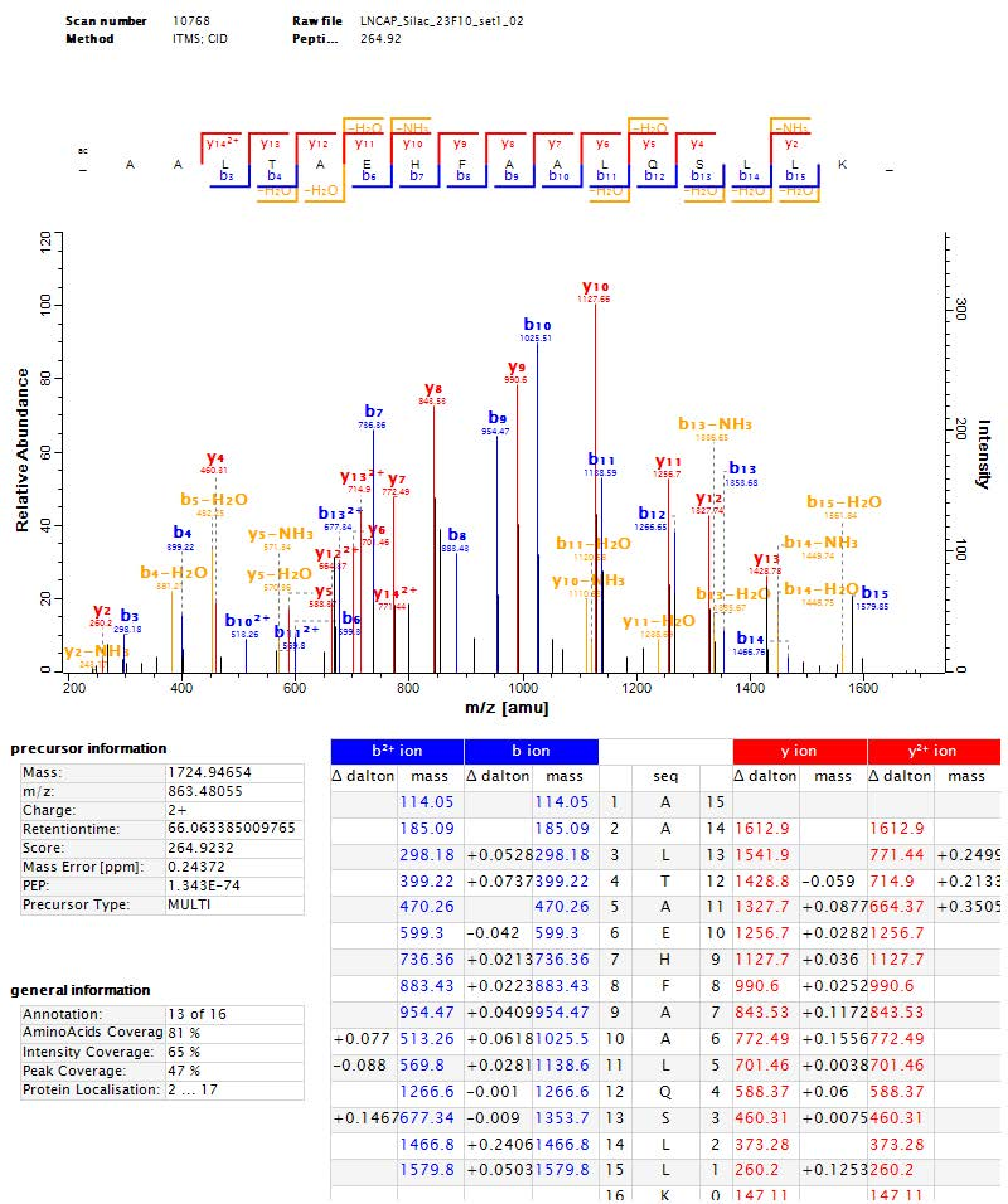
precursor information

Mass:	1635.85448
m/z:	818.93452
Charge:	2+
Retentiontime:	65.704528808593
Score:	156.5997
Mass Error [ppm]:	0.38229
PEP:	1.5278E-45
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	49 %
Peak Coverage:	33 %
Protein Localisation:	2 ... 16

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.04		100.04	1	G	14				
	215.07		215.07	2	D	13	1536.9		1536.9	
	328.15	+0.0533	328.15	3	I	12	1421.8		711.42	+0.217
	441.23	-0.075	441.23	4	L	11	1308.8	+0.0552	654.88	+0.1299
	512.27		512.27	5	A	10	1195.7	-0.04	1195.7	
	649.33	-0.035	649.33	6	H	9	1124.6	-0.015	562.82	+0.1615
	778.37	+0.1822	778.37	7	E	8	987.57	+0.1166	987.57	
	865.41	+0.2751	865.41	8	S	7	858.53	+0.0674	858.53	
	994.45	+0.0841	994.45	9	E	6	771.5		771.5	
+0.204	554.27		1107.5	10	L	5	642.45		642.45	
	1220.6	-0.079	1220.6	11	L	4	529.37	+0.1725	529.37	
+0.1938	639.32	+0.036	1277.6	12	G	3	416.29	+0.0671	416.29	
	1390.7	+0.158	1390.7	13	L	2	359.27		359.27	
	1489.8	-0.103	1489.8	14	V	1	246.18	+0.2148	246.18	
				15	K	0	147.11		147.11	



Scan number	10768	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	264.92

precursor information

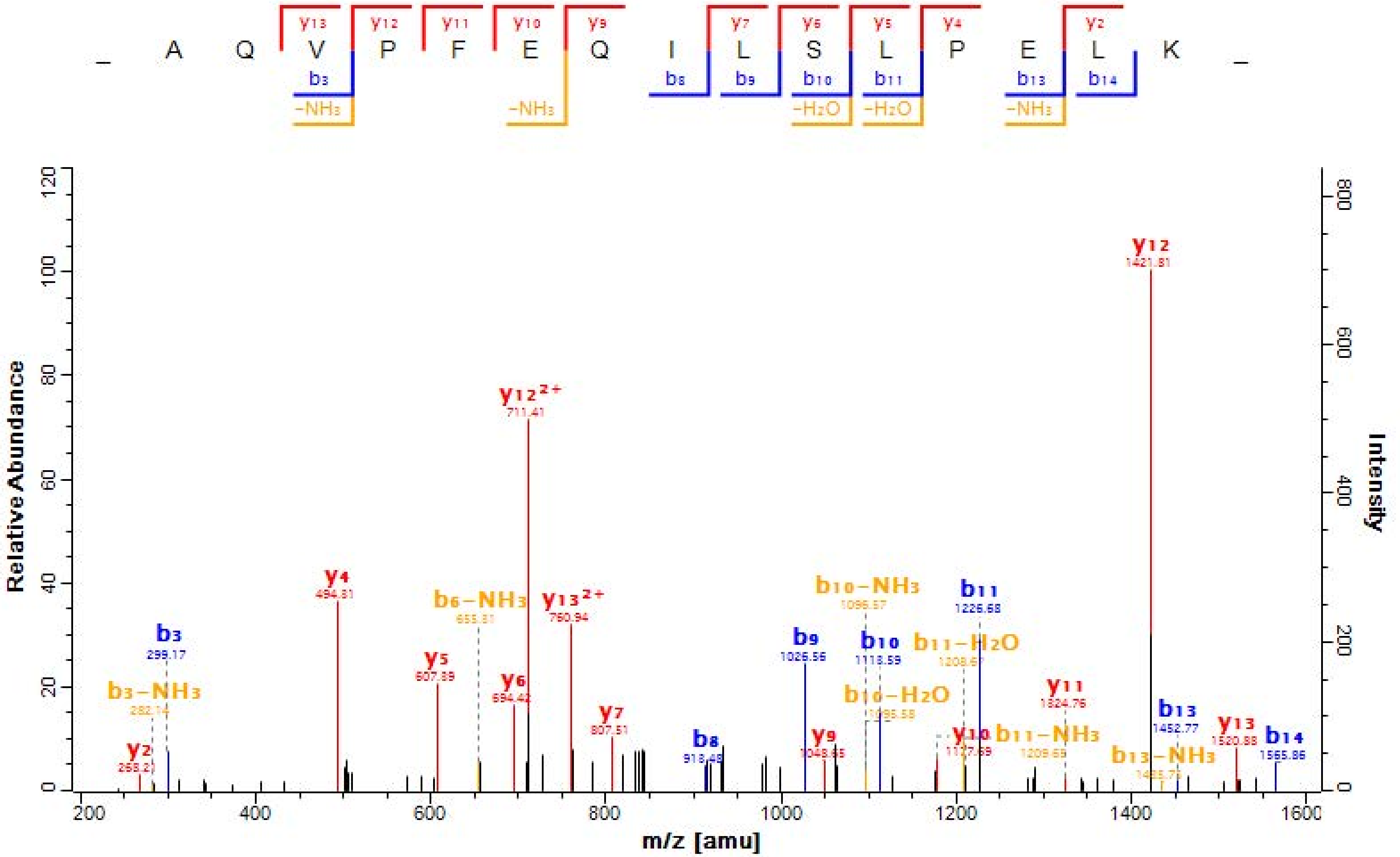
Mass:	1724.94654
m/z:	863.48055
Charge:	2+
Retentiontime:	66.063385009765
Score:	264.9232
Mass Error [ppm]:	0.24372
PEP:	1.343E-74
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	65 %
Peak Coverage:	47 %
Protein Localisation:	2 ... 17

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.05		114.05	1	A	15				
	185.09		185.09	2	A	14	1612.9		1612.9	
	298.18	+0.0528	298.18	3	L	13	1541.9		771.44	+0.249
	399.22	+0.0737	399.22	4	T	12	1428.8	-0.059	714.9	+0.213
	470.26		470.26	5	A	11	1327.7	+0.0877	664.37	+0.350
	599.3	-0.042	599.3	6	E	10	1256.7	+0.0282	1256.7	
	736.36	+0.0213	736.36	7	H	9	1127.7	+0.036	1127.7	
	883.43	+0.0223	883.43	8	F	8	990.6	+0.0252	990.6	
	954.47	+0.0409	954.47	9	A	7	843.53	+0.1172	843.53	
+0.077	513.26	+0.0618	1025.5	10	A	6	772.49	+0.1556	772.49	
-0.088	569.8	+0.0281	1138.6	11	L	5	701.46	+0.0038	701.46	
	1266.6	-0.001	1266.6	12	Q	4	588.37	+0.06	588.37	
+0.1467	677.34	-0.009	1353.7	13	S	3	460.31	+0.0075	460.31	
	1466.8	+0.2406	1466.8	14	L	2	373.28		373.28	
	1579.8	+0.0503	1579.8	15	L	1	260.2	+0.1253	260.2	
				16	K	0	147.11		147.11	

Scan number	10887	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	124.78



precursor information

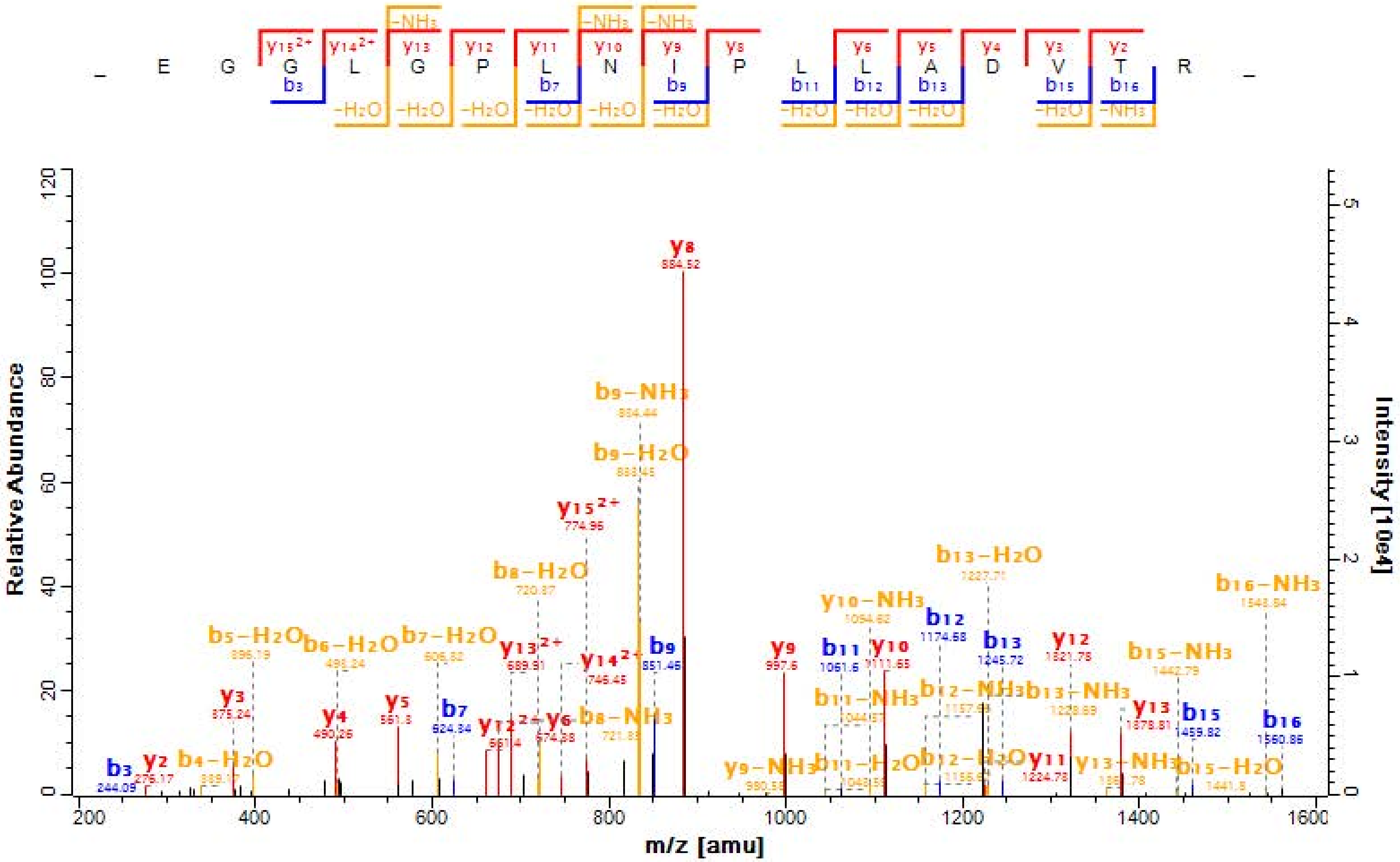
Mass:	1718.96896
m/z:	860.49176
Charge:	2+
Retentiontime:	66.902740478515
Score:	124.7764
Mass Error [ppm]:	-0.49931
PEP:	2.4585E-06
Precursor Type:	ISO

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	62 %
Peak Coverage:	32 %
Protein Localisation:	51 ... 65

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	14				
	200.103	2	Q	13	1648.94		1648.94	
+0.100011	299.1714	3	V	12	1520.881	+0.103579	760.9443	+0.039423
	396.2241	4	P	11	1421.813	-0.13709	711.4101	+0.017722
	543.2926	5	F	10	1324.76	+0.326075	1324.76	
	672.3352	6	E	9	1177.692	-0.10881	1177.692	
	800.3937	7	Q	8	1048.649	+0.126169	1048.649	
+0.042958	913.4778	8	I	7	920.5906		920.5906	
+0.115266	1026.562	9	L	6	807.5066	+0.141552	807.5066	
-0.05287	1113.594	10	S	5	694.4225	+0.184173	694.4225	
-0.06528	1226.678	11	L	4	607.3905	+0.049759	607.3905	
	1323.731	12	P	3	494.3064	+0.117892	494.3064	
+0.418343	1452.773	13	E	2	397.2537		397.2537	
-0.02864	1565.857	14	L	1	268.2111	+0.086571	268.2111	
		15	K	0	155.127		155.127	

Scan number	11120	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	227.67



precursor information

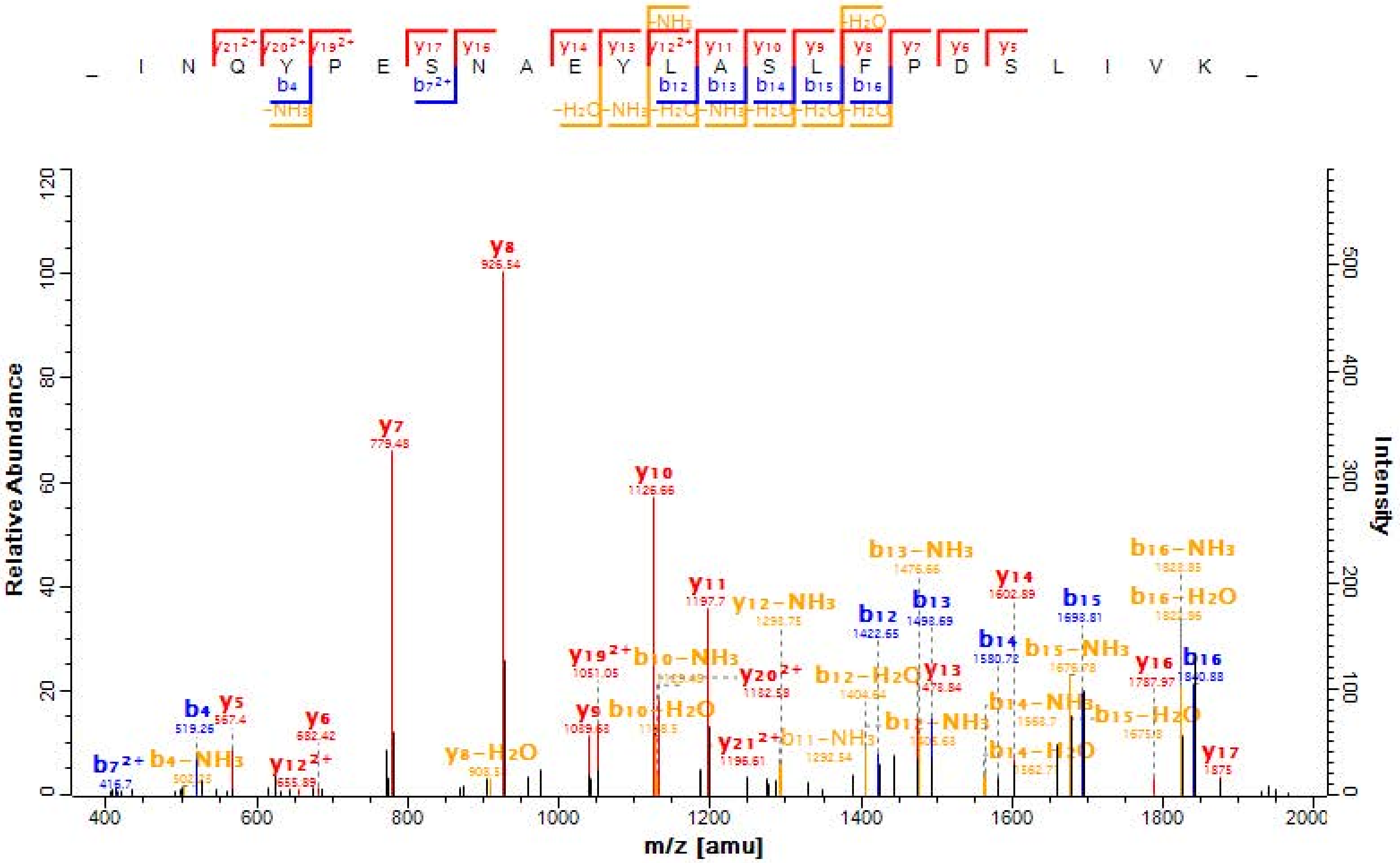
Mass:	1733.96688
m/z:	867.99071
Charge:	2+
Retentiontime:	68.743461608886
Score:	227.6734
Mass Error [ppm]:	-0.40848
PEP:	6.0539E-48
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	74 %
Peak Coverage:	53 %
Protein Localisation:	93 ... 109

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	16				
	187.0713	2	G	15	1605.932		1605.932	
+0.18238	244.0928	3	G	14	1548.911		774.959	+0.069158
	357.1769	4	L	13	1491.889		746.4483	+0.371577
	414.1983	5	G	12	1378.805	+0.033835	689.9063	+0.275303
	511.2511	6	P	11	1321.784	+0.047608	661.3955	+0.269922
+0.084403	624.3352	7	L	10	1224.731	-0.03146	1224.731	
	738.3781	8	N	9	1111.647	-1.2E-05	1111.647	
-0.0421	851.4621	9	I	8	997.6041	+0.041145	997.6041	
	948.5149	10	P	7	884.52	+0.090114	884.52	
+0.03323	1061.599	11	L	6	787.4672		787.4672	
+0.105538	1174.683	12	L	5	674.3832	+0.157667	674.3832	
+0.064518	1245.72	13	A	4	561.2991	+0.010591	561.2991	
	1360.747	14	D	3	490.262	+0.111181	490.262	
+0.187545	1459.816	15	V	2	375.235	+0.094271	375.235	
-0.05398	1560.863	16	T	1	276.1666	+0.090602	276.1666	
		17	R	0	175.119		175.119	

Scan number	11251	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	154.6



precursor information

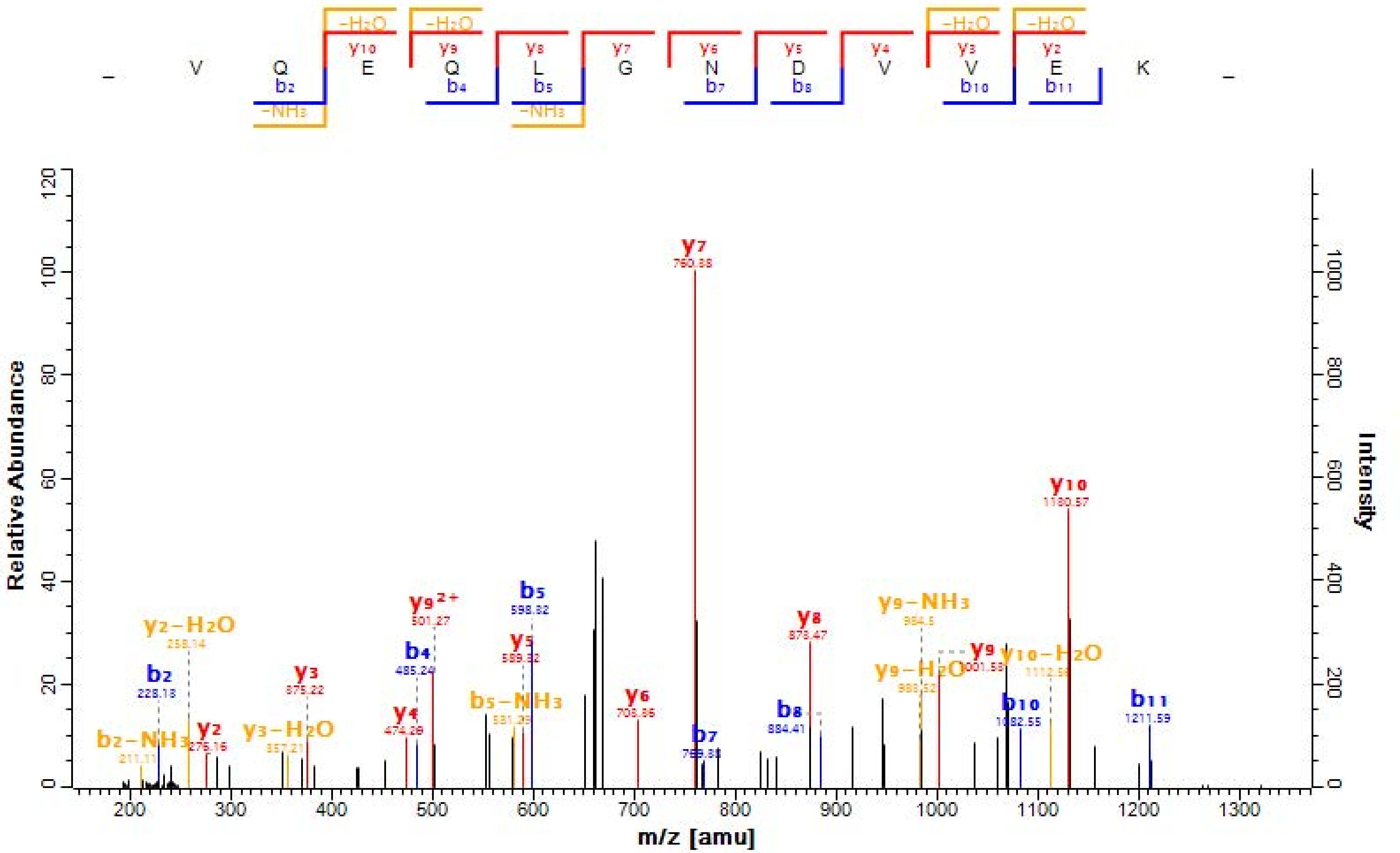
Mass:	2610.32078
m/z:	1306.16767
Charge:	2+
Retentiontime:	69.754623413085
Score:	154.6024
Mass Error [ppm]:	-0.36553
PEP:	8.239E-29
Precursor Type:	MULTI

general information

Annotation:	16 of 23
AminoAcids Coverag	70 %
Intensity Coverage:	65 %
Peak Coverage:	37 %
Protein Localisation:	122 … 144

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	I	22				
	228.13		228.13	2	N	21	2506.3		2506.3	
	356.19		356.19	3	Q	20	2392.2		1196.6	-0.006
	519.26	+0.1012	519.26	4	Y	19	2264.2		1132.6	+0.2316
	616.31		616.31	5	P	18	2101.1		1051.1	+0.0837
	745.35		745.35	6	E	17	2004		2004	
-0.241	416.7		832.38	7	S	16	1875	+0.1628	1875	
	946.43		946.43	8	N	15	1788	+0.4624	1788	
	1017.5		1017.5	9	A	14	1673.9		1673.9	
	1146.5		1146.5	10	E	13	1602.9	+0.0014	1602.9	
	1309.6		1309.6	11	Y	12	1473.8	+0.0126	1473.8	
	1422.7	-0.099	1422.7	12	L	11	1310.8		655.89	-0.3
	1493.7	-0.089	1493.7	13	A	10	1197.7	+0.0013	1197.7	
	1580.7	+0.0602	1580.7	14	S	9	1126.7	-0.003	1126.7	
	1693.8	-0.193	1693.8	15	L	8	1039.6	+0.0647	1039.6	
	1840.9	-0.038	1840.9	16	F	7	926.54	+0.0206	926.54	
	1937.9		1937.9	17	P	6	779.48	+0.0317	779.48	
	2053		2053	18	D	5	682.42	-0.06	682.42	
	2140		2140	19	S	4	567.4	+0.0914	567.4	
	2253.1		2253.1	20	L	3	480.36		480.36	
	2366.2		2366.2	21	I	2	367.28		367.28	
	2465.2		2465.2	22	V	1	254.2		254.2	
				23	K	0	155.13		155.13	

Scan number	1171	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	121.18



precursor information

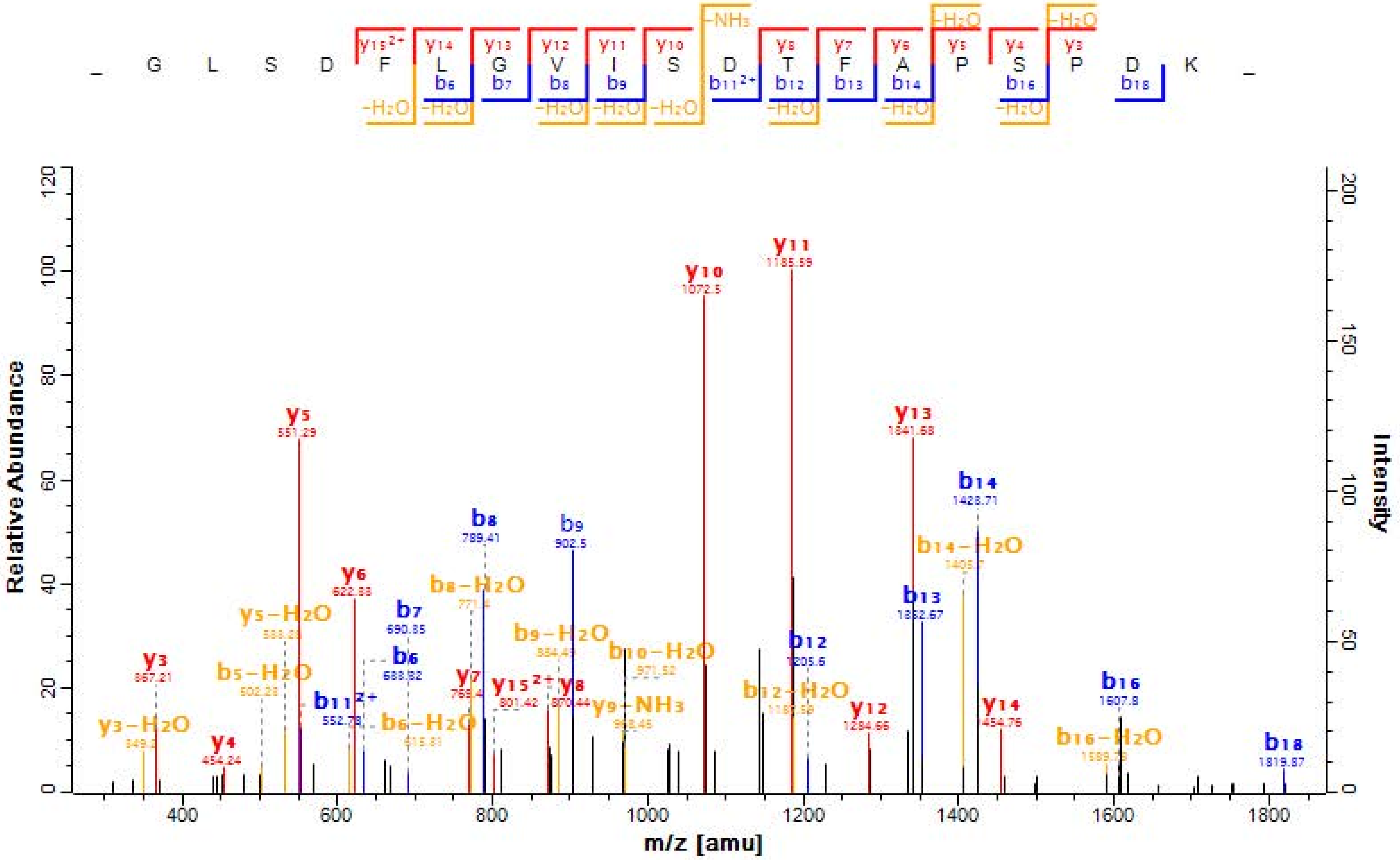
Mass:	1356.68836
m/z:	679.35146
Charge:	2+
Retentiontime:	13.051728248596
Score:	121.1825
Mass Error [ppm]:	-0.10671
PEP:	2.0404E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	44 %
Peak Coverage:	25 %
Protein Localisation:	52 ... 63

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	11				
+0.039362	228.1343	2	Q	10	1258.627		1258.627	
	357.1769	3	E	9	1130.569	-0.02973	1130.569	
+0.004247	485.2354	4	Q	8	1001.526	-0.01894	501.2667	-0.01637
+0.015764	598.3195	5	L	7	873.4676	-0.04264	873.4676	
	655.341	6	G	6	760.3836	+0.007493	760.3836	
+0.070147	769.3839	7	N	5	703.3621	-0.06919	703.3621	
+0.073355	884.4108	8	D	4	589.3192	+0.08641	589.3192	
	983.4793	9	V	3	474.2922	+0.123668	474.2922	
-0.08612	1082.548	10	V	2	375.2238	+0.150578	375.2238	
-0.04399	1211.59	11	E	1	276.1554	-0.0293	276.1554	
		12	K	0	147.1128		147.1128	

Scan number	11722	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	155.79



precursor information

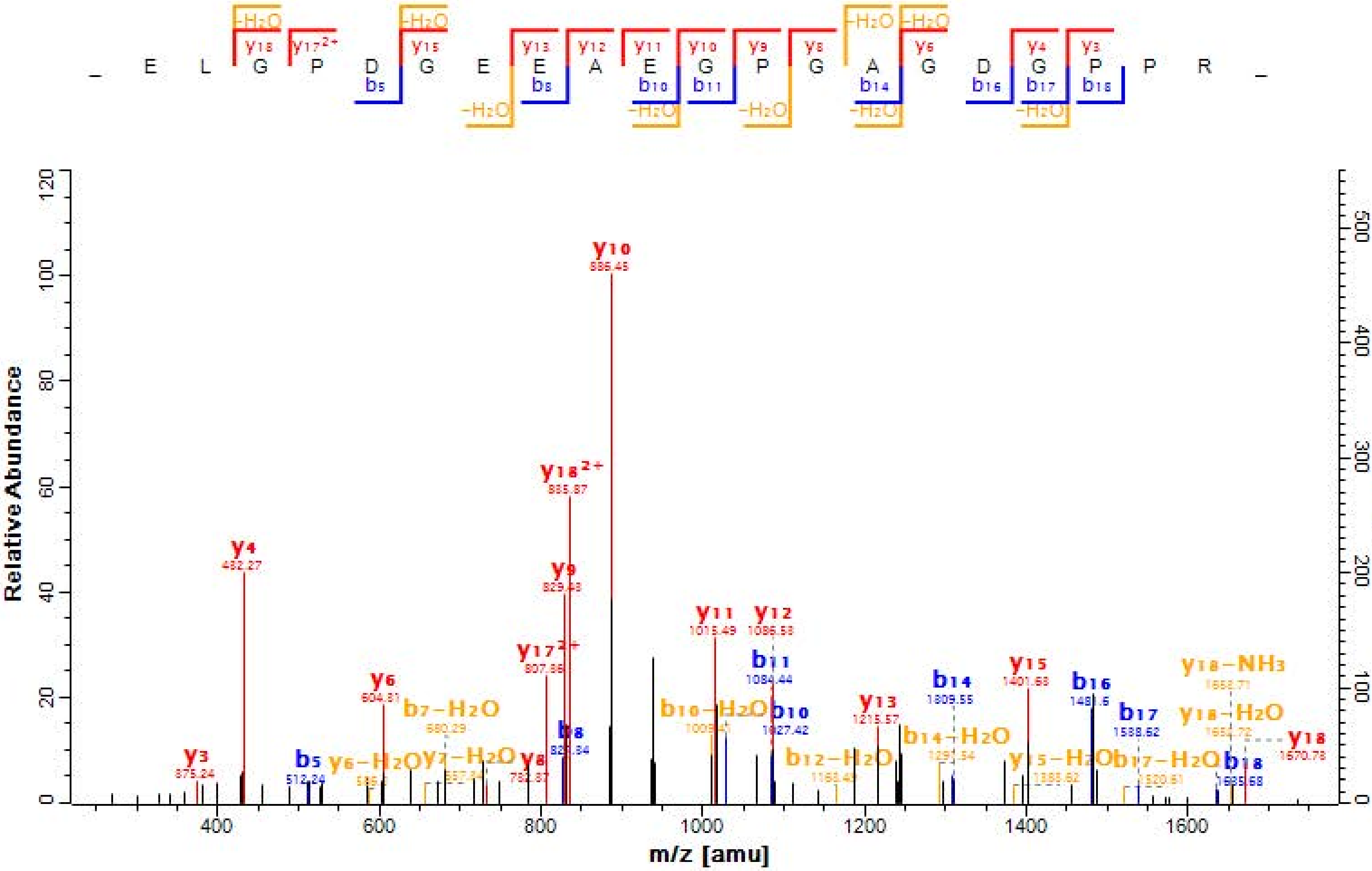
Mass:	1964.97166
m/z:	983.49311
Charge:	2+
Retentiontime:	74.122528076171
Score:	155.7944
Mass Error [ppm]:	-0.74225
PEP:	3.1468E-26
Precursor Type:	MULTI

general information

Annotation:	15 of 19
AminoAcids Coverag	79 %
Intensity Coverage:	65 %
Peak Coverage:	39 %
Protein Localisation:	94 ... 112

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	18				
	171.11		171.11	2	L	17	1917		1917	
	258.14		258.14	3	S	16	1803.9		1803.9	
	373.17		373.17	4	D	15	1716.9		1716.9	
	520.24		520.24	5	F	14	1601.8		801.42	+0.2434
	633.32	+0.0824	633.32	6	L	13	1454.8	-0.055	1454.8	
	690.35	+0.0707	690.35	7	G	12	1341.7	-0.09	1341.7	
	789.41	-0.138	789.41	8	V	11	1284.7	-0.017	1284.7	
	902.5	+0.0333	902.5	9	I	10	1185.6	-0.079	1185.6	
	989.53		989.53	10	S	9	1072.5	-0.032	1072.5	
-0.44	552.78		1104.6	11	D	8	985.47		985.47	
	1205.6	-0.099	1205.6	12	T	7	870.44	+0.1871	870.44	
	1352.7	-0.002	1352.7	13	F	6	769.4	+0.2197	769.4	
	1423.7	-0.08	1423.7	14	A	5	622.33	+0.1334	622.33	
	1520.8		1520.8	15	P	4	551.29	+0.0903	551.29	
	1607.8	+0.1786	1607.8	16	S	3	454.24	+0.2341	454.24	
	1704.8		1704.8	17	P	2	367.21	+0.0265	367.21	
	1819.9	+0.052	1819.9	18	D	1	270.15		270.15	
				19	K	0	155.13		155.13	

Scan number	1186	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	131.25



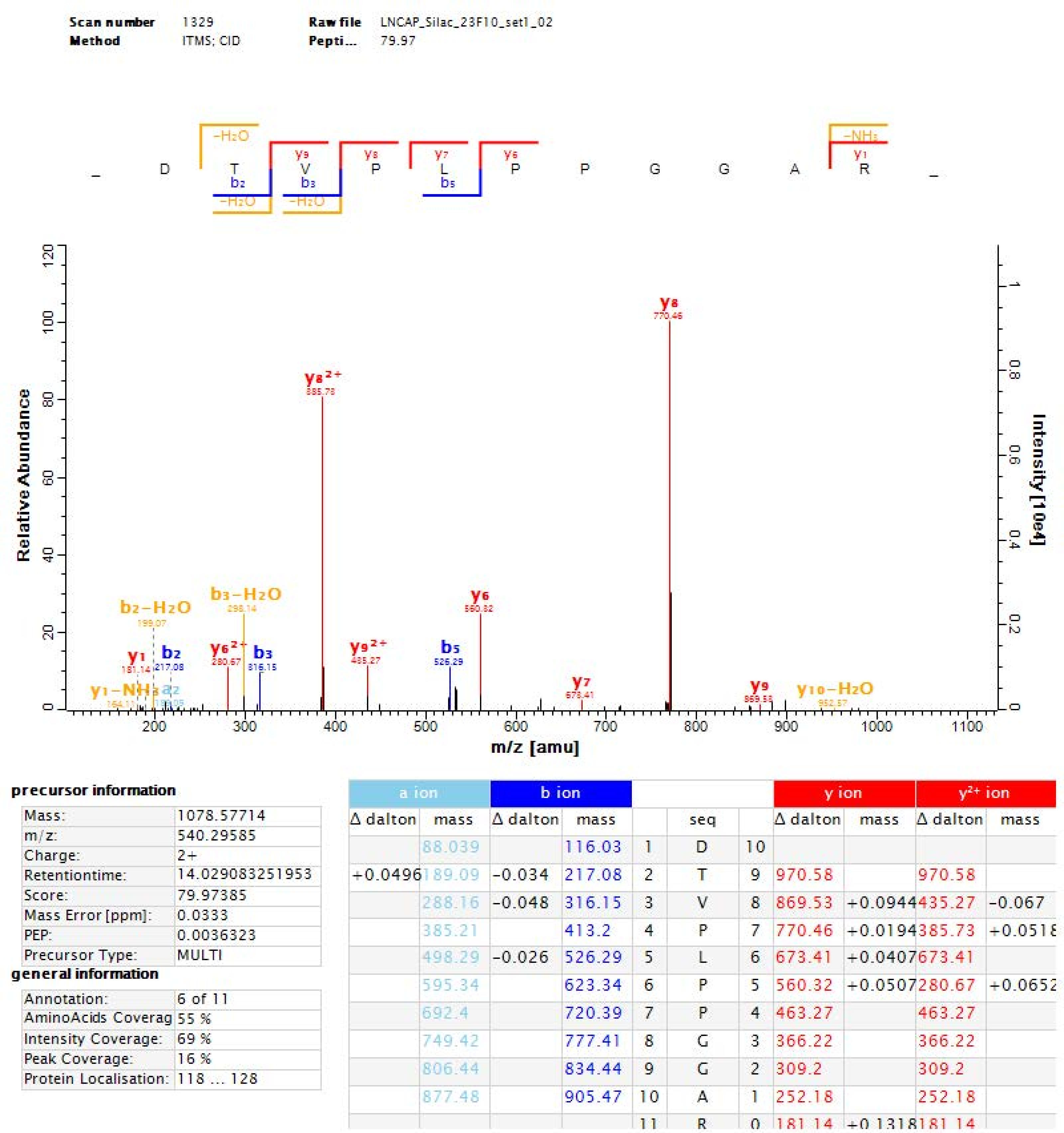
precursor information

Mass:	1905.83295
m/z:	953.92375
Charge:	2+
Retentiontime:	13.150157928466
Score:	131.2486
Mass Error [ppm]:	-0.57993
PEP:	2.7031E-13
Precursor Type:	MULTI

general information

Annotation:	16 of 20
AminoAcids Coverag	80 %
Intensity Coverage:	54 %
Peak Coverage:	33 %
Protein Localisation:	152 ... 171

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	19				
	243.1339	2	L	18	1783.819		1783.819	
	300.1554	3	G	17	1670.735	-0.15302	835.871	+0.151051
	397.2082	4	P	16	1613.713		807.3603	-0.05587
-0.11413	512.2351	5	D	15	1516.661		1516.661	
	569.2566	6	G	14	1401.634	-0.05613	1401.634	
	698.2992	7	E	13	1344.612		1344.612	
+0.146039	827.3418	8	E	12	1215.57	-0.03931	1215.57	
	898.3789	9	A	11	1086.527	-0.07826	1086.527	
-0.14595	1027.421	10	E	10	1015.49	-0.11372	1015.49	
-0.13384	1084.443	11	G	9	886.4473	+0.037518	886.4473	
	1181.496	12	P	8	829.4258	+0.069724	829.4258	
	1238.517	13	G	7	732.3731	-0.00147	732.3731	
-0.32807	1309.554	14	A	6	675.3516		675.3516	
	1366.576	15	G	5	604.3145	+0.147435	604.3145	
-0.10499	1481.603	16	D	4	547.293		547.293	
-0.1477	1538.624	17	G	3	432.2661	+0.024882	432.2661	
-0.13857	1635.677	18	P	2	375.2446	+0.049733	375.2446	
	1732.73	19	P	1	278.1918		278.1918	
		20	R	0	181.1391		181.1391	



Scan number	1329	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	79.97

precursor information

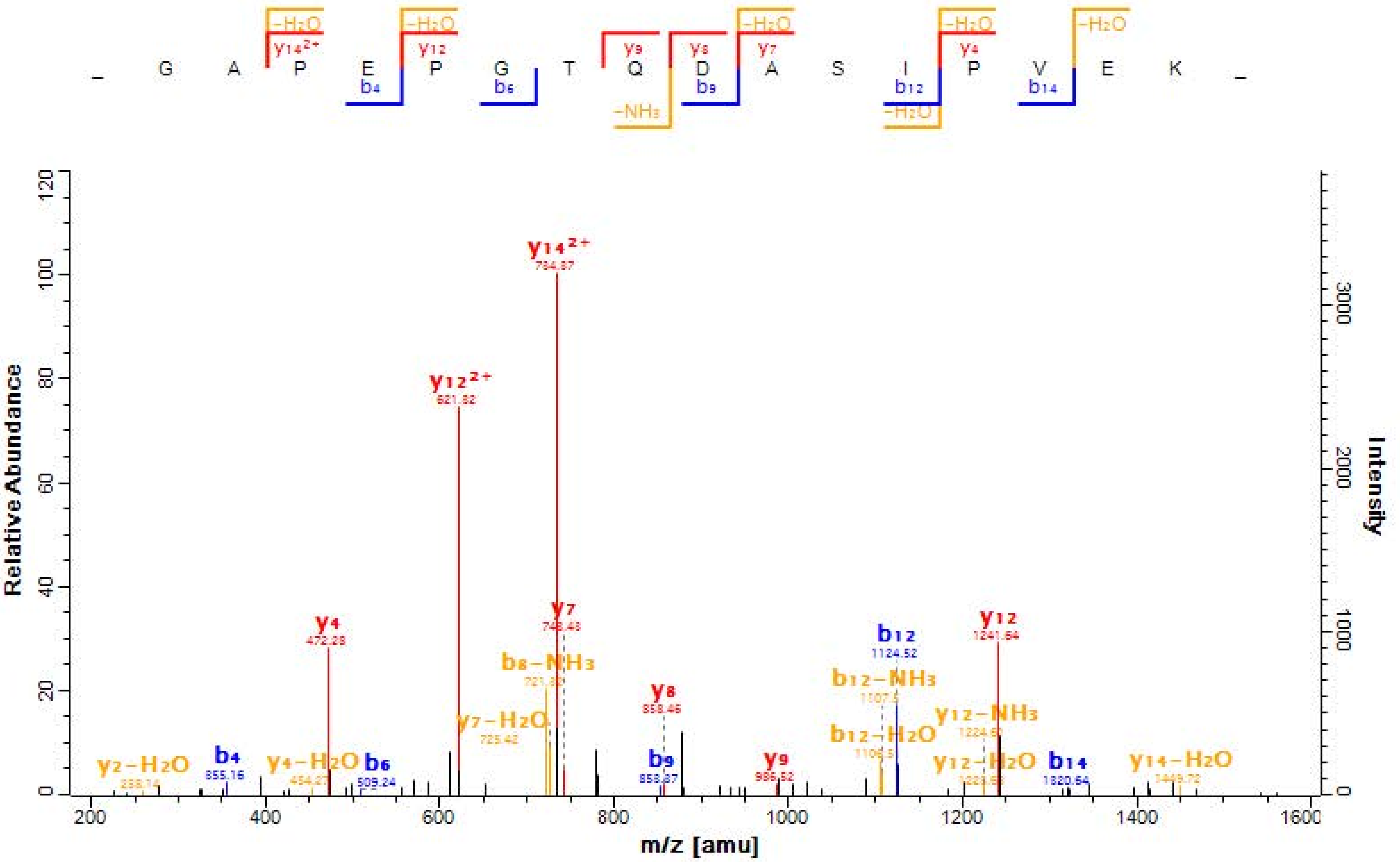
Mass:	1078.57714
m/z:	540.29585
Charge:	2+
Retentiontime:	14.029083251953
Score:	79.97385
Mass Error [ppm]:	0.0333
PEP:	0.0036323
Precursor Type:	MULTI

general information

Annotation:	6 of 11
AminoAcids Coverag	55 %
Intensity Coverage:	69 %
Peak Coverage:	16 %
Protein Localisation:	118 ... 128

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	10				
+0.0496	189.09	-0.034	217.08	2	T	9	970.58		970.58	
	288.16	-0.048	316.15	3	V	8	869.53	+0.0944	435.27	-0.067
	385.21		413.2	4	P	7	770.46	+0.0194	385.73	+0.051
	498.29	-0.026	526.29	5	L	6	673.41	+0.0407	673.41	
	595.34		623.34	6	P	5	560.32	+0.0507	280.67	+0.0652
	692.4		720.39	7	P	4	463.27		463.27	
	749.42		777.41	8	G	3	366.22		366.22	
	806.44		834.44	9	G	2	309.2		309.2	
	877.48		905.47	10	A	1	252.18		252.18	
				11	R	0	181.14	+0.1318	181.14	

Scan number	1521	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	77.07



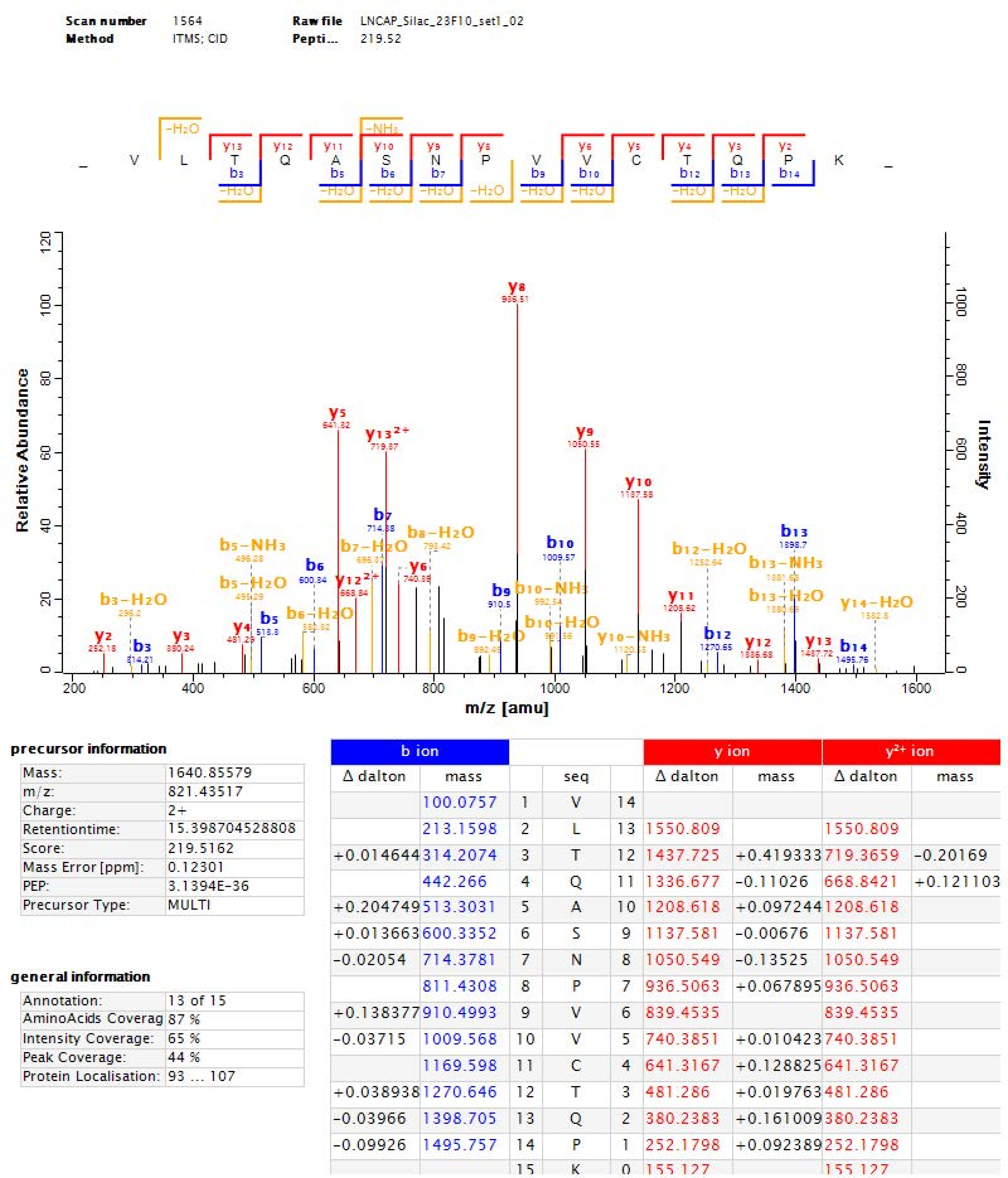
precursor information

Mass:	1594.78314
m/z:	798.39885
Charge:	2+
Retentiontime:	15.152011871337
Score:	77.06827
Mass Error [ppm]:	-0.45487
PEP:	0.0002916
Precursor Type:	MULTI

general information

Annotation:	11 of 16
AminoAcids Coverag	69 %
Intensity Coverage:	67 %
Peak Coverage:	27 %
Protein Localisation:	188 ... 203

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	15				
	129.0659	2	A	14	1538.77		1538.77	
	226.1186	3	P	13	1467.733		734.3699	+0.193739
+0.101423	355.1612	4	E	12	1370.68		1370.68	
	452.214	5	P	11	1241.637	-0.04248	621.3222	+0.221215
-0.00985	509.2354	6	G	10	1144.584		1144.584	
	610.2831	7	T	9	1087.563		1087.563	
	738.3417	8	Q	8	986.5153	+0.061847	986.5153	
+0.130447	853.3686	9	D	7	858.4567	+0.019228	858.4567	
	924.4058	10	A	6	743.4298	-0.01029	743.4298	
	1011.438	11	S	5	672.3927		672.3927	
-0.02526	1124.522	12	I	4	585.3606		585.3606	
	1221.575	13	P	3	472.2766	+0.136389	472.2766	
-0.1064	1320.643	14	V	2	375.2238		375.2238	
	1449.686	15	E	1	276.1554		276.1554	
		16	K	0	147.1128		147.1128	



Scan number	1564	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	219.52

precursor information

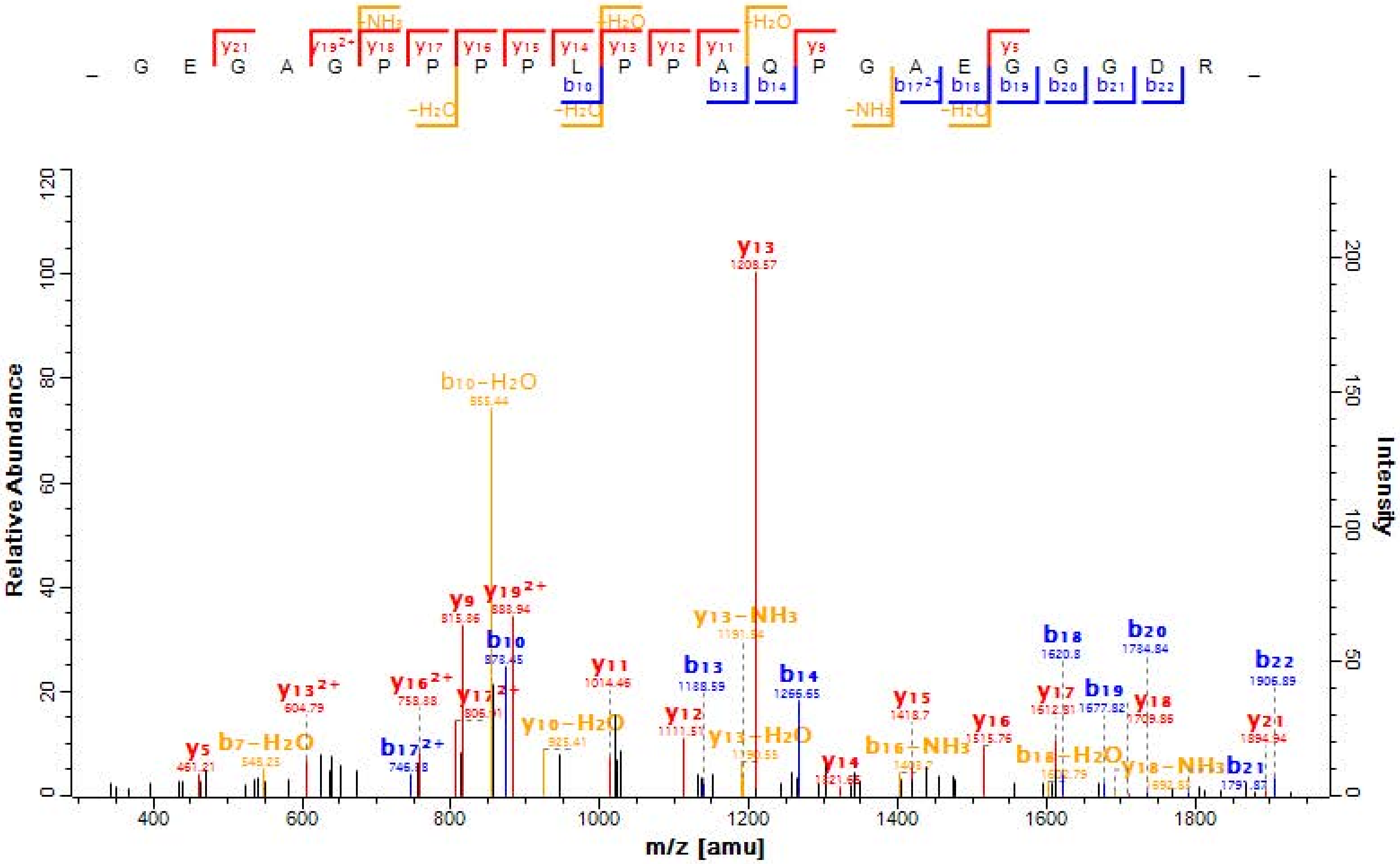
Mass:	1640.85579
m/z:	821.43517
Charge:	2+
Retentiontime:	15.398704528808
Score:	219.5162
Mass Error [ppm]:	0.12301
PEP:	3.1394E-36
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	65 %
Peak Coverage:	44 %
Protein Localisation:	93 ... 107

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	14				
	213.1598	2	L	13	1550.809		1550.809	
+0.014644	314.2074	3	T	12	1437.725	+0.419333	719.3659	-0.20169
	442.266	4	Q	11	1336.677	-0.11026	668.8421	+0.121103
+0.204749	513.3031	5	A	10	1208.618	+0.097244	1208.618	
+0.013663	600.3352	6	S	9	1137.581	-0.00676	1137.581	
-0.02054	714.3781	7	N	8	1050.549	-0.13525	1050.549	
	811.4308	8	P	7	936.5063	+0.067895	936.5063	
+0.138377	910.4993	9	V	6	839.4535		839.4535	
-0.03715	1009.568	10	V	5	740.3851	+0.010423	740.3851	
	1169.598	11	C	4	641.3167	+0.128825	641.3167	
+0.038938	1270.646	12	T	3	481.286	+0.019763	481.286	
-0.03966	1398.705	13	Q	2	380.2383	+0.161009	380.2383	
-0.09926	1495.757	14	P	1	252.1798	+0.092389	252.1798	
		15	K	0	155.127		155.127	

Scan number	1648	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	114.63



precursor information

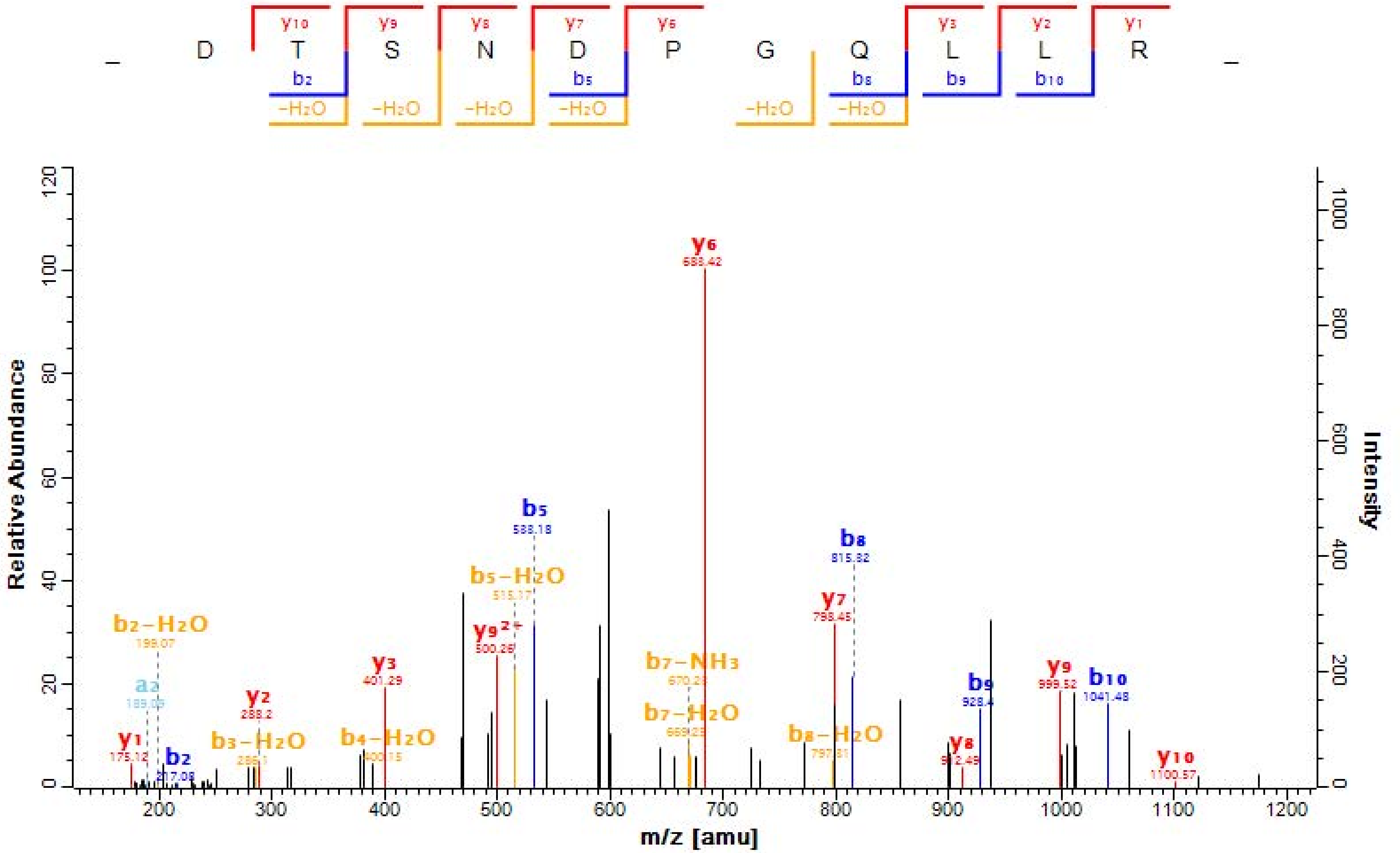
Mass:	2077.93333
m/z:	1039.97394
Charge:	2+
Retentiontime:	15.869448661804
Score:	114.6299
Mass Error [ppm]:	-0.25178
PEP:	9.0511E-24
Precursor Type:	MULTI

general information

Annotation:	19 of 23
AminoAcids Coverag	83 %
Intensity Coverage:	63 %
Peak Coverage:	36 %
Protein Localisation:	13 ... 35

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	22				
	187.07		187.07	2	E	21	2024		2024	
	244.09		244.09	3	G	20	1894.9	+0.0284	1894.9	
	315.13		315.13	4	A	19	1837.9		1837.9	
	372.15		372.15	5	G	18	1766.9		883.94	-0.145
	469.2		469.2	6	P	17	1709.9	+0.3965	1709.9	
	566.26		566.26	7	P	16	1612.8	-0.131	806.91	+0.0453
	663.31		663.31	8	P	15	1515.8	+0.113	758.38	-0.173
	760.36		760.36	9	P	14	1418.7	-0.323	1418.7	
	873.45	-0.004	873.45	10	L	13	1321.6	+0.3741	1321.6	
	970.5		970.5	11	P	12	1208.6	-0.039	604.79	+0.027
	1067.6		1067.6	12	P	11	1111.5	-0.043	1111.5	
	1138.6	+0.188	1138.6	13	A	10	1014.5	+0.0667	1014.5	
	1266.6	-0.134	1266.6	14	Q	9	943.42		943.42	
	1363.7		1363.7	15	P	8	815.36	+0.2035	815.36	
	1420.7		1420.7	16	G	7	718.31		718.31	
+0.3606	746.38		1491.8	17	A	6	661.29		661.29	
	1620.8	-0.118	1620.8	18	E	5	590.25		590.25	
	1677.8	+0.0883	1677.8	19	G	4	461.21	-0.109	461.21	
	1734.8	-0.071	1734.8	20	G	3	404.19		404.19	
	1791.9	-0.008	1791.9	21	G	2	347.17		347.17	
	1906.9	-0.077	1906.9	22	D	1	290.15		290.15	
				23	R	0	175.12		175.12	

Scan number	2060	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	86.91



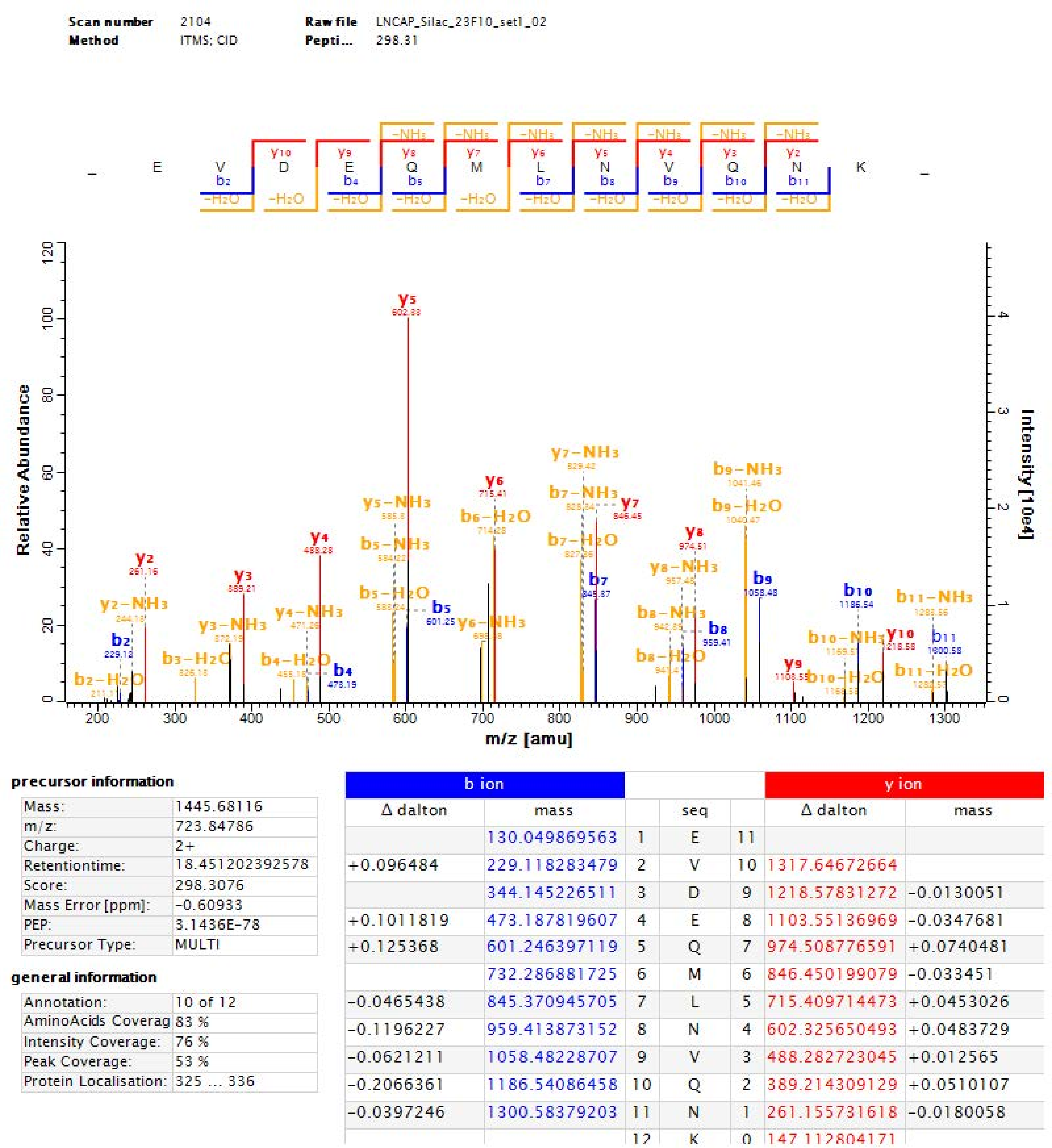
precursor information

Mass:	1214.58897
m/z:	608.30176
Charge:	2+
Retentiontime:	18.208929061889
Score:	86.91063
Mass Error [ppm]:	-0.12734
PEP:	0.0021501
Precursor Type:	MULTI

general information

Annotation:	10 of 11
AminoAcids Coverag	91 %
Intensity Coverage:	42 %
Peak Coverage:	27 %
Protein Localisation:	264 ... 274

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	10				
+0.2285	189.09	-0.056	217.08	2	T	9	1100.6	+0.1486	1100.6	
	276.12		304.11	3	S	8	999.52	-0.098	500.26	+0.044
	390.16		418.16	4	N	7	912.49	+0.0483	912.49	
	505.19	+0.087	533.18	5	D	6	798.45	-0.015	798.45	
	602.24		630.24	6	P	5	683.42	-0.011	683.42	
	659.26		687.26	7	G	4	586.37		586.37	
	787.32	-0.047	815.32	8	Q	3	529.35		529.35	
	900.41	+0.0102	928.4	9	L	2	401.29	+0.0993	401.29	
	1013.5	+0.0437	1041.5	10	L	1	288.2	+0.0819	288.2	
				11	R	0	175.12	+0.1062	175.12	



Scan number	2104	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	298.31

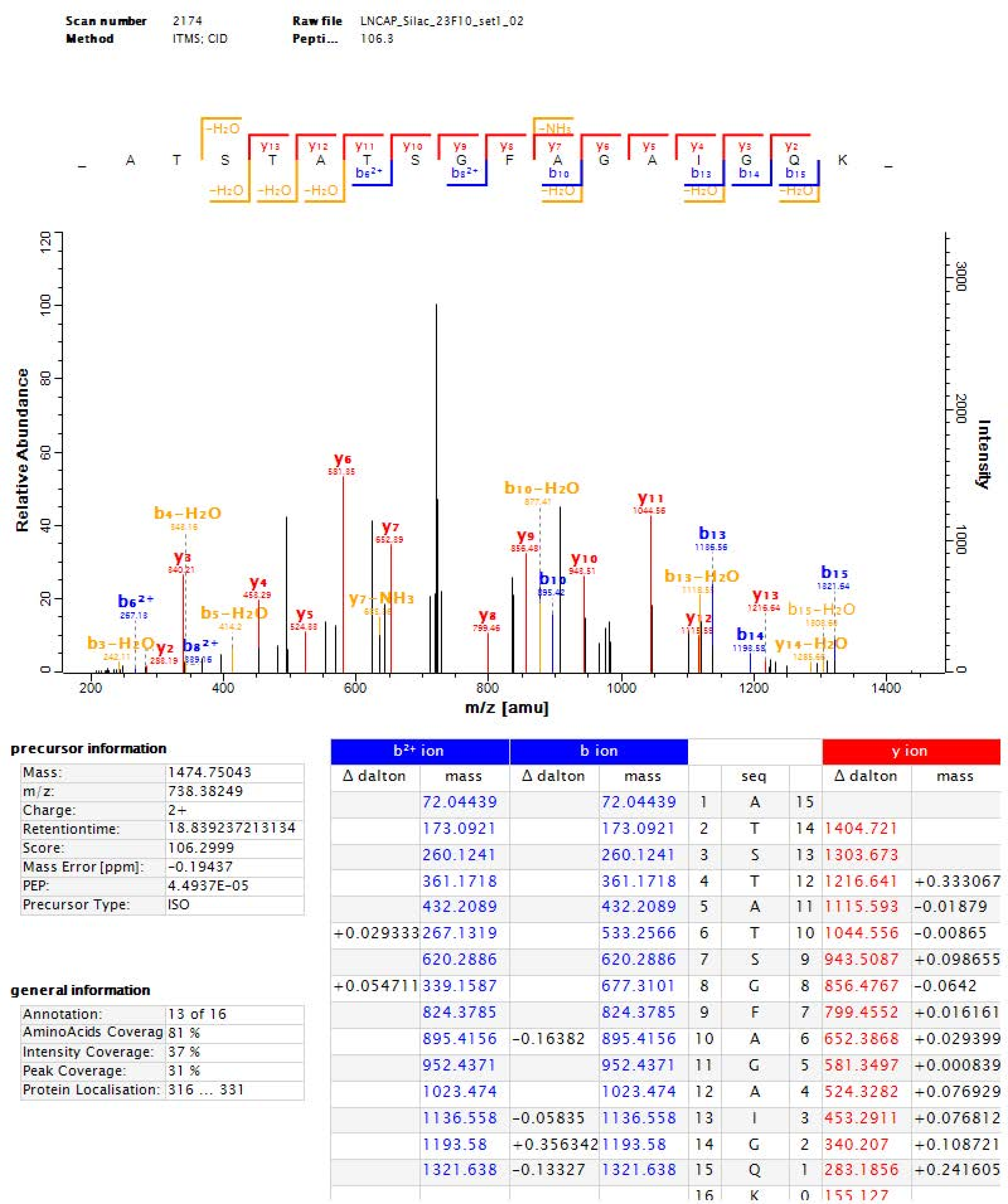
precursor information

Mass:	1445.68116
m/z:	723.84786
Charge:	2+
Retentiontime:	18.451202392578
Score:	298.3076
Mass Error [ppm]:	-0.60933
PEP:	3.1436E-78
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	76 %
Peak Coverage:	53 %
Protein Localisation:	325 ... 336

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	130.049869563	1	E	11		
+0.096484	229.118283479	2	V	10	1317.64672664	
	344.145226511	3	D	9	1218.57831272	-0.0130051
+0.1011819	473.187819607	4	E	8	1103.55136969	-0.0347681
+0.125368	601.246397119	5	Q	7	974.508776591	+0.0740481
	732.286881725	6	M	6	846.450199079	-0.033451
-0.0465438	845.370945705	7	L	5	715.409714473	+0.0453026
-0.1196227	959.413873152	8	N	4	602.325650493	+0.0483729
-0.0621211	1058.48228707	9	V	3	488.282723045	+0.012565
-0.2066361	1186.54086458	10	Q	2	389.214309129	+0.0510107
-0.0397246	1300.58379203	11	N	1	261.155731618	-0.0180058
		12	K	0	147.112804171	



Scan number 2174
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set1_02
Pepti... 106.3

precursor information

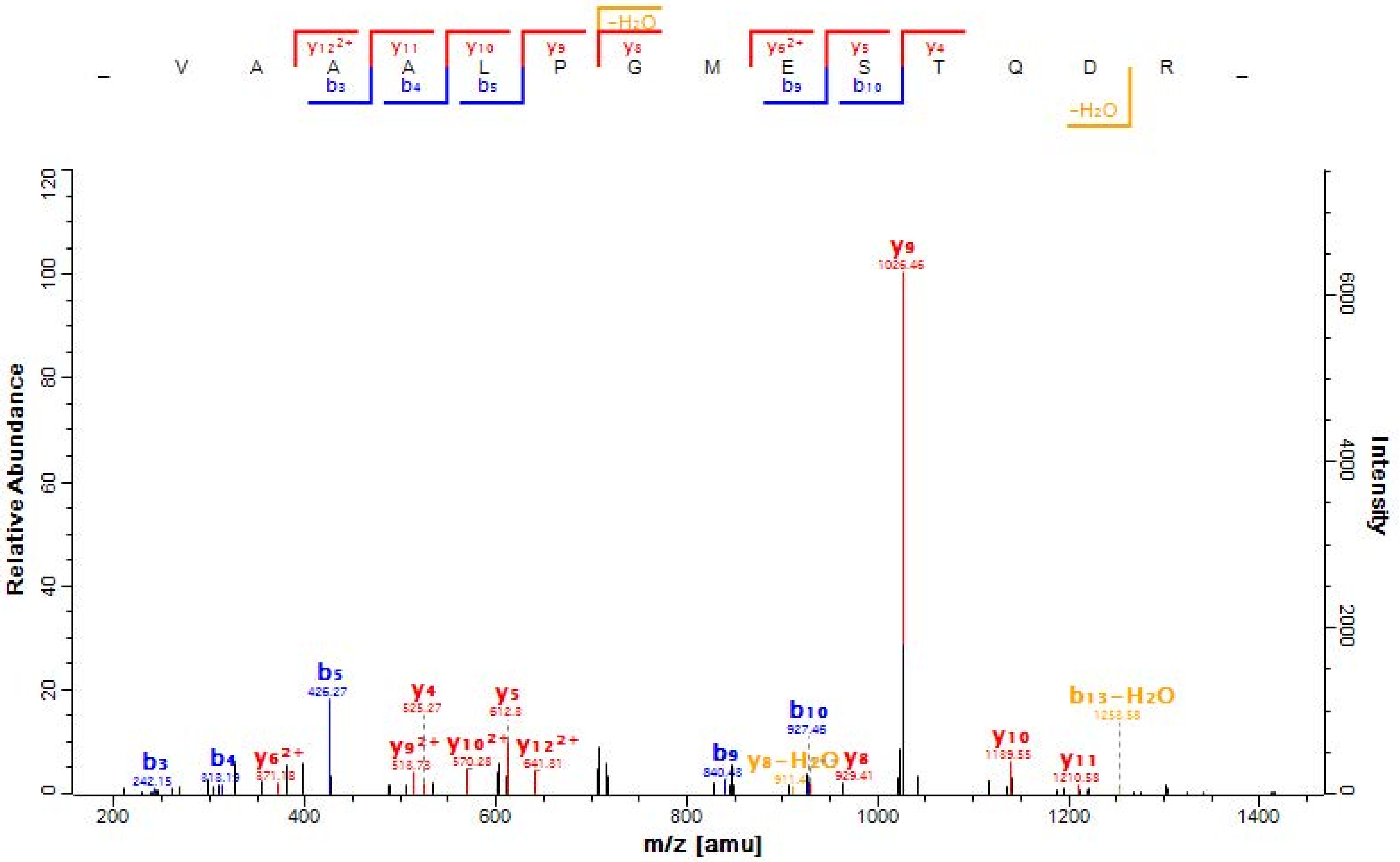
Mass:	1474.75043
m/z:	738.38249
Charge:	2+
Retentiontime:	18.839237213134
Score:	106.2999
Mass Error [ppm]:	-0.19437
PEP:	4.4937E-05
Precursor Type:	ISO

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	37 %
Peak Coverage:	31 %
Protein Localisation:	316 ... 331

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	72.04439		72.04439	1	A	15		
	173.0921		173.0921	2	T	14	1404.721	
	260.1241		260.1241	3	S	13	1303.673	
	361.1718		361.1718	4	T	12	1216.641	+0.333067
	432.2089		432.2089	5	A	11	1115.593	-0.01879
+0.029333	267.1319		533.2566	6	T	10	1044.556	-0.00865
	620.2886		620.2886	7	S	9	943.5087	+0.098655
+0.054711	339.1587		677.3101	8	G	8	856.4767	-0.0642
	824.3785		824.3785	9	F	7	799.4552	+0.016161
	895.4156	-0.16382	895.4156	10	A	6	652.3868	+0.029399
	952.4371		952.4371	11	G	5	581.3497	+0.000839
	1023.474		1023.474	12	A	4	524.3282	+0.076929
	1136.558	-0.05835	1136.558	13	I	3	453.2911	+0.076812
	1193.58	+0.356342	1193.58	14	G	2	340.207	+0.108721
	1321.638	-0.13327	1321.638	15	Q	1	283.1856	+0.241605
				16	K	0	155.127	

Scan number	2359	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	80.31



precursor information

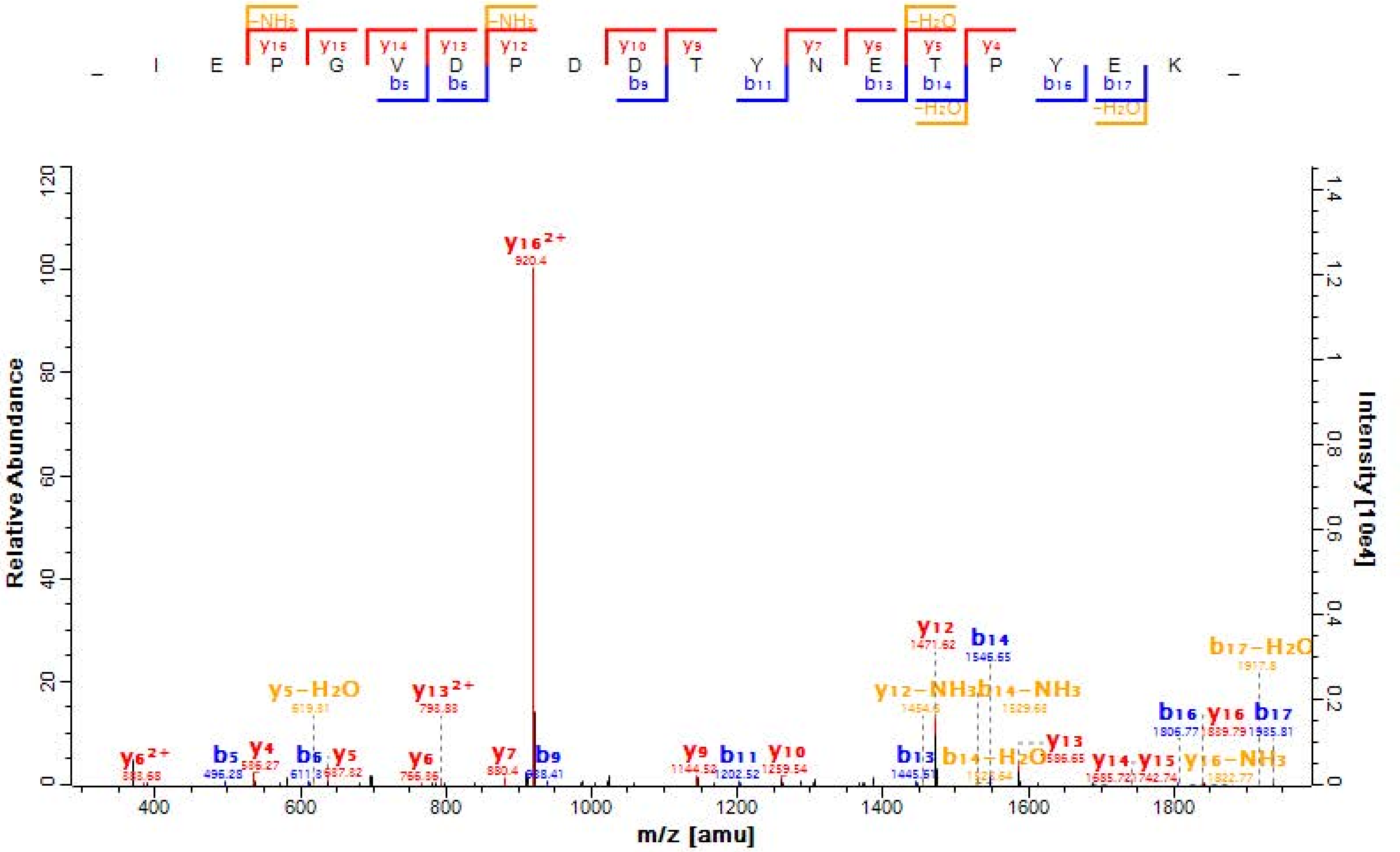
Mass:	1444.69884
m/z:	723.3567
Charge:	2+
Retentiontime:	19.858392715454
Score:	80.31177
Mass Error [ppm]:	0.5586
PEP:	0.00098105
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	48 %
Peak Coverage:	19 %
Protein Localisation:	170 ... 183

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	13				
	171.1128	2	A	12	1352.657		1352.657	
+0.107406	242.1499	3	A	11	1281.62		641.3136	-0.0451
+0.006389	313.187	4	A	10	1210.583	-0.12124	1210.583	
-0.0214	426.2711	5	L	9	1139.546	+0.021949	570.2765	+0.273633
	523.3239	6	P	8	1026.462	-0.05036	513.7344	+0.017203
	580.3453	7	G	7	929.4089	+0.273767	929.4089	
	711.3858	8	M	6	872.3874		872.3874	
-0.25158	840.4284	9	E	5	741.3469		371.1771	+0.280858
-0.00193	927.4604	10	S	4	612.3043	-0.03301	612.3043	
	1028.508	11	T	3	525.2723	+0.12689	525.2723	
	1156.567	12	Q	2	424.2246		424.2246	
	1271.594	13	D	1	296.166		296.166	
		14	R	0	181.1391		181.1391	

Scan number	2517	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	124.84



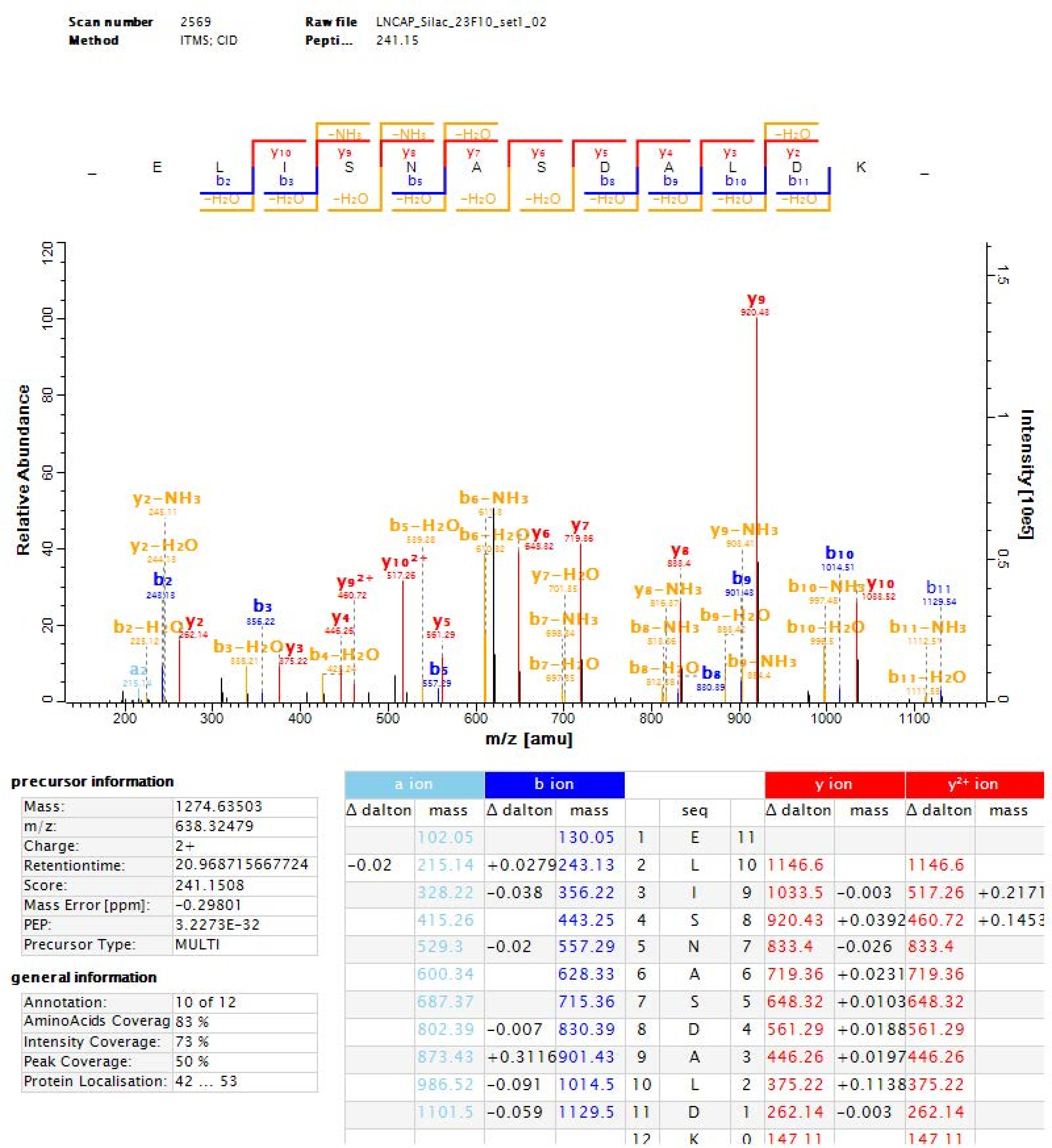
precursor information

Mass:	2080.91113
m/z:	1041.46284
Charge:	2+
Retentiontime:	20.691112518310
Score:	124.844
Mass Error [ppm]:	-0.089082
PEP:	2.1154E-12
Precursor Type:	MULTI

general information

Annotation:	14 of 18
AminoAcids Coverag	78 %
Intensity Coverage:	67 %
Peak Coverage:	29 %
Protein Localisation:	407 ... 424

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	I	17				
	243.1339	2	E	16	1968.835		1968.835	
	340.1867	3	P	15	1839.792	-0.30621	920.3996	+0.270807
	397.2082	4	G	14	1742.739	+0.07663	1742.739	
+0.070471	496.2766	5	V	13	1685.718	-0.15435	1685.718	
+0.004526	611.3035	6	D	12	1586.649	-0.10949	793.8283	-0.03299
	708.3563	7	P	11	1471.622	-0.04398	1471.622	
	823.3832	8	D	10	1374.57		1374.57	
+0.042347	938.4102	9	D	9	1259.543	+0.033411	1259.543	
	1039.458	10	T	8	1144.516	+0.048269	1144.516	
-0.01214	1202.521	11	Y	7	1043.468		1043.468	
	1316.564	12	N	6	880.4047	-0.08181	880.4047	
-0.05897	1445.607	13	E	5	766.3618	+0.228815	383.6845	-0.26573
-0.22579	1546.654	14	T	4	637.3192	+0.09996	637.3192	
	1643.707	15	P	3	536.2715	+0.172297	536.2715	
-0.27254	1806.77	16	Y	2	439.2187		439.2187	
-0.21308	1935.813	17	E	1	276.1554		276.1554	
		18	K	0	147.1128		147.1128	



Scan number	2569	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	241.15

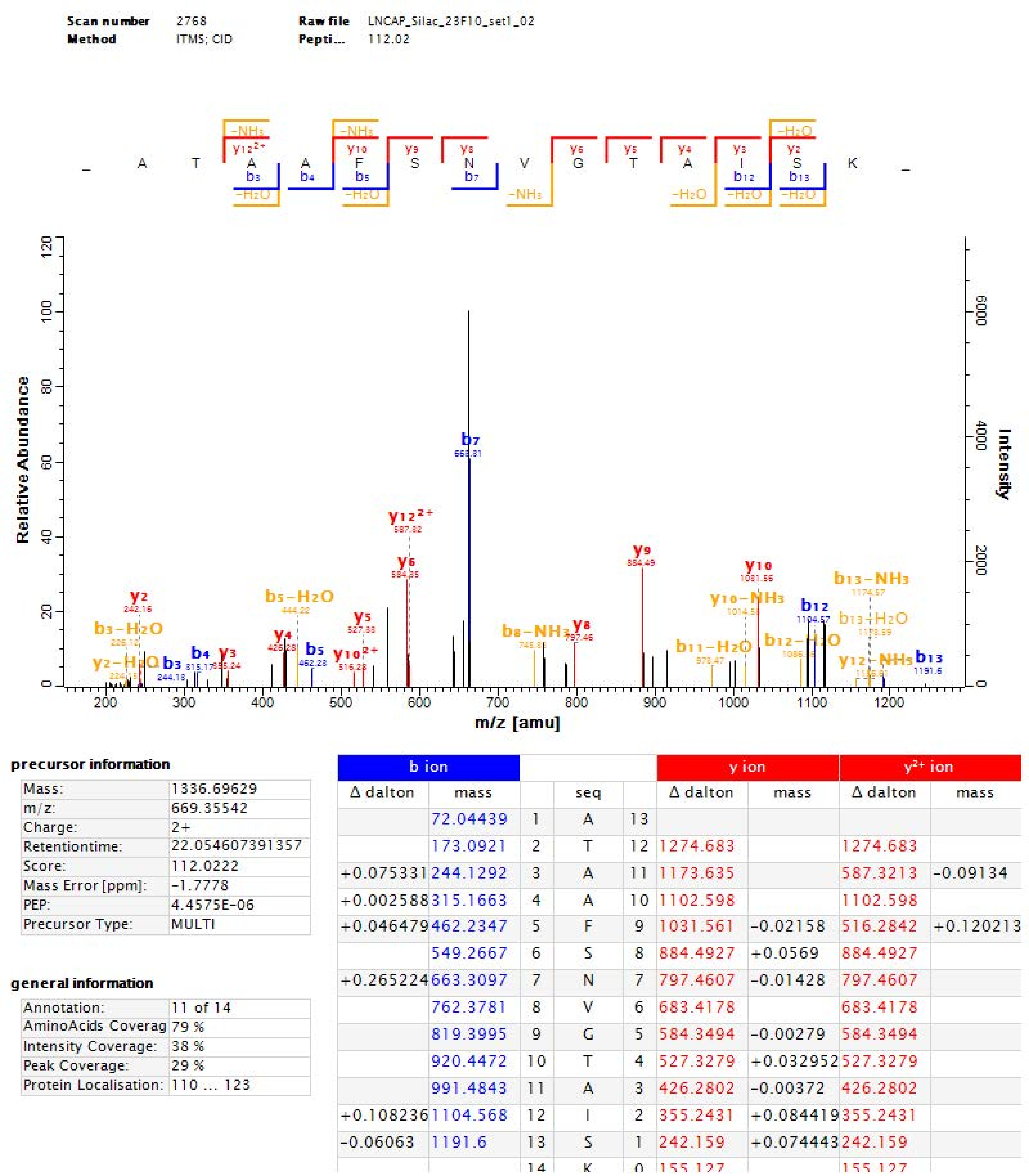
precursor information

Mass:	1274.63503
m/z:	638.32479
Charge:	2+
Retentiontime:	20.968715667724
Score:	241.1508
Mass Error [ppm]:	-0.29801
PEP:	3.2273E-32
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	73 %
Peak Coverage:	50 %
Protein Localisation:	42 ... 53

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	11				
-0.02	215.14	+0.0279	243.13	2	L	10	1146.6		1146.6	
	328.22	-0.038	356.22	3	I	9	1033.5	-0.003	517.26	+0.2171
	415.26		443.25	4	S	8	920.43	+0.0392	460.72	+0.1453
	529.3	-0.02	557.29	5	N	7	833.4	-0.026	833.4	
	600.34		628.33	6	A	6	719.36	+0.0231	719.36	
	687.37		715.36	7	S	5	648.32	+0.0103	648.32	
	802.39	-0.007	830.39	8	D	4	561.29	+0.0188	561.29	
	873.43	+0.3116	901.43	9	A	3	446.26	+0.0197	446.26	
	986.52	-0.091	1014.5	10	L	2	375.22	+0.1138	375.22	
	1101.5	-0.059	1129.5	11	D	1	262.14	-0.003	262.14	
				12	K	0	147.11		147.11	



Scan number	2768	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	112.02

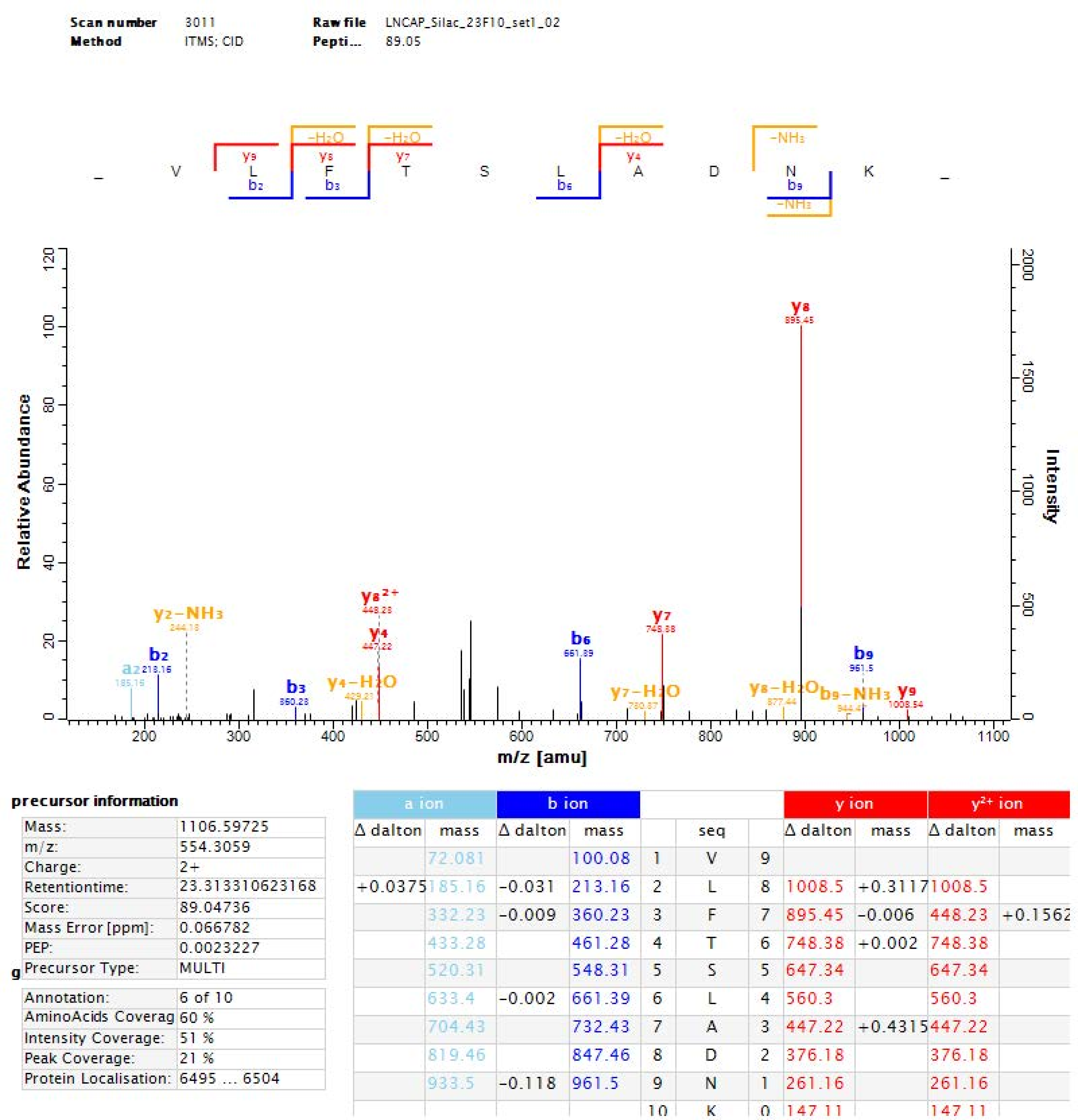
precursor information

Mass:	1336.69629
m/z:	669.35542
Charge:	2+
Retentiontime:	22.054607391357
Score:	112.0222
Mass Error [ppm]:	-1.7778
PEP:	4.4575E-06
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	38 %
Peak Coverage:	29 %
Protein Localisation:	110 ... 123

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	13				
	173.0921	2	T	12	1274.683		1274.683	
+0.075331	244.1292	3	A	11	1173.635		587.3213	-0.09134
+0.002588	315.1663	4	A	10	1102.598		1102.598	
+0.046479	462.2347	5	F	9	1031.561	-0.02158	516.2842	+0.120213
	549.2667	6	S	8	884.4927	+0.0569	884.4927	
+0.265224	663.3097	7	N	7	797.4607	-0.01428	797.4607	
	762.3781	8	V	6	683.4178		683.4178	
	819.3995	9	G	5	584.3494	-0.00279	584.3494	
	920.4472	10	T	4	527.3279	+0.032952	527.3279	
	991.4843	11	A	3	426.2802	-0.00372	426.2802	
+0.108236	1104.568	12	I	2	355.2431	+0.084419	355.2431	
-0.06063	1191.6	13	S	1	242.159	+0.074443	242.159	
		14	K	0	155.127		155.127	



Scan number	3011	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	89.05

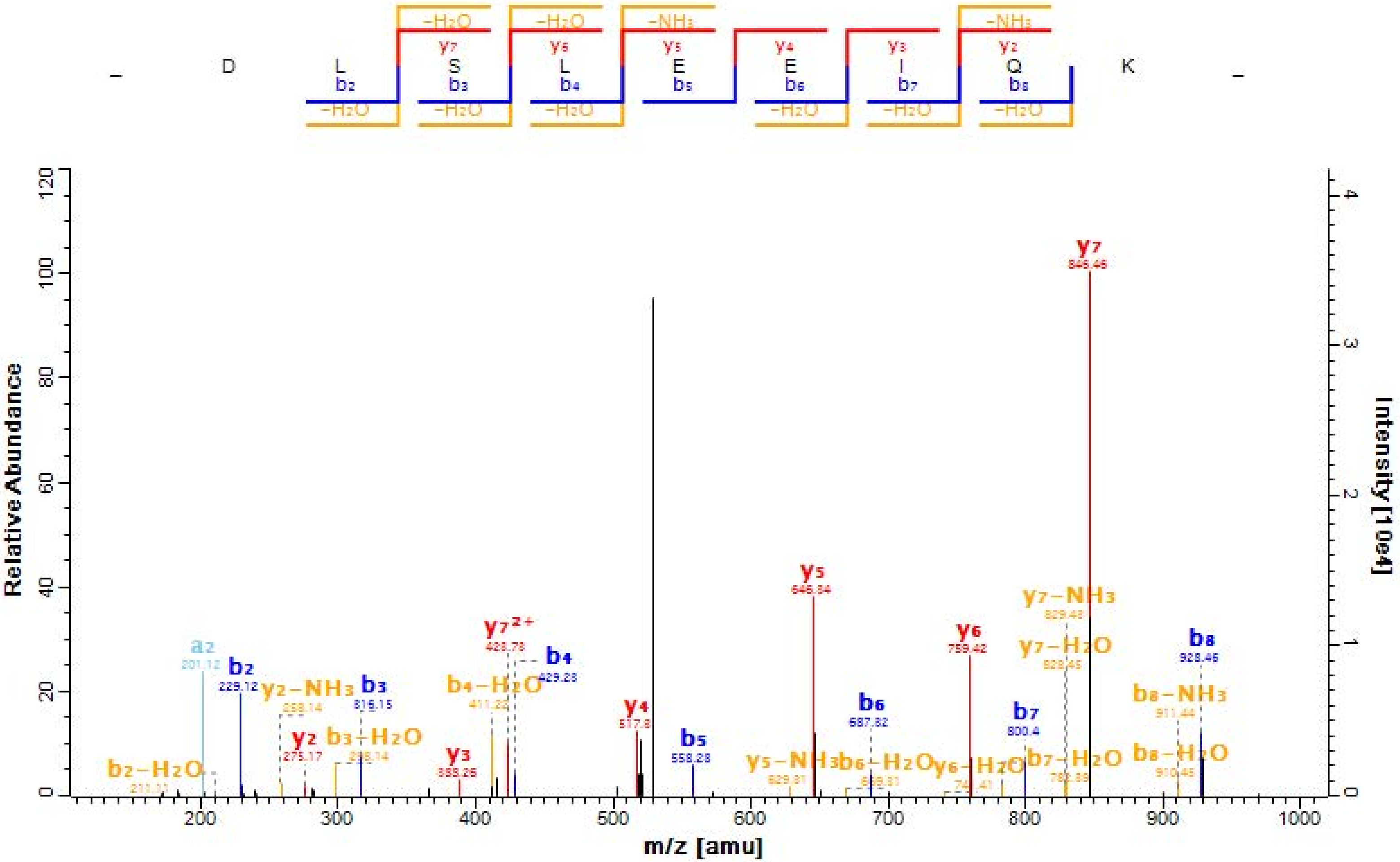
precursor information

Mass:	1106.59725
m/z:	554.3059
Charge:	2+
Retentiontime:	23.313310623168
Score:	89.04736
Mass Error [ppm]:	0.066782
PEP:	0.0023227
Precursor Type:	MULTI

Annotation:	6 of 10
AminoAcids Coverag	60 %
Intensity Coverage:	51 %
Peak Coverage:	21 %
Protein Localisation:	6495 ... 6504

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.081		100.08	1	V	9				
+0.0375	185.16	-0.031	213.16	2	L	8	1008.5	+0.3117	1008.5	
	332.23	-0.009	360.23	3	F	7	895.45	-0.006	448.23	+0.1562
	433.28		461.28	4	T	6	748.38	+0.002	748.38	
	520.31		548.31	5	S	5	647.34		647.34	
	633.4	-0.002	661.39	6	L	4	560.3		560.3	
	704.43		732.43	7	A	3	447.22	+0.4315	447.22	
	819.46		847.46	8	D	2	376.18		376.18	
	933.5	-0.118	961.5	9	N	1	261.16		261.16	
				10	K	0	147.11		147.11	

Scan number	3258	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	217.64

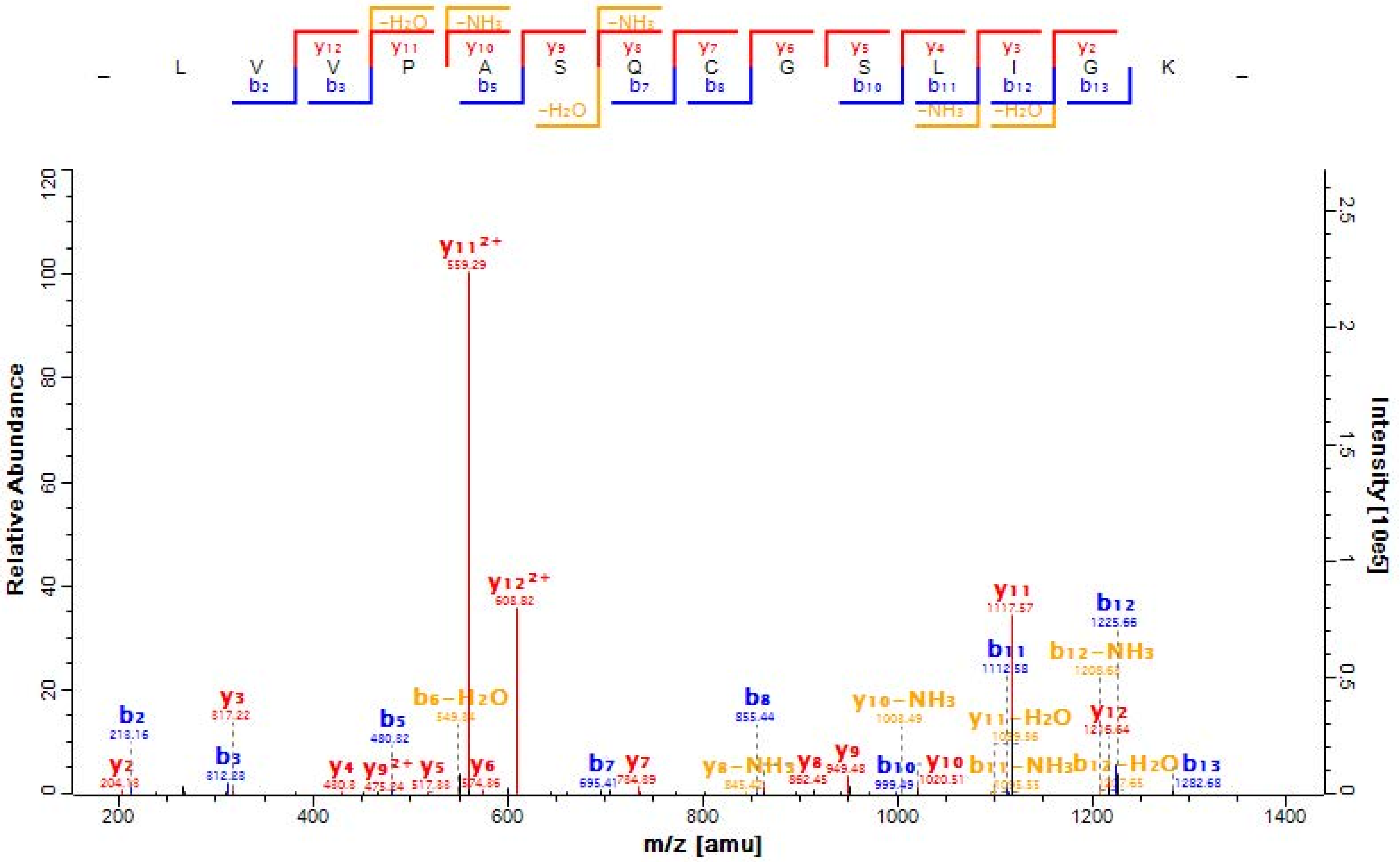


precursor information

Mass:	1073.56049
m/z:	537.78752
Charge:	2+
Retentiontime:	24.614988327026
Score:	217.641
Mass Error [ppm]:	0.034209
PEP:	9.9135E-19
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	61 %
Peak Coverage:	41 %
Protein Localisation:	44 ... 52

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	8				
+0.03	201.12	-0.104	229.12	2	L	7	959.54		959.54	
	288.16	+0.0795	316.15	3	S	6	846.46	+0.0337	423.73	+0.212
	401.24	+0.0296	429.23	4	L	5	759.42	+0.0073	759.42	
	530.28	+0.0966	558.28	5	E	4	646.34	+0.0512	646.34	
	659.32	+0.0314	687.32	6	E	3	517.3	+0.0414	517.3	
	772.41	-0.104	800.4	7	I	2	388.26	+0.1101	388.26	
	900.47	-0.128	928.46	8	Q	1	275.17	+0.0803	275.17	
				9	K	0	147.11		147.11	

Scan number	3399	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	162.94



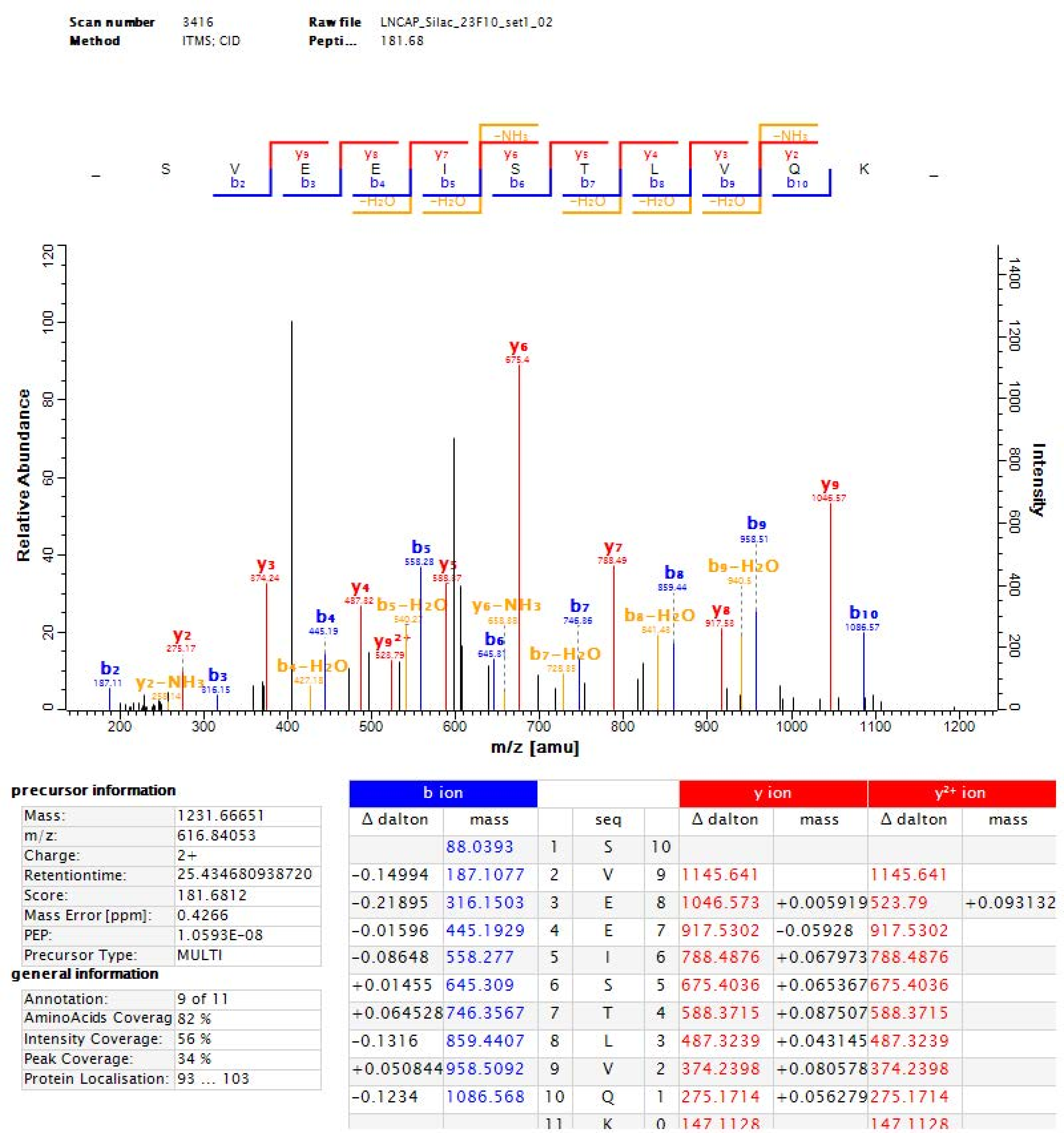
precursor information

Mass:	1427.78068
m/z:	714.89762
Charge:	2+
Retentiontime:	25.347267150878
Score:	162.9437
Mass Error [ppm]:	0.031923
PEP:	1.1644E-10
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	85 %
Peak Coverage:	40 %
Protein Localisation:	102 ... 115

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	13				
-0.04409	213.1598	2	V	12	1315.704		1315.704	
-0.01717	312.2282	3	V	11	1216.635	-0.08551	608.8214	+0.197871
	409.2809	4	P	10	1117.567	-3.1E-06	559.2871	+0.178611
+0.079659	480.318	5	A	9	1020.514	+0.031948	1020.514	
	567.3501	6	S	8	949.4771	-0.01858	475.2422	+0.402017
+0.345376	695.4087	7	Q	7	862.4451	+0.029679	862.4451	
+0.073945	855.4393	8	C	6	734.3865	+0.093322	734.3865	
	912.4608	9	G	5	574.3559	+0.020089	574.3559	
+0.027899	999.4928	10	S	4	517.3344	-7.4E-05	517.3344	
-0.0688	1112.577	11	L	3	430.3024	+0.177707	430.3024	
-0.12247	1225.661	12	I	2	317.2183	-0.02039	317.2183	
-0.08705	1282.682	13	G	1	204.1343	+0.111093	204.1343	
		14	K	0	147.1128		147.1128	



Scan number	3416	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	181.68

precursor information

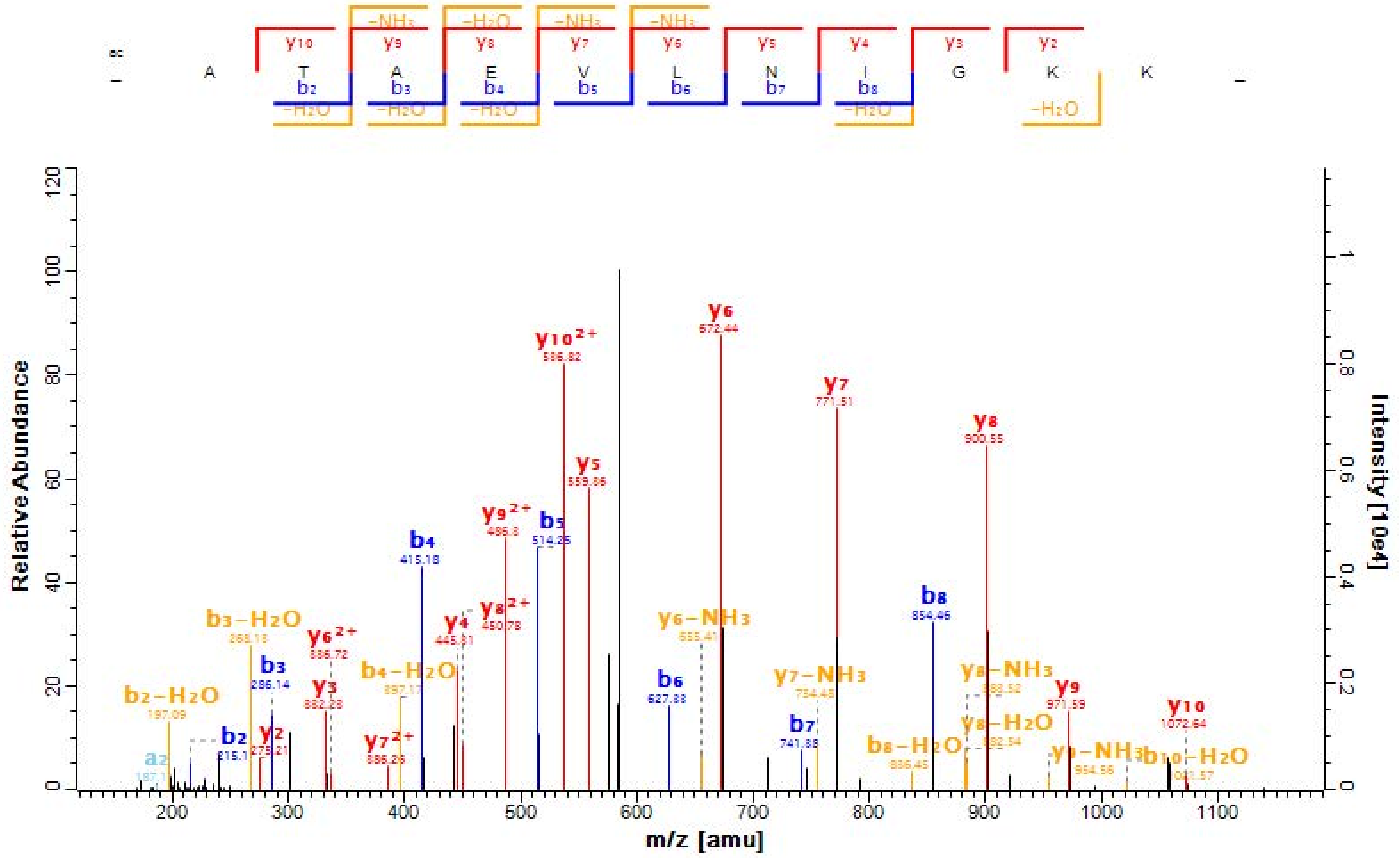
Mass:	1231.66651
m/z:	616.84053
Charge:	2+
Retentiontime:	25.434680938720
Score:	181.6812
Mass Error [ppm]:	0.4266
PEP:	1.0593E-08
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	56 %
Peak Coverage:	34 %
Protein Localisation:	93 ... 103

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	10				
-0.14994	187.1077	2	V	9	1145.641		1145.641	
-0.21895	316.1503	3	E	8	1046.573	+0.005919	523.79	+0.093132
-0.01596	445.1929	4	E	7	917.5302	-0.05928	917.5302	
-0.08648	558.277	5	I	6	788.4876	+0.067973	788.4876	
+0.01455	645.309	6	S	5	675.4036	+0.065367	675.4036	
+0.064528	746.3567	7	T	4	588.3715	+0.087507	588.3715	
-0.1316	859.4407	8	L	3	487.3239	+0.043145	487.3239	
+0.050844	958.5092	9	V	2	374.2398	+0.080578	374.2398	
-0.1234	1086.568	10	Q	1	275.1714	+0.056279	275.1714	
		11	K	0	147.1128		147.1128	

Scan number	3689	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	240.1



precursor information

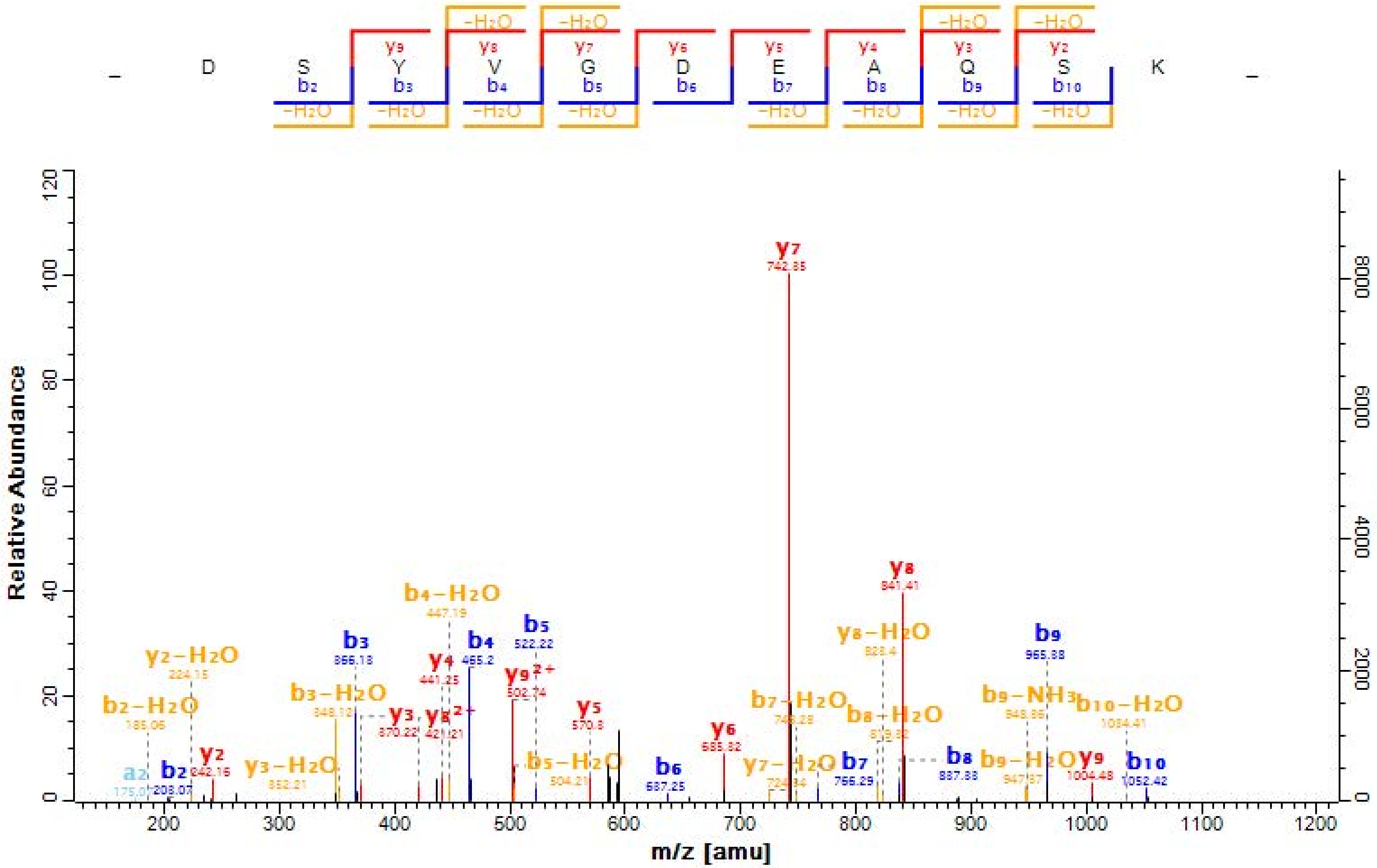
Mass:	1184.6767
m/z:	593.34562
Charge:	2+
Retentiontime:	26.816455841064
Score:	240.0957
Mass Error [ppm]:	0.17517
PEP:	7.3412E-29
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	68 %
Peak Coverage:	36 %
Protein Localisation:	2 ... 12

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.06		114.05	1	A	10				
+0.0117	187.11	+0.1103	215.1	2	T	9	1072.6	−0.029	536.82	+0.2537
	258.14	−0.106	286.14	3	A	8	971.59	+0.0506	486.3	+0.2315
	387.19	−0.049	415.18	4	E	7	900.55	+0.0336	450.78	−0.003
	486.26	−0.108	514.25	5	V	6	771.51	+0.0047	386.26	+0.212
	599.34	+0.0023	627.33	6	L	5	672.44	+0.0344	336.72	−0.034
	713.38	−0.001	741.38	7	N	4	559.36	+0.0951	559.36	
	826.47	−0.023	854.46	8	I	3	445.31	+0.1041	445.31	
	883.49		911.48	9	G	2	332.23	+0.0849	332.23	
	1011.6		1039.6	10	K	1	275.21	+0.0628	275.21	
				11	K	0	147.11		147.11	

Scan number	375	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	250.7



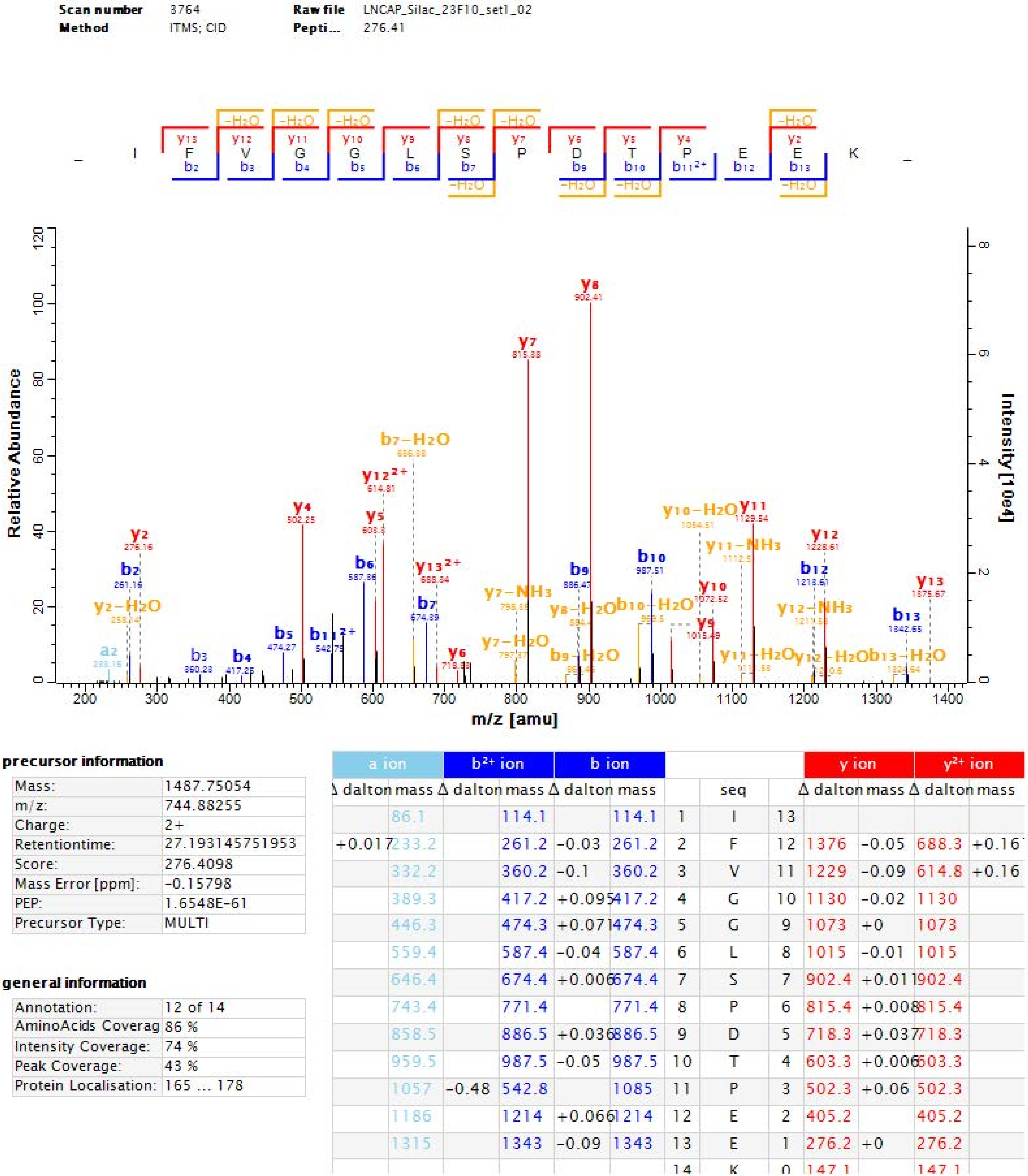
precursor information

Mass:	1197.51516
m/z:	599.76486
Charge:	2+
Retentiontime:	7.3600916862487
Score:	250.6963
Mass Error [ppm]:	0.16632
PEP:	3.0267E-38
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	76 %
Peak Coverage:	40 %
Protein Localisation:	51 ... 61

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	10				
+0.0378	175.07	-0.034	203.07	2	S	9	1091.5		1091.5	
	338.13	-0.069	366.13	3	Y	8	1004.5	+0.0074	502.74	+0.0602
	437.2	-0.059	465.2	4	V	7	841.41	-0.054	421.21	+0.0209
	494.22	-0.035	522.22	5	G	6	742.35	-0.043	742.35	
	609.25	+0.113	637.25	6	D	5	685.32	-0.036	685.32	
	738.29	+0.0944	766.29	7	E	4	570.3	-0.04	570.3	
	809.33	-0.032	837.33	8	A	3	441.25	+0.0924	441.25	
	937.39	+0.0283	965.38	9	Q	2	370.22	+0.0387	370.22	
	1024.4	-0.105	1052.4	10	S	1	242.16	+0.0234	242.16	
				11	K	0	155.13		155.13	



Scan number	3764	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	276.41

precursor information

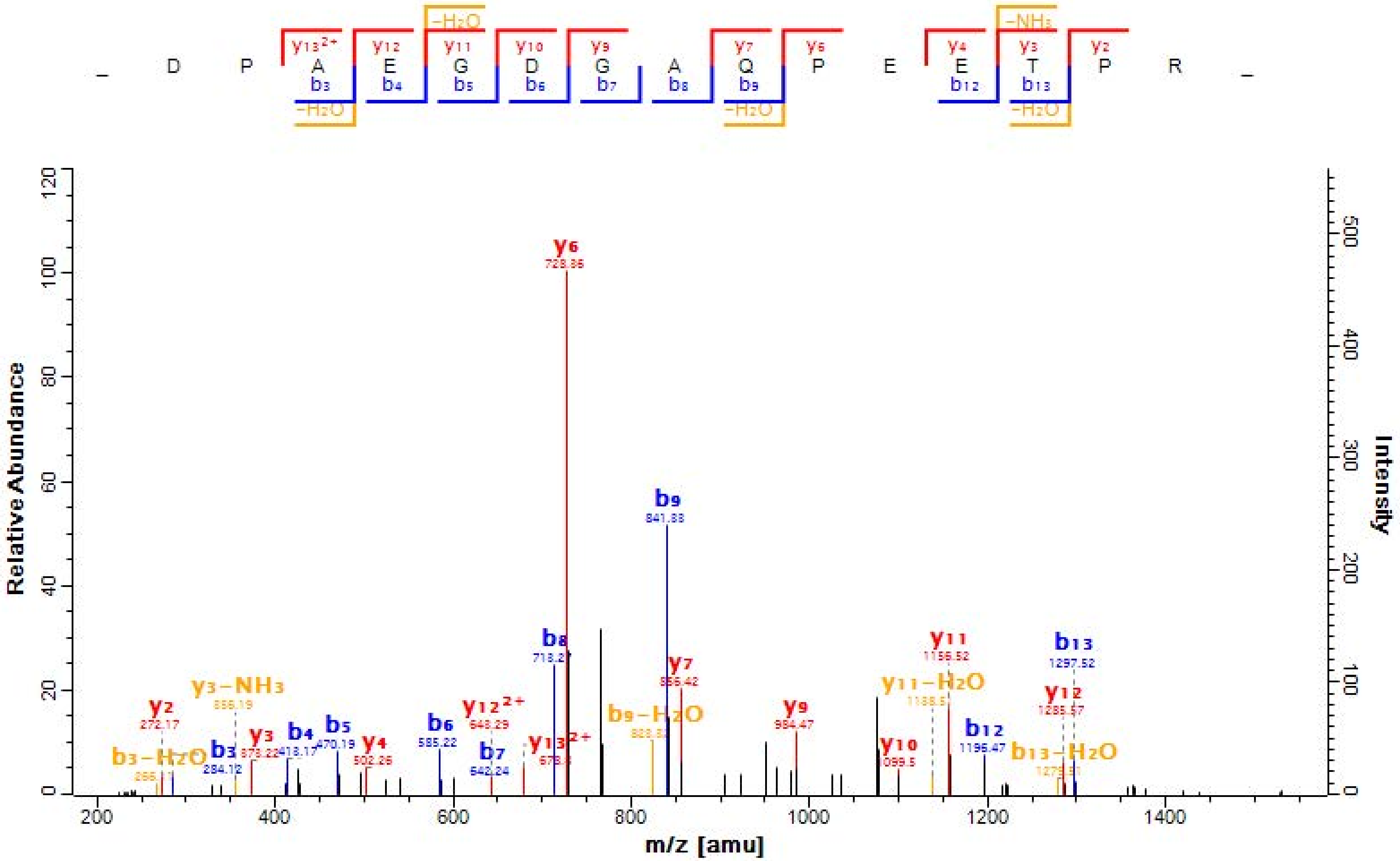
Mass:	1487.75054
m/z:	744.88255
Charge:	2+
Retentiontime:	27.193145751953
Score:	276.4098
Mass Error [ppm]:	-0.15798
PEP:	1.6548E-61
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	74 %
Peak Coverage:	43 %
Protein Localisation:	165 ... 178

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	I	13				
+0.017	233.2		261.2	-0.03	261.2	2	F	12	1376	-0.05	688.3	+0.16
	332.2		360.2	-0.1	360.2	3	V	11	1229	-0.09	614.8	+0.16
	389.3		417.2	+0.095	417.2	4	G	10	1130	-0.02	1130	
	446.3		474.3	+0.071	474.3	5	G	9	1073	+0	1073	
	559.4		587.4	-0.04	587.4	6	L	8	1015	-0.01	1015	
	646.4		674.4	+0.006	674.4	7	S	7	902.4	+0.011	902.4	
	743.4		771.4		771.4	8	P	6	815.4	+0.008	815.4	
	858.5		886.5	+0.036	886.5	9	D	5	718.3	+0.037	718.3	
	959.5		987.5	-0.05	987.5	10	T	4	603.3	+0.006	603.3	
	1057	-0.48	542.8		1085	11	P	3	502.3	+0.06	502.3	
	1186		1214	+0.066	1214	12	E	2	405.2		405.2	
	1315		1343	-0.09	1343	13	E	1	276.2	+0	276.2	
						14	K	0	147.1		147.1	

Scan number	385	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	154.6



precursor information

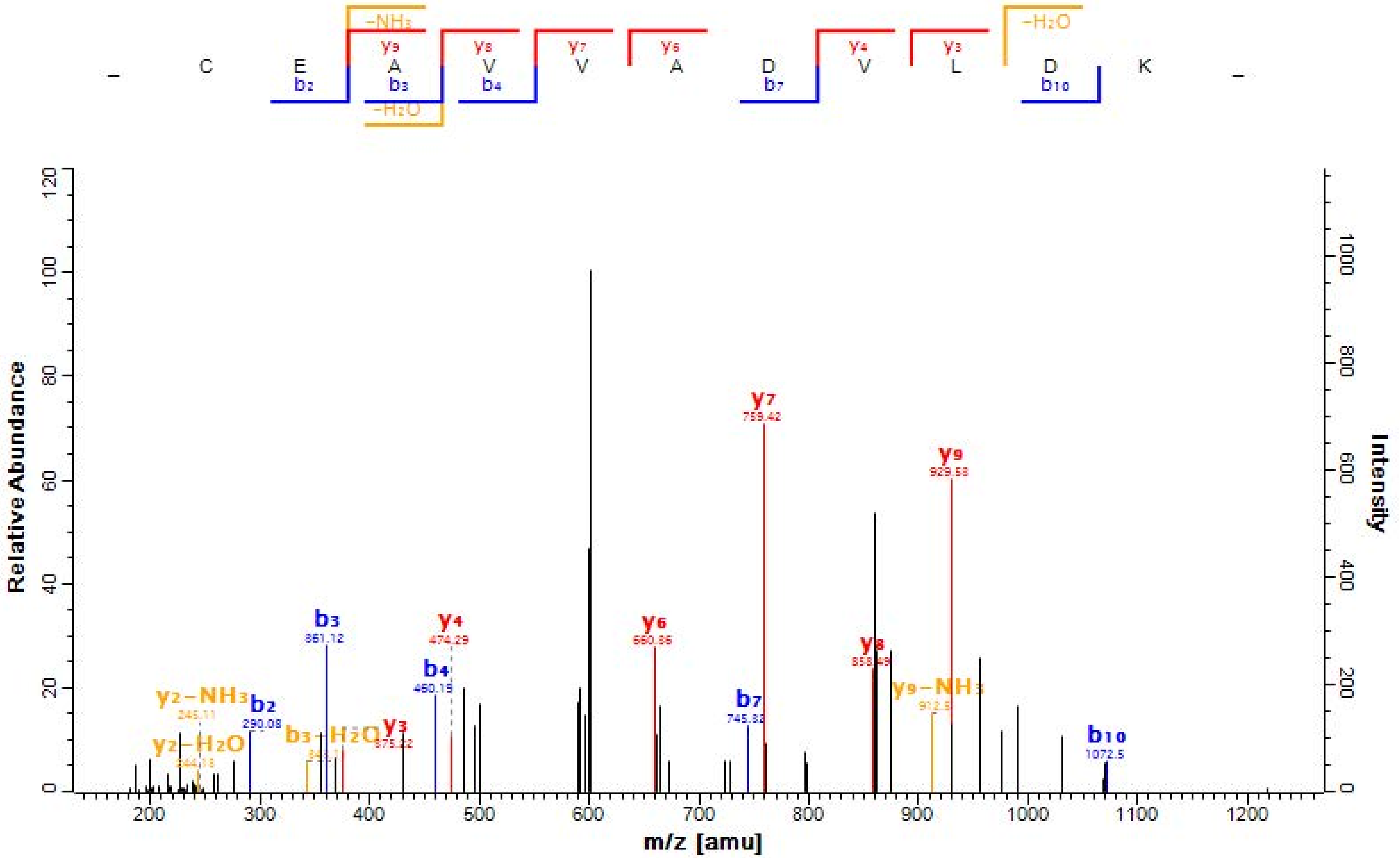
Mass:	1567.67587
m/z:	784.84521
Charge:	2+
Retentiontime:	7.4568734169006
Score:	154.5955
Mass Error [ppm]:	0.52977
PEP:	4.6845E-14
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	55 %
Peak Coverage:	31 %
Protein Localisation:	243 ... 257

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342	1	D	14				
	213.087	2	P	13	1453.655		1453.655	
+0.164111	284.1241	3	A	12	1356.603		678.8049	+0.153368
-0.04419	413.1667	4	E	11	1285.565	-0.0904	643.2864	+0.189259
+0.066607	470.1882	5	G	10	1156.523	+0.001752	1156.523	
+0.111624	585.2151	6	D	9	1099.501	+0.126487	1099.501	
+0.077953	642.2366	7	G	8	984.4745	+0.008105	984.4745	
-0.03948	713.2737	8	A	7	927.453		927.453	
+0.044884	841.3323	9	Q	6	856.4159	-0.01333	856.4159	
	938.385	10	P	5	728.3573	+0.002885	728.3573	
	1067.428	11	E	4	631.3046		631.3046	
-0.0205	1196.47	12	E	3	502.262	+0.069311	502.262	
+0.032901	1297.518	13	T	2	373.2194	+0.058132	373.2194	
	1394.571	14	P	1	272.1717	-0.04092	272.1717	
		15	R	0	175.119		175.119	

Scan number	3885	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	57.17



precursor information

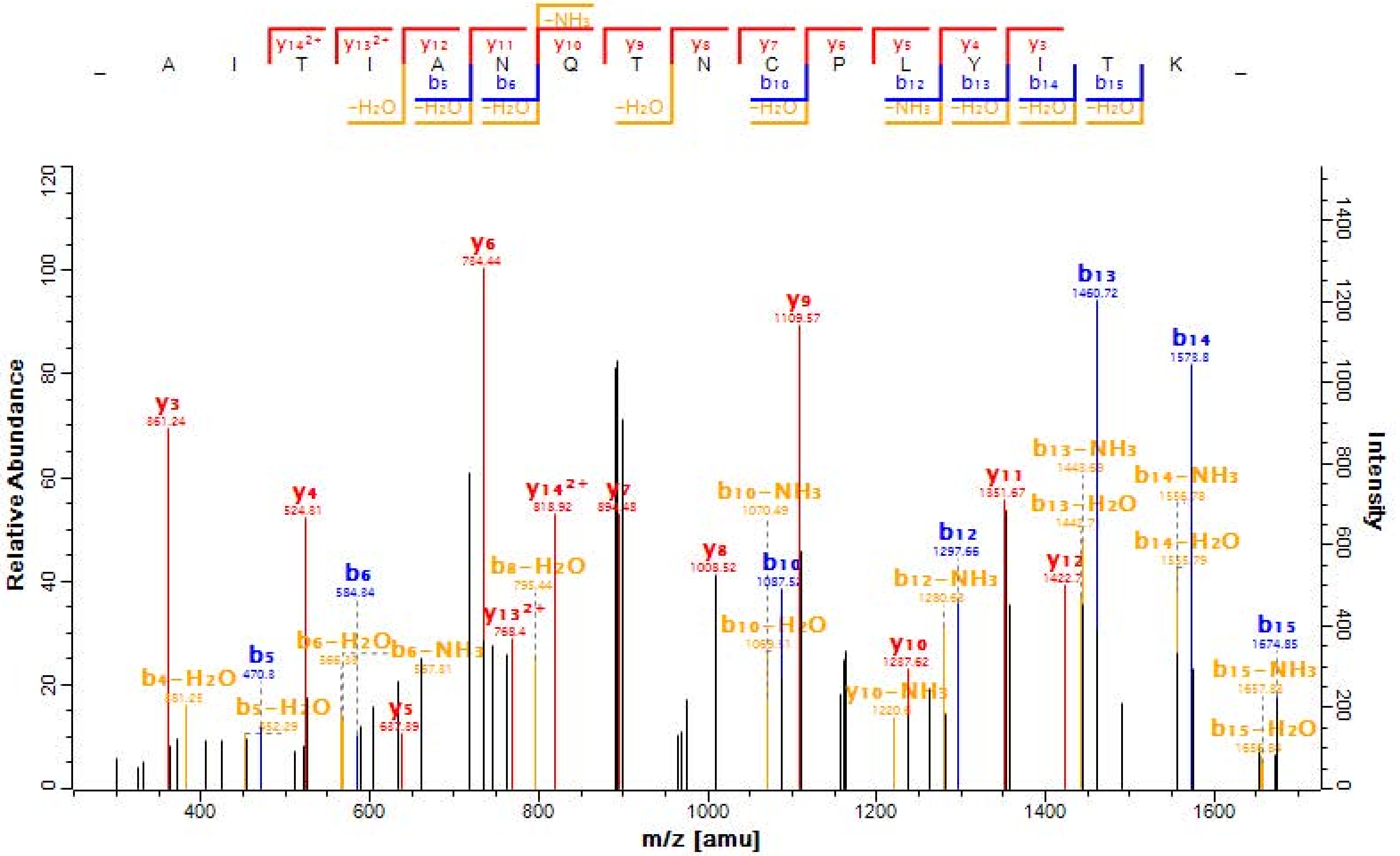
Mass:	1217.59724
m/z:	609.8059
Charge:	2+
Retentiontime:	27.816537857055
Score:	57.17472
Mass Error [ppm]:	0.86365
PEP:	0.016341
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	32 %
Peak Coverage:	18 %
Protein Localisation:	425 ... 435

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	161.037924668	1	C	10		
+0.019824	290.080517764	2	E	9	1058.57281664	
-0.0033127	361.117631552	3	A	8	929.530223539	-0.0572621
+0.1117451	460.186045468	4	V	7	858.493109751	+0.1469659
	559.254459384	5	V	6	759.424695835	+0.1183339
	630.291573172	6	A	5	660.356281919	+0.0604051
+0.0157733	745.318516204	7	D	4	589.319168131	
	844.38693012	8	V	3	474.292225099	+0.0782583
	957.470994101	9	L	2	375.223811183	+0.1853075
-0.0284547	1072.49793713	10	D	1	262.139747203	
		11	K	0	147.112804171	

Scan number	4541	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	174.39



precursor information

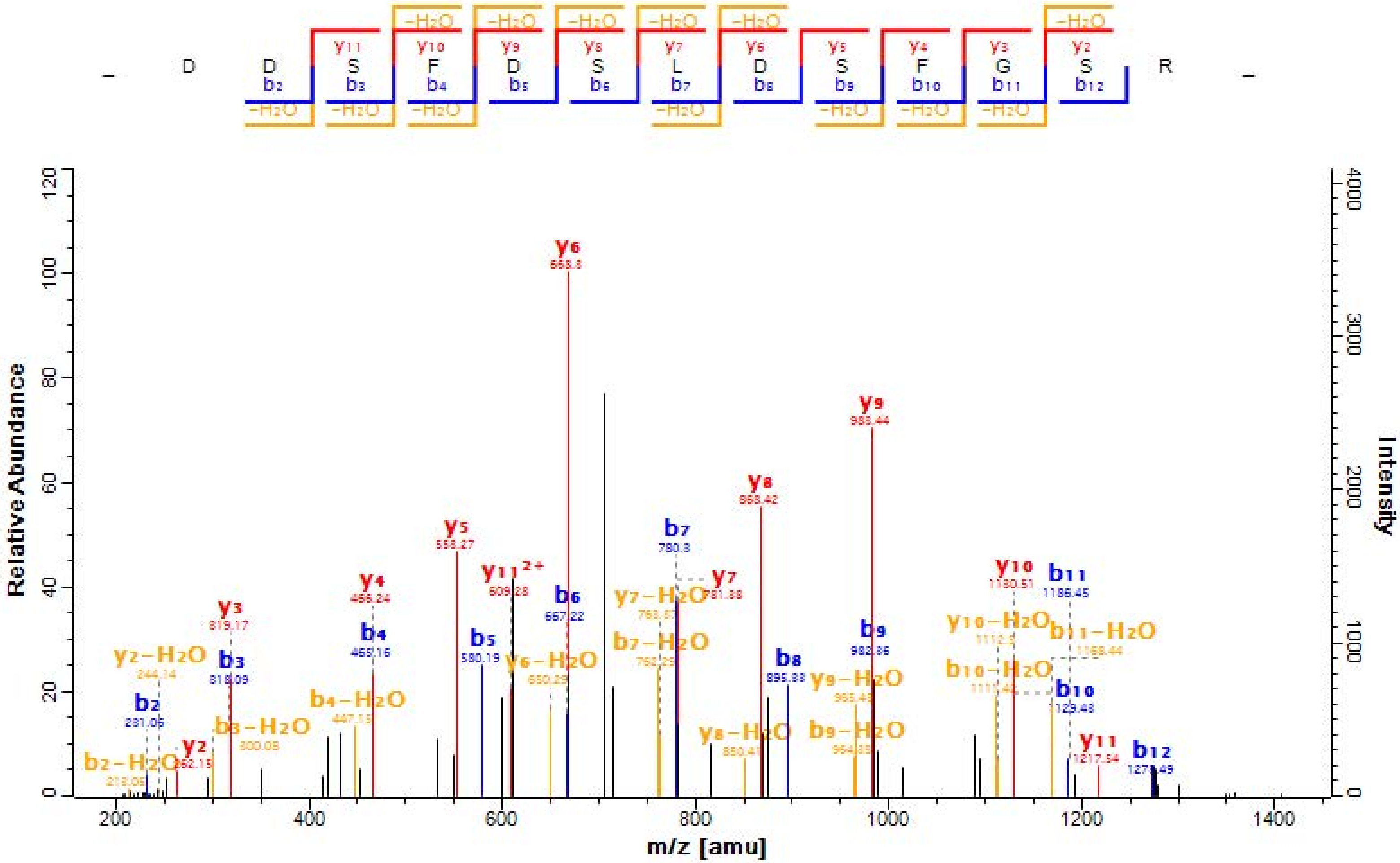
Mass:	1819.95068
m/z:	910.98262
Charge:	2+
Retentiontime:	31.232454299926
Score:	174.3949
Mass Error [ppm]:	0.25477
PEP:	1.7665E-22
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	51 %
Peak Coverage:	41 %
Protein Localisation:	239 ... 254

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	15				
	185.1285	2	I	14	1749.92		1749.92	
	286.1761	3	T	13	1636.836		818.9218	+0.250932
	399.2602	4	I	12	1535.789		768.398	+0.080557
−0.01728	470.2973	5	A	11	1422.705	−0.07128	1422.705	
−0.37887	584.3402	6	N	10	1351.667	+0.032611	1351.667	
	712.3988	7	Q	9	1237.625	−0.03603	1237.625	
	813.4465	8	T	8	1109.566	−0.00639	1109.566	
	927.4894	9	N	7	1008.518	−0.05075	1008.518	
+0.091014	1087.52	10	C	6	894.4754	+0.009939	894.4754	
	1184.573	11	P	5	734.4447	+0.080749	734.4447	
−0.10624	1297.657	12	L	4	637.3919	+0.059782	637.3919	
−0.19935	1460.72	13	Y	3	524.3079	−0.10737	524.3079	
−0.10373	1573.804	14	I	2	361.2445	+0.125662	361.2445	
−0.23258	1674.852	15	T	1	248.1605		248.1605	
		16	K	0	147.1128		147.1128	

Scan number	4913	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	227.06



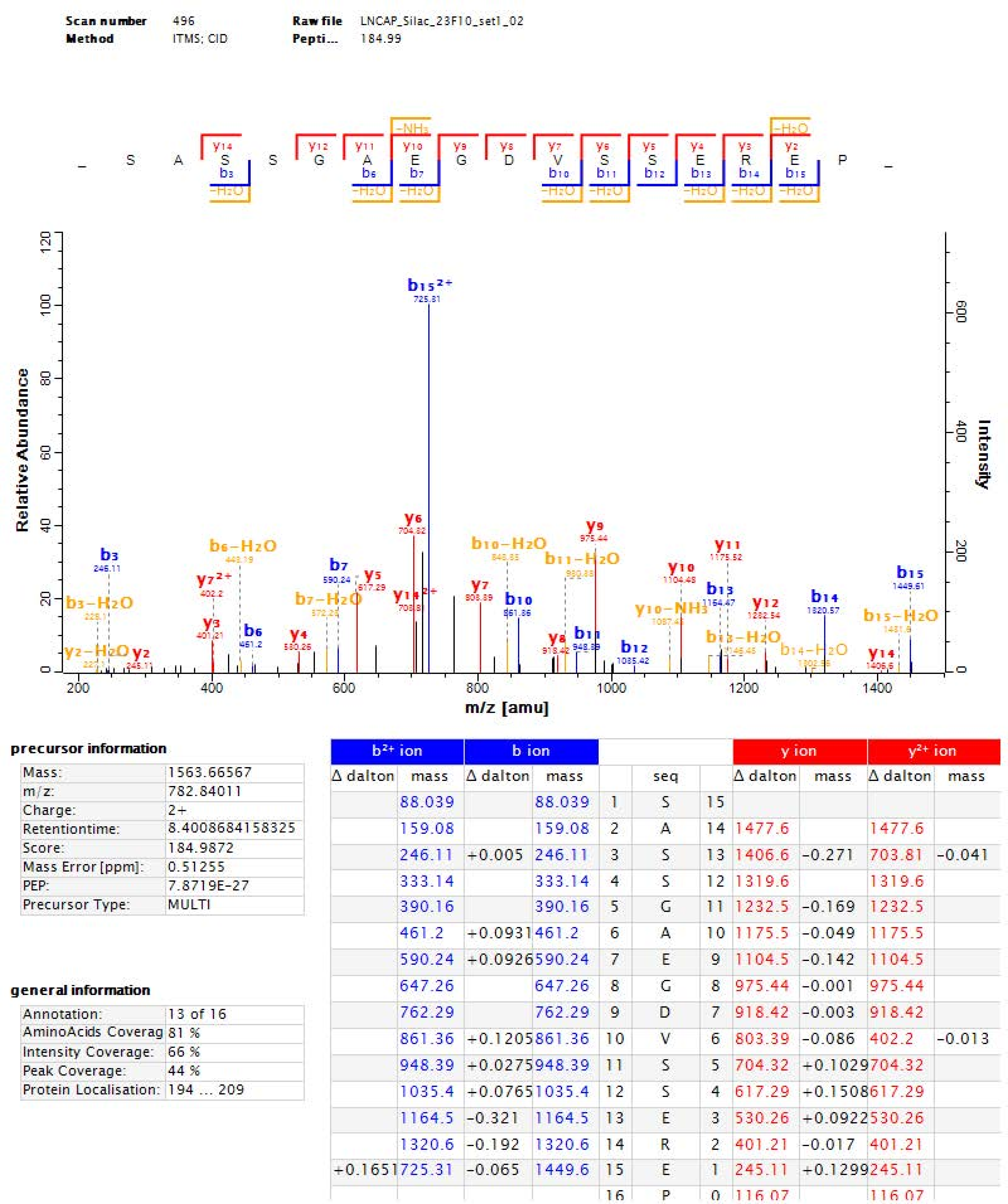
precursor information

Mass:	1446.58998
m/z:	724.30227
Charge:	2+
Retentiontime:	33.163055419921
Score:	227.0594
Mass Error [ppm]:	0.045372
PEP:	9.2468E-29
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	65 %
Peak Coverage:	43 %
Protein Localisation:	199 ... 211

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342	1	D	12				
-0.05674	231.0612	2	D	11	1332.57		1332.57	
+0.390635	318.0932	3	S	10	1217.543	-0.09983	609.2753	-0.06881
-0.07164	465.1616	4	F	9	1130.511	+0.001172	1130.511	
+0.019582	580.1885	5	D	8	983.4429	-0.00518	983.4429	
+0.070317	667.2206	6	S	7	868.4159	+0.017855	868.4159	
+0.00908	780.3046	7	L	6	781.3839	+0.064654	781.3839	
-0.09159	895.3316	8	D	5	668.2998	+0.069616	668.2998	
+0.073217	982.3636	9	S	4	553.2729	+0.150575	553.2729	
-0.10976	1129.432	10	F	3	466.2409	+0.047167	466.2409	
-0.15442	1186.453	11	G	2	319.1724	+0.149638	319.1724	
+0.059038	1273.486	12	S	1	262.151	+0.211568	262.151	
		13	R	0	175.119		175.119	



Scan number	496	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	184.99

precursor information

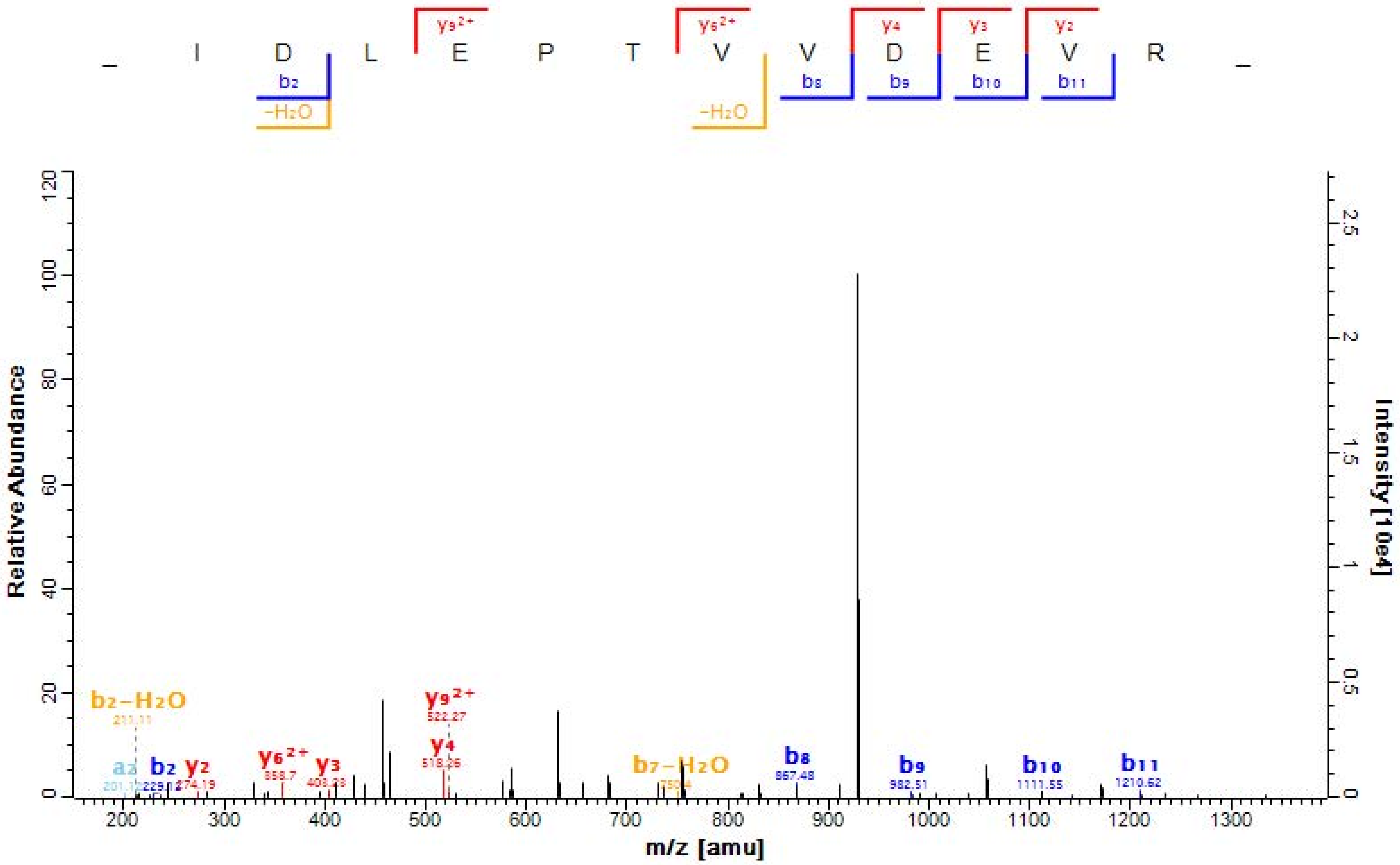
Mass:	1563.66567
m/z:	782.84011
Charge:	2+
Retentiontime:	8.4008684158325
Score:	184.9872
Mass Error [ppm]:	0.51255
PEP:	7.8719E-27
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	66 %
Peak Coverage:	44 %
Protein Localisation:	194 ... 209

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	15				
	159.08		159.08	2	A	14	1477.6		1477.6	
	246.11	+0.005	246.11	3	S	13	1406.6	-0.271	703.81	-0.041
	333.14		333.14	4	S	12	1319.6		1319.6	
	390.16		390.16	5	G	11	1232.5	-0.169	1232.5	
	461.2	+0.0931	461.2	6	A	10	1175.5	-0.049	1175.5	
	590.24	+0.0926	590.24	7	E	9	1104.5	-0.142	1104.5	
	647.26		647.26	8	G	8	975.44	-0.001	975.44	
	762.29		762.29	9	D	7	918.42	-0.003	918.42	
	861.36	+0.1205	861.36	10	V	6	803.39	-0.086	402.2	-0.013
	948.39	+0.0275	948.39	11	S	5	704.32	+0.1029	704.32	
	1035.4	+0.0765	1035.4	12	S	4	617.29	+0.1508	617.29	
	1164.5	-0.321	1164.5	13	E	3	530.26	+0.0922	530.26	
	1320.6	-0.192	1320.6	14	R	2	401.21	-0.017	401.21	
+0.1651	725.31	-0.065	1449.6	15	E	1	245.11	+0.1299	245.11	
				16	P	0	116.07		116.07	

Scan number	5048	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	56.23



precursor information

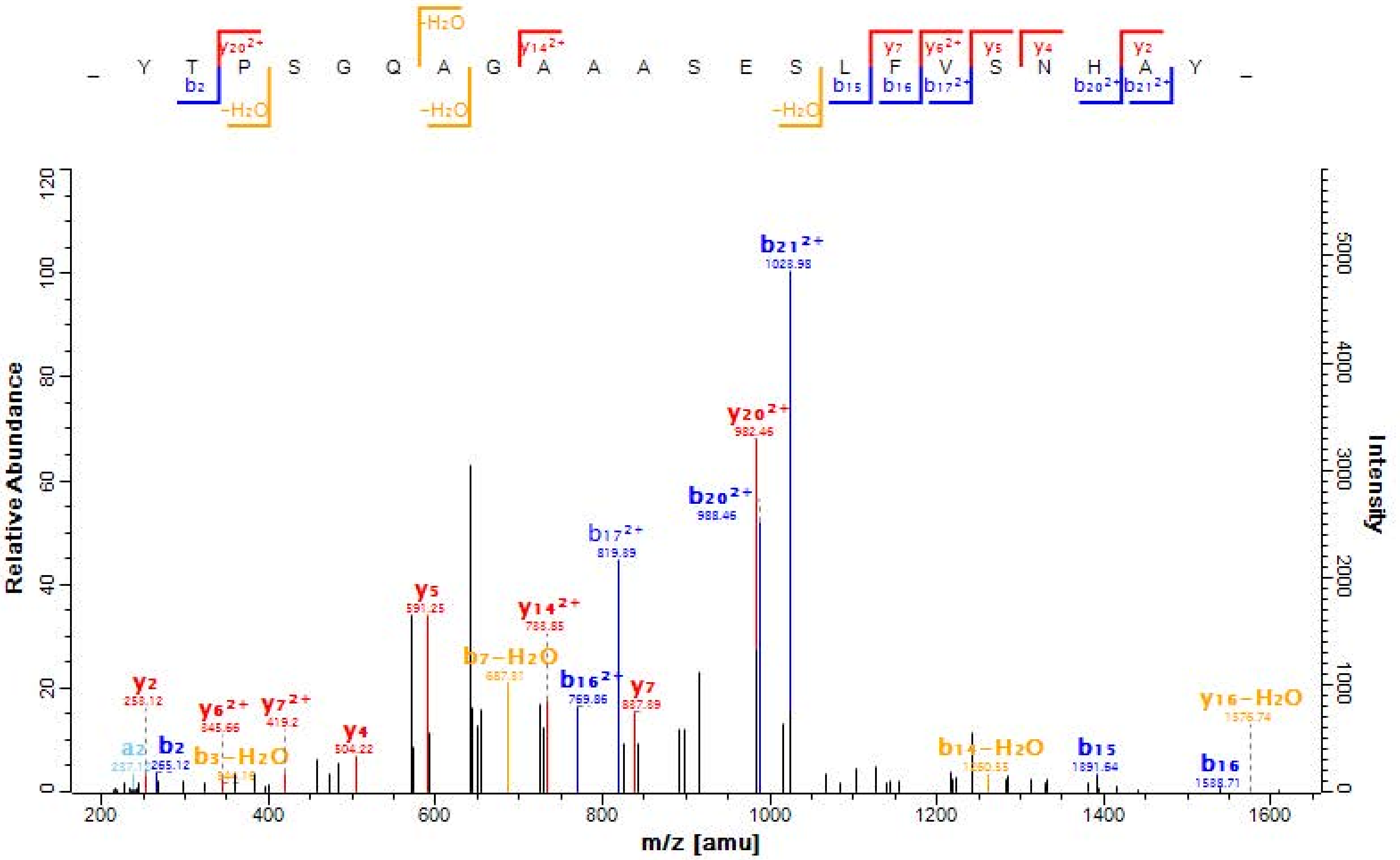
Mass:	1383.72505
m/z:	692.8698
Charge:	2+
Retentiontime:	33.844264984130
Score:	56.22507
Mass Error [ppm]:	0.35218
PEP:	0.014011
Precursor Type:	MULTI

general information

Annotation:	7 of 12
AminoAcids Coverag	58 %
Intensity Coverage:	7 %
Peak Coverage:	15 %
Protein Localisation:	92 ... 103

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	11				
-0.02	201.12	-0.038	229.12	2	D	10	1271.6		1271.6	
	314.21		342.2	3	L	9	1156.6		1156.6	
	443.25		471.24	4	E	8	1043.5		522.27	+0.3865
	540.3		568.3	5	P	7	914.49		914.49	
	641.35		669.35	6	T	6	817.44		817.44	
	740.42		768.41	7	V	5	716.39		358.7	-0.486
	839.49	+0.0007	867.48	8	V	4	617.33		617.33	
	954.51	-0.131	982.51	9	D	3	518.26	+0.0847	518.26	
	1083.6	-0.28	1111.6	10	E	2	403.23	+0.0801	403.23	
	1182.6	-0.057	1210.6	11	V	1	274.19	-0.084	274.19	
				12	R	0	175.12		175.12	

Scan number	5184	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	75.24



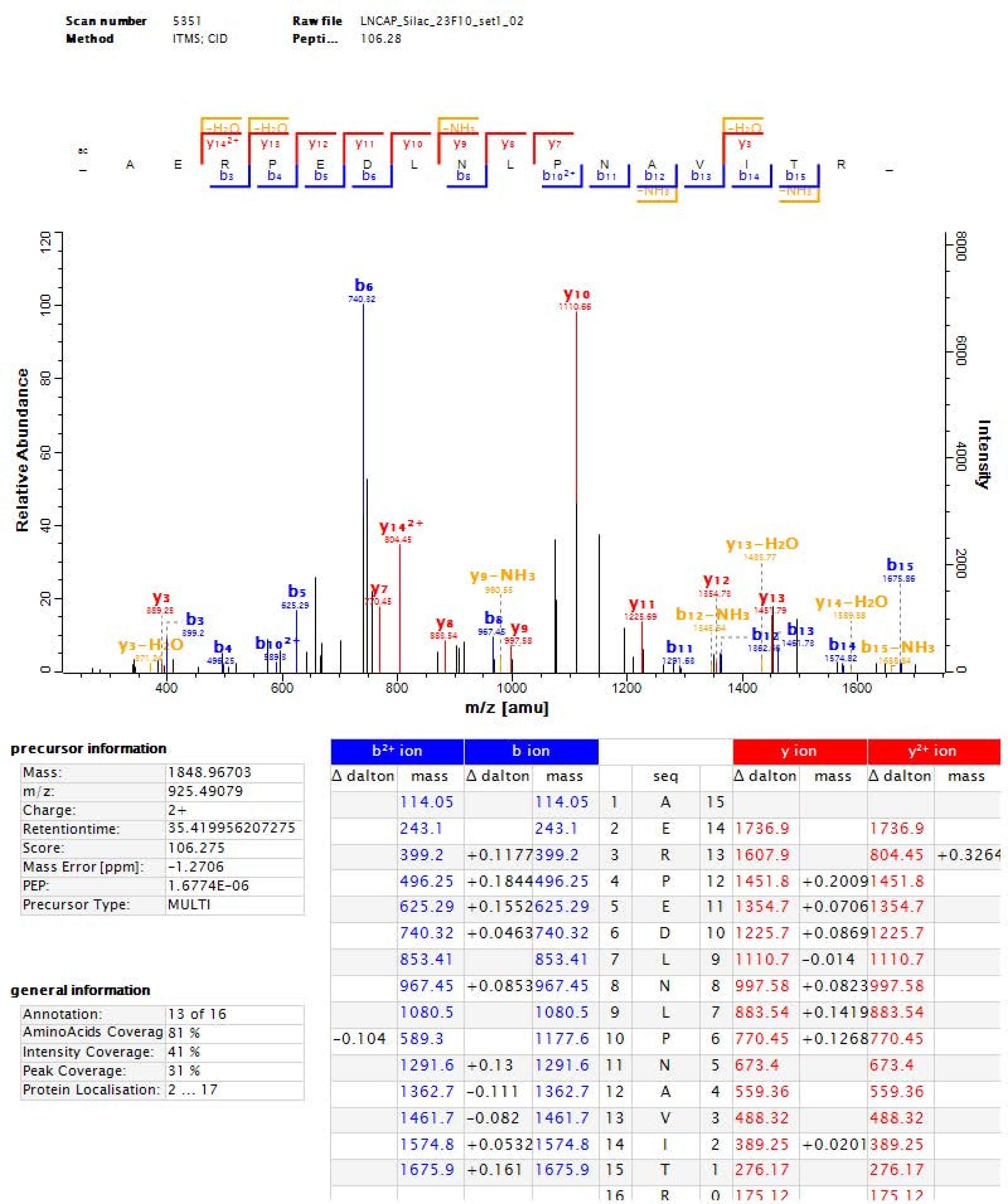
precursor information

Mass:	2227.01847
m/z:	743.34677
Charge:	3+
Retentiontime:	34.569225311279
Score:	75.23901
Mass Error [ppm]:	0.13077
PEP:	0.0020916
Precursor Type:	ISO

general information

Annotation:	12 of 22
AminoAcids Coverag	55 %
Intensity Coverage:	48 %
Peak Coverage:	23 %
Protein Localisation:	397 ... 418

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.1		164.1		164.1	1	Y	21				
+0.023	237.1		265.1	-0.12	265.1	2	T	20	2065		2065	
	334.2		362.2		362.2	3	P	19	1964		982.5	+0.20
	421.2		449.2		449.2	4	S	18	1867		1867	
	478.2		506.2		506.2	5	G	17	1780		1780	
	606.3		634.3		634.3	6	Q	16	1723		1723	
	677.3		705.3		705.3	7	A	15	1595		1595	
	734.3		762.3		762.3	8	G	14	1524		1524	
	805.4		833.4		833.4	9	A	13	1467		733.8	-0.15
	876.4		904.4		904.4	10	A	12	1396		1396	
	947.5		975.5		975.5	11	A	11	1325		1325	
	1034		1062		1062	12	S	10	1254		1254	
	1164		1192		1192	13	E	9	1167		1167	
	1251		1279		1279	14	S	8	1038		1038	
	1364		1392	+0.067	1392	15	L	7	950.5		950.5	
	1511	-0.01	769.9	-0.15	1539	16	F	6	837.4	+0.048	419.2	+0.20
	1610	+0.292	819.4		1638	17	V	5	690.3		345.7	-0.23
	1697		1725		1725	18	S	4	591.3	+0.112	591.3	
	1811		1839		1839	19	N	3	504.2	-0.02	504.2	
	1948	+0.317	988.5		1976	20	H	2	390.2		390.2	
	2019	+0.222	1024		2047	21	A	1	253.1	-0.06	253.1	
						22	Y	0	182.1		182.1	



Scan number 5351
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set1_02
Pepti... 106.28

precursor information

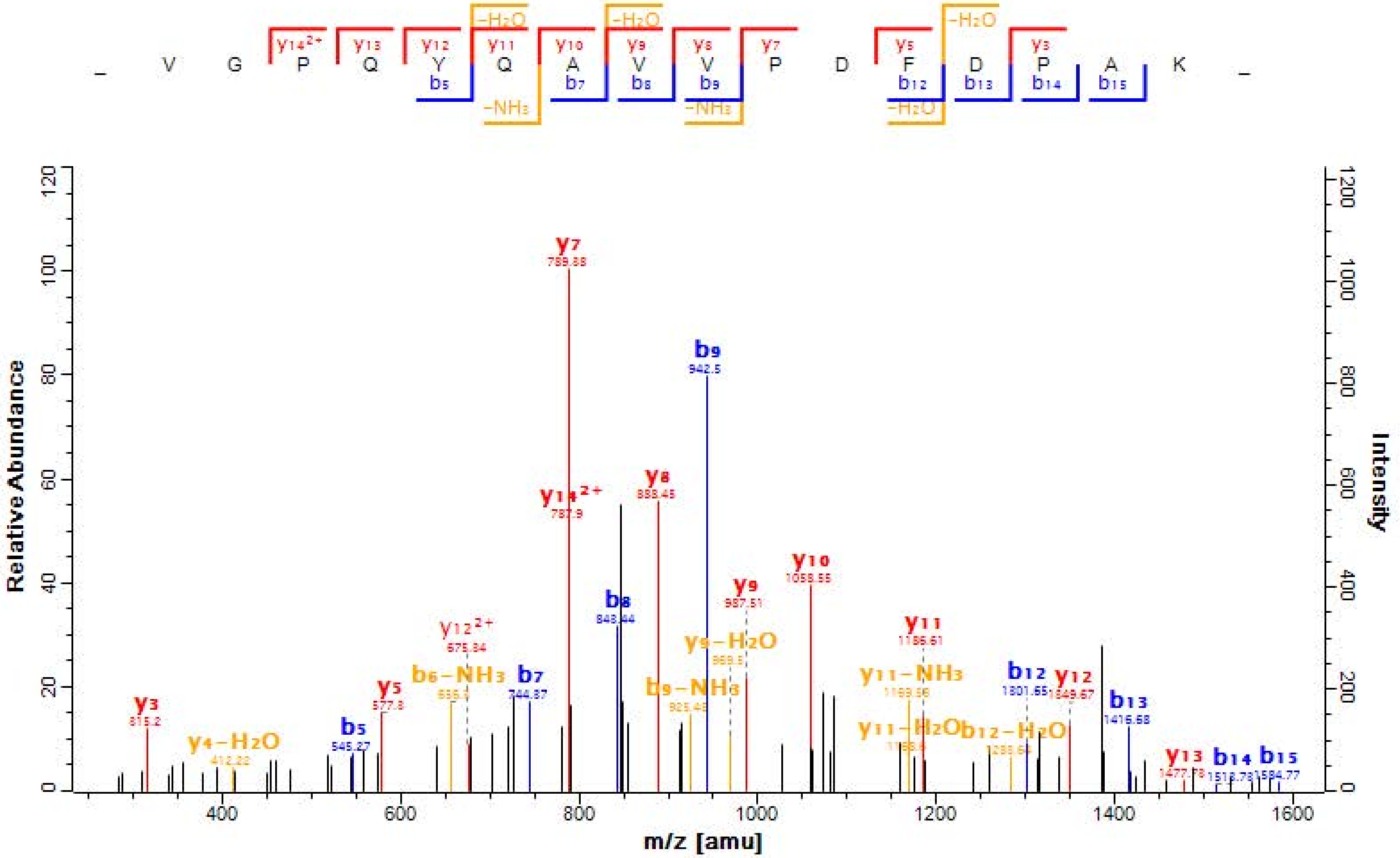
Mass:	1848.96703
m/z:	925.49079
Charge:	2+
Retentiontime:	35.419956207275
Score:	106.275
Mass Error [ppm]:	-1.2706
PEP:	1.6774E-06
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	41 %
Peak Coverage:	31 %
Protein Localisation:	2 ... 17

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.05		114.05	1	A	15				
	243.1		243.1	2	E	14	1736.9		1736.9	
	399.2	+0.1177	399.2	3	R	13	1607.9		804.45	+0.3264
	496.25	+0.1844	496.25	4	P	12	1451.8	+0.2009	1451.8	
	625.29	+0.1552	625.29	5	E	11	1354.7	+0.0706	1354.7	
	740.32	+0.0463	740.32	6	D	10	1225.7	+0.0869	1225.7	
	853.41		853.41	7	L	9	1110.7	-0.014	1110.7	
	967.45	+0.0853	967.45	8	N	8	997.58	+0.0823	997.58	
	1080.5		1080.5	9	L	7	883.54	+0.1419	883.54	
-0.104	589.3		1177.6	10	P	6	770.45	+0.1268	770.45	
	1291.6	+0.13	1291.6	11	N	5	673.4		673.4	
	1362.7	-0.111	1362.7	12	A	4	559.36		559.36	
	1461.7	-0.082	1461.7	13	V	3	488.32		488.32	
	1574.8	+0.0532	1574.8	14	I	2	389.25	+0.0201	389.25	
	1675.9	+0.161	1675.9	15	T	1	276.17		276.17	
				16	R	0	175.12		175.12	

Scan number	5513	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	124.25



precursor information

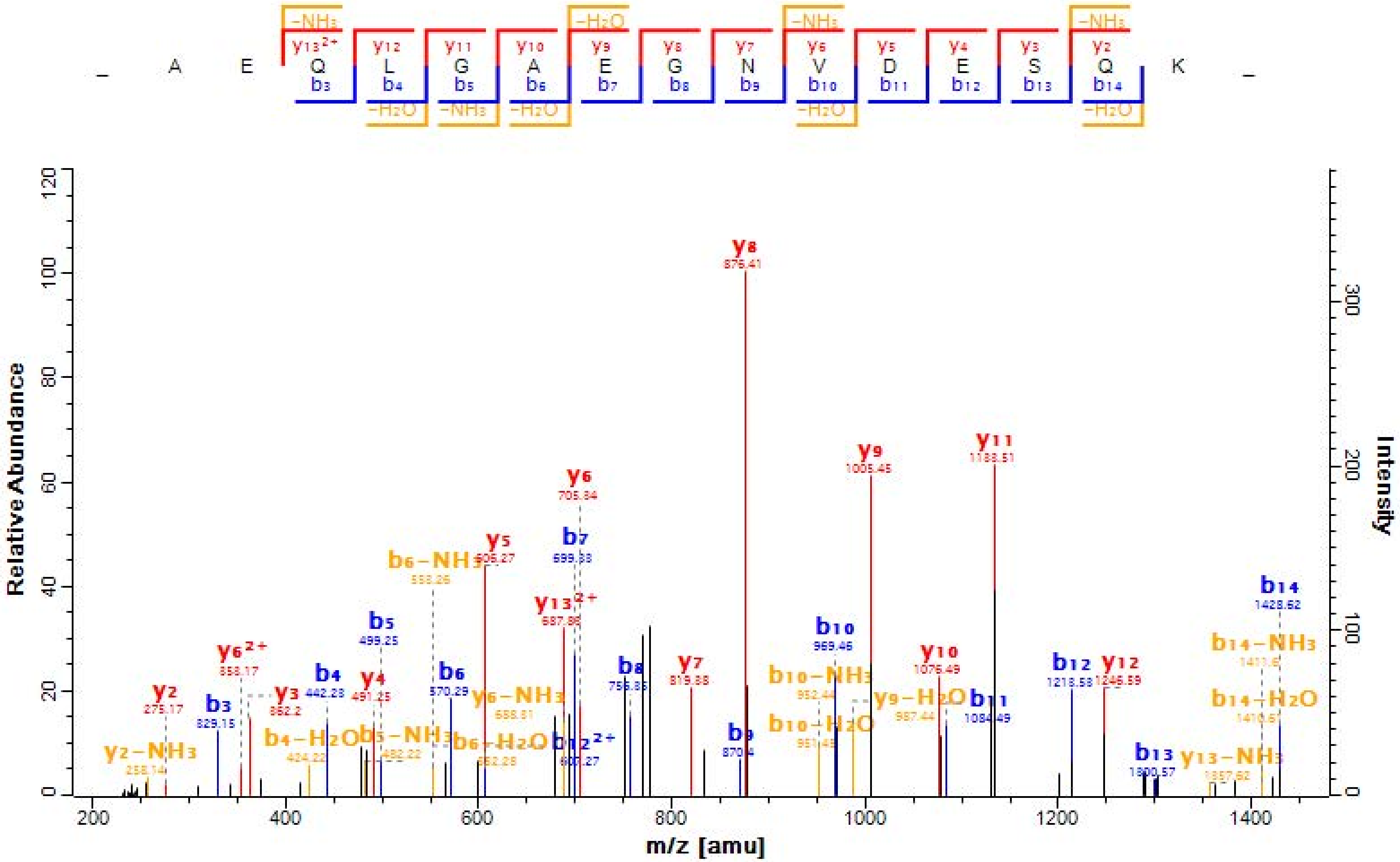
Mass:	1729.87077
m/z:	865.94266
Charge:	2+
Retentiontime:	36.265056610107
Score:	124.2509
Mass Error [ppm]:	1.868
PEP:	6.3574E-10
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	53 %
Peak Coverage:	31 %
Protein Localisation:	104 ... 119

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	15				
	157.0972	2	G	14	1631.806		1631.806	
	254.1499	3	P	13	1574.785		787.8961	+0.115918
	382.2085	4	Q	12	1477.732	+0.2555	1477.732	
+0.201504	545.2718	5	Y	11	1349.674	+0.083487	675.3404	+0.262287
	673.3304	6	Q	10	1186.61	-0.02408	1186.61	
-0.07638	744.3675	7	A	9	1058.552	-0.02581	1058.552	
-0.0381	843.4359	8	V	8	987.5146	-0.03728	987.5146	
+0.10137	942.5043	9	V	7	888.4462	-0.00457	888.4462	
	1039.557	10	P	6	789.3777	+0.02179	789.3777	
	1154.584	11	D	5	692.325		692.325	
-0.26233	1301.652	12	F	4	577.298	+0.060787	577.298	
-0.17343	1416.679	13	D	3	430.2296		430.2296	
-0.1842	1513.732	14	P	2	315.2027	+0.200547	315.2027	
+0.055667	1584.769	15	A	1	218.1499		218.1499	
		16	K	0	147.1128		147.1128	

Scan number	573	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	209.89



precursor information

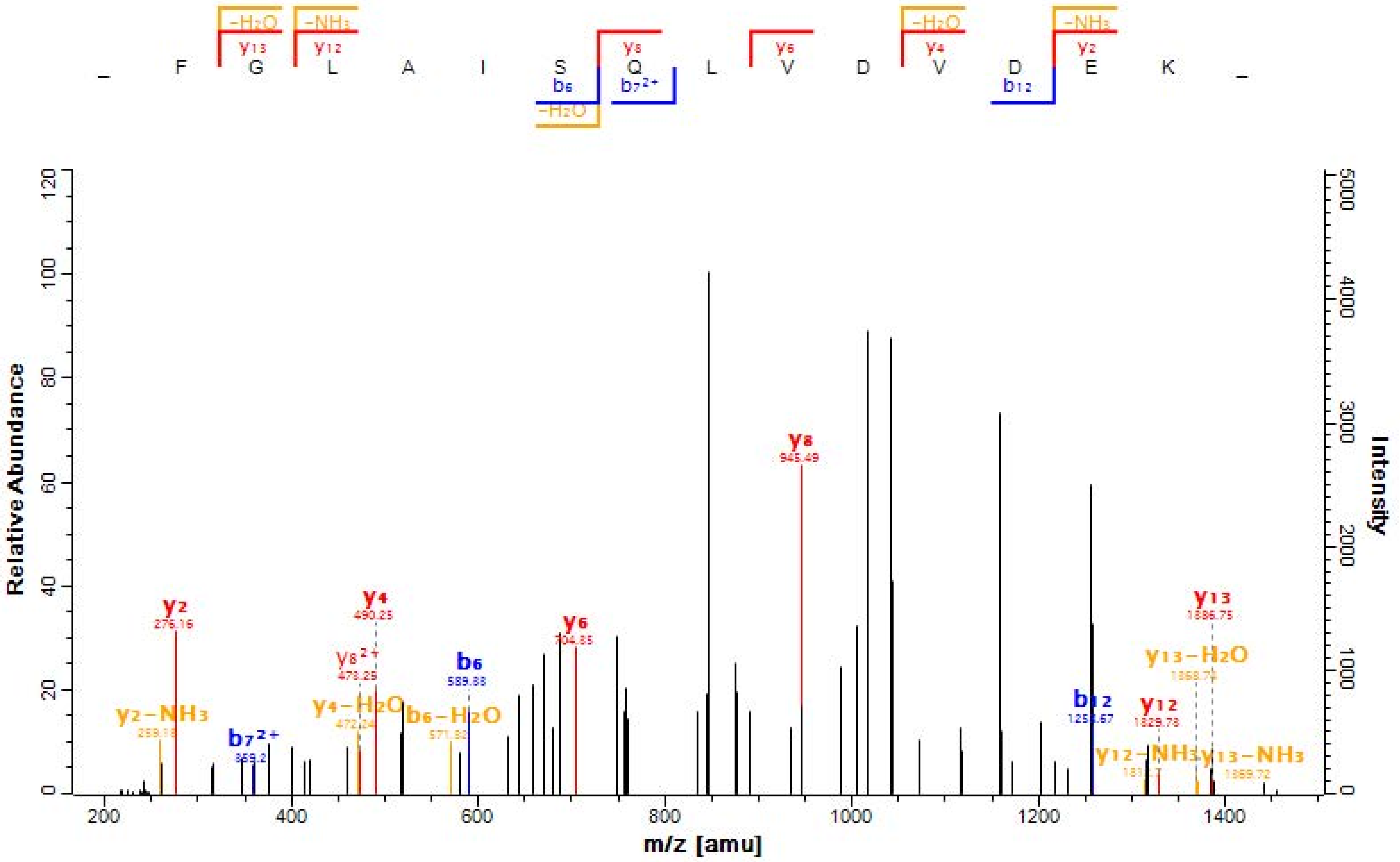
Mass:	0
m/z:	787.86835
Charge:	0+
Retentiontime:	9.0170564651489
Score:	209.8947
Mass Error [ppm]:	0.095272
PEP:	2.0906E-38
Precursor Type:	PEAK

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	61 %
Peak Coverage:	45 %
Protein Localisation:	140 ... 154

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	14				
	201.09		201.09	2	E	13	1503.7		1503.7	
	329.15	+0.0446	329.15	3	Q	12	1374.6		687.83	+0.0855
	442.23	+0.1114	442.23	4	L	11	1246.6	-0.039	1246.6	
	499.25	+0.1058	499.25	5	G	10	1133.5	-0.064	1133.5	
	570.29	+0.0772	570.29	6	A	9	1076.5	-0.003	1076.5	
	699.33	-0.03	699.33	7	E	8	1005.4	+0.0043	1005.4	
	756.35	+0.1324	756.35	8	G	7	876.41	+0.014	876.41	
	870.4	+0.1216	870.4	9	N	6	819.38	+0.0784	819.38	
	969.46	-0.063	969.46	10	V	5	705.34	+0.267	353.17	+0.1442
	1084.5	+0.0466	1084.5	11	D	4	606.27	+0.0392	606.27	
+0.1078	607.27	-0.135	1213.5	12	E	3	491.25	+0.2243	491.25	
	1300.6	-0.383	1300.6	13	S	2	362.2	+0.0666	362.2	
	1428.6	+0.0057	1428.6	14	Q	1	275.17	+0.056	275.17	
				15	K	0	147.11		147.11	

Scan number	6368	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	68.17



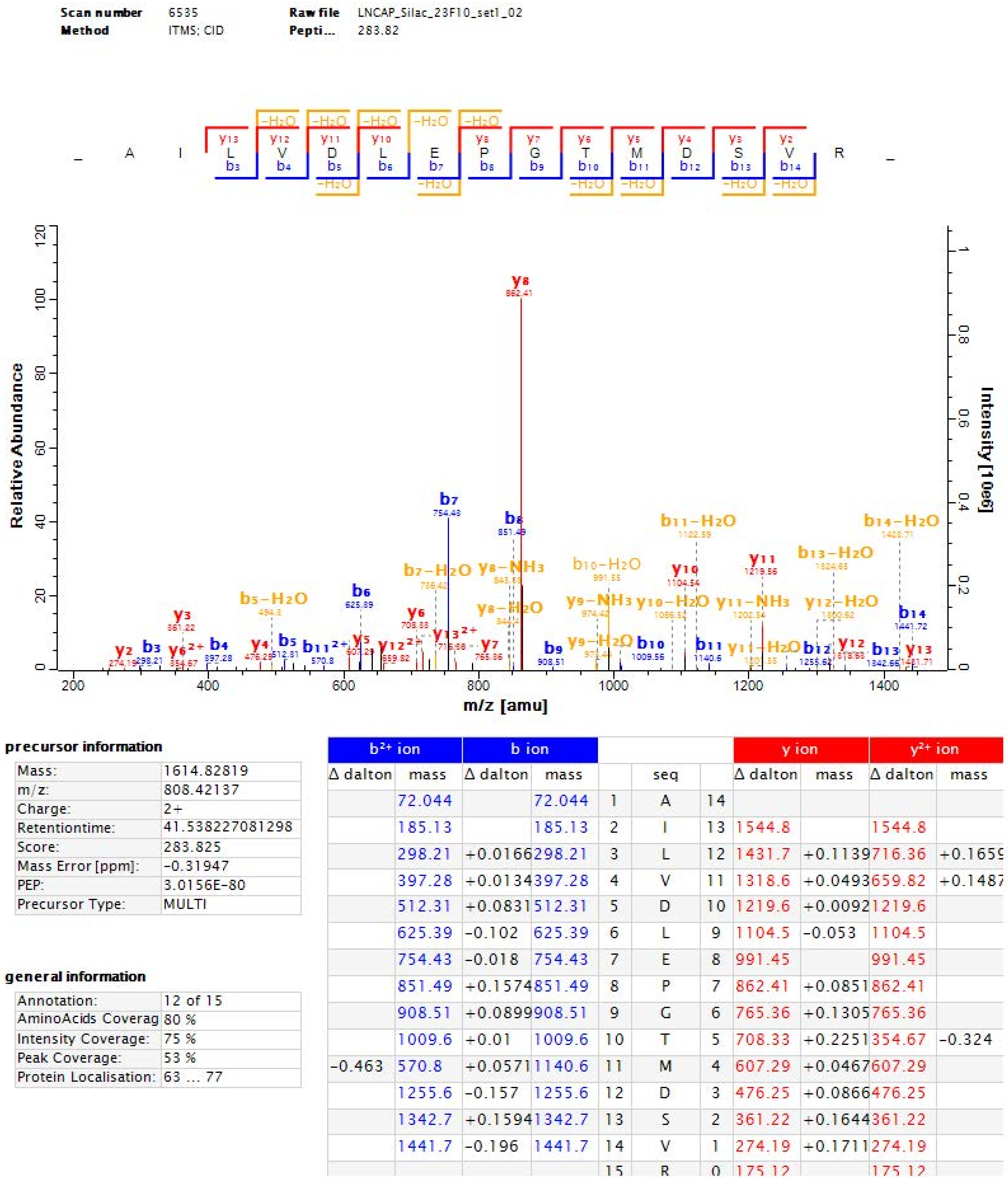
precursor information

Mass:	1532.8079
m/z:	767.41123
Charge:	2+
Retentiontime:	40.656078338623
Score:	68.17118
Mass Error [ppm]:	-0.4704
PEP:	0.0032842
Precursor Type:	MULTI

general information

Annotation:	8 of 14
AminoAcids Coverag	57 %
Intensity Coverage:	16 %
Peak Coverage:	18 %
Protein Localisation:	76 ... 89

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.08		148.08	1	F	13				
	205.1		205.1	2	G	12	1386.7	+0.3771	1386.7	
	318.18		318.18	3	L	11	1329.7	-0.188	1329.7	
	389.22		389.22	4	A	10	1216.6		1216.6	
	502.3		502.3	5	I	9	1145.6		1145.6	
	589.33	+0.0703	589.33	6	S	8	1032.5		1032.5	
+0.2187	359.2		717.39	7	Q	7	945.49	+0.0825	473.25	+0.1097
	830.48		830.48	8	L	6	817.43		817.43	
	929.55		929.55	9	V	5	704.35	+0.0957	704.35	
	1044.6		1044.6	10	D	4	605.28		605.28	
	1143.6		1143.6	11	V	3	490.25	+0.1399	490.25	
	1258.7	+0.0323	1258.7	12	D	2	391.18		391.18	
	1387.7		1387.7	13	E	1	276.16	+0.0969	276.16	
				14	K	0	147.11		147.11	



Scan number	6535	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	283.82

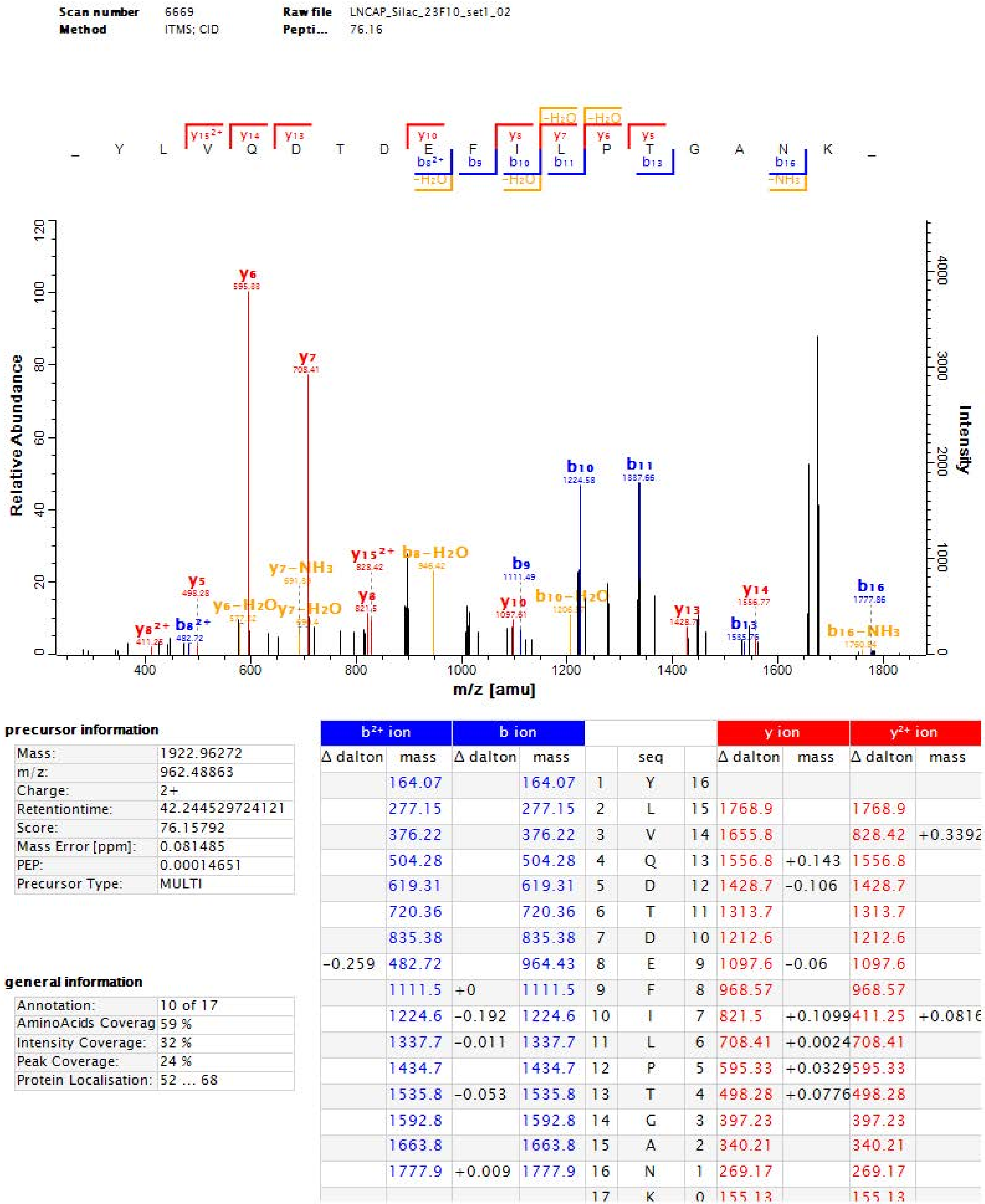
precursor information

Mass:	1614.82819
m/z:	808.42137
Charge:	2+
Retentiontime:	41.538227081298
Score:	283.825
Mass Error [ppm]:	-0.31947
PEP:	3.0156E-80
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	75 %
Peak Coverage:	53 %
Protein Localisation:	63 ... 77

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	14				
	185.13		185.13	2	I	13	1544.8		1544.8	
	298.21	+0.0166	298.21	3	L	12	1431.7	+0.1139	716.36	+0.1659
	397.28	+0.0134	397.28	4	V	11	1318.6	+0.0493	659.82	+0.1487
	512.31	+0.0831	512.31	5	D	10	1219.6	+0.0092	1219.6	
	625.39	-0.102	625.39	6	L	9	1104.5	-0.053	1104.5	
	754.43	-0.018	754.43	7	E	8	991.45		991.45	
	851.49	+0.1574	851.49	8	P	7	862.41	+0.0851	862.41	
	908.51	+0.0899	908.51	9	G	6	765.36	+0.1305	765.36	
	1009.6	+0.01	1009.6	10	T	5	708.33	+0.2251	354.67	-0.324
-0.463	570.8	+0.0571	1140.6	11	M	4	607.29	+0.0467	607.29	
	1255.6	-0.157	1255.6	12	D	3	476.25	+0.0866	476.25	
	1342.7	+0.1594	1342.7	13	S	2	361.22	+0.1644	361.22	
	1441.7	-0.196	1441.7	14	V	1	274.19	+0.1711	274.19	
				15	R	0	175.12		175.12	



Scan number	6669	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	76.16

precursor information

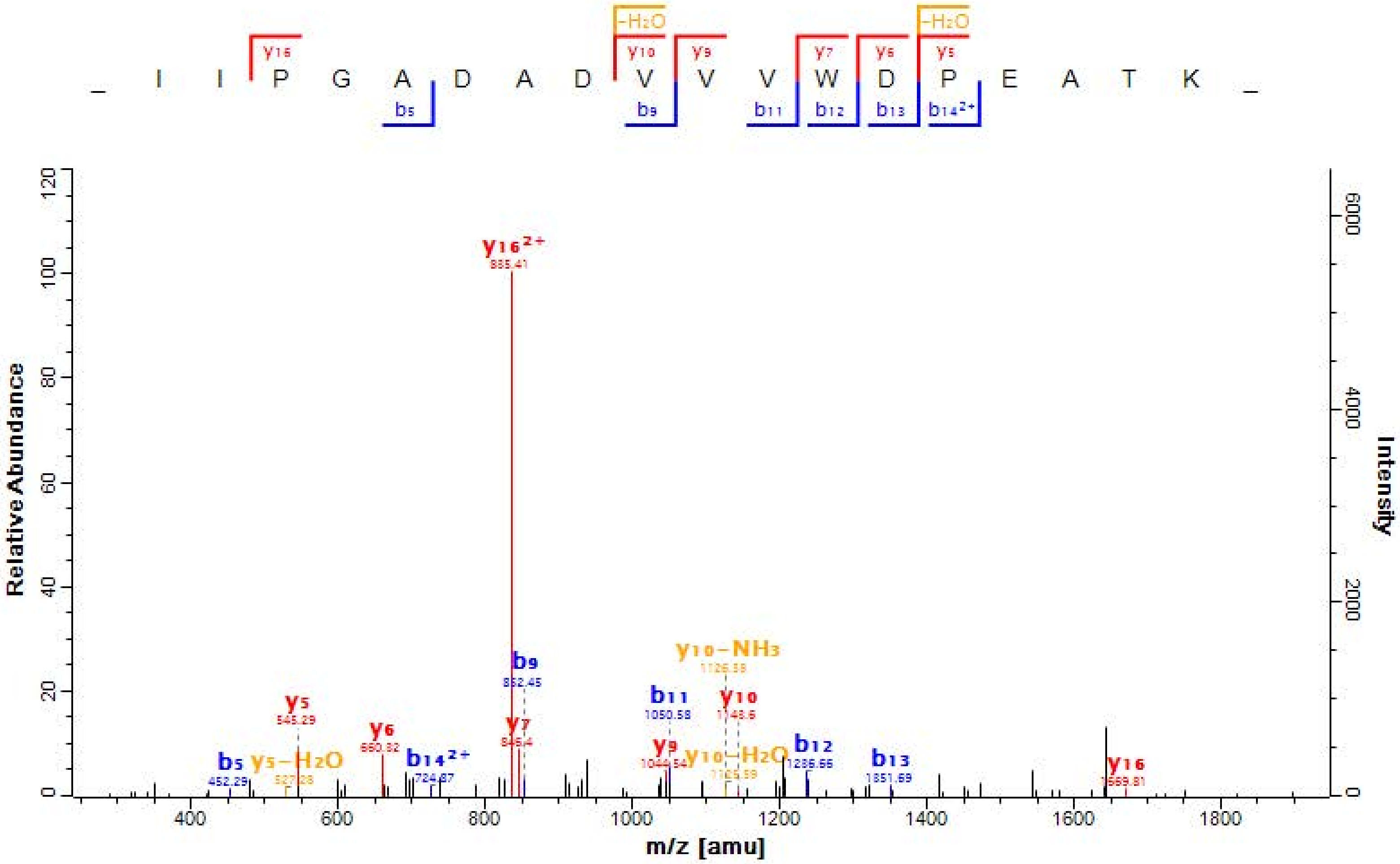
Mass:	1922.96272
m/z:	962.48863
Charge:	2+
Retentiontime:	42.244529724121
Score:	76.15792
Mass Error [ppm]:	0.081485
PEP:	0.00014651
Precursor Type:	MULTI

general information

Annotation:	10 of 17
AminoAcids Coverag	59 %
Intensity Coverage:	32 %
Peak Coverage:	24 %
Protein Localisation:	52 ... 68

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	164.07		164.07	1	Y	16				
	277.15		277.15	2	L	15	1768.9		1768.9	
	376.22		376.22	3	V	14	1655.8		828.42	+0.3392
	504.28		504.28	4	Q	13	1556.8	+0.143	1556.8	
	619.31		619.31	5	D	12	1428.7	-0.106	1428.7	
	720.36		720.36	6	T	11	1313.7		1313.7	
	835.38		835.38	7	D	10	1212.6		1212.6	
-0.259	482.72		964.43	8	E	9	1097.6	-0.06	1097.6	
	1111.5	+0	1111.5	9	F	8	968.57		968.57	
	1224.6	-0.192	1224.6	10	I	7	821.5	+0.1099	411.25	+0.0816
	1337.7	-0.011	1337.7	11	L	6	708.41	+0.0024	708.41	
	1434.7		1434.7	12	P	5	595.33	+0.0329	595.33	
	1535.8	-0.053	1535.8	13	T	4	498.28	+0.0776	498.28	
	1592.8		1592.8	14	G	3	397.23		397.23	
	1663.8		1663.8	15	A	2	340.21		340.21	
	1777.9	+0.009	1777.9	16	N	1	269.17		269.17	
				17	K	0	155.13		155.13	

Scan number	6752	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	61.96



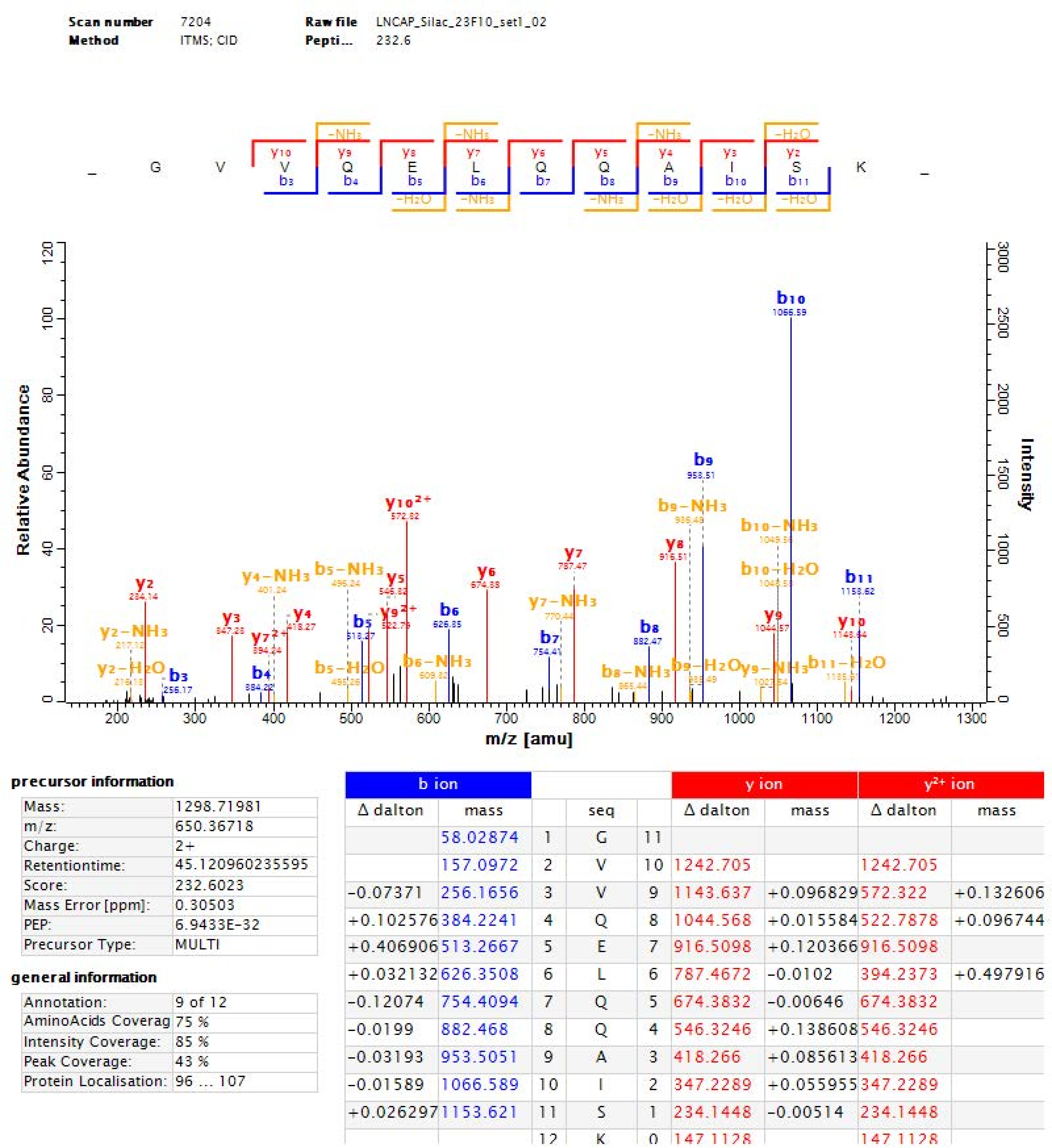
precursor information

Mass:	1894.96966
m/z:	948.49211
Charge:	2+
Retentiontime:	42.687789916992
Score:	61.96206
Mass Error [ppm]:	1.0654
PEP:	0.0016759
Precursor Type:	MULTI

general information

Annotation:	8 of 18
AminoAcids Coverag	44 %
Intensity Coverage:	48 %
Peak Coverage:	17 %
Protein Localisation:	394 ... 411

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	I	17				
	227.18		227.18	2	I	16	1782.9		1782.9	
	324.23		324.23	3	P	15	1669.8	-0.042	835.41	+0.344
	381.25		381.25	4	G	14	1572.8		1572.8	
	452.29	+0.1352	452.29	5	A	13	1515.7		1515.7	
	567.31		567.31	6	D	12	1444.7		1444.7	
	638.35		638.35	7	A	11	1329.7		1329.7	
	753.38		753.38	8	D	10	1258.6		1258.6	
	852.45	+0.01	852.45	9	V	9	1143.6	+0.3528	1143.6	
	951.51		951.51	10	V	8	1044.5	+0.0447	1044.5	
	1050.6	-0.044	1050.6	11	V	7	945.47		945.47	
	1236.7	+0.0015	1236.7	12	W	6	846.4	+0.0966	846.4	
	1351.7	-0.153	1351.7	13	D	5	660.32	-0.018	660.32	
+0.4367	724.87		1448.7	14	P	4	545.29	+0.0779	545.29	
	1577.8		1577.8	15	E	3	448.24		448.24	
	1648.8		1648.8	16	A	2	319.2		319.2	
	1749.9		1749.9	17	T	1	248.16		248.16	
				18	K	0	147.11		147.11	



Scan number	7204	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	232.6

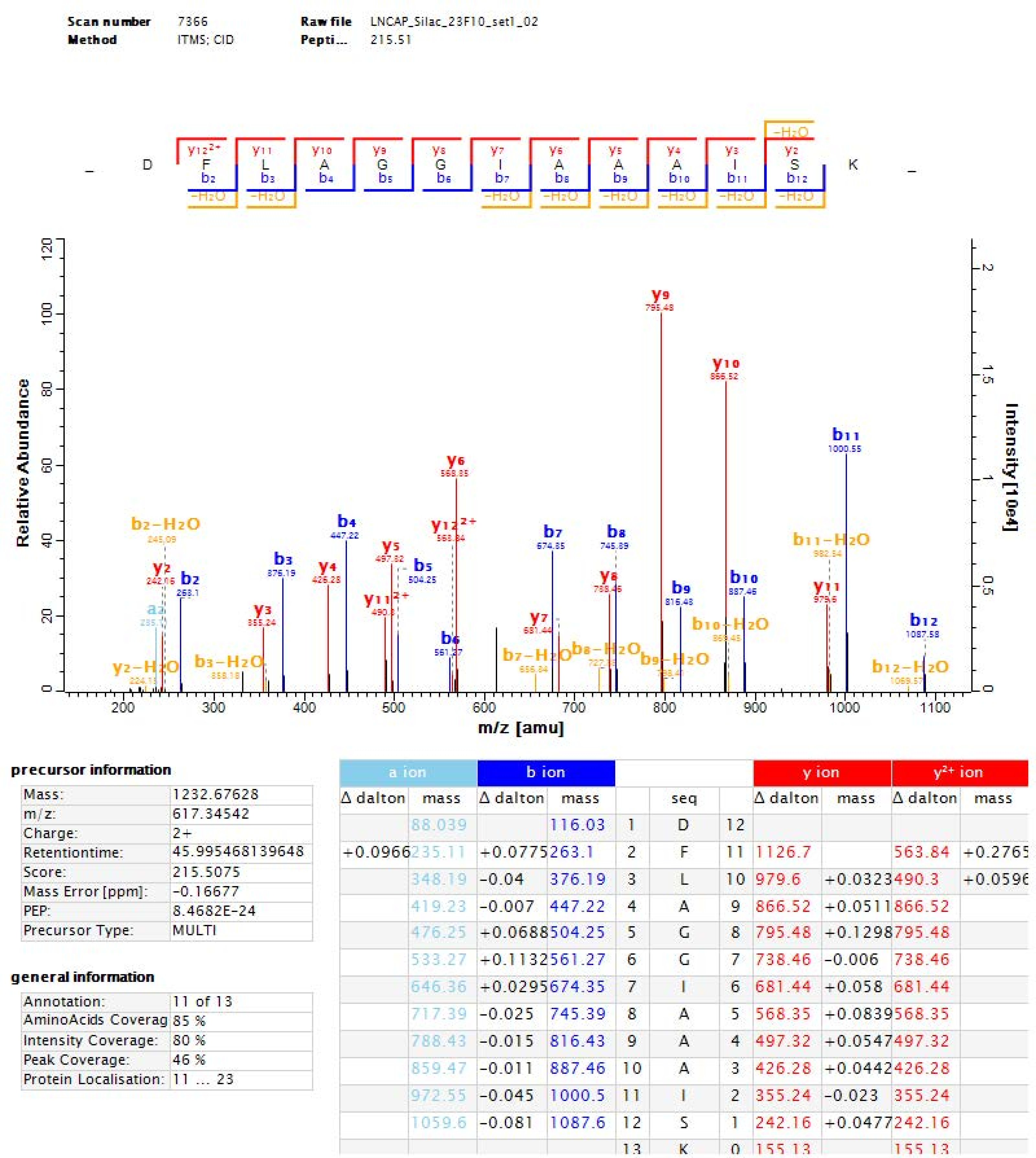
precursor information

Mass:	1298.71981
m/z:	650.36718
Charge:	2+
Retentiontime:	45.120960235595
Score:	232.6023
Mass Error [ppm]:	0.30503
PEP:	6.9433E-32
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	85 %
Peak Coverage:	43 %
Protein Localisation:	96 ... 107

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	11				
	157.0972	2	V	10	1242.705		1242.705	
-0.07371	256.1656	3	V	9	1143.637	+0.096829	572.322	+0.132606
+0.102576	384.2241	4	Q	8	1044.568	+0.015584	522.7878	+0.096744
+0.406906	513.2667	5	E	7	916.5098	+0.120366	916.5098	
+0.032132	626.3508	6	L	6	787.4672	-0.0102	394.2373	+0.497916
-0.12074	754.4094	7	Q	5	674.3832	-0.00646	674.3832	
-0.0199	882.468	8	Q	4	546.3246	+0.138608	546.3246	
-0.03193	953.5051	9	A	3	418.266	+0.085613	418.266	
-0.01589	1066.589	10	I	2	347.2289	+0.055955	347.2289	
+0.026297	1153.621	11	S	1	234.1448	-0.00514	234.1448	
		12	K	0	147.1128		147.1128	



Scan number	7366	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	215.51

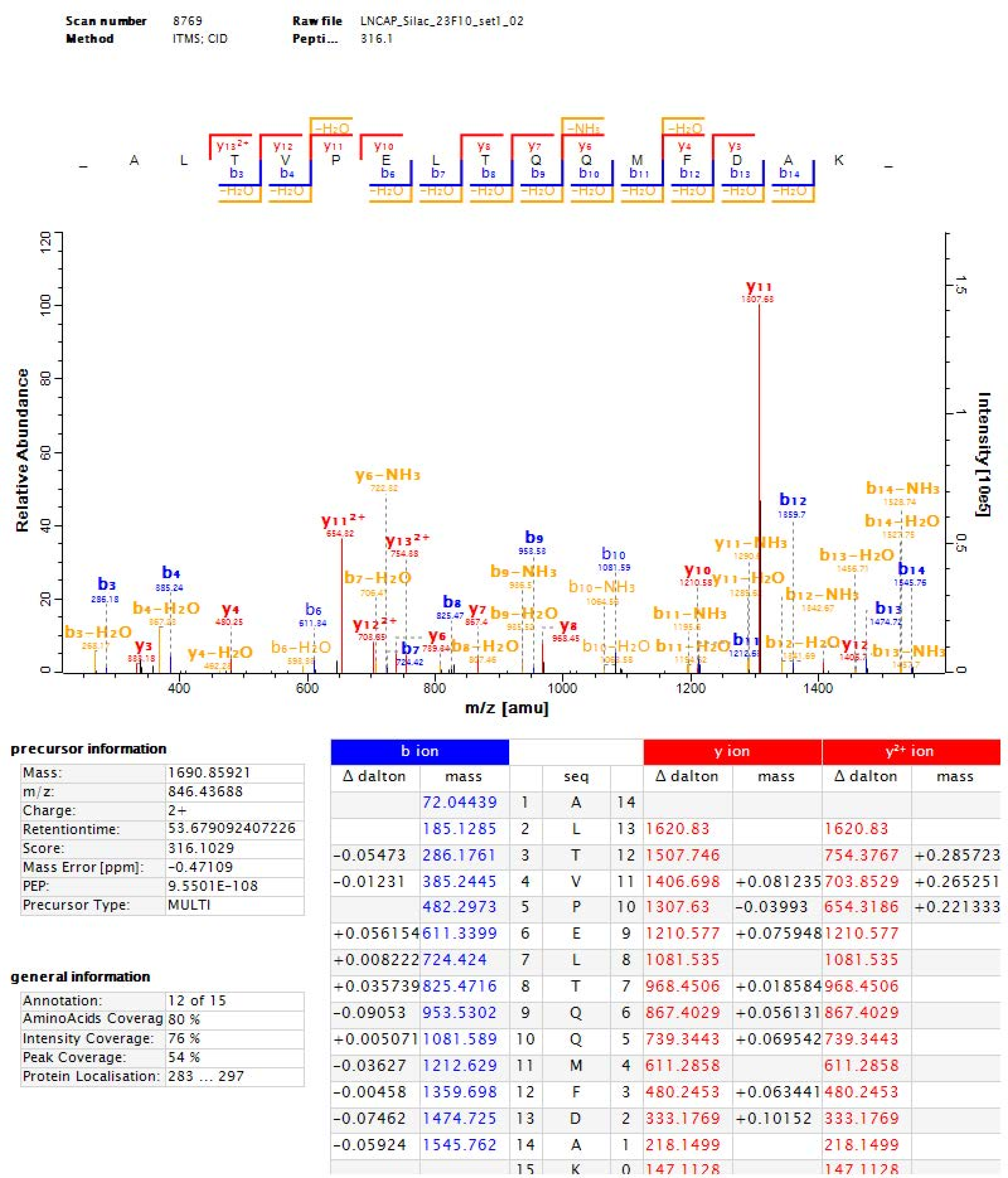
precursor information

Mass:	1232.67628
m/z:	617.34542
Charge:	2+
Retentiontime:	45.995468139648
Score:	215.5075
Mass Error [ppm]:	-0.16677
PEP:	8.4682E-24
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	80 %
Peak Coverage:	46 %
Protein Localisation:	11 ... 23

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	12				
+0.0966	235.11	+0.0775	263.1	2	F	11	1126.7		563.84	+0.2765
	348.19	-0.04	376.19	3	L	10	979.6	+0.0323	490.3	+0.0596
	419.23	-0.007	447.22	4	A	9	866.52	+0.0511	866.52	
	476.25	+0.0688	504.25	5	G	8	795.48	+0.1298	795.48	
	533.27	+0.1132	561.27	6	G	7	738.46	-0.006	738.46	
	646.36	+0.0295	674.35	7	I	6	681.44	+0.058	681.44	
	717.39	-0.025	745.39	8	A	5	568.35	+0.0839	568.35	
	788.43	-0.015	816.43	9	A	4	497.32	+0.0547	497.32	
	859.47	-0.011	887.46	10	A	3	426.28	+0.0442	426.28	
	972.55	-0.045	1000.5	11	I	2	355.24	-0.023	355.24	
	1059.6	-0.081	1087.6	12	S	1	242.16	+0.0477	242.16	
				13	K	0	155.13		155.13	



Scan number	8769	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	316.1

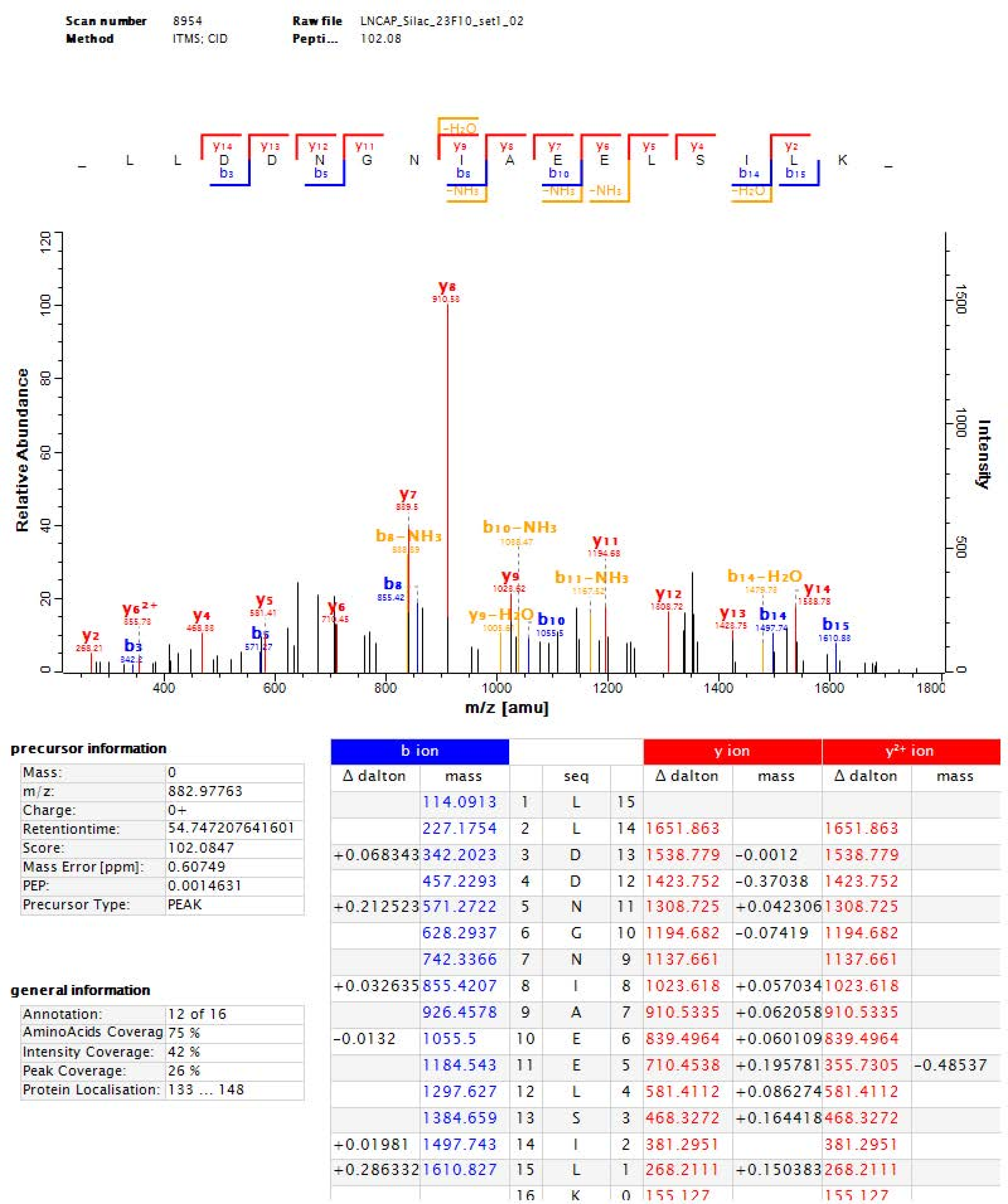
precursor information

Mass:	1690.85921
m/z:	846.43688
Charge:	2+
Retentiontime:	53.679092407226
Score:	316.1029
Mass Error [ppm]:	-0.47109
PEP:	9.5501E-108
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	76 %
Peak Coverage:	54 %
Protein Localisation:	283 ... 297

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	14				
	185.1285	2	L	13	1620.83		1620.83	
-0.05473	286.1761	3	T	12	1507.746		754.3767	+0.285723
-0.01231	385.2445	4	V	11	1406.698	+0.081235	703.8529	+0.265251
	482.2973	5	P	10	1307.63	-0.03993	654.3186	+0.221333
+0.056154	611.3399	6	E	9	1210.577	+0.075948	1210.577	
+0.008222	724.424	7	L	8	1081.535		1081.535	
+0.035739	825.4716	8	T	7	968.4506	+0.018584	968.4506	
-0.09053	953.5302	9	Q	6	867.4029	+0.056131	867.4029	
+0.005071	1081.589	10	Q	5	739.3443	+0.069542	739.3443	
-0.03627	1212.629	11	M	4	611.2858		611.2858	
-0.00458	1359.698	12	F	3	480.2453	+0.063441	480.2453	
-0.07462	1474.725	13	D	2	333.1769	+0.10152	333.1769	
-0.05924	1545.762	14	A	1	218.1499		218.1499	
		15	K	0	147.1128		147.1128	



Scan number	8954	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	102.08

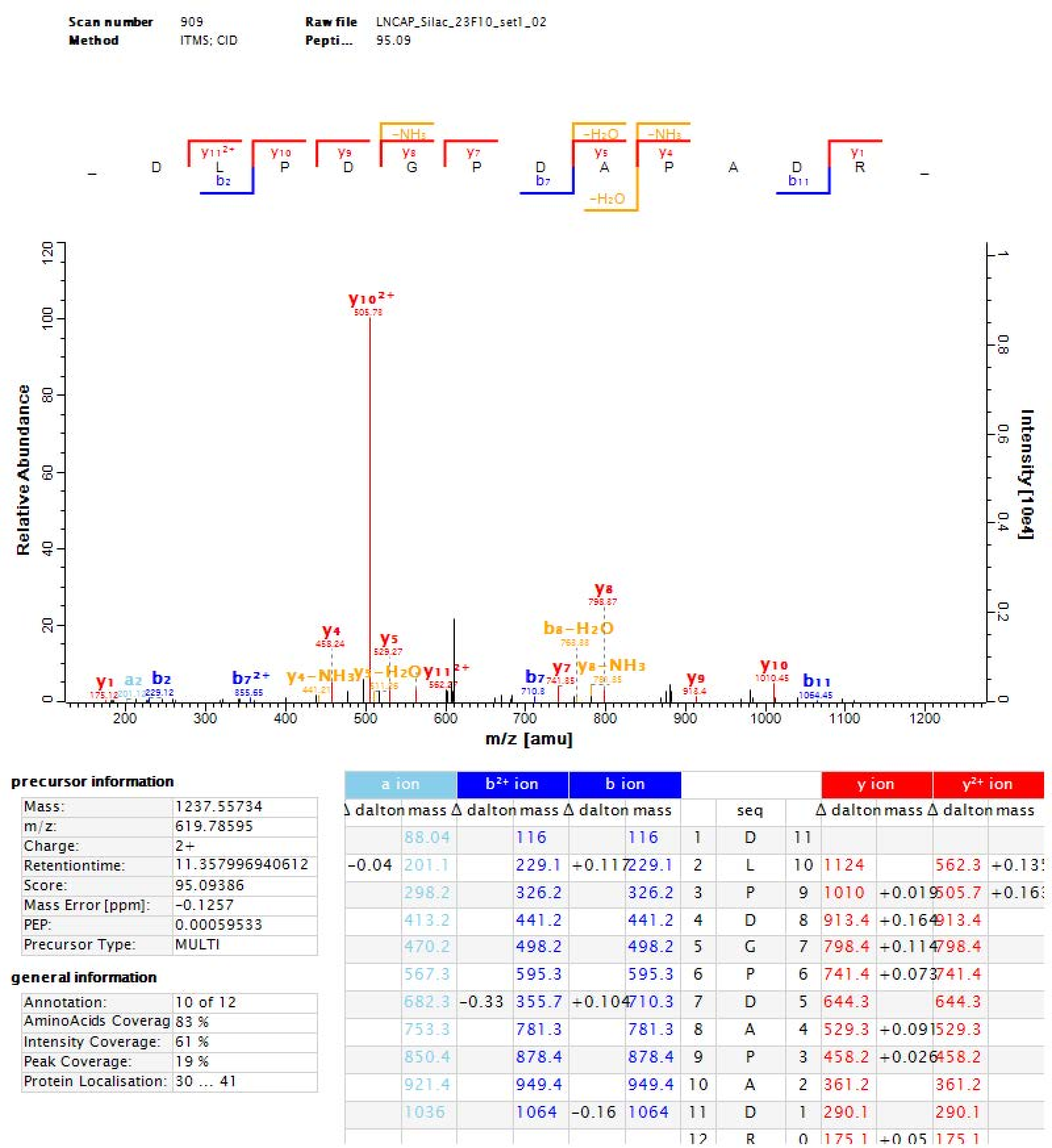
precursor information

Mass:	0
m/z:	882.97763
Charge:	0+
Retentiontime:	54.747207641601
Score:	102.0847
Mass Error [ppm]:	0.60749
PEP:	0.0014631
Precursor Type:	PEAK

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	42 %
Peak Coverage:	26 %
Protein Localisation:	133 ... 148

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	15				
	227.1754	2	L	14	1651.863		1651.863	
+0.068343	342.2023	3	D	13	1538.779	-0.0012	1538.779	
	457.2293	4	D	12	1423.752	-0.37038	1423.752	
+0.212523	571.2722	5	N	11	1308.725	+0.042306	1308.725	
	628.2937	6	G	10	1194.682	-0.07419	1194.682	
	742.3366	7	N	9	1137.661		1137.661	
+0.032635	855.4207	8	I	8	1023.618	+0.057034	1023.618	
	926.4578	9	A	7	910.5335	+0.062058	910.5335	
-0.0132	1055.5	10	E	6	839.4964	+0.060109	839.4964	
	1184.543	11	E	5	710.4538	+0.195781	355.7305	-0.48537
	1297.627	12	L	4	581.4112	+0.086274	581.4112	
	1384.659	13	S	3	468.3272	+0.164418	468.3272	
+0.01981	1497.743	14	I	2	381.2951		381.2951	
+0.286332	1610.827	15	L	1	268.2111	+0.150383	268.2111	
		16	K	0	155.127		155.127	



Scan number	909	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	95.09

precursor information

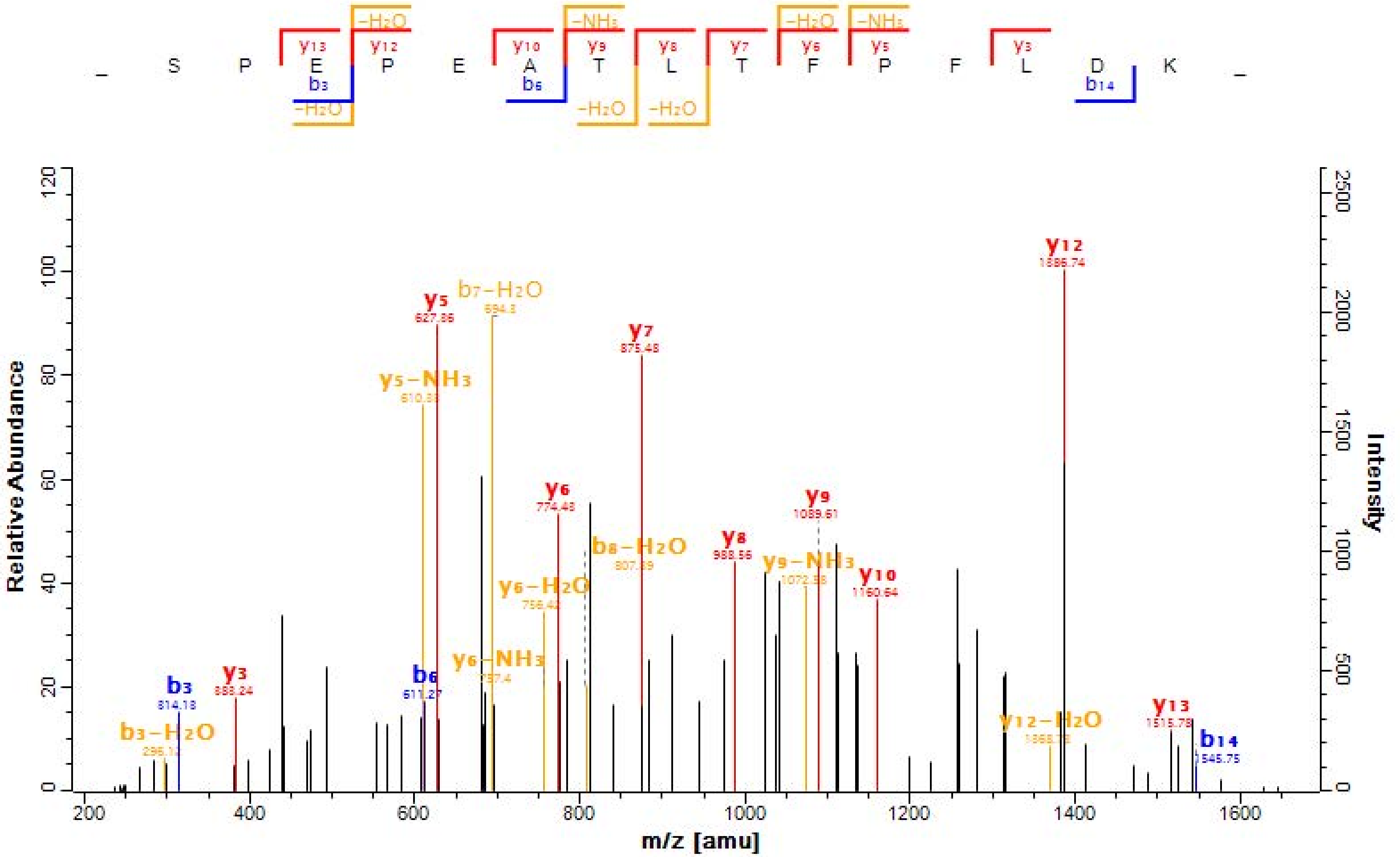
Mass:	1237.55734
m/z:	619.78595
Charge:	2+
Retentiontime:	11.357996940612
Score:	95.09386
Mass Error [ppm]:	-0.1257
PEP:	0.00059533
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	61 %
Peak Coverage:	19 %
Protein Localisation:	30 ... 41

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.04		116		116	1	D	11				
-0.04	201.1		229.1	+0.117	229.1	2	L	10	1124		562.3	+0.13
	298.2		326.2		326.2	3	P	9	1010	+0.019	505.7	+0.16
	413.2		441.2		441.2	4	D	8	913.4	+0.164	913.4	
	470.2		498.2		498.2	5	G	7	798.4	+0.114	798.4	
	567.3		595.3		595.3	6	P	6	741.4	+0.073	741.4	
	682.3	-0.33	355.7	+0.104	710.3	7	D	5	644.3		644.3	
	753.3		781.3		781.3	8	A	4	529.3	+0.091	529.3	
	850.4		878.4		878.4	9	P	3	458.2	+0.026	458.2	
	921.4		949.4		949.4	10	A	2	361.2		361.2	
	1036		1064	-0.16	1064	11	D	1	290.1		290.1	
						12	R	0	175.1	+0.05	175.1	

Scan number	9235	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	102.28



precursor information

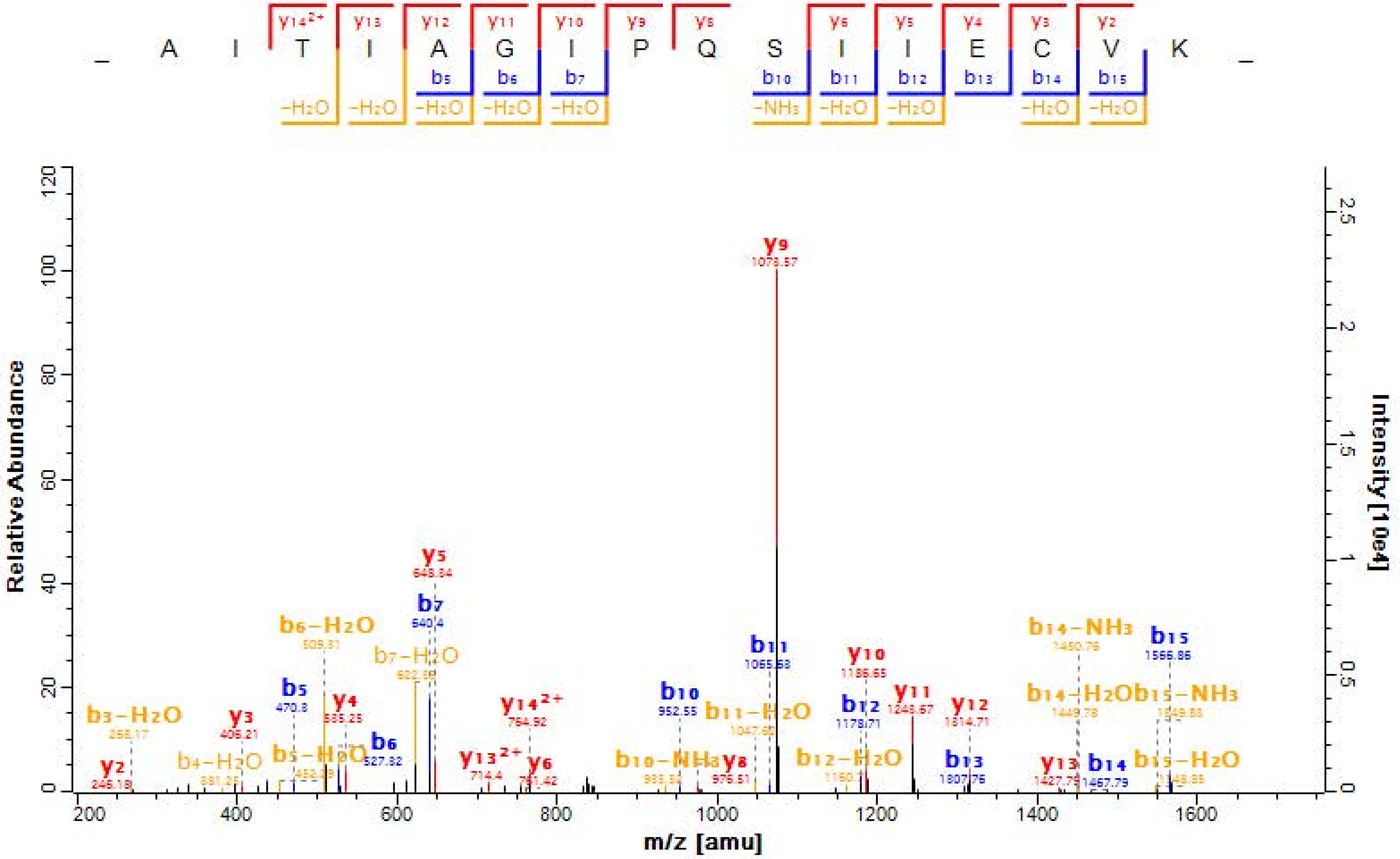
Mass:	1690.8464
m/z:	846.43048
Charge:	2+
Retentiontime:	56.421833038330
Score:	102.2768
Mass Error [ppm]:	0.58789
PEP:	1.4583E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 15
AminoAcids Coverag	67 %
Intensity Coverage:	39 %
Peak Coverage:	22 %
Protein Localisation:	718 ... 732

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	88.039304876	1	S	14		
	185.092068728	2	P	13	1612.83485029	
+0.0410279	314.134661825	3	E	12	1515.78208644	−0.105939
	411.187425677	4	P	11	1386.73949335	+0.0269861
	540.230018773	5	E	10	1289.68672949	
+0.1256897	611.267132561	6	A	9	1160.6441364	−0.0457477
	712.314811035	7	T	8	1089.60702261	+0.0733973
	825.398875015	8	L	7	988.559344135	+0.1015445
	926.446553489	9	T	6	875.475280155	−0.0065912
	1073.51496741	10	F	5	774.427601681	+0.1092636
	1170.56773126	11	P	4	627.359187764	+0.0875285
	1317.63614517	12	F	3	530.306423912	
	1430.72020915	13	L	2	383.238009996	+0.157864
+0.0810949	1545.74715219	14	D	1	270.153946016	
		15	K	0	155.127002984	

Scan number	9401	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	183.23



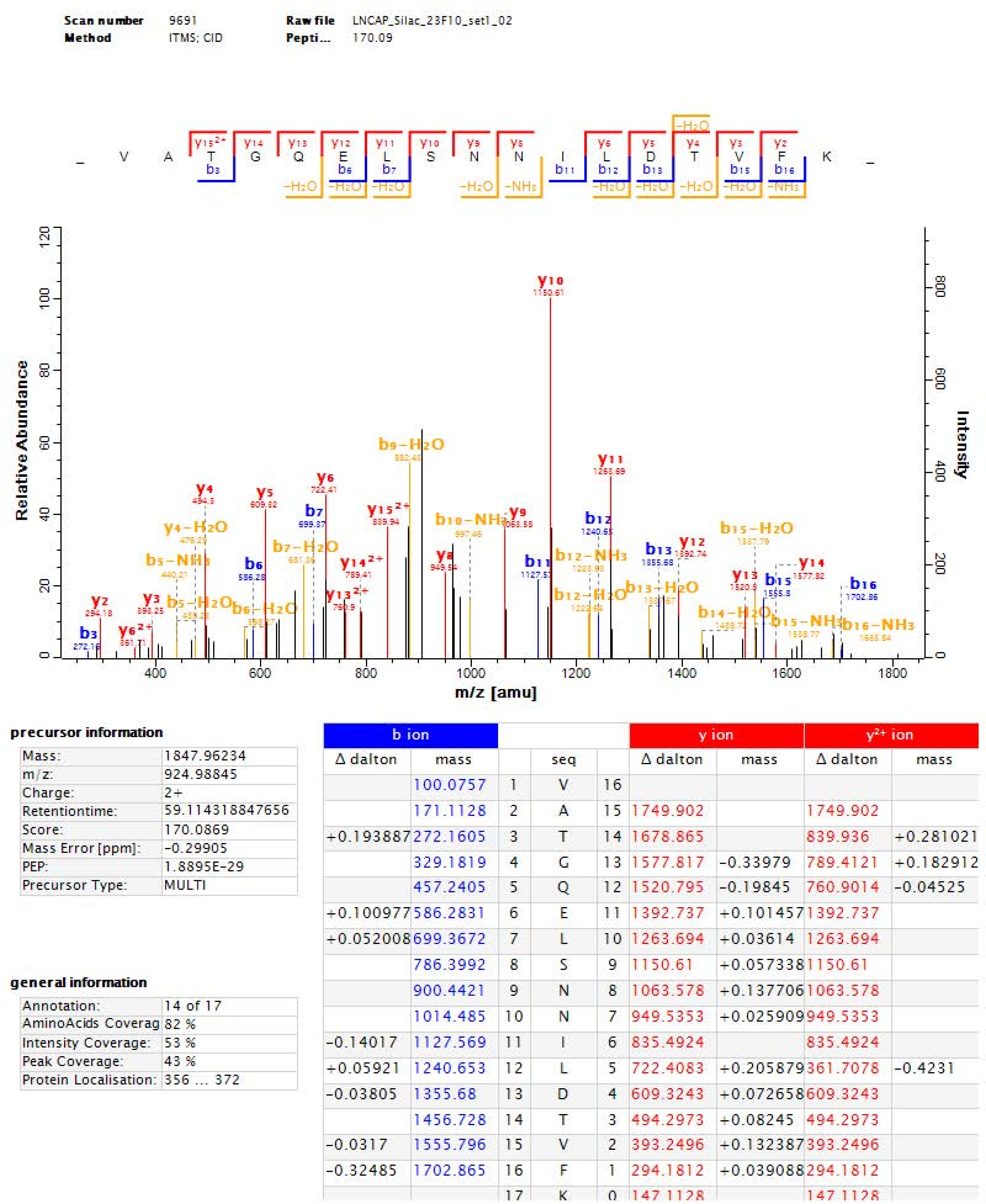
precursor information

Mass:	1711.95431
m/z:	856.98443
Charge:	2+
Retentiontime:	57.395809173584
Score:	183.2319
Mass Error [ppm]:	0.038865
PEP:	1.3254E-23
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	65 %
Peak Coverage:	42 %
Protein Localisation:	145 ... 160

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	15				
	185.1285	2	I	14	1641.924		1641.924	
	286.1761	3	T	13	1528.84		764.9238	-0.00071
	399.2602	4	I	12	1427.793	+0.081239	714.4	+0.285394
-0.04432	470.2973	5	A	11	1314.709	+0.177754	1314.709	
+0.016431	527.3188	6	G	10	1243.671	+0.039941	1243.671	
-0.01734	640.4028	7	I	9	1186.65	-0.01501	1186.65	
	737.4556	8	P	8	1073.566	-0.01103	1073.566	
	865.5142	9	Q	7	976.5132	+0.201712	976.5132	
+0.07275	952.5462	10	S	6	848.4546		848.4546	
+0.204933	1065.63	11	I	5	761.4226	-0.08622	761.4226	
-0.11497	1178.714	12	I	4	648.3385	+0.146401	648.3385	
+0.465361	1307.757	13	E	3	535.2545	+0.108578	535.2545	
+0.023824	1467.788	14	C	2	406.2119	+0.077501	406.2119	
-0.12149	1566.856	15	V	1	246.1812	-0.07467	246.1812	
		16	K	0	147.1128		147.1128	



Scan number	9691	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	170.09

precursor information

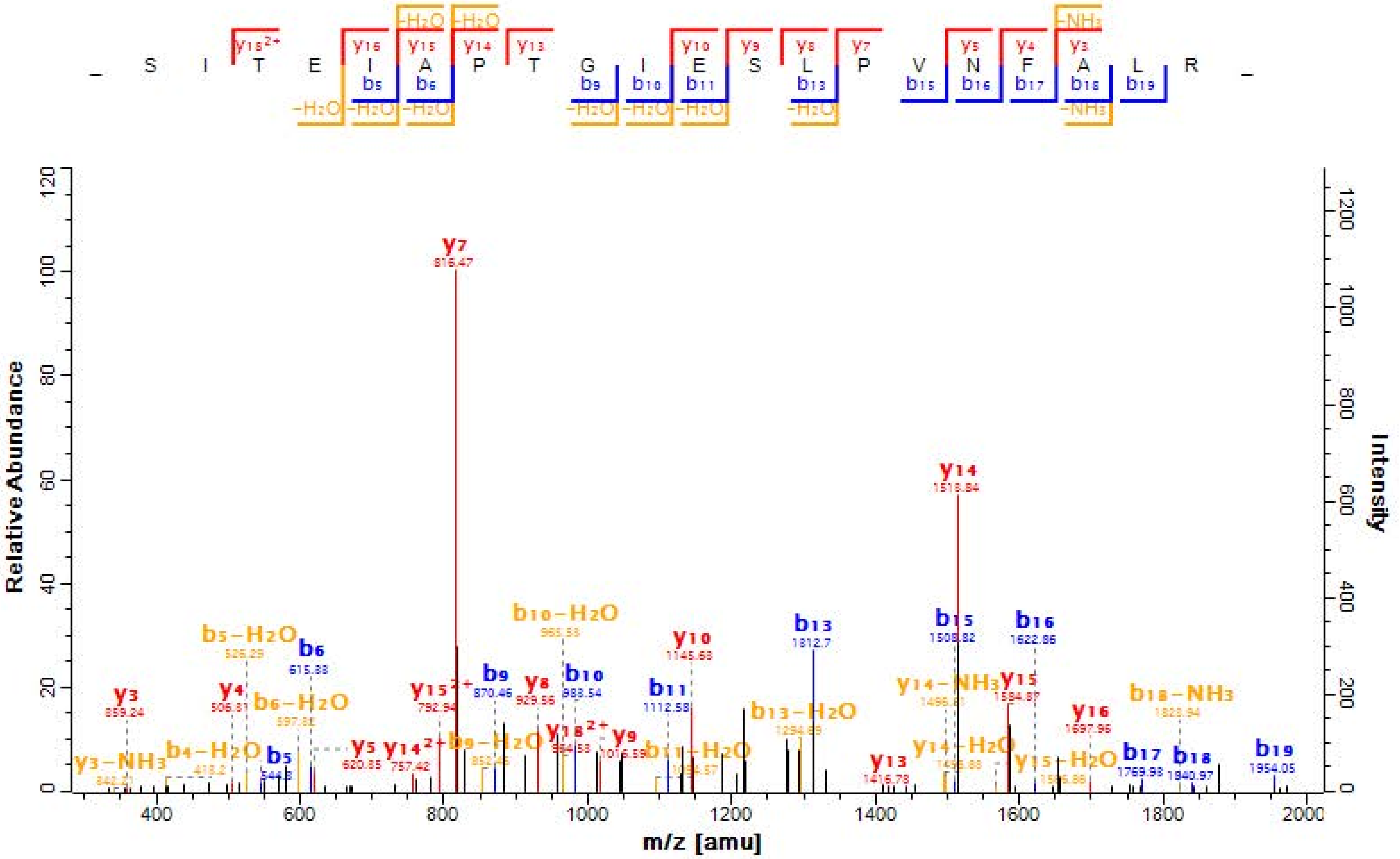
Mass:	1847.96234
m/z:	924.98845
Charge:	2+
Retentiontime:	59.114318847656
Score:	170.0869
Mass Error [ppm]:	-0.29905
PEP:	1.8895E-29
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	53 %
Peak Coverage:	43 %
Protein Localisation:	356 ... 372

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	16				
	171.1128	2	A	15	1749.902		1749.902	
+0.193887	272.1605	3	T	14	1678.865		839.936	+0.281021
	329.1819	4	G	13	1577.817	-0.33979	789.4121	+0.182912
	457.2405	5	Q	12	1520.795	-0.19845	760.9014	-0.04525
+0.100977	586.2831	6	E	11	1392.737	+0.101457	1392.737	
+0.052008	699.3672	7	L	10	1263.694	+0.03614	1263.694	
	786.3992	8	S	9	1150.61	+0.057338	1150.61	
	900.4421	9	N	8	1063.578	+0.137706	1063.578	
	1014.485	10	N	7	949.5353	+0.025909	949.5353	
-0.14017	1127.569	11	I	6	835.4924		835.4924	
+0.05921	1240.653	12	L	5	722.4083	+0.205879	361.7078	-0.4231
-0.03805	1355.68	13	D	4	609.3243	+0.072658	609.3243	
	1456.728	14	T	3	494.2973	+0.08245	494.2973	
-0.0317	1555.796	15	V	2	393.2496	+0.132387	393.2496	
-0.32485	1702.865	16	F	1	294.1812	+0.039088	294.1812	
		17	K	0	147.1128		147.1128	

Scan number	9711	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	186.98



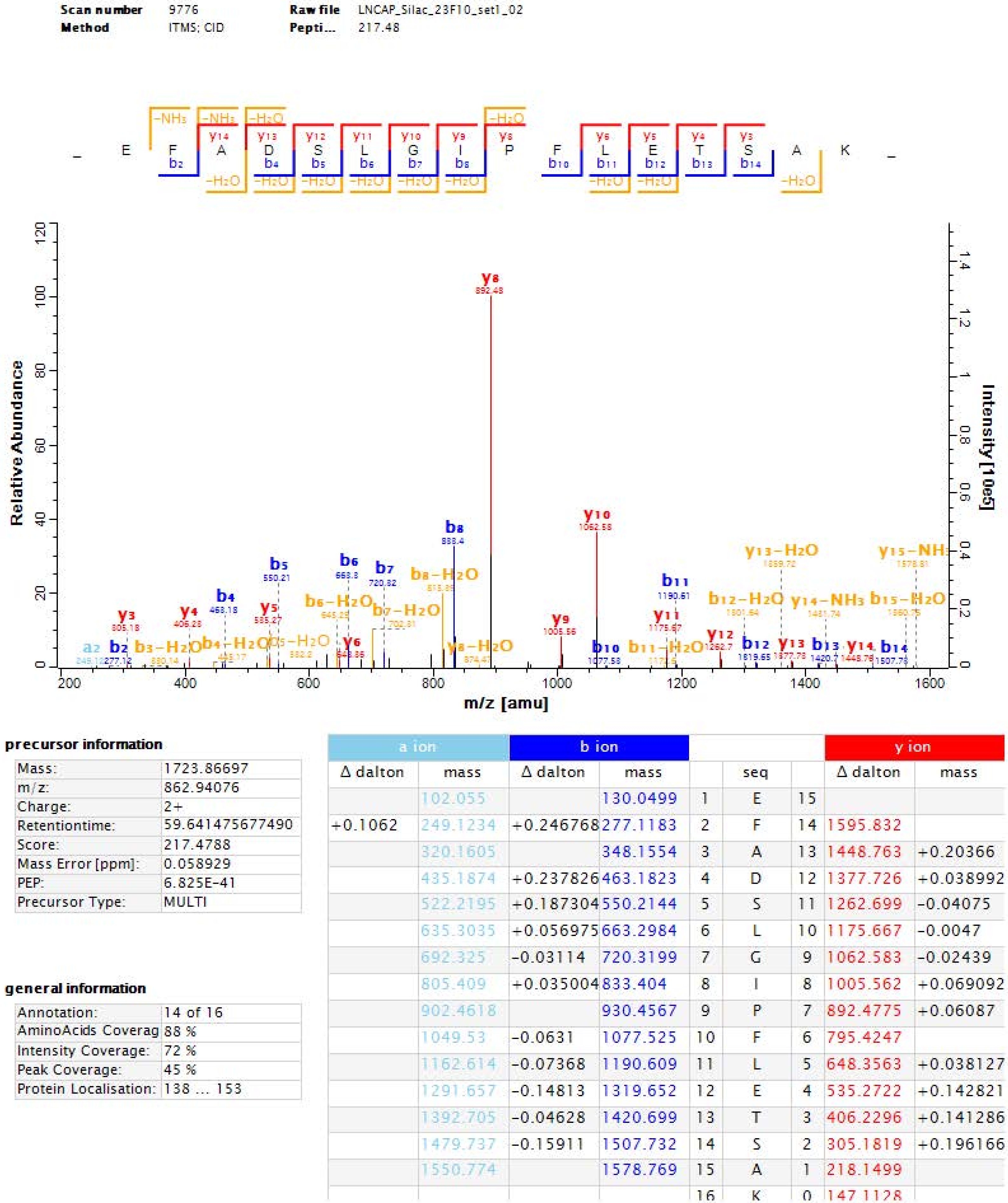
precursor information

Mass:	2127.15737
m/z:	1064.58596
Charge:	2+
Retentiontime:	59.226970672607
Score:	186.9782
Mass Error [ppm]:	-0.095916
PEP:	2.5741E-47
Precursor Type:	MULTI

general information

Annotation:	17 of 20
AminoAcids Coverag	85 %
Intensity Coverage:	54 %
Peak Coverage:	36 %
Protein Localisation:	61 ... 80

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	19				
	201.1234	2	I	18	2041.133		2041.133	
	302.171	3	T	17	1928.049		964.528	+0.041687
	431.2136	4	E	16	1827.001		1827.001	
-0.11301	544.2977	5	I	15	1697.958	+0.431532	1697.958	
+0.031393	615.3348	6	A	14	1584.874	-0.02652	792.9408	+0.282663
	712.3876	7	P	13	1513.837	+0.001929	757.4223	+0.209362
	813.4353	8	T	12	1416.785	+0.082647	1416.785	
+0.067568	870.4567	9	G	11	1315.737		1315.737	
+0.042342	983.5408	10	I	10	1258.715		1258.715	
-0.01698	1112.583	11	E	9	1145.631	+0.000257	1145.631	
	1199.615	12	S	8	1016.589	-0.0747	1016.589	
-0.04115	1312.699	13	L	7	929.5567	-0.00764	929.5567	
	1409.752	14	P	6	816.4726	+0.055549	816.4726	
-0.0615	1508.821	15	V	5	719.4199		719.4199	
-0.04754	1622.864	16	N	4	620.3515	+0.169647	620.3515	
+0.138686	1769.932	17	F	3	506.3085	+0.201039	506.3085	
-0.28979	1840.969	18	A	2	359.2401	+0.132429	359.2401	
+0.056815	1954.053	19	L	1	288.203		288.203	
		20	R	0	175.119		175.119	



Scan number	9776	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	217.48

precursor information

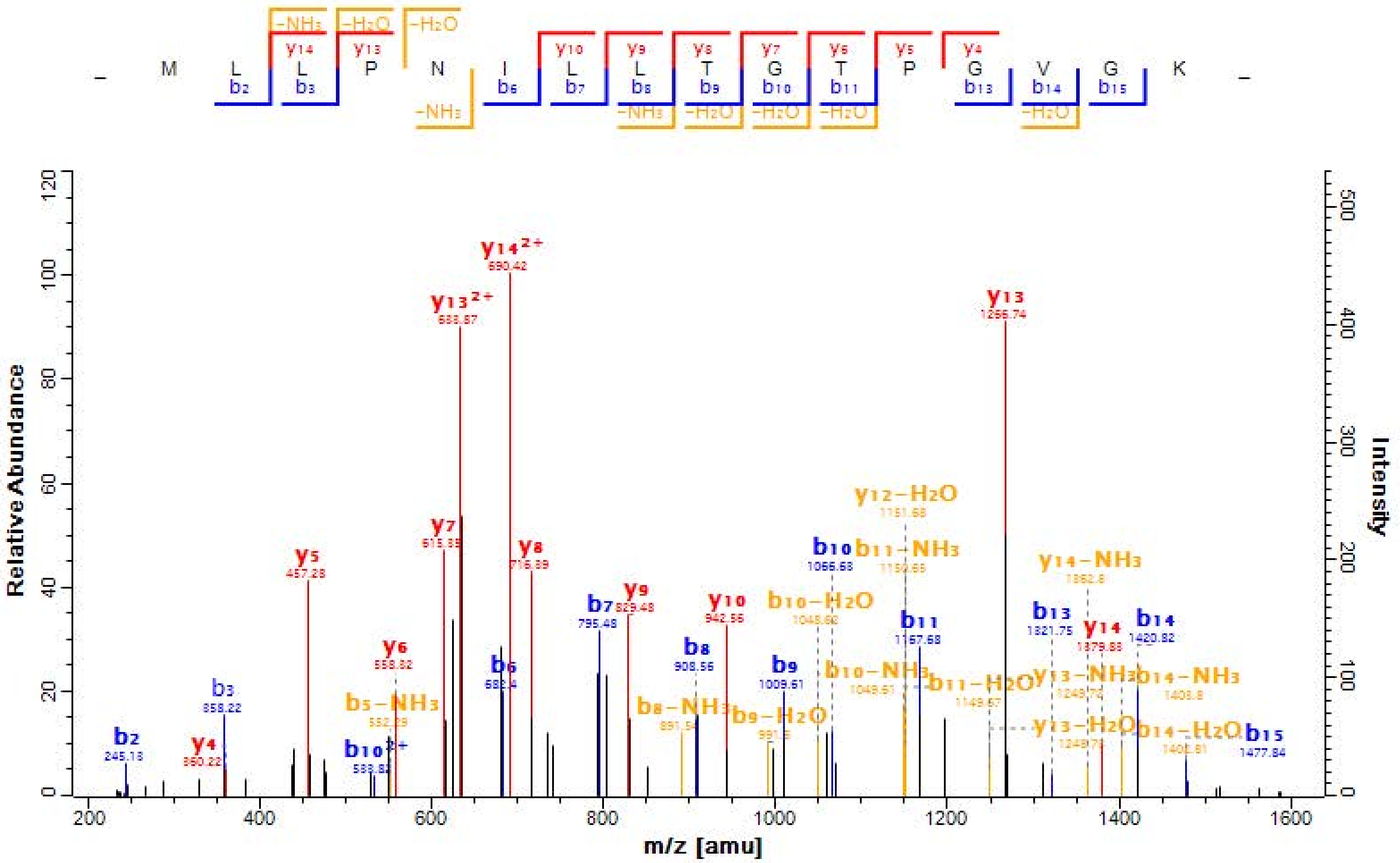
Mass:	1723.86697
m/z:	862.94076
Charge:	2+
Retentiontime:	59.641475677490
Score:	217.4788
Mass Error [ppm]:	0.058929
PEP:	6.825E-41
Precursor Type:	MULTI

general information

Annotation:	14 of 16
AminoAcids Coverag	88 %
Intensity Coverage:	72 %
Peak Coverage:	45 %
Protein Localisation:	138 ... 153

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	102.055		130.0499	1	E	15		
+0.1062	249.1234	+0.246768	277.1183	2	F	14	1595.832	
	320.1605		348.1554	3	A	13	1448.763	+0.20366
	435.1874	+0.237826	463.1823	4	D	12	1377.726	+0.038992
	522.2195	+0.187304	550.2144	5	S	11	1262.699	-0.04075
	635.3035	+0.056975	663.2984	6	L	10	1175.667	-0.0047
	692.325	-0.03114	720.3199	7	G	9	1062.583	-0.02439
	805.409	+0.035004	833.404	8	I	8	1005.562	+0.069092
	902.4618		930.4567	9	P	7	892.4775	+0.06087
	1049.53	-0.0631	1077.525	10	F	6	795.4247	
	1162.614	-0.07368	1190.609	11	L	5	648.3563	+0.038127
	1291.657	-0.14813	1319.652	12	E	4	535.2722	+0.142821
	1392.705	-0.04628	1420.699	13	T	3	406.2296	+0.141286
	1479.737	-0.15911	1507.732	14	S	2	305.1819	+0.196166
	1550.774		1578.769	15	A	1	218.1499	
				16	K	0	147.1128	

Scan number	9802	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	201.3



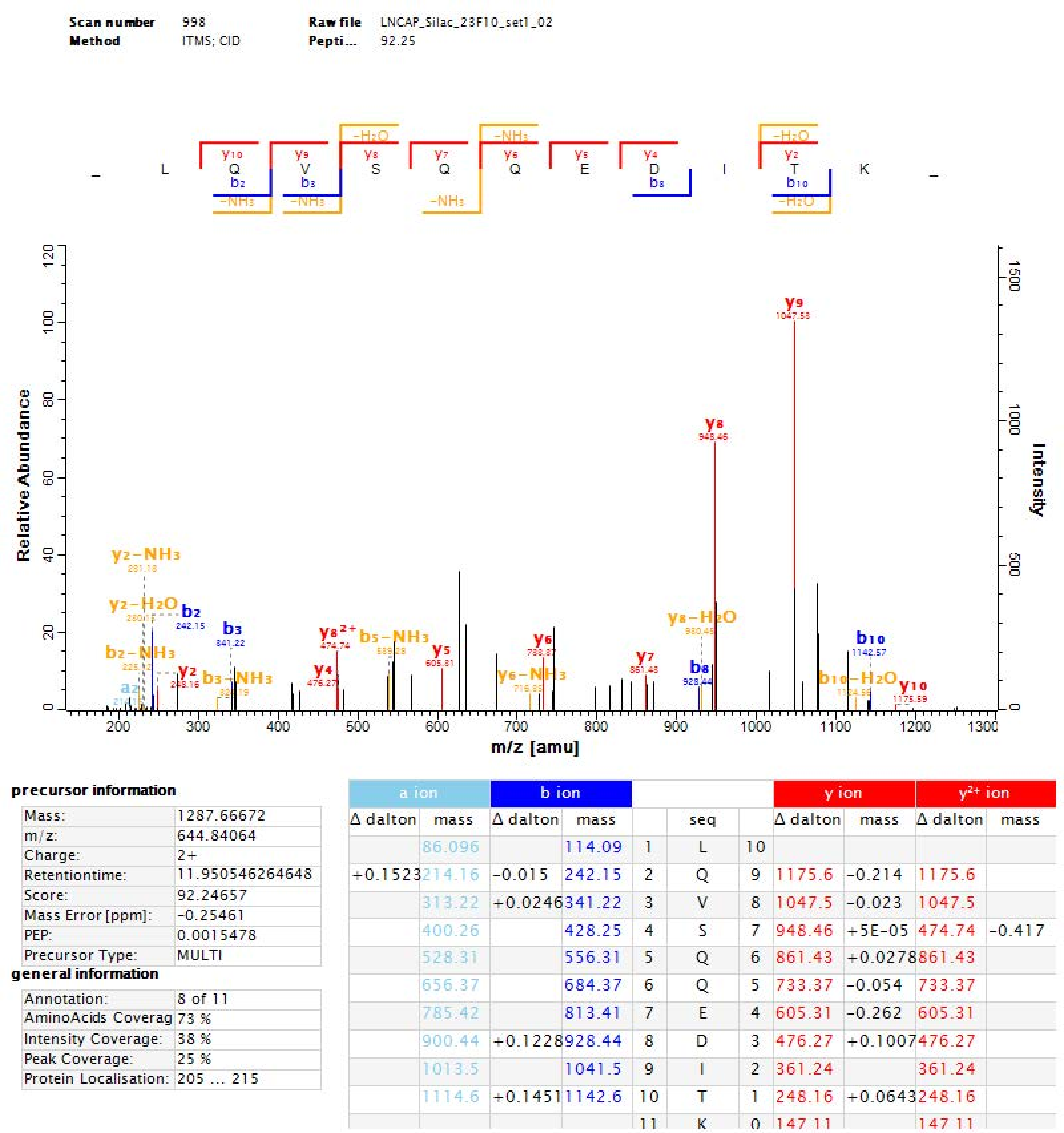
precursor information

Mass:	1622.94361
m/z:	812.47908
Charge:	2+
Retentiontime:	59.788963317871
Score:	201.3038
Mass Error [ppm]:	0.40571
PEP:	9.8581E-28
Precursor Type:	ISO

general information

Annotation:	14 of 16
AminoAcids Coverag	88 %
Intensity Coverage:	61 %
Peak Coverage:	41 %
Protein Localisation:	1 ... 16

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	132.05		132.05	1	M	15				
	245.13	-0.003	245.13	2	L	14	1492.9		1492.9	
	358.22	+0.179	358.22	3	L	13	1379.8	-0.097	690.42	+0.315
	455.27		455.27	4	P	12	1266.7	-0.061	633.87	+0.0767
	569.31		569.31	5	N	11	1169.7		1169.7	
	682.4	+0.0759	682.4	6	I	10	1055.6		1055.6	
	795.48	+0.0848	795.48	7	L	9	942.56	+0.1198	942.56	
	908.56	+0.0906	908.56	8	L	8	829.48	+0.085	829.48	
	1009.6	+0.0892	1009.6	9	T	7	716.39	+0.1371	716.39	
-0.496	533.82	+0.0143	1066.6	10	G	6	615.35	+0.0728	615.35	
	1167.7	-0.112	1167.7	11	T	5	558.32	+0.0999	558.32	
	1264.7		1264.7	12	P	4	457.28	+0.0684	457.28	
	1321.8	-0.296	1321.8	13	G	3	360.22	+0.0901	360.22	
	1420.8	-0.036	1420.8	14	V	2	303.2		303.2	
	1477.8	-0.354	1477.8	15	G	1	204.13		204.13	
				16	K	0	147.11		147.11	



Scan number	998	**Raw file**	LNCAP_Silac_23F10_set1_02
Method	ITMS; CID	**Pepti...**	92.25

precursor information

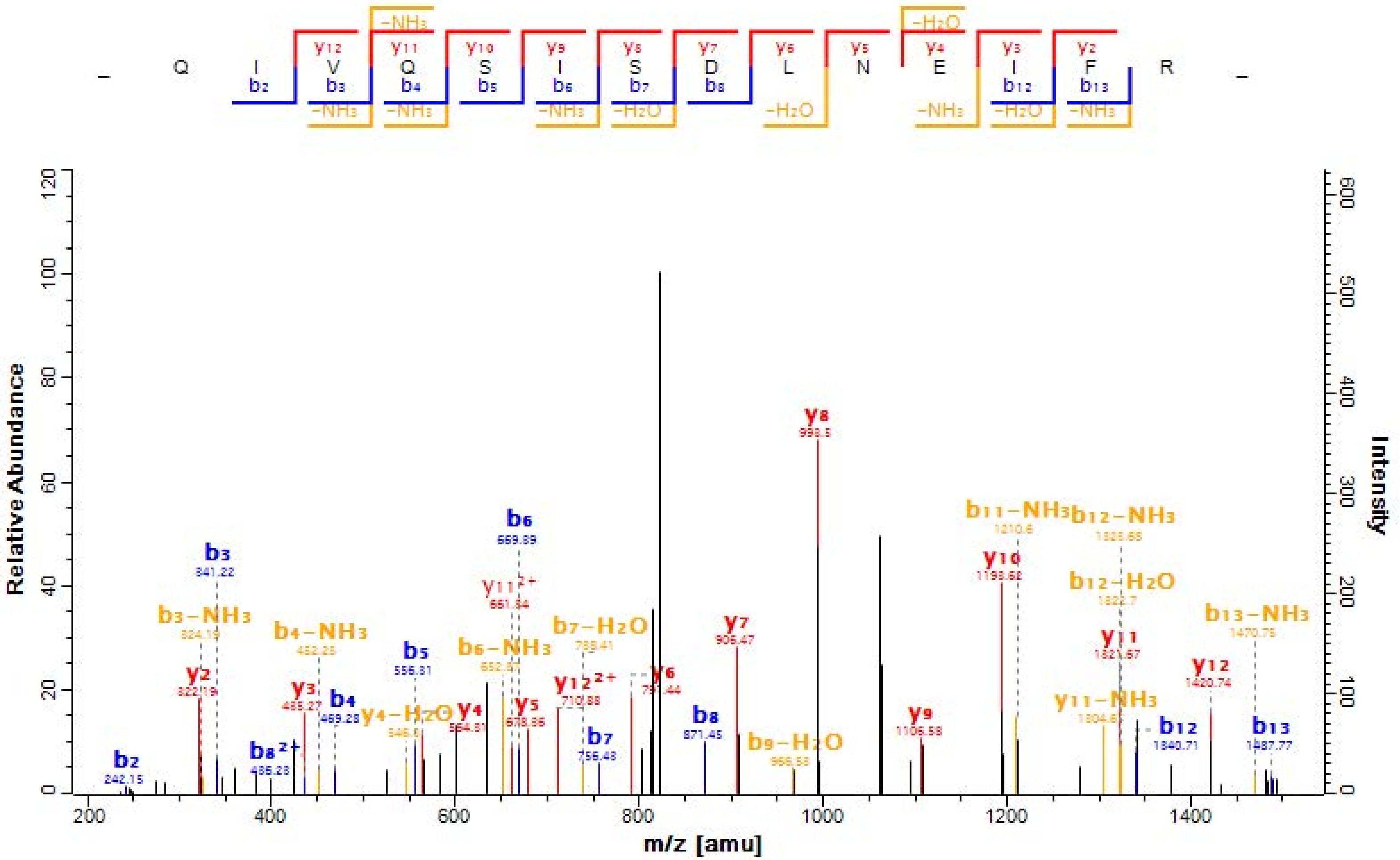
Mass:	1287.66672
m/z:	644.84064
Charge:	2+
Retentiontime:	11.950546264648
Score:	92.24657
Mass Error [ppm]:	-0.25461
PEP:	0.0015478
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	38 %
Peak Coverage:	25 %
Protein Localisation:	205 ... 215

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	10				
+0.1523	214.16	-0.015	242.15	2	Q	9	1175.6	-0.214	1175.6	
	313.22	+0.0246	341.22	3	V	8	1047.5	-0.023	1047.5	
	400.26		428.25	4	S	7	948.46	+5E-05	474.74	-0.417
	528.31		556.31	5	Q	6	861.43	+0.0278	861.43	
	656.37		684.37	6	Q	5	733.37	-0.054	733.37	
	785.42		813.41	7	E	4	605.31	-0.262	605.31	
	900.44	+0.1228	928.44	8	D	3	476.27	+0.1007	476.27	
	1013.5		1041.5	9	I	2	361.24		361.24	
	1114.6	+0.1451	1142.6	10	T	1	248.16	+0.0643	248.16	
				11	K	0	147.11		147.11	

Scan number 10072 **Raw file** LNCAP_Silac_23F10_set1_03
Method ITMS; CID **Pepti...** 186.05



precursor information

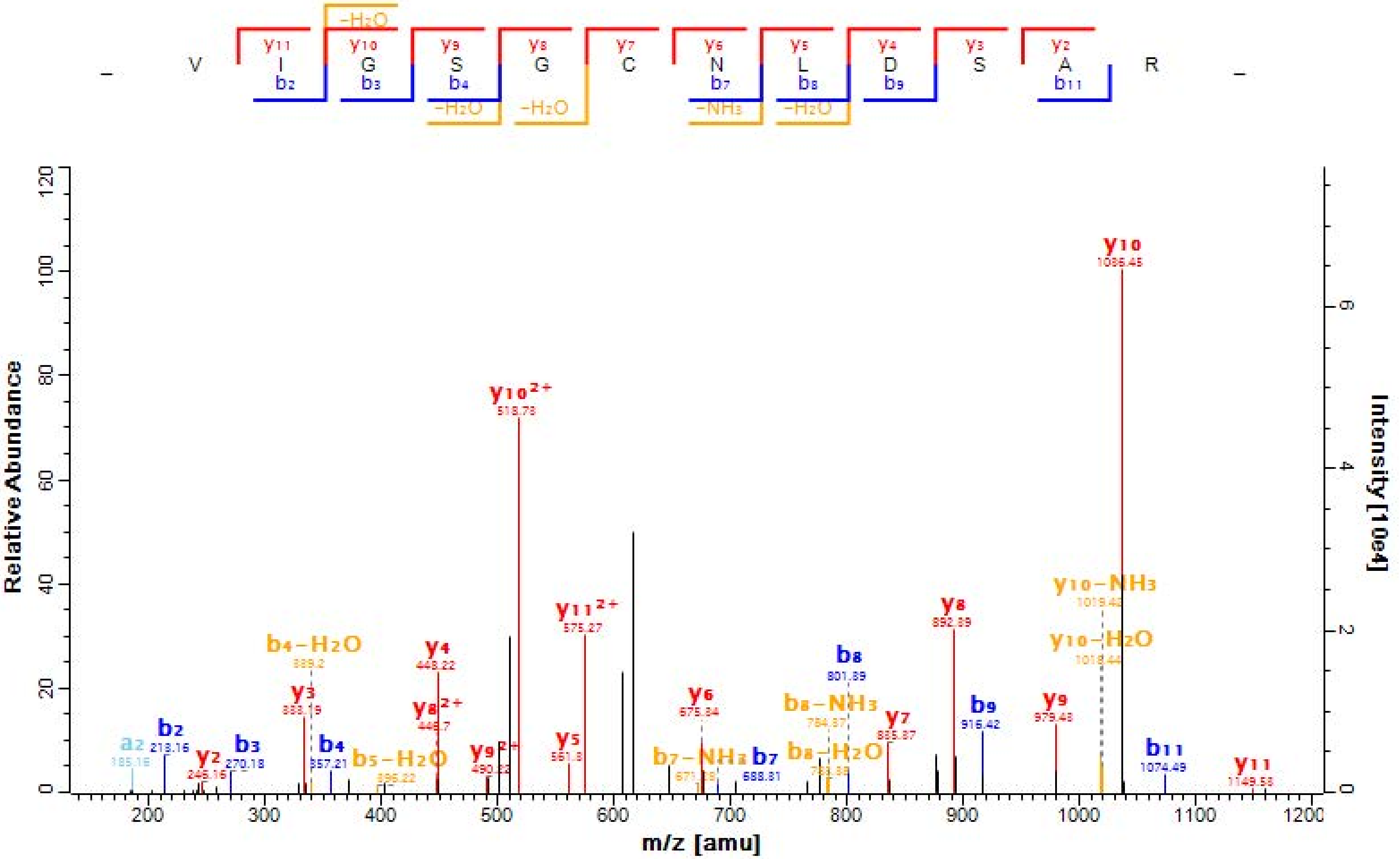
Mass:	1663.75805
m/z:	832.8863
Charge:	2+
Retentiontime:	55.281185150146
Score:	186.0512
Mass Error [ppm]:	-0.27852
PEP:	1.4098E-59
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	42 %
Peak Coverage:	43 %
Protein Localisation:	243 ... 256

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.07		129.07	1	Q	13				
	242.15	+0.1111	242.15	2	I	12	1533.8		1533.8	
	341.22	-0.132	341.22	3	V	11	1420.7	+0.0805	710.88	+0.2667
	469.28	+0.0372	469.28	4	Q	10	1321.7	-0.02	661.34	+0.3937
	556.31	+0.1488	556.31	5	S	9	1193.6	+0.1056	1193.6	
	669.39	+0.1243	669.39	6	I	8	1106.6	+0.1376	1106.6	
	756.43	-0.396	756.43	7	S	7	993.5	-0.006	993.5	
+0.2186	436.23	-0.116	871.45	8	D	6	906.47	+0.0366	906.47	
	984.54		984.54	9	L	5	791.44	-0.031	791.44	
	1098.6		1098.6	10	N	4	678.36	+0.1438	678.36	
	1227.6		1227.6	11	E	3	564.31	-0.006	564.31	
	1340.7	-0.1	1340.7	12	I	2	435.27	-0.03	435.27	
	1487.8	+0.1035	1487.8	13	F	1	322.19	+0.0719	322.19	
				14	R	0	175.12		175.12	

Scan number	1010	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	184.31



precursor information

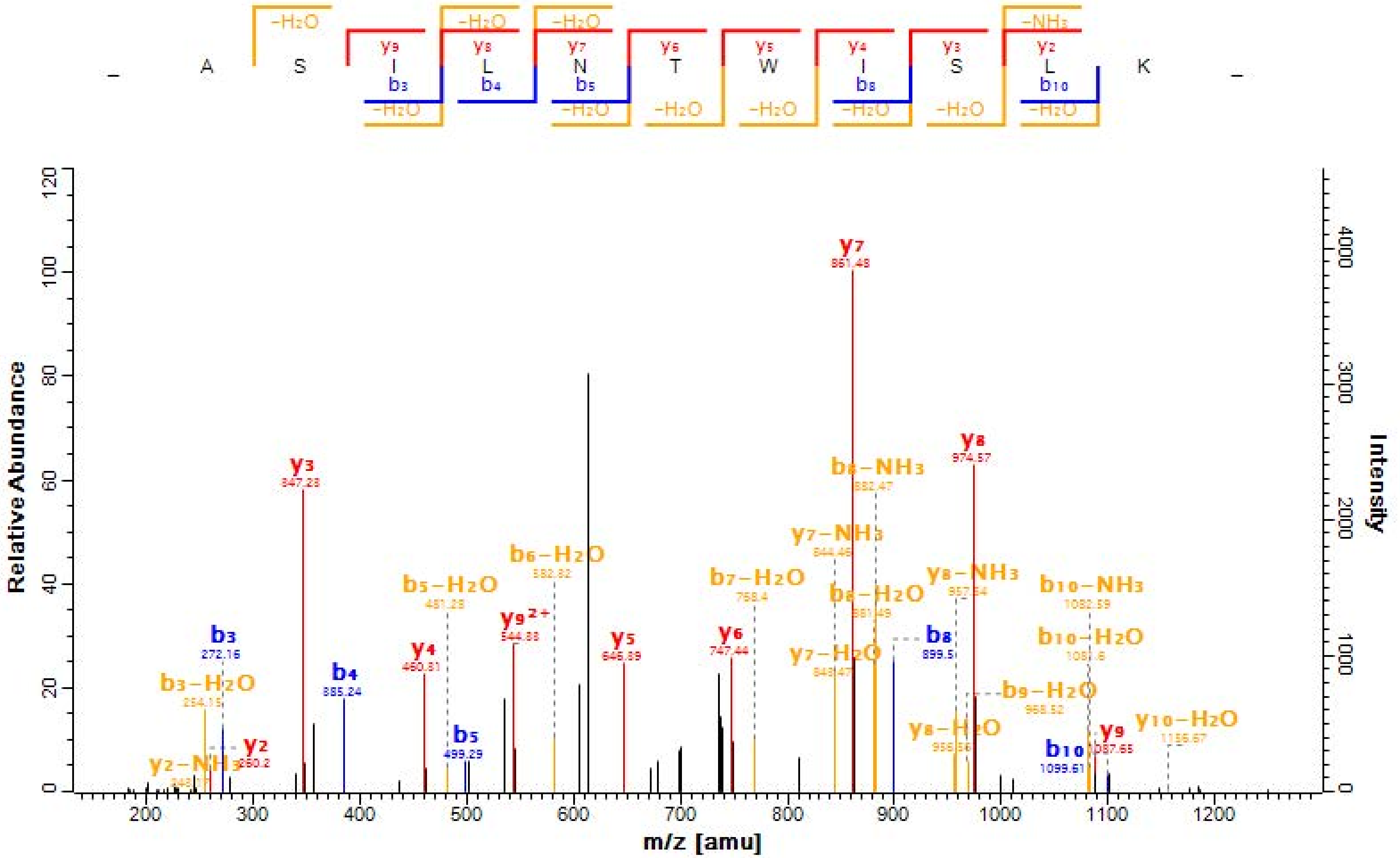
Mass:	1247.59228
m/z:	624.80342
Charge:	2+
Retentiontime:	10.886320114135
Score:	184.3138
Mass Error [ppm]:	-0.446
PEP:	3.9059E-14
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	62 %
Peak Coverage:	38 %
Protein Localisation:	187 ... 198

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.081		100.08	1	V	11				
+0.0251	185.16	-0.128	213.16	2	I	10	1149.5	-0.176	575.27	+0.2556
	242.19	-0.043	270.18	3	G	9	1036.4	+0.004	518.73	+0.2021
	329.22	+0.0191	357.21	4	S	8	979.43	-0.016	490.22	+0.2642
	386.24		414.23	5	G	7	892.39	+0.0451	446.7	+0.0138
	546.27		574.27	6	C	6	835.37	-0.022	835.37	
	660.31	+0.1367	688.31	7	N	5	675.34	-0.008	675.34	
	773.4	+0.1053	801.39	8	L	4	561.3	+0.1432	561.3	
	888.42	+0.0767	916.42	9	D	3	448.22	+0.0518	448.22	
	975.46		1003.5	10	S	2	333.19	+0.0315	333.19	
	1046.5	+0.0334	1074.5	11	A	1	246.16	-0.02	246.16	
				12	R	0	175.12		175.12	

Scan number	10226	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	151.79



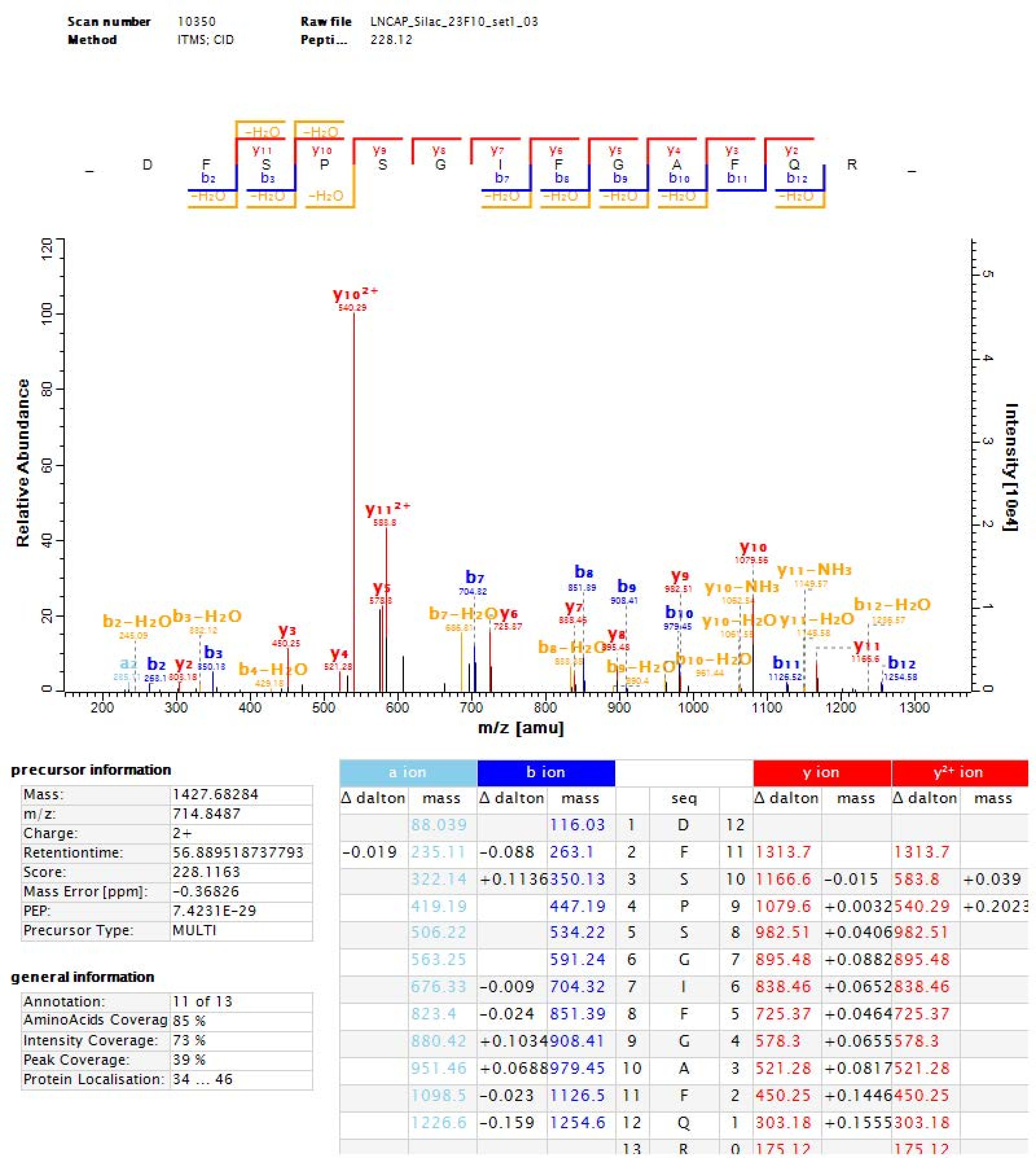
precursor information

Mass:	1244.71314
m/z:	623.36384
Charge:	2+
Retentiontime:	56.155422210693
Score:	151.7877
Mass Error [ppm]:	0.21069
PEP:	3.8263E-06
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	63 %
Peak Coverage:	34 %
Protein Localisation:	430 … 440

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	10				
	159.0764	2	S	9	1174.683		1174.683	
−0.06362	272.1605	3	I	8	1087.651	+0.004266	544.3291	+0.053793
+0.103781	385.2445	4	L	7	974.5669	−0.00615	974.5669	
+0.073732	499.2875	5	N	6	861.4829	+0.0383	861.4829	
	600.3352	6	T	5	747.44	+0.050649	747.44	
	786.4145	7	W	4	646.3923	+0.07434	646.3923	
−0.01995	899.4985	8	I	3	460.313	+0.04141	460.313	
	986.5306	9	S	2	347.2289	+0.01323	347.2289	
+0.020876	1099.615	10	L	1	260.1969	+0.05005	260.1969	
		11	K	0	147.1128		147.1128	



Scan number	10350	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	228.12

precursor information

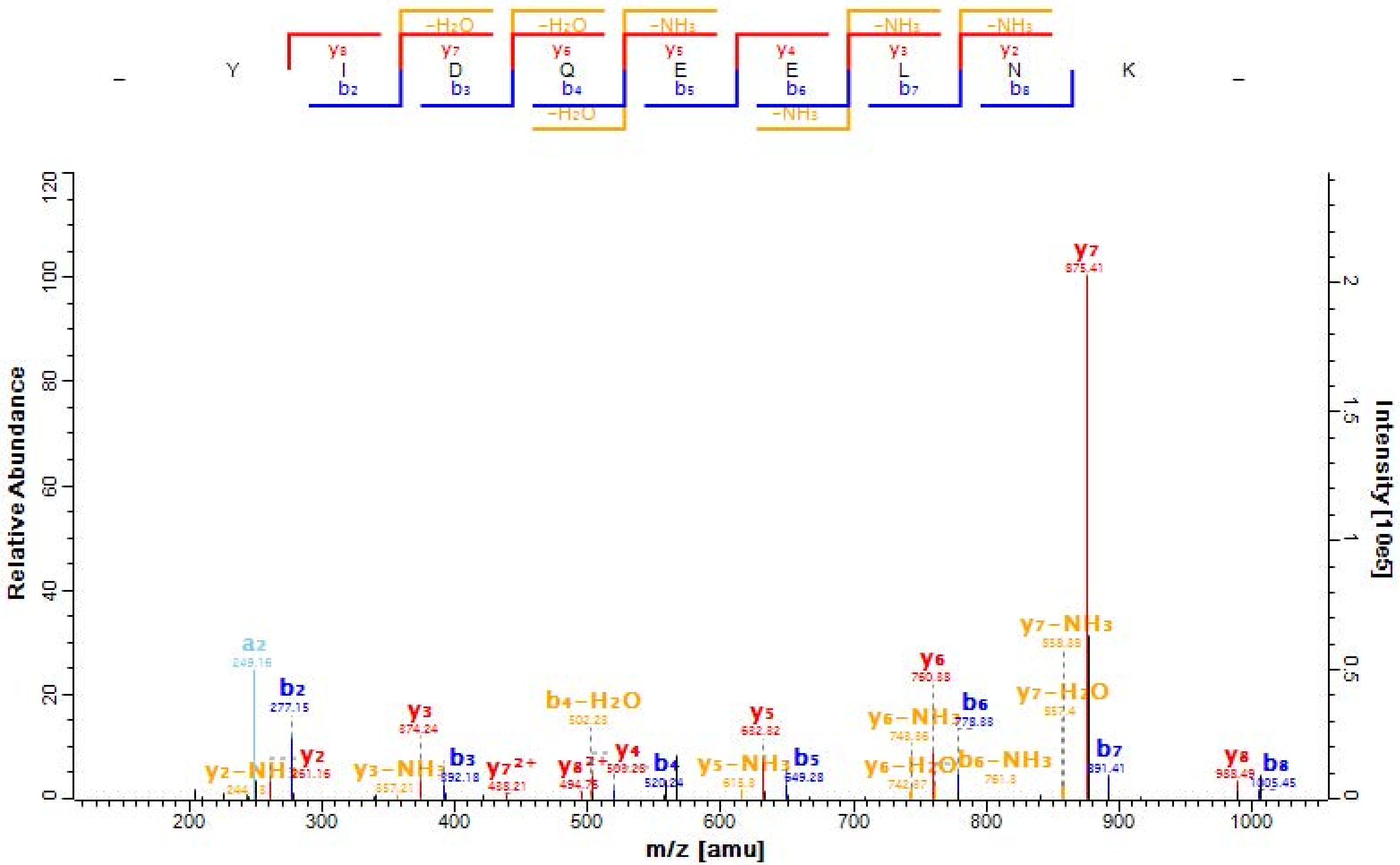
Mass:	1427.68284
m/z:	714.8487
Charge:	2+
Retentiontime:	56.889518737793
Score:	228.1163
Mass Error [ppm]:	-0.36826
PEP:	7.4231E-29
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	73 %
Peak Coverage:	39 %
Protein Localisation:	34 ... 46

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	12				
-0.019	235.11	-0.088	263.1	2	F	11	1313.7		1313.7	
	322.14	+0.1136	350.13	3	S	10	1166.6	-0.015	583.8	+0.039
	419.19		447.19	4	P	9	1079.6	+0.0032	540.29	+0.2023
	506.22		534.22	5	S	8	982.51	+0.0406	982.51	
	563.25		591.24	6	G	7	895.48	+0.0882	895.48	
	676.33	-0.009	704.32	7	I	6	838.46	+0.0652	838.46	
	823.4	-0.024	851.39	8	F	5	725.37	+0.0464	725.37	
	880.42	+0.1034	908.41	9	G	4	578.3	+0.0655	578.3	
	951.46	+0.0688	979.45	10	A	3	521.28	+0.0817	521.28	
	1098.5	-0.023	1126.5	11	F	2	450.25	+0.1446	450.25	
	1226.6	-0.159	1254.6	12	Q	1	303.18	+0.1555	303.18	
				13	R	0	175.12		175.12	

Scan number	1045	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	204.52



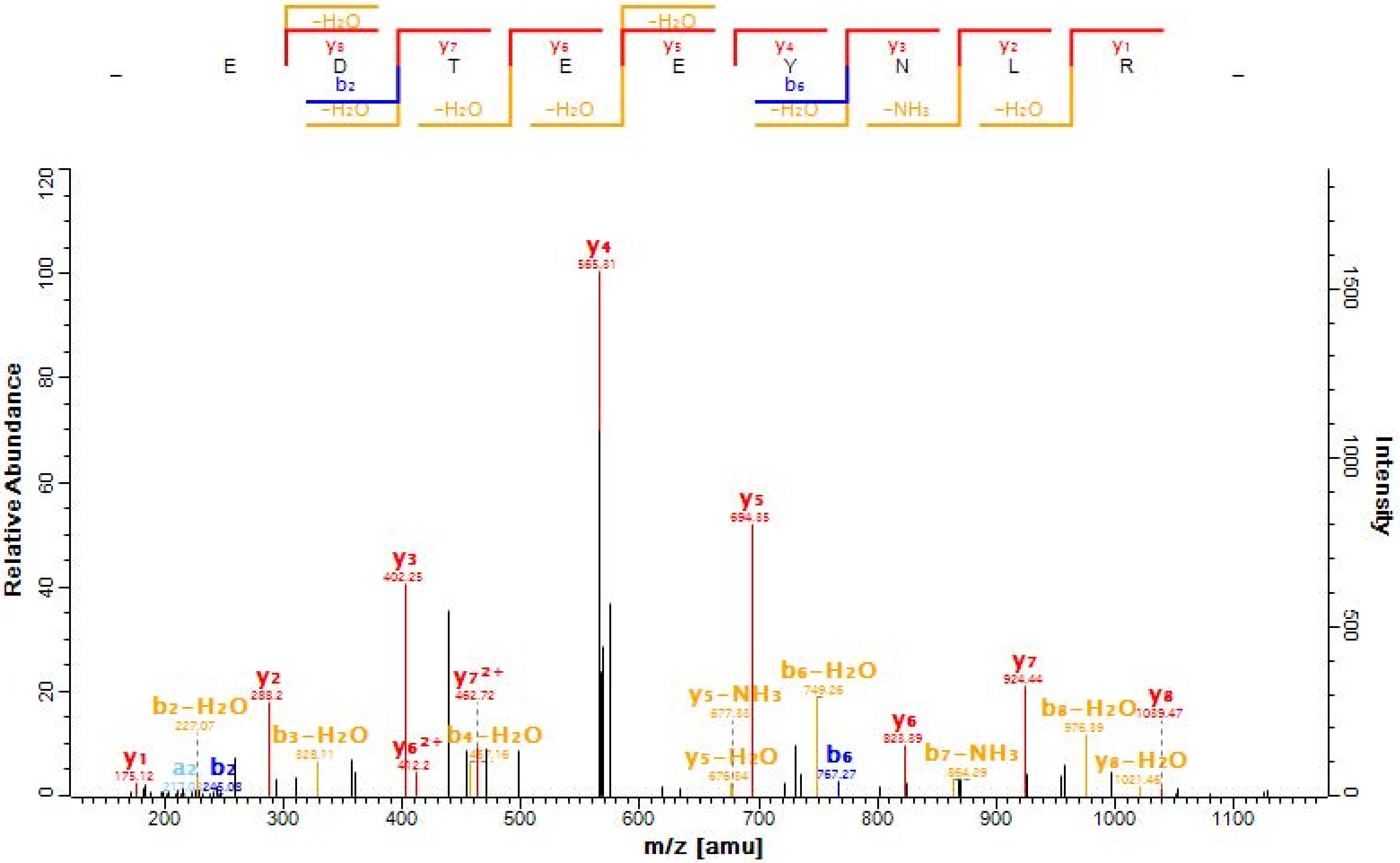
precursor information

Mass:	1150.55047
m/z:	576.28251
Charge:	2+
Retentiontime:	11.048258781433
Score:	204.5235
Mass Error [ppm]:	-0.13211
PEP:	1.3675E-12
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	74 %
Peak Coverage:	40 %
Protein Localisation:	406 ... 414

g

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.08		164.07	1	Y	8				
-0.043	249.16	-0.037	277.15	2	I	7	988.49	+0.0068	494.75	+0.2322
	364.19	+0.0611	392.18	3	D	6	875.41	-0.038	438.21	+0.2148
	492.25	+0.0696	520.24	4	Q	5	760.38	+0.035	760.38	
	621.29	-0.001	649.28	5	E	4	632.32	+0.0045	632.32	
	750.33	-0.021	778.33	6	E	3	503.28	-0.002	503.28	
	863.41	-0.053	891.41	7	L	2	374.24	+0.134	374.24	
	977.46	+0.144	1005.5	8	N	1	261.16	+0.0723	261.16	
				9	K	0	147.11		147.11	

Scan number	1050	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	115.71

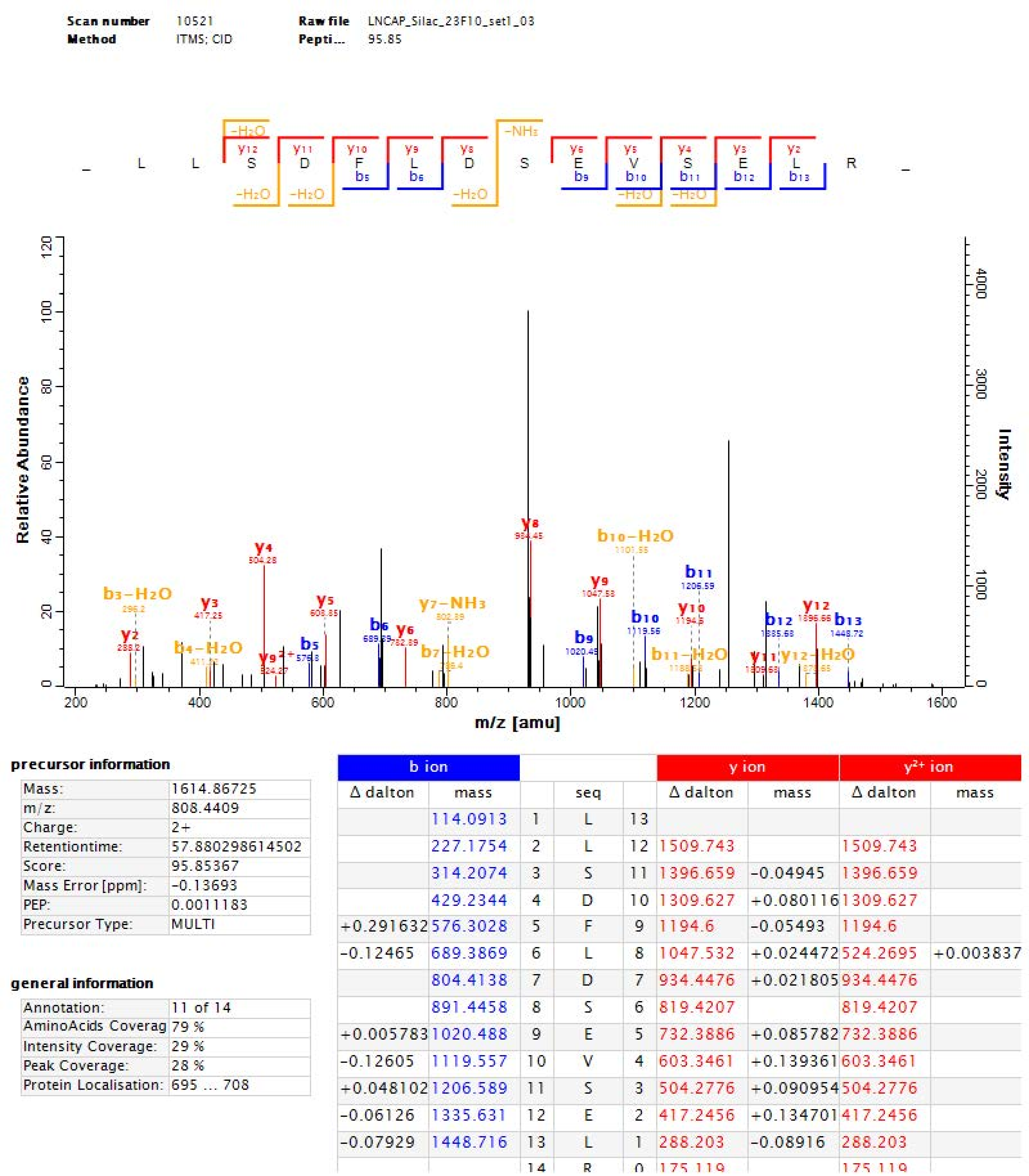


precursor information

Mass:	1167.50411
m/z:	584.75933
Charge:	2+
Retentiontime:	11.068449974060
Score:	115.7144
Mass Error [ppm]:	-0.24308
PEP:	0.00043883
Precursor Type:	ISO
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	47 %
Peak Coverage:	28 %
Protein Localisation:	135 ... 143

g

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	8				
+0.0743	217.08	+0.1919	245.08	2	D	7	1039.5	-0.061	1039.5	
	318.13		346.12	3	T	6	924.44	+0.0117	462.72	-0.022
	447.17		475.17	4	E	5	823.39	+0.1497	412.2	-0.017
	576.21		604.21	5	E	4	694.35	+0.012	694.35	
	739.28	+0.0853	767.27	6	Y	3	565.31	+0.0281	565.31	
	853.32		881.32	7	N	2	402.25	+0.0324	402.25	
	966.41		994.4	8	L	1	288.2	+0.0806	288.2	
				9	R	0	175.12	-0.014	175.12	



Scan number	10521	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	95.85

precursor information

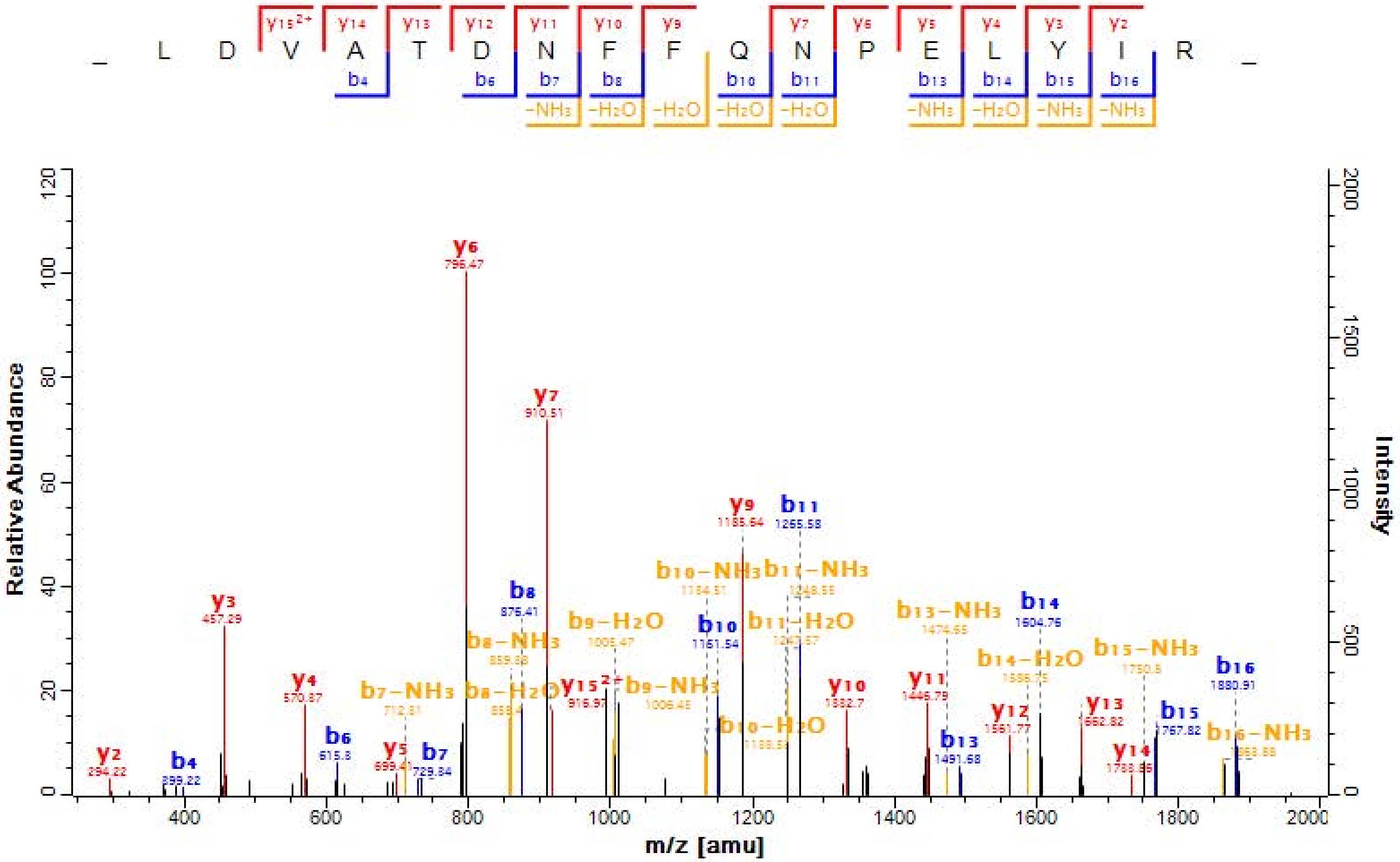
Mass:	1614.86725
m/z:	808.4409
Charge:	2+
Retentiontime:	57.880298614502
Score:	95.85367
Mass Error [ppm]:	-0.13693
PEP:	0.0011183
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	29 %
Peak Coverage:	28 %
Protein Localisation:	695 ... 708

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	13				
	227.1754	2	L	12	1509.743		1509.743	
	314.2074	3	S	11	1396.659	-0.04945	1396.659	
	429.2344	4	D	10	1309.627	+0.080116	1309.627	
+0.291632	576.3028	5	F	9	1194.6	-0.05493	1194.6	
-0.12465	689.3869	6	L	8	1047.532	+0.024472	524.2695	+0.003837
	804.4138	7	D	7	934.4476	+0.021805	934.4476	
	891.4458	8	S	6	819.4207		819.4207	
+0.005783	1020.488	9	E	5	732.3886	+0.085782	732.3886	
-0.12605	1119.557	10	V	4	603.3461	+0.139361	603.3461	
+0.048102	1206.589	11	S	3	504.2776	+0.090954	504.2776	
-0.06126	1335.631	12	E	2	417.2456	+0.134701	417.2456	
-0.07929	1448.716	13	L	1	288.203	-0.08916	288.203	
		14	R	0	175.119		175.119	

Scan number	10570	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	208.43



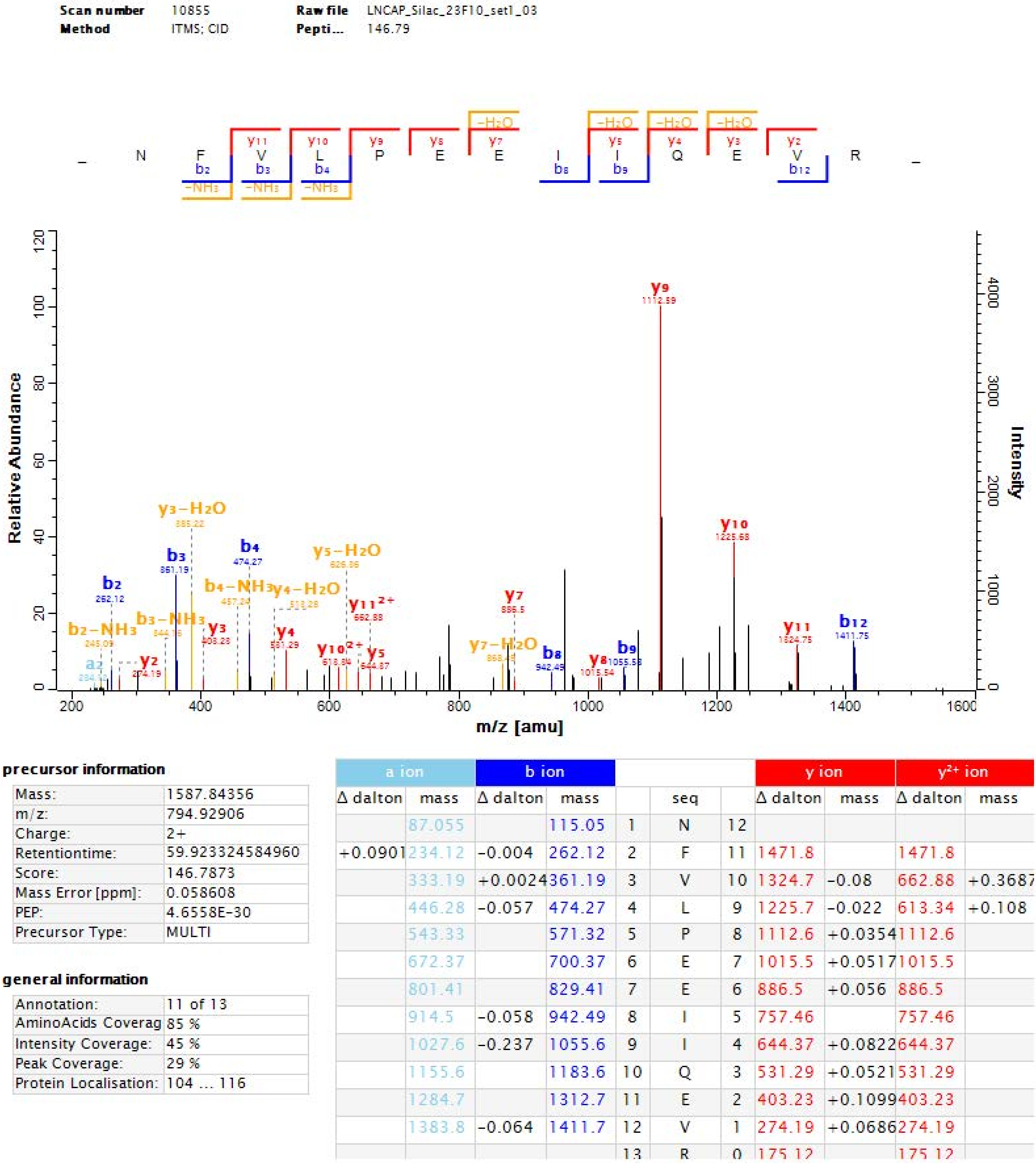
precursor information

Mass:	2054.01104
m/z:	1028.0128
Charge:	2+
Retentiontime:	58.155178070068
Score:	208.4329
Mass Error [ppm]:	0.067368
PEP:	5.2887E-40
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	58 %
Peak Coverage:	38 %
Protein Localisation:	37 ... 53

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	16				
	229.1183	2	D	15	1947.954		1947.954	
	328.1867	3	V	14	1832.927		916.9673	+0.317378
+0.046575	399.2238	4	A	13	1733.859	+0.009884	1733.859	
	500.2715	5	T	12	1662.822	-0.08996	1662.822	
+0.144255	615.2984	6	D	11	1561.774	+0.019969	1561.774	
+0.238596	729.3414	7	N	10	1446.747	-0.01132	1446.747	
-0.0775	876.4098	8	F	9	1332.704	+0.038815	1332.704	
	1023.478	9	F	8	1185.636	+0.151784	1185.636	
-0.12551	1151.537	10	Q	7	1038.567		1038.567	
-0.07847	1265.58	11	N	6	910.5088	+0.052945	910.5088	
	1362.632	12	P	5	796.4659	-0.03486	796.4659	
+0.00244	1491.675	13	E	4	699.4131	+0.143876	699.4131	
-0.01729	1604.759	14	L	3	570.3705	+0.073066	570.3705	
-0.13958	1767.822	15	Y	2	457.2865	+0.091486	457.2865	
+0.034045	1880.907	16	I	1	294.2231	+0.043884	294.2231	
		17	R	0	181.1391		181.1391	



Scan number	10855	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	146.79

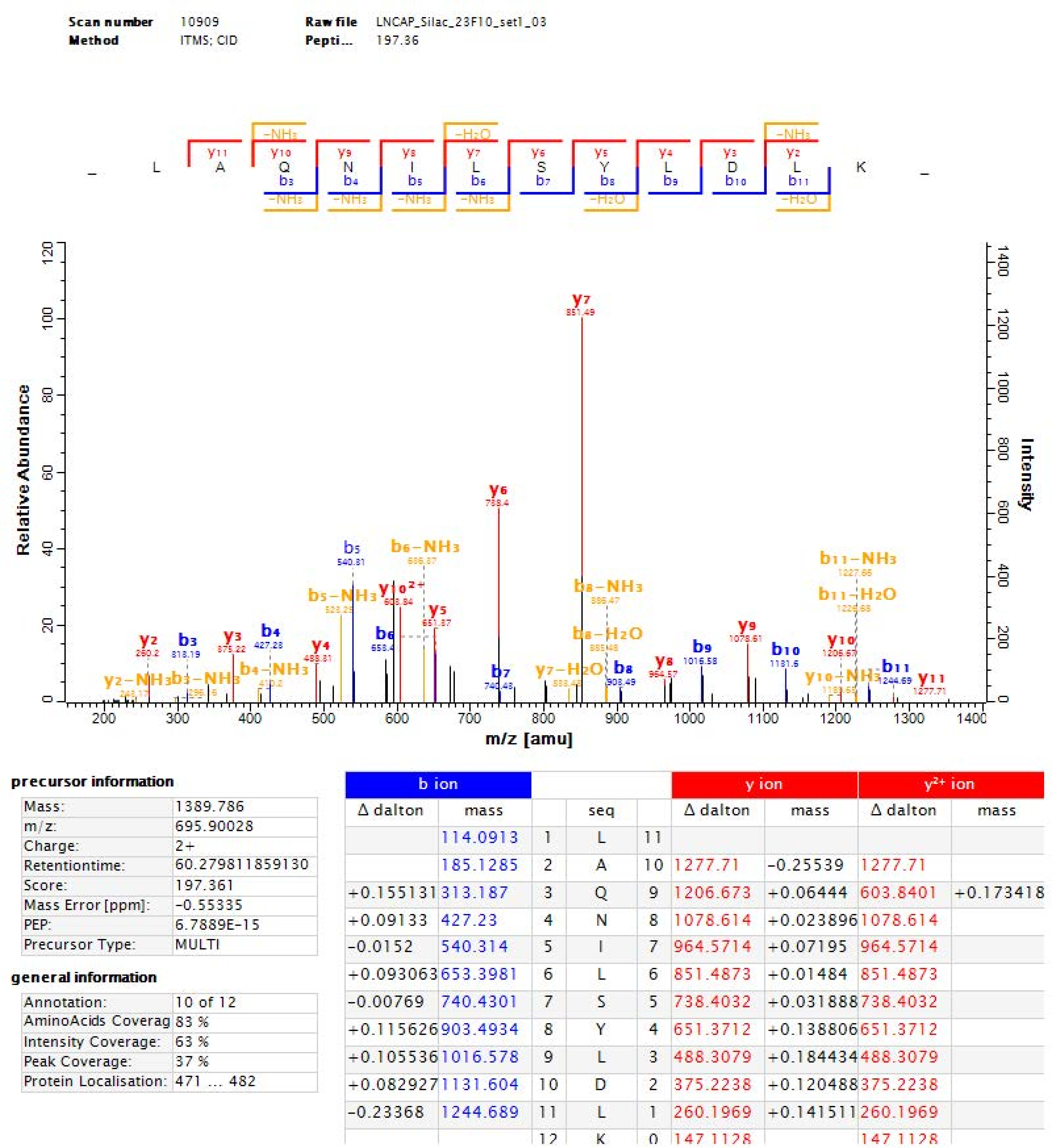
precursor information

Mass:	1587.84356
m/z:	794.92906
Charge:	2+
Retentiontime:	59.923324584960
Score:	146.7873
Mass Error [ppm]:	0.058608
PEP:	4.6558E-30
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	45 %
Peak Coverage:	29 %
Protein Localisation:	104 ... 116

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	87.055		115.05	1	N	12				
+0.0901	234.12	-0.004	262.12	2	F	11	1471.8		1471.8	
	333.19	+0.0024	361.19	3	V	10	1324.7	-0.08	662.88	+0.3687
	446.28	-0.057	474.27	4	L	9	1225.7	-0.022	613.34	+0.108
	543.33		571.32	5	P	8	1112.6	+0.0354	1112.6	
	672.37		700.37	6	E	7	1015.5	+0.0517	1015.5	
	801.41		829.41	7	E	6	886.5	+0.056	886.5	
	914.5	-0.058	942.49	8	I	5	757.46		757.46	
	1027.6	-0.237	1055.6	9	I	4	644.37	+0.0822	644.37	
	1155.6		1183.6	10	Q	3	531.29	+0.0521	531.29	
	1284.7		1312.7	11	E	2	403.23	+0.1099	403.23	
	1383.8	-0.064	1411.7	12	V	1	274.19	+0.0686	274.19	
				13	R	0	175.12		175.12	



Scan number	10909	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	197.36

precursor information

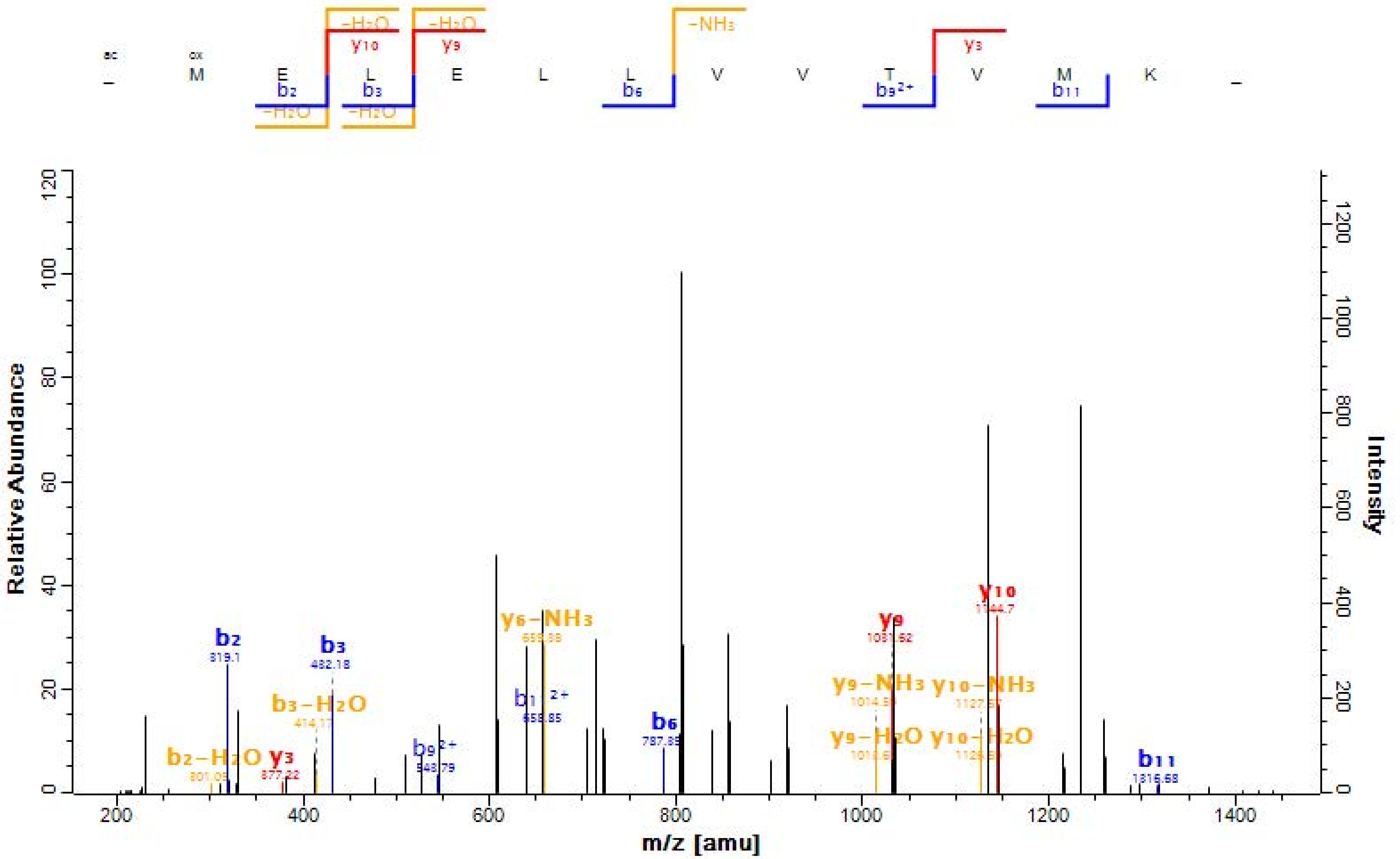
Mass:	1389.786
m/z:	695.90028
Charge:	2+
Retentiontime:	60.279811859130
Score:	197.361
Mass Error [ppm]:	-0.55335
PEP:	6.7889E-15
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	63 %
Peak Coverage:	37 %
Protein Localisation:	471 ... 482

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	11				
	185.1285	2	A	10	1277.71	-0.25539	1277.71	
+0.155131	313.187	3	Q	9	1206.673	+0.06444	603.8401	+0.173418
+0.09133	427.23	4	N	8	1078.614	+0.023896	1078.614	
-0.0152	540.314	5	I	7	964.5714	+0.07195	964.5714	
+0.093063	653.3981	6	L	6	851.4873	+0.01484	851.4873	
-0.00769	740.4301	7	S	5	738.4032	+0.031888	738.4032	
+0.115626	903.4934	8	Y	4	651.3712	+0.138806	651.3712	
+0.105536	1016.578	9	L	3	488.3079	+0.184434	488.3079	
+0.082927	1131.604	10	D	2	375.2238	+0.120488	375.2238	
-0.23368	1244.689	11	L	1	260.1969	+0.141511	260.1969	
		12	K	0	147.1128		147.1128	

Scan number	10974	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	78.49



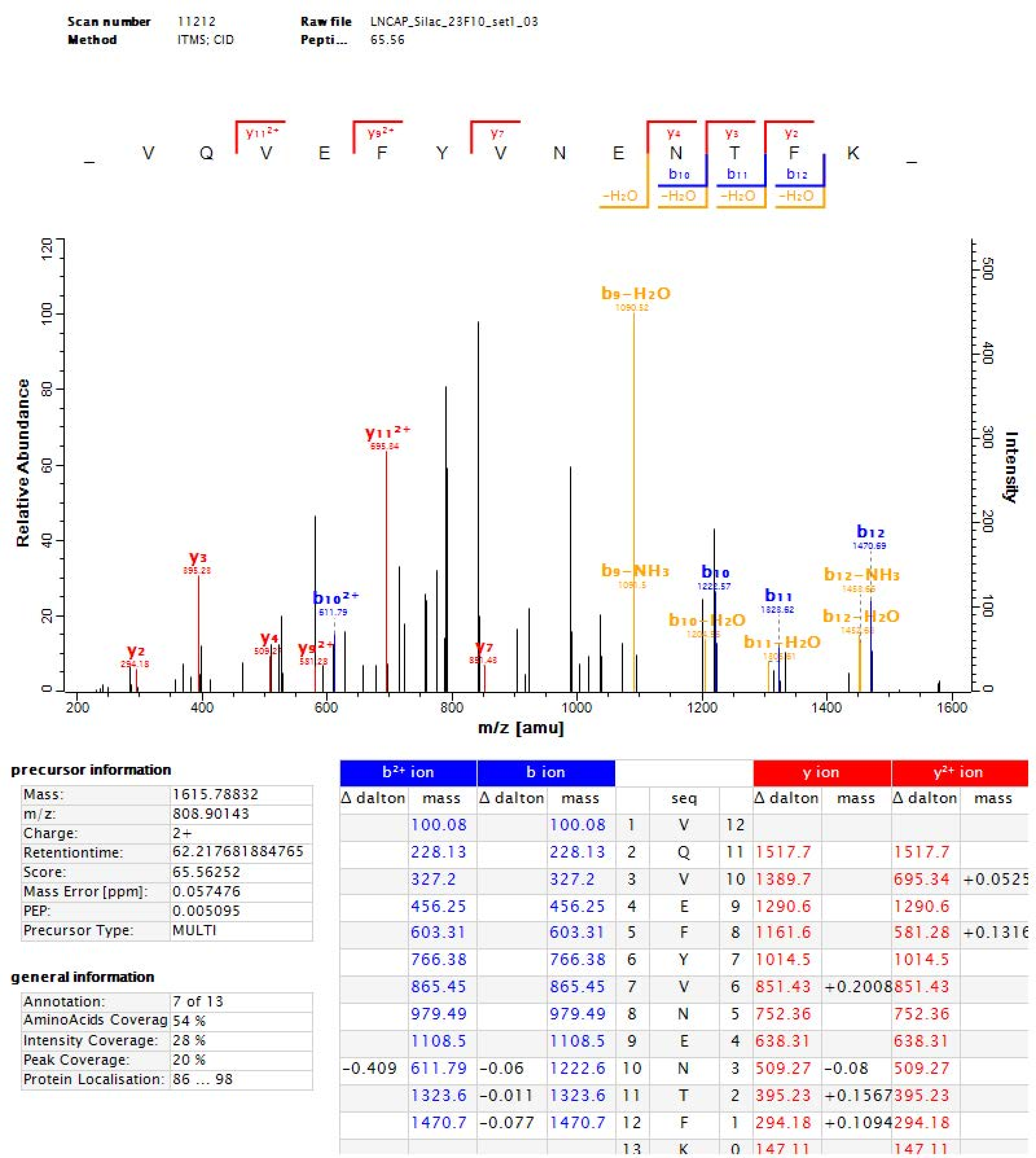
precursor information

Mass:	1461.78336
m/z:	731.89895
Charge:	2+
Retentiontime:	60.685070037841
Score:	78.48815
Mass Error [ppm]:	0.74046
PEP:	0.010877
Precursor Type:	MULTI

general information

Annotation:	8 of 12
AminoAcids Coverag	67 %
Intensity Coverage:	18 %
Peak Coverage:	20 %
Protein Localisation:	1 ... 12

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	190.0532		190.0532	1	M	11		
	319.0958	+0.163566	319.0958	2	E	10	1273.744	
	432.1799	+0.099521	432.1799	3	L	9	1144.701	-0.16376
	561.2225		561.2225	4	E	8	1031.617	-0.10289
	674.3066		674.3066	5	L	7	902.5743	
	787.3906	+0.119574	787.3906	6	L	6	789.4903	
	886.459		886.459	7	V	5	676.4062	
	985.5274		985.5274	8	V	4	577.3378	
-0.25714	543.7912		1086.575	9	T	3	478.2694	
	1185.644		1185.644	10	V	2	377.2217	+0.260109
-0.06654	658.8456	-0.14997	1316.684	11	M	1	278.1533	
				12	K	0	147.1128	



Scan number	11212	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	65.56

precursor information

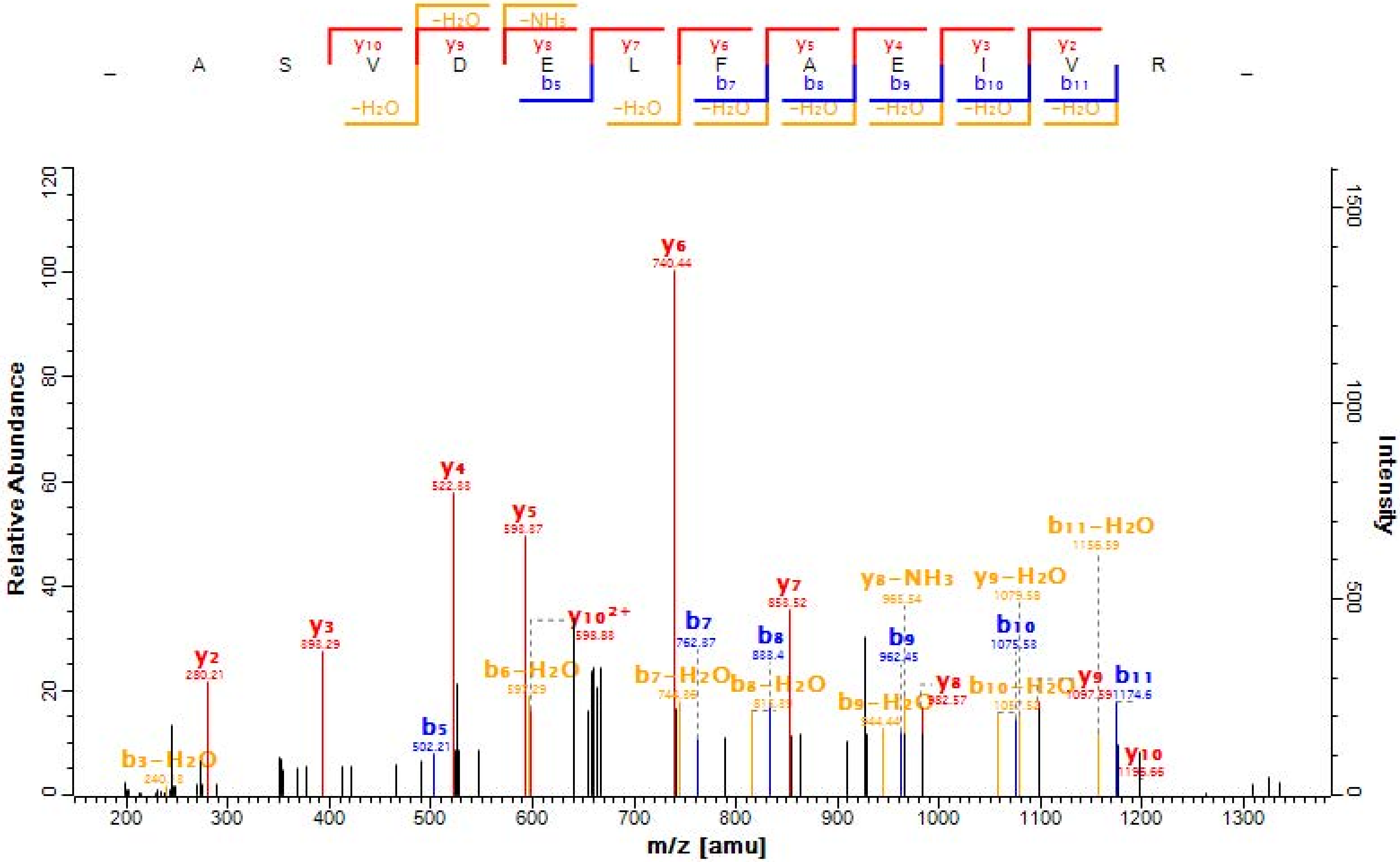
Mass:	1615.78832
m/z:	808.90143
Charge:	2+
Retentiontime:	62.217681884765
Score:	65.56252
Mass Error [ppm]:	0.057476
PEP:	0.005095
Precursor Type:	MULTI

general information

Annotation:	7 of 13
AminoAcids Coverag	54 %
Intensity Coverage:	28 %
Peak Coverage:	20 %
Protein Localisation:	86 ... 98

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	12				
	228.13		228.13	2	Q	11	1517.7		1517.7	
	327.2		327.2	3	V	10	1389.7		695.34	+0.0525
	456.25		456.25	4	E	9	1290.6		1290.6	
	603.31		603.31	5	F	8	1161.6		581.28	+0.1316
	766.38		766.38	6	Y	7	1014.5		1014.5	
	865.45		865.45	7	V	6	851.43	+0.2008	851.43	
	979.49		979.49	8	N	5	752.36		752.36	
	1108.5		1108.5	9	E	4	638.31		638.31	
-0.409	611.79	-0.06	1222.6	10	N	3	509.27	-0.08	509.27	
	1323.6	-0.011	1323.6	11	T	2	395.23	+0.1567	395.23	
	1470.7	-0.077	1470.7	12	F	1	294.18	+0.1094	294.18	
				13	K	0	147.11		147.11	

Scan number	11240	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	134.49



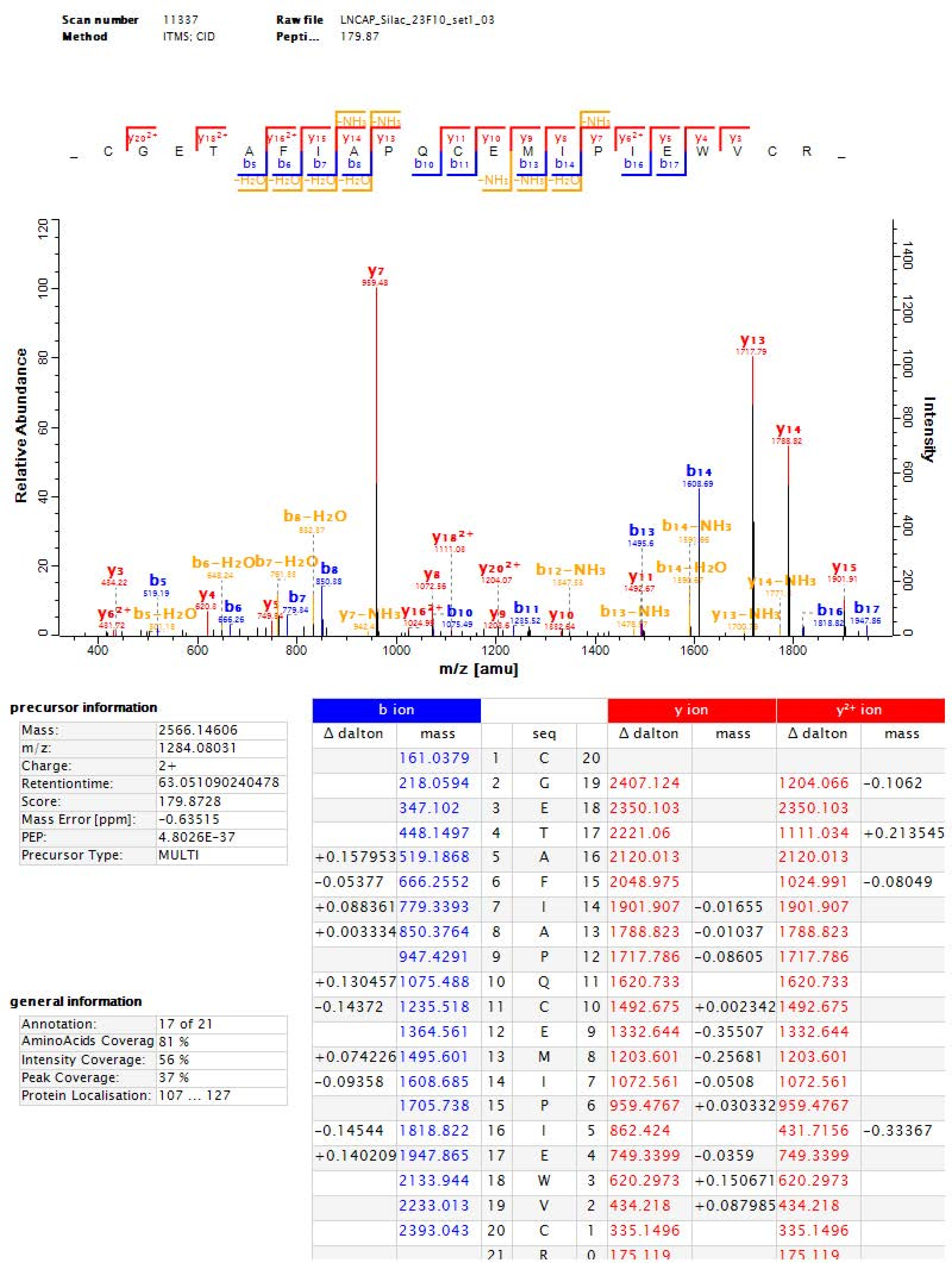
precursor information

Mass:	1347.70291
m/z:	674.85873
Charge:	2+
Retentiontime:	62.410984039306
Score:	134.4899
Mass Error [ppm]:	-0.3878
PEP:	2.5331E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	54 %
Peak Coverage:	29 %
Protein Localisation:	151 ... 162

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	11				
	159.0764	2	S	10	1283.694		1283.694	
	258.1448	3	V	9	1196.662	-0.05085	598.8345	+0.10747
	373.1718	4	D	8	1097.593	+0.035992	1097.593	
+0.066149	502.2144	5	E	7	982.5663	+0.144906	982.5663	
	615.2984	6	L	6	853.5237	+0.104979	853.5237	
-0.02987	762.3668	7	F	5	740.4397	+0.04262	740.4397	
-0.04465	833.404	8	A	4	593.3713	+0.049999	593.3713	
+0.013835	962.4466	9	E	3	522.3342	+0.023941	522.3342	
-0.04661	1075.531	10	I	2	393.2916	+0.028875	393.2916	
-0.18839	1174.599	11	V	1	280.2075	+0.032312	280.2075	
		12	R	0	181.1391		181.1391	



Scan number	11337	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	179.87

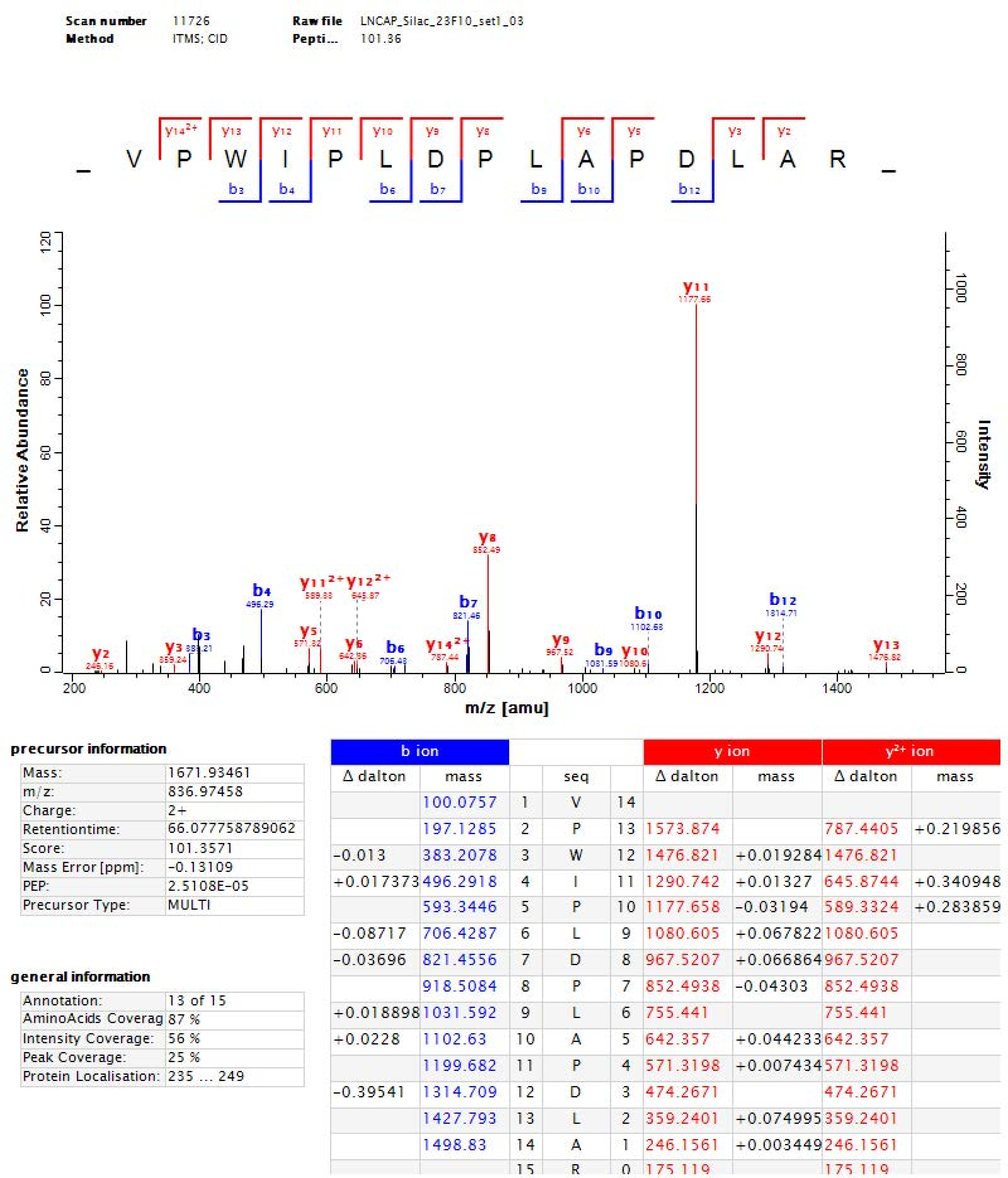
precursor information

Mass:	2566.14606
m/z:	1284.08031
Charge:	2+
Retentiontime:	63.051090240478
Score:	179.8728
Mass Error [ppm]:	-0.63515
PEP:	4.8026E-37
Precursor Type:	MULTI

general information

Annotation:	17 of 21
AminoAcids Coverag	81 %
Intensity Coverage:	56 %
Peak Coverage:	37 %
Protein Localisation:	107 ... 127

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	161.0379	1	C	20				
	218.0594	2	G	19	2407.124		1204.066	-0.1062
	347.102	3	E	18	2350.103		2350.103	
	448.1497	4	T	17	2221.06		1111.034	+0.213545
+0.157953	519.1868	5	A	16	2120.013		2120.013	
-0.05377	666.2552	6	F	15	2048.975		1024.991	-0.08049
+0.088361	779.3393	7	I	14	1901.907	-0.01655	1901.907	
+0.003334	850.3764	8	A	13	1788.823	-0.01037	1788.823	
	947.4291	9	P	12	1717.786	-0.08605	1717.786	
+0.130457	1075.488	10	Q	11	1620.733		1620.733	
-0.14372	1235.518	11	C	10	1492.675	+0.002342	1492.675	
	1364.561	12	E	9	1332.644	-0.35507	1332.644	
+0.074226	1495.601	13	M	8	1203.601	-0.25681	1203.601	
-0.09358	1608.685	14	I	7	1072.561	-0.0508	1072.561	
	1705.738	15	P	6	959.4767	+0.030332	959.4767	
-0.14544	1818.822	16	I	5	862.424		431.7156	-0.33367
+0.140209	1947.865	17	E	4	749.3399	-0.0359	749.3399	
	2133.944	18	W	3	620.2973	+0.150671	620.2973	
	2233.013	19	V	2	434.218	+0.087985	434.218	
	2393.043	20	C	1	335.1496		335.1496	
		21	R	0	175.119		175.119	



Scan number	11726	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	101.36

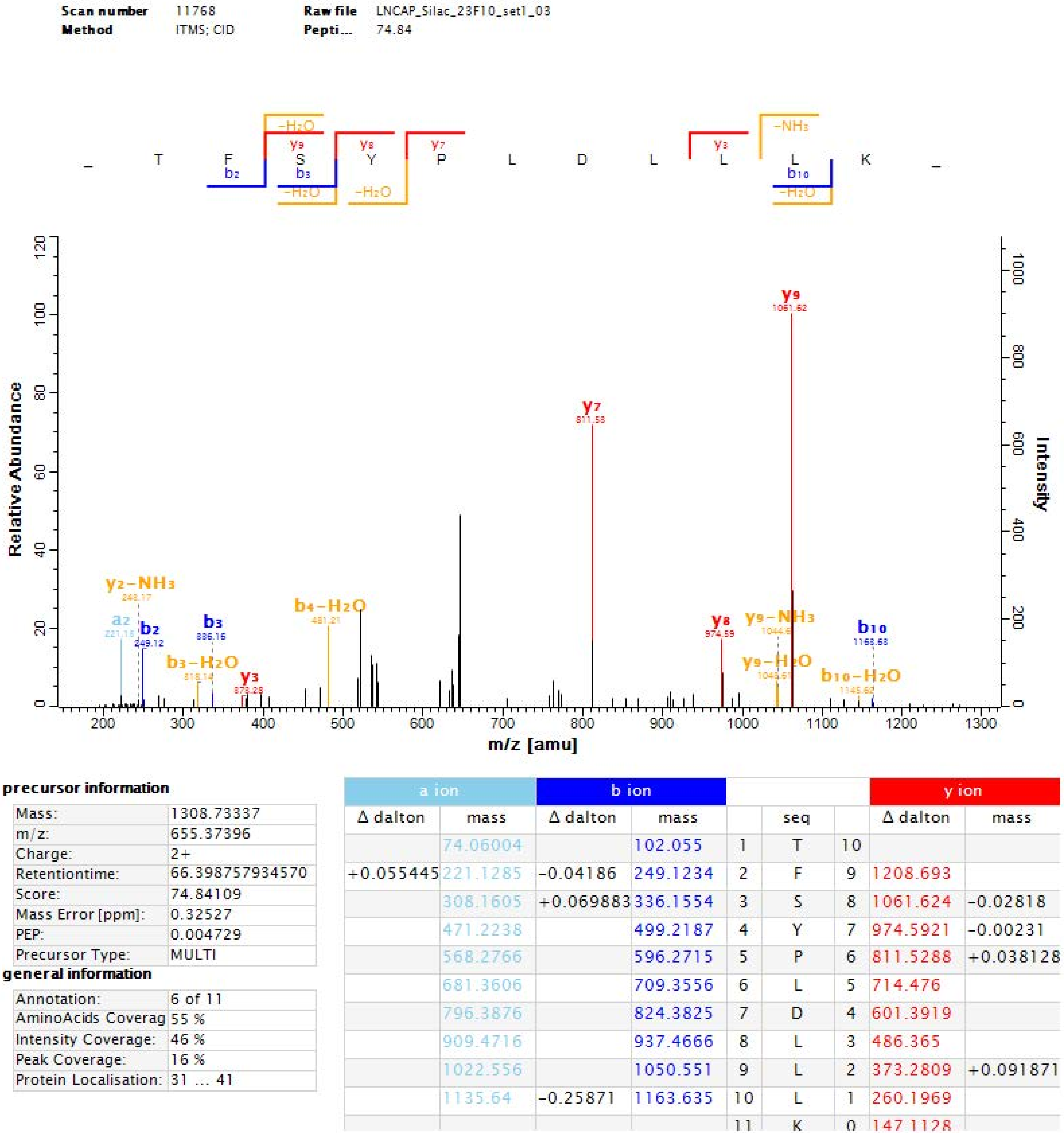
precursor information

Mass:	1671.93461
m/z:	836.97458
Charge:	2+
Retentiontime:	66.077758789062
Score:	101.3571
Mass Error [ppm]:	-0.13109
PEP:	2.5108E-05
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	56 %
Peak Coverage:	25 %
Protein Localisation:	235 ... 249

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	14				
	197.1285	2	P	13	1573.874		787.4405	+0.219856
-0.013	383.2078	3	W	12	1476.821	+0.019284	1476.821	
+0.017373	496.2918	4	I	11	1290.742	+0.01327	645.8744	+0.340948
	593.3446	5	P	10	1177.658	-0.03194	589.3324	+0.283859
-0.08717	706.4287	6	L	9	1080.605	+0.067822	1080.605	
-0.03696	821.4556	7	D	8	967.5207	+0.066864	967.5207	
	918.5084	8	P	7	852.4938	-0.04303	852.4938	
+0.018898	1031.592	9	L	6	755.441		755.441	
+0.0228	1102.63	10	A	5	642.357	+0.044233	642.357	
	1199.682	11	P	4	571.3198	+0.007434	571.3198	
-0.39541	1314.709	12	D	3	474.2671		474.2671	
	1427.793	13	L	2	359.2401	+0.074995	359.2401	
	1498.83	14	A	1	246.1561	+0.003449	246.1561	
		15	R	0	175.119		175.119	



Scan number	11768	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	74.84

precursor information

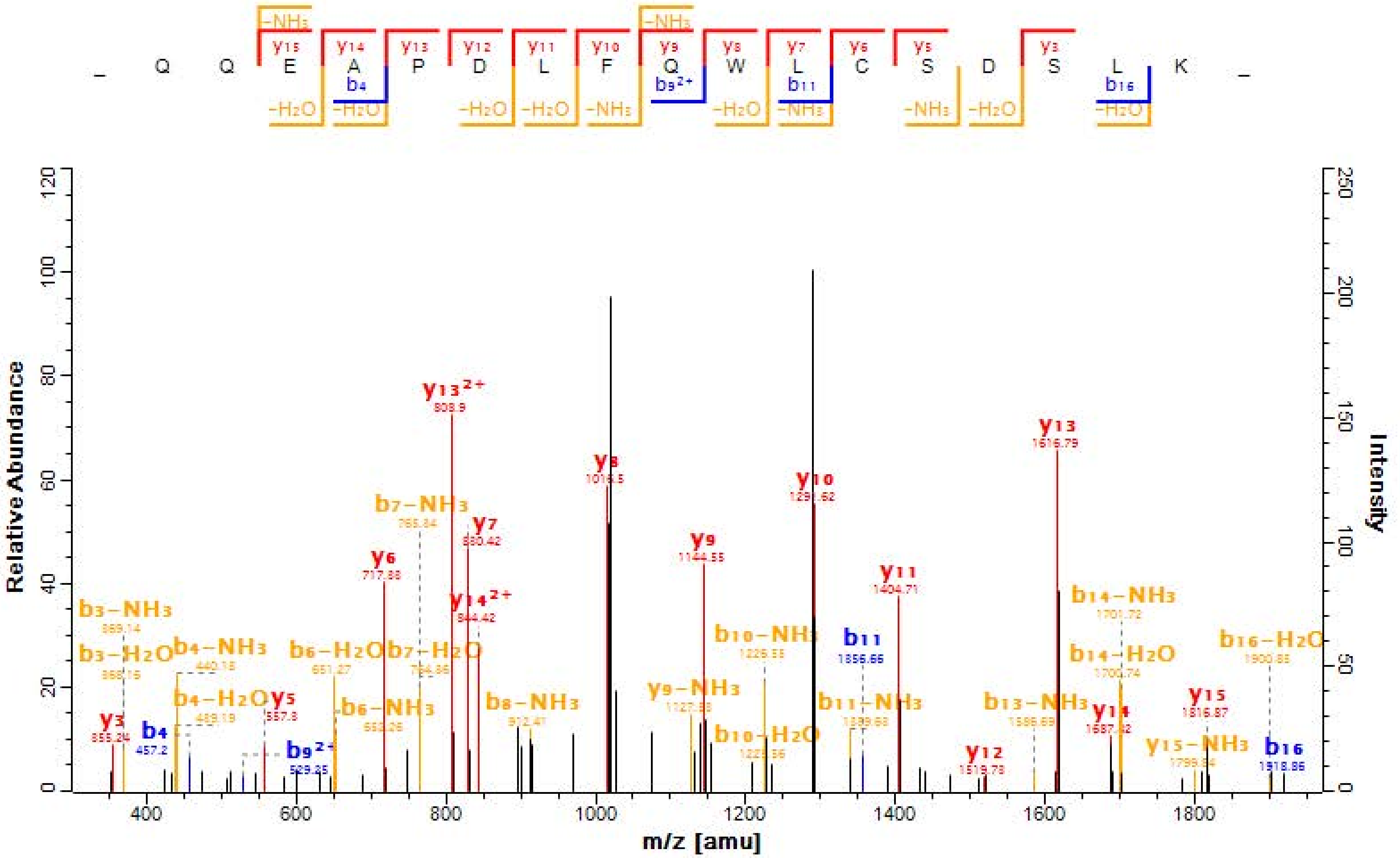
Mass:	1308.73337
m/z:	655.37396
Charge:	2+
Retentiontime:	66.398757934570
Score:	74.84109
Mass Error [ppm]:	0.32527
PEP:	0.004729
Precursor Type:	MULTI

general information

Annotation:	6 of 11
AminoAcids Coverag	55 %
Intensity Coverage:	46 %
Peak Coverage:	16 %
Protein Localisation:	31 ... 41

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	74.06004		102.055	1	T	10		
+0.055445	221.1285	-0.04186	249.1234	2	F	9	1208.693	
	308.1605	+0.069883	336.1554	3	S	8	1061.624	-0.02818
	471.2238		499.2187	4	Y	7	974.5921	-0.00231
	568.2766		596.2715	5	P	6	811.5288	+0.038128
	681.3606		709.3556	6	L	5	714.476	
	796.3876		824.3825	7	D	4	601.3919	
	909.4716		937.4666	8	L	3	486.365	
	1022.556		1050.551	9	L	2	373.2809	+0.091871
	1135.64	-0.25871	1163.635	10	L	1	260.1969	
				11	K	0	147.1128	

Scan number	11876	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	127.83



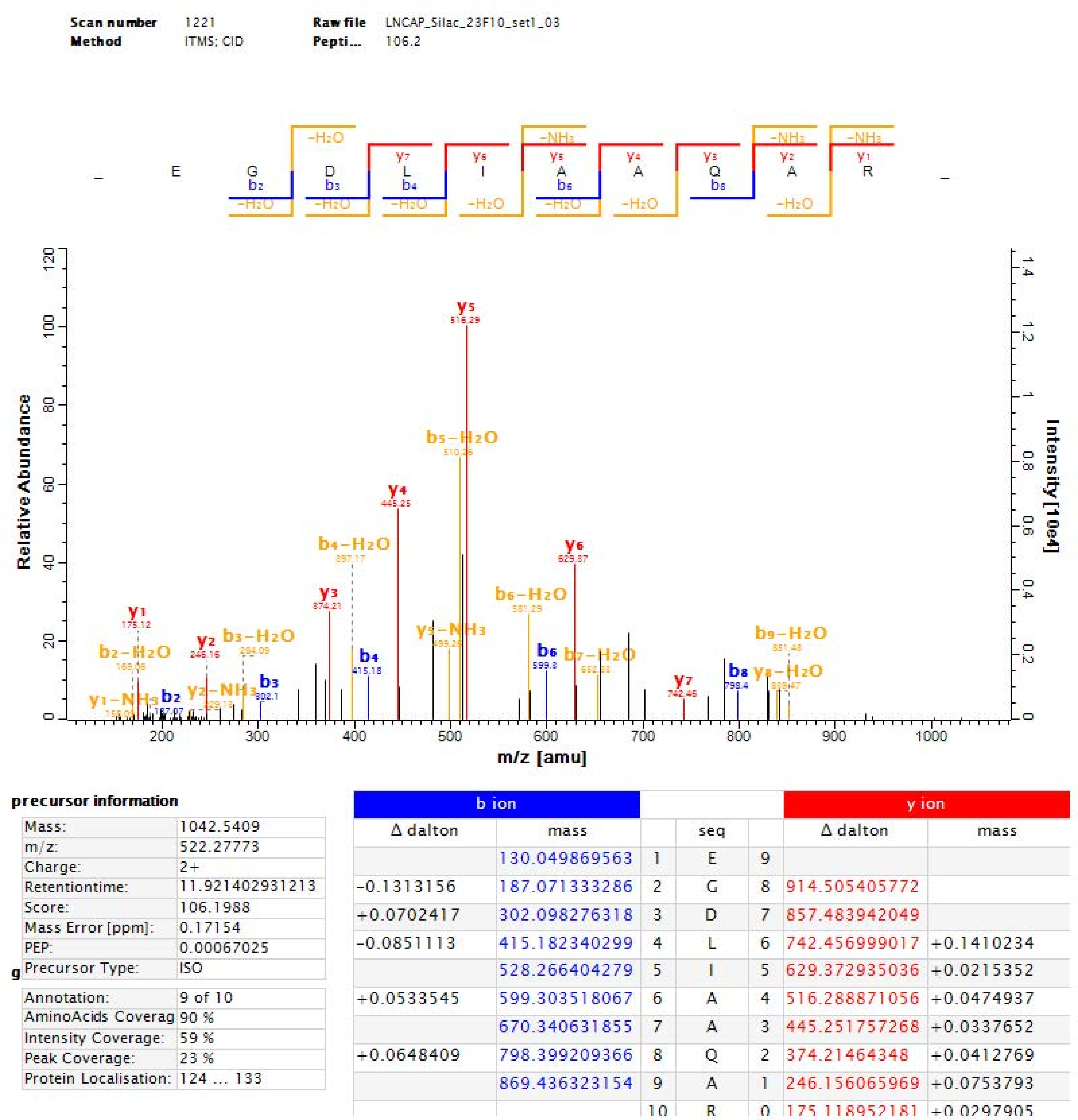
precursor information

Mass:	2063.96242
m/z:	1032.98849
Charge:	2+
Retentiontime:	67.277984619140
Score:	127.8341
Mass Error [ppm]:	0.085224
PEP:	3.6389E-12
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	48 %
Peak Coverage:	37 %
Protein Localisation:	124 ... 140

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.07		129.07	1	Q	16				
	257.12		257.12	2	Q	15	1944.9		1944.9	
	386.17		386.17	3	E	14	1816.9	-0.086	1816.9	
	457.2	+0.1042	457.2	4	A	13	1687.8	-0.156	844.42	+0.3365
	554.26		554.26	5	P	12	1616.8	+0.0554	808.9	+0.2351
	669.28		669.28	6	D	11	1519.7	-0.149	1519.7	
	782.37		782.37	7	L	10	1404.7	+0.0311	1404.7	
	929.44		929.44	8	F	9	1291.6	-0.032	1291.6	
+0.0607	529.25		1057.5	9	Q	8	1144.6	+0.0365	1144.6	
	1243.6		1243.6	10	W	7	1016.5	-0.025	1016.5	
	1356.7	+0.0463	1356.7	11	L	6	830.42	+0.0089	830.42	
	1516.7		1516.7	12	C	5	717.33	+0.0356	717.33	
	1603.7		1603.7	13	S	4	557.3	+0.017	557.3	
	1718.7		1718.7	14	D	3	470.27		470.27	
	1805.8		1805.8	15	S	2	355.24	+0.0512	355.24	
	1918.9	-0.089	1918.9	16	L	1	268.21		268.21	
				17	K	0	155.13		155.13	



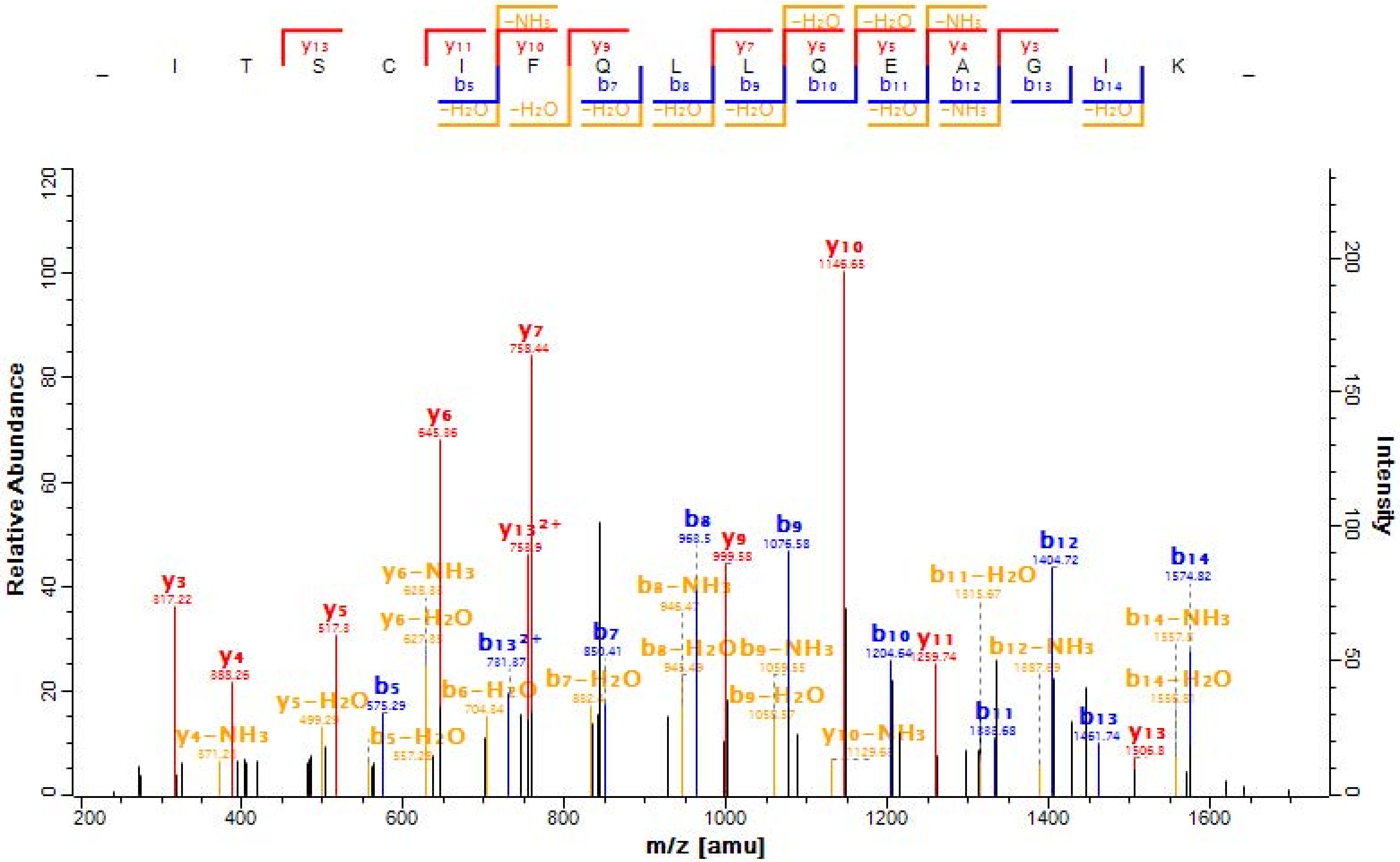
Scan number	1221	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	106.2

precursor information

Mass:	1042.5409
m/z:	522.27773
Charge:	2+
Retentiontime:	11.921402931213
Score:	106.1988
Mass Error [ppm]:	0.17154
PEP:	0.00067025
Precursor Type:	ISO
Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	59 %
Peak Coverage:	23 %
Protein Localisation:	124 ... 133

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	130.049869563	1	E	9		
-0.1313156	187.071333286	2	G	8	914.505405772	
+0.0702417	302.098276318	3	D	7	857.483942049	
-0.0851113	415.182340299	4	L	6	742.456999017	+0.1410234
	528.266404279	5	I	5	629.372935036	+0.0215352
+0.0533545	599.303518067	6	A	4	516.288871056	+0.0474937
	670.340631855	7	A	3	445.251757268	+0.0337652
+0.0648409	798.399209366	8	Q	2	374.21464348	+0.0412769
	869.436323154	9	A	1	246.156065969	+0.0753793
		10	R	0	175.118952181	+0.0297905

Scan number	12249	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	246.5



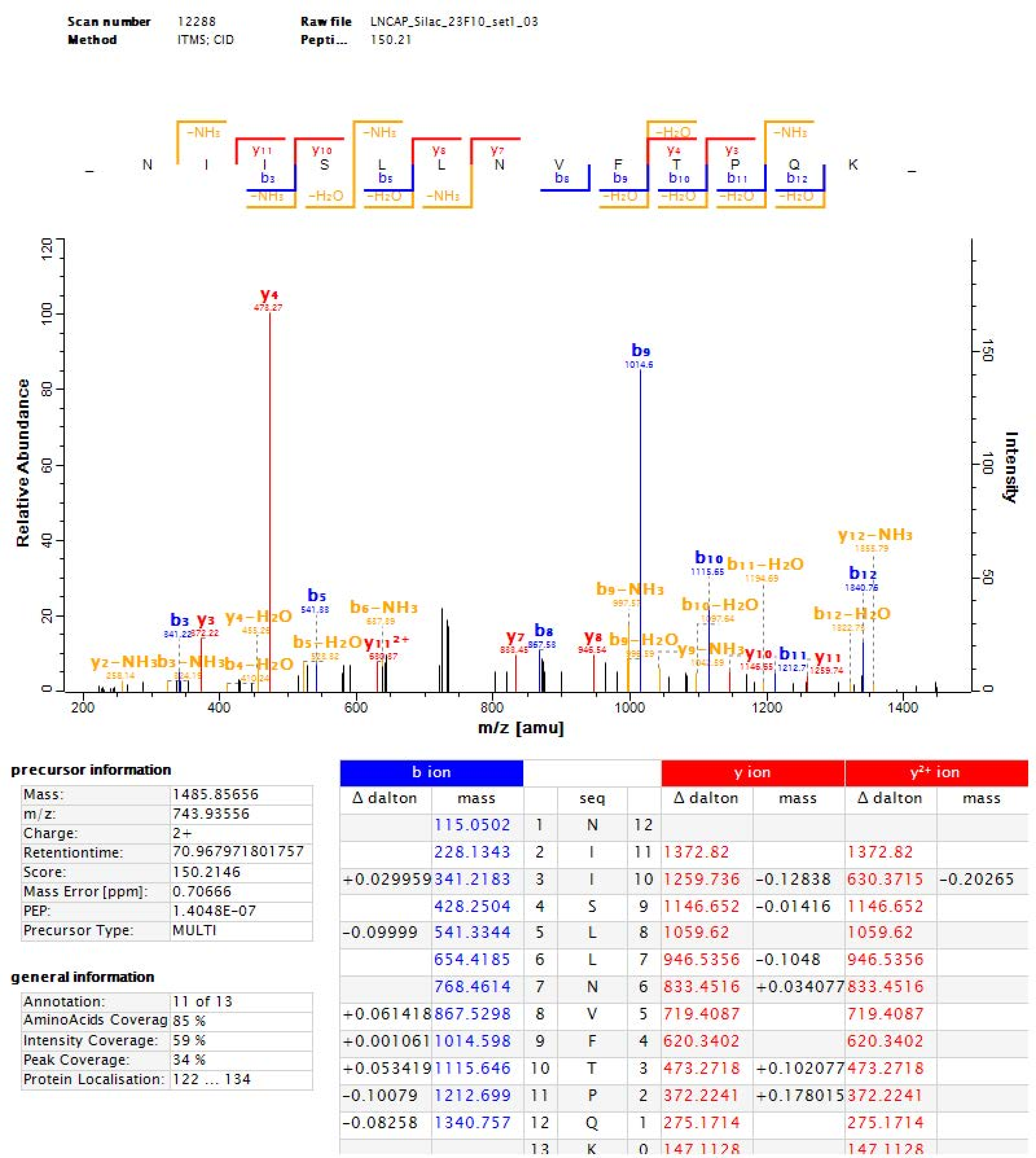
precursor information

Mass:	1719.92353
m/z:	860.96904
Charge:	2+
Retentiontime:	70.593521118164
Score:	246.5004
Mass Error [ppm]:	0.34146
PEP:	6.1525E-47
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	60 %
Peak Coverage:	41 %
Protein Localisation:	86 ... 100

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	I	14				
	215.14		215.14	2	T	13	1607.8		1607.8	
	302.17		302.17	3	S	12	1506.8	-0.392	753.9	-0.068
	462.2		462.2	4	C	11	1419.8		1419.8	
	575.29	+0.0198	575.29	5	I	10	1259.7	+0.0556	1259.7	
	722.35		722.35	6	F	9	1146.7	-0.122	1146.7	
	850.41	-0.131	850.41	7	Q	8	999.58	+0.0095	999.58	
	963.5	+0.1121	963.5	8	L	7	871.52		871.52	
	1076.6	-0.016	1076.6	9	L	6	758.44	+0.0224	758.44	
	1204.6	-0.247	1204.6	10	Q	5	645.36	+0.069	645.36	
	1333.7	-0.392	1333.7	11	E	4	517.3	+0.0749	517.3	
	1404.7	-0.095	1404.7	12	A	3	388.26	+0.0398	388.26	
-0.206	731.37	-0.023	1461.7	13	G	2	317.22	+0.0194	317.22	
	1574.8	+0.0617	1574.8	14	I	1	260.2		260.2	
				15	K	0	147.11		147.11	



Scan number	12288	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	150.21

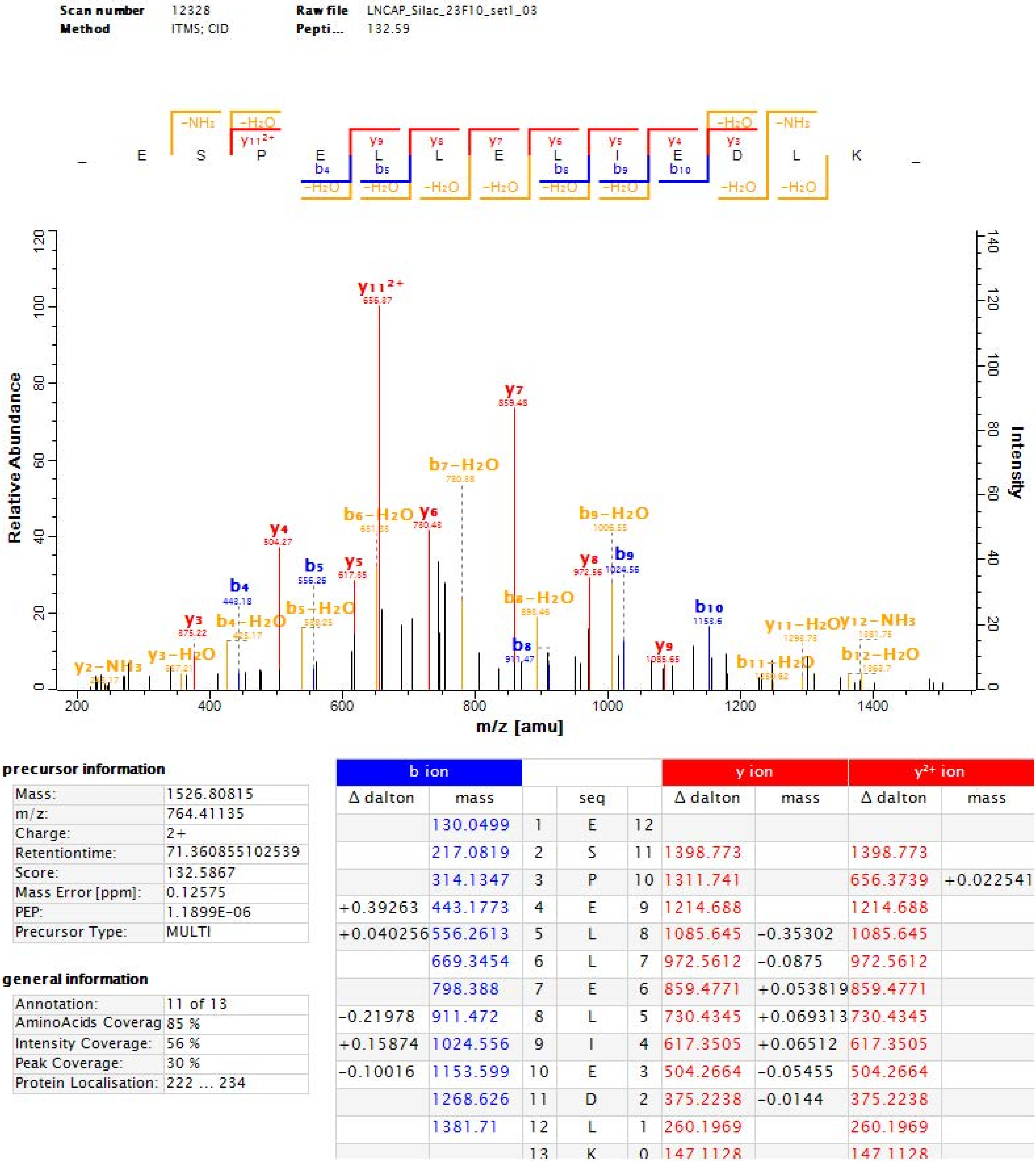
precursor information

Mass:	1485.85656
m/z:	743.93556
Charge:	2+
Retentiontime:	70.967971801757
Score:	150.2146
Mass Error [ppm]:	0.70666
PEP:	1.4048E-07
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	59 %
Peak Coverage:	34 %
Protein Localisation:	122 ... 134

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502	1	N	12				
	228.1343	2	I	11	1372.82		1372.82	
+0.029959	341.2183	3	I	10	1259.736	-0.12838	630.3715	-0.20265
	428.2504	4	S	9	1146.652	-0.01416	1146.652	
-0.09999	541.3344	5	L	8	1059.62		1059.62	
	654.4185	6	L	7	946.5356	-0.1048	946.5356	
	768.4614	7	N	6	833.4516	+0.034077	833.4516	
+0.061418	867.5298	8	V	5	719.4087		719.4087	
+0.001061	1014.598	9	F	4	620.3402		620.3402	
+0.053419	1115.646	10	T	3	473.2718	+0.102077	473.2718	
-0.10079	1212.699	11	P	2	372.2241	+0.178015	372.2241	
-0.08258	1340.757	12	Q	1	275.1714		275.1714	
		13	K	0	147.1128		147.1128	



Scan number	12328	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	132.59

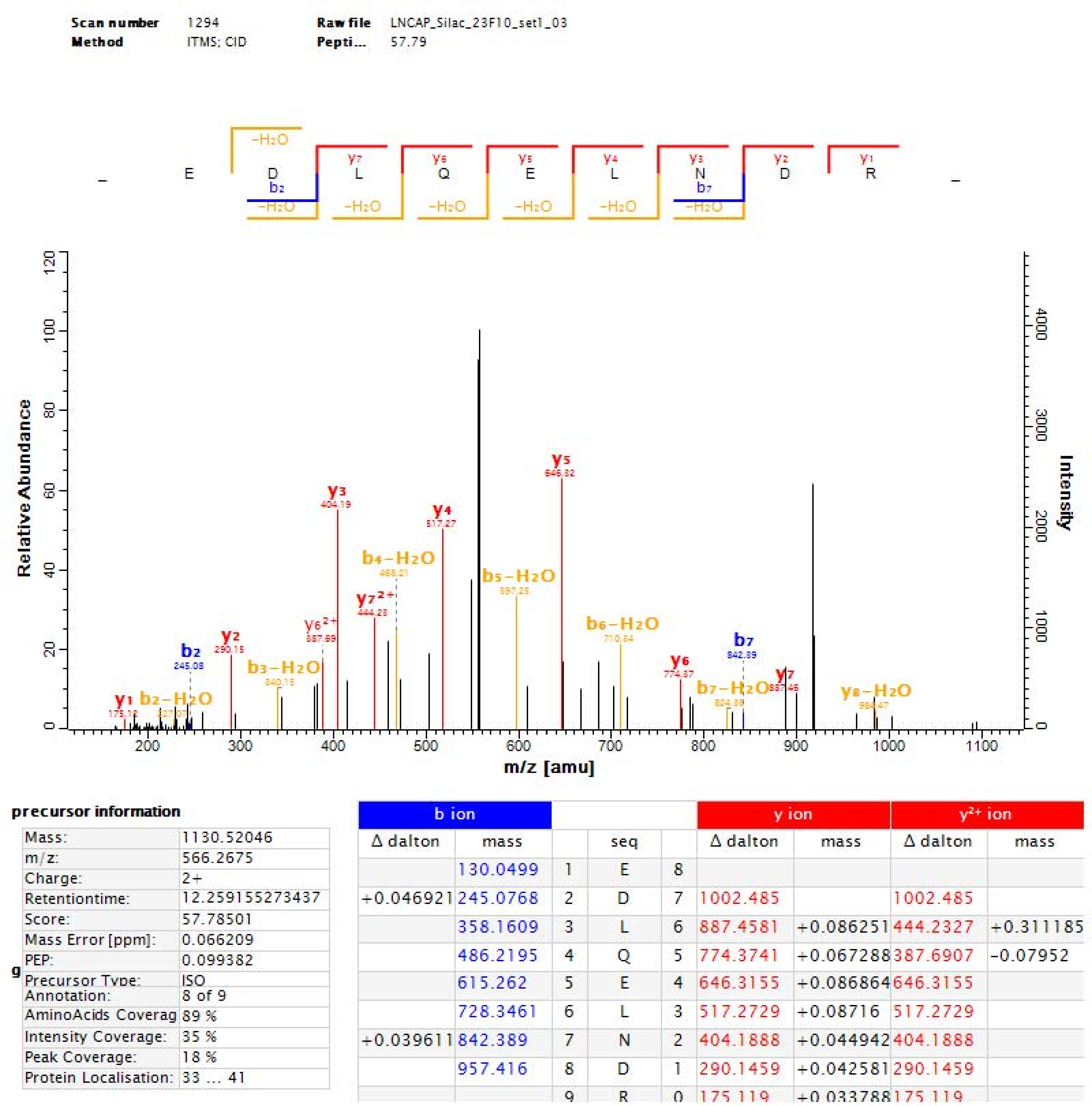
precursor information

Mass:	1526.80815
m/z:	764.41135
Charge:	2+
Retentiontime:	71.360855102539
Score:	132.5867
Mass Error [ppm]:	0.12575
PEP:	1.1899E-06
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	56 %
Peak Coverage:	30 %
Protein Localisation:	222 ... 234

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	12				
	217.0819	2	S	11	1398.773		1398.773	
	314.1347	3	P	10	1311.741		656.3739	+0.022541
+0.39263	443.1773	4	E	9	1214.688		1214.688	
+0.040256	556.2613	5	L	8	1085.645	-0.35302	1085.645	
	669.3454	6	L	7	972.5612	-0.0875	972.5612	
	798.388	7	E	6	859.4771	+0.053819	859.4771	
-0.21978	911.472	8	L	5	730.4345	+0.069313	730.4345	
+0.15874	1024.556	9	I	4	617.3505	+0.06512	617.3505	
-0.10016	1153.599	10	E	3	504.2664	-0.05455	504.2664	
	1268.626	11	D	2	375.2238	-0.0144	375.2238	
	1381.71	12	L	1	260.1969		260.1969	
		13	K	0	147.1128		147.1128	

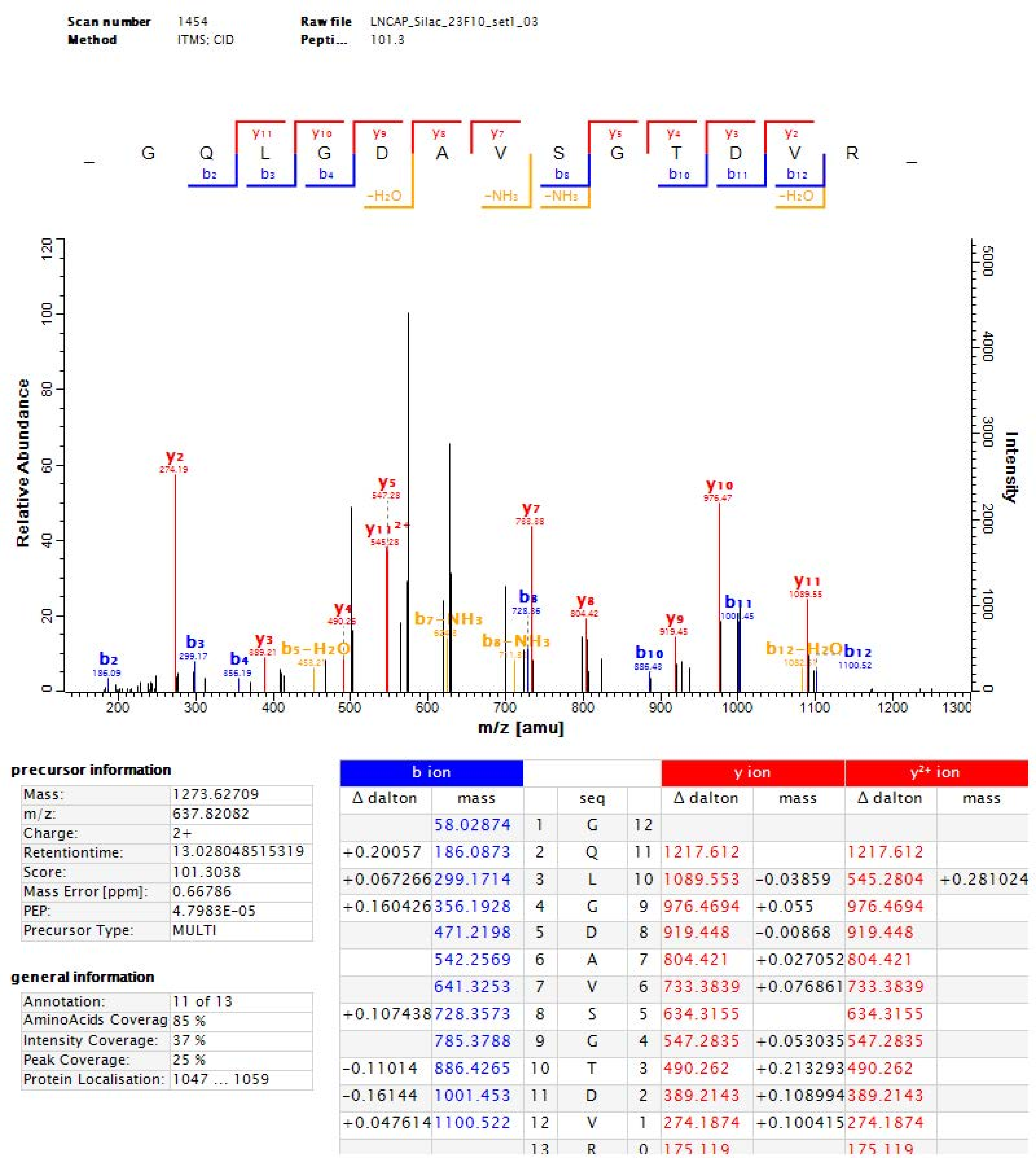


Scan number	1294	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	57.79

precursor information

Mass:	1130.52046
m/z:	566.2675
Charge:	2+
Retentiontime:	12.259155273437
Score:	57.78501
Mass Error [ppm]:	0.066209
PEP:	0.099382
Precursor Type:	ISO
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	35 %
Peak Coverage:	18 %
Protein Localisation:	33 ... 41

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	8				
+0.046921	245.0768	2	D	7	1002.485		1002.485	
	358.1609	3	L	6	887.4581	+0.086251	444.2327	+0.311185
	486.2195	4	Q	5	774.3741	+0.067288	387.6907	-0.07952
	615.262	5	E	4	646.3155	+0.086864	646.3155	
	728.3461	6	L	3	517.2729	+0.08716	517.2729	
+0.039611	842.389	7	N	2	404.1888	+0.044942	404.1888	
	957.416	8	D	1	290.1459	+0.042581	290.1459	
		9	R	0	175.119	+0.033788	175.119	



Scan number	1454	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	101.3

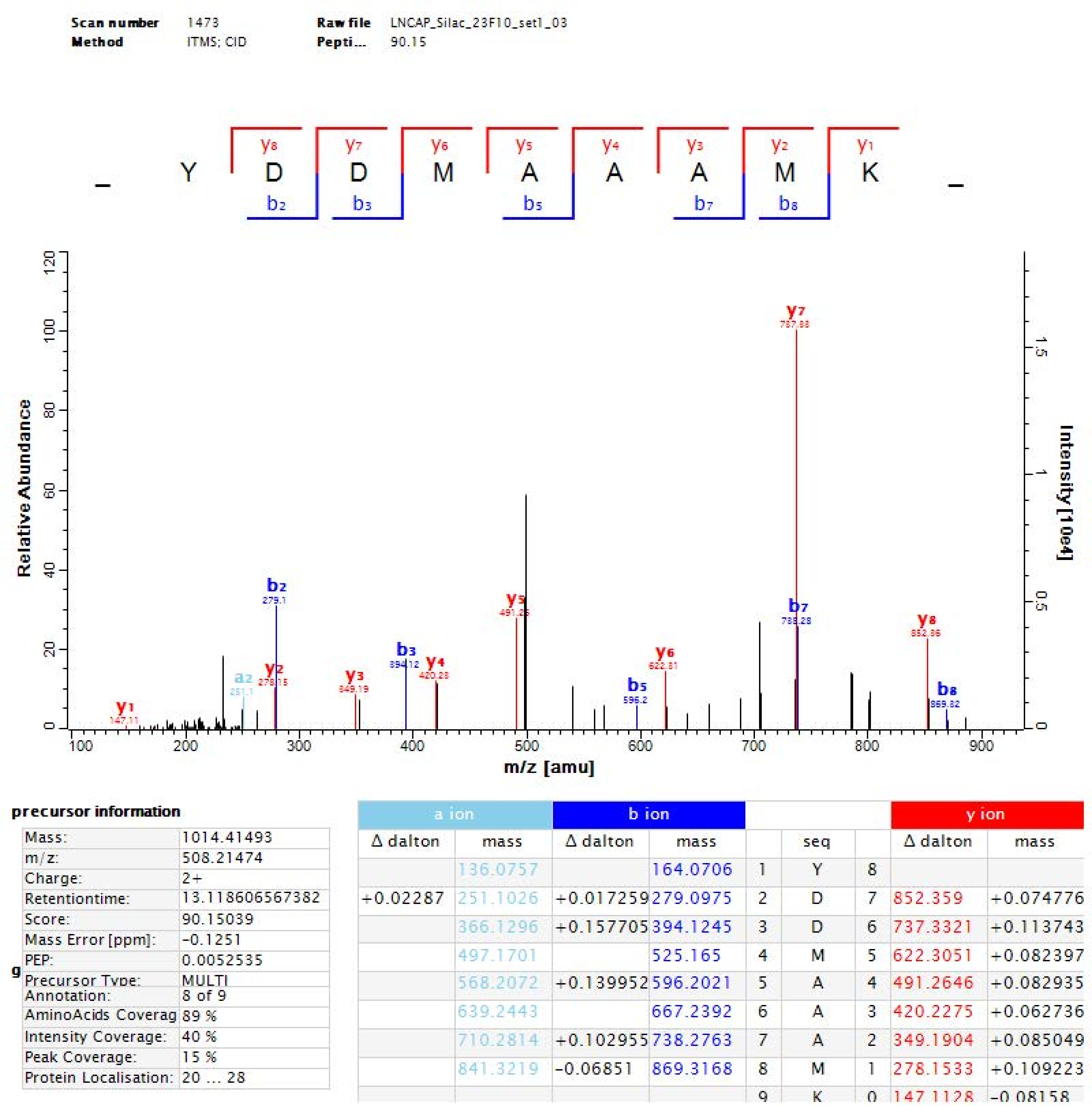
precursor information

Mass:	1273.62709
m/z:	637.82082
Charge:	2+
Retentiontime:	13.028048515319
Score:	101.3038
Mass Error [ppm]:	0.66786
PEP:	4.7983E-05
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	37 %
Peak Coverage:	25 %
Protein Localisation:	1047 ... 1059

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	12				
+0.20057	186.0873	2	Q	11	1217.612		1217.612	
+0.067266	299.1714	3	L	10	1089.553	-0.03859	545.2804	+0.281024
+0.160426	356.1928	4	G	9	976.4694	+0.055	976.4694	
	471.2198	5	D	8	919.448	-0.00868	919.448	
	542.2569	6	A	7	804.421	+0.027052	804.421	
	641.3253	7	V	6	733.3839	+0.076861	733.3839	
+0.107438	728.3573	8	S	5	634.3155		634.3155	
	785.3788	9	G	4	547.2835	+0.053035	547.2835	
-0.11014	886.4265	10	T	3	490.262	+0.213293	490.262	
-0.16144	1001.453	11	D	2	389.2143	+0.108994	389.2143	
+0.047614	1100.522	12	V	1	274.1874	+0.100415	274.1874	
		13	R	0	175.119		175.119	

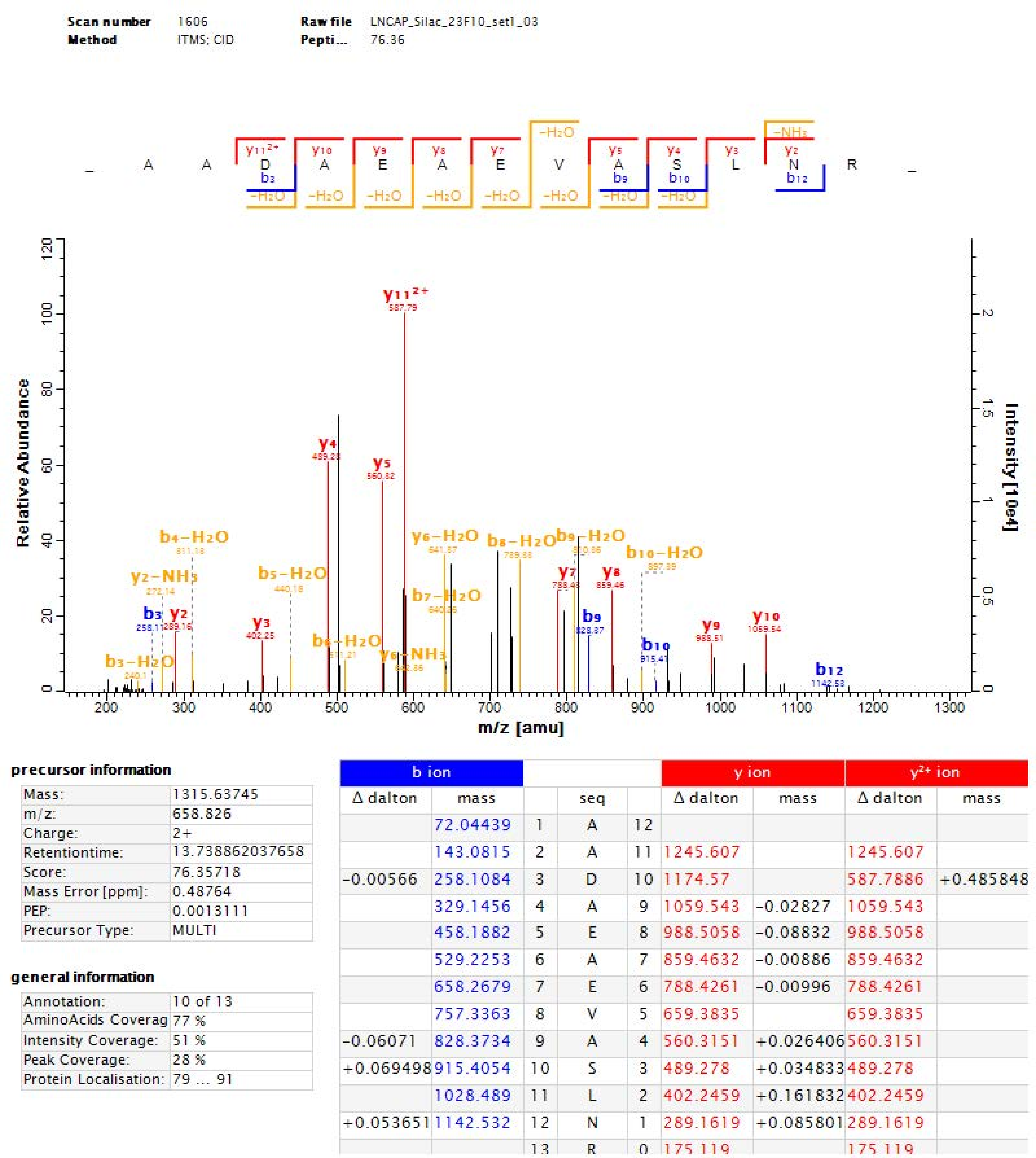


Scan number	1473	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	90.15

precursor information

Mass:	1014.41493
m/z:	508.21474
Charge:	2+
Retentiontime:	13.118606567382
Score:	90.15039
Mass Error [ppm]:	-0.1251
PEP:	0.0052535
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	40 %
Peak Coverage:	15 %
Protein Localisation:	20 ... 28

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	136.0757		164.0706	1	Y	8		
+0.02287	251.1026	+0.017259	279.0975	2	D	7	852.359	+0.074776
	366.1296	+0.157705	394.1245	3	D	6	737.3321	+0.113743
	497.1701		525.165	4	M	5	622.3051	+0.082397
	568.2072	+0.139952	596.2021	5	A	4	491.2646	+0.082935
	639.2443		667.2392	6	A	3	420.2275	+0.062736
	710.2814	+0.102955	738.2763	7	A	2	349.1904	+0.085049
	841.3219	-0.06851	869.3168	8	M	1	278.1533	+0.109223
				9	K	0	147.1128	-0.08158



Scan number	1606	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	76.36

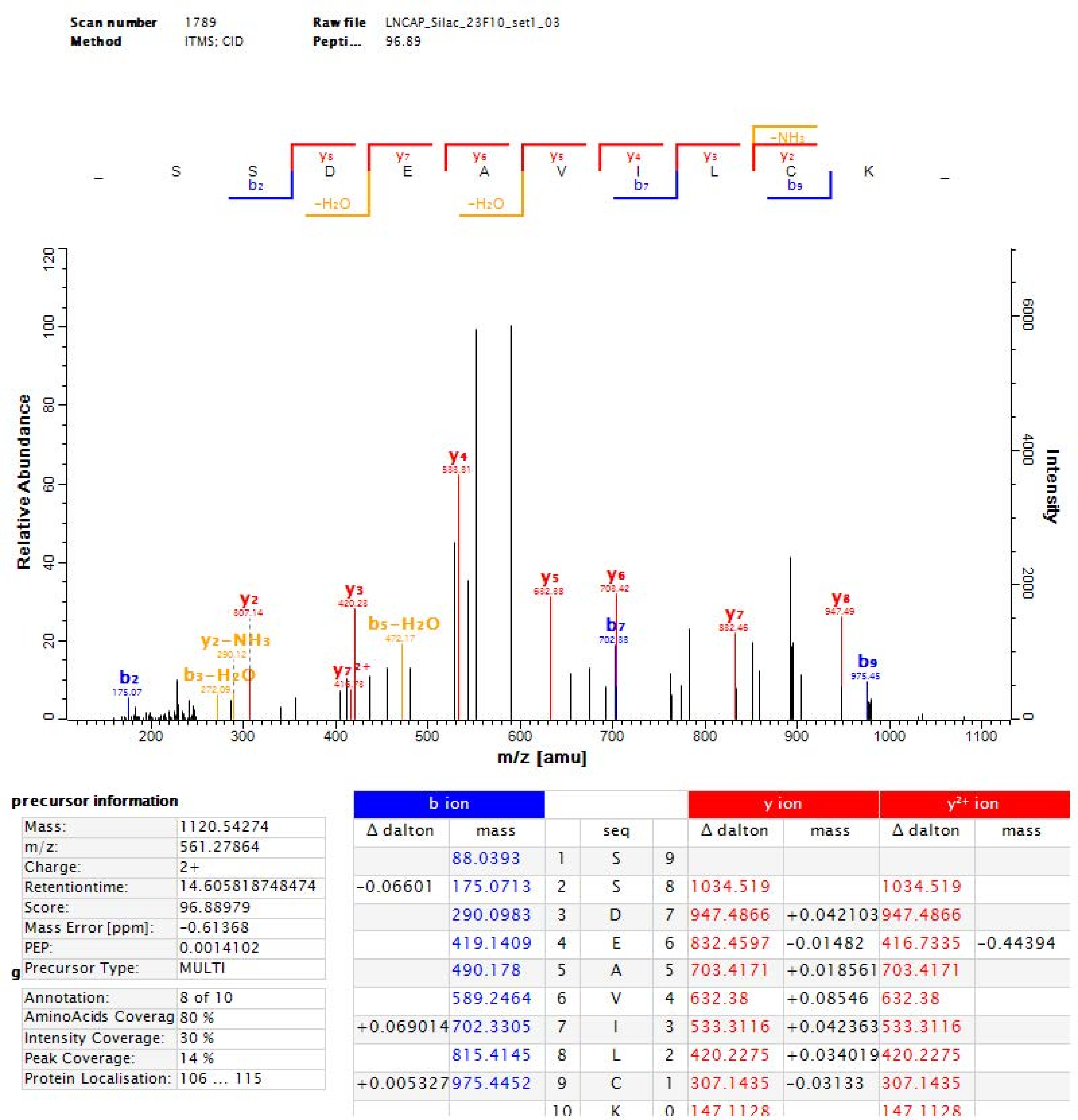
precursor information

Mass:	1315.63745
m/z:	658.826
Charge:	2+
Retentiontime:	13.738862037658
Score:	76.35718
Mass Error [ppm]:	0.48764
PEP:	0.0013111
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	51 %
Peak Coverage:	28 %
Protein Localisation:	79 ... 91

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	12				
	143.0815	2	A	11	1245.607		1245.607	
-0.00566	258.1084	3	D	10	1174.57		587.7886	+0.485848
	329.1456	4	A	9	1059.543	-0.02827	1059.543	
	458.1882	5	E	8	988.5058	-0.08832	988.5058	
	529.2253	6	A	7	859.4632	-0.00886	859.4632	
	658.2679	7	E	6	788.4261	-0.00996	788.4261	
	757.3363	8	V	5	659.3835		659.3835	
-0.06071	828.3734	9	A	4	560.3151	+0.026406	560.3151	
+0.069498	915.4054	10	S	3	489.278	+0.034833	489.278	
	1028.489	11	L	2	402.2459	+0.161832	402.2459	
+0.053651	1142.532	12	N	1	289.1619	+0.085801	289.1619	
		13	R	0	175.119		175.119	



Scan number	1789	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	96.89

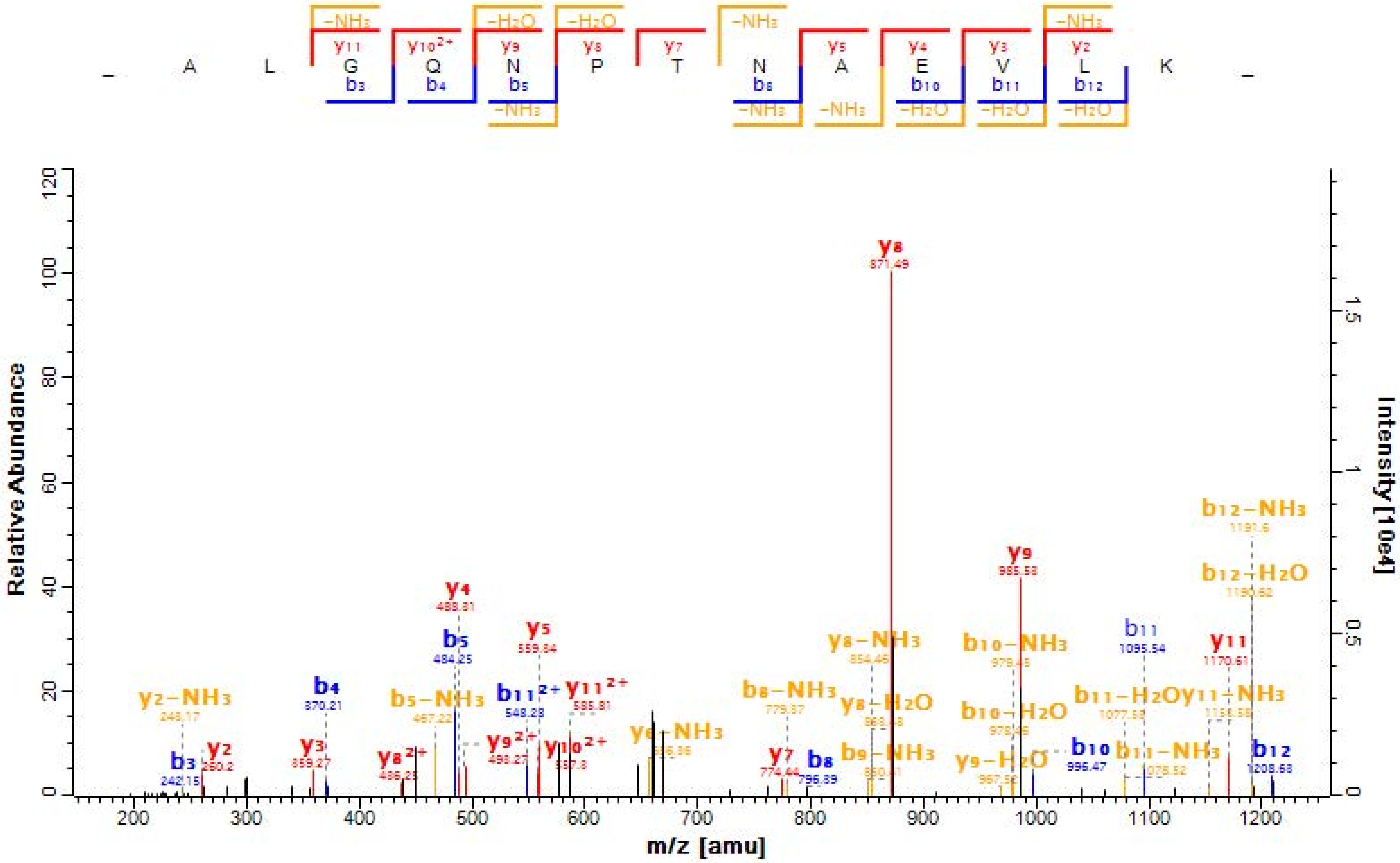
precursor information

Mass:	1120.54274
m/z:	561.27864
Charge:	2+
Retentiontime:	14.605818748474
Score:	96.88979
Mass Error [ppm]:	-0.61368
PEP:	0.0014102
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	30 %
Peak Coverage:	14 %
Protein Localisation:	106 ... 115

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	9				
-0.06601	175.0713	2	S	8	1034.519		1034.519	
	290.0983	3	D	7	947.4866	+0.042103	947.4866	
	419.1409	4	E	6	832.4597	-0.01482	416.7335	-0.44394
	490.178	5	A	5	703.4171	+0.018561	703.4171	
	589.2464	6	V	4	632.38	+0.08546	632.38	
+0.069014	702.3305	7	I	3	533.3116	+0.042363	533.3116	
	815.4145	8	L	2	420.2275	+0.034019	420.2275	
+0.005327	975.4452	9	C	1	307.1435	-0.03133	307.1435	
		10	K	0	147.1128		147.1128	

Scan number	2011	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	222.25



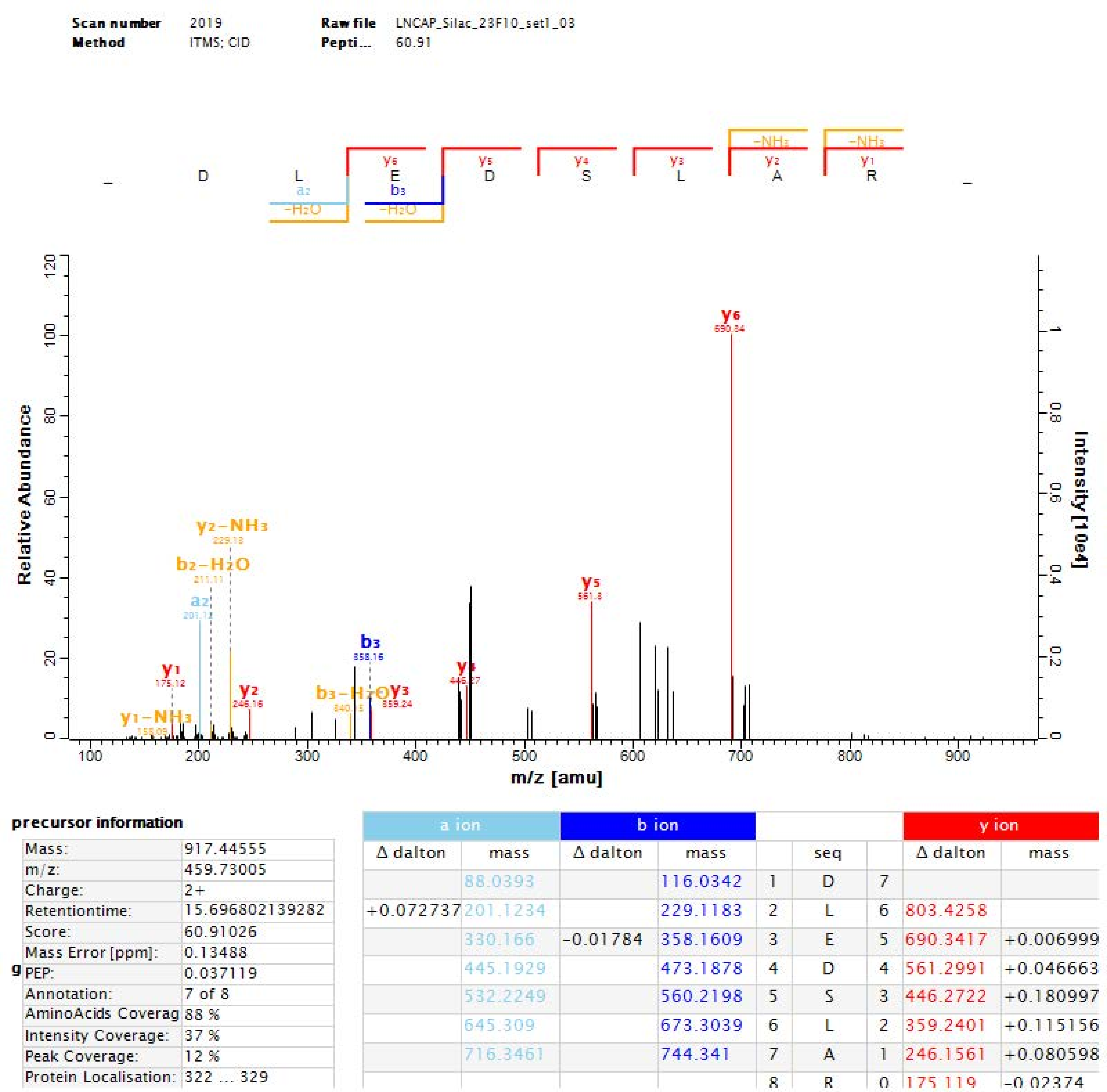
precursor information

Mass:	1353.72453
m/z:	677.86954
Charge:	2+
Retentiontime:	15.658533096313
Score:	222.254
Mass Error [ppm]:	-0.51423
PEP:	1.7539E-28
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	61 %
Peak Coverage:	40 %
Protein Localisation:	131 ... 143

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	12				
	185.13		185.13	2	L	11	1283.7		1283.7	
	242.15	+0.0357	242.15	3	G	10	1170.6	+0.0295	585.81	-0.005
	370.21	+0.0919	370.21	4	Q	9	1113.6		557.3	+0.3801
	484.25	+0.0696	484.25	5	N	8	985.53	+0.0012	493.27	+0.3362
	581.3		581.3	6	P	7	871.49	+0.009	436.25	+0.284
	682.35		682.35	7	T	6	774.44	+0.0776	774.44	
	796.39	-0.047	796.39	8	N	5	673.39		673.39	
	867.43		867.43	9	A	4	559.34	+0.0117	559.34	
	996.47	+0.0214	996.47	10	E	3	488.31	+0.0727	488.31	
+0.3469	548.28	-0.064	1095.5	11	V	2	359.27	+0.0942	359.27	
	1208.6	-0.055	1208.6	12	L	1	260.2	+0.0735	260.2	
				13	K	0	147.11		147.11	



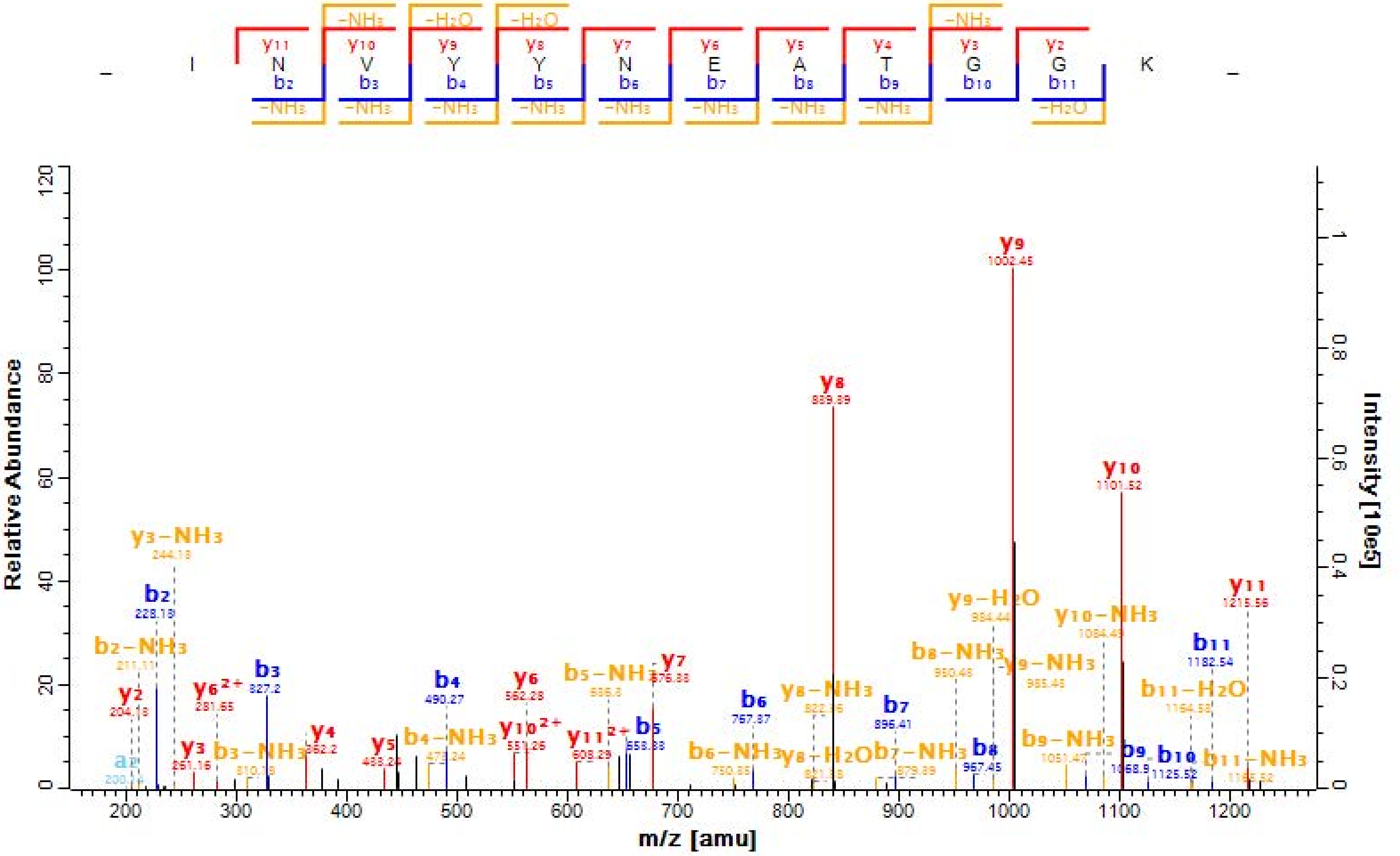
Scan number	2019	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	60.91

precursor information

Mass:	917.44555
m/z:	459.73005
Charge:	2+
Retentiontime:	15.696802139282
Score:	60.91026
Mass Error [ppm]:	0.13488
PEP:	0.037119
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	37 %
Peak Coverage:	12 %
Protein Localisation:	322 ... 329

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	88.0393		116.0342	1	D	7		
+0.072737	201.1234		229.1183	2	L	6	803.4258	
	330.166	-0.01784	358.1609	3	E	5	690.3417	+0.006999
	445.1929		473.1878	4	D	4	561.2991	+0.046663
	532.2249		560.2198	5	S	3	446.2722	+0.180997
	645.309		673.3039	6	L	2	359.2401	+0.115156
	716.3461		744.341	7	A	1	246.1561	+0.080598
				8	R	0	175.119	-0.02374

Scan number	2033	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	296.17



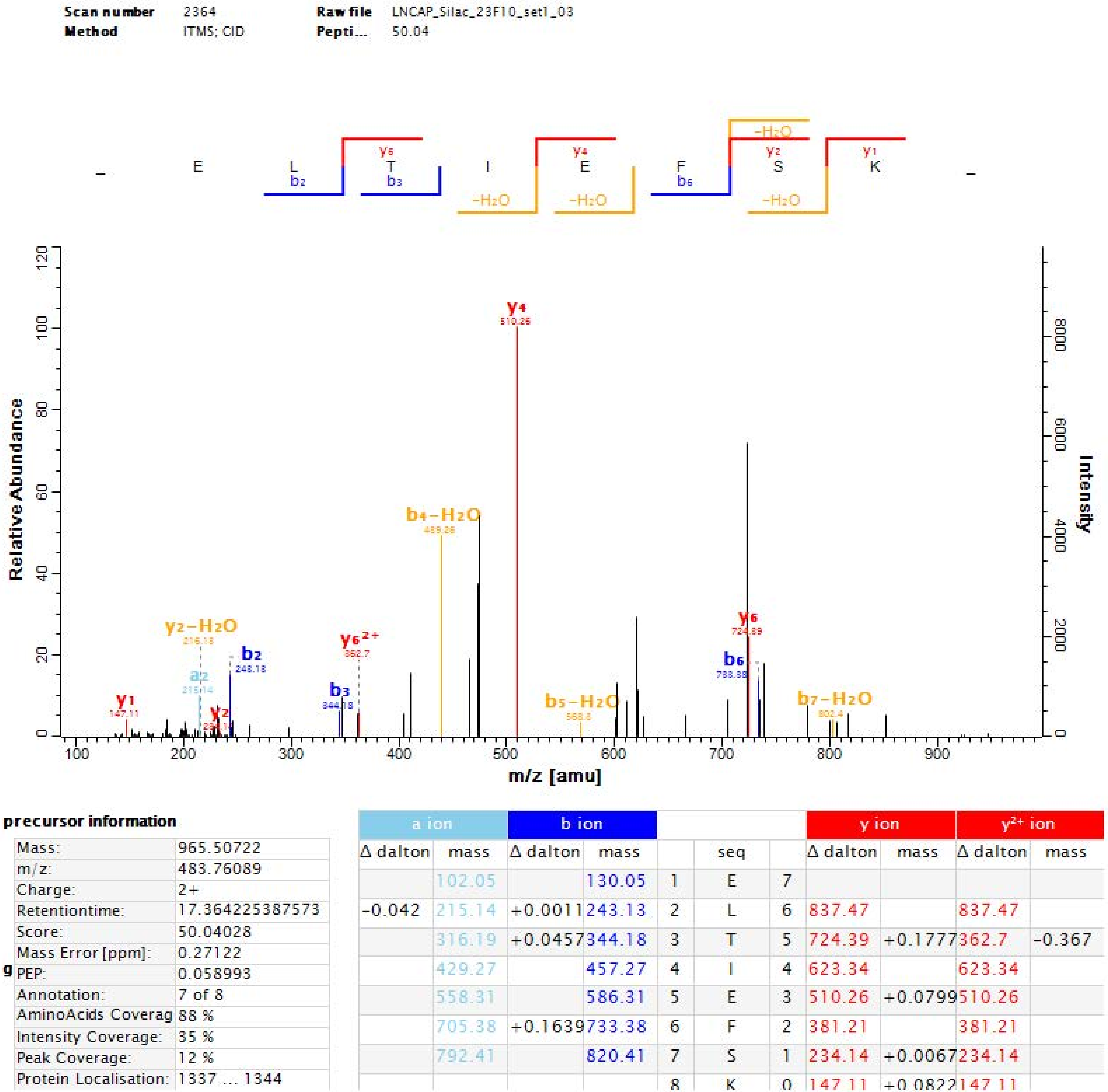
precursor information

Mass:	1327.64075
m/z:	664.82765
Charge:	2+
Retentiontime:	15.766888618469
Score:	296.165
Mass Error [ppm]:	-0.062885
PEP:	4.4124E-66
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	72 %
Peak Coverage:	53 %
Protein Localisation:	47 ... 58

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	11				
-0.061	200.14	-0.014	228.13	2	N	10	1215.6	+0.0278	608.29	+0.066
	299.21	-0.01	327.2	3	V	9	1101.5	+0.0111	551.26	-0.043
	462.27	-0.001	490.27	4	Y	8	1002.5	-0.032	1002.5	
	625.33	+0.0197	653.33	5	Y	7	839.39	-0.009	839.39	
	739.38	-0.026	767.37	6	N	6	676.33	+0.0842	676.33	
	868.42	+0.1057	896.41	7	E	5	562.28	+0.1773	281.65	+0.4941
	939.46	+0.0574	967.45	8	A	4	433.24	+0.0867	433.24	
	1040.5	-0.117	1068.5	9	T	3	362.2	+0.0556	362.2	
	1097.5	+3E-06	1125.5	10	G	2	261.16	+0.1066	261.16	
	1154.5	+0.1085	1182.5	11	G	1	204.13	+0.1345	204.13	
				12	K	0	147.11		147.11	



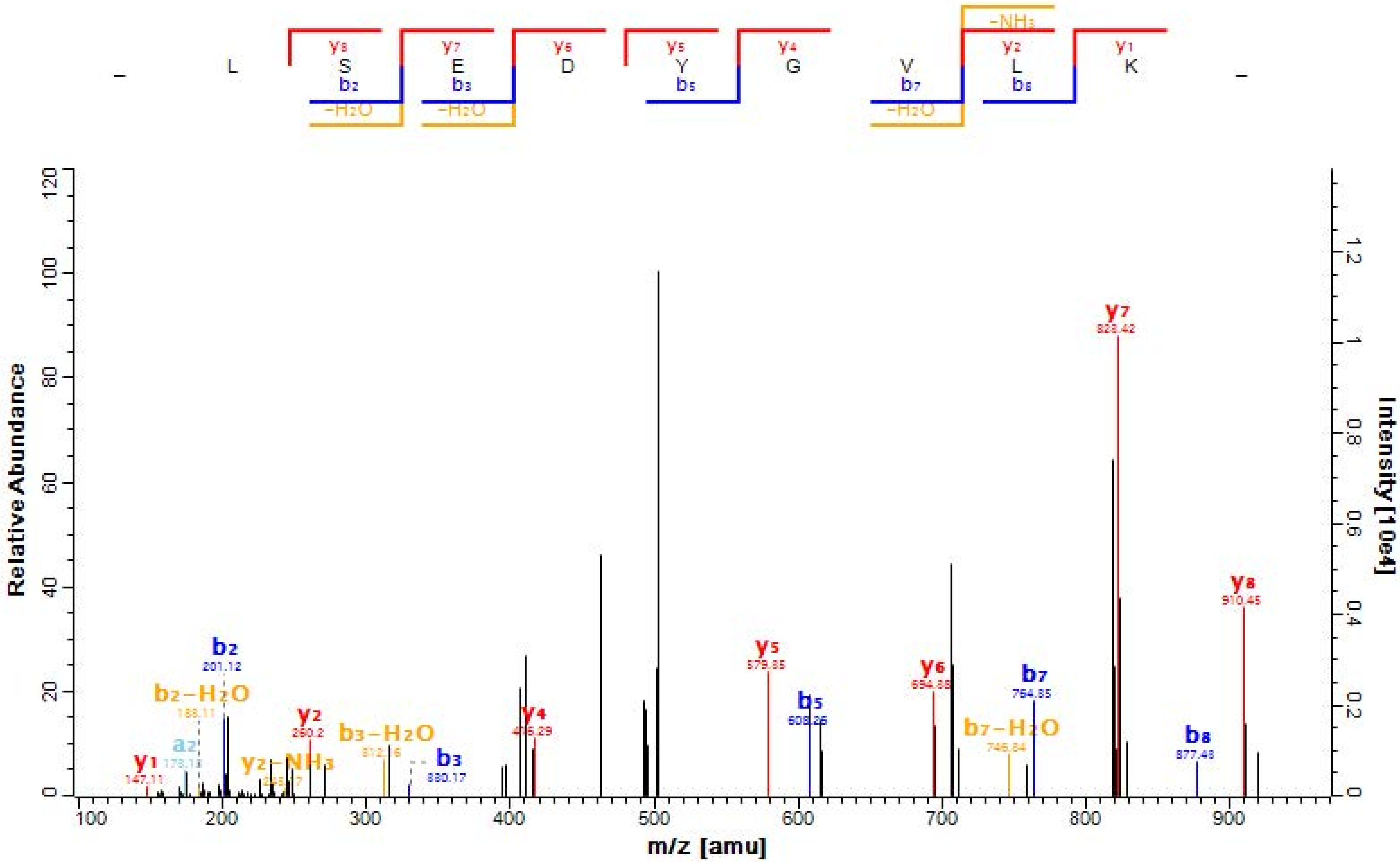
Scan number	2364	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	50.04

precursor information

Mass:	965.50722
m/z:	483.76089
Charge:	2+
Retentiontime:	17.364225387573
Score:	50.04028
Mass Error [ppm]:	0.27122
PEP:	0.058993
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	35 %
Peak Coverage:	12 %
Protein Localisation:	1337 ... 1344

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	7				
-0.042	215.14	+0.0011	243.13	2	L	6	837.47		837.47	
	316.19	+0.0457	344.18	3	T	5	724.39	+0.1777	362.7	-0.367
	429.27		457.27	4	I	4	623.34		623.34	
	558.31		586.31	5	E	3	510.26	+0.0799	510.26	
	705.38	+0.1639	733.38	6	F	2	381.21		381.21	
	792.41		820.41	7	S	1	234.14	+0.0067	234.14	
				8	K	0	147.11	+0.0822	147.11	

Scan number	2437	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	100.02

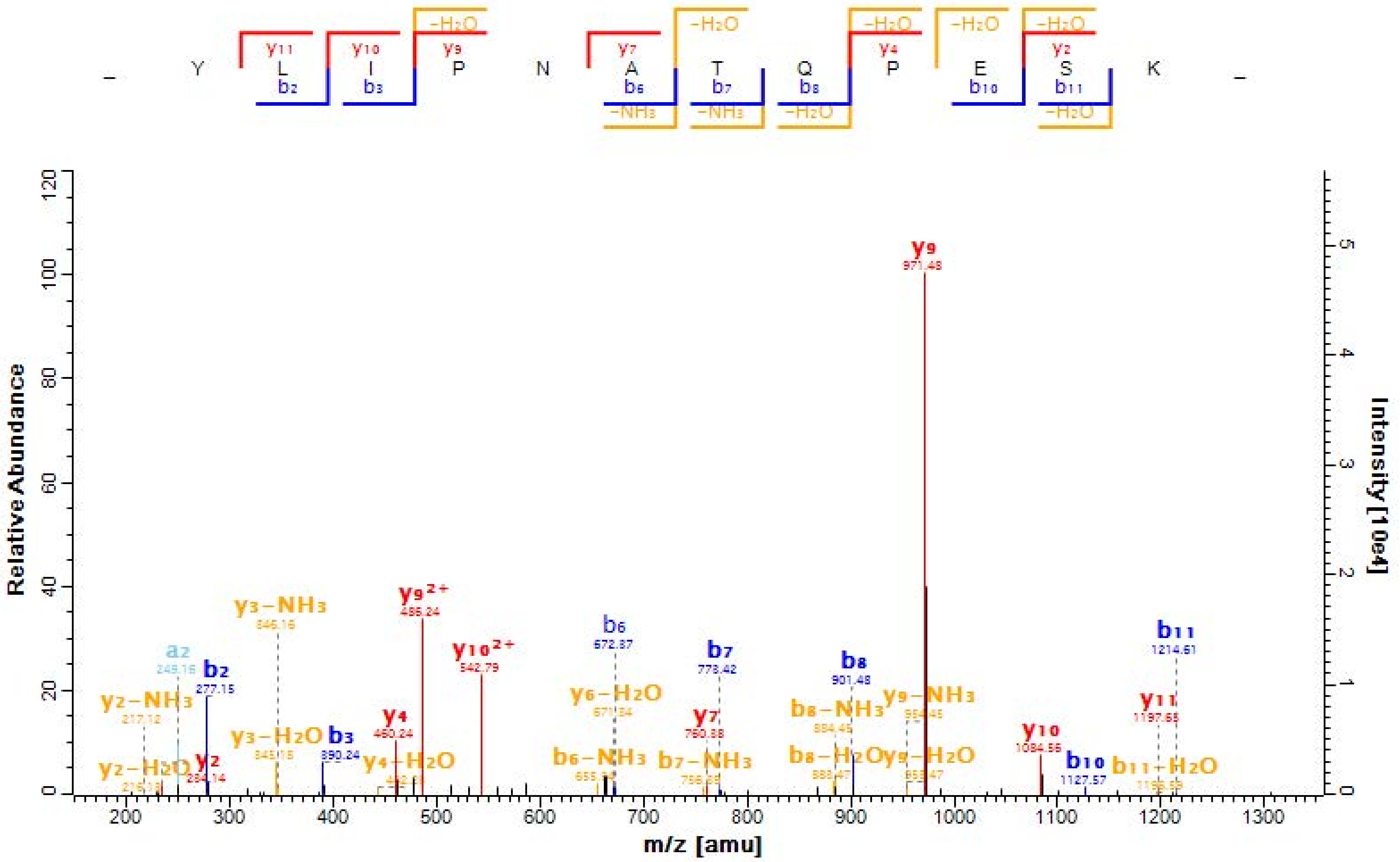


precursor information

Mass:	1022.5291
m/z:	512.27183
Charge:	2+
Retentiontime:	17.702489852905
Score:	100.017
Mass Error [ppm]:	0.65839
PEP:	0.0034806
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	28 %
Peak Coverage:	19 %
Protein Localisation:	111 ... 119

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	86.09643		114.0913	1	L	8		
+0.021372	173.1285	+0.063322	201.1234	2	S	7	910.4516	+0.086447
	302.171	-0.12281	330.166	3	E	6	823.4196	+0.030158
	417.198		445.1929	4	D	5	694.377	+0.02319
	580.2613	+0.105888	608.2562	5	Y	4	579.3501	+0.04702
	637.2828		665.2777	6	G	3	416.2867	+0.053464
	736.3512	-0.0554	764.3461	7	V	2	359.2653	
	849.4353	+0.093323	877.4302	8	L	1	260.1969	+0.13437
				9	K	0	147.1128	-0.05433

Scan number	2479	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	164.9



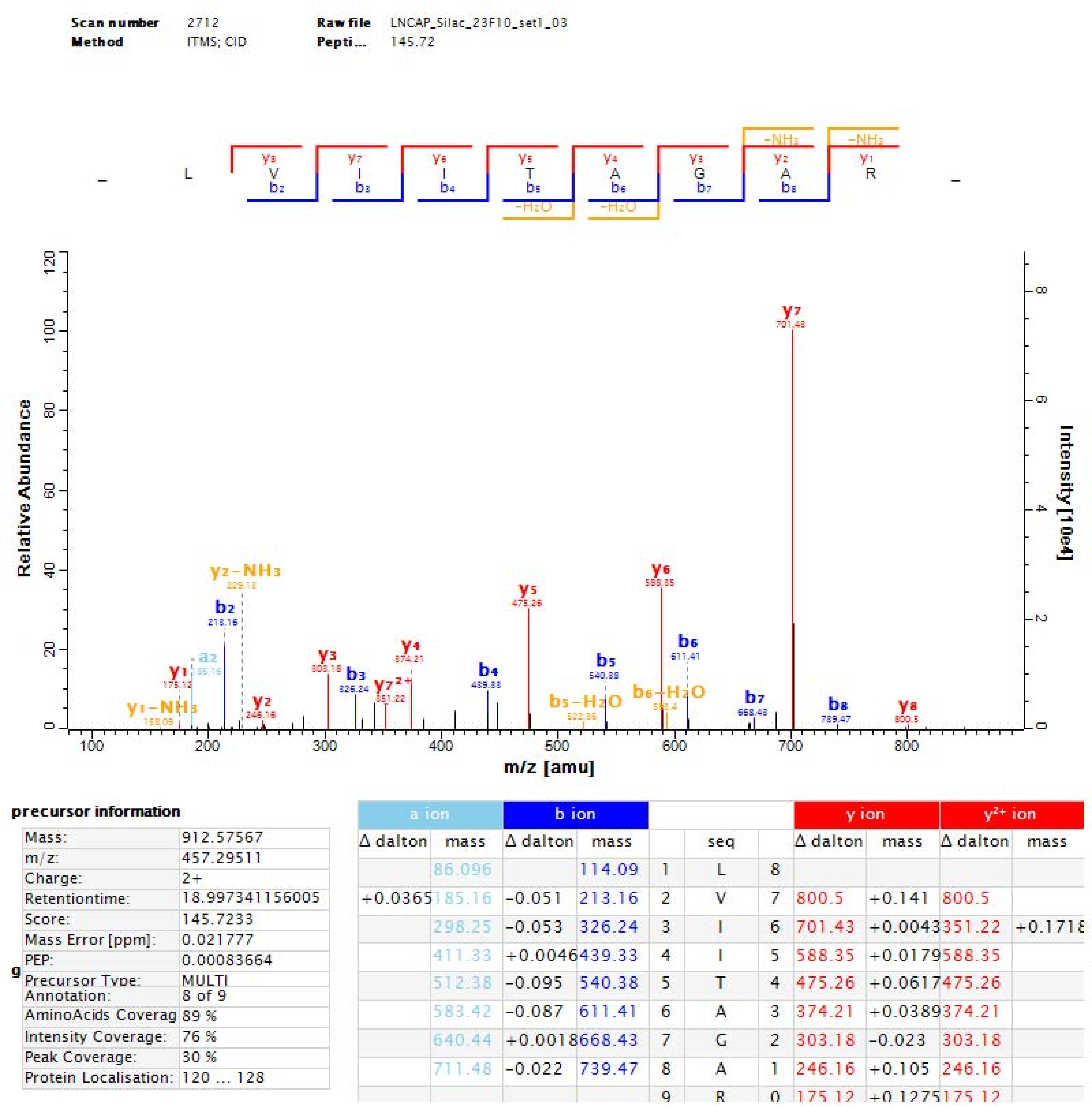
precursor information

Mass:	1359.70336
m/z:	680.85895
Charge:	2+
Retentiontime:	17.894138336181
Score:	164.9017
Mass Error [ppm]:	-0.055182
PEP:	1.1436E-07
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	73 %
Peak Coverage:	34 %
Protein Localisation:	106 ... 117

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.08		164.07	1	Y	11				
-0.001	249.16	-0.017	277.15	2	L	10	1197.6	-0.023	1197.6	
	362.24	-0.073	390.24	3	I	9	1084.6	-0.09	542.79	+0.1944
	459.3		487.29	4	P	8	971.48	-0.018	486.24	+0.231
	573.34		601.33	5	N	7	874.43		874.43	
	644.38	+0.2455	672.37	6	A	6	760.38	-0.152	760.38	
	745.42	+0.0855	773.42	7	T	5	689.35		689.35	
	873.48	+0.1709	901.48	8	Q	4	588.3		588.3	
	970.54		998.53	9	P	3	460.24	+0.0441	460.24	
	1099.6	+0.0194	1127.6	10	E	2	363.19		363.19	
	1186.6	-0.213	1214.6	11	S	1	234.14	+0.0761	234.14	
				12	K	0	147.11		147.11	



Scan number 2712

Raw file LNCAP_Silac_23F10_set1_03

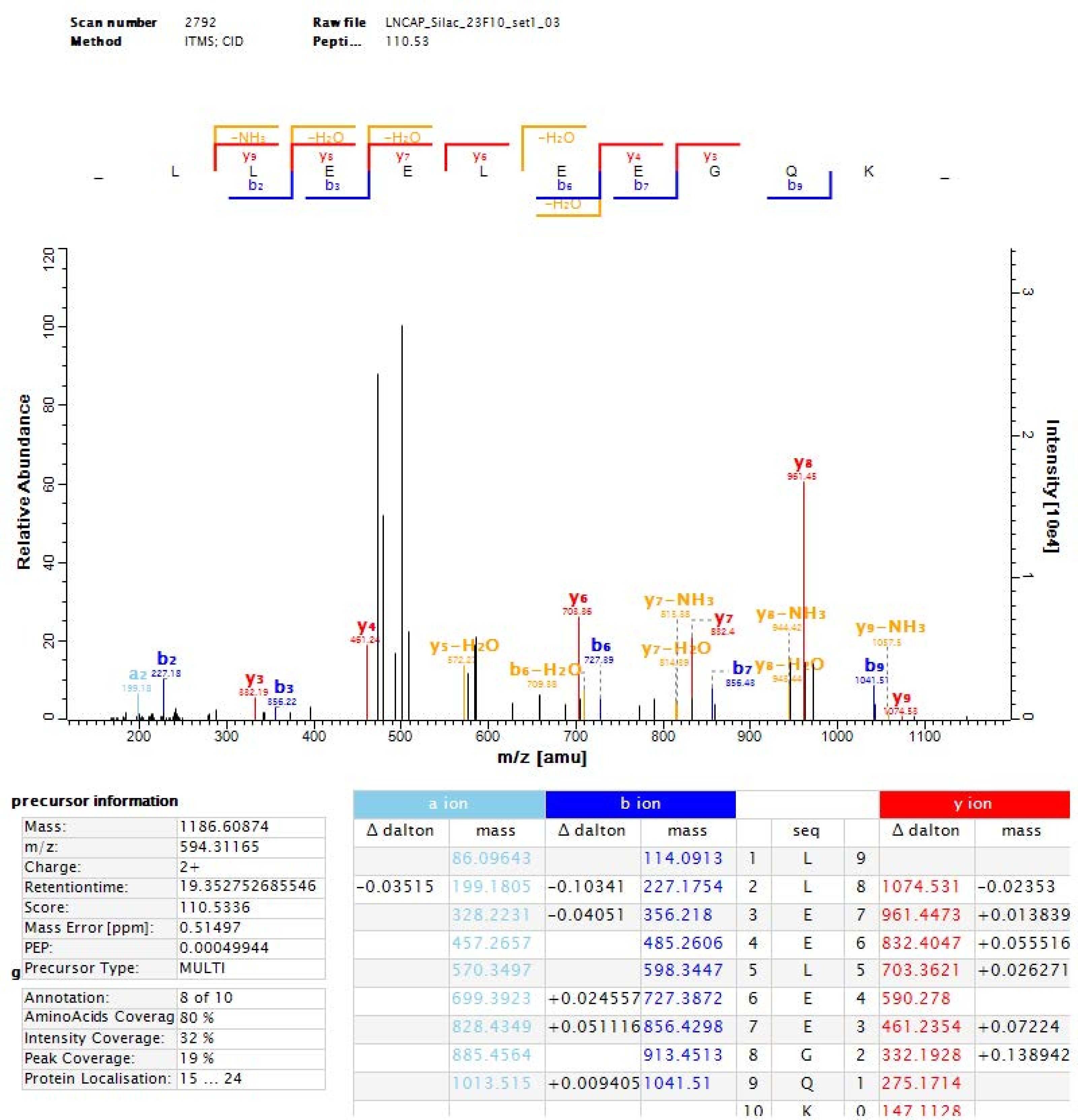
Method ITMS; CID

Pepti... 145.72

precursor information

Mass:	912.57567
m/z:	457.29511
Charge:	2+
Retentiontime:	18.997341156005
Score:	145.7233
Mass Error [ppm]:	0.021777
PEP:	0.00083664
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	76 %
Peak Coverage:	30 %
Protein Localisation:	120 ... 128

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	8				
+0.0365	185.16	-0.051	213.16	2	V	7	800.5	+0.141	800.5	
	298.25	-0.053	326.24	3	I	6	701.43	+0.0043	351.22	+0.171
	411.33	+0.0046	439.33	4	I	5	588.35	+0.0179	588.35	
	512.38	-0.095	540.38	5	T	4	475.26	+0.0617	475.26	
	583.42	-0.087	611.41	6	A	3	374.21	+0.0389	374.21	
	640.44	+0.0018	668.43	7	G	2	303.18	-0.023	303.18	
	711.48	-0.022	739.47	8	A	1	246.16	+0.105	246.16	
				9	R	0	175.12	+0.1275	175.12	



Scan number	2792	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	110.53

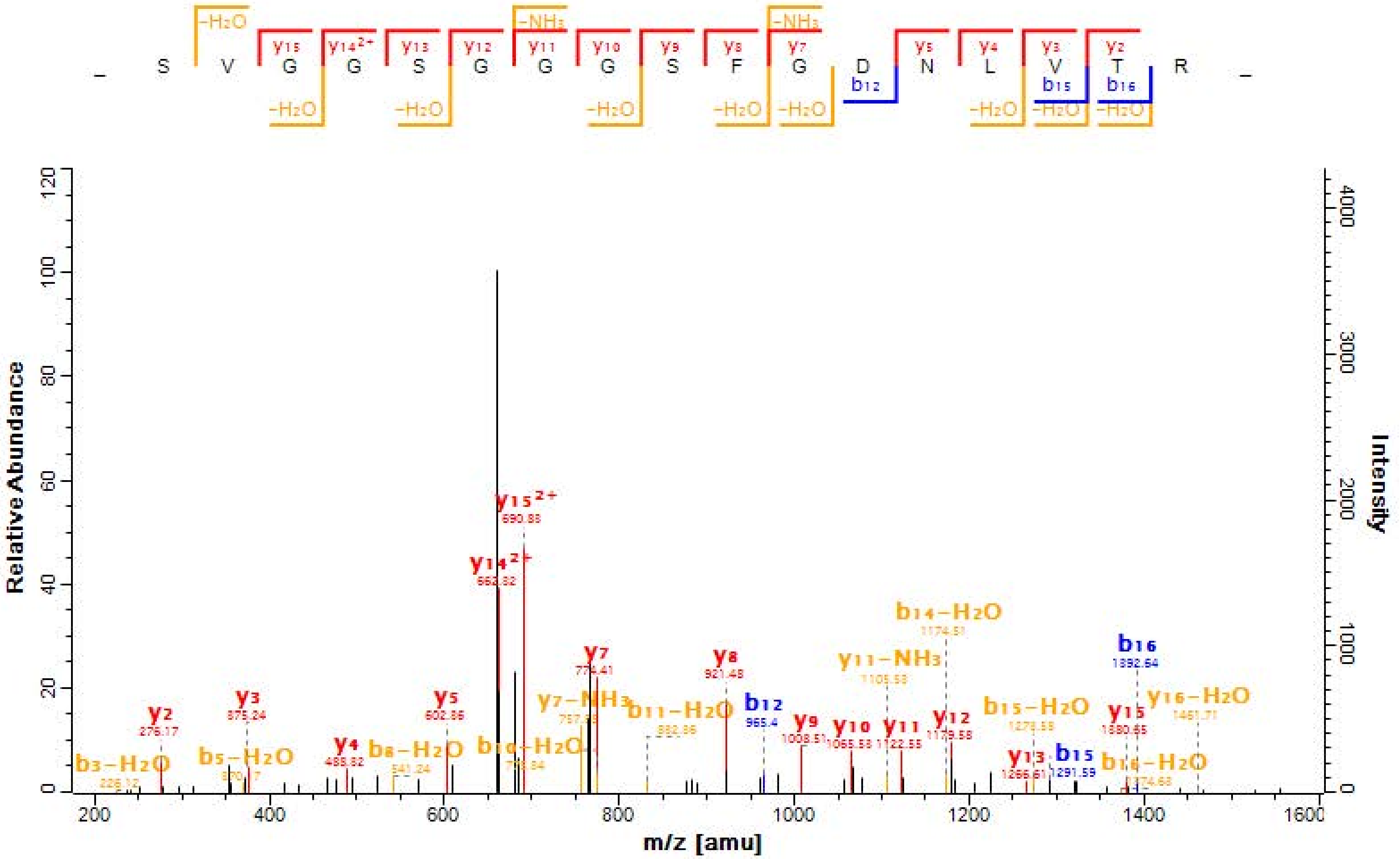
precursor information

Mass:	1186.60874
m/z:	594.31165
Charge:	2+
Retentiontime:	19.352752685546
Score:	110.5336
Mass Error [ppm]:	0.51497
PEP:	0.00049944
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	32 %
Peak Coverage:	19 %
Protein Localisation:	15 ... 24

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	86.09643		114.0913	1	L	9		
-0.03515	199.1805	-0.10341	227.1754	2	L	8	1074.531	-0.02353
	328.2231	-0.04051	356.218	3	E	7	961.4473	+0.013839
	457.2657		485.2606	4	E	6	832.4047	+0.055516
	570.3497		598.3447	5	L	5	703.3621	+0.026271
	699.3923	+0.024557	727.3872	6	E	4	590.278	
	828.4349	+0.051116	856.4298	7	E	3	461.2354	+0.07224
	885.4564		913.4513	8	G	2	332.1928	+0.138942
	1013.515	+0.009405	1041.51	9	Q	1	275.1714	
				10	K	0	147.1128	

Scan number	3022	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	99.57



precursor information

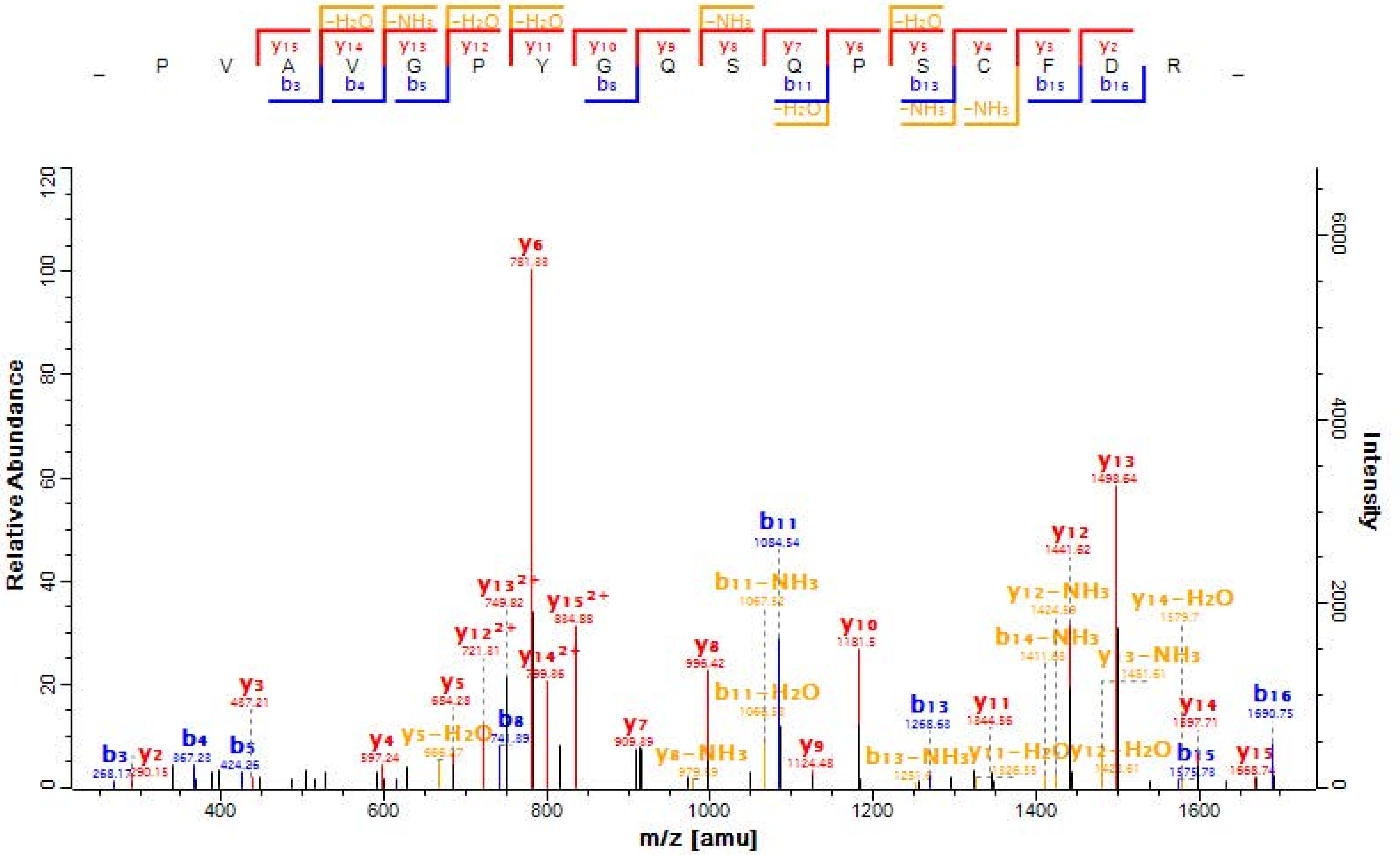
Mass:	1565.7429
m/z:	783.87873
Charge:	2+
Retentiontime:	20.412982940673
Score:	99.56905
Mass Error [ppm]:	-0.31807
PEP:	0.00086168
Precursor Type:	ISO

general information

Annotation:	15 of 17
AminoAcids Coverag	88 %
Intensity Coverage:	44 %
Peak Coverage:	36 %
Protein Localisation:	628 ... 644

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	16				
	187.1077	2	V	15	1479.719		1479.719	
	244.1292	3	G	14	1380.65	+0.116492	690.8288	+0.167706
	301.1506	4	G	13	1323.629		662.318	-0.24374
	388.1827	5	S	12	1266.607	-0.03956	1266.607	
	445.2041	6	G	11	1179.575	-0.14583	1179.575	
	502.2256	7	G	10	1122.554	-0.0294	1122.554	
	559.2471	8	G	9	1065.532	+0.049927	1065.532	
	646.2791	9	S	8	1008.511	-0.07339	1008.511	
	793.3475	10	F	7	921.4789	+0.003321	921.4789	
	850.369	11	G	6	774.4104	+0.084552	774.4104	
+0.097188	965.3959	12	D	5	717.389		717.389	
	1079.439	13	N	4	602.362	+0.045618	602.362	
	1192.523	14	L	3	488.3191	+0.00041	488.3191	
-0.07801	1291.591	15	V	2	375.235	+0.174562	375.235	
+0.139322	1392.639	16	T	1	276.1666	+0.063258	276.1666	
		17	R	0	175.119		175.119	

Scan number	3138	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	197.75



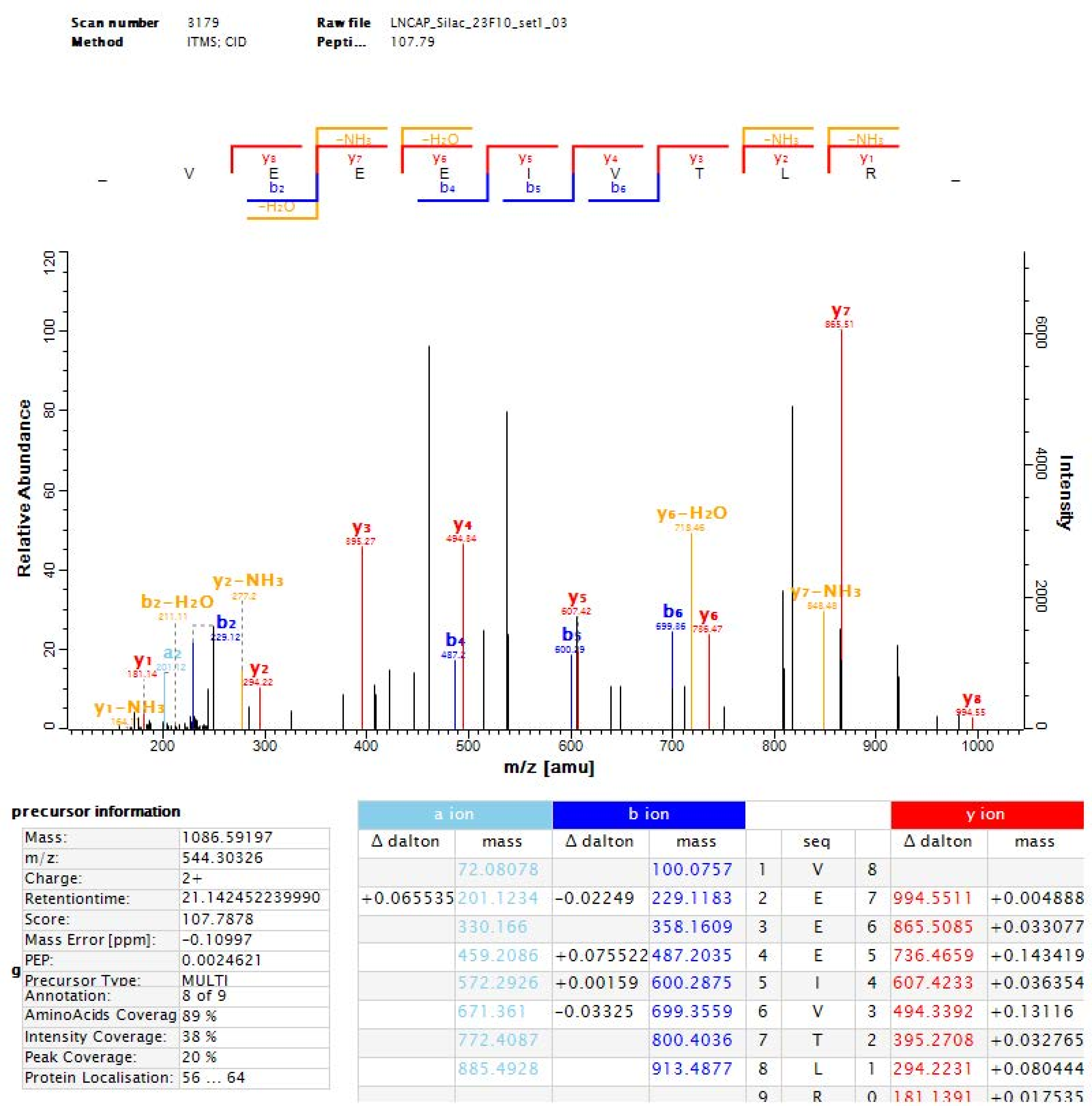
precursor information

Mass:	1863.85743
m/z:	932.93599
Charge:	2+
Retentiontime:	20.952625274658
Score:	197.7513
Mass Error [ppm]:	0.027832
PEP:	1.5793E-34
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	63 %
Peak Coverage:	45 %
Protein Localisation:	2 ... 18

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	98.06004	1	P	16				
	197.1285	2	V	15	1767.812		1767.812	
-0.02424	268.1656	3	A	14	1668.743	+0.214405	834.8754	+0.249255
+0.105343	367.234	4	V	13	1597.706	-0.00288	799.3568	+0.119253
+0.114427	424.2554	5	G	12	1498.638	-0.00734	749.8226	+0.080156
	521.3082	6	P	11	1441.616	-0.03482	721.3119	+0.317939
	684.3715	7	Y	10	1344.564	+0.301509	1344.564	
+0.184574	741.393	8	G	9	1181.5	+0.016937	1181.5	
	869.4516	9	Q	8	1124.479	+0.039622	1124.479	
	956.4836	10	S	7	996.4204	+0.026239	996.4204	
+0.005666	1084.542	11	Q	6	909.3883	+0.117898	909.3883	
	1181.595	12	P	5	781.3297	+0.068444	781.3297	
-0.02859	1268.627	13	S	4	684.277	-0.0713	684.277	
	1428.658	14	C	3	597.245	+0.001808	597.245	
-0.44027	1575.726	15	F	2	437.2143	+0.265244	437.2143	
-0.12298	1690.753	16	D	1	290.1459	-0.05178	290.1459	
		17	R	0	175.119		175.119	

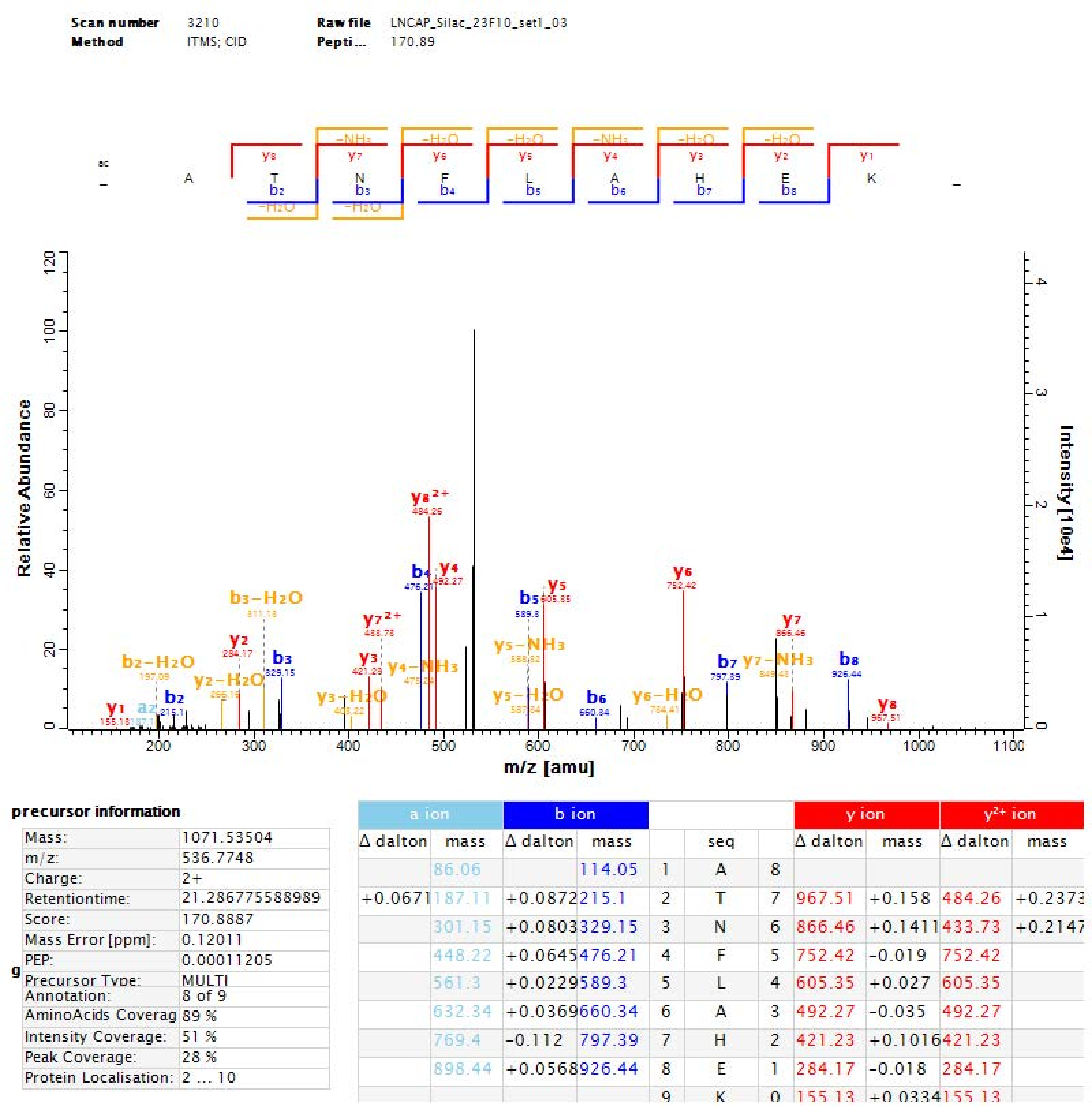


Scan number	3179	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	107.79

precursor information

Mass:	1086.59197
m/z:	544.30326
Charge:	2+
Retentiontime:	21.142452239990
Score:	107.7878
Mass Error [ppm]:	-0.10997
PEP:	0.0024621
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	38 %
Peak Coverage:	20 %
Protein Localisation:	56 ... 64

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	72.08078		100.0757	1	V	8		
+0.065535	201.1234	-0.02249	229.1183	2	E	7	994.5511	+0.004888
	330.166		358.1609	3	E	6	865.5085	+0.033077
	459.2086	+0.075522	487.2035	4	E	5	736.4659	+0.143419
	572.2926	+0.00159	600.2875	5	I	4	607.4233	+0.036354
	671.361	-0.03325	699.3559	6	V	3	494.3392	+0.13116
	772.4087		800.4036	7	T	2	395.2708	+0.032765
	885.4928		913.4877	8	L	1	294.2231	+0.080444
				9	R	0	181.1391	+0.017535

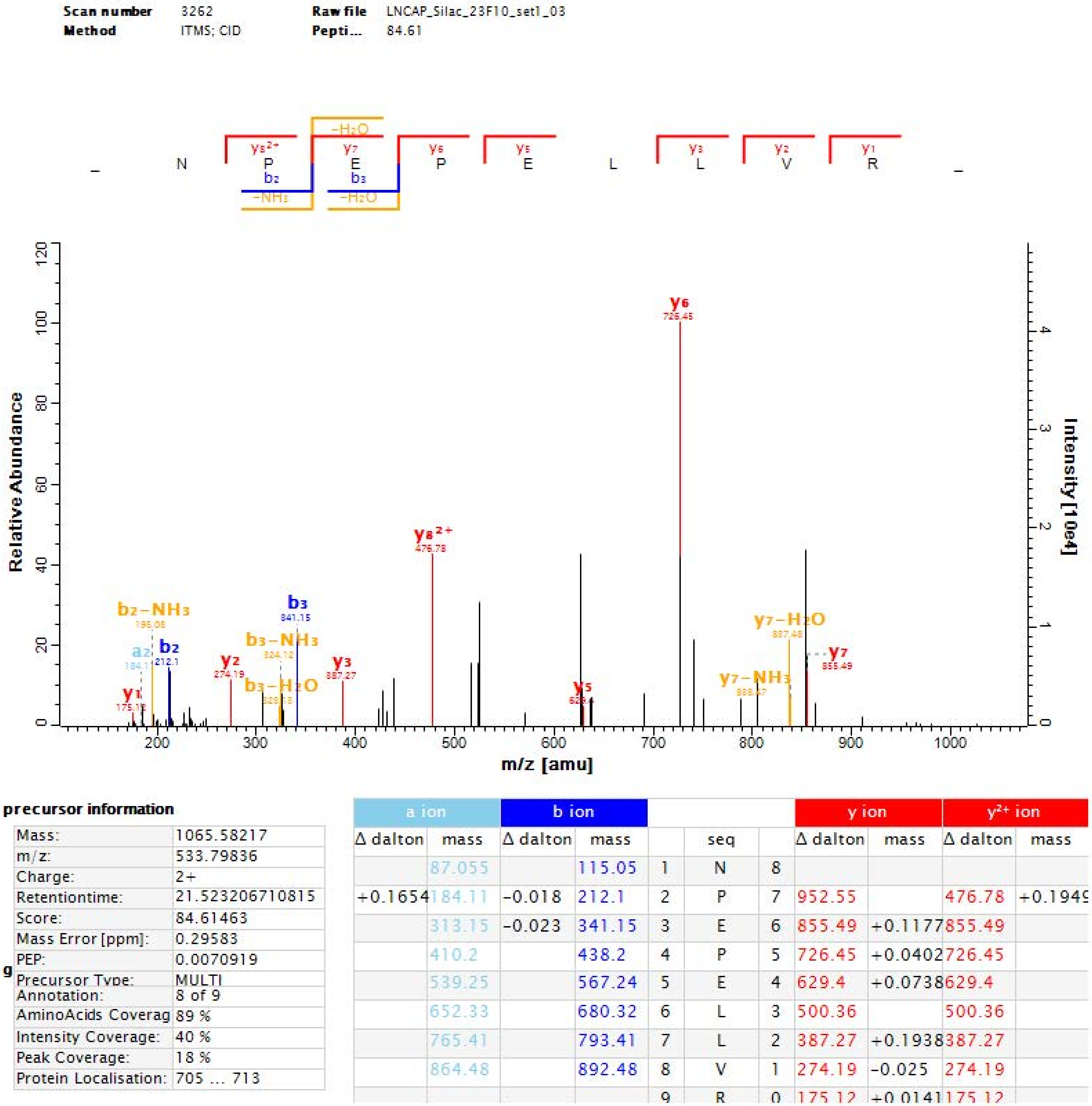


Scan number	3210	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	170.89

precursor information

Mass:	1071.53504
m/z:	536.7748
Charge:	2+
Retentiontime:	21.286775588989
Score:	170.8887
Mass Error [ppm]:	0.12011
PEP:	0.00011205
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	51 %
Peak Coverage:	28 %
Protein Localisation:	2 ... 10

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.06		114.05	1	A	8				
+0.0671	187.11	+0.0872	215.1	2	T	7	967.51	+0.158	484.26	+0.2373
	301.15	+0.0803	329.15	3	N	6	866.46	+0.1411	433.73	+0.2147
	448.22	+0.0645	476.21	4	F	5	752.42	−0.019	752.42	
	561.3	+0.0229	589.3	5	L	4	605.35	+0.027	605.35	
	632.34	+0.0369	660.34	6	A	3	492.27	−0.035	492.27	
	769.4	−0.112	797.39	7	H	2	421.23	+0.1016	421.23	
	898.44	+0.0568	926.44	8	E	1	284.17	−0.018	284.17	
				9	K	0	155.13	+0.0334	155.13	



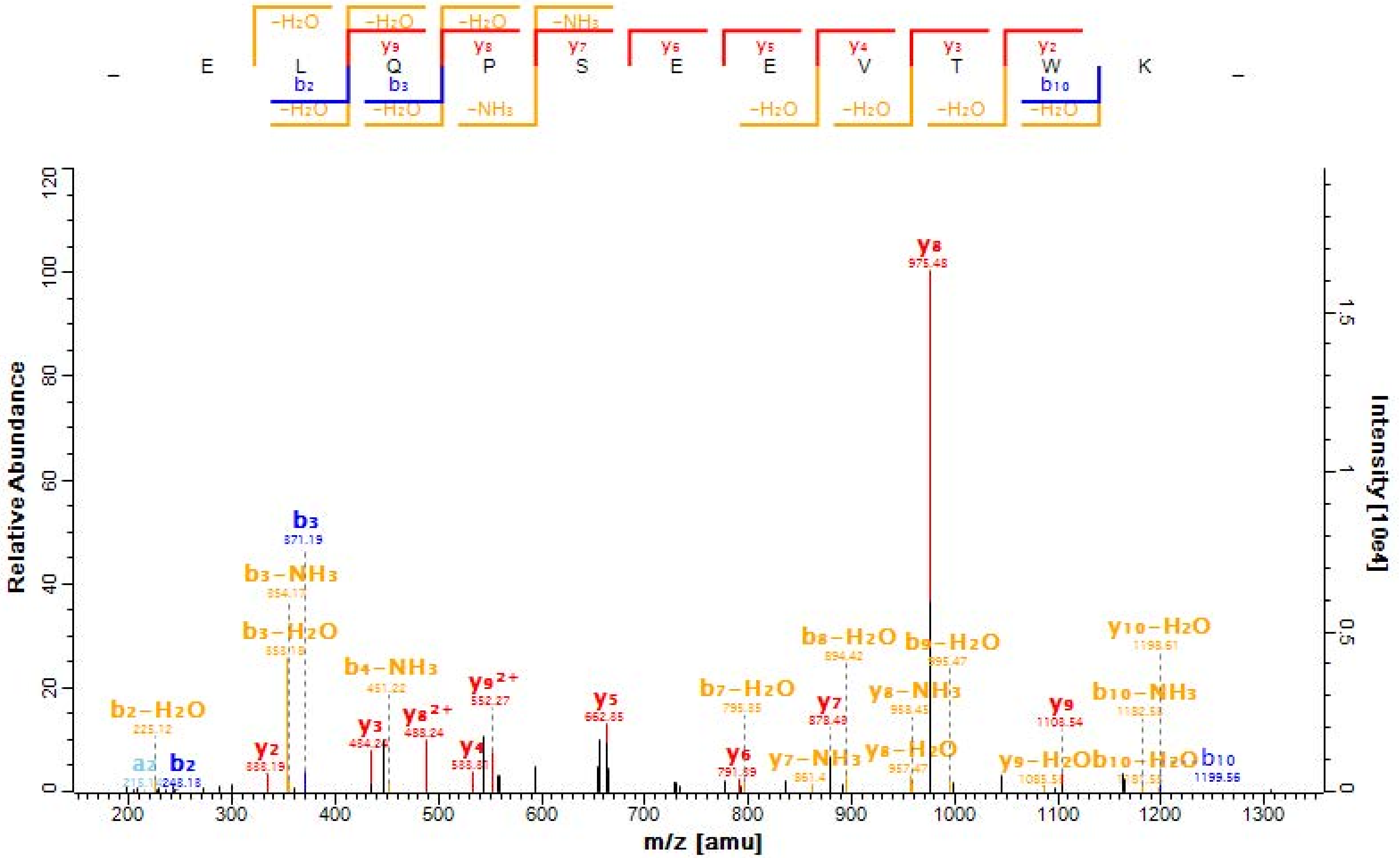
Scan number	3262	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	84.61

precursor information

Mass:	1065.58217
m/z:	533.79836
Charge:	2+
Retentiontime:	21.523206710815
Score:	84.61463
Mass Error [ppm]:	0.29583
PEP:	0.0070919
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	40 %
Peak Coverage:	18 %
Protein Localisation:	705 ... 713

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	87.055		115.05	1	N	8				
+0.1654	184.11	-0.018	212.1	2	P	7	952.55		476.78	+0.194
	313.15	-0.023	341.15	3	E	6	855.49	+0.1177	855.49	
	410.2		438.2	4	P	5	726.45	+0.0402	726.45	
	539.25		567.24	5	E	4	629.4	+0.0738	629.4	
	652.33		680.32	6	L	3	500.36		500.36	
	765.41		793.41	7	L	2	387.27	+0.1938	387.27	
	864.48		892.48	8	V	1	274.19	-0.025	274.19	
				9	R	0	175.12	+0.0141	175.12	

Scan number	3280	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	129.82



precursor information

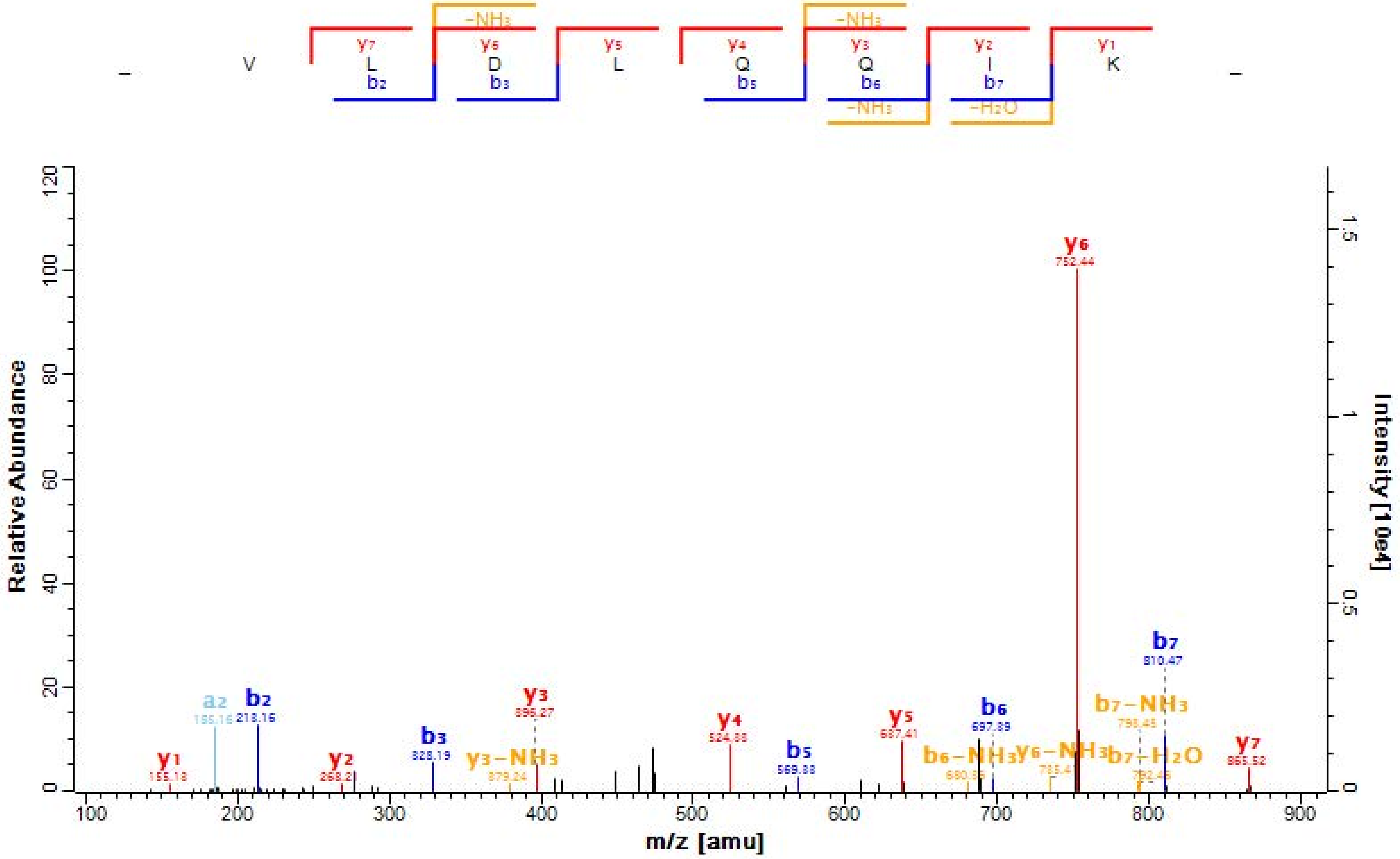
Mass:	1344.65667
m/z:	673.33561
Charge:	2+
Retentiontime:	21.607357025146
Score:	129.8187
Mass Error [ppm]:	0.39089
PEP:	0.0001863
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	60 %
Peak Coverage:	35 %
Protein Localisation:	95 ... 105

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	10				
-0.04	215.14	+0.0132	243.13	2	L	9	1216.6		1216.6	
	343.2	+0.0019	371.19	3	Q	8	1103.5	+0.0465	552.27	+0.03
	440.25		468.25	4	P	7	975.48	-0.006	488.24	+0.109
	527.28		555.28	5	S	6	878.43	-0.032	878.43	
	656.32		684.32	6	E	5	791.39	+0.185	791.39	
	785.37		813.36	7	E	4	662.35	+0.2121	662.35	
	884.44		912.43	8	V	3	533.31	+0.1872	533.31	
	985.48		1013.5	9	T	2	434.24	+0.0288	434.24	
	1171.6	-0.145	1199.6	10	W	1	333.19	+0.193	333.19	
				11	K	0	147.11		147.11	

Scan number	3577	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	130.56

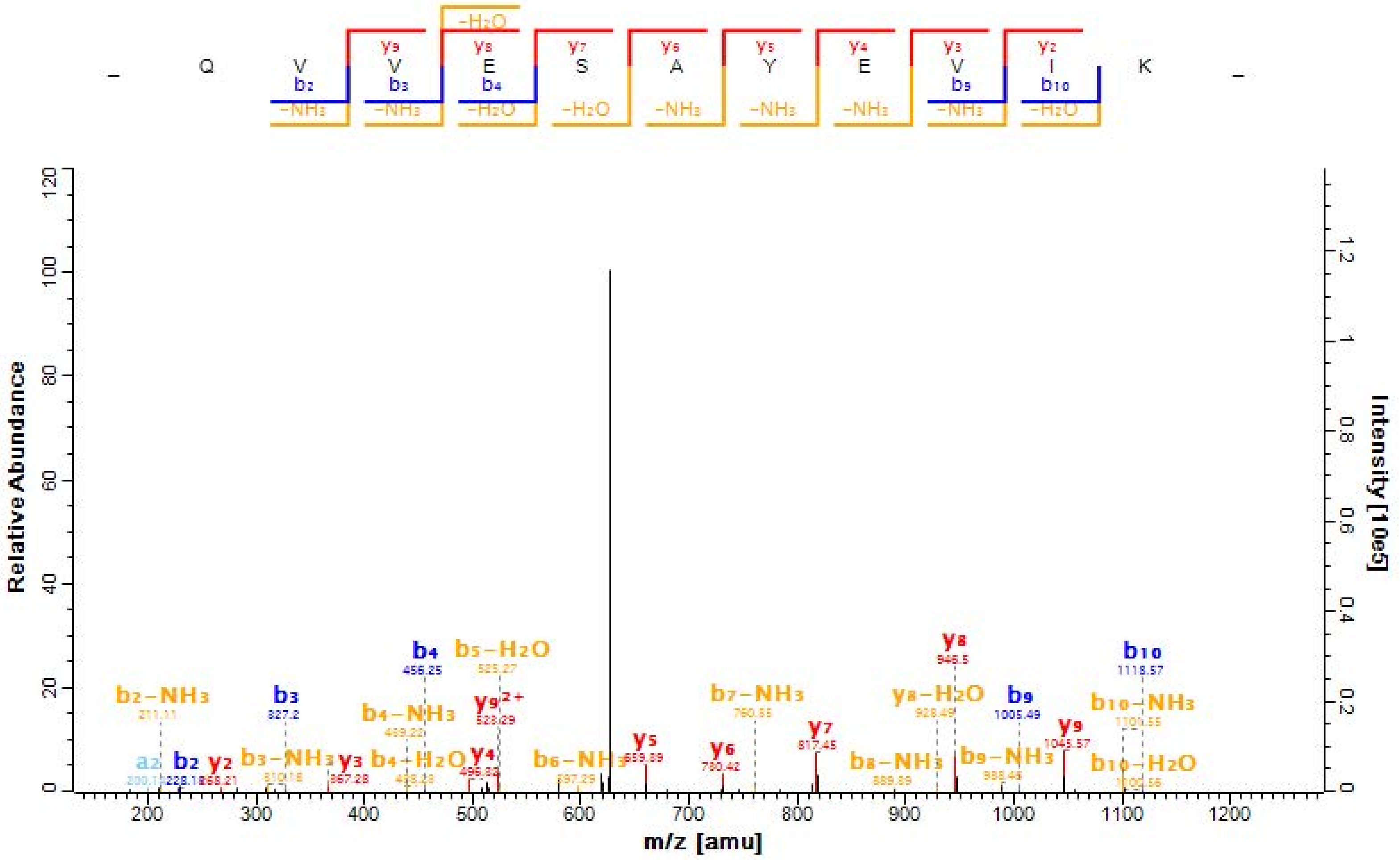


precursor information

Mass:	955.57015
m/z:	478.79235
Charge:	2+
Retentiontime:	23.014547348022
Score:	130.5618
Mass Error [ppm]:	-0.087316
PEP:	0.0005295
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	69 %
Peak Coverage:	23 %
Protein Localisation:	340 ... 347

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	72.08078		100.0757	1	V	7		
-0.01906	185.1648	+0.036809	213.1598	2	L	6	865.5233	+0.004478
	300.1918	+0.028726	328.1867	3	D	5	752.4392	+0.09257
	413.2758		441.2708	4	L	4	637.4123	-0.01544
	541.3344	+0.086372	569.3293	5	Q	3	524.3282	+0.0469
	669.393	+0.115502	697.3879	6	Q	2	396.2696	+0.182626
	782.4771	+0.009953	810.472	7	I	1	268.2111	+0.078545
				8	K	0	155.127	-0.10921

Scan number	3662	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	148.28



precursor information

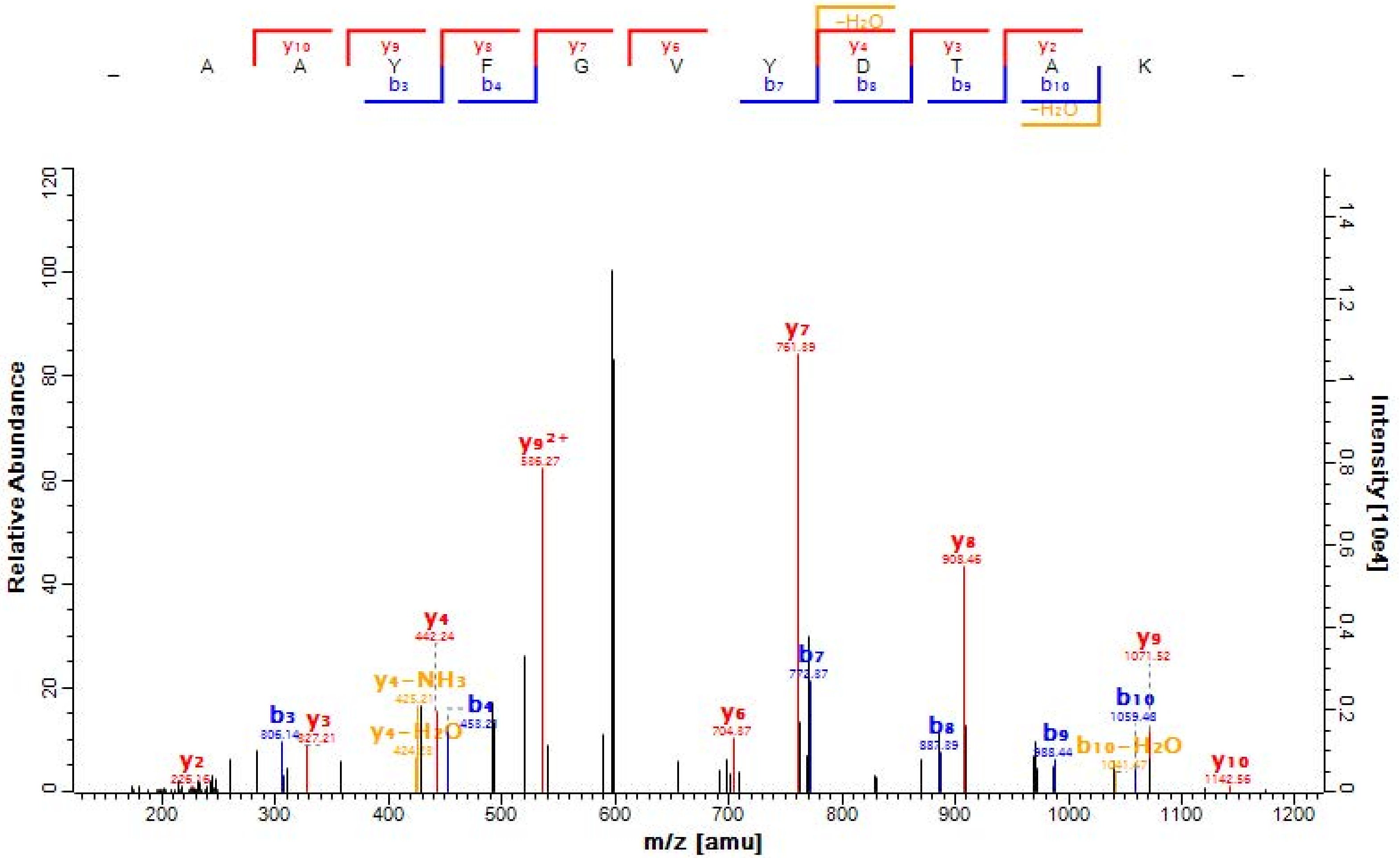
Mass:	1263.67076
m/z:	632.84266
Charge:	2+
Retentiontime:	23.406057357788
Score:	148.2801
Mass Error [ppm]:	-0.24238
PEP:	4.0733E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	29 %
Peak Coverage:	33 %
Protein Localisation:	262 ... 272

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	101.07		129.07	1	Q	10				
+0.0351	200.14	+0.0606	228.13	2	V	9	1144.6		1144.6	
	299.21	-0.017	327.2	3	V	8	1045.6	-0.015	523.29	+0.2344
	428.25	+0.0379	456.25	4	E	7	946.5	+0.0407	946.5	
	515.28		543.28	5	S	6	817.45	+0.1498	817.45	
	586.32		614.31	6	A	5	730.42	+0.1703	730.42	
	749.38		777.38	7	Y	4	659.39	+0.1209	659.39	
	878.43		906.42	8	E	3	496.32	+0.1302	496.32	
	977.49	-0.456	1005.5	9	V	2	367.28	-0.06	367.28	
	1090.6	+0.0579	1118.6	10	I	1	268.21	+0.0676	268.21	
				11	K	0	155.13		155.13	

Scan number	3729	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	91.31



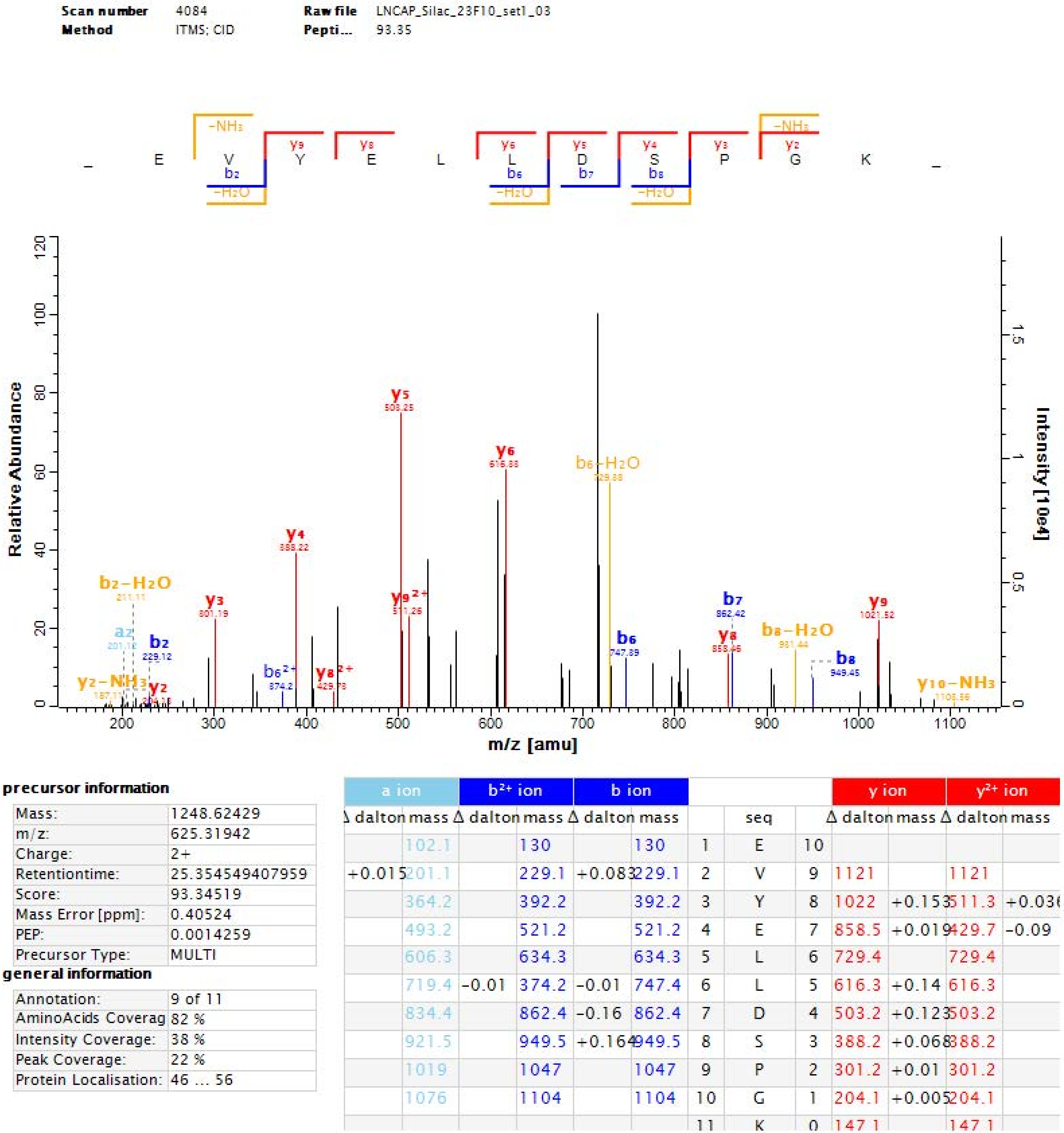
precursor information

Mass:	1204.57676
m/z:	603.29566
Charge:	2+
Retentiontime:	23.713668823242
Score:	91.31331
Mass Error [ppm]:	0.26836
PEP:	0.0016514
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	39 %
Peak Coverage:	18 %
Protein Localisation:	189 ... 199

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	10				
	143.0815	2	A	9	1142.561	+0.284902	1142.561	
+0.058842	306.1448	3	Y	8	1071.524	-0.10816	536.2655	+0.117392
-0.0067	453.2132	4	F	7	908.4604	+0.068389	908.4604	
	510.2347	5	G	6	761.3919	+0.039269	761.3919	
	609.3031	6	V	5	704.3705	+0.111941	704.3705	
+0.143008	772.3665	7	Y	4	605.3021		605.3021	
+0.146826	887.3934	8	D	3	442.2387	+0.100617	442.2387	
-0.03287	988.4411	9	T	2	327.2118	+0.11456	327.2118	
+0.095176	1059.478	10	A	1	226.1641	+0.359138	226.1641	
		11	K	0	155.127		155.127	



Scan number	4084	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	93.35

precursor information

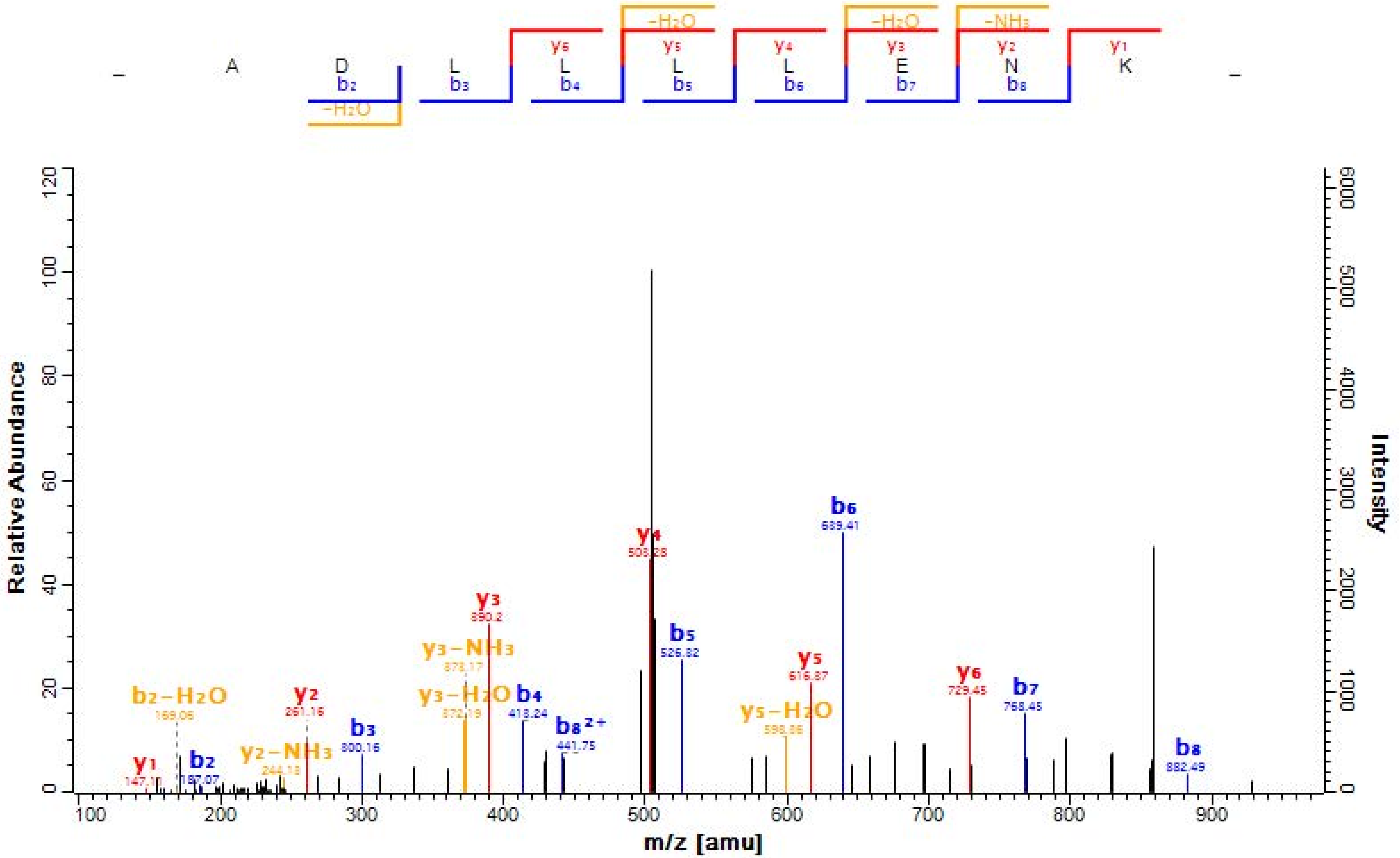
Mass:	1248.62429
m/z:	625.31942
Charge:	2+
Retentiontime:	25.354549407959
Score:	93.34519
Mass Error [ppm]:	0.40524
PEP:	0.0014259
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	38 %
Peak Coverage:	22 %
Protein Localisation:	46 ... 56

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.1		130		130	1	E	10				
+0.015	201.1		229.1	+0.083	229.1	2	V	9	1121		1121	
	364.2		392.2		392.2	3	Y	8	1022	+0.153	511.3	+0.03
	493.2		521.2		521.2	4	E	7	858.5	+0.019	429.7	-0.09
	606.3		634.3		634.3	5	L	6	729.4		729.4	
	719.4	-0.01	374.2	-0.01	747.4	6	L	5	616.3	+0.14	616.3	
	834.4		862.4	-0.16	862.4	7	D	4	503.2	+0.123	503.2	
	921.5		949.5	+0.164	949.5	8	S	3	388.2	+0.068	388.2	
	1019		1047		1047	9	P	2	301.2	+0.01	301.2	
	1076		1104		1104	10	G	1	204.1	+0.005	204.1	
						11	K	0	147.1		147.1	

Scan number	4159	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	105.2

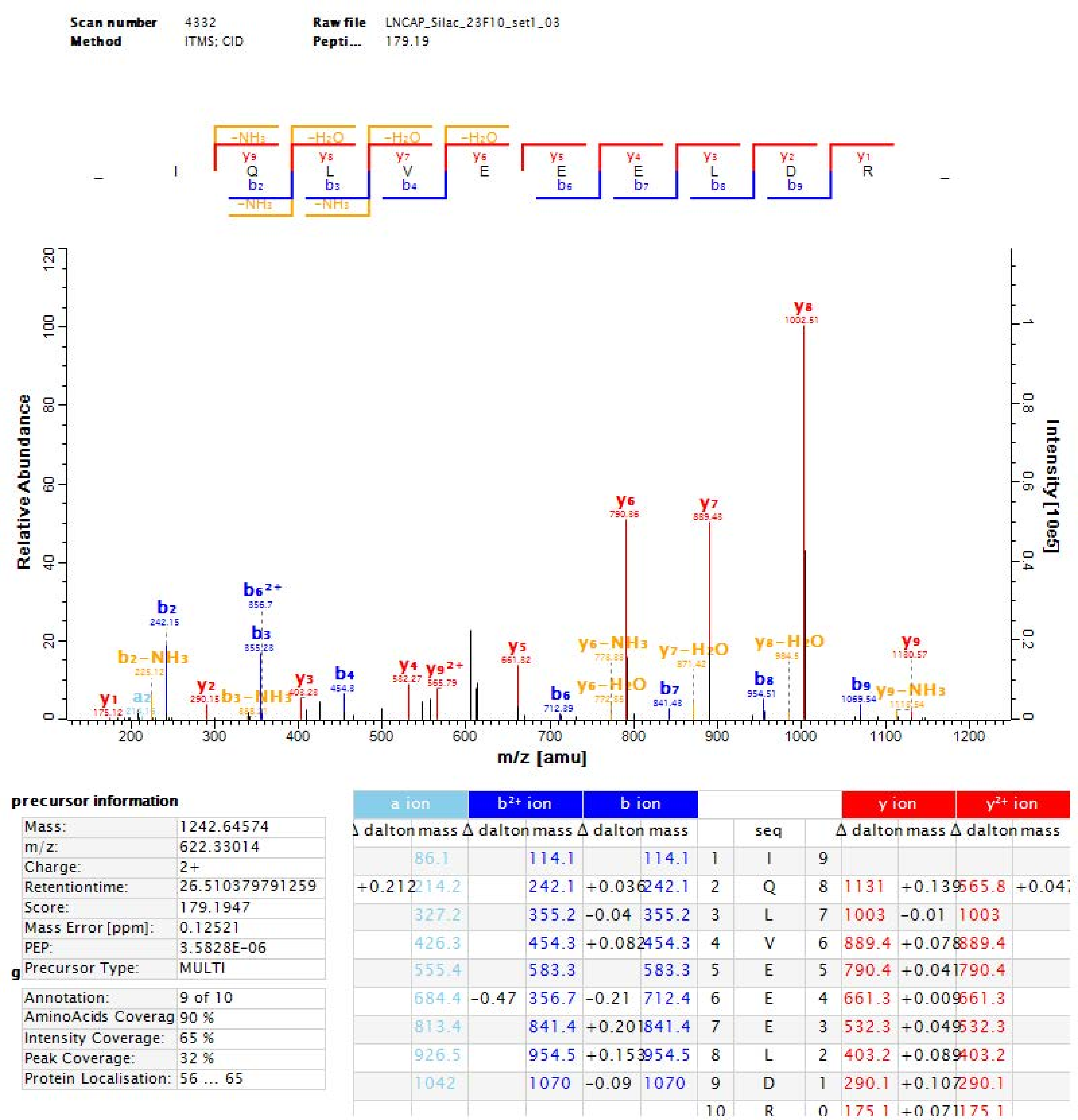


precursor information

g

Mass:	1027.59219
m/z:	514.80337
Charge:	2+
Retentiontime:	25.704471588134
Score:	105.1952
Mass Error [ppm]:	0.81014
PEP:	0.0027161
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	39 %
Peak Coverage:	20 %
Protein Localisation:	653 ... 661

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	72.04439		72.04439	1	A	8		
	187.0713	−0.15845	187.0713	2	D	7	957.5615	
	300.1554	+0.05493	300.1554	3	L	6	842.5346	
	413.2395	+0.107402	413.2395	4	L	5	729.4505	+0.075728
	526.3235	+0.031272	526.3235	5	L	4	616.3665	+0.229617
	639.4076	−0.01263	639.4076	6	L	3	503.2824	+0.06484
	768.4502	+0.066175	768.4502	7	E	2	390.1983	+0.024271
−0.40992	441.7502	+0.221673	882.4931	8	N	1	261.1557	+0.079437
				9	K	0	147.1128	−0.06341



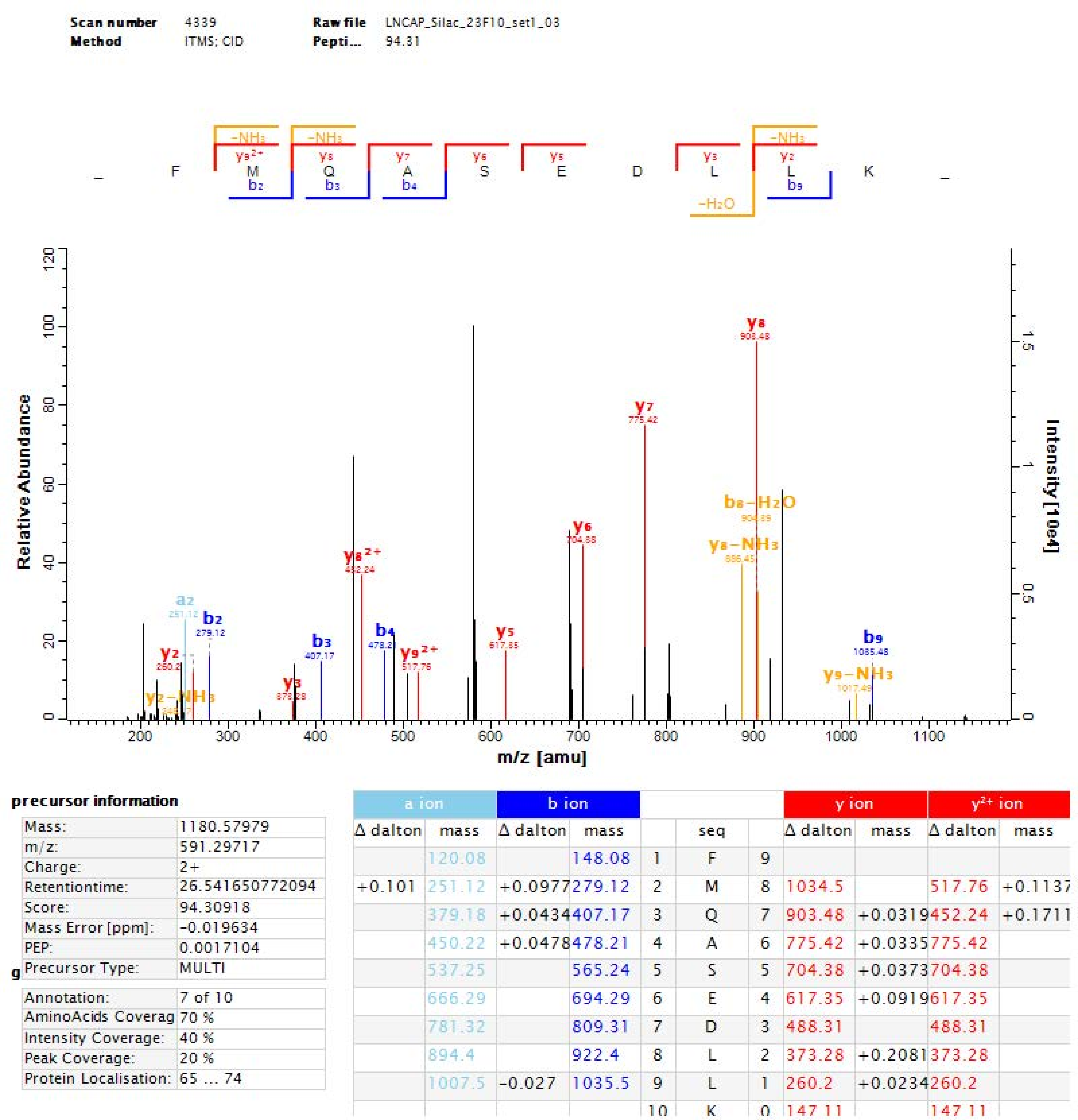
Scan number	4332	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	179.19

precursor information

Mass:	1242.64574
m/z:	622.33014
Charge:	2+
Retentiontime:	26.510379791259
Score:	179.1947
Mass Error [ppm]:	0.12521
PEP:	3.5828E-06
Precursor Type:	MULTI

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	65 %
Peak Coverage:	32 %
Protein Localisation:	56 ... 65

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	I	9				
+0.212	214.2		242.1	+0.036	242.1	2	Q	8	1131	+0.139	565.8	+0.04
	327.2		355.2	−0.04	355.2	3	L	7	1003	−0.01	1003	
	426.3		454.3	+0.082	454.3	4	V	6	889.4	+0.078	889.4	
	555.4		583.3		583.3	5	E	5	790.4	+0.041	790.4	
	684.4	−0.47	356.7	−0.21	712.4	6	E	4	661.3	+0.009	661.3	
	813.4		841.4	+0.201	841.4	7	E	3	532.3	+0.049	532.3	
	926.5		954.5	+0.153	954.5	8	L	2	403.2	+0.089	403.2	
	1042		1070	−0.09	1070	9	D	1	290.1	+0.107	290.1	
						10	R	0	175.1	+0.071	175.1	



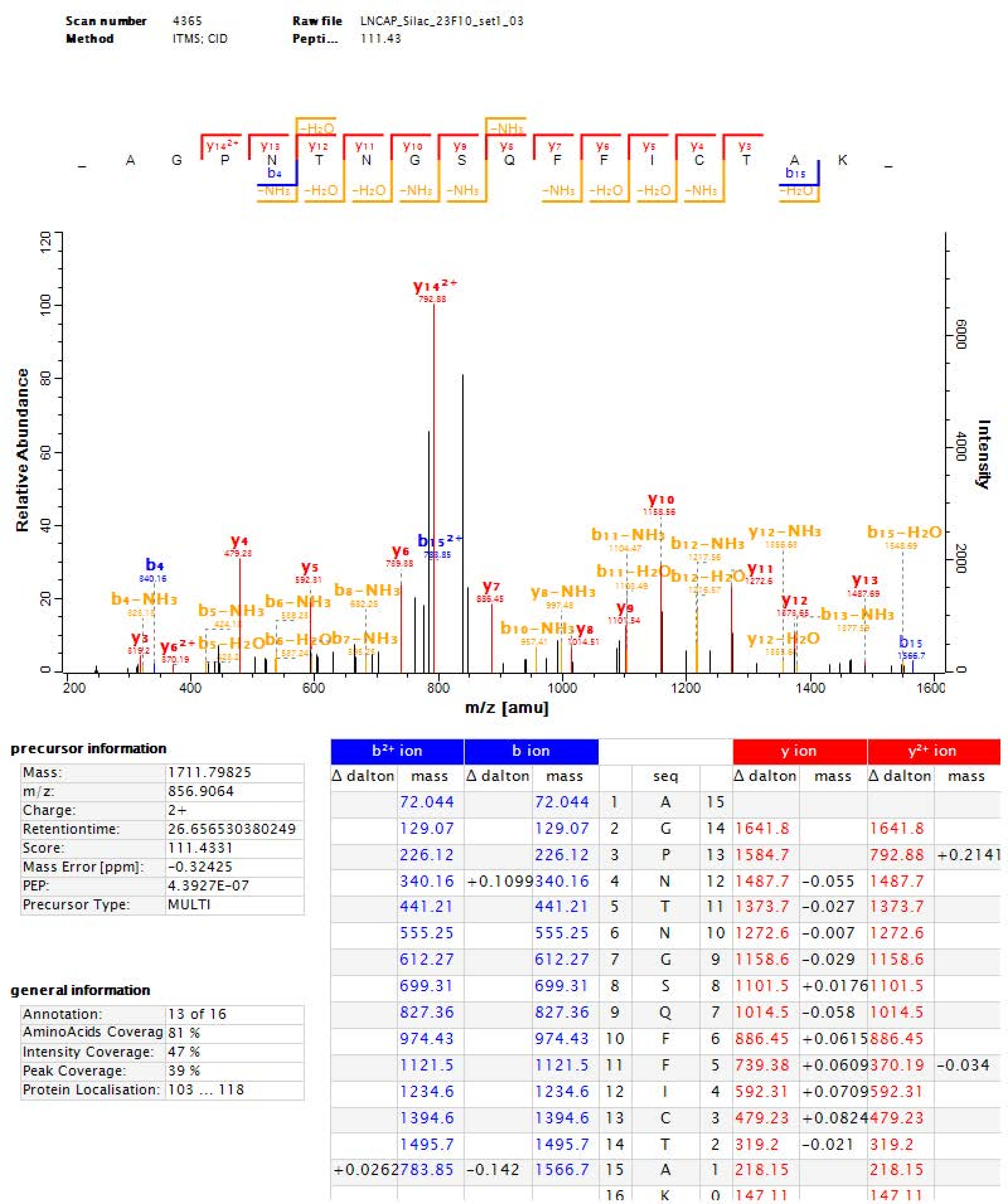
Scan number	4339	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	94.31

precursor information

Mass:	1180.57979
m/z:	591.29717
Charge:	2+
Retentiontime:	26.541650772094
Score:	94.30918
Mass Error [ppm]:	-0.019634
PEP:	0.0017104
Precursor Type:	MULTI

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	40 %
Peak Coverage:	20 %
Protein Localisation:	65 ... 74

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08		148.08	1	F	9				
+0.101	251.12	+0.0977	279.12	2	M	8	1034.5		517.76	+0.1137
	379.18	+0.0434	407.17	3	Q	7	903.48	+0.0319	452.24	+0.1711
	450.22	+0.0478	478.21	4	A	6	775.42	+0.0335	775.42	
	537.25		565.24	5	S	5	704.38	+0.0373	704.38	
	666.29		694.29	6	E	4	617.35	+0.0919	617.35	
	781.32		809.31	7	D	3	488.31		488.31	
	894.4		922.4	8	L	2	373.28	+0.2081	373.28	
	1007.5	-0.027	1035.5	9	L	1	260.2	+0.0234	260.2	
				10	K	0	147.11		147.11	



Scan number	4365	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	111.43

precursor information

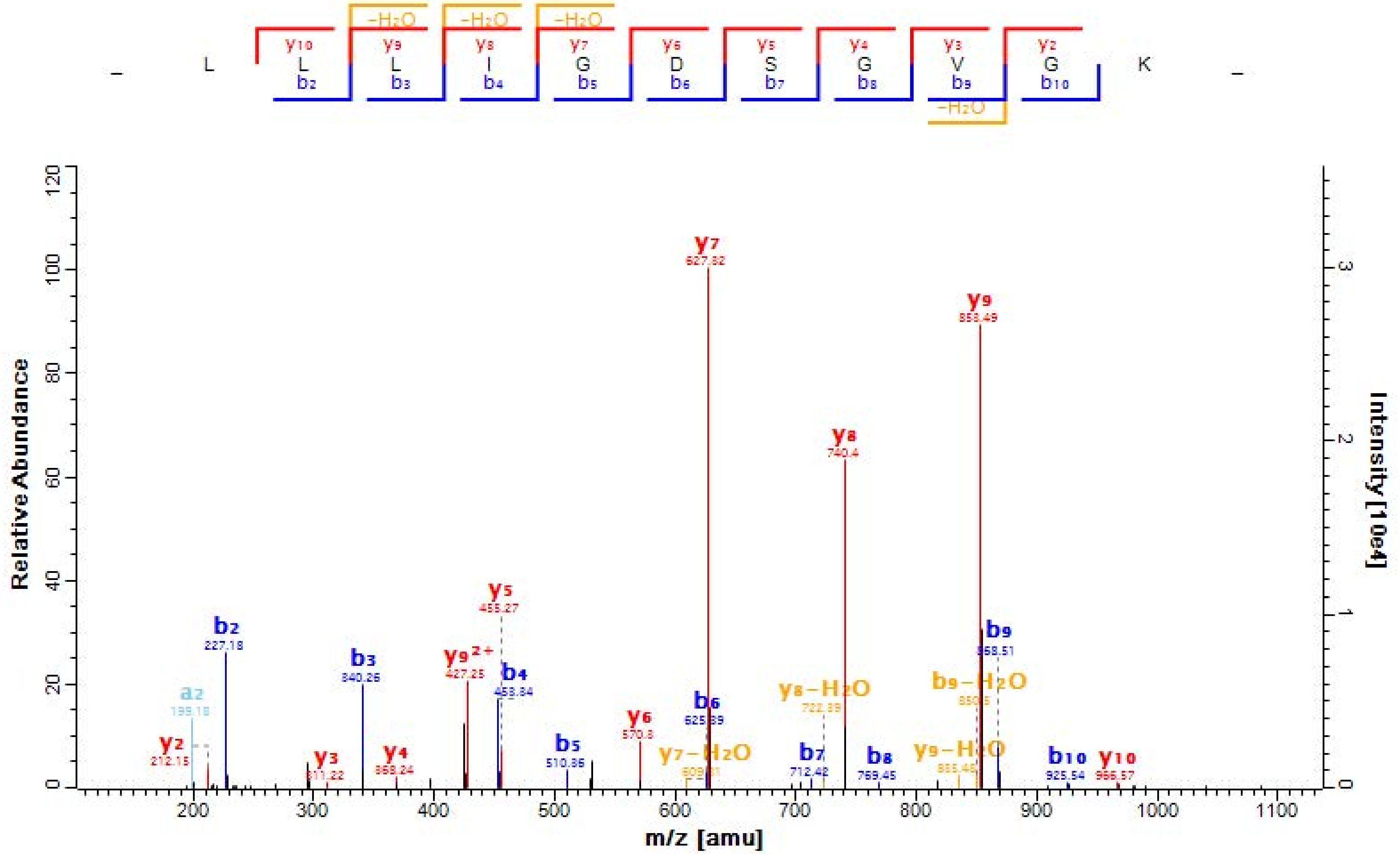
Mass:	1711.79825
m/z:	856.9064
Charge:	2+
Retentiontime:	26.656530380249
Score:	111.4331
Mass Error [ppm]:	-0.32425
PEP:	4.3927E-07
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	47 %
Peak Coverage:	39 %
Protein Localisation:	103 ... 118

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	15				
	129.07		129.07	2	G	14	1641.8		1641.8	
	226.12		226.12	3	P	13	1584.7		792.88	+0.2141
	340.16	+0.1099	340.16	4	N	12	1487.7	-0.055	1487.7	
	441.21		441.21	5	T	11	1373.7	-0.027	1373.7	
	555.25		555.25	6	N	10	1272.6	-0.007	1272.6	
	612.27		612.27	7	G	9	1158.6	-0.029	1158.6	
	699.31		699.31	8	S	8	1101.5	+0.0176	1101.5	
	827.36		827.36	9	Q	7	1014.5	-0.058	1014.5	
	974.43		974.43	10	F	6	886.45	+0.0615	886.45	
	1121.5		1121.5	11	F	5	739.38	+0.0609	370.19	-0.034
	1234.6		1234.6	12	I	4	592.31	+0.0709	592.31	
	1394.6		1394.6	13	C	3	479.23	+0.0824	479.23	
	1495.7		1495.7	14	T	2	319.2	-0.021	319.2	
+0.0262	783.85	-0.142	1566.7	15	A	1	218.15		218.15	
				16	K	0	147.11		147.11	

Scan number	5080	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	159.09



precursor information

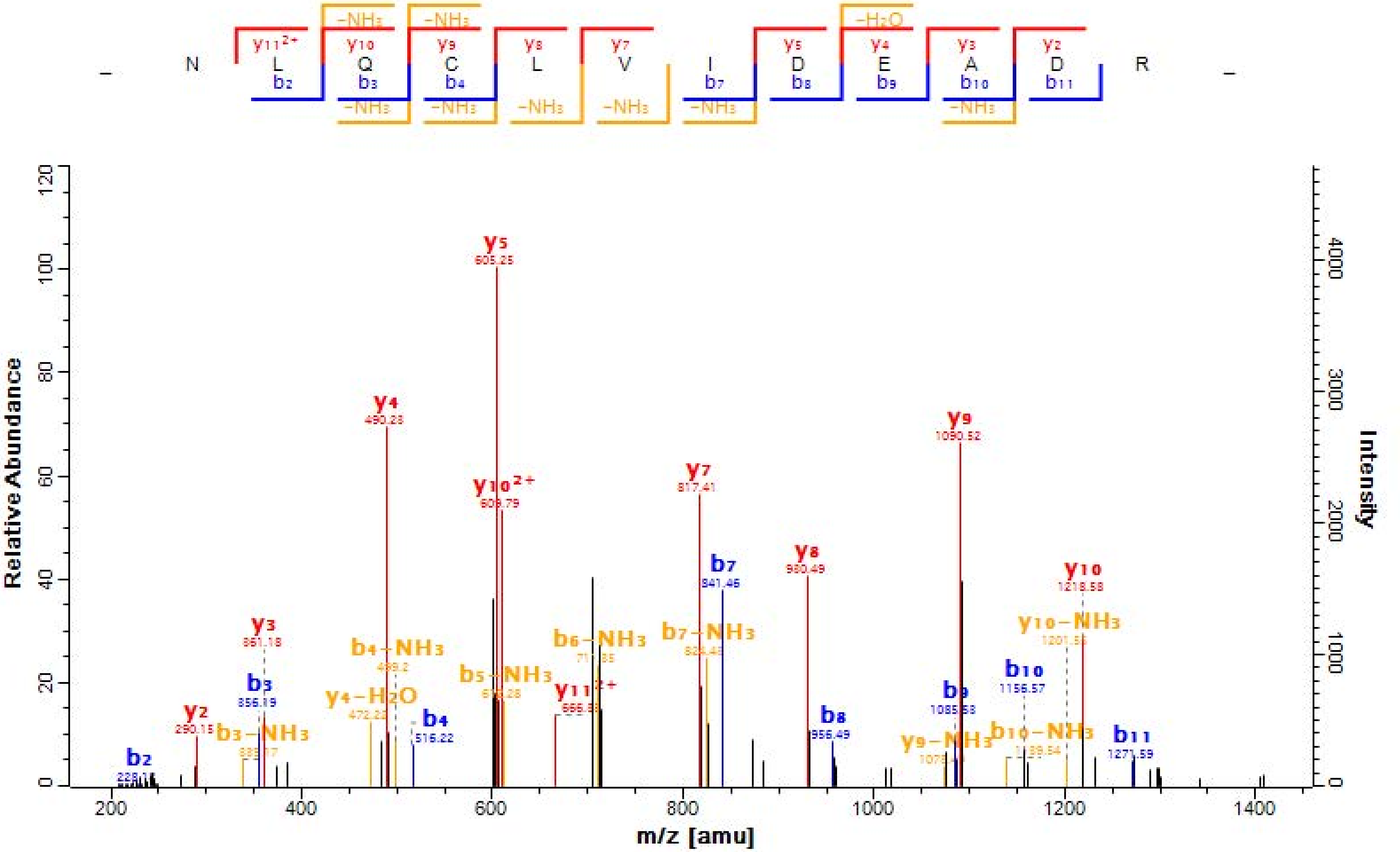
Mass:	1070.63338
m/z:	536.32397
Charge:	2+
Retentiontime:	29.993888854980
Score:	159.0863
Mass Error [ppm]:	-0.16606
PEP:	2.1152E-06
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	77 %
Peak Coverage:	31 %
Protein Localisation:	11 ... 21

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	10				
-0.046	199.18	-0.076	227.18	2	L	9	966.57	+0.0802	966.57	
	312.26	-0.031	340.26	3	L	8	853.49	-0.02	427.25	+0.1549
	425.35	-0.09	453.34	4	I	7	740.4	+0.0752	740.4	
	482.37	-0.033	510.36	5	G	6	627.32	-0.004	627.32	
	597.4	+0.005	625.39	6	D	5	570.3	+0.1632	570.3	
	684.43	+0.0587	712.42	7	S	4	455.27	+0.0938	455.27	
	741.45	-0.017	769.45	8	G	3	368.24	+0.1186	368.24	
	840.52	+0.0067	868.51	9	V	2	311.22	+0.0876	311.22	
	897.54	-0.066	925.54	10	G	1	212.15	+0.0875	212.15	
				11	K	0	155.13		155.13	

Scan number	5316	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	133.15



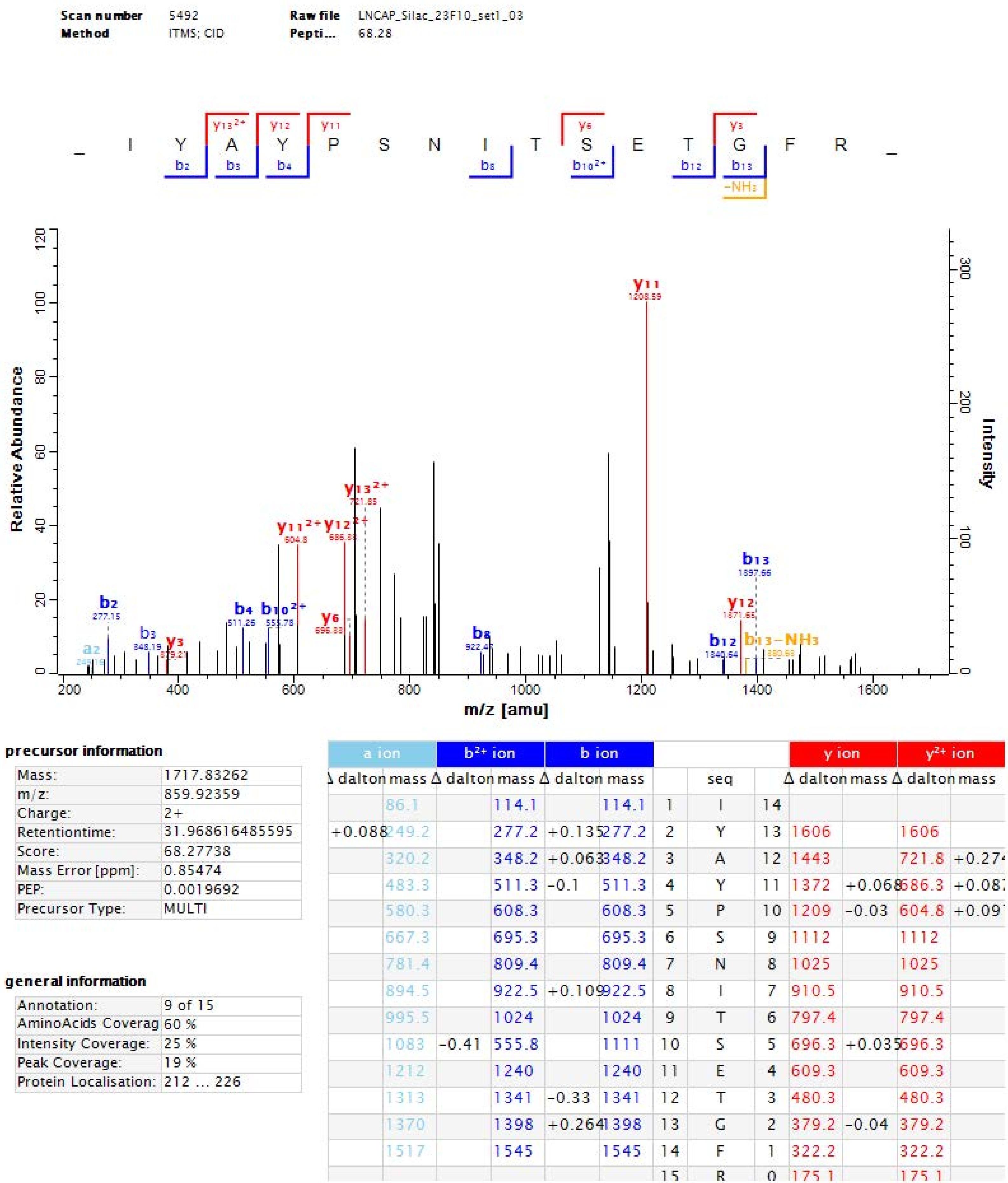
precursor information

Mass:	1444.6977
m/z:	723.35613
Charge:	2+
Retentiontime:	31.130268096923
Score:	133.1483
Mass Error [ppm]:	-0.22369
PEP:	6.8343E-05
Precursor Type:	ISO

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	62 %
Peak Coverage:	31 %
Protein Localisation:	326 ... 337

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502	1	N	11				
-0.17699	228.1343	2	L	10	1331.662		666.3348	+0.076367
+0.061305	356.1928	3	Q	9	1218.578	-0.01862	609.7928	+0.02825
+0.145098	516.2235	4	C	8	1090.52	+0.009073	1090.52	
	629.3076	5	L	7	930.4891	+0.048267	930.4891	
	728.376	6	V	6	817.405	+0.143622	817.405	
-0.07899	841.46	7	I	5	718.3366		718.3366	
+0.12557	956.487	8	D	4	605.2525	+0.003497	605.2525	
-0.11295	1085.53	9	E	3	490.2256	+0.063399	490.2256	
+0.203822	1156.567	10	A	2	361.183	+0.090062	361.183	
-0.03674	1271.594	11	D	1	290.1459	+0.100687	290.1459	
		12	R	0	175.119		175.119	



Scan number	5492	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	68.28

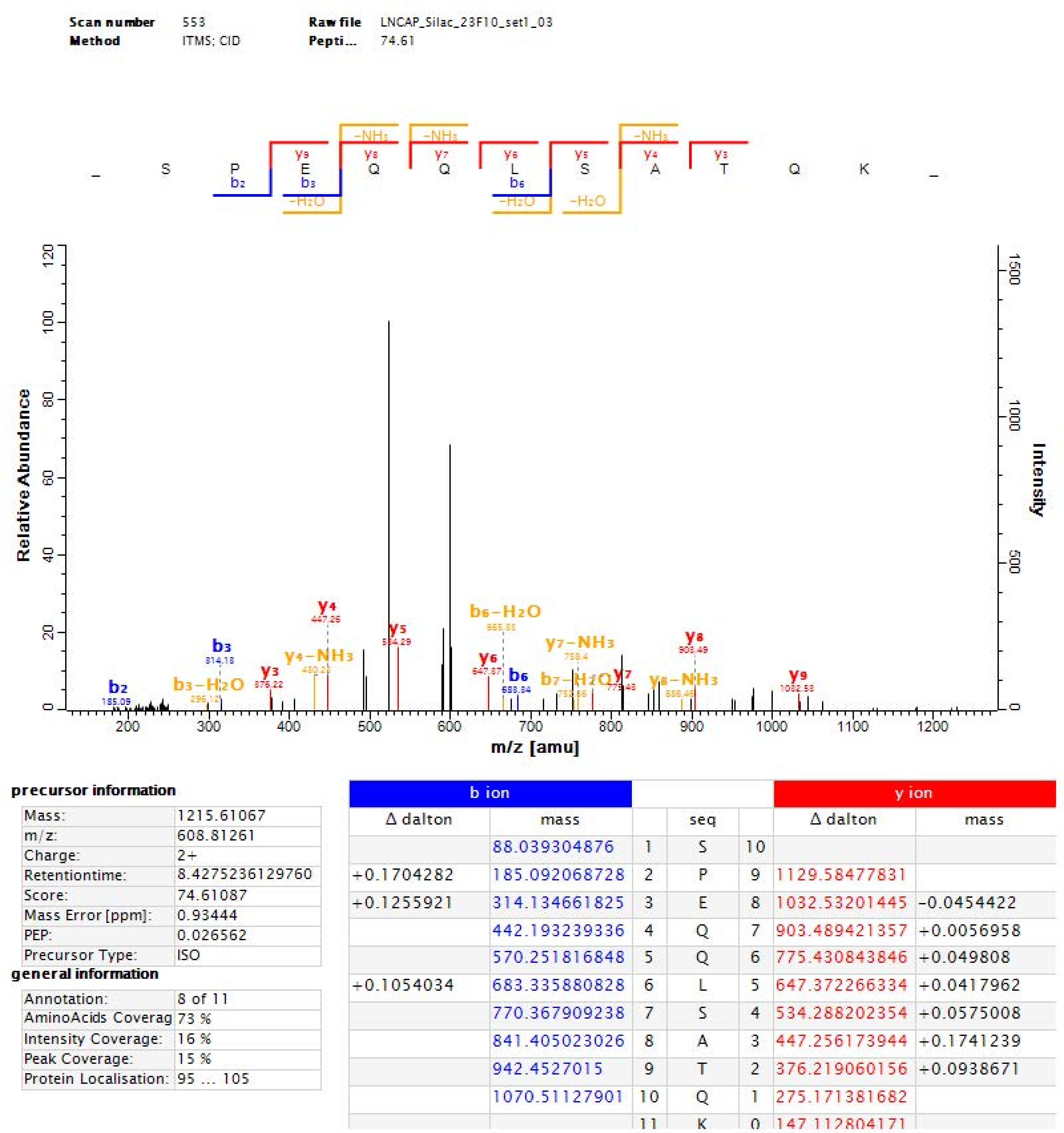
precursor information

Mass:	1717.83262
m/z:	859.92359
Charge:	2+
Retentiontime:	31.968616485595
Score:	68.27738
Mass Error [ppm]:	0.85474
PEP:	0.0019692
Precursor Type:	MULTI

general information

Annotation:	9 of 15
AminoAcids Coverag	60 %
Intensity Coverage:	25 %
Peak Coverage:	19 %
Protein Localisation:	212 ... 226

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	I	14				
+0.088	249.2		277.2	+0.135	277.2	2	Y	13	1606		1606	
	320.2		348.2	+0.063	348.2	3	A	12	1443		721.8	+0.27
	483.3		511.3	-0.1	511.3	4	Y	11	1372	+0.068	686.3	+0.08
	580.3		608.3		608.3	5	P	10	1209	-0.03	604.8	+0.09
	667.3		695.3		695.3	6	S	9	1112		1112	
	781.4		809.4		809.4	7	N	8	1025		1025	
	894.5		922.5	+0.109	922.5	8	I	7	910.5		910.5	
	995.5		1024		1024	9	T	6	797.4		797.4	
	1083	-0.41	555.8		1111	10	S	5	696.3	+0.035	696.3	
	1212		1240		1240	11	E	4	609.3		609.3	
	1313		1341	-0.33	1341	12	T	3	480.3		480.3	
	1370		1398	+0.264	1398	13	G	2	379.2	-0.04	379.2	
	1517		1545		1545	14	F	1	322.2		322.2	
						15	R	0	175.1		175.1	



Scan number 553 **Raw file** LNCAP_Silac_23F10_set1_03

Method ITMS; CID **Pepti...** 74.61

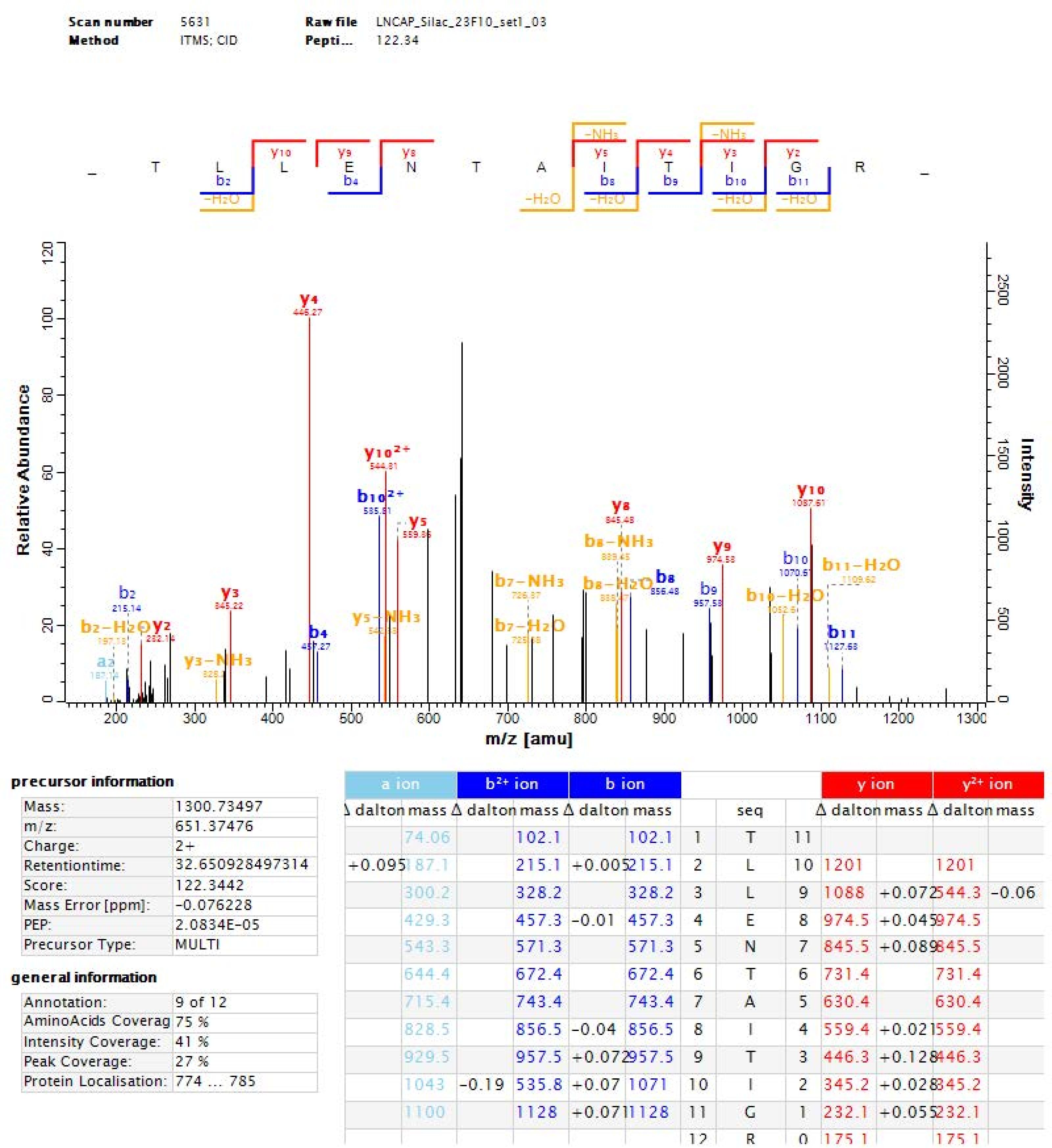
precursor information

Mass:	1215.61067
m/z:	608.81261
Charge:	2+
Retentiontime:	8.4275236129760
Score:	74.61087
Mass Error [ppm]:	0.93444
PEP:	0.026562
Precursor Type:	ISO

general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	16 %
Peak Coverage:	15 %
Protein Localisation:	95 ... 105

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	88.039304876	1	S	10		
+0.1704282	185.092068728	2	P	9	1129.58477831	
+0.1255921	314.134661825	3	E	8	1032.53201445	-0.0454422
	442.193239336	4	Q	7	903.489421357	+0.0056958
	570.251816848	5	Q	6	775.430843846	+0.049808
+0.1054034	683.335880828	6	L	5	647.372266334	+0.0417962
	770.367909238	7	S	4	534.288202354	+0.0575008
	841.405023026	8	A	3	447.256173944	+0.1741239
	942.4527015	9	T	2	376.219060156	+0.0938671
	1070.51127901	10	Q	1	275.171381682	
		11	K	0	147.112804171	



Scan number	5631	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	122.34

precursor information

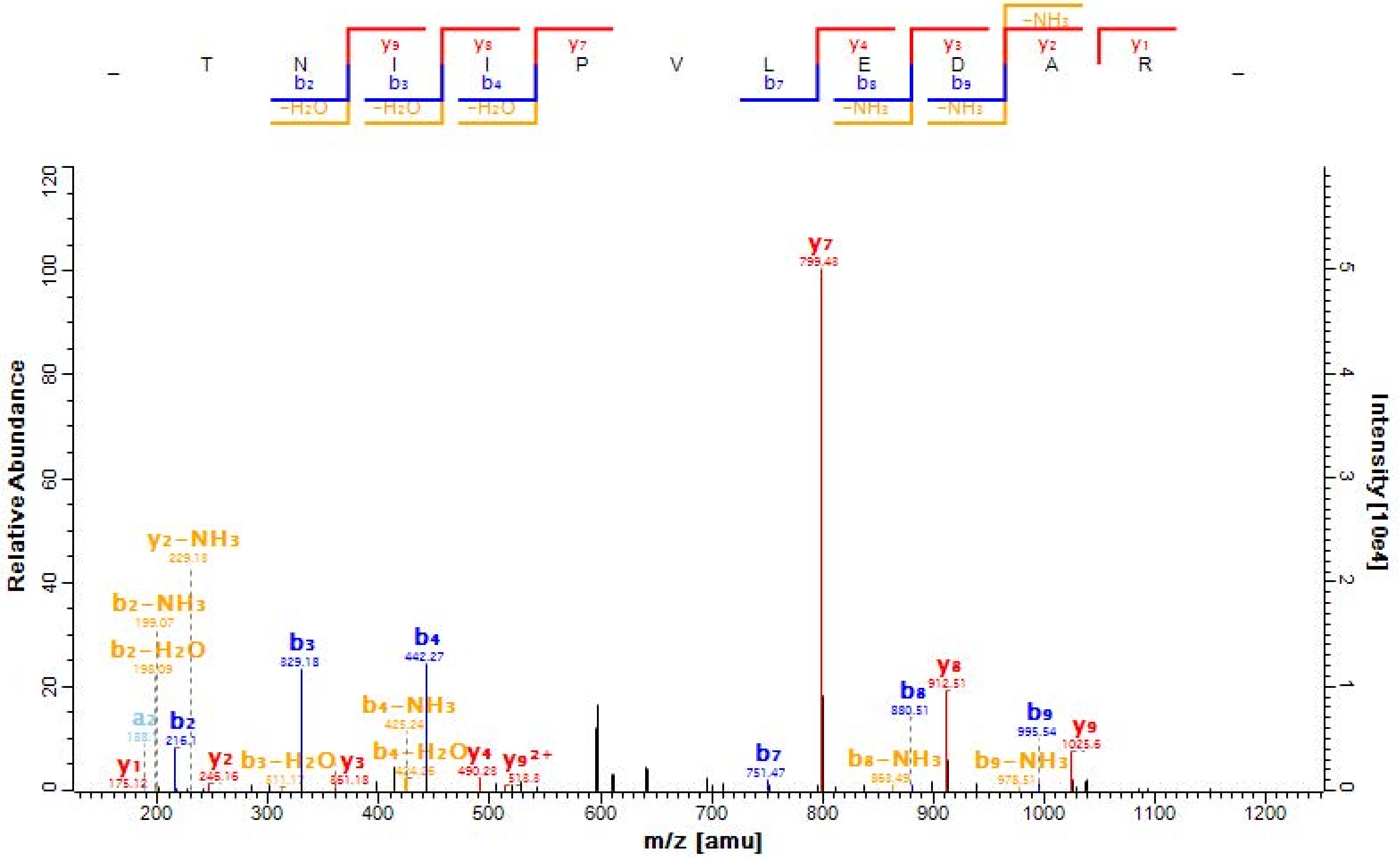
Mass:	1300.73497
m/z:	651.37476
Charge:	2+
Retentiontime:	32.650928497314
Score:	122.3442
Mass Error [ppm]:	-0.076228
PEP:	2.0834E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	41 %
Peak Coverage:	27 %
Protein Localisation:	774 ... 785

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.1		102.1	1	T	11				
+0.095	187.1		215.1	+0.005	215.1	2	L	10	1201		1201	
	300.2		328.2		328.2	3	L	9	1088	+0.072	544.3	-0.06
	429.3		457.3	-0.01	457.3	4	E	8	974.5	+0.045	974.5	
	543.3		571.3		571.3	5	N	7	845.5	+0.089	845.5	
	644.4		672.4		672.4	6	T	6	731.4		731.4	
	715.4		743.4		743.4	7	A	5	630.4		630.4	
	828.5		856.5	-0.04	856.5	8	I	4	559.4	+0.021	559.4	
	929.5		957.5	+0.072	957.5	9	T	3	446.3	+0.128	446.3	
	1043	-0.19	535.8	+0.07	1071	10	I	2	345.2	+0.028	345.2	
	1100		1128	+0.071	1128	11	G	1	232.1	+0.055	232.1	
						12	R	0	175.1		175.1	

Scan number	5766	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	101.89



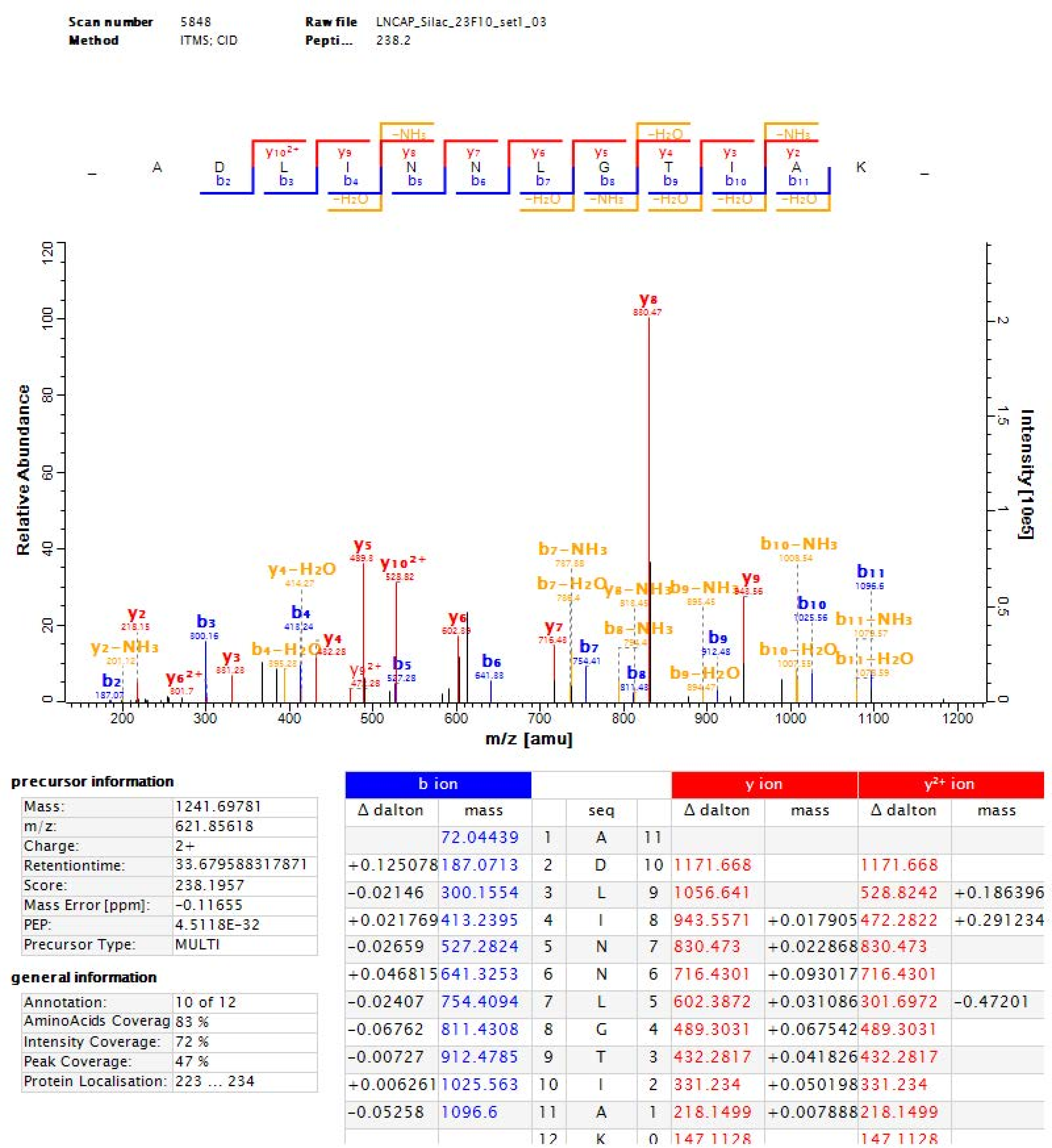
precursor information

Mass:	1239.68201
m/z:	620.84828
Charge:	2+
Retentiontime:	33.289150238037
Score:	101.8882
Mass Error [ppm]:	-0.23374
PEP:	0.00047755
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	65 %
Peak Coverage:	30 %
Protein Localisation:	220 ... 230

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.05	1	T	10				
+0.1706	188.1	-0.055	216.1	2	N	9	1139.6		1139.6	
	301.19	-0.031	329.18	3	I	8	1025.6	+0.1009	513.3	+0.1274
	414.27	-0.025	442.27	4	I	7	912.51	+0.0276	912.51	
	511.32		539.32	5	P	6	799.43	+0.0529	799.43	
	610.39		638.39	6	V	5	702.38		702.38	
	723.48	+0.1104	751.47	7	L	4	603.31		603.31	
	852.52	+0.1465	880.51	8	E	3	490.23	+0.2045	490.23	
	967.55	-0.027	995.54	9	D	2	361.18	+0.1181	361.18	
	1038.6		1066.6	10	A	1	246.16	+0.0258	246.16	
				11	R	0	175.12	-0.062	175.12	



Scan number	5848	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	238.2

precursor information

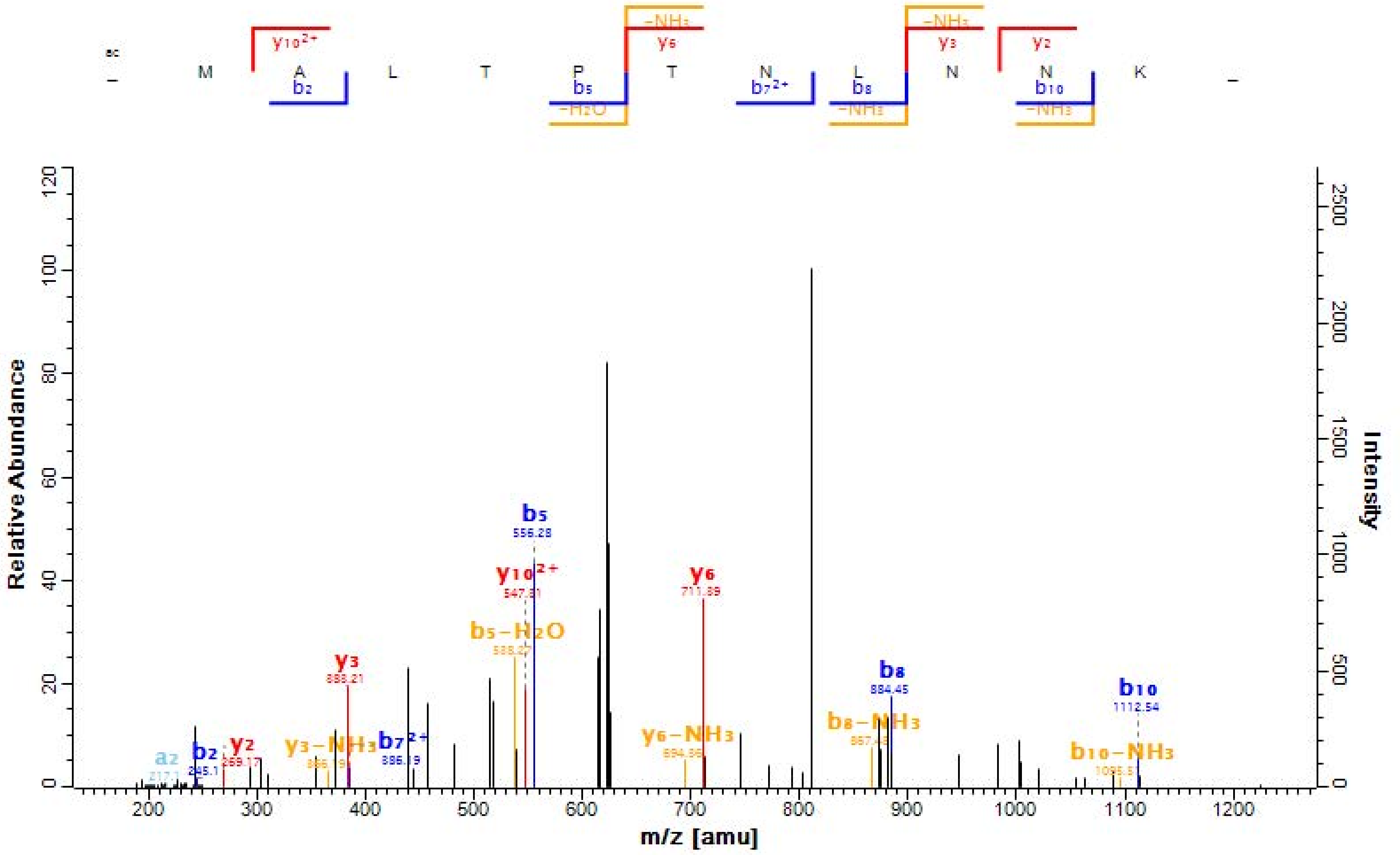
Mass:	1241.69781
m/z:	621.85618
Charge:	2+
Retentiontime:	33.679588317871
Score:	238.1957
Mass Error [ppm]:	-0.11655
PEP:	4.5118E-32
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	72 %
Peak Coverage:	47 %
Protein Localisation:	223 ... 234

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	11				
+0.125078	187.0713	2	D	10	1171.668		1171.668	
-0.02146	300.1554	3	L	9	1056.641		528.8242	+0.186396
+0.021769	413.2395	4	I	8	943.5571	+0.017905	472.2822	+0.291234
-0.02659	527.2824	5	N	7	830.473	+0.022868	830.473	
+0.046815	641.3253	6	N	6	716.4301	+0.093017	716.4301	
-0.02407	754.4094	7	L	5	602.3872	+0.031086	301.6972	-0.47201
-0.06762	811.4308	8	G	4	489.3031	+0.067542	489.3031	
-0.00727	912.4785	9	T	3	432.2817	+0.041826	432.2817	
+0.006261	1025.563	10	I	2	331.234	+0.050198	331.234	
-0.05258	1096.6	11	A	1	218.1499	+0.007888	218.1499	
		12	K	0	147.1128		147.1128	

Scan number	590	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	96.14



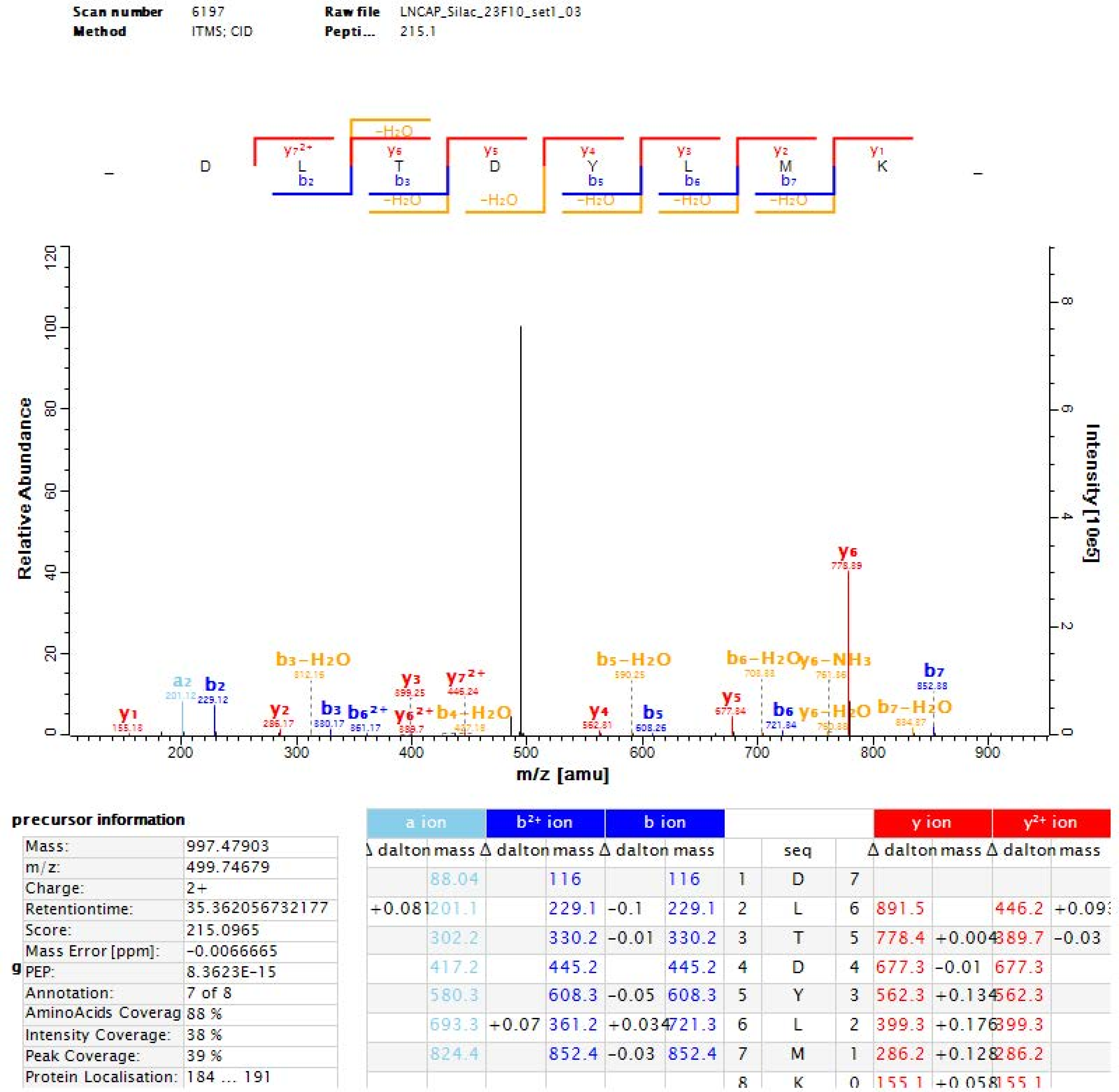
precursor information

Mass:	0
m/z:	633.83021
Charge:	0+
Retentiontime:	8.6660203933715
Score:	96.14293
Mass Error [ppm]:	-5.5665
PEP:	0.0048514
Precursor Type:	PEAK

general information

Annotation:	7 of 11
AminoAcids Coverag	64 %
Intensity Coverage:	24 %
Peak Coverage:	17 %
Protein Localisation:	1 ... 11

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	146.1		174.1		174.1	1	M	10				
+0.005	217.1		245.1	+0.051	245.1	2	A	9	1094		547.3	-0.26
	330.2		358.2		358.2	3	L	8	1023		1023	
	431.2		459.2		459.2	4	T	7	909.5		909.5	
	528.3		556.3	-0.15	556.3	5	P	6	808.4		808.4	
	629.3		657.3		657.3	6	T	5	711.4	-0.05	711.4	
	743.4	-0.03	386.2		771.4	7	N	4	610.3		610.3	
	856.5		884.5	+0.003	884.5	8	L	3	496.3		496.3	
	970.5		998.5		998.5	9	N	2	383.2	+0.158	383.2	
	1085		1113	-0.13	1113	10	N	1	269.2	-0.26	269.2	
						11	K	0	155.1		155.1	

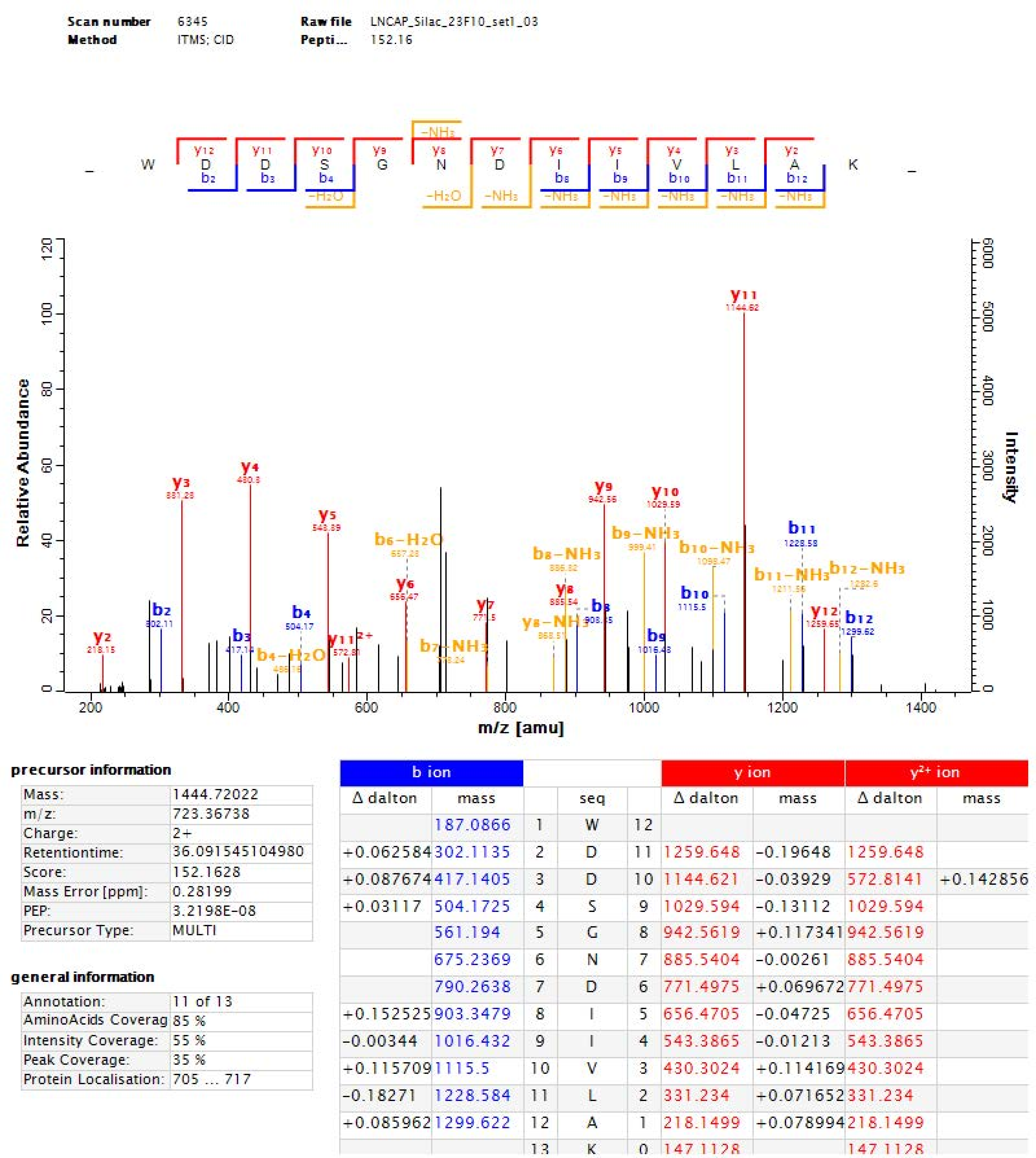


Scan number	6197	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	215.1

precursor information

Mass:	997.47903
m/z:	499.74679
Charge:	2+
Retentiontime:	35.362056732177
Score:	215.0965
Mass Error [ppm]:	-0.0066665
PEP:	8.3623E-15
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	38 %
Peak Coverage:	39 %
Protein Localisation:	184 ... 191

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.04		116		116	1	D	7				
+0.081	201.1		229.1	-0.1	229.1	2	L	6	891.5		446.2	+0.09
	302.2		330.2	-0.01	330.2	3	T	5	778.4	+0.004	389.7	-0.03
	417.2		445.2		445.2	4	D	4	677.3	-0.01	677.3	
	580.3		608.3	-0.05	608.3	5	Y	3	562.3	+0.134	562.3	
	693.3	+0.07	361.2	+0.034	721.3	6	L	2	399.3	+0.176	399.3	
	824.4		852.4	-0.03	852.4	7	M	1	286.2	+0.128	286.2	
						8	K	0	155.1	+0.058	155.1	



Scan number	6345	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	152.16

precursor information

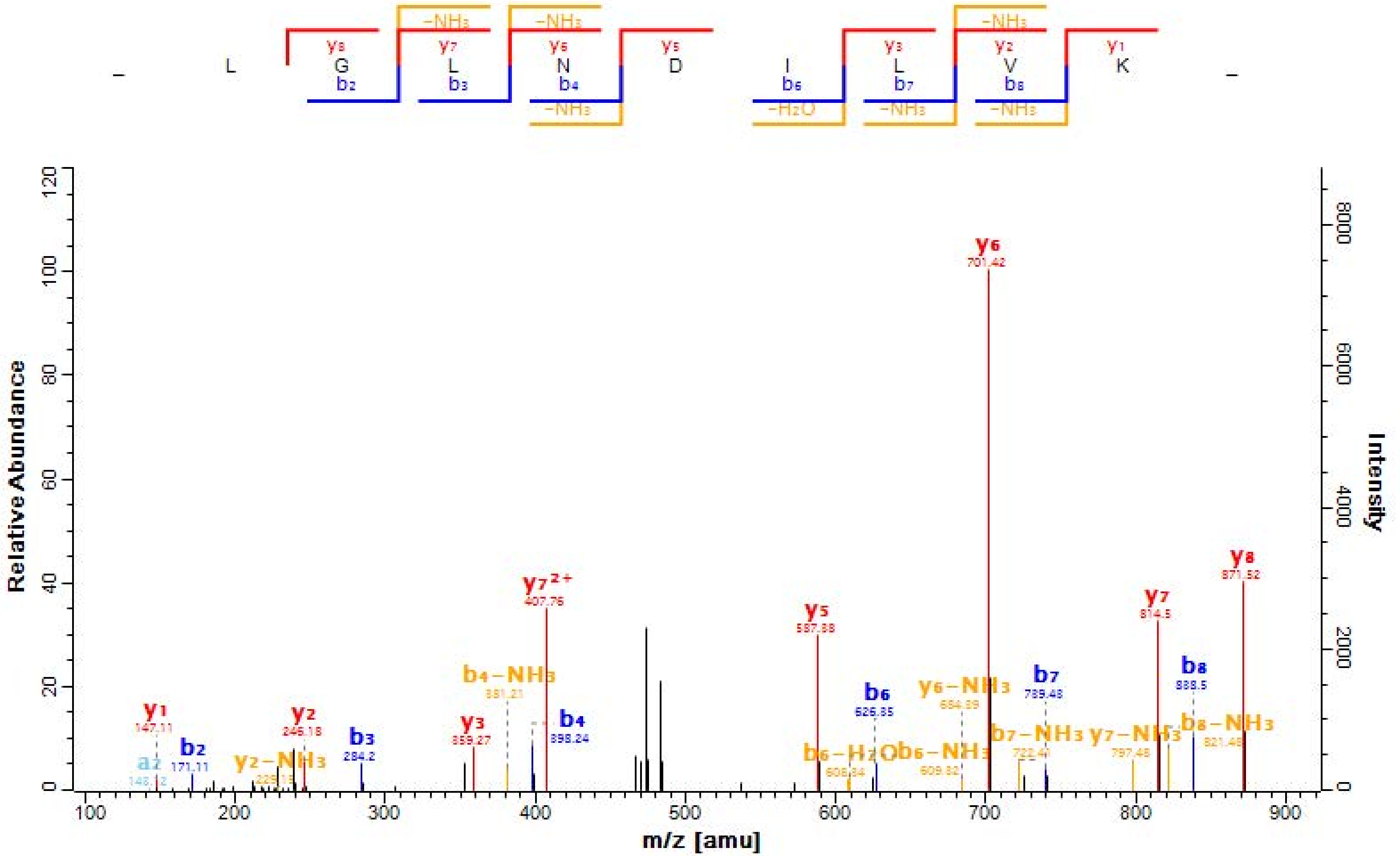
Mass:	1444.72022
m/z:	723.36738
Charge:	2+
Retentiontime:	36.091545104980
Score:	152.1628
Mass Error [ppm]:	0.28199
PEP:	3.2198E-08
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	55 %
Peak Coverage:	35 %
Protein Localisation:	705 ... 717

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	187.0866	1	W	12				
+0.062584	302.1135	2	D	11	1259.648	-0.19648	1259.648	
+0.087674	417.1405	3	D	10	1144.621	-0.03929	572.8141	+0.142856
+0.03117	504.1725	4	S	9	1029.594	-0.13112	1029.594	
	561.194	5	G	8	942.5619	+0.117341	942.5619	
	675.2369	6	N	7	885.5404	-0.00261	885.5404	
	790.2638	7	D	6	771.4975	+0.069672	771.4975	
+0.152525	903.3479	8	I	5	656.4705	-0.04725	656.4705	
-0.00344	1016.432	9	I	4	543.3865	-0.01213	543.3865	
+0.115709	1115.5	10	V	3	430.3024	+0.114169	430.3024	
-0.18271	1228.584	11	L	2	331.234	+0.071652	331.234	
+0.085962	1299.622	12	A	1	218.1499	+0.078994	218.1499	
		13	K	0	147.1128		147.1128	

Scan number	6810	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	162.88

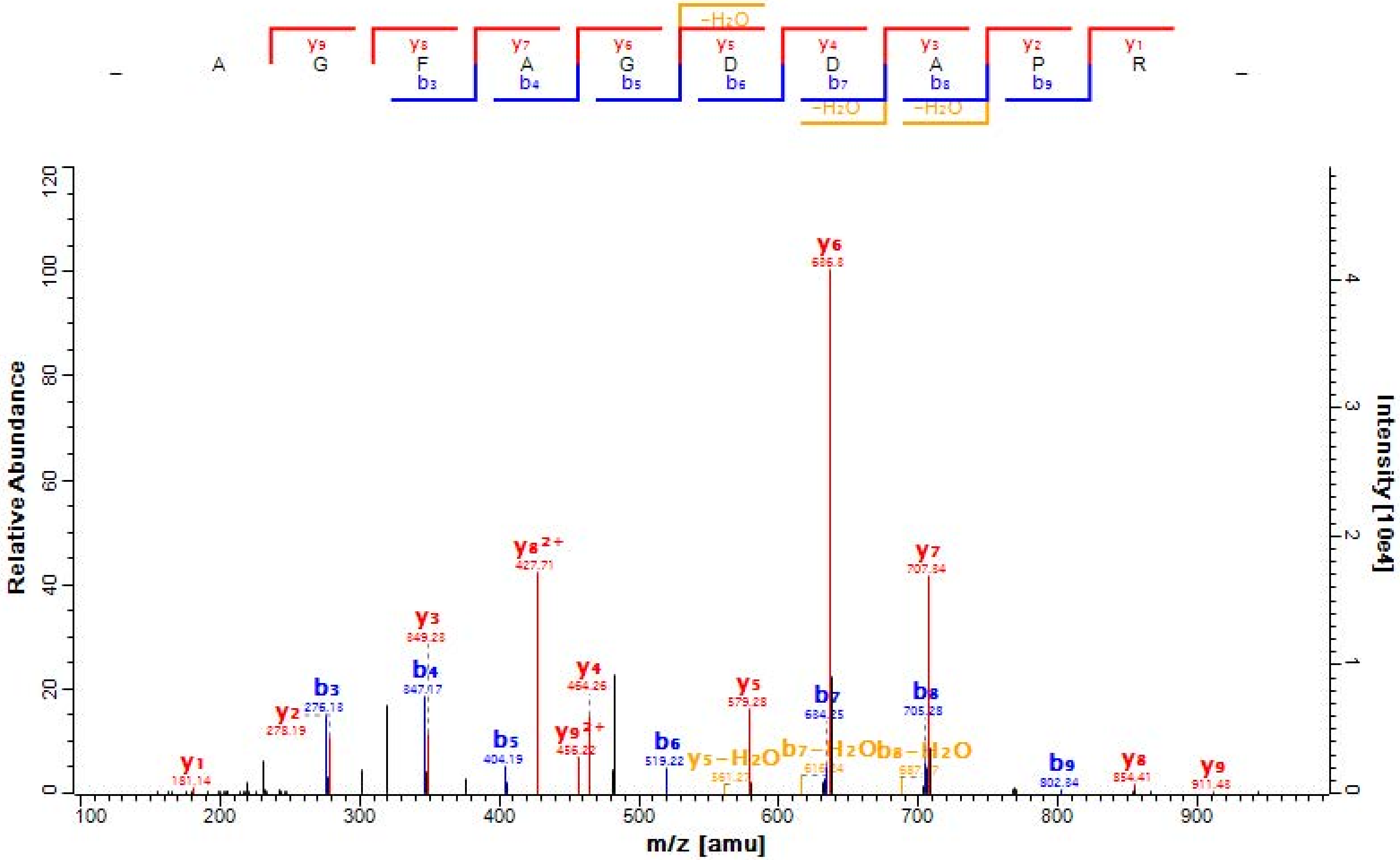


precursor information

Mass:	983.60124
m/z:	492.80789
Charge:	2+
Retentiontime:	38.328197479248
Score:	162.8769
Mass Error [ppm]:	-0.30107
PEP:	0.00025611
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	65 %
Peak Coverage:	31 %
Protein Localisation:	613 ... 621

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	8				
-0.103	143.12	+0.0192	171.11	2	G	7	871.52	-0.012	871.52	
	256.2	-0.07	284.2	3	L	6	814.5	+0.0396	407.76	+0.2023
	370.24	+0.0798	398.24	4	N	5	701.42	+0.0762	701.42	
	485.27		513.27	5	D	4	587.38	+0.0226	587.38	
	598.36	+0.138	626.35	6	I	3	472.35		472.35	
	711.44	+0.1185	739.43	7	L	2	359.27	+0.0643	359.27	
	810.51	+0.0073	838.5	8	V	1	246.18	+0.0905	246.18	
				9	K	0	147.11	+0.0341	147.11	

Scan number	696	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	152.54



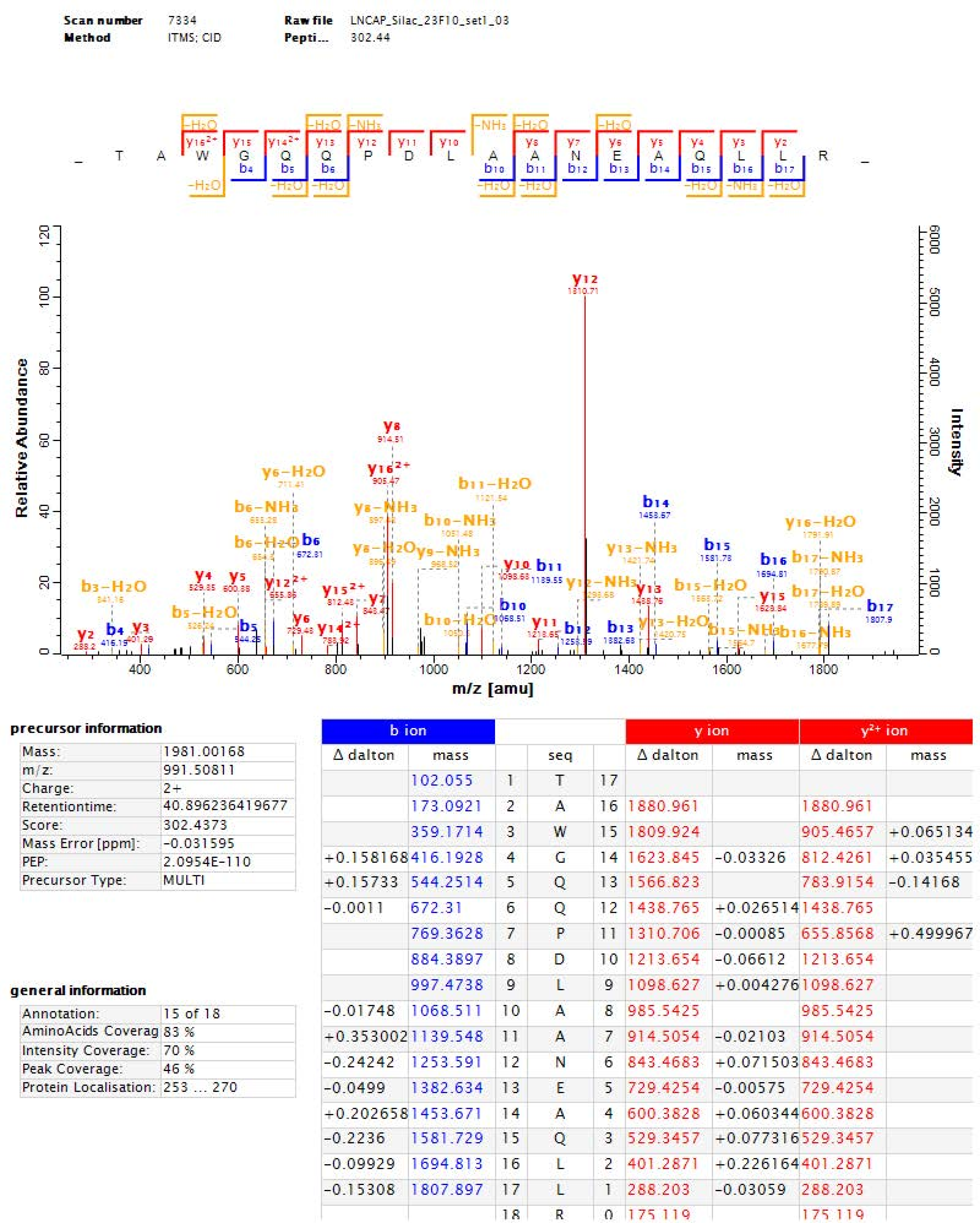
precursor information

Mass:	975.44093
m/z:	488.72774
Charge:	2+
Retentiontime:	9.2692966461181
Score:	152.5395
Mass Error [ppm]:	-0.079382
PEP:	0.00013938
Precursor Type:	MULTI

g

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	71 %
Peak Coverage:	21 %
Protein Localisation:	19 ... 28

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	9				
	129.0659	2	G	8	911.4313	-0.22335	456.2193	+0.116191
-0.09182	276.1343	3	F	7	854.4098	+0.110183	427.7086	+0.204194
-0.05395	347.1714	4	A	6	707.3414	+0.015816	707.3414	
-0.03577	404.1928	5	G	5	636.3043	-0.11589	636.3043	
+0.00183	519.2198	6	D	4	579.2828	-0.02821	579.2828	
+0.050754	634.2467	7	D	3	464.2559	+0.089038	464.2559	
+0.044219	705.2838	8	A	2	349.229	+0.13829	349.229	
-0.14612	802.3366	9	P	1	278.1918	-0.02095	278.1918	
		10	R	0	181.1391	+0.133212	181.1391	



Scan number 7334
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set1_03
Pepti... 302.44

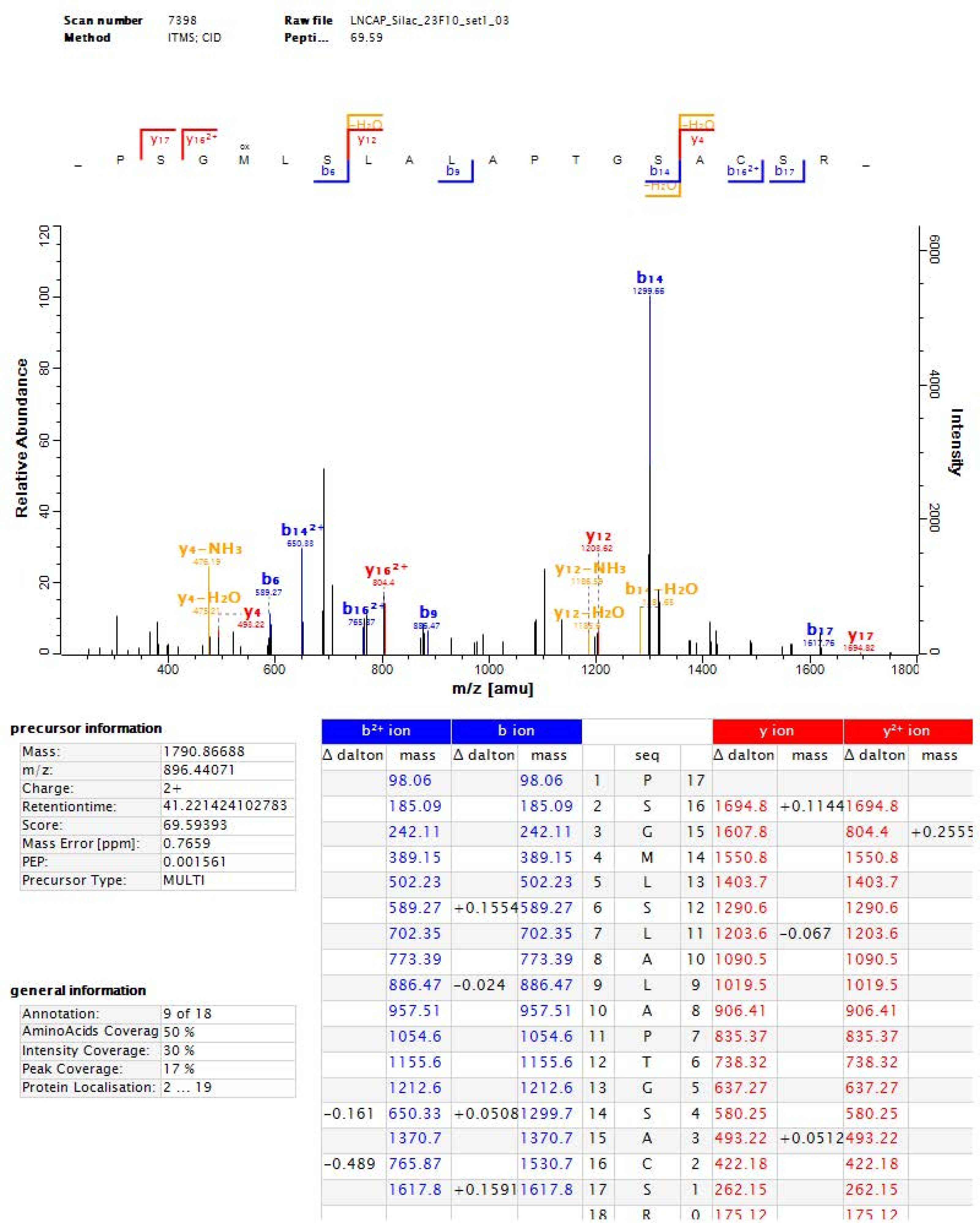
precursor information

Mass:	1981.00168
m/z:	991.50811
Charge:	2+
Retentiontime:	40.896236419677
Score:	302.4373
Mass Error [ppm]:	-0.031595
PEP:	2.0954E-110
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	70 %
Peak Coverage:	46 %
Protein Localisation:	253 ... 270

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055	1	T	17				
	173.0921	2	A	16	1880.961		1880.961	
	359.1714	3	W	15	1809.924		905.4657	+0.065134
+0.158168	416.1928	4	G	14	1623.845	-0.03326	812.4261	+0.035455
+0.15733	544.2514	5	Q	13	1566.823		783.9154	-0.14168
-0.0011	672.31	6	Q	12	1438.765	+0.026514	1438.765	
	769.3628	7	P	11	1310.706	-0.00085	655.8568	+0.499967
	884.3897	8	D	10	1213.654	-0.06612	1213.654	
	997.4738	9	L	9	1098.627	+0.004276	1098.627	
-0.01748	1068.511	10	A	8	985.5425		985.5425	
+0.353002	1139.548	11	A	7	914.5054	-0.02103	914.5054	
-0.24242	1253.591	12	N	6	843.4683	+0.071503	843.4683	
-0.0499	1382.634	13	E	5	729.4254	-0.00575	729.4254	
+0.202658	1453.671	14	A	4	600.3828	+0.060344	600.3828	
-0.2236	1581.729	15	Q	3	529.3457	+0.077316	529.3457	
-0.09929	1694.813	16	L	2	401.2871	+0.226164	401.2871	
-0.15308	1807.897	17	L	1	288.203	-0.03059	288.203	
		18	R	0	175.119		175.119	



Scan number	7398	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	69.59

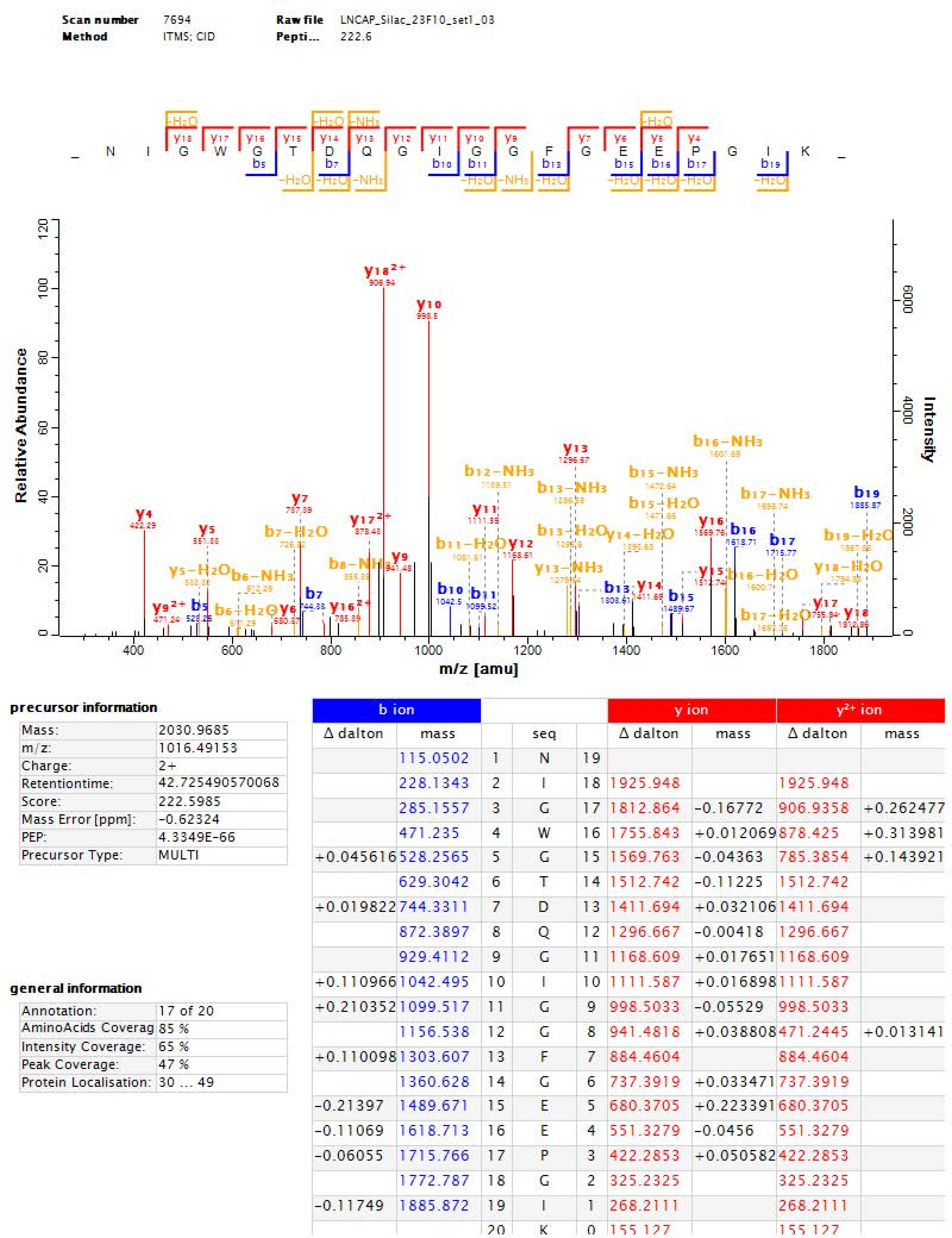
precursor information

Mass:	1790.86688
m/z:	896.44071
Charge:	2+
Retentiontime:	41.221424102783
Score:	69.59393
Mass Error [ppm]:	0.7659
PEP:	0.001561
Precursor Type:	MULTI

general information

Annotation:	9 of 18
AminoAcids Coverag	50 %
Intensity Coverage:	30 %
Peak Coverage:	17 %
Protein Localisation:	2 ... 19

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	98.06		98.06	1	P	17				
	185.09		185.09	2	S	16	1694.8	+0.1144	1694.8	
	242.11		242.11	3	G	15	1607.8		804.4	+0.2555
	389.15		389.15	4	M	14	1550.8		1550.8	
	502.23		502.23	5	L	13	1403.7		1403.7	
	589.27	+0.1554	589.27	6	S	12	1290.6		1290.6	
	702.35		702.35	7	L	11	1203.6	-0.067	1203.6	
	773.39		773.39	8	A	10	1090.5		1090.5	
	886.47	-0.024	886.47	9	L	9	1019.5		1019.5	
	957.51		957.51	10	A	8	906.41		906.41	
	1054.6		1054.6	11	P	7	835.37		835.37	
	1155.6		1155.6	12	T	6	738.32		738.32	
	1212.6		1212.6	13	G	5	637.27		637.27	
-0.161	650.33	+0.0508	1299.7	14	S	4	580.25		580.25	
	1370.7		1370.7	15	A	3	493.22	+0.0512	493.22	
-0.489	765.87		1530.7	16	C	2	422.18		422.18	
	1617.8	+0.1591	1617.8	17	S	1	262.15		262.15	
				18	R	0	175.12		175.12	



Scan number	7694	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	222.6

precursor information

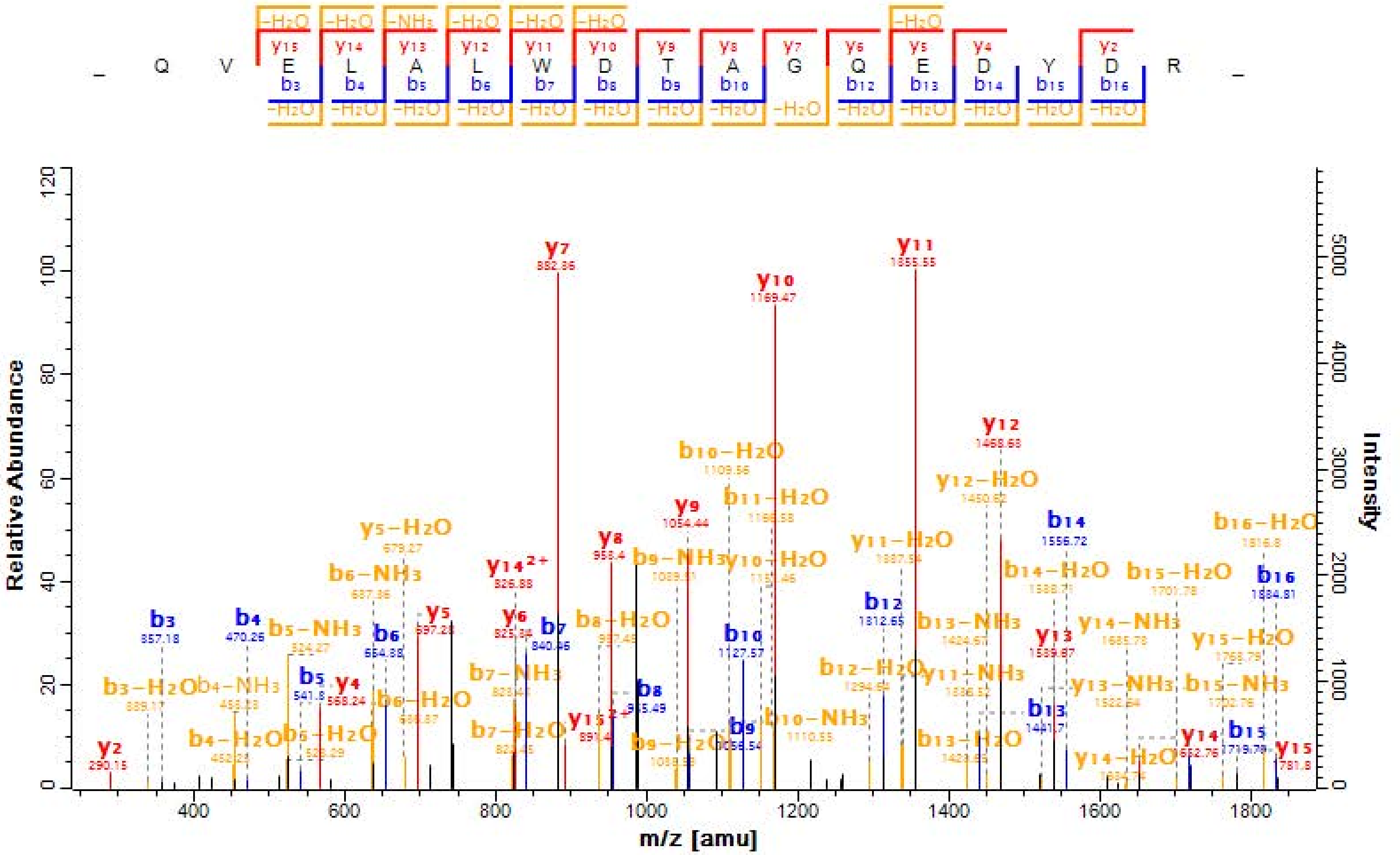
Mass:	2030.9685
m/z:	1016.49153
Charge:	2+
Retentiontime:	42.725490570068
Score:	222.5985
Mass Error [ppm]:	-0.62324
PEP:	4.3349E-66
Precursor Type:	MULTI

general information

Annotation:	17 of 20
AminoAcids Coverag	85 %
Intensity Coverage:	65 %
Peak Coverage:	47 %
Protein Localisation:	30 ... 49

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502	1	N	19				
	228.1343	2	I	18	1925.948		1925.948	
	285.1557	3	G	17	1812.864	-0.16772	906.9358	+0.262477
	471.235	4	W	16	1755.843	+0.012069	878.425	+0.313981
+0.045616	528.2565	5	G	15	1569.763	-0.04363	785.3854	+0.143921
	629.3042	6	T	14	1512.742	-0.11225	1512.742	
+0.019822	744.3311	7	D	13	1411.694	+0.032106	1411.694	
	872.3897	8	Q	12	1296.667	-0.00418	1296.667	
	929.4112	9	G	11	1168.609	+0.017651	1168.609	
+0.110966	1042.495	10	I	10	1111.587	+0.016898	1111.587	
+0.210352	1099.517	11	G	9	998.5033	-0.05529	998.5033	
	1156.538	12	G	8	941.4818	+0.038808	471.2445	+0.013141
+0.110098	1303.607	13	F	7	884.4604		884.4604	
	1360.628	14	G	6	737.3919	+0.033471	737.3919	
-0.21397	1489.671	15	E	5	680.3705	+0.223391	680.3705	
-0.11069	1618.713	16	E	4	551.3279	-0.0456	551.3279	
-0.06055	1715.766	17	P	3	422.2853	+0.050582	422.2853	
	1772.787	18	G	2	325.2325		325.2325	
-0.11749	1885.872	19	I	1	268.2111		268.2111	
		20	K	0	155.127		155.127	

Scan number	7864	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	409.19



precursor information

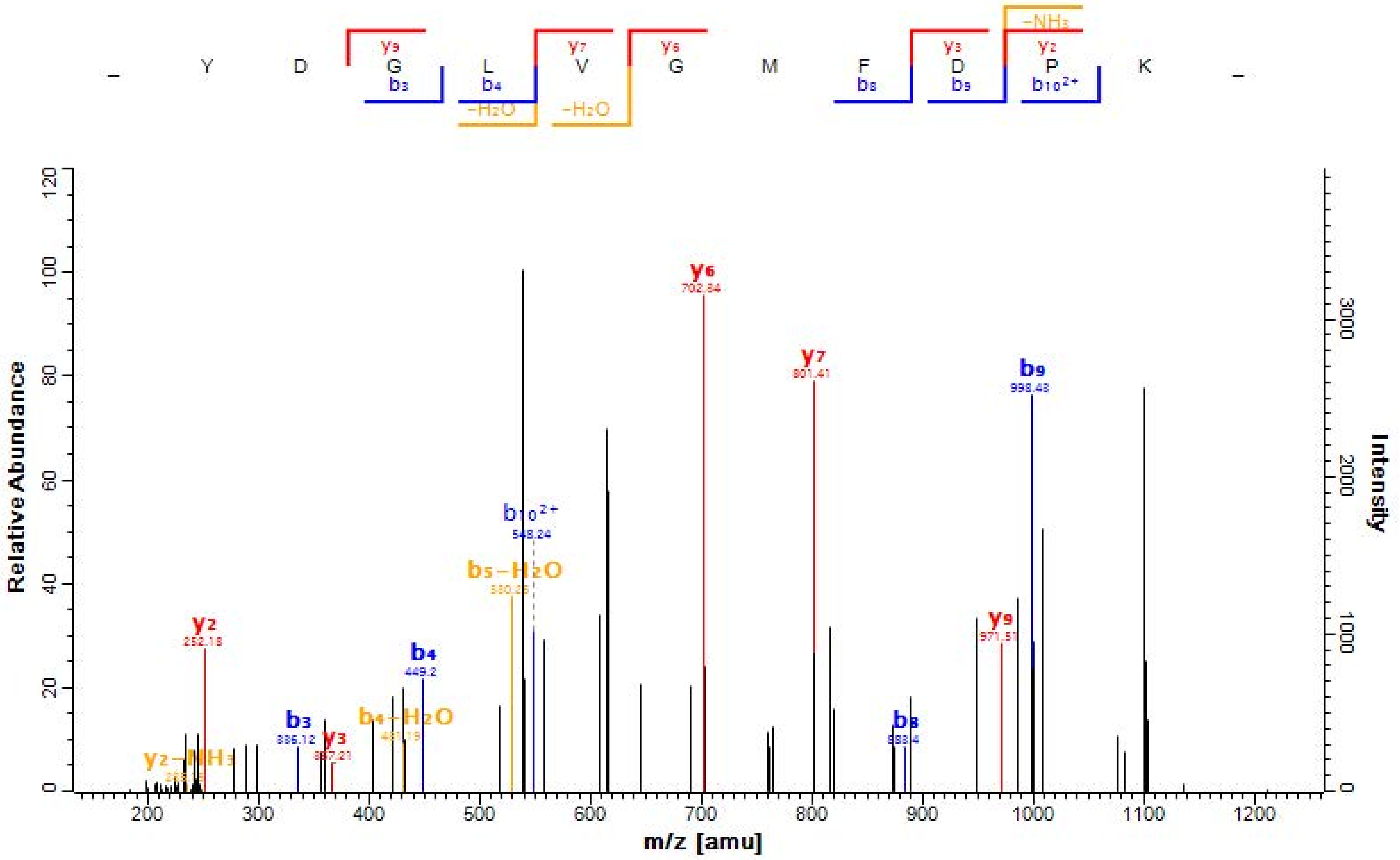
Mass:	2007.91724
m/z:	1004.96589
Charge:	2+
Retentiontime:	43.588634490966
Score:	409.1888
Mass Error [ppm]:	-0.080883
PEP:	1.2009E-221
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	74 %
Peak Coverage:	62 %
Protein Localisation:	52 ... 68

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.0659	1	Q	16				
	228.1343	2	V	15	1880.866		1880.866	
+0.207508	357.1769	3	E	14	1781.798	-0.17476	891.4025	-0.07387
+0.023407	470.2609	4	L	13	1652.755	-0.07076	826.8812	-0.39913
+0.01849	541.298	5	A	12	1539.671	-0.04224	1539.671	
-0.01943	654.3821	6	L	11	1468.634	-0.10205	1468.634	
+0.061289	840.4614	7	W	10	1355.55	-0.04143	1355.55	
-0.01302	955.4884	8	D	9	1169.471	+0.010054	1169.471	
-0.10342	1056.536	9	T	8	1054.444	+0.06312	1054.444	
-0.05167	1127.573	10	A	7	953.3959	+0.069051	953.3959	
	1184.595	11	G	6	882.3588	+0.004236	882.3588	
-0.03857	1312.653	12	Q	5	825.3373	+0.007389	825.3373	
+0.009659	1441.696	13	E	4	697.2788	+0.104785	697.2788	
+0.147755	1556.723	14	D	3	568.2362	+0.094705	568.2362	
+0.031936	1719.786	15	Y	2	453.2092		453.2092	
-0.41774	1834.813	16	D	1	290.1459	+0.063242	290.1459	
		17	R	0	175.119		175.119	

Scan number	7985	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	51.25



precursor information

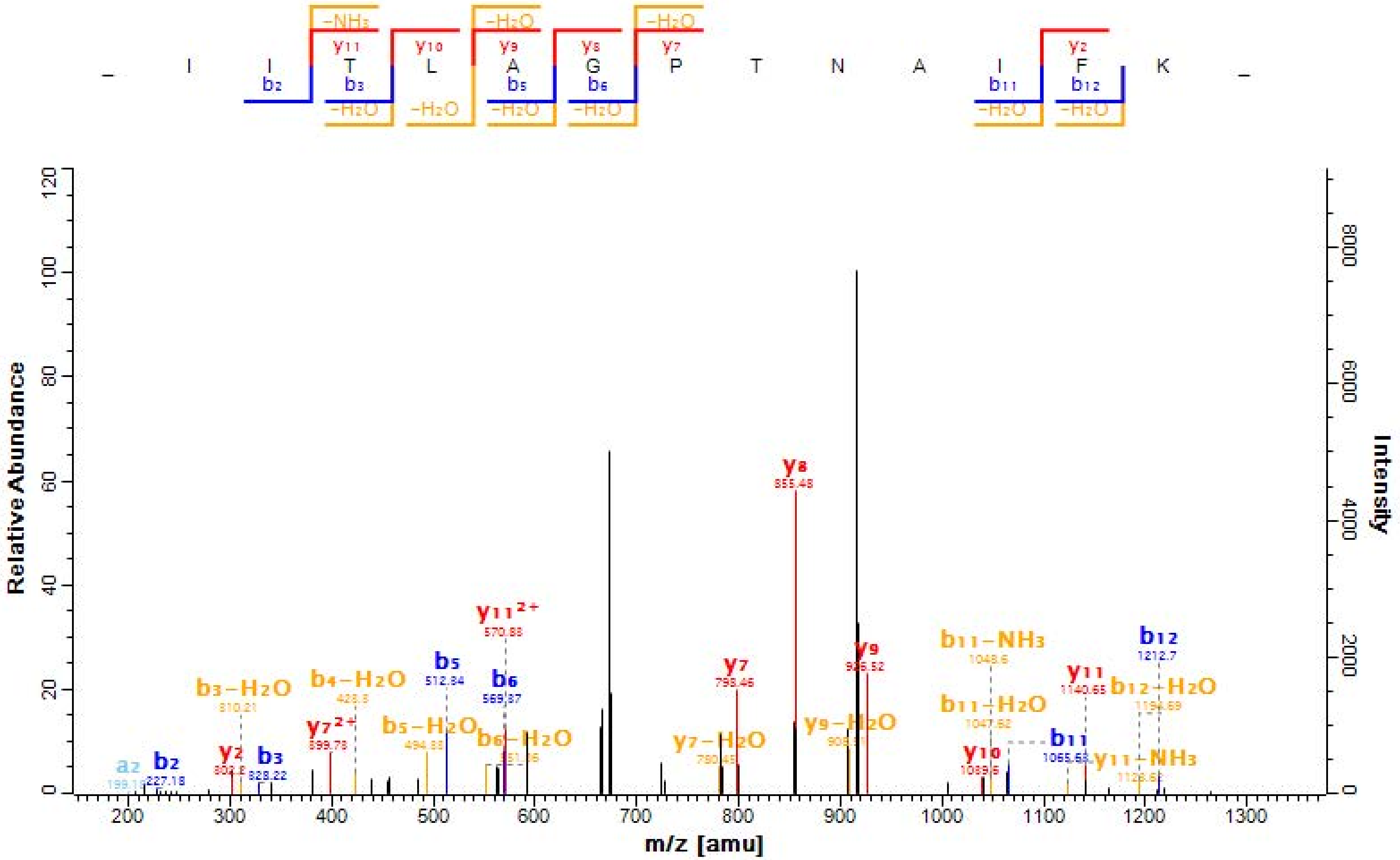
Mass:	1240.58011
m/z:	621.29733
Charge:	2+
Retentiontime:	44.214679718017
Score:	51.25192
Mass Error [ppm]:	0.24415
PEP:	0.02987
Precursor Type:	MULTI

general information

Annotation:	7 of 11
AminoAcids Coverag	64 %
Intensity Coverage:	28 %
Peak Coverage:	15 %
Protein Localisation:	363 ... 373

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	164.0706		164.0706	1	Y	10		
	279.0975		279.0975	2	D	9	1086.538	
	336.119	+0.177924	336.119	3	G	8	971.511	+0.0134
	449.2031	+0.055347	449.2031	4	L	7	914.4896	
	548.2715		548.2715	5	V	6	801.4055	+0.056611
	605.293		605.293	6	G	5	702.3371	+0.109034
	736.3334		736.3334	7	M	4	645.3156	
	883.4019	+0.43848	883.4019	8	F	3	514.2751	
	998.4288	−0.12429	998.4288	9	D	2	367.2067	−0.0189
−0.03134	548.2444		1095.482	10	P	1	252.1798	+0.103574
				11	K	0	155.127	

Scan number 8054 **Raw file** LNCAP_Silac_23F10_set1_03
Method ITMS; CID **Pepti...** 151.26



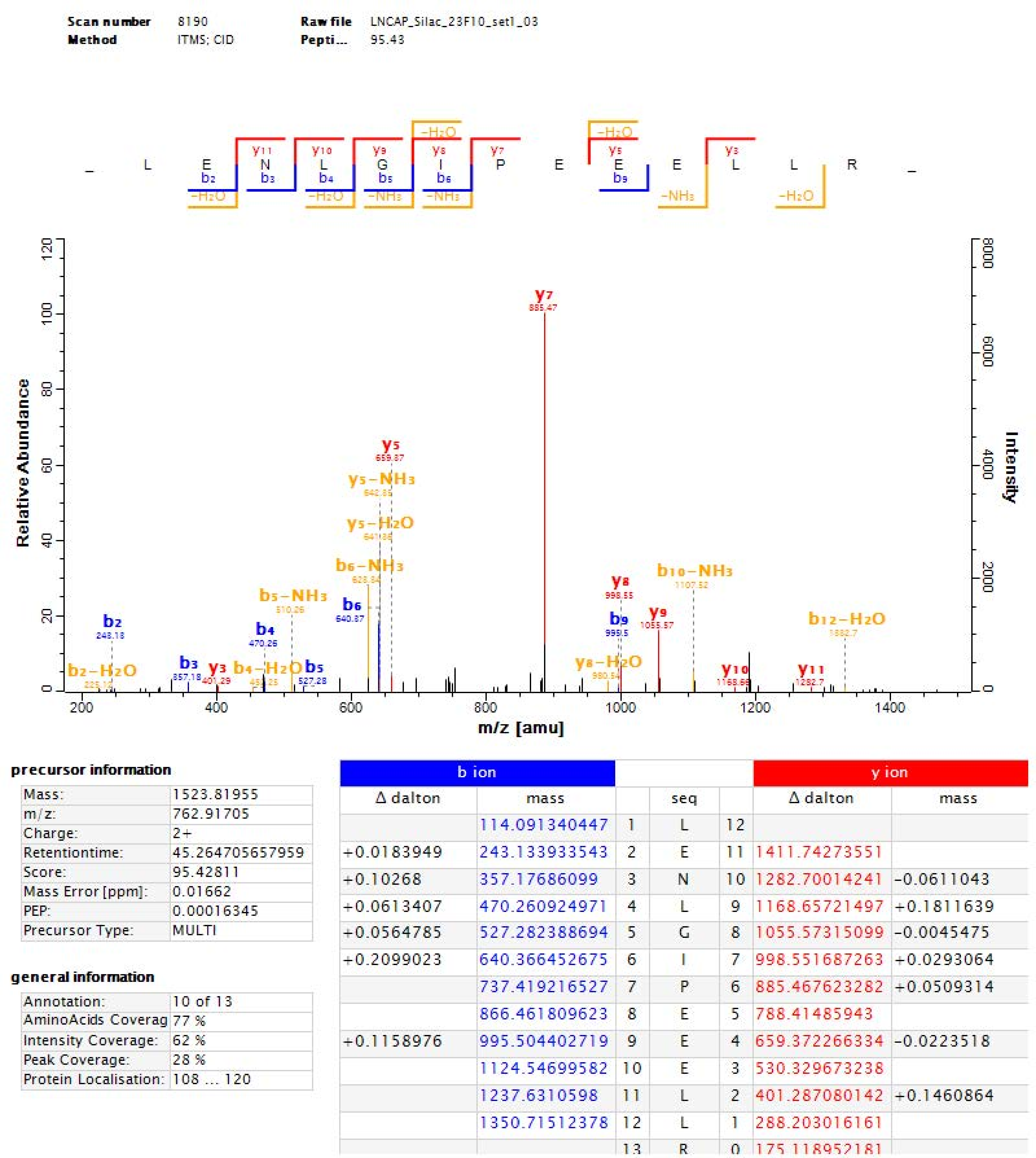
precursor information

Mass:	1357.79712
m/z:	679.90583
Charge:	2+
Retentiontime:	44.571655273437
Score:	151.2568
Mass Error [ppm]:	0.13042
PEP:	6.1813E-08
Precursor Type:	MULTI

general information

Annotation:	8 of 13
AminoAcids Coverag	62 %
Intensity Coverage:	35 %
Peak Coverage:	31 %
Protein Localisation:	58 ... 70

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	12				
-0.044	199.18	-0.013	227.18	2	I	11	1253.7		1253.7	
	300.23	+0.0884	328.22	3	T	10	1140.7	+0.052	570.83	+0.0432
	413.31		441.31	4	L	9	1039.6	+0.0704	1039.6	
	484.35	+0.0454	512.34	5	A	8	926.52	-0.004	926.52	
	541.37	-0.093	569.37	6	G	7	855.48	+0.0438	855.48	
	638.42		666.42	7	P	6	798.46	+0.0265	399.73	-0.401
	739.47		767.47	8	T	5	701.41		701.41	
	853.51		881.51	9	N	4	600.36		600.36	
	924.55		952.55	10	A	3	486.32		486.32	
	1037.6	-0.038	1065.6	11	I	2	415.28		415.28	
	1184.7	-0.101	1212.7	12	F	1	302.2	+0.1356	302.2	
				13	K	0	155.13		155.13	



Scan number	8190	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	95.43

precursor information

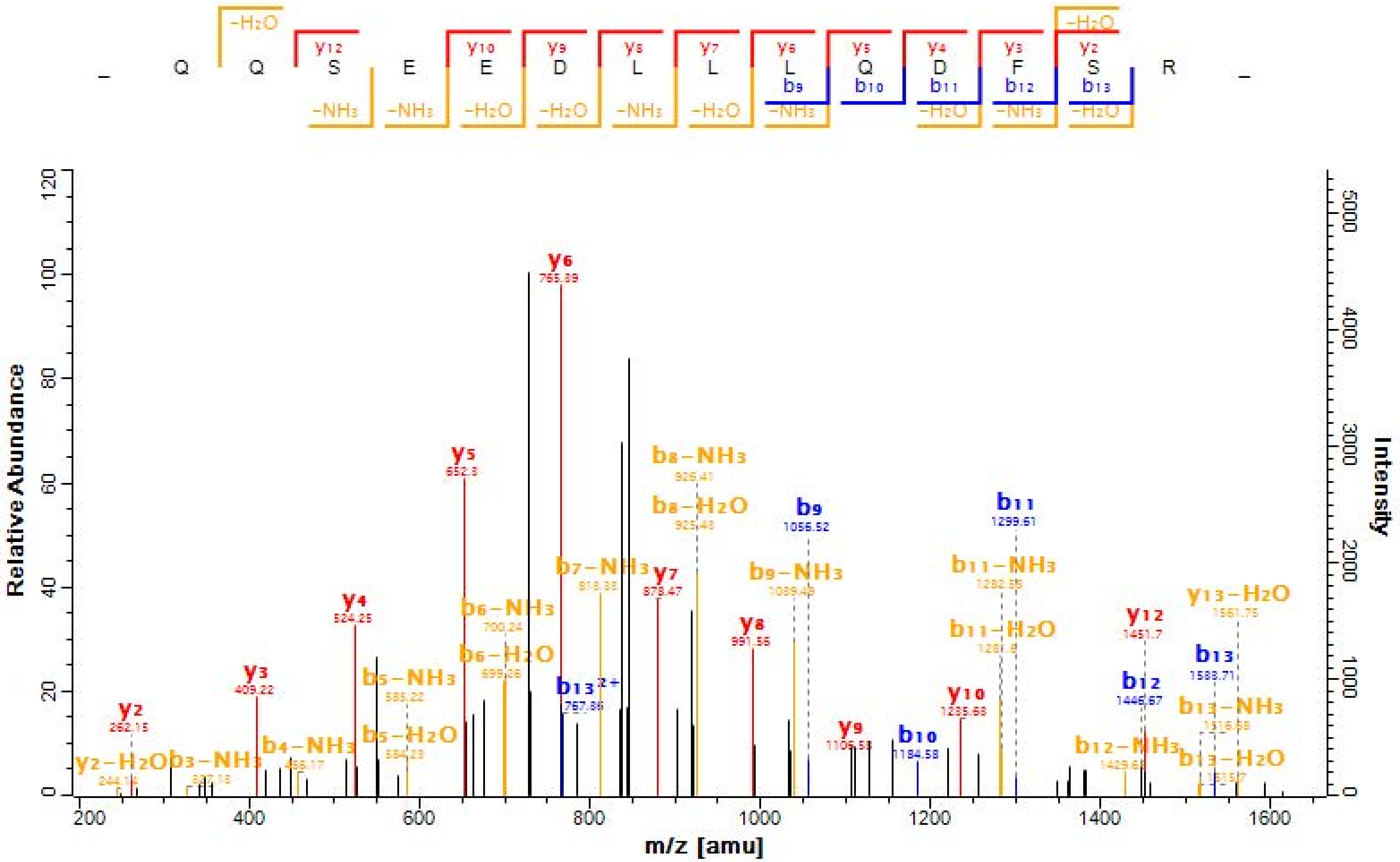
Mass:	1523.81955
m/z:	762.91705
Charge:	2+
Retentiontime:	45.264705657959
Score:	95.42811
Mass Error [ppm]:	0.01662
PEP:	0.00016345
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	62 %
Peak Coverage:	28 %
Protein Localisation:	108 ... 120

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	114.091340447	1	L	12		
+0.0183949	243.133933543	2	E	11	1411.74273551	
+0.10268	357.17686099	3	N	10	1282.70014241	-0.0611043
+0.0613407	470.260924971	4	L	9	1168.65721497	+0.1811639
+0.0564785	527.282388694	5	G	8	1055.57315099	-0.0045475
+0.2099023	640.366452675	6	I	7	998.551687263	+0.0293064
	737.419216527	7	P	6	885.467623282	+0.0509314
	866.461809623	8	E	5	788.41485943	
+0.1158976	995.504402719	9	E	4	659.372266334	-0.0223518
	1124.54699582	10	E	3	530.329673238	
	1237.6310598	11	L	2	401.287080142	+0.1460864
	1350.71512378	12	L	1	288.203016161	
		13	R	0	175.118952181	

Scan number	8348	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	114.31



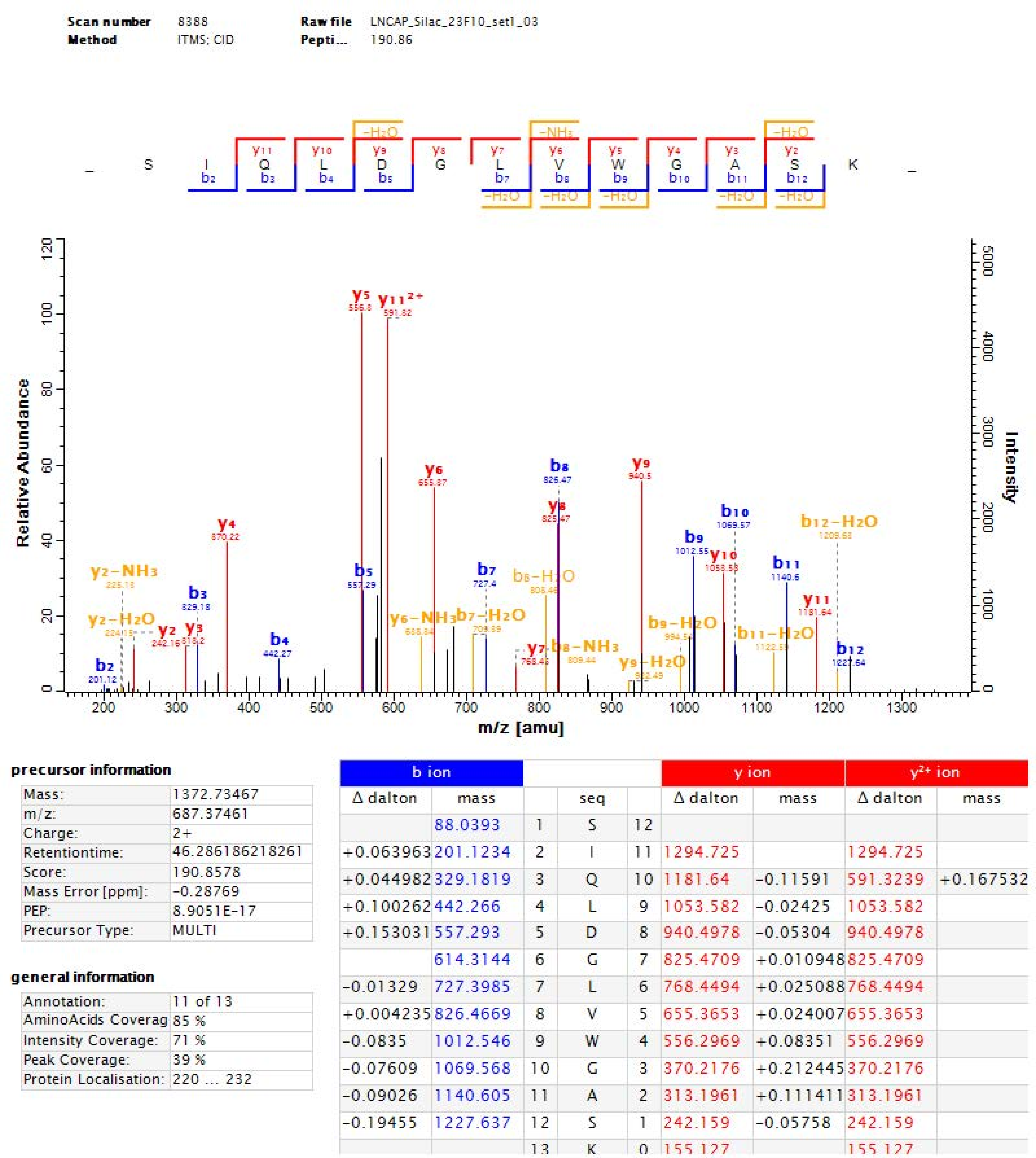
precursor information

Mass:	1706.81162
m/z:	854.41309
Charge:	2+
Retentiontime:	46.081710815429
Score:	114.3098
Mass Error [ppm]:	0.28159
PEP:	0.00021926
Precursor Type:	ISO

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	46 %
Peak Coverage:	39 %
Protein Localisation:	9 ... 22

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	129.0659		129.0659	1	Q	13		
	257.1244		257.1244	2	Q	12	1579.76	
	344.1565		344.1565	3	S	11	1451.701	-0.09299
	473.1991		473.1991	4	E	10	1364.669	
	602.2416		602.2416	5	E	9	1235.627	+0.001287
	717.2686		717.2686	6	D	8	1106.584	+0.169002
	830.3527		830.3527	7	L	7	991.5571	+0.042319
	943.4367		943.4367	8	L	6	878.473	+0.177897
	1056.521	-0.03763	1056.521	9	L	5	765.389	+0.04431
	1184.579	-0.07203	1184.579	10	Q	4	652.3049	+0.018999
	1299.606	-0.09641	1299.606	11	D	3	524.2463	+0.004517
	1446.675	-0.12479	1446.675	12	F	2	409.2194	+0.13229
+0.175338	767.357	-0.21053	1533.707	13	S	1	262.151	+0.074056
				14	R	0	175.119	



Scan number	8388	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	190.86

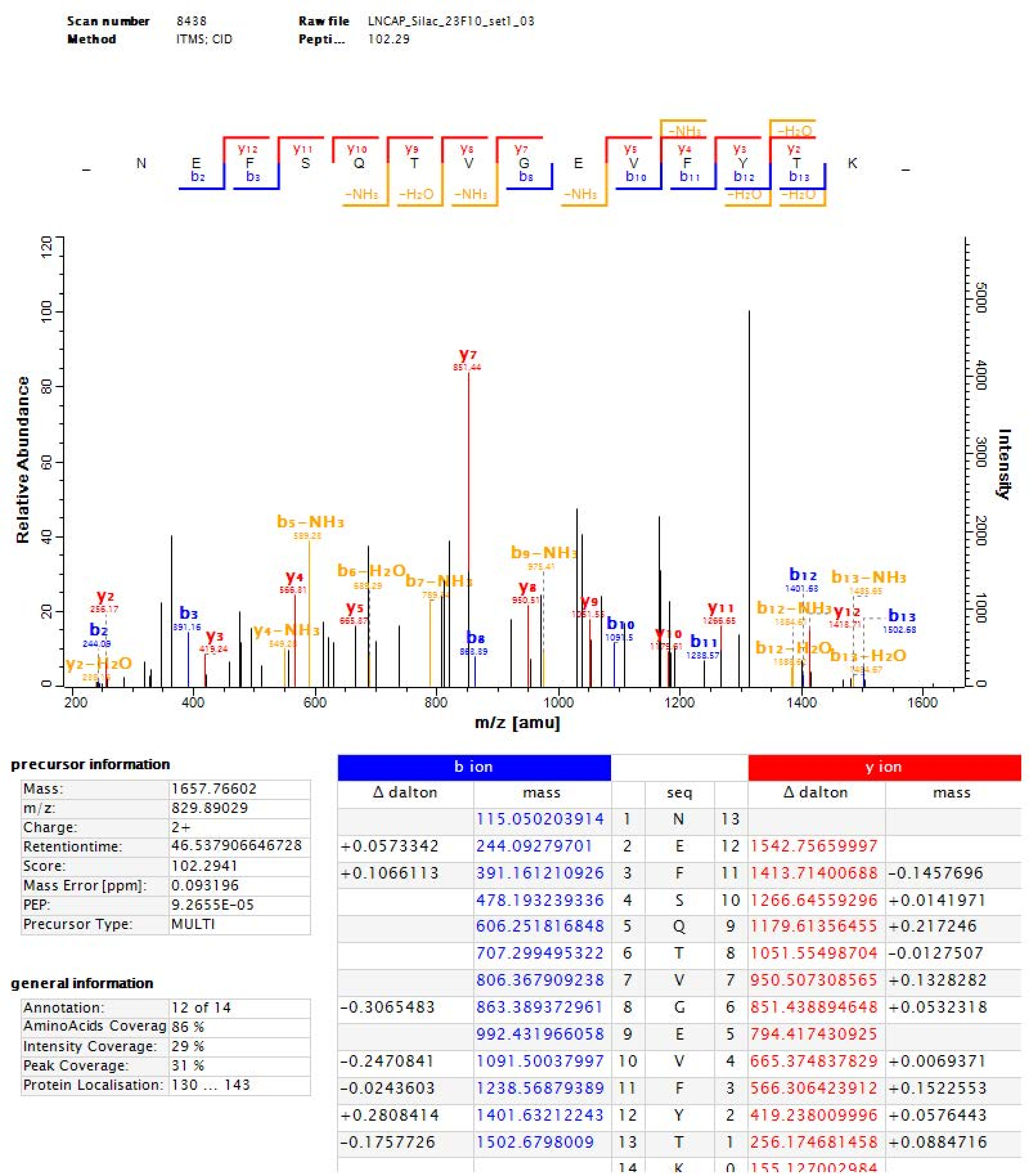
precursor information

Mass:	1372.73467
m/z:	687.37461
Charge:	2+
Retentiontime:	46.286186218261
Score:	190.8578
Mass Error [ppm]:	-0.28769
PEP:	8.9051E-17
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	71 %
Peak Coverage:	39 %
Protein Localisation:	220 ... 232

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	12				
+0.063963	201.1234	2	I	11	1294.725		1294.725	
+0.044982	329.1819	3	Q	10	1181.64	-0.11591	591.3239	+0.167532
+0.100262	442.266	4	L	9	1053.582	-0.02425	1053.582	
+0.153031	557.293	5	D	8	940.4978	-0.05304	940.4978	
	614.3144	6	G	7	825.4709	+0.010948	825.4709	
-0.01329	727.3985	7	L	6	768.4494	+0.025088	768.4494	
+0.004235	826.4669	8	V	5	655.3653	+0.024007	655.3653	
-0.0835	1012.546	9	W	4	556.2969	+0.08351	556.2969	
-0.07609	1069.568	10	G	3	370.2176	+0.212445	370.2176	
-0.09026	1140.605	11	A	2	313.1961	+0.111411	313.1961	
-0.19455	1227.637	12	S	1	242.159	-0.05758	242.159	
		13	K	0	155.127		155.127	



Scan number	8438	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	102.29

precursor information

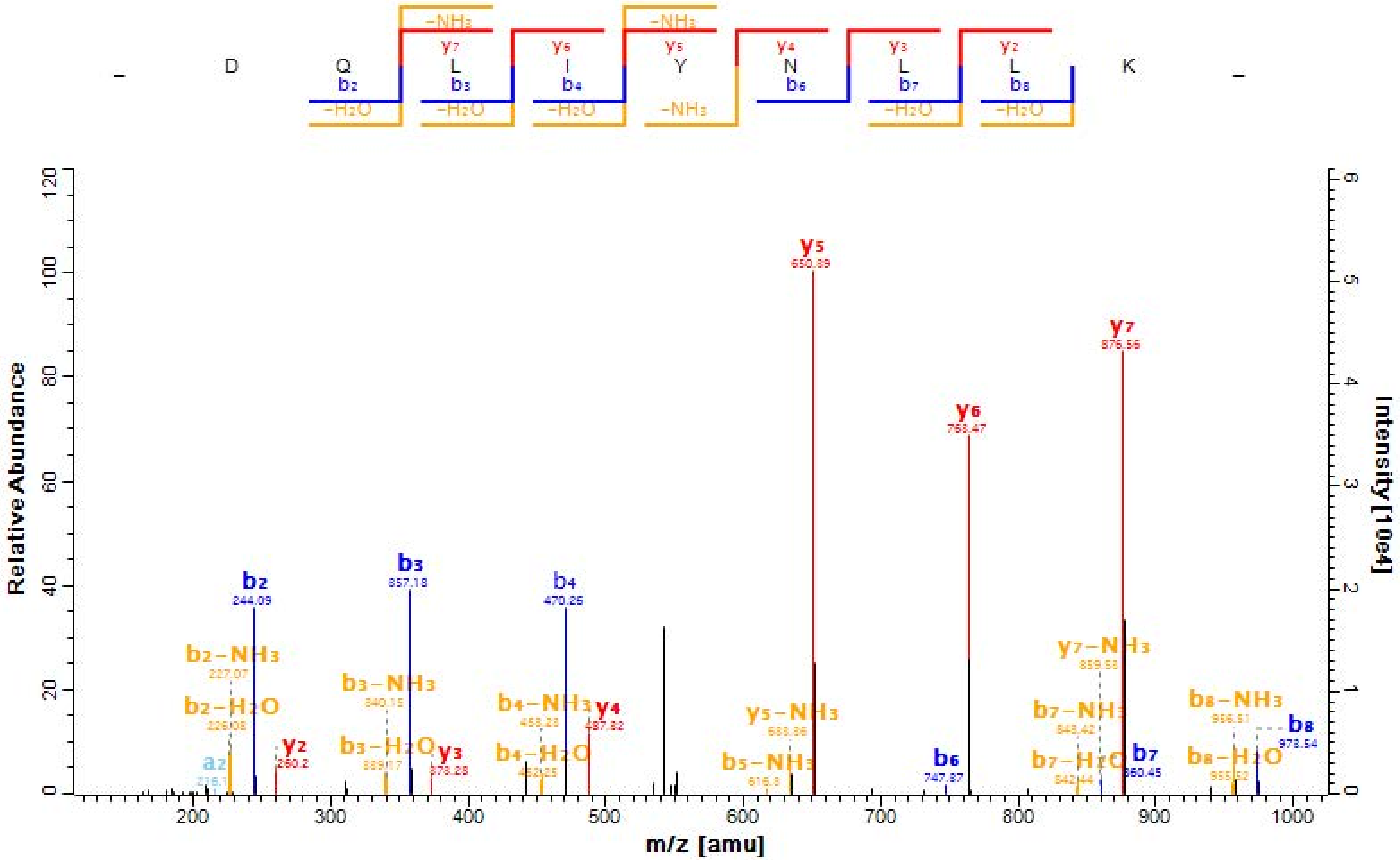
Mass:	1657.76602
m/z:	829.89029
Charge:	2+
Retentiontime:	46.537906646728
Score:	102.2941
Mass Error [ppm]:	0.093196
PEP:	9.2655E-05
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	29 %
Peak Coverage:	31 %
Protein Localisation:	130 ... 143

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	115.050203914	1	N	13		
+0.0573342	244.09279701	2	E	12	1542.75659997	
+0.1066113	391.161210926	3	F	11	1413.71400688	-0.1457696
	478.193239336	4	S	10	1266.64559296	+0.0141971
	606.251816848	5	Q	9	1179.61356455	+0.217246
	707.299495322	6	T	8	1051.55498704	-0.0127507
	806.367909238	7	V	7	950.507308565	+0.1328282
-0.3065483	863.389372961	8	G	6	851.438894648	+0.0532318
	992.431966058	9	E	5	794.417430925	
-0.2470841	1091.50037997	10	V	4	665.374837829	+0.0069371
-0.0243603	1238.56879389	11	F	3	566.306423912	+0.1522553
+0.2808414	1401.63212243	12	Y	2	419.238009996	+0.0576443
-0.1757726	1502.6798009	13	T	1	256.174681458	+0.0884716
		14	K	0	155.127002984	

Scan number 8456 **Raw file** LNCAP_Silac_23F10_set1_03
Method ITMS; CID **Pepti...** 195.79

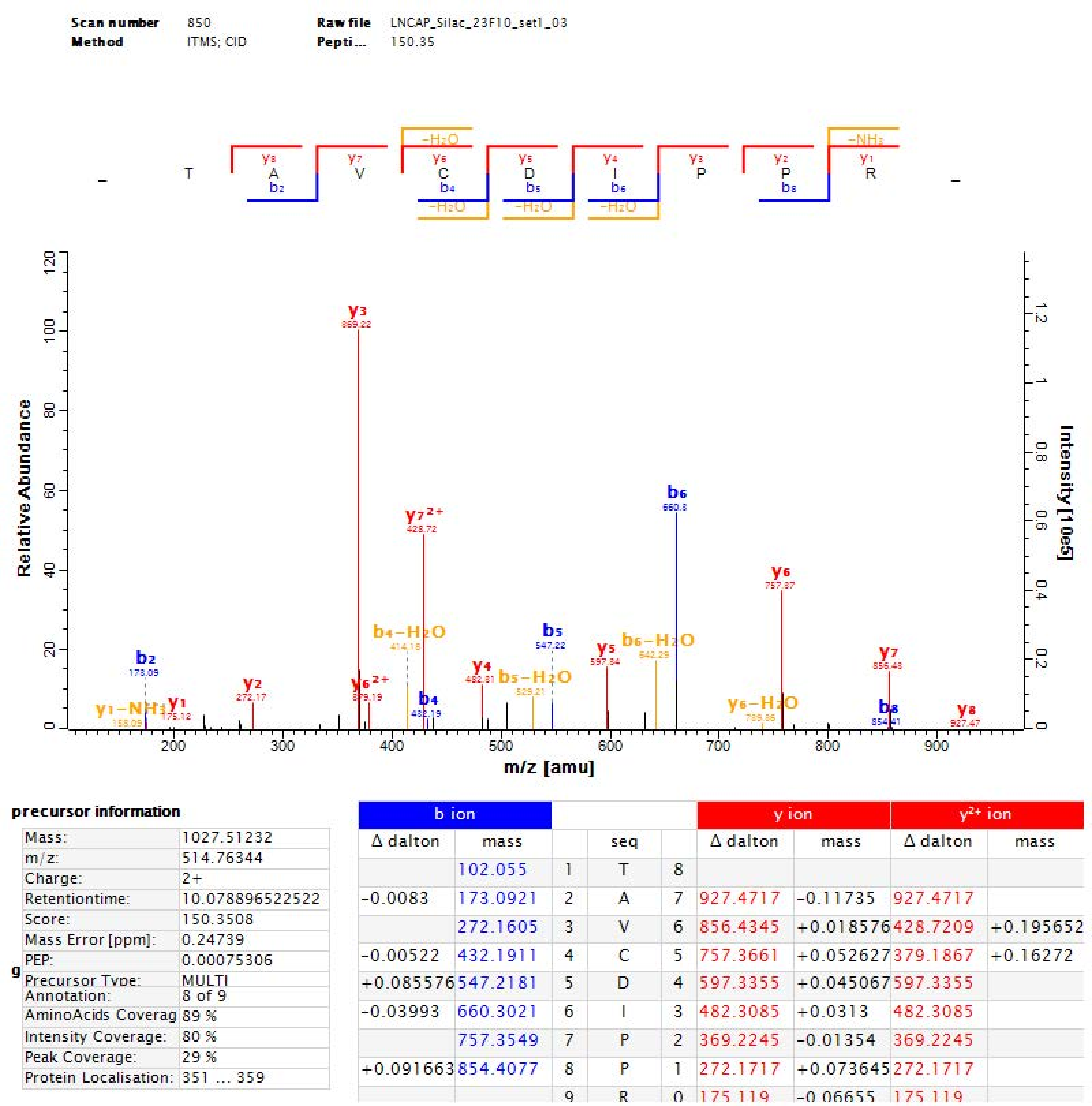


g

precursor information

Mass:	1118.63336
m/z:	560.32395
Charge:	2+
Retentiontime:	46.628013610839
Score:	195.7864
Mass Error [ppm]:	-0.18282
PEP:	1.8085E-08
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	72 %
Peak Coverage:	35 %
Protein Localisation:	35 ... 43

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	88.0393		116.0342	1	D	8		
+0.087298	216.0979	-0.00773	244.0928	2	Q	7	1004.614	
	329.1819	+0.049946	357.1769	3	L	6	876.5553	+0.031171
	442.266	-0.00372	470.2609	4	I	5	763.4713	+0.021851
	605.3293		633.3243	5	Y	4	650.3872	+0.033893
	719.3723	+0.084967	747.3672	6	N	3	487.3239	+0.010857
	832.4563	+0.155933	860.4512	7	L	2	373.2809	+0.137464
	945.5404	-0.00424	973.5353	8	L	1	260.1969	-0.00888
				9	K	0	147.1128	

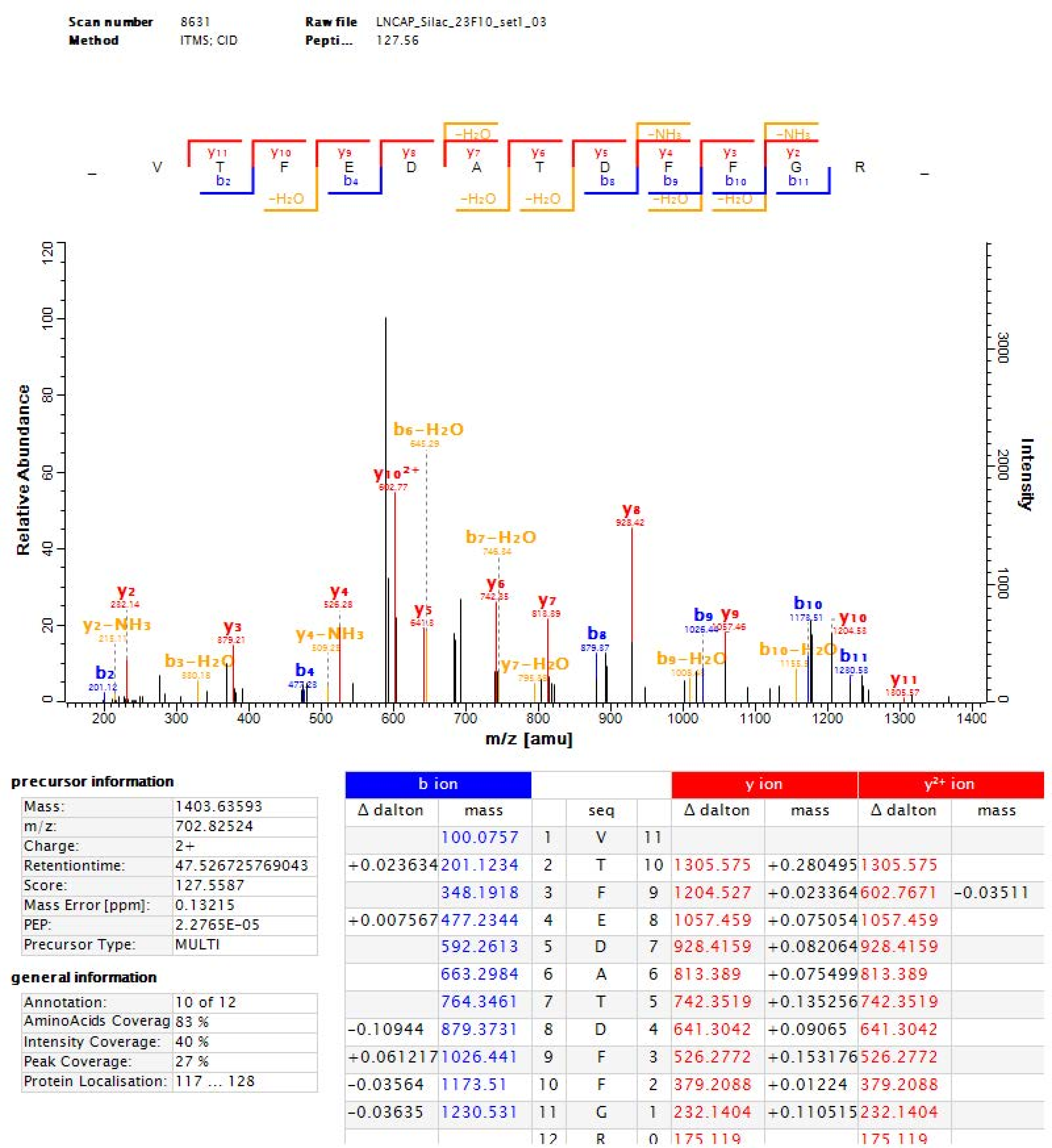


Scan number	850	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	150.35

precursor information

Mass:	1027.51232
m/z:	514.76344
Charge:	2+
Retentiontime:	10.078896522522
Score:	150.3508
Mass Error [ppm]:	0.24739
PEP:	0.00075306
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	80 %
Peak Coverage:	29 %
Protein Localisation:	351 ... 359

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055	1	T	8				
−0.0083	173.0921	2	A	7	927.4717	−0.11735	927.4717	
	272.1605	3	V	6	856.4345	+0.018576	428.7209	+0.195652
−0.00522	432.1911	4	C	5	757.3661	+0.052627	379.1867	+0.16272
+0.085576	547.2181	5	D	4	597.3355	+0.045067	597.3355	
−0.03993	660.3021	6	I	3	482.3085	+0.0313	482.3085	
	757.3549	7	P	2	369.2245	−0.01354	369.2245	
+0.091663	854.4077	8	P	1	272.1717	+0.073645	272.1717	
		9	R	0	175.119	−0.06655	175.119	



Scan number	8631	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	127.56

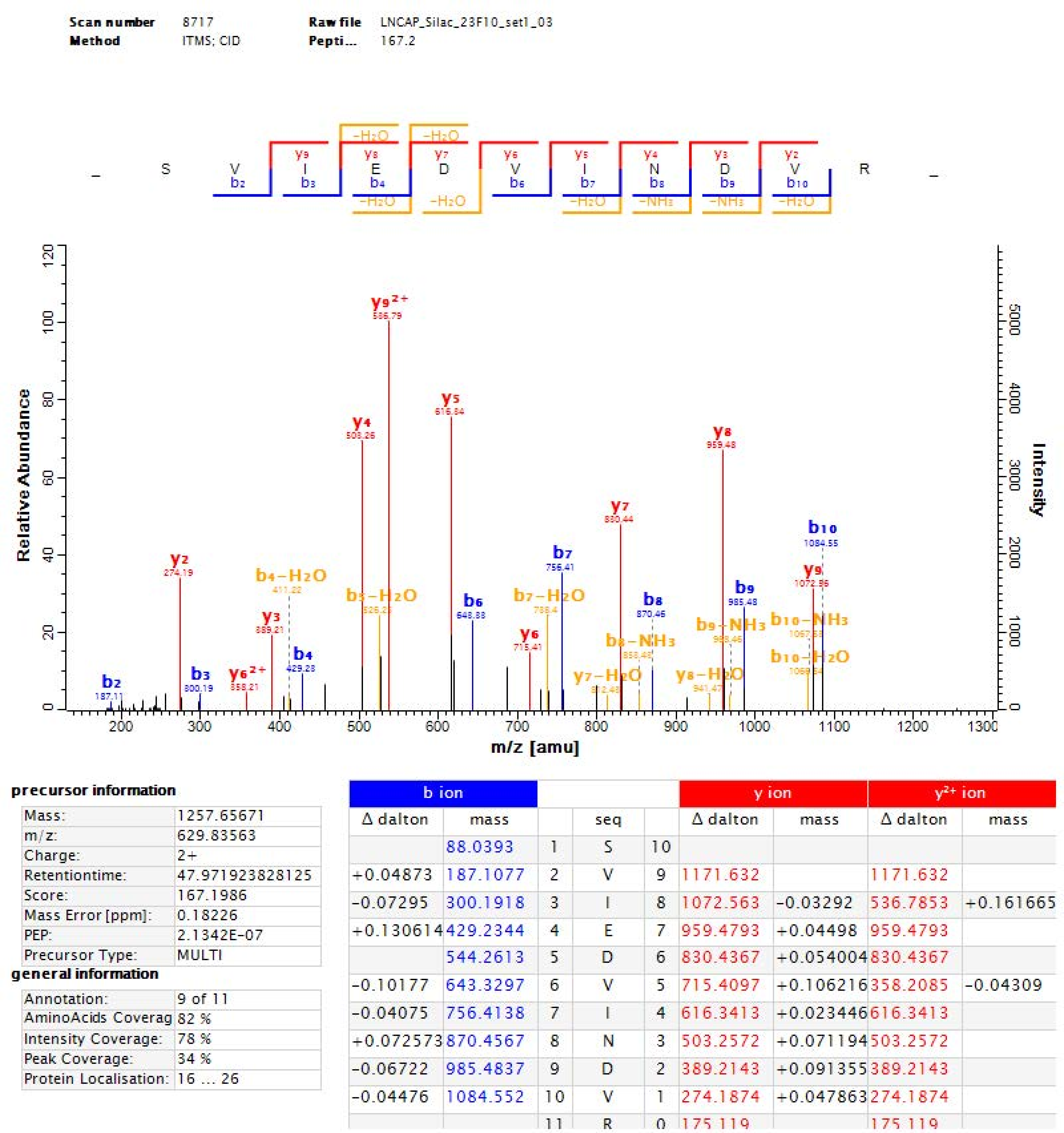
precursor information

Mass:	1403.63593
m/z:	702.82524
Charge:	2+
Retentiontime:	47.526725769043
Score:	127.5587
Mass Error [ppm]:	0.13215
PEP:	2.2765E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	40 %
Peak Coverage:	27 %
Protein Localisation:	117 ... 128

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	11				
+0.023634	201.1234	2	T	10	1305.575	+0.280495	1305.575	
	348.1918	3	F	9	1204.527	+0.023364	602.7671	-0.03511
+0.007567	477.2344	4	E	8	1057.459	+0.075054	1057.459	
	592.2613	5	D	7	928.4159	+0.082064	928.4159	
	663.2984	6	A	6	813.389	+0.075499	813.389	
	764.3461	7	T	5	742.3519	+0.135256	742.3519	
-0.10944	879.3731	8	D	4	641.3042	+0.09065	641.3042	
+0.061217	1026.441	9	F	3	526.2772	+0.153176	526.2772	
-0.03564	1173.51	10	F	2	379.2088	+0.01224	379.2088	
-0.03635	1230.531	11	G	1	232.1404	+0.110515	232.1404	
		12	R	0	175.119		175.119	



Scan number	8717	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	167.2

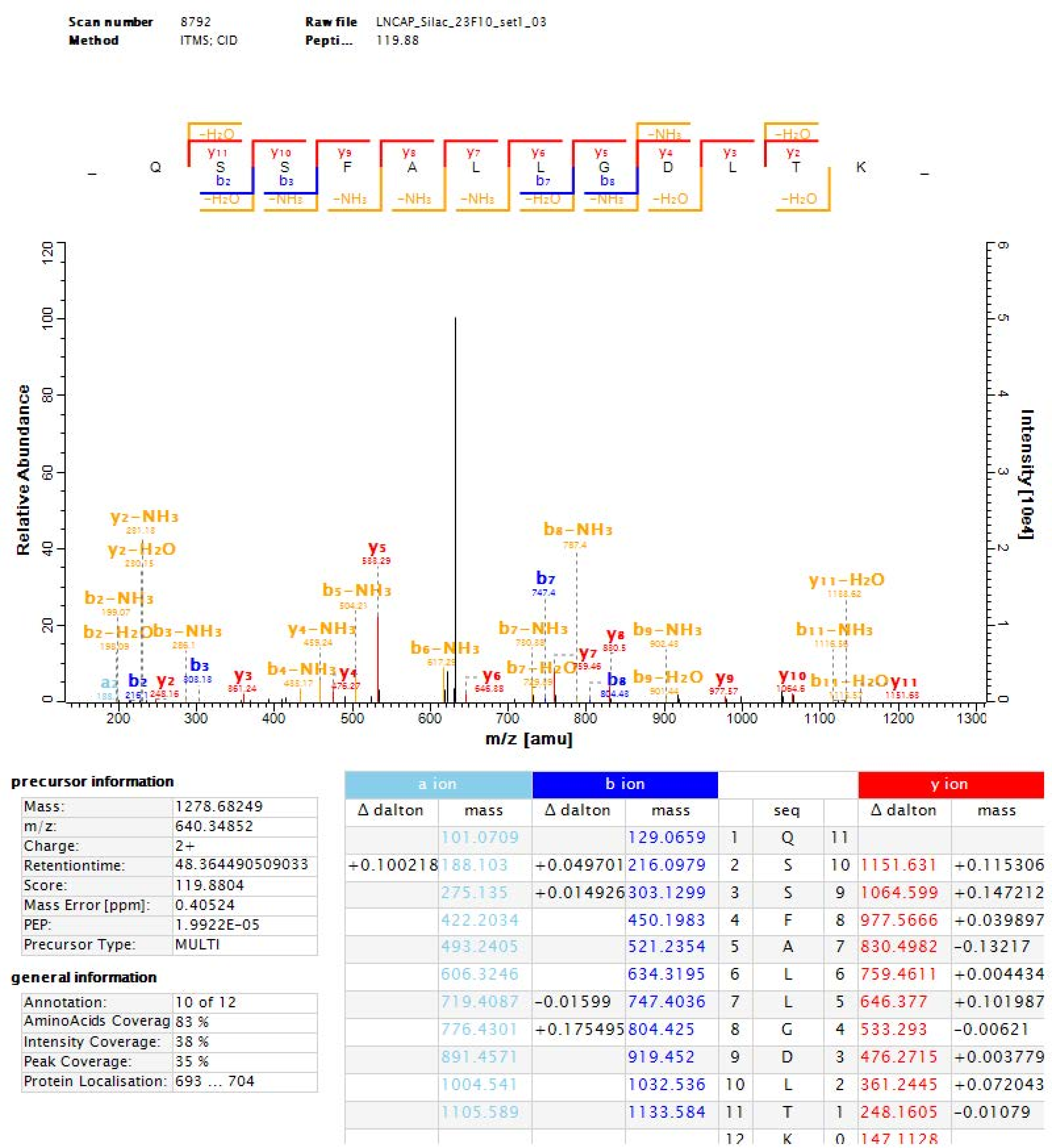
precursor information

Mass:	1257.65671
m/z:	629.83563
Charge:	2+
Retentiontime:	47.971923828125
Score:	167.1986
Mass Error [ppm]:	0.18226
PEP:	2.1342E-07
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	78 %
Peak Coverage:	34 %
Protein Localisation:	16 ... 26

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	10				
+0.04873	187.1077	2	V	9	1171.632		1171.632	
−0.07295	300.1918	3	I	8	1072.563	−0.03292	536.7853	+0.161665
+0.130614	429.2344	4	E	7	959.4793	+0.04498	959.4793	
	544.2613	5	D	6	830.4367	+0.054004	830.4367	
−0.10177	643.3297	6	V	5	715.4097	+0.106216	358.2085	−0.04309
−0.04075	756.4138	7	I	4	616.3413	+0.023446	616.3413	
+0.072573	870.4567	8	N	3	503.2572	+0.071194	503.2572	
−0.06722	985.4837	9	D	2	389.2143	+0.091355	389.2143	
−0.04476	1084.552	10	V	1	274.1874	+0.047863	274.1874	
		11	R	0	175.119		175.119	



Scan number	8792	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	119.88

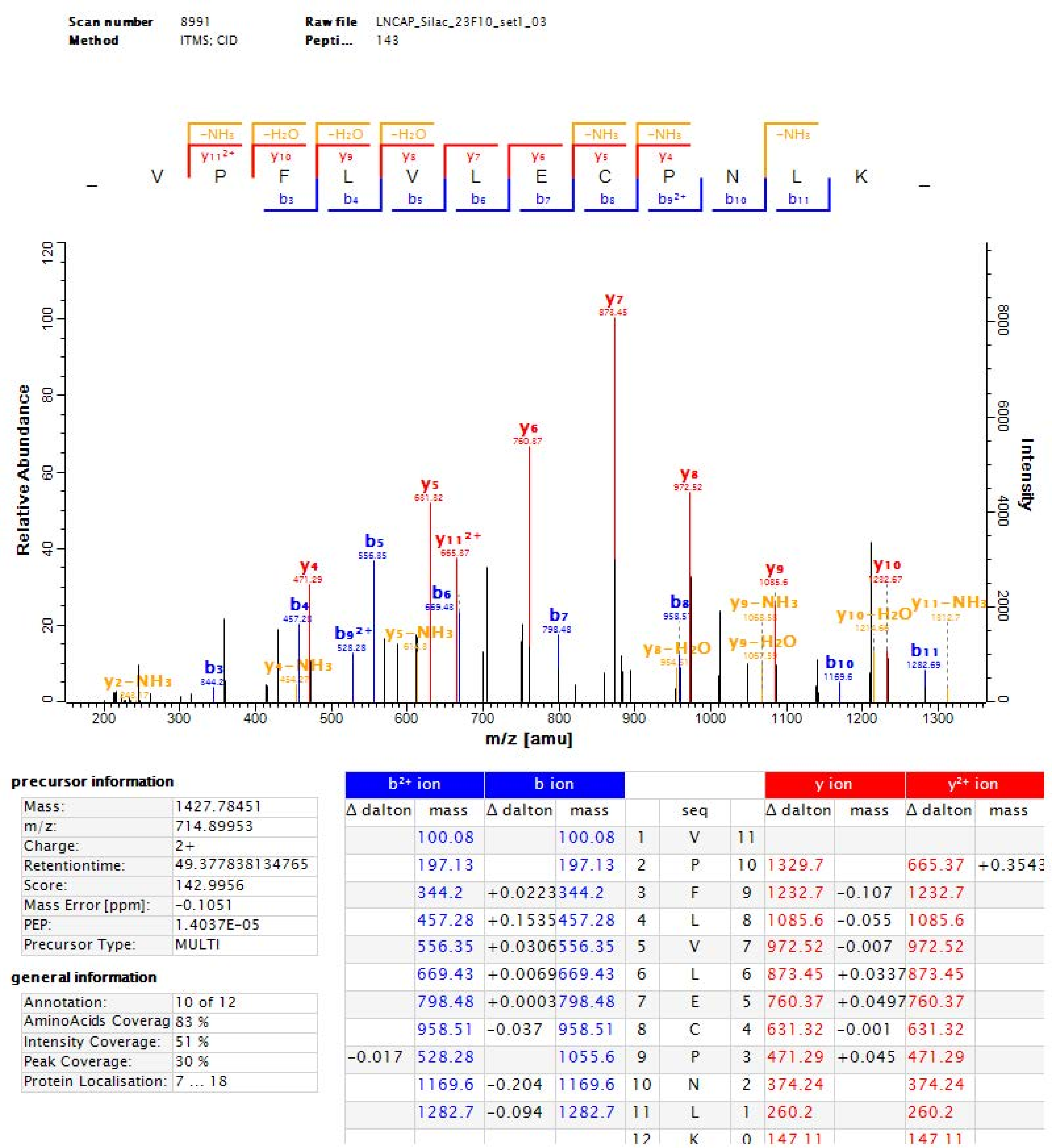
precursor information

Mass:	1278.68249
m/z:	640.34852
Charge:	2+
Retentiontime:	48.364490509033
Score:	119.8804
Mass Error [ppm]:	0.40524
PEP:	1.9922E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	38 %
Peak Coverage:	35 %
Protein Localisation:	693 ... 704

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	101.0709		129.0659	1	Q	11		
+0.100218	188.103	+0.049701	216.0979	2	S	10	1151.631	+0.115306
	275.135	+0.014926	303.1299	3	S	9	1064.599	+0.147212
	422.2034		450.1983	4	F	8	977.5666	+0.039897
	493.2405		521.2354	5	A	7	830.4982	-0.13217
	606.3246		634.3195	6	L	6	759.4611	+0.004434
	719.4087	-0.01599	747.4036	7	L	5	646.377	+0.101987
	776.4301	+0.175495	804.425	8	G	4	533.293	-0.00621
	891.4571		919.452	9	D	3	476.2715	+0.003779
	1004.541		1032.536	10	L	2	361.2445	+0.072043
	1105.589		1133.584	11	T	1	248.1605	-0.01079
				12	K	0	147.1128	



Scan number	8991	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	143

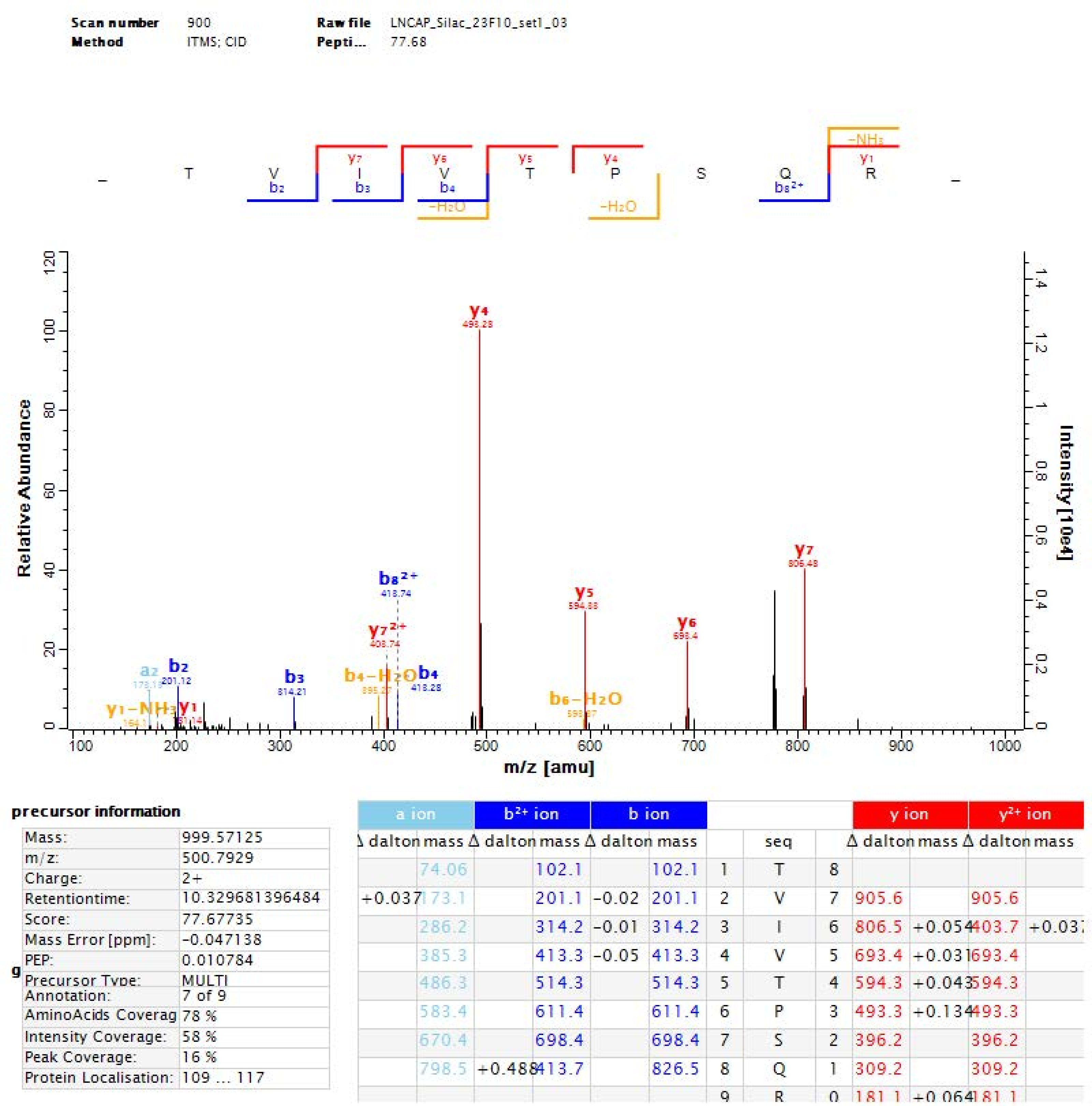
precursor information

Mass:	1427.78451
m/z:	714.89953
Charge:	2+
Retentiontime:	49.377838134765
Score:	142.9956
Mass Error [ppm]:	-0.1051
PEP:	1.4037E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	51 %
Peak Coverage:	30 %
Protein Localisation:	7 ... 18

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	11				
	197.13		197.13	2	P	10	1329.7		665.37	+0.3543
	344.2	+0.0223	344.2	3	F	9	1232.7	-0.107	1232.7	
	457.28	+0.1535	457.28	4	L	8	1085.6	-0.055	1085.6	
	556.35	+0.0306	556.35	5	V	7	972.52	-0.007	972.52	
	669.43	+0.0069	669.43	6	L	6	873.45	+0.0337	873.45	
	798.48	+0.0003	798.48	7	E	5	760.37	+0.0497	760.37	
	958.51	-0.037	958.51	8	C	4	631.32	-0.001	631.32	
-0.017	528.28		1055.6	9	P	3	471.29	+0.045	471.29	
	1169.6	-0.204	1169.6	10	N	2	374.24		374.24	
	1282.7	-0.094	1282.7	11	L	1	260.2		260.2	
				12	K	0	147.11		147.11	



Scan number	900	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	77.68

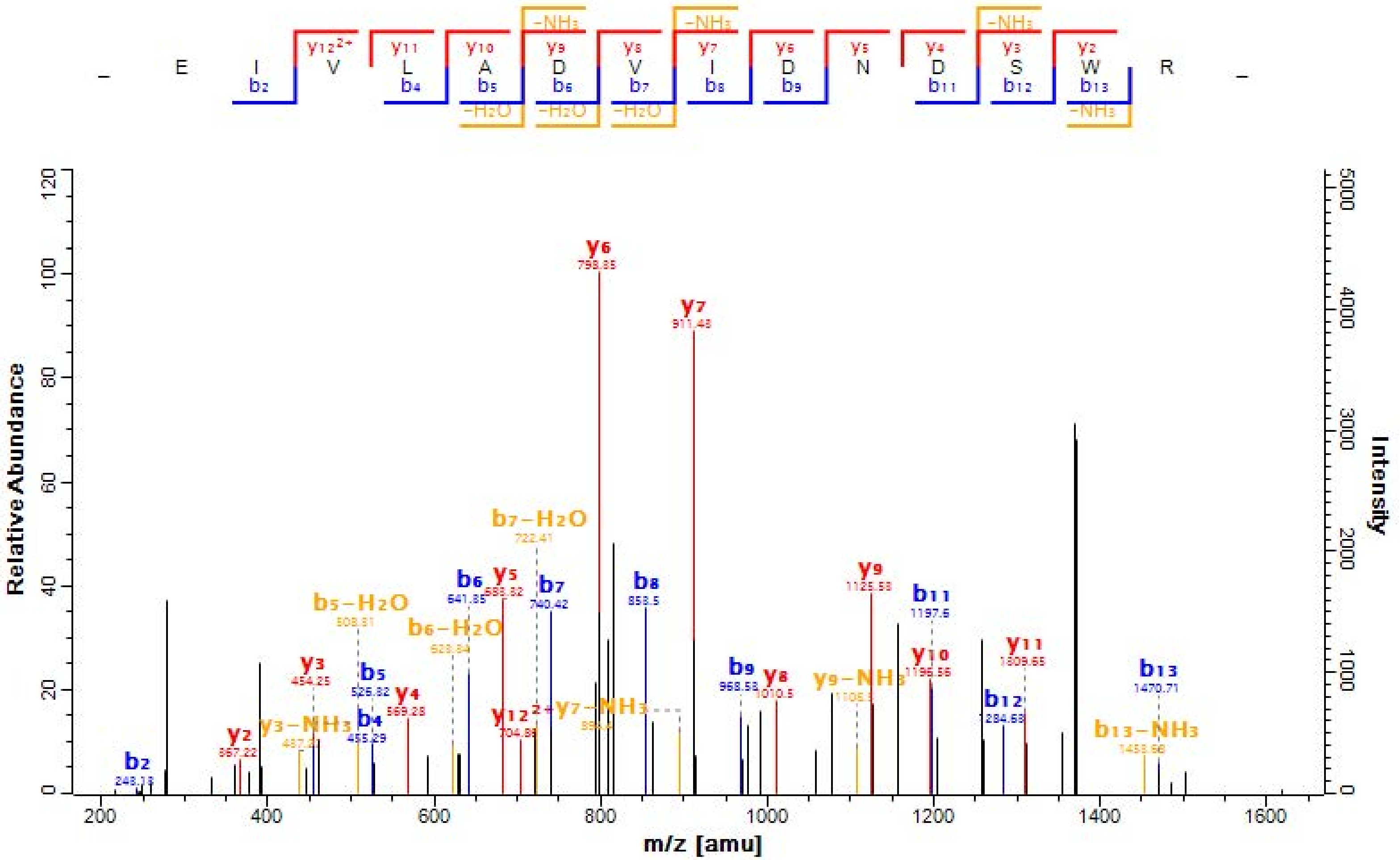
precursor information

Mass:	999.57125
m/z:	500.7929
Charge:	2+
Retentiontime:	10.329681396484
Score:	77.67735
Mass Error [ppm]:	−0.047138
PEP:	0.010784
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	58 %
Peak Coverage:	16 %
Protein Localisation:	109 ... 117

g

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.1		102.1	1	T	8				
+0.037	173.1		201.1	−0.02	201.1	2	V	7	905.6		905.6	
	286.2		314.2	−0.01	314.2	3	I	6	806.5	+0.054	403.7	+0.03
	385.3		413.3	−0.05	413.3	4	V	5	693.4	+0.031	693.4	
	486.3		514.3		514.3	5	T	4	594.3	+0.043	594.3	
	583.4		611.4		611.4	6	P	3	493.3	+0.134	493.3	
	670.4		698.4		698.4	7	S	2	396.2		396.2	
	798.5	+0.488	413.7		826.5	8	Q	1	309.2		309.2	
						9	R	0	181.1	+0.064	181.1	

Scan number	9871	**Raw file**	LNCAP_Silac_23F10_set1_03
Method	ITMS; CID	**Pepti...**	151.07



precursor information

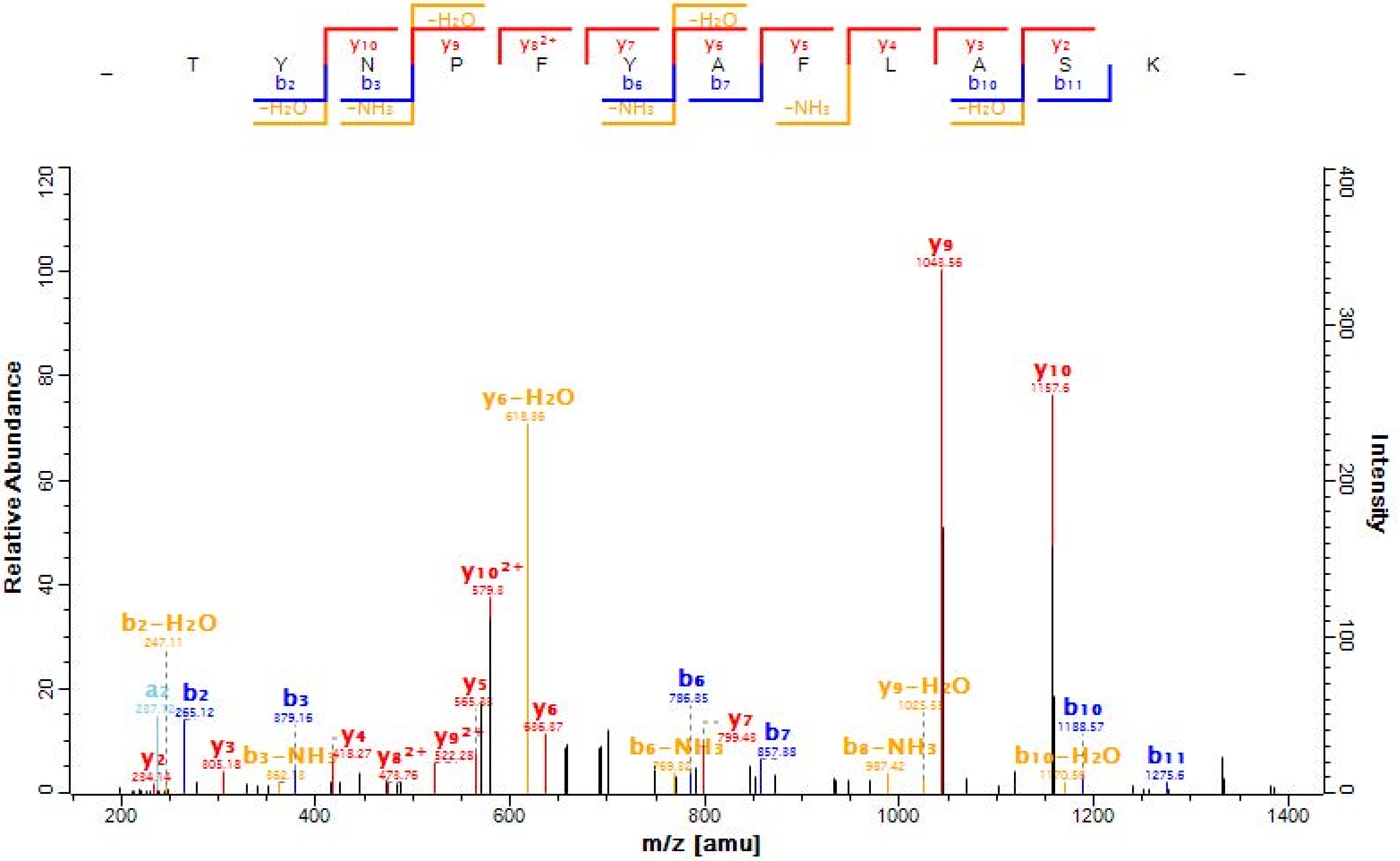
Mass:	1643.81542
m/z:	822.91499
Charge:	2+
Retentiontime:	54.144031524658
Score:	151.0698
Mass Error [ppm]:	-0.048414
PEP:	6.9829E-10
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	43 %
Peak Coverage:	33 %
Protein Localisation:	228 ... 241

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	13				
+0.07618	243.1339	2	I	12	1521.8		1521.8	
	342.2023	3	V	11	1408.716		704.8618	-0.07709
+0.113247	455.2864	4	L	10	1309.648	+0.011711	1309.648	
-0.15391	526.3235	5	A	9	1196.564	+0.001415	1196.564	
+0.019893	641.3505	6	D	8	1125.527	+0.062454	1125.527	
+0.068484	740.4189	7	V	7	1010.5	-0.07326	1010.5	
-0.06636	853.5029	8	I	6	911.4313	-0.00521	911.4313	
-0.12956	968.5299	9	D	5	798.3472	+0.029351	798.3472	
	1082.573	10	N	4	683.3203	+0.047566	683.3203	
-0.04397	1197.6	11	D	3	569.2774	+0.120645	569.2774	
-0.20564	1284.632	12	S	2	454.2504	+0.148564	454.2504	
+0.005818	1470.711	13	W	1	367.2184	+0.146047	367.2184	
		14	R	0	181.1391		181.1391	

Scan number	10157	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	141.58



precursor information

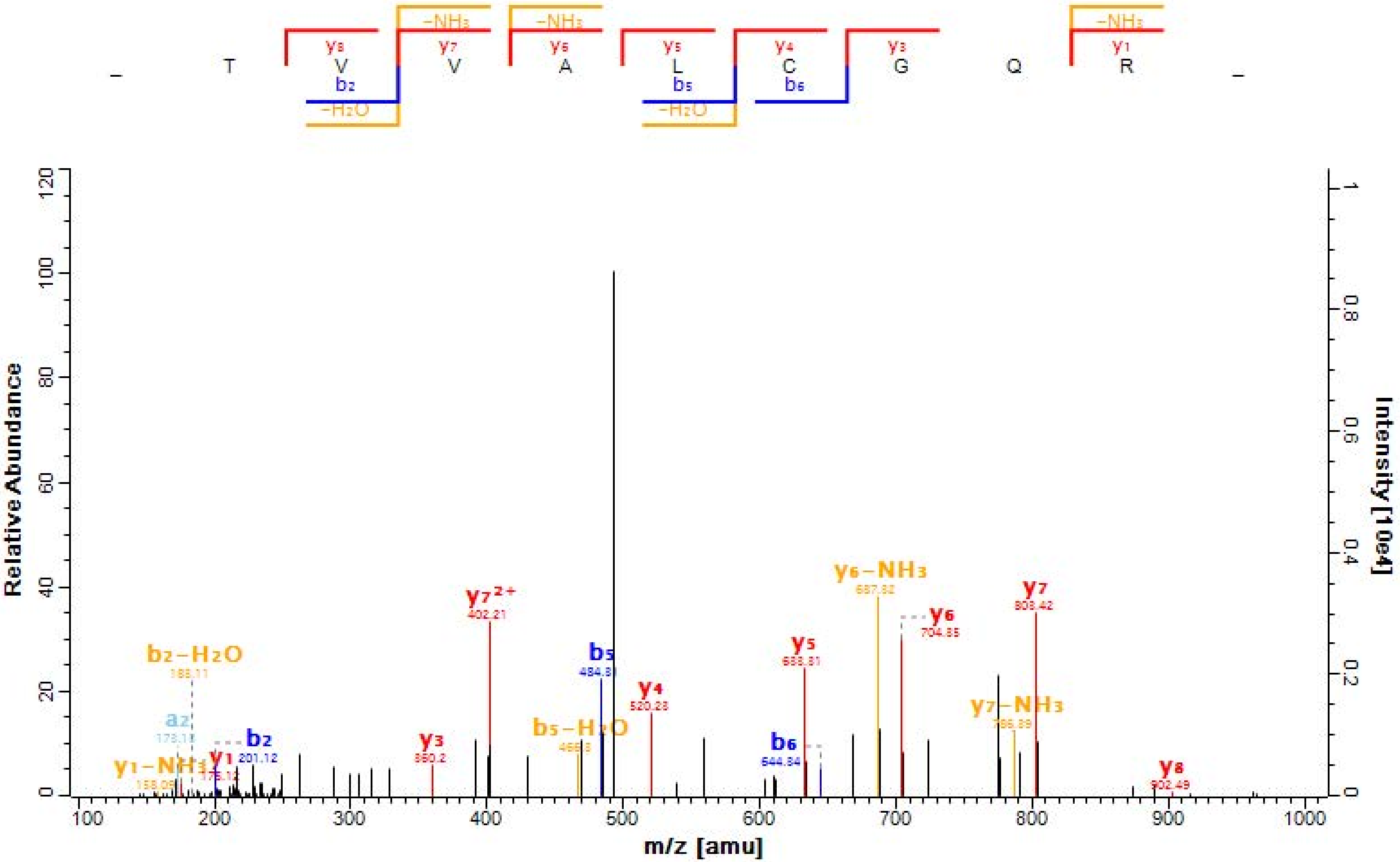
Mass:	1420.70262
m/z:	711.35859
Charge:	2+
Retentiontime:	62.981800079345
Score:	141.5814
Mass Error [ppm]:	-0.054749
PEP:	1.623E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	55 %
Peak Coverage:	30 %
Protein Localisation:	702 ... 713

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.05	1	T	11				
-0.005	237.12	+0.0682	265.12	2	Y	10	1320.7		1320.7	
	351.17	+0.1045	379.16	3	N	9	1157.6	-0.019	579.3	+0.0243
	448.22		476.21	4	P	8	1043.6	-0.007	522.28	+0.379
	595.29		623.28	5	F	7	946.5		473.76	+0.2115
	758.35	+0.0093	786.35	6	Y	6	799.43	+0.1453	799.43	
	829.39	-0.101	857.38	7	A	5	636.37	+0.0497	636.37	
	976.46		1004.5	8	F	4	565.33	+0.0614	565.33	
	1089.5		1117.5	9	L	3	418.27	+0.0832	418.27	
	1160.6	+0.0287	1188.6	10	A	2	305.18	+0.1035	305.18	
	1247.6	+0.2134	1275.6	11	S	1	234.14	+0.0119	234.14	
				12	K	0	147.11		147.11	

Scan number	1196	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	100.02

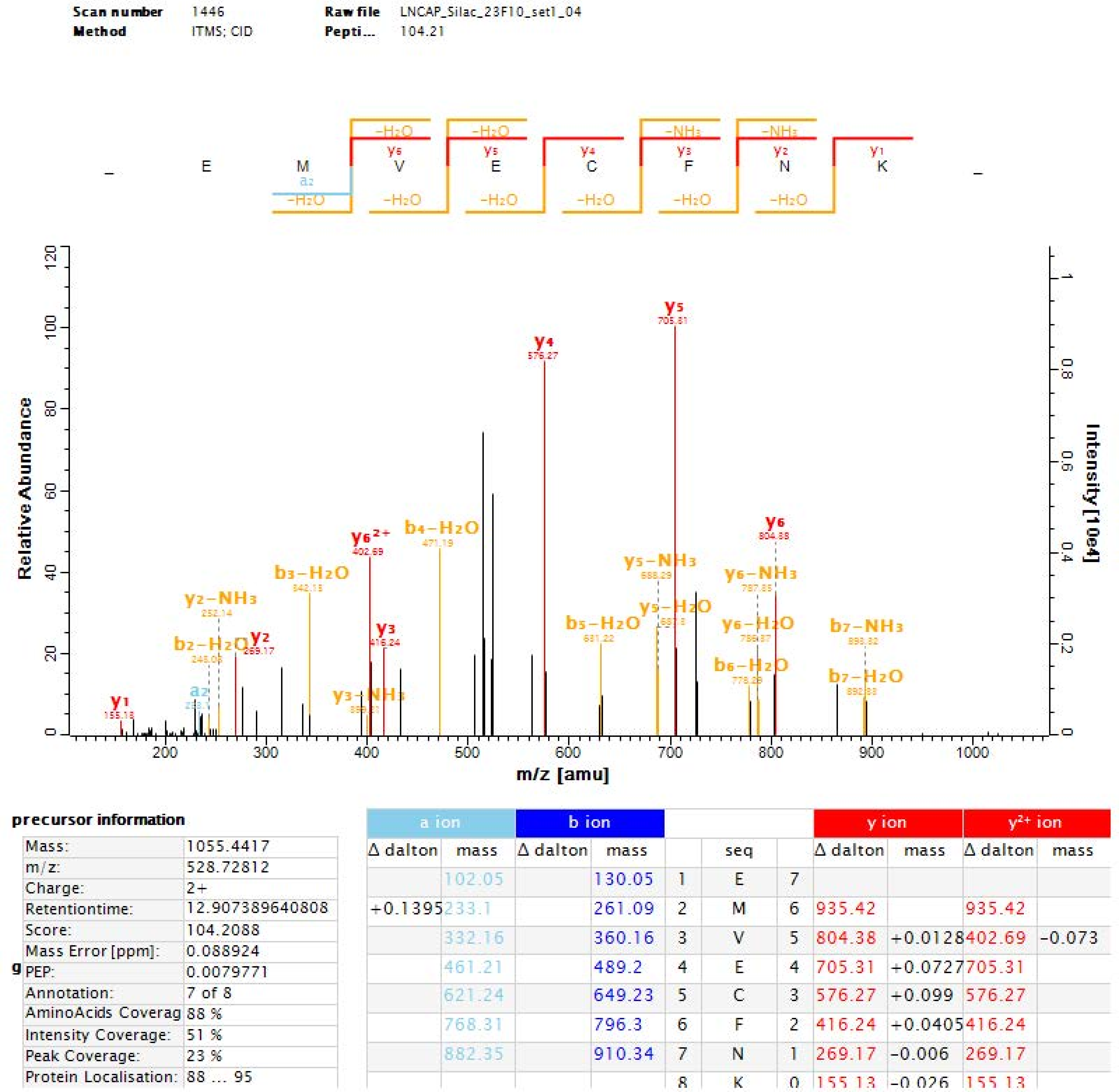


precursor information

g

Mass:	1002.52841
m/z:	502.27148
Charge:	2+
Retentiontime:	11.632506370544
Score:	100.0171
Mass Error [ppm]:	0.35598
PEP:	0.0034806
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	37 %
Peak Coverage:	16 %
Protein Localisation:	187 ... 195

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.05	1	T	8				
−0.033	173.13	+0.0491	201.12	2	V	7	902.49	+0.1407	902.49	
	272.2		300.19	3	V	6	803.42	+0.0344	402.21	−0.113
	343.23		371.23	4	A	5	704.35	+0.0292	704.35	
	456.32	−0.081	484.31	5	L	4	633.31	+0.0832	633.31	
	616.35	+0.165	644.34	6	C	3	520.23	+0.1121	520.23	
	673.37		701.37	7	G	2	360.2	−0.01	360.2	
	801.43		829.42	8	Q	1	303.18		303.18	
				9	R	0	175.12	+0.1168	175.12	

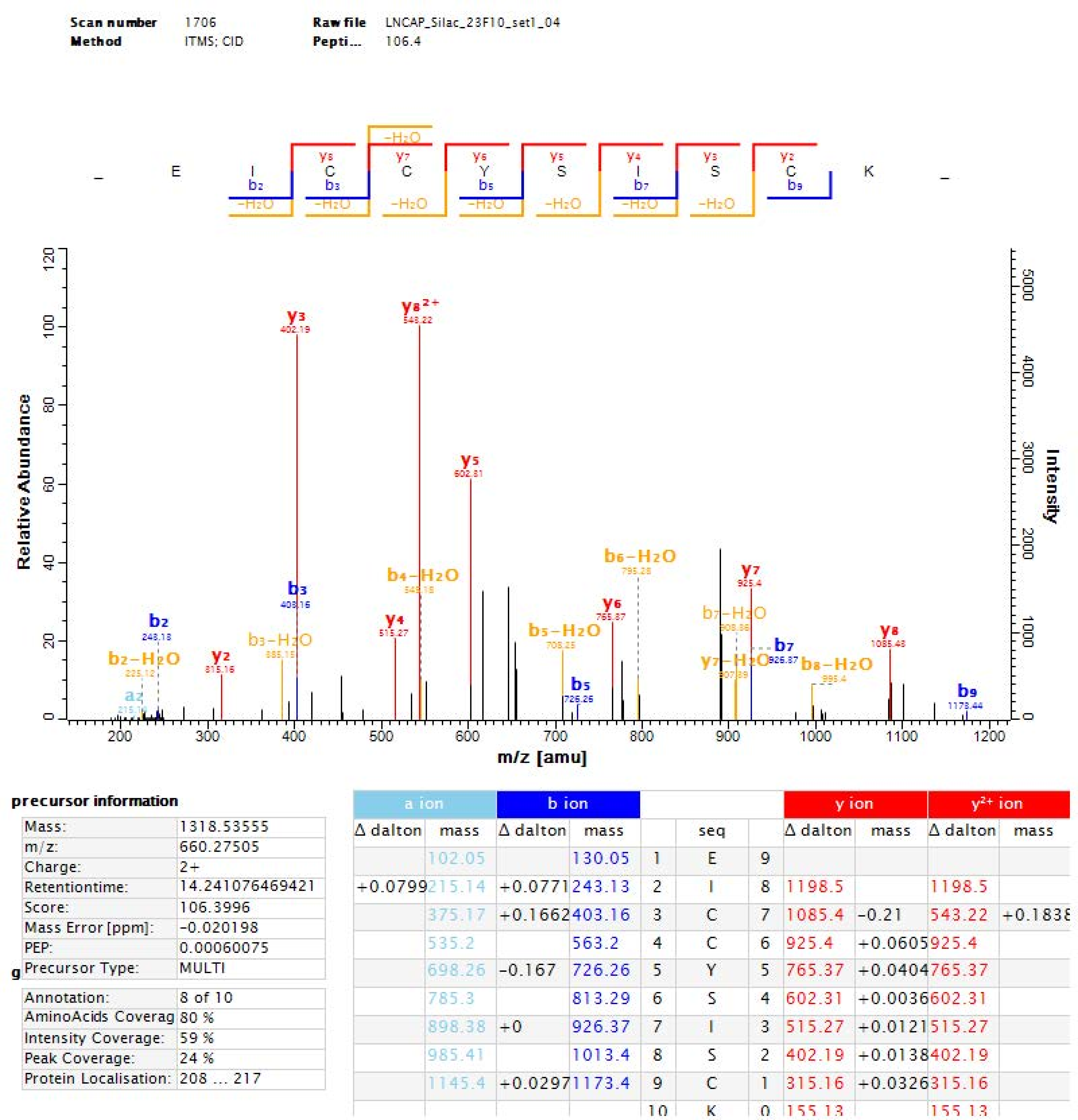


Scan number 1446
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set1_04
Pepti... 104.21

precursor information

Mass:	1055.4417
m/z:	528.72812
Charge:	2+
Retentiontime:	12.907389640808
Score:	104.2088
Mass Error [ppm]:	0.088924
PEP:	0.0079771
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	51 %
Peak Coverage:	23 %
Protein Localisation:	88 ... 95

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	7				
+0.1395	233.1		261.09	2	M	6	935.42		935.42	
	332.16		360.16	3	V	5	804.38	+0.0128	402.69	-0.073
	461.21		489.2	4	E	4	705.31	+0.0727	705.31	
	621.24		649.23	5	C	3	576.27	+0.099	576.27	
	768.31		796.3	6	F	2	416.24	+0.0405	416.24	
	882.35		910.34	7	N	1	269.17	-0.006	269.17	
				8	K	0	155.13	-0.026	155.13	



Scan number	1706	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	106.4

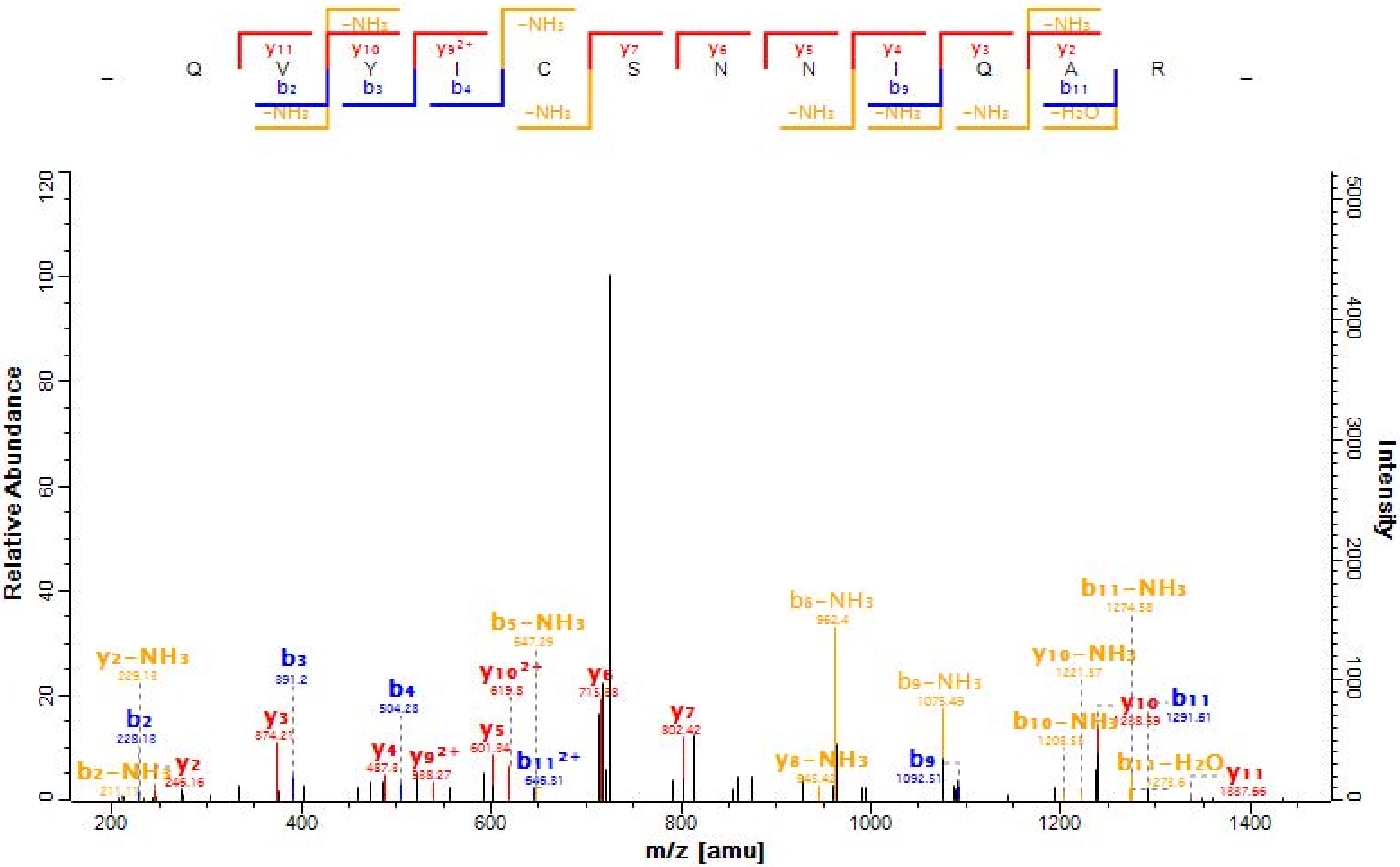
precursor information

Mass:	1318.53555
m/z:	660.27505
Charge:	2+
Retentiontime:	14.241076469421
Score:	106.3996
Mass Error [ppm]:	-0.020198
PEP:	0.00060075
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	59 %
Peak Coverage:	24 %
Protein Localisation:	208 ... 217

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	9				
+0.0799	215.14	+0.0771	243.13	2	I	8	1198.5		1198.5	
	375.17	+0.1662	403.16	3	C	7	1085.4	-0.21	543.22	+0.183
	535.2		563.2	4	C	6	925.4	+0.0605	925.4	
	698.26	-0.167	726.26	5	Y	5	765.37	+0.0404	765.37	
	785.3		813.29	6	S	4	602.31	+0.0036	602.31	
	898.38	+0	926.37	7	I	3	515.27	+0.0121	515.27	
	985.41		1013.4	8	S	2	402.19	+0.0138	402.19	
	1145.4	+0.0297	1173.4	9	C	1	315.16	+0.0326	315.16	
				10	K	0	155.13		155.13	

Scan number	1906	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	140.14



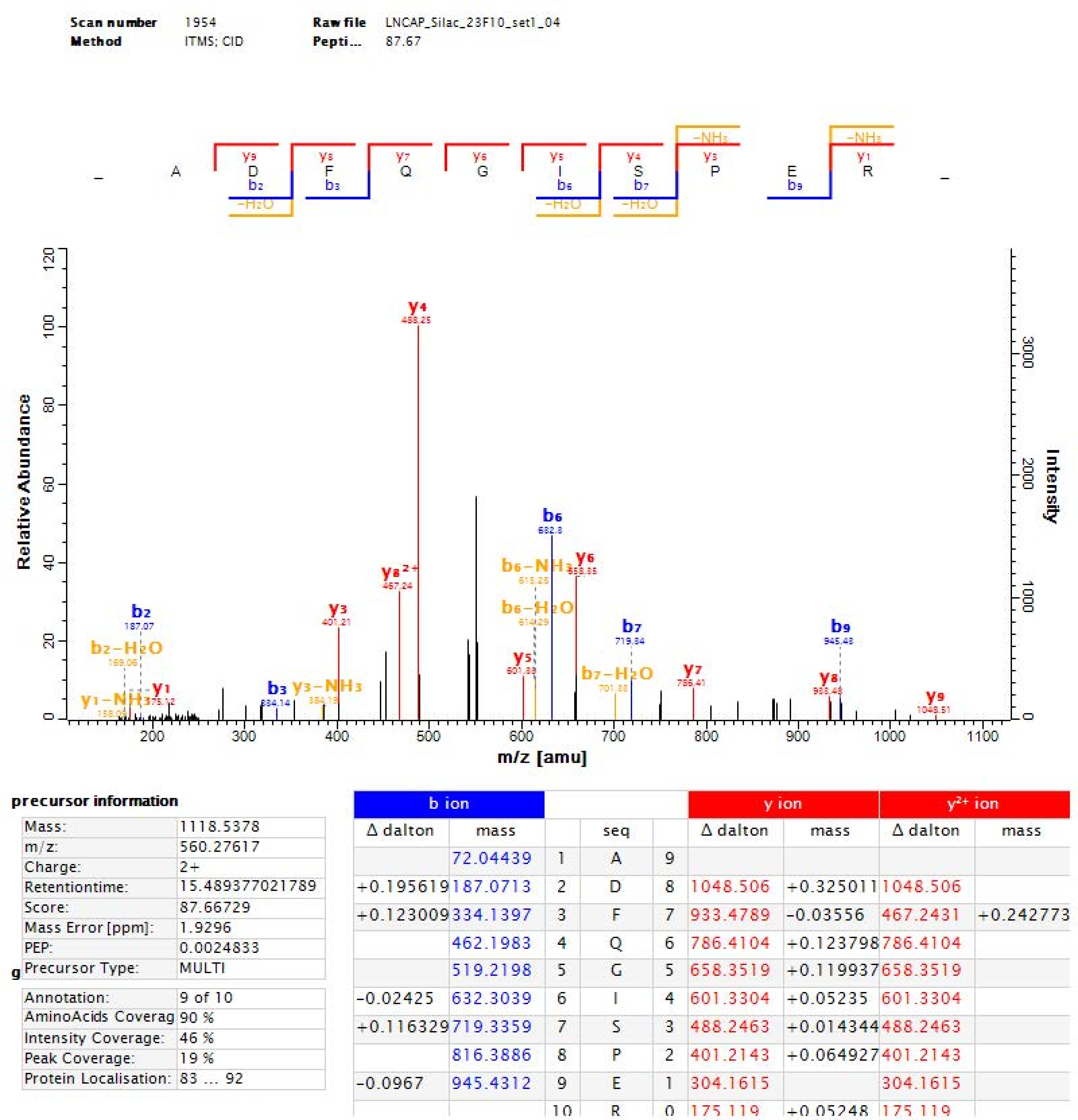
precursor information

Mass:	1464.71425
m/z:	733.3644
Charge:	2+
Retentiontime:	15.247585296630
Score:	140.1416
Mass Error [ppm]:	-0.06309
PEP:	1.8463E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	34 %
Peak Coverage:	28 %
Protein Localisation:	164 ... 175

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.07		129.07	1	Q	11				
	228.13	-0.006	228.13	2	V	10	1337.7	-0.073	1337.7	
	391.2	+0.1235	391.2	3	Y	9	1238.6	-0.026	619.8	-0.08
	504.28	+0.1091	504.28	4	I	8	1075.5		538.27	+0.1208
	664.31		664.31	5	C	7	962.45		962.45	
	751.34		751.34	6	S	6	802.42	+0.0852	802.42	
	865.39		865.39	7	N	5	715.38	+0.1626	715.38	
	979.43		979.43	8	N	4	601.34	-0.137	601.34	
	1092.5	-0.183	1092.5	9	I	3	487.3	+0.1591	487.3	
	1220.6		1220.6	10	Q	2	374.21	+0.0702	374.21	
-0.024	646.31	-0.207	1291.6	11	A	1	246.16	-0.04	246.16	
				12	R	0	175.12		175.12	



Scan number	1954	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	87.67

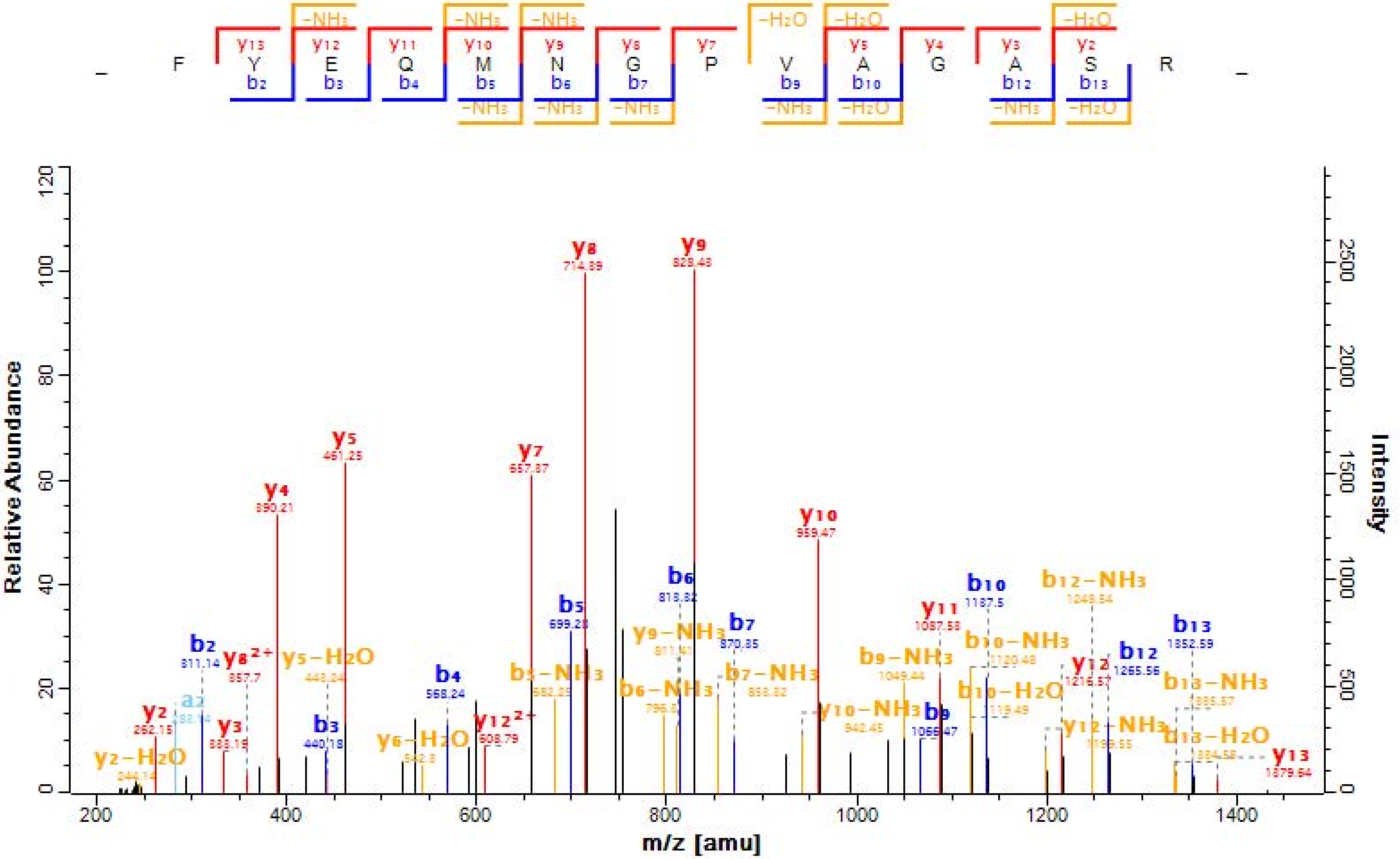
precursor information

Mass:	1118.5378
m/z:	560.27617
Charge:	2+
Retentiontime:	15.489377021789
Score:	87.66729
Mass Error [ppm]:	1.9296
PEP:	0.0024833
Precursor Type:	MULTI

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	46 %
Peak Coverage:	19 %
Protein Localisation:	83 ... 92

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	9				
+0.195619	187.0713	2	D	8	1048.506	+0.325011	1048.506	
+0.123009	334.1397	3	F	7	933.4789	−0.03556	467.2431	+0.242773
	462.1983	4	Q	6	786.4104	+0.123798	786.4104	
	519.2198	5	G	5	658.3519	+0.119937	658.3519	
−0.02425	632.3039	6	I	4	601.3304	+0.05235	601.3304	
+0.116329	719.3359	7	S	3	488.2463	+0.014344	488.2463	
	816.3886	8	P	2	401.2143	+0.064927	401.2143	
−0.0967	945.4312	9	E	1	304.1615		304.1615	
		10	R	0	175.119	+0.05248	175.119	

Scan number	2295	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	242.91



precursor information

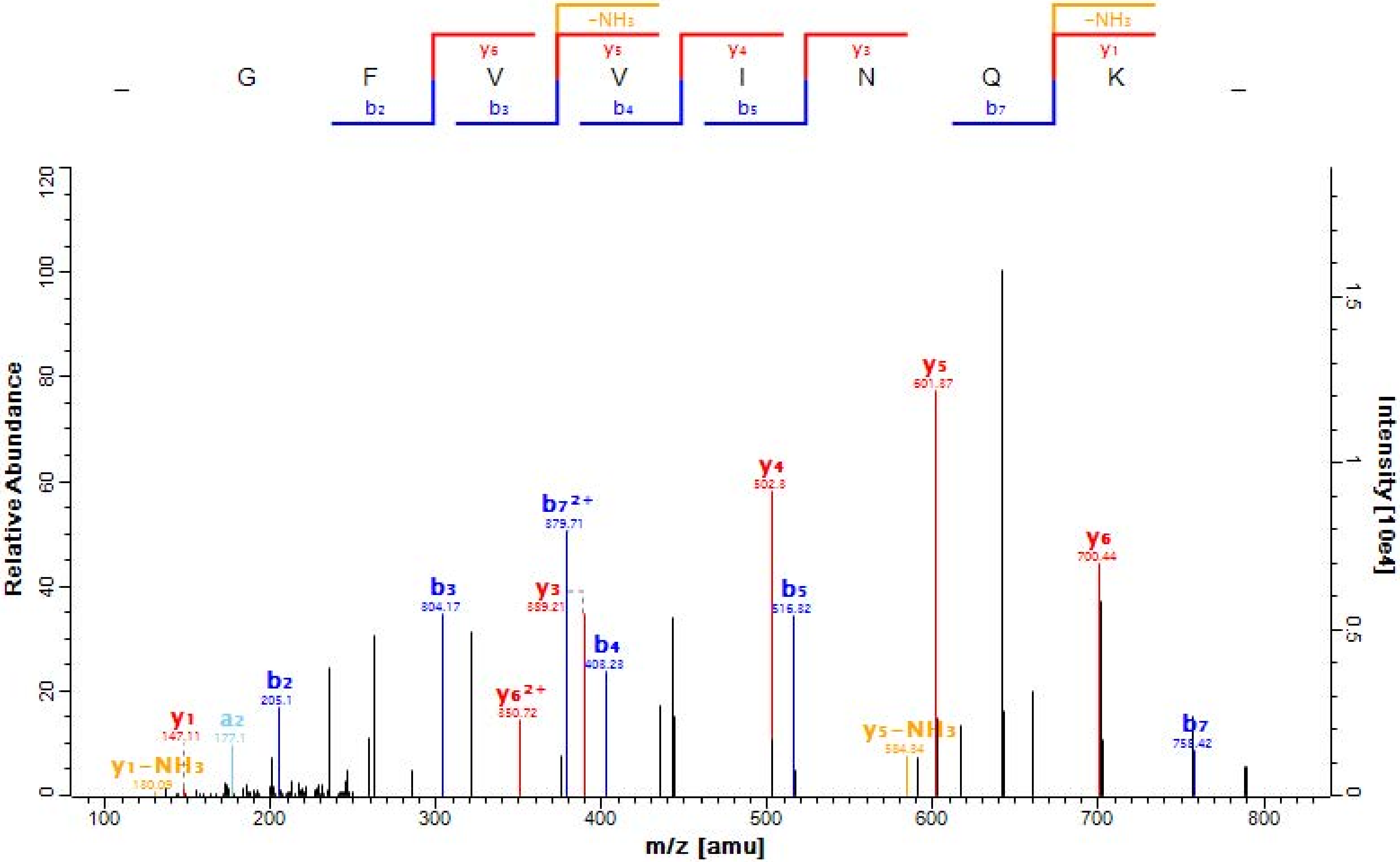
Mass:	1525.69932
m/z:	763.85693
Charge:	2+
Retentiontime:	17.233478546142
Score:	242.9063
Mass Error [ppm]:	0.62571
PEP:	1.4136E-41
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	67 %
Peak Coverage:	46 %
Protein Localisation:	25 ... 38

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08		148.08	1	F	13				
-0.008	283.14	+0.0982	311.14	2	Y	12	1379.6	+0.3761	1379.6	
	412.19	+0.17	440.18	3	E	11	1216.6	-0.053	608.79	+0.056
	540.25	+0.1257	568.24	4	Q	10	1087.5	+0.0748	1087.5	
	671.29	-0.025	699.28	5	M	9	959.47	-0.015	959.47	
	785.33	+0.0345	813.32	6	N	8	828.43	+0.0098	828.43	
	842.35	-0.042	870.35	7	G	7	714.39	+0.0379	357.7	-0.406
	939.4		967.4	8	P	6	657.37	+0.1013	657.37	
	1038.5	+0.0411	1066.5	9	V	5	560.32		560.32	
	1109.5	-0.038	1137.5	10	A	4	461.25	+0.0769	461.25	
	1166.5		1194.5	11	G	3	390.21	+0.0212	390.21	
	1237.6	-0.089	1265.6	12	A	2	333.19	+0.0692	333.19	
	1324.6	+0.0707	1352.6	13	S	1	262.15	+0.0748	262.15	
				14	R	0	175.12		175.12	

Scan number	2315	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	121.29

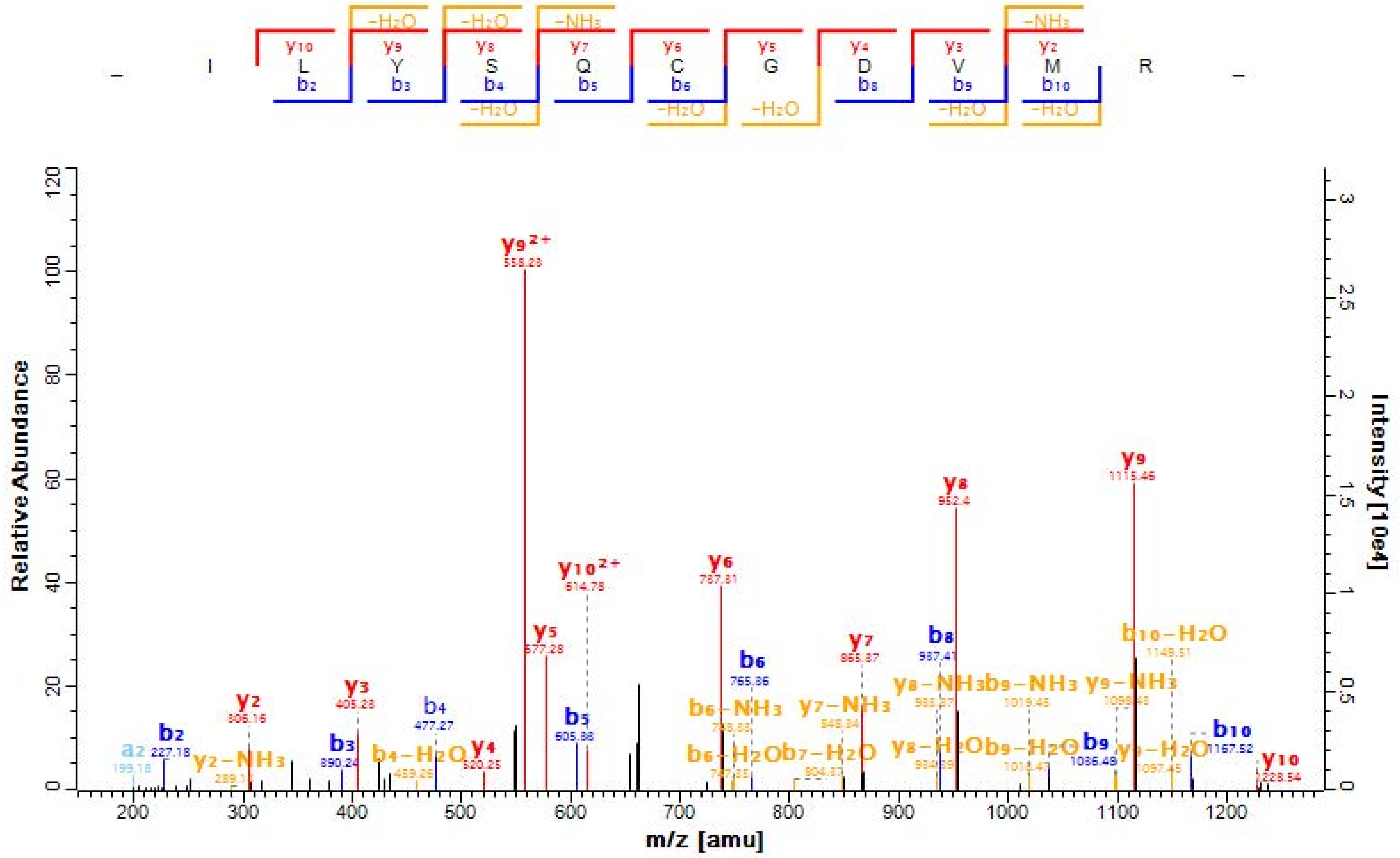


precursor information

Mass:	903.51757
m/z:	452.76606
Charge:	2+
Retentiontime:	17.332700729370
Score:	121.2923
Mass Error [ppm]:	-0.25542
PEP:	0.0012395
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	44 %
Peak Coverage:	15 %
Protein Localisation:	288 ... 295

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	30.03		58.03		58.03	1	G	7				
+0.02	177.1		205.1	-0.11	205.1	2	F	6	847.5		847.5	
	276.2		304.2	-0.01	304.2	3	V	5	700.4	-0.02	350.7	+0.07
	375.2		403.2	-0.08	403.2	4	V	4	601.4	+0.041	601.4	
	488.3		516.3	-0.04	516.3	5	I	3	502.3	+0.04	502.3	
	602.4		630.4		630.4	6	N	2	389.2	+0.093	389.2	
	730.4	-0.32	379.7	+0.137	758.4	7	Q	1	275.2		275.2	
						8	K	0	147.1	-0.1	147.1	

Scan number	2539	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	261.75



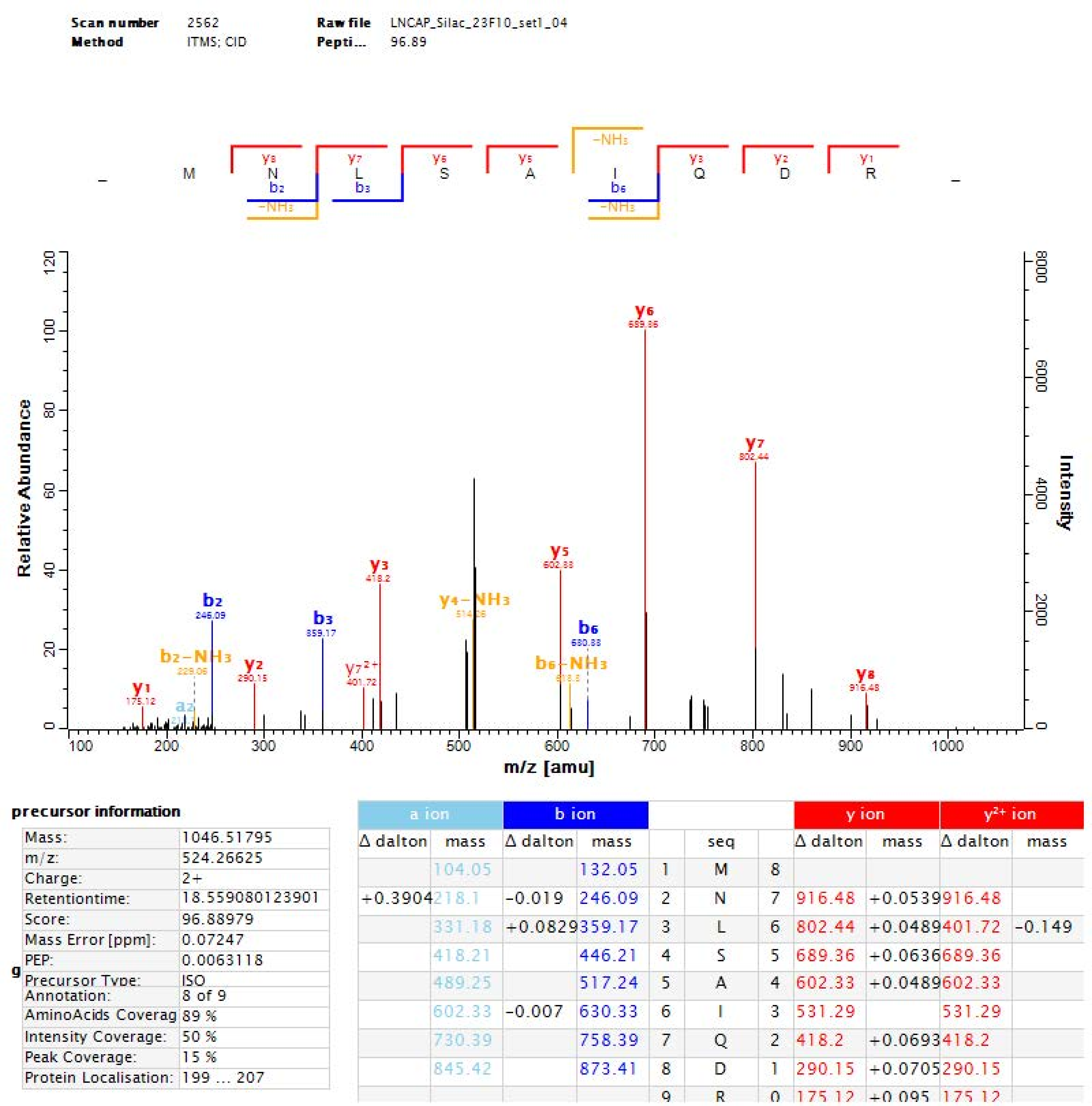
precursor information

Mass:	1340.62135
m/z:	671.31795
Charge:	2+
Retentiontime:	18.446458816528
Score:	261.7532
Mass Error [ppm]:	-0.25462
PEP:	6.423E-39
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	70 %
Peak Coverage:	41 %
Protein Localisation:	120 ... 130

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	10				
+0.0903	199.18	-0.099	227.18	2	L	9	1228.5	+0.1159	614.78	+0.1886
	362.24	+0.0066	390.24	3	Y	8	1115.5	+0.0094	558.23	+0.2459
	449.28	-0.121	477.27	4	S	7	952.4	-0.017	952.4	
	577.33	+0.0969	605.33	5	Q	6	865.37	+0.0102	865.37	
	737.37	+0.0413	765.36	6	C	5	737.31	+0.0426	737.31	
	794.39		822.38	7	G	4	577.28	+0.0663	577.28	
	909.41	-0.09	937.41	8	D	3	520.25	+0.2376	520.25	
	1008.5	+0.0416	1036.5	9	V	2	405.23	+0.0897	405.23	
	1139.5	+0.0293	1167.5	10	M	1	306.16	+0.0546	306.16	
				11	R	0	175.12		175.12	

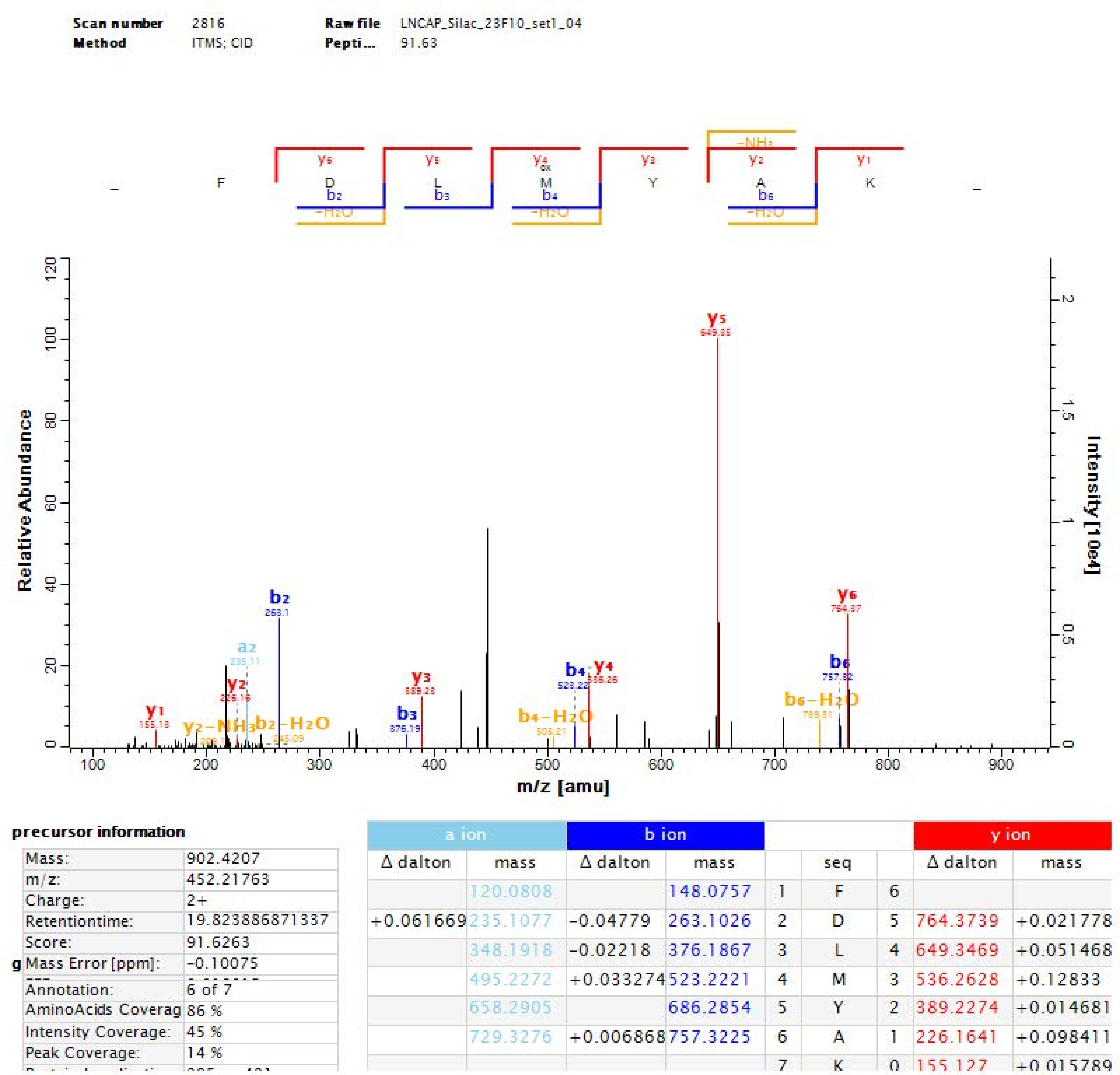


Scan number	2562	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	96.89

precursor information

Mass:	1046.51795
m/z:	524.26625
Charge:	2+
Retentiontime:	18.559080123901
Score:	96.88979
Mass Error [ppm]:	0.07247
PEP:	0.0063118
Precursor Type:	ISO
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	50 %
Peak Coverage:	15 %
Protein Localisation:	199 ... 207

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	104.05		132.05	1	M	8				
+0.3904	218.1	-0.019	246.09	2	N	7	916.48	+0.0539	916.48	
	331.18	+0.0829	359.17	3	L	6	802.44	+0.0489	401.72	-0.149
	418.21		446.21	4	S	5	689.36	+0.0636	689.36	
	489.25		517.24	5	A	4	602.33	+0.0489	602.33	
	602.33	-0.007	630.33	6	I	3	531.29		531.29	
	730.39		758.39	7	Q	2	418.2	+0.0693	418.2	
	845.42		873.41	8	D	1	290.15	+0.0705	290.15	
				9	R	0	175.12	+0.095	175.12	



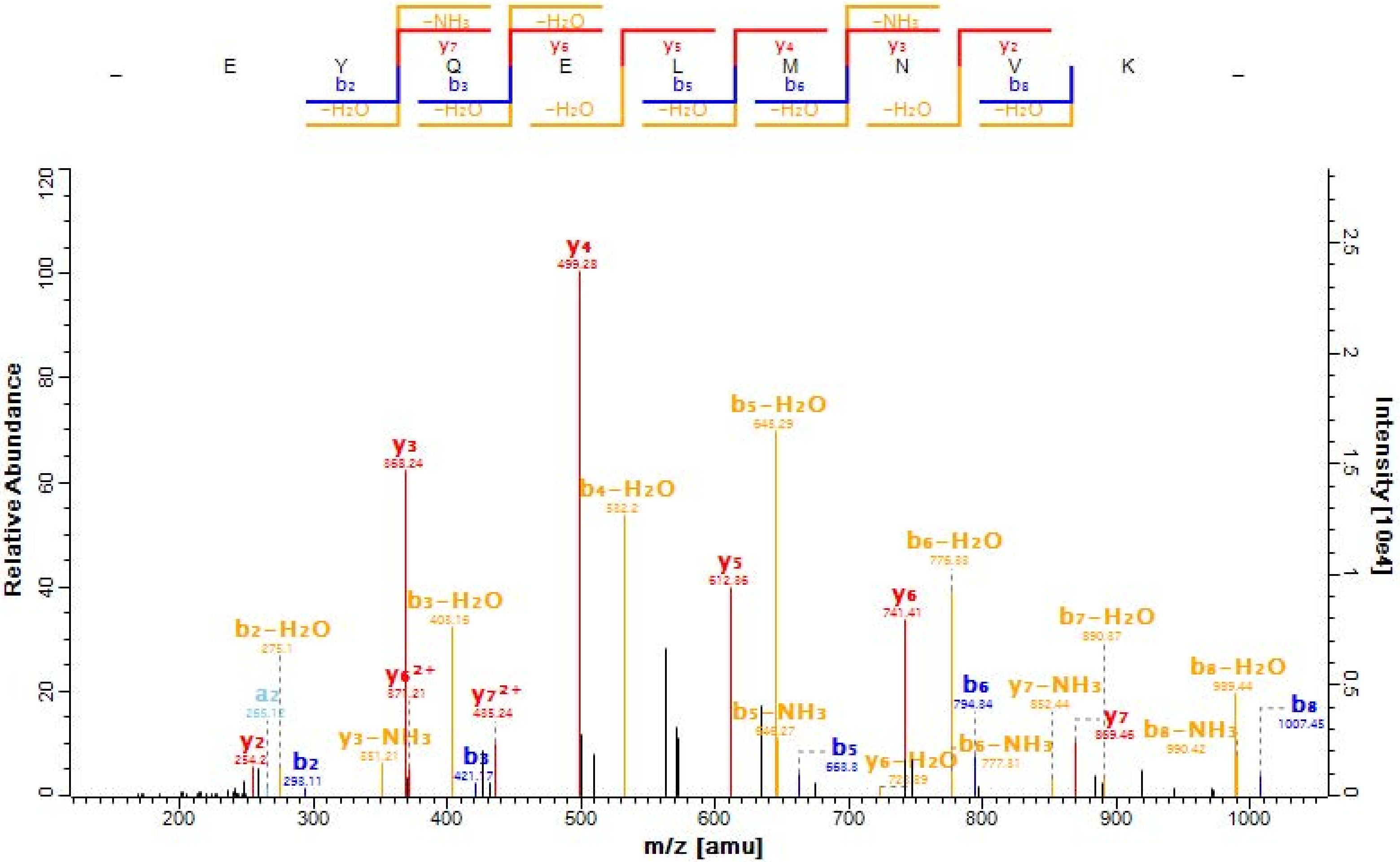
Scan number	2816	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	91.63

precursor information

Mass:	902.4207
m/z:	452.21763
Charge:	2+
Retentiontime:	19.823886871337
Score:	91.6263
Mass Error [ppm]:	-0.10075
Annotation:	6 of 7
AminoAcids Coverag	86 %
Intensity Coverage:	45 %
Peak Coverage:	14 %

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	120.0808		148.0757	1	F	6		
+0.061669	235.1077	-0.04779	263.1026	2	D	5	764.3739	+0.021778
	348.1918	-0.02218	376.1867	3	L	4	649.3469	+0.051468
	495.2272	+0.033274	523.2221	4	M	3	536.2628	+0.12833
	658.2905		686.2854	5	Y	2	389.2274	+0.014681
	729.3276	+0.006868	757.3225	6	A	1	226.1641	+0.098411
				7	K	0	155.127	+0.015789

Scan number	2829	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	207.29



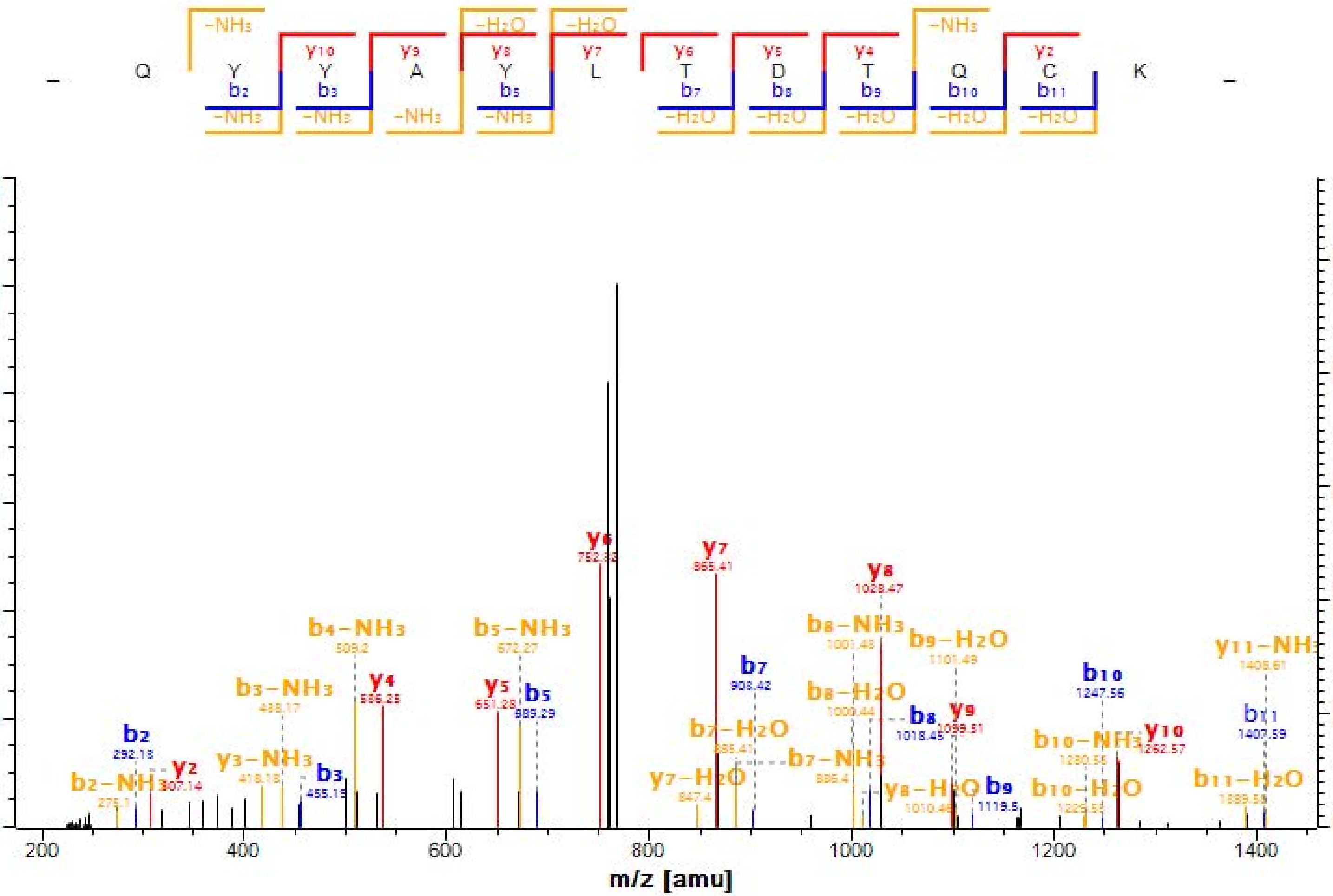
precursor information

g

Mass:	1152.54844
m/z:	577.2815
Charge:	2+
Retentiontime:	19.891582489013
Score:	207.2877
Mass Error [ppm]:	-0.061339
PEP:	1.0455E-12
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	78 %
Peak Coverage:	33 %
Protein Localisation:	373 ... 381

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	8				
-0.043	265.12	+0.1064	293.11	2	Y	7	1032.5		1032.5	
	393.18	-0.012	421.17	3	Q	6	869.46	+0.0034	435.24	-0.004
	522.22		550.21	4	E	5	741.41	+0.0627	371.21	+0.154
	635.3	+0.1021	663.3	5	L	4	612.36	+0.0235	612.36	
	766.34	+0.0101	794.34	6	M	3	499.28	+0.0143	499.28	
	880.39		908.38	7	N	2	368.24	+0.0518	368.24	
	979.46	+0.0721	1007.5	8	V	1	254.2	+0.0125	254.2	
				9	K	0	155.13		155.13	

Scan number	3199	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	186.76



precursor information

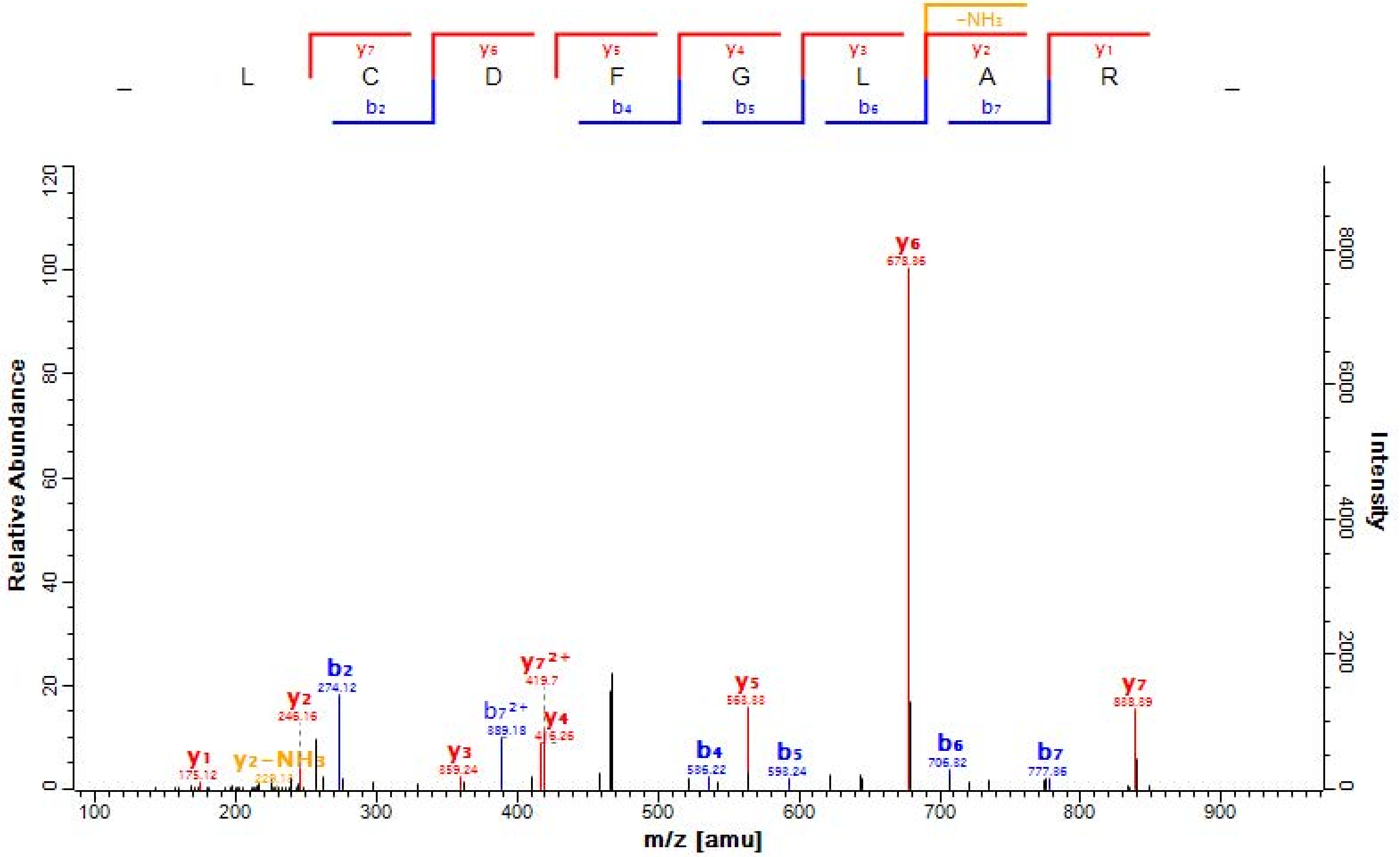
Mass:	1552.68506
m/z:	777.34981
Charge:	2+
Retentiontime:	21.731882095336
Score:	186.7626
Mass Error [ppm]:	-1.1144
PEP:	3.3002E-14
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	44 %
Peak Coverage:	37 %
Protein Localisation:	337 ... 348

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	129.065853978	1	Q	11		
+0.0332931	292.129182516	2	Y	10	1425.63549325	
+0.0639587	455.192511055	3	Y	9	1262.57216471	+0.0649203
	526.229624842	4	A	8	1099.50883617	+0.0124041
+0.0042268	689.292953381	5	Y	7	1028.47172238	-0.0190857
	802.377017361	6	L	6	865.408393844	-0.0117874
-0.2969493	903.424695835	7	T	5	752.324329864	+0.048778
+0.2671722	1018.45163887	8	D	4	651.27665139	+0.0188198
-0.0764658	1119.49931734	9	T	3	536.249708358	+0.0195177
-0.0600921	1247.55789485	10	Q	2	435.202029883	
+0.0159491	1407.58854305	11	C	1	307.143452372	+0.0837205
		12	K	0	147.112804171	

Scan number	3408	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	111.95

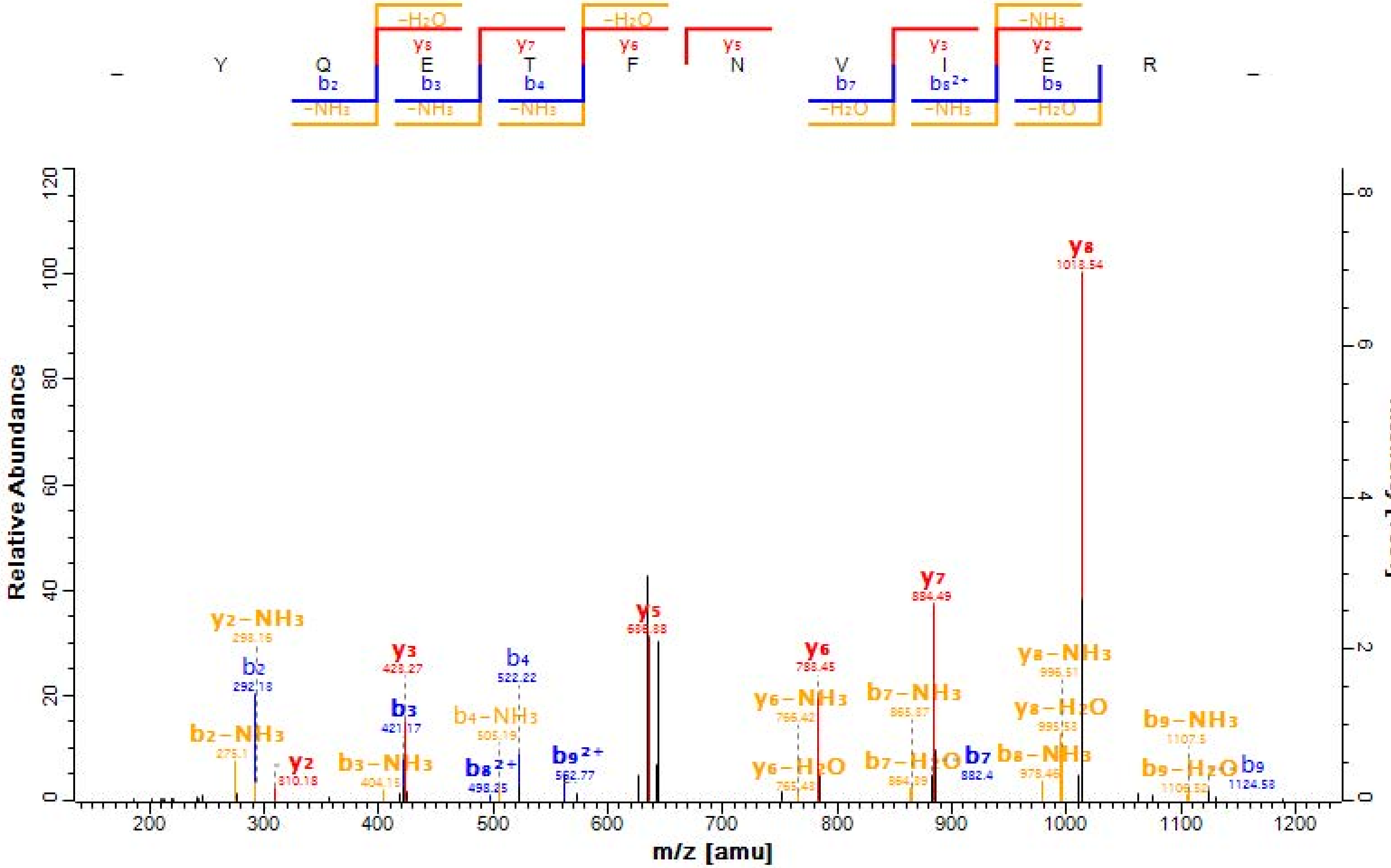


precursor information

Mass:	950.46492
m/z:	476.23974
Charge:	2+
Retentiontime:	22.825452804565
Score:	111.9471
Mass Error [ppm]:	0.56099
PEP:	0.0046044
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	60 %
Peak Coverage:	14 %
Protein Localisation:	153 ... 160

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	7				
	274.12	-0.028	274.12	2	C	6	838.39	+0.0245	419.7	-0.015
	389.15		389.15	3	D	5	678.36	+0.0232	678.36	
	536.22	+0.0718	536.22	4	F	4	563.33	+0.0615	563.33	
	593.24	+0.099	593.24	5	G	3	416.26	+0.0839	416.26	
	706.32	+0.1813	706.32	6	L	2	359.24	+0.1074	359.24	
-0.015	389.18	-0.004	777.36	7	A	1	246.16	+0.0094	246.16	
				8	R	0	175.12	+0.0501	175.12	

Scan number	3853	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti…**	174.77

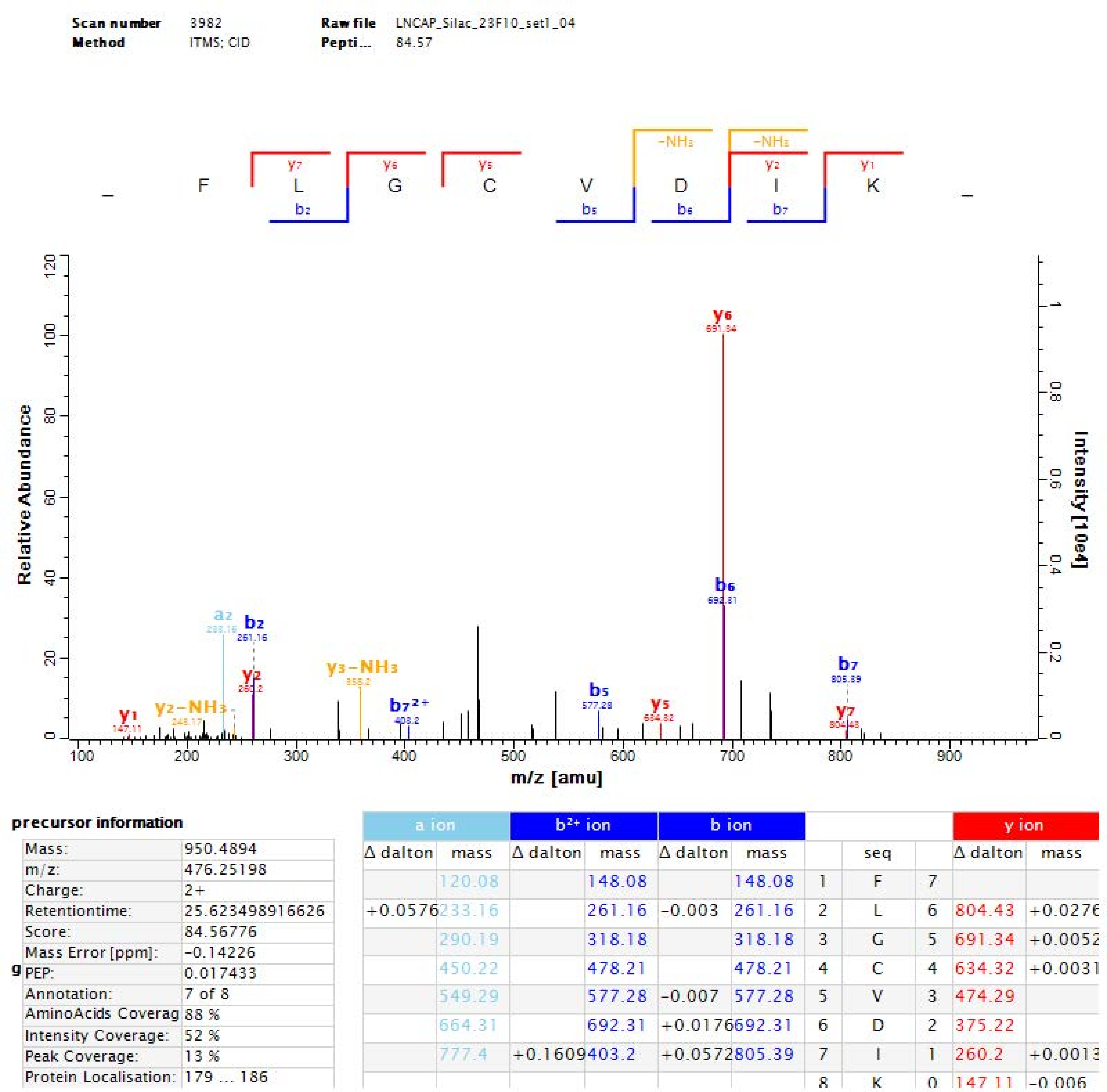


precursor information

Mass:	1297.62999
m/z:	649.82227
Charge:	2+
Retentiontime:	25.002014160156
Score:	174.7679
Mass Error [ppm]:	-0.20838
PEP:	6.9005E-06
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	62 %
Peak Coverage:	36 %
Protein Localisation:	149 … 158

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	164.0706		164.0706	1	Y	9		
	292.1292	-0.03012	292.1292	2	Q	8	1141.594	
	421.1718	+0.070839	421.1718	3	E	7	1013.536	-0.03528
	522.2195	+0.032743	522.2195	4	T	6	884.4932	+0.040336
	669.2879		669.2879	5	F	5	783.4455	-0.04303
	783.3308		783.3308	6	N	4	636.3771	-0.09003
	882.3992	-0.04563	882.3992	7	V	3	522.3342	
-0.28122	498.2453		995.4833	8	I	2	423.2657	+0.125619
+0.340423	562.7666	-0.40087	1124.526	9	E	1	310.1817	+0.075528
				10	R	0	181.1391	

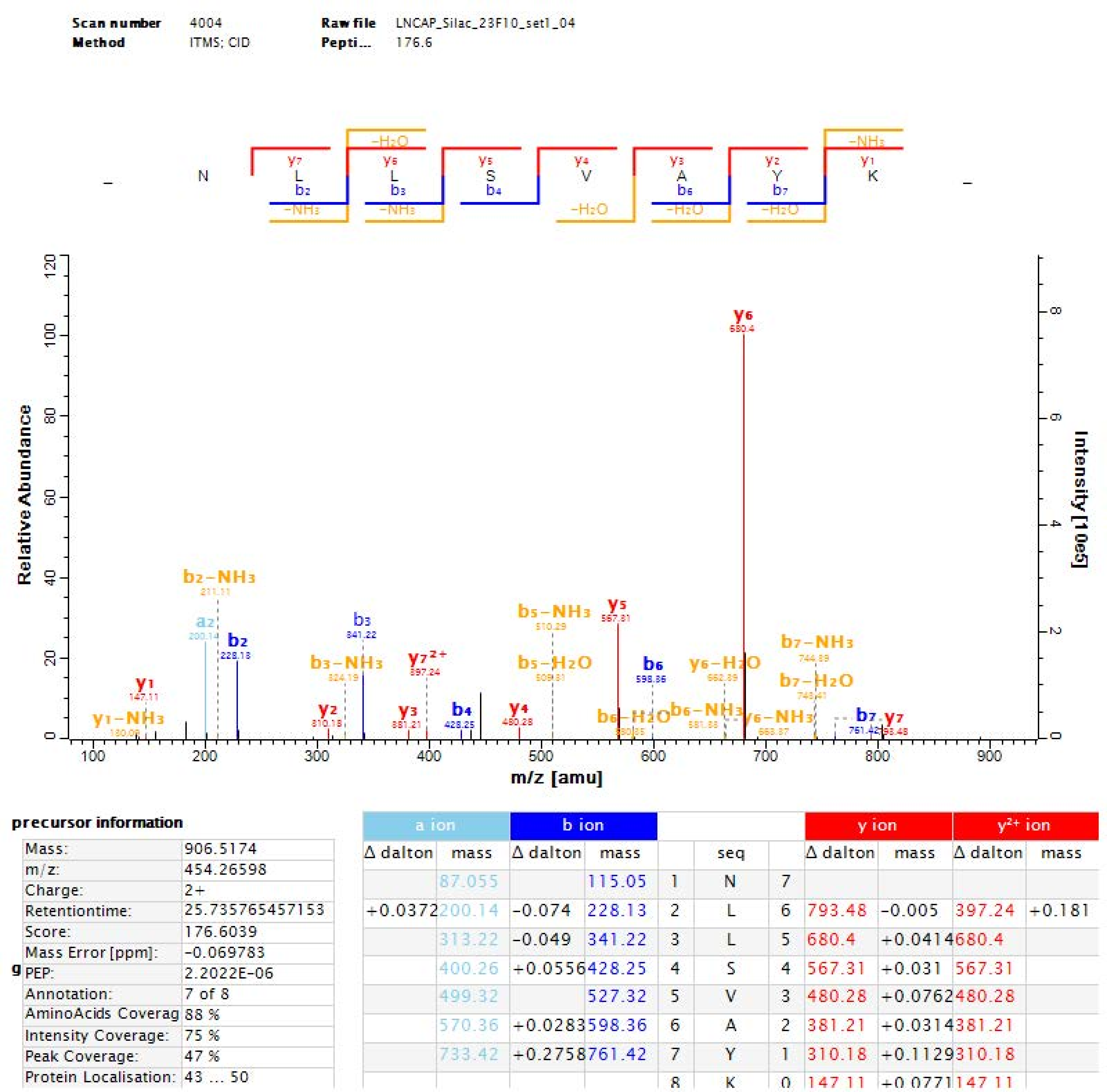


Scan number	3982	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	84.57

precursor information

Mass:	950.4894
m/z:	476.25198
Charge:	2+
Retentiontime:	25.623498916626
Score:	84.56776
Mass Error [ppm]:	-0.14226
PEP:	0.017433
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	52 %
Peak Coverage:	13 %
Protein Localisation:	179 ... 186

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	120.08		148.08		148.08	1	F	7		
+0.0576	233.16		261.16	-0.003	261.16	2	L	6	804.43	+0.0276
	290.19		318.18		318.18	3	G	5	691.34	+0.0052
	450.22		478.21		478.21	4	C	4	634.32	+0.0031
	549.29		577.28	-0.007	577.28	5	V	3	474.29	
	664.31		692.31	+0.0176	692.31	6	D	2	375.22	
	777.4	+0.1609	403.2	+0.0572	805.39	7	I	1	260.2	+0.0013
						8	K	0	147.11	-0.006



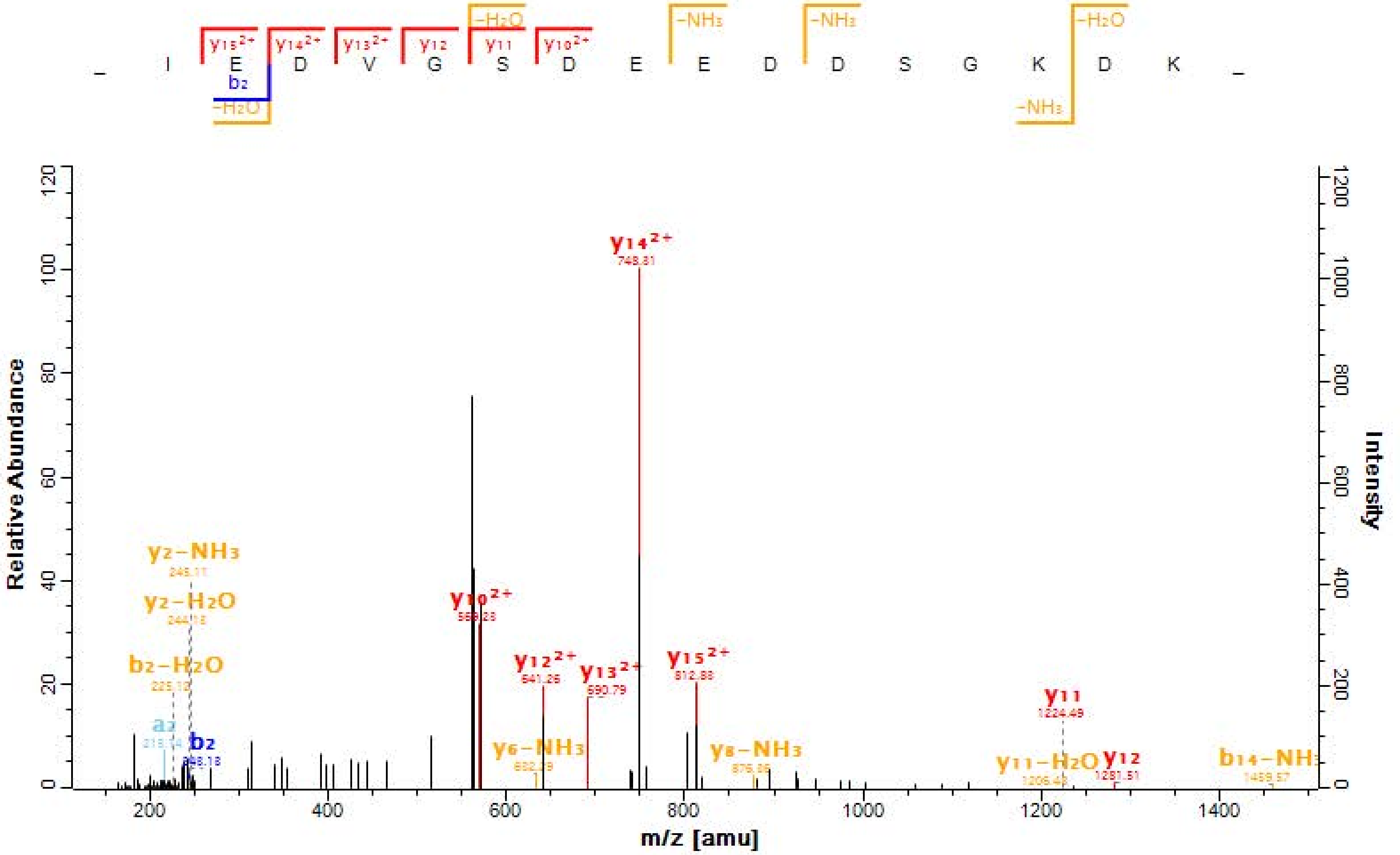
Scan number	4004	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	176.6

precursor information

Mass:	906.5174
m/z:	454.26598
Charge:	2+
Retentiontime:	25.735765457153
Score:	176.6039
Mass Error [ppm]:	-0.069783
PEP:	2.2022E-06
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	75 %
Peak Coverage:	47 %
Protein Localisation:	43 ... 50

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	87.055		115.05	1	N	7				
+0.0372	200.14	-0.074	228.13	2	L	6	793.48	-0.005	397.24	+0.181
	313.22	-0.049	341.22	3	L	5	680.4	+0.0414	680.4	
	400.26	+0.0556	428.25	4	S	4	567.31	+0.031	567.31	
	499.32		527.32	5	V	3	480.28	+0.0762	480.28	
	570.36	+0.0283	598.36	6	A	2	381.21	+0.0314	381.21	
	733.42	+0.2758	761.42	7	Y	1	310.18	+0.1129	310.18	
				8	K	0	147.11	+0.0771	147.11	

Scan number	402	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	39.51



precursor information

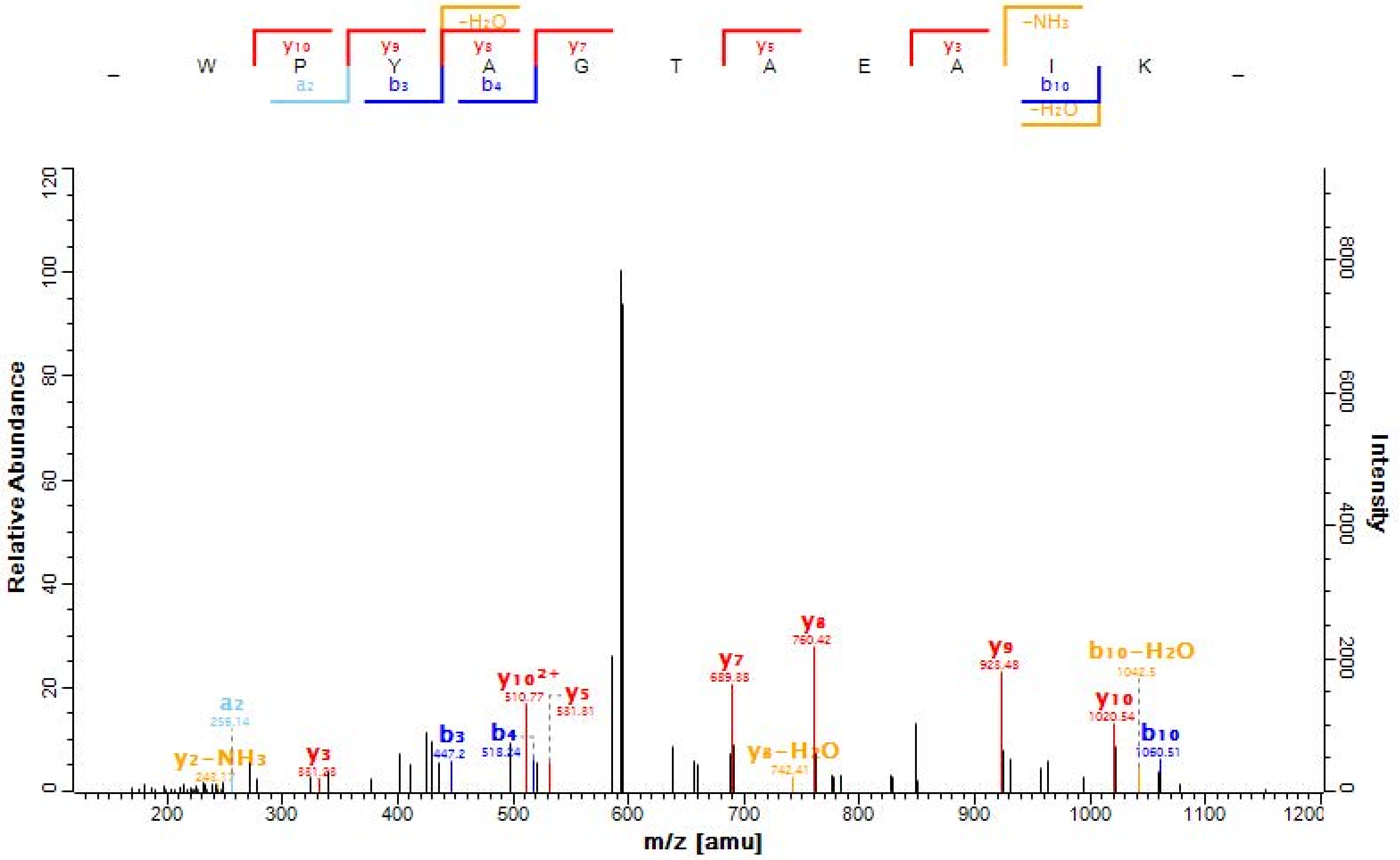
Mass:	1736.72133
m/z:	579.91439
Charge:	3+
Retentiontime:	7.2645649909973
Score:	39.509
Mass Error [ppm]:	-0.64426
PEP:	0.032174
Precursor Type:	MULTI

general information

Annotation:	10 of 16
AminoAcids Coverag	62 %
Intensity Coverage:	31 %
Peak Coverage:	13 %
Protein Localisation:	250 ... 265

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	15				
+0.1127	215.14	+0.0468	243.13	2	E	14	1624.6		812.83	-0.08
	330.17		358.16	3	D	13	1495.6		748.31	+0.0233
	429.23		457.23	4	V	12	1380.6		690.79	+0.3761
	486.26		514.25	5	G	11	1281.5	+0.1719	641.26	+0.0289
	573.29		601.28	6	S	10	1224.5	+0.3935	1224.5	
	688.31		716.31	7	D	9	1137.5		569.23	+0.4486
	817.36		845.35	8	E	8	1022.4		1022.4	
	946.4		974.39	9	E	7	893.38		893.38	
	1061.4		1089.4	10	D	6	764.34		764.34	
	1176.5		1204.4	11	D	5	649.32		649.32	
	1263.5		1291.5	12	S	4	534.29		534.29	
	1320.5		1348.5	13	G	3	447.26		447.26	
	1448.6		1476.6	14	K	2	390.23		390.23	
	1563.6		1591.6	15	D	1	262.14		262.14	
				16	K	0	147.11		147.11	

Scan number	4052	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	72.2



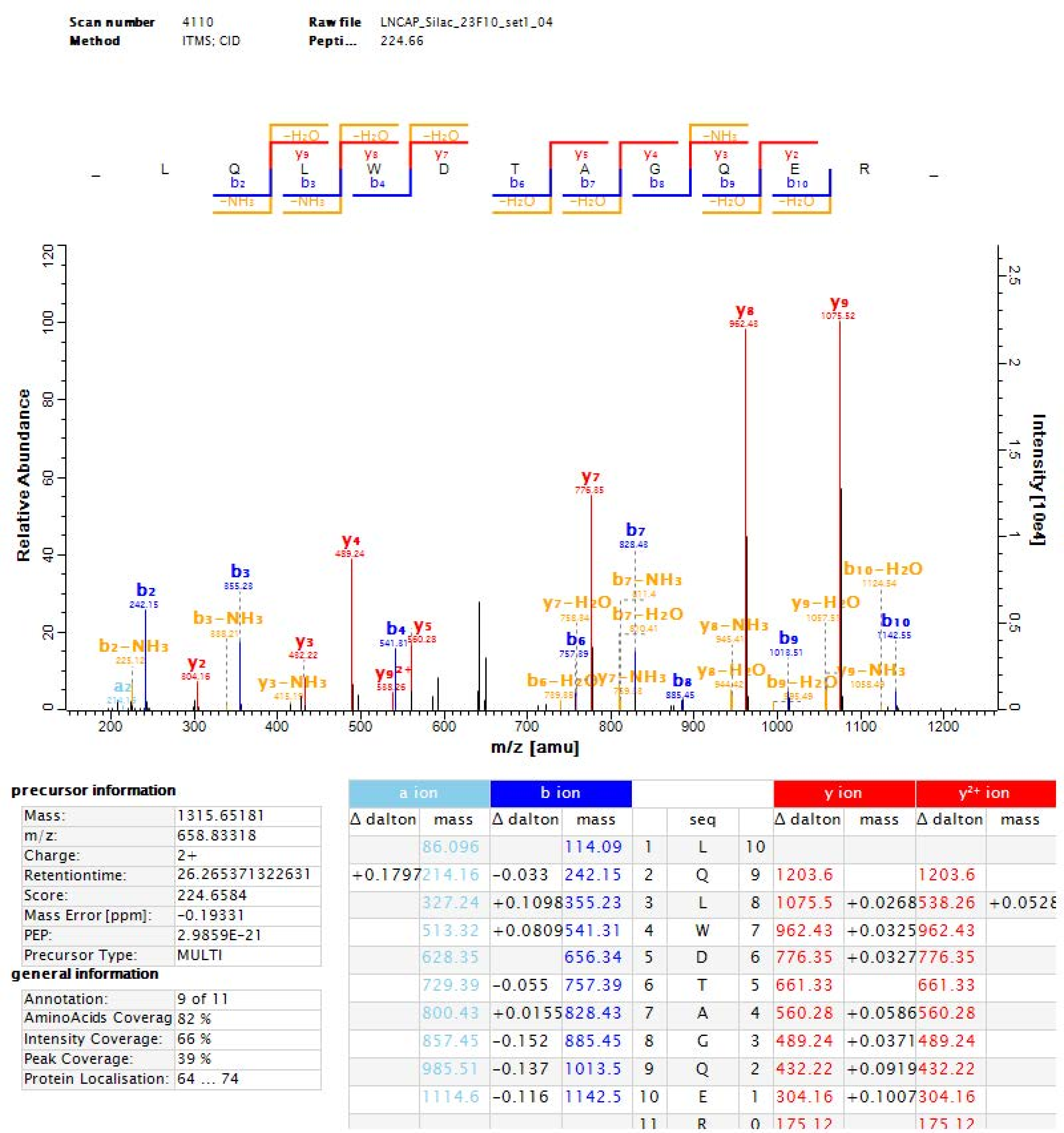
precursor information

Mass:	1205.60766
m/z:	603.81111
Charge:	2+
Retentiontime:	25.972467422485
Score:	72.20042
Mass Error [ppm]:	-0.34535
PEP:	0.0052933
Precursor Type:	MULTI

general information

Annotation:	7 of 11
AminoAcids Coverag	64 %
Intensity Coverage:	23 %
Peak Coverage:	15 %
Protein Localisation:	204 ... 214

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	159.09		187.09	1	W	10				
-0.019	256.14		284.14	2	P	9	1020.5	-0.057	510.77	+0.1427
	419.21	+0.0164	447.2	3	Y	8	923.48	+0.0114	923.48	
	490.24	+0.1446	518.24	4	A	7	760.42	+0.0649	760.42	
	547.27		575.26	5	G	6	689.38	+0.0777	689.38	
	648.31		676.31	6	T	5	632.36		632.36	
	719.35		747.35	7	A	4	531.31	+0.0515	531.31	
	848.39		876.39	8	E	3	460.28		460.28	
	919.43		947.43	9	A	2	331.23	+0.1187	331.23	
	1032.5	+0.1574	1060.5	10	I	1	260.2		260.2	
				11	K	0	147.11		147.11	



Scan number	4110	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	224.66

precursor information

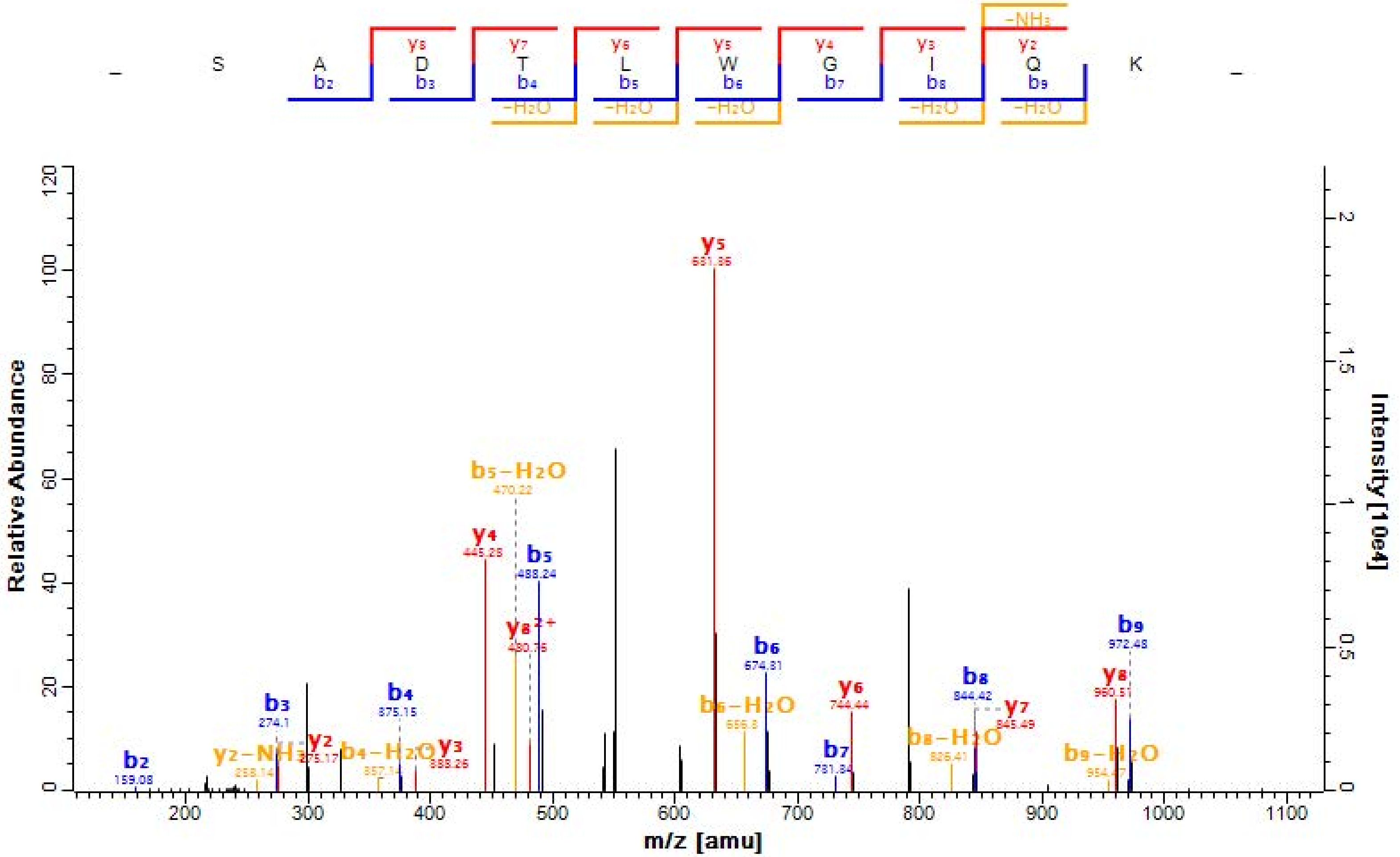
Mass:	1315.65181
m/z:	658.83318
Charge:	2+
Retentiontime:	26.265371322631
Score:	224.6584
Mass Error [ppm]:	-0.19331
PEP:	2.9859E-21
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	66 %
Peak Coverage:	39 %
Protein Localisation:	64 ... 74

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	10				
+0.1797	214.16	-0.033	242.15	2	Q	9	1203.6		1203.6	
	327.24	+0.1098	355.23	3	L	8	1075.5	+0.0268	538.26	+0.052
	513.32	+0.0809	541.31	4	W	7	962.43	+0.0325	962.43	
	628.35		656.34	5	D	6	776.35	+0.0327	776.35	
	729.39	-0.055	757.39	6	T	5	661.33		661.33	
	800.43	+0.0155	828.43	7	A	4	560.28	+0.0586	560.28	
	857.45	-0.152	885.45	8	G	3	489.24	+0.0371	489.24	
	985.51	-0.137	1013.5	9	Q	2	432.22	+0.0919	432.22	
	1114.6	-0.116	1142.5	10	E	1	304.16	+0.1007	304.16	
				11	R	0	175.12		175.12	

Scan number	4425	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	151.22



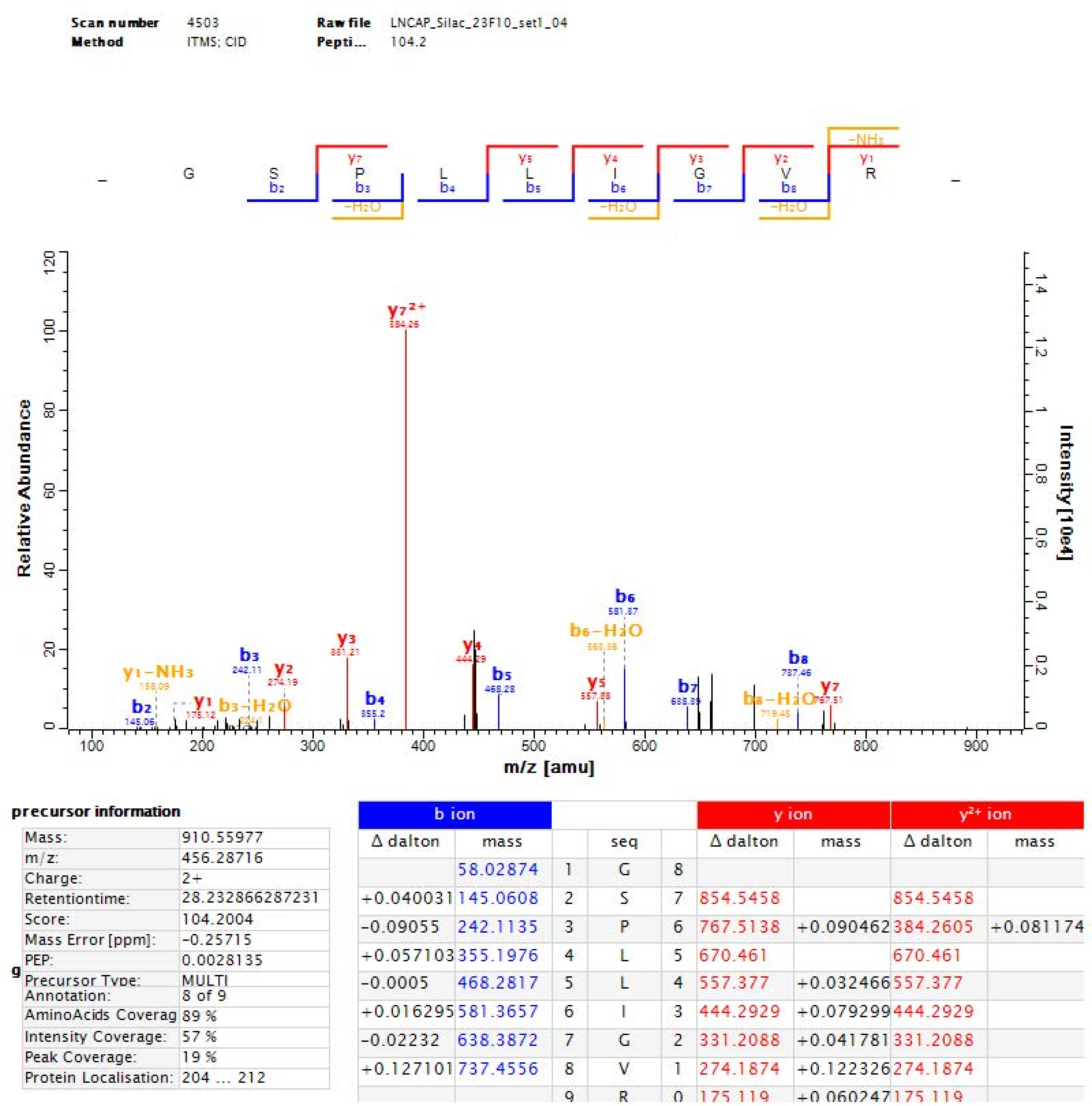
precursor information

Mass:	1117.57686
m/z:	559.7957
Charge:	2+
Retentiontime:	27.856187820434
Score:	151.2159
Mass Error [ppm]:	0.074509
PEP:	1.1767E-09
Precursor Type:	ISO

g

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	52 %
Peak Coverage:	27 %
Protein Localisation:	348 ... 357

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	9				
-0.10614	159.0764	2	A	8	1031.552		1031.552	
+0.072786	274.1034	3	D	7	960.5149	-0.03084	480.7611	+0.060929
+0.037375	375.151	4	T	6	845.488	+0.094127	845.488	
-0.01892	488.2351	5	L	5	744.4403	+0.043051	744.4403	
+0.036596	674.3144	6	W	4	631.3562	+0.007059	631.3562	
+0.082149	731.3359	7	G	3	445.2769	+0.044624	445.2769	
-0.00051	844.4199	8	I	2	388.2554	+0.075426	388.2554	
-0.10621	972.4785	9	Q	1	275.1714	+0.081548	275.1714	
		10	K	0	147.1128		147.1128	



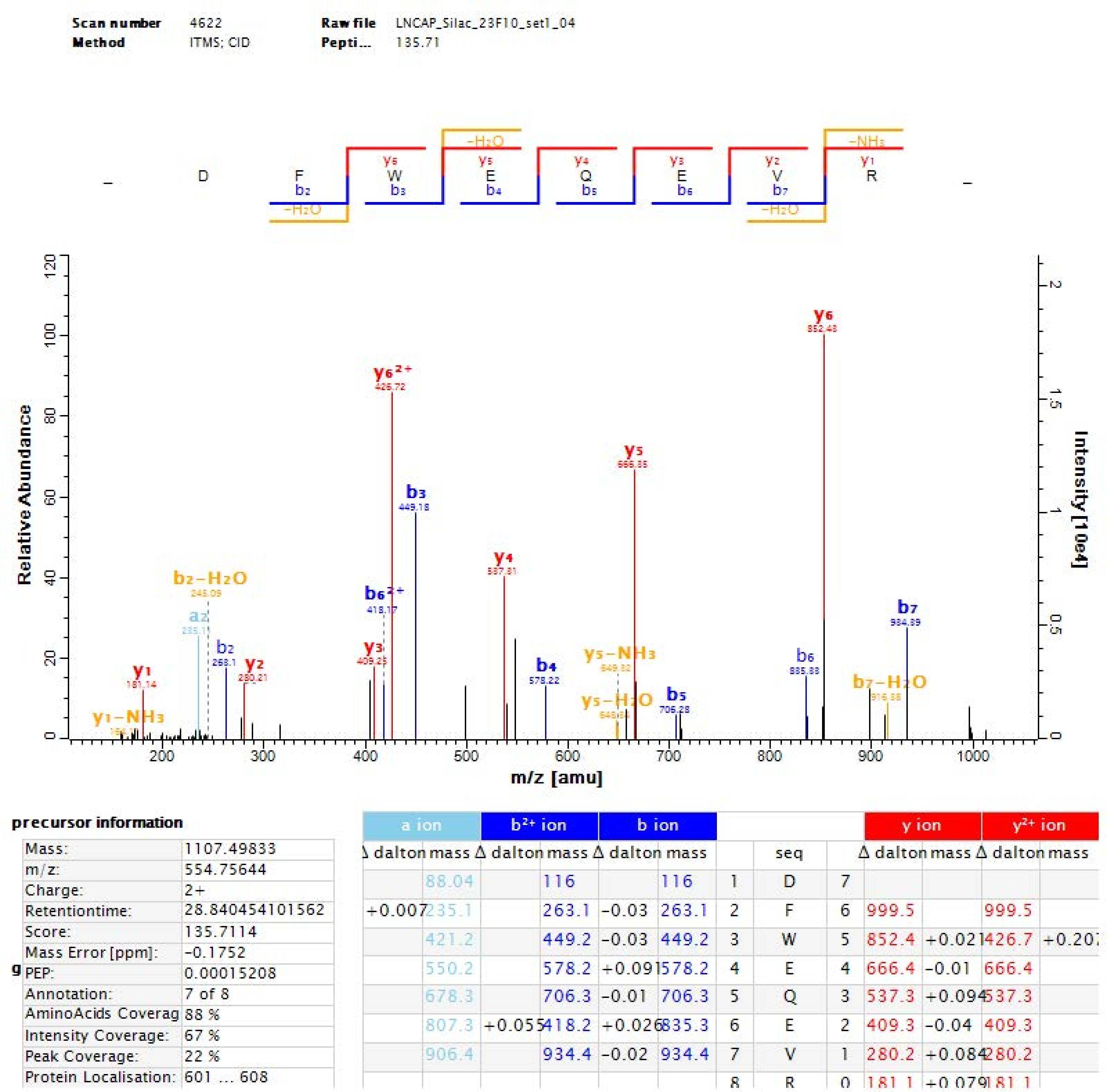
Scan number	4503	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	104.2

precursor information

g

Mass:	910.55977
m/z:	456.28716
Charge:	2+
Retentiontime:	28.232866287231
Score:	104.2004
Mass Error [ppm]:	-0.25715
PEP:	0.0028135
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	57 %
Peak Coverage:	19 %
Protein Localisation:	204 ... 212

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	8				
+0.040031	145.0608	2	S	7	854.5458		854.5458	
-0.09055	242.1135	3	P	6	767.5138	+0.090462	384.2605	+0.081174
+0.057103	355.1976	4	L	5	670.461		670.461	
-0.0005	468.2817	5	L	4	557.377	+0.032466	557.377	
+0.016295	581.3657	6	I	3	444.2929	+0.079299	444.2929	
-0.02232	638.3872	7	G	2	331.2088	+0.041781	331.2088	
+0.127101	737.4556	8	V	1	274.1874	+0.122326	274.1874	
		9	R	0	175.119	+0.060247	175.119	



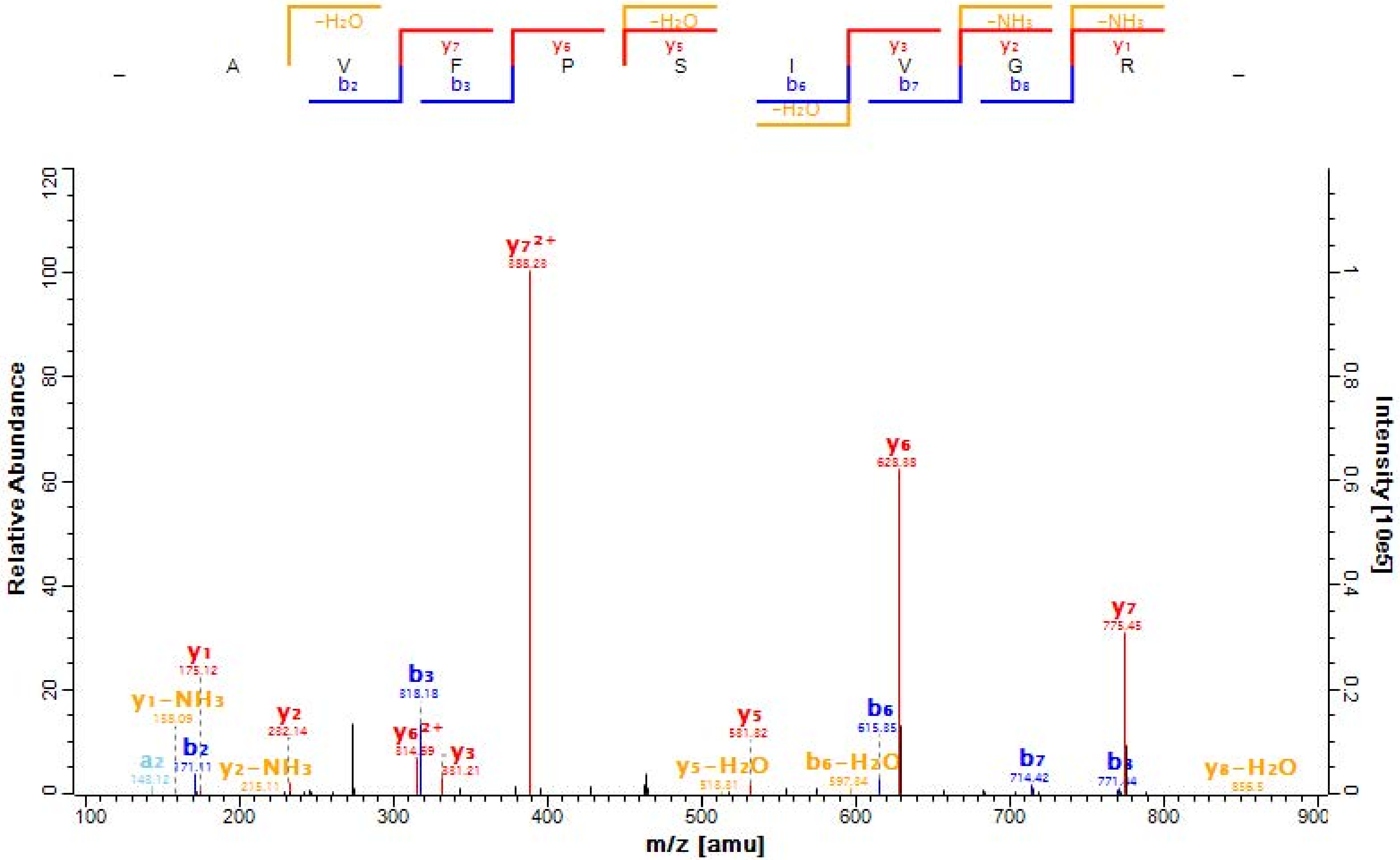
Scan number 4622
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set1_04
Pepti... 135.71

precursor information

Mass:	1107.49833
m/z:	554.75644
Charge:	2+
Retentiontime:	28.840454101562
Score:	135.7114
Mass Error [ppm]:	-0.1752
PEP:	0.00015208
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	67 %
Peak Coverage:	22 %
Protein Localisation:	601 ... 608

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.04		116		116	1	D	7				
+0.007	235.1		263.1	-0.03	263.1	2	F	6	999.5		999.5	
	421.2		449.2	-0.03	449.2	3	W	5	852.4	+0.021	426.7	+0.20
	550.2		578.2	+0.091	578.2	4	E	4	666.4	-0.01	666.4	
	678.3		706.3	-0.01	706.3	5	Q	3	537.3	+0.094	537.3	
	807.3	+0.055	418.2	+0.026	835.3	6	E	2	409.3	-0.04	409.3	
	906.4		934.4	-0.02	934.4	7	V	1	280.2	+0.084	280.2	
						8	R	0	181.1	+0.079	181.1	

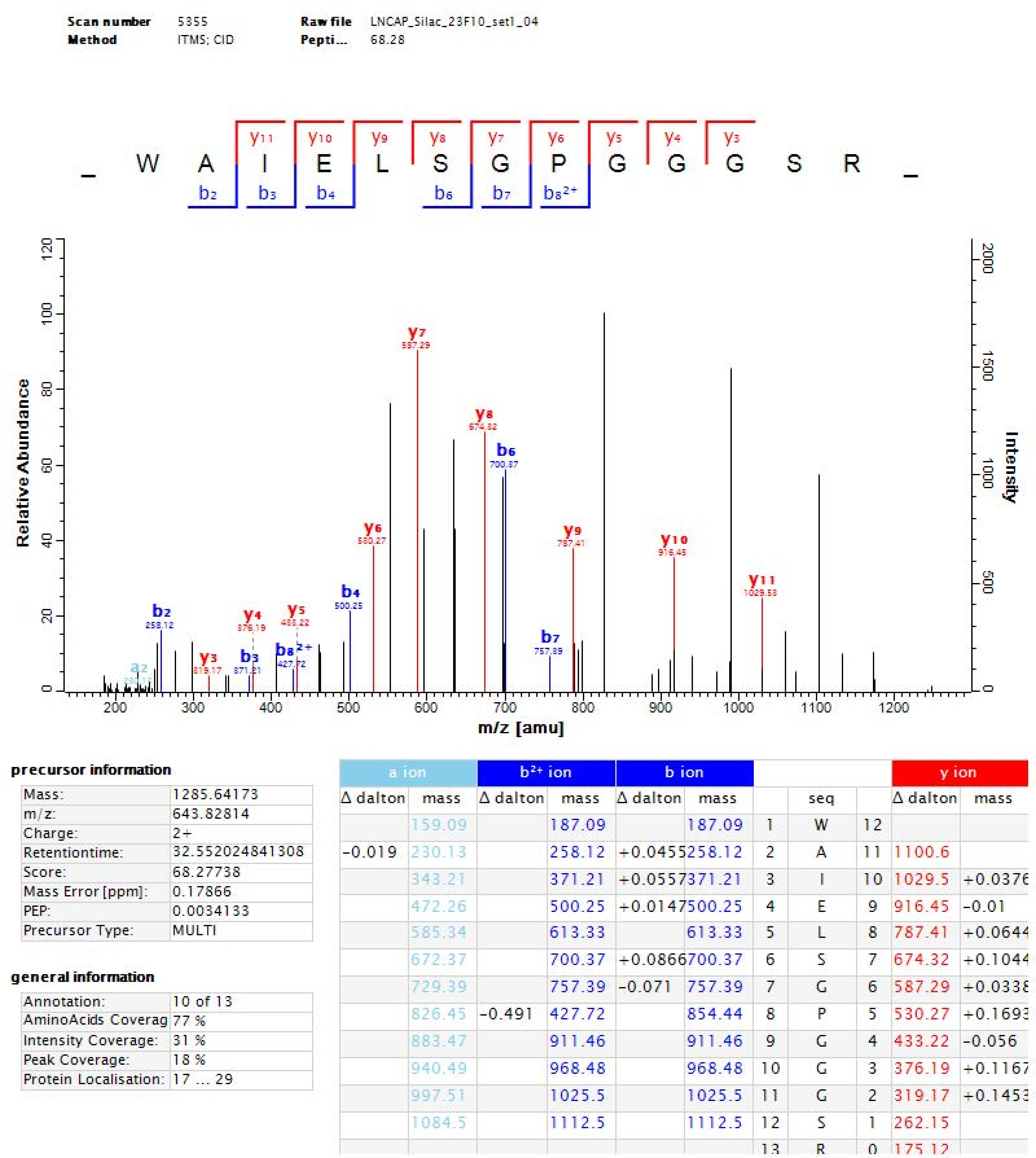
Scan number	4847	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	124.23



precursor information

Mass:	944.5443
m/z:	473.27943
Charge:	2+
Retentiontime:	29.979841232299
Score:	124.2303
Mass Error [ppm]:	-0.050586
PEP:	0.0012377
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	80 %
Peak Coverage:	26 %
Protein Localisation:	29 ... 37

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	44.049		72.044	1	A	8				
+0.0275	143.12	+0.0154	171.11	2	V	7	874.51		874.51	
	290.19	+0.0279	318.18	3	F	6	775.45	+0.0252	388.23	+0.1519
	387.24		415.23	4	P	5	628.38	+0.0522	314.69	+0.223
	474.27		502.27	5	S	4	531.32	+0.0569	531.32	
	587.36	+0.0148	615.35	6	I	3	444.29		444.29	
	686.42	+0.0506	714.42	7	V	2	331.21	+0.1203	331.21	
	743.45	+0	771.44	8	G	1	232.14	+0.0686	232.14	
				9	R	0	175.12	-0.014	175.12	



Scan number	5355	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	68.28

precursor information

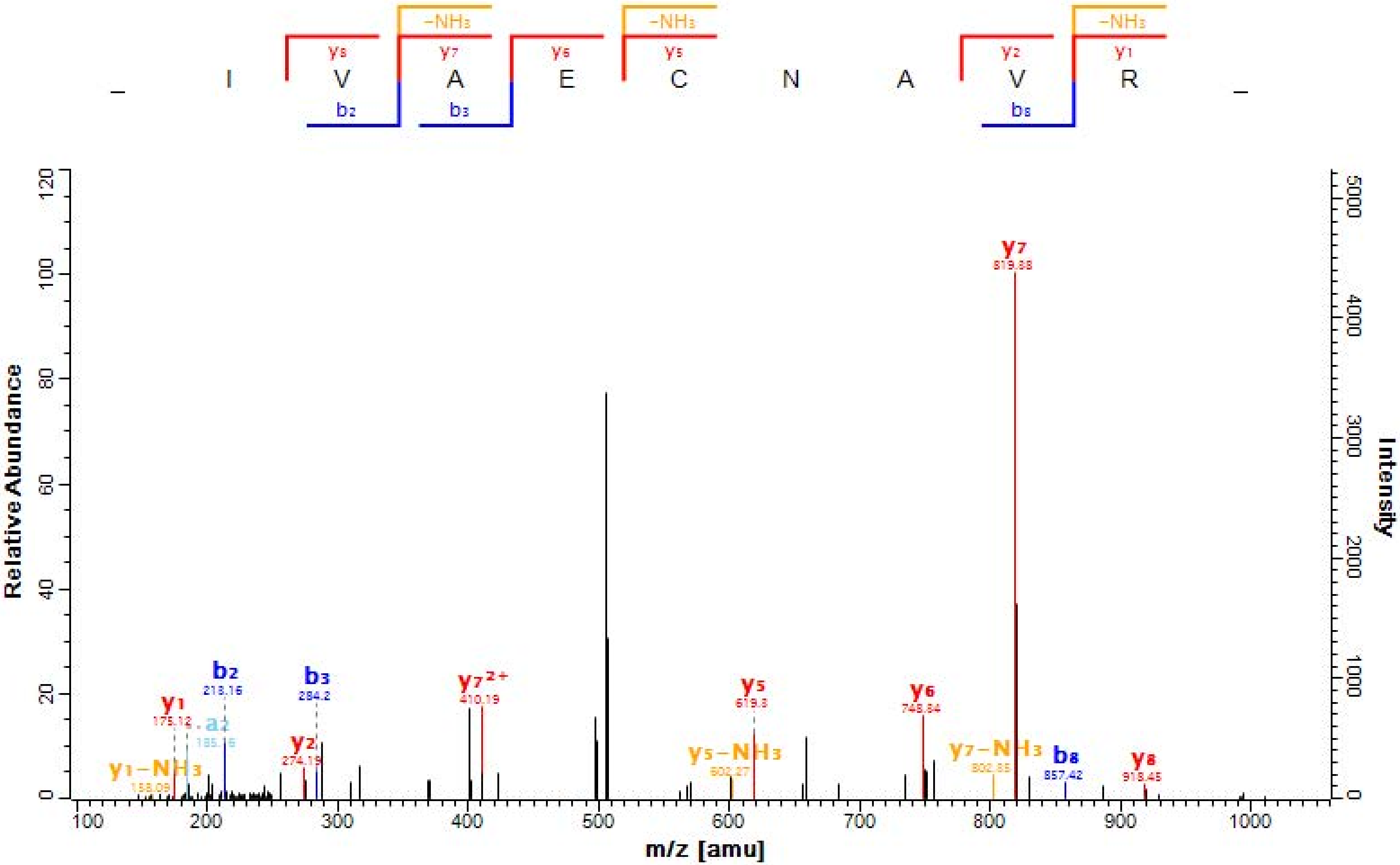
Mass:	1285.64173
m/z:	643.82814
Charge:	2+
Retentiontime:	32.552024841308
Score:	68.27738
Mass Error [ppm]:	0.17866
PEP:	0.0034133
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	31 %
Peak Coverage:	18 %
Protein Localisation:	17 … 29

a ion		b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	159.09		187.09		187.09	1	W	12		
-0.019	230.13		258.12	+0.0455	258.12	2	A	11	1100.6	
	343.21		371.21	+0.0557	371.21	3	I	10	1029.5	+0.0376
	472.26		500.25	+0.0147	500.25	4	E	9	916.45	-0.01
	585.34		613.33		613.33	5	L	8	787.41	+0.0644
	672.37		700.37	+0.0866	700.37	6	S	7	674.32	+0.1044
	729.39		757.39	-0.071	757.39	7	G	6	587.29	+0.0338
	826.45	-0.491	427.72		854.44	8	P	5	530.27	+0.1693
	883.47		911.46		911.46	9	G	4	433.22	-0.056
	940.49		968.48		968.48	10	G	3	376.19	+0.1167
	997.51		1025.5		1025.5	11	G	2	319.17	+0.1453
	1084.5		1112.5		1112.5	12	S	1	262.15	
						13	R	0	175.12	

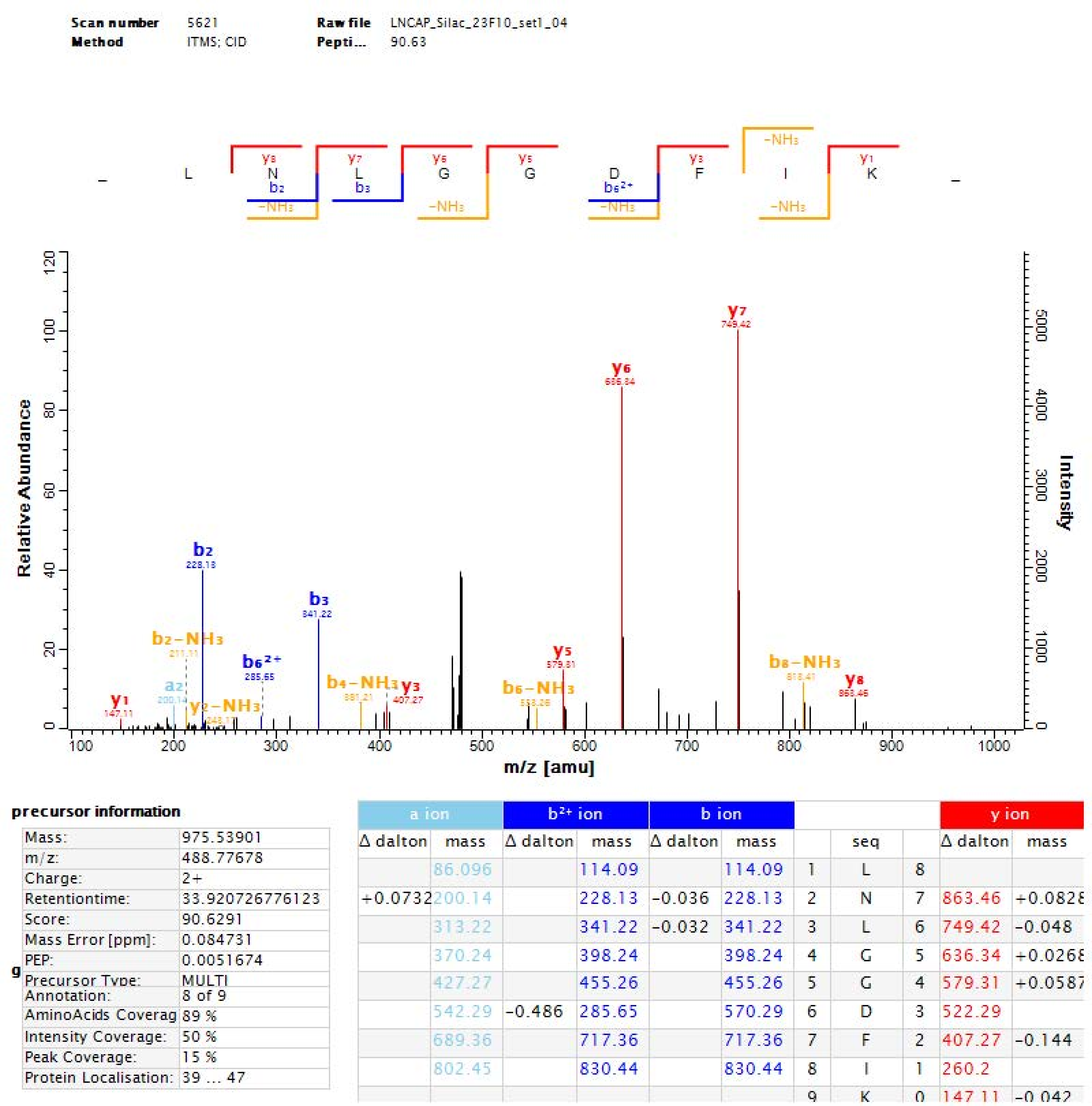
Scan number	548	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	97.43



precursor information

Mass:	1030.52303
m/z:	516.26879
Charge:	2+
Retentiontime:	8.1562929153442
Score:	97.43056
Mass Error [ppm]:	0.063135
PEP:	0.0039453
Precursor Type:	MULTI
Annotation:	6 of 9
AminoAcids Coverag	67 %
Intensity Coverage:	34 %
Peak Coverage:	12 %
Protein Localisation:	333 ... 341

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	8				
+0.0248	185.16	-0.041	213.16	2	V	7	918.45	+0.0118	918.45	
	256.2	-0.094	284.2	3	A	6	819.38	+0.0053	410.19	+0.004
	385.24		413.24	4	E	5	748.34	+0.0278	748.34	
	545.28		573.27	5	C	4	619.3	+0.0693	619.3	
	659.32		687.31	6	N	3	459.27		459.27	
	730.36		758.35	7	A	2	345.22		345.22	
	829.42	-0.097	857.42	8	V	1	274.19	-0.004	274.19	
				9	R	0	175.12	+0.0633	175.12	



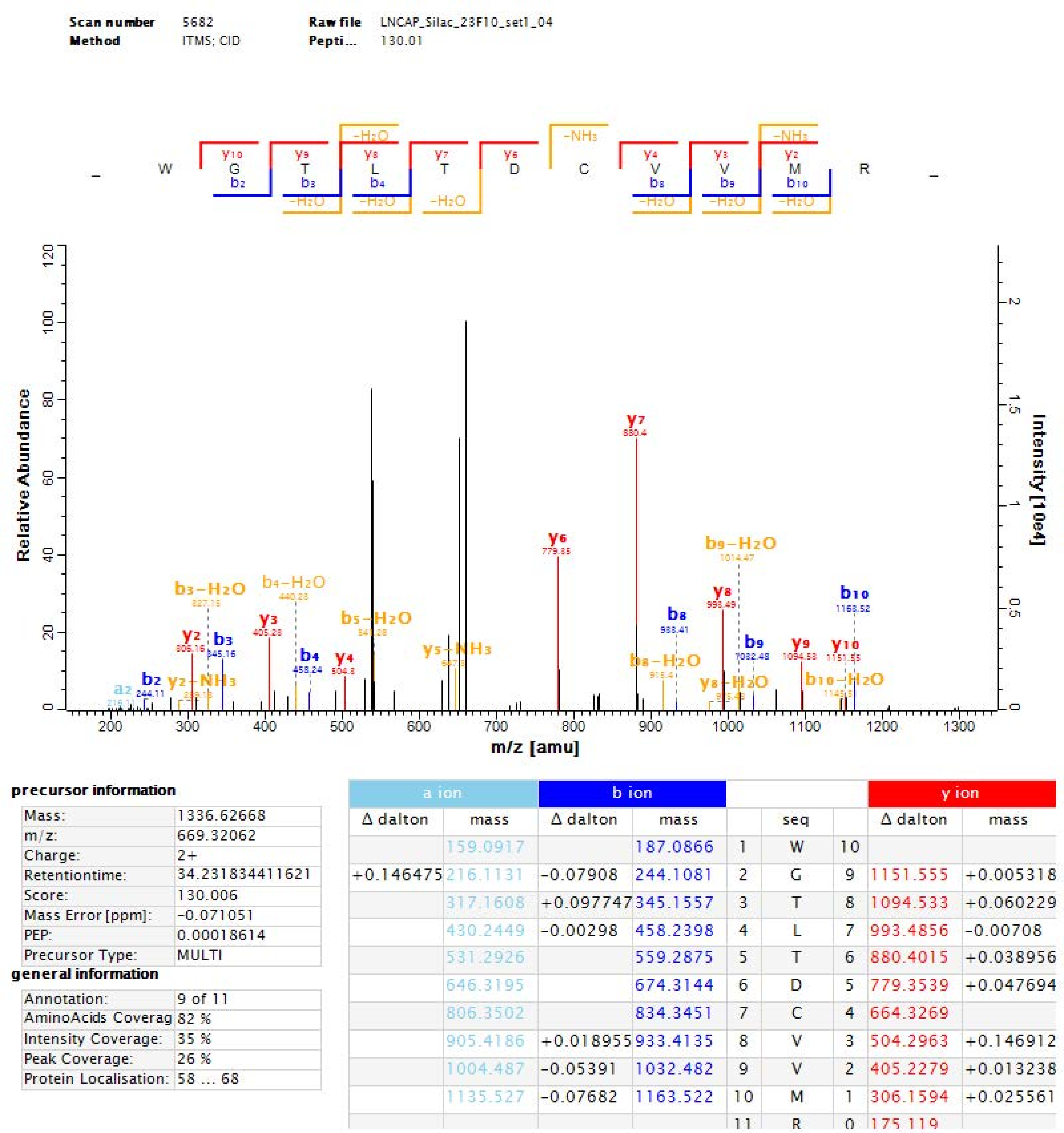
Scan number	5621	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	90.63

precursor information

Mass:	975.53901
m/z:	488.77678
Charge:	2+
Retentiontime:	33.920726776123
Score:	90.6291
Mass Error [ppm]:	0.084731
PEP:	0.0051674
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	50 %
Peak Coverage:	15 %
Protein Localisation:	39 ... 47

g

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	86.096		114.09		114.09	1	L	8		
+0.0732	200.14		228.13	−0.036	228.13	2	N	7	863.46	+0.082
	313.22		341.22	−0.032	341.22	3	L	6	749.42	−0.048
	370.24		398.24		398.24	4	G	5	636.34	+0.026
	427.27		455.26		455.26	5	G	4	579.31	+0.0587
	542.29	−0.486	285.65		570.29	6	D	3	522.29	
	689.36		717.36		717.36	7	F	2	407.27	−0.144
	802.45		830.44		830.44	8	I	1	260.2	
						9	K	0	147.11	−0.042



Scan number	5682	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	130.01

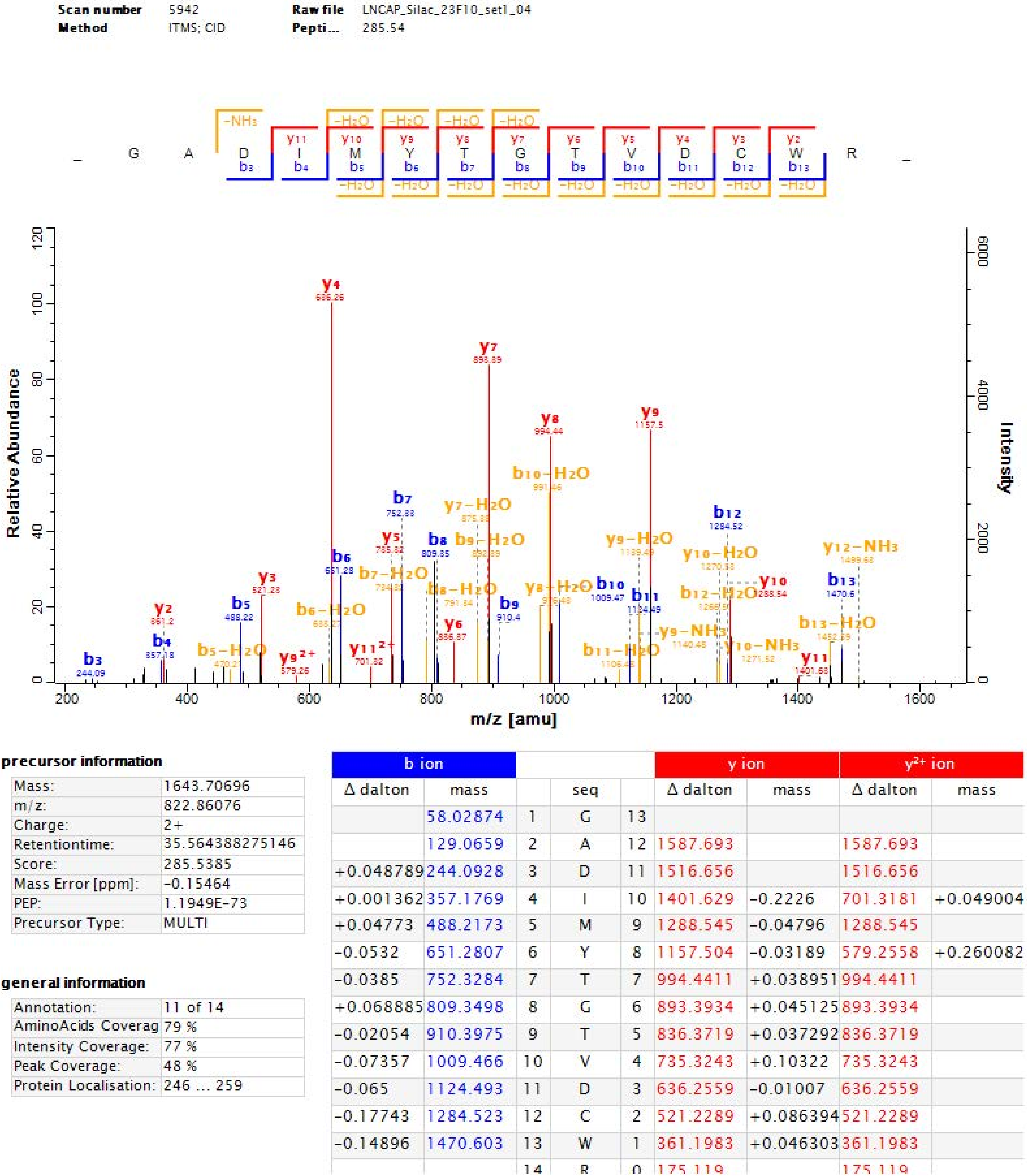
precursor information

Mass:	1336.62668
m/z:	669.32062
Charge:	2+
Retentiontime:	34.231834411621
Score:	130.006
Mass Error [ppm]:	-0.071051
PEP:	0.00018614
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	35 %
Peak Coverage:	26 %
Protein Localisation:	58 ... 68

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	159.0917		187.0866	1	W	10		
+0.146475	216.1131	-0.07908	244.1081	2	G	9	1151.555	+0.005318
	317.1608	+0.097747	345.1557	3	T	8	1094.533	+0.060229
	430.2449	-0.00298	458.2398	4	L	7	993.4856	-0.00708
	531.2926		559.2875	5	T	6	880.4015	+0.038956
	646.3195		674.3144	6	D	5	779.3539	+0.047694
	806.3502		834.3451	7	C	4	664.3269	
	905.4186	+0.018955	933.4135	8	V	3	504.2963	+0.146912
	1004.487	-0.05391	1032.482	9	V	2	405.2279	+0.013238
	1135.527	-0.07682	1163.522	10	M	1	306.1594	+0.025561
				11	R	0	175.119	



Scan number	5942	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	285.54

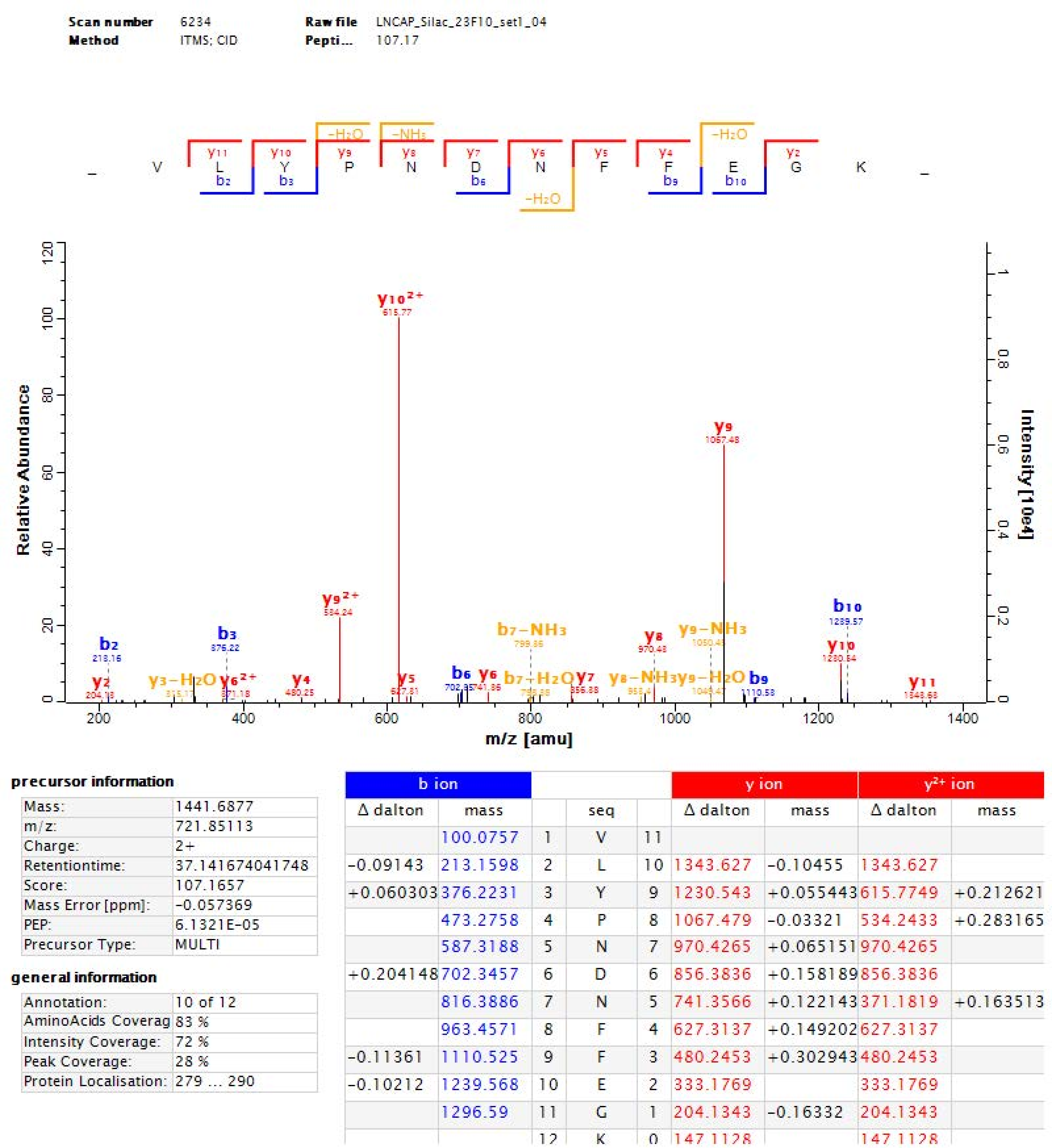
precursor information

Mass:	1643.70696
m/z:	822.86076
Charge:	2+
Retentiontime:	35.564388275146
Score:	285.5385
Mass Error [ppm]:	-0.15464
PEP:	1.1949E-73
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	77 %
Peak Coverage:	48 %
Protein Localisation:	246 ... 259

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	13				
	129.0659	2	A	12	1587.693		1587.693	
+0.048789	244.0928	3	D	11	1516.656		1516.656	
+0.001362	357.1769	4	I	10	1401.629	-0.2226	701.3181	+0.049004
+0.04773	488.2173	5	M	9	1288.545	-0.04796	1288.545	
-0.0532	651.2807	6	Y	8	1157.504	-0.03189	579.2558	+0.260082
-0.0385	752.3284	7	T	7	994.4411	+0.038951	994.4411	
+0.068885	809.3498	8	G	6	893.3934	+0.045125	893.3934	
-0.02054	910.3975	9	T	5	836.3719	+0.037292	836.3719	
-0.07357	1009.466	10	V	4	735.3243	+0.10322	735.3243	
-0.065	1124.493	11	D	3	636.2559	-0.01007	636.2559	
-0.17743	1284.523	12	C	2	521.2289	+0.086394	521.2289	
-0.14896	1470.603	13	W	1	361.1983	+0.046303	361.1983	
		14	R	0	175.119		175.119	



Scan number	6234	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	107.17

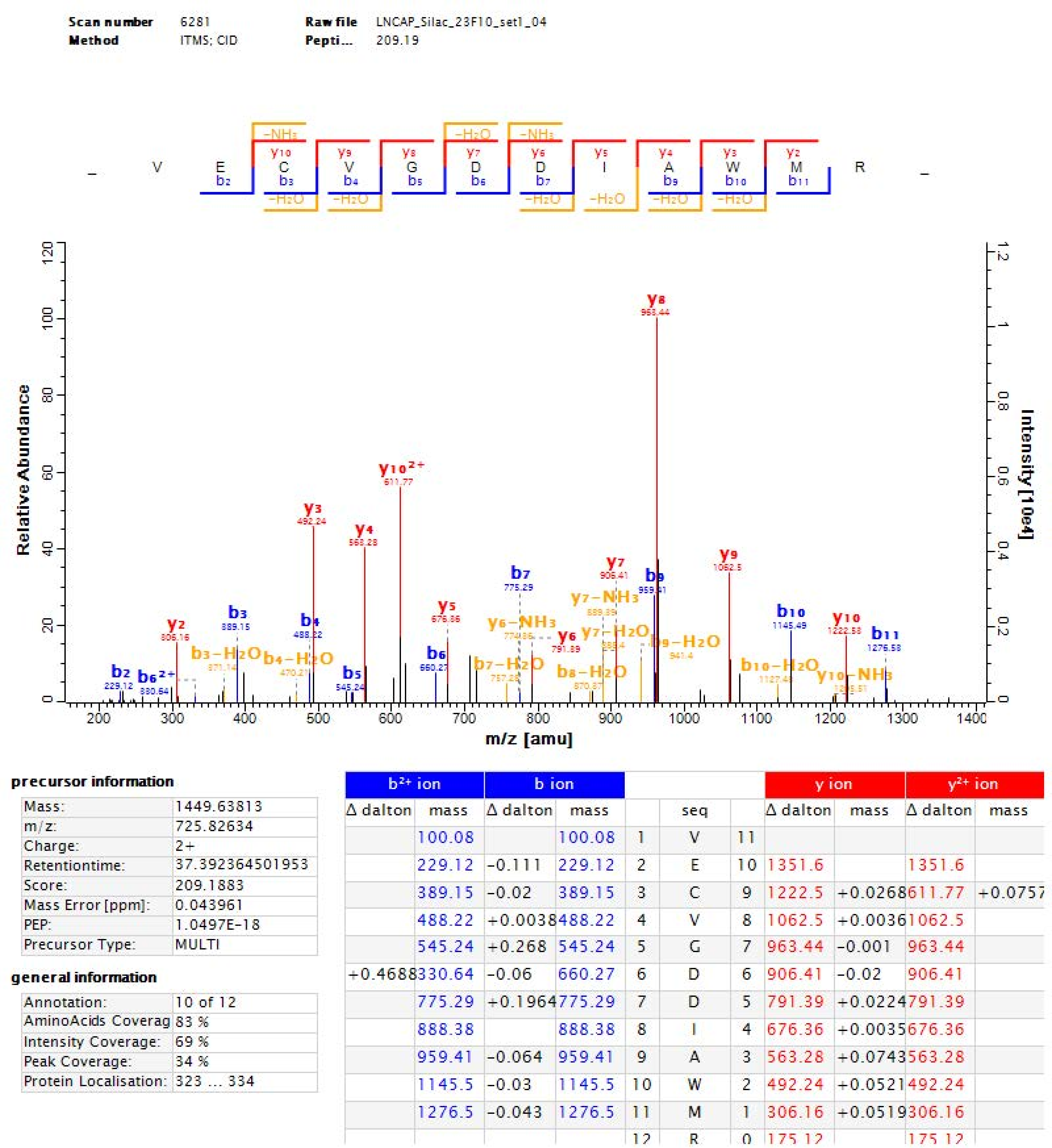
precursor information

Mass:	1441.6877
m/z:	721.85113
Charge:	2+
Retentiontime:	37.141674041748
Score:	107.1657
Mass Error [ppm]:	-0.057369
PEP:	6.1321E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	72 %
Peak Coverage:	28 %
Protein Localisation:	279 ... 290

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	11				
-0.09143	213.1598	2	L	10	1343.627	-0.10455	1343.627	
+0.060303	376.2231	3	Y	9	1230.543	+0.055443	615.7749	+0.212621
	473.2758	4	P	8	1067.479	-0.03321	534.2433	+0.283165
	587.3188	5	N	7	970.4265	+0.065151	970.4265	
+0.204148	702.3457	6	D	6	856.3836	+0.158189	856.3836	
	816.3886	7	N	5	741.3566	+0.122143	371.1819	+0.163513
	963.4571	8	F	4	627.3137	+0.149202	627.3137	
-0.11361	1110.525	9	F	3	480.2453	+0.302943	480.2453	
-0.10212	1239.568	10	E	2	333.1769		333.1769	
	1296.59	11	G	1	204.1343	-0.16332	204.1343	
		12	K	0	147.1128		147.1128	



Scan number	6281	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	209.19

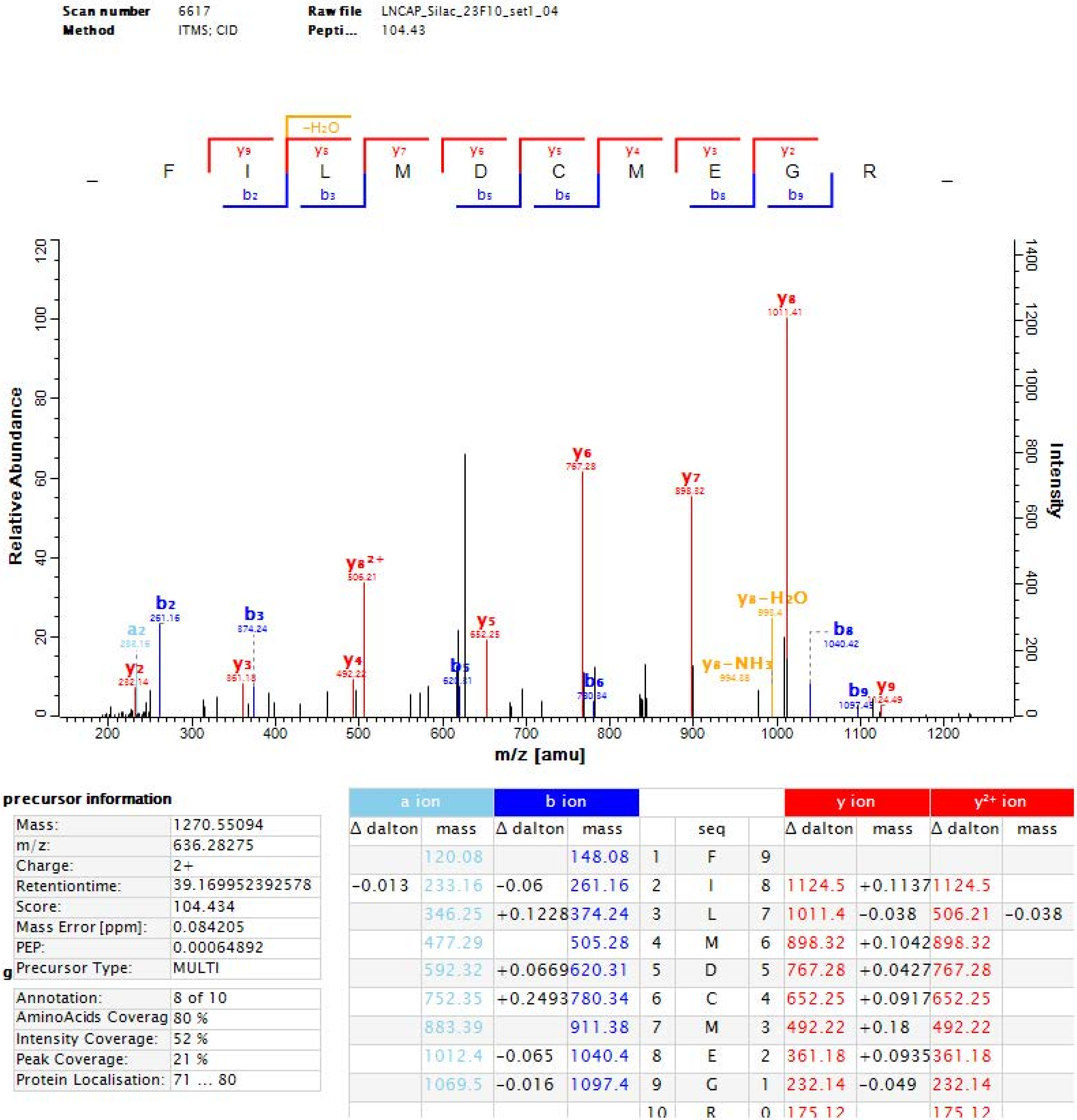
precursor information

Mass:	1449.63813
m/z:	725.82634
Charge:	2+
Retentiontime:	37.392364501953
Score:	209.1883
Mass Error [ppm]:	0.043961
PEP:	1.0497E-18
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	69 %
Peak Coverage:	34 %
Protein Localisation:	323 ... 334

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	11				
	229.12	-0.111	229.12	2	E	10	1351.6		1351.6	
	389.15	-0.02	389.15	3	C	9	1222.5	+0.0268	611.77	+0.0757
	488.22	+0.0038	488.22	4	V	8	1062.5	+0.0036	1062.5	
	545.24	+0.268	545.24	5	G	7	963.44	-0.001	963.44	
+0.4688	330.64	-0.06	660.27	6	D	6	906.41	-0.02	906.41	
	775.29	+0.1964	775.29	7	D	5	791.39	+0.0224	791.39	
	888.38		888.38	8	I	4	676.36	+0.0035	676.36	
	959.41	-0.064	959.41	9	A	3	563.28	+0.0743	563.28	
	1145.5	-0.03	1145.5	10	W	2	492.24	+0.0521	492.24	
	1276.5	-0.043	1276.5	11	M	1	306.16	+0.0519	306.16	
				12	R	0	175.12		175.12	



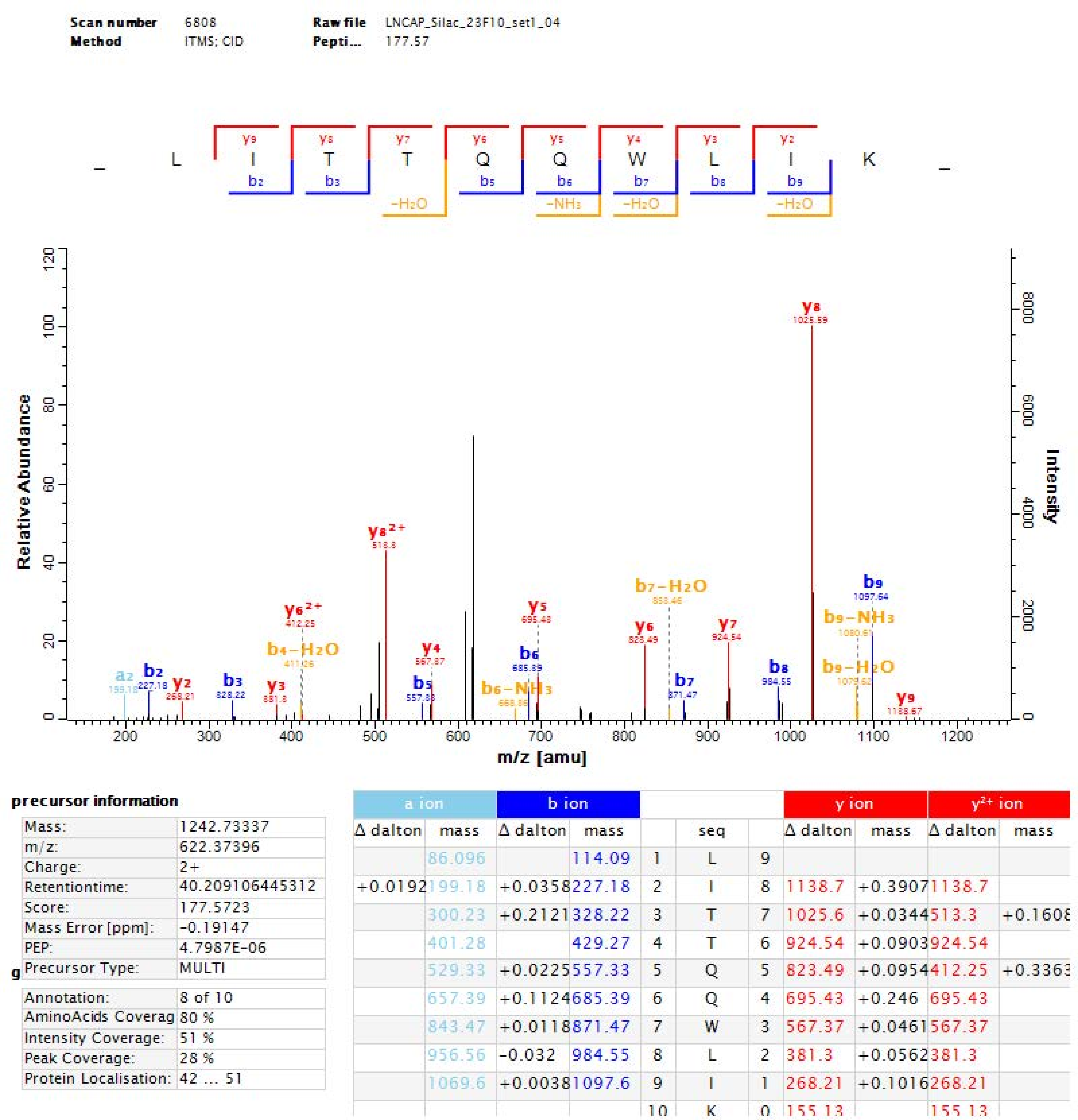
Scan number	6617	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	104.43

precursor information

Mass:	1270.55094
m/z:	636.28275
Charge:	2+
Retentiontime:	39.169952392578
Score:	104.434
Mass Error [ppm]:	0.084205
PEP:	0.00064892
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	52 %
Peak Coverage:	21 %
Protein Localisation:	71 ... 80

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08		148.08	1	F	9				
-0.013	233.16	-0.06	261.16	2	I	8	1124.5	+0.1137	1124.5	
	346.25	+0.1228	374.24	3	L	7	1011.4	-0.038	506.21	-0.038
	477.29		505.28	4	M	6	898.32	+0.1042	898.32	
	592.32	+0.0669	620.31	5	D	5	767.28	+0.0427	767.28	
	752.35	+0.2493	780.34	6	C	4	652.25	+0.0917	652.25	
	883.39		911.38	7	M	3	492.22	+0.18	492.22	
	1012.4	-0.065	1040.4	8	E	2	361.18	+0.0935	361.18	
	1069.5	-0.016	1097.4	9	G	1	232.14	-0.049	232.14	
				10	R	0	175.12		175.12	



Scan number	6808	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	177.57

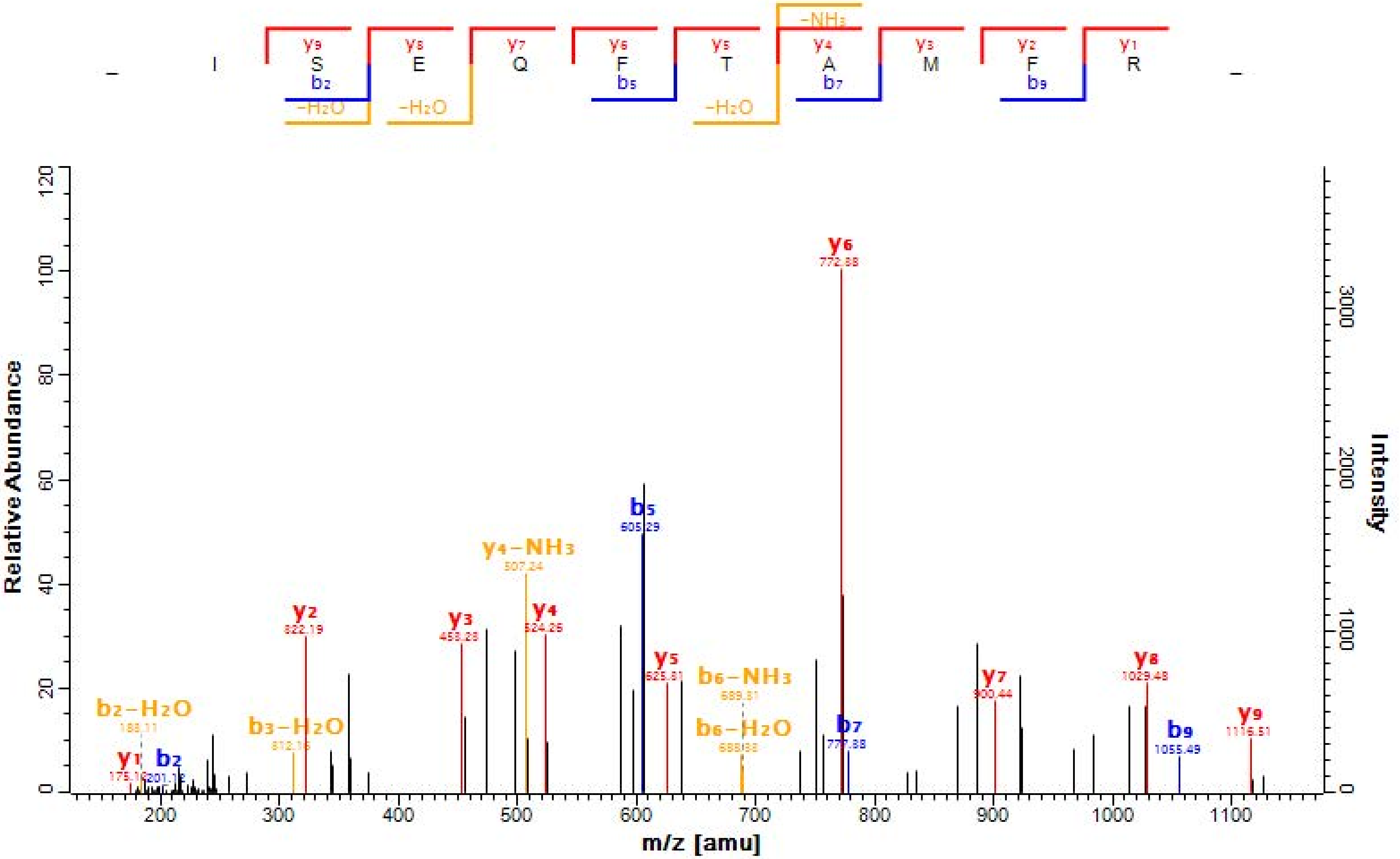
precursor information

Mass:	1242.73337
m/z:	622.37396
Charge:	2+
Retentiontime:	40.209106445312
Score:	177.5723
Mass Error [ppm]:	-0.19147
PEP:	4.7987E-06
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	51 %
Peak Coverage:	28 %
Protein Localisation:	42 ... 51

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	9				
+0.0192	199.18	+0.0358	227.18	2	I	8	1138.7	+0.3907	1138.7	
	300.23	+0.2121	328.22	3	T	7	1025.6	+0.0344	513.3	+0.1608
	401.28		429.27	4	T	6	924.54	+0.0903	924.54	
	529.33	+0.0225	557.33	5	Q	5	823.49	+0.0954	412.25	+0.3363
	657.39	+0.1124	685.39	6	Q	4	695.43	+0.246	695.43	
	843.47	+0.0118	871.47	7	W	3	567.37	+0.0461	567.37	
	956.56	-0.032	984.55	8	L	2	381.3	+0.0562	381.3	
	1069.6	+0.0038	1097.6	9	I	1	268.21	+0.1016	268.21	
				10	K	0	155.13		155.13	

Scan number	6928	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	56.09



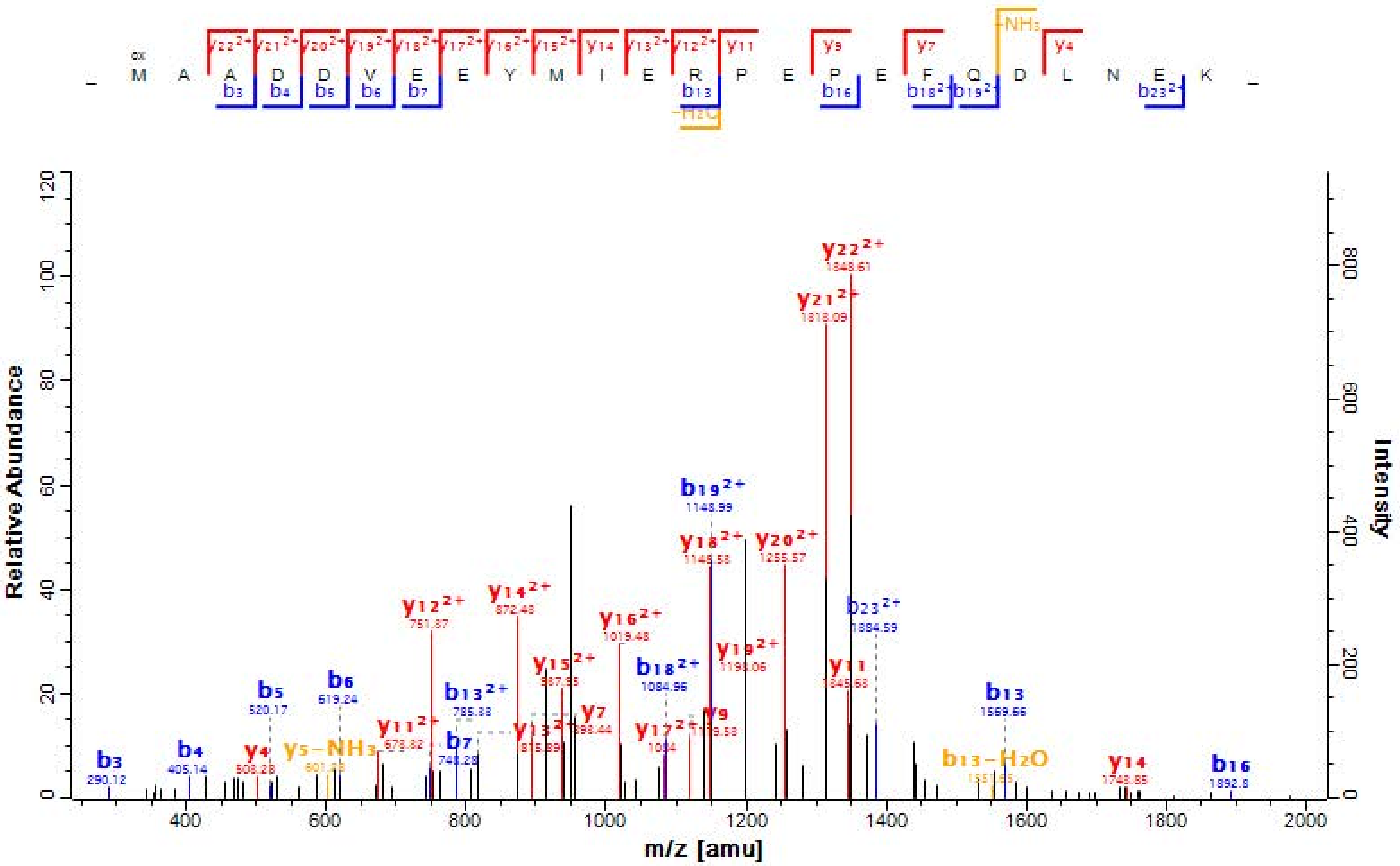
precursor information

Mass:	1228.59149
m/z:	615.30302
Charge:	2+
Retentiontime:	40.864376068115
Score:	56.08672
Mass Error [ppm]:	0.36417
PEP:	0.0258
Precursor Type:	MULTI

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	39 %
Peak Coverage:	19 %
Protein Localisation:	381 ... 390

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	114.091340447	1	I	9		
+0.2853836	201.123368857	2	S	8	1116.5142559	+0.1256367
	330.165961953	3	E	7	1029.48222749	+0.195751
	458.224539464	4	Q	6	900.439634393	+0.1248187
+0.1291047	605.292953381	5	F	5	772.381056882	+0.0115823
	706.340631855	6	T	4	625.312642965	+0.1301061
+0.1422129	777.377745643	7	A	3	524.264964491	+0.0229383
	908.418230249	8	M	2	453.227850703	+0.0472347
-0.114818	1055.48664416	9	F	1	322.187366097	+0.0500301
		10	R	0	175.118952181	+0.0355125

Scan number	7310	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	132.74



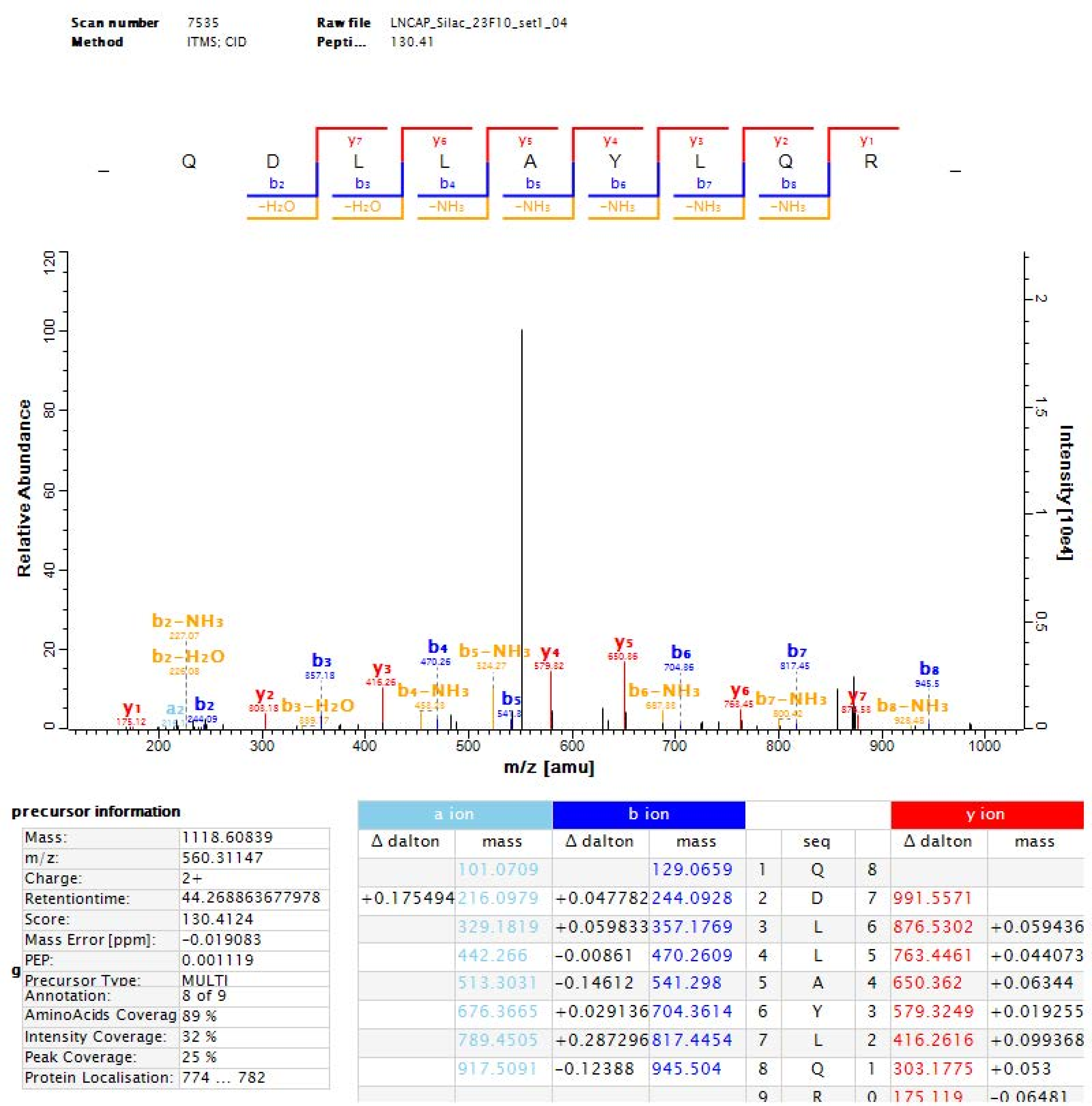
precursor information

Mass:	2913.26899
m/z:	972.09694
Charge:	3+
Retentiontime:	42.965671539306
Score:	132.735
Mass Error [ppm]:	0.18242
PEP:	7.5782E-16
Precursor Type:	MULTI

general information

Annotation:	19 of 24
AminoAcids Coverag	79 %
Intensity Coverage:	54 %
Peak Coverage:	31 %
Protein Localisation:	83 ... 106

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.04		148.04	1	M	23				
	219.08		219.08	2	A	22	2767.2		2767.2	
	290.12	-0.17	290.12	3	A	21	2696.2		1348.6	+0.2182
	405.14	+0.1853	405.14	4	D	20	2625.2		1313.1	+0.2882
	520.17	-0.078	520.17	5	D	19	2510.1		1255.6	+0.1912
	619.24	+0.193	619.24	6	V	18	2395.1		1198.1	-0.009
	748.28	-0.194	748.28	7	E	17	2296		1148.5	-0.062
	877.32		877.32	8	E	16	2167		1084	+0.0197
	1040.4		1040.4	9	Y	15	2038		1019.5	+0.4135
	1171.4		1171.4	10	M	14	1874.9		937.95	+0.1908
	1284.5		1284.5	11	I	13	1743.9	+0.0269	872.43	+0.2682
	1413.6		1413.6	12	E	12	1630.8		815.89	-0.08
+0.0529	785.33	+0.0509	1569.7	13	R	11	1501.7		751.37	+0.1888
	1666.7		1666.7	14	P	10	1345.6	+0.0339	673.32	+0.2214
	1795.8		1795.8	15	E	9	1248.6		1248.6	
	1892.8	-0.398	1892.8	16	P	8	1119.5	-0.004	1119.5	
	2021.8		2021.8	17	E	7	1022.5		1022.5	
-0.167	1085		2168.9	18	F	6	893.44	+0.2486	893.44	
+0.2526	1149		2297	19	Q	5	746.37		746.37	
	2412		2412	20	D	4	618.31		618.31	
	2525.1		2525.1	21	L	3	503.28	-0.039	503.28	
	2639.1		2639.1	22	N	2	390.2		390.2	
-0.18	1384.6		2768.2	23	E	1	276.16		276.16	
				24	K	0	147.11		147.11	



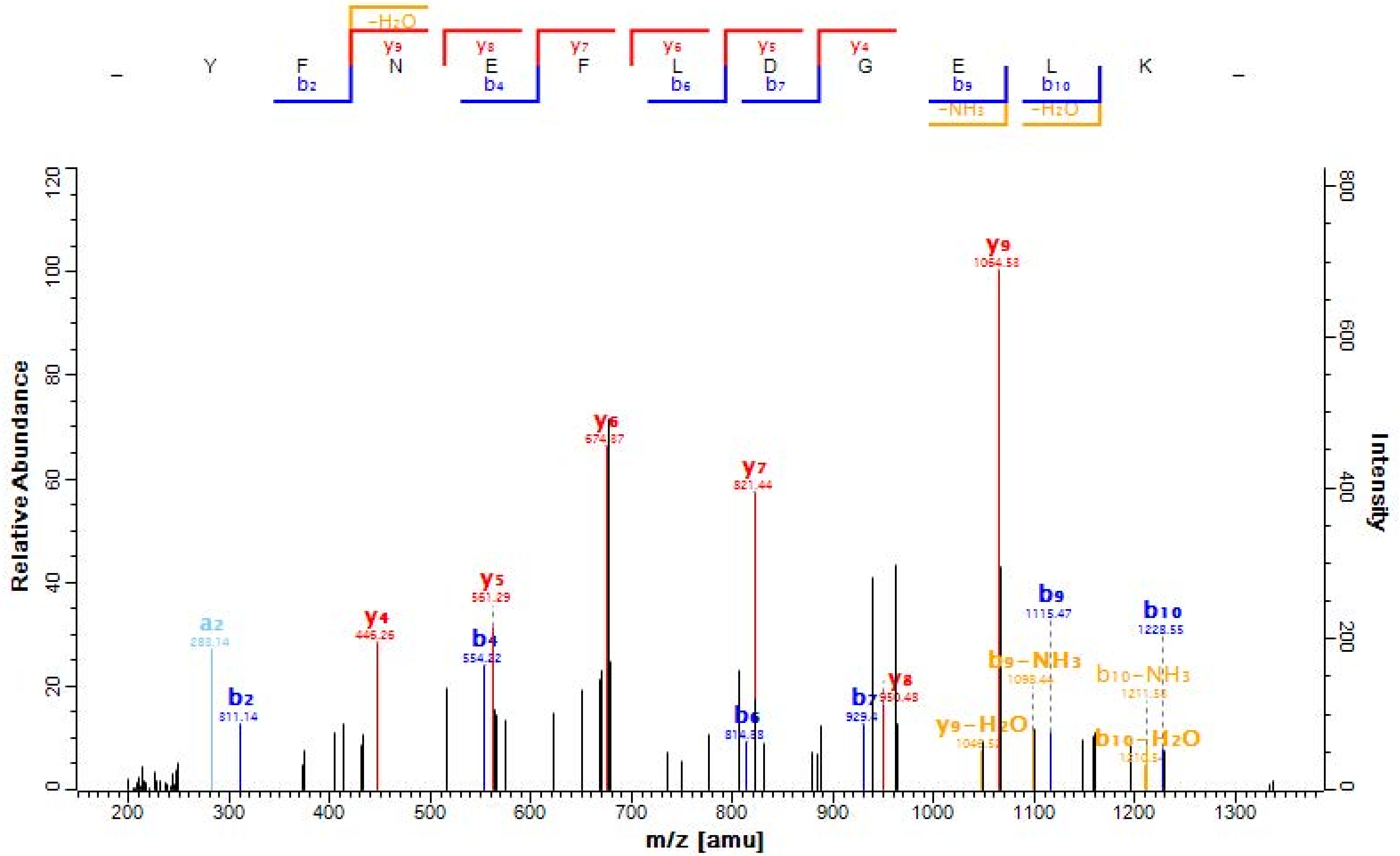
Scan number	7535	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	130.41

precursor information

Mass:	1118.60839
m/z:	560.31147
Charge:	2+
Retentiontime:	44.268863677978
Score:	130.4124
Mass Error [ppm]:	-0.019083
PEP:	0.001119
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	32 %
Peak Coverage:	25 %
Protein Localisation:	774 ... 782

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	101.0709		129.0659	1	Q	8		
+0.175494	216.0979	+0.047782	244.0928	2	D	7	991.5571	
	329.1819	+0.059833	357.1769	3	L	6	876.5302	+0.059436
	442.266	-0.00861	470.2609	4	L	5	763.4461	+0.044073
	513.3031	-0.14612	541.298	5	A	4	650.362	+0.06344
	676.3665	+0.029136	704.3614	6	Y	3	579.3249	+0.019255
	789.4505	+0.287296	817.4454	7	L	2	416.2616	+0.099368
	917.5091	-0.12388	945.504	8	Q	1	303.1775	+0.053
				9	R	0	175.119	-0.06481

Scan number	7672	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	92.19



precursor information

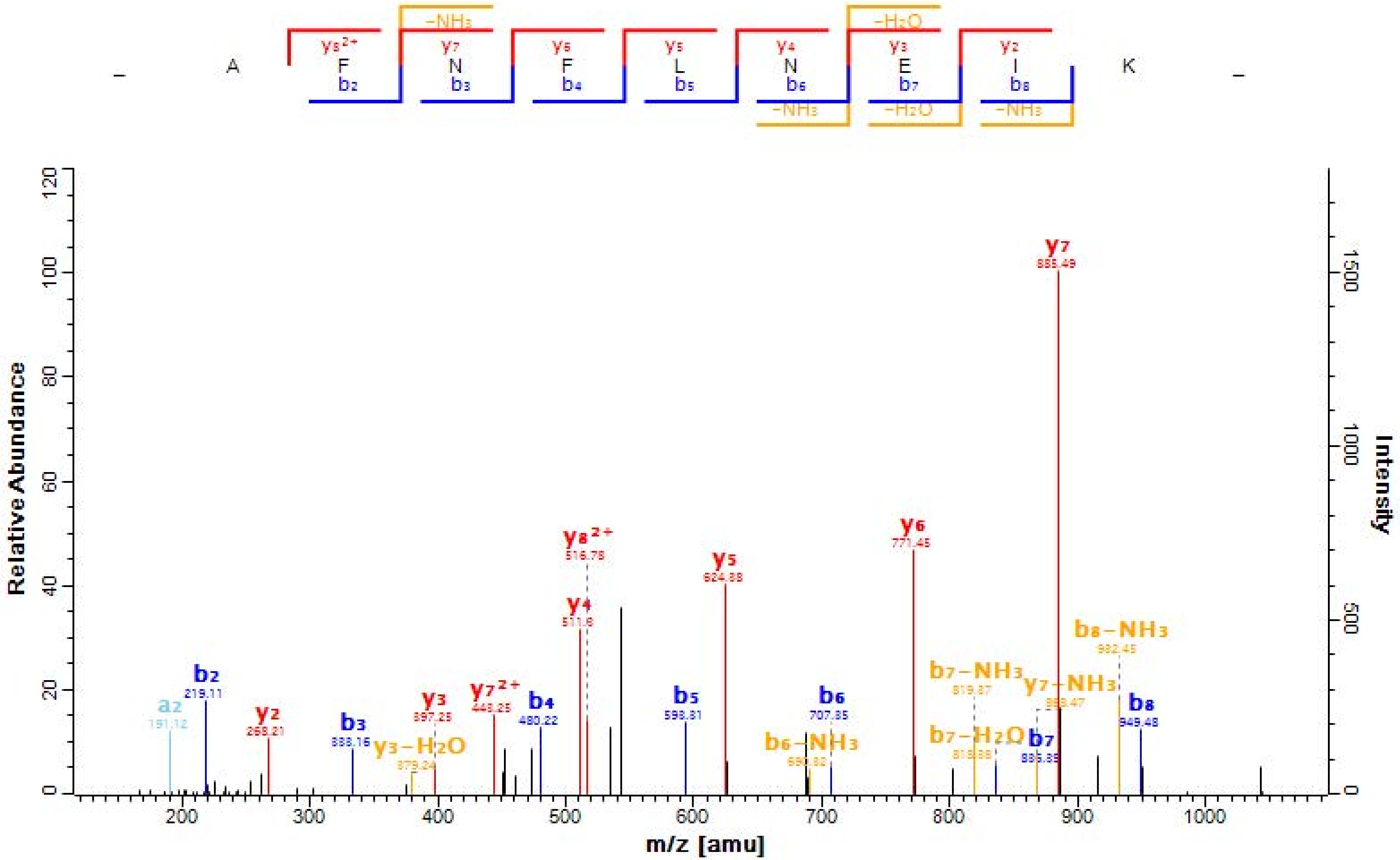
Mass:	1373.65072
m/z:	687.83264
Charge:	2+
Retentiontime:	45.082679748535
Score:	92.18982
Mass Error [ppm]:	0.28043
PEP:	0.0015541
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	40 %
Peak Coverage:	21 %
Protein Localisation:	136 ... 146

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	136.0757		164.0706	1	Y	10		
+0.18927	283.1441	+0.088276	311.139	2	F	9	1211.594	
	397.187		425.1819	3	N	8	1064.526	+0.035169
	526.2296	-0.08623	554.2245	4	E	7	950.4829	+0.060091
	673.298		701.293	5	F	6	821.4403	+0.034569
	786.3821	-0.08899	814.377	6	L	5	674.3719	+0.164628
	901.409	+0.22342	929.404	7	D	4	561.2879	+0.150181
	958.4305		986.4254	8	G	3	446.2609	+0.144715
	1087.473	-0.04358	1115.468	9	E	2	389.2395	
	1200.557	-0.27535	1228.552	10	L	1	260.1969	
				11	K	0	147.1128	

Scan number	8157	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	182.65



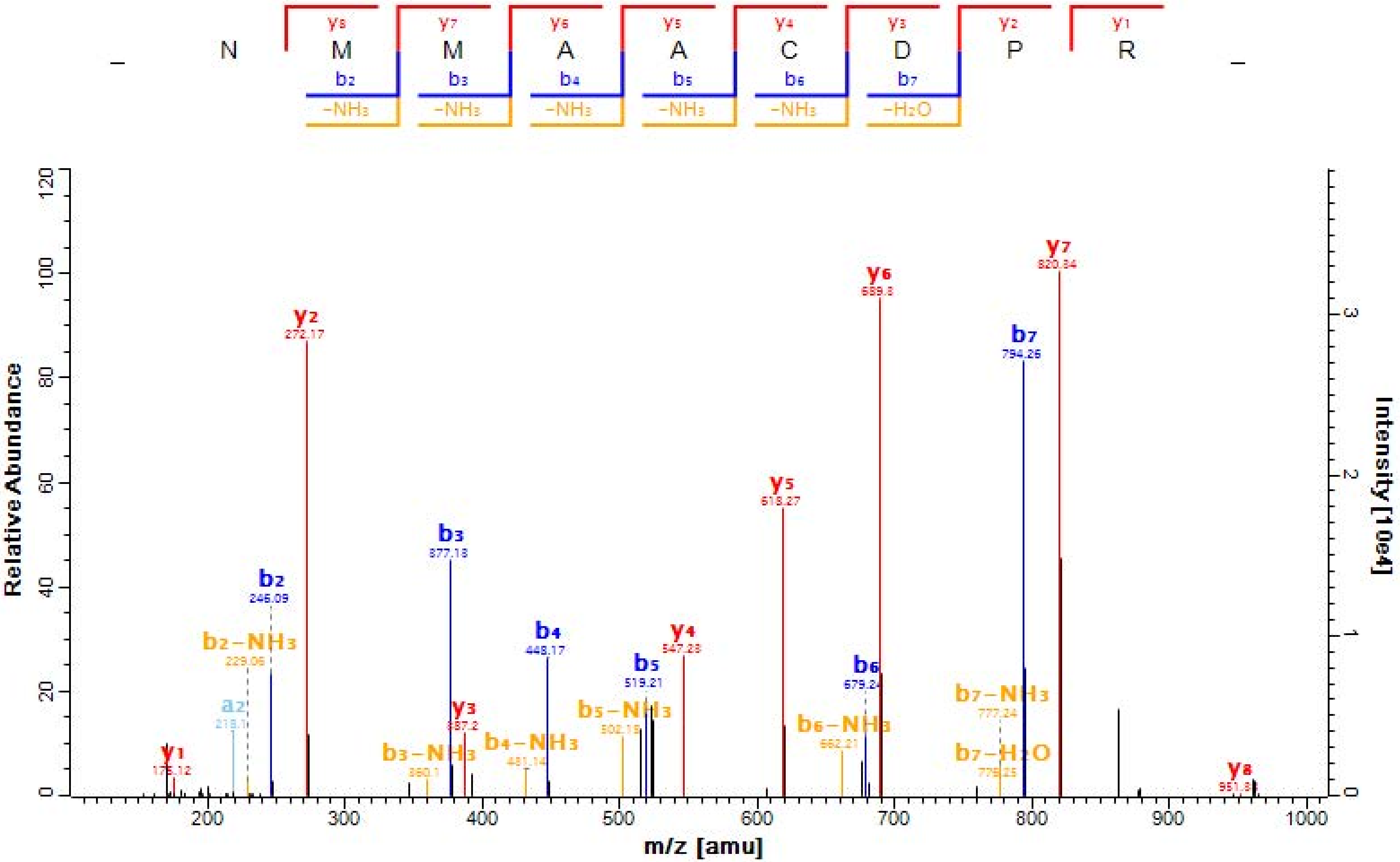
precursor information

g

Mass:	1094.57604
m/z:	548.2953
Charge:	2+
Retentiontime:	47.896610260009
Score:	182.6465
Mass Error [ppm]:	-0.0056447
PEP:	4.01E-06
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	68 %
Peak Coverage:	29 %
Protein Localisation:	75 ... 83

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	44.049		72.044	1	A	8				
+0.0172	191.12	+0.0051	219.11	2	F	7	1032.6		516.78	-0.061
	305.16	+0.1602	333.16	3	N	6	885.49	+0.0366	443.25	+0.0745
	452.23	-0.148	480.22	4	F	5	771.45	-0.011	771.45	
	565.31	-0.086	593.31	5	L	4	624.38	+0.0947	624.38	
	679.36	+0.2113	707.35	6	N	3	511.3	+0.0639	511.3	
	808.4	-0.092	836.39	7	E	2	397.25	+0.0497	397.25	
	921.48	-0.022	949.48	8	I	1	268.21	+0.0549	268.21	
				9	K	0	155.13		155.13	

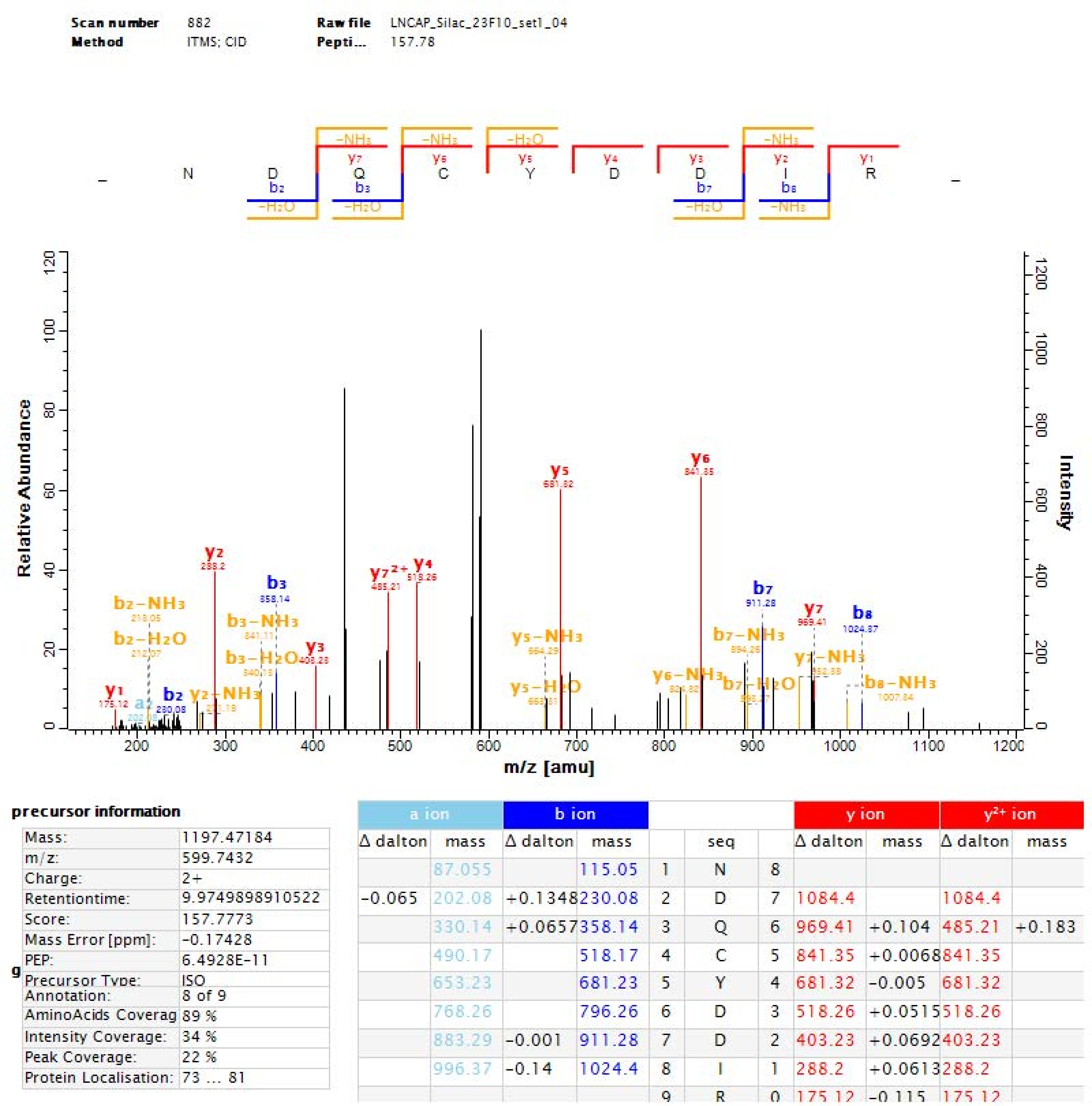
Scan number	829	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	153.97



precursor information

Mass:	1064.41947
m/z:	533.21701
Charge:	2+
Retentiontime:	9.6935062408447
Score:	153.9702
Mass Error [ppm]:	-0.64502
PEP:	0.00063145
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	72 %
Peak Coverage:	28 %
Protein Localisation:	298 ... 306

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	87.05529		115.0502	1	N	8		
+0.072531	218.0958	-0.00582	246.0907	2	M	7	951.3845	+0.223711
	349.1363	+0.034781	377.1312	3	M	6	820.344	+0.013341
	420.1734	-0.0428	448.1683	4	A	5	689.3035	+0.049309
	491.2105	+0.063337	519.2054	5	A	4	618.2664	-0.01184
	651.2411	-0.03445	679.236	6	C	3	547.2293	-0.00818
	766.2681	-0.01641	794.263	7	D	2	387.1987	+0.105174
	863.3208		891.3158	8	P	1	272.1717	-0.0082
				9	R	0	175.119	-0.06234

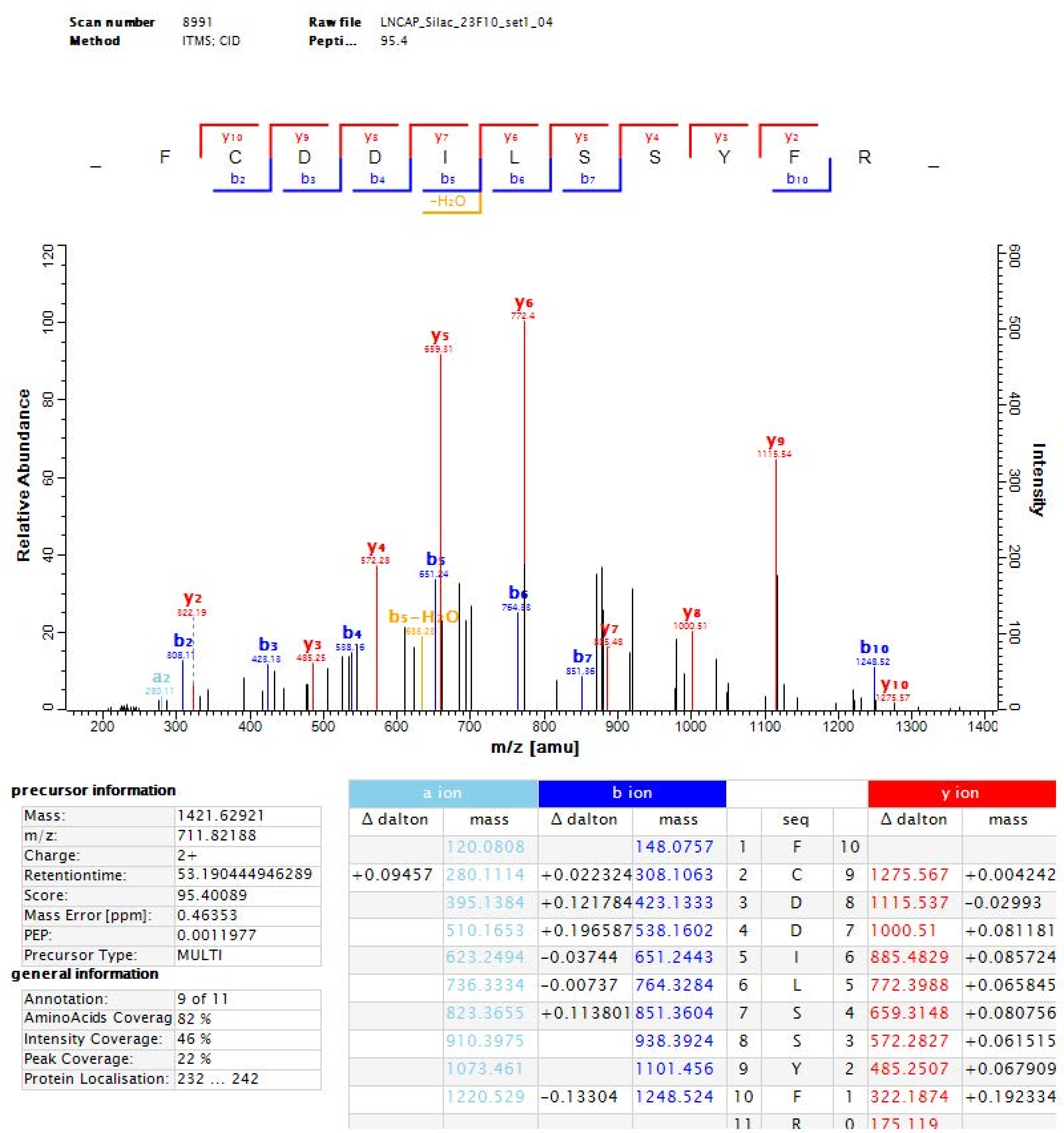


Scan number 882
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set1_04
Pepti... 157.78

precursor information

Mass:	1197.47184
m/z:	599.7432
Charge:	2+
Retentiontime:	9.9749898910522
Score:	157.7773
Mass Error [ppm]:	-0.17428
PEP:	6.4928E-11
Precursor Type:	ISO
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	34 %
Peak Coverage:	22 %
Protein Localisation:	73 ... 81

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	87.055		115.05	1	N	8				
-0.065	202.08	+0.1348	230.08	2	D	7	1084.4		1084.4	
	330.14	+0.0657	358.14	3	Q	6	969.41	+0.104	485.21	+0.183
	490.17		518.17	4	C	5	841.35	+0.0068	841.35	
	653.23		681.23	5	Y	4	681.32	-0.005	681.32	
	768.26		796.26	6	D	3	518.26	+0.0515	518.26	
	883.29	-0.001	911.28	7	D	2	403.23	+0.0692	403.23	
	996.37	-0.14	1024.4	8	I	1	288.2	+0.0613	288.2	
				9	R	0	175.12	-0.115	175.12	



Scan number	8991	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	95.4

precursor information

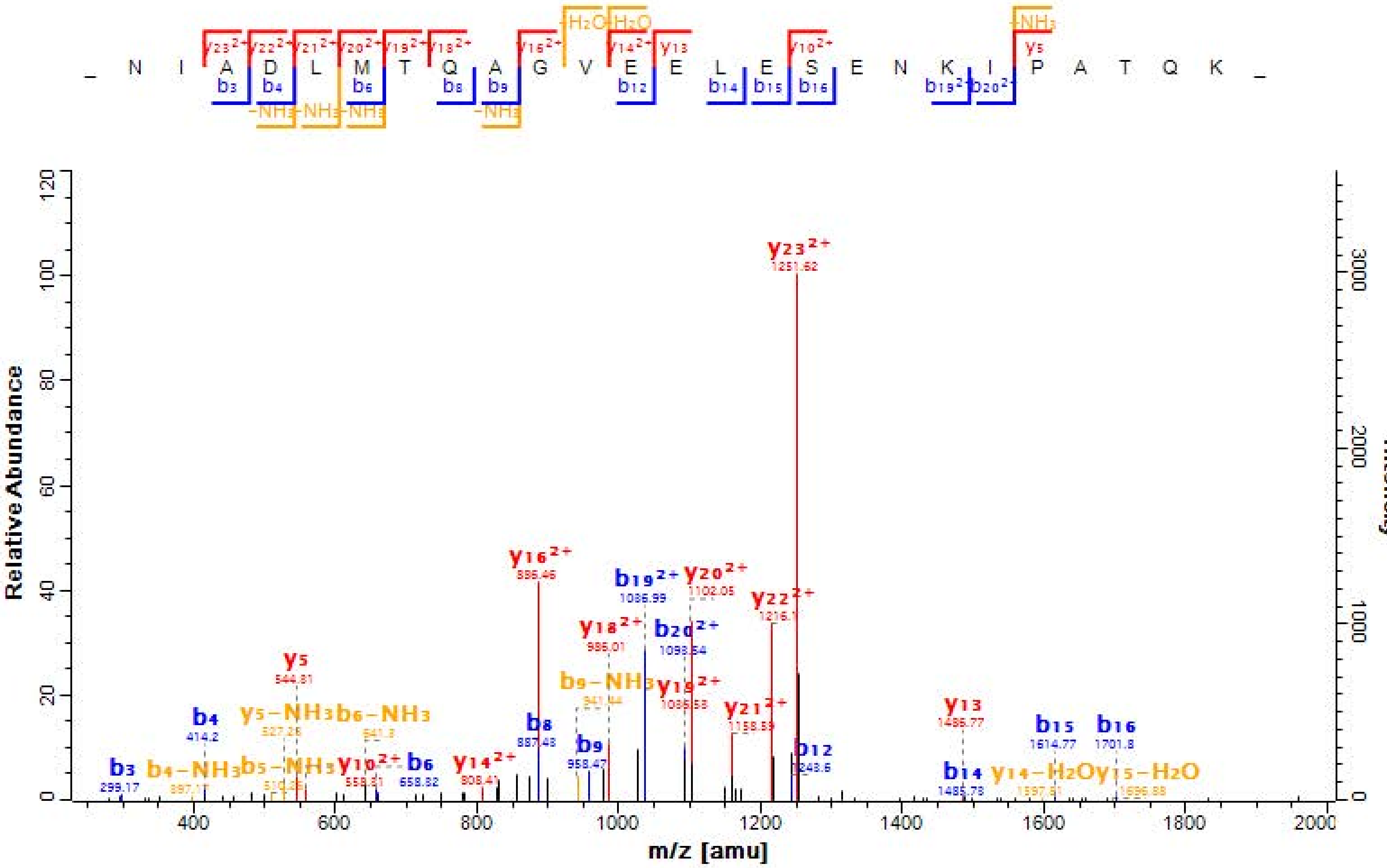
Mass:	1421.62921
m/z:	711.82188
Charge:	2+
Retentiontime:	53.190444946289
Score:	95.40089
Mass Error [ppm]:	0.46353
PEP:	0.0011977
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	46 %
Peak Coverage:	22 %
Protein Localisation:	232 ... 242

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	120.0808		148.0757	1	F	10		
+0.09457	280.1114	+0.022324	308.1063	2	C	9	1275.567	+0.004242
	395.1384	+0.121784	423.1333	3	D	8	1115.537	-0.02993
	510.1653	+0.196587	538.1602	4	D	7	1000.51	+0.081181
	623.2494	-0.03744	651.2443	5	I	6	885.4829	+0.085724
	736.3334	-0.00737	764.3284	6	L	5	772.3988	+0.065845
	823.3655	+0.113801	851.3604	7	S	4	659.3148	+0.080756
	910.3975		938.3924	8	S	3	572.2827	+0.061515
	1073.461		1101.456	9	Y	2	485.2507	+0.067909
	1220.529	-0.13304	1248.524	10	F	1	322.1874	+0.192334
				11	R	0	175.119	

Scan number	9005	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	136.96



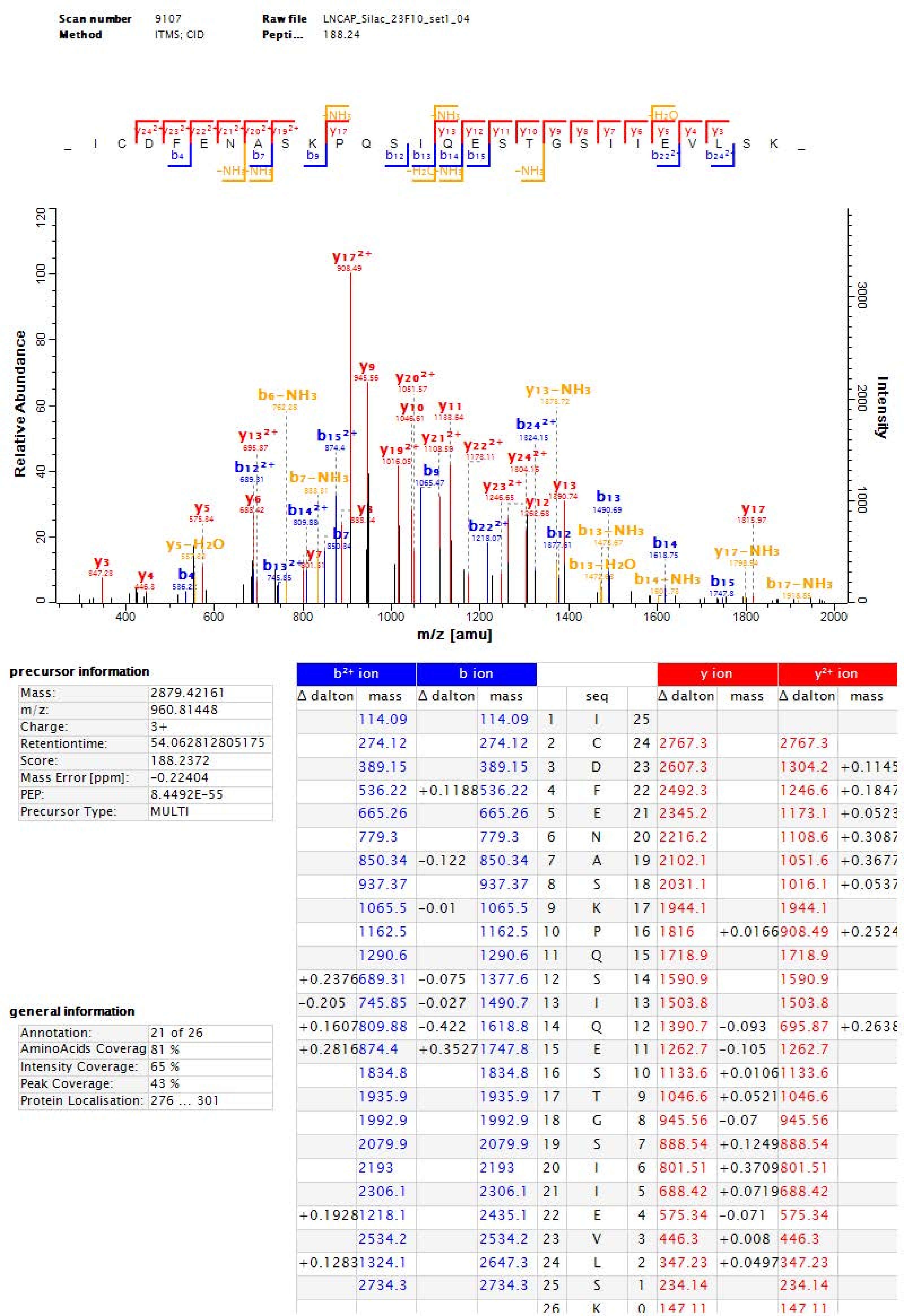
precursor information

Mass:	2728.36045
m/z:	910.46076
Charge:	3+
Retentiontime:	53.296188354492
Score:	136.9649
Mass Error [ppm]:	0.56013
PEP:	5.0752E-23
Precursor Type:	MULTI

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.05		115.05	1	N	24				
	228.13		228.13	2	I	23	2615.3		2615.3	
	299.17	+0.1492	299.17	3	A	22	2502.2		1251.6	+0.3877
	414.2	+0.089	414.2	4	D	21	2431.2		1216.1	+0.3077
	527.28		527.28	5	L	20	2316.2		1158.6	+0.3283
	658.32	+0.0927	658.32	6	M	19	2203.1		1102	+0.3505
	759.37		759.37	7	T	18	2072.1		1036.5	-0.054
	887.43	+0.1665	887.43	8	Q	17	1971		986.01	+0.312
	958.47	+0.0392	958.47	9	A	16	1842.9		1842.9	
	1015.5		1015.5	10	G	15	1771.9		886.46	+0.3331
	1114.6		1114.6	11	V	14	1714.9		1714.9	
	1243.6	+0.267	1243.6	12	E	13	1615.8		808.41	+0.2765
	1372.6		1372.6	13	E	12	1486.8	-0.448	1486.8	
	1485.7	-0.178	1485.7	14	L	11	1357.7		1357.7	
	1614.8	+0.2469	1614.8	15	E	10	1244.6		1244.6	
	1701.8	-0.316	1701.8	16	S	9	1115.6		558.31	+0.2567
	1830.8		1830.8	17	E	8	1028.6		1028.6	
	1944.9		1944.9	18	N	7	899.53		899.53	
+0.2016	1037		2073	19	K	6	785.49		785.49	
-0.163	1093.5		2186.1	20	I	5	657.39		657.39	
	2283.1		2283.1	21	P	4	544.31	-0.022	544.31	
	2354.2		2354.2	22	A	3	447.26		447.26	
	2455.2		2455.2	23	T	2	376.22		376.22	
	2583.3		2583.3	24	Q	1	275.17		275.17	
				25	K	0	147.11		147.11	

general information

Annotation:	17 of 25
AminoAcids Coverag	68 %
Intensity Coverage:	72 %
Peak Coverage:	33 %
Protein Localisation:	51 ... 75



Scan number	9107	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	188.24

precursor information

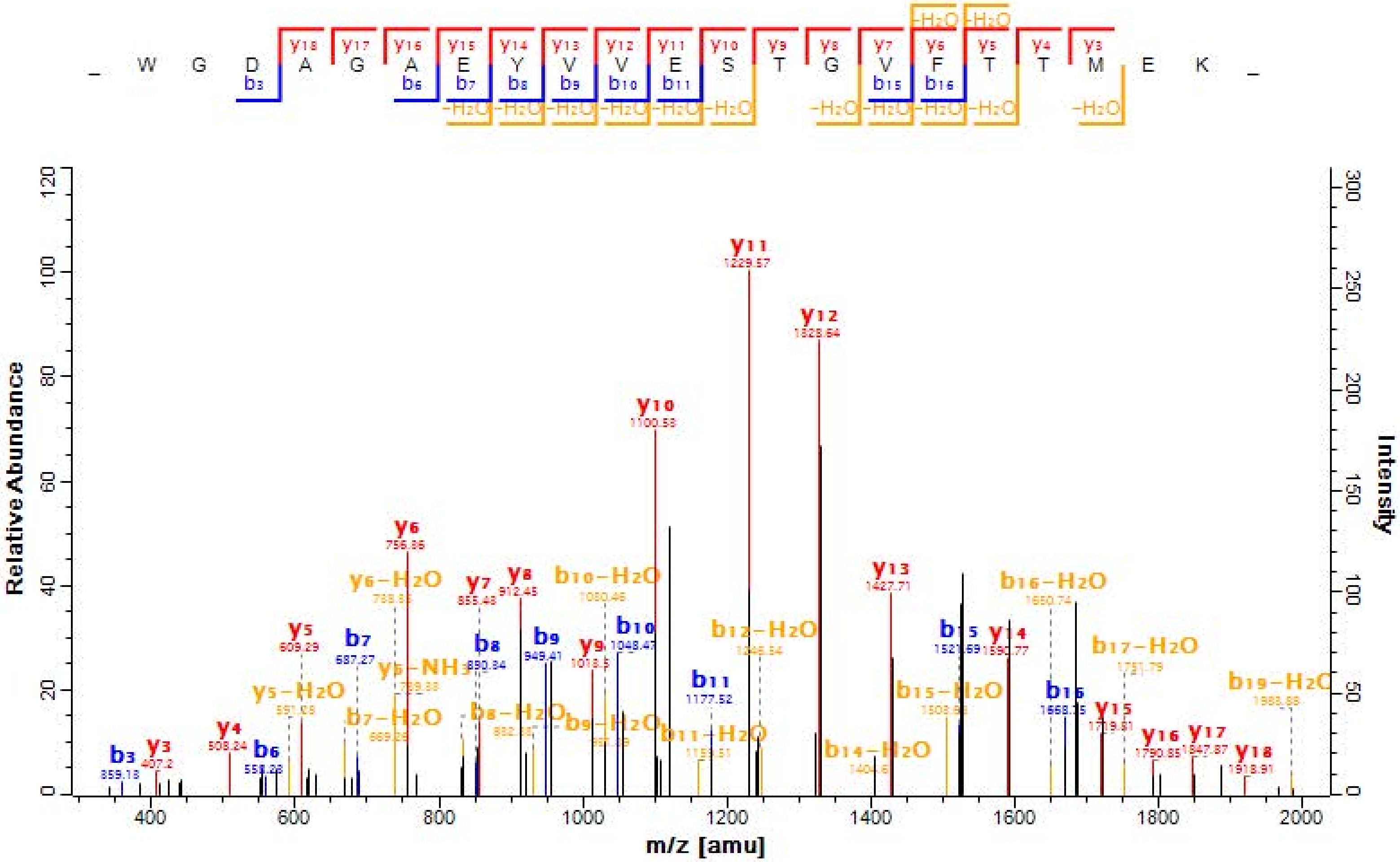
Mass:	2879.42161
m/z:	960.81448
Charge:	3+
Retentiontime:	54.062812805175
Score:	188.2372
Mass Error [ppm]:	-0.22404
PEP:	8.4492E-55
Precursor Type:	MULTI

general information

Annotation:	21 of 26
AminoAcids Coverag	81 %
Intensity Coverage:	65 %
Peak Coverage:	43 %
Protein Localisation:	276 ... 301

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	I	25				
	274.12		274.12	2	C	24	2767.3		2767.3	
	389.15		389.15	3	D	23	2607.3		1304.2	+0.1145
	536.22	+0.1188	536.22	4	F	22	2492.3		1246.6	+0.1847
	665.26		665.26	5	E	21	2345.2		1173.1	+0.0523
	779.3		779.3	6	N	20	2216.2		1108.6	+0.3087
	850.34	-0.122	850.34	7	A	19	2102.1		1051.6	+0.3677
	937.37		937.37	8	S	18	2031.1		1016.1	+0.0537
	1065.5	-0.01	1065.5	9	K	17	1944.1		1944.1	
	1162.5		1162.5	10	P	16	1816	+0.0166	908.49	+0.2524
	1290.6		1290.6	11	Q	15	1718.9		1718.9	
+0.2376	689.31	-0.075	1377.6	12	S	14	1590.9		1590.9	
-0.205	745.85	-0.027	1490.7	13	I	13	1503.8		1503.8	
+0.1607	809.88	-0.422	1618.8	14	Q	12	1390.7	-0.093	695.87	+0.2638
+0.2816	874.4	+0.3527	1747.8	15	E	11	1262.7	-0.105	1262.7	
	1834.8		1834.8	16	S	10	1133.6	+0.0106	1133.6	
	1935.9		1935.9	17	T	9	1046.6	+0.0521	1046.6	
	1992.9		1992.9	18	G	8	945.56	-0.07	945.56	
	2079.9		2079.9	19	S	7	888.54	+0.1249	888.54	
	2193		2193	20	I	6	801.51	+0.3709	801.51	
	2306.1		2306.1	21	I	5	688.42	+0.0719	688.42	
+0.1928	1218.1		2435.1	22	E	4	575.34	-0.071	575.34	
	2534.2		2534.2	23	V	3	446.3	+0.008	446.3	
+0.1283	1324.1		2647.3	24	L	2	347.23	+0.0497	347.23	
	2734.3		2734.3	25	S	1	234.14		234.14	
				26	K	0	147.11		147.11	

Scan number	9362	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	182.22



precursor information

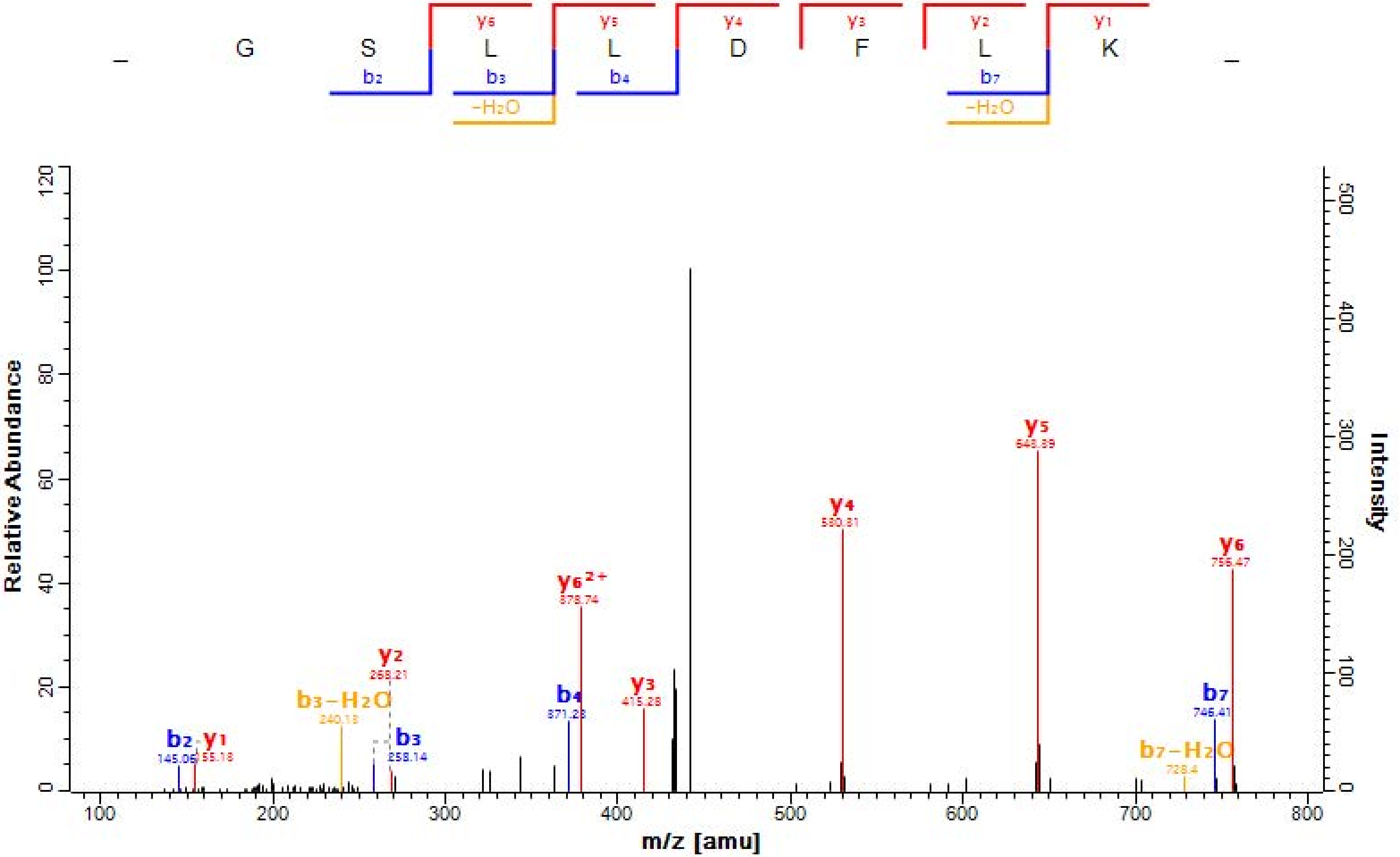
Mass:	2276.03037
m/z:	1139.02246
Charge:	2+
Retentiontime:	55.974071502685
Score:	182.2159
Mass Error [ppm]:	-0.15052
PEP:	2.442E-28
Precursor Type:	ISO

general information

Annotation:	17 of 21
AminoAcids Coverag	81 %
Intensity Coverage:	49 %
Peak Coverage:	38 %
Protein Localisation:	87 ... 107

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	187.08658942	1	W	20		
	244.108053144	2	G	19	2090.95867788	
+0.1418288	359.134996176	3	D	18	2033.93721416	
	430.172109963	4	A	17	1918.91027112	+0.1189037
	487.193573687	5	G	16	1847.87315734	-0.1608771
+0.0182139	558.230687475	6	A	15	1790.85169361	-0.190927
+0.0638776	687.273280571	7	E	14	1719.81457982	-0.0564011
+0.0740354	850.336609109	8	Y	13	1590.77198673	-0.0141742
-0.1259703	949.405023026	9	V	12	1427.70865819	+0.0026455
+0.043775	1048.47343694	10	V	11	1328.64024427	+0.0117333
+0.0996926	1177.51603004	11	E	10	1229.57183036	+0.0231403
	1264.54805845	12	S	9	1100.52923726	-0.0277724
	1365.59573692	13	T	8	1013.49720885	-0.0006268
	1422.61720065	14	G	7	912.449530377	-0.0670841
-0.1787786	1521.68561456	15	V	6	855.428066654	+0.0658298
-0.1979982	1668.75402848	16	F	5	756.359652737	+0.0259063
	1769.80170695	17	T	4	609.291238821	+0.0338344
	1870.84938543	18	T	3	508.243560347	+0.1348576
	2001.88987003	19	M	2	407.195881873	+0.2130537
	2130.93246313	20	E	1	276.155397267	
		21	K	0	147.112804171	

Scan number	9370	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	90.66

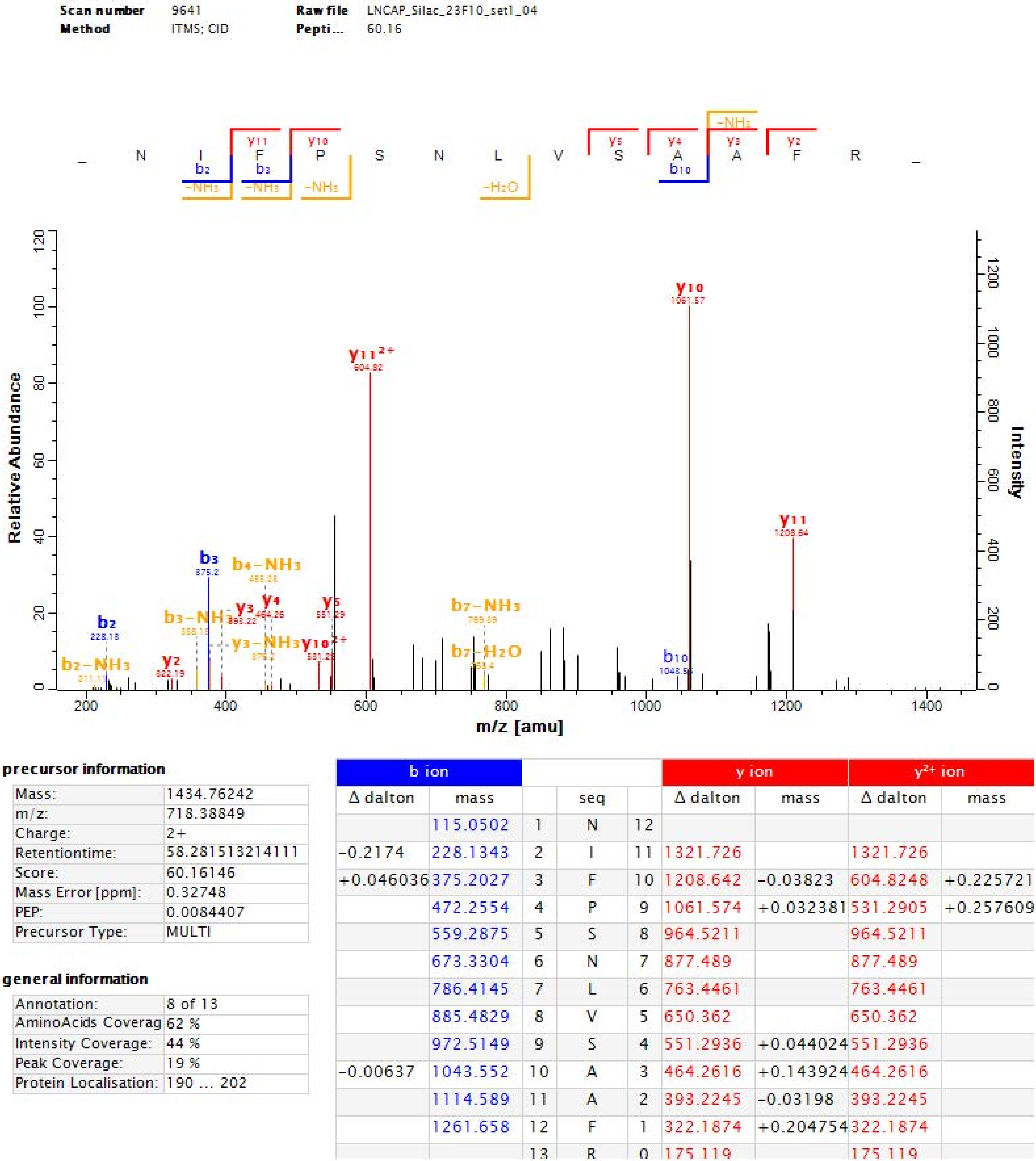


precursor information

g

Mass:	899.52
m/z:	450.76728
Charge:	2+
Retentiontime:	56.042755126953
Score:	90.65661
Mass Error [ppm]:	-0.85573
PEP:	0.016489
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	50 %
Peak Coverage:	14 %
Protein Localisation:	353 ... 360

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	7				
+0.006446	145.0608	2	S	6	843.5066		843.5066	
-0.03216	258.1448	3	L	5	756.4746	-0.01154	378.7409	-0.00974
+0.03682	371.2289	4	L	4	643.3905	+0.014847	643.3905	
	486.2558	5	D	3	530.3064	+0.134677	530.3064	
	633.3243	6	F	2	415.2795	+0.066833	415.2795	
+0.004952	746.4083	7	L	1	268.2111	+0.162773	268.2111	
		8	K	0	155.127	-0.05071	155.127	



Scan number	9641	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	60.16

precursor information

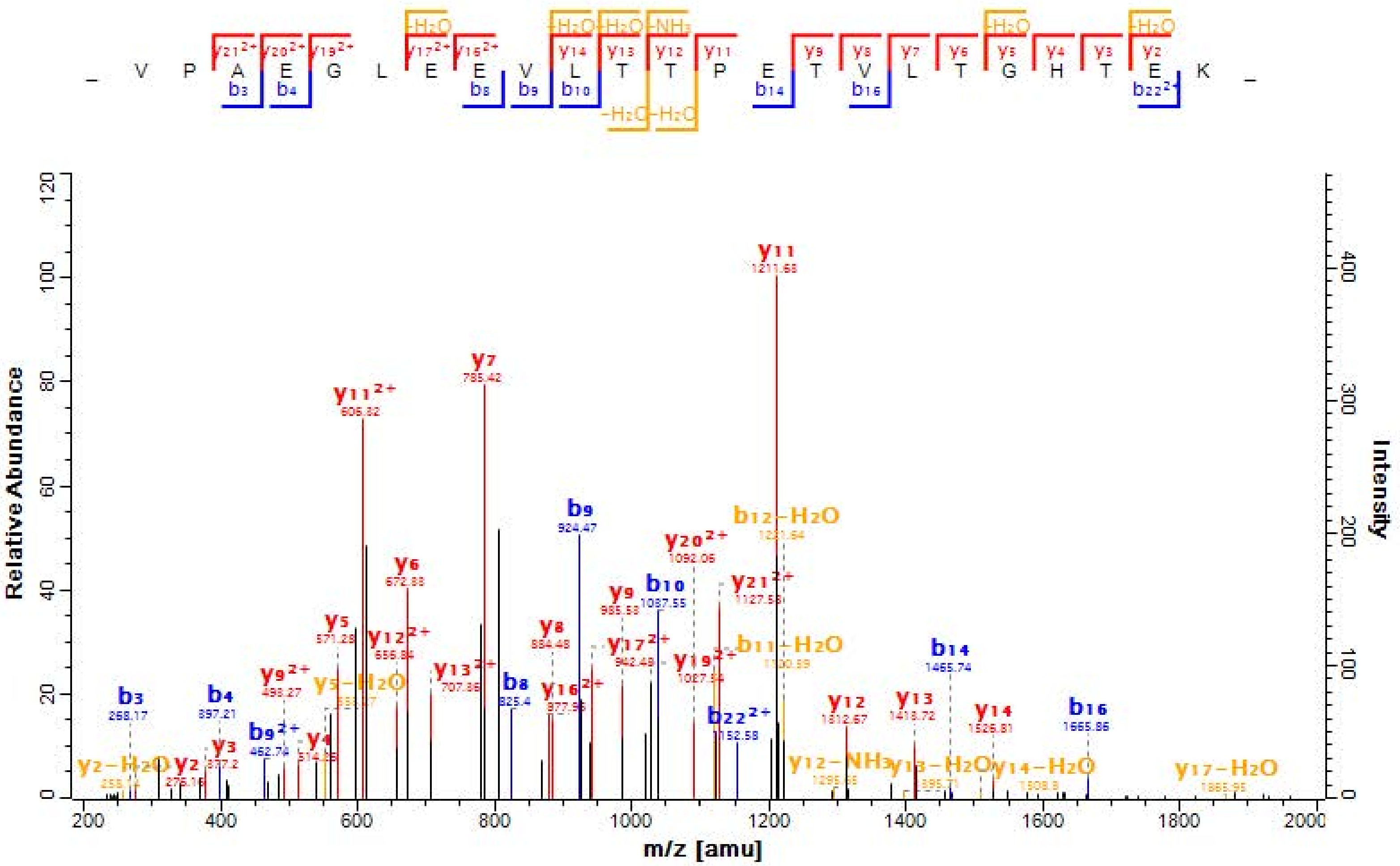
Mass:	1434.76242
m/z:	718.38849
Charge:	2+
Retentiontime:	58.281513214111
Score:	60.16146
Mass Error [ppm]:	0.32748
PEP:	0.0084407
Precursor Type:	MULTI

general information

Annotation:	8 of 13
AminoAcids Coverag	62 %
Intensity Coverage:	44 %
Peak Coverage:	19 %
Protein Localisation:	190 ... 202

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502	1	N	12				
-0.2174	228.1343	2	I	11	1321.726		1321.726	
+0.046036	375.2027	3	F	10	1208.642	-0.03823	604.8248	+0.225721
	472.2554	4	P	9	1061.574	+0.032381	531.2905	+0.257609
	559.2875	5	S	8	964.5211		964.5211	
	673.3304	6	N	7	877.489		877.489	
	786.4145	7	L	6	763.4461		763.4461	
	885.4829	8	V	5	650.362		650.362	
	972.5149	9	S	4	551.2936	+0.044024	551.2936	
-0.00637	1043.552	10	A	3	464.2616	+0.143924	464.2616	
	1114.589	11	A	2	393.2245	-0.03198	393.2245	
	1261.658	12	F	1	322.1874	+0.204754	322.1874	
		13	R	0	175.119		175.119	

Scan number	9867	**Raw file**	LNCAP_Silac_23F10_set1_04
Method	ITMS; CID	**Pepti...**	186.11



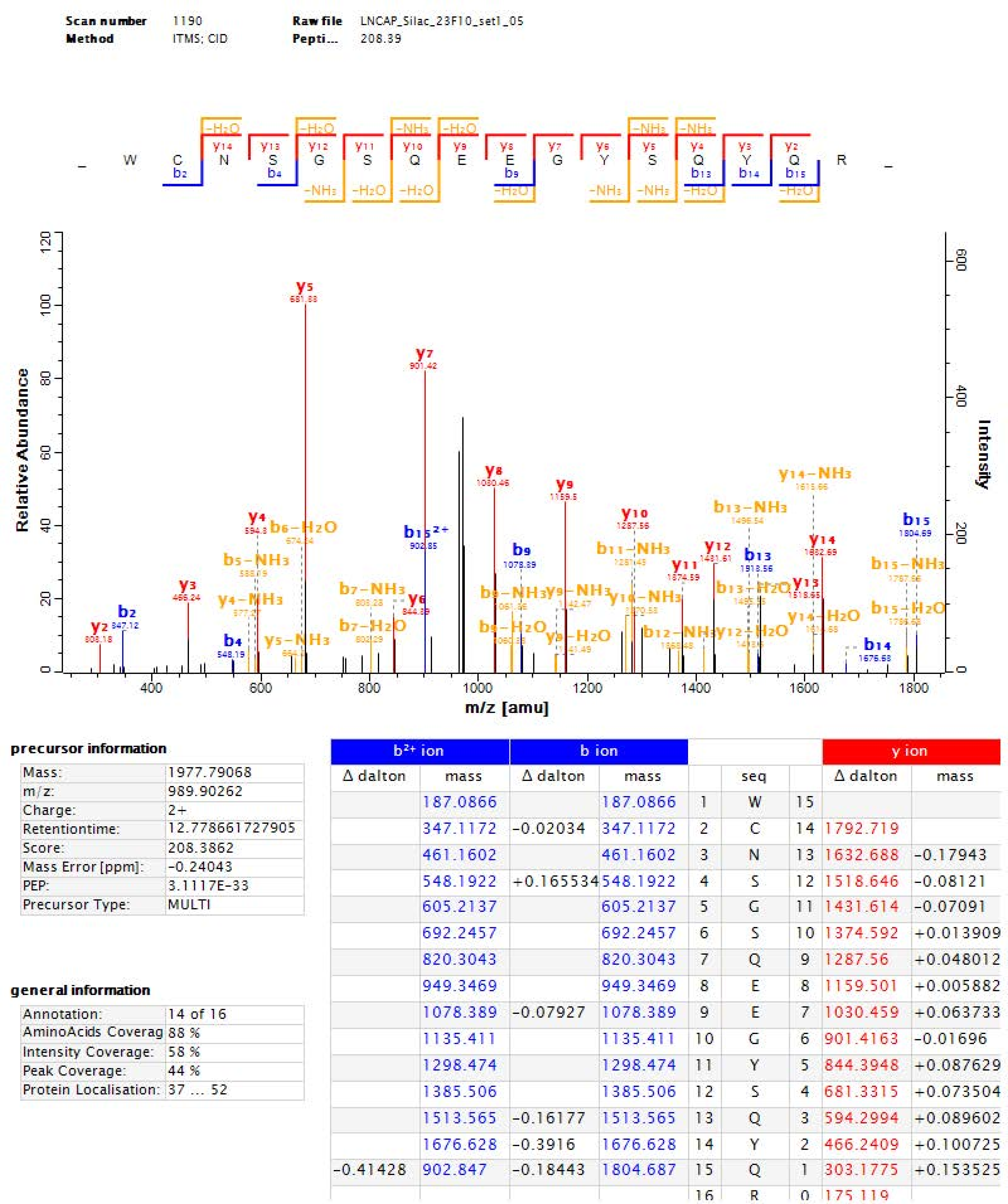
precursor information

Mass:	2449.25941
m/z:	817.42708
Charge:	3+
Retentiontime:	60.231098175048
Score:	186.1136
Mass Error [ppm]:	0.24808
PEP:	3.9849E-49
Precursor Type:	MULTI

general information

Annotation:	19 of 23
AminoAcids Coverag	83 %
Intensity Coverage:	56 %
Peak Coverage:	36 %
Protein Localisation:	574 ... 596

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	22				
	197.13		197.13	2	P	21	2351.2		2351.2	
	268.17	-0.036	268.17	3	A	20	2254.1		1127.6	+0.3359
	397.21	+0.0711	397.21	4	E	19	2183.1		1092.1	+0.265
	454.23		454.23	5	G	18	2054.1		1027.5	-0.056
	567.31		567.31	6	L	17	1997		1997	
	696.36		696.36	7	E	16	1884		942.48	+0.2091
	825.4	+0.05	825.4	8	E	15	1754.9		877.96	+0.4681
+0.2455	462.74	+0.0147	924.47	9	V	14	1625.9		1625.9	
	1037.6	+0.0232	1037.6	10	L	13	1526.8	+0.0942	1526.8	
	1138.6		1138.6	11	T	12	1413.7	-0.123	707.36	-0.004
	1239.6		1239.6	12	T	11	1312.7	-0.061	656.84	-0.031
	1336.7		1336.7	13	P	10	1211.6	-0.011	606.32	+0.2567
	1465.7	+0.3479	1465.7	14	E	9	1114.6		1114.6	
	1566.8		1566.8	15	T	8	985.53	-0.009	493.27	+0.2271
	1665.9	-0.318	1665.9	16	V	7	884.48	+0.0694	884.48	
	1778.9		1778.9	17	L	6	785.42	-0.093	785.42	
	1880		1880	18	T	5	672.33	+0.0707	672.33	
	1937		1937	19	G	4	571.28	+0.0189	571.28	
	2074.1		2074.1	20	H	3	514.26	+0.1618	514.26	
	2175.1		2175.1	21	T	2	377.2	-0.106	377.2	
+0.4573	1152.6		2304.2	22	E	1	276.16	+0.0577	276.16	
				23	K	0	147.11		147.11	



Scan number	1190	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	208.39

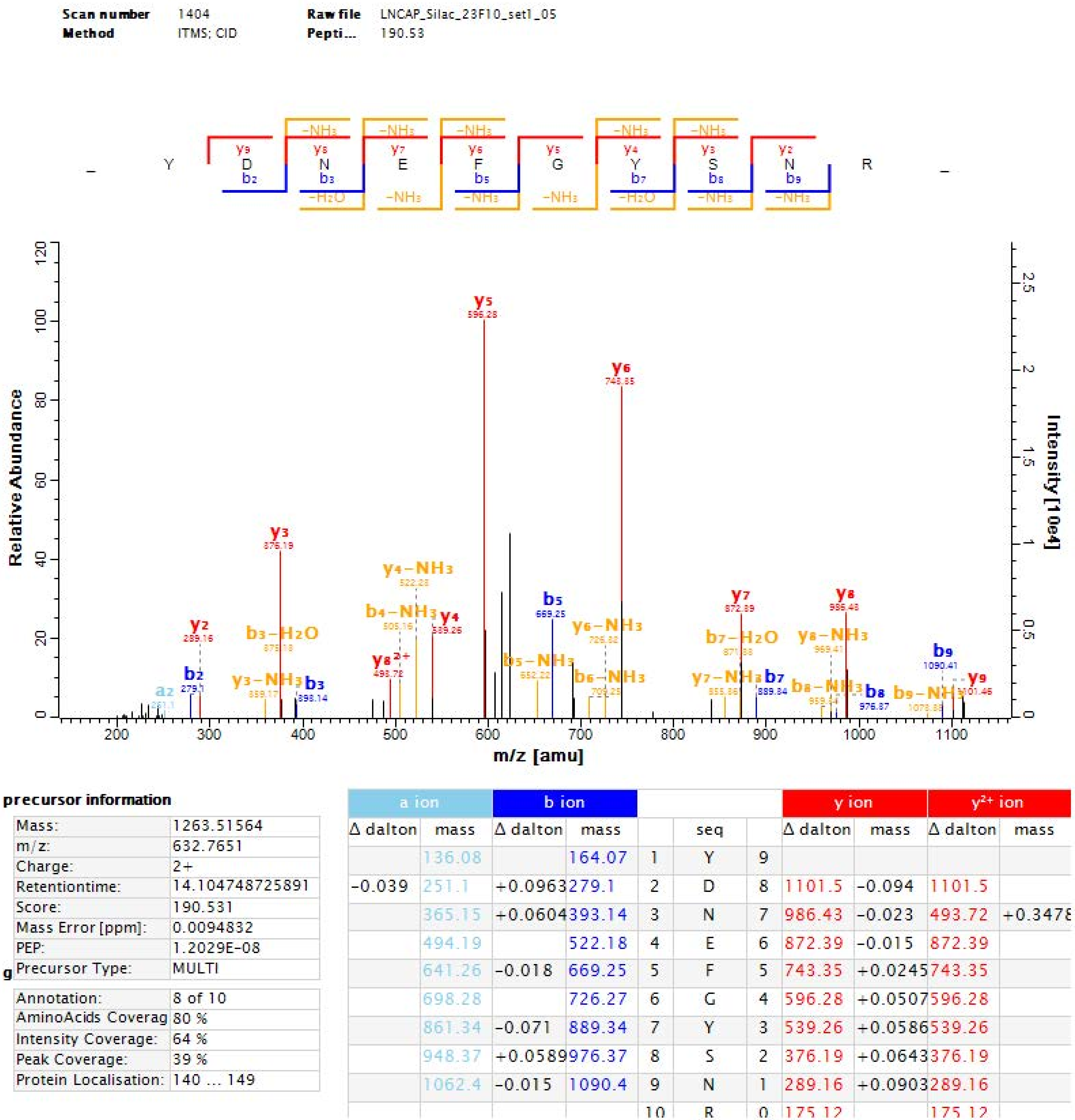
precursor information

Mass:	1977.79068
m/z:	989.90262
Charge:	2+
Retentiontime:	12.778661727905
Score:	208.3862
Mass Error [ppm]:	-0.24043
PEP:	3.1117E-33
Precursor Type:	MULTI

general information

Annotation:	14 of 16
AminoAcids Coverag	88 %
Intensity Coverage:	58 %
Peak Coverage:	44 %
Protein Localisation:	37 ... 52

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	187.0866		187.0866	1	W	15		
	347.1172	-0.02034	347.1172	2	C	14	1792.719	
	461.1602		461.1602	3	N	13	1632.688	-0.17943
	548.1922	+0.165534	548.1922	4	S	12	1518.646	-0.08121
	605.2137		605.2137	5	G	11	1431.614	-0.07091
	692.2457		692.2457	6	S	10	1374.592	+0.013909
	820.3043		820.3043	7	Q	9	1287.56	+0.048012
	949.3469		949.3469	8	E	8	1159.501	+0.005882
	1078.389	-0.07927	1078.389	9	E	7	1030.459	+0.063733
	1135.411		1135.411	10	G	6	901.4163	-0.01696
	1298.474		1298.474	11	Y	5	844.3948	+0.087629
	1385.506		1385.506	12	S	4	681.3315	+0.073504
	1513.565	-0.16177	1513.565	13	Q	3	594.2994	+0.089602
	1676.628	-0.3916	1676.628	14	Y	2	466.2409	+0.100725
-0.41428	902.847	-0.18443	1804.687	15	Q	1	303.1775	+0.153525
				16	R	0	175.119	



Scan number	1404	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	190.53

precursor information

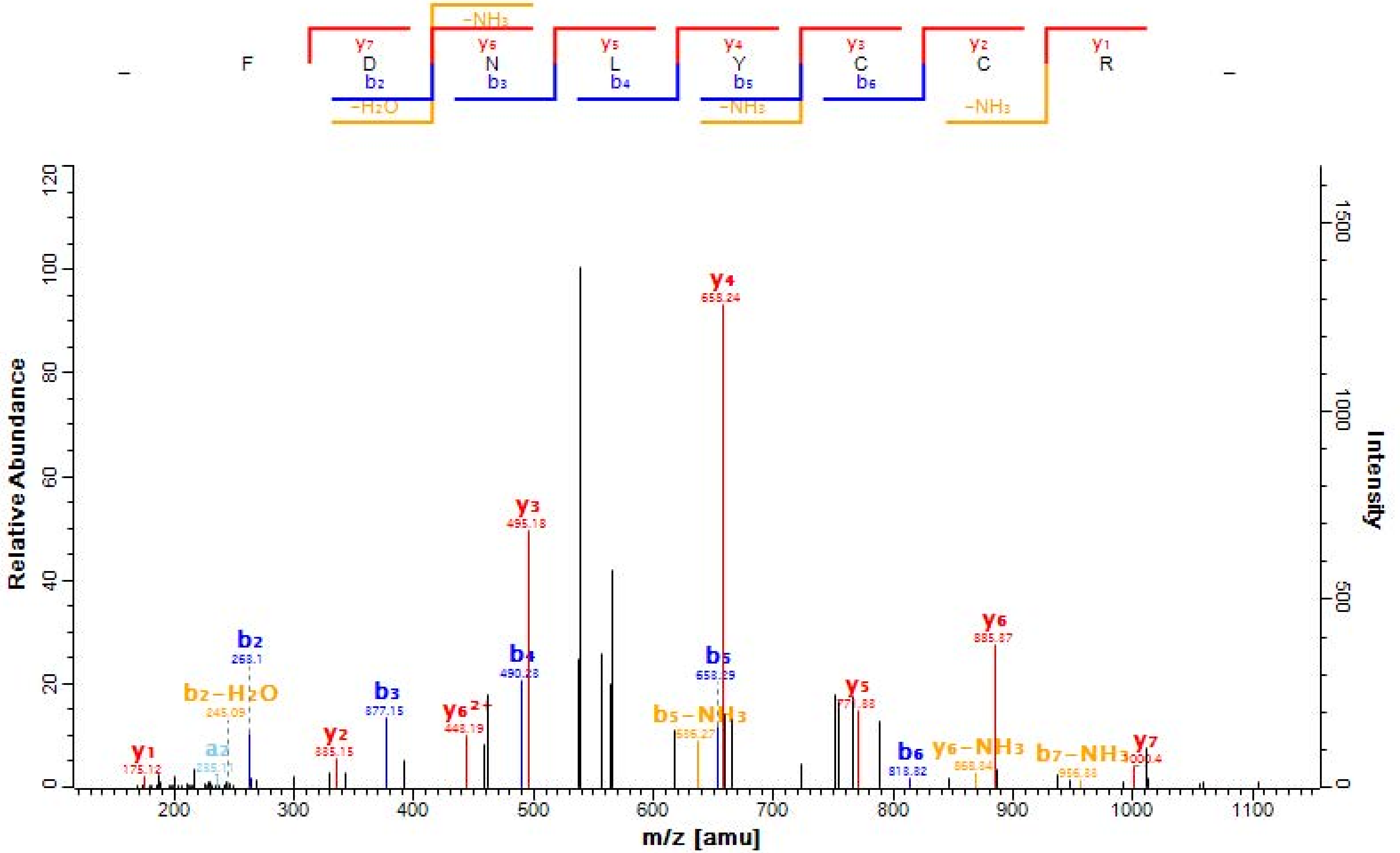
Mass:	1263.51564
m/z:	632.7651
Charge:	2+
Retentiontime:	14.104748725891
Score:	190.531
Mass Error [ppm]:	0.0094832
PEP:	1.2029E-08
Precursor Type:	MULTI

g

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	64 %
Peak Coverage:	39 %
Protein Localisation:	140 ... 149

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.08		164.07	1	Y	9				
-0.039	251.1	+0.0963	279.1	2	D	8	1101.5	-0.094	1101.5	
	365.15	+0.0604	393.14	3	N	7	986.43	-0.023	493.72	+0.347
	494.19		522.18	4	E	6	872.39	-0.015	872.39	
	641.26	-0.018	669.25	5	F	5	743.35	+0.0245	743.35	
	698.28		726.27	6	G	4	596.28	+0.0507	596.28	
	861.34	-0.071	889.34	7	Y	3	539.26	+0.0586	539.26	
	948.37	+0.0589	976.37	8	S	2	376.19	+0.0643	376.19	
	1062.4	-0.015	1090.4	9	N	1	289.16	+0.0903	289.16	
				10	R	0	175.12		175.12	

Scan number	1825	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	117.89

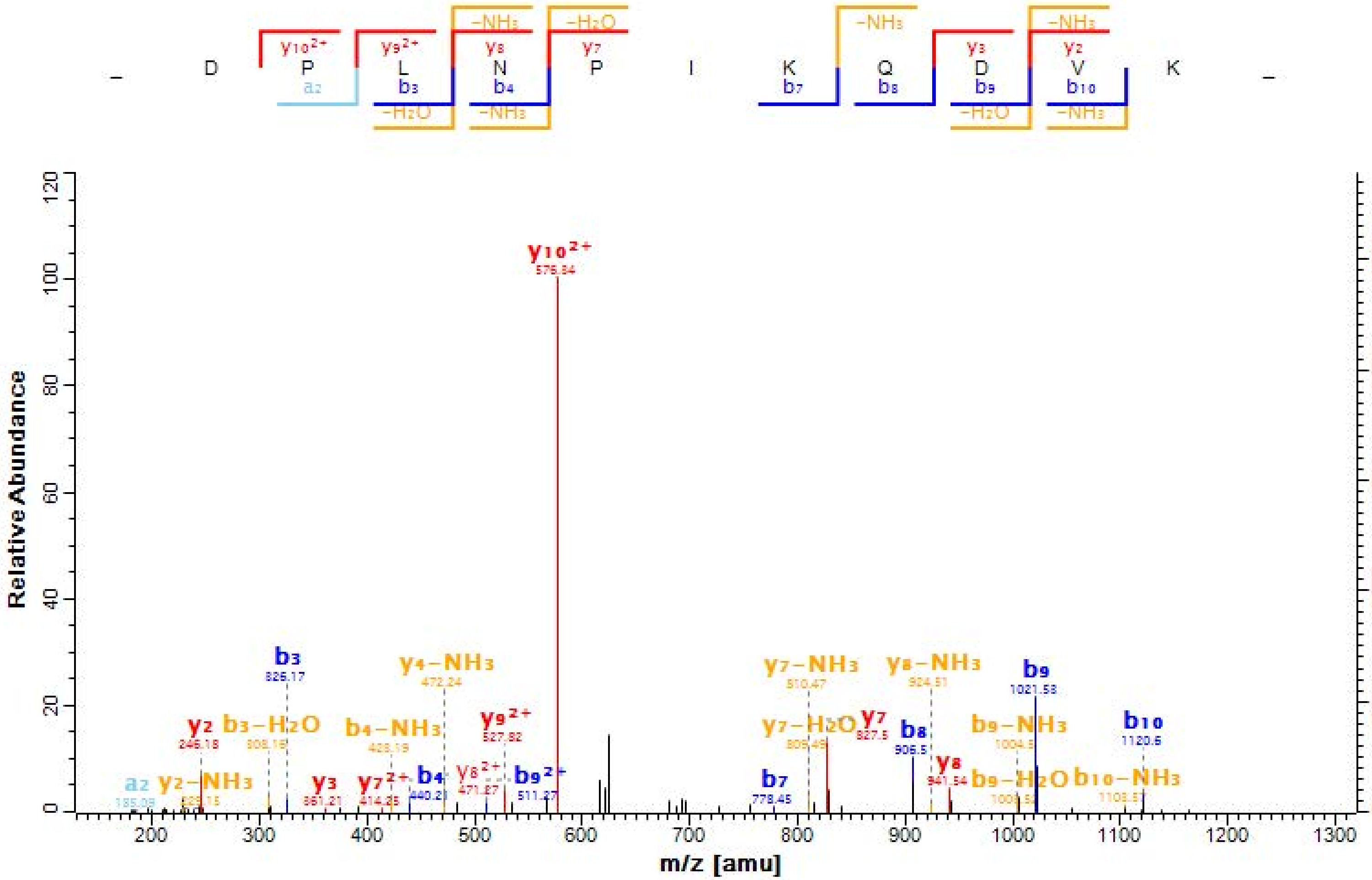


precursor information

Mass:	1146.45878
m/z:	574.23667
Charge:	2+
Retentiontime:	16.636901855468
Score:	117.8897
Mass Error [ppm]:	0.11565
PEP:	0.0020144
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	39 %
Peak Coverage:	19 %
Protein Localisation:	368 ... 375

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08		148.08	1	F	7				
+0.0111	235.11	-0.026	263.1	2	D	6	1000.4	+0.12	1000.4	
	349.15	+0.0875	377.15	3	N	5	885.37	+0.0329	443.19	+0.197
	462.23	-0.013	490.23	4	L	4	771.33	+0.0554	771.33	
	625.3	+0.0551	653.29	5	Y	3	658.24	+0.0563	658.24	
	785.33	-0.005	813.32	6	C	2	495.18	+0.1479	495.18	
	945.36		973.35	7	C	1	335.15	+0.0292	335.15	
				8	R	0	175.12	+0.0905	175.12	

Scan number	1833	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	164.33



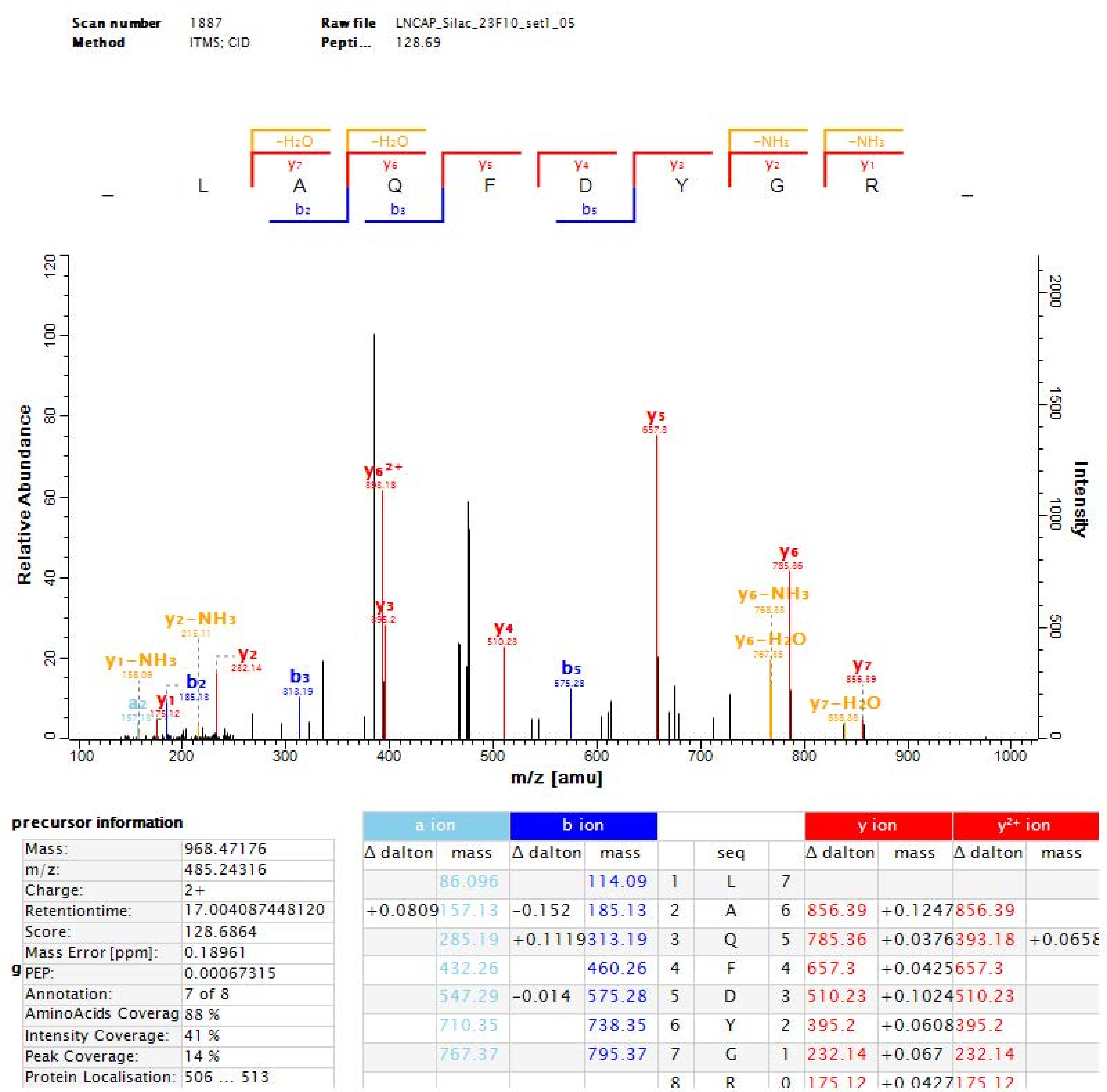
precursor information

Mass:	1265.69775
m/z:	633.85615
Charge:	2+
Retentiontime:	16.681453704834
Score:	164.3349
Mass Error [ppm]:	-0.15779
PEP:	7.229E-07
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	66 %
Peak Coverage:	25 %
Protein Localisation:	64 ... 74

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.04		116		116	1	D	10				
+0.266	185.1		213.1		213.1	2	P	9	1152		576.3	+0.21
	298.2		326.2	+0.1	326.2	3	L	8	1055		527.8	+0.29
	412.2		440.2	+0.071	440.2	4	N	7	941.5	+0.094	471.3	+0
	509.3		537.3		537.3	5	P	6	827.5	+0.055	414.3	-0.03
	622.4		650.4		650.4	6	I	5	730.4		730.4	
	750.5		778.4	-0.05	778.4	7	K	4	617.4		617.4	
	878.5		906.5	-0.01	906.5	8	Q	3	489.3		489.3	
	993.5	+0.229	511.3	-0.04	1022	9	D	2	361.2	+0.207	361.2	
	1093		1121	+0.044	1121	10	V	1	246.2	+0.037	246.2	
						11	K	0	147.1		147.1	

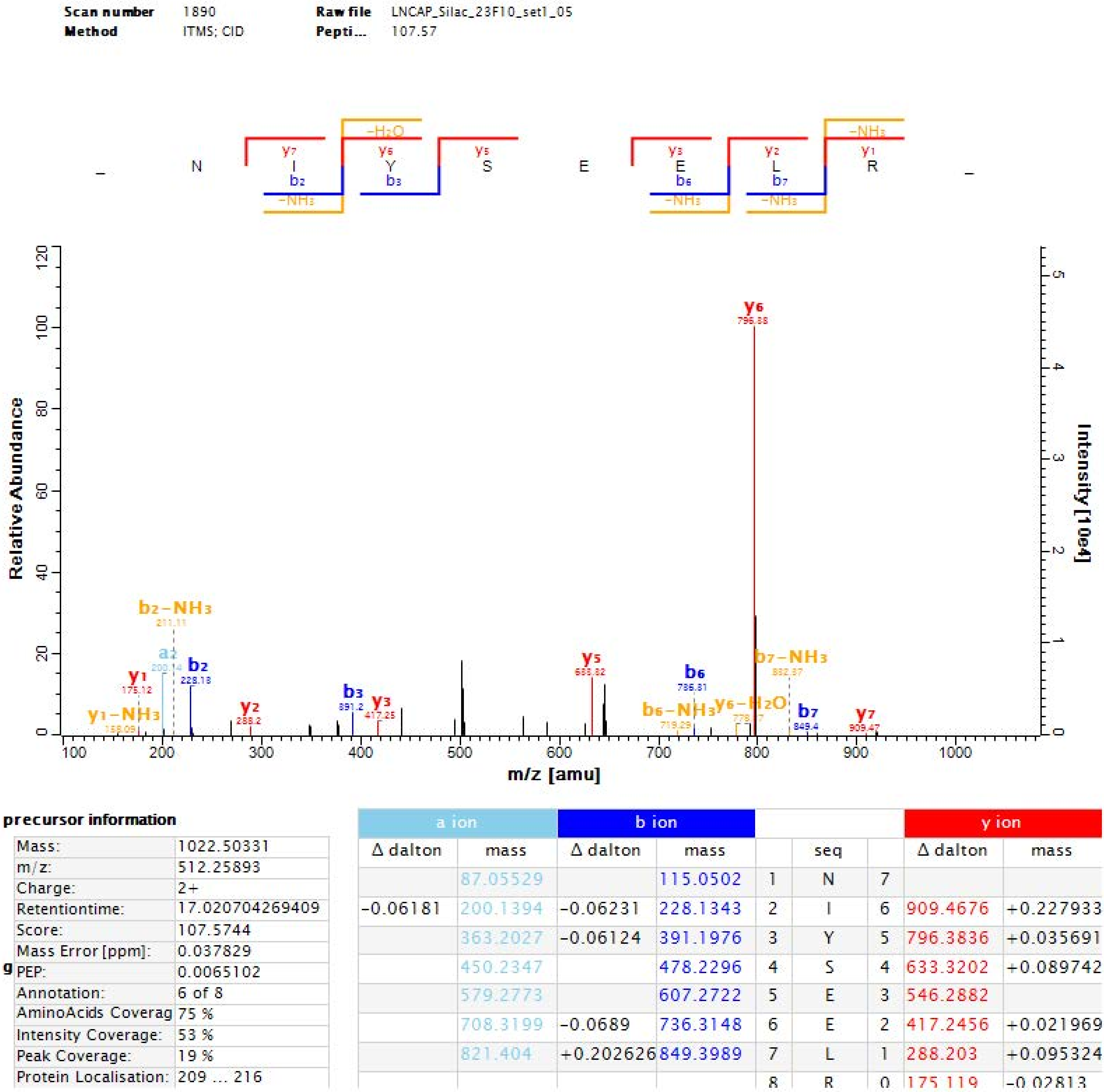


Scan number 1887
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set1_05
Pepti... 128.69

precursor information

Mass:	968.47176
m/z:	485.24316
Charge:	2+
Retentiontime:	17.004087448120
Score:	128.6864
Mass Error [ppm]:	0.18961
PEP:	0.00067315
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	41 %
Peak Coverage:	14 %
Protein Localisation:	506 ... 513

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	7				
+0.0809	157.13	-0.152	185.13	2	A	6	856.39	+0.1247	856.39	
	285.19	+0.1119	313.19	3	Q	5	785.36	+0.0376	393.18	+0.0658
	432.26		460.26	4	F	4	657.3	+0.0425	657.3	
	547.29	-0.014	575.28	5	D	3	510.23	+0.1024	510.23	
	710.35		738.35	6	Y	2	395.2	+0.0608	395.2	
	767.37		795.37	7	G	1	232.14	+0.067	232.14	
				8	R	0	175.12	+0.0427	175.12	



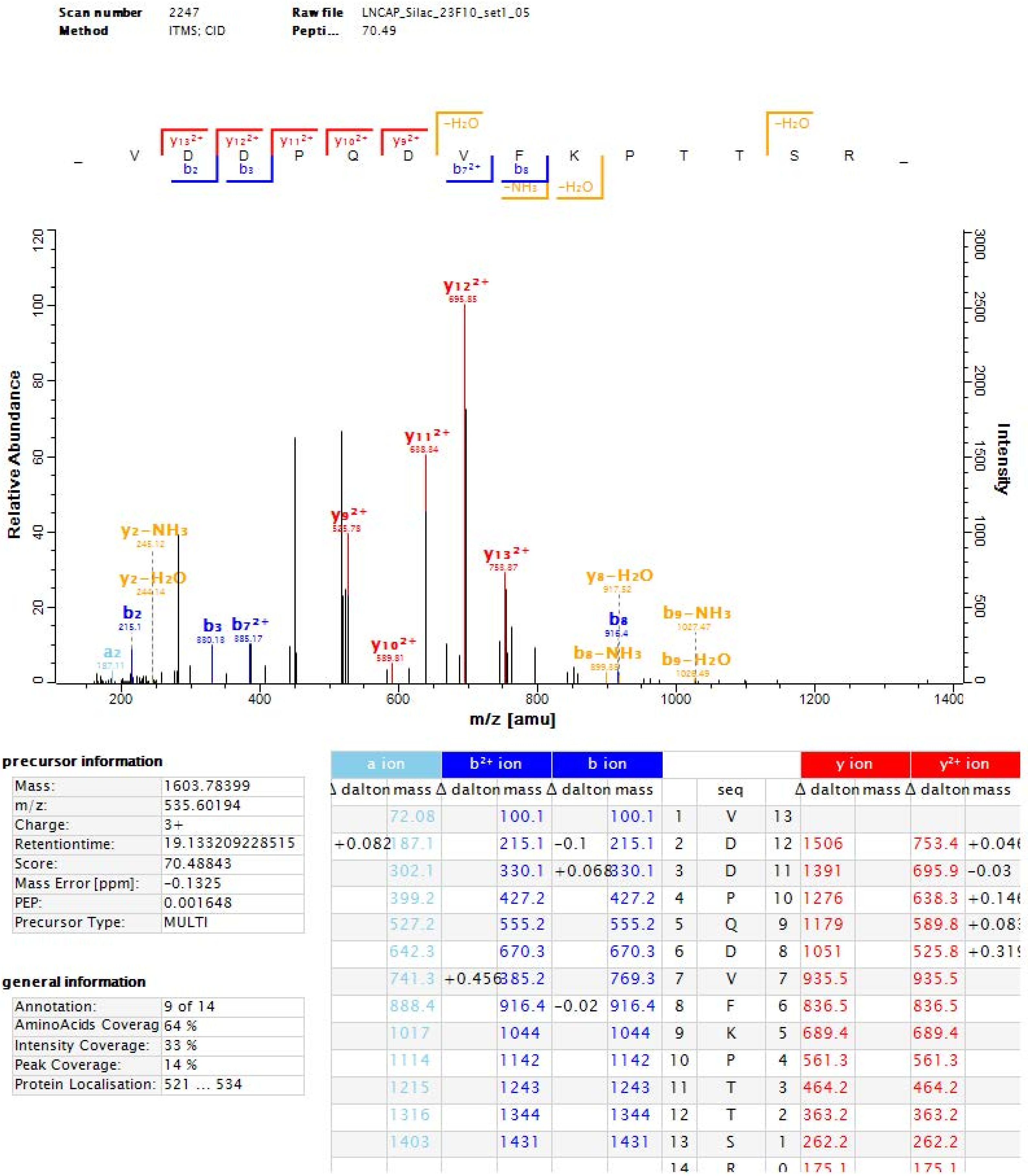
Scan number 1890
Raw file LNCAP_Silac_23F10_set1_05
Method ITMS; CID
Pepti... 107.57

precursor information

g

Mass:	1022.50331
m/z:	512.25893
Charge:	2+
Retentiontime:	17.020704269409
Score:	107.5744
Mass Error [ppm]:	0.037829
PEP:	0.0065102
Annotation:	6 of 8
AminoAcids Coverag	75 %
Intensity Coverage:	53 %
Peak Coverage:	19 %
Protein Localisation:	209 ... 216

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	87.05529		115.0502	1	N	7		
-0.06181	200.1394	-0.06231	228.1343	2	I	6	909.4676	+0.227933
	363.2027	-0.06124	391.1976	3	Y	5	796.3836	+0.035691
	450.2347		478.2296	4	S	4	633.3202	+0.089742
	579.2773		607.2722	5	E	3	546.2882	
	708.3199	-0.0689	736.3148	6	E	2	417.2456	+0.021969
	821.404	+0.202626	849.3989	7	L	1	288.203	+0.095324
				8	R	0	175.119	-0.02813



Scan number	2247	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	70.49

precursor information

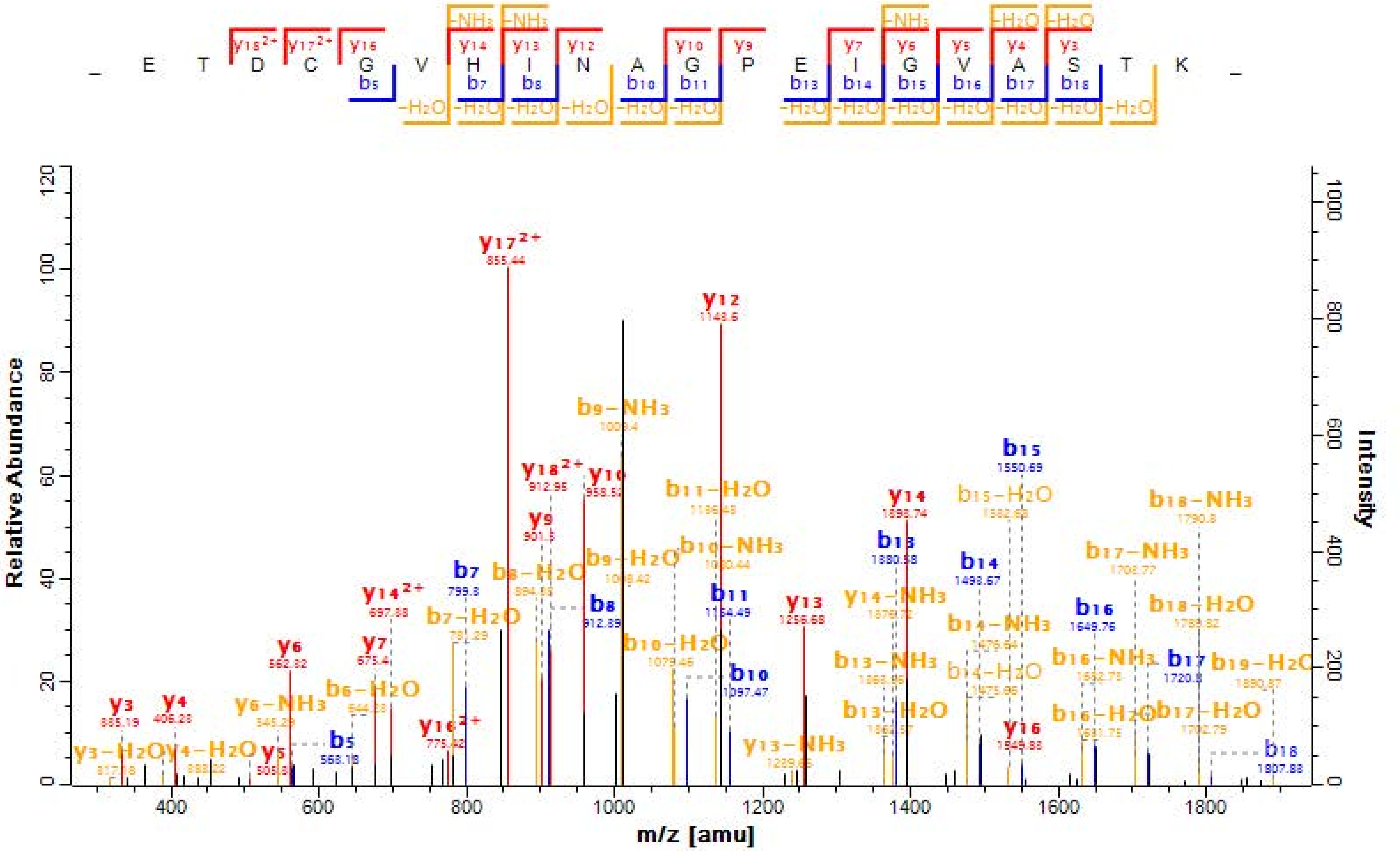
Mass:	1603.78399
m/z:	535.60194
Charge:	3+
Retentiontime:	19.133209228515
Score:	70.48843
Mass Error [ppm]:	-0.1325
PEP:	0.001648
Precursor Type:	MULTI

general information

Annotation:	9 of 14
AminoAcids Coverag	64 %
Intensity Coverage:	33 %
Peak Coverage:	14 %
Protein Localisation:	521 ... 534

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.08		100.1		100.1	1	V	13				
+0.082	187.1		215.1	-0.1	215.1	2	D	12	1506		753.4	+0.04
	302.1		330.1	+0.068	330.1	3	D	11	1391		695.9	-0.03
	399.2		427.2		427.2	4	P	10	1276		638.3	+0.14
	527.2		555.2		555.2	5	Q	9	1179		589.8	+0.08
	642.3		670.3		670.3	6	D	8	1051		525.8	+0.31
	741.3	+0.456	385.2		769.3	7	V	7	935.5		935.5	
	888.4		916.4	-0.02	916.4	8	F	6	836.5		836.5	
	1017		1044		1044	9	K	5	689.4		689.4	
	1114		1142		1142	10	P	4	561.3		561.3	
	1215		1243		1243	11	T	3	464.2		464.2	
	1316		1344		1344	12	T	2	363.2		363.2	
	1403		1431		1431	13	S	1	262.2		262.2	
						14	R	0	175.1		175.1	

Scan number	2856	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	320.23



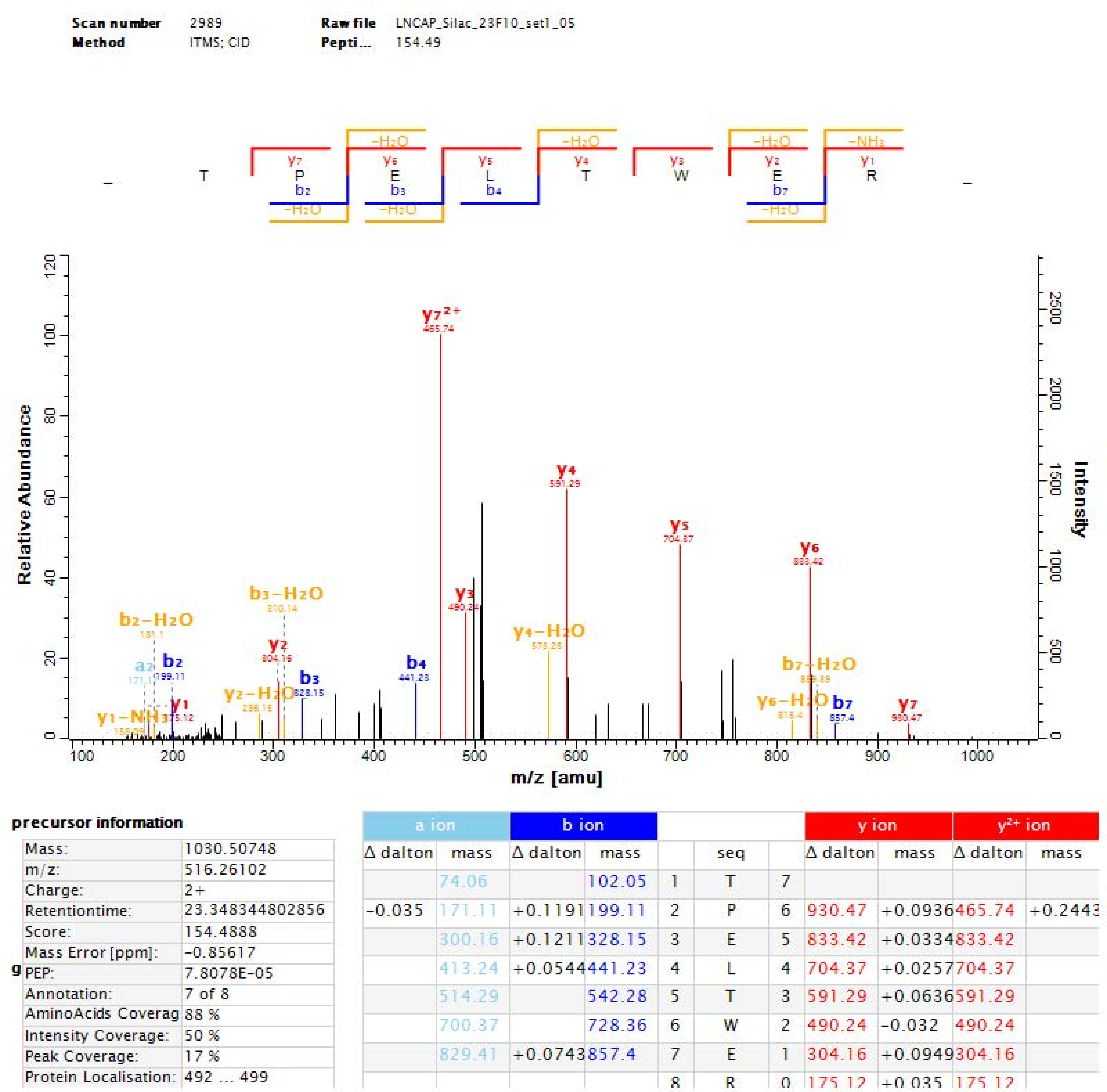
precursor information

Mass:	2053.97445
m/z:	1027.9945
Charge:	2+
Retentiontime:	22.603683471679
Score:	320.2345
Mass Error [ppm]:	0.28311
PEP:	1.419E-142
Precursor Type:	MULTI

general information

Annotation:	17 of 20
AminoAcids Coverag	85 %
Intensity Coverage:	73 %
Peak Coverage:	55 %
Protein Localisation:	475 ... 494

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	19				
	231.0975	2	T	18	1925.939		1925.939	
	346.1245	3	D	17	1824.891		912.9491	+0.290061
	506.1551	4	C	16	1709.864		855.4356	+0.288762
+0.23868	563.1766	5	G	15	1549.833	-0.12149	775.4203	-0.0805
	662.245	6	V	14	1492.812		1492.812	
+0.16299	799.3039	7	H	13	1393.743	-0.01037	697.3753	+0.059657
-0.04876	912.388	8	I	12	1256.684	+0.062456	1256.684	
	1026.431	9	N	11	1143.6	+0.040685	1143.6	
-0.00954	1097.468	10	A	10	1029.558		1029.558	
+0.081791	1154.489	11	G	9	958.5204	-0.00403	958.5204	
	1251.542	12	P	8	901.4989	+0.050149	901.4989	
-0.08461	1380.585	13	E	7	804.4462		804.4462	
-0.01413	1493.669	14	I	6	675.4036	+0.214353	675.4036	
+0.081102	1550.69	15	G	5	562.3195	+0.072099	562.3195	
+0.044182	1649.759	16	V	4	505.298	+0.360714	505.298	
-0.1111	1720.796	17	A	3	406.2296	+0.088002	406.2296	
-0.08551	1807.828	18	S	2	335.1925	+0.052576	335.1925	
	1908.876	19	T	1	248.1605		248.1605	
		20	K	0	147.1128		147.1128	

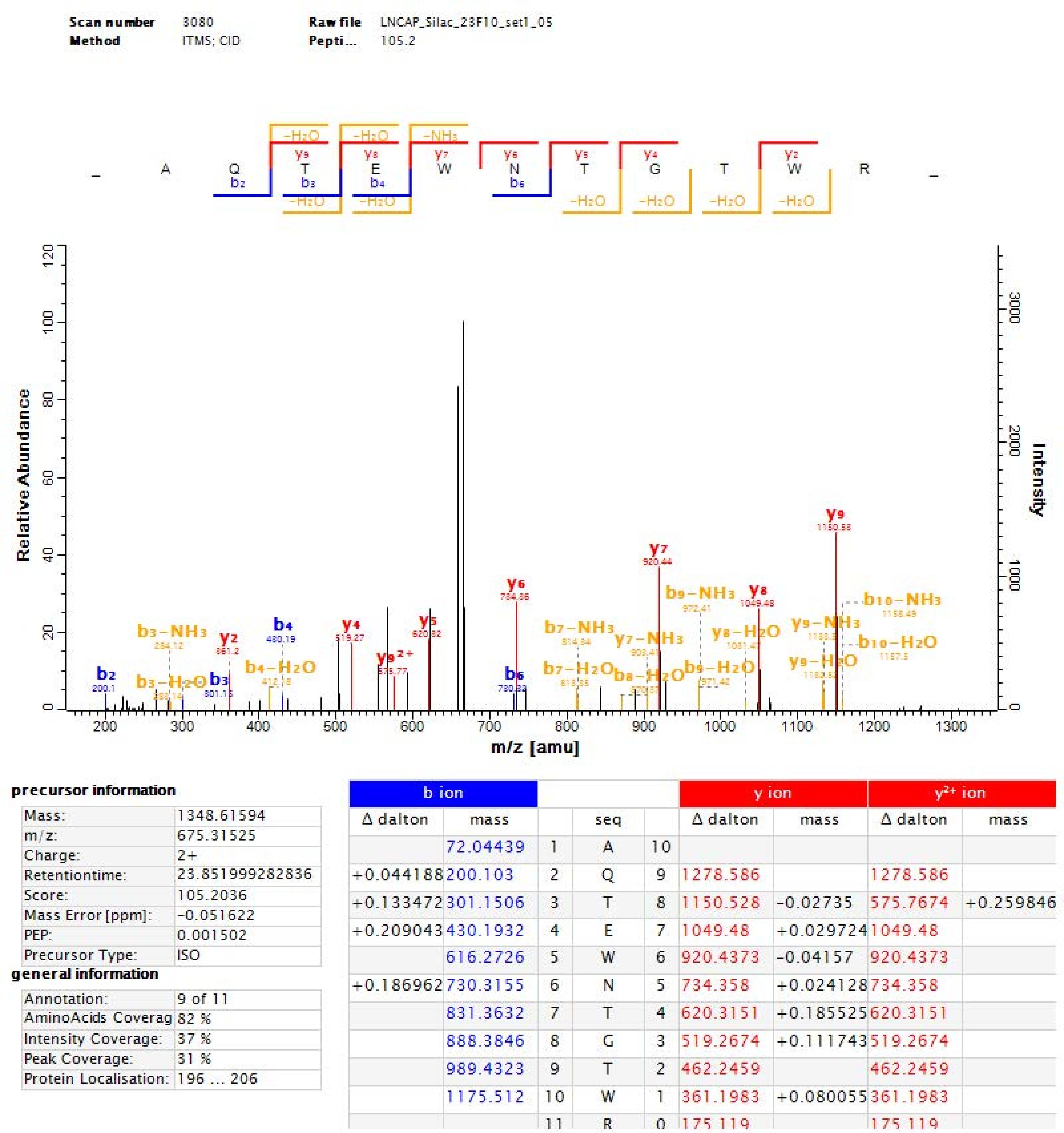


Scan number 2989
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set1_05
Pepti... 154.49

precursor information

Mass:	1030.50748
m/z:	516.26102
Charge:	2+
Retentiontime:	23.348344802856
Score:	154.4888
Mass Error [ppm]:	-0.85617
PEP:	7.8078E-05
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	50 %
Peak Coverage:	17 %
Protein Localisation:	492 ... 499

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.05	1	T	7				
-0.035	171.11	+0.1191	199.11	2	P	6	930.47	+0.0936	465.74	+0.2443
	300.16	+0.1211	328.15	3	E	5	833.42	+0.0334	833.42	
	413.24	+0.0544	441.23	4	L	4	704.37	+0.0257	704.37	
	514.29		542.28	5	T	3	591.29	+0.0636	591.29	
	700.37		728.36	6	W	2	490.24	-0.032	490.24	
	829.41	+0.0743	857.4	7	E	1	304.16	+0.0949	304.16	
				8	R	0	175.12	+0.035	175.12	



Scan number	3080	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	105.2

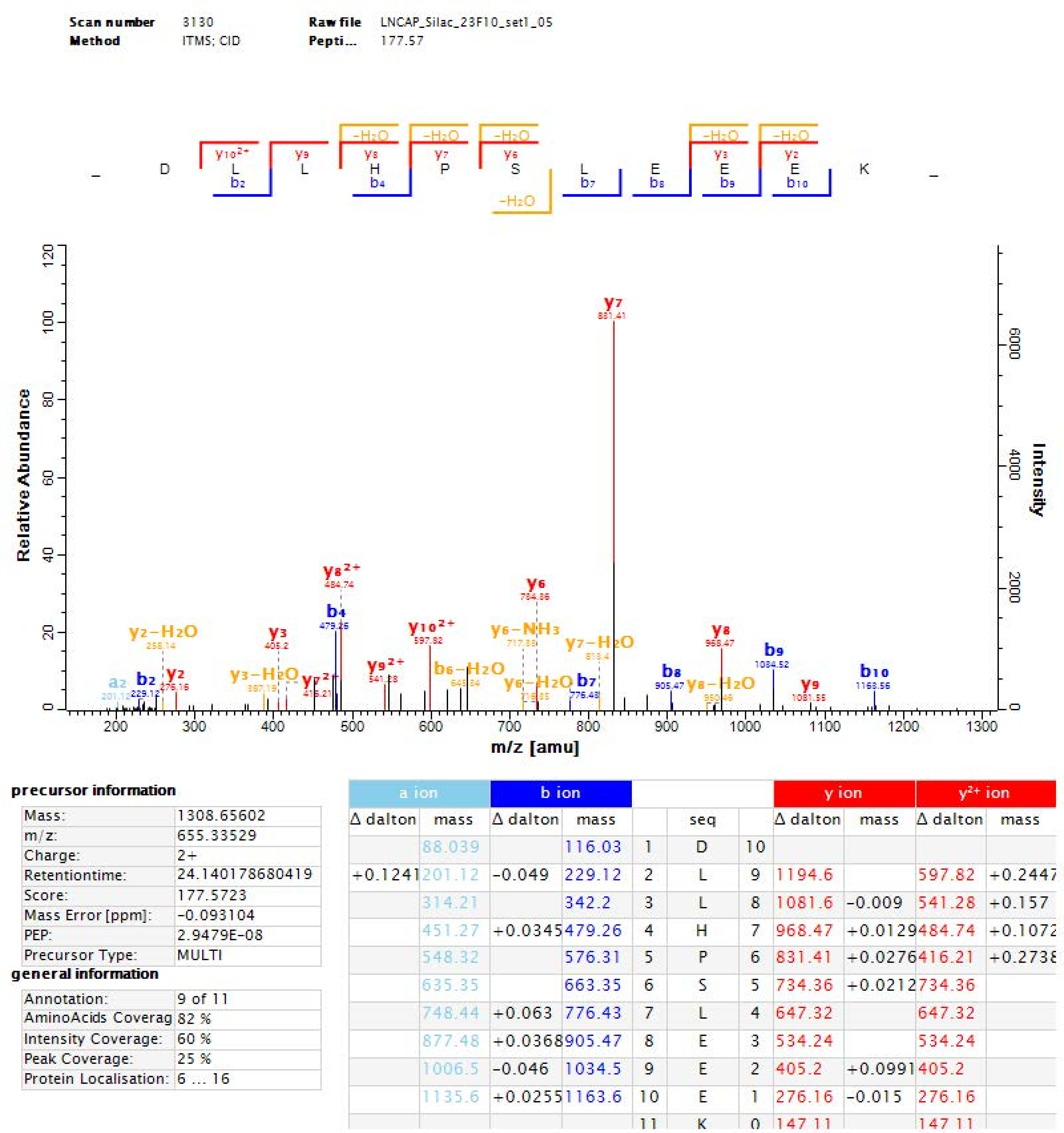
precursor information

Mass:	1348.61594
m/z:	675.31525
Charge:	2+
Retentiontime:	23.851999282836
Score:	105.2036
Mass Error [ppm]:	-0.051622
PEP:	0.001502
Precursor Type:	ISO

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	37 %
Peak Coverage:	31 %
Protein Localisation:	196 ... 206

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	10				
+0.044188	200.103	2	Q	9	1278.586		1278.586	
+0.133472	301.1506	3	T	8	1150.528	-0.02735	575.7674	+0.259846
+0.209043	430.1932	4	E	7	1049.48	+0.029724	1049.48	
	616.2726	5	W	6	920.4373	-0.04157	920.4373	
+0.186962	730.3155	6	N	5	734.358	+0.024128	734.358	
	831.3632	7	T	4	620.3151	+0.185525	620.3151	
	888.3846	8	G	3	519.2674	+0.111743	519.2674	
	989.4323	9	T	2	462.2459		462.2459	
	1175.512	10	W	1	361.1983	+0.080055	361.1983	
		11	R	0	175.119		175.119	



Scan number	3130	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	177.57

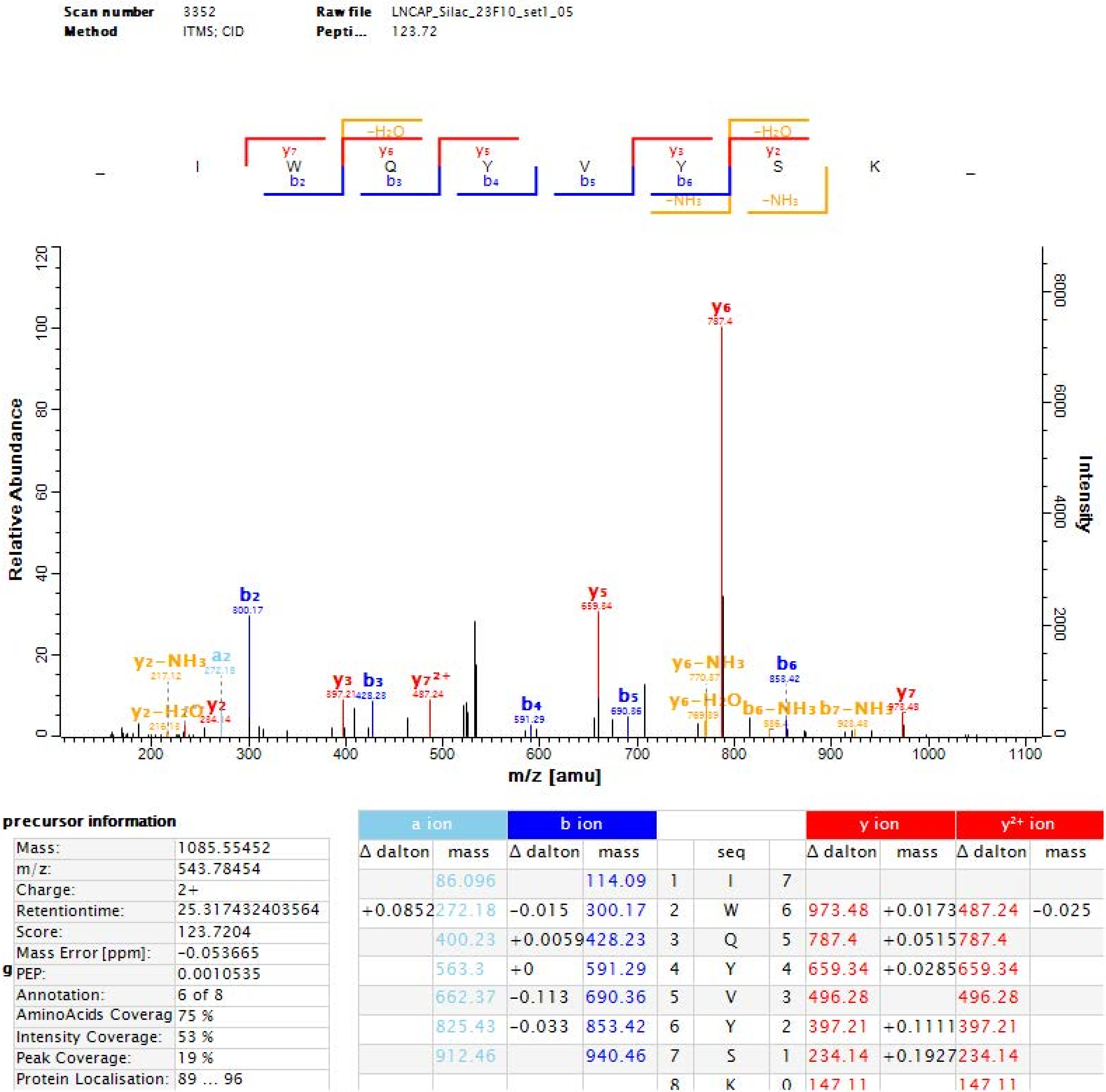
precursor information

Mass:	1308.65602
m/z:	655.33529
Charge:	2+
Retentiontime:	24.140178680419
Score:	177.5723
Mass Error [ppm]:	-0.093104
PEP:	2.9479E-08
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	60 %
Peak Coverage:	25 %
Protein Localisation:	6 ... 16

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	10				
+0.1241	201.12	-0.049	229.12	2	L	9	1194.6		597.82	+0.2447
	314.21		342.2	3	L	8	1081.6	-0.009	541.28	+0.157
	451.27	+0.0345	479.26	4	H	7	968.47	+0.0129	484.74	+0.1072
	548.32		576.31	5	P	6	831.41	+0.0276	416.21	+0.273
	635.35		663.35	6	S	5	734.36	+0.0212	734.36	
	748.44	+0.063	776.43	7	L	4	647.32		647.32	
	877.48	+0.0368	905.47	8	E	3	534.24		534.24	
	1006.5	-0.046	1034.5	9	E	2	405.2	+0.0991	405.2	
	1135.6	+0.0255	1163.6	10	E	1	276.16	-0.015	276.16	
				11	K	0	147.11		147.11	

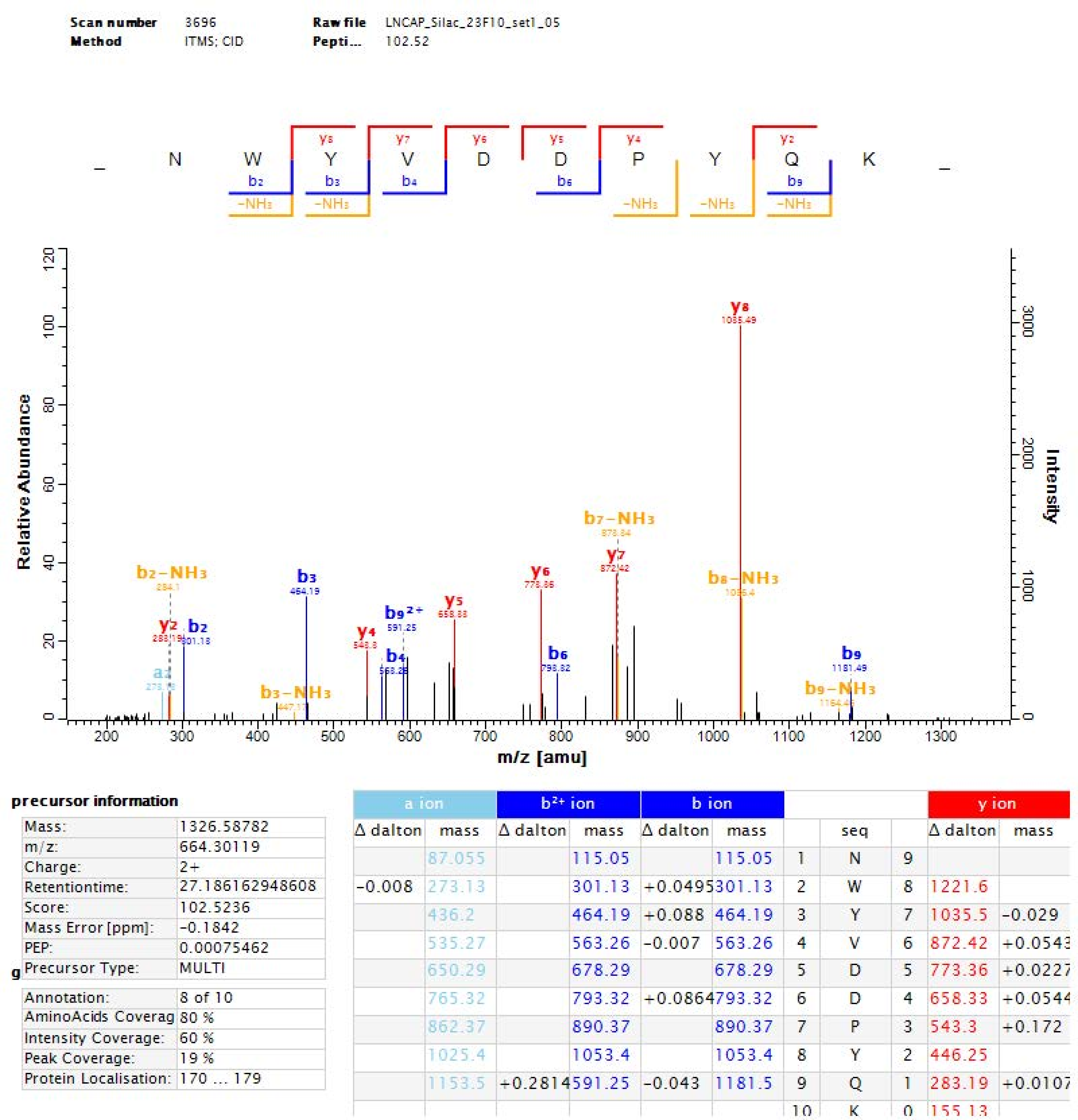


Scan number 3352 **Raw file** LNCAP_Silac_23F10_set1_05
Method ITMS; CID **Pepti...** 123.72

precursor information

Mass:	1085.55452
m/z:	543.78454
Charge:	2+
Retentiontime:	25.317432403564
Score:	123.7204
Mass Error [ppm]:	-0.053665
PEP:	0.0010535
Annotation:	6 of 8
AminoAcids Coverag	75 %
Intensity Coverage:	53 %
Peak Coverage:	19 %
Protein Localisation:	89 ... 96

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	7				
+0.0852	272.18	-0.015	300.17	2	W	6	973.48	+0.0173	487.24	-0.025
	400.23	+0.0059	428.23	3	Q	5	787.4	+0.0515	787.4	
	563.3	+0	591.29	4	Y	4	659.34	+0.0285	659.34	
	662.37	-0.113	690.36	5	V	3	496.28		496.28	
	825.43	-0.033	853.42	6	Y	2	397.21	+0.1111	397.21	
	912.46		940.46	7	S	1	234.14	+0.1927	234.14	
				8	K	0	147.11		147.11	



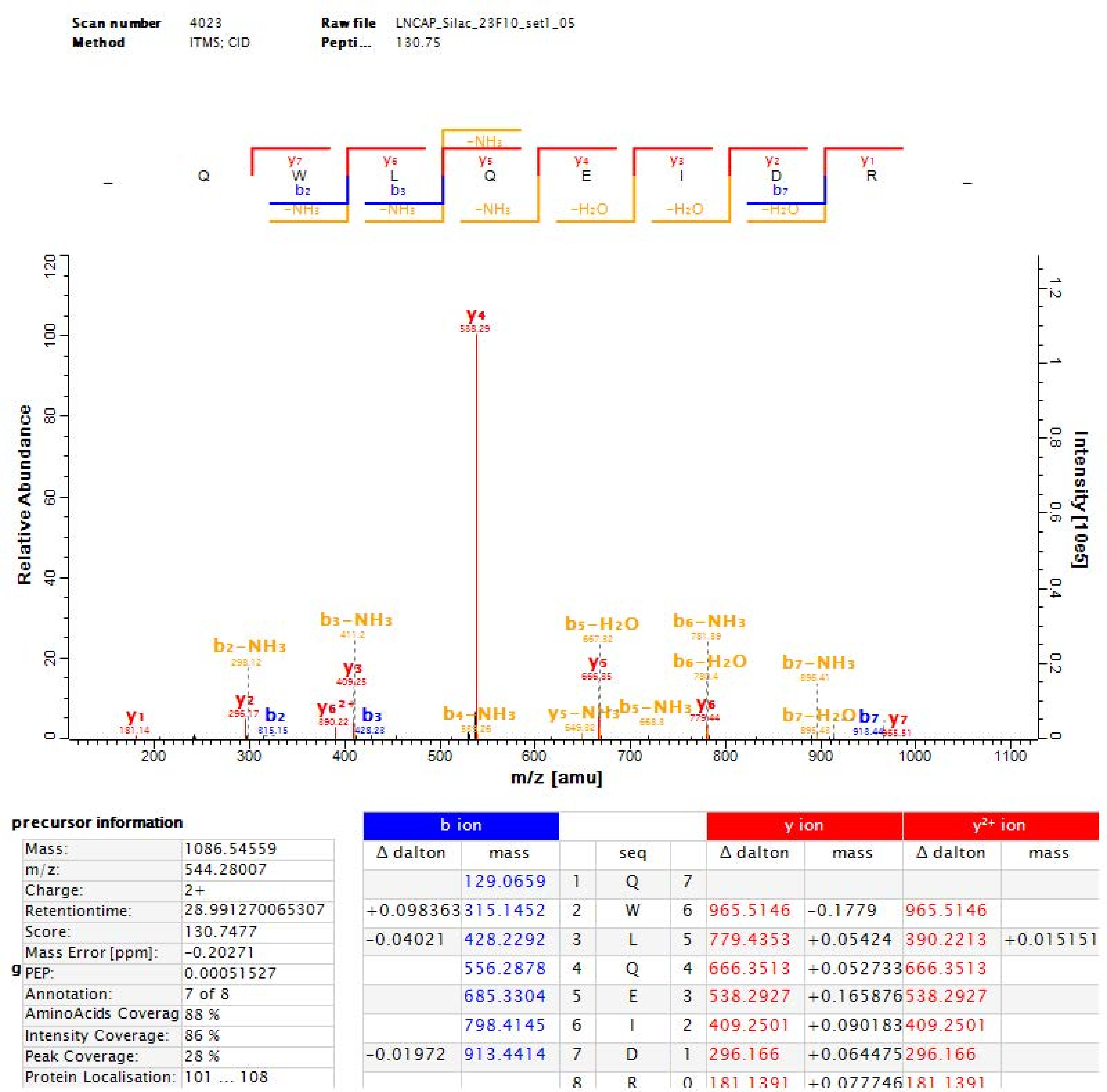
Scan number	3696	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	102.52

precursor information

Mass:	1326.58782
m/z:	664.30119
Charge:	2+
Retentiontime:	27.186162948608
Score:	102.5236
Mass Error [ppm]:	-0.1842
PEP:	0.00075462
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	60 %
Peak Coverage:	19 %
Protein Localisation:	170 ... 179

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	87.055		115.05		115.05	1	N	9		
-0.008	273.13		301.13	+0.0495	301.13	2	W	8	1221.6	
	436.2		464.19	+0.088	464.19	3	Y	7	1035.5	-0.029
	535.27		563.26	-0.007	563.26	4	V	6	872.42	+0.0543
	650.29		678.29		678.29	5	D	5	773.36	+0.0227
	765.32		793.32	+0.0864	793.32	6	D	4	658.33	+0.0544
	862.37		890.37		890.37	7	P	3	543.3	+0.172
	1025.4		1053.4		1053.4	8	Y	2	446.25	
	1153.5	+0.2814	591.25	-0.043	1181.5	9	Q	1	283.19	+0.0107
						10	K	0	155.13	



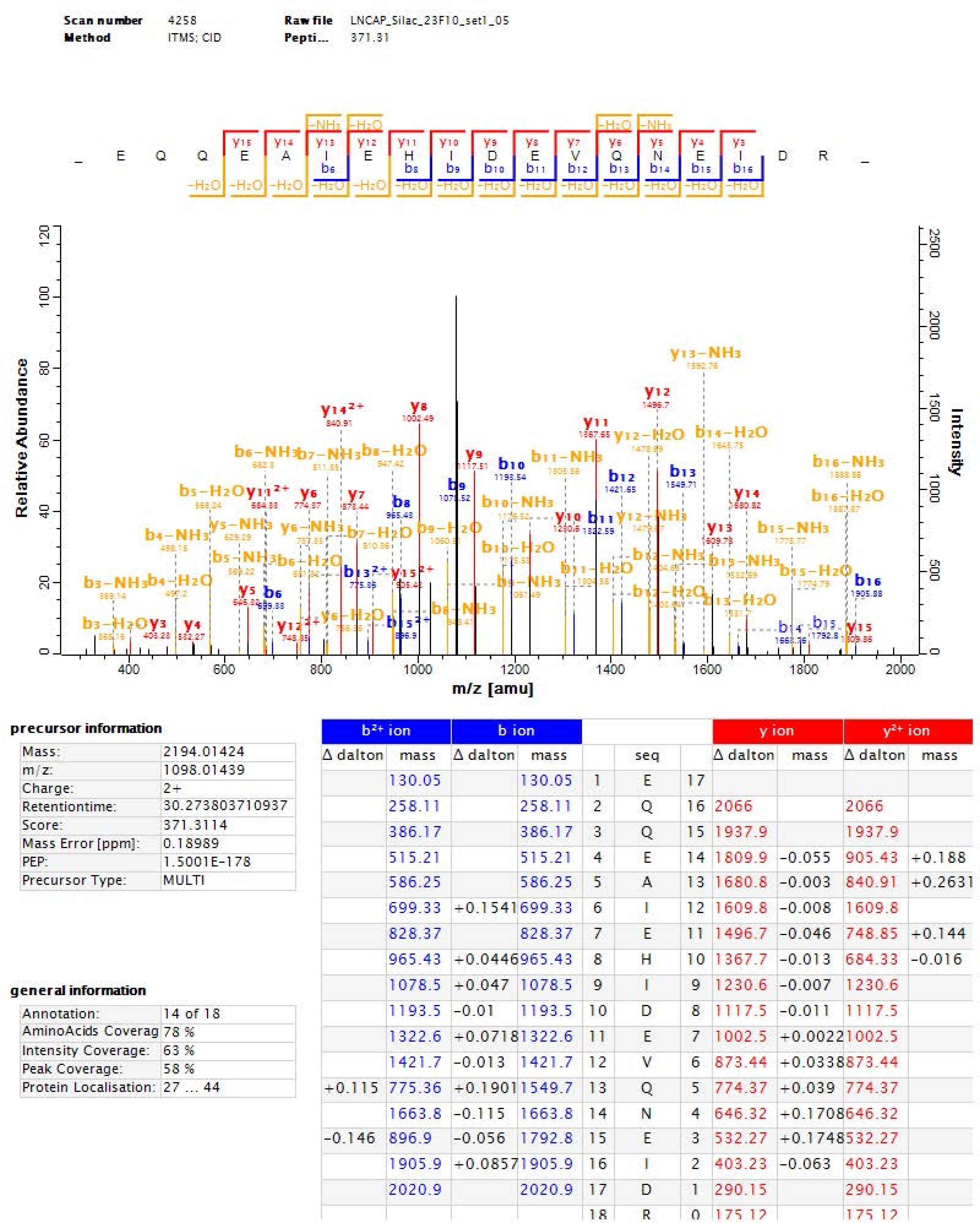
Scan number	4023	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	130.75

precursor information

Mass:	1086.54559
m/z:	544.28007
Charge:	2+
Retentiontime:	28.991270065307
Score:	130.7477
Mass Error [ppm]:	-0.20271
PEP:	0.00051527
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	86 %
Peak Coverage:	28 %
Protein Localisation:	101 ... 108

g

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.0659	1	Q	7				
+0.098363	315.1452	2	W	6	965.5146	-0.1779	965.5146	
-0.04021	428.2292	3	L	5	779.4353	+0.05424	390.2213	+0.015151
	556.2878	4	Q	4	666.3513	+0.052733	666.3513	
	685.3304	5	E	3	538.2927	+0.165876	538.2927	
	798.4145	6	I	2	409.2501	+0.090183	409.2501	
-0.01972	913.4414	7	D	1	296.166	+0.064475	296.166	
		8	R	0	181.1391	+0.077746	181.1391	



Scan number	4258	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	371.31

precursor information

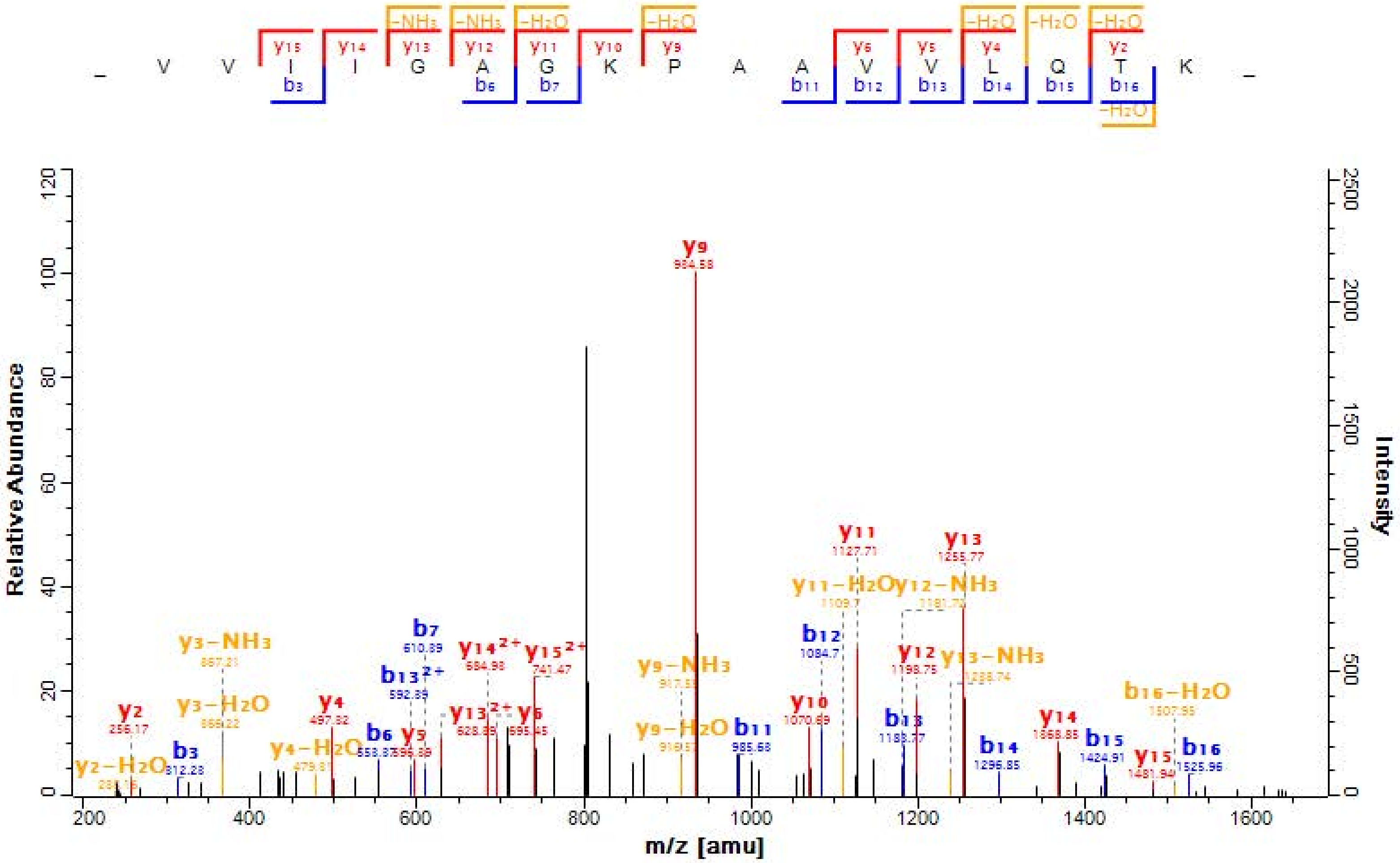
Mass:	2194.01424
m/z:	1098.01439
Charge:	2+
Retentiontime:	30.273803710937
Score:	371.3114
Mass Error [ppm]:	0.18989
PEP:	1.5001E-178
Precursor Type:	MULTI

general information

Annotation:	14 of 18
AminoAcids Coverag	78 %
Intensity Coverage:	63 %
Peak Coverage:	58 %
Protein Localisation:	27 ... 44

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	17				
	258.11		258.11	2	Q	16	2066		2066	
	386.17		386.17	3	Q	15	1937.9		1937.9	
	515.21		515.21	4	E	14	1809.9	-0.055	905.43	+0.188
	586.25		586.25	5	A	13	1680.8	-0.003	840.91	+0.2631
	699.33	+0.1541	699.33	6	I	12	1609.8	-0.008	1609.8	
	828.37		828.37	7	E	11	1496.7	-0.046	748.85	+0.144
	965.43	+0.0446	965.43	8	H	10	1367.7	-0.013	684.33	-0.016
	1078.5	+0.047	1078.5	9	I	9	1230.6	-0.007	1230.6	
	1193.5	-0.01	1193.5	10	D	8	1117.5	-0.011	1117.5	
	1322.6	+0.0718	1322.6	11	E	7	1002.5	+0.0022	1002.5	
	1421.7	-0.013	1421.7	12	V	6	873.44	+0.0338	873.44	
+0.115	775.36	+0.1901	1549.7	13	Q	5	774.37	+0.039	774.37	
	1663.8	-0.115	1663.8	14	N	4	646.32	+0.1708	646.32	
-0.146	896.9	-0.056	1792.8	15	E	3	532.27	+0.1748	532.27	
	1905.9	+0.0857	1905.9	16	I	2	403.23	-0.063	403.23	
	2020.9		2020.9	17	D	1	290.15		290.15	
				18	R	0	175.12		175.12	

Scan number	4294	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	186.77



precursor information

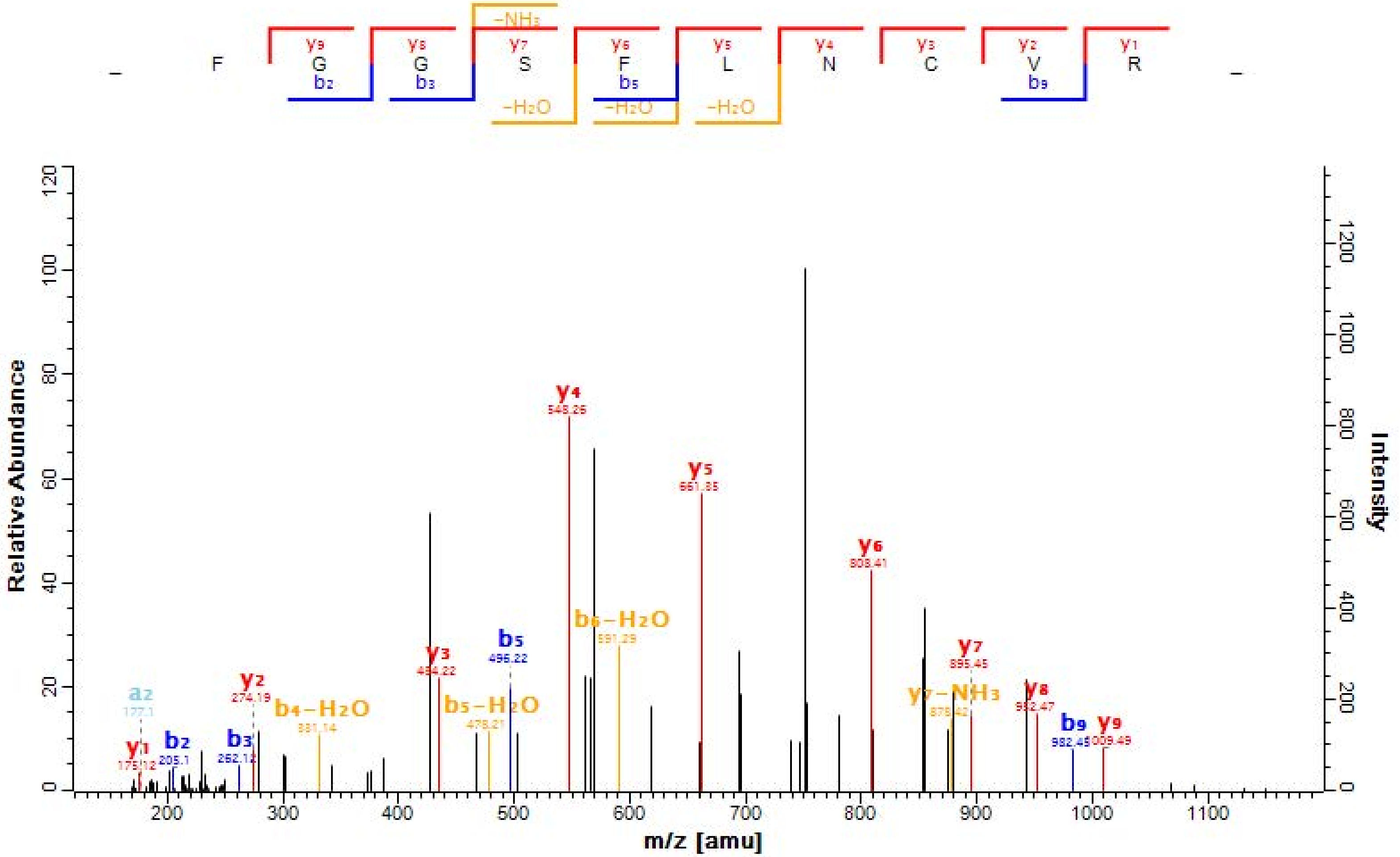
Mass:	1663.04012
m/z:	832.52733
Charge:	2+
Retentiontime:	30.465564727783
Score:	186.7722
Mass Error [ppm]:	0.29075
PEP:	7.3096E-34
Precursor Type:	MULTI

general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	51 %
Peak Coverage:	37 %
Protein Localisation:	943 ... 959

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	16				
	199.14		199.14	2	V	15	1581		1581	
	312.23	+0.0684	312.23	3	I	14	1481.9	+0.0394	741.47	+0.0421
	425.31		425.31	4	I	13	1368.9	-0.061	684.93	+0.3324
	482.33		482.33	5	G	12	1255.8	-0.093	628.39	+0.061
	553.37	+0.0734	553.37	6	A	11	1198.7	-0.091	1198.7	
	610.39	+0.108	610.39	7	G	10	1127.7	+0.0333	1127.7	
	746.5		746.5	8	K	9	1070.7	+0.0831	1070.7	
	843.55		843.55	9	P	8	934.58	+0	934.58	
	914.59		914.59	10	A	7	837.53		837.53	
	985.63	+0.0024	985.63	11	A	6	766.49		766.49	
	1084.7	-0.014	1084.7	12	V	5	695.45	+0.1636	695.45	
-0.006	592.39	-0.076	1183.8	13	V	4	596.39	+0.1954	596.39	
	1296.8	+0.0603	1296.8	14	L	3	497.32	+0.0896	497.32	
	1424.9	+0.1835	1424.9	15	Q	2	384.23		384.23	
	1526	+0.1075	1526	16	T	1	256.17	+0.0405	256.17	
				17	K	0	155.13		155.13	

Scan number	4773	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	82.26

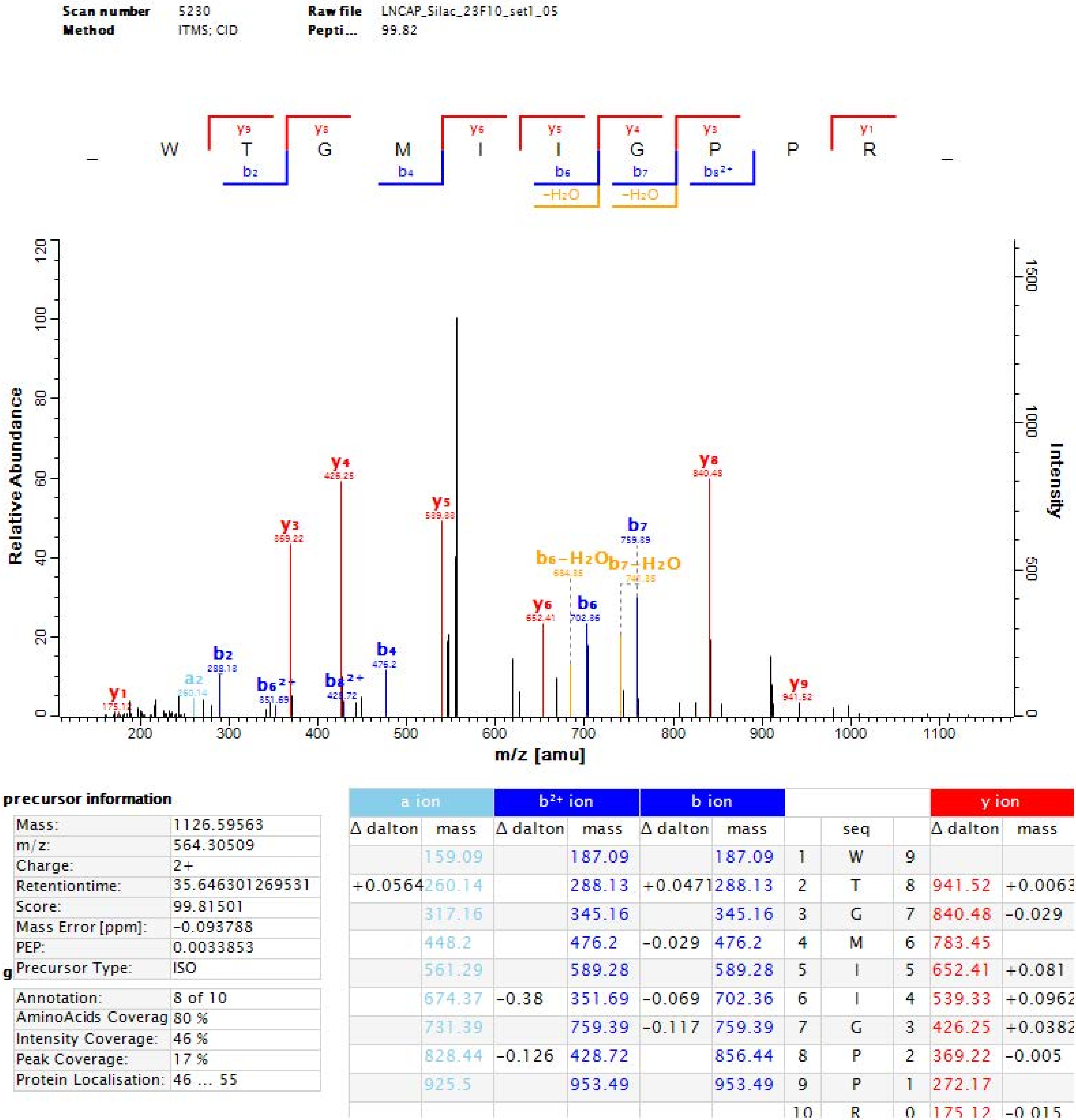


precursor information

Mass:	1155.54984
m/z:	578.7822
Charge:	2+
Retentiontime:	33.146770477294
Score:	82.26067
Mass Error [ppm]:	0.28479
PEP:	0.0046008
Precursor Type:	MULTI

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	34 %
Peak Coverage:	19 %
Protein Localisation:	163 ... 172

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	120.0808		148.0757	1	F	9		
+0.131785	177.1022	+0.03221	205.0972	2	G	8	1009.488	+0.054776
	234.1237	+0.036961	262.1186	3	G	7	952.4669	+0.1623
	321.1557		349.1506	4	S	6	895.4454	+0.073656
	468.2241	+0.382441	496.2191	5	F	5	808.4134	-0.00168
	581.3082		609.3031	6	L	4	661.345	+0.117214
	695.3511		723.3461	7	N	3	548.2609	+0.070662
	855.3818		883.3767	8	C	2	434.218	+0.039127
	954.4502	+0.109513	982.4451	9	V	1	274.1874	+0.08186
				10	R	0	175.119	+0.058752



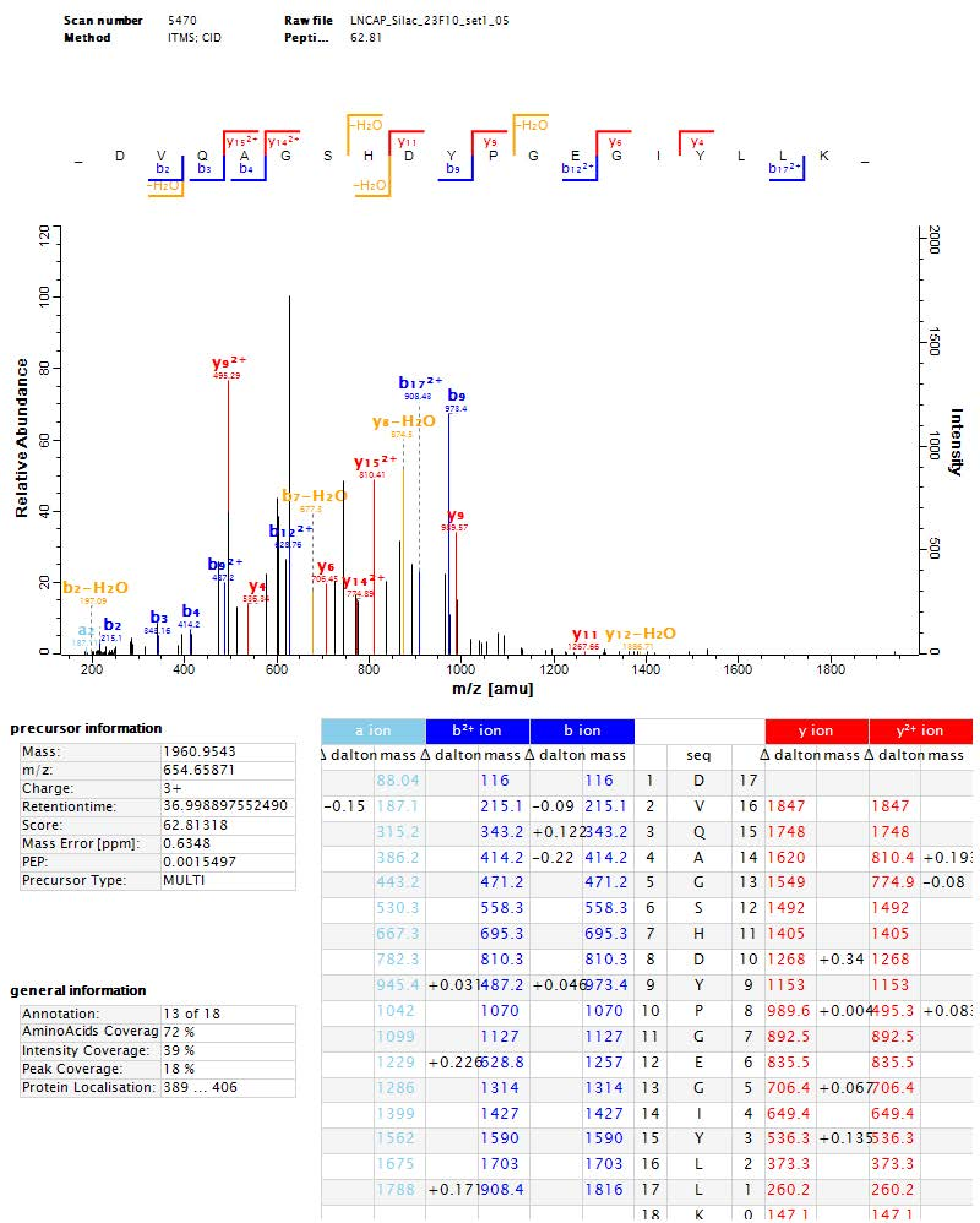
Scan number	5230	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	99.82

precursor information

Mass:	1126.59563
m/z:	564.30509
Charge:	2+
Retentiontime:	35.646301269531
Score:	99.81501
Mass Error [ppm]:	-0.093788
PEP:	0.0033853
Precursor Type:	ISO

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	46 %
Peak Coverage:	17 %
Protein Localisation:	46 ... 55

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	159.09		187.09		187.09	1	W	9		
+0.0564	260.14		288.13	+0.0471	288.13	2	T	8	941.52	+0.0063
	317.16		345.16		345.16	3	G	7	840.48	-0.029
	448.2		476.2	-0.029	476.2	4	M	6	783.45	
	561.29		589.28		589.28	5	I	5	652.41	+0.081
	674.37	-0.38	351.69	-0.069	702.36	6	I	4	539.33	+0.0962
	731.39		759.39	-0.117	759.39	7	G	3	426.25	+0.0382
	828.44	-0.126	428.72		856.44	8	P	2	369.22	-0.005
	925.5		953.49		953.49	9	P	1	272.17	
						10	R	0	175.12	-0.015



Scan number	5470	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	62.81

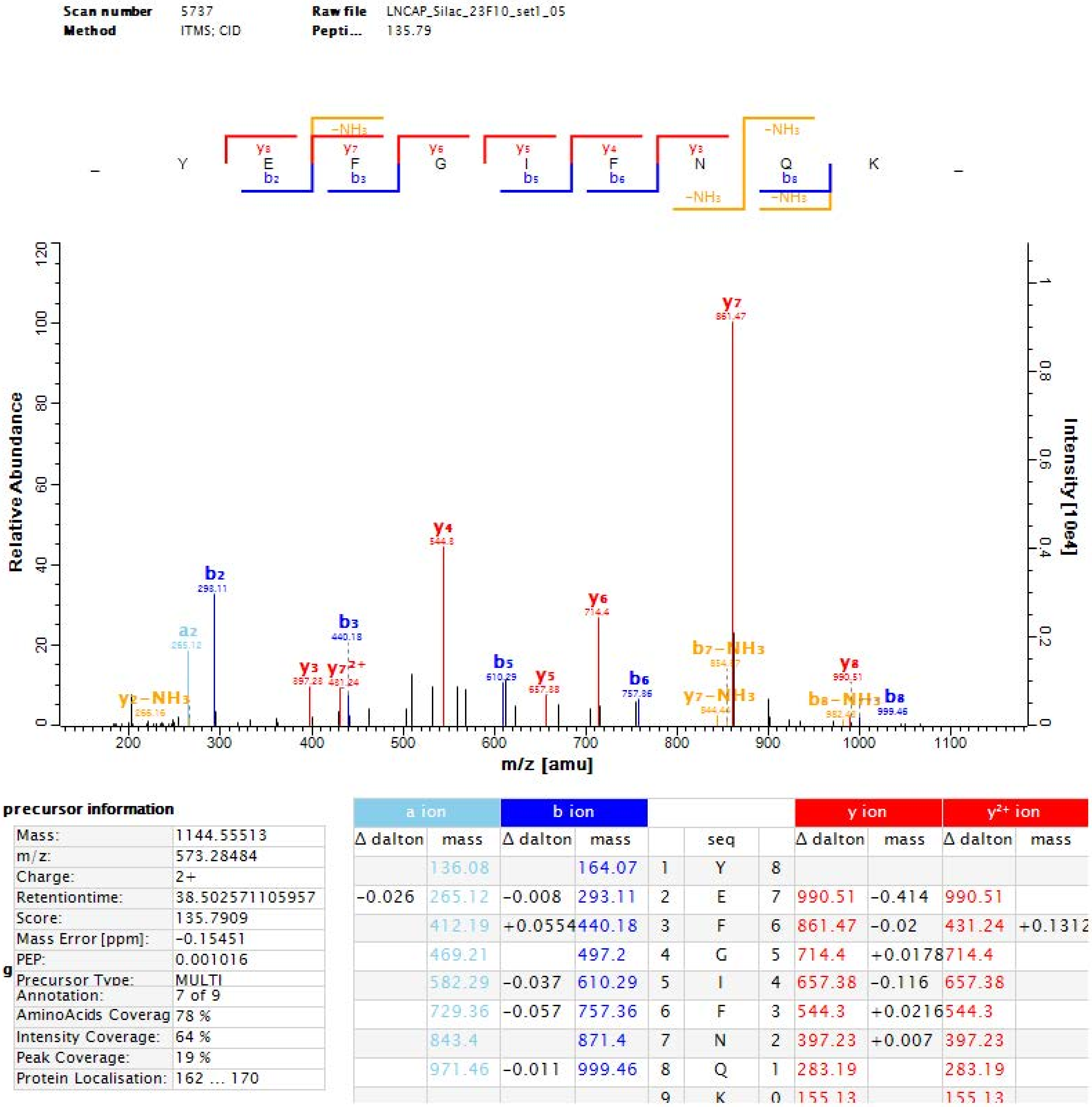
precursor information

Mass:	1960.9543
m/z:	654.65871
Charge:	3+
Retentiontime:	36.998897552490
Score:	62.81318
Mass Error [ppm]:	0.6348
PEP:	0.0015497
Precursor Type:	MULTI

general information

Annotation:	13 of 18
AminoAcids Coverag	72 %
Intensity Coverage:	39 %
Peak Coverage:	18 %
Protein Localisation:	389 ... 406

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.04		116		116	1	D	17				
-0.15	187.1		215.1	-0.09	215.1	2	V	16	1847		1847	
	315.2		343.2	+0.122	343.2	3	Q	15	1748		1748	
	386.2		414.2	-0.22	414.2	4	A	14	1620		810.4	+0.19
	443.2		471.2		471.2	5	G	13	1549		774.9	-0.08
	530.3		558.3		558.3	6	S	12	1492		1492	
	667.3		695.3		695.3	7	H	11	1405		1405	
	782.3		810.3		810.3	8	D	10	1268	+0.34	1268	
	945.4	+0.031	487.2	+0.046	973.4	9	Y	9	1153		1153	
	1042		1070		1070	10	P	8	989.6	+0.004	495.3	+0.08
	1099		1127		1127	11	G	7	892.5		892.5	
	1229	+0.226	628.8		1257	12	E	6	835.5		835.5	
	1286		1314		1314	13	G	5	706.4	+0.067	706.4	
	1399		1427		1427	14	I	4	649.4		649.4	
	1562		1590		1590	15	Y	3	536.3	+0.135	536.3	
	1675		1703		1703	16	L	2	373.3		373.3	
	1788	+0.171	908.4		1816	17	L	1	260.2		260.2	
						18	K	0	147.1		147.1	



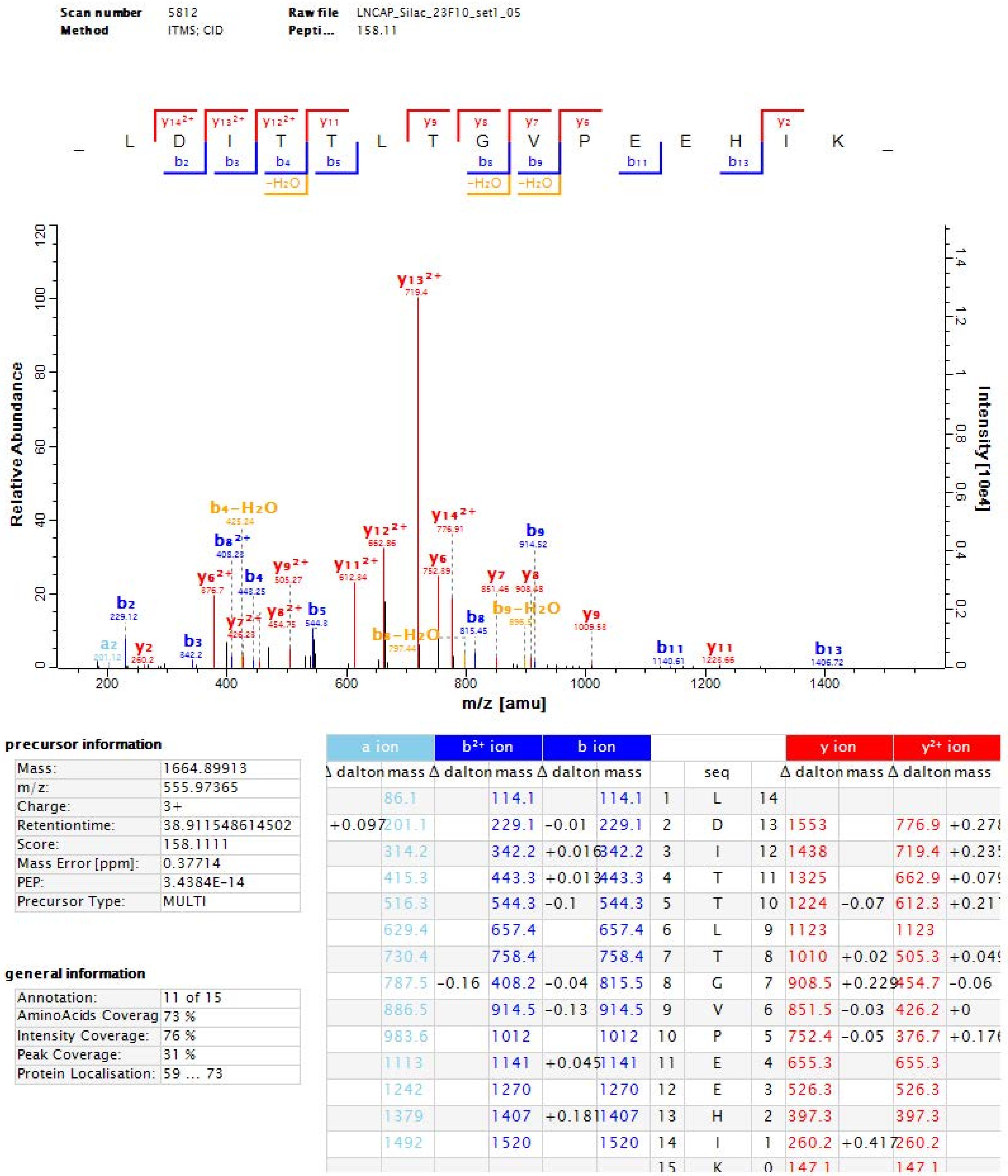
Scan number	5737	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	135.79

precursor information

g

Mass:	1144.55513
m/z:	573.28484
Charge:	2+
Retentiontime:	38.502571105957
Score:	135.7909
Mass Error [ppm]:	-0.15451
PEP:	0.001016
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	64 %
Peak Coverage:	19 %
Protein Localisation:	162 ... 170

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.08		164.07	1	Y	8				
-0.026	265.12	-0.008	293.11	2	E	7	990.51	-0.414	990.51	
	412.19	+0.0554	440.18	3	F	6	861.47	-0.02	431.24	+0.1312
	469.21		497.2	4	G	5	714.4	+0.0178	714.4	
	582.29	-0.037	610.29	5	I	4	657.38	-0.116	657.38	
	729.36	-0.057	757.36	6	F	3	544.3	+0.0216	544.3	
	843.4		871.4	7	N	2	397.23	+0.007	397.23	
	971.46	-0.011	999.46	8	Q	1	283.19		283.19	
				9	K	0	155.13		155.13	



Scan number	5812	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	158.11

precursor information

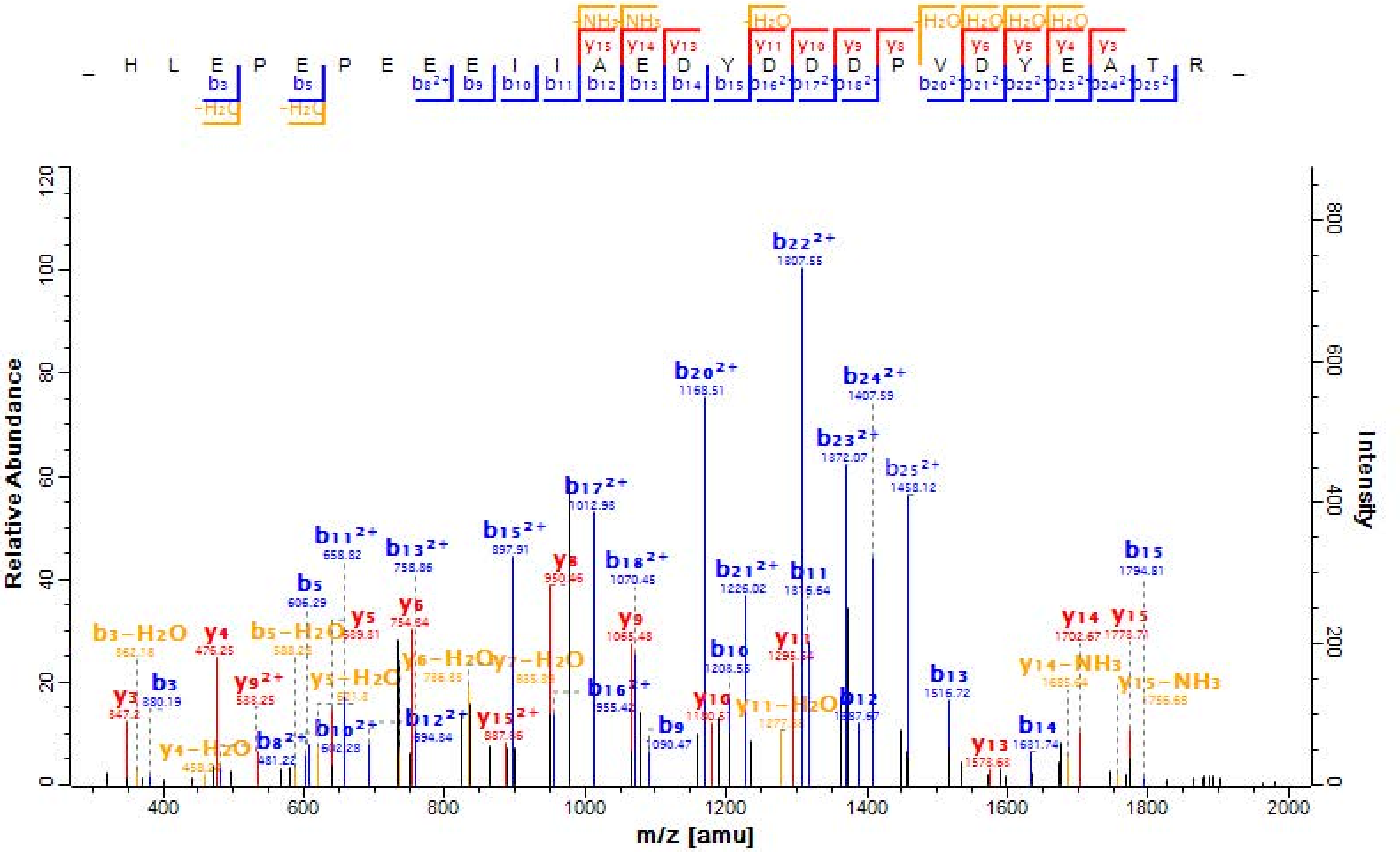
Mass:	1664.89913
m/z:	555.97365
Charge:	3+
Retentiontime:	38.911548614502
Score:	158.1111
Mass Error [ppm]:	0.37714
PEP:	3.4384E-14
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	76 %
Peak Coverage:	31 %
Protein Localisation:	59 ... 73

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	14				
+0.097	201.1		229.1	-0.01	229.1	2	D	13	1553		776.9	+0.27
	314.2		342.2	+0.016	342.2	3	I	12	1438		719.4	+0.23
	415.3		443.3	+0.013	443.3	4	T	11	1325		662.9	+0.07
	516.3		544.3	-0.1	544.3	5	T	10	1224	-0.07	612.3	+0.21
	629.4		657.4		657.4	6	L	9	1123		1123	
	730.4		758.4		758.4	7	T	8	1010	+0.02	505.3	+0.04
	787.5	-0.16	408.2	-0.04	815.5	8	G	7	908.5	+0.229	454.7	-0.06
	886.5		914.5	-0.13	914.5	9	V	6	851.5	-0.03	426.2	+0
	983.6		1012		1012	10	P	5	752.4	-0.05	376.7	+0.17
	1113		1141	+0.045	1141	11	E	4	655.3		655.3	
	1242		1270		1270	12	E	3	526.3		526.3	
	1379		1407	+0.181	1407	13	H	2	397.3		397.3	
	1492		1520		1520	14	I	1	260.2	+0.417	260.2	
						15	K	0	147.1		147.1	

Scan number	5988	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	232.29



precursor information

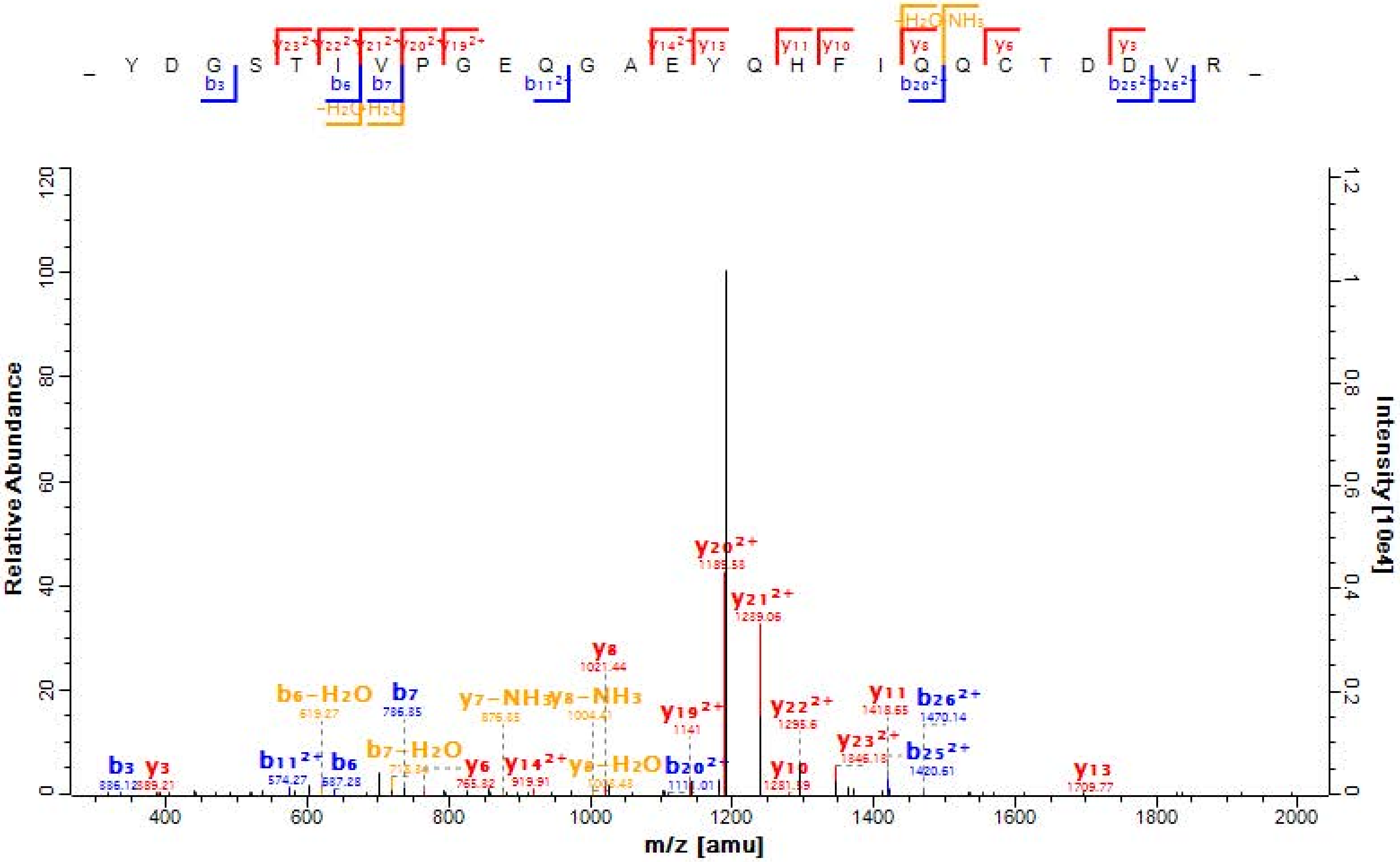
Mass:	3088.33105
m/z:	1030.45096
Charge:	3+
Retentiontime:	39.923168182373
Score:	232.2893
Mass Error [ppm]:	0.044294
PEP:	1.9191E-83
Precursor Type:	MULTI

general information

Annotation:	20 of 26
AminoAcids Coverag	77 %
Intensity Coverage:	68 %
Peak Coverage:	46 %
Protein Localisation:	19 ... 44

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.07		138.07	1	H	25				
	251.15		251.15	2	L	24	2952.3		2952.3	
	380.19	+0.2443	380.19	3	E	23	2839.2		2839.2	
	477.25		477.25	4	P	22	2710.2		2710.2	
	606.29	+0.16	606.29	5	E	21	2613.1		2613.1	
	703.34		703.34	6	P	20	2484.1		2484.1	
	832.38		832.38	7	E	19	2387		2387	
+0.036	481.22		961.43	8	E	18	2258		2258	
	1090.5	+0.1119	1090.5	9	E	17	2128.9		2128.9	
+0.2164	602.28	-0.024	1203.6	10	I	16	1999.9		1999.9	
+0.2496	658.82	+0.023	1316.6	11	I	15	1886.8		1886.8	
+0.0699	694.34	+0.0578	1387.7	12	A	14	1773.7	-0.096	887.36	+0.0645
+0.3315	758.86	-0.038	1516.7	13	E	13	1702.7	+0.0681	1702.7	
	1631.7	+0.125	1631.7	14	D	12	1573.6	+0.1376	1573.6	
+0.1913	897.91	-0.242	1794.8	15	Y	11	1458.6		1458.6	
+0.0316	955.42		1909.8	16	D	10	1295.5	+0.0875	1295.5	
+0.0936	1012.9		2024.9	17	D	9	1180.5	+0.0925	1180.5	
+0.1807	1070.4		2139.9	18	D	8	1065.5	+0.0426	533.25	+0.3101
	2236.9		2236.9	19	P	7	950.46	-0.025	950.46	
+0.3052	1168.5		2336	20	V	6	853.41		853.41	
+0.1955	1226		2451	21	D	5	754.34	+0.1107	754.34	
+0.1505	1307.6		2614.1	22	Y	4	639.31	+0.1471	639.31	
-0.045	1372.1		2743.1	23	E	3	476.25	+0.0706	476.25	
+0.15	1407.6		2814.2	24	A	2	347.2	+0.1028	347.2	
+0.2135	1458.1		2915.2	25	T	1	276.17		276.17	
				26	R	0	175.12		175.12	

Scan number	6158	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	69.4



precursor information

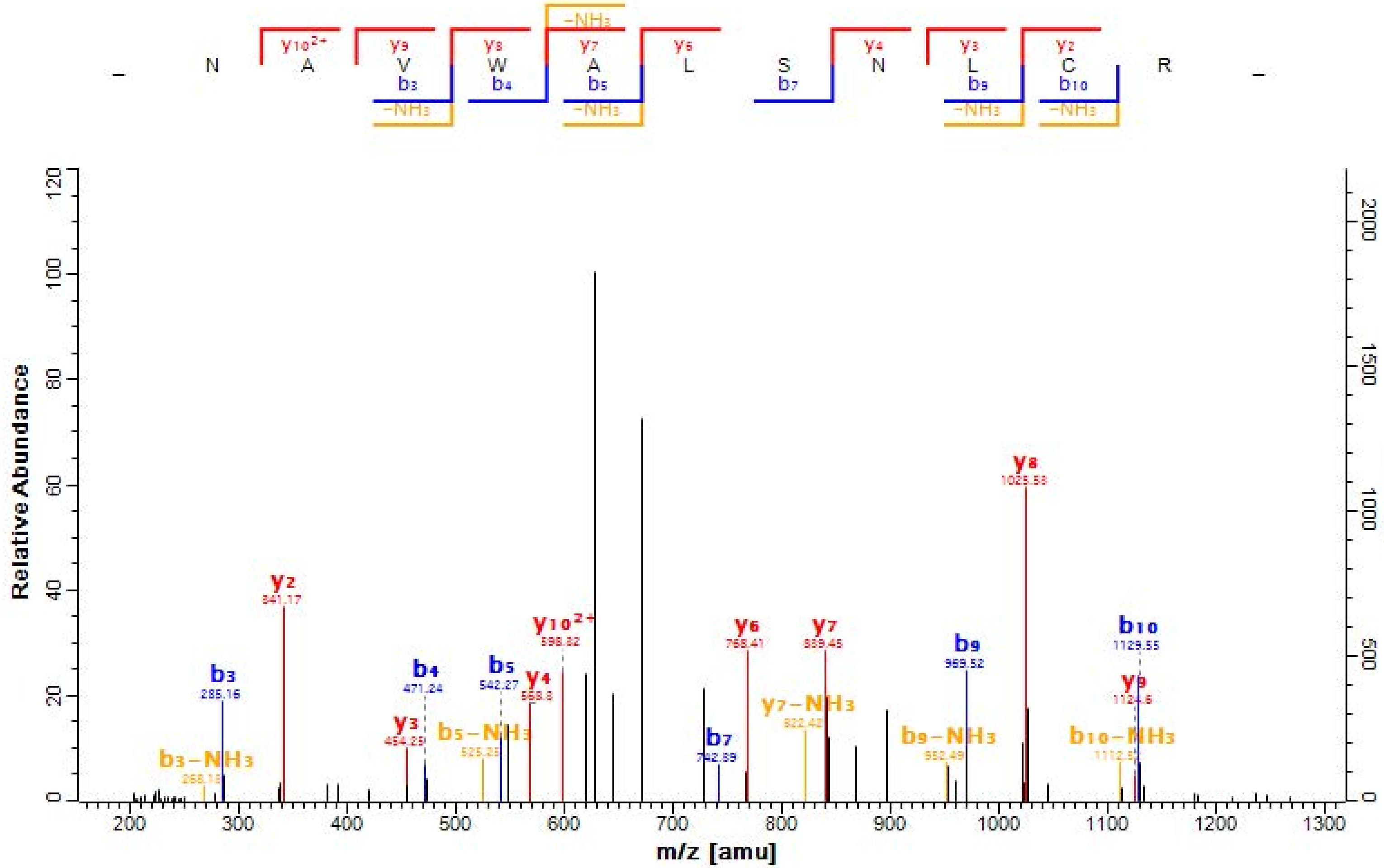
Mass:	3112.38213
m/z:	1038.46799
Charge:	3+
Retentiontime:	40.917778015136
Score:	69.3985
Mass Error [ppm]:	-0.35834
PEP:	6.6074E-06
Precursor Type:	MULTI

general information

Annotation:	16 of 27
AminoAcids Coverag	59 %
Intensity Coverage:	38 %
Peak Coverage:	24 %
Protein Localisation:	31 ... 57

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	164.07		164.07	1	Y	26				
	279.1		279.1	2	D	25	2950.3		2950.3	
	336.12	+0.0426	336.12	3	G	24	2835.3		2835.3	
	423.15		423.15	4	S	23	2778.3		2778.3	
	524.2		524.2	5	T	22	2691.2		1346.1	+0.3455
	637.28	-0.046	637.28	6	I	21	2590.2		1295.6	+0.1224
	736.35	-0.064	736.35	7	V	20	2477.1		1239.1	+0.3435
	833.4		833.4	8	P	19	2378		1189.5	+0.0378
	890.43		890.43	9	G	18	2281		1141	+0.3007
	1019.5		1019.5	10	E	17	2224		2224	
+0.2262	574.27		1147.5	11	Q	16	2094.9		2094.9	
	1204.5		1204.5	12	G	15	1966.9		1966.9	
	1275.6		1275.6	13	A	14	1909.8		1909.8	
	1404.6		1404.6	14	E	13	1838.8		919.91	-0.146
	1567.7		1567.7	15	Y	12	1709.8	-0.023	1709.8	
	1695.7		1695.7	16	Q	11	1546.7		1546.7	
	1832.8		1832.8	17	H	10	1418.6	+0.4739	1418.6	
	1979.9		1979.9	18	F	9	1281.6	-0.117	1281.6	
	2093		2093	19	I	8	1134.5		1134.5	
+0.0372	1111		2221	20	Q	7	1021.4	-0.053	1021.4	
	2349.1		2349.1	21	Q	6	893.38		893.38	
	2509.1		2509.1	22	C	5	765.32	-0.067	765.32	
	2610.2		2610.2	23	T	4	605.29		605.29	
	2725.2		2725.2	24	D	3	504.24		504.24	
+0.2951	1420.6		2840.2	25	D	2	389.21	+0.4819	389.21	
-0.026	1470.1		2939.3	26	V	1	274.19		274.19	
				27	R	0	175.12		175.12	

Scan number	6174	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	135.99



precursor information

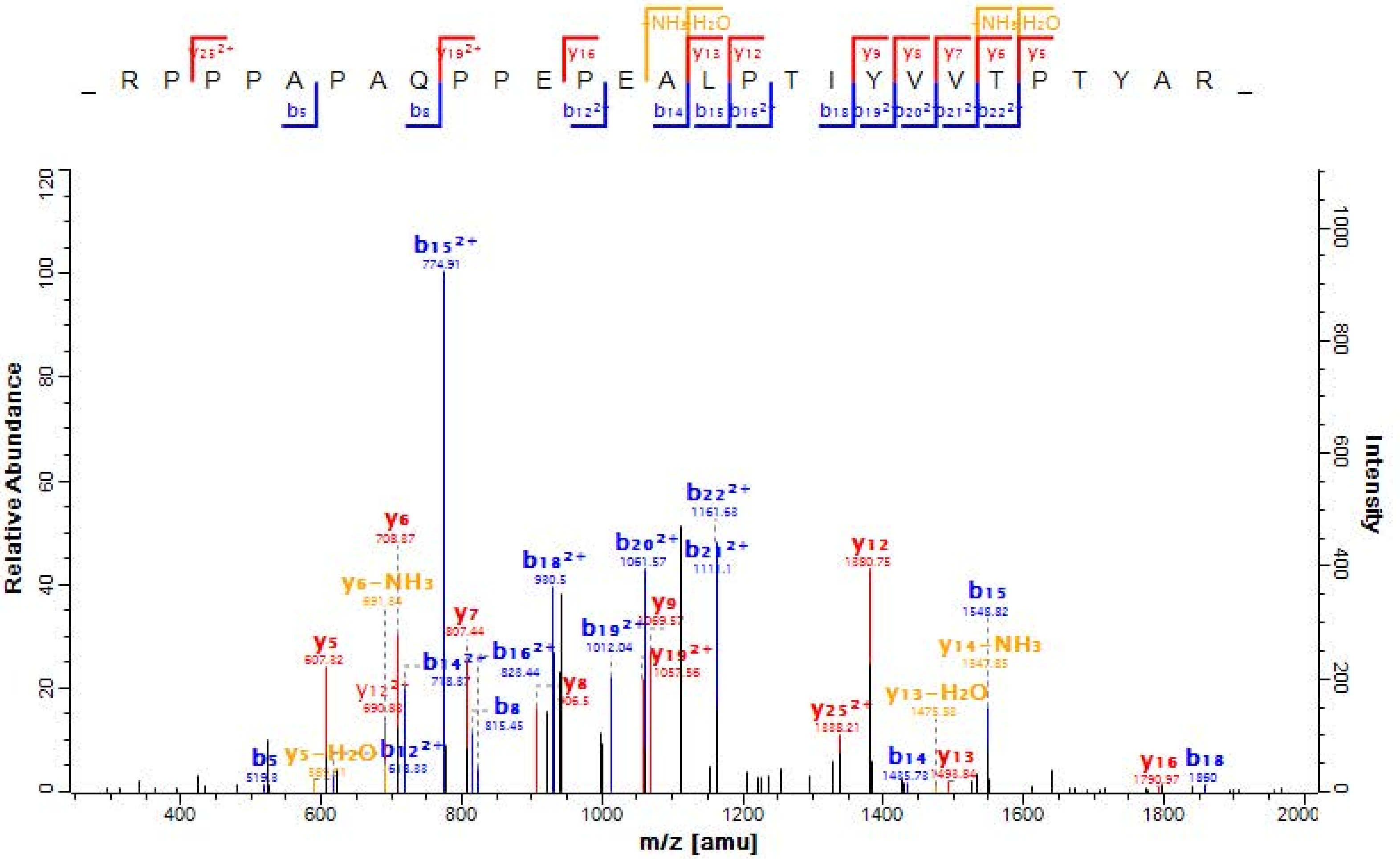
Mass:	1302.65077
m/z:	652.33266
Charge:	2+
Retentiontime:	41.013126373291
Score:	135.9866
Mass Error [ppm]:	0.36391
PEP:	0.00017585
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	40 %
Peak Coverage:	23 %
Protein Localisation:	231 ... 241

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502	1	N	10				
	186.0873	2	A	9	1195.635		598.321	-0.06937
-0.04501	285.1557	3	V	8	1124.598	+0.002688	1124.598	
+0.072328	471.235	4	W	7	1025.529	-0.03986	1025.529	
+0.113584	542.2722	5	A	6	839.4499	+0.063073	839.4499	
	655.3562	6	L	5	768.4128	+0.038237	768.4128	
-0.04517	742.3883	7	S	4	655.3287		655.3287	
	856.4312	8	N	3	568.2967	-0.0889	568.2967	
-0.08922	969.5152	9	L	2	454.2538	+0.175894	454.2538	
-0.05224	1129.546	10	C	1	341.1697	-0.075	341.1697	
		11	R	0	181.1391		181.1391	

Scan number	6907	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	98.21



precursor information

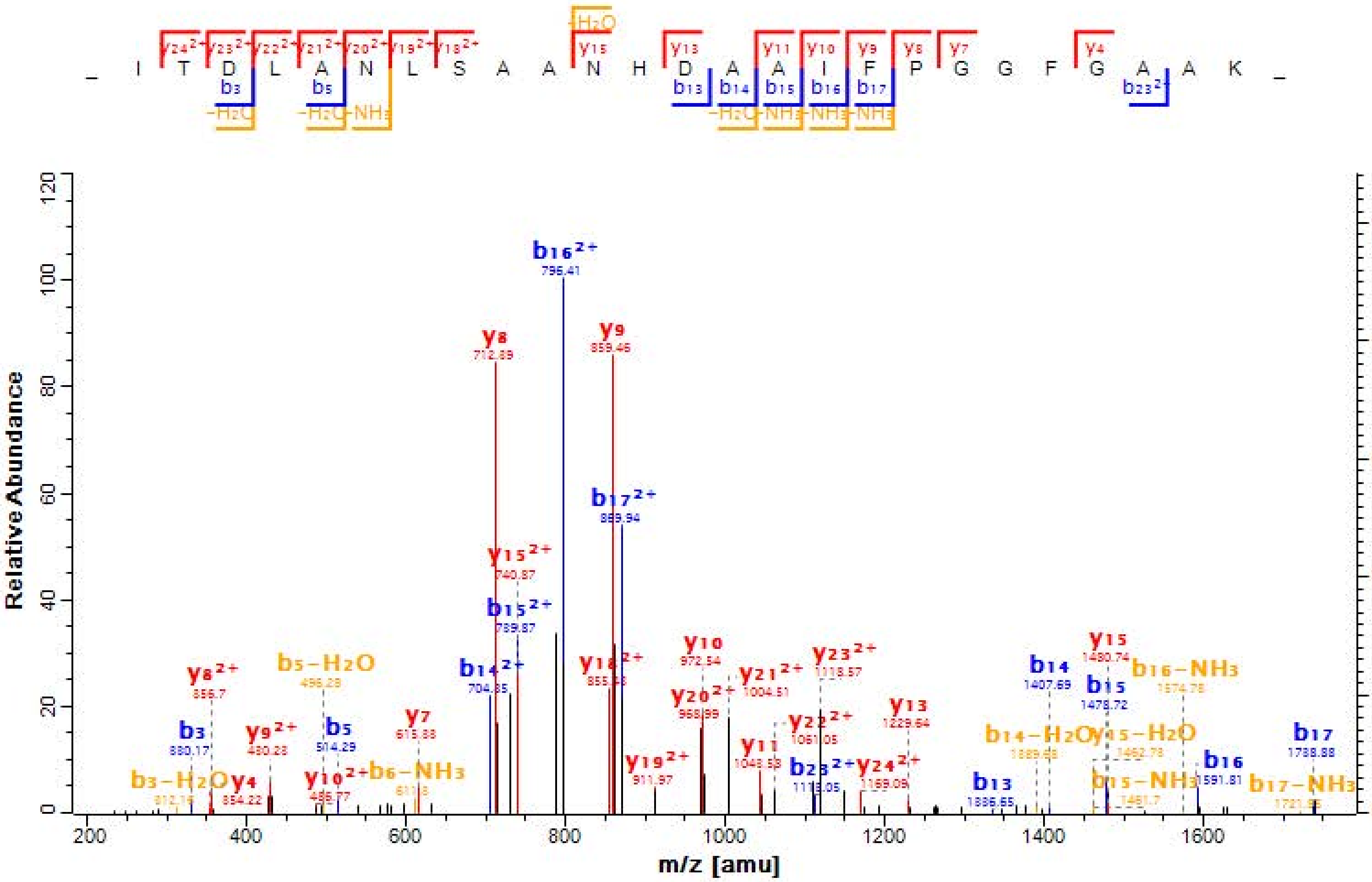
Mass:	2927.55511
m/z:	976.85898
Charge:	3+
Retentiontime:	45.365871429443
Score:	98.21014
Mass Error [ppm]:	0.19864
PEP:	1.3009E-10
Precursor Type:	MULTI

general information

Annotation:	14 of 27
AminoAcids Coverag	52 %
Intensity Coverage:	60 %
Peak Coverage:	31 %
Protein Localisation:	70 ... 96

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	157.11		157.11	1	R	26				
	254.16		254.16	2	P	25	2772.5		2772.5	
	351.21		351.21	3	P	24	2675.4		1338.2	+0.227
	448.27		448.27	4	P	23	2578.4		2578.4	
	519.3	+0.2206	519.3	5	A	22	2481.3		2481.3	
	616.36		616.36	6	P	21	2410.3		2410.3	
	687.39		687.39	7	A	20	2313.2		2313.2	
	815.45	+0.0861	815.45	8	Q	19	2242.2		2242.2	
	912.51		912.51	9	P	18	2114.1		1057.6	+0.3367
	1009.6		1009.6	10	P	17	2017.1		2017.1	
	1138.6		1138.6	11	E	16	1920		1920	
-0.207	618.33		1235.7	12	P	15	1791	+0.3984	1791	
	1364.7		1364.7	13	E	14	1693.9		1693.9	
+0.2506	718.37	-0.059	1435.7	14	A	13	1564.9		1564.9	
+0.2638	774.91	+0.0345	1548.8	15	L	12	1493.8	+0.0789	1493.8	
+0.0793	823.44		1645.9	16	P	11	1380.8	-0.053	690.88	-0.099
	1746.9		1746.9	17	T	10	1283.7		1283.7	
+0.0248	930.5	-0.488	1860	18	I	9	1182.7		1182.7	
+0.2601	1012		2023.1	19	Y	8	1069.6	-0.032	1069.6	
+0.3298	1061.6		2122.1	20	V	7	906.5	-0.109	906.5	
-0.075	1111.1		2221.2	21	V	6	807.44	+0.0427	807.44	
+0.2565	1161.6		2322.2	22	T	5	708.37	+0.0154	708.37	
	2419.3		2419.3	23	P	4	607.32	+0.1301	607.32	
	2520.3		2520.3	24	T	3	510.27		510.27	
	2683.4		2683.4	25	Y	2	409.22		409.22	
	2754.5		2754.5	26	A	1	246.16		246.16	
				27	R	0	175.12		175.12	

Scan number	7290	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	216.3



precursor information

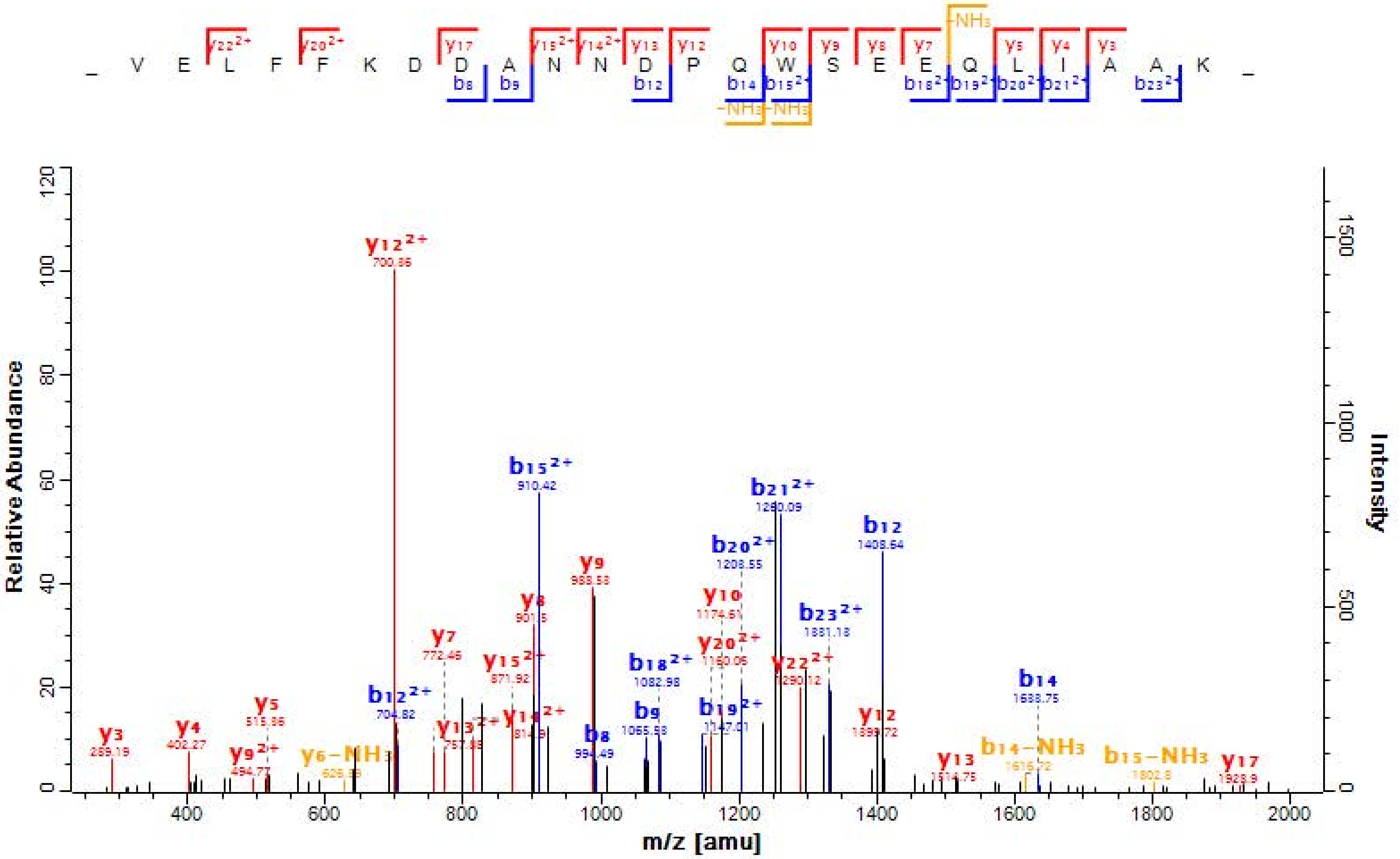
Mass:	2441.23377
m/z:	814.75187
Charge:	3+
Retentiontime:	47.678062438964
Score:	216.304
Mass Error [ppm]:	-0.060577
PEP:	5.3119E-78
Precursor Type:	MULTI

general information

Annotation:	18 of 25
AminoAcids Coverag	72 %
Intensity Coverage:	64 %
Peak Coverage:	40 %
Protein Localisation:	117 ... 141

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	I	24				
	215.14		215.14	2	T	23	2337.2		1169.1	+0.0557
	330.17	+0.1305	330.17	3	D	22	2236.1		1118.6	-0.027
	443.25		443.25	4	L	21	2121.1		1061.1	-0.192
	514.29	-0.116	514.29	5	A	20	2008		1004.5	-0.091
	628.33		628.33	6	N	19	1937		968.99	+0.0286
	741.41		741.41	7	L	18	1822.9		911.97	-0.163
	828.45		828.45	8	S	17	1709.8		855.43	+0.2994
	899.48		899.48	9	A	16	1622.8		1622.8	
	970.52		970.52	10	A	15	1551.8		1551.8	
	1084.6		1084.6	11	N	14	1480.7	-0.041	740.87	-0.197
	1221.6		1221.6	12	H	13	1366.7		1366.7	
	1336.6	-0.138	1336.6	13	D	12	1229.6	-0.254	1229.6	
+0.1213	704.35	+0.006	1407.7	14	A	11	1114.6		1114.6	
+0.002	739.87	+0.1923	1478.7	15	A	10	1043.6	+0.0423	1043.6	
+0.2599	796.41	+0.2099	1591.8	16	I	9	972.54	+0.0545	486.77	-0.061
+0.2533	869.94	-0.313	1738.9	17	F	8	859.46	-0.043	430.23	+0.1127
	1835.9		1835.9	18	P	7	712.39	+0.0715	356.7	+0.1392
	1893		1893	19	G	6	615.33	+0.1514	615.33	
	1950		1950	20	G	5	558.31		558.31	
	2097		2097	21	F	4	501.29		501.29	
	2154.1		2154.1	22	G	3	354.22	+0.2591	354.22	
+0.3173	1113.1		2225.1	23	A	2	297.2		297.2	
	2296.1		2296.1	24	A	1	226.16		226.16	
				25	K	0	155.13		155.13	

Scan number	7357	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	119.87



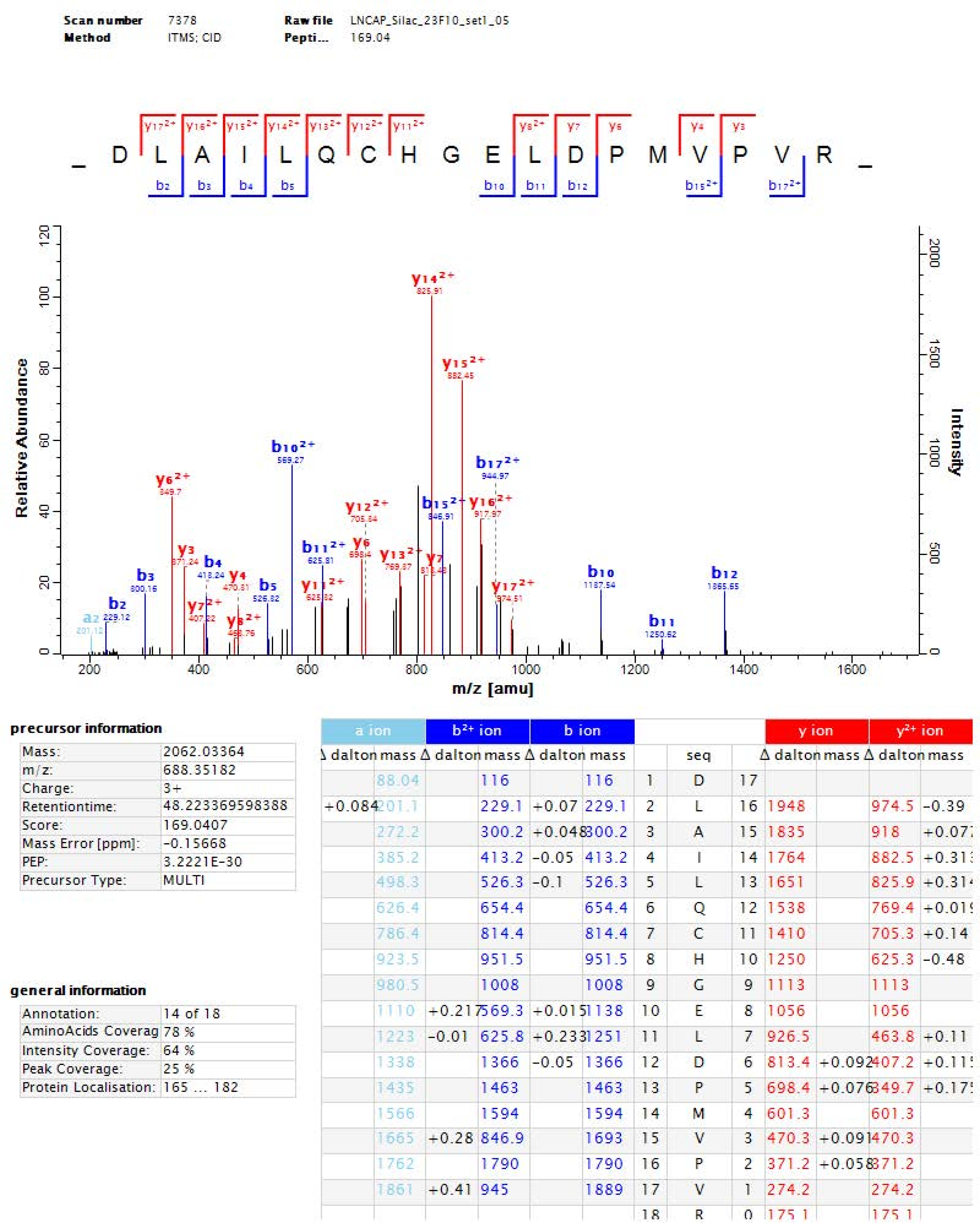
precursor information

Mass:	2806.34488
m/z:	936.45557
Charge:	3+
Retentiontime:	48.095981597900
Score:	119.8729
Mass Error [ppm]:	-0.039114
PEP:	1.503E-15
Precursor Type:	MULTI

general information

Annotation:	18 of 24
AminoAcids Coverag	75 %
Intensity Coverage:	53 %
Peak Coverage:	30 %
Protein Localisation:	152 ... 175

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	23				
	229.12		229.12	2	E	22	2708.3		2708.3	
	342.2		342.2	3	L	21	2579.2		1290.1	+0.259
	489.27		489.27	4	F	20	2466.2		2466.2	
	636.34		636.34	5	F	19	2319.1		1160	+0.471
	764.43		764.43	6	K	18	2172		2172	
	879.46		879.46	7	D	17	2043.9		2043.9	
	994.49	+0.1065	994.49	8	D	16	1928.9	-0.341	1928.9	
	1065.5	-0.051	1065.5	9	A	15	1813.9		1813.9	
	1179.6		1179.6	10	N	14	1742.8		871.92	+0.285
	1293.6		1293.6	11	N	13	1628.8		814.9	-0.048
+0.1889	704.82	+0.0289	1408.6	12	D	12	1514.7	-0.115	757.88	+0.0224
	1505.7		1505.7	13	P	11	1399.7	-0.116	700.36	+0.3362
	1633.7	-0.041	1633.7	14	Q	10	1302.7		1302.7	
+0.3716	910.42		1819.8	15	W	9	1174.6	-0.043	1174.6	
	1906.9		1906.9	16	S	8	988.53	-0.033	494.77	+0.4181
	2035.9		2035.9	17	E	7	901.5	+0.1264	901.5	
+0.232	1083		2164.9	18	E	6	772.46	+0.1902	772.46	
+0.3662	1147		2293	19	Q	5	643.41		643.41	
+0.3076	1203.5		2406.1	20	L	4	515.36	+0.3	515.36	
+0.4238	1260.1		2519.2	21	I	3	402.27	-0.053	402.27	
	2590.2		2590.2	22	A	2	289.19	+0.069	289.19	
+0.1955	1331.1		2661.2	23	A	1	218.15		218.15	
				24	K	0	147.11		147.11	



Scan number	7378	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	169.04

precursor information

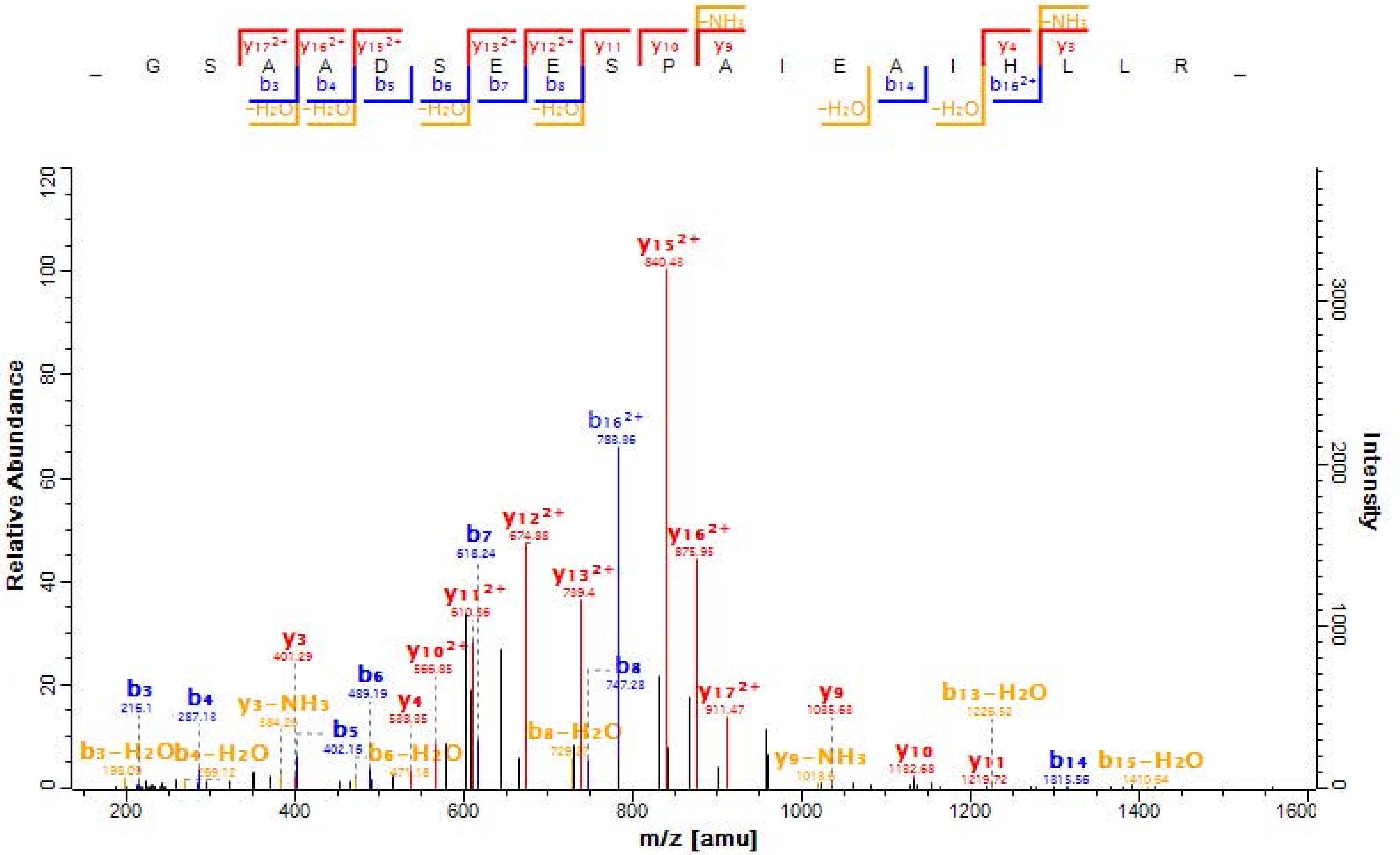
Mass:	2062.03364
m/z:	688.35182
Charge:	3+
Retentiontime:	48.223369598388
Score:	169.0407
Mass Error [ppm]:	-0.15668
PEP:	3.2221E-30
Precursor Type:	MULTI

general information

Annotation:	14 of 18
AminoAcids Coverag	78 %
Intensity Coverage:	64 %
Peak Coverage:	25 %
Protein Localisation:	165 ... 182

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.04		116		116	1	D	17				
+0.084	201.1		229.1	+0.07	229.1	2	L	16	1948		974.5	-0.39
	272.2		300.2	+0.048	300.2	3	A	15	1835		918	+0.07
	385.2		413.2	-0.05	413.2	4	I	14	1764		882.5	+0.31
	498.3		526.3	-0.1	526.3	5	L	13	1651		825.9	+0.31
	626.4		654.4		654.4	6	Q	12	1538		769.4	+0.01
	786.4		814.4		814.4	7	C	11	1410		705.3	+0.14
	923.5		951.5		951.5	8	H	10	1250		625.3	-0.48
	980.5		1008		1008	9	G	9	1113		1113	
	1110	+0.217	569.3	+0.015	1138	10	E	8	1056		1056	
	1223	-0.01	625.8	+0.233	1251	11	L	7	926.5		463.8	+0.11
	1338		1366	-0.05	1366	12	D	6	813.4	+0.092	407.2	+0.11
	1435		1463		1463	13	P	5	698.4	+0.076	349.7	+0.17
	1566		1594		1594	14	M	4	601.3		601.3	
	1665	+0.28	846.9		1693	15	V	3	470.3	+0.091	470.3	
	1762		1790		1790	16	P	2	371.2	+0.058	371.2	
	1861	+0.41	945		1889	17	V	1	274.2		274.2	
						18	R	0	175.1		175.1	

Scan number	7418	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	145.52



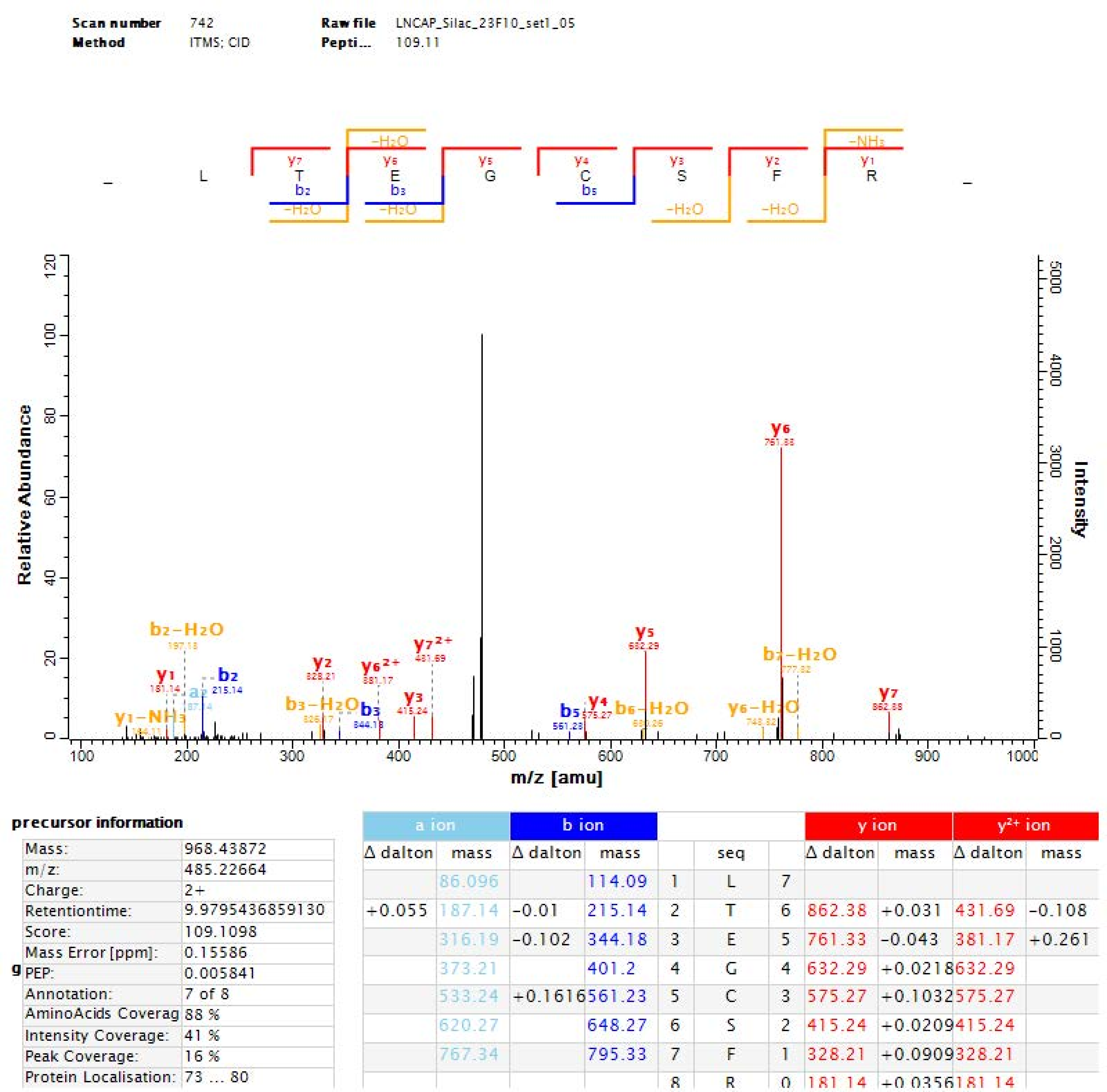
precursor information

Mass:	1964.97948
m/z:	656.00044
Charge:	3+
Retentiontime:	48.475803375244
Score:	145.5203
Mass Error [ppm]:	-0.43377
PEP:	5.0555E-19
Precursor Type:	MULTI

general information

Annotation:	14 of 19
AminoAcids Coverag	74 %
Intensity Coverage:	64 %
Peak Coverage:	27 %
Protein Localisation:	120 ... 138

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	18				
	145.06		145.06	2	S	17	1909		1909	
	216.1	+0.088	216.1	3	A	16	1821.9		911.47	+0.3737
	287.13	+0.018	287.13	4	A	15	1750.9		875.95	+0.196
	402.16	-0.021	402.16	5	D	14	1679.9		840.43	+0.2351
	489.19	+0.0686	489.19	6	S	13	1564.8		1564.8	
	618.24	+0.1165	618.24	7	E	12	1477.8		739.4	+0.302
	747.28	+0.0023	747.28	8	E	11	1348.8		674.88	+0.3031
	834.31		834.31	9	S	10	1219.7	+0.1528	610.36	+0.256
	931.36		931.36	10	P	9	1132.7	+0.0233	566.85	+0.074
	1002.4		1002.4	11	A	8	1035.6	-0.087	1035.6	
	1115.5		1115.5	12	I	7	964.59		964.59	
	1244.5		1244.5	13	E	6	851.51		851.51	
	1315.6	+0.1531	1315.6	14	A	5	722.47		722.47	
	1428.6		1428.6	15	I	4	651.43		651.43	
-0.181	783.36		1565.7	16	H	3	538.35	+0.0536	538.35	
	1678.8		1678.8	17	L	2	401.29	+0.068	401.29	
	1791.9		1791.9	18	L	1	288.2		288.2	
				19	R	0	175.12		175.12	



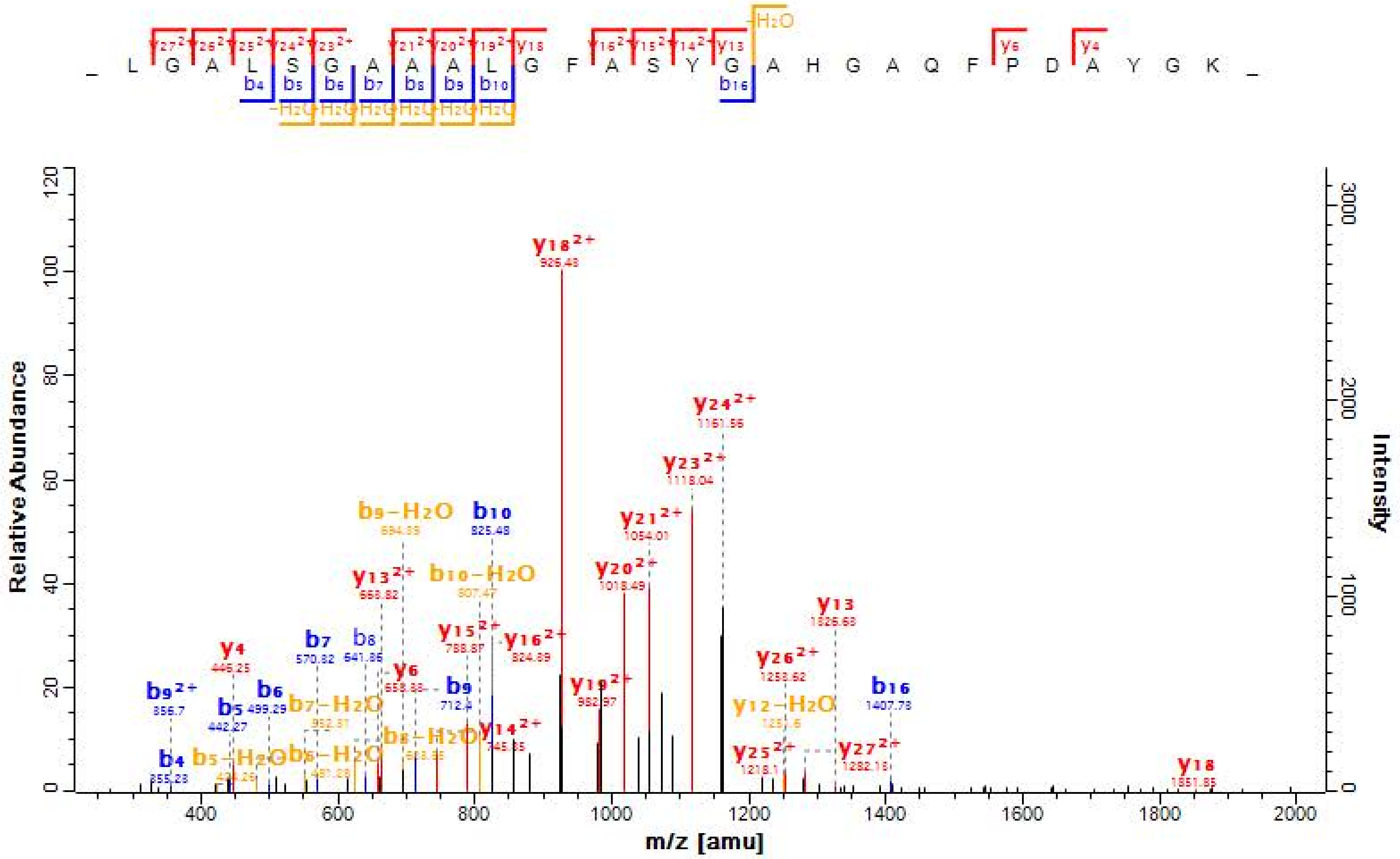
Scan number	742	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	109.11

precursor information

Mass:	968.43872
m/z:	485.22664
Charge:	2+
Retentiontime:	9.9795436859130
Score:	109.1098
Mass Error [ppm]:	0.15586
PEP:	0.005841
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	41 %
Peak Coverage:	16 %
Protein Localisation:	73 ... 80

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	7				
+0.055	187.14	-0.01	215.14	2	T	6	862.38	+0.031	431.69	-0.108
	316.19	-0.102	344.18	3	E	5	761.33	-0.043	381.17	+0.261
	373.21		401.2	4	G	4	632.29	+0.0218	632.29	
	533.24	+0.1616	561.23	5	C	3	575.27	+0.1032	575.27	
	620.27		648.27	6	S	2	415.24	+0.0209	415.24	
	767.34		795.33	7	F	1	328.21	+0.0909	328.21	
				8	R	0	181.14	+0.0356	181.14	

Scan number	7762	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	153.36



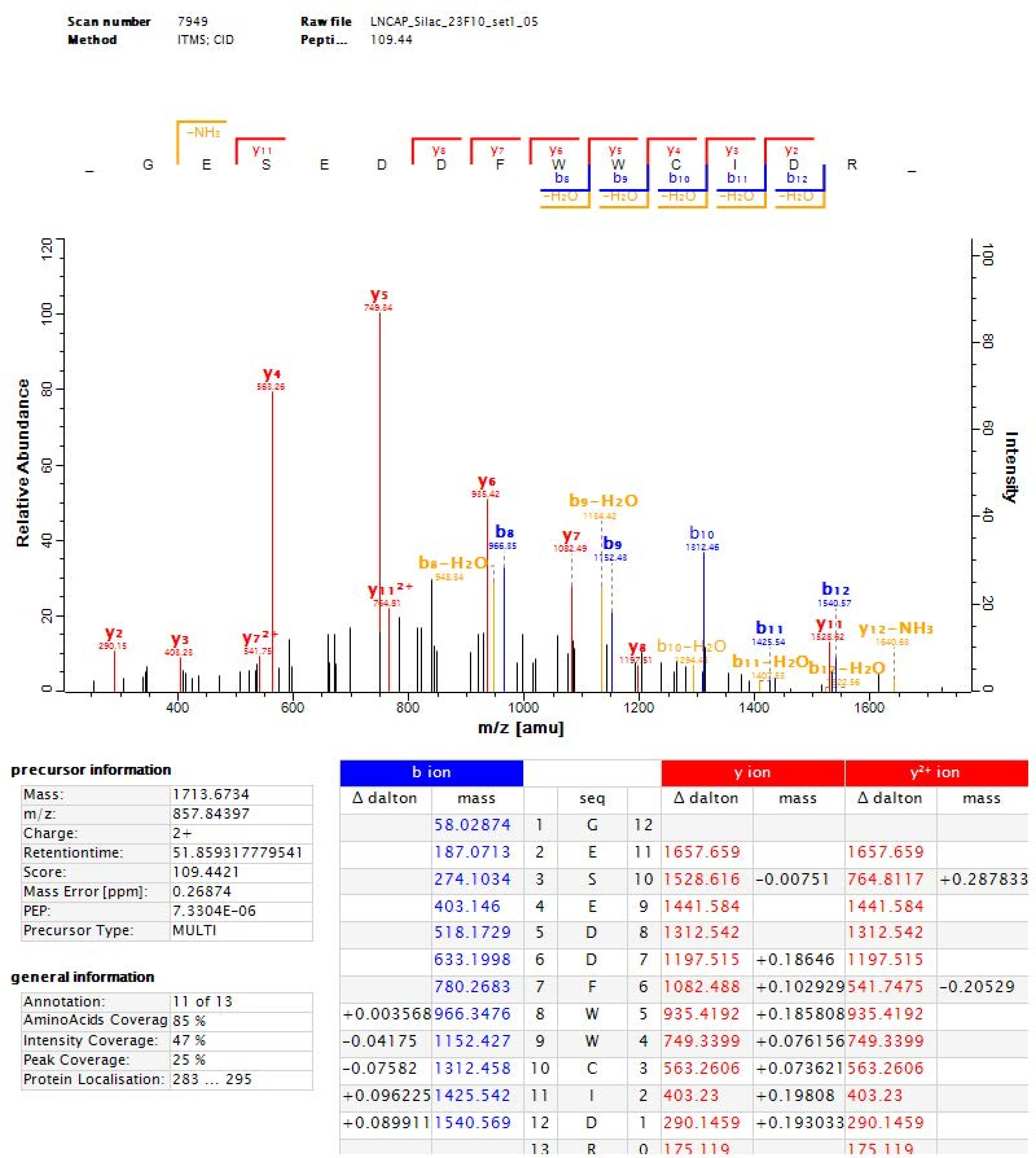
precursor information

Mass:	2667.30799
m/z:	890.10994
Charge:	3+
Retentiontime:	50.614284515380
Score:	153.3561
Mass Error [ppm]:	-0.058962
PEP:	6.2245E-36
Precursor Type:	MULTI

general information

Annotation:	17 of 28
AminoAcids Coverag	61 %
Intensity Coverage:	56 %
Peak Coverage:	32 %
Protein Localisation:	11 ... 38

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	27				
	171.11		171.11	2	G	26	2563.2		1282.1	+0.2846
	242.15		242.15	3	A	25	2506.2		1253.6	+0.3376
	355.23	-0.11	355.23	4	L	24	2435.2		1218.1	+0.1886
	442.27	-0.024	442.27	5	S	23	2322.1		1161.6	-0.091
	499.29	+0.1318	499.29	6	G	22	2235.1		1118	+0.3343
	570.32	-0.039	570.32	7	A	21	2178		2178	
	641.36	+0.1144	641.36	8	A	20	2107		1054	+0.2832
-0.285	356.7	+0.006	712.4	9	A	19	2036		1018.5	+0.3103
	825.48	+0.1772	825.48	10	L	18	1964.9		982.97	-0.014
	882.5		882.5	11	G	17	1851.9	-0.016	926.43	+0.2871
	1029.6		1029.6	12	F	16	1794.8		1794.8	
	1100.6		1100.6	13	A	15	1647.8		824.39	+0.249
	1187.6		1187.6	14	S	14	1576.7		788.87	+0.3296
	1350.7		1350.7	15	Y	13	1489.7		745.35	+0.1184
	1407.7	-0.104	1407.7	16	G	12	1326.6	-0.169	663.82	+0.2429
	1478.8		1478.8	17	A	11	1269.6		1269.6	
	1615.8		1615.8	18	H	10	1198.6		1198.6	
	1672.8		1672.8	19	G	9	1061.5		1061.5	
	1743.9		1743.9	20	A	8	1004.5		1004.5	
	1871.9		1871.9	21	Q	7	933.46		933.46	
	2019		2019	22	F	6	805.4		805.4	
	2116.1		2116.1	23	P	5	658.33	+0.166	658.33	
	2231.1		2231.1	24	D	4	561.28		561.28	
	2302.1		2302.1	25	A	3	446.25	+0.1863	446.25	
	2465.2		2465.2	26	Y	2	375.21		375.21	
	2522.2		2522.2	27	G	1	212.15		212.15	
				28	K	0	155.13		155.13	



Scan number	7949	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	109.44

precursor information

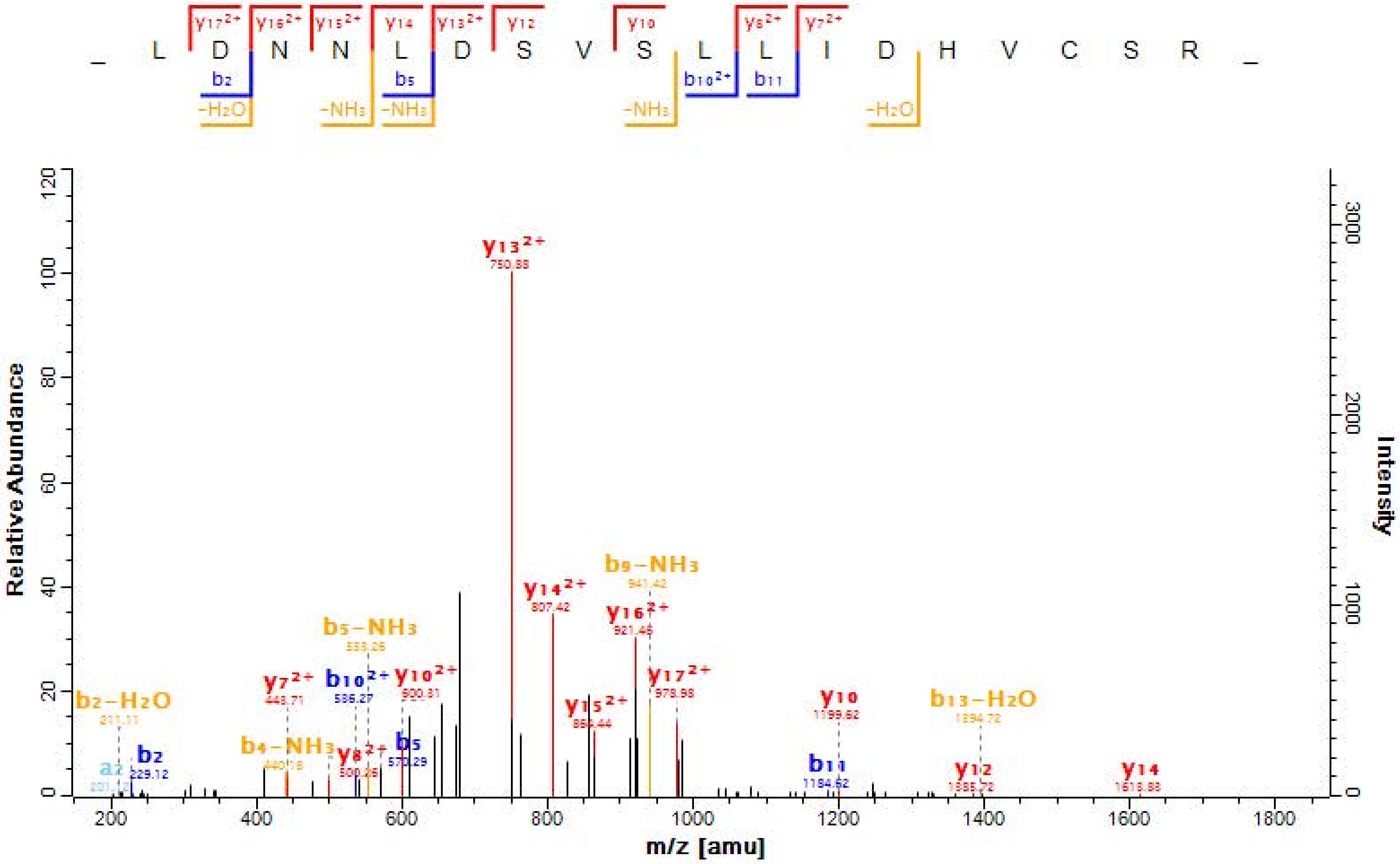
Mass:	1713.6734
m/z:	857.84397
Charge:	2+
Retentiontime:	51.859317779541
Score:	109.4421
Mass Error [ppm]:	0.26874
PEP:	7.3304E-06
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	47 %
Peak Coverage:	25 %
Protein Localisation:	283 ... 295

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	12				
	187.0713	2	E	11	1657.659		1657.659	
	274.1034	3	S	10	1528.616	-0.00751	764.8117	+0.287833
	403.146	4	E	9	1441.584		1441.584	
	518.1729	5	D	8	1312.542		1312.542	
	633.1998	6	D	7	1197.515	+0.18646	1197.515	
	780.2683	7	F	6	1082.488	+0.102929	541.7475	-0.20529
+0.003568	966.3476	8	W	5	935.4192	+0.185808	935.4192	
-0.04175	1152.427	9	W	4	749.3399	+0.076156	749.3399	
-0.07582	1312.458	10	C	3	563.2606	+0.073621	563.2606	
+0.096225	1425.542	11	I	2	403.23	+0.19808	403.23	
+0.089911	1540.569	12	D	1	290.1459	+0.193033	290.1459	
		13	R	0	175.119		175.119	

Scan number	7968	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	79.65



precursor information

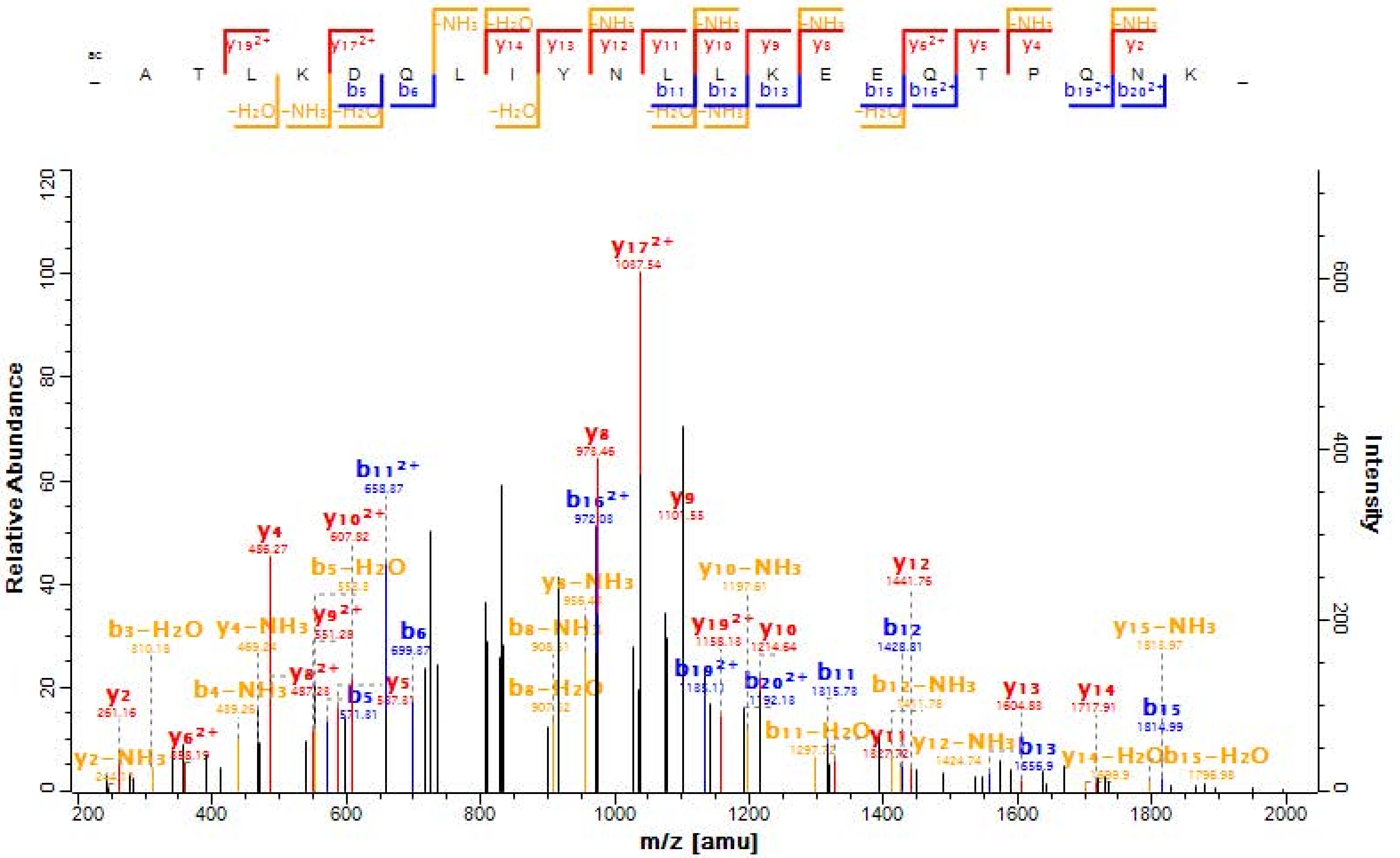
Mass:	2069.02125
m/z:	690.68102
Charge:	3+
Retentiontime:	51.998573303222
Score:	79.65154
Mass Error [ppm]:	0.044615
PEP:	0.00018012
Precursor Type:	MULTI

general information

Annotation:	11 of 18
AminoAcids Coverag	61 %
Intensity Coverage:	45 %
Peak Coverage:	22 %
Protein Localisation:	323 ... 340

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	17				
+0.114	201.1		229.1	+0.025	229.1	2	D	16	1957		979	+0
	315.2		343.2		343.2	3	N	15	1842		921.5	+0.04
	429.2		457.2		457.2	4	N	14	1728		864.4	+0.24
	542.3		570.3	+0.061	570.3	5	L	13	1614	-0.21	807.4	+0.35
	657.3		685.3		685.3	6	D	12	1501		750.9	+0.32
	744.4		772.3		772.3	7	S	11	1386	+0.305	1386	
	843.4		871.4		871.4	8	V	10	1299		1299	
	930.5		958.4		958.4	9	S	9	1200	-0.02	600.3	+0.07
	1044	+0.088	536.3		1072	10	L	8	1113		1113	
	1157		1185	+0.048	1185	11	L	7	999.5		500.3	+0.32
	1270		1298		1298	12	I	6	886.4		443.7	-0.14
	1385		1413		1413	13	D	5	773.3		773.3	
	1522		1550		1550	14	H	4	658.3		658.3	
	1621		1649		1649	15	V	3	521.3		521.3	
	1781		1809		1809	16	C	2	422.2		422.2	
	1868		1896		1896	17	S	1	262.2		262.2	
						18	R	0	175.1		175.1	

Scan number	8337	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	183.6



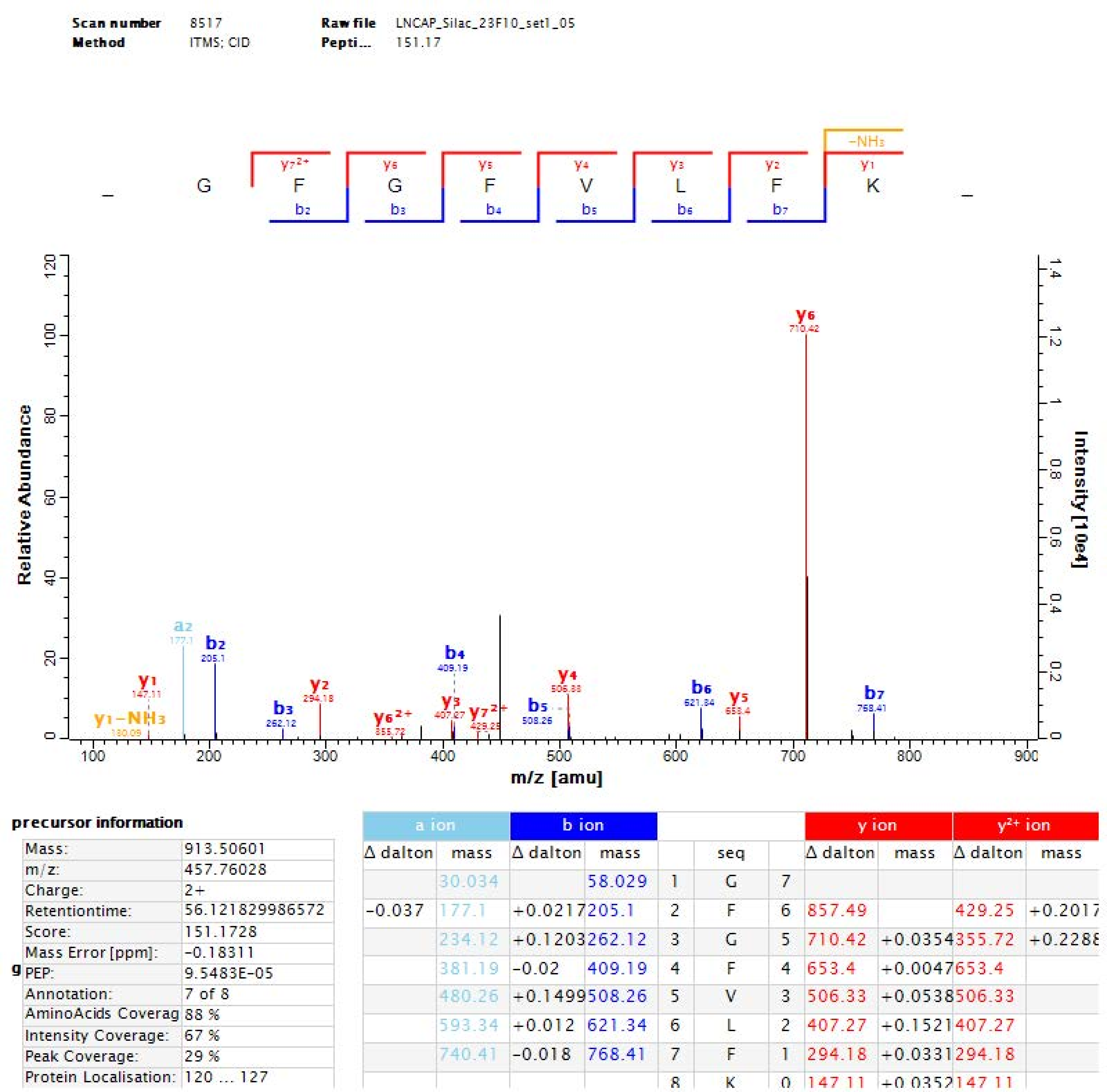
precursor information

Mass:	2528.34952
m/z:	843.79045
Charge:	3+
Retentiontime:	54.765014648437
Score:	183.5978
Mass Error [ppm]:	0.35805
PEP:	9.4661E-38
Precursor Type:	MULTI

general information

Annotation:	18 of 21
AminoAcids Coverag	86 %
Intensity Coverage:	42 %
Peak Coverage:	39 %
Protein Localisation:	2 ... 22

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.05		114.05	1	A	20				
	215.1		215.1	2	T	19	2416.3		2416.3	
	328.19		328.19	3	L	18	2315.3		1158.1	+0.4296
	456.28		456.28	4	K	17	2202.2		2202.2	
	571.31	+0.2891	571.31	5	D	16	2074.1		1037.5	+0.3365
	699.37	+0.288	699.37	6	Q	15	1959.1		1959.1	
	812.45		812.45	7	L	14	1831		1831	
	925.54		925.54	8	I	13	1717.9	+0.0576	1717.9	
	1088.6		1088.6	9	Y	12	1604.8	+0.3837	1604.8	
	1202.6		1202.6	10	N	11	1441.8	-0.054	1441.8	
+0.2588	658.37	+0.0755	1315.7	11	L	10	1327.7	+0.0266	1327.7	
	1428.8	-0.086	1428.8	12	L	9	1214.6	-0.03	607.82	+0.2502
	1556.9	-0.174	1556.9	13	K	8	1101.6	-0.033	551.28	+0.0093
	1685.9		1685.9	14	E	7	973.46	+0.0242	487.23	+0.292
	1815	+0.2788	1815	15	E	6	844.42		844.42	
-0.279	972.03		1943	16	Q	5	715.37		358.19	+0.0106
	2044.1		2044.1	17	T	4	587.31	+0.0559	587.31	
	2141.1		2141.1	18	P	3	486.27	+0.0653	486.27	
-0.229	1135.1		2269.2	19	Q	2	389.21		389.21	
+0.3994	1192.1		2383.3	20	N	1	261.16	+0.1216	261.16	
				21	K	0	147.11		147.11	



Scan number 8517
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set1_05
Pepti... 151.17

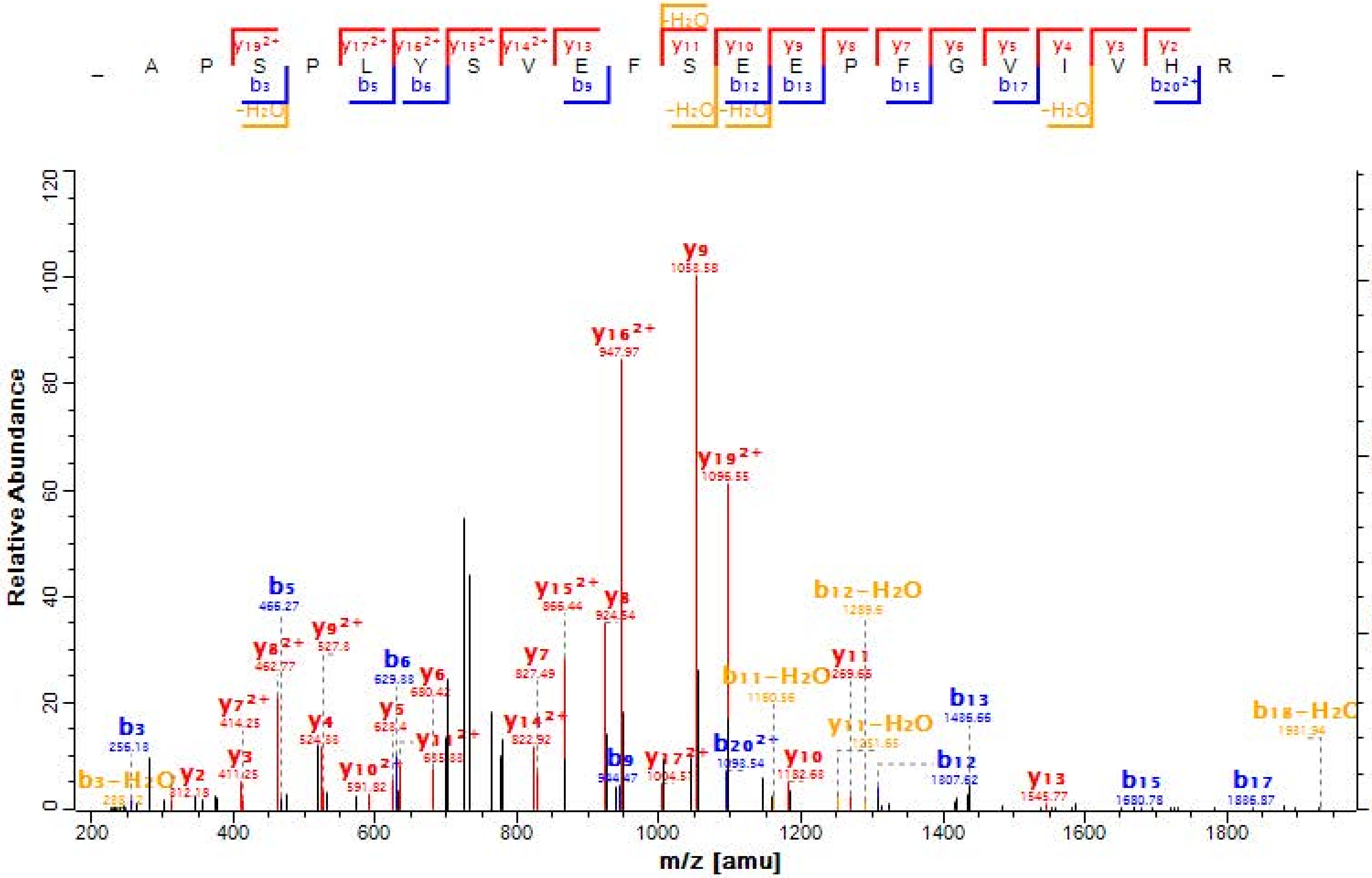
precursor information

Mass:	913.50601
m/z:	457.76028
Charge:	2+
Retentiontime:	56.121829986572
Score:	151.1728
Mass Error [ppm]:	-0.18311
PEP:	9.5483E-05
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	67 %
Peak Coverage:	29 %
Protein Localisation:	120 ... 127

g

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	30.034		58.029	1	G	7				
-0.037	177.1	+0.0217	205.1	2	F	6	857.49		429.25	+0.2017
	234.12	+0.1203	262.12	3	G	5	710.42	+0.0354	355.72	+0.2288
	381.19	-0.02	409.19	4	F	4	653.4	+0.0047	653.4	
	480.26	+0.1499	508.26	5	V	3	506.33	+0.0538	506.33	
	593.34	+0.012	621.34	6	L	2	407.27	+0.1521	407.27	
	740.41	-0.018	768.41	7	F	1	294.18	+0.0331	294.18	
				8	K	0	147.11	+0.0352	147.11	

Scan number	8700	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	166.77



precursor information

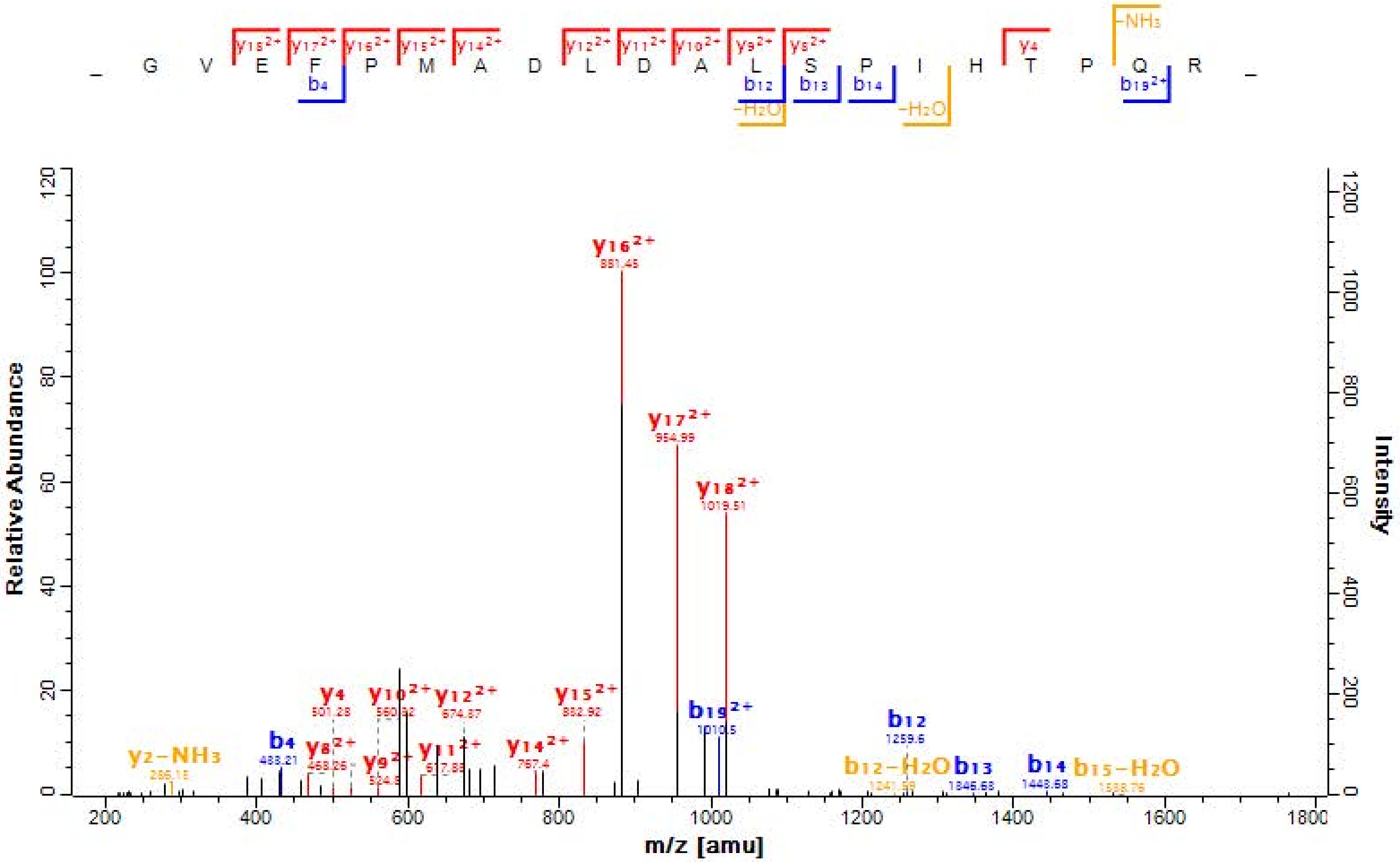
Mass:	2359.18534
m/z:	787.40239
Charge:	3+
Retentiontime:	57.596488952636
Score:	166.7736
Mass Error [ppm]:	0.2079
PEP:	3.6002E-28
Precursor Type:	MULTI

general information

Annotation:	17 of 21
AminoAcids Coverag	81 %
Intensity Coverage:	53 %
Peak Coverage:	32 %
Protein Localisation:	204 ... 224

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	20				
	169.1		169.1	2	P	19	2289.2		2289.2	
	256.13	+0.0204	256.13	3	S	18	2192.1		1096.6	+0.4267
	353.18		353.18	4	P	17	2105.1		2105.1	
	466.27	-0.096	466.27	5	L	16	2008		1004.5	-0.011
	629.33	+0.0547	629.33	6	Y	15	1894.9		947.97	+0.2314
	716.36		716.36	7	S	14	1731.9		866.44	+0.28
	815.43		815.43	8	V	13	1644.8		822.92	+0.2915
	944.47	+0.0962	944.47	9	E	12	1545.8	-0.112	1545.8	
	1091.5		1091.5	10	F	11	1416.7		1416.7	
	1178.6		1178.6	11	S	10	1269.7	+0.1497	635.33	+0.1917
	1307.6	+0.1623	1307.6	12	E	9	1182.6	+0.0415	591.82	+0.1348
	1436.7	-0.144	1436.7	13	E	8	1053.6	-0.207	527.3	+0.1901
	1533.7		1533.7	14	P	7	924.54	+0.1274	462.77	+0.2369
	1680.8	+0.1459	1680.8	15	F	6	827.49	+0.1253	414.25	+0.0272
	1737.8		1737.8	16	G	5	680.42	+0.1196	680.42	
	1836.9	+0.0488	1836.9	17	V	4	623.4	+0.1079	623.4	
	1950		1950	18	I	3	524.33	+0.0915	524.33	
	2049		2049	19	V	2	411.25	+0.1331	411.25	
+0.346	1093.5		2186.1	20	H	1	312.18	+0.2167	312.18	
				21	R	0	175.12		175.12	

Scan number	8808	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	70.41



precursor information

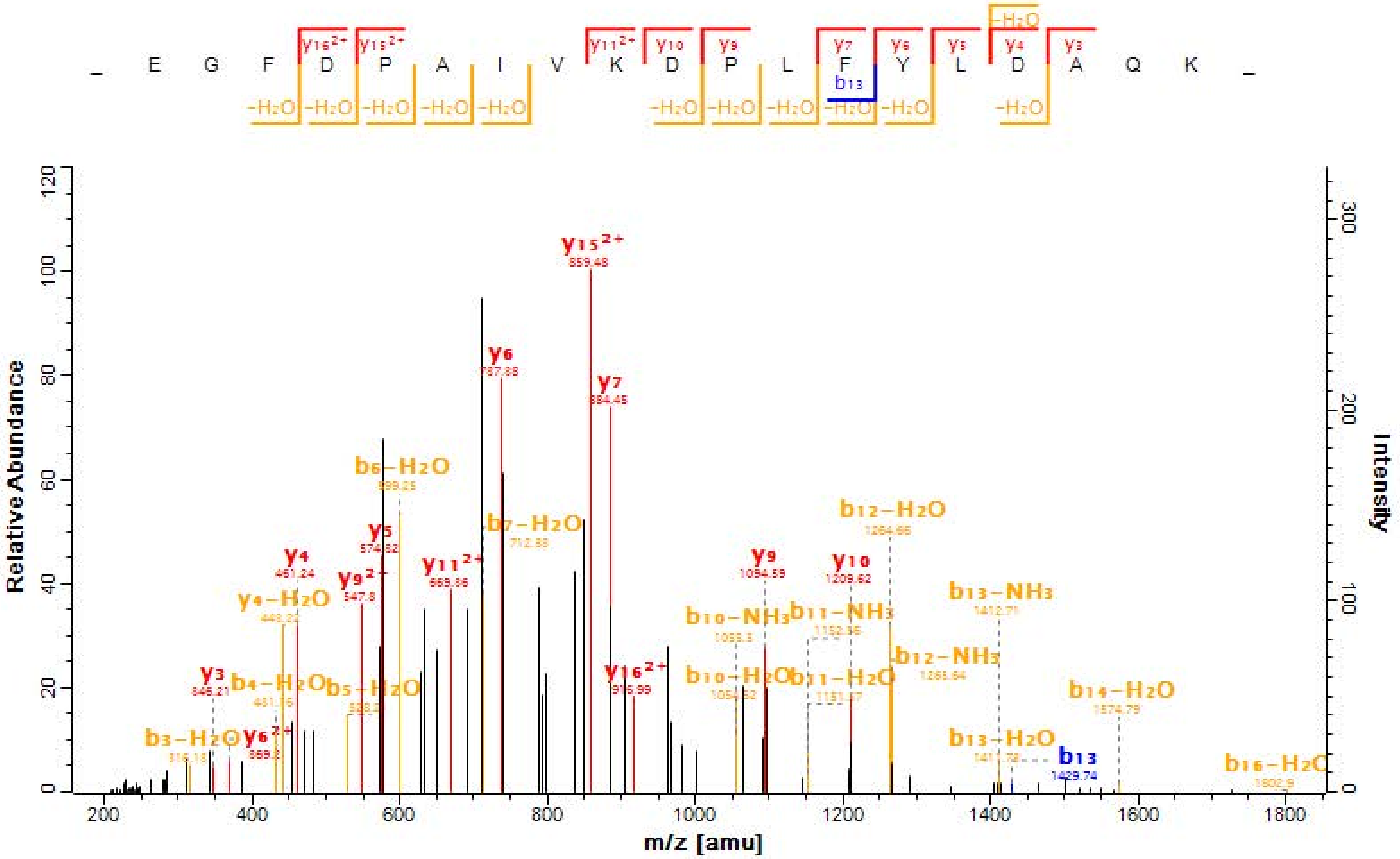
Mass:	2193.08754
m/z:	732.03646
Charge:	3+
Retentiontime:	58.521709442138
Score:	70.41049
Mass Error [ppm]:	-0.59229
PEP:	0.00030086
Precursor Type:	MULTI

general information

Annotation:	14 of 20
AminoAcids Coverag	70 %
Intensity Coverage:	53 %
Peak Coverage:	23 %
Protein Localisation:	148 ... 167

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	19				
	157.1		157.1	2	V	18	2137.1		2137.1	
	286.14		286.14	3	E	17	2038		1019.5	+0.2989
	433.21	-0.017	433.21	4	F	16	1909		954.99	+0.3304
	530.26		530.26	5	P	15	1761.9		881.45	+0.1106
	661.3		661.3	6	M	14	1664.8		832.92	+0.2736
	732.34		732.34	7	A	13	1533.8		767.4	+0.2966
	847.37		847.37	8	D	12	1462.8		1462.8	
	960.45		960.45	9	L	11	1347.7		674.37	-0.269
	1075.5		1075.5	10	D	10	1234.7		617.83	+0.132
	1146.5		1146.5	11	A	9	1119.6		560.32	+0.0414
	1259.6	-0.138	1259.6	12	L	8	1048.6		524.8	+0.069
	1346.6	+0.2081	1346.6	13	S	7	935.51		468.26	+0.3037
	1443.7	+0.1509	1443.7	14	P	6	848.47		848.47	
	1556.8		1556.8	15	I	5	751.42		751.42	
	1693.8		1693.8	16	H	4	638.34		638.34	
	1794.9		1794.9	17	T	3	501.28	+0.1366	501.28	
	1891.9		1891.9	18	P	2	400.23		400.23	
+0.4501	1010.5		2020	19	Q	1	303.18		303.18	
				20	R	0	175.12		175.12	

Scan number	8911	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	71.7



precursor information

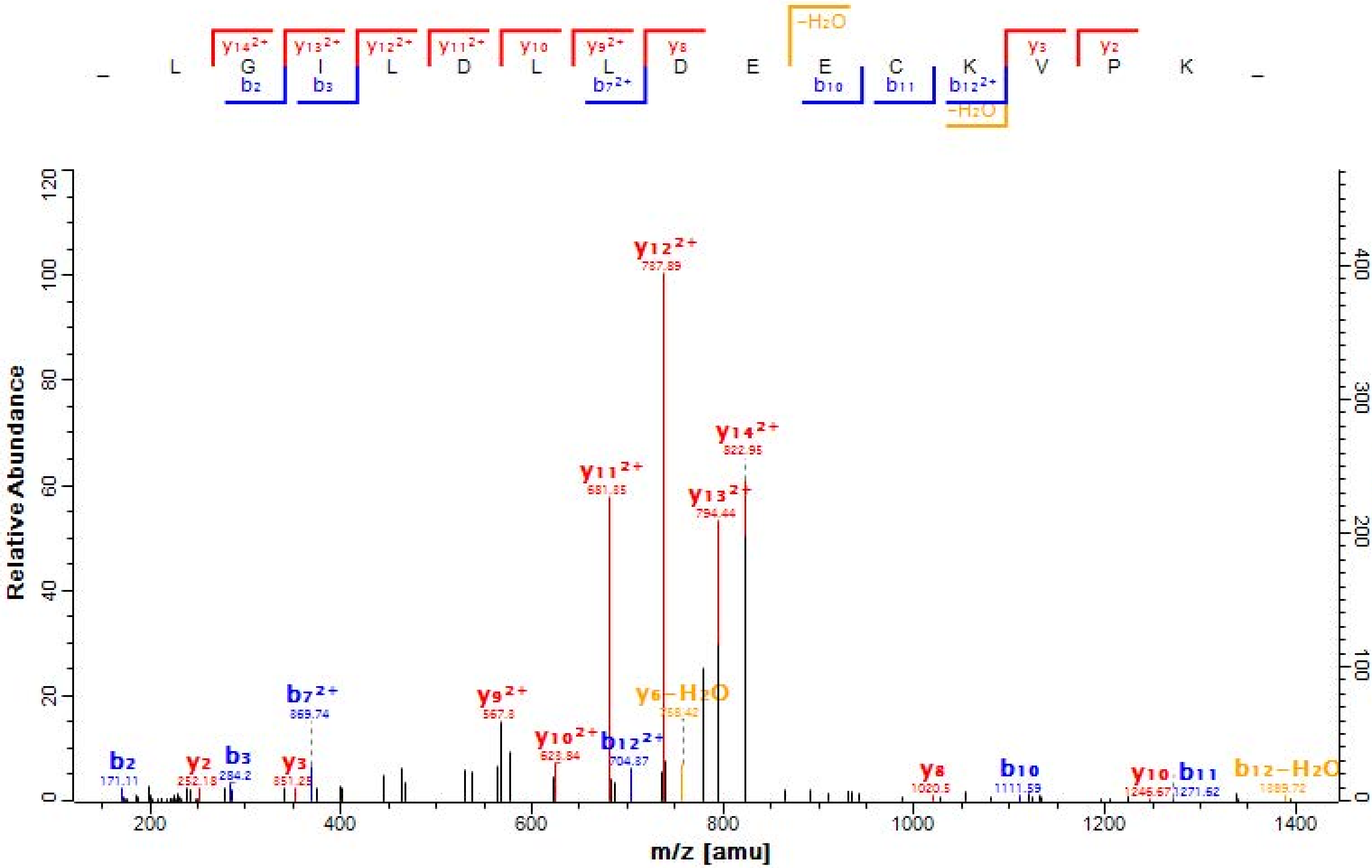
Mass:	2165.10541
m/z:	722.70908
Charge:	3+
Retentiontime:	59.367465972900
Score:	71.69701
Mass Error [ppm]:	0.43189
PEP:	0.00021836
Precursor Type:	MULTI

general information

Annotation:	14 of 19
AminoAcids Coverag	74 %
Intensity Coverage:	45 %
Peak Coverage:	28 %
Protein Localisation:	604 ... 622

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	18				
	187.0713	2	G	17	2037.069		2037.069	
	334.1397	3	F	16	1980.048		1980.048	
	449.1667	4	D	15	1832.979		916.9933	+0.248483
	546.2195	5	P	14	1717.952		859.4798	+0.264274
	617.2566	6	A	13	1620.9		1620.9	
	730.3406	7	I	12	1549.862		1549.862	
	829.409	8	V	11	1436.778		1436.778	
	957.504	9	K	10	1337.71		669.3586	+0.265884
	1072.531	10	D	9	1209.615	+0.031102	1209.615	
	1169.584	11	P	8	1094.588	-0.16449	547.7977	+0.236871
	1282.668	12	L	7	997.5353		997.5353	
-0.00109	1429.736	13	F	6	884.4512	+0.029956	884.4512	
	1592.8	14	Y	5	737.3828	+0.052106	369.1951	+0.103469
	1705.884	15	L	4	574.3195	+0.010515	574.3195	
	1820.911	16	D	3	461.2354	+9.62E-05	461.2354	
	1891.948	17	A	2	346.2085	+0.085877	346.2085	
	2020.006	18	Q	1	275.1714		275.1714	
		19	K	0	147.1128		147.1128	

Scan number	8950	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	95.42



precursor information

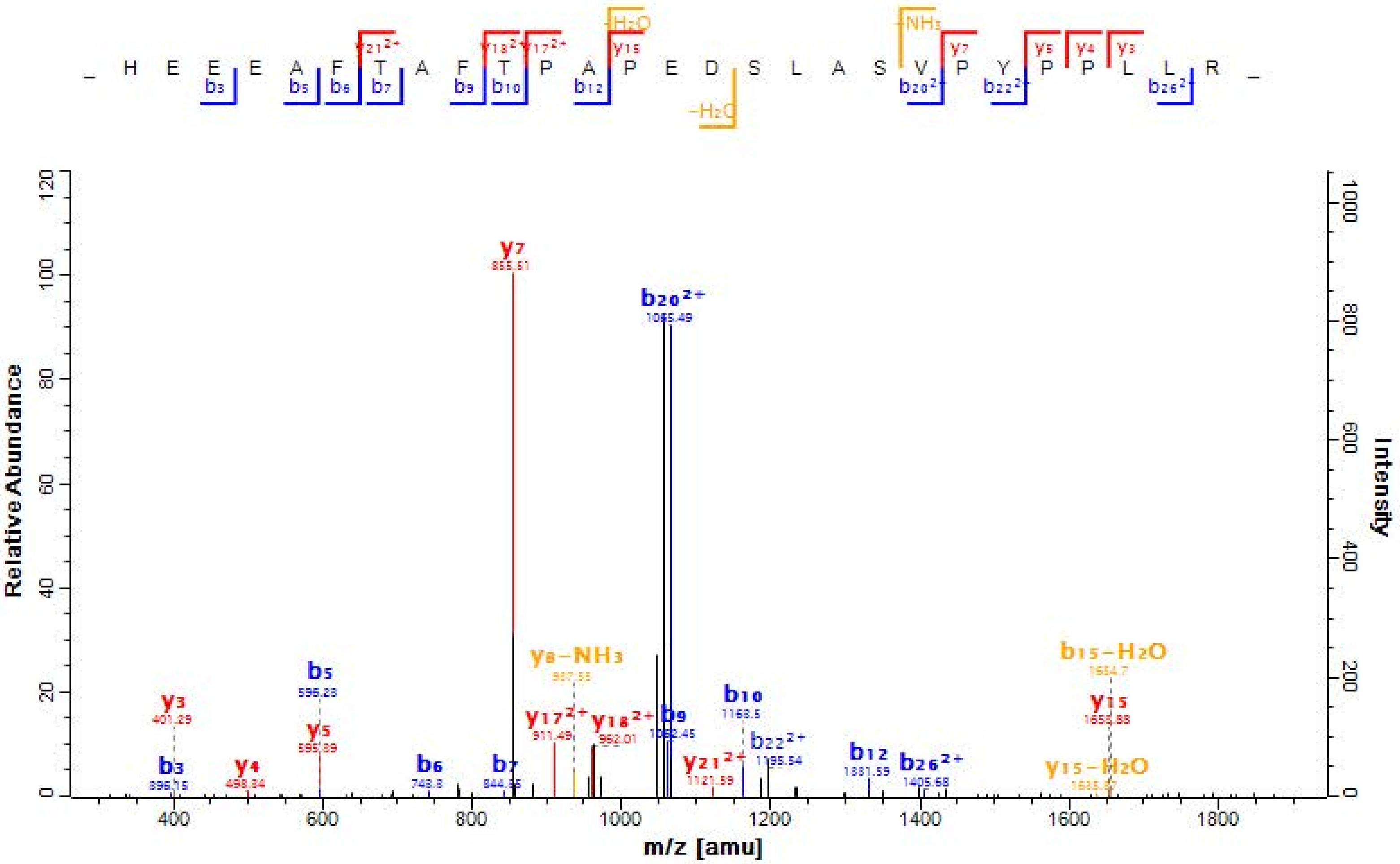
Mass:	1740.93417
m/z:	581.31867
Charge:	3+
Retentiontime:	59.703971862793
Score:	95.41728
Mass Error [ppm]:	0.56815
PEP:	7.6055E-05
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	57 %
Peak Coverage:	19 %
Protein Localisation:	504 ... 518

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	14				
	171.11	+0.1424	171.11	2	G	13	1644.9		822.95	-0.017
	284.2	+0.0343	284.2	3	I	12	1587.9		794.44	+0.1445
	397.28		397.28	4	L	11	1474.8		737.89	+0.1185
	512.31		512.31	5	D	10	1361.7		681.35	+0.113
	625.39		625.39	6	L	9	1246.7	+0.2074	623.84	+0.037
-0.448	369.74		738.48	7	L	8	1133.6		567.3	+0.011
	853.5		853.5	8	D	7	1020.5	-0.408	1020.5	
	982.55		982.55	9	E	6	905.47		905.47	
	1111.6	+0.0299	1111.6	10	E	5	776.43		776.43	
	1271.6	-0.174	1271.6	11	C	4	647.39		647.39	
-0.115	704.37		1407.7	12	K	3	487.36		487.36	
	1506.8		1506.8	13	V	2	351.25	+0.1109	351.25	
	1603.8		1603.8	14	P	1	252.18	+0.0103	252.18	
				15	K	0	155.13		155.13	

Scan number	9265	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	72.99



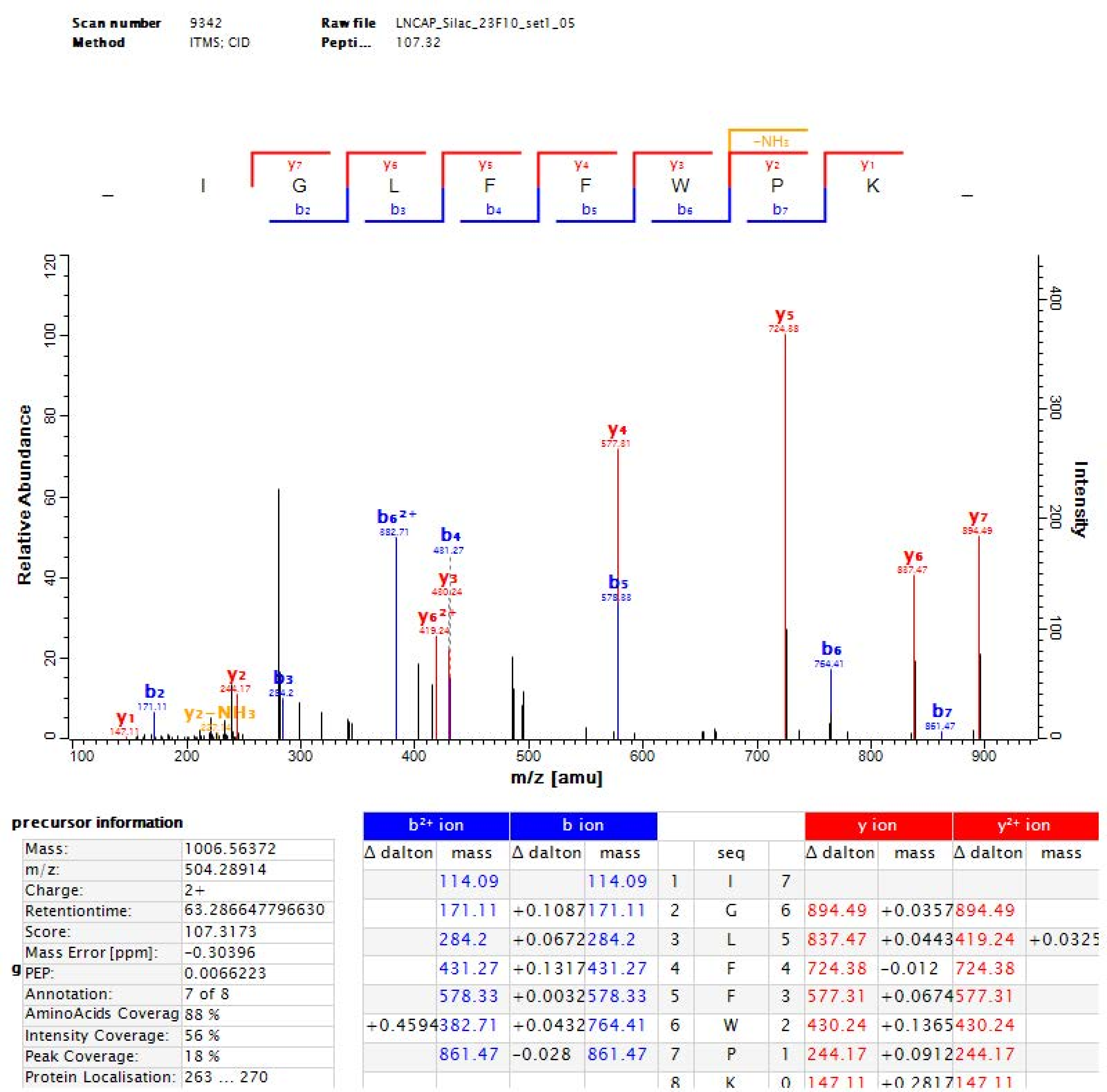
precursor information

Mass:	2983.46074
m/z:	995.49419
Charge:	3+
Retentiontime:	62.558944702148
Score:	72.98977
Mass Error [ppm]:	0.13076
PEP:	5.1913E-08
Precursor Type:	MULTI

general information

Annotation:	18 of 27
AminoAcids Coverag	67 %
Intensity Coverage:	52 %
Peak Coverage:	23 %
Protein Localisation:	152 ... 178

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.07		138.07	1	H	26				
	267.11		267.11	2	E	25	2847.4		2847.4	
	396.15	+0.1145	396.15	3	E	24	2718.4		2718.4	
	525.19		525.19	4	E	23	2589.3		2589.3	
	596.23	+0.2719	596.23	5	A	22	2460.3		2460.3	
	743.3	+0.2133	743.3	6	F	21	2389.2		2389.2	
	844.35	-0.001	844.35	7	T	20	2242.2		1121.6	+0.1667
	915.38		915.38	8	A	19	2141.1		2141.1	
	1062.5	-0.018	1062.5	9	F	18	2070.1		2070.1	
	1163.5	-0.159	1163.5	10	T	17	1923		962.01	+0.08
	1260.6		1260.6	11	P	16	1822		911.49	+0.2604
	1331.6	-0.045	1331.6	12	A	15	1724.9		1724.9	
	1428.6		1428.6	13	P	14	1653.9	-0.071	1653.9	
	1557.7		1557.7	14	E	13	1556.8		1556.8	
	1672.7		1672.7	15	D	12	1427.8		1427.8	
	1759.7		1759.7	16	S	11	1312.8		1312.8	
	1872.8		1872.8	17	L	10	1225.7		1225.7	
	1943.9		1943.9	18	A	9	1112.6		1112.6	
	2030.9		2030.9	19	S	8	1041.6		1041.6	
+0.294	1065.5		2130	20	V	7	954.58		954.58	
	2227		2227	21	P	6	855.51	+0.0847	855.51	
-0.026	1195.5		2390.1	22	Y	5	758.46		758.46	
	2487.1		2487.1	23	P	4	595.39	+0.0859	595.39	
	2584.2		2584.2	24	P	3	498.34	+0.3257	498.34	
	2697.3		2697.3	25	L	2	401.29	-0.05	401.29	
+0.3864	1405.7		2810.4	26	L	1	288.2		288.2	
				27	R	0	175.12		175.12	



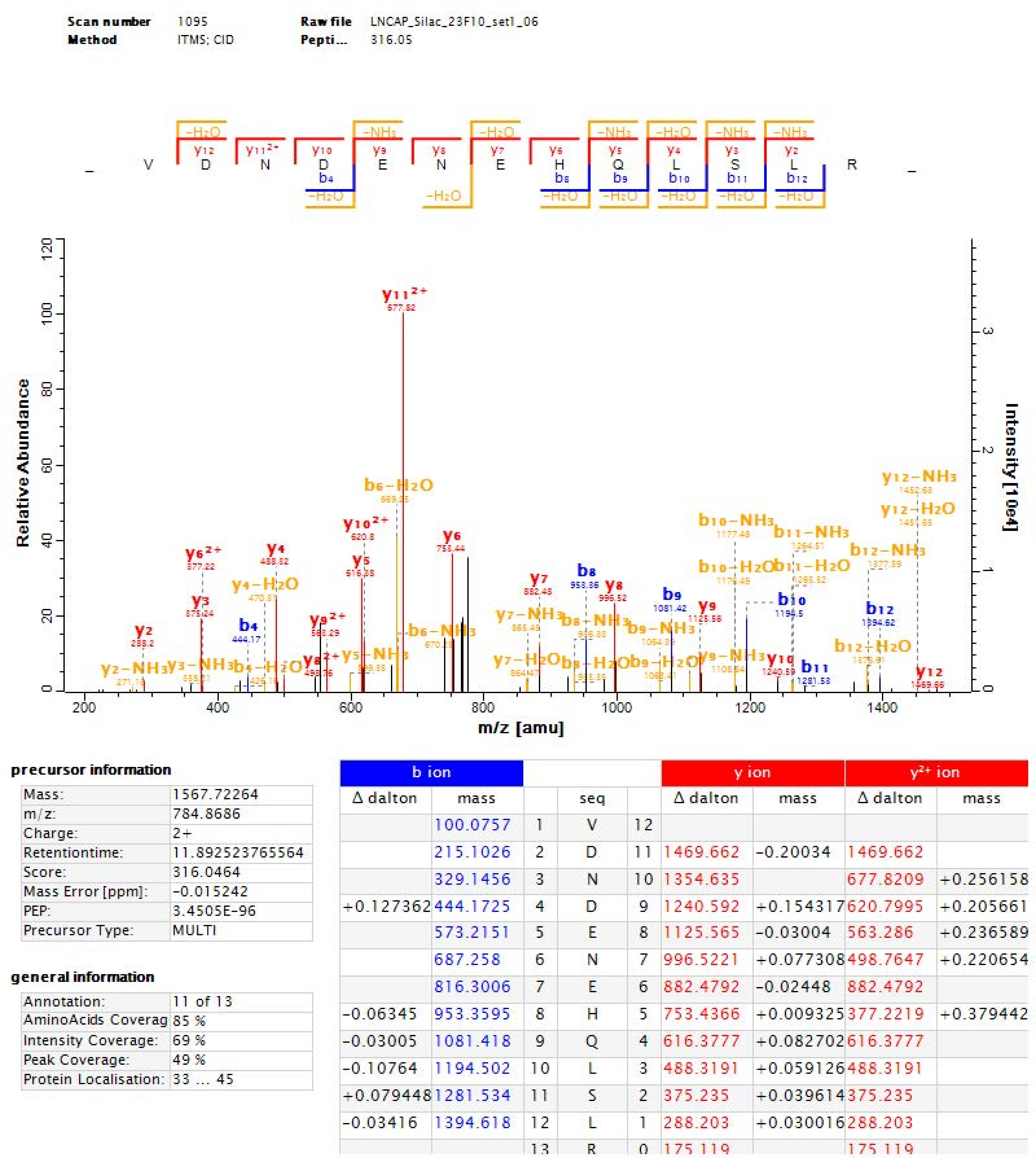
Scan number	9342	**Raw file**	LNCAP_Silac_23F10_set1_05
Method	ITMS; CID	**Pepti...**	107.32

precursor information

g

Mass:	1006.56372
m/z:	504.28914
Charge:	2+
Retentiontime:	63.286647796630
Score:	107.3173
Mass Error [ppm]:	-0.30396
PEP:	0.0066223
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	56 %
Peak Coverage:	18 %
Protein Localisation:	263 ... 270

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	I	7				
	171.11	+0.1087	171.11	2	G	6	894.49	+0.0357	894.49	
	284.2	+0.0672	284.2	3	L	5	837.47	+0.0443	419.24	+0.0325
	431.27	+0.1317	431.27	4	F	4	724.38	-0.012	724.38	
	578.33	+0.0032	578.33	5	F	3	577.31	+0.0674	577.31	
+0.4594	382.71	+0.0432	764.41	6	W	2	430.24	+0.1365	430.24	
	861.47	-0.028	861.47	7	P	1	244.17	+0.0912	244.17	
				8	K	0	147.11	+0.2817	147.11	



Scan number 1095 **Raw file** LNCAP_Silac_23F10_set1_06

Method ITMS; CID **Pepti...** 316.05

precursor information

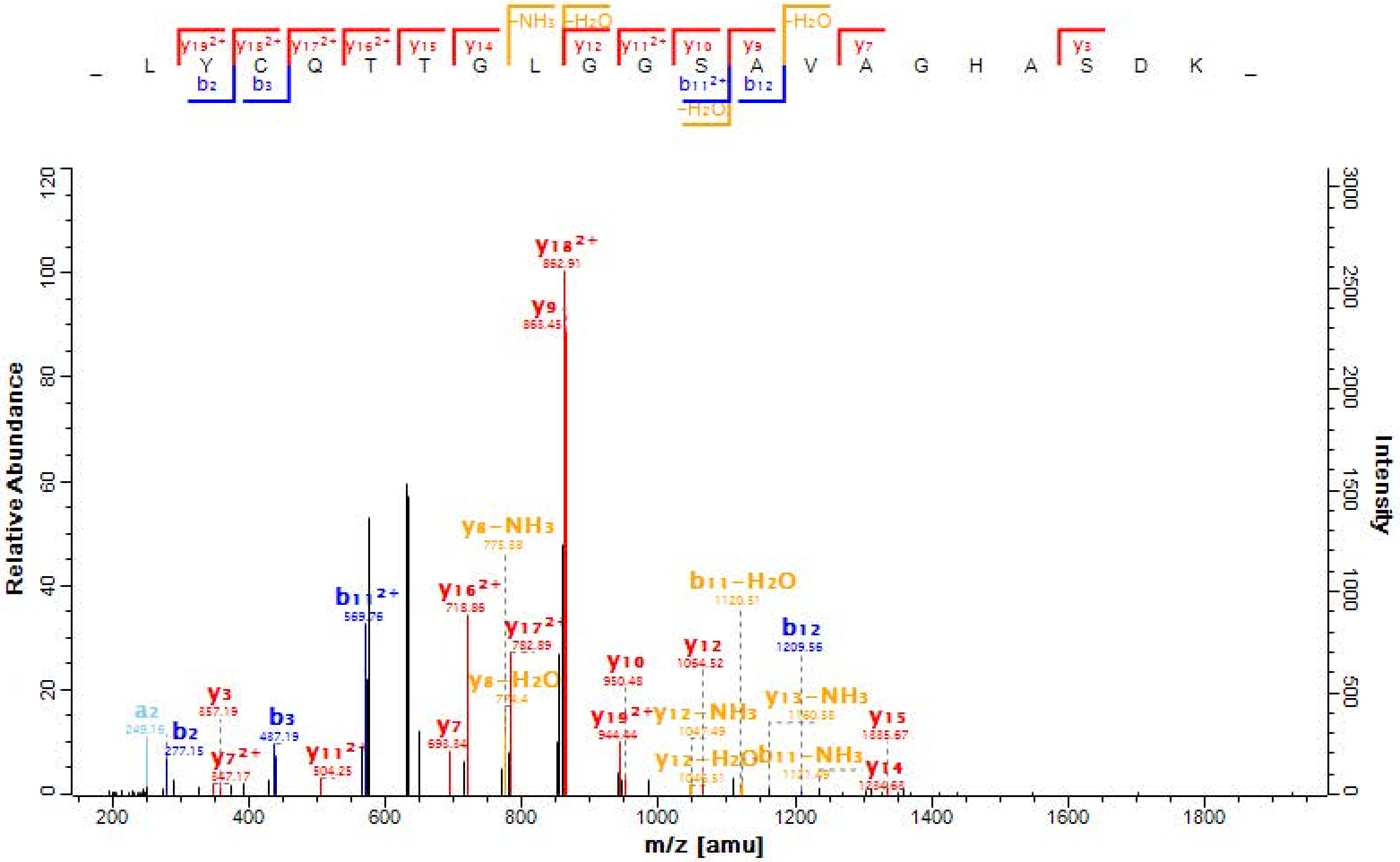
Mass:	1567.72264
m/z:	784.8686
Charge:	2+
Retentiontime:	11.892523765564
Score:	316.0464
Mass Error [ppm]:	-0.015242
PEP:	3.4505E-96
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	69 %
Peak Coverage:	49 %
Protein Localisation:	33 ... 45

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	12				
	215.1026	2	D	11	1469.662	-0.20034	1469.662	
	329.1456	3	N	10	1354.635		677.8209	+0.256158
+0.127362	444.1725	4	D	9	1240.592	+0.154317	620.7995	+0.205661
	573.2151	5	E	8	1125.565	-0.03004	563.286	+0.236589
	687.258	6	N	7	996.5221	+0.077308	498.7647	+0.220654
	816.3006	7	E	6	882.4792	-0.02448	882.4792	
-0.06345	953.3595	8	H	5	753.4366	+0.009325	377.2219	+0.379442
-0.03005	1081.418	9	Q	4	616.3777	+0.082702	616.3777	
-0.10764	1194.502	10	L	3	488.3191	+0.059126	488.3191	
+0.079448	1281.534	11	S	2	375.235	+0.039614	375.235	
-0.03416	1394.618	12	L	1	288.203	+0.030016	288.203	
		13	R	0	175.119		175.119	

Scan number	1497	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	93.23



precursor information

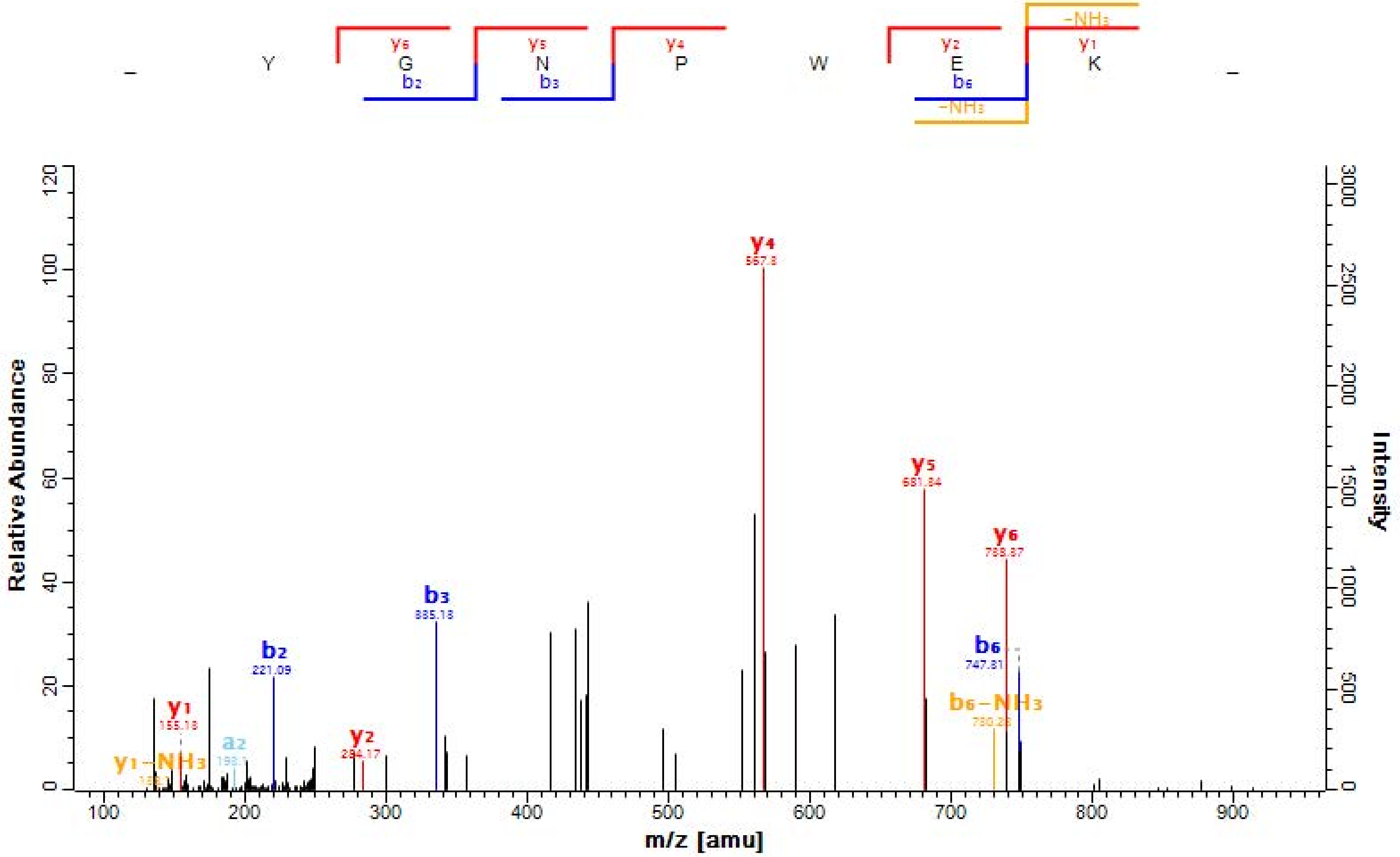
Mass:	1991.93706
m/z:	664.9863
Charge:	3+
Retentiontime:	14.320529937744
Score:	93.22573
Mass Error [ppm]:	-0.013336
PEP:	4.8377E-06
Precursor Type:	MULTI

general information

Annotation:	15 of 20
AminoAcids Coverag	75 %
Intensity Coverage:	48 %
Peak Coverage:	25 %
Protein Localisation:	119 ... 138

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	19				
-0.02	249.2		277.2	+0.081	277.2	2	Y	18	1888		944.4	+0.34
	409.2		437.2	-0.12	437.2	3	C	17	1725		862.9	+0.00
	537.2		565.2		565.2	4	Q	16	1565		782.9	+0.33
	638.3		666.3		666.3	5	T	15	1437		718.9	+0.25
	739.3		767.3		767.3	6	T	14	1336	-0.06	1336	
	796.4		824.4		824.4	7	G	13	1235	+0.078	1235	
	909.4		937.4		937.4	8	L	12	1178		1178	
	966.5		994.5		994.5	9	G	11	1065	+0.085	1065	
	1023		1051		1051	10	G	10	1007		504.3	-0.09
	1111	+0.173	569.8		1139	11	S	9	950.5	-0.1	950.5	
	1182		1210	+0.123	1210	12	A	8	863.4	+0.138	863.4	
	1281		1309		1309	13	V	7	792.4		792.4	
	1352		1380		1380	14	A	6	693.3	+0.042	347.2	+0.39
	1409		1437		1437	15	G	5	622.3		622.3	
	1546		1574		1574	16	H	4	565.3		565.3	
	1617		1645		1645	17	A	3	428.2		428.2	
	1704		1732		1732	18	S	2	357.2	+0.201	357.2	
	1819		1847		1847	19	D	1	270.2		270.2	
						20	K	0	155.1		155.1	

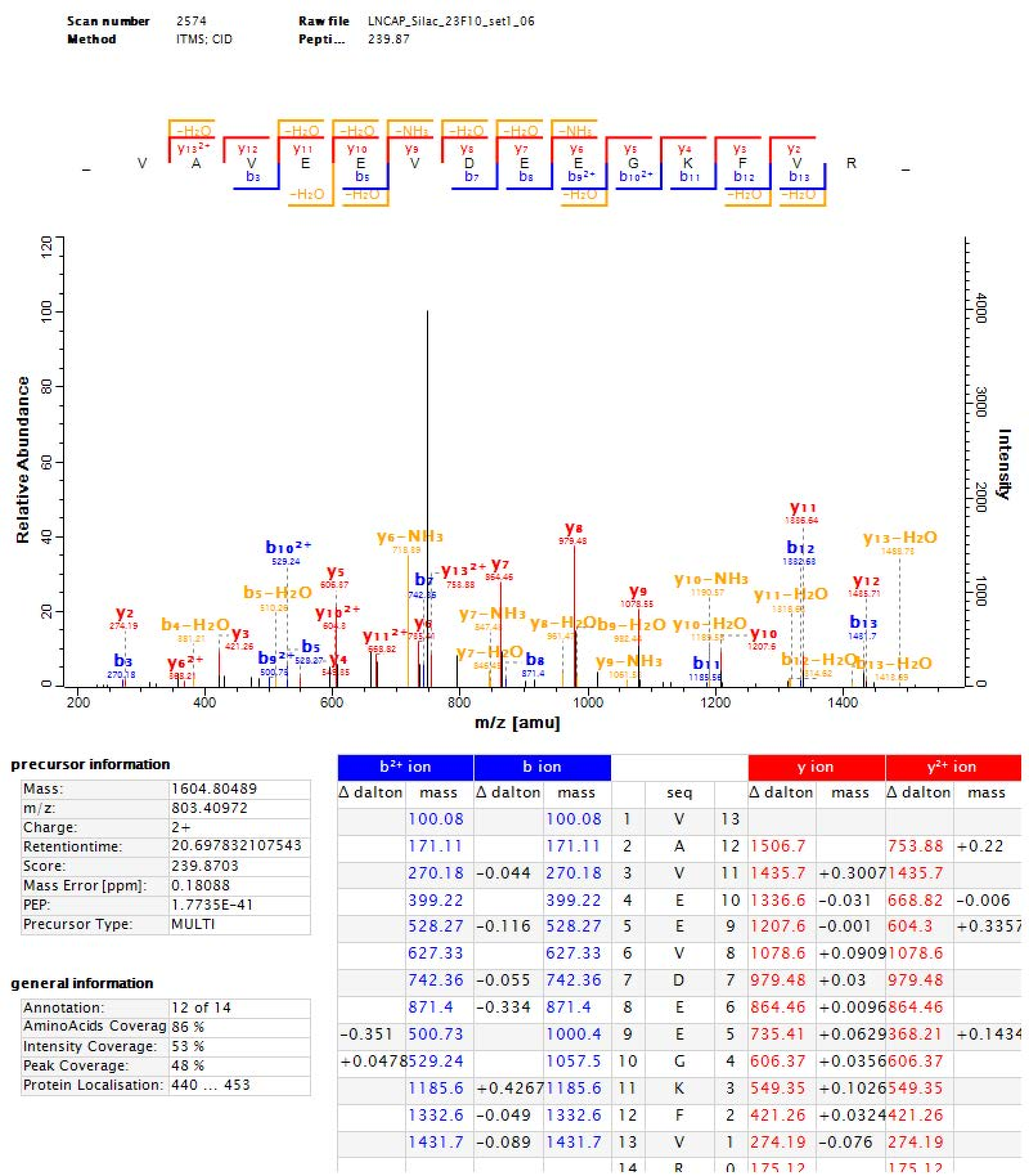
Scan number	1564	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	58.82



precursor information

Mass:	900.42254
m/z:	451.21855
Charge:	2+
Retentiontime:	14.730946540832
Score:	58.815
Mass Error [ppm]:	0.47014
Annotation:	5 of 7
AminoAcids Coverag	71 %
Intensity Coverage:	35 %
Peak Coverage:	9 %

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	136.0757		164.0706	1	Y	6		
-0.00751	193.0972	-0.01513	221.0921	2	G	5	738.3661	+0.00094
	307.1401	-0.04888	335.135	3	N	4	681.3446	-0.02276
	404.1928		432.1878	4	P	3	567.3017	+0.06228
	590.2722		618.2671	5	W	2	470.2489	
	719.3148	+0.034389	747.3097	6	E	1	284.1696	+0.053548
				7	K	0	155.127	+0.029552



Scan number	2574	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	239.87

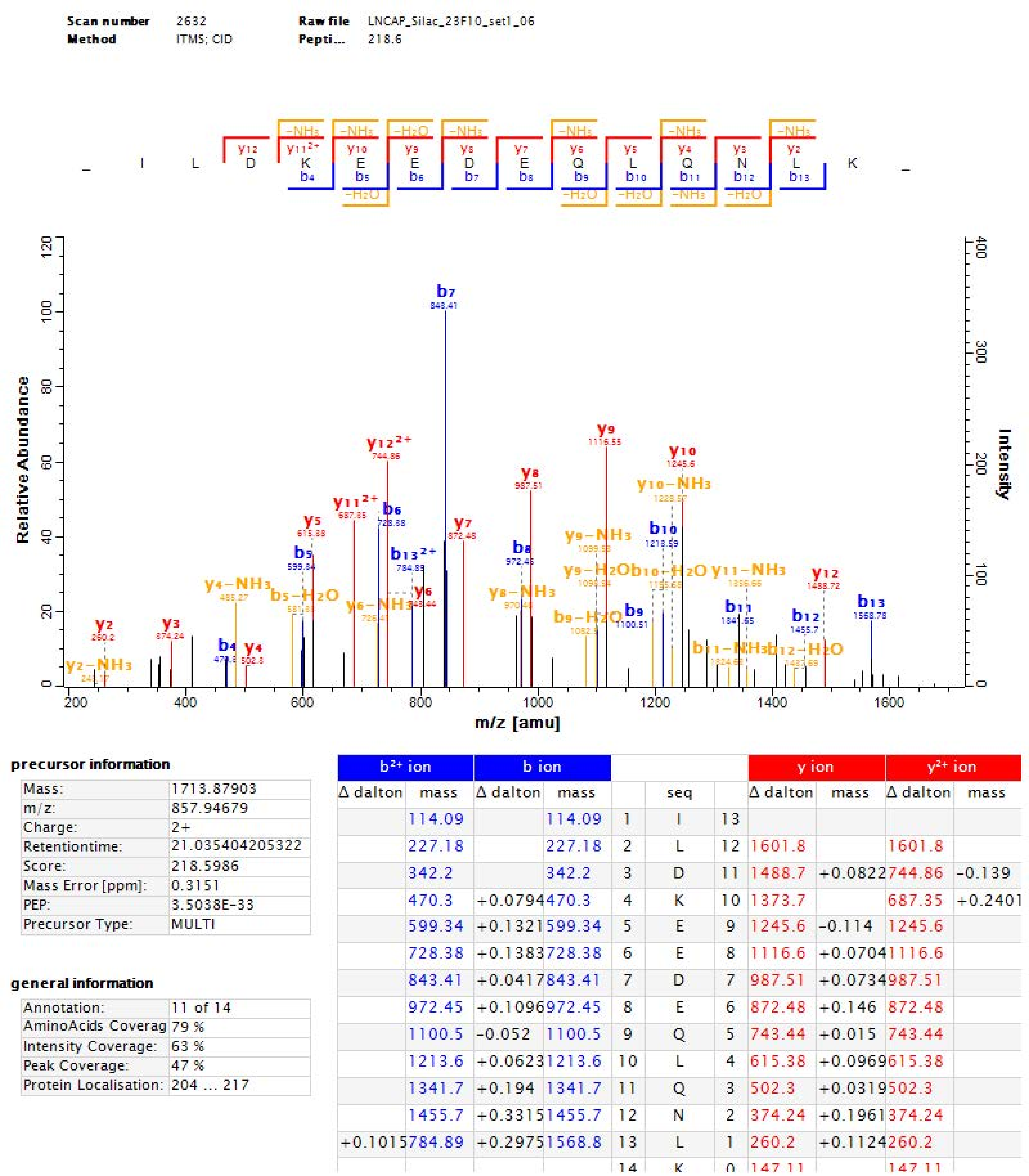
precursor information

Mass:	1604.80489
m/z:	803.40972
Charge:	2+
Retentiontime:	20.697832107543
Score:	239.8703
Mass Error [ppm]:	0.18088
PEP:	1.7735E-41
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	53 %
Peak Coverage:	48 %
Protein Localisation:	440 ... 453

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	13				
	171.11		171.11	2	A	12	1506.7		753.88	+0.22
	270.18	-0.044	270.18	3	V	11	1435.7	+0.3007	1435.7	
	399.22		399.22	4	E	10	1336.6	-0.031	668.82	-0.006
	528.27	-0.116	528.27	5	E	9	1207.6	-0.001	604.3	+0.3357
	627.33		627.33	6	V	8	1078.6	+0.0909	1078.6	
	742.36	-0.055	742.36	7	D	7	979.48	+0.03	979.48	
	871.4	-0.334	871.4	8	E	6	864.46	+0.0096	864.46	
-0.351	500.73		1000.4	9	E	5	735.41	+0.0629	368.21	+0.1434
+0.0478	529.24		1057.5	10	G	4	606.37	+0.0356	606.37	
	1185.6	+0.4267	1185.6	11	K	3	549.35	+0.1026	549.35	
	1332.6	-0.049	1332.6	12	F	2	421.26	+0.0324	421.26	
	1431.7	-0.089	1431.7	13	V	1	274.19	-0.076	274.19	
				14	R	0	175.12		175.12	



Scan number	2632	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	218.6

precursor information

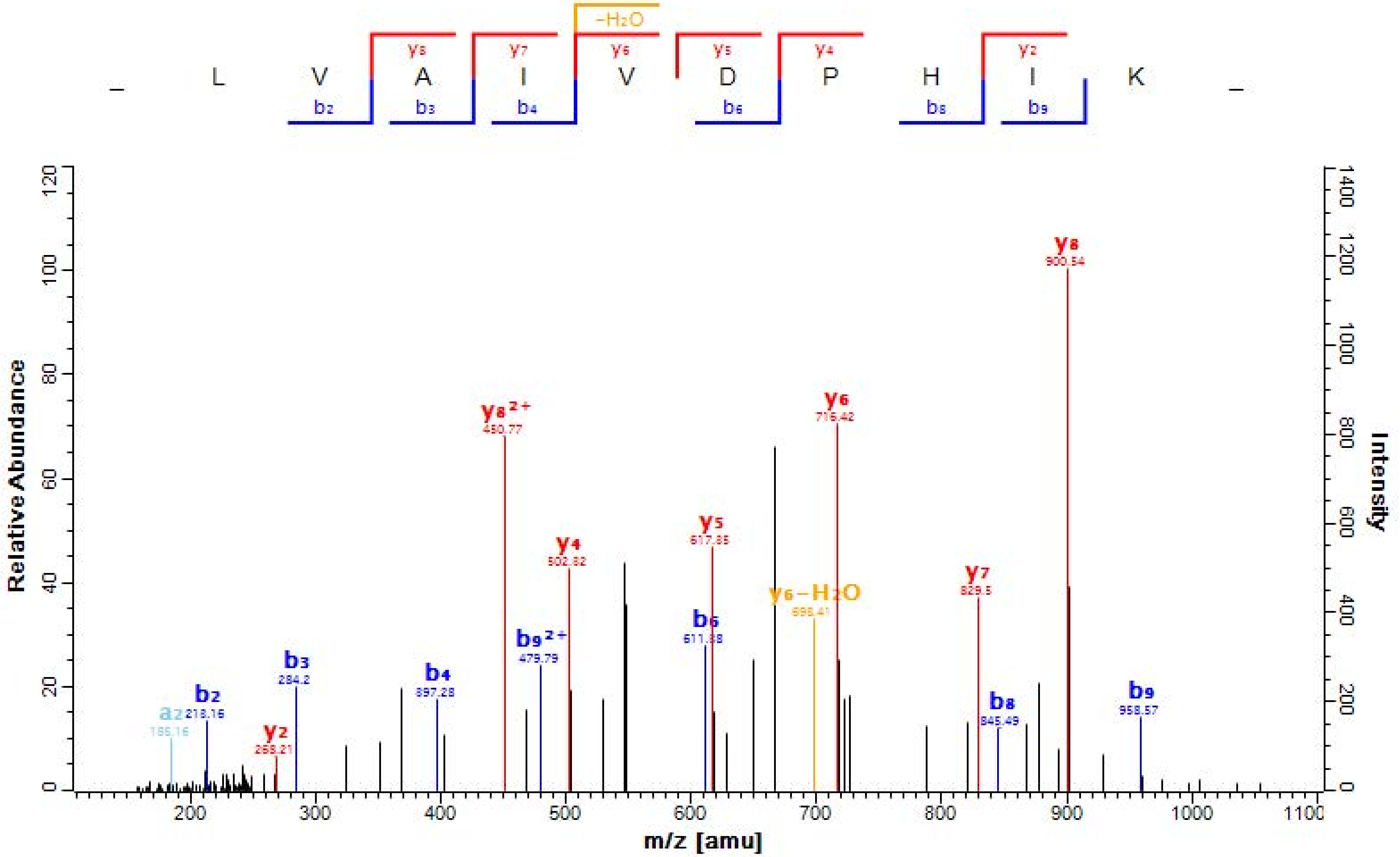
Mass:	1713.87903
m/z:	857.94679
Charge:	2+
Retentiontime:	21.035404205322
Score:	218.5986
Mass Error [ppm]:	0.3151
PEP:	3.5038E-33
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	63 %
Peak Coverage:	47 %
Protein Localisation:	204 ... 217

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	I	13				
	227.18		227.18	2	L	12	1601.8		1601.8	
	342.2		342.2	3	D	11	1488.7	+0.0822	744.86	-0.139
	470.3	+0.0794	470.3	4	K	10	1373.7		687.35	+0.2401
	599.34	+0.1321	599.34	5	E	9	1245.6	-0.114	1245.6	
	728.38	+0.1383	728.38	6	E	8	1116.6	+0.0704	1116.6	
	843.41	+0.0417	843.41	7	D	7	987.51	+0.0734	987.51	
	972.45	+0.1096	972.45	8	E	6	872.48	+0.146	872.48	
	1100.5	-0.052	1100.5	9	Q	5	743.44	+0.015	743.44	
	1213.6	+0.0623	1213.6	10	L	4	615.38	+0.0969	615.38	
	1341.7	+0.194	1341.7	11	Q	3	502.3	+0.0319	502.3	
	1455.7	+0.3315	1455.7	12	N	2	374.24	+0.1961	374.24	
+0.1015	784.89	+0.2975	1568.8	13	L	1	260.2	+0.1124	260.2	
				14	K	0	147.11		147.11	

Scan number	3157	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	127.4



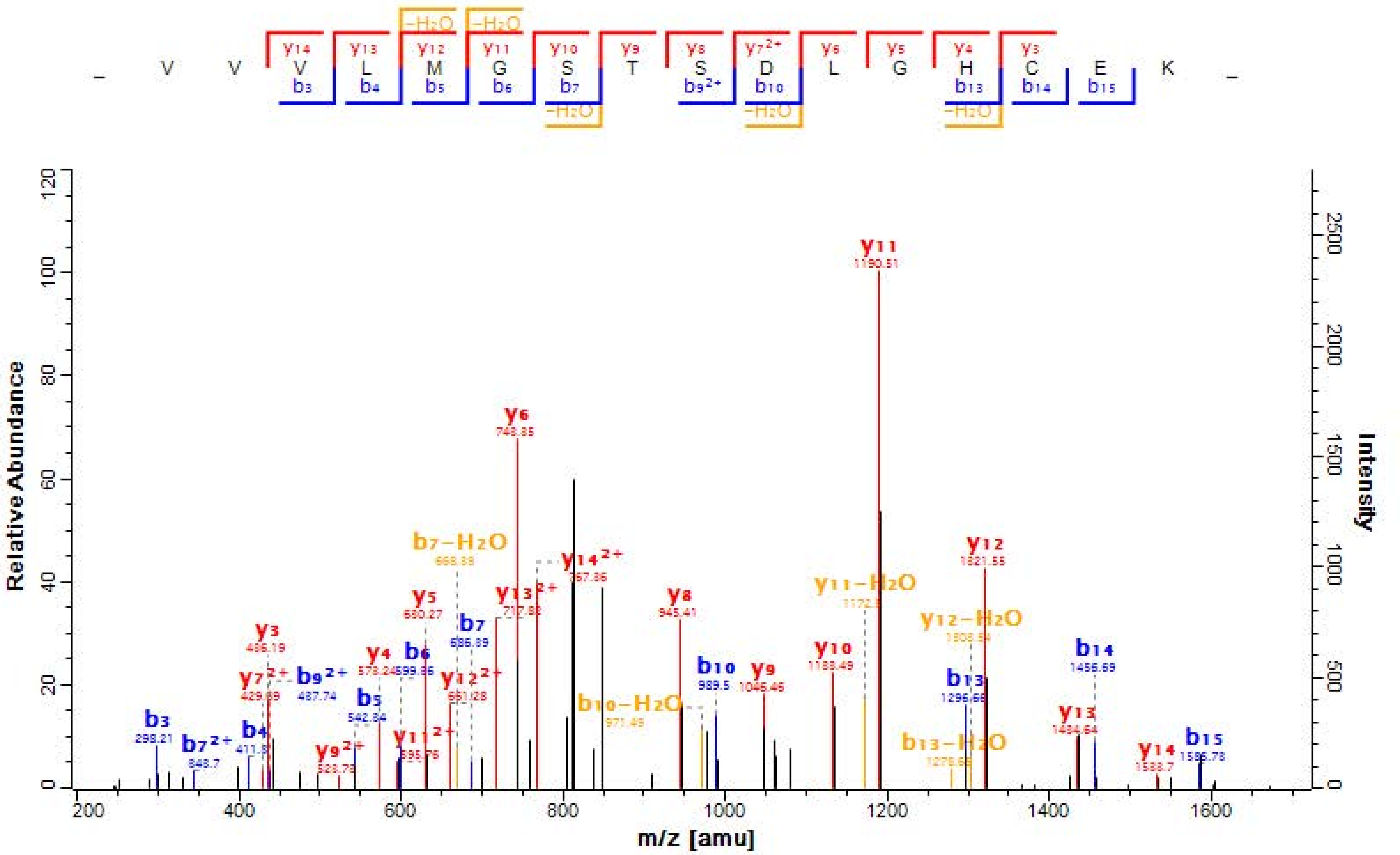
precursor information

Mass:	1103.67034
m/z:	552.84245
Charge:	2+
Retentiontime:	24.012029647827
Score:	127.3975
Mass Error [ppm]:	0.056709
PEP:	0.00025448
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	47 %
Peak Coverage:	15 %
Protein Localisation:	514 ... 523

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	9				
-0.03	185.2		213.2	+0.037	213.2	2	V	8	999.6		999.6	
	256.2		284.2	-0.02	284.2	3	A	7	900.5	-0.1	450.8	+0.19
	369.3		397.3	+0.052	397.3	4	I	6	829.5	+0.064	829.5	
	468.4		496.3		496.3	5	V	5	716.4	+0.054	716.4	
	583.4		611.4	-0.17	611.4	6	D	4	617.3	-0.02	617.3	
	680.4		708.4		708.4	7	P	3	502.3	+0.085	502.3	
	817.5		845.5	+0.061	845.5	8	H	2	405.3		405.3	
	930.6	-0.32	479.8	+0.017	958.6	9	I	1	268.2	+0.127	268.2	
						10	K	0	155.1		155.1	

Scan number	3223	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	196.67



precursor information

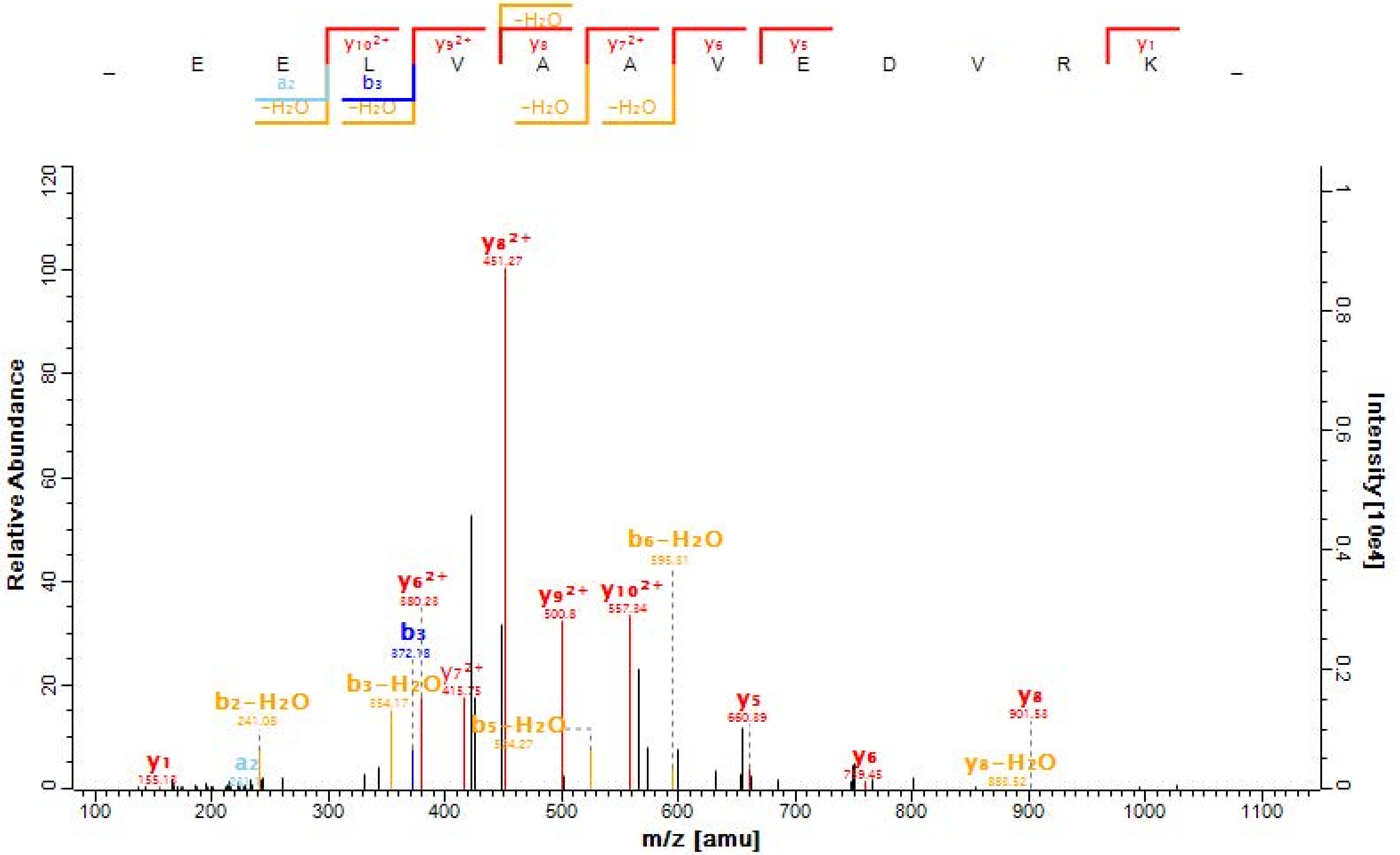
Mass:	1730.83292
m/z:	866.42374
Charge:	2+
Retentiontime:	24.379335403442
Score:	196.6749
Mass Error [ppm]:	-0.12777
PEP:	2.1859E-27
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	55 %
Peak Coverage:	39 %
Protein Localisation:	294 ... 309

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	15				
	199.14		199.14	2	V	14	1632.8		1632.8	
	298.21	+0.0378	298.21	3	V	13	1533.7	-0.06	767.36	+0.2665
	411.3	+0.0593	411.3	4	L	12	1434.6	-0.007	717.82	+0.1882
	542.34	-0.029	542.34	5	M	11	1321.6	-0.004	661.28	+0.2041
	599.36	-0.079	599.36	6	G	10	1190.5	-0.015	595.76	-0.487
+0.4917	343.7	-0.154	686.39	7	S	9	1133.5	+0.0938	1133.5	
	787.44		787.44	8	T	8	1046.5	-0.014	523.73	-0.289
-0.384	437.74		874.47	9	S	7	945.41	+0.0309	945.41	
	989.5	-0.077	989.5	10	D	6	858.38		429.69	-0.307
	1102.6		1102.6	11	L	5	743.35	+0.0365	743.35	
	1159.6		1159.6	12	G	4	630.27	+0.0687	630.27	
	1296.7	-0.065	1296.7	13	H	3	573.24	+0.1037	573.24	
	1456.7	-0.088	1456.7	14	C	2	436.19	-0.015	436.19	
	1585.7	-0.234	1585.7	15	E	1	276.16		276.16	
				16	K	0	147.11		147.11	

Scan number	3410	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	44.61



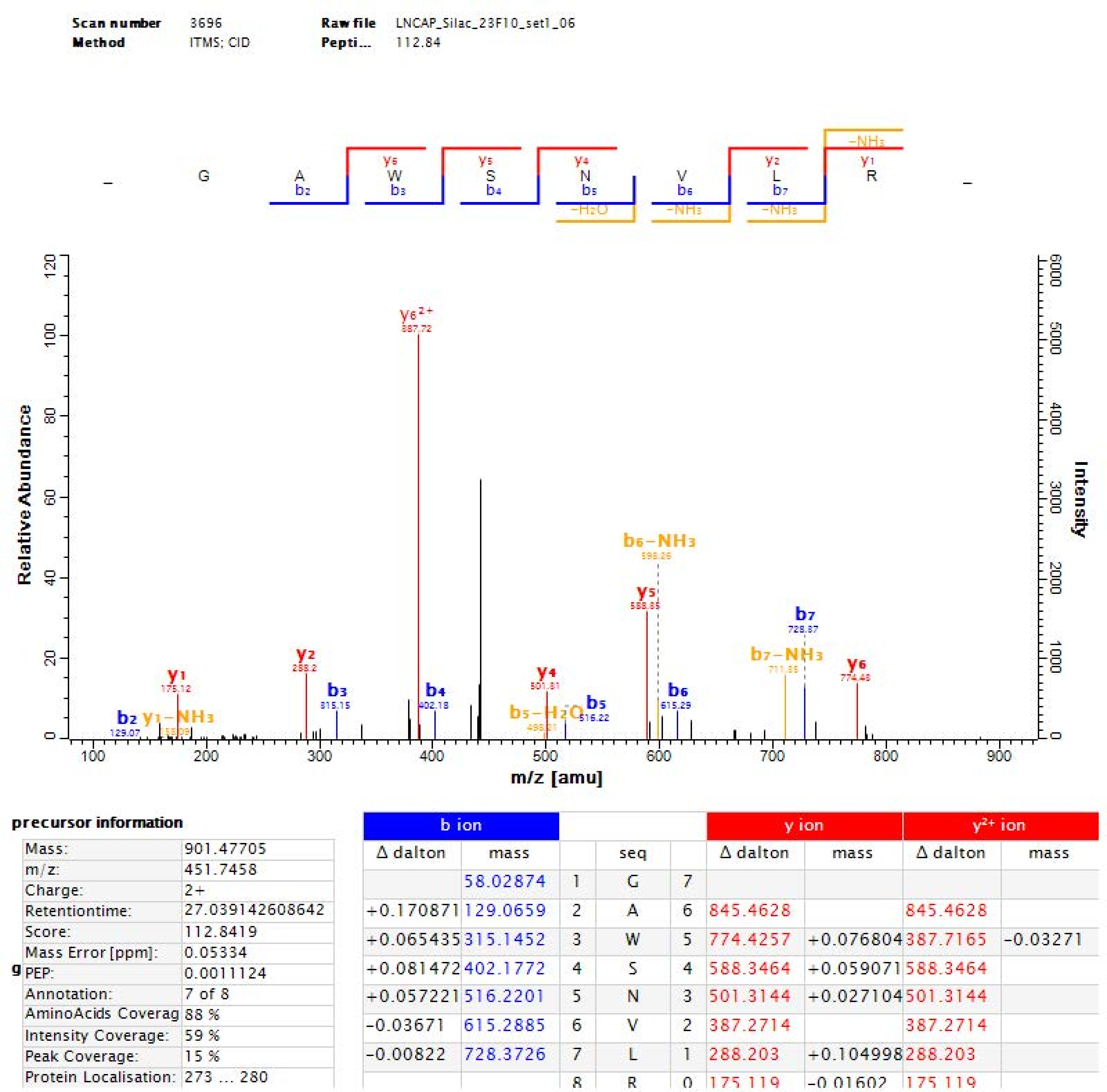
precursor information

Mass:	1356.72483
m/z:	453.24889
Charge:	3+
Retentiontime:	25.431894302368
Score:	44.61188
Mass Error [ppm]:	-0.045812
PEP:	0.025221
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	52 %
Peak Coverage:	19 %
Protein Localisation:	88 ... 99

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	11				
-0.333	231.1		259.09	2	E	10	1242.7		1242.7	
	344.18	-0.298	372.18	3	L	9	1113.7		557.34	+0.1403
	443.25		471.24	4	V	8	1000.6		500.8	-0.019
	514.29		542.28	5	A	7	901.53	+0.1342	451.27	-0.026
	585.32		613.32	6	A	6	830.49		415.75	+0.1353
	684.39		712.39	7	V	5	759.45	+0.0555	380.23	+0.0162
	813.44		841.43	8	E	4	660.39	+0.0238	660.39	
	928.46		956.46	9	D	3	531.34		531.34	
	1027.5		1055.5	10	V	2	416.32		416.32	
	1189.7		1217.6	11	R	1	317.25		317.25	
				12	K	0	155.13	+0.0143	155.13	



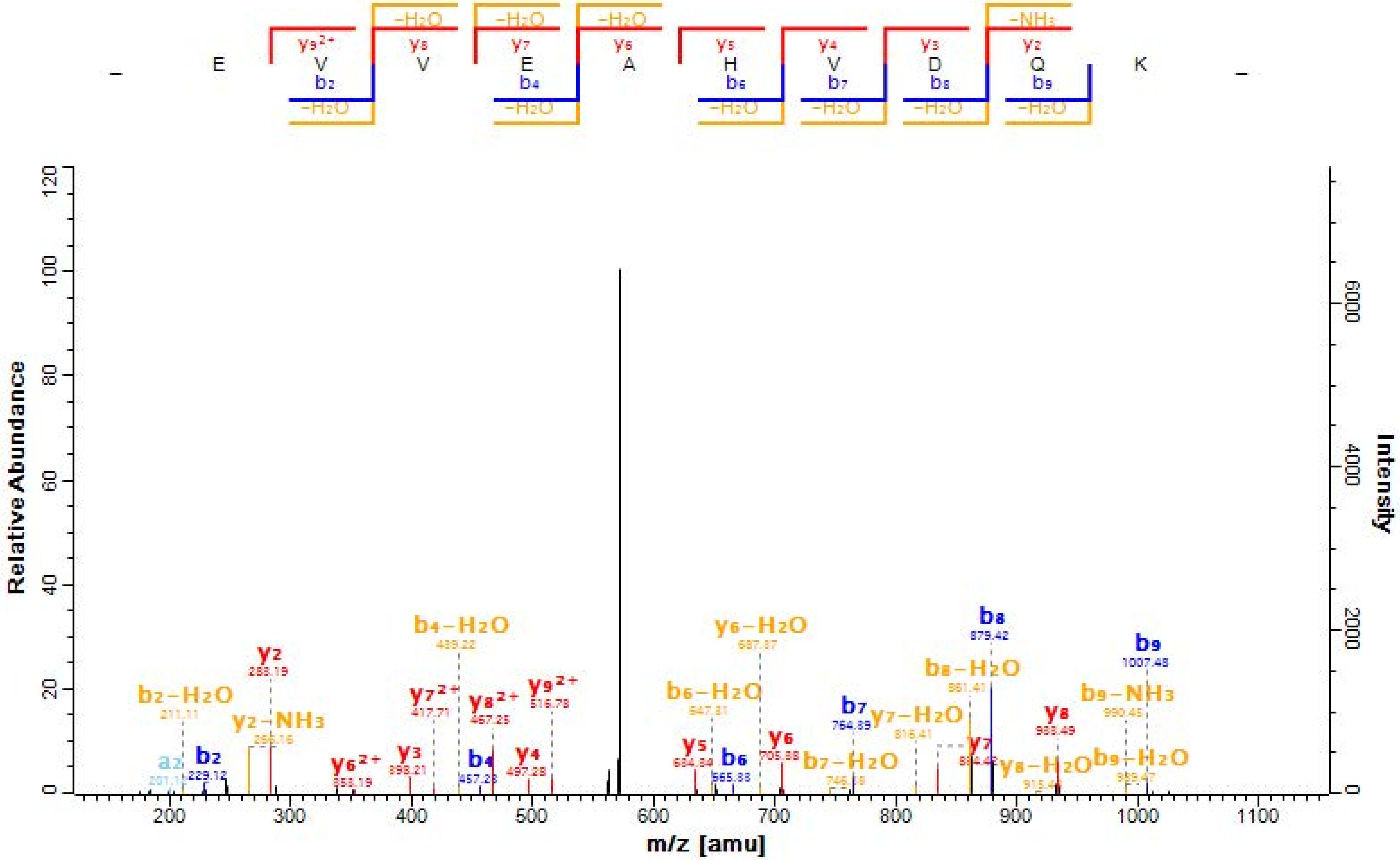
Scan number	3696	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	112.84

precursor information

Mass:	901.47705
m/z:	451.7458
Charge:	2+
Retentiontime:	27.039142608642
Score:	112.8419
Mass Error [ppm]:	0.05334
PEP:	0.0011124
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	59 %
Peak Coverage:	15 %
Protein Localisation:	273 ... 280

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	7				
+0.170871	129.0659	2	A	6	845.4628		845.4628	
+0.065435	315.1452	3	W	5	774.4257	+0.076804	387.7165	-0.03271
+0.081472	402.1772	4	S	4	588.3464	+0.059071	588.3464	
+0.057221	516.2201	5	N	3	501.3144	+0.027104	501.3144	
-0.03671	615.2885	6	V	2	387.2714		387.2714	
-0.00822	728.3726	7	L	1	288.203	+0.104998	288.203	
		8	R	0	175.119	-0.01602	175.119	

Scan number	373	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	236.32



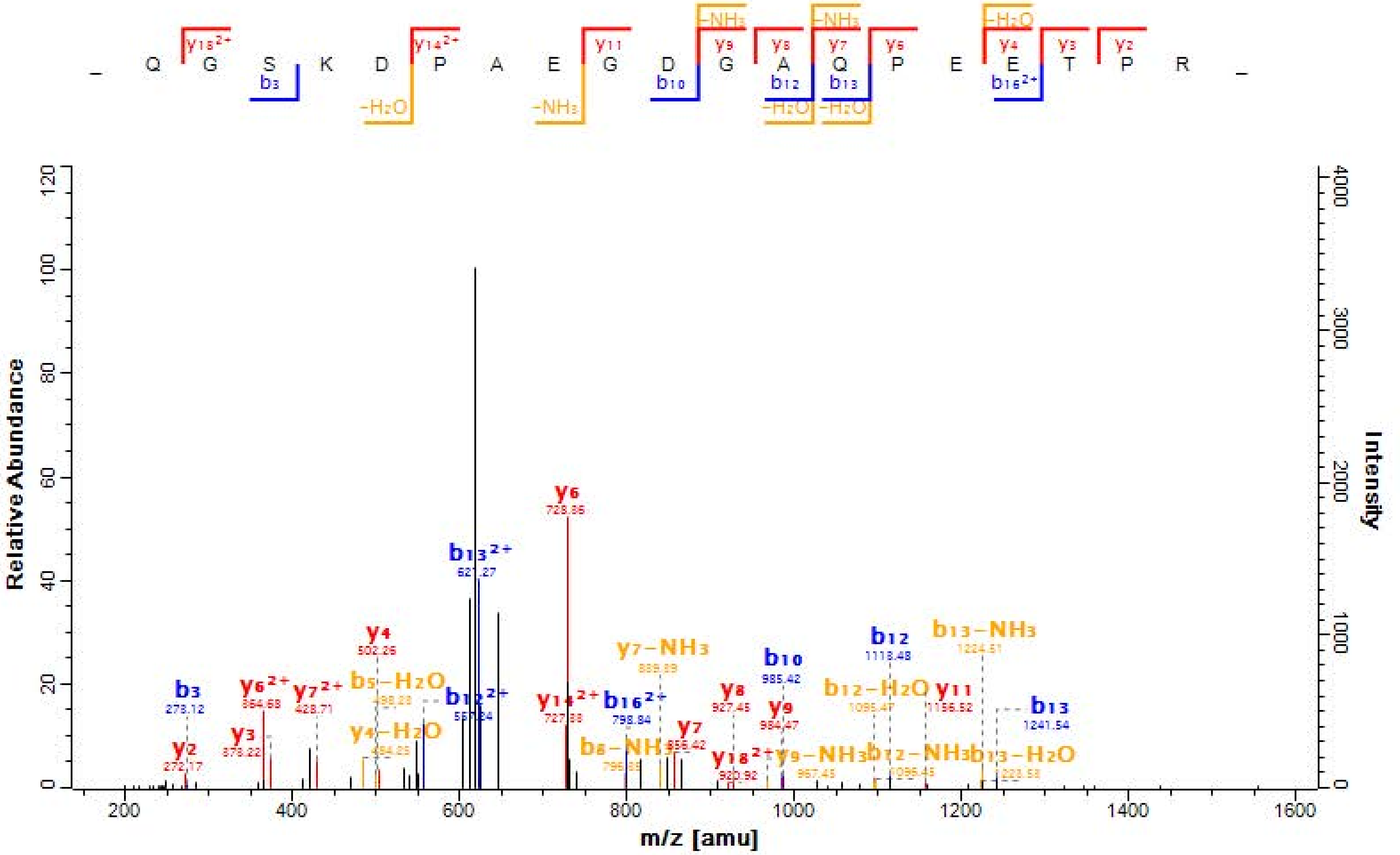
precursor information

Mass:	1152.57727
m/z:	577.29591
Charge:	2+
Retentiontime:	7.1489267349243
Score:	236.3153
Mass Error [ppm]:	-0.19743
PEP:	3.4933E-27
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	42 %
Peak Coverage:	31 %
Protein Localisation:	224 ... 233

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	9				
+0.0501	201.12	+0.032	229.12	2	V	8	1032.6		516.78	+0.0211
	300.19		328.19	3	V	7	933.49	+0.0106	467.25	+0.1879
	429.23	+0.3266	457.23	4	E	6	834.42	+0.0414	417.71	+0.0333
	500.27		528.27	5	A	5	705.38	+0.091	353.19	+0.3714
	637.33	+0.0467	665.33	6	H	4	634.34	+0.1487	634.34	
	736.4	+0.192	764.39	7	V	3	497.28	+0.0122	497.28	
	851.43	+0.0039	879.42	8	D	2	398.21	+0.1911	398.21	
	979.48	+0.0618	1007.5	9	Q	1	283.19	+0.0585	283.19	
				10	K	0	155.13		155.13	

Scan number 381 **Raw file** LNCAP_Silac_23F10_set1_06
Method ITMS; CID **Pepti...** 146.3



precursor information

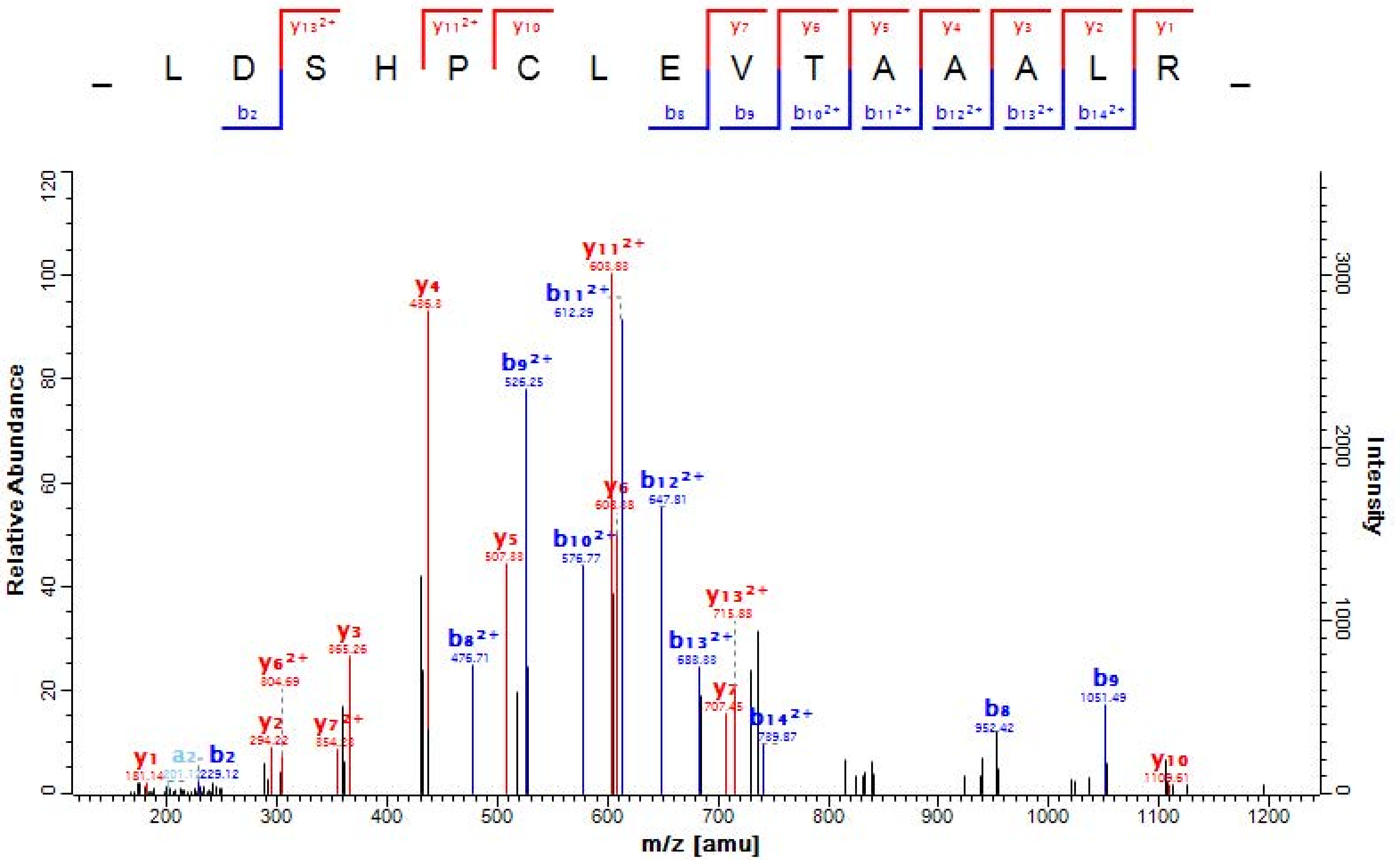
Mass:	1967.88305
m/z:	656.96829
Charge:	3+
Retentiontime:	7.2028932571411
Score:	146.2959
Mass Error [ppm]:	0.49396
PEP:	3.6066E-19
Precursor Type:	MULTI

general information

Annotation:	14 of 19
AminoAcids Coverag	74 %
Intensity Coverage:	40 %
Peak Coverage:	28 %
Protein Localisation:	210 ... 228

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.07		129.07	1	Q	18				
	186.09		186.09	2	G	17	1840.8		920.92	-0.068
	273.12	+0.3189	273.12	3	S	16	1783.8		1783.8	
	401.21		401.21	4	K	15	1696.8		1696.8	
	516.24		516.24	5	D	14	1568.7		1568.7	
	613.29		613.29	6	P	13	1453.7		727.33	+0.4359
	684.33		684.33	7	A	12	1356.6		1356.6	
	813.37		813.37	8	E	11	1285.6		1285.6	
	870.4		870.4	9	G	10	1156.5	+0.2223	1156.5	
	985.42	+0.178	985.42	10	D	9	1099.5		1099.5	
	1042.4		1042.4	11	G	8	984.47	+0.0109	984.47	
+0.1082	557.24	+0.0548	1113.5	12	A	7	927.45	+0.0546	927.45	
+0.2019	621.27	+0.054	1241.5	13	Q	6	856.42	+0.0753	428.71	+0.3608
	1338.6		1338.6	14	P	5	728.36	+0.0737	364.68	+0.2042
	1467.6		1467.6	15	E	4	631.3		631.3	
+0.1407	798.84		1596.7	16	E	3	502.26	+0.1015	502.26	
	1697.7		1697.7	17	T	2	373.22	+0.0955	373.22	
	1794.8		1794.8	18	P	1	272.17	+0.0656	272.17	
				19	R	0	175.12		175.12	

Scan number	4091	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	132.79



precursor information

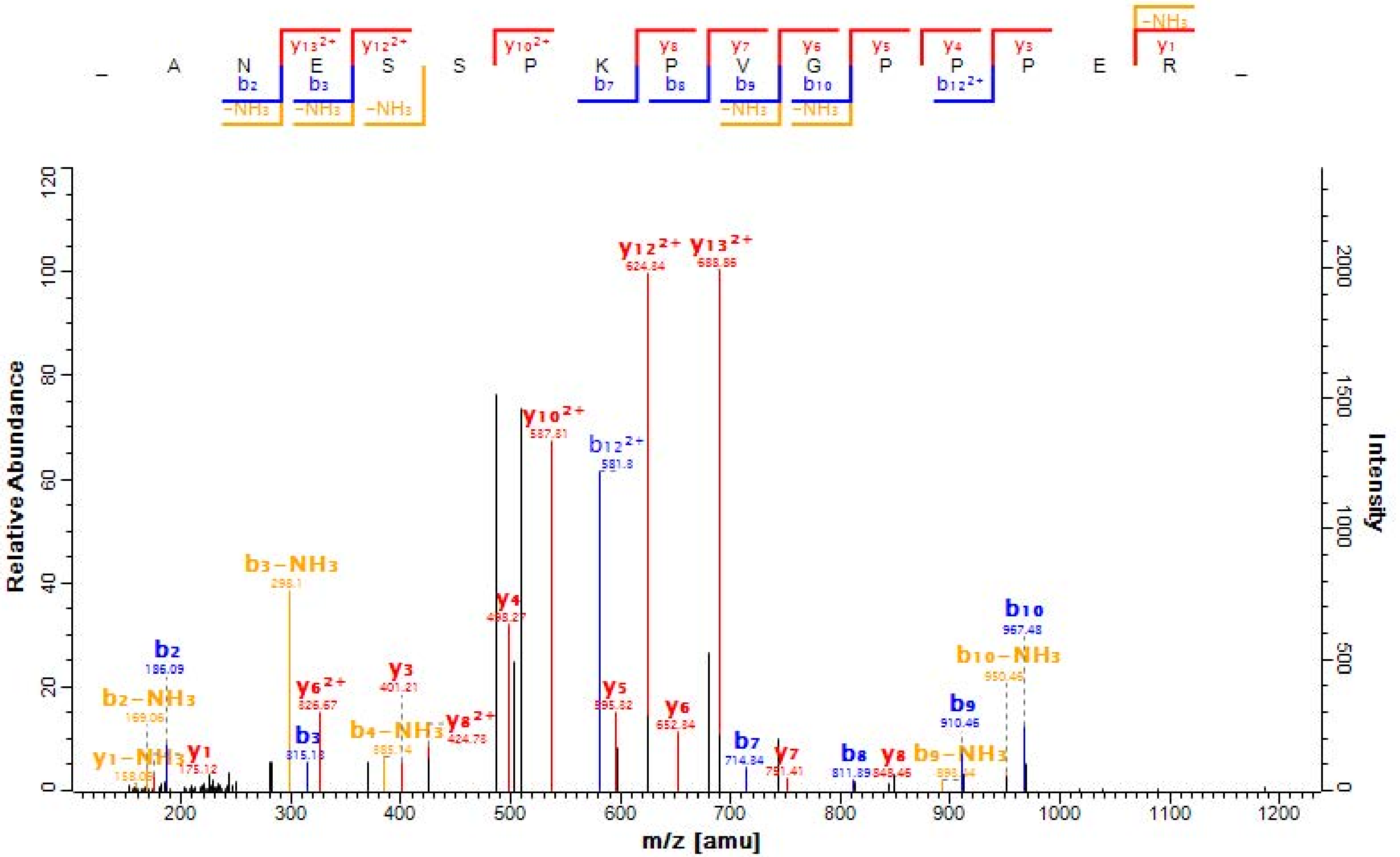
Mass:	1651.83535
m/z:	551.61906
Charge:	3+
Retentiontime:	29.285007476806
Score:	132.7903
Mass Error [ppm]:	0.095453
PEP:	5.7481E-10
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	65 %
Peak Coverage:	23 %
Protein Localisation:	88 ... 102

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	14				
+0.152	201.1		229.1	+0.036	229.1	2	D	13	1546		1546	
	288.2		316.2		316.2	3	S	12	1431		715.9	-0.25
	425.2		453.2		453.2	4	H	11	1344		1344	
	522.3		550.3		550.3	5	P	10	1207		603.8	-0.26
	682.3		710.3		710.3	6	C	9	1110	+0.031	1110	
	795.4		823.4		823.4	7	L	8	949.6		949.6	
	924.4	+0.234	476.7	+0.082	952.4	8	E	7	836.5		836.5	
	1023	+0.242	526.2	+0.049	1051	9	V	6	707.5	+0.293	354.2	+0.12
	1125	+0.257	576.8		1153	10	T	5	608.4	-0.02	304.7	+0.05
	1196	+0.22	612.3		1224	11	A	4	507.3	+0.055	507.3	
	1267	+0.264	647.8		1295	12	A	3	436.3	+0.104	436.3	
	1338	+0.146	683.3		1366	13	A	2	365.3	+0.037	365.3	
	1451	+0.293	739.9		1479	14	L	1	294.2	+0.008	294.2	
						15	R	0	181.1	+0.095	181.1	

Scan number	451	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	126.71



precursor information

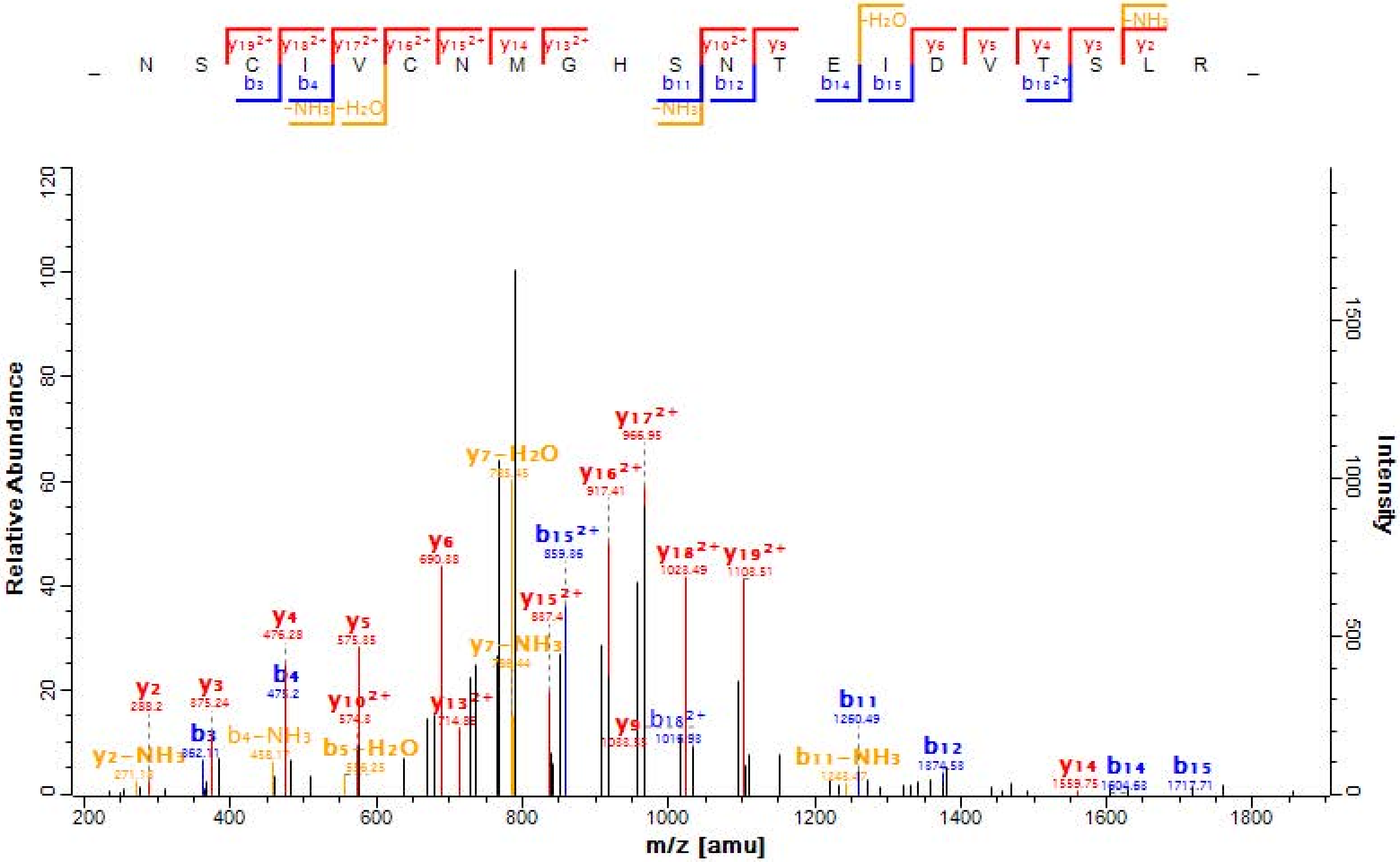
Mass:	1560.78948
m/z:	521.27044
Charge:	3+
Retentiontime:	7.6911034584045
Score:	126.7053
Mass Error [ppm]:	-0.086911
PEP:	1.5313E-09
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	60 %
Peak Coverage:	23 %
Protein Localisation:	156 ... 170

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	14				
	186.09	+0.0191	186.09	2	N	13	1490.8		1490.8	
	315.13	+0.031	315.13	3	E	12	1376.7		688.86	+0.3151
	402.16		402.16	4	S	11	1247.7		624.34	+0.3127
	489.19		489.19	5	S	10	1160.6		1160.6	
	586.25		586.25	6	P	9	1073.6		537.31	+0.2704
	714.34	-0.043	714.34	7	K	8	976.56		976.56	
	811.39	+0.3544	811.39	8	P	7	848.46	+0.0902	424.73	-0.027
	910.46	+0.1441	910.46	9	V	6	751.41	+0.3963	751.41	
	967.48	+0.0371	967.48	10	G	5	652.34	-0.043	326.67	+0.0893
	1064.5		1064.5	11	P	4	595.32	+0.086	595.32	
-0.189	581.3		1161.6	12	P	3	498.27	-0.024	498.27	
	1258.6		1258.6	13	P	2	401.21	+0.0406	401.21	
	1387.7		1387.7	14	E	1	304.16		304.16	
				15	R	0	175.12	-0.041	175.12	

Scan number	4540	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	122.49



precursor information

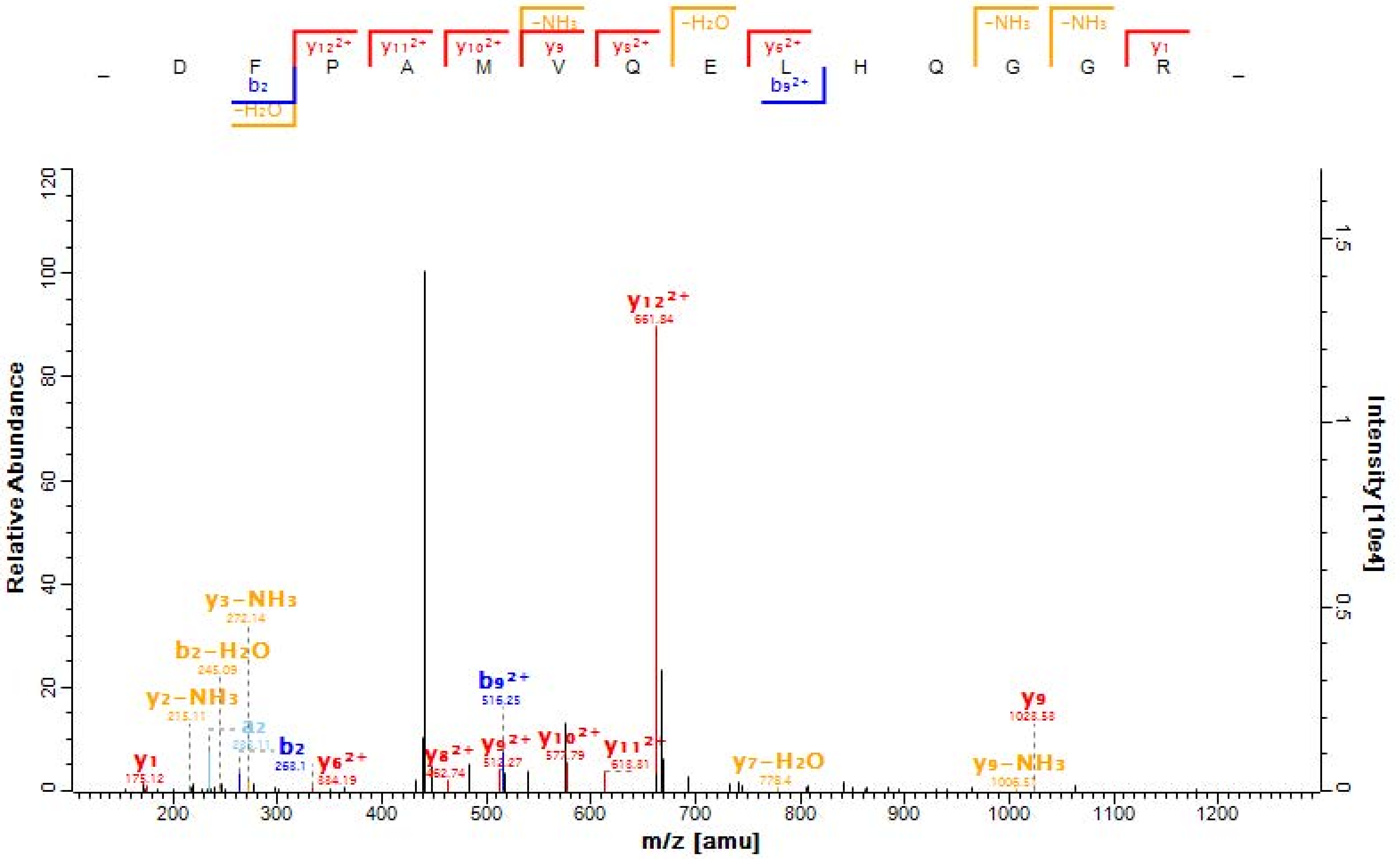
Mass:	2406.07259
m/z:	803.03147
Charge:	3+
Retentiontime:	31.77880859375
Score:	122.4872
Mass Error [ppm]:	-0.0079439
PEP:	2.73E-13
Precursor Type:	MULTI

general information

Annotation:	17 of 21
AminoAcids Coverag	81 %
Intensity Coverage:	46 %
Peak Coverage:	33 %
Protein Localisation:	390 ... 410

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.05		115.05	1	N	20				
	202.08		202.08	2	S	19	2293		2293	
	362.11	+0.1306	362.11	3	C	18	2206		1103.5	+0.2407
	475.2	+0.0579	475.2	4	I	17	2046		1023.5	+0.2106
	574.27		574.27	5	V	16	1932.9		966.95	-0.082
	734.3		734.3	6	C	15	1833.8		917.41	-0.018
	848.34		848.34	7	N	14	1673.8		837.4	-0.069
	979.38		979.38	8	M	13	1559.7	+0.0712	1559.7	
	1036.4		1036.4	9	G	12	1428.7		714.86	+0.2534
	1173.5		1173.5	10	H	11	1371.7		1371.7	
	1260.5	+0.4165	1260.5	11	S	10	1234.6		1234.6	
	1374.5	+0.2105	1374.5	12	N	9	1147.6		574.3	+0.0626
	1475.6		1475.6	13	T	8	1033.6	+0.0239	1033.6	
	1604.6	-0.076	1604.6	14	E	7	932.5		932.5	
+0.2613	859.36	-0.168	1717.7	15	I	6	803.46		803.46	
	1832.7		1832.7	16	D	5	690.38	+0.0949	690.38	
	1931.8		1931.8	17	V	4	575.35	+0.0436	575.35	
-0.011	1016.9		2032.9	18	T	3	476.28	+0.1565	476.28	
	2119.9		2119.9	19	S	2	375.24	-0.058	375.24	
	2233		2233	20	L	1	288.2	+0.0392	288.2	
				21	R	0	175.12		175.12	

Scan number	4936	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	58.17



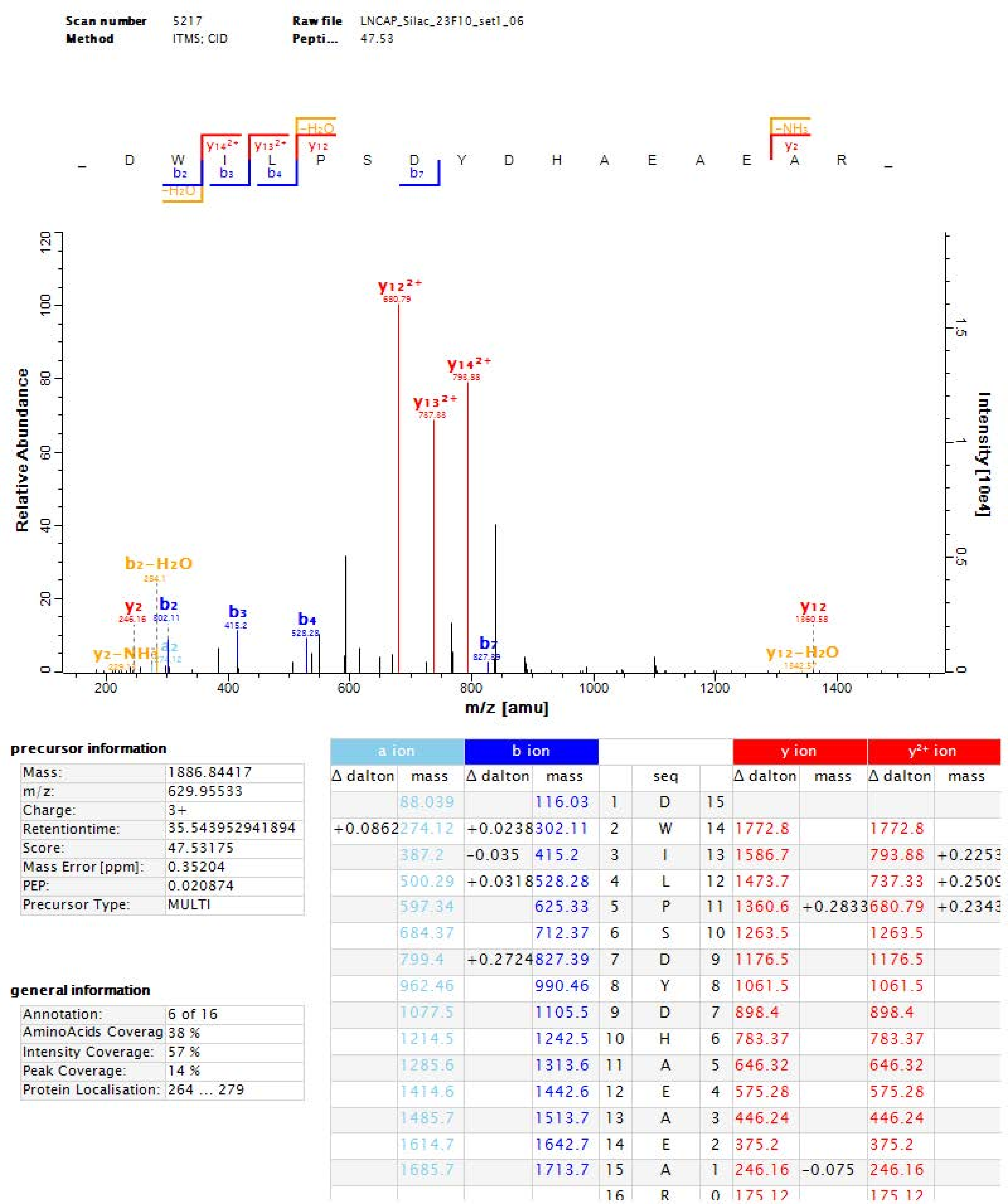
precursor information

Mass:	1583.75126
m/z:	528.92436
Charge:	3+
Retentiontime:	33.976543426513
Score:	58.17212
Mass Error [ppm]:	-0.12411
PEP:	0.0087523
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	38 %
Peak Coverage:	17 %
Protein Localisation:	423 ... 436

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.04		116		116	1	D	13				
-0.06	235.1		263.1	+0.024	263.1	2	F	12	1470		1470	
	332.2		360.2		360.2	3	P	11	1323		661.8	+0.24
	403.2		431.2		431.2	4	A	10	1226		613.3	+0.16
	534.2		562.2		562.2	5	M	9	1155		577.8	+0.24
	633.3		661.3		661.3	6	V	8	1024	+0.103	512.3	+0.07
	761.4		789.4		789.4	7	Q	7	924.5		462.7	+0.26
	890.4		918.4		918.4	8	E	6	796.4		796.4	
	1003	-0.23	516.2		1031	9	L	5	667.4		334.2	+0.08
	1141		1169		1169	10	H	4	554.3		554.3	
	1269		1297		1297	11	Q	3	417.2		417.2	
	1326		1354		1354	12	G	2	289.2		289.2	
	1383		1411		1411	13	G	1	232.1		232.1	
						14	R	0	175.1	+0.01	175.1	



Scan number	5217	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	47.53

precursor information

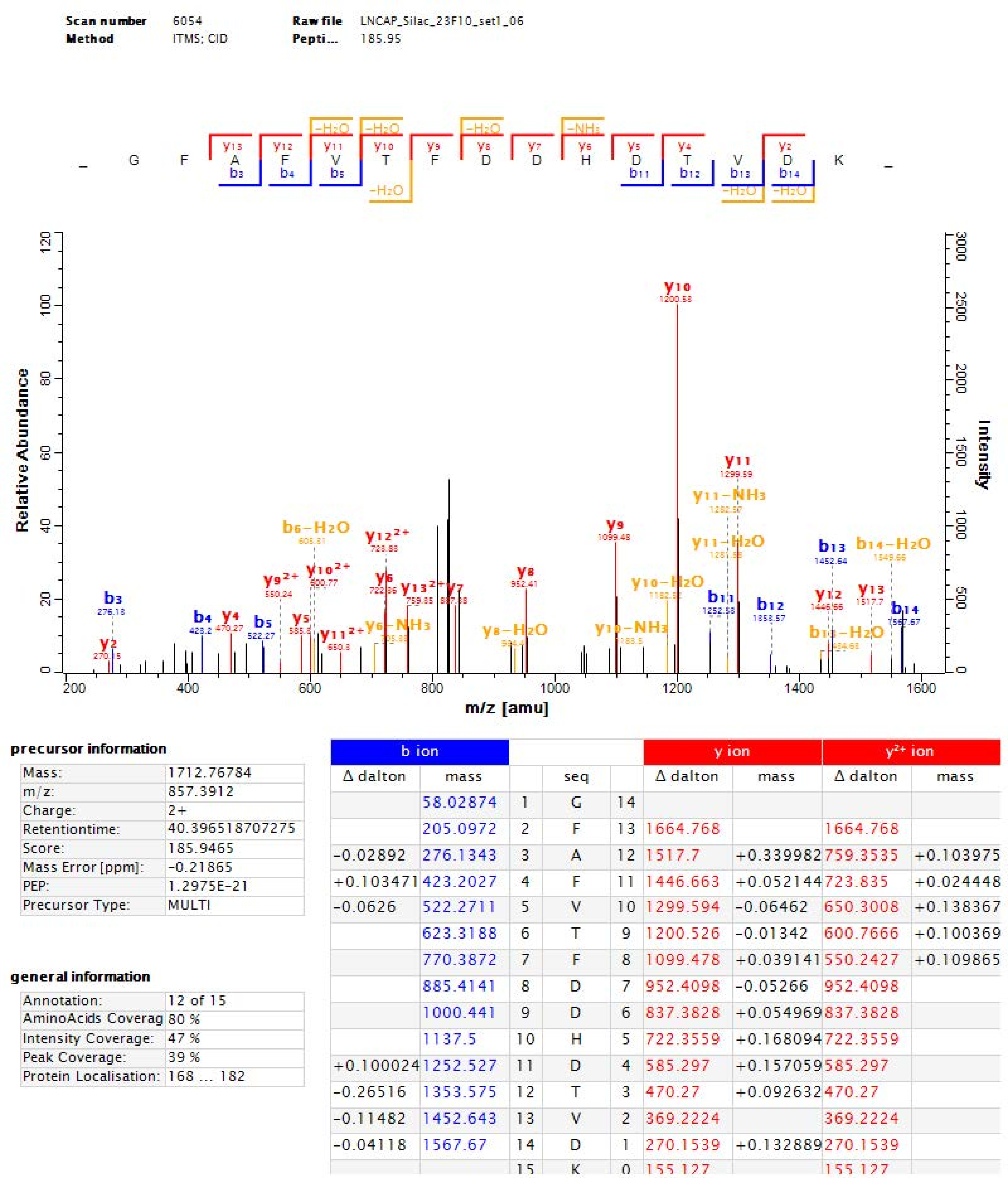
Mass:	1886.84417
m/z:	629.95533
Charge:	3+
Retentiontime:	35.543952941894
Score:	47.53175
Mass Error [ppm]:	0.35204
PEP:	0.020874
Precursor Type:	MULTI

general information

Annotation:	6 of 16
AminoAcids Coverag	38 %
Intensity Coverage:	57 %
Peak Coverage:	14 %
Protein Localisation:	264 ... 279

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	15				
+0.0862	274.12	+0.0238	302.11	2	W	14	1772.8		1772.8	
	387.2	-0.035	415.2	3	I	13	1586.7		793.88	+0.2253
	500.29	+0.0318	528.28	4	L	12	1473.7		737.33	+0.2509
	597.34		625.33	5	P	11	1360.6	+0.2833	680.79	+0.2343
	684.37		712.37	6	S	10	1263.5		1263.5	
	799.4	+0.2724	827.39	7	D	9	1176.5		1176.5	
	962.46		990.46	8	Y	8	1061.5		1061.5	
	1077.5		1105.5	9	D	7	898.4		898.4	
	1214.5		1242.5	10	H	6	783.37		783.37	
	1285.6		1313.6	11	A	5	646.32		646.32	
	1414.6		1442.6	12	E	4	575.28		575.28	
	1485.7		1513.7	13	A	3	446.24		446.24	
	1614.7		1642.7	14	E	2	375.2		375.2	
	1685.7		1713.7	15	A	1	246.16	-0.075	246.16	
				16	R	0	175.12		175.12	

Scan number 6054 **Raw file** LNCAP_Silac_23F10_set1_06
Method ITMS; CID **Pepti...** 185.95



precursor information

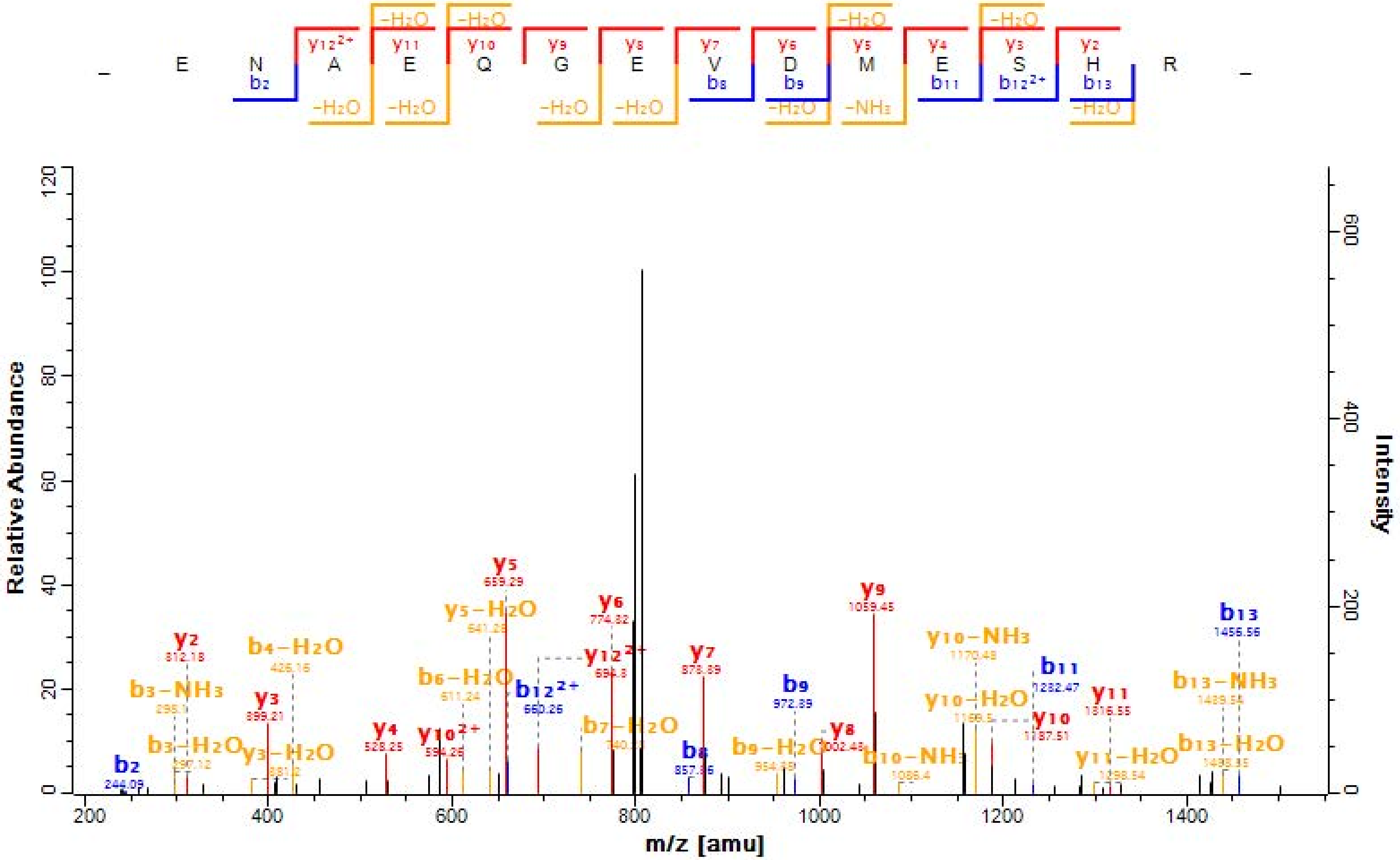
Mass:	1712.76784
m/z:	857.3912
Charge:	2+
Retentiontime:	40.396518707275
Score:	185.9465
Mass Error [ppm]:	-0.21865
PEP:	1.2975E-21
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	47 %
Peak Coverage:	39 %
Protein Localisation:	168 ... 182

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	14				
	205.0972	2	F	13	1664.768		1664.768	
-0.02892	276.1343	3	A	12	1517.7	+0.339982	759.3535	+0.103975
+0.103471	423.2027	4	F	11	1446.663	+0.052144	723.835	+0.024448
-0.0626	522.2711	5	V	10	1299.594	-0.06462	650.3008	+0.138367
	623.3188	6	T	9	1200.526	-0.01342	600.7666	+0.100369
	770.3872	7	F	8	1099.478	+0.039141	550.2427	+0.109865
	885.4141	8	D	7	952.4098	-0.05266	952.4098	
	1000.441	9	D	6	837.3828	+0.054969	837.3828	
	1137.5	10	H	5	722.3559	+0.168094	722.3559	
+0.100024	1252.527	11	D	4	585.297	+0.157059	585.297	
-0.26516	1353.575	12	T	3	470.27	+0.092632	470.27	
-0.11482	1452.643	13	V	2	369.2224		369.2224	
-0.04118	1567.67	14	D	1	270.1539	+0.132889	270.1539	
		15	K	0	155.127		155.127	

Scan number	614	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	136.83



precursor information

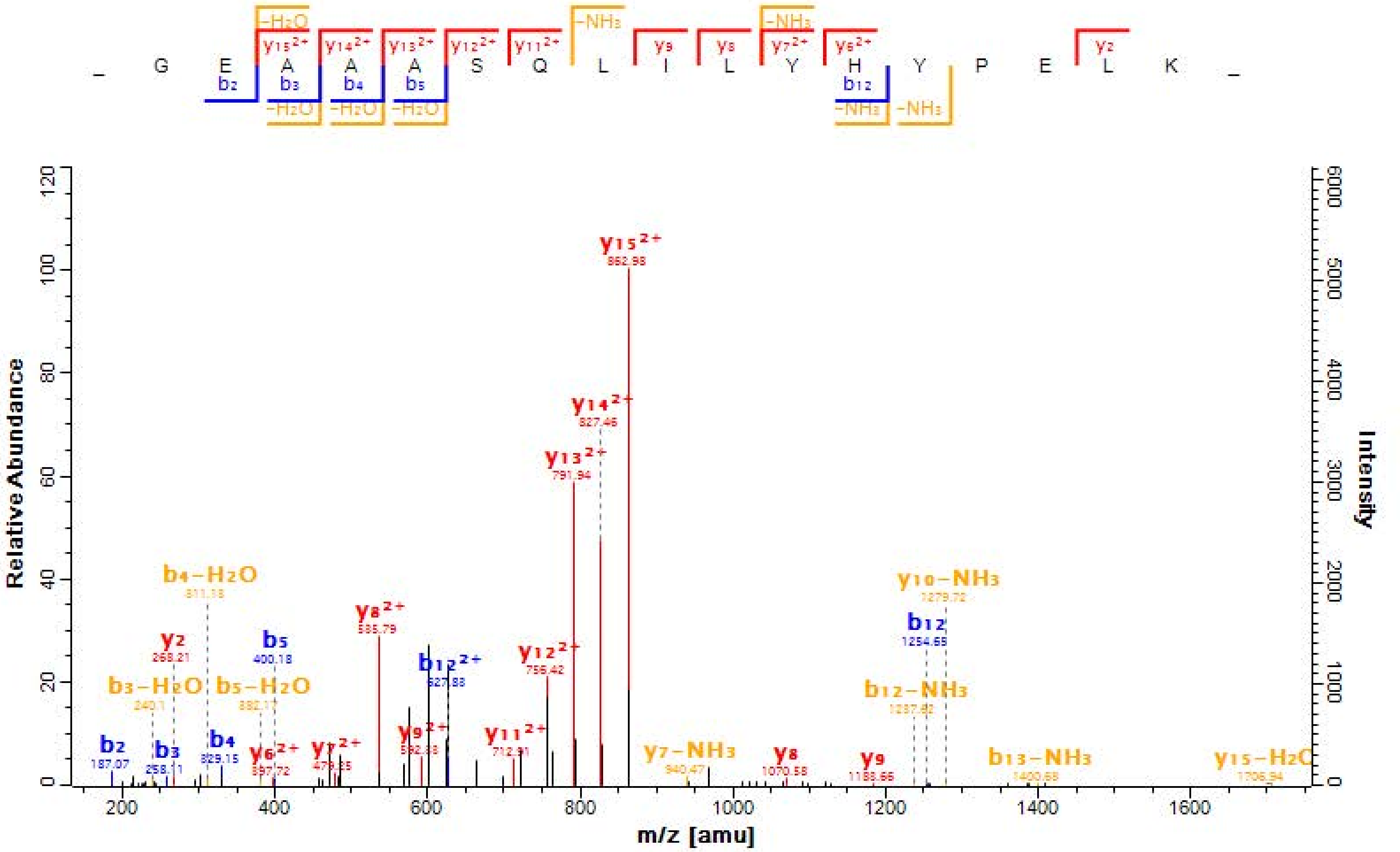
Mass:	1629.66941
m/z:	815.84198
Charge:	2+
Retentiontime:	8.8113946914672
Score:	136.8258
Mass Error [ppm]:	0.30822
PEP:	8.5359E-09
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	42 %
Peak Coverage:	42 %
Protein Localisation:	157 ... 170

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	13				
	244.09	+0.1471	244.09	2	N	12	1501.6		1501.6	
	315.13		315.13	3	A	11	1387.6		694.3	+0.11
	444.17		444.17	4	E	10	1316.6	+0.0432	1316.6	
	572.23		572.23	5	Q	9	1187.5	-0.043	594.26	+0.0304
	629.25		629.25	6	G	8	1059.5	-0.02	1059.5	
	758.3		758.3	7	E	7	1002.4	-0.002	1002.4	
	857.36	+0.0771	857.36	8	V	6	873.39	+0.0149	873.39	
	972.39	-0.195	972.39	9	D	5	774.32	-3E-05	774.32	
	1103.4		1103.4	10	M	4	659.29	-0.076	659.29	
	1232.5	-0.292	1232.5	11	E	3	528.25	+0.07	528.25	
+0.0085	660.26		1319.5	12	S	2	399.21	+0.0281	399.21	
	1456.6	+0.1287	1456.6	13	H	1	312.18	-0.012	312.18	
				14	R	0	175.12		175.12	

Scan number	6211	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	114.7



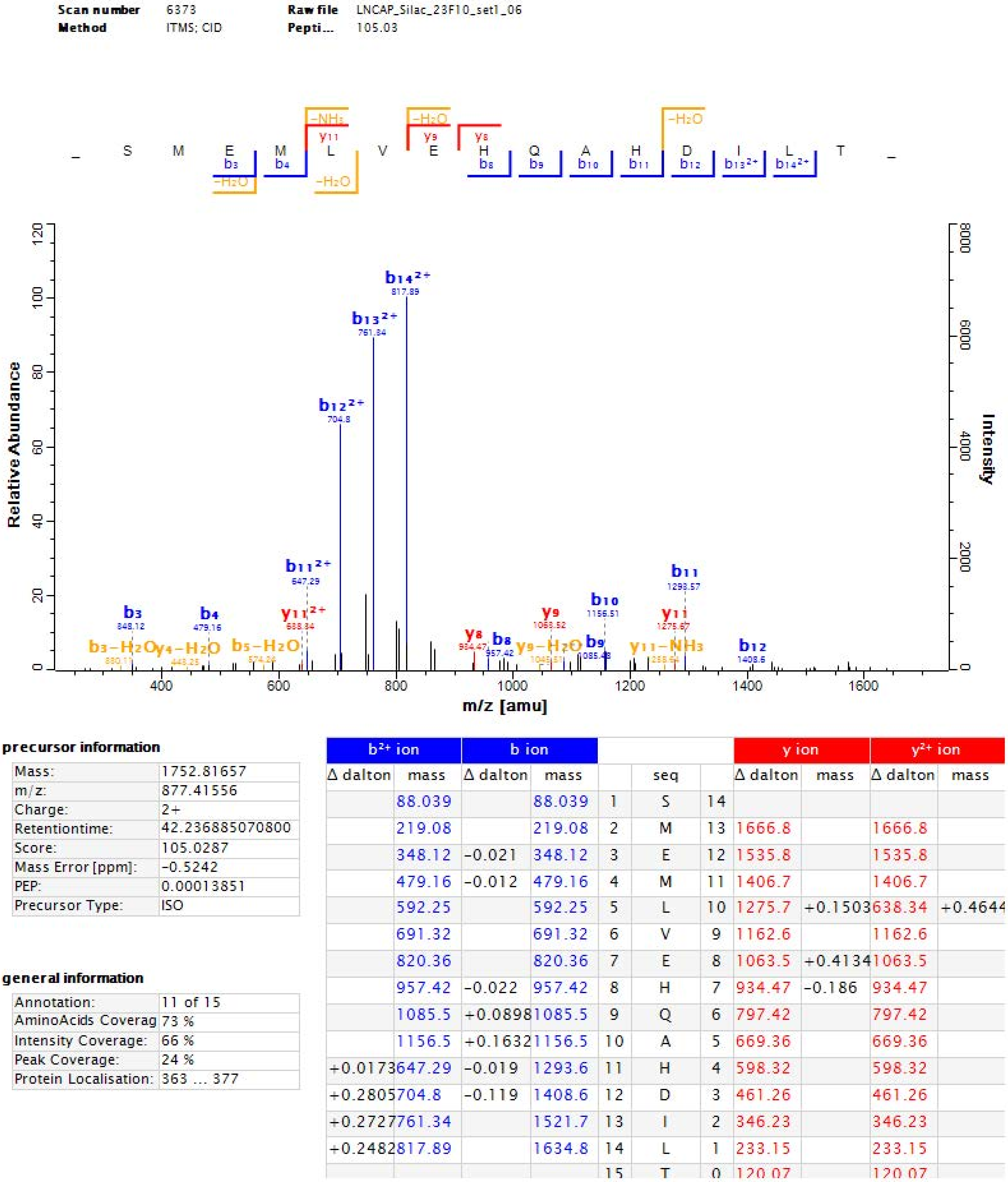
precursor information

Mass:	1901.98895
m/z:	635.00359
Charge:	3+
Retentiontime:	41.302028656005
Score:	114.7048
Mass Error [ppm]:	0.12431
PEP:	8.5072E-09
Precursor Type:	MULTI

general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	59 %
Peak Coverage:	28 %
Protein Localisation:	231 ... 247

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	16				
	187.07	-0.028	187.07	2	E	15	1854		1854	
	258.11	+0.0177	258.11	3	A	14	1724.9		862.98	+0.2713
	329.15	+0.0526	329.15	4	A	13	1653.9		827.46	+0.302
	400.18	+0.2982	400.18	5	A	12	1582.9		791.94	+0.2022
	487.21		487.21	6	S	11	1511.8		756.42	-0.018
	615.27		615.27	7	Q	10	1424.8		712.91	+0.2547
	728.36		728.36	8	L	9	1296.7		1296.7	
	841.44		841.44	9	I	8	1183.7	+0.3437	592.33	+0.201
	954.53		954.53	10	L	7	1070.6	-0.125	535.79	+0.2304
	1117.6		1117.6	11	Y	6	957.49		479.25	+0.4885
-0.109	627.83	-0.011	1254.6	12	H	5	794.43		397.72	+0.1407
	1417.7		1417.7	13	Y	4	657.37		657.37	
	1514.8		1514.8	14	P	3	494.31		494.31	
	1643.8		1643.8	15	E	2	397.25		397.25	
	1756.9		1756.9	16	L	1	268.21	-0.08	268.21	
				17	K	0	155.13		155.13	



Scan number	6373	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	105.03

precursor information

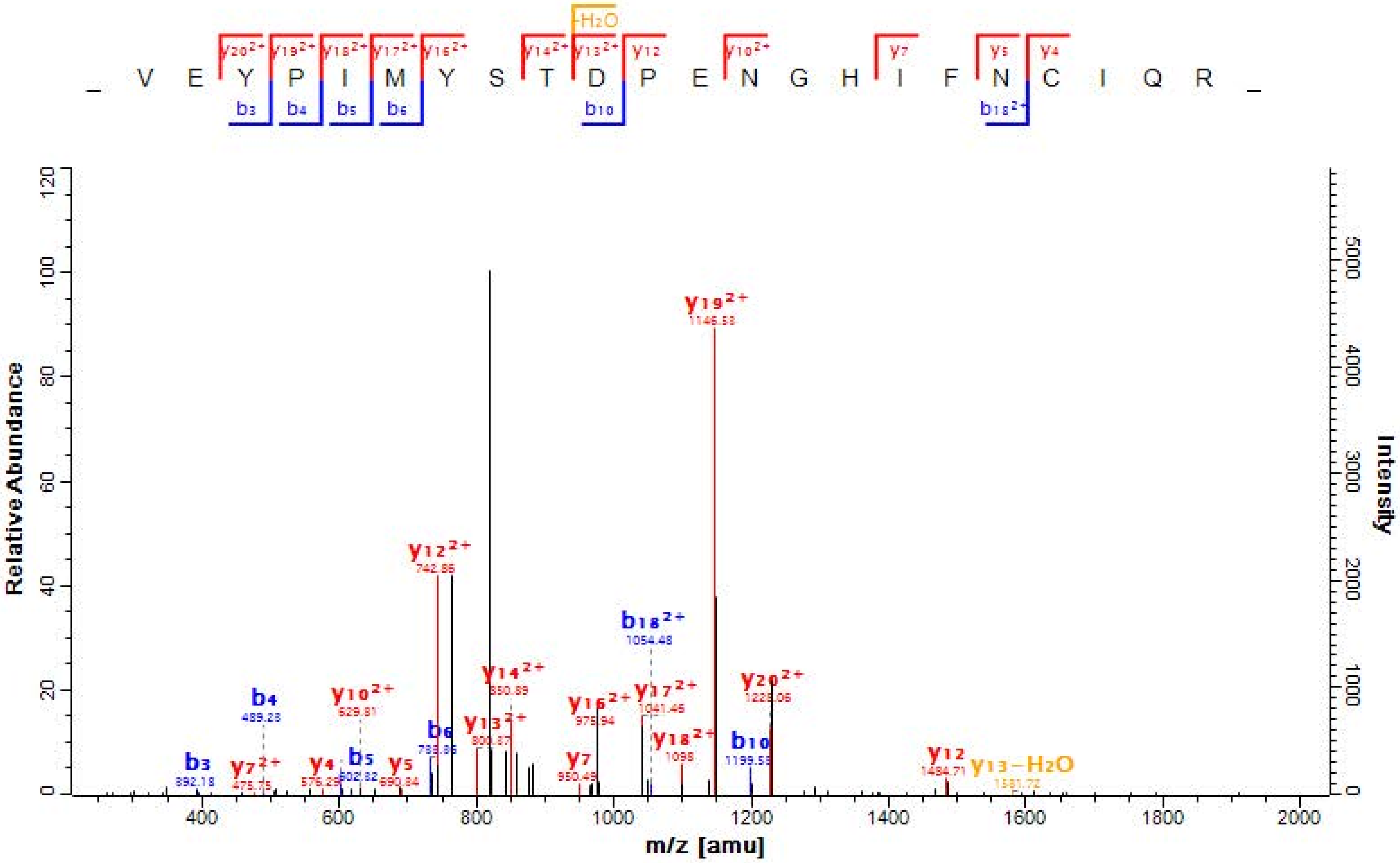
Mass:	1752.81657
m/z:	877.41556
Charge:	2+
Retentiontime:	42.236885070800
Score:	105.0287
Mass Error [ppm]:	-0.5242
PEP:	0.00013851
Precursor Type:	ISO

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	66 %
Peak Coverage:	24 %
Protein Localisation:	363 ... 377

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	14				
	219.08		219.08	2	M	13	1666.8		1666.8	
	348.12	-0.021	348.12	3	E	12	1535.8		1535.8	
	479.16	-0.012	479.16	4	M	11	1406.7		1406.7	
	592.25		592.25	5	L	10	1275.7	+0.1503	638.34	+0.4644
	691.32		691.32	6	V	9	1162.6		1162.6	
	820.36		820.36	7	E	8	1063.5	+0.4134	1063.5	
	957.42	-0.022	957.42	8	H	7	934.47	-0.186	934.47	
	1085.5	+0.0898	1085.5	9	Q	6	797.42		797.42	
	1156.5	+0.1632	1156.5	10	A	5	669.36		669.36	
+0.0173	647.29	-0.019	1293.6	11	H	4	598.32		598.32	
+0.2805	704.8	-0.119	1408.6	12	D	3	461.26		461.26	
+0.2727	761.34		1521.7	13	I	2	346.23		346.23	
+0.2482	817.89		1634.8	14	L	1	233.15		233.15	
				15	T	0	120.07		120.07	

Scan number	6666	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	82.88



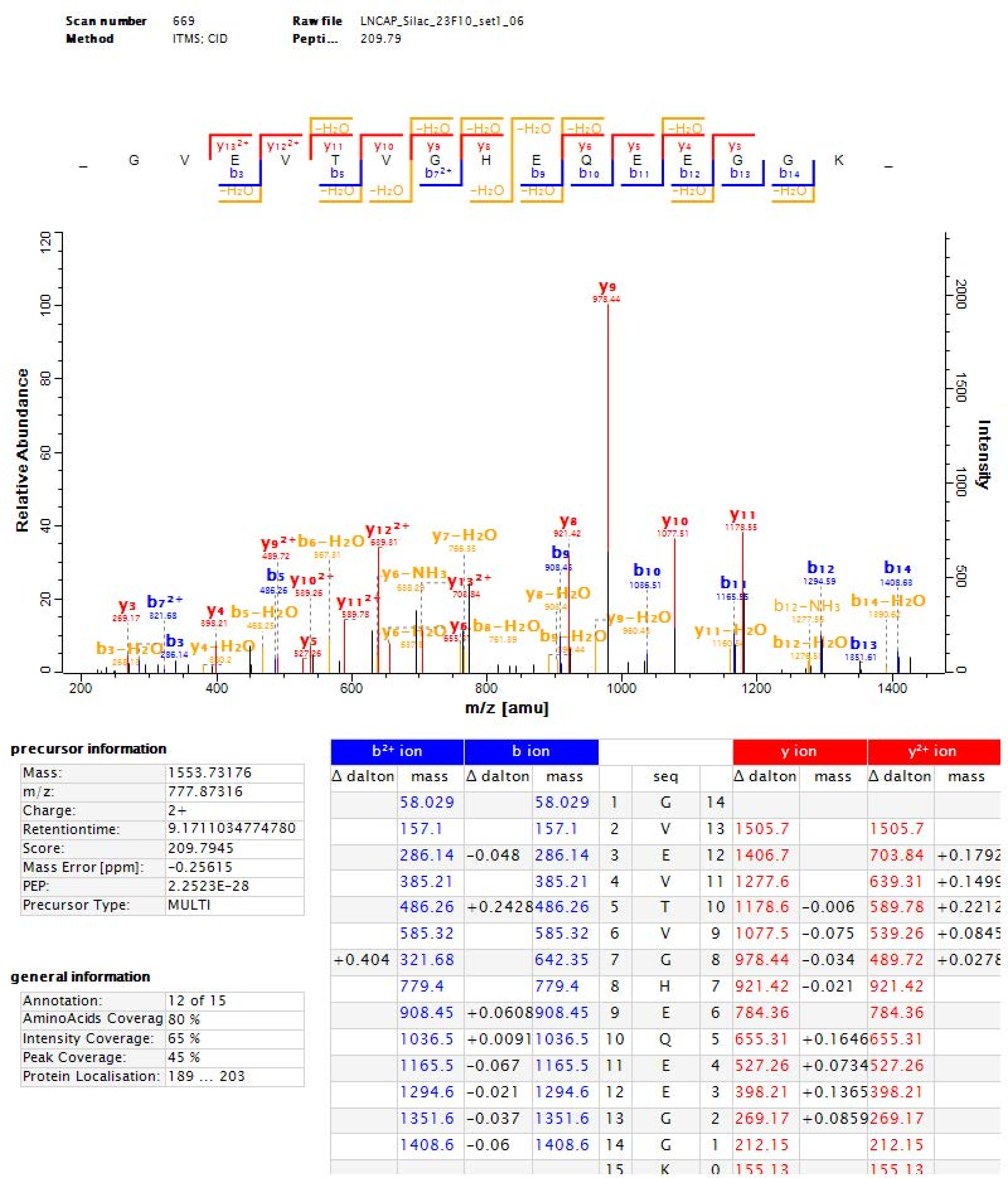
precursor information

Mass:	2682.2209
m/z:	895.08091
Charge:	3+
Retentiontime:	43.964550018310
Score:	82.8772
Mass Error [ppm]:	0.089207
PEP:	0.00012651
Precursor Type:	MULTI

general information

Annotation:	12 of 22
AminoAcids Coverag	55 %
Intensity Coverage:	41 %
Peak Coverage:	23 %
Protein Localisation:	52 ... 73

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	21				
	229.12		229.12	2	E	20	2584.2		2584.2	
	392.18	+0.022	392.18	3	Y	19	2455.1		1228.1	-0.017
	489.23	+0.1395	489.23	4	P	18	2292.1		1146.5	+0.291
	602.32	+0.1583	602.32	5	I	17	2195		1098	+0.4441
	733.36	+0.069	733.36	6	M	16	2081.9		1041.5	+0.093
	896.42		896.42	7	Y	15	1950.9		975.94	+0.003
	983.45		983.45	8	S	14	1787.8		1787.8	
	1084.5		1084.5	9	T	13	1700.8		850.89	+0.326
	1199.5	-0.204	1199.5	10	D	12	1599.7		800.37	+0.157
	1296.6		1296.6	11	P	11	1484.7	+0.0846	742.86	+0.2801
	1425.6		1425.6	12	E	10	1387.7		1387.7	
	1539.7		1539.7	13	N	9	1258.6		629.81	+0.465
	1596.7		1596.7	14	G	8	1144.6		1144.6	
	1733.7		1733.7	15	H	7	1087.5		1087.5	
	1846.8		1846.8	16	I	6	950.49	-0.086	475.75	-0.418
	1993.9		1993.9	17	F	5	837.4		837.4	
-0.431	1054.5		2107.9	18	N	4	690.34	+0.3391	690.34	
	2268		2268	19	C	3	576.29	-0.113	576.29	
	2381.1		2381.1	20	I	2	416.26		416.26	
	2509.1		2509.1	21	Q	1	303.18		303.18	
				22	R	0	175.12		175.12	



Scan number	669	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	209.79

precursor information

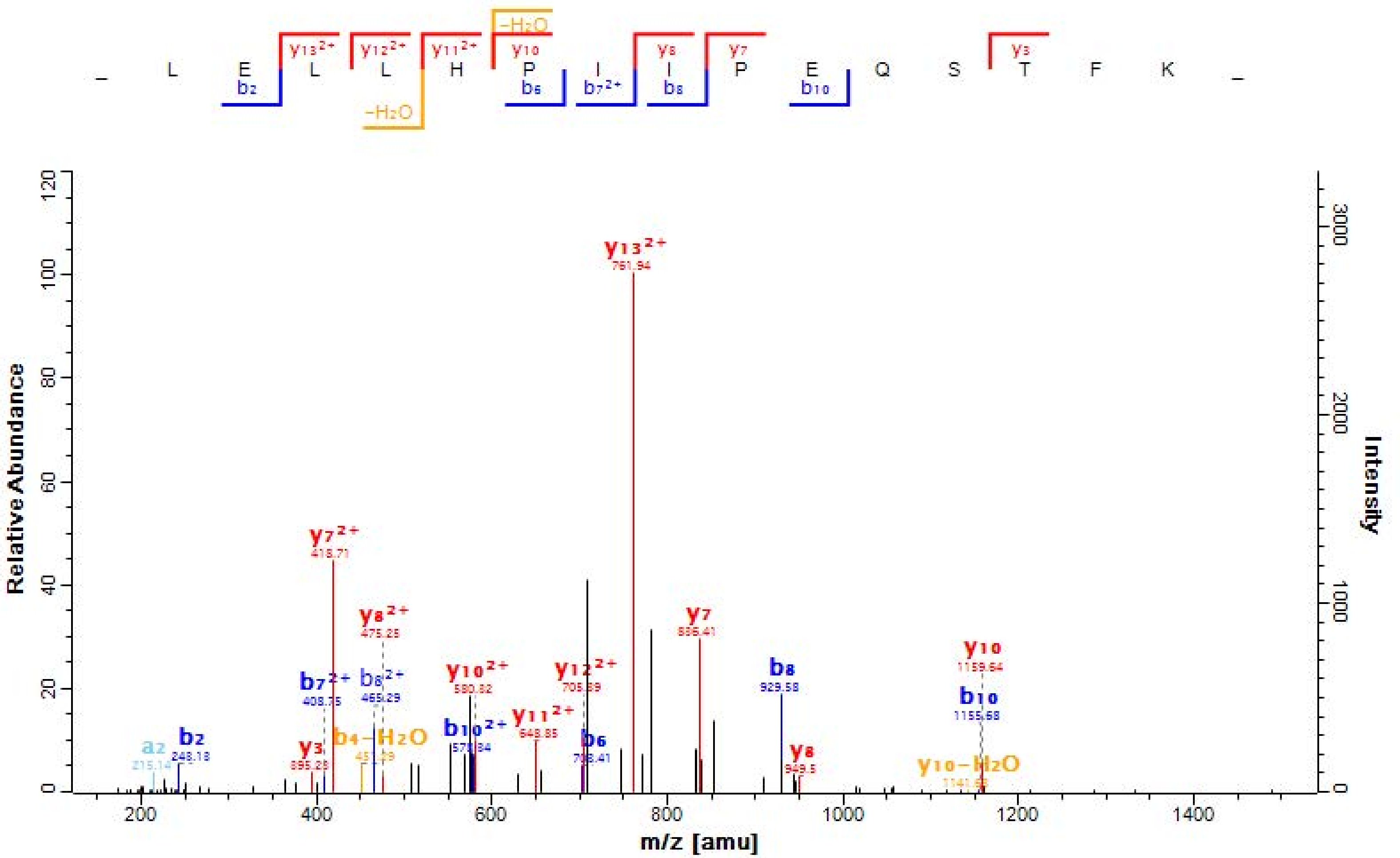
Mass:	1553.73176
m/z:	777.87316
Charge:	2+
Retentiontime:	9.1711034774780
Score:	209.7945
Mass Error [ppm]:	-0.25615
PEP:	2.2523E-28
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	65 %
Peak Coverage:	45 %
Protein Localisation:	189 ... 203

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	14				
	157.1		157.1	2	V	13	1505.7		1505.7	
	286.14	-0.048	286.14	3	E	12	1406.7		703.84	+0.1792
	385.21		385.21	4	V	11	1277.6		639.31	+0.1499
	486.26	+0.2428	486.26	5	T	10	1178.6	-0.006	589.78	+0.2212
	585.32		585.32	6	V	9	1077.5	-0.075	539.26	+0.0845
+0.404	321.68		642.35	7	G	8	978.44	-0.034	489.72	+0.0278
	779.4		779.4	8	H	7	921.42	-0.021	921.42	
	908.45	+0.0608	908.45	9	E	6	784.36		784.36	
	1036.5	+0.0091	1036.5	10	Q	5	655.31	+0.1646	655.31	
	1165.5	-0.067	1165.5	11	E	4	527.26	+0.0734	527.26	
	1294.6	-0.021	1294.6	12	E	3	398.21	+0.1365	398.21	
	1351.6	-0.037	1351.6	13	G	2	269.17	+0.0859	269.17	
	1408.6	-0.06	1408.6	14	G	1	212.15		212.15	
				15	K	0	155.13		155.13	

Scan number	6908	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	96.06



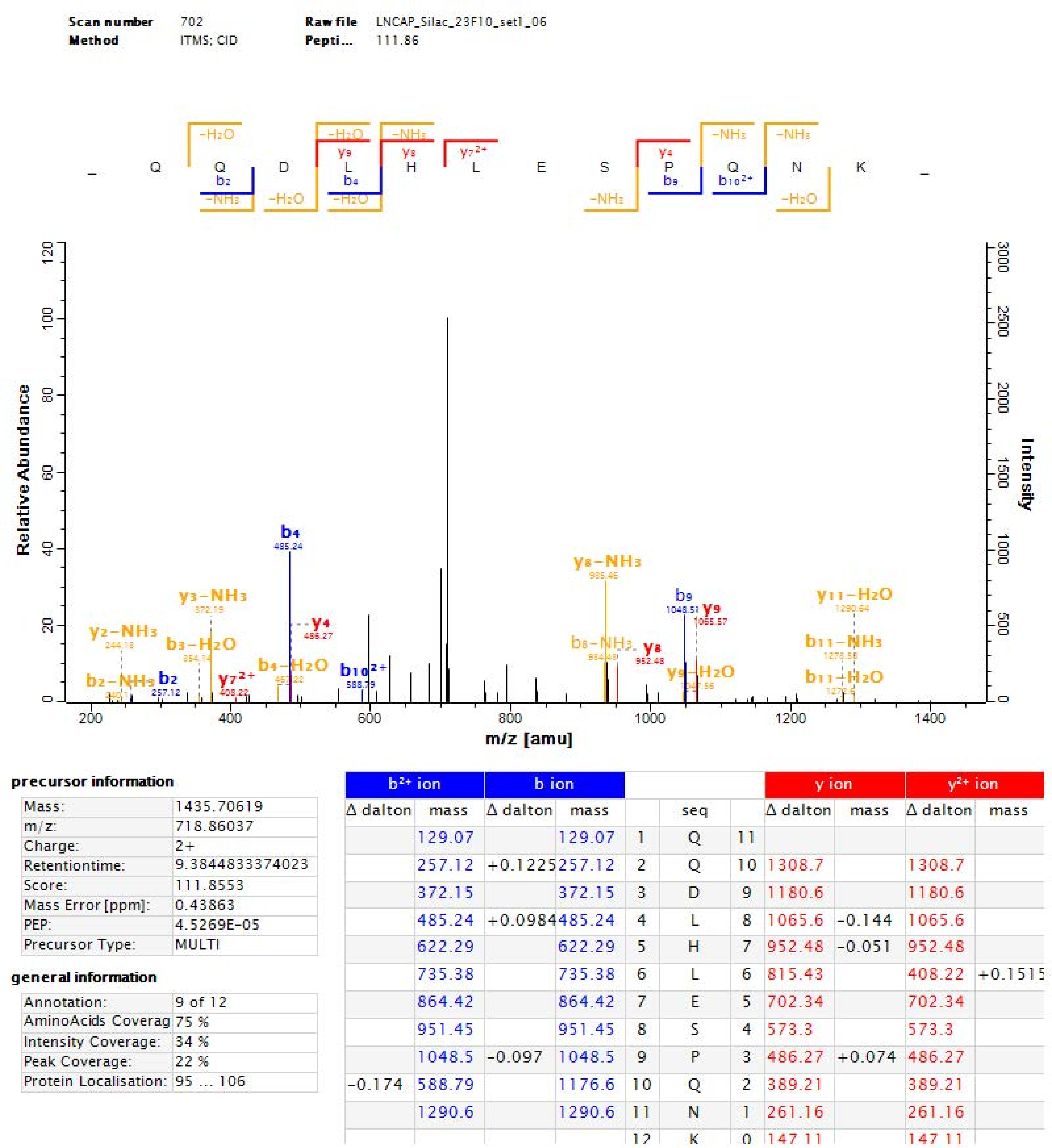
precursor information

Mass:	1763.98259
m/z:	589.00147
Charge:	3+
Retentiontime:	45.433322906494
Score:	96.0589
Mass Error [ppm]:	0.23784
PEP:	8.5743E-05
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	54 %
Peak Coverage:	21 %
Protein Localisation:	222 ... 236

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	14				
+0	215.1		243.1	+0.077	243.1	2	E	13	1652		1652	
	328.2		356.2		356.2	3	L	12	1523		761.9	+0.25
	441.3		469.3		469.3	4	L	11	1410		705.4	+0.26
	578.4		606.4		606.4	5	H	10	1297		648.9	+0.26
	675.4		703.4	-0.2	703.4	6	P	9	1160	+0.072	580.3	-0.15
	788.5	+0.116	408.8		816.5	7	I	8	1063		1063	
	901.6	+0.221	465.3	+0.007	929.6	8	I	7	949.5	+0.101	475.3	-0.04
	998.6		1027		1027	9	P	6	836.4	+0.056	418.7	+0.14
	1128	+0.493	578.3	-0.22	1156	10	E	5	739.4		739.4	
	1256		1284		1284	11	Q	4	610.3		610.3	
	1343		1371		1371	12	S	3	482.3		482.3	
	1444		1472		1472	13	T	2	395.2	-0.27	395.2	
	1591		1619		1619	14	F	1	294.2		294.2	
						15	K	0	147.1		147.1	



Scan number	702	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	111.86

precursor information

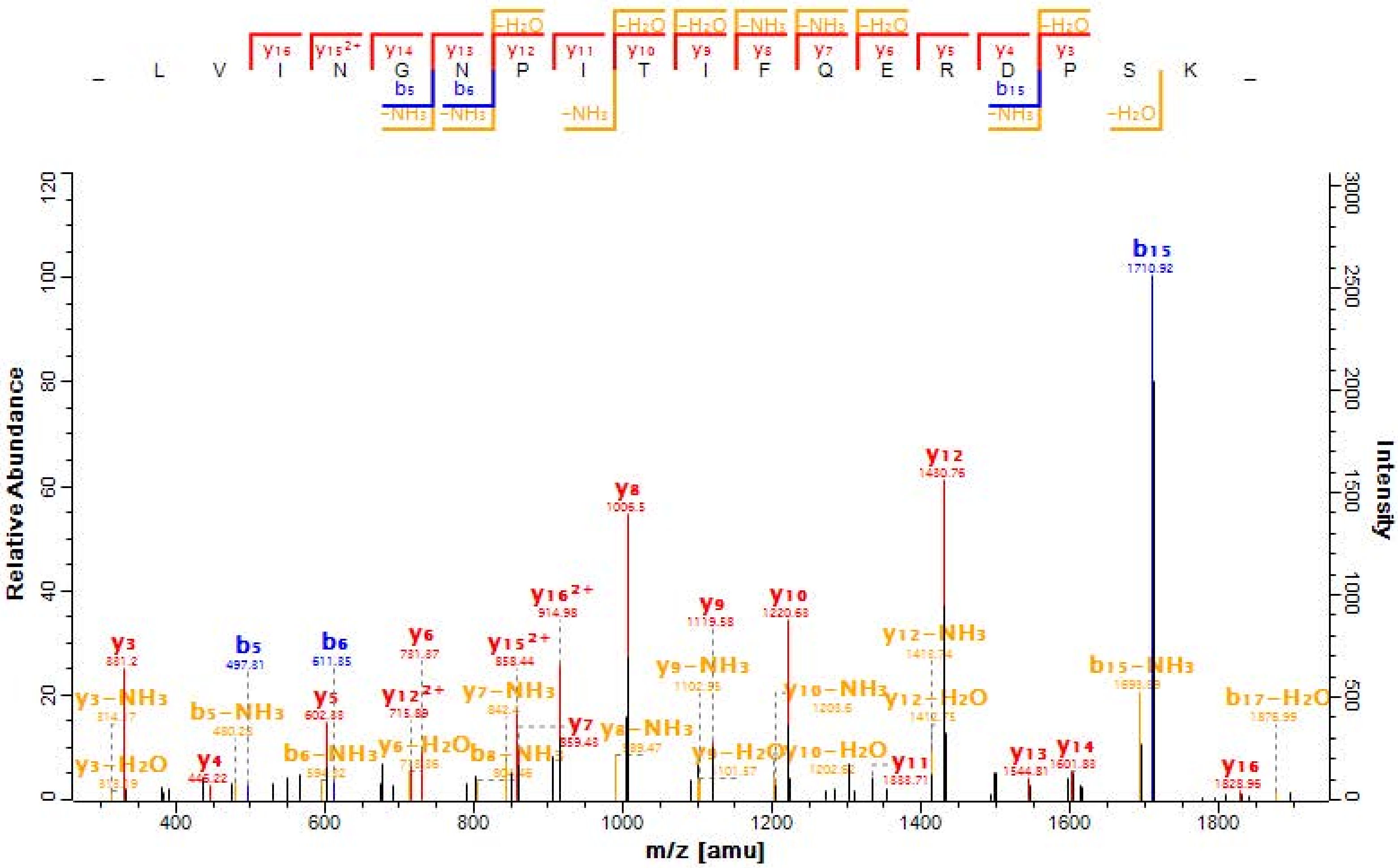
Mass:	1435.70619
m/z:	718.86037
Charge:	2+
Retentiontime:	9.3844833374023
Score:	111.8553
Mass Error [ppm]:	0.43863
PEP:	4.5269E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	34 %
Peak Coverage:	22 %
Protein Localisation:	95 ... 106

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.07		129.07	1	Q	11				
	257.12	+0.1225	257.12	2	Q	10	1308.7		1308.7	
	372.15		372.15	3	D	9	1180.6		1180.6	
	485.24	+0.0984	485.24	4	L	8	1065.6	-0.144	1065.6	
	622.29		622.29	5	H	7	952.48	-0.051	952.48	
	735.38		735.38	6	L	6	815.43		408.22	+0.1515
	864.42		864.42	7	E	5	702.34		702.34	
	951.45		951.45	8	S	4	573.3		573.3	
	1048.5	-0.097	1048.5	9	P	3	486.27	+0.074	486.27	
-0.174	588.79		1176.6	10	Q	2	389.21		389.21	
	1290.6		1290.6	11	N	1	261.16		261.16	
				12	K	0	147.11		147.11	

Scan number	7169	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	178.14



precursor information

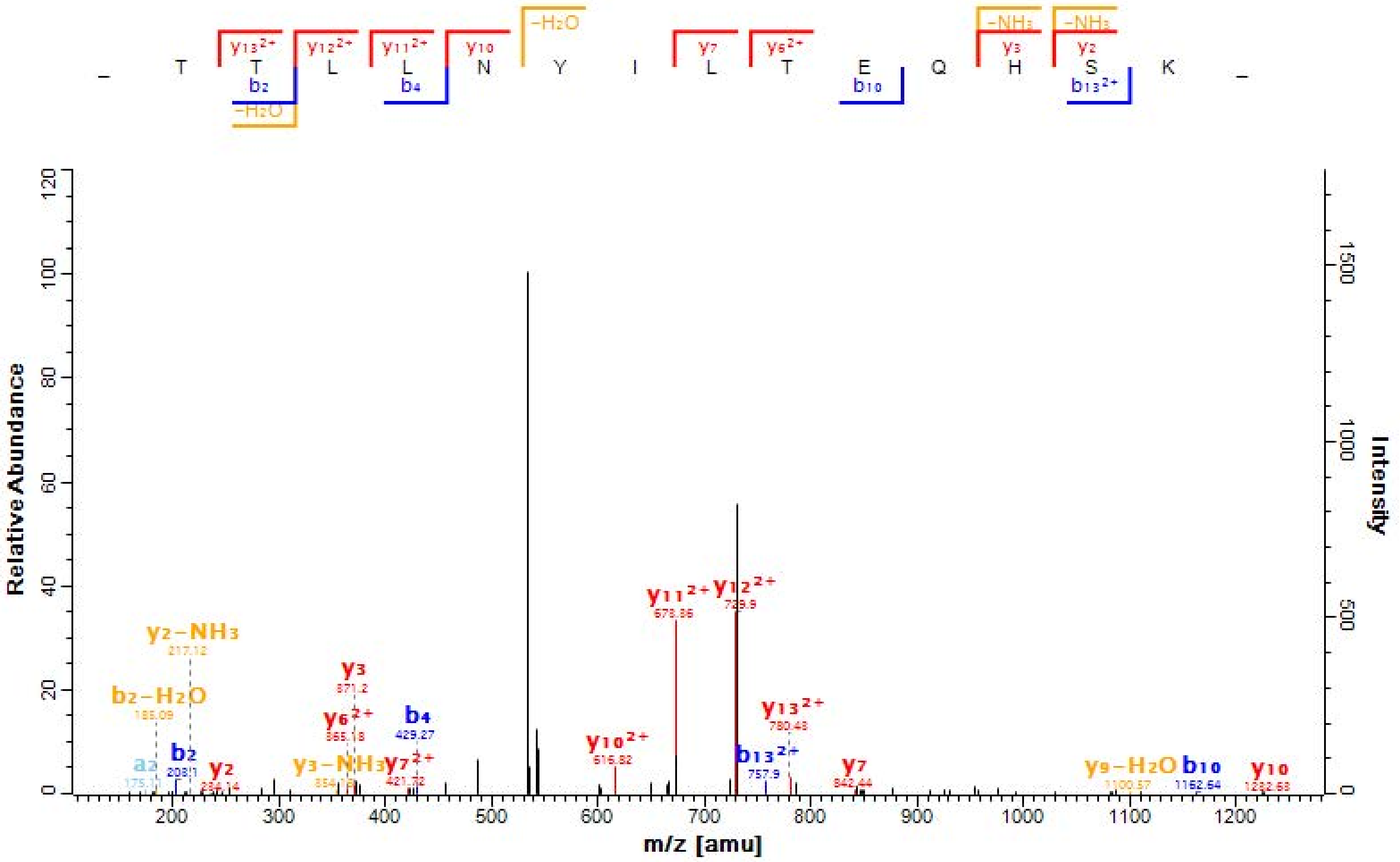
Mass:	2040.10014
m/z:	1021.05735
Charge:	2+
Retentiontime:	46.990718841552
Score:	178.1361
Mass Error [ppm]:	-0.12203
PEP:	1.0265E-30
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	52 %
Peak Coverage:	37 %
Protein Localisation:	67 ... 84

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	17				
	213.1598	2	V	16	1928.024		1928.024	
	326.2438	3	I	15	1828.955	-0.22484	914.9812	+0.193084
	440.2867	4	N	14	1715.871		858.4392	+0.294442
+0.181109	497.3082	5	G	13	1601.828	+0.049001	1601.828	
+0.104368	611.3511	6	N	12	1544.807	+0.008575	1544.807	
	708.4039	7	P	11	1430.764	+0.007313	715.8855	+0.045306
	821.488	8	I	10	1333.711	-0.00877	1333.711	
	922.5356	9	T	9	1220.627	-0.027	1220.627	
	1035.62	10	I	8	1119.579	+0.158738	1119.579	
	1182.688	11	F	7	1006.495	-0.02282	1006.495	
	1310.747	12	Q	6	859.4268	+0.073423	859.4268	
	1439.789	13	E	5	731.3682	+0.066998	731.3682	
	1595.89	14	R	4	602.3257	-0.05771	602.3257	
+0.027356	1710.917	15	D	3	446.2245	+0.102487	446.2245	
	1807.97	16	P	2	331.1976	+0.035558	331.1976	
	1895.002	17	S	1	234.1448		234.1448	
		18	K	0	147.1128		147.1128	

Scan number	7650	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	73.88



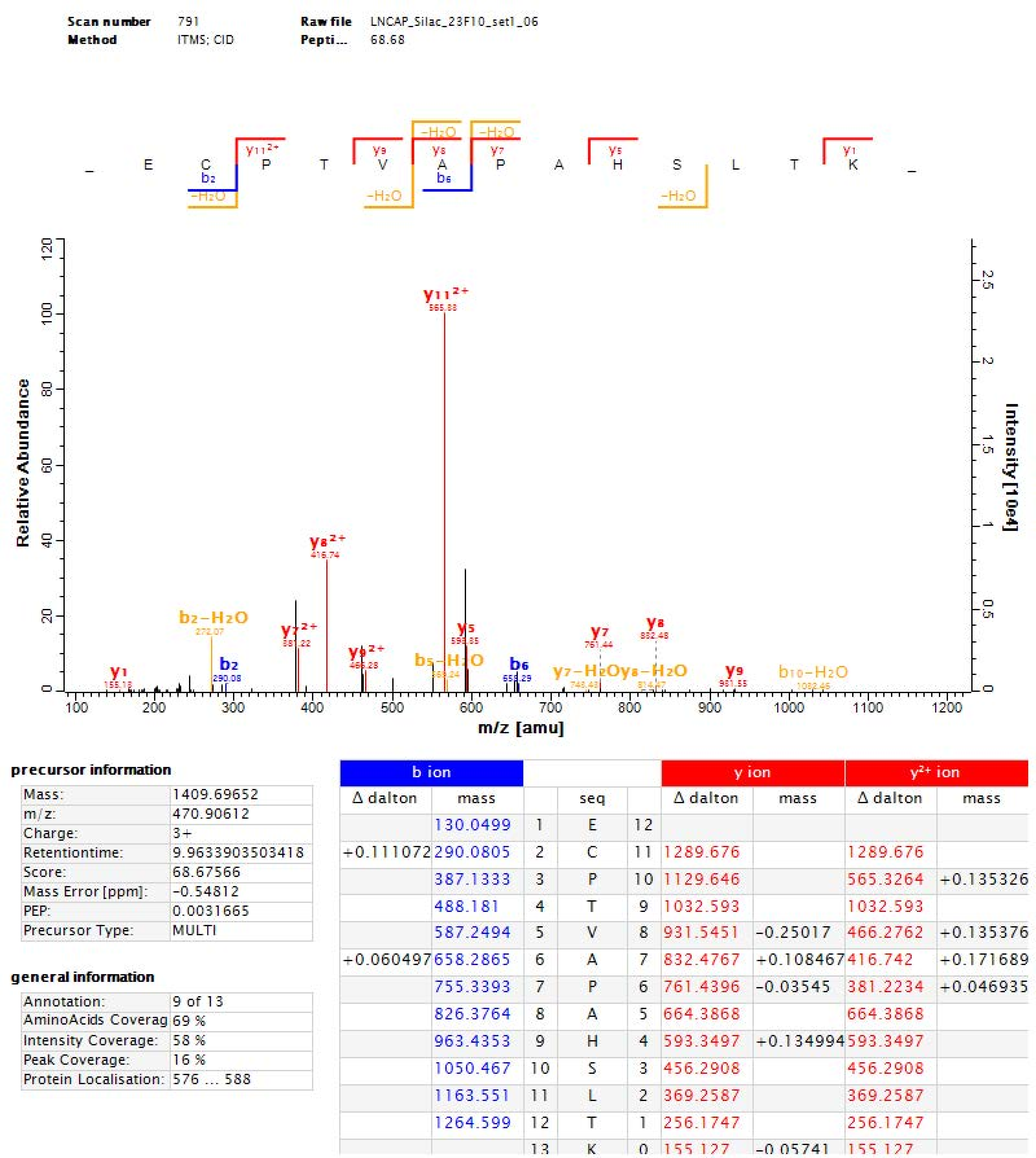
precursor information

Mass:	1659.88371
m/z:	554.30185
Charge:	3+
Retentiontime:	50.029216766357
Score:	73.88116
Mass Error [ppm]:	0.31461
PEP:	0.0015503
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	26 %
Peak Coverage:	19 %
Protein Localisation:	56 ... 69

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.1		102.1	1	T	13				
−0.05	175.1		203.1	+0.028	203.1	2	T	12	1560		780.4	+0.40
	288.2		316.2		316.2	3	L	11	1459		729.9	−0.01
	401.3		429.3	−0.01	429.3	4	L	10	1346		673.4	+0.28
	515.3		543.3		543.3	5	N	9	1233	−0.4	616.8	+0.29
	678.4		706.4		706.4	6	Y	8	1119		1119	
	791.5		819.5		819.5	7	I	7	955.5		955.5	
	904.6		932.5		932.5	8	L	6	842.4	−0.18	421.7	+0.18
	1006		1034		1034	9	T	5	729.4		365.2	−0.14
	1135		1163	−0.45	1163	10	E	4	628.3		628.3	
	1263		1291		1291	11	Q	3	499.3		499.3	
	1400		1428		1428	12	H	2	371.2	+0.086	371.2	
	1487	−0.21	757.9		1515	13	S	1	234.1	+0.122	234.1	
						14	K	0	147.1		147.1	



Scan number	791	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	68.68

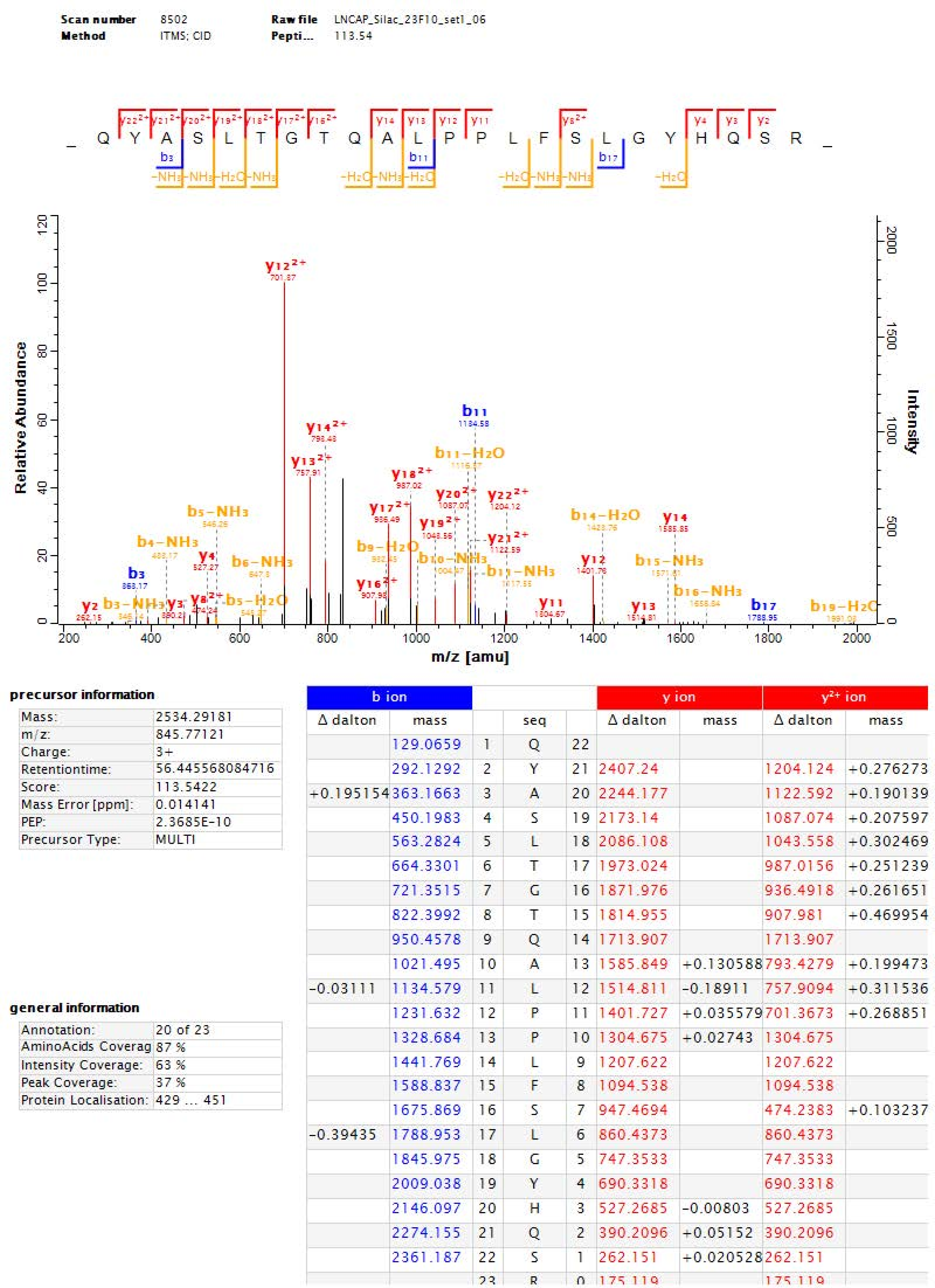
precursor information

Mass:	1409.69652
m/z:	470.90612
Charge:	3+
Retentiontime:	9.9633903503418
Score:	68.67566
Mass Error [ppm]:	-0.54812
PEP:	0.0031665
Precursor Type:	MULTI

general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	58 %
Peak Coverage:	16 %
Protein Localisation:	576 … 588

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	12				
+0.111072	290.0805	2	C	11	1289.676		1289.676	
	387.1333	3	P	10	1129.646		565.3264	+0.135326
	488.181	4	T	9	1032.593		1032.593	
	587.2494	5	V	8	931.5451	-0.25017	466.2762	+0.135376
+0.060497	658.2865	6	A	7	832.4767	+0.108467	416.742	+0.171689
	755.3393	7	P	6	761.4396	-0.03545	381.2234	+0.046935
	826.3764	8	A	5	664.3868		664.3868	
	963.4353	9	H	4	593.3497	+0.134994	593.3497	
	1050.467	10	S	3	456.2908		456.2908	
	1163.551	11	L	2	369.2587		369.2587	
	1264.599	12	T	1	256.1747		256.1747	
		13	K	0	155.127	-0.05741	155.127	



Scan number 8502
Raw file LNCAP_Silac_23F10_set1_06
Method ITMS; CID
Pepti... 113.54

precursor information

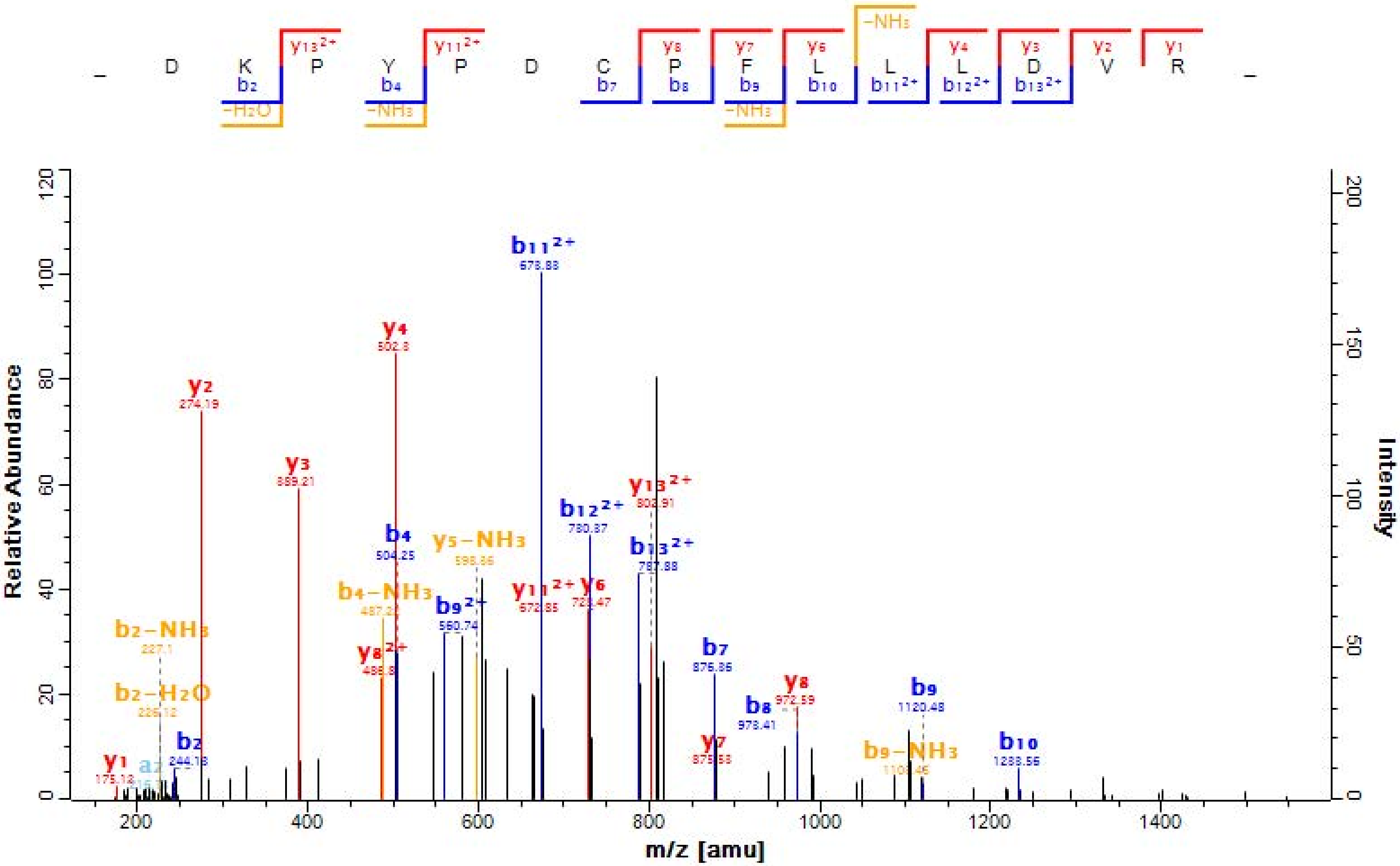
Mass:	2534.29181
m/z:	845.77121
Charge:	3+
Retentiontime:	56.445568084716
Score:	113.5422
Mass Error [ppm]:	0.014141
PEP:	2.3685E-10
Precursor Type:	MULTI

general information

Annotation:	20 of 23
AminoAcids Coverag	87 %
Intensity Coverage:	63 %
Peak Coverage:	37 %
Protein Localisation:	429 ... 451

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.0659	1	Q	22				
	292.1292	2	Y	21	2407.24		1204.124	+0.276273
+0.195154	363.1663	3	A	20	2244.177		1122.592	+0.190139
	450.1983	4	S	19	2173.14		1087.074	+0.207597
	563.2824	5	L	18	2086.108		1043.558	+0.302469
	664.3301	6	T	17	1973.024		987.0156	+0.251239
	721.3515	7	G	16	1871.976		936.4918	+0.261651
	822.3992	8	T	15	1814.955		907.981	+0.469954
	950.4578	9	Q	14	1713.907		1713.907	
	1021.495	10	A	13	1585.849	+0.130588	793.4279	+0.199473
-0.03111	1134.579	11	L	12	1514.811	-0.18911	757.9094	+0.311536
	1231.632	12	P	11	1401.727	+0.035579	701.3673	+0.268851
	1328.684	13	P	10	1304.675	+0.02743	1304.675	
	1441.769	14	L	9	1207.622		1207.622	
	1588.837	15	F	8	1094.538		1094.538	
	1675.869	16	S	7	947.4694		474.2383	+0.103237
-0.39435	1788.953	17	L	6	860.4373		860.4373	
	1845.975	18	G	5	747.3533		747.3533	
	2009.038	19	Y	4	690.3318		690.3318	
	2146.097	20	H	3	527.2685	-0.00803	527.2685	
	2274.155	21	Q	2	390.2096	+0.05152	390.2096	
	2361.187	22	S	1	262.151	+0.020528	262.151	
		23	R	0	175.119		175.119	

Scan number	8577	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	125.97



precursor information

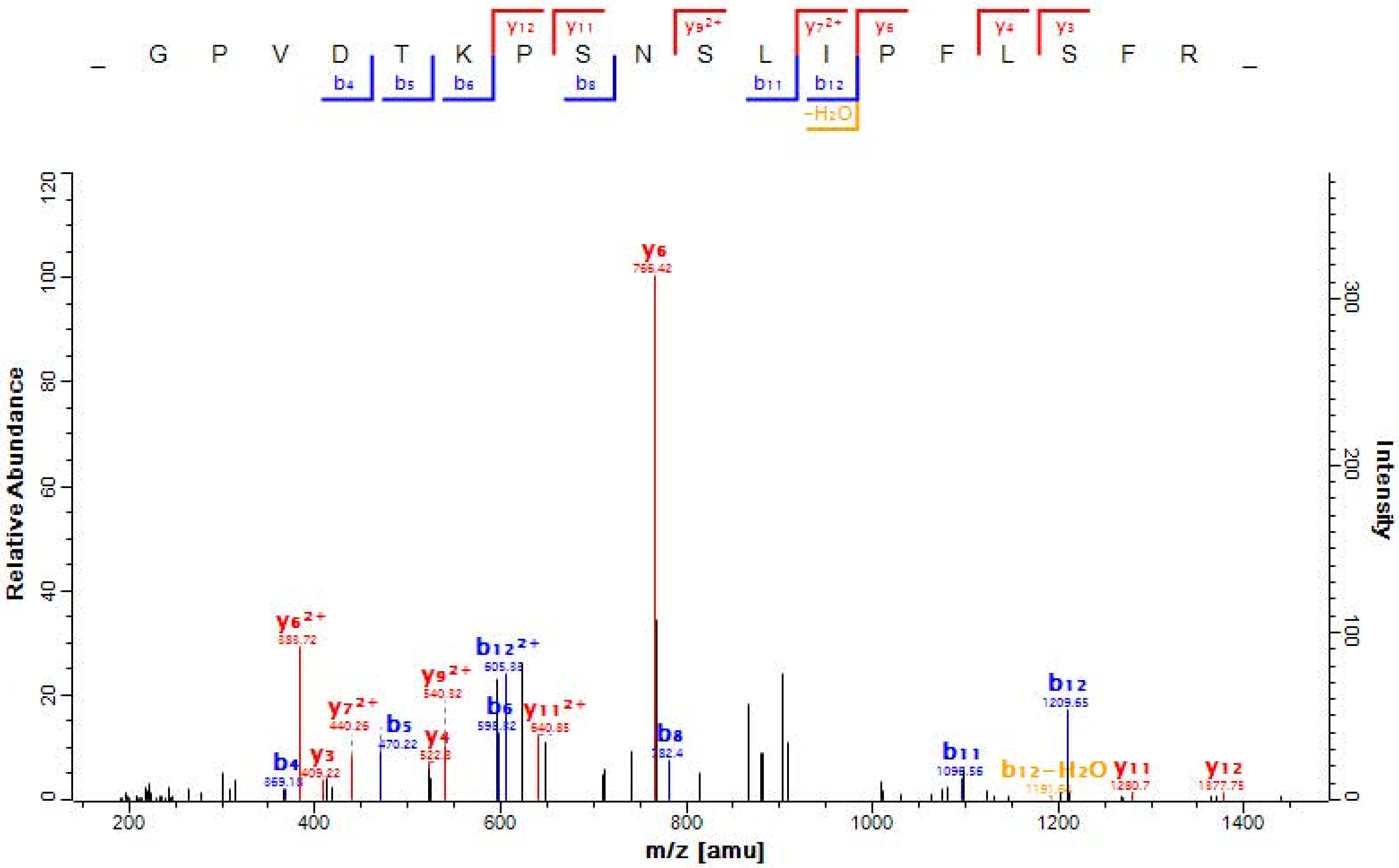
Mass:	1846.93037
m/z:	616.65073
Charge:	3+
Retentiontime:	57.130912780761
Score:	125.9748
Mass Error [ppm]:	0.87495
PEP:	1.6587E-09
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	54 %
Peak Coverage:	24 %
Protein Localisation:	165 ... 179

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.04		116		116	1	D	14				
+0.114	216.1		244.1	+0.007	244.1	2	K	13	1733		1733	
	313.2		341.2		341.2	3	P	12	1605		802.9	+0.31
	476.3		504.2	+0.187	504.2	4	Y	11	1508		1508	
	573.3		601.3		601.3	5	P	10	1345		672.9	+0.38
	688.3		716.3		716.3	6	D	9	1248		1248	
	848.4		876.4	+0.047	876.4	7	C	8	1133		1133	
	945.4		973.4	+0.404	973.4	8	P	7	972.6	-0.19	486.8	+0
	1092	-0.11	560.7	+0.208	1120	9	F	6	875.5	+0.095	875.5	
	1206		1234	-0.17	1234	10	L	5	728.5	+0.106	728.5	
	1319	+0.242	673.8		1347	11	L	4	615.4		615.4	
	1432	+0.089	730.4		1460	12	L	3	502.3	+0.014	502.3	
	1547	+0.046	787.9		1575	13	D	2	389.2	+0.01	389.2	
	1646		1674		1674	14	V	1	274.2	-0.01	274.2	
						15	R	0	175.1	-0.09	175.1	

Scan number	8903	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	56.12



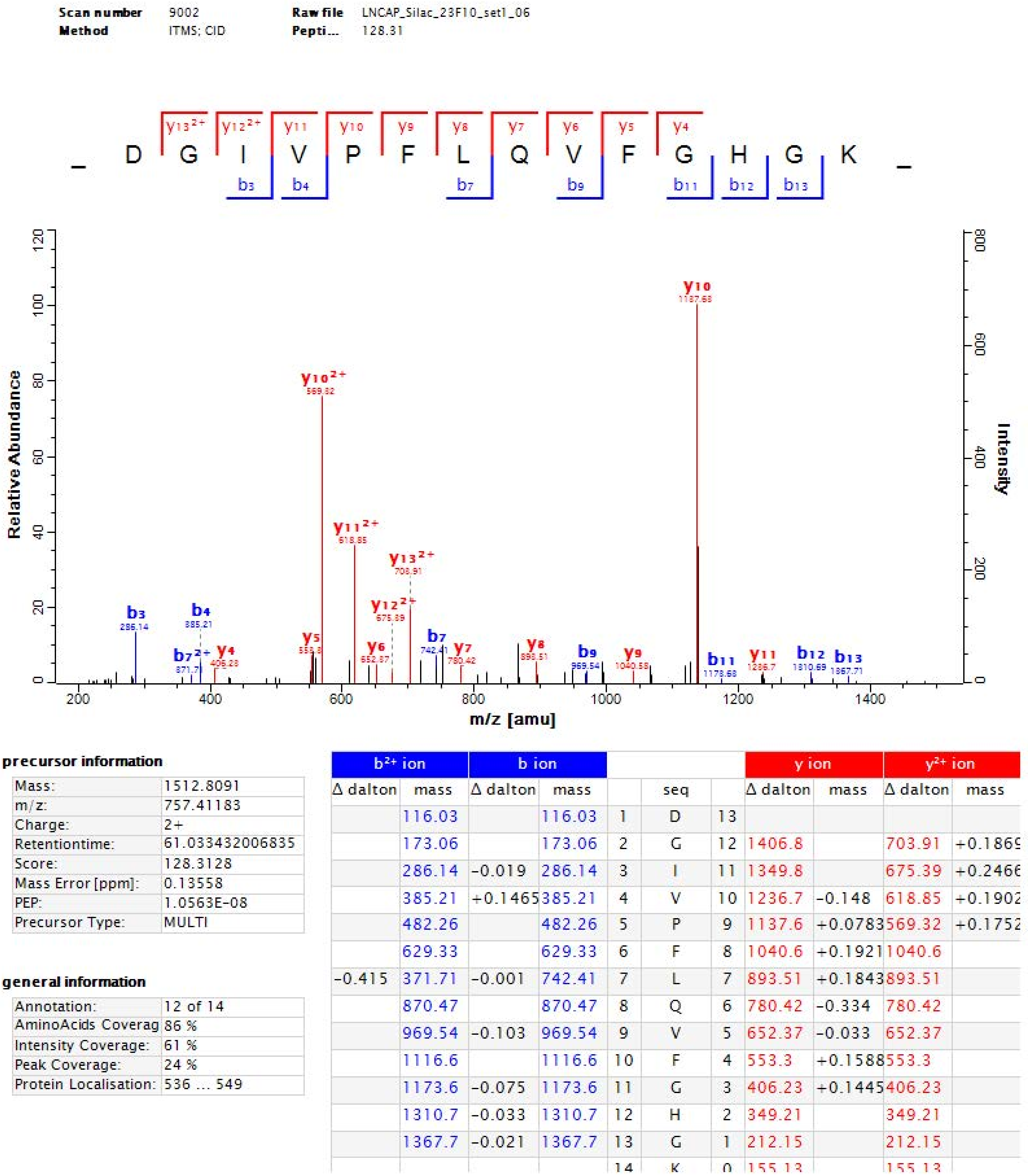
precursor information

Mass:	1974.05839
m/z:	659.02674
Charge:	3+
Retentiontime:	60.100646972656
Score:	56.12079
Mass Error [ppm]:	0.47058
PEP:	0.0020769
Precursor Type:	MULTI

general information

Annotation:	11 of 18
AminoAcids Coverag	61 %
Intensity Coverage:	44 %
Peak Coverage:	20 %
Protein Localisation:	802 ... 819

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	17				
	155.08		155.08	2	P	16	1918		1918	
	254.15		254.15	3	V	15	1821		1821	
	369.18	+0.1723	369.18	4	D	14	1721.9		1721.9	
	470.22	+0.0905	470.22	5	T	13	1606.9		1606.9	
	598.32	+0.0898	598.32	6	K	12	1505.8		1505.8	
	695.37		695.37	7	P	11	1377.8	-0.102	1377.8	
	782.4	+0.0358	782.4	8	S	10	1280.7	-0.2	640.85	-0.411
	896.45		896.45	9	N	9	1193.7		1193.7	
	983.48		983.48	10	S	8	1079.6		540.32	-0.386
	1096.6	-0.002	1096.6	11	L	7	992.59		992.59	
+0.1034	605.33	-0.122	1209.6	12	I	6	879.51		440.26	+0.4686
	1306.7		1306.7	13	P	5	766.42	+0.0073	383.72	+0.1543
	1453.8		1453.8	14	F	4	669.37		669.37	
	1566.9		1566.9	15	L	3	522.3	-0.058	522.3	
	1653.9		1653.9	16	S	2	409.22	+0.052	409.22	
	1801		1801	17	F	1	322.19		322.19	
				18	R	0	175.12		175.12	



Scan number	9002	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	128.31

precursor information

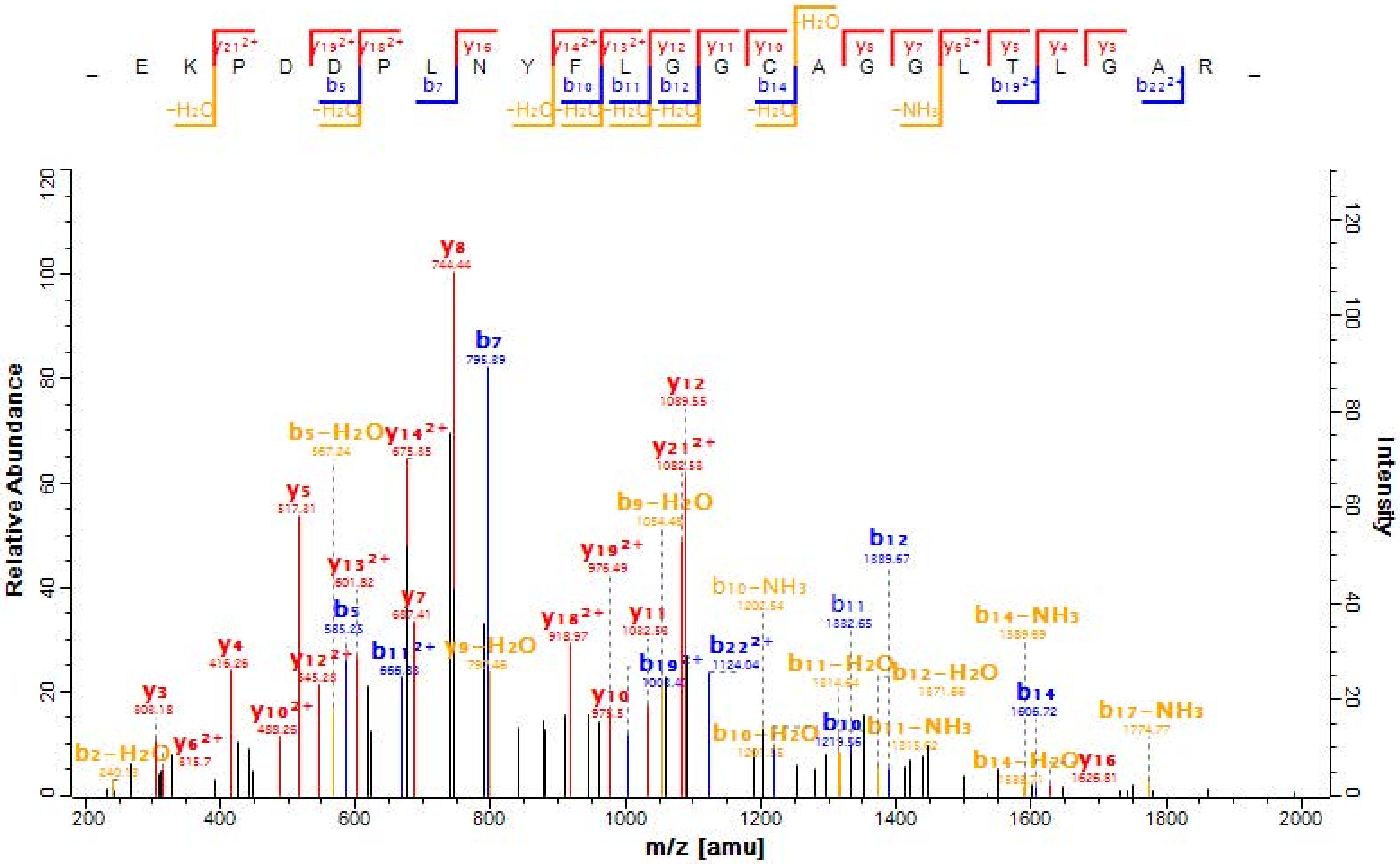
Mass:	1512.8091
m/z:	757.41183
Charge:	2+
Retentiontime:	61.033432006835
Score:	128.3128
Mass Error [ppm]:	0.13558
PEP:	1.0563E-08
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	61 %
Peak Coverage:	24 %
Protein Localisation:	536 ... 549

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	13				
	173.06		173.06	2	G	12	1406.8		703.91	+0.1869
	286.14	-0.019	286.14	3	I	11	1349.8		675.39	+0.2466
	385.21	+0.1465	385.21	4	V	10	1236.7	-0.148	618.85	+0.1902
	482.26		482.26	5	P	9	1137.6	+0.0783	569.32	+0.1752
	629.33		629.33	6	F	8	1040.6	+0.1921	1040.6	
-0.415	371.71	-0.001	742.41	7	L	7	893.51	+0.1843	893.51	
	870.47		870.47	8	Q	6	780.42	-0.334	780.42	
	969.54	-0.103	969.54	9	V	5	652.37	-0.033	652.37	
	1116.6		1116.6	10	F	4	553.3	+0.1588	553.3	
	1173.6	-0.075	1173.6	11	G	3	406.23	+0.1445	406.23	
	1310.7	-0.033	1310.7	12	H	2	349.21		349.21	
	1367.7	-0.021	1367.7	13	G	1	212.15		212.15	
				14	K	0	155.13		155.13	

Scan number	9097	**Raw file**	LNCAP_Silac_23F10_set1_06
Method	ITMS; CID	**Pepti...**	153.36



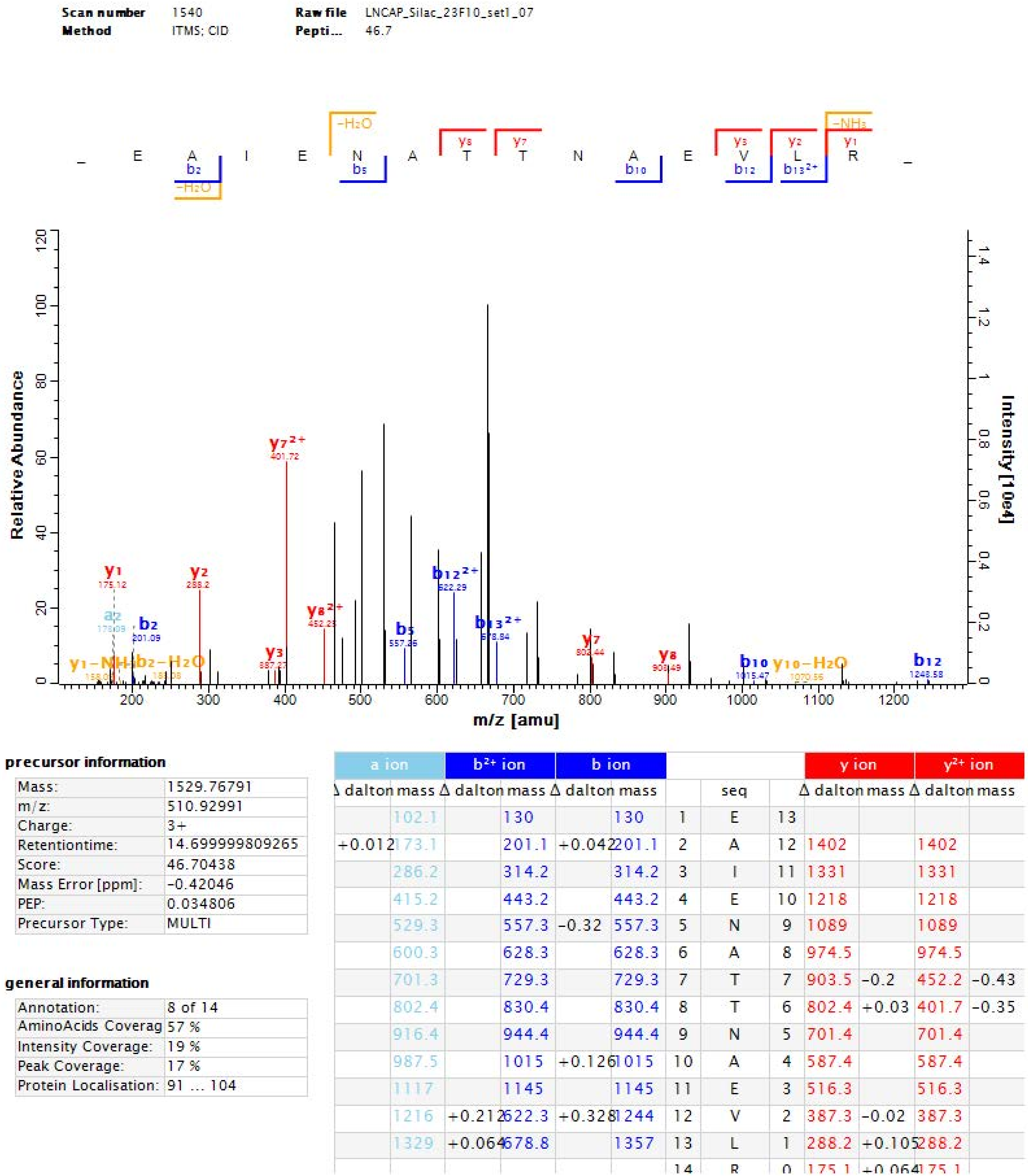
precursor information

Mass:	2420.17969
m/z:	807.73384
Charge:	3+
Retentiontime:	61.977073669433
Score:	153.3647
Mass Error [ppm]:	0.10006
PEP:	7.3633E-29
Precursor Type:	MULTI

general information

Annotation:	20 of 23
AminoAcids Coverag	87 %
Intensity Coverage:	59 %
Peak Coverage:	43 %
Protein Localisation:	82 ... 104

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	22				
	258.14		258.14	2	K	21	2292.1		2292.1	
	355.2		355.2	3	P	20	2164		1082.5	+0.1573
	470.22		470.22	4	D	19	2067		2067	
	585.25	+0.2392	585.25	5	D	18	1952		976.49	+0.2323
	682.3		682.3	6	P	17	1836.9		918.97	+0.3352
	795.39	+0.1336	795.39	7	L	16	1739.9		1739.9	
	909.43		909.43	8	N	15	1626.8	+0.1112	1626.8	
	1072.5		1072.5	9	Y	14	1512.8		1512.8	
	1219.6	+0.072	1219.6	10	F	13	1349.7		675.35	-0.142
+0.2977	666.83	-0.106	1332.6	11	L	12	1202.6		601.82	-0.113
	1389.7	+0.3732	1389.7	12	G	11	1089.5	+0.061	545.28	+0.1839
	1446.7		1446.7	13	G	10	1032.5	+0.006	1032.5	
	1606.7	+0.0286	1606.7	14	C	9	975.5	+0.1097	488.26	+0.1528
	1677.8		1677.8	15	A	8	815.47		815.47	
	1734.8		1734.8	16	G	7	744.44	+0.0029	744.44	
	1791.8		1791.8	17	G	6	687.41	+0.0534	687.41	
	1904.9		1904.9	18	L	5	630.39		315.7	+0.3078
+0.1607	1003.5		2005.9	19	T	4	517.31	+0.0602	517.31	
	2119		2119	20	L	3	416.26	+0.0538	416.26	
	2176		2176	21	G	2	303.18	+0.1406	303.18	
+0.0129	1124		2247.1	22	A	1	246.16		246.16	
				23	R	0	175.12		175.12	



Scan number	1540	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	46.7

precursor information

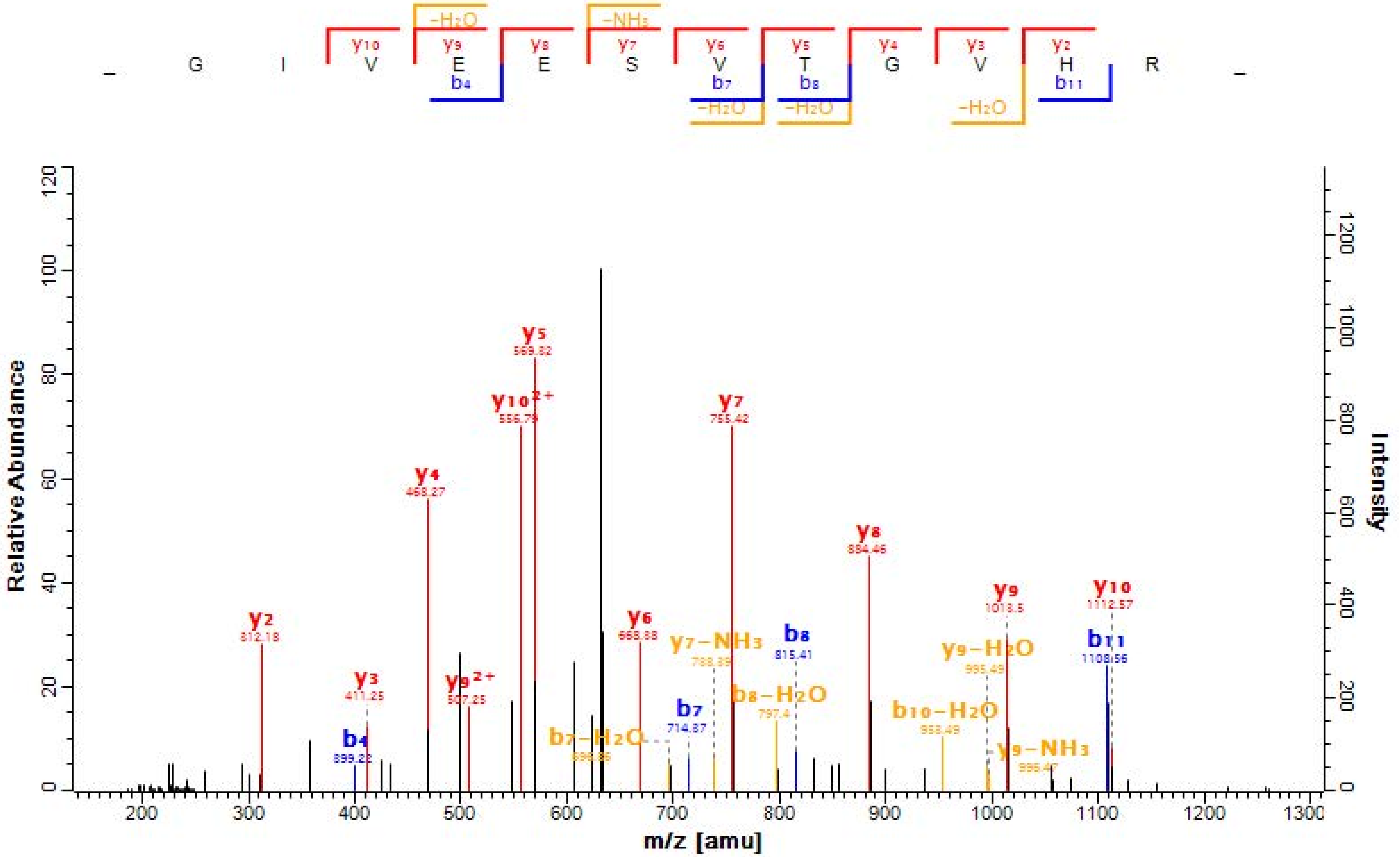
Mass:	1529.76791
m/z:	510.92991
Charge:	3+
Retentiontime:	14.699999809265
Score:	46.70438
Mass Error [ppm]:	-0.42046
PEP:	0.034806
Precursor Type:	MULTI

general information

Annotation:	8 of 14
AminoAcids Coverag	57 %
Intensity Coverage:	19 %
Peak Coverage:	17 %
Protein Localisation:	91 ... 104

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.1		130		130	1	E	13				
+0.012	173.1		201.1	+0.042	201.1	2	A	12	1402		1402	
	286.2		314.2		314.2	3	I	11	1331		1331	
	415.2		443.2		443.2	4	E	10	1218		1218	
	529.3		557.3	-0.32	557.3	5	N	9	1089		1089	
	600.3		628.3		628.3	6	A	8	974.5		974.5	
	701.3		729.3		729.3	7	T	7	903.5	-0.2	452.2	-0.43
	802.4		830.4		830.4	8	T	6	802.4	+0.03	401.7	-0.35
	916.4		944.4		944.4	9	N	5	701.4		701.4	
	987.5		1015	+0.126	1015	10	A	4	587.4		587.4	
	1117		1145		1145	11	E	3	516.3		516.3	
	1216	+0.212	622.3	+0.328	1244	12	V	2	387.3	-0.02	387.3	
	1329	+0.064	678.8		1357	13	L	1	288.2	+0.105	288.2	
						14	R	0	175.1	+0.064	175.1	

Scan number	1603	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	124.12



precursor information

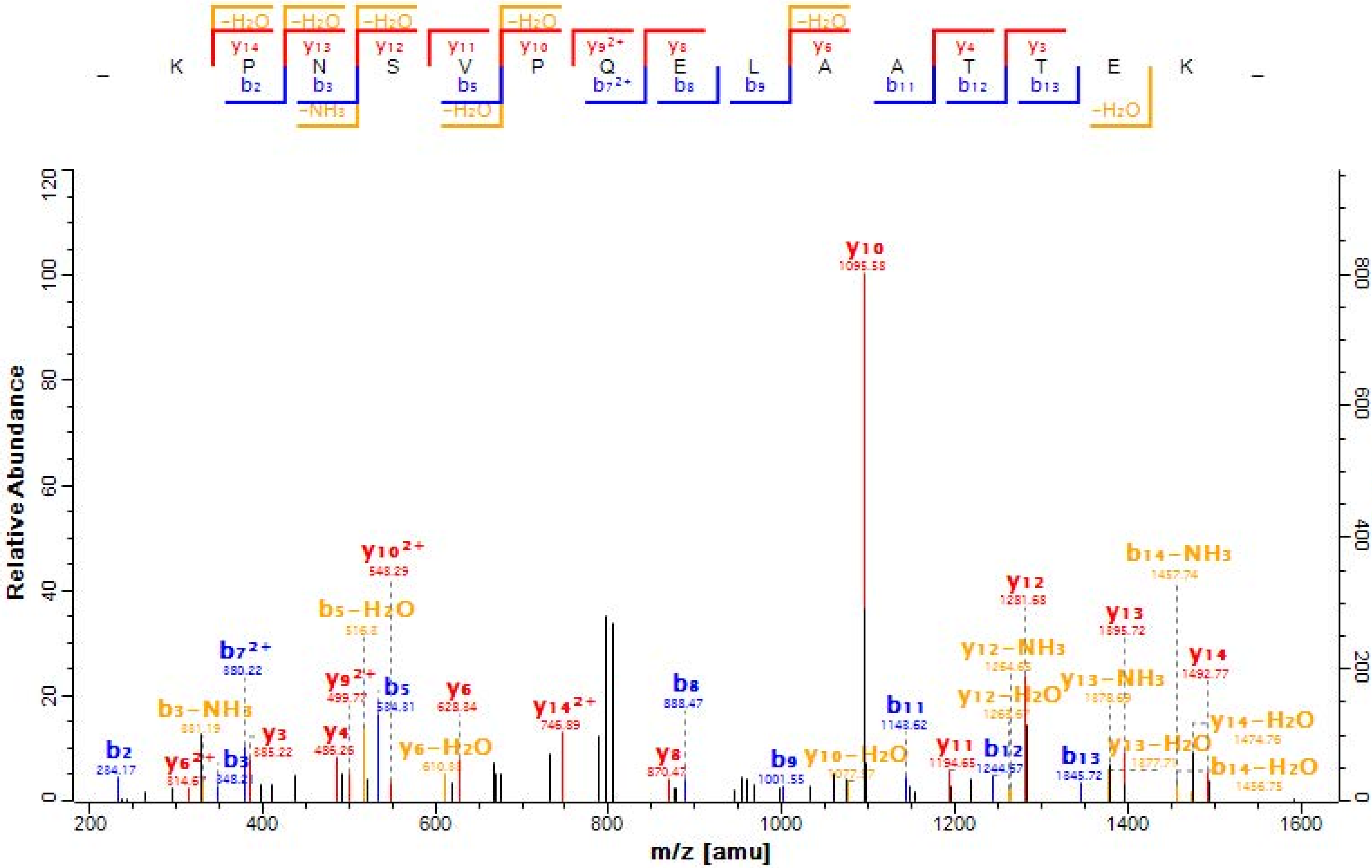
Mass:	1281.66775
m/z:	641.84115
Charge:	2+
Retentiontime:	15.078287124633
Score:	124.1237
Mass Error [ppm]:	0.030955
PEP:	2.1493E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	54 %
Peak Coverage:	22 %
Protein Localisation:	331 ... 342

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	11				
	171.1128	2	I	10	1225.654		1225.654	
	270.1812	3	V	9	1112.569	+0.069209	556.7884	+0.189047
+0.043157	399.2238	4	E	8	1013.501	+0.080555	507.2542	+0.040881
	528.2664	5	E	7	884.4585	+0.02891	884.4585	
	615.2984	6	S	6	755.4159	+0.051117	755.4159	
+0.042699	714.3668	7	V	5	668.3838	+0.091752	668.3838	
-0.18064	815.4145	8	T	4	569.3154	+0.000498	569.3154	
	872.436	9	G	3	468.2677	+0.0378	468.2677	
	971.5044	10	V	2	411.2463	+0.173095	411.2463	
-0.02096	1108.563	11	H	1	312.1779	+0.024406	312.1779	
		12	R	0	175.119		175.119	

Scan number	1861	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	190.41



precursor information

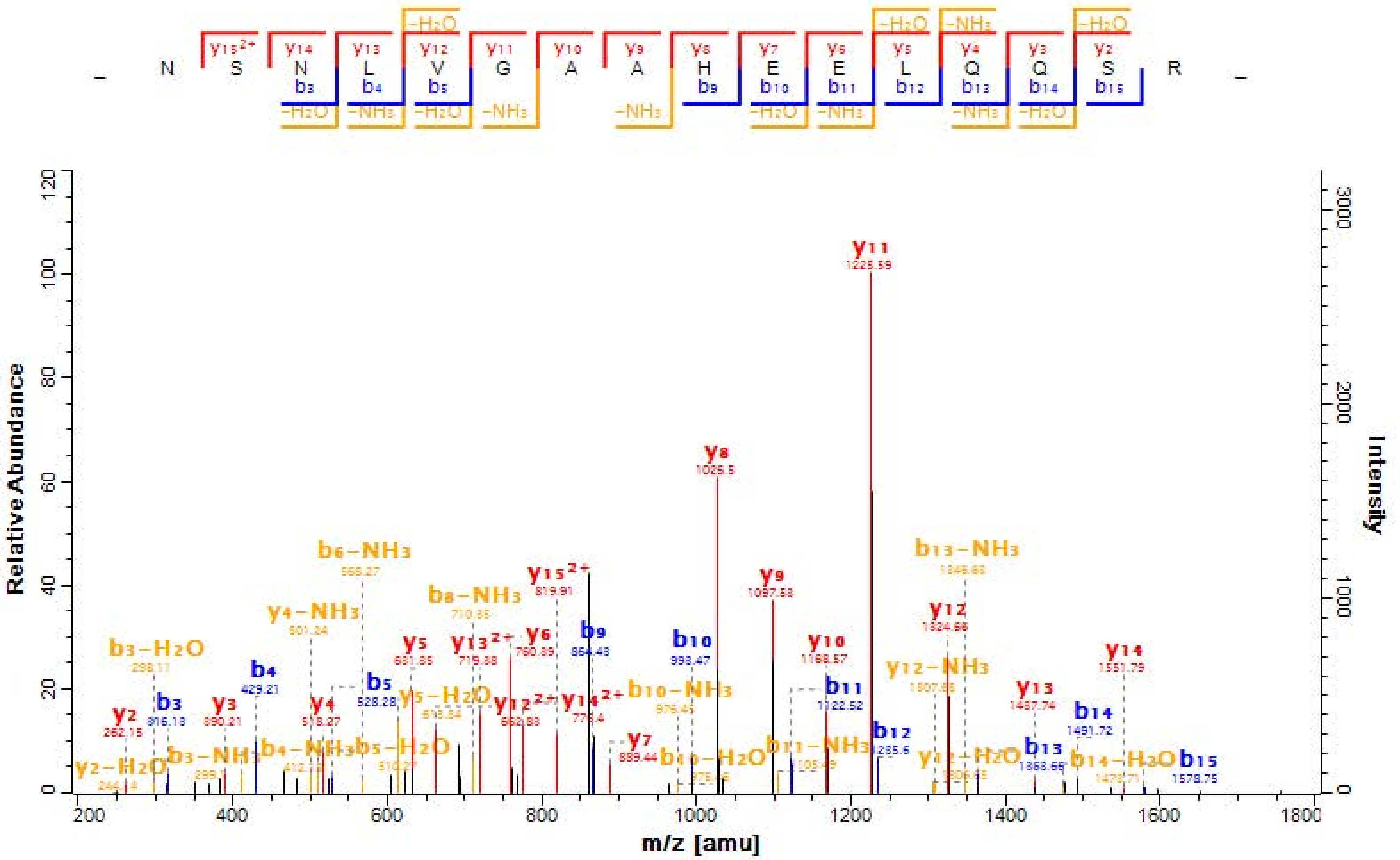
Mass:	1611.84664
m/z:	806.9306
Charge:	2+
Retentiontime:	16.640384674072
Score:	190.407
Mass Error [ppm]:	-0.099444
PEP:	4.5597E-22
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	48 %
Peak Coverage:	43 %
Protein Localisation:	618 ... 632

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	137.12		137.12	1	K	14				
	234.17	+0.0525	234.17	2	P	13	1492.8	-0.231	746.89	+0.2622
	348.21	+0.0691	348.21	3	N	12	1395.7	-0.24	1395.7	
	435.24		435.24	4	S	11	1281.7	+0.0542	1281.7	
	534.31	-0.131	534.31	5	V	10	1194.6	-0.036	1194.6	
	631.37		631.37	6	P	9	1095.6	+0.0331	548.29	+0.1585
+0.049	380.22		759.42	7	Q	8	998.52		499.77	-0.251
	888.47	-0.038	888.47	8	E	7	870.47	+0.0881	870.47	
	1001.6	-0.115	1001.6	9	L	6	741.42		741.42	
	1072.6		1072.6	10	A	5	628.34	+0.1322	314.67	-0.317
	1143.6	-0.103	1143.6	11	A	4	557.3		557.3	
	1244.7	+0.0081	1244.7	12	T	3	486.26	+0.0897	486.26	
	1345.7	-0.053	1345.7	13	T	2	385.22	+0.1314	385.22	
	1474.8		1474.8	14	E	1	284.17		284.17	
				15	K	0	155.13		155.13	

Scan number	2476	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	248.97



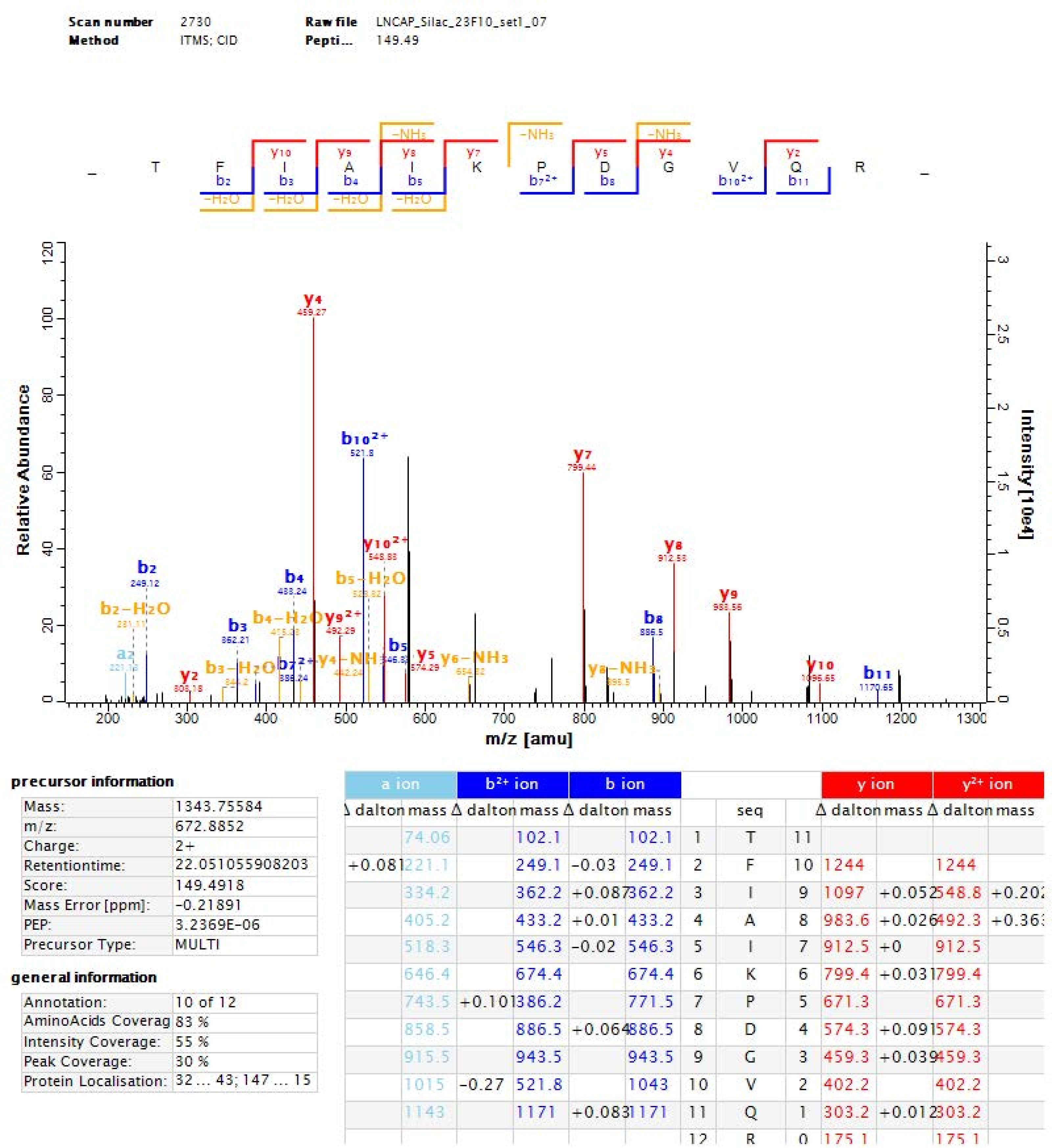
precursor information

Mass:	1751.85483
m/z:	876.93469
Charge:	2+
Retentiontime:	20.520244598388
Score:	248.9714
Mass Error [ppm]:	-0.13906
PEP:	4.6904E-62
Precursor Type:	MULTI

general information

Annotation:	14 of 16
AminoAcids Coverag	88 %
Intensity Coverage:	61 %
Peak Coverage:	50 %
Protein Localisation:	281 ... 296

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502	1	N	15				
	202.0822	2	S	14	1638.819		819.9133	+0.269573
+0.070153	316.1252	3	N	13	1551.787	+0.066488	776.3973	+0.212101
+0.049382	429.2092	4	L	12	1437.744	+0.110269	719.3759	+0.223433
-0.05315	528.2776	5	V	11	1324.66	-0.01221	662.8338	+0.221092
	585.2991	6	G	10	1225.592	-0.04096	1225.592	
	656.3362	7	A	9	1168.571	+0.011628	1168.571	
	727.3733	8	A	8	1097.533	+0.00028	1097.533	
+0.1291	864.4322	9	H	7	1026.496	+0.015665	1026.496	
+0.137776	993.4748	10	E	6	889.4374	+0.183342	889.4374	
-0.077	1122.517	11	E	5	760.3948	+0.068769	760.3948	
+0.009105	1235.601	12	L	4	631.3522	+0.042881	631.3522	
-0.08219	1363.66	13	Q	3	518.2681	+0.039909	518.2681	
-0.02419	1491.719	14	Q	2	390.2096	+0.112006	390.2096	
-0.32209	1578.751	15	S	1	262.151	+0.019124	262.151	
		16	R	0	175.119		175.119	



Scan number	2730	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	149.49

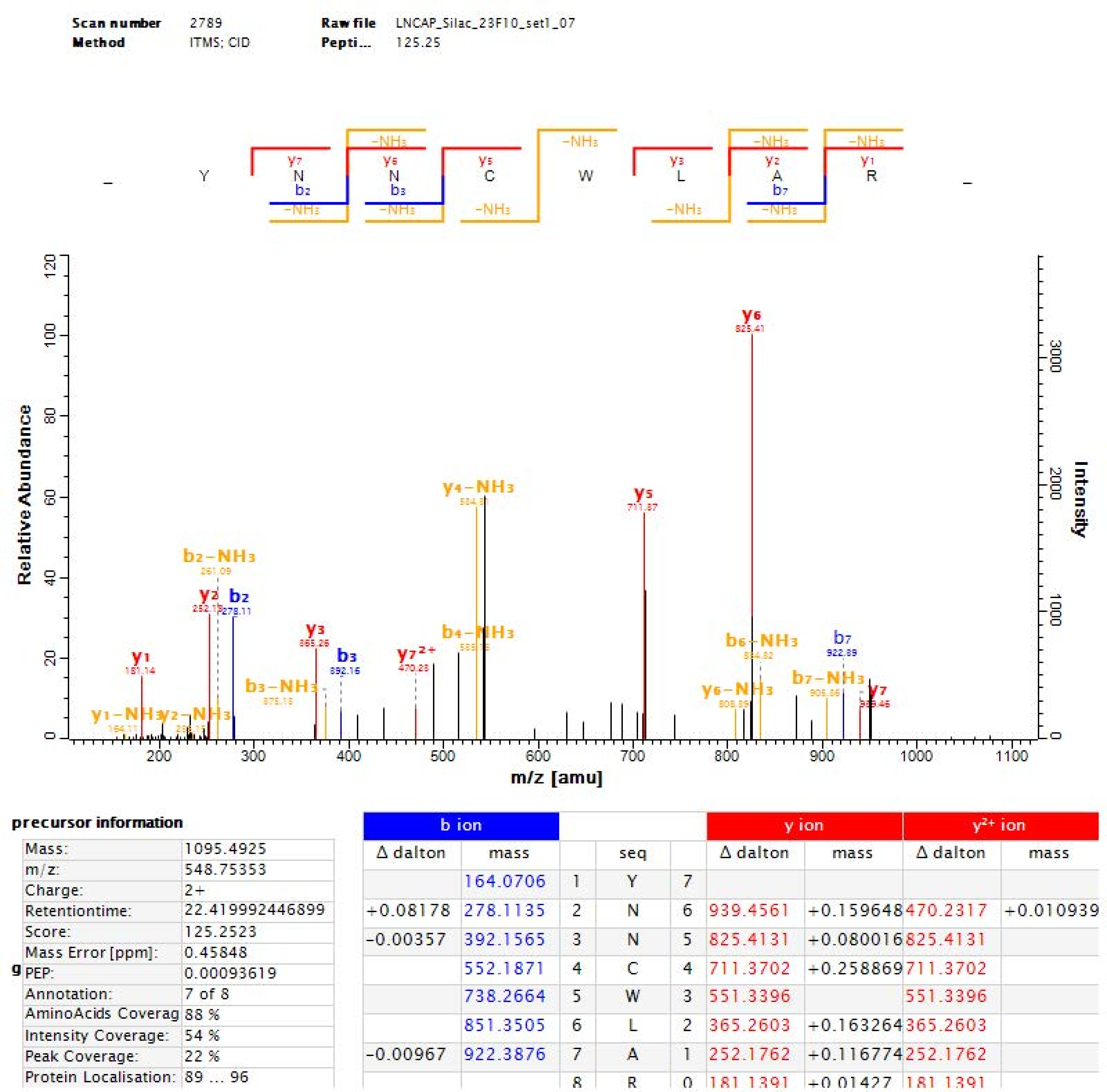
precursor information

Mass:	1343.75584
m/z:	672.8852
Charge:	2+
Retentiontime:	22.051055908203
Score:	149.4918
Mass Error [ppm]:	-0.21891
PEP:	3.2369E-06
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	55 %
Peak Coverage:	30 %
Protein Localisation:	32 ... 43; 147 ... 15

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.1		102.1	1	T	11				
+0.081	221.1		249.1	-0.03	249.1	2	F	10	1244		1244	
	334.2		362.2	+0.087	362.2	3	I	9	1097	+0.052	548.8	+0.20
	405.2		433.2	+0.01	433.2	4	A	8	983.6	+0.026	492.3	+0.36
	518.3		546.3	-0.02	546.3	5	I	7	912.5	+0	912.5	
	646.4		674.4		674.4	6	K	6	799.4	+0.031	799.4	
	743.5	+0.101	386.2		771.5	7	P	5	671.3		671.3	
	858.5		886.5	+0.064	886.5	8	D	4	574.3	+0.091	574.3	
	915.5		943.5		943.5	9	G	3	459.3	+0.039	459.3	
	1015	-0.27	521.8		1043	10	V	2	402.2		402.2	
	1143		1171	+0.083	1171	11	Q	1	303.2	+0.012	303.2	
						12	R	0	175.1		175.1	



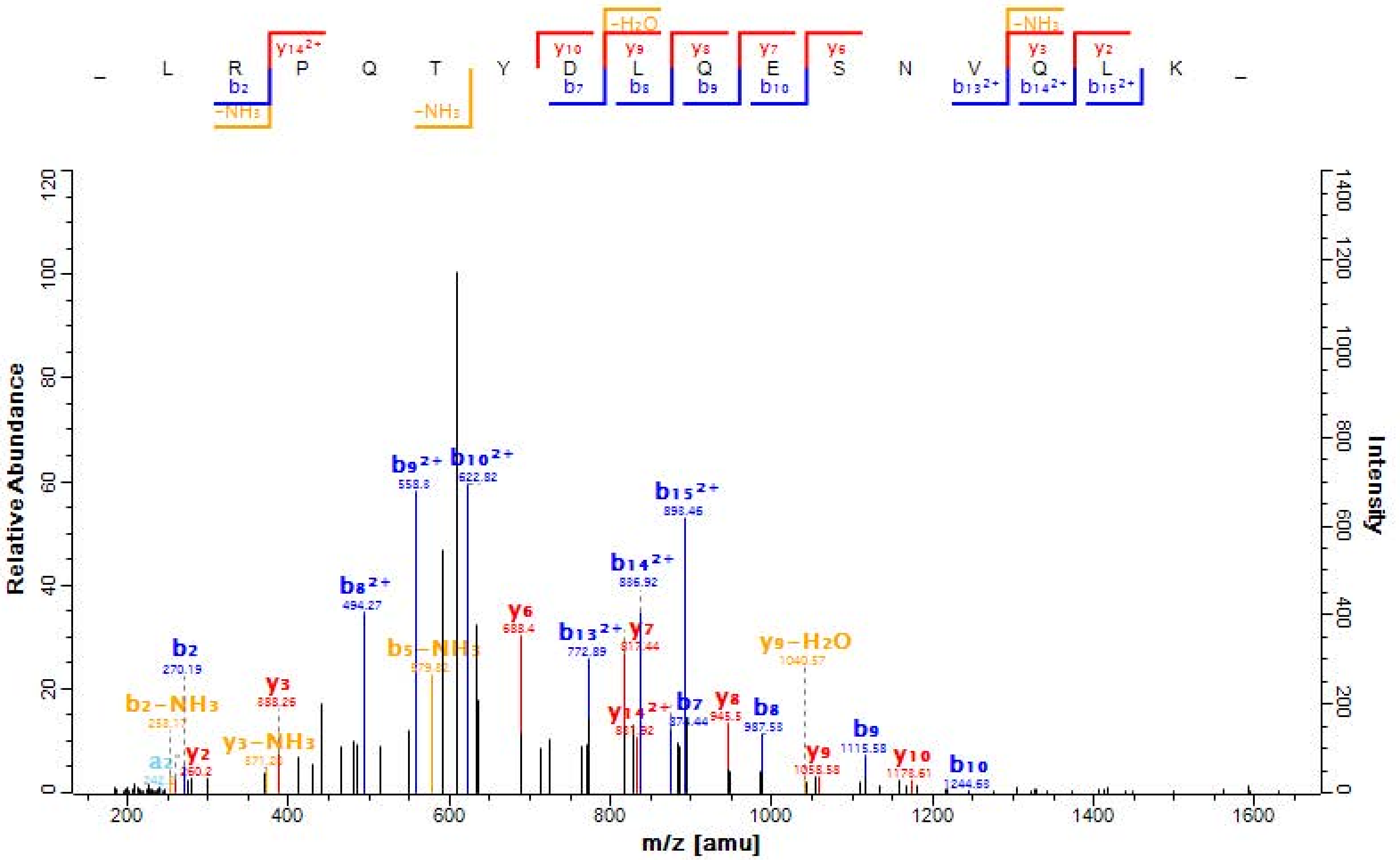
Scan number 2789 **Raw file** LNCAP_Silac_23F10_set1_07
Method ITMS; CID **Pepti...** 125.25

precursor information

Mass:	1095.4925
m/z:	548.75353
Charge:	2+
Retentiontime:	22.419992446899
Score:	125.2523
Mass Error [ppm]:	0.45848
PEP:	0.00093619
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	54 %
Peak Coverage:	22 %
Protein Localisation:	89 ... 96

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	164.0706	1	Y	7				
+0.08178	278.1135	2	N	6	939.4561	+0.159648	470.2317	+0.010939
−0.00357	392.1565	3	N	5	825.4131	+0.080016	825.4131	
	552.1871	4	C	4	711.3702	+0.258869	711.3702	
	738.2664	5	W	3	551.3396		551.3396	
	851.3505	6	L	2	365.2603	+0.163264	365.2603	
−0.00967	922.3876	7	A	1	252.1762	+0.116774	252.1762	
		8	R	0	181.1391	+0.01427	181.1391	

Scan number	3028	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	126.48



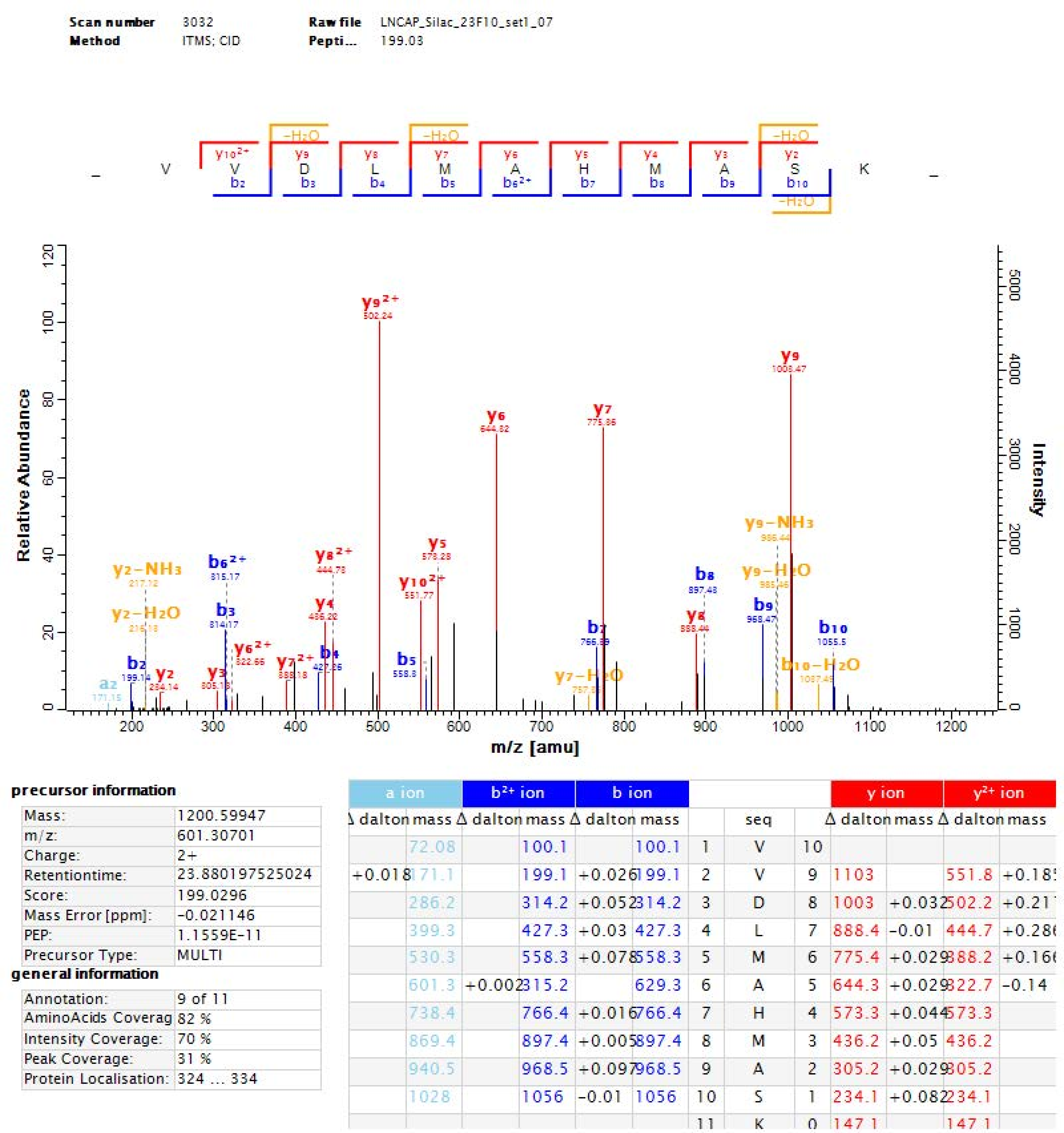
precursor information

Mass:	1931.0104
m/z:	644.67741
Charge:	3+
Retentiontime:	23.853332519531
Score:	126.4845
Mass Error [ppm]:	-0.43303
PEP:	4.161E-10
Precursor Type:	MULTI

general information

Annotation:	11 of 16
AminoAcids Coverag	69 %
Intensity Coverage:	46 %
Peak Coverage:	21 %
Protein Localisation:	83 ... 98

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	15				
+0.358	242.2		270.2	+0.039	270.2	2	R	14	1819		1819	
	339.3		367.2		367.2	3	P	13	1663		831.9	+0.16
	467.3		495.3		495.3	4	Q	12	1566		1566	
	568.4		596.4		596.4	5	T	11	1438		1438	
	731.4		759.4		759.4	6	Y	10	1337		1337	
	846.4		874.4	+0.064	874.4	7	D	9	1174	+0.05	1174	
	959.5	+0.207	494.3	+0.029	987.5	8	L	8	1059	+0.198	1059	
	1088	+0.252	558.3	-0.03	1116	9	Q	7	945.5	-0.08	945.5	
	1217	+0.304	622.8	+0.038	1245	10	E	6	817.4	+0.052	817.4	
	1304		1332		1332	11	S	5	688.4	+0.072	688.4	
	1418		1446		1446	12	N	4	601.4		601.4	
	1517	+0.007	772.9		1545	13	V	3	487.3		487.3	
	1645	+0.326	836.9		1673	14	Q	2	388.3	+0.11	388.3	
	1758	+0.213	893.5		1786	15	L	1	260.2	+0.026	260.2	
						16	K	0	147.1		147.1	



Scan number	3032	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	199.03

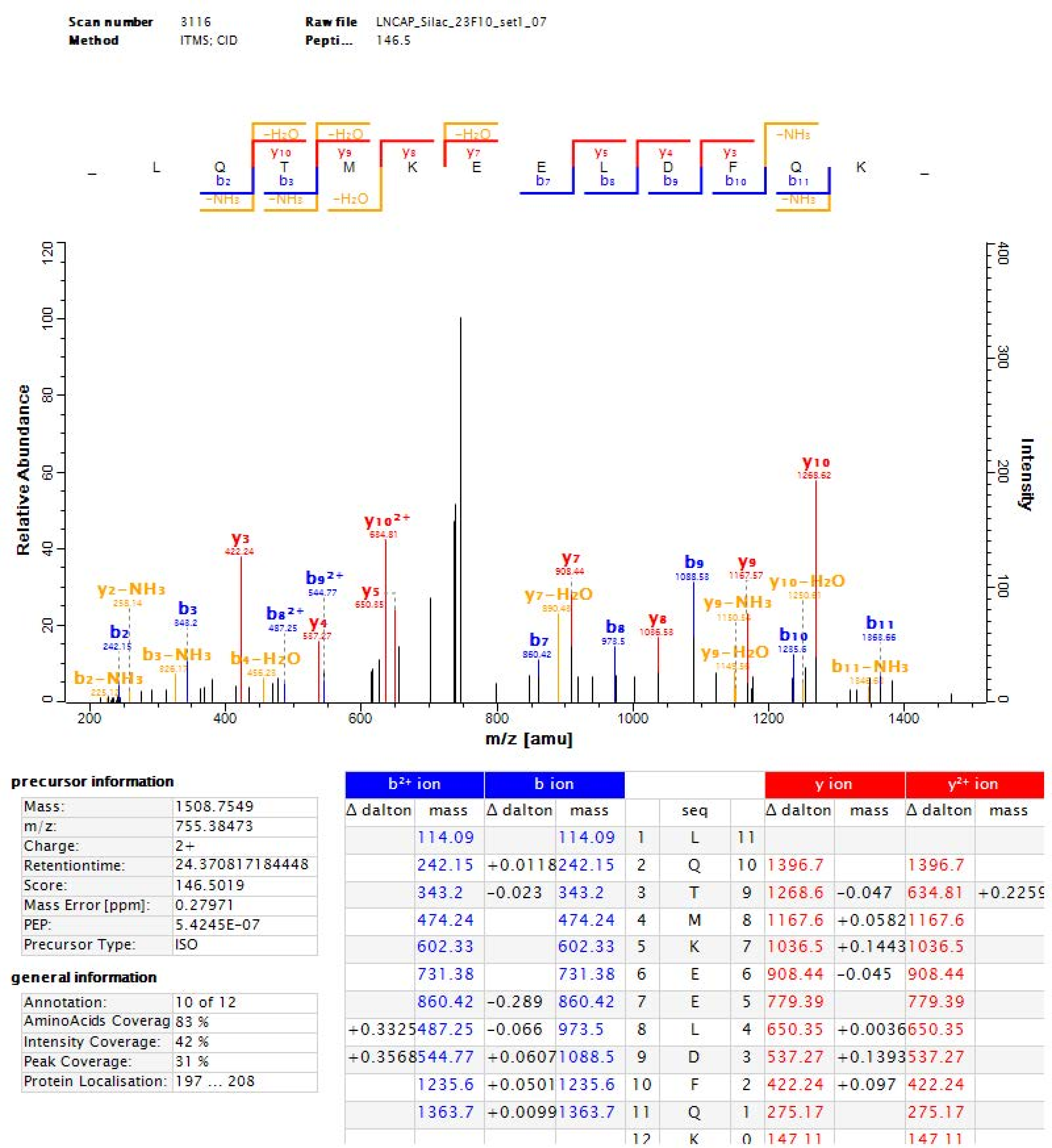
precursor information

Mass:	1200.59947
m/z:	601.30701
Charge:	2+
Retentiontime:	23.880197525024
Score:	199.0296
Mass Error [ppm]:	-0.021146
PEP:	1.1559E-11
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	70 %
Peak Coverage:	31 %
Protein Localisation:	324 ... 334

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.08		100.1		100.1	1	V	10				
+0.018	171.1		199.1	+0.026	199.1	2	V	9	1103		551.8	+0.18
	286.2		314.2	+0.052	314.2	3	D	8	1003	+0.032	502.2	+0.21
	399.3		427.3	+0.03	427.3	4	L	7	888.4	-0.01	444.7	+0.28
	530.3		558.3	+0.078	558.3	5	M	6	775.4	+0.029	388.2	+0.16
	601.3	+0.002	315.2		629.3	6	A	5	644.3	+0.029	322.7	-0.14
	738.4		766.4	+0.016	766.4	7	H	4	573.3	+0.044	573.3	
	869.4		897.4	+0.005	897.4	8	M	3	436.2	+0.05	436.2	
	940.5		968.5	+0.097	968.5	9	A	2	305.2	+0.029	305.2	
	1028		1056	-0.01	1056	10	S	1	234.1	+0.082	234.1	
						11	K	0	147.1		147.1	



Scan number	3116	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	146.5

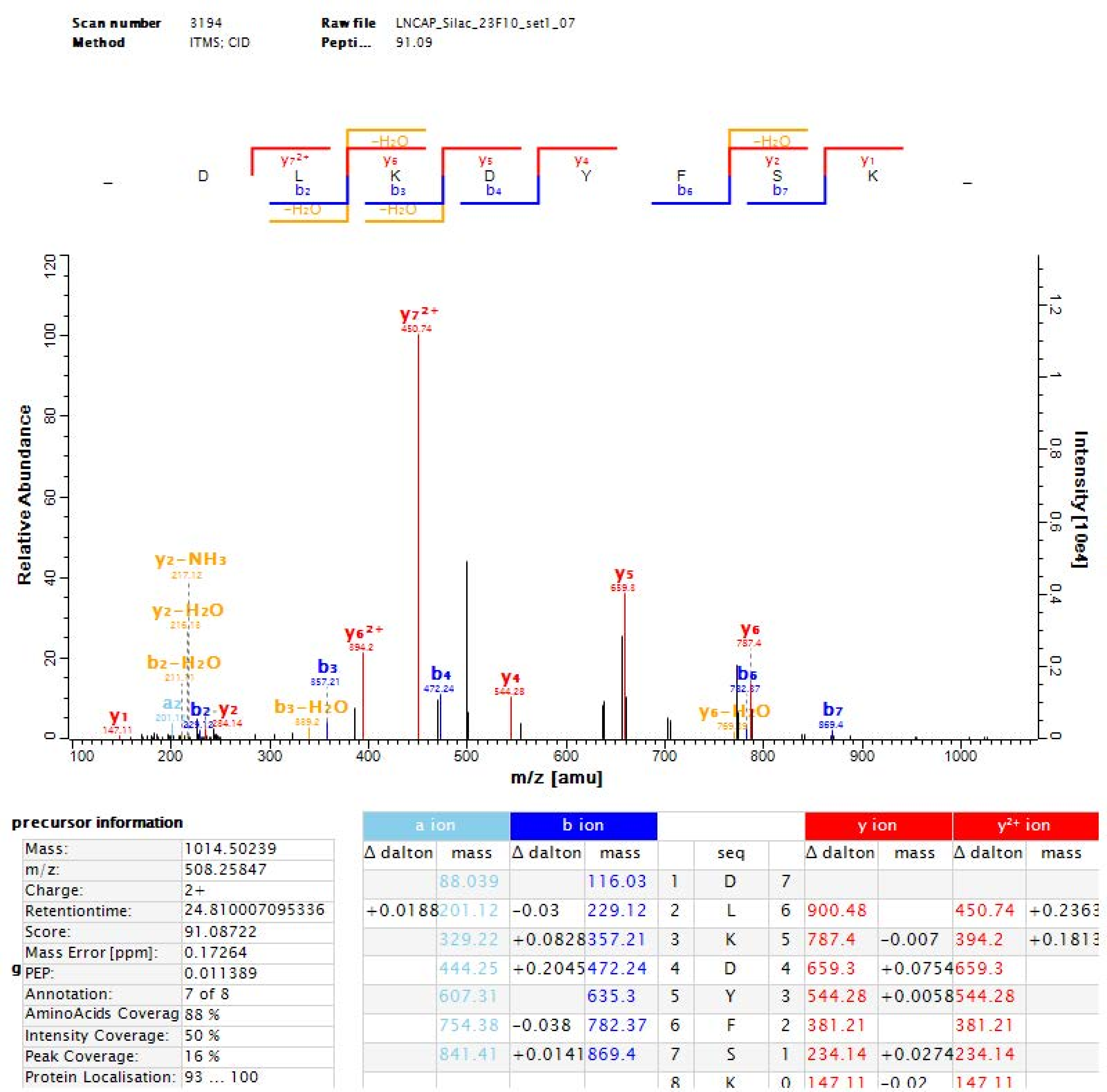
precursor information

Mass:	1508.7549
m/z:	755.38473
Charge:	2+
Retentiontime:	24.370817184448
Score:	146.5019
Mass Error [ppm]:	0.27971
PEP:	5.4245E-07
Precursor Type:	ISO

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	42 %
Peak Coverage:	31 %
Protein Localisation:	197 ... 208

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	11				
	242.15	+0.0118	242.15	2	Q	10	1396.7		1396.7	
	343.2	-0.023	343.2	3	T	9	1268.6	-0.047	634.81	+0.2259
	474.24		474.24	4	M	8	1167.6	+0.0582	1167.6	
	602.33		602.33	5	K	7	1036.5	+0.1443	1036.5	
	731.38		731.38	6	E	6	908.44	-0.045	908.44	
	860.42	-0.289	860.42	7	E	5	779.39		779.39	
+0.3325	487.25	-0.066	973.5	8	L	4	650.35	+0.0036	650.35	
+0.3568	544.77	+0.0607	1088.5	9	D	3	537.27	+0.1393	537.27	
	1235.6	+0.0501	1235.6	10	F	2	422.24	+0.097	422.24	
	1363.7	+0.0099	1363.7	11	Q	1	275.17		275.17	
				12	K	0	147.11		147.11	

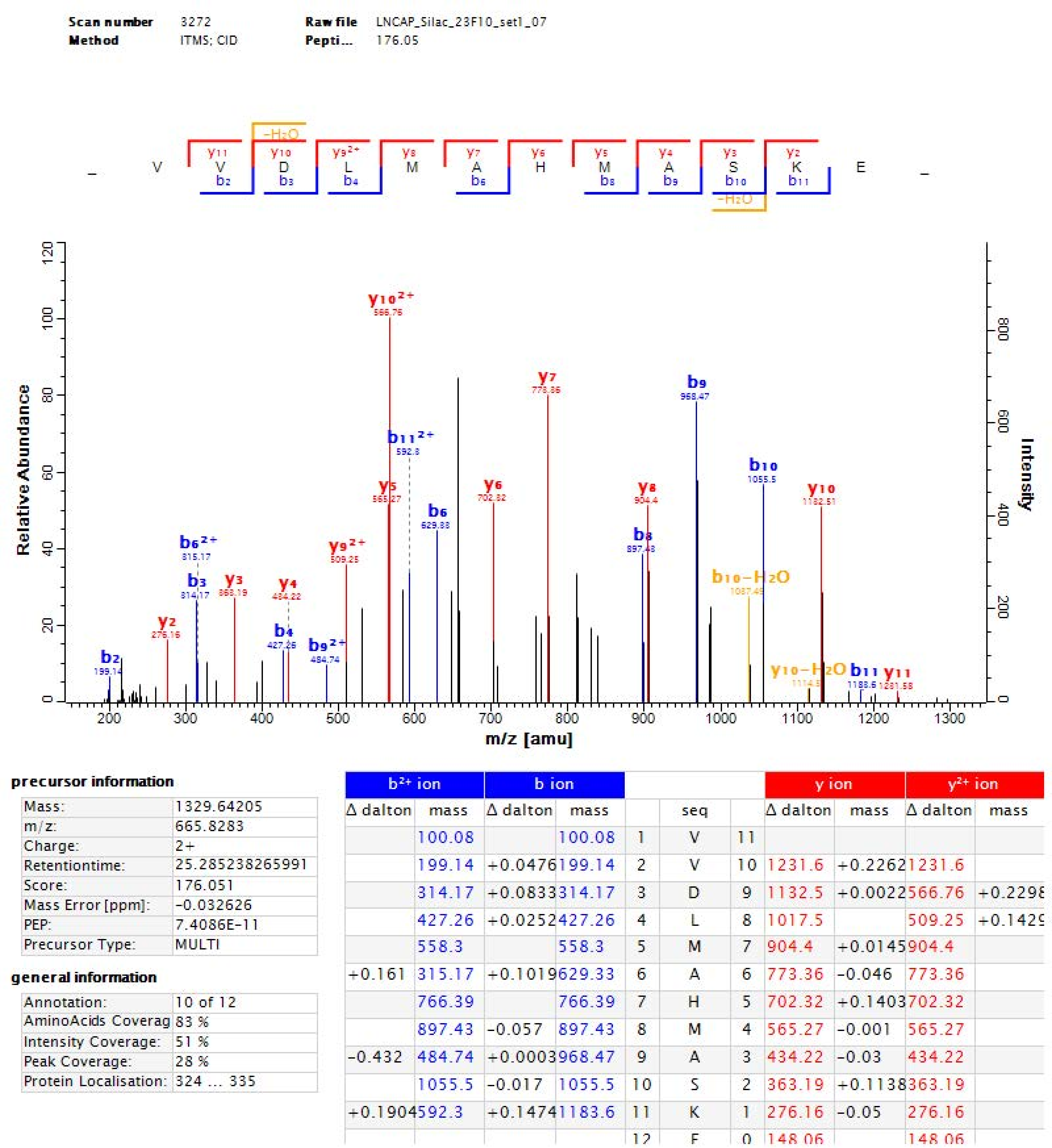


Scan number	3194	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	91.09

precursor information

Mass:	1014.50239
m/z:	508.25847
Charge:	2+
Retentiontime:	24.810007095336
Score:	91.08722
Mass Error [ppm]:	0.17264
PEP:	0.011389
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	50 %
Peak Coverage:	16 %
Protein Localisation:	93 ... 100

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	7				
+0.0188	201.12	-0.03	229.12	2	L	6	900.48		450.74	+0.2363
	329.22	+0.0828	357.21	3	K	5	787.4	-0.007	394.2	+0.1813
	444.25	+0.2045	472.24	4	D	4	659.3	+0.0754	659.3	
	607.31		635.3	5	Y	3	544.28	+0.0058	544.28	
	754.38	-0.038	782.37	6	F	2	381.21		381.21	
	841.41	+0.0141	869.4	7	S	1	234.14	+0.0274	234.14	
				8	K	0	147.11	-0.02	147.11	



Scan number	3272	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	176.05

precursor information

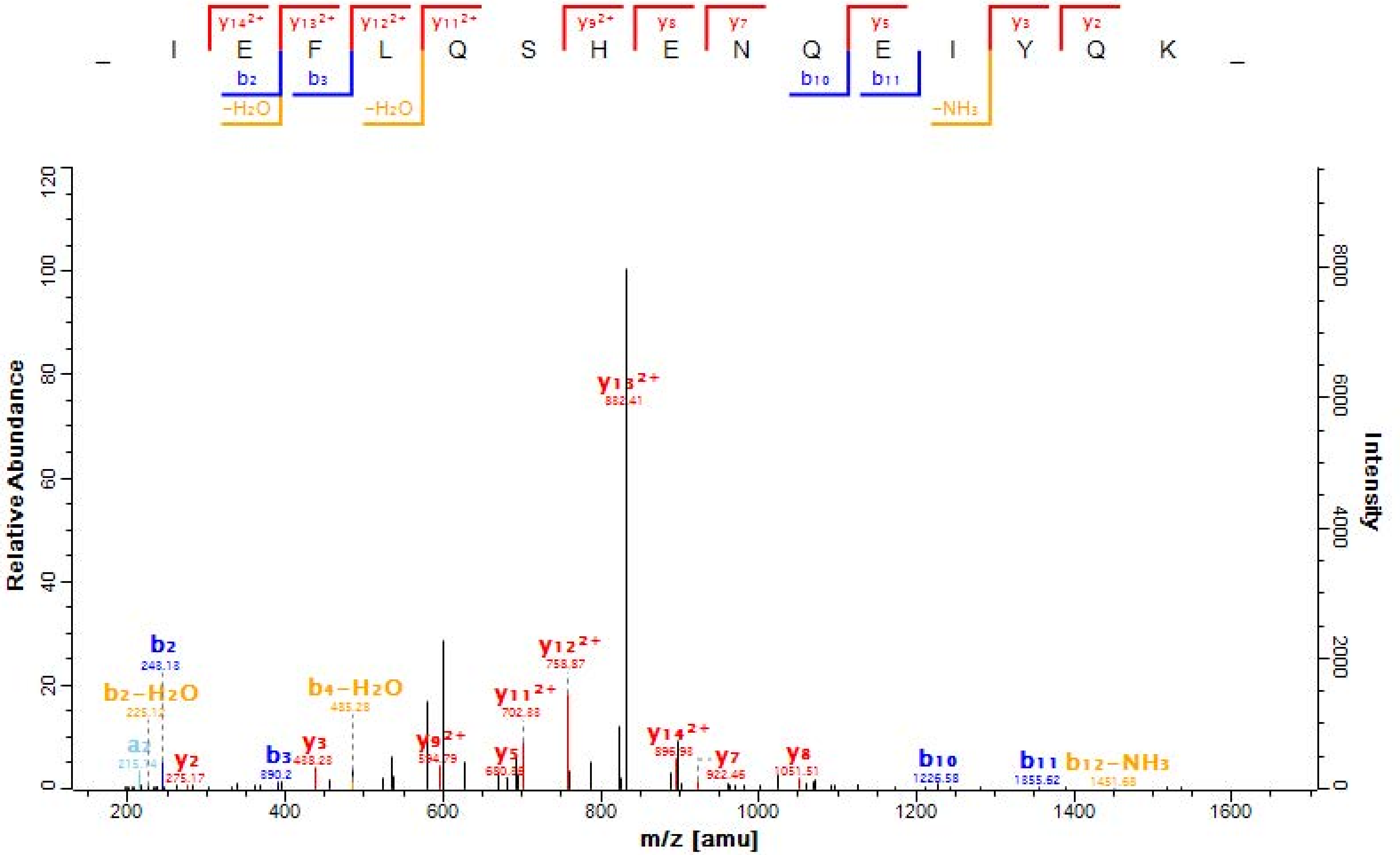
Mass:	1329.64205
m/z:	665.8283
Charge:	2+
Retentiontime:	25.285238265991
Score:	176.051
Mass Error [ppm]:	-0.032626
PEP:	7.4086E-11
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	51 %
Peak Coverage:	28 %
Protein Localisation:	324 ... 335

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	11				
	199.14	+0.0476	199.14	2	V	10	1231.6	+0.2262	1231.6	
	314.17	+0.0833	314.17	3	D	9	1132.5	+0.0022	566.76	+0.229
	427.26	+0.0252	427.26	4	L	8	1017.5		509.25	+0.142
	558.3		558.3	5	M	7	904.4	+0.0145	904.4	
+0.161	315.17	+0.1019	629.33	6	A	6	773.36	-0.046	773.36	
	766.39		766.39	7	H	5	702.32	+0.1403	702.32	
	897.43	-0.057	897.43	8	M	4	565.27	-0.001	565.27	
-0.432	484.74	+0.0003	968.47	9	A	3	434.22	-0.03	434.22	
	1055.5	-0.017	1055.5	10	S	2	363.19	+0.1138	363.19	
+0.1904	592.3	+0.1474	1183.6	11	K	1	276.16	-0.05	276.16	
				12	E	0	148.06		148.06	

Scan number	3360	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	75.46



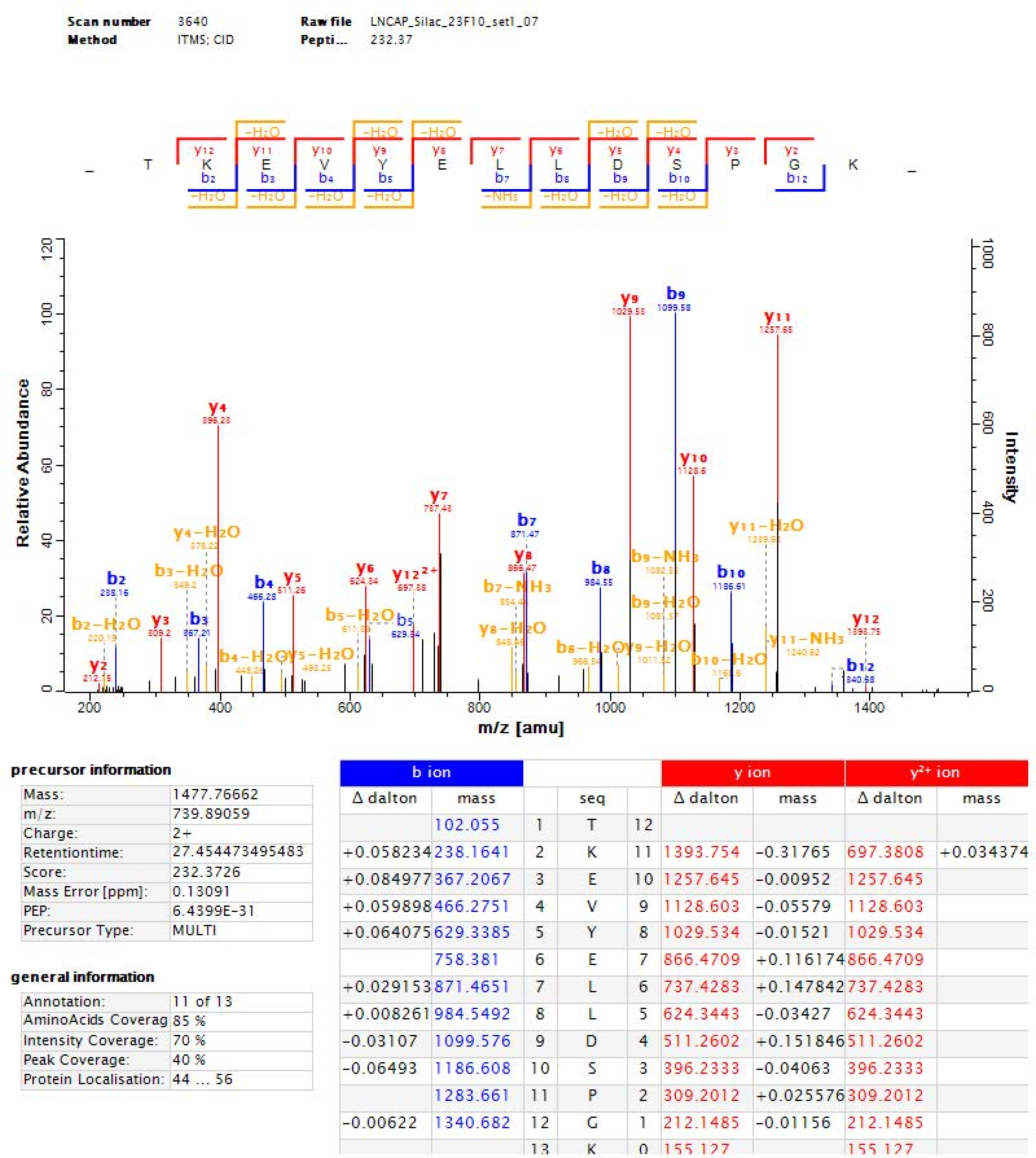
precursor information

Mass:	1904.92692
m/z:	635.98292
Charge:	3+
Retentiontime:	25.823421478271
Score:	75.46223
Mass Error [ppm]:	0.042638
PEP:	0.00080469
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	32 %
Peak Coverage:	17 %
Protein Localisation:	481 ... 495

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	14				
+0.0103	215.14	-0.024	243.13	2	E	13	1792.9		896.93	-0.068
	362.21	-0.005	390.2	3	F	12	1663.8		832.41	+0.0751
	475.29		503.29	4	L	11	1516.7		758.87	+0.3355
	603.35		631.34	5	Q	10	1403.7		702.33	+0.288
	690.38		718.38	6	S	9	1275.6		1275.6	
	827.44		855.44	7	H	8	1188.6		594.79	+0.0475
	956.48		984.48	8	E	7	1051.5	+0.0664	1051.5	
	1070.5		1098.5	9	N	6	922.46	-0.033	922.46	
	1198.6	-0.055	1226.6	10	Q	5	808.42		808.42	
	1327.6	-0.055	1355.6	11	E	4	680.36	+0.1694	680.36	
	1440.7		1468.7	12	I	3	551.32		551.32	
	1603.8		1631.8	13	Y	2	438.23	+0.0671	438.23	
	1731.8		1759.8	14	Q	1	275.17	+0.0703	275.17	
				15	K	0	147.11		147.11	



Scan number	3640	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	232.37

precursor information

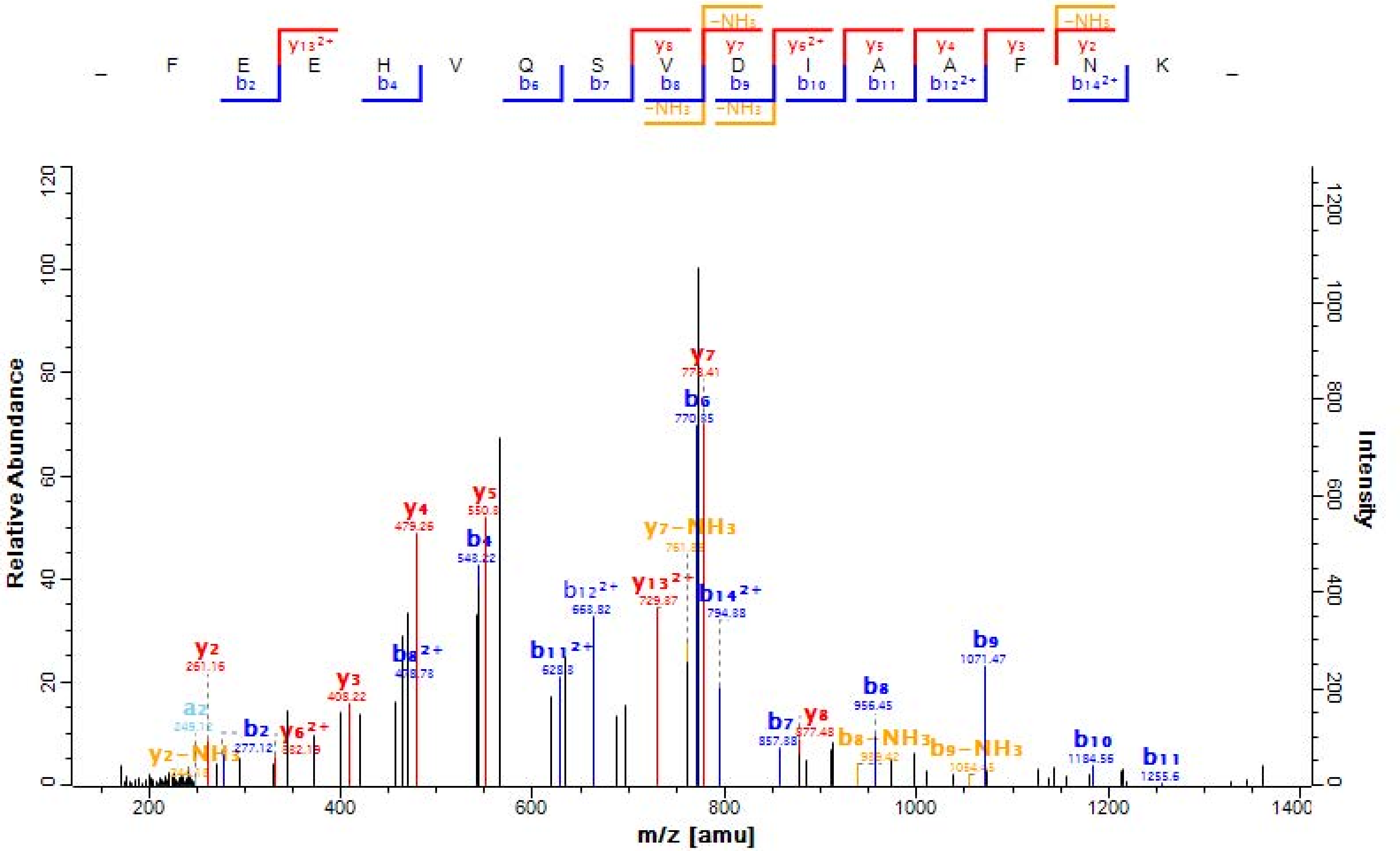
Mass:	1477.76662
m/z:	739.89059
Charge:	2+
Retentiontime:	27.454473495483
Score:	232.3726
Mass Error [ppm]:	0.13091
PEP:	6.4399E-31
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	70 %
Peak Coverage:	40 %
Protein Localisation:	44 ... 56

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055	1	T	12				
+0.058234	238.1641	2	K	11	1393.754	-0.31765	697.3808	+0.034374
+0.084977	367.2067	3	E	10	1257.645	-0.00952	1257.645	
+0.059898	466.2751	4	V	9	1128.603	-0.05579	1128.603	
+0.064075	629.3385	5	Y	8	1029.534	-0.01521	1029.534	
	758.381	6	E	7	866.4709	+0.116174	866.4709	
+0.029153	871.4651	7	L	6	737.4283	+0.147842	737.4283	
+0.008261	984.5492	8	L	5	624.3443	-0.03427	624.3443	
-0.03107	1099.576	9	D	4	511.2602	+0.151846	511.2602	
-0.06493	1186.608	10	S	3	396.2333	-0.04063	396.2333	
	1283.661	11	P	2	309.2012	+0.025576	309.2012	
-0.00622	1340.682	12	G	1	212.1485	-0.01156	212.1485	
		13	K	0	155.127		155.127	

Scan number	4265	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	118.51



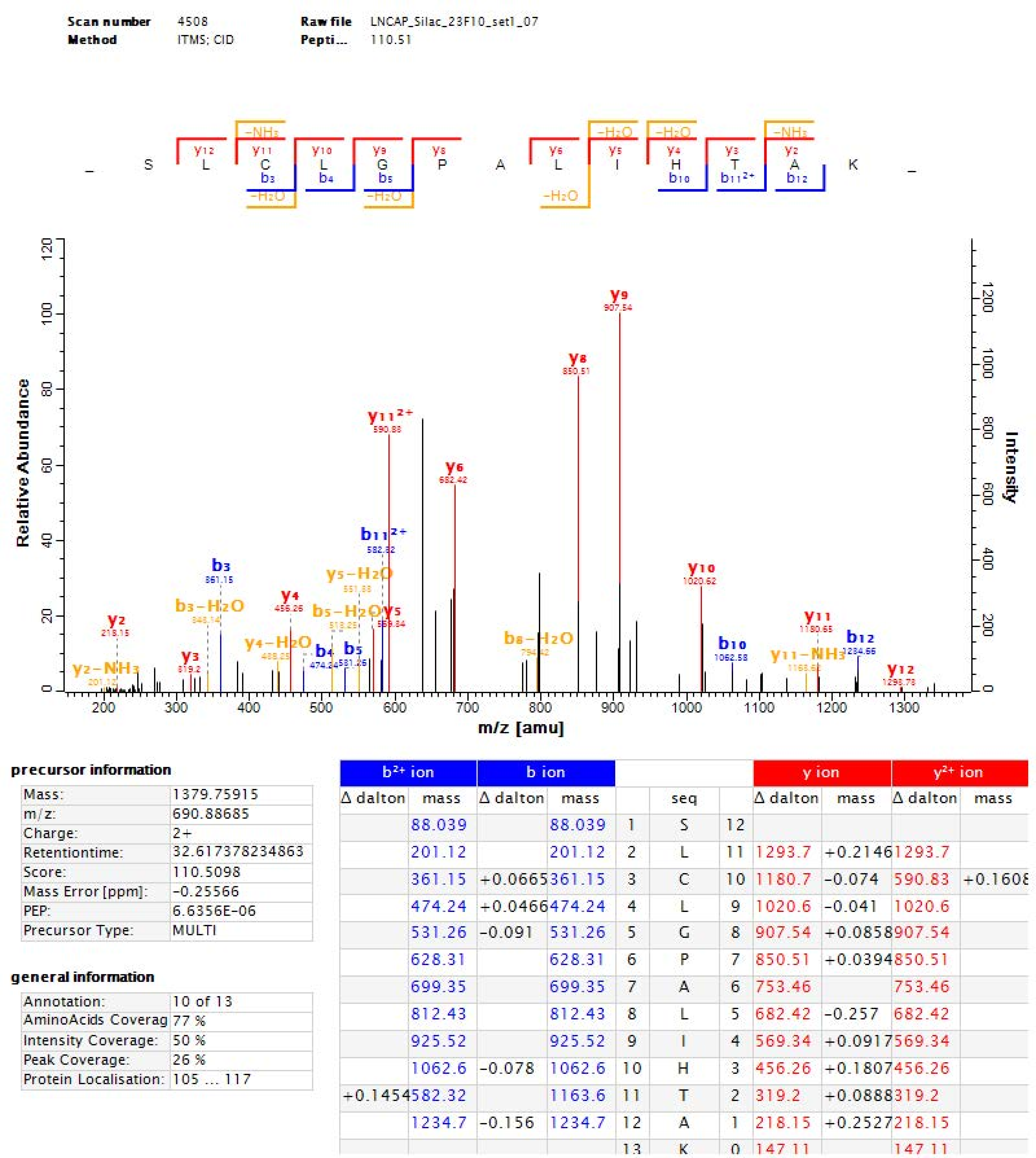
precursor information

Mass:	1732.8418
m/z:	578.62121
Charge:	3+
Retentiontime:	31.162668228149
Score:	118.5074
Mass Error [ppm]:	-0.14442
PEP:	2.2605E-07
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	45 %
Peak Coverage:	23 %
Protein Localisation:	266 ... 280

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.1		148.1		148.1	1	F	14				
-0.31	249.1		277.1	+0.083	277.1	2	E	13	1587		1587	
	378.2		406.2		406.2	3	E	12	1458		729.4	+0.07
	515.2		543.2	-0.19	543.2	4	H	11	1329		1329	
	614.3		642.3		642.3	5	V	10	1192		1192	
	742.4		770.3	+0.46	770.3	6	Q	9	1093		1093	
	829.4		857.4	+0.264	857.4	7	S	8	964.5		964.5	
	928.5	+0.002	478.7	+0.059	956.4	8	V	7	877.5	+0.117	877.5	
	1043		1071	-0.08	1071	9	D	6	778.4	+0.015	778.4	
	1157		1185	+0.008	1185	10	I	5	663.4		332.2	-0.07
	1228	+0.103	628.3	+0.206	1256	11	A	4	550.3	+0.116	550.3	
	1299	-0.1	663.8		1327	12	A	3	479.3	+0.133	479.3	
	1446		1474		1474	13	F	2	408.2	-0.03	408.2	
	1560	+0.488	794.4		1588	14	N	1	261.2	+0.129	261.2	
						15	K	0	147.1		147.1	



Scan number 4508 **Raw file** LNCAP_Silac_23F10_set1_07
Method ITMS; CID **Pepti...** 110.51

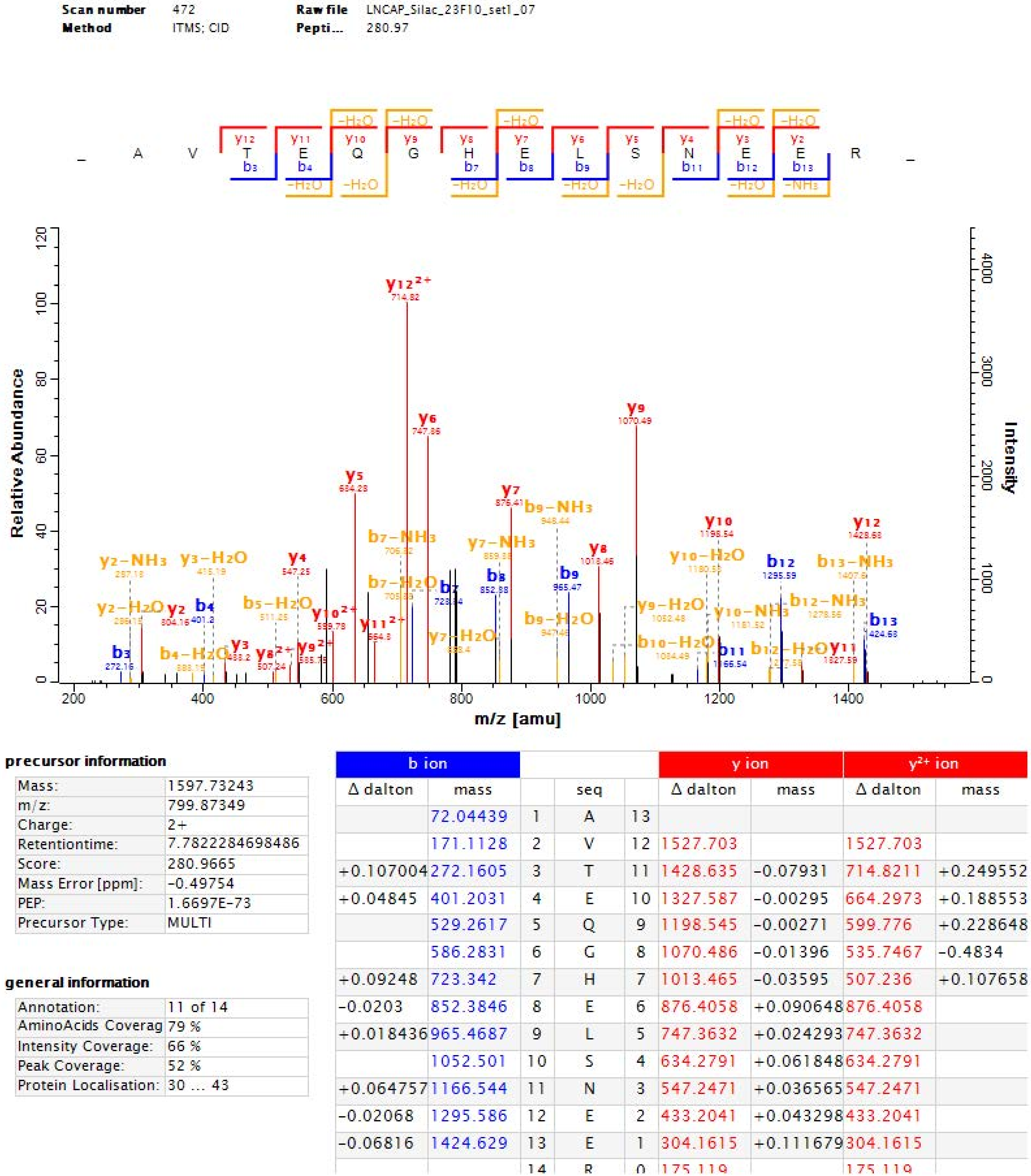
precursor information

Mass:	1379.75915
m/z:	690.88685
Charge:	2+
Retentiontime:	32.617378234863
Score:	110.5098
Mass Error [ppm]:	-0.25566
PEP:	6.6356E-06
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	50 %
Peak Coverage:	26 %
Protein Localisation:	105 ... 117

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	12				
	201.12		201.12	2	L	11	1293.7	+0.2146	1293.7	
	361.15	+0.0665	361.15	3	C	10	1180.7	-0.074	590.83	+0.1608
	474.24	+0.0466	474.24	4	L	9	1020.6	-0.041	1020.6	
	531.26	-0.091	531.26	5	G	8	907.54	+0.0858	907.54	
	628.31		628.31	6	P	7	850.51	+0.0394	850.51	
	699.35		699.35	7	A	6	753.46		753.46	
	812.43		812.43	8	L	5	682.42	-0.257	682.42	
	925.52		925.52	9	I	4	569.34	+0.0917	569.34	
	1062.6	-0.078	1062.6	10	H	3	456.26	+0.1807	456.26	
+0.1454	582.32		1163.6	11	T	2	319.2	+0.0888	319.2	
	1234.7	-0.156	1234.7	12	A	1	218.15	+0.2527	218.15	
				13	K	0	147.11		147.11	



Scan number 472
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set1_07
Pepti... 280.97

precursor information

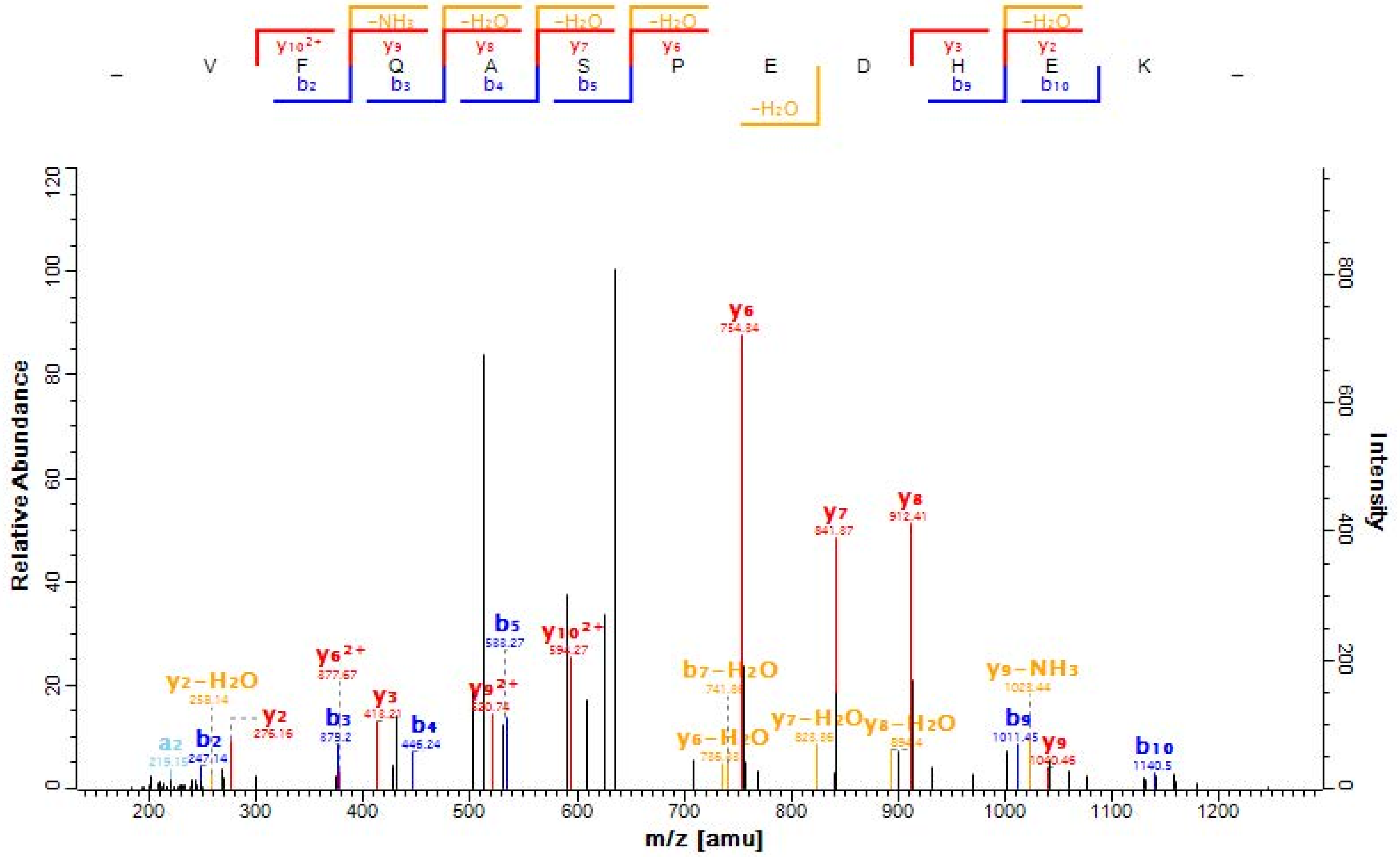
Mass:	1597.73243
m/z:	799.87349
Charge:	2+
Retentiontime:	7.7822284698486
Score:	280.9665
Mass Error [ppm]:	-0.49754
PEP:	1.6697E-73
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	66 %
Peak Coverage:	52 %
Protein Localisation:	30 ... 43

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	13				
	171.1128	2	V	12	1527.703		1527.703	
+0.107004	272.1605	3	T	11	1428.635	-0.07931	714.8211	+0.249552
+0.04845	401.2031	4	E	10	1327.587	-0.00295	664.2973	+0.188553
	529.2617	5	Q	9	1198.545	-0.00271	599.776	+0.228648
	586.2831	6	G	8	1070.486	-0.01396	535.7467	-0.4834
+0.09248	723.342	7	H	7	1013.465	-0.03595	507.236	+0.107658
-0.0203	852.3846	8	E	6	876.4058	+0.090648	876.4058	
+0.018436	965.4687	9	L	5	747.3632	+0.024293	747.3632	
	1052.501	10	S	4	634.2791	+0.061848	634.2791	
+0.064757	1166.544	11	N	3	547.2471	+0.036565	547.2471	
-0.02068	1295.586	12	E	2	433.2041	+0.043298	433.2041	
-0.06816	1424.629	13	E	1	304.1615	+0.111679	304.1615	
		14	R	0	175.119		175.119	

Scan number	489	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	129.82



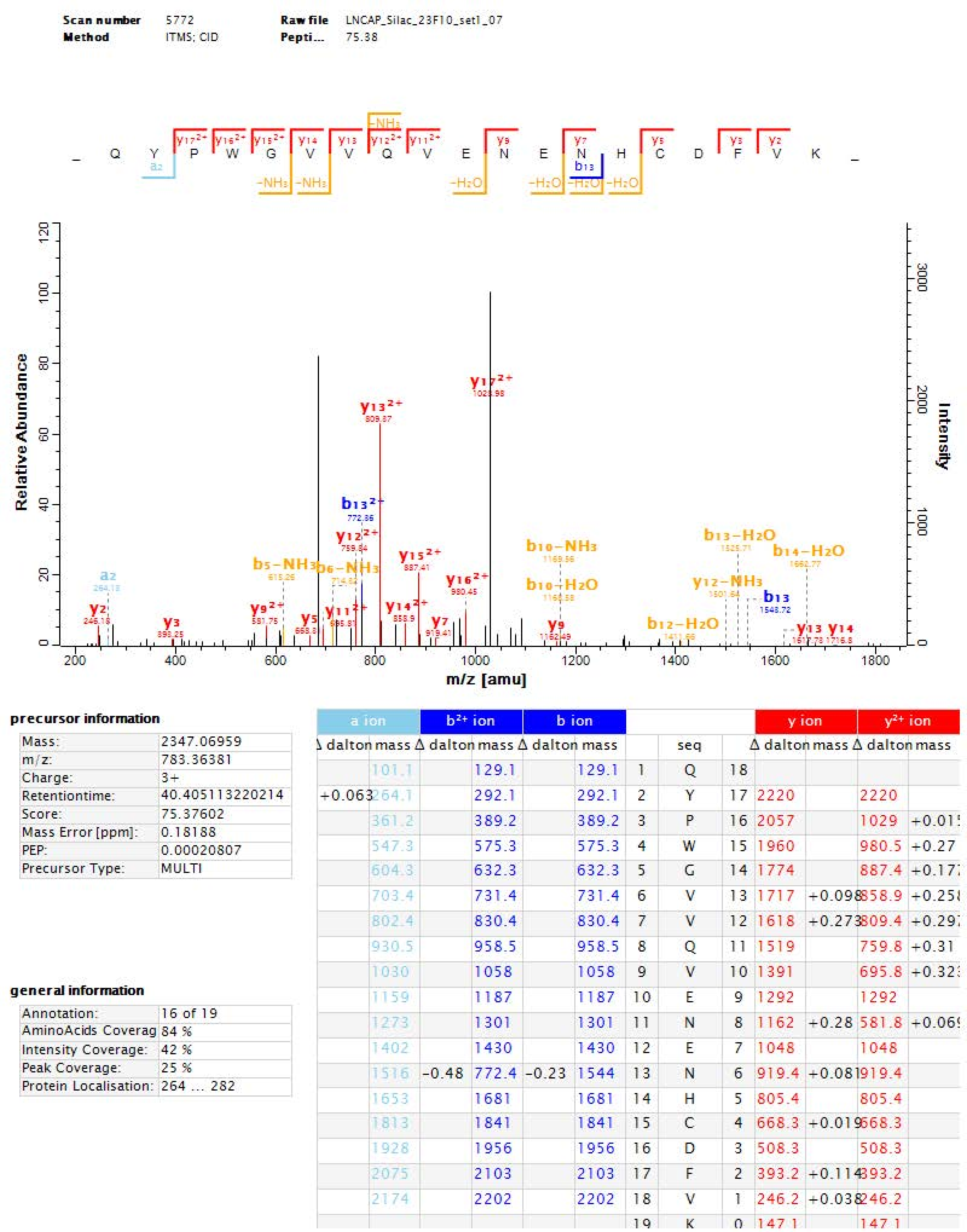
precursor information

Mass:	1285.59405
m/z:	643.8043
Charge:	2+
Retentiontime:	7.8962616920471
Score:	129.8187
Mass Error [ppm]:	0.13213
PEP:	0.0001863
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	40 %
Peak Coverage:	25 %
Protein Localisation:	75 ... 85

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.081		100.08	1	V	10				
+0.0375	219.15	-0.047	247.14	2	F	9	1187.5		594.27	+0.1436
	347.21	+0.1767	375.2	3	Q	8	1040.5	-0.001	520.74	+0.2561
	418.24	+0.0236	446.24	4	A	7	912.41	-0.065	912.41	
	505.28	+0.1226	533.27	5	S	6	841.37	+0.0178	841.37	
	602.33		630.32	6	P	5	754.34	+0.0315	377.67	+0.1887
	731.37		759.37	7	E	4	657.28		657.28	
	846.4		874.39	8	D	3	528.24		528.24	
	983.46	+0.0868	1011.5	9	H	2	413.21	+0.0126	413.21	
	1112.5	+0.1222	1140.5	10	E	1	276.16	+0.1745	276.16	
				11	K	0	147.11		147.11	



Scan number	5772	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	75.38

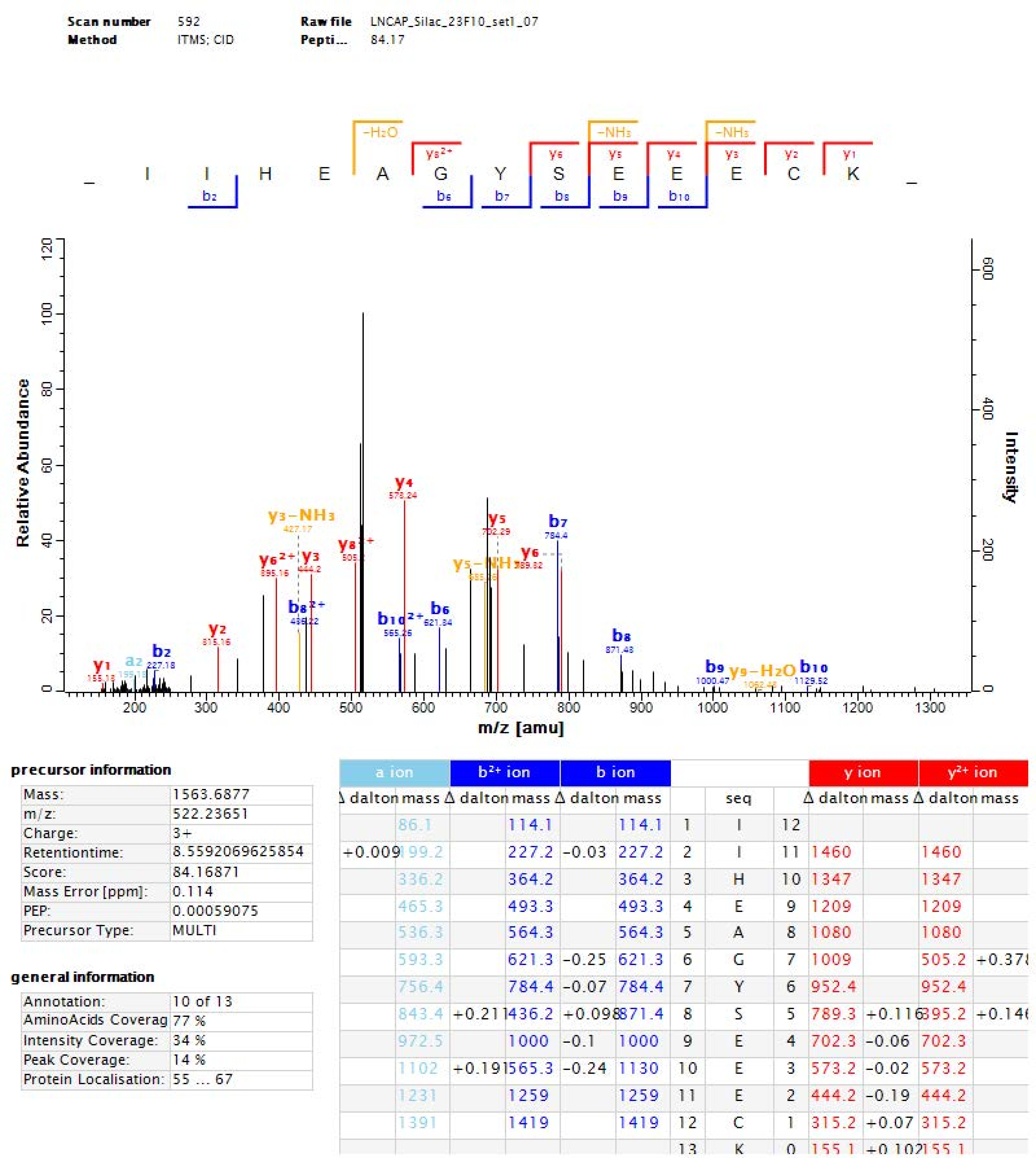
precursor information

Mass:	2347.06959
m/z:	783.36381
Charge:	3+
Retentiontime:	40.405113220214
Score:	75.37602
Mass Error [ppm]:	0.18188
PEP:	0.00020807
Precursor Type:	MULTI

general information

Annotation:	16 of 19
AminoAcids Coverag	84 %
Intensity Coverage:	42 %
Peak Coverage:	25 %
Protein Localisation:	264 ... 282

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	101.1		129.1		129.1	1	Q	18				
+0.063	264.1		292.1		292.1	2	Y	17	2220		2220	
	361.2		389.2		389.2	3	P	16	2057		1029	+0.01
	547.3		575.3		575.3	4	W	15	1960		980.5	+0.27
	604.3		632.3		632.3	5	G	14	1774		887.4	+0.17
	703.4		731.4		731.4	6	V	13	1717	+0.098	858.9	+0.25
	802.4		830.4		830.4	7	V	12	1618	+0.273	809.4	+0.29
	930.5		958.5		958.5	8	Q	11	1519		759.8	+0.31
	1030		1058		1058	9	V	10	1391		695.8	+0.32
	1159		1187		1187	10	E	9	1292		1292	
	1273		1301		1301	11	N	8	1162	+0.28	581.8	+0.06
	1402		1430		1430	12	E	7	1048		1048	
	1516	-0.48	772.4	-0.23	1544	13	N	6	919.4	+0.081	919.4	
	1653		1681		1681	14	H	5	805.4		805.4	
	1813		1841		1841	15	C	4	668.3	+0.019	668.3	
	1928		1956		1956	16	D	3	508.3		508.3	
	2075		2103		2103	17	F	2	393.2	+0.114	393.2	
	2174		2202		2202	18	V	1	246.2	+0.038	246.2	
						19	K	0	147.1		147.1	



Scan number	592	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	84.17

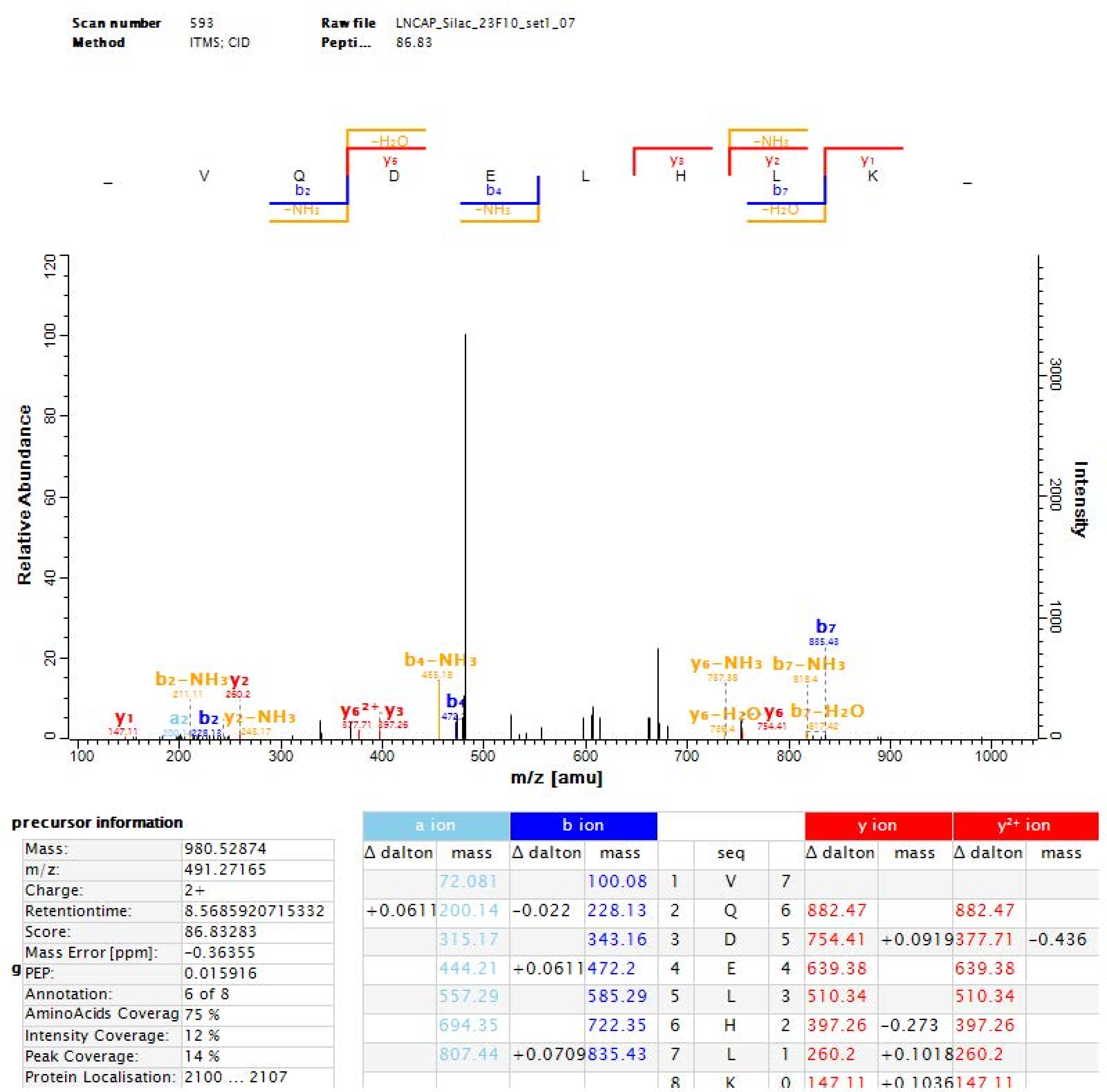
precursor information

Mass:	1563.6877
m/z:	522.23651
Charge:	3+
Retentiontime:	8.5592069625854
Score:	84.16871
Mass Error [ppm]:	0.114
PEP:	0.00059075
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	34 %
Peak Coverage:	14 %
Protein Localisation:	55 ... 67

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	I	12				
+0.009	199.2		227.2	-0.03	227.2	2	I	11	1460		1460	
	336.2		364.2		364.2	3	H	10	1347		1347	
	465.3		493.3		493.3	4	E	9	1209		1209	
	536.3		564.3		564.3	5	A	8	1080		1080	
	593.3		621.3	-0.25	621.3	6	G	7	1009		505.2	+0.37
	756.4		784.4	-0.07	784.4	7	Y	6	952.4		952.4	
	843.4	+0.211	436.2	+0.098	871.4	8	S	5	789.3	+0.116	395.2	+0.14
	972.5		1000	-0.1	1000	9	E	4	702.3	-0.06	702.3	
	1102	+0.191	565.3	-0.24	1130	10	E	3	573.2	-0.02	573.2	
	1231		1259		1259	11	E	2	444.2	-0.19	444.2	
	1391		1419		1419	12	C	1	315.2	+0.07	315.2	
						13	K	0	155.1	+0.102	155.1	



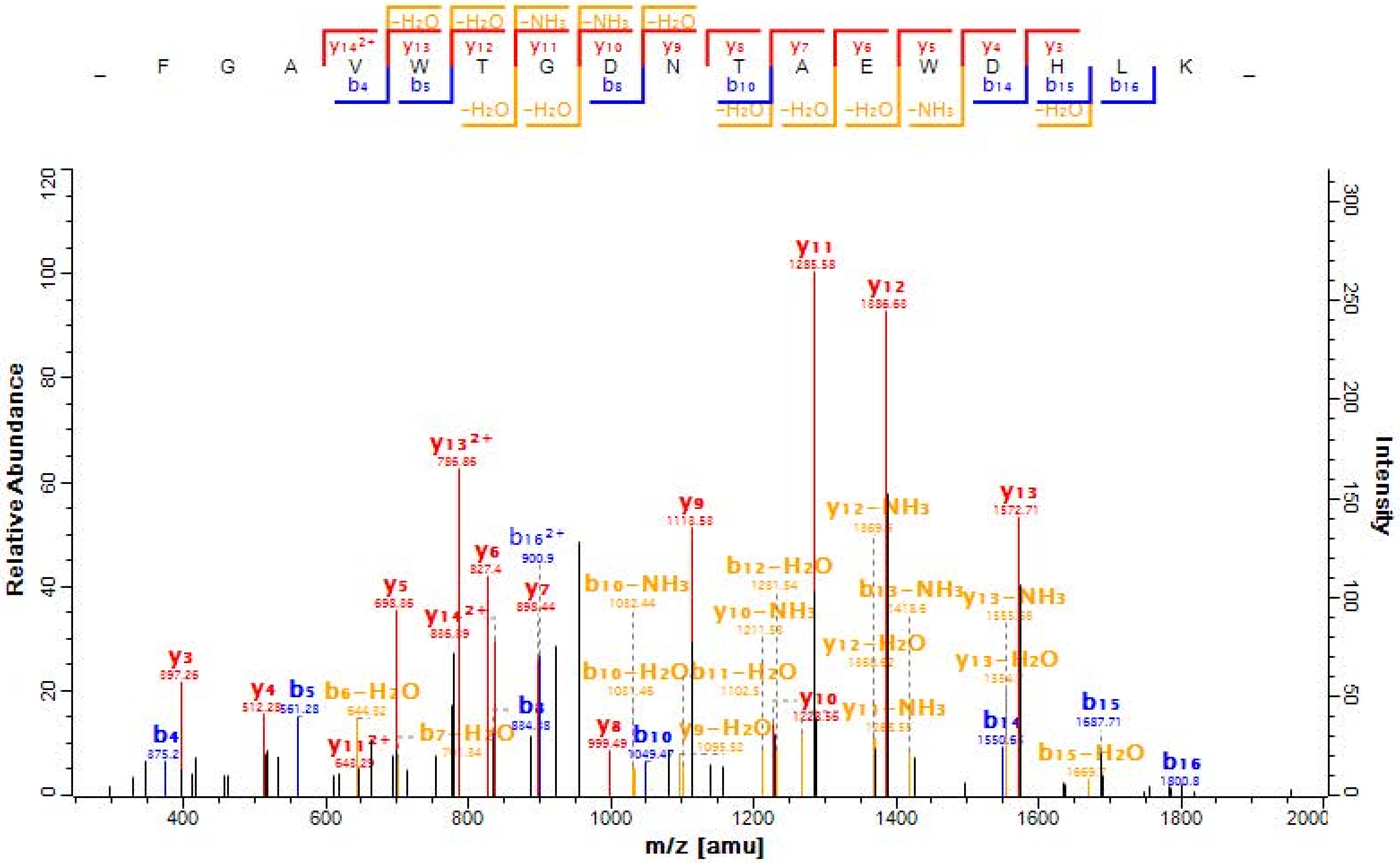
Scan number	593	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	86.83

precursor information

Mass:	980.52874
m/z:	491.27165
Charge:	2+
Retentiontime:	8.5685920715332
Score:	86.83283
Mass Error [ppm]:	-0.36355
PEP:	0.015916
Annotation:	6 of 8
AminoAcids Coverag	75 %
Intensity Coverage:	12 %
Peak Coverage:	14 %
Protein Localisation:	2100 ... 2107

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.081		100.08	1	V	7				
+0.0611	200.14	-0.022	228.13	2	Q	6	882.47		882.47	
	315.17		343.16	3	D	5	754.41	+0.0919	377.71	-0.436
	444.21	+0.0611	472.2	4	E	4	639.38		639.38	
	557.29		585.29	5	L	3	510.34		510.34	
	694.35		722.35	6	H	2	397.26	-0.273	397.26	
	807.44	+0.0709	835.43	7	L	1	260.2	+0.1018	260.2	
				8	K	0	147.11	+0.1036	147.11	

Scan number	5999	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	190.11



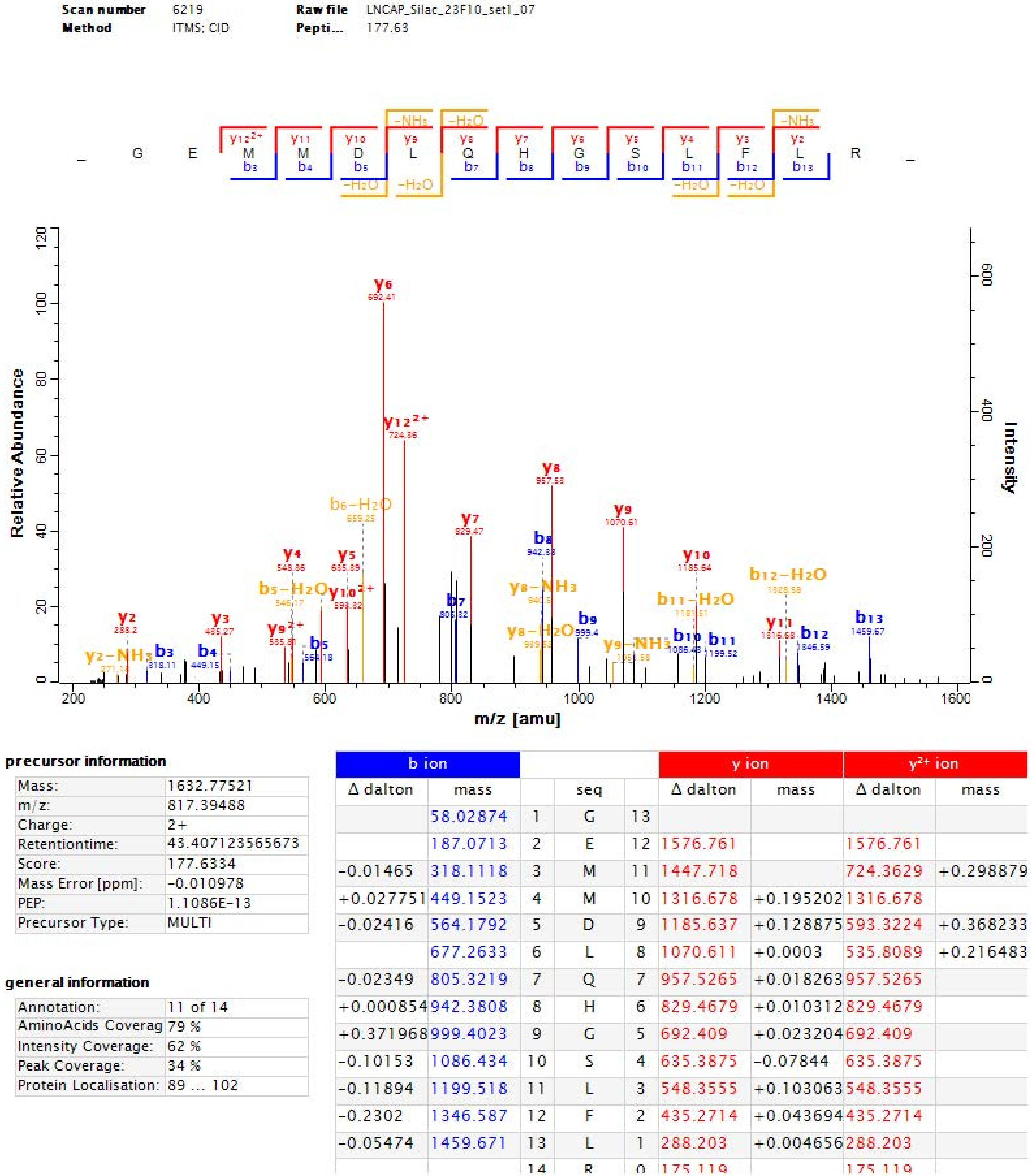
precursor information

Mass:	1945.89749
m/z:	973.95602
Charge:	2+
Retentiontime:	41.896690368652
Score:	190.1081
Mass Error [ppm]:	0.82819
PEP:	6.7079E-34
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	57 %
Peak Coverage:	41 %
Protein Localisation:	662 ... 678

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.08		148.08	1	F	16				
	205.1		205.1	2	G	15	1799.8		1799.8	
	276.13		276.13	3	A	14	1742.8		1742.8	
	375.2	+0.1115	375.2	4	V	13	1671.8		836.39	+0.2076
	561.28	+0.096	561.28	5	W	12	1572.7	-0.04	786.86	+0.3021
	662.33		662.33	6	T	11	1386.6	+0.0018	1386.6	
	719.35		719.35	7	G	10	1285.6	+0.0018	643.29	-0.103
	834.38	+0.0841	834.38	8	D	9	1228.6	+0.0913	1228.6	
	948.42		948.42	9	N	8	1113.5	+0.0502	1113.5	
	1049.5	-0.064	1049.5	10	T	7	999.49	+0.0181	999.49	
	1120.5		1120.5	11	A	6	898.44	-0.005	898.44	
	1249.5		1249.5	12	E	5	827.4	+0.1541	827.4	
	1435.6		1435.6	13	W	4	698.36	+0.1711	698.36	
	1550.7	-0.137	1550.7	14	D	3	512.28	+0.0625	512.28	
	1687.7	+0.0761	1687.7	15	H	2	397.26	+0.0943	397.26	
-0.135	900.9	-0.041	1800.8	16	L	1	260.2		260.2	
				17	K	0	147.11		147.11	



Scan number	6219	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	177.63

precursor information

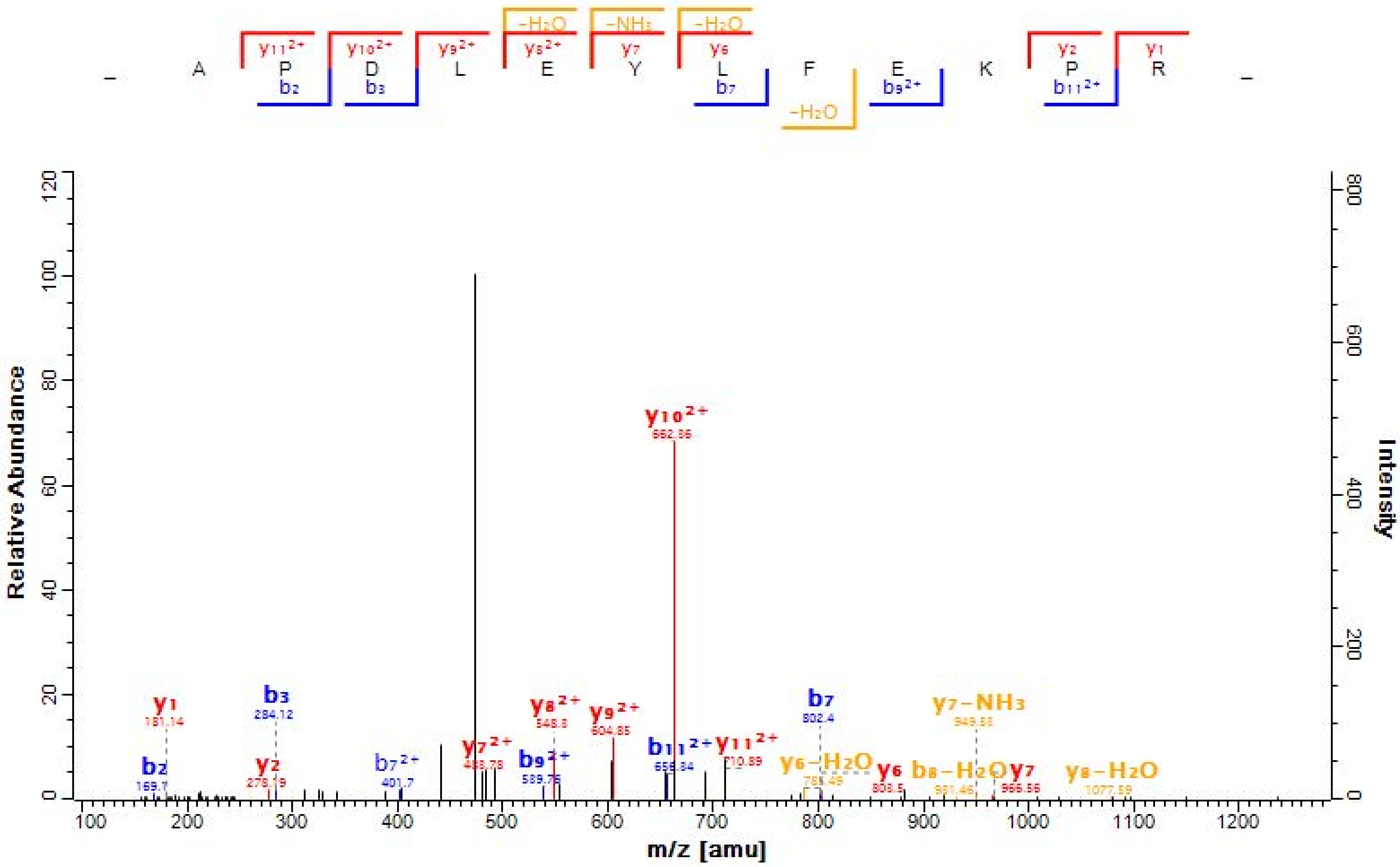
Mass:	1632.77521
m/z:	817.39488
Charge:	2+
Retentiontime:	43.407123565673
Score:	177.6334
Mass Error [ppm]:	-0.010978
PEP:	1.1086E-13
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	62 %
Peak Coverage:	34 %
Protein Localisation:	89 ... 102

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	13				
	187.0713	2	E	12	1576.761		1576.761	
-0.01465	318.1118	3	M	11	1447.718		724.3629	+0.298879
+0.027751	449.1523	4	M	10	1316.678	+0.195202	1316.678	
-0.02416	564.1792	5	D	9	1185.637	+0.128875	593.3224	+0.368233
	677.2633	6	L	8	1070.611	+0.0003	535.8089	+0.216483
-0.02349	805.3219	7	Q	7	957.5265	+0.018263	957.5265	
+0.000854	942.3808	8	H	6	829.4679	+0.010312	829.4679	
+0.371968	999.4023	9	G	5	692.409	+0.023204	692.409	
-0.10153	1086.434	10	S	4	635.3875	-0.07844	635.3875	
-0.11894	1199.518	11	L	3	548.3555	+0.103063	548.3555	
-0.2302	1346.587	12	F	2	435.2714	+0.043694	435.2714	
-0.05474	1459.671	13	L	1	288.203	+0.004656	288.203	
		14	R	0	175.119		175.119	

Scan number 6252 **Raw file** LNCAP_Silac_23F10_set1_07
Method ITMS; CID **Pepti...** 99.57



precursor information

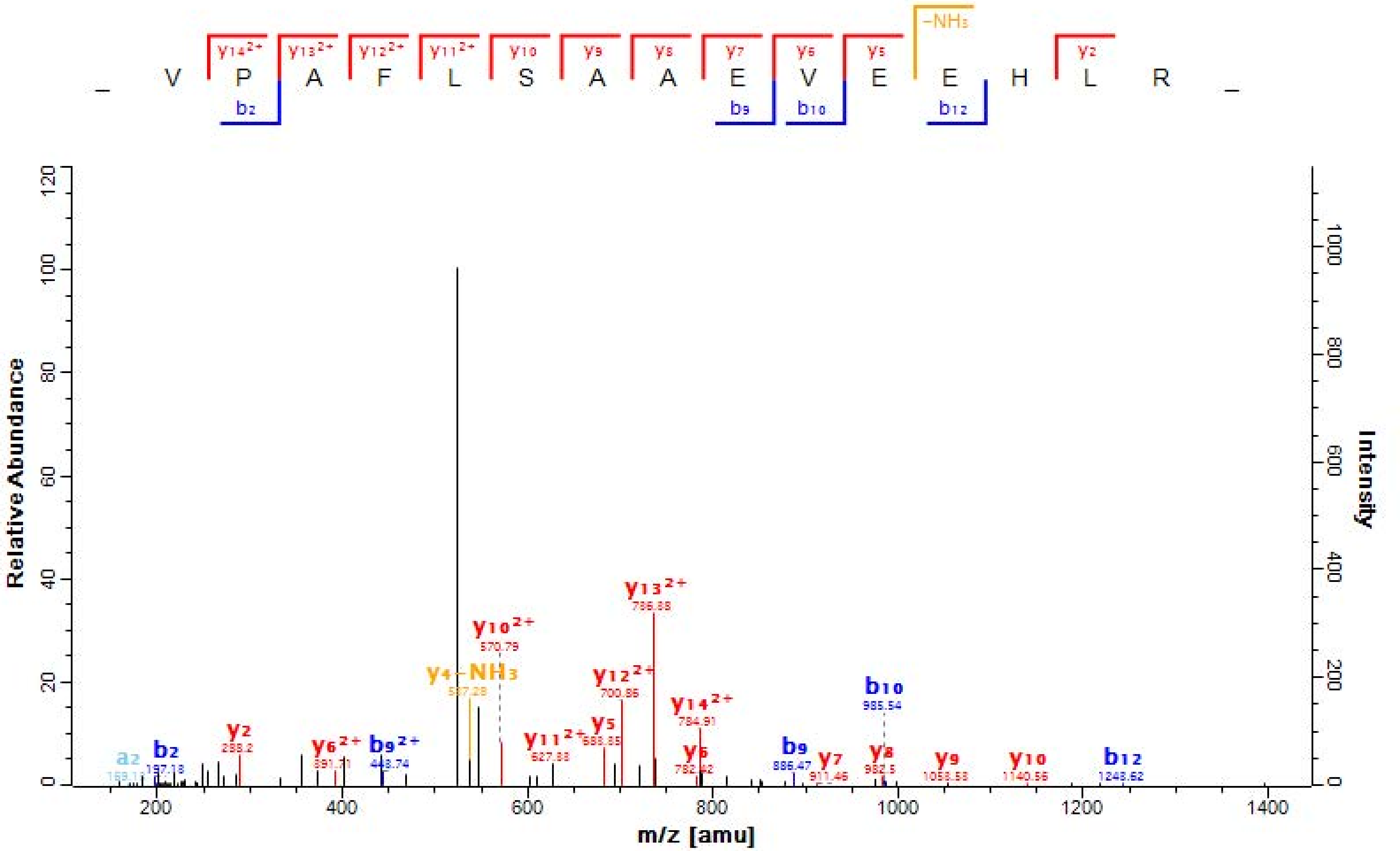
Mass:	1494.81219
m/z:	499.27801
Charge:	3+
Retentiontime:	43.644962310791
Score:	99.56806
Mass Error [ppm]:	-0.42974
PEP:	0.00048726
Precursor Type:	ISO

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	38 %
Peak Coverage:	18 %
Protein Localisation:	155 ... 166

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	11				
	169.1	+0.0905	169.1	2	P	10	1420.8		710.89	-0.006
	284.12	+0.0343	284.12	3	D	9	1323.7		662.36	+0.2183
	397.21		397.21	4	L	8	1208.7		604.85	+0.2891
	526.25		526.25	5	E	7	1095.6		548.3	+0.308
	689.31		689.31	6	Y	6	966.56	-0.13	483.78	-0.123
+0.268	401.7	-0.012	802.4	7	L	5	803.5	-0.219	803.5	
	949.47		949.47	8	F	4	690.41		690.41	
-0.418	539.76		1078.5	9	E	3	543.34		543.34	
	1214.6		1214.6	10	K	2	414.3		414.3	
-0.266	656.34		1311.7	11	P	1	278.19	-0.392	278.19	
				12	R	0	181.14	-0.118	181.14	

Scan number	6771	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	96.46



precursor information

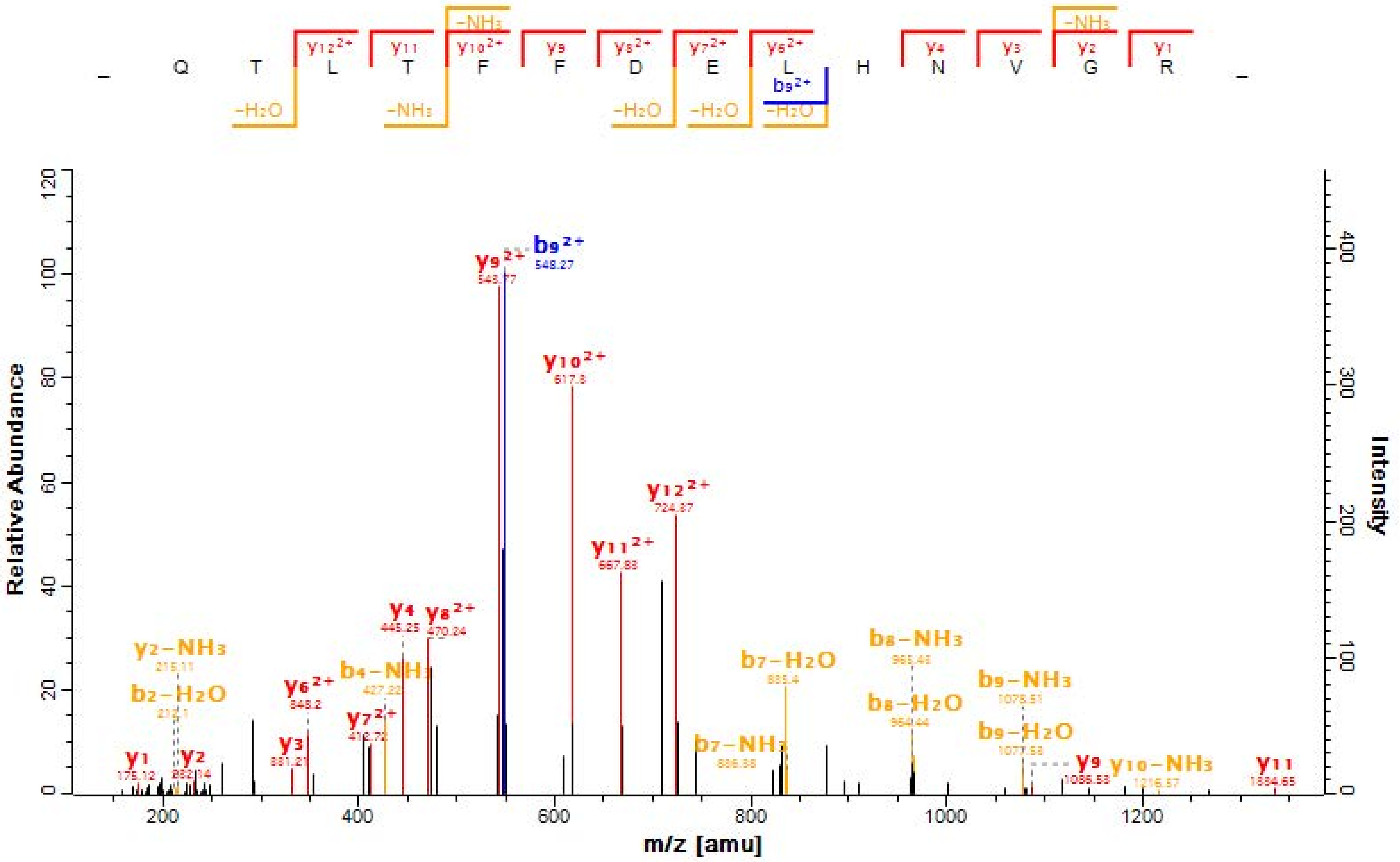
Mass:	1666.86865
m/z:	556.63016
Charge:	3+
Retentiontime:	47.334087371826
Score:	96.46406
Mass Error [ppm]:	0.4657
PEP:	0.0016412
Precursor Type:	ISO

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	35 %
Peak Coverage:	20 %
Protein Localisation:	4 ... 18

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.08		100.1		100.1	1	V	14				
+0.035	169.1		197.1	-0.11	197.1	2	P	13	1569		784.9	+0.31
	240.2		268.2		268.2	3	A	12	1472		736.4	+0.28
	387.2		415.2		415.2	4	F	11	1401		700.9	+0.31
	500.3		528.3		528.3	5	L	10	1254		627.3	+0.02
	587.4		615.4		615.4	6	S	9	1141	+0.078	570.8	+0.24
	658.4		686.4		686.4	7	A	8	1054	-0.22	1054	
	729.4		757.4		757.4	8	A	7	982.5	+0.34	982.5	
	858.5	-0.34	443.7	+0.144	886.5	9	E	6	911.5	+0.079	911.5	
	957.5		985.5	-0.33	985.5	10	V	5	782.4	+0.139	391.7	-0.04
	1087		1115		1115	11	E	4	683.3	+0.036	683.3	
	1216		1244	-0.12	1244	12	E	3	554.3		554.3	
	1353		1381		1381	13	H	2	425.3		425.3	
	1466		1494		1494	14	L	1	288.2	+0.017	288.2	
						15	R	0	175.1		175.1	

Scan number	6867	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	91.96



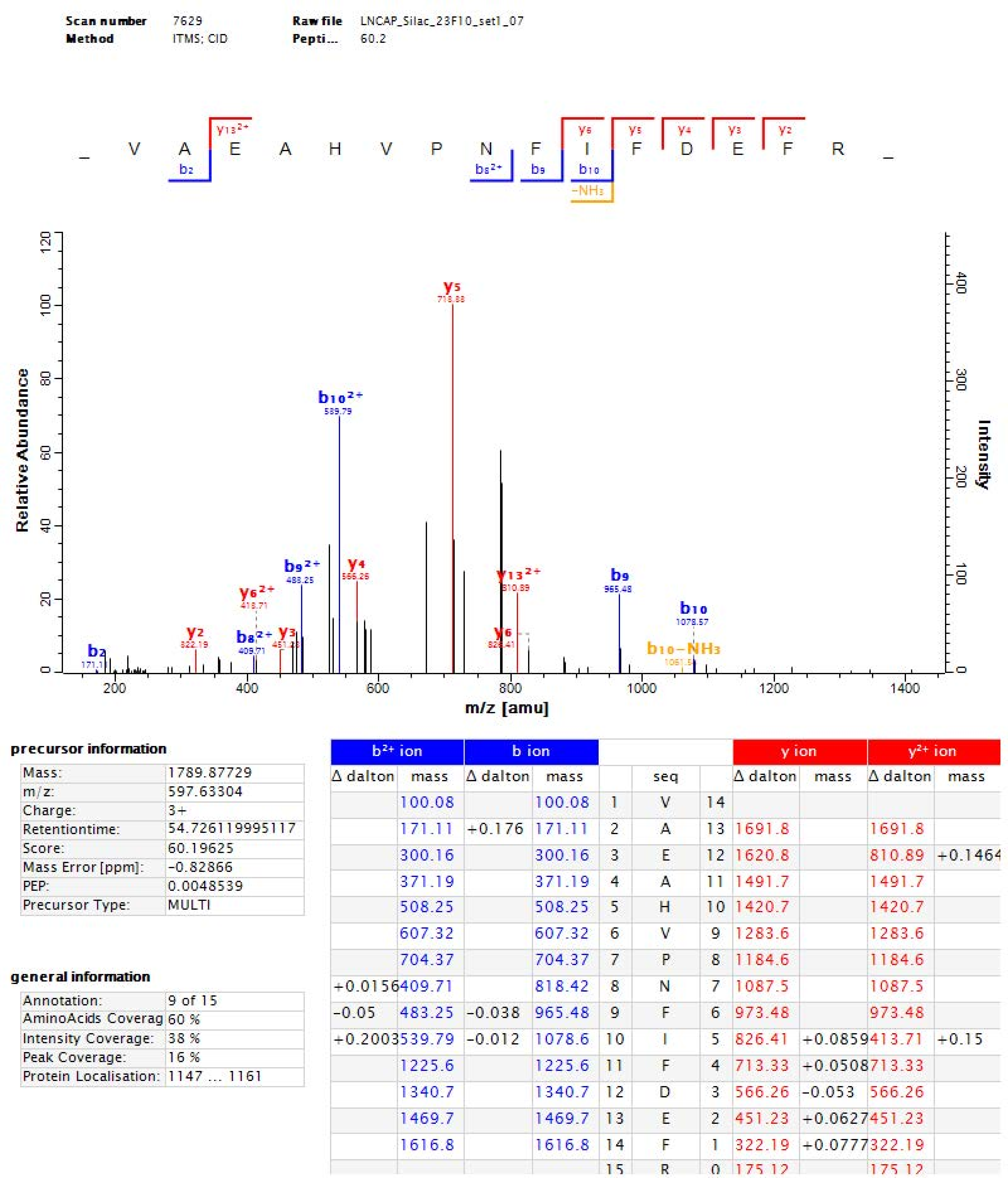
precursor information

Mass:	1675.83251
m/z:	559.61811
Charge:	3+
Retentiontime:	48.053188323974
Score:	91.96123
Mass Error [ppm]:	0.4142
PEP:	0.00027225
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	57 %
Peak Coverage:	25 %
Protein Localisation:	154 ... 167

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.07		129.07	1	Q	13				
	230.11		230.11	2	T	12	1548.8		1548.8	
	343.2		343.2	3	L	11	1447.7		724.37	+0.3287
	444.25		444.25	4	T	10	1334.6	-0.218	667.83	+0.1765
	591.31		591.31	5	F	9	1233.6		617.3	+0.2802
	738.38		738.38	6	F	8	1086.5	+0.0391	543.77	+0.1958
	853.41		853.41	7	D	7	939.46		470.24	-0.143
	982.45		982.45	8	E	6	824.44		412.72	+0.0137
+0.087	548.27		1095.5	9	L	5	695.39		348.2	+0.0034
	1232.6		1232.6	10	H	4	582.31		582.31	
	1346.6		1346.6	11	N	3	445.25	+0.0695	445.25	
	1445.7		1445.7	12	V	2	331.21	-0.156	331.21	
	1502.7		1502.7	13	G	1	232.14	+0.0263	232.14	
				14	R	0	175.12	-0.035	175.12	



Scan number	7629	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	60.2

precursor information

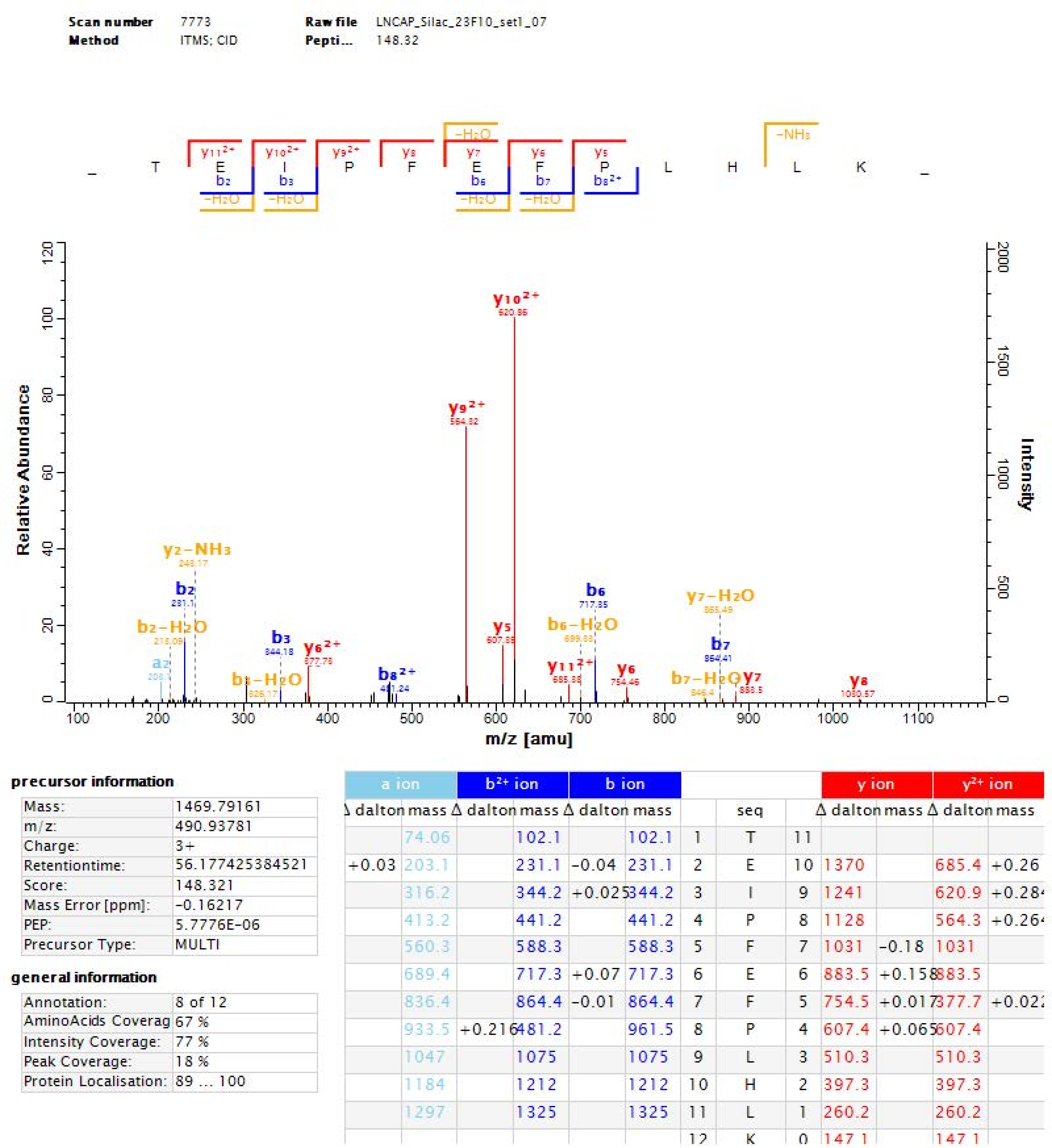
Mass:	1789.87729
m/z:	597.63304
Charge:	3+
Retentiontime:	54.726119995117
Score:	60.19625
Mass Error [ppm]:	-0.82866
PEP:	0.0048539
Precursor Type:	MULTI

general information

Annotation:	9 of 15
AminoAcids Coverag	60 %
Intensity Coverage:	38 %
Peak Coverage:	16 %
Protein Localisation:	1147 ... 1161

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	14				
	171.11	+0.176	171.11	2	A	13	1691.8		1691.8	
	300.16		300.16	3	E	12	1620.8		810.89	+0.1464
	371.19		371.19	4	A	11	1491.7		1491.7	
	508.25		508.25	5	H	10	1420.7		1420.7	
	607.32		607.32	6	V	9	1283.6		1283.6	
	704.37		704.37	7	P	8	1184.6		1184.6	
+0.0156	409.71		818.42	8	N	7	1087.5		1087.5	
-0.05	483.25	-0.038	965.48	9	F	6	973.48		973.48	
+0.2003	539.79	-0.012	1078.6	10	I	5	826.41	+0.0859	413.71	+0.15
	1225.6		1225.6	11	F	4	713.33	+0.0508	713.33	
	1340.7		1340.7	12	D	3	566.26	-0.053	566.26	
	1469.7		1469.7	13	E	2	451.23	+0.0627	451.23	
	1616.8		1616.8	14	F	1	322.19	+0.0777	322.19	
				15	R	0	175.12		175.12	

Scan number	7773	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	148.32



precursor information

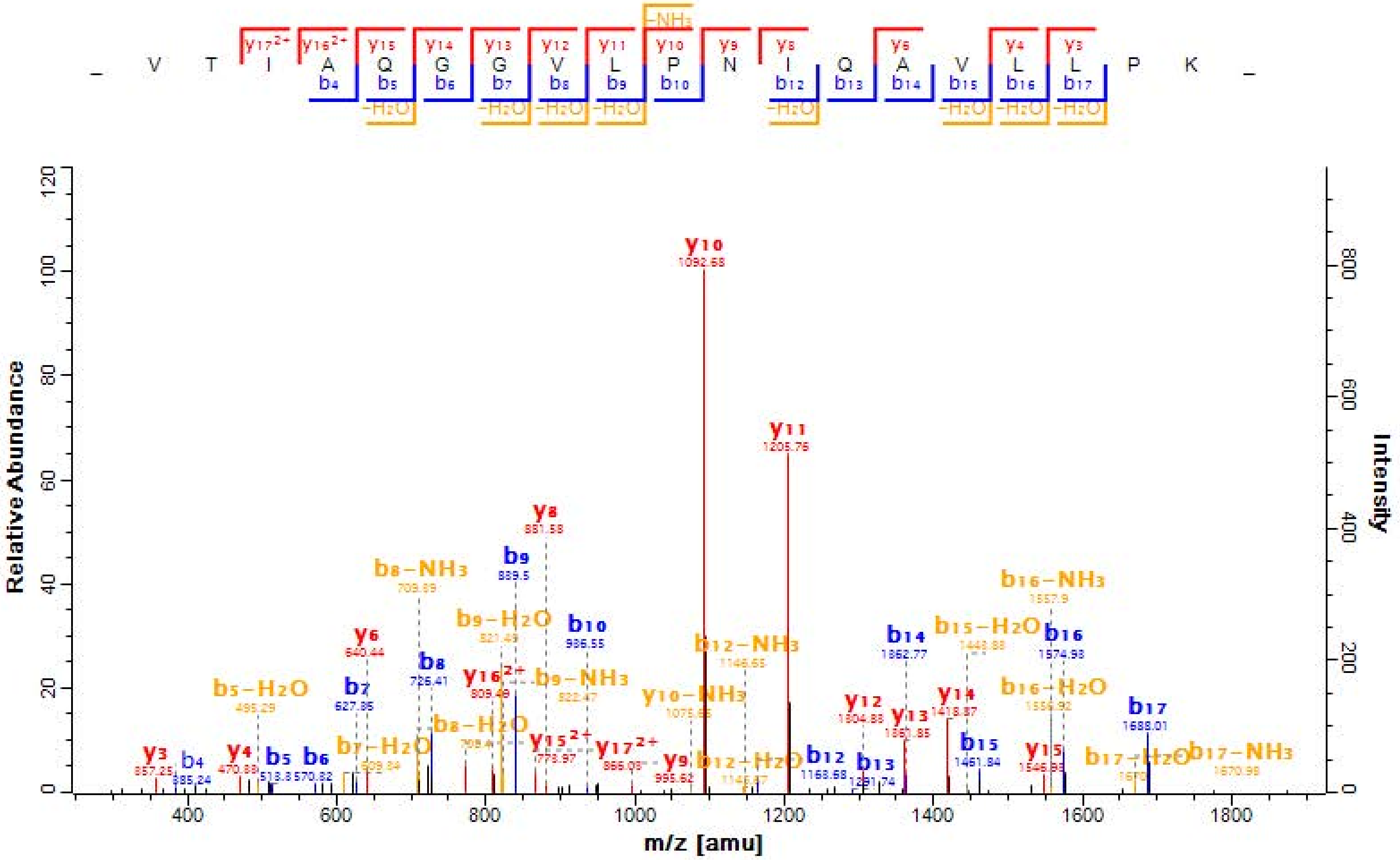
Mass:	1469.79161
m/z:	490.93781
Charge:	3+
Retentiontime:	56.177425384521
Score:	148.321
Mass Error [ppm]:	-0.16217
PEP:	5.7776E-06
Precursor Type:	MULTI

general information

Annotation:	8 of 12
AminoAcids Coverag	67 %
Intensity Coverage:	77 %
Peak Coverage:	18 %
Protein Localisation:	89 ... 100

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.1		102.1	1	T	11				
+0.03	203.1		231.1	-0.04	231.1	2	E	10	1370		685.4	+0.26
	316.2		344.2	+0.025	344.2	3	I	9	1241		620.9	+0.28
	413.2		441.2		441.2	4	P	8	1128		564.3	+0.26
	560.3		588.3		588.3	5	F	7	1031	-0.18	1031	
	689.4		717.3	+0.07	717.3	6	E	6	883.5	+0.158	883.5	
	836.4		864.4	-0.01	864.4	7	F	5	754.5	+0.017	377.7	+0.02
	933.5	+0.216	481.2		961.5	8	P	4	607.4	+0.065	607.4	
	1047		1075		1075	9	L	3	510.3		510.3	
	1184		1212		1212	10	H	2	397.3		397.3	
	1297		1325		1325	11	L	1	260.2		260.2	
						12	K	0	147.1		147.1	

Scan number	8373	**Raw file**	LNCAP_Silac_23F10_set1_07
Method	ITMS; CID	**Pepti...**	237.46



precursor information

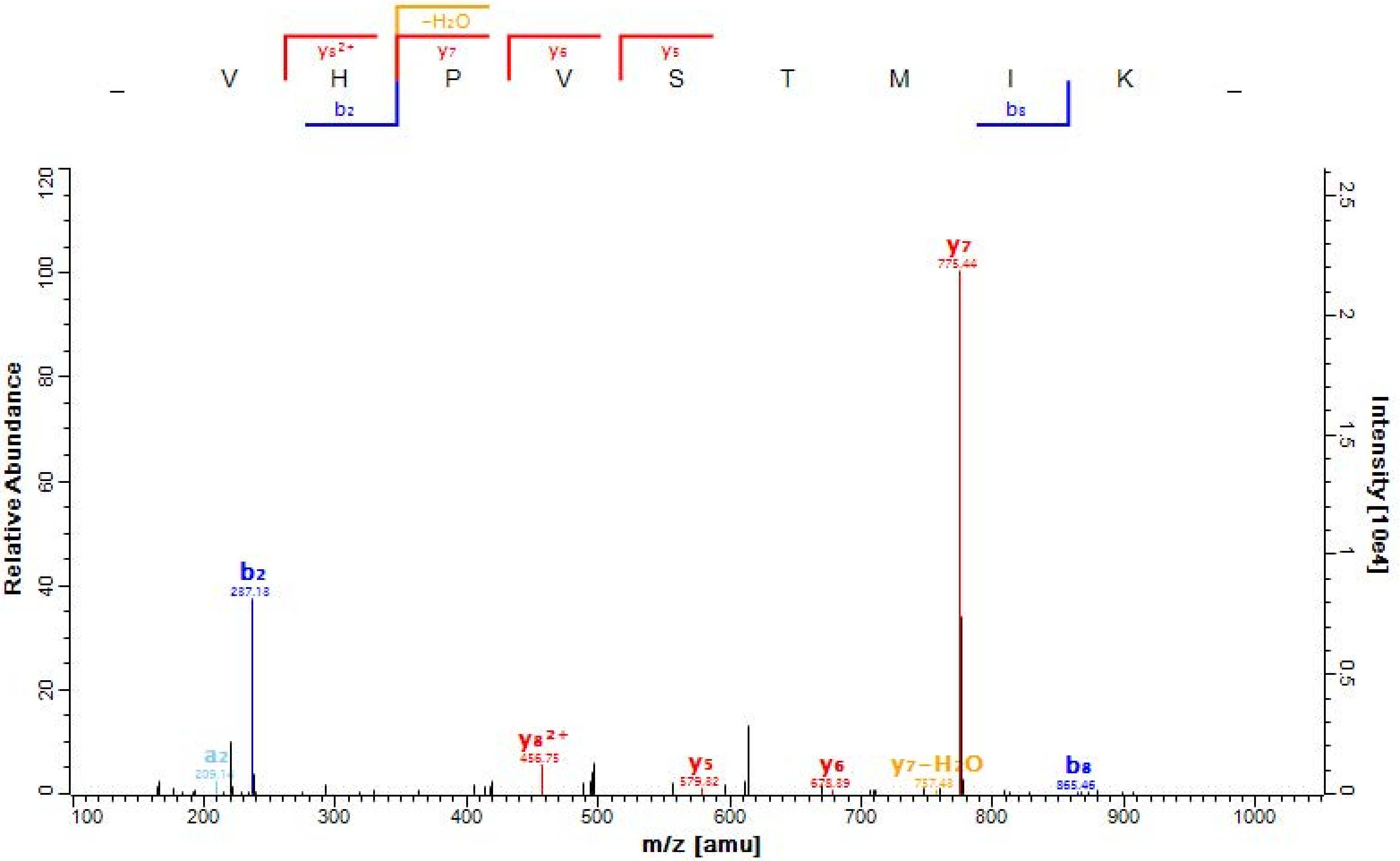
Mass:	1930.16157
m/z:	966.08806
Charge:	2+
Retentiontime:	62.929134368896
Score:	237.4612
Mass Error [ppm]:	0.020742
PEP:	1.7643E-65
Precursor Type:	MULTI

general information

Annotation:	15 of 19
AminoAcids Coverag	79 %
Intensity Coverage:	75 %
Peak Coverage:	47 %
Protein Localisation:	101 ... 119

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	18				
	201.1234	2	T	17	1832.1		1832.1	
	314.2074	3	I	16	1731.053		866.03	+0.212862
-0.10014	385.2445	4	A	15	1617.969		809.488	+0.226513
+0.037818	513.3031	5	Q	14	1546.932	+0.037577	773.9694	+0.124281
+0.151975	570.3246	6	G	13	1418.873	-0.12845	1418.873	
+0.093707	627.3461	7	G	12	1361.851	-0.1026	1361.851	
-0.01084	726.4145	8	V	11	1304.83	-0.13814	1304.83	
-0.03869	839.4985	9	L	10	1205.762	-0.08755	1205.762	
+0.018836	936.5513	10	P	9	1092.678	-0.06379	1092.678	
	1050.594	11	N	8	995.6248	+0.337671	995.6248	
-0.32672	1163.678	12	I	7	881.5819	-0.07851	881.5819	
-0.04851	1291.737	13	Q	6	768.4978		768.4978	
-0.01506	1362.774	14	A	5	640.4392	-0.00685	640.4392	
-0.11314	1461.842	15	V	4	569.4021		569.4021	
-0.30231	1574.926	16	L	3	470.3337	-0.07961	470.3337	
-0.22915	1688.011	17	L	2	357.2496	+0.117617	357.2496	
	1785.063	18	P	1	244.1656		244.1656	
		19	K	0	147.1128		147.1128	

Scan number	1114	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	36.38

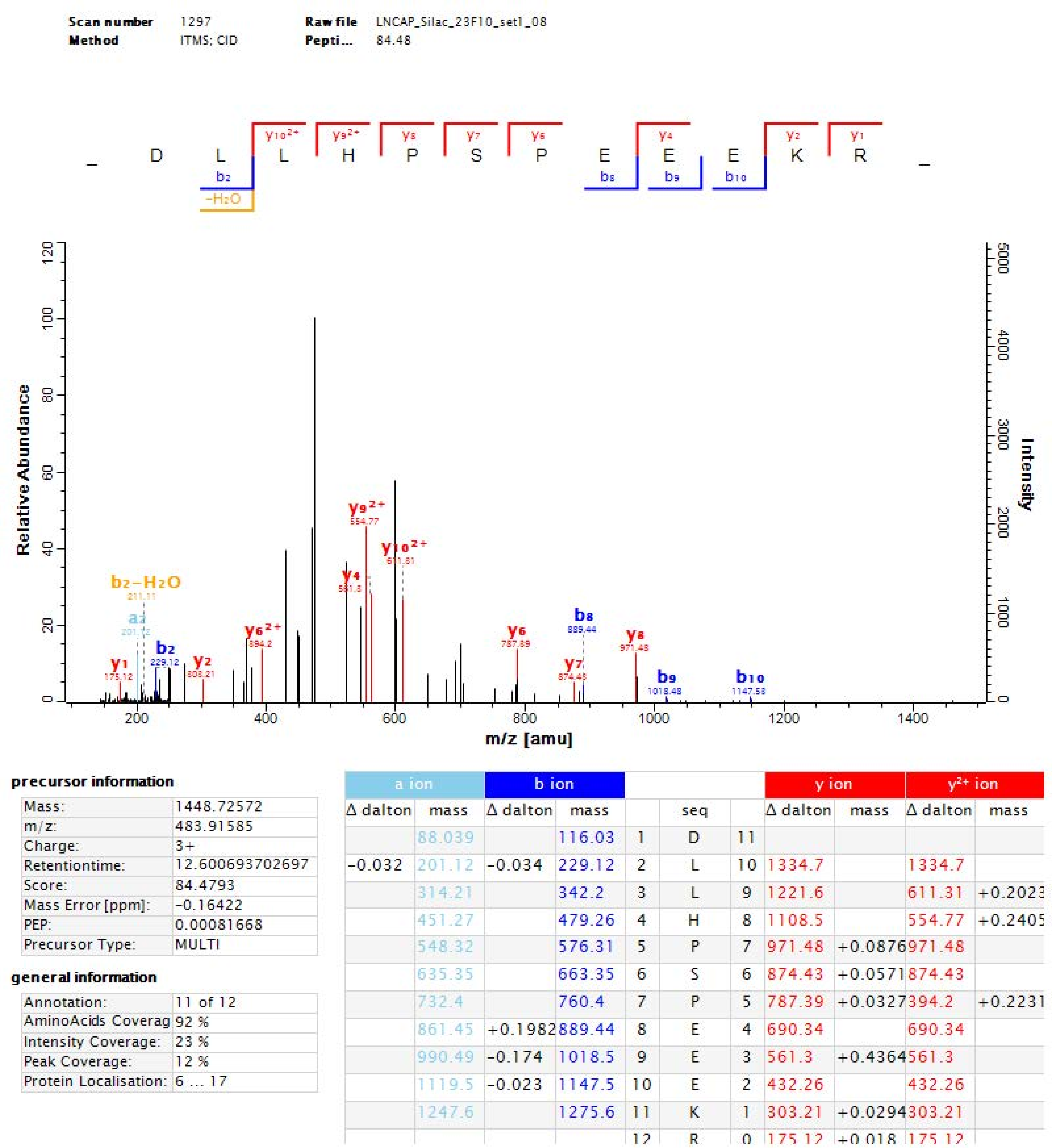


precursor information

Mass:	1010.55862
m/z:	506.28659
Charge:	2+
Retentiontime:	11.468678474426
Score:	36.38147
Mass Error [ppm]:	0.33168
PEP:	0.11773
Precursor Type:	MULTI
Annotation:	5 of 9
AminoAcids Coverag	56 %
Intensity Coverage:	55 %
Peak Coverage:	10 %
Protein Localisation:	299 ... 307

g

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.081		100.08	1	V	8				
-0.019	209.14	-0.002	237.13	2	H	7	912.5		456.75	+0.332
	306.19		334.19	3	P	6	775.44	+0.0284	775.44	
	405.26		433.26	4	V	5	678.39	+0.0249	678.39	
	492.29		520.29	5	S	4	579.32	+0.0324	579.32	
	593.34		621.34	6	T	3	492.29		492.29	
	724.38		752.38	7	M	2	391.24		391.24	
	837.47	-0.145	865.46	8	I	1	260.2		260.2	
				9	K	0	147.11		147.11	



Scan number	1297	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	84.48

precursor information

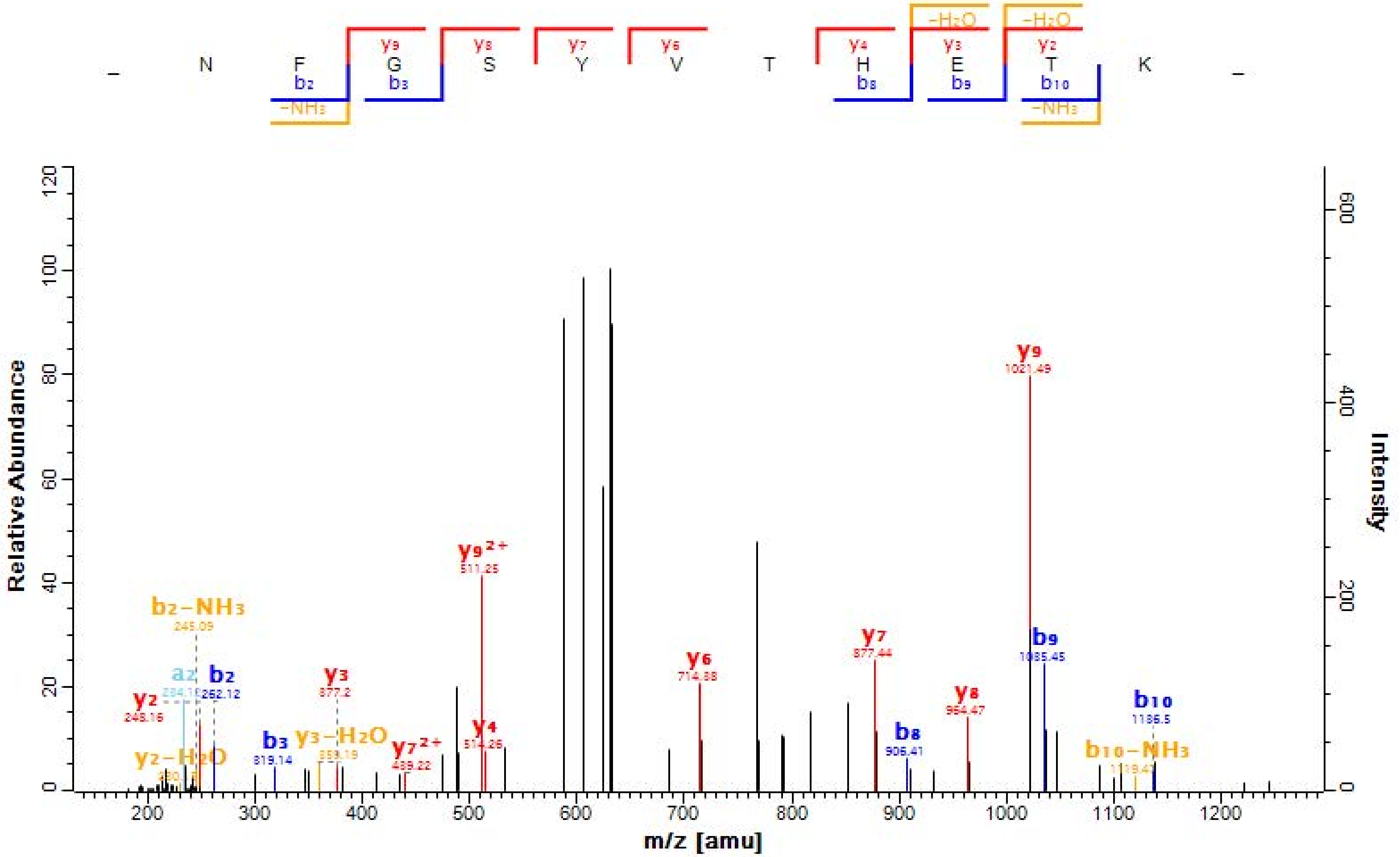
Mass:	1448.72572
m/z:	483.91585
Charge:	3+
Retentiontime:	12.600693702697
Score:	84.4793
Mass Error [ppm]:	-0.16422
PEP:	0.00081668
Precursor Type:	MULTI

general information

Annotation:	11 of 12
AminoAcids Coverag	92 %
Intensity Coverage:	23 %
Peak Coverage:	12 %
Protein Localisation:	6 ... 17

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	11				
-0.032	201.12	-0.034	229.12	2	L	10	1334.7		1334.7	
	314.21		342.2	3	L	9	1221.6		611.31	+0.2023
	451.27		479.26	4	H	8	1108.5		554.77	+0.2405
	548.32		576.31	5	P	7	971.48	+0.0876	971.48	
	635.35		663.35	6	S	6	874.43	+0.0571	874.43	
	732.4		760.4	7	P	5	787.39	+0.0327	394.2	+0.2231
	861.45	+0.1982	889.44	8	E	4	690.34		690.34	
	990.49	-0.174	1018.5	9	E	3	561.3	+0.4364	561.3	
	1119.5	-0.023	1147.5	10	E	2	432.26		432.26	
	1247.6		1275.6	11	K	1	303.21	+0.0294	303.21	
				12	R	0	175.12	+0.018	175.12	

Scan number	1552	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	105.03



precursor information

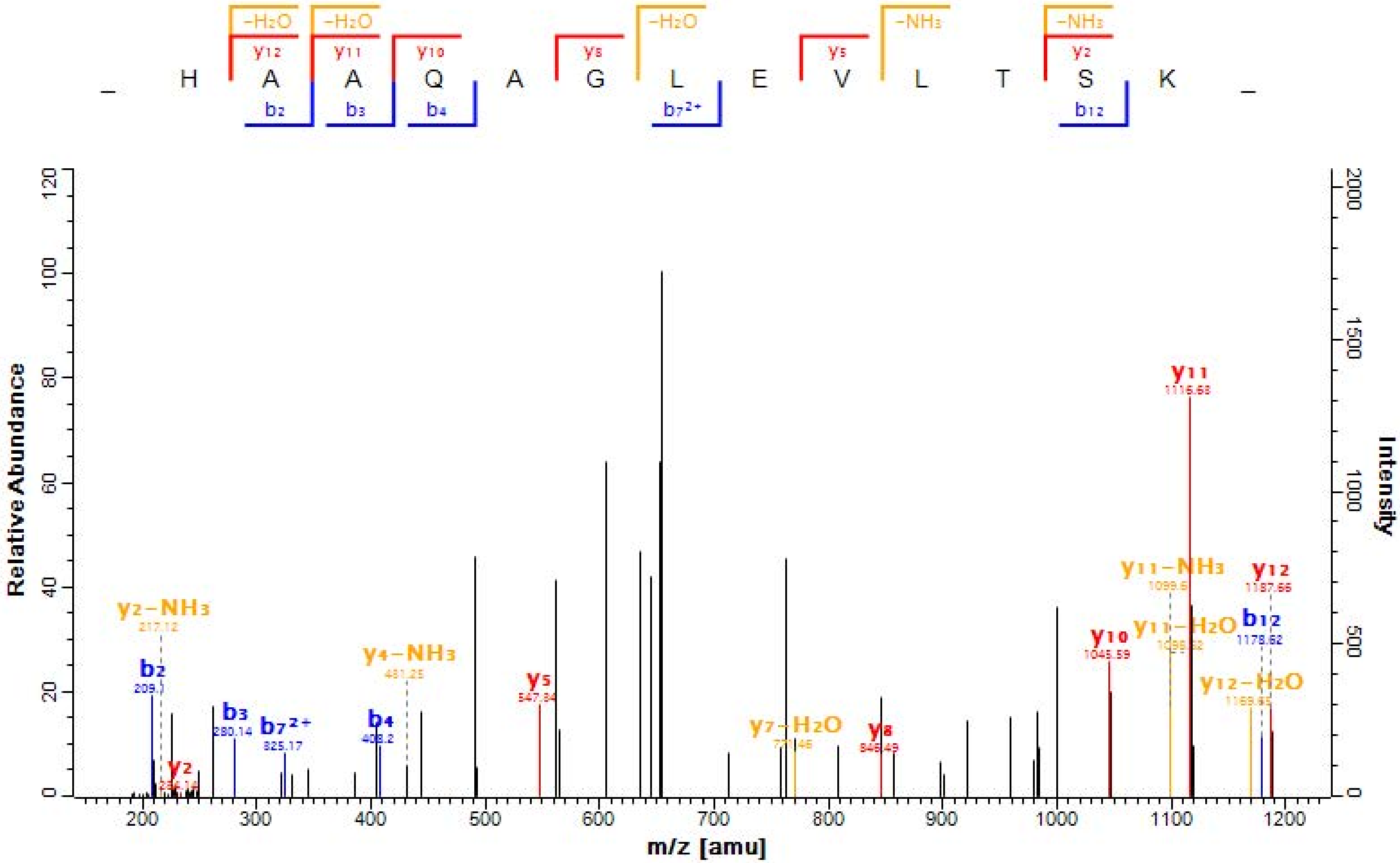
Mass:	1281.59884
m/z:	641.80669
Charge:	2+
Retentiontime:	14.130715370178
Score:	105.0319
Mass Error [ppm]:	-0.10173
PEP:	0.00031962
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	25 %
Peak Coverage:	22 %
Protein Localisation:	61 ... 71

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	87.055		115.05	1	N	10				
+0.0671	234.12	-0.027	262.12	2	F	9	1168.6		1168.6	
	291.15	+0.0859	319.14	3	G	8	1021.5	-0.017	511.25	+0.1945
	378.18		406.17	4	S	7	964.47	+0.1002	964.47	
	541.24		569.24	5	Y	6	877.44	+0.1053	439.22	+0.0991
	640.31		668.3	6	V	5	714.38	+0.0846	714.38	
	741.36		769.35	7	T	4	615.31		615.31	
	878.42	+0.1511	906.41	8	H	3	514.26	+0.2128	514.26	
	1007.5	+0.1209	1035.5	9	E	2	377.2	+0.138	377.2	
	1108.5	+0.1748	1136.5	10	T	1	248.16	+0.0937	248.16	
				11	K	0	147.11		147.11	

Scan number	1820	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	69.03



precursor information

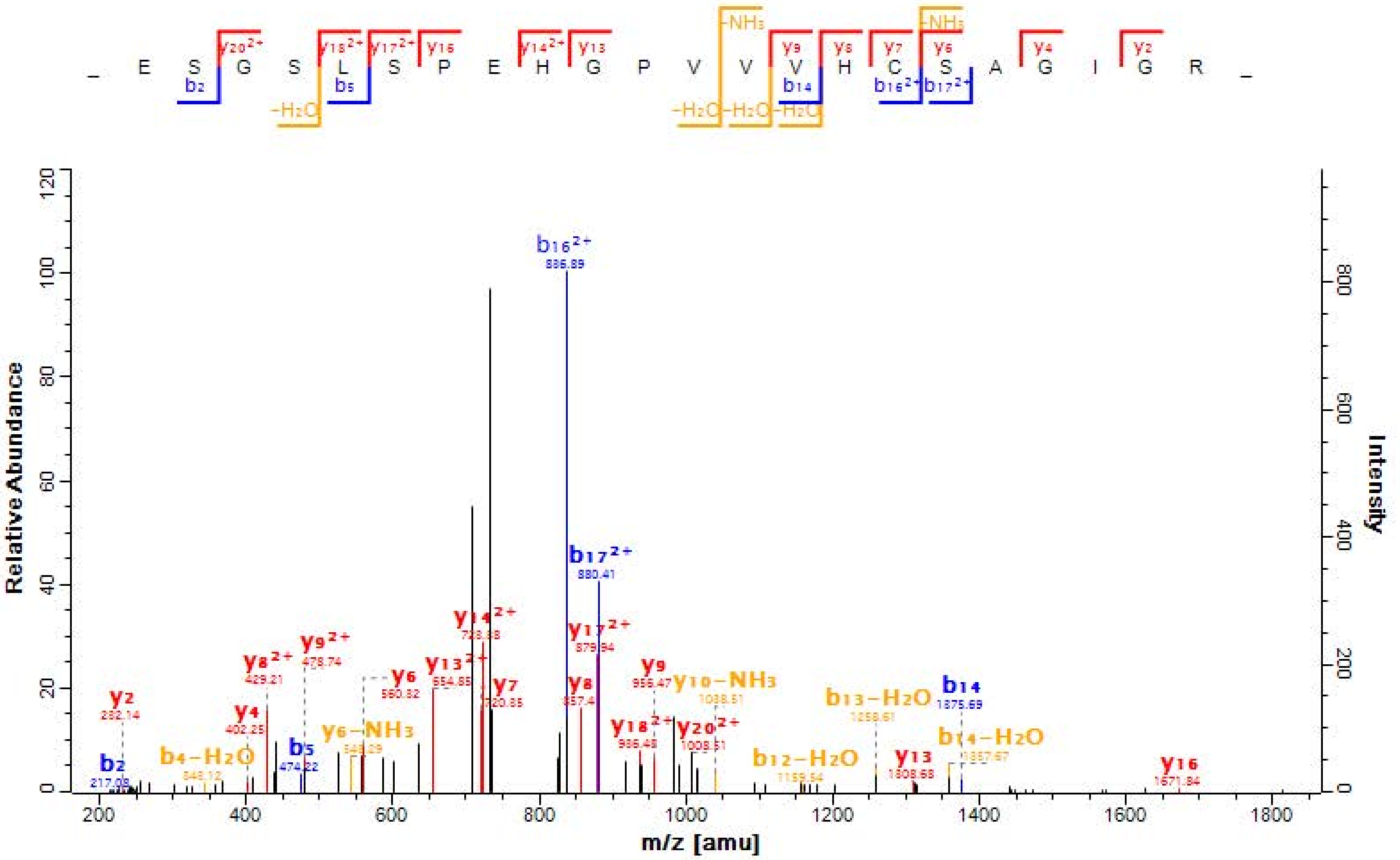
Mass:	1323.71356
m/z:	662.86406
Charge:	2+
Retentiontime:	15.680751800537
Score:	69.03009
Mass Error [ppm]:	-0.83505
PEP:	0.002947
Precursor Type:	MULTI

general information

Annotation:	8 of 13
AminoAcids Coverag	62 %
Intensity Coverage:	22 %
Peak Coverage:	20 %
Protein Localisation:	5 ... 17

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	138.0662		138.0662	1	H	12		
	209.1033	+0.056976	209.1033	2	A	11	1187.663	-0.0213
	280.1404	+0.121608	280.1404	3	A	10	1116.626	-0.10272
	408.199	+0.002301	408.199	4	Q	9	1045.589	-0.05511
	479.2361		479.2361	5	A	8	917.5302	
	536.2576		536.2576	6	G	7	846.4931	-0.00367
+0.019331	325.1745		649.3416	7	L	6	789.4716	
	778.3842		778.3842	8	E	5	676.3876	
	877.4526		877.4526	9	V	4	547.345	-0.03072
	990.5367		990.5367	10	L	3	448.2766	
	1091.584		1091.584	11	T	2	335.1925	
	1178.616	-0.08419	1178.616	12	S	1	234.1448	+0.023518
				13	K	0	147.1128	

Scan number	2133	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	69.36



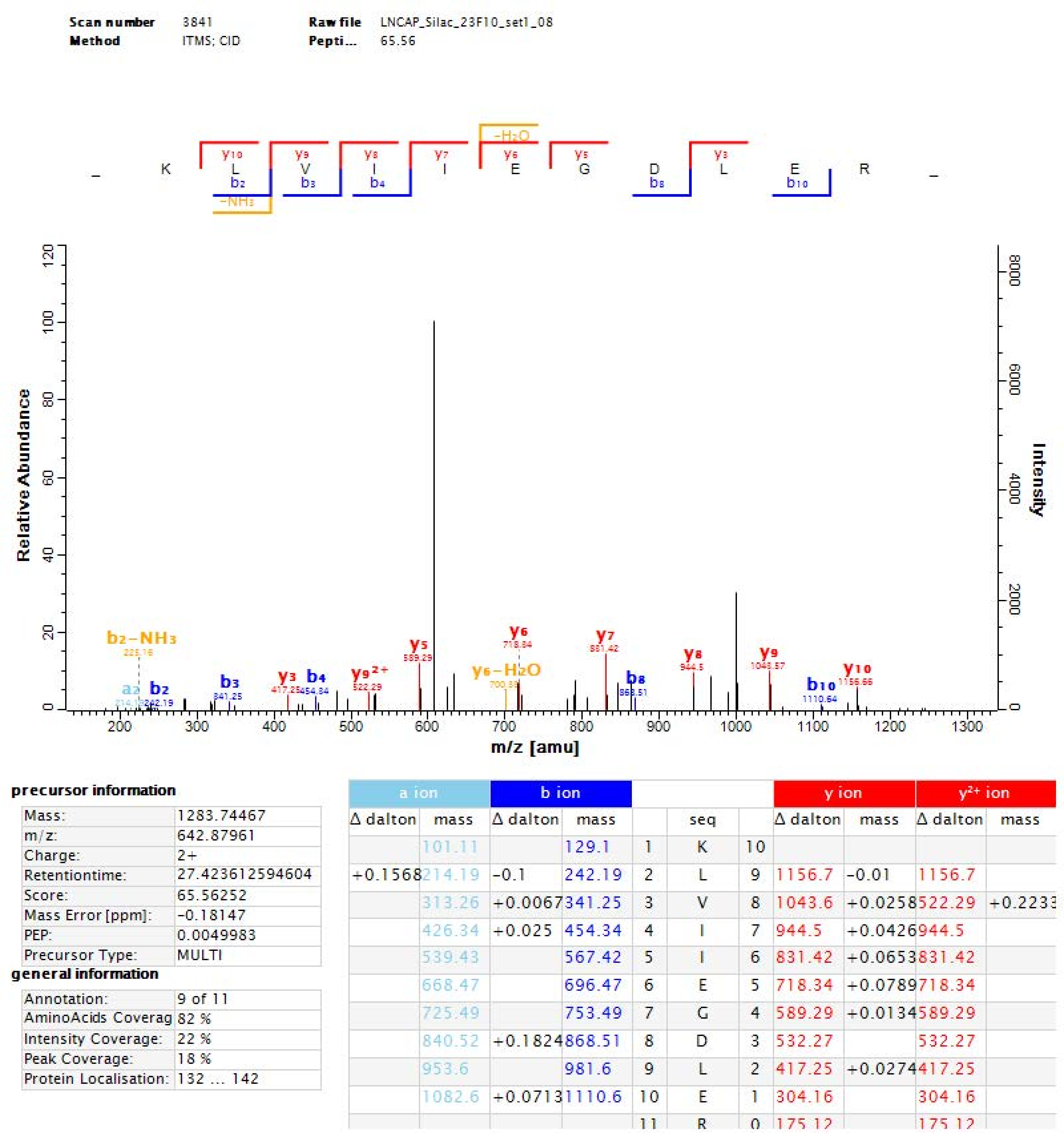
precursor information

Mass:	2231.0751
m/z:	744.69898
Charge:	3+
Retentiontime:	17.502246856689
Score:	69.36105
Mass Error [ppm]:	-0.093832
PEP:	0.00341
Precursor Type:	ISO

general information

Annotation:	16 of 22
AminoAcids Coverag	73 %
Intensity Coverage:	48 %
Peak Coverage:	28 %
Protein Localisation:	200 ... 221

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	21				
	217.08	-0.085	217.08	2	S	20	2103		2103	
	274.1		274.1	3	G	19	2016		1008.5	-0.124
	361.14		361.14	4	S	18	1959		1959	
	474.22	+0.1878	474.22	5	L	17	1872		936.48	+0.279
	561.25		561.25	6	S	16	1758.9		879.94	-0.012
	658.3		658.3	7	P	15	1671.8	+0.3546	1671.8	
	787.35		787.35	8	E	14	1574.8		1574.8	
	924.41		924.41	9	H	13	1445.7		723.38	+0.376
	981.43		981.43	10	G	12	1308.7	+0.0898	654.85	+0.1745
	1078.5		1078.5	11	P	11	1251.7		1251.7	
	1177.5		1177.5	12	V	10	1154.6		1154.6	
	1276.6		1276.6	13	V	9	1055.5		1055.5	
	1375.7	-0.138	1375.7	14	V	8	956.47	+0.0904	478.74	-0.055
	1512.7		1512.7	15	H	7	857.4	-0.054	429.21	+0.0973
-0.174	836.89		1672.8	16	C	6	720.35	+0.0703	720.35	
+0.1479	880.41		1759.8	17	S	5	560.32	+0.0169	560.32	
	1830.8		1830.8	18	A	4	473.28		473.28	
	1887.9		1887.9	19	G	3	402.25	+0.217	402.25	
	2000.9		2000.9	20	I	2	345.22		345.22	
	2058		2058	21	G	1	232.14	-0.146	232.14	
				22	R	0	175.12		175.12	



Scan number	3841	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	65.56

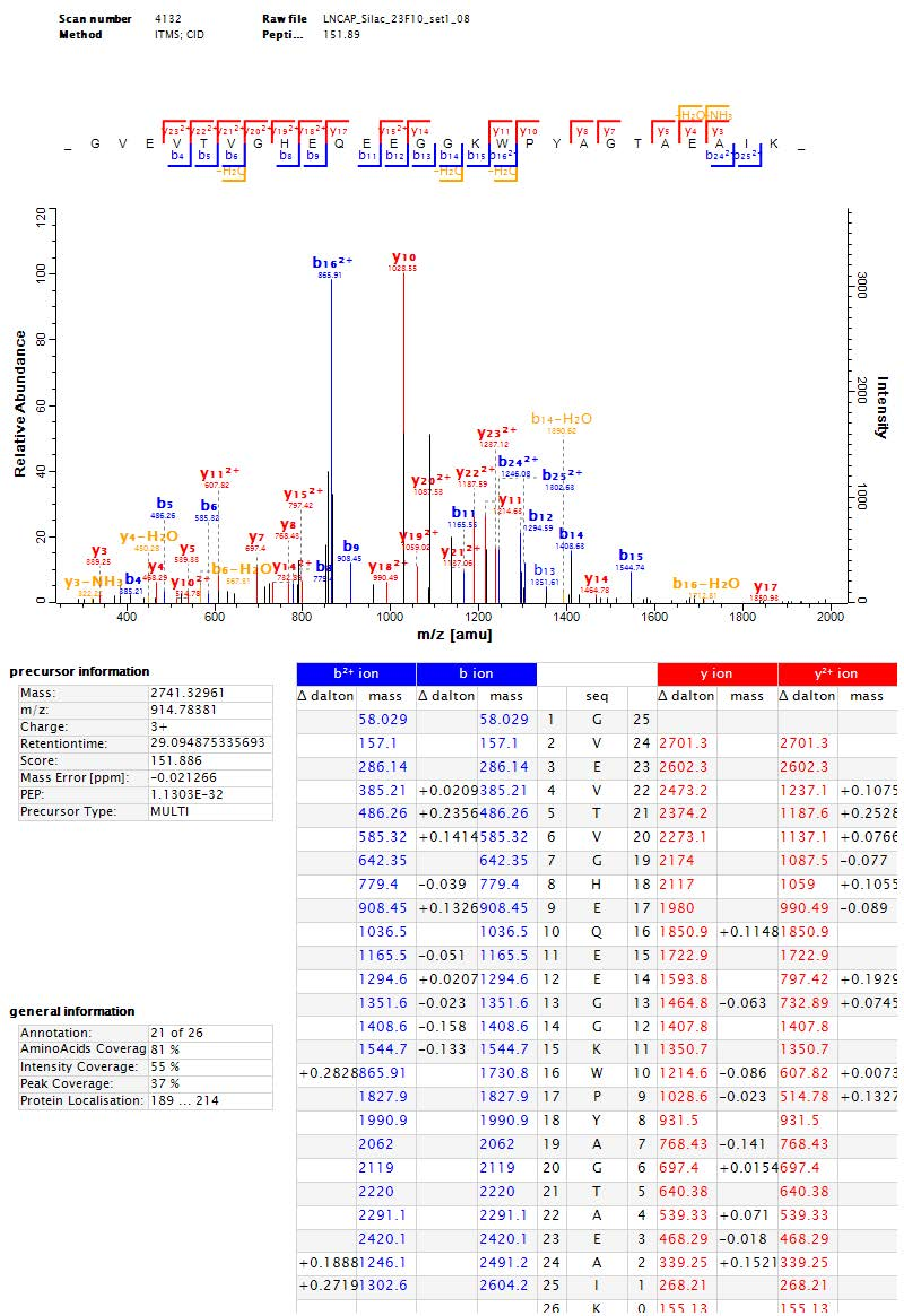
precursor information

Mass:	1283.74467
m/z:	642.87961
Charge:	2+
Retentiontime:	27.423612594604
Score:	65.56252
Mass Error [ppm]:	-0.18147
PEP:	0.0049983
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	22 %
Peak Coverage:	18 %
Protein Localisation:	132 ... 142

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	101.11		129.1	1	K	10				
+0.1568	214.19	-0.1	242.19	2	L	9	1156.7	-0.01	1156.7	
	313.26	+0.0067	341.25	3	V	8	1043.6	+0.0258	522.29	+0.2233
	426.34	+0.025	454.34	4	I	7	944.5	+0.0426	944.5	
	539.43		567.42	5	I	6	831.42	+0.0653	831.42	
	668.47		696.47	6	E	5	718.34	+0.0789	718.34	
	725.49		753.49	7	G	4	589.29	+0.0134	589.29	
	840.52	+0.1824	868.51	8	D	3	532.27		532.27	
	953.6		981.6	9	L	2	417.25	+0.0274	417.25	
	1082.6	+0.0713	1110.6	10	E	1	304.16		304.16	
				11	R	0	175.12		175.12	



Scan number	4132	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	151.89

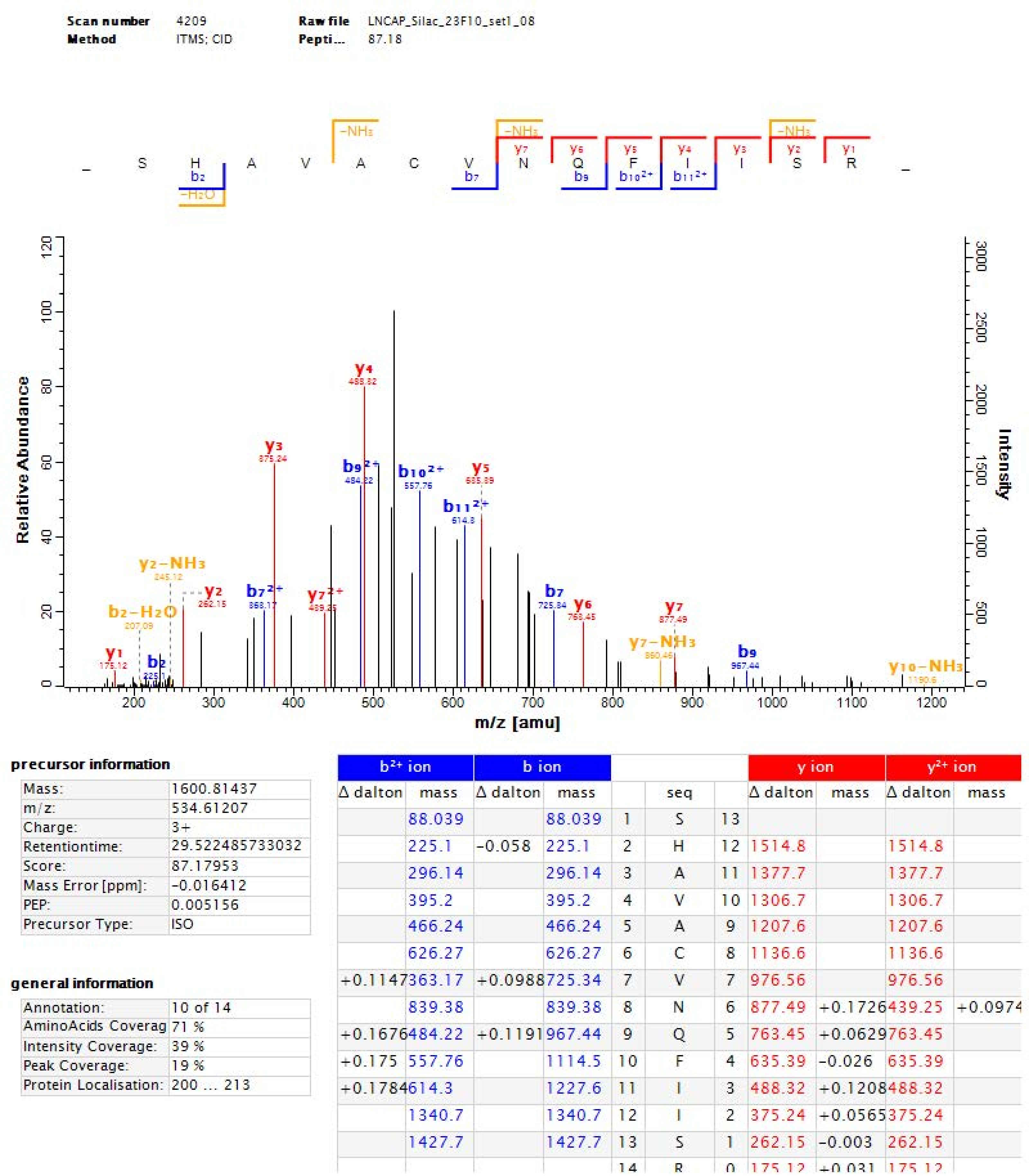
precursor information

Mass:	2741.32961
m/z:	914.78381
Charge:	3+
Retentiontime:	29.094875335693
Score:	151.886
Mass Error [ppm]:	-0.021266
PEP:	1.1303E-32
Precursor Type:	MULTI

general information

Annotation:	21 of 26
AminoAcids Coverag	81 %
Intensity Coverage:	55 %
Peak Coverage:	37 %
Protein Localisation:	189 ... 214

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	25				
	157.1		157.1	2	V	24	2701.3		2701.3	
	286.14		286.14	3	E	23	2602.3		2602.3	
	385.21	+0.0209	385.21	4	V	22	2473.2		1237.1	+0.1075
	486.26	+0.2356	486.26	5	T	21	2374.2		1187.6	+0.2528
	585.32	+0.1414	585.32	6	V	20	2273.1		1137.1	+0.0766
	642.35		642.35	7	G	19	2174		1087.5	-0.077
	779.4	-0.039	779.4	8	H	18	2117		1059	+0.1055
	908.45	+0.1326	908.45	9	E	17	1980		990.49	-0.089
	1036.5		1036.5	10	Q	16	1850.9	+0.1148	1850.9	
	1165.5	-0.051	1165.5	11	E	15	1722.9		1722.9	
	1294.6	+0.0207	1294.6	12	E	14	1593.8		797.42	+0.1929
	1351.6	-0.023	1351.6	13	G	13	1464.8	-0.063	732.89	+0.0745
	1408.6	-0.158	1408.6	14	G	12	1407.8		1407.8	
	1544.7	-0.133	1544.7	15	K	11	1350.7		1350.7	
+0.2828	865.91		1730.8	16	W	10	1214.6	-0.086	607.82	+0.0073
	1827.9		1827.9	17	P	9	1028.6	-0.023	514.78	+0.1327
	1990.9		1990.9	18	Y	8	931.5		931.5	
	2062		2062	19	A	7	768.43	-0.141	768.43	
	2119		2119	20	G	6	697.4	+0.0154	697.4	
	2220		2220	21	T	5	640.38		640.38	
	2291.1		2291.1	22	A	4	539.33	+0.071	539.33	
	2420.1		2420.1	23	E	3	468.29	-0.018	468.29	
+0.1888	1246.1		2491.2	24	A	2	339.25	+0.1521	339.25	
+0.2719	1302.6		2604.2	25	I	1	268.21		268.21	
				26	K	0	155.13		155.13	



Scan number	4209	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	87.18

precursor information

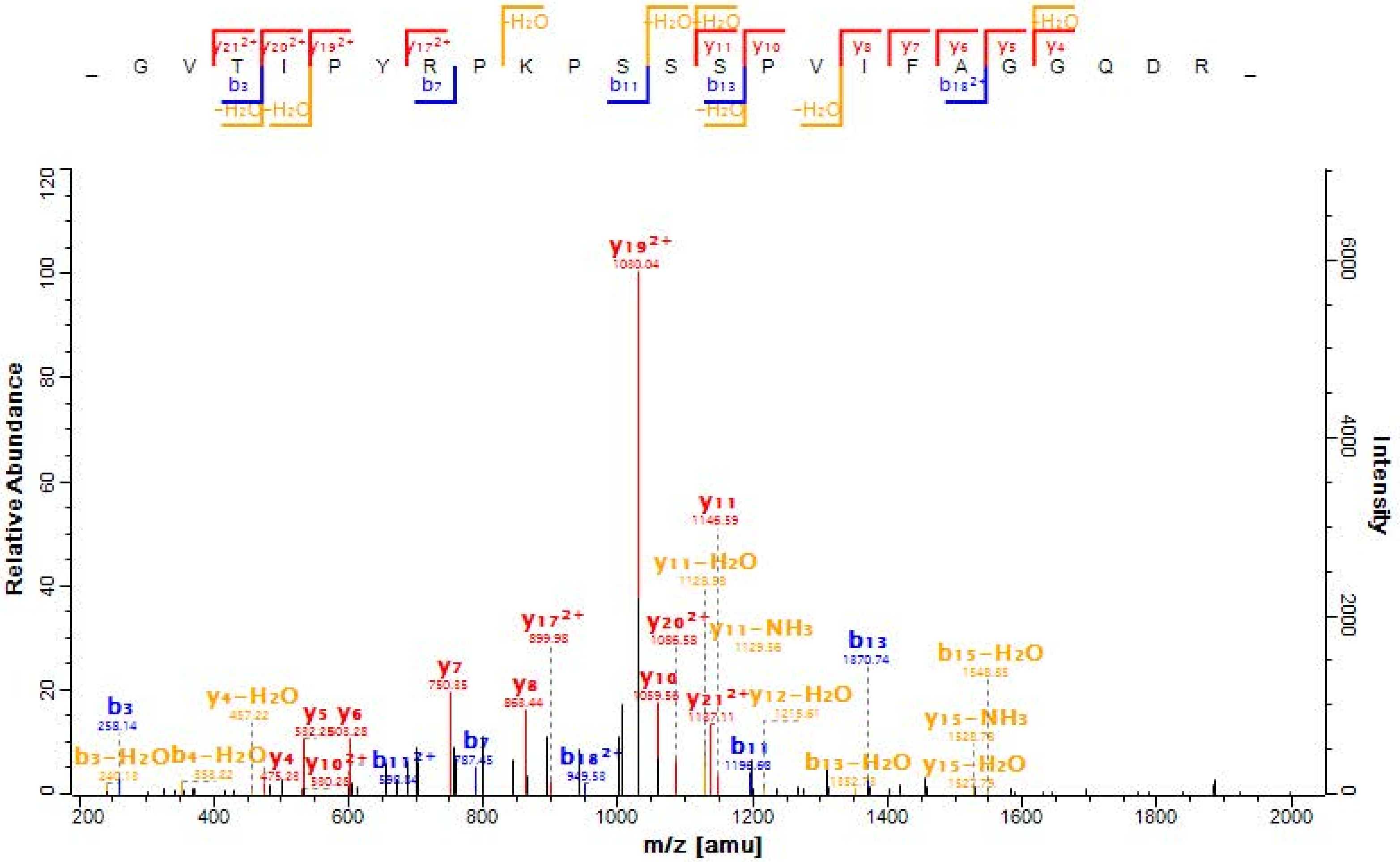
Mass:	1600.81437
m/z:	534.61207
Charge:	3+
Retentiontime:	29.522485733032
Score:	87.17953
Mass Error [ppm]:	-0.016412
PEP:	0.005156
Precursor Type:	ISO

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	39 %
Peak Coverage:	19 %
Protein Localisation:	200 ... 213

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	13				
	225.1	-0.058	225.1	2	H	12	1514.8		1514.8	
	296.14		296.14	3	A	11	1377.7		1377.7	
	395.2		395.2	4	V	10	1306.7		1306.7	
	466.24		466.24	5	A	9	1207.6		1207.6	
	626.27		626.27	6	C	8	1136.6		1136.6	
+0.1147	363.17	+0.0988	725.34	7	V	7	976.56		976.56	
	839.38		839.38	8	N	6	877.49	+0.1726	439.25	+0.0974
+0.1676	484.22	+0.1191	967.44	9	Q	5	763.45	+0.0629	763.45	
+0.175	557.76		1114.5	10	F	4	635.39	-0.026	635.39	
+0.1784	614.3		1227.6	11	I	3	488.32	+0.1208	488.32	
	1340.7		1340.7	12	I	2	375.24	+0.0565	375.24	
	1427.7		1427.7	13	S	1	262.15	-0.003	262.15	
				14	R	0	175.12	+0.031	175.12	

Scan number	4332	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	78.71



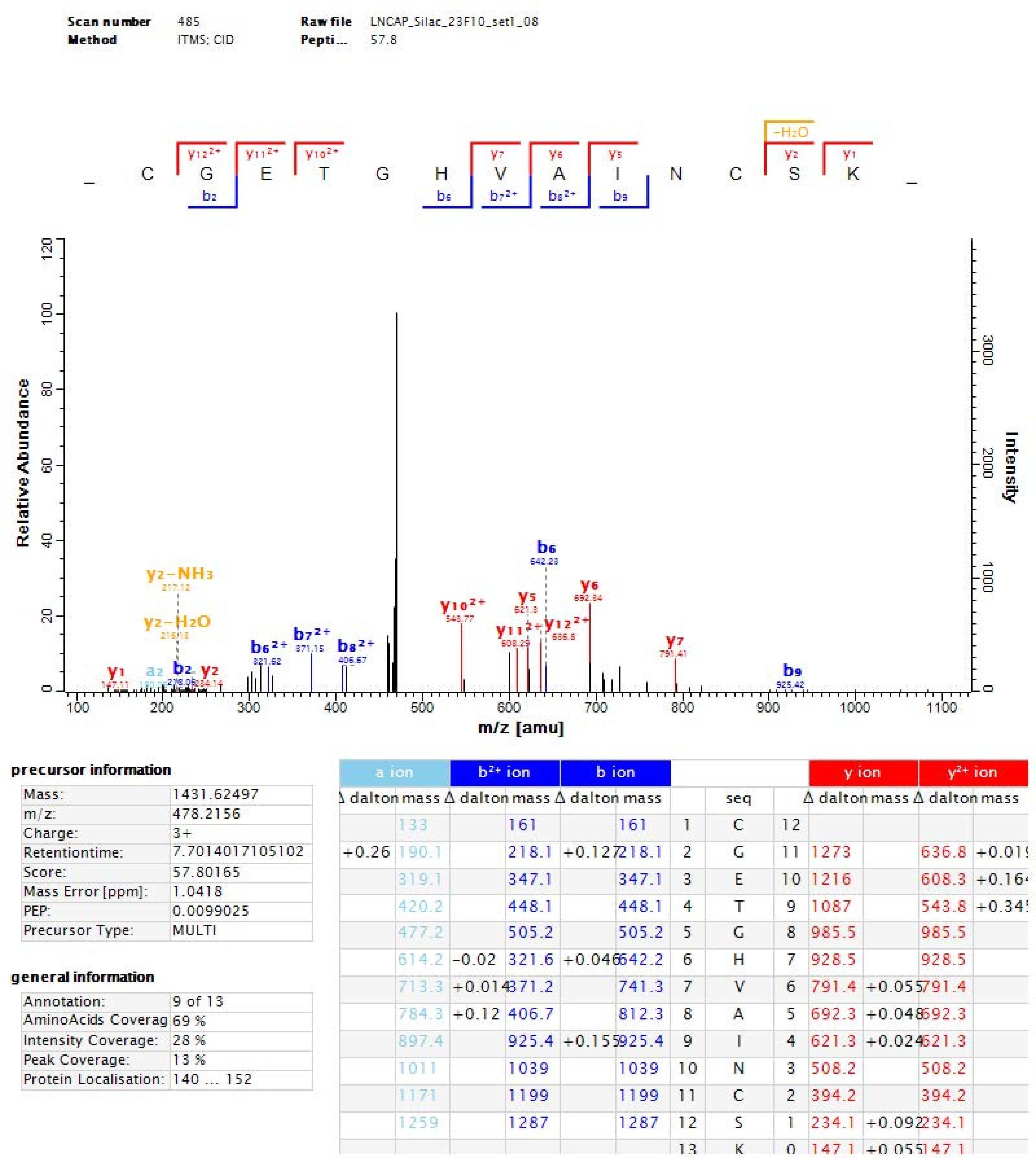
precursor information

Mass:	2428.28768
m/z:	810.4365
Charge:	3+
Retentiontime:	30.221952438354
Score:	78.70789
Mass Error [ppm]:	0.57241
PEP:	0.004811
Precursor Type:	ISO

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	22				
	157.1		157.1	2	V	21	2372.3		2372.3	
	258.14	+0.1104	258.14	3	T	20	2273.2		1137.1	+0.3237
	371.23		371.23	4	I	19	2172.2		1086.6	+0.2001
	468.28		468.28	5	P	18	2059.1		1030	+0.2457
	631.34		631.34	6	Y	17	1962		1962	
	787.45	-0.187	787.45	7	R	16	1799		899.98	+0.3649
	884.5		884.5	8	P	15	1642.9		1642.9	
	1012.6		1012.6	9	K	14	1545.8		1545.8	
	1109.6		1109.6	10	P	13	1417.7		1417.7	
-0.125	598.84	-0.073	1196.7	11	S	12	1320.7		1320.7	
	1283.7		1283.7	12	S	11	1233.6		1233.6	
	1370.7	-0.147	1370.7	13	S	10	1146.6	-0.196	1146.6	
	1467.8		1467.8	14	P	9	1059.6	+0.0678	530.28	+0.1682
	1566.9		1566.9	15	V	8	962.51		962.51	
	1679.9		1679.9	16	I	7	863.44	+0.1016	863.44	
	1827		1827	17	F	6	750.35	-0.006	750.35	
+0.3085	949.53		1898.1	18	A	5	603.28	+0.0938	603.28	
	1955.1		1955.1	19	G	4	532.25	+0.073	532.25	
	2012.1		2012.1	20	G	3	475.23	+0.0625	475.23	
	2140.2		2140.2	21	Q	2	418.2		418.2	
	2255.2		2255.2	22	D	1	290.15		290.15	
				23	R	0	175.12		175.12	

general information

Annotation:	16 of 23
AminoAcids Coverag	70 %
Intensity Coverage:	51 %
Peak Coverage:	28 %
Protein Localisation:	177 ... 199



Scan number 485

Method ITMS; CID

Raw file LNCAP_Silac_23F10_set1_08

Pepti... 57.8

precursor information

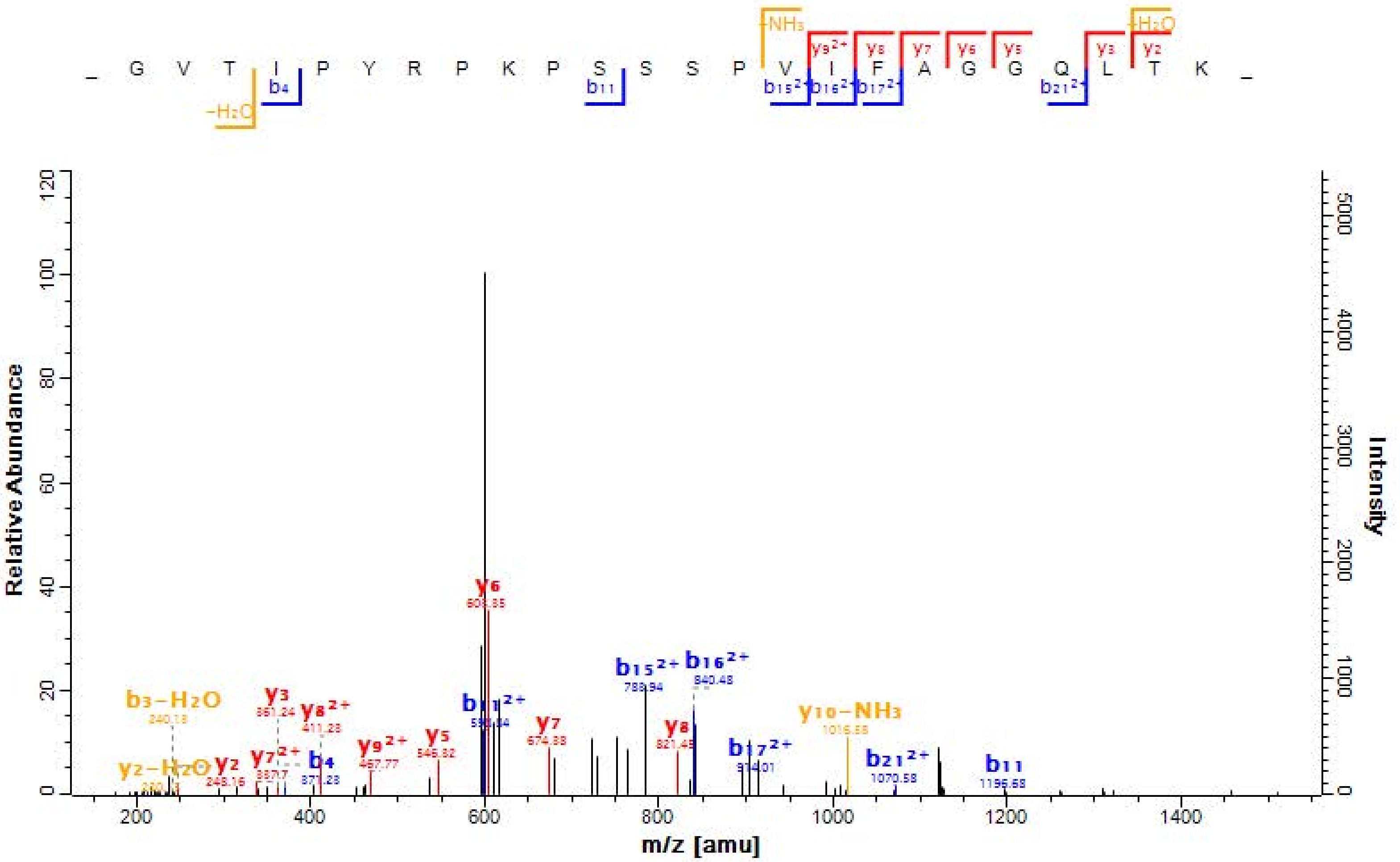
Mass:	1431.62497
m/z:	478.2156
Charge:	3+
Retentiontime:	7.7014017105102
Score:	57.80165
Mass Error [ppm]:	1.0418
PEP:	0.0099025
Precursor Type:	MULTI

general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	28 %
Peak Coverage:	13 %
Protein Localisation:	140 ... 152

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	133		161		161	1	C	12				
+0.26	190.1		218.1	+0.127	218.1	2	G	11	1273		636.8	+0.01
	319.1		347.1		347.1	3	E	10	1216		608.3	+0.16
	420.2		448.1		448.1	4	T	9	1087		543.8	+0.34
	477.2		505.2		505.2	5	G	8	985.5		985.5	
	614.2	-0.02	321.6	+0.046	642.2	6	H	7	928.5		928.5	
	713.3	+0.014	371.2		741.3	7	V	6	791.4	+0.055	791.4	
	784.3	+0.12	406.7		812.3	8	A	5	692.3	+0.048	692.3	
	897.4		925.4	+0.155	925.4	9	I	4	621.3	+0.024	621.3	
	1011		1039		1039	10	N	3	508.2		508.2	
	1171		1199		1199	11	C	2	394.2		394.2	
	1259		1287		1287	12	S	1	234.1	+0.092	234.1	
						13	K	0	147.1	+0.055	147.1	

Scan number	5281	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	45.4



precursor information

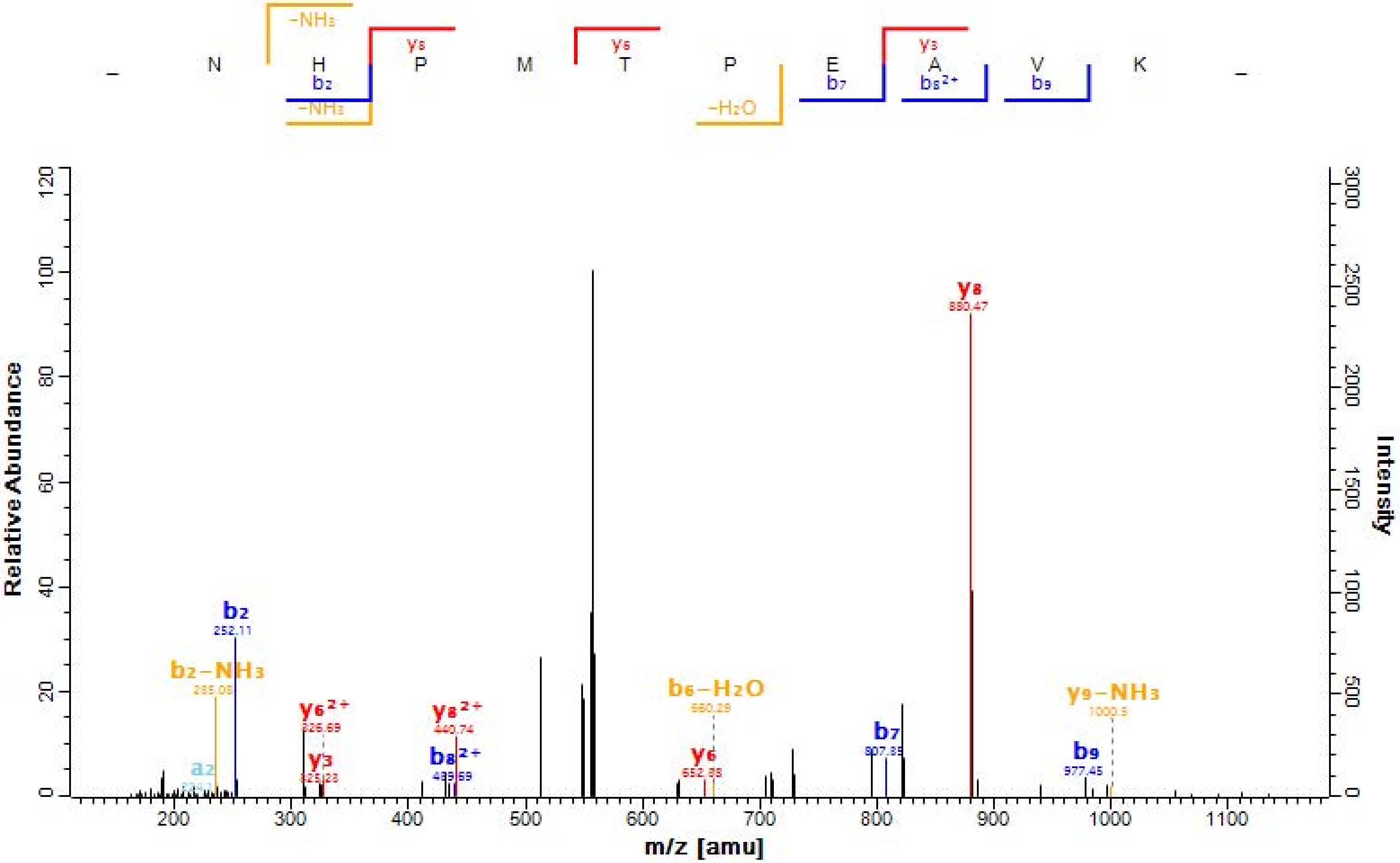
Mass:	2499.38481
m/z:	625.85348
Charge:	4+
Retentiontime:	35.764331817627
Score:	45.39541
Mass Error [ppm]:	-0.055613
PEP:	0.0059418
Precursor Type:	MULTI

general information

Annotation:	13 of 24
AminoAcids Coverag	54 %
Intensity Coverage:	30 %
Peak Coverage:	17 %
Protein Localisation:	139 ... 162

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	23				
	157.1		157.1	2	V	22	2443.4		2443.4	
	258.14		258.14	3	T	21	2344.3		2344.3	
	371.23	+0.1331	371.23	4	I	20	2243.3		2243.3	
	468.28		468.28	5	P	19	2130.2		2130.2	
	631.34		631.34	6	Y	18	2033.1		2033.1	
	787.45		787.45	7	R	17	1870.1		1870.1	
	884.5		884.5	8	P	16	1714		1714	
	1012.6		1012.6	9	K	15	1616.9		1616.9	
	1109.6		1109.6	10	P	14	1488.8		1488.8	
-0.027	598.84	-0.059	1196.7	11	S	13	1391.8		1391.8	
	1283.7		1283.7	12	S	12	1304.7		1304.7	
	1370.7		1370.7	13	S	11	1217.7		1217.7	
	1467.8		1467.8	14	P	10	1130.7		1130.7	
+0.029	783.94		1566.9	15	V	9	1033.6		1033.6	
-0.053	840.48		1679.9	16	I	8	934.54		467.77	+0.1037
+0.0508	914.01		1827	17	F	7	821.45	+0.1322	411.23	+0.14
	1898.1		1898.1	18	A	6	674.38	+0.0927	337.7	+0.3456
	1955.1		1955.1	19	G	5	603.35	+0.0297	603.35	
	2012.1		2012.1	20	G	4	546.32	+0.004	546.32	
+0.2883	1070.6		2140.2	21	Q	3	489.3		489.3	
	2253.2		2253.2	22	L	2	361.24	-0.013	361.24	
	2354.3		2354.3	23	T	1	248.16	+0.0737	248.16	
				24	K	0	147.11		147.11	

Scan number	553	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	59.91



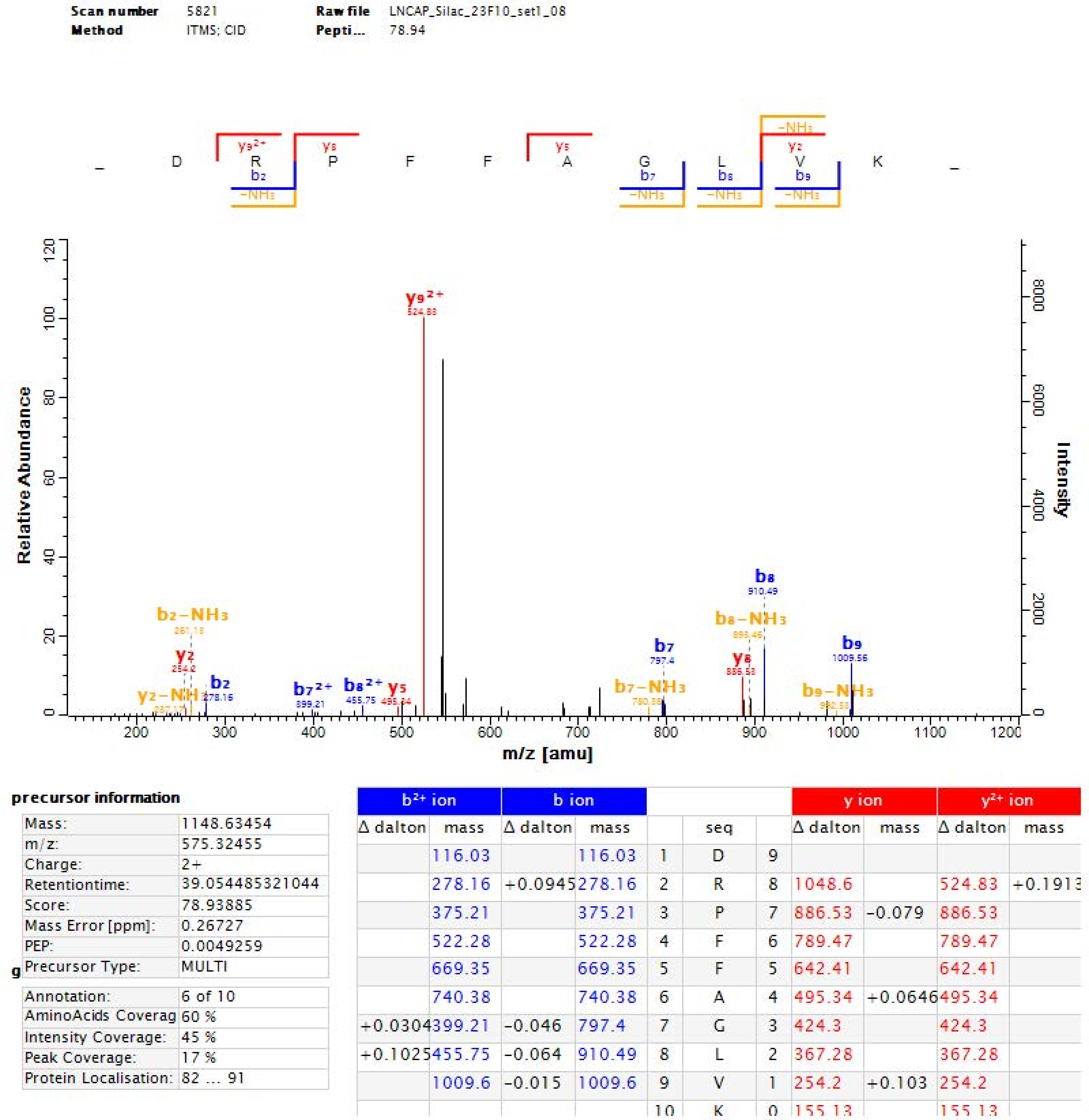
precursor information

Mass:	1122.54899
m/z:	562.28177
Charge:	2+
Retentiontime:	8.0938034057617
Score:	59.90757
Mass Error [ppm]:	-0.16651
PEP:	0.021583
Precursor Type:	MULTI

g

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	30 %
Peak Coverage:	13 %
Protein Localisation:	261 ... 270

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	87.06		115.1		115.1	1	N	9				
+0.195	224.1		252.1	+0.051	252.1	2	H	8	1018		1018	
	321.2		349.2		349.2	3	P	7	880.5	+0.015	440.7	+0.11
	452.2		480.2		480.2	4	M	6	783.4		783.4	
	553.3		581.3		581.3	5	T	5	652.4	+0.127	326.7	+0.28
	650.3		678.3		678.3	6	P	4	551.3		551.3	
	779.4		807.3	-0.19	807.3	7	E	3	454.3		454.3	
	850.4	-0.19	439.7		878.4	8	A	2	325.2	+0.082	325.2	
	949.5		977.5	+0.185	977.5	9	V	1	254.2		254.2	
						10	K	0	155.1		155.1	



Scan number	5821	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	78.94

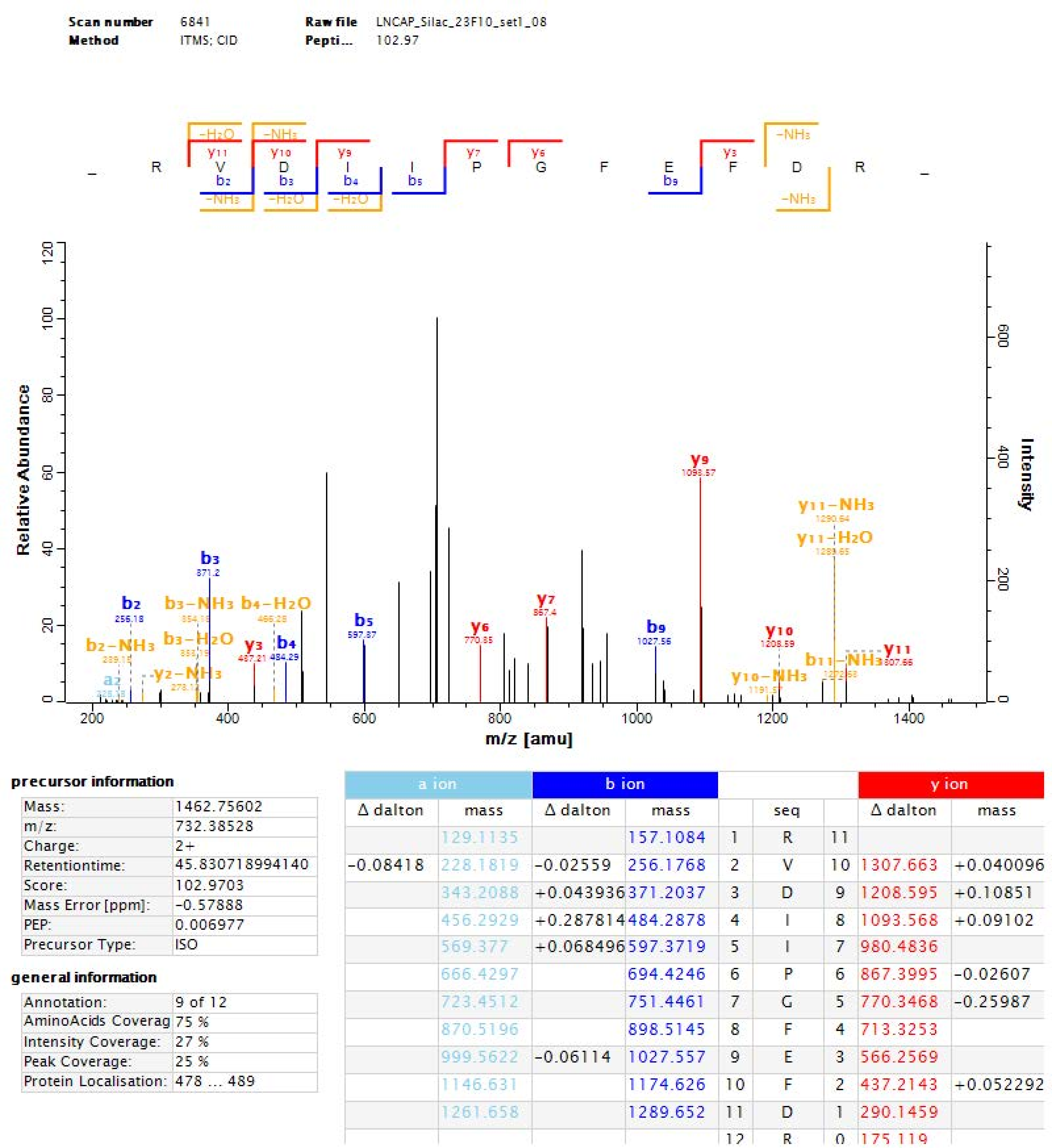
precursor information

Mass:	1148.63454
m/z:	575.32455
Charge:	2+
Retentiontime:	39.054485321044
Score:	78.93885
Mass Error [ppm]:	0.26727
PEP:	0.0049259
Precursor Type:	MULTI

g

Annotation:	6 of 10
AminoAcids Coverag	60 %
Intensity Coverage:	45 %
Peak Coverage:	17 %
Protein Localisation:	82 ... 91

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	9				
	278.16	+0.0945	278.16	2	R	8	1048.6		524.83	+0.1913
	375.21		375.21	3	P	7	886.53	-0.079	886.53	
	522.28		522.28	4	F	6	789.47		789.47	
	669.35		669.35	5	F	5	642.41		642.41	
	740.38		740.38	6	A	4	495.34	+0.0646	495.34	
+0.0304	399.21	-0.046	797.4	7	G	3	424.3		424.3	
+0.1025	455.75	-0.064	910.49	8	L	2	367.28		367.28	
	1009.6	-0.015	1009.6	9	V	1	254.2	+0.103	254.2	
				10	K	0	155.13		155.13	



Scan number	6841	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	102.97

precursor information

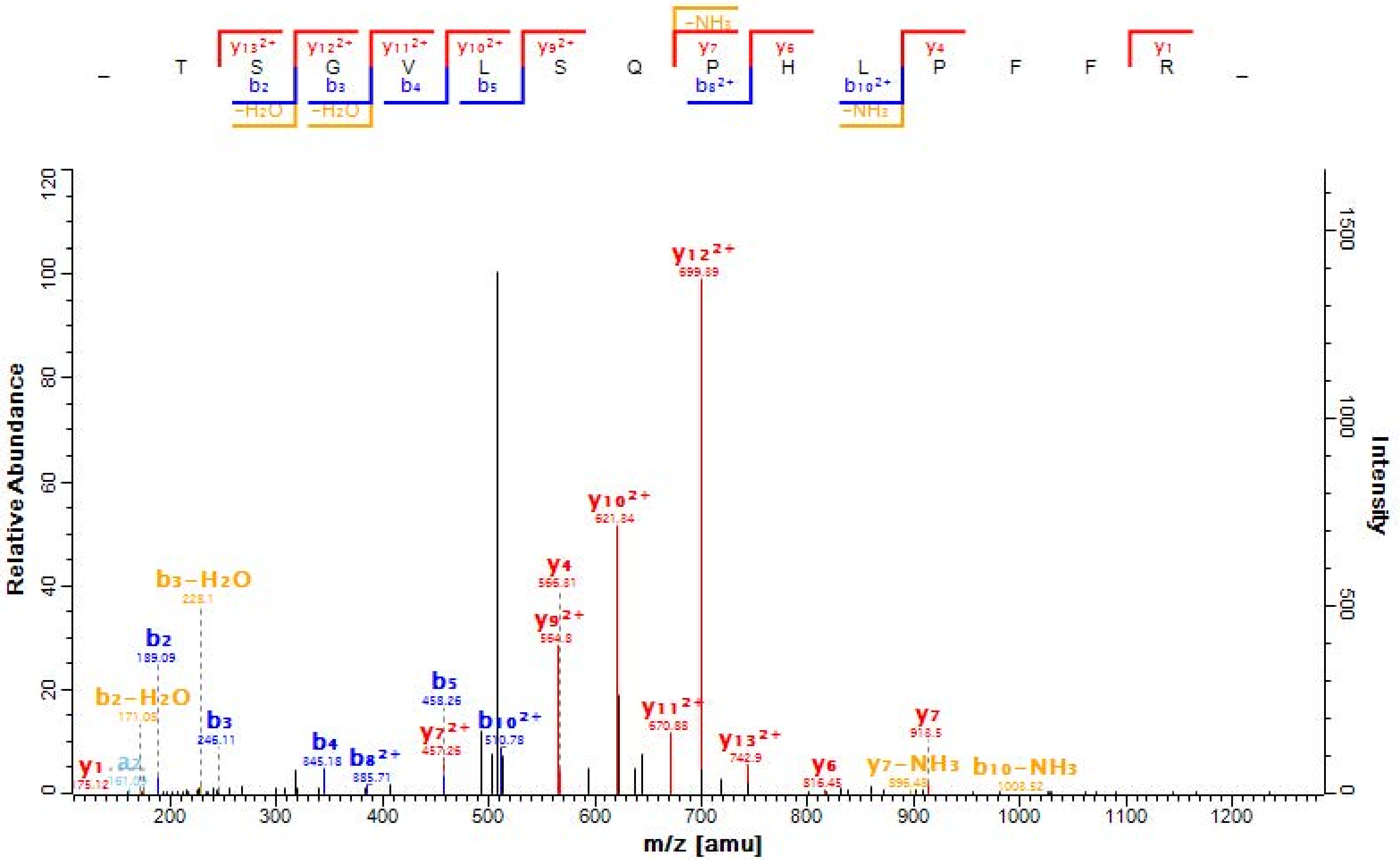
Mass:	1462.75602
m/z:	732.38528
Charge:	2+
Retentiontime:	45.830718994140
Score:	102.9703
Mass Error [ppm]:	-0.57888
PEP:	0.006977
Precursor Type:	ISO

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	27 %
Peak Coverage:	25 %
Protein Localisation:	478 ... 489

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	129.1135		157.1084	1	R	11		
-0.08418	228.1819	-0.02559	256.1768	2	V	10	1307.663	+0.040096
	343.2088	+0.043936	371.2037	3	D	9	1208.595	+0.10851
	456.2929	+0.287814	484.2878	4	I	8	1093.568	+0.09102
	569.377	+0.068496	597.3719	5	I	7	980.4836	
	666.4297		694.4246	6	P	6	867.3995	-0.02607
	723.4512		751.4461	7	G	5	770.3468	-0.25987
	870.5196		898.5145	8	F	4	713.3253	
	999.5622	-0.06114	1027.557	9	E	3	566.2569	
	1146.631		1174.626	10	F	2	437.2143	+0.052292
	1261.658		1289.652	11	D	1	290.1459	
				12	R	0	175.119	

Scan number	7056	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	113.22



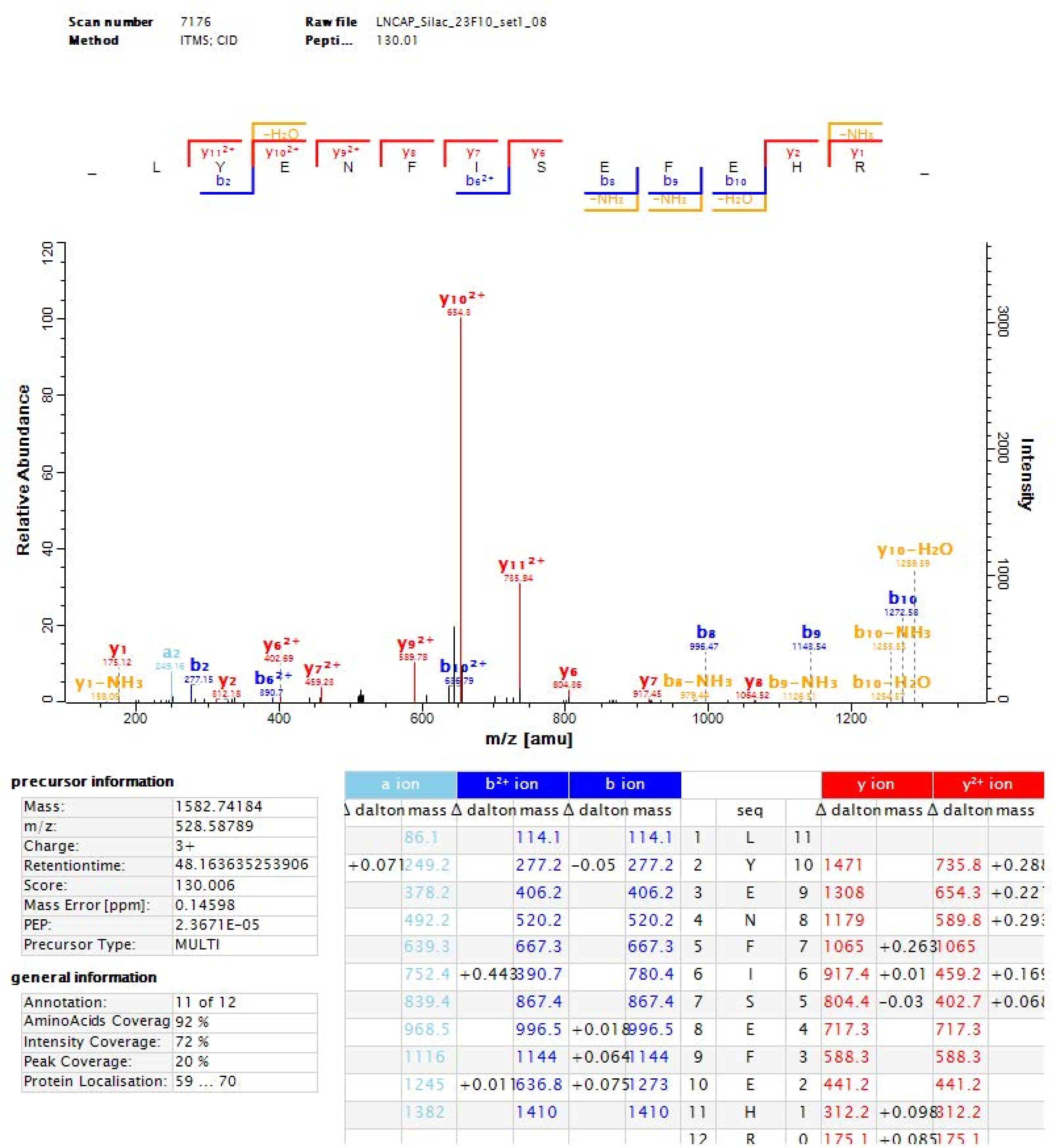
precursor information

Mass:	1584.84233
m/z:	529.28805
Charge:	3+
Retentiontime:	47.326187133789
Score:	113.2243
Mass Error [ppm]:	0.67453
PEP:	0.00024115
Precursor Type:	ISO

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	54 %
Peak Coverage:	24 %
Protein Localisation:	449 ... 462

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.1		102.1	1	T	13				
+0.088	161.1		189.1	+0.043	189.1	2	S	12	1485		742.9	+0.24
	218.1		246.1	+0.073	246.1	3	G	11	1398		699.4	+0.24
	317.2		345.2	+0.058	345.2	4	V	10	1341		670.9	-0.14
	430.3		458.3	+0.078	458.3	5	L	9	1242		621.3	+0.10
	517.3		545.3		545.3	6	S	8	1129		564.8	+0.16
	645.4		673.4		673.4	7	Q	7	1042		1042	
	742.4	-0.48	385.7		770.4	8	P	6	913.5	-0.02	457.3	+0.22
	879.5		907.5		907.5	9	H	5	816.5	+0.104	816.5	
	992.6	+0.433	510.8		1021	10	L	4	679.4		679.4	
	1090		1118		1118	11	P	3	566.3	+0.213	566.3	
	1237		1265		1265	12	F	2	469.3		469.3	
	1384		1412		1412	13	F	1	322.2		322.2	
						14	R	0	175.1	+0.129	175.1	



Scan number	7176	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	130.01

precursor information

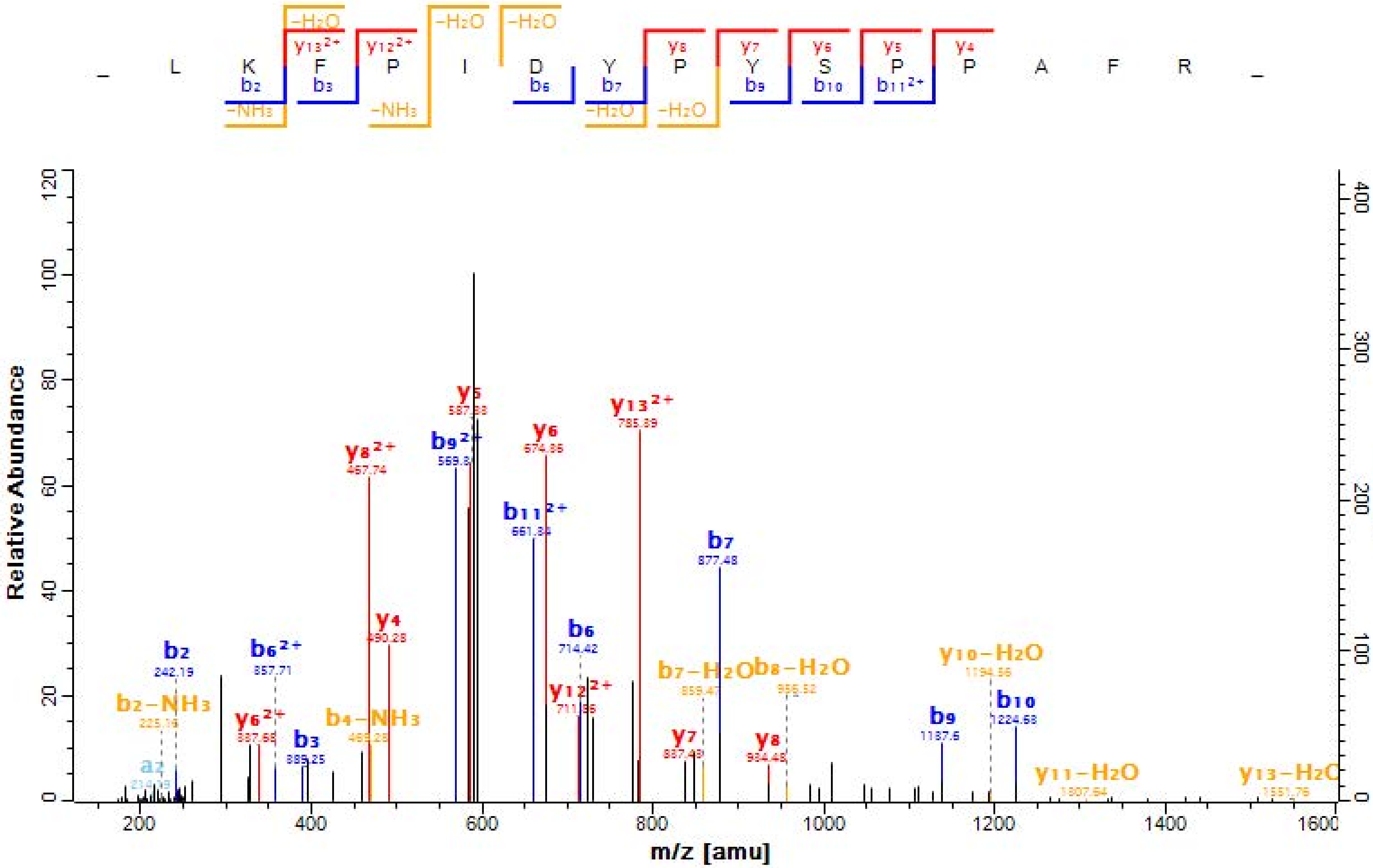
Mass:	1582.74184
m/z:	528.58789
Charge:	3+
Retentiontime:	48.163635253906
Score:	130.006
Mass Error [ppm]:	0.14598
PEP:	2.3671E-05
Precursor Type:	MULTI

general information

Annotation:	11 of 12
AminoAcids Coverag	92 %
Intensity Coverage:	72 %
Peak Coverage:	20 %
Protein Localisation:	59 ... 70

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	11				
+0.071	249.2		277.2	-0.05	277.2	2	Y	10	1471		735.8	+0.28
	378.2		406.2		406.2	3	E	9	1308		654.3	+0.22
	492.2		520.2		520.2	4	N	8	1179		589.8	+0.29
	639.3		667.3		667.3	5	F	7	1065	+0.263	1065	
	752.4	+0.443	390.7		780.4	6	I	6	917.4	+0.01	459.2	+0.16
	839.4		867.4		867.4	7	S	5	804.4	-0.03	402.7	+0.06
	968.5		996.5	+0.018	996.5	8	E	4	717.3		717.3	
	1116		1144	+0.064	1144	9	F	3	588.3		588.3	
	1245	+0.011	636.8	+0.075	1273	10	E	2	441.2		441.2	
	1382		1410		1410	11	H	1	312.2	+0.098	312.2	
						12	R	0	175.1	+0.085	175.1	

Scan number	7417	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	88.28



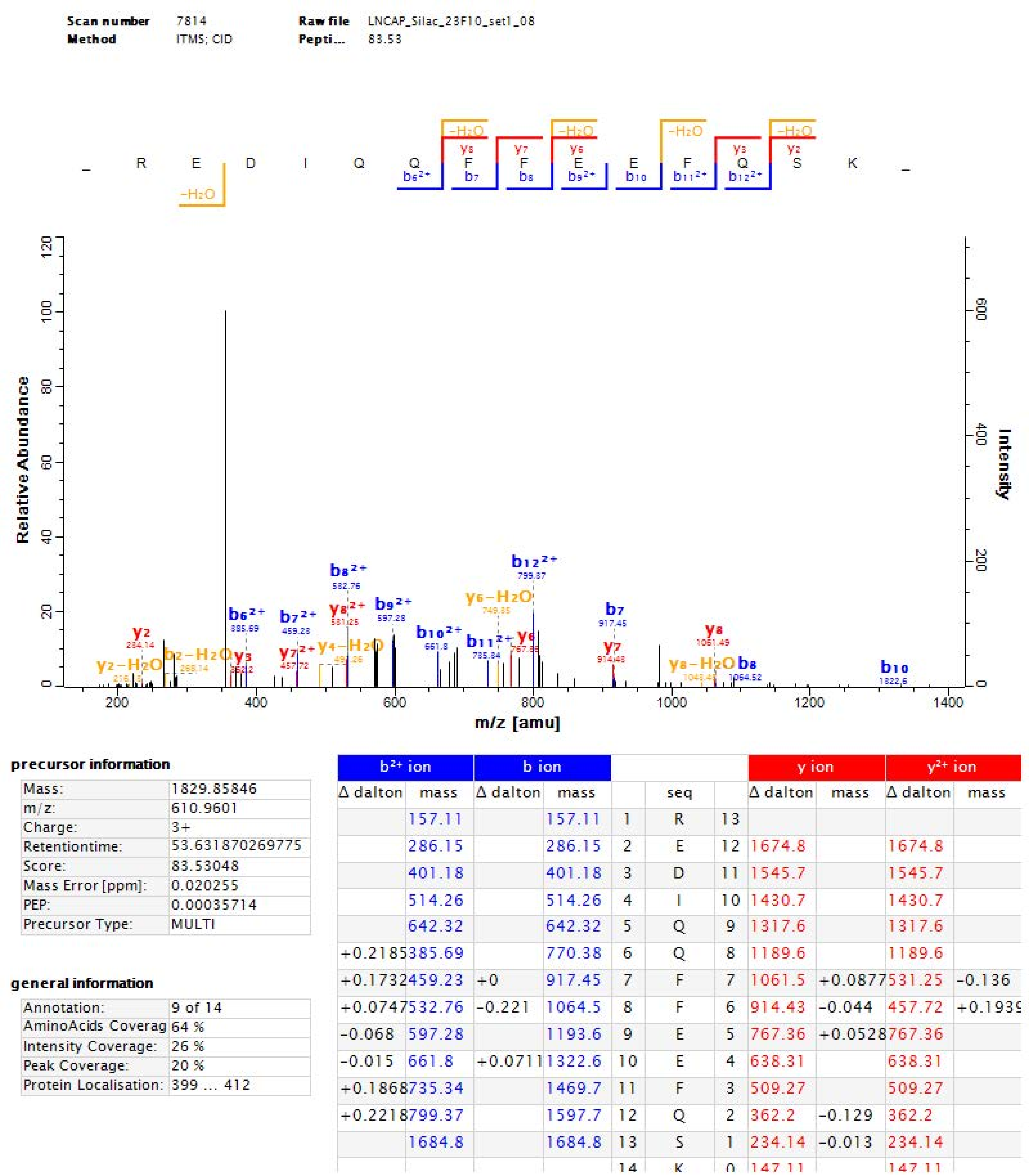
precursor information

Mass:	1809.94533
m/z:	604.32239
Charge:	3+
Retentiontime:	50.101516723632
Score:	88.28183
Mass Error [ppm]:	-0.032006
PEP:	0.00014278
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	49 %
Peak Coverage:	24 %
Protein Localisation:	62 ... 76

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	14				
+0.05	214.2		242.2	-0.03	242.2	2	K	13	1698		1698	
	361.3		389.3	+0.093	389.3	3	F	12	1570		785.4	+0.26
	458.3		486.3		486.3	4	P	11	1423		711.9	+0.32
	571.4		599.4		599.4	5	I	10	1326		1326	
	686.4	-0.48	357.7	-0.16	714.4	6	D	9	1213		1213	
	849.5		877.5	+0.048	877.5	7	Y	8	1098		1098	
	946.5		974.5		974.5	8	P	7	934.5	-0.1	467.7	+0.14
	1110	+0.158	569.3	+0.008	1138	9	Y	6	837.4	+0.079	837.4	
	1197		1225	+0.05	1225	10	S	5	674.4	+0.044	337.7	+0.20
	1294	-0.2	661.3		1322	11	P	4	587.3	-0.04	587.3	
	1391		1419		1419	12	P	3	490.3	+0.114	490.3	
	1462		1490		1490	13	A	2	393.2		393.2	
	1609		1637		1637	14	F	1	322.2		322.2	
						15	R	0	175.1		175.1	



Scan number	7814	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	83.53

precursor information

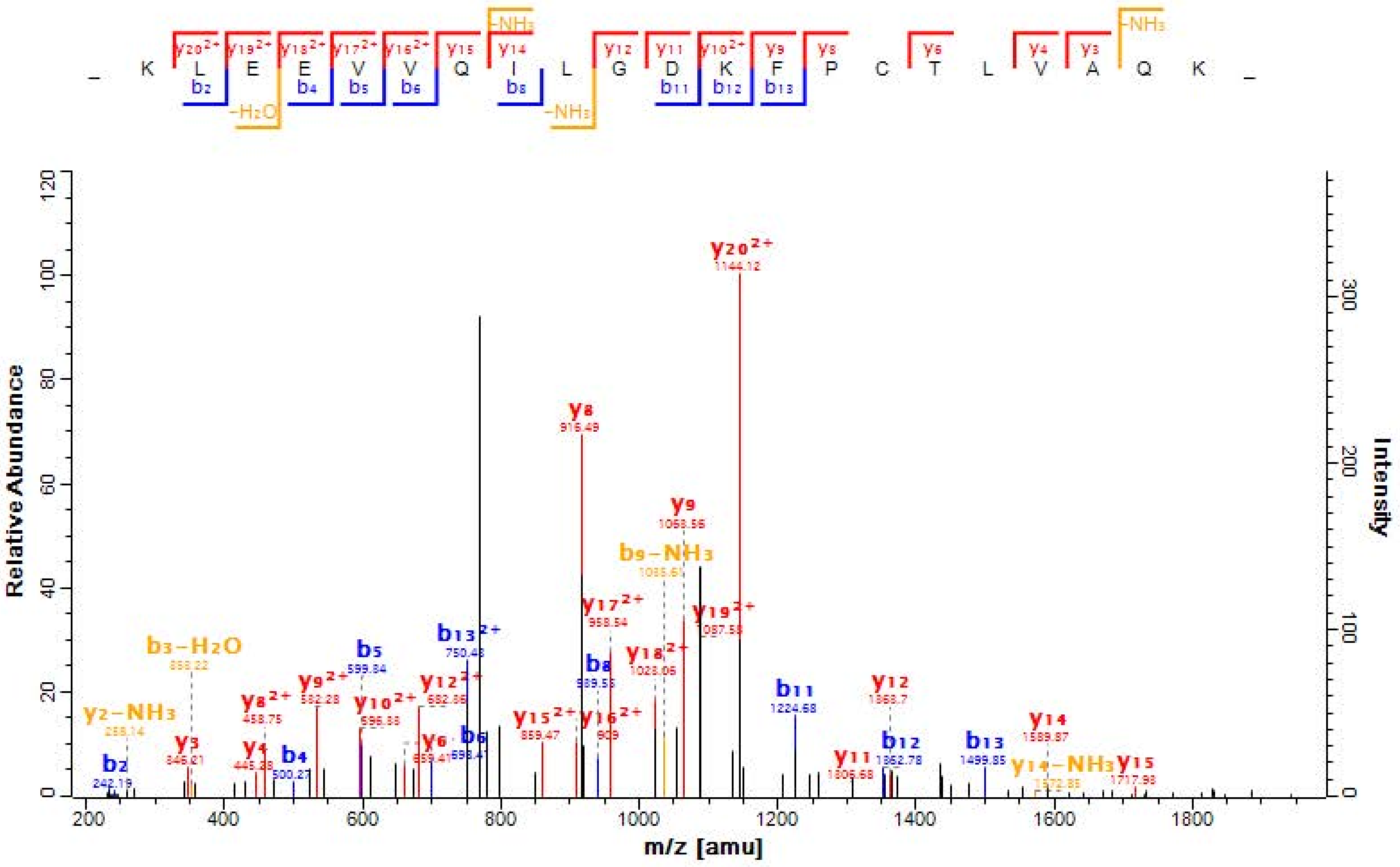
Mass:	1829.85846
m/z:	610.9601
Charge:	3+
Retentiontime:	53.631870269775
Score:	83.53048
Mass Error [ppm]:	0.020255
PEP:	0.00035714
Precursor Type:	MULTI

general information

Annotation:	9 of 14
AminoAcids Coverag	64 %
Intensity Coverage:	26 %
Peak Coverage:	20 %
Protein Localisation:	399 ... 412

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	157.11		157.11	1	R	13				
	286.15		286.15	2	E	12	1674.8		1674.8	
	401.18		401.18	3	D	11	1545.7		1545.7	
	514.26		514.26	4	I	10	1430.7		1430.7	
	642.32		642.32	5	Q	9	1317.6		1317.6	
+0.2185	385.69		770.38	6	Q	8	1189.6		1189.6	
+0.1732	459.23	+0	917.45	7	F	7	1061.5	+0.0877	531.25	−0.136
+0.0747	532.76	−0.221	1064.5	8	F	6	914.43	−0.044	457.72	+0.1939
−0.068	597.28		1193.6	9	E	5	767.36	+0.0528	767.36	
−0.015	661.8	+0.0711	1322.6	10	E	4	638.31		638.31	
+0.1868	735.34		1469.7	11	F	3	509.27		509.27	
+0.2218	799.37		1597.7	12	Q	2	362.2	−0.129	362.2	
	1684.8		1684.8	13	S	1	234.14	−0.013	234.14	
				14	K	0	147.11		147.11	

Scan number	7844	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	128.74



precursor information

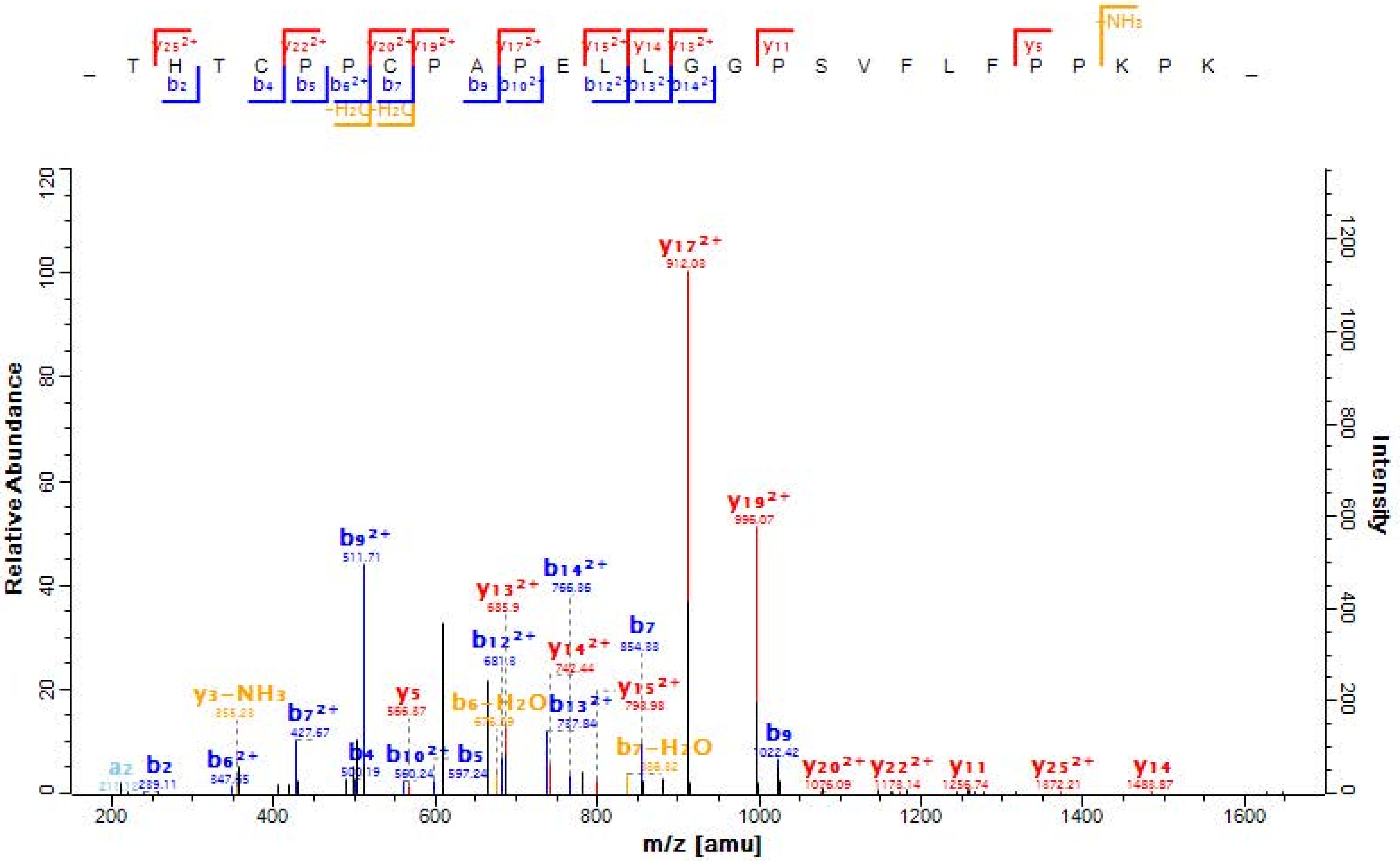
Mass:	2414.32232
m/z:	805.78138
Charge:	3+
Retentiontime:	53.915332794189
Score:	128.743
Mass Error [ppm]:	-0.82871
PEP:	1.1473E-13
Precursor Type:	MULTI

general information

Annotation:	17 of 21
AminoAcids Coverag	81 %
Intensity Coverage:	52 %
Peak Coverage:	32 %
Protein Localisation:	19 ... 39

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.1		129.1	1	K	20				
	242.19	+0.0444	242.19	2	L	19	2287.2		1144.1	+0.2275
	371.23		371.23	3	E	18	2174.2		1087.6	-0.15
	500.27	+0.0746	500.27	4	E	17	2045.1		1023.1	+0.2768
	599.34	+0.0781	599.34	5	V	16	1916.1		958.54	+0.4517
	698.41	-0.072	698.41	6	V	15	1817		909	+0.4351
	826.47		826.47	7	Q	14	1717.9	-0.152	859.47	+0.2144
	939.55	+0.0034	939.55	8	I	13	1589.9	+0.1194	1589.9	
	1052.6		1052.6	9	L	12	1476.8		1476.8	
	1109.7		1109.7	10	G	11	1363.7	+0.0053	682.36	+0.1938
	1224.7	+0.0367	1224.7	11	D	10	1306.7	+0.186	1306.7	
	1352.8	-0.23	1352.8	12	K	9	1191.7		596.33	+0.0697
+0.2018	750.43	+0.2274	1499.8	13	F	8	1063.6	+0.0113	532.28	+0.3426
	1596.9		1596.9	14	P	7	916.49	-0.02	458.75	+0.3612
	1756.9		1756.9	15	C	6	819.44		819.44	
	1858		1858	16	T	5	659.41	+0.0661	659.41	
	1971.1		1971.1	17	L	4	558.36		558.36	
	2070.1		2070.1	18	V	3	445.28	+0.0704	445.28	
	2141.2		2141.2	19	A	2	346.21	+0.0182	346.21	
	2269.2		2269.2	20	Q	1	275.17		275.17	
				21	K	0	147.11		147.11	

Scan number	8012	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	107.41



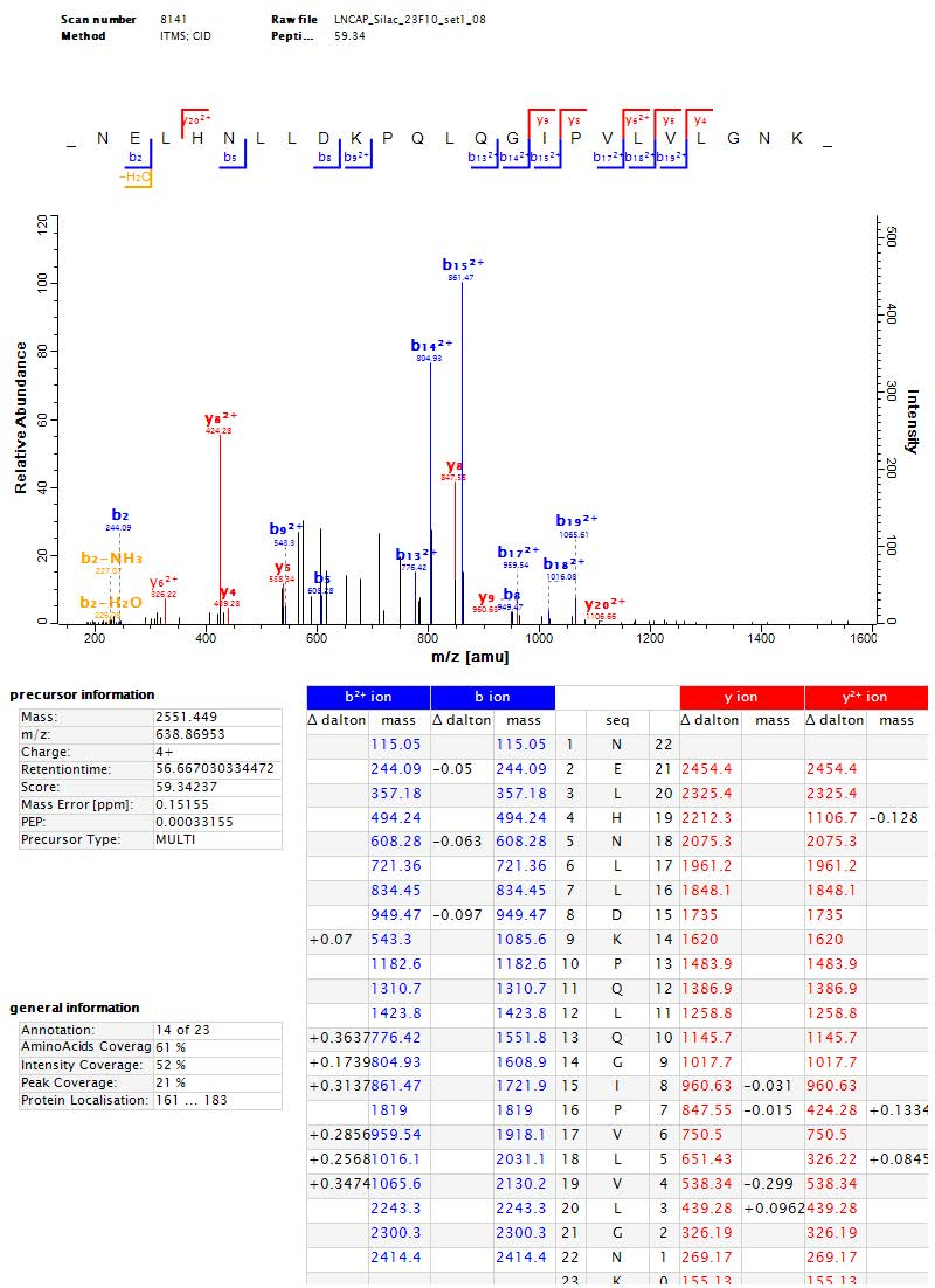
precursor information

Mass:	2843.45161
m/z:	711.87018
Charge:	4+
Retentiontime:	55.369087219238
Score:	107.4089
Mass Error [ppm]:	0.47498
PEP:	4.1411E-11
Precursor Type:	ISO

general information

Annotation:	14 of 26
AminoAcids Coverag	54 %
Intensity Coverage:	60 %
Peak Coverage:	36 %
Protein Localisation:	258 ... 283

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.1		102.1	1	T	25				
-0.07	211.1		239.1	+0.008	239.1	2	H	24	2743		1372	+0.46
	312.2		340.2		340.2	3	T	23	2606		2606	
	472.2		500.2	-0.03	500.2	4	C	22	2505		2505	
	569.3		597.2	+0.055	597.2	5	P	21	2345		1173	+0.10
	666.3	-0.01	347.7		694.3	6	P	20	2248		2248	
	826.3	+0.227	427.7	+0.084	854.3	7	C	19	2151		1076	+0.24
	923.4		951.4		951.4	8	P	18	1991		996.1	+0.2
	994.4	+0.225	511.7	-0.02	1022	9	A	17	1894		1894	
	1091	+0.182	560.2		1119	10	P	16	1823		912	+0.25
	1221		1249		1249	11	E	15	1726		1726	
	1334	+0.233	681.3		1362	12	L	14	1597		799	+0.39
	1447	+0.31	737.8		1475	13	L	13	1484	+0.408	742.4	+0.30
	1504	+0.17	766.4		1532	14	G	12	1371		685.9	-0.18
	1561		1589		1589	15	G	11	1314		1314	
	1658		1686		1686	16	P	10	1257	-0.05	1257	
	1745		1773		1773	17	S	9	1160		1160	
	1844		1872		1872	18	V	8	1073		1073	
	1991		2019		2019	19	F	7	973.6		973.6	
	2104		2132		2132	20	L	6	826.5		826.5	
	2251		2279		2279	21	F	5	713.4		713.4	
	2348		2376		2376	22	P	4	566.4	-0.04	566.4	
	2445		2473		2473	23	P	3	469.3		469.3	
	2573		2601		2601	24	K	2	372.3		372.3	
	2670		2698		2698	25	P	1	244.2		244.2	
						26	K	0	147.1		147.1	



Scan number 8141
Raw file LNCAP_Silac_23F10_set1_08
Method ITMS; CID
Pepti... 59.34

precursor information

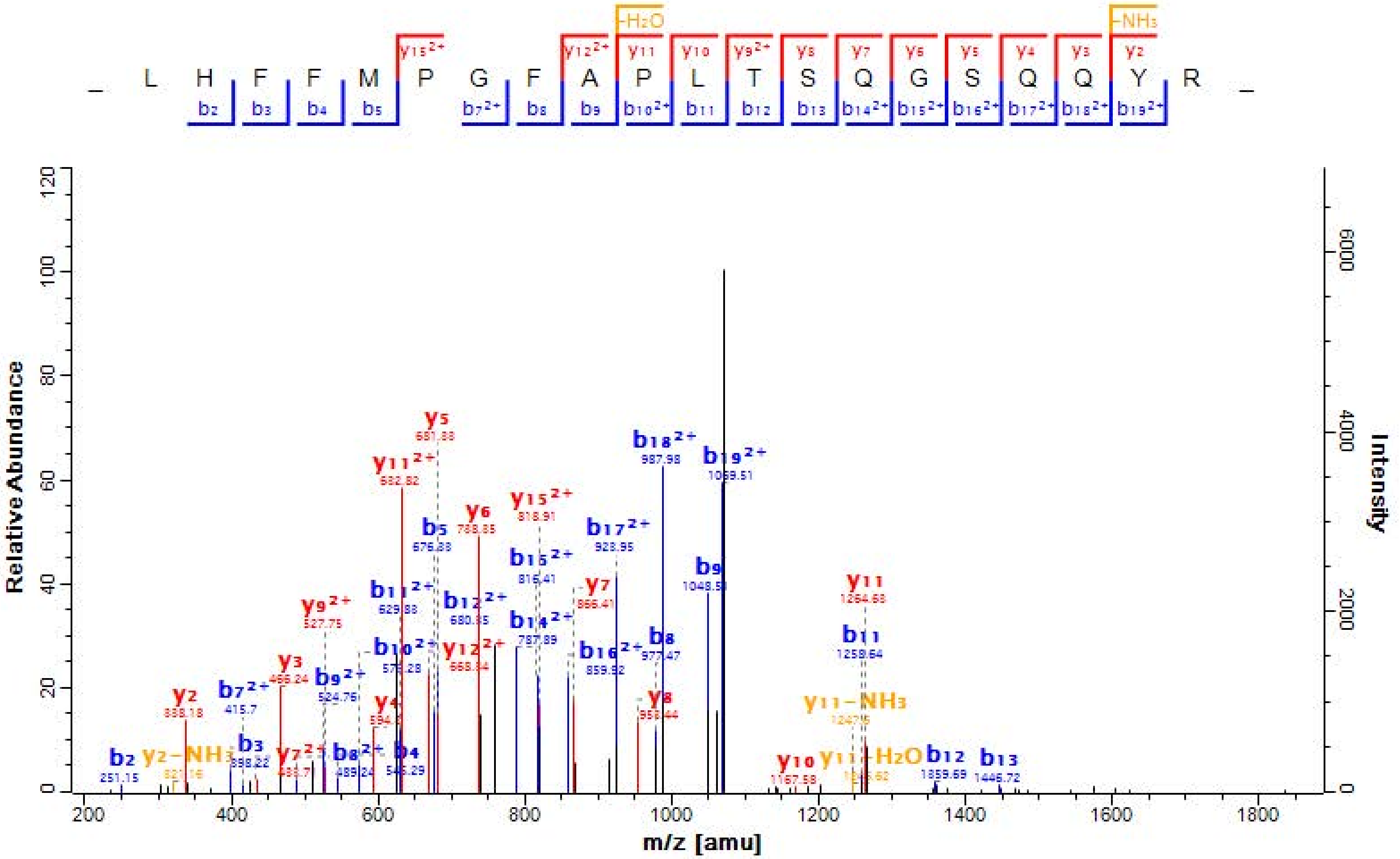
Mass:	2551.449
m/z:	638.86953
Charge:	4+
Retentiontime:	56.667030334472
Score:	59.34237
Mass Error [ppm]:	0.15155
PEP:	0.00033155
Precursor Type:	MULTI

general information

Annotation:	14 of 23
AminoAcids Coverag	61 %
Intensity Coverage:	52 %
Peak Coverage:	21 %
Protein Localisation:	161 ... 183

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.05		115.05	1	N	22				
	244.09	-0.05	244.09	2	E	21	2454.4		2454.4	
	357.18		357.18	3	L	20	2325.4		2325.4	
	494.24		494.24	4	H	19	2212.3		1106.7	-0.128
	608.28	-0.063	608.28	5	N	18	2075.3		2075.3	
	721.36		721.36	6	L	17	1961.2		1961.2	
	834.45		834.45	7	L	16	1848.1		1848.1	
	949.47	-0.097	949.47	8	D	15	1735		1735	
+0.07	543.3		1085.6	9	K	14	1620		1620	
	1182.6		1182.6	10	P	13	1483.9		1483.9	
	1310.7		1310.7	11	Q	12	1386.9		1386.9	
	1423.8		1423.8	12	L	11	1258.8		1258.8	
+0.3637	776.42		1551.8	13	Q	10	1145.7		1145.7	
+0.1739	804.93		1608.9	14	G	9	1017.7		1017.7	
+0.3137	861.47		1721.9	15	I	8	960.63	-0.031	960.63	
	1819		1819	16	P	7	847.55	-0.015	424.28	+0.1334
+0.2856	959.54		1918.1	17	V	6	750.5		750.5	
+0.2568	1016.1		2031.1	18	L	5	651.43		326.22	+0.0845
+0.3474	1065.6		2130.2	19	V	4	538.34	-0.299	538.34	
	2243.3		2243.3	20	L	3	439.28	+0.0962	439.28	
	2300.3		2300.3	21	G	2	326.19		326.19	
	2414.4		2414.4	22	N	1	269.17		269.17	
				23	K	0	155.13		155.13	

Scan number	8172	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	238.07



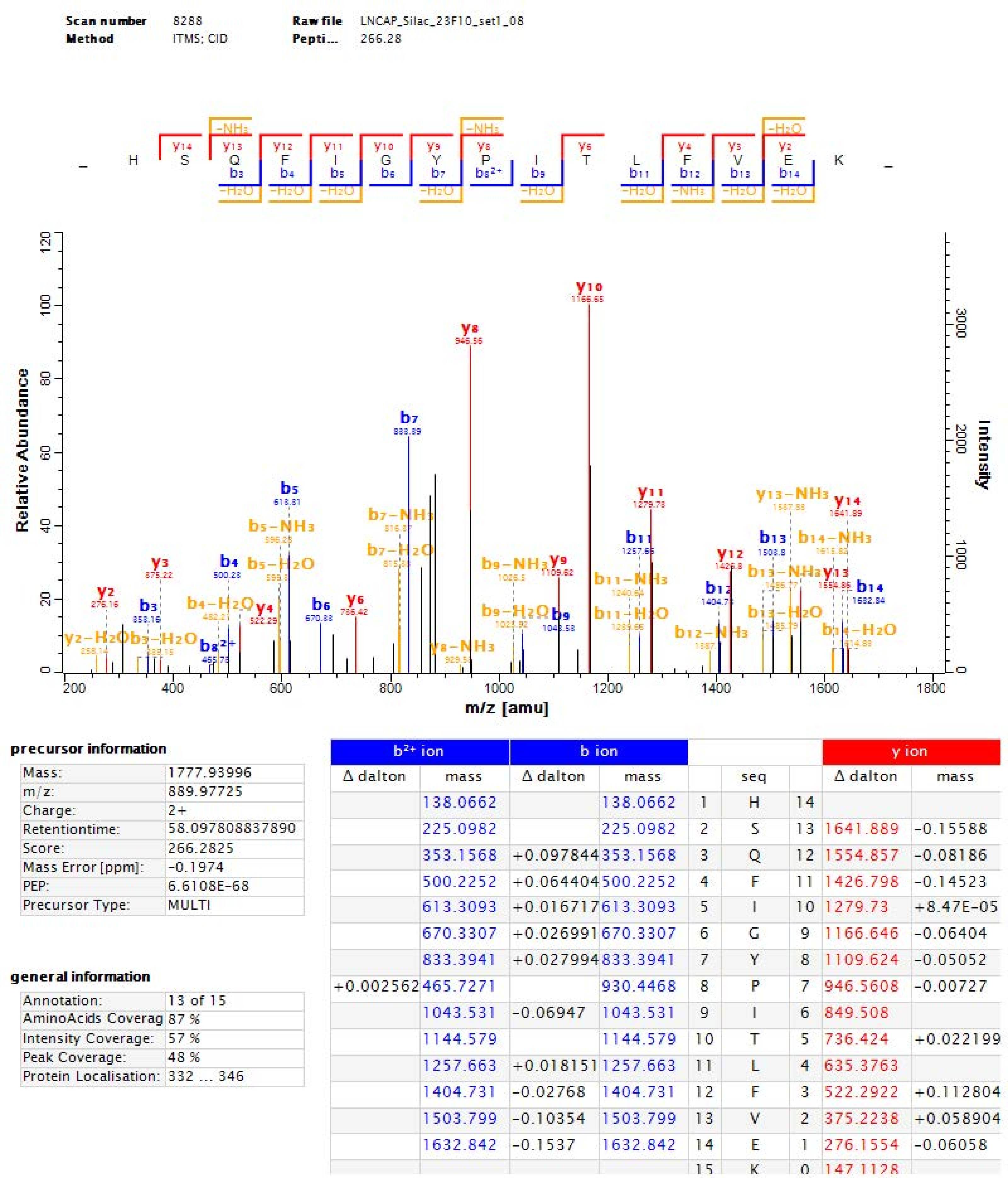
precursor information

Mass:	2311.12002
m/z:	771.38062
Charge:	3+
Retentiontime:	57.002693176269
Score:	238.0663
Mass Error [ppm]:	-0.33963
PEP:	3.8747E-75
Precursor Type:	MULTI

general information

Annotation:	18 of 20
AminoAcids Coverag	90 %
Intensity Coverage:	66 %
Peak Coverage:	45 %
Protein Localisation:	263 ... 282

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	19				
	251.15	+0.0265	251.15	2	H	18	2199		2199	
	398.22	+0.1087	398.22	3	F	17	2062		2062	
	545.29	-0.29	545.29	4	F	16	1914.9		1914.9	
	676.33	+0.0009	676.33	5	M	15	1767.8		1767.8	
	773.38		773.38	6	P	14	1636.8		818.91	+0.0518
+0.1557	415.7		830.4	7	G	13	1539.8		1539.8	
+0.3523	489.24	-0.082	977.47	8	F	12	1482.7		1482.7	
+0.0984	524.76	+0.0053	1048.5	9	A	11	1335.7		668.34	+0.2937
+0.0997	573.28		1145.6	10	P	10	1264.6	-0.029	632.82	+0.2556
+0.2547	629.83	+0.0009	1258.6	11	L	9	1167.6	-0.006	1167.6	
+0.1827	680.35	+0.0471	1359.7	12	T	8	1054.5		527.75	-0.11
	1446.7	+0.3111	1446.7	13	S	7	953.44	+0.1351	953.44	
+0.2228	787.89		1574.8	14	Q	6	866.41	+0.0489	433.71	+0.2279
+0.1212	816.41		1631.8	15	G	5	738.35	+0.0384	738.35	
+0.2154	859.92		1718.8	16	S	4	681.33	+0.0728	681.33	
+0.2652	923.95		1846.9	17	Q	3	594.3	+0.0276	594.3	
+0.2468	987.98		1975	18	Q	2	466.24	+0.1305	466.24	
-0.015	1069.5		2138	19	Y	1	338.18	+0.1193	338.18	
				20	R	0	175.12		175.12	



Scan number	8288	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	266.28

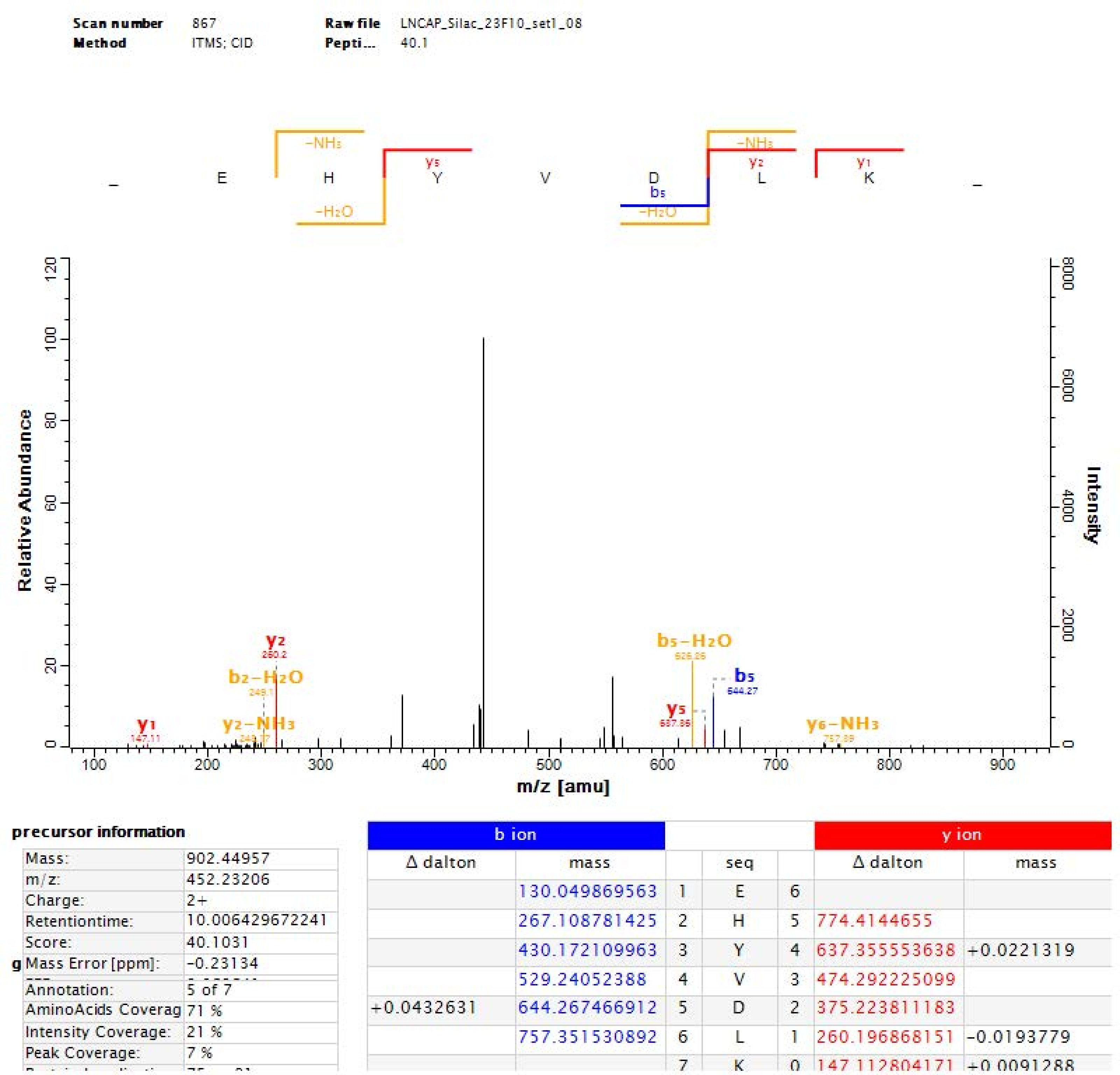
precursor information

Mass:	1777.93996
m/z:	889.97725
Charge:	2+
Retentiontime:	58.097808837890
Score:	266.2825
Mass Error [ppm]:	-0.1974
PEP:	6.6108E-68
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	57 %
Peak Coverage:	48 %
Protein Localisation:	332 ... 346

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	138.0662		138.0662	1	H	14		
	225.0982		225.0982	2	S	13	1641.889	-0.15588
	353.1568	+0.097844	353.1568	3	Q	12	1554.857	-0.08186
	500.2252	+0.064404	500.2252	4	F	11	1426.798	-0.14523
	613.3093	+0.016717	613.3093	5	I	10	1279.73	+8.47E-05
	670.3307	+0.026991	670.3307	6	G	9	1166.646	-0.06404
	833.3941	+0.027994	833.3941	7	Y	8	1109.624	-0.05052
+0.002562	465.7271		930.4468	8	P	7	946.5608	-0.00727
	1043.531	-0.06947	1043.531	9	I	6	849.508	
	1144.579		1144.579	10	T	5	736.424	+0.022199
	1257.663	+0.018151	1257.663	11	L	4	635.3763	
	1404.731	-0.02768	1404.731	12	F	3	522.2922	+0.112804
	1503.799	-0.10354	1503.799	13	V	2	375.2238	+0.058904
	1632.842	-0.1537	1632.842	14	E	1	276.1554	-0.06058
				15	K	0	147.1128	



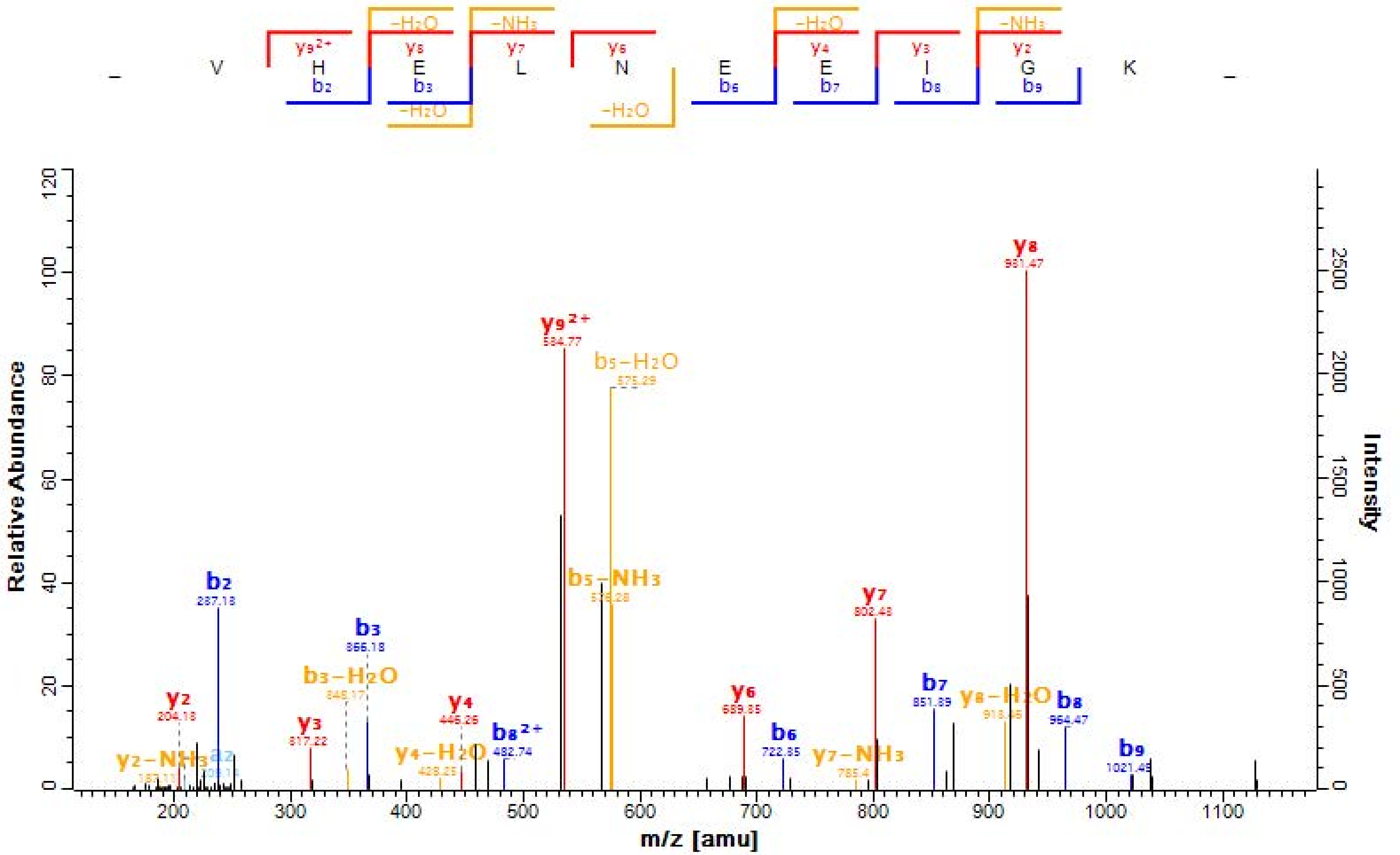
Scan number	867	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	40.1

precursor information

Mass:	902.44957
m/z:	452.23206
Charge:	2+
Retentiontime:	10.006429672241
Score:	40.1031
Mass Error [ppm]:	−0.23134
Annotation:	5 of 7
AminoAcids Coverag	71 %
Intensity Coverage:	21 %
Peak Coverage:	7 %

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	130.049869563	1	E	6		
	267.108781425	2	H	5	774.4144655	
	430.172109963	3	Y	4	637.355553638	+0.0221319
	529.24052388	4	V	3	474.292225099	
+0.0432631	644.267466912	5	D	2	375.223811183	
	757.351530892	6	L	1	260.196868151	−0.0193779
		7	K	0	147.112804171	+0.0091288

Scan number	934	**Raw file**	LNCAP_Silac_23F10_set1_08
Method	ITMS; CID	**Pepti...**	141.88



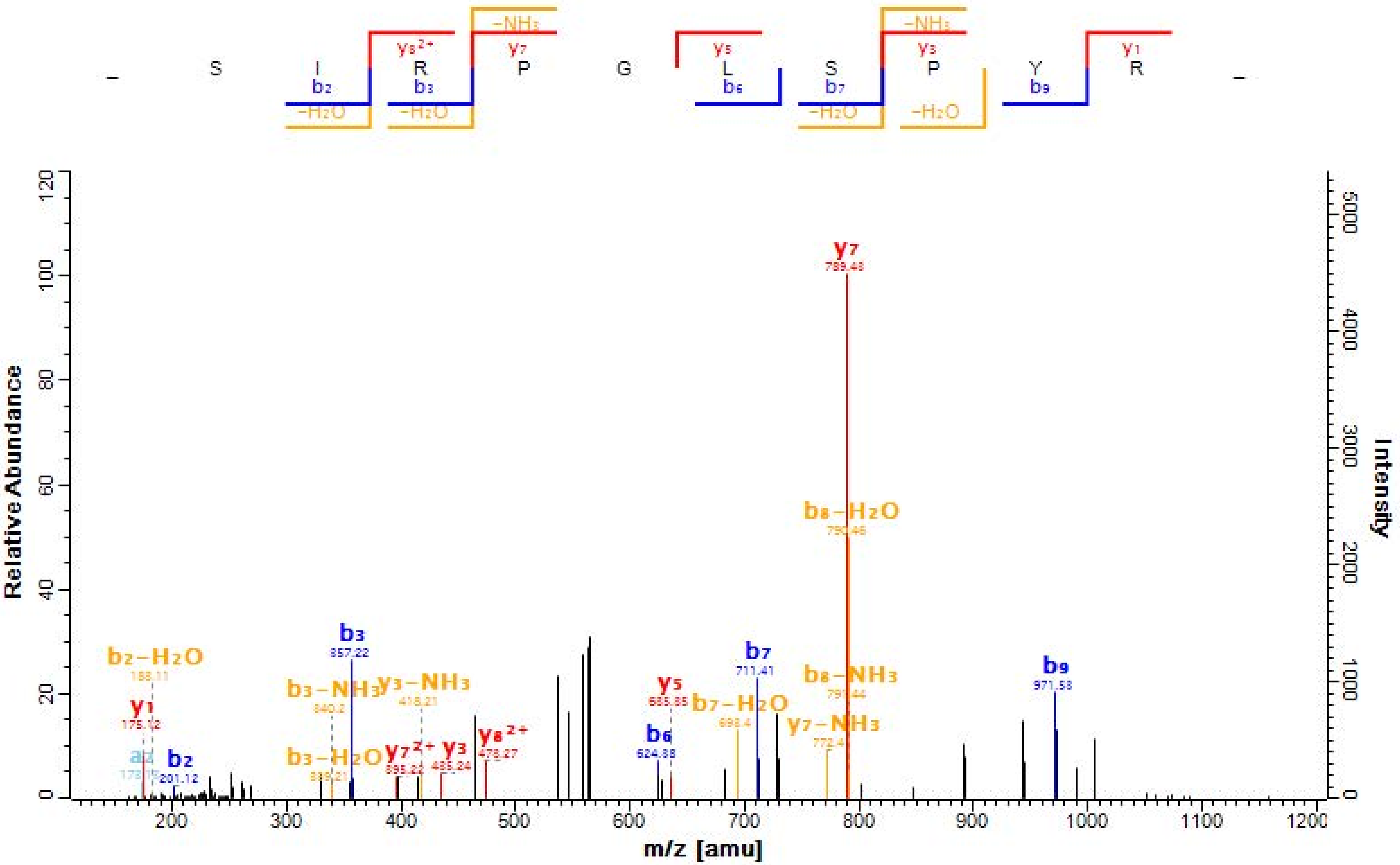
precursor information

Mass:	1166.59354
m/z:	584.30404
Charge:	2+
Retentiontime:	10.395719528198
Score:	141.8786
Mass Error [ppm]:	0.3298
PEP:	0.00019399
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	61 %
Peak Coverage:	22 %
Protein Localisation:	192 ... 201

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.08		100.1		100.1	1	V	9				
+0.066	209.1		237.1	+0.074	237.1	2	H	8	1069		534.8	+0.24
	338.2		366.2	+0.068	366.2	3	E	7	931.5	+0.004	931.5	
	451.3		479.3		479.3	4	L	6	802.4	+0.022	802.4	
	565.3		593.3		593.3	5	N	5	689.3	+0.129	689.3	
	694.4		722.3	+0.059	722.3	6	E	4	575.3		575.3	
	823.4		851.4	-0.01	851.4	7	E	3	446.3	+0.124	446.3	
	936.5	-0.14	482.7	-0.06	964.5	8	I	2	317.2	-0.01	317.2	
	993.5		1021	+0.066	1021	9	G	1	204.1	+0.075	204.1	
						10	K	0	147.1		147.1	

Scan number	1502	**Raw file**	LNCAP_Silac_23F10_set1_09
Method	ITMS; CID	**Pepti...**	101.97



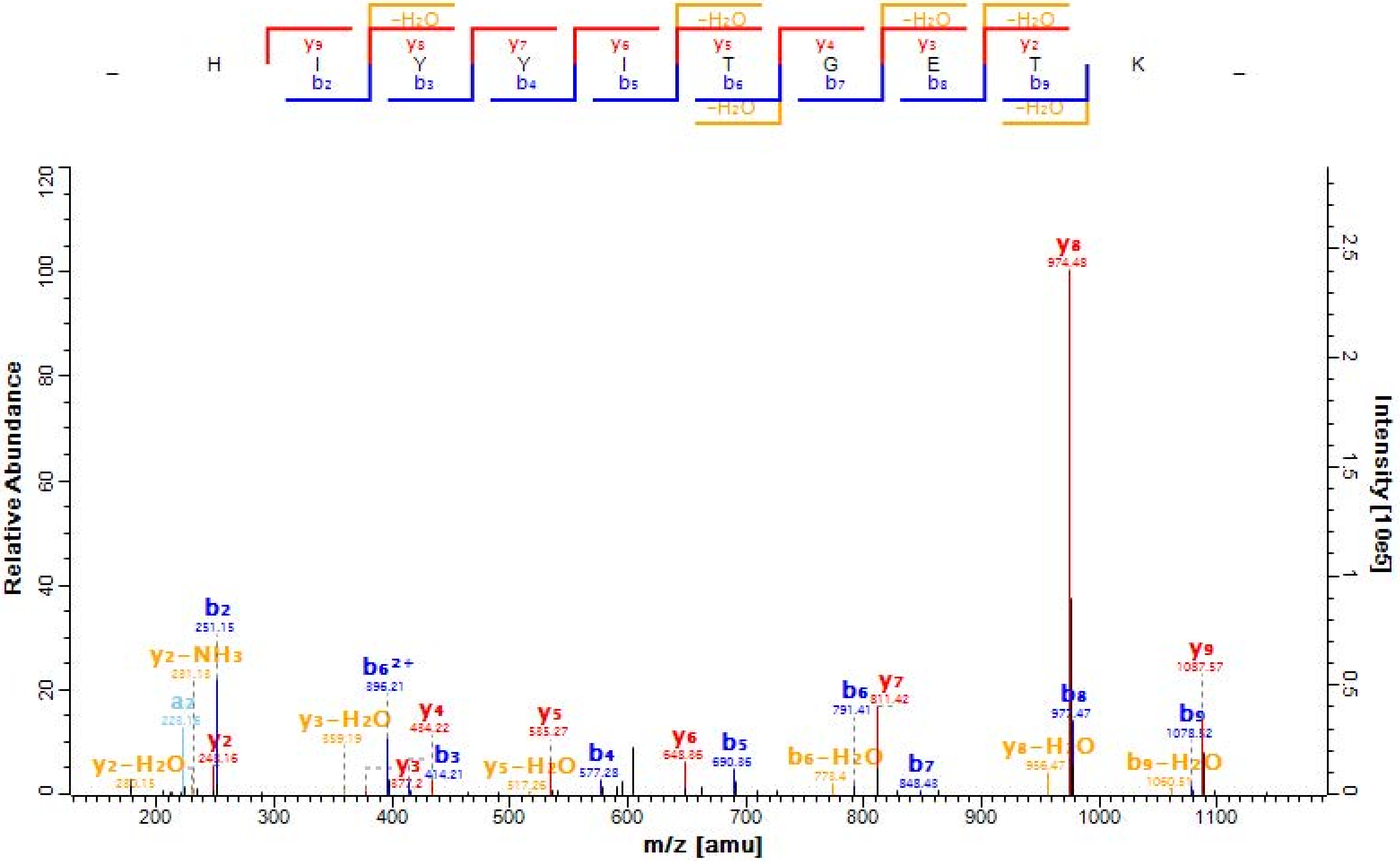
precursor information

Mass:	1144.63553
m/z:	573.32504
Charge:	2+
Retentiontime:	13.566512107849
Score:	101.9741
Mass Error [ppm]:	0.20649
PEP:	0.0051846
Precursor Type:	ISO

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	45 %
Peak Coverage:	18 %
Protein Localisation:	103 ... 112

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	60.044		88.039	1	S	9				
+0.0055	173.13	+0.034	201.12	2	I	8	1058.6		1058.6	
	329.23	+0.0412	357.22	3	R	7	945.53		473.27	+0.3187
	426.28		454.28	4	P	6	789.43	+0.0365	395.22	+0.216
	483.3		511.3	5	G	5	692.37		692.37	
	596.39	+0.0238	624.38	6	L	4	635.35	+0.0864	635.35	
	683.42	-0.023	711.41	7	S	3	522.27		522.27	
	780.47		808.47	8	P	2	435.24	+0.1693	435.24	
	943.54	+0.0265	971.53	9	Y	1	338.18		338.18	
				10	R	0	175.12	+0.0402	175.12	

Scan number 1660 **Raw file** LNCAP_Silac_23F10_set1_09
Method ITMS; CID **Pepti...** 182.64

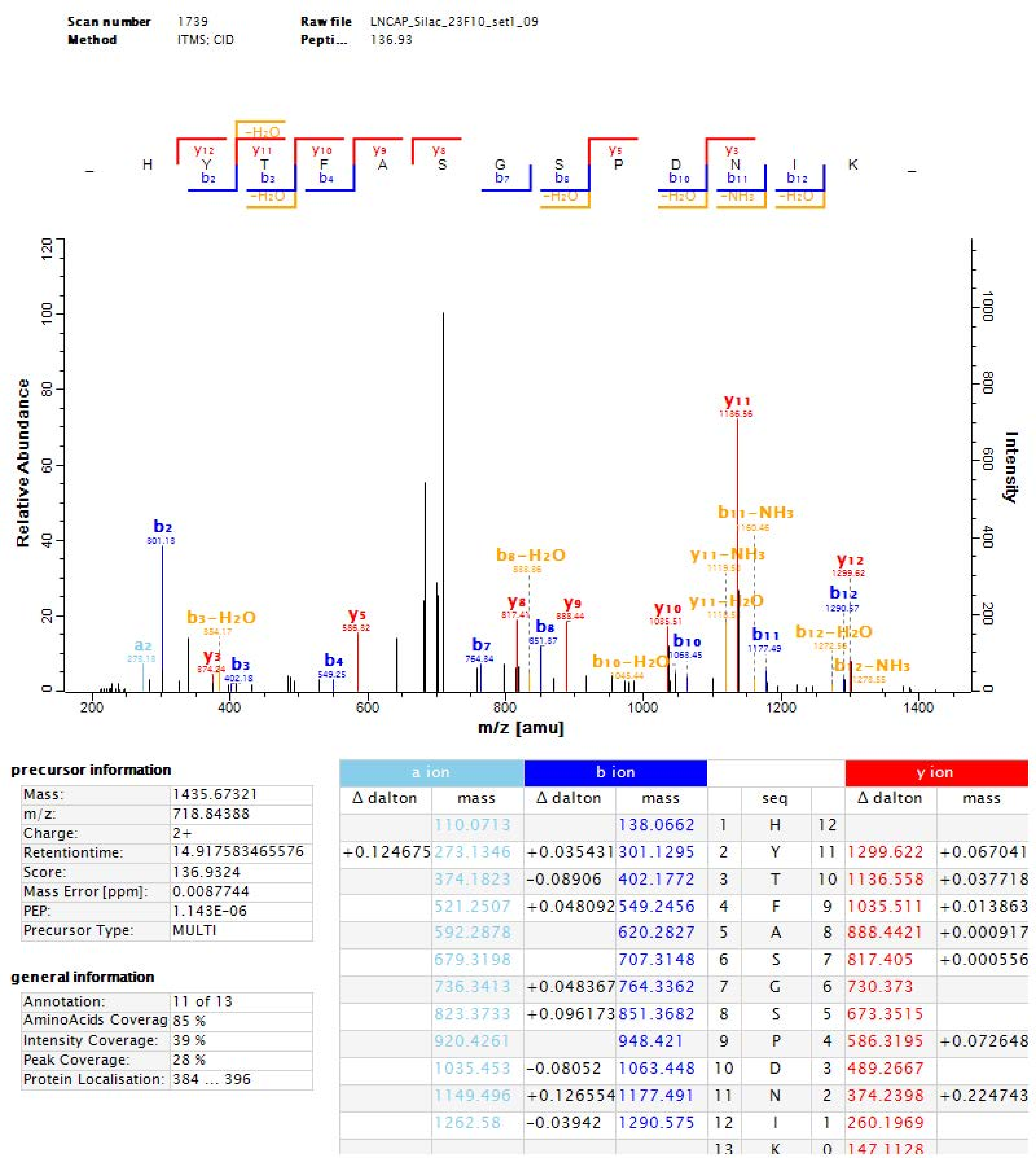


precursor information

Mass:	1223.61852
m/z:	612.81654
Charge:	2+
Retentiontime:	14.455381393432
Score:	182.6384
Mass Error [ppm]:	-0.092898
PEP:	1.0019E-06
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	70 %
Peak Coverage:	36 %
Protein Localisation:	612 ... 621

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	110.07		138.07		138.07	1	H	9		
-0.028	223.16		251.15	-0.023	251.15	2	I	8	1087.6	-0.031
	386.22		414.21	+0.0826	414.21	3	Y	7	974.48	+0.0157
	549.28		577.28	+0.1244	577.28	4	Y	6	811.42	+0.0283
	662.37		690.36	-0.084	690.36	5	I	5	648.36	-0.002
	763.41	+0.0123	396.21	-0.052	791.41	6	T	4	535.27	+0.0744
	820.44		848.43	+0.1961	848.43	7	G	3	434.22	+0.0344
	949.48		977.47	+0.0062	977.47	8	E	2	377.2	+0.1709
	1050.5		1078.5	-0.025	1078.5	9	T	1	248.16	+0.049
						10	K	0	147.11	



Scan number	1739	**Raw file**	LNCAP_Silac_23F10_set1_09
Method	ITMS; CID	**Pepti...**	136.93

precursor information

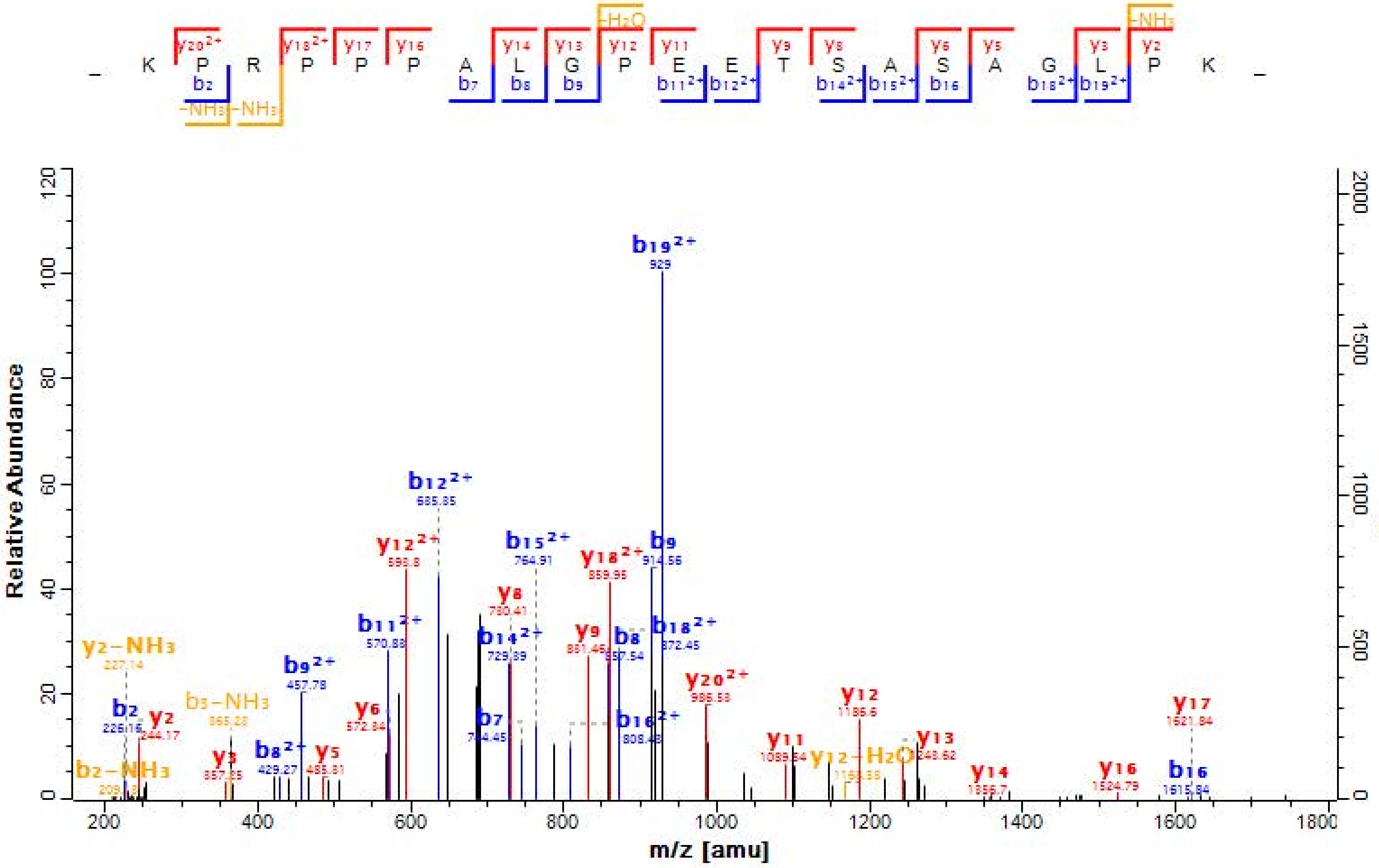
Mass:	1435.67321
m/z:	718.84388
Charge:	2+
Retentiontime:	14.917583465576
Score:	136.9324
Mass Error [ppm]:	0.0087744
PEP:	1.143E-06
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	39 %
Peak Coverage:	28 %
Protein Localisation:	384 ... 396

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	110.0713		138.0662	1	H	12		
+0.124675	273.1346	+0.035431	301.1295	2	Y	11	1299.622	+0.067041
	374.1823	-0.08906	402.1772	3	T	10	1136.558	+0.037718
	521.2507	+0.048092	549.2456	4	F	9	1035.511	+0.013863
	592.2878		620.2827	5	A	8	888.4421	+0.000917
	679.3198		707.3148	6	S	7	817.405	+0.000556
	736.3413	+0.048367	764.3362	7	G	6	730.373	
	823.3733	+0.096173	851.3682	8	S	5	673.3515	
	920.4261		948.421	9	P	4	586.3195	+0.072648
	1035.453	-0.08052	1063.448	10	D	3	489.2667	
	1149.496	+0.126554	1177.491	11	N	2	374.2398	+0.224743
	1262.58	-0.03942	1290.575	12	I	1	260.1969	
				13	K	0	147.1128	

Scan number	2393	**Raw file**	LNCAP_Silac_23F10_set1_09
Method	ITMS; CID	**Pepti...**	170.61



precursor information

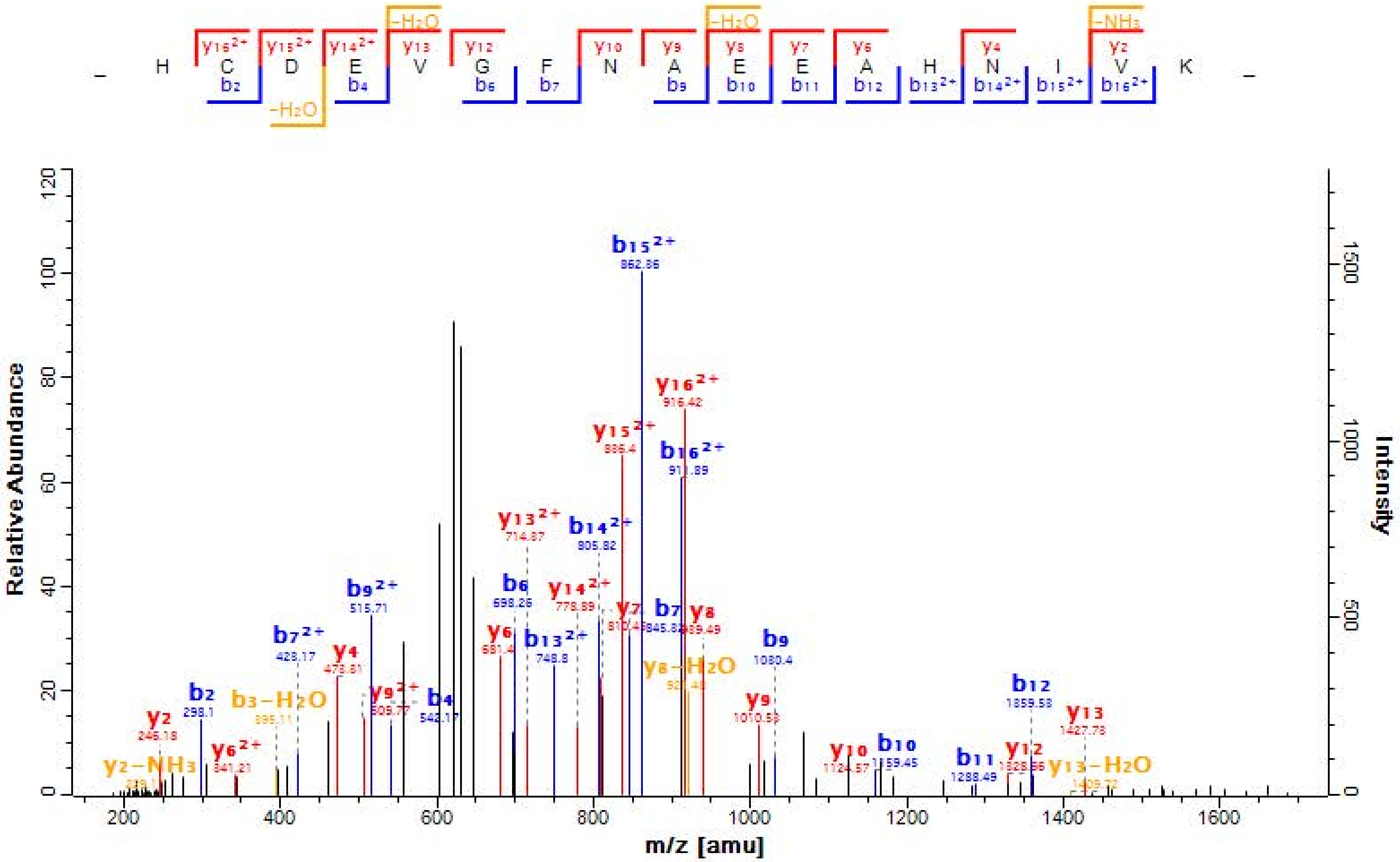
Mass:	2099.13685
m/z:	700.71956
Charge:	3+
Retentiontime:	18.694150924682
Score:	170.608
Mass Error [ppm]:	-0.30918
PEP:	1.2744E-36
Precursor Type:	MULTI

general information

Annotation:	19 of 21
AminoAcids Coverag	90 %
Intensity Coverage:	61 %
Peak Coverage:	33 %
Protein Localisation:	15 ... 35

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.1		129.1	1	K	20				
	226.16	+0.1007	226.16	2	P	19	1972		986.53	+0.0247
	382.26		382.26	3	R	18	1875		1875	
	479.31		479.31	4	P	17	1718.9		859.95	+0.348
	576.36		576.36	5	P	16	1621.8	+0.1438	1621.8	
	673.41		673.41	6	P	15	1524.8	+0.1147	1524.8	
	744.45	+0.0213	744.45	7	A	14	1427.7		1427.7	
+0.094	429.27	+0.0037	857.54	8	L	13	1356.7	-0.04	1356.7	
+0.244	457.78	-0.061	914.56	9	G	12	1243.6	-0.042	1243.6	
	1011.6		1011.6	10	P	11	1186.6	+0.0326	593.8	+0.2175
+0.2244	570.83		1140.7	11	E	10	1089.5	+0.2602	1089.5	
+0.1813	635.35		1269.7	12	E	9	960.5		960.5	
	1370.7		1370.7	13	T	8	831.46	+0.0594	831.46	
+0.2662	729.39		1457.8	14	S	7	730.41	+0.045	730.41	
+0.1135	764.91		1528.8	15	A	6	643.38		643.38	
+0.2594	808.43	-0.137	1615.8	16	S	5	572.34	-0.045	572.34	
	1686.9		1686.9	17	A	4	485.31	+0.0614	485.31	
+0.3085	872.45		1743.9	18	G	3	414.27		414.27	
+0.2973	929		1857	19	L	2	357.25	+0.0348	357.25	
	1954		1954	20	P	1	244.17	-0.014	244.17	
				21	K	0	147.11		147.11	

Scan number	2903	**Raw file**	LNCAP_Silac_23F10_set1_09
Method	ITMS; CID	**Pepti...**	192.32



precursor information

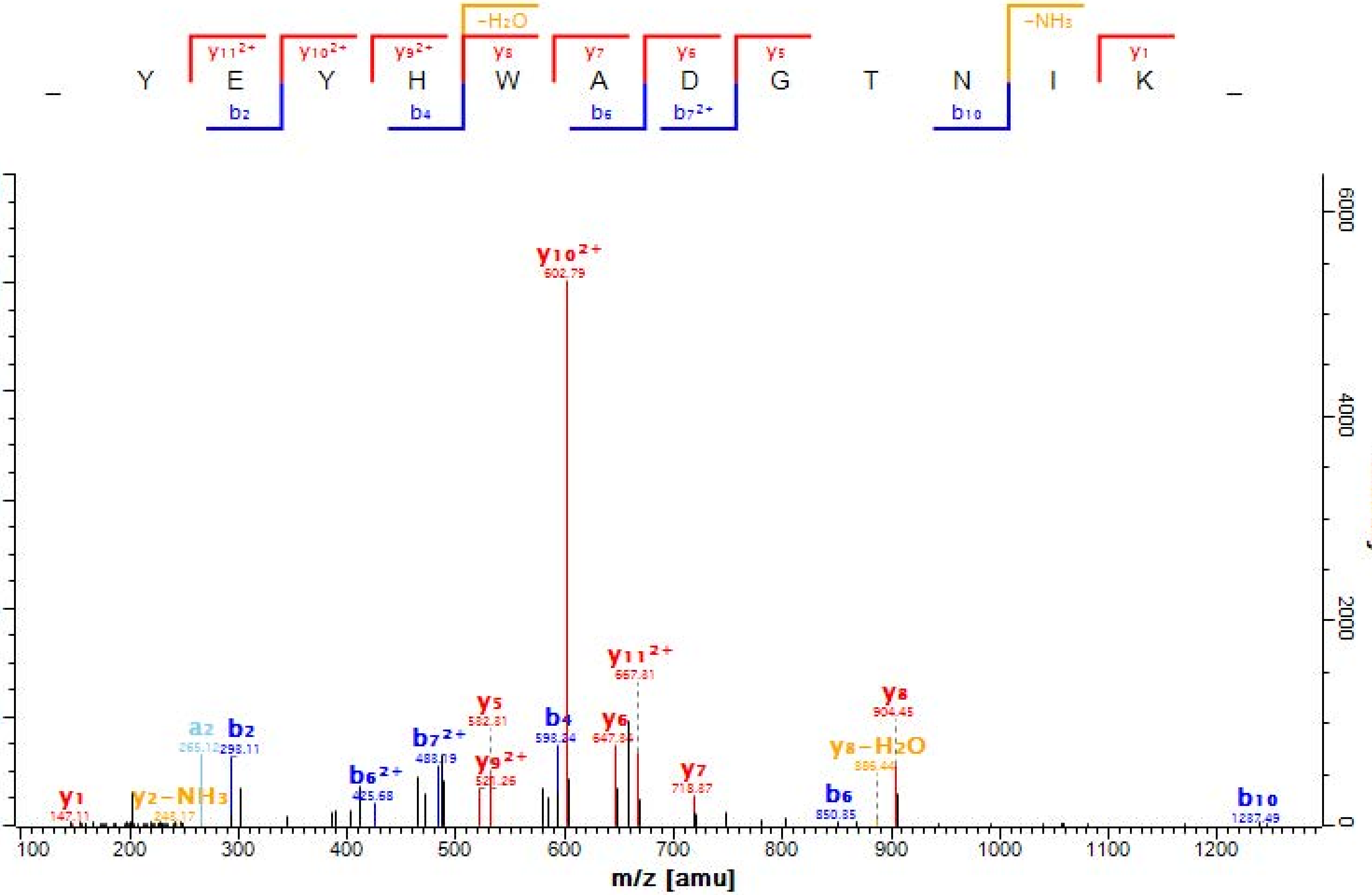
Mass:	1967.87906
m/z:	656.96696
Charge:	3+
Retentiontime:	21.679357528686
Score:	192.3154
Mass Error [ppm]:	-0.26043
PEP:	5.2268E-34
Precursor Type:	MULTI

general information

Annotation:	15 of 17
AminoAcids Coverag	88 %
Intensity Coverage:	52 %
Peak Coverage:	31 %
Protein Localisation:	7 ... 23

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.07		138.07	1	H	16				
	298.1	+0.02	298.1	2	C	15	1831.8		916.42	+0.4227
	413.12		413.12	3	D	14	1671.8		836.4	+0.3854
	542.17	+0.1289	542.17	4	E	13	1556.8		778.89	+0.2394
	641.23		641.23	5	V	12	1427.7	-0.089	714.37	+0.1549
	698.26	+0.0288	698.26	6	G	11	1328.7	+0.0157	1328.7	
+0.2627	423.17	-0.001	845.32	7	F	10	1271.6		1271.6	
	959.37		959.37	8	N	9	1124.6	+0.1381	1124.6	
+0.2487	515.71	+0.0357	1030.4	9	A	8	1010.5	+0.4525	505.77	+0.2746
	1159.4	+0.0184	1159.4	10	E	7	939.49	-0.071	939.49	
	1288.5	-0.15	1288.5	11	E	6	810.45	-0.13	810.45	
	1359.5	-0.026	1359.5	12	A	5	681.4	+0.0747	341.21	+0.2718
+0.3355	748.8		1496.6	13	H	4	610.37		610.37	
+0.1443	805.82		1610.6	14	N	3	473.31	+0.1188	473.31	
+0.2828	862.36		1723.7	15	I	2	359.27		359.27	
+0.2446	911.89		1822.8	16	V	1	246.18	-0.141	246.18	
				17	K	0	147.11		147.11	

Scan number	3053	**Raw file**	LNCAP_Silac_23F10_set1_09
Method	ITMS; CID	**Pepti...**	91.31



precursor information

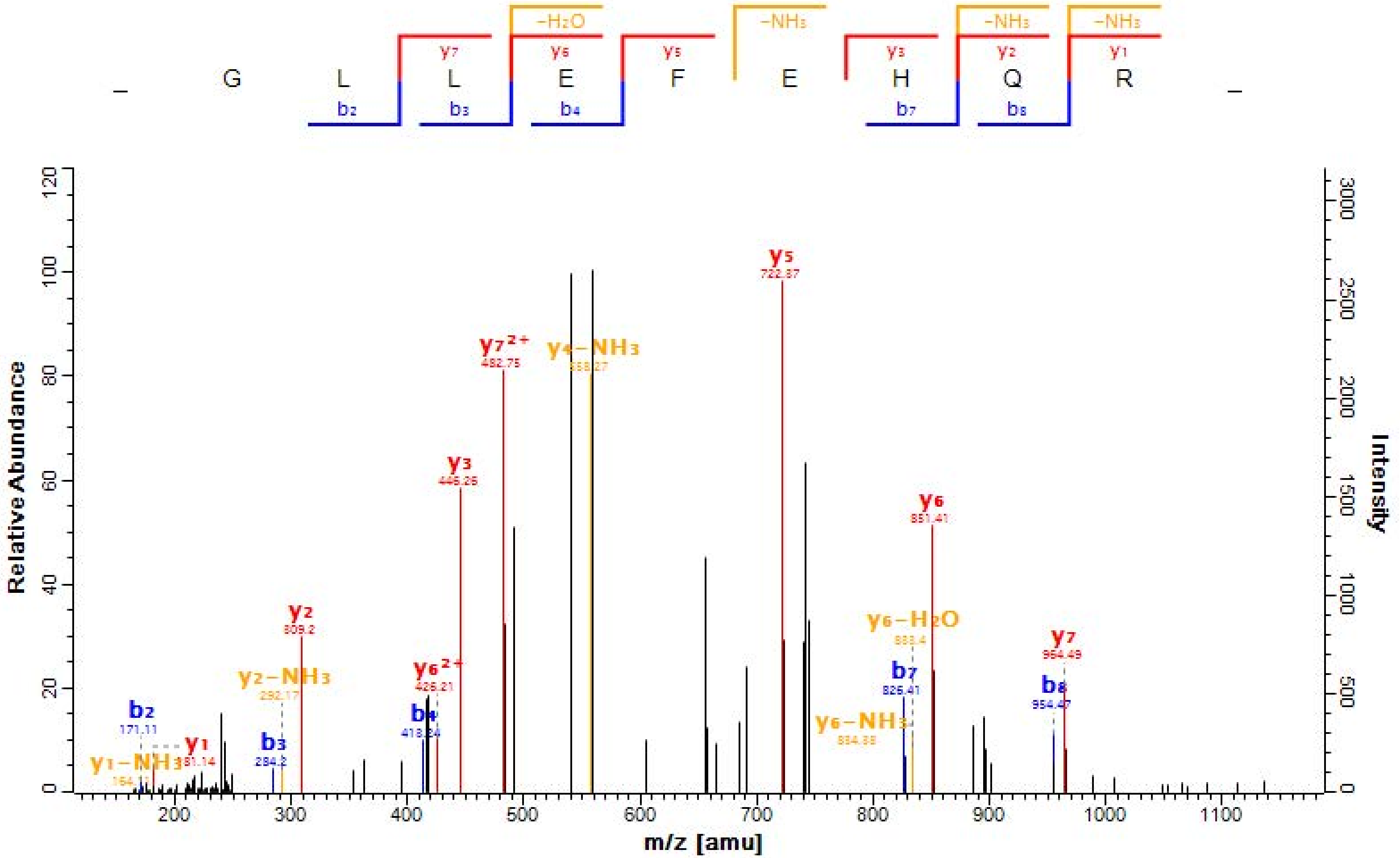
Mass:	1495.67312
m/z:	499.56498
Charge:	3+
Retentiontime:	22.589340209960
Score:	91.31331
Mass Error [ppm]:	-0.048146
PEP:	0.00083906
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	57 %
Peak Coverage:	13 %
Protein Localisation:	98 ... 109

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.1		164.1		164.1	1	Y	11				
+0.048	265.1		293.1	+0.034	293.1	2	E	10	1334		667.3	+0.15
	428.2		456.2		456.2	3	Y	9	1205		602.8	+0.20
	565.2		593.2	+0.438	593.2	4	H	8	1042		521.3	-0.01
	751.3		779.3		779.3	5	W	7	904.5	-0.01	904.5	
	822.4	+0.115	425.7	+0.14	850.4	6	A	6	718.4	-0.06	718.4	
	937.4	+0	483.2		965.4	7	D	5	647.3	+0.069	647.3	
	994.4		1022		1022	8	G	4	532.3	+0.09	532.3	
	1095		1123		1123	9	T	3	475.3		475.3	
	1209		1237	+0.398	1237	10	N	2	374.2		374.2	
	1323		1351		1351	11	I	1	260.2		260.2	
						12	K	0	147.1	+0.026	147.1	

Scan number	3153	**Raw file**	LNCAP_Silac_23F10_set1_09
Method	ITMS; CID	**Pepti...**	116.05

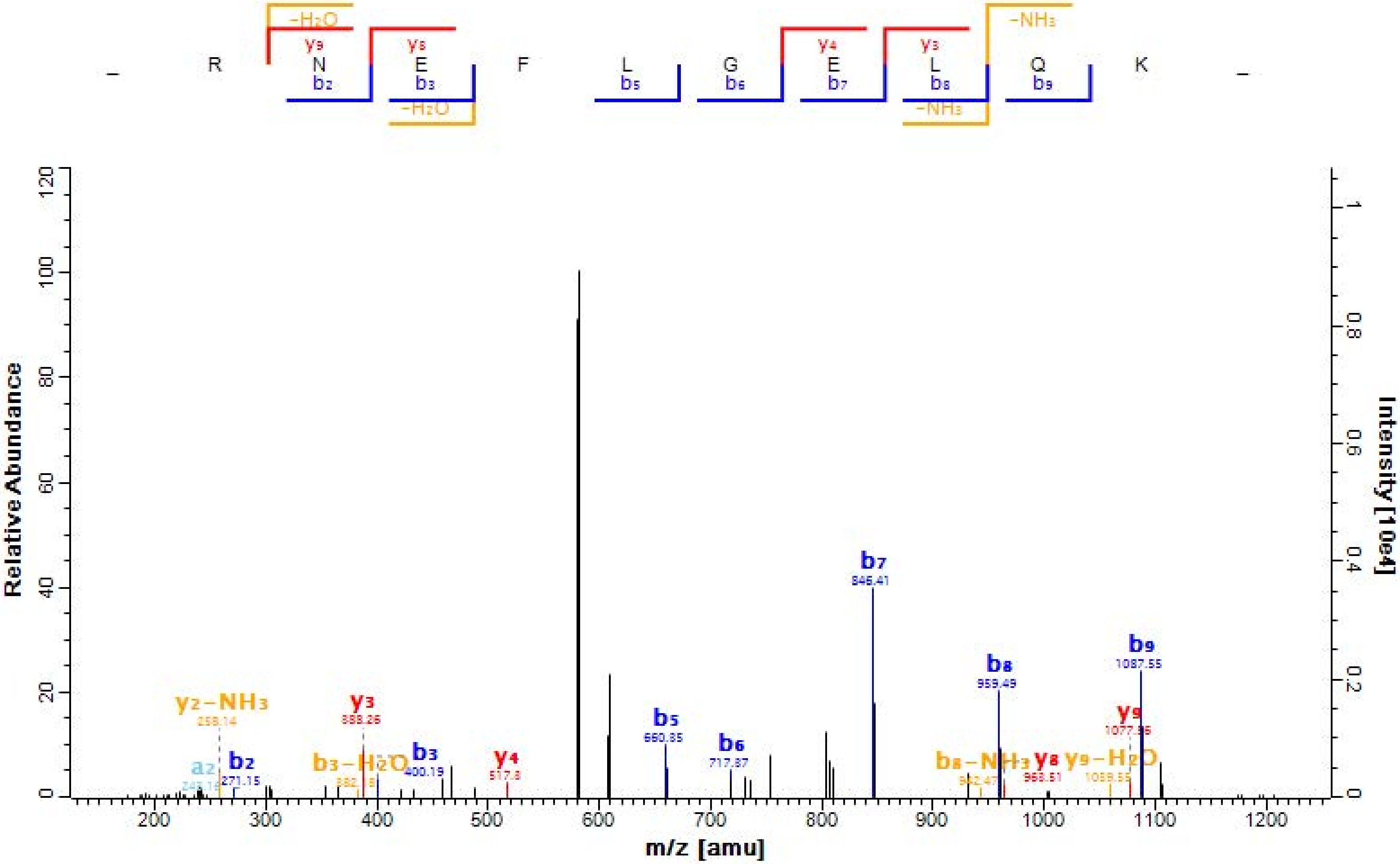


precursor information

Mass:	1127.5723
m/z:	564.79342
Charge:	2+
Retentiontime:	23.226873397827
Score:	116.0506
Mass Error [ppm]:	-0.054077
PEP:	0.0016525
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	37 %
Peak Coverage:	17 %
Protein Localisation:	225 ... 233

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	8				
-0.00793	171.1128	2	L	7	1077.578		1077.578	
+0.190766	284.1969	3	L	6	964.4942	+0.023832	482.7508	+0.026832
+0.108195	413.2395	4	E	5	851.4102	+0.064439	426.2087	+0.096269
	560.3079	5	F	4	722.3676	+0.078162	722.3676	
	689.3505	6	E	3	575.2992		575.2992	
+0.042585	826.4094	7	H	2	446.2566	-0.01859	446.2566	
+0.003905	954.468	8	Q	1	309.1977	+0.011173	309.1977	
		9	R	0	181.1391	+0.014117	181.1391	

Scan number	3170	**Raw file**	LNCAP_Silac_23F10_set1_09
Method	ITMS; CID	**Pepti...**	65.23

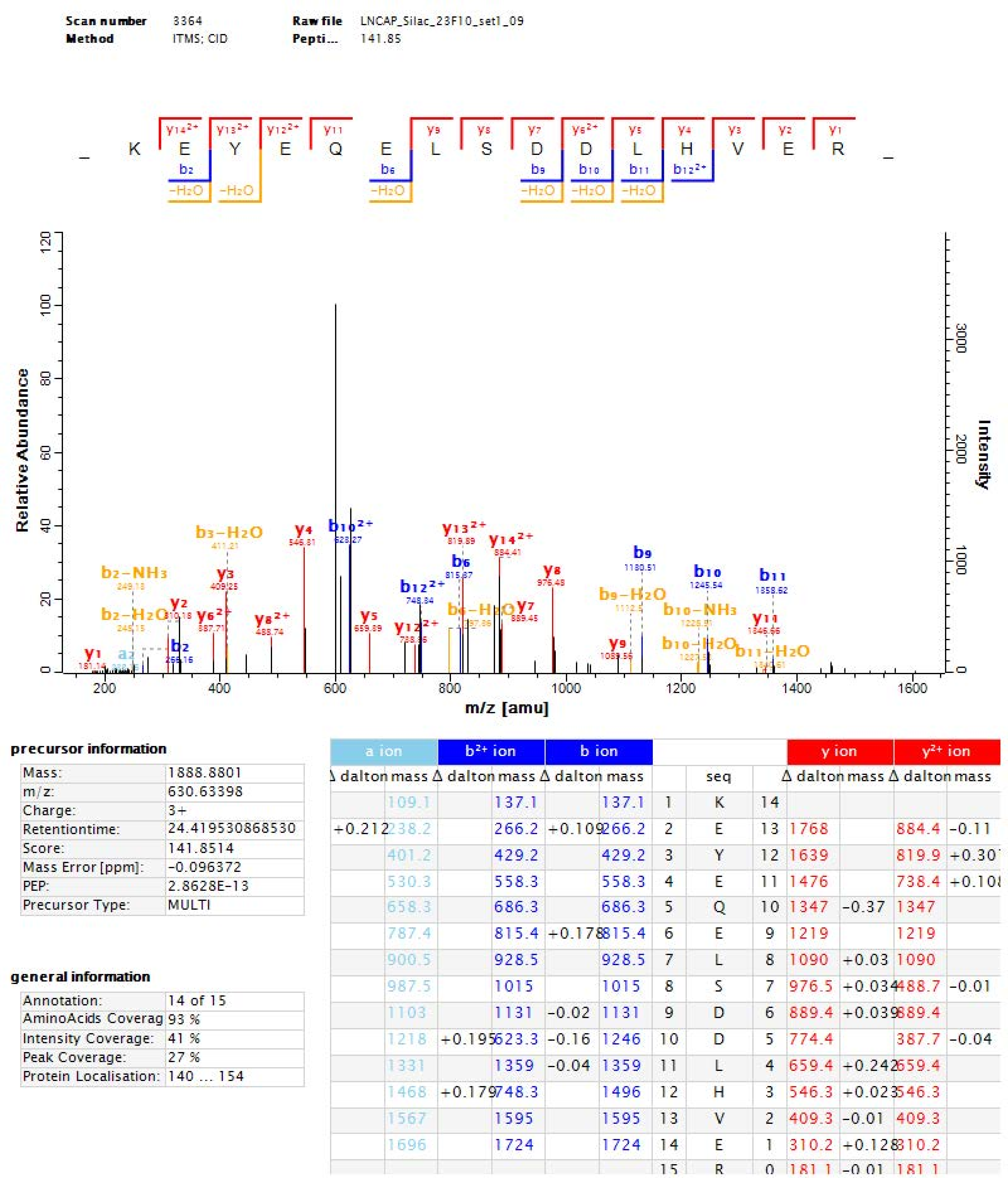


precursor information

Mass:	1232.6516
m/z:	617.33308
Charge:	2+
Retentiontime:	23.324785232543
Score:	65.23174
Mass Error [ppm]:	0.21398
PEP:	0.0080588
Precursor Type:	MULTI

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	24 %
Peak Coverage:	16 %
Protein Localisation:	337 ... 346

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	129.1135		157.1084	1	R	9		
+0.01639	243.1564	+0.034323	271.1513	2	N	8	1077.558	+0.039301
	372.199	+0.05127	400.1939	3	E	7	963.5146	+0.16017
	519.2674		547.2623	4	F	6	834.472	
	632.3515	+0.093739	660.3464	5	L	5	687.4036	
	689.3729	+0.014414	717.3678	6	G	4	574.3195	
	818.4155	+0.014179	846.4104	7	E	3	517.298	-0.00037
	931.4996	+0.00824	959.4945	8	L	2	388.2554	+0.097643
	1059.558	+0.066423	1087.553	9	Q	1	275.1714	
				10	K	0	147.1128	



Scan number	3364	**Raw file**	LNCAP_Silac_23F10_set1_09
Method	ITMS; CID	**Pepti...**	141.85

precursor information

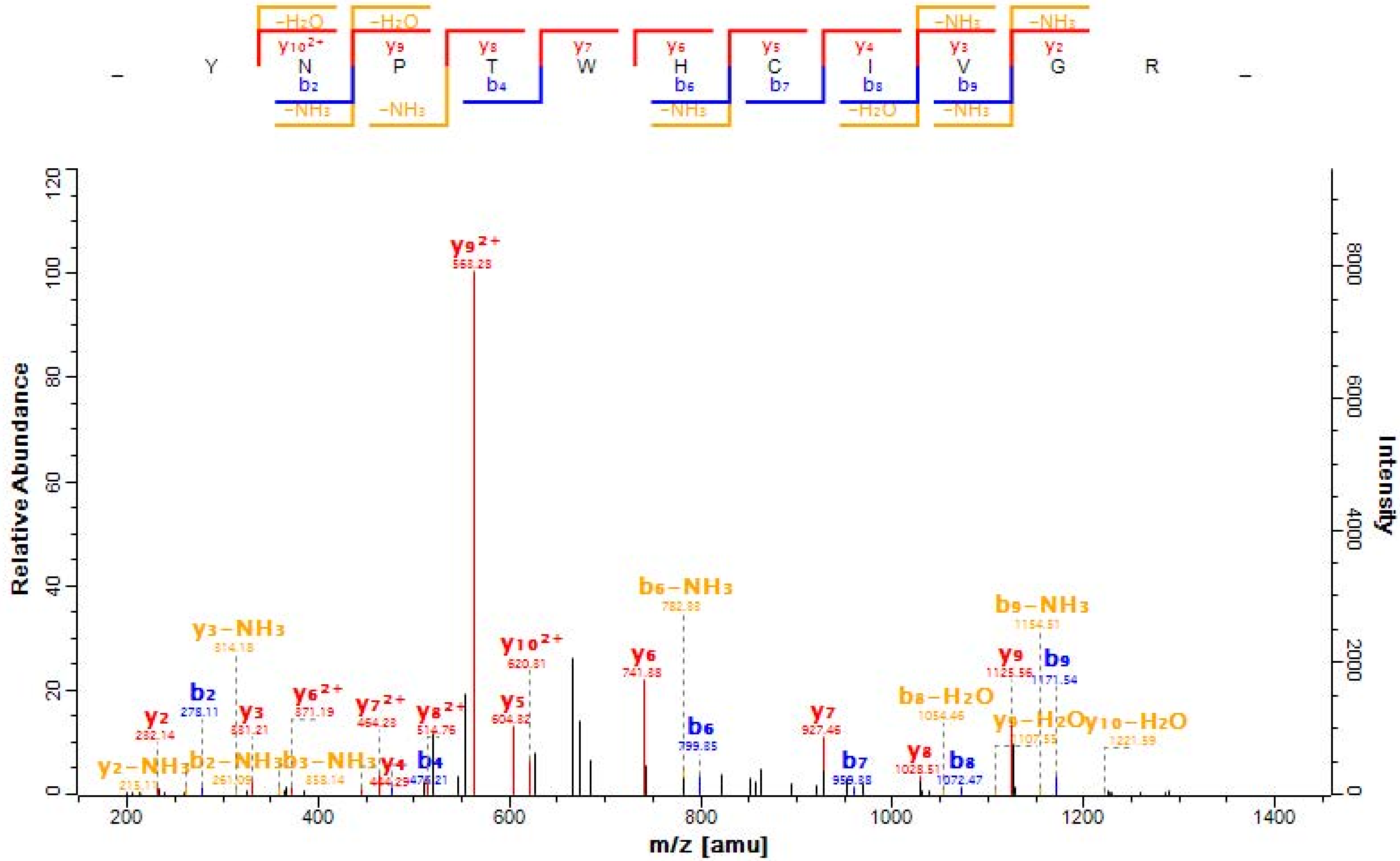
Mass:	1888.8801
m/z:	630.63398
Charge:	3+
Retentiontime:	24.419530868530
Score:	141.8514
Mass Error [ppm]:	-0.096372
PEP:	2.8628E-13
Precursor Type:	MULTI

general information

Annotation:	14 of 15
AminoAcids Coverag	93 %
Intensity Coverage:	41 %
Peak Coverage:	27 %
Protein Localisation:	140 ... 154

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	109.1		137.1		137.1	1	K	14				
+0.212	238.2		266.2	+0.109	266.2	2	E	13	1768		884.4	-0.11
	401.2		429.2		429.2	3	Y	12	1639		819.9	+0.30
	530.3		558.3		558.3	4	E	11	1476		738.4	+0.10
	658.3		686.3		686.3	5	Q	10	1347	-0.37	1347	
	787.4		815.4	+0.178	815.4	6	E	9	1219		1219	
	900.5		928.5		928.5	7	L	8	1090	+0.03	1090	
	987.5		1015		1015	8	S	7	976.5	+0.034	488.7	-0.01
	1103		1131	-0.02	1131	9	D	6	889.4	+0.039	889.4	
	1218	+0.195	623.3	-0.16	1246	10	D	5	774.4		387.7	-0.04
	1331		1359	-0.04	1359	11	L	4	659.4	+0.242	659.4	
	1468	+0.179	748.3		1496	12	H	3	546.3	+0.023	546.3	
	1567		1595		1595	13	V	2	409.3	-0.01	409.3	
	1696		1724		1724	14	E	1	310.2	+0.128	310.2	
						15	R	0	181.1	-0.01	181.1	

Scan number	3373	**Raw file**	LNCAP_Silac_23F10_set1_09
Method	ITMS; CID	**Pepti...**	168.22



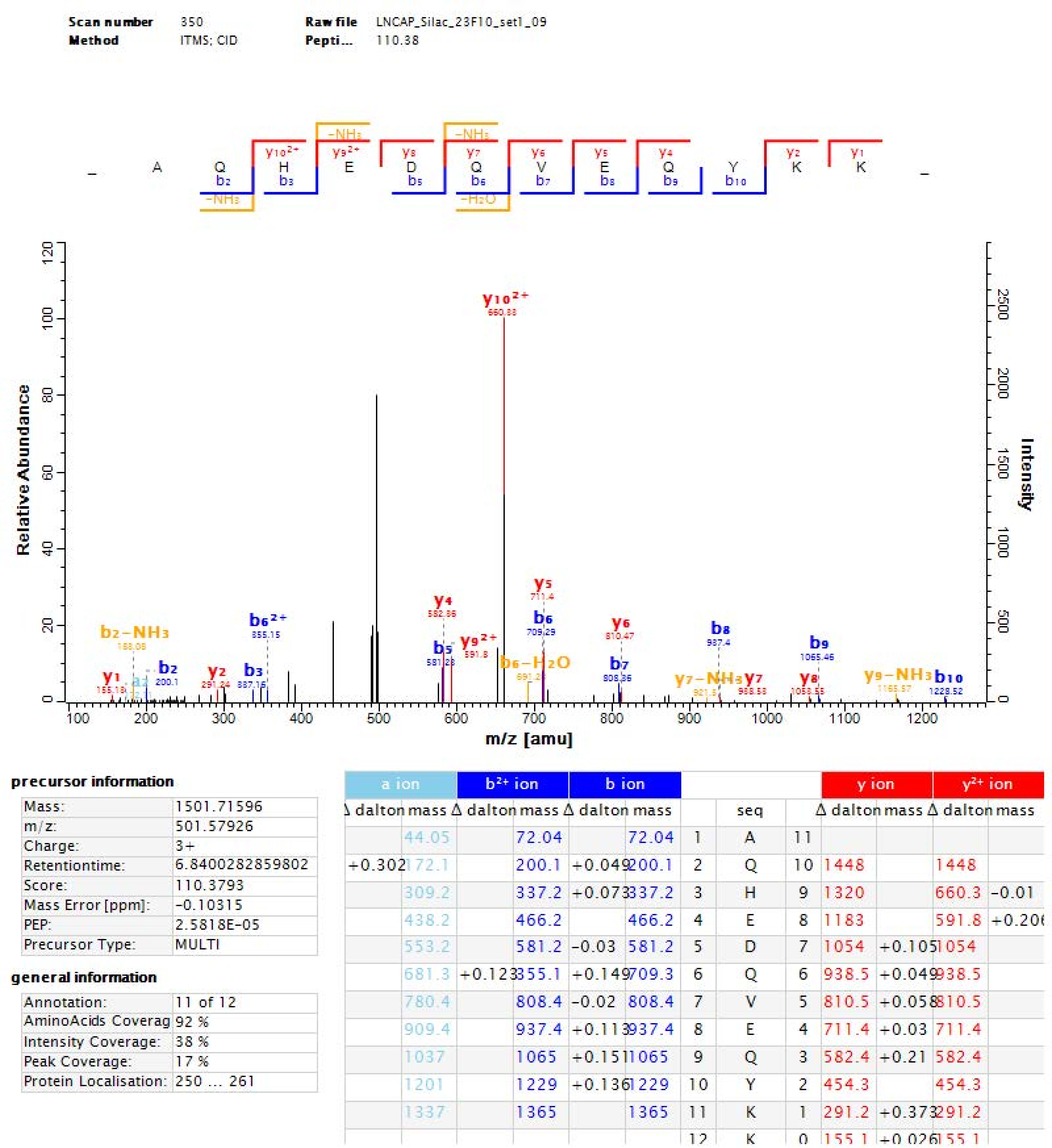
precursor information

Mass:	1401.66143
m/z:	701.83799
Charge:	2+
Retentiontime:	24.467107772827
Score:	168.2202
Mass Error [ppm]:	0.1733
PEP:	7.2464E-08
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	53 %
Peak Coverage:	31 %
Protein Localisation:	50 ... 60

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	164.0706	1	Y	10				
+0.077355	278.1135	2	N	9	1239.605		620.3062	+0.176765
	375.1663	3	P	8	1125.562	+0.030808	563.2847	+0.219102
+0.150222	476.214	4	T	7	1028.509	+0.201736	514.7584	+0.344727
	662.2933	5	W	6	927.4618	-0.03141	464.2345	+0.208472
+0.009861	799.3522	6	H	5	741.3825	+0.093315	371.1949	+0.016744
+0.009547	959.3828	7	C	4	604.3235	-0.02288	604.3235	
-0.02514	1072.467	8	I	3	444.2929	+0.184767	444.2929	
+0.112379	1171.535	9	V	2	331.2088	+0.160006	331.2088	
	1228.557	10	G	1	232.1404	+0.034969	232.1404	
		11	R	0	175.119		175.119	



Scan number	350	**Raw file**	LNCAP_Silac_23F10_set1_09
Method	ITMS; CID	**Pepti...**	110.38

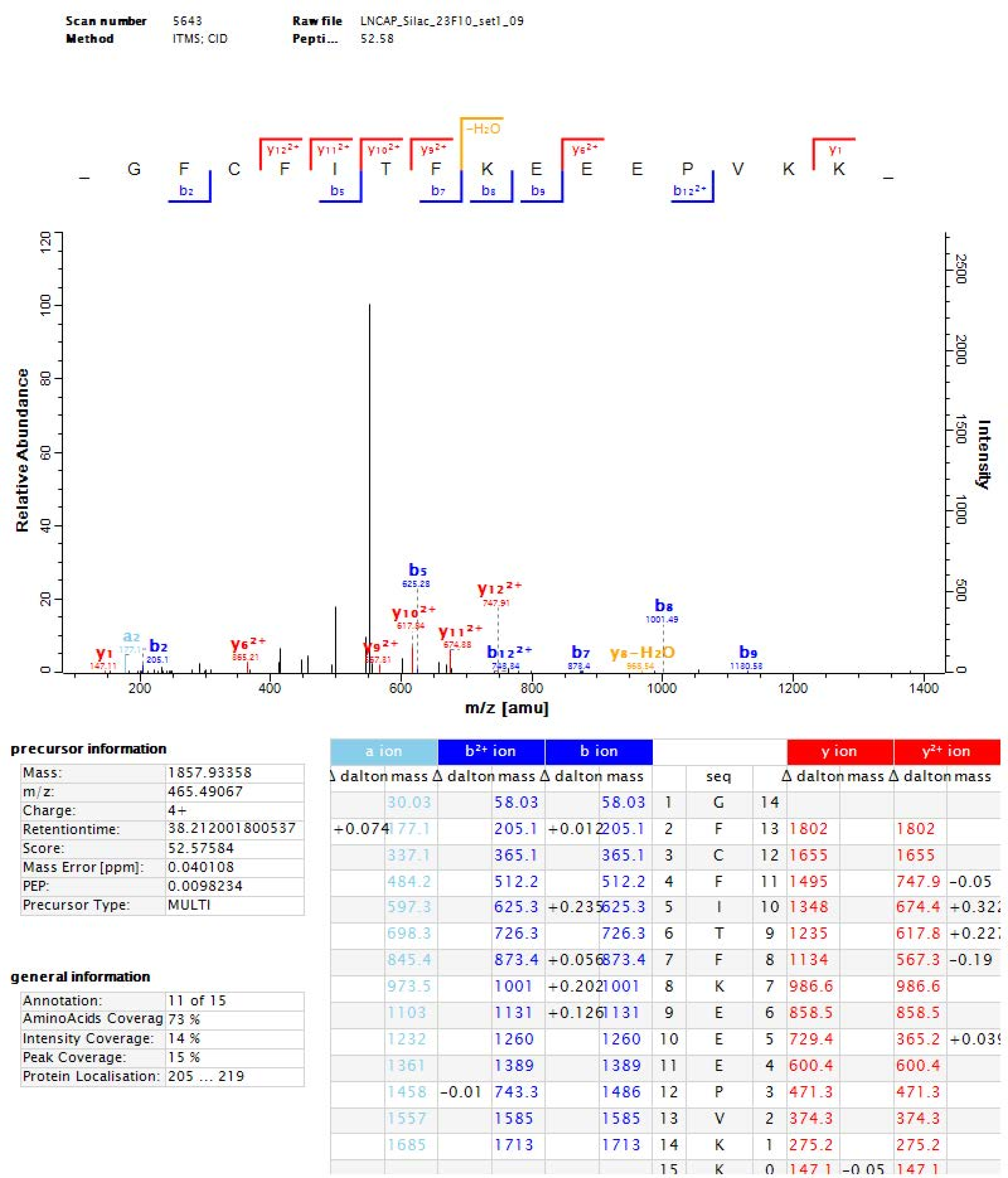
precursor information

Mass:	1501.71596
m/z:	501.57926
Charge:	3+
Retentiontime:	6.8400282859802
Score:	110.3793
Mass Error [ppm]:	-0.10315
PEP:	2.5818E-05
Precursor Type:	MULTI

general information

Annotation:	11 of 12
AminoAcids Coverag	92 %
Intensity Coverage:	38 %
Peak Coverage:	17 %
Protein Localisation:	250 ... 261

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	44.05		72.04		72.04	1	A	11				
+0.302	172.1		200.1	+0.049	200.1	2	Q	10	1448		1448	
	309.2		337.2	+0.073	337.2	3	H	9	1320		660.3	-0.01
	438.2		466.2		466.2	4	E	8	1183		591.8	+0.20
	553.2		581.2	-0.03	581.2	5	D	7	1054	+0.105	1054	
	681.3	+0.123	355.1	+0.149	709.3	6	Q	6	938.5	+0.049	938.5	
	780.4		808.4	-0.02	808.4	7	V	5	810.5	+0.058	810.5	
	909.4		937.4	+0.113	937.4	8	E	4	711.4	+0.03	711.4	
	1037		1065	+0.151	1065	9	Q	3	582.4	+0.21	582.4	
	1201		1229	+0.136	1229	10	Y	2	454.3		454.3	
	1337		1365		1365	11	K	1	291.2	+0.373	291.2	
						12	K	0	155.1	+0.026	155.1	



Scan number	5643	**Raw file**	LNCAP_Silac_23F10_set1_09
Method	ITMS; CID	**Pepti...**	52.58

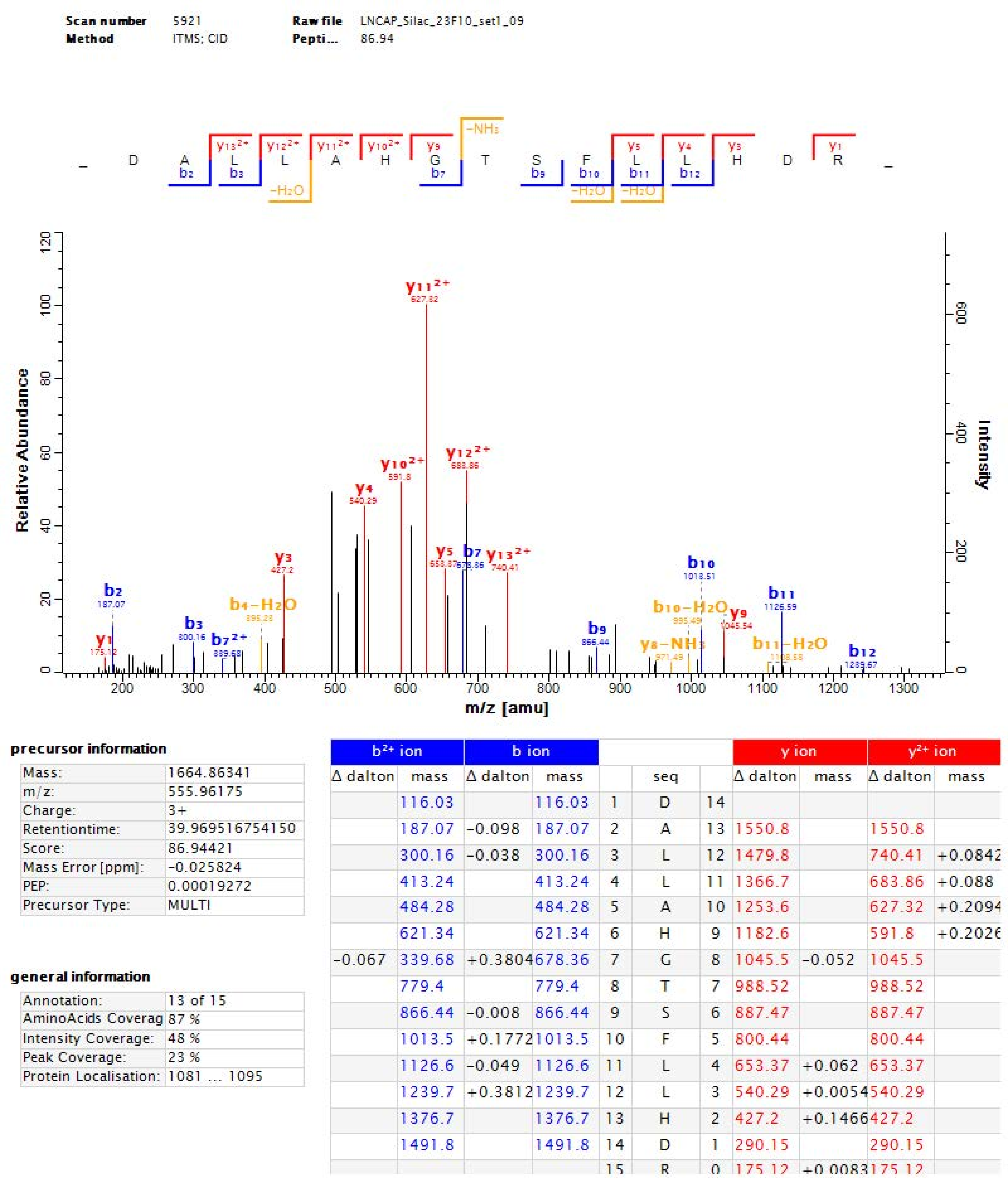
precursor information

Mass:	1857.93358
m/z:	465.49067
Charge:	4+
Retentiontime:	38.212001800537
Score:	52.57584
Mass Error [ppm]:	0.040108
PEP:	0.0098234
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	14 %
Peak Coverage:	15 %
Protein Localisation:	205 ... 219

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	30.03		58.03		58.03	1	G	14				
+0.074	177.1		205.1	+0.012	205.1	2	F	13	1802		1802	
	337.1		365.1		365.1	3	C	12	1655		1655	
	484.2		512.2		512.2	4	F	11	1495		747.9	-0.05
	597.3		625.3	+0.235	625.3	5	I	10	1348		674.4	+0.32
	698.3		726.3		726.3	6	T	9	1235		617.8	+0.22
	845.4		873.4	+0.056	873.4	7	F	8	1134		567.3	-0.19
	973.5		1001	+0.202	1001	8	K	7	986.6		986.6	
	1103		1131	+0.126	1131	9	E	6	858.5		858.5	
	1232		1260		1260	10	E	5	729.4		365.2	+0.03
	1361		1389		1389	11	E	4	600.4		600.4	
	1458	-0.01	743.3		1486	12	P	3	471.3		471.3	
	1557		1585		1585	13	V	2	374.3		374.3	
	1685		1713		1713	14	K	1	275.2		275.2	
						15	K	0	147.1	-0.05	147.1	



Scan number	5921	**Raw file**	LNCAP_Silac_23F10_set1_09
Method	ITMS; CID	**Pepti...**	86.94

precursor information

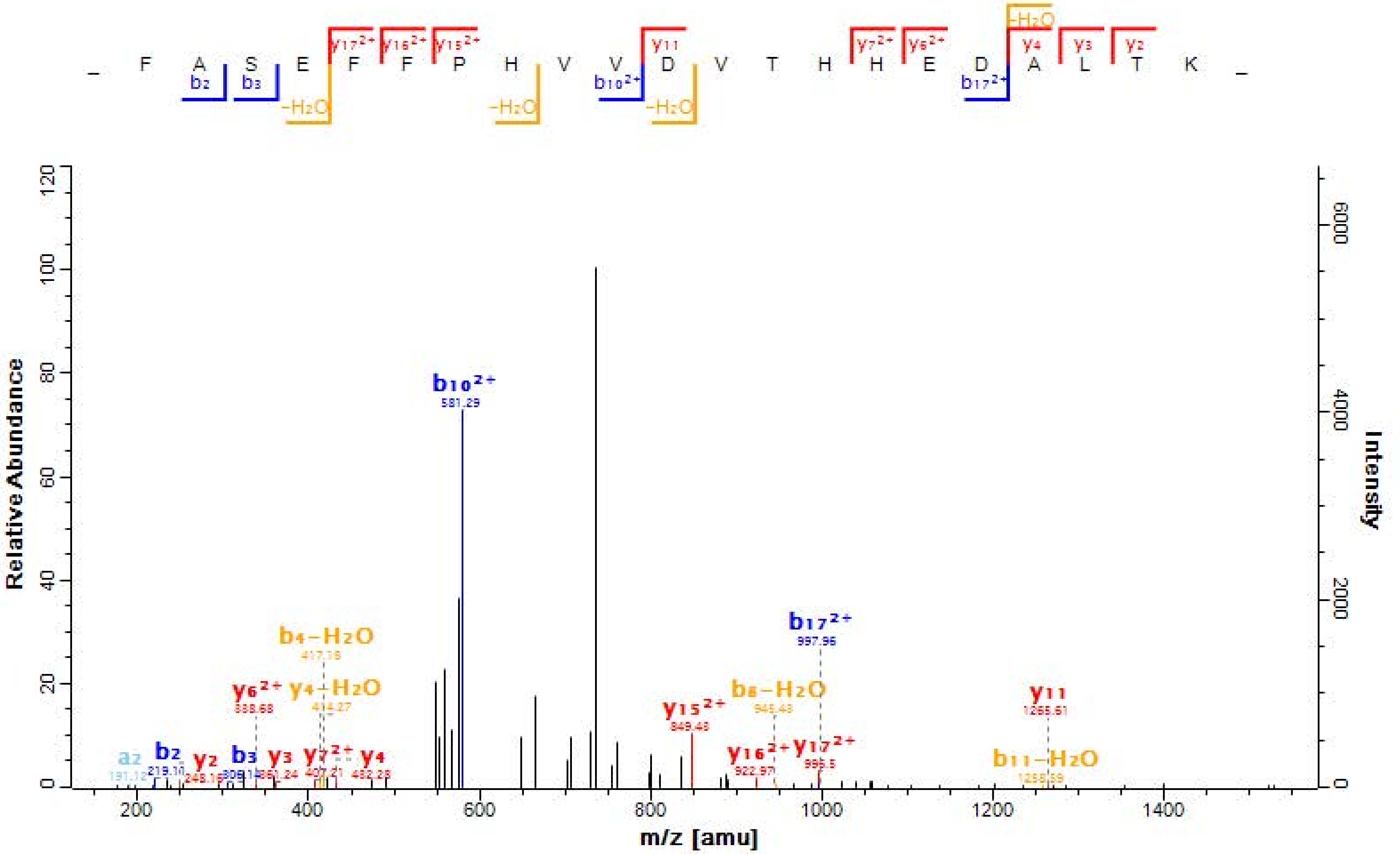
Mass:	1664.86341
m/z:	555.96175
Charge:	3+
Retentiontime:	39.969516754150
Score:	86.94421
Mass Error [ppm]:	-0.025824
PEP:	0.00019272
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	48 %
Peak Coverage:	23 %
Protein Localisation:	1081 ... 1095

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	14				
	187.07	-0.098	187.07	2	A	13	1550.8		1550.8	
	300.16	-0.038	300.16	3	L	12	1479.8		740.41	+0.0842
	413.24		413.24	4	L	11	1366.7		683.86	+0.088
	484.28		484.28	5	A	10	1253.6		627.32	+0.2094
	621.34		621.34	6	H	9	1182.6		591.8	+0.2026
-0.067	339.68	+0.3804	678.36	7	G	8	1045.5	-0.052	1045.5	
	779.4		779.4	8	T	7	988.52		988.52	
	866.44	-0.008	866.44	9	S	6	887.47		887.47	
	1013.5	+0.1772	1013.5	10	F	5	800.44		800.44	
	1126.6	-0.049	1126.6	11	L	4	653.37	+0.062	653.37	
	1239.7	+0.3812	1239.7	12	L	3	540.29	+0.0054	540.29	
	1376.7		1376.7	13	H	2	427.2	+0.1466	427.2	
	1491.8		1491.8	14	D	1	290.15		290.15	
				15	R	0	175.12	+0.0083	175.12	

Scan number	6038	**Raw file**	LNCAP_Silac_23F10_set1_09
Method	ITMS; CID	**Pepti...**	44.58



precursor information

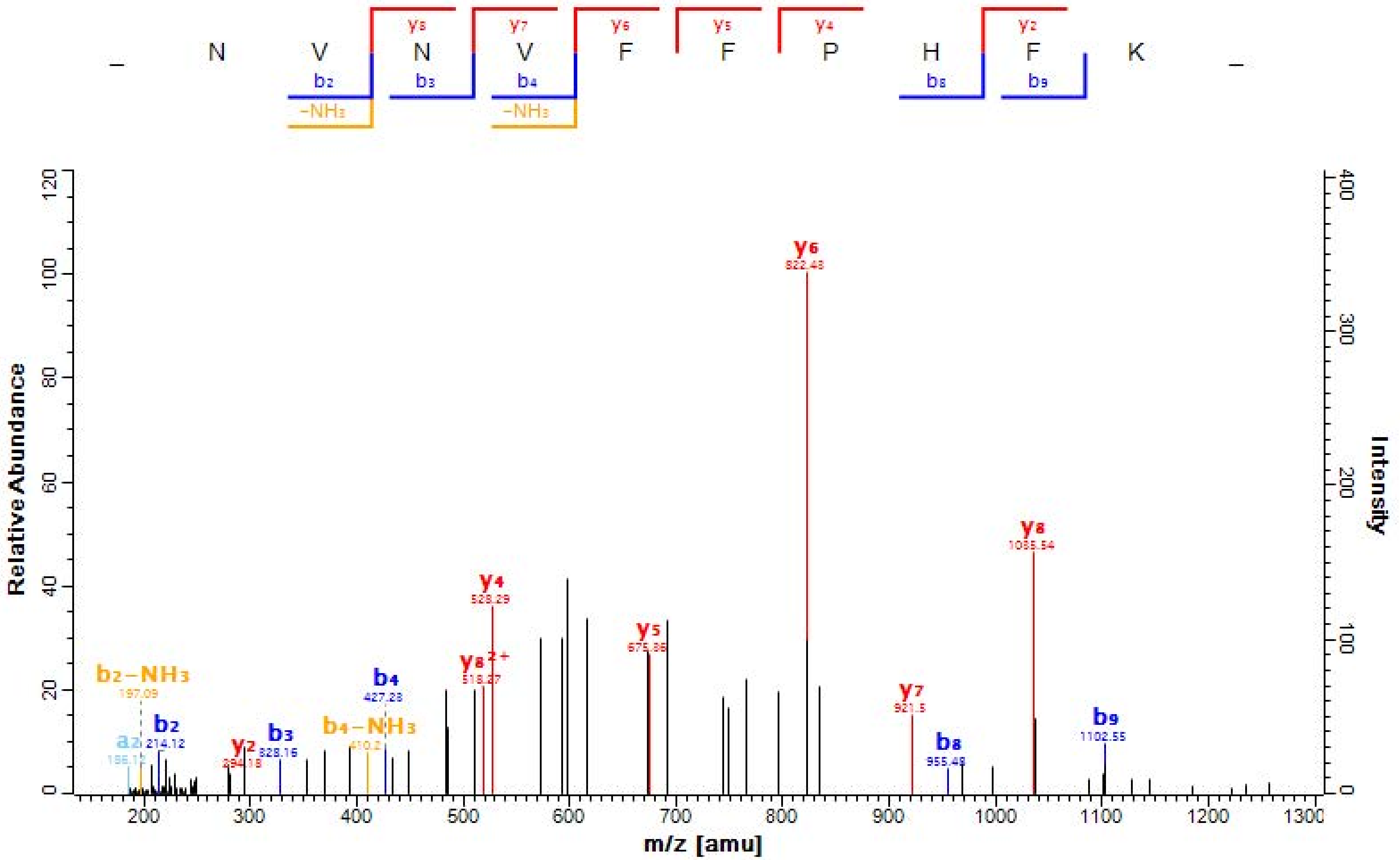
Mass:	2425.1697
m/z:	607.2997
Charge:	4+
Retentiontime:	40.699810028076
Score:	44.57743
Mass Error [ppm]:	-0.23257
PEP:	0.011809
Precursor Type:	MULTI

general information

Annotation:	15 of 21
AminoAcids Coverag	71 %
Intensity Coverage:	24 %
Peak Coverage:	19 %
Protein Localisation:	65 ... 85

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.1		148.1		148.1	1	F	20				
-0.06	191.1		219.1	+0.088	219.1	2	A	19	2279		2279	
	278.1		306.1	+0.091	306.1	3	S	18	2208		2208	
	407.2		435.2		435.2	4	E	17	2121		2121	
	554.3		582.3		582.3	5	F	16	1992		996.5	+0.23
	701.3		729.3		729.3	6	F	15	1845		923	+0.00
	798.4		826.4		826.4	7	P	14	1698		849.4	+0.24
	935.4		963.4		963.4	8	H	13	1601		1601	
	1035		1063		1063	9	V	12	1464		1464	
	1134	-0.4	581.3		1162	10	V	11	1365		1365	
	1249		1277		1277	11	D	10	1266	+0.296	1266	
	1348		1376		1376	12	V	9	1151		1151	
	1449		1477		1477	13	T	8	1052		1052	
	1586		1614		1614	14	H	7	950.5		950.5	
	1723		1751		1751	15	H	6	813.4		407.2	+0.24
	1852		1880		1880	16	E	5	676.4		338.7	+0.49
	1967	-0.4	998		1995	17	D	4	547.3		547.3	
	2038		2066		2066	18	A	3	432.3	+0.015	432.3	
	2151		2179		2179	19	L	2	361.2	-0.12	361.2	
	2252		2280		2280	20	T	1	248.2	+0.03	248.2	
						21	K	0	147.1		147.1	

Scan number	6440	**Raw file**	LNCAP_Silac_23F10_set1_09
Method	ITMS; CID	**Pepti...**	100.02

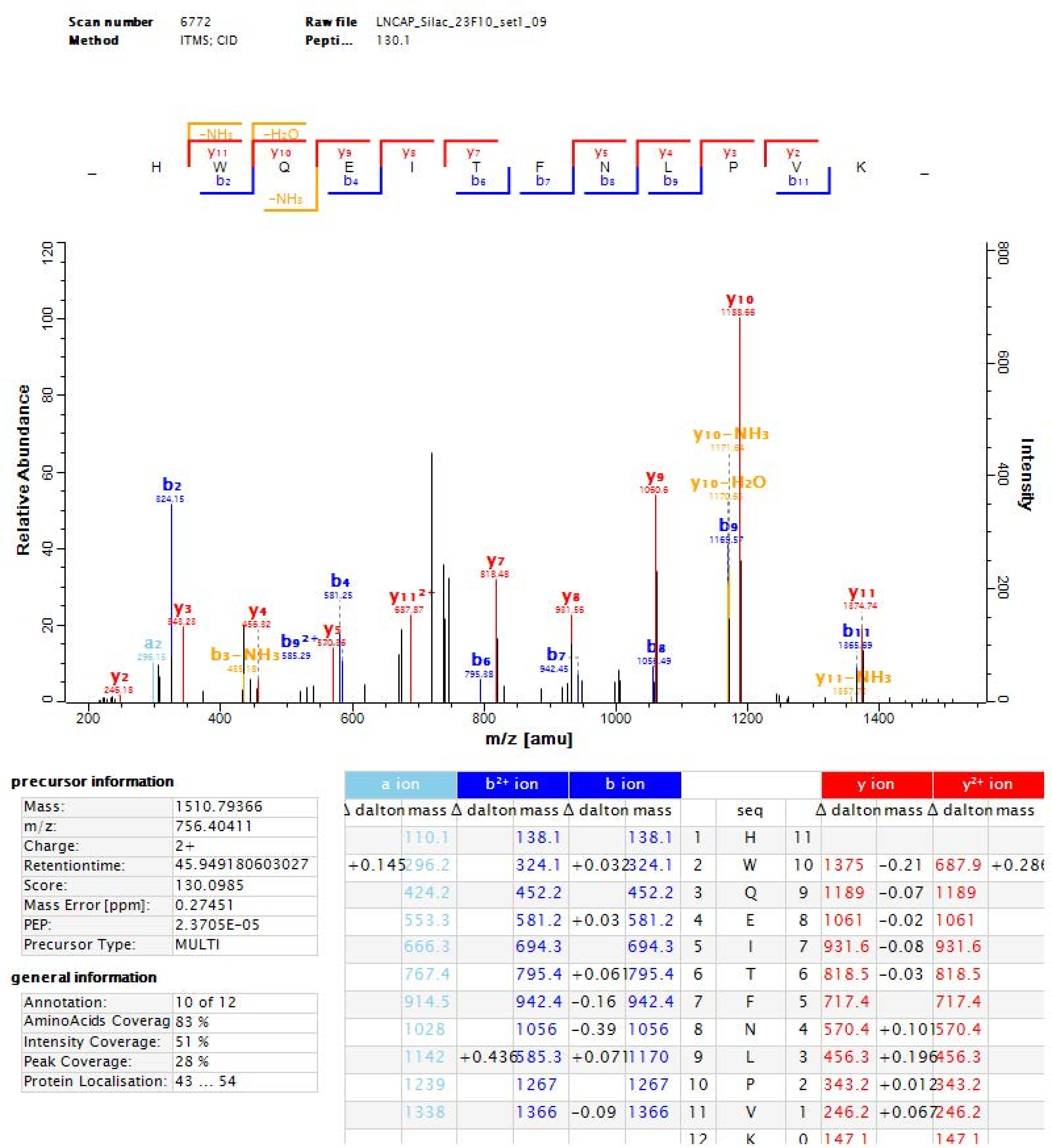


precursor information

Mass:	1247.64573
m/z:	624.83014
Charge:	2+
Retentiontime:	43.407024383544
Score:	100.017
Mass Error [ppm]:	0.47952
PEP:	0.0032869
Precursor Type:	ISO

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	33 %
Peak Coverage:	16 %
Protein Localisation:	27 ... 36

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	87.055		115.05	1	N	9				
-0.094	186.12	-0.016	214.12	2	V	8	1134.6		1134.6	
	300.17	+0.0921	328.16	3	N	7	1035.5	-0.033	518.27	+0.0947
	399.24	+0.0575	427.23	4	V	6	921.5	-0.029	921.5	
	546.3		574.3	5	F	5	822.43	-0.181	822.43	
	693.37		721.37	6	F	4	675.36	+0.1468	675.36	
	790.42		818.42	7	P	3	528.29	+0.0732	528.29	
	927.48	+0.0066	955.48	8	H	2	431.24		431.24	
	1074.6	+0.0767	1102.5	9	F	1	294.18	+0.1163	294.18	
				10	K	0	147.11		147.11	



Scan number 6772
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set1_09
Pepti... 130.1

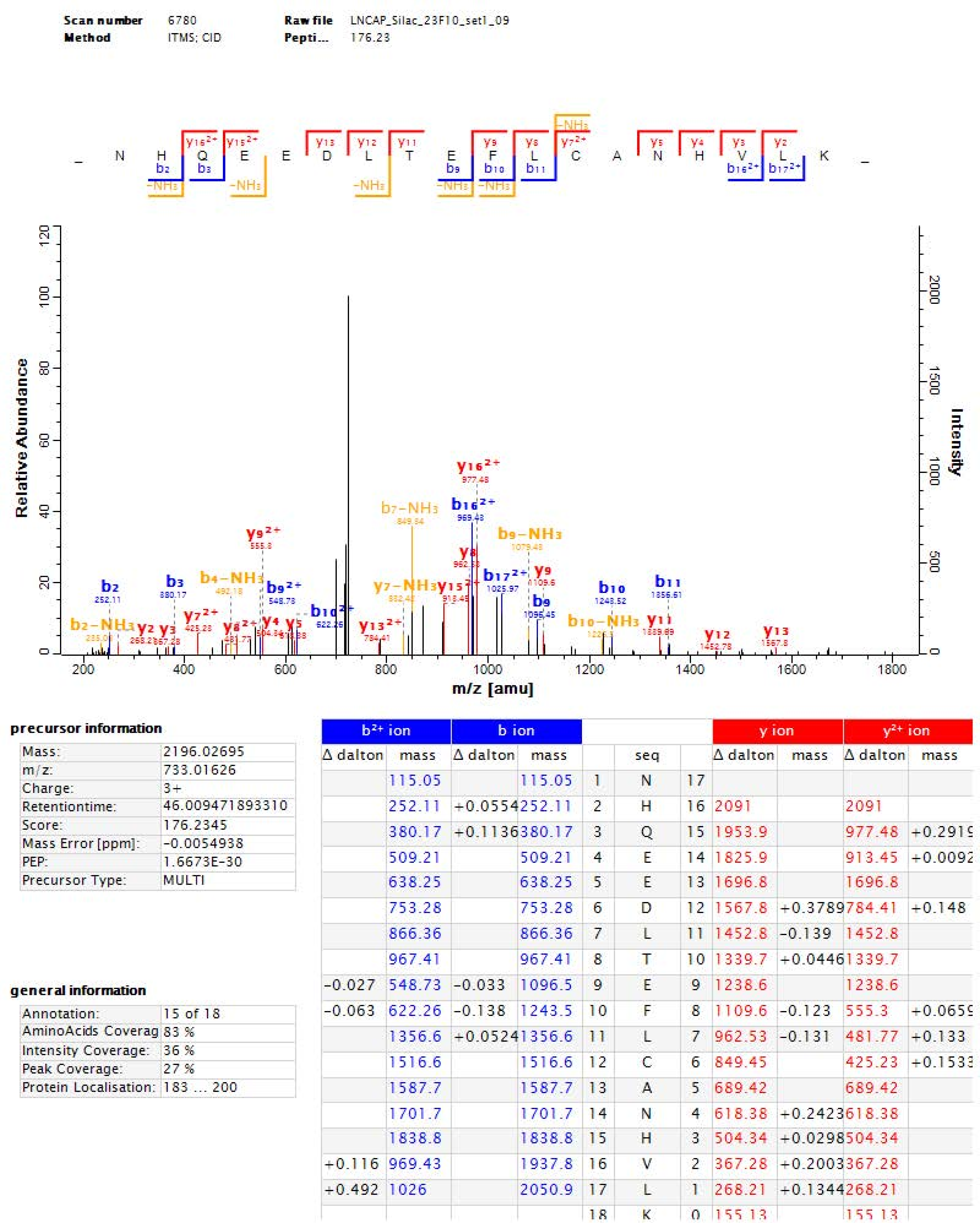
precursor information

Mass:	1510.79366
m/z:	756.40411
Charge:	2+
Retentiontime:	45.949180603027
Score:	130.0985
Mass Error [ppm]:	0.27451
PEP:	2.3705E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	51 %
Peak Coverage:	28 %
Protein Localisation:	43 ... 54

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	110.1		138.1		138.1	1	H	11				
+0.145	296.2		324.1	+0.032	324.1	2	W	10	1375	-0.21	687.9	+0.28
	424.2		452.2		452.2	3	Q	9	1189	-0.07	1189	
	553.3		581.2	+0.03	581.2	4	E	8	1061	-0.02	1061	
	666.3		694.3		694.3	5	I	7	931.6	-0.08	931.6	
	767.4		795.4	+0.061	795.4	6	T	6	818.5	-0.03	818.5	
	914.5		942.4	-0.16	942.4	7	F	5	717.4		717.4	
	1028		1056	-0.39	1056	8	N	4	570.4	+0.101	570.4	
	1142	+0.436	585.3	+0.071	1170	9	L	3	456.3	+0.196	456.3	
	1239		1267		1267	10	P	2	343.2	+0.012	343.2	
	1338		1366	-0.09	1366	11	V	1	246.2	+0.067	246.2	
						12	K	0	147.1		147.1	



Scan number	6780	**Raw file**	LNCAP_Silac_23F10_set1_09
Method	ITMS; CID	**Pepti...**	176.23

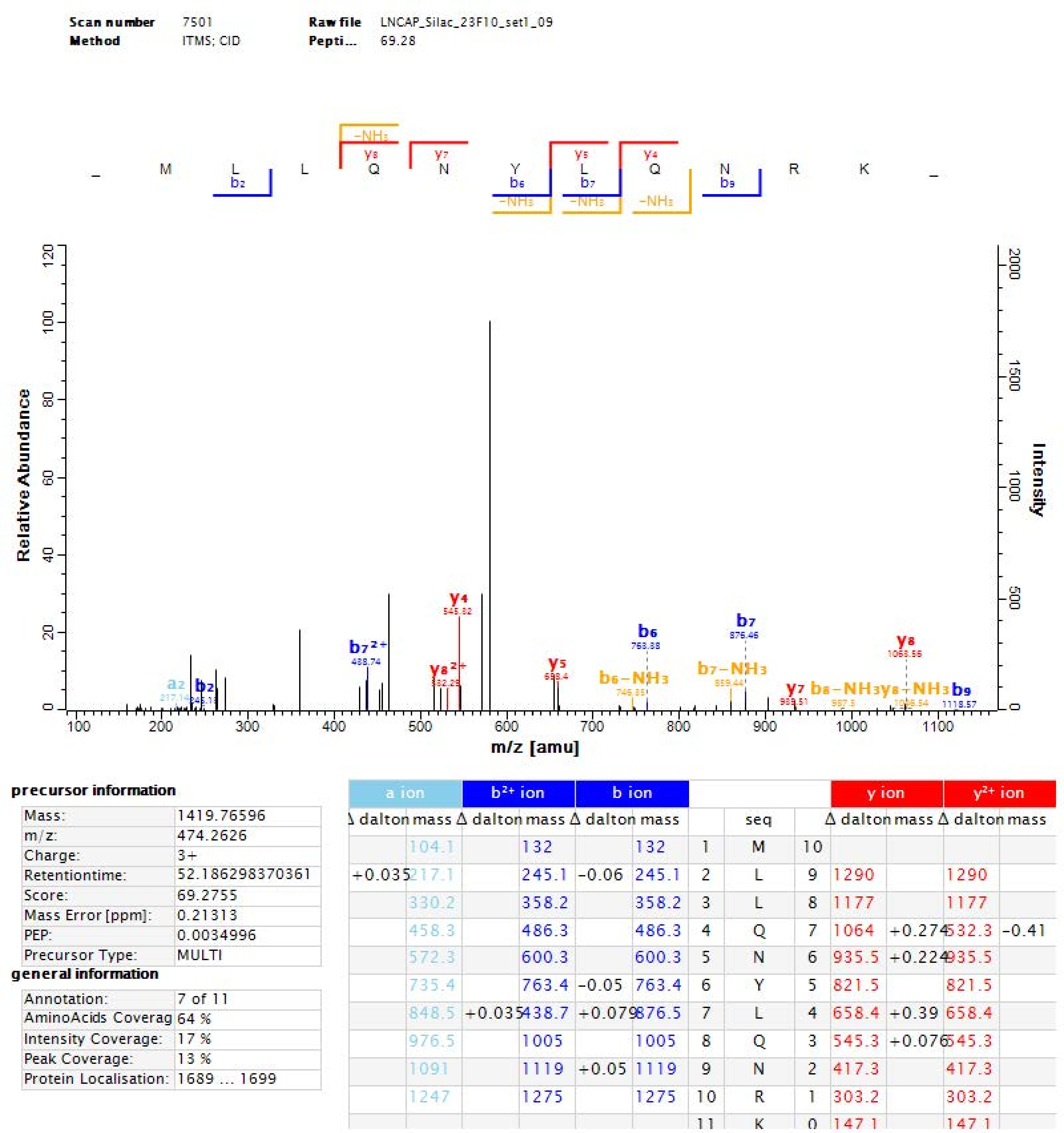
precursor information

Mass:	2196.02695
m/z:	733.01626
Charge:	3+
Retentiontime:	46.009471893310
Score:	176.2345
Mass Error [ppm]:	-0.0054938
PEP:	1.6673E-30
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	36 %
Peak Coverage:	27 %
Protein Localisation:	183 ... 200

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.05		115.05	1	N	17				
	252.11	+0.0554	252.11	2	H	16	2091		2091	
	380.17	+0.1136	380.17	3	Q	15	1953.9		977.48	+0.2919
	509.21		509.21	4	E	14	1825.9		913.45	+0.0092
	638.25		638.25	5	E	13	1696.8		1696.8	
	753.28		753.28	6	D	12	1567.8	+0.3789	784.41	+0.148
	866.36		866.36	7	L	11	1452.8	-0.139	1452.8	
	967.41		967.41	8	T	10	1339.7	+0.0446	1339.7	
-0.027	548.73	-0.033	1096.5	9	E	9	1238.6		1238.6	
-0.063	622.26	-0.138	1243.5	10	F	8	1109.6	-0.123	555.3	+0.0659
	1356.6	+0.0524	1356.6	11	L	7	962.53	-0.131	481.77	+0.133
	1516.6		1516.6	12	C	6	849.45		425.23	+0.1533
	1587.7		1587.7	13	A	5	689.42		689.42	
	1701.7		1701.7	14	N	4	618.38	+0.2423	618.38	
	1838.8		1838.8	15	H	3	504.34	+0.0298	504.34	
+0.116	969.43		1937.8	16	V	2	367.28	+0.2003	367.28	
+0.492	1026		2050.9	17	L	1	268.21	+0.1344	268.21	
				18	K	0	155.13		155.13	



Scan number 7501
Raw file LNCAP_Silac_23F10_set1_09
Method ITMS; CID
Pepti... 69.28

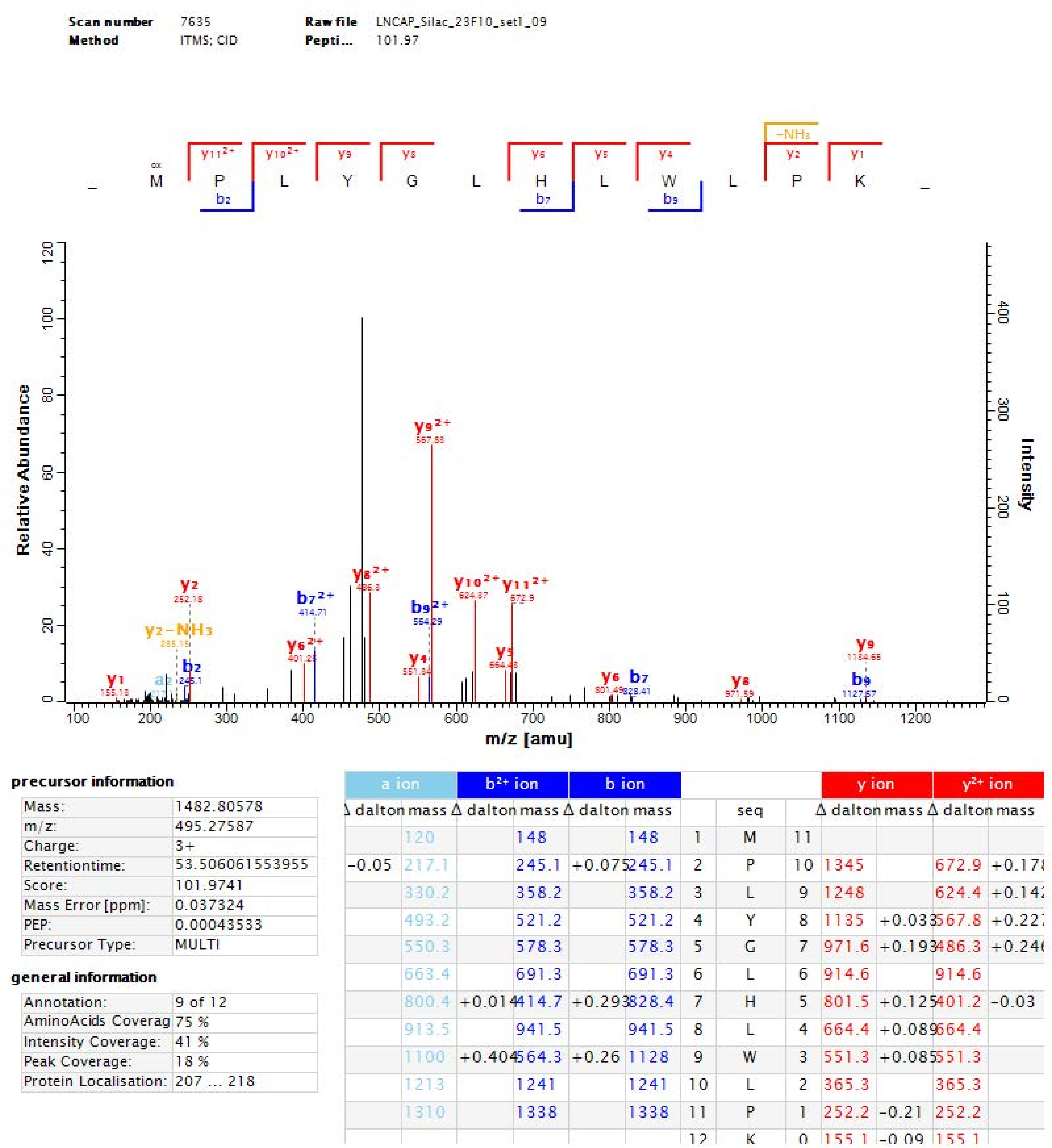
precursor information

Mass:	1419.76596
m/z:	474.2626
Charge:	3+
Retentiontime:	52.186298370361
Score:	69.2755
Mass Error [ppm]:	0.21313
PEP:	0.0034996
Precursor Type:	MULTI

general information

Annotation:	7 of 11
AminoAcids Coverag	64 %
Intensity Coverage:	17 %
Peak Coverage:	13 %
Protein Localisation:	1689 ... 1699

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	104.1		132		132	1	M	10				
+0.035	217.1		245.1	-0.06	245.1	2	L	9	1290		1290	
	330.2		358.2		358.2	3	L	8	1177		1177	
	458.3		486.3		486.3	4	Q	7	1064	+0.274	532.3	-0.41
	572.3		600.3		600.3	5	N	6	935.5	+0.224	935.5	
	735.4		763.4	-0.05	763.4	6	Y	5	821.5		821.5	
	848.5	+0.035	438.7	+0.079	876.5	7	L	4	658.4	+0.39	658.4	
	976.5		1005		1005	8	Q	3	545.3	+0.076	545.3	
	1091		1119	+0.05	1119	9	N	2	417.3		417.3	
	1247		1275		1275	10	R	1	303.2		303.2	
						11	K	0	147.1		147.1	



Scan number	7635	**Raw file**	LNCAP_Silac_23F10_set1_09
Method	ITMS; CID	**Pepti...**	101.97

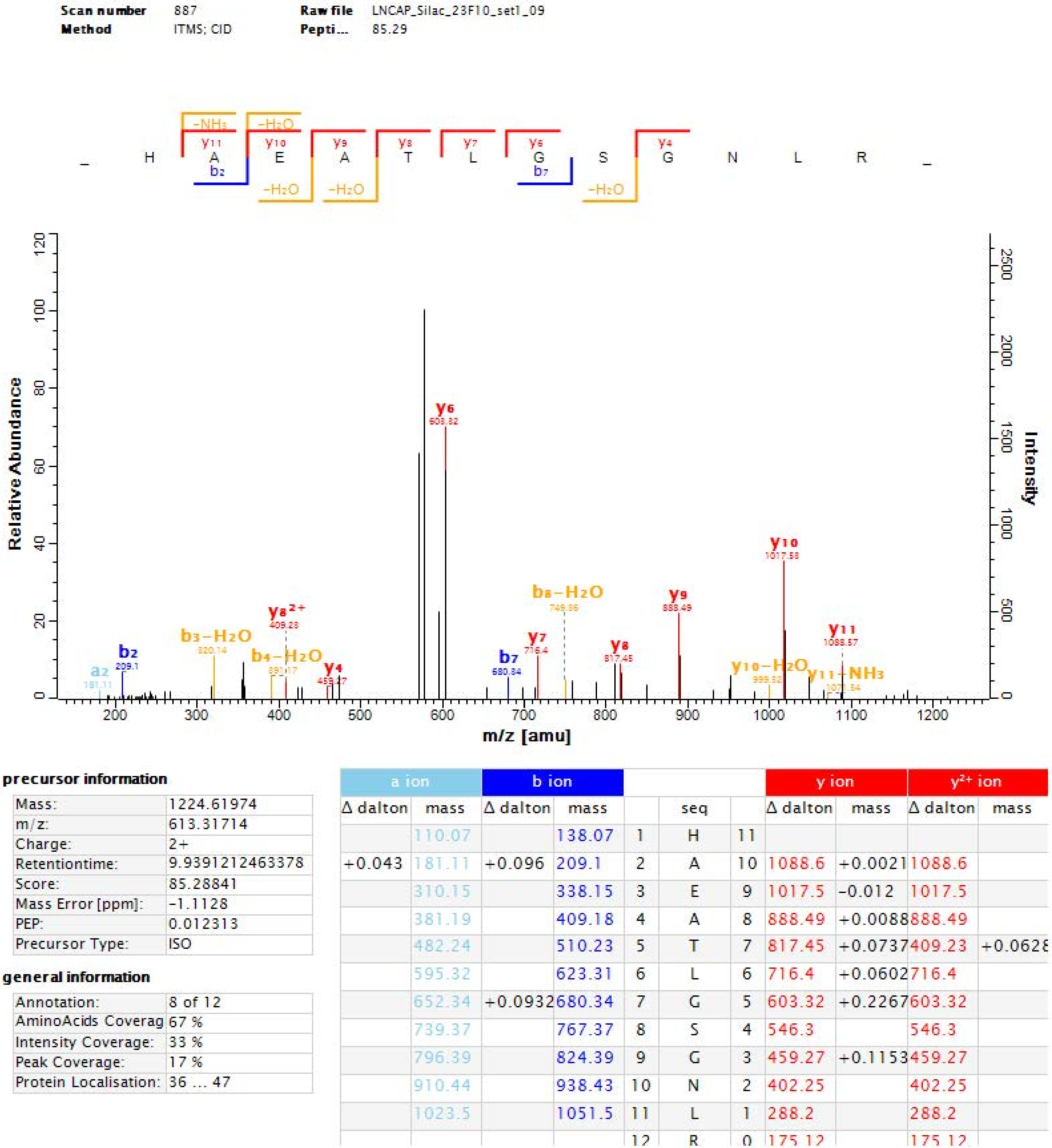
precursor information

Mass:	1482.80578
m/z:	495.27587
Charge:	3+
Retentiontime:	53.506061553955
Score:	101.9741
Mass Error [ppm]:	0.037324
PEP:	0.00043533
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	41 %
Peak Coverage:	18 %
Protein Localisation:	207 ... 218

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120		148		148	1	M	11				
-0.05	217.1		245.1	+0.075	245.1	2	P	10	1345		672.9	+0.17
	330.2		358.2		358.2	3	L	9	1248		624.4	+0.14
	493.2		521.2		521.2	4	Y	8	1135	+0.033	567.8	+0.22
	550.3		578.3		578.3	5	G	7	971.6	+0.193	486.3	+0.24
	663.4		691.3		691.3	6	L	6	914.6		914.6	
	800.4	+0.014	414.7	+0.293	828.4	7	H	5	801.5	+0.125	401.2	-0.03
	913.5		941.5		941.5	8	L	4	664.4	+0.089	664.4	
	1100	+0.404	564.3	+0.26	1128	9	W	3	551.3	+0.085	551.3	
	1213		1241		1241	10	L	2	365.3		365.3	
	1310		1338		1338	11	P	1	252.2	-0.21	252.2	
						12	K	0	155.1	-0.09	155.1	



Scan number	887	**Raw file**	LNCAP_Silac_23F10_set1_09
Method	ITMS; CID	**Pepti...**	85.29

precursor information

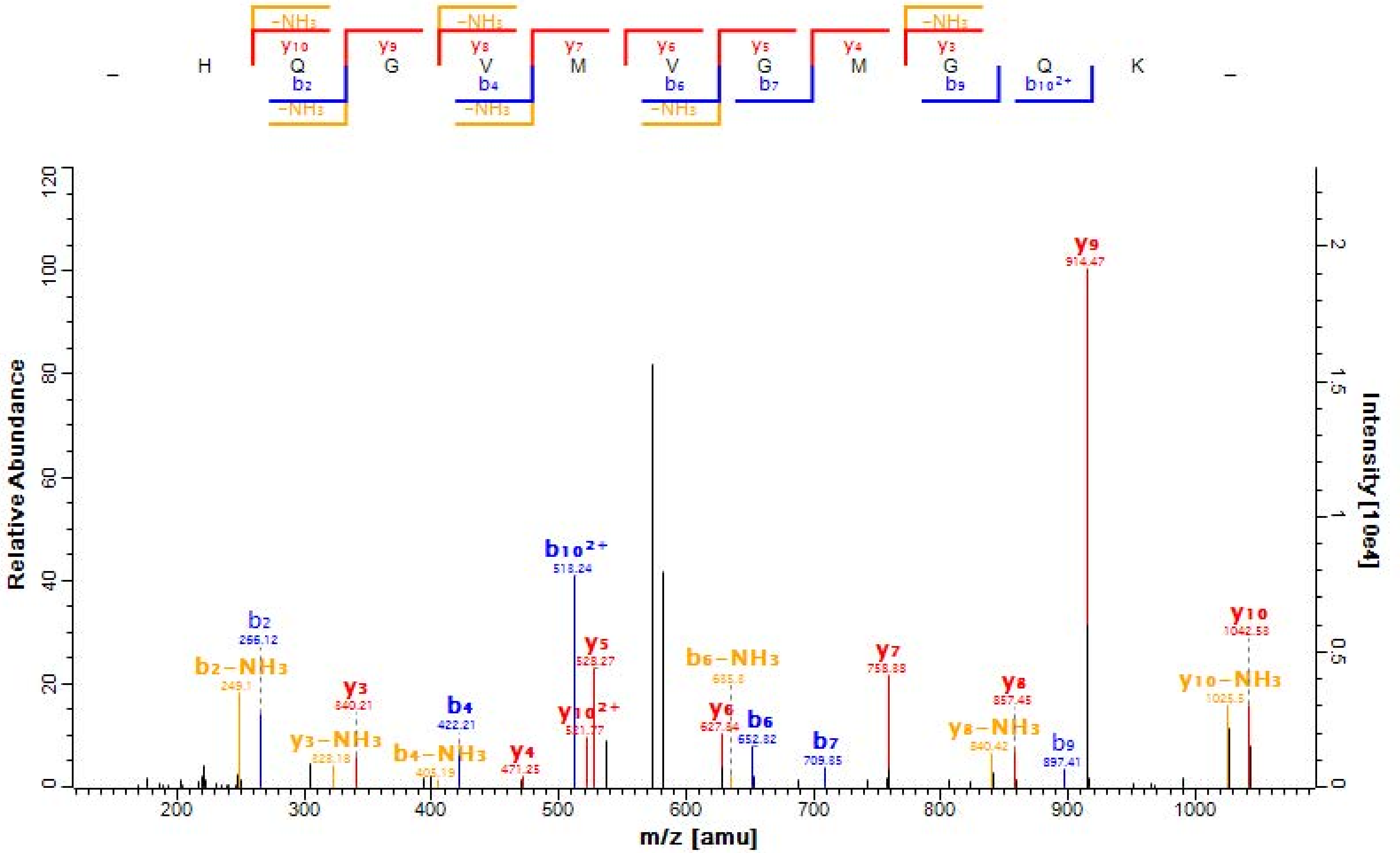
Mass:	1224.61974
m/z:	613.31714
Charge:	2+
Retentiontime:	9.9391212463378
Score:	85.28841
Mass Error [ppm]:	-1.1128
PEP:	0.012313
Precursor Type:	ISO

general information

Annotation:	8 of 12
AminoAcids Coverag	67 %
Intensity Coverage:	33 %
Peak Coverage:	17 %
Protein Localisation:	36 ... 47

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	110.07		138.07	1	H	11				
+0.043	181.11	+0.096	209.1	2	A	10	1088.6	+0.0021	1088.6	
	310.15		338.15	3	E	9	1017.5	-0.012	1017.5	
	381.19		409.18	4	A	8	888.49	+0.0088	888.49	
	482.24		510.23	5	T	7	817.45	+0.0737	409.23	+0.062
	595.32		623.31	6	L	6	716.4	+0.0602	716.4	
	652.34	+0.0932	680.34	7	G	5	603.32	+0.2267	603.32	
	739.37		767.37	8	S	4	546.3		546.3	
	796.39		824.39	9	G	3	459.27	+0.1153	459.27	
	910.44		938.43	10	N	2	402.25		402.25	
	1023.5		1051.5	11	L	1	288.2		288.2	
				12	R	0	175.12		175.12	

Scan number	977	**Raw file**	LNCAP_Silac_23F10_set1_09
Method	ITMS; CID	**Pepti...**	169.37



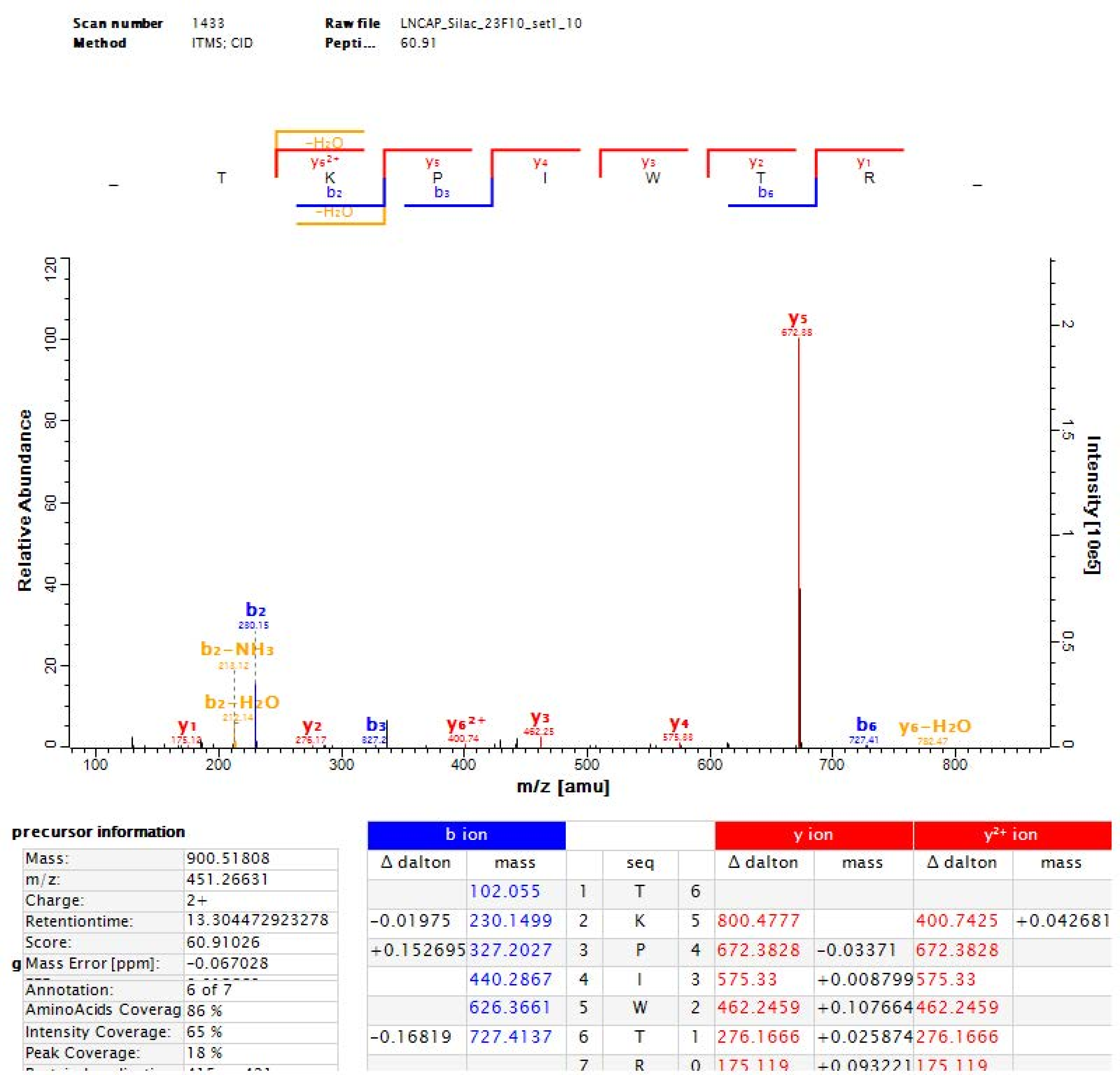
precursor information

Mass:	1170.56323
m/z:	586.28889
Charge:	2+
Retentiontime:	10.437109947204
Score:	169.374
Mass Error [ppm]:	-0.46786
PEP:	6.7161E-08
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	56 %
Peak Coverage:	29 %
Protein Localisation:	40 ... 50

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.07		138.07	1	H	10				
	266.12	-0.072	266.12	2	Q	9	1042.5	-0.041	521.77	+0.1447
	323.15		323.15	3	G	8	914.47	-0.042	914.47	
	422.21	-0.022	422.21	4	V	7	857.45	-0.06	857.45	
	553.26		553.26	5	M	6	758.38	+0.105	758.38	
	652.32	+0.0416	652.32	6	V	5	627.34	+0.0164	627.34	
	709.35	-0.053	709.35	7	G	4	528.27	-0.026	528.27	
	840.39		840.39	8	M	3	471.25	+0.0816	471.25	
	897.41	-0.088	897.41	9	G	2	340.21	+0.0623	340.21	
-0.301	513.24		1025.5	10	Q	1	283.19		283.19	
				11	K	0	155.13		155.13	



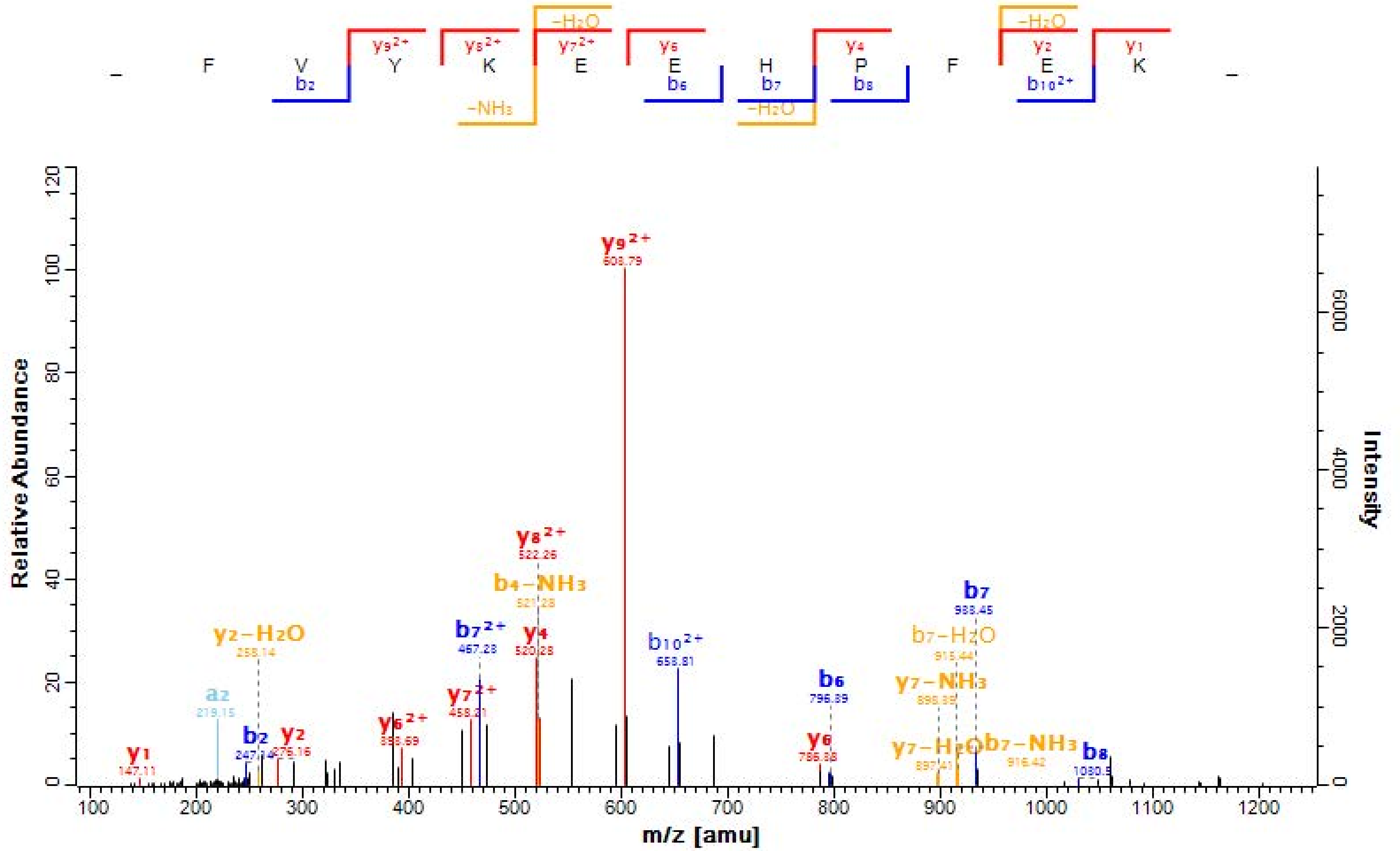
Scan number 1433 **Raw file** LNCAP_Silac_23F10_set1_10
Method ITMS; CID **Pepti...** 60.91

precursor information

Mass:	900.51808
m/z:	451.26631
Charge:	2+
Retentiontime:	13.304472923278
Score:	60.91026
Mass Error [ppm]:	-0.067028
Annotation:	6 of 7
AminoAcids Coverag	86 %
Intensity Coverage:	65 %
Peak Coverage:	18 %

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055	1	T	6				
-0.01975	230.1499	2	K	5	800.4777		400.7425	+0.042681
+0.152695	327.2027	3	P	4	672.3828	-0.03371	672.3828	
	440.2867	4	I	3	575.33	+0.008799	575.33	
	626.3661	5	W	2	462.2459	+0.107664	462.2459	
-0.16819	727.4137	6	T	1	276.1666	+0.025874	276.1666	
		7	R	0	175.119	+0.093221	175.119	

Scan number	1707	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	125.74



precursor information

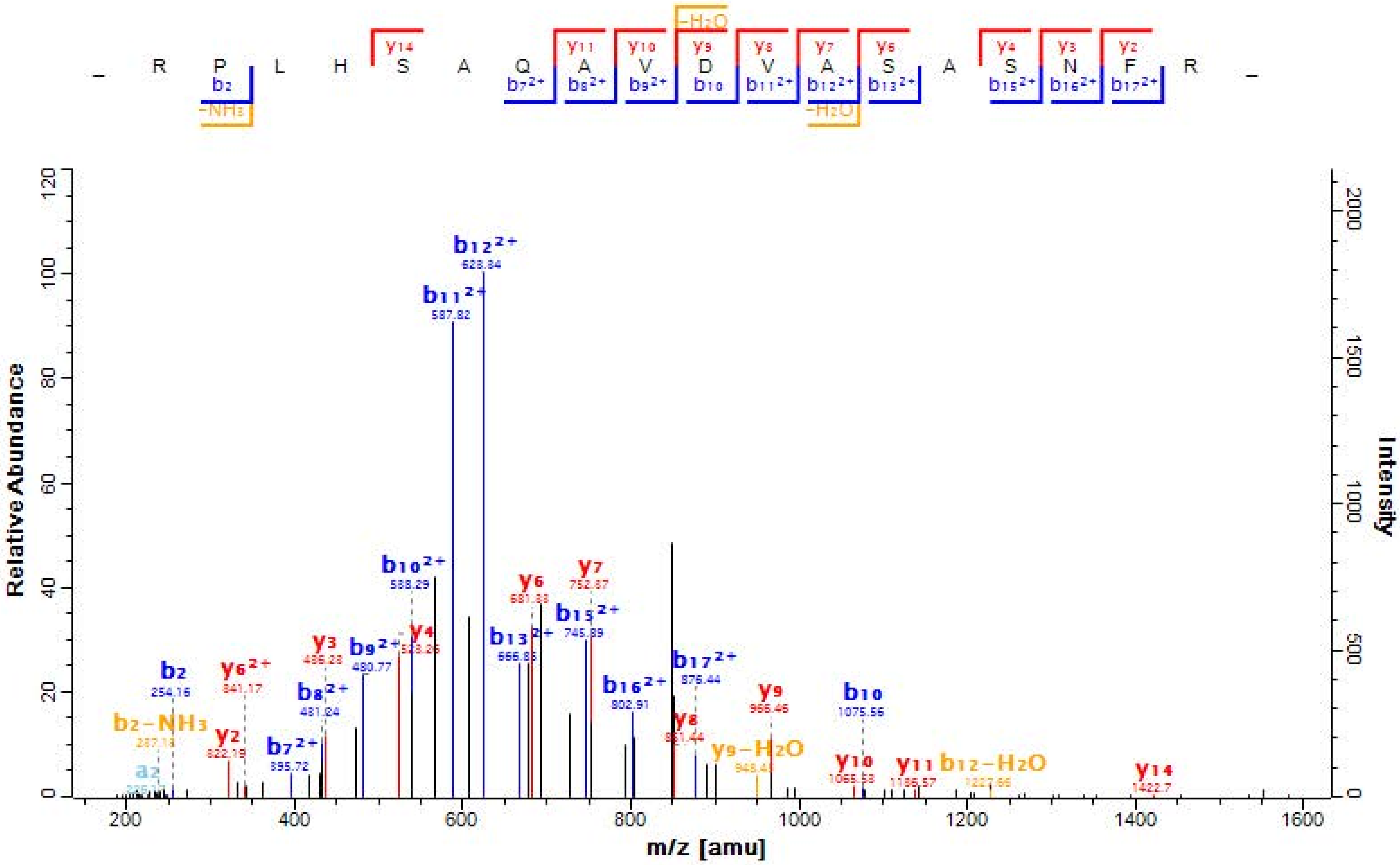
Mass:	1451.70881
m/z:	484.91021
Charge:	3+
Retentiontime:	14.980576515197
Score:	125.7365
Mass Error [ppm]:	0.20155
PEP:	0.00015508
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	56 %
Peak Coverage:	16 %
Protein Localisation:	3 ... 13

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.1		148.1		148.1	1	F	10				
-0.04	219.1		247.1	+0.07	247.1	2	V	9	1306		1306	
	382.2		410.2		410.2	3	Y	8	1207		603.8	+0.24
	510.3		538.3		538.3	4	K	7	1044		522.3	+0.29
	639.4		667.3		667.3	5	E	6	915.4		458.2	-0.27
	768.4		796.4	+0.168	796.4	6	E	5	786.4	-0.04	393.7	-0.04
	905.5	+0.141	467.2	+0.064	933.4	7	H	4	657.3		657.3	
	1003		1030	+0.224	1030	8	P	3	520.3	-0.04	520.3	
	1150		1178		1178	9	F	2	423.2		423.2	
	1279	-0.13	653.8		1307	10	E	1	276.2	+0.141	276.2	
						11	K	0	147.1	-0.08	147.1	

Scan number	2093	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	114.27



precursor information

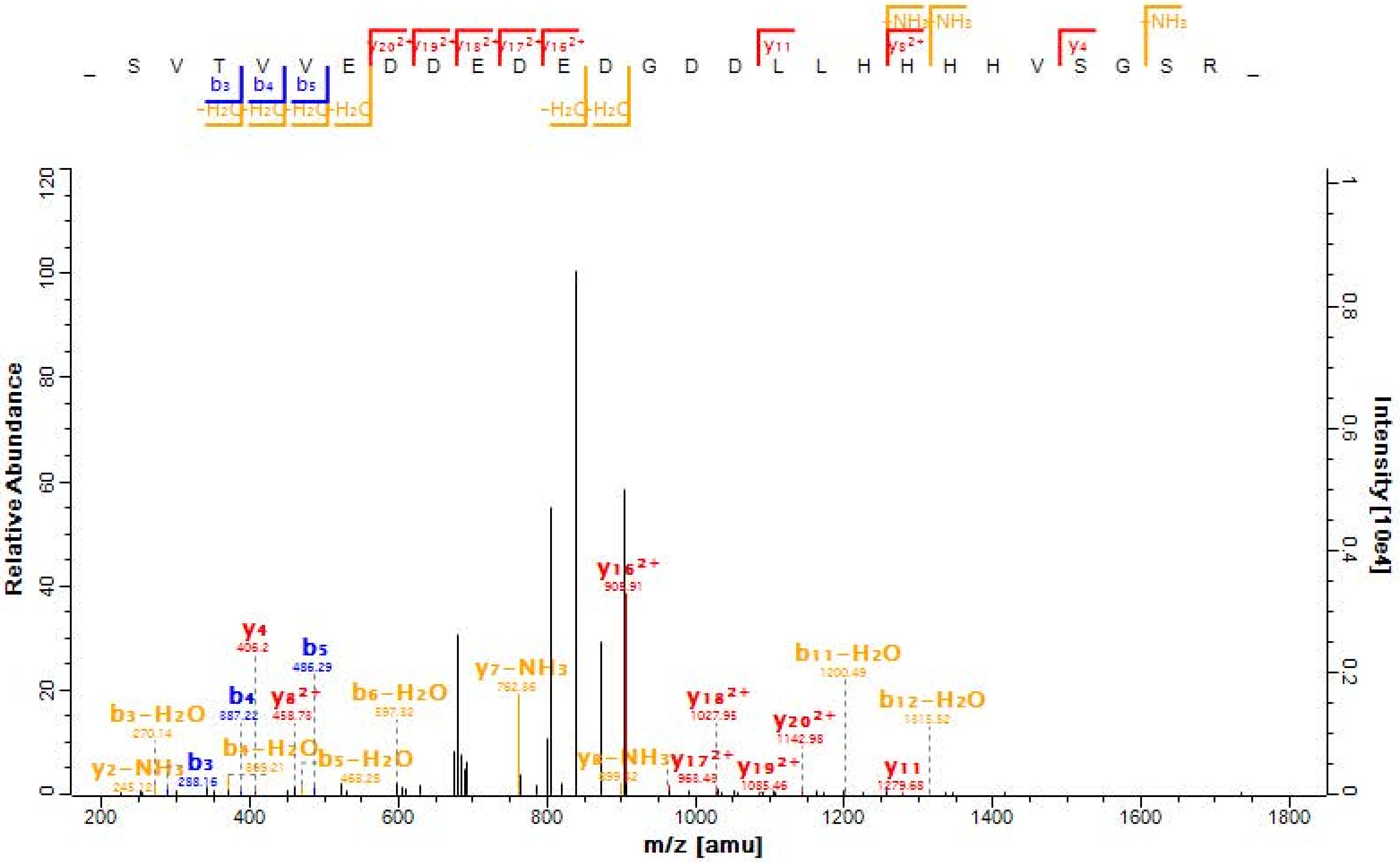
Mass:	1924.98748
m/z:	642.66977
Charge:	3+
Retentiontime:	17.430215835571
Score:	114.2746
Mass Error [ppm]:	0.37463
PEP:	0.00012851
Precursor Type:	ISO

general information

Annotation:	12 of 18
AminoAcids Coverag	67 %
Intensity Coverage:	55 %
Peak Coverage:	28 %
Protein Localisation:	15 ... 32

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.1		157.1		157.1	1	R	17				
-0.16	226.2		254.2	+0.148	254.2	2	P	16	1770		1770	
	339.3		367.2		367.2	3	L	15	1673		1673	
	476.3		504.3		504.3	4	H	14	1560		1560	
	563.3		591.3		591.3	5	S	13	1423	-0.27	1423	
	634.4		662.4		662.4	6	A	12	1336		1336	
	762.4	-0.06	395.7		790.4	7	Q	11	1265		1265	
	833.5	+0.054	431.2		861.5	8	A	10	1137	+0.248	1137	
	932.5	+0.253	480.8		960.5	9	V	9	1066	-0.08	1066	
	1048	+0.027	538.3	-0.06	1076	10	D	8	966.5	+0.205	966.5	
	1147	+0.268	587.8		1175	11	V	7	851.4	+0.127	851.4	
	1218	+0.26	623.3		1246	12	A	6	752.4	+0.067	752.4	
	1305	-0.03	666.9		1333	13	S	5	681.3	+0.078	341.2	+0.11
	1376		1404		1404	14	A	4	594.3		594.3	
	1463	+0.259	745.9		1491	15	S	3	523.3	+0.01	523.3	
	1577	+0.039	802.9		1605	16	N	2	436.2	+0.129	436.2	
	1724	+0.203	876.4		1752	17	F	1	322.2	+0.052	322.2	
						18	R	0	175.1		175.1	

Scan number	2342	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	38.24



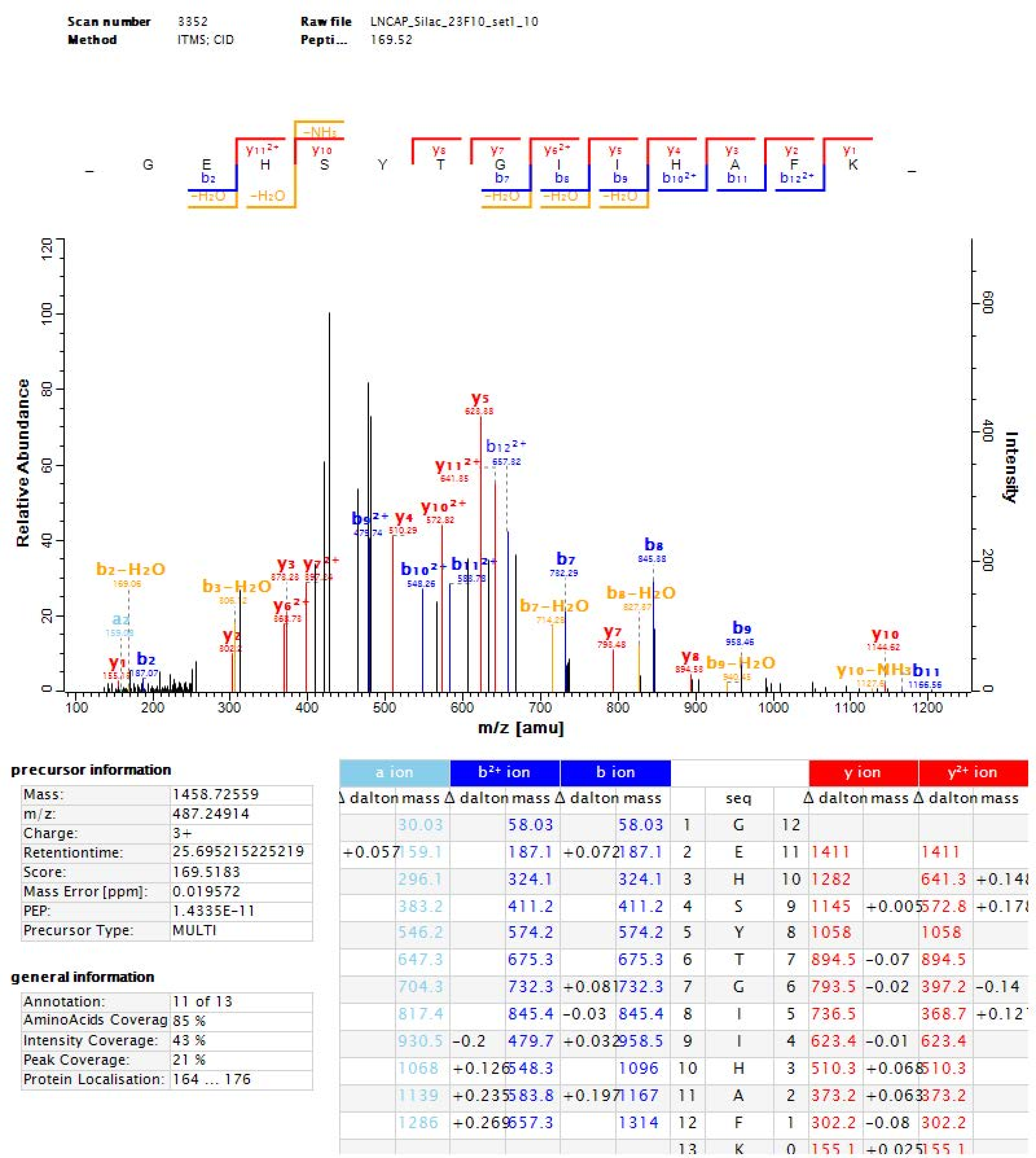
precursor information

Mass:	2898.26638
m/z:	725.57387
Charge:	4+
Retentiontime:	19.008152008056
Score:	38.23733
Mass Error [ppm]:	0.39395
PEP:	0.012984
Precursor Type:	MULTI

general information

Annotation:	15 of 26
AminoAcids Coverag	58 %
Intensity Coverage:	18 %
Peak Coverage:	23 %
Protein Localisation:	546 ... 571

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	25				
	187.1077	2	V	24	2812.24		2812.24	
+0.024656	288.1554	3	T	23	2713.172		2713.172	
+0.024602	387.2238	4	V	22	2612.124		2612.124	
-0.01915	486.2922	5	V	21	2513.056		2513.056	
	615.3348	6	E	20	2413.988		2413.988	
	730.3618	7	D	19	2284.945		1142.976	+0.417187
	845.3887	8	D	18	2169.918		1085.463	-0.13514
	974.4313	9	E	17	2054.891		1027.949	+0.075234
	1089.458	10	D	16	1925.848		963.4279	+0.27695
	1218.501	11	E	15	1810.822		905.9144	-0.02843
	1333.528	12	D	14	1681.779		1681.779	
	1390.549	13	G	13	1566.752		1566.752	
	1505.576	14	D	12	1509.731		1509.731	
	1620.603	15	D	11	1394.704		1394.704	
	1733.687	16	L	10	1279.677	-0.09024	1279.677	
	1846.771	17	L	9	1166.593		1166.593	
	1983.83	18	H	8	1053.509		1053.509	
	2120.889	19	H	7	916.4496		458.7284	-0.08294
	2257.948	20	H	6	779.3907		779.3907	
	2395.007	21	H	5	642.3318		642.3318	
	2494.075	22	V	4	505.2729		505.2729	
	2581.107	23	S	3	406.2045	+0.188472	406.2045	
	2638.129	24	G	2	319.1724		319.1724	
	2725.161	25	S	1	262.151		262.151	
		26	R	0	175.119		175.119	



Scan number	3352	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	169.52

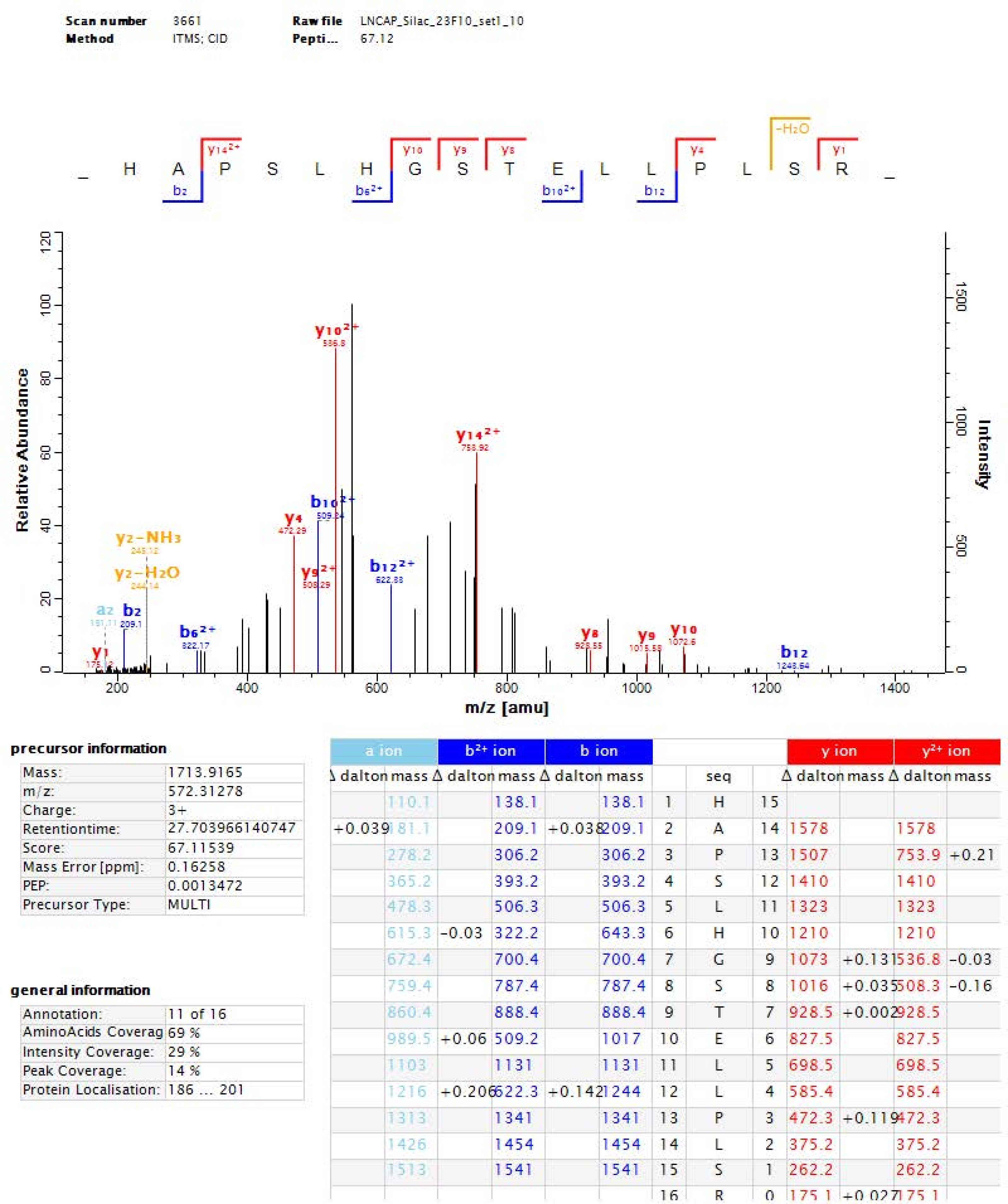
precursor information

Mass:	1458.72559
m/z:	487.24914
Charge:	3+
Retentiontime:	25.695215225219
Score:	169.5183
Mass Error [ppm]:	0.019572
PEP:	1.4335E-11
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	43 %
Peak Coverage:	21 %
Protein Localisation:	164 ... 176

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	30.03		58.03		58.03	1	G	12				
+0.057	159.1		187.1	+0.072	187.1	2	E	11	1411		1411	
	296.1		324.1		324.1	3	H	10	1282		641.3	+0.14
	383.2		411.2		411.2	4	S	9	1145	+0.005	572.8	+0.17
	546.2		574.2		574.2	5	Y	8	1058		1058	
	647.3		675.3		675.3	6	T	7	894.5	-0.07	894.5	
	704.3		732.3	+0.081	732.3	7	G	6	793.5	-0.02	397.2	-0.14
	817.4		845.4	-0.03	845.4	8	I	5	736.5		368.7	+0.12
	930.5	-0.2	479.7	+0.032	958.5	9	I	4	623.4	-0.01	623.4	
	1068	+0.126	548.3		1096	10	H	3	510.3	+0.068	510.3	
	1139	+0.235	583.8	+0.197	1167	11	A	2	373.2	+0.063	373.2	
	1286	+0.269	657.3		1314	12	F	1	302.2	-0.08	302.2	
						13	K	0	155.1	+0.025	155.1	



Scan number 3661 **Raw file** LNCAP_Silac_23F10_set1_10

Method ITMS; CID **Pepti...** 67.12

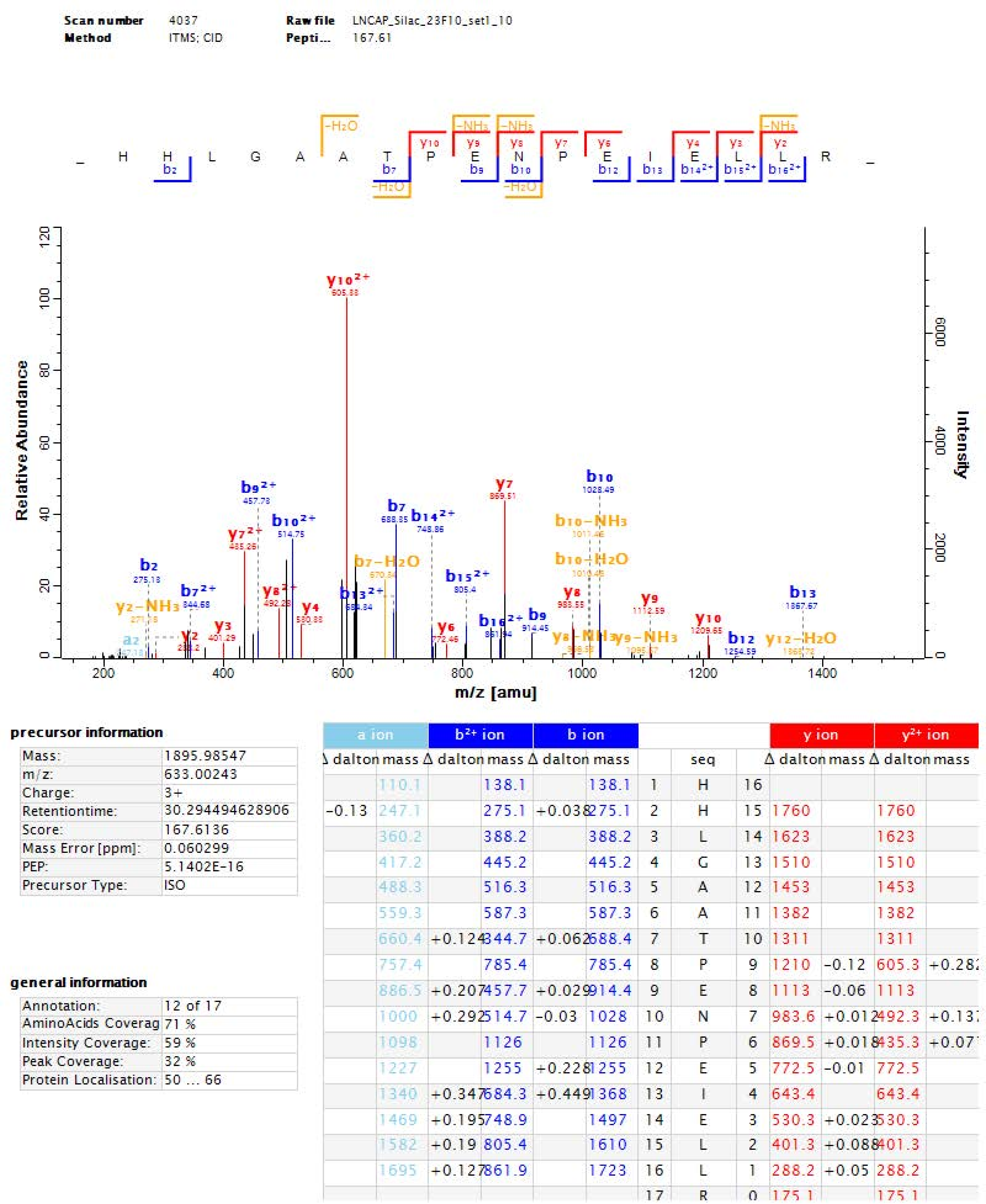
precursor information

Mass:	1713.9165
m/z:	572.31278
Charge:	3+
Retentiontime:	27.703966140747
Score:	67.11539
Mass Error [ppm]:	0.16258
PEP:	0.0013472
Precursor Type:	MULTI

general information

Annotation:	11 of 16
AminoAcids Coverag	69 %
Intensity Coverage:	29 %
Peak Coverage:	14 %
Protein Localisation:	186 ... 201

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	110.1		138.1		138.1	1	H	15				
+0.039	181.1		209.1	+0.038	209.1	2	A	14	1578		1578	
	278.2		306.2		306.2	3	P	13	1507		753.9	+0.21
	365.2		393.2		393.2	4	S	12	1410		1410	
	478.3		506.3		506.3	5	L	11	1323		1323	
	615.3	-0.03	322.2		643.3	6	H	10	1210		1210	
	672.4		700.4		700.4	7	G	9	1073	+0.131	536.8	-0.03
	759.4		787.4		787.4	8	S	8	1016	+0.035	508.3	-0.16
	860.4		888.4		888.4	9	T	7	928.5	+0.002	928.5	
	989.5	+0.06	509.2		1017	10	E	6	827.5		827.5	
	1103		1131		1131	11	L	5	698.5		698.5	
	1216	+0.206	622.3	+0.142	1244	12	L	4	585.4		585.4	
	1313		1341		1341	13	P	3	472.3	+0.119	472.3	
	1426		1454		1454	14	L	2	375.2		375.2	
	1513		1541		1541	15	S	1	262.2		262.2	
						16	R	0	175.1	+0.027	175.1	



Scan number	4037	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	167.61

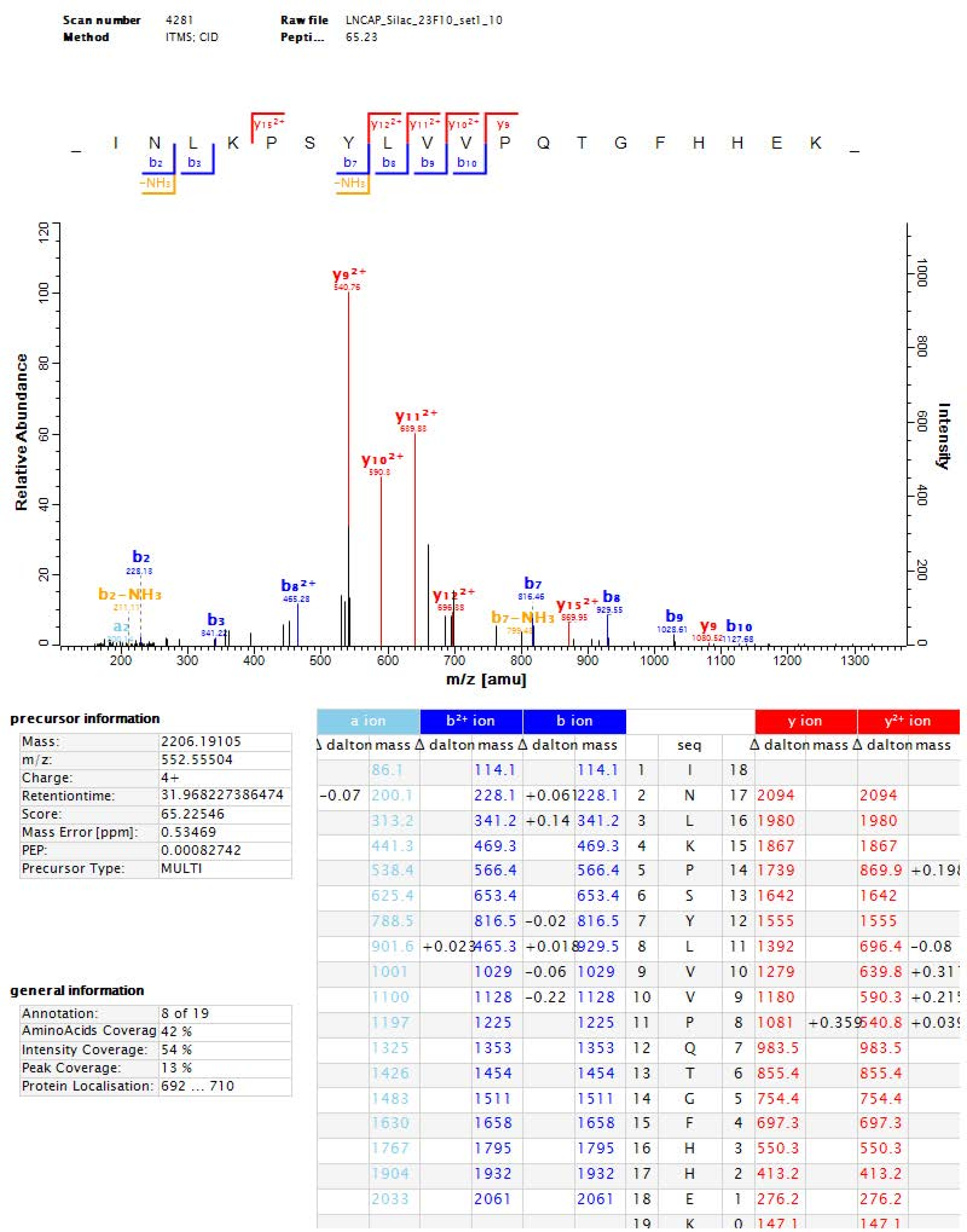
precursor information

Mass:	1895.98547
m/z:	633.00243
Charge:	3+
Retentiontime:	30.294494628906
Score:	167.6136
Mass Error [ppm]:	0.060299
PEP:	5.1402E-16
Precursor Type:	ISO

general information

Annotation:	12 of 17
AminoAcids Coverag	71 %
Intensity Coverage:	59 %
Peak Coverage:	32 %
Protein Localisation:	50 ... 66

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	110.1		138.1		138.1	1	H	16				
-0.13	247.1		275.1	+0.038	275.1	2	H	15	1760		1760	
	360.2		388.2		388.2	3	L	14	1623		1623	
	417.2		445.2		445.2	4	G	13	1510		1510	
	488.3		516.3		516.3	5	A	12	1453		1453	
	559.3		587.3		587.3	6	A	11	1382		1382	
	660.4	+0.124	344.7	+0.062	688.4	7	T	10	1311		1311	
	757.4		785.4		785.4	8	P	9	1210	-0.12	605.3	+0.28
	886.5	+0.207	457.7	+0.029	914.4	9	E	8	1113	-0.06	1113	
	1000	+0.292	514.7	-0.03	1028	10	N	7	983.6	+0.012	492.3	+0.13
	1098		1126		1126	11	P	6	869.5	+0.018	435.3	+0.07
	1227		1255	+0.228	1255	12	E	5	772.5	-0.01	772.5	
	1340	+0.347	684.3	+0.449	1368	13	I	4	643.4		643.4	
	1469	+0.195	748.9		1497	14	E	3	530.3	+0.023	530.3	
	1582	+0.19	805.4		1610	15	L	2	401.3	+0.088	401.3	
	1695	+0.127	861.9		1723	16	L	1	288.2	+0.05	288.2	
						17	R	0	175.1		175.1	



Scan number	4281	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	65.23

precursor information

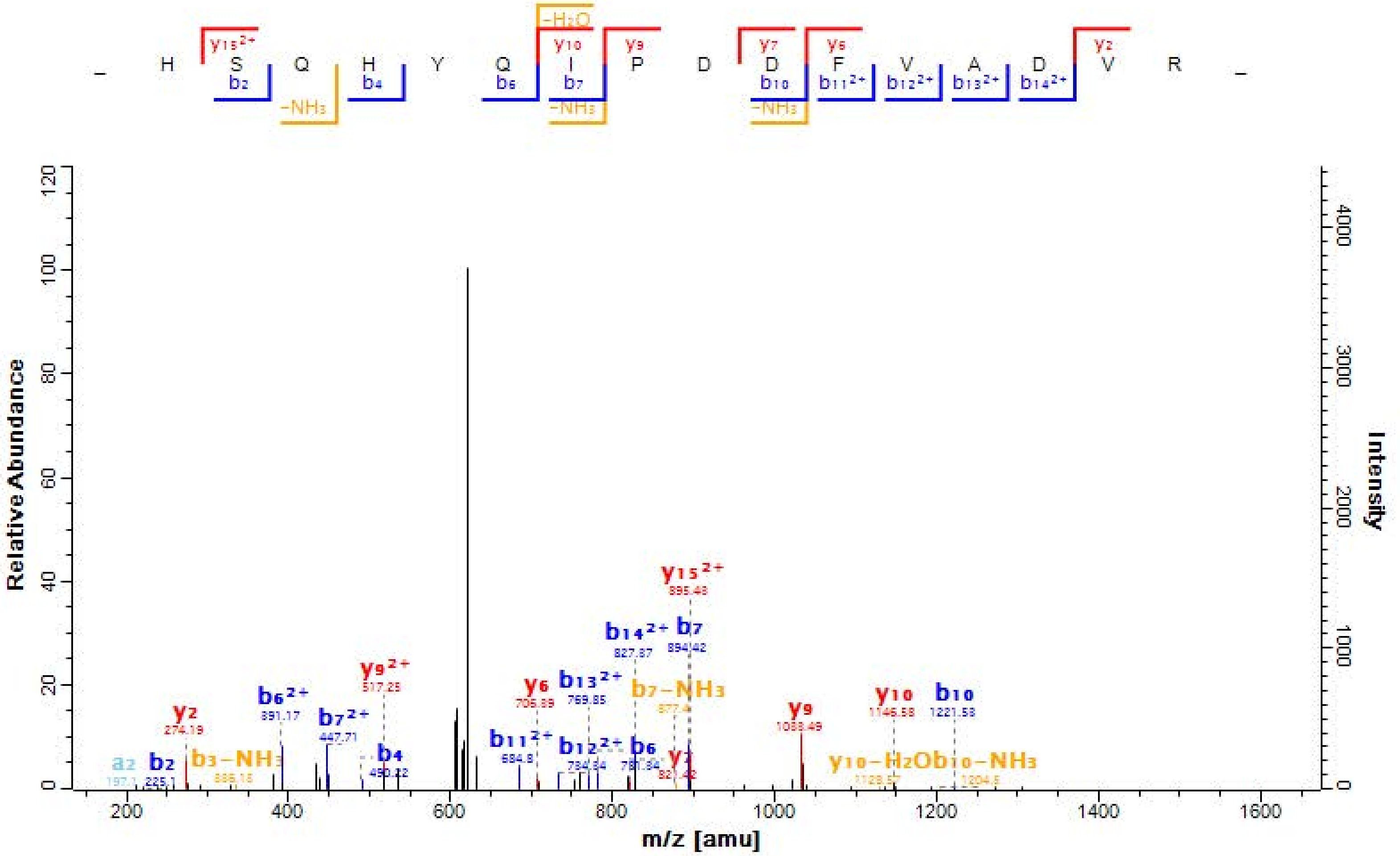
Mass:	2206.19105
m/z:	552.55504
Charge:	4+
Retentiontime:	31.968227386474
Score:	65.22546
Mass Error [ppm]:	0.53469
PEP:	0.00082742
Precursor Type:	MULTI

general information

Annotation:	8 of 19
AminoAcids Coverag	42 %
Intensity Coverage:	54 %
Peak Coverage:	13 %
Protein Localisation:	692 ... 710

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	I	18				
-0.07	200.1		228.1	+0.061	228.1	2	N	17	2094		2094	
	313.2		341.2	+0.14	341.2	3	L	16	1980		1980	
	441.3		469.3		469.3	4	K	15	1867		1867	
	538.4		566.4		566.4	5	P	14	1739		869.9	+0.19
	625.4		653.4		653.4	6	S	13	1642		1642	
	788.5		816.5	-0.02	816.5	7	Y	12	1555		1555	
	901.6	+0.023	465.3	+0.018	929.5	8	L	11	1392		696.4	-0.08
	1001		1029	-0.06	1029	9	V	10	1279		639.8	+0.31
	1100		1128	-0.22	1128	10	V	9	1180		590.3	+0.21
	1197		1225		1225	11	P	8	1081	+0.359	540.8	+0.03
	1325		1353		1353	12	Q	7	983.5		983.5	
	1426		1454		1454	13	T	6	855.4		855.4	
	1483		1511		1511	14	G	5	754.4		754.4	
	1630		1658		1658	15	F	4	697.3		697.3	
	1767		1795		1795	16	H	3	550.3		550.3	
	1904		1932		1932	17	H	2	413.2		413.2	
	2033		2061		2061	18	E	1	276.2		276.2	
						19	K	0	147.1		147.1	

Scan number	4430	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	95.85



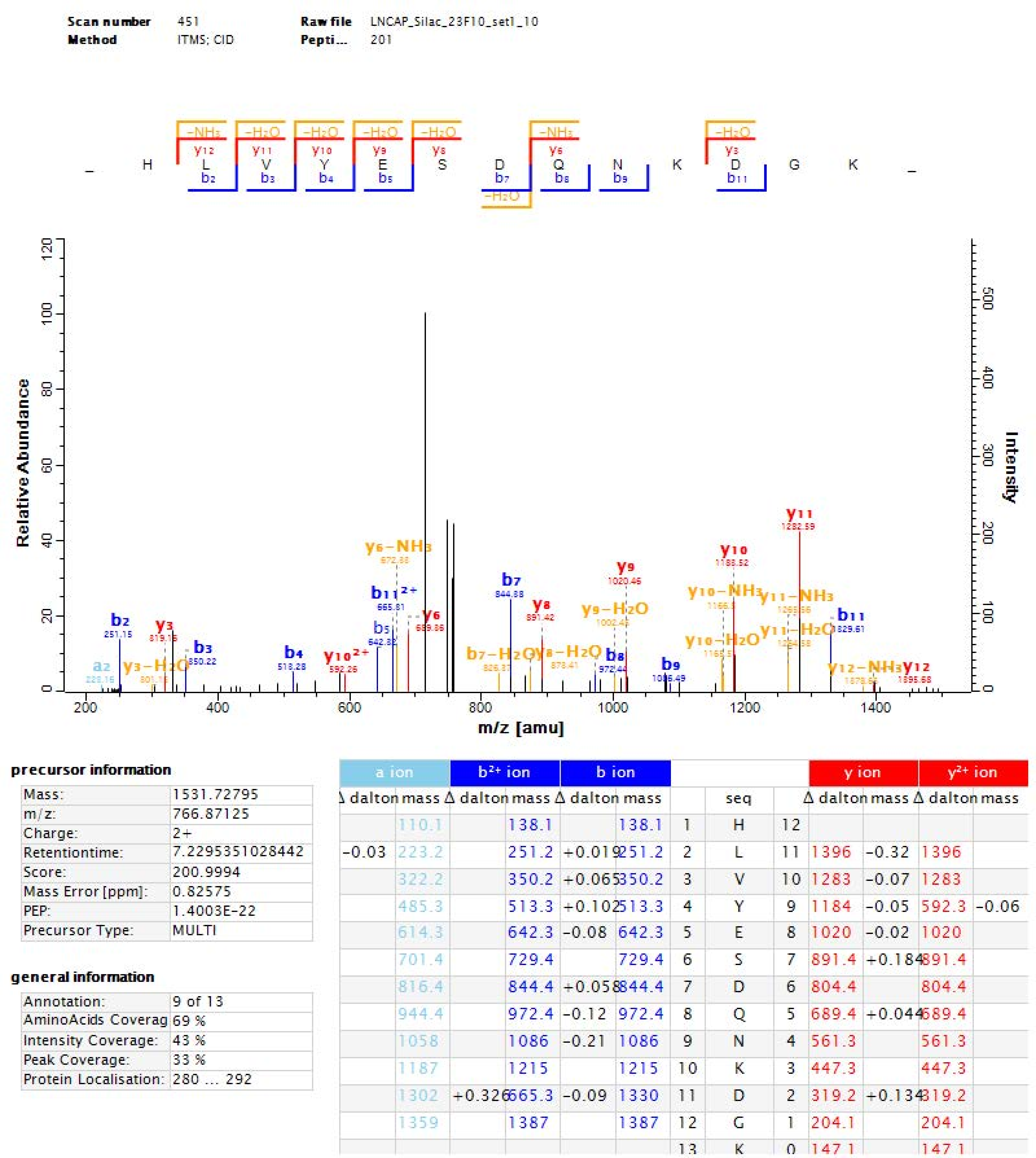
precursor information

Mass:	1925.9028
m/z:	642.97488
Charge:	3+
Retentiontime:	33.062602996826
Score:	95.85367
Mass Error [ppm]:	0.40155
PEP:	2.2628E-05
Precursor Type:	MULTI

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	28 %
Peak Coverage:	26 %
Protein Localisation:	1014 ... 1029

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	110.1		138.1		138.1	1	H	15				
+0.486	197.1		225.1	+0.251	225.1	2	S	14	1790		895.4	−0.08
	325.2		353.2		353.2	3	Q	13	1703		1703	
	462.2		490.2	+0.214	490.2	4	H	12	1575		1575	
	625.3		653.3		653.3	5	Y	11	1438		1438	
	753.3	+0.268	391.2	−0.09	781.3	6	Q	10	1275		1275	
	866.4	+0.221	447.7	−0.06	894.4	7	I	9	1147	+0.041	1147	
	963.5		991.5		991.5	8	P	8	1033	−0.03	517.3	+0.03
	1079		1107		1107	9	D	7	936.4		936.4	
	1194		1222	+0.085	1222	10	D	6	821.4	−0.09	821.4	
	1341	+0.326	684.8		1369	11	F	5	706.4	+0.044	706.4	
	1440	+0.019	734.3		1468	12	V	4	559.3		559.3	
	1511	+0.245	769.9		1539	13	A	3	460.3		460.3	
	1626	−0.01	827.4		1654	14	D	2	389.2		389.2	
	1725		1753		1753	15	V	1	274.2	+0.12	274.2	
						16	R	0	175.1		175.1	



Scan number	451	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	201

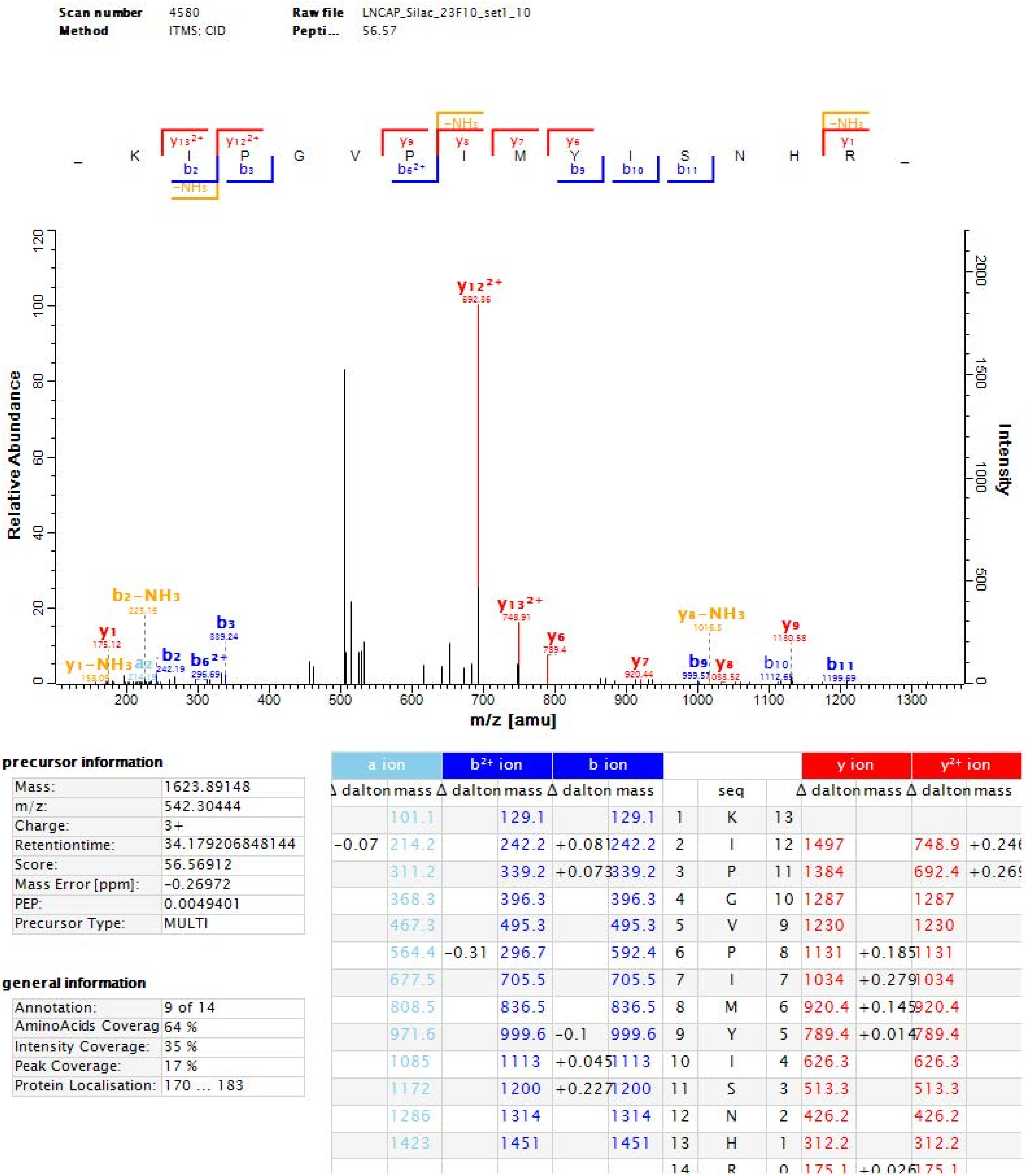
precursor information

Mass:	1531.72795
m/z:	766.87125
Charge:	2+
Retentiontime:	7.2295351028442
Score:	200.9994
Mass Error [ppm]:	0.82575
PEP:	1.4003E-22
Precursor Type:	MULTI

general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	43 %
Peak Coverage:	33 %
Protein Localisation:	280 ... 292

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	110.1		138.1		138.1	1	H	12				
-0.03	223.2		251.2	+0.019	251.2	2	L	11	1396	-0.32	1396	
	322.2		350.2	+0.065	350.2	3	V	10	1283	-0.07	1283	
	485.3		513.3	+0.102	513.3	4	Y	9	1184	-0.05	592.3	-0.06
	614.3		642.3	-0.08	642.3	5	E	8	1020	-0.02	1020	
	701.4		729.4		729.4	6	S	7	891.4	+0.184	891.4	
	816.4		844.4	+0.058	844.4	7	D	6	804.4		804.4	
	944.4		972.4	-0.12	972.4	8	Q	5	689.4	+0.044	689.4	
	1058		1086	-0.21	1086	9	N	4	561.3		561.3	
	1187		1215		1215	10	K	3	447.3		447.3	
	1302	+0.326	665.3	-0.09	1330	11	D	2	319.2	+0.134	319.2	
	1359		1387		1387	12	G	1	204.1		204.1	
						13	K	0	147.1		147.1	



Scan number	4580	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	56.57

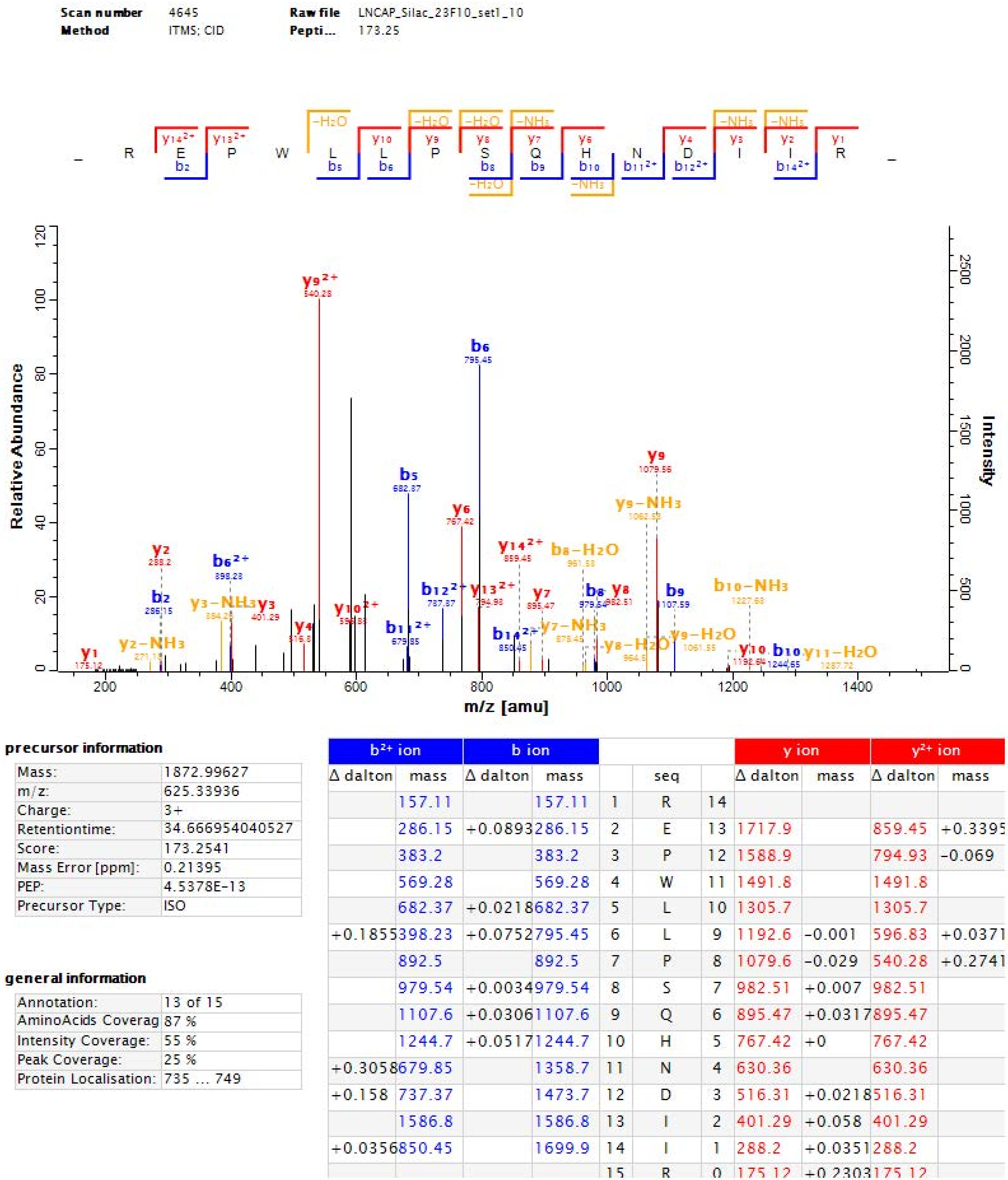
precursor information

Mass:	1623.89148
m/z:	542.30444
Charge:	3+
Retentiontime:	34.179206848144
Score:	56.56912
Mass Error [ppm]:	-0.26972
PEP:	0.0049401
Precursor Type:	MULTI

general information

Annotation:	9 of 14
AminoAcids Coverag	64 %
Intensity Coverage:	35 %
Peak Coverage:	17 %
Protein Localisation:	170 ... 183

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	101.1		129.1		129.1	1	K	13				
-0.07	214.2		242.2	+0.081	242.2	2	I	12	1497		748.9	+0.24
	311.2		339.2	+0.073	339.2	3	P	11	1384		692.4	+0.26
	368.3		396.3		396.3	4	G	10	1287		1287	
	467.3		495.3		495.3	5	V	9	1230		1230	
	564.4	-0.31	296.7		592.4	6	P	8	1131	+0.185	1131	
	677.5		705.5		705.5	7	I	7	1034	+0.279	1034	
	808.5		836.5		836.5	8	M	6	920.4	+0.145	920.4	
	971.6		999.6	-0.1	999.6	9	Y	5	789.4	+0.014	789.4	
	1085		1113	+0.045	1113	10	I	4	626.3		626.3	
	1172		1200	+0.227	1200	11	S	3	513.3		513.3	
	1286		1314		1314	12	N	2	426.2		426.2	
	1423		1451		1451	13	H	1	312.2		312.2	
						14	R	0	175.1	+0.026	175.1	



Scan number	4645	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	173.25

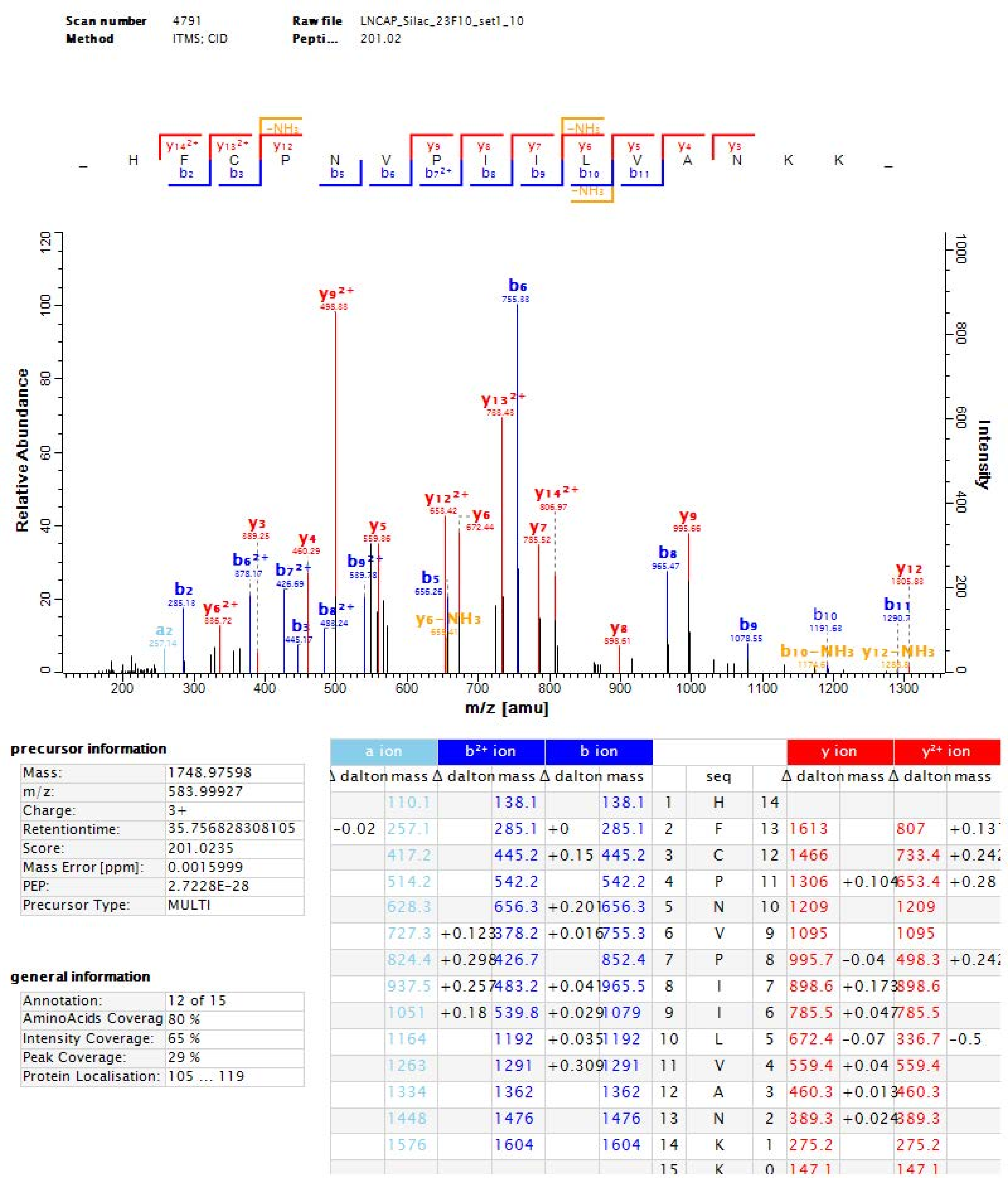
precursor information

Mass:	1872.99627
m/z:	625.33936
Charge:	3+
Retentiontime:	34.666954040527
Score:	173.2541
Mass Error [ppm]:	0.21395
PEP:	4.5378E-13
Precursor Type:	ISO

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	55 %
Peak Coverage:	25 %
Protein Localisation:	735 … 749

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	157.11		157.11	1	R	14				
	286.15	+0.0893	286.15	2	E	13	1717.9		859.45	+0.3395
	383.2		383.2	3	P	12	1588.9		794.93	-0.069
	569.28		569.28	4	W	11	1491.8		1491.8	
	682.37	+0.0218	682.37	5	L	10	1305.7		1305.7	
+0.1855	398.23	+0.0752	795.45	6	L	9	1192.6	-0.001	596.83	+0.0371
	892.5		892.5	7	P	8	1079.6	-0.029	540.28	+0.2741
	979.54	+0.0034	979.54	8	S	7	982.51	+0.007	982.51	
	1107.6	+0.0306	1107.6	9	Q	6	895.47	+0.0317	895.47	
	1244.7	+0.0517	1244.7	10	H	5	767.42	+0	767.42	
+0.3058	679.85		1358.7	11	N	4	630.36		630.36	
+0.158	737.37		1473.7	12	D	3	516.31	+0.0218	516.31	
	1586.8		1586.8	13	I	2	401.29	+0.058	401.29	
+0.0356	850.45		1699.9	14	I	1	288.2	+0.0351	288.2	
				15	R	0	175.12	+0.2303	175.12	



Scan number	4791	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	201.02

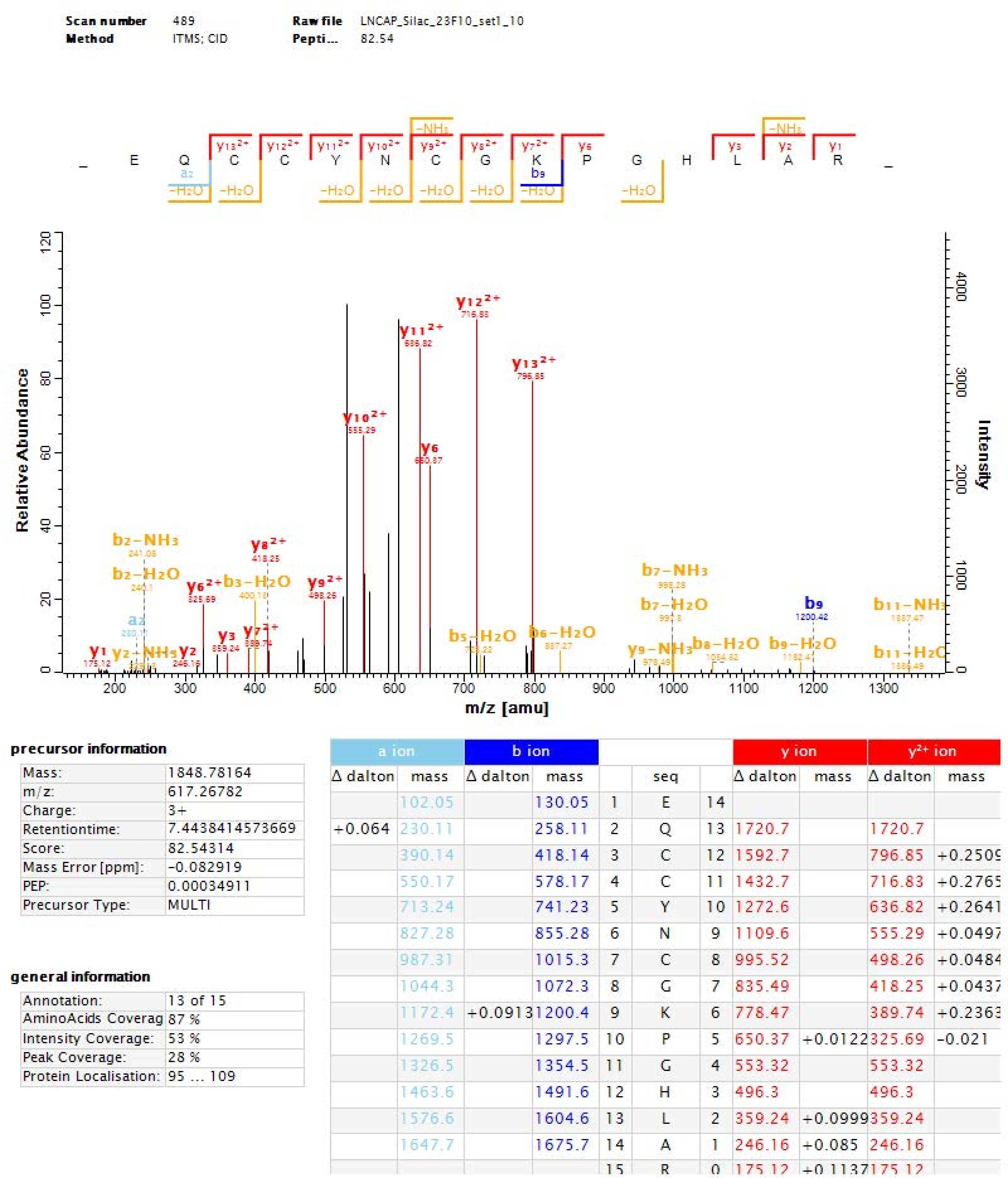
precursor information

Mass:	1748.97598
m/z:	583.99927
Charge:	3+
Retentiontime:	35.756828308105
Score:	201.0235
Mass Error [ppm]:	0.0015999
PEP:	2.7228E-28
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	65 %
Peak Coverage:	29 %
Protein Localisation:	105 ... 119

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	110.1		138.1		138.1	1	H	14				
-0.02	257.1		285.1	+0	285.1	2	F	13	1613		807	+0.13
	417.2		445.2	+0.15	445.2	3	C	12	1466		733.4	+0.24
	514.2		542.2		542.2	4	P	11	1306	+0.104	653.4	+0.28
	628.3		656.3	+0.201	656.3	5	N	10	1209		1209	
	727.3	+0.123	378.2	+0.016	755.3	6	V	9	1095		1095	
	824.4	+0.298	426.7		852.4	7	P	8	995.7	-0.04	498.3	+0.24
	937.5	+0.257	483.2	+0.041	965.5	8	I	7	898.6	+0.173	898.6	
	1051	+0.18	539.8	+0.029	1079	9	I	6	785.5	+0.047	785.5	
	1164		1192	+0.035	1192	10	L	5	672.4	-0.07	336.7	-0.5
	1263		1291	+0.309	1291	11	V	4	559.4	+0.04	559.4	
	1334		1362		1362	12	A	3	460.3	+0.013	460.3	
	1448		1476		1476	13	N	2	389.3	+0.024	389.3	
	1576		1604		1604	14	K	1	275.2		275.2	
						15	K	0	147.1		147.1	



Scan number 489 **Raw file** LNCAP_Silac_23F10_set1_10
Method ITMS; CID **Pepti...** 82.54

precursor information

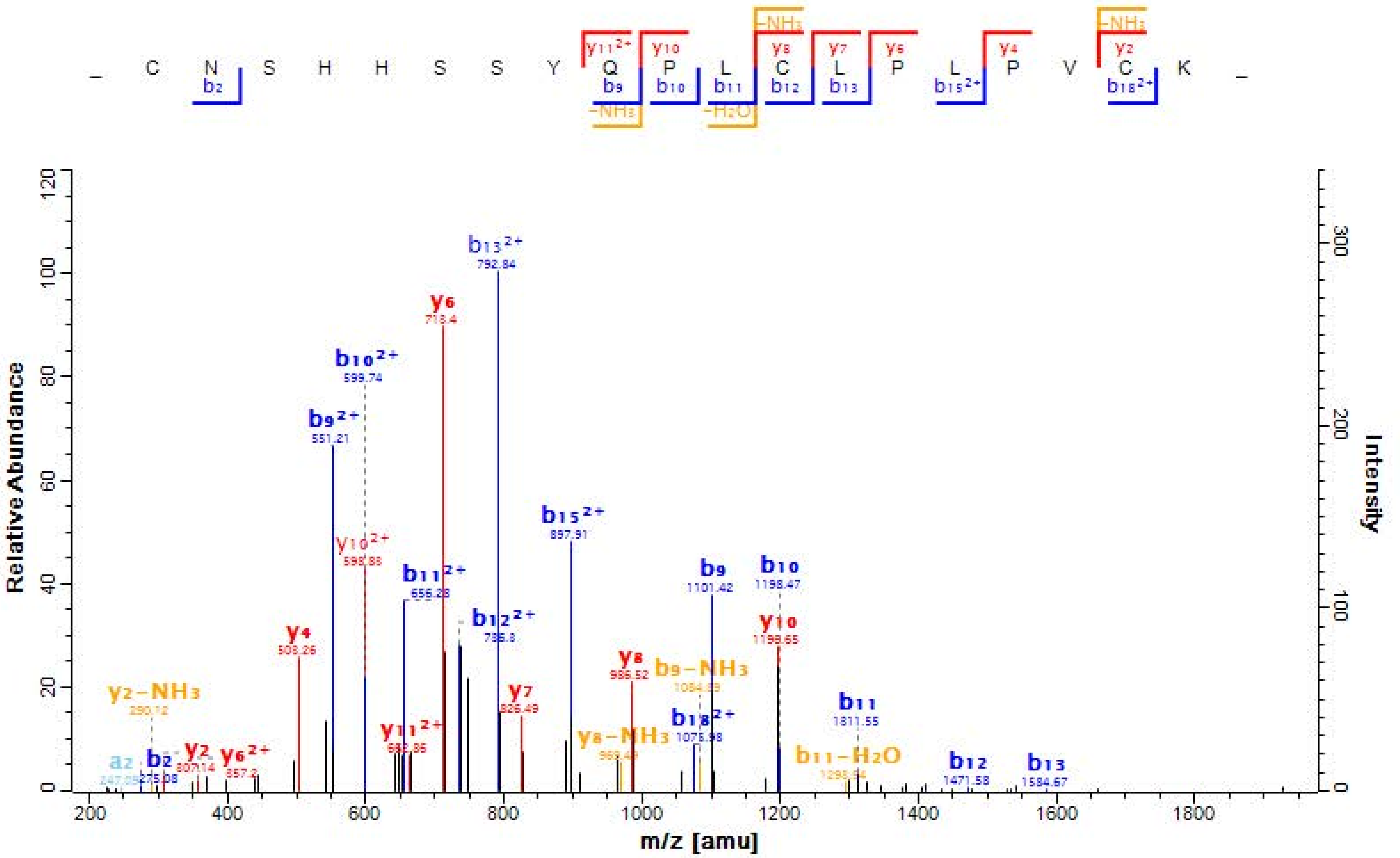
Mass:	1848.78164
m/z:	617.26782
Charge:	3+
Retentiontime:	7.4438414573669
Score:	82.54314
Mass Error [ppm]:	-0.082919
PEP:	0.00034911
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	53 %
Peak Coverage:	28 %
Protein Localisation:	95 ... 109

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	14				
+0.064	230.11		258.11	2	Q	13	1720.7		1720.7	
	390.14		418.14	3	C	12	1592.7		796.85	+0.2509
	550.17		578.17	4	C	11	1432.7		716.83	+0.2765
	713.24		741.23	5	Y	10	1272.6		636.82	+0.2641
	827.28		855.28	6	N	9	1109.6		555.29	+0.0497
	987.31		1015.3	7	C	8	995.52		498.26	+0.0484
	1044.3		1072.3	8	G	7	835.49		418.25	+0.0437
	1172.4	+0.0913	1200.4	9	K	6	778.47		389.74	+0.2363
	1269.5		1297.5	10	P	5	650.37	+0.0122	325.69	-0.021
	1326.5		1354.5	11	G	4	553.32		553.32	
	1463.6		1491.6	12	H	3	496.3		496.3	
	1576.6		1604.6	13	L	2	359.24	+0.0999	359.24	
	1647.7		1675.7	14	A	1	246.16	+0.085	246.16	
				15	R	0	175.12	+0.1137	175.12	

Scan number	5097	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	144.29



precursor information

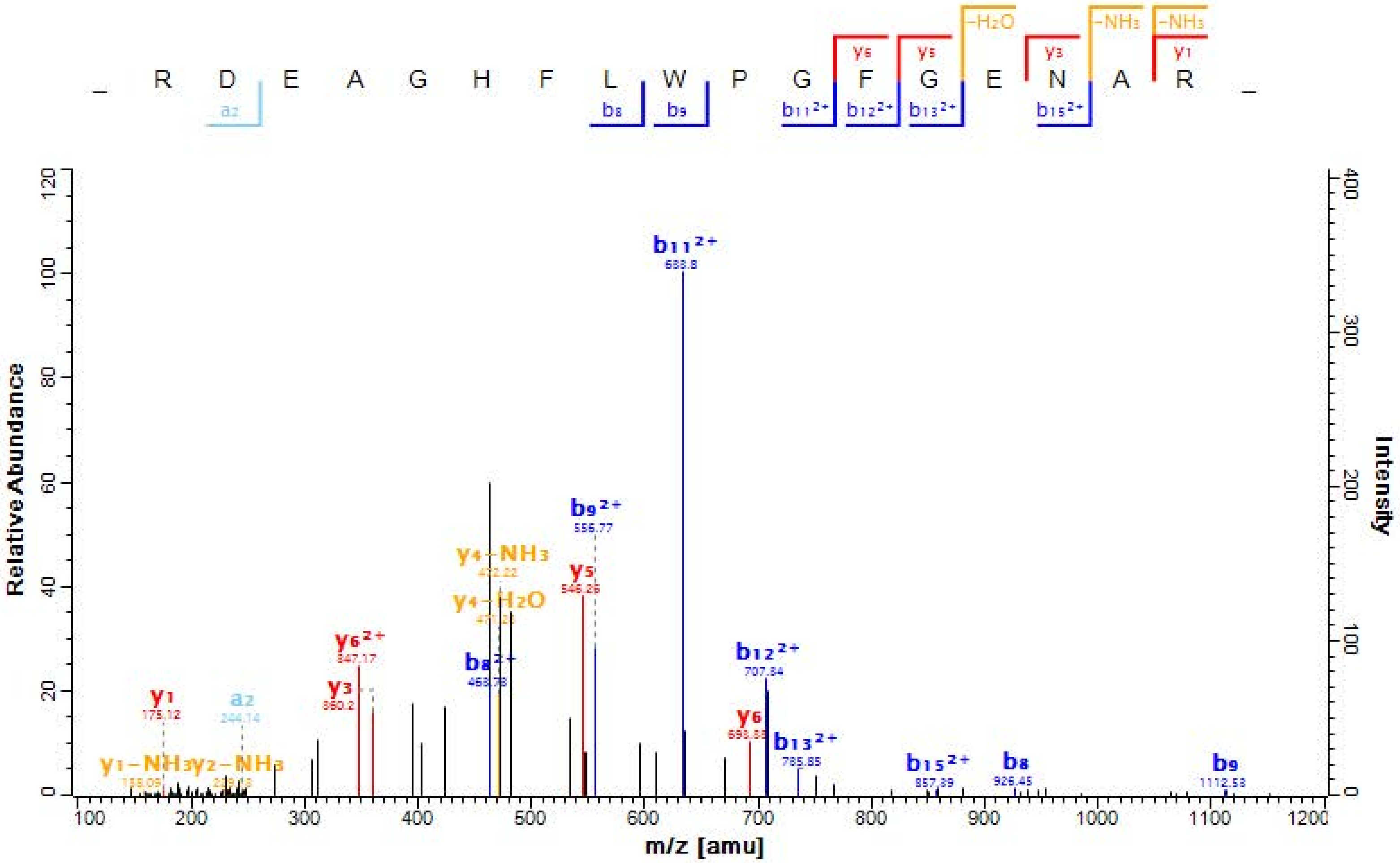
Mass:	2296.05481
m/z:	766.35888
Charge:	3+
Retentiontime:	38.262657165527
Score:	144.2888
Mass Error [ppm]:	-0.13255
PEP:	6.0737E-19
Precursor Type:	MULTI

general information

Annotation:	11 of 19
AminoAcids Coverag	58 %
Intensity Coverage:	67 %
Peak Coverage:	33 %
Protein Localisation:	503 ... 521

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	133		161		161	1	C	18				
+0.107	247.1		275.1	+0.037	275.1	2	N	17	2137		2137	
	334.1		362.1		362.1	3	S	16	2023		2023	
	471.2		499.2		499.2	4	H	15	1936		1936	
	608.2		636.2		636.2	5	H	14	1799		1799	
	695.3		723.3		723.3	6	S	13	1662		1662	
	782.3		810.3		810.3	7	S	12	1575		1575	
	945.4		973.4		973.4	8	Y	11	1488		1488	
	1073	+0.253	551.2	-0.05	1101	9	Q	10	1325		662.9	+0.33
	1170	+0.425	599.7	+0.098	1198	10	P	9	1197	-0.01	598.8	+0.18
	1284	+0.322	656.3	+0.251	1312	11	L	8	1100		1100	
	1444	-0.04	736.3	+0.02	1472	12	C	7	986.5	-0.04	986.5	
	1557	+0.189	792.8	+0.421	1585	13	L	6	826.5	-0.02	826.5	
	1654		1682		1682	14	P	5	713.4	-0.06	357.2	+0.05
	1767	+0.104	897.9		1795	15	L	4	616.3		616.3	
	1864		1892		1892	16	P	3	503.3	+0.074	503.3	
	1963		1991		1991	17	V	2	406.2		406.2	
	2123	-0.01	1076		2151	18	C	1	307.1	+0.007	307.1	
						19	K	0	147.1		147.1	

Scan number	5530	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	49.59



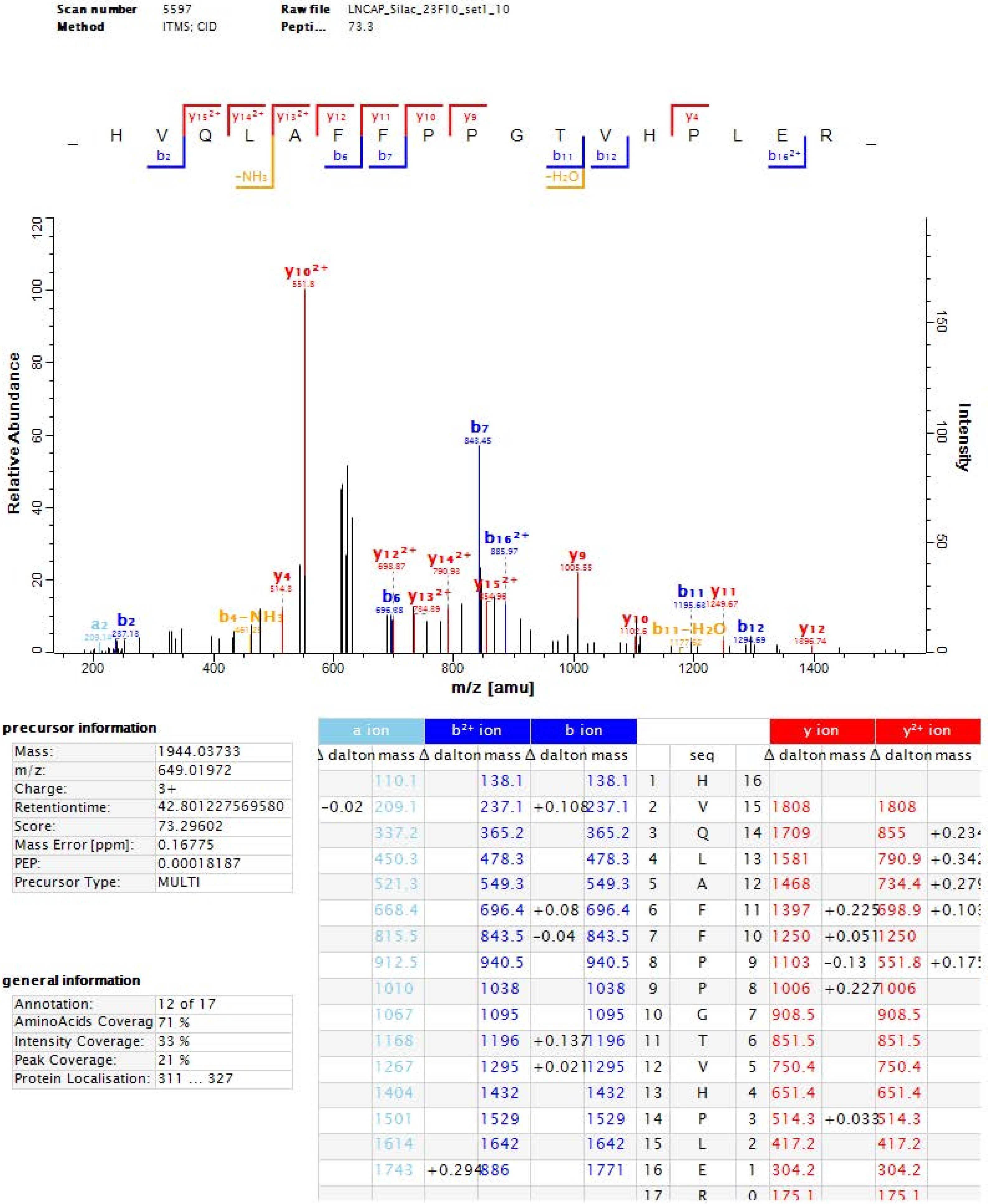
precursor information

Mass:	1957.91728
m/z:	490.4866
Charge:	4+
Retentiontime:	42.120121002197
Score:	49.59457
Mass Error [ppm]:	-0.54336
PEP:	0.0076928
Precursor Type:	MULTI

general information

Annotation:	11 of 17
AminoAcids Coverag	65 %
Intensity Coverage:	48 %
Peak Coverage:	16 %
Protein Localisation:	537 ... 553

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.1		157.1		157.1	1	R	16				
+0.109	244.1		272.1		272.1	2	D	15	1803		1803	
	373.2		401.2		401.2	3	E	14	1688		1688	
	444.2		472.2		472.2	4	A	13	1559		1559	
	501.2		529.2		529.2	5	G	12	1488		1488	
	638.3		666.3		666.3	6	H	11	1431		1431	
	785.4		813.4		813.4	7	F	10	1294		1294	
	898.5	+0.073	463.7	-0.06	926.4	8	L	9	1147		1147	
	1085	+0.16	556.8	-0.2	1113	9	W	8	1033		1033	
	1182		1210		1210	10	P	7	847.4		847.4	
	1239	+0.2	633.8		1267	11	G	6	750.4		750.4	
	1386	-0.01	707.3		1414	12	F	5	693.3	+0.201	347.2	+0.07
	1443	+0.092	735.8		1471	13	G	4	546.3	+0.004	546.3	
	1572		1600		1600	14	E	3	489.2		489.2	
	1686	+0.471	857.4		1714	15	N	2	360.2	+0.108	360.2	
	1757		1785		1785	16	A	1	246.2		246.2	
						17	R	0	175.1	+0.1	175.1	



Scan number	5597	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	73.3

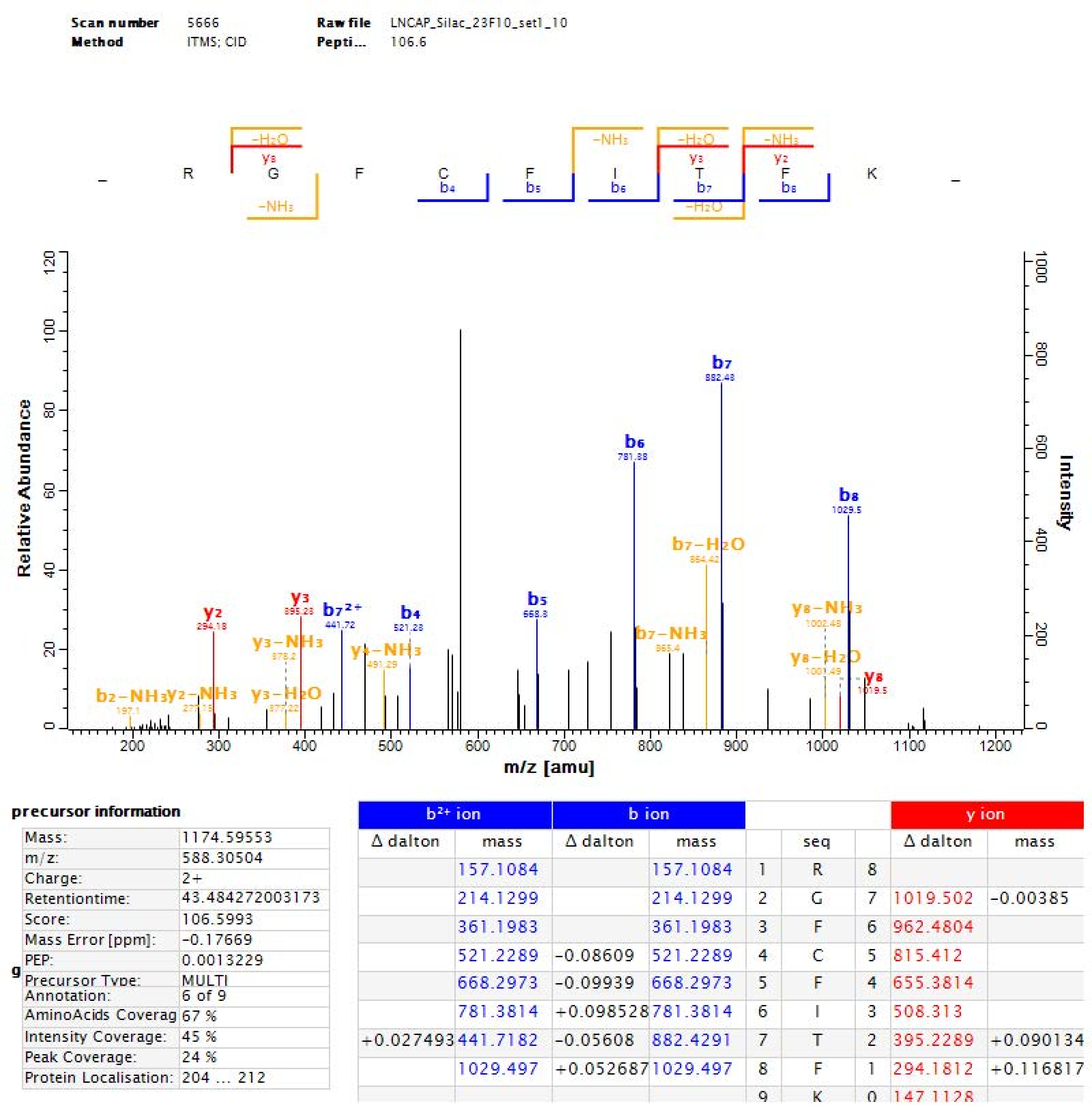
precursor information

Mass:	1944.03733
m/z:	649.01972
Charge:	3+
Retentiontime:	42.801227569580
Score:	73.29602
Mass Error [ppm]:	0.16775
PEP:	0.00018187
Precursor Type:	MULTI

general information

Annotation:	12 of 17
AminoAcids Coverag	71 %
Intensity Coverage:	33 %
Peak Coverage:	21 %
Protein Localisation:	311 ... 327

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	110.1		138.1		138.1	1	H	16				
-0.02	209.1		237.1	+0.108	237.1	2	V	15	1808		1808	
	337.2		365.2		365.2	3	Q	14	1709		855	+0.23
	450.3		478.3		478.3	4	L	13	1581		790.9	+0.34
	521.3		549.3		549.3	5	A	12	1468		734.4	+0.27
	668.4		696.4	+0.08	696.4	6	F	11	1397	+0.225	698.9	+0.10
	815.5		843.5	-0.04	843.5	7	F	10	1250	+0.051	1250	
	912.5		940.5		940.5	8	P	9	1103	-0.13	551.8	+0.17
	1010		1038		1038	9	P	8	1006	+0.227	1006	
	1067		1095		1095	10	G	7	908.5		908.5	
	1168		1196	+0.137	1196	11	T	6	851.5		851.5	
	1267		1295	+0.021	1295	12	V	5	750.4		750.4	
	1404		1432		1432	13	H	4	651.4		651.4	
	1501		1529		1529	14	P	3	514.3	+0.033	514.3	
	1614		1642		1642	15	L	2	417.2		417.2	
	1743	+0.294	886		1771	16	E	1	304.2		304.2	
						17	R	0	175.1		175.1	

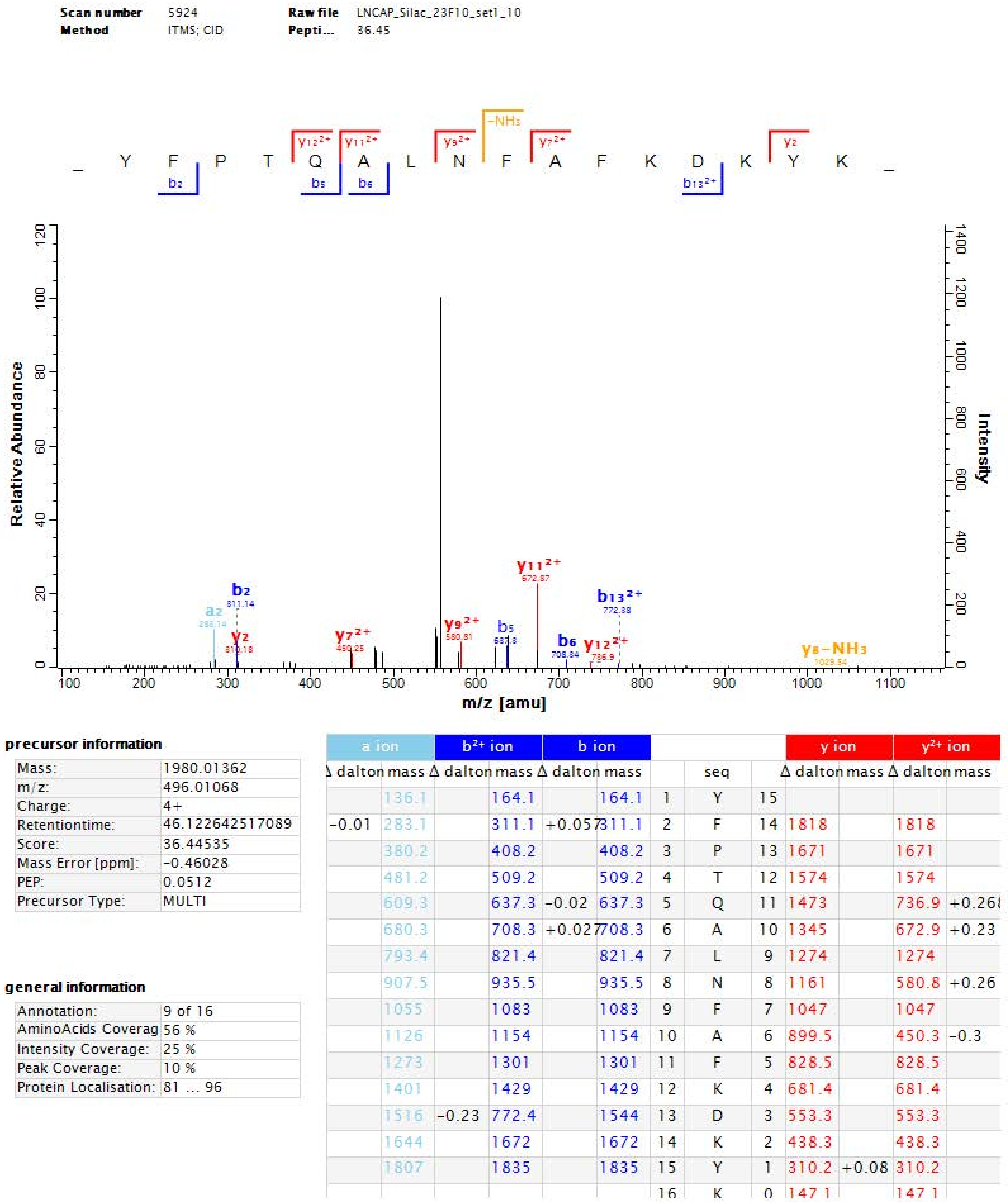


Scan number	5666	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	106.6

precursor information

Mass:	1174.59553
m/z:	588.30504
Charge:	2+
Retentiontime:	43.484272003173
Score:	106.5993
Mass Error [ppm]:	-0.17669
PEP:	0.0013229
Precursor Type:	MULTI
Annotation:	6 of 9
AminoAcids Coverag	67 %
Intensity Coverage:	45 %
Peak Coverage:	24 %
Protein Localisation:	204 ... 212

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	157.1084		157.1084	1	R	8		
	214.1299		214.1299	2	G	7	1019.502	-0.00385
	361.1983		361.1983	3	F	6	962.4804	
	521.2289	-0.08609	521.2289	4	C	5	815.412	
	668.2973	-0.09939	668.2973	5	F	4	655.3814	
	781.3814	+0.098528	781.3814	6	I	3	508.313	
+0.027493	441.7182	-0.05608	882.4291	7	T	2	395.2289	+0.090134
	1029.497	+0.052687	1029.497	8	F	1	294.1812	+0.116817
				9	K	0	147.1128	



Scan number	5924	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	36.45

precursor information

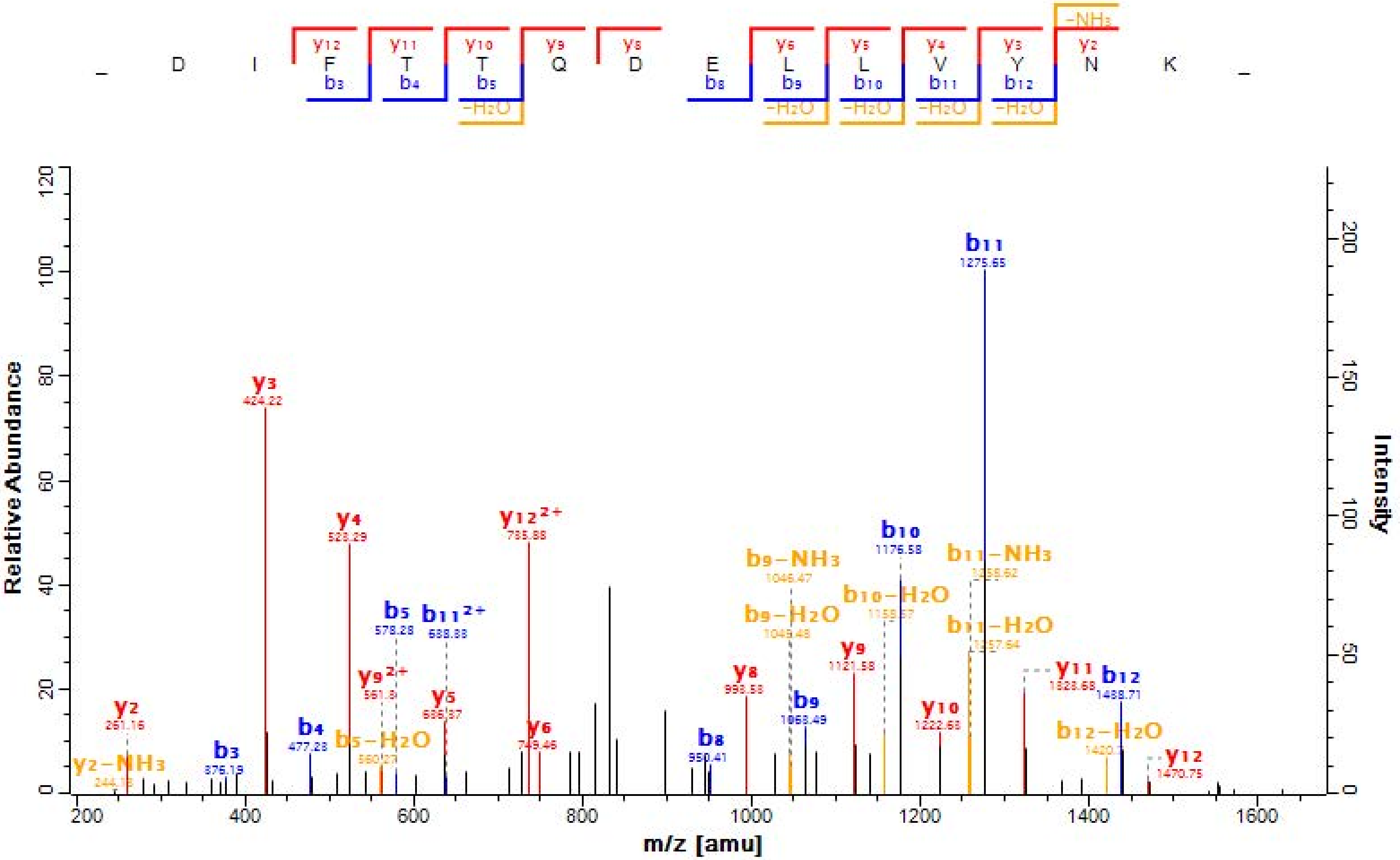
Mass:	1980.01362
m/z:	496.01068
Charge:	4+
Retentiontime:	46.122642517089
Score:	36.44535
Mass Error [ppm]:	-0.46028
PEP:	0.0512
Precursor Type:	MULTI

general information

Annotation:	9 of 16
AminoAcids Coverag	56 %
Intensity Coverage:	25 %
Peak Coverage:	10 %
Protein Localisation:	81 ... 96

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.1		164.1		164.1	1	Y	15				
-0.01	283.1		311.1	+0.057	311.1	2	F	14	1818		1818	
	380.2		408.2		408.2	3	P	13	1671		1671	
	481.2		509.2		509.2	4	T	12	1574		1574	
	609.3		637.3	-0.02	637.3	5	Q	11	1473		736.9	+0.26
	680.3		708.3	+0.027	708.3	6	A	10	1345		672.9	+0.23
	793.4		821.4		821.4	7	L	9	1274		1274	
	907.5		935.5		935.5	8	N	8	1161		580.8	+0.26
	1055		1083		1083	9	F	7	1047		1047	
	1126		1154		1154	10	A	6	899.5		450.3	-0.3
	1273		1301		1301	11	F	5	828.5		828.5	
	1401		1429		1429	12	K	4	681.4		681.4	
	1516	-0.23	772.4		1544	13	D	3	553.3		553.3	
	1644		1672		1672	14	K	2	438.3		438.3	
	1807		1835		1835	15	Y	1	310.2	+0.08	310.2	
						16	K	0	147.1		147.1	

Scan number	5966	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	178.84



precursor information

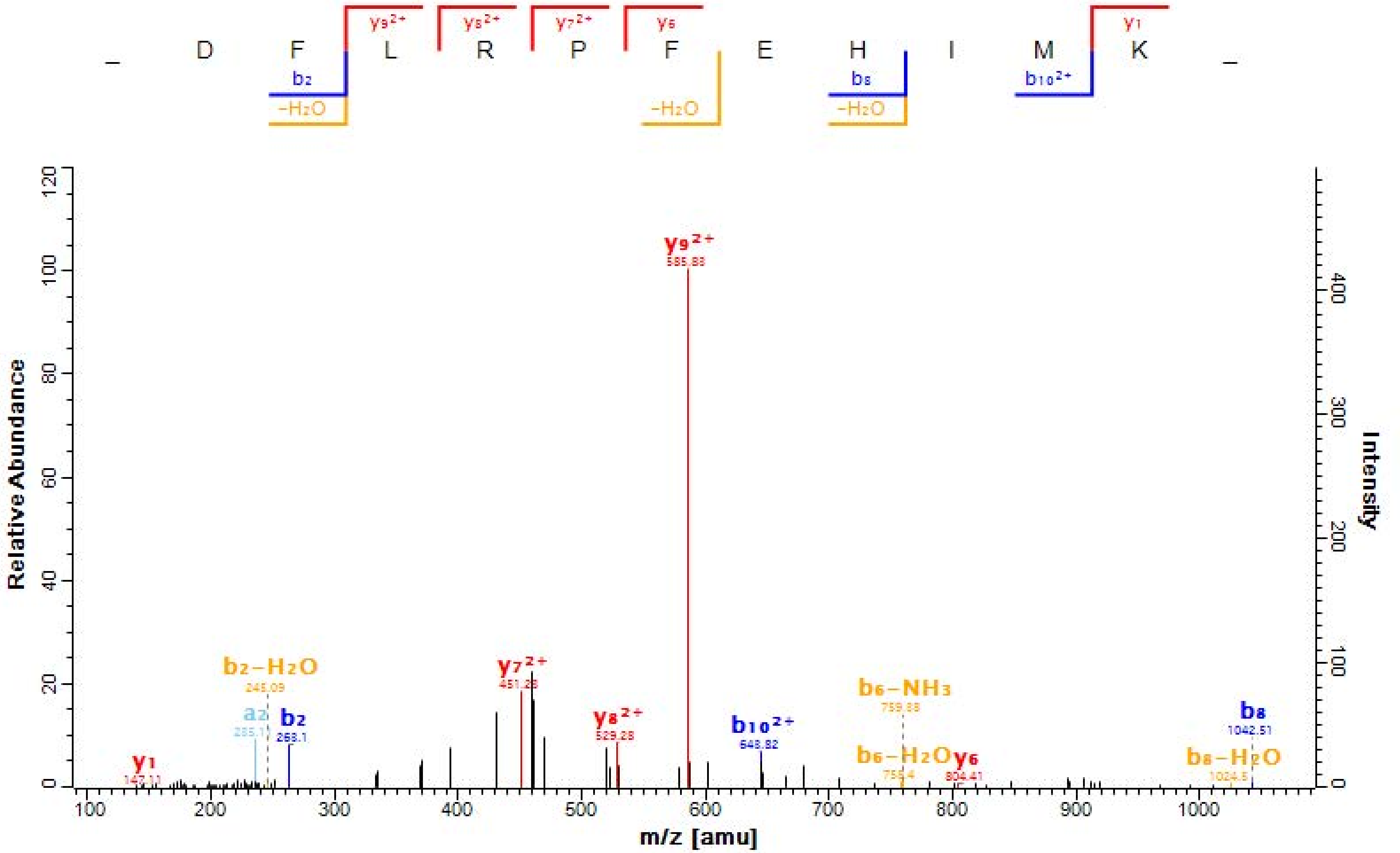
Mass:	1697.85132
m/z:	849.93294
Charge:	2+
Retentiontime:	46.572704315185
Score:	178.8359
Mass Error [ppm]:	0.059369
PEP:	4.1643E-18
Precursor Type:	ISO

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	58 %
Peak Coverage:	34 %
Protein Localisation:	252 ... 265

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	13				
	229.12		229.12	2	I	12	1583.8		1583.8	
	376.19	+0.0584	376.19	3	F	11	1470.7	-0.139	735.88	+0.2115
	477.23	+0.067	477.23	4	T	10	1323.7	-0.031	1323.7	
	578.28	+0.141	578.28	5	T	9	1222.6	+0.1279	1222.6	
	706.34		706.34	6	Q	8	1121.6	+0.0415	561.3	-0.026
	821.37		821.37	7	D	7	993.53	+0.1585	993.53	
	950.41	-0.02	950.41	8	E	6	878.5		878.5	
	1063.5	-0.032	1063.5	9	L	5	749.46	+0.0615	749.46	
	1176.6	-0.064	1176.6	10	L	4	636.37	-0.065	636.37	
+0.359	638.33	-0.088	1275.6	11	V	3	523.29	+0.1155	523.29	
	1438.7	+0.0044	1438.7	12	Y	2	424.22	+0.0117	424.22	
	1552.8		1552.8	13	N	1	261.16	+0.1154	261.16	
				14	K	0	147.11		147.11	

Scan number	5973	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	51.93



precursor information

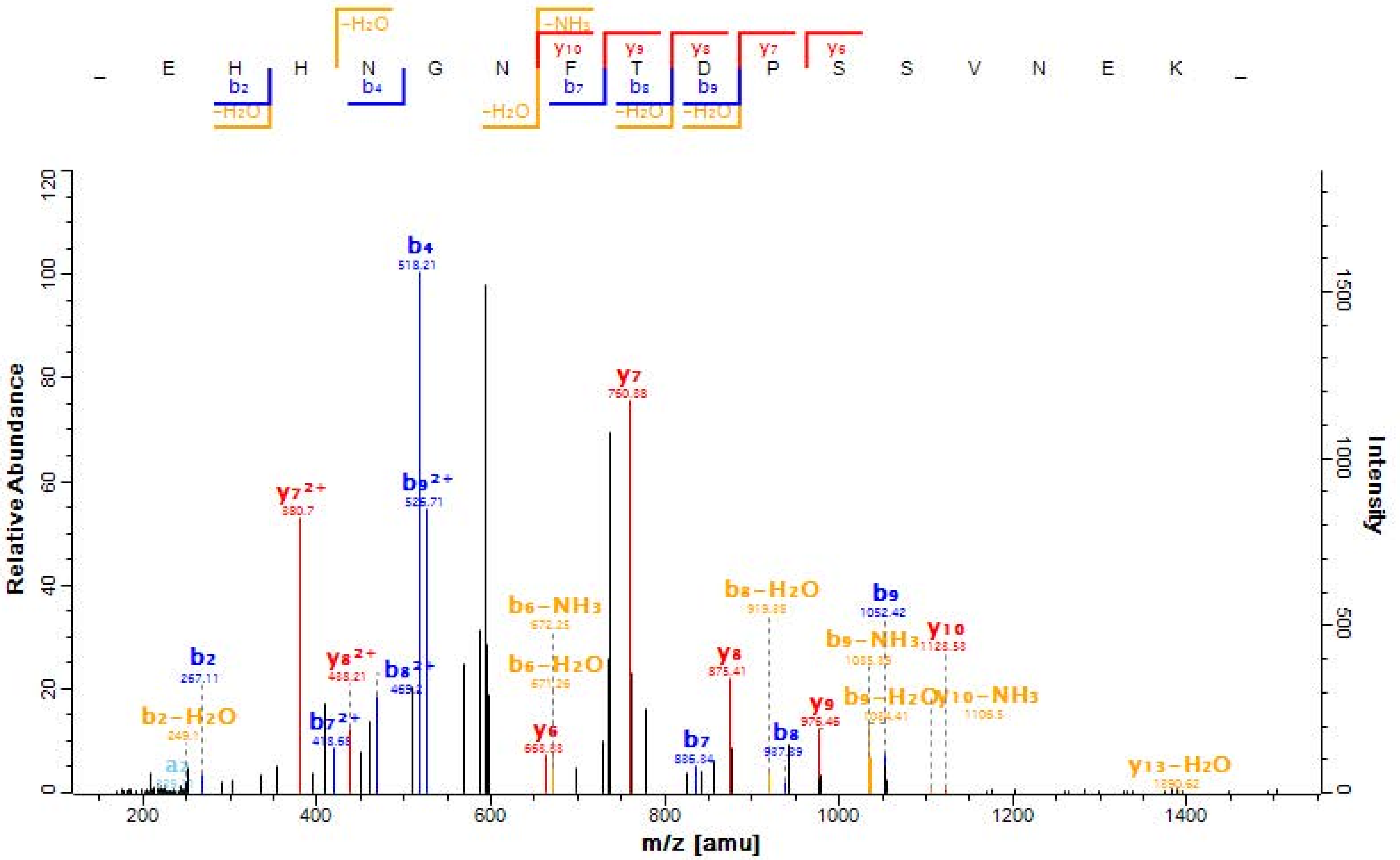
Mass:	1431.73269
m/z:	478.25151
Charge:	3+
Retentiontime:	46.643508911132
Score:	51.92667
Mass Error [ppm]:	-0.42101
PEP:	0.022551
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	45 %
Peak Coverage:	12 %
Protein Localisation:	1182 ... 1192

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.04		116		116	1	D	10				
+0.046	235.1		263.1	+0.045	263.1	2	F	9	1318		1318	
	348.2		376.2		376.2	3	L	8	1171		585.8	+0.287
	504.3		532.3		532.3	4	R	7	1058		529.3	-0.1
	601.3		629.3		629.3	5	P	6	901.5		451.2	-0.02
	748.4		776.4		776.4	6	F	5	804.4	-0.37	804.4	
	877.5		905.5		905.5	7	E	4	657.3		657.3	
	1015		1043	+0.141	1043	8	H	3	528.3		528.3	
	1128		1156		1156	9	I	2	391.2		391.2	
	1259	+0.343	643.8		1287	10	M	1	278.2		278.2	
						11	K	0	147.1	-0.06	147.1	

Scan number	630	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	88.56



precursor information

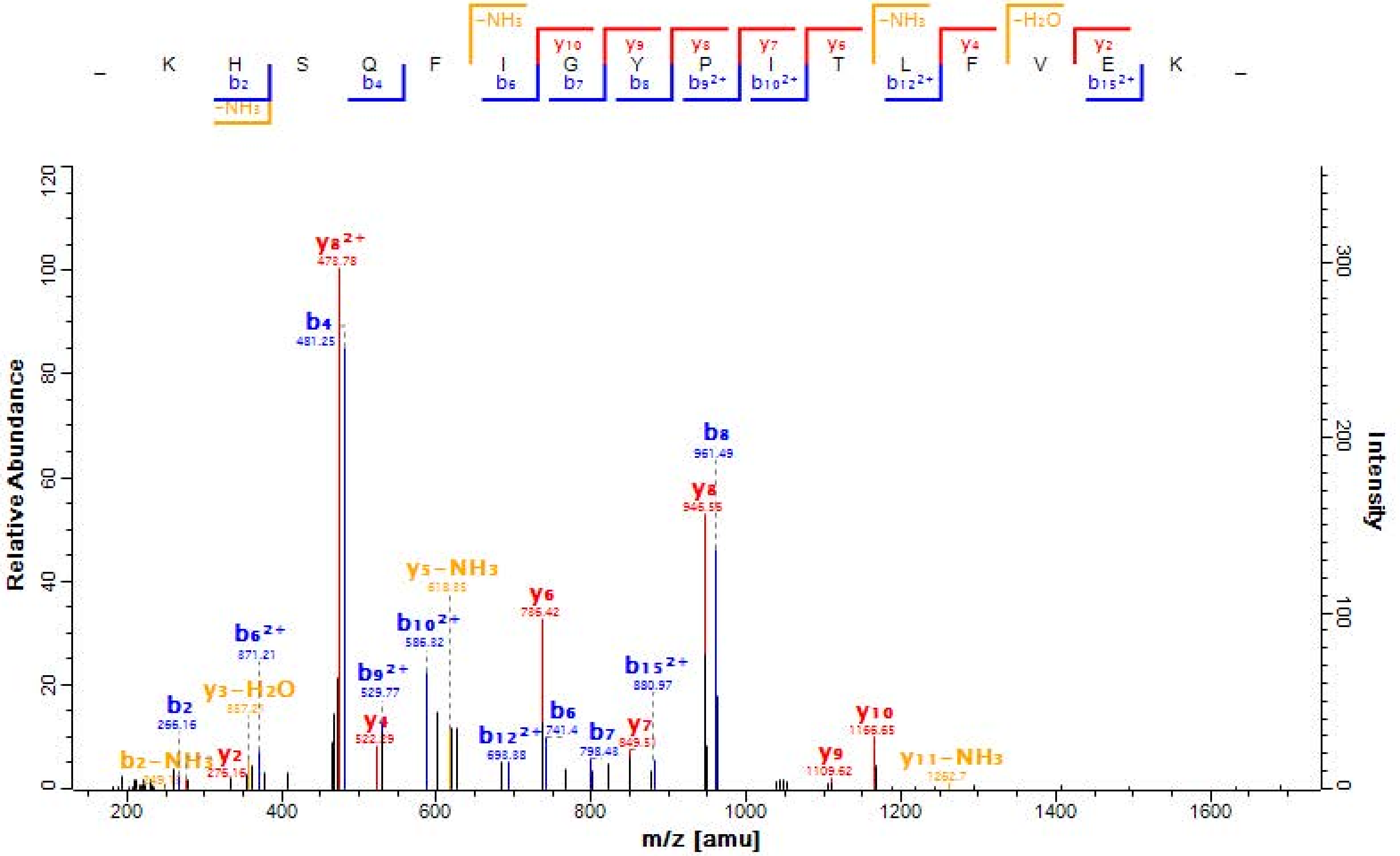
Mass:	1810.78759
m/z:	604.60314
Charge:	3+
Retentiontime:	8.3005332946777
Score:	88.56142
Mass Error [ppm]:	0.2938
PEP:	4.4302E-05
Precursor Type:	MULTI

general information

Annotation:	8 of 16
AminoAcids Coverag	50 %
Intensity Coverage:	44 %
Peak Coverage:	20 %
Protein Localisation:	18 ... 33

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.1		130		130	1	E	15				
-0.07	239.1		267.1	+0.021	267.1	2	H	14	1683		1683	
	376.2		404.2		404.2	3	H	13	1546		1546	
	490.2		518.2	-0.34	518.2	4	N	12	1409		1409	
	547.2		575.2		575.2	5	G	11	1295		1295	
	661.3		689.3		689.3	6	N	10	1238		1238	
	808.3	+0.296	418.7	+0.219	836.3	7	F	9	1124	-0.11	1124	
	909.4	+0.016	469.2	+0.023	937.4	8	T	8	976.5	+0.051	976.5	
	1024	+0.272	526.7	+0.078	1052	9	D	7	875.4	+0.037	438.2	-0.03
	1121		1149		1149	10	P	6	760.4	+0.054	380.7	+0.16
	1209		1237		1237	11	S	5	663.3	+0.053	663.3	
	1296		1324		1324	12	S	4	576.3		576.3	
	1395		1423		1423	13	V	3	489.3		489.3	
	1509		1537		1537	14	N	2	390.2		390.2	
	1638		1666		1666	15	E	1	276.2		276.2	
						16	K	0	147.1		147.1	

Scan number	6450	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	86.38



precursor information

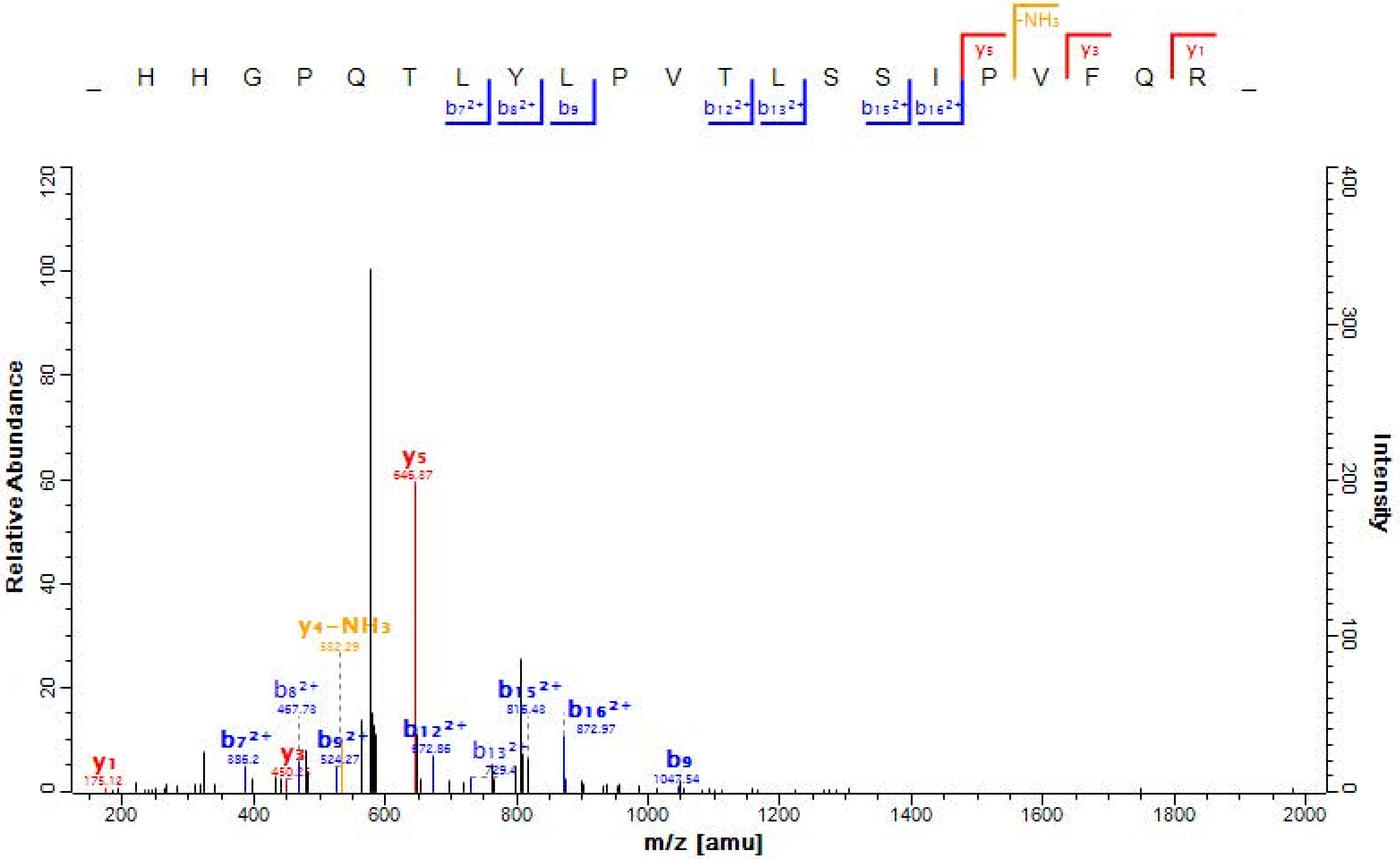
Mass:	1906.03512
m/z:	636.35232
Charge:	3+
Retentiontime:	52.618999481201
Score:	86.37751
Mass Error [ppm]:	-0.078655
PEP:	3.2995E-05
Precursor Type:	MULTI

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	62 %
Peak Coverage:	24 %
Protein Localisation:	331 ... 346

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.1		129.1	1	K	15				
	266.16	+0.1212	266.16	2	H	14	1778.9		1778.9	
	353.19		353.19	3	S	13	1641.9		1641.9	
	481.25	+0.159	481.25	4	Q	12	1554.9		1554.9	
	628.32		628.32	5	F	11	1426.8		1426.8	
+0.1861	371.21	-0.074	741.4	6	I	10	1279.7		1279.7	
	798.43	+0.2038	798.43	7	G	9	1166.6	-0.086	1166.6	
	961.49	-0.018	961.49	8	Y	8	1109.6	+0.1587	1109.6	
-0.107	529.77		1058.5	9	P	7	946.56	-0.025	473.78	+0.1565
+0.2639	586.32		1171.6	10	I	6	849.51	-0.431	849.51	
	1272.7		1272.7	11	T	5	736.42	+0.0166	736.42	
+0.0526	693.38		1385.8	12	L	4	635.38		635.38	
	1532.8		1532.8	13	F	3	522.29	-0.178	522.29	
	1631.9		1631.9	14	V	2	375.22		375.22	
+0.2382	880.97		1760.9	15	E	1	276.16	-0.029	276.16	
				16	K	0	147.11		147.11	

Scan number	6850	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	30.95



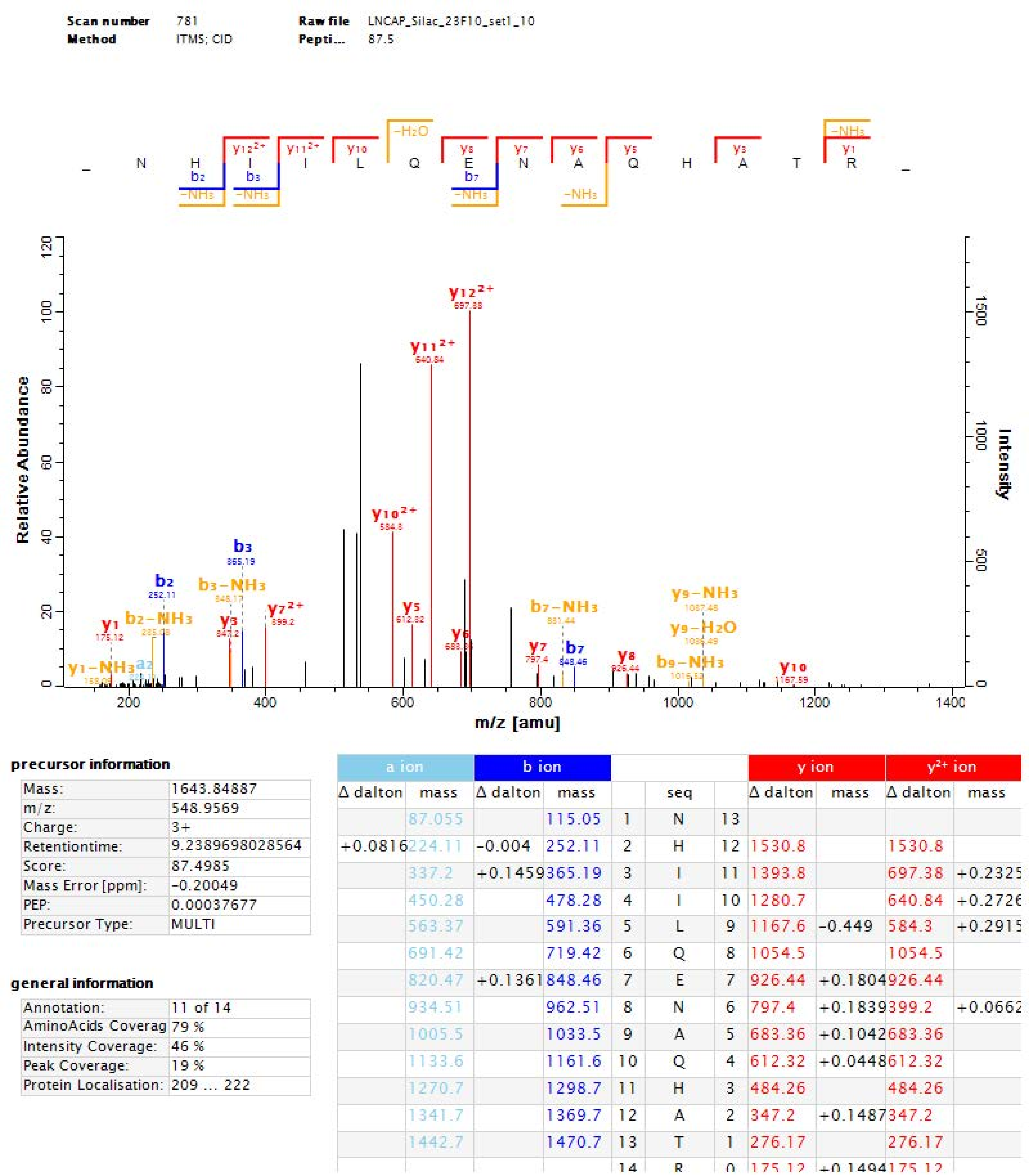
precursor information

Mass:	2389.29093
m/z:	598.33001
Charge:	4+
Retentiontime:	59.439029693603
Score:	30.94517
Mass Error [ppm]:	0.11711
PEP:	0.085984
Precursor Type:	MULTI

general information

Annotation:	12 of 21
AminoAcids Coverag	57 %
Intensity Coverage:	28 %
Peak Coverage:	16 %
Protein Localisation:	836 ... 856

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	138.0662		138.0662	1	H	20		
	275.1251		275.1251	2	H	19	2253.239	
	332.1466		332.1466	3	G	18	2116.18	
	429.1993		429.1993	4	P	17	2059.159	
	557.2579		557.2579	5	Q	16	1962.106	
	658.3056		658.3056	6	T	15	1834.047	
+0.066003	386.1985		771.3896	7	L	14	1733	
-0.08645	467.7301		934.453	8	Y	13	1619.916	
+0.245603	524.2722	-0.03081	1047.537	9	L	12	1456.852	
	1144.59		1144.59	10	P	11	1343.768	
	1243.658		1243.658	11	V	10	1246.715	
+0.155376	672.8566		1344.706	12	T	9	1147.647	
-0.01513	729.3986		1457.79	13	L	8	1046.599	
	1544.822		1544.822	14	S	7	933.5152	
+0.038469	816.4306		1631.854	15	S	6	846.4832	
+0.13694	872.9727		1744.938	16	I	5	759.4512	
	1841.991		1841.991	17	P	4	646.3671	-0.00048
	1941.059		1941.059	18	V	3	549.3144	
	2088.128		2088.128	19	F	2	450.2459	+0.128202
	2216.186		2216.186	20	Q	1	303.1775	
				21	R	0	175.119	-0.0577



Scan number	781	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	87.5

precursor information

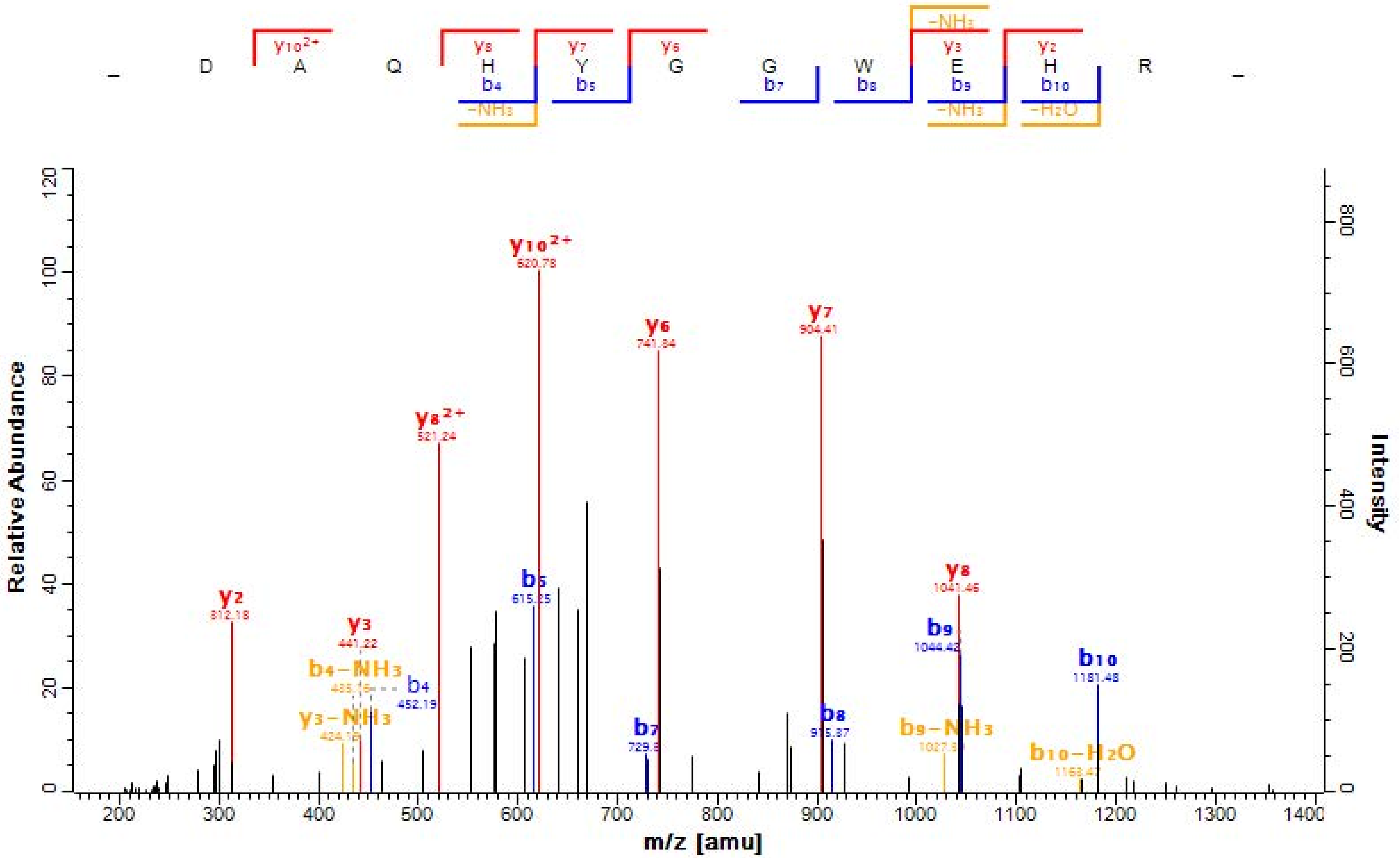
Mass:	1643.84887
m/z:	548.9569
Charge:	3+
Retentiontime:	9.2389698028564
Score:	87.4985
Mass Error [ppm]:	-0.20049
PEP:	0.00037677
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	46 %
Peak Coverage:	19 %
Protein Localisation:	209 ... 222

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	87.055		115.05	1	N	13				
+0.0816	224.11	-0.004	252.11	2	H	12	1530.8		1530.8	
	337.2	+0.1459	365.19	3	I	11	1393.8		697.38	+0.2325
	450.28		478.28	4	I	10	1280.7		640.84	+0.2726
	563.37		591.36	5	L	9	1167.6	-0.449	584.3	+0.2915
	691.42		719.42	6	Q	8	1054.5		1054.5	
	820.47	+0.1361	848.46	7	E	7	926.44	+0.1804	926.44	
	934.51		962.51	8	N	6	797.4	+0.1839	399.2	+0.0662
	1005.5		1033.5	9	A	5	683.36	+0.1042	683.36	
	1133.6		1161.6	10	Q	4	612.32	+0.0448	612.32	
	1270.7		1298.7	11	H	3	484.26		484.26	
	1341.7		1369.7	12	A	2	347.2	+0.1487	347.2	
	1442.7		1470.7	13	T	1	276.17		276.17	
				14	R	0	175.12	+0.1494	175.12	

Scan number	818	**Raw file**	LNCAP_Silac_23F10_set1_10
Method	ITMS; CID	**Pepti...**	86.91



precursor information

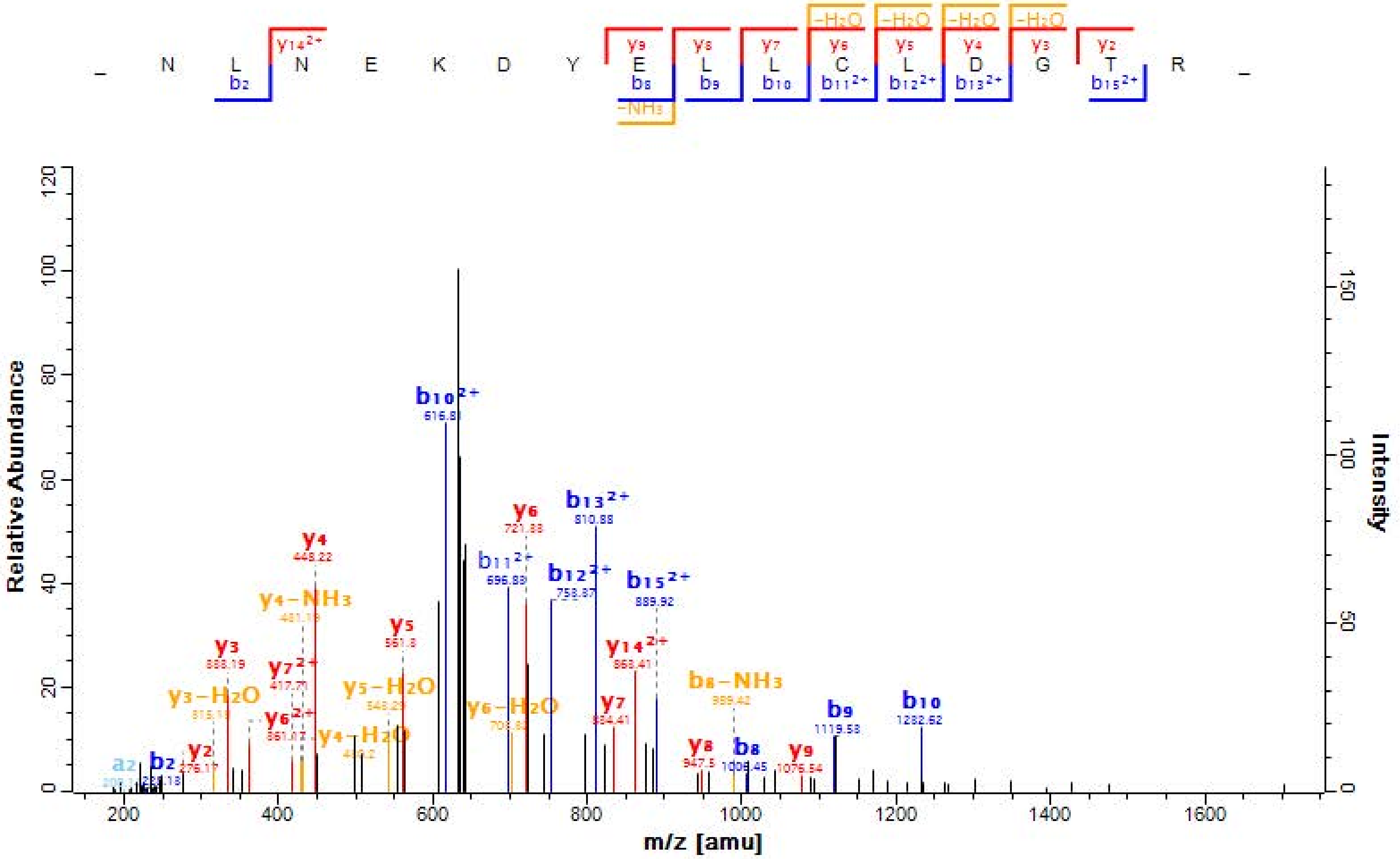
Mass:	1354.58044
m/z:	678.2975
Charge:	2+
Retentiontime:	9.4535512924194
Score:	86.91063
Mass Error [ppm]:	0.10674
PEP:	0.0021501
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	49 %
Peak Coverage:	22 %
Protein Localisation:	610 ... 620

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342	1	D	10				
	187.0713	2	A	9	1240.561		620.784	+0.182783
	315.1299	3	Q	8	1169.524		1169.524	
+0.087178	452.1888	4	H	7	1041.465	+0.038968	521.2361	+0.174354
-0.04103	615.2522	5	Y	6	904.406	+0.052226	904.406	
	672.2736	6	G	5	741.3427	+0.030105	741.3427	
+0.062526	729.2951	7	G	4	684.3212		684.3212	
+0.108335	915.3744	8	W	3	627.2998		627.2998	
+0.120613	1044.417	9	E	2	441.2205	+0.1261	441.2205	
-0.06501	1181.476	10	H	1	312.1779	+0.047112	312.1779	
		11	R	0	175.119		175.119	

Scan number	3138	**Raw file**	LNCAP_Silac_23F10_set1_11
Method	ITMS; CID	**Pepti...**	131.96



precursor information

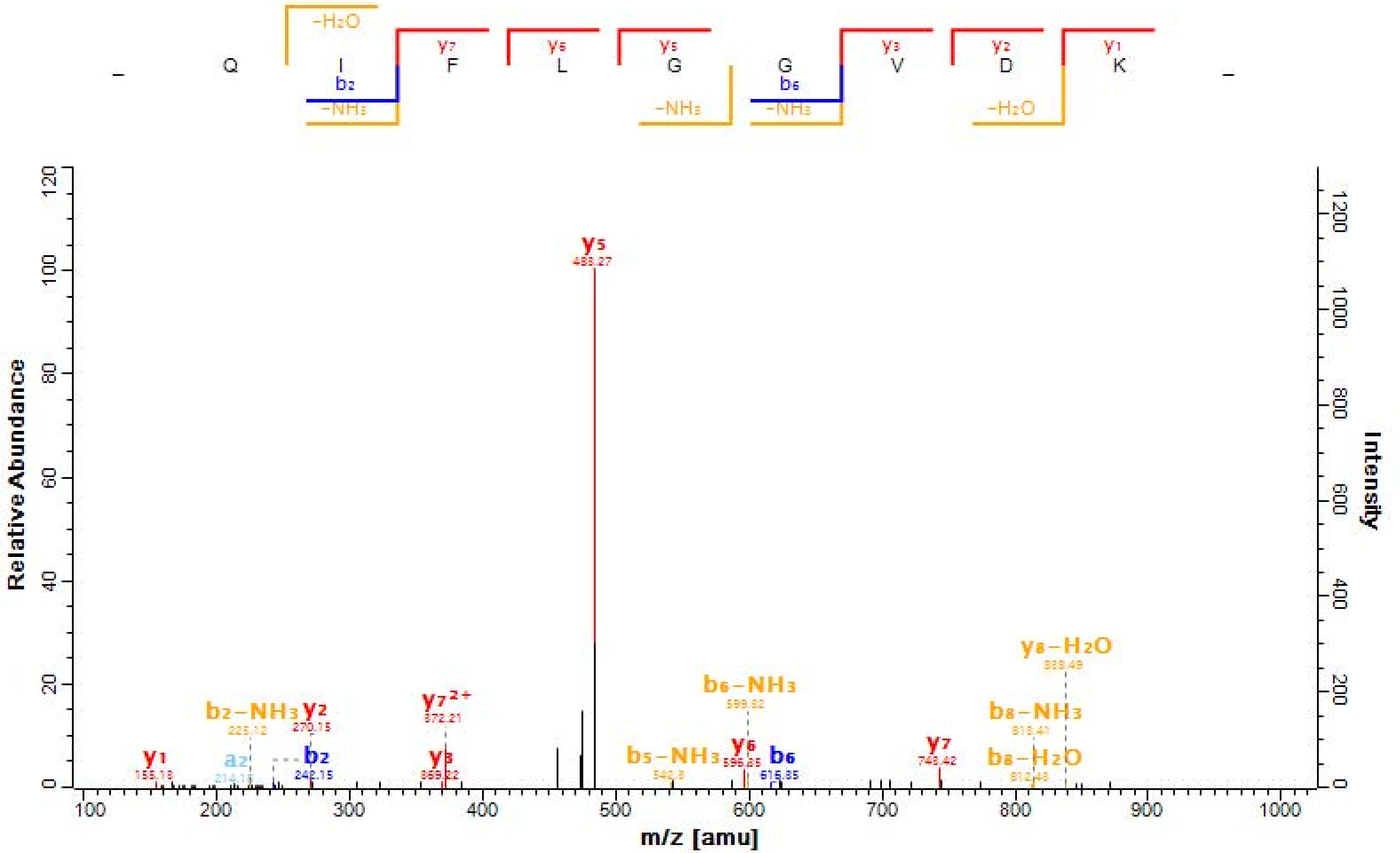
Mass:	1951.93151
m/z:	651.65111
Charge:	3+
Retentiontime:	37.447799682617
Score:	131.958
Mass Error [ppm]:	0.29258
PEP:	2.2364E-07
Precursor Type:	ISO

general information

Annotation:	11 of 16
AminoAcids Coverag	69 %
Intensity Coverage:	47 %
Peak Coverage:	30 %
Protein Localisation:	572 ... 587

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	87.06		115.1		115.1	1	N	15				
+0.1	200.1		228.1	+0.216	228.1	2	L	14	1839		1839	
	314.2		342.2		342.2	3	N	13	1726		863.4	-0.23
	443.2		471.2		471.2	4	E	12	1612		1612	
	571.3		599.3		599.3	5	K	11	1483		1483	
	686.3		714.3		714.3	6	D	10	1355		1355	
	849.4		877.4		877.4	7	Y	9	1240		1240	
	978.5		1006	-0.08	1006	8	E	8	1077	+0.265	1077	
	1092		1120	+0	1120	9	L	7	947.5	+0	947.5	
	1205	+0.202	616.8	-0.12	1233	10	L	6	834.4	+0.017	417.7	+0.15
	1365	+0.225	696.8		1393	11	C	5	721.3	-0.04	361.2	+0.46
	1478	+0.172	753.4		1506	12	L	4	561.3	-0.05	561.3	
	1593	+0.356	810.9		1621	13	D	3	448.2	+0.106	448.2	
	1650		1678		1678	14	G	2	333.2	+0.086	333.2	
	1751	+0.388	889.9		1779	15	T	1	276.2	+0.047	276.2	
						16	R	0	175.1		175.1	

Scan number	1985	**Raw file**	LNCAP_Silac_23F10_set1_12
Method	ITMS; CID	**Pepti...**	54.07

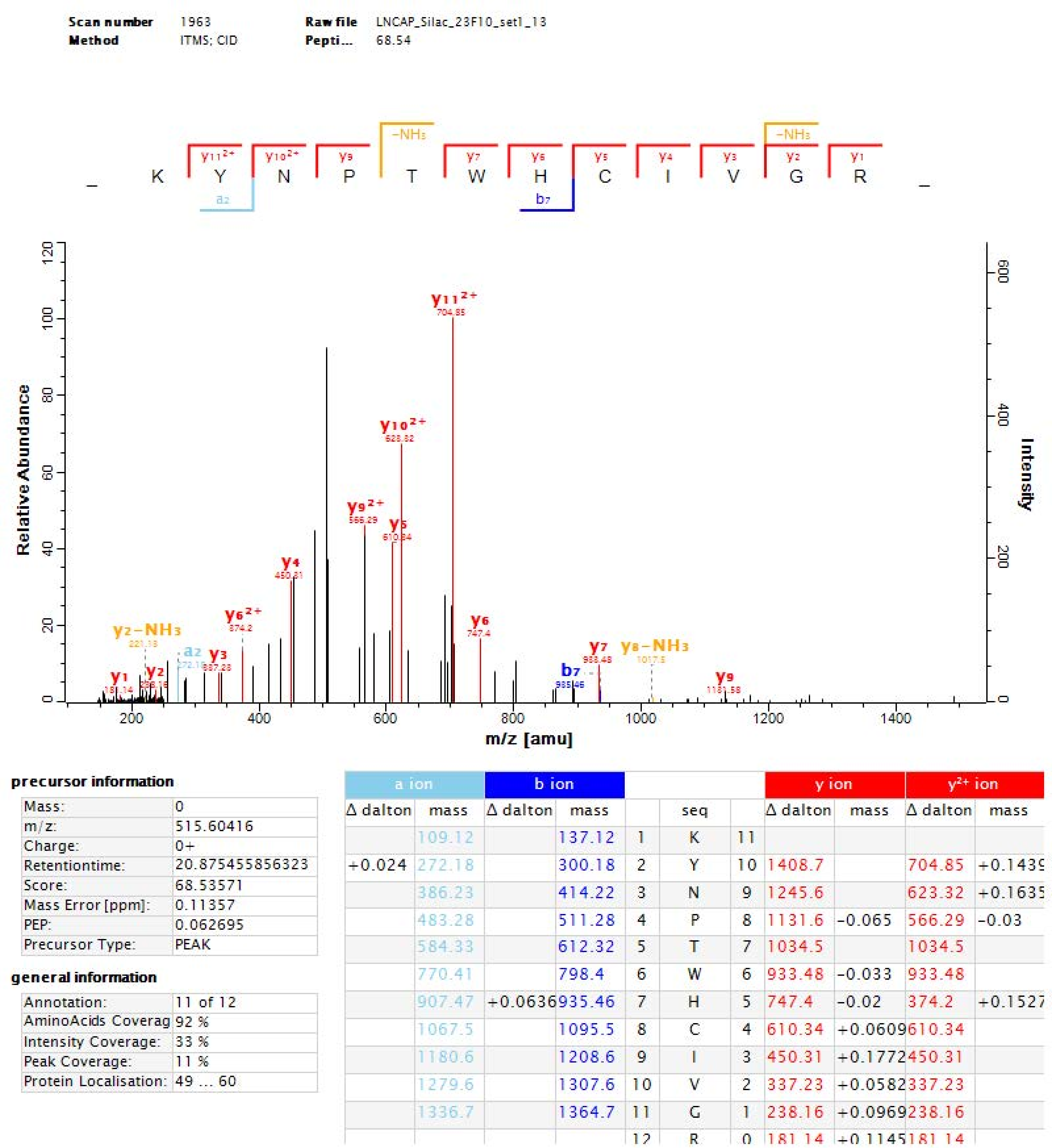


precursor information

Mass:	975.53889
m/z:	488.77672
Charge:	2+
Retentiontime:	25.164915084838
Score:	54.06599
Mass Error [ppm]:	-0.045968
PEP:	0.035479
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	56 %
Peak Coverage:	16 %
Protein Localisation:	97 ... 105

g

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	101.07		129.07	1	Q	8				
+0.0826	214.16	+0.0172	242.15	2	I	7	856.5		856.5	
	361.22		389.22	3	F	6	743.42	+0.0266	372.21	+0.032
	474.31		502.3	4	L	5	596.35	+0.0657	596.35	
	531.33		559.32	5	G	4	483.27	+0.4443	483.27	
	588.35	-0.146	616.35	6	G	3	426.24		426.24	
	687.42		715.41	7	V	2	369.22	+0.1927	369.22	
	802.45		830.44	8	D	1	270.15	+0.0944	270.15	
				9	K	0	155.13	+0.0107	155.13	



Scan number	1963	**Raw file**	LNCAP_Silac_23F10_set1_13
Method	ITMS; CID	**Pepti...**	68.54

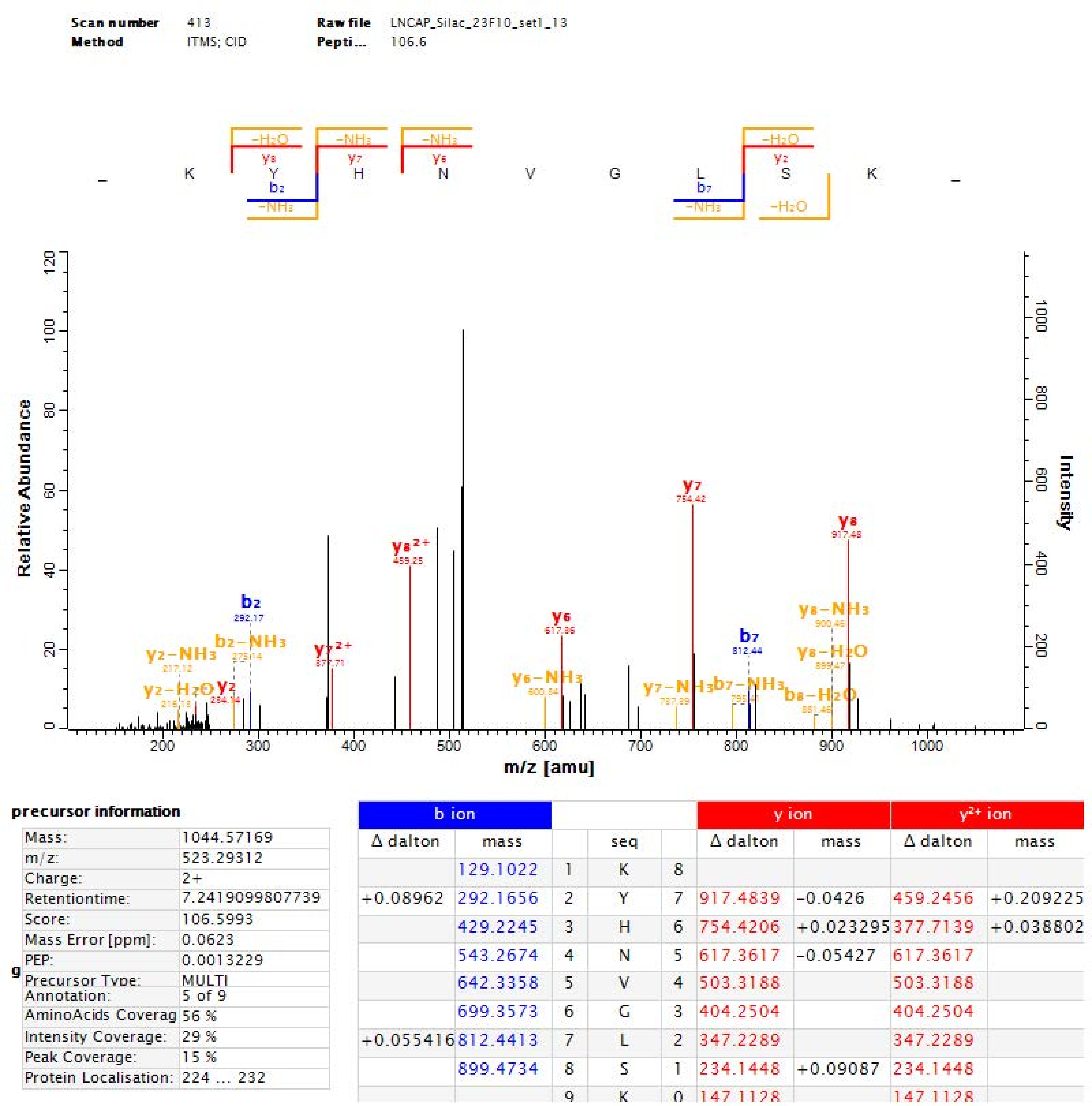
precursor information

Mass:	0
m/z:	515.60416
Charge:	0+
Retentiontime:	20.875455856323
Score:	68.53571
Mass Error [ppm]:	0.11357
PEP:	0.062695
Precursor Type:	PEAK

general information

Annotation:	11 of 12
AminoAcids Coverag	92 %
Intensity Coverage:	33 %
Peak Coverage:	11 %
Protein Localisation:	49 ... 60

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	109.12		137.12	1	K	11				
+0.024	272.18		300.18	2	Y	10	1408.7		704.85	+0.1439
	386.23		414.22	3	N	9	1245.6		623.32	+0.1635
	483.28		511.28	4	P	8	1131.6	−0.065	566.29	−0.03
	584.33		612.32	5	T	7	1034.5		1034.5	
	770.41		798.4	6	W	6	933.48	−0.033	933.48	
	907.47	+0.0636	935.46	7	H	5	747.4	−0.02	374.2	+0.1527
	1067.5		1095.5	8	C	4	610.34	+0.0609	610.34	
	1180.6		1208.6	9	I	3	450.31	+0.1772	450.31	
	1279.6		1307.6	10	V	2	337.23	+0.0582	337.23	
	1336.7		1364.7	11	G	1	238.16	+0.0969	238.16	
				12	R	0	181.14	+0.1145	181.14	

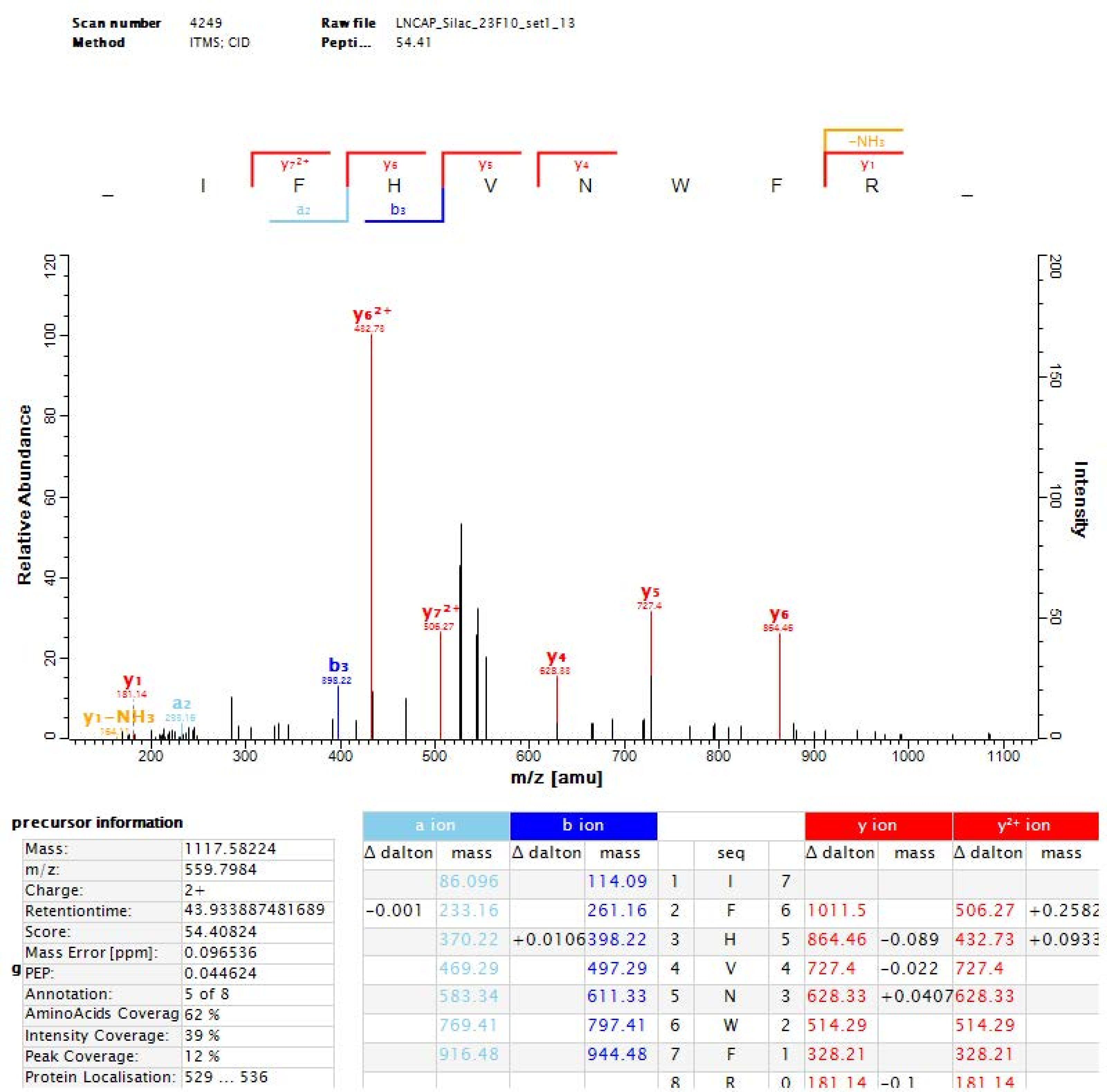


Scan number	413	**Raw file**	LNCAP_Silac_23F10_set1_13
Method	ITMS; CID	**Pepti...**	106.6

precursor information

Mass:	1044.57169
m/z:	523.29312
Charge:	2+
Retentiontime:	7.2419099807739
Score:	106.5993
Mass Error [ppm]:	0.0623
PEP:	0.0013229
Precursor Type:	MULTI
Annotation:	5 of 9
AminoAcids Coverag	56 %
Intensity Coverage:	29 %
Peak Coverage:	15 %
Protein Localisation:	224 ... 232

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.1022	1	K	8				
+0.08962	292.1656	2	Y	7	917.4839	-0.0426	459.2456	+0.209225
	429.2245	3	H	6	754.4206	+0.023295	377.7139	+0.038802
	543.2674	4	N	5	617.3617	-0.05427	617.3617	
	642.3358	5	V	4	503.3188		503.3188	
	699.3573	6	G	3	404.2504		404.2504	
+0.055416	812.4413	7	L	2	347.2289		347.2289	
	899.4734	8	S	1	234.1448	+0.09087	234.1448	
		9	K	0	147.1128		147.1128	

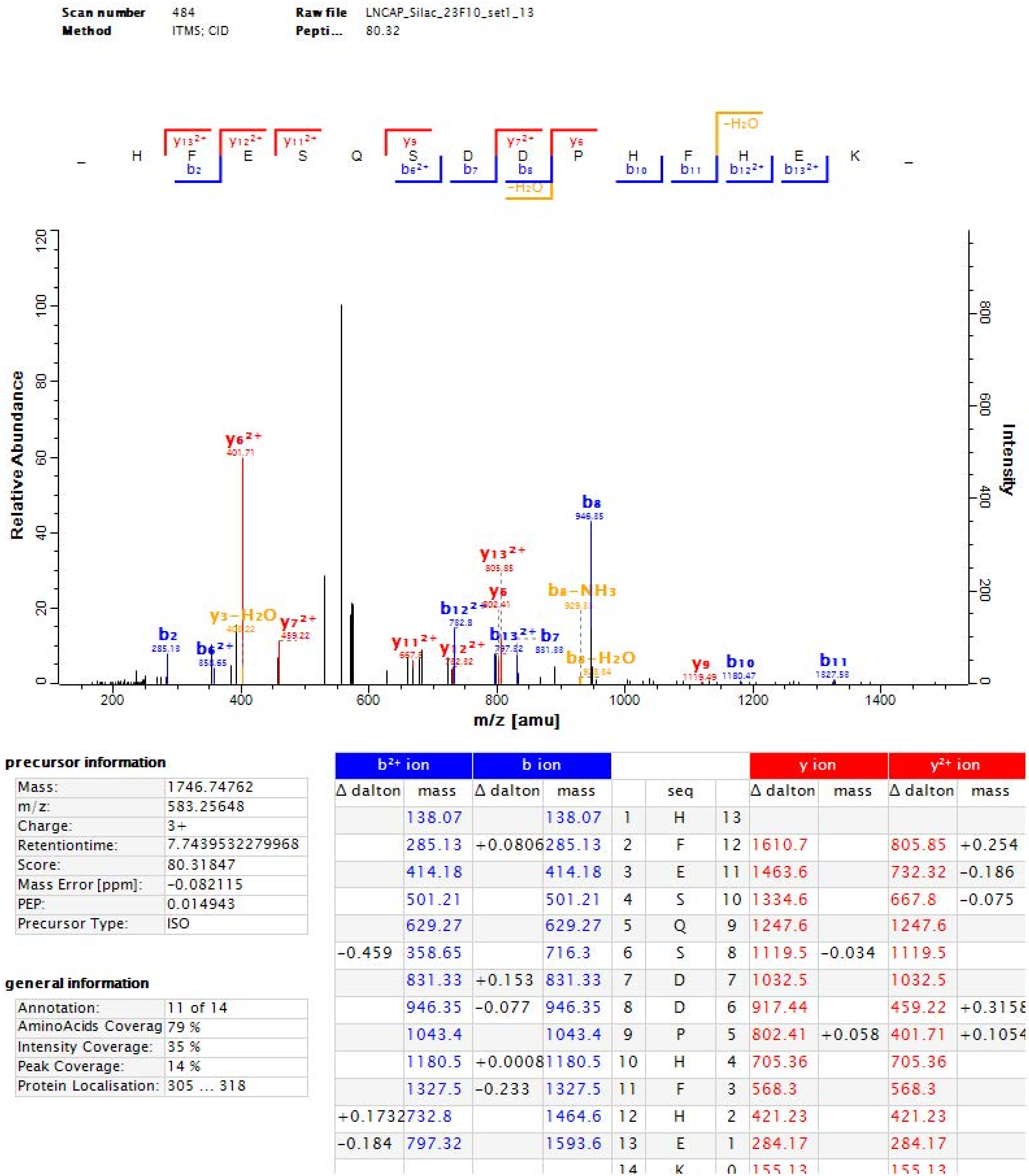


Scan number	4249	**Raw file**	LNCAP_Silac_23F10_set1_13
Method	ITMS; CID	**Pepti...**	54.41

precursor information

Mass:	1117.58224
m/z:	559.7984
Charge:	2+
Retentiontime:	43.933887481689
Score:	54.40824
Mass Error [ppm]:	0.096536
PEP:	0.044624
Annotation:	5 of 8
AminoAcids Coverag	62 %
Intensity Coverage:	39 %
Peak Coverage:	12 %
Protein Localisation:	529 ... 536

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	7				
-0.001	233.16		261.16	2	F	6	1011.5		506.27	+0.2582
	370.22	+0.0106	398.22	3	H	5	864.46	-0.089	432.73	+0.0933
	469.29		497.29	4	V	4	727.4	-0.022	727.4	
	583.34		611.33	5	N	3	628.33	+0.0407	628.33	
	769.41		797.41	6	W	2	514.29		514.29	
	916.48		944.48	7	F	1	328.21		328.21	
				8	R	0	181.14	-0.1	181.14	



Scan number	484	**Raw file**	LNCAP_Silac_23F10_set1_13
Method	ITMS; CID	**Pepti...**	80.32

precursor information

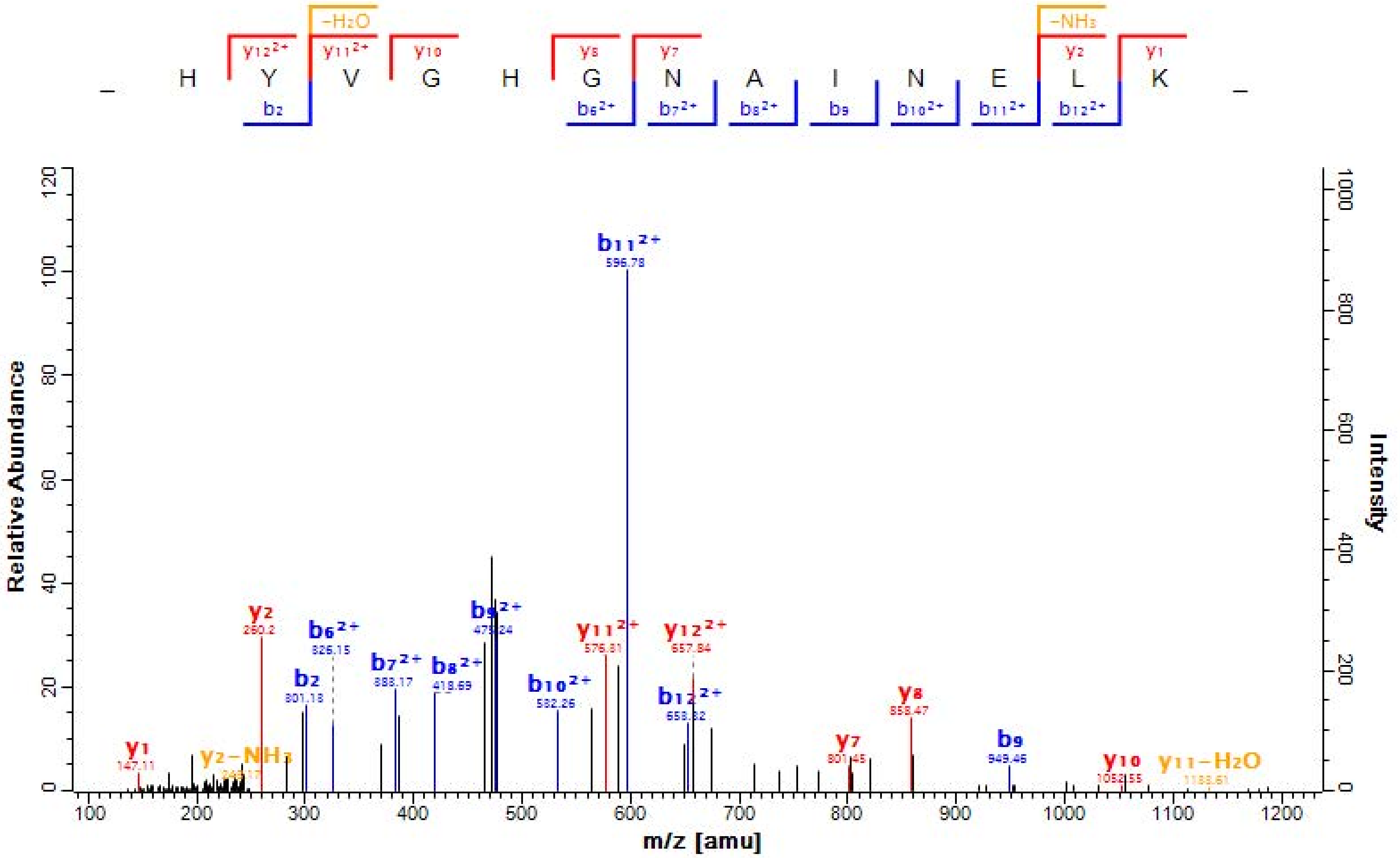
Mass:	1746.74762
m/z:	583.25648
Charge:	3+
Retentiontime:	7.7439532279968
Score:	80.31847
Mass Error [ppm]:	-0.082115
PEP:	0.014943
Precursor Type:	ISO

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	35 %
Peak Coverage:	14 %
Protein Localisation:	305 ... 318

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.07		138.07	1	H	13				
	285.13	+0.0806	285.13	2	F	12	1610.7		805.85	+0.254
	414.18		414.18	3	E	11	1463.6		732.32	-0.186
	501.21		501.21	4	S	10	1334.6		667.8	-0.075
	629.27		629.27	5	Q	9	1247.6		1247.6	
-0.459	358.65		716.3	6	S	8	1119.5	-0.034	1119.5	
	831.33	+0.153	831.33	7	D	7	1032.5		1032.5	
	946.35	-0.077	946.35	8	D	6	917.44		459.22	+0.3158
	1043.4		1043.4	9	P	5	802.41	+0.058	401.71	+0.1054
	1180.5	+0.0008	1180.5	10	H	4	705.36		705.36	
	1327.5	-0.233	1327.5	11	F	3	568.3		568.3	
+0.1732	732.8		1464.6	12	H	2	421.23		421.23	
-0.184	797.32		1593.6	13	E	1	284.17		284.17	
				14	K	0	155.13		155.13	

Scan number	802	**Raw file**	LNCAP_Silac_23F10_set1_13
Method	ITMS; CID	**Pepti...**	101.93



precursor information

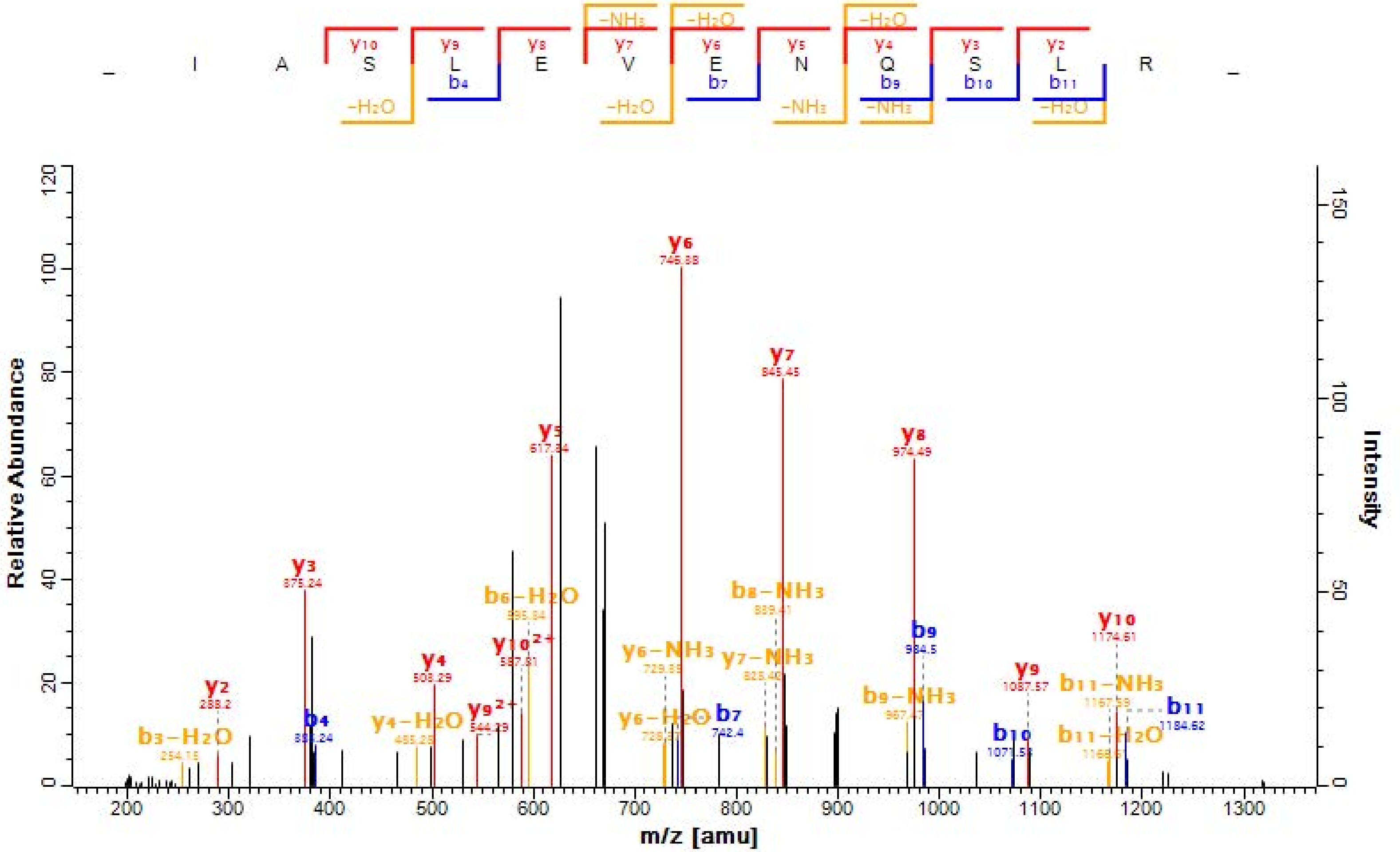
Mass:	0
m/z:	484.58452
Charge:	0+
Retentiontime:	10.360164642334
Score:	101.9286
Mass Error [ppm]:	0.022073
PEP:	0.0022053
Precursor Type:	PEAK

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	43 %
Peak Coverage:	14 %
Protein Localisation:	185 ... 197

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.07		138.07	1	H	12				
	301.13	−0.067	301.13	2	Y	11	1314.7		657.84	−0.008
	400.2		400.2	3	V	10	1151.6		576.31	+0.2297
	457.22		457.22	4	G	9	1052.5	−0.008	1052.5	
	594.28		594.28	5	H	8	995.53		995.53	
+0.2403	326.15		651.3	6	G	7	858.47	+0.1346	858.47	
+0.1812	383.17		765.34	7	N	6	801.45	−0.117	801.45	
+0.2282	418.69		836.38	8	A	5	687.4		687.4	
+0.3367	475.24	−0.071	949.46	9	I	4	616.37		616.37	
−0.075	532.26		1063.5	10	N	3	503.28		503.28	
+0.2377	596.78		1192.5	11	E	2	389.24		389.24	
+0.3066	653.32		1305.6	12	L	1	260.2	+0.039	260.2	
				13	K	0	147.11	+0.0875	147.11	

Scan number	2027	**Raw file**	LNCAP_Silac_23F10_set1_14
Method	ITMS; CID	**Pepti...**	128.68



precursor information

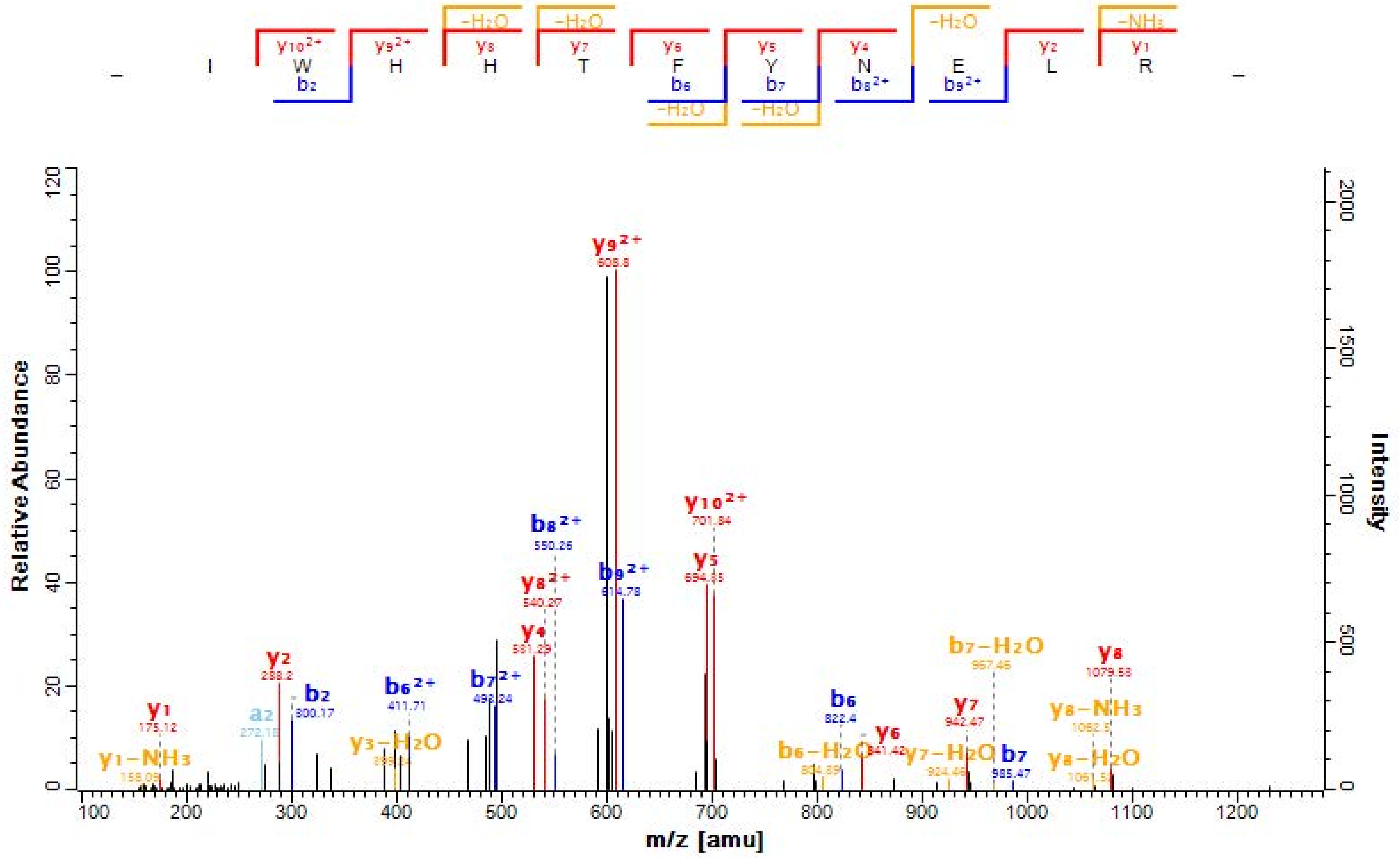
Mass:	1357.71929
m/z:	679.86692
Charge:	2+
Retentiontime:	23.433917999267
Score:	128.6753
Mass Error [ppm]:	-0.62485
PEP:	2.3178E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	46 %
Peak Coverage:	32 %
Protein Localisation:	84 ... 95

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	I	11				
	185.1285	2	A	10	1245.643		1245.643	
	272.1605	3	S	9	1174.606	-0.0026	587.8068	-0.13263
+0.132223	385.2445	4	L	8	1087.574	-0.04516	544.2907	-0.13639
	514.2871	5	E	7	974.4901	-0.00571	974.4901	
	613.3556	6	V	6	845.4476	+0.046462	845.4476	
+0.144761	742.3981	7	E	5	746.3791	+0.006233	746.3791	
	856.4411	8	N	4	617.3365	+0.141234	617.3365	
+0.172223	984.4997	9	Q	3	503.2936	+0.06795	503.2936	
+0.334043	1071.532	10	S	2	375.235	+0.13489	375.235	
-0.30715	1184.616	11	L	1	288.203	-0.01234	288.203	
		12	R	0	175.119		175.119	

Scan number	2129	**Raw file**	LNCAP_Silac_23F10_set1_14
Method	ITMS; CID	**Pepti...**	175.93



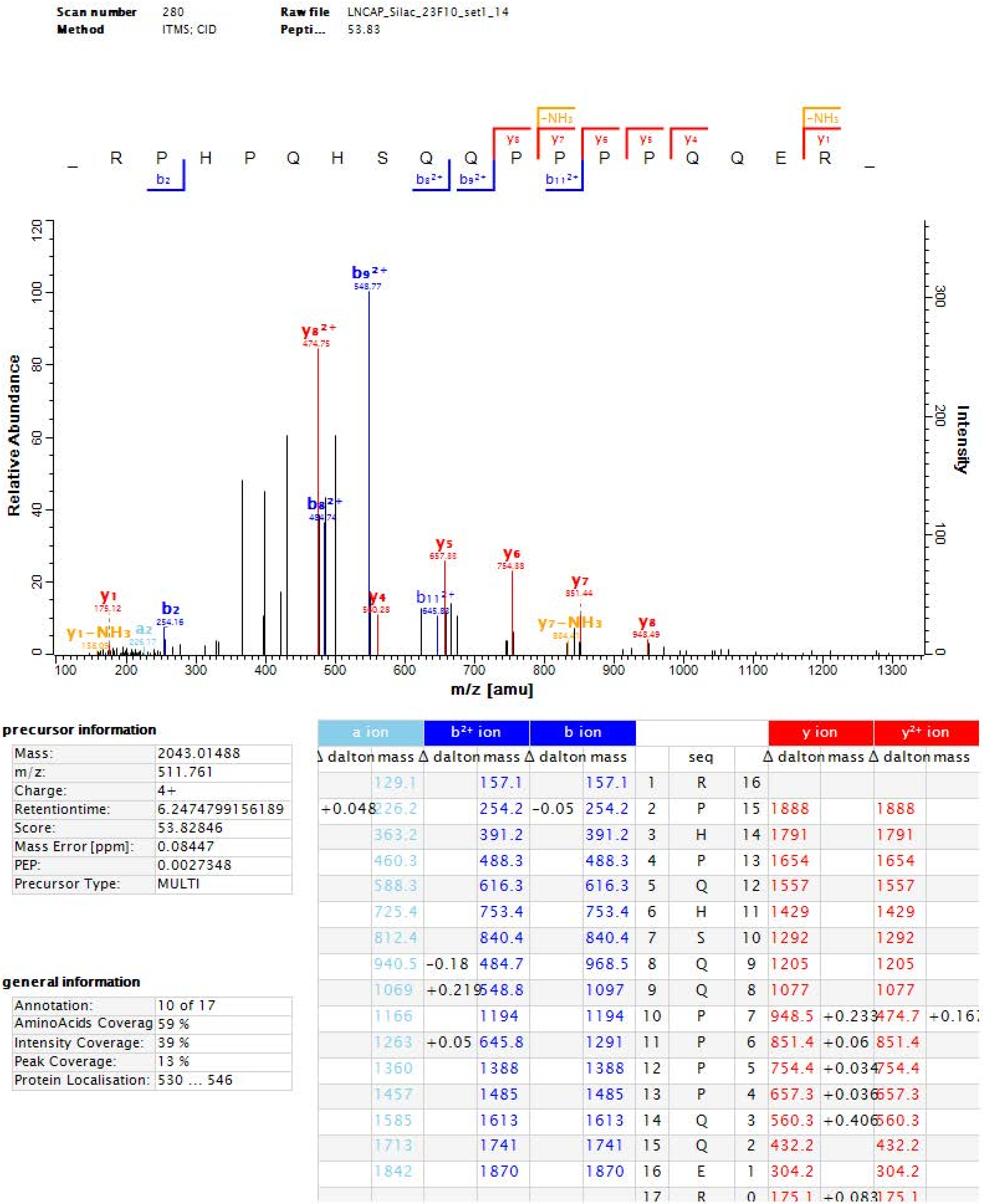
precursor information

Mass:	1514.74188
m/z:	505.92124
Charge:	3+
Retentiontime:	24.452590942382
Score:	175.9339
Mass Error [ppm]:	-0.00031296
PEP:	3.7009E-08
Precursor Type:	MULTI

general information

Annotation:	10 of 11
AminoAcids Coverag	91 %
Intensity Coverage:	50 %
Peak Coverage:	23 %
Protein Localisation:	85 ... 95

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	I	10				
-0.09	272.2		300.2	+0.086	300.2	2	W	9	1403		701.8	+0.26
	409.2		437.2		437.2	3	H	8	1217		608.8	+0.21
	546.3		574.3		574.3	4	H	7	1080	-0.02	540.3	+0.24
	647.3		675.3		675.3	5	T	6	942.5	-0.03	942.5	
	794.4	-0.01	411.7	+0.249	822.4	6	F	5	841.4	+0.143	841.4	
	957.5	+0.316	493.2	+0.041	985.5	7	Y	4	694.4	-0.1	694.4	
	1072	+0.217	550.3		1100	8	N	3	531.3	+0.028	531.3	
	1201	+0.292	614.8		1229	9	E	2	417.2		417.2	
	1314		1342		1342	10	L	1	288.2	+0.118	288.2	
						11	R	0	175.1	+0.139	175.1	



Scan number 280
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set1_14
Pepti... 53.83

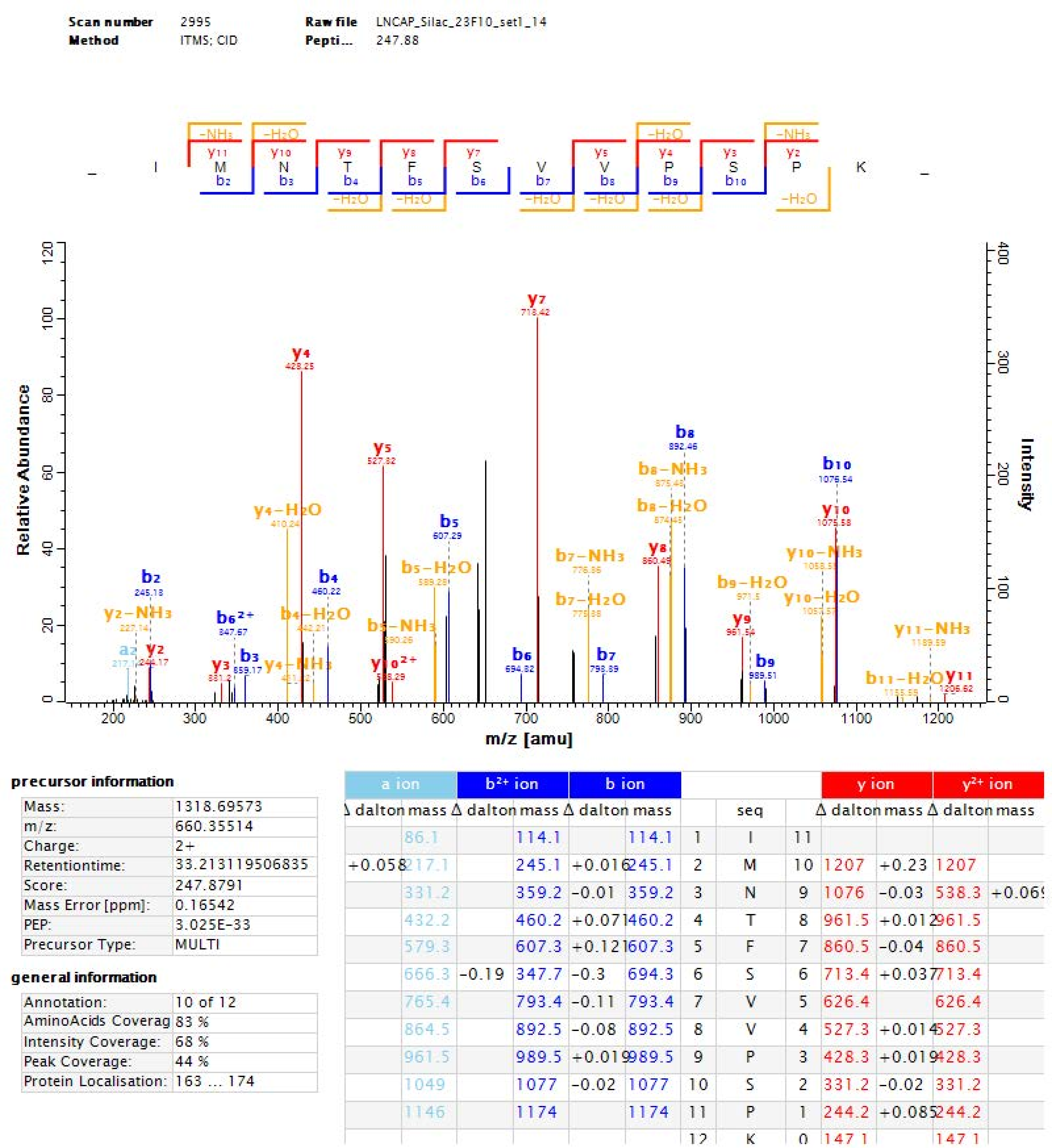
precursor information

Mass:	2043.01488
m/z:	511.761
Charge:	4+
Retentiontime:	6.2474799156189
Score:	53.82846
Mass Error [ppm]:	0.08447
PEP:	0.0027348
Precursor Type:	MULTI

general information

Annotation:	10 of 17
AminoAcids Coverag	59 %
Intensity Coverage:	39 %
Peak Coverage:	13 %
Protein Localisation:	530 ... 546

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.1		157.1		157.1	1	R	16				
+0.048	226.2		254.2	-0.05	254.2	2	P	15	1888		1888	
	363.2		391.2		391.2	3	H	14	1791		1791	
	460.3		488.3		488.3	4	P	13	1654		1654	
	588.3		616.3		616.3	5	Q	12	1557		1557	
	725.4		753.4		753.4	6	H	11	1429		1429	
	812.4		840.4		840.4	7	S	10	1292		1292	
	940.5	-0.18	484.7		968.5	8	Q	9	1205		1205	
	1069	+0.219	548.8		1097	9	Q	8	1077		1077	
	1166		1194		1194	10	P	7	948.5	+0.233	474.7	+0.16
	1263	+0.05	645.8		1291	11	P	6	851.4	+0.06	851.4	
	1360		1388		1388	12	P	5	754.4	+0.034	754.4	
	1457		1485		1485	13	P	4	657.3	+0.036	657.3	
	1585		1613		1613	14	Q	3	560.3	+0.406	560.3	
	1713		1741		1741	15	Q	2	432.2		432.2	
	1842		1870		1870	16	E	1	304.2		304.2	
						17	R	0	175.1	+0.083	175.1	



Scan number	2995	**Raw file**	LNCAP_Silac_23F10_set1_14
Method	ITMS; CID	**Pepti...**	247.88

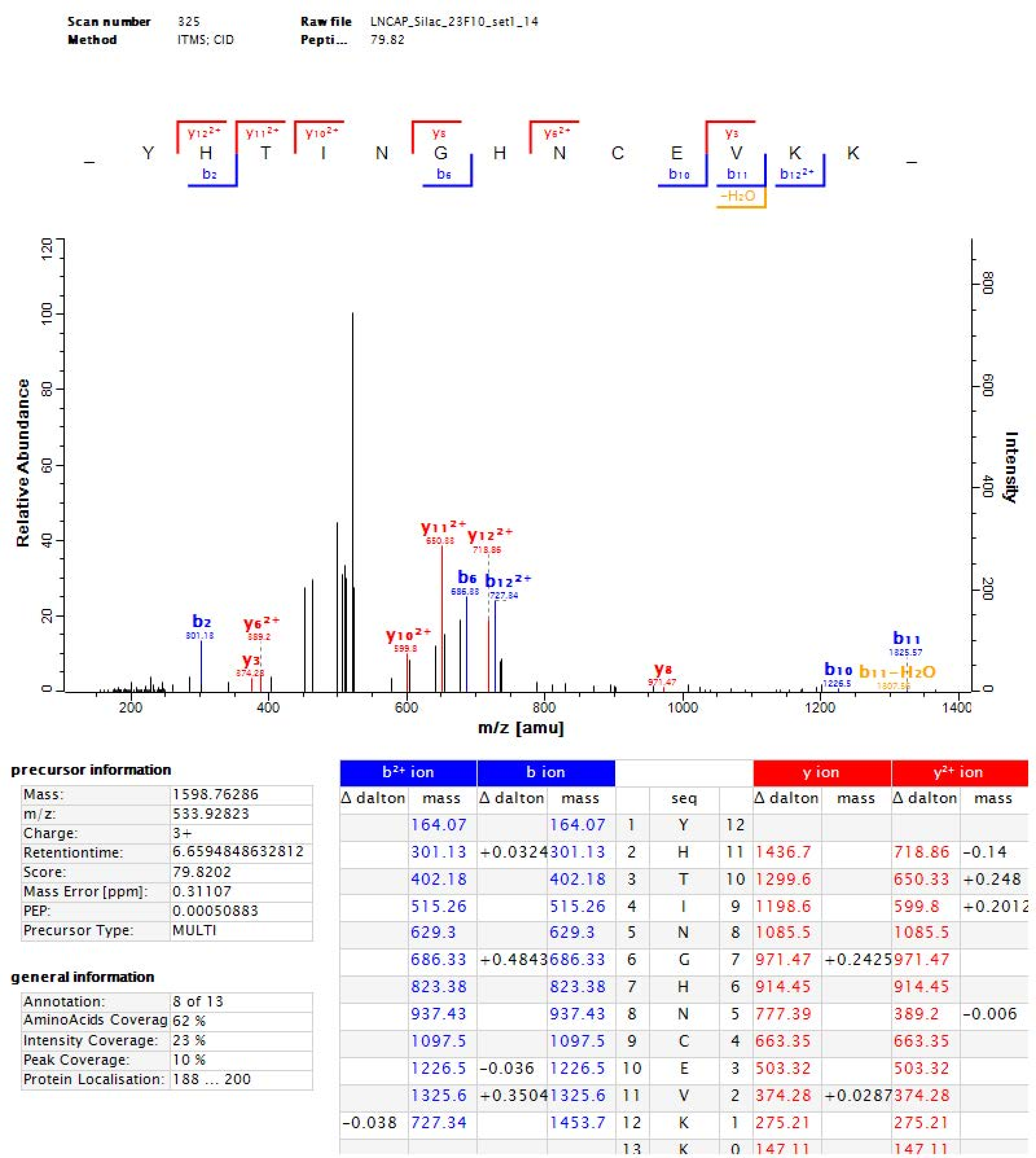
precursor information

Mass:	1318.69573
m/z:	660.35514
Charge:	2+
Retentiontime:	33.213119506835
Score:	247.8791
Mass Error [ppm]:	0.16542
PEP:	3.025E-33
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	68 %
Peak Coverage:	44 %
Protein Localisation:	163 ... 174

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	I	11				
+0.058	217.1		245.1	+0.016	245.1	2	M	10	1207	+0.23	1207	
	331.2		359.2	-0.01	359.2	3	N	9	1076	-0.03	538.3	+0.06
	432.2		460.2	+0.071	460.2	4	T	8	961.5	+0.012	961.5	
	579.3		607.3	+0.121	607.3	5	F	7	860.5	-0.04	860.5	
	666.3	-0.19	347.7	-0.3	694.3	6	S	6	713.4	+0.037	713.4	
	765.4		793.4	-0.11	793.4	7	V	5	626.4		626.4	
	864.5		892.5	-0.08	892.5	8	V	4	527.3	+0.014	527.3	
	961.5		989.5	+0.019	989.5	9	P	3	428.3	+0.019	428.3	
	1049		1077	-0.02	1077	10	S	2	331.2	-0.02	331.2	
	1146		1174		1174	11	P	1	244.2	+0.085	244.2	
						12	K	0	147.1		147.1	



Scan number 325
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set1_14
Pepti... 79.82

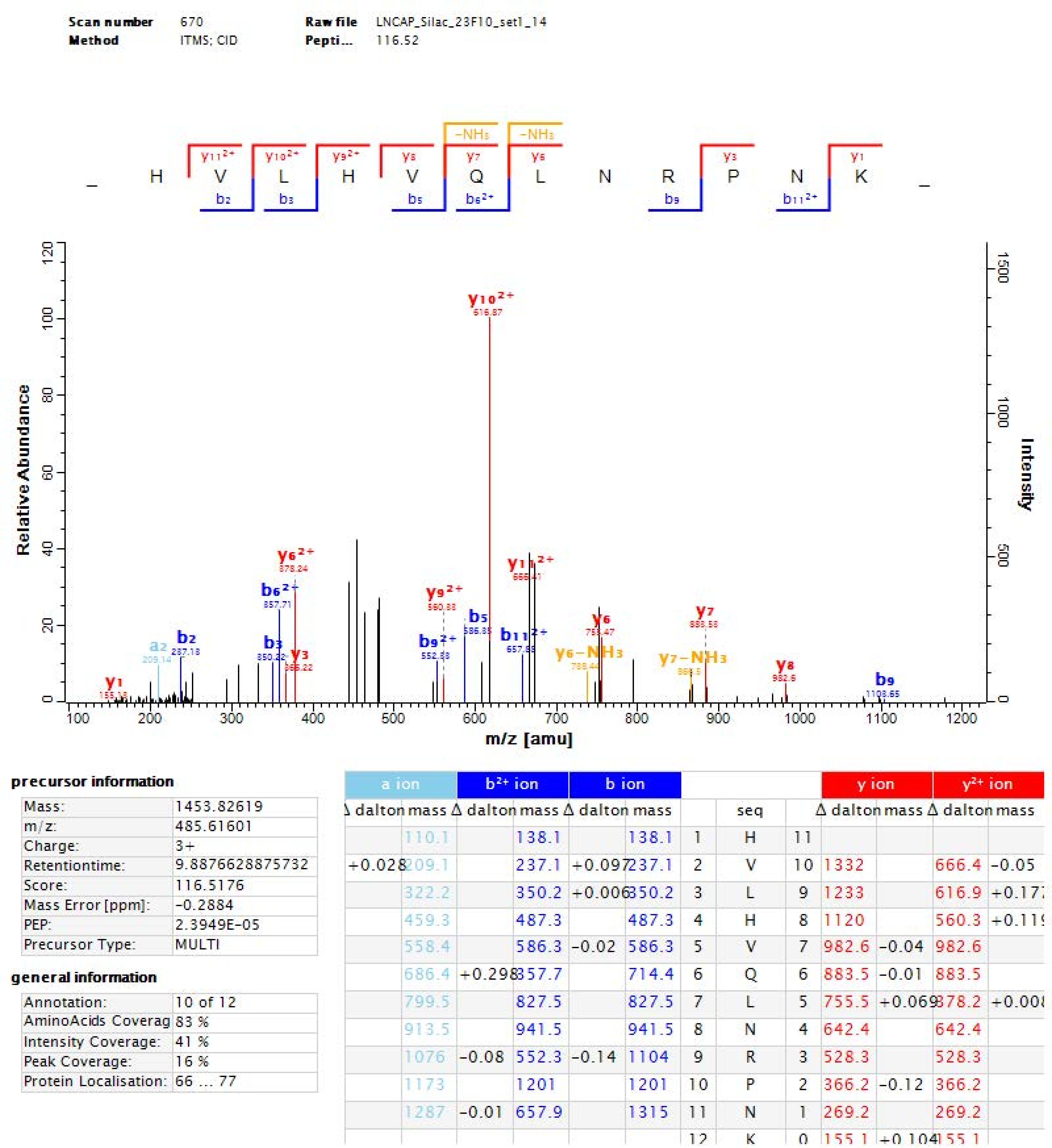
precursor information

Mass:	1598.76286
m/z:	533.92823
Charge:	3+
Retentiontime:	6.6594848632812
Score:	79.8202
Mass Error [ppm]:	0.31107
PEP:	0.00050883
Precursor Type:	MULTI

general information

Annotation:	8 of 13
AminoAcids Coverag	62 %
Intensity Coverage:	23 %
Peak Coverage:	10 %
Protein Localisation:	188 ... 200

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	164.07		164.07	1	Y	12				
	301.13	+0.0324	301.13	2	H	11	1436.7		718.86	-0.14
	402.18		402.18	3	T	10	1299.6		650.33	+0.248
	515.26		515.26	4	I	9	1198.6		599.8	+0.2012
	629.3		629.3	5	N	8	1085.5		1085.5	
	686.33	+0.4843	686.33	6	G	7	971.47	+0.2425	971.47	
	823.38		823.38	7	H	6	914.45		914.45	
	937.43		937.43	8	N	5	777.39		389.2	-0.006
	1097.5		1097.5	9	C	4	663.35		663.35	
	1226.5	-0.036	1226.5	10	E	3	503.32		503.32	
	1325.6	+0.3504	1325.6	11	V	2	374.28	+0.0287	374.28	
-0.038	727.34		1453.7	12	K	1	275.21		275.21	
				13	K	0	147.11		147.11	



Scan number	670	**Raw file**	LNCAP_Silac_23F10_set1_14
Method	ITMS; CID	**Pepti...**	116.52

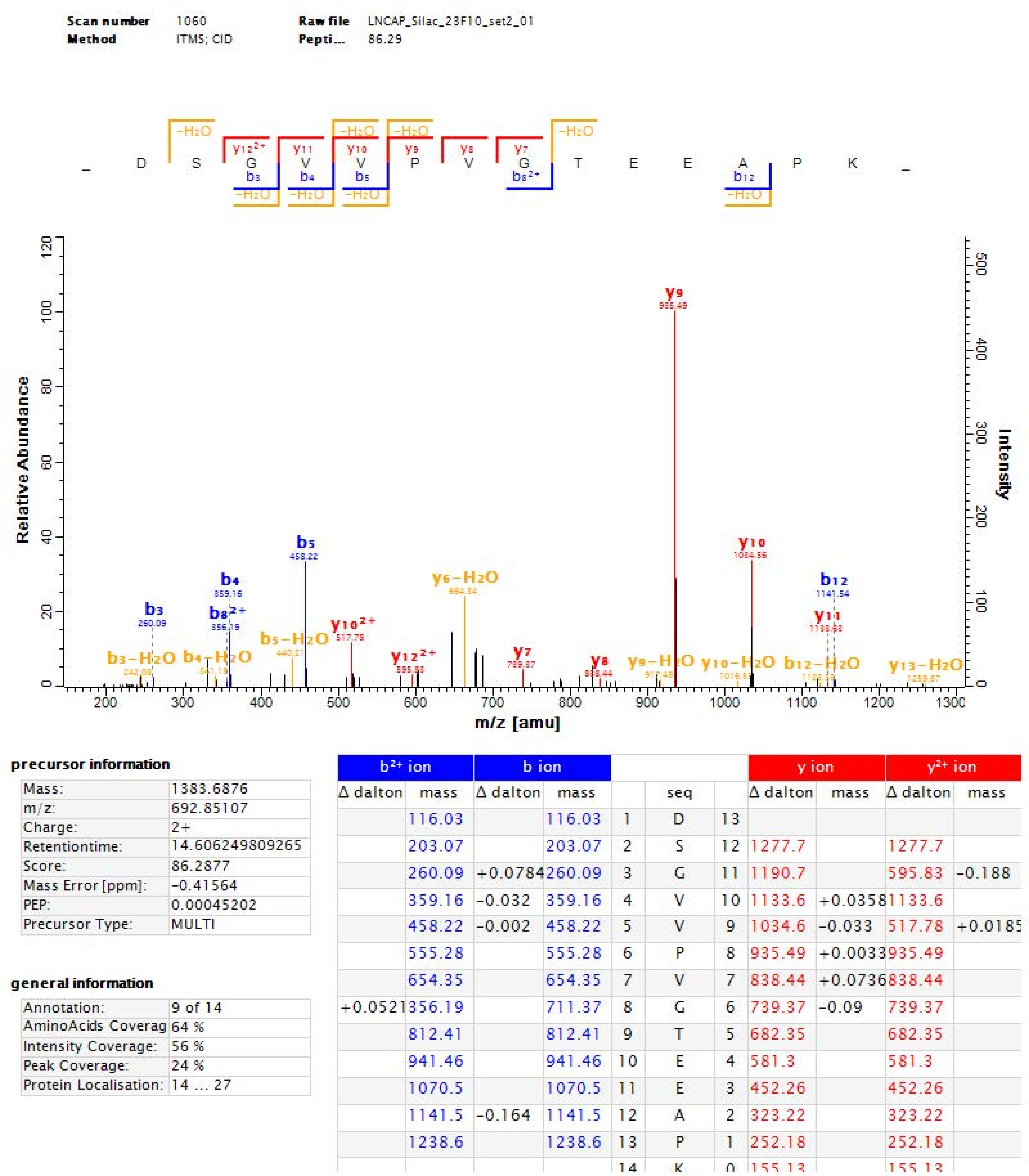
precursor information

Mass:	1453.82619
m/z:	485.61601
Charge:	3+
Retentiontime:	9.8876628875732
Score:	116.5176
Mass Error [ppm]:	-0.2884
PEP:	2.3949E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	41 %
Peak Coverage:	16 %
Protein Localisation:	66 ... 77

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	110.1		138.1		138.1	1	H	11				
+0.028	209.1		237.1	+0.097	237.1	2	V	10	1332		666.4	-0.05
	322.2		350.2	+0.006	350.2	3	L	9	1233		616.9	+0.17
	459.3		487.3		487.3	4	H	8	1120		560.3	+0.11
	558.4		586.3	-0.02	586.3	5	V	7	982.6	-0.04	982.6	
	686.4	+0.298	357.7		714.4	6	Q	6	883.5	-0.01	883.5	
	799.5		827.5		827.5	7	L	5	755.5	+0.069	378.2	+0.00
	913.5		941.5		941.5	8	N	4	642.4		642.4	
	1076	-0.08	552.3	-0.14	1104	9	R	3	528.3		528.3	
	1173		1201		1201	10	P	2	366.2	-0.12	366.2	
	1287	-0.01	657.9		1315	11	N	1	269.2		269.2	
						12	K	0	155.1	+0.104	155.1	



Scan number	1060	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	86.29

precursor information

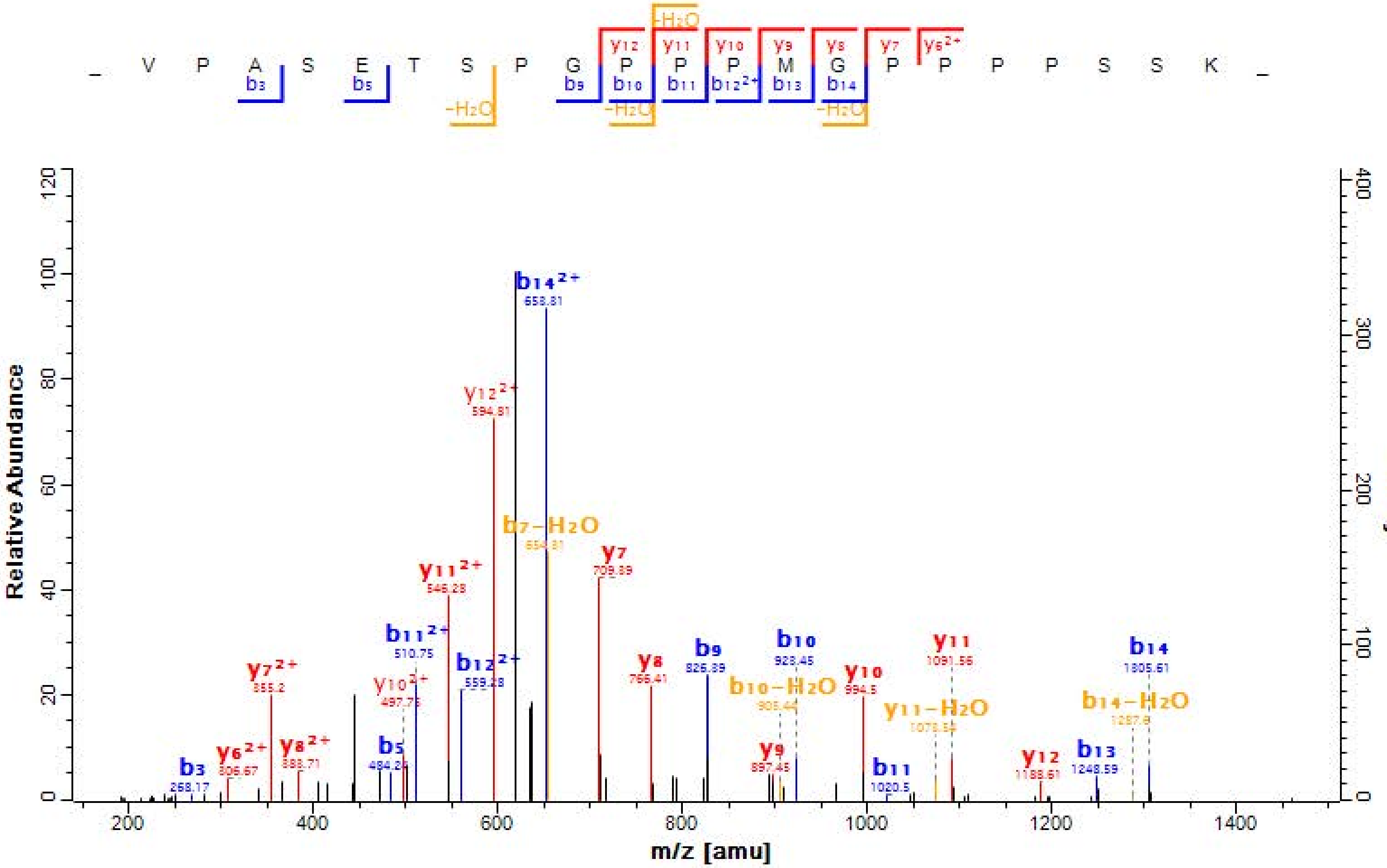
Mass:	1383.6876
m/z:	692.85107
Charge:	2+
Retentiontime:	14.606249809265
Score:	86.2877
Mass Error [ppm]:	-0.41564
PEP:	0.00045202
Precursor Type:	MULTI

general information

Annotation:	9 of 14
AminoAcids Coverag	64 %
Intensity Coverage:	56 %
Peak Coverage:	24 %
Protein Localisation:	14 ... 27

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	13				
	203.07		203.07	2	S	12	1277.7		1277.7	
	260.09	+0.0784	260.09	3	G	11	1190.7		595.83	-0.188
	359.16	-0.032	359.16	4	V	10	1133.6	+0.0358	1133.6	
	458.22	-0.002	458.22	5	V	9	1034.6	-0.033	517.78	+0.0185
	555.28		555.28	6	P	8	935.49	+0.0033	935.49	
	654.35		654.35	7	V	7	838.44	+0.0736	838.44	
+0.0521	356.19		711.37	8	G	6	739.37	-0.09	739.37	
	812.41		812.41	9	T	5	682.35		682.35	
	941.46		941.46	10	E	4	581.3		581.3	
	1070.5		1070.5	11	E	3	452.26		452.26	
	1141.5	-0.164	1141.5	12	A	2	323.22		323.22	
	1238.6		1238.6	13	P	1	252.18		252.18	
				14	K	0	155.13		155.13	

Scan number	1188	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	126.88



precursor information

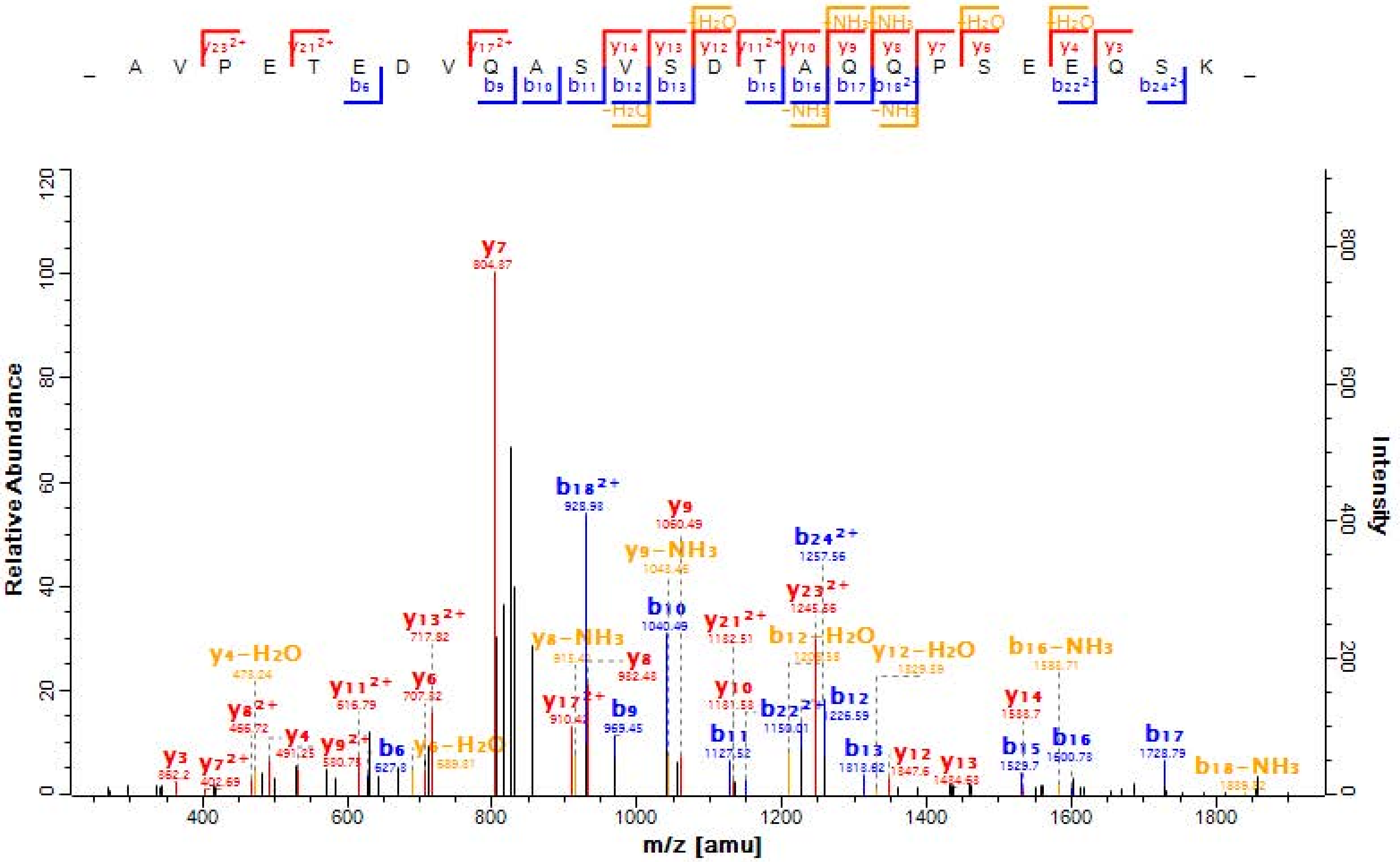
Mass:	2012.98813
m/z:	672.00332
Charge:	3+
Retentiontime:	15.854846954345
Score:	126.8845
Mass Error [ppm]:	0.19793
PEP:	1.8059E-13
Precursor Type:	MULTI

general information

Annotation:	13 of 21
AminoAcids Coverag	62 %
Intensity Coverage:	64 %
Peak Coverage:	32 %
Protein Localisation:	63 ... 83

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	20				
	197.13		197.13	2	P	19	1914.9		1914.9	
	268.17	-0.002	268.17	3	A	18	1817.9		1817.9	
	355.2		355.2	4	S	17	1746.8		1746.8	
	484.24	+0.0611	484.24	5	E	16	1659.8		1659.8	
	585.29		585.29	6	T	15	1530.8		1530.8	
	672.32		672.32	7	S	14	1429.7		1429.7	
	769.37		769.37	8	P	13	1342.7		1342.7	
	826.39	+0.0462	826.39	9	G	12	1245.6		1245.6	
	923.45	+0.056	923.45	10	P	11	1188.6	-0.206	594.81	+0.1914
+0.28	510.75	-0.061	1020.5	11	P	10	1091.6	-0.11	546.28	+0.1344
+0.1456	559.28		1117.6	12	P	9	994.5	+0.0178	497.75	+0.0665
	1248.6	-0.186	1248.6	13	M	8	897.45	-0.08	897.45	
+0.0829	653.31	-0.293	1305.6	14	G	7	766.41	+0.0566	383.71	+0.1911
	1402.7		1402.7	15	P	6	709.39	-0.085	355.2	+0.1043
	1499.7		1499.7	16	P	5	612.34		306.67	-0.045
	1596.8		1596.8	17	P	4	515.28		515.28	
	1693.8		1693.8	18	P	3	418.23		418.23	
	1780.9		1780.9	19	S	2	321.18		321.18	
	1867.9		1867.9	20	S	1	234.14		234.14	
				21	K	0	147.11		147.11	

Scan number	1503	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	158.91



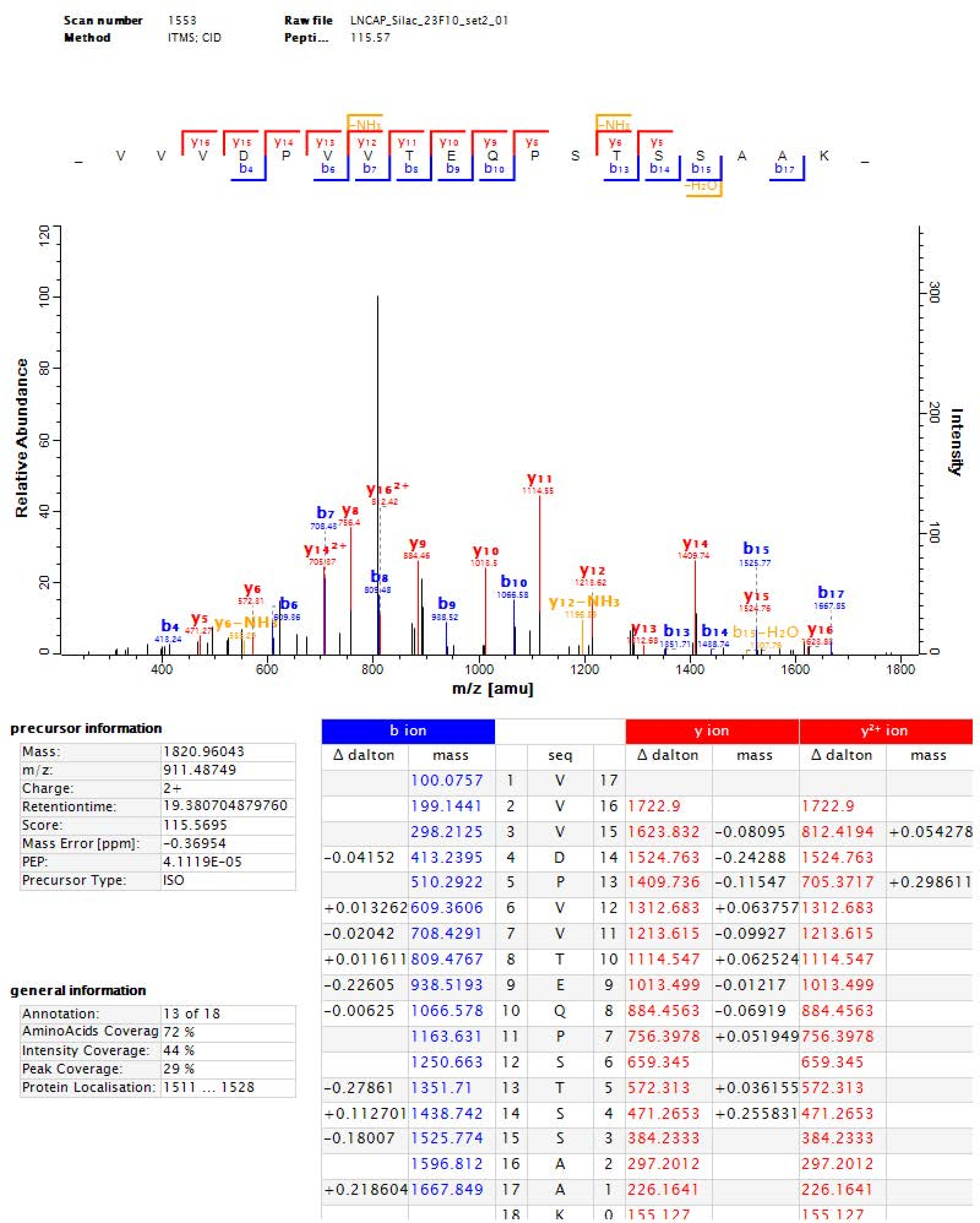
precursor information

Mass:	2659.21002
m/z:	887.41062
Charge:	3+
Retentiontime:	18.895931243896
Score:	158.9069
Mass Error [ppm]:	0.1272
PEP:	1.1484E-31
Precursor Type:	MULTI

general information

Annotation:	18 of 25
AminoAcids Coverag	72 %
Intensity Coverage:	54 %
Peak Coverage:	40 %
Protein Localisation:	113 ... 137

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	24				
	171.11		171.11	2	V	23	2589.2		2589.2	
	268.17		268.17	3	P	22	2490.1		1245.6	+0.2046
	397.21		397.21	4	E	21	2393.1		2393.1	
	498.26		498.26	5	T	20	2264		1132.5	+0.2409
	627.3	-0.057	627.3	6	E	19	2163		2163	
	742.33		742.33	7	D	18	2033.9		2033.9	
	841.39		841.39	8	V	17	1918.9		1918.9	
	969.45	-0.004	969.45	9	Q	16	1819.8		910.42	+0.3842
	1040.5	-0.054	1040.5	10	A	15	1691.8		1691.8	
	1127.5	+0.0149	1127.5	11	S	14	1620.7		1620.7	
	1226.6	-0.147	1226.6	12	V	13	1533.7	-0.014	1533.7	
	1313.6	-0.322	1313.6	13	S	12	1434.6	-0.204	717.82	+0.1395
	1428.6		1428.6	14	D	11	1347.6	-0.051	1347.6	
	1529.7	+0.0931	1529.7	15	T	10	1232.6		616.79	+0.1735
	1600.7	-0.209	1600.7	16	A	9	1131.5	+0.0698	1131.5	
	1728.8	-0.253	1728.8	17	Q	8	1060.5	+0.2057	530.75	-0.001
+0.1117	928.93		1856.9	18	Q	7	932.43	+0.1366	466.72	+0.3147
	1953.9		1953.9	19	P	6	804.37	+0.0023	402.69	-0.138
	2040.9		2040.9	20	S	5	707.32	+0.1175	707.32	
	2170		2170	21	E	4	620.29		620.29	
-0.352	1150		2299	22	E	3	491.25	+0.1675	491.25	
	2427.1		2427.1	23	Q	2	362.2	+0.0625	362.2	
+0.3714	1257.6		2514.1	24	S	1	234.14		234.14	
				25	K	0	147.11		147.11	



Scan number	1553	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	115.57

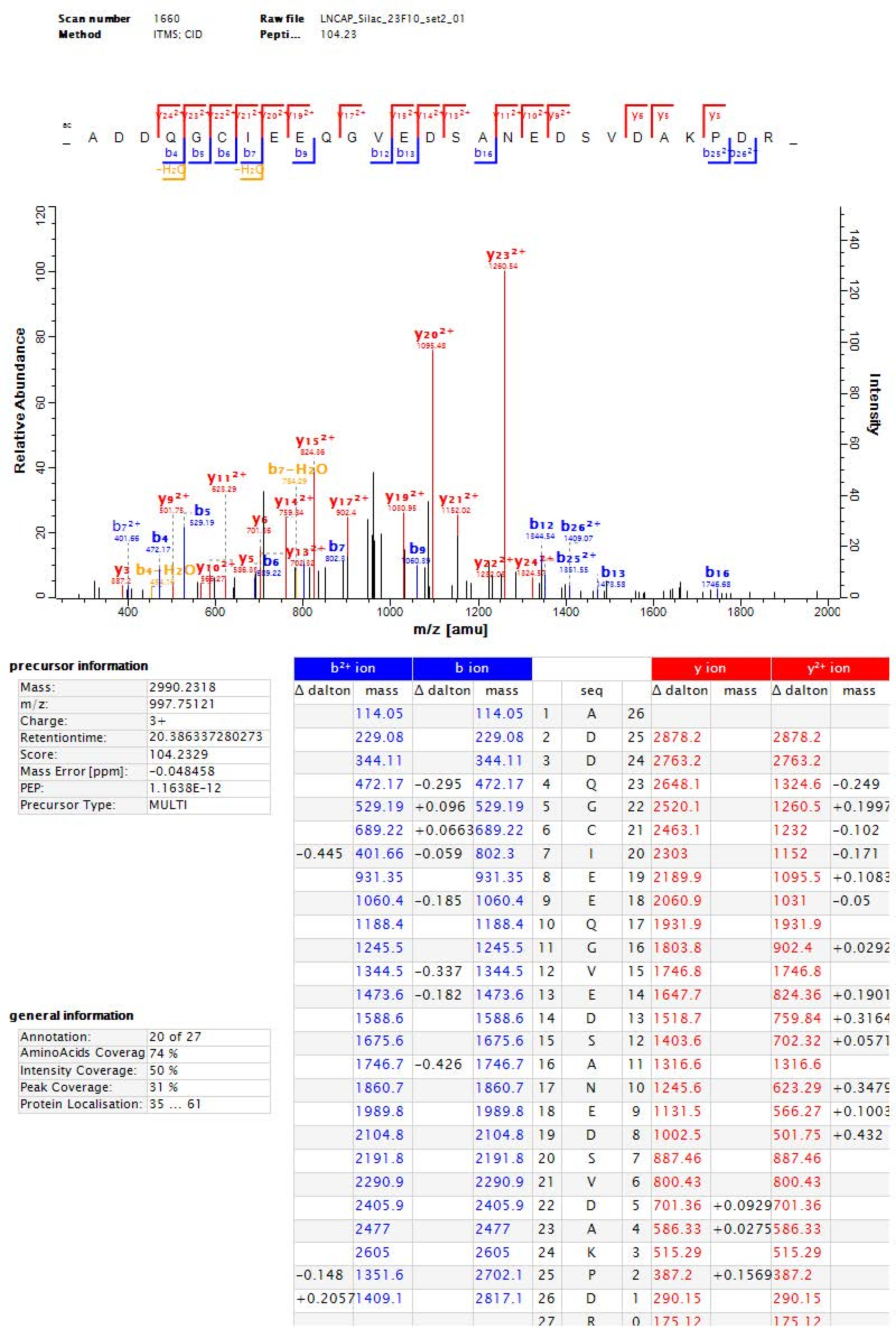
precursor information

Mass:	1820.96043
m/z:	911.48749
Charge:	2+
Retentiontime:	19.380704879760
Score:	115.5695
Mass Error [ppm]:	-0.36954
PEP:	4.1119E-05
Precursor Type:	ISO

general information

Annotation:	13 of 18
AminoAcids Coverag	72 %
Intensity Coverage:	44 %
Peak Coverage:	29 %
Protein Localisation:	1511 ... 1528

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	17				
	199.1441	2	V	16	1722.9		1722.9	
	298.2125	3	V	15	1623.832	-0.08095	812.4194	+0.054278
-0.04152	413.2395	4	D	14	1524.763	-0.24288	1524.763	
	510.2922	5	P	13	1409.736	-0.11547	705.3717	+0.298611
+0.013262	609.3606	6	V	12	1312.683	+0.063757	1312.683	
-0.02042	708.4291	7	V	11	1213.615	-0.09927	1213.615	
+0.011611	809.4767	8	T	10	1114.547	+0.062524	1114.547	
-0.22605	938.5193	9	E	9	1013.499	-0.01217	1013.499	
-0.00625	1066.578	10	Q	8	884.4563	-0.06919	884.4563	
	1163.631	11	P	7	756.3978	+0.051949	756.3978	
	1250.663	12	S	6	659.345		659.345	
-0.27861	1351.71	13	T	5	572.313	+0.036155	572.313	
+0.112701	1438.742	14	S	4	471.2653	+0.255831	471.2653	
-0.18007	1525.774	15	S	3	384.2333		384.2333	
	1596.812	16	A	2	297.2012		297.2012	
+0.218604	1667.849	17	A	1	226.1641		226.1641	
		18	K	0	155.127		155.127	



Scan number	1660	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	104.23

precursor information

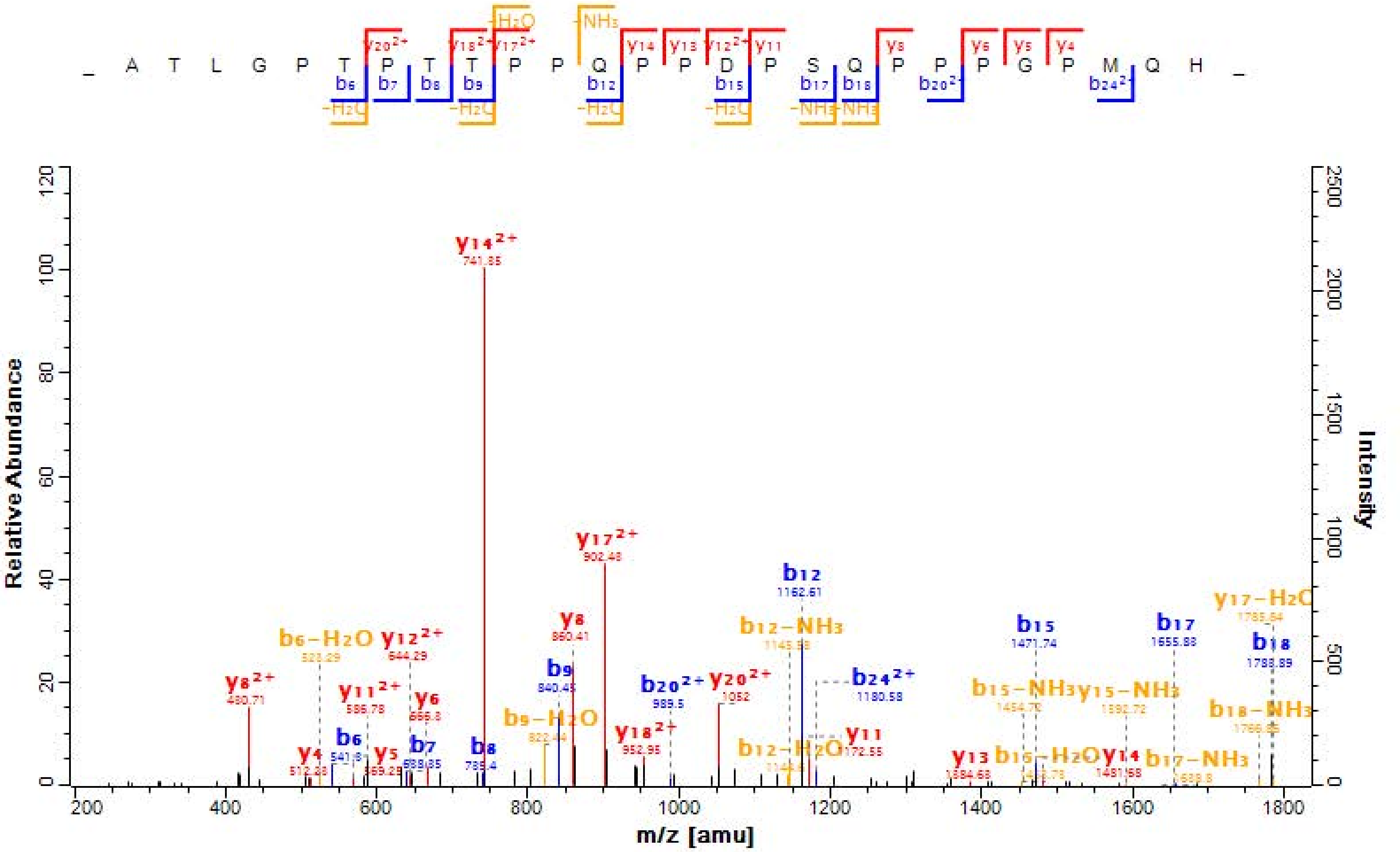
Mass:	2990.2318
m/z:	997.75121
Charge:	3+
Retentiontime:	20.386337280273
Score:	104.2329
Mass Error [ppm]:	-0.048458
PEP:	1.1638E-12
Precursor Type:	MULTI

general information

Annotation:	20 of 27
AminoAcids Coverag	74 %
Intensity Coverage:	50 %
Peak Coverage:	31 %
Protein Localisation:	35 ... 61

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.05		114.05	1	A	26				
	229.08		229.08	2	D	25	2878.2		2878.2	
	344.11		344.11	3	D	24	2763.2		2763.2	
	472.17	-0.295	472.17	4	Q	23	2648.1		1324.6	-0.249
	529.19	+0.096	529.19	5	G	22	2520.1		1260.5	+0.1997
	689.22	+0.0663	689.22	6	C	21	2463.1		1232	-0.102
-0.445	401.66	-0.059	802.3	7	I	20	2303		1152	-0.171
	931.35		931.35	8	E	19	2189.9		1095.5	+0.1083
	1060.4	-0.185	1060.4	9	E	18	2060.9		1031	-0.05
	1188.4		1188.4	10	Q	17	1931.9		1931.9	
	1245.5		1245.5	11	G	16	1803.8		902.4	+0.0292
	1344.5	-0.337	1344.5	12	V	15	1746.8		1746.8	
	1473.6	-0.182	1473.6	13	E	14	1647.7		824.36	+0.1901
	1588.6		1588.6	14	D	13	1518.7		759.84	+0.3164
	1675.6		1675.6	15	S	12	1403.6		702.32	+0.0571
	1746.7	-0.426	1746.7	16	A	11	1316.6		1316.6	
	1860.7		1860.7	17	N	10	1245.6		623.29	+0.3479
	1989.8		1989.8	18	E	9	1131.5		566.27	+0.1003
	2104.8		2104.8	19	D	8	1002.5		501.75	+0.432
	2191.8		2191.8	20	S	7	887.46		887.46	
	2290.9		2290.9	21	V	6	800.43		800.43	
	2405.9		2405.9	22	D	5	701.36	+0.0929	701.36	
	2477		2477	23	A	4	586.33	+0.0275	586.33	
	2605		2605	24	K	3	515.29		515.29	
-0.148	1351.6		2702.1	25	P	2	387.2	+0.1569	387.2	
+0.2057	1409.1		2817.1	26	D	1	290.15		290.15	
				27	R	0	175.12		175.12	

Scan number	2239	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	131.56



precursor information

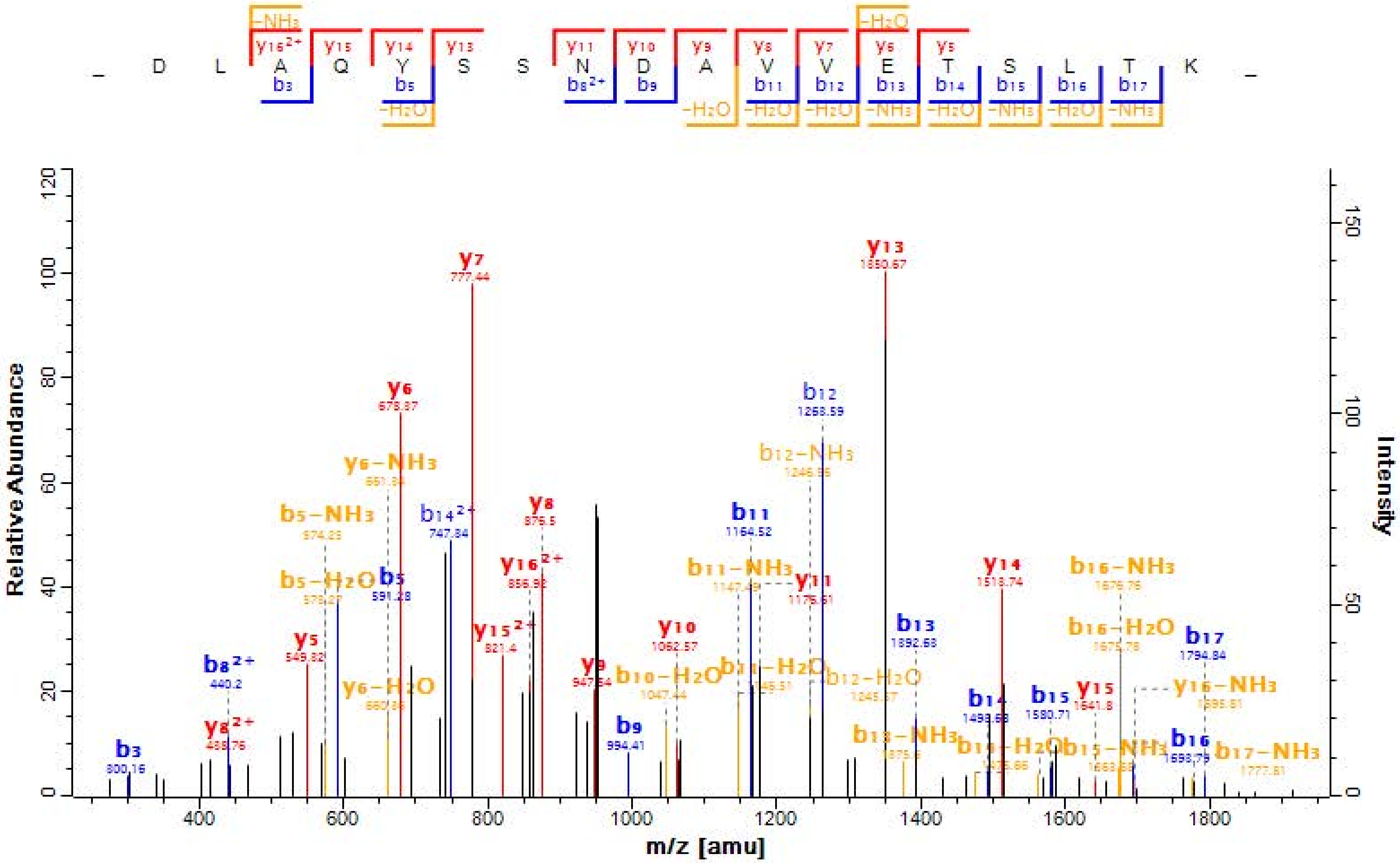
Mass:	2642.28033
m/z:	881.76739
Charge:	3+
Retentiontime:	25.658084869384
Score:	131.5595
Mass Error [ppm]:	0.16752
PEP:	1.5075E-16
Precursor Type:	ISO

general information

Annotation:	18 of 26
AminoAcids Coverag	69 %
Intensity Coverage:	73 %
Peak Coverage:	38 %
Protein Localisation:	101 ... 126

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	25				
	173.09		173.09	2	T	24	2572.3		2572.3	
	286.18		286.18	3	L	23	2471.2		2471.2	
	343.2		343.2	4	G	22	2358.1		2358.1	
	440.25		440.25	5	P	21	2301.1		2301.1	
	541.3	+0.0734	541.3	6	T	20	2204		2204	
	638.35	-0.037	638.35	7	P	19	2103		1052	+0.3026
	739.4	+0.0362	739.4	8	T	18	2005.9		2005.9	
	840.45	-0.046	840.45	9	T	17	1904.9		952.95	-0.307
	937.5		937.5	10	P	16	1803.8		902.43	+0.2487
	1034.6		1034.6	11	P	15	1706.8		1706.8	
	1162.6	-0.042	1162.6	12	Q	14	1609.7		1609.7	
	1259.7		1259.7	13	P	13	1481.7	-0.029	741.35	+0.3178
	1356.7		1356.7	14	P	12	1384.6	+0.0265	1384.6	
	1471.7	-0.144	1471.7	15	D	11	1287.6		644.29	+0.2434
	1568.8		1568.8	16	P	10	1172.6	+0.021	586.78	-0.008
	1655.8	+0.4613	1655.8	17	S	9	1075.5		1075.5	
	1783.9	-0.288	1783.9	18	Q	8	988.47		988.47	
	1880.9		1880.9	19	P	7	860.41	-0.089	430.71	+0.0249
+0.054	989.5		1978	20	P	6	763.36		763.36	
	2075		2075	21	P	5	666.3	+0.0637	666.3	
	2132.1		2132.1	22	G	4	569.25	+0.1843	569.25	
	2229.1		2229.1	23	P	3	512.23	+0.134	512.23	
-0.334	1180.6		2360.2	24	M	2	415.18		415.18	
	2488.2		2488.2	25	Q	1	284.14		284.14	
				26	H	0	156.08		156.08	

Scan number	2856	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	211.06



precursor information

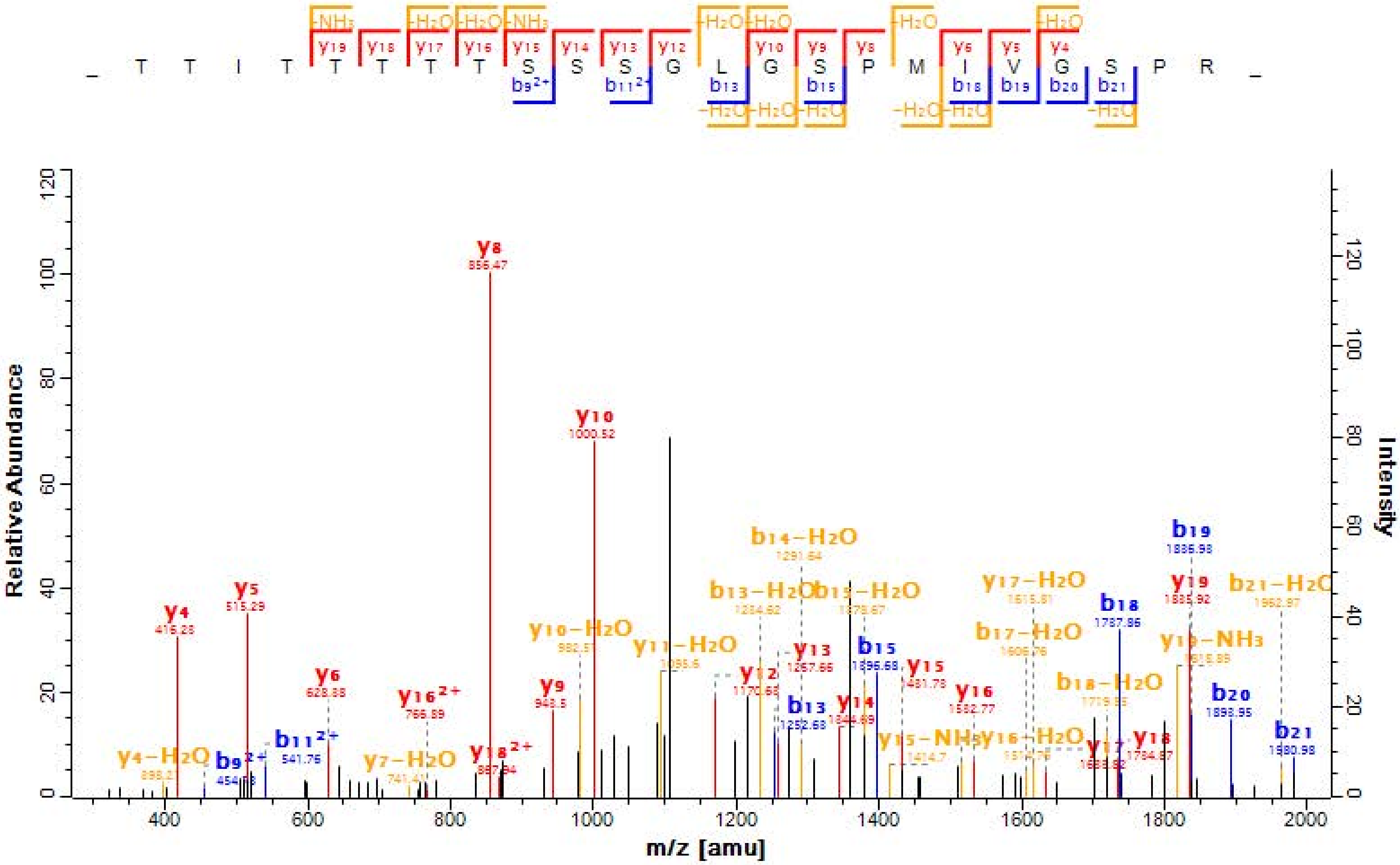
Mass:	1939.93883
m/z:	970.97669
Charge:	2+
Retentiontime:	31.145492553710
Score:	211.0629
Mass Error [ppm]:	0.70179
PEP:	5.5671E-41
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	54 %
Peak Coverage:	43 %
Protein Localisation:	65 ... 82

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	17				
	229.12		229.12	2	L	16	1825.9		1825.9	
	300.16	-0.05	300.16	3	A	15	1712.8		856.92	+0.0584
	428.21		428.21	4	Q	14	1641.8	+0.4043	821.4	+0.0293
	591.28	+0.0769	591.28	5	Y	13	1513.7	+0.0184	1513.7	
	678.31		678.31	6	S	12	1350.7	-0.081	1350.7	
	765.34		765.34	7	S	11	1263.6		1263.6	
-0.064	440.2		879.38	8	N	10	1176.6	+0.0461	1176.6	
	994.41	+0.1232	994.41	9	D	9	1062.6	+0.1874	1062.6	
	1065.4		1065.4	10	A	8	947.54	-0.06	947.54	
	1164.5	-0.067	1164.5	11	V	7	876.5	-0.206	438.76	+0.4233
	1263.6	+0.0115	1263.6	12	V	6	777.44	-0.068	777.44	
	1392.6	-0.038	1392.6	13	E	5	678.37	-0.012	678.37	
+0.1257	747.34	-0.047	1493.7	14	T	4	549.32	+0.0514	549.32	
	1580.7	-0.08	1580.7	15	S	3	448.28		448.28	
	1693.8	-0.267	1693.8	16	L	2	361.24		361.24	
	1794.8	-0.017	1794.8	17	T	1	248.16		248.16	
				18	K	0	147.11		147.11	

Scan number	2885	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	174.2



precursor information

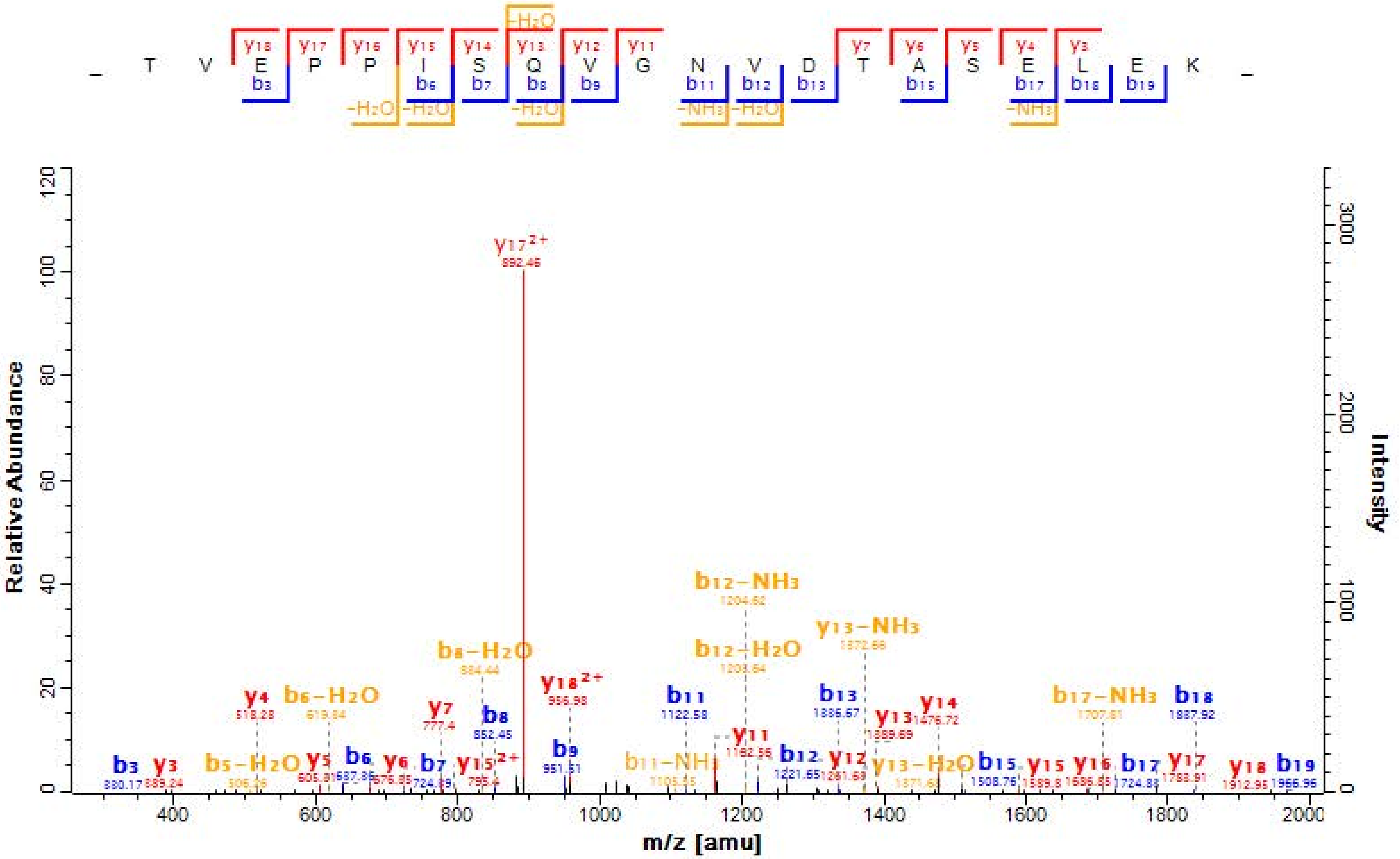
Mass:	2251.13651
m/z:	1126.57553
Charge:	2+
Retentiontime:	31.406850814819
Score:	174.2027
Mass Error [ppm]:	-0.029536
PEP:	3.0472E-38
Precursor Type:	MULTI

general information

Annotation:	17 of 23
AminoAcids Coverag	74 %
Intensity Coverage:	58 %
Peak Coverage:	38 %
Protein Localisation:	8 … 30

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	22				
	203.1		203.1	2	T	21	2151.1		2151.1	
	316.19		316.19	3	I	20	2050		2050	
	417.23		417.23	4	T	19	1937		1937	
	518.28		518.28	5	T	18	1835.9	+0.4717	1835.9	
	619.33		619.33	6	T	17	1734.9	-0.125	867.94	+0.2532
	720.38		720.38	7	T	16	1633.8	-0.437	1633.8	
	821.43		821.43	8	T	15	1532.8	+0.0031	766.89	+0.0121
-0.332	454.73		908.46	9	S	14	1431.7	+0.1259	1431.7	
	995.49		995.49	10	S	13	1344.7	+0.0412	1344.7	
+0.1334	541.76		1082.5	11	S	12	1257.7	-0.063	1257.7	
	1139.5		1139.5	12	G	11	1170.6	+0.0418	1170.6	
	1252.6	-0.005	1252.6	13	L	10	1113.6		1113.6	
	1309.6		1309.6	14	G	9	1000.5	+0.0557	1000.5	
	1396.7	-0.245	1396.7	15	S	8	943.5	+0.1864	943.5	
	1493.7		1493.7	16	P	7	856.47	+0.0076	856.47	
	1624.8		1624.8	17	M	6	759.42		759.42	
	1737.9	-0.322	1737.9	18	I	5	628.38	+0.0788	628.38	
	1836.9	+0.2569	1836.9	19	V	4	515.29	+0.1356	515.29	
	1893.9	-0.183	1893.9	20	G	3	416.23	+0.0429	416.23	
	1981	-0.073	1981	21	S	2	359.2		359.2	
	2078		2078	22	P	1	272.17		272.17	
				23	R	0	175.12		175.12	

Scan number	3049	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	174



precursor information

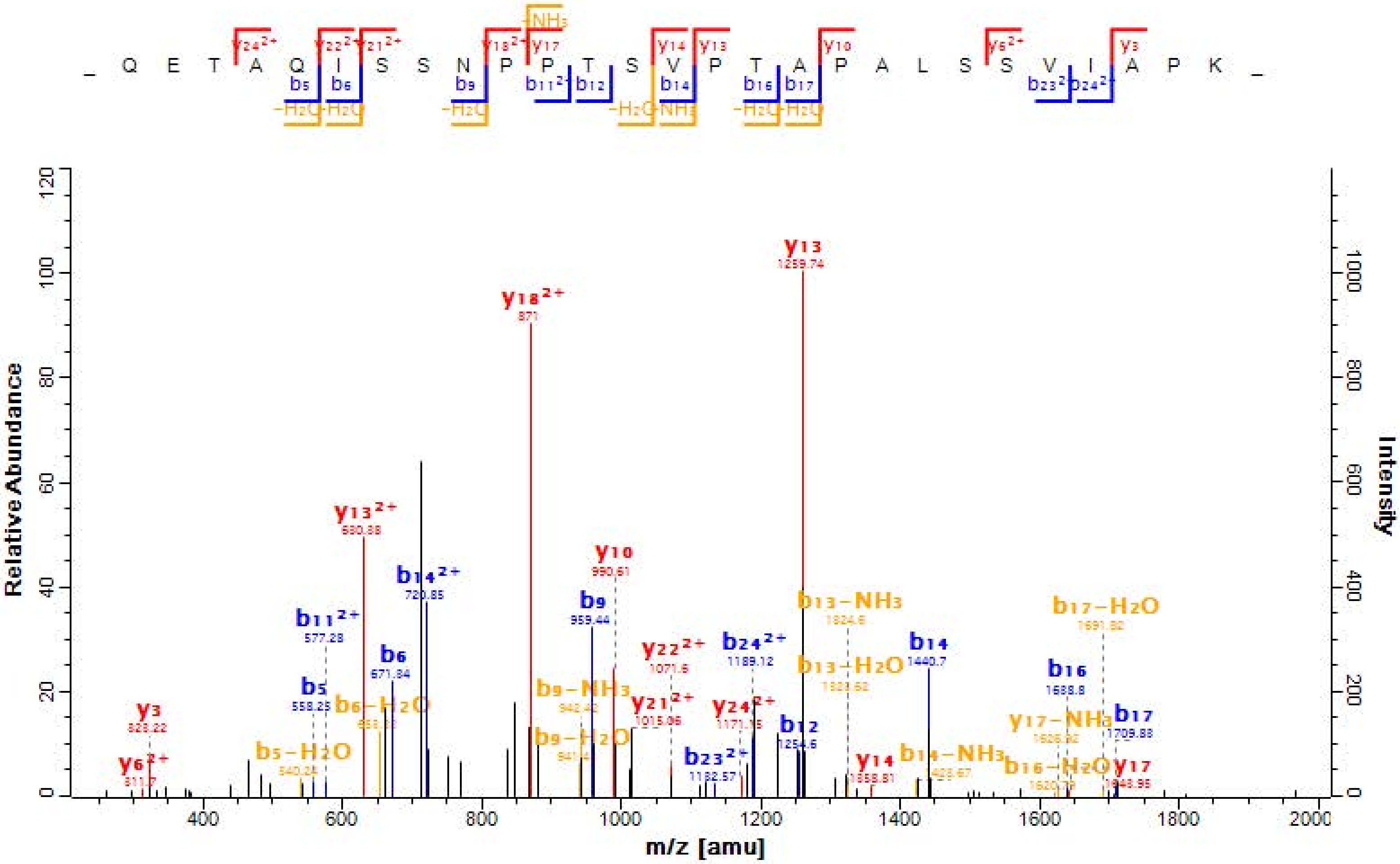
Mass:	2112.05911
m/z:	1057.03683
Charge:	2+
Retentiontime:	32.881526947021
Score:	174.0004
Mass Error [ppm]:	0.22292
PEP:	3.328E-36
Precursor Type:	MULTI

general information

Annotation:	17 of 20
AminoAcids Coverag	85 %
Intensity Coverage:	79 %
Peak Coverage:	37 %
Protein Localisation:	1092 ... 1111

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055	1	T	19				
	201.1234	2	V	18	2012.018		2012.018	
+0.368431	330.166	3	E	17	1912.95	+0.384889	956.9786	+0.060022
	427.2187	4	P	16	1783.907	-0.01148	892.4573	+0.250996
	524.2715	5	P	15	1686.854	-0.10655	1686.854	
+0.038062	637.3556	6	I	14	1589.802	-0.12263	795.4045	+0.374683
+0.137503	724.3876	7	S	13	1476.718	-0.11547	1476.718	
+0.041878	852.4462	8	Q	12	1389.686	+0.137872	1389.686	
+0.012282	951.5146	9	V	11	1261.627	+0.002113	1261.627	
	1008.536	10	G	10	1162.559	-0.02859	1162.559	
+0.296035	1122.579	11	N	9	1105.537		1105.537	
+0.018271	1221.647	12	V	8	991.4942		991.4942	
-0.08594	1336.674	13	D	7	892.4258		892.4258	
	1437.722	14	T	6	777.3989	-0.00752	777.3989	
-0.13338	1508.759	15	A	5	676.3512	-0.22217	676.3512	
	1595.791	16	S	4	605.3141	+0.009159	605.3141	
+0.129766	1724.834	17	E	3	518.2821	+0.075123	518.2821	
-0.18574	1837.918	18	L	2	389.2395	+0.119548	389.2395	
-0.10663	1966.96	19	E	1	276.1554		276.1554	
		20	K	0	147.1128		147.1128	

Scan number	4052	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	110.57



precursor information

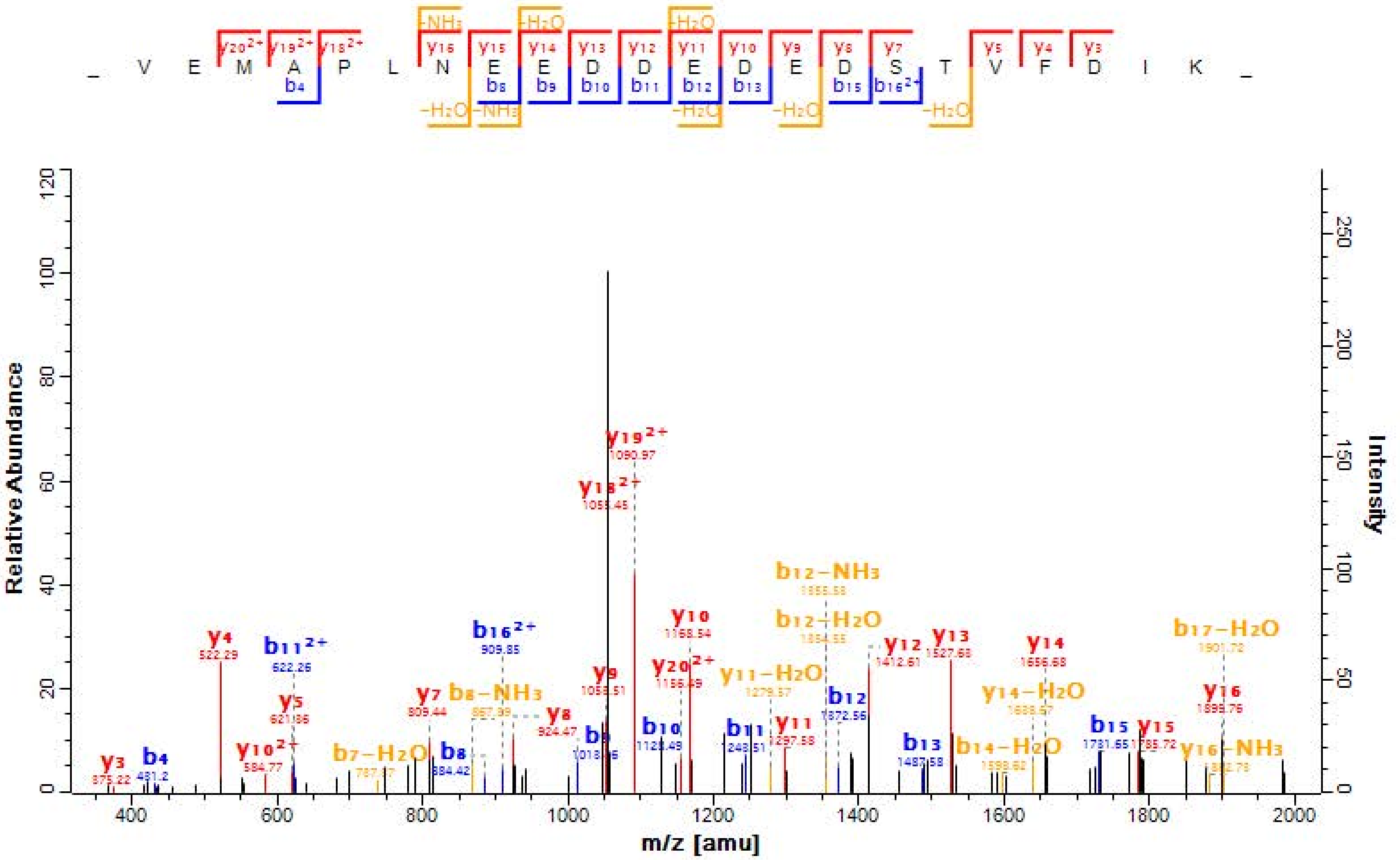
Mass:	2690.41349
m/z:	897.81177
Charge:	3+
Retentiontime:	41.396366119384
Score:	110.5715
Mass Error [ppm]:	0.30274
PEP:	2.9206E-13
Precursor Type:	MULTI

general information

Annotation:	18 of 27
AminoAcids Coverag	67 %
Intensity Coverage:	53 %
Peak Coverage:	34 %
Protein Localisation:	165 ... 191

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.07		129.07	1	Q	26				
	258.11		258.11	2	E	25	2571.4		2571.4	
	359.16		359.16	3	T	24	2442.3		2442.3	
	430.19		430.19	4	A	23	2341.3		1171.1	+0.2868
	558.25	+0.1091	558.25	5	Q	22	2270.2		2270.2	
	671.34	+0.008	671.34	6	I	21	2142.2		1071.6	-0.362
	758.37		758.37	7	S	20	2029.1		1015.1	-0.117
	845.4		845.4	8	S	19	1942.1		1942.1	
	959.44	-0.022	959.44	9	N	18	1855		1855	
	1056.5		1056.5	10	P	17	1741		871	+0.1871
+0.0831	577.28		1153.5	11	P	16	1643.9	-0.325	1643.9	
	1254.6	-0.003	1254.6	12	T	15	1546.9		1546.9	
	1341.6		1341.6	13	S	14	1445.8		1445.8	
+0.0755	720.85	-0.086	1440.7	14	V	13	1358.8	+0.0423	1358.8	
	1537.7		1537.7	15	P	12	1259.7	-0.155	630.38	+0.1626
	1638.8	+0.071	1638.8	16	T	11	1162.7		1162.7	
	1709.8	+0.0721	1709.8	17	A	10	1061.6		1061.6	
	1806.9		1806.9	18	P	9	990.61	-0.153	990.61	
	1877.9		1877.9	19	A	8	893.55		893.55	
	1991		1991	20	L	7	822.52		822.52	
	2078		2078	21	S	6	709.43		709.43	
	2165.1		2165.1	22	S	5	622.4		311.7	+0.4072
+0.404	1132.6		2264.1	23	V	4	535.37		535.37	
-0.298	1189.1		2377.2	24	I	3	436.3		436.3	
	2448.3		2448.3	25	A	2	323.22	+0.0232	323.22	
	2545.3		2545.3	26	P	1	252.18		252.18	
				27	K	0	155.13		155.13	

Scan number	4420	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	136.02



precursor information

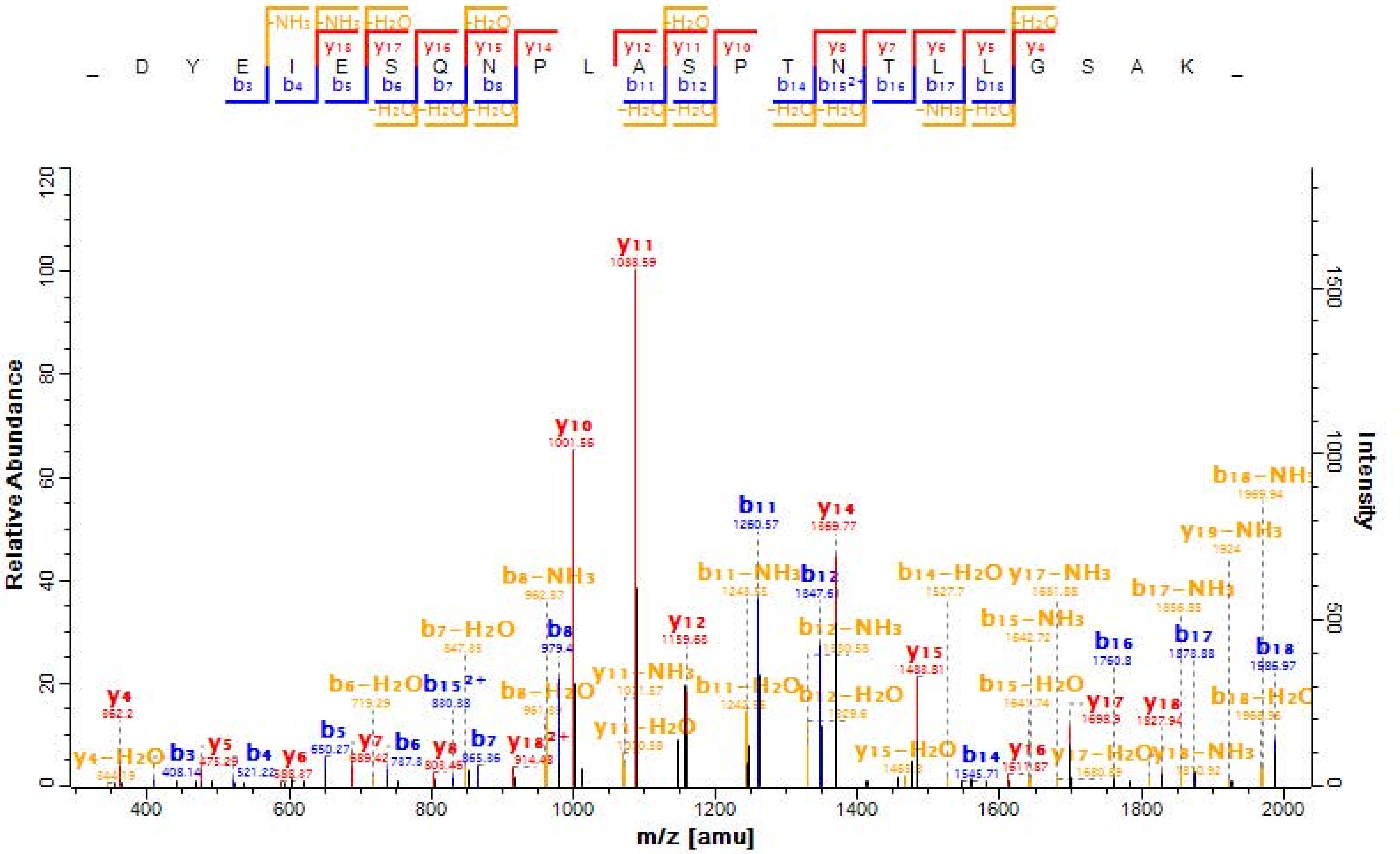
Mass:	2539.08043
m/z:	1270.54749
Charge:	2+
Retentiontime:	44.489040374755
Score:	136.0206
Mass Error [ppm]:	0.33522
PEP:	1.4162E-20
Precursor Type:	MULTI

general information

Annotation:	17 of 22
AminoAcids Coverag	77 %
Intensity Coverage:	45 %
Peak Coverage:	36 %
Protein Localisation:	136 ... 157

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	21				
	229.12		229.12	2	E	20	2441		2441	
	360.16		360.16	3	M	19	2312		1156.5	+0.4015
	431.2	-0.036	431.2	4	A	18	2180.9		1091	+0.2568
	528.25		528.25	5	P	17	2109.9		1055.5	-0.019
	641.33		641.33	6	L	16	2012.8		2012.8	
	755.38		755.38	7	N	15	1899.8	+0.1066	1899.8	
	884.42	-0.016	884.42	8	E	14	1785.7	-0.146	1785.7	
	1013.5	-0.032	1013.5	9	E	13	1656.7	-0.237	1656.7	
	1128.5	-0.166	1128.5	10	D	12	1527.6	-0.155	1527.6	
+0.2319	622.26	-0.014	1243.5	11	D	11	1412.6	-0.013	1412.6	
	1372.6	-0.114	1372.6	12	E	10	1297.6	+0.1901	1297.6	
	1487.6	-0.317	1487.6	13	D	9	1168.5	+0.2569	584.77	-0.229
	1616.6		1616.6	14	E	8	1053.5	-0.023	1053.5	
	1731.7	-0.145	1731.7	15	D	7	924.47	-0.125	924.47	
-0.334	909.85		1818.7	16	S	6	809.44	+0.0078	809.44	
	1919.7		1919.7	17	T	5	722.41		722.41	
	2018.8		2018.8	18	V	4	621.36	+0.0575	621.36	
	2165.9		2165.9	19	F	3	522.29	+0.104	522.29	
	2280.9		2280.9	20	D	2	375.22	-0.002	375.22	
	2394		2394	21	I	1	260.2		260.2	
				22	K	0	147.11		147.11	

Scan number	4554	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	263.31



precursor information

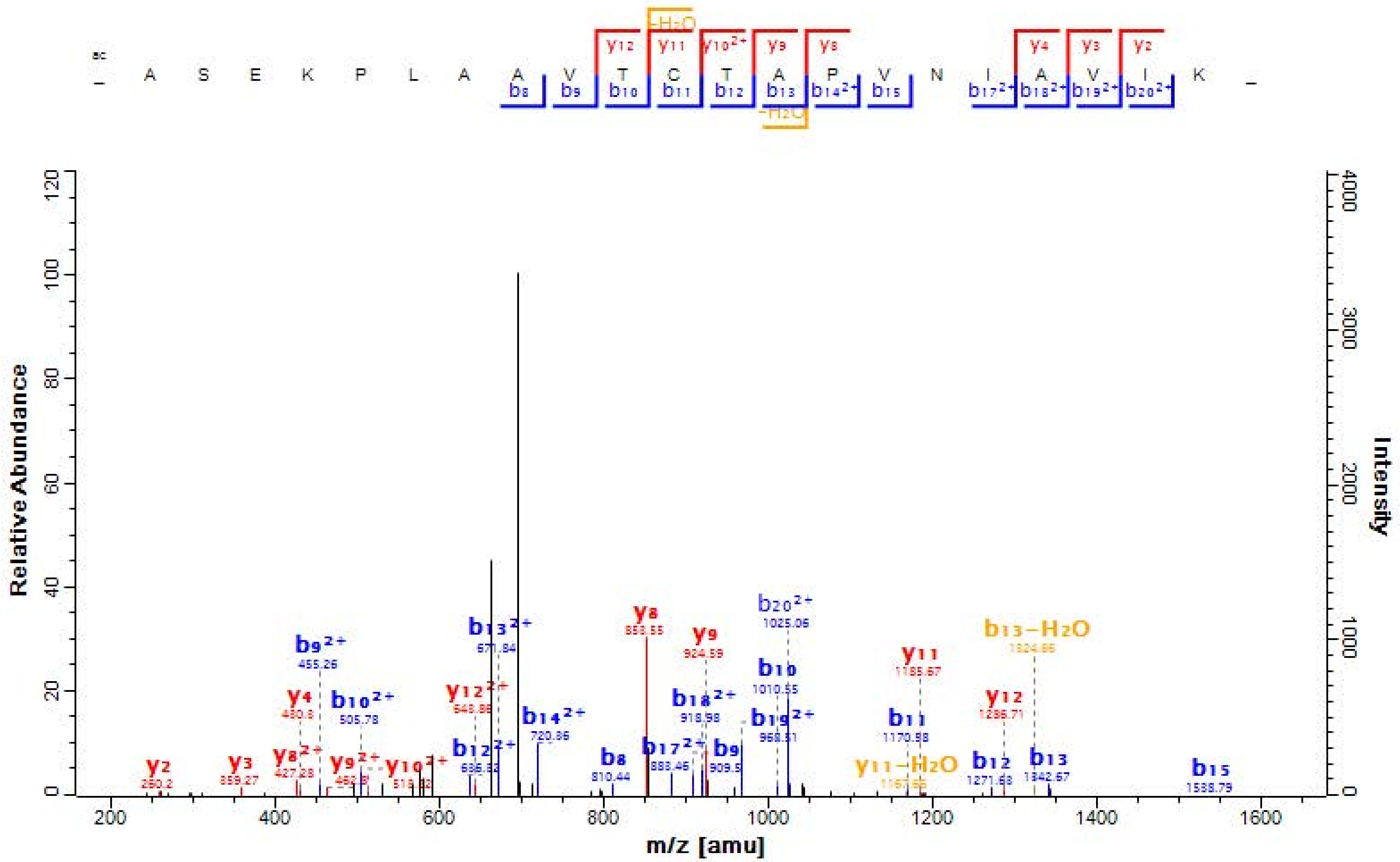
Mass:	2347.15461
m/z:	1174.58458
Charge:	2+
Retentiontime:	45.622333526611
Score:	263.3145
Mass Error [ppm]:	0.11688
PEP:	3.4764E-98
Precursor Type:	MULTI

general information

Annotation:	16 of 22
AminoAcids Coverag	73 %
Intensity Coverage:	66 %
Peak Coverage:	49 %
Protein Localisation:	618 ... 639

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	21				
	279.1		279.1	2	Y	20	2233.1		2233.1	
	408.14	+0.1962	408.14	3	E	19	2070.1		2070.1	
	521.22	-0.021	521.22	4	I	18	1941		1941	
	650.27	-0.062	650.27	5	E	17	1827.9	-0.027	914.48	+0.0981
	737.3	-0.003	737.3	6	S	16	1698.9	-0.202	1698.9	
	865.36	+0.0446	865.36	7	Q	15	1611.9	+0.0388	1611.9	
	979.4	-0.028	979.4	8	N	14	1483.8	-0.111	1483.8	
	1076.5		1076.5	9	P	13	1369.8	-0.058	1369.8	
	1189.5		1189.5	10	L	12	1272.7		1272.7	
	1260.6	-0.165	1260.6	11	A	11	1159.6	+0.0306	1159.6	
	1347.6	-0.133	1347.6	12	S	10	1088.6	-0.044	1088.6	
	1444.7		1444.7	13	P	9	1001.6	-0.054	1001.6	
	1545.7	-0.396	1545.7	14	T	8	904.51		904.51	
+0.0117	830.38		1659.7	15	N	7	803.46	-0.257	803.46	
	1760.8	-0.075	1760.8	16	T	6	689.42	-0.08	689.42	
	1873.9	-0.193	1873.9	17	L	5	588.37	+0.0806	588.37	
	1987	-0.062	1987	18	L	4	475.29	+0.042	475.29	
	2044		2044	19	G	3	362.2	+0.1255	362.2	
	2131		2131	20	S	2	305.18		305.18	
	2202.1		2202.1	21	A	1	218.15		218.15	
				22	K	0	147.11		147.11	

Scan number 4598 **Raw file** LNCAP_Silac_23F10_set2_01
Method ITMS; CID **Pepti...** 148.15



precursor information

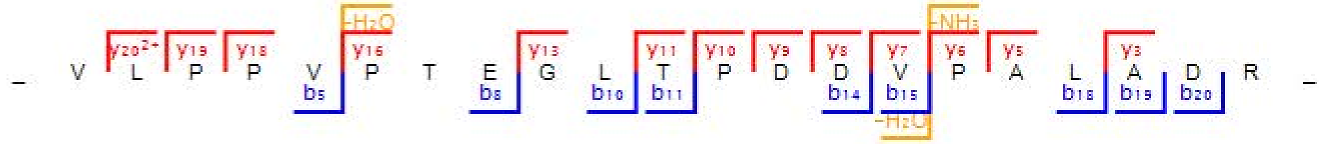
Mass:	2194.20274
m/z:	732.40819
Charge:	3+
Retentiontime:	45.968639373779
Score:	148.1532
Mass Error [ppm]:	-0.18036
PEP:	1.6817E-19
Precursor Type:	MULTI

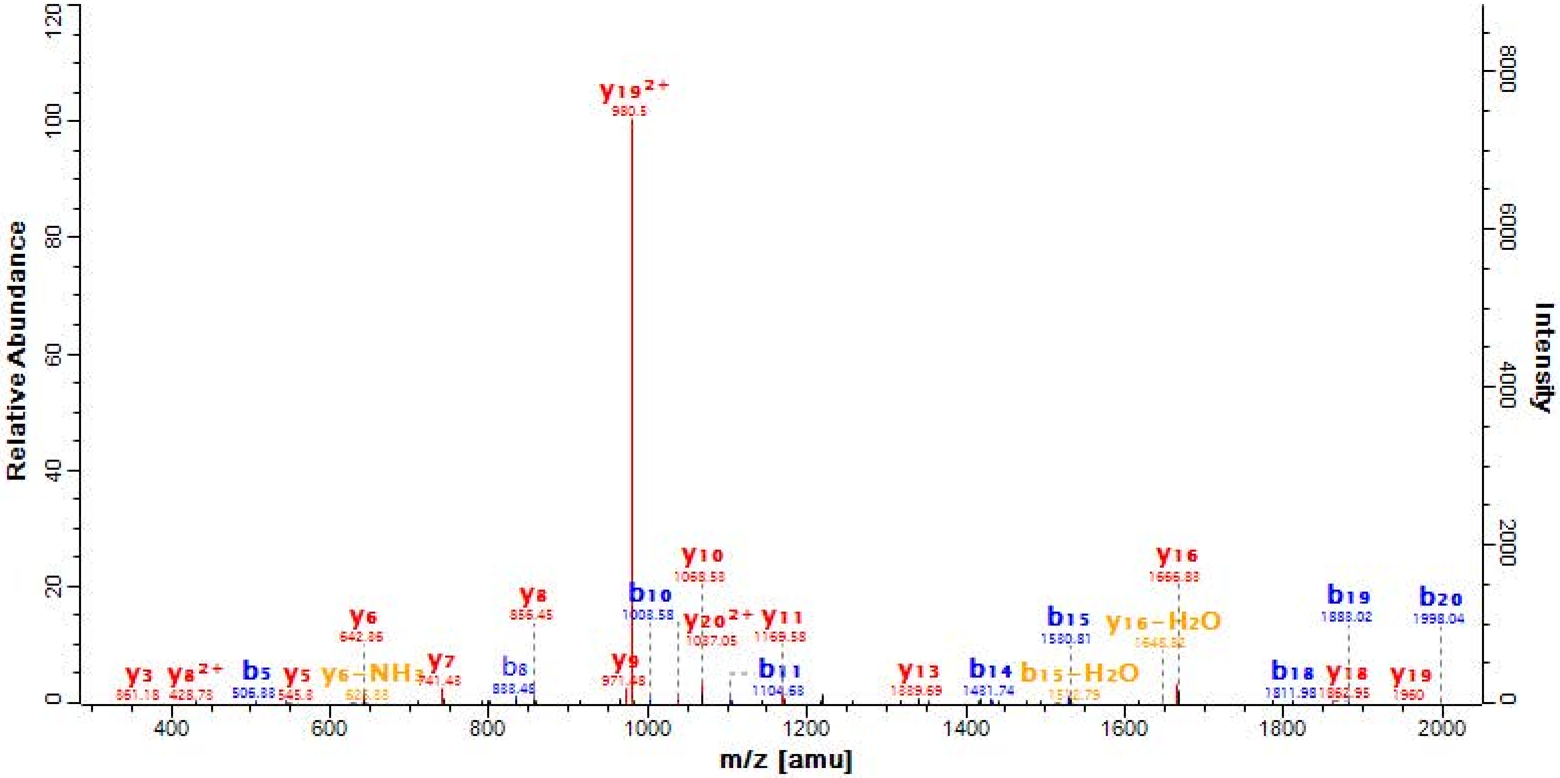
general information

Annotation:	12 of 21
AminoAcids Coverag	57 %
Intensity Coverage:	39 %
Peak Coverage:	31 %
Protein Localisation:	2 ... 22

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.05		114.05	1	A	20				
	201.09		201.09	2	S	19	2082.2		2082.2	
	330.13		330.13	3	E	18	1995.1		1995.1	
	458.22		458.22	4	K	17	1866.1		1866.1	
	555.28		555.28	5	P	16	1738		1738	
	668.36		668.36	6	L	15	1640.9		1640.9	
	739.4		739.4	7	A	14	1527.9		1527.9	
	810.44	+0.1832	810.44	8	A	13	1456.8		1456.8	
-0.106	455.26	+0.0832	909.5	9	V	12	1385.8		1385.8	
+0.075	505.78	-0.075	1010.6	10	T	11	1286.7	+0.1282	643.86	+0.0031
	1170.6	-0.118	1170.6	11	C	10	1185.7	+0.0173	1185.7	
+0.0524	636.32	-0.152	1271.6	12	T	9	1025.6		513.32	+0.169
+0.0158	671.84	+0.0298	1342.7	13	A	8	924.59	-0.009	462.8	+0.0041
+0.4628	720.36		1439.7	14	P	7	853.55	+0	427.28	+0.201
	1538.8	-0.013	1538.8	15	V	6	756.5		756.5	
	1652.8		1652.8	16	N	5	657.43		657.43	
+0.1378	883.46		1765.9	17	I	4	543.39		543.39	
+0.2296	918.98		1837	18	A	3	430.3	+0.1658	430.3	
+0.2875	968.51		1936	19	V	2	359.27	+0.0216	359.27	
+0.2166	1025.1		2049.1	20	I	1	260.2	+0.032	260.2	
				21	K	0	147.11		147.11	

Scan number	4795	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	121.82





precursor information

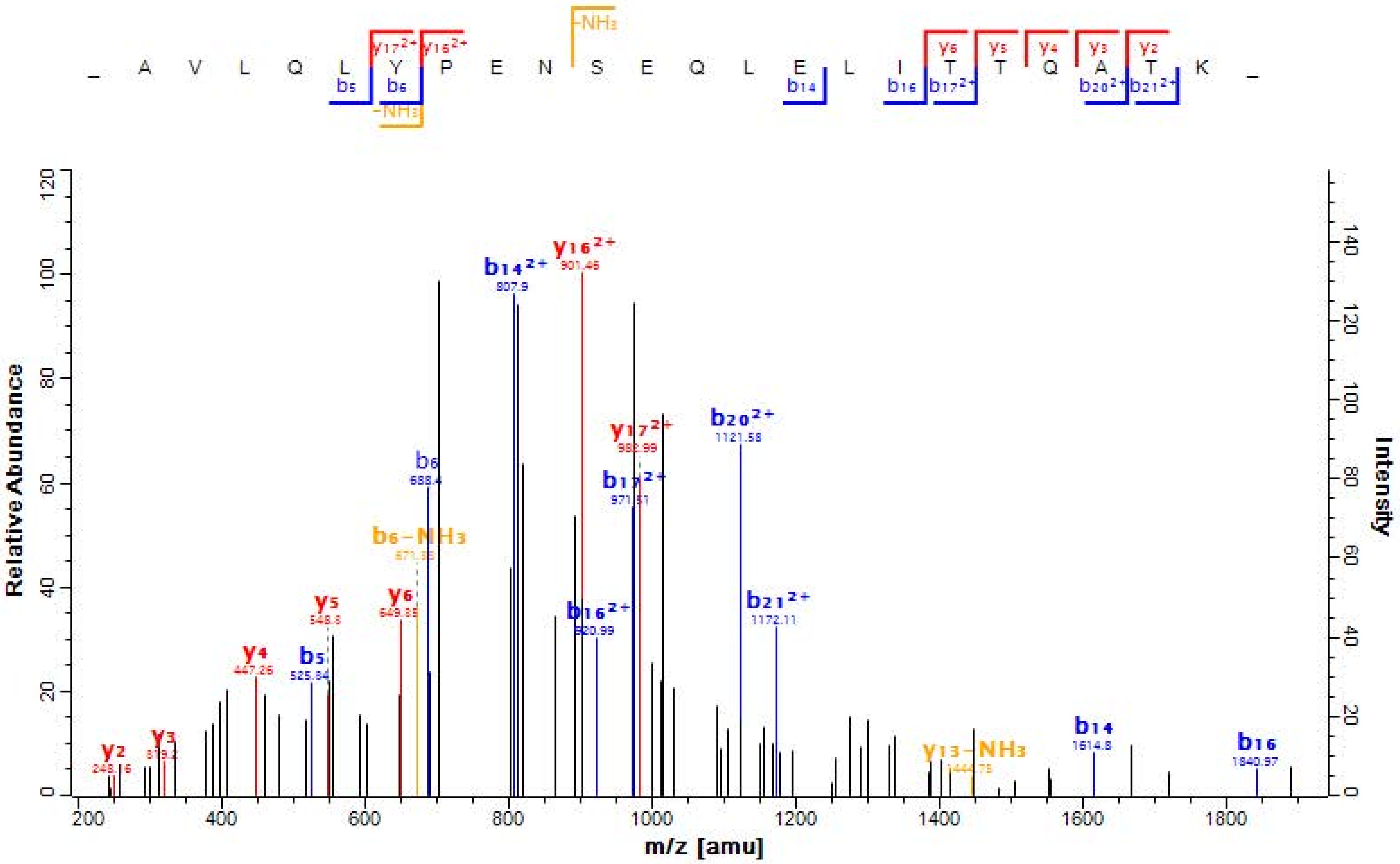
Mass:	2171.14741
m/z:	1086.58098
Charge:	2+
Retentiontime:	47.478794097900
Score:	121.8175
Mass Error [ppm]:	0.0028389
PEP:	2.8707E-13
Precursor Type:	MULTI

general information

Annotation:	18 of 21
AminoAcids Coverag	86 %
Intensity Coverage:	84 %
Peak Coverage:	27 %
Protein Localisation:	233 ... 253

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	20				
	213.1598	2	L	19	2073.086		1037.047	+0.199447
	310.2125	3	P	18	1960.002	+0.005249	980.5047	+0.308984
	407.2653	4	P	17	1862.949	-0.14047	1862.949	
+0.159956	506.3337	5	V	16	1765.897		1765.897	
	603.3865	6	P	15	1666.828	-0.10108	1666.828	
	704.4341	7	T	14	1569.775		1569.775	
+0.198928	833.4767	8	E	13	1468.728		1468.728	
	890.4982	9	G	12	1339.685	+0.085043	1339.685	
+0.108171	1003.582	10	L	11	1282.664		1282.664	
-0.10211	1104.63	11	T	10	1169.58	-0.06443	1169.58	
	1201.683	12	P	9	1068.532	-0.00223	1068.532	
	1316.71	13	D	8	971.4793	+0.395749	971.4793	
-0.10121	1431.737	14	D	7	856.4523	+0.118127	428.7298	+0.333135
-0.11311	1530.805	15	V	6	741.4254	+0.066701	741.4254	
	1627.858	16	P	5	642.357	+0.059309	642.357	
	1698.895	17	A	4	545.3042	+0.233167	545.3042	
-0.10468	1811.979	18	L	3	474.2671		474.2671	
-0.10846	1883.016	19	A	2	361.183	+0.145543	361.183	
+0.459564	1998.043	20	D	1	290.1459		290.1459	
		21	R	0	175.119		175.119	

Scan number	5446	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	62.62



precursor information

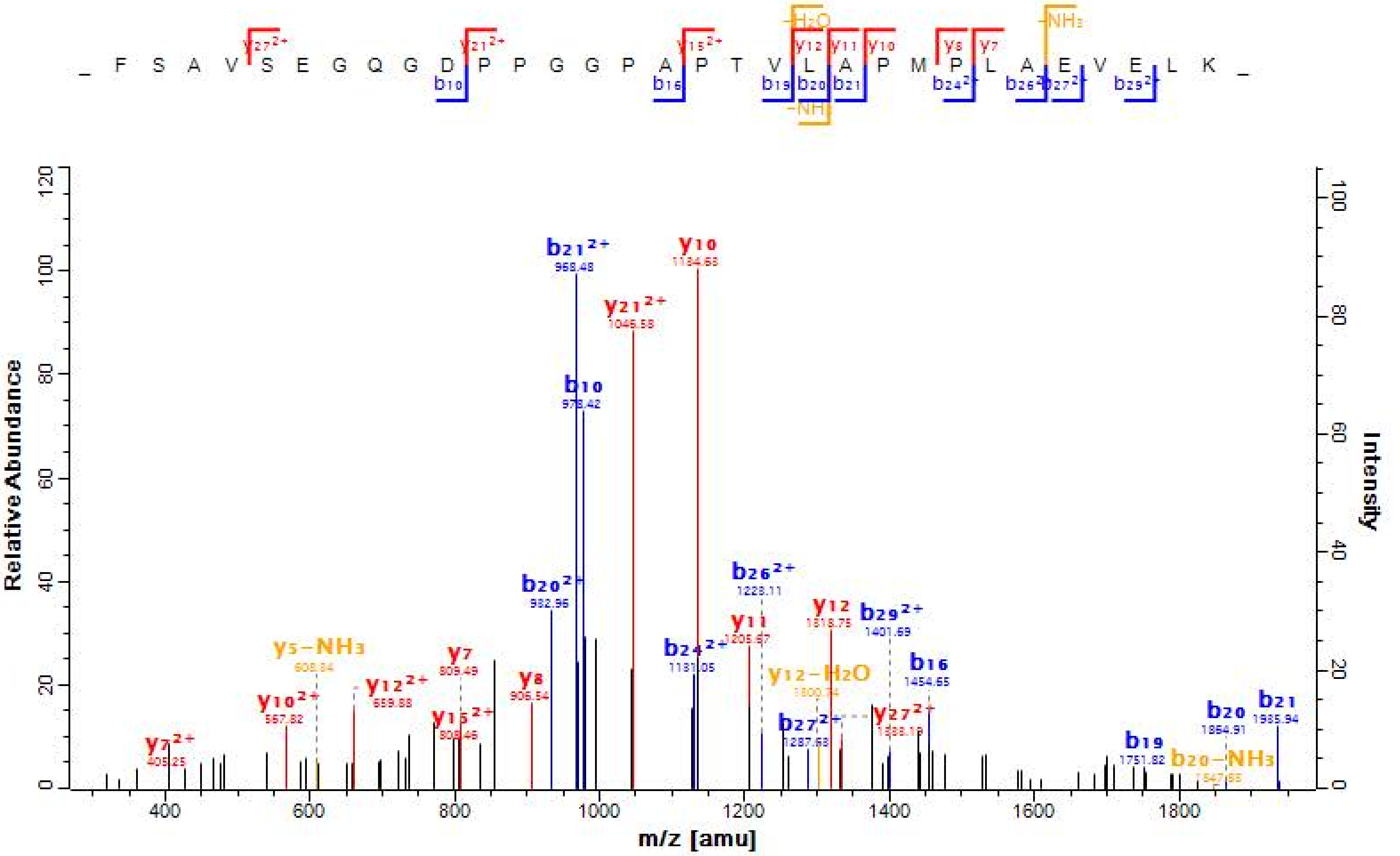
Mass:	2488.30652
m/z:	830.44278
Charge:	3+
Retentiontime:	52.763751983642
Score:	62.61666
Mass Error [ppm]:	0.17605
PEP:	0.00092432
Precursor Type:	MULTI

general information

Annotation:	12 of 22
AminoAcids Coverag	55 %
Intensity Coverage:	31 %
Peak Coverage:	21 %
Protein Localisation:	159 ... 180

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	21				
	171.11		171.11	2	V	20	2418.3		2418.3	
	284.2		284.2	3	L	19	2319.2		2319.2	
	412.26		412.26	4	Q	18	2206.1		2206.1	
	525.34	+0.2354	525.34	5	L	17	2078.1		2078.1	
	688.4	-0.134	688.4	6	Y	16	1965		982.99	+0.1923
	785.46		785.46	7	P	15	1801.9		901.46	+0.0414
	914.5		914.5	8	E	14	1704.9		1704.9	
	1028.5		1028.5	9	N	13	1575.8		1575.8	
	1115.6		1115.6	10	S	12	1461.8		1461.8	
	1244.6		1244.6	11	E	11	1374.7		1374.7	
	1372.7		1372.7	12	Q	10	1245.7		1245.7	
	1485.8		1485.8	13	L	9	1117.6		1117.6	
+0.1073	807.9	+0.1354	1614.8	14	E	8	1004.6		1004.6	
	1727.9		1727.9	15	L	7	875.52		875.52	
+0.4515	920.99	-0.097	1841	16	I	6	762.44		762.44	
+0.3354	971.51		1942	17	T	5	649.35	-0.059	649.35	
	2043.1		2043.1	18	T	4	548.3	-0.093	548.3	
	2171.1		2171.1	19	Q	3	447.26	+0.0267	447.26	
+0.0777	1121.6		2242.2	20	A	2	319.2	-0.079	319.2	
+0.2095	1172.1		2343.2	21	T	1	248.16	+0.2653	248.16	
				22	K	0	147.11		147.11	

Scan number	5987	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	78.75



precursor information

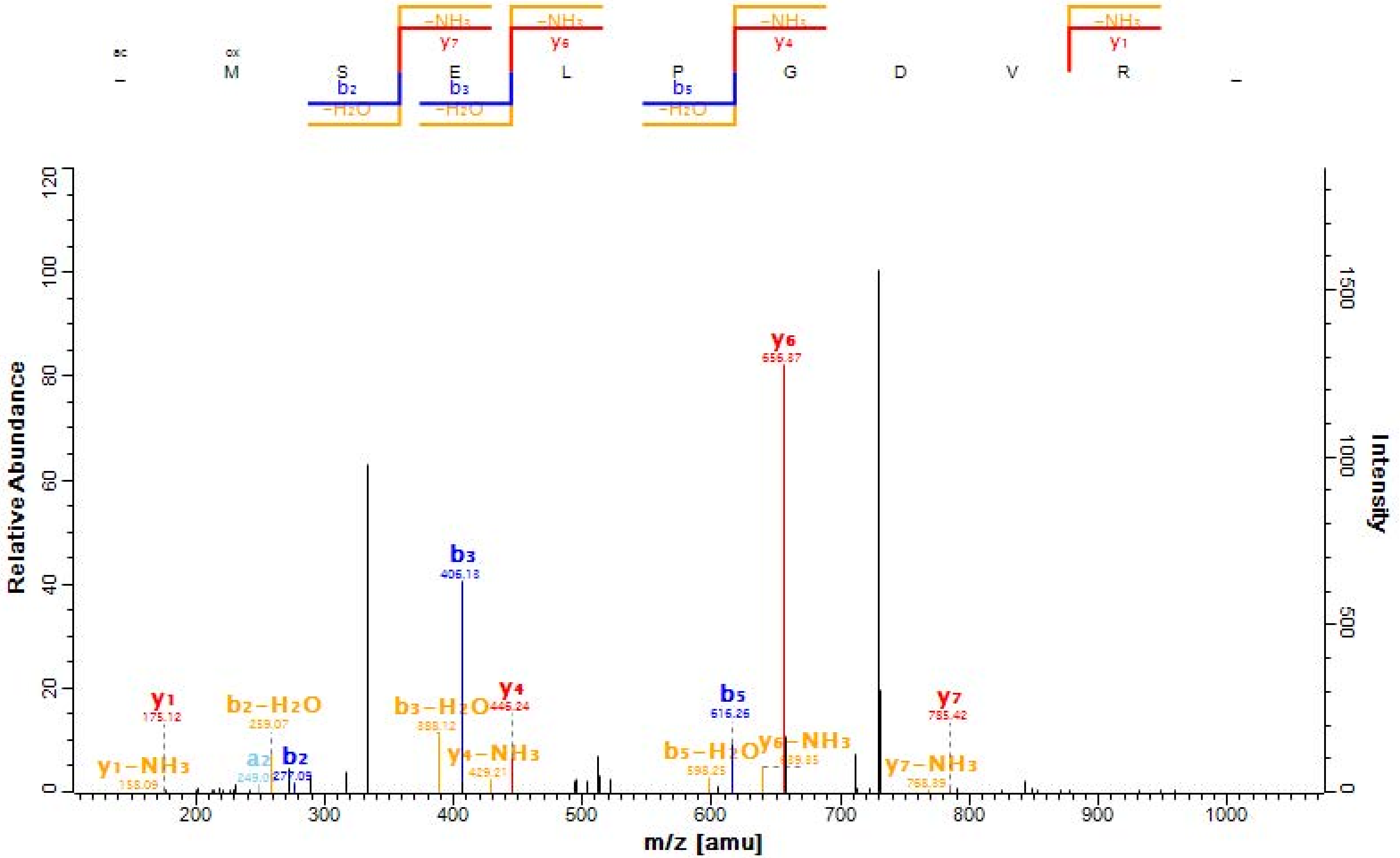
Mass:	3060.54831
m/z:	1021.19005
Charge:	3+
Retentiontime:	57.557941436767
Score:	78.75172
Mass Error [ppm]:	0.17003
PEP:	3.1813E-10
Precursor Type:	MULTI

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.08		148.08	1	F	30				
	235.11		235.11	2	S	29	2922.5		2922.5	
	306.14		306.14	3	A	28	2835.5		2835.5	
	405.21		405.21	4	V	27	2764.4		2764.4	
	492.25		492.25	5	S	26	2665.4		1333.2	-0.106
	621.29		621.29	6	E	25	2578.3		2578.3	
	678.31		678.31	7	G	24	2449.3		2449.3	
	806.37		806.37	8	Q	23	2392.3		2392.3	
	863.39		863.39	9	G	22	2264.2		2264.2	
	978.42	-0.01	978.42	10	D	21	2207.2		2207.2	
	1075.5		1075.5	11	P	20	2092.2		1046.6	+0.1095
	1172.5		1172.5	12	P	19	1995.1		1995.1	
	1229.5		1229.5	13	G	18	1898.1		1898.1	
	1286.6		1286.6	14	G	17	1841		1841	
	1383.6		1383.6	15	P	16	1784		1784	
	1454.7	+0.2024	1454.7	16	A	15	1687		1687	
	1551.7		1551.7	17	P	14	1615.9		808.46	-0.273
	1652.8		1652.8	18	T	13	1518.9		1518.9	
	1751.8	-0.363	1751.8	19	V	12	1417.8		1417.8	
+0.2939	932.96	-0.082	1864.9	20	L	11	1318.8	+0.0517	659.88	+0.1795
+0.1424	968.48	-0.129	1935.9	21	A	10	1205.7	+0.0449	1205.7	
	2033		2033	22	P	9	1134.6	+0.0112	567.82	-0.044
	2164		2164	23	M	8	1037.6		1037.6	
-0.484	1131		2261.1	24	P	7	906.54	+0.1945	906.54	
	2374.2		2374.2	25	L	6	809.49	-0.203	405.25	+0.2389
+0.2449	1223.1		2445.2	26	A	5	696.4		696.4	
+0.3804	1287.6		2574.3	27	E	4	625.36		625.36	
	2673.3		2673.3	28	V	3	496.32		496.32	
-0.048	1401.7		2802.4	29	E	2	397.25		397.25	
	2915.4		2915.4	30	L	1	268.21		268.21	
				31	K	0	155.13		155.13	

general information

Annotation:	16 of 31
AminoAcids Coverag	52 %
Intensity Coverage:	54 %
Peak Coverage:	27 %
Protein Localisation:	165 ... 195

Scan number	5992	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	87.64



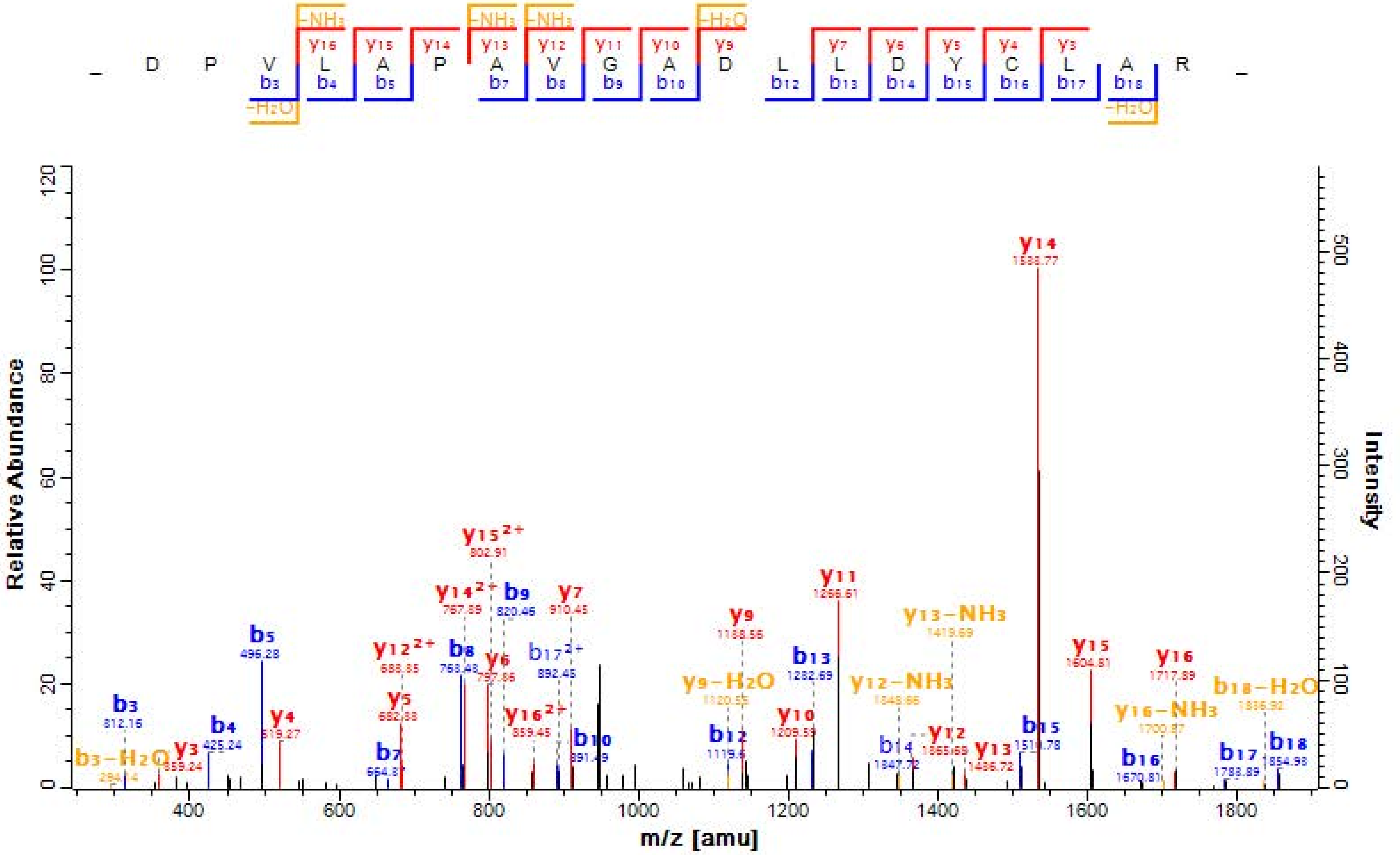
precursor information

g

Mass:	1060.48636
m/z:	531.25046
Charge:	2+
Retentiontime:	57.604183197021
Score:	87.6395
Mass Error [ppm]:	0.42595
PEP:	0.0032525
Precursor Type:	ISO
Annotation:	6 of 9
AminoAcids Coverag	67 %
Intensity Coverage:	40 %
Peak Coverage:	21 %
Protein Localisation:	1 ... 9

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	162.0583		190.0532	1	M	8		
+0.028329	249.0904	−0.02314	277.0853	2	S	7	872.4472	
	378.1329	+0.028449	406.1279	3	E	6	785.4152	+0.083036
	491.217		519.2119	4	L	5	656.3726	−0.01884
	588.2698	+0.145467	616.2647	5	P	4	543.2885	
	645.2912		673.2862	6	G	3	446.2358	+0.002875
	760.3182		788.3131	7	D	2	389.2143	
	859.3866		887.3815	8	V	1	274.1874	
				9	R	0	175.119	−0.09007

Scan number	6252	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	210.98



precursor information

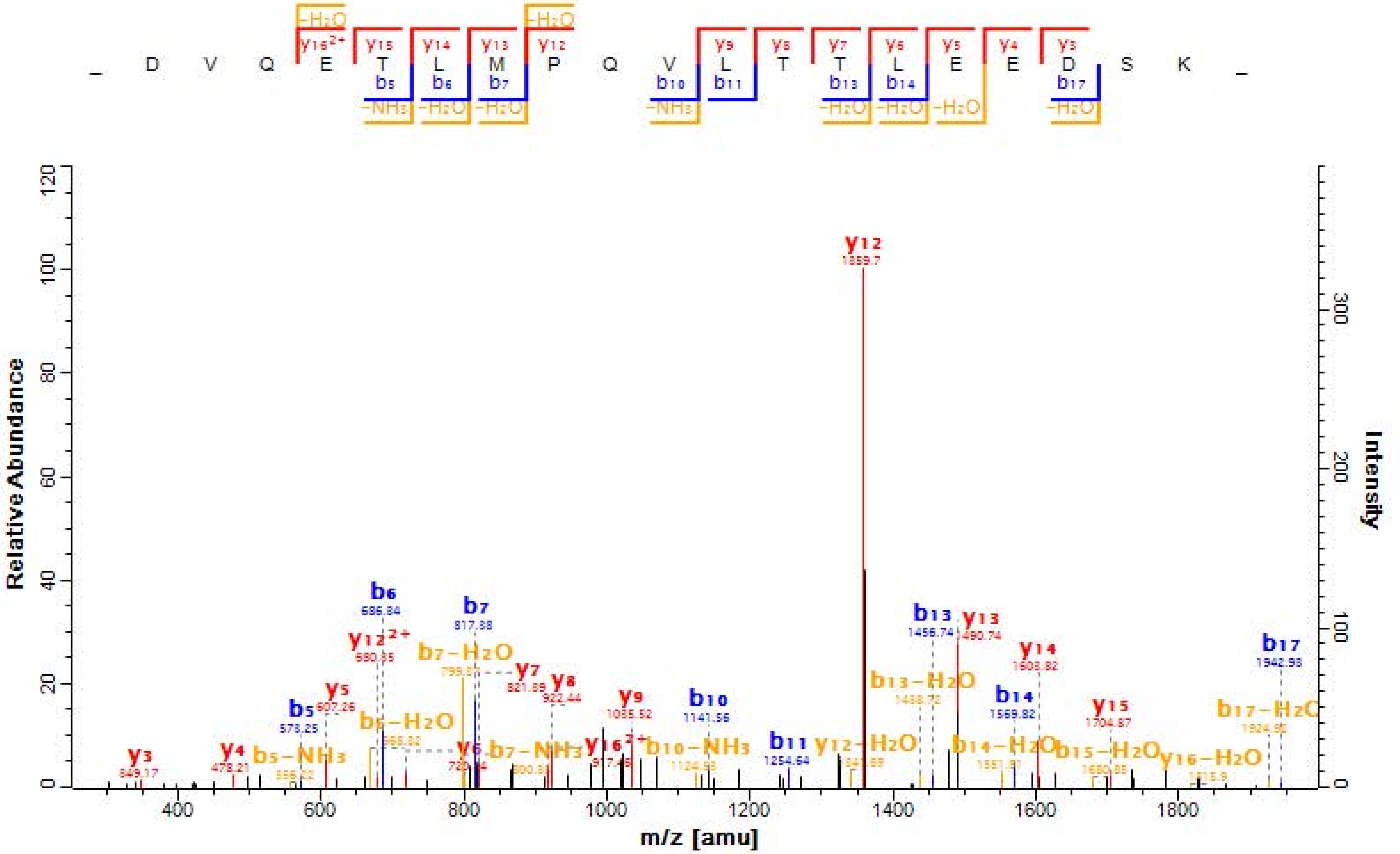
Mass:	2028.03368
m/z:	1015.02412
Charge:	2+
Retentiontime:	60.061389923095
Score:	210.9766
Mass Error [ppm]:	-0.6569
PEP:	5.0361E-49
Precursor Type:	MULTI

general information

Annotation:	16 of 19
AminoAcids Coverag	84 %
Intensity Coverage:	57 %
Peak Coverage:	39 %
Protein Localisation:	1207 ... 1225

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	18				
	213.09		213.09	2	P	17	1914		1914	
	312.16	-0.029	312.16	3	V	16	1817		1817	
	425.24	+0.0573	425.24	4	L	15	1717.9	-0.256	859.45	-0.03
	496.28	-0.037	496.28	5	A	14	1604.8	-0.091	802.91	+0.2345
	593.33		593.33	6	P	13	1533.8	-0.081	767.39	+0.2784
	664.37	+0.0091	664.37	7	A	12	1436.7	+0.0876	1436.7	
	763.43	-0.072	763.43	8	V	11	1365.7	+0.0452	683.35	+0.0117
	820.46	-0.045	820.46	9	G	10	1266.6	-0.028	1266.6	
	891.49	-0.079	891.49	10	A	9	1209.6	-0.007	1209.6	
	1006.5		1006.5	11	D	8	1138.6	-0.093	1138.6	
	1119.6	-0.266	1119.6	12	L	7	1023.5		1023.5	
	1232.7	-0.445	1232.7	13	L	6	910.45	-0.053	910.45	
	1347.7	+0.0671	1347.7	14	D	5	797.36	+0.0075	797.36	
	1510.8	-0.182	1510.8	15	Y	4	682.33	+0.0377	682.33	
	1670.8	+0.1394	1670.8	16	C	3	519.27	+0.0943	519.27	
+0.2145	892.45	-0.046	1783.9	17	L	2	359.24	+0.1561	359.24	
	1854.9	-0.287	1854.9	18	A	1	246.16		246.16	
				19	R	0	175.12		175.12	

Scan number	6587	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	156.39



precursor information

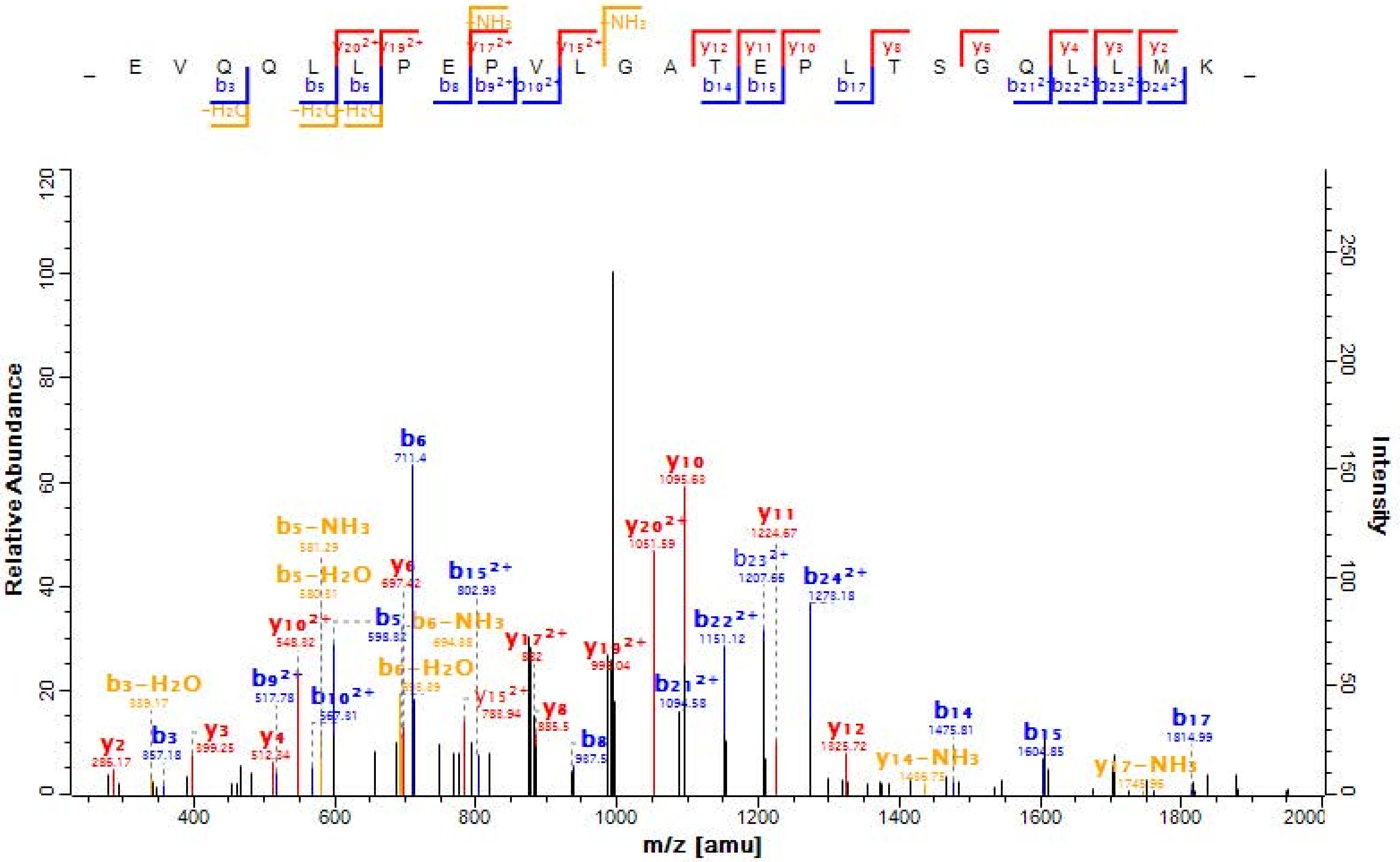
Mass:	2175.06144
m/z:	1088.538
Charge:	2+
Retentiontime:	63.106166839599
Score:	156.3896
Mass Error [ppm]:	-0.11101
PEP:	2.9907E-26
Precursor Type:	MULTI

general information

Annotation:	13 of 19
AminoAcids Coverag	68 %
Intensity Coverage:	56 %
Peak Coverage:	34 %
Protein Localisation:	697 ... 715

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342	1	D	18				
	215.1026	2	V	17	2061.042		2061.042	
	343.1612	3	Q	16	1961.974		1961.974	
	472.2038	4	E	15	1833.915		917.4611	-0.02121
+0.01634	573.2515	5	T	14	1704.872	-0.37695	1704.872	
+0.019068	686.3355	6	L	13	1603.825	-0.09062	1603.825	
-0.00274	817.376	7	M	12	1490.741	-0.14535	1490.741	
	914.4288	8	P	11	1359.7	-0.09168	680.3537	-0.06315
	1042.487	9	Q	10	1262.647		1262.647	
-0.1969	1141.556	10	V	9	1134.589		1134.589	
+0.015911	1254.64	11	L	8	1035.52	-0.01666	1035.52	
	1355.688	12	T	7	922.4364	+0.066791	922.4364	
-0.13047	1456.735	13	T	6	821.3887	+0.206755	821.3887	
-0.24029	1569.819	14	L	5	720.341	-0.01278	720.341	
	1698.862	15	E	4	607.257	+0.112301	607.257	
	1827.904	16	E	3	478.2144	+0.083666	478.2144	
+0.328731	1942.931	17	D	2	349.1718	+0.114723	349.1718	
	2029.963	18	S	1	234.1448		234.1448	
		19	K	0	147.1128		147.1128	

Scan number	6664	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	133.74



precursor information

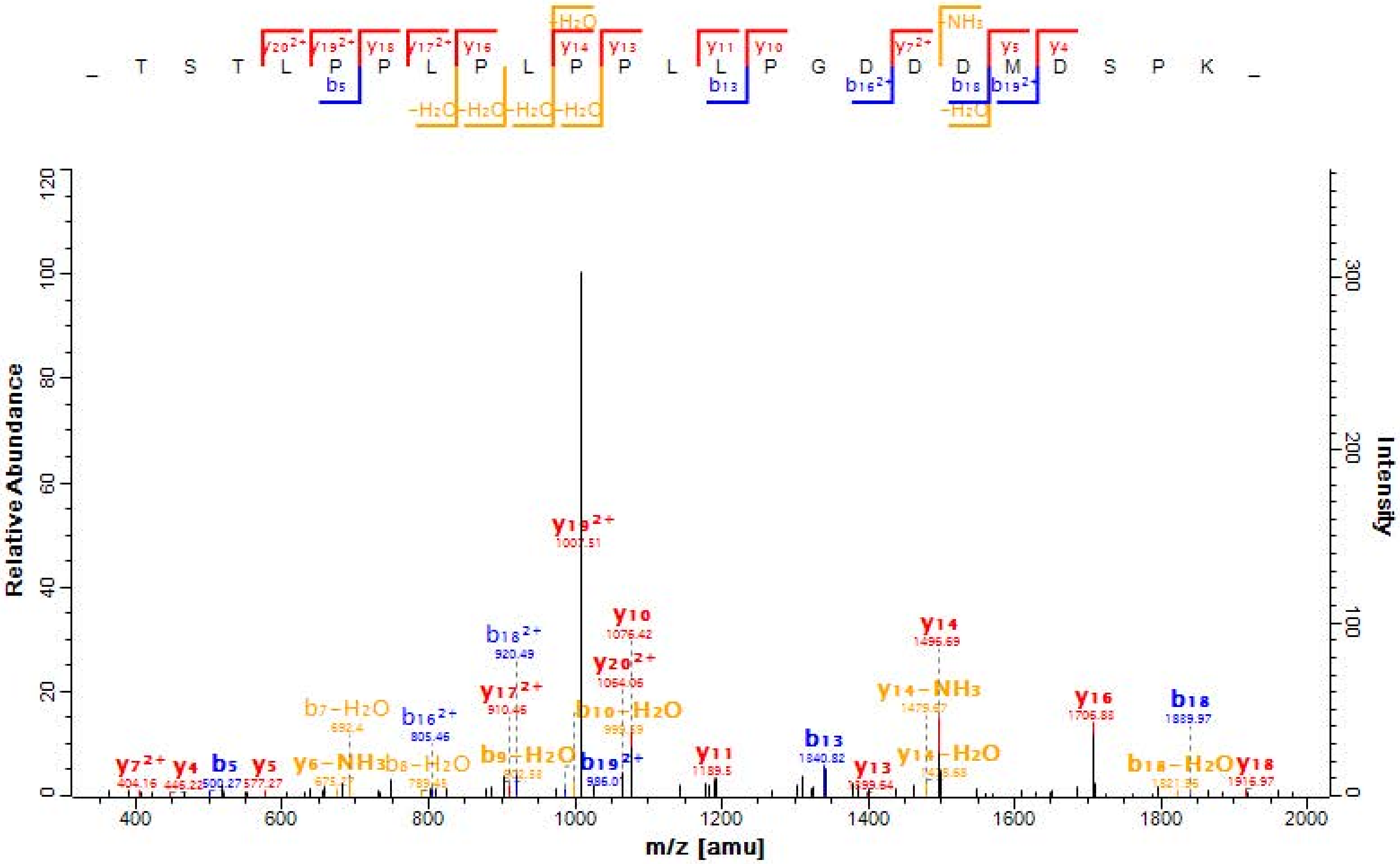
Mass:	2690.45597
m/z:	897.82593
Charge:	3+
Retentiontime:	63.856506347656
Score:	133.744
Mass Error [ppm]:	-0.17917
PEP:	5.4512E-17
Precursor Type:	MULTI

general information

Annotation:	20 of 25
AminoAcids Coverag	80 %
Intensity Coverage:	46 %
Peak Coverage:	31 %
Protein Localisation:	423 ... 447

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	24				
	229.12		229.12	2	V	23	2570.4		2570.4	
	357.18	+0.078	357.18	3	Q	22	2471.4		2471.4	
	485.24		485.24	4	Q	21	2343.3		2343.3	
	598.32	+0.0216	598.32	5	L	20	2215.2		2215.2	
	711.4	-0.088	711.4	6	L	19	2102.2		1051.6	+0.2414
	808.46		808.46	7	P	18	1989.1		995.04	-0.315
	937.5	+0.0108	937.5	8	E	17	1892		1892	
+0.4584	517.78		1034.6	9	P	16	1763		882	-0.121
+0.0042	567.31		1133.6	10	V	15	1665.9		1665.9	
	1246.7		1246.7	11	L	14	1566.9		783.94	+0.2417
	1303.7		1303.7	12	G	13	1453.8		1453.8	
	1374.8		1374.8	13	A	12	1396.8		1396.8	
	1475.8	+0.1606	1475.8	14	T	11	1325.7	-0.057	1325.7	
+0.2062	802.93	+0.0623	1604.9	15	E	10	1224.7	-0.159	1224.7	
	1701.9		1701.9	16	P	9	1095.6	+0.0062	548.32	+0.2774
	1815	-0.066	1815	17	L	8	998.58		998.58	
	1916		1916	18	T	7	885.5	+0.0388	885.5	
	2003.1		2003.1	19	S	6	784.45		784.45	
	2060.1		2060.1	20	G	5	697.42	+0.1377	697.42	
+0.3857	1094.6		2188.1	21	Q	4	640.39		640.39	
+0.22	1151.1		2301.2	22	L	3	512.34	-0.09	512.34	
+0.3347	1207.7		2414.3	23	L	2	399.25	-0.014	399.25	
+0.4163	1273.2		2545.4	24	M	1	286.17	+0.2143	286.17	
				25	K	0	155.13		155.13	

Scan number	6676	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	99.41



precursor information

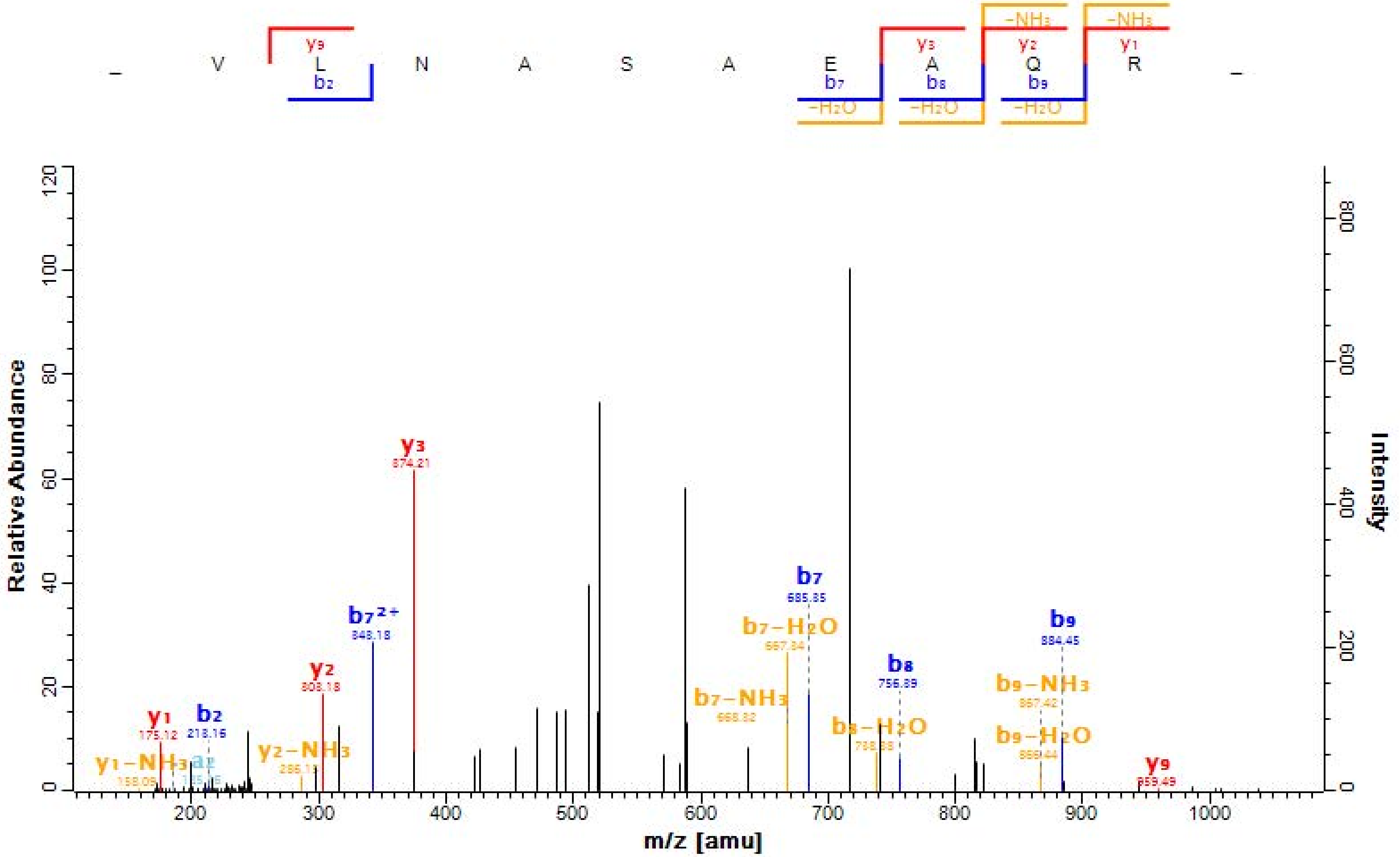
Mass:	2415.22341
m/z:	1208.61898
Charge:	2+
Retentiontime:	63.976642608642
Score:	99.4091
Mass Error [ppm]:	-0.38191
PEP:	5.25E-07
Precursor Type:	MULTI

general information

Annotation:	15 of 23
AminoAcids Coverag	65 %
Intensity Coverage:	37 %
Peak Coverage:	27 %
Protein Localisation:	624 ... 646

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	22				
	189.09		189.09	2	S	21	2315.2		2315.2	
	290.13		290.13	3	T	20	2228.2		2228.2	
	403.22		403.22	4	L	19	2127.1		1064.1	+0.318
	500.27	+0.0565	500.27	5	P	18	2014		1007.5	+0.023
	597.32		597.32	6	P	17	1917	-0.401	1917	
	710.41		710.41	7	L	16	1819.9		910.46	+0.1252
	807.46		807.46	8	P	15	1706.8	-0.101	1706.8	
	920.55		920.55	9	L	14	1609.8		1609.8	
	1017.6		1017.6	10	P	13	1496.7	-0.113	1496.7	
	1114.7		1114.7	11	P	12	1399.6	+0.0789	1399.6	
	1227.7		1227.7	12	L	11	1302.6		1302.6	
	1340.8	-0.021	1340.8	13	L	10	1189.5	+0.0537	1189.5	
	1437.9		1437.9	14	P	9	1076.4	+0.0203	1076.4	
	1494.9		1494.9	15	G	8	979.37		979.37	
-0.023	805.46		1609.9	16	D	7	922.35		922.35	
	1724.9		1724.9	17	D	6	807.32		404.16	+0.023
-0.14	920.49	+0.0425	1840	18	D	5	692.29		692.29	
+0.0239	986.01		1971	19	M	4	577.27	-0.011	577.27	
	2086		2086	20	D	3	446.22	-0.256	446.22	
	2173.1		2173.1	21	S	2	331.2		331.2	
	2270.1		2270.1	22	P	1	244.17		244.17	
				23	K	0	147.11		147.11	

Scan number	678	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	89.05

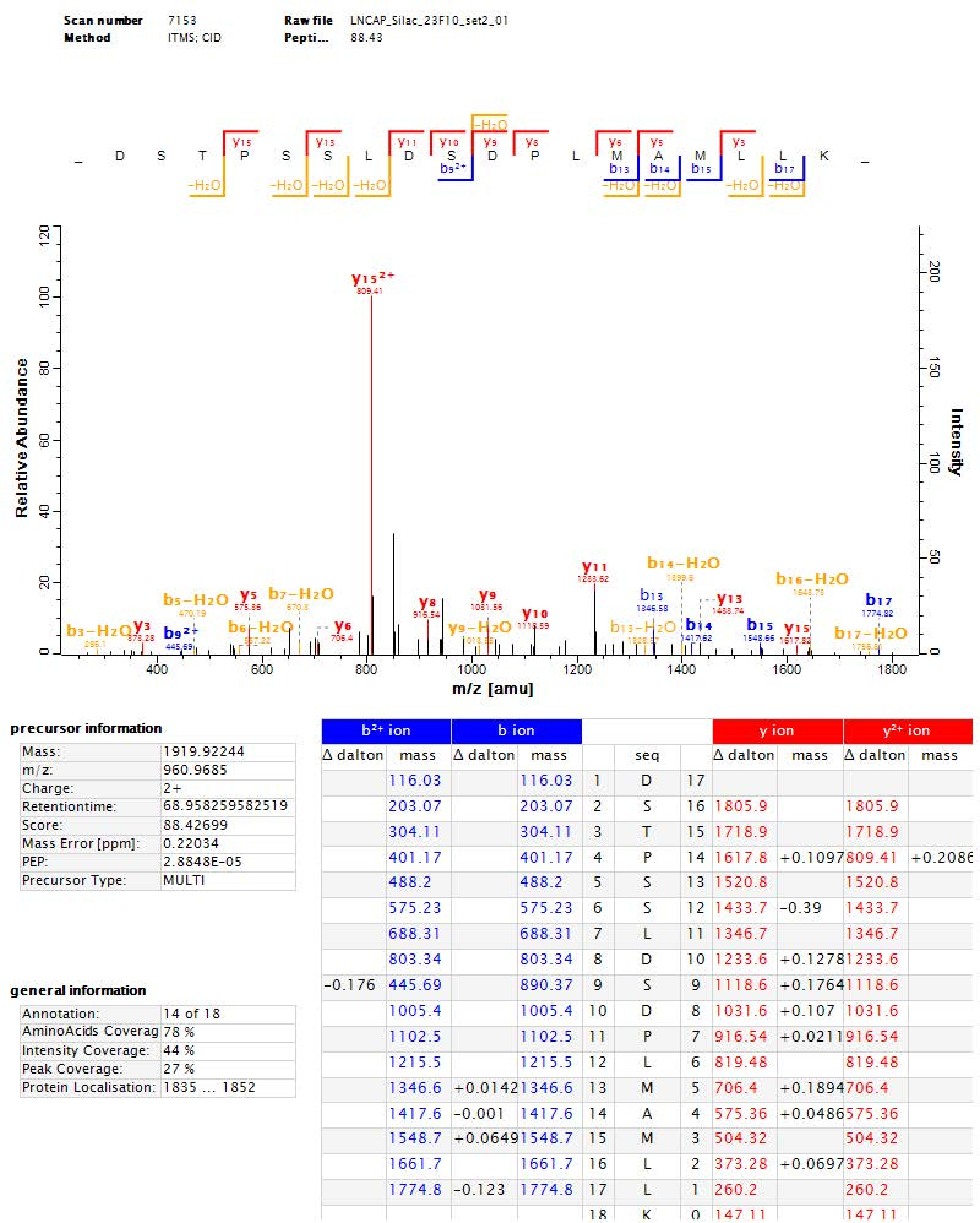


precursor information

Mass:	1057.55136
m/z:	529.78296
Charge:	2+
Retentiontime:	10.787036895752
Score:	89.04736
Mass Error [ppm]:	-0.24774
PEP:	0.0023227
Precursor Type:	MULTI

Annotation:	5 of 10
AminoAcids Coverag	50 %
Intensity Coverage:	28 %
Peak Coverage:	17 %
Protein Localisation:	143 ... 152

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	72.081		100.08		100.08	1	V	9		
-0.074	185.16		213.16	-0.068	213.16	2	L	8	959.49	-0.089
	299.21		327.2		327.2	3	N	7	846.41	
	370.24		398.24		398.24	4	A	6	732.36	
	457.28		485.27		485.27	5	S	5	661.33	
	528.31		556.31		556.31	6	A	4	574.29	
	657.36	-0.059	343.18	+0.0337	685.35	7	E	3	503.26	
	728.39		756.39	-0.135	756.39	8	A	2	374.21	+0.013
	856.45		884.45	+0.0282	884.45	9	Q	1	303.18	+0.0042
						10	R	0	175.12	+0.0725



Scan number	7153	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	88.43

precursor information

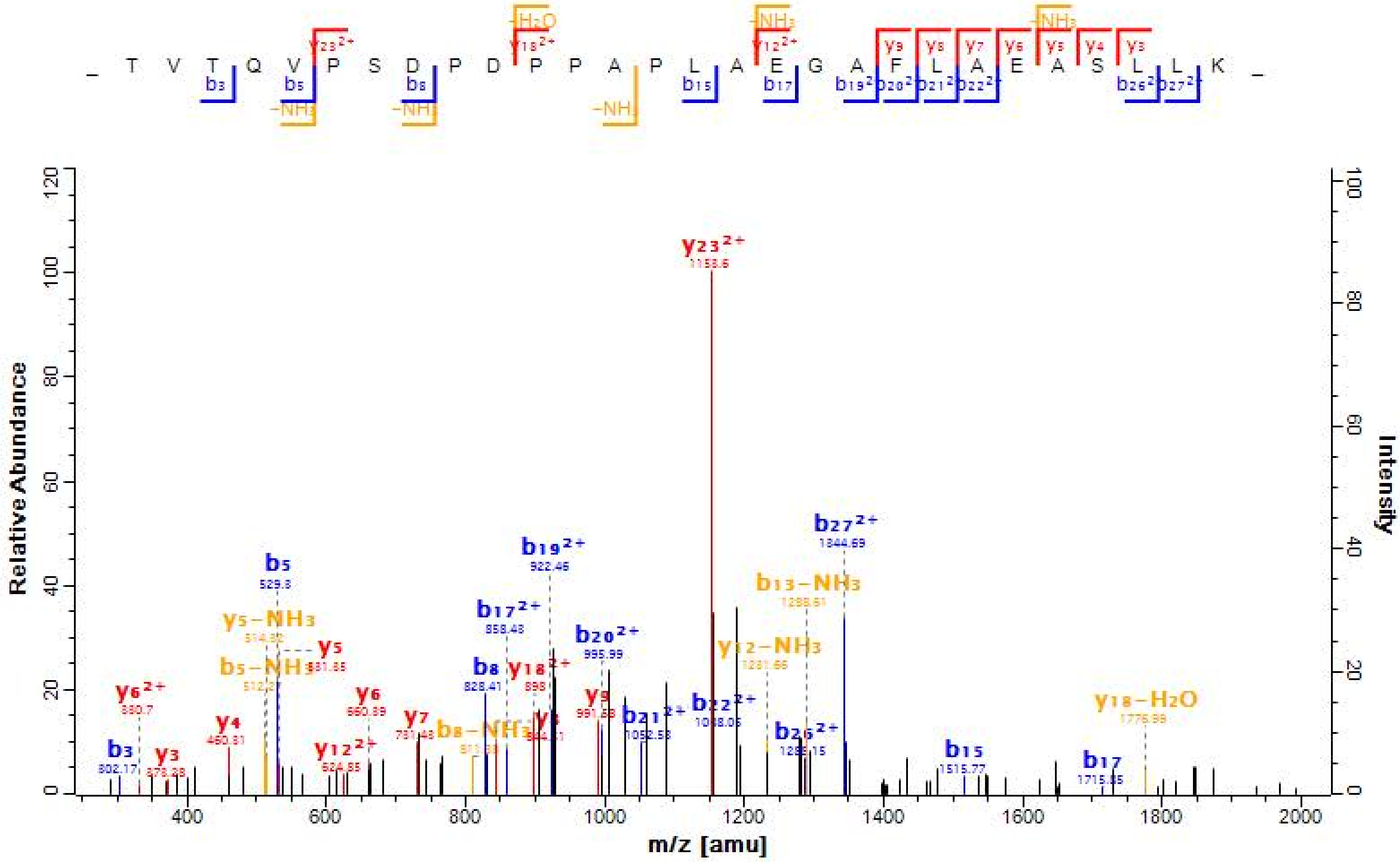
Mass:	1919.92244
m/z:	960.9685
Charge:	2+
Retentiontime:	68.958259582519
Score:	88.42699
Mass Error [ppm]:	0.22034
PEP:	2.8848E-05
Precursor Type:	MULTI

general information

Annotation:	14 of 18
AminoAcids Coverag	78 %
Intensity Coverage:	44 %
Peak Coverage:	27 %
Protein Localisation:	1835 ... 1852

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	17				
	203.07		203.07	2	S	16	1805.9		1805.9	
	304.11		304.11	3	T	15	1718.9		1718.9	
	401.17		401.17	4	P	14	1617.8	+0.1097	809.41	+0.2086
	488.2		488.2	5	S	13	1520.8		1520.8	
	575.23		575.23	6	S	12	1433.7	-0.39	1433.7	
	688.31		688.31	7	L	11	1346.7		1346.7	
	803.34		803.34	8	D	10	1233.6	+0.1278	1233.6	
-0.176	445.69		890.37	9	S	9	1118.6	+0.1764	1118.6	
	1005.4		1005.4	10	D	8	1031.6	+0.107	1031.6	
	1102.5		1102.5	11	P	7	916.54	+0.0211	916.54	
	1215.5		1215.5	12	L	6	819.48		819.48	
	1346.6	+0.0142	1346.6	13	M	5	706.4	+0.1894	706.4	
	1417.6	-0.001	1417.6	14	A	4	575.36	+0.0486	575.36	
	1548.7	+0.0649	1548.7	15	M	3	504.32		504.32	
	1661.7		1661.7	16	L	2	373.28	+0.0697	373.28	
	1774.8	-0.123	1774.8	17	L	1	260.2		260.2	
				18	K	0	147.11		147.11	

Scan number	7337	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	86.62



precursor information

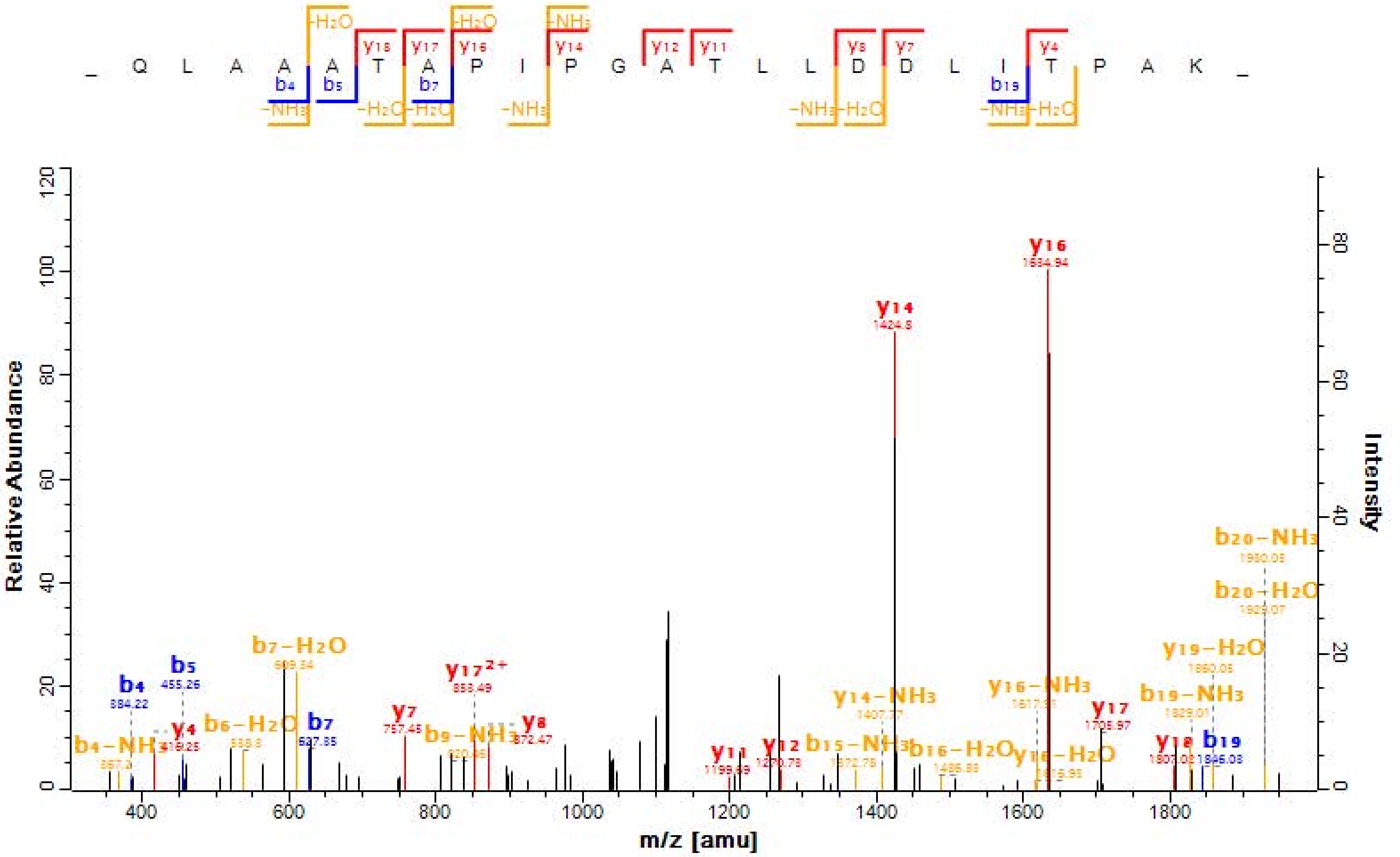
Mass:	2833.47582
m/z:	945.49922
Charge:	3+
Retentiontime:	71.060409545898
Score:	86.61732
Mass Error [ppm]:	0.30973
PEP:	3.6757E-10
Precursor Type:	MULTI

general information

Annotation:	18 of 28
AminoAcids Coverag	64 %
Intensity Coverage:	41 %
Peak Coverage:	28 %
Protein Localisation:	345 ... 372

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	27				
	201.12		201.12	2	V	26	2733.4		2733.4	
	302.17	+0.2901	302.17	3	T	25	2634.4		2634.4	
	430.23		430.23	4	Q	24	2533.3		2533.3	
	529.3	+0.0688	529.3	5	V	23	2405.3		2405.3	
	626.35		626.35	6	P	22	2306.2		1153.6	+0.0801
	713.38		713.38	7	S	21	2209.1		2209.1	
	828.41	+0	828.41	8	D	20	2122.1		2122.1	
	925.46		925.46	9	P	19	2007.1		2007.1	
	1040.5		1040.5	10	D	18	1910		1910	
	1137.5		1137.5	11	P	17	1795		898	-0.146
	1234.6		1234.6	12	P	16	1697.9		1697.9	
	1305.6		1305.6	13	A	15	1600.9		1600.9	
	1402.7		1402.7	14	P	14	1529.9		1529.9	
	1515.8	+0.3183	1515.8	15	L	13	1432.8		1432.8	
	1586.8		1586.8	16	A	12	1319.7		1319.7	
-0.136	858.43	-0.412	1715.8	17	E	11	1248.7		624.85	+0.3116
	1772.9		1772.9	18	G	10	1119.6		1119.6	
+0.1656	922.46		1843.9	19	A	9	1062.6		1062.6	
-0.112	995.99		1991	20	F	8	991.58	+0.148	991.58	
+0.3909	1052.5		2104.1	21	L	7	844.51	+0.0374	844.51	
+0.0405	1088.1		2175.1	22	A	6	731.43	+0.0439	731.43	
	2304.1		2304.1	23	E	5	660.39	+0.1839	330.7	-0.261
	2375.2		2375.2	24	A	4	531.35	+0.0783	531.35	
	2462.2		2462.2	25	S	3	460.31	+0.0226	460.31	
-0.017	1288.1		2575.3	26	L	2	373.28	-0.434	373.28	
-0.133	1344.7		2688.4	27	L	1	260.2		260.2	
				28	K	0	147.11		147.11	

Scan number	7475	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	68.29



precursor information

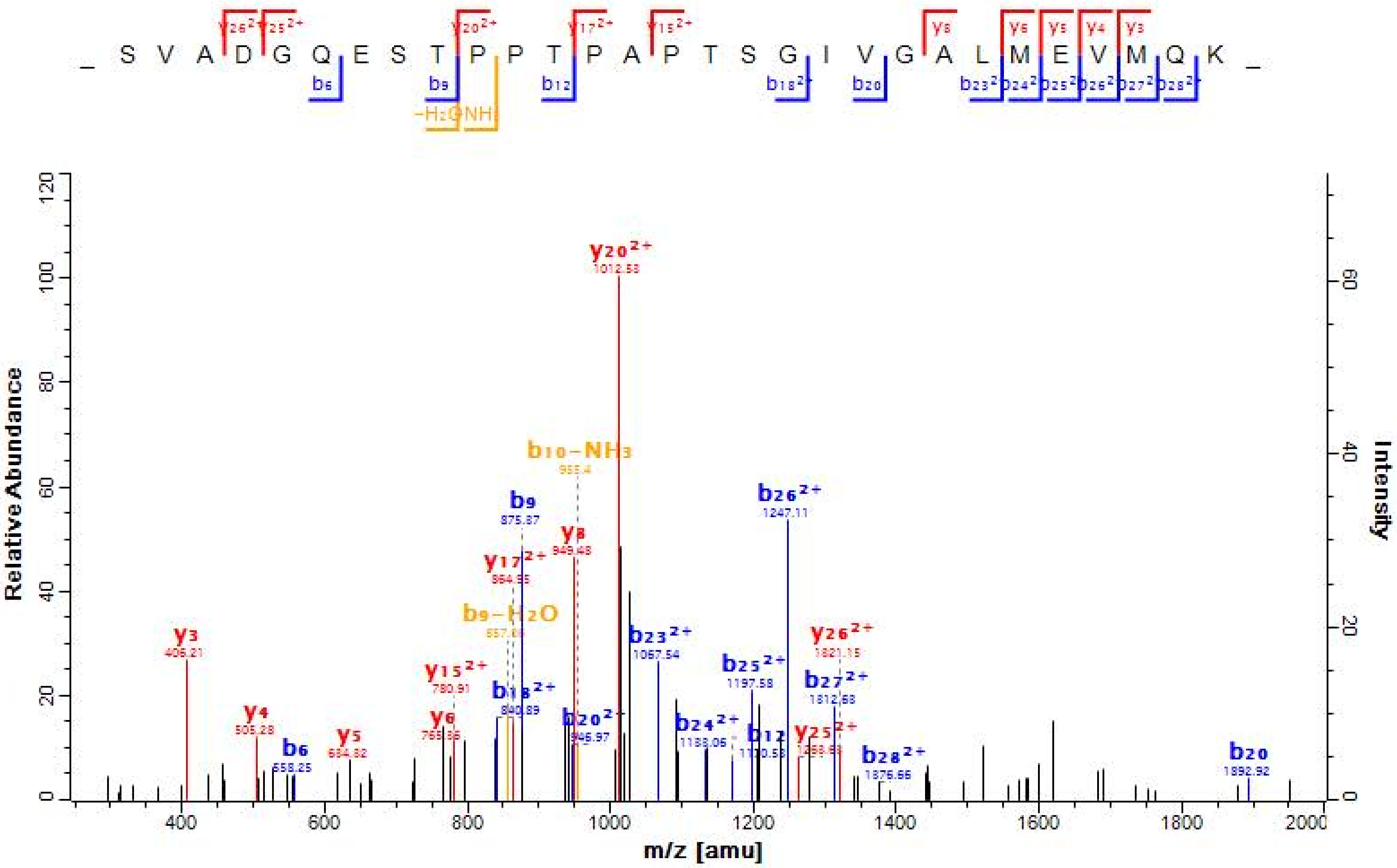
Mass:	2260.26831
m/z:	1131.14143
Charge:	2+
Retentiontime:	72.691169738769
Score:	68.29145
Mass Error [ppm]:	0.20424
PEP:	0.00021451
Precursor Type:	MULTI

general information

Annotation:	14 of 23
AminoAcids Coverag	61 %
Intensity Coverage:	38 %
Peak Coverage:	30 %
Protein Localisation:	130 ... 152

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.0659	1	Q	22				
	242.1499	2	L	21	2133.217		2133.217	
	313.187	3	A	20	2020.132		2020.132	
-0.27108	384.2241	4	A	19	1949.095		1949.095	
+0.026338	455.2613	5	A	18	1878.058		1878.058	
	556.3089	6	T	17	1807.021	-0.34939	1807.021	
-0.23094	627.3461	7	A	16	1705.973	+0.024705	853.4904	+0.006334
	724.3988	8	P	15	1634.936	-0.1573	1634.936	
	837.4829	9	I	14	1537.884		1537.884	
	934.5356	10	P	13	1424.8	-0.01498	1424.8	
	991.5571	11	G	12	1327.747		1327.747	
	1062.594	12	A	11	1270.725	+0.098192	1270.725	
	1163.642	13	T	10	1199.688	+0.354178	1199.688	
	1276.726	14	L	9	1098.641		1098.641	
	1389.81	15	L	8	985.5564		985.5564	
	1504.837	16	D	7	872.4724	+0.449134	872.4724	
	1619.864	17	D	6	757.4454	+0.03107	757.4454	
	1732.948	18	L	5	642.4185		642.4185	
-0.19098	1846.032	19	I	4	529.3344		529.3344	
	1947.08	20	T	3	416.2504	+0.187994	416.2504	
	2044.132	21	P	2	315.2027		315.2027	
	2115.17	22	A	1	218.1499		218.1499	
		23	K	0	147.1128		147.1128	

Scan number	7704	**Raw file**	LNCAP_Silac_23F10_set2_01
Method	ITMS; CID	**Pepti...**	72.93



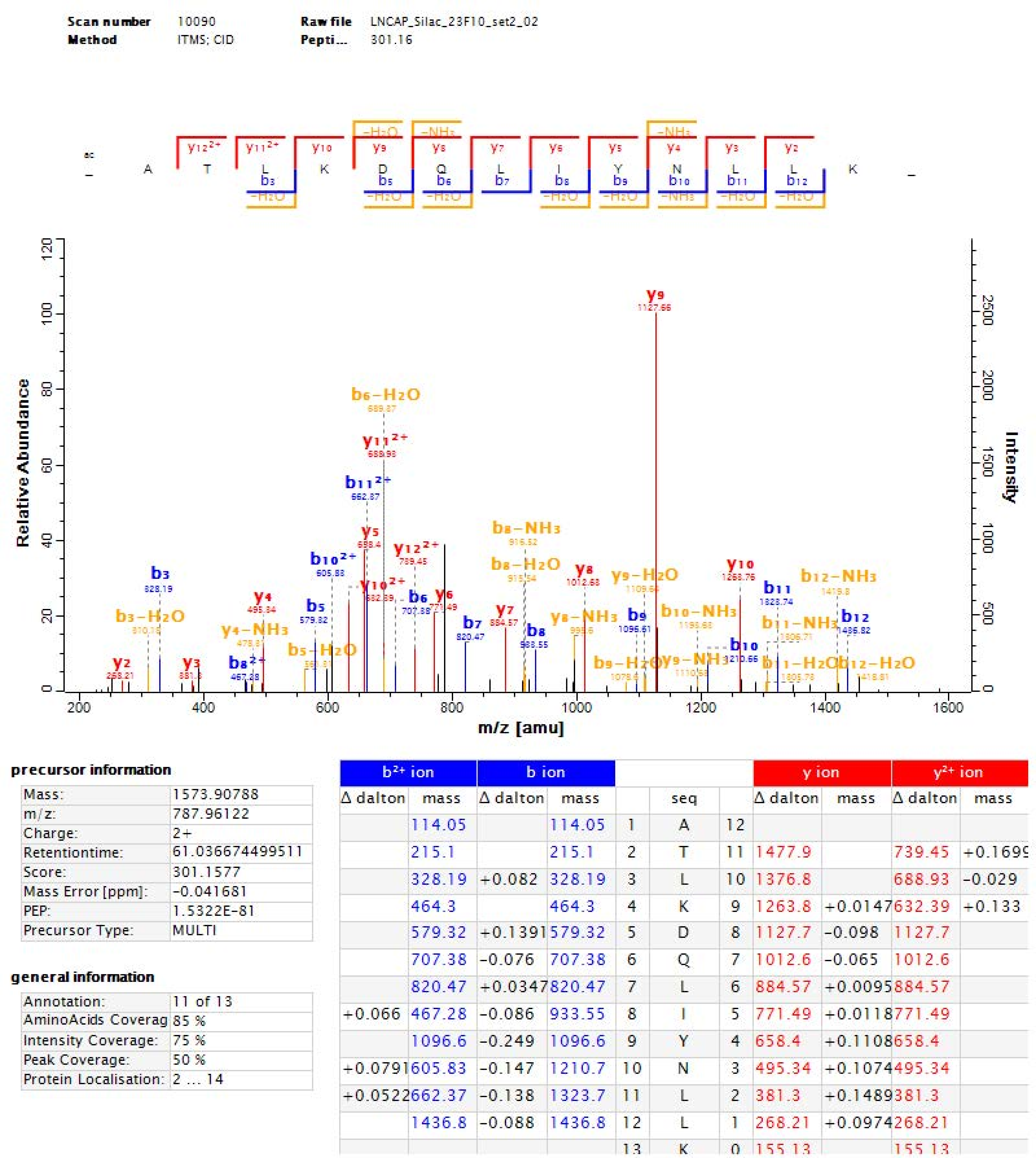
precursor information

Mass:	2897.41488
m/z:	966.81224
Charge:	3+
Retentiontime:	76.022361755371
Score:	72.93469
Mass Error [ppm]:	-0.063429
PEP:	6.7434E-09
Precursor Type:	MULTI

general information

Annotation:	18 of 29
AminoAcids Coverag	62 %
Intensity Coverage:	48 %
Peak Coverage:	26 %
Protein Localisation:	449 ... 477

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	28				
	187.11		187.11	2	V	27	2811.4		2811.4	
	258.14		258.14	3	A	26	2712.3		2712.3	
	373.17		373.17	4	D	25	2641.3		1321.1	-0.099
	430.19		430.19	5	G	24	2526.3		1263.6	-0.036
	558.25	-0.237	558.25	6	Q	23	2469.2		2469.2	
	687.29		687.29	7	E	22	2341.2		2341.2	
	774.33		774.33	8	S	21	2212.1		2212.1	
	875.37	+0.0793	875.37	9	T	20	2125.1		2125.1	
	972.43		972.43	10	P	19	2024.1		1012.5	+0.2786
	1069.5		1069.5	11	P	18	1927		1927	
	1170.5	-0.27	1170.5	12	T	17	1829.9		1829.9	
	1267.6		1267.6	13	P	16	1728.9		864.95	+0.0265
	1338.6		1338.6	14	A	15	1631.8		1631.8	
	1435.7		1435.7	15	P	14	1560.8		780.91	+0.1317
	1536.7		1536.7	16	T	13	1463.8		1463.8	
	1623.7		1623.7	17	S	12	1362.7		1362.7	
-0.272	840.89		1680.8	18	G	11	1275.7		1275.7	
	1793.9		1793.9	19	I	10	1218.7		1218.7	
-0.087	946.97	-0.174	1892.9	20	V	9	1105.6		1105.6	
	1949.9		1949.9	21	G	8	1006.5		1006.5	
	2021		2021	22	A	7	949.48	-0.488	949.48	
-0.272	1067.5		2134.1	23	L	6	878.45		878.45	
-0.029	1133.1		2265.1	24	M	5	765.36	-0.131	765.36	
-0.154	1197.6		2394.1	25	E	4	634.32	+0.1384	634.32	
+0.2664	1247.1		2493.2	26	V	3	505.28	+0.0368	505.28	
-0.148	1312.6		2624.3	27	M	2	406.21	+0.1625	406.21	
-0.137	1376.7		2752.3	28	Q	1	275.17		275.17	
				29	K	0	147.11		147.11	



Scan number	10090	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	301.16

precursor information

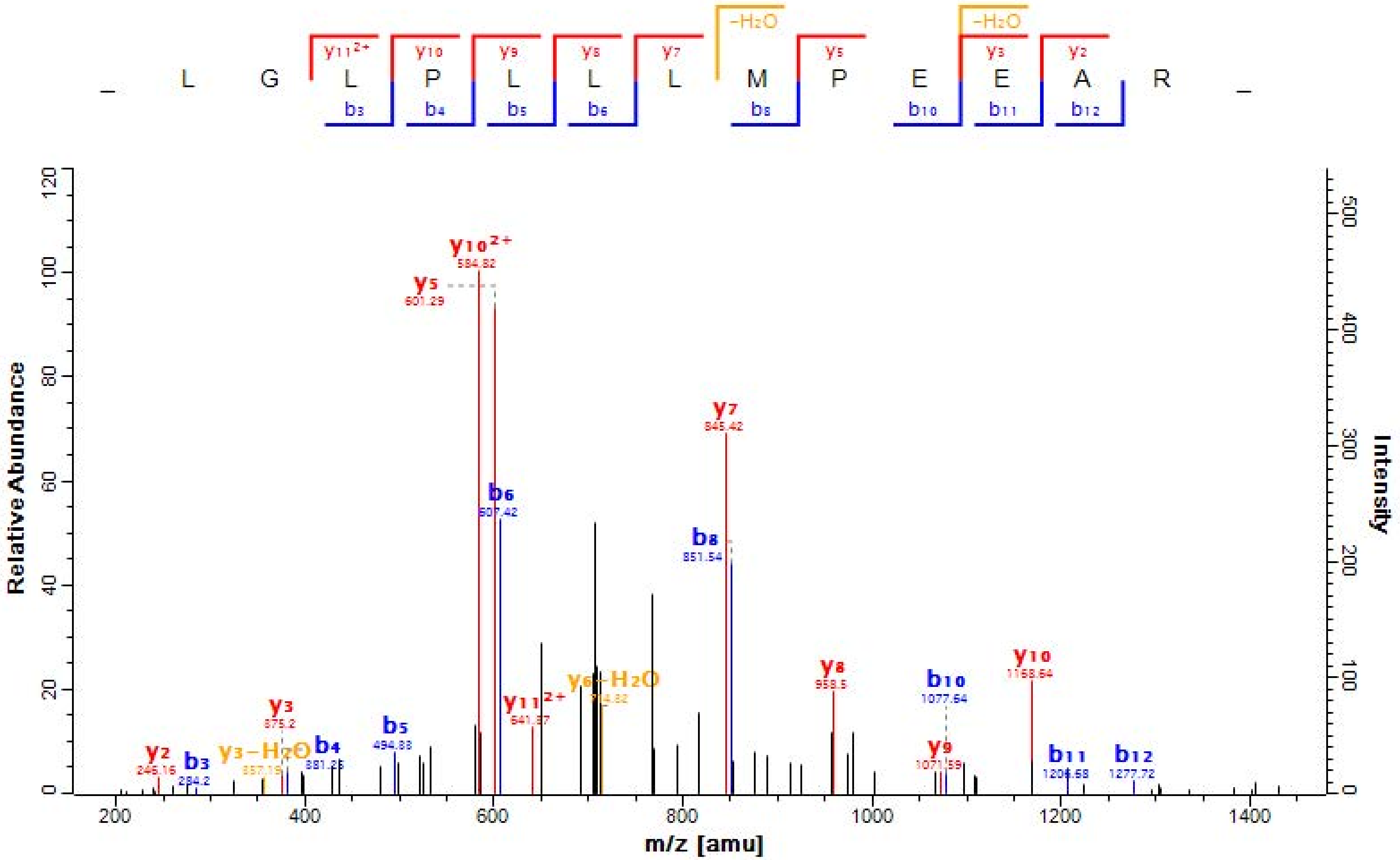
Mass:	1573.90788
m/z:	787.96122
Charge:	2+
Retentiontime:	61.036674499511
Score:	301.1577
Mass Error [ppm]:	-0.041681
PEP:	1.5322E-81
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	75 %
Peak Coverage:	50 %
Protein Localisation:	2 ... 14

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.05		114.05	1	A	12				
	215.1		215.1	2	T	11	1477.9		739.45	+0.1699
	328.19	+0.082	328.19	3	L	10	1376.8		688.93	-0.029
	464.3		464.3	4	K	9	1263.8	+0.0147	632.39	+0.133
	579.32	+0.1391	579.32	5	D	8	1127.7	-0.098	1127.7	
	707.38	-0.076	707.38	6	Q	7	1012.6	-0.065	1012.6	
	820.47	+0.0347	820.47	7	L	6	884.57	+0.0095	884.57	
+0.066	467.28	-0.086	933.55	8	I	5	771.49	+0.0118	771.49	
	1096.6	-0.249	1096.6	9	Y	4	658.4	+0.1108	658.4	
+0.0791	605.83	-0.147	1210.7	10	N	3	495.34	+0.1074	495.34	
+0.0522	662.37	-0.138	1323.7	11	L	2	381.3	+0.1489	381.3	
	1436.8	-0.088	1436.8	12	L	1	268.21	+0.0974	268.21	
				13	K	0	155.13		155.13	

Scan number	10471	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	101.89



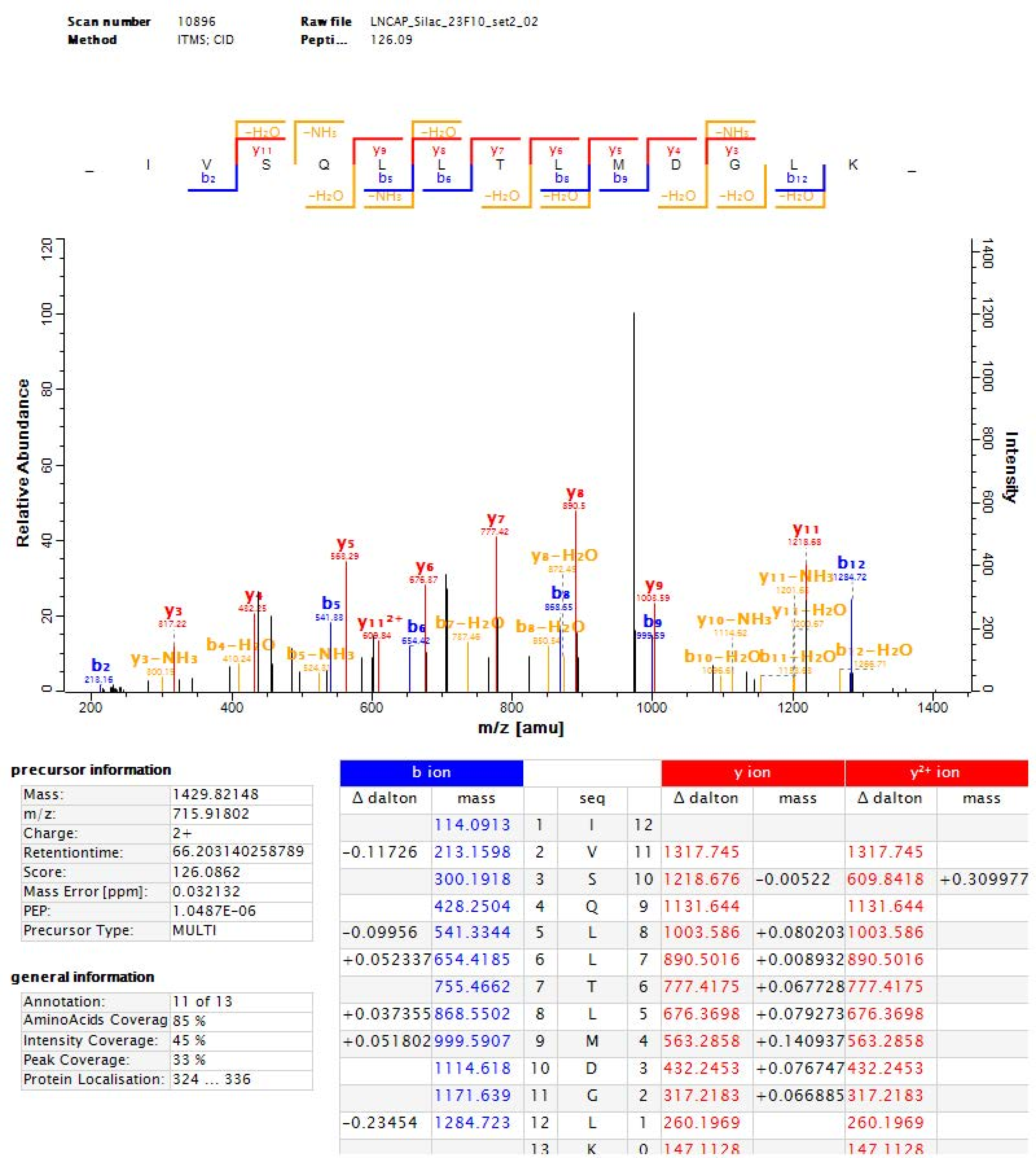
precursor information

Mass:	1450.82207
m/z:	726.41831
Charge:	2+
Retentiontime:	63.416202545166
Score:	101.8882
Mass Error [ppm]:	0.20799
PEP:	3.6499E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	52 %
Peak Coverage:	25 %
Protein Localisation:	46 ... 58

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	12				
	171.1128	2	G	11	1338.745		1338.745	
-0.00278	284.1969	3	L	10	1281.724		641.3654	+0.159382
-0.09021	381.2496	4	P	9	1168.639	+0.043405	584.8234	+0.056211
+0.047896	494.3337	5	L	8	1071.587	+0.122048	1071.587	
-0.01914	607.4178	6	L	7	958.5026	-0.09858	958.5026	
	720.5018	7	L	6	845.4186	-0.04723	845.4186	
-0.04121	851.5423	8	M	5	732.3345		732.3345	
	948.5951	9	P	4	601.294	+0.13323	601.294	
-0.06748	1077.638	10	E	3	504.2413		504.2413	
+0.275918	1206.68	11	E	2	375.1987	+0.188121	375.1987	
-0.1036	1277.717	12	A	1	246.1561	-0.00857	246.1561	
		13	R	0	175.119		175.119	



Scan number	10896	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	126.09

precursor information

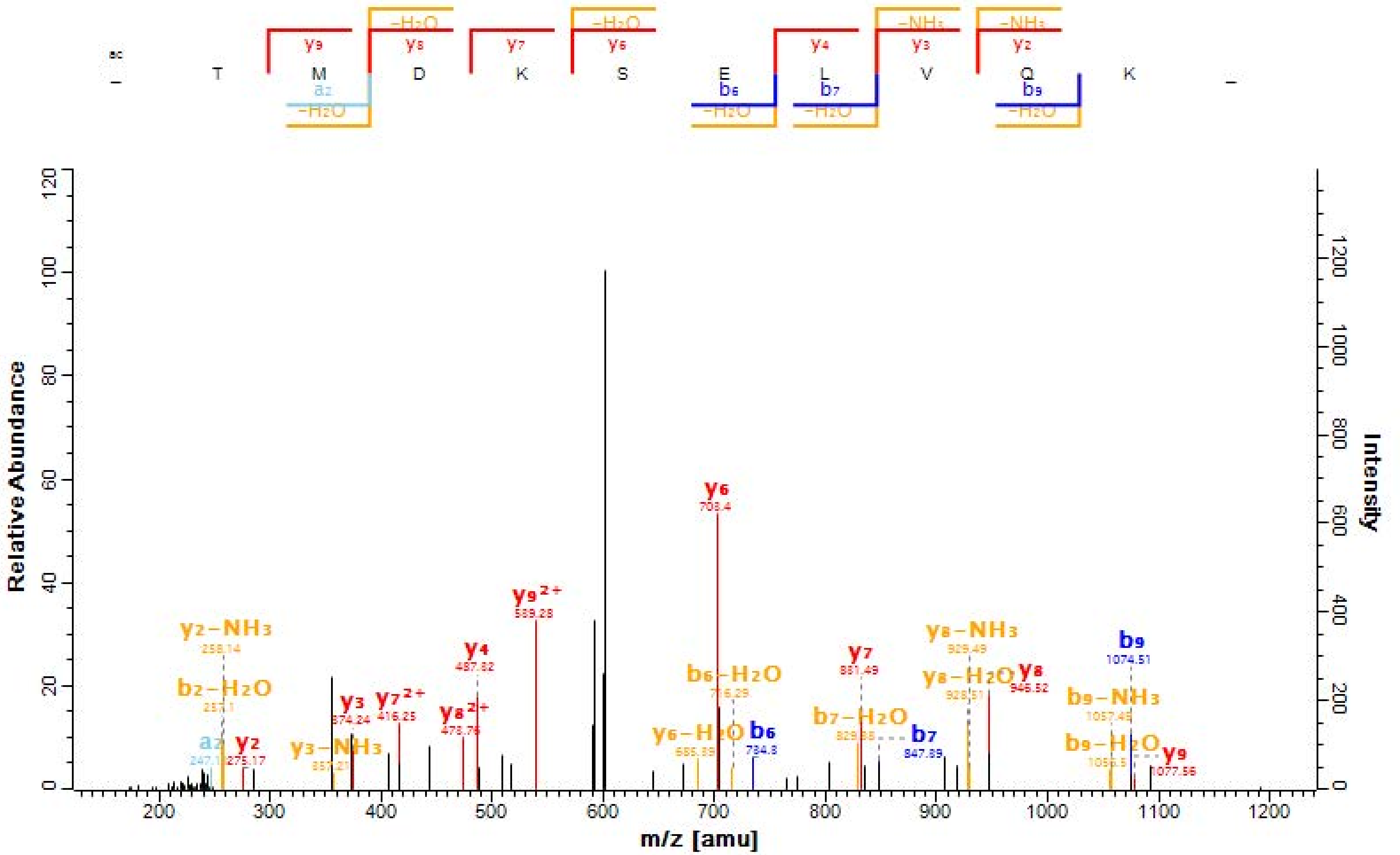
Mass:	1429.82148
m/z:	715.91802
Charge:	2+
Retentiontime:	66.203140258789
Score:	126.0862
Mass Error [ppm]:	0.032132
PEP:	1.0487E-06
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	45 %
Peak Coverage:	33 %
Protein Localisation:	324 ... 336

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	I	12				
-0.11726	213.1598	2	V	11	1317.745		1317.745	
	300.1918	3	S	10	1218.676	-0.00522	609.8418	+0.309977
	428.2504	4	Q	9	1131.644		1131.644	
-0.09956	541.3344	5	L	8	1003.586	+0.080203	1003.586	
+0.052337	654.4185	6	L	7	890.5016	+0.008932	890.5016	
	755.4662	7	T	6	777.4175	+0.067728	777.4175	
+0.037355	868.5502	8	L	5	676.3698	+0.079273	676.3698	
+0.051802	999.5907	9	M	4	563.2858	+0.140937	563.2858	
	1114.618	10	D	3	432.2453	+0.076747	432.2453	
	1171.639	11	G	2	317.2183	+0.066885	317.2183	
-0.23454	1284.723	12	L	1	260.1969		260.1969	
		13	K	0	147.1128		147.1128	

Scan number	1092	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	169.93



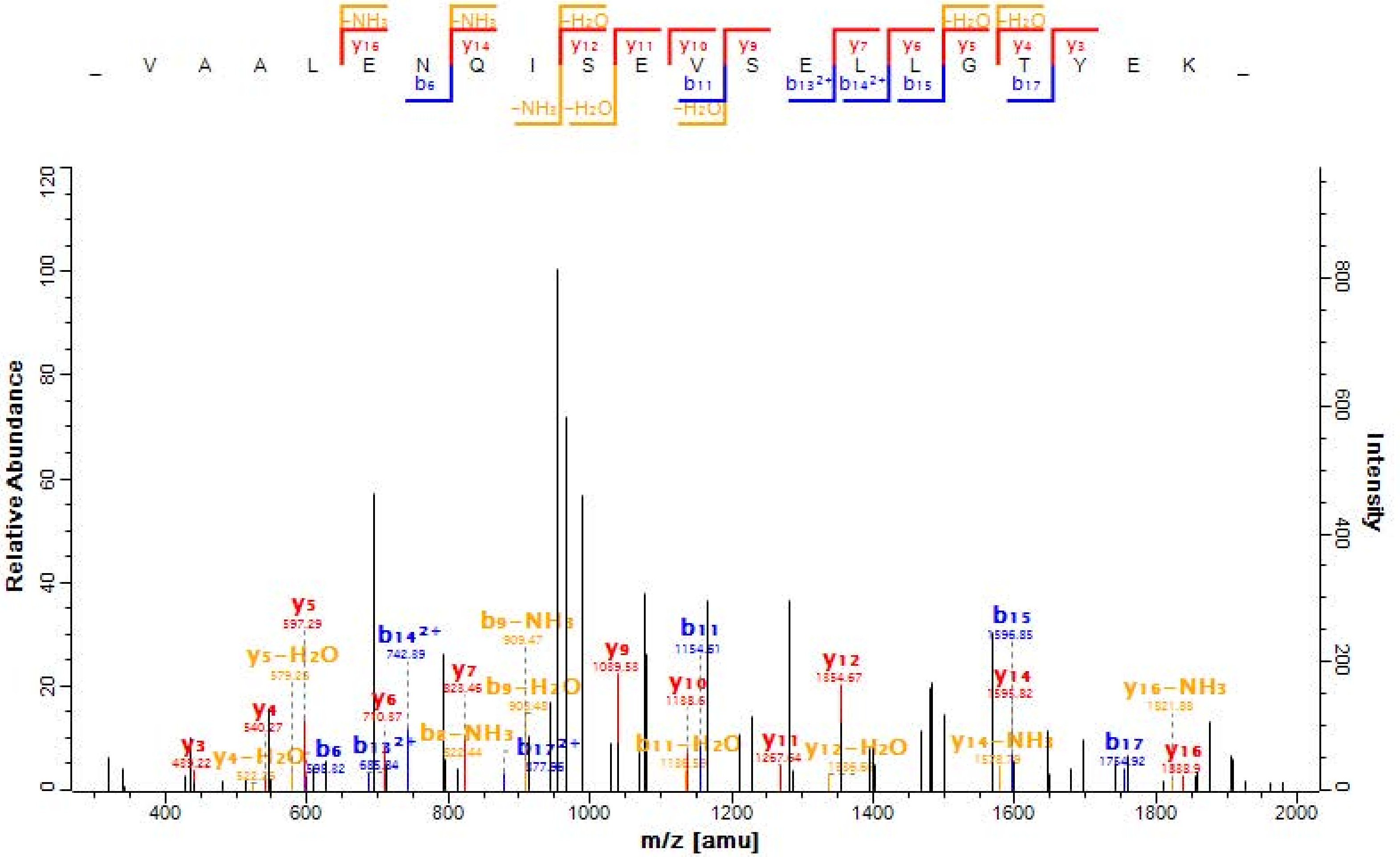
precursor information

Mass:	1219.61227
m/z:	610.81341
Charge:	2+
Retentiontime:	12.752985000610
Score:	169.9348
Mass Error [ppm]:	0.35356
PEP:	2.4315E-05
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	43 %
Peak Coverage:	27 %
Protein Localisation:	2 ... 11

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.07		144.07	1	T	9				
+0.0284	247.11		275.11	2	M	8	1077.6	+0.143	539.28	+0.1022
	362.14		390.13	3	D	7	946.52	-0.03	473.76	+0.1191
	490.23		518.23	4	K	6	831.49	-0.013	416.25	+0.0503
	577.27		605.26	5	S	5	703.4	-0.042	703.4	
	706.31	+0.0827	734.3	6	E	4	616.37		616.37	
	819.39	+0.1313	847.39	7	L	3	487.32	+0.0121	487.32	
	918.46		946.46	8	V	2	374.24	+0.0363	374.24	
	1046.5	+0.0748	1074.5	9	Q	1	275.17	+0.01	275.17	
				10	K	0	147.11		147.11	

Scan number	11116	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	87.55



precursor information

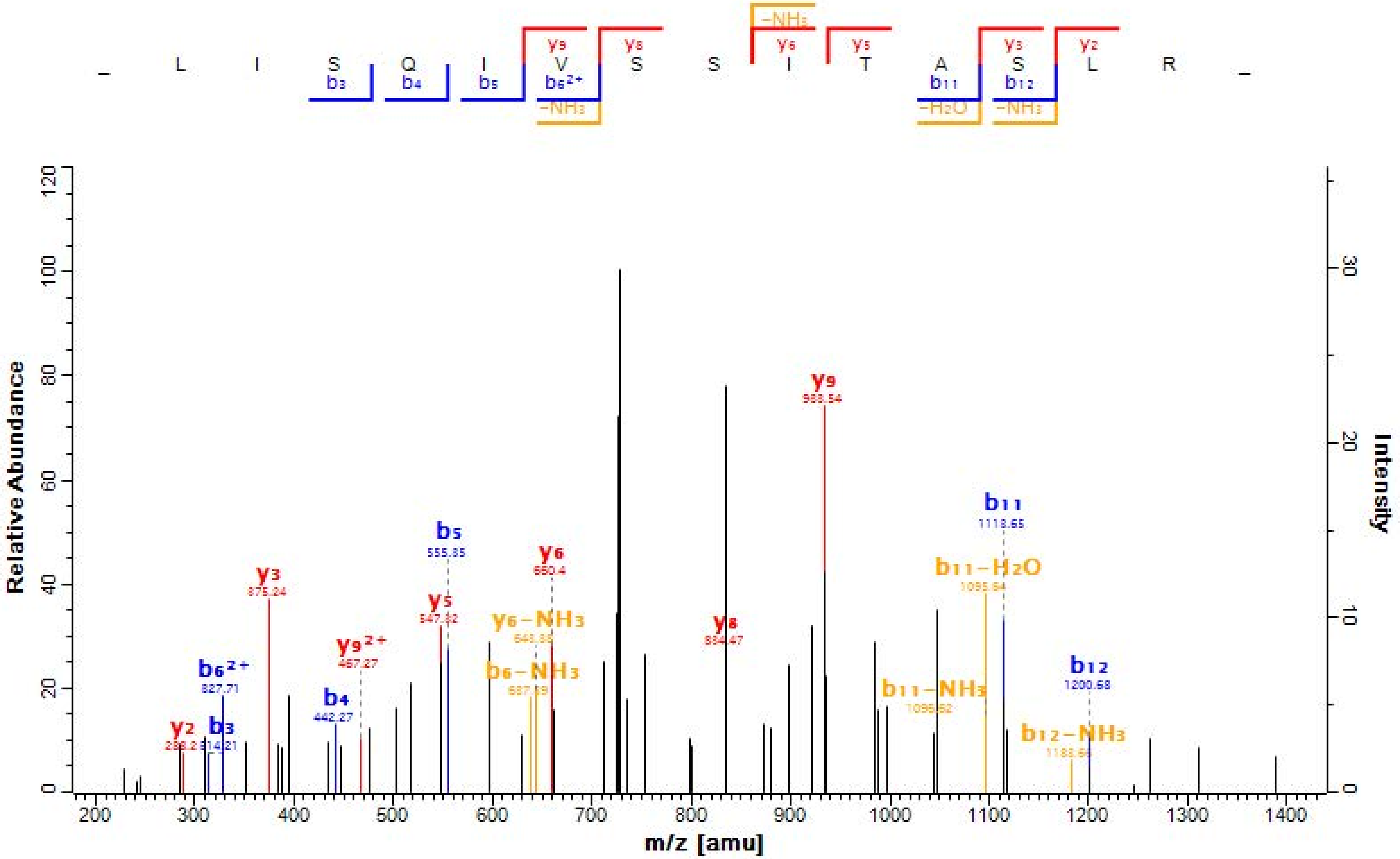
Mass:	2192.06158
m/z:	1097.03807
Charge:	2+
Retentiontime:	67.691619873046
Score:	87.5537
Mass Error [ppm]:	-0.51705
PEP:	0.00029903
Precursor Type:	MULTI

general information

Annotation:	14 of 20
AminoAcids Coverag	70 %
Intensity Coverage:	16 %
Peak Coverage:	26 %
Protein Localisation:	363 ... 382

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	100.0757		100.0757	1	V	19		
	171.1128		171.1128	2	A	18	2094.06	
	242.1499		242.1499	3	A	17	2023.023	
	355.234		355.234	4	L	16	1951.986	
	484.2766		484.2766	5	E	15	1838.902	-0.12728
	598.3195	-0.04814	598.3195	6	N	14	1709.859	
	726.3781		726.3781	7	Q	13	1595.816	+0.209829
	839.4621		839.4621	8	I	12	1467.758	
	926.4942		926.4942	9	S	11	1354.674	-0.04792
	1055.537		1055.537	10	E	10	1267.642	+0.056618
	1154.605	-0.09419	1154.605	11	V	9	1138.599	-0.05875
	1241.637		1241.637	12	S	8	1039.531	+0.001609
+0.450712	685.8435		1370.68	13	E	7	952.4986	
-0.00947	742.3856		1483.764	14	L	6	823.456	+0.000303
	1596.848	-0.08682	1596.848	15	L	5	710.3719	+0.146501
	1653.869		1653.869	16	G	4	597.2879	-0.0043
+0.498031	877.9622	-0.26778	1754.917	17	T	3	540.2664	+0.079848
	1917.98		1917.98	18	Y	2	439.2187	+0.077966
	2047.023		2047.023	19	E	1	276.1554	
				20	K	0	147.1128	

Scan number	11251	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	77.78



precursor information

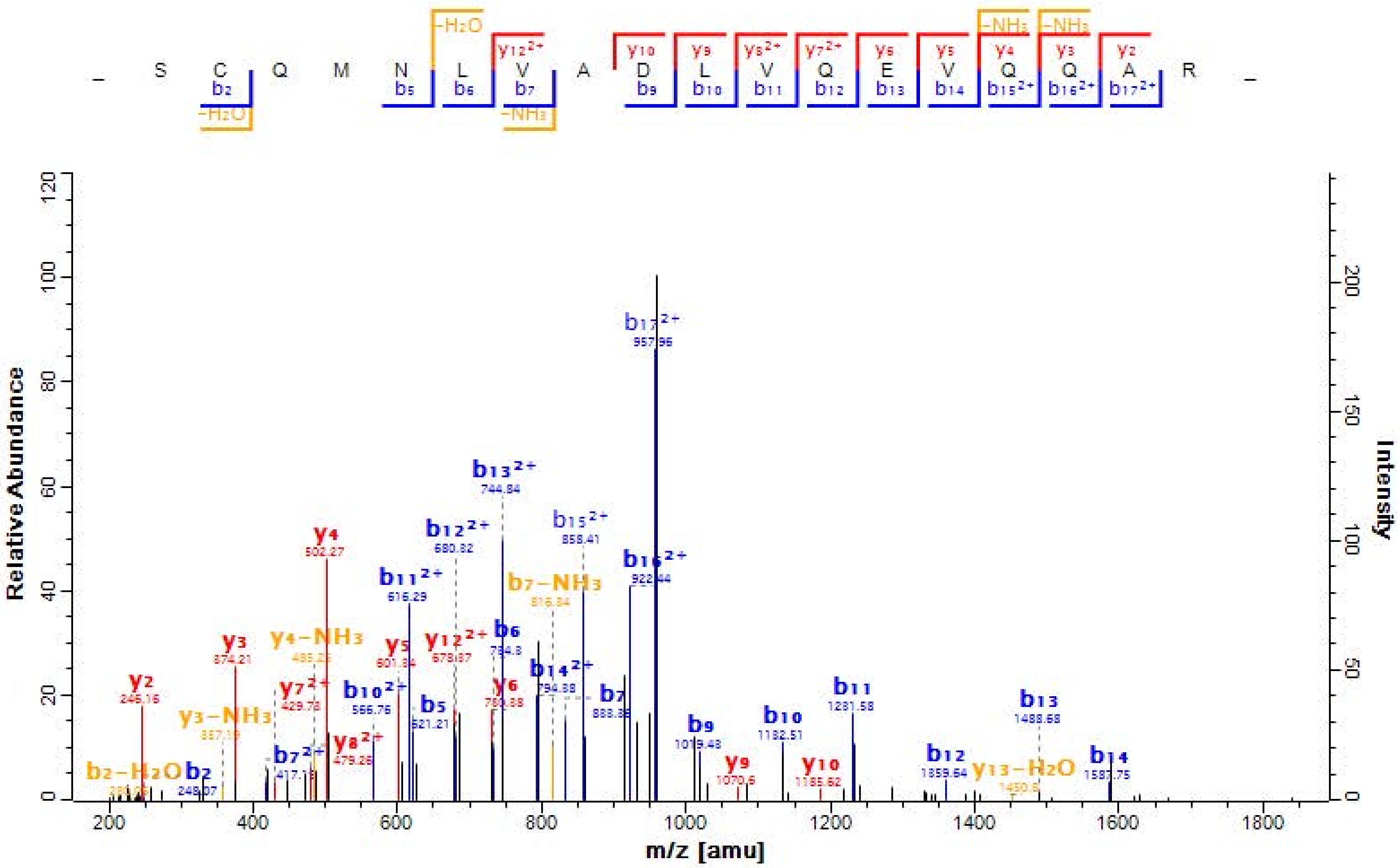
Mass:	1486.87178
m/z:	744.44317
Charge:	2+
Retentiontime:	68.683578491210
Score:	77.77563
Mass Error [ppm]:	-0.076075
PEP:	0.0012056
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	31 %
Peak Coverage:	28 %
Protein Localisation:	230 ... 243

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	13				
	227.18		227.18	2	I	12	1374.8		1374.8	
	314.21	+0.1748	314.21	3	S	11	1261.7		1261.7	
	442.27	+0.2289	442.27	4	Q	10	1174.7		1174.7	
	555.35	-0.083	555.35	5	I	9	1046.6		1046.6	
+0.0801	327.71		654.42	6	V	8	933.54	+0.1838	467.27	-0.118
	741.45		741.45	7	S	7	834.47	-0.003	834.47	
	828.48		828.48	8	S	6	747.44		747.44	
	941.57		941.57	9	I	5	660.4	-0.135	660.4	
	1042.6		1042.6	10	T	4	547.32	+0.0995	547.32	
	1113.7	-0.04	1113.7	11	A	3	446.27		446.27	
	1200.7	+0.0971	1200.7	12	S	2	375.24	+0.1456	375.24	
	1313.8		1313.8	13	L	1	288.2	-0.111	288.2	
				14	R	0	175.12		175.12	

Scan number	11698	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	158.45



precursor information

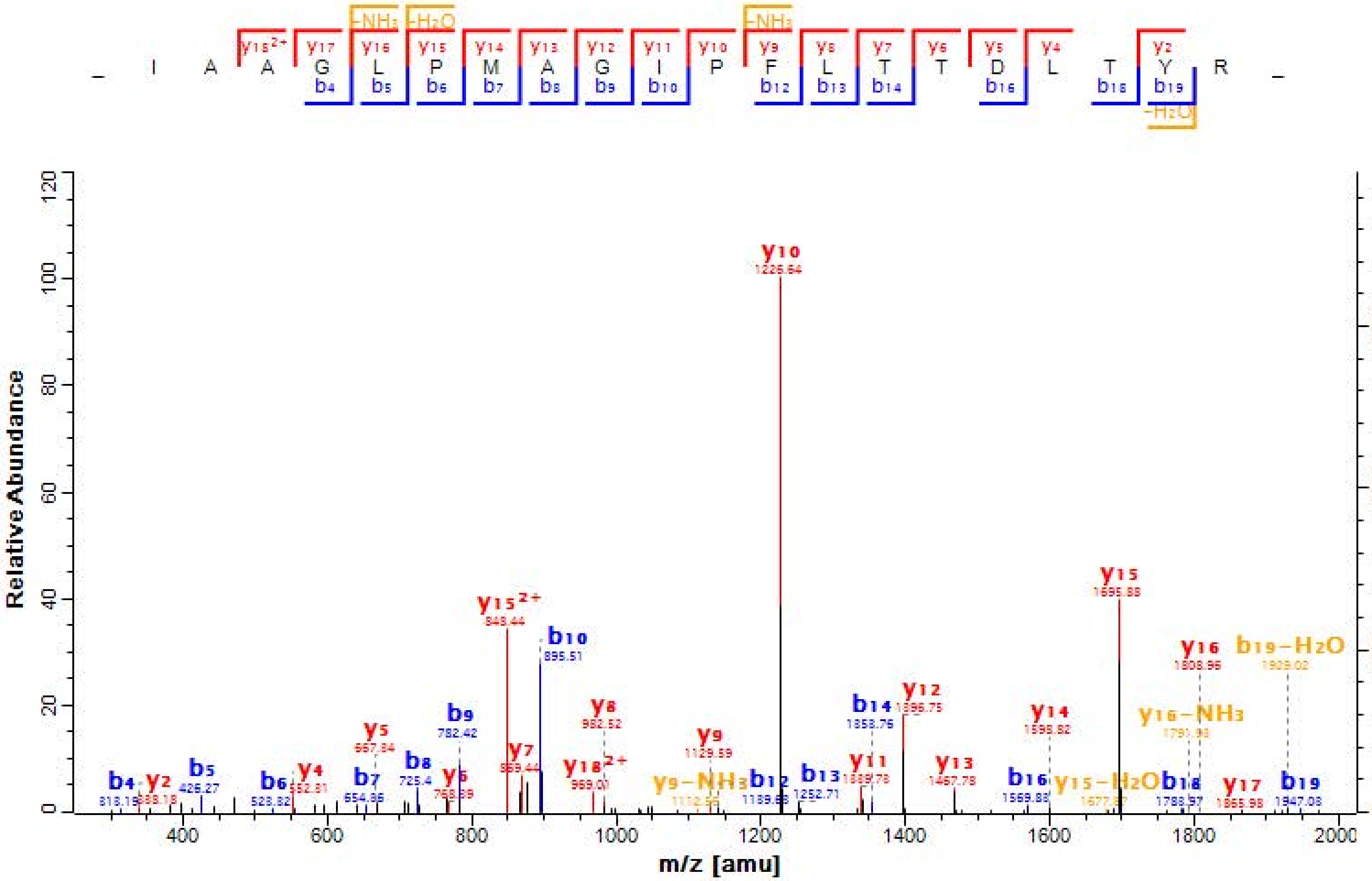
Mass:	2088.00822
m/z:	697.01002
Charge:	3+
Retentiontime:	72.248626708984
Score:	158.4521
Mass Error [ppm]:	-0.47204
PEP:	1.5002E-23
Precursor Type:	MULTI

general information

Annotation:	13 of 18
AminoAcids Coverag	72 %
Intensity Coverage:	57 %
Peak Coverage:	35 %
Protein Localisation:	167 ... 184

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	17				
	248.07	+0.2115	248.07	2	C	16	2002		2002	
	376.13		376.13	3	Q	15	1842		1842	
	507.17		507.17	4	M	14	1713.9		1713.9	
	621.21	-0.094	621.21	5	N	13	1582.9		1582.9	
	734.3	-0.102	734.3	6	L	12	1468.8		1468.8	
+0.4396	417.19	-0.043	833.36	7	V	11	1355.7		678.37	-0.295
	904.4		904.4	8	A	10	1256.7		1256.7	
	1019.4	-0.192	1019.4	9	D	9	1185.6	+0.2649	1185.6	
+0.1083	566.76	+0.0581	1132.5	10	L	8	1070.6	-0.008	1070.6	
+0.2665	616.29	-0.203	1231.6	11	V	7	957.51		479.26	+0.2351
+0.0772	680.32	-0.054	1359.6	12	Q	6	858.44		429.73	+0.3325
+0.2083	744.84	-0.474	1488.7	13	E	5	730.38	+0.0633	730.38	
-0.121	794.38	-0.165	1587.8	14	V	4	601.34	+0.0887	601.34	
+0.0068	858.41		1715.8	15	Q	3	502.27	+0.0555	502.27	
+0.353	922.44		1843.9	16	Q	2	374.21	+0.0707	374.21	
-0.066	957.96		1914.9	17	A	1	246.16	+0.0441	246.16	
				18	R	0	175.12		175.12	

Scan number	11745	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	188.41



precursor information

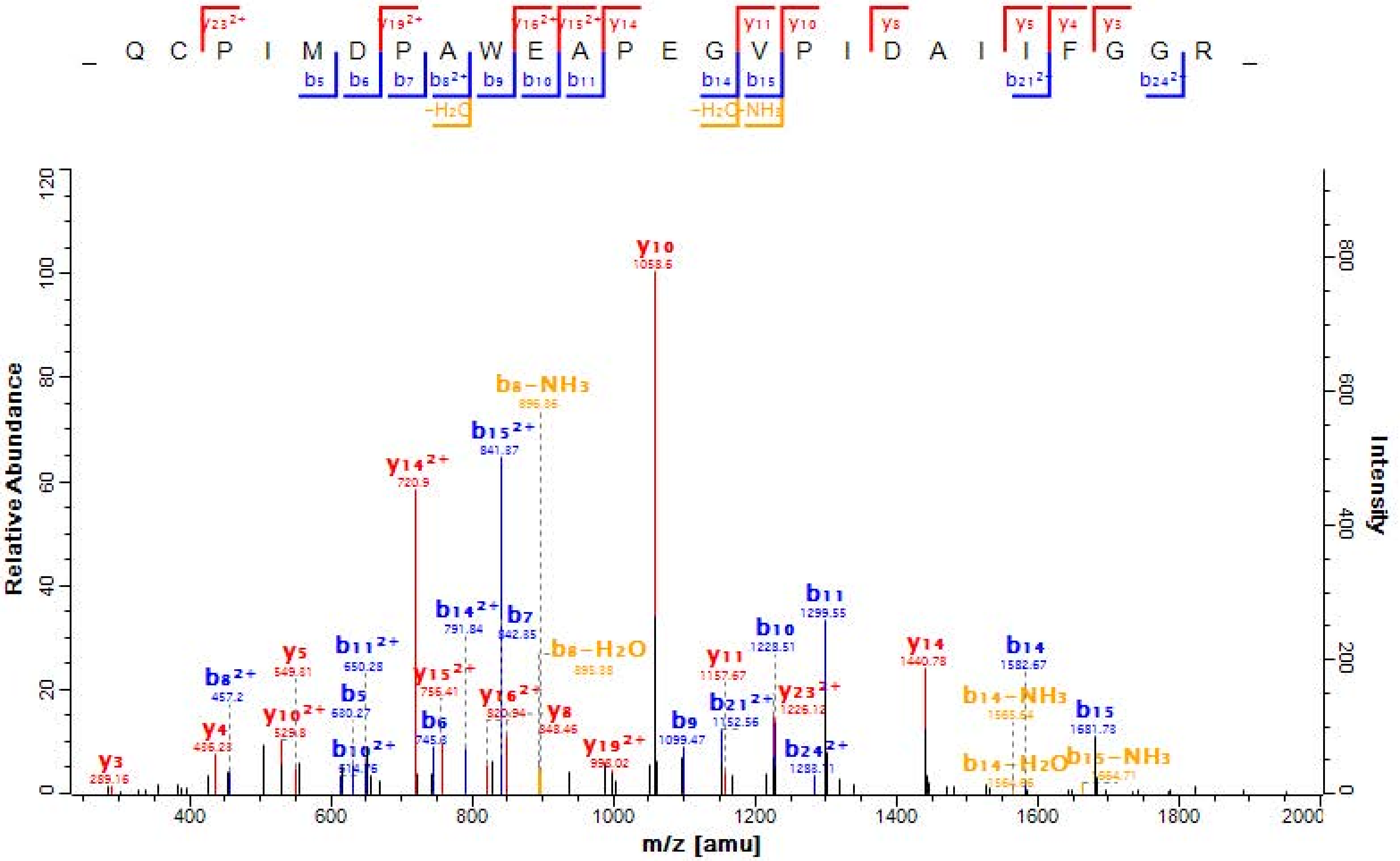
Mass:	2120.13302
m/z:	1061.07379
Charge:	2+
Retentiontime:	72.686325073242
Score:	188.4109
Mass Error [ppm]:	-0.45932
PEP:	2.2932E-47
Precursor Type:	MULTI

general information

Annotation:	17 of 20
AminoAcids Coverag	85 %
Intensity Coverage:	64 %
Peak Coverage:	34 %
Protein Localisation:	65 ... 84

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	I	19				
	185.1285	2	A	18	2008.057		2008.057	
	256.1656	3	A	17	1937.02		969.0137	+0.365952
+0.109324	313.187	4	G	16	1865.983	-0.10481	1865.983	
-0.04466	426.2711	5	L	15	1808.962	+0.155913	1808.962	
+0.142815	523.3239	6	P	14	1695.877	-0.06166	848.4424	+0.302019
+0.077611	654.3643	7	M	13	1598.825	+0.298234	1598.825	
+0.000397	725.4015	8	A	12	1467.784	-0.11392	1467.784	
-0.00215	782.4229	9	G	11	1396.747	-0.00478	1396.747	
-0.05716	895.507	10	I	10	1339.726	+0.041339	1339.726	
	992.5597	11	P	9	1226.642	-0.02413	1226.642	
-0.11278	1139.628	12	F	8	1129.589	-0.12774	1129.589	
-0.21882	1252.712	13	L	7	982.5204	-0.00183	982.5204	
-0.02736	1353.76	14	T	6	869.4363	+0.107256	869.4363	
	1454.808	15	T	5	768.3886	-0.00058	768.3886	
+0.016913	1569.835	16	D	4	667.341	+0.178565	667.341	
	1682.919	17	L	3	552.314	+0.012881	552.314	
-0.25765	1783.966	18	T	2	439.23		439.23	
+0.044254	1947.03	19	Y	1	338.1823	+0.104249	338.1823	
		20	R	0	175.119		175.119	

Scan number	11809	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	132.83



precursor information

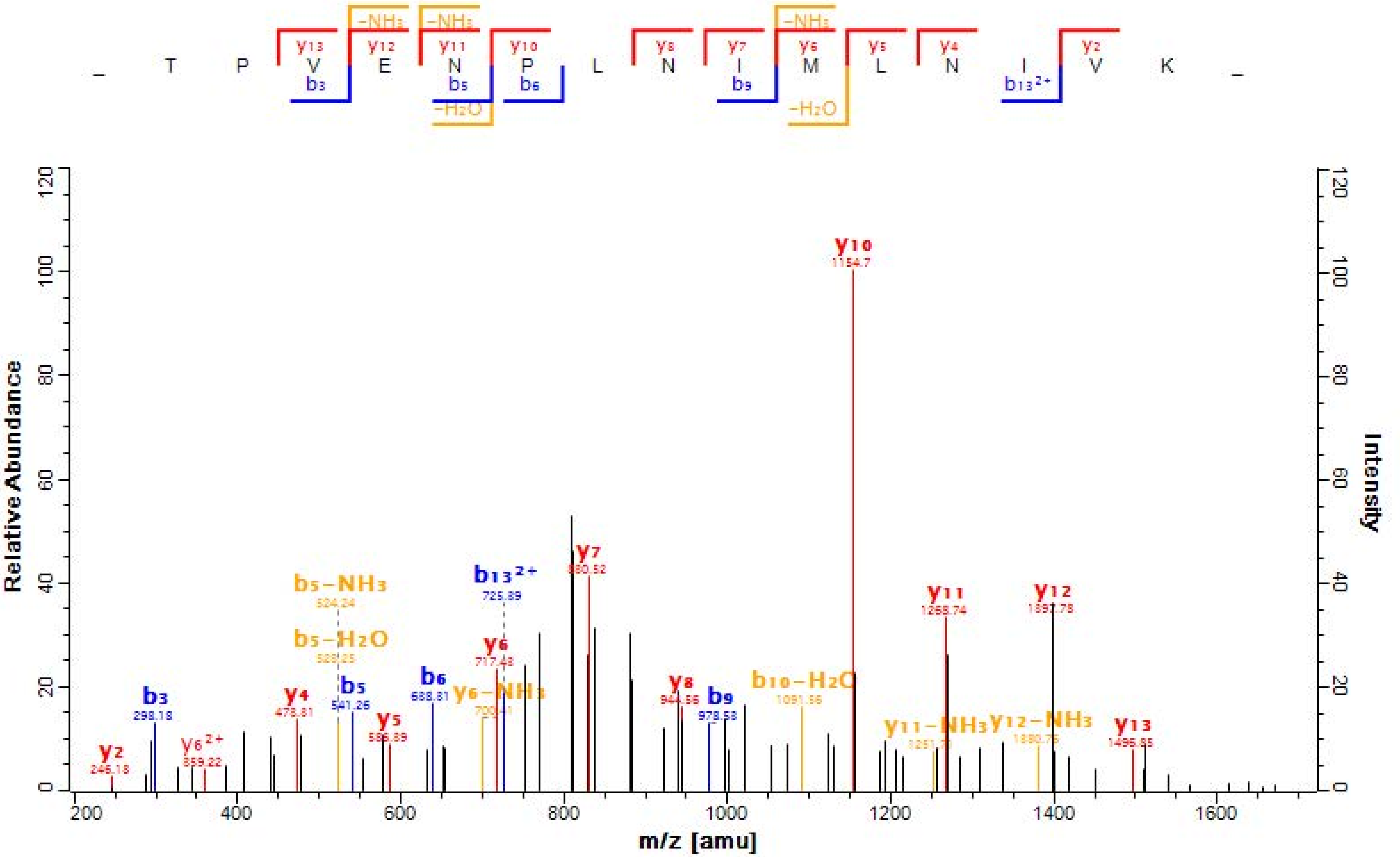
Mass:	2738.31924
m/z:	913.78036
Charge:	3+
Retentiontime:	73.276000976562
Score:	132.8275
Mass Error [ppm]:	-0.14544
PEP:	8.3323E-17
Precursor Type:	MULTI

general information

Annotation:	18 of 25
AminoAcids Coverag	72 %
Intensity Coverage:	64 %
Peak Coverage:	35 %
Protein Localisation:	430 ... 454

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.07		129.07	1	Q	24				
	289.1		289.1	2	C	23	2611.3		2611.3	
	386.15		386.15	3	P	22	2451.2		1226.1	+0.1152
	499.23		499.23	4	I	21	2354.2		2354.2	
	630.27	+0.1281	630.27	5	M	20	2241.1		2241.1	
	745.3	-0.047	745.3	6	D	19	2110.1		2110.1	
	842.35	+0.1783	842.35	7	P	18	1995		998.02	+0.1937
+0.129	457.2		913.39	8	A	17	1898		1898	
	1099.5	-0.108	1099.5	9	W	16	1826.9		1826.9	
+0.0865	614.76	-0.096	1228.5	10	E	15	1640.9		820.94	+0.0813
-0.193	650.28	-0.077	1299.5	11	A	14	1511.8		756.41	+0.268
	1396.6		1396.6	12	P	13	1440.8	-0.027	720.9	+0.1682
	1525.6		1525.6	13	E	12	1343.7		1343.7	
+0.0533	791.84	+0.2873	1582.7	14	G	11	1214.7		1214.7	
+0.228	841.37	-0.231	1681.7	15	V	10	1157.7	+0.0898	1157.7	
	1778.8		1778.8	16	P	9	1058.6	+0.0453	529.8	+0.0761
	1891.9		1891.9	17	I	8	961.55		961.55	
	2006.9		2006.9	18	D	7	848.46	+0.0071	848.46	
	2077.9		2077.9	19	A	6	733.44		733.44	
	2191		2191	20	I	5	662.4		662.4	
+0.3753	1152.6		2304.1	21	I	4	549.31	+0.0766	549.31	
	2451.2		2451.2	22	F	3	436.23	+0.0189	436.23	
	2508.2		2508.2	23	G	2	289.16	+0.0367	289.16	
+0.1403	1283.1		2565.2	24	G	1	232.14		232.14	
				25	R	0	175.12		175.12	

Scan number	12263	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	98.58



precursor information

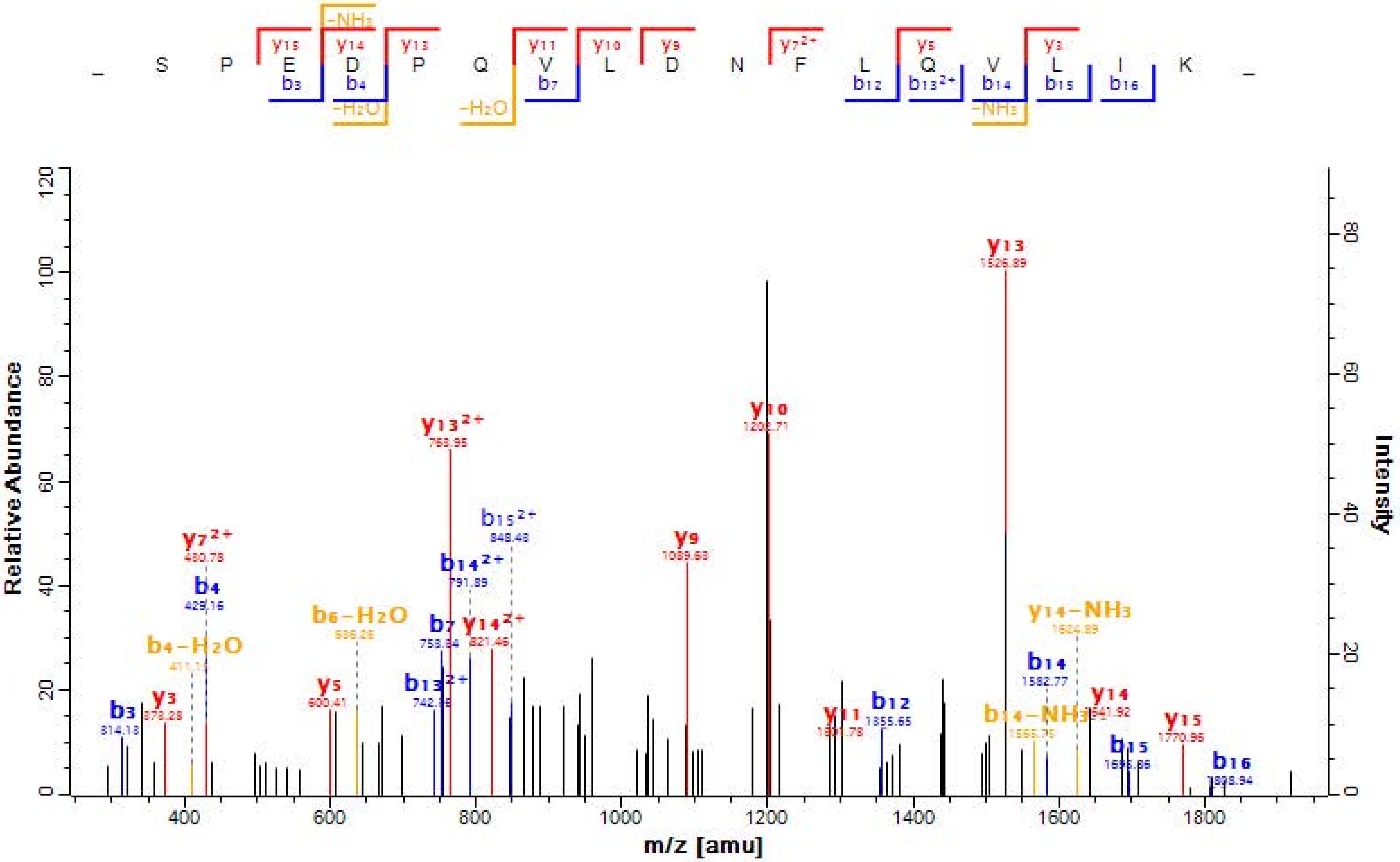
Mass:	1693.94474
m/z:	847.97964
Charge:	2+
Retentiontime:	77.516677856445
Score:	98.58204
Mass Error [ppm]:	0.62447
PEP:	0.0012696
Precursor Type:	ISO

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	38 %
Peak Coverage:	27 %
Protein Localisation:	1497 ... 1511

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	14				
	199.11		199.11	2	P	13	1593.9		1593.9	
	298.18	-0.041	298.18	3	V	12	1496.9	-0.015	1496.9	
	427.22		427.22	4	E	11	1397.8	-0.201	1397.8	
	541.26	+0.252	541.26	5	N	10	1268.7	-0.194	1268.7	
	638.31	+0.0886	638.31	6	P	9	1154.7	+0.0571	1154.7	
	751.4		751.4	7	L	8	1057.6		1057.6	
	865.44		865.44	8	N	7	944.56	-0.196	944.56	
	978.53	-0.014	978.53	9	I	6	830.52	+0.1555	830.52	
	1109.6		1109.6	10	M	5	717.43	-0.052	359.22	+0.0015
	1222.7		1222.7	11	L	4	586.39	-0.106	586.39	
	1336.7		1336.7	12	N	3	473.31	-0.079	473.31	
+0.2859	725.39		1449.8	13	I	2	359.27		359.27	
	1548.8		1548.8	14	V	1	246.18	+0.0179	246.18	
				15	K	0	147.11		147.11	

Scan number	12270	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	113.01



precursor information

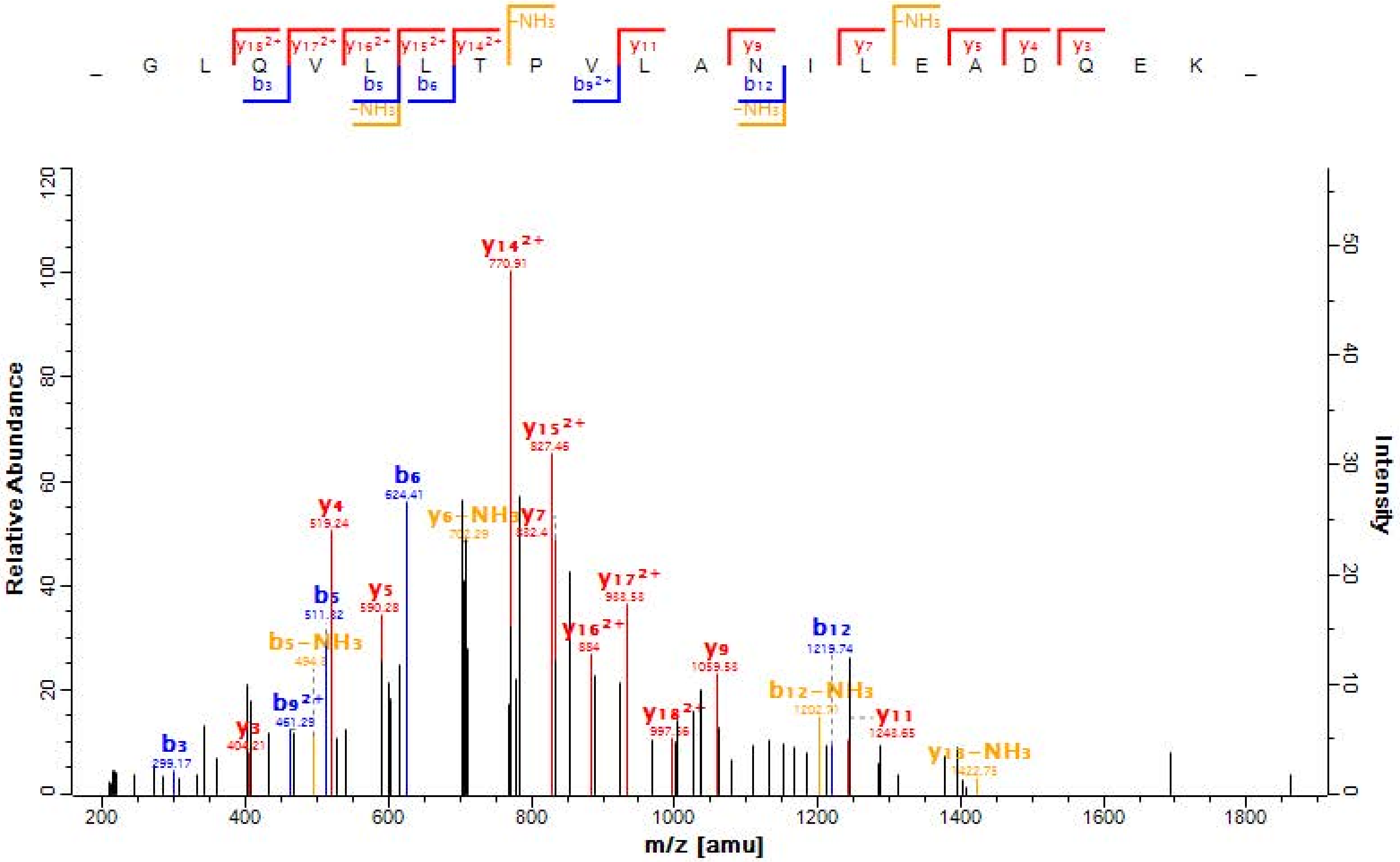
Mass:	1954.03967
m/z:	978.02711
Charge:	2+
Retentiontime:	77.589752197265
Score:	113.0145
Mass Error [ppm]:	-0.75629
PEP:	1.1619E-08
Precursor Type:	MULTI

general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	38 %
Peak Coverage:	26 %
Protein Localisation:	98 ... 114

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	16				
	185.09		185.09	2	P	15	1868		1868	
	314.13	+0.0441	314.13	3	E	14	1771	+0.257	1771	
	429.16	+0.1088	429.16	4	D	13	1641.9	-0.313	821.46	-0.263
	526.21		526.21	5	P	12	1526.9	-0.176	763.95	+0.2783
	654.27		654.27	6	Q	11	1429.8		1429.8	
	753.34	+0.0019	753.34	7	V	10	1301.8	+0.3182	1301.8	
	866.43		866.43	8	L	9	1202.7	-0.008	1202.7	
	981.45		981.45	9	D	8	1089.6	+0.0825	1089.6	
	1095.5		1095.5	10	N	7	974.6		974.6	
	1242.6		1242.6	11	F	6	860.56		430.78	-0.497
	1355.6	+0.1596	1355.6	12	L	5	713.49		713.49	
+0.132	742.36		1483.7	13	Q	4	600.41	-0.027	600.41	
-0.009	791.89	+0.1742	1582.8	14	V	3	472.35		472.35	
+0.1114	848.43	+0.1747	1695.9	15	L	2	373.28	+0.0919	373.28	
	1808.9	+0.0949	1808.9	16	I	1	260.2		260.2	
				17	K	0	147.11		147.11	

Scan number	12412	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	75.55



precursor information

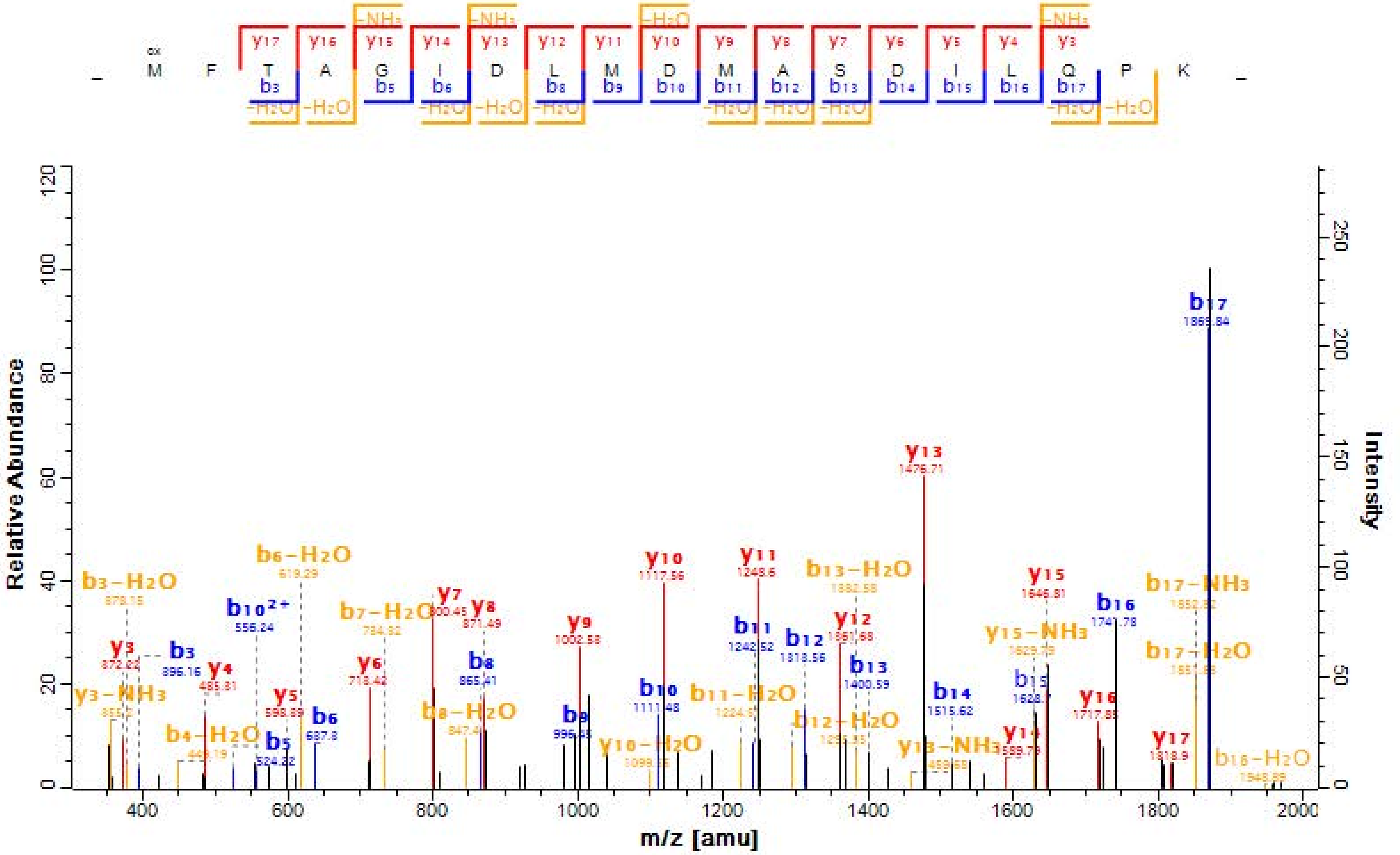
Mass:	2163.21615
m/z:	722.07933
Charge:	3+
Retentiontime:	78.948104858398
Score:	75.54819
Mass Error [ppm]:	0.49108
PEP:	0.0001799
Precursor Type:	MULTI

general information

Annotation:	14 of 20
AminoAcids Coverag	70 %
Intensity Coverage:	39 %
Peak Coverage:	24 %
Protein Localisation:	272 ... 291

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	19				
	171.11		171.11	2	L	18	2107.2		2107.2	
	299.17	+0.0366	299.17	3	Q	17	1994.1		997.56	-0.119
	398.24		398.24	4	V	16	1866.1		933.53	+0.2864
	511.32	+0.1547	511.32	5	L	15	1767		884	-0.231
	624.41	-0.086	624.41	6	L	14	1653.9		827.46	-0.086
	725.46		725.46	7	T	13	1540.8		770.91	-0.005
	822.51		822.51	8	P	12	1439.8		1439.8	
+0.151	461.29		921.58	9	V	11	1342.7		1342.7	
	1034.7		1034.7	10	L	10	1243.7	-0.247	1243.7	
	1105.7		1105.7	11	A	9	1130.6		1130.6	
	1219.7	+0.2916	1219.7	12	N	8	1059.5	-0.114	1059.5	
	1332.8		1332.8	13	I	7	945.49		945.49	
	1445.9		1445.9	14	L	6	832.4	+0.1408	832.4	
	1575		1575	15	E	5	719.32		719.32	
	1646		1646	16	A	4	590.28	+0.0733	590.28	
	1761		1761	17	D	3	519.24	+0.0337	519.24	
	1889.1		1889.1	18	Q	2	404.21	+0.0517	404.21	
	2018.1		2018.1	19	E	1	276.16		276.16	
				20	K	0	147.11		147.11	

Scan number 12512
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set2_02
Pepti... 227.46



precursor information

Mass:	2111.99352
m/z:	1057.00404
Charge:	2+
Retentiontime:	80.002891540527
Score:	227.4564
Mass Error [ppm]:	-0.29223
PEP:	4.1025E-56
Precursor Type:	MULTI

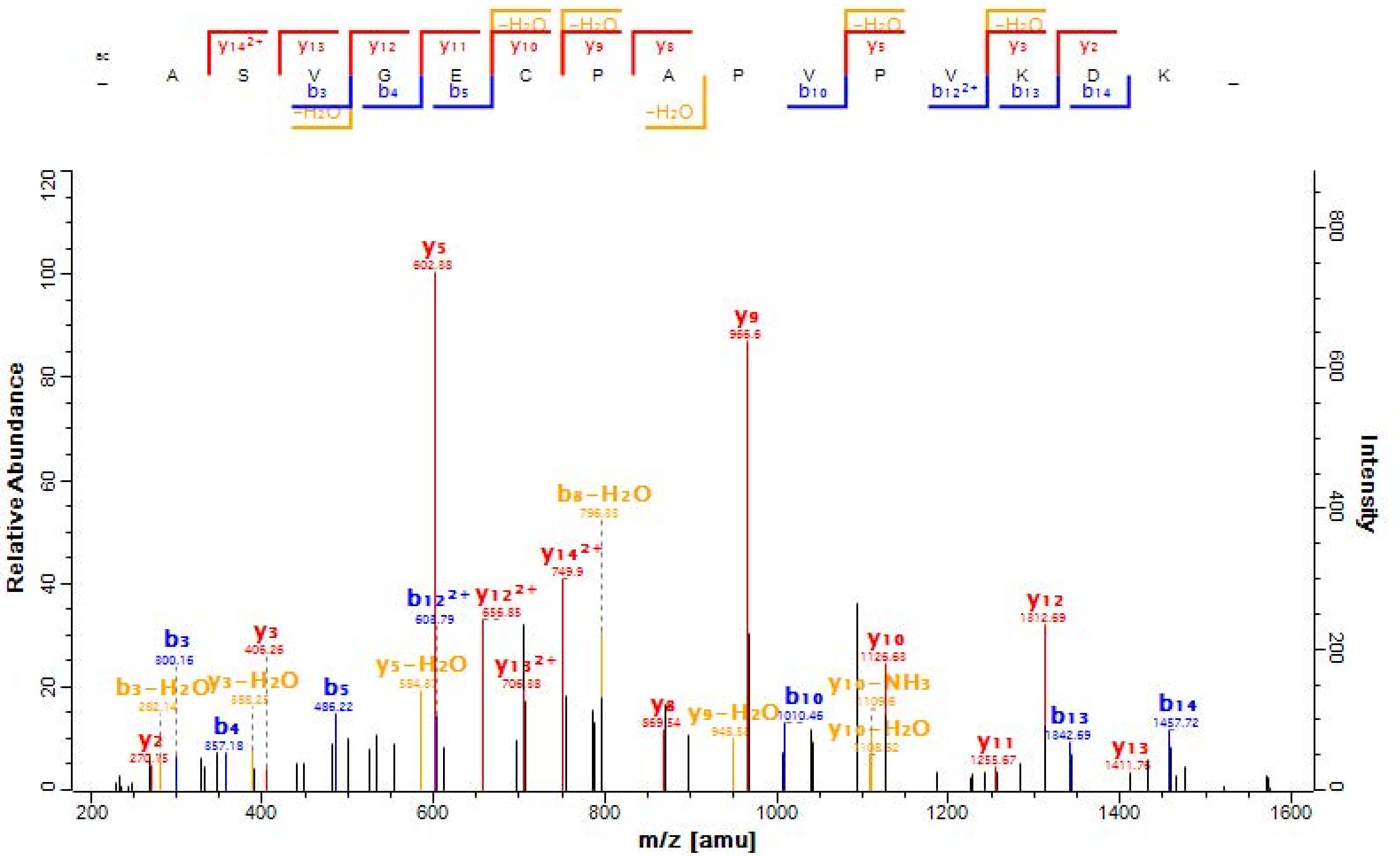
general information

Annotation:	17 of 19
AminoAcids Coverag	89 %
Intensity Coverage:	53 %
Peak Coverage:	45 %
Protein Localisation:	113 ... 131

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	148.0427		148.0427	1	M	18		
	295.1111		295.1111	2	F	17	1965.966	
	396.1588	-0.04286	396.1588	3	T	16	1818.898	-0.35475
	467.1959		467.1959	4	A	15	1717.85	-0.09858
	524.2173	+0.172547	524.2173	5	G	14	1646.813	-0.04938
	637.3014	+0.088361	637.3014	6	I	13	1589.791	+0.391519
	752.3284		752.3284	7	D	12	1476.707	-0.15943
	865.4124	+0.016905	865.4124	8	L	11	1361.68	-0.03873
	996.4529	-0.10085	996.4529	9	M	10	1248.596	-0.08577
+0.20755	556.2436	-0.11083	1111.48	10	D	9	1117.556	-0.12939
	1242.52	-0.15046	1242.52	11	M	8	1002.529	-0.0496
	1313.557	-0.16645	1313.557	12	A	7	871.4884	-0.02754
	1400.589	-0.11022	1400.589	13	S	6	800.4512	+0.078296
	1515.616	-0.07491	1515.616	14	D	5	713.4192	+0.10239
	1628.7	-0.34831	1628.7	15	I	4	598.3923	+0.088806
	1741.785	-0.25537	1741.785	16	L	3	485.3082	+0.11629
	1869.843	-0.17344	1869.843	17	Q	2	372.2241	+0.114844
	1966.896		1966.896	18	P	1	244.1656	
				19	K	0	147.1128	

Scan number 1460
Method ITMS; CID

Raw file LNCAP_Silac_23F10_set2_02
Pepti... 133.47



precursor information

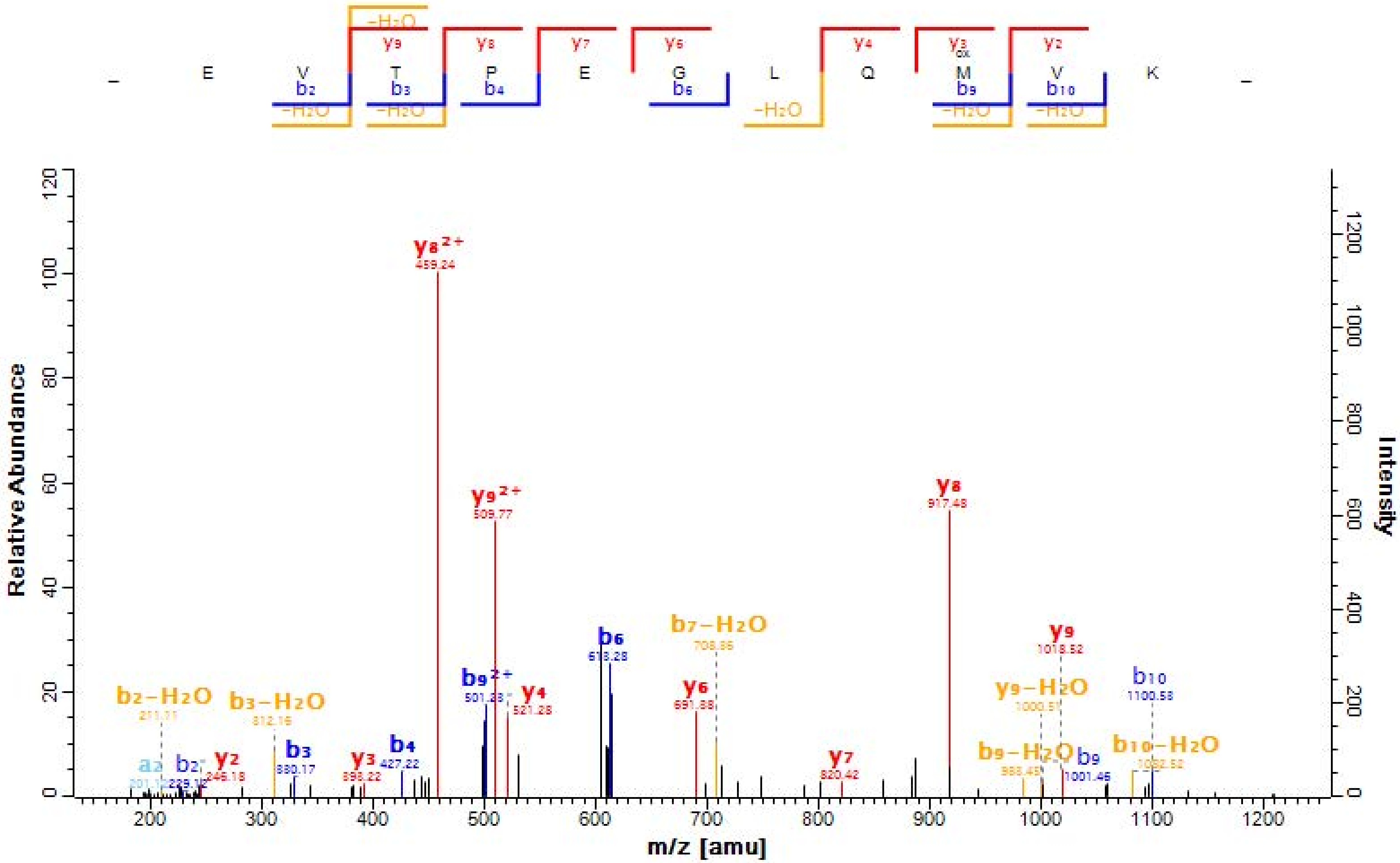
Mass:	1594.80215
m/z:	798.40835
Charge:	2+
Retentiontime:	15.029078483581
Score:	133.4698
Mass Error [ppm]:	-0.21526
PEP:	9.9295E-10
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	51 %
Peak Coverage:	31 %
Protein Localisation:	2 ... 16

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.05		114.05	1	A	14				
	201.09		201.09	2	S	13	1498.8		749.9	+0.191
	300.16	-0.065	300.16	3	V	12	1411.8	+0.4657	706.38	-0.208
	357.18	+0.0768	357.18	4	G	11	1312.7	+0.0784	656.85	+0.076
	486.22	-0.018	486.22	5	E	10	1255.7	-0.002	1255.7	
	646.25		646.25	6	C	9	1126.6	-0.17	1126.6	
	743.3		743.3	7	P	8	966.6	-0.076	966.6	
	814.34		814.34	8	A	7	869.54	-0.051	869.54	
	911.39		911.39	9	P	6	798.51		798.51	
	1010.5	-0.382	1010.5	10	V	5	701.45		701.45	
	1107.5		1107.5	11	P	4	602.38	+0.0658	602.38	
-0.441	603.79		1206.6	12	V	3	505.33		505.33	
	1342.7	+0.0056	1342.7	13	K	2	406.26	-0.229	406.26	
	1457.7	-0.093	1457.7	14	D	1	270.15	+0.0533	270.15	
				15	K	0	155.13		155.13	

Scan number	1702	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	149.23



precursor information

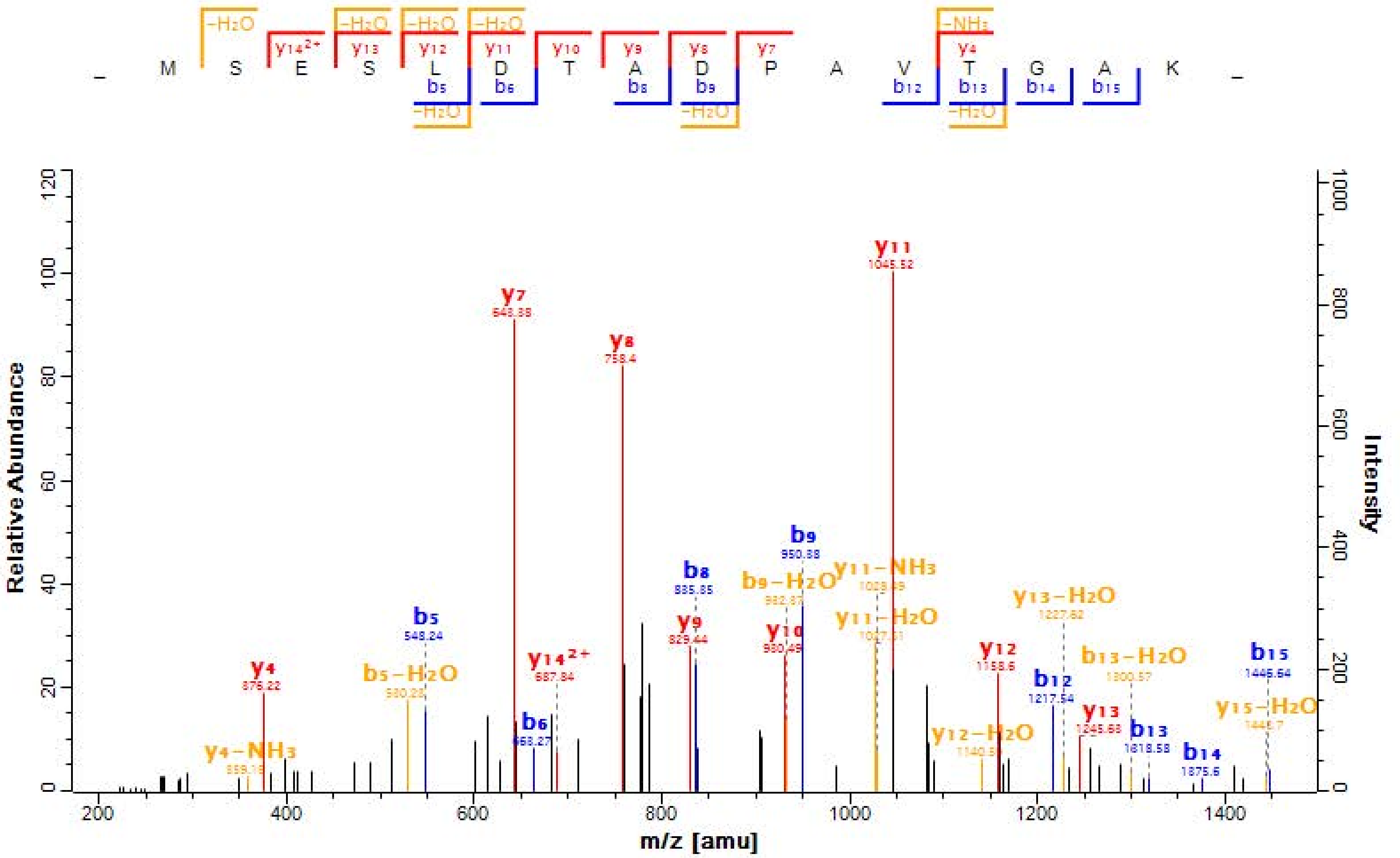
Mass:	1245.62707
m/z:	623.82081
Charge:	2+
Retentiontime:	16.404220581054
Score:	149.2311
Mass Error [ppm]:	-0.33508
PEP:	8.6858E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	61 %
Peak Coverage:	25 %
Protein Localisation:	262 ... 272

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.1		130		130	1	E	10				
-0.34	201.1		229.1	+0	229.1	2	V	9	1118		1118	
	302.2		330.2	+0.055	330.2	3	T	8	1019	+0.125	509.8	+0.03
	399.2		427.2	-0.08	427.2	4	P	7	917.5	+0	459.2	+0.07
	528.3		556.3		556.3	5	E	6	820.4	+0.004	820.4	
	585.3		613.3	+0.288	613.3	6	G	5	691.4	+0	691.4	
	698.4		726.4		726.4	7	L	4	634.4		634.4	
	826.4		854.4		854.4	8	Q	3	521.3	+0.077	521.3	
	973.5	+0.177	501.2	+0.015	1001	9	M	2	393.2	+0.062	393.2	
	1073		1101	-0.07	1101	10	V	1	246.2	-0.06	246.2	
						11	K	0	147.1		147.1	

Scan number	1972	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	130.72



precursor information

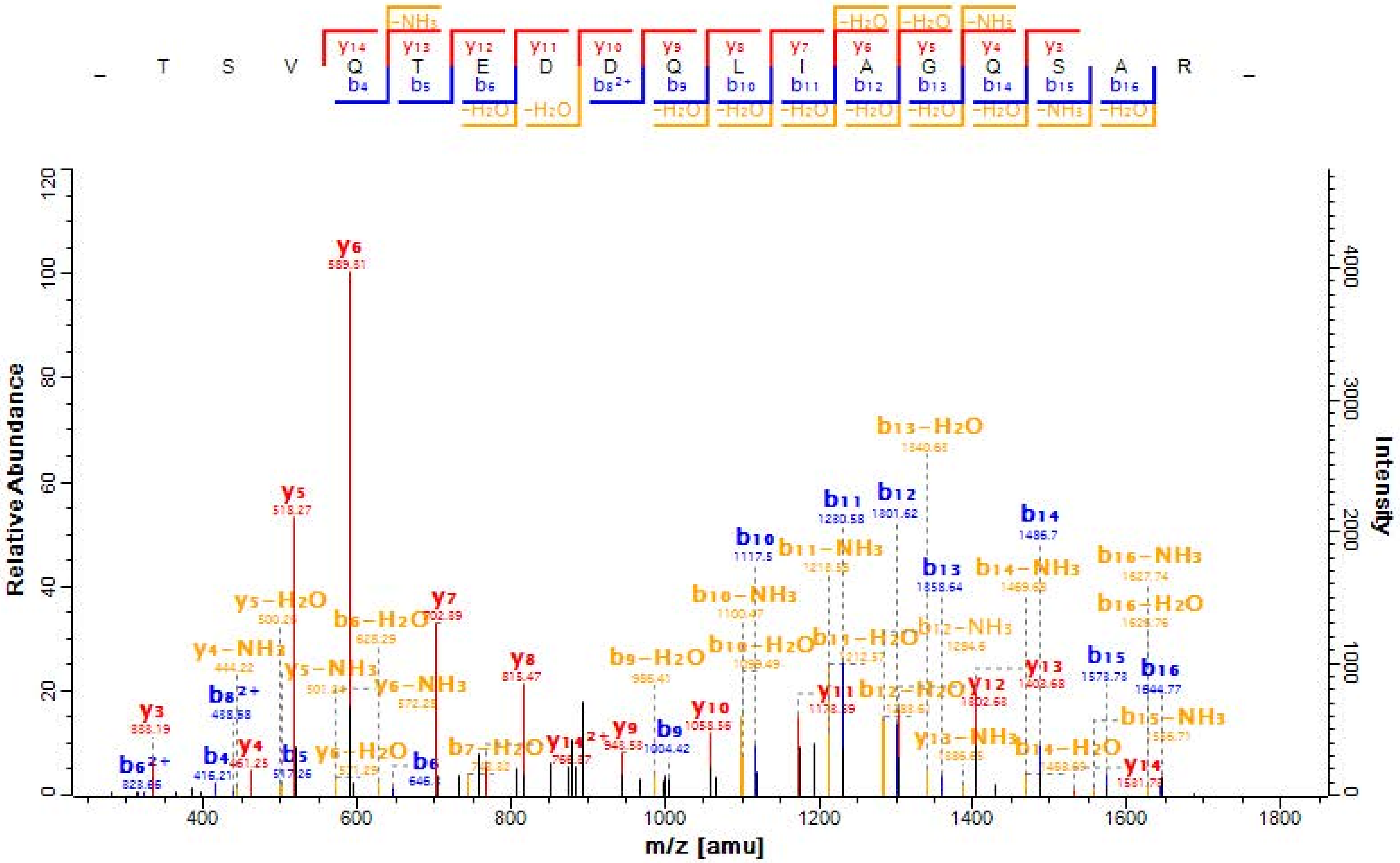
Mass:	1591.74034
m/z:	796.87744
Charge:	2+
Retentiontime:	17.934617996215
Score:	130.7175
Mass Error [ppm]:	0.24164
PEP:	2.6958E-10
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	59 %
Peak Coverage:	32 %
Protein Localisation:	259 ... 274

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	132.0478	1	M	15				
	219.0798	2	S	14	1461.707		1461.707	
	348.1224	3	E	13	1374.675		687.841	-0.13067
	435.1544	4	S	12	1245.632	+0.125202	1245.632	
+0.014272	548.2385	5	L	11	1158.6	-0.05517	1158.6	
+0.178247	663.2654	6	D	10	1045.516	+0.012656	1045.516	
	764.3131	7	T	9	930.4891	+0.157886	930.4891	
+0.080515	835.3502	8	A	8	829.4414	+0.029966	829.4414	
-0.05806	950.3772	9	D	7	758.4043	+0.062441	758.4043	
	1047.43	10	P	6	643.3774	-0.05026	643.3774	
	1118.467	11	A	5	546.3246		546.3246	
-0.101	1217.535	12	V	4	475.2875		475.2875	
-0.0747	1318.583	13	T	3	376.2191	+0.118281	376.2191	
+0.103543	1375.605	14	G	2	275.1714		275.1714	
+0.348289	1446.642	15	A	1	218.1499		218.1499	
		16	K	0	147.1128		147.1128	

Scan number	2012	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	312.66



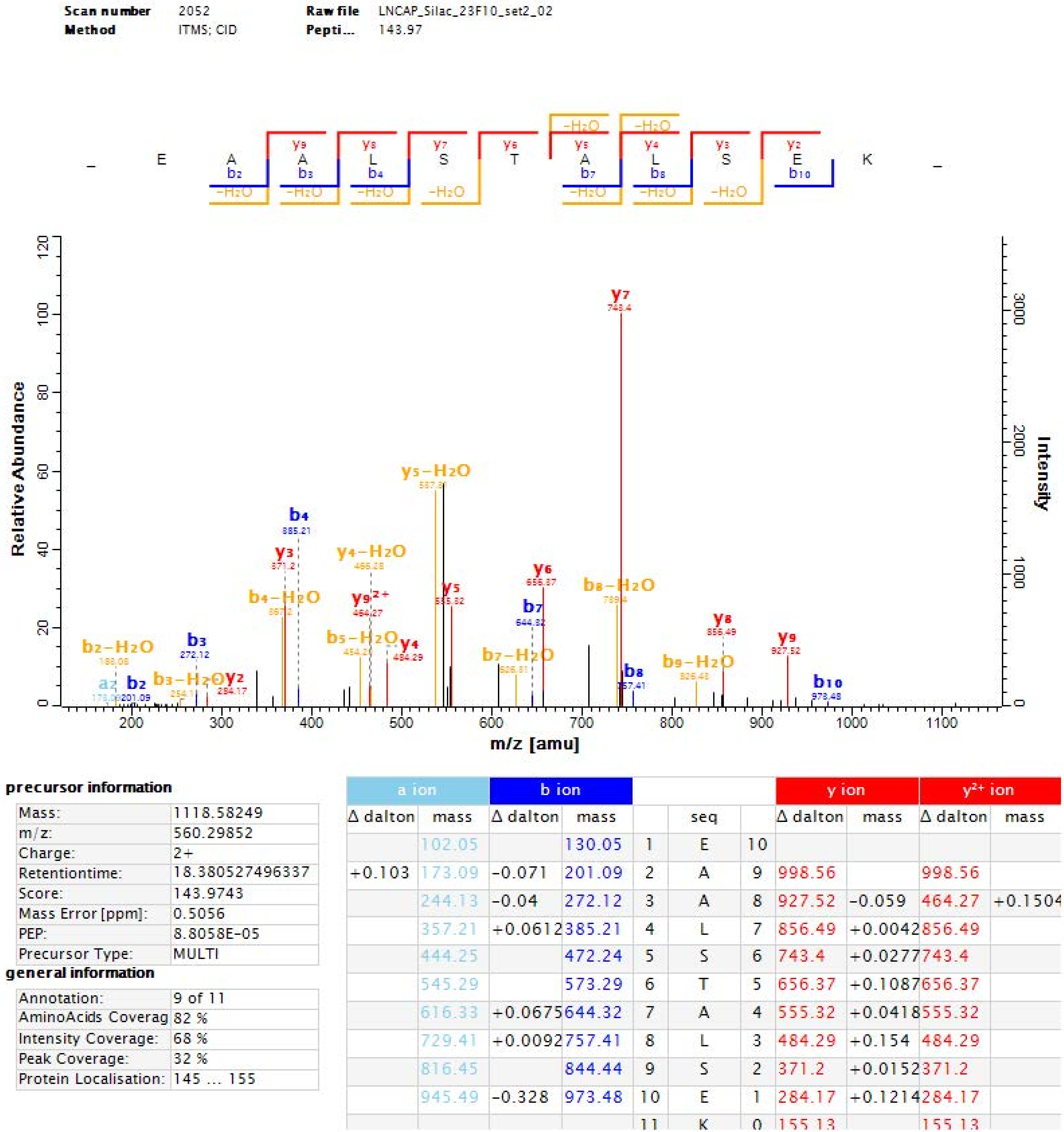
precursor information

Mass:	1817.87509
m/z:	909.94482
Charge:	2+
Retentiontime:	18.165054321289
Score:	312.6553
Mass Error [ppm]:	-0.24375
PEP:	6.7109E-111
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	72 %
Peak Coverage:	54 %
Protein Localisation:	654 ... 670

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	16				
	189.09		189.09	2	S	15	1717.8		1717.8	
	288.16		288.16	3	V	14	1630.8		1630.8	
	416.21	+0.0814	416.21	4	Q	13	1531.7	+0.0169	766.37	-0.063
	517.26	-0.012	517.26	5	T	12	1403.7	-0.032	1403.7	
-0.356	323.66	+0.1166	646.3	6	E	11	1302.6	-0.126	1302.6	
	761.33		761.33	7	D	10	1173.6	-0.012	1173.6	
-0.288	438.68		876.36	8	D	9	1058.6	+0.025	1058.6	
	1004.4	-0.019	1004.4	9	Q	8	943.53	+0.0254	943.53	
	1117.5	+0.073	1117.5	10	L	7	815.47	+0.141	815.47	
	1230.6	-0.031	1230.6	11	I	6	702.39	+0.0758	702.39	
	1301.6	-0.054	1301.6	12	A	5	589.31	+0.042	589.31	
	1358.6	-0.013	1358.6	13	G	4	518.27	+0.0344	518.27	
	1486.7	-0.15	1486.7	14	Q	3	461.25	-0.028	461.25	
	1573.7	-0.09	1573.7	15	S	2	333.19	-0.012	333.19	
	1644.8	-0.101	1644.8	16	A	1	246.16		246.16	
				17	R	0	175.12		175.12	



Scan number 2052 **Raw file** LNCAP_Silac_23F10_set2_02

Method ITMS; CID **Pepti...** 143.97

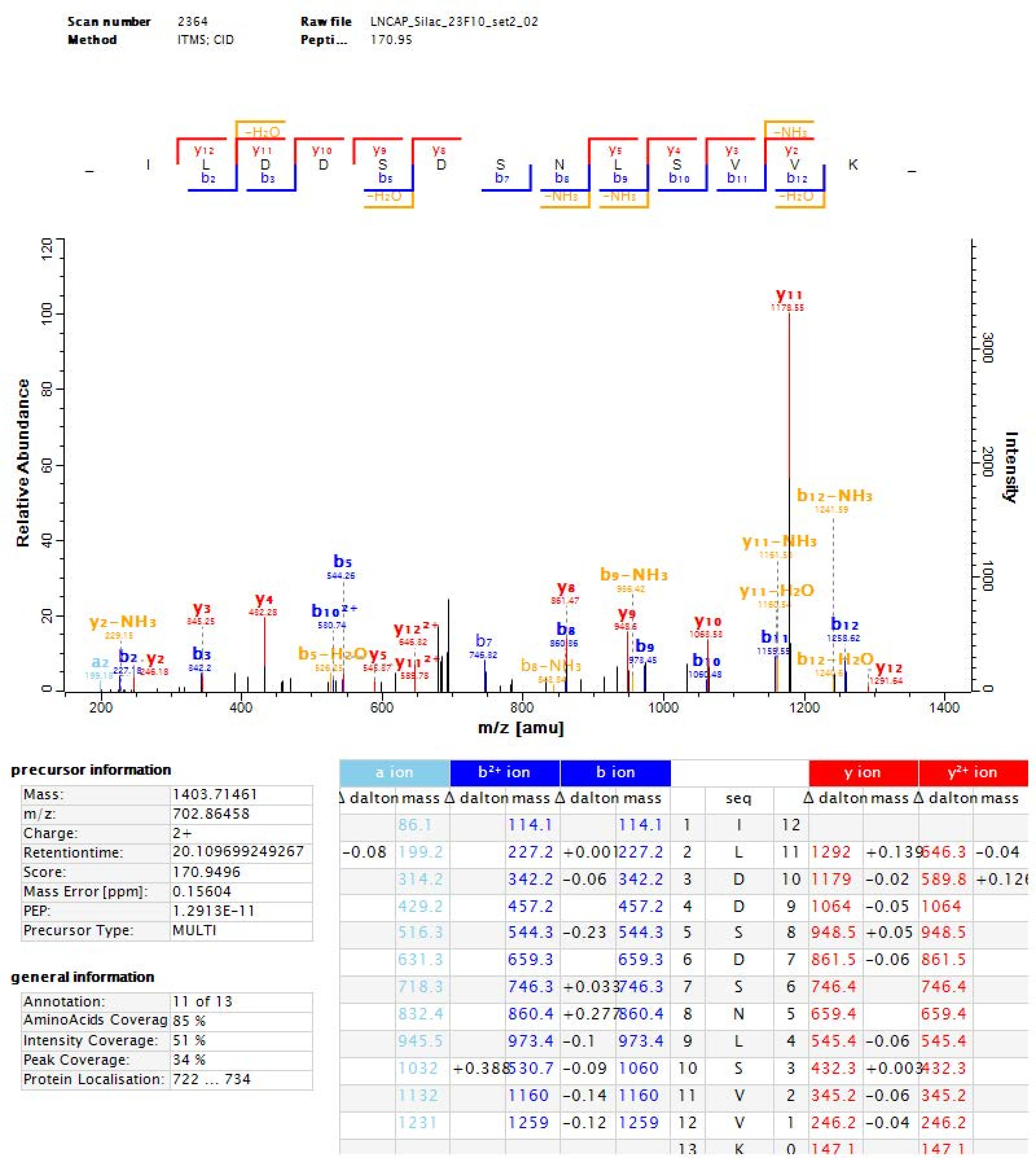
precursor information

Mass:	1118.58249
m/z:	560.29852
Charge:	2+
Retentiontime:	18.380527496337
Score:	143.9743
Mass Error [ppm]:	0.5056
PEP:	8.8058E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	68 %
Peak Coverage:	32 %
Protein Localisation:	145 ... 155

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	10				
+0.103	173.09	-0.071	201.09	2	A	9	998.56		998.56	
	244.13	-0.04	272.12	3	A	8	927.52	-0.059	464.27	+0.1504
	357.21	+0.0612	385.21	4	L	7	856.49	+0.0042	856.49	
	444.25		472.24	5	S	6	743.4	+0.0277	743.4	
	545.29		573.29	6	T	5	656.37	+0.1087	656.37	
	616.33	+0.0675	644.32	7	A	4	555.32	+0.0418	555.32	
	729.41	+0.0092	757.41	8	L	3	484.29	+0.154	484.29	
	816.45		844.44	9	S	2	371.2	+0.0152	371.2	
	945.49	-0.328	973.48	10	E	1	284.17	+0.1214	284.17	
				11	K	0	155.13		155.13	



Scan number 2364
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set2_02
Pepti... 170.95

precursor information

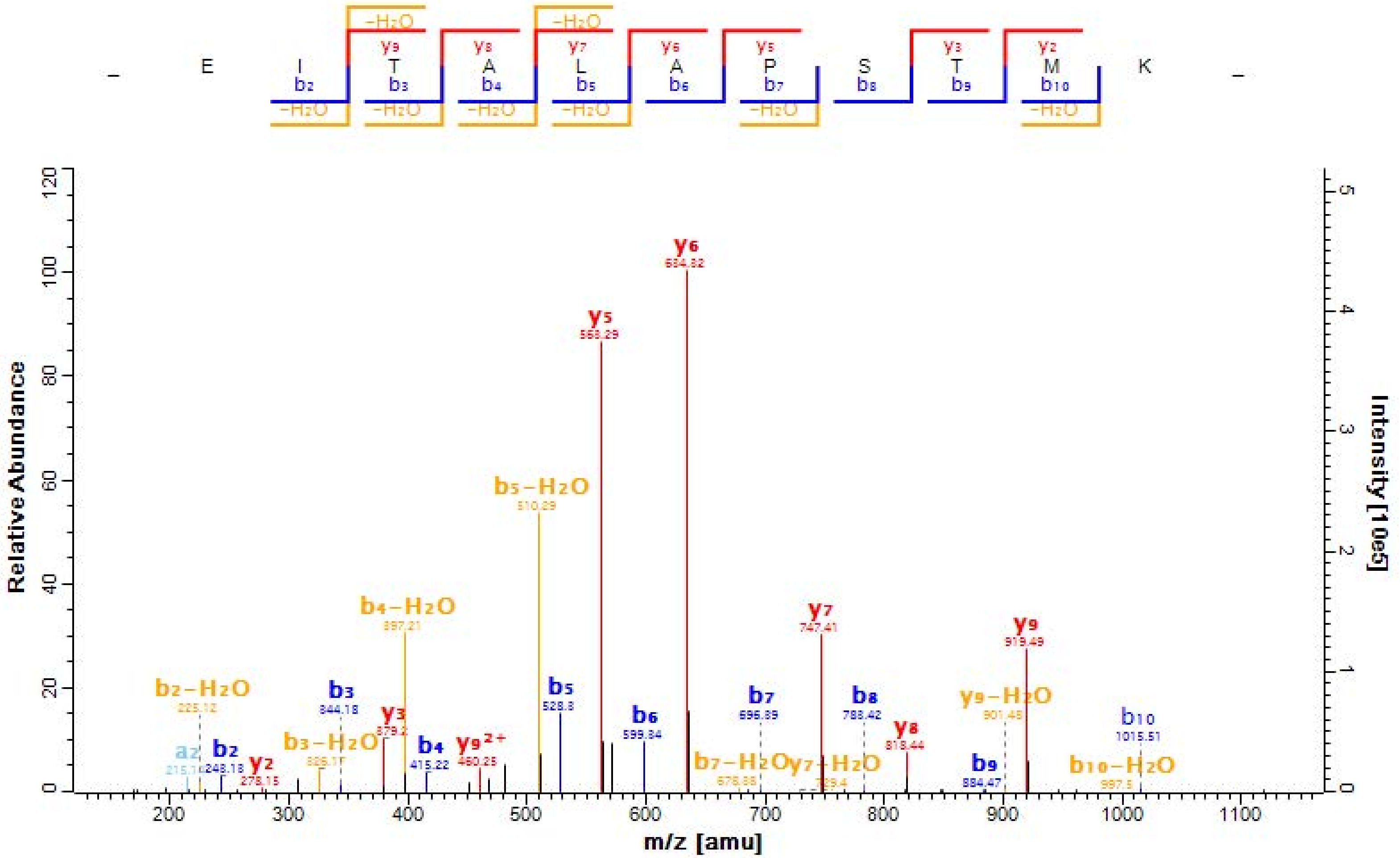
Mass:	1403.71461
m/z:	702.86458
Charge:	2+
Retentiontime:	20.109699249267
Score:	170.9496
Mass Error [ppm]:	0.15604
PEP:	1.2913E-11
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	51 %
Peak Coverage:	34 %
Protein Localisation:	722 ... 734

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	I	12				
-0.08	199.2		227.2	+0.001	227.2	2	L	11	1292	+0.139	646.3	-0.04
	314.2		342.2	-0.06	342.2	3	D	10	1179	-0.02	589.8	+0.12
	429.2		457.2		457.2	4	D	9	1064	-0.05	1064	
	516.3		544.3	-0.23	544.3	5	S	8	948.5	+0.05	948.5	
	631.3		659.3		659.3	6	D	7	861.5	-0.06	861.5	
	718.3		746.3	+0.033	746.3	7	S	6	746.4		746.4	
	832.4		860.4	+0.277	860.4	8	N	5	659.4		659.4	
	945.5		973.4	-0.1	973.4	9	L	4	545.4	-0.06	545.4	
	1032	+0.388	530.7	-0.09	1060	10	S	3	432.3	+0.003	432.3	
	1132		1160	-0.14	1160	11	V	2	345.2	-0.06	345.2	
	1231		1259	-0.12	1259	12	V	1	246.2	-0.04	246.2	
						13	K	0	147.1		147.1	

Scan number	2514	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	184.24



precursor information

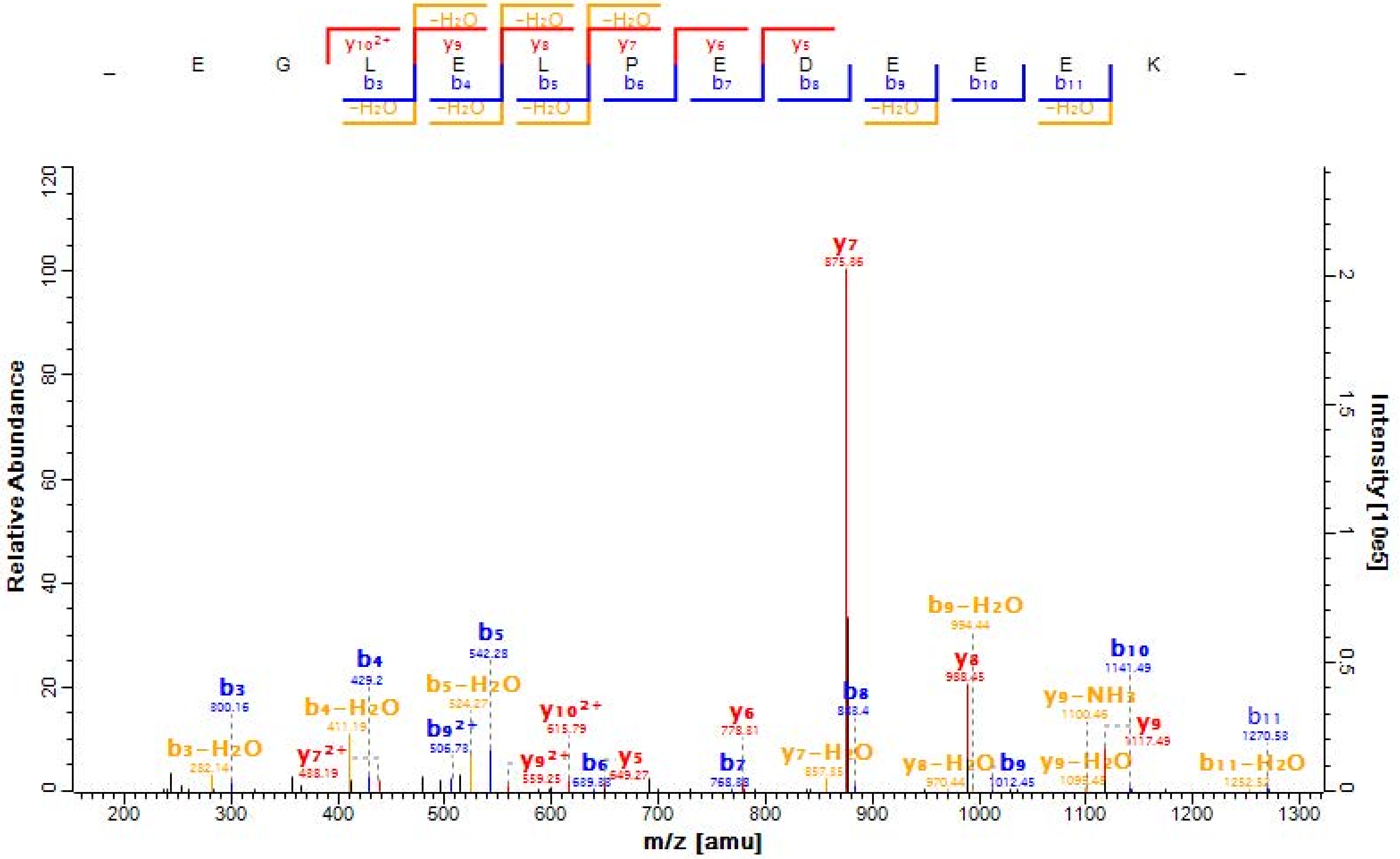
Mass:	1160.61107
m/z:	581.31281
Charge:	2+
Retentiontime:	20.920673370361
Score:	184.2389
Mass Error [ppm]:	-0.031167
PEP:	1.7045E-10
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	83 %
Peak Coverage:	37 %
Protein Localisation:	316 ... 326

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	10				
-0.059	215.14	+0.0351	243.13	2	I	9	1032.6		1032.6	
	316.19	-0.014	344.18	3	T	8	919.49	-0.041	460.25	+0.0595
	387.22	+0.0161	415.22	4	A	7	818.44	+0.0871	818.44	
	500.31	-0.108	528.3	5	L	6	747.41	+0.0367	747.41	
	571.34	-0.057	599.34	6	A	5	634.32	+0.0383	634.32	
	668.4	+0.0969	696.39	7	P	4	563.29	+0.0708	563.29	
	755.43	+0.1939	783.42	8	S	3	466.23		466.23	
	856.48	-0.132	884.47	9	T	2	379.2	+0.0379	379.2	
	987.52	-0.267	1015.5	10	M	1	278.15	+0.088	278.15	
				11	K	0	147.11		147.11	

Scan number	2632	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	206.97



precursor information

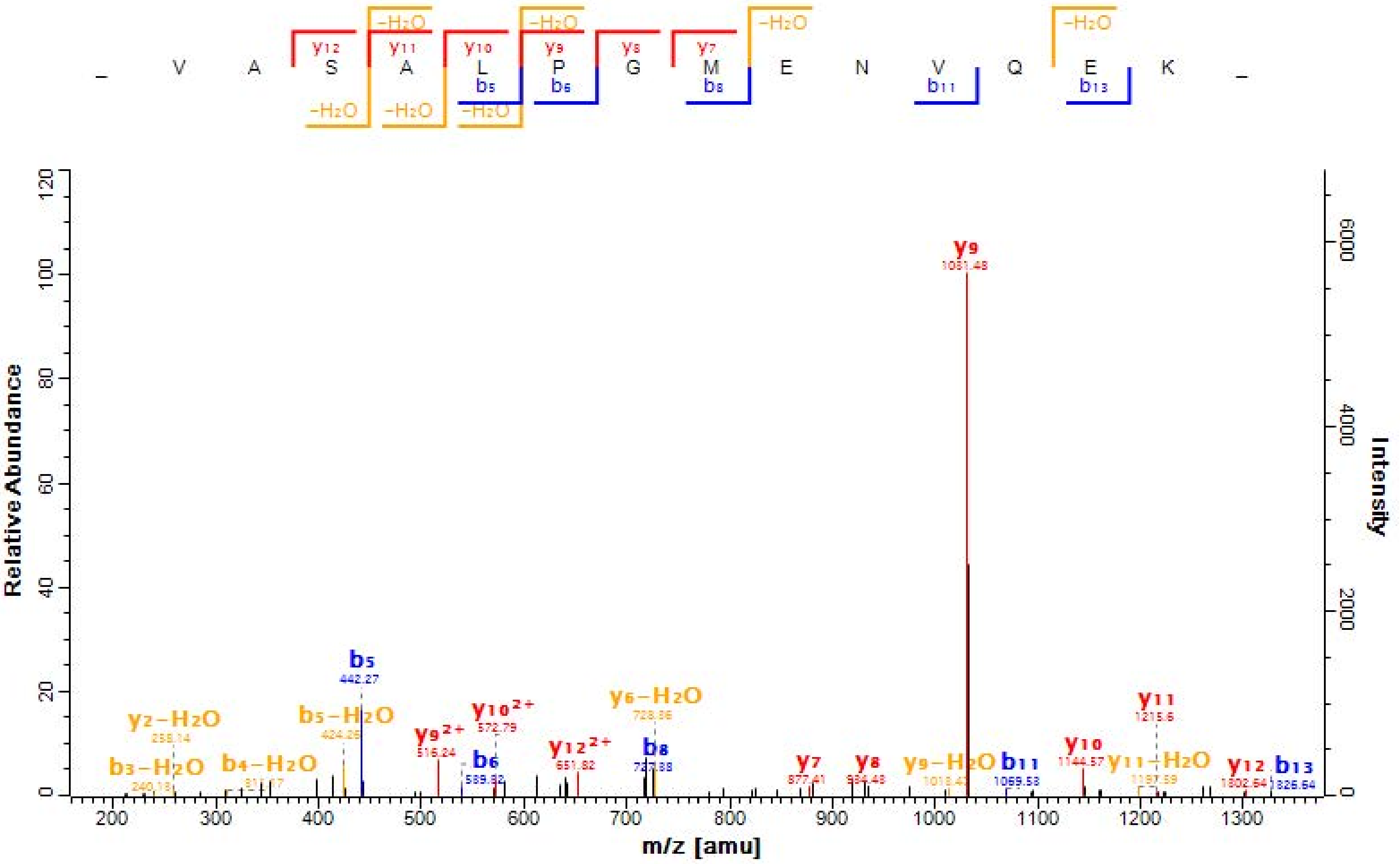
Mass:	1415.63035
m/z:	708.82245
Charge:	2+
Retentiontime:	21.575054168701
Score:	206.9699
Mass Error [ppm]:	-0.027999
PEP:	1.379E-18
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	72 %
Peak Coverage:	40 %
Protein Localisation:	669 ... 680

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	11				
	187.07		187.07	2	G	10	1287.6		1287.6	
	300.16	+0.0645	300.16	3	L	9	1230.6		615.79	+0.2844
	429.2	-0.041	429.2	4	E	8	1117.5	-0.003	559.25	+0.0287
	542.28	-0.061	542.28	5	L	7	988.45	-0.001	988.45	
	639.33	+0.1728	639.33	6	P	6	875.36	+0.0177	438.19	+0.152
	768.38	+0.1413	768.38	7	E	5	778.31	+0.1422	778.31	
	883.4	+0.0753	883.4	8	D	4	649.27	+0.0812	649.27	
-0.387	506.73	+0.0343	1012.4	9	E	3	534.24		534.24	
	1141.5	-0.189	1141.5	10	E	2	405.2		405.2	
	1270.5	-0.311	1270.5	11	E	1	276.16		276.16	
				12	K	0	147.11		147.11	

Scan number	2678	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	79.61



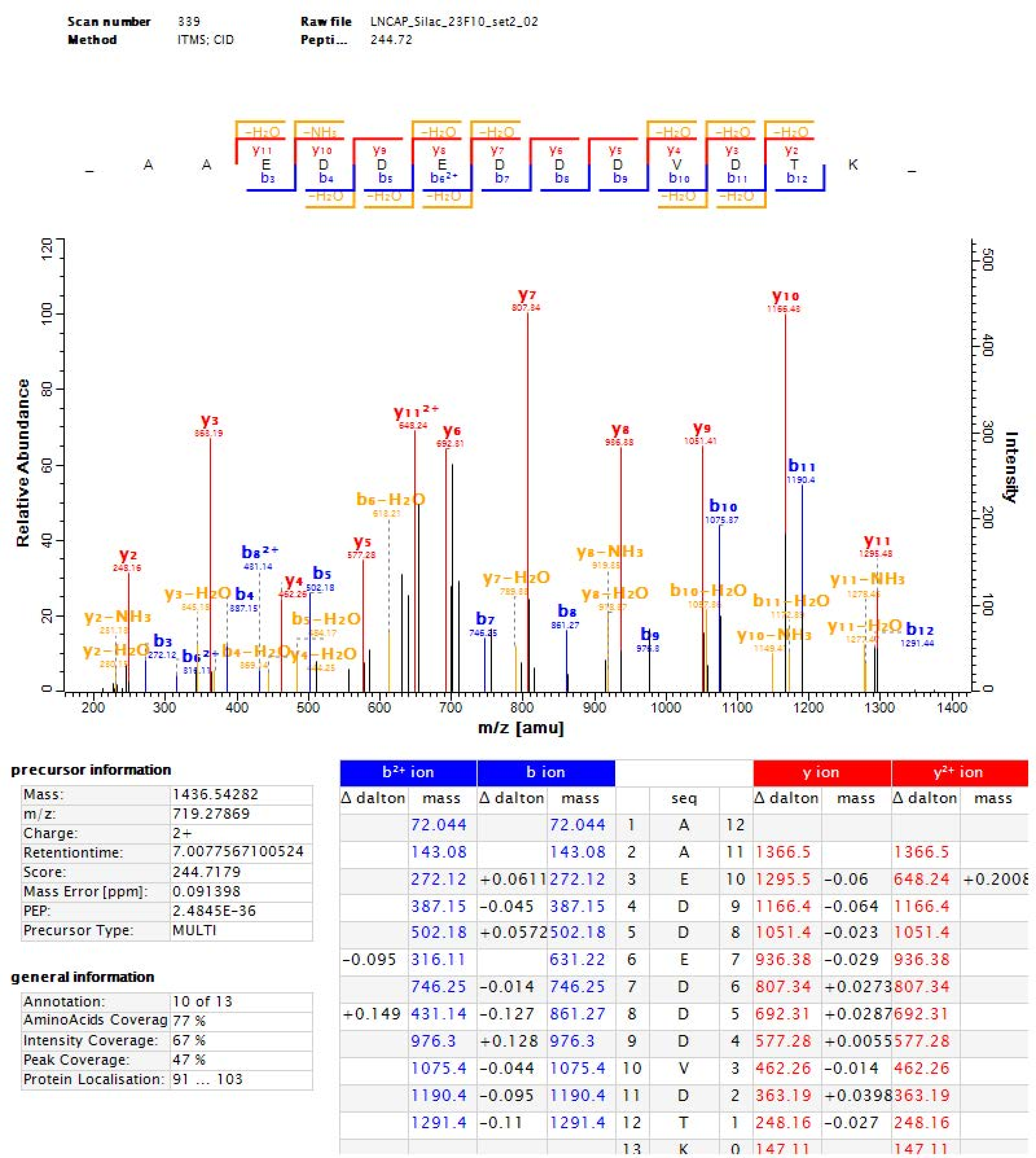
precursor information

Mass:	1471.73418
m/z:	736.87437
Charge:	2+
Retentiontime:	21.831764221191
Score:	79.61386
Mass Error [ppm]:	0.068064
PEP:	0.0010428
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	54 %
Peak Coverage:	25 %
Protein Localisation:	170 ... 183

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	13				
	171.1128	2	A	12	1373.673		1373.673	
	258.1448	3	S	11	1302.636	+0.072791	651.8216	+0.245709
	329.1819	4	A	10	1215.604	+0.013999	1215.604	
-0.00588	442.266	5	L	9	1144.567	-0.18375	572.787	+0.372138
+0.083447	539.3188	6	P	8	1031.483	-0.03145	516.2449	+0.067856
	596.3402	7	G	7	934.4299	+0.103162	934.4299	
-0.40593	727.3807	8	M	6	877.4084	+0.024651	877.4084	
	856.4233	9	E	5	746.3679		746.3679	
	970.4662	10	N	4	617.3253		617.3253	
+0.104869	1069.535	11	V	3	503.2824		503.2824	
	1197.593	12	Q	2	404.214		404.214	
-0.16158	1326.636	13	E	1	276.1554		276.1554	
		14	K	0	147.1128		147.1128	



Scan number	339	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	244.72

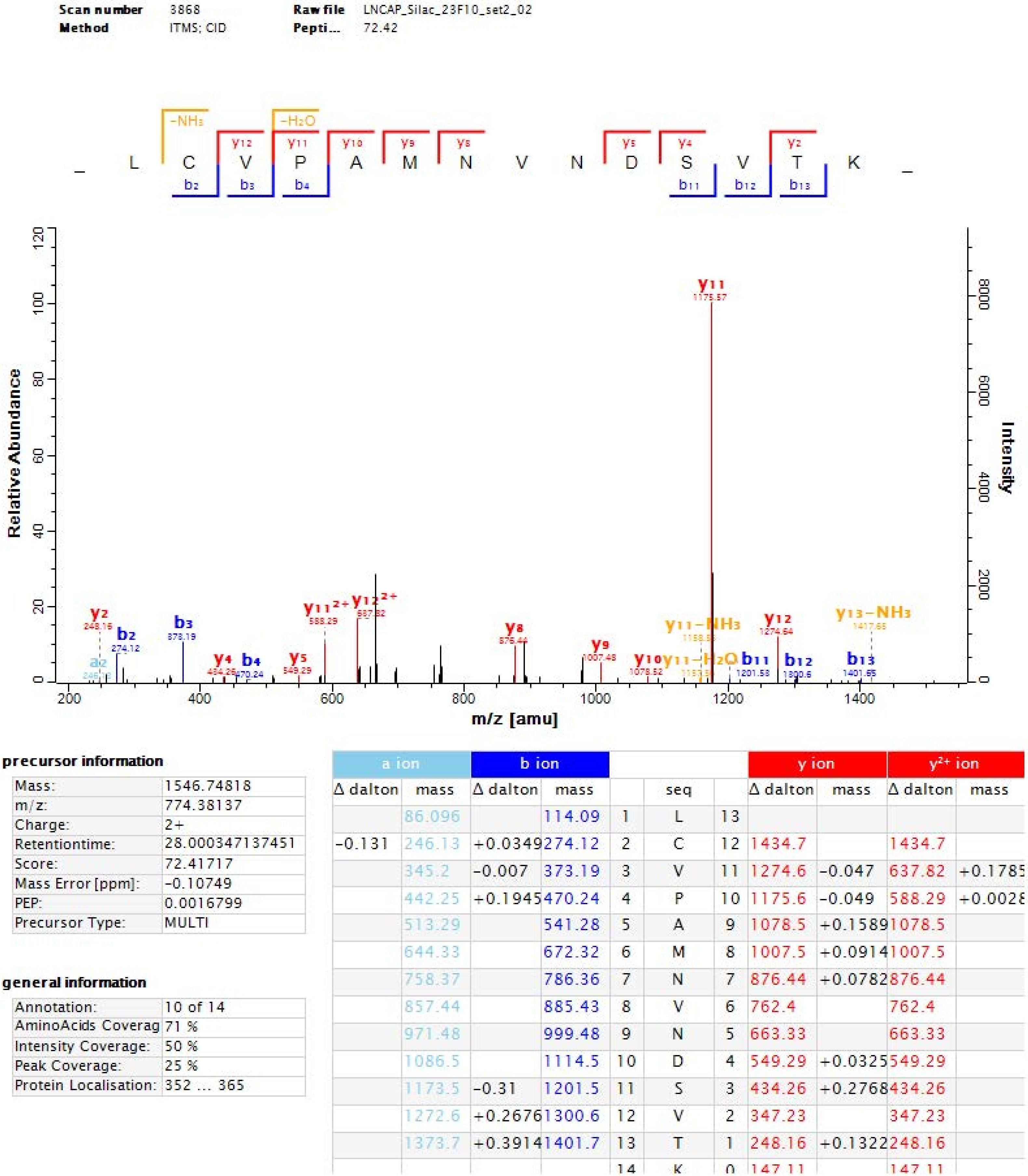
precursor information

Mass:	1436.54282
m/z:	719.27869
Charge:	2+
Retentiontime:	7.0077567100524
Score:	244.7179
Mass Error [ppm]:	0.091398
PEP:	2.4845E-36
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	67 %
Peak Coverage:	47 %
Protein Localisation:	91 ... 103

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	12				
	143.08		143.08	2	A	11	1366.5		1366.5	
	272.12	+0.0611	272.12	3	E	10	1295.5	-0.06	648.24	+0.2008
	387.15	-0.045	387.15	4	D	9	1166.4	-0.064	1166.4	
	502.18	+0.0572	502.18	5	D	8	1051.4	-0.023	1051.4	
-0.095	316.11		631.22	6	E	7	936.38	-0.029	936.38	
	746.25	-0.014	746.25	7	D	6	807.34	+0.0273	807.34	
+0.149	431.14	-0.127	861.27	8	D	5	692.31	+0.0287	692.31	
	976.3	+0.128	976.3	9	D	4	577.28	+0.0055	577.28	
	1075.4	-0.044	1075.4	10	V	3	462.26	-0.014	462.26	
	1190.4	-0.095	1190.4	11	D	2	363.19	+0.0398	363.19	
	1291.4	-0.11	1291.4	12	T	1	248.16	-0.027	248.16	
				13	K	0	147.11		147.11	



Scan number	3868	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	72.42

precursor information

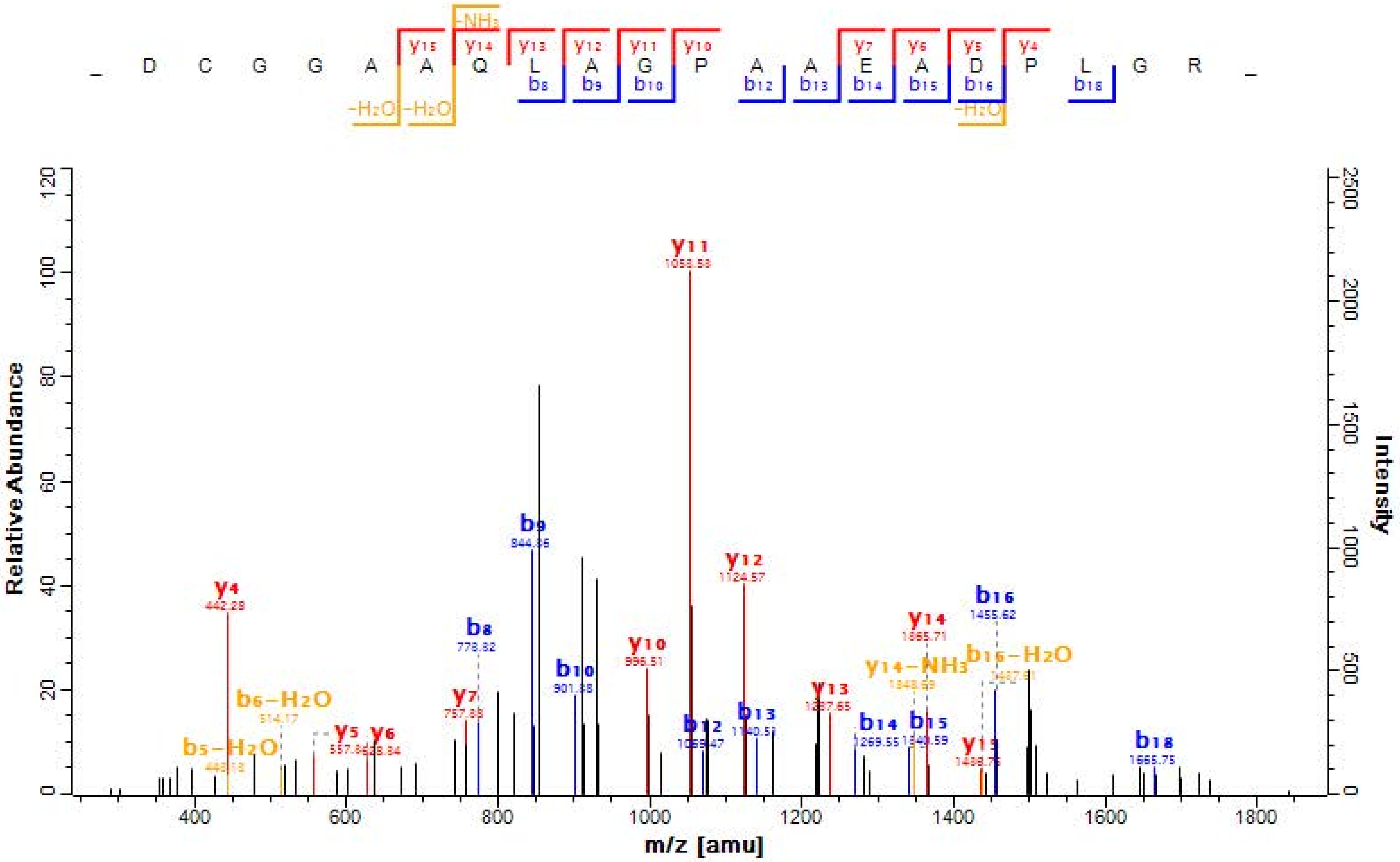
Mass:	1546.74818
m/z:	774.38137
Charge:	2+
Retentiontime:	28.000347137451
Score:	72.41717
Mass Error [ppm]:	-0.10749
PEP:	0.0016799
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	50 %
Peak Coverage:	25 %
Protein Localisation:	352 ... 365

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	13				
-0.131	246.13	+0.0349	274.12	2	C	12	1434.7		1434.7	
	345.2	-0.007	373.19	3	V	11	1274.6	-0.047	637.82	+0.1785
	442.25	+0.1945	470.24	4	P	10	1175.6	-0.049	588.29	+0.0028
	513.29		541.28	5	A	9	1078.5	+0.1589	1078.5	
	644.33		672.32	6	M	8	1007.5	+0.0914	1007.5	
	758.37		786.36	7	N	7	876.44	+0.0782	876.44	
	857.44		885.43	8	V	6	762.4		762.4	
	971.48		999.48	9	N	5	663.33		663.33	
	1086.5		1114.5	10	D	4	549.29	+0.0325	549.29	
	1173.5	-0.31	1201.5	11	S	3	434.26	+0.2768	434.26	
	1272.6	+0.2676	1300.6	12	V	2	347.23		347.23	
	1373.7	+0.3914	1401.7	13	T	1	248.16	+0.1322	248.16	
				14	K	0	147.11		147.11	

Scan number	3999	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	75.77



precursor information

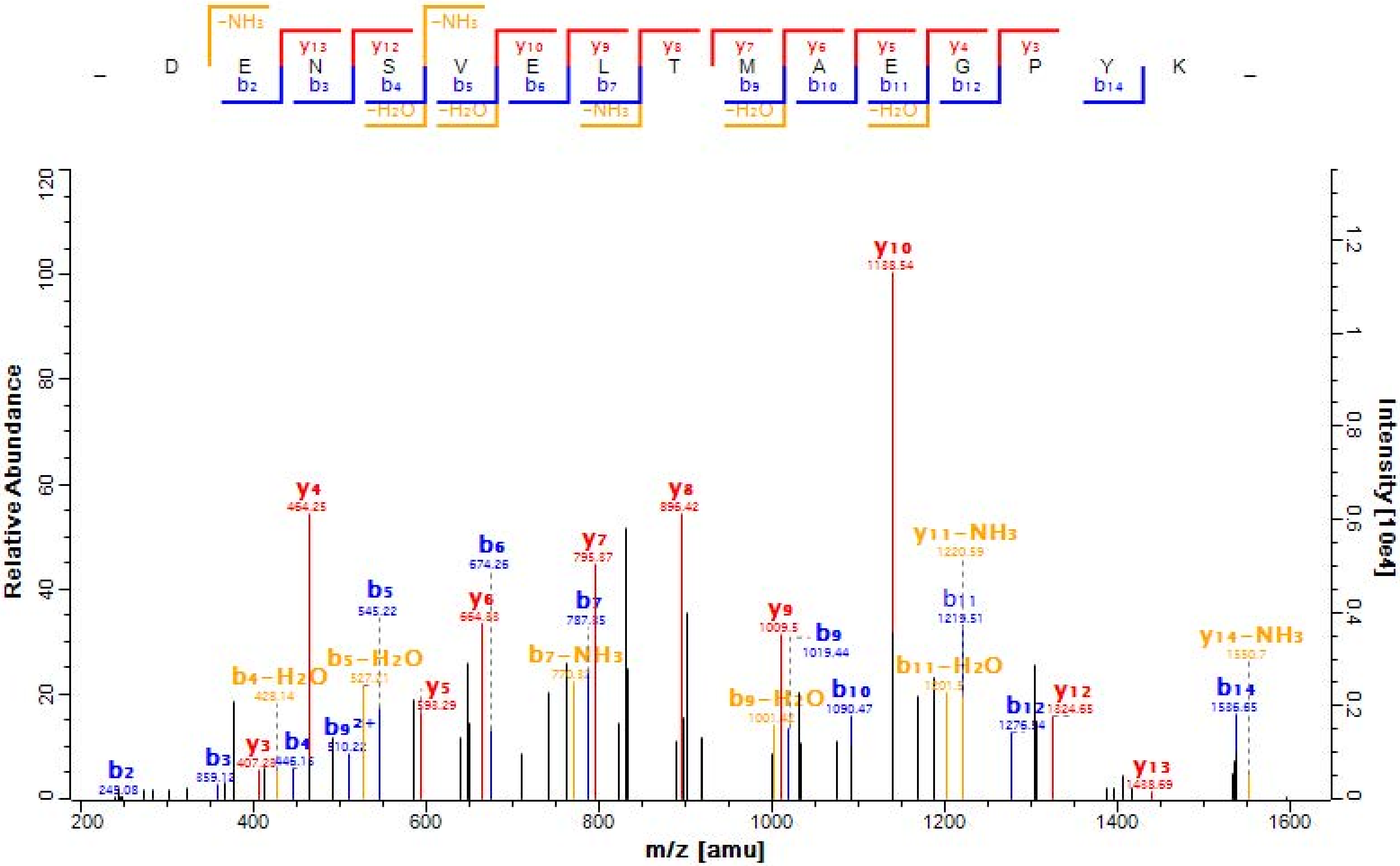
Mass:	1895.88149
m/z:	948.94802
Charge:	2+
Retentiontime:	28.651065826416
Score:	75.77346
Mass Error [ppm]:	1.0133
PEP:	0.0043013
Precursor Type:	ISO

general information

Annotation:	14 of 20
AminoAcids Coverag	70 %
Intensity Coverage:	38 %
Peak Coverage:	27 %
Protein Localisation:	7 ... 26

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	116.034219499	1	D	19		
	276.0648677	2	C	18	1781.85990731	
	333.086331424	3	G	17	1621.82925911	
	390.107795147	4	G	16	1564.80779538	
	461.144908935	5	A	15	1507.78633166	
	532.182022723	6	A	14	1436.74921787	−0.0838126
	660.240600234	7	Q	13	1365.71210408	+0.0463188
−0.1097594	773.324664215	8	L	12	1237.65352657	−0.0754016
−0.0117414	844.361778002	9	A	11	1124.56946259	−0.0052536
−0.0353413	901.383241726	10	G	10	1053.5323488	+0.0042723
	998.436005578	11	P	9	996.510885081	+0.0616857
+0.0005134	1069.47311937	12	A	8	899.458121229	
−0.0444128	1140.51023315	13	A	7	828.421007441	
+0.0492245	1269.55282625	14	E	6	757.383893653	+0.0229667
−0.1581773	1340.58994004	15	A	5	628.341300557	+0.1278157
−0.1561897	1455.61688307	16	D	4	557.304186769	+0.2606326
	1552.66964692	17	P	3	442.277243737	+0.104287
−0.066333	1665.7537109	18	L	2	345.224479885	
	1722.77517463	19	G	1	232.140415905	
		20	R	0	175.118952181	

Scan number	4131	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	124.68



precursor information

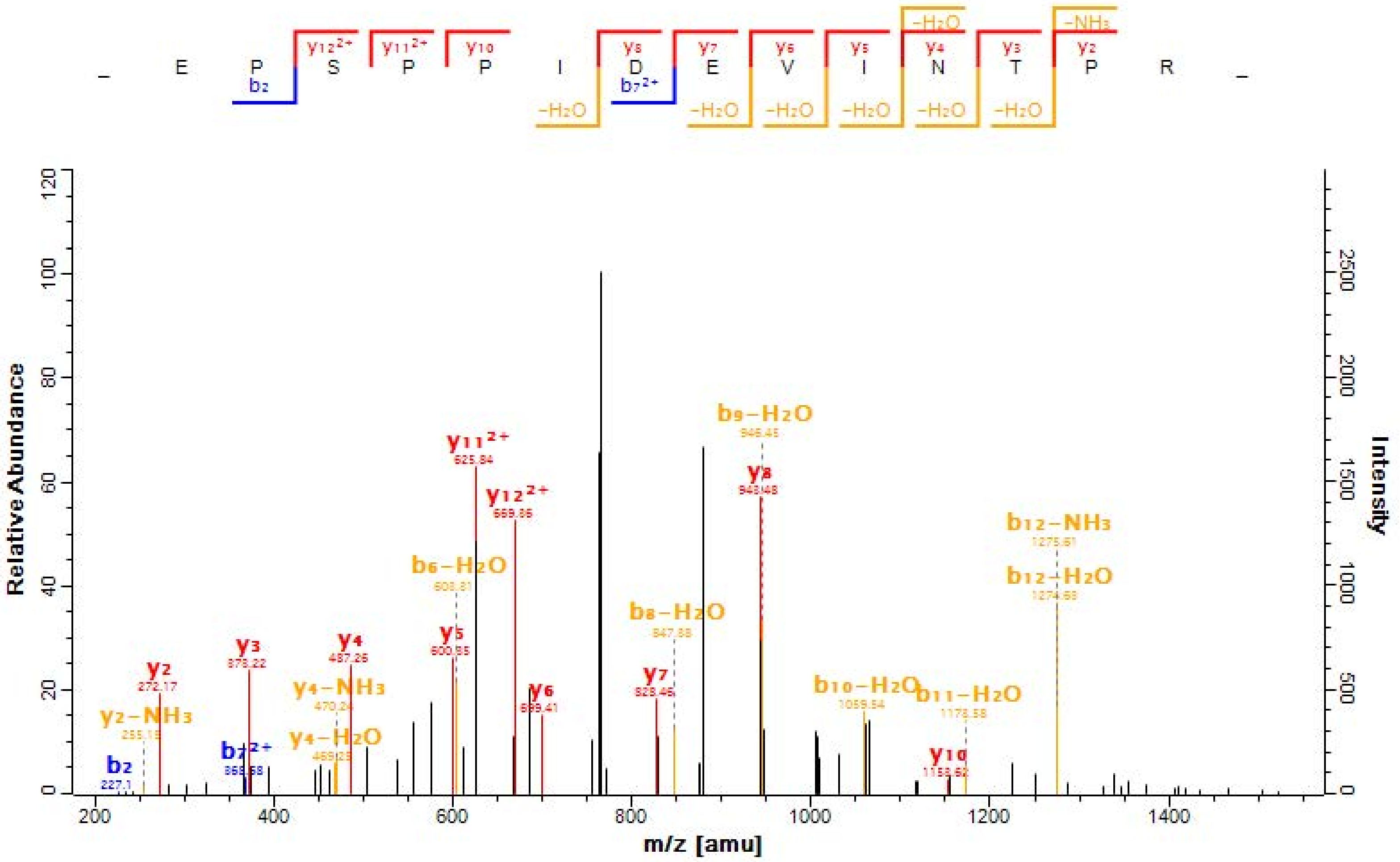
Mass:	1681.75072
m/z:	841.88264
Charge:	2+
Retentiontime:	29.348617553710
Score:	124.6754
Mass Error [ppm]:	0.12212
PEP:	2.3076E-09
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	51 %
Peak Coverage:	36 %
Protein Localisation:	185 ... 199

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	116.0342		116.0342	1	D	14		
	245.0768	+0.018692	245.0768	2	E	13	1567.731	
	359.1197	+0.239696	359.1197	3	N	12	1438.688	-0.14272
	446.1518	+0.036159	446.1518	4	S	11	1324.645	+0.031306
	545.2202	-0.004	545.2202	5	V	10	1237.613	
	674.2628	+0.069866	674.2628	6	E	9	1138.545	+0.021031
	787.3468	-0.01701	787.3468	7	L	8	1009.502	-0.00785
	888.3945		888.3945	8	T	7	896.4182	-0.00282
-0.25727	510.2211	-0.1186	1019.435	9	M	6	795.3706	+0.038018
	1090.472	-0.05976	1090.472	10	A	5	664.3301	+0.040416
	1219.515	-0.08551	1219.515	11	E	4	593.293	+0.032791
	1276.536	-0.14762	1276.536	12	G	3	464.2504	+0.061957
	1373.589		1373.589	13	P	2	407.2289	+0.008408
	1536.652	-0.09697	1536.652	14	Y	1	310.1761	
				15	K	0	147.1128	

Scan number	4227	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	72.89



precursor information

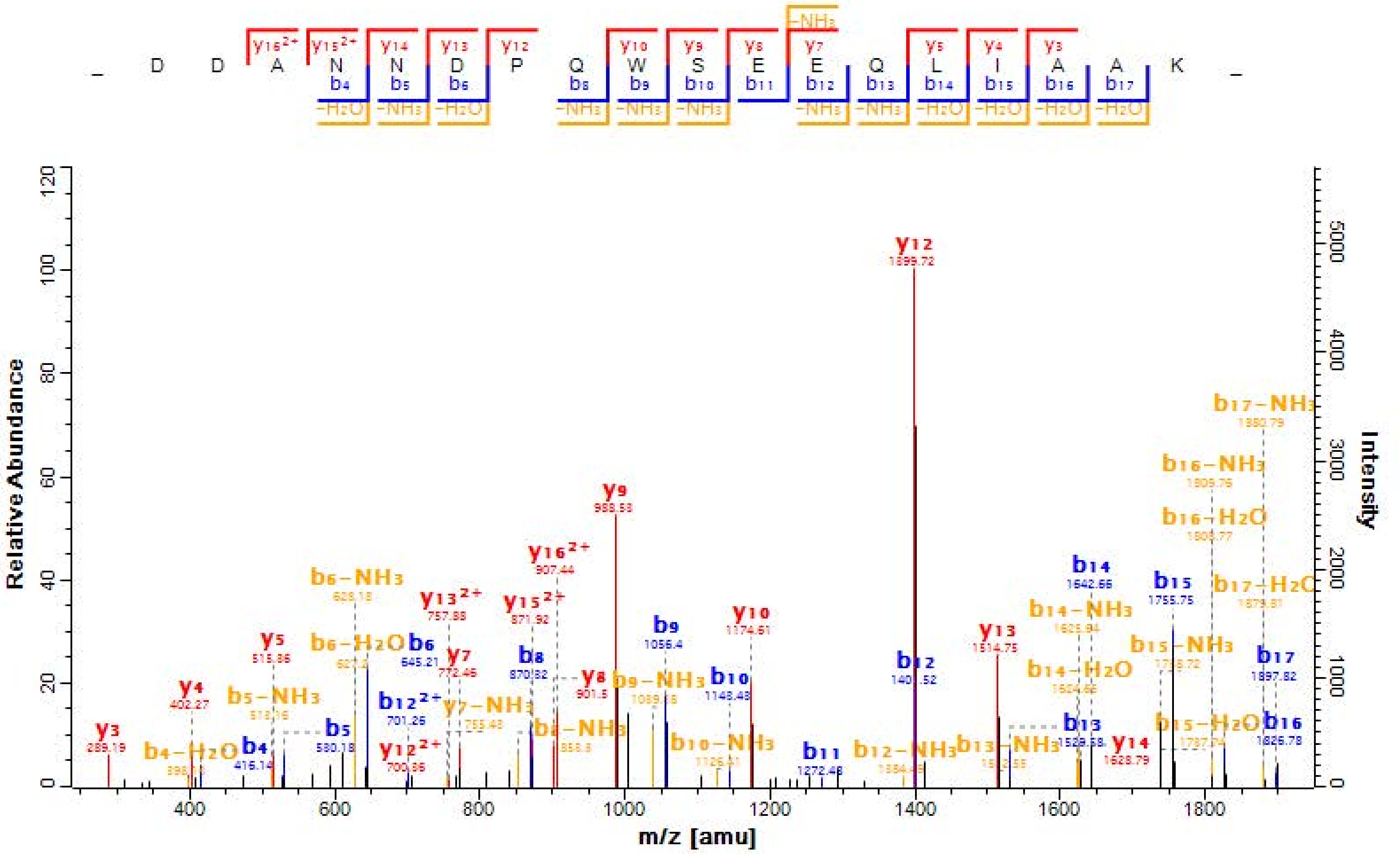
Mass:	1562.79362
m/z:	782.40409
Charge:	2+
Retentiontime:	29.841358184814
Score:	72.89124
Mass Error [ppm]:	-0.26617
PEP:	0.001638
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	43 %
Peak Coverage:	28 %
Protein Localisation:	116 ... 129

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	13				
	227.1	-0.071	227.1	2	P	12	1434.8		1434.8	
	314.13		314.13	3	S	11	1337.7		669.36	+0.2323
	411.19		411.19	4	P	10	1250.7		625.84	-0.061
	508.24		508.24	5	P	9	1153.6	+0.1083	1153.6	
	621.32		621.32	6	I	8	1056.6		1056.6	
-0.248	368.68		736.35	7	D	7	943.48	-0.071	943.48	
	865.39		865.39	8	E	6	828.46	+0.0284	828.46	
	964.46		964.46	9	V	5	699.41	+0.1443	699.41	
	1077.5		1077.5	10	I	4	600.35	+0.0766	600.35	
	1191.6		1191.6	11	N	3	487.26	+0.1427	487.26	
	1292.6		1292.6	12	T	2	373.22	+0.0637	373.22	
	1389.7		1389.7	13	P	1	272.17	-0.035	272.17	
				14	R	0	175.12		175.12	

Scan number	4363	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	307.21



precursor information

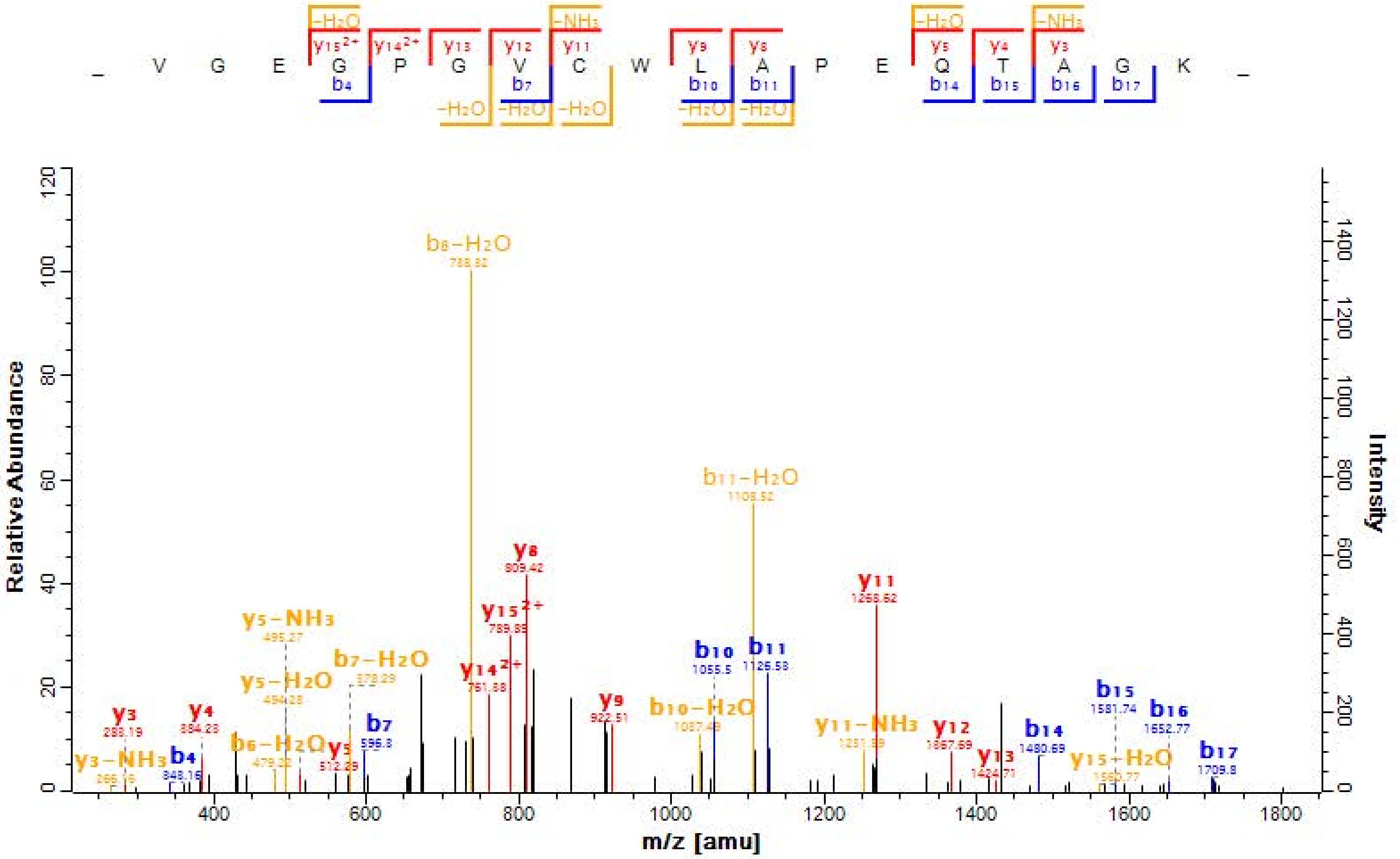
Mass:	2042.91799
m/z:	1022.46627
Charge:	2+
Retentiontime:	30.547027587890
Score:	307.205
Mass Error [ppm]:	-0.065154
PEP:	1.1673E-110
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	61 %
Peak Coverage:	46 %
Protein Localisation:	158 ... 175

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	17				
	231.06		231.06	2	D	16	1928.9		1928.9	
	302.1		302.1	3	A	15	1813.9		907.44	+0.2507
	416.14	+0.0086	416.14	4	N	14	1742.8		871.92	-0.25
	530.18	+0.0435	530.18	5	N	13	1628.8	-0.238	1628.8	
	645.21	+0.0642	645.21	6	D	12	1514.7	-0.18	757.88	+0.4788
	742.26		742.26	7	P	11	1399.7	-0.099	700.36	+0.0301
	870.32	-0.008	870.32	8	Q	10	1302.7		1302.7	
	1056.4	-0.071	1056.4	9	W	9	1174.6	-0.074	1174.6	
	1143.4	+0.0476	1143.4	10	S	8	988.53	-0.086	988.53	
	1272.5	-0.025	1272.5	11	E	7	901.5	-0.039	901.5	
-0.175	701.26	+0.1332	1401.5	12	E	6	772.46	+0.0625	772.46	
	1529.6	-0.115	1529.6	13	Q	5	643.41		643.41	
	1642.7	-0.163	1642.7	14	L	4	515.36	-0.024	515.36	
	1755.7	-0.153	1755.7	15	I	3	402.27	+0.1249	402.27	
	1826.8	-0.161	1826.8	16	A	2	289.19	-0.03	289.19	
	1897.8	-0.114	1897.8	17	A	1	218.15		218.15	
				18	K	0	147.11		147.11	

Scan number	5025	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	151.04



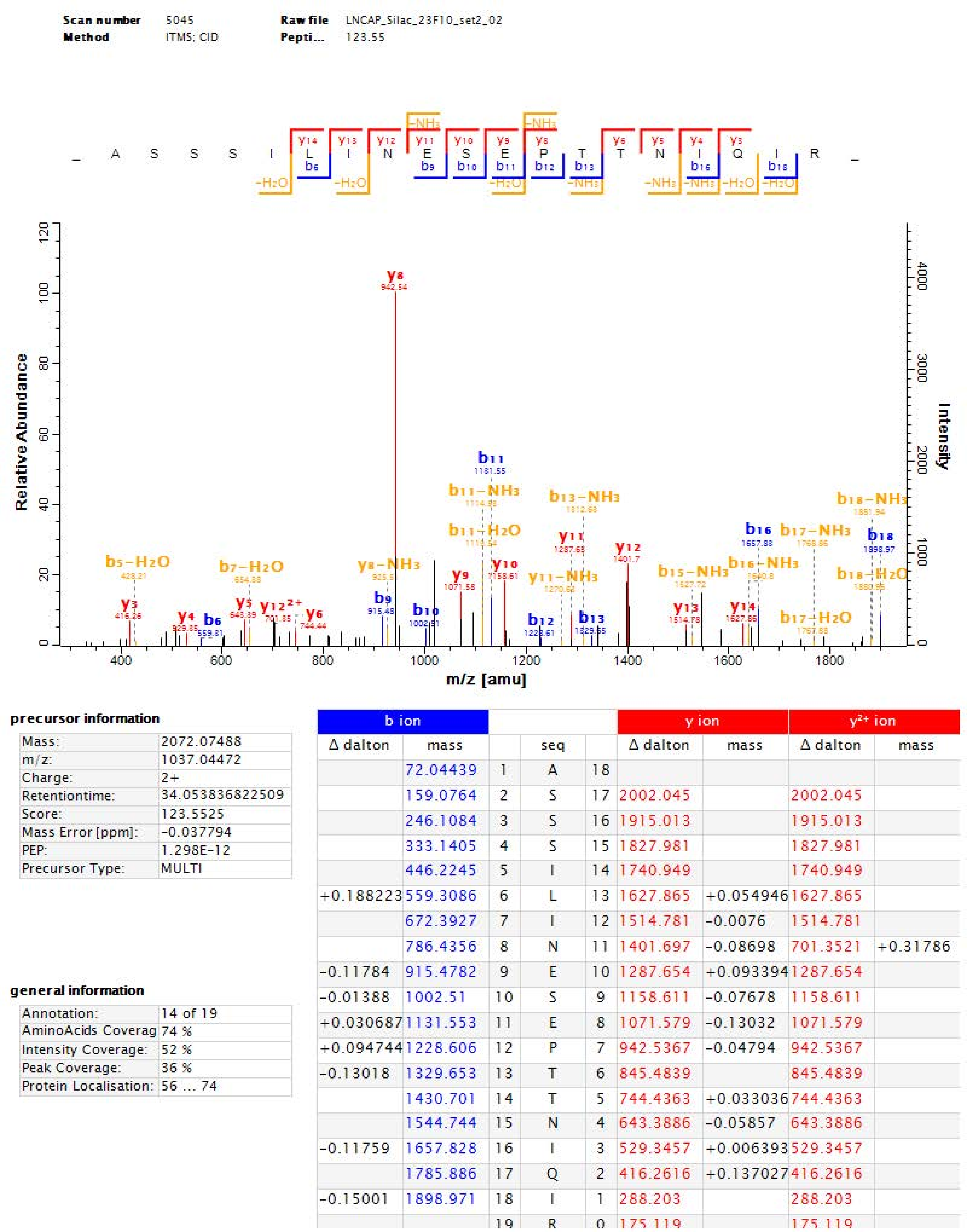
precursor information

Mass:	1854.89343
m/z:	928.45399
Charge:	2+
Retentiontime:	33.947914123535
Score:	151.0435
Mass Error [ppm]:	0.00037632
PEP:	1.4342E-18
Precursor Type:	MULTI

general information

Annotation:	13 of 18
AminoAcids Coverag	72 %
Intensity Coverage:	55 %
Peak Coverage:	30 %
Protein Localisation:	152 ... 169

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	17				
	157.0972	2	G	16	1764.846		1764.846	
	286.1397	3	E	15	1707.825		1707.825	
+0.059492	343.1612	4	G	14	1578.782		789.8949	+0.182169
	440.214	5	P	13	1521.761		761.3841	+0.080902
	497.2354	6	G	12	1424.708	+0.043865	1424.708	
+0.119671	596.3039	7	V	11	1367.687	-0.07041	1367.687	
	756.3345	8	C	10	1268.618	-0.00713	1268.618	
	942.4138	9	W	9	1108.588		1108.588	
-0.10078	1055.498	10	L	8	922.5084	+0.079519	922.5084	
+0.068402	1126.535	11	A	7	809.4243	+0.09498	809.4243	
	1223.588	12	P	6	738.3872		738.3872	
	1352.63	13	E	5	641.3344		641.3344	
+0.121499	1480.689	14	Q	4	512.2918	+0.312351	512.2918	
+0.331999	1581.737	15	T	3	384.2333	-0.06297	384.2333	
-0.41569	1652.774	16	A	2	283.1856	+0.231839	283.1856	
-0.43935	1709.795	17	G	1	212.1485		212.1485	
		18	K	0	155.127		155.127	



Scan number	5045	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	123.55

precursor information

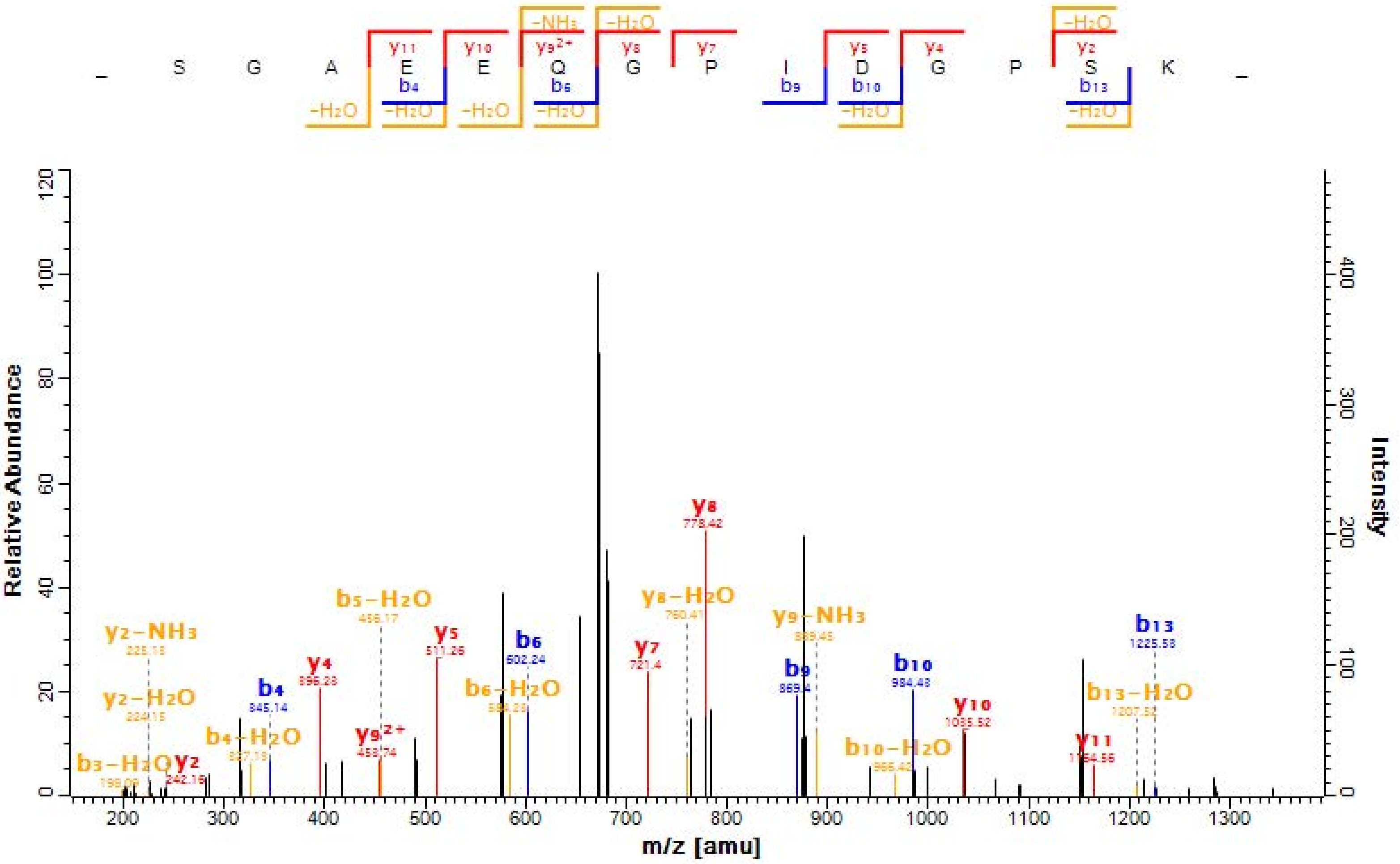
Mass:	2072.07488
m/z:	1037.04472
Charge:	2+
Retentiontime:	34.053836822509
Score:	123.5525
Mass Error [ppm]:	-0.037794
PEP:	1.298E-12
Precursor Type:	MULTI

general information

Annotation:	14 of 19
AminoAcids Coverag	74 %
Intensity Coverage:	52 %
Peak Coverage:	36 %
Protein Localisation:	56 ... 74

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	18				
	159.0764	2	S	17	2002.045		2002.045	
	246.1084	3	S	16	1915.013		1915.013	
	333.1405	4	S	15	1827.981		1827.981	
	446.2245	5	I	14	1740.949		1740.949	
+0.188223	559.3086	6	L	13	1627.865	+0.054946	1627.865	
	672.3927	7	I	12	1514.781	-0.0076	1514.781	
	786.4356	8	N	11	1401.697	-0.08698	701.3521	+0.31786
-0.11784	915.4782	9	E	10	1287.654	+0.093394	1287.654	
-0.01388	1002.51	10	S	9	1158.611	-0.07678	1158.611	
+0.030687	1131.553	11	E	8	1071.579	-0.13032	1071.579	
+0.094744	1228.606	12	P	7	942.5367	-0.04794	942.5367	
-0.13018	1329.653	13	T	6	845.4839		845.4839	
	1430.701	14	T	5	744.4363	+0.033036	744.4363	
	1544.744	15	N	4	643.3886	-0.05857	643.3886	
-0.11759	1657.828	16	I	3	529.3457	+0.006393	529.3457	
	1785.886	17	Q	2	416.2616	+0.137027	416.2616	
-0.15001	1898.971	18	I	1	288.203		288.203	
		19	R	0	175.119		175.119	

Scan number	525	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	74.85



precursor information

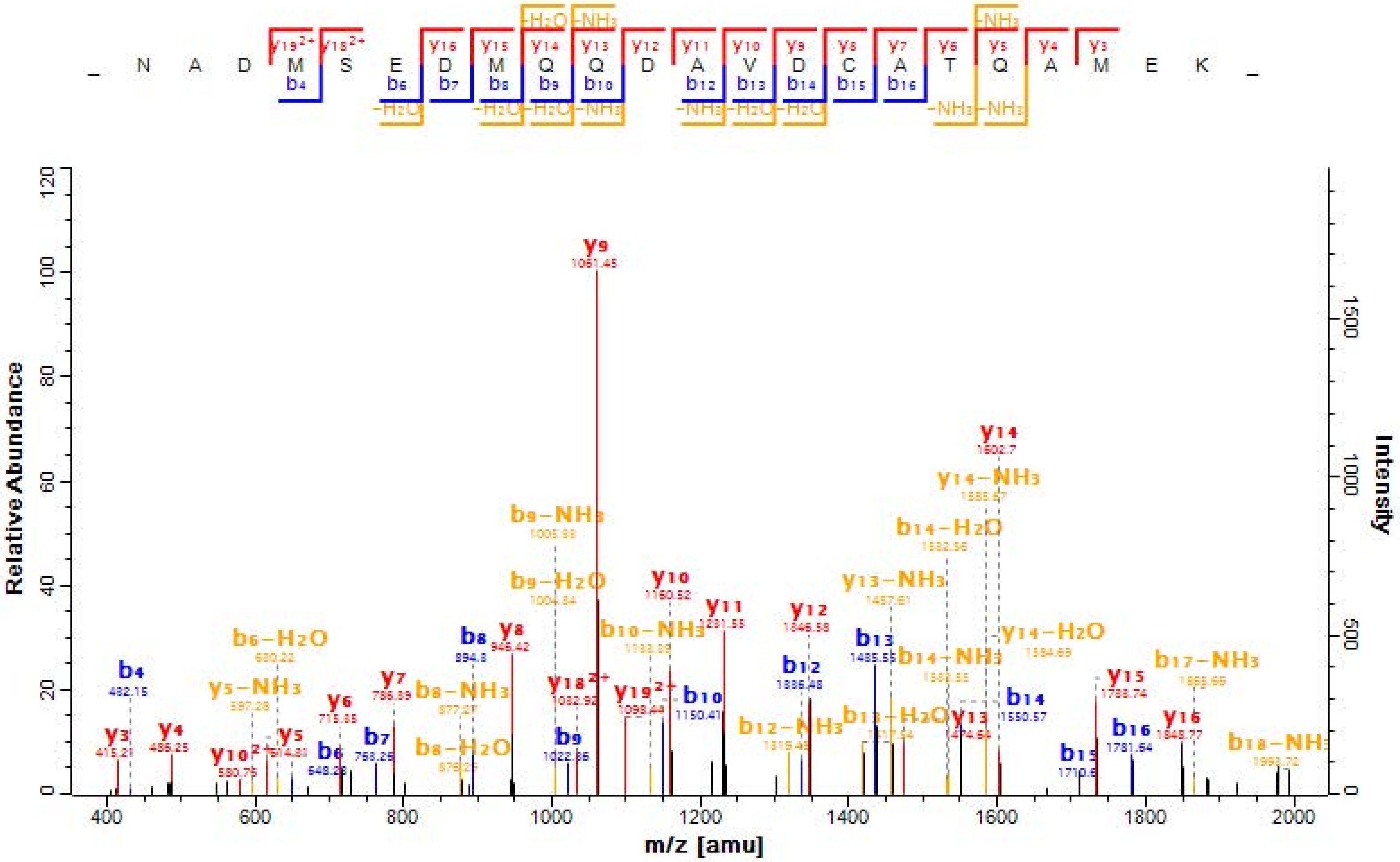
Mass:	1370.63022
m/z:	686.32239
Charge:	2+
Retentiontime:	8.6645650863647
Score:	74.85336
Mass Error [ppm]:	-0.8491
PEP:	0.0014643
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	26 %
Peak Coverage:	28 %
Protein Localisation:	224 ... 237

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	13				
	145.0608	2	G	12	1292.621		1292.621	
	216.0979	3	A	11	1235.599		1235.599	
+0.025357	345.1405	4	E	10	1164.562	+0.355711	1164.562	
	474.1831	5	E	9	1035.52	+0.05785	1035.52	
+0.088249	602.2416	6	Q	8	906.4771		453.7422	+0.169081
	659.2631	7	G	7	778.4185	-0.01133	778.4185	
	756.3159	8	P	6	721.397	+0.036503	721.397	
+0.035121	869.3999	9	I	5	624.3443		624.3443	
+0.026305	984.4269	10	D	4	511.2602	+0.063101	511.2602	
	1041.448	11	G	3	396.2333	-0.01512	396.2333	
	1138.501	12	P	2	339.2118		339.2118	
-0.07037	1225.533	13	S	1	242.159	+0.07191	242.159	
		14	K	0	155.127		155.127	

Scan number	5688	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	230.71



precursor information

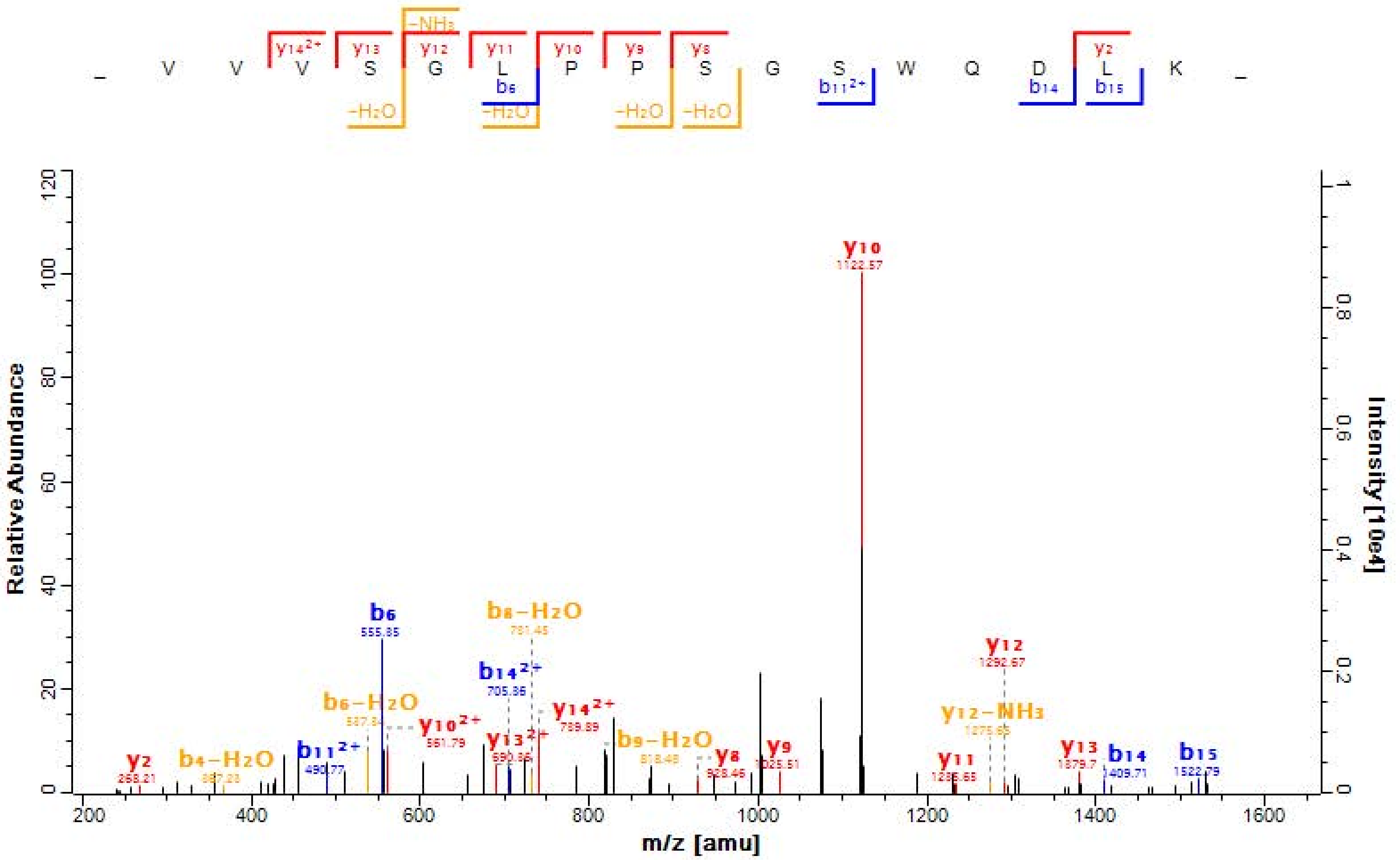
Mass:	2486.96582
m/z:	1244.49019
Charge:	2+
Retentiontime:	37.376995086669
Score:	230.7101
Mass Error [ppm]:	-0.0020538
PEP:	7.467E-76
Precursor Type:	MULTI

general information

Annotation:	17 of 22
AminoAcids Coverag	77 %
Intensity Coverage:	62 %
Peak Coverage:	46 %
Protein Localisation:	10 ... 31

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502	1	N	21				
	186.0873	2	A	20	2381.944		2381.944	
	301.1143	3	D	19	2310.907		2310.907	
-0.04671	432.1547	4	M	18	2195.88		1098.444	+0.35137
	519.1868	5	S	17	2064.84		1032.924	+0.217682
+0.167362	648.2294	6	E	16	1977.808		1977.808	
+0.025978	763.2563	7	D	15	1848.765	+0.044239	1848.765	
-0.00737	894.2968	8	M	14	1733.738	-0.06236	1733.738	
-0.10049	1022.355	9	Q	13	1602.698	-0.3024	1602.698	
+0.074698	1150.414	10	Q	12	1474.639	-0.11101	1474.639	
	1265.441	11	D	11	1346.581	+0.006166	1346.581	
-0.07859	1336.478	12	A	10	1231.554	+0.039212	1231.554	
+0.081876	1435.546	13	V	9	1160.517	+0.025057	580.7619	-0.42098
-0.15771	1550.573	14	D	8	1061.448	-0.11368	1061.448	
+0.017937	1710.604	15	C	7	946.4212	+0.06597	946.4212	
-0.18812	1781.641	16	A	6	786.3906	+0.032592	786.3906	
	1882.689	17	T	5	715.3535	+0.104069	715.3535	
	2010.747	18	Q	4	614.3058	-0.05187	614.3058	
	2081.784	19	A	3	486.2472	+0.070921	486.2472	
	2212.825	20	M	2	415.2101	+0.02048	415.2101	
	2341.868	21	E	1	284.1696		284.1696	
		22	K	0	155.127		155.127	

Scan number	5759	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	75.32



precursor information

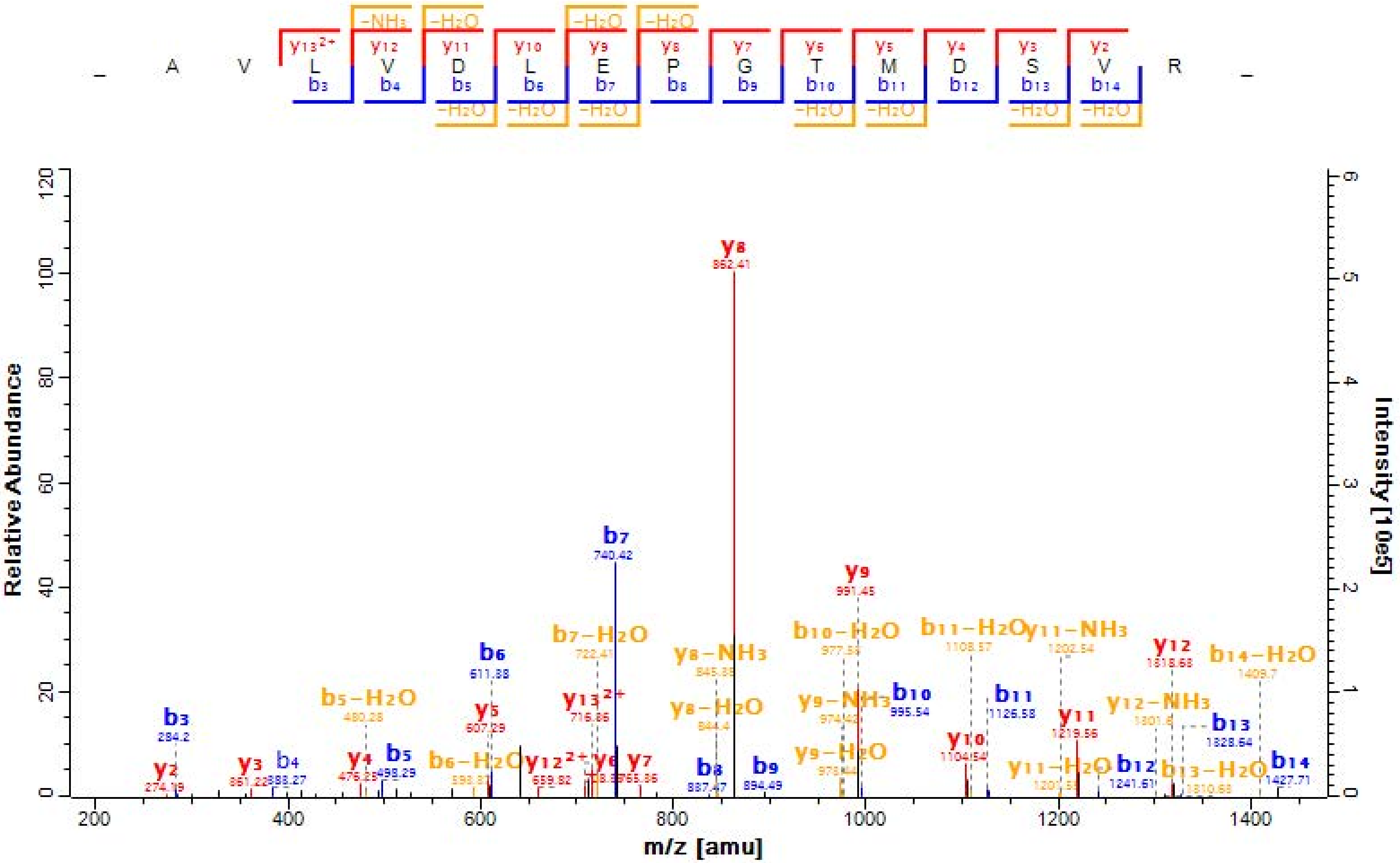
Mass:	1667.88863
m/z:	834.95159
Charge:	2+
Retentiontime:	37.760238647460
Score:	75.31638
Mass Error [ppm]:	0.2161
PEP:	0.00033437
Precursor Type:	MULTI

general information

Annotation:	10 of 16
AminoAcids Coverag	62 %
Intensity Coverage:	39 %
Peak Coverage:	24 %
Protein Localisation:	123 ... 138

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	15				
	199.14		199.14	2	V	14	1577.8		1577.8	
	298.21		298.21	3	V	13	1478.8		739.89	+0.079
	385.24		385.24	4	S	12	1379.7	-0.145	690.36	-0.247
	442.27		442.27	5	G	11	1292.7	+0.0884	1292.7	
	555.35	-0.024	555.35	6	L	10	1235.7	-0.035	1235.7	
	652.4		652.4	7	P	9	1122.6	-0.024	561.79	+0.0314
	749.46		749.46	8	P	8	1025.5	-0.111	1025.5	
	836.49		836.49	9	S	7	928.46	+0.3156	928.46	
	893.51		893.51	10	G	6	841.43		841.43	
-0.386	490.77		980.54	11	S	5	784.41		784.41	
	1166.6		1166.6	12	W	4	697.38		697.38	
	1294.7		1294.7	13	Q	3	511.3		511.3	
-0.003	705.36	+0.1113	1409.7	14	D	2	383.24		383.24	
	1522.8	+0.1022	1522.8	15	L	1	268.21	+0.0499	268.21	
				16	K	0	155.13		155.13	

Scan number	5797	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	265.12



precursor information

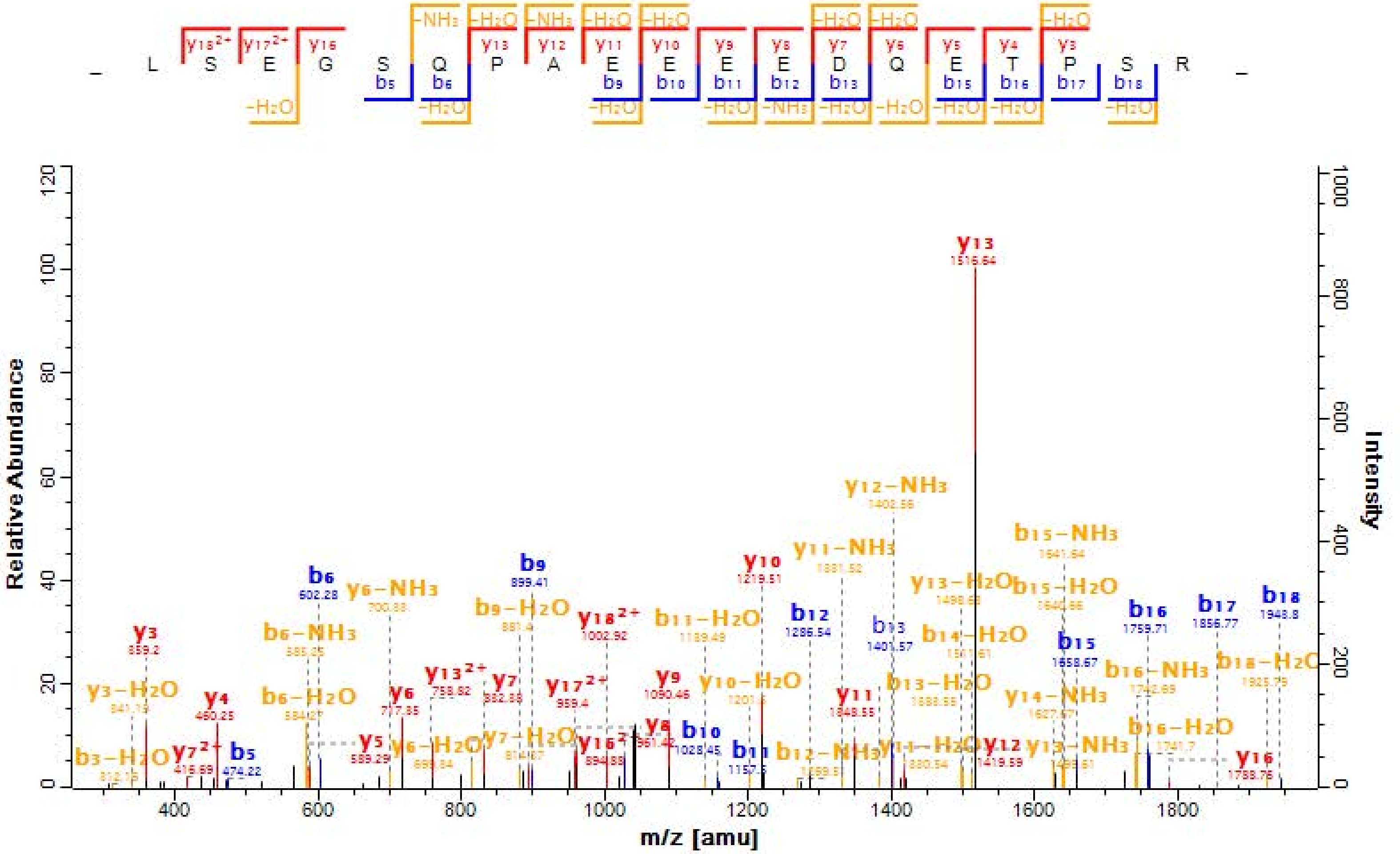
Mass:	1600.81297
m/z:	801.41376
Charge:	2+
Retentiontime:	37.947242736816
Score:	265.1235
Mass Error [ppm]:	-0.054164
PEP:	7.1354E-68
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	73 %
Peak Coverage:	51 %
Protein Localisation:	63 ... 77

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	14				
	171.1128	2	V	13	1530.783		1530.783	
+0.011018	284.1969	3	L	12	1431.715		716.361	+0.156537
-0.00228	383.2653	4	V	11	1318.631	-0.04908	659.819	+0.169699
+0.071605	498.2922	5	D	10	1219.562	-0.01594	1219.562	
+0.172234	611.3763	6	L	9	1104.535	-0.06139	1104.535	
-0.03399	740.4189	7	E	8	991.4513	+0.041416	991.4513	
-0.12643	837.4716	8	P	7	862.4087	+0.037866	862.4087	
+0.004144	894.4931	9	G	6	765.356	+0.122429	765.356	
-0.02242	995.5408	10	T	5	708.3345	+0.076083	708.3345	
-0.10276	1126.581	11	M	4	607.2868	+0.115033	607.2868	
-0.1756	1241.608	12	D	3	476.2463	+0.064698	476.2463	
-0.19139	1328.64	13	S	2	361.2194	+0.123745	361.2194	
-0.07426	1427.709	14	V	1	274.1874	+0.254071	274.1874	
		15	R	0	175.119		175.119	

Scan number 588 **Raw file** LNCAP_Silac_23F10_set2_02
Method ITMS; CID **Pepti...** 299.93



precursor information

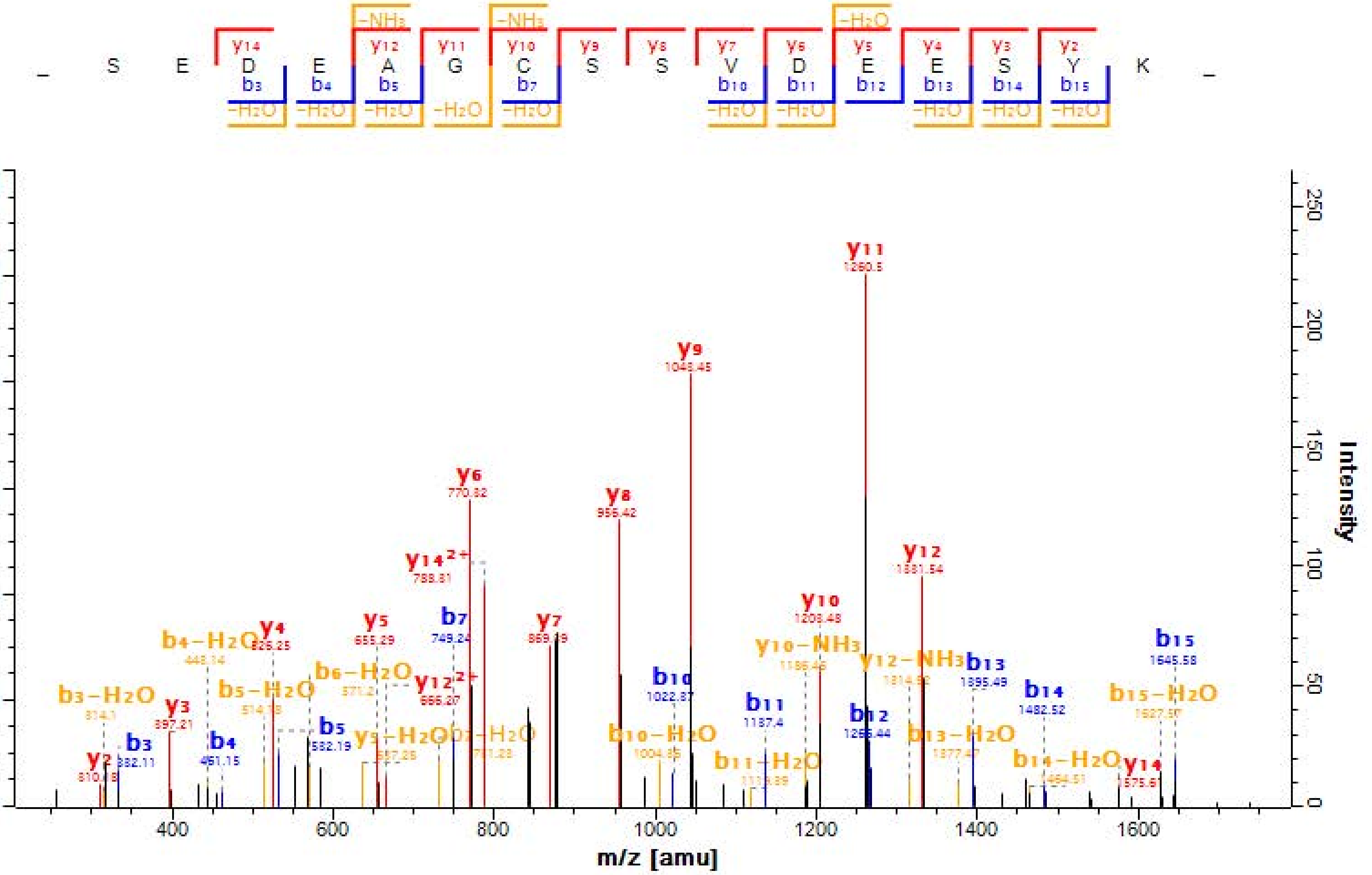
Mass:	2116.90308
m/z:	1059.45882
Charge:	2+
Retentiontime:	9.1949701309204
Score:	299.9317
Mass Error [ppm]:	-0.087027
PEP:	2.4157E-117
Precursor Type:	MULTI

general information

Annotation:	17 of 19
AminoAcids Coverag	89 %
Intensity Coverage:	62 %
Peak Coverage:	54 %
Protein Localisation:	141 ... 159

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	18				
	201.1234	2	S	17	2004.826		1002.917	+0.021844
	330.166	3	E	16	1917.794		959.4009	-0.05736
	387.1874	4	G	15	1788.752	+0.317236	894.8796	+0.353954
+0.019987	474.2195	5	S	14	1731.73		1731.73	
+0.123824	602.278	6	Q	13	1644.698		1644.698	
	699.3308	7	P	12	1516.64	-0.04933	758.8235	+0.174821
	770.3679	8	A	11	1419.587	+0.032118	1419.587	
+0.107808	899.4105	9	E	10	1348.55	-0.00071	1348.55	
+0.079864	1028.453	10	E	9	1219.507	+0.056283	1219.507	
-0.03207	1157.496	11	E	8	1090.465	+0.002684	1090.465	
-0.04927	1286.538	12	E	7	961.4221	+0.139516	961.4221	
-0.1508	1401.565	13	D	6	832.3795	+0.070537	416.6934	-0.45772
	1529.624	14	Q	5	717.3526	+0.028815	717.3526	
-0.02833	1658.666	15	E	4	589.294	+0.086233	589.294	
-0.16354	1759.714	16	T	3	460.2514	+0.054302	460.2514	
-0.29186	1856.767	17	P	2	359.2037	+0.034049	359.2037	
+0.138756	1943.799	18	S	1	262.151		262.151	
		19	R	0	175.119		175.119	

Scan number	625	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	226.24



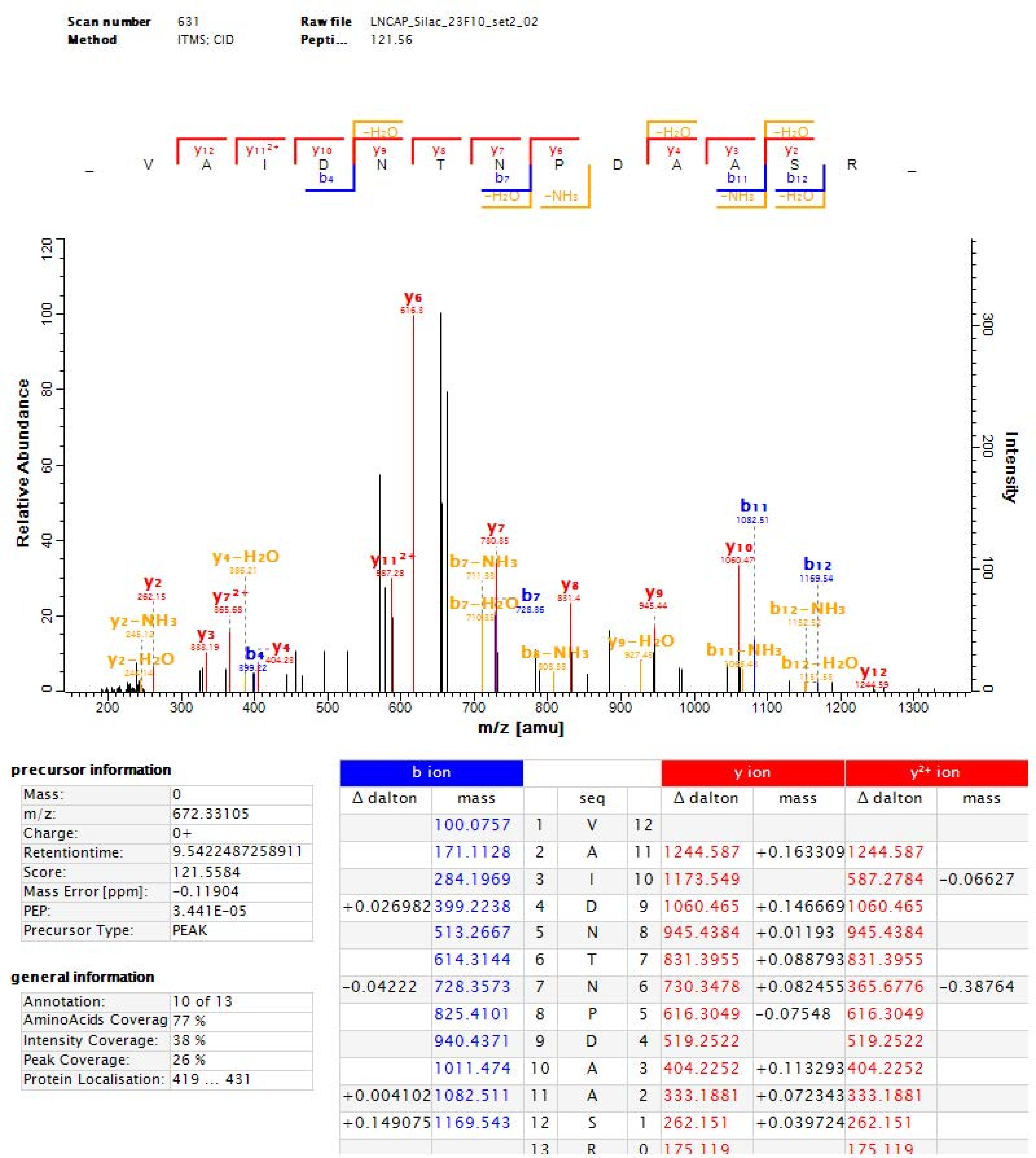
precursor information

Mass:	1790.67856
m/z:	896.34656
Charge:	2+
Retentiontime:	9.4921684265136
Score:	226.2415
Mass Error [ppm]:	-0.17222
PEP:	2.8218E-41
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	57 %
Peak Coverage:	43 %
Protein Localisation:	376 ... 391

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	15				
	217.0819	2	E	14	1704.654		1704.654	
+0.067856	332.1088	3	D	13	1575.612	-0.01521	788.3094	+0.131701
-0.01716	461.1514	4	E	12	1460.585		1460.585	
+0.101674	532.1885	5	A	11	1331.542	-0.02563	666.2746	-0.0878
	589.21	6	G	10	1260.505	-0.01525	1260.505	
+0.198	749.2407	7	C	9	1203.483	+0.00829	1203.483	
	836.2727	8	S	8	1043.453	-0.00952	1043.453	
	923.3047	9	S	7	956.4207	+0.021223	956.4207	
-0.07656	1022.373	10	V	6	869.3887	-0.13278	869.3887	
-0.03252	1137.4	11	D	5	770.3203	-0.0341	770.3203	
-0.03874	1266.443	12	E	4	655.2933	+0.08678	655.2933	
-0.0845	1395.485	13	E	3	526.2508	+0.03782	526.2508	
-0.15584	1482.517	14	S	2	397.2082	+0.060333	397.2082	
-0.10857	1645.581	15	Y	1	310.1761	+0.130142	310.1761	
		16	K	0	147.1128		147.1128	



Scan number	631	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	121.56

precursor information

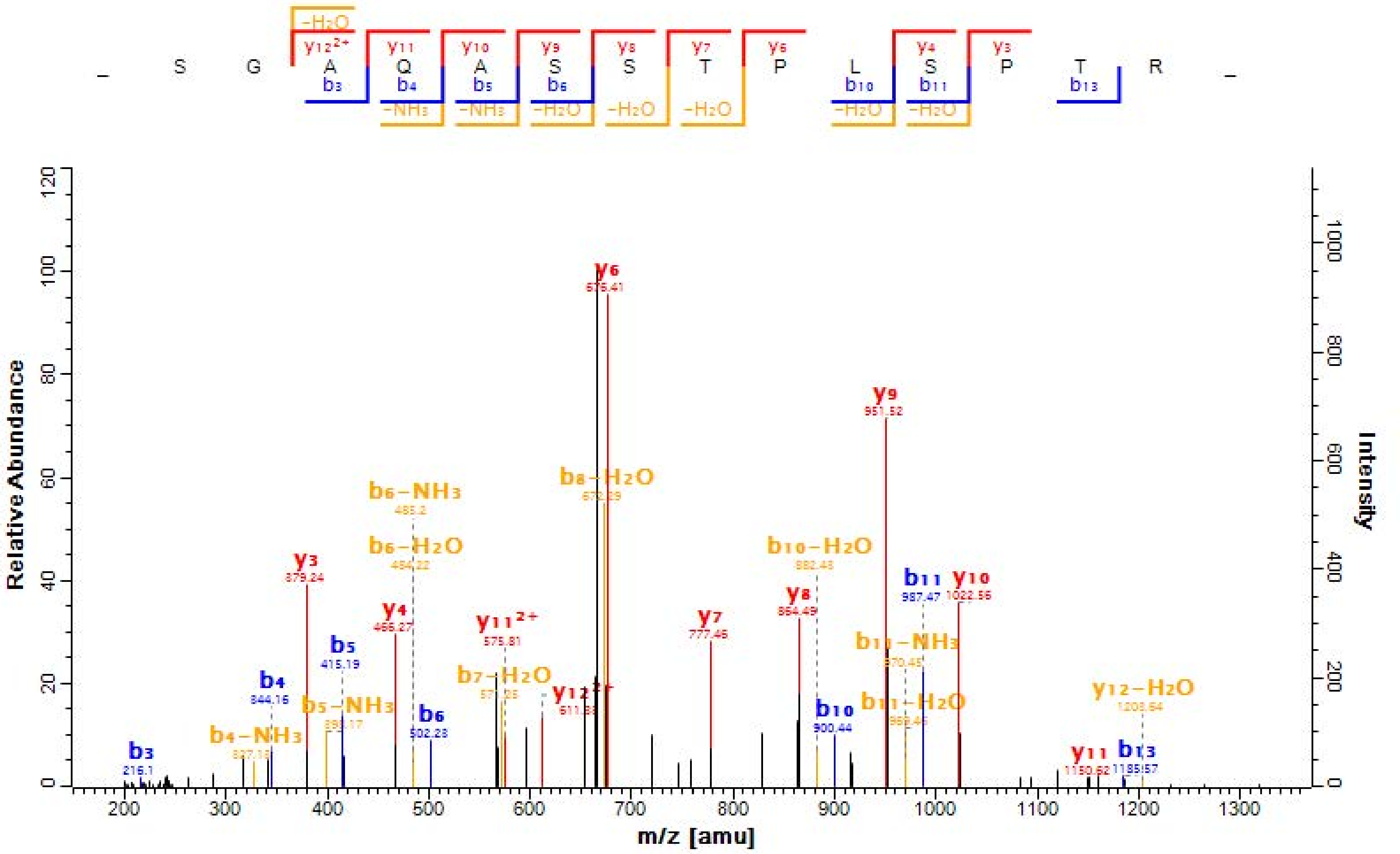
Mass:	0
m/z:	672.33105
Charge:	0+
Retentiontime:	9.5422487258911
Score:	121.5584
Mass Error [ppm]:	-0.11904
PEP:	3.441E-05
Precursor Type:	PEAK

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	38 %
Peak Coverage:	26 %
Protein Localisation:	419 ... 431

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	12				
	171.1128	2	A	11	1244.587	+0.163309	1244.587	
	284.1969	3	I	10	1173.549		587.2784	-0.06627
+0.026982	399.2238	4	D	9	1060.465	+0.146669	1060.465	
	513.2667	5	N	8	945.4384	+0.01193	945.4384	
	614.3144	6	T	7	831.3955	+0.088793	831.3955	
-0.04222	728.3573	7	N	6	730.3478	+0.082455	365.6776	-0.38764
	825.4101	8	P	5	616.3049	-0.07548	616.3049	
	940.4371	9	D	4	519.2522		519.2522	
	1011.474	10	A	3	404.2252	+0.113293	404.2252	
+0.004102	1082.511	11	A	2	333.1881	+0.072343	333.1881	
+0.149075	1169.543	12	S	1	262.151	+0.039724	262.151	
		13	R	0	175.119		175.119	

Scan number	664	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	135.02



precursor information

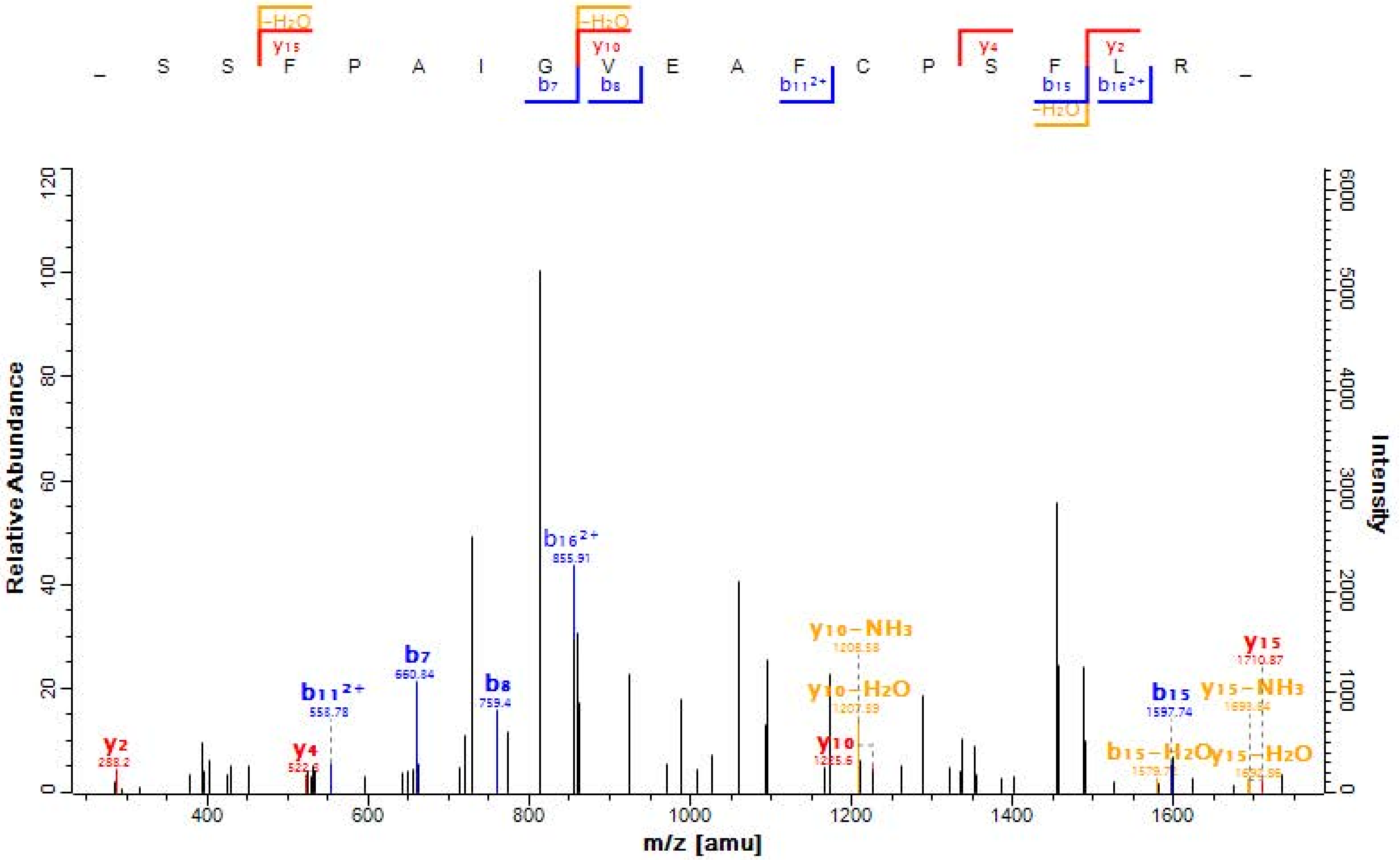
Mass:	1358.67943
m/z:	680.34699
Charge:	2+
Retentiontime:	9.7836666107177
Score:	135.0247
Mass Error [ppm]:	0.31353
PEP:	9.3589E-09
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	58 %
Peak Coverage:	31 %
Protein Localisation:	12 ... 25

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	13				
	145.0608	2	G	12	1278.674		1278.674	
+0.033313	216.0979	3	A	11	1221.653		611.3301	+0.206218
+0.104465	344.1565	4	Q	10	1150.616	+0.30204	575.8115	+0.122724
+0.104278	415.1936	5	A	9	1022.557	-0.01695	1022.557	
+0.017928	502.2256	6	S	8	951.5201	-0.07022	951.5201	
	589.2576	7	S	7	864.4881	+0.089245	864.4881	
	690.3053	8	T	6	777.4561	+0.114376	777.4561	
	787.3581	9	P	5	676.4084	-0.02819	676.4084	
+0.024599	900.4421	10	L	4	579.3556		579.3556	
-0.00133	987.4742	11	S	3	466.2716	-0.01325	466.2716	
	1084.527	12	P	2	379.2395	+0.024392	379.2395	
-0.19155	1185.575	13	T	1	282.1868		282.1868	
		14	R	0	181.1391		181.1391	

Scan number	7021	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	54.81



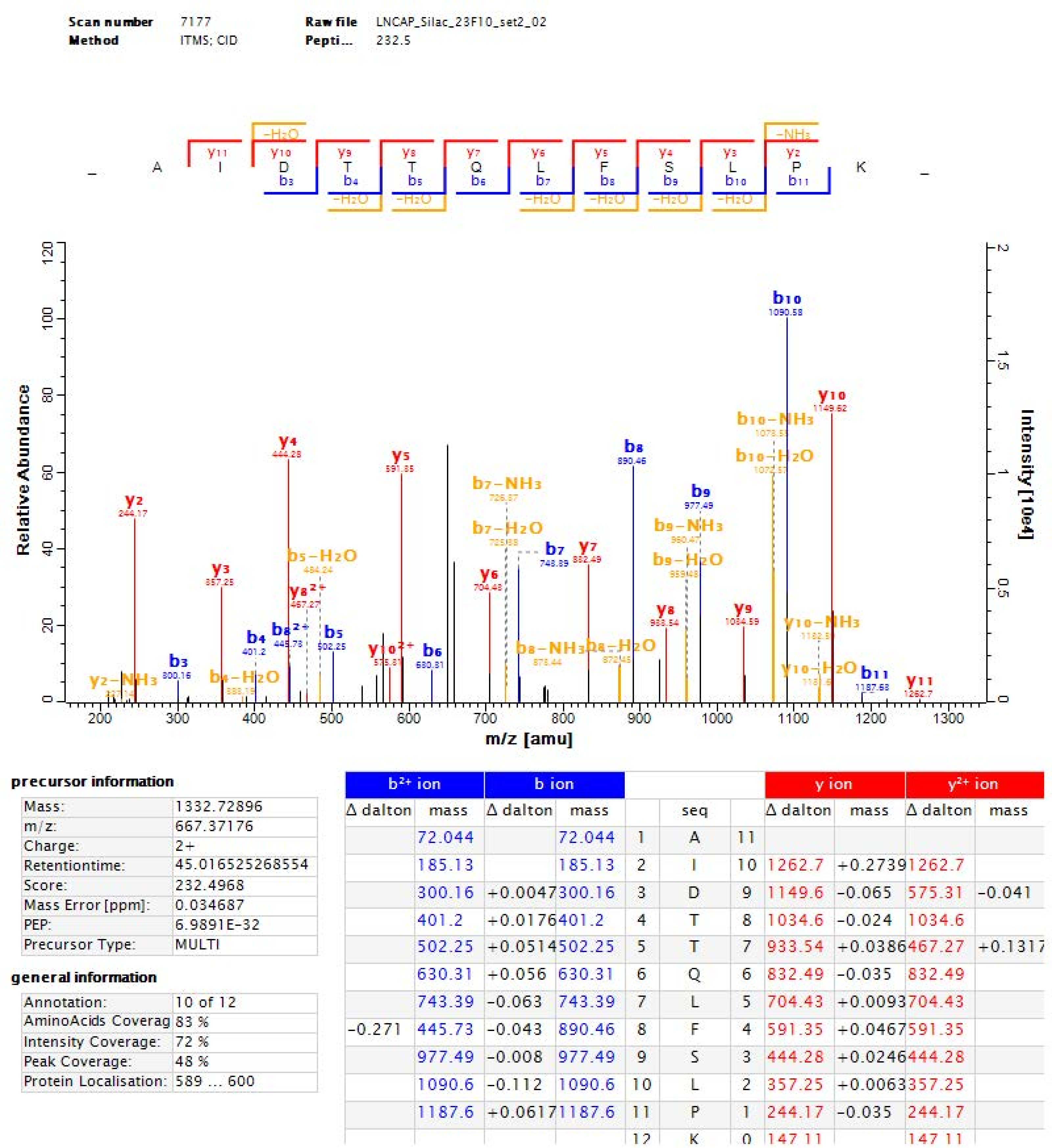
precursor information

Mass:	1883.92403
m/z:	942.96929
Charge:	2+
Retentiontime:	44.185081481933
Score:	54.81177
Mass Error [ppm]:	0.013859
PEP:	0.0033309
Precursor Type:	MULTI

general information

Annotation:	7 of 17
AminoAcids Coverag	41 %
Intensity Coverage:	15 %
Peak Coverage:	17 %
Protein Localisation:	188 ... 204

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	88.0393		88.0393	1	S	16		
	175.0713		175.0713	2	S	15	1797.899	
	322.1397		322.1397	3	F	14	1710.867	-0.00761
	419.1925		419.1925	4	P	13	1563.799	
	490.2296		490.2296	5	A	12	1466.746	
	603.3137		603.3137	6	I	11	1395.709	
	660.3352	+0.065238	660.3352	7	G	10	1282.625	
	759.4036	+0.03607	759.4036	8	V	9	1225.603	+0.145496
	888.4462		888.4462	9	E	8	1126.535	
	959.4833		959.4833	10	A	7	997.4924	
-0.40204	553.7795		1106.552	11	F	6	926.4553	
	1266.582		1266.582	12	C	5	779.3869	
	1363.635		1363.635	13	P	4	619.3562	
	1450.667		1450.667	14	S	3	522.3035	+0.030587
	1597.736	-0.07844	1597.736	15	F	2	435.2714	
-0.00658	855.9134		1710.82	16	L	1	288.203	-0.00105
				17	R	0	175.119	



Scan number 7177
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set2_02
Pepti... 232.5

precursor information

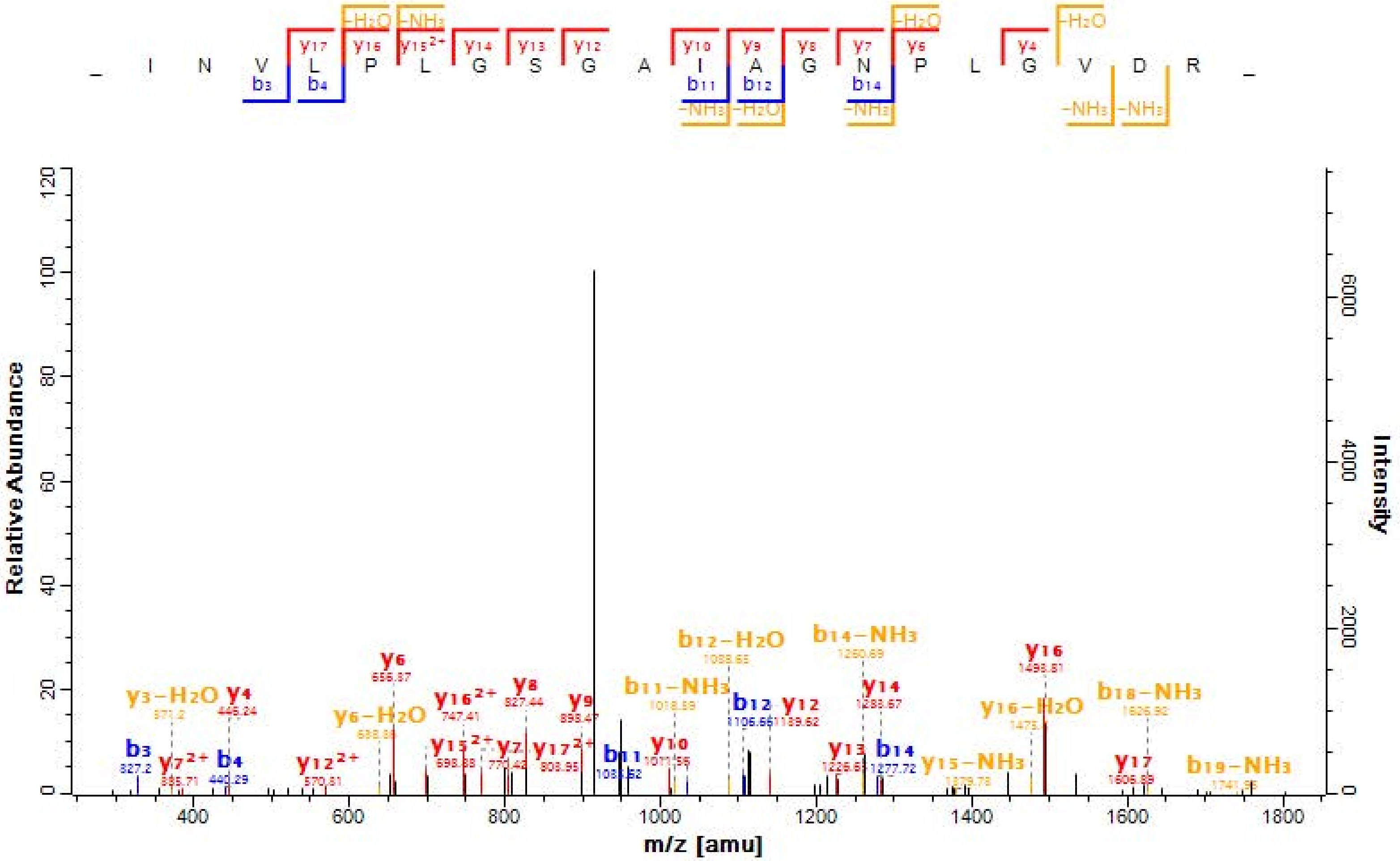
Mass:	1332.72896
m/z:	667.37176
Charge:	2+
Retentiontime:	45.01652526855
Score:	232.4968
Mass Error [ppm]:	0.034687
PEP:	6.9891E-32
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	72 %
Peak Coverage:	48 %
Protein Localisation:	589 ... 600

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	11				
	185.13		185.13	2	I	10	1262.7	+0.2739	1262.7	
	300.16	+0.0047	300.16	3	D	9	1149.6	-0.065	575.31	-0.041
	401.2	+0.0176	401.2	4	T	8	1034.6	-0.024	1034.6	
	502.25	+0.0514	502.25	5	T	7	933.54	+0.0386	467.27	+0.1317
	630.31	+0.056	630.31	6	Q	6	832.49	-0.035	832.49	
	743.39	-0.063	743.39	7	L	5	704.43	+0.0093	704.43	
-0.271	445.73	-0.043	890.46	8	F	4	591.35	+0.0467	591.35	
	977.49	-0.008	977.49	9	S	3	444.28	+0.0246	444.28	
	1090.6	-0.112	1090.6	10	L	2	357.25	+0.0063	357.25	
	1187.6	+0.0617	1187.6	11	P	1	244.17	-0.035	244.17	
				12	K	0	147.11		147.11	

Scan number	8134	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	103.41



precursor information

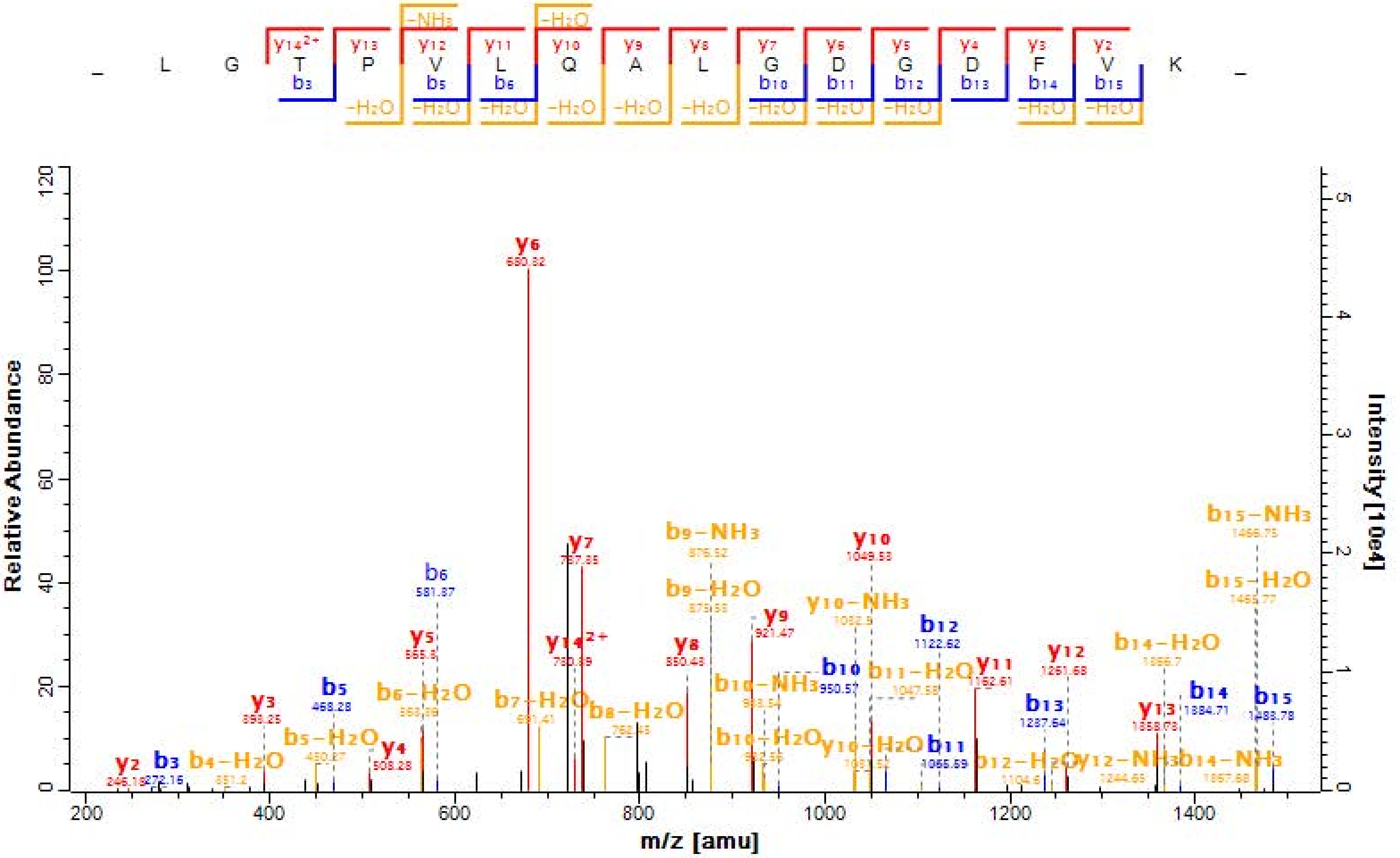
Mass:	1933.87574
m/z:	967.94515
Charge:	2+
Retentiontime:	50.12222900390
Score:	103.4126
Mass Error [ppm]:	-0.55933
PEP:	1.2753E-07
Precursor Type:	MULTI

general information

Annotation:	15 of 20
AminoAcids Coverag	75 %
Intensity Coverage:	31 %
Peak Coverage:	34 %
Protein Localisation:	194 ... 213

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	I	19				
	228.1343	2	N	18	1820.002		1820.002	
+0.064988	327.2027	3	V	17	1705.96		1705.96	
+0.137815	440.2867	4	L	16	1606.891	-0.11598	803.9492	+0.43428
	537.3395	5	P	15	1493.807	-0.08356	747.4072	+0.012018
	650.4236	6	L	14	1396.754		698.8808	+0.424203
	707.445	7	G	13	1283.67	+0.03667	1283.67	
	794.4771	8	S	12	1226.649	+0.105985	1226.649	
	851.4985	9	G	11	1139.617	+0.080763	570.312	+0.279297
	922.5356	10	A	10	1082.595		1082.595	
-0.04964	1035.62	11	I	9	1011.558	+0.031369	1011.558	
-0.24422	1106.657	12	A	8	898.4741	-0.0377	898.4741	
	1163.678	13	G	7	827.437	+0.04012	827.437	
+0.02537	1277.721	14	N	6	770.4155	+0.108642	385.7114	-0.31901
	1374.774	15	P	5	656.3726	+0.114277	656.3726	
	1487.858	16	L	4	559.3198		559.3198	
	1544.88	17	G	3	446.2358	+0.098456	446.2358	
	1643.948	18	V	2	389.2143		389.2143	
	1758.975	19	D	1	290.1459		290.1459	
		20	R	0	175.119		175.119	

Scan number	8262	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	197.17



precursor information

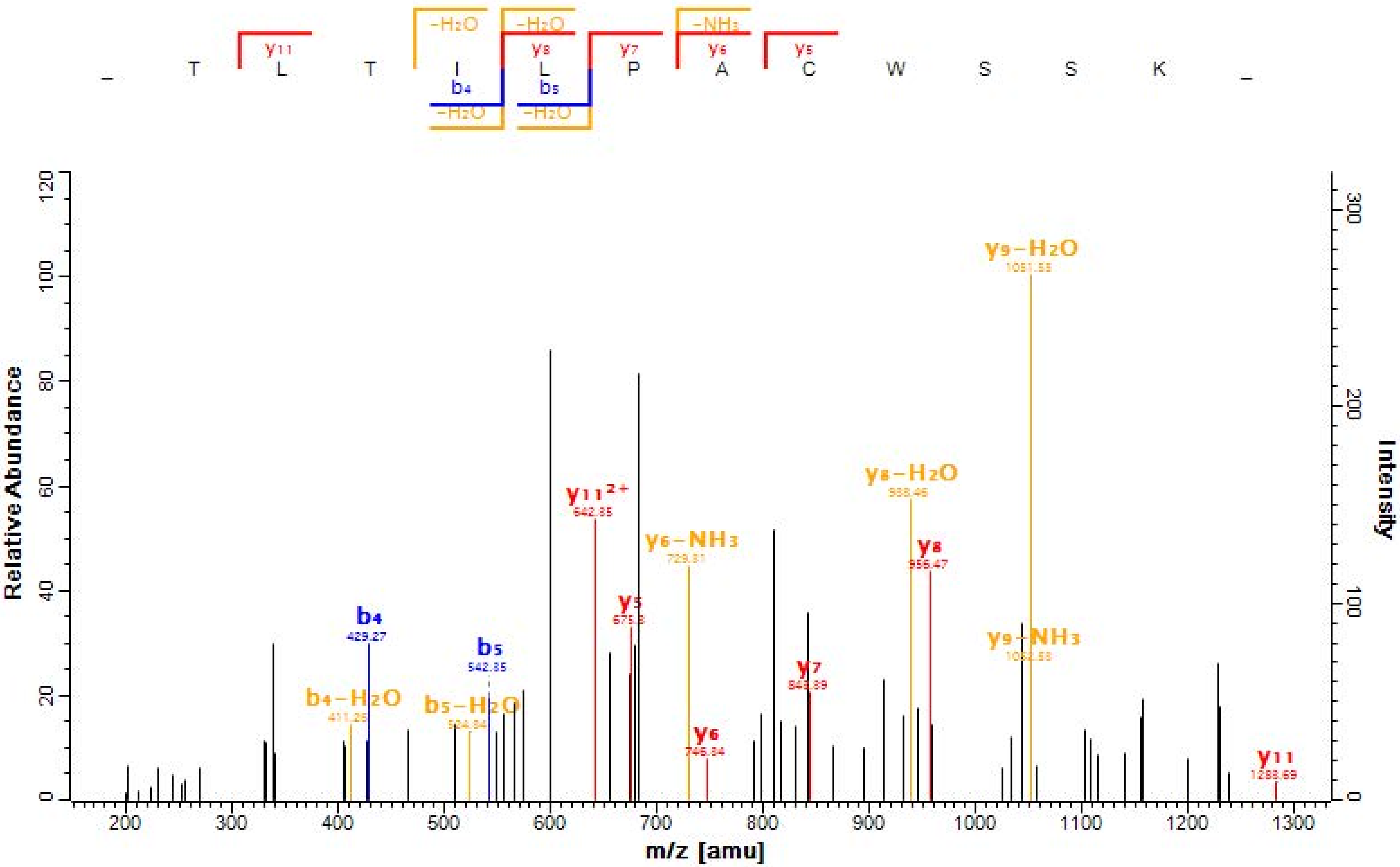
Mass:	1628.87719
m/z:	815.44587
Charge:	2+
Retentiontime:	50.797710418701
Score:	197.1731
Mass Error [ppm]:	-0.11347
PEP:	1.8684E-27
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	72 %
Peak Coverage:	51 %
Protein Localisation:	194 ... 209

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	15				
	171.1128	2	G	14	1516.801		1516.801	
-0.19201	272.1605	3	T	13	1459.779		730.3932	-0.01991
	369.2132	4	P	12	1358.731	-0.0133	1358.731	
+0.278215	468.2817	5	V	11	1261.679	-0.087	1261.679	
+0.188292	581.3657	6	L	10	1162.61	+0.045009	1162.61	
	709.4243	7	Q	9	1049.526	+0.097334	1049.526	
	780.4614	8	A	8	921.4676	+0.02725	921.4676	
	893.5455	9	L	7	850.4305	+0.049898	850.4305	
-0.00133	950.5669	10	G	6	737.3464	-0.00788	737.3464	
-0.09413	1065.594	11	D	5	680.325	-0.20395	680.325	
+0.109503	1122.615	12	G	4	565.298	+0.093746	565.298	
-0.09041	1237.642	13	D	3	508.2766	-0.02041	508.2766	
-0.33095	1384.711	14	F	2	393.2496	+0.017702	393.2496	
-0.11445	1483.779	15	V	1	246.1812	-0.116	246.1812	
		16	K	0	147.1128		147.1128	

Scan number	8404	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	70.49



precursor information

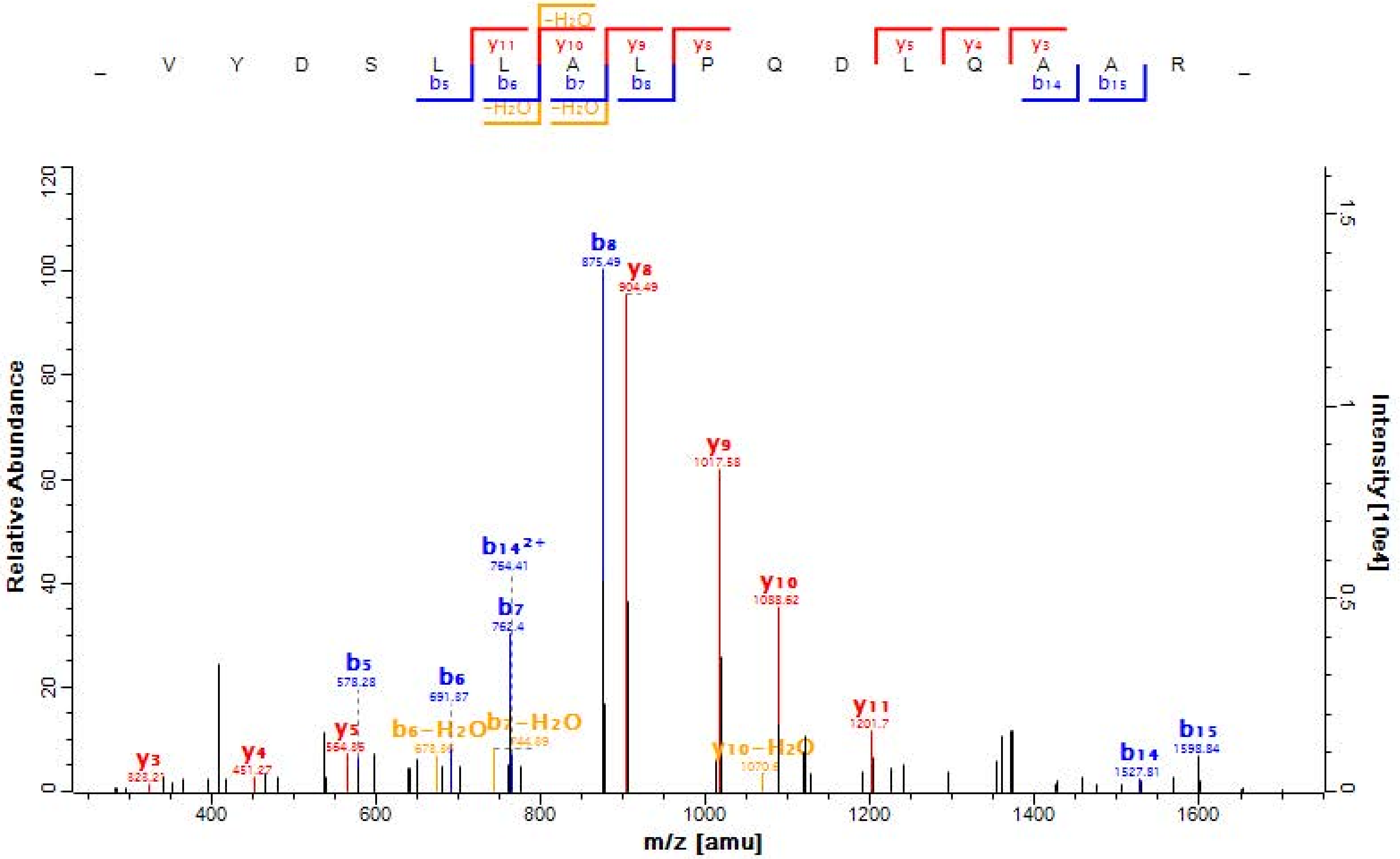
Mass:	1375.71722
m/z:	688.86589
Charge:	2+
Retentiontime:	51.586090087890
Score:	70.48843
Mass Error [ppm]:	0.17899
PEP:	0.0043974
Precursor Type:	MULTI

general information

Annotation:	6 of 12
AminoAcids Coverag	50 %
Intensity Coverage:	34 %
Peak Coverage:	21 %
Protein Localisation:	328 ... 339

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055	1	T	11				
	215.139	2	L	10	1283.691	-0.25095	642.349	+0.249305
	316.1867	3	T	9	1170.607		1170.607	
-0.01124	429.2708	4	I	8	1069.559		1069.559	
+0.246005	542.3548	5	L	7	956.475	+0.089246	956.475	
	639.4076	6	P	6	843.3909	+0.188874	843.3909	
	710.4447	7	A	5	746.3381	+0.349792	746.3381	
	870.4754	8	C	4	675.301	+0.096684	675.301	
	1056.555	9	W	3	515.2704		515.2704	
	1143.587	10	S	2	329.1911		329.1911	
	1230.619	11	S	1	242.159		242.159	
		12	K	0	155.127		155.127	

Scan number	8428	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	88.56



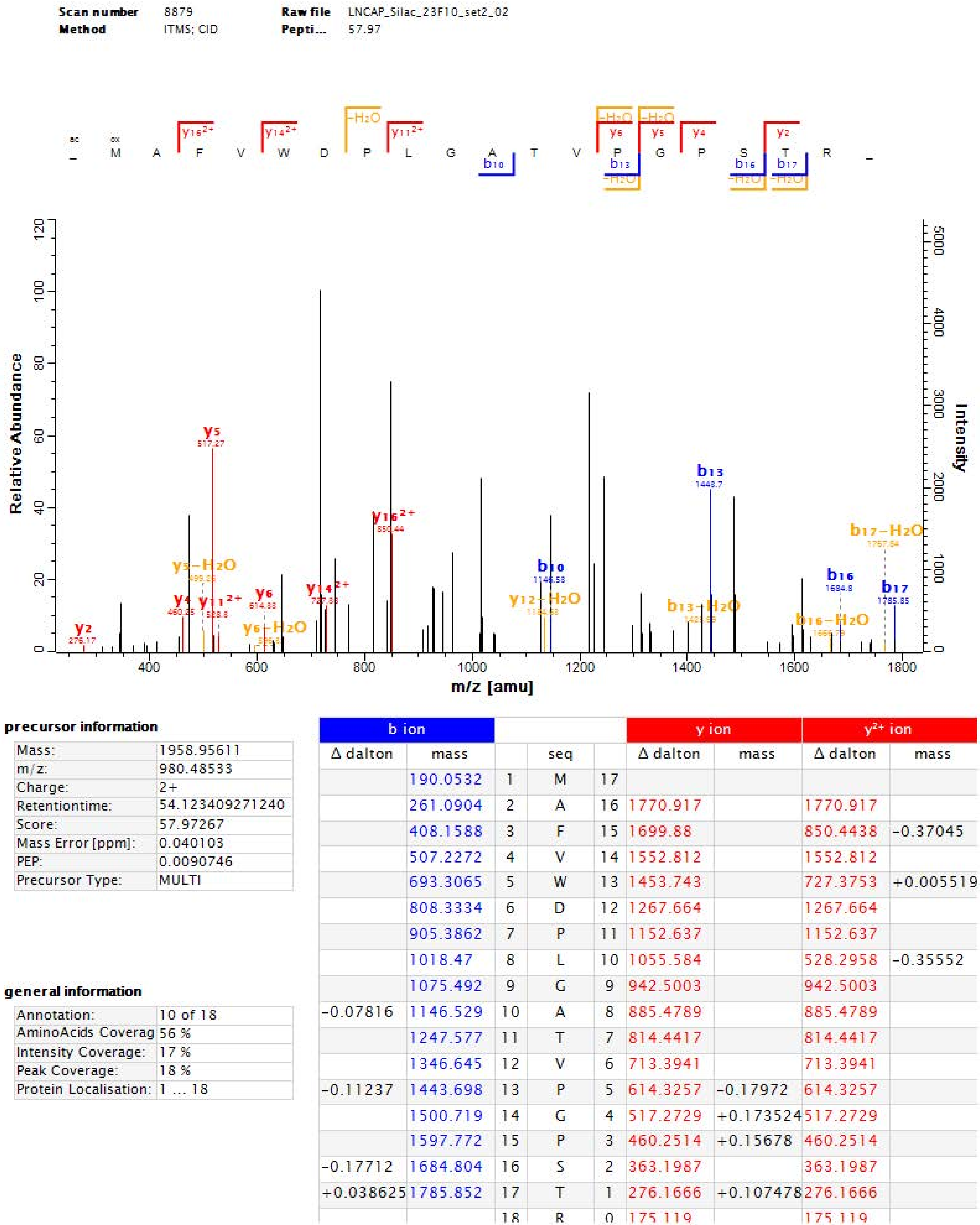
precursor information

Mass:	1771.94589
m/z:	886.98022
Charge:	2+
Retentiontime:	51.715183258056
Score:	88.56142
Mass Error [ppm]:	-0.54117
PEP:	4.4302E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 16
AminoAcids Coverag	56 %
Intensity Coverage:	48 %
Peak Coverage:	21 %
Protein Localisation:	65 ... 80

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	100.0757		100.0757	1	V	15		
	263.139		263.139	2	Y	14	1679.906	
	378.166		378.166	3	D	13	1516.843	
	465.198		465.198	4	S	12	1401.816	
	578.2821	-0.00587	578.2821	5	L	11	1314.784	
	691.3661	-0.08456	691.3661	6	L	10	1201.699	-0.04262
	762.4032	-0.08988	762.4032	7	A	9	1088.615	-0.09686
	875.4873	-0.05913	875.4873	8	L	8	1017.578	-0.02843
	972.5401		972.5401	9	P	7	904.4942	+0.073697
	1100.599		1100.599	10	Q	6	807.4415	
	1215.626		1215.626	11	D	5	679.3829	
	1328.71		1328.71	12	L	4	564.356	+0.042853
	1456.768		1456.768	13	Q	3	451.2719	+0.14419
+0.122197	764.4063	+0.055748	1527.805	14	A	2	323.2133	+0.168588
	1598.842	-0.22636	1598.842	15	A	1	252.1762	
				16	R	0	181.1391	



Scan number	8879	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	57.97

precursor information

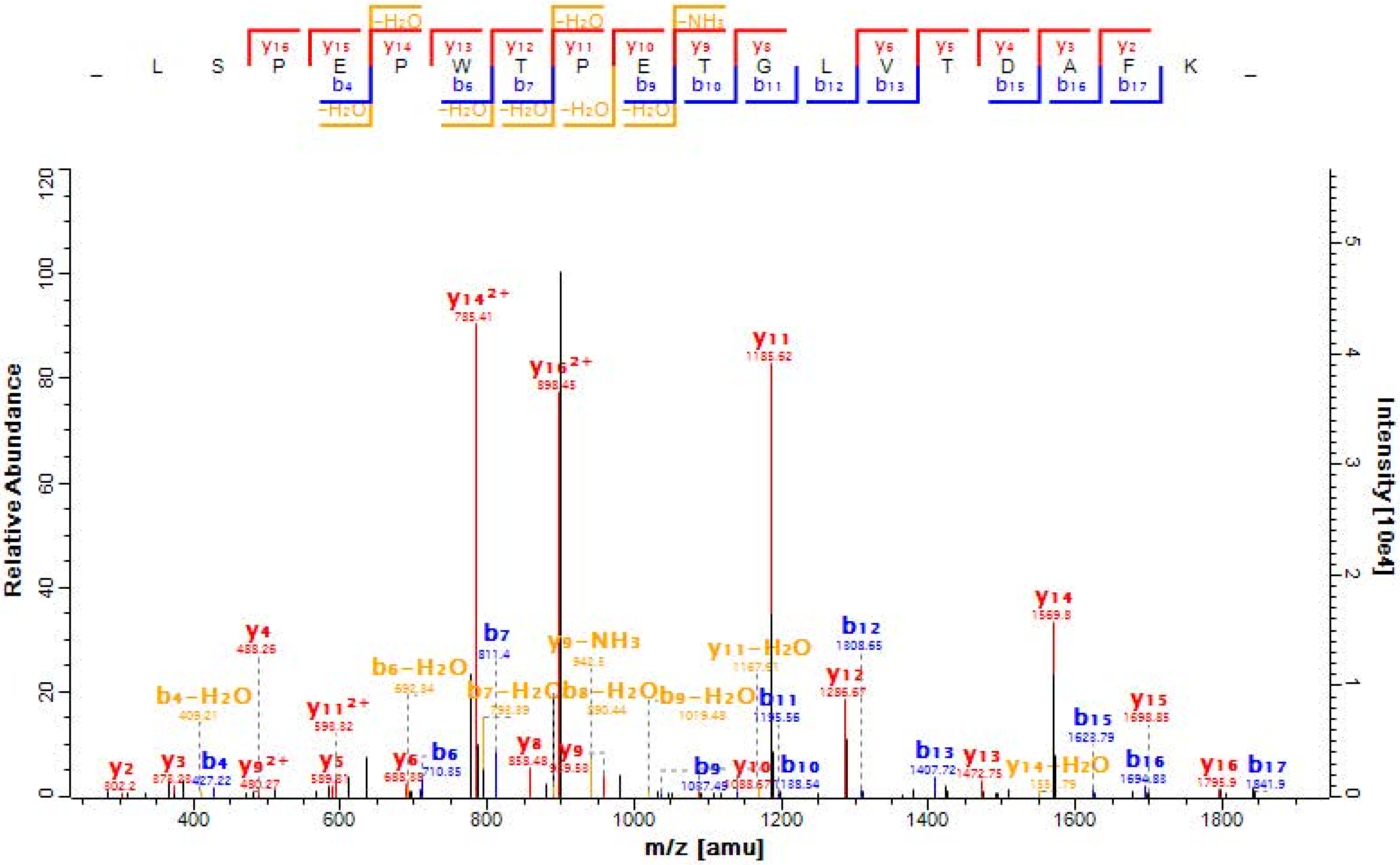
Mass:	1958.95611
m/z:	980.48533
Charge:	2+
Retentiontime:	54.123409271240
Score:	57.97267
Mass Error [ppm]:	0.040103
PEP:	0.0090746
Precursor Type:	MULTI

general information

Annotation:	10 of 18
AminoAcids Coverag	56 %
Intensity Coverage:	17 %
Peak Coverage:	18 %
Protein Localisation:	1 ... 18

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	190.0532	1	M	17				
	261.0904	2	A	16	1770.917		1770.917	
	408.1588	3	F	15	1699.88		850.4438	-0.37045
	507.2272	4	V	14	1552.812		1552.812	
	693.3065	5	W	13	1453.743		727.3753	+0.005519
	808.3334	6	D	12	1267.664		1267.664	
	905.3862	7	P	11	1152.637		1152.637	
	1018.47	8	L	10	1055.584		528.2958	-0.35552
	1075.492	9	G	9	942.5003		942.5003	
-0.07816	1146.529	10	A	8	885.4789		885.4789	
	1247.577	11	T	7	814.4417		814.4417	
	1346.645	12	V	6	713.3941		713.3941	
-0.11237	1443.698	13	P	5	614.3257	-0.17972	614.3257	
	1500.719	14	G	4	517.2729	+0.173524	517.2729	
	1597.772	15	P	3	460.2514	+0.15678	460.2514	
-0.17712	1684.804	16	S	2	363.1987		363.1987	
+0.038625	1785.852	17	T	1	276.1666	+0.107478	276.1666	
		18	R	0	175.119		175.119	

Scan number	8905	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	207.53



precursor information

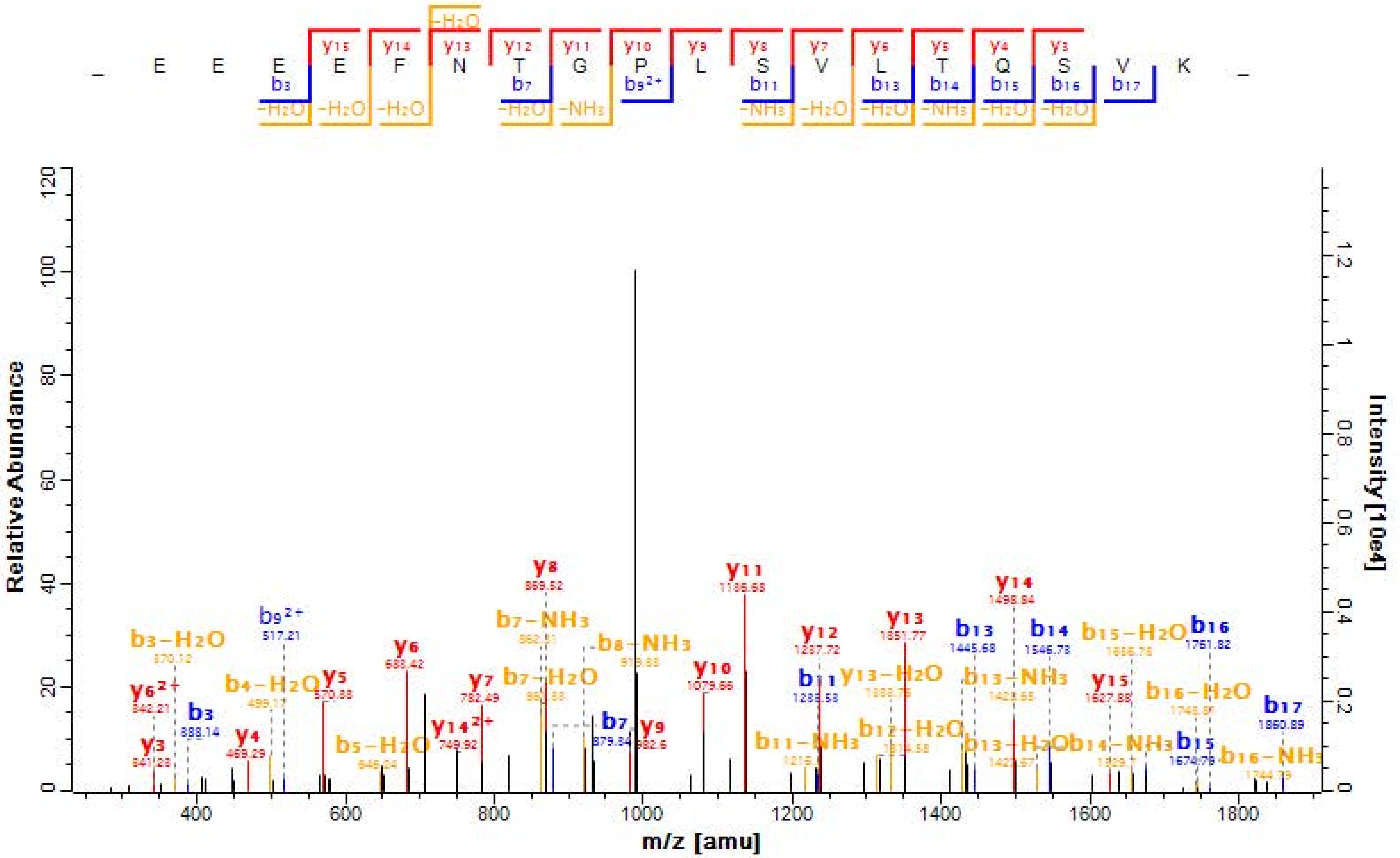
Mass:	1986.99361
m/z:	994.50408
Charge:	2+
Retentiontime:	54.267658233642
Score:	207.5324
Mass Error [ppm]:	-0.1244
PEP:	9.3477E-41
Precursor Type:	MULTI

general information

Annotation:	16 of 18
AminoAcids Coverag	89 %
Intensity Coverage:	55 %
Peak Coverage:	38 %
Protein Localisation:	682 ... 699

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	17				
	201.1234	2	S	16	1882.931		1882.931	
	298.1761	3	P	15	1795.899	-0.03022	898.4533	-0.02626
+0.166406	427.2187	4	E	14	1698.846	+0.000446	1698.846	
	524.2715	5	P	13	1569.804	-0.06963	785.4056	+0.255186
+0.016995	710.3508	6	W	12	1472.751	-0.15066	1472.751	
+0.007036	811.3985	7	T	11	1286.672	-0.0827	1286.672	
	908.4512	8	P	10	1185.624	-0.05357	593.3157	+0.131929
+0.047178	1037.494	9	E	9	1088.571	-0.1584	1088.571	
+0.186633	1138.542	10	T	8	959.5288	+0.057531	480.268	+0.252422
+0.192147	1195.563	11	G	7	858.4811	+0.018296	858.4811	
-0.16694	1308.647	12	L	6	801.4596		801.4596	
+0.003048	1407.715	13	V	5	688.3756	-0.00545	688.3756	
	1508.763	14	T	4	589.3072	+0.084205	589.3072	
+0.034383	1623.79	15	D	3	488.2595	+0.312456	488.2595	
+0.050492	1694.827	16	A	2	373.2325	+0.041731	373.2325	
+0.134422	1841.896	17	F	1	302.1954	-0.07841	302.1954	
		18	K	0	155.127		155.127	

Scan number	9024	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	183.6



precursor information

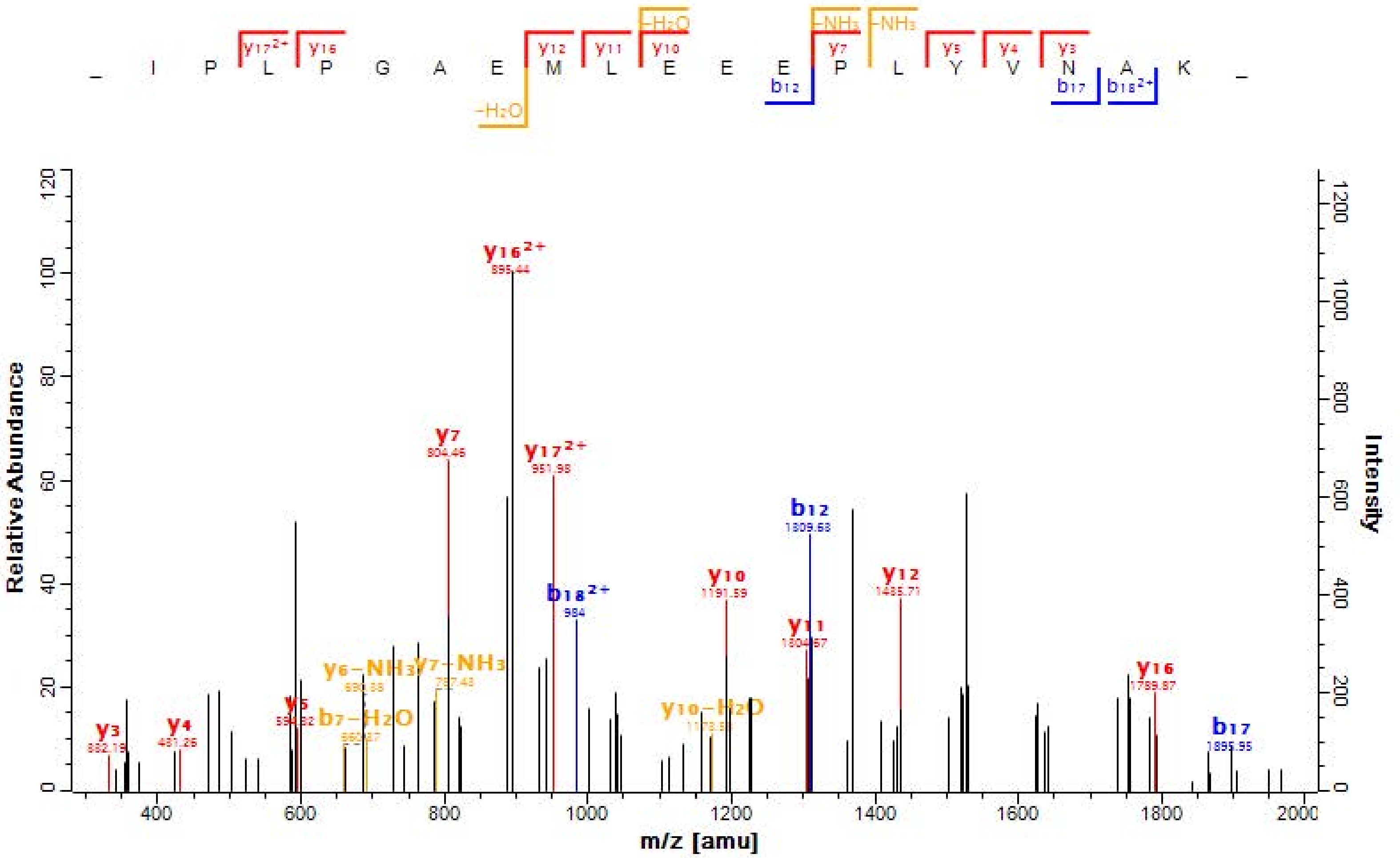
Mass:	2005.98463
m/z:	1003.99959
Charge:	2+
Retentiontime:	54.930931091308
Score:	183.5978
Mass Error [ppm]:	0.10662
PEP:	7.5898E-32
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	46 %
Peak Coverage:	41 %
Protein Localisation:	20 ... 37

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	17				
	259.09		259.09	2	E	16	1886		1886	
	388.14	+0.1102	388.14	3	E	15	1756.9		1756.9	
	517.18		517.18	4	E	14	1627.9	-0.191	1627.9	
	664.25		664.25	5	F	13	1498.8	+0.0376	749.92	-0.326
	778.29		778.29	6	N	12	1351.8	-0.053	1351.8	
	879.34	+0.2781	879.34	7	T	11	1237.7	-0.062	1237.7	
	936.36		936.36	8	G	10	1136.7	+0.0217	1136.7	
+0.1565	517.21		1033.4	9	P	9	1079.7	+0.0039	1079.7	
	1146.5		1146.5	10	L	8	982.6	-0.013	982.6	
	1233.5	+0.2875	1233.5	11	S	7	869.52	-0.006	869.52	
	1332.6		1332.6	12	V	6	782.49	-0.024	782.49	
	1445.7	+0.0094	1445.7	13	L	5	683.42	+0.0451	342.21	+0.2978
	1546.7	+0.0636	1546.7	14	T	4	570.33	+0.1221	570.33	
	1674.8	-0.292	1674.8	15	Q	3	469.29	+0.099	469.29	
	1761.8	+0.1718	1761.8	16	S	2	341.23	+0.0087	341.23	
	1860.9	-0.293	1860.9	17	V	1	254.2		254.2	
				18	K	0	155.13		155.13	

Scan number	9133	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	54.97



precursor information

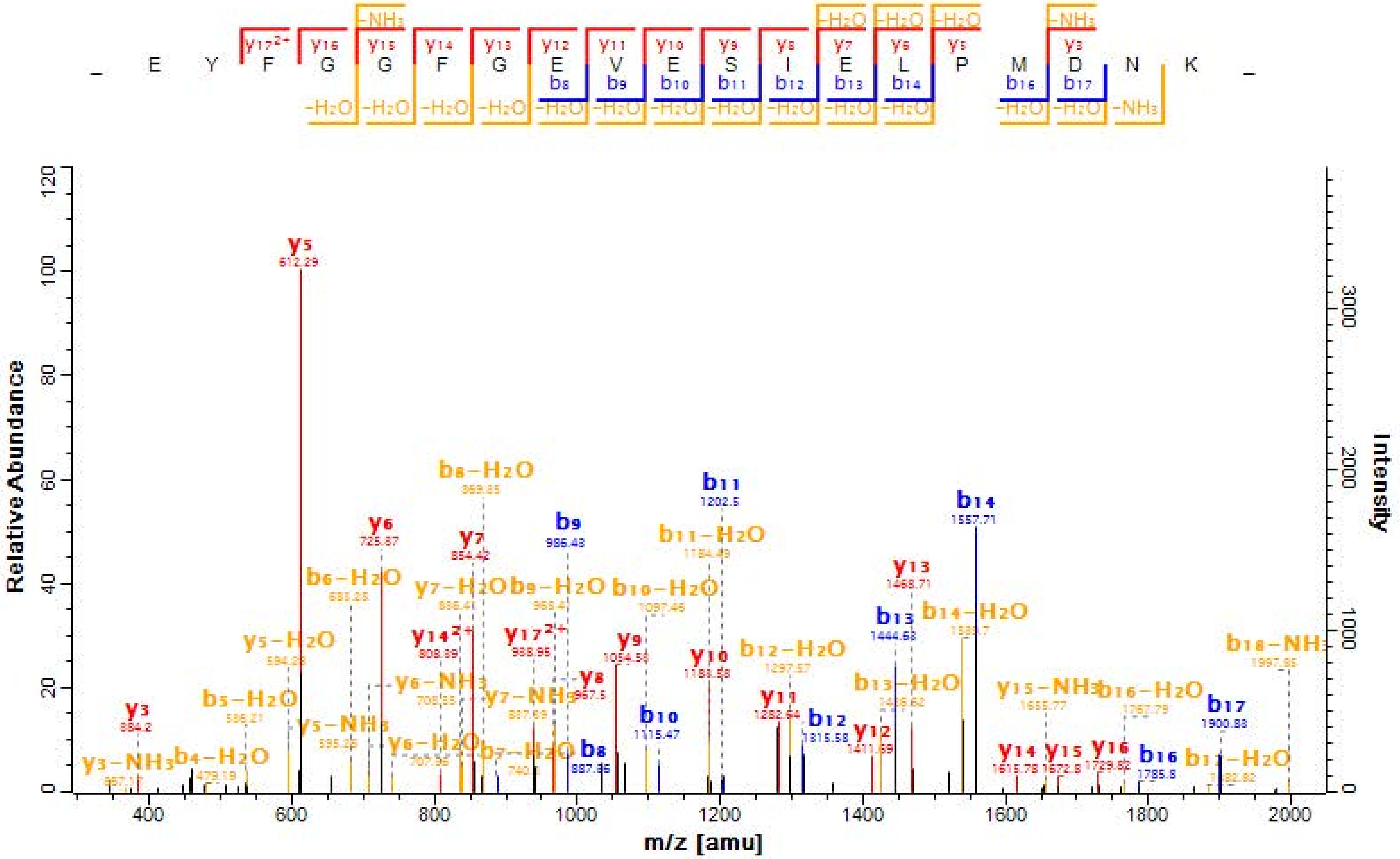
Mass:	2112.08253
m/z:	1057.04854
Charge:	2+
Retentiontime:	55.549900054931
Score:	54.97353
Mass Error [ppm]:	0.58439
PEP:	0.0023463
Precursor Type:	MULTI

general information

Annotation:	13 of 19
AminoAcids Coverag	68 %
Intensity Coverage:	26 %
Peak Coverage:	17 %
Protein Localisation:	252 ... 270

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	I	18				
	211.14		211.14	2	P	17	2000		2000	
	324.23		324.23	3	L	16	1903		951.98	+0.2567
	421.28		421.28	4	P	15	1789.9	+0.194	895.44	+0.0907
	478.3		478.3	5	G	14	1692.8		1692.8	
	549.34		549.34	6	A	13	1635.8		1635.8	
	678.38		678.38	7	E	12	1564.8		1564.8	
	809.42		809.42	8	M	11	1435.7	-0.027	1435.7	
	922.51		922.51	9	L	10	1304.7	-0.147	1304.7	
	1051.5		1051.5	10	E	9	1191.6	-0.066	1191.6	
	1180.6		1180.6	11	E	8	1062.5		1062.5	
	1309.6	-0.104	1309.6	12	E	7	933.5		933.5	
	1406.7		1406.7	13	P	6	804.46	+0.1127	804.46	
	1519.8		1519.8	14	L	5	707.41		707.41	
	1682.8		1682.8	15	Y	4	594.32	+0.0156	594.32	
	1781.9		1781.9	16	V	3	431.26	+0.1418	431.26	
	1895.9	+0.2644	1895.9	17	N	2	332.19	+0.193	332.19	
+0.3086	984		1967	18	A	1	218.15		218.15	
				19	K	0	147.11		147.11	

Scan number	9325	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	269.51



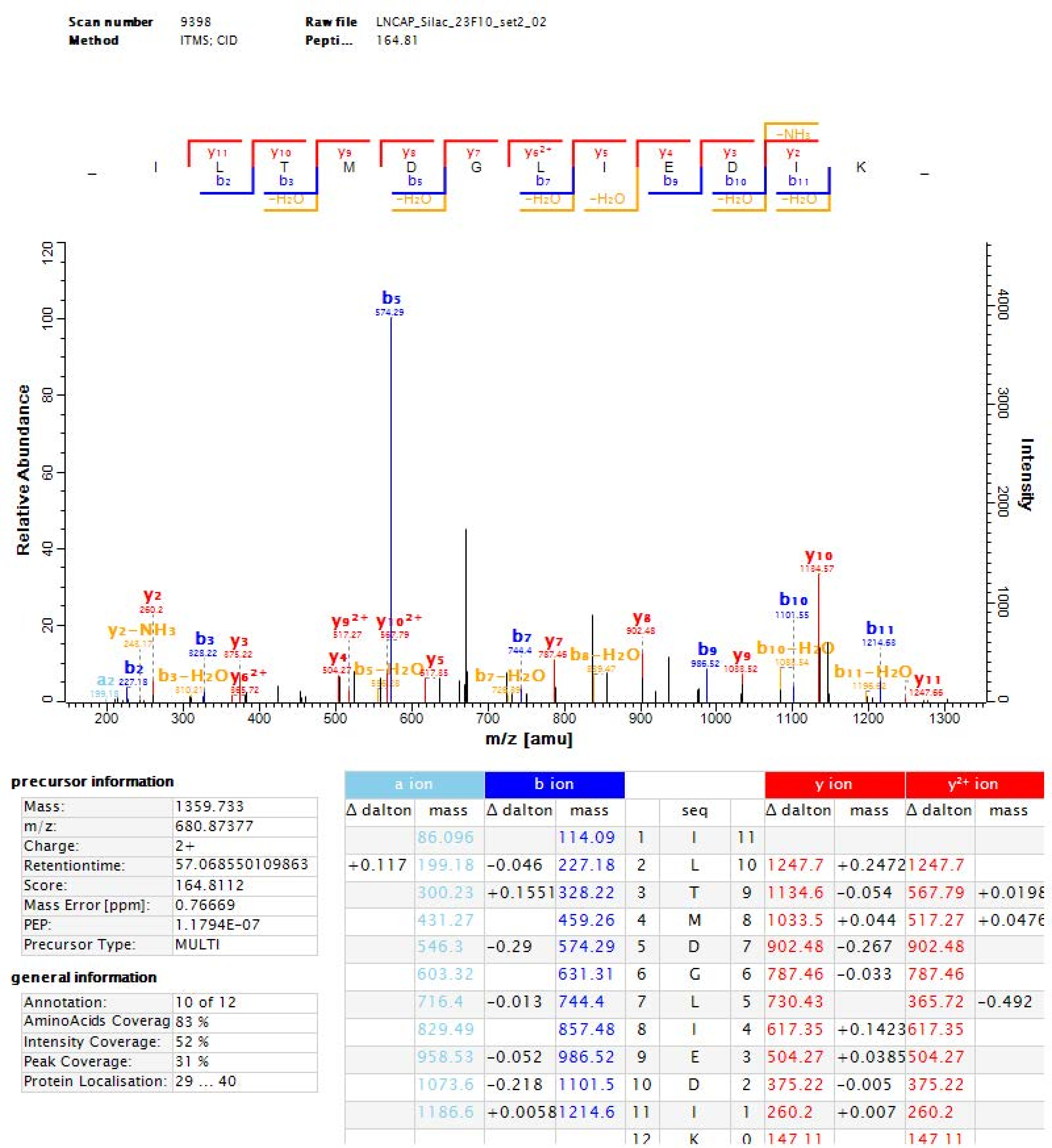
precursor information

Mass:	2159.97207
m/z:	1080.99331
Charge:	2+
Retentiontime:	56.667125701904
Score:	269.5136
Mass Error [ppm]:	-0.03195
PEP:	3.0326E-89
Precursor Type:	MULTI

general information

Annotation:	16 of 19
AminoAcids Coverag	84 %
Intensity Coverage:	71 %
Peak Coverage:	47 %
Protein Localisation:	181 ... 199

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	18				
	293.1132	2	Y	17	2039.951		2039.951	
	440.1816	3	F	16	1876.888		938.9475	-0.00571
	497.2031	4	G	15	1729.819	-0.26874	1729.819	
	554.2245	5	G	14	1672.798	-0.17001	1672.798	
	701.293	6	F	13	1615.776	+0.254413	808.3918	+0.462191
	758.3144	7	G	12	1468.708	-0.11357	1468.708	
+0.340377	887.357	8	E	11	1411.686	+0.047049	1411.686	
-0.12159	986.4254	9	V	10	1282.644	-0.05184	1282.644	
+0.212525	1115.468	10	E	9	1183.575	+0.076025	1183.575	
-0.15385	1202.5	11	S	8	1054.533	+0.032925	1054.533	
-0.12024	1315.584	12	I	7	967.5008	+0.071056	967.5008	
-0.16149	1444.627	13	E	6	854.4168	+0.029022	854.4168	
-0.12983	1557.711	14	L	5	725.3742	+0.000936	725.3742	
	1654.764	15	P	4	612.2901	-0.01791	612.2901	
-0.0246	1785.804	16	M	3	515.2374		515.2374	
-0.11575	1900.831	17	D	2	384.1969	+0.07339	384.1969	
	2014.874	18	N	1	269.1699		269.1699	
		19	K	0	155.127		155.127	



Scan number	9398	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	164.81

precursor information

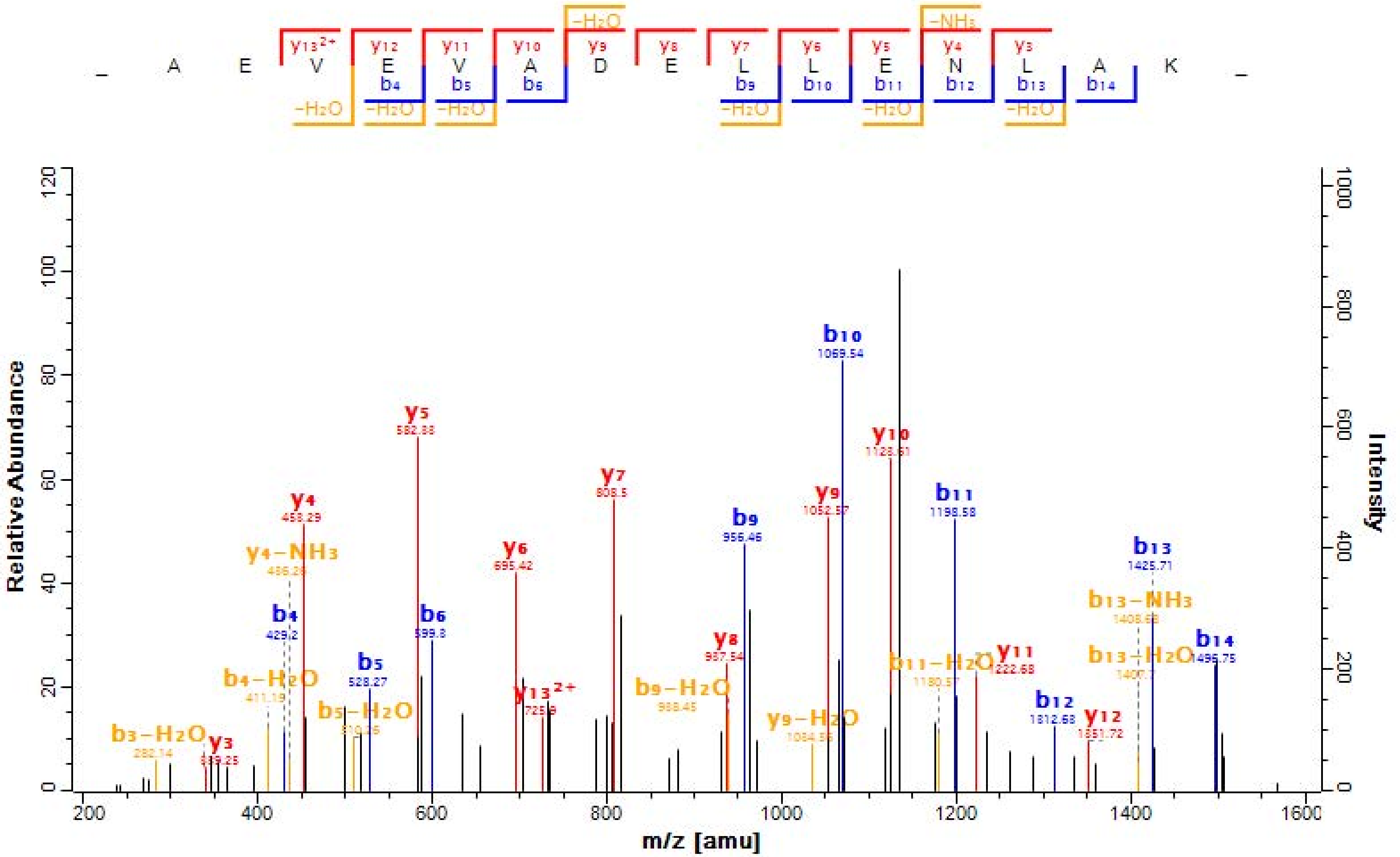
Mass:	1359.733
m/z:	680.87377
Charge:	2+
Retentiontime:	57.068550109863
Score:	164.8112
Mass Error [ppm]:	0.76669
PEP:	1.1794E-07
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	52 %
Peak Coverage:	31 %
Protein Localisation:	29 ... 40

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	11				
+0.117	199.18	-0.046	227.18	2	L	10	1247.7	+0.2472	1247.7	
	300.23	+0.1551	328.22	3	T	9	1134.6	-0.054	567.79	+0.019
	431.27		459.26	4	M	8	1033.5	+0.044	517.27	+0.047
	546.3	-0.29	574.29	5	D	7	902.48	-0.267	902.48	
	603.32		631.31	6	G	6	787.46	-0.033	787.46	
	716.4	-0.013	744.4	7	L	5	730.43		365.72	-0.492
	829.49		857.48	8	I	4	617.35	+0.1423	617.35	
	958.53	-0.052	986.52	9	E	3	504.27	+0.0385	504.27	
	1073.6	-0.218	1101.5	10	D	2	375.22	-0.005	375.22	
	1186.6	+0.0058	1214.6	11	I	1	260.2	+0.007	260.2	
				12	K	0	147.11		147.11	

Scan number	9715	**Raw file**	LNCAP_Silac_23F10_set2_02
Method	ITMS; CID	**Pepti...**	147.56



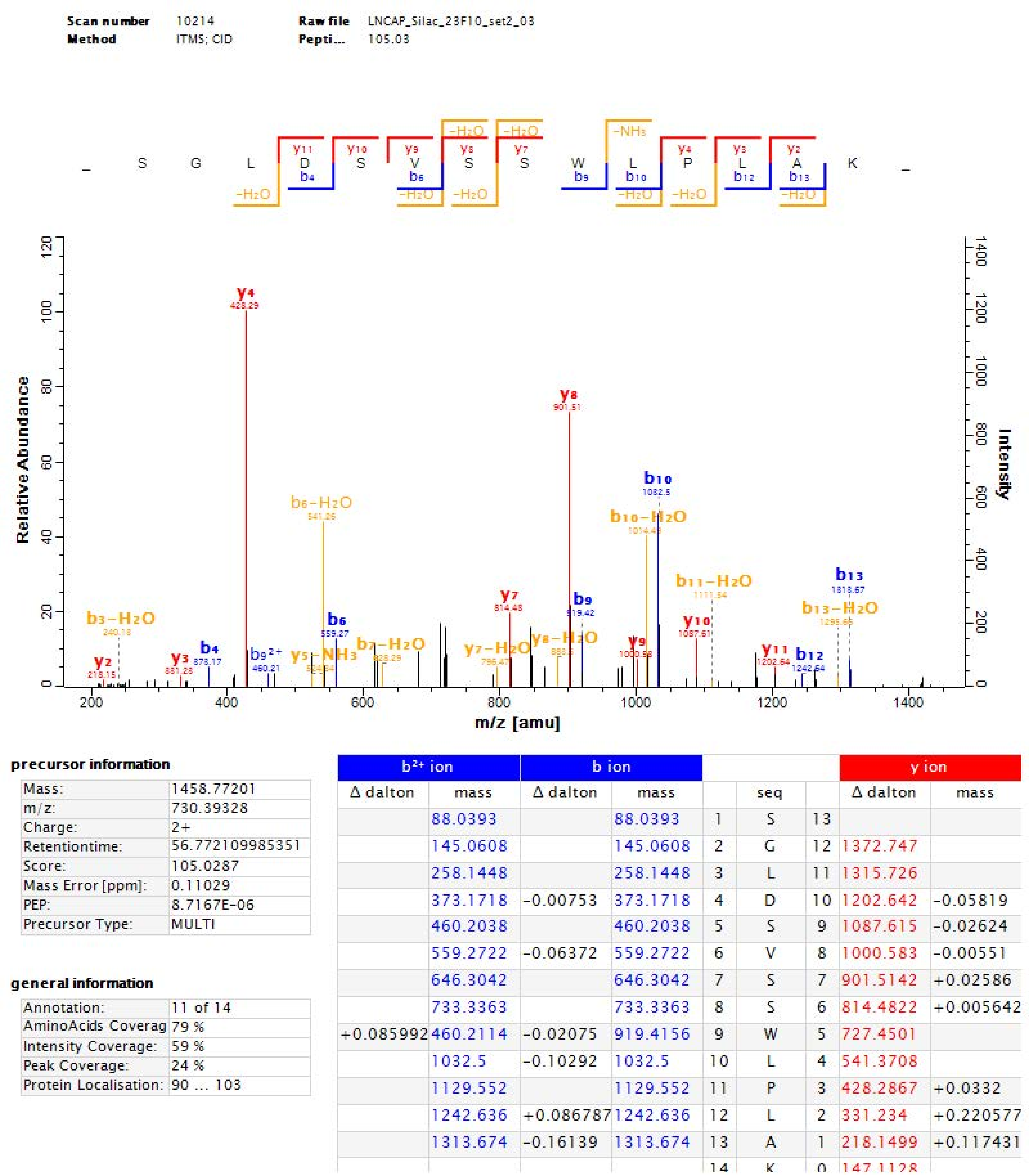
precursor information

Mass:	1641.84689
m/z:	821.93072
Charge:	2+
Retentiontime:	58.860866546630
Score:	147.5608
Mass Error [ppm]:	0.45938
PEP:	2.6582E-13
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	55 %
Peak Coverage:	38 %
Protein Localisation:	97 ... 111

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	14				
	201.087	2	E	13	1579.83		1579.83	
	300.1554	3	V	12	1450.788		725.8976	+0.206721
-0.05108	429.198	4	E	11	1351.719	-0.18164	1351.719	
-0.06535	528.2664	5	V	10	1222.677	-0.07985	1222.677	
+0.021555	599.3035	6	A	9	1123.608	+0.124431	1123.608	
	714.3305	7	D	8	1052.571	-0.03169	1052.571	
	843.3731	8	E	7	937.5444	-0.24224	937.5444	
+0.008885	956.4571	9	L	6	808.5018	+0.038271	808.5018	
-0.02482	1069.541	10	L	5	695.4178	+0.133077	695.4178	
-0.17679	1198.584	11	E	4	582.3337	+0.01133	582.3337	
-0.06994	1312.627	12	N	3	453.2911	+0.126128	453.2911	
-0.07649	1425.711	13	L	2	339.2482	+0.044941	339.2482	
-0.01351	1496.748	14	A	1	226.1641		226.1641	
		15	K	0	155.127		155.127	



precursor information

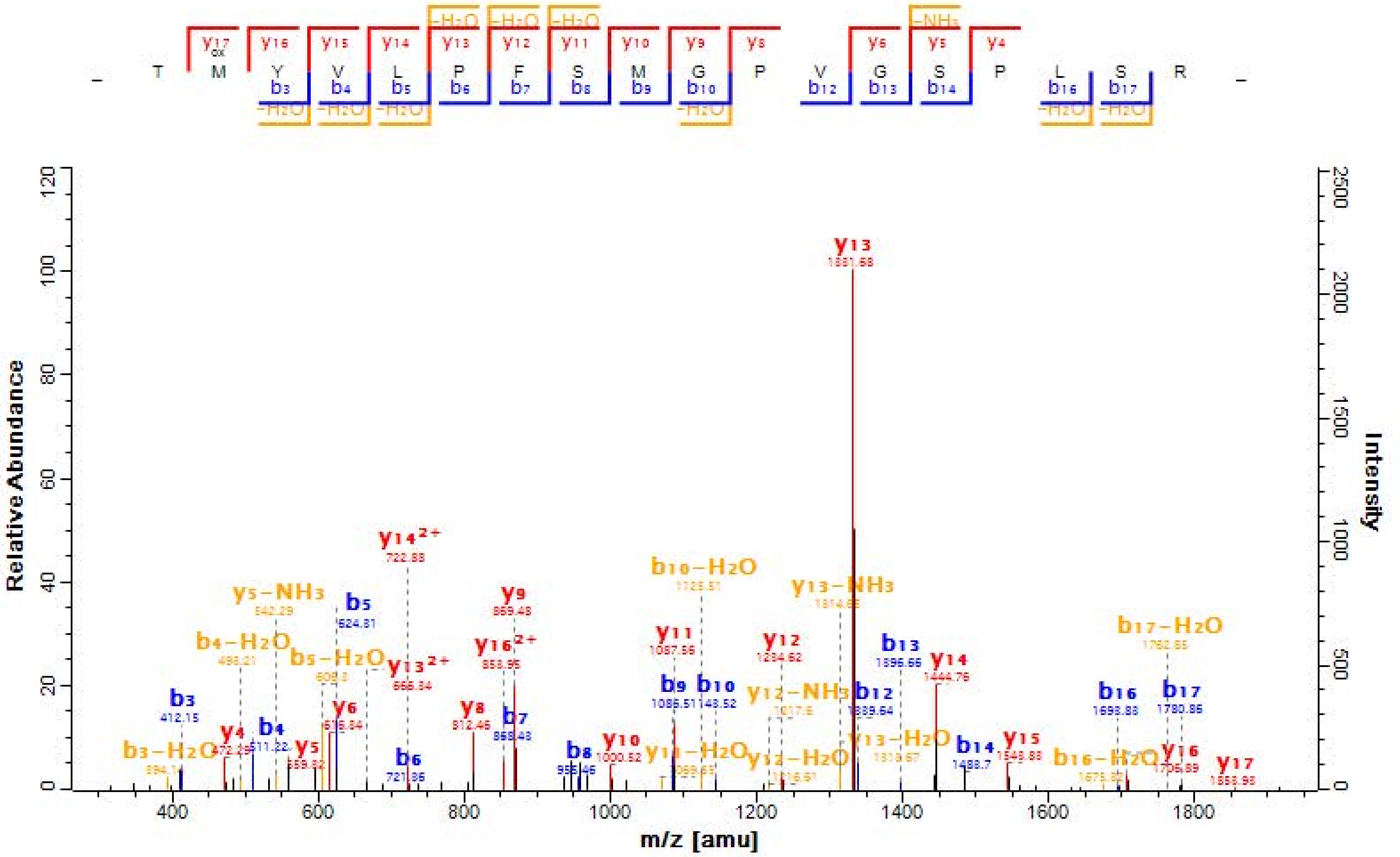
Mass:	1458.77201
m/z:	730.39328
Charge:	2+
Retentiontime:	56.772109985351
Score:	105.0287
Mass Error [ppm]:	0.11029
PEP:	8.7167E-06
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	59 %
Peak Coverage:	24 %
Protein Localisation:	90 ... 103

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	88.0393		88.0393	1	S	13		
	145.0608		145.0608	2	G	12	1372.747	
	258.1448		258.1448	3	L	11	1315.726	
	373.1718	−0.00753	373.1718	4	D	10	1202.642	−0.05819
	460.2038		460.2038	5	S	9	1087.615	−0.02624
	559.2722	−0.06372	559.2722	6	V	8	1000.583	−0.00551
	646.3042		646.3042	7	S	7	901.5142	+0.02586
	733.3363		733.3363	8	S	6	814.4822	+0.005642
+0.085992	460.2114	−0.02075	919.4156	9	W	5	727.4501	
	1032.5	−0.10292	1032.5	10	L	4	541.3708	
	1129.552		1129.552	11	P	3	428.2867	+0.0332
	1242.636	+0.086787	1242.636	12	L	2	331.234	+0.220577
	1313.674	−0.16139	1313.674	13	A	1	218.1499	+0.117431
				14	K	0	147.1128	

Scan number	10295	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	239.55



precursor information

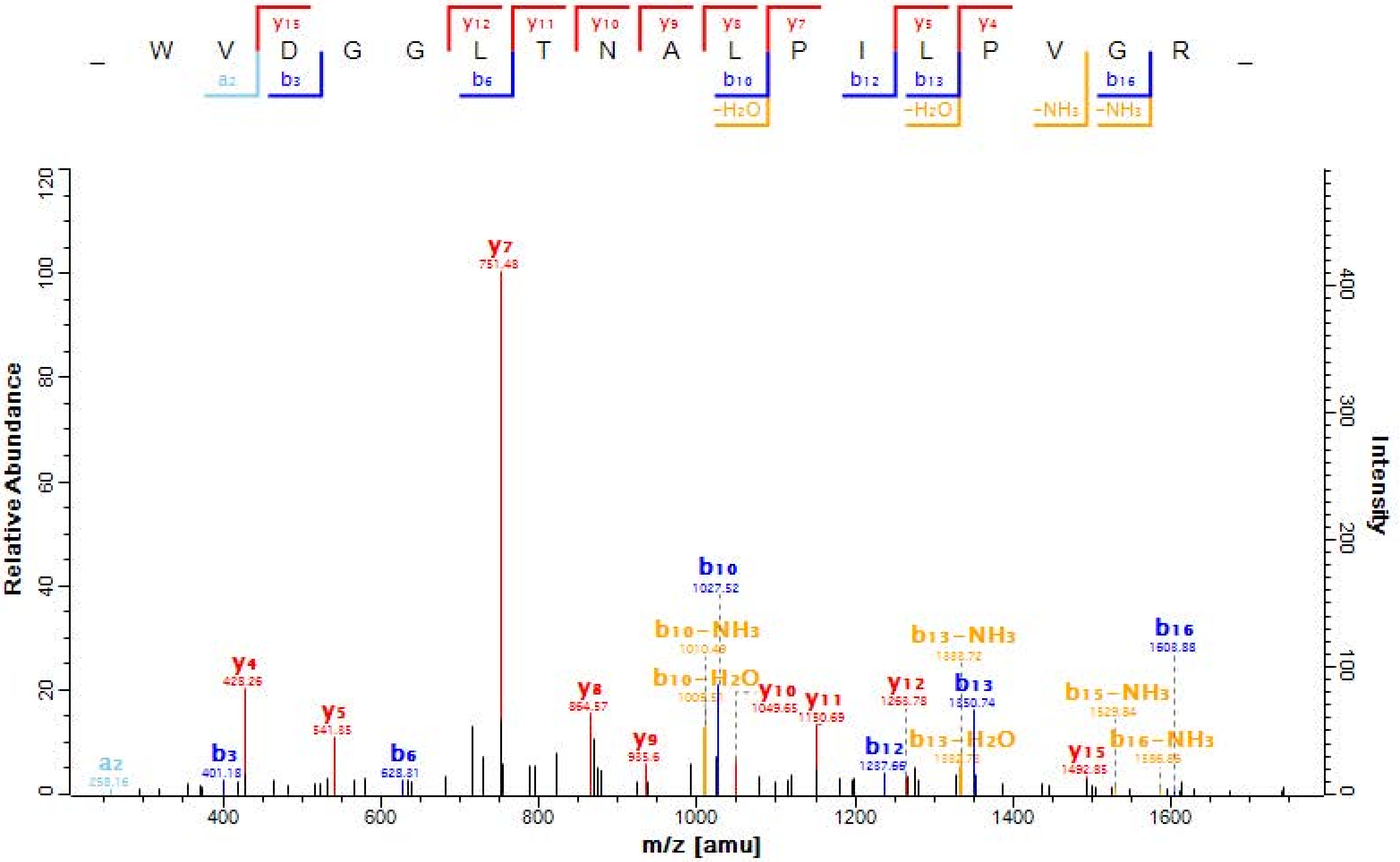
Mass:	1953.96988
m/z:	977.99222
Charge:	2+
Retentiontime:	57.293136596679
Score:	239.5532
Mass Error [ppm]:	0.32982
PEP:	1.7118E-57
Precursor Type:	MULTI

general information

Annotation:	16 of 18
AminoAcids Coverag	89 %
Intensity Coverage:	63 %
Peak Coverage:	45 %
Protein Localisation:	156 ... 173

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055	1	T	17				
	249.0904	2	M	16	1853.929	+0.187495	1853.929	
-0.0592	412.1537	3	Y	15	1706.893	+0.092767	853.9504	+0.208761
+0.016185	511.2221	4	V	14	1543.83	-0.01187	1543.83	
-0.00947	624.3062	5	L	13	1444.762	+0.040427	722.8845	+0.178563
+0.092431	721.3589	6	P	12	1331.678	-0.04641	666.3425	+0.256056
+0.002654	868.4273	7	F	11	1234.625	+0.161264	1234.625	
+0.105086	955.4594	8	S	10	1087.556	-0.04864	1087.556	
-0.22348	1086.5	9	M	9	1000.524	+0.002734	1000.524	
-0.03877	1143.521	10	G	8	869.4839	+0.010138	869.4839	
	1240.574	11	P	7	812.4625	-0.02589	812.4625	
-0.11613	1339.642	12	V	6	715.4097		715.4097	
-0.09743	1396.664	13	G	5	616.3413	+0.133858	616.3413	
+0.005675	1483.696	14	S	4	559.3198	+0.09215	559.3198	
	1580.749	15	P	3	472.2878	+0.063327	472.2878	
-0.27239	1693.833	16	L	2	375.235		375.235	
-0.06052	1780.865	17	S	1	262.151		262.151	
		18	R	0	175.119		175.119	

Scan number	10455	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	120.66



precursor information

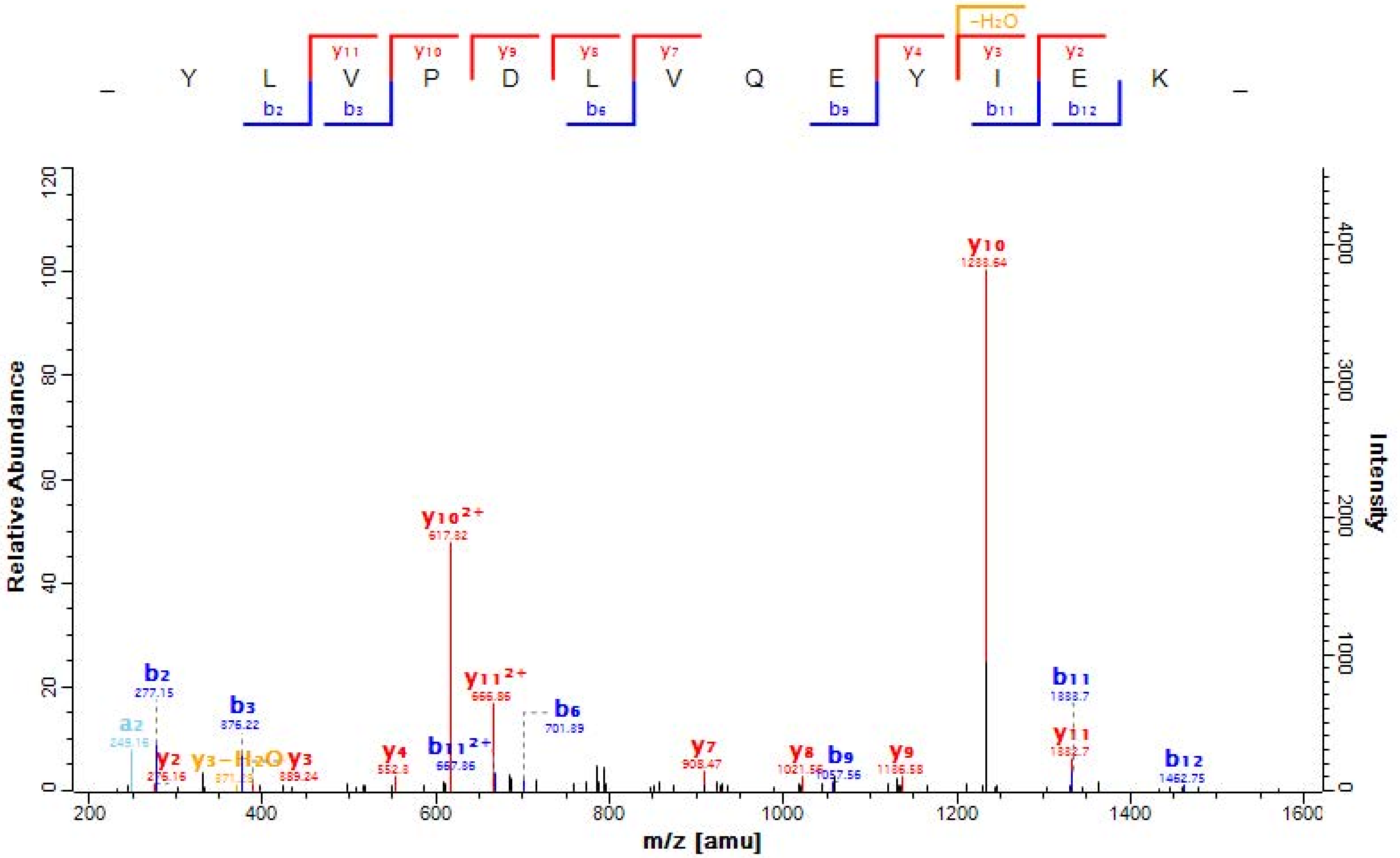
Mass:	1776.9889
m/z:	889.50173
Charge:	2+
Retentiontime:	58.305435180664
Score:	120.663
Mass Error [ppm]:	0.13902
PEP:	7.0524E-12
Precursor Type:	MULTI

general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	55 %
Peak Coverage:	26 %
Protein Localisation:	161 ... 177

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	159.0917		187.0866	1	W	16		
+0.244117	258.1601		286.155	2	V	15	1591.917	
	373.187	-0.05493	401.1819	3	D	14	1492.848	-0.04571
	430.2085		458.2034	4	G	13	1377.821	
	487.23		515.2249	5	G	12	1320.8	
	600.314	+0.151511	628.3089	6	L	11	1263.778	+0.244616
	701.3617		729.3566	7	T	10	1150.694	+0.021429
	815.4046		843.3995	8	N	9	1049.647	+0.211686
	886.4417		914.4367	9	A	8	935.6037	-0.01919
	999.5258	-0.24631	1027.521	10	L	7	864.5665	+0.012735
	1096.579		1124.573	11	P	6	751.4825	-0.01099
	1209.663	-0.20064	1237.658	12	I	5	654.4297	
	1322.747	-0.16324	1350.742	13	L	4	541.3457	+0.130539
	1419.799		1447.794	14	P	3	428.2616	+0.01691
	1518.868		1546.863	15	V	2	331.2088	
	1575.889	+0.358177	1603.884	16	G	1	232.1404	
				17	R	0	175.119	

Scan number	10724	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	120.14



precursor information

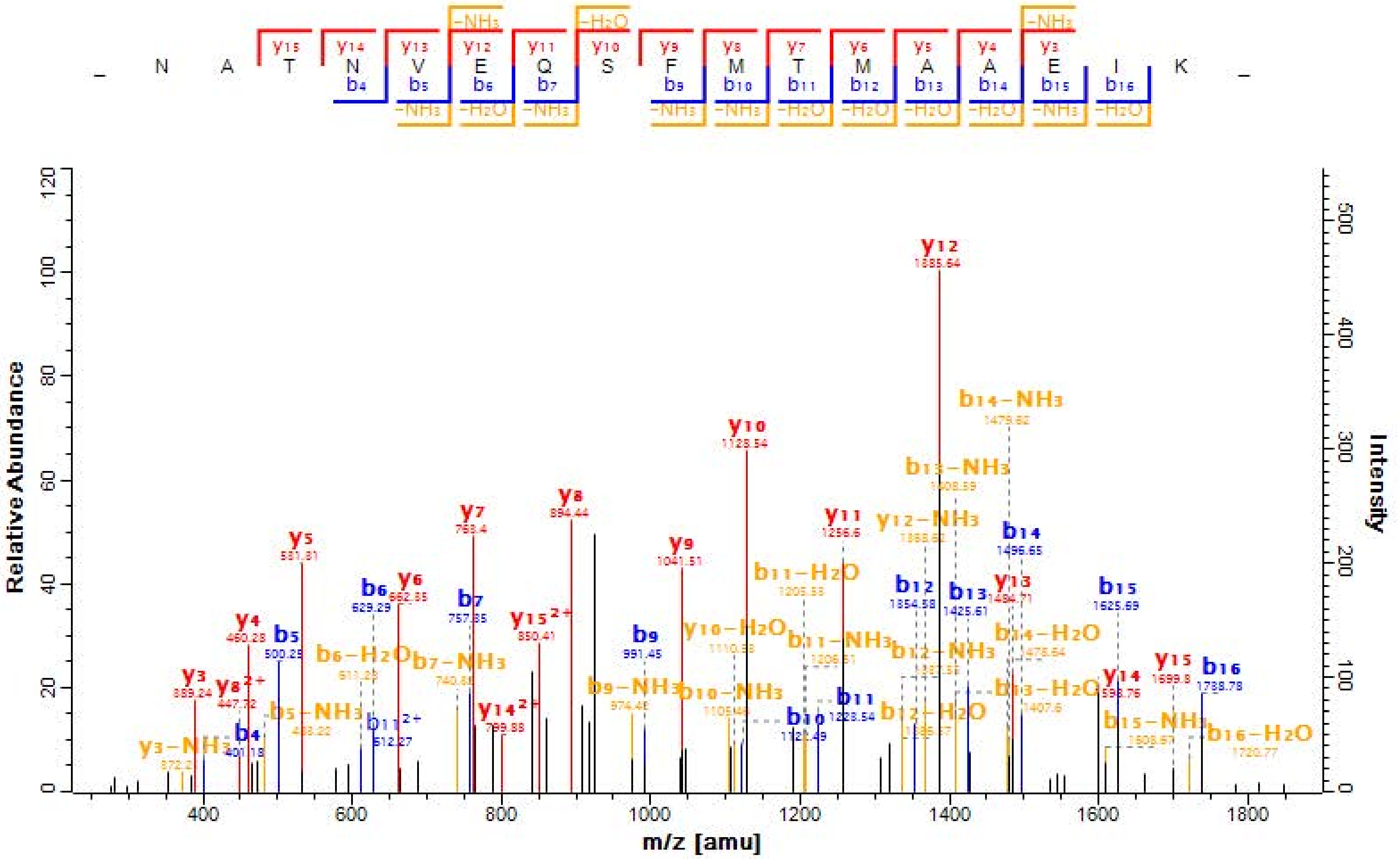
Mass:	1607.84571
m/z:	804.93013
Charge:	2+
Retentiontime:	60.021999359130
Score:	120.1359
Mass Error [ppm]:	0.64384
PEP:	9.1937E-07
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	68 %
Peak Coverage:	24 %
Protein Localisation:	238 ... 250

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.1		164.1		164.1	1	Y	12				
-0.03	249.2		277.2	-0.08	277.2	2	L	11	1446		1446	
	348.2		376.2	+0	376.2	3	V	10	1333	-0.22	666.9	+0.04
	445.3		473.3		473.3	4	P	9	1234	-0.02	617.3	+0.13
	560.3		588.3		588.3	5	D	8	1137	-0.07	1137	
	673.4		701.4	+0.108	701.4	6	L	7	1022	+0.014	1022	
	772.5		800.5		800.5	7	V	6	908.5	+0.014	908.5	
	900.5		928.5		928.5	8	Q	5	809.4		809.4	
	1030		1058	+0.057	1058	9	E	4	681.3		681.3	
	1193		1221		1221	10	Y	3	552.3	+0.118	552.3	
	1306	+0.295	667.4	-0.15	1334	11	I	2	389.2	+0.059	389.2	
	1435		1463	-0.18	1463	12	E	1	276.2	+0.118	276.2	
						13	K	0	147.1		147.1	

Scan number	10761	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	289.32



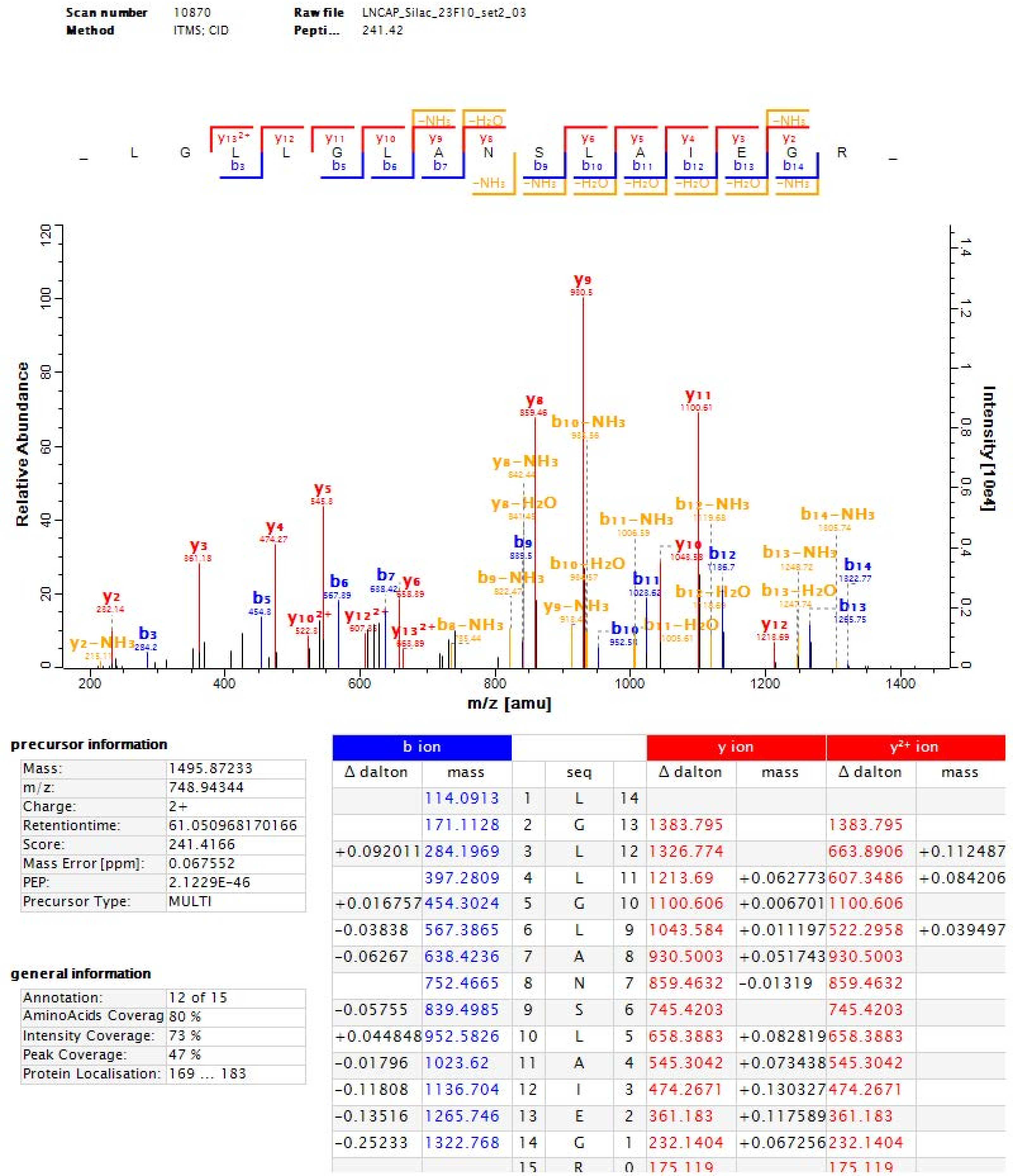
precursor information

Mass:	1883.87688
m/z:	942.94572
Charge:	2+
Retentiontime:	60.284439086914
Score:	289.321
Mass Error [ppm]:	0.60802
PEP:	5.7331E-95
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	65 %
Peak Coverage:	48 %
Protein Localisation:	157 ... 173

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.05		115.05	1	N	16				
	186.09		186.09	2	A	15	1770.8		1770.8	
	287.13		287.13	3	T	14	1699.8	-0.249	850.41	+0.2171
	401.18	+0.0407	401.18	4	N	13	1598.8	-0.025	799.88	-0.273
	500.25	+0.1508	500.25	5	V	12	1484.7	-0.225	1484.7	
	629.29	+0.0347	629.29	6	E	11	1385.6	-0.024	1385.6	
	757.35	+0.0391	757.35	7	Q	10	1256.6	-0.088	1256.6	
	844.38		844.38	8	S	9	1128.5	-0.091	1128.5	
	991.45	-0.208	991.45	9	F	8	1041.5	-0.002	1041.5	
	1122.5	-0.211	1122.5	10	M	7	894.44	-0.053	447.72	+0.4413
+0.0448	612.27	-0.088	1223.5	11	T	6	763.4	-0.023	763.4	
	1354.6	-0.205	1354.6	12	M	5	662.35	+0.0026	662.35	
	1425.6	-0.192	1425.6	13	A	4	531.31	+0.0525	531.31	
	1496.7	+0.1596	1496.7	14	A	3	460.28	+0.13	460.28	
	1625.7	-0.042	1625.7	15	E	2	389.24	+0.1061	389.24	
	1738.8	-0.209	1738.8	16	I	1	260.2		260.2	
				17	K	0	147.11		147.11	



Scan number	10870	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	241.42

precursor information

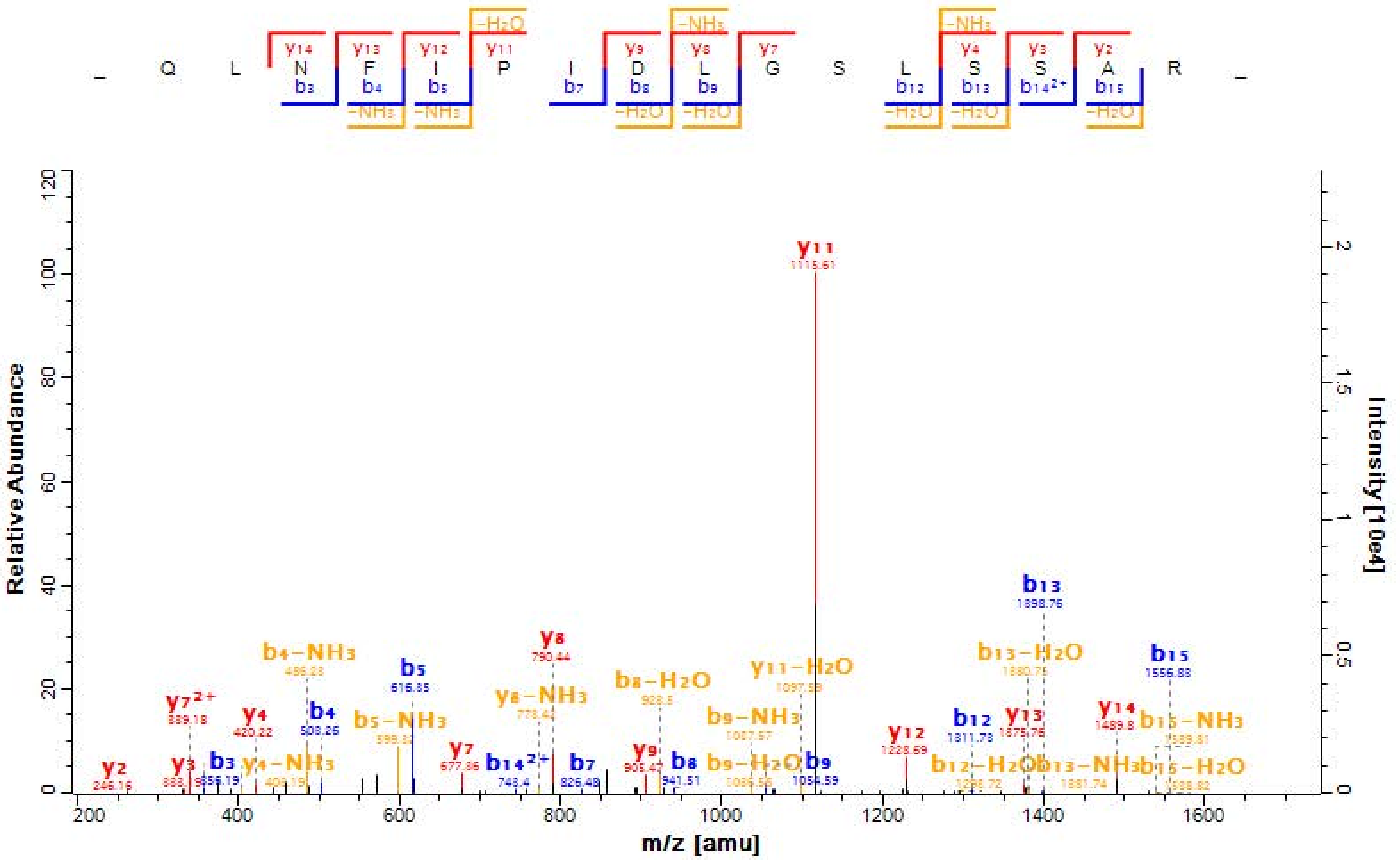
Mass:	1495.87233
m/z:	748.94344
Charge:	2+
Retentiontime:	61.050968170166
Score:	241.4166
Mass Error [ppm]:	0.067552
PEP:	2.1229E-46
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	73 %
Peak Coverage:	47 %
Protein Localisation:	169 ... 183

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	14				
	171.1128	2	G	13	1383.795		1383.795	
+0.092011	284.1969	3	L	12	1326.774		663.8906	+0.112487
	397.2809	4	L	11	1213.69	+0.062773	607.3486	+0.084206
+0.016757	454.3024	5	G	10	1100.606	+0.006701	1100.606	
-0.03838	567.3865	6	L	9	1043.584	+0.011197	522.2958	+0.039497
-0.06267	638.4236	7	A	8	930.5003	+0.051743	930.5003	
	752.4665	8	N	7	859.4632	-0.01319	859.4632	
-0.05755	839.4985	9	S	6	745.4203		745.4203	
+0.044848	952.5826	10	L	5	658.3883	+0.082819	658.3883	
-0.01796	1023.62	11	A	4	545.3042	+0.073438	545.3042	
-0.11808	1136.704	12	I	3	474.2671	+0.130327	474.2671	
-0.13516	1265.746	13	E	2	361.183	+0.117589	361.183	
-0.25233	1322.768	14	G	1	232.1404	+0.067256	232.1404	
		15	R	0	175.119		175.119	

Scan number	10893	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	194.77



precursor information

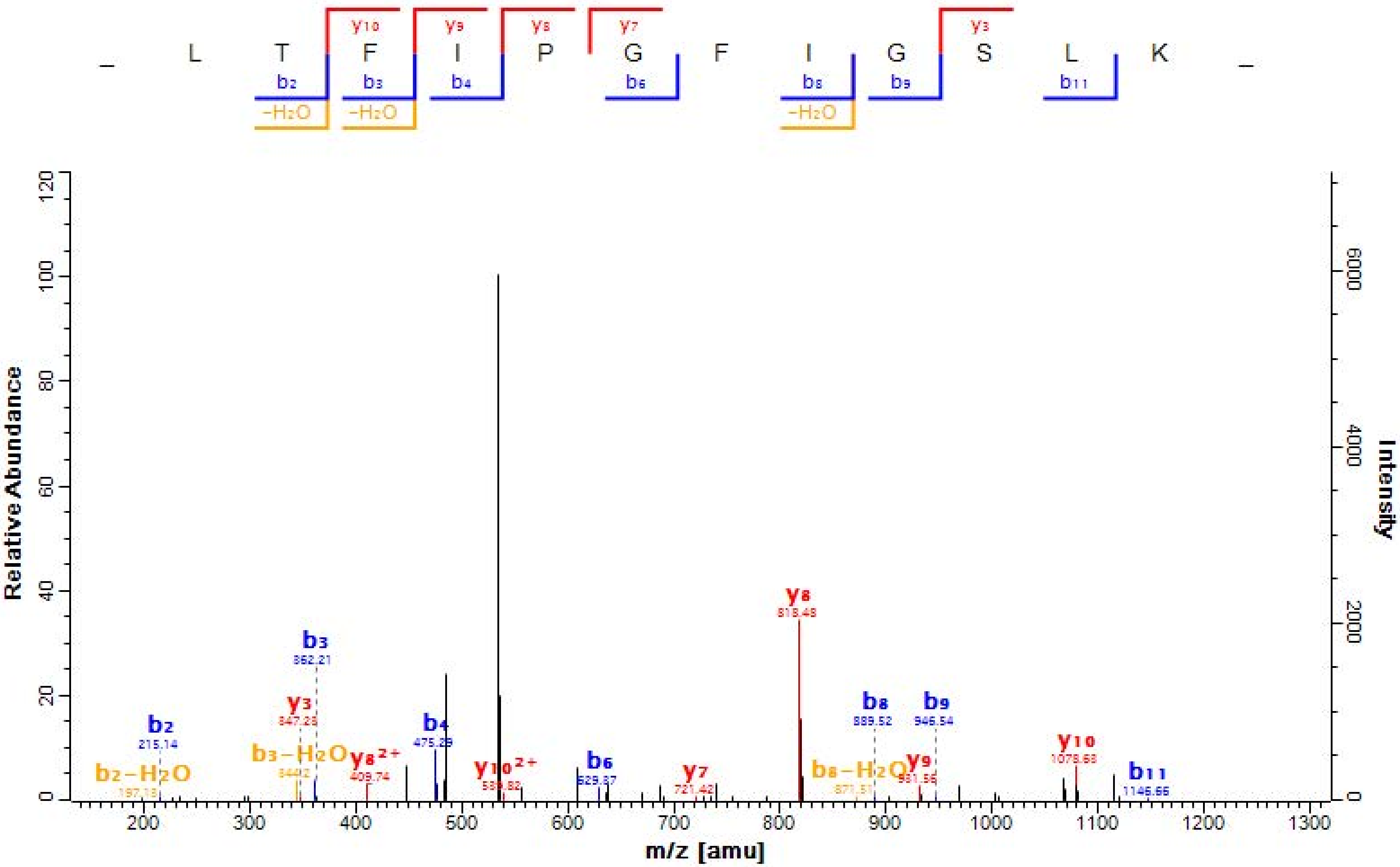
Mass:	1729.93622
m/z:	865.97539
Charge:	2+
Retentiontime:	61.200981140136
Score:	194.773
Mass Error [ppm]:	-0.038245
PEP:	3.398E-27
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	67 %
Peak Coverage:	39 %
Protein Localisation:	184 ... 199

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.07		129.07	1	Q	15				
	242.15		242.15	2	L	14	1602.9		1602.9	
	356.19	+0.0139	356.19	3	N	13	1489.8	-0.033	1489.8	
	503.26	-0.144	503.26	4	F	12	1375.8	-0.003	1375.8	
	616.35	-0.016	616.35	5	I	11	1228.7	+0.006	1228.7	
	713.4		713.4	6	P	10	1115.6	-0.016	1115.6	
	826.48	-0.267	826.48	7	I	9	1018.6		1018.6	
	941.51	-0.13	941.51	8	D	8	905.47	+0.0126	905.47	
	1054.6	-0.008	1054.6	9	L	7	790.44	+0.0089	790.44	
	1111.6		1111.6	10	G	6	677.36	+0.0583	339.18	+0.0782
	1198.6		1198.6	11	S	5	620.34		620.34	
	1311.7	-0.045	1311.7	12	L	4	533.3		533.3	
	1398.8	-0.18	1398.8	13	S	3	420.22	+0.0197	420.22	
-0.019	743.4		1485.8	14	S	2	333.19	+0.0192	333.19	
	1556.8	-0.18	1556.8	15	A	1	246.16	-0.082	246.16	
				16	R	0	175.12		175.12	

Scan number	10909	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	100.93



precursor information

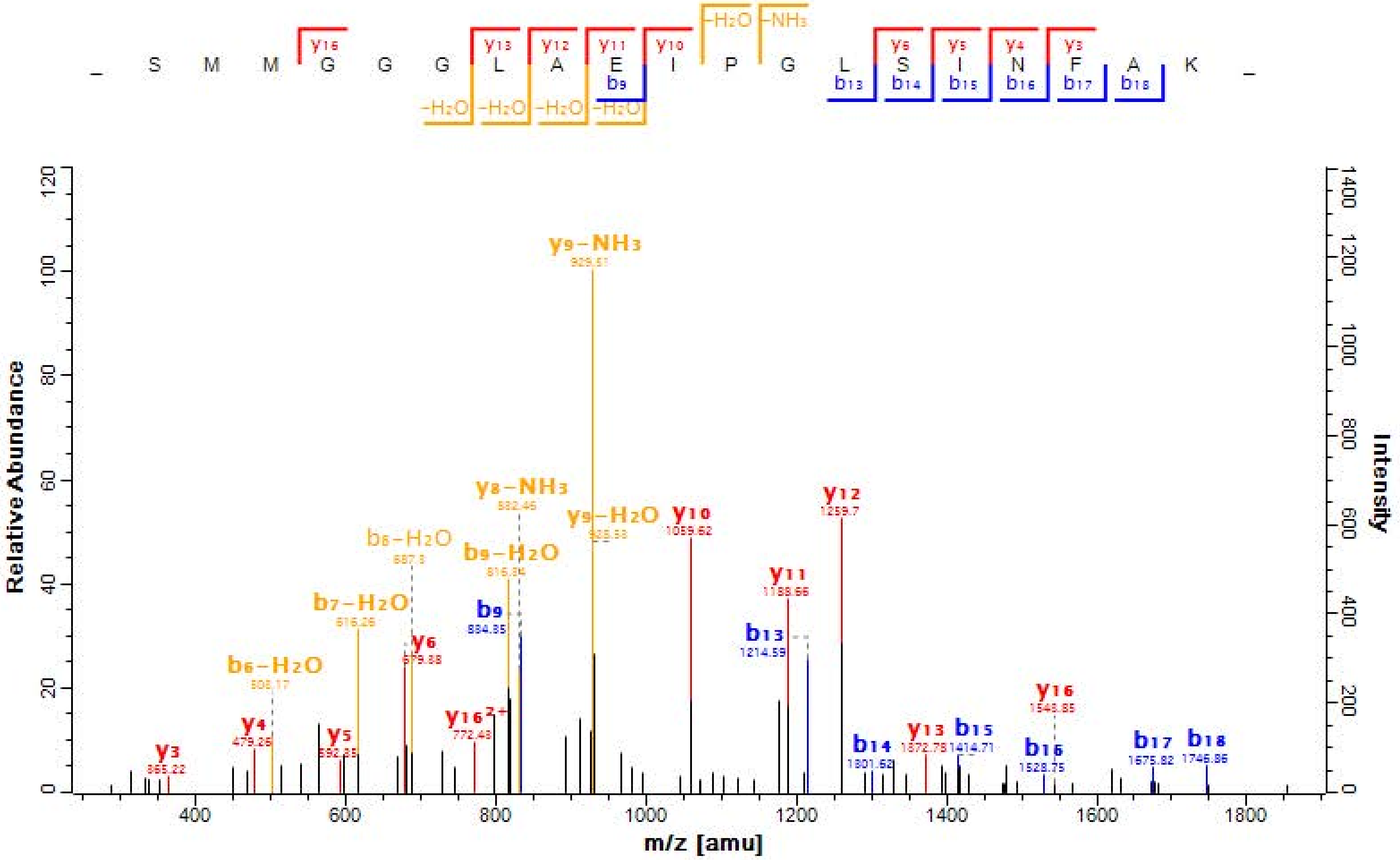
Mass:	1288.59723
m/z:	645.30589
Charge:	2+
Retentiontime:	61.305160522460
Score:	100.9311
Mass Error [ppm]:	0.064282
PEP:	0.00025118
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	24 %
Peak Coverage:	22 %
Protein Localisation:	219 ... 230

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	11				
-0.02647	215.139	2	T	10	1179.677		1179.677	
-0.07773	362.2074	3	F	9	1078.63	+0.048801	539.8184	+0.178172
+0.008552	475.2915	4	I	8	931.5611	-0.1337	931.5611	
	572.3443	5	P	7	818.4771	+0.017502	409.7422	+0.176957
+0.426817	629.3657	6	G	6	721.4243	+0.065627	721.4243	
	776.4341	7	F	5	664.4028		664.4028	
+0.070482	889.5182	8	I	4	517.3344		517.3344	
-0.03814	946.5397	9	G	3	404.2504		404.2504	
	1033.572	10	S	2	347.2289	-0.0038	347.2289	
-0.281	1146.656	11	L	1	260.1969		260.1969	
		12	K	0	147.1128		147.1128	

Scan number	10948	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	86.48



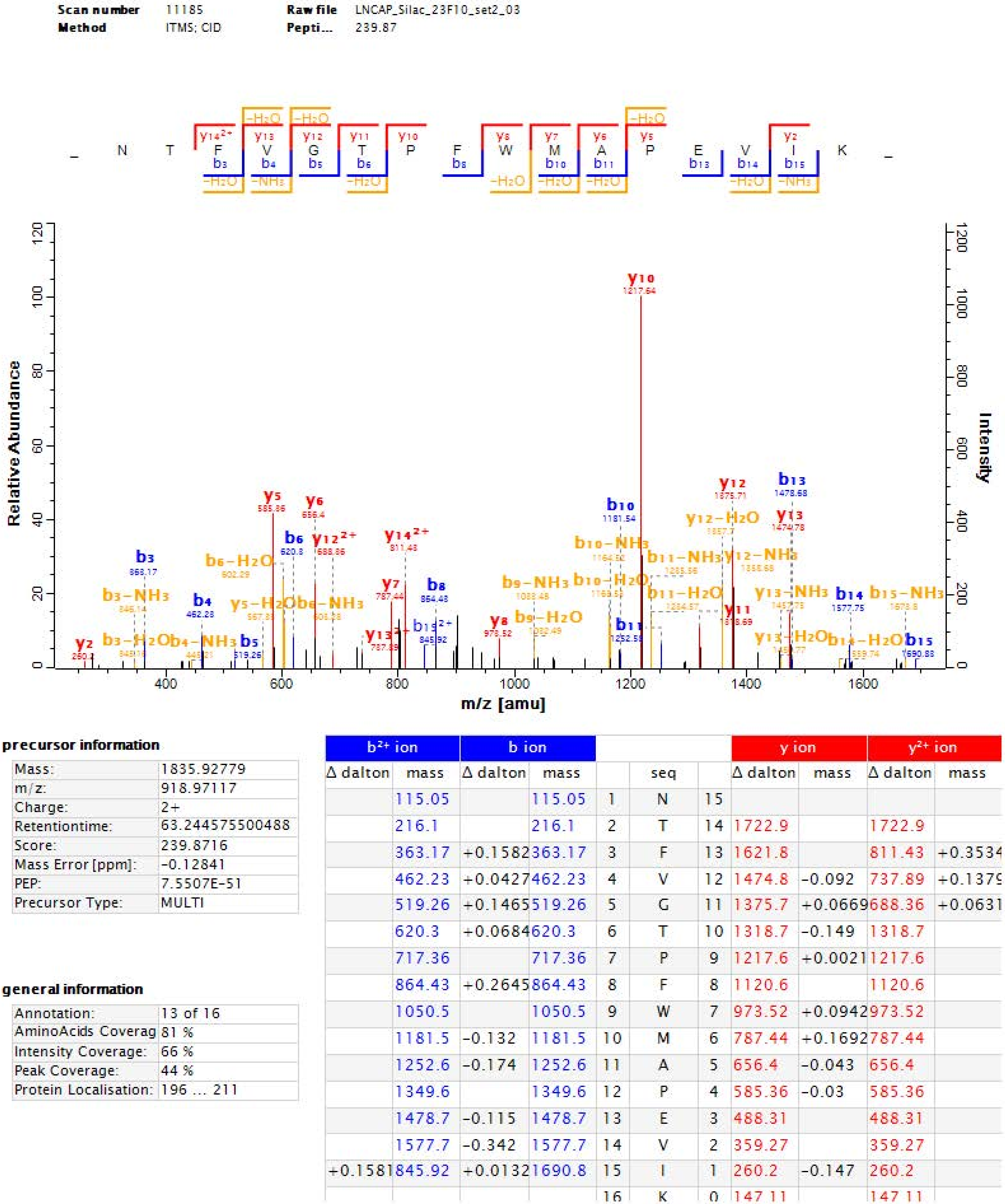
precursor information

Mass:	1891.95368
m/z:	946.98412
Charge:	2+
Retentiontime:	61.571578979492
Score:	86.4794
Mass Error [ppm]:	0.045836
PEP:	2.945E-05
Precursor Type:	MULTI

general information

Annotation:	14 of 19
AminoAcids Coverag	74 %
Intensity Coverage:	58 %
Peak Coverage:	28 %
Protein Localisation:	385 ... 403

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	18				
	219.0798	2	M	17	1805.929		1805.929	
	350.1203	3	M	16	1674.888		1674.888	
	407.1417	4	G	15	1543.848	-0.08993	772.4276	-0.00759
	464.1632	5	G	14	1486.826		1486.826	
	521.1847	6	G	13	1429.805		1429.805	
	634.2687	7	L	12	1372.783	+0.047943	1372.783	
	705.3058	8	A	11	1259.699	-0.10908	1259.699	
-0.02391	834.3484	9	E	10	1188.662	-0.06818	1188.662	
	947.4325	10	I	9	1059.62	-0.01961	1059.62	
	1044.485	11	P	8	946.5356		946.5356	
	1101.507	12	G	7	849.4829		849.4829	
-0.08689	1214.591	13	L	6	792.4614		792.4614	
-0.13661	1301.623	14	S	5	679.3774	+0.114103	679.3774	
-0.13083	1414.707	15	I	4	592.3453	+0.043898	592.3453	
-0.04925	1528.75	16	N	3	479.2613	+0.107271	479.2613	
+0.1255	1675.818	17	F	2	365.2183	-0.03141	365.2183	
-0.17541	1746.855	18	A	1	218.1499		218.1499	
		19	K	0	147.1128		147.1128	



Scan number	11185	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	239.87

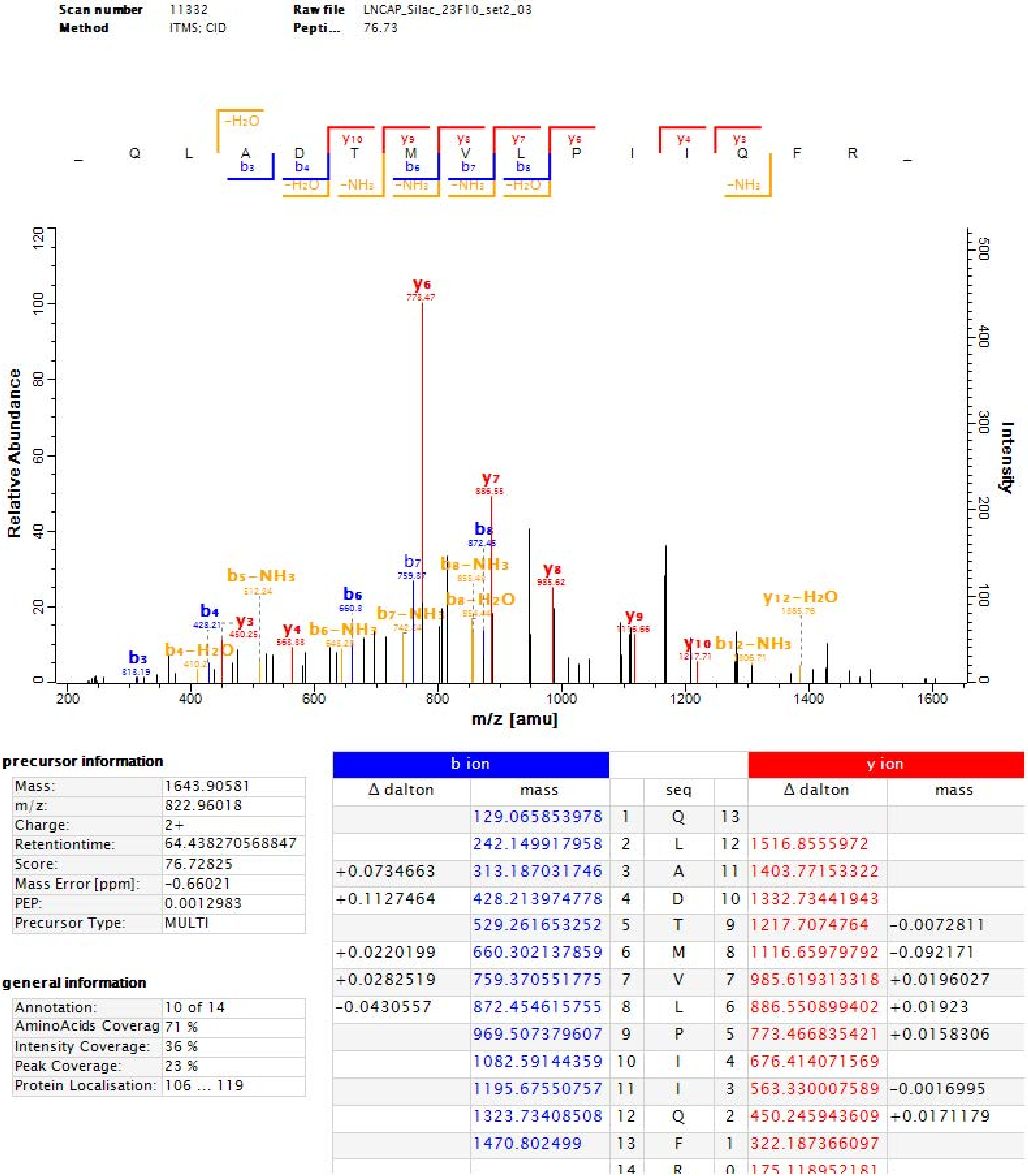
precursor information

Mass:	1835.92779
m/z:	918.97117
Charge:	2+
Retentiontime:	63.244575500488
Score:	239.8716
Mass Error [ppm]:	-0.12841
PEP:	7.5507E-51
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	66 %
Peak Coverage:	44 %
Protein Localisation:	196 ... 211

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.05		115.05	1	N	15				
	216.1		216.1	2	T	14	1722.9		1722.9	
	363.17	+0.1582	363.17	3	F	13	1621.8		811.43	+0.3534
	462.23	+0.0427	462.23	4	V	12	1474.8	-0.092	737.89	+0.137
	519.26	+0.1465	519.26	5	G	11	1375.7	+0.0669	688.36	+0.0631
	620.3	+0.0684	620.3	6	T	10	1318.7	-0.149	1318.7	
	717.36		717.36	7	P	9	1217.6	+0.0021	1217.6	
	864.43	+0.2645	864.43	8	F	8	1120.6		1120.6	
	1050.5		1050.5	9	W	7	973.52	+0.0942	973.52	
	1181.5	-0.132	1181.5	10	M	6	787.44	+0.1692	787.44	
	1252.6	-0.174	1252.6	11	A	5	656.4	-0.043	656.4	
	1349.6		1349.6	12	P	4	585.36	-0.03	585.36	
	1478.7	-0.115	1478.7	13	E	3	488.31		488.31	
	1577.7	-0.342	1577.7	14	V	2	359.27		359.27	
+0.1581	845.92	+0.0132	1690.8	15	I	1	260.2	-0.147	260.2	
				16	K	0	147.11		147.11	



Scan number	11332	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	76.73

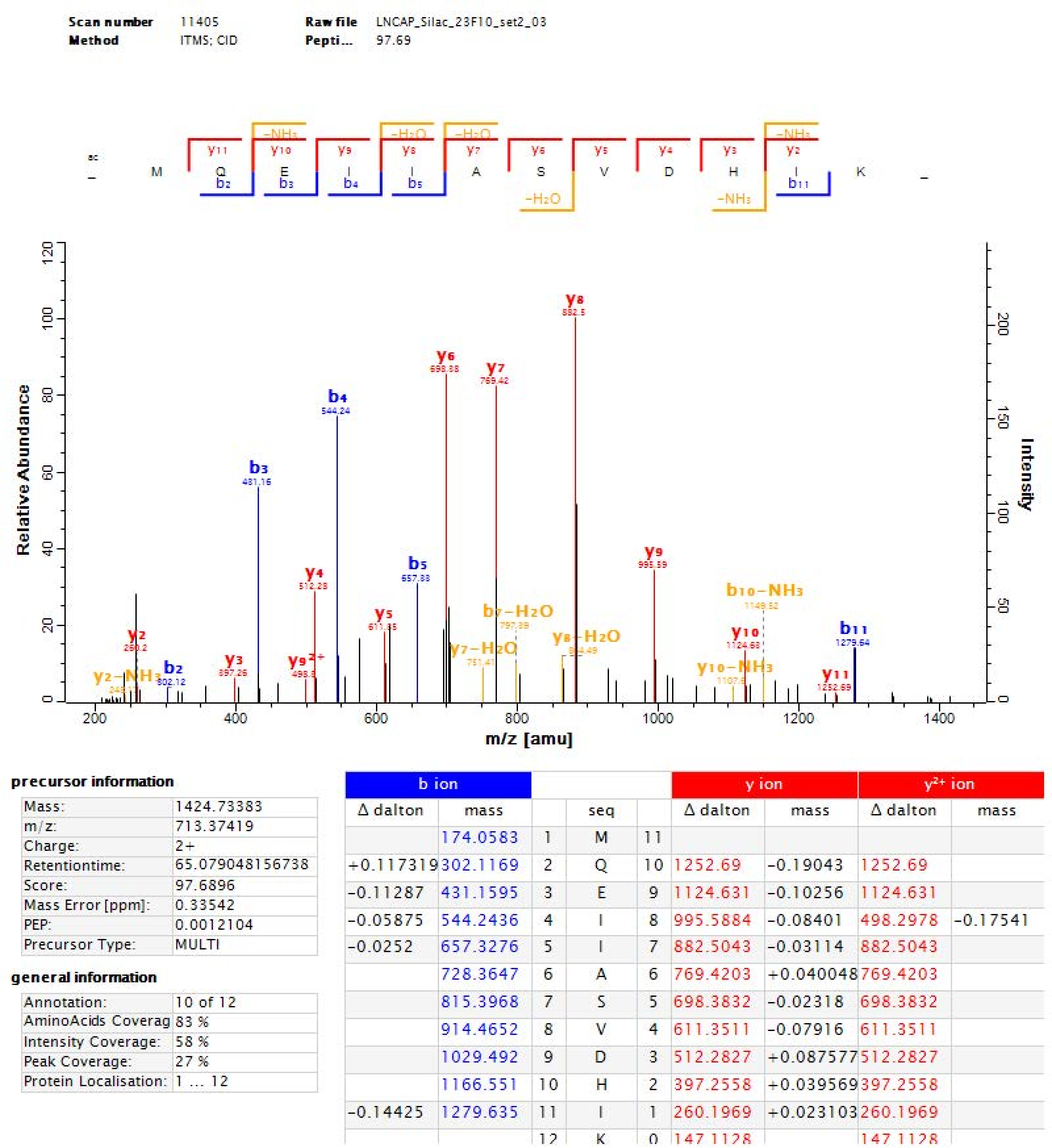
precursor information

Mass:	1643.90581
m/z:	822.96018
Charge:	2+
Retentiontime:	64.438270568847
Score:	76.72825
Mass Error [ppm]:	-0.66021
PEP:	0.0012983
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	36 %
Peak Coverage:	23 %
Protein Localisation:	106 ... 119

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	129.065853978	1	Q	13		
	242.149917958	2	L	12	1516.8555972	
+0.0734663	313.187031746	3	A	11	1403.77153322	
+0.1127464	428.213974778	4	D	10	1332.73441943	
	529.261653252	5	T	9	1217.7074764	-0.0072811
+0.0220199	660.302137859	6	M	8	1116.65979792	-0.092171
+0.0282519	759.370551775	7	V	7	985.619313318	+0.0196027
-0.0430557	872.454615755	8	L	6	886.550899402	+0.01923
	969.507379607	9	P	5	773.466835421	+0.0158306
	1082.59144359	10	I	4	676.414071569	
	1195.67550757	11	I	3	563.330007589	-0.0016995
	1323.73408508	12	Q	2	450.245943609	+0.0171179
	1470.802499	13	F	1	322.187366097	
		14	R	0	175.118952181	



Scan number	11405	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	97.69

precursor information

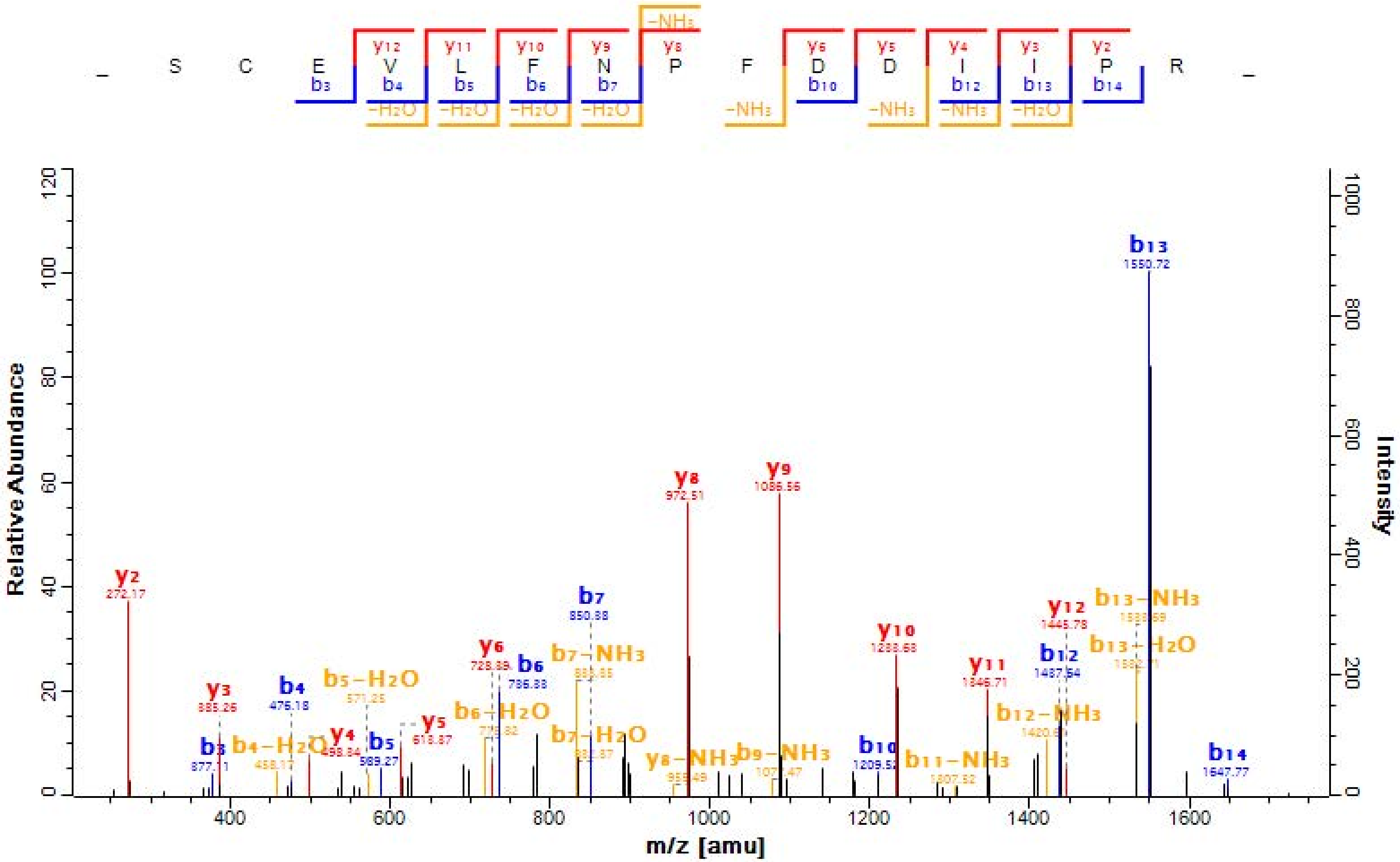
Mass:	1424.73383
m/z:	713.37419
Charge:	2+
Retentiontime:	65.079048156738
Score:	97.6896
Mass Error [ppm]:	0.33542
PEP:	0.0012104
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	58 %
Peak Coverage:	27 %
Protein Localisation:	1 ... 12

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	174.0583	1	M	11				
+0.117319	302.1169	2	Q	10	1252.69	-0.19043	1252.69	
-0.11287	431.1595	3	E	9	1124.631	-0.10256	1124.631	
-0.05875	544.2436	4	I	8	995.5884	-0.08401	498.2978	-0.17541
-0.0252	657.3276	5	I	7	882.5043	-0.03114	882.5043	
	728.3647	6	A	6	769.4203	+0.040048	769.4203	
	815.3968	7	S	5	698.3832	-0.02318	698.3832	
	914.4652	8	V	4	611.3511	-0.07916	611.3511	
	1029.492	9	D	3	512.2827	+0.087577	512.2827	
	1166.551	10	H	2	397.2558	+0.039569	397.2558	
-0.14425	1279.635	11	I	1	260.1969	+0.023103	260.1969	
		12	K	0	147.1128		147.1128	

Scan number	11689	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	163.23



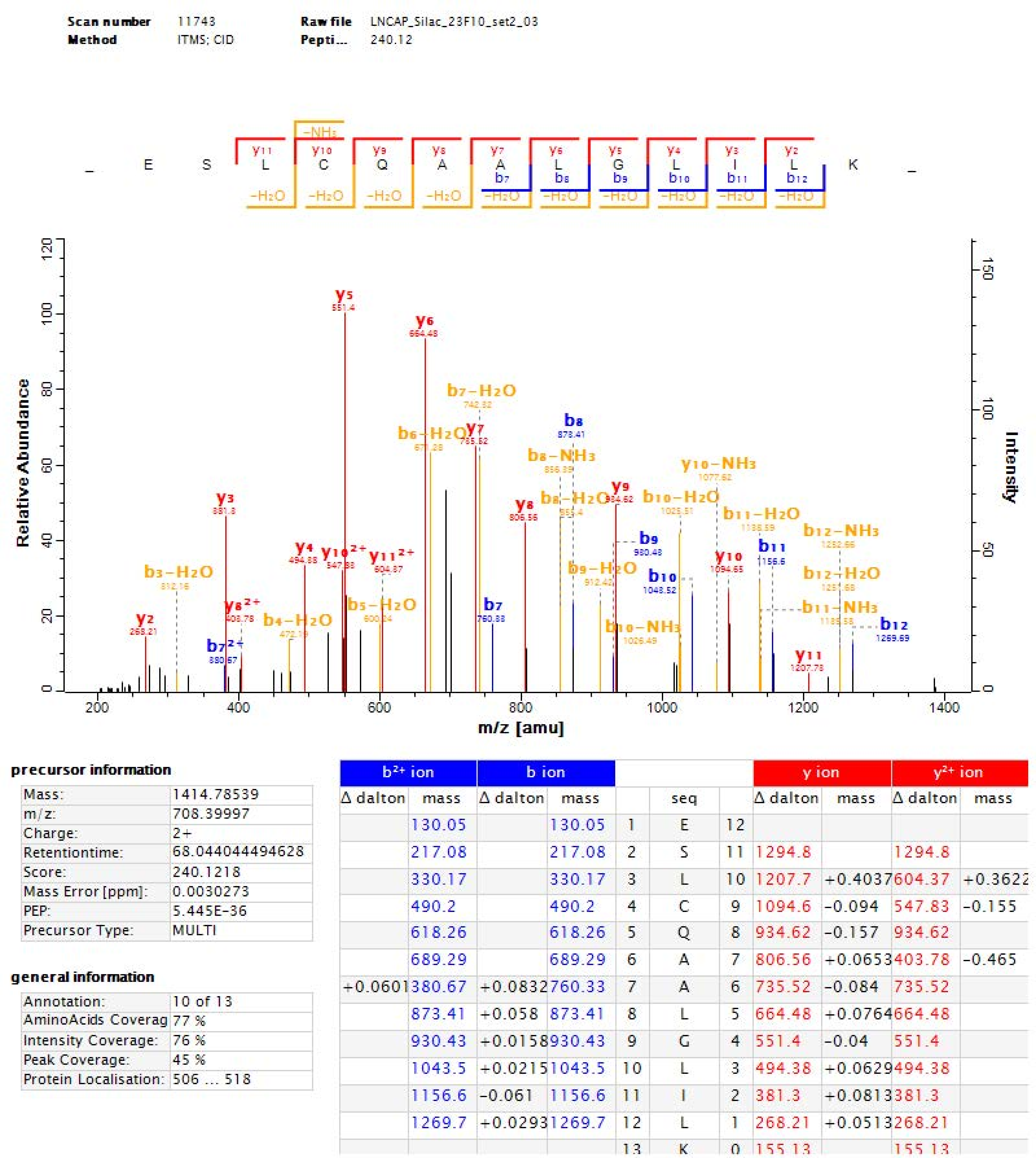
precursor information

Mass:	1820.87718
m/z:	911.44587
Charge:	2+
Retentiontime:	67.571876525878
Score:	163.2325
Mass Error [ppm]:	0.25191
PEP:	1.6231E-14
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	55 %
Peak Coverage:	34 %
Protein Localisation:	163 ... 177

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	88.039304876	1	S	14		
	248.069953078	2	C	13	1734.85196838	
+0.0199001	377.112546174	3	E	12	1574.82132018	
-0.0021881	476.18096009	4	V	11	1445.77872709	-0.0918374
-0.0269259	589.265024071	5	L	10	1346.71031317	+0.0090472
-0.0962554	736.333437987	6	F	9	1233.62624919	+0.0446492
-0.0448835	850.376365434	7	N	8	1086.55783527	-0.0088851
	947.429129286	8	P	7	972.514907826	-0.0715485
	1094.4975432	9	F	6	875.462143974	
+0.0983165	1209.52448623	10	D	5	728.393730058	+0.101082
	1324.55142927	11	D	4	613.366787026	+0.0500221
-0.1030225	1437.63549325	12	I	3	498.339843994	+0.0219114
-0.2233414	1550.71955723	13	I	2	385.255780013	-0.0012939
-0.1945623	1647.77232108	14	P	1	272.171716033	+0.038367
		15	R	0	175.118952181	



Scan number 11743 **Raw file** LNCAP_Silac_23F10_set2_03
Method ITMS; CID **Pepti...** 240.12

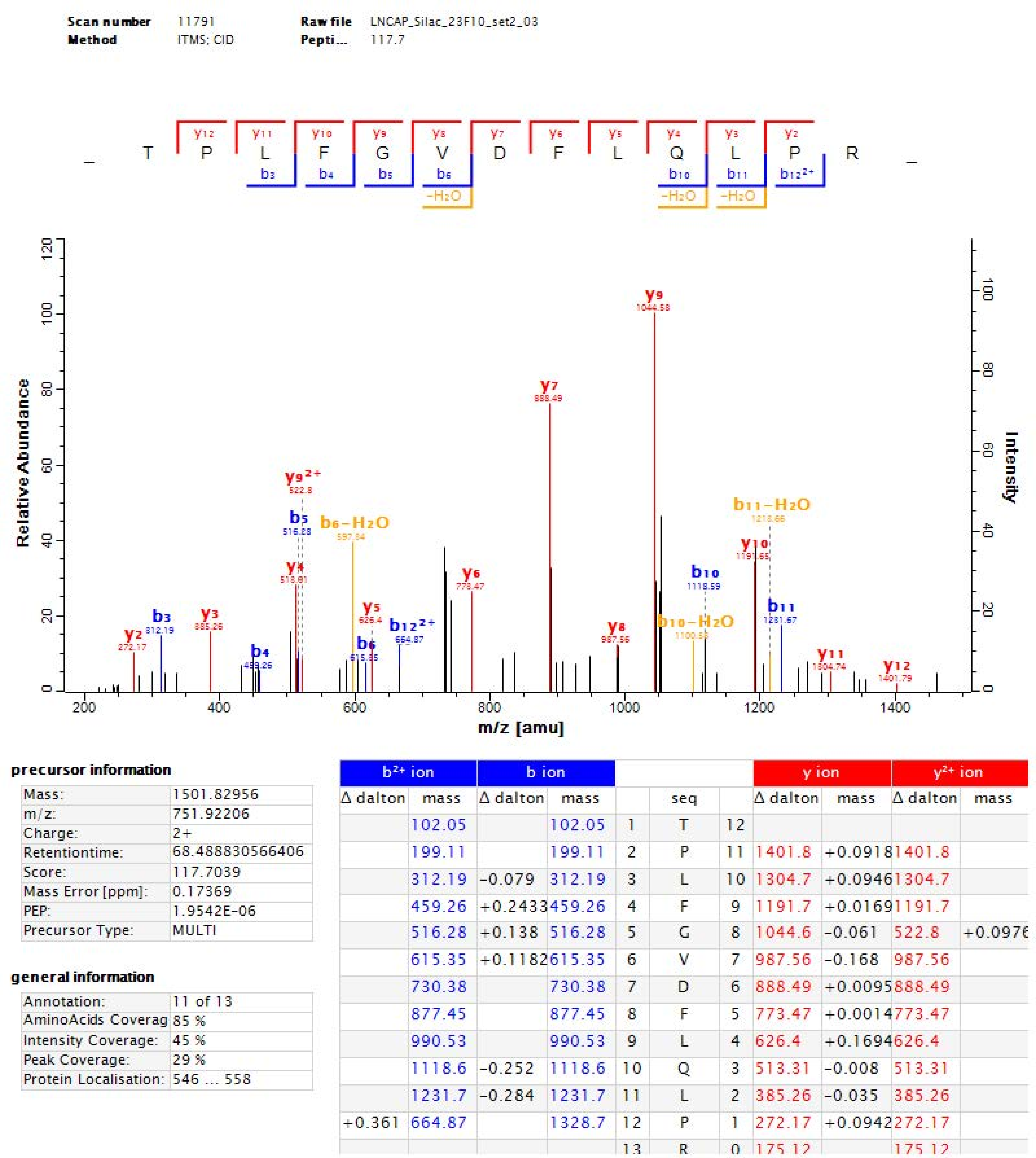
precursor information

Mass:	1414.78539
m/z:	708.39997
Charge:	2+
Retentiontime:	68.044044494628
Score:	240.1218
Mass Error [ppm]:	0.0030273
PEP:	5.445E-36
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	76 %
Peak Coverage:	45 %
Protein Localisation:	506 ... 518

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	12				
	217.08		217.08	2	S	11	1294.8		1294.8	
	330.17		330.17	3	L	10	1207.7	+0.4037	604.37	+0.3622
	490.2		490.2	4	C	9	1094.6	-0.094	547.83	-0.155
	618.26		618.26	5	Q	8	934.62	-0.157	934.62	
	689.29		689.29	6	A	7	806.56	+0.0653	403.78	-0.465
+0.0601	380.67	+0.0832	760.33	7	A	6	735.52	-0.084	735.52	
	873.41	+0.058	873.41	8	L	5	664.48	+0.0764	664.48	
	930.43	+0.0158	930.43	9	G	4	551.4	-0.04	551.4	
	1043.5	+0.0215	1043.5	10	L	3	494.38	+0.0629	494.38	
	1156.6	-0.061	1156.6	11	I	2	381.3	+0.0813	381.3	
	1269.7	+0.0293	1269.7	12	L	1	268.21	+0.0513	268.21	
				13	K	0	155.13		155.13	



Scan number	11791	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	117.7

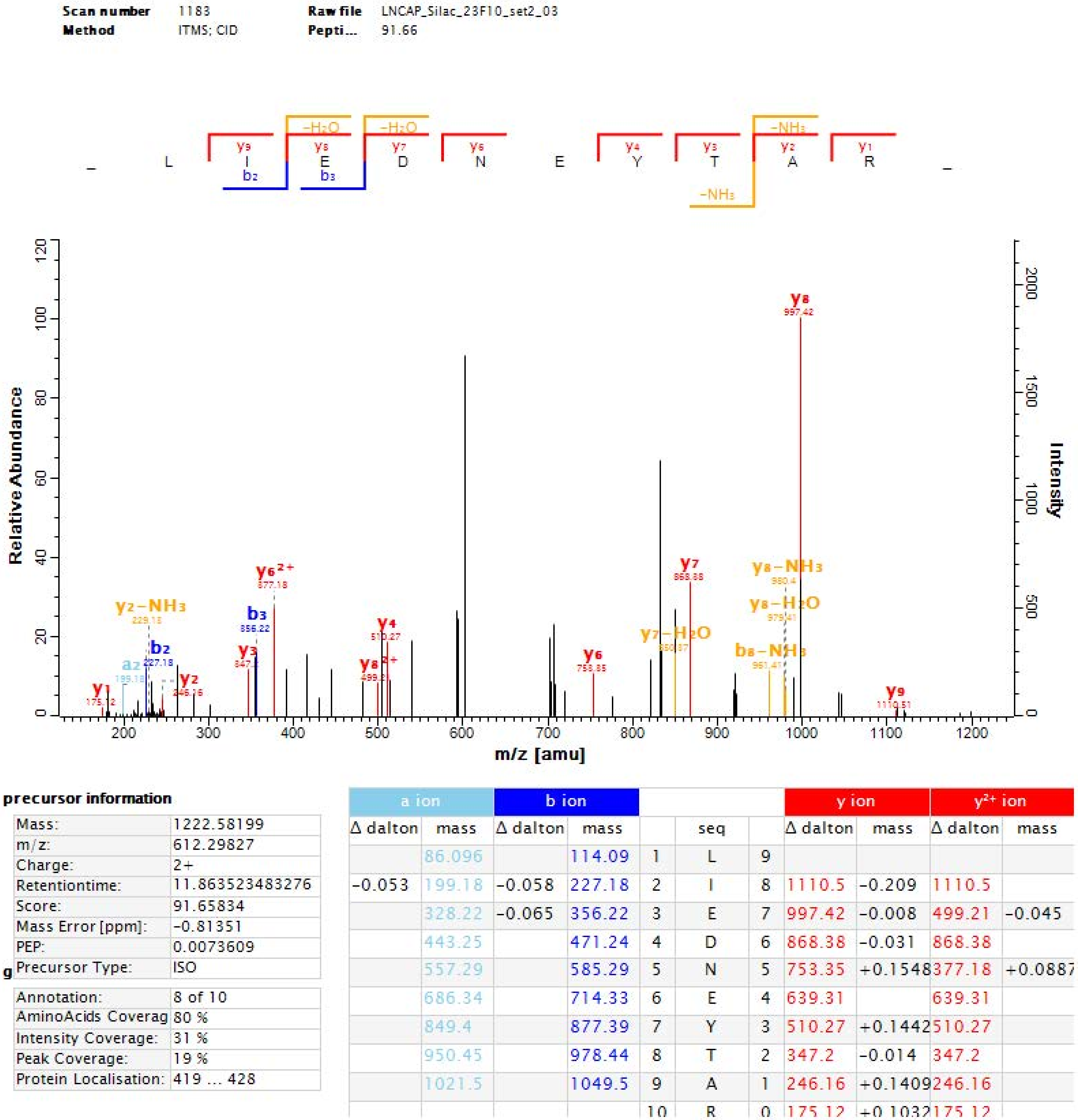
precursor information

Mass:	1501.82956
m/z:	751.92206
Charge:	2+
Retentiontime:	68.488830566406
Score:	117.7039
Mass Error [ppm]:	0.17369
PEP:	1.9542E-06
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	45 %
Peak Coverage:	29 %
Protein Localisation:	546 ... 558

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	12				
	199.11		199.11	2	P	11	1401.8	+0.0918	1401.8	
	312.19	-0.079	312.19	3	L	10	1304.7	+0.0946	1304.7	
	459.26	+0.2433	459.26	4	F	9	1191.7	+0.0169	1191.7	
	516.28	+0.138	516.28	5	G	8	1044.6	-0.061	522.8	+0.0976
	615.35	+0.1182	615.35	6	V	7	987.56	-0.168	987.56	
	730.38		730.38	7	D	6	888.49	+0.0095	888.49	
	877.45		877.45	8	F	5	773.47	+0.0014	773.47	
	990.53		990.53	9	L	4	626.4	+0.1694	626.4	
	1118.6	-0.252	1118.6	10	Q	3	513.31	-0.008	513.31	
	1231.7	-0.284	1231.7	11	L	2	385.26	-0.035	385.26	
+0.361	664.87		1328.7	12	P	1	272.17	+0.0942	272.17	
				13	R	0	175.12		175.12	



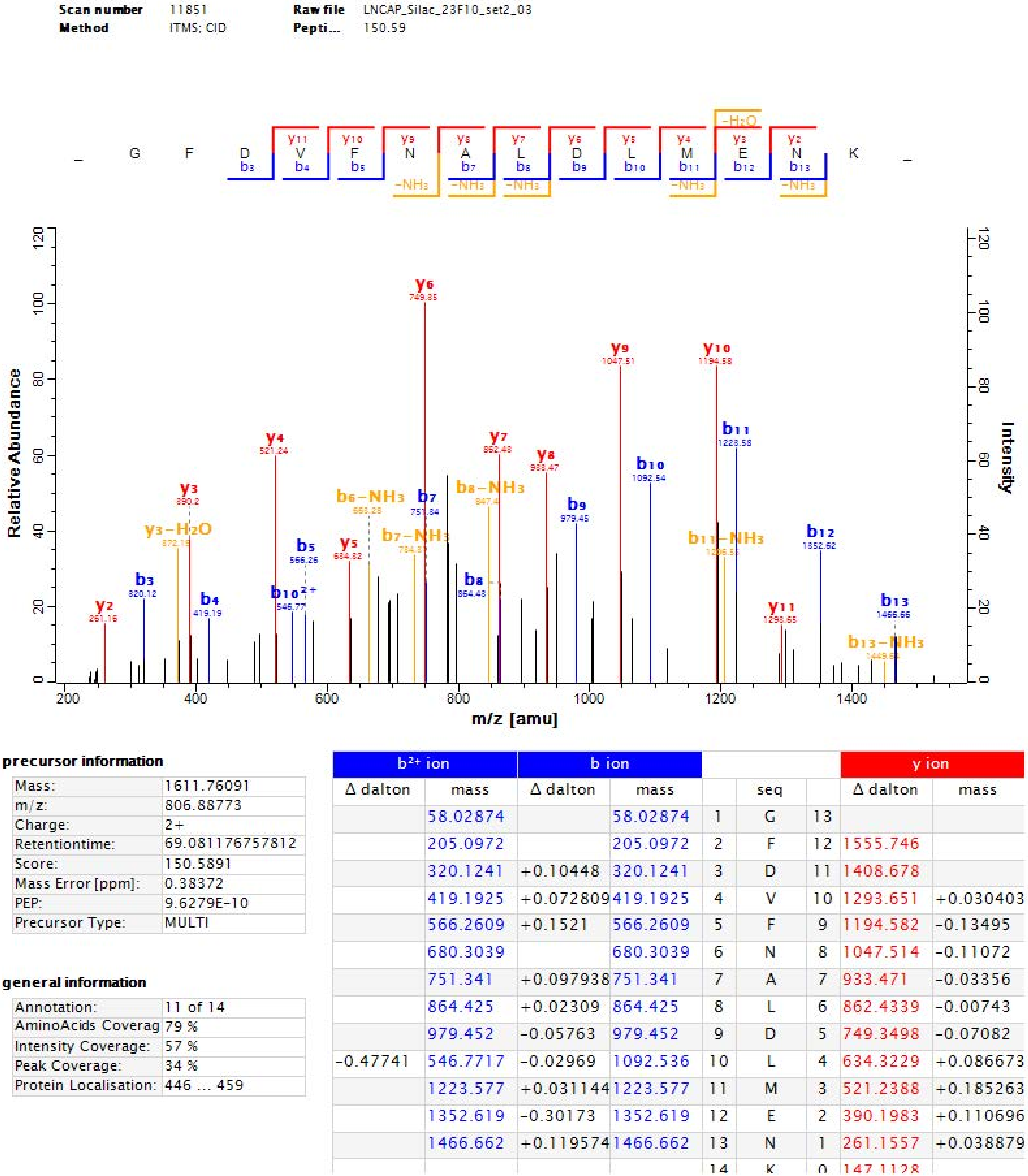
Scan number	1183
Method	ITMS; CID
Raw file	LNCAP_Silac_23F10_set2_03
Pepti...	91.66

precursor information

Mass:	1222.58199
m/z:	612.29827
Charge:	2+
Retentiontime:	11.863523483276
Score:	91.65834
Mass Error [ppm]:	-0.81351
PEP:	0.0073609
Precursor Type:	ISO

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	31 %
Peak Coverage:	19 %
Protein Localisation:	419 ... 428

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	9				
-0.053	199.18	-0.058	227.18	2	I	8	1110.5	-0.209	1110.5	
	328.22	-0.065	356.22	3	E	7	997.42	-0.008	499.21	-0.045
	443.25		471.24	4	D	6	868.38	-0.031	868.38	
	557.29		585.29	5	N	5	753.35	+0.1548	377.18	+0.0887
	686.34		714.33	6	E	4	639.31		639.31	
	849.4		877.39	7	Y	3	510.27	+0.1442	510.27	
	950.45		978.44	8	T	2	347.2	-0.014	347.2	
	1021.5		1049.5	9	A	1	246.16	+0.1409	246.16	
				10	R	0	175.12	+0.1032	175.12	



Scan number	11851	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	150.59

precursor information

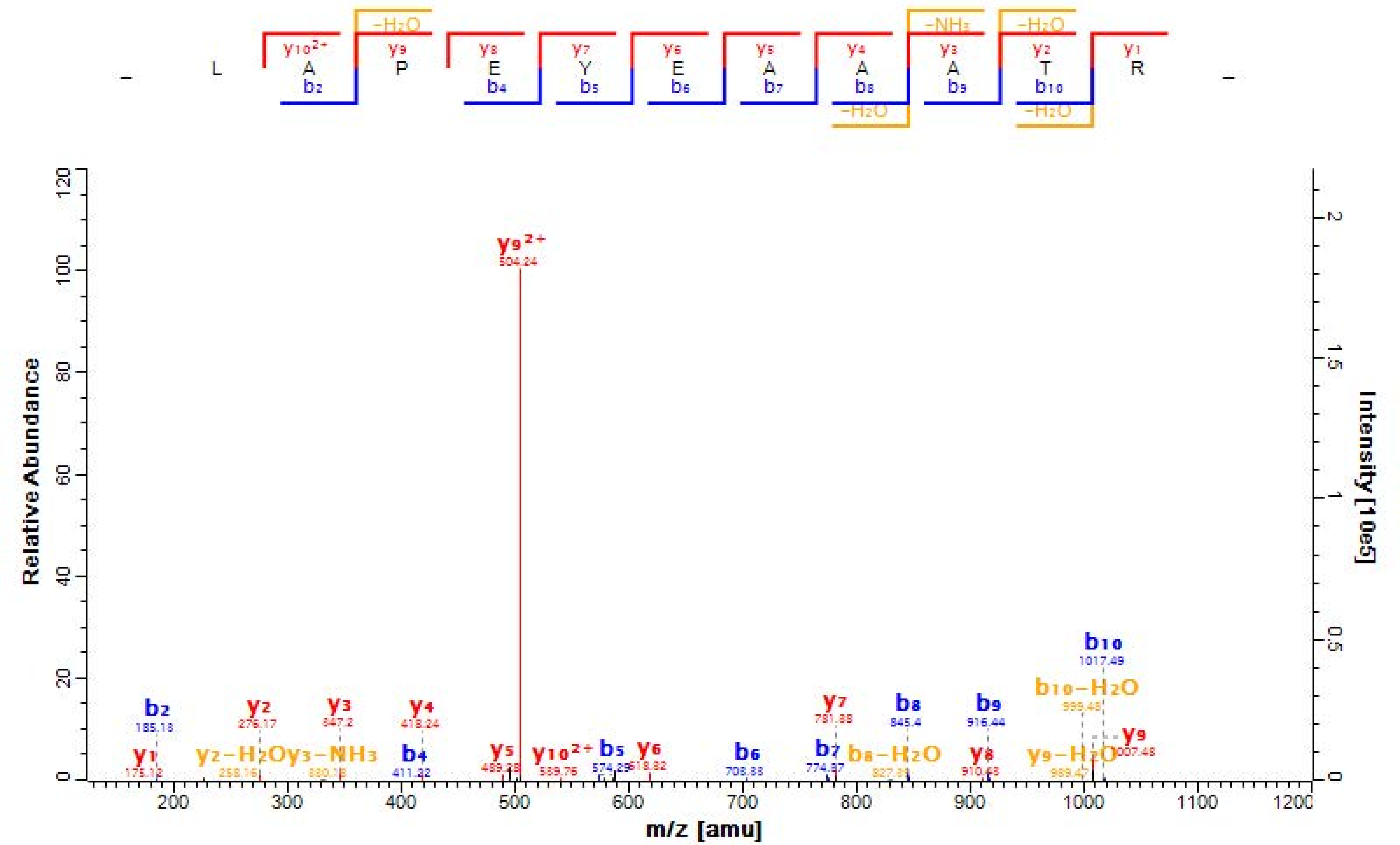
Mass:	1611.76091
m/z:	806.88773
Charge:	2+
Retentiontime:	69.081176757812
Score:	150.5891
Mass Error [ppm]:	0.38372
PEP:	9.6279E-10
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	57 %
Peak Coverage:	34 %
Protein Localisation:	446 ... 459

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	58.02874		58.02874	1	G	13		
	205.0972		205.0972	2	F	12	1555.746	
	320.1241	+0.10448	320.1241	3	D	11	1408.678	
	419.1925	+0.072809	419.1925	4	V	10	1293.651	+0.030403
	566.2609	+0.1521	566.2609	5	F	9	1194.582	-0.13495
	680.3039		680.3039	6	N	8	1047.514	-0.11072
	751.341	+0.097938	751.341	7	A	7	933.471	-0.03356
	864.425	+0.02309	864.425	8	L	6	862.4339	-0.00743
	979.452	-0.05763	979.452	9	D	5	749.3498	-0.07082
-0.47741	546.7717	-0.02969	1092.536	10	L	4	634.3229	+0.086673
	1223.577	+0.031144	1223.577	11	M	3	521.2388	+0.185263
	1352.619	-0.30173	1352.619	12	E	2	390.1983	+0.110696
	1466.662	+0.119574	1466.662	13	N	1	261.1557	+0.038879
				14	K	0	147.1128	

Scan number	1213	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	149.49



precursor information

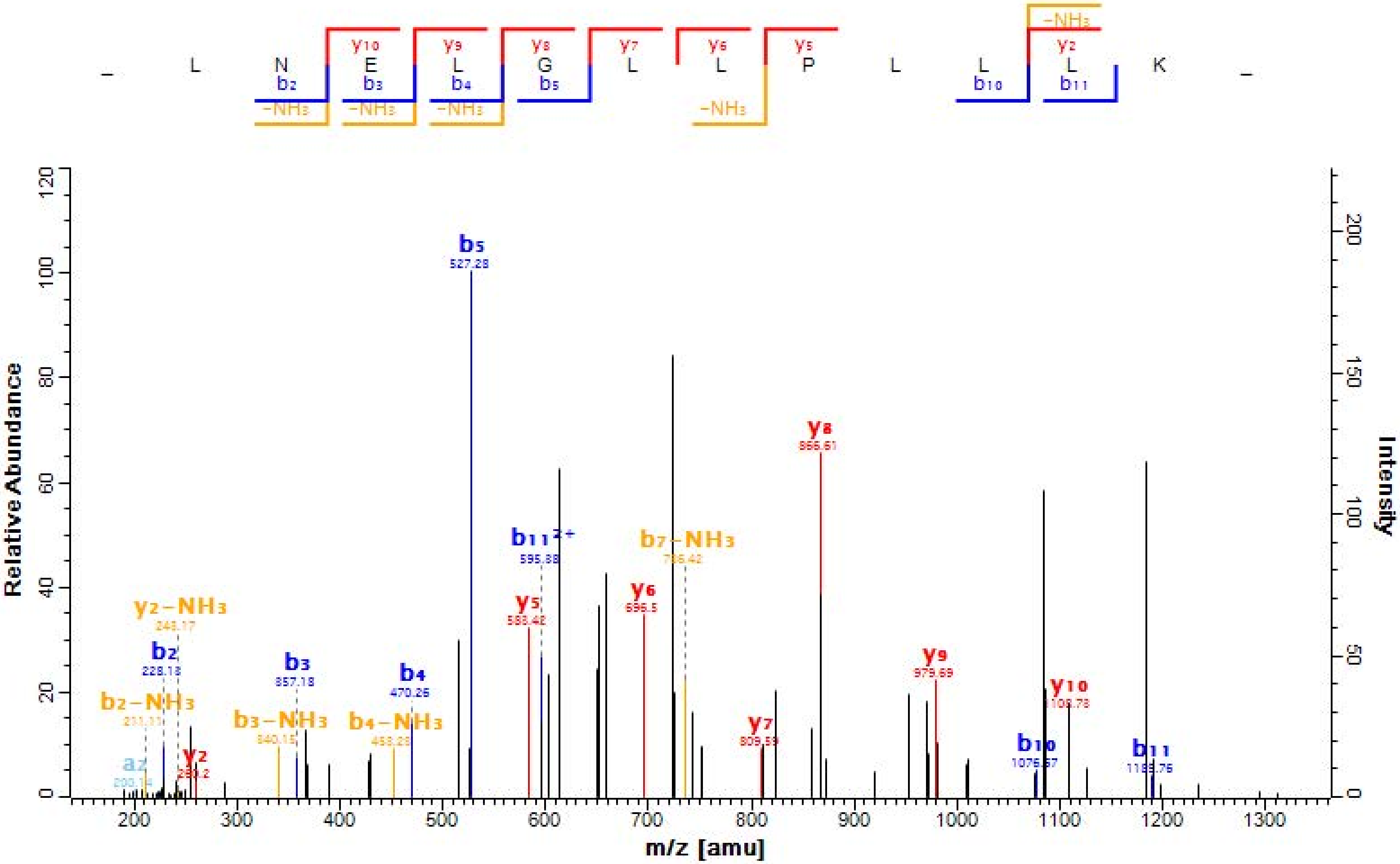
Mass:	1190.5929
m/z:	596.30372
Charge:	2+
Retentiontime:	12.025785446167
Score:	149.4918
Mass Error [ppm]:	-0.21558
PEP:	2.7415E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 11
AminoAcids Coverag	91 %
Intensity Coverage:	91 %
Peak Coverage:	36 %
Protein Localisation:	63 ... 73

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	10				
-0.07731	185.1285	2	A	9	1078.516		539.7618	+0.13619
	282.1812	3	P	8	1007.479	-0.01197	504.2433	+0.2098
+0.128972	411.2238	4	E	7	910.4265	+0.123013	910.4265	
-0.00729	574.2871	5	Y	6	781.3839	+0.095904	781.3839	
-0.01717	703.3297	6	E	5	618.3206	+0.0783	618.3206	
-0.04775	774.3668	7	A	4	489.278	+0.129804	489.278	
+0.004548	845.404	8	A	3	418.2409	+0.044115	418.2409	
-0.05881	916.4411	9	A	2	347.2037	+0.030447	347.2037	
-0.18876	1017.489	10	T	1	276.1666	+0.064906	276.1666	
		11	R	0	175.119	-0.05837	175.119	

Scan number	12268	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	88.02



precursor information

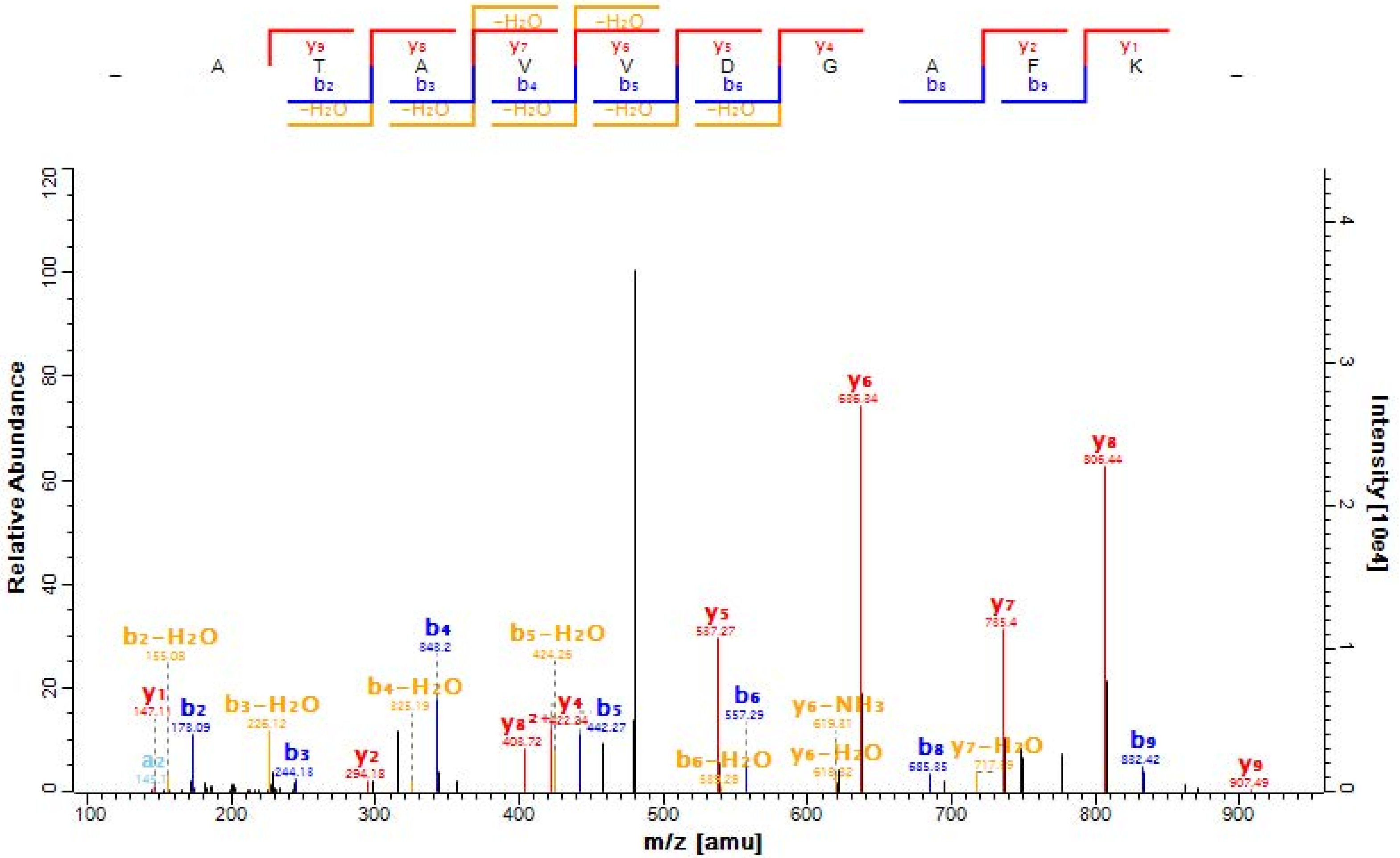
Mass:	1328.65396
m/z:	665.33426
Charge:	2+
Retentiontime:	73.231643676757
Score:	88.02058
Mass Error [ppm]:	0.26843
PEP:	0.00419
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	32 %
Peak Coverage:	23 %
Protein Localisation:	259 ... 270

a ion		b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	86.096		114.09		114.09	1	L	11		
+0.3567	200.14		228.13	+0.0544	228.13	2	N	10	1222.8	
	329.18		357.18	+0.1888	357.18	3	E	9	1108.7	-0.154
	442.27		470.26	+0.0524	470.26	4	L	8	979.69	-0.024
	499.29		527.28	+0.208	527.28	5	G	7	866.61	-0.01
	612.37		640.37		640.37	6	L	6	809.59	-0.03
	725.46		753.45		753.45	7	L	5	696.5	-0.083
	822.51		850.5		850.5	8	P	4	583.42	-0.059
	935.59		963.59		963.59	9	L	3	486.36	
	1048.7		1076.7	-0.002	1076.7	10	L	2	373.28	
	1161.8	+0.0702	595.38	-0.249	1189.8	11	L	1	260.2	-0.014
						12	K	0	147.11	

Scan number	1848	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti…**	174.98

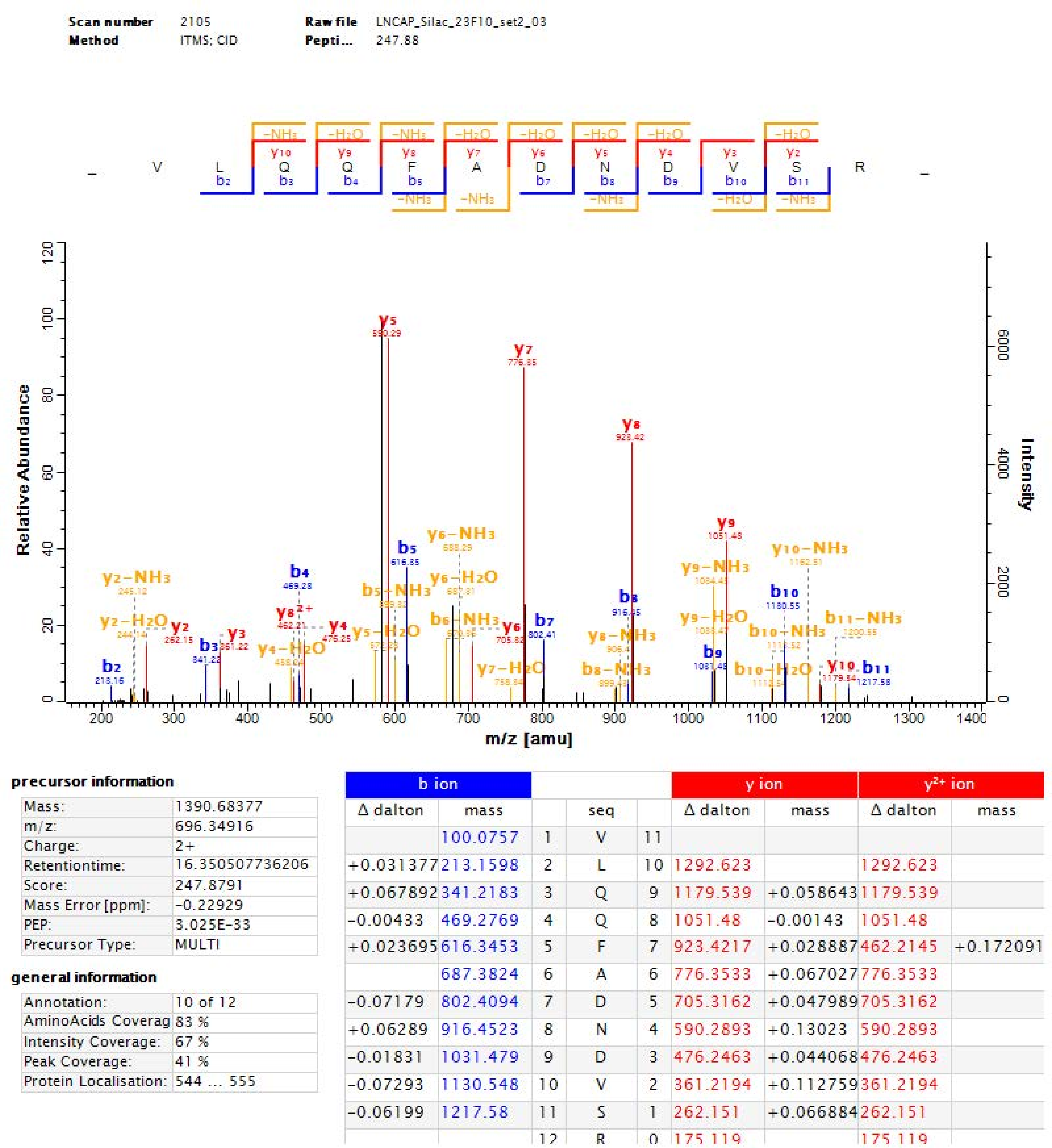


precursor information

Mass:	977.51801
m/z:	489.76628
Charge:	2+
Retentiontime:	15.109158515930
Score:	174.9809
Mass Error [ppm]:	-0.18793
PEP:	6.7409E-06
Precursor Type:	MULTI

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	54 %
Peak Coverage:	30 %
Protein Localisation:	17 … 26

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	44.049		72.044	1	A	9				
+0.1253	145.1	-0.008	173.09	2	T	8	907.49	+0.1564	907.49	
	216.13	+0.1206	244.13	3	A	7	806.44	+0.0351	403.72	+0.1483
	315.2	+0.0028	343.2	4	V	6	735.4	+0.0576	735.4	
	414.27	+0.0323	442.27	5	V	5	636.34	-0.016	636.34	
	529.3	+0.0648	557.29	6	D	4	537.27	+0.0224	537.27	
	586.32		614.31	7	G	3	422.24	+0.0637	422.24	
	657.36	-0.017	685.35	8	A	2	365.22		365.22	
	804.43	-0.149	832.42	9	F	1	294.18	+0.0322	294.18	
				10	K	0	147.11	+0.0347	147.11	



Scan number	2105	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	247.88

precursor information

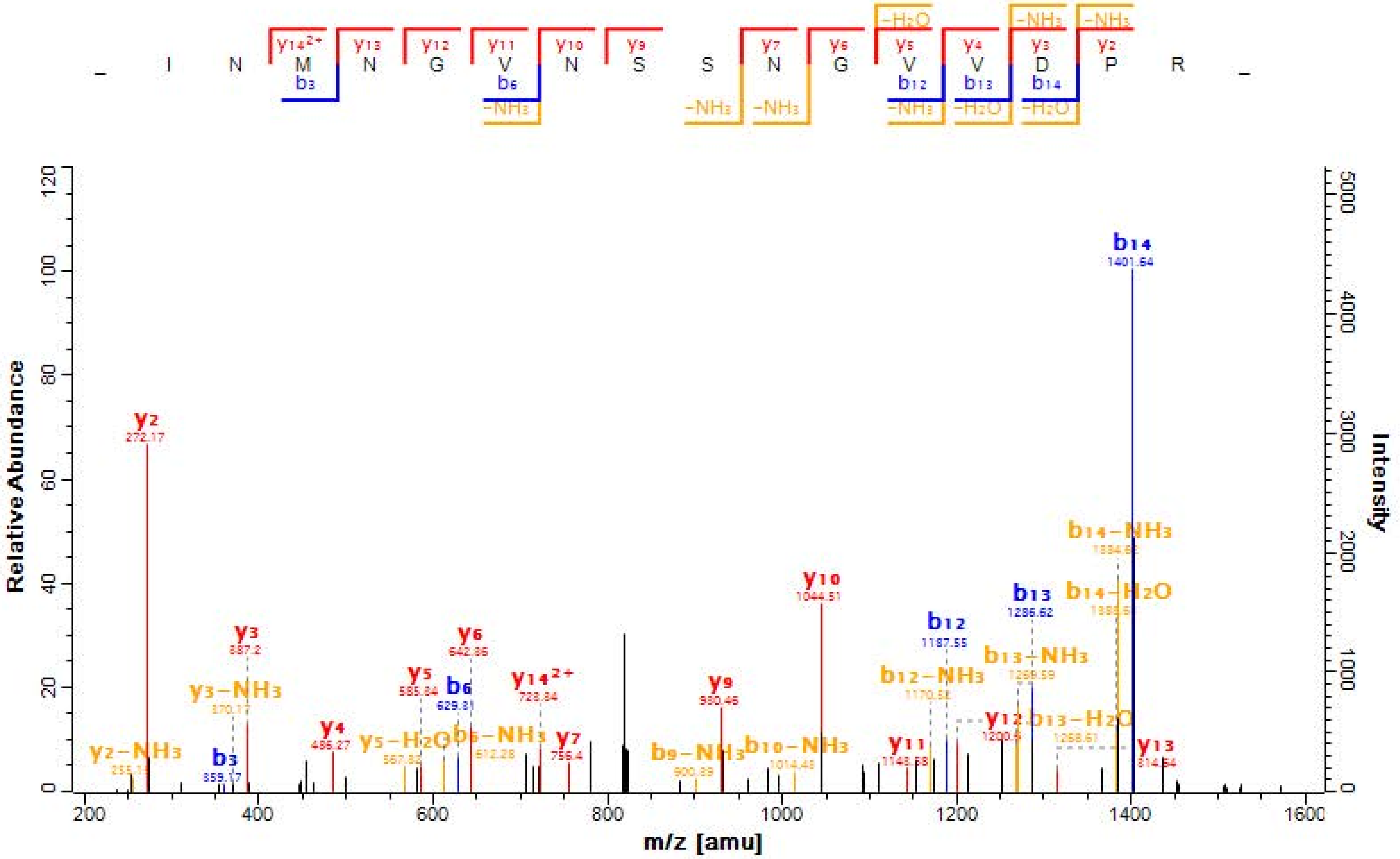
Mass:	1390.68377
m/z:	696.34916
Charge:	2+
Retentiontime:	16.350507736206
Score:	247.8791
Mass Error [ppm]:	-0.22929
PEP:	3.025E-33
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	67 %
Peak Coverage:	41 %
Protein Localisation:	544 ... 555

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	11				
+0.031377	213.1598	2	L	10	1292.623		1292.623	
+0.067892	341.2183	3	Q	9	1179.539	+0.058643	1179.539	
-0.00433	469.2769	4	Q	8	1051.48	-0.00143	1051.48	
+0.023695	616.3453	5	F	7	923.4217	+0.028887	462.2145	+0.172091
	687.3824	6	A	6	776.3533	+0.067027	776.3533	
-0.07179	802.4094	7	D	5	705.3162	+0.047989	705.3162	
+0.06289	916.4523	8	N	4	590.2893	+0.13023	590.2893	
-0.01831	1031.479	9	D	3	476.2463	+0.044068	476.2463	
-0.07293	1130.548	10	V	2	361.2194	+0.112759	361.2194	
-0.06199	1217.58	11	S	1	262.151	+0.066884	262.151	
		12	R	0	175.119		175.119	

Scan number	2341	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	132.81



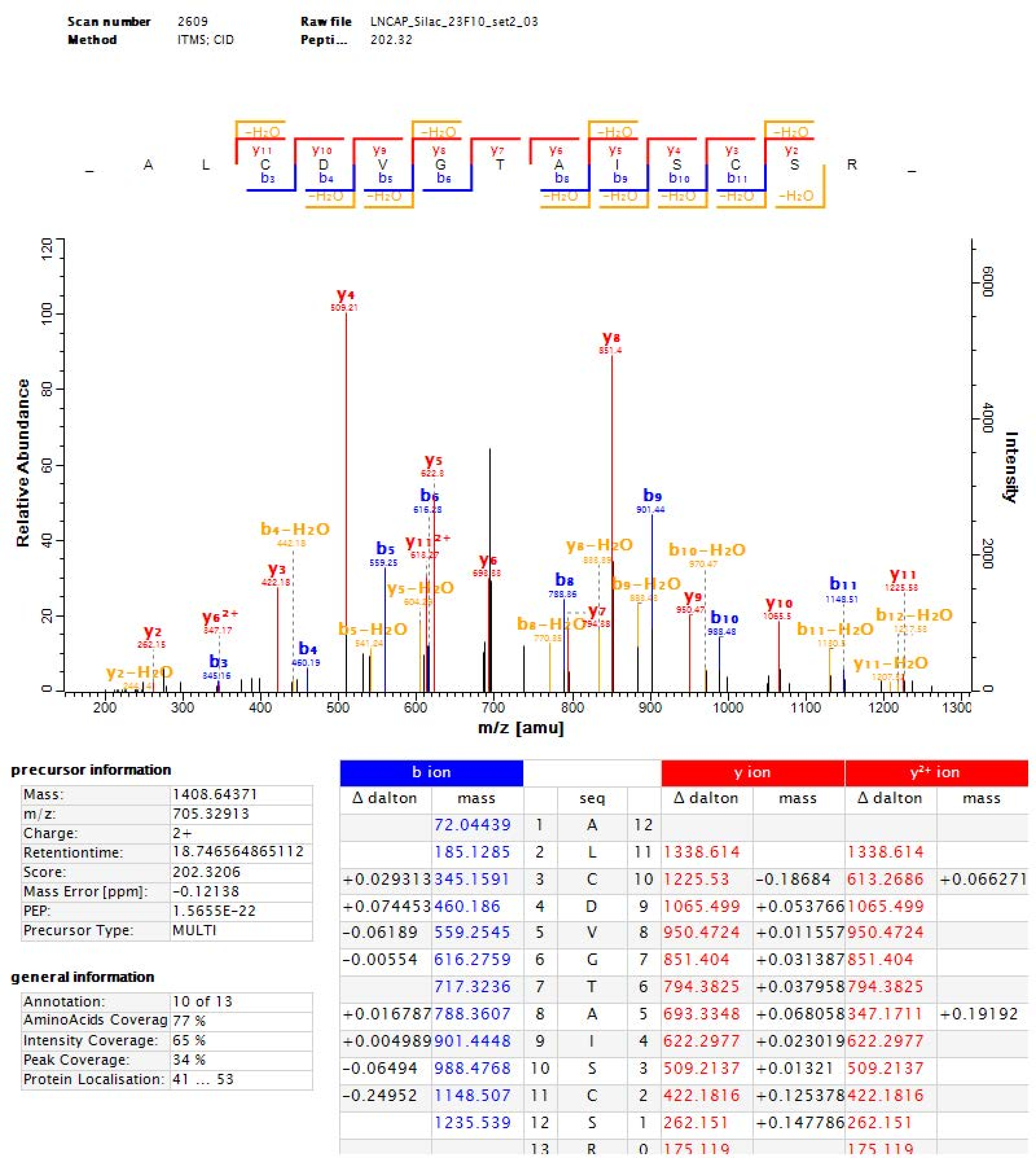
precursor information

Mass:	1671.80069
m/z:	836.90762
Charge:	2+
Retentiontime:	17.500610351562
Score:	132.8108
Mass Error [ppm]:	0.49405
PEP:	1.5105E-10
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	58 %
Peak Coverage:	33 %
Protein Localisation:	311 ... 326

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	I	15				
	228.1343	2	N	14	1559.723		1559.723	
+0.046561	359.1748	3	M	13	1445.68		723.3437	+0.300878
	473.2177	4	N	12	1314.64	+0.029156	1314.64	
	530.2391	5	G	11	1200.597	+0.066102	1200.597	
+0.054381	629.3076	6	V	10	1143.575	+0.072917	1143.575	
	743.3505	7	N	9	1044.507	-0.09329	1044.507	
	830.3825	8	S	8	930.4639	-0.00098	930.4639	
	917.4145	9	S	7	843.4319		843.4319	
	1031.457	10	N	6	756.3999	+0.002405	756.3999	
	1088.479	11	G	5	642.357	+0.148787	642.357	
-0.15025	1187.547	12	V	4	585.3355	+0.128319	585.3355	
-0.12077	1286.616	13	V	3	486.2671	+0.017656	486.2671	
-0.1543	1401.643	14	D	2	387.1987	+0.164988	387.1987	
	1498.695	15	P	1	272.1717	-0.02734	272.1717	
		16	R	0	175.119		175.119	



Scan number	2609	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	202.32

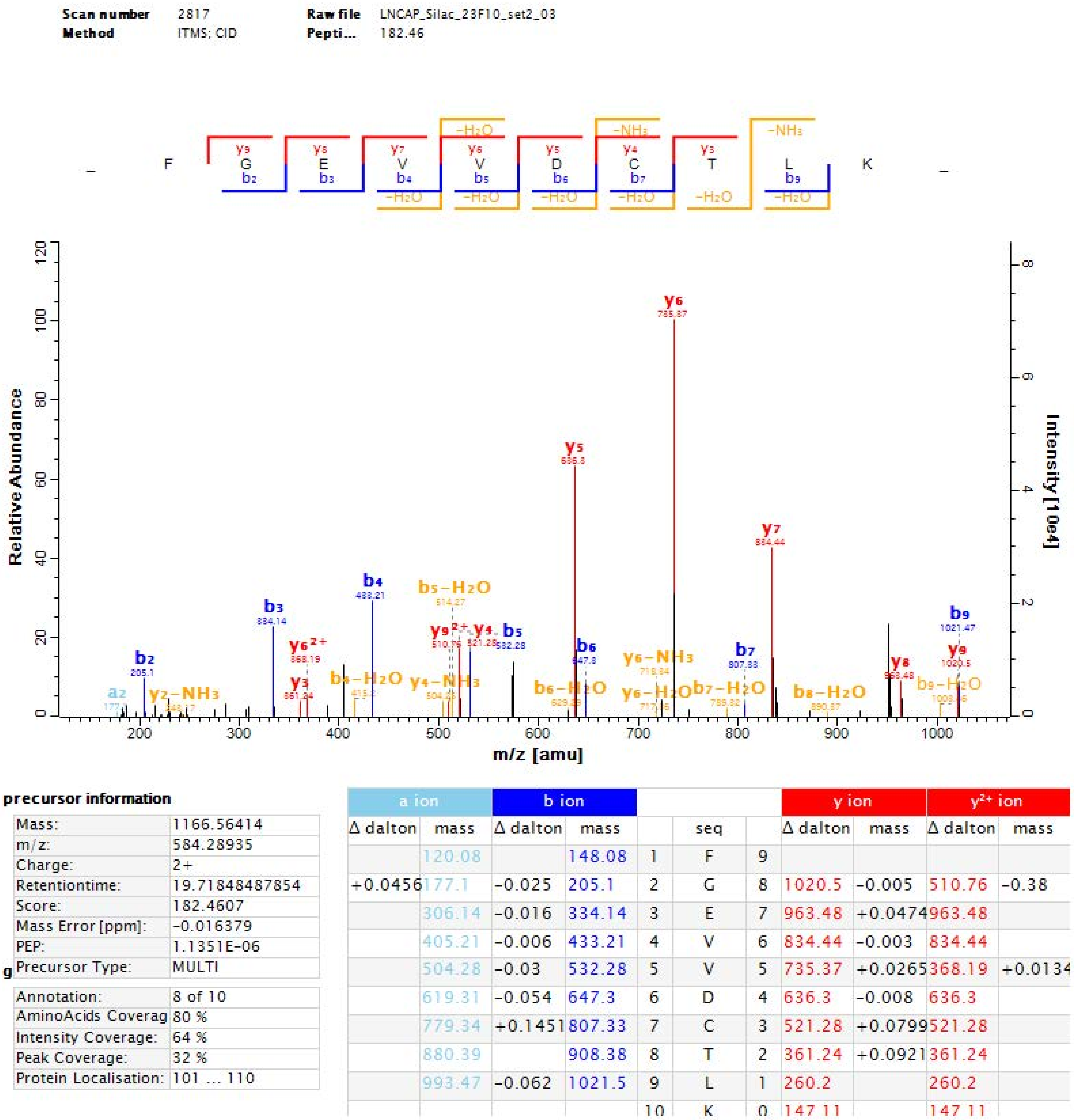
precursor information

Mass:	1408.64371
m/z:	705.32913
Charge:	2+
Retentiontime:	18.746564865112
Score:	202.3206
Mass Error [ppm]:	-0.12138
PEP:	1.5655E-22
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	65 %
Peak Coverage:	34 %
Protein Localisation:	41 … 53

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	12				
	185.1285	2	L	11	1338.614		1338.614	
+0.029313	345.1591	3	C	10	1225.53	-0.18684	613.2686	+0.066271
+0.074453	460.186	4	D	9	1065.499	+0.053766	1065.499	
-0.06189	559.2545	5	V	8	950.4724	+0.011557	950.4724	
-0.00554	616.2759	6	G	7	851.404	+0.031387	851.404	
	717.3236	7	T	6	794.3825	+0.037958	794.3825	
+0.016787	788.3607	8	A	5	693.3348	+0.068058	347.1711	+0.19192
+0.004989	901.4448	9	I	4	622.2977	+0.023019	622.2977	
-0.06494	988.4768	10	S	3	509.2137	+0.01321	509.2137	
-0.24952	1148.507	11	C	2	422.1816	+0.125378	422.1816	
	1235.539	12	S	1	262.151	+0.147786	262.151	
		13	R	0	175.119		175.119	



Scan number	2817	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	182.46

precursor information

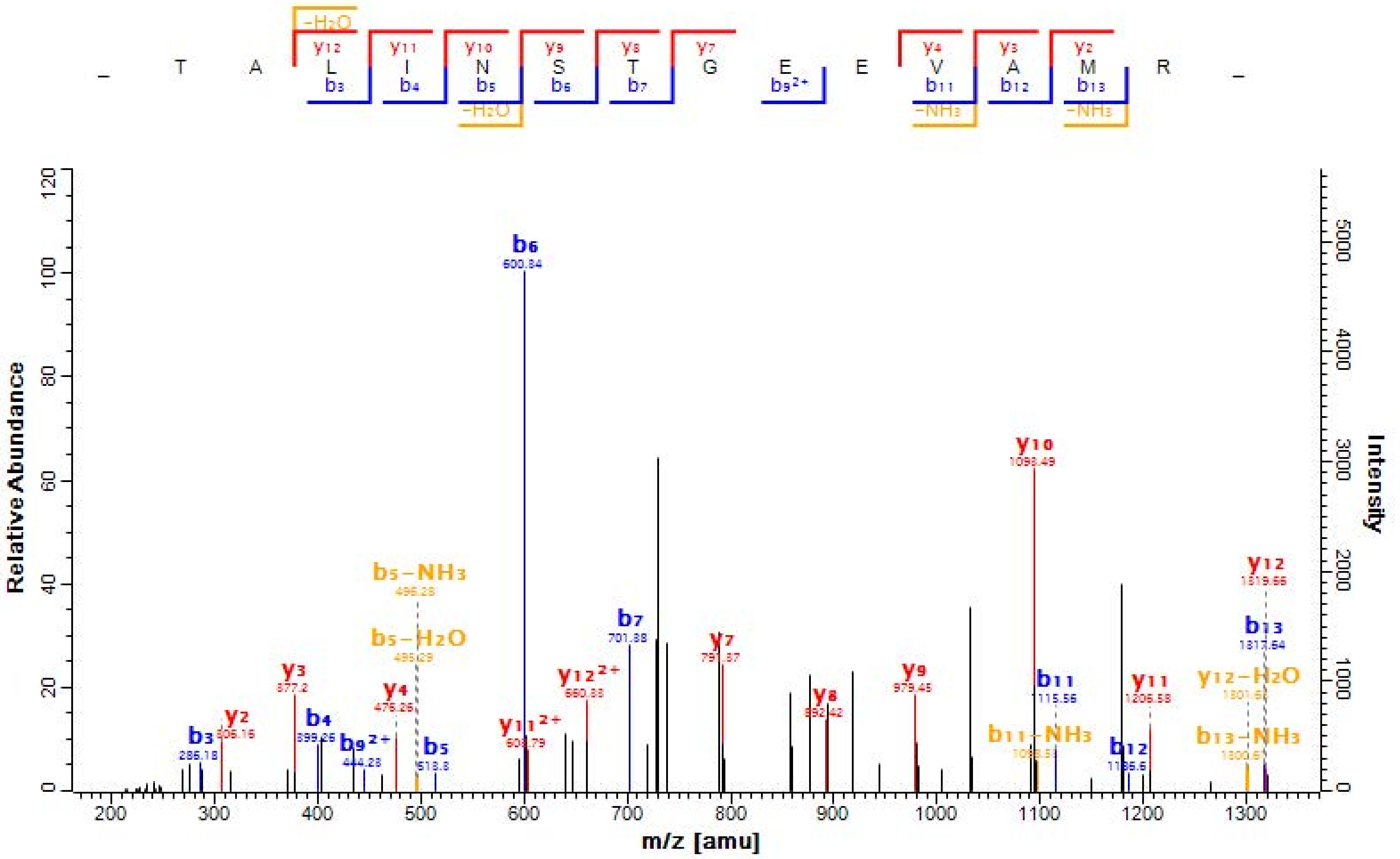
Mass:	1166.56414
m/z:	584.28935
Charge:	2+
Retentiontime:	19.71848487854
Score:	182.4607
Mass Error [ppm]:	-0.016379
PEP:	1.1351E-06
Precursor Type:	MULTI

g

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	64 %
Peak Coverage:	32 %
Protein Localisation:	101 ... 110

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08		148.08	1	F	9				
+0.0456	177.1	-0.025	205.1	2	G	8	1020.5	-0.005	510.76	-0.38
	306.14	-0.016	334.14	3	E	7	963.48	+0.0474	963.48	
	405.21	-0.006	433.21	4	V	6	834.44	-0.003	834.44	
	504.28	-0.03	532.28	5	V	5	735.37	+0.0265	368.19	+0.0134
	619.31	-0.054	647.3	6	D	4	636.3	-0.008	636.3	
	779.34	+0.1451	807.33	7	C	3	521.28	+0.0799	521.28	
	880.39		908.38	8	T	2	361.24	+0.0921	361.24	
	993.47	-0.062	1021.5	9	L	1	260.2		260.2	
				10	K	0	147.11		147.11	

Scan number	3318	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	135.02



precursor information

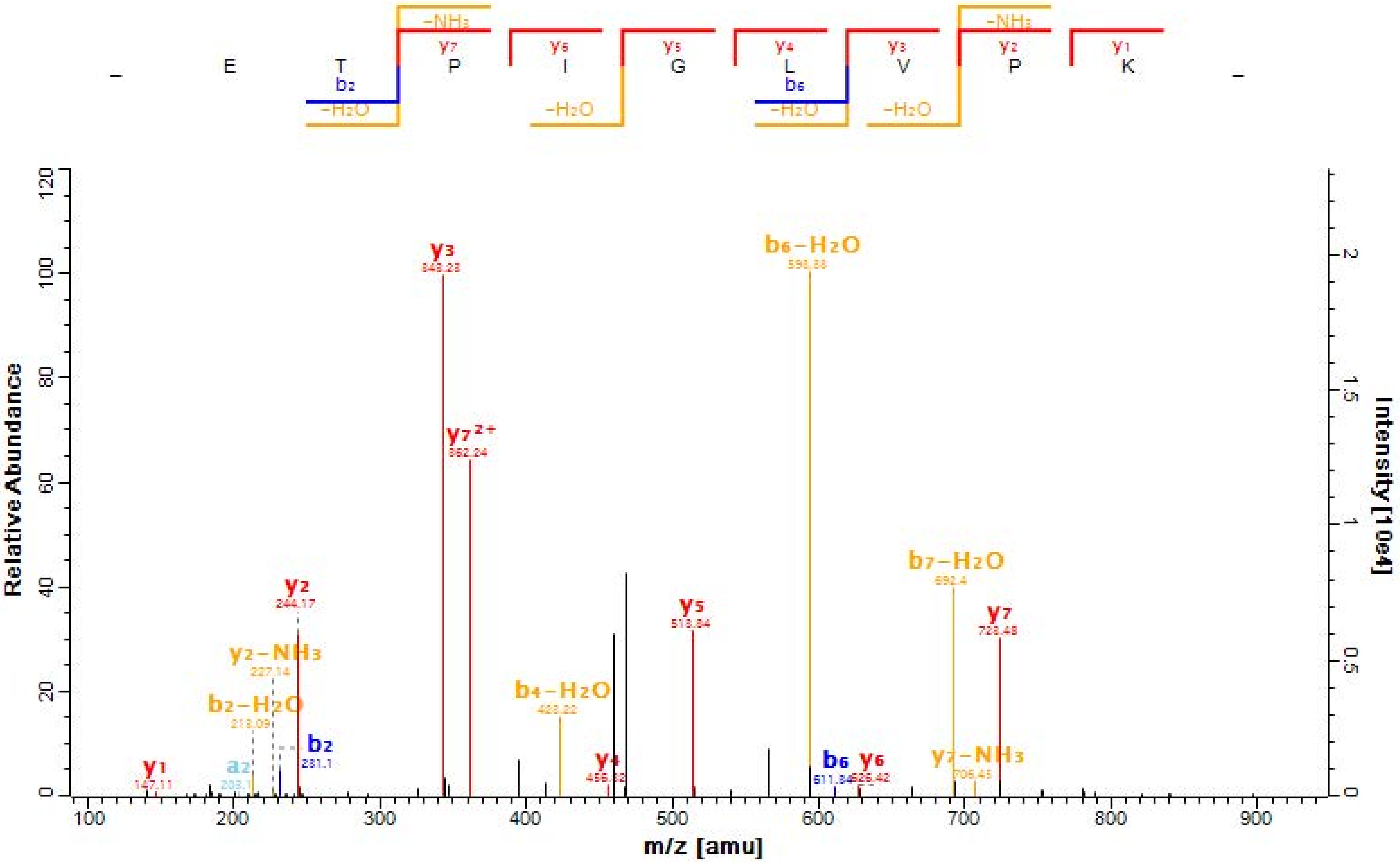
Mass:	1476.6871
m/z:	739.35083
Charge:	2+
Retentiontime:	22.122484207153
Score:	135.0247
Mass Error [ppm]:	0.62713
PEP:	8.5526E-27
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	42 %
Peak Coverage:	30 %
Protein Localisation:	528 ... 541

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	13				
	173.09		173.09	2	A	12	1390.7		1390.7	
	286.18	-0.008	286.18	3	L	11	1319.7	-0.247	660.33	-0.014
	399.26	+0.0765	399.26	4	I	10	1206.6	-0.038	603.79	+0.0852
	513.3	+0.0367	513.3	5	N	9	1093.5	+0.0206	1093.5	
	600.34	+0.0375	600.34	6	S	8	979.45	-0.017	979.45	
	701.38	+0.0844	701.38	7	T	7	892.42	+0.0139	892.42	
	758.4		758.4	8	G	6	791.37	+0.0132	791.37	
+0.0387	444.23		887.45	9	E	5	734.35		734.35	
	1016.5		1016.5	10	E	4	605.31		605.31	
	1115.6	-0.219	1115.6	11	V	3	476.26	+0.0403	476.26	
	1186.6	-0.023	1186.6	12	A	2	377.2	+0.1034	377.2	
	1317.6	-0.207	1317.6	13	M	1	306.16	-0.04	306.16	
				14	R	0	175.12		175.12	

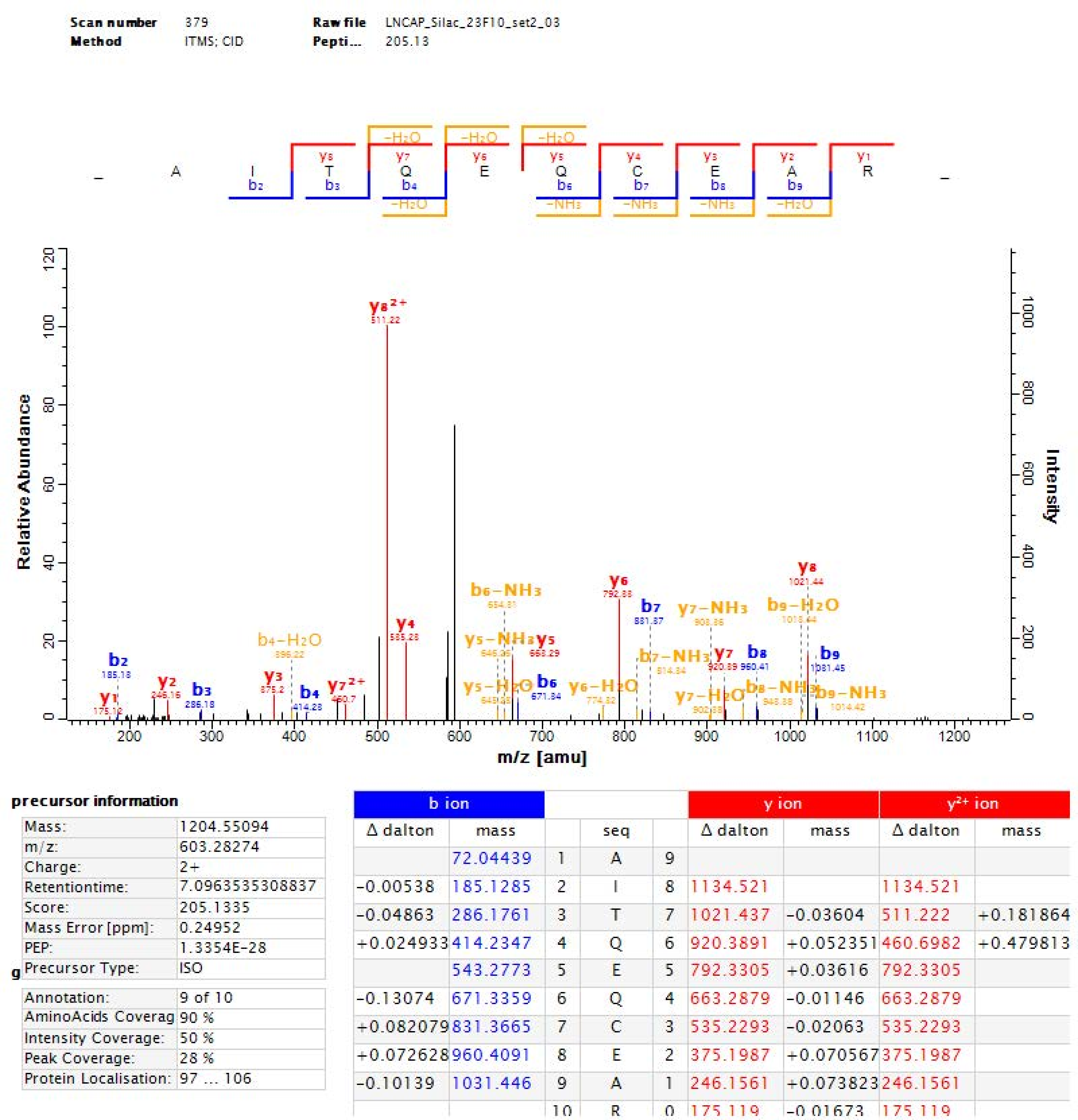
Scan number	3328	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	89.7



precursor information

Mass:	952.55957
m/z:	477.28706
Charge:	2+
Retentiontime:	22.174257278442
Score:	89.69799
Mass Error [ppm]:	0.24588
PEP:	0.0053347
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	76 %
Peak Coverage:	21 %
Protein Localisation:	570 ... 578

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	8				
-0.043	203.1	-0.011	231.1	2	T	7	824.52		824.52	
	300.16		328.15	3	P	6	723.48	-0.007	362.24	+0.054
	413.24		441.23	4	I	5	626.42	+0.0213	626.42	
	470.26		498.26	5	G	4	513.34	+0.0204	513.34	
	583.34	+0.1992	611.34	6	L	3	456.32	+0.0805	456.32	
	682.41		710.41	7	V	2	343.23	+0.0465	343.23	
	779.47		807.46	8	P	1	244.17	-0.013	244.17	
				9	K	0	147.11	+0.0293	147.11	



Scan number 379

Method ITMS; CID

Raw file LNCAP_Silac_23F10_set2_03

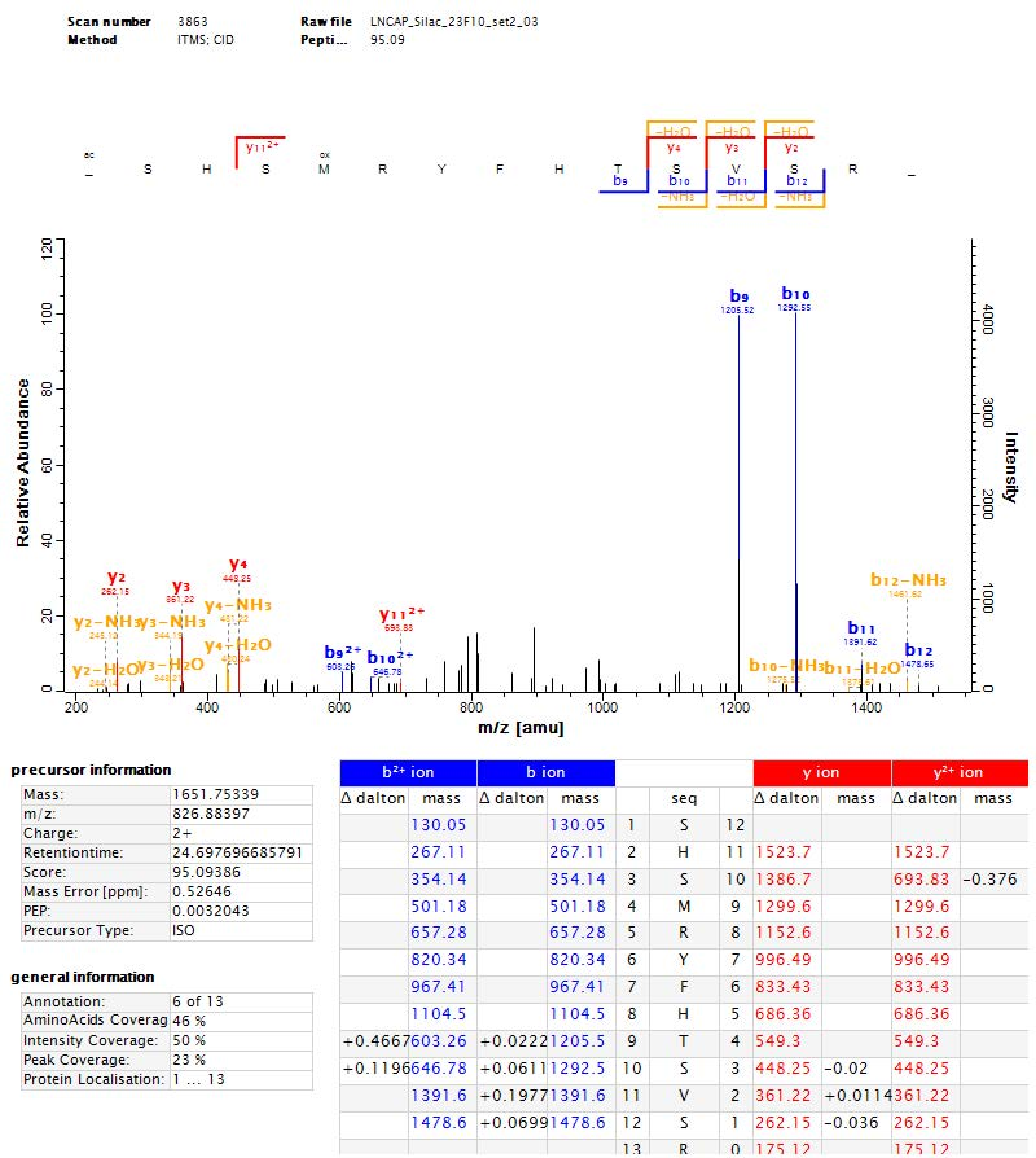
Pepti... 205.13

precursor information

Mass:	1204.55094
m/z:	603.28274
Charge:	2+
Retentiontime:	7.0963535308837
Score:	205.1335
Mass Error [ppm]:	0.24952
PEP:	1.3354E-28
Precursor Type:	ISO

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	50 %
Peak Coverage:	28 %
Protein Localisation:	97 ... 106

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	9				
-0.00538	185.1285	2	I	8	1134.521		1134.521	
-0.04863	286.1761	3	T	7	1021.437	-0.03604	511.222	+0.181864
+0.024933	414.2347	4	Q	6	920.3891	+0.052351	460.6982	+0.479813
	543.2773	5	E	5	792.3305	+0.03616	792.3305	
-0.13074	671.3359	6	Q	4	663.2879	-0.01146	663.2879	
+0.082079	831.3665	7	C	3	535.2293	-0.02063	535.2293	
+0.072628	960.4091	8	E	2	375.1987	+0.070567	375.1987	
-0.10139	1031.446	9	A	1	246.1561	+0.073823	246.1561	
		10	R	0	175.119	-0.01673	175.119	



Scan number	3863	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	95.09

precursor information

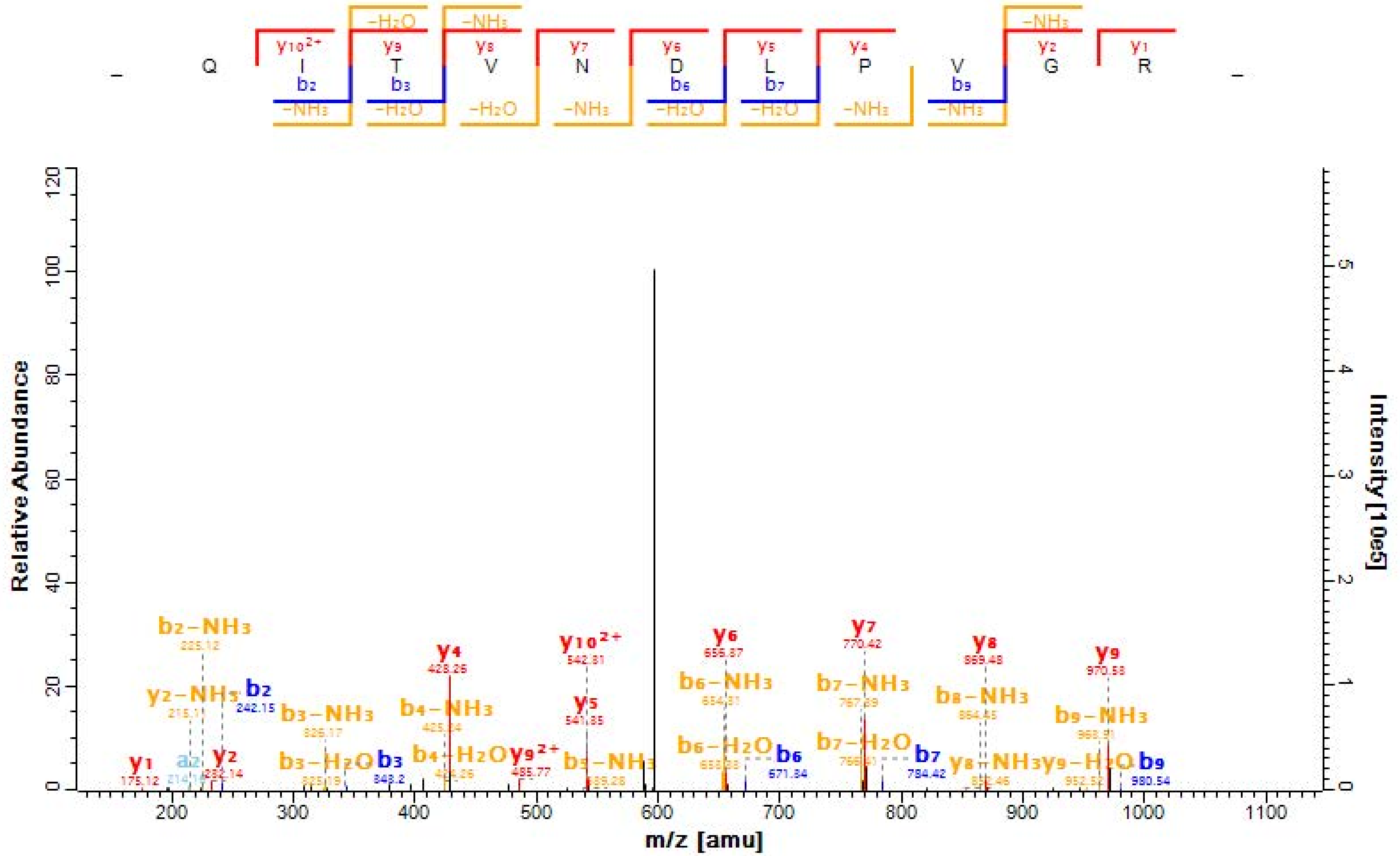
Mass:	1651.75339
m/z:	826.88397
Charge:	2+
Retentiontime:	24.697696685791
Score:	95.09386
Mass Error [ppm]:	0.52646
PEP:	0.0032043
Precursor Type:	ISO

general information

Annotation:	6 of 13
AminoAcids Coverag	46 %
Intensity Coverage:	50 %
Peak Coverage:	23 %
Protein Localisation:	1 ... 13

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	S	12				
	267.11		267.11	2	H	11	1523.7		1523.7	
	354.14		354.14	3	S	10	1386.7		693.83	-0.376
	501.18		501.18	4	M	9	1299.6		1299.6	
	657.28		657.28	5	R	8	1152.6		1152.6	
	820.34		820.34	6	Y	7	996.49		996.49	
	967.41		967.41	7	F	6	833.43		833.43	
	1104.5		1104.5	8	H	5	686.36		686.36	
+0.4667	603.26	+0.0222	1205.5	9	T	4	549.3		549.3	
+0.1196	646.78	+0.0611	1292.5	10	S	3	448.25	-0.02	448.25	
	1391.6	+0.1977	1391.6	11	V	2	361.22	+0.0114	361.22	
	1478.6	+0.0699	1478.6	12	S	1	262.15	-0.036	262.15	
				13	R	0	175.12		175.12	

Scan number	3928	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	180.19



precursor information

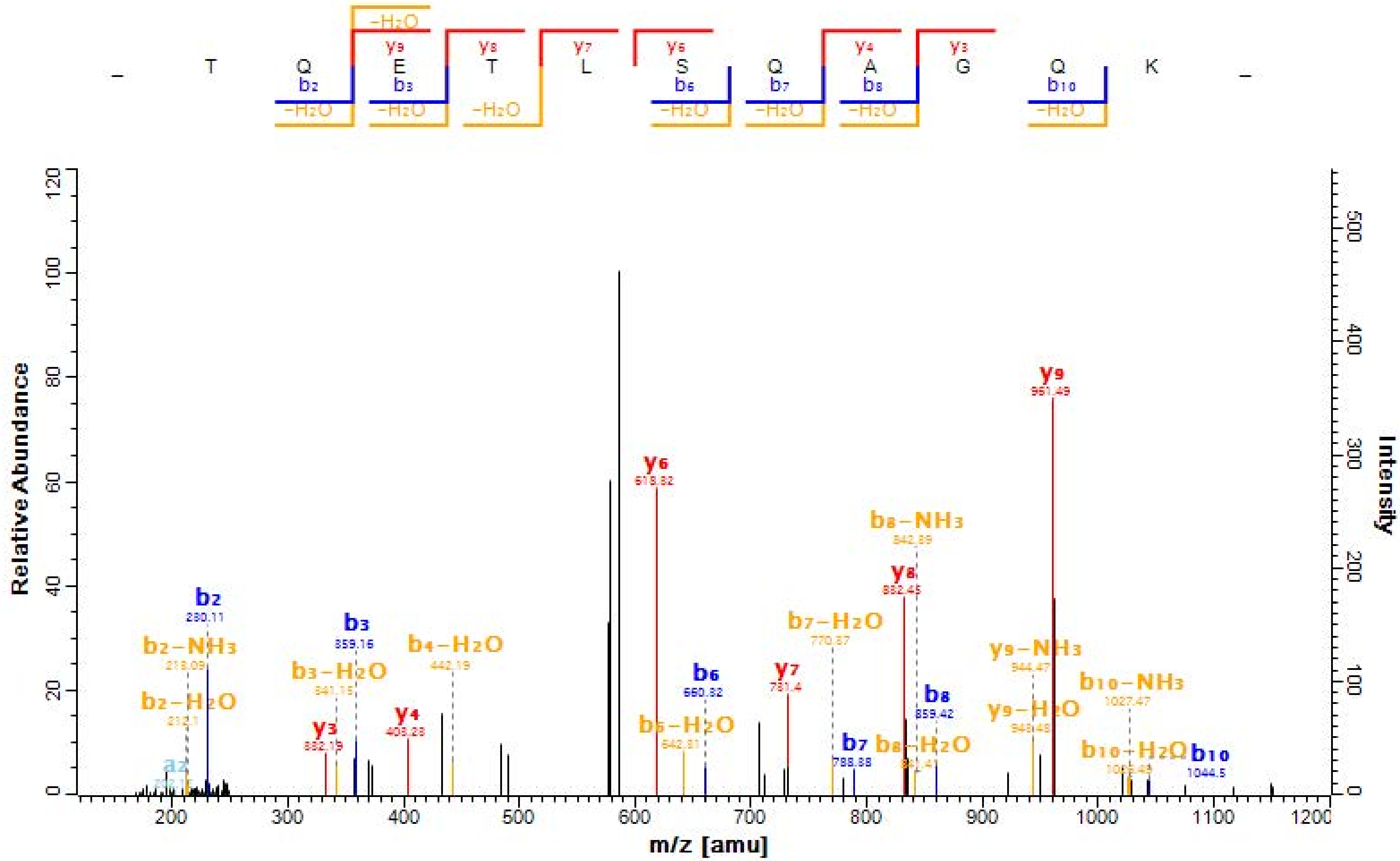
Mass:	1210.66675
m/z:	606.34065
Charge:	2+
Retentiontime:	25.000156402587
Score:	180.1916
Mass Error [ppm]:	-0.19086
PEP:	1.744E-08
Precursor Type:	MULTI

general information

Annotation:	10 of 11
AminoAcids Coverag	91 %
Intensity Coverage:	43 %
Peak Coverage:	44 %
Protein Localisation:	141 ... 151

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	101.07		129.07	1	Q	10				
+0.0608	214.16	+0.0757	242.15	2	I	9	1083.6		542.31	+0.0495
	315.2	+0.1136	343.2	3	T	8	970.53	-0.04	485.77	+0.2371
	414.27		442.27	4	V	7	869.48	+0.0041	869.48	
	528.31		556.31	5	N	6	770.42	+0.0126	770.42	
	643.34	+0.0187	671.34	6	D	5	656.37	+0.0147	656.37	
	756.43	-0.074	784.42	7	L	4	541.35	+0.0241	541.35	
	853.48		881.47	8	P	3	428.26	+0.0347	428.26	
	952.55	-0.085	980.54	9	V	2	331.21		331.21	
	1009.6		1037.6	10	G	1	232.14	-0.013	232.14	
				11	R	0	175.12	+0.0103	175.12	

Scan number	404	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	132.17



precursor information

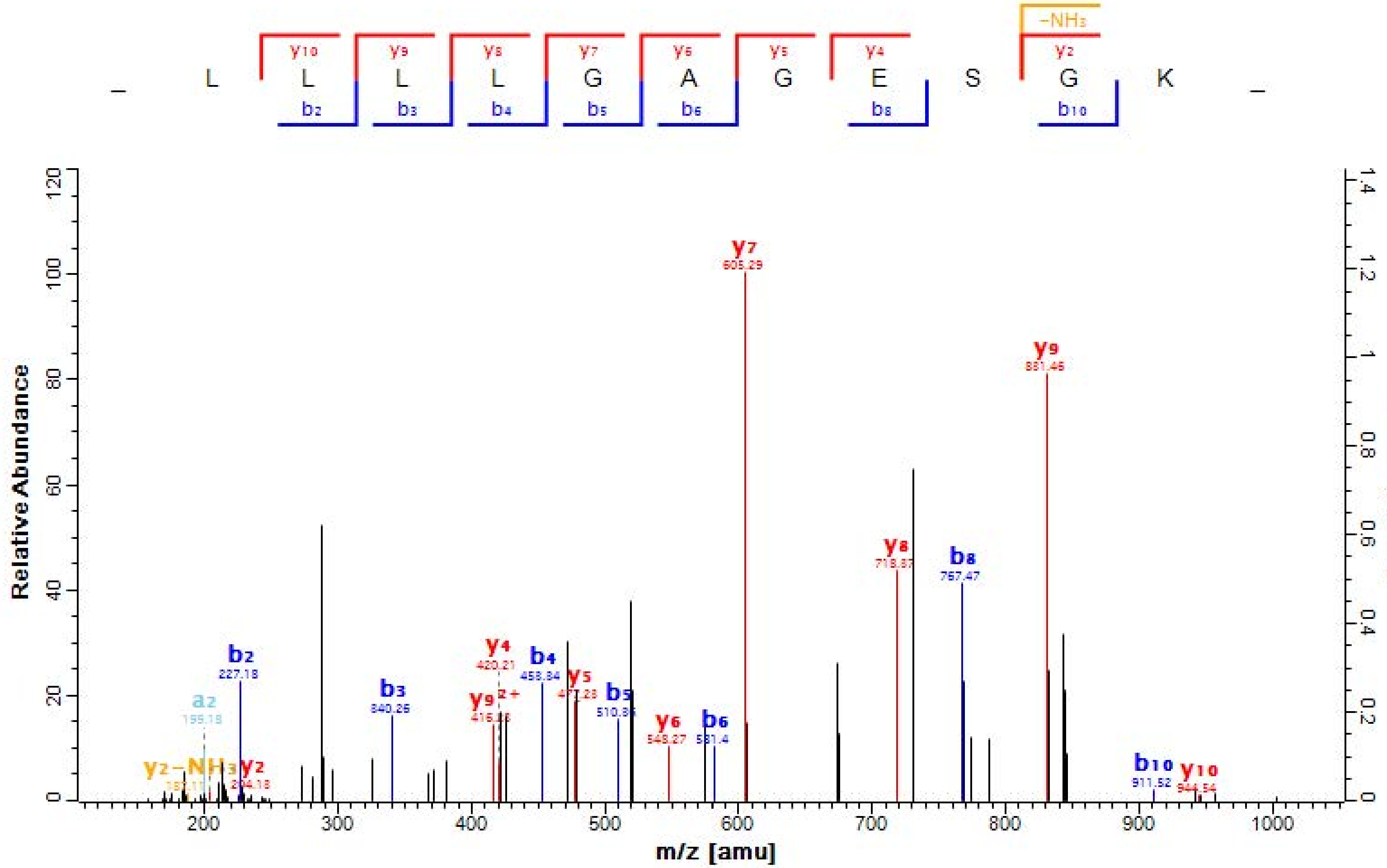
Mass:	1189.59372
m/z:	595.80413
Charge:	2+
Retentiontime:	7.2942566871643
Score:	132.1712
Mass Error [ppm]:	-0.13857
PEP:	0.00018428
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	40 %
Peak Coverage:	24 %
Protein Localisation:	109 ... 119

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	74.06004		102.055	1	T	10		
−0.08978	202.1186	−0.05332	230.1135	2	Q	9	1089.553	
	331.1612	+0.008975	359.1561	3	E	8	961.4949	−0.00998
	432.2089		460.2038	4	T	7	832.4523	−0.04026
	545.293		573.2879	5	L	6	731.4046	+0.04758
	632.325	+0.083363	660.3199	6	S	5	618.3206	−0.01392
	760.3836	+0.00916	788.3785	7	Q	4	531.2885	
	831.4207	−0.0166	859.4156	8	A	3	403.23	+0.080405
	888.4421		916.4371	9	G	2	332.1928	+0.052455
	1016.501	−0.0779	1044.496	10	Q	1	275.1714	
				11	K	0	147.1128	

Scan number	4382	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	81.52



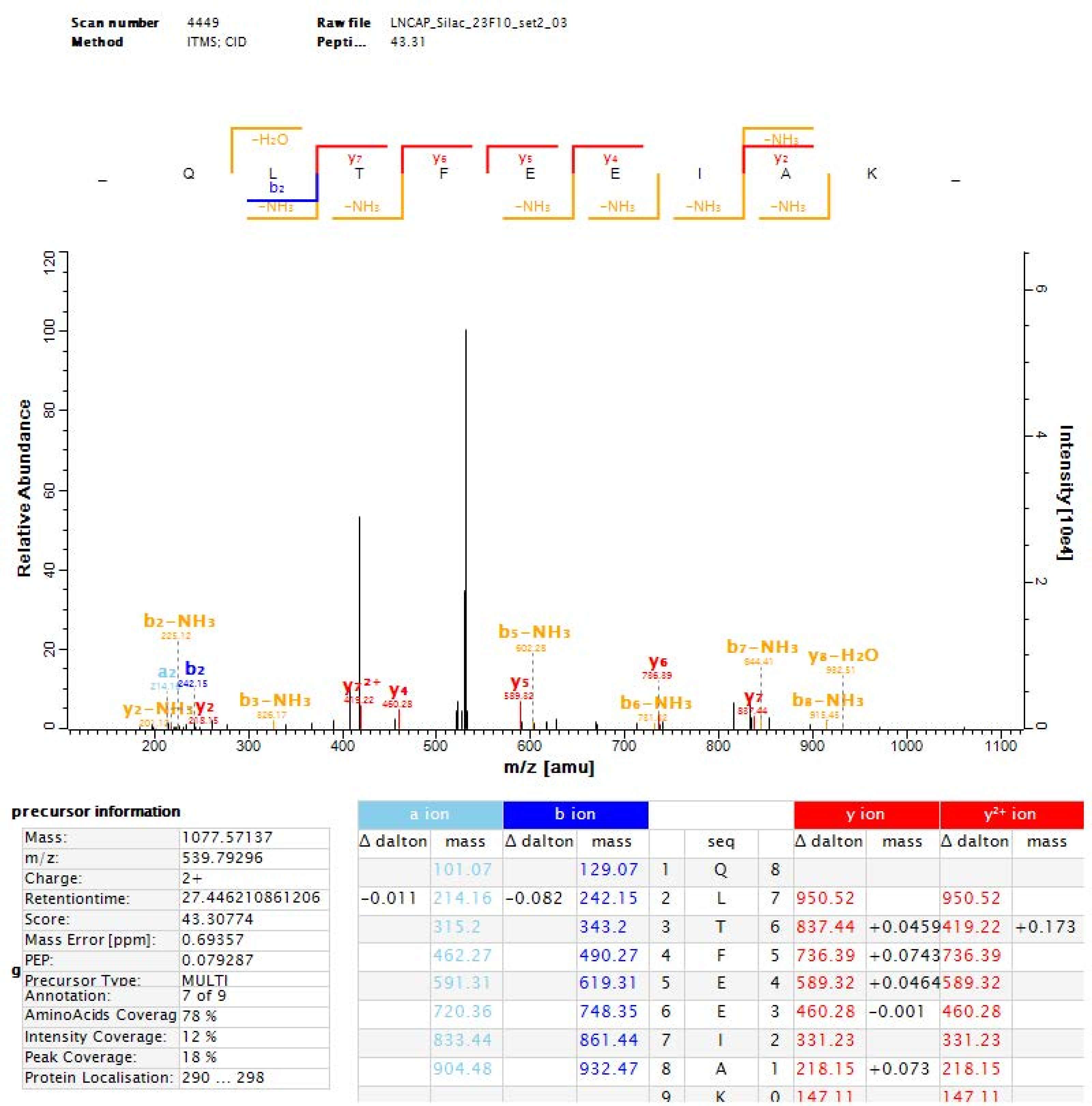
precursor information

Mass:	1056.61777
m/z:	529.31616
Charge:	2+
Retentiontime:	27.134902954101
Score:	81.52473
Mass Error [ppm]:	-0.13594
PEP:	0.0033009
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	42 %
Peak Coverage:	20 %
Protein Localisation:	686 ... 696

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	10				
-0.025	199.18	-0.073	227.18	2	L	9	944.54	-0.096	944.54	
	312.26	+0.0533	340.26	3	L	8	831.46	-0.003	416.23	+0.1134
	425.35	-0.207	453.34	4	L	7	718.37	+0.079	718.37	
	482.37	+0.0945	510.36	5	G	6	605.29	-0.026	605.29	
	553.41	+0.104	581.4	6	A	5	548.27	+0.1108	548.27	
	610.43		638.42	7	G	4	477.23	-0.025	477.23	
	739.47	+0.0239	767.47	8	E	3	420.21	+0.1879	420.21	
	826.5		854.5	9	S	2	291.17		291.17	
	883.52	+0.034	911.52	10	G	1	204.13	+0.1276	204.13	
				11	K	0	147.11		147.11	



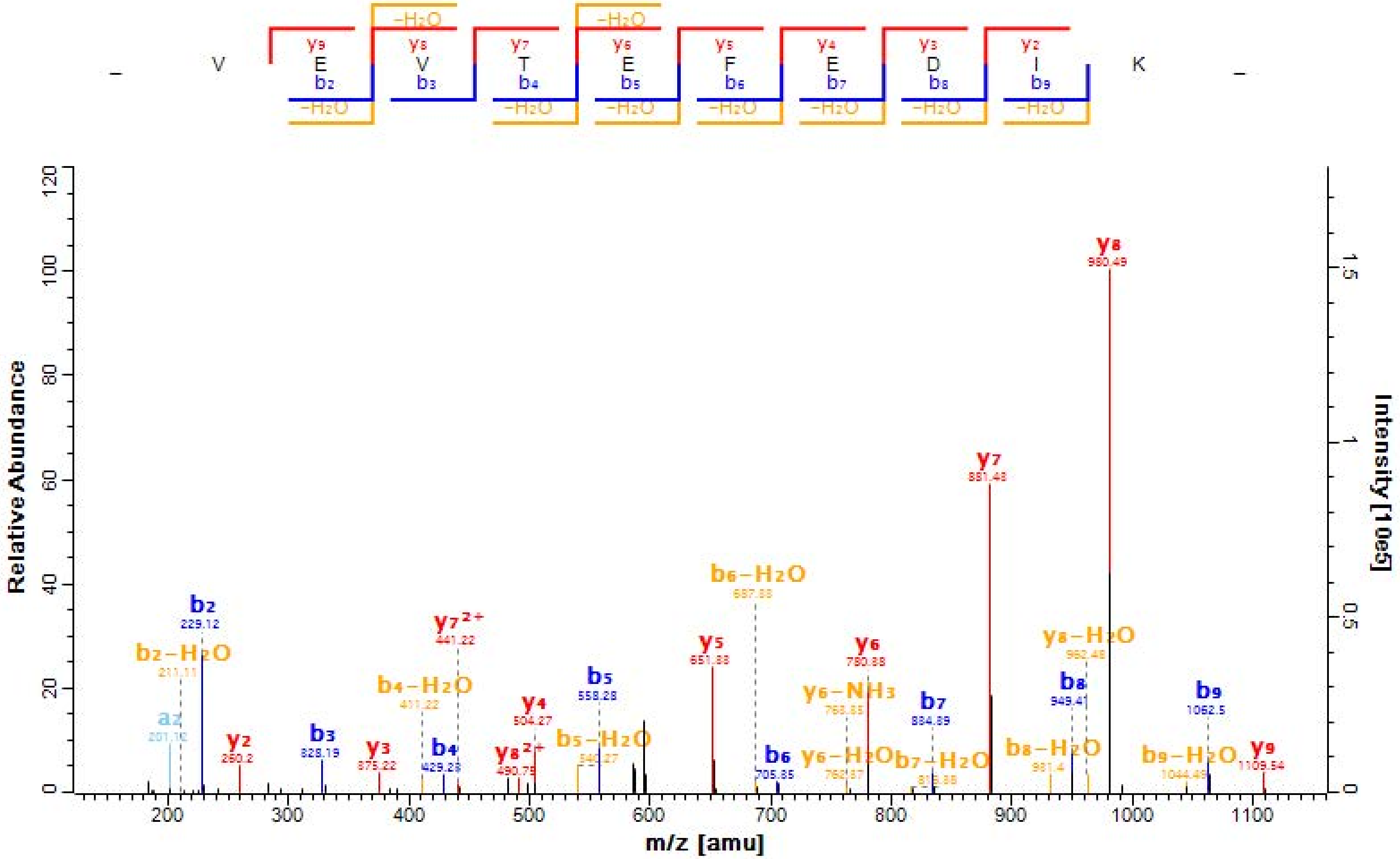
Scan number	4449	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	43.31

precursor information

Mass:	1077.57137
m/z:	539.79296
Charge:	2+
Retentiontime:	27.446210861206
Score:	43.30774
Mass Error [ppm]:	0.69357
PEP:	0.079287
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	12 %
Peak Coverage:	18 %
Protein Localisation:	290 ... 298

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	101.07		129.07	1	Q	8				
-0.011	214.16	-0.082	242.15	2	L	7	950.52		950.52	
	315.2		343.2	3	T	6	837.44	+0.0459	419.22	+0.173
	462.27		490.27	4	F	5	736.39	+0.0743	736.39	
	591.31		619.31	5	E	4	589.32	+0.0464	589.32	
	720.36		748.35	6	E	3	460.28	-0.001	460.28	
	833.44		861.44	7	I	2	331.23		331.23	
	904.48		932.47	8	A	1	218.15	+0.073	218.15	
				9	K	0	147.11		147.11	

Scan number	4517	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	219.03



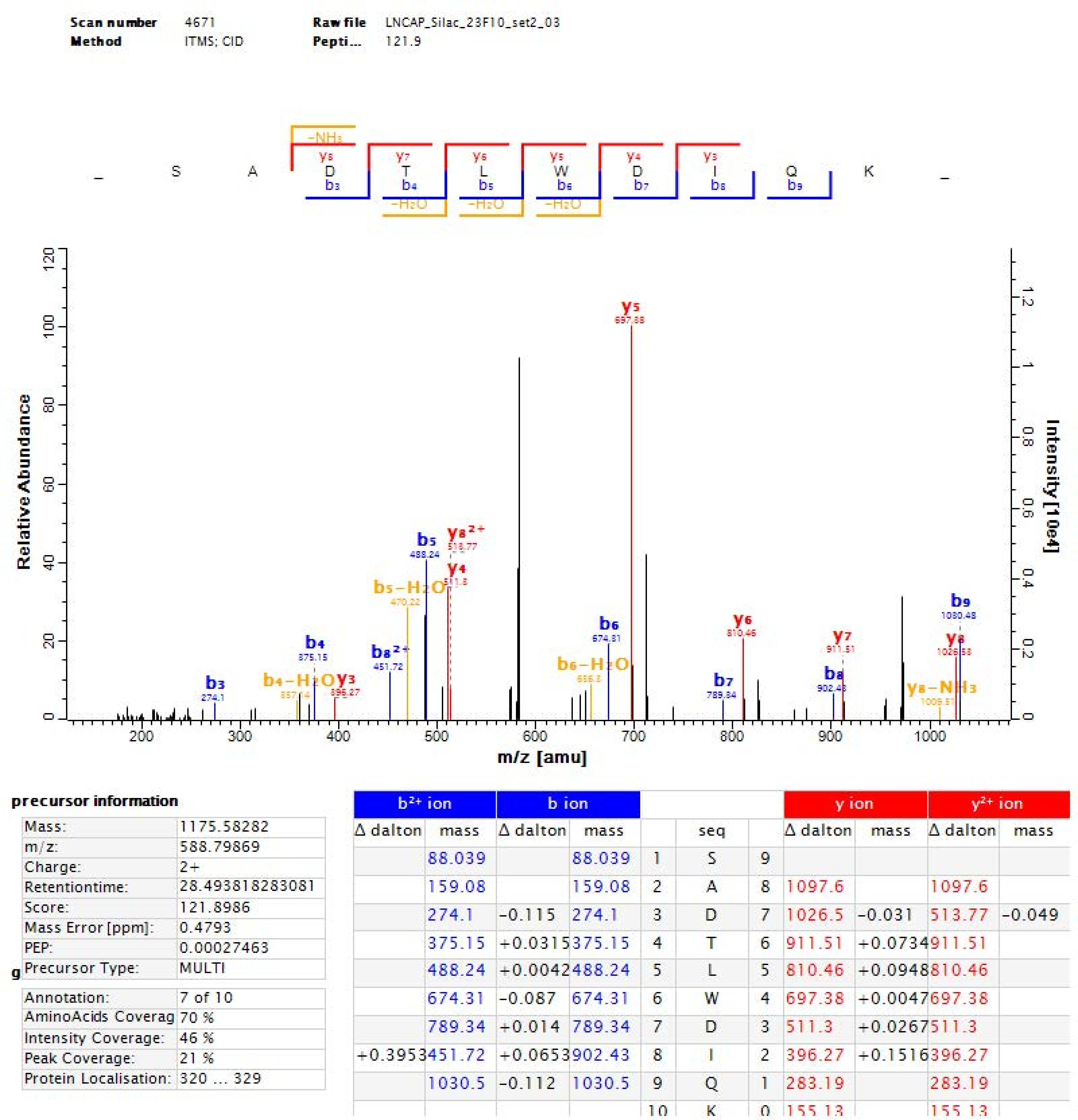
precursor information

Mass:	1207.59699
m/z:	604.80577
Charge:	2+
Retentiontime:	27.768495559692
Score:	219.0326
Mass Error [ppm]:	-0.20174
PEP:	3.4357E-19
Precursor Type:	MULTI

g

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	70 %
Peak Coverage:	35 %
Protein Localisation:	110 ... 119

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.081		100.08	1	V	9				
-0.035	201.12	-0.036	229.12	2	E	8	1109.5	-0.07	1109.5	
	300.19	-0.067	328.19	3	V	7	980.49	-0.004	490.75	+0.2037
	401.24	+0.0673	429.23	4	T	6	881.43	-0.012	441.22	-0.045
	530.28	-0.003	558.28	5	E	5	780.38	+0.0296	780.38	
	677.35	-0.038	705.35	6	F	4	651.33	+0.0097	651.33	
	806.39	-0.037	834.39	7	E	3	504.27	+0.0123	504.27	
	921.42	-0.042	949.41	8	D	2	375.22	+0.0945	375.22	
	1034.5	-0.123	1062.5	9	I	1	260.2	-0.018	260.2	
				10	K	0	147.11		147.11	



Scan number	4671	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	121.9

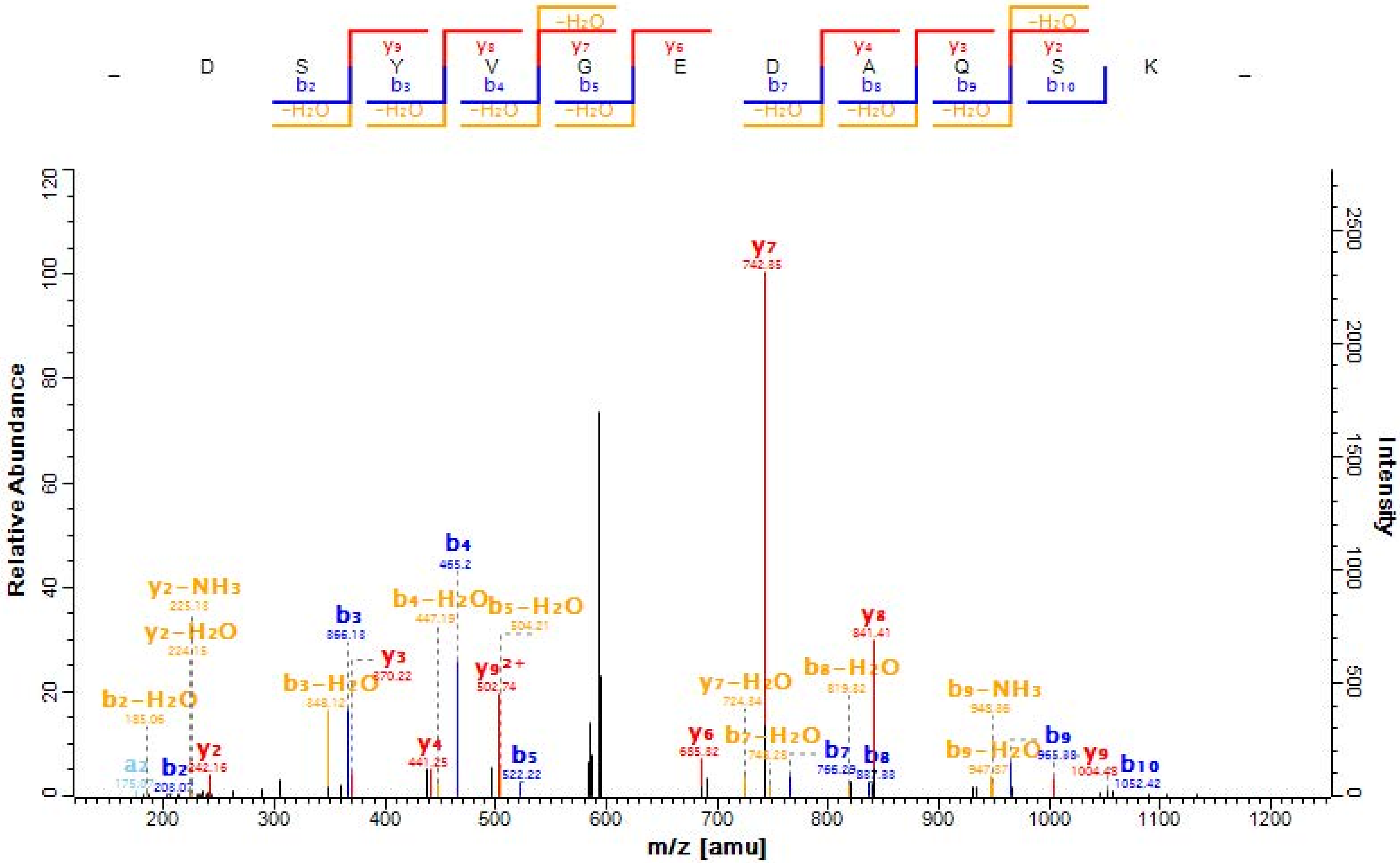
precursor information

Mass:	1175.58282
m/z:	588.79869
Charge:	2+
Retentiontime:	28.493818283081
Score:	121.8986
Mass Error [ppm]:	0.4793
PEP:	0.00027463
Precursor Type:	MULTI

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	46 %
Peak Coverage:	21 %
Protein Localisation:	320 ... 329

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	9				
	159.08		159.08	2	A	8	1097.6		1097.6	
	274.1	-0.115	274.1	3	D	7	1026.5	-0.031	513.77	-0.049
	375.15	+0.0315	375.15	4	T	6	911.51	+0.0734	911.51	
	488.24	+0.0042	488.24	5	L	5	810.46	+0.0948	810.46	
	674.31	-0.087	674.31	6	W	4	697.38	+0.0047	697.38	
	789.34	+0.014	789.34	7	D	3	511.3	+0.0267	511.3	
+0.3953	451.72	+0.0653	902.43	8	I	2	396.27	+0.1516	396.27	
	1030.5	-0.112	1030.5	9	Q	1	283.19		283.19	
				10	K	0	155.13		155.13	

Scan number	482	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	167.18



precursor information

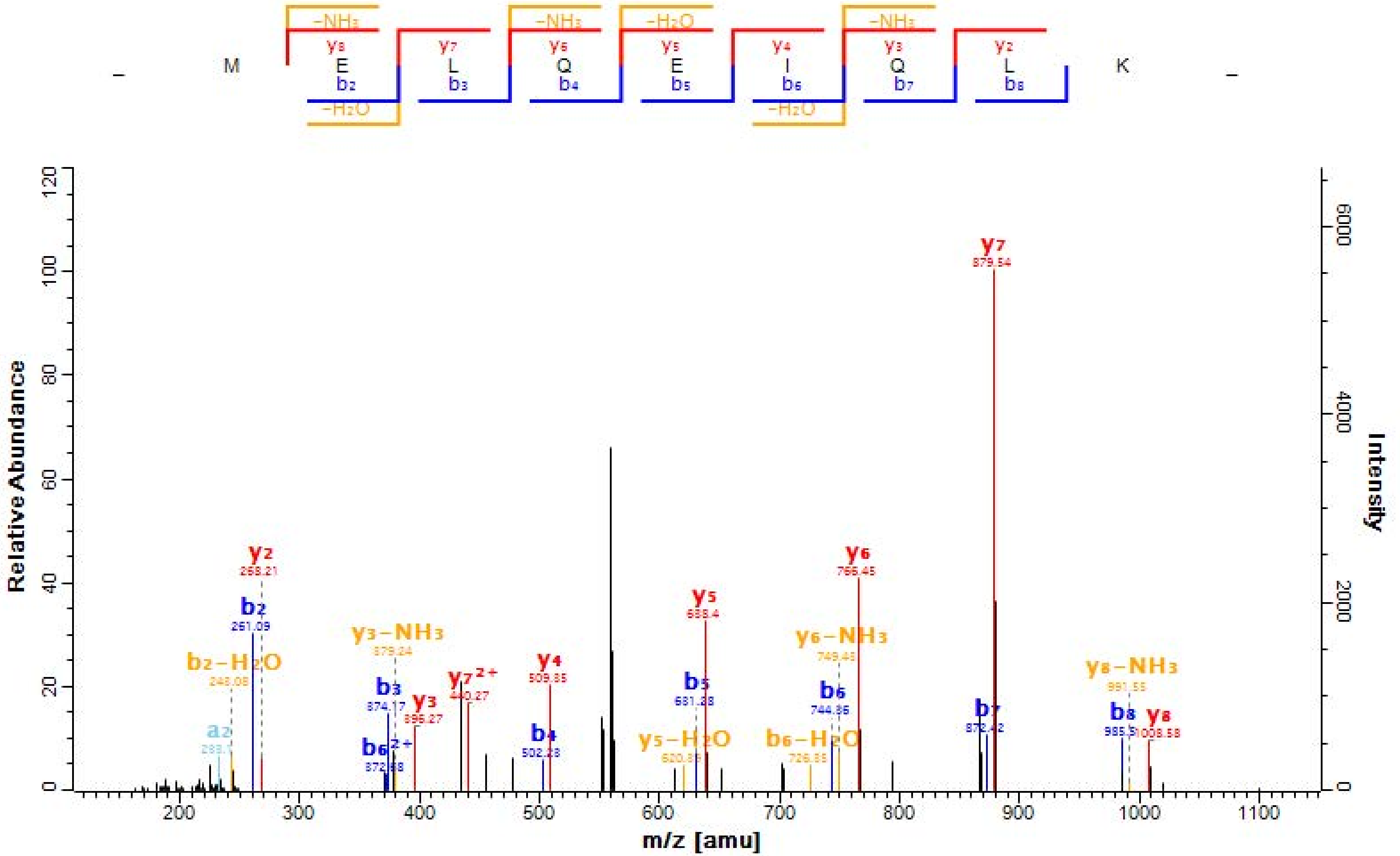
Mass:	1197.51515
m/z:	599.76485
Charge:	2+
Retentiontime:	7.8564882278442
Score:	167.1786
Mass Error [ppm]:	0.15619
PEP:	2.1811E-07
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	58 %
Peak Coverage:	28 %
Protein Localisation:	240 ... 250

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	10				
+0.1686	175.07	-0.155	203.07	2	S	9	1091.5		1091.5	
	338.13	+0.0015	366.13	3	Y	8	1004.5	-0.074	502.74	+0.1591
	437.2	-0.032	465.2	4	V	7	841.41	+0.0294	841.41	
	494.22	+0.0074	522.22	5	G	6	742.35	+0.0104	742.35	
	623.27		651.26	6	E	5	685.32	-0.064	685.32	
	738.29	-0.032	766.29	7	D	4	556.28		556.28	
	809.33	+0.1078	837.33	8	A	3	441.25	+0.0099	441.25	
	937.39	-0.133	965.38	9	Q	2	370.22	+0.1315	370.22	
	1024.4	-0.008	1052.4	10	S	1	242.16	+0.0309	242.16	
				11	K	0	155.13		155.13	

Scan number	4886	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	160.53



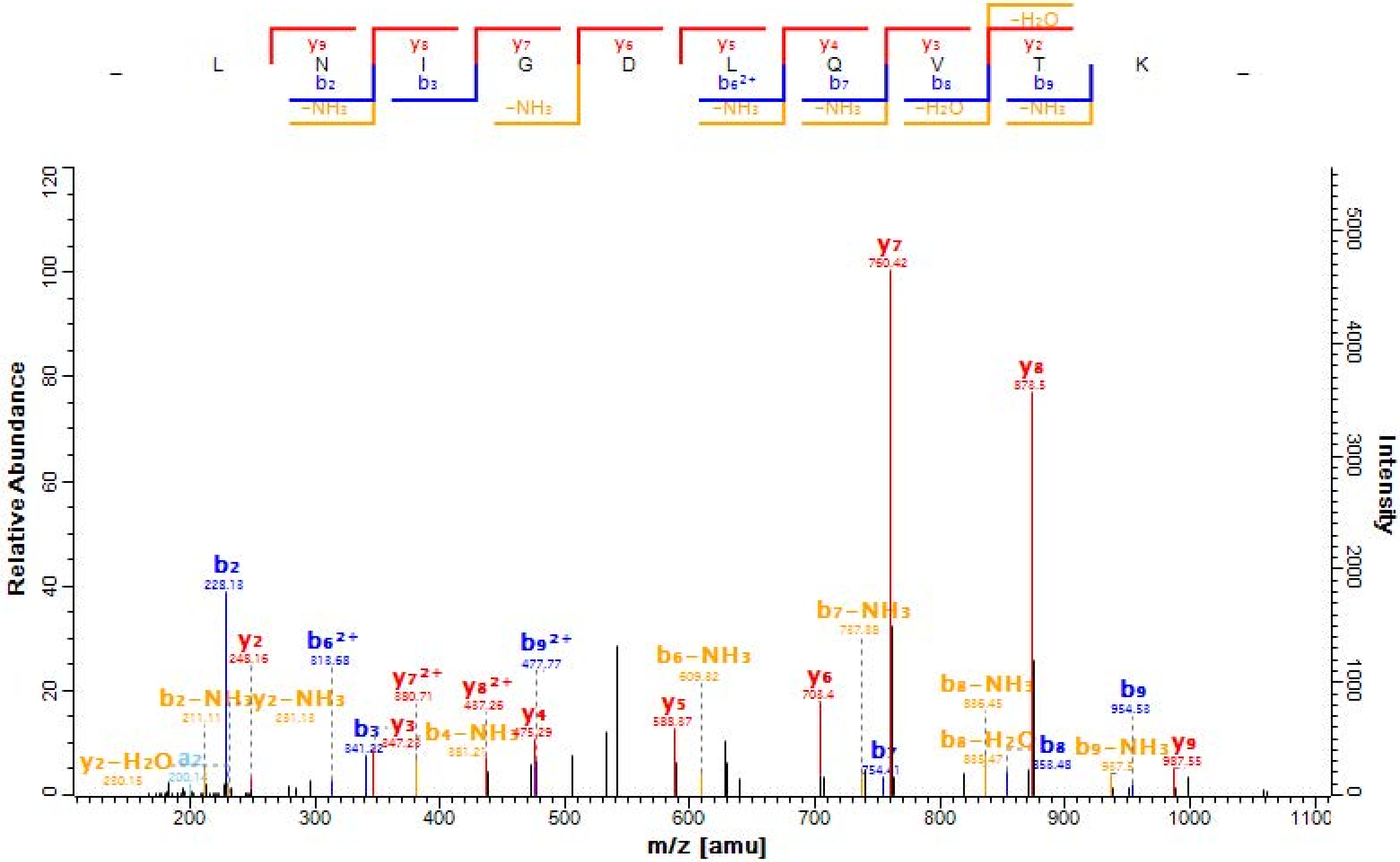
precursor information

g

Mass:	1138.61489
m/z:	570.31472
Charge:	2+
Retentiontime:	29.493478775024
Score:	160.5311
Mass Error [ppm]:	0.12851
PEP:	2.1299E-15
Precursor Type:	ISO
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	52 %
Peak Coverage:	25 %
Protein Localisation:	105 ... 113

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	104.1		132		132	1	M	8				
+0.083	233.1		261.1	-0.03	261.1	2	E	7	1009	-0.01	1009	
	346.2		374.2	+0.029	374.2	3	L	6	879.5	-0.02	440.3	+0.08
	474.2		502.2	-0.02	502.2	4	Q	5	766.5	+0.047	766.5	
	603.3		631.3	+0.038	631.3	5	E	4	638.4	+0.005	638.4	
	716.4	-0.18	372.7	-0.18	744.4	6	I	3	509.4	+0.132	509.4	
	844.4		872.4	-0.05	872.4	7	Q	2	396.3	+0.094	396.3	
	957.5		985.5	-0.02	985.5	8	L	1	268.2	+0.085	268.2	
						9	K	0	155.1		155.1	

Scan number 5026 **Raw file** LNCAP_Silac_23F10_set2_03
Method ITMS; CID **Pepti...** 136.5

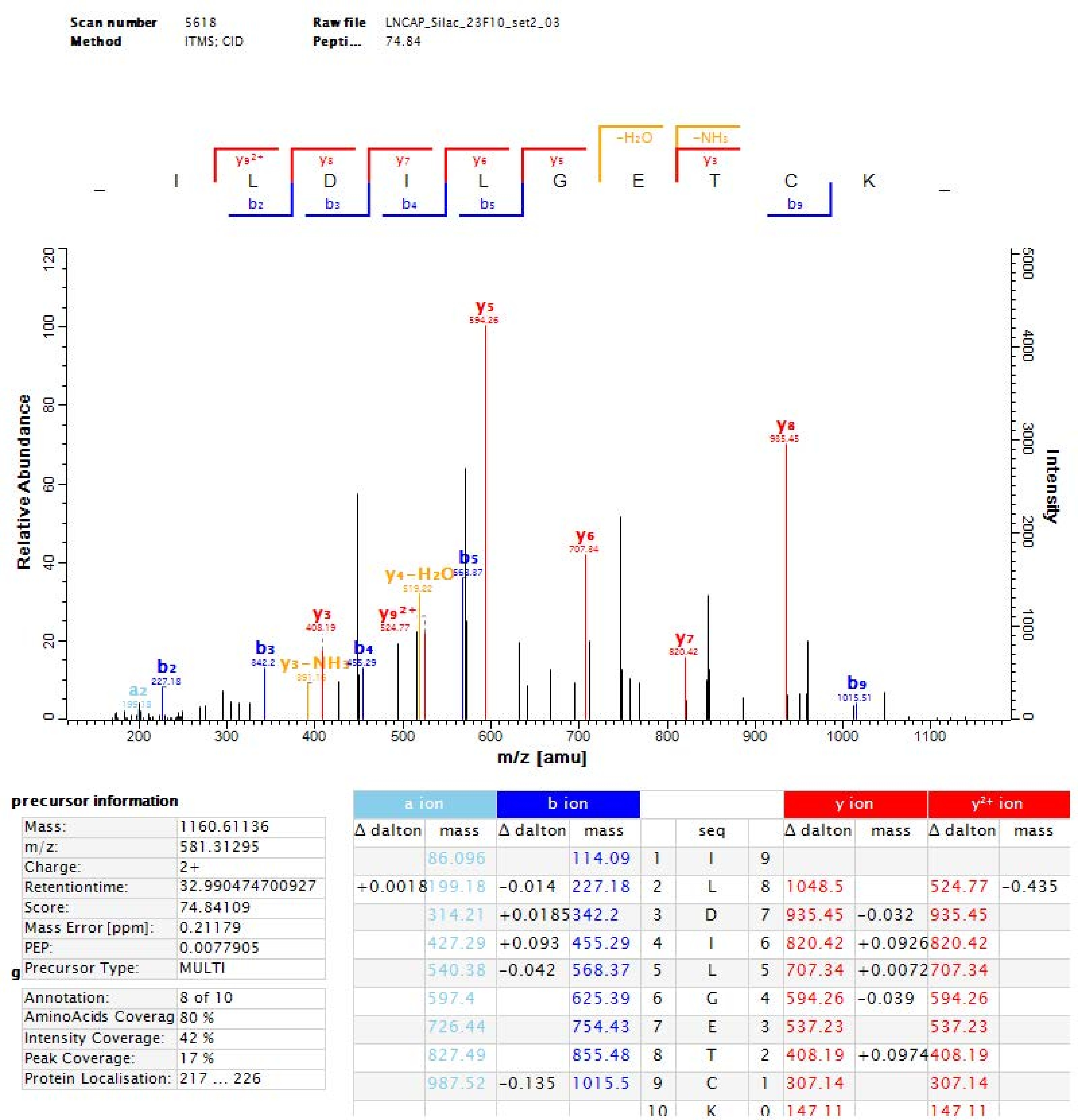


precursor information

Mass:	1099.62345
m/z:	550.819
Charge:	2+
Retentiontime:	30.168365478515
Score:	136.5002
Mass Error [ppm]:	-0.25326
PEP:	0.00021993
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	59 %
Peak Coverage:	28 %
Protein Localisation:	123 ... 132

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	9				
+0.116	200.1		228.1	-0.07	228.1	2	N	8	987.5	+0.051	987.5	
	313.2		341.2	+0.072	341.2	3	I	7	873.5	-0.03	437.3	-0.09
	370.2		398.2		398.2	4	G	6	760.4	+0	380.7	-0.43
	485.3		513.3		513.3	5	D	5	703.4	+0.041	703.4	
	598.4	-0.45	313.7		626.4	6	L	4	588.4	+0.017	588.4	
	726.4		754.4	-0.06	754.4	7	Q	3	475.3	+0.08	475.3	
	825.5		853.5	+0.019	853.5	8	V	2	347.2	-0.07	347.2	
	926.5	-0.39	477.8	-0.13	954.5	9	T	1	248.2	+0.092	248.2	
						10	K	0	147.1		147.1	



Scan number	5618	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	74.84

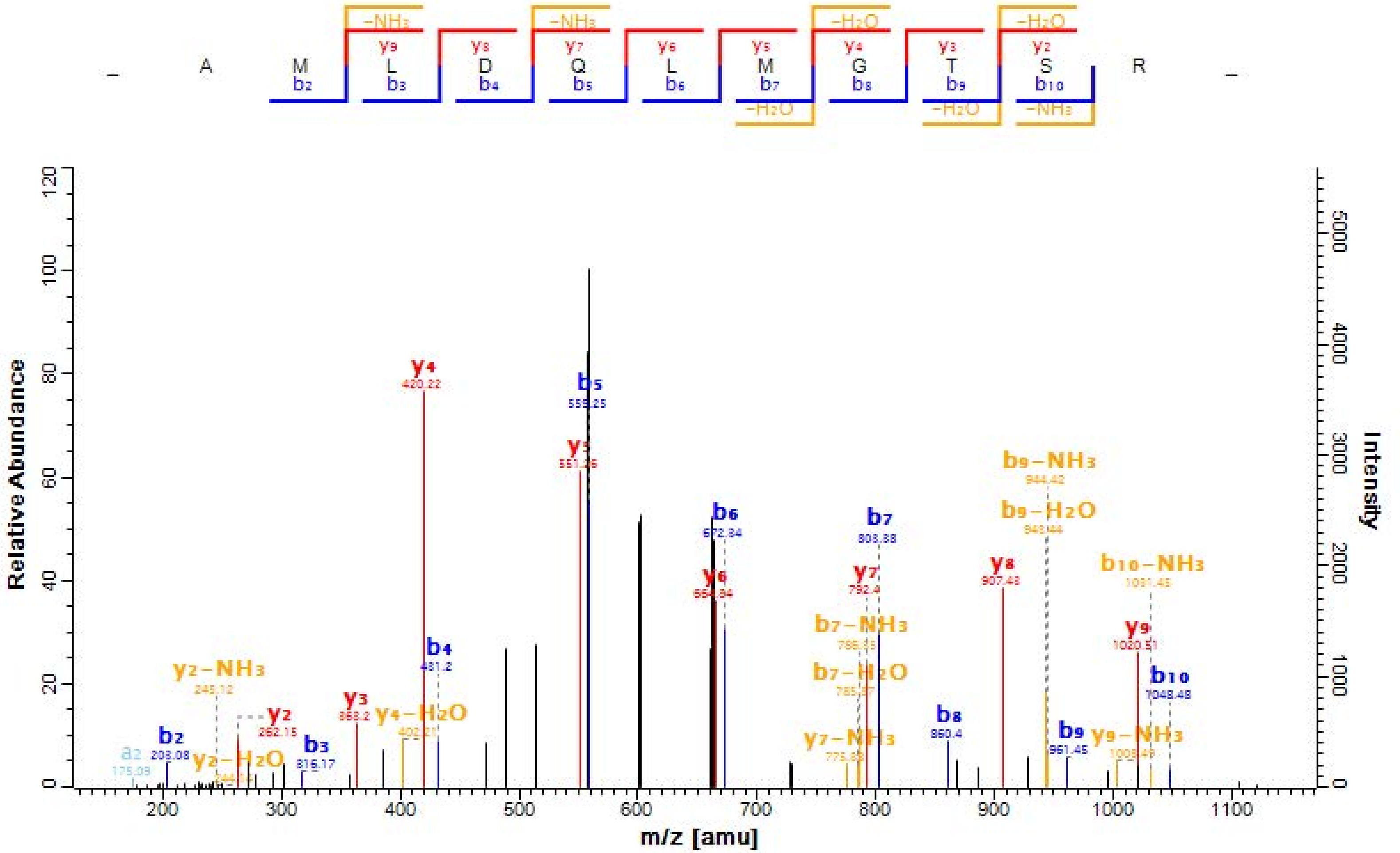
precursor information

Mass:	1160.61136
m/z:	581.31295
Charge:	2+
Retentiontime:	32.990474700927
Score:	74.84109
Mass Error [ppm]:	0.21179
PEP:	0.0077905
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	42 %
Peak Coverage:	17 %
Protein Localisation:	217 ... 226

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	9				
+0.0018	199.18	-0.014	227.18	2	L	8	1048.5		524.77	-0.435
	314.21	+0.0185	342.2	3	D	7	935.45	-0.032	935.45	
	427.29	+0.093	455.29	4	I	6	820.42	+0.0926	820.42	
	540.38	-0.042	568.37	5	L	5	707.34	+0.0072	707.34	
	597.4		625.39	6	G	4	594.26	-0.039	594.26	
	726.44		754.43	7	E	3	537.23		537.23	
	827.49		855.48	8	T	2	408.19	+0.0974	408.19	
	987.52	-0.135	1015.5	9	C	1	307.14		307.14	
				10	K	0	147.11		147.11	

Scan number 5658 **Raw file** LNCAP_Silac_23F10_set2_03
Method ITMS; CID **Pepti...** 165.58



precursor information

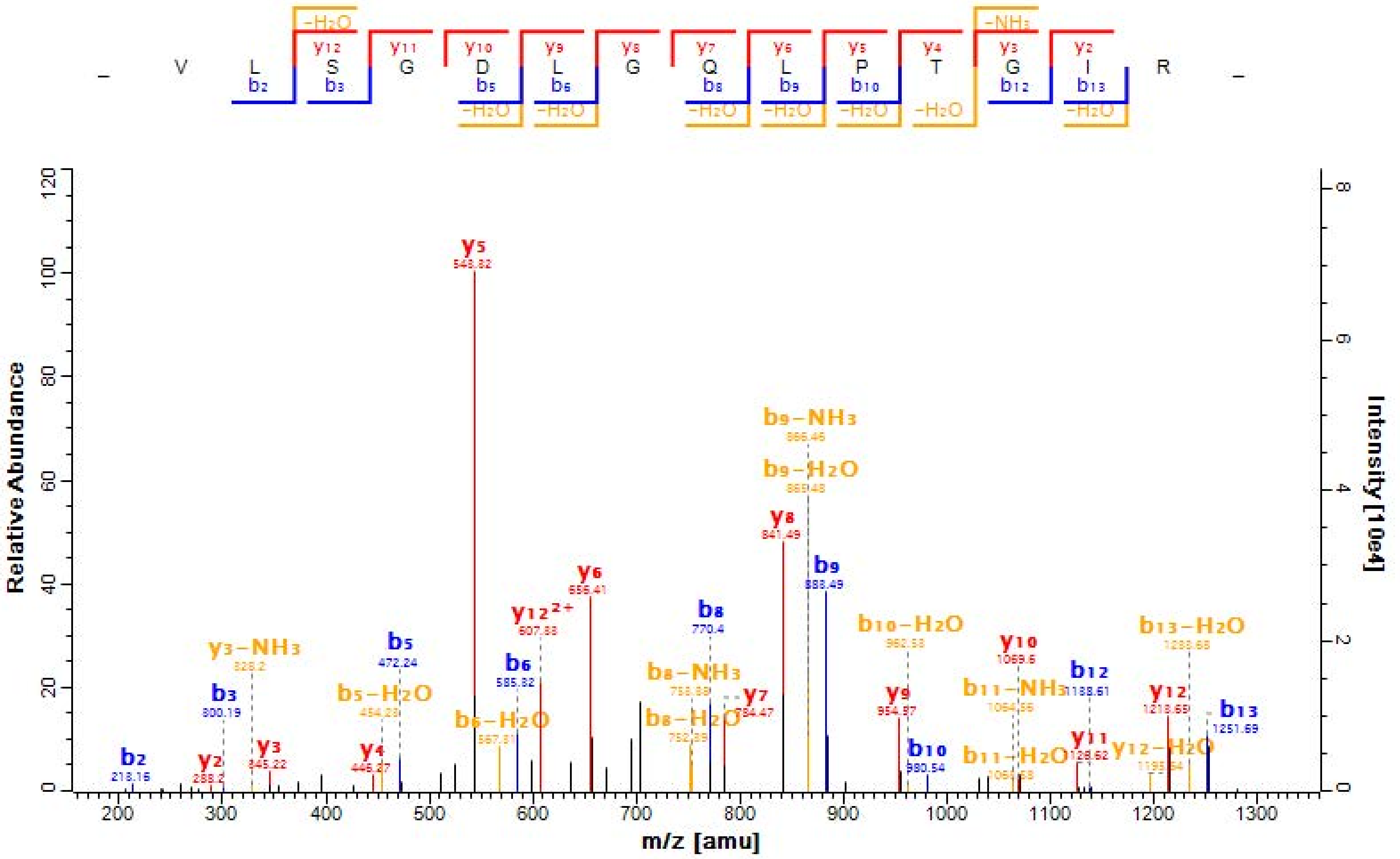
Mass:	1221.58484
m/z:	611.7997
Charge:	2+
Retentiontime:	33.177593231201
Score:	165.5837
Mass Error [ppm]:	0.2183
PEP:	5.9201E-07
Precursor Type:	MULTI

general information

Annotation:	10 of 11
AminoAcids Coverag	91 %
Intensity Coverage:	48 %
Peak Coverage:	38 %
Protein Localisation:	9 ... 19

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	44.04948		72.04439	1	A	10		
-0.06367	175.09	-0.10639	203.0849	2	M	9	1151.555	
	288.174	+0.028113	316.1689	3	L	8	1020.514	-0.04038
	403.201	-0.02529	431.1959	4	D	7	907.4302	+0.006881
	531.2595	+0.069393	559.2545	5	Q	6	792.4032	+0.061168
	644.3436	+0.055642	672.3385	6	L	5	664.3447	+0.085077
	775.3841	-0.0366	803.379	7	M	4	551.2606	+0.028638
	832.4056	+0.018168	860.4005	8	G	3	420.2201	+0.03946
	933.4532	+0.102387	961.4482	9	T	2	363.1987	+0.083018
	1020.485	-0.08736	1048.48	10	S	1	262.151	+0.071889
				11	R	0	175.119	

Scan number	5944	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	180.11



precursor information

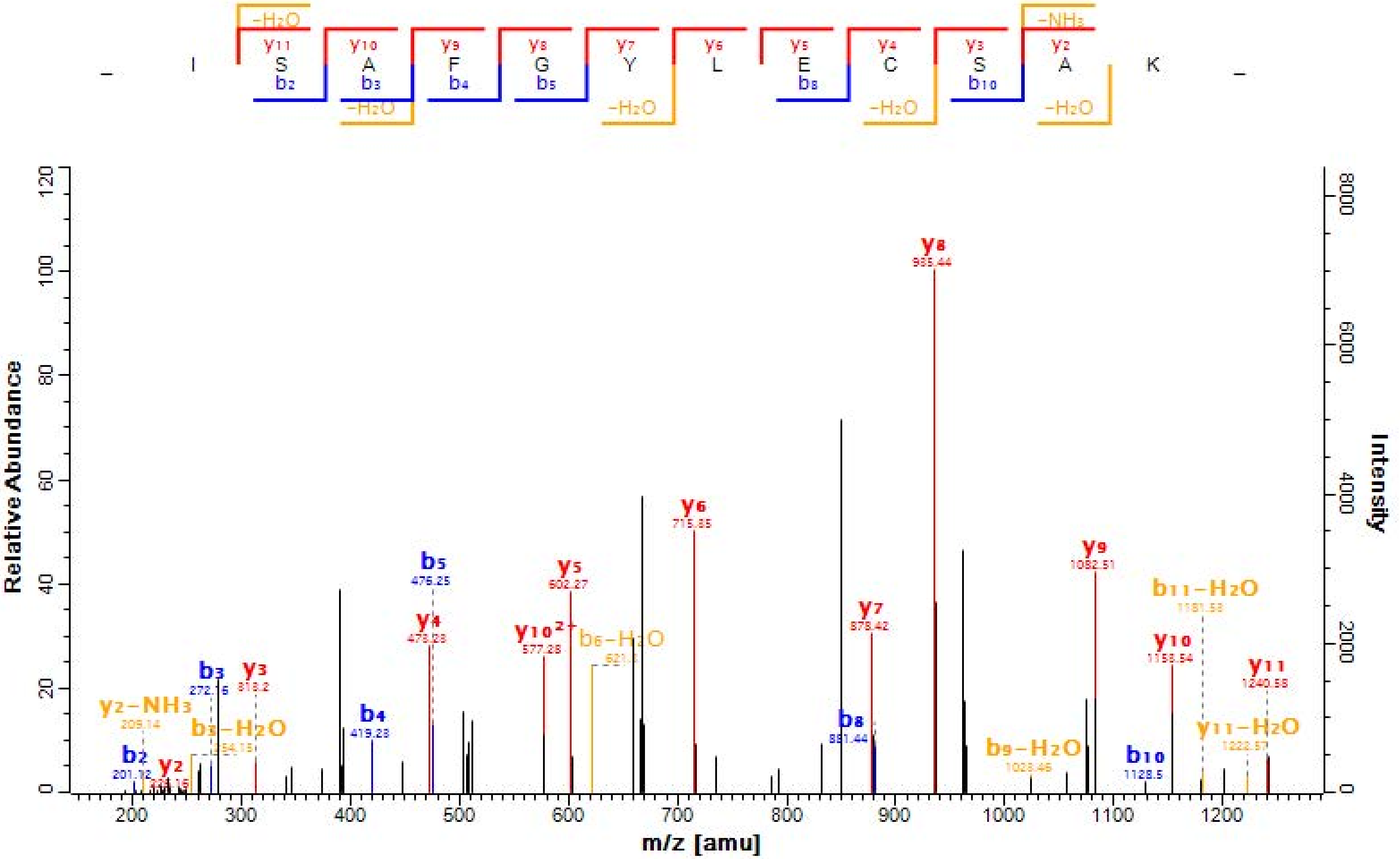
Mass:	1424.79844
m/z:	713.40649
Charge:	2+
Retentiontime:	34.550453186035
Score:	180.1071
Mass Error [ppm]:	-0.20472
PEP:	6.7433E-14
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	72 %
Peak Coverage:	45 %
Protein Localisation:	32 ... 45

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	13				
-0.04391	213.1598	2	L	12	1326.738		1326.738	
+0.251332	300.1918	3	S	11	1213.654	+0.007728	607.3304	+0.119306
	357.2132	4	G	10	1126.621	+0.068199	1126.621	
+0.073653	472.2402	5	D	9	1069.6	-0.08294	1069.6	
-0.07767	585.3243	6	L	8	954.5731	-0.03324	954.5731	
	642.3457	7	G	7	841.489	+0.013902	841.489	
-0.04339	770.4043	8	Q	6	784.4676	+0.012722	784.4676	
-0.06844	883.4884	9	L	5	656.409	-0.0255	656.409	
+0.10878	980.5411	10	P	4	543.3249	+0.054289	543.3249	
	1081.589	11	T	3	446.2722	+0.133176	446.2722	
+0.048427	1138.61	12	G	2	345.2245	-0.0115	345.2245	
-0.21386	1251.694	13	I	1	288.203	+0.058184	288.203	
		14	R	0	175.119		175.119	

Scan number	5987	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	104.17



precursor information

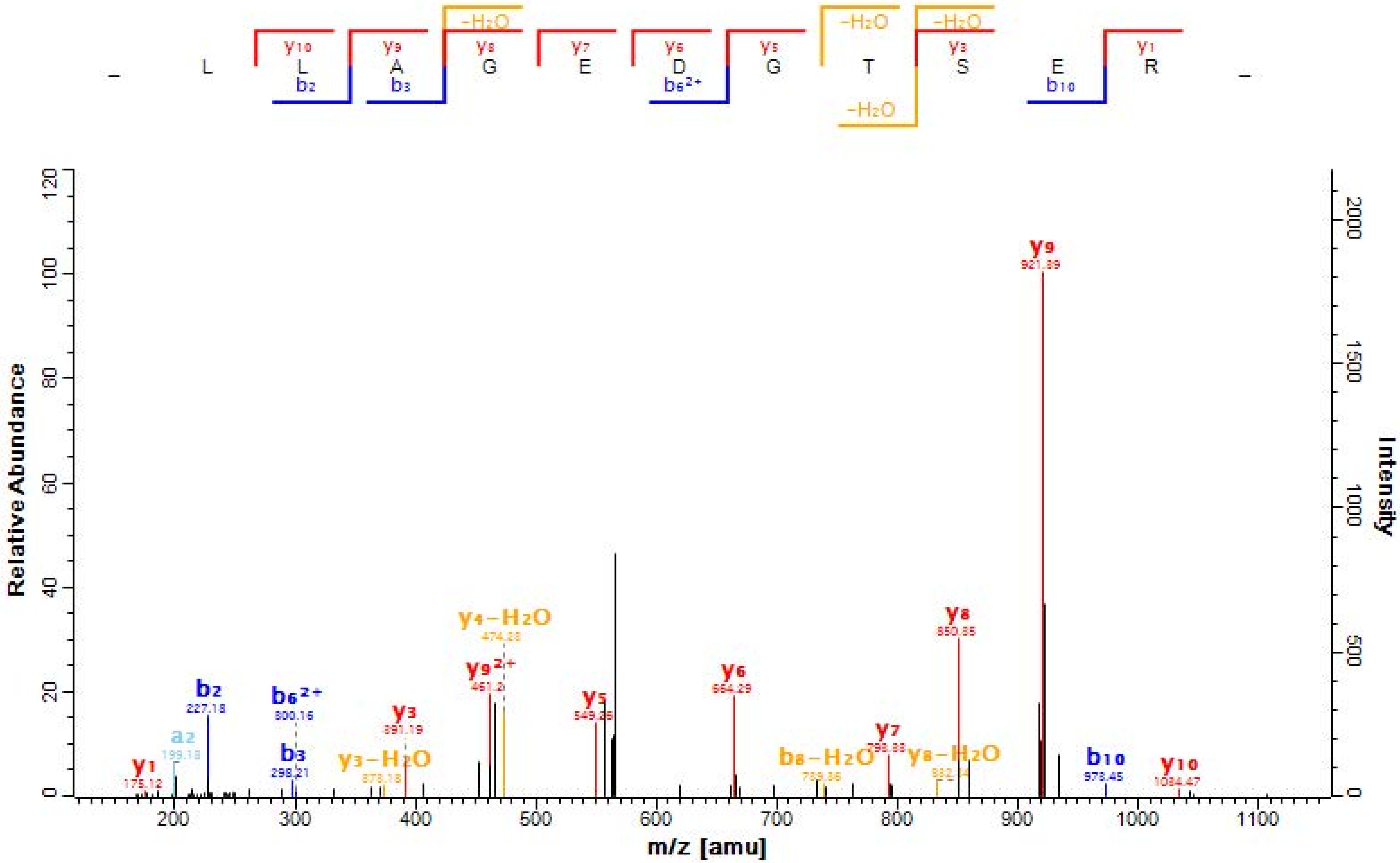
Mass:	1344.63927
m/z:	673.32691
Charge:	2+
Retentiontime:	34.757106781005
Score:	104.1745
Mass Error [ppm]:	0.65089
PEP:	7.1559E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	40 %
Peak Coverage:	27 %
Protein Localisation:	151 ... 162

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	I	11				
+0.006544	201.1234	2	S	10	1240.576	-0.13036	1240.576	
+0.037851	272.1605	3	A	9	1153.544	-0.12409	577.2755	-0.11103
-0.10011	419.2289	4	F	8	1082.507	-0.11518	1082.507	
+0.08985	476.2504	5	G	7	935.4382	-0.00971	935.4382	
	639.3137	6	Y	6	878.4168	-0.004	878.4168	
	752.3978	7	L	5	715.3535	+0.016239	715.3535	
-0.13029	881.4403	8	E	4	602.2694	+0.005516	602.2694	
	1041.471	9	C	3	473.2268	-0.12572	473.2268	
+0.141265	1128.503	10	S	2	313.1961	+0.027366	313.1961	
	1199.54	11	A	1	226.1641	+0.025977	226.1641	
		12	K	0	155.127		155.127	

Scan number	647	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	94.47



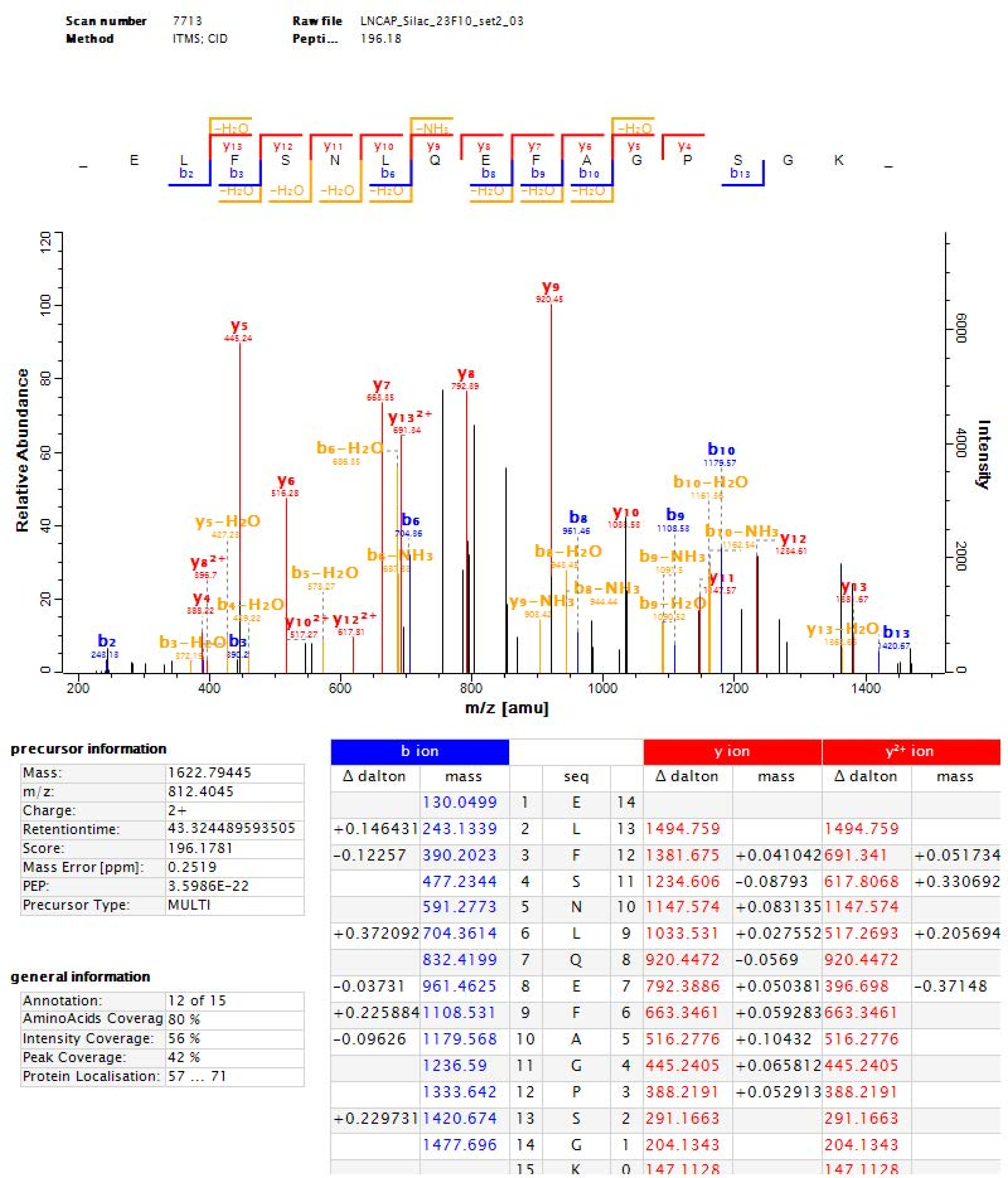
precursor information

Mass:	1146.55159
m/z:	574.28307
Charge:	2+
Retentiontime:	8.9340362548828
Score:	94.46532
Mass Error [ppm]:	-0.082438
PEP:	0.0013015
Precursor Type:	MULTI

general information

Annotation:	10 of 11
AminoAcids Coverag	91 %
Intensity Coverage:	49 %
Peak Coverage:	19 %
Protein Localisation:	395 ... 405

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	10				
-0.01	199.2		227.2	-0.02	227.2	2	L	9	1034	+0.262	1034	
	270.2		298.2	+0.047	298.2	3	A	8	921.4	-0.06	461.2	+0.02
	327.2		355.2		355.2	4	G	7	850.4	+0.058	850.4	
	456.3		484.3		484.3	5	E	6	793.3	+0.003	793.3	
	571.3	-0.02	300.2		599.3	6	D	5	664.3	+0.045	664.3	
	628.3		656.3		656.3	7	G	4	549.3	+0.07	549.3	
	729.4		757.4		757.4	8	T	3	492.2		492.2	
	816.4		844.4		844.4	9	S	2	391.2	-0.02	391.2	
	945.5		973.4	-0.05	973.4	10	E	1	304.2		304.2	
						11	R	0	175.1	+0.062	175.1	



Scan number	7713	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	196.18

precursor information

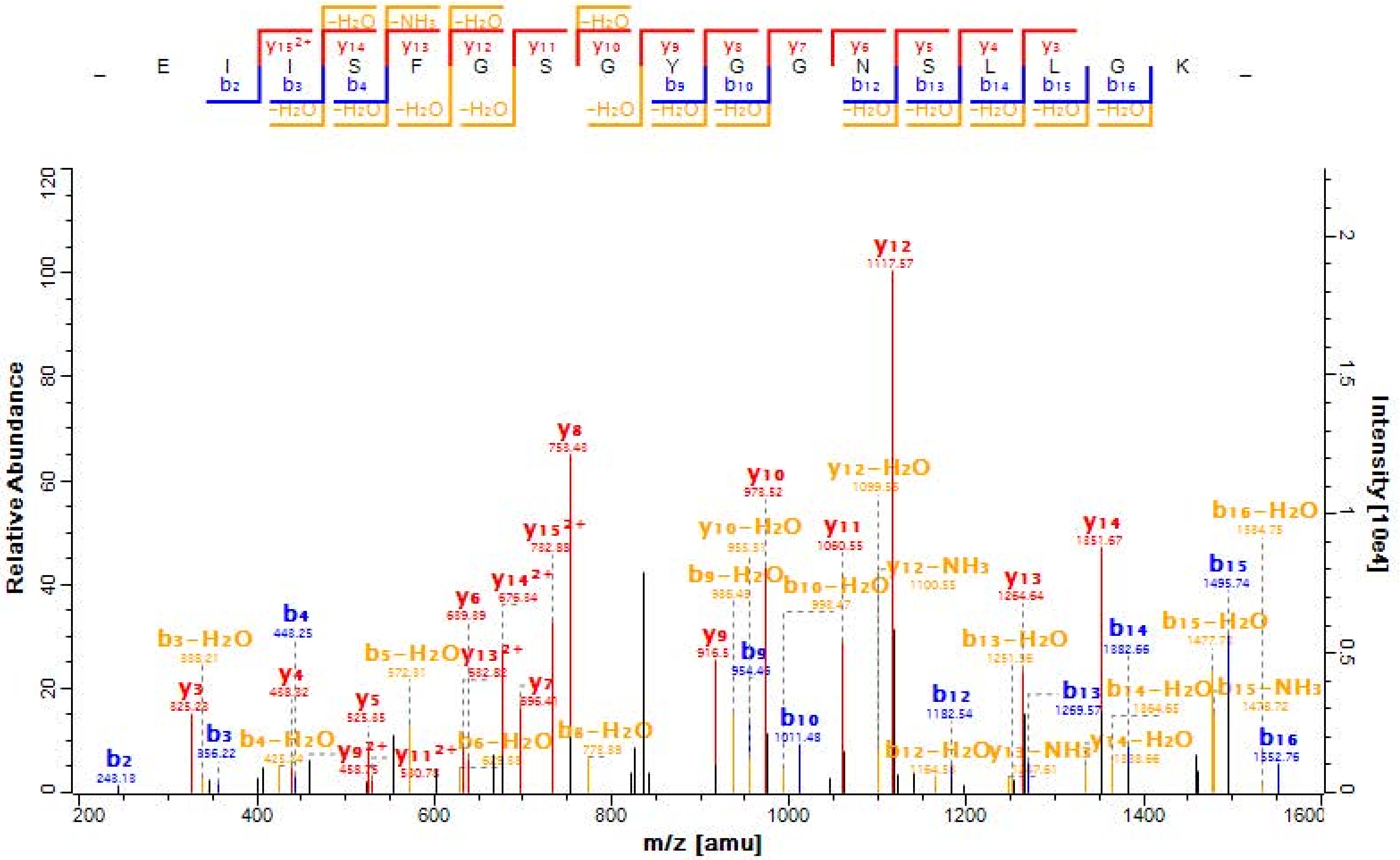
Mass:	1622.79445
m/z:	812.4045
Charge:	2+
Retentiontime:	43.324489593505
Score:	196.1781
Mass Error [ppm]:	0.2519
PEP:	3.5986E-22
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	56 %
Peak Coverage:	42 %
Protein Localisation:	57 ... 71

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	14				
+0.146431	243.1339	2	L	13	1494.759		1494.759	
-0.12257	390.2023	3	F	12	1381.675	+0.041042	691.341	+0.051734
	477.2344	4	S	11	1234.606	-0.08793	617.8068	+0.330692
	591.2773	5	N	10	1147.574	+0.083135	1147.574	
+0.372092	704.3614	6	L	9	1033.531	+0.027552	517.2693	+0.205694
	832.4199	7	Q	8	920.4472	-0.0569	920.4472	
-0.03731	961.4625	8	E	7	792.3886	+0.050381	396.698	-0.37148
+0.225884	1108.531	9	F	6	663.3461	+0.059283	663.3461	
-0.09626	1179.568	10	A	5	516.2776	+0.10432	516.2776	
	1236.59	11	G	4	445.2405	+0.065812	445.2405	
	1333.642	12	P	3	388.2191	+0.052913	388.2191	
+0.229731	1420.674	13	S	2	291.1663		291.1663	
	1477.696	14	G	1	204.1343		204.1343	
		15	K	0	147.1128		147.1128	

Scan number	7763	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	264.03



precursor information

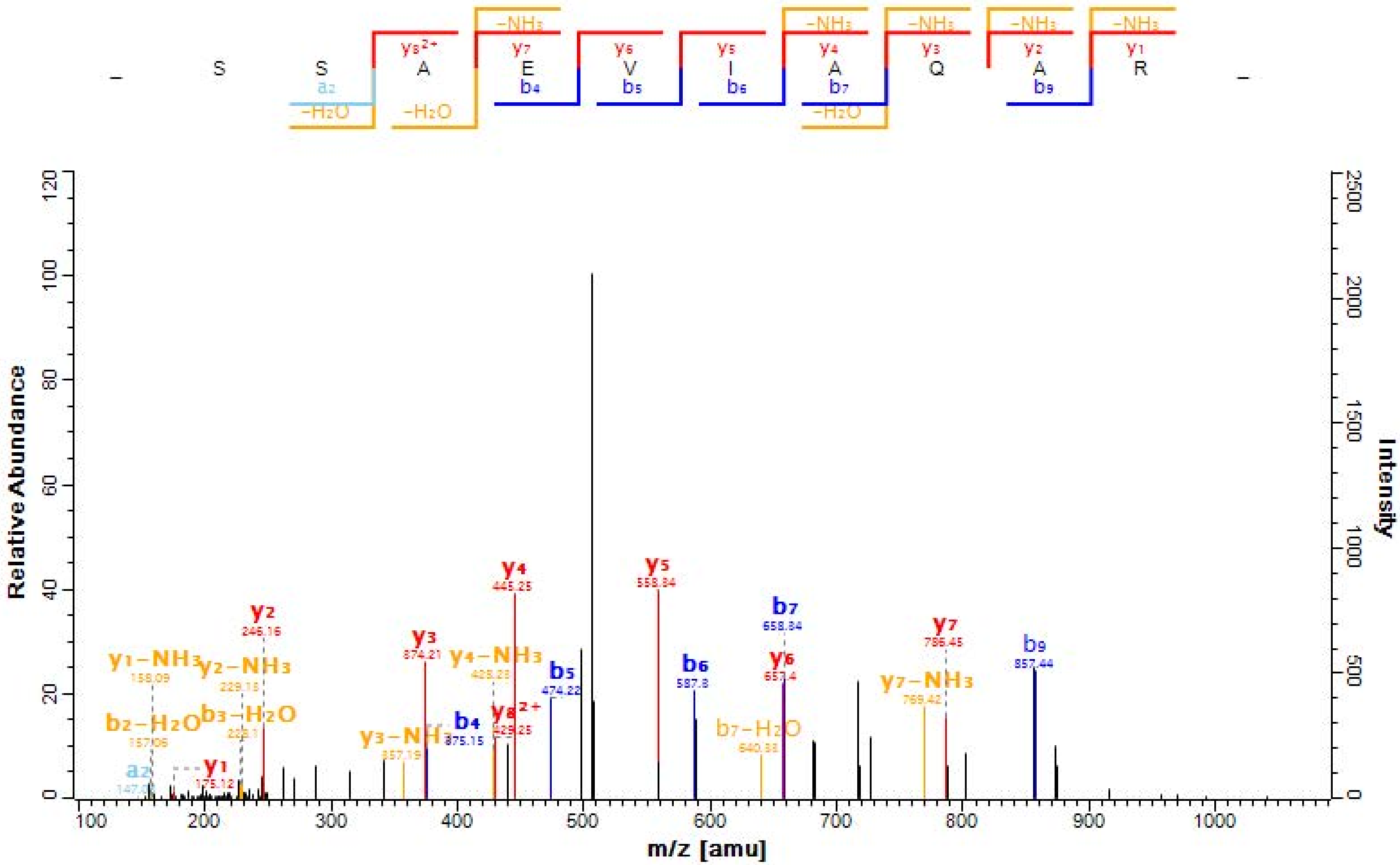
Mass:	1697.86241
m/z:	849.93848
Charge:	2+
Retentiontime:	43.583534240722
Score:	264.0251
Mass Error [ppm]:	-0.025645
PEP:	1.7246E-69
Precursor Type:	MULTI

general information

Annotation:	15 of 17
AminoAcids Coverag	88 %
Intensity Coverage:	70 %
Peak Coverage:	57 %
Protein Localisation:	245 ... 261

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	16				
-0.08463	243.1339	2	I	15	1577.841		1577.841	
-0.05119	356.218	3	I	14	1464.757		732.8823	+0.20867
+0.033788	443.25	4	S	13	1351.673	-0.01403	676.3402	+0.069977
	590.3184	5	F	12	1264.641	-0.12165	632.8242	+0.111992
	647.3399	6	G	11	1117.573	-0.08643	1117.573	
	734.3719	7	S	10	1060.551	-0.05716	530.7793	-0.42028
	791.3934	8	G	9	973.5193	-0.04198	973.5193	
-0.08948	954.4567	9	Y	8	916.4978	-0.01044	458.7525	-0.16221
+0.018211	1011.478	10	G	7	753.4345	+0.027253	753.4345	
	1068.5	11	G	6	696.413	+0.124522	696.413	
+0.066796	1182.543	12	N	5	639.3916	+0.066701	639.3916	
+0.02195	1269.575	13	S	4	525.3486	+0.158579	525.3486	
-0.1063	1382.659	14	L	3	438.3166	+0.037226	438.3166	
-0.12152	1495.743	15	L	2	325.2325	+0.010389	325.2325	
-0.13493	1552.764	16	G	1	212.1485		212.1485	
		17	K	0	155.127		155.127	

Scan number	781	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	104.82

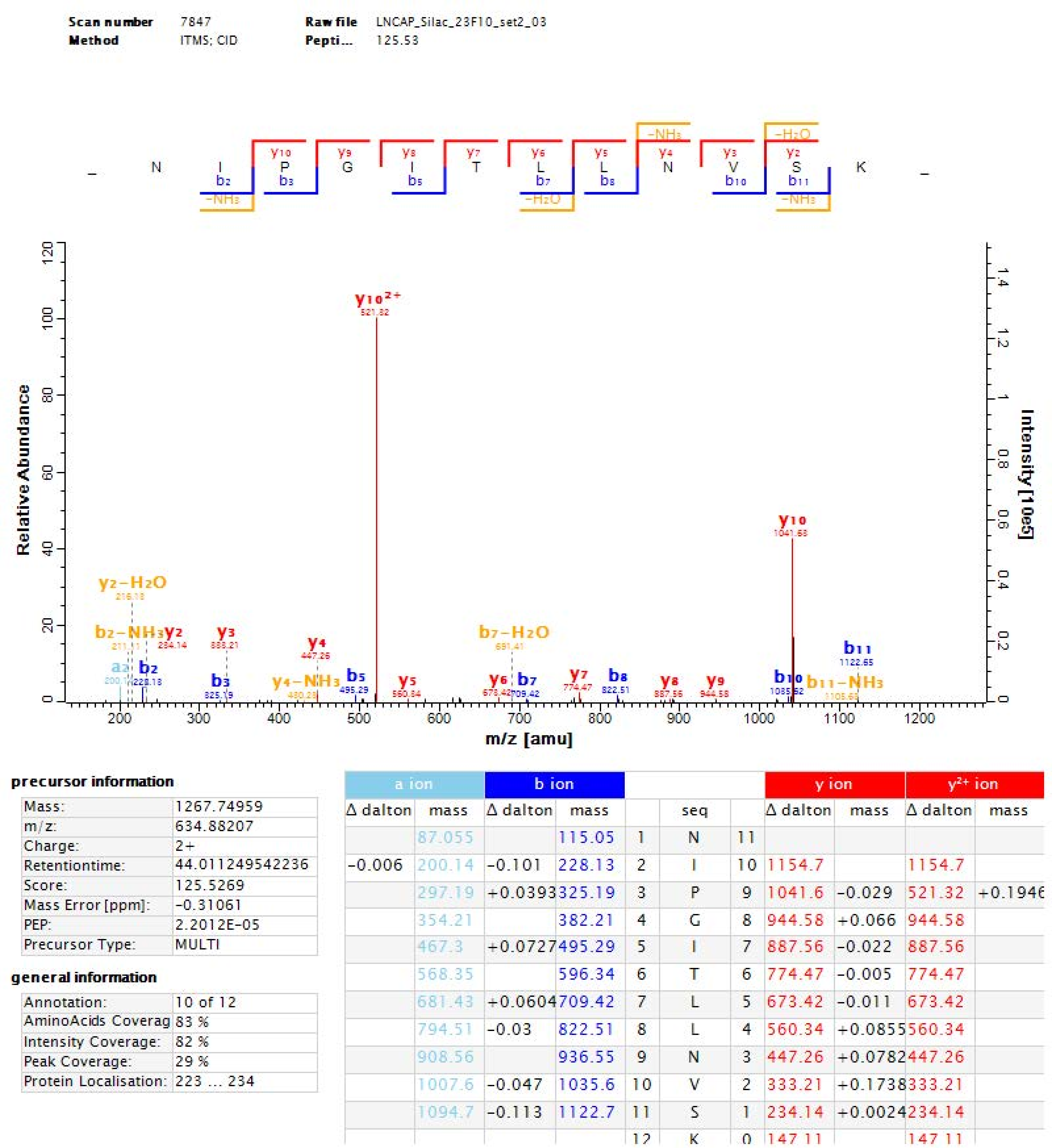


precursor information

Mass:	1030.54173
m/z:	516.27814
Charge:	2+
Retentiontime:	9.7214536666870
Score:	104.8239
Mass Error [ppm]:	0.97941
PEP:	0.00094399
Precursor Type:	ISO

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	41 %
Peak Coverage:	20 %
Protein Localisation:	259 ... 268

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	60.044		88.039	1	S	9				
-0.093	147.08		175.07	2	S	8	944.52		944.52	
	218.11		246.11	3	A	7	857.48		429.25	+0.3189
	347.16	+0.0804	375.15	4	E	6	786.45	+0.0399	786.45	
	446.22	+0.0697	474.22	5	V	5	657.4	-0.021	657.4	
	559.31	+0.0206	587.3	6	I	4	558.34	+0.1024	558.34	
	630.35	+0.0796	658.34	7	A	3	445.25	-0.001	445.25	
	758.4		786.4	8	Q	2	374.21	-0.015	374.21	
	829.44	-0.049	857.44	9	A	1	246.16	+0.0941	246.16	
				10	R	0	175.12	+0.0258	175.12	



Scan number	7847	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	125.53

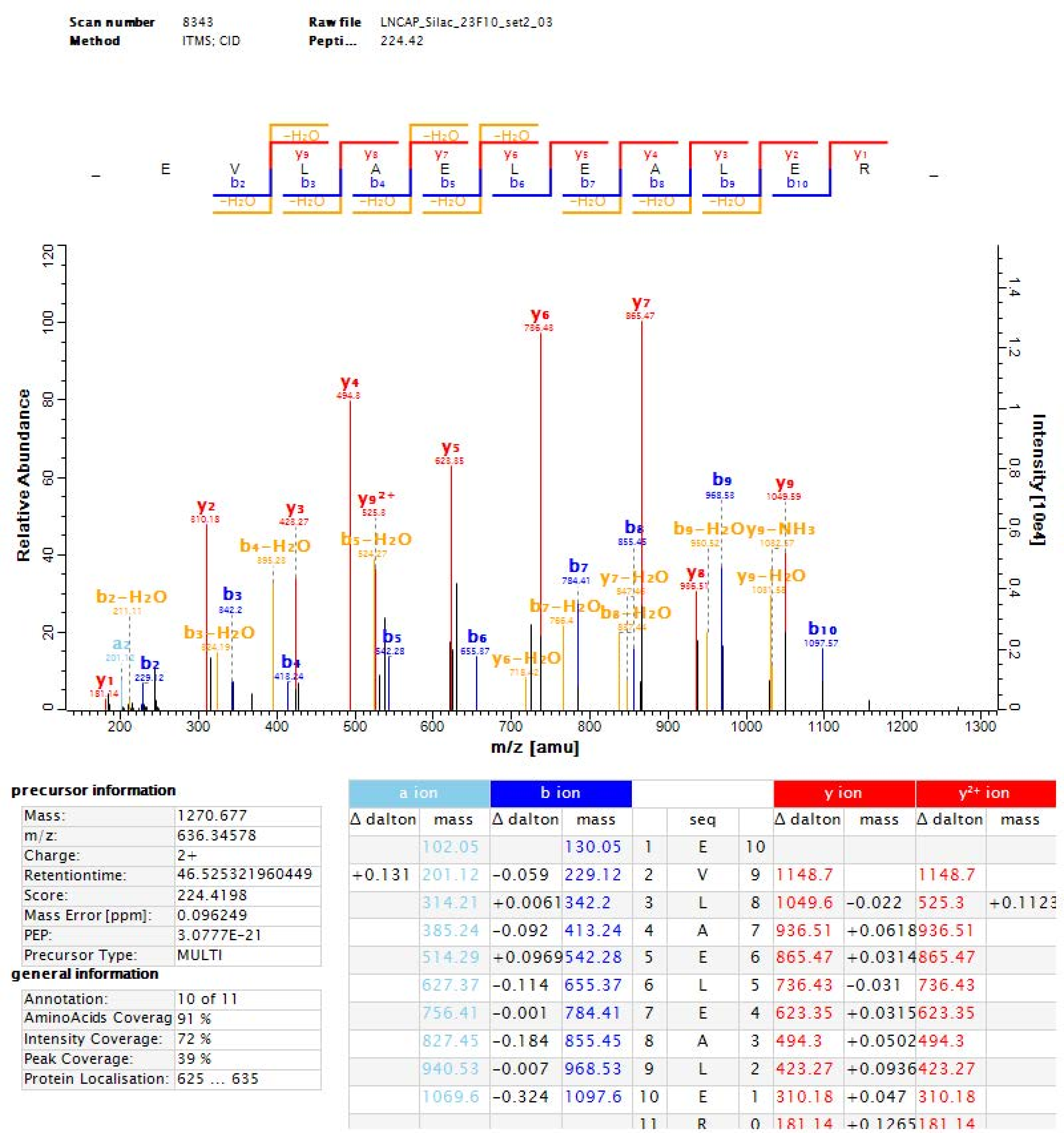
precursor information

Mass:	1267.74959
m/z:	634.88207
Charge:	2+
Retentiontime:	44.011249542236
Score:	125.5269
Mass Error [ppm]:	-0.31061
PEP:	2.2012E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	82 %
Peak Coverage:	29 %
Protein Localisation:	223 ... 234

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	87.055		115.05	1	N	11				
-0.006	200.14	-0.101	228.13	2	I	10	1154.7		1154.7	
	297.19	+0.0393	325.19	3	P	9	1041.6	-0.029	521.32	+0.194
	354.21		382.21	4	G	8	944.58	+0.066	944.58	
	467.3	+0.0727	495.29	5	I	7	887.56	-0.022	887.56	
	568.35		596.34	6	T	6	774.47	-0.005	774.47	
	681.43	+0.0604	709.42	7	L	5	673.42	-0.011	673.42	
	794.51	-0.03	822.51	8	L	4	560.34	+0.0855	560.34	
	908.56		936.55	9	N	3	447.26	+0.0782	447.26	
	1007.6	-0.047	1035.6	10	V	2	333.21	+0.1738	333.21	
	1094.7	-0.113	1122.7	11	S	1	234.14	+0.0024	234.14	
				12	K	0	147.11		147.11	



Scan number	8343	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	224.42

precursor information

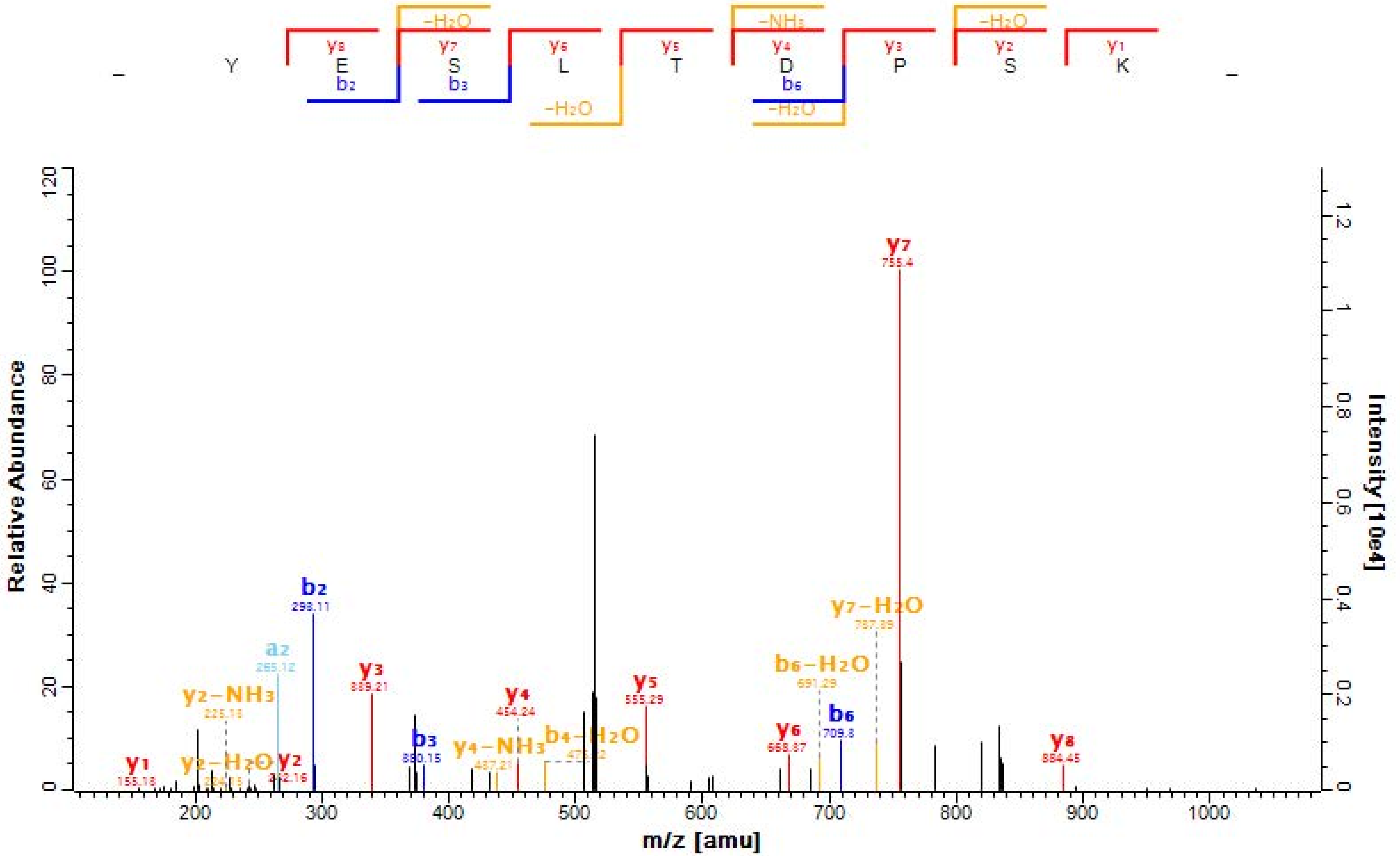
Mass:	1270.677
m/z:	636.34578
Charge:	2+
Retentiontime:	46.525321960449
Score:	224.4198
Mass Error [ppm]:	0.096249
PEP:	3.0777E-21
Precursor Type:	MULTI

general information

Annotation:	10 of 11
AminoAcids Coverag	91 %
Intensity Coverage:	72 %
Peak Coverage:	39 %
Protein Localisation:	625 ... 635

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	10				
+0.131	201.12	-0.059	229.12	2	V	9	1148.7		1148.7	
	314.21	+0.0061	342.2	3	L	8	1049.6	-0.022	525.3	+0.1123
	385.24	-0.092	413.24	4	A	7	936.51	+0.0618	936.51	
	514.29	+0.0969	542.28	5	E	6	865.47	+0.0314	865.47	
	627.37	-0.114	655.37	6	L	5	736.43	-0.031	736.43	
	756.41	-0.001	784.41	7	E	4	623.35	+0.0315	623.35	
	827.45	-0.184	855.45	8	A	3	494.3	+0.0502	494.3	
	940.53	-0.007	968.53	9	L	2	423.27	+0.0936	423.27	
	1069.6	-0.324	1097.6	10	E	1	310.18	+0.047	310.18	
				11	R	0	181.14	+0.1265	181.14	

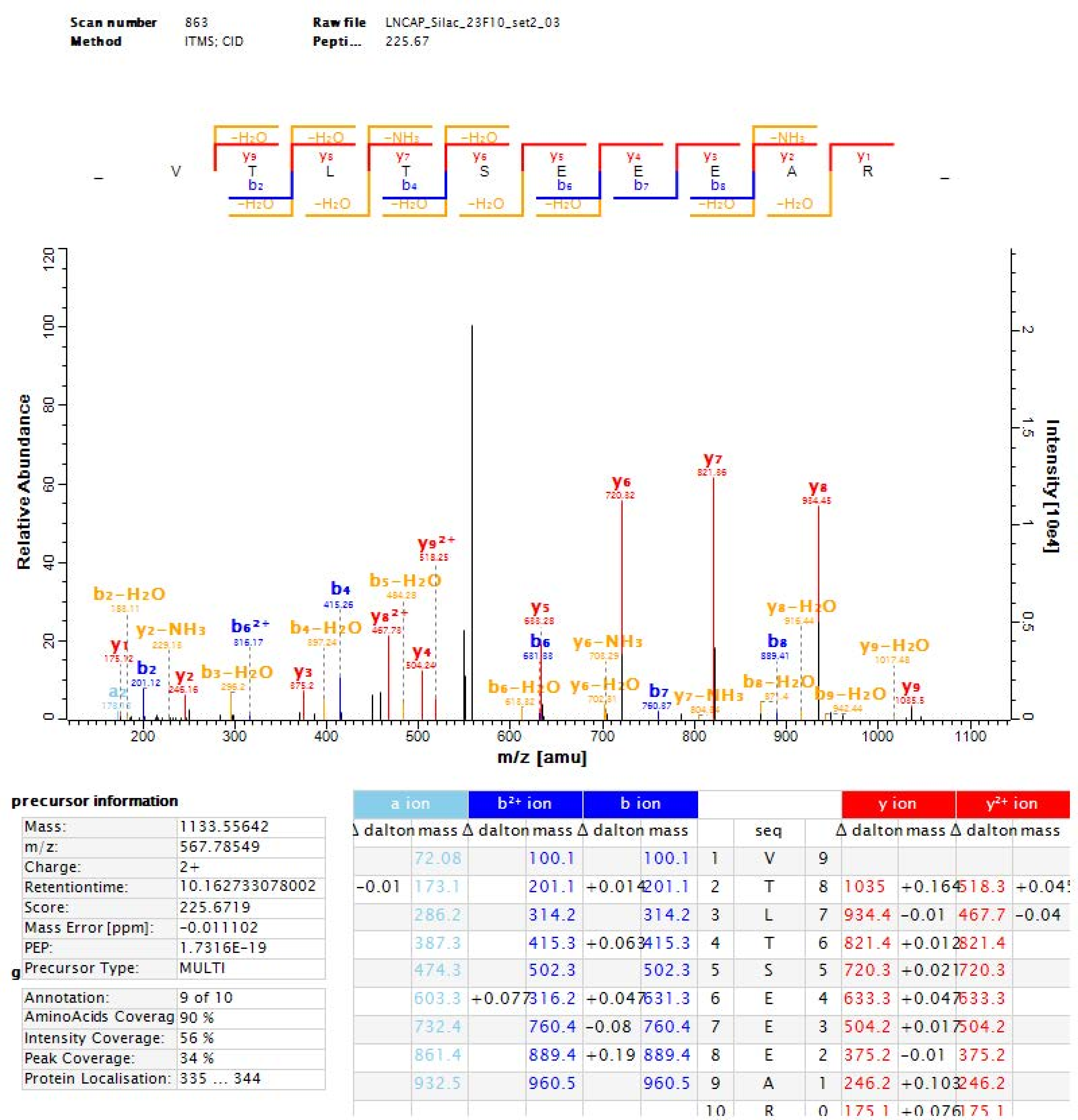
Scan number	856	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	85.35



precursor information

Mass:	1038.48695
m/z:	520.25075
Charge:	2+
Retentiontime:	10.120121955871
Score:	85.35461
Mass Error [ppm]:	-0.0021924
PEP:	0.0066981
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	47 %
Peak Coverage:	22 %
Protein Localisation:	183 ... 191

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	136.0757		164.0706	1	Y	8		
+0.053592	265.1183	-0.04075	293.1132	2	E	7	884.4451	+0.049588
	352.1503	+0.09336	380.1452	3	S	6	755.4025	-0.06859
	465.2344		493.2293	4	L	5	668.3705	+0.139102
	566.2821		594.277	5	T	4	555.2864	-0.02311
	681.309	-0.05263	709.3039	6	D	3	454.2387	+0.070283
	778.3618		806.3567	7	P	2	339.2118	+0.052304
	865.3938		893.3887	8	S	1	242.159	-0.03595
				9	K	0	155.127	+0.097835



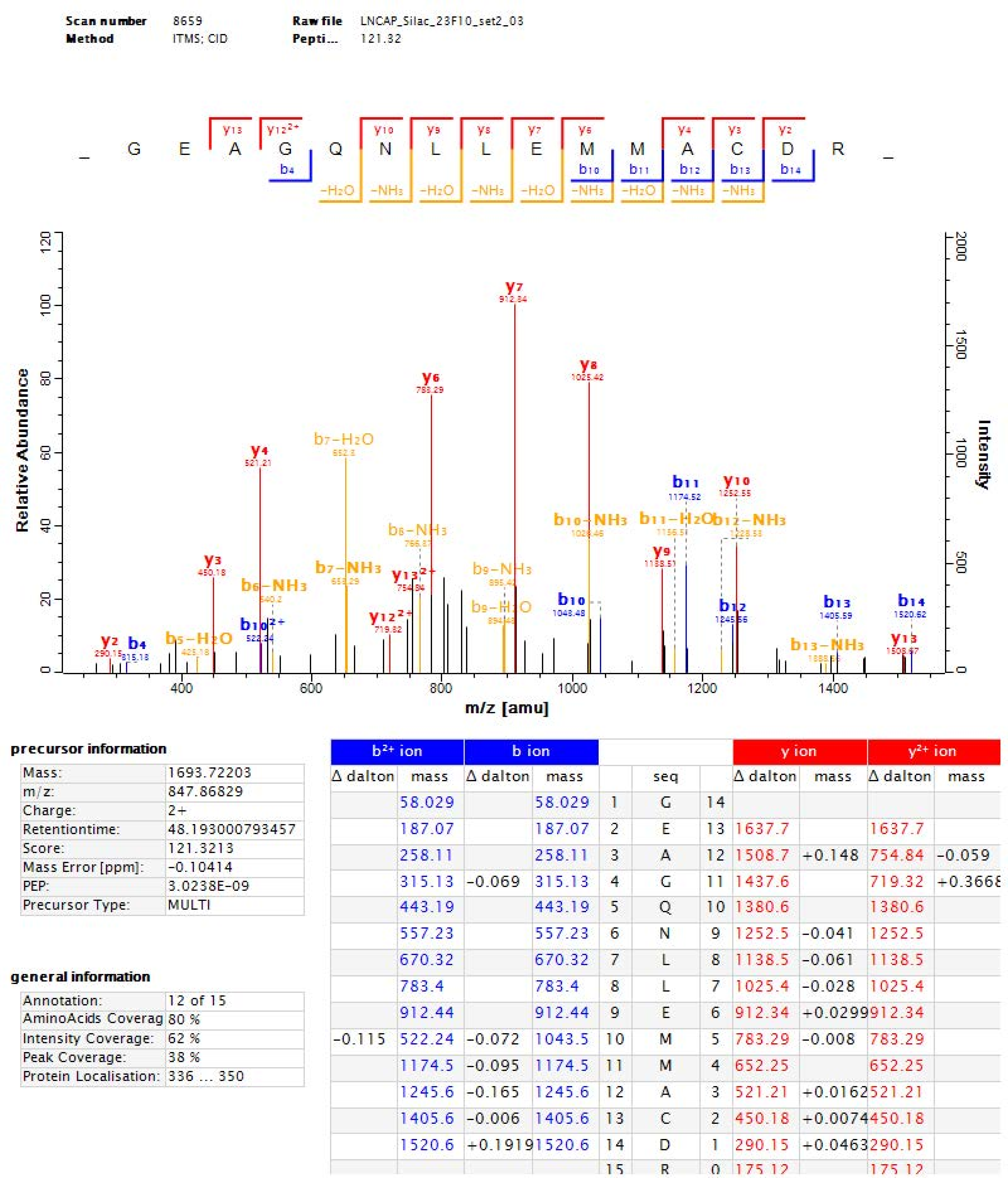
Scan number	863	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	225.67

precursor information

Mass:	1133.55642
m/z:	567.78549
Charge:	2+
Retentiontime:	10.162733078002
Score:	225.6719
Mass Error [ppm]:	-0.011102
PEP:	1.7316E-19
Precursor Type:	MULTI

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	56 %
Peak Coverage:	34 %
Protein Localisation:	335 ... 344

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.08		100.1		100.1	1	V	9				
-0.01	173.1		201.1	+0.014	201.1	2	T	8	1035	+0.164	518.3	+0.04
	286.2		314.2		314.2	3	L	7	934.4	-0.01	467.7	-0.04
	387.3		415.3	+0.063	415.3	4	T	6	821.4	+0.012	821.4	
	474.3		502.3		502.3	5	S	5	720.3	+0.021	720.3	
	603.3	+0.077	316.2	+0.047	631.3	6	E	4	633.3	+0.047	633.3	
	732.4		760.4	-0.08	760.4	7	E	3	504.2	+0.017	504.2	
	861.4		889.4	+0.19	889.4	8	E	2	375.2	-0.01	375.2	
	932.5		960.5		960.5	9	A	1	246.2	+0.103	246.2	
						10	R	0	175.1	+0.076	175.1	



Scan number 8659 **Raw file** LNCAP_Silac_23F10_set2_03
Method ITMS; CID **Pepti...** 121.32

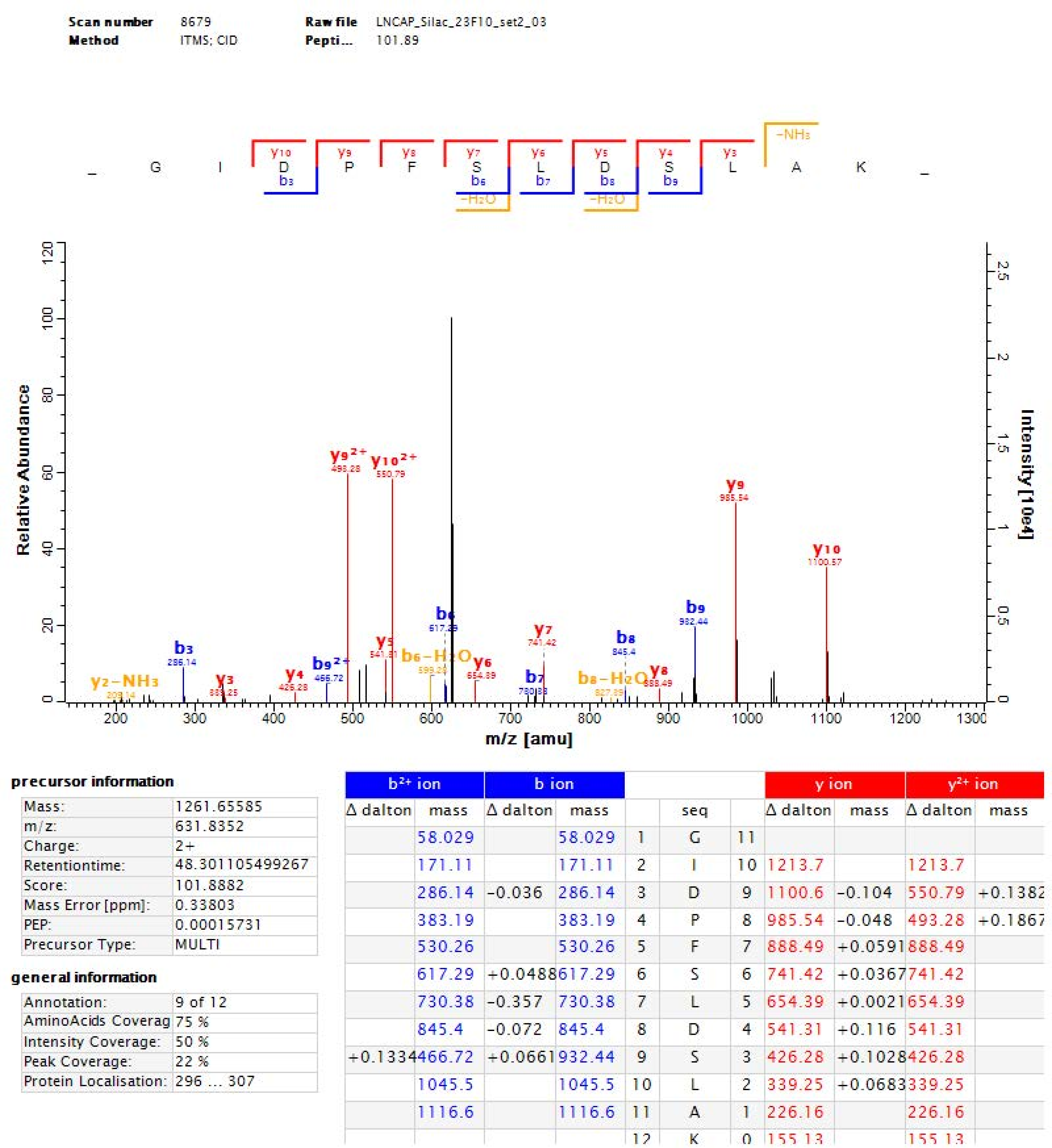
precursor information

Mass:	1693.72203
m/z:	847.86829
Charge:	2+
Retentiontime:	48.193000793457
Score:	121.3213
Mass Error [ppm]:	-0.10414
PEP:	3.0238E-09
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	62 %
Peak Coverage:	38 %
Protein Localisation:	336 ... 350

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	14				
	187.07		187.07	2	E	13	1637.7		1637.7	
	258.11		258.11	3	A	12	1508.7	+0.148	754.84	-0.059
	315.13	-0.069	315.13	4	G	11	1437.6		719.32	+0.3668
	443.19		443.19	5	Q	10	1380.6		1380.6	
	557.23		557.23	6	N	9	1252.5	-0.041	1252.5	
	670.32		670.32	7	L	8	1138.5	-0.061	1138.5	
	783.4		783.4	8	L	7	1025.4	-0.028	1025.4	
	912.44		912.44	9	E	6	912.34	+0.0299	912.34	
-0.115	522.24	-0.072	1043.5	10	M	5	783.29	-0.008	783.29	
	1174.5	-0.095	1174.5	11	M	4	652.25		652.25	
	1245.6	-0.165	1245.6	12	A	3	521.21	+0.0162	521.21	
	1405.6	-0.006	1405.6	13	C	2	450.18	+0.0074	450.18	
	1520.6	+0.1919	1520.6	14	D	1	290.15	+0.0463	290.15	
				15	R	0	175.12		175.12	



Scan number	8679	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	101.89

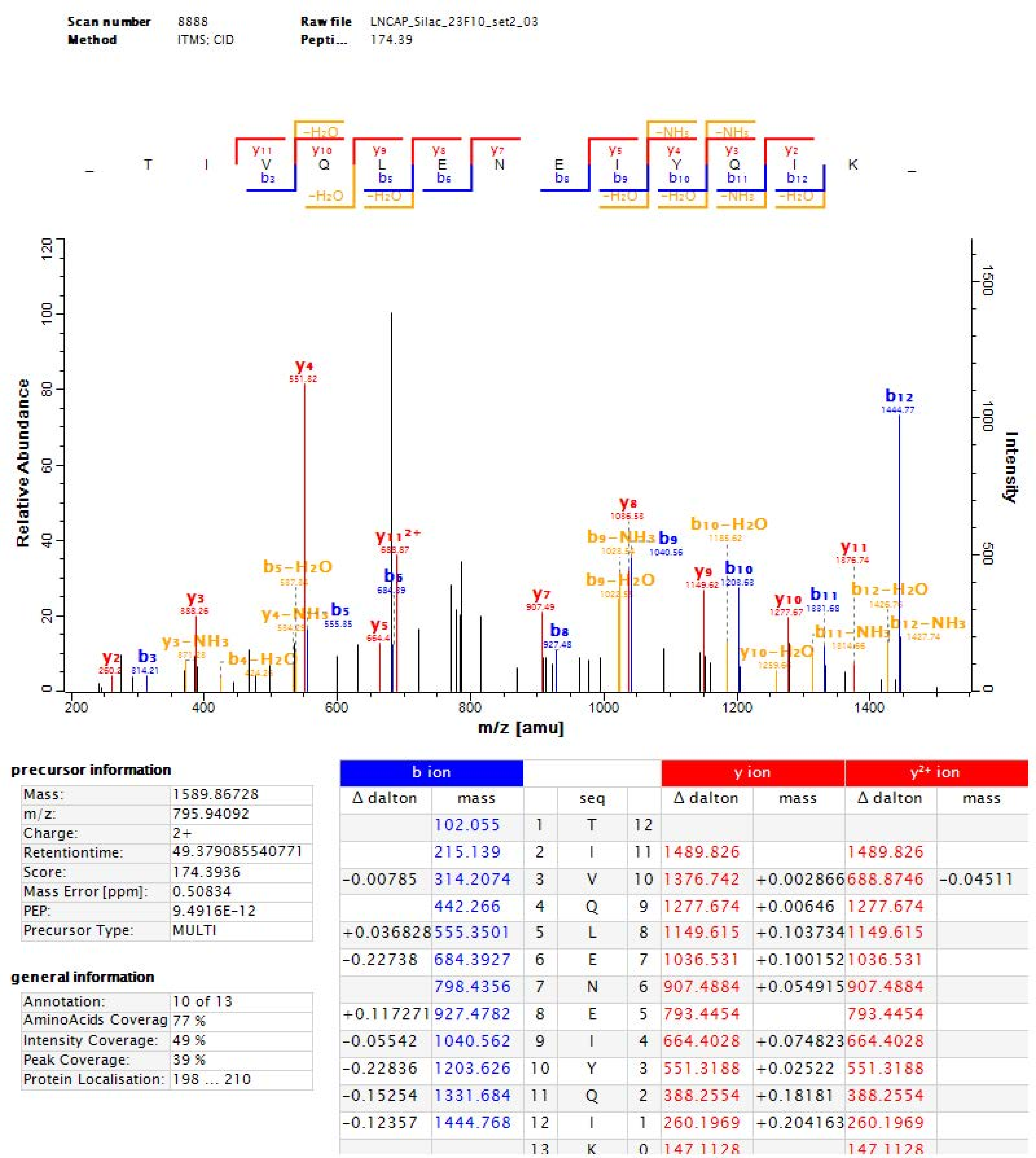
precursor information

Mass:	1261.65585
m/z:	631.8352
Charge:	2+
Retentiontime:	48.301105499267
Score:	101.8882
Mass Error [ppm]:	0.33803
PEP:	0.00015731
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	50 %
Peak Coverage:	22 %
Protein Localisation:	296 ... 307

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	11				
	171.11		171.11	2	I	10	1213.7		1213.7	
	286.14	-0.036	286.14	3	D	9	1100.6	-0.104	550.79	+0.1382
	383.19		383.19	4	P	8	985.54	-0.048	493.28	+0.1867
	530.26		530.26	5	F	7	888.49	+0.0591	888.49	
	617.29	+0.0488	617.29	6	S	6	741.42	+0.0367	741.42	
	730.38	-0.357	730.38	7	L	5	654.39	+0.0021	654.39	
	845.4	-0.072	845.4	8	D	4	541.31	+0.116	541.31	
+0.1334	466.72	+0.0661	932.44	9	S	3	426.28	+0.1028	426.28	
	1045.5		1045.5	10	L	2	339.25	+0.0683	339.25	
	1116.6		1116.6	11	A	1	226.16		226.16	
				12	K	0	155.13		155.13	



Scan number	8888	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	174.39

precursor information

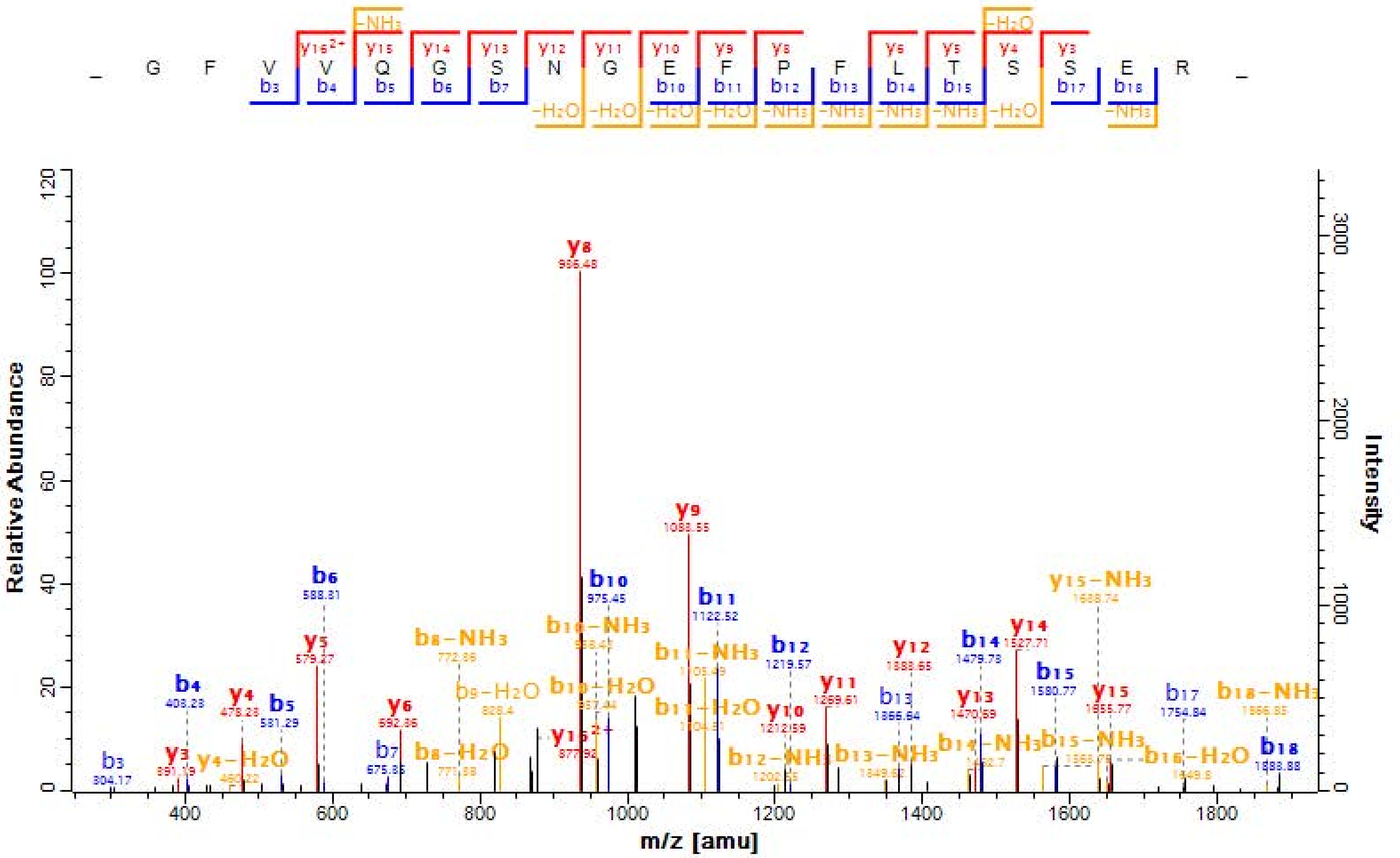
Mass:	1589.86728
m/z:	795.94092
Charge:	2+
Retentiontime:	49.379085540771
Score:	174.3936
Mass Error [ppm]:	0.50834
PEP:	9.4916E-12
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	49 %
Peak Coverage:	39 %
Protein Localisation:	198 ... 210

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055	1	T	12				
	215.139	2	I	11	1489.826		1489.826	
-0.00785	314.2074	3	V	10	1376.742	+0.002866	688.8746	-0.04511
	442.266	4	Q	9	1277.674	+0.00646	1277.674	
+0.036828	555.3501	5	L	8	1149.615	+0.103734	1149.615	
-0.22738	684.3927	6	E	7	1036.531	+0.100152	1036.531	
	798.4356	7	N	6	907.4884	+0.054915	907.4884	
+0.117271	927.4782	8	E	5	793.4454		793.4454	
-0.05542	1040.562	9	I	4	664.4028	+0.074823	664.4028	
-0.22836	1203.626	10	Y	3	551.3188	+0.02522	551.3188	
-0.15254	1331.684	11	Q	2	388.2554	+0.18181	388.2554	
-0.12357	1444.768	12	I	1	260.1969	+0.204163	260.1969	
		13	K	0	147.1128		147.1128	

Scan number	9080	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	203.06



precursor information

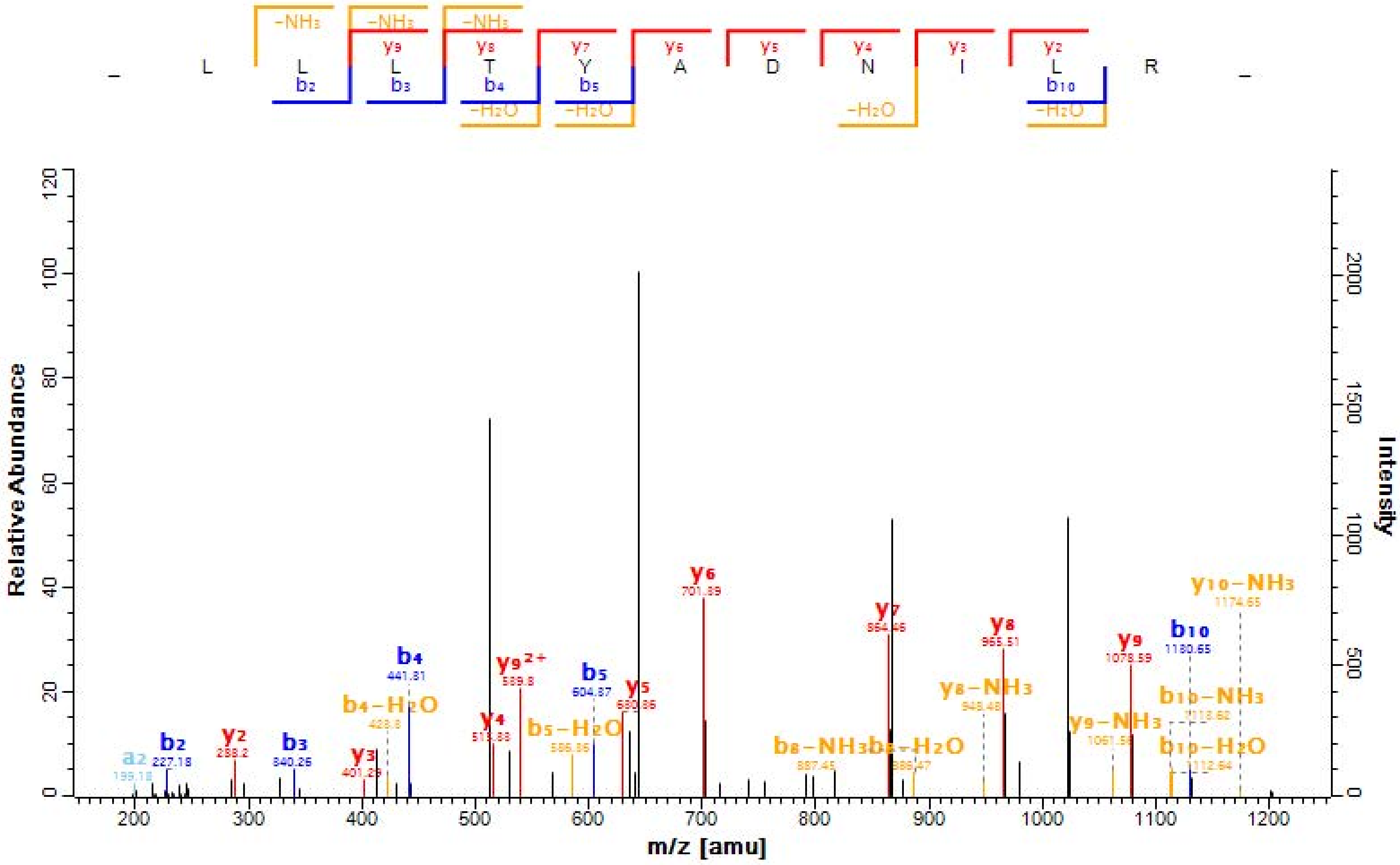
Mass:	2056.98623
m/z:	1029.50039
Charge:	2+
Retentiontime:	50.360656738281
Score:	203.0634
Mass Error [ppm]:	0.39298
PEP:	1.2577E-48
Precursor Type:	MULTI

general information

Annotation:	16 of 19
AminoAcids Coverag	84 %
Intensity Coverage:	62 %
Peak Coverage:	43 %
Protein Localisation:	71 ... 89

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	18				
	205.0972	2	F	17	2000.971		2000.971	
+0.093526	304.1656	3	V	16	1853.903		1853.903	
+0.116573	403.234	4	V	15	1754.834		877.9208	-0.0976
-0.14192	531.2926	5	Q	14	1655.766	-0.10168	1655.766	
+0.082644	588.314	6	G	13	1527.707	-0.0193	1527.707	
+0.122454	675.3461	7	S	12	1470.686	-0.05765	1470.686	
	789.389	8	N	11	1383.654	-0.09227	1383.654	
	846.4104	9	G	10	1269.611	+0.082855	1269.611	
-0.08499	975.453	10	E	9	1212.59	+0.181467	1212.59	
-0.07199	1122.521	11	F	8	1083.547	-0.02594	1083.547	
-0.05566	1219.574	12	P	7	936.4785	-0.02674	936.4785	
+0.08894	1366.643	13	F	6	839.4258		839.4258	
-0.068	1479.727	14	L	5	692.3573	-0.00963	692.3573	
-0.03182	1580.774	15	T	4	579.2733	-0.04318	579.2733	
	1667.806	16	S	3	478.2256	+0.086867	478.2256	
+0.208204	1754.838	17	S	2	391.1936	+0.137725	391.1936	
-0.07475	1883.881	18	E	1	304.1615		304.1615	
		19	R	0	175.119		175.119	

Scan number	9109	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	136.02



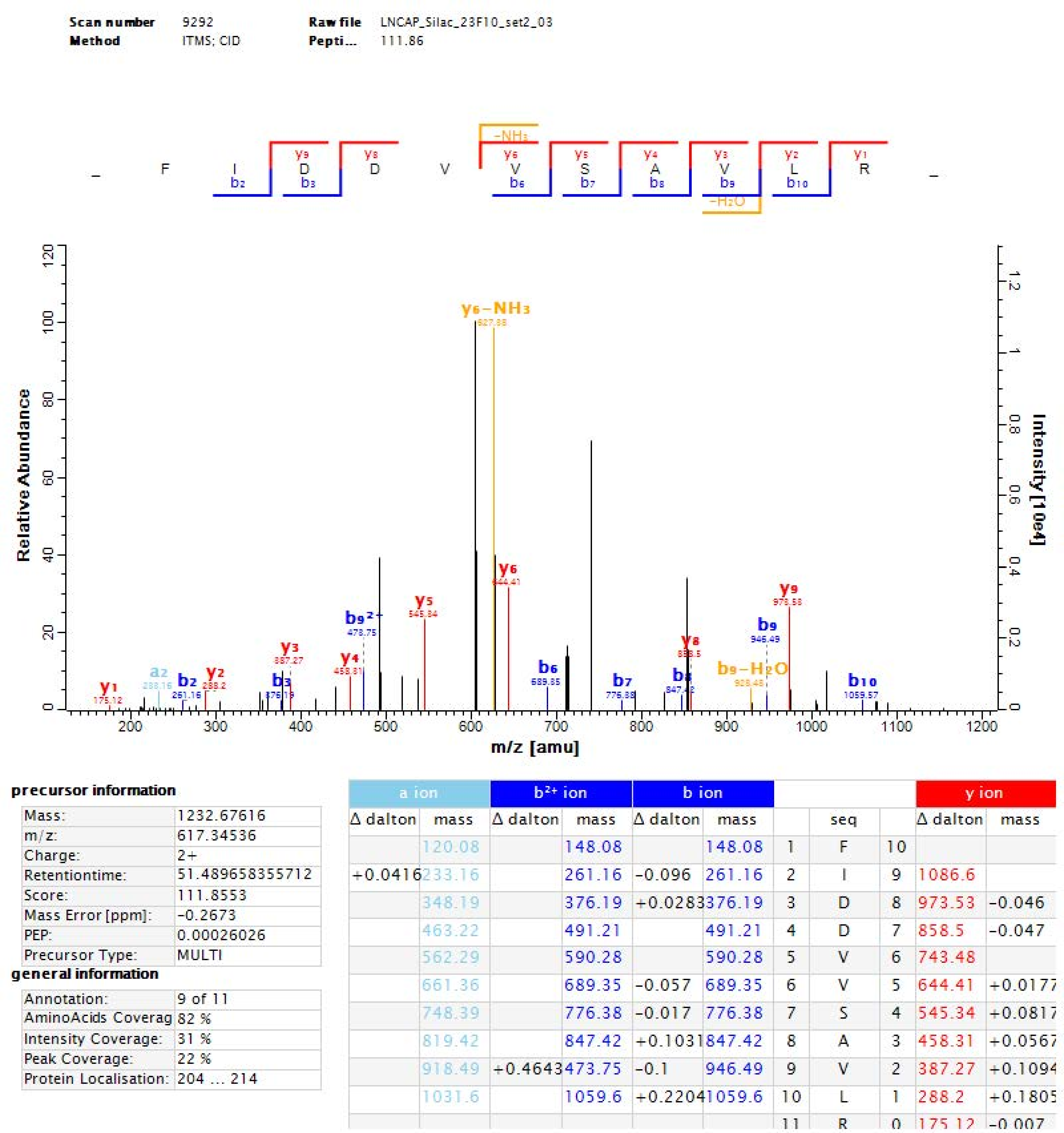
precursor information

Mass:	1306.65587
m/z:	654.33521
Charge:	2+
Retentiontime:	50.518951416015
Score:	136.0225
Mass Error [ppm]:	-0.067521
PEP:	5.0939E-12
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	36 %
Peak Coverage:	32 %
Protein Localisation:	34 ... 44

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	10				
-0.002	199.18	+0.0248	227.18	2	L	9	1191.7		1191.7	
	312.26	-0.069	340.26	3	L	8	1078.6	-0.049	539.8	+0.171
	413.31	-0.005	441.31	4	T	7	965.51	-0.004	965.51	
	576.38	-0.127	604.37	5	Y	6	864.46	-0.045	864.46	
	647.41		675.41	6	A	5	701.39	+0.0287	701.39	
	762.44		790.43	7	D	4	630.36	+0.2299	630.36	
	876.48		904.48	8	N	3	515.33	-0.006	515.33	
	989.57		1017.6	9	I	2	401.29	+0.1485	401.29	
	1102.7	-0.003	1130.6	10	L	1	288.2	+0.0929	288.2	
				11	R	0	175.12		175.12	



Scan number	9292	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	111.86

precursor information

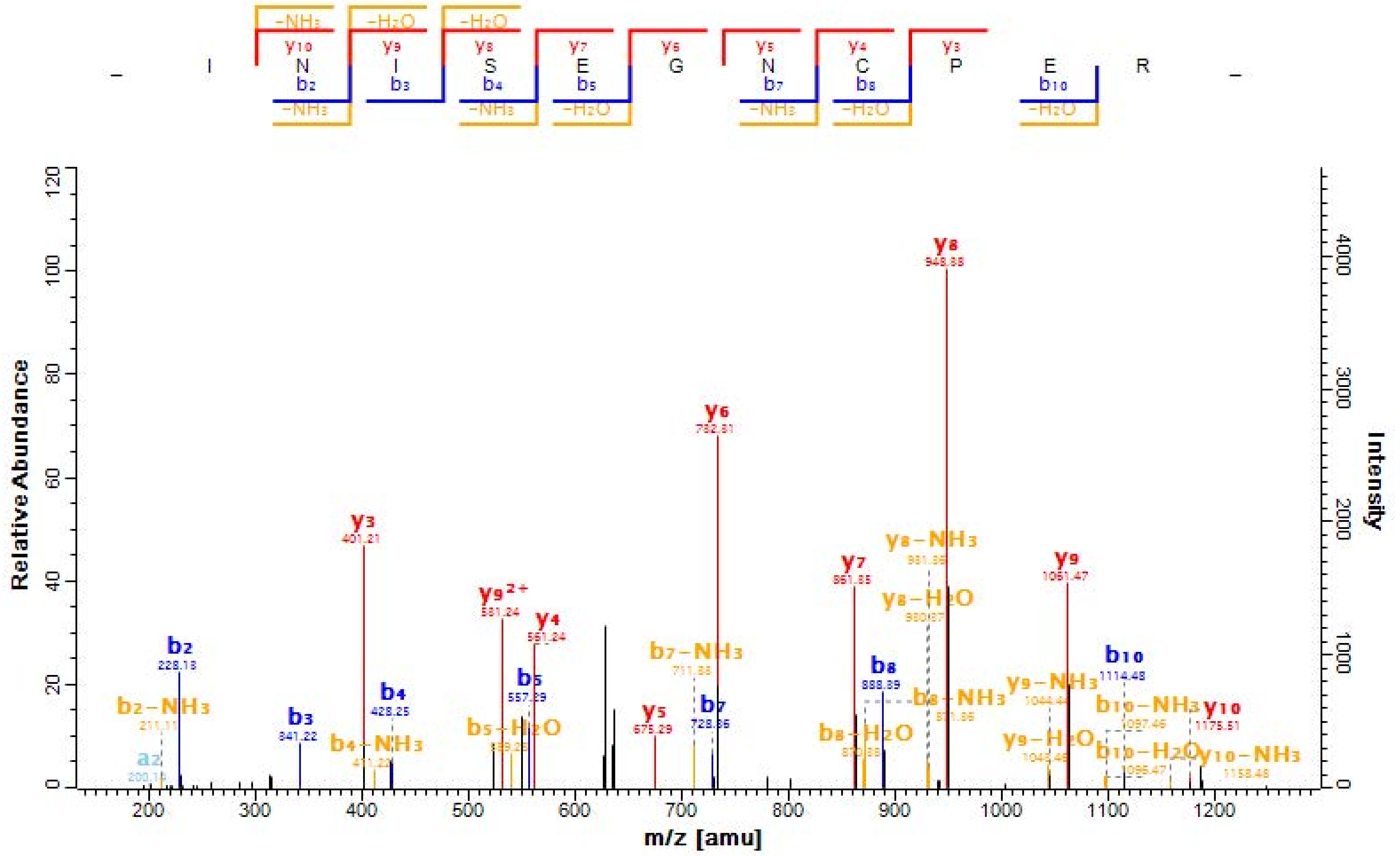
Mass:	1232.67616
m/z:	617.34536
Charge:	2+
Retentiontime:	51.489658355712
Score:	111.8553
Mass Error [ppm]:	-0.2673
PEP:	0.00026026
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	31 %
Peak Coverage:	22 %
Protein Localisation:	204 ... 214

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	120.08		148.08		148.08	1	F	10		
+0.0416	233.16		261.16	-0.096	261.16	2	I	9	1086.6	
	348.19		376.19	+0.0283	376.19	3	D	8	973.53	-0.046
	463.22		491.21		491.21	4	D	7	858.5	-0.047
	562.29		590.28		590.28	5	V	6	743.48	
	661.36		689.35	-0.057	689.35	6	V	5	644.41	+0.0177
	748.39		776.38	-0.017	776.38	7	S	4	545.34	+0.0817
	819.42		847.42	+0.1031	847.42	8	A	3	458.31	+0.0567
	918.49	+0.4643	473.75	-0.1	946.49	9	V	2	387.27	+0.1094
	1031.6		1059.6	+0.2204	1059.6	10	L	1	288.2	+0.1805
						11	R	0	175.12	-0.007

Scan number	934	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	209.19



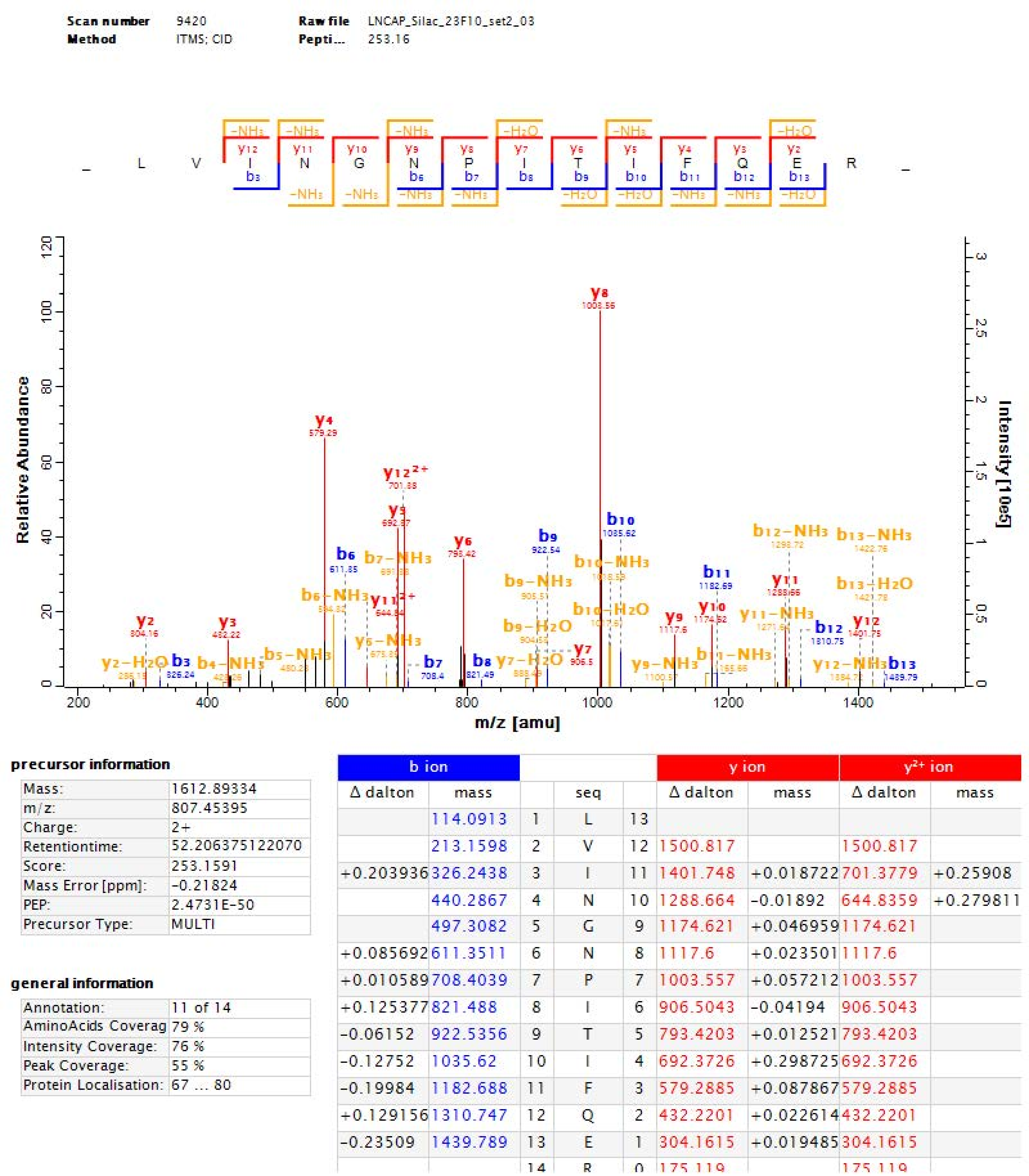
precursor information

Mass:	1287.58756
m/z:	644.80106
Charge:	2+
Retentiontime:	10.552663803100
Score:	209.1883
Mass Error [ppm]:	-0.1466
PEP:	3.2085E-15
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	67 %
Peak Coverage:	33 %
Protein Localisation:	47 ... 57

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	10				
+0.016	200.14	-0.038	228.13	2	N	9	1175.5	+0.0352	1175.5	
	313.22	-0.009	341.22	3	I	8	1061.5	-0.032	531.24	+0.2006
	400.26	-0.006	428.25	4	S	7	948.38	+0.003	948.38	
	529.3	+0.0317	557.29	5	E	6	861.35	+0.0058	861.35	
	586.32		614.31	6	G	5	732.31	+0.0023	732.31	
	700.36	+0.1052	728.36	7	N	4	675.29	+0.0785	675.29	
	860.39	-0.034	888.39	8	C	3	561.24	+0.0514	561.24	
	957.45		985.44	9	P	2	401.21	+0.0386	401.21	
	1086.5	-0.063	1114.5	10	E	1	304.16		304.16	
				11	R	0	175.12		175.12	



Scan number	9420	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	253.16

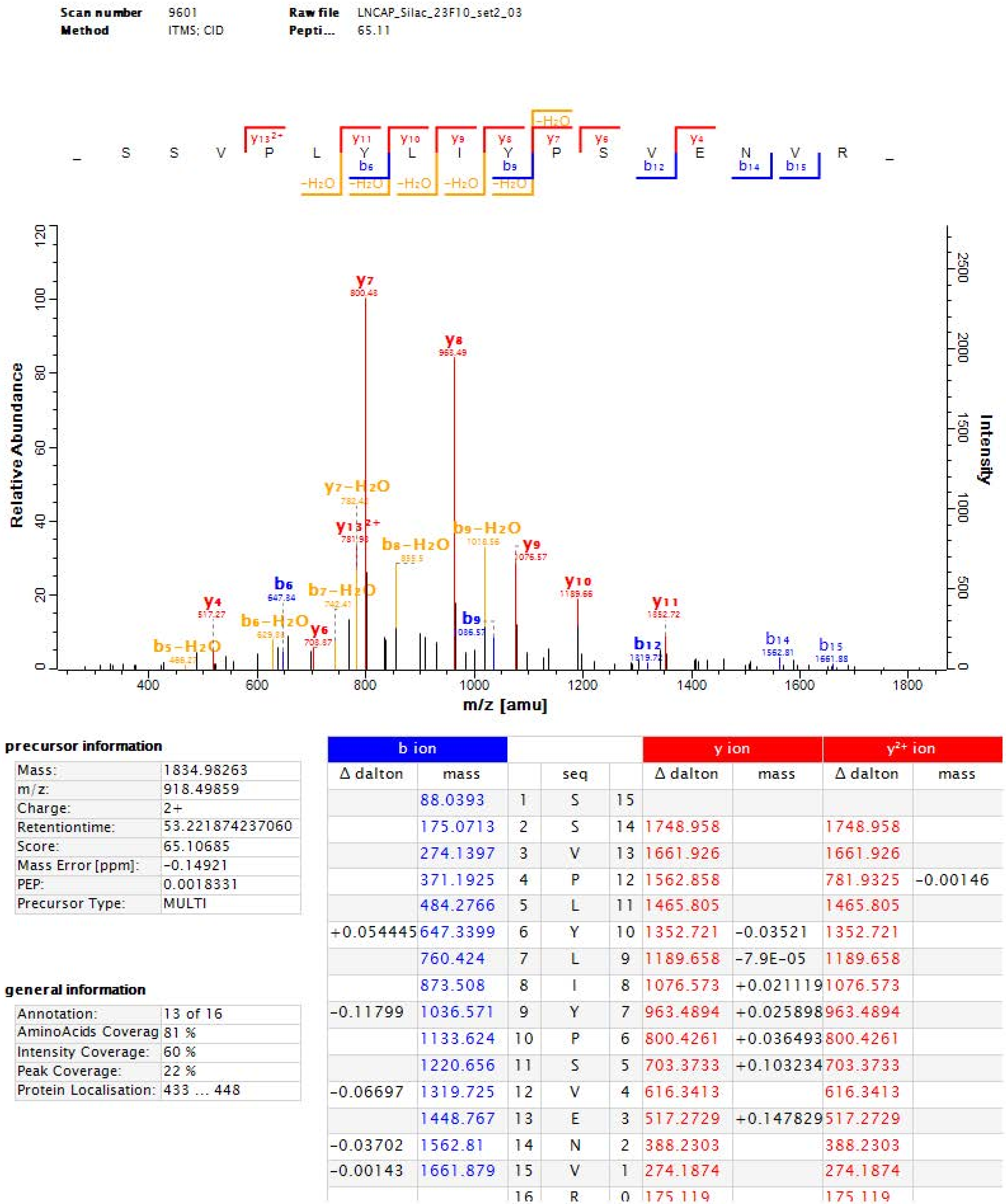
precursor information

Mass:	1612.89334
m/z:	807.45395
Charge:	2+
Retentiontime:	52.206375122070
Score:	253.1591
Mass Error [ppm]:	-0.21824
PEP:	2.4731E-50
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	76 %
Peak Coverage:	55 %
Protein Localisation:	67 ... 80

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	13				
	213.1598	2	V	12	1500.817		1500.817	
+0.203936	326.2438	3	I	11	1401.748	+0.018722	701.3779	+0.25908
	440.2867	4	N	10	1288.664	-0.01892	644.8359	+0.279811
	497.3082	5	G	9	1174.621	+0.046959	1174.621	
+0.085692	611.3511	6	N	8	1117.6	+0.023501	1117.6	
+0.010589	708.4039	7	P	7	1003.557	+0.057212	1003.557	
+0.125377	821.488	8	I	6	906.5043	-0.04194	906.5043	
-0.06152	922.5356	9	T	5	793.4203	+0.012521	793.4203	
-0.12752	1035.62	10	I	4	692.3726	+0.298725	692.3726	
-0.19984	1182.688	11	F	3	579.2885	+0.087867	579.2885	
+0.129156	1310.747	12	Q	2	432.2201	+0.022614	432.2201	
-0.23509	1439.789	13	E	1	304.1615	+0.019485	304.1615	
		14	R	0	175.119		175.119	



Scan number	9601	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	65.11

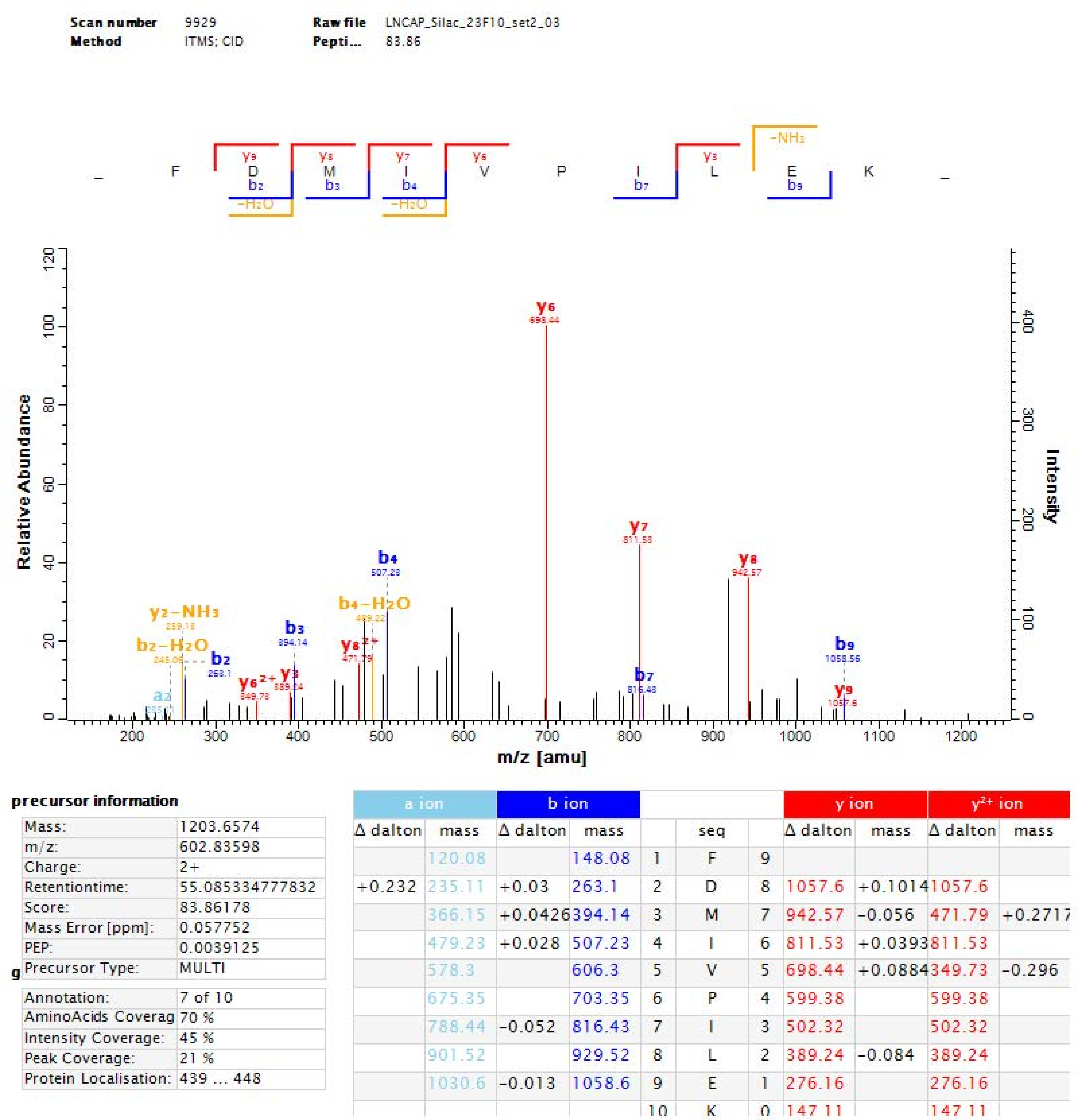
precursor information

Mass:	1834.98263
m/z:	918.49859
Charge:	2+
Retentiontime:	53.221874237060
Score:	65.10685
Mass Error [ppm]:	-0.14921
PEP:	0.0018331
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	60 %
Peak Coverage:	22 %
Protein Localisation:	433 ... 448

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	15				
	175.0713	2	S	14	1748.958		1748.958	
	274.1397	3	V	13	1661.926		1661.926	
	371.1925	4	P	12	1562.858		781.9325	-0.00146
	484.2766	5	L	11	1465.805		1465.805	
+0.054445	647.3399	6	Y	10	1352.721	-0.03521	1352.721	
	760.424	7	L	9	1189.658	-7.9E-05	1189.658	
	873.508	8	I	8	1076.573	+0.021119	1076.573	
-0.11799	1036.571	9	Y	7	963.4894	+0.025898	963.4894	
	1133.624	10	P	6	800.4261	+0.036493	800.4261	
	1220.656	11	S	5	703.3733	+0.103234	703.3733	
-0.06697	1319.725	12	V	4	616.3413		616.3413	
	1448.767	13	E	3	517.2729	+0.147829	517.2729	
-0.03702	1562.81	14	N	2	388.2303		388.2303	
-0.00143	1661.879	15	V	1	274.1874		274.1874	
		16	R	0	175.119		175.119	



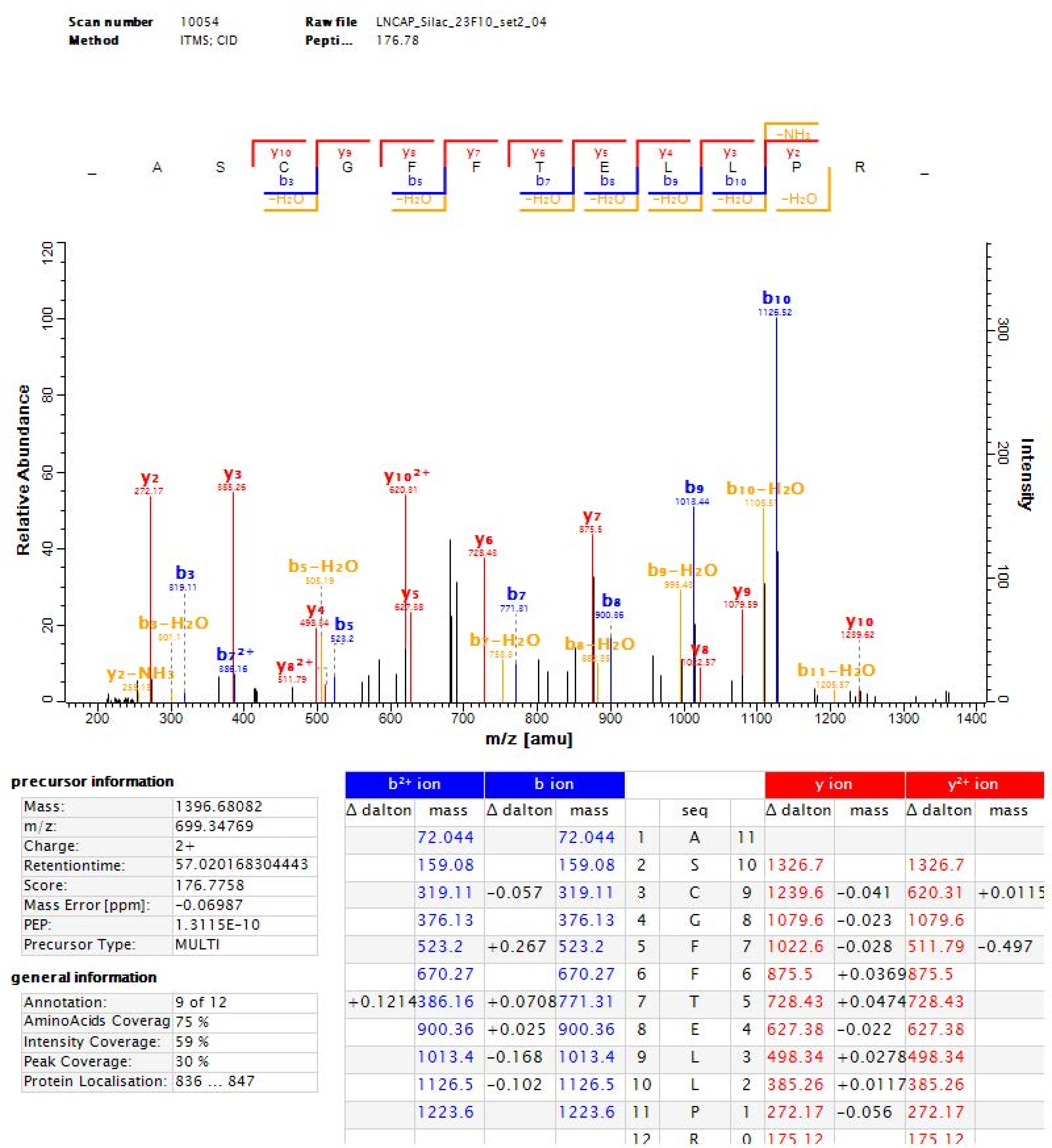
Scan number	9929	**Raw file**	LNCAP_Silac_23F10_set2_03
Method	ITMS; CID	**Pepti...**	83.86

precursor information

Mass:	1203.6574
m/z:	602.83598
Charge:	2+
Retentiontime:	55.085334777832
Score:	83.86178
Mass Error [ppm]:	0.057752
PEP:	0.0039125
Precursor Type:	MULTI

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	45 %
Peak Coverage:	21 %
Protein Localisation:	439 ... 448

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08		148.08	1	F	9				
+0.232	235.11	+0.03	263.1	2	D	8	1057.6	+0.1014	1057.6	
	366.15	+0.0426	394.14	3	M	7	942.57	-0.056	471.79	+0.2717
	479.23	+0.028	507.23	4	I	6	811.53	+0.0393	811.53	
	578.3		606.3	5	V	5	698.44	+0.0884	349.73	-0.296
	675.35		703.35	6	P	4	599.38		599.38	
	788.44	-0.052	816.43	7	I	3	502.32		502.32	
	901.52		929.52	8	L	2	389.24	-0.084	389.24	
	1030.6	-0.013	1058.6	9	E	1	276.16		276.16	
				10	K	0	147.11		147.11	



Scan number	10054	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	176.78

precursor information

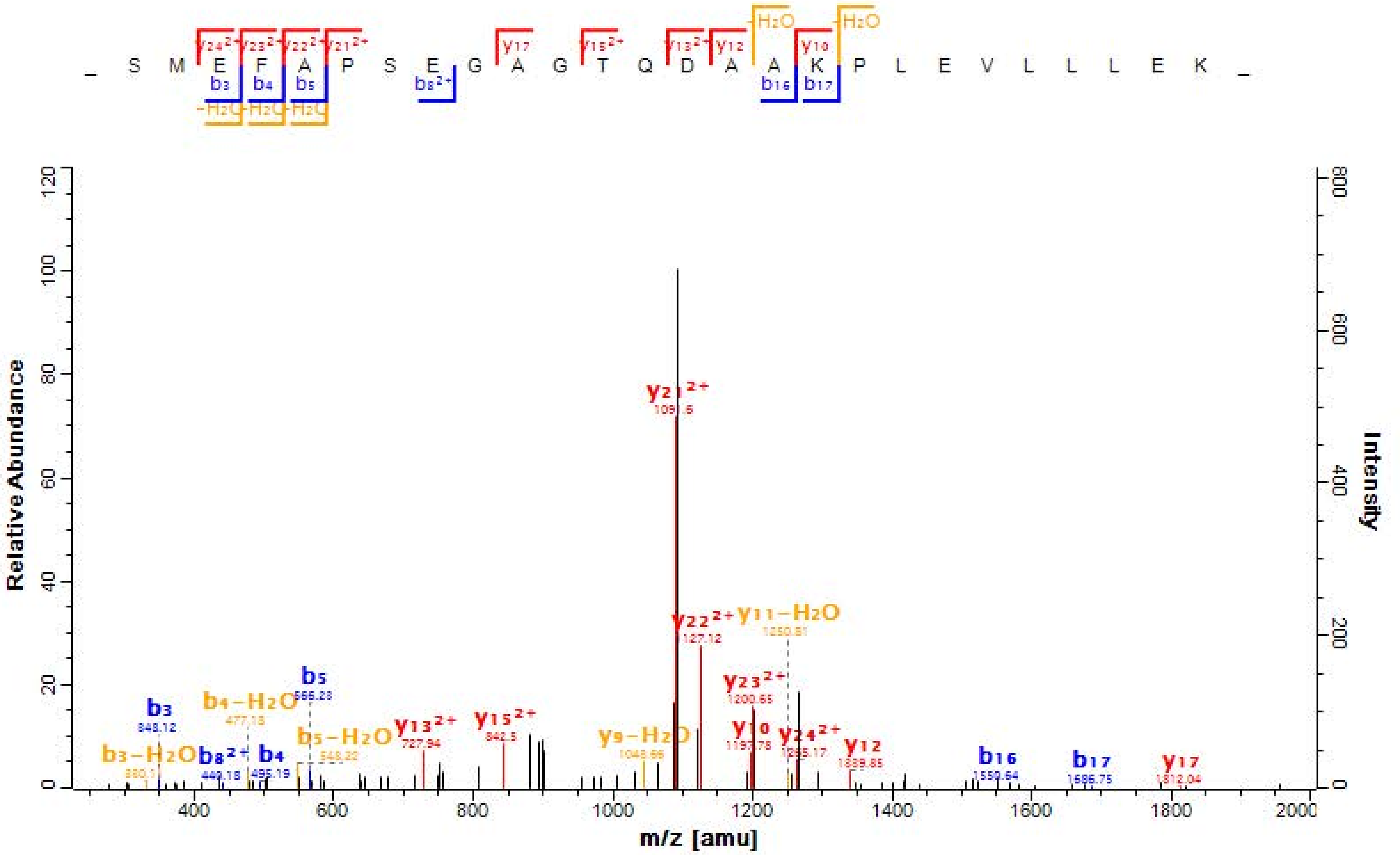
Mass:	1396.68082
m/z:	699.34769
Charge:	2+
Retentiontime:	57.020168304443
Score:	176.7758
Mass Error [ppm]:	-0.06987
PEP:	1.3115E-10
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	59 %
Peak Coverage:	30 %
Protein Localisation:	836 ... 847

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	11				
	159.08		159.08	2	S	10	1326.7		1326.7	
	319.11	-0.057	319.11	3	C	9	1239.6	-0.041	620.31	+0.0115
	376.13		376.13	4	G	8	1079.6	-0.023	1079.6	
	523.2	+0.267	523.2	5	F	7	1022.6	-0.028	511.79	-0.497
	670.27		670.27	6	F	6	875.5	+0.0369	875.5	
+0.1214	386.16	+0.0708	771.31	7	T	5	728.43	+0.0474	728.43	
	900.36	+0.025	900.36	8	E	4	627.38	-0.022	627.38	
	1013.4	-0.168	1013.4	9	L	3	498.34	+0.0278	498.34	
	1126.5	-0.102	1126.5	10	L	2	385.26	+0.0117	385.26	
	1223.6		1223.6	11	P	1	272.17	-0.056	272.17	
				12	R	0	175.12		175.12	

Scan number	10279	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	63.17



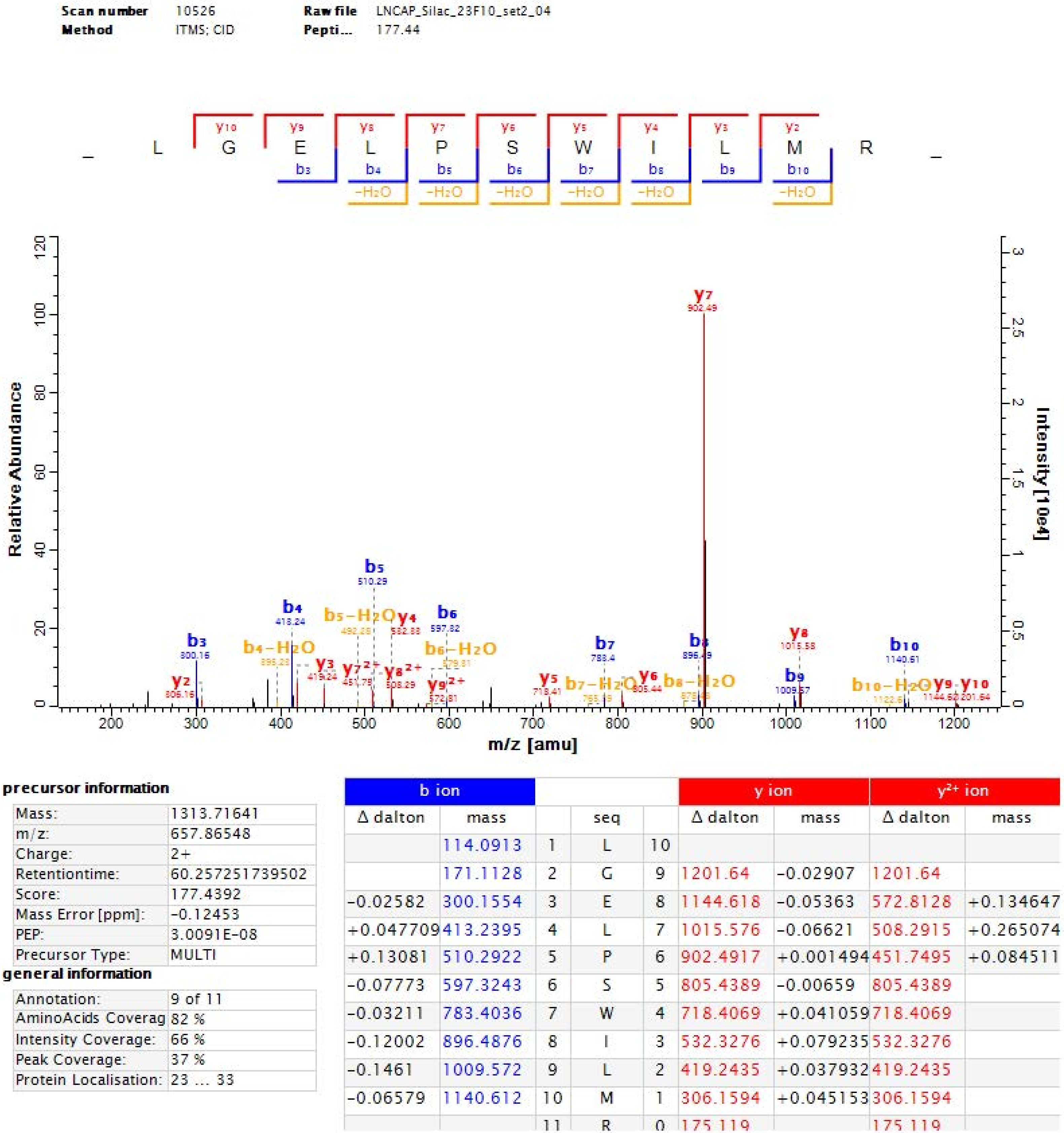
precursor information

Mass:	2730.38001
m/z:	911.13395
Charge:	3+
Retentiontime:	58.537189483642
Score:	63.16536
Mass Error [ppm]:	0.51346
PEP:	4.4306E-05
Precursor Type:	MULTI

general information

Annotation:	12 of 26
AminoAcids Coverag	46 %
Intensity Coverage:	35 %
Peak Coverage:	22 %
Protein Localisation:	374 ... 399

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	25				
	219.08		219.08	2	M	24	2660.4		2660.4	
	348.12	+0.2817	348.12	3	E	23	2529.3		1265.2	-0.317
	495.19	+0.3984	495.19	4	F	22	2400.3		1200.7	-0.038
	566.23	+0.0809	566.23	5	A	21	2253.2		1127.1	+0.1707
	663.28		663.28	6	P	20	2182.2		1091.6	-0.045
	750.31		750.31	7	S	19	2085.1		2085.1	
-0.024	440.18		879.36	8	E	18	1998.1		1998.1	
	936.38		936.38	9	G	17	1869.1		1869.1	
	1007.4		1007.4	10	A	16	1812	+0.4727	1812	
	1064.4		1064.4	11	G	15	1741		1741	
	1165.5		1165.5	12	T	14	1684		842.5	+0.0804
	1293.5		1293.5	13	Q	13	1582.9		1582.9	
	1408.6		1408.6	14	D	12	1454.9		727.94	+0.2444
	1479.6		1479.6	15	A	11	1339.9	-0.138	1339.9	
	1550.6	-0.166	1550.6	16	A	10	1268.8		1268.8	
	1686.8	-0.279	1686.8	17	K	9	1197.8	+0.2466	1197.8	
	1783.8		1783.8	18	P	8	1061.7		1061.7	
	1896.9		1896.9	19	L	7	964.62		964.62	
	2025.9		2025.9	20	E	6	851.53		851.53	
	2125		2125	21	V	5	722.49		722.49	
	2238.1		2238.1	22	L	4	623.42		623.42	
	2351.2		2351.2	23	L	3	510.34		510.34	
	2464.3		2464.3	24	L	2	397.25		397.25	
	2593.3		2593.3	25	E	1	284.17		284.17	
				26	K	0	155.13		155.13	



Scan number	10526	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	177.44

precursor information

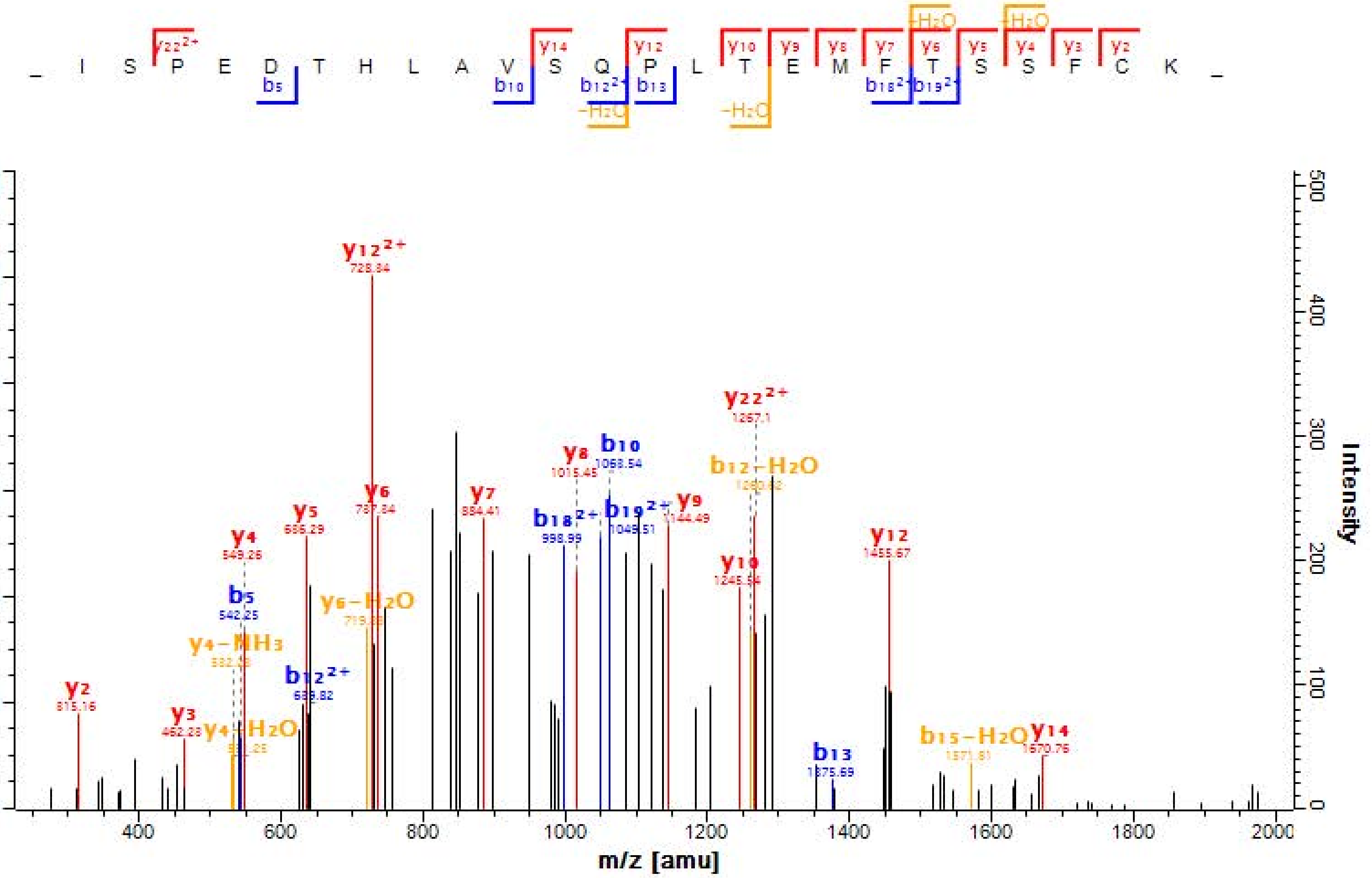
Mass:	1313.71641
m/z:	657.86548
Charge:	2+
Retentiontime:	60.257251739502
Score:	177.4392
Mass Error [ppm]:	-0.12453
PEP:	3.0091E-08
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	66 %
Peak Coverage:	37 %
Protein Localisation:	23 ... 33

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	10				
	171.1128	2	G	9	1201.64	-0.02907	1201.64	
-0.02582	300.1554	3	E	8	1144.618	-0.05363	572.8128	+0.134647
+0.047709	413.2395	4	L	7	1015.576	-0.06621	508.2915	+0.265074
+0.13081	510.2922	5	P	6	902.4917	+0.001494	451.7495	+0.084511
-0.07773	597.3243	6	S	5	805.4389	-0.00659	805.4389	
-0.03211	783.4036	7	W	4	718.4069	+0.041059	718.4069	
-0.12002	896.4876	8	I	3	532.3276	+0.079235	532.3276	
-0.1461	1009.572	9	L	2	419.2435	+0.037932	419.2435	
-0.06579	1140.612	10	M	1	306.1594	+0.045153	306.1594	
		11	R	0	175.119		175.119	

Scan number	10568	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	84.18



precursor information

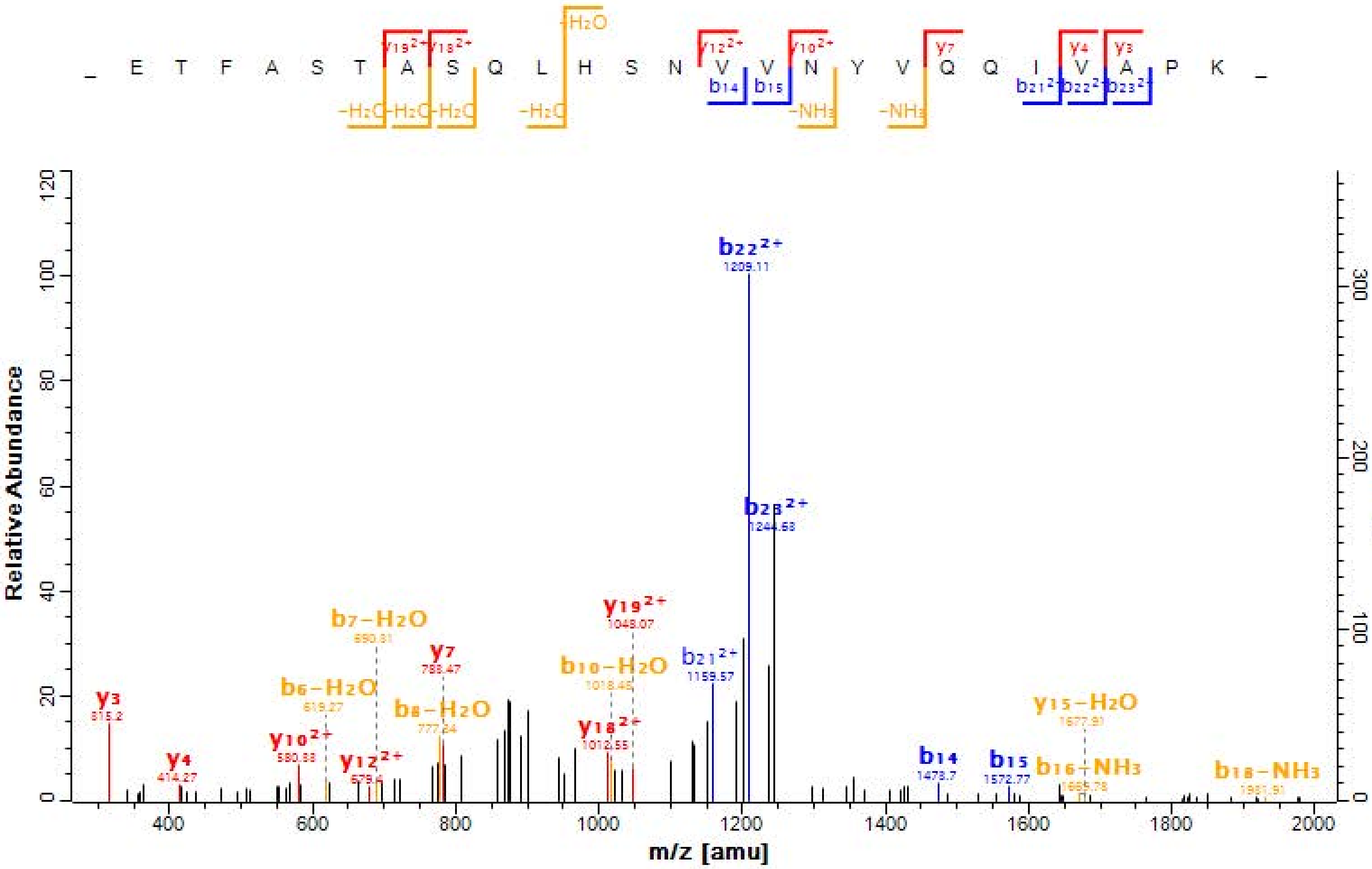
Mass:	2724.27952
m/z:	909.10045
Charge:	3+
Retentiontime:	60.564037322998
Score:	84.18081
Mass Error [ppm]:	0.73692
PEP:	7.0891E-06
Precursor Type:	MULTI

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	I	23				
	201.12		201.12	2	S	22	2620.2		2620.2	
	298.18		298.18	3	P	21	2533.2		1267.1	-0.153
	427.22		427.22	4	E	20	2436.1		2436.1	
	542.25	+0.025	542.25	5	D	19	2307.1		2307.1	
	643.29		643.29	6	T	18	2192.1		2192.1	
	780.35		780.35	7	H	17	2091		2091	
	893.44		893.44	8	L	16	1954		1954	
	964.47		964.47	9	A	15	1840.9		1840.9	
	1063.5	+0.122	1063.5	10	V	14	1769.8		1769.8	
	1150.6		1150.6	11	S	13	1670.8	+0.2697	1670.8	
-0.038	639.82		1278.6	12	Q	12	1583.7		1583.7	
	1375.7	-0.306	1375.7	13	P	11	1455.7	-0.116	728.34	+0.4026
	1488.8		1488.8	14	L	10	1358.6		1358.6	
	1589.8		1589.8	15	T	9	1245.5	-0.029	1245.5	
	1718.9		1718.9	16	E	8	1144.5	+0.0122	1144.5	
	1849.9		1849.9	17	M	7	1015.4	-0.03	1015.4	
+0.4372	998.99		1997	18	F	6	884.41	-0.005	884.41	
+0.2507	1049.5		2098	19	T	5	737.34	-0.089	737.34	
	2185		2185	20	S	4	636.29	+0.0086	636.29	
	2272.1		2272.1	21	S	3	549.26	+0.0583	549.26	
	2419.1		2419.1	22	F	2	462.23	+0.0671	462.23	
	2579.2		2579.2	23	C	1	315.16	+0.1872	315.16	
				24	K	0	155.13		155.13	

general information

Annotation:	15 of 24
AminoAcids Coverag	62 %
Intensity Coverage:	41 %
Peak Coverage:	26 %
Protein Localisation:	45 ... 68

Scan number	10998	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	39.09



precursor information

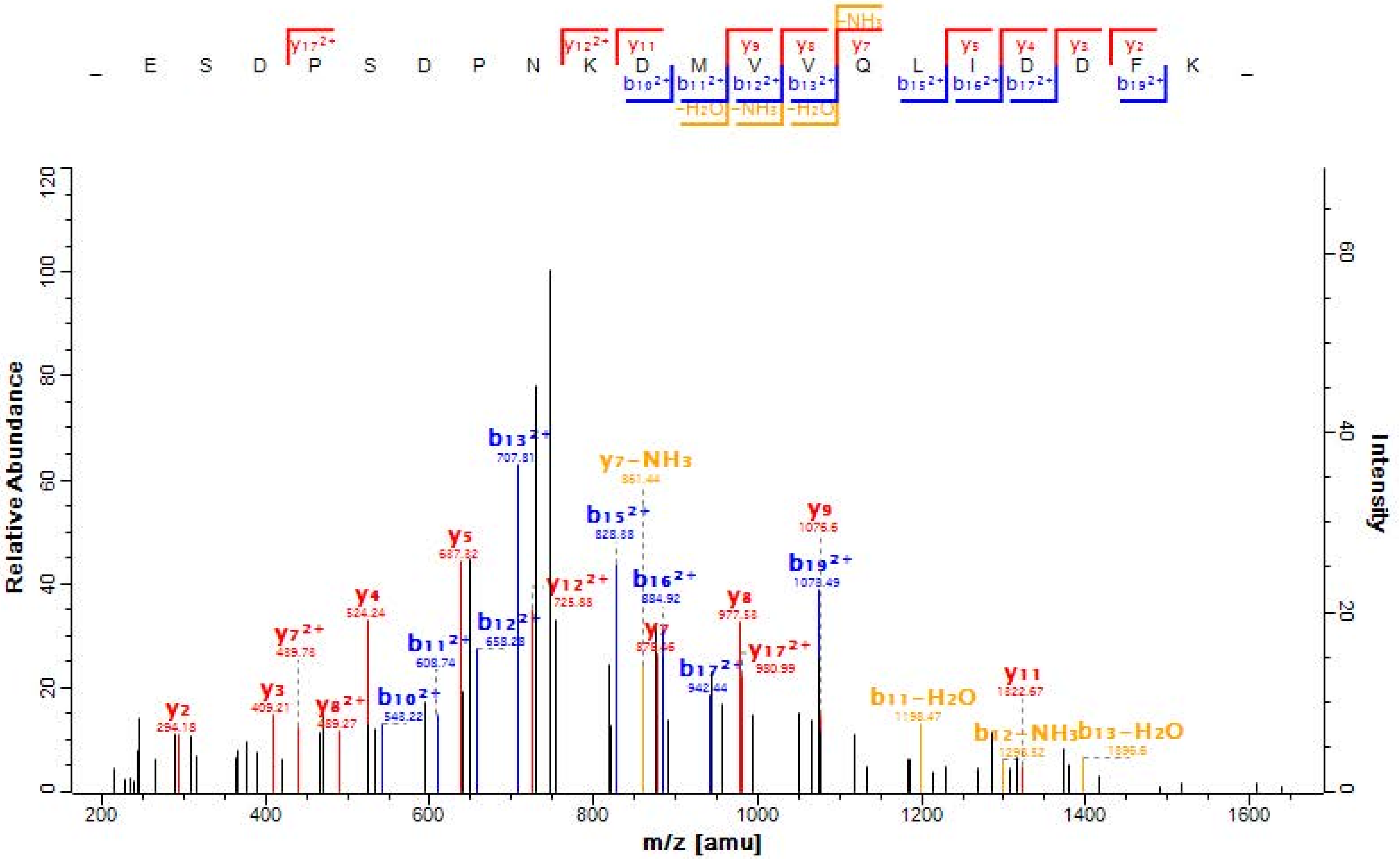
Mass:	2730.39912
m/z:	911.14032
Charge:	3+
Retentiontime:	64.100265502929
Score:	39.08555
Mass Error [ppm]:	0.52252
PEP:	0.011744
Precursor Type:	MULTI

general information

Annotation:	13 of 25
AminoAcids Coverag	52 %
Intensity Coverage:	37 %
Peak Coverage:	20 %
Protein Localisation:	632 ... 656

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	24				
	231.1		231.1	2	T	23	2602.4		2602.4	
	378.17		378.17	3	F	22	2501.3		2501.3	
	449.2		449.2	4	A	21	2354.2		2354.2	
	536.24		536.24	5	S	20	2283.2		2283.2	
	637.28		637.28	6	T	19	2196.2		2196.2	
	708.32		708.32	7	A	18	2095.1		1048.1	+0.145
	795.35		795.35	8	S	17	2024.1		1012.5	+0.0106
	923.41		923.41	9	Q	16	1937.1		1937.1	
	1036.5		1036.5	10	L	15	1809		1809	
	1173.6		1173.6	11	H	14	1695.9		1695.9	
	1260.6		1260.6	12	S	13	1558.9		1558.9	
	1374.6		1374.6	13	N	12	1471.8		1471.8	
	1473.7	-0.009	1473.7	14	V	11	1357.8		679.4	-0.472
	1572.8	+0.0959	1572.8	15	V	10	1258.7		1258.7	
	1686.8		1686.8	16	N	9	1159.6		580.33	+0.0866
	1849.9		1849.9	17	Y	8	1045.6		1045.6	
	1948.9		1948.9	18	V	7	882.54		882.54	
	2077		2077	19	Q	6	783.47	-0.088	783.47	
	2205.1		2205.1	20	Q	5	655.41		655.41	
-0.017	1159.6		2318.1	21	I	4	527.36		527.36	
+0.1954	1209.1		2417.2	22	V	3	414.27	+0.2716	414.27	
-0.087	1244.6		2488.2	23	A	2	315.2	+0.0224	315.2	
	2585.3		2585.3	24	P	1	244.17		244.17	
				25	K	0	147.11		147.11	

Scan number	11067	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	80.54



precursor information

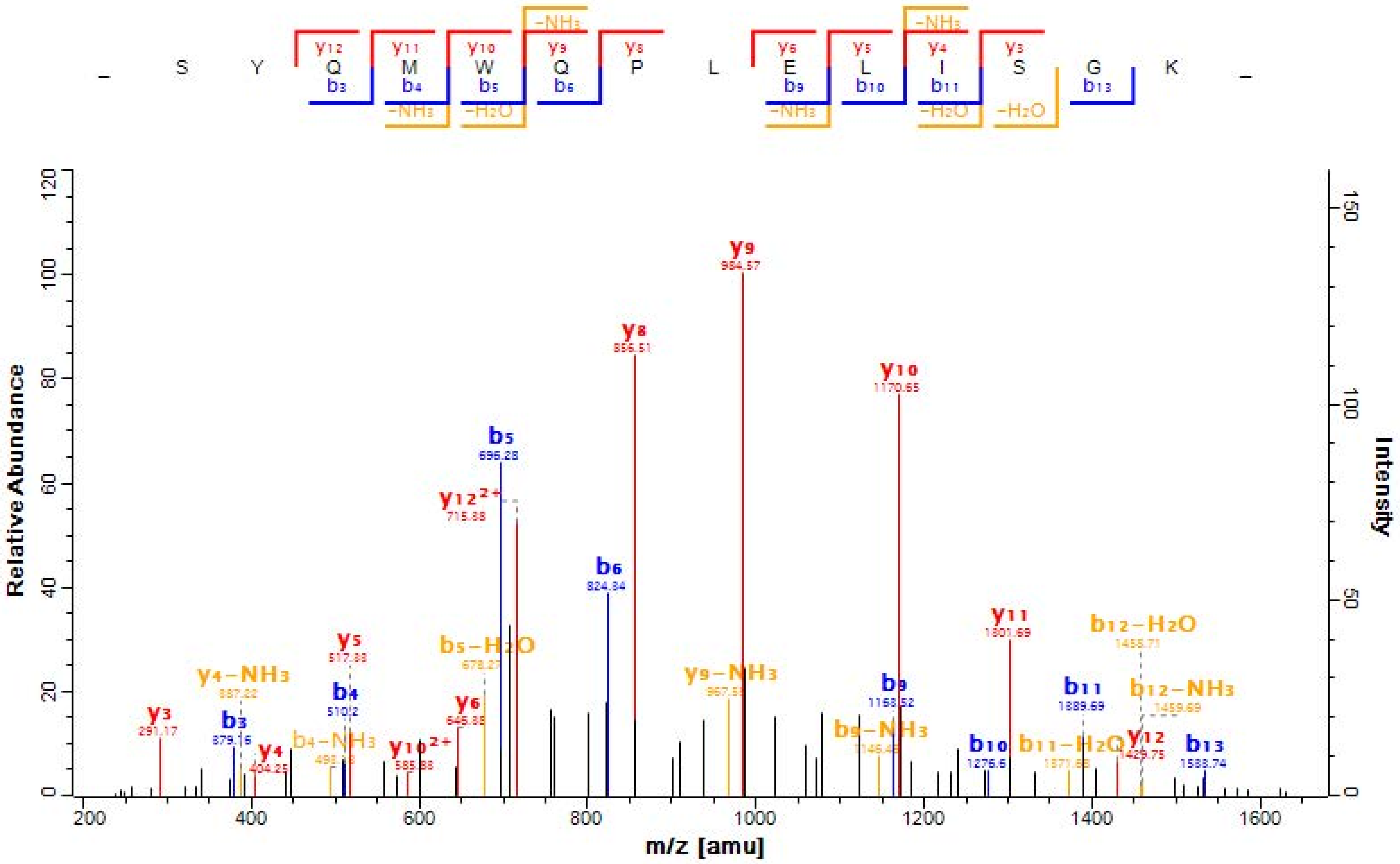
Mass:	2291.0634
m/z:	764.69508
Charge:	3+
Retentiontime:	64.729248046875
Score:	80.54491
Mass Error [ppm]:	0.28551
PEP:	8.5693E-05
Precursor Type:	MULTI

general information

Annotation:	12 of 20
AminoAcids Coverag	60 %
Intensity Coverage:	42 %
Peak Coverage:	30 %
Protein Localisation:	176 ... 195

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	19				
	217.08		217.08	2	S	18	2163		2163	
	332.11		332.11	3	D	17	2076		2076	
	429.16		429.16	4	P	16	1961		980.99	+0.4235
	516.19		516.19	5	S	15	1863.9		1863.9	
	631.22		631.22	6	D	14	1776.9		1776.9	
	728.27		728.27	7	P	13	1661.9		1661.9	
	842.32		842.32	8	N	12	1564.8		1564.8	
	970.41		970.41	9	K	11	1450.8		725.88	-0.463
-0.02	543.22		1085.4	10	D	10	1322.7	-0.091	1322.7	
+0.4423	608.74		1216.5	11	M	9	1207.6		1207.6	
+0.2843	658.28		1315.5	12	V	8	1076.6	-0.249	1076.6	
-0.083	707.81		1414.6	13	V	7	977.53	-0.009	489.27	+0.0716
	1542.7		1542.7	14	Q	6	878.46	+0.1225	439.73	+0.4468
+0.0934	828.38		1655.8	15	L	5	750.4		750.4	
+0.2261	884.92		1768.8	16	I	4	637.32	+0.1777	637.32	
-0.035	942.44		1883.9	17	D	3	524.24	+0.0654	524.24	
	1998.9		1998.9	18	D	2	409.21	+0.038	409.21	
-0.097	1073.5		2146	19	F	1	294.18	+0.2599	294.18	
				20	K	0	147.11		147.11	

Scan number	11082	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	127.57



precursor information

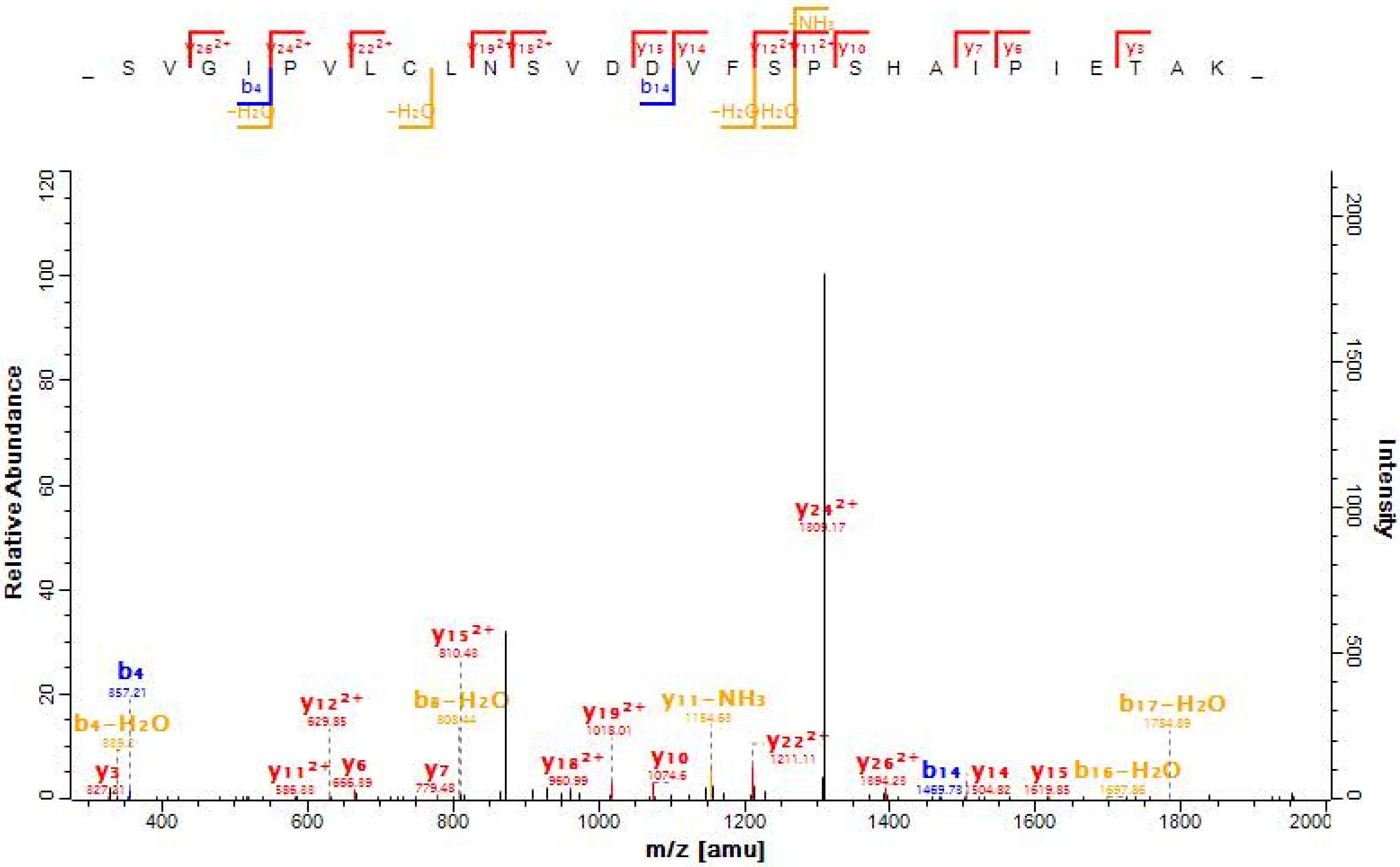
Mass:	1678.8401
m/z:	840.42733
Charge:	2+
Retentiontime:	64.871635437011
Score:	127.5703
Mass Error [ppm]:	0.72894
PEP:	1.0697E-08
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	56 %
Peak Coverage:	31 %
Protein Localisation:	190 ... 203

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	13				
	251.1026	2	Y	12	1592.814		1592.814	
-0.02077	379.1612	3	Q	11	1429.751	-0.16059	715.379	+0.209647
+0.261928	510.2017	4	M	10	1301.692	-0.10323	1301.692	
-0.1073	696.281	5	W	9	1170.652	-0.03369	585.8295	+0.185387
-0.0396	824.3396	6	Q	8	984.5724	-0.01719	984.5724	
	921.3923	7	P	7	856.5138	+0.101938	856.5138	
	1034.476	8	L	6	759.4611		759.4611	
-0.11508	1163.519	9	E	5	646.377	-0.12305	646.377	
-0.48637	1276.603	10	L	4	517.3344	-0.04731	517.3344	
+0.074706	1389.687	11	I	3	404.2504	+0.186468	404.2504	
	1476.719	12	S	2	291.1663	-0.03892	291.1663	
+0.07346	1533.741	13	G	1	204.1343		204.1343	
		14	K	0	147.1128		147.1128	

Scan number	11177	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	50.5



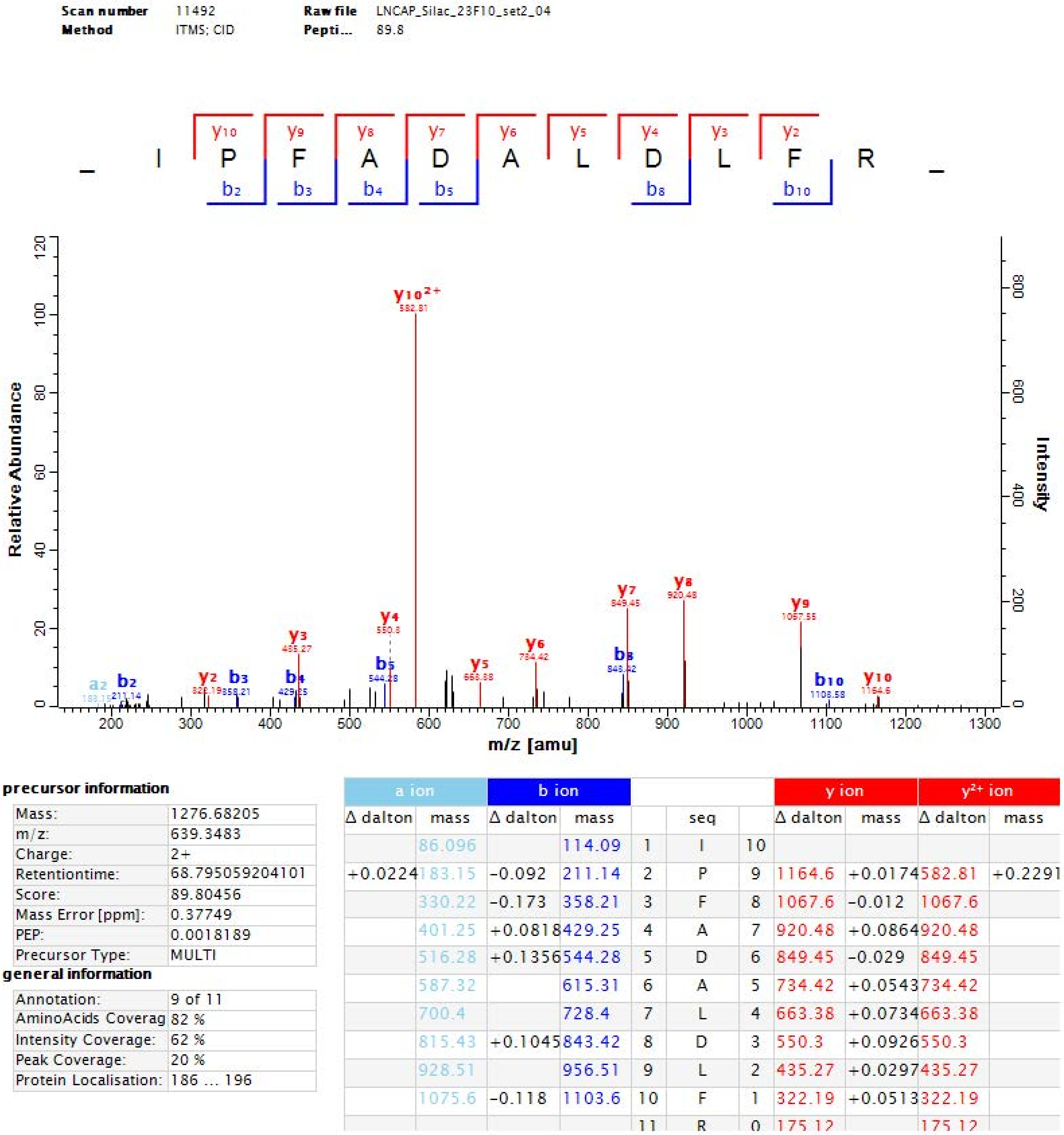
precursor information

Mass:	2964.52622
m/z:	989.18268
Charge:	3+
Retentiontime:	65.777084350585
Score:	50.4978
Mass Error [ppm]:	-0.14762
PEP:	0.001785
Precursor Type:	MULTI

general information

Annotation:	17 of 28
AminoAcids Coverag	61 %
Intensity Coverage:	27 %
Peak Coverage:	21 %
Protein Localisation:	333 ... 360

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	27				
	187.1077	2	V	26	2886.516		2886.516	
	244.1292	3	G	25	2787.448		1394.227	+0.244073
-0.05962	357.2132	4	I	24	2730.426		2730.426	
	454.266	5	P	23	2617.342		1309.175	-0.12138
	553.3344	6	V	22	2520.289		2520.289	
	666.4185	7	L	21	2421.221		1211.114	+0.191289
	826.4491	8	C	20	2308.137		2308.137	
	939.5332	9	L	19	2148.106		2148.106	
	1053.576	10	N	18	2035.022		1018.015	+0.101468
	1140.608	11	S	17	1920.979		960.9933	+0.202521
	1239.677	12	V	16	1833.947		1833.947	
	1354.704	13	D	15	1734.879		1734.879	
-0.19567	1469.73	14	D	14	1619.852	-0.14181	810.4296	-0.30324
	1568.799	15	V	13	1504.825	-0.41712	1504.825	
	1715.867	16	F	12	1405.757		1405.757	
	1802.899	17	S	11	1258.688		629.8477	+0.353715
	1899.952	18	P	10	1171.656		586.3317	+0.045144
	1986.984	19	S	9	1074.603	+0.005308	1074.603	
	2124.043	20	H	8	987.5713		987.5713	
	2195.08	21	A	7	850.5124		850.5124	
	2308.164	22	I	6	779.4753	+0.229066	779.4753	
	2405.217	23	P	5	666.3912	-0.01023	666.3912	
	2518.301	24	I	4	569.3385		569.3385	
	2647.344	25	E	3	456.2544		456.2544	
	2748.391	26	T	2	327.2118	+0.168545	327.2118	
	2819.428	27	A	1	226.1641		226.1641	
		28	K	0	155.127		155.127	



Scan number	11492	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	89.8

precursor information

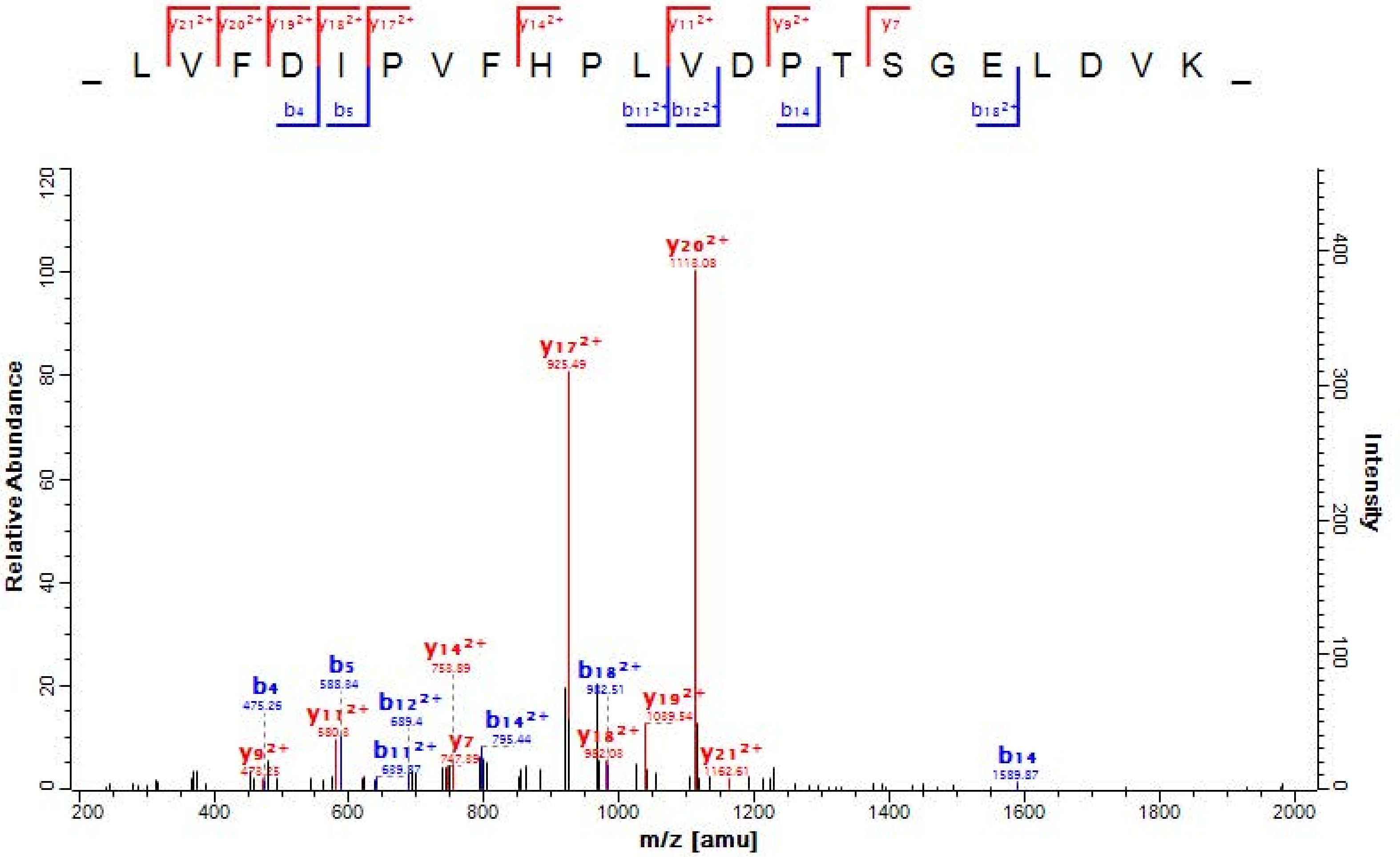
Mass:	1276.68205
m/z:	639.3483
Charge:	2+
Retentiontime:	68.795059204101
Score:	89.80456
Mass Error [ppm]:	0.37749
PEP:	0.0018189
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	62 %
Peak Coverage:	20 %
Protein Localisation:	186 ... 196

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	10				
+0.0224	183.15	-0.092	211.14	2	P	9	1164.6	+0.0174	582.81	+0.2291
	330.22	-0.173	358.21	3	F	8	1067.6	-0.012	1067.6	
	401.25	+0.0818	429.25	4	A	7	920.48	+0.0864	920.48	
	516.28	+0.1356	544.28	5	D	6	849.45	-0.029	849.45	
	587.32		615.31	6	A	5	734.42	+0.0543	734.42	
	700.4		728.4	7	L	4	663.38	+0.0734	663.38	
	815.43	+0.1045	843.42	8	D	3	550.3	+0.0926	550.3	
	928.51		956.51	9	L	2	435.27	+0.0297	435.27	
	1075.6	-0.118	1103.6	10	F	1	322.19	+0.0513	322.19	
				11	R	0	175.12		175.12	

Scan number	11530	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	51.09



precursor information

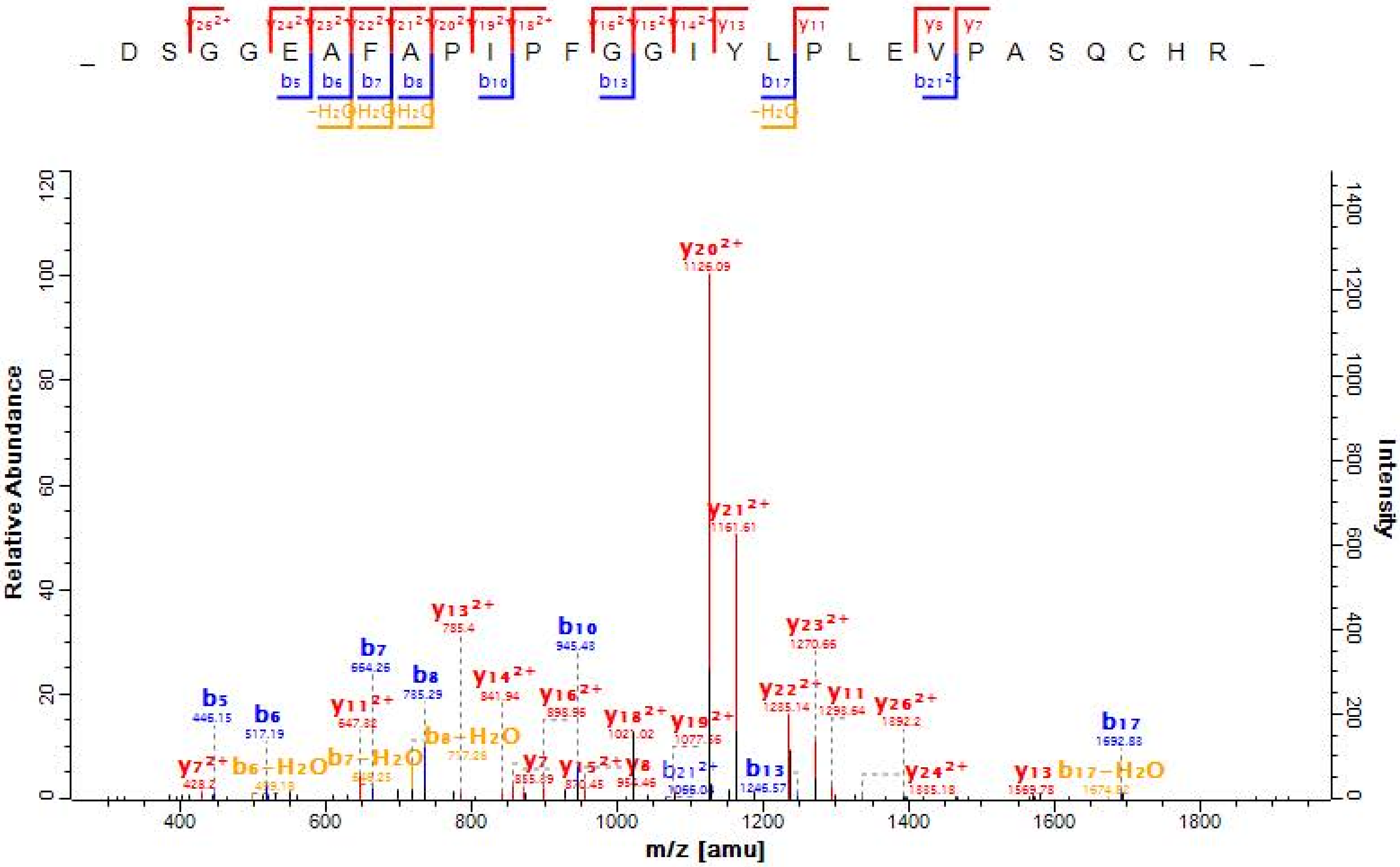
Mass:	2436.29525
m/z:	813.10569
Charge:	3+
Retentiontime:	69.183265686035
Score:	51.08867
Mass Error [ppm]:	0.48552
PEP:	0.004197
Precursor Type:	MULTI

general information

Annotation:	12 of 22
AminoAcids Coverag	55 %
Intensity Coverage:	53 %
Peak Coverage:	17 %
Protein Localisation:	140 ... 161

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	21				
	213.16		213.16	2	V	20	2324.2		1162.6	+0.02
	360.23		360.23	3	F	19	2225.1		1113.1	+0.2496
	475.26	+0.3643	475.26	4	D	18	2078.1		1039.5	+0.0059
	588.34	-0.048	588.34	5	I	17	1963.1		982.03	-0.068
	685.39		685.39	6	P	16	1850		925.49	+0.2494
	784.46		784.46	7	V	15	1752.9		1752.9	
	931.53		931.53	8	F	14	1653.8		1653.8	
	1068.6		1068.6	9	H	13	1506.8		753.89	-0.033
	1165.6		1165.6	10	P	12	1369.7		1369.7	
+0.4942	639.87		1278.7	11	L	11	1272.7		1272.7	
-0.186	689.4		1377.8	12	V	10	1159.6		580.3	-0.063
	1492.8		1492.8	13	D	9	1060.5		1060.5	
+0	795.44	+0.1397	1589.9	14	P	8	945.49		473.25	+0.2806
	1690.9		1690.9	15	T	7	848.44		848.44	
	1778		1778	16	S	6	747.39	+0.1127	747.39	
	1835		1835	17	G	5	660.36		660.36	
+0.1937	982.51		1964	18	E	4	603.33		603.33	
	2077.1		2077.1	19	L	3	474.29		474.29	
	2192.1		2192.1	20	D	2	361.21		361.21	
	2291.2		2291.2	21	V	1	246.18		246.18	
				22	K	0	147.11		147.11	

Scan number	11577	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	142.99



precursor information

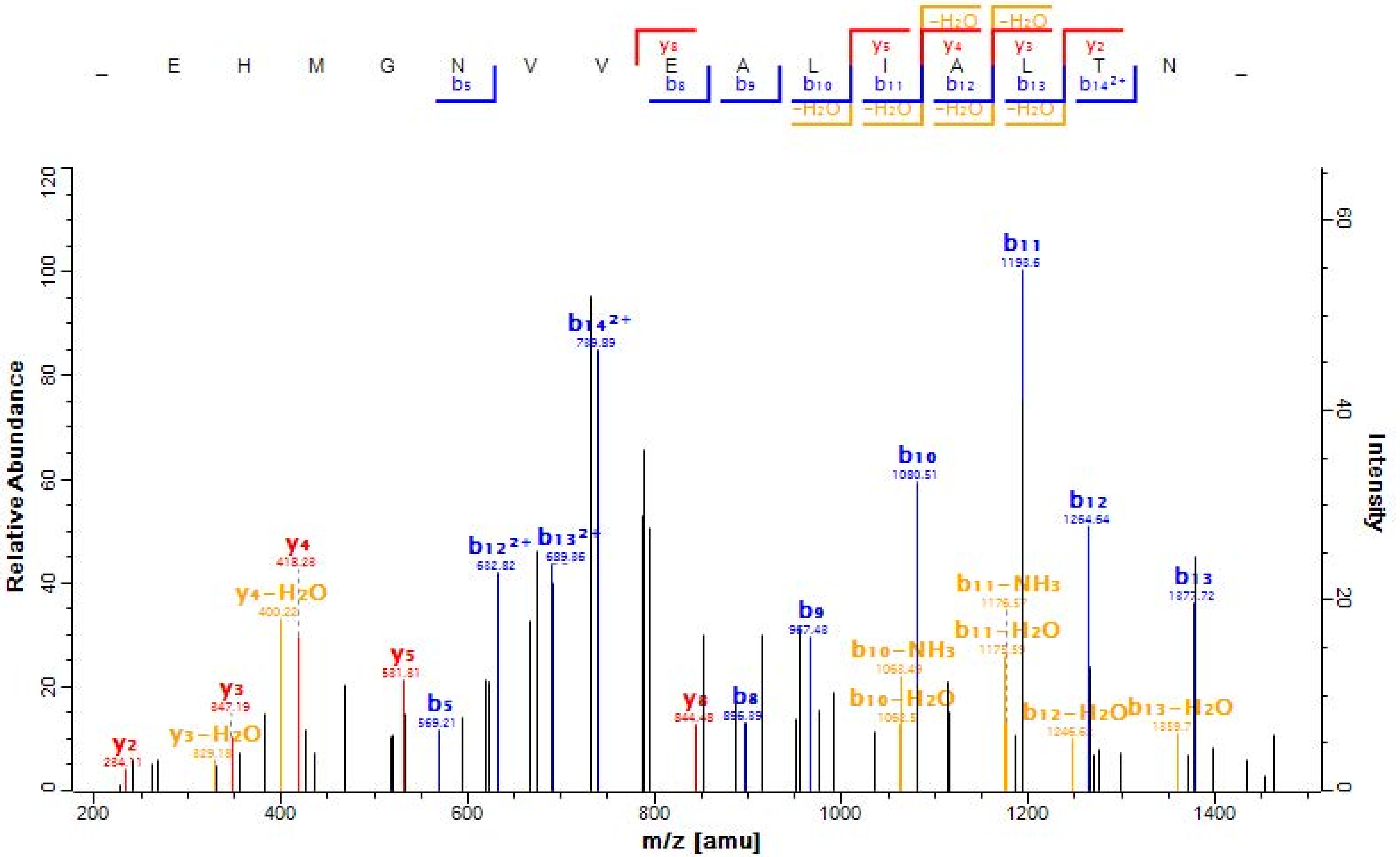
Mass:	2984.44881
m/z:	995.82355
Charge:	3+
Retentiontime:	69.657081604003
Score:	142.9873
Mass Error [ppm]:	-0.087988
PEP:	5.5879E-28
Precursor Type:	MULTI

general information

Annotation:	17 of 28
AminoAcids Coverag	61 %
Intensity Coverage:	70 %
Peak Coverage:	33 %
Protein Localisation:	320 ... 347

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	27				
	203.07		203.07	2	S	26	2870.4		2870.4	
	260.09		260.09	3	G	25	2783.4		1392.2	-0.152
	317.11		317.11	4	G	24	2726.4		2726.4	
	446.15	+0.015	446.15	5	E	23	2669.4		1335.2	+0.1009
	517.19	+0.0882	517.19	6	A	22	2540.3		1270.7	+0.1957
	664.26	+0.1086	664.26	7	F	21	2469.3		1235.1	+0.2055
	735.29	+0.0973	735.29	8	A	20	2322.2		1161.6	+0.2567
	832.35		832.35	9	P	19	2251.2		1126.1	+0.2308
	945.43	-0.078	945.43	10	I	18	2154.1		1077.6	+0.2509
	1042.5		1042.5	11	P	17	2041		1021	-0.014
	1189.6		1189.6	12	F	16	1944		1944	
	1246.6	-0.028	1246.6	13	G	15	1796.9		898.96	+0.3491
	1303.6		1303.6	14	G	14	1739.9		870.45	+0.4264
	1416.7		1416.7	15	I	13	1682.9		841.94	-0.43
	1579.7		1579.7	16	Y	12	1569.8	+0.0515	785.4	+0.1956
	1692.8	+0.1544	1692.8	17	L	11	1406.7		1406.7	
	1789.9		1789.9	18	P	10	1293.6	+0.1607	647.32	+0.1214
	1903		1903	19	L	9	1196.6		1196.6	
	2032		2032	20	E	8	1083.5		1083.5	
-0.089	1066		2131.1	21	V	7	954.46	+0.0707	954.46	
	2228.1		2228.1	22	P	6	855.39	+0.1508	428.2	+0.0449
	2299.2		2299.2	23	A	5	758.34		758.34	
	2386.2		2386.2	24	S	4	687.3		687.3	
	2514.3		2514.3	25	Q	3	600.27		600.27	
	2674.3		2674.3	26	C	2	472.21		472.21	
	2811.3		2811.3	27	H	1	312.18		312.18	
				28	R	0	175.12		175.12	

Scan number	11792	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	136.33



precursor information

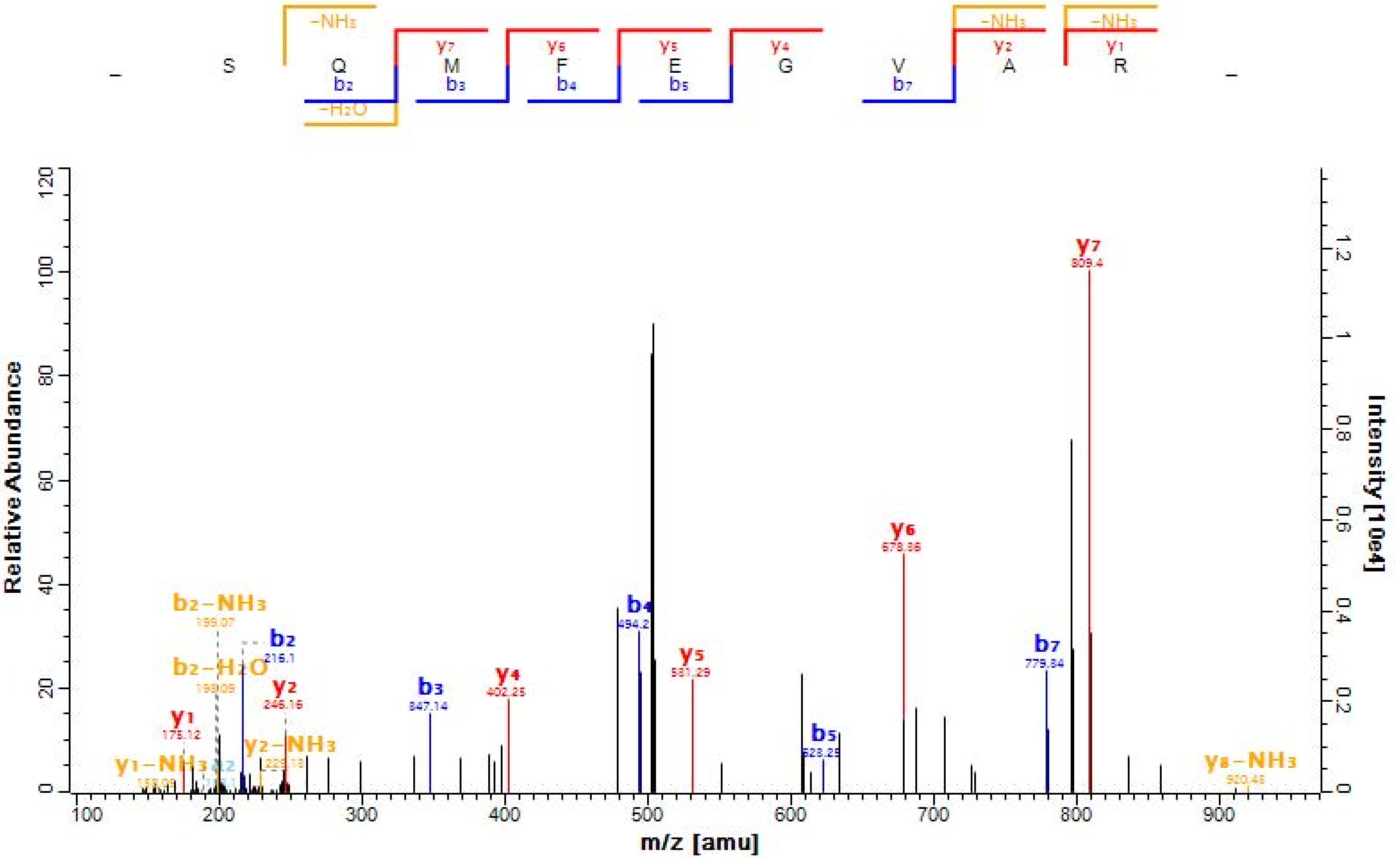
Mass:	1609.81296
m/z:	805.91376
Charge:	2+
Retentiontime:	71.957252502441
Score:	136.3266
Mass Error [ppm]:	-0.26682
PEP:	7.3503E-07
Precursor Type:	ISO

general information

Annotation:	8 of 15
AminoAcids Coverag	53 %
Intensity Coverage:	38 %
Peak Coverage:	31 %
Protein Localisation:	161 ... 175

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	130.0499		130.0499	1	E	14		
	267.1088		267.1088	2	H	13	1481.778	
	398.1493		398.1493	3	M	12	1344.719	
	455.1707		455.1707	4	G	11	1213.679	
	569.2137	-0.12259	569.2137	5	N	10	1156.657	
	668.2821		668.2821	6	V	9	1042.614	
	767.3505		767.3505	7	V	8	943.5459	
	896.3931	-0.06544	896.3931	8	E	7	844.4775	+0.063007
	967.4302	+0.058578	967.4302	9	A	6	715.4349	
	1080.514	-0.09812	1080.514	10	L	5	644.3978	
	1193.598	-0.13958	1193.598	11	I	4	531.3137	+0.094026
+0.295527	632.8214	+0.015323	1264.635	12	A	3	418.2296	-0.03822
+0.254899	689.3634	-0.14906	1377.719	13	L	2	347.1925	+0.292352
+0.034099	739.8872		1478.767	14	T	1	234.1084	-0.21497
				15	N	0	133.0608	

Scan number	2018	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	54.78

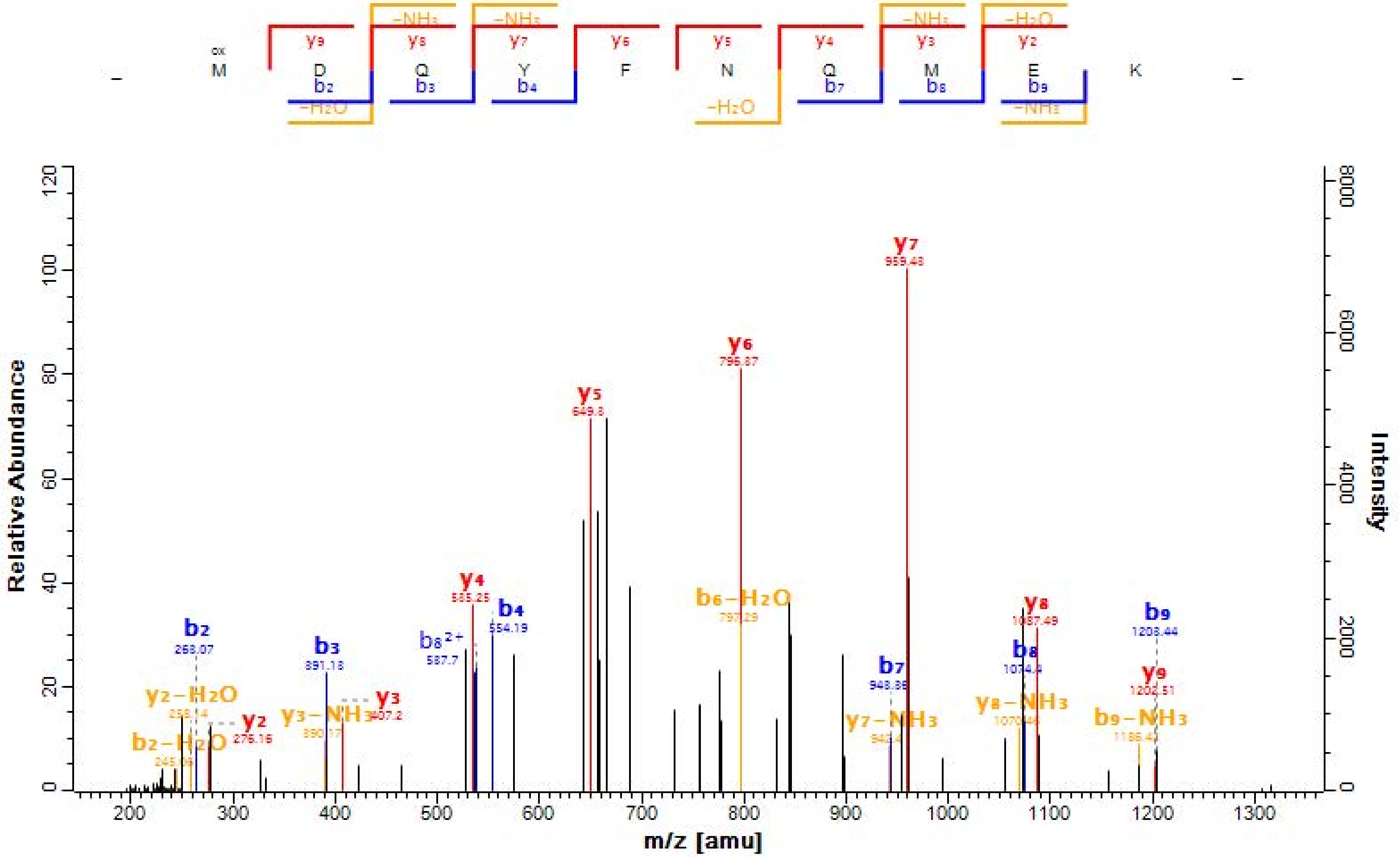


precursor information

Mass:	1023.48114
m/z:	512.74785
Charge:	2+
Retentiontime:	15.747982025146
Score:	54.78384
Mass Error [ppm]:	0.37106
PEP:	0.11337
Precursor Type:	ISO
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	33 %
Peak Coverage:	17 %
Protein Localisation:	589 ... 597

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	60.04439		88.0393	1	S	8		
-0.12355	188.103	+0.077563	216.0979	2	Q	7	937.456	
	319.1435	-0.09546	347.1384	3	M	6	809.3974	-0.02012
	466.2119	-0.17504	494.2068	4	F	5	678.357	+0.033674
	595.2545	+0.043167	623.2494	5	E	4	531.2885	+0.030982
	652.2759		680.2708	6	G	3	402.2459	+0.031888
	751.3443	+0.055158	779.3393	7	V	2	345.2245	
	822.3815		850.3764	8	A	1	246.1561	+0.114045
				9	R	0	175.119	+0.100774

Scan number	2097	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	113.61



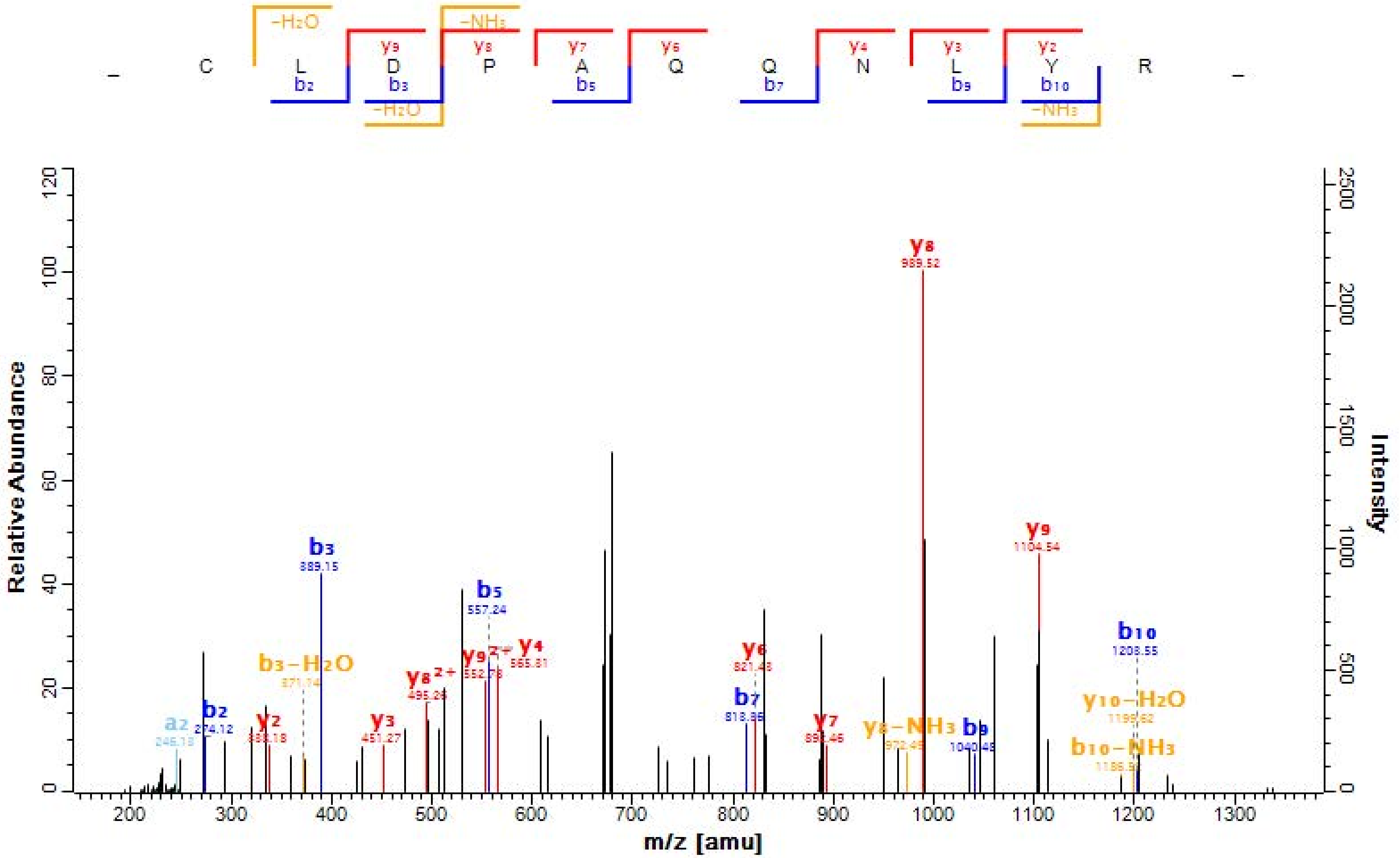
precursor information

Mass:	1348.54275
m/z:	675.27865
Charge:	2+
Retentiontime:	16.134061813354
Score:	113.609
Mass Error [ppm]:	-0.020397
PEP:	0.0012164
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	43 %
Peak Coverage:	24 %
Protein Localisation:	962 ... 971

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	148.0427		148.0427	1	M	9		
	263.0696	+0.011863	263.0696	2	D	8	1202.515	+0.478514
	391.1282	+0.135537	391.1282	3	Q	7	1087.488	-0.02299
	554.1915	+0.043705	554.1915	4	Y	6	959.4291	+0.008371
	701.2599		701.2599	5	F	5	796.3658	+0.017073
	815.3029		815.3029	6	N	4	649.2974	-0.00662
	943.3614	-0.0006	943.3614	7	Q	3	535.2545	+0.191036
-0.24568	537.7046	+0.118091	1074.402	8	M	2	407.1959	+0.08018
	1203.445	+0.170103	1203.445	9	E	1	276.1554	+0.054869
				10	K	0	147.1128	

Scan number	2162	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	115.57



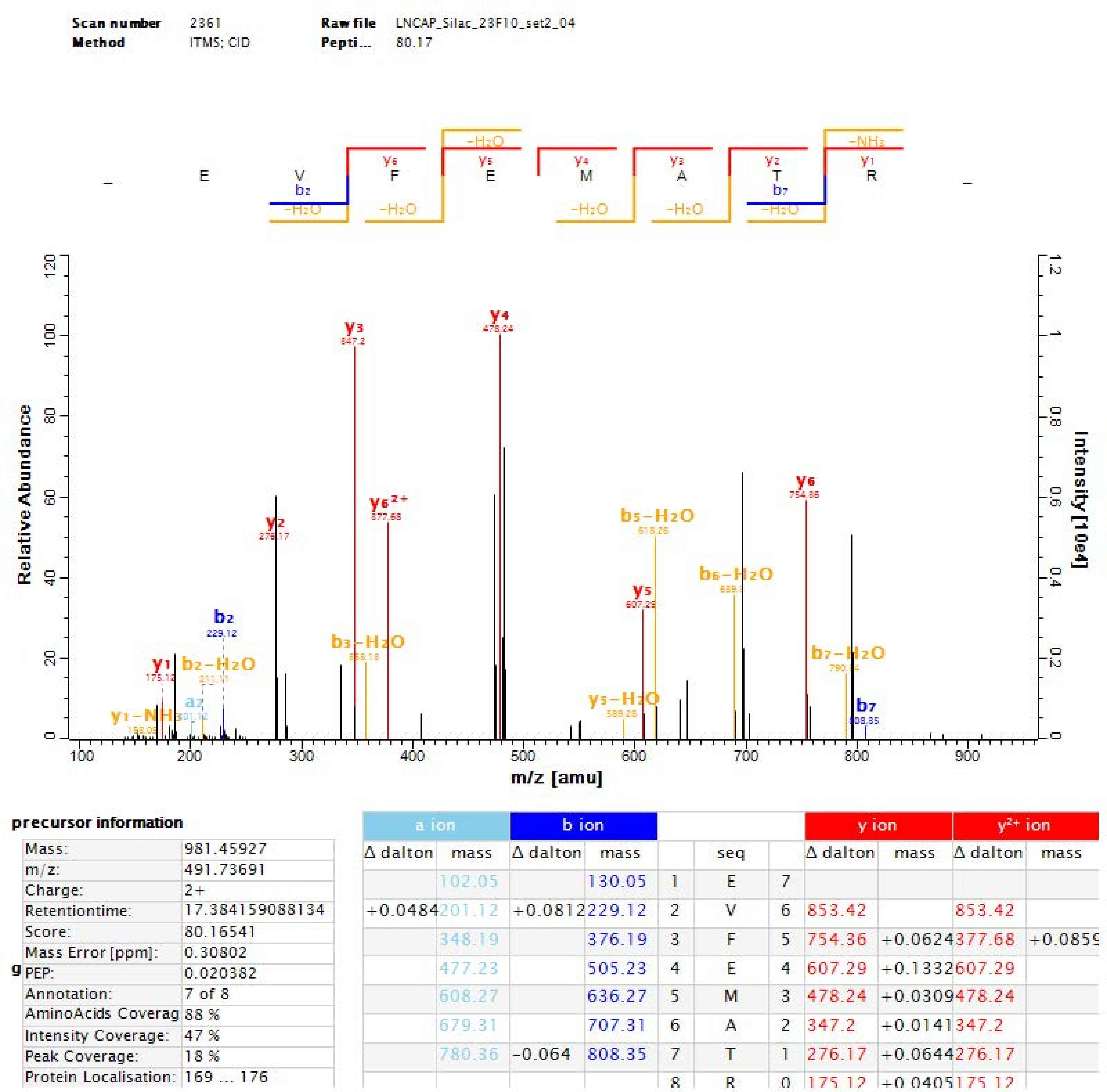
precursor information

Mass:	1376.65005
m/z:	689.3323
Charge:	2+
Retentiontime:	16.454347610473
Score:	115.5738
Mass Error [ppm]:	-0.46183
PEP:	0.00022791
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	32 %
Peak Coverage:	21 %
Protein Localisation:	20 ... 30

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	133.04		161.04	1	C	10				
+0.1172	246.13	+0.0665	274.12	2	L	9	1217.6		1217.6	
	361.15	+0.0892	389.15	3	D	8	1104.5	-0.04	552.78	-0.057
	458.21		486.2	4	P	7	989.52	+0.0249	495.26	+0.0209
	529.24	-0.173	557.24	5	A	6	892.46	+0.0198	892.46	
	657.3		685.3	6	Q	5	821.43	-0.008	821.43	
	785.36	+0.0584	813.36	7	Q	4	693.37		693.37	
	899.4		927.4	8	N	3	565.31	+0.0665	565.31	
	1012.5	-0.052	1040.5	9	L	2	451.27	+0.0733	451.27	
	1175.6	-0.267	1203.5	10	Y	1	338.18	+0.0602	338.18	
				11	R	0	175.12		175.12	



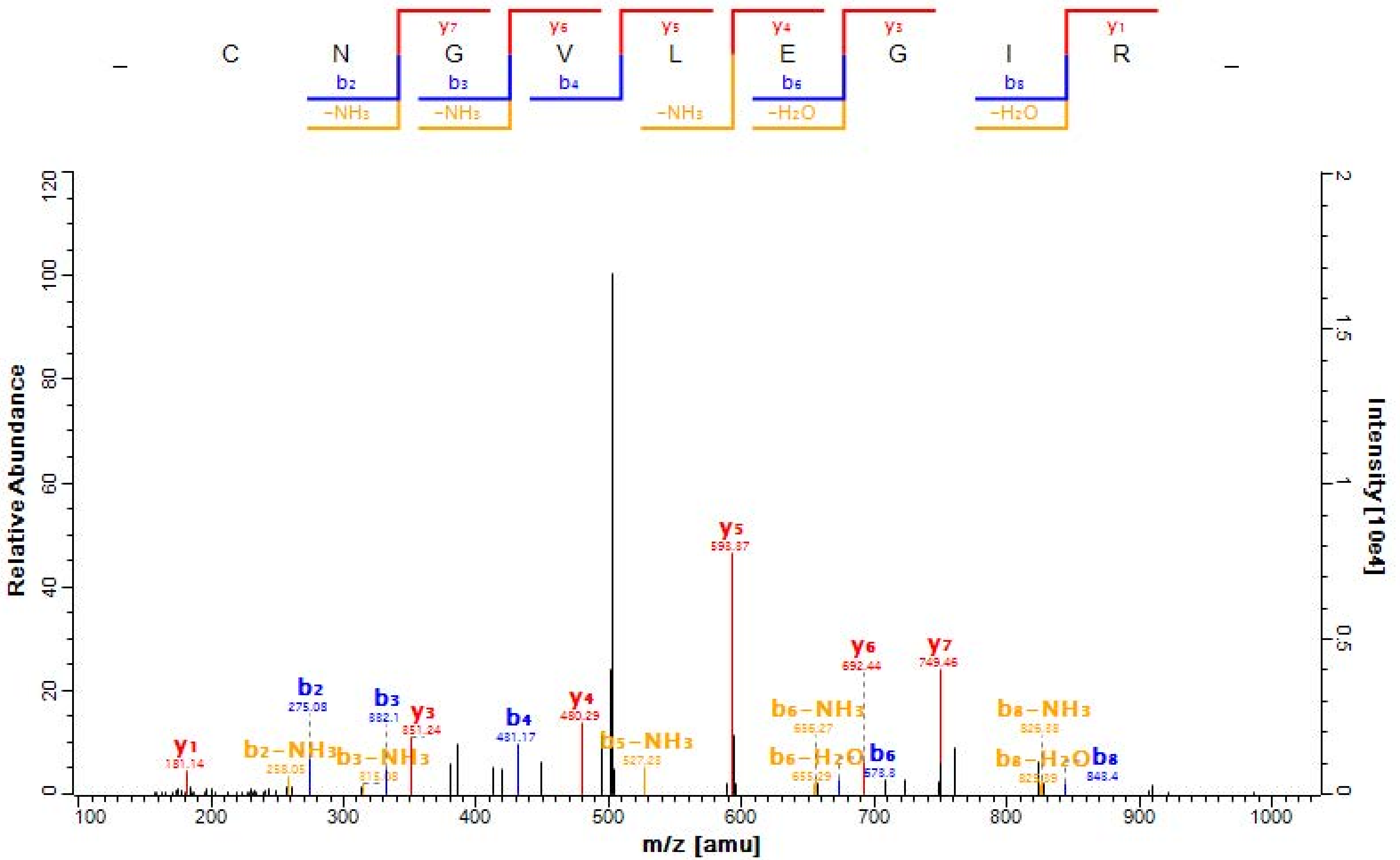
Scan number	2361	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	80.17

precursor information

Mass:	981.45927
m/z:	491.73691
Charge:	2+
Retentiontime:	17.384159088134
Score:	80.16541
Mass Error [ppm]:	0.30802
PEP:	0.020382
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	47 %
Peak Coverage:	18 %
Protein Localisation:	169 ... 176

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	7				
+0.0484	201.12	+0.0812	229.12	2	V	6	853.42		853.42	
	348.19		376.19	3	F	5	754.36	+0.0624	377.68	+0.0859
	477.23		505.23	4	E	4	607.29	+0.1332	607.29	
	608.27		636.27	5	M	3	478.24	+0.0309	478.24	
	679.31		707.31	6	A	2	347.2	+0.0141	347.2	
	780.36	-0.064	808.35	7	T	1	276.17	+0.0644	276.17	
				8	R	0	175.12	+0.0405	175.12	

Scan number	2444	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	109.66

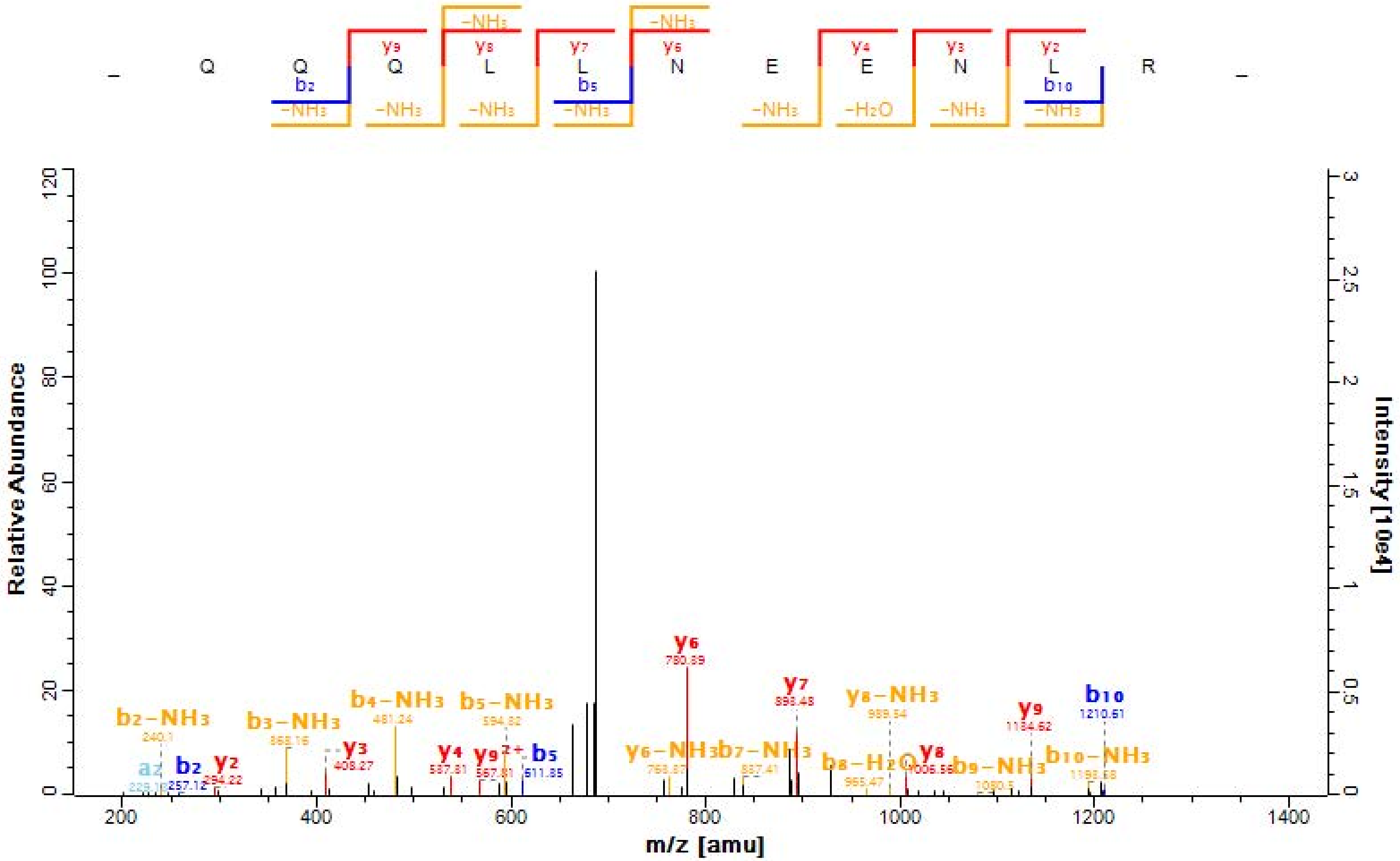


precursor information

Mass:	1016.50738
m/z:	509.26097
Charge:	2+
Retentiontime:	17.777385711669
Score:	109.6637
Mass Error [ppm]:	0.064281
PEP:	0.0022783
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	37 %
Peak Coverage:	17 %
Protein Localisation:	694 ... 702

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	161.037924668	1	C	8		
+0.02953	275.080852115	2	N	7	863.504071075	
-0.0032558	332.102315839	3	G	6	749.461143628	+0.0274428
-0.0092307	431.170729755	4	V	5	692.439679905	+0.0548269
	544.254793735	5	L	4	593.371265988	+0.0405382
+0.1548226	673.297386832	6	E	3	480.287202008	+0.0419606
	730.318850555	7	G	2	351.244608912	+0.0763139
+0.0069365	843.402914536	8	I	1	294.223145188	
		9	R	0	181.139081208	+0.0473202

Scan number	2673	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	108.7



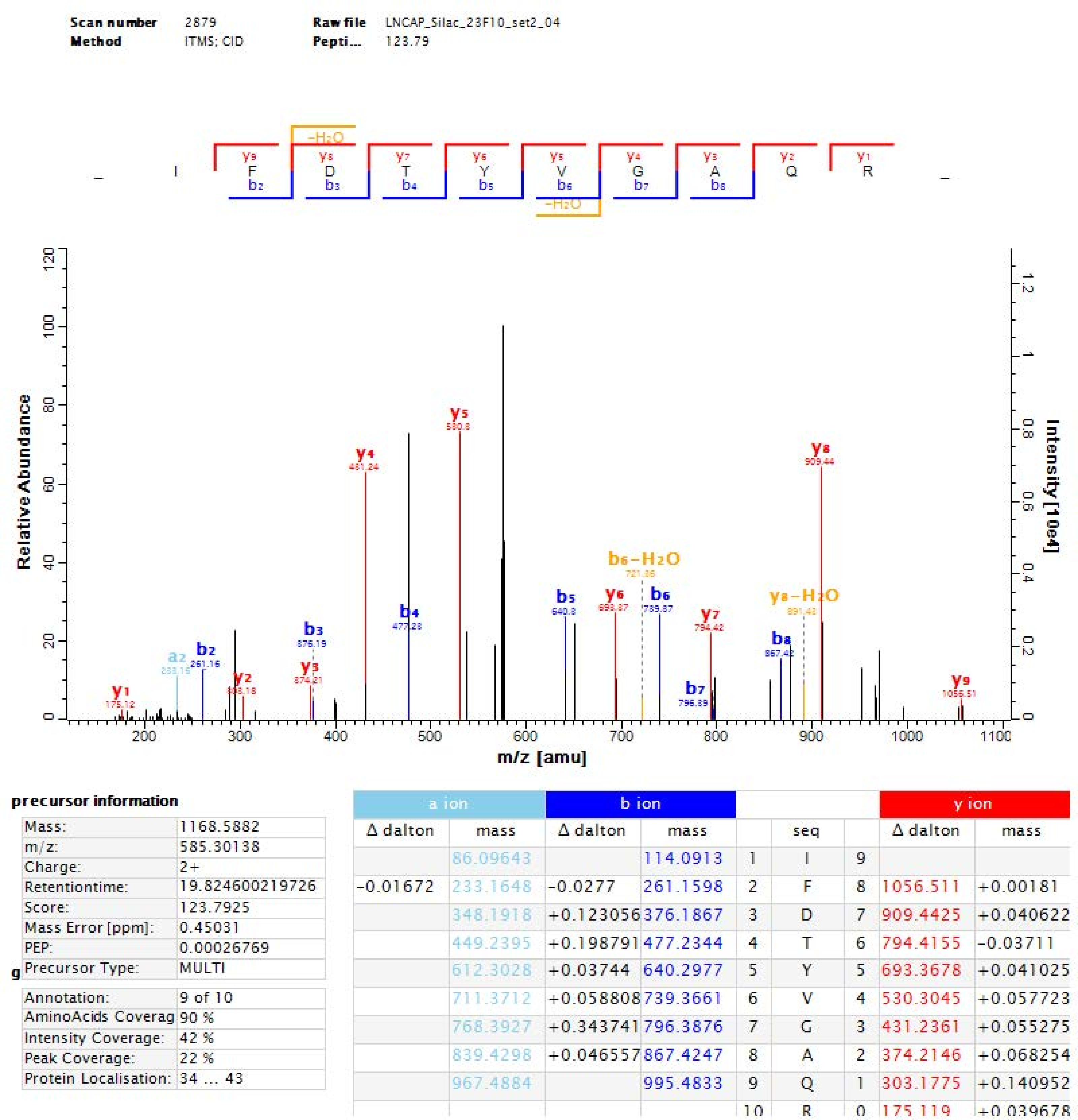
precursor information

Mass:	1383.71052
m/z:	692.86254
Charge:	2+
Retentiontime:	18.850095748901
Score:	108.6968
Mass Error [ppm]:	-0.088179
PEP:	0.00028774
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	29 %
Peak Coverage:	27 %
Protein Localisation:	147 ... 157

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	101.07		129.07	1	Q	10				
+0.0885	229.13	+0.0146	257.12	2	Q	9	1262.7		1262.7	
	357.19		385.18	3	Q	8	1134.6	+0.2255	567.81	-0.127
	470.27		498.27	4	L	7	1006.6	+0.0413	1006.6	
	583.36	-0.008	611.35	5	L	6	893.48	-0.013	893.48	
	697.4		725.39	6	N	5	780.39	+0.0346	780.39	
	826.44		854.44	7	E	4	666.35		666.35	
	955.48		983.48	8	E	3	537.31	+0.1128	537.31	
	1069.5		1097.5	9	N	2	408.27	+0.0931	408.27	
	1182.6	-0.172	1210.6	10	L	1	294.22	+0.1202	294.22	
				11	R	0	181.14		181.14	



Scan number	2879	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	123.79

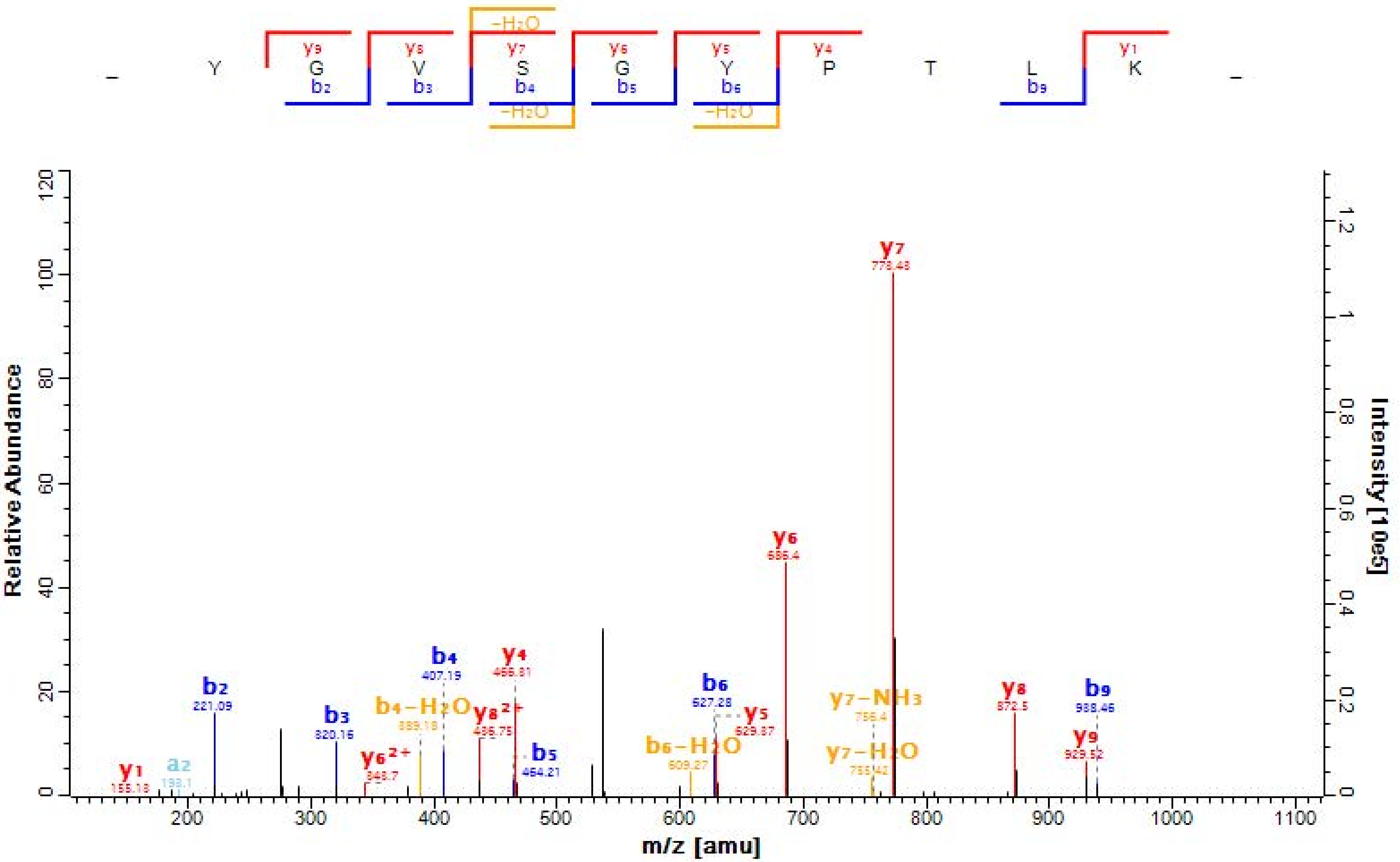
precursor information

Mass:	1168.5882
m/z:	585.30138
Charge:	2+
Retentiontime:	19.824600219726
Score:	123.7925
Mass Error [ppm]:	0.45031
PEP:	0.00026769
Precursor Type:	MULTI

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	42 %
Peak Coverage:	22 %
Protein Localisation:	34 ... 43

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	86.09643		114.0913	1	I	9		
-0.01672	233.1648	-0.0277	261.1598	2	F	8	1056.511	+0.00181
	348.1918	+0.123056	376.1867	3	D	7	909.4425	+0.040622
	449.2395	+0.198791	477.2344	4	T	6	794.4155	-0.03711
	612.3028	+0.03744	640.2977	5	Y	5	693.3678	+0.041025
	711.3712	+0.058808	739.3661	6	V	4	530.3045	+0.057723
	768.3927	+0.343741	796.3876	7	G	3	431.2361	+0.055275
	839.4298	+0.046557	867.4247	8	A	2	374.2146	+0.068254
	967.4884		995.4833	9	Q	1	303.1775	+0.140952
				10	R	0	175.119	+0.039678

Scan number	2932	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	145.89



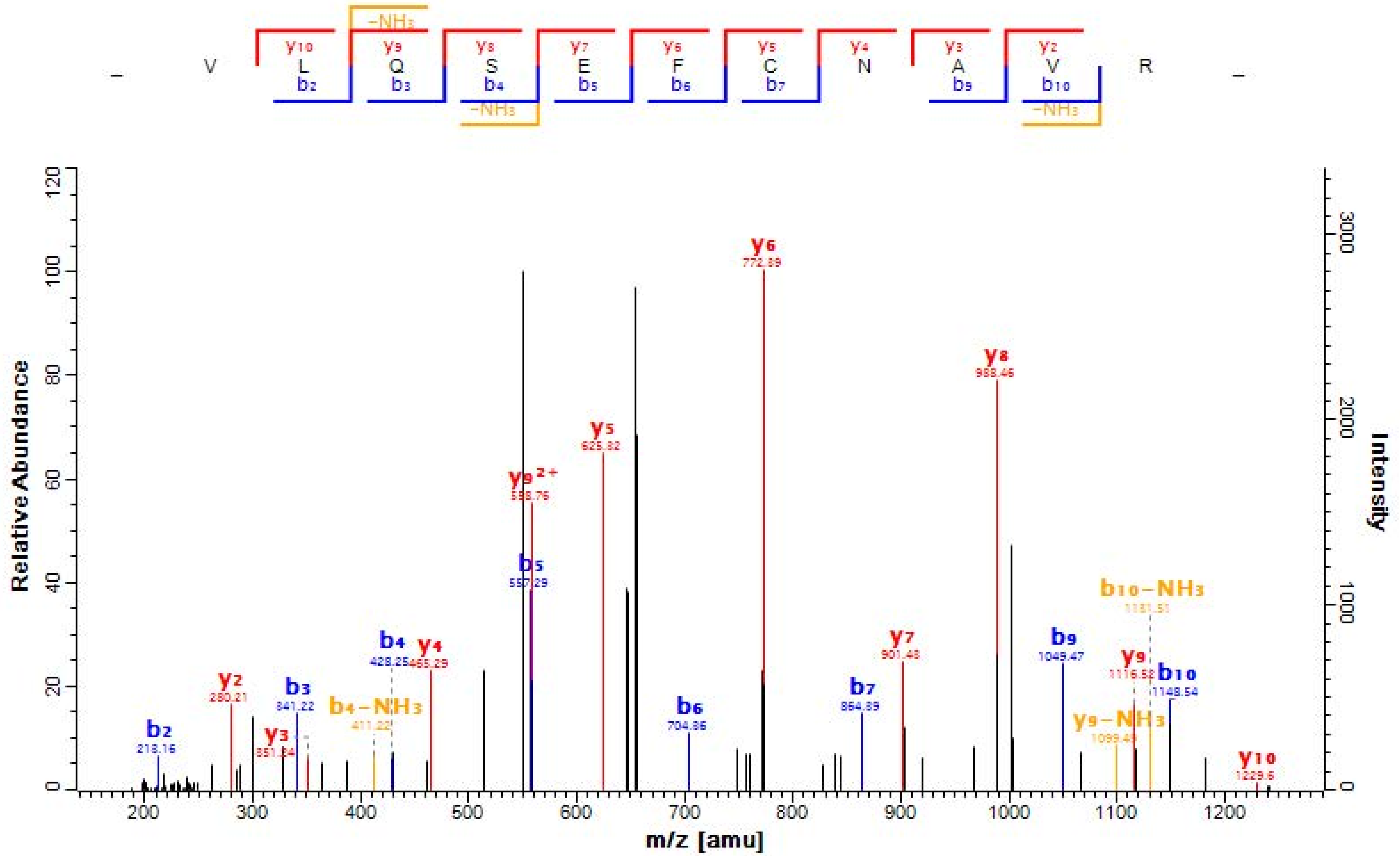
precursor information

Mass:	1083.56061
m/z:	542.78758
Charge:	2+
Retentiontime:	20.077526092529
Score:	145.8865
Mass Error [ppm]:	0.50461
PEP:	0.00017465
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	67 %
Peak Coverage:	27 %
Protein Localisation:	95 ... 104

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.08		164.07	1	Y	9				
-0.056	193.1	+0.0203	221.09	2	G	8	929.52	+0.0045	929.52	
	292.17	-0.044	320.16	3	V	7	872.5	+0.0237	436.75	-0.112
	379.2	-0.038	407.19	4	S	6	773.43	-0.025	773.43	
	436.22	-0.021	464.21	5	G	5	686.4	-0.018	343.7	+0.457
	599.28	-0.018	627.28	6	Y	4	629.37	-0.008	629.37	
	696.34		724.33	7	P	3	466.31	+0.0654	466.31	
	797.38		825.38	8	T	2	369.26		369.26	
	910.47	+0.0079	938.46	9	L	1	268.21		268.21	
				10	K	0	155.13	+0.147	155.13	

Scan number	2967	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	136.7



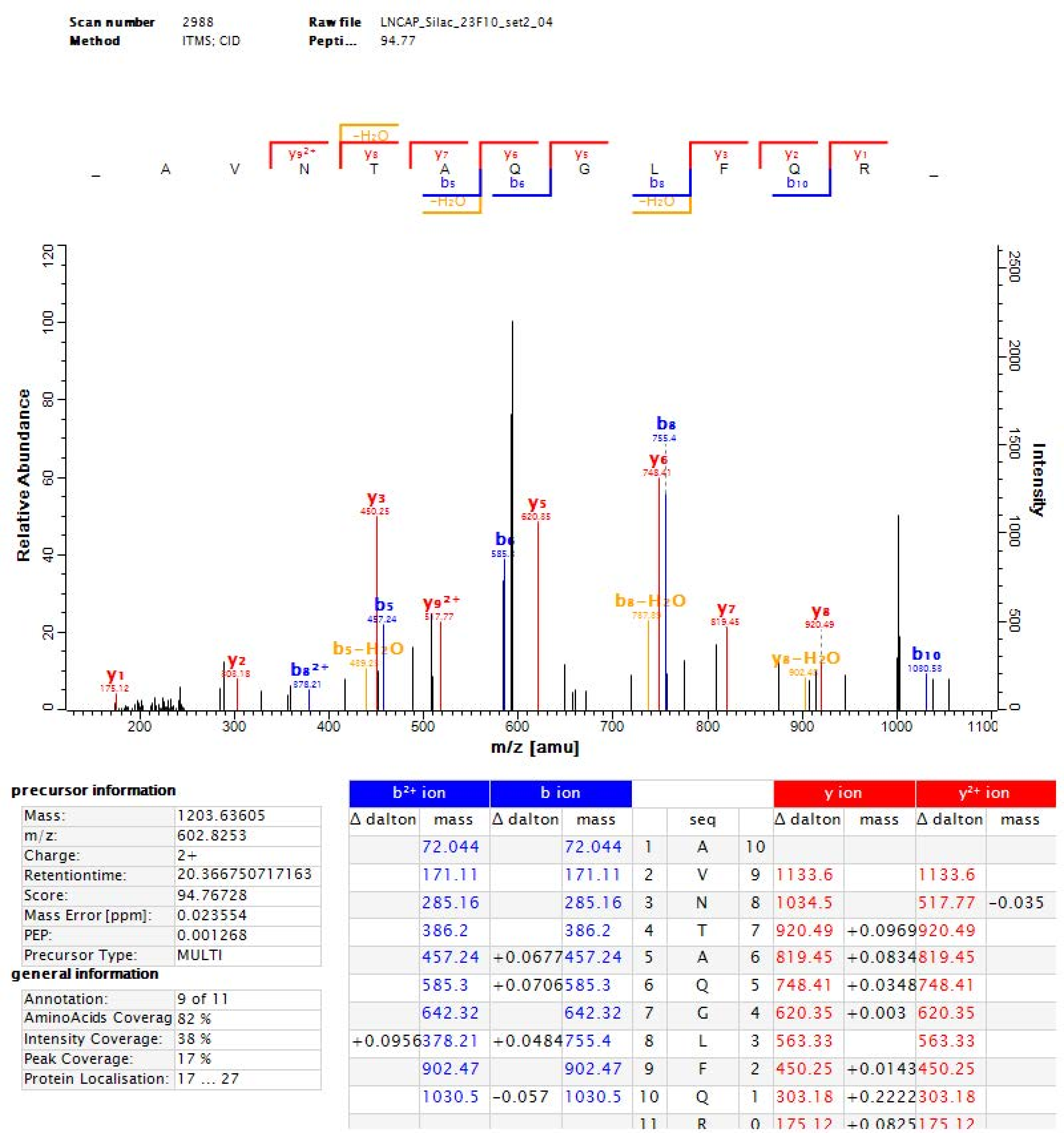
precursor information

Mass:	1321.64491
m/z:	661.82973
Charge:	2+
Retentiontime:	20.268697738647
Score:	136.6982
Mass Error [ppm]:	0.033149
PEP:	0.00016803
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	41 %
Peak Coverage:	23 %
Protein Localisation:	41 ... 51

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	10				
+0.005285	213.1598	2	L	9	1229.604	+0.291768	1229.604	
+0.040884	341.2183	3	Q	8	1116.52	+0.095193	558.7635	−0.06694
+0.003302	428.2504	4	S	7	988.4612	−0.00663	988.4612	
−0.03099	557.293	5	E	6	901.4292	−0.04711	901.4292	
+0.029441	704.3614	6	F	5	772.3866	+0.072447	772.3866	
+0.025038	864.392	7	C	4	625.3182	−0.02448	625.3182	
	978.4349	8	N	3	465.2875	−0.01398	465.2875	
−0.12074	1049.472	9	A	2	351.2446	+0.198567	351.2446	
−0.14643	1148.54	10	V	1	280.2075	+0.044733	280.2075	
		11	R	0	181.1391		181.1391	



Scan number	2988	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	94.77

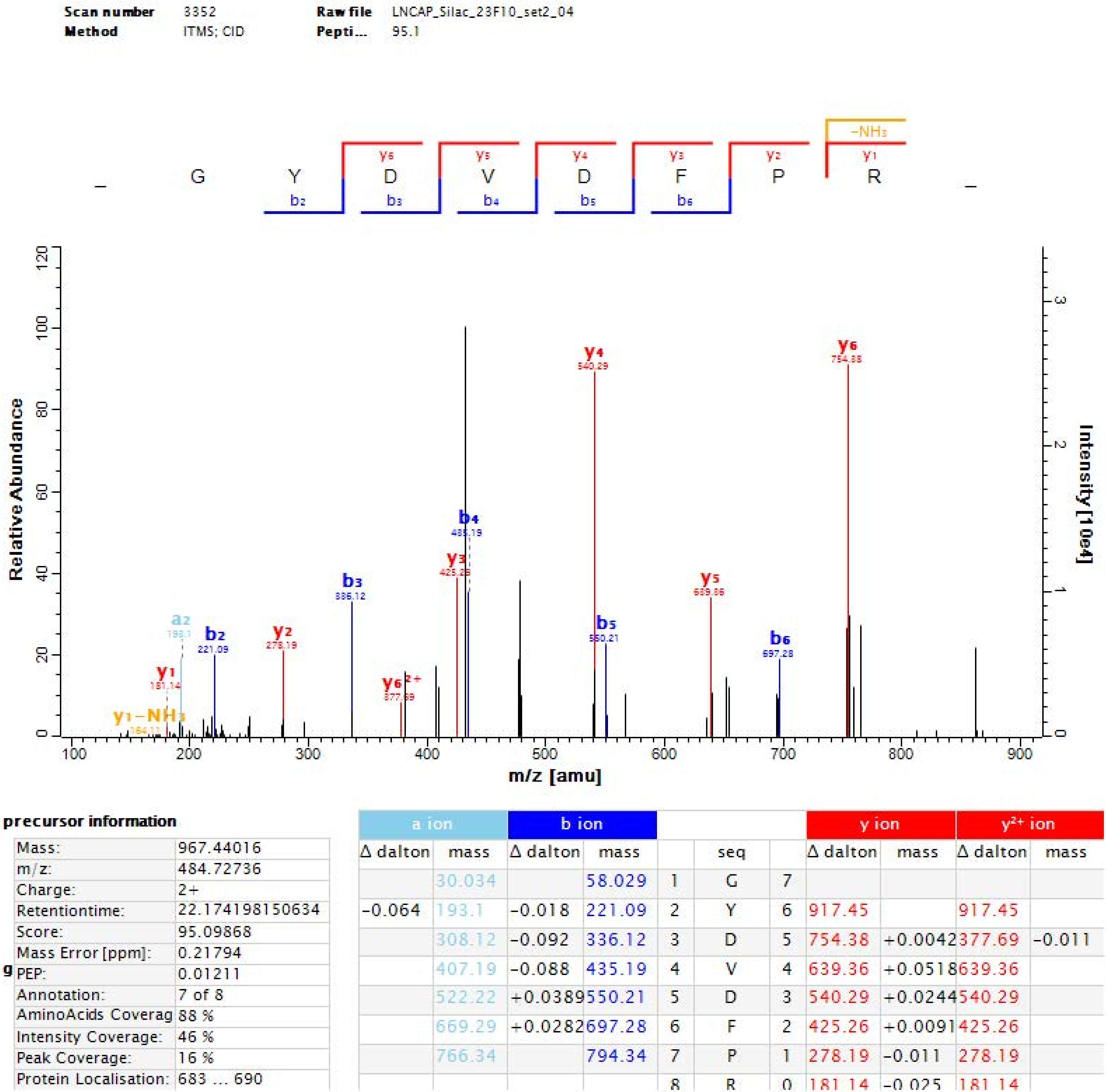
precursor information

Mass:	1203.63605
m/z:	602.8253
Charge:	2+
Retentiontime:	20.366750717163
Score:	94.76728
Mass Error [ppm]:	0.023554
PEP:	0.001268
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	38 %
Peak Coverage:	17 %
Protein Localisation:	17 ... 27

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	10				
	171.11		171.11	2	V	9	1133.6		1133.6	
	285.16		285.16	3	N	8	1034.5		517.77	−0.035
	386.2		386.2	4	T	7	920.49	+0.0969	920.49	
	457.24	+0.0677	457.24	5	A	6	819.45	+0.0834	819.45	
	585.3	+0.0706	585.3	6	Q	5	748.41	+0.0348	748.41	
	642.32		642.32	7	G	4	620.35	+0.003	620.35	
+0.0956	378.21	+0.0484	755.4	8	L	3	563.33		563.33	
	902.47		902.47	9	F	2	450.25	+0.0143	450.25	
	1030.5	−0.057	1030.5	10	Q	1	303.18	+0.2222	303.18	
				11	R	0	175.12	+0.0825	175.12	



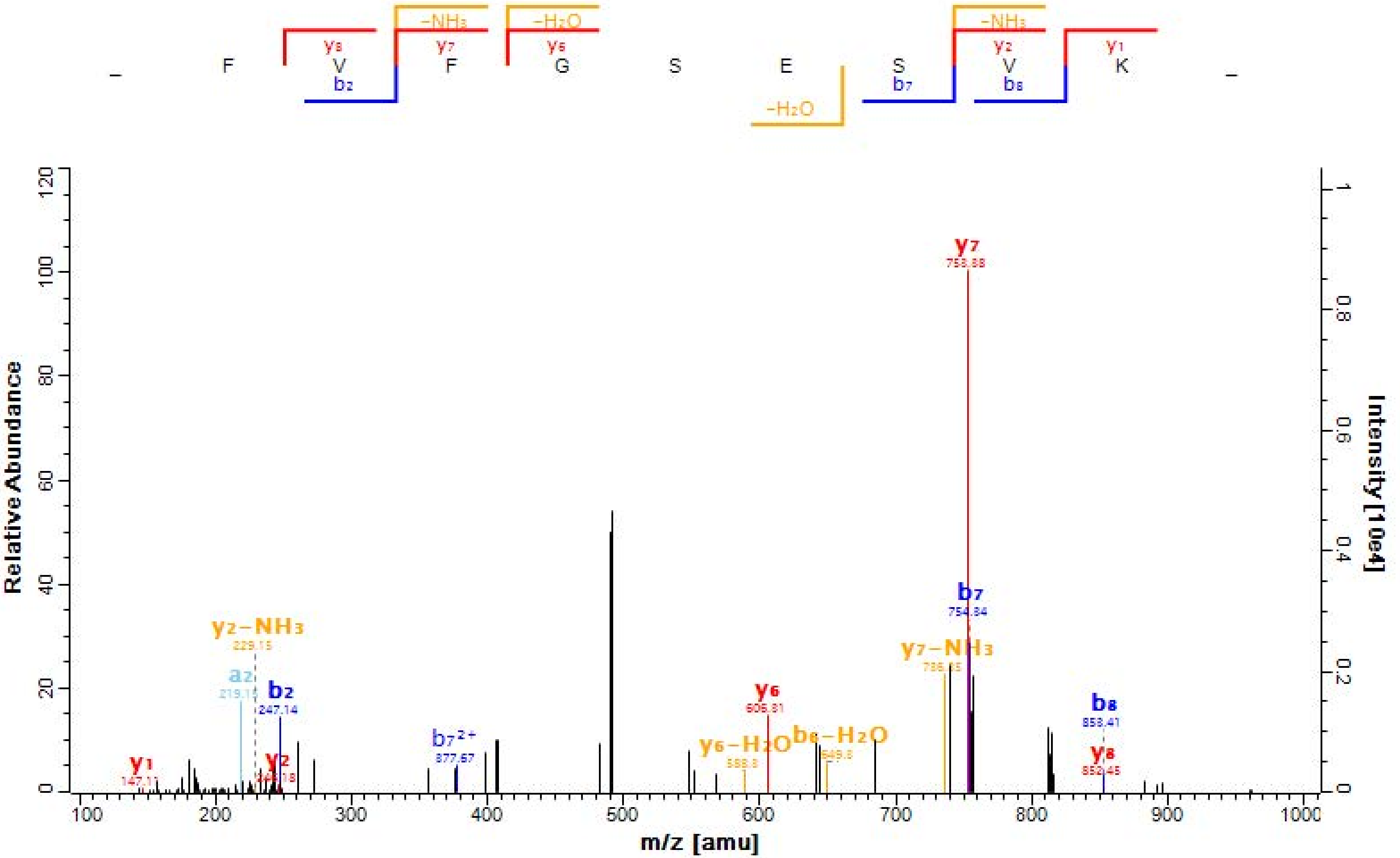
Scan number	3352	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	95.1

precursor information

Mass:	967.44016
m/z:	484.72736
Charge:	2+
Retentiontime:	22.174198150634
Score:	95.09868
Mass Error [ppm]:	0.21794
PEP:	0.01211
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	46 %
Peak Coverage:	16 %
Protein Localisation:	683 ... 690

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	30.034		58.029	1	G	7				
-0.064	193.1	-0.018	221.09	2	Y	6	917.45		917.45	
	308.12	-0.092	336.12	3	D	5	754.38	+0.0042	377.69	-0.011
	407.19	-0.088	435.19	4	V	4	639.36	+0.0518	639.36	
	522.22	+0.0389	550.21	5	D	3	540.29	+0.0244	540.29	
	669.29	+0.0282	697.28	6	F	2	425.26	+0.0091	425.26	
	766.34		794.34	7	P	1	278.19	-0.011	278.19	
				8	R	0	181.14	-0.025	181.14	

Scan number	3464	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	49.42

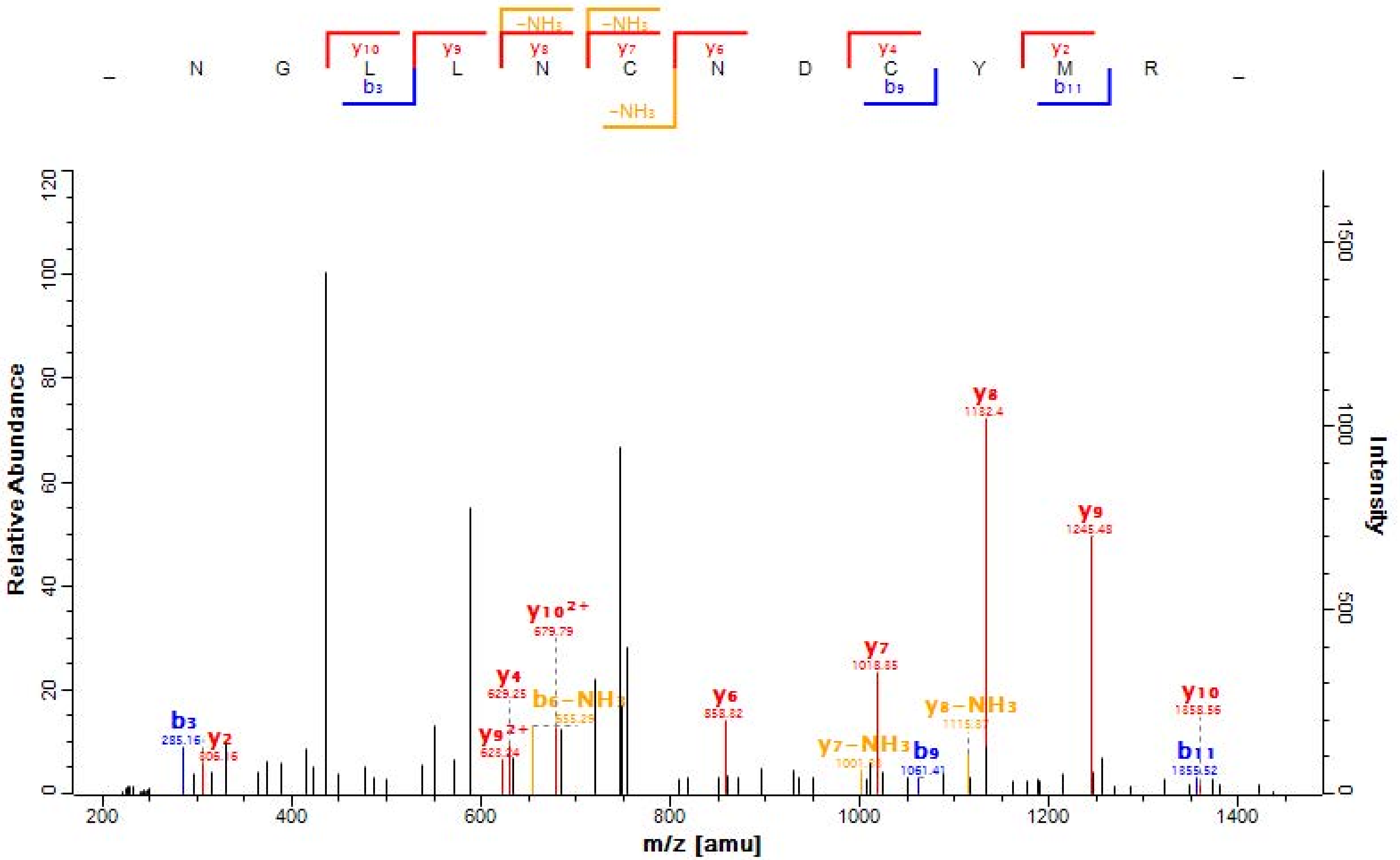


precursor information

Mass:	998.5072
m/z:	500.26088
Charge:	2+
Retentiontime:	22.701210021972
Score:	49.41815
Mass Error [ppm]:	-0.09499
PEP:	0.054405
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	34 %
Peak Coverage:	14 %
Protein Localisation:	2514 ... 2522

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	120.08		148.08		148.08	1	F	8		
+0.0508	219.15		247.14	+0.0197	247.14	2	V	7	852.45	-0.18
	366.22		394.21		394.21	3	F	6	753.38	+0.0231
	423.24		451.23		451.23	4	G	5	606.31	-0.109
	510.27		538.27		538.27	5	S	4	549.29	
	639.31		667.31		667.31	6	E	3	462.26	
	726.35	-0.139	377.67	+0.1128	754.34	7	S	2	333.21	
	825.41		853.41	+0.0828	853.41	8	V	1	246.18	-0.176
						9	K	0	147.11	+0.0577

Scan number	3503	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	65.56



precursor information

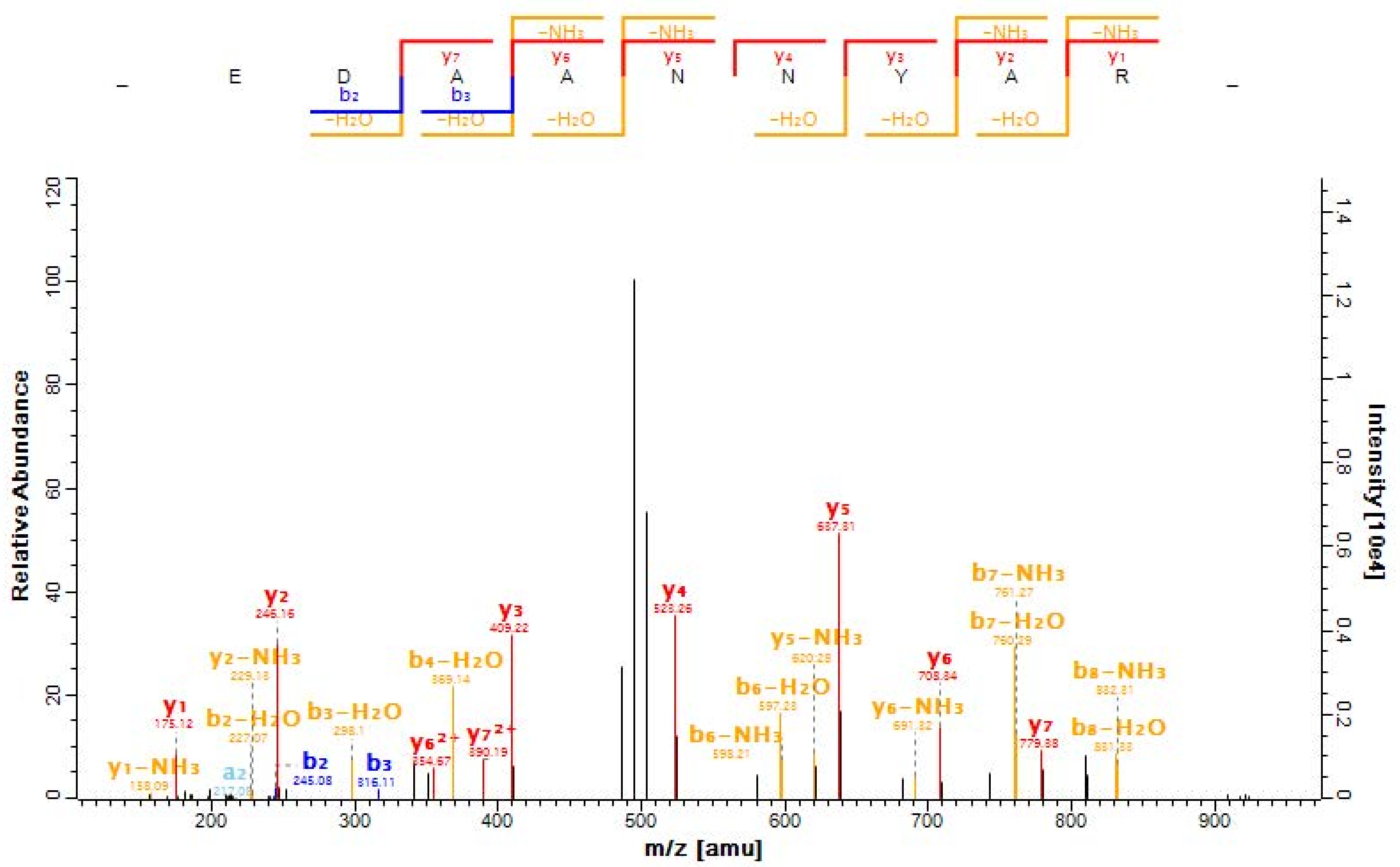
Mass:	1528.62111
m/z:	765.31783
Charge:	2+
Retentiontime:	22.879905700683
Score:	65.56252
Mass Error [ppm]:	-0.64907
PEP:	0.0077176
Precursor Type:	MULTI

general information

Annotation:	7 of 12
AminoAcids Coverag	58 %
Intensity Coverage:	29 %
Peak Coverage:	17 %
Protein Localisation:	1062 ... 1073

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502	1	N	11				
	172.0717	2	G	10	1415.586		1415.586	
+0.082885	285.1557	3	L	9	1358.565	+0.126785	679.7861	-0.10522
	398.2398	4	L	8	1245.481	-0.03415	623.2441	+0.143046
	512.2827	5	N	7	1132.397	-0.02552	1132.397	
	672.3134	6	C	6	1018.354	+0.078441	1018.354	
	786.3563	7	N	5	858.3233	+0.075215	858.3233	
	901.3832	8	D	4	744.2804		744.2804	
+0.130788	1061.414	9	C	3	629.2534	+0.124699	629.2534	
	1224.477	10	Y	2	469.2228		469.2228	
+0.107053	1355.518	11	M	1	306.1594	+0.006609	306.1594	
		12	R	0	175.119		175.119	

Scan number	353	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	127.56

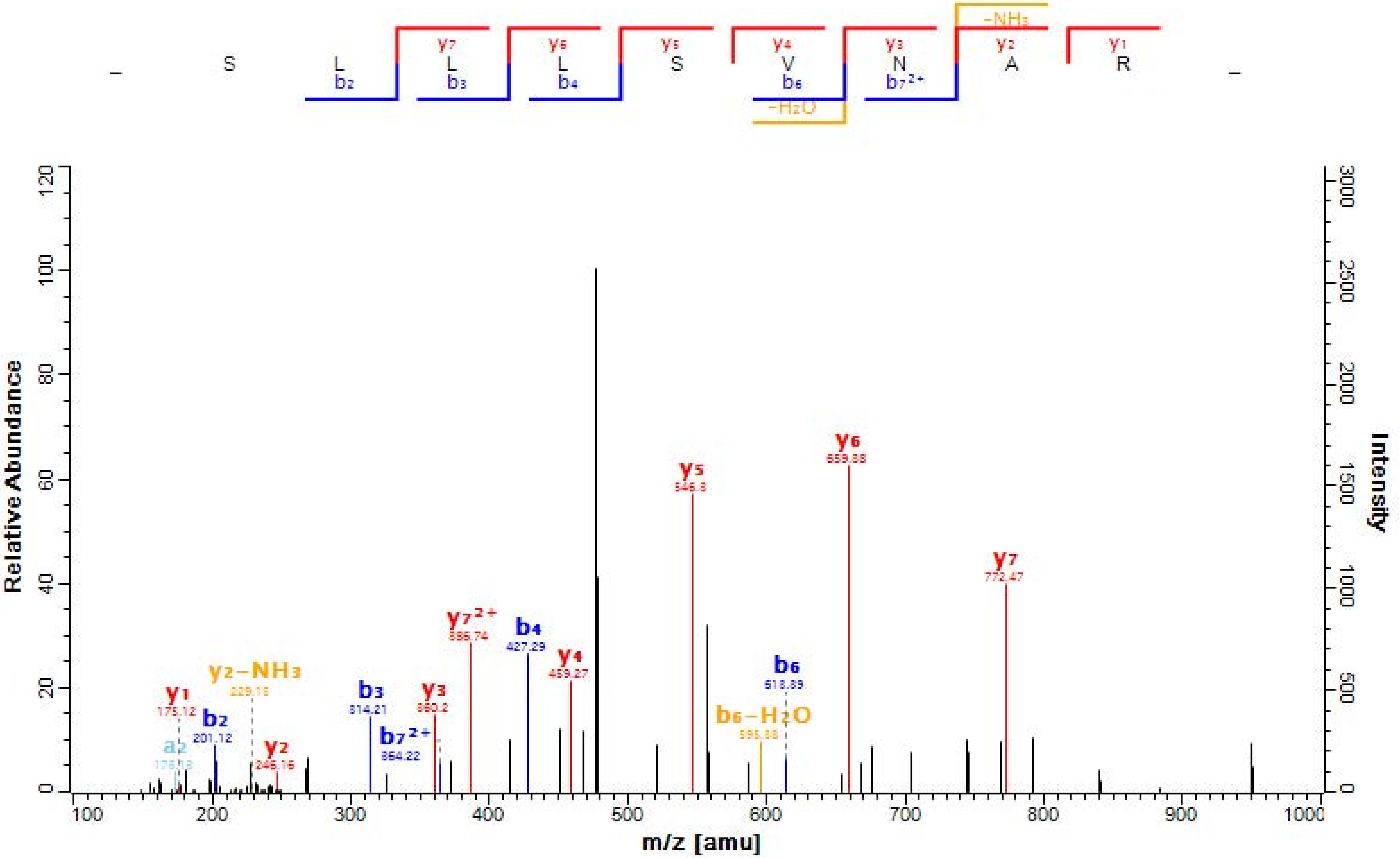


precursor information

Mass:	1022.4417
m/z:	512.22813
Charge:	2+
Retentiontime:	6.9462800025939
Score:	127.5647
Mass Error [ppm]:	-0.03855
PEP:	0.0011737
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	50 %
Peak Coverage:	34 %
Protein Localisation:	97 ... 105

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	8				
-0.367	217.08	-0.055	245.08	2	D	7	894.41		894.41	
	288.12	+0.0728	316.11	3	A	6	779.38	-0.004	390.19	+0.0185
	359.16		387.15	4	A	5	708.34	+0.0995	354.67	+0.07
	473.2		501.19	5	N	4	637.31	+0.0342	637.31	
	587.24		615.24	6	N	3	523.26	+0.0038	523.26	
	750.31		778.3	7	Y	2	409.22	+0.115	409.22	
	821.34		849.34	8	A	1	246.16	-0.032	246.16	
				9	R	0	175.12	+0.0207	175.12	

Scan number	3964	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	91.87

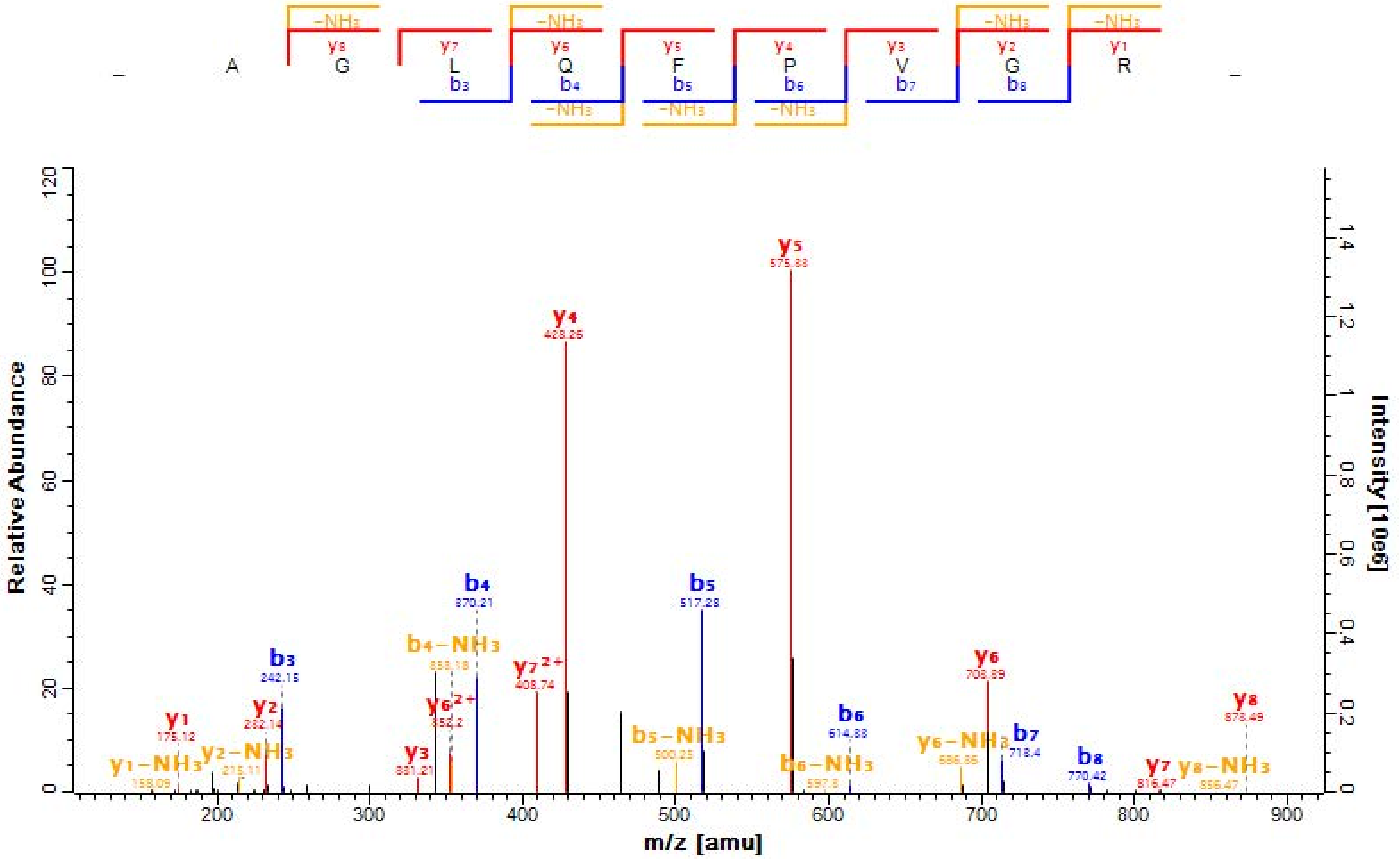


precursor information

Mass:	971.57608
m/z:	486.79532
Charge:	2+
Retentiontime:	25.063606262207
Score:	91.86671
Mass Error [ppm]:	-0.30388
PEP:	0.0094571
Precursor Type:	ISO
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	44 %
Peak Coverage:	19 %
Protein Localisation:	216 ... 224

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	60.04		88.04		88.04	1	S	8				
-0.06	173.1		201.1	-0.04	201.1	2	L	7	885.6		885.6	
	286.2		314.2	-0.04	314.2	3	L	6	772.5	+0.16	386.7	+0.24
	399.3		427.3	-0.01	427.3	4	L	5	659.4	+0.08	659.4	
	486.3		514.3		514.3	5	S	4	546.3	+0.006	546.3	
	585.4		613.4	+0.12	613.4	6	V	3	459.3	+0.02	459.3	
	699.4	+0.433	364.2		727.4	7	N	2	360.2	+0	360.2	
	770.5		798.5		798.5	8	A	1	246.2	-0.02	246.2	
						9	R	0	175.1	+0.084	175.1	

Scan number	4036	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	212.58



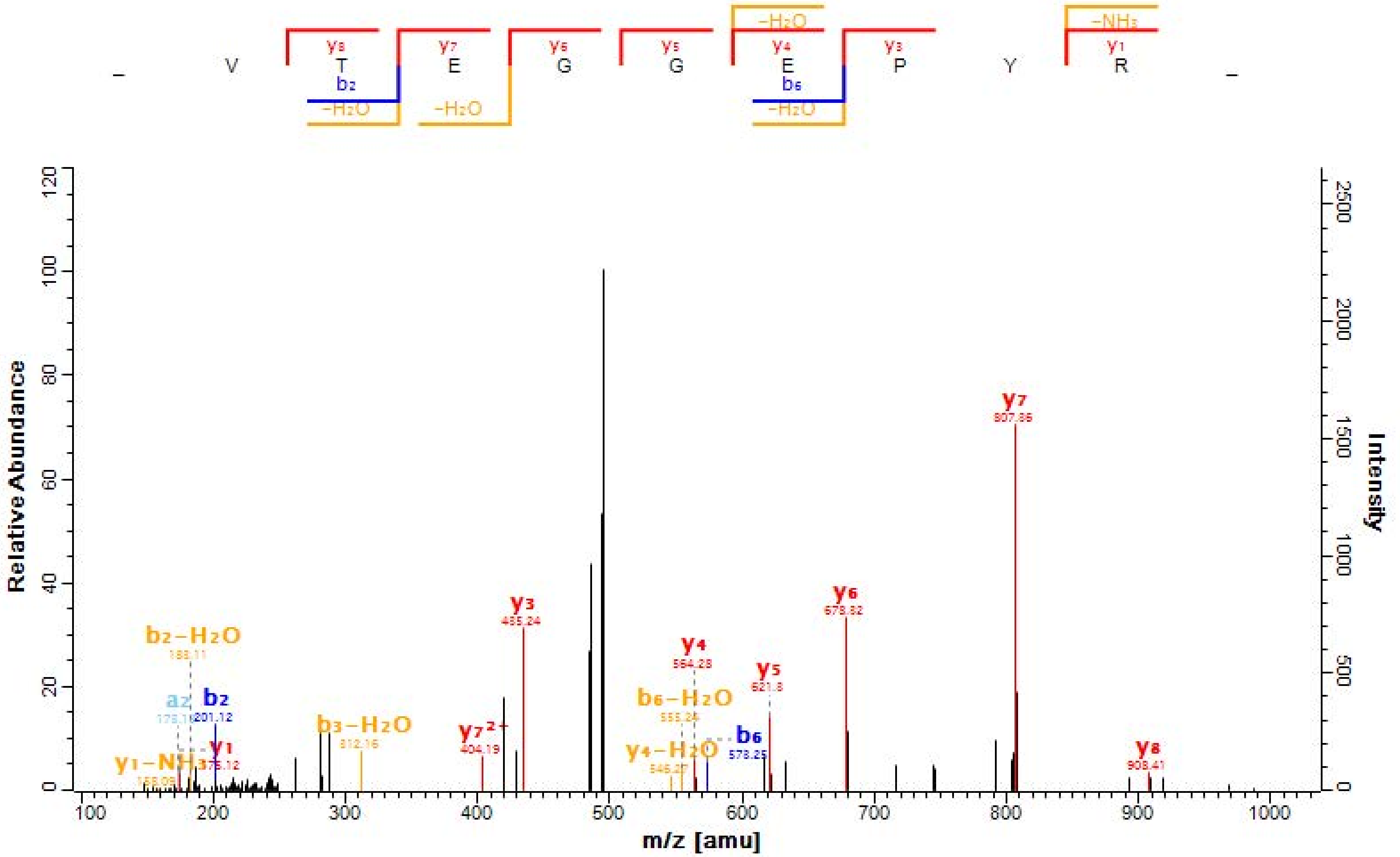
g

precursor information

Mass:	943.52354
m/z:	472.76904
Charge:	2+
Retentiontime:	25.423799514770
Score:	212.5806
Mass Error [ppm]:	-0.43951
PEP:	4.2885E-13
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	73 %
Peak Coverage:	37 %
Protein Localisation:	22 ... 30

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	8				
	129.0659	2	G	7	873.4941	+0.03201	873.4941	
−0.00615	242.1499	3	L	6	816.4726	−0.01806	408.74	+0.272702
−0.03497	370.2085	4	Q	5	703.3886	+0.010524	352.1979	−0.02932
−0.06158	517.2769	5	F	4	575.33	+0.040537	575.33	
+0.006081	614.3297	6	P	3	428.2616	+0.03287	428.2616	
+0.024459	713.3981	7	V	2	331.2088	+0.018892	331.2088	
+0.179082	770.4196	8	G	1	232.1404	+0.110927	232.1404	
		9	R	0	175.119	+0.16361	175.119	

Scan number	445	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	91.87

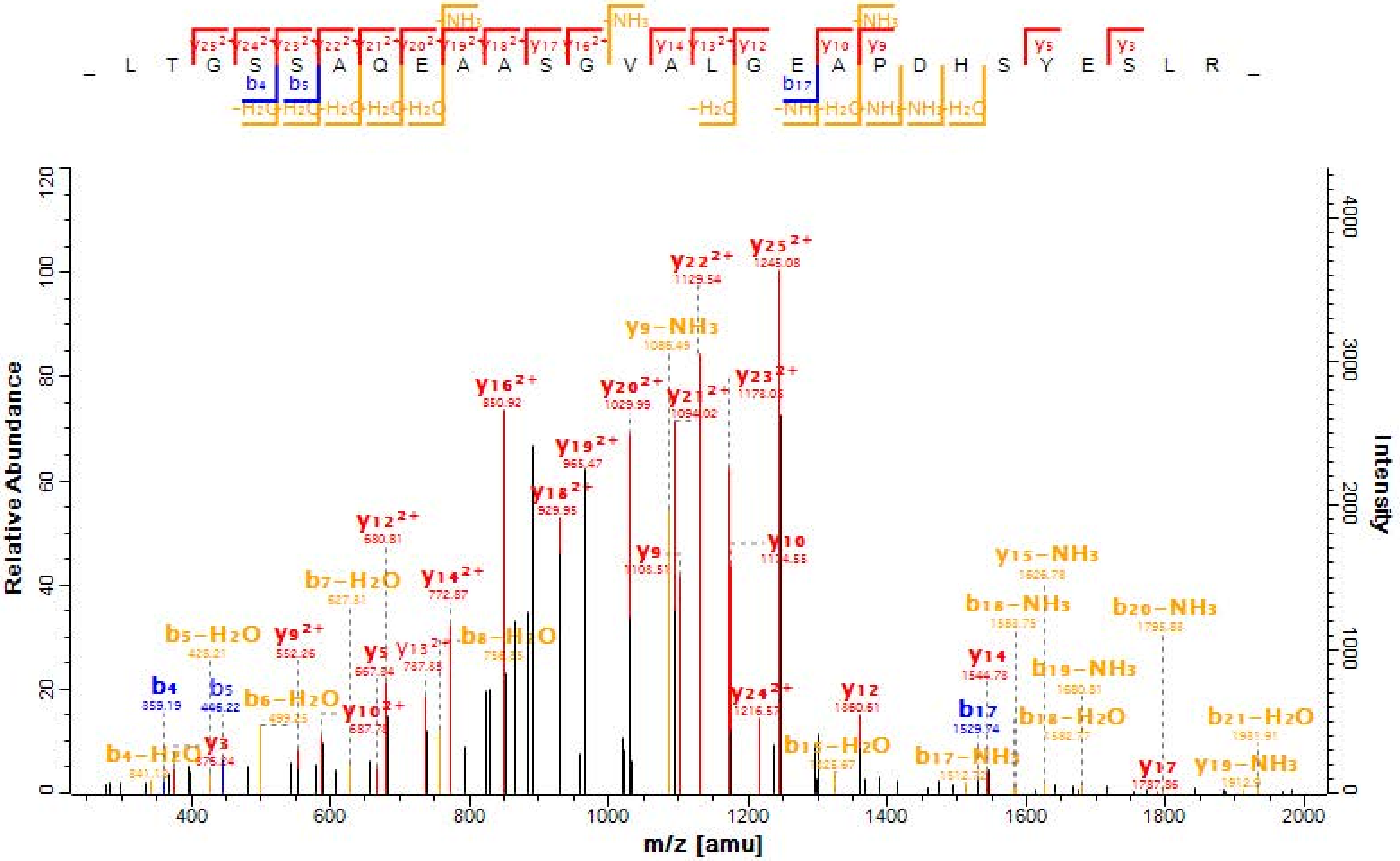


precursor information

Mass:	1006.47135
m/z:	504.24295
Charge:	2+
Retentiontime:	7.5758252143859
Score:	91.86671
Mass Error [ppm]:	-0.62125
PEP:	0.0049451
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	31 %
Peak Coverage:	14 %
Protein Localisation:	321 ... 329

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.081		100.08	1	V	8				
+0.0903	173.13	+0.05	201.12	2	T	7	908.41	-0.088	908.41	
	302.17		330.17	3	E	6	807.36	-0.044	404.19	+0.1213
	359.19		387.19	4	G	5	678.32	-0.025	678.32	
	416.21		444.21	5	G	4	621.3	+0.0453	621.3	
	545.26	+0.0921	573.25	6	E	3	564.28	-0.012	564.28	
	642.31		670.3	7	P	2	435.24	+0.0055	435.24	
	805.37		833.37	8	Y	1	338.18		338.18	
				9	R	0	175.12	+0.0621	175.12	

Scan number	4592	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	108.08



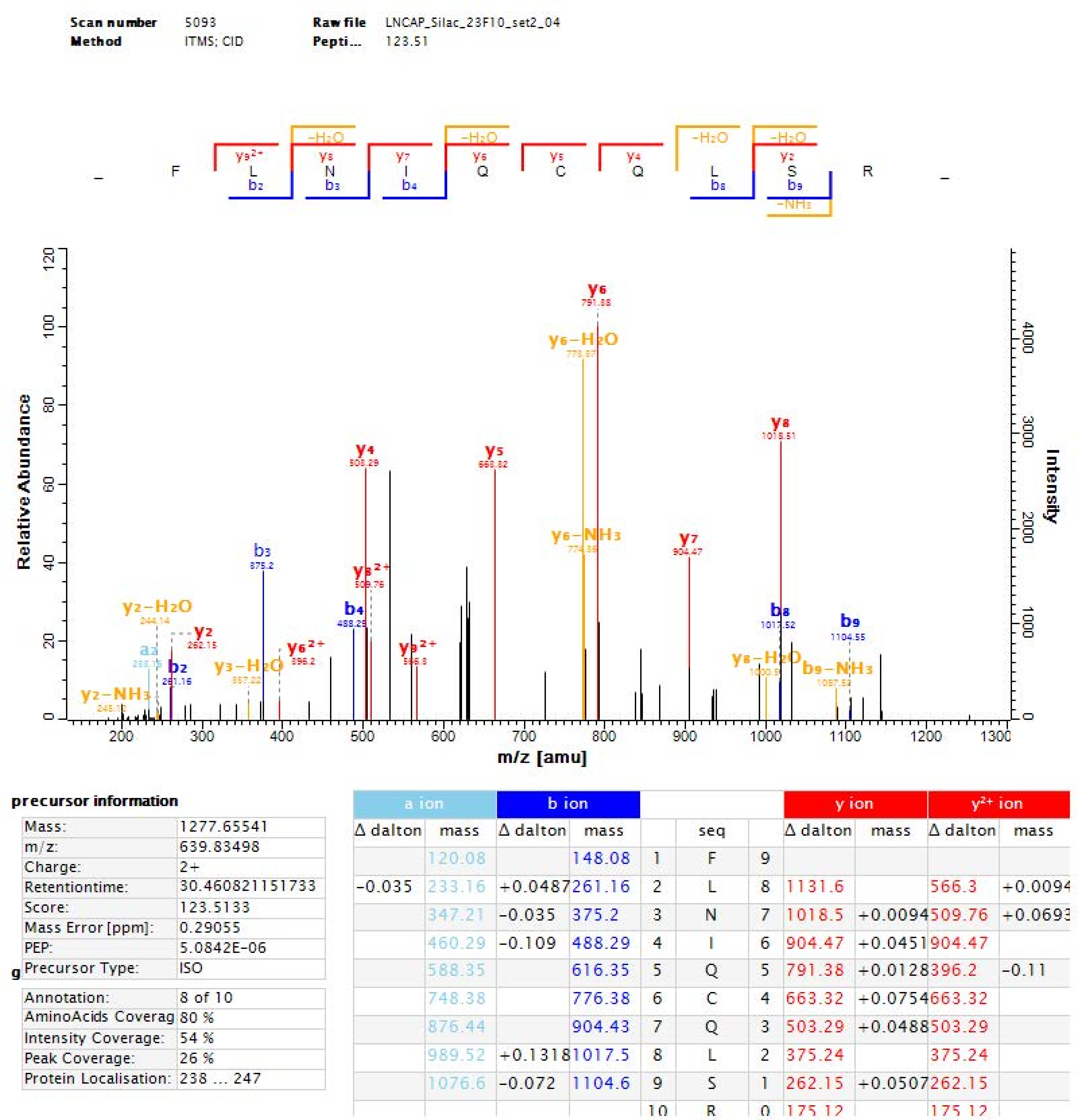
precursor information

Mass:	2702.27898
m/z:	901.76694
Charge:	3+
Retentiontime:	28.066053390502
Score:	108.0798
Mass Error [ppm]:	0.22895
PEP:	3.7523E-13
Precursor Type:	MULTI

general information

Annotation:	22 of 27
AminoAcids Coverag	81 %
Intensity Coverage:	56 %
Peak Coverage:	38 %
Protein Localisation:	33 ... 59

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	26				
	215.139	2	T	25	2590.202		2590.202	
	272.1605	3	G	24	2489.154		1245.081	+0.210916
-0.45252	359.1925	4	S	23	2432.132		1216.57	+0.057707
+0.104318	446.2245	5	S	22	2345.1		1173.054	+0.292959
	517.2617	6	A	21	2258.068		1129.538	+0.234877
	645.3202	7	Q	20	2187.031		1094.019	+0.226578
	774.3628	8	E	19	2058.973		1029.99	+0.294319
	845.3999	9	A	18	1929.93		965.4687	+0.028934
	916.4371	10	A	17	1858.893		929.9501	+0.009588
	1003.469	11	S	16	1787.856	-0.23343	1787.856	
	1060.491	12	G	15	1700.824		850.9156	+0.203522
	1159.559	13	V	14	1643.802		1643.802	
	1230.596	14	A	13	1544.734	-0.00459	772.8706	+0.342149
	1343.68	15	L	12	1473.697		737.3521	+0.211353
	1400.702	16	G	11	1360.613	-0.03185	680.81	+0.118253
-0.12761	1529.744	17	E	10	1303.591		1303.591	
	1600.781	18	A	9	1174.549	-0.17641	587.778	+0.010572
	1697.834	19	P	8	1103.512	-0.05727	552.2594	+0.076859
	1812.861	20	D	7	1006.459		1006.459	
	1949.92	21	H	6	891.4319		891.4319	
	2036.952	22	S	5	754.373		754.373	
	2200.015	23	Y	4	667.341	-0.0732	667.341	
	2329.058	24	E	3	504.2776		504.2776	
	2416.09	25	S	2	375.235	+0.112093	375.235	
	2529.174	26	L	1	288.203		288.203	
		27	R	0	175.119		175.119	



Scan number 5093 **Raw file** LNCAP_Silac_23F10_set2_04
Method ITMS; CID **Pepti...** 123.51

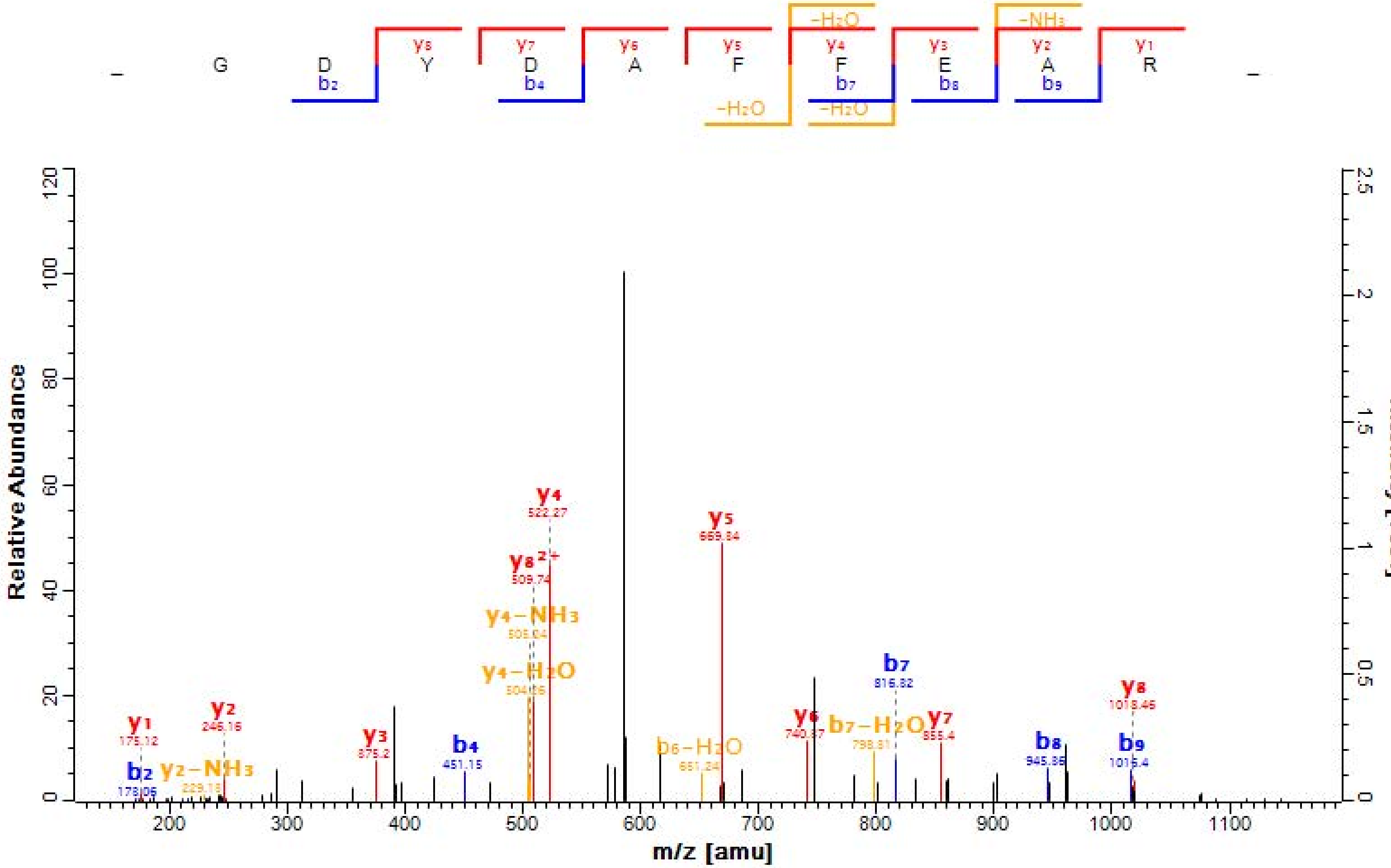
precursor information

Mass:	1277.65541
m/z:	639.83498
Charge:	2+
Retentiontime:	30.460821151733
Score:	123.5133
Mass Error [ppm]:	0.29055
PEP:	5.0842E-06
Precursor Type:	ISO

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	54 %
Peak Coverage:	26 %
Protein Localisation:	238 ... 247

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08		148.08	1	F	9				
-0.035	233.16	+0.0487	261.16	2	L	8	1131.6		566.3	+0.0094
	347.21	-0.035	375.2	3	N	7	1018.5	+0.0094	509.76	+0.0693
	460.29	-0.109	488.29	4	I	6	904.47	+0.0451	904.47	
	588.35		616.35	5	Q	5	791.38	+0.0128	396.2	-0.11
	748.38		776.38	6	C	4	663.32	+0.0754	663.32	
	876.44		904.43	7	Q	3	503.29	+0.0488	503.29	
	989.52	+0.1318	1017.5	8	L	2	375.24		375.24	
	1076.6	-0.072	1104.6	9	S	1	262.15	+0.0507	262.15	
				10	R	0	175.12		175.12	
]

Scan number	5643	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	129.89

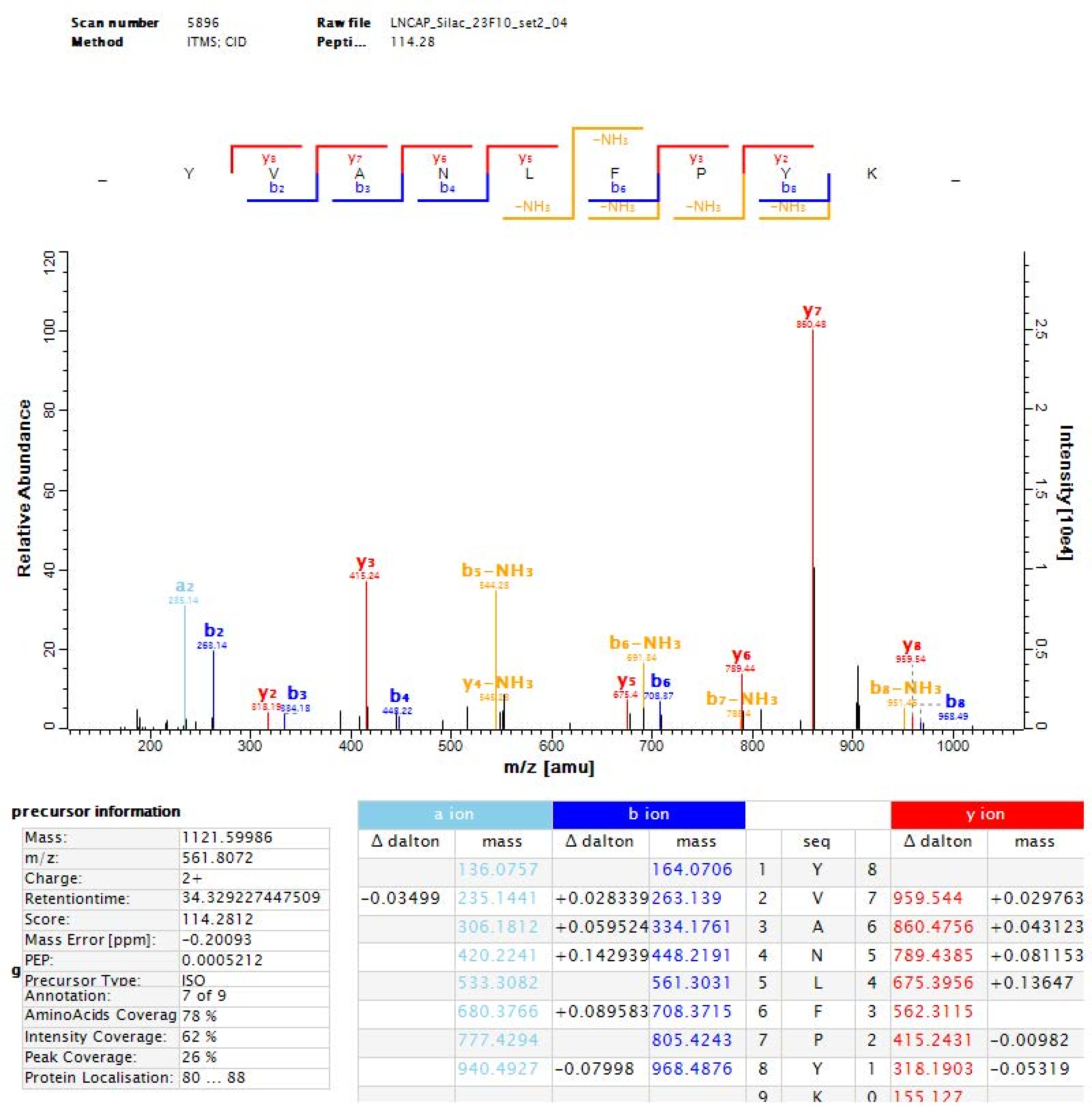


precursor information

Mass:	1189.50454
m/z:	595.75955
Charge:	2+
Retentiontime:	33.100513458252
Score:	129.8889
Mass Error [ppm]:	0.45147
PEP:	0.00024535
Precursor Type:	MULTI

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	42 %
Peak Coverage:	22 %
Protein Localisation:	77 ... 86

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	9				
+0.182751	173.0557	2	D	8	1133.49		1133.49	
	336.119	3	Y	7	1018.463	+0.047321	509.7351	-0.08645
-0.03182	451.146	4	D	6	855.3995	+0.07122	855.3995	
	522.1831	5	A	5	740.3726	+0.036335	740.3726	
	669.2515	6	F	4	669.3355	+0.009423	669.3355	
+0.014759	816.3199	7	F	3	522.2671	+0.064165	522.2671	
+0.070067	945.3625	8	E	2	375.1987	-0.04638	375.1987	
-0.21992	1016.4	9	A	1	246.1561	+0.02028	246.1561	
		10	R	0	175.119	+0.012731	175.119	



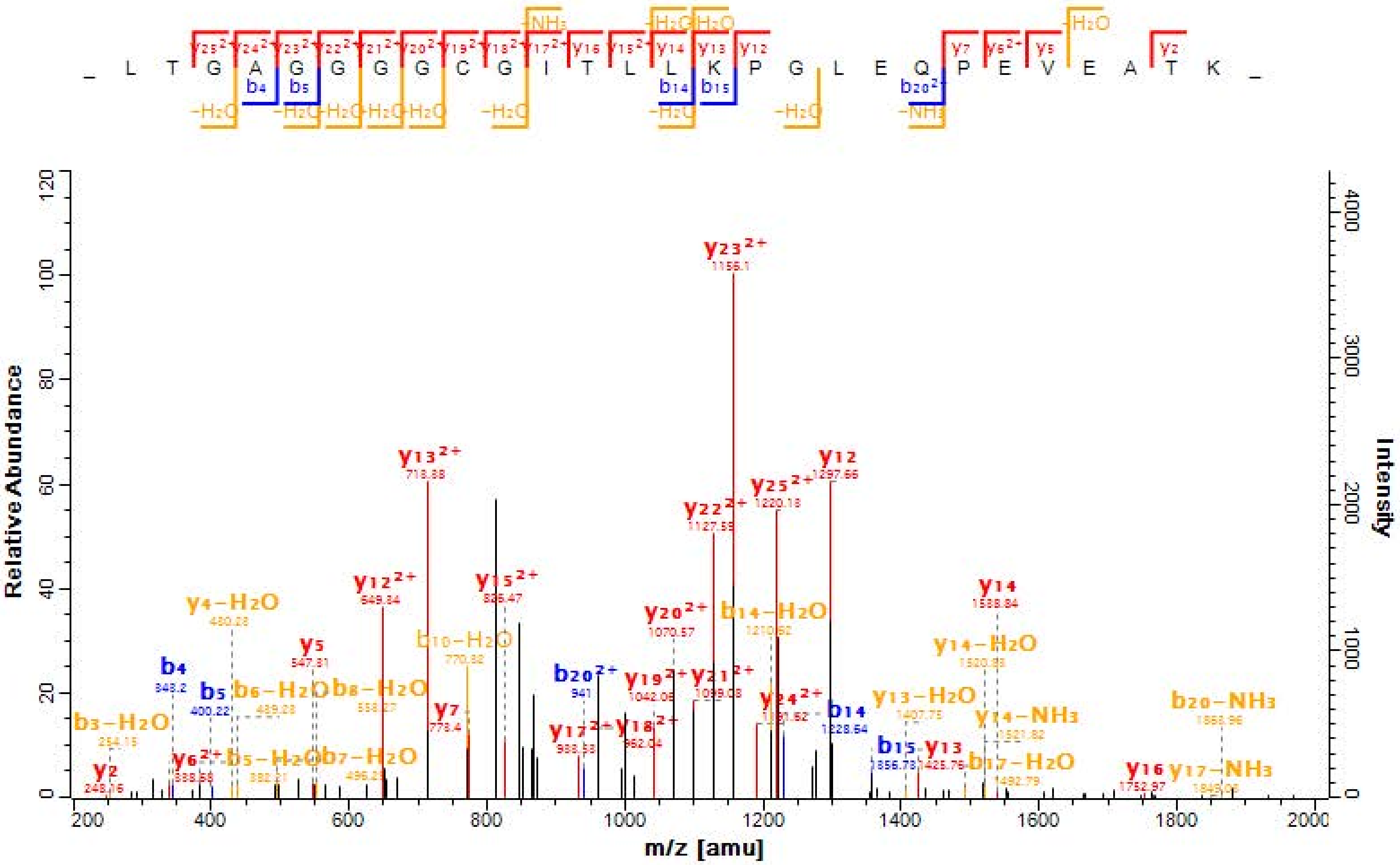
Scan number	5896	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	114.28

precursor information

Mass:	1121.59986
m/z:	561.8072
Charge:	2+
Retentiontime:	34.329227447509
Score:	114.2812
Mass Error [ppm]:	-0.20093
PEP:	0.0005212
Precursor Type:	ISO
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	62 %
Peak Coverage:	26 %
Protein Localisation:	80 ... 88

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	136.0757		164.0706	1	Y	8		
-0.03499	235.1441	+0.028339	263.139	2	V	7	959.544	+0.029763
	306.1812	+0.059524	334.1761	3	A	6	860.4756	+0.043123
	420.2241	+0.142939	448.2191	4	N	5	789.4385	+0.081153
	533.3082		561.3031	5	L	4	675.3956	+0.13647
	680.3766	+0.089583	708.3715	6	F	3	562.3115	
	777.4294		805.4243	7	P	2	415.2431	-0.00982
	940.4927	-0.07998	968.4876	8	Y	1	318.1903	-0.05319
				9	K	0	155.127	

Scan number	6158	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	122.18



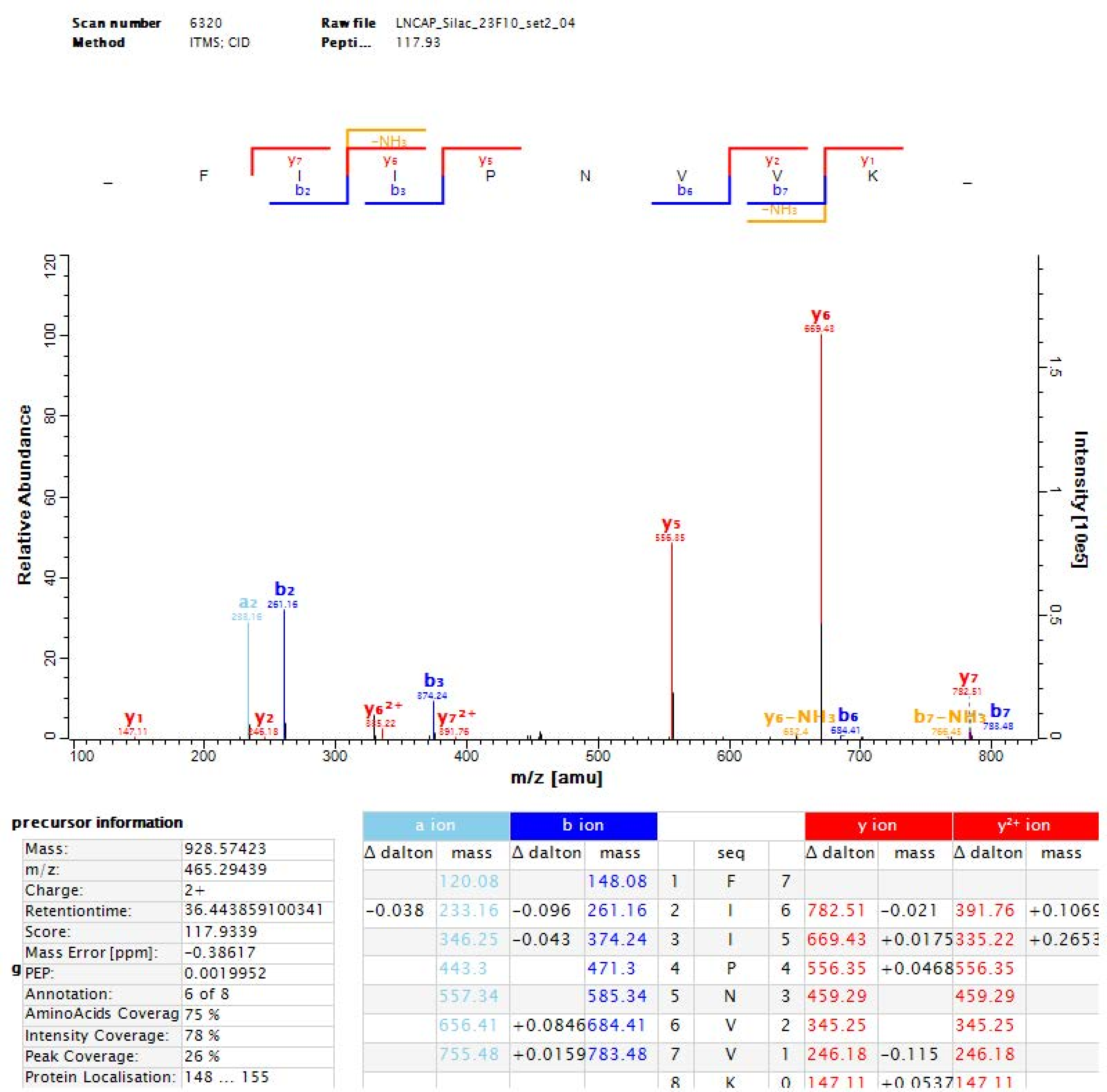
precursor information

Mass:	2652.37925
m/z:	885.13369
Charge:	3+
Retentiontime:	35.645549774169
Score:	122.1781
Mass Error [ppm]:	-0.0062823
PEP:	4.2434E-18
Precursor Type:	MULTI

general information

Annotation:	22 of 27
AminoAcids Coverag	81 %
Intensity Coverage:	53 %
Peak Coverage:	37 %
Protein Localisation:	331 ... 357

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	26				
	215.14		215.14	2	T	25	2540.3		2540.3	
	272.16		272.16	3	G	24	2439.3		1220.1	+0.3038
	343.2	+0.0923	343.2	4	A	23	2382.2		1191.6	+0.0353
	400.22	+0.4115	400.22	5	G	22	2311.2		1156.1	+0.2577
	457.24		457.24	6	G	21	2254.2		1127.6	+0.1585
	514.26		514.26	7	G	20	2197.2		1099.1	-0.004
	571.28		571.28	8	G	19	2140.1		1070.6	+0.0137
	731.31		731.31	9	C	18	2083.1		1042.1	+0.4834
	788.34		788.34	10	G	17	1923.1		962.04	+0.0088
	901.42		901.42	11	I	16	1866.1		933.53	+0.3176
	1002.5		1002.5	12	T	15	1753	+0.0295	1753	
	1115.6		1115.6	13	L	14	1651.9		826.47	+0.2701
	1228.6	-0.012	1228.6	14	L	13	1538.8	-0.19	1538.8	
	1356.7	-0.178	1356.7	15	K	12	1425.8	-0.01	713.38	+0.2193
	1453.8		1453.8	16	P	11	1297.7	-0.008	649.34	+0.2493
	1510.8		1510.8	17	G	10	1200.6		1200.6	
	1623.9		1623.9	18	L	9	1143.6		1143.6	
	1752.9		1752.9	19	E	8	1030.5		1030.5	
+0.3036	941		1881	20	Q	7	901.46		901.46	
	1978		1978	21	P	6	773.4	+0.1218	773.4	
	2107.1		2107.1	22	E	5	676.35		338.68	+0.3506
	2206.2		2206.2	23	V	4	547.31	+0.0488	547.31	
	2335.2		2335.2	24	E	3	448.24		448.24	
	2406.2		2406.2	25	A	2	319.2		319.2	
	2507.3		2507.3	26	T	1	248.16	+0.2767	248.16	
				27	K	0	147.11		147.11	

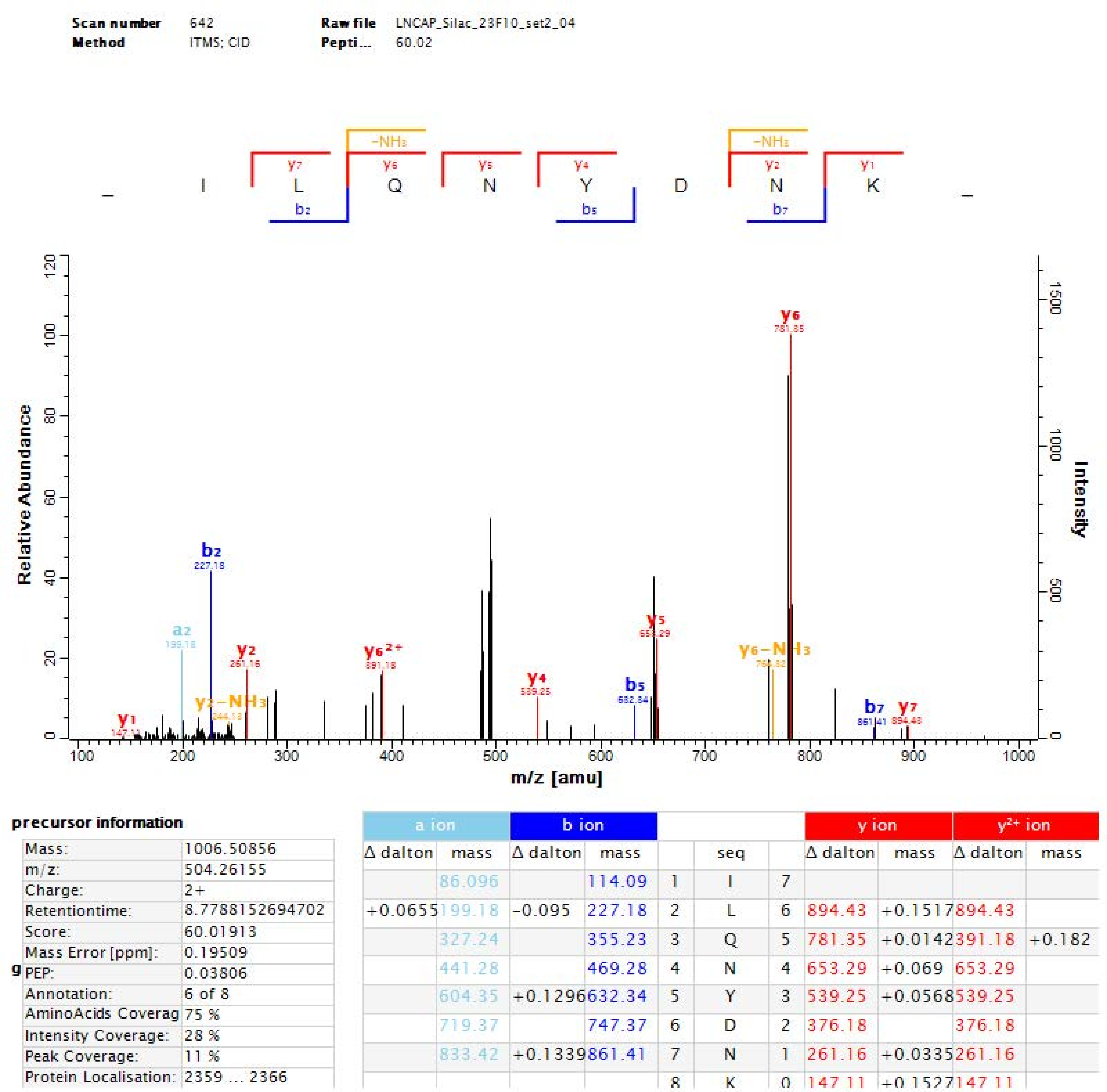


Scan number	6320	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	117.93

precursor information

Mass:	928.57423
m/z:	465.29439
Charge:	2+
Retentiontime:	36.443859100341
Score:	117.9339
Mass Error [ppm]:	-0.38617
PEP:	0.0019952
Annotation:	6 of 8
AminoAcids Coverag	75 %
Intensity Coverage:	78 %
Peak Coverage:	26 %
Protein Localisation:	148 ... 155

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08		148.08	1	F	7				
-0.038	233.16	-0.096	261.16	2	I	6	782.51	-0.021	391.76	+0.1069
	346.25	-0.043	374.24	3	I	5	669.43	+0.0175	335.22	+0.2653
	443.3		471.3	4	P	4	556.35	+0.0468	556.35	
	557.34		585.34	5	N	3	459.29		459.29	
	656.41	+0.0846	684.41	6	V	2	345.25		345.25	
	755.48	+0.0159	783.48	7	V	1	246.18	-0.115	246.18	
				8	K	0	147.11	+0.0537	147.11	



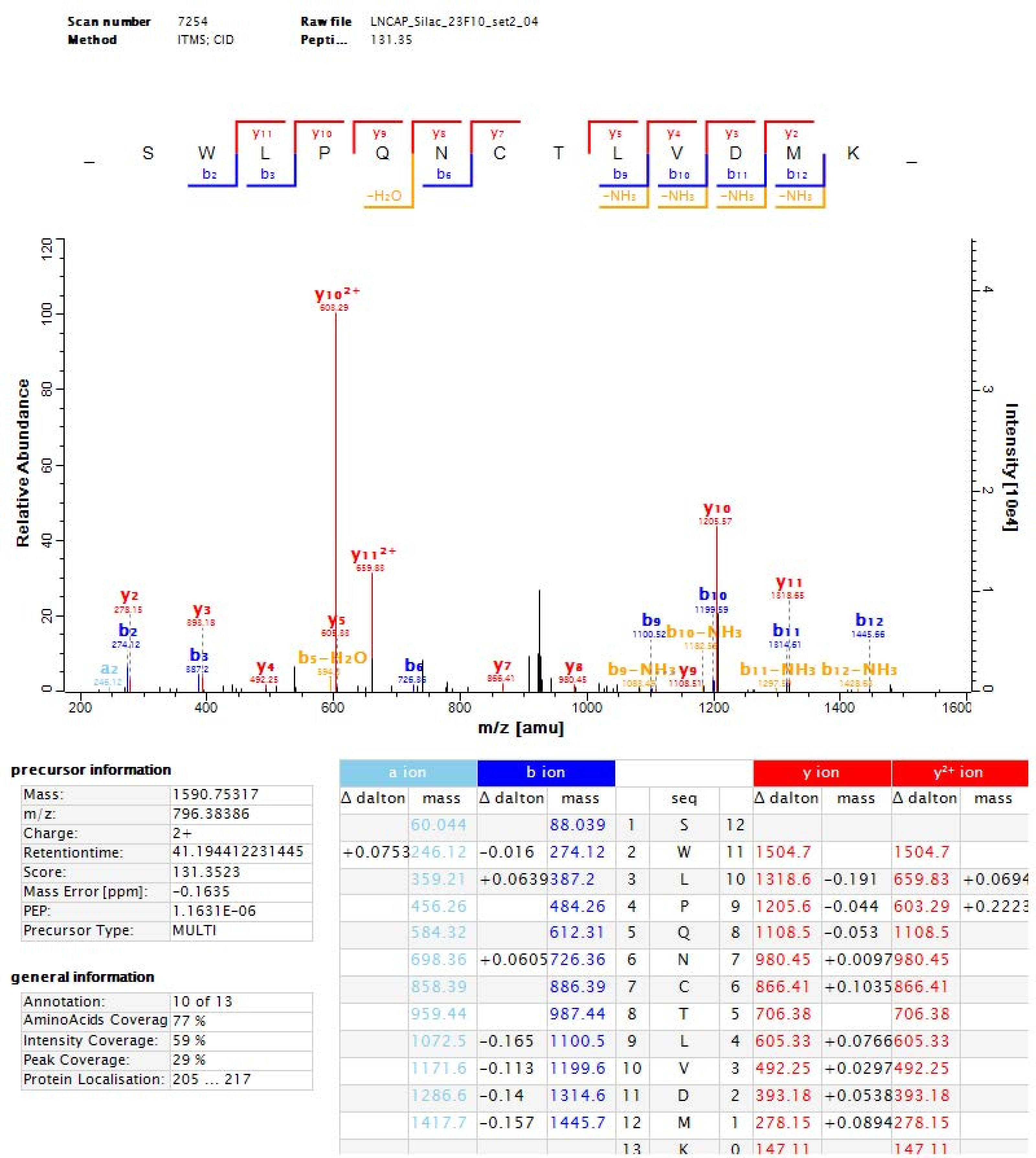
Scan number	642	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	60.02

precursor information

g

Mass:	1006.50856
m/z:	504.26155
Charge:	2+
Retentiontime:	8.7788152694702
Score:	60.01913
Mass Error [ppm]:	0.19509
PEP:	0.03806
Annotation:	6 of 8
AminoAcids Coverag	75 %
Intensity Coverage:	28 %
Peak Coverage:	11 %
Protein Localisation:	2359 ... 2366

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	7				
+0.0655	199.18	-0.095	227.18	2	L	6	894.43	+0.1517	894.43	
	327.24		355.23	3	Q	5	781.35	+0.0142	391.18	+0.182
	441.28		469.28	4	N	4	653.29	+0.069	653.29	
	604.35	+0.1296	632.34	5	Y	3	539.25	+0.0568	539.25	
	719.37		747.37	6	D	2	376.18		376.18	
	833.42	+0.1339	861.41	7	N	1	261.16	+0.0335	261.16	
				8	K	0	147.11	+0.1527	147.11	



Scan number	7254	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	131.35

precursor information

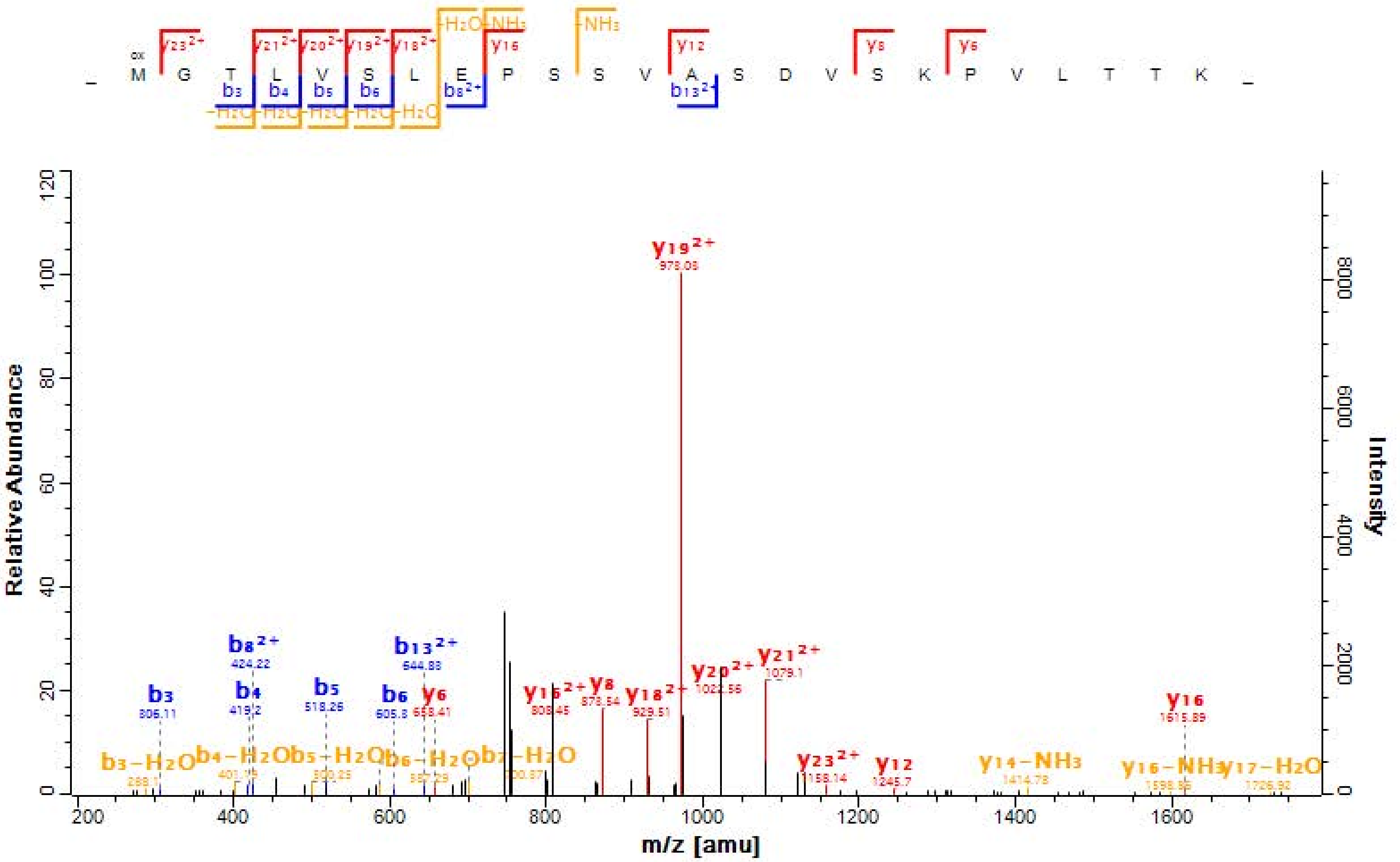
Mass:	1590.75317
m/z:	796.38386
Charge:	2+
Retentiontime:	41.194412231445
Score:	131.3523
Mass Error [ppm]:	-0.1635
PEP:	1.1631E-06
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	59 %
Peak Coverage:	29 %
Protein Localisation:	205 ... 217

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	60.044		88.039	1	S	12				
+0.0753	246.12	-0.016	274.12	2	W	11	1504.7		1504.7	
	359.21	+0.0639	387.2	3	L	10	1318.6	-0.191	659.83	+0.0694
	456.26		484.26	4	P	9	1205.6	-0.044	603.29	+0.2223
	584.32		612.31	5	Q	8	1108.5	-0.053	1108.5	
	698.36	+0.0605	726.36	6	N	7	980.45	+0.0097	980.45	
	858.39		886.39	7	C	6	866.41	+0.1035	866.41	
	959.44		987.44	8	T	5	706.38		706.38	
	1072.5	-0.165	1100.5	9	L	4	605.33	+0.0766	605.33	
	1171.6	-0.113	1199.6	10	V	3	492.25	+0.0297	492.25	
	1286.6	-0.14	1314.6	11	D	2	393.18	+0.0538	393.18	
	1417.7	-0.157	1445.7	12	M	1	278.15	+0.0894	278.15	
				13	K	0	147.11		147.11	

Scan number	7290	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	76.7



precursor information

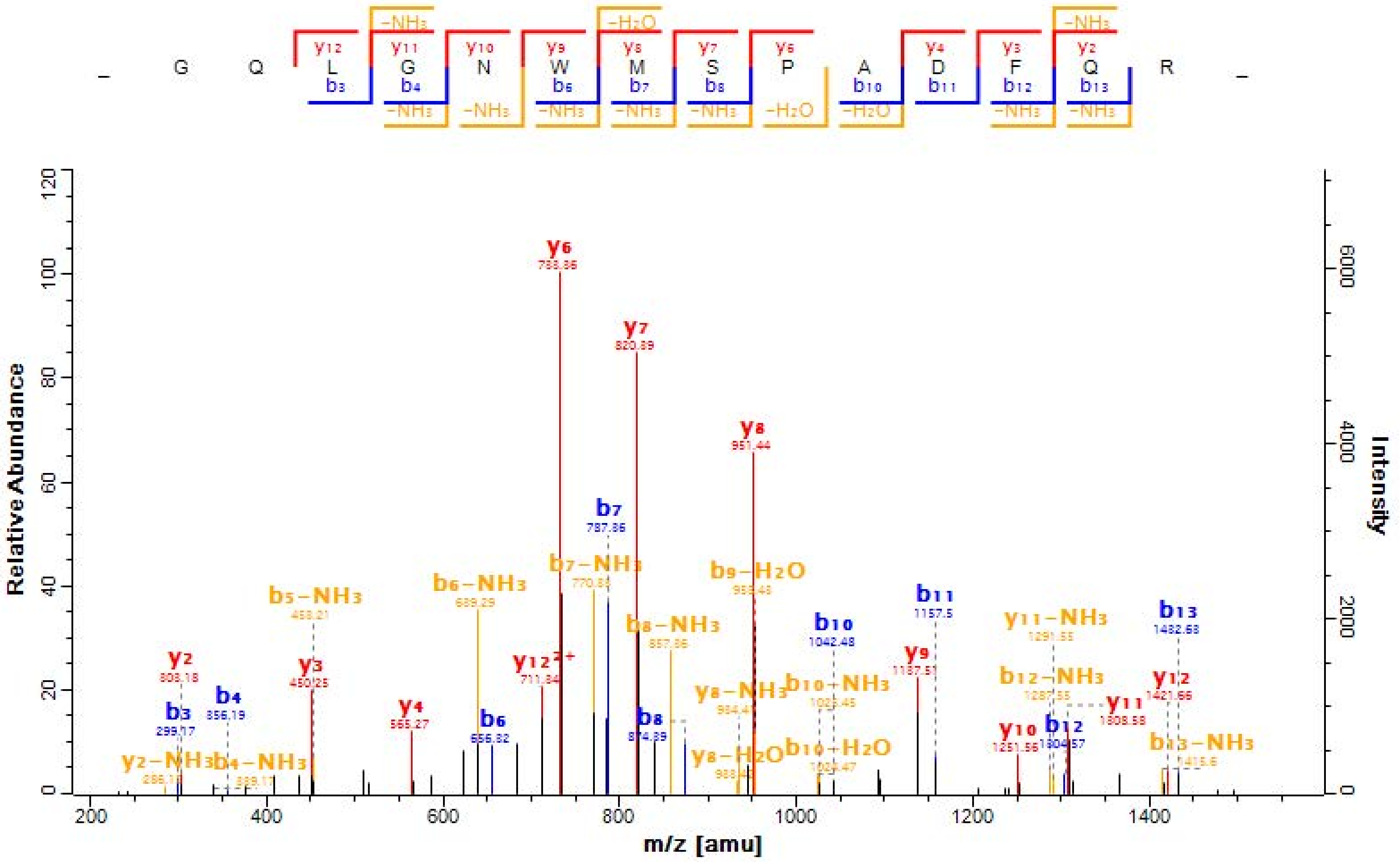
Mass:	2461.299
m/z:	821.44028
Charge:	3+
Retentiontime:	41.375064849853
Score:	76.70426
Mass Error [ppm]:	0.17894
PEP:	5.6097E-05
Precursor Type:	MULTI

general information

Annotation:	13 of 24
AminoAcids Coverag	54 %
Intensity Coverage:	50 %
Peak Coverage:	27 %
Protein Localisation:	42 ... 65

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.04		148.04	1	M	23				
	205.06		205.06	2	G	22	2315.3		1158.1	+0.206
	306.11	+0.1002	306.11	3	T	21	2258.2		2258.2	
	419.2	-0.136	419.2	4	L	20	2157.2		1079.1	+0.2636
	518.26	+0.1033	518.26	5	V	19	2044.1		1022.6	-0.043
	605.3	+0.0059	605.3	6	S	18	1945		973.03	+0.2689
	718.38		718.38	7	L	17	1858		929.51	+0.2228
+0.1569	424.22		847.42	8	E	16	1744.9		1744.9	
	944.48		944.48	9	P	15	1615.9	+0.3558	808.45	+0.0267
	1031.5		1031.5	10	S	14	1518.8		1518.8	
	1118.5		1118.5	11	S	13	1431.8		1431.8	
	1217.6		1217.6	12	V	12	1344.8		1344.8	
-0.107	644.83		1288.6	13	A	11	1245.7	-0.298	1245.7	
	1375.7		1375.7	14	S	10	1174.7		1174.7	
	1490.7		1490.7	15	D	9	1087.6		1087.6	
	1589.8		1589.8	16	V	8	972.61		972.61	
	1676.8		1676.8	17	S	7	873.54	-0.239	873.54	
	1804.9		1804.9	18	K	6	786.51		786.51	
	1902		1902	19	P	5	658.41	-0.105	658.41	
	2001		2001	20	V	4	561.36		561.36	
	2114.1		2114.1	21	L	3	462.29		462.29	
	2215.2		2215.2	22	T	2	349.21		349.21	
	2316.2		2316.2	23	T	1	248.16		248.16	
				24	K	0	147.11		147.11	

Scan number	7531	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	196.33



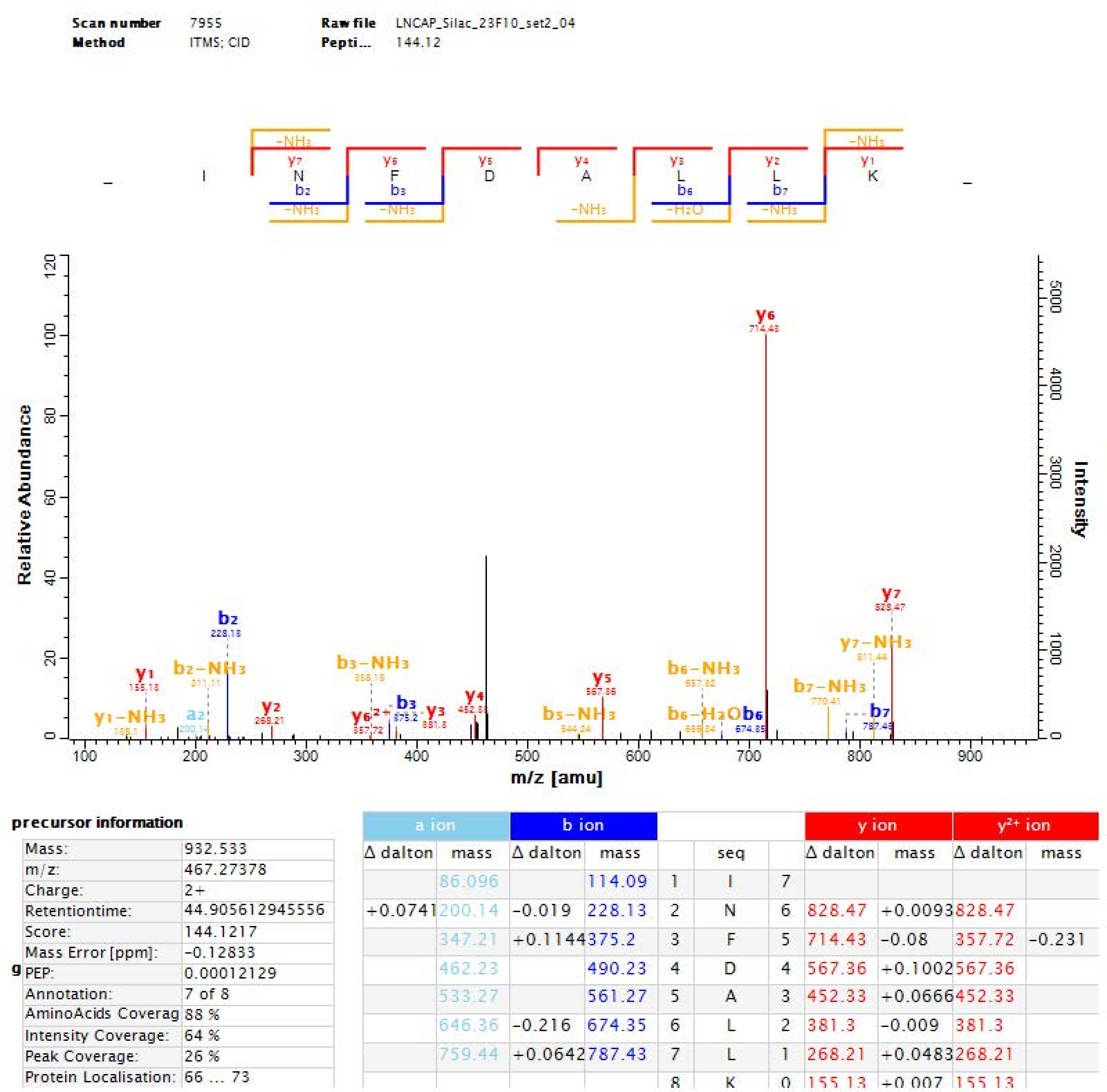
precursor information

Mass:	1605.73591
m/z:	803.87523
Charge:	2+
Retentiontime:	42.652976989746
Score:	196.3342
Mass Error [ppm]:	0.062758
PEP:	9.0273E-19
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	66 %
Peak Coverage:	42 %
Protein Localisation:	129 ... 142

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	13				
	186.0873	2	Q	12	1549.722		1549.722	
+0.021428	299.1714	3	L	11	1421.663	+0.213175	711.3352	+0.020186
+0.142054	356.1928	4	G	10	1308.579	+0.020262	1308.579	
	470.2358	5	N	9	1251.558	+0.066994	1251.558	
+0.062295	656.3151	6	W	8	1137.515	+0.005918	1137.515	
-0.22941	787.3556	7	M	7	951.4353	+0.015834	951.4353	
+0.019139	874.3876	8	S	6	820.3948	+0.02519	820.3948	
	971.4404	9	P	5	733.3628	-0.00656	733.3628	
-0.04791	1042.477	10	A	4	636.31		636.31	
-0.02029	1157.504	11	D	3	565.2729	+0.124635	565.2729	
-0.01729	1304.573	12	F	2	450.2459	+0.034452	450.2459	
-0.15058	1432.631	13	Q	1	303.1775	+0.105948	303.1775	
		14	R	0	175.119		175.119	



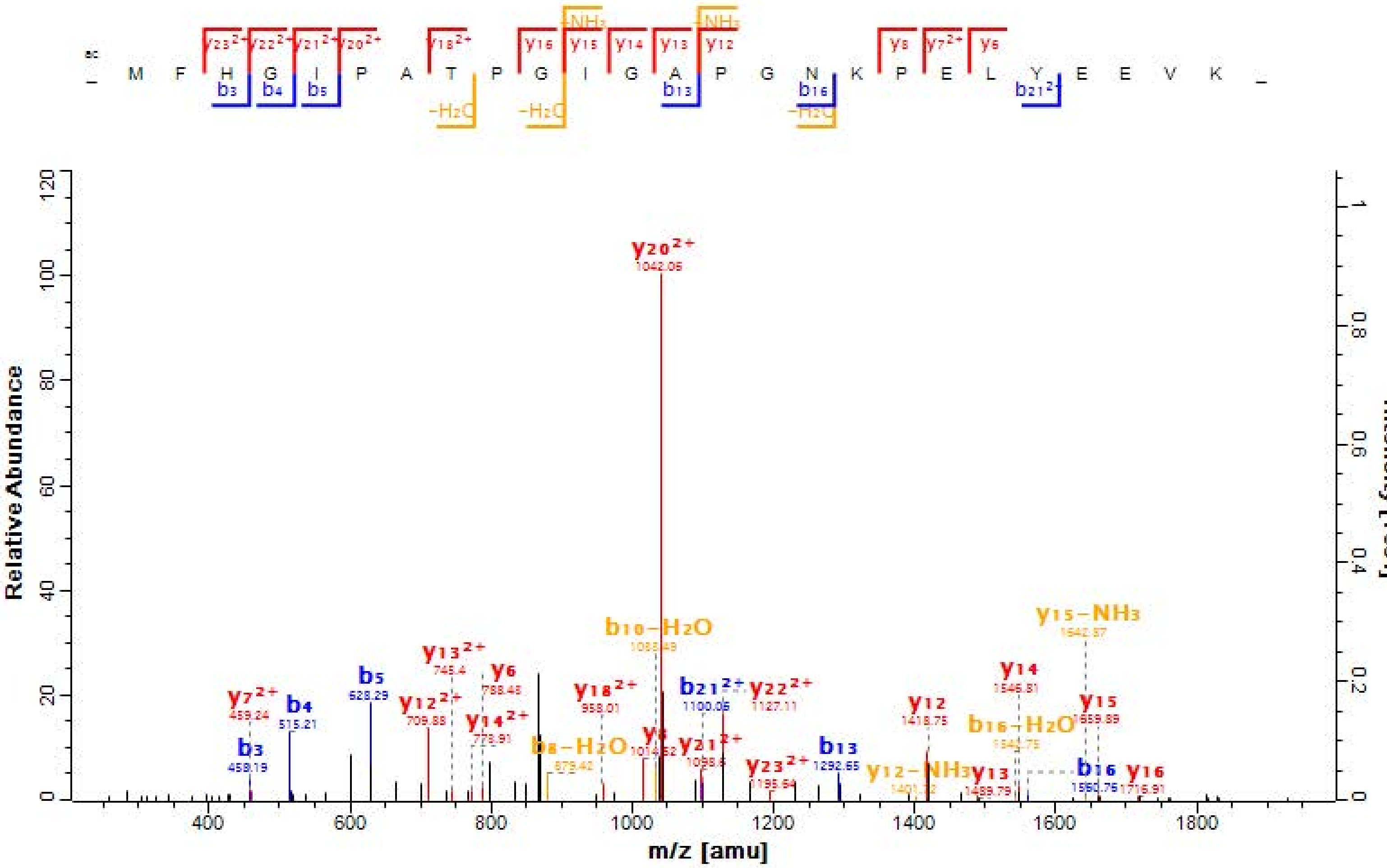
Scan number 7955
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set2_04
Pepti... 144.12

precursor information

Mass:	932.533
m/z:	467.27378
Charge:	2+
Retentiontime:	44.905612945556
Score:	144.1217
Mass Error [ppm]:	-0.12833
PEP:	0.00012129
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	64 %
Peak Coverage:	26 %
Protein Localisation:	66 ... 73

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	7				
+0.0741	200.14	-0.019	228.13	2	N	6	828.47	+0.0093	828.47	
	347.21	+0.1144	375.2	3	F	5	714.43	-0.08	357.72	-0.231
	462.23		490.23	4	D	4	567.36	+0.1002	567.36	
	533.27		561.27	5	A	3	452.33	+0.0666	452.33	
	646.36	-0.216	674.35	6	L	2	381.3	-0.009	381.3	
	759.44	+0.0642	787.43	7	L	1	268.21	+0.0483	268.21	
				8	K	0	155.13	+0.007	155.13	

Scan number	8153	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	96.55



precursor information

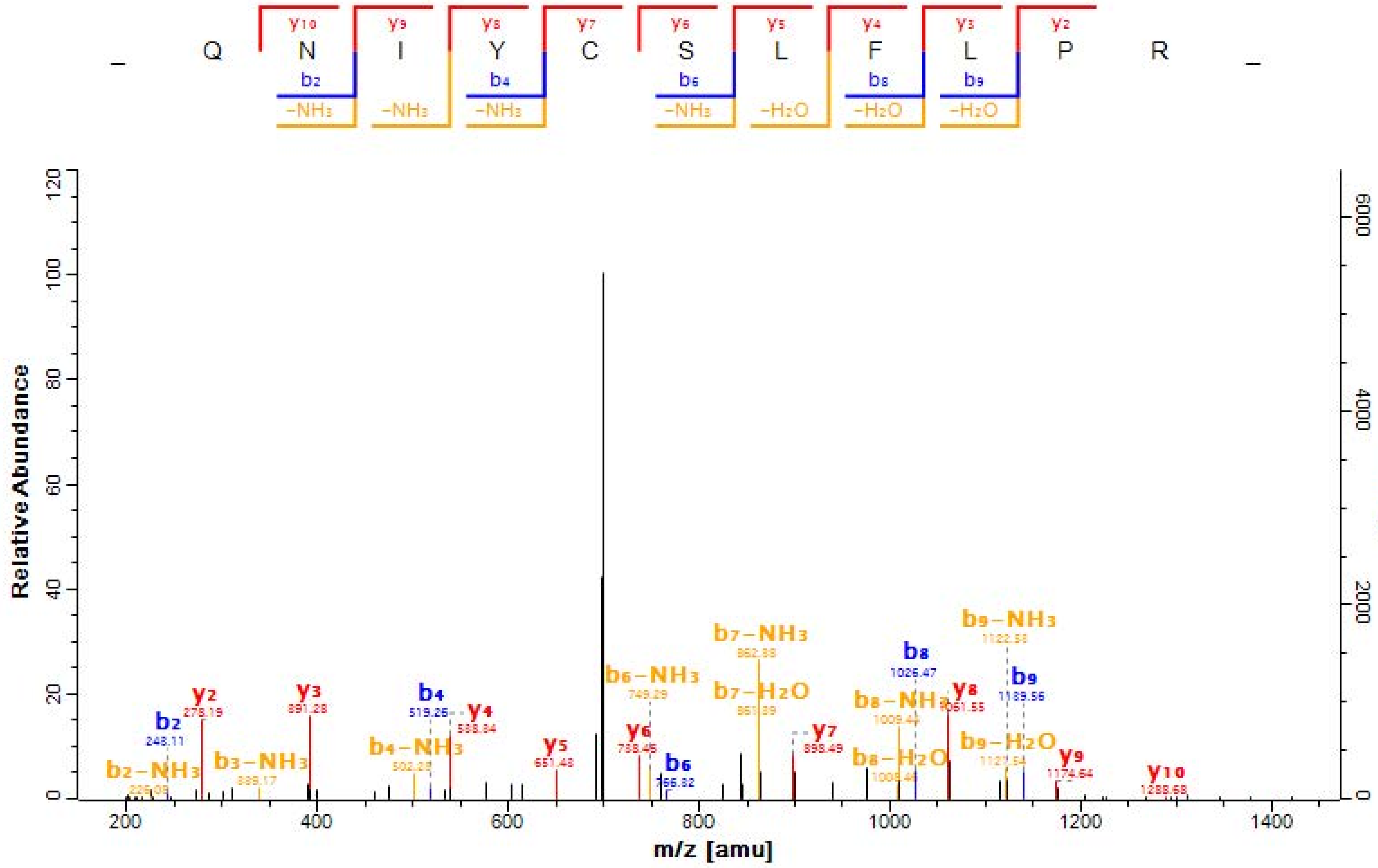
Mass:	2693.35267
m/z:	898.7915
Charge:	3+
Retentiontime:	45.949150085449
Score:	96.5498
Mass Error [ppm]:	0.12665
PEP:	1.7692E-07
Precursor Type:	MULTI

general information

Annotation:	15 of 25
AminoAcids Coverag	60 %
Intensity Coverage:	54 %
Peak Coverage:	27 %
Protein Localisation:	1 ... 25

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	174.06		174.06	1	M	24				
	321.13		321.13	2	F	23	2537.3		2537.3	
	458.19	-0.066	458.19	3	H	22	2390.3		1195.6	+0.3848
	515.21	+0.042	515.21	4	G	21	2253.2		1127.1	+0.038
	628.29	+0.0669	628.29	5	I	20	2196.2		1098.6	-0.007
	725.34		725.34	6	P	19	2083.1		1042.1	+0.1936
	796.38		796.38	7	A	18	1986.1		1986.1	
	897.43		897.43	8	T	17	1915		958.01	+0.351
	994.48		994.48	9	P	16	1814		1814	
	1051.5		1051.5	10	G	15	1716.9	+0.3888	1716.9	
	1164.6		1164.6	11	I	14	1659.9	+0.1906	1659.9	
	1221.6		1221.6	12	G	13	1546.8	-0.177	773.91	-0.303
	1292.6	+0.0652	1292.6	13	A	12	1489.8	+0.1978	745.4	+0.2972
	1389.7		1389.7	14	P	11	1418.7	-0.126	709.88	+0.3377
	1446.7		1446.7	15	G	10	1321.7		1321.7	
	1560.8	-0.057	1560.8	16	N	9	1264.7		1264.7	
	1696.9		1696.9	17	K	8	1150.6		1150.6	
	1793.9		1793.9	18	P	7	1014.5	+0.067	1014.5	
	1923		1923	19	E	6	917.47		459.24	+0.0277
	2036.1		2036.1	20	L	5	788.43	+0.1797	788.43	
-0.406	1100.1		2199.1	21	Y	4	675.34		675.34	
	2328.2		2328.2	22	E	3	512.28		512.28	
	2457.2		2457.2	23	E	2	383.24		383.24	
	2556.3		2556.3	24	V	1	254.2		254.2	
				25	K	0	155.13		155.13	

Scan number	8478	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti…**	125.97



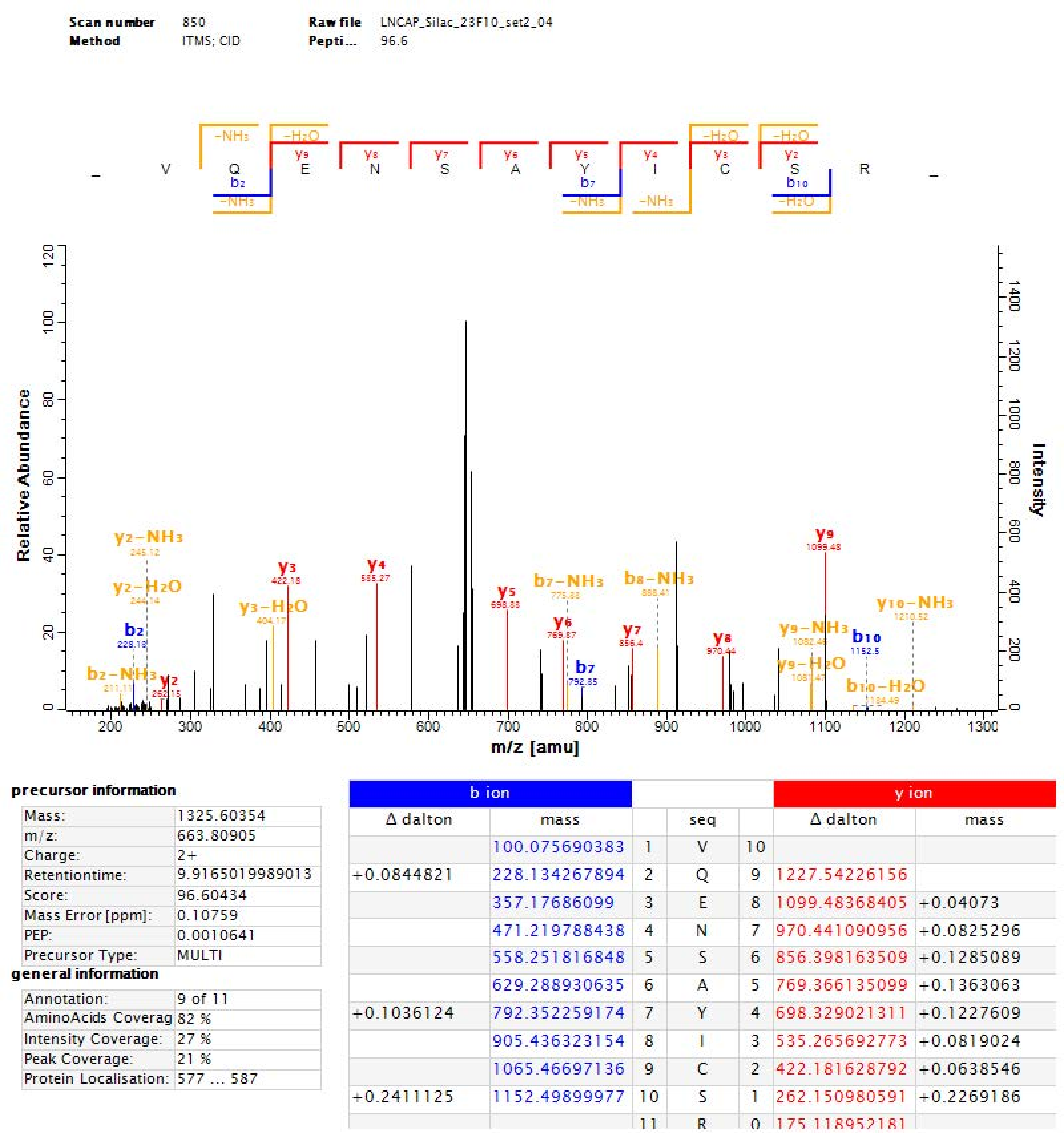
precursor information

Mass:	1409.71271
m/z:	705.86363
Charge:	2+
Retentiontime:	47.686119079589
Score:	125.9703
Mass Error [ppm]:	0.11213
PEP:	0.0001896
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	37 %
Peak Coverage:	27 %
Protein Localisation:	170 … 180

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	129.065853978	1	Q	10		
+0.1070389	243.108781425	2	N	9	1288.68138351	-0.1669792
	356.192845406	3	I	8	1174.63845607	-0.0165078
+0.0845853	519.256173944	4	Y	7	1061.55439209	+0.0239771
	679.286822145	5	C	6	898.491063548	+0.1476694
+0.2647676	766.318850555	6	S	5	738.460415347	-0.0125394
	879.402914536	7	L	4	651.428386937	-0.0218318
-0.0506742	1026.47132845	8	F	3	538.344322956	+0.0318367
-0.2029754	1139.55539243	9	L	2	391.27590904	+0.1288151
	1236.60815628	10	P	1	278.19184506	+0.0421027
		11	R	0	181.139081208	



Scan number	850	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti…**	96.6

precursor information

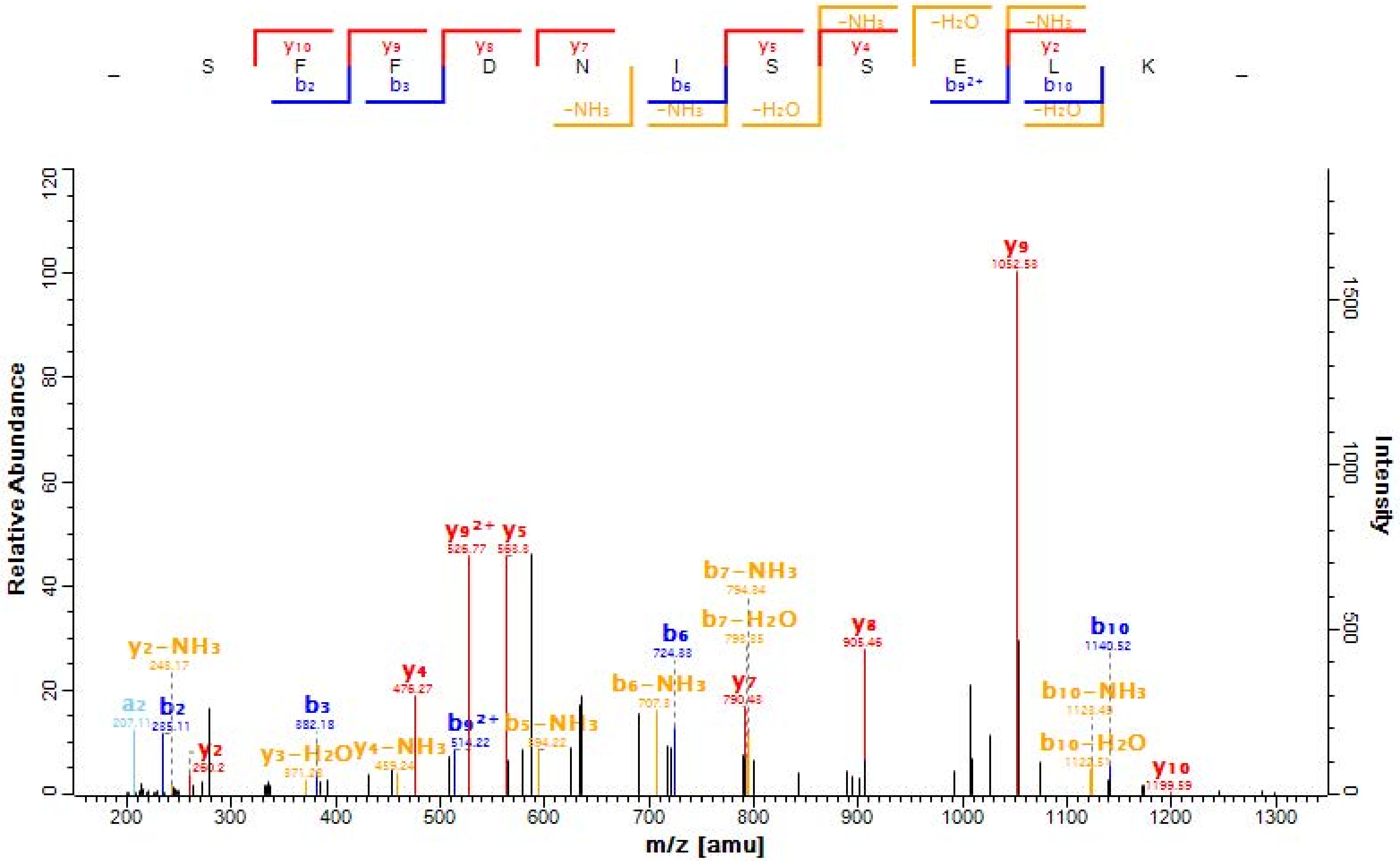
Mass:	1325.60354
m/z:	663.80905
Charge:	2+
Retentiontime:	9.9165019989013
Score:	96.60434
Mass Error [ppm]:	0.10759
PEP:	0.0010641
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	27 %
Peak Coverage:	21 %
Protein Localisation:	577 … 587

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	100.075690383	1	V	10		
+0.0844821	228.134267894	2	Q	9	1227.54226156	
	357.17686099	3	E	8	1099.48368405	+0.04073
	471.219788438	4	N	7	970.441090956	+0.0825296
	558.251816848	5	S	6	856.398163509	+0.1285089
	629.288930635	6	A	5	769.366135099	+0.1363063
+0.1036124	792.352259174	7	Y	4	698.329021311	+0.1227609
	905.436323154	8	I	3	535.265692773	+0.0819024
	1065.46697136	9	C	2	422.181628792	+0.0638546
+0.2411125	1152.49899977	10	S	1	262.150980591	+0.2269186
		11	R	0	175.118952181	

Scan number	8501	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	126.19



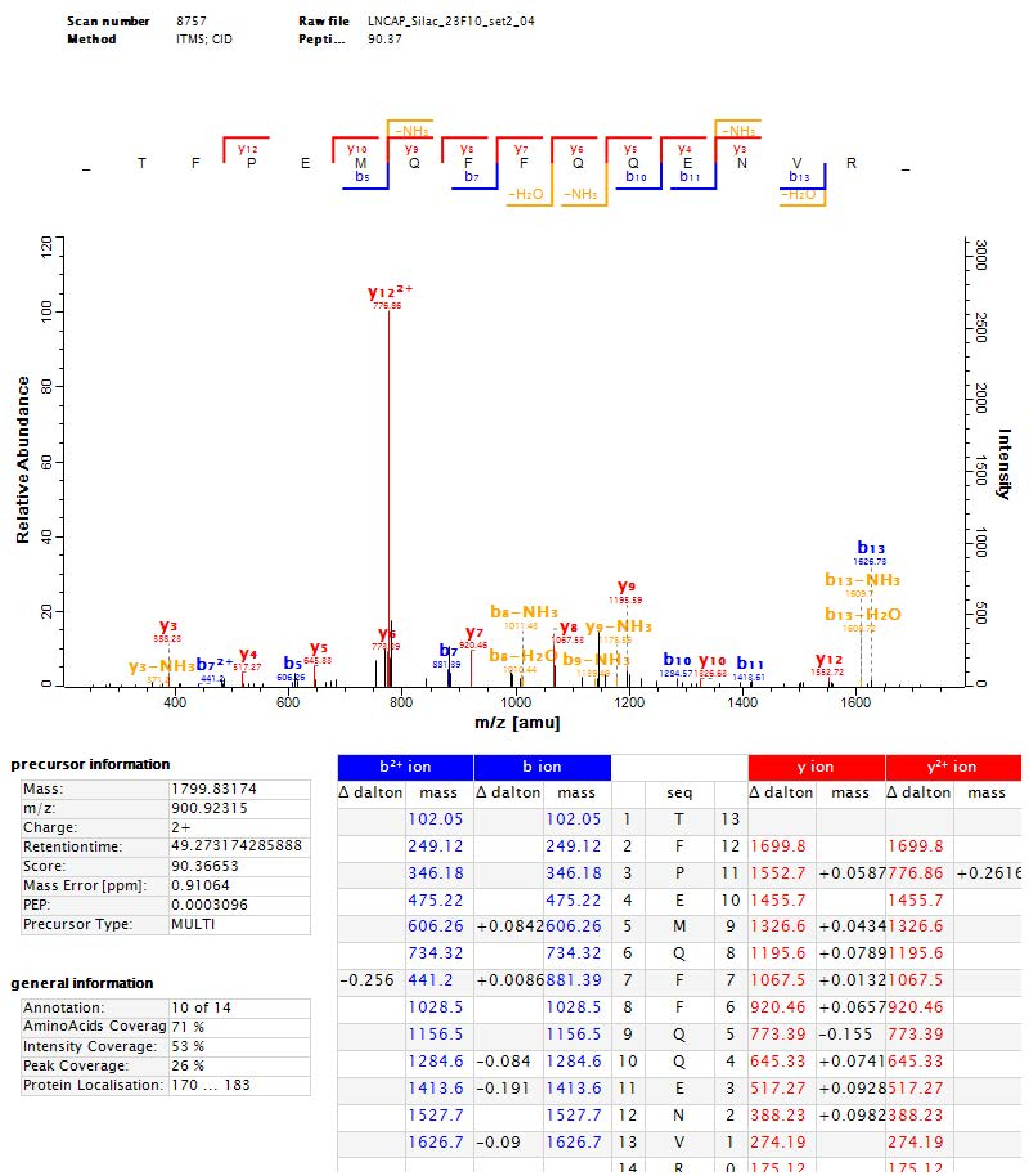
precursor information

Mass:	1285.61942
m/z:	643.81699
Charge:	2+
Retentiontime:	47.816772460937
Score:	126.1938
Mass Error [ppm]:	0.3038
PEP:	7.8407E-05
Precursor Type:	ISO

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	53 %
Peak Coverage:	27 %
Protein Localisation:	317 ... 327

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	60.04		88.04		88.04	1	S	10				
+0.074	207.1		235.1	-0.17	235.1	2	F	9	1200	-0.04	1200	
	354.2		382.2	+0.013	382.2	3	F	8	1053	-0.03	526.8	+0.28
	469.2		497.2		497.2	4	D	7	905.5	-0.06	905.5	
	583.3		611.2		611.2	5	N	6	790.4	+0.245	790.4	
	696.3		724.3	-0.16	724.3	6	I	5	676.4		676.4	
	783.4		811.4		811.4	7	S	4	563.3	+0.132	563.3	
	870.4		898.4		898.4	8	S	3	476.3	+0.172	476.3	
	999.4	+0.182	514.2		1027	9	E	2	389.2		389.2	
	1113		1141	-0.05	1141	10	L	1	260.2	+0	260.2	
						11	K	0	147.1		147.1	



Scan number	8757	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	90.37

precursor information

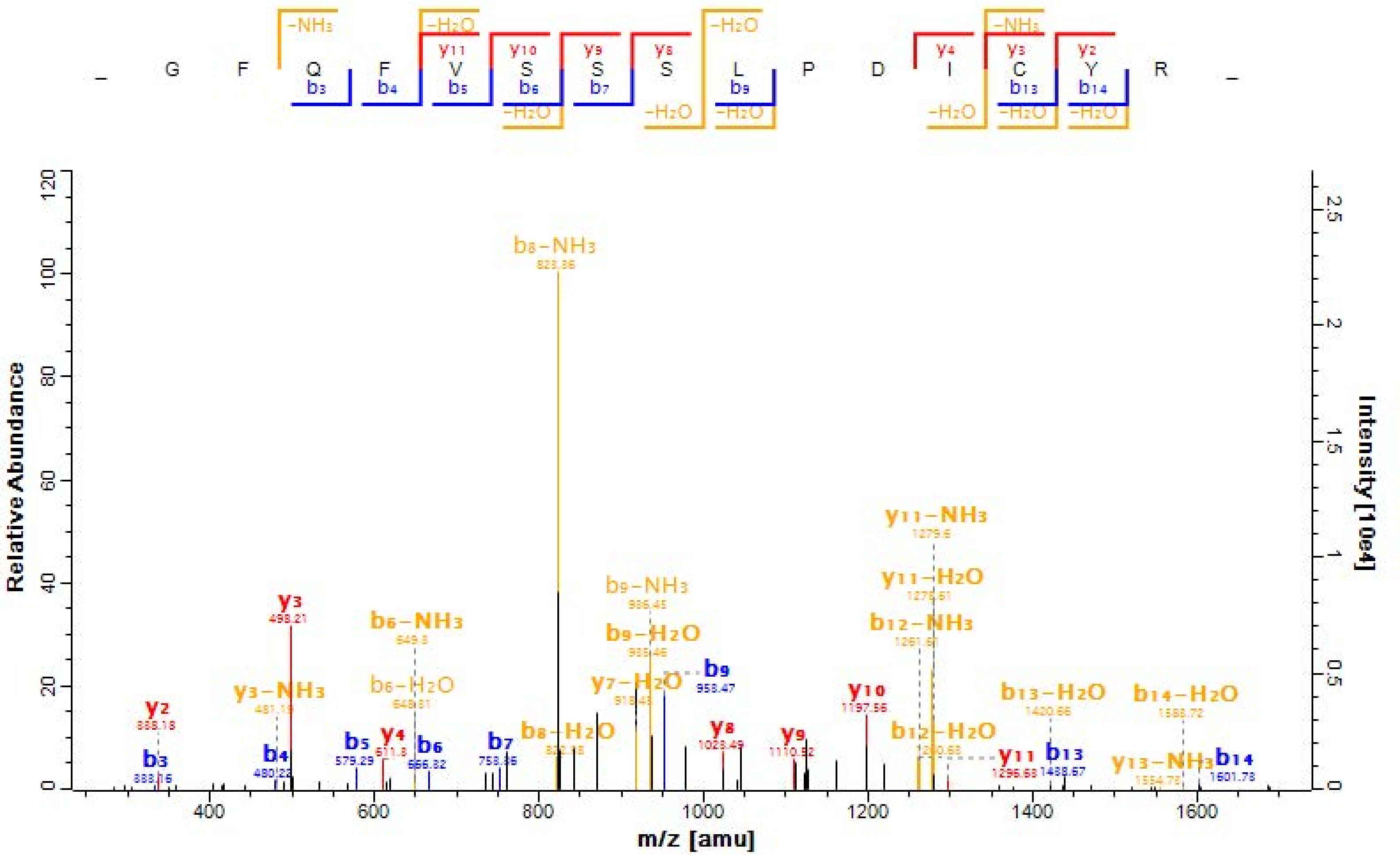
Mass:	1799.83174
m/z:	900.92315
Charge:	2+
Retentiontime:	49.273174285888
Score:	90.36653
Mass Error [ppm]:	0.91064
PEP:	0.0003096
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	53 %
Peak Coverage:	26 %
Protein Localisation:	170 ... 183

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	13				
	249.12		249.12	2	F	12	1699.8		1699.8	
	346.18		346.18	3	P	11	1552.7	+0.0587	776.86	+0.2616
	475.22		475.22	4	E	10	1455.7		1455.7	
	606.26	+0.0842	606.26	5	M	9	1326.6	+0.0434	1326.6	
	734.32		734.32	6	Q	8	1195.6	+0.0789	1195.6	
-0.256	441.2	+0.0086	881.39	7	F	7	1067.5	+0.0132	1067.5	
	1028.5		1028.5	8	F	6	920.46	+0.0657	920.46	
	1156.5		1156.5	9	Q	5	773.39	-0.155	773.39	
	1284.6	-0.084	1284.6	10	Q	4	645.33	+0.0741	645.33	
	1413.6	-0.191	1413.6	11	E	3	517.27	+0.0928	517.27	
	1527.7		1527.7	12	N	2	388.23	+0.0982	388.23	
	1626.7	-0.09	1626.7	13	V	1	274.19		274.19	
				14	R	0	175.12		175.12	

Scan number	8766	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	147.56



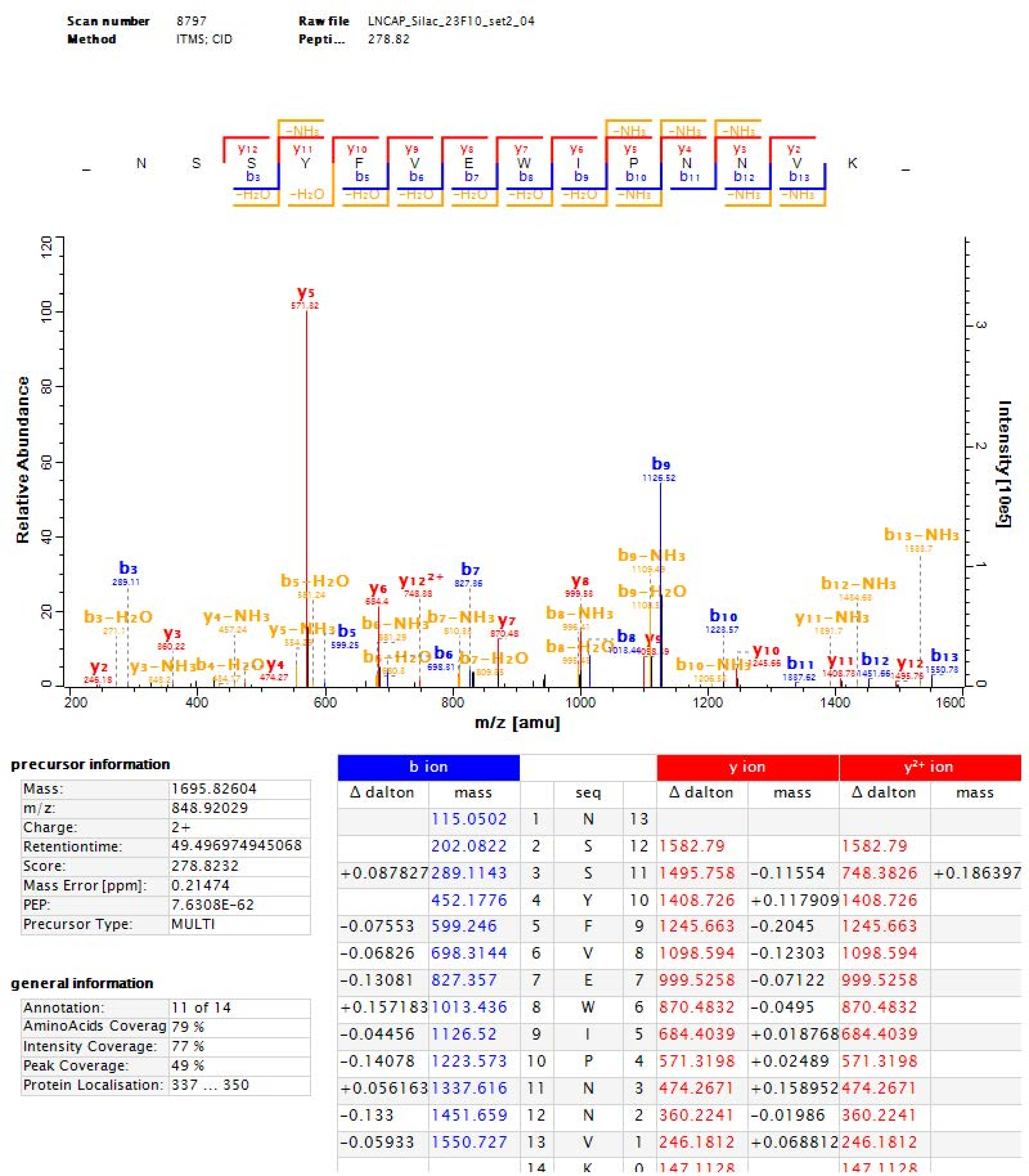
precursor information

Mass:	1774.83465
m/z:	888.4246
Charge:	2+
Retentiontime:	49.325603485107
Score:	147.5608
Mass Error [ppm]:	-0.11745
PEP:	6.8065E-09
Precursor Type:	ISO

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	60 %
Peak Coverage:	36 %
Protein Localisation:	42 ... 56

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	58.02874019	1	G	14		
	205.097154106	2	F	13	1718.82066826	
+0.0194698	333.155731618	3	Q	12	1571.75225434	
+0.0154785	480.224145534	4	F	11	1443.69367683	
+0.0275089	579.29255945	5	V	10	1296.62526291	-0.104633
+0.0805635	666.32458786	6	S	9	1197.556849	-0.0338998
-0.1653931	753.35661627	7	S	8	1110.52482059	-0.0132239
	840.38864468	8	S	7	1023.49279218	-0.0027409
-0.1055822	953.47270866	9	L	6	936.460763766	
	1050.52547251	10	P	5	823.376699785	
	1165.55241554	11	D	4	726.323935933	
	1278.63647952	12	I	3	611.296992901	+0.2068523
-0.0971814	1438.66712773	13	C	2	498.212928921	+0.0350569
-0.2150754	1601.73045626	14	Y	1	338.182280719	-0.0932915
		15	R	0	175.118952181	



Scan number	8797	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	278.82

precursor information

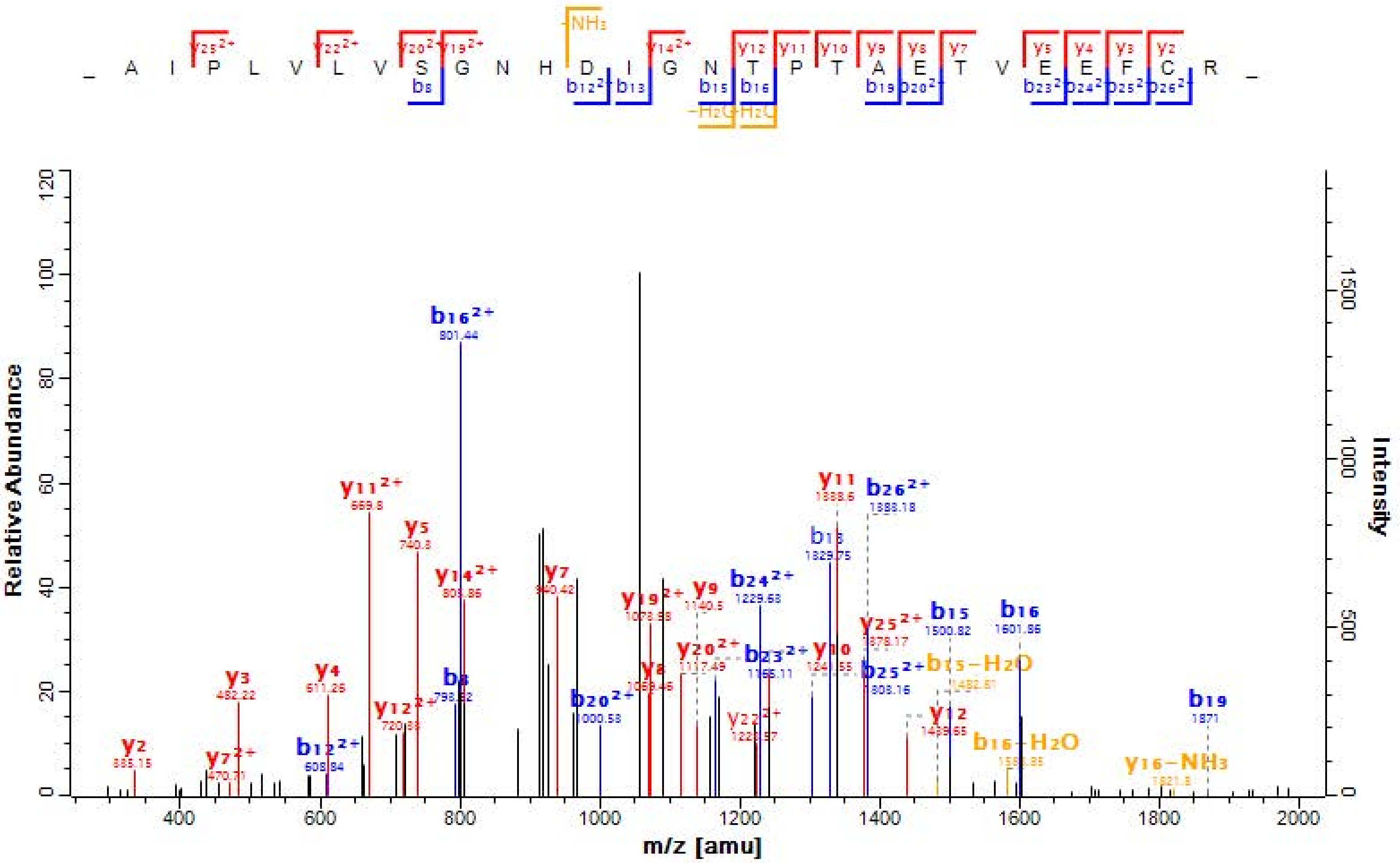
Mass:	1695.82604
m/z:	848.92029
Charge:	2+
Retentiontime:	49.496974945068
Score:	278.8232
Mass Error [ppm]:	0.21474
PEP:	7.6308E-62
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	77 %
Peak Coverage:	49 %
Protein Localisation:	337 ... 350

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502	1	N	13				
	202.0822	2	S	12	1582.79		1582.79	
+0.087827	289.1143	3	S	11	1495.758	-0.11554	748.3826	+0.186397
	452.1776	4	Y	10	1408.726	+0.117909	1408.726	
-0.07553	599.246	5	F	9	1245.663	-0.2045	1245.663	
-0.06826	698.3144	6	V	8	1098.594	-0.12303	1098.594	
-0.13081	827.357	7	E	7	999.5258	-0.07122	999.5258	
+0.157183	1013.436	8	W	6	870.4832	-0.0495	870.4832	
-0.04456	1126.52	9	I	5	684.4039	+0.018768	684.4039	
-0.14078	1223.573	10	P	4	571.3198	+0.02489	571.3198	
+0.056163	1337.616	11	N	3	474.2671	+0.158952	474.2671	
-0.133	1451.659	12	N	2	360.2241	-0.01986	360.2241	
-0.05933	1550.727	13	V	1	246.1812	+0.068812	246.1812	
		14	K	0	147.1128		147.1128	

Scan number	8872	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	121.39



precursor information

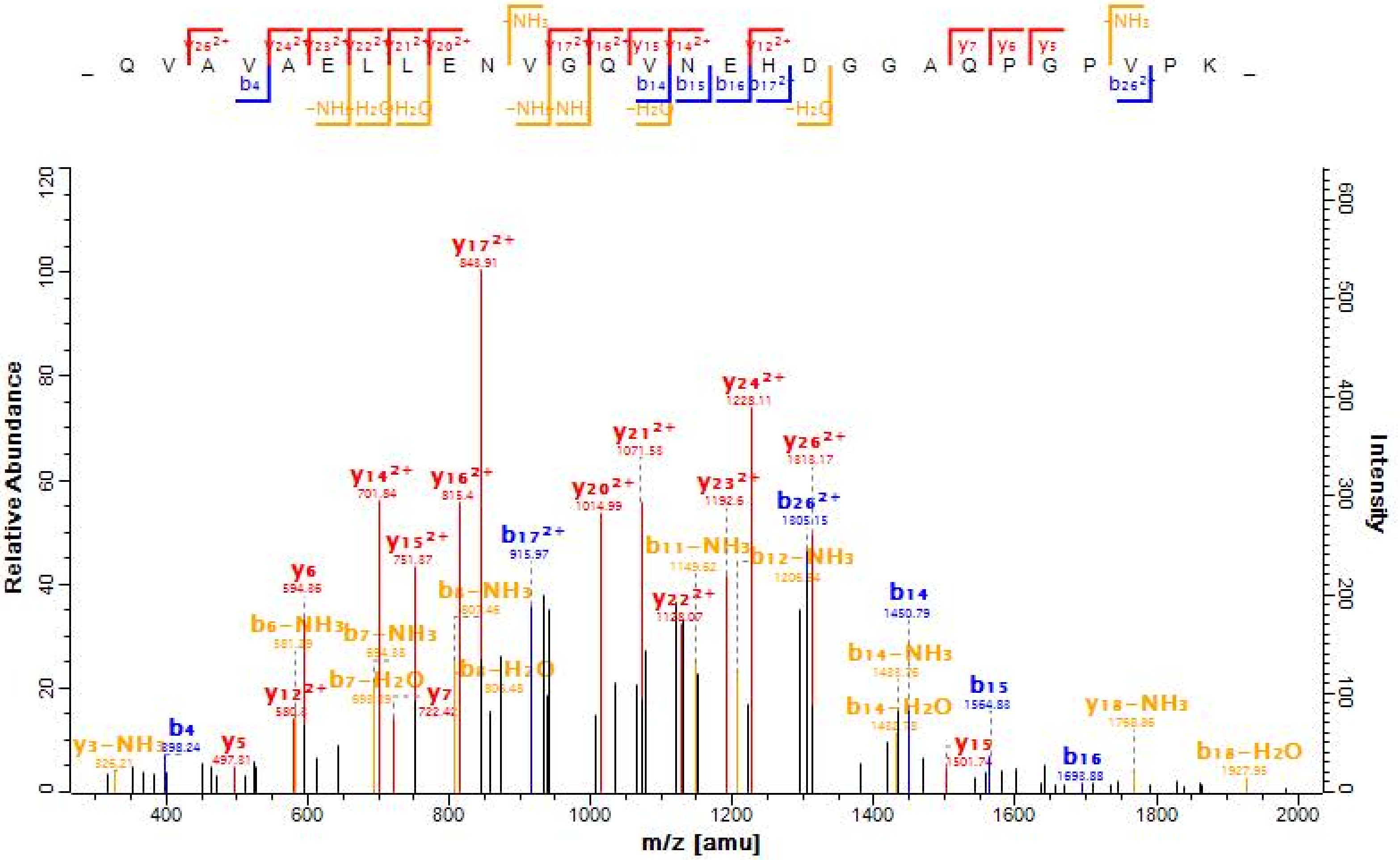
Mass:	2938.4484
m/z:	980.49008
Charge:	3+
Retentiontime:	49.905361175537
Score:	121.3915
Mass Error [ppm]:	-0.36496
PEP:	5.5008E-18
Precursor Type:	MULTI

general information

Annotation:	20 of 27
AminoAcids Coverag	74 %
Intensity Coverage:	53 %
Peak Coverage:	36 %
Protein Localisation:	118 ... 144

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	26				
	185.13		185.13	2	I	25	2868.4		2868.4	
	282.18		282.18	3	P	24	2755.3		1378.2	+0.1512
	395.27		395.27	4	L	23	2658.3		2658.3	
	494.33		494.33	5	V	22	2545.2		2545.2	
	607.42		607.42	6	L	21	2446.1		1223.6	+0.3523
	706.49		706.49	7	V	20	2333		2333	
	793.52	-0.14	793.52	8	S	19	2234		1117.5	+0.0809
	850.54		850.54	9	G	18	2146.9		1074	+0.1493
	964.58		964.58	10	N	17	2089.9		2089.9	
	1101.6		1101.6	11	H	16	1975.9		1975.9	
-0.283	608.84		1216.7	12	D	15	1838.8		1838.8	
	1329.8	-0.047	1329.8	13	I	14	1723.8		1723.8	
	1386.8		1386.8	14	G	13	1610.7		805.86	-0.032
	1500.8	-0.087	1500.8	15	N	12	1553.7		1553.7	
+0.073	801.44	-0.124	1601.9	16	T	11	1439.6	-0.065	720.33	+0.0804
	1698.9		1698.9	17	P	10	1338.6	-0.075	669.8	+0.2197
	1800		1800	18	T	9	1241.5	+0.3654	1241.5	
	1871	-0.113	1871	19	A	8	1140.5	+0.0103	1140.5	
+0.0144	1000.5		2000	20	E	7	1069.5	-0.025	1069.5	
	2101.1		2101.1	21	T	6	940.42	+0.0708	470.71	-0.033
	2200.2		2200.2	22	V	5	839.37		839.37	
+0.1876	1165.1		2329.2	23	E	4	740.3	+0.0266	740.3	
+0.2032	1229.6		2458.2	24	E	3	611.26	+0.037	611.26	
+0.4955	1303.2		2605.3	25	F	2	482.22	+0.1289	482.22	
+0.1158	1383.2		2765.3	26	C	1	335.15	+0.0726	335.15	
				27	R	0	175.12		175.12	

Scan number	8949	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	108.25



precursor information

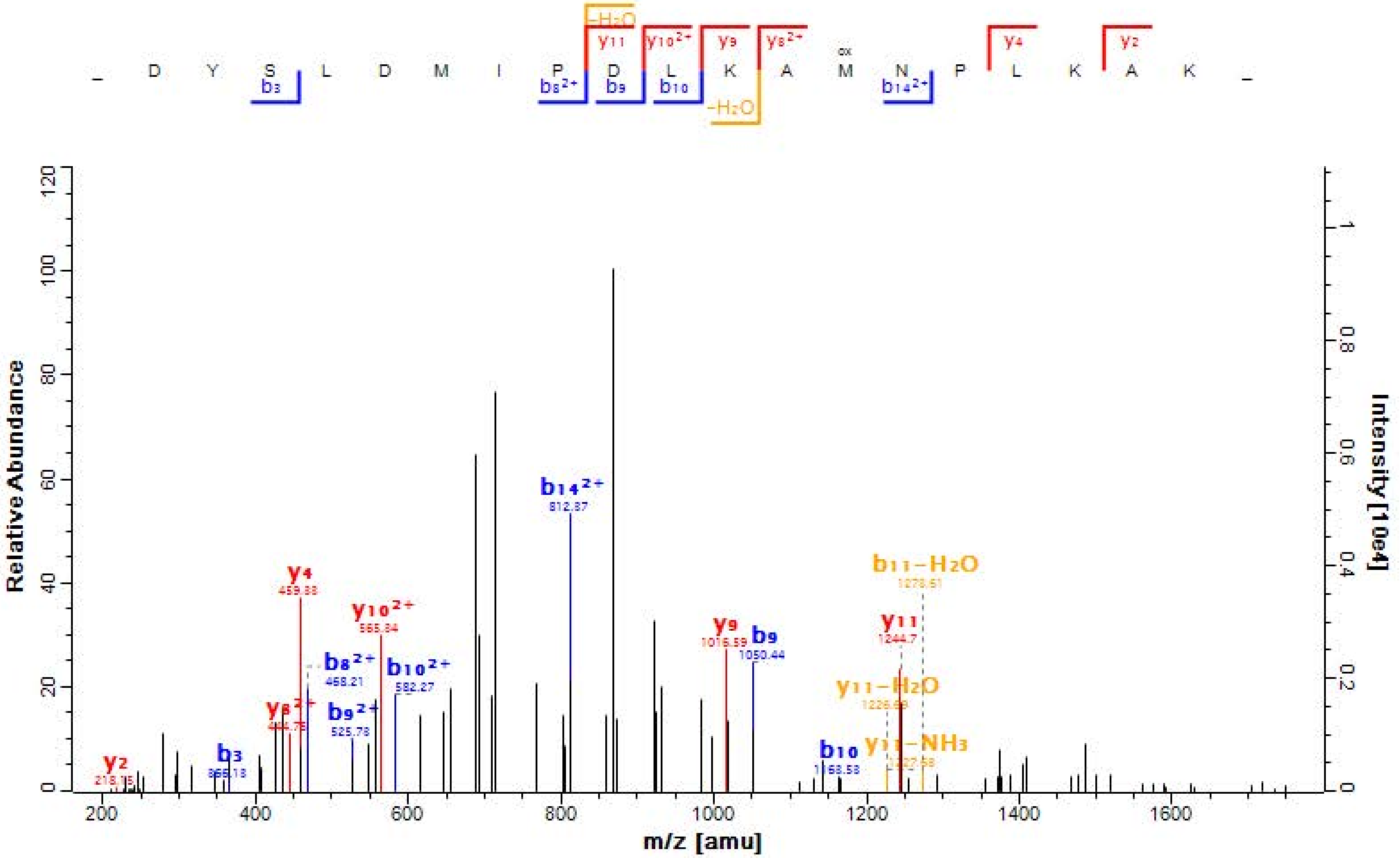
Mass:	2851.4471
m/z:	951.48964
Charge:	3+
Retentiontime:	50.327705383300
Score:	108.2531
Mass Error [ppm]:	0.23191
PEP:	1.0717E-16
Precursor Type:	MULTI

general information

Annotation:	19 of 28
AminoAcids Coverag	68 %
Intensity Coverage:	57 %
Peak Coverage:	36 %
Protein Localisation:	194 ... 221

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.07		129.07	1	Q	27				
	228.13		228.13	2	V	26	2724.4		2724.4	
	299.17		299.17	3	A	25	2625.3		1313.2	+0.2063
	398.24	-0.051	398.24	4	V	24	2554.3		2554.3	
	469.28		469.28	5	A	23	2455.2		1228.1	+0.2156
	598.32		598.32	6	E	22	2384.2		1192.6	+0.0811
	711.4		711.4	7	L	21	2255.1		1128.1	+0.0509
	824.49		824.49	8	L	20	2142.1		1071.5	+0.2515
	953.53		953.53	9	E	19	2029		1015	+0.3224
	1067.6		1067.6	10	N	18	1899.9		1899.9	
	1166.6		1166.6	11	V	17	1785.9		1785.9	
	1223.7		1223.7	12	G	16	1686.8		843.91	+0.2848
	1351.7		1351.7	13	Q	15	1629.8		815.4	+0.2918
	1450.8	-0.161	1450.8	14	V	14	1501.7	+0.1222	751.37	+0.2537
	1564.8	-0.143	1564.8	15	N	13	1402.7		701.84	+0.1024
	1693.9	+0.0261	1693.9	16	E	12	1288.6		1288.6	
+0.2715	915.97		1830.9	17	H	11	1159.6		580.3	-0.042
	1946		1946	18	D	10	1022.5		1022.5	
	2003		2003	19	G	9	907.5		907.5	
	2060		2060	20	G	8	850.48		850.48	
	2131		2131	21	A	7	793.46		793.46	
	2259.1		2259.1	22	Q	6	722.42	+0.1123	722.42	
	2356.2		2356.2	23	P	5	594.36	+0.0759	594.36	
	2413.2		2413.2	24	G	4	497.31	-0.135	497.31	
	2510.2		2510.2	25	P	3	440.29		440.29	
-0.016	1305.2		2609.3	26	V	2	343.23		343.23	
	2706.3		2706.3	27	P	1	244.17		244.17	
				28	K	0	147.11		147.11	

Scan number	9144	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	51.26



precursor information

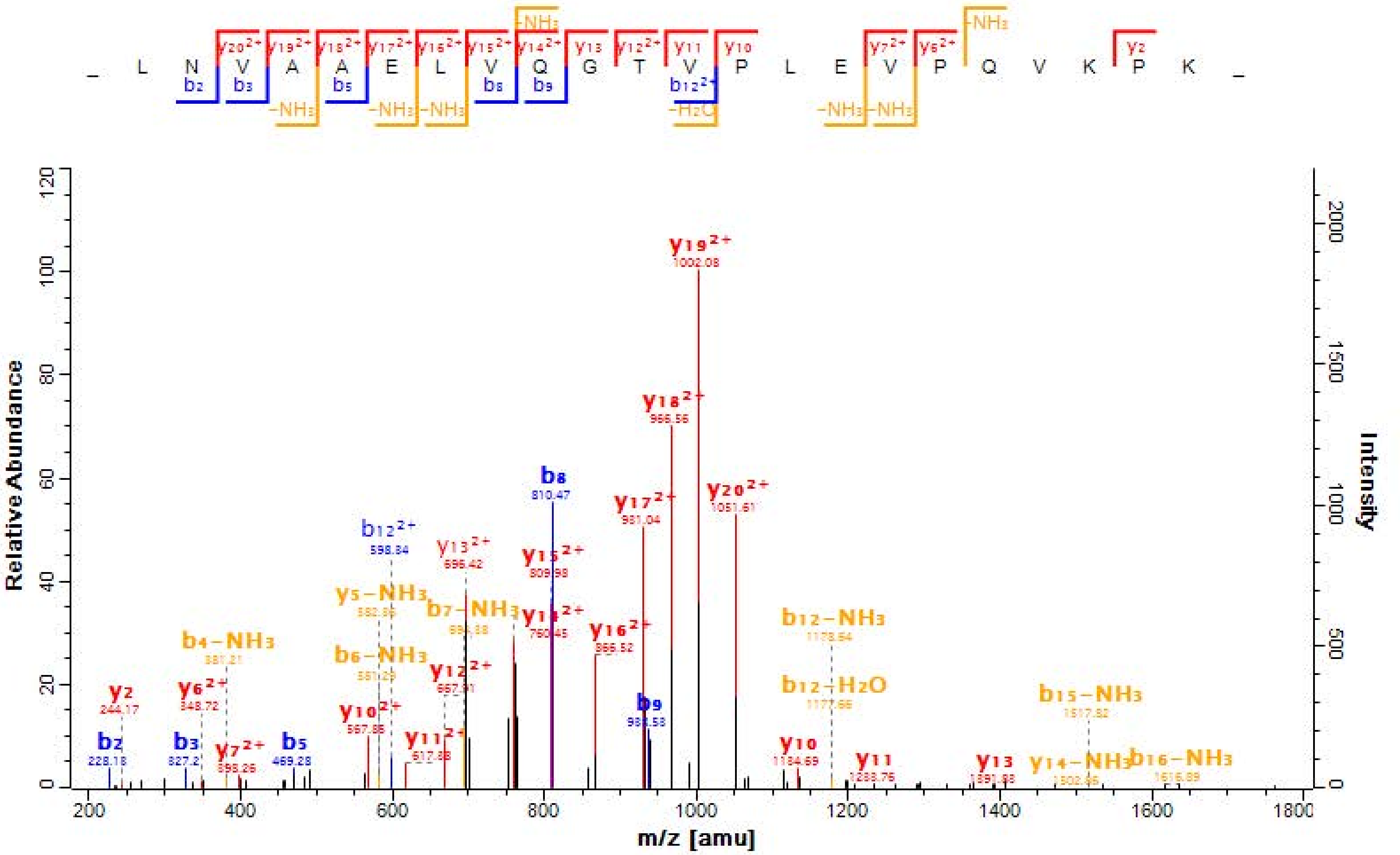
Mass:	2178.10627
m/z:	727.0427
Charge:	3+
Retentiontime:	51.423927307128
Score:	51.26491
Mass Error [ppm]:	−0.086044
PEP:	0.01971
Precursor Type:	MULTI

general information

Annotation:	9 of 19
AminoAcids Coverag	47 %
Intensity Coverage:	24 %
Peak Coverage:	16 %
Protein Localisation:	100 ... 118

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	18				
	279.1		279.1	2	Y	17	2064.1		2064.1	
	366.13	+0.2063	366.13	3	S	16	1901		1901	
	479.21		479.21	4	L	15	1814		1814	
	594.24		594.24	5	D	14	1700.9		1700.9	
	725.28		725.28	6	M	13	1585.9		1585.9	
	838.37		838.37	7	I	12	1454.8		1454.8	
+0.074	468.21		935.42	8	P	11	1341.8		1341.8	
+0.2957	525.73	+0.0555	1050.4	9	D	10	1244.7	−0.248	1244.7	
+0.1512	582.27	+0.1247	1163.5	10	L	9	1129.7		565.34	+0.0443
	1291.6		1291.6	11	K	8	1016.6	−0.061	1016.6	
	1362.7		1362.7	12	A	7	888.5		444.75	−0.396
	1509.7		1509.7	13	M	6	817.46		817.46	
−0.245	812.37		1623.7	14	N	5	670.42		670.42	
	1720.8		1720.8	15	P	4	556.38		556.38	
	1833.9		1833.9	16	L	3	459.33	−0.004	459.33	
	1962		1962	17	K	2	346.24		346.24	
	2033		2033	18	A	1	218.15	+0.11	218.15	
				19	K	0	147.11		147.11	

Scan number	9194	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	103.1



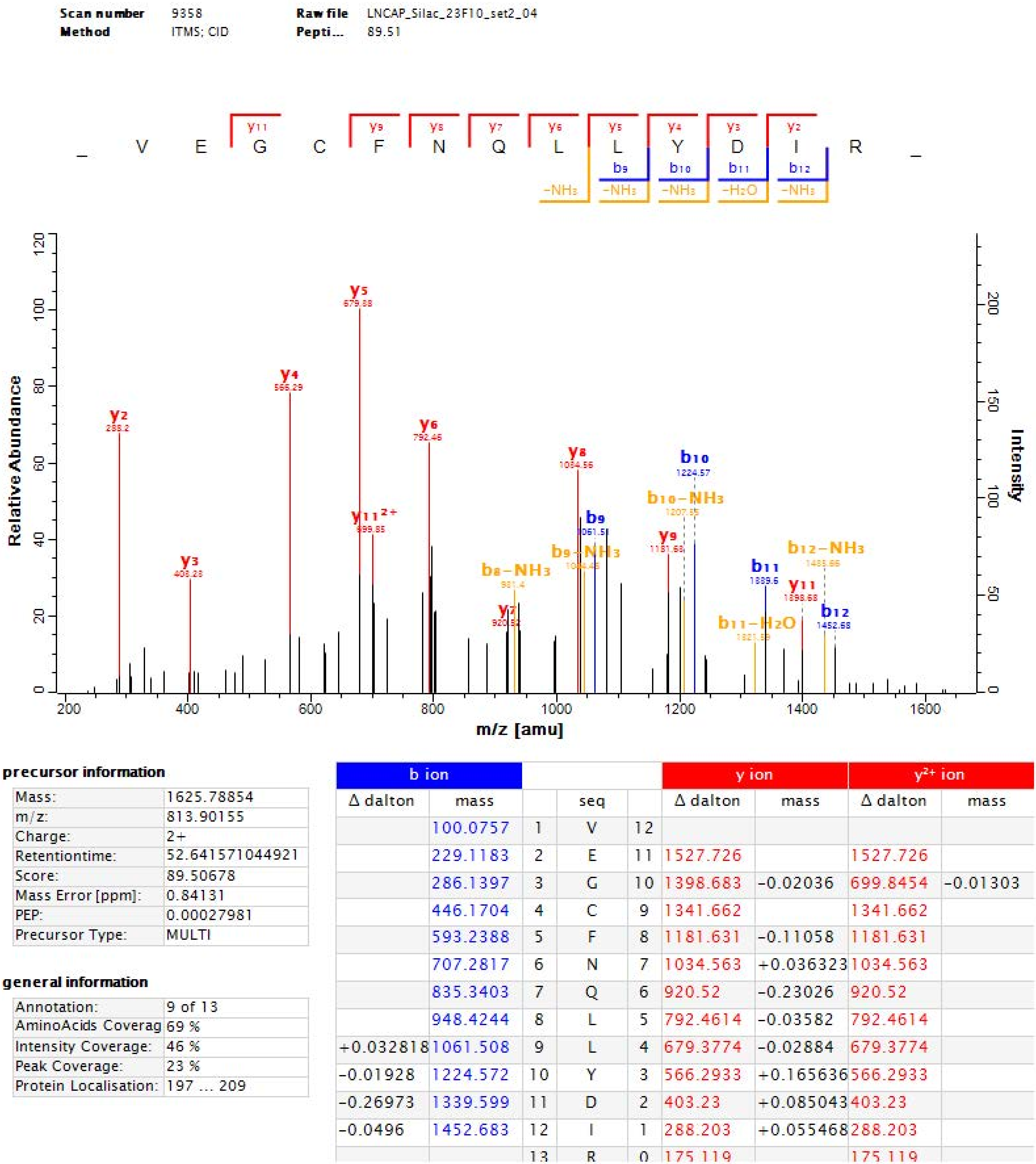
precursor information

Mass:	2328.34135
m/z:	777.12106
Charge:	3+
Retentiontime:	51.702125549316
Score:	103.1036
Mass Error [ppm]:	-0.1422
PEP:	1.9234E-08
Precursor Type:	MULTI

general information

Annotation:	17 of 22
AminoAcids Coverag	77 %
Intensity Coverage:	66 %
Peak Coverage:	35 %
Protein Localisation:	196 ... 217

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	21				
	228.13	+0.0933	228.13	2	N	20	2216.3		2216.3	
	327.2	+0.0343	327.2	3	V	19	2102.2		1051.6	+0.3136
	398.24		398.24	4	A	18	2003.2		1002.1	+0.214
	469.28	+0.1394	469.28	5	A	17	1932.1		966.56	+0.2665
	598.32		598.32	6	E	16	1861.1		931.04	+0.2064
	711.4		711.4	7	L	15	1732		866.52	+0.2456
	810.47	+0.1958	810.47	8	V	14	1619		809.98	+0.0065
	938.53	-0.222	938.53	9	Q	13	1519.9		760.45	+0.0085
	995.55		995.55	10	G	12	1391.8	+0.0741	696.42	-0.087
	1096.6		1096.6	11	T	11	1334.8		667.91	+0.3219
+0.0592	598.34		1195.7	12	V	10	1233.8	-0.097	617.38	+0.2507
	1292.7		1292.7	13	P	9	1134.7	-0.176	567.85	+0.2577
	1405.8		1405.8	14	L	8	1037.6		1037.6	
	1534.8		1534.8	15	E	7	924.55		924.55	
	1633.9		1633.9	16	V	6	795.51		398.26	+0.2101
	1731		1731	17	P	5	696.44		348.72	+0.2704
	1859		1859	18	Q	4	599.39		599.39	
	1958.1		1958.1	19	V	3	471.33		471.33	
	2086.2		2086.2	20	K	2	372.26		372.26	
	2183.2		2183.2	21	P	1	244.17	+0.0379	244.17	
				22	K	0	147.11		147.11	



Scan number 9358
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set2_04
Pepti... 89.51

precursor information

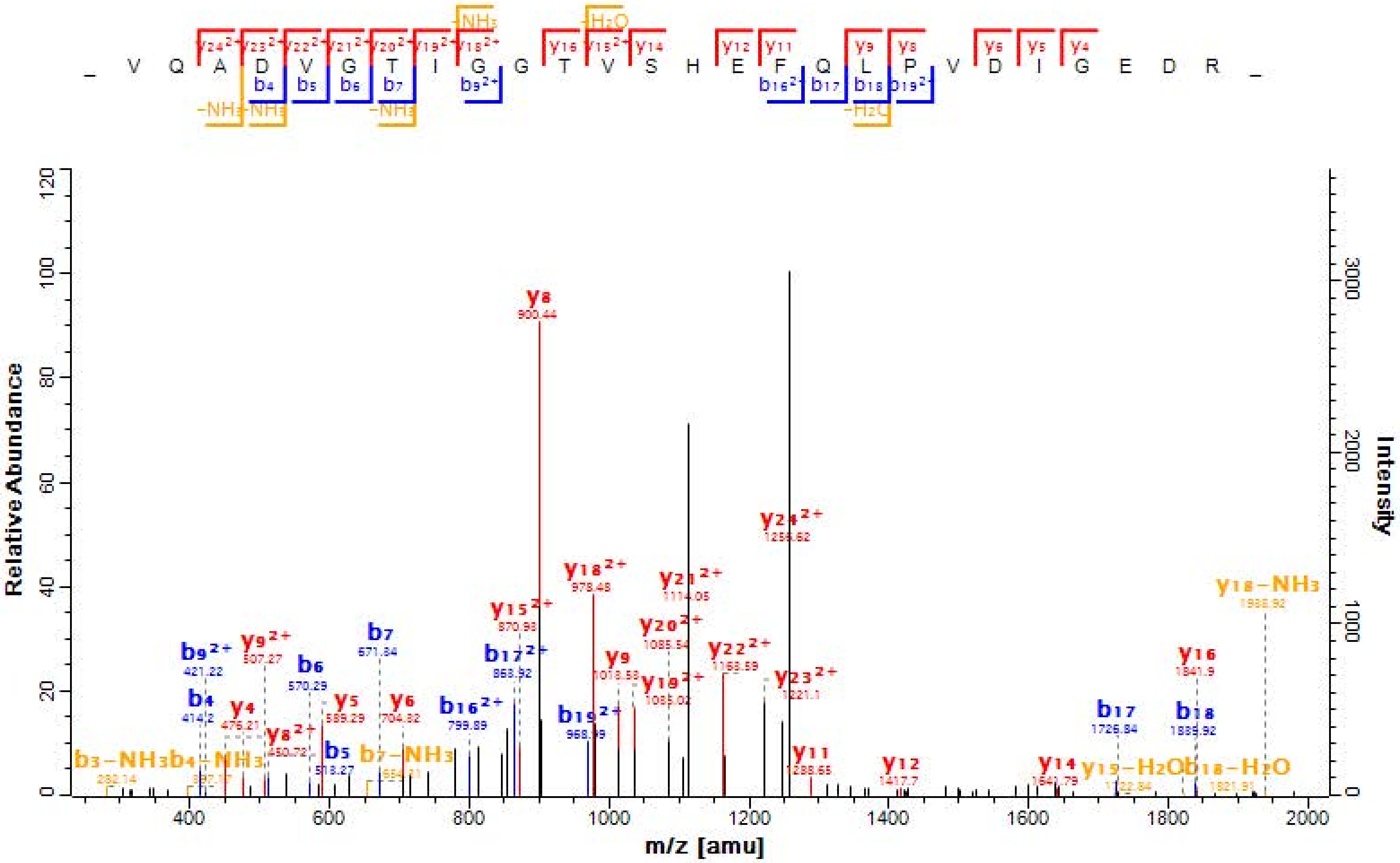
Mass:	1625.78854
m/z:	813.90155
Charge:	2+
Retentiontime:	52.641571044921
Score:	89.50678
Mass Error [ppm]:	0.84131
PEP:	0.00027981
Precursor Type:	MULTI

general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	46 %
Peak Coverage:	23 %
Protein Localisation:	197 ... 209

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	12				
	229.1183	2	E	11	1527.726		1527.726	
	286.1397	3	G	10	1398.683	-0.02036	699.8454	-0.01303
	446.1704	4	C	9	1341.662		1341.662	
	593.2388	5	F	8	1181.631	-0.11058	1181.631	
	707.2817	6	N	7	1034.563	+0.036323	1034.563	
	835.3403	7	Q	6	920.52	-0.23026	920.52	
	948.4244	8	L	5	792.4614	-0.03582	792.4614	
+0.032818	1061.508	9	L	4	679.3774	-0.02884	679.3774	
-0.01928	1224.572	10	Y	3	566.2933	+0.165636	566.2933	
-0.26973	1339.599	11	D	2	403.23	+0.085043	403.23	
-0.0496	1452.683	12	I	1	288.203	+0.055468	288.203	
		13	R	0	175.119		175.119	

Scan number	9383	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	135.54



precursor information

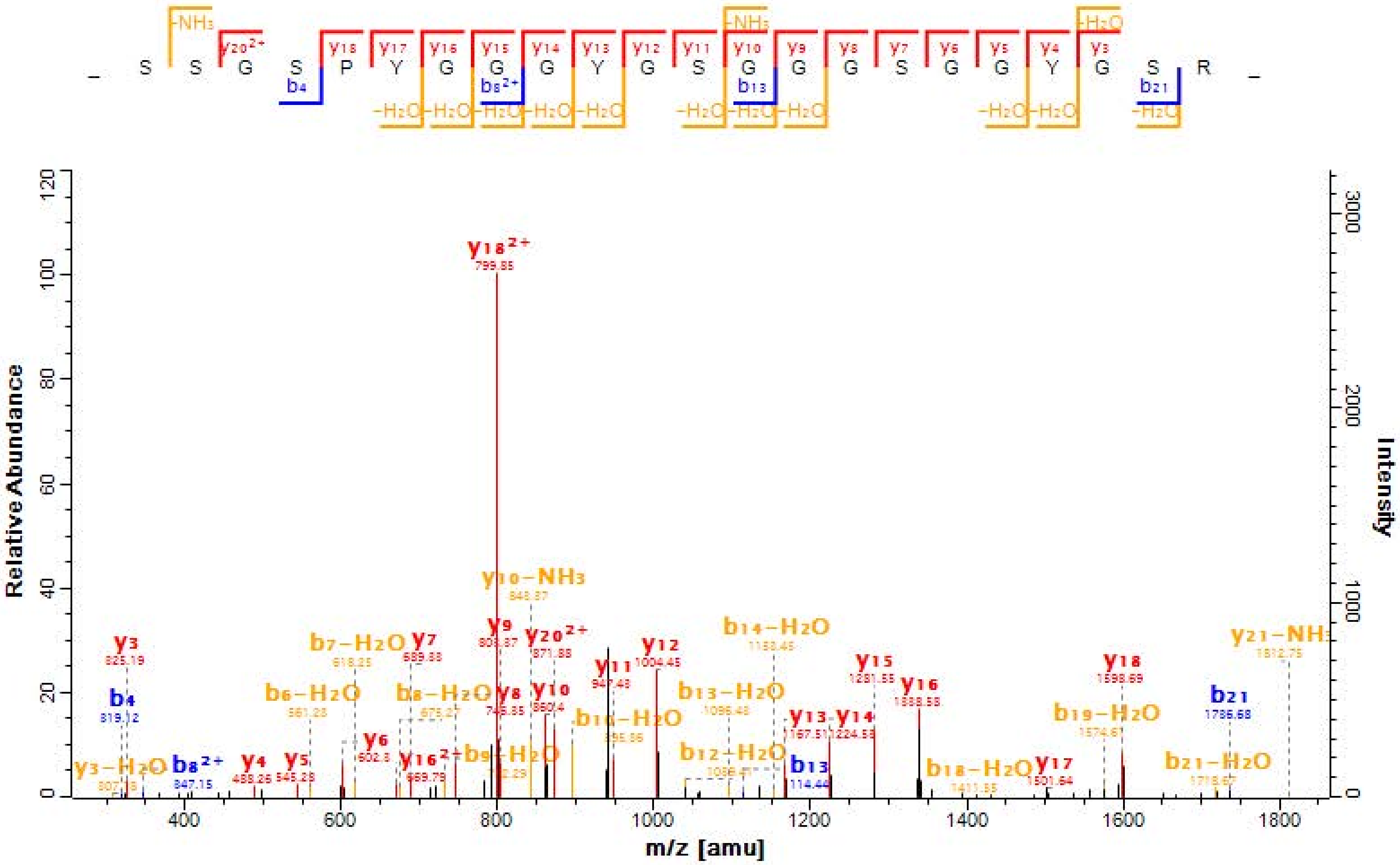
Mass:	2738.3525
m/z:	913.79144
Charge:	3+
Retentiontime:	52.792716979980
Score:	135.5363
Mass Error [ppm]:	0.4986
PEP:	3.5468E-24
Precursor Type:	MULTI

general information

Annotation:	18 of 26
AminoAcids Coverag	69 %
Intensity Coverage:	48 %
Peak Coverage:	35 %
Protein Localisation:	244 ... 269

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	25				
	228.13		228.13	2	Q	24	2640.3		2640.3	
	299.17		299.17	3	A	23	2512.2		1256.6	-0.112
	414.2	+0.1915	414.2	4	D	22	2441.2		1221.1	-0.144
	513.27	+0.126	513.27	5	V	21	2326.2		1163.6	+0.1754
	570.29	+0.3259	570.29	6	G	20	2227.1		1114.1	-0.034
	671.34	-0.034	671.34	7	T	19	2170.1		1085.5	+0.2037
	784.42		784.42	8	I	18	2069		1035	+0.4284
+0.0637	421.22		841.44	9	G	17	1955.9		978.48	+0.1434
	898.46		898.46	10	G	16	1898.9		1898.9	
	999.51		999.51	11	T	15	1841.9	+0.1024	1841.9	
	1098.6		1098.6	12	V	14	1740.9		870.93	+0.4755
	1185.6		1185.6	13	S	13	1641.8	+0.1847	1641.8	
	1322.7		1322.7	14	H	12	1554.8		1554.8	
	1451.7		1451.7	15	E	11	1417.7	-0.29	1417.7	
+0.3455	799.89		1598.8	16	F	10	1288.7	-0.001	1288.7	
+0.1159	863.92	-0.025	1726.8	17	Q	9	1141.6		1141.6	
	1839.9	-0.206	1839.9	18	L	8	1013.5	+0.0494	507.27	+0.1235
+0.4758	968.99		1937	19	P	7	900.44	-0.007	450.72	+0.3049
	2036		2036	20	V	6	803.39		803.39	
	2151.1		2151.1	21	D	5	704.32	-0.052	704.32	
	2264.2		2264.2	22	I	4	589.29	+0.1556	589.29	
	2321.2		2321.2	23	G	3	476.21	+0.2033	476.21	
	2450.2		2450.2	24	E	2	419.19		419.19	
	2565.2		2565.2	25	D	1	290.15		290.15	
				26	R	0	175.12		175.12	

Scan number	942	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	153.21



precursor information

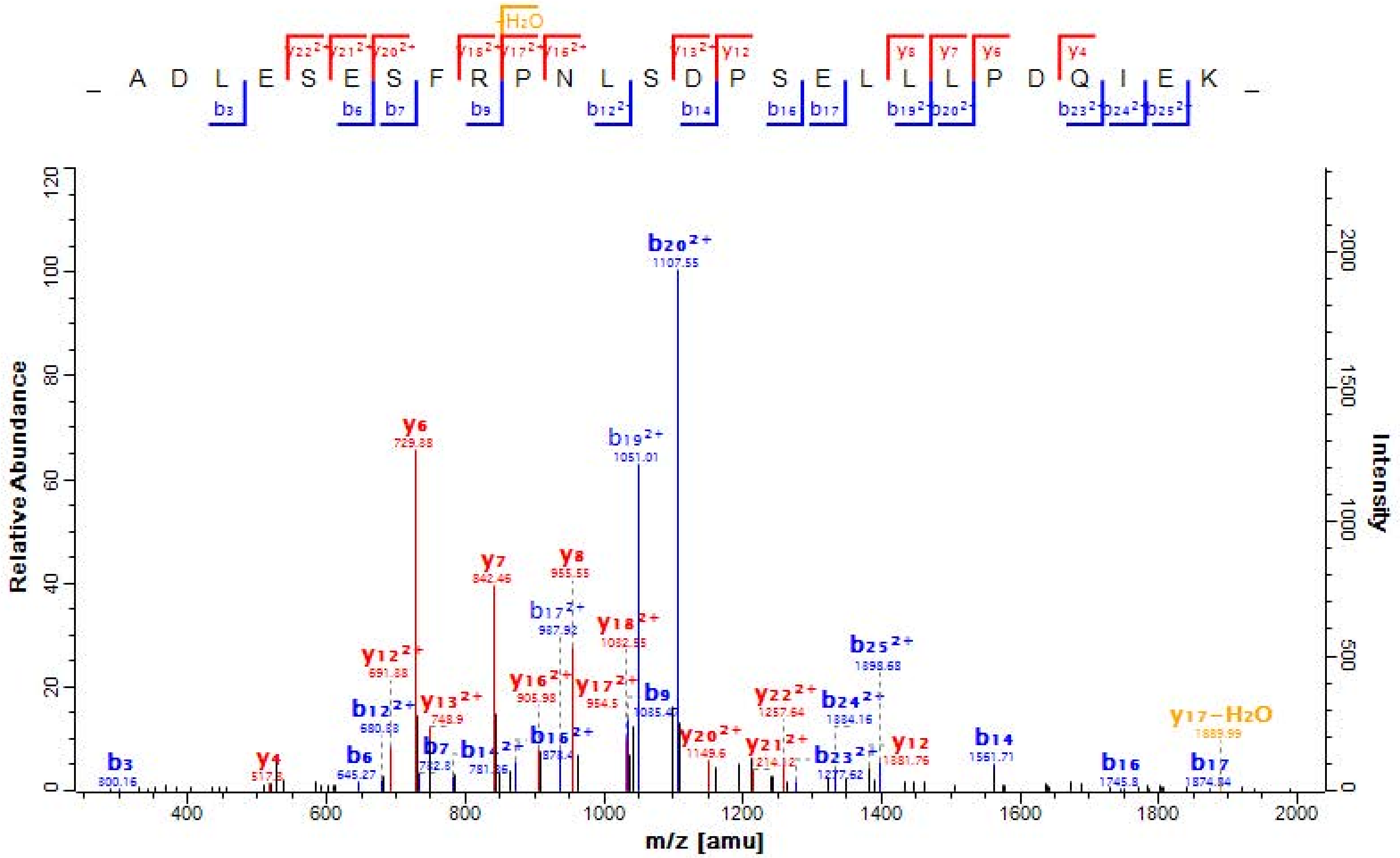
Mass:	1909.78321
m/z:	955.89888
Charge:	2+
Retentiontime:	10.393086433410
Score:	153.21
Mass Error [ppm]:	0.26852
PEP:	3.6701E-28
Precursor Type:	MULTI

general information

Annotation:	20 of 22
AminoAcids Coverag	91 %
Intensity Coverage:	64 %
Peak Coverage:	40 %
Protein Localisation:	355 ... 376

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	21				
	175.07		175.07	2	S	20	1829.8		1829.8	
	232.09		232.09	3	G	19	1742.7		871.88	+0.0649
	319.12	+0.1601	319.12	4	S	18	1685.7		1685.7	
	416.18		416.18	5	P	17	1598.7	-0.056	799.85	+0.3048
	579.24		579.24	6	Y	16	1501.6	+0.0189	1501.6	
	636.26		636.26	7	G	15	1338.6	+0.0103	669.79	+0.1141
+0.2662	347.15		693.28	8	G	14	1281.6	+0.1276	1281.6	
	750.31		750.31	9	G	13	1224.5	-0.12	1224.5	
	913.37		913.37	10	Y	12	1167.5	+0.1293	1167.5	
	970.39		970.39	11	G	11	1004.4	+0.019	1004.4	
	1057.4		1057.4	12	S	10	947.43	+0.1059	947.43	
	1114.4	-0.089	1114.4	13	G	9	860.4	+0.0952	860.4	
	1171.5		1171.5	14	G	8	803.37	+0.0323	803.37	
	1228.5		1228.5	15	G	7	746.35	+0.0133	746.35	
	1315.5		1315.5	16	S	6	689.33	+0.18	689.33	
	1372.5		1372.5	17	G	5	602.3	+0.0817	602.3	
	1429.6		1429.6	18	G	4	545.28	+0.0041	545.28	
	1592.6		1592.6	19	Y	3	488.26	+0.1389	488.26	
	1649.6		1649.6	20	G	2	325.19	+0.0846	325.19	
	1736.7	-0.097	1736.7	21	S	1	268.17		268.17	
				22	R	0	181.14		181.14	

Scan number	9431	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	112.36



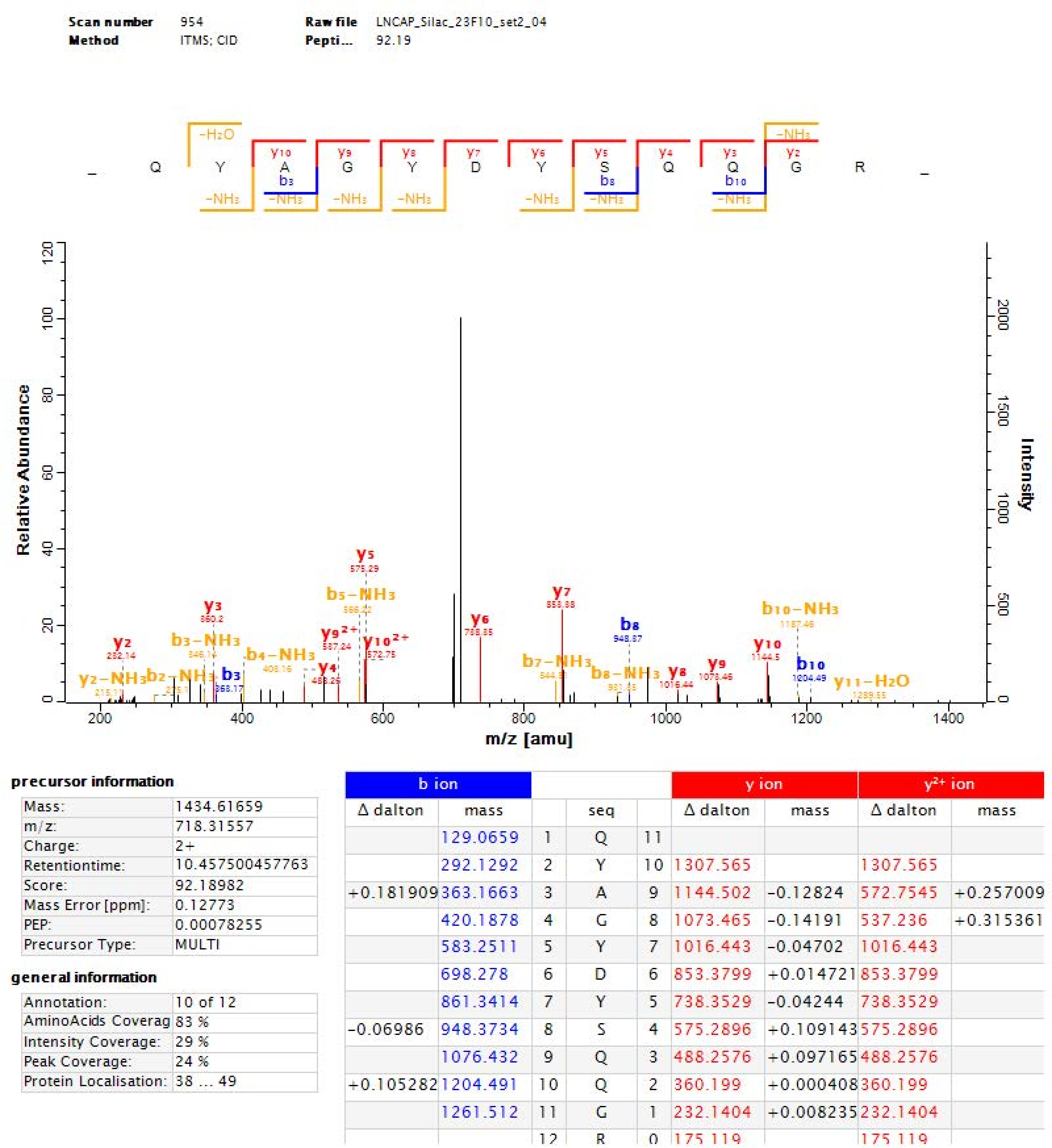
precursor information

Mass:	2941.45748
m/z:	981.4931
Charge:	3+
Retentiontime:	53.085021972656
Score:	112.362
Mass Error [ppm]:	0.61916
PEP:	2.8462E-11
Precursor Type:	ISO

general information

Annotation:	19 of 26
AminoAcids Coverag	73 %
Intensity Coverage:	67 %
Peak Coverage:	29 %
Protein Localisation:	697 ... 722

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	25				
	187.07		187.07	2	D	24	2871.4		2871.4	
	300.16	+0.1025	300.16	3	L	23	2756.4		2756.4	
	429.2		429.2	4	E	22	2643.3		2643.3	
	516.23		516.23	5	S	21	2514.3		1257.6	+0.2352
	645.27	+0.0728	645.27	6	E	20	2427.2		1214.1	+0.3992
	732.3	-0.006	732.3	7	S	19	2298.2		1149.6	+0.224
	879.37		879.37	8	F	18	2211.2		2211.2	
	1035.5	+0.0345	1035.5	9	R	17	2064.1		1032.6	+0.191
	1132.5		1132.5	10	P	16	1908		954.5	-0.067
	1246.6		1246.6	11	N	15	1810.9		905.98	+0.395
+0.104	680.33		1359.7	12	L	14	1696.9		1696.9	
	1446.7		1446.7	13	S	13	1583.8		1583.8	
+0.0802	781.36	-0.27	1561.7	14	D	12	1496.8		748.9	-0.49
	1658.8		1658.8	15	P	11	1381.8	-0.105	691.38	-0.006
-0.339	873.4	+0.1277	1745.8	16	S	10	1284.7		1284.7	
+0.1855	937.92	+0.4412	1874.8	17	E	9	1197.7		1197.7	
	1987.9		1987.9	18	L	8	1068.6		1068.6	
+0.2579	1051		2101	19	L	7	955.55	-0.112	955.55	
+0.2389	1107.5		2214.1	20	L	6	842.46	+0.0384	842.46	
	2311.1		2311.1	21	P	5	729.38	+0.0452	729.38	
	2426.2		2426.2	22	D	4	632.32		632.32	
+0.0563	1277.6		2554.2	23	Q	3	517.3	+0.1337	517.3	
+0.0125	1334.2		2667.3	24	I	2	389.24		389.24	
+0.3018	1398.7		2796.4	25	E	1	276.16		276.16	
				26	K	0	147.11		147.11	



Scan number	954	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	92.19

precursor information

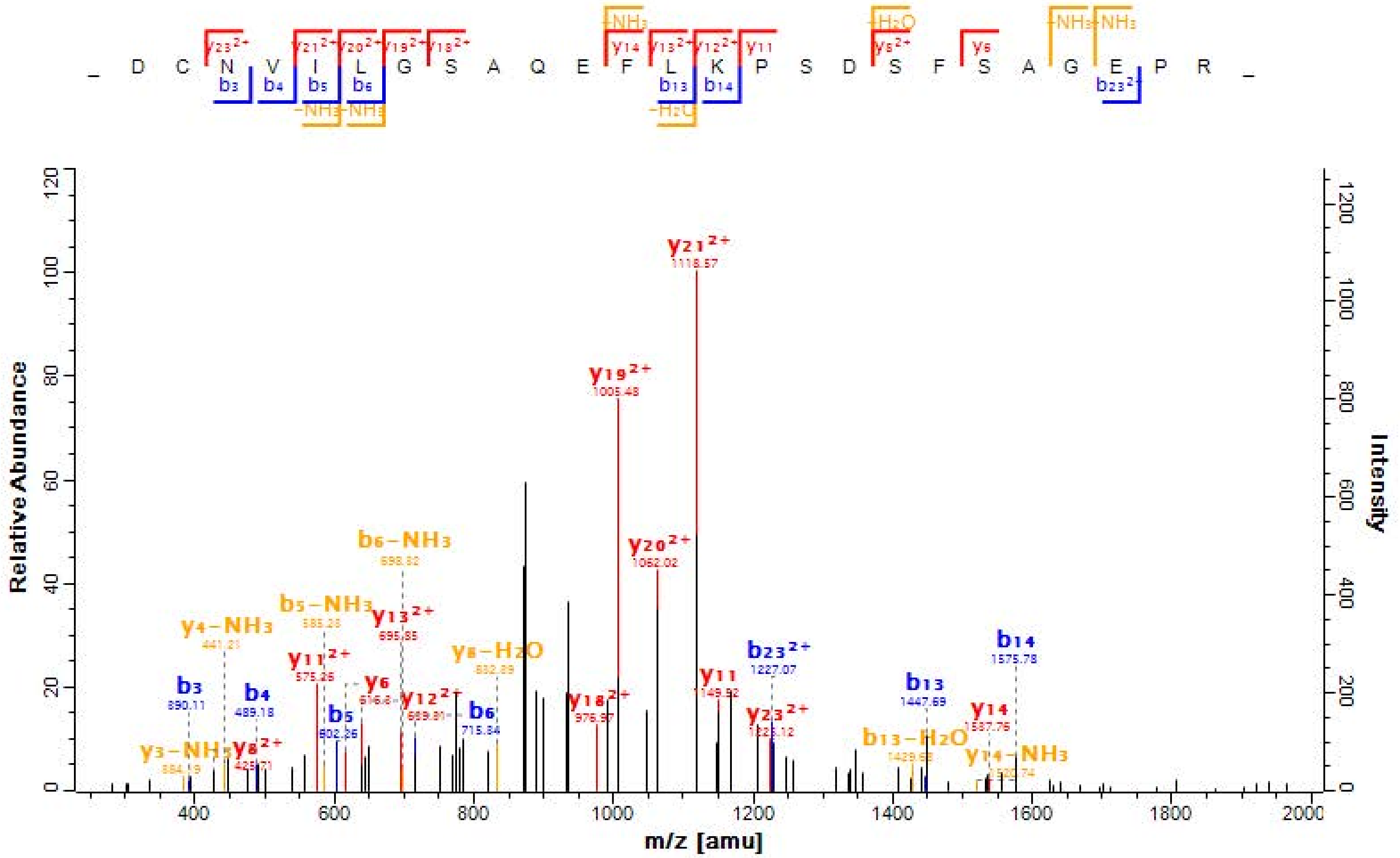
Mass:	1434.61659
m/z:	718.31557
Charge:	2+
Retentiontime:	10.457500457763
Score:	92.18982
Mass Error [ppm]:	0.12773
PEP:	0.00078255
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	29 %
Peak Coverage:	24 %
Protein Localisation:	38 ... 49

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.0659	1	Q	11				
	292.1292	2	Y	10	1307.565		1307.565	
+0.181909	363.1663	3	A	9	1144.502	-0.12824	572.7545	+0.257009
	420.1878	4	G	8	1073.465	-0.14191	537.236	+0.315361
	583.2511	5	Y	7	1016.443	-0.04702	1016.443	
	698.278	6	D	6	853.3799	+0.014721	853.3799	
	861.3414	7	Y	5	738.3529	-0.04244	738.3529	
-0.06986	948.3734	8	S	4	575.2896	+0.109143	575.2896	
	1076.432	9	Q	3	488.2576	+0.097165	488.2576	
+0.105282	1204.491	10	Q	2	360.199	+0.000408	360.199	
	1261.512	11	G	1	232.1404	+0.008235	232.1404	
		12	R	0	175.119		175.119	

Scan number 9667 **Raw file** LNCAP_Silac_23F10_set2_04
Method ITMS; CID **Pepti...** 80.75



precursor information

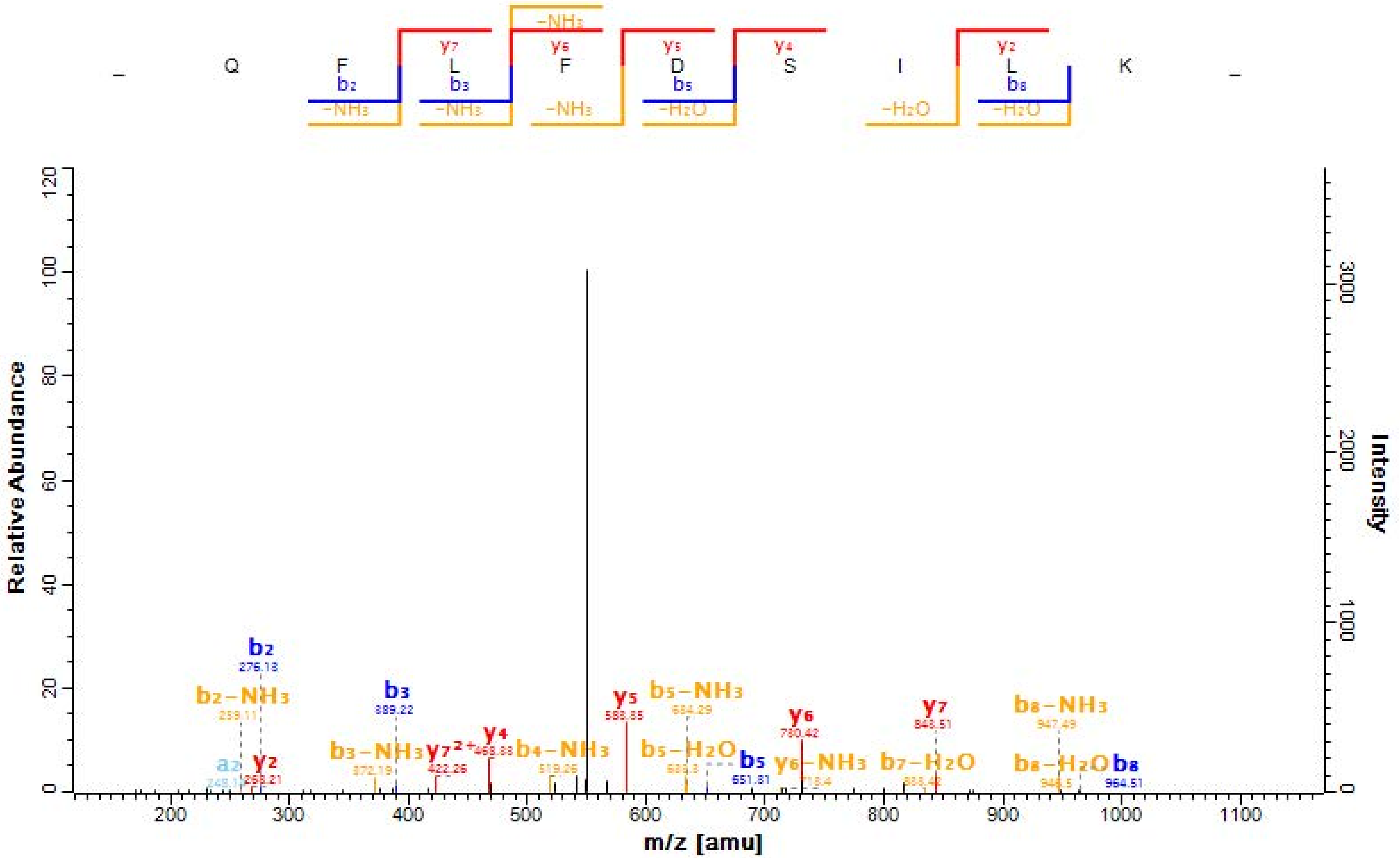
Mass:	2723.28925
m/z:	908.77036
Charge:	3+
Retentiontime:	54.555961608886
Score:	80.75249
Mass Error [ppm]:	1.1583
PEP:	0.00061384
Precursor Type:	ISO

general information

Annotation:	14 of 25
AminoAcids Coverag	56 %
Intensity Coverage:	38 %
Peak Coverage:	26 %
Protein Localisation:	121 ... 145

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	24				
	276.06		276.06	2	C	23	2609.3		2609.3	
	390.11	+0.074	390.11	3	N	22	2449.2		1225.1	-0.109
	489.18	-0.083	489.18	4	V	21	2335.2		2335.2	
	602.26	-0.09	602.26	5	I	20	2236.1		1118.6	+0.2137
	715.34	-0.077	715.34	6	L	19	2123		1062	+0.181
	772.37		772.37	7	G	18	2010		1005.5	+0.2042
	859.4		859.4	8	S	17	1952.9		976.97	+0.3029
	930.43		930.43	9	A	16	1865.9		1865.9	
	1058.5		1058.5	10	Q	15	1794.9		1794.9	
	1187.5		1187.5	11	E	14	1666.8		1666.8	
	1334.6		1334.6	12	F	13	1537.8	+0.0776	1537.8	
	1447.7	-0.233	1447.7	13	L	12	1390.7		695.85	+0.2475
	1575.8	-0.036	1575.8	14	K	11	1277.6		639.31	+0.1023
	1672.8		1672.8	15	P	10	1149.5	+0.0148	575.26	+0.1339
	1759.9		1759.9	16	S	9	1052.5		1052.5	
	1874.9		1874.9	17	D	8	965.43		965.43	
	1961.9		1961.9	18	S	7	850.41		425.71	+0.029
	2109		2109	19	F	6	763.37		763.37	
	2196		2196	20	S	5	616.3	-0.008	616.3	
	2267.1		2267.1	21	A	4	529.27		529.27	
	2324.1		2324.1	22	G	3	458.24		458.24	
-0.08	1227.1		2453.1	23	E	2	401.21		401.21	
	2550.2		2550.2	24	P	1	272.17		272.17	
				25	R	0	175.12		175.12	

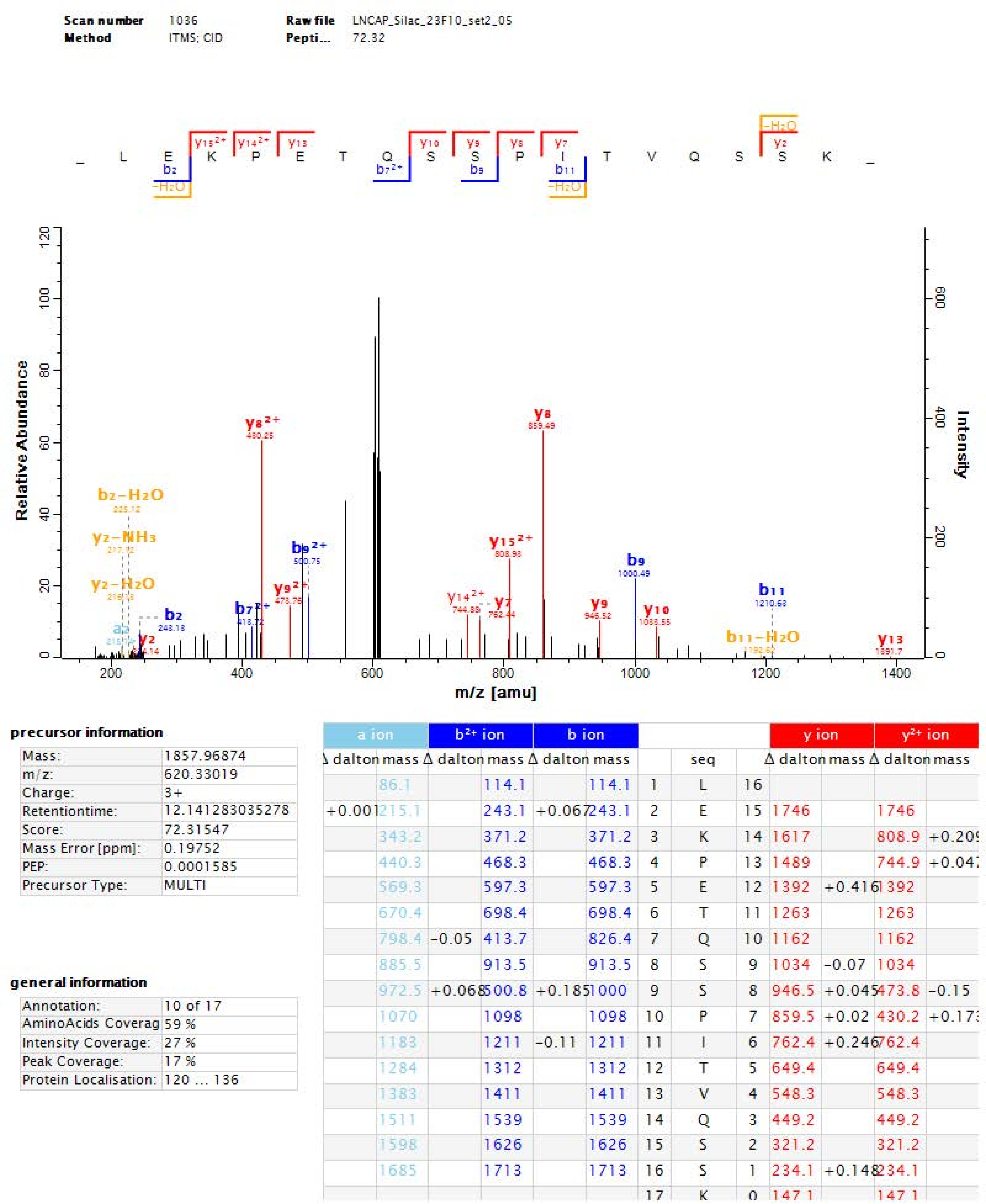
Scan number	9980	**Raw file**	LNCAP_Silac_23F10_set2_04
Method	ITMS; CID	**Pepti...**	138.98



precursor information

Mass:	1109.61217
m/z:	555.81336
Charge:	2+
Retentiontime:	56.520709991455
Score:	138.9753
Mass Error [ppm]:	0.070131
PEP:	0.00095852
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	31 %
Peak Coverage:	26 %
Protein Localisation:	302 ... 310

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	101.07		129.07	1	Q	8				
-0.133	248.14	-0.057	276.13	2	F	7	990.57		990.57	
	361.22	+0.1603	389.22	3	L	6	843.51	+0.0718	422.26	-0.075
	508.29		536.29	4	F	5	730.42	+0.0195	730.42	
	623.32	+0.1869	651.31	5	D	4	583.35	-0.003	583.35	
	710.35		738.35	6	S	3	468.33	+0.0354	468.33	
	823.43		851.43	7	I	2	381.3		381.3	
	936.52	+0.1857	964.51	8	L	1	268.21	+0.1321	268.21	
				9	K	0	155.13		155.13	



Scan number	1036	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	72.32

precursor information

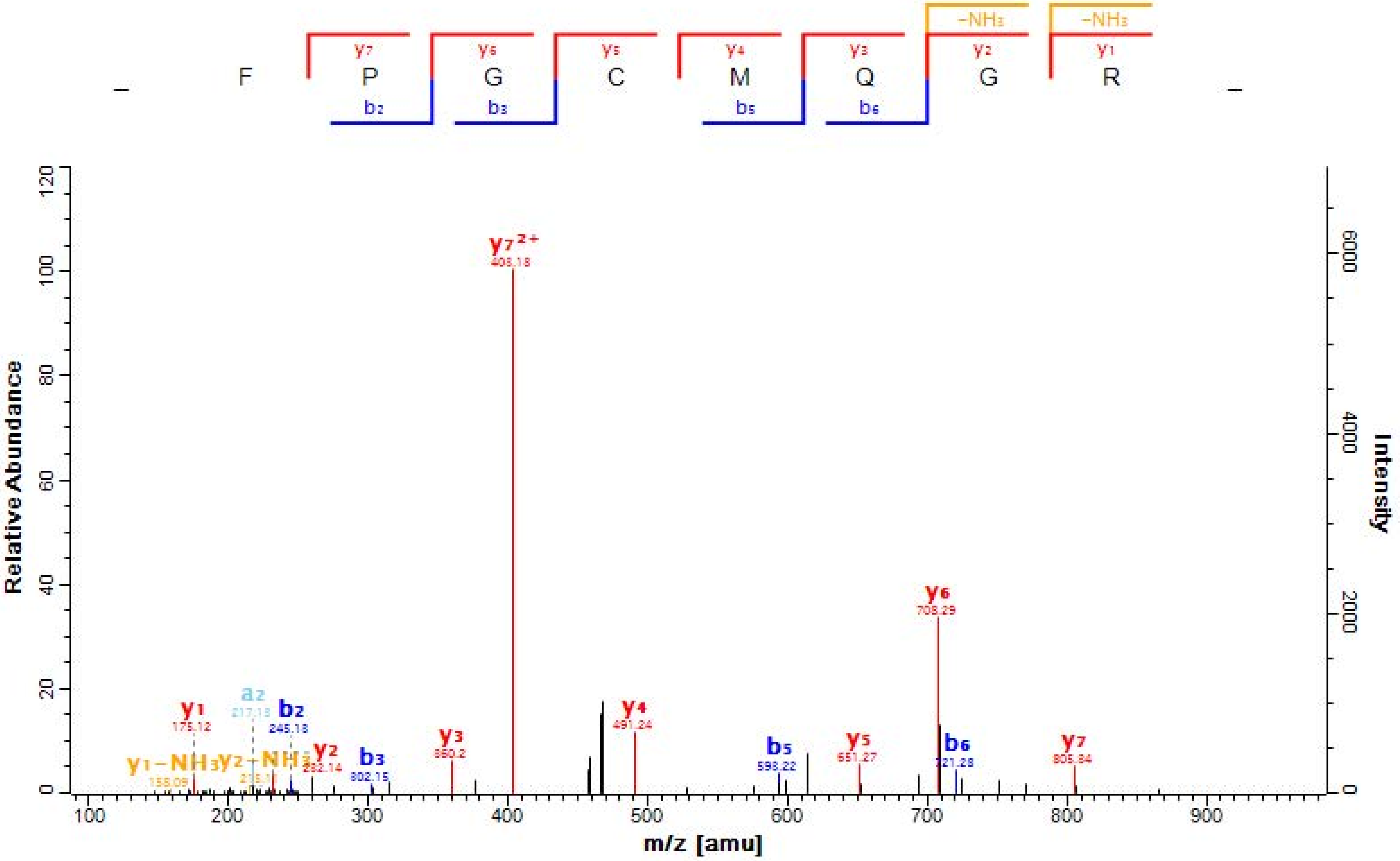
Mass:	1857.96874
m/z:	620.33019
Charge:	3+
Retentiontime:	12.141283035278
Score:	72.31547
Mass Error [ppm]:	0.19752
PEP:	0.0001585
Precursor Type:	MULTI

general information

Annotation:	10 of 17
AminoAcids Coverag	59 %
Intensity Coverage:	27 %
Peak Coverage:	17 %
Protein Localisation:	120 ... 136

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	16				
+0.001	215.1		243.1	+0.067	243.1	2	E	15	1746		1746	
	343.2		371.2		371.2	3	K	14	1617		808.9	+0.20
	440.3		468.3		468.3	4	P	13	1489		744.9	+0.04
	569.3		597.3		597.3	5	E	12	1392	+0.416	1392	
	670.4		698.4		698.4	6	T	11	1263		1263	
	798.4	-0.05	413.7		826.4	7	Q	10	1162		1162	
	885.5		913.5		913.5	8	S	9	1034	-0.07	1034	
	972.5	+0.068	500.8	+0.185	1000	9	S	8	946.5	+0.045	473.8	-0.15
	1070		1098		1098	10	P	7	859.5	+0.02	430.2	+0.17
	1183		1211	-0.11	1211	11	I	6	762.4	+0.246	762.4	
	1284		1312		1312	12	T	5	649.4		649.4	
	1383		1411		1411	13	V	4	548.3		548.3	
	1511		1539		1539	14	Q	3	449.2		449.2	
	1598		1626		1626	15	S	2	321.2		321.2	
	1685		1713		1713	16	S	1	234.1	+0.148	234.1	
						17	K	0	147.1		147.1	

Scan number	1039	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	129.4

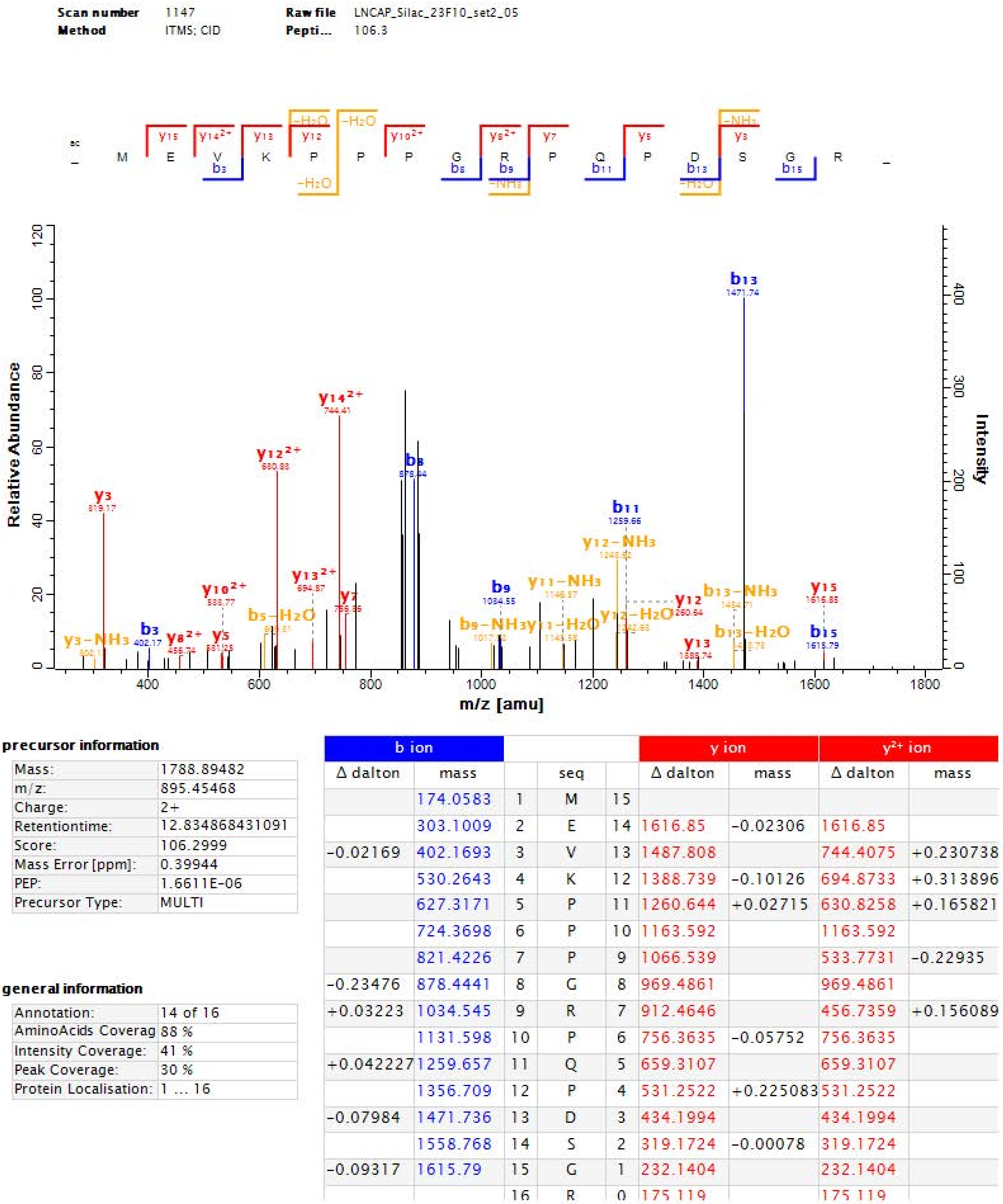


precursor information

Mass:	951.40584
m/z:	476.7102
Charge:	2+
Retentiontime:	12.162103652954
Score:	129.3973
Mass Error [ppm]:	0.36602
PEP:	0.0006187
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	59 %
Peak Coverage:	13 %
Protein Localisation:	148 ... 155

g

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08		148.08	1	F	7				
-0.11	217.13	+0.1019	245.13	2	P	6	805.34	+0.0143	403.18	+0.146
	274.16	-0.027	302.15	3	G	5	708.29	-0.018	708.29	
	434.19		462.18	4	C	4	651.27	+0.0995	651.27	
	565.23	+0.1267	593.22	5	M	3	491.24	+0.0816	491.24	
	693.28	+0.0485	721.28	6	Q	2	360.2	+0.059	360.2	
	750.31		778.3	7	G	1	232.14	+0.06	232.14	
				8	R	0	175.12	-0.08	175.12	



Scan number	1147	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	106.3

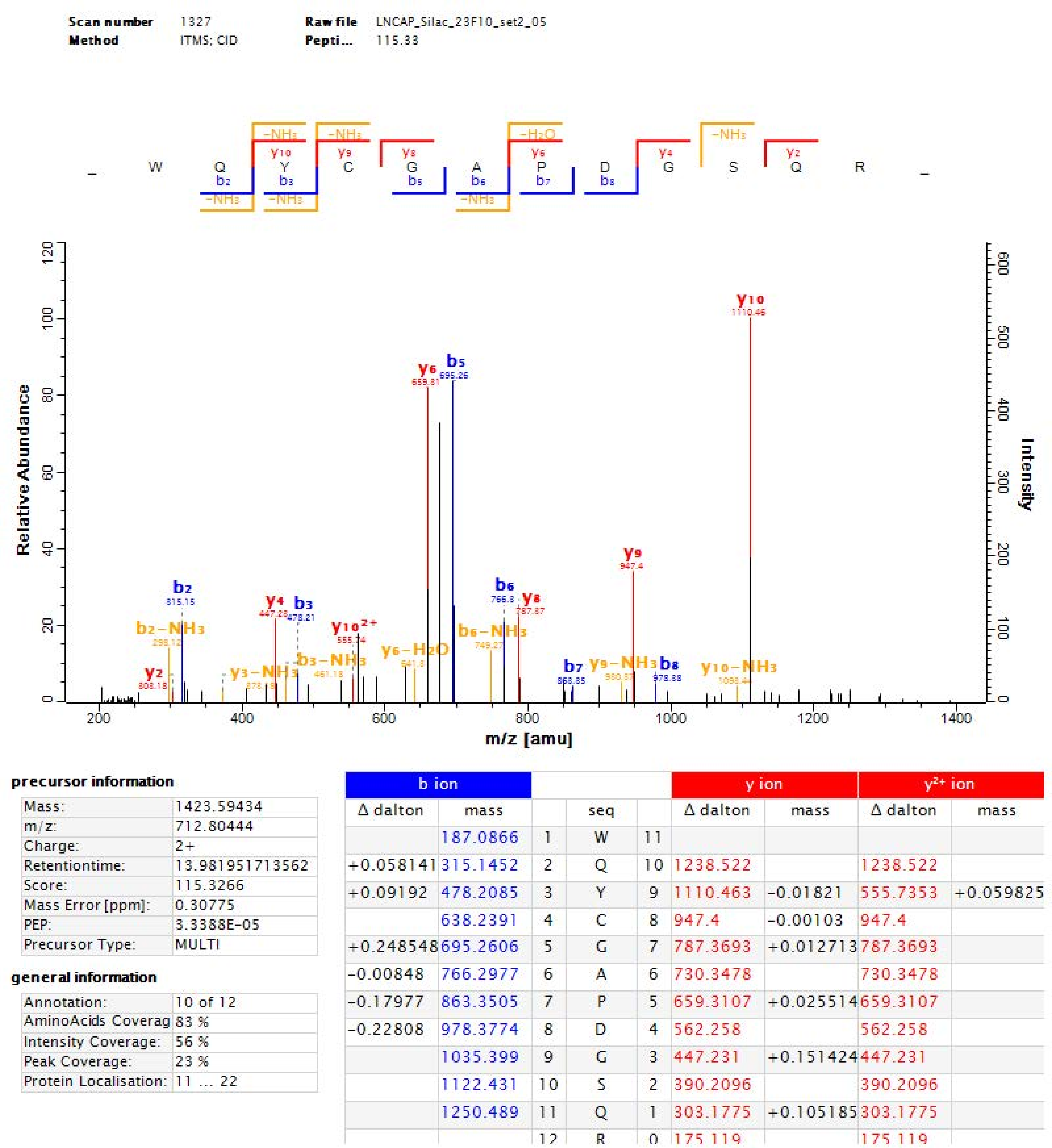
precursor information

Mass:	1788.89482
m/z:	895.45468
Charge:	2+
Retentiontime:	12.834868431091
Score:	106.2999
Mass Error [ppm]:	0.39944
PEP:	1.6611E-06
Precursor Type:	MULTI

general information

Annotation:	14 of 16
AminoAcids Coverag	88 %
Intensity Coverage:	41 %
Peak Coverage:	30 %
Protein Localisation:	1 ... 16

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	174.0583	1	M	15				
	303.1009	2	E	14	1616.85	−0.02306	1616.85	
−0.02169	402.1693	3	V	13	1487.808		744.4075	+0.230738
	530.2643	4	K	12	1388.739	−0.10126	694.8733	+0.313896
	627.3171	5	P	11	1260.644	+0.02715	630.8258	+0.165821
	724.3698	6	P	10	1163.592		1163.592	
	821.4226	7	P	9	1066.539		533.7731	−0.22935
−0.23476	878.4441	8	G	8	969.4861		969.4861	
+0.03223	1034.545	9	R	7	912.4646		456.7359	+0.156089
	1131.598	10	P	6	756.3635	−0.05752	756.3635	
+0.042227	1259.657	11	Q	5	659.3107		659.3107	
	1356.709	12	P	4	531.2522	+0.225083	531.2522	
−0.07984	1471.736	13	D	3	434.1994		434.1994	
	1558.768	14	S	2	319.1724	−0.00078	319.1724	
−0.09317	1615.79	15	G	1	232.1404		232.1404	
		16	R	0	175.119		175.119	



Scan number	1327	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	115.33

precursor information

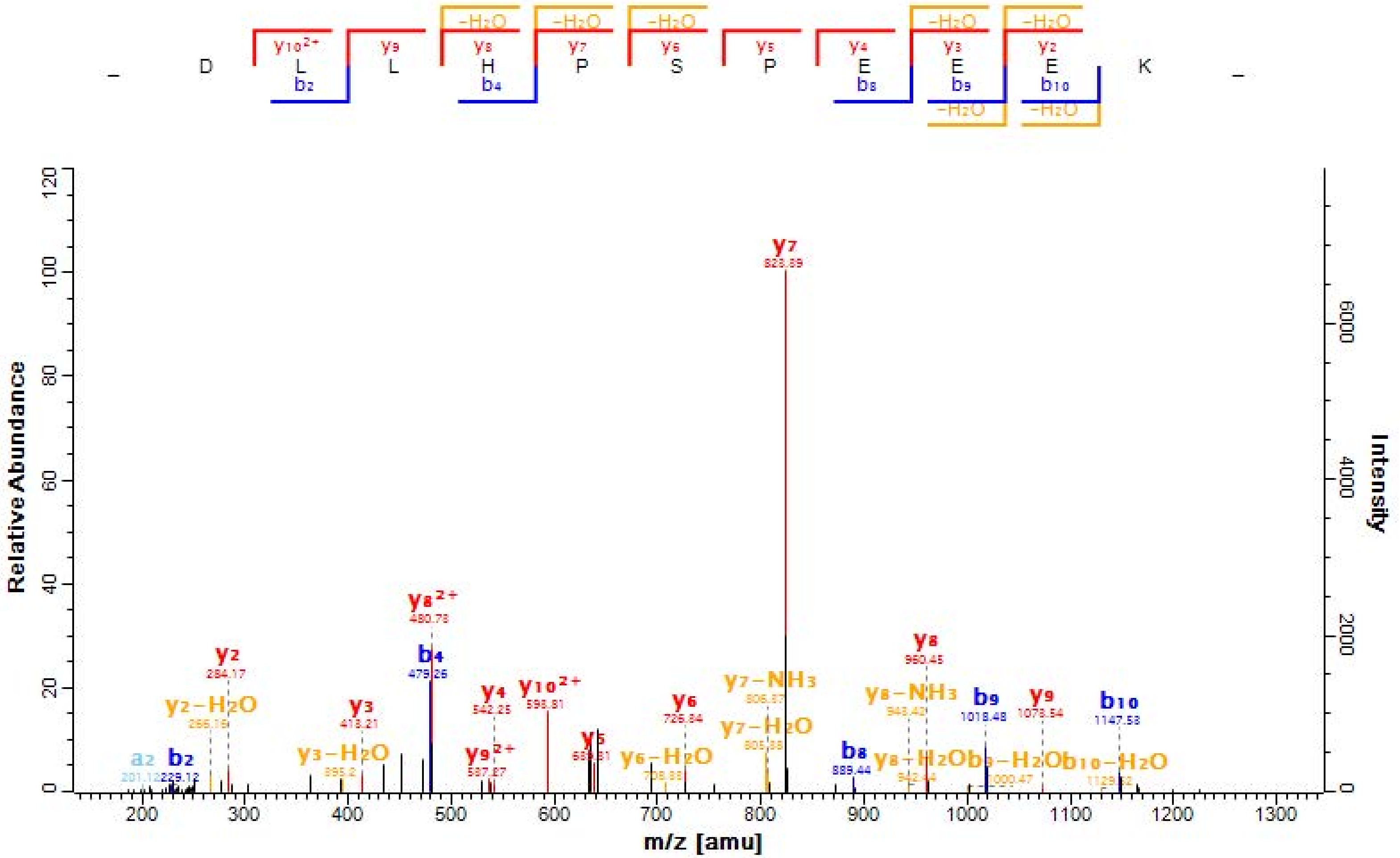
Mass:	1423.59434
m/z:	712.80444
Charge:	2+
Retentiontime:	13.981951713562
Score:	115.3266
Mass Error [ppm]:	0.30775
PEP:	3.3388E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	56 %
Peak Coverage:	23 %
Protein Localisation:	11 ... 22

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	187.0866	1	W	11				
+0.058141	315.1452	2	Q	10	1238.522		1238.522	
+0.09192	478.2085	3	Y	9	1110.463	-0.01821	555.7353	+0.059825
	638.2391	4	C	8	947.4	-0.00103	947.4	
+0.248548	695.2606	5	G	7	787.3693	+0.012713	787.3693	
-0.00848	766.2977	6	A	6	730.3478		730.3478	
-0.17977	863.3505	7	P	5	659.3107	+0.025514	659.3107	
-0.22808	978.3774	8	D	4	562.258		562.258	
	1035.399	9	G	3	447.231	+0.151424	447.231	
	1122.431	10	S	2	390.2096		390.2096	
	1250.489	11	Q	1	303.1775	+0.105185	303.1775	
		12	R	0	175.119		175.119	

Scan number	1487	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	180.19



precursor information

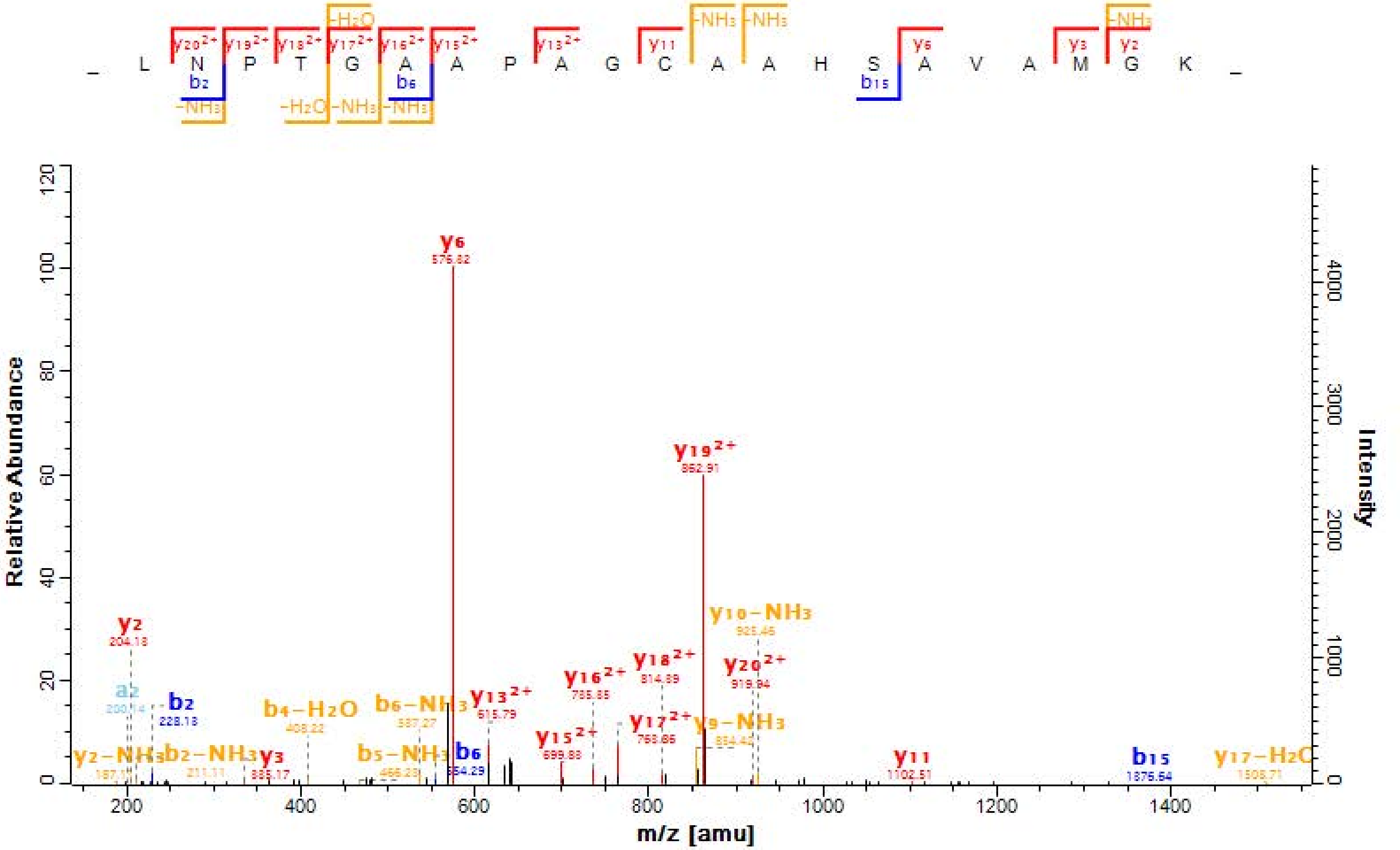
Mass:	1292.62489
m/z:	647.31972
Charge:	2+
Retentiontime:	14.982003211975
Score:	180.1916
Mass Error [ppm]:	0.036428
PEP:	1.744E-08
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	59 %
Peak Coverage:	28 %
Protein Localisation:	6 ... 16

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	10				
-0.048	201.12	+0.0095	229.12	2	L	9	1186.6		593.81	+0.2374
	314.21		342.2	3	L	8	1073.5	+0.1223	537.27	+0.0133
	451.27	+0.0229	479.26	4	H	7	960.45	-0.025	480.73	-0.069
	548.32		576.31	5	P	6	823.39	-0.002	823.39	
	635.35		663.35	6	S	5	726.34	-0.037	726.34	
	732.4		760.4	7	P	4	639.31	+0.0814	639.31	
	861.45	+0.1522	889.44	8	E	3	542.25	+0.2331	542.25	
	990.49	-0.026	1018.5	9	E	2	413.21	-0.163	413.21	
	1119.5	-0.065	1147.5	10	E	1	284.17	-0.059	284.17	
				11	K	0	155.13		155.13	

Scan number	1614	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	54.76



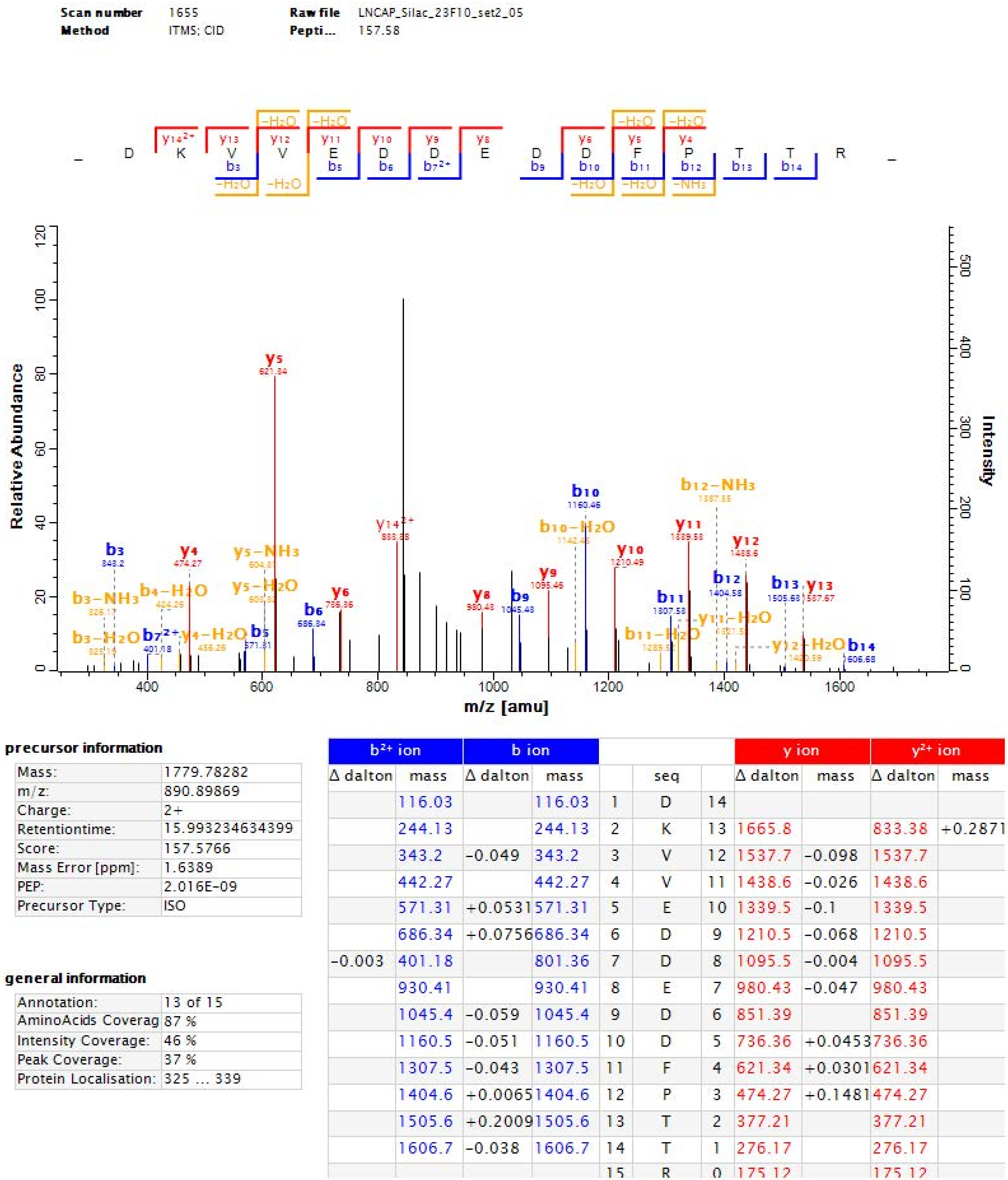
precursor information

Mass:	1950.94016
m/z:	651.32066
Charge:	3+
Retentiontime:	15.730754852294
Score:	54.76434
Mass Error [ppm]:	-0.12461
PEP:	0.0018969
Precursor Type:	MULTI

general information

Annotation:	14 of 21
AminoAcids Coverag	67 %
Intensity Coverage:	74 %
Peak Coverage:	23 %
Protein Localisation:	233 ... 253

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	20				
+0.2199	200.14	+0.0671	228.13	2	N	19	1838.9		919.94	+0.3056
	297.19		325.19	3	P	18	1724.8		862.91	+0.247
	398.24		426.23	4	T	17	1627.8		814.39	+0.1476
	455.26		483.26	5	G	16	1526.7		763.86	+0.235
	526.3	+0.3508	554.29	6	A	15	1469.7		735.35	+0.2088
	597.34		625.33	7	A	14	1398.7		699.83	+0.1495
	694.39		722.38	8	P	13	1327.6		1327.6	
	765.43		793.42	9	A	12	1230.6		615.79	-0.336
	822.45		850.44	10	G	11	1159.5		1159.5	
	982.48		1010.5	11	C	10	1102.5	+0.0792	1102.5	
	1053.5		1081.5	12	A	9	942.48		942.48	
	1124.6		1152.5	13	A	8	871.45		871.45	
	1261.6		1289.6	14	H	7	800.41		800.41	
	1348.6	-0.143	1376.6	15	S	6	663.35		663.35	
	1419.7		1447.7	16	A	5	576.32	-0.426	576.32	
	1518.7		1546.7	17	V	4	505.28		505.28	
	1589.8		1617.8	18	A	3	406.21		406.21	
	1720.8		1748.8	19	M	2	335.17	+0.4287	335.17	
	1777.8		1805.8	20	G	1	204.13	-0.016	204.13	
				21	K	0	147.11		147.11	



Scan number	1655	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	157.58

precursor information

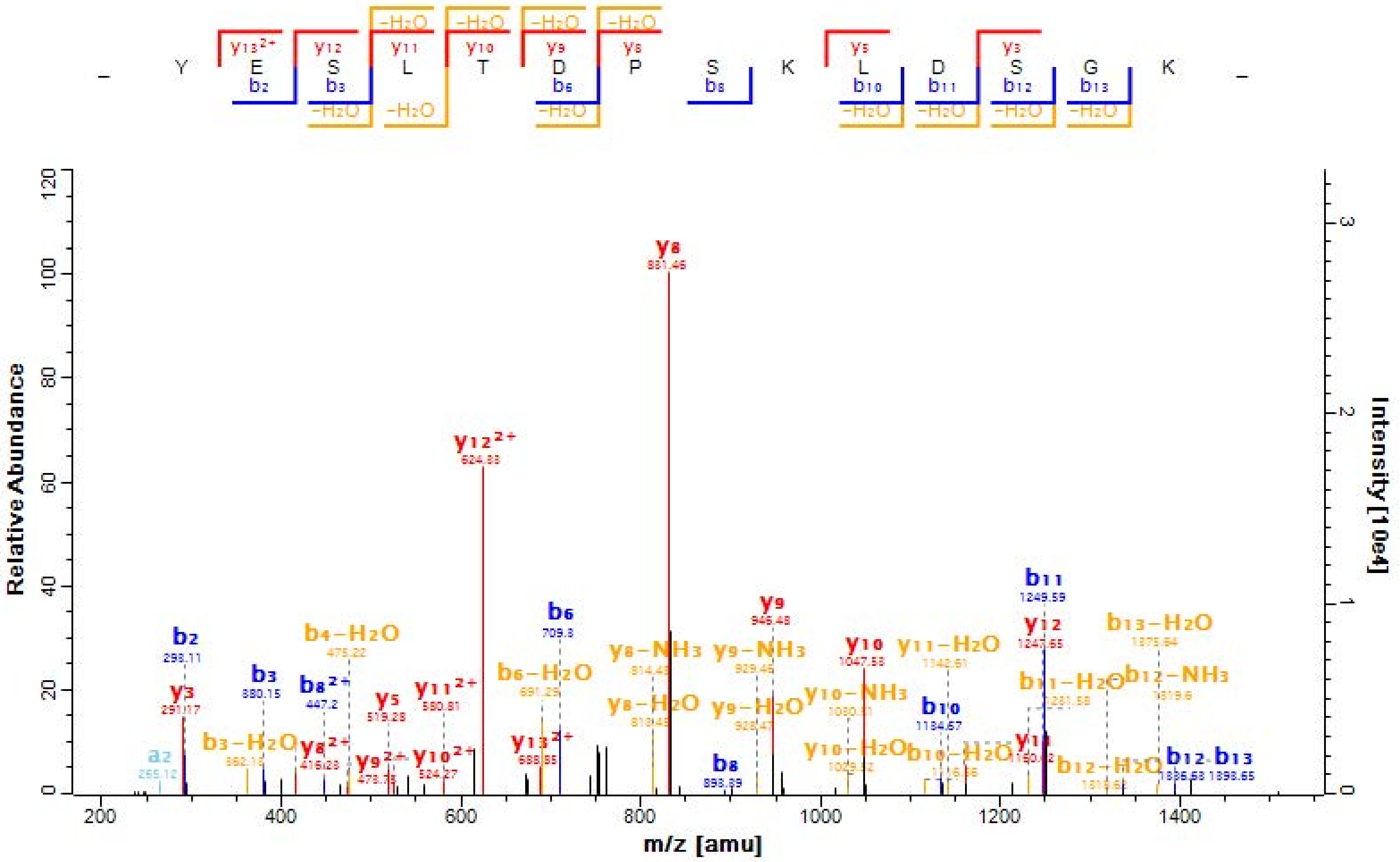
Mass:	1779.78282
m/z:	890.89869
Charge:	2+
Retentiontime:	15.993234634399
Score:	157.5766
Mass Error [ppm]:	1.6389
PEP:	2.016E-09
Precursor Type:	ISO

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	46 %
Peak Coverage:	37 %
Protein Localisation:	325 ... 339

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	14				
	244.13		244.13	2	K	13	1665.8		833.38	+0.2871
	343.2	-0.049	343.2	3	V	12	1537.7	-0.098	1537.7	
	442.27		442.27	4	V	11	1438.6	-0.026	1438.6	
	571.31	+0.0531	571.31	5	E	10	1339.5	-0.1	1339.5	
	686.34	+0.0756	686.34	6	D	9	1210.5	-0.068	1210.5	
-0.003	401.18		801.36	7	D	8	1095.5	-0.004	1095.5	
	930.41		930.41	8	E	7	980.43	-0.047	980.43	
	1045.4	-0.059	1045.4	9	D	6	851.39		851.39	
	1160.5	-0.051	1160.5	10	D	5	736.36	+0.0453	736.36	
	1307.5	-0.043	1307.5	11	F	4	621.34	+0.0301	621.34	
	1404.6	+0.0065	1404.6	12	P	3	474.27	+0.1481	474.27	
	1505.6	+0.2009	1505.6	13	T	2	377.21		377.21	
	1606.7	-0.038	1606.7	14	T	1	276.17		276.17	
				15	R	0	175.12		175.12	

Scan number 1750
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set2_05
Pepti... 281.26



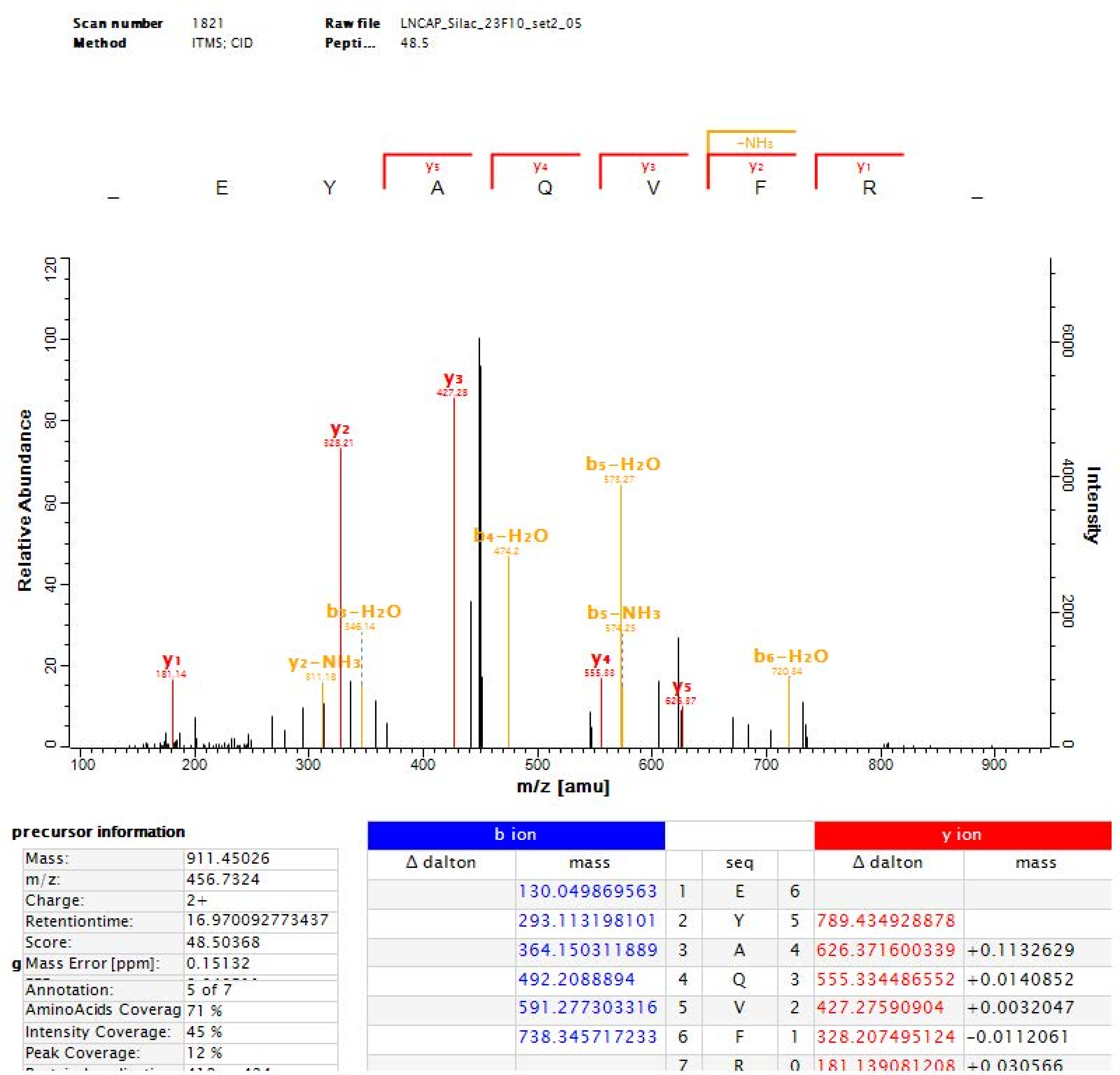
precursor information

Mass:	1538.74645
m/z:	770.3805
Charge:	2+
Retentiontime:	16.558956146240
Score:	281.2599
Mass Error [ppm]:	0.021031
PEP:	1.3393E-73
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	71 %
Peak Coverage:	47 %
Protein Localisation:	183 ... 196

a ion		b2+ ion		b ion					y ion		y2+ ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.1		164.1		164.1	1	Y	13				
+0.007	265.1		293.1	+0.038	293.1	2	E	12	1377		688.8	+0.20
	352.2		380.1	−0.03	380.1	3	S	11	1248	+0.053	624.3	+0.18
	465.2		493.2		493.2	4	L	10	1161	+0.039	580.8	−0.07
	566.3		594.3		594.3	5	T	9	1048	+0	524.3	+0.36
	681.3		709.3	+0.047	709.3	6	D	8	946.5	−0.06	473.7	−0.14
	778.4		806.4		806.4	7	P	7	831.5	−0.01	416.2	+0.49
	865.4	−0.01	447.2	+0.492	893.4	8	S	6	734.4		734.4	
	993.5		1021		1021	9	K	5	647.4		647.4	
	1107		1135	+0.062	1135	10	L	4	519.3	+0.097	519.3	
	1222		1250	+0.01	1250	11	D	3	406.2		406.2	
	1309		1337	−0.02	1337	12	S	2	291.2	−0.02	291.2	
	1366		1394	+0.029	1394	13	G	1	204.1		204.1	
						14	K	0	147.1		147.1	

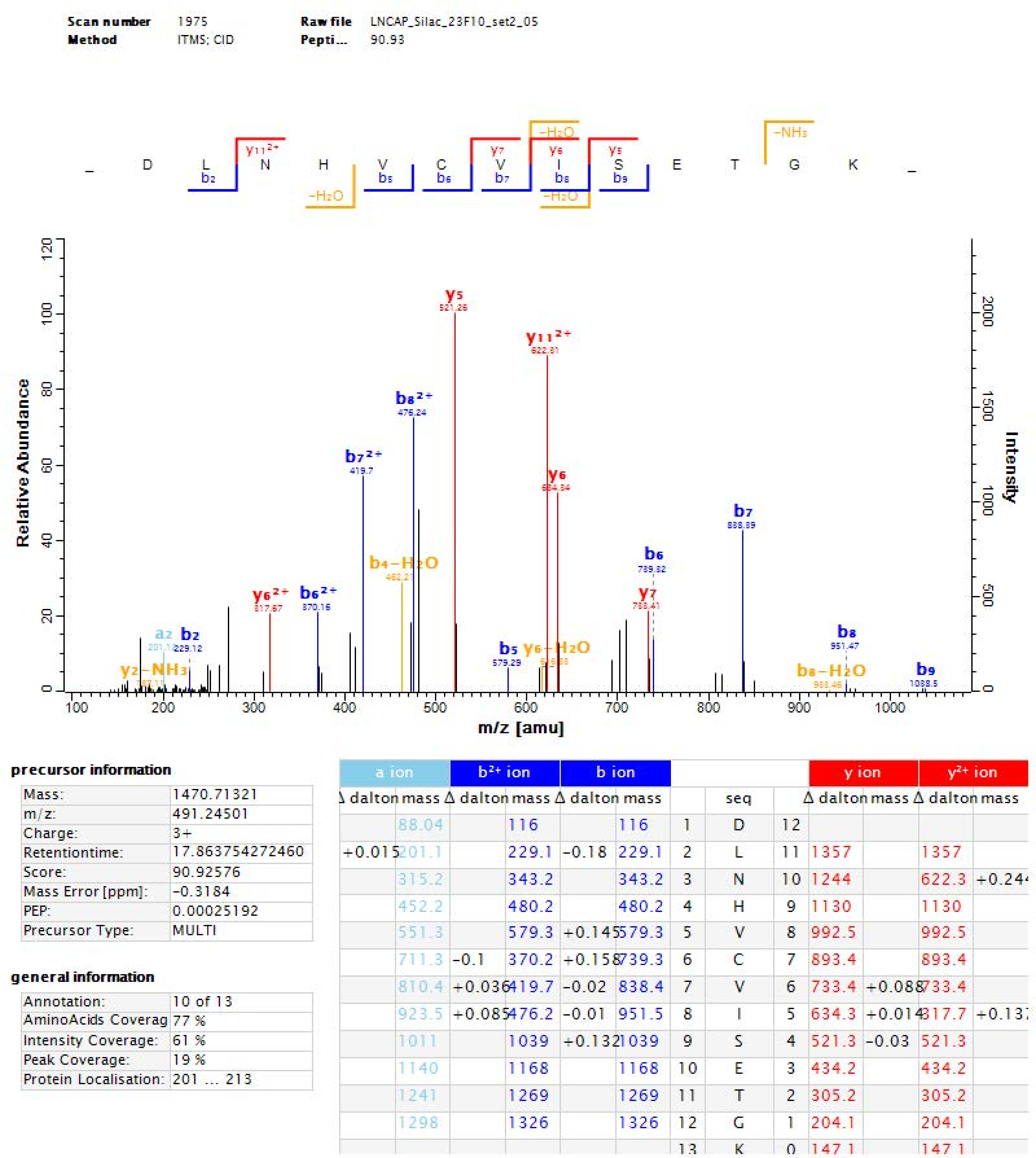


Scan number	1821	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	48.5

precursor information

Mass:	911.45026
m/z:	456.7324
Charge:	2+
Retentiontime:	16.970092773437
Score:	48.50368
Mass Error [ppm]:	0.15132
Annotation:	5 of 7
AminoAcids Coverag	71 %
Intensity Coverage:	45 %
Peak Coverage:	12 %

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	130.049869563	1	E	6		
	293.113198101	2	Y	5	789.434928878	
	364.150311889	3	A	4	626.371600339	+0.1132629
	492.2088894	4	Q	3	555.334486552	+0.0140852
	591.277303316	5	V	2	427.27590904	+0.0032047
	738.345717233	6	F	1	328.207495124	-0.0112061
		7	R	0	181.139081208	+0.030566



Scan number 1975 **Raw file** LNCAP_Silac_23F10_set2_05
Method ITMS; CID **Pepti...** 90.93

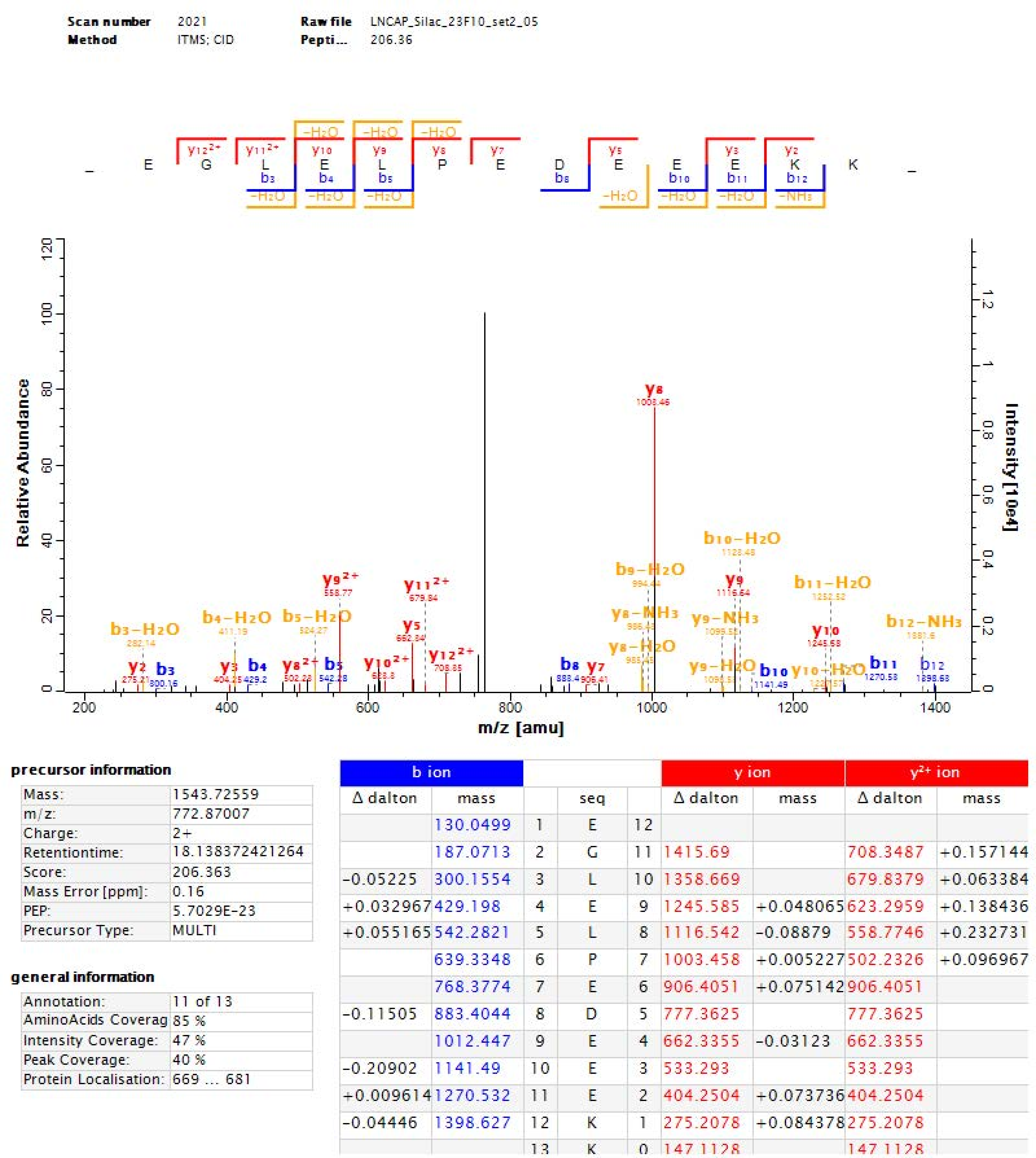
precursor information

Mass:	1470.71321
m/z:	491.24501
Charge:	3+
Retentiontime:	17.863754272460
Score:	90.92576
Mass Error [ppm]:	-0.3184
PEP:	0.00025192
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	61 %
Peak Coverage:	19 %
Protein Localisation:	201 ... 213

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.04		116		116	1	D	12				
+0.015	201.1		229.1	-0.18	229.1	2	L	11	1357		1357	
	315.2		343.2		343.2	3	N	10	1244		622.3	+0.24
	452.2		480.2		480.2	4	H	9	1130		1130	
	551.3		579.3	+0.145	579.3	5	V	8	992.5		992.5	
	711.3	-0.1	370.2	+0.158	739.3	6	C	7	893.4		893.4	
	810.4	+0.036	419.7	-0.02	838.4	7	V	6	733.4	+0.088	733.4	
	923.5	+0.085	476.2	-0.01	951.5	8	I	5	634.3	+0.014	317.7	+0.13
	1011		1039	+0.132	1039	9	S	4	521.3	-0.03	521.3	
	1140		1168		1168	10	E	3	434.2		434.2	
	1241		1269		1269	11	T	2	305.2		305.2	
	1298		1326		1326	12	G	1	204.1		204.1	
						13	K	0	147.1		147.1	



Scan number 2021 **Raw file** LNCAP_Silac_23F10_set2_05

Method ITMS; CID **Pepti...** 206.36

precursor information

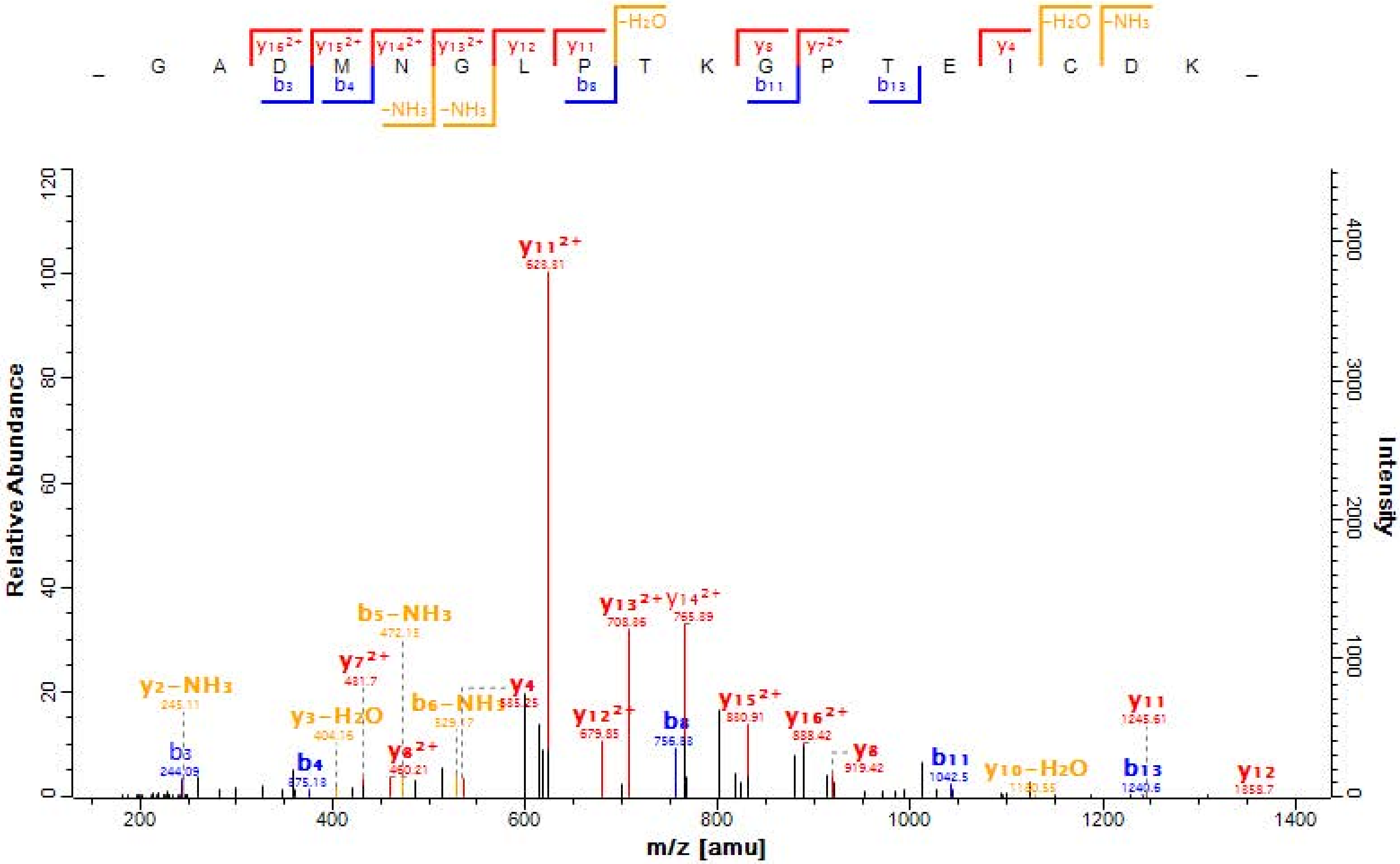
Mass:	1543.72559
m/z:	772.87007
Charge:	2+
Retentiontime:	18.138372421264
Score:	206.363
Mass Error [ppm]:	0.16
PEP:	5.7029E-23
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	47 %
Peak Coverage:	40 %
Protein Localisation:	669 … 681

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	12				
	187.0713	2	G	11	1415.69		708.3487	+0.157144
-0.05225	300.1554	3	L	10	1358.669		679.8379	+0.063384
+0.032967	429.198	4	E	9	1245.585	+0.048065	623.2959	+0.138436
+0.055165	542.2821	5	L	8	1116.542	-0.08879	558.7746	+0.232731
	639.3348	6	P	7	1003.458	+0.005227	502.2326	+0.096967
	768.3774	7	E	6	906.4051	+0.075142	906.4051	
-0.11505	883.4044	8	D	5	777.3625		777.3625	
	1012.447	9	E	4	662.3355	-0.03123	662.3355	
-0.20902	1141.49	10	E	3	533.293		533.293	
+0.009614	1270.532	11	E	2	404.2504	+0.073736	404.2504	
-0.04446	1398.627	12	K	1	275.2078	+0.084378	275.2078	
		13	K	0	147.1128		147.1128	

Scan number	2284	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	72.45



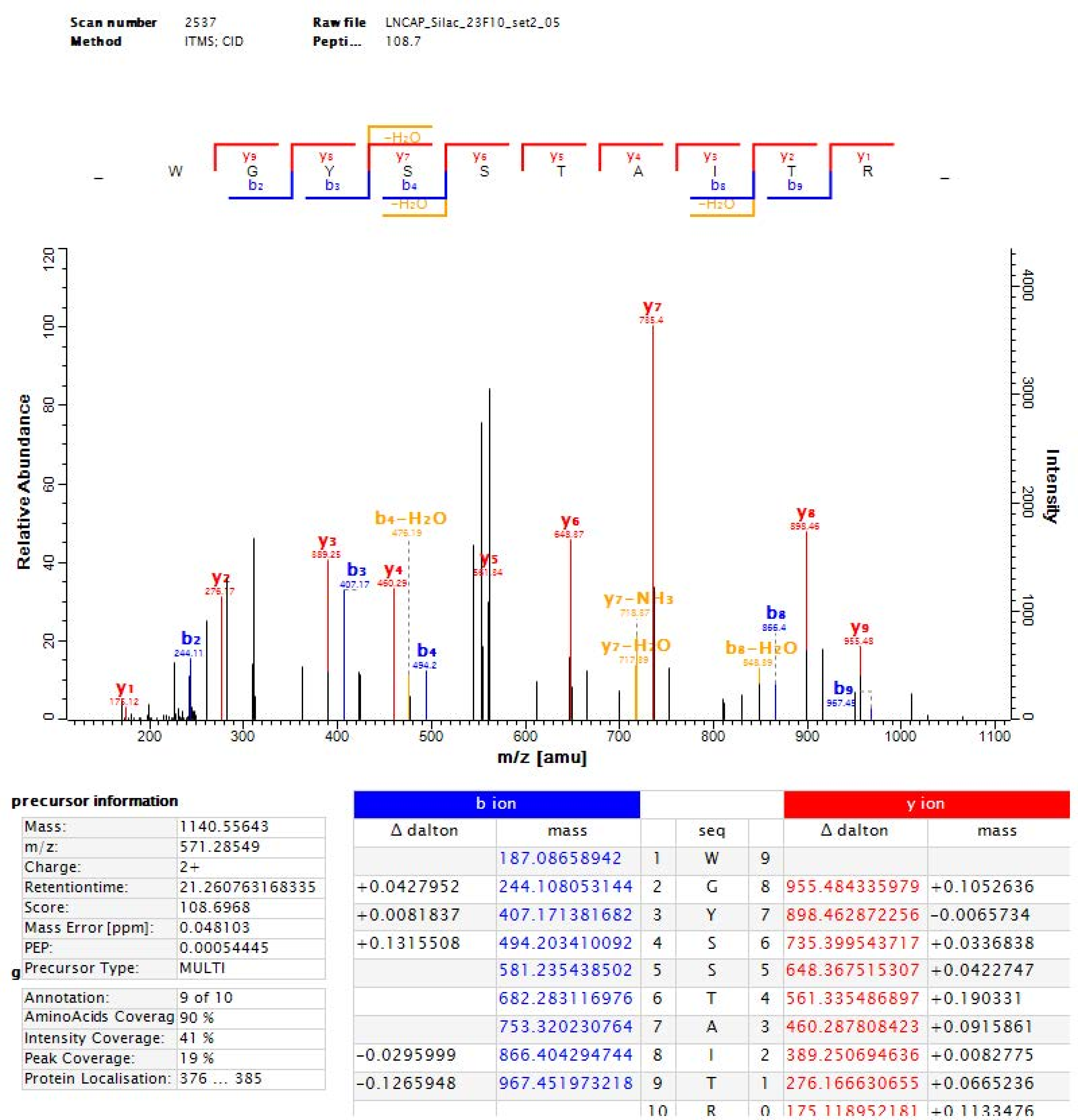
precursor information

Mass:	1902.88164
m/z:	635.30116
Charge:	3+
Retentiontime:	19.737129211425
Score:	72.44628
Mass Error [ppm]:	0.050315
PEP:	0.000266
Precursor Type:	MULTI

general information

Annotation:	13 of 18
AminoAcids Coverag	72 %
Intensity Coverage:	56 %
Peak Coverage:	22 %
Protein Localisation:	56 … 73

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	17				
	129.0659	2	A	16	1846.867		1846.867	
-0.13931	244.0928	3	D	15	1775.83		888.4188	-0.01666
+0.030048	375.1333	4	M	14	1660.803		830.9053	+0.174971
	489.1762	5	N	13	1529.763		765.385	+0.100731
	546.1977	6	G	12	1415.72		708.3636	+0.229861
	659.2817	7	L	11	1358.698	-0.06391	679.8529	+0.123771
+0.420199	756.3345	8	P	10	1245.614	-0.20994	623.3108	+0.276155
	857.3822	9	T	9	1148.562		1148.562	
	985.4771	10	K	8	1047.514		1047.514	
-0.27143	1042.499	11	G	7	919.419	-0.04304	460.2131	+0.321001
	1139.551	12	P	6	862.3975		431.7024	+0.015205
+0.481396	1240.599	13	T	5	765.3447		765.3447	
	1369.642	14	E	4	664.2971		664.2971	
	1482.726	15	I	3	535.2545	+0.373409	535.2545	
	1642.756	16	C	2	422.1704		422.1704	
	1757.783	17	D	1	262.1397		262.1397	
		18	K	0	147.1128		147.1128	



Scan number 2537 **Raw file** LNCAP_Silac_23F10_set2_05
Method ITMS; CID **Pepti...** 108.7

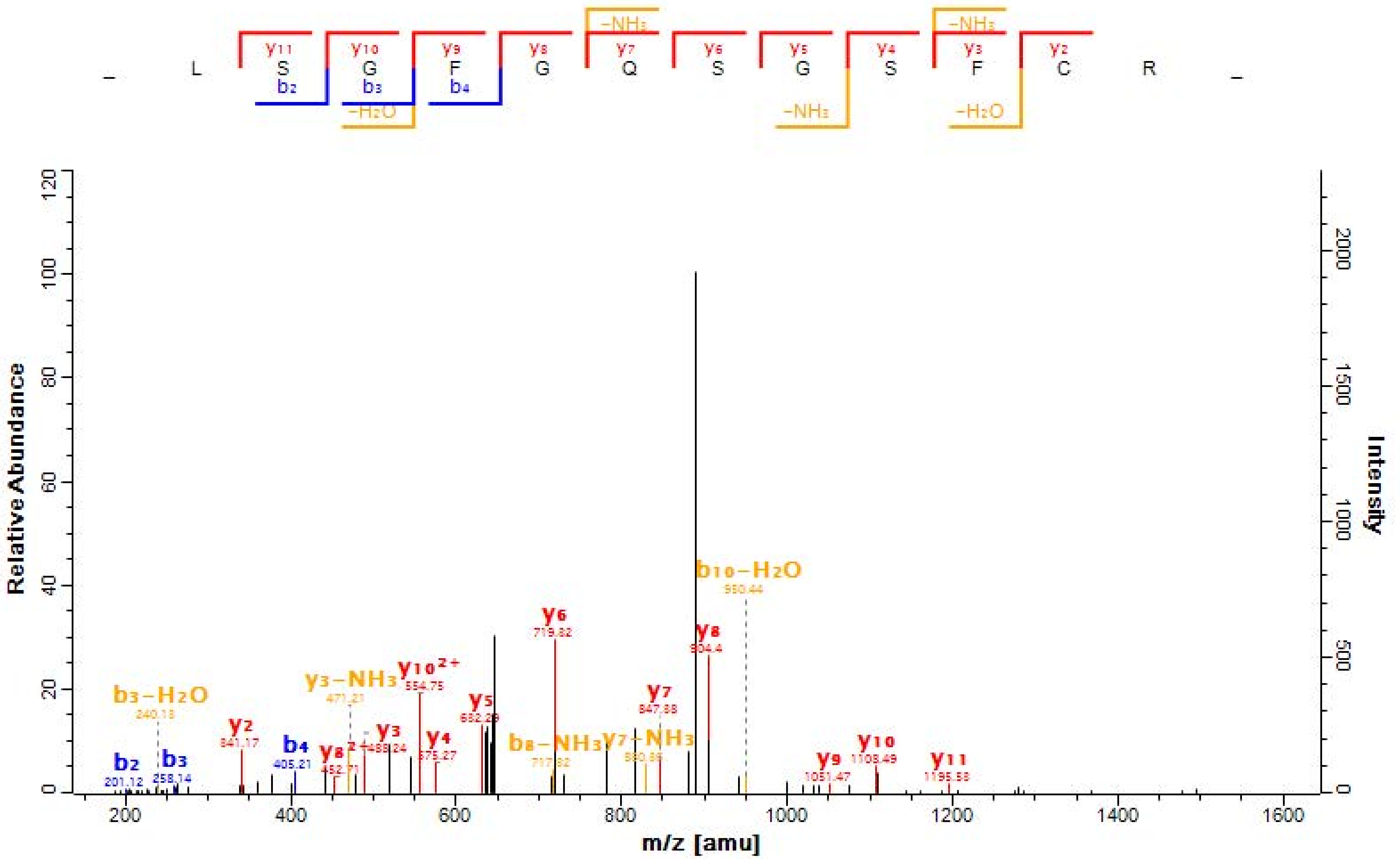
precursor information

Mass:	1140.55643
m/z:	571.28549
Charge:	2+
Retentiontime:	21.260763168335
Score:	108.6968
Mass Error [ppm]:	0.048103
PEP:	0.00054445
Precursor Type:	MULTI

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	41 %
Peak Coverage:	19 %
Protein Localisation:	376 ... 385

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	187.08658942	1	W	9		
+0.0427952	244.108053144	2	G	8	955.484335979	+0.1052636
+0.0081837	407.171381682	3	Y	7	898.462872256	-0.0065734
+0.1315508	494.203410092	4	S	6	735.399543717	+0.0336838
	581.235438502	5	S	5	648.367515307	+0.0422747
	682.283116976	6	T	4	561.335486897	+0.190331
	753.320230764	7	A	3	460.287808423	+0.0915861
-0.0295999	866.404294744	8	I	2	389.250694636	+0.0082775
-0.1265948	967.451973218	9	T	1	276.166630655	+0.0665236
		10	R	0	175.118952181	+0.1133476

Scan number 2567 **Raw file** LNCAP_Silac_23F10_set2_05
Method ITMS; CID **Pepti...** 91.86



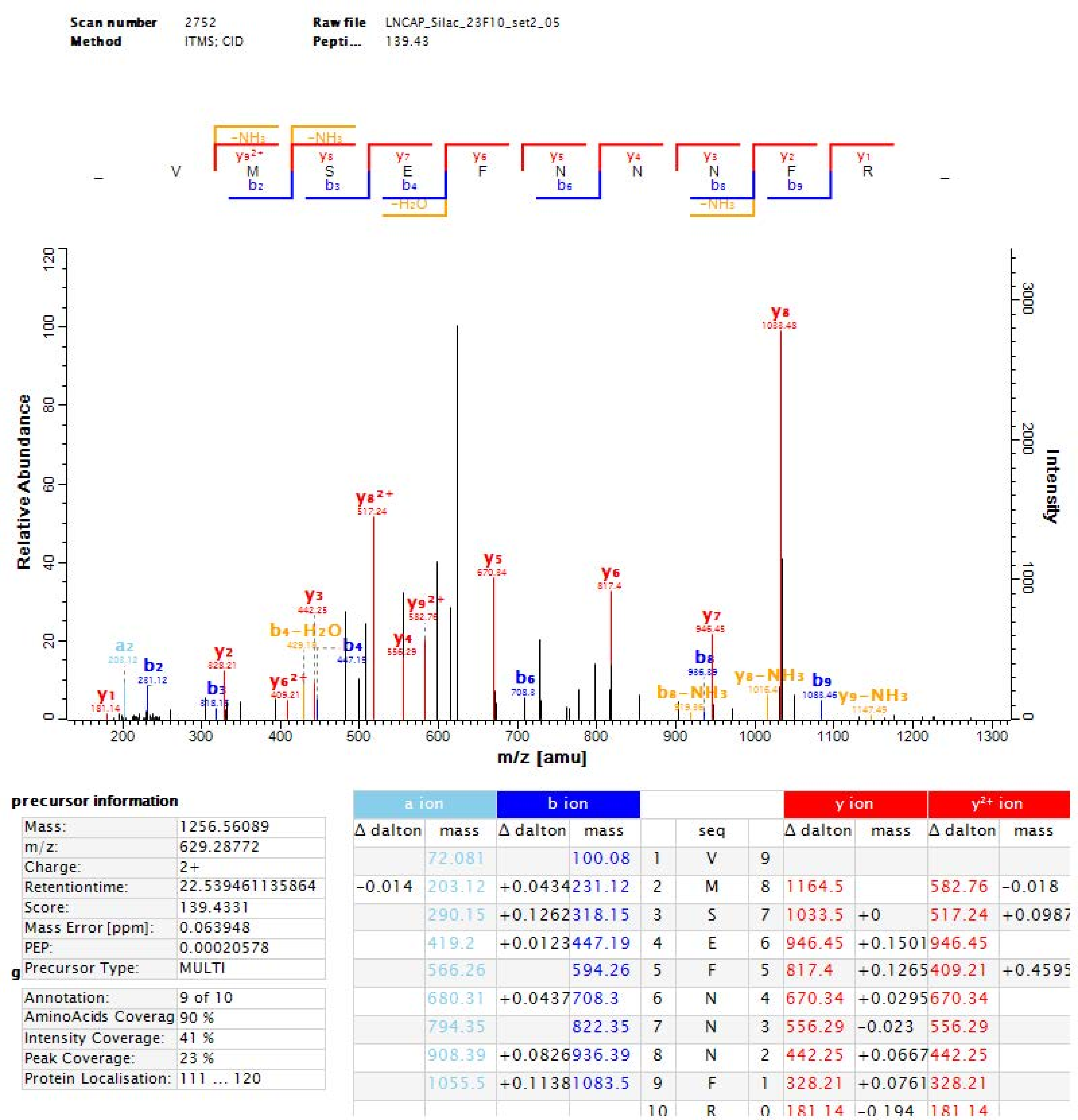
precursor information

Mass:	1960.94905
m/z:	654.65696
Charge:	3+
Retentiontime:	21.440256118774
Score:	91.85767
Mass Error [ppm]:	0.61747
PEP:	0.0024941
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	32 %
Peak Coverage:	21 %
Protein Localisation:	107 ... 118

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	11				
+0.011488	201.1234	2	S	10	1195.526	+0.006005	1195.526	
+0.047062	258.1448	3	G	9	1108.494	-0.02325	554.7504	+0.295469
+0.190928	405.2132	4	F	8	1051.472	+0.225757	1051.472	
	462.2347	5	G	7	904.4037	+0.053814	452.7055	+0.30635
	590.2933	6	Q	6	847.3822	+0.060935	847.3822	
	677.3253	7	S	5	719.3237	+0.050237	719.3237	
	734.3468	8	G	4	632.2916	+0.033987	632.2916	
	821.3788	9	S	3	575.2702	+0.024323	575.2702	
	968.4472	10	F	2	488.2381	+0.070145	488.2381	
	1128.478	11	C	1	341.1697	+0.164682	341.1697	
		12	R	0	181.1391		181.1391	



Scan number	2752	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	139.43

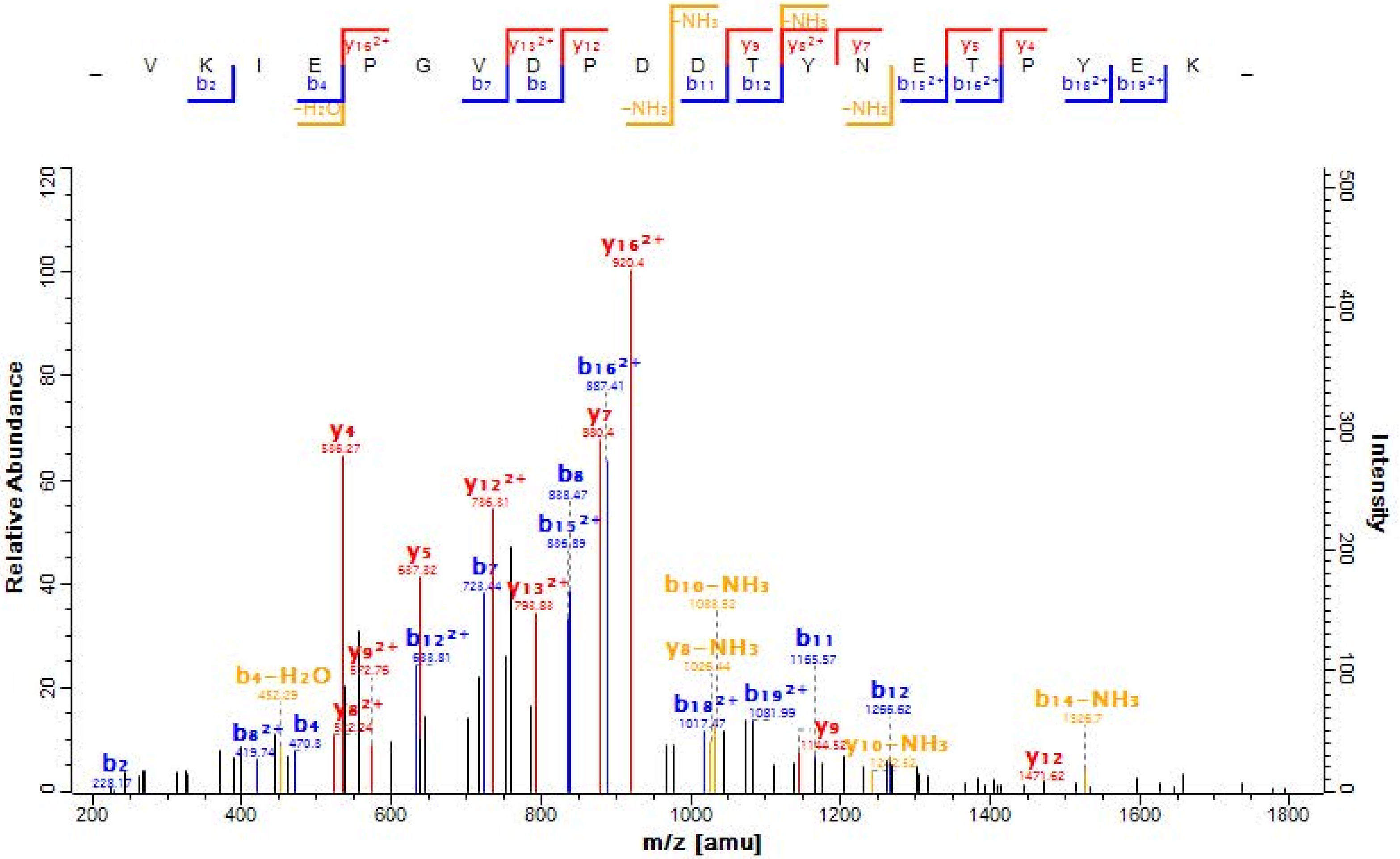
precursor information

Mass:	1256.56089
m/z:	629.28772
Charge:	2+
Retentiontime:	22.539461135864
Score:	139.4331
Mass Error [ppm]:	0.063948
PEP:	0.00020578
Precursor Type:	MULTI

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	41 %
Peak Coverage:	23 %
Protein Localisation:	111 ... 120

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.081		100.08	1	V	9				
-0.014	203.12	+0.0434	231.12	2	M	8	1164.5		582.76	-0.018
	290.15	+0.1262	318.15	3	S	7	1033.5	+0	517.24	+0.0987
	419.2	+0.0123	447.19	4	E	6	946.45	+0.1501	946.45	
	566.26		594.26	5	F	5	817.4	+0.1265	409.21	+0.4595
	680.31	+0.0437	708.3	6	N	4	670.34	+0.0295	670.34	
	794.35		822.35	7	N	3	556.29	-0.023	556.29	
	908.39	+0.0826	936.39	8	N	2	442.25	+0.0667	442.25	
	1055.5	+0.1138	1083.5	9	F	1	328.21	+0.0761	328.21	
				10	R	0	181.14	-0.194	181.14	

Scan number	2753	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	99.89



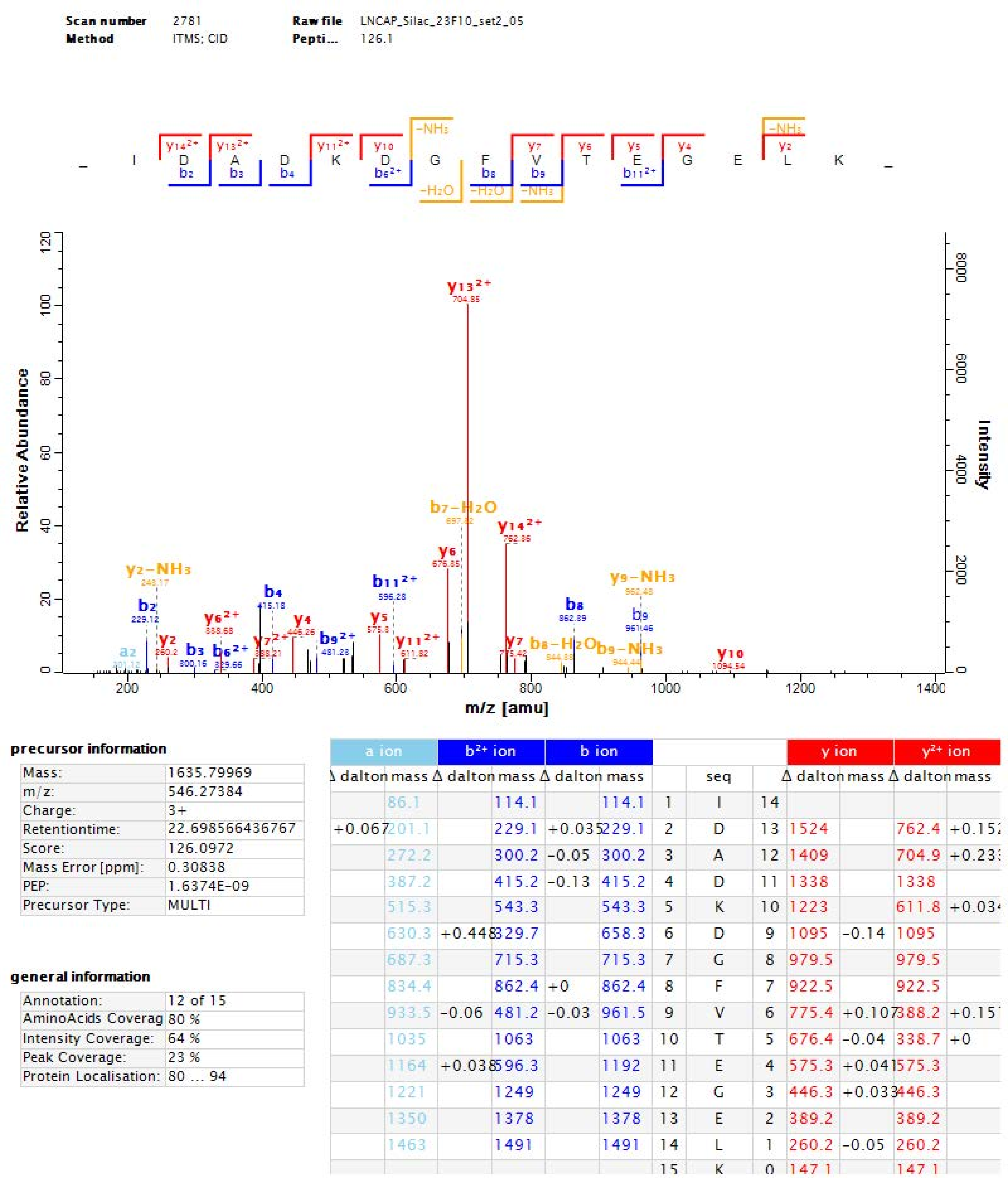
precursor information

Mass:	2308.07512
m/z:	770.36565
Charge:	3+
Retentiontime:	22.544143676757
Score:	99.89084
Mass Error [ppm]:	0.18837
PEP:	1.3125E-06
Precursor Type:	MULTI

general information

Annotation:	16 of 20
AminoAcids Coverag	80 %
Intensity Coverage:	60 %
Peak Coverage:	31 %
Protein Localisation:	405 ... 424

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	19				
	228.17	+0.0728	228.17	2	K	18	2210		2210	
	341.25		341.25	3	I	17	2081.9		2081.9	
	470.3	-0.003	470.3	4	E	16	1968.8		1968.8	
	567.35		567.35	5	P	15	1839.8		920.4	+0.241
	624.37		624.37	6	G	14	1742.7		1742.7	
	723.44	+0.0157	723.44	7	V	13	1685.7		1685.7	
+0.3603	419.74	-0.021	838.47	8	D	12	1586.6		793.83	+0.1468
	935.52		935.52	9	P	11	1471.6	+0.1784	736.31	+0.2958
	1050.5		1050.5	10	D	10	1374.6		1374.6	
	1165.6	-0.189	1165.6	11	D	9	1259.5		1259.5	
+0.1655	633.81	-0.008	1266.6	12	T	8	1144.5	-0.138	572.76	+0.0517
	1429.7		1429.7	13	Y	7	1043.5		522.24	-0.068
	1543.7		1543.7	14	N	6	880.4	-0.072	880.4	
+0.2627	836.89		1672.8	15	E	5	766.36		766.36	
+0.237	887.41		1773.8	16	T	4	637.32	+0.0806	637.32	
	1870.9		1870.9	17	P	3	536.27	-0.025	536.27	
+0.4176	1017.5		2033.9	18	Y	2	439.22		439.22	
-0.109	1082		2163	19	E	1	276.16		276.16	
				20	K	0	147.11		147.11	



Scan number	2781	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	126.1

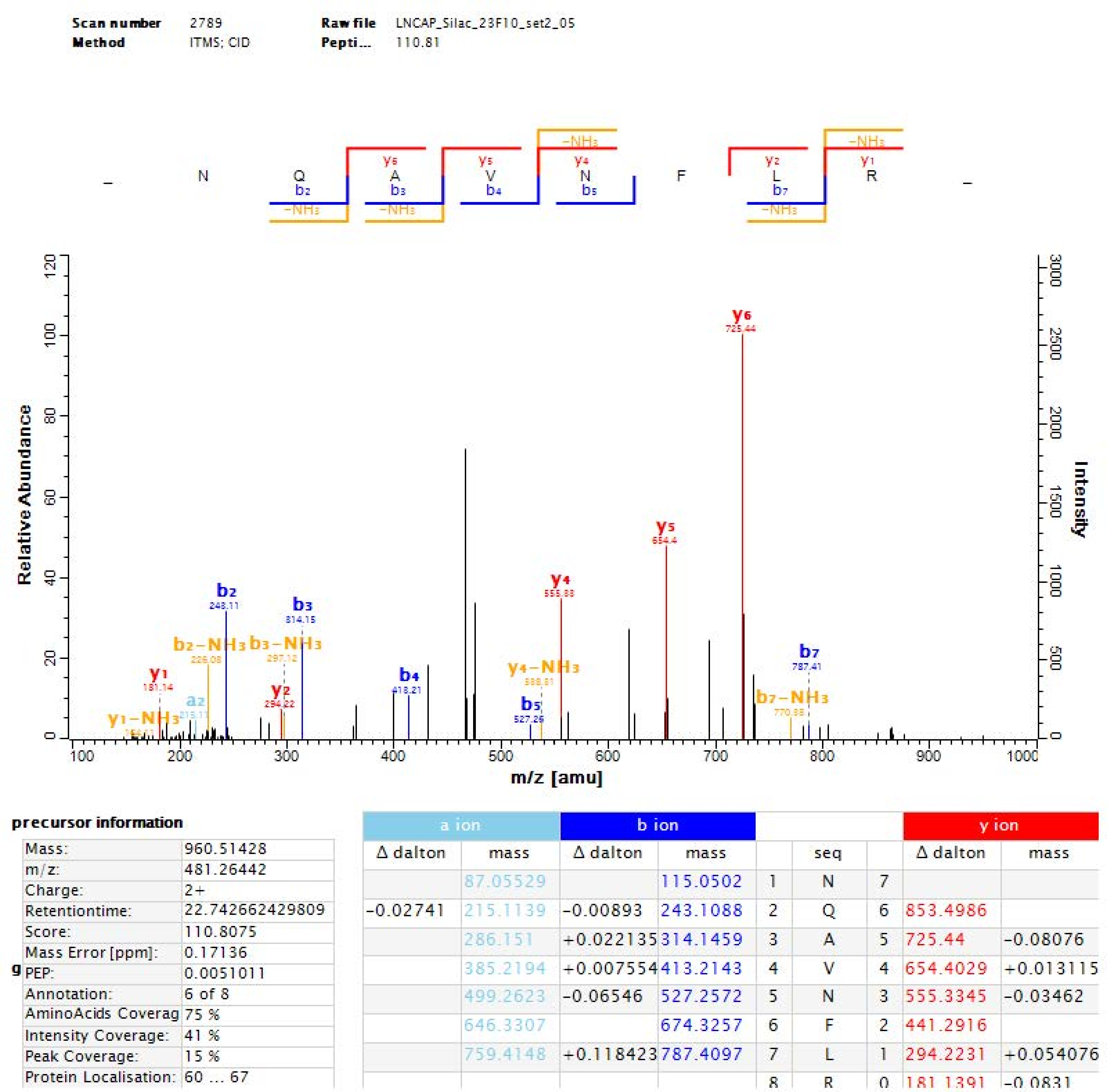
precursor information

Mass:	1635.79969
m/z:	546.27384
Charge:	3+
Retentiontime:	22.698566436767
Score:	126.0972
Mass Error [ppm]:	0.30838
PEP:	1.6374E-09
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	64 %
Peak Coverage:	23 %
Protein Localisation:	80 ... 94

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	I	14				
+0.067	201.1		229.1	+0.035	229.1	2	D	13	1524		762.4	+0.15
	272.2		300.2	-0.05	300.2	3	A	12	1409		704.9	+0.23
	387.2		415.2	-0.13	415.2	4	D	11	1338		1338	
	515.3		543.3		543.3	5	K	10	1223		611.8	+0.03
	630.3	+0.448	329.7		658.3	6	D	9	1095	-0.14	1095	
	687.3		715.3		715.3	7	G	8	979.5		979.5	
	834.4		862.4	+0	862.4	8	F	7	922.5		922.5	
	933.5	-0.06	481.2	-0.03	961.5	9	V	6	775.4	+0.107	388.2	+0.15
	1035		1063		1063	10	T	5	676.4	-0.04	338.7	+0
	1164	+0.038	596.3		1192	11	E	4	575.3	+0.041	575.3	
	1221		1249		1249	12	G	3	446.3	+0.033	446.3	
	1350		1378		1378	13	E	2	389.2		389.2	
	1463		1491		1491	14	L	1	260.2	-0.05	260.2	
						15	K	0	147.1		147.1	



Scan number	2789	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	110.81

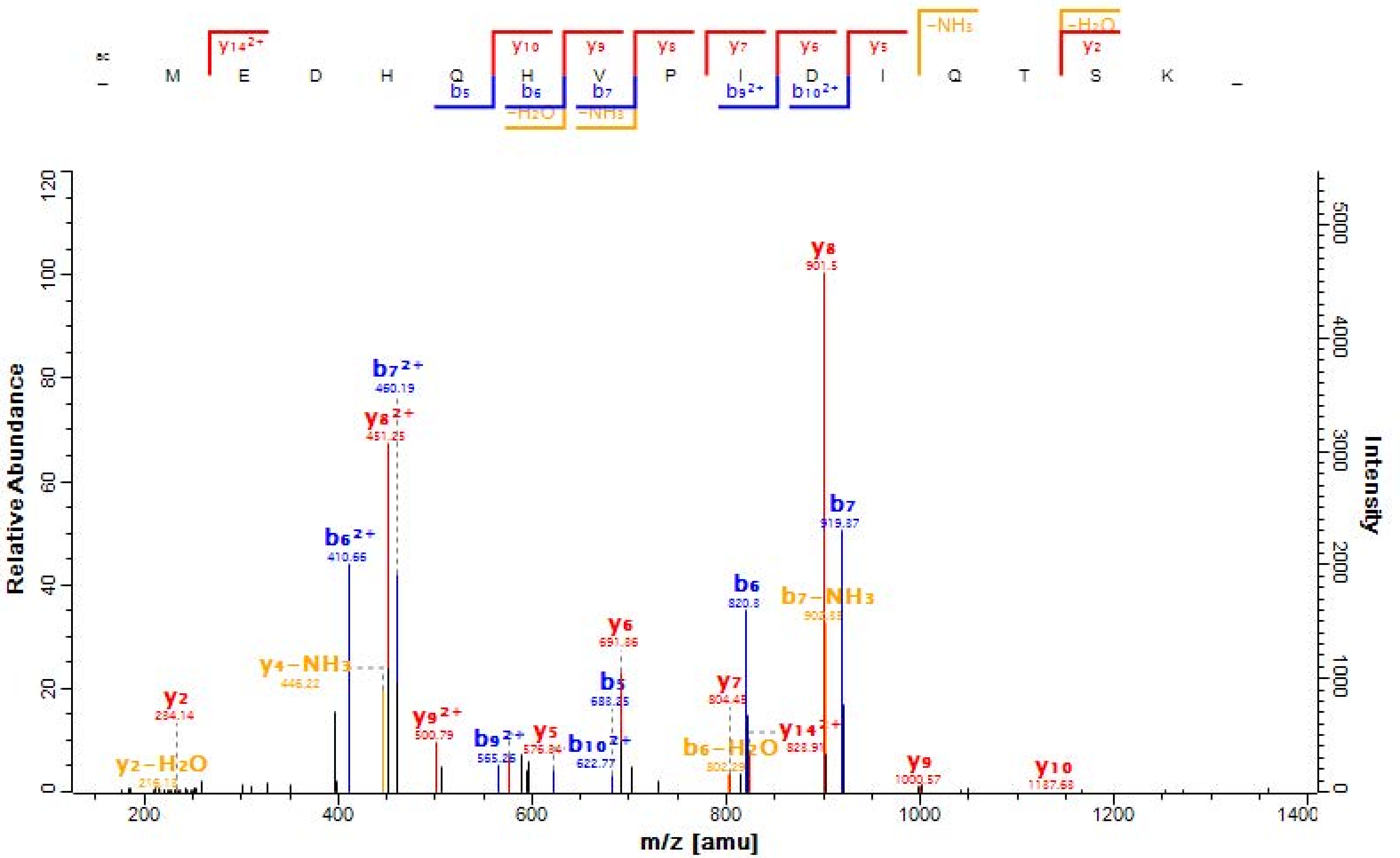
precursor information

g

Mass:	960.51428
m/z:	481.26442
Charge:	2+
Retentiontime:	22.742662429809
Score:	110.8075
Mass Error [ppm]:	0.17136
PEP:	0.0051011
Annotation:	6 of 8
AminoAcids Coverag	75 %
Intensity Coverage:	41 %
Peak Coverage:	15 %
Protein Localisation:	60 ... 67

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	87.05529		115.0502	1	N	7		
-0.02741	215.1139	-0.00893	243.1088	2	Q	6	853.4986	
	286.151	+0.022135	314.1459	3	A	5	725.44	-0.08076
	385.2194	+0.007554	413.2143	4	V	4	654.4029	+0.013115
	499.2623	-0.06546	527.2572	5	N	3	555.3345	-0.03462
	646.3307		674.3257	6	F	2	441.2916	
	759.4148	+0.118423	787.4097	7	L	1	294.2231	+0.054076
				8	R	0	181.1391	-0.0831

Scan number	2808	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	77.42



precursor information

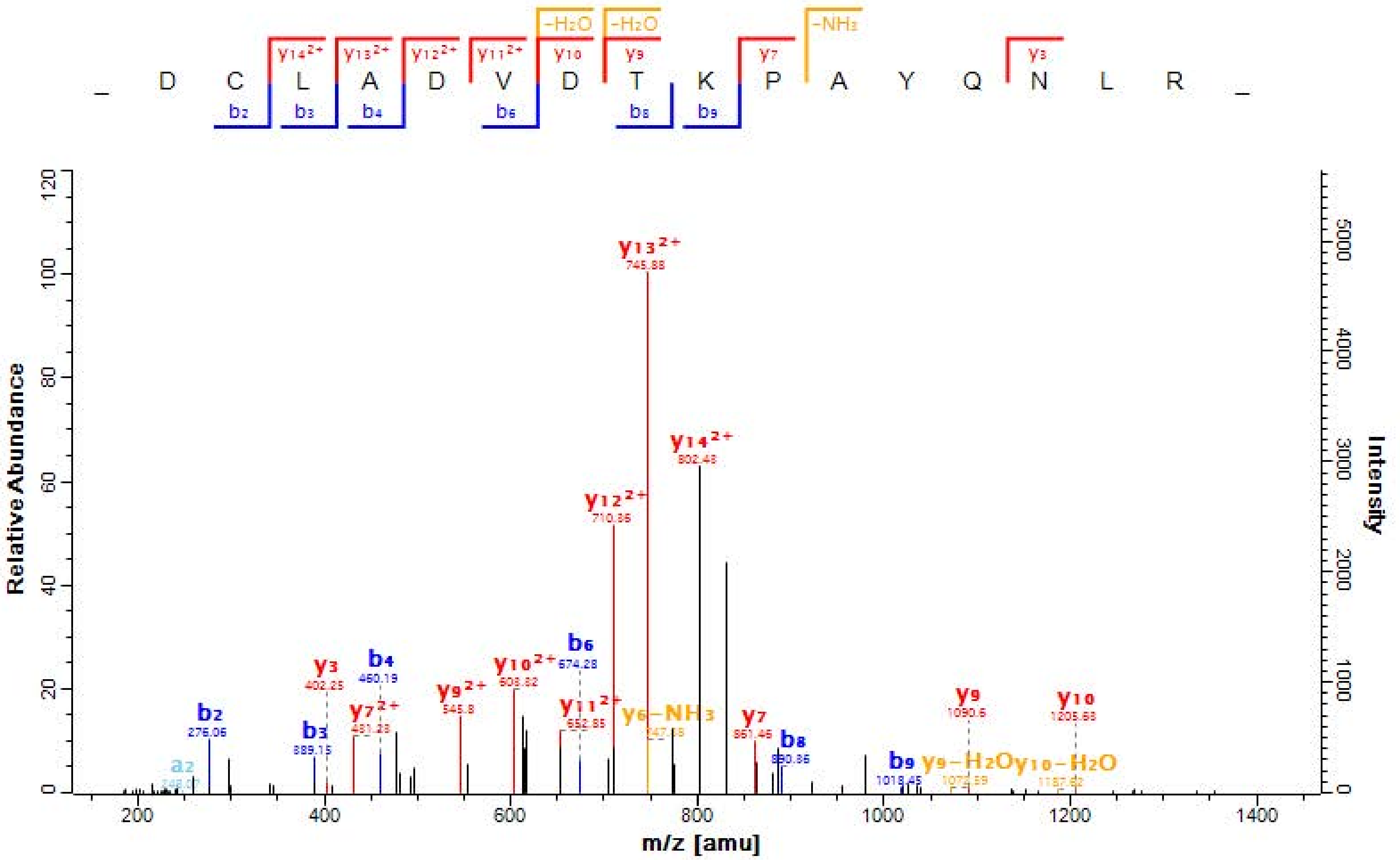
Mass:	1818.85798
m/z:	607.29327
Charge:	3+
Retentiontime:	22.850254058837
Score:	77.42032
Mass Error [ppm]:	0.51123
PEP:	0.0019806
Precursor Type:	MULTI

general information

Annotation:	10 of 15
AminoAcids Coverag	67 %
Intensity Coverage:	72 %
Peak Coverage:	26 %
Protein Localisation:	1 ... 15

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	174.06		174.06	1	M	14				
	303.1		303.1	2	E	13	1646.8		823.91	+0.304
	418.13		418.13	3	D	12	1517.8		1517.8	
	555.19		555.19	4	H	11	1402.7		1402.7	
	683.25	−0.022	683.25	5	Q	10	1265.7		1265.7	
+0.1526	410.66	−0.034	820.3	6	H	9	1137.6	+0.31	1137.6	
−0.004	460.19	−0.006	919.37	7	V	8	1000.6	+0.1148	500.79	+0.233
	1016.4		1016.4	8	P	7	901.5	−0.01	451.25	+0.0357
+0.0302	565.26		1129.5	9	I	6	804.45	+0.1702	804.45	
+0.2603	622.77		1244.5	10	D	5	691.36	+0	691.36	
	1357.6		1357.6	11	I	4	576.34	+0.0564	576.34	
	1485.7		1485.7	12	Q	3	463.25		463.25	
	1586.7		1586.7	13	T	2	335.19		335.19	
	1673.8		1673.8	14	S	1	234.14	+0.2246	234.14	
				15	K	0	147.11		147.11	

Scan number	2895	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	95.26



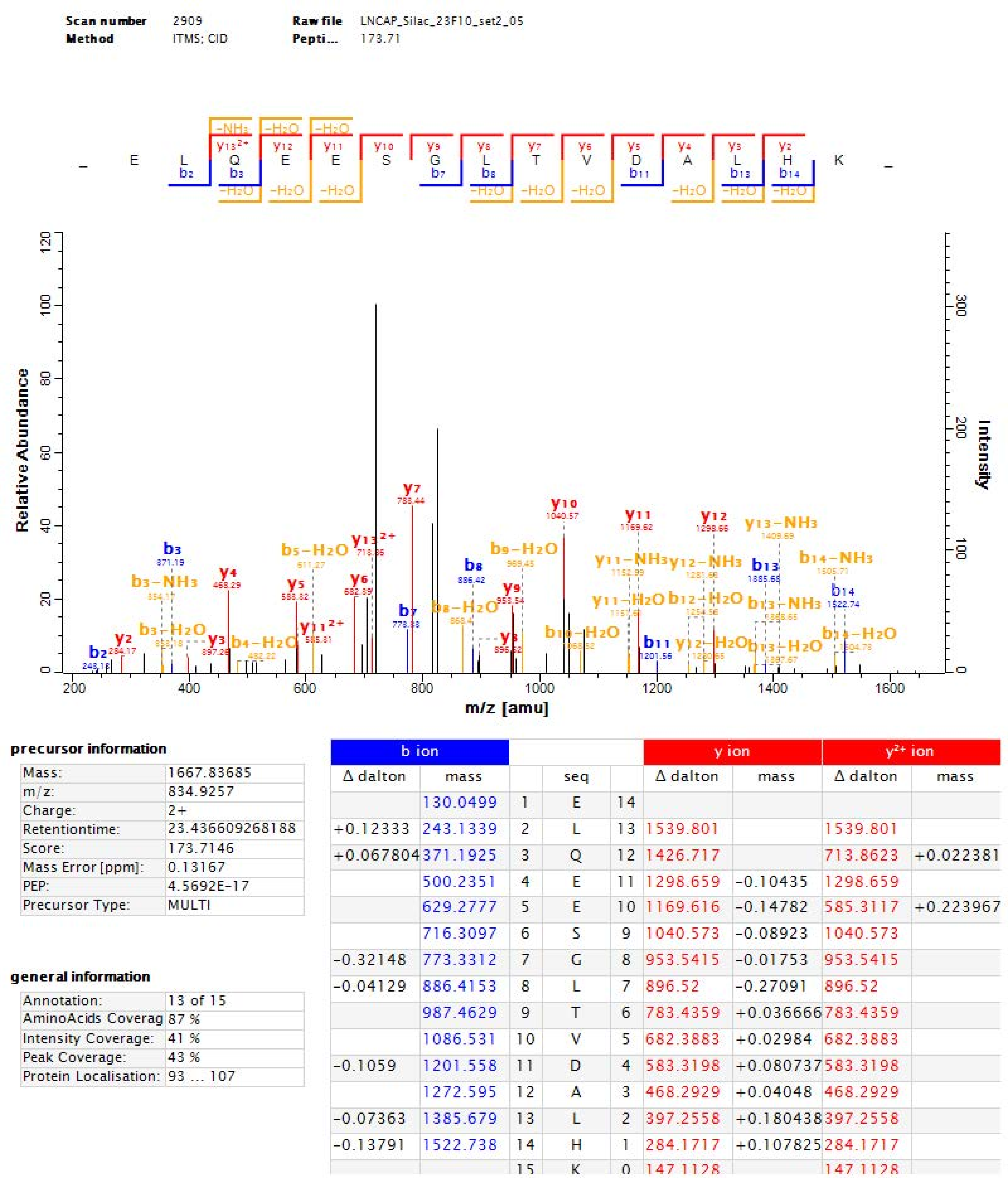
precursor information

Mass:	1877.89348
m/z:	626.97177
Charge:	3+
Retentiontime:	23.356206893920
Score:	95.26447
Mass Error [ppm]:	-0.36127
PEP:	1.9919E-05
Precursor Type:	MULTI

general information

Annotation:	11 of 16
AminoAcids Coverag	69 %
Intensity Coverage:	53 %
Peak Coverage:	20 %
Protein Localisation:	73 ... 88

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	15				
-0.032	248.07	+0.0247	276.06	2	C	14	1763.9		1763.9	
	361.15	+0.0154	389.15	3	L	13	1603.8		802.43	+0.0731
	432.19	+0.0364	460.19	4	A	12	1490.8		745.88	+0.2848
	547.22		575.21	5	D	11	1419.7		710.36	+0.2233
	646.29	-0.011	674.28	6	V	10	1304.7		652.85	+0.0334
	761.31		789.31	7	D	9	1205.6	+0.2147	603.32	+0.1922
	862.36	-0.053	890.36	8	T	8	1090.6	+0.125	545.8	+0.14
	990.46	+0.0171	1018.5	9	K	7	989.55		989.55	
	1087.5		1115.5	10	P	6	861.46	+0.0299	431.23	+0.1153
	1158.5		1186.5	11	A	5	764.4		764.4	
	1321.6		1349.6	12	Y	4	693.37		693.37	
	1449.7		1477.7	13	Q	3	530.3		530.3	
	1563.7		1591.7	14	N	2	402.25	+0.0837	402.25	
	1676.8		1704.8	15	L	1	288.2		288.2	
				16	R	0	175.12		175.12	



Scan number	2909	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	173.71

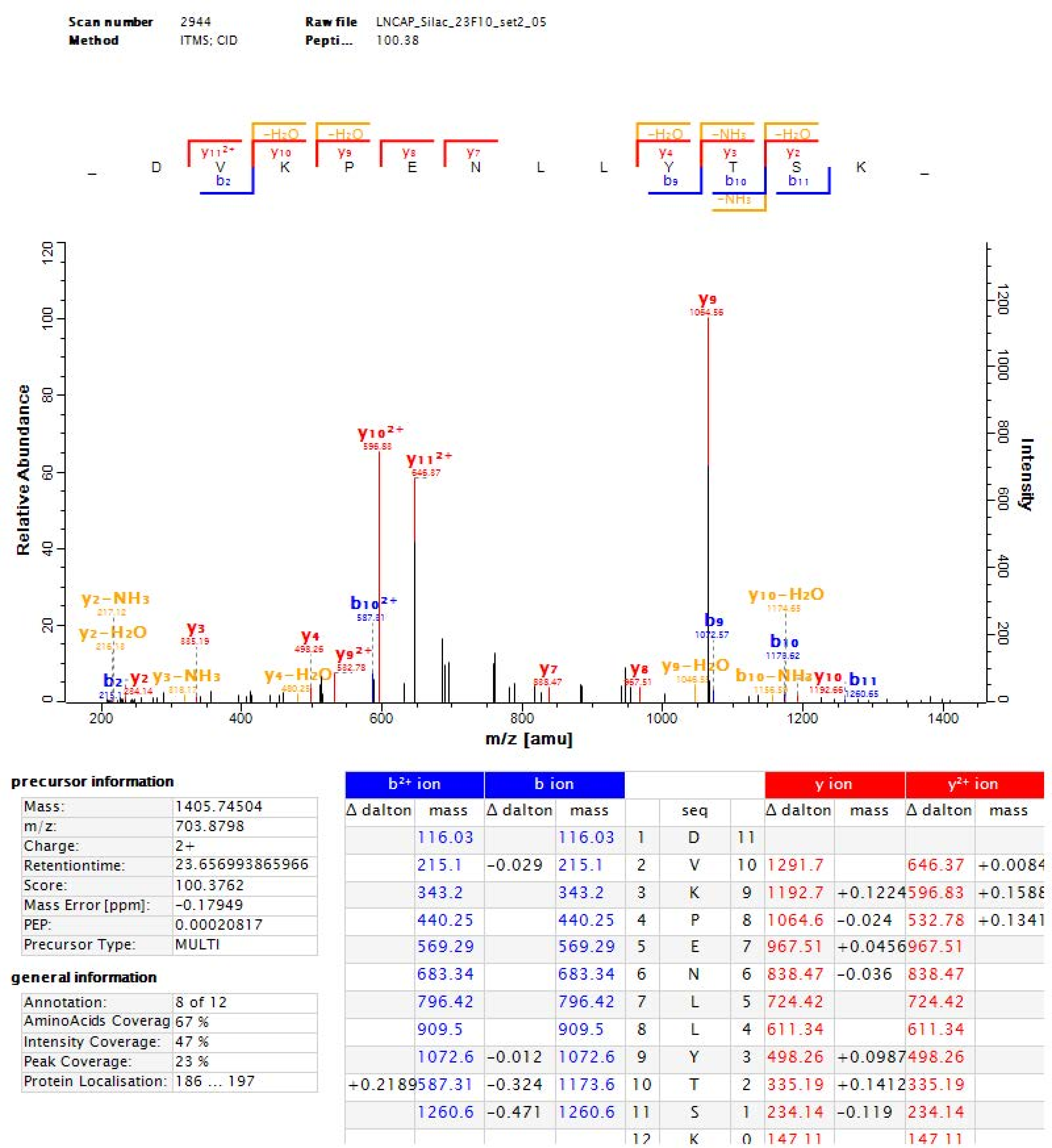
precursor information

Mass:	1667.83685
m/z:	834.9257
Charge:	2+
Retentiontime:	23.436609268188
Score:	173.7146
Mass Error [ppm]:	0.13167
PEP:	4.5692E-17
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	41 %
Peak Coverage:	43 %
Protein Localisation:	93 ... 107

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	14				
+0.12333	243.1339	2	L	13	1539.801		1539.801	
+0.067804	371.1925	3	Q	12	1426.717		713.8623	+0.022381
	500.2351	4	E	11	1298.659	-0.10435	1298.659	
	629.2777	5	E	10	1169.616	-0.14782	585.3117	+0.223967
	716.3097	6	S	9	1040.573	-0.08923	1040.573	
-0.32148	773.3312	7	G	8	953.5415	-0.01753	953.5415	
-0.04129	886.4153	8	L	7	896.52	-0.27091	896.52	
	987.4629	9	T	6	783.4359	+0.036666	783.4359	
	1086.531	10	V	5	682.3883	+0.02984	682.3883	
-0.1059	1201.558	11	D	4	583.3198	+0.080737	583.3198	
	1272.595	12	A	3	468.2929	+0.04048	468.2929	
-0.07363	1385.679	13	L	2	397.2558	+0.180438	397.2558	
-0.13791	1522.738	14	H	1	284.1717	+0.107825	284.1717	
		15	K	0	147.1128		147.1128	



Scan number	2944	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	100.38

precursor information

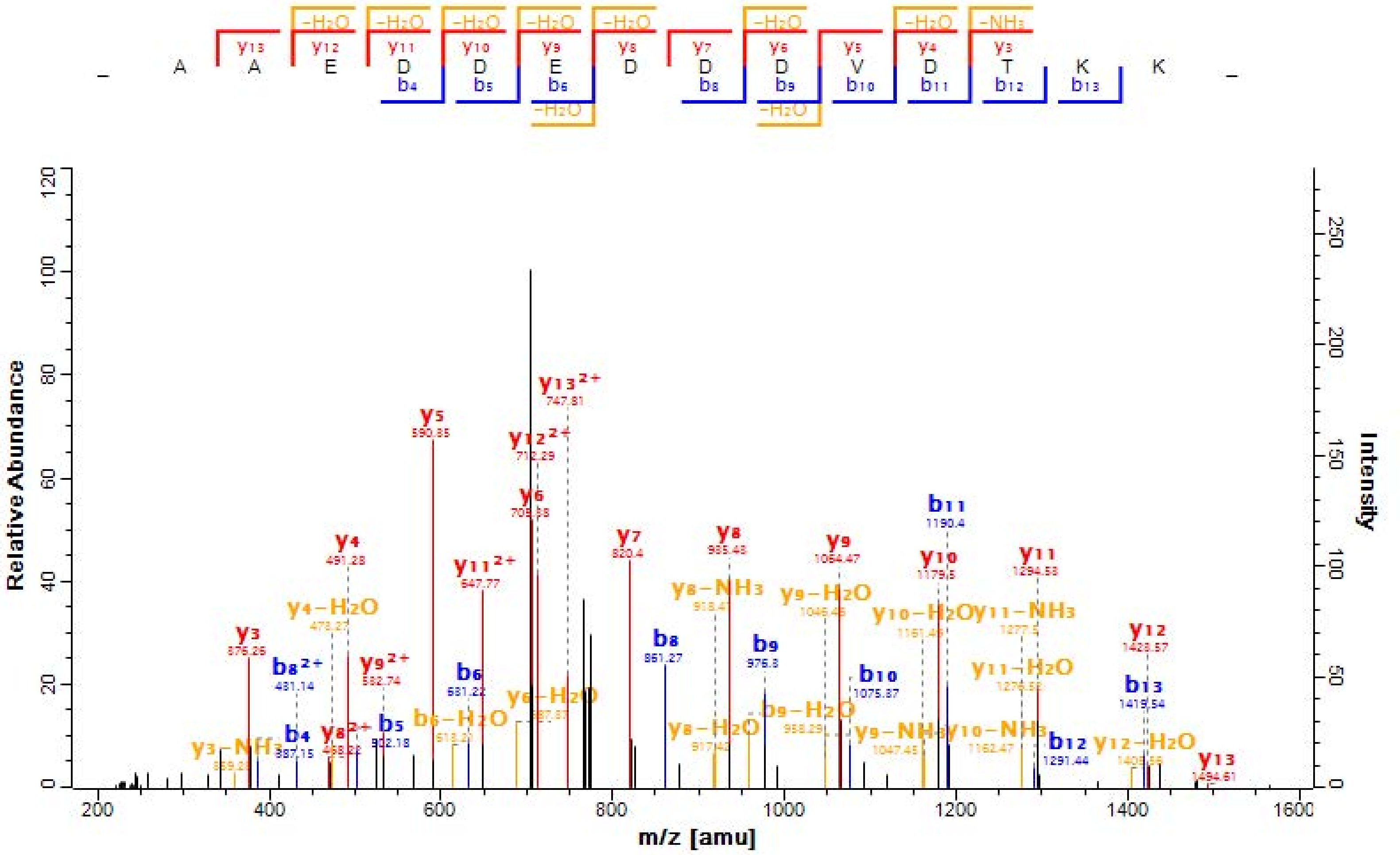
Mass:	1405.74504
m/z:	703.8798
Charge:	2+
Retentiontime:	23.656993865966
Score:	100.3762
Mass Error [ppm]:	-0.17949
PEP:	0.00020817
Precursor Type:	MULTI

general information

Annotation:	8 of 12
AminoAcids Coverag	67 %
Intensity Coverage:	47 %
Peak Coverage:	23 %
Protein Localisation:	186 ... 197

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	11				
	215.1	-0.029	215.1	2	V	10	1291.7		646.37	+0.0084
	343.2		343.2	3	K	9	1192.7	+0.1224	596.83	+0.158
	440.25		440.25	4	P	8	1064.6	-0.024	532.78	+0.1341
	569.29		569.29	5	E	7	967.51	+0.0456	967.51	
	683.34		683.34	6	N	6	838.47	-0.036	838.47	
	796.42		796.42	7	L	5	724.42		724.42	
	909.5		909.5	8	L	4	611.34		611.34	
	1072.6	-0.012	1072.6	9	Y	3	498.26	+0.0987	498.26	
+0.2189	587.31	-0.324	1173.6	10	T	2	335.19	+0.1412	335.19	
	1260.6	-0.471	1260.6	11	S	1	234.14	-0.119	234.14	
				12	K	0	147.11		147.11	

Scan number	306	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	286.26



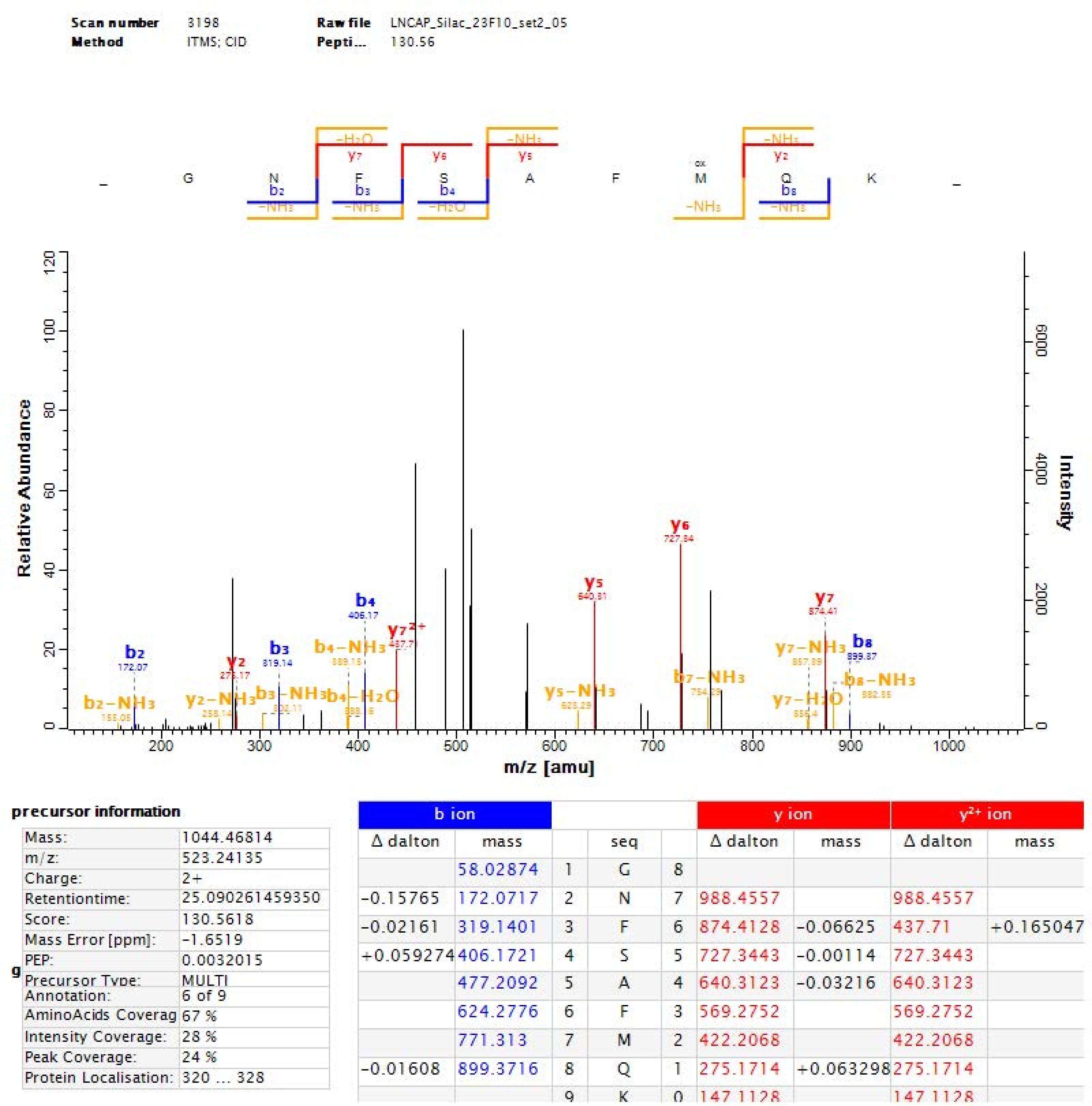
precursor information

Mass:	1564.63821
m/z:	783.32638
Charge:	2+
Retentiontime:	6.7152915000915
Score:	286.2632
Mass Error [ppm]:	0.35452
PEP:	2.754E-90
Precursor Type:	ISO

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	61 %
Peak Coverage:	43 %
Protein Localisation:	91 ... 104

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	13				
	143.08		143.08	2	A	12	1494.6	-0.019	747.81	-0.179
	272.12		272.12	3	E	11	1423.6	-0.087	712.29	+0.2431
	387.15	+0.0214	387.15	4	D	10	1294.5	-0.043	647.77	+0.0867
	502.18	+0.1839	502.18	5	D	9	1179.5	-0.028	1179.5	
	631.22	+0.223	631.22	6	E	8	1064.5	+0.0084	532.74	+0.058
	746.25		746.25	7	D	7	935.43	-0.068	468.22	+0.1235
+0.1171	431.14	-0.012	861.27	8	D	6	820.4	+0.01	820.4	
	976.3	-0.07	976.3	9	D	5	705.38	+0.0701	705.38	
	1075.4	+0.0784	1075.4	10	V	4	590.35	-0.005	590.35	
	1190.4	-0.064	1190.4	11	D	3	491.28	-0.009	491.28	
	1291.4	+0.1505	1291.4	12	T	2	376.26	+0.0355	376.26	
	1419.5	-0.33	1419.5	13	K	1	275.21		275.21	
				14	K	0	147.11		147.11	



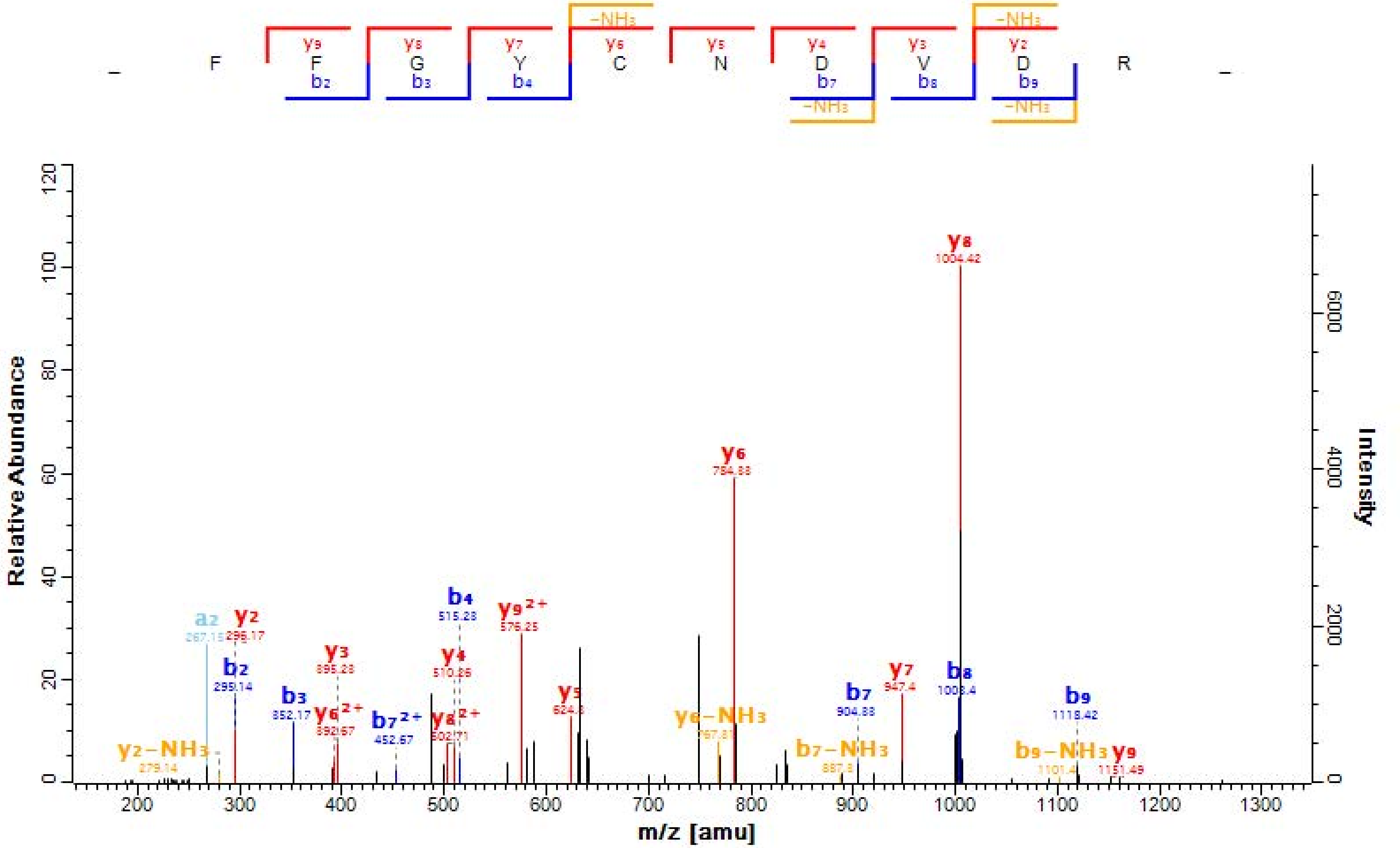
Scan number	3198	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	130.56

precursor information

Mass:	1044.46814
m/z:	523.24135
Charge:	2+
Retentiontime:	25.090261459350
Score:	130.5618
Mass Error [ppm]:	-1.6519
PEP:	0.0032015
Precursor Type:	MULTI
Annotation:	6 of 9
AminoAcids Coverag	67 %
Intensity Coverage:	28 %
Peak Coverage:	24 %
Protein Localisation:	320 ... 328

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	8				
-0.15765	172.0717	2	N	7	988.4557		988.4557	
-0.02161	319.1401	3	F	6	874.4128	-0.06625	437.71	+0.165047
+0.059274	406.1721	4	S	5	727.3443	-0.00114	727.3443	
	477.2092	5	A	4	640.3123	-0.03216	640.3123	
	624.2776	6	F	3	569.2752		569.2752	
	771.313	7	M	2	422.2068		422.2068	
-0.01608	899.3716	8	Q	1	275.1714	+0.063298	275.1714	
		9	K	0	147.1128		147.1128	

Scan number	3320	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	169.65



precursor information

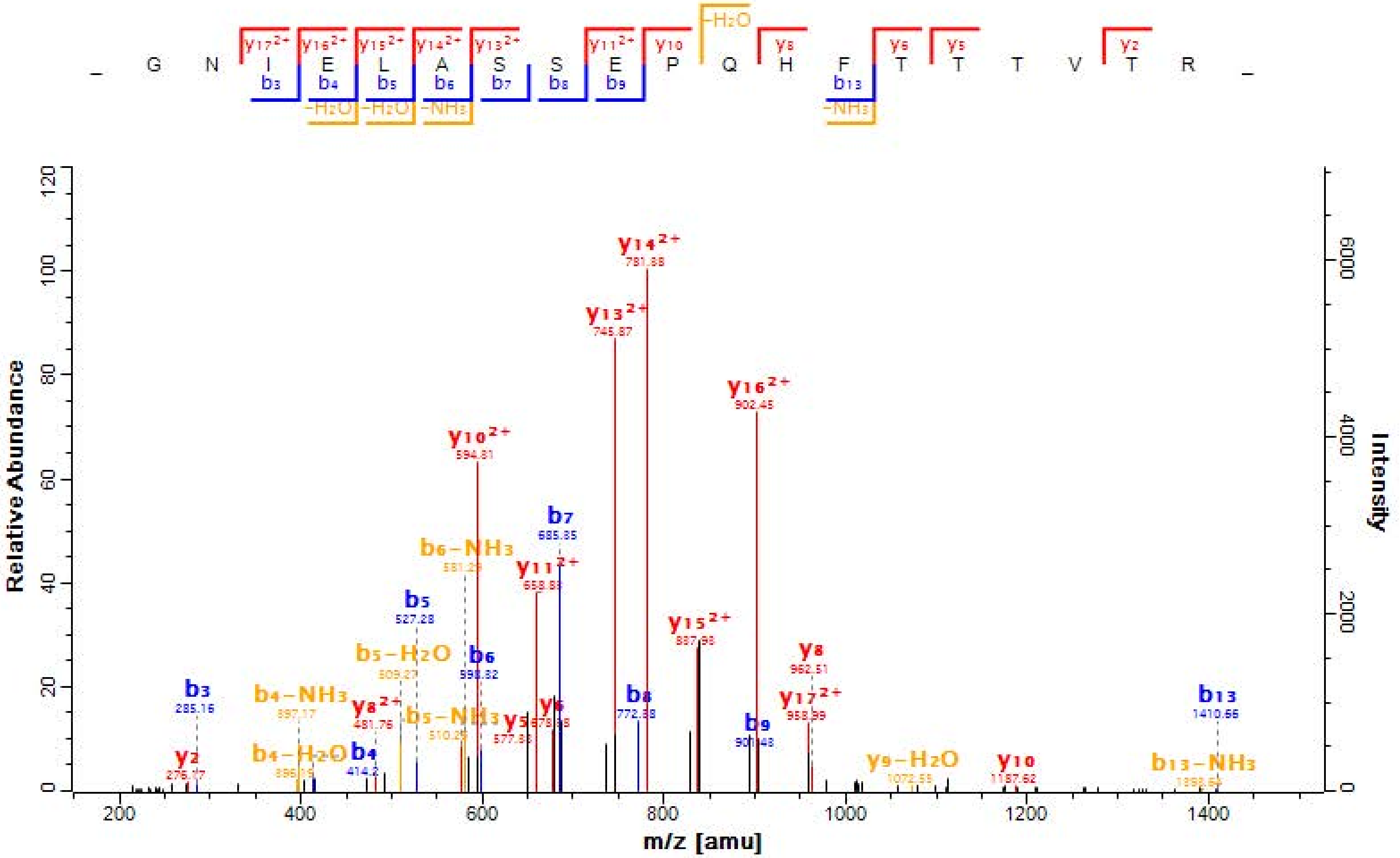
Mass:	1291.52924
m/z:	646.7719
Charge:	2+
Retentiontime:	25.774934768676
Score:	169.6546
Mass Error [ppm]:	0.05316
PEP:	1.0733E-05
Precursor Type:	MULTI

g

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	57 %
Peak Coverage:	26 %
Protein Localisation:	33 ... 42

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.1		148.1		148.1	1	F	9				
-0.05	267.1		295.1	+0	295.1	2	F	8	1151	-0.08	576.2	+0.20
	324.2		352.2	-0.02	352.2	3	G	7	1004	+0.029	502.7	+0.05
	487.2		515.2	-0.15	515.2	4	Y	6	947.4	+0	947.4	
	647.3		675.3		675.3	5	C	5	784.3	-0.04	392.7	+0.26
	761.3		789.3		789.3	6	N	4	624.3	+0.035	624.3	
	876.3	-0.49	452.7	+0.071	904.3	7	D	3	510.3	+0.083	510.3	
	975.4		1003	+0.173	1003	8	V	2	395.2	+0.049	395.2	
	1090		1118	-0.12	1118	9	D	1	296.2	+0.076	296.2	
						10	R	0	181.1		181.1	

Scan number	3334	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	143.67



precursor information

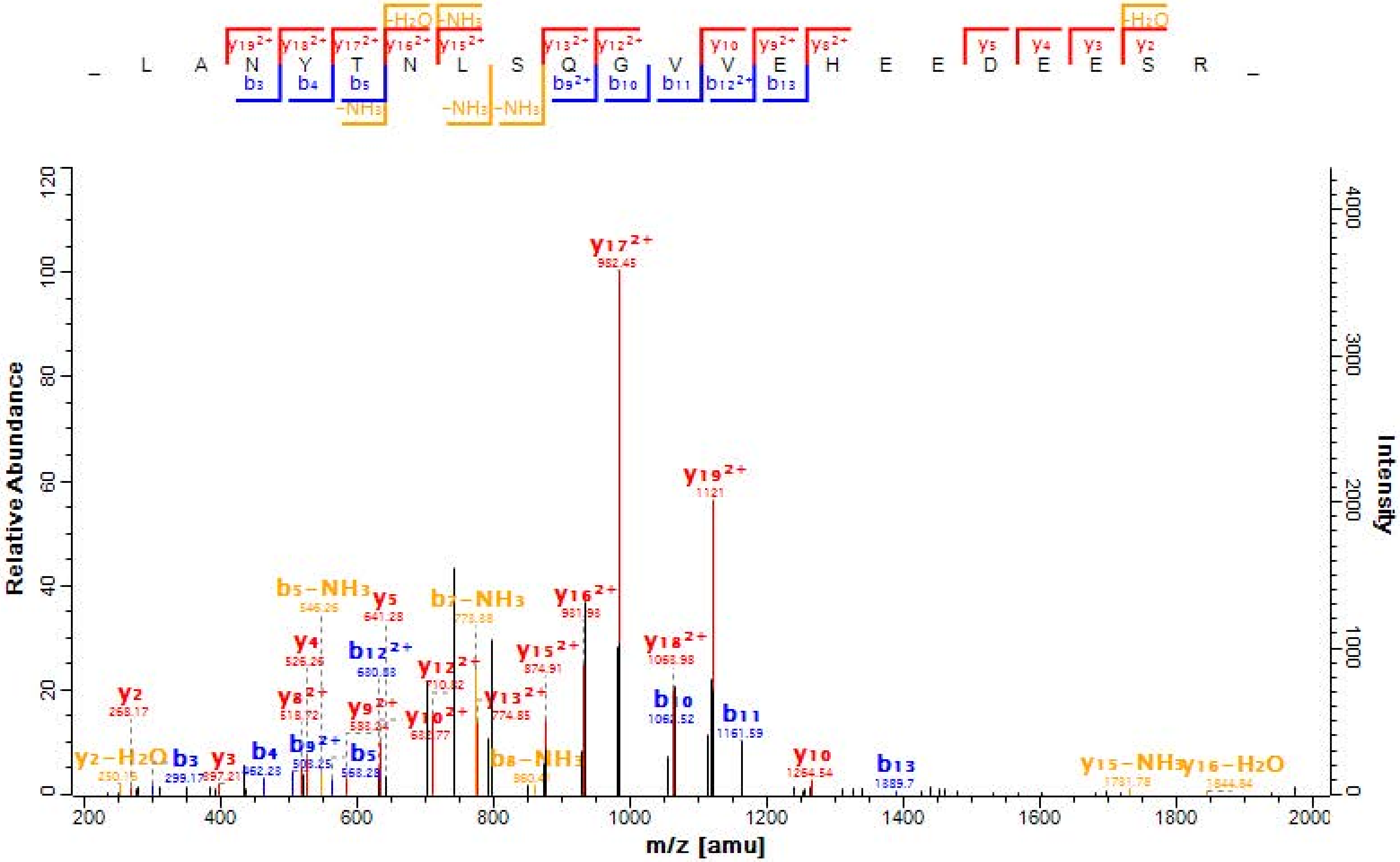
Mass:	2087.02844
m/z:	696.68342
Charge:	3+
Retentiontime:	25.844264984130
Score:	143.6723
Mass Error [ppm]:	0.045902
PEP:	6.5834E-19
Precursor Type:	MULTI

general information

Annotation:	14 of 19
AminoAcids Coverag	74 %
Intensity Coverage:	73 %
Peak Coverage:	27 %
Protein Localisation:	650 ... 668

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	18				
	172.0717	2	N	17	2031.014		2031.014	
+0.138092	285.1557	3	I	16	1916.971		958.9893	+0.001041
+0.103006	414.1983	4	E	15	1803.887		902.4472	+0.303327
-0.05894	527.2824	5	L	14	1674.845		837.9259	-8.3E-05
+0.09926	598.3195	6	A	13	1561.761		781.3839	+0.238909
-0.1716	685.3515	7	S	12	1490.723		745.8653	+0.281148
+0.228318	772.3836	8	S	11	1403.691		1403.691	
-0.09113	901.4262	9	E	10	1316.659		658.8333	+0.288823
	998.4789	10	P	9	1187.617	-0.0811	594.312	+0.231872
	1126.537	11	Q	8	1090.564		1090.564	
	1263.596	12	H	7	962.5054	+0.1907	481.7563	-0.22326
+0.361181	1410.665	13	F	6	825.4465		825.4465	
	1511.712	14	T	5	678.3781	-0.13913	678.3781	
	1612.76	15	T	4	577.3304	-0.1277	577.3304	
	1713.808	16	T	3	476.2827		476.2827	
	1812.876	17	V	2	375.235		375.235	
	1913.924	18	T	1	276.1666	+0.075862	276.1666	
		19	R	0	175.119		175.119	

Scan number	3598	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	106.67



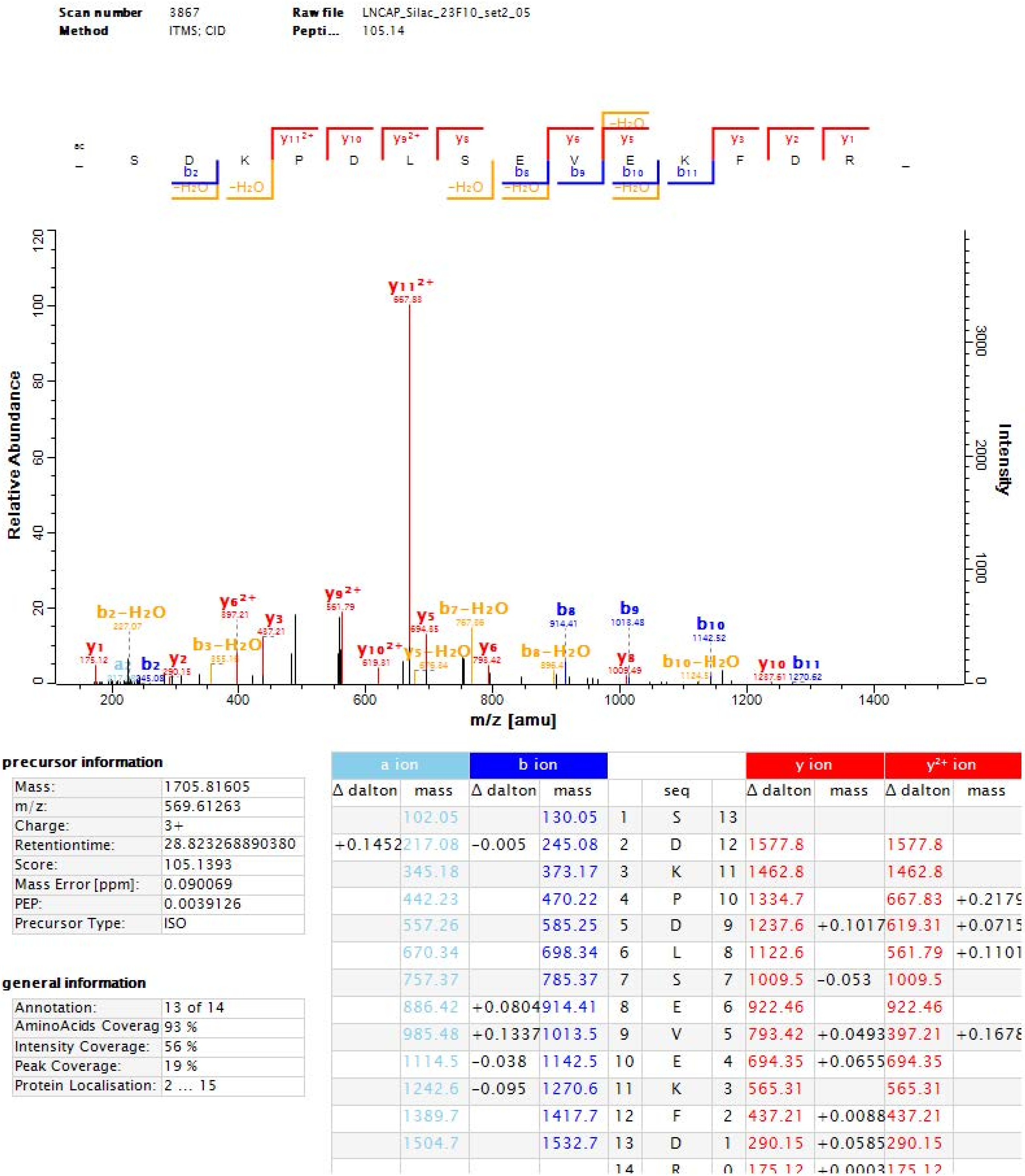
precursor information

Mass:	2418.09408
m/z:	807.03864
Charge:	3+
Retentiontime:	27.353333251953
Score:	106.6661
Mass Error [ppm]:	0.22967
PEP:	5.7842E-09
Precursor Type:	MULTI

general information

Annotation:	16 of 21
AminoAcids Coverag	76 %
Intensity Coverage:	48 %
Peak Coverage:	33 %
Protein Localisation:	89 ... 109

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	20				
	185.13		185.13	2	A	19	2312		2312	
	299.17	-0.043	299.17	3	N	18	2241		1121	+0.3078
	462.23	+0.2206	462.23	4	Y	17	2127		1064	-0.115
	563.28	+0.0614	563.28	5	T	16	1963.9		982.45	+0.2269
	677.33		677.33	6	N	15	1862.8		931.93	-0.083
	790.41		790.41	7	L	14	1748.8		874.91	-0.037
	877.44		877.44	8	S	13	1635.7		1635.7	
+0.214	503.25		1005.5	9	Q	12	1548.7		774.85	+0.1563
	1062.5	-0.424	1062.5	10	G	11	1420.6		710.82	+0.2897
	1161.6	+0.2873	1161.6	11	V	10	1363.6		1363.6	
-0.154	630.83		1260.7	12	V	9	1264.5	+0.3756	632.77	+0.0148
	1389.7	+0.2468	1389.7	13	E	8	1165.5		583.24	+0.1846
	1526.8		1526.8	14	H	7	1036.4		518.72	+0.0743
	1655.8		1655.8	15	E	6	899.37		899.37	
	1784.8		1784.8	16	E	5	770.33		770.33	
	1899.9		1899.9	17	D	4	641.28	+0.1195	641.28	
	2028.9		2028.9	18	E	3	526.26	+0.1945	526.26	
	2158		2158	19	E	2	397.21	-0.08	397.21	
	2245		2245	20	S	1	268.17	+0.4166	268.17	
				21	R	0	181.14		181.14	



Scan number	3867	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	105.14

precursor information

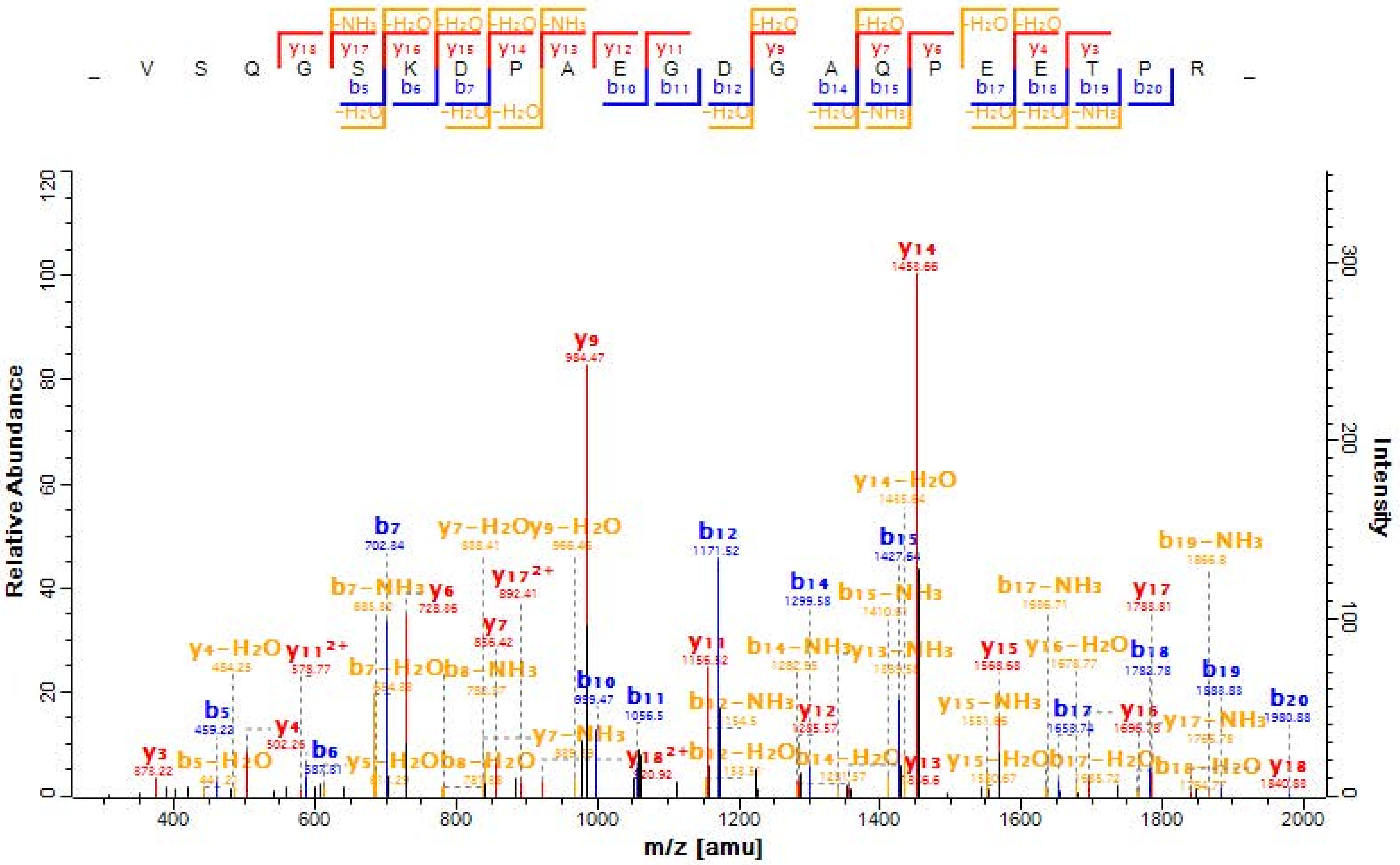
Mass:	1705.81605
m/z:	569.61263
Charge:	3+
Retentiontime:	28.823268890380
Score:	105.1393
Mass Error [ppm]:	0.090069
PEP:	0.0039126
Precursor Type:	ISO

general information

Annotation:	13 of 14
AminoAcids Coverag	93 %
Intensity Coverage:	56 %
Peak Coverage:	19 %
Protein Localisation:	2 ... 15

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	S	13				
+0.1452	217.08	-0.005	245.08	2	D	12	1577.8		1577.8	
	345.18		373.17	3	K	11	1462.8		1462.8	
	442.23		470.22	4	P	10	1334.7		667.83	+0.2179
	557.26		585.25	5	D	9	1237.6	+0.1017	619.31	+0.0715
	670.34		698.34	6	L	8	1122.6		561.79	+0.1101
	757.37		785.37	7	S	7	1009.5	-0.053	1009.5	
	886.42	+0.0804	914.41	8	E	6	922.46		922.46	
	985.48	+0.1337	1013.5	9	V	5	793.42	+0.0493	397.21	+0.1678
	1114.5	-0.038	1142.5	10	E	4	694.35	+0.0655	694.35	
	1242.6	-0.095	1270.6	11	K	3	565.31		565.31	
	1389.7		1417.7	12	F	2	437.21	+0.0088	437.21	
	1504.7		1532.7	13	D	1	290.15	+0.0585	290.15	
				14	R	0	175.12	+0.0003	175.12	

Scan number	391	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	286.7



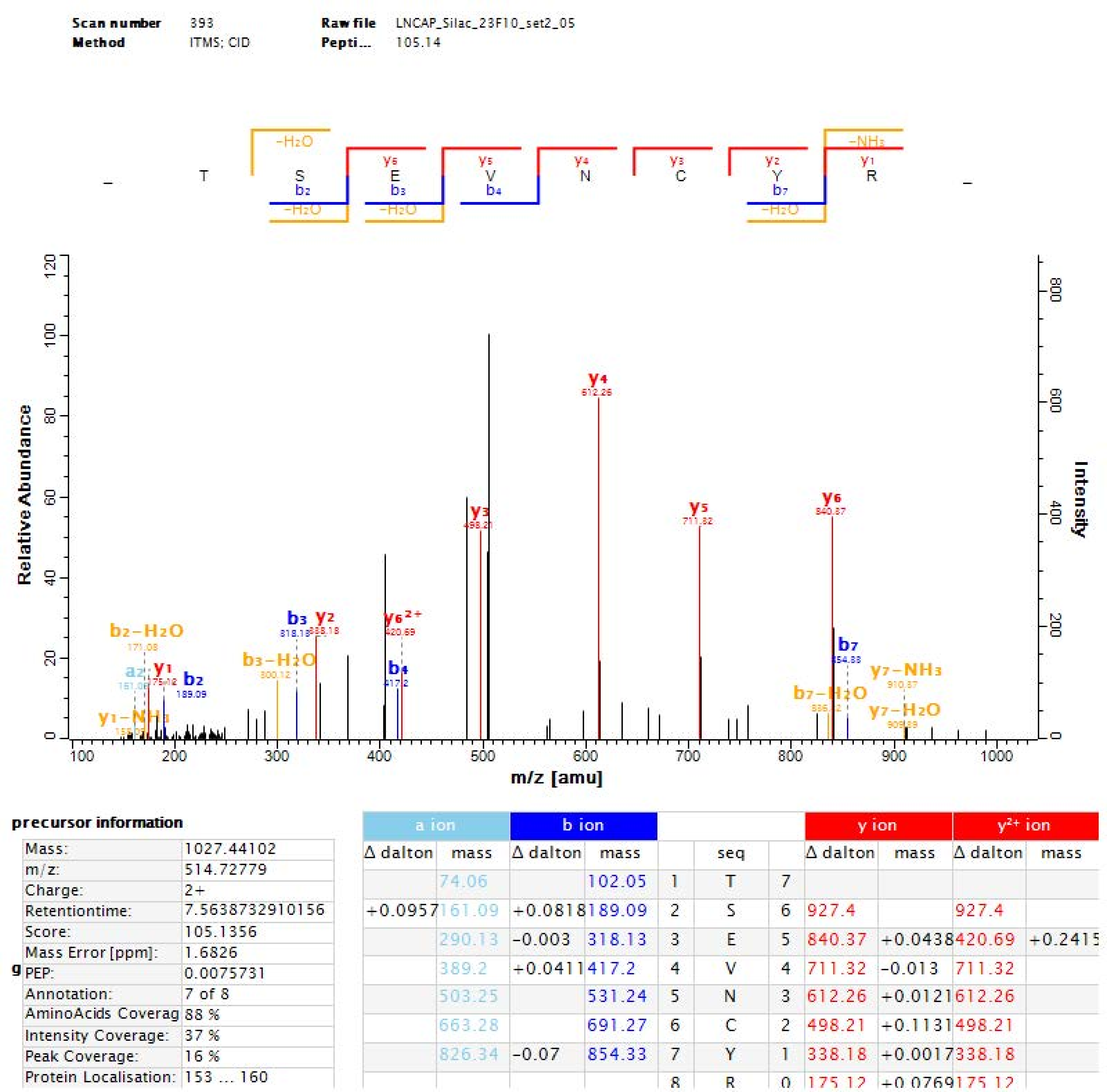
precursor information

Mass:	2153.98371
m/z:	1077.99913
Charge:	2+
Retentiontime:	7.5454382896423
Score:	286.6989
Mass Error [ppm]:	0.553
PEP:	1.1338E-112
Precursor Type:	MULTI

general information

Annotation:	17 of 21
AminoAcids Coverag	81 %
Intensity Coverage:	72 %
Peak Coverage:	57 %
Protein Localisation:	237 ... 257

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	20				
	187.1077	2	S	19	2055.921		2055.921	
	315.1663	3	Q	18	1968.889		1968.889	
	372.1878	4	G	17	1840.831	-0.01168	920.919	+0.041668
+0.052795	459.2198	5	S	16	1783.809	+0.000625	892.4083	+0.125886
-0.14922	587.3148	6	K	15	1696.777	+0.327941	1696.777	
+0.019145	702.3417	7	D	14	1568.682	-0.0384	1568.682	
	799.3945	8	P	13	1453.655	-0.10716	1453.655	
	870.4316	9	A	12	1356.603	+0.345995	1356.603	
-0.21159	999.4742	10	E	11	1285.565	-0.09675	1285.565	
+0.11753	1056.496	11	G	10	1156.523	-0.02083	578.7651	-0.0583
-0.04918	1171.523	12	D	9	1099.501		1099.501	
	1228.544	13	G	8	984.4745	-0.03261	984.4745	
-0.14878	1299.581	14	A	7	927.453		927.453	
+0.055585	1427.64	15	Q	6	856.4159	+0.044527	856.4159	
	1524.692	16	P	5	728.3573	-0.00334	728.3573	
+0.005272	1653.735	17	E	4	631.3046		631.3046	
-0.12997	1782.778	18	E	3	502.262	+0.144262	502.262	
-0.00724	1883.825	19	T	2	373.2194	+0.179165	373.2194	
+0.028741	1980.878	20	P	1	272.1717		272.1717	
		21	R	0	175.119		175.119	

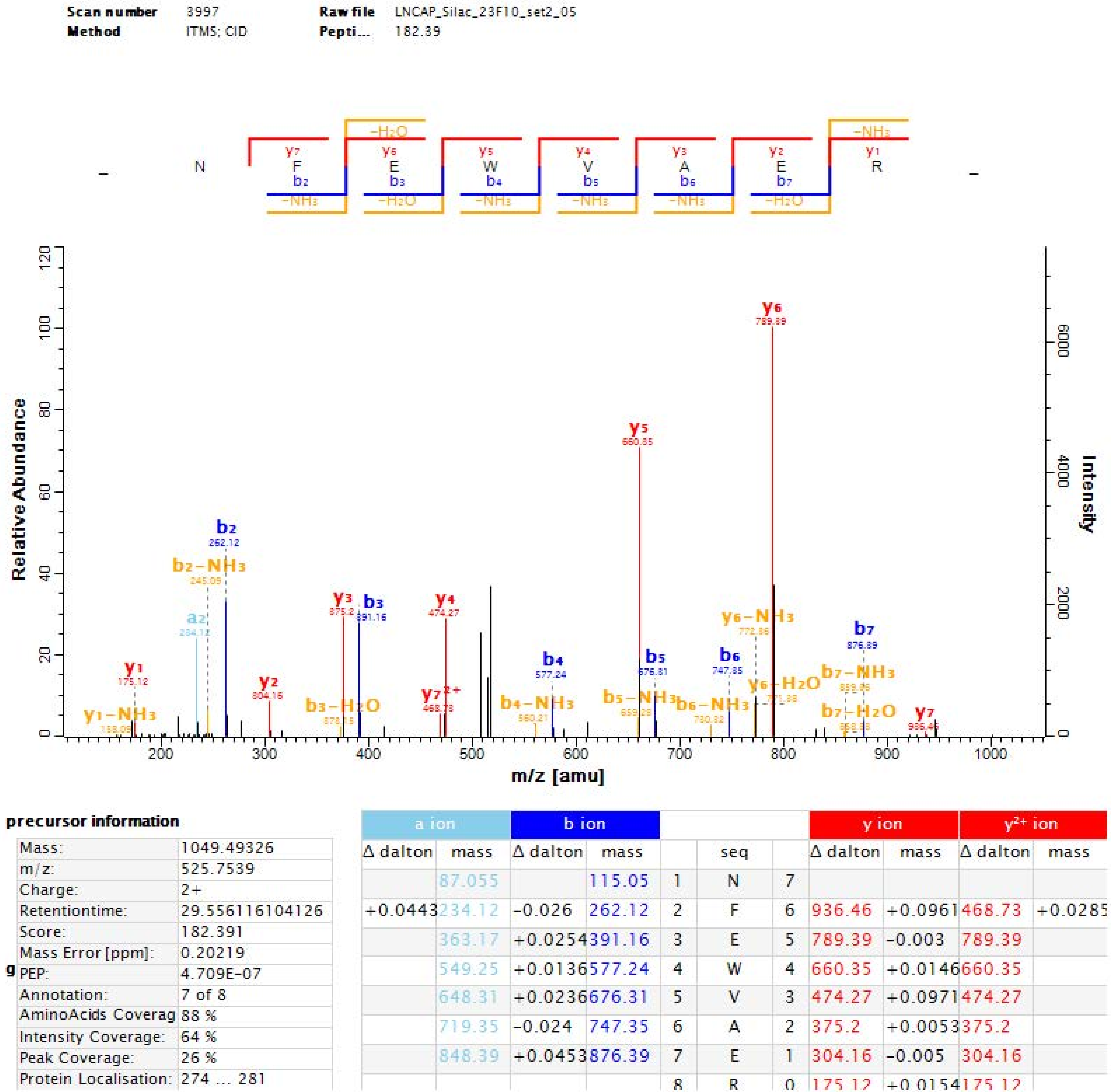


Scan number	393	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	105.14

precursor information

Mass:	1027.44102
m/z:	514.72779
Charge:	2+
Retentiontime:	7.5638732910156
Score:	105.1356
Mass Error [ppm]:	1.6826
PEP:	0.0075731
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	37 %
Peak Coverage:	16 %
Protein Localisation:	153 ... 160

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.05	1	T	7				
+0.0957	161.09	+0.0818	189.09	2	S	6	927.4		927.4	
	290.13	-0.003	318.13	3	E	5	840.37	+0.0438	420.69	+0.2415
	389.2	+0.0411	417.2	4	V	4	711.32	-0.013	711.32	
	503.25		531.24	5	N	3	612.26	+0.0121	612.26	
	663.28		691.27	6	C	2	498.21	+0.1131	498.21	
	826.34	-0.07	854.33	7	Y	1	338.18	+0.0017	338.18	
				8	R	0	175.12	+0.0769	175.12	



Scan number 3997 **Raw file** LNCAP_Silac_23F10_set2_05

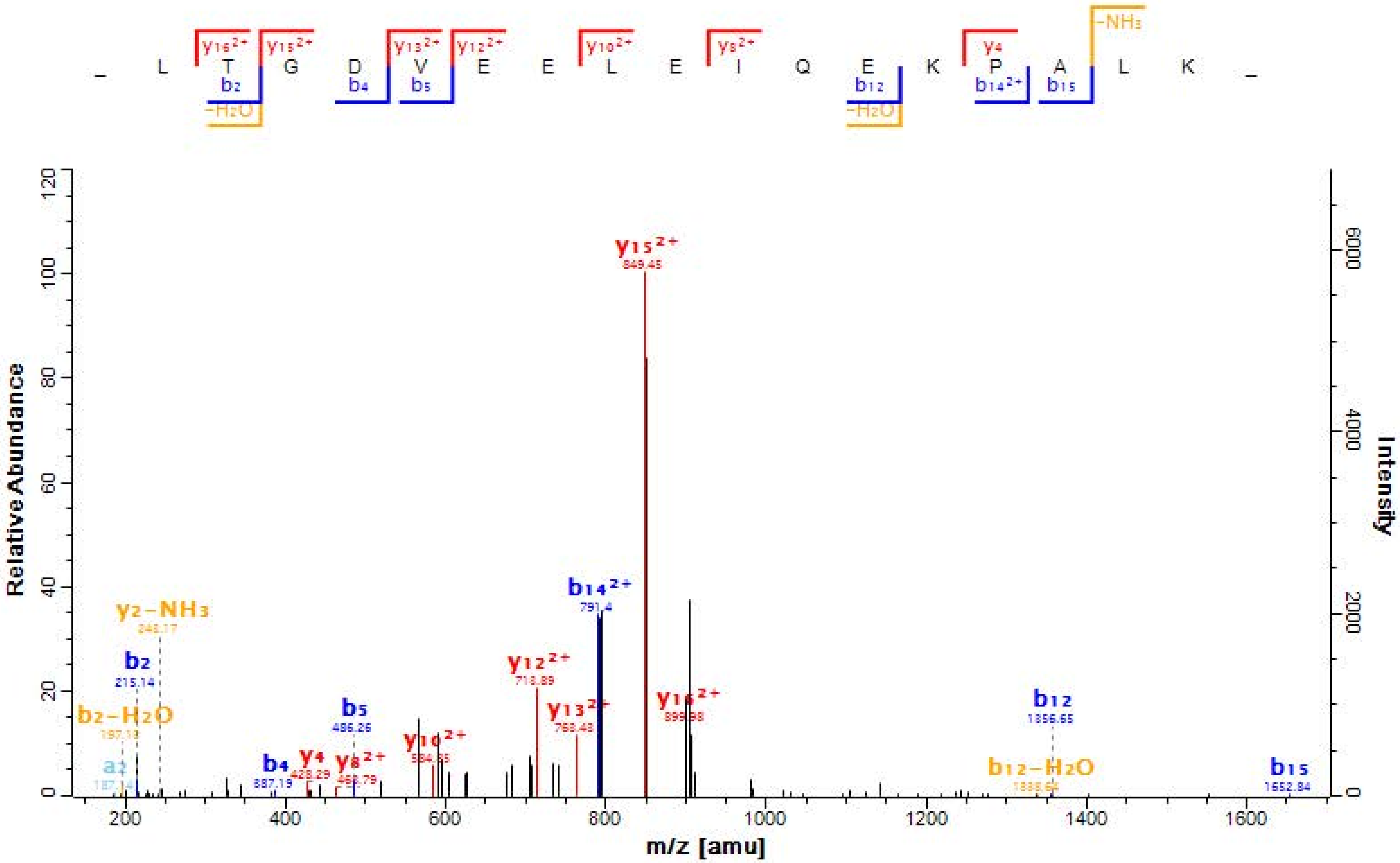
Method ITMS; CID **Pepti...** 182.39

precursor information

Mass:	1049.49326
m/z:	525.7539
Charge:	2+
Retentiontime:	29.556116104126
Score:	182.391
Mass Error [ppm]:	0.20219
PEP:	4.709E-07
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	64 %
Peak Coverage:	26 %
Protein Localisation:	274 ... 281

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	87.055		115.05	1	N	7				
+0.0443	234.12	-0.026	262.12	2	F	6	936.46	+0.0961	468.73	+0.0285
	363.17	+0.0254	391.16	3	E	5	789.39	-0.003	789.39	
	549.25	+0.0136	577.24	4	W	4	660.35	+0.0146	660.35	
	648.31	+0.0236	676.31	5	V	3	474.27	+0.0971	474.27	
	719.35	-0.024	747.35	6	A	2	375.2	+0.0053	375.2	
	848.39	+0.0453	876.39	7	E	1	304.16	-0.005	304.16	
				8	R	0	175.12	+0.0154	175.12	

Scan number	4039	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	65.22



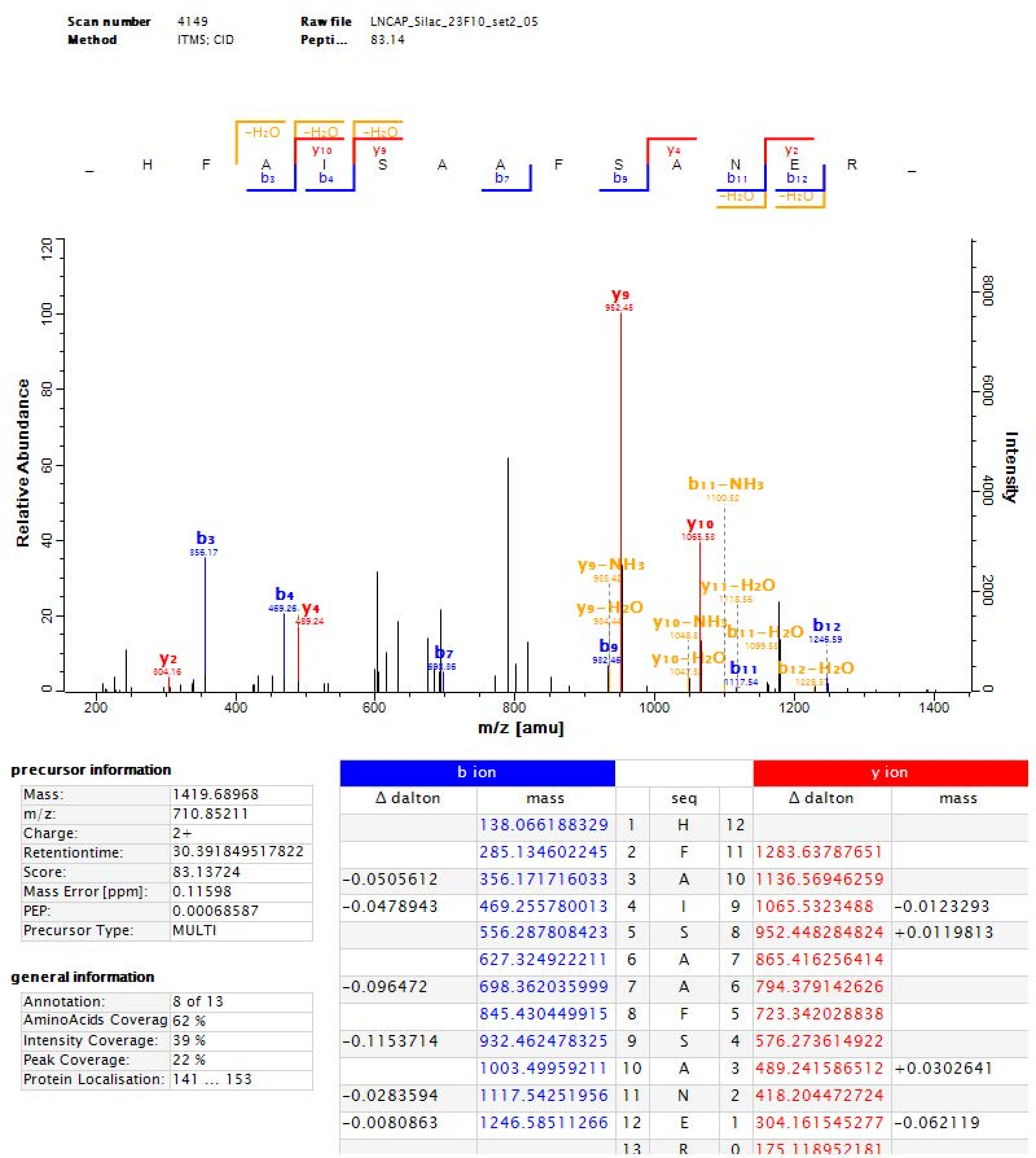
precursor information

Mass:	1911.01985
m/z:	638.01389
Charge:	3+
Retentiontime:	29.787187576293
Score:	65.2186
Mass Error [ppm]:	-0.11692
PEP:	0.0010681
Precursor Type:	MULTI

general information

Annotation:	11 of 17
AminoAcids Coverag	65 %
Intensity Coverage:	30 %
Peak Coverage:	17 %
Protein Localisation:	533 ... 549

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	16				
+0.213	187.1		215.1	+0.036	215.1	2	T	15	1799		900	-0.01
	244.2		272.2		272.2	3	G	14	1698		849.5	-0.01
	359.2		387.2	+0.133	387.2	4	D	13	1641		1641	
	458.3		486.3	-0.03	486.3	5	V	12	1526		763.4	+0.00
	587.3		615.3		615.3	6	E	11	1427		713.9	+0.15
	716.3		744.3		744.3	7	E	10	1298		1298	
	829.4		857.4		857.4	8	L	9	1169		584.9	-0.21
	958.5		986.5		986.5	9	E	8	1056		1056	
	1072		1100		1100	10	I	7	926.6		463.8	-0.28
	1200		1228		1228	11	Q	6	813.5		813.5	
	1329		1357	-0.13	1357	12	E	5	685.4		685.4	
	1457		1485		1485	13	K	4	556.4		556.4	
	1554	+0.051	791.4		1582	14	P	3	428.3	+0.124	428.3	
	1625		1653	-0.09	1653	15	A	2	331.2		331.2	
	1738		1766		1766	16	L	1	260.2		260.2	
						17	K	0	147.1		147.1	



Scan number	4149	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	83.14

precursor information

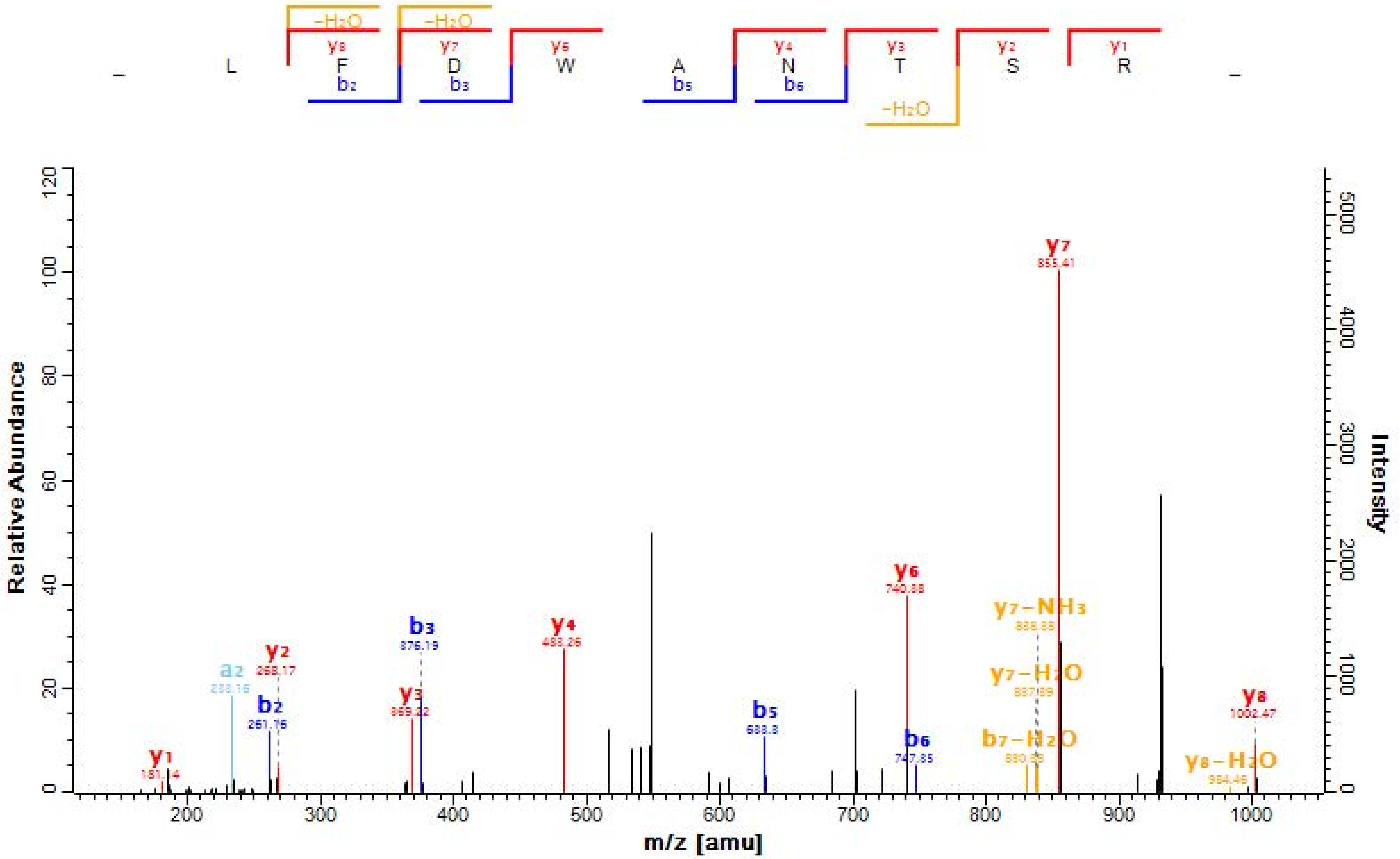
Mass:	1419.68968
m/z:	710.85211
Charge:	2+
Retentiontime:	30.391849517822
Score:	83.13724
Mass Error [ppm]:	0.11598
PEP:	0.00068587
Precursor Type:	MULTI

general information

Annotation:	8 of 13
AminoAcids Coverag	62 %
Intensity Coverage:	39 %
Peak Coverage:	22 %
Protein Localisation:	141 ... 153

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	138.066188329	1	H	12		
	285.134602245	2	F	11	1283.63787651	
-0.0505612	356.171716033	3	A	10	1136.56946259	
-0.0478943	469.255780013	4	I	9	1065.5323488	-0.0123293
	556.287808423	5	S	8	952.448284824	+0.0119813
	627.324922211	6	A	7	865.416256414	
-0.096472	698.362035999	7	A	6	794.379142626	
	845.430449915	8	F	5	723.342028838	
-0.1153714	932.462478325	9	S	4	576.273614922	
	1003.49959211	10	A	3	489.241586512	+0.0302641
-0.0283594	1117.54251956	11	N	2	418.204472724	
-0.0080863	1246.58511266	12	E	1	304.161545277	-0.062119
		13	R	0	175.118952181	

Scan number	4417	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti…**	90.11



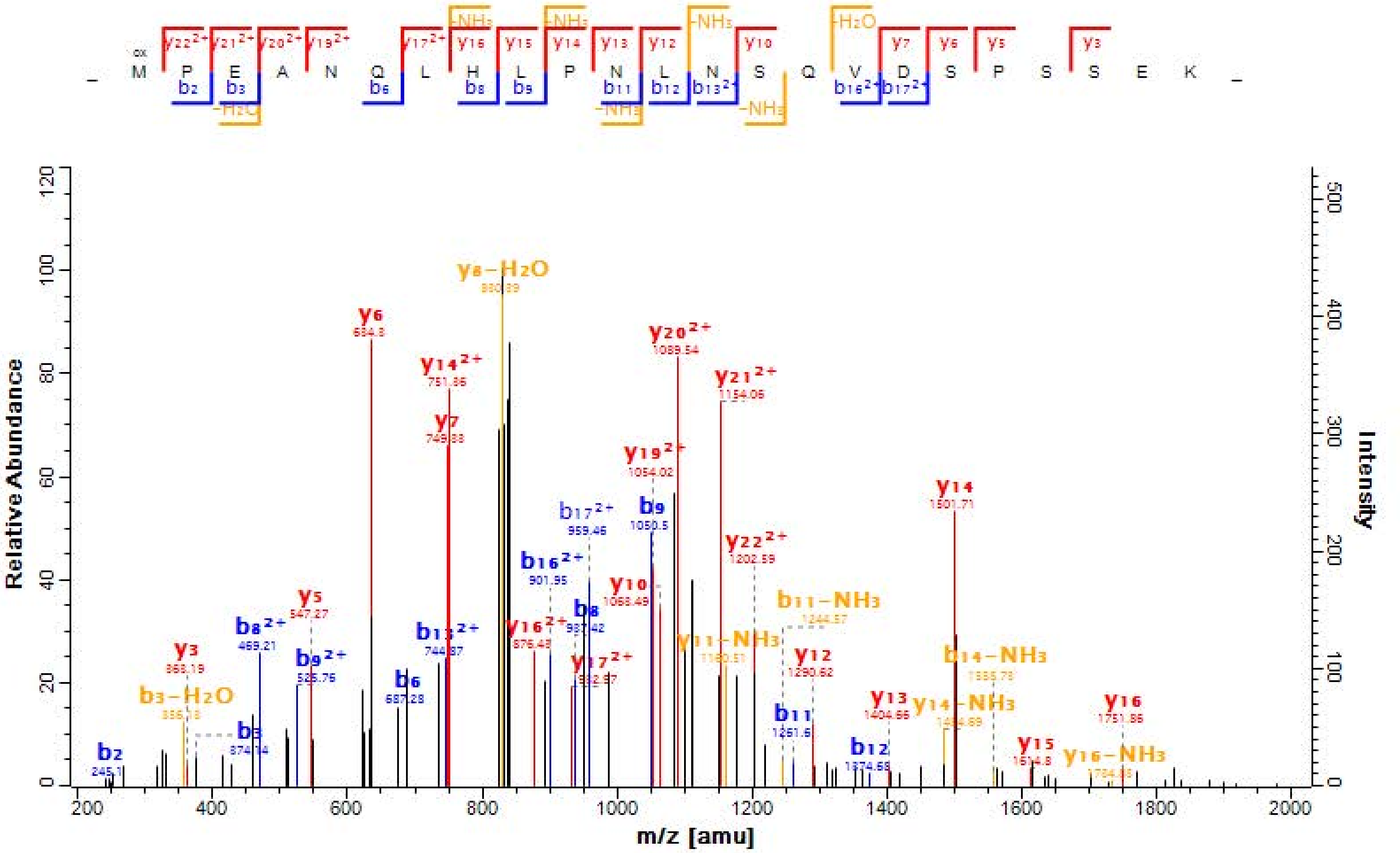
precursor information

g

Mass:	1108.53045
m/z:	555.2725
Charge:	2+
Retentiontime:	31.942998886108
Score:	90.10822
Mass Error [ppm]:	0.26025
PEP:	0.005261
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	46 %
Peak Coverage:	21 %
Protein Localisation:	395 … 403

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	86.09643		114.0913	1	L	8		
+0.002091	233.1648	-0.0762	261.1598	2	F	7	1002.473	+0.037426
	348.1918	+0.076486	376.1867	3	D	6	855.4051	+0.0221
	534.2711		562.266	4	W	5	740.3781	-0.03055
	605.3082	-0.07247	633.3031	5	A	4	554.2988	
	719.3511	-0.0142	747.3461	6	N	3	483.2617	-0.01239
	820.3988		848.3937	7	T	2	369.2188	+0.071312
	907.4308		935.4258	8	S	1	268.1711	+0.137423
				9	R	0	181.1391	-0.08493

Scan number	4439	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	143.52



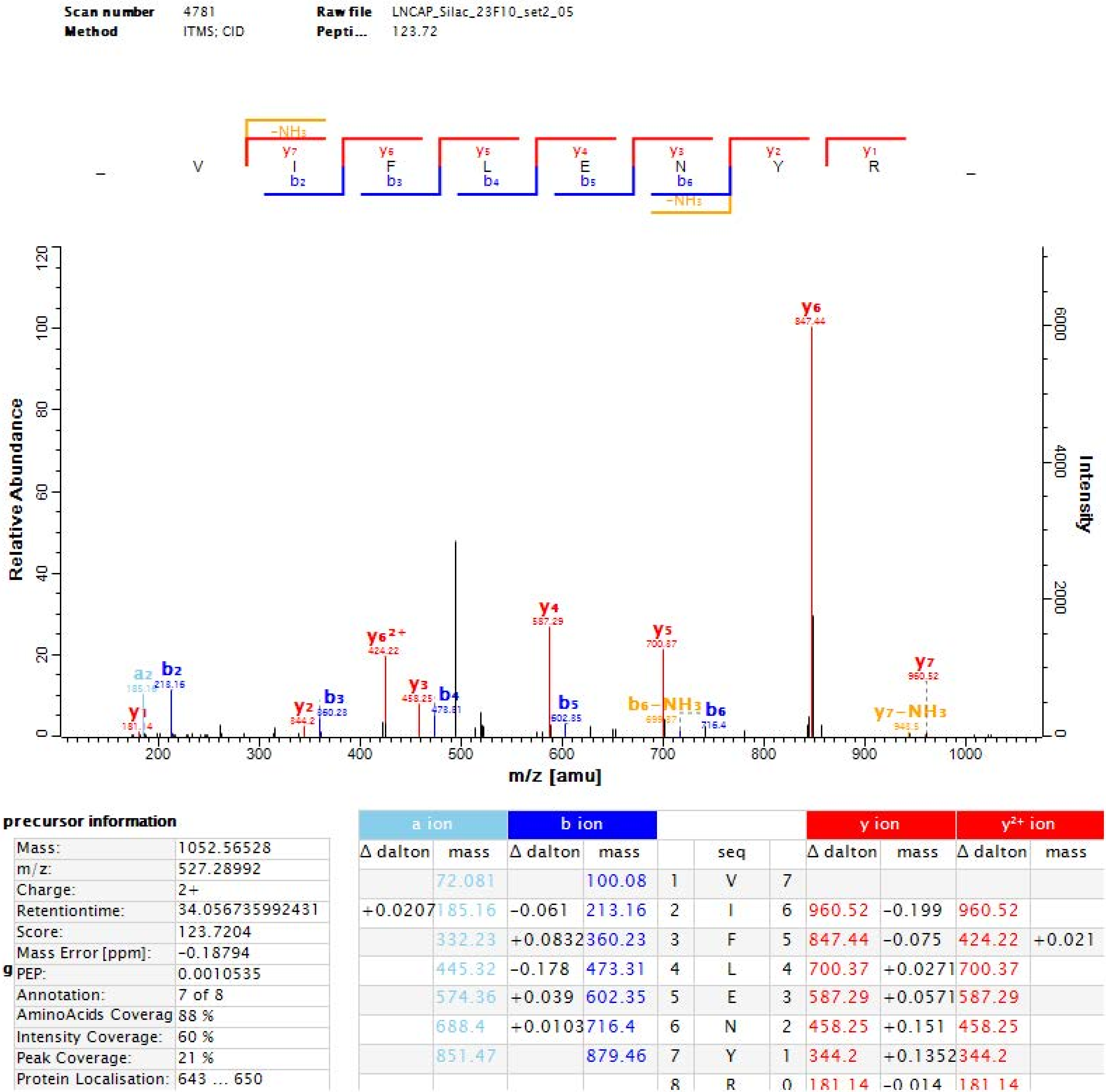
precursor information

Mass:	2550.20058
m/z:	851.07414
Charge:	3+
Retentiontime:	32.071010589599
Score:	143.5151
Mass Error [ppm]:	-0.56825
PEP:	5.6095E-21
Precursor Type:	MULTI

general information

Annotation:	20 of 23
AminoAcids Coverag	87 %
Intensity Coverage:	49 %
Peak Coverage:	33 %
Protein Localisation:	733 ... 755

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.04		148.04	1	M	22				
	245.1	+0.0445	245.1	2	P	21	2404.2		1202.6	+0.23
	374.14	-0.015	374.14	3	E	20	2307.1		1154.1	+0.0527
	445.18		445.18	4	A	19	2178.1		1089.5	+0.3157
	559.22		559.22	5	N	18	2107		1054	+0.025
	687.28	+0.1345	687.28	6	Q	17	1993		1993	
	800.36		800.36	7	L	16	1864.9		932.97	+0.2099
+0.1274	469.21	+0.1636	937.42	8	H	15	1751.9	-0.108	876.43	+0.1251
+0.4554	525.76	-0.054	1050.5	9	L	14	1614.8	-0.085	1614.8	
	1147.6		1147.6	10	P	13	1501.7	-0.134	751.36	+0.3256
	1261.6	+0.0575	1261.6	11	N	12	1404.7	+0.0603	1404.7	
	1374.7	+0.265	1374.7	12	L	11	1290.6	+0.3788	1290.6	
-0.003	744.87		1488.7	13	N	10	1177.5		1177.5	
	1575.8		1575.8	14	S	9	1063.5	-0.041	1063.5	
	1703.8		1703.8	15	Q	8	976.46		976.46	
+0.1319	901.95		1802.9	16	V	7	848.4		848.4	
+0.2726	959.46		1917.9	17	D	6	749.33	+0.0287	749.33	
	2004.9		2004.9	18	S	5	634.3	+0.0206	634.3	
	2102		2102	19	P	4	547.27	+0.0771	547.27	
	2189		2189	20	S	3	450.22		450.22	
	2276.1		2276.1	21	S	2	363.19	+0.1015	363.19	
	2405.1		2405.1	22	E	1	276.16		276.16	
				23	K	0	147.11		147.11	



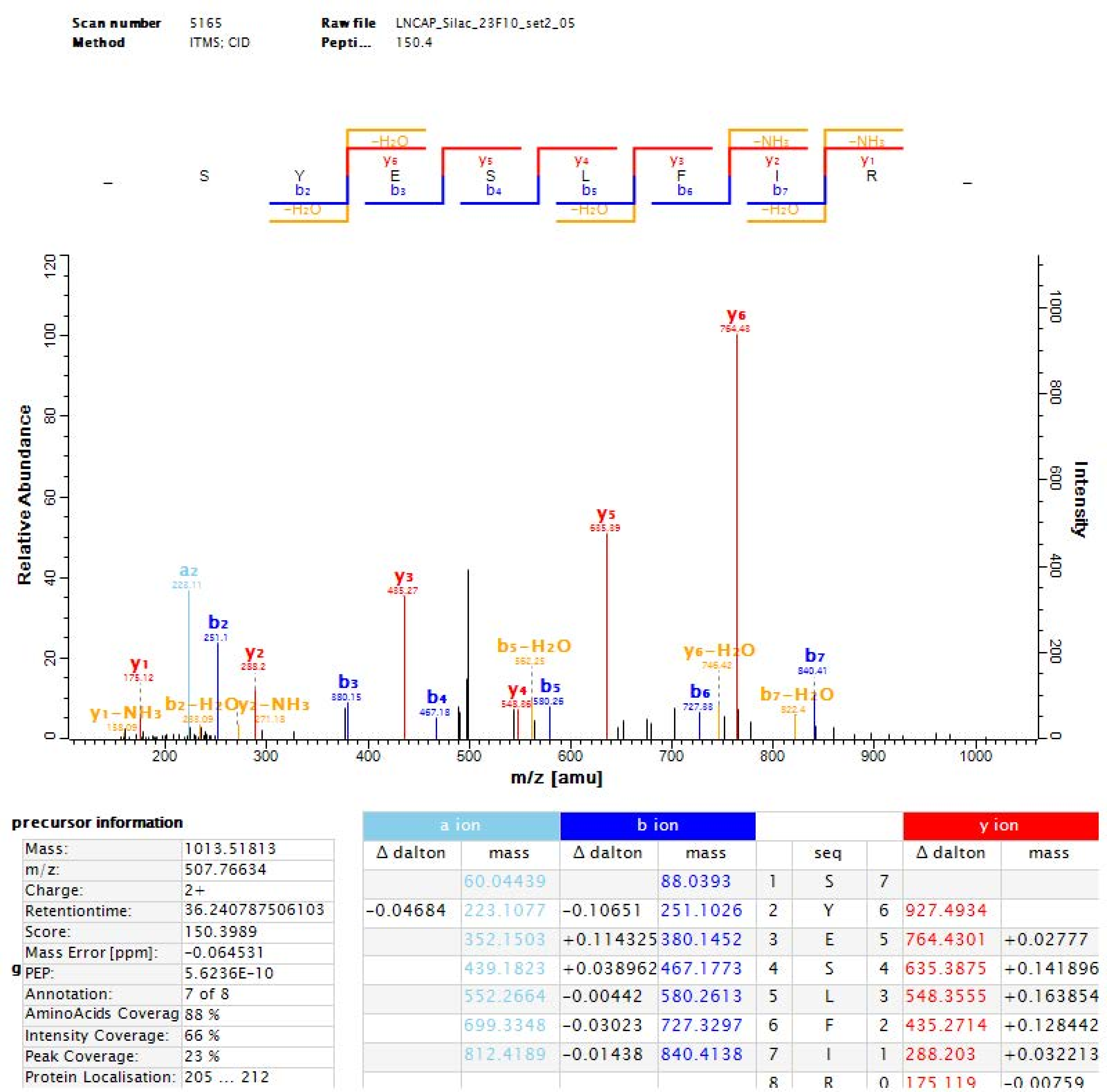
Scan number 4781 **Raw file** LNCAP_Silac_23F10_set2_05
Method ITMS; CID **Pepti...** 123.72

precursor information

Mass:	1052.56528
m/z:	527.28992
Charge:	2+
Retentiontime:	34.056735992431
Score:	123.7204
Mass Error [ppm]:	-0.18794
PEP:	0.0010535
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	60 %
Peak Coverage:	21 %
Protein Localisation:	643 ... 650

g

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.081		100.08	1	V	7				
+0.0207	185.16	-0.061	213.16	2	I	6	960.52	-0.199	960.52	
	332.23	+0.0832	360.23	3	F	5	847.44	-0.075	424.22	+0.021
	445.32	-0.178	473.31	4	L	4	700.37	+0.0271	700.37	
	574.36	+0.039	602.35	5	E	3	587.29	+0.0571	587.29	
	688.4	+0.0103	716.4	6	N	2	458.25	+0.151	458.25	
	851.47		879.46	7	Y	1	344.2	+0.1352	344.2	
				8	R	0	181.14	-0.014	181.14	

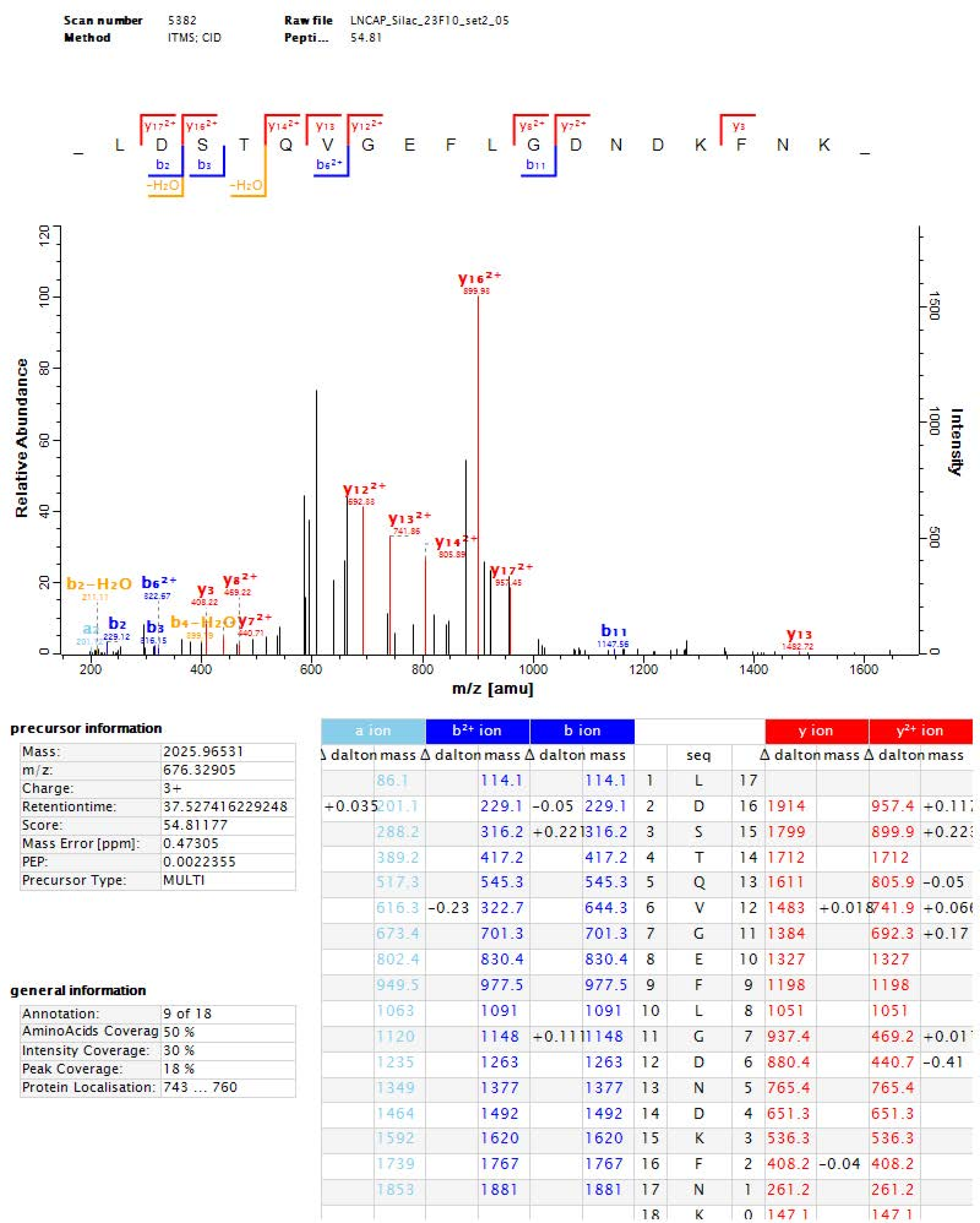


Scan number	5165	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	150.4

precursor information

Mass:	1013.51813
m/z:	507.76634
Charge:	2+
Retentiontime:	36.240787506103
Score:	150.3989
Mass Error [ppm]:	-0.064531
PEP:	5.6236E-10
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	66 %
Peak Coverage:	23 %
Protein Localisation:	205 ... 212

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	60.04439		88.0393	1	S	7		
-0.04684	223.1077	-0.10651	251.1026	2	Y	6	927.4934	
	352.1503	+0.114325	380.1452	3	E	5	764.4301	+0.02777
	439.1823	+0.038962	467.1773	4	S	4	635.3875	+0.141896
	552.2664	-0.00442	580.2613	5	L	3	548.3555	+0.163854
	699.3348	-0.03023	727.3297	6	F	2	435.2714	+0.128442
	812.4189	-0.01438	840.4138	7	I	1	288.203	+0.032213
				8	R	0	175.119	-0.00759



Scan number	5382	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	54.81

precursor information

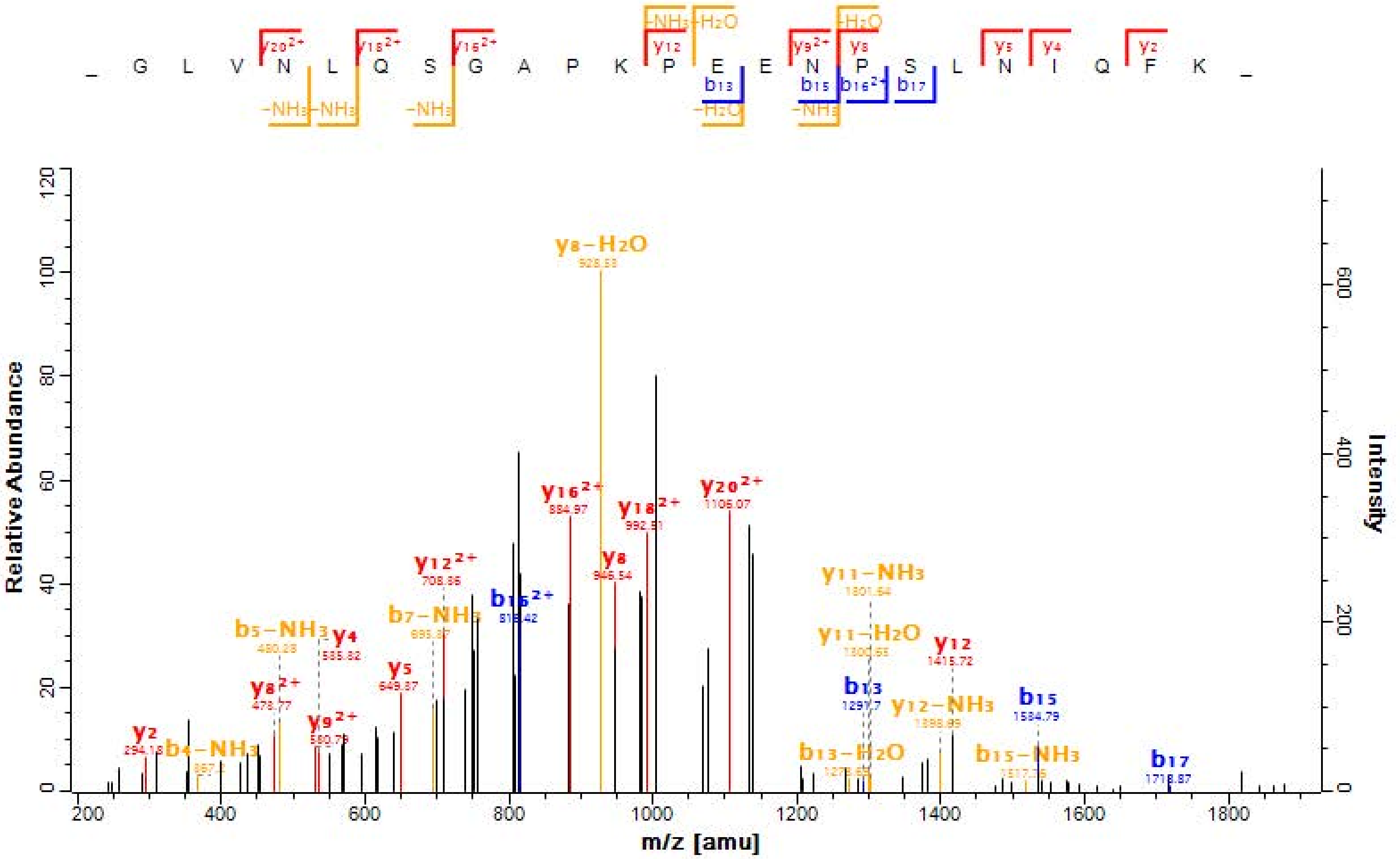
Mass:	2025.96531
m/z:	676.32905
Charge:	3+
Retentiontime:	37.527416229248
Score:	54.81177
Mass Error [ppm]:	0.47305
PEP:	0.0022355
Precursor Type:	MULTI

general information

Annotation:	9 of 18
AminoAcids Coverag	50 %
Intensity Coverage:	30 %
Peak Coverage:	18 %
Protein Localisation:	743 ... 760

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	17				
+0.035	201.1		229.1	-0.05	229.1	2	D	16	1914		957.4	+0.11
	288.2		316.2	+0.221	316.2	3	S	15	1799		899.9	+0.22
	389.2		417.2		417.2	4	T	14	1712		1712	
	517.3		545.3		545.3	5	Q	13	1611		805.9	-0.05
	616.3	-0.23	322.7		644.3	6	V	12	1483	+0.018	741.9	+0.06
	673.4		701.3		701.3	7	G	11	1384		692.3	+0.17
	802.4		830.4		830.4	8	E	10	1327		1327	
	949.5		977.5		977.5	9	F	9	1198		1198	
	1063		1091		1091	10	L	8	1051		1051	
	1120		1148	+0.111	1148	11	G	7	937.4		469.2	+0.01
	1235		1263		1263	12	D	6	880.4		440.7	-0.41
	1349		1377		1377	13	N	5	765.4		765.4	
	1464		1492		1492	14	D	4	651.3		651.3	
	1592		1620		1620	15	K	3	536.3		536.3	
	1739		1767		1767	16	F	2	408.2	-0.04	408.2	
	1853		1881		1881	17	N	1	261.2		261.2	
						18	K	0	147.1		147.1	

Scan number	5911	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	69.36



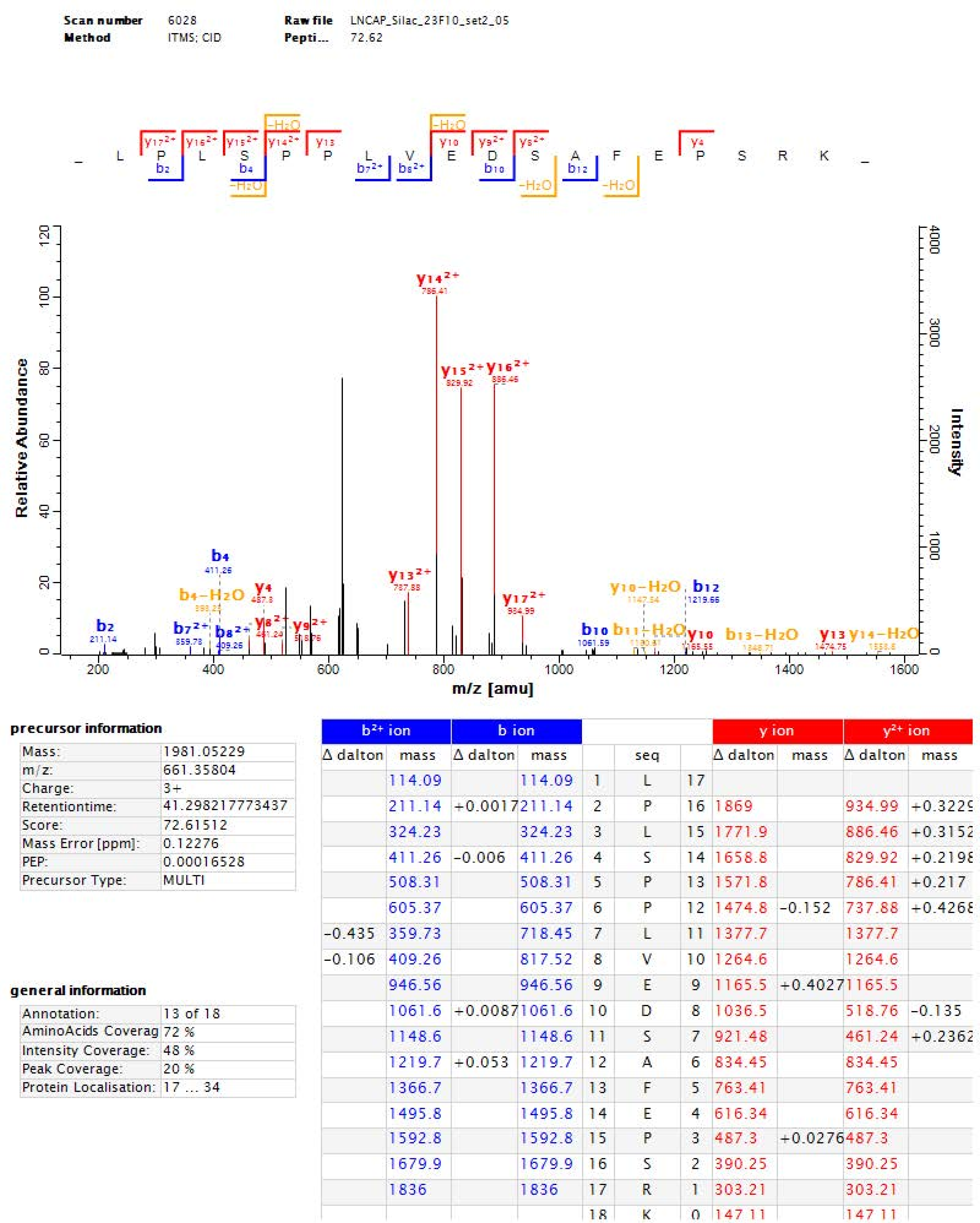
precursor information

Mass:	2479.30838
m/z:	827.4434
Charge:	3+
Retentiontime:	40.582332611084
Score:	69.36105
Mass Error [ppm]:	0.52189
PEP:	0.00015658
Precursor Type:	MULTI

general information

Annotation:	13 of 23
AminoAcids Coverag	57 %
Intensity Coverage:	32 %
Peak Coverage:	25 %
Protein Localisation:	356 ... 378

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	22				
	171.11		171.11	2	L	21	2423.3		2423.3	
	270.18		270.18	3	V	20	2310.2		2310.2	
	384.22		384.22	4	N	19	2211.1		1106.1	+0.0861
	497.31		497.31	5	L	18	2097.1		2097.1	
	625.37		625.37	6	Q	17	1984		992.51	+0.2972
	712.4		712.4	7	S	16	1856		1856	
	769.42		769.42	8	G	15	1768.9		884.97	+0.0022
	840.46		840.46	9	A	14	1711.9		1711.9	
	937.51		937.51	10	P	13	1640.9		1640.9	
	1065.6		1065.6	11	K	12	1543.8		1543.8	
	1162.7		1162.7	12	P	11	1415.7	-0.149	708.36	+0.0254
	1291.7	-0.127	1291.7	13	E	10	1318.7		1318.7	
	1420.7		1420.7	14	E	9	1189.6		1189.6	
	1534.8	+0.0808	1534.8	15	N	8	1060.6		530.79	+0.3484
-0.392	816.42		1631.8	16	P	7	946.54	-0.097	473.77	+0.3078
	1718.9	+0.0114	1718.9	17	S	6	849.48		849.48	
	1832		1832	18	L	5	762.45		762.45	
	1946		1946	19	N	4	649.37	+0.0902	649.37	
	2059.1		2059.1	20	I	3	535.32	+0.0939	535.32	
	2187.1		2187.1	21	Q	2	422.24		422.24	
	2334.2		2334.2	22	F	1	294.18	-0.04	294.18	
				23	K	0	147.11		147.11	



Scan number 6028
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set2_05
Pepti... 72.62

precursor information

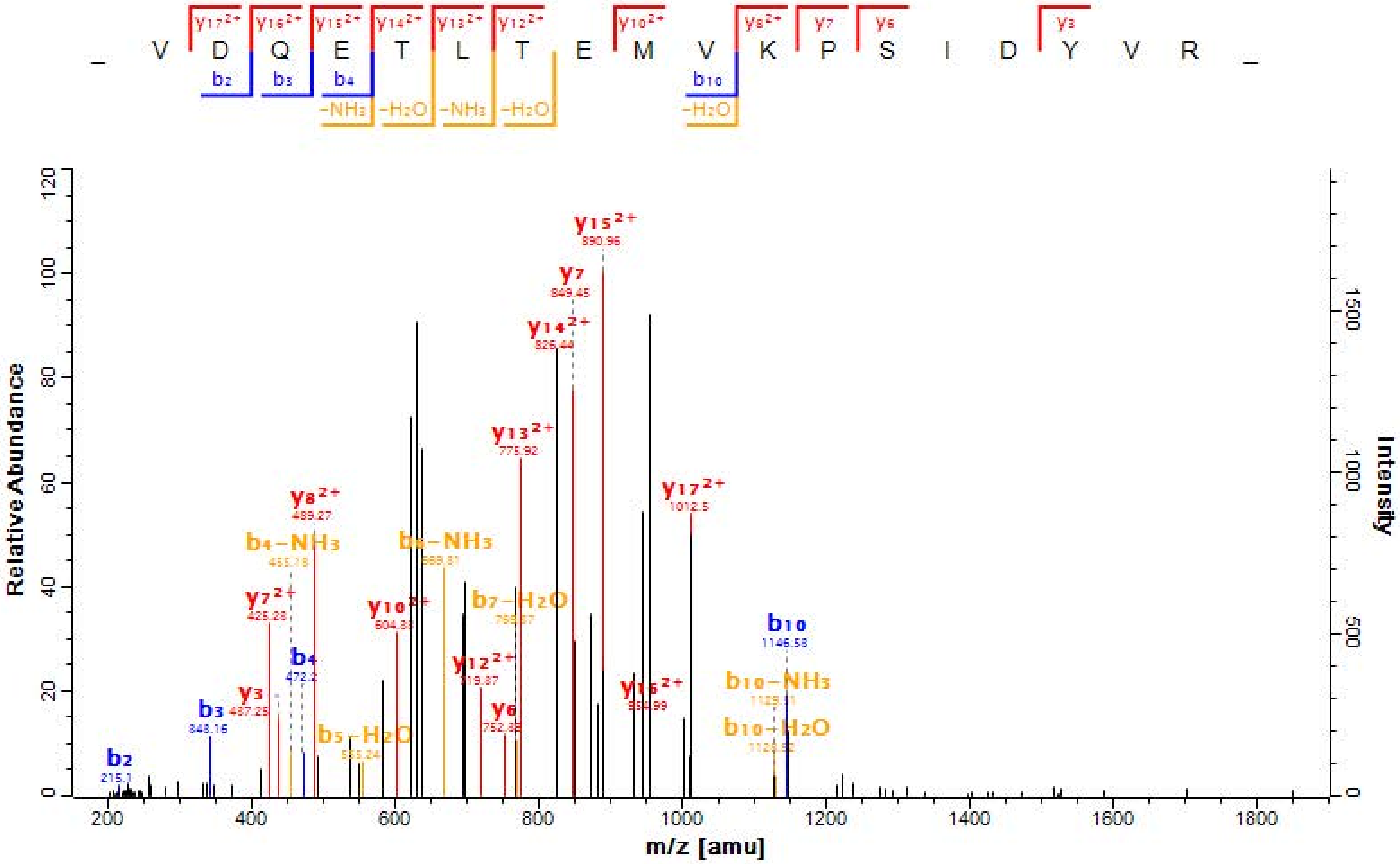
Mass:	1981.05229
m/z:	661.35804
Charge:	3+
Retentiontime:	41.298217773437
Score:	72.61512
Mass Error [ppm]:	0.12276
PEP:	0.00016528
Precursor Type:	MULTI

general information

Annotation:	13 of 18
AminoAcids Coverag	72 %
Intensity Coverage:	48 %
Peak Coverage:	20 %
Protein Localisation:	17 ... 34

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	17				
	211.14	+0.0017	211.14	2	P	16	1869		934.99	+0.322
	324.23		324.23	3	L	15	1771.9		886.46	+0.315
	411.26	-0.006	411.26	4	S	14	1658.8		829.92	+0.219
	508.31		508.31	5	P	13	1571.8		786.41	+0.217
	605.37		605.37	6	P	12	1474.8	-0.152	737.88	+0.426
-0.435	359.73		718.45	7	L	11	1377.7		1377.7	
-0.106	409.26		817.52	8	V	10	1264.6		1264.6	
	946.56		946.56	9	E	9	1165.5	+0.4027	1165.5	
	1061.6	+0.0087	1061.6	10	D	8	1036.5		518.76	-0.135
	1148.6		1148.6	11	S	7	921.48		461.24	+0.236
	1219.7	+0.053	1219.7	12	A	6	834.45		834.45	
	1366.7		1366.7	13	F	5	763.41		763.41	
	1495.8		1495.8	14	E	4	616.34		616.34	
	1592.8		1592.8	15	P	3	487.3	+0.0276	487.3	
	1679.9		1679.9	16	S	2	390.25		390.25	
	1836		1836	17	R	1	303.21		303.21	
				18	K	0	147.11		147.11	

Scan number	6110	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	81.45



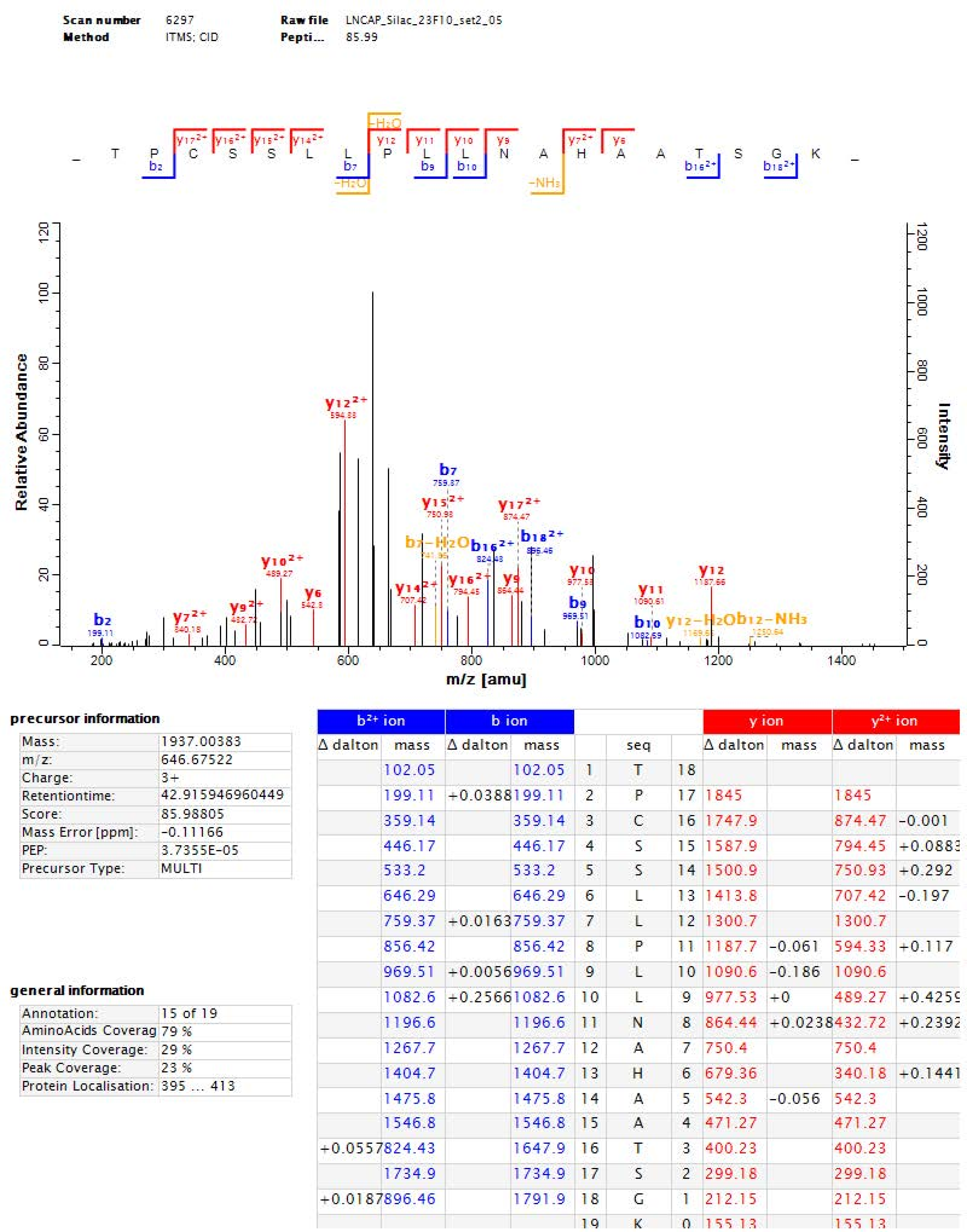
precursor information

Mass:	2122.06194
m/z:	708.36126
Charge:	3+
Retentiontime:	41.790824890136
Score:	81.44754
Mass Error [ppm]:	0.15128
PEP:	0.00011754
Precursor Type:	MULTI

general information

Annotation:	12 of 18
AminoAcids Coverag	67 %
Intensity Coverage:	42 %
Peak Coverage:	22 %
Protein Localisation:	280 ... 297

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	17				
+0.072293	215.1026	2	D	16	2024		1012.504	-0.05497
+0.022749	343.1612	3	Q	15	1908.974		954.9904	-0.1682
+0.178276	472.2038	4	E	14	1780.915		890.9611	+0.291261
	573.2515	5	T	13	1651.872		826.4398	+0.054074
	686.3355	6	L	12	1550.825		775.916	+0.388948
	787.3832	7	T	11	1437.741		719.374	+0.384166
	916.4258	8	E	10	1336.693		1336.693	
	1047.466	9	M	9	1207.65		604.3288	+0.142803
-0.23357	1146.535	10	V	8	1076.61		1076.61	
	1274.63	11	K	7	977.5415		489.2744	+0.257372
	1371.682	12	P	6	849.4465	+0.007547	425.2269	+0.153181
	1458.714	13	S	5	752.3937	-0.01525	752.3937	
	1571.799	14	I	4	665.3617		665.3617	
	1686.825	15	D	3	552.2776		552.2776	
	1849.889	16	Y	2	437.2507	+0.061561	437.2507	
	1948.957	17	V	1	274.1874		274.1874	
		18	R	0	175.119		175.119	



Scan number	6297	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	85.99

precursor information

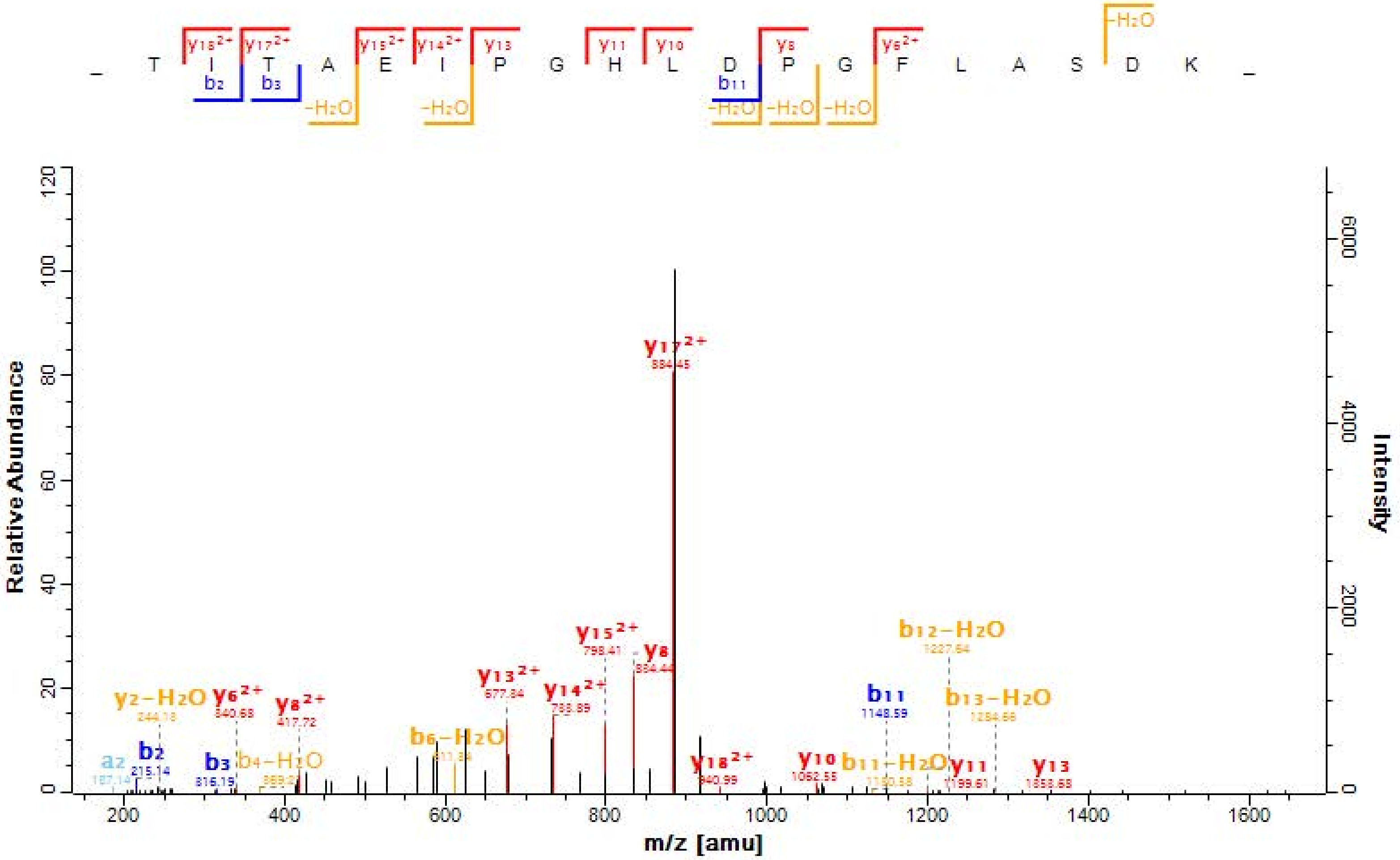
Mass:	1937.00383
m/z:	646.67522
Charge:	3+
Retentiontime:	42.915946960449
Score:	85.98805
Mass Error [ppm]:	-0.11166
PEP:	3.7355E-05
Precursor Type:	MULTI

general information

Annotation:	15 of 19
AminoAcids Coverag	79 %
Intensity Coverage:	29 %
Peak Coverage:	23 %
Protein Localisation:	395 ... 413

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	18				
	199.11	+0.0388	199.11	2	P	17	1845		1845	
	359.14		359.14	3	C	16	1747.9		874.47	-0.001
	446.17		446.17	4	S	15	1587.9		794.45	+0.0883
	533.2		533.2	5	S	14	1500.9		750.93	+0.292
	646.29		646.29	6	L	13	1413.8		707.42	-0.197
	759.37	+0.0163	759.37	7	L	12	1300.7		1300.7	
	856.42		856.42	8	P	11	1187.7	-0.061	594.33	+0.117
	969.51	+0.0056	969.51	9	L	10	1090.6	-0.186	1090.6	
	1082.6	+0.2566	1082.6	10	L	9	977.53	+0	489.27	+0.4259
	1196.6		1196.6	11	N	8	864.44	+0.0238	432.72	+0.2392
	1267.7		1267.7	12	A	7	750.4		750.4	
	1404.7		1404.7	13	H	6	679.36		340.18	+0.1441
	1475.8		1475.8	14	A	5	542.3	-0.056	542.3	
	1546.8		1546.8	15	A	4	471.27		471.27	
+0.0557	824.43		1647.9	16	T	3	400.23		400.23	
	1734.9		1734.9	17	S	2	299.18		299.18	
+0.0187	896.46		1791.9	18	G	1	212.15		212.15	
				19	K	0	155.13		155.13	

Scan number	6302	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	75.91



precursor information

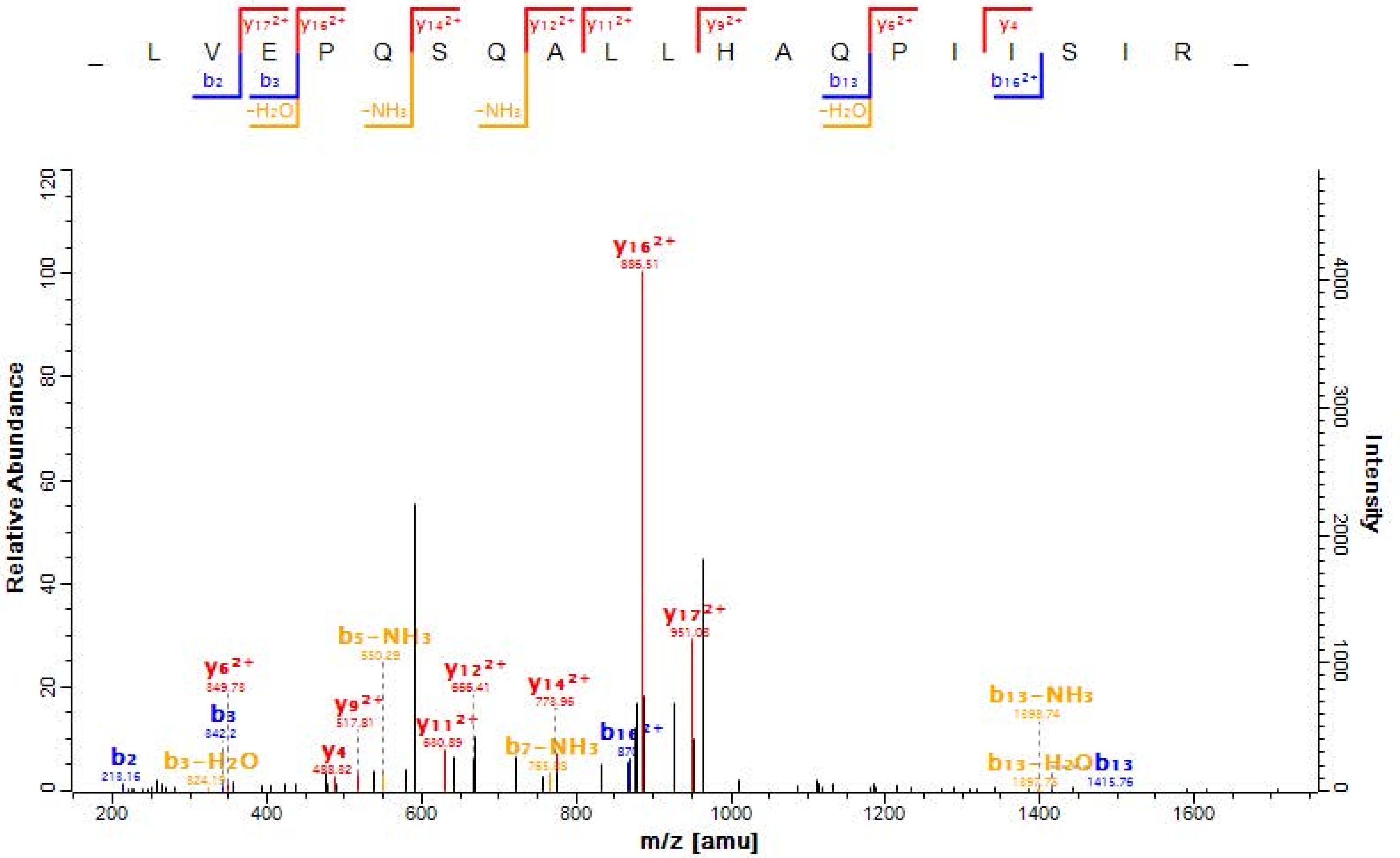
Mass:	1981.01639
m/z:	661.34607
Charge:	3+
Retentiontime:	42.949020385742
Score:	75.91064
Mass Error [ppm]:	0.37125
PEP:	0.00019947
Precursor Type:	MULTI

general information

Annotation:	13 of 19
AminoAcids Coverag	68 %
Intensity Coverage:	40 %
Peak Coverage:	20 %
Protein Localisation:	232 ... 250

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.05	1	T	18				
+0.0724	187.14	+0.0063	215.14	2	I	17	1881		940.99	-0.234
	288.19	-0.102	316.19	3	T	16	1767.9		884.45	-0.006
	359.23		387.22	4	A	15	1666.8		1666.8	
	488.27		516.27	5	E	14	1595.8		798.41	+0.2202
	601.36		629.35	6	I	13	1466.8		733.89	+0.1991
	698.41		726.4	7	P	12	1353.7	+0.1995	677.34	-0.029
	755.43		783.42	8	G	11	1256.6		1256.6	
	892.49		920.48	9	H	10	1199.6	+0.1949	1199.6	
	1005.6		1033.6	10	L	9	1062.5	-0.206	1062.5	
	1120.6	-0.205	1148.6	11	D	8	949.46		949.46	
	1217.7		1245.6	12	P	7	834.44	-0.147	417.72	+0.2916
	1274.7		1302.7	13	G	6	737.38		737.38	
	1421.7		1449.7	14	F	5	680.36		340.68	+0.3802
	1534.8		1562.8	15	L	4	533.29		533.29	
	1605.9		1633.9	16	A	3	420.21		420.21	
	1692.9		1720.9	17	S	2	349.17		349.17	
	1807.9		1835.9	18	D	1	262.14		262.14	
				19	K	0	147.11		147.11	

Scan number	6353	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	53.17



precursor information

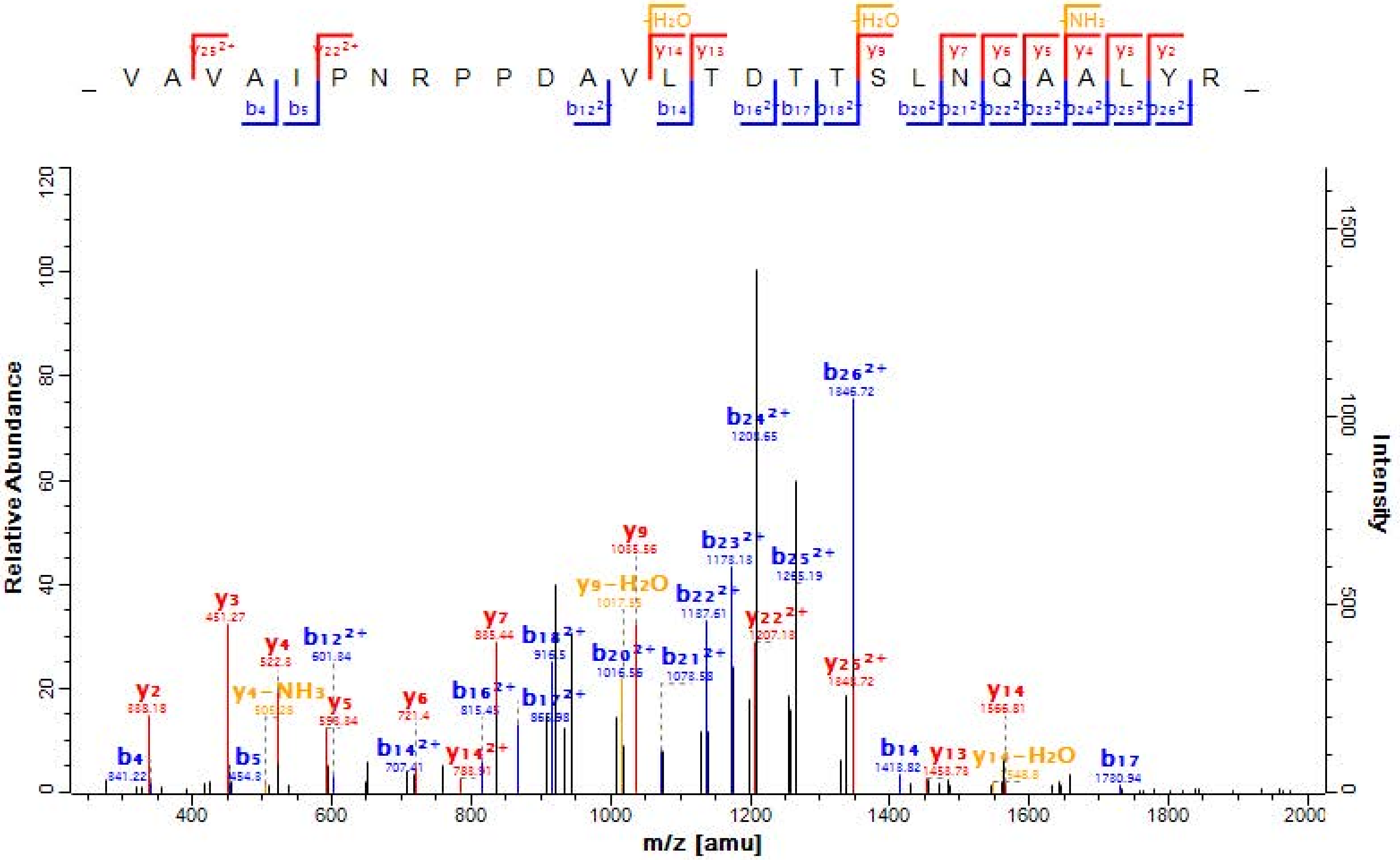
Mass:	2112.20608
m/z:	705.07597
Charge:	3+
Retentiontime:	43.282321929931
Score:	53.16797
Mass Error [ppm]:	0.26214
PEP:	0.005095
Precursor Type:	MULTI

general information

Annotation:	12 of 19
AminoAcids Coverag	63 %
Intensity Coverage:	38 %
Peak Coverage:	20 %
Protein Localisation:	433 ... 451

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	18				
	213.16	+0.0156	213.16	2	V	17	2000.1		2000.1	
	342.2	-0.043	342.2	3	E	16	1901.1		951.03	+0.266
	439.26		439.26	4	P	15	1772		886.51	+0.227
	567.31		567.31	5	Q	14	1675		1675	
	654.35		654.35	6	S	13	1546.9		773.96	+0.285
	782.4		782.4	7	Q	12	1459.9		1459.9	
	853.44		853.44	8	A	11	1331.8		666.41	-0.127
	966.53		966.53	9	L	10	1260.8		630.89	+0.124
	1079.6		1079.6	10	L	9	1147.7		1147.7	
	1216.7		1216.7	11	H	8	1034.6		517.81	+0.297
	1287.7		1287.7	12	A	7	897.55		897.55	
	1415.8	+0.0553	1415.8	13	Q	6	826.51		826.51	
	1512.8		1512.8	14	P	5	698.46		349.73	+0.1032
	1625.9		1625.9	15	I	4	601.4		601.4	
-0.28	870		1739	16	I	3	488.32	+0.0695	488.32	
	1826		1826	17	S	2	375.24		375.24	
	1939.1		1939.1	18	I	1	288.2		288.2	
				19	R	0	175.12		175.12	

Scan number	6705	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	154.34



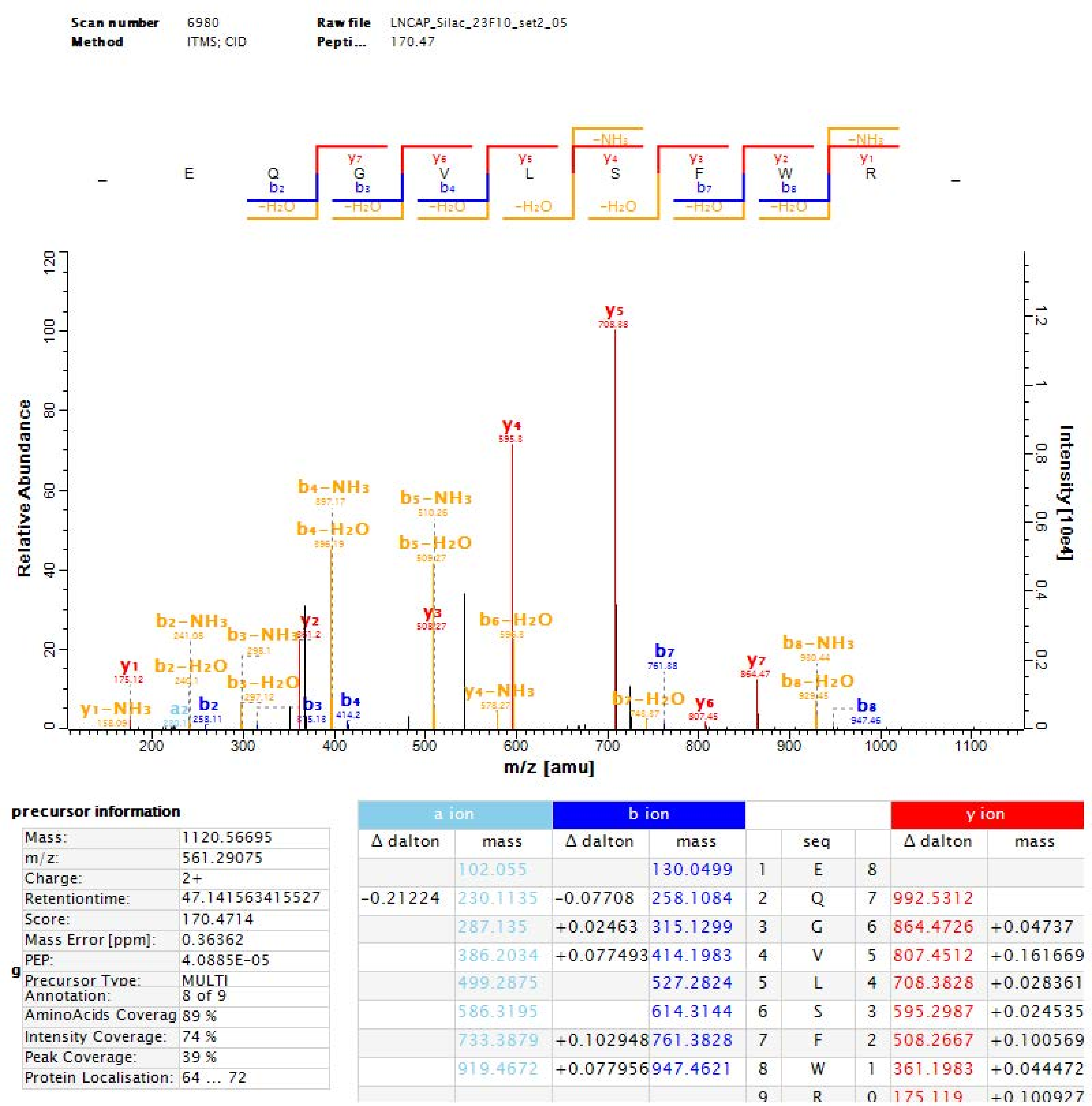
precursor information

Mass:	2865.53476
m/z:	956.18553
Charge:	3+
Retentiontime:	45.459671020507
Score:	154.336
Mass Error [ppm]:	-0.033219
PEP:	3.3243E-33
Precursor Type:	MULTI

general information

Annotation:	18 of 27
AminoAcids Coverag	67 %
Intensity Coverage:	49 %
Peak Coverage:	30 %
Protein Localisation:	480 ... 506

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	26				
	171.11		171.11	2	A	25	2767.5		2767.5	
	270.18		270.18	3	V	24	2696.4		1348.7	-0.421
	341.22	-0.355	341.22	4	A	23	2597.4		2597.4	
	454.3	+0.0736	454.3	5	I	22	2526.3		2526.3	
	551.36		551.36	6	P	21	2413.2		1207.1	+0.0518
	665.4		665.4	7	N	20	2316.2		2316.2	
	821.5		821.5	8	R	19	2202.2		2202.2	
	918.55		918.55	9	P	18	2046.1		2046.1	
	1015.6		1015.6	10	P	17	1949		1949	
	1130.6		1130.6	11	D	16	1851.9		1851.9	
+0.112	601.34		1201.7	12	A	15	1736.9		1736.9	
	1300.7		1300.7	13	V	14	1665.9		1665.9	
+0.0146	707.41	-0.101	1413.8	14	L	13	1566.8	+0.246	783.91	-0.076
	1514.9		1514.9	15	T	12	1453.7	-0.123	1453.7	
-0.144	815.45		1629.9	16	D	11	1352.7		1352.7	
+0.2351	865.98	-0.261	1730.9	17	T	10	1237.7		1237.7	
+0.2974	916.5		1832	18	T	9	1136.6		1136.6	
	1919		1919	19	S	8	1035.6	-0.027	1035.6	
-0.11	1016.6		2032.1	20	L	7	948.53		948.53	
+0.3402	1073.6		2146.2	21	N	6	835.44	+0.0673	835.44	
+0.2491	1137.6		2274.2	22	Q	5	721.4	+0.1989	721.4	
+0.2309	1173.1		2345.2	23	A	4	593.34	+0.0121	593.34	
-0.424	1208.6		2416.3	24	A	3	522.3	+0.0776	522.3	
-0.09	1265.2		2529.4	25	L	2	451.27	+0.1003	451.27	
+0.2246	1346.7		2692.4	26	Y	1	338.18	+0.0936	338.18	
				27	R	0	175.12		175.12	



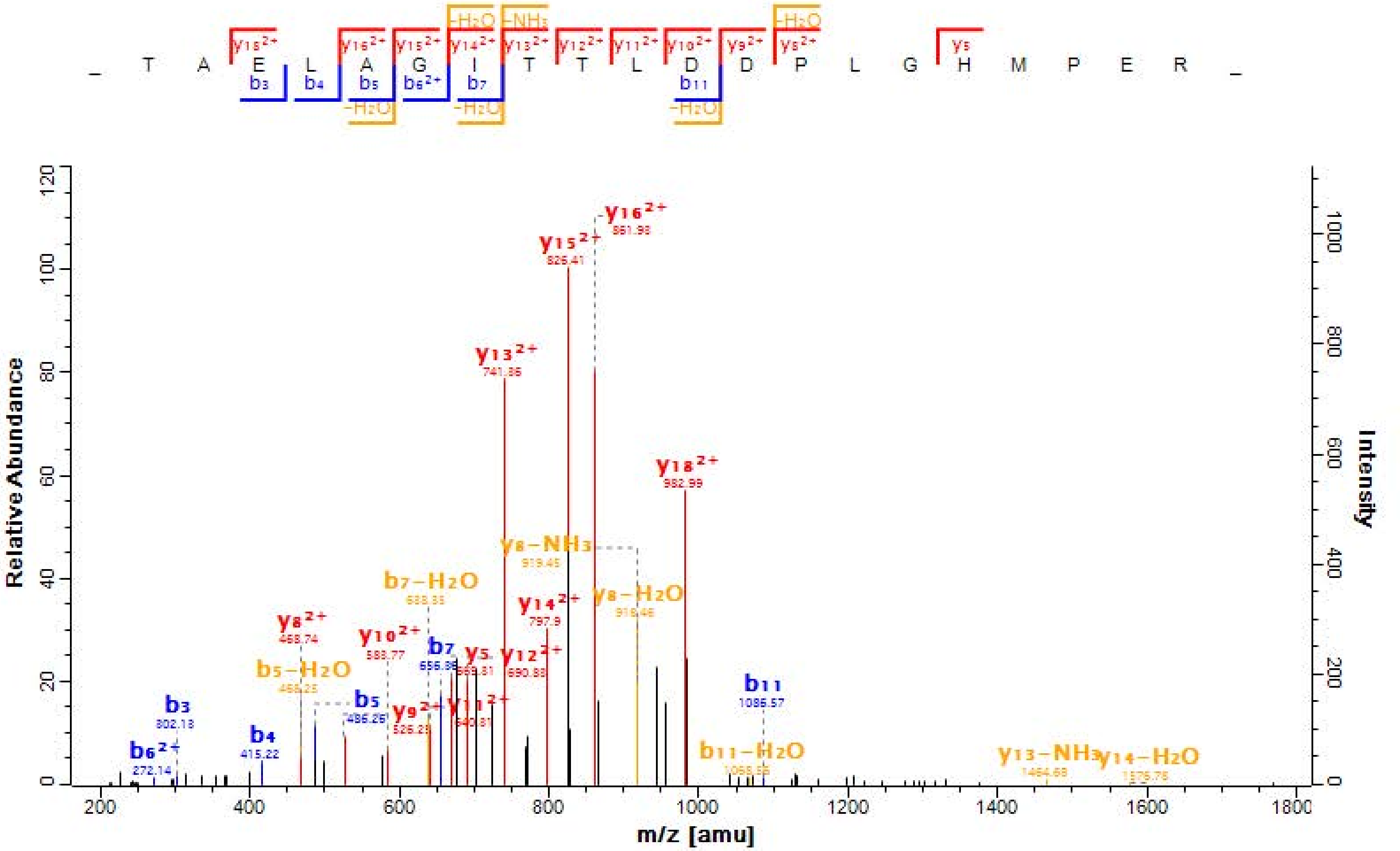
Scan number	6980	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	170.47

precursor information

Mass:	1120.56695
m/z:	561.29075
Charge:	2+
Retentiontime:	47.141563415527
Score:	170.4714
Mass Error [ppm]:	0.36362
PEP:	4.0885E-05
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	74 %
Peak Coverage:	39 %
Protein Localisation:	64 ... 72

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	102.055		130.0499	1	E	8		
-0.21224	230.1135	-0.07708	258.1084	2	Q	7	992.5312	
	287.135	+0.02463	315.1299	3	G	6	864.4726	+0.04737
	386.2034	+0.077493	414.1983	4	V	5	807.4512	+0.161669
	499.2875		527.2824	5	L	4	708.3828	+0.028361
	586.3195		614.3144	6	S	3	595.2987	+0.024535
	733.3879	+0.102948	761.3828	7	F	2	508.2667	+0.100569
	919.4672	+0.077956	947.4621	8	W	1	361.1983	+0.044472
				9	R	0	175.119	+0.100927

Scan number	7037	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	89.51



precursor information

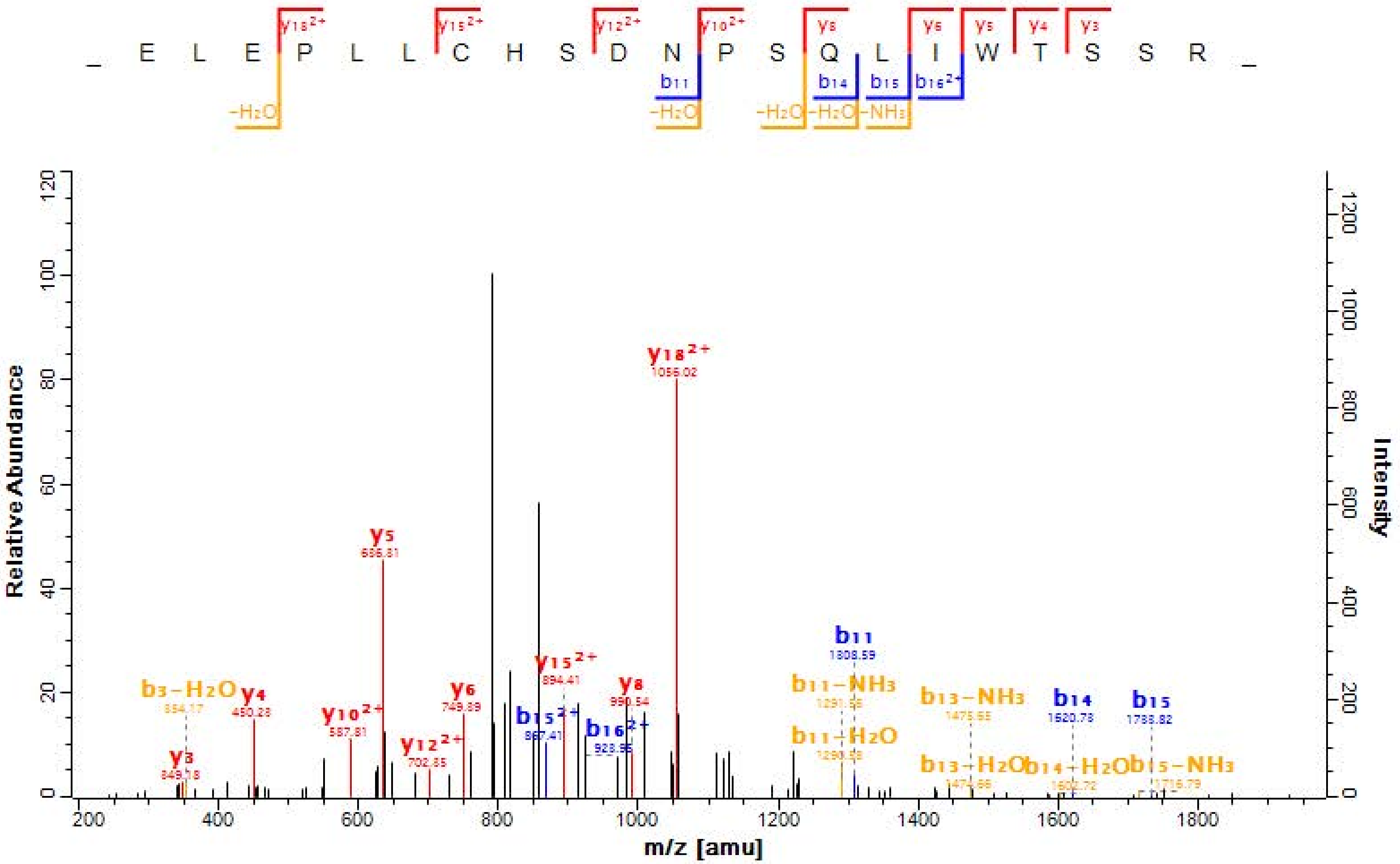
Mass:	2136.05349
m/z:	713.02511
Charge:	3+
Retentiontime:	47.487735748291
Score:	89.50639
Mass Error [ppm]:	0.64036
PEP:	6.6408E-06
Precursor Type:	MULTI

general information

Annotation:	12 of 20
AminoAcids Coverag	60 %
Intensity Coverage:	65 %
Peak Coverage:	30 %
Protein Localisation:	153 ... 172

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	19				
	173.09		173.09	2	A	18	2036		2036	
	302.13	+0.1355	302.13	3	E	17	1965		982.99	-0.011
	415.22	-0.083	415.22	4	L	16	1835.9		1835.9	
	486.26	-0.094	486.26	5	A	15	1722.8		861.93	+0.211
+0.0287	272.14		543.28	6	G	14	1651.8		826.41	+0.0382
	656.36	-0.351	656.36	7	I	13	1594.8		797.9	+0.2132
	757.41		757.41	8	T	12	1481.7		741.36	+0.1443
	858.46		858.46	9	T	11	1380.7		690.83	+0.0433
	971.54		971.54	10	L	10	1279.6		640.31	+0.3421
	1086.6	+0.2667	1086.6	11	D	9	1166.5		583.77	-0.039
	1201.6		1201.6	12	D	8	1051.5		526.25	+0.083
	1298.6		1298.6	13	P	7	936.47		468.74	+0.3523
	1411.7		1411.7	14	L	6	839.42		839.42	
	1468.8		1468.8	15	G	5	726.34		726.34	
	1605.8		1605.8	16	H	4	669.31	+0.1496	669.31	
	1736.9		1736.9	17	M	3	532.25		532.25	
	1833.9		1833.9	18	P	2	401.21		401.21	
	1962.9		1962.9	19	E	1	304.16		304.16	
				20	R	0	175.12		175.12	

Scan number	7170	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	66.61



precursor information

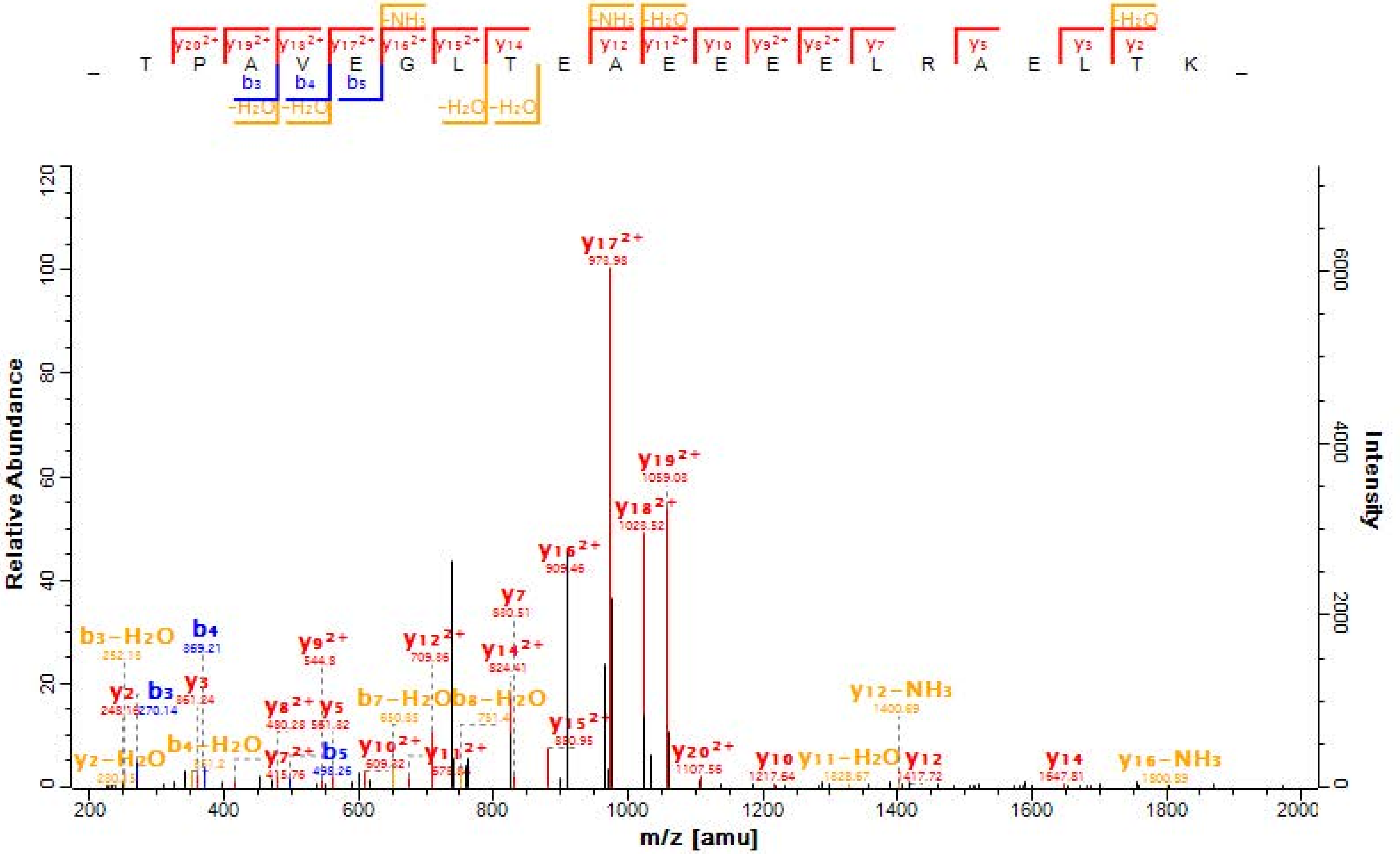
Mass:	2481.19557
m/z:	828.07247
Charge:	3+
Retentiontime:	48.324138641357
Score:	66.60609
Mass Error [ppm]:	-0.10077
PEP:	0.00088585
Precursor Type:	MULTI

general information

Annotation:	13 of 21
AminoAcids Coverag	62 %
Intensity Coverage:	33 %
Peak Coverage:	22 %
Protein Localisation:	152 ... 172

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	20				
	243.13		243.13	2	L	19	2353.2		2353.2	
	372.18		372.18	3	E	18	2240.1		2240.1	
	469.23		469.23	4	P	17	2111		1056	+0.1992
	582.31		582.31	5	L	16	2014		2014	
	695.4		695.4	6	L	15	1900.9		1900.9	
	855.43		855.43	7	C	14	1787.8		894.41	+0.3139
	992.49		992.49	8	H	13	1627.8		1627.8	
	1079.5		1079.5	9	S	12	1490.7		1490.7	
	1194.5		1194.5	10	D	11	1403.7		702.35	+0.4605
	1308.6	-0.069	1308.6	11	N	10	1288.7		1288.7	
	1405.6		1405.6	12	P	9	1174.6		587.81	+0.2338
	1492.7		1492.7	13	S	8	1077.6		1077.6	
	1620.7	+0.1722	1620.7	14	Q	7	990.54	+0.218	990.54	
-0.105	867.41	+0.0764	1733.8	15	L	6	862.48		862.48	
-0.049	923.95		1846.9	16	I	5	749.39	+0.0343	749.39	
	2033		2033	17	W	4	636.31	+0.0988	636.31	
	2134		2134	18	T	3	450.23	+0.0739	450.23	
	2221.1		2221.1	19	S	2	349.18	+0.0782	349.18	
	2308.1		2308.1	20	S	1	262.15		262.15	
				21	R	0	175.12		175.12	

Scan number	7249	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	139.67



precursor information

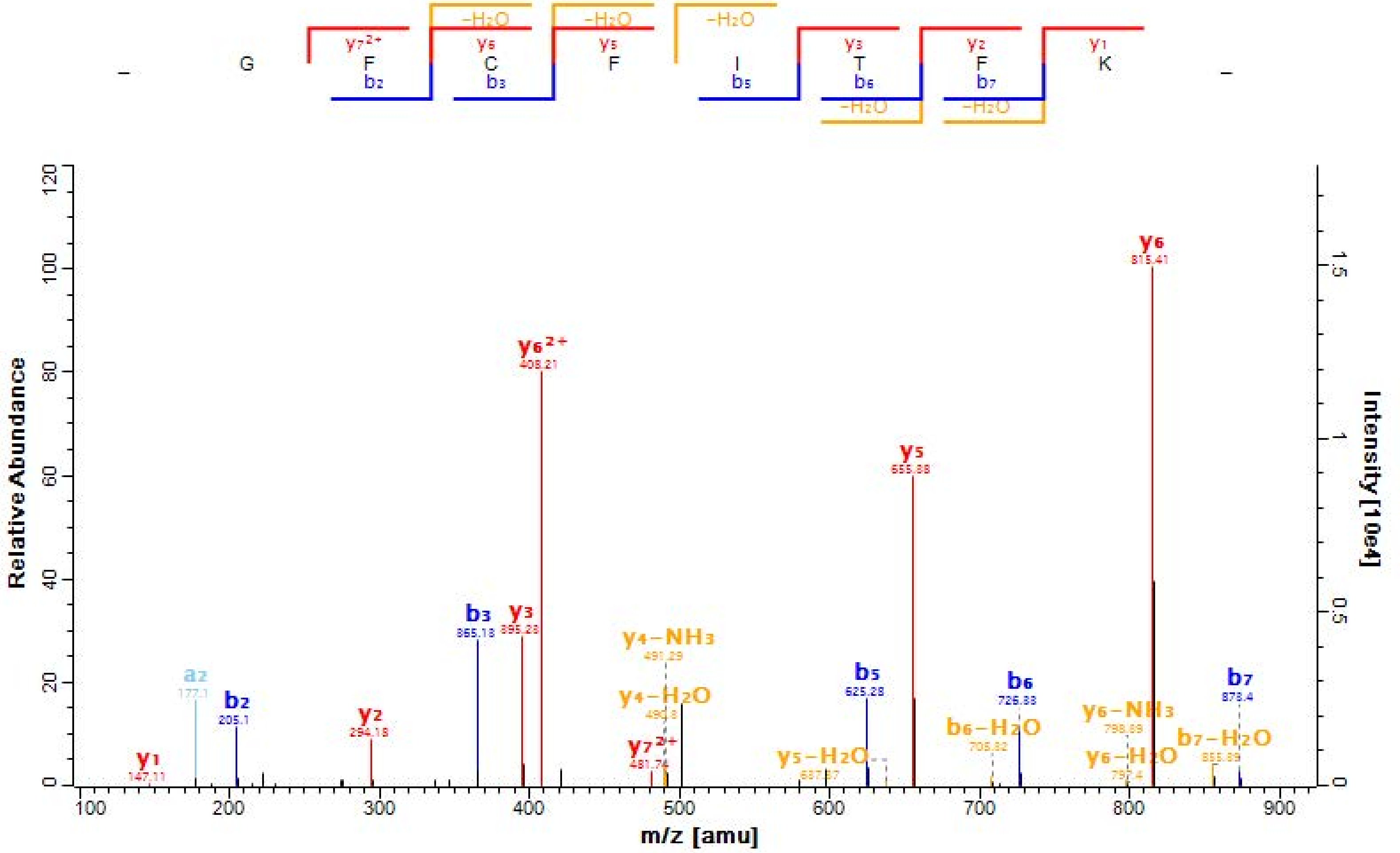
Mass:	2314.15355
m/z:	772.39179
Charge:	3+
Retentiontime:	48.8662109375
Score:	139.6694
Mass Error [ppm]:	-0.19433
PEP:	2.0436E-19
Precursor Type:	MULTI

general information

Annotation:	16 of 21
AminoAcids Coverag	76 %
Intensity Coverage:	56 %
Peak Coverage:	29 %
Protein Localisation:	35 ... 55

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055	1	T	20				
	199.1077	2	P	19	2214.114		1107.56	+0.051623
+0.101383	270.1448	3	A	18	2117.061		1059.034	+0.319216
+0.086131	369.2132	4	V	17	2046.024		1023.515	+0.23029
+0.038899	498.2558	5	E	16	1946.955		973.9813	+0.278291
	555.2773	6	G	15	1817.913		909.46	+0.005398
	668.3614	7	L	14	1760.891		880.9493	+0.387346
	769.409	8	T	13	1647.807	-0.38702	824.4072	+0.056025
	898.4516	9	E	12	1546.76		1546.76	
	969.4888	10	A	11	1417.717	+0.043461	709.3621	+0.190944
	1098.531	11	E	10	1346.68		673.8435	+0.108793
	1227.574	12	E	9	1217.637	-0.16919	609.3222	+0.22445
	1356.617	13	E	8	1088.595		544.8009	+0.228168
	1485.659	14	E	7	959.552		480.2796	+0.030349
	1598.743	15	L	6	830.5094	+0.010408	415.7584	+0.190439
	1754.844	16	R	5	717.4254		717.4254	
	1825.881	17	A	4	561.3243	+0.227077	561.3243	
	1954.924	18	E	3	490.2871		490.2871	
	2068.008	19	L	2	361.2445	-0.05967	361.2445	
	2169.056	20	T	1	248.1605	-0.04351	248.1605	
		21	K	0	147.1128		147.1128	

Scan number	7306	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	166.17

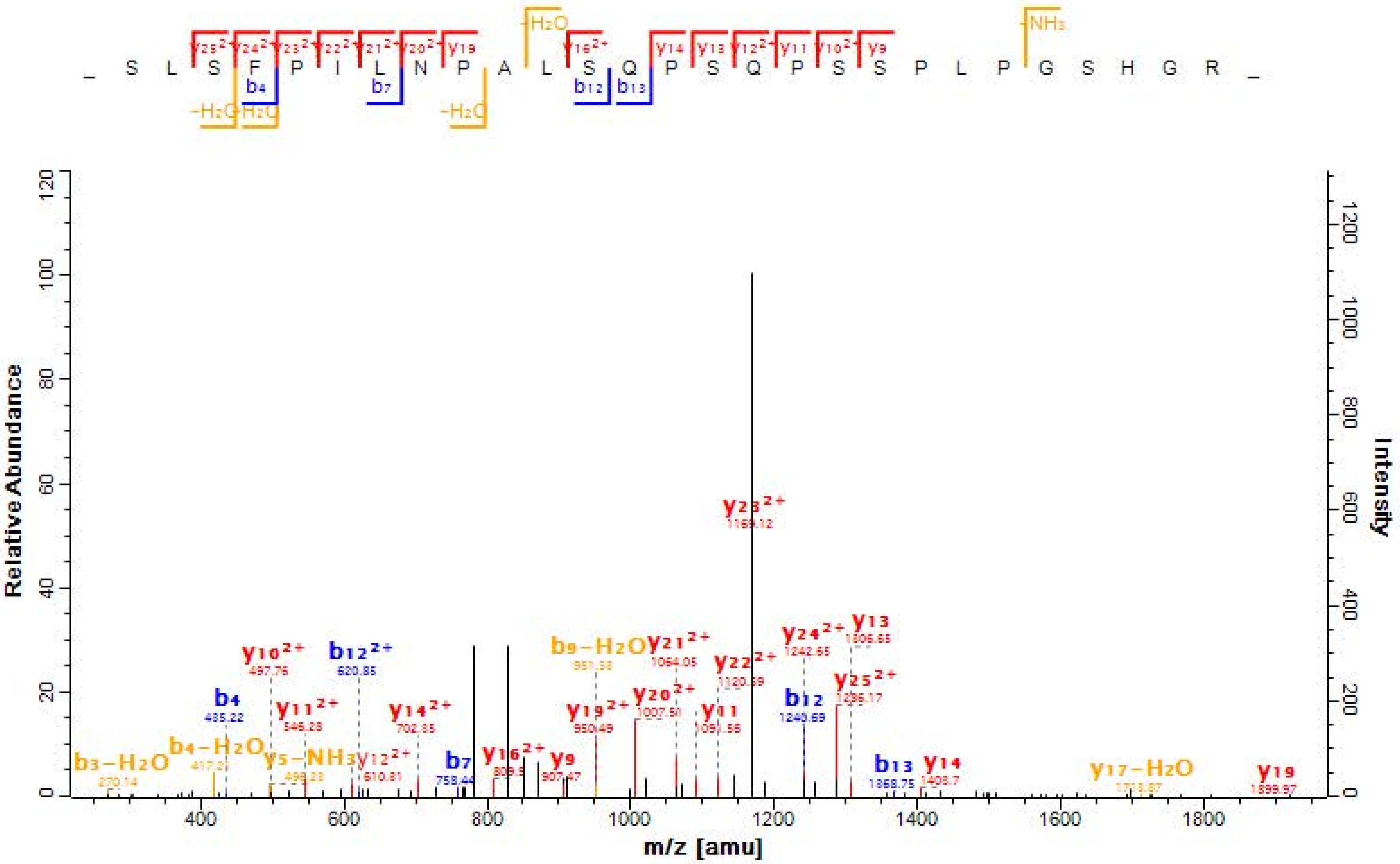


precursor information

Mass:	1018.49497
m/z:	510.25476
Charge:	2+
Retentiontime:	49.221870422363
Score:	166.1692
Mass Error [ppm]:	0.33723
PEP:	1.377E-05
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	77 %
Peak Coverage:	33 %
Protein Localisation:	205 ... 212

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	30.034		58.029	1	G	7				
+0.0209	177.1	+0.0018	205.1	2	F	6	962.48		481.74	+0.3203
	337.13	+0.0025	365.13	3	C	5	815.41	−0.036	408.21	+0.1796
	484.2		512.2	4	F	4	655.38	−0.019	655.38	
	597.29	−0.027	625.28	5	I	3	508.31		508.31	
	698.33	−0.061	726.33	6	T	2	395.23	+0.0052	395.23	
	845.4	−0.052	873.4	7	F	1	294.18	+0.0572	294.18	
				8	K	0	147.11	−0.072	147.11	

Scan number	7676	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	74.56



precursor information

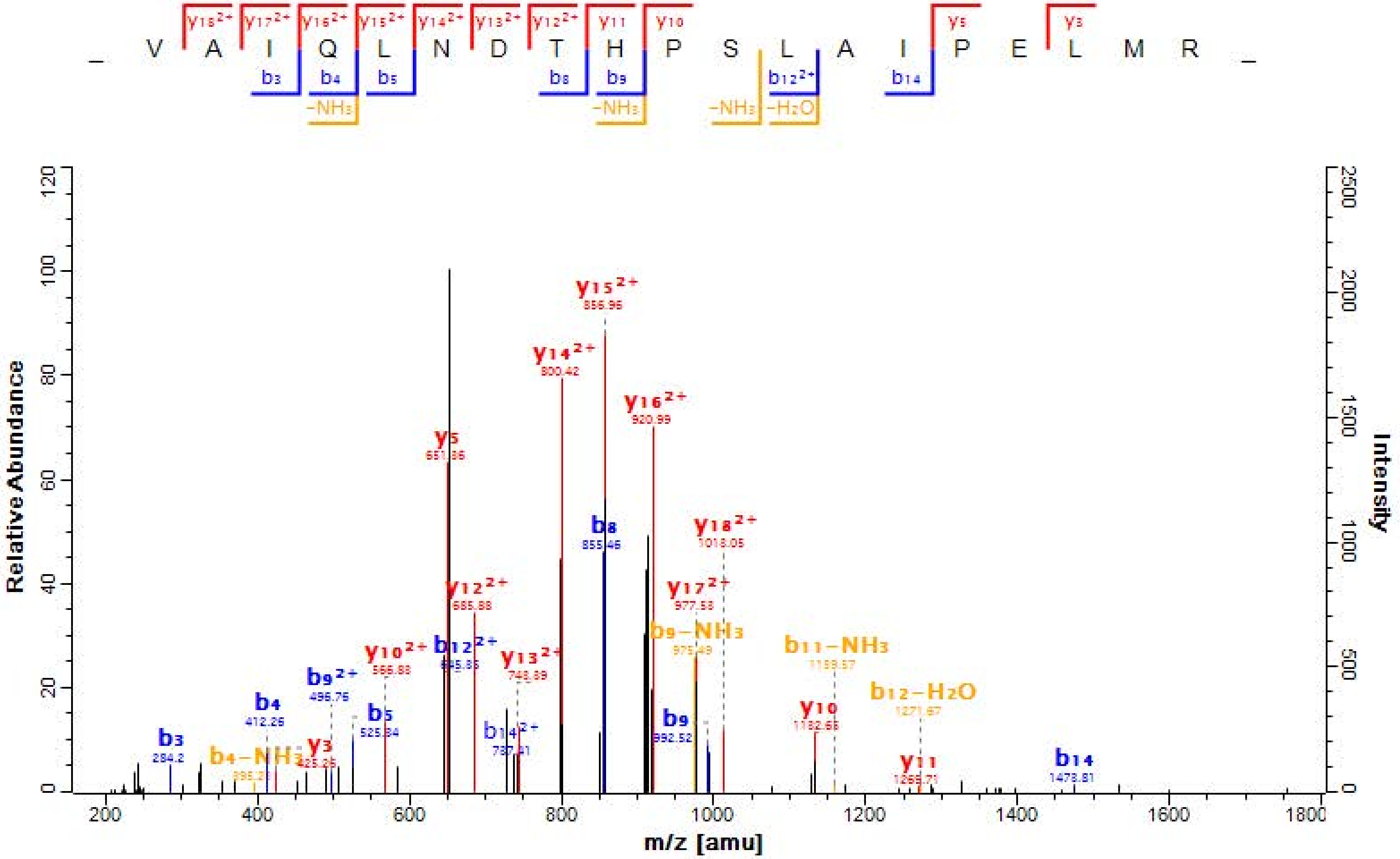
Mass:	2770.44016
m/z:	924.48733
Charge:	3+
Retentiontime:	51.716648101806
Score:	74.56078
Mass Error [ppm]:	-0.022439
PEP:	4.6188E-08
Precursor Type:	MULTI

general information

Annotation:	18 of 27
AminoAcids Coverag	67 %
Intensity Coverage:	38 %
Peak Coverage:	28 %
Protein Localisation:	483 ... 509

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	26				
	201.12		201.12	2	L	25	2684.4		2684.4	
	288.16		288.16	3	S	24	2571.3		1286.2	+0.3134
	435.22	-0.058	435.22	4	F	23	2484.3		1242.7	-0.326
	532.28		532.28	5	P	22	2337.2		1169.1	-0.015
	645.36		645.36	6	I	21	2240.2		1120.6	-0.024
	758.44	-0.105	758.44	7	L	20	2127.1		1064.1	+0.403
	872.49		872.49	8	N	19	2014		1007.5	+0.198
	969.54		969.54	9	P	18	1900	-0.255	950.49	+0.2447
	1040.6		1040.6	10	A	17	1802.9		1802.9	
	1153.7		1153.7	11	L	16	1731.9		1731.9	
+0.3158	620.85	+0.4805	1240.7	12	S	15	1618.8		809.9	-0.05
	1368.8	-0.234	1368.8	13	Q	14	1531.8		1531.8	
	1465.8		1465.8	14	P	13	1403.7	-0.046	702.35	+0.162
	1552.8		1552.8	15	S	12	1306.6	+0.0483	1306.6	
	1680.9		1680.9	16	Q	11	1219.6		610.31	+0.1809
	1777.9		1777.9	17	P	10	1091.6	+0.0457	546.28	+0.4409
	1865		1865	18	S	9	994.51		497.76	-0.098
	1952		1952	19	S	8	907.47	+0.083	907.47	
	2049.1		2049.1	20	P	7	820.44		820.44	
	2162.1		2162.1	21	L	6	723.39		723.39	
	2259.2		2259.2	22	P	5	610.31		610.31	
	2316.2		2316.2	23	G	4	513.25		513.25	
	2403.3		2403.3	24	S	3	456.23		456.23	
	2540.3		2540.3	25	H	2	369.2		369.2	
	2597.3		2597.3	26	G	1	232.14		232.14	
				27	R	0	175.12		175.12	

Scan number	7746	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	101.01



precursor information

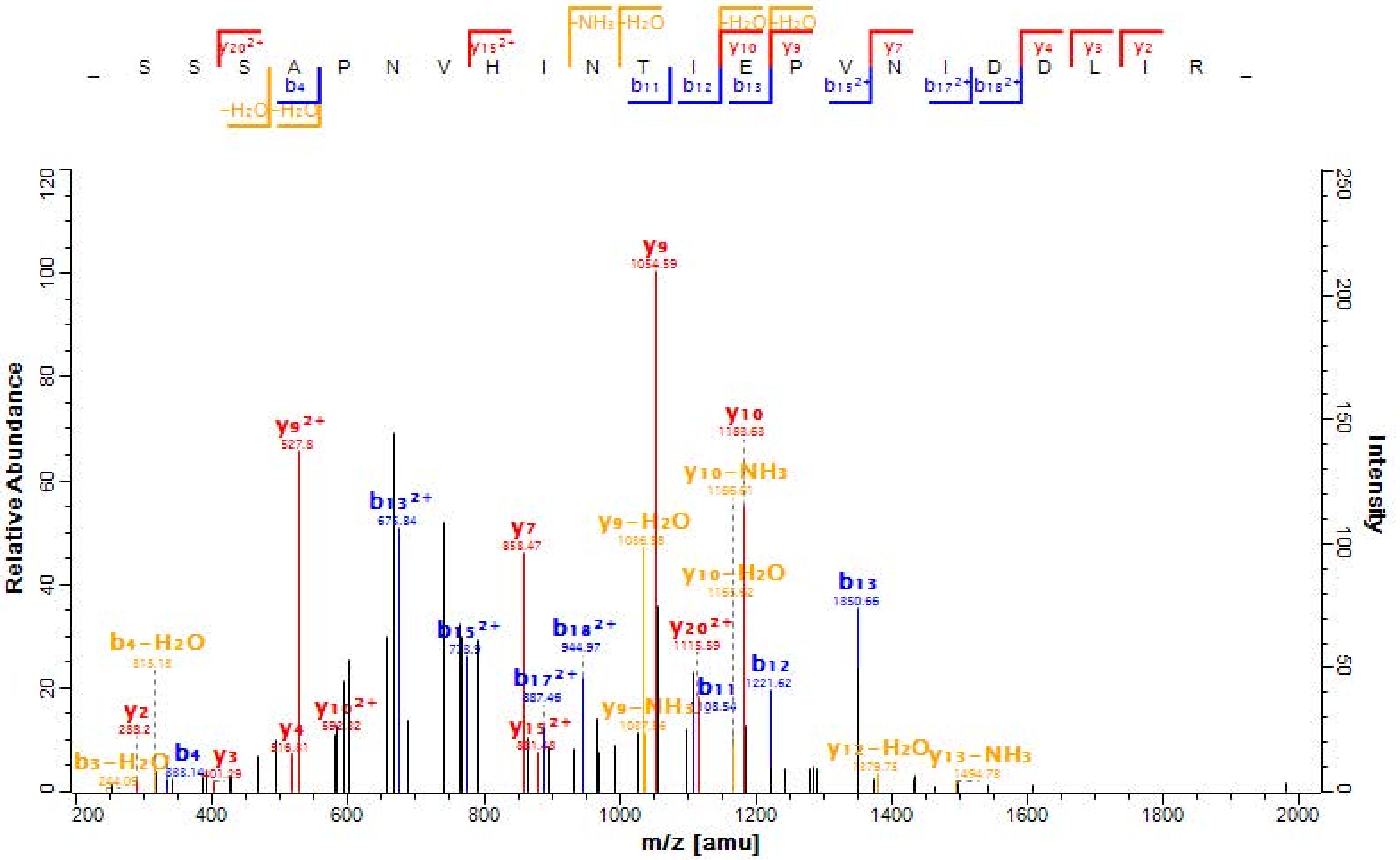
Mass:	2117.12973
m/z:	706.71719
Charge:	3+
Retentiontime:	52.212528228759
Score:	101.0086
Mass Error [ppm]:	-0.27352
PEP:	2.8338E-06
Precursor Type:	MULTI

general information

Annotation:	14 of 19
AminoAcids Coverag	74 %
Intensity Coverage:	47 %
Peak Coverage:	26 %
Protein Localisation:	334 ... 352

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	18				
	171.11		171.11	2	A	17	2025.1		1013	-0.05
	284.2	+0.0214	284.2	3	I	16	1954.1		977.53	+0.0622
	412.26	+0.0939	412.26	4	Q	15	1841		920.99	+0.2972
	525.34	+0.0035	525.34	5	L	14	1712.9		856.96	+0.028
	639.38		639.38	6	N	13	1599.8		800.42	+0.127
	754.41		754.41	7	D	12	1485.8		743.39	+0.229
	855.46	-0.229	855.46	8	T	11	1370.8		685.88	+0.2227
+0.0487	496.76	+0.0087	992.52	9	H	10	1269.7	+0.1066	1269.7	
	1089.6		1089.6	10	P	9	1132.6	-0.008	566.83	+0.1625
	1176.6		1176.6	11	S	8	1035.6		1035.6	
-0.101	645.35		1289.7	12	L	7	948.56		948.56	
	1360.7		1360.7	13	A	6	835.48		835.48	
+0.0872	737.41	+0.4656	1473.8	14	I	5	764.44		764.44	
	1570.9		1570.9	15	P	4	651.36	+0.1163	651.36	
	1699.9		1699.9	16	E	3	554.31		554.31	
	1813		1813	17	L	2	425.26	+0.0355	425.26	
	1944		1944	18	M	1	312.18		312.18	
				19	R	0	181.14		181.14	

Scan number	7845	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	92.39



precursor information

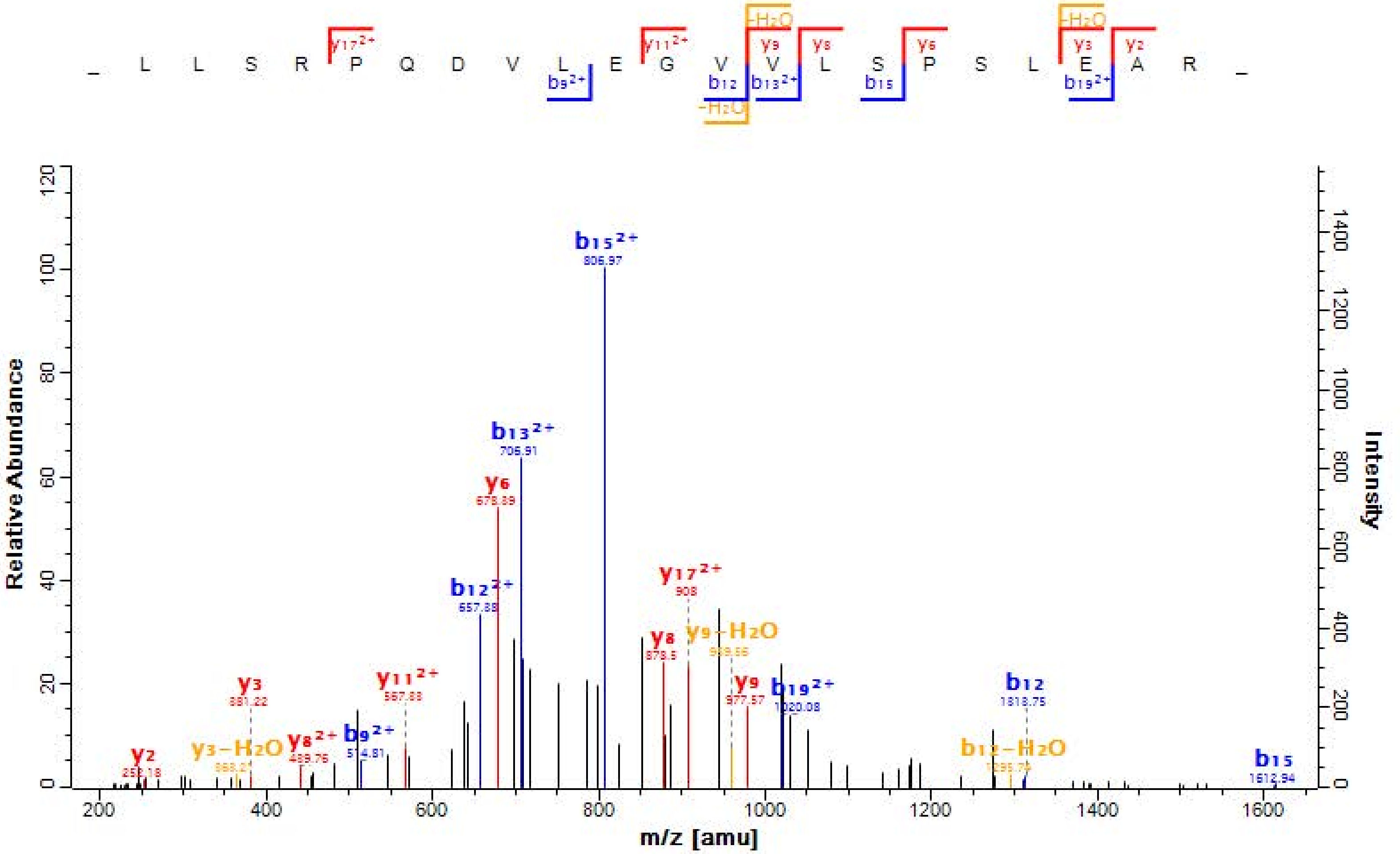
Mass:	2403.23988
m/z:	802.08724
Charge:	3+
Retentiontime:	52.963550567627
Score:	92.39011
Mass Error [ppm]:	0.2007
PEP:	3.9E-06
Precursor Type:	MULTI

general information

Annotation:	16 of 22
AminoAcids Coverag	73 %
Intensity Coverage:	48 %
Peak Coverage:	35 %
Protein Localisation:	363 ... 384

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	21				
	175.07		175.07	2	S	20	2317.2		2317.2	
	262.1		262.1	3	S	19	2230.2		1115.6	+0.2141
	333.14	+0.0469	333.14	4	A	18	2143.2		2143.2	
	430.19		430.19	5	P	17	2072.1		2072.1	
	544.24		544.24	6	N	16	1975.1		1975.1	
	643.3		643.3	7	V	15	1861		1861	
	780.36		780.36	8	H	14	1761.9		881.48	+0.0259
	893.45		893.45	9	I	13	1624.9		1624.9	
	1007.5		1007.5	10	N	12	1511.8		1511.8	
	1108.5	+0.2548	1108.5	11	T	11	1397.8		1397.8	
	1221.6	+0.1076	1221.6	12	I	10	1296.7		1296.7	
-0.083	675.84	-0.052	1350.7	13	E	9	1183.6	-0.011	592.32	+0.306
	1447.7		1447.7	14	P	8	1054.6	+0.0564	527.8	+0.1338
+0.1446	773.9		1546.8	15	V	7	957.54		957.54	
	1660.8		1660.8	16	N	6	858.47	+0.0635	858.47	
-0.161	887.46		1773.9	17	I	5	744.43		744.43	
-0.112	944.97		1888.9	18	D	4	631.34		631.34	
	2004		2004	19	D	3	516.31	+0.1026	516.31	
	2117.1		2117.1	20	L	2	401.29	+0.2782	401.29	
	2230.1		2230.1	21	I	1	288.2	+0.1526	288.2	
				22	R	0	175.12		175.12	

Scan number 7852 **Raw file** LNCAP_Silac_23F10_set2_05
Method ITMS; CID **Pepti...** 69.08



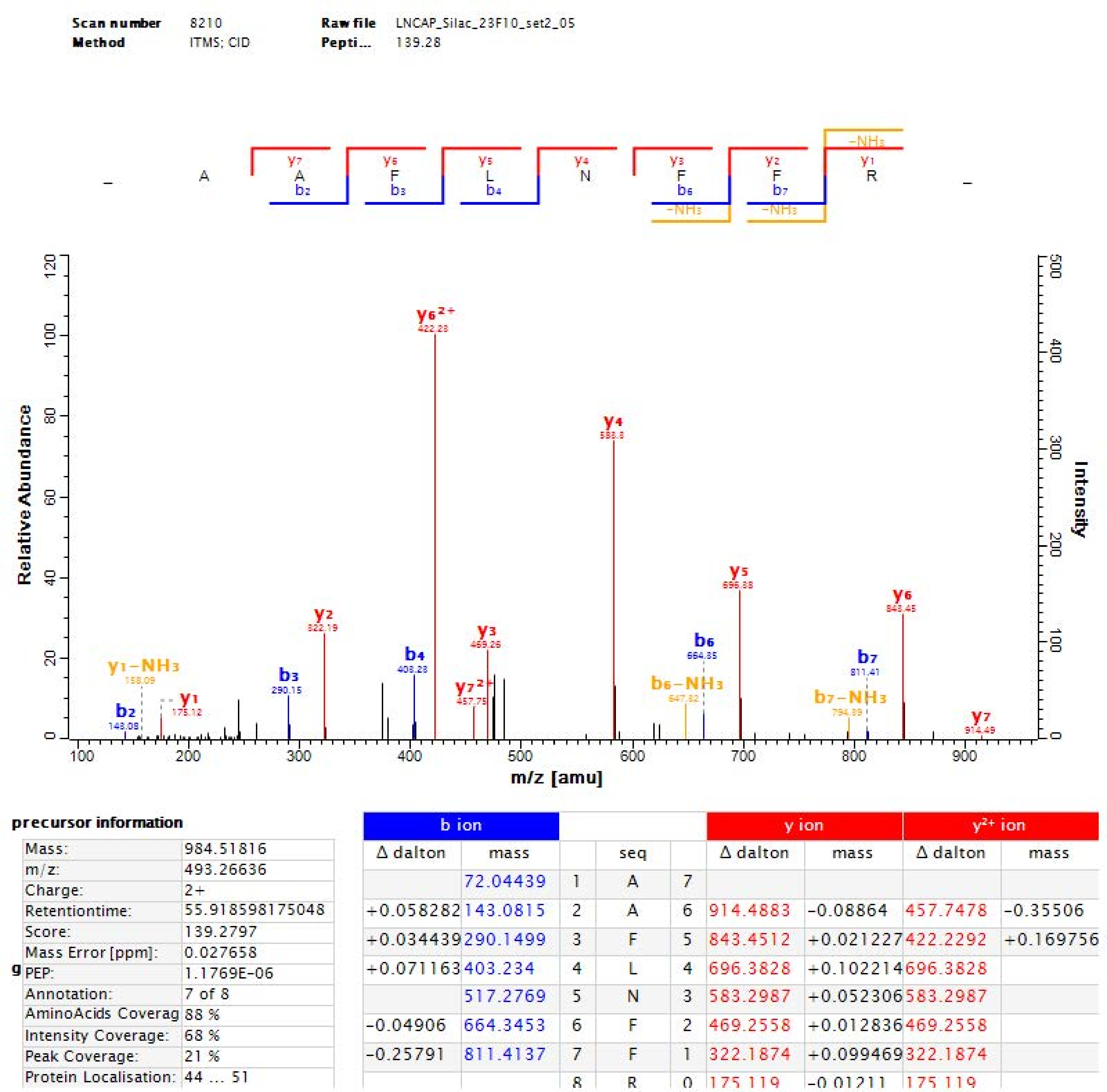
precursor information

Mass:	2277.26955
m/z:	760.09713
Charge:	3+
Retentiontime:	53.021354675293
Score:	69.08141
Mass Error [ppm]:	0.13482
PEP:	0.0005511
Precursor Type:	MULTI

general information

Annotation:	10 of 21
AminoAcids Coverag	48 %
Intensity Coverage:	42 %
Peak Coverage:	20 %
Protein Localisation:	307 ... 327

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	20				
	227.18		227.18	2	L	19	2177.2		2177.2	
	314.21		314.21	3	S	18	2064.1		2064.1	
	476.33		476.33	4	R	17	1977.1		1977.1	
	573.38		573.38	5	P	16	1815		908	+0.1812
	701.44		701.44	6	Q	15	1717.9		1717.9	
	816.47		816.47	7	D	14	1589.9		1589.9	
	915.54		915.54	8	V	13	1474.9		1474.9	
-0.139	514.81		1028.6	9	L	12	1375.8		1375.8	
	1157.7		1157.7	10	E	11	1262.7		1262.7	
	1214.7		1214.7	11	G	10	1133.7		567.33	-0.008
+0.0384	657.38	-0.06	1313.8	12	V	9	1076.6		1076.6	
+0.0354	706.91		1412.8	13	V	8	977.57	+0.0102	977.57	
	1525.9		1525.9	14	L	7	878.5	-0.049	439.76	+0.4365
+0.1033	806.97	+0.0141	1612.9	15	S	6	765.42		765.42	
	1710		1710	16	P	5	678.39	+0.0499	678.39	
	1797		1797	17	S	4	581.33		581.33	
	1910.1		1910.1	18	L	3	494.3		494.3	
-0.451	1020.1		2039.1	19	E	2	381.22	+0.0208	381.22	
	2110.2		2110.2	20	A	1	252.18	+0.1182	252.18	
				21	R	0	181.14		181.14	



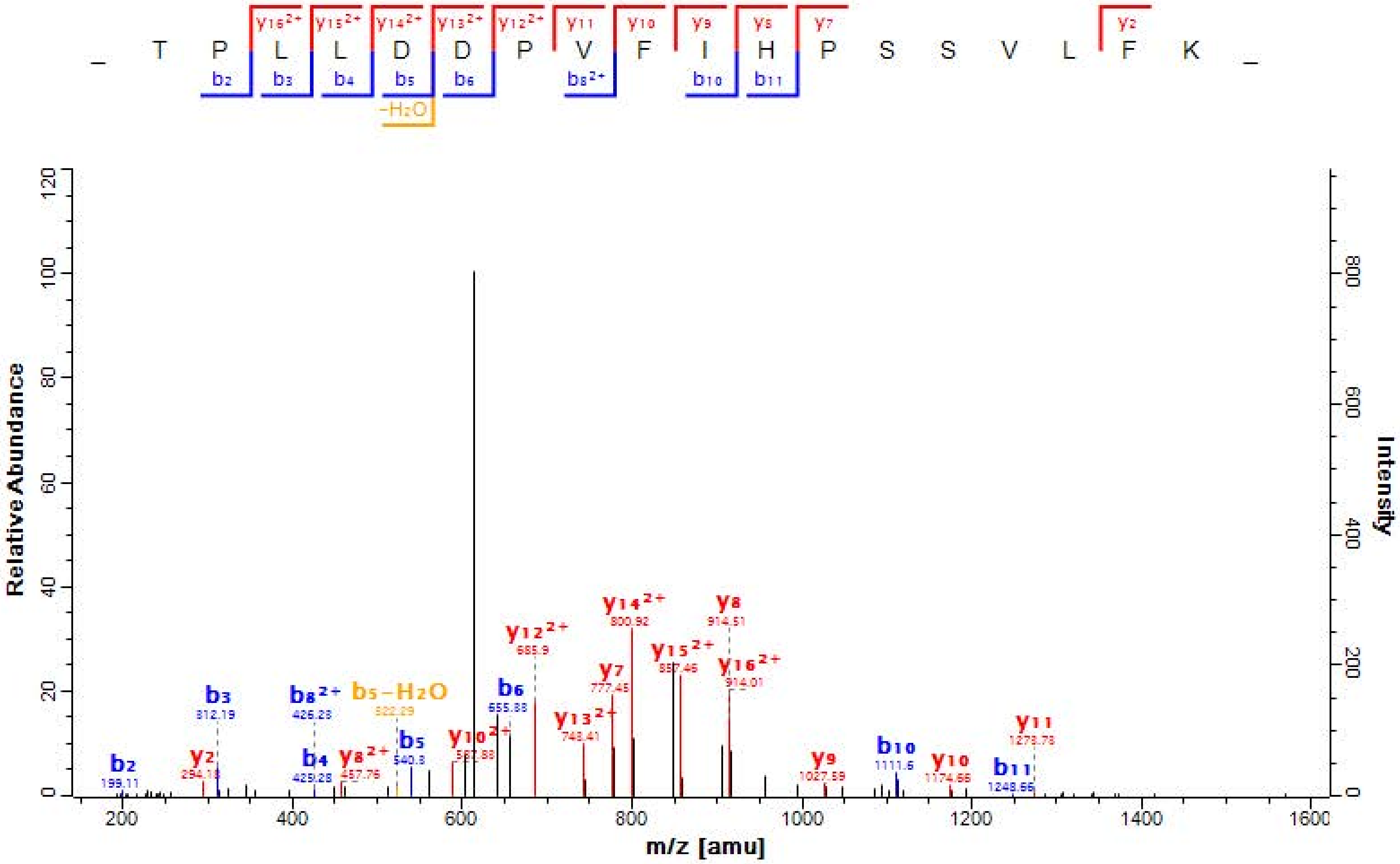
Scan number	8210	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	139.28

precursor information

Mass:	984.51816
m/z:	493.26636
Charge:	2+
Retentiontime:	55.918598175048
Score:	139.2797
Mass Error [ppm]:	0.027658
PEP:	1.1769E-06
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	68 %
Peak Coverage:	21 %
Protein Localisation:	44 ... 51

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	7				
+0.058282	143.0815	2	A	6	914.4883	-0.08864	457.7478	-0.35506
+0.034439	290.1499	3	F	5	843.4512	+0.021227	422.2292	+0.169756
+0.071163	403.234	4	L	4	696.3828	+0.102214	696.3828	
	517.2769	5	N	3	583.2987	+0.052306	583.2987	
-0.04906	664.3453	6	F	2	469.2558	+0.012836	469.2558	
-0.25791	811.4137	7	F	1	322.1874	+0.099469	322.1874	
		8	R	0	175.119	-0.01211	175.119	

Scan number	8712	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	139.65



precursor information

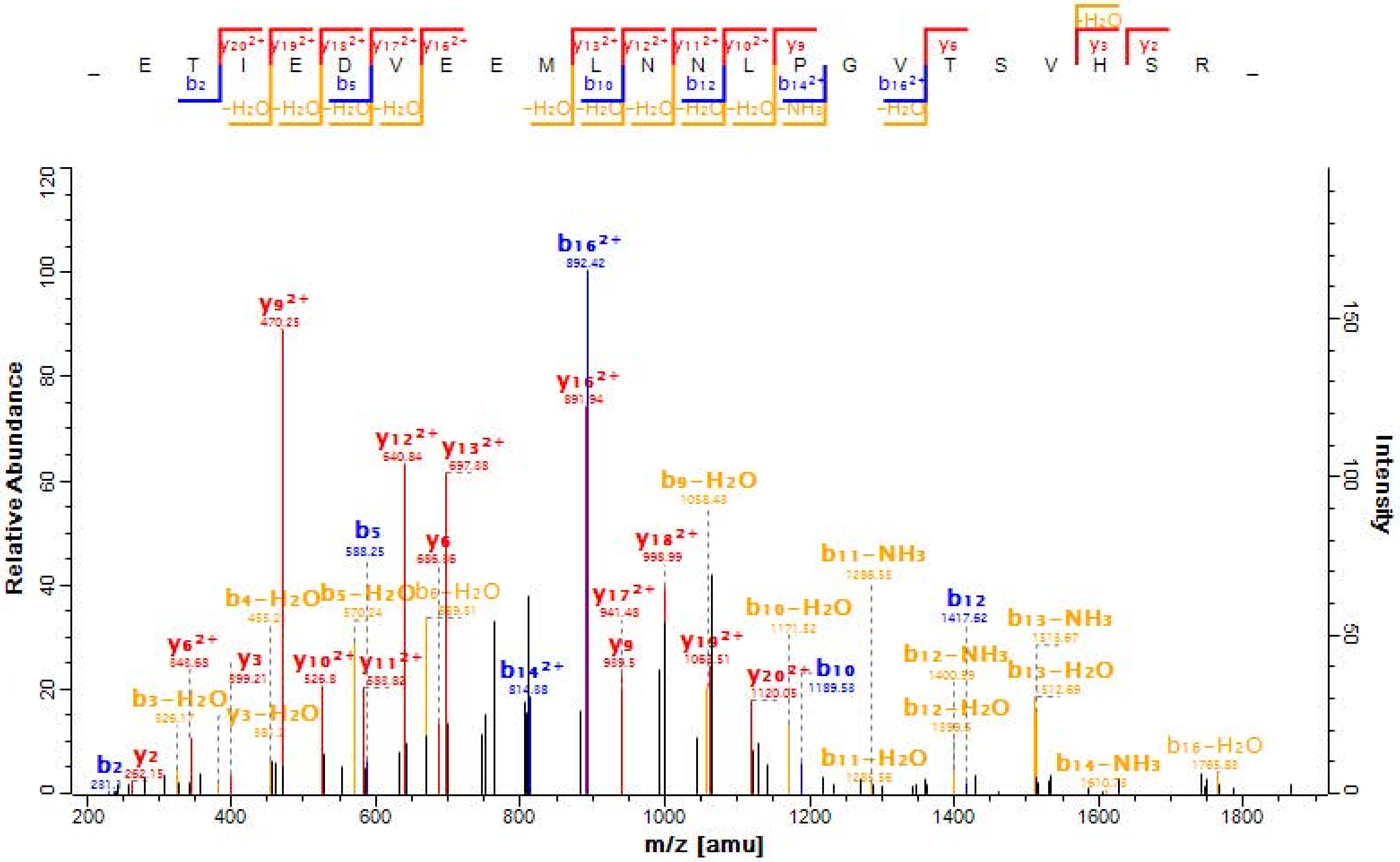
Mass:	2024.09809
m/z:	675.70664
Charge:	3+
Retentiontime:	60.425247192382
Score:	139.6463
Mass Error [ppm]:	-0.086907
PEP:	2.908E-17
Precursor Type:	MULTI

general information

Annotation:	12 of 18
AminoAcids Coverag	67 %
Intensity Coverage:	38 %
Peak Coverage:	22 %
Protein Localisation:	957 ... 974

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	17				
	199.11	+0.0187	199.11	2	P	16	1924.1		1924.1	
	312.19	+0.0769	312.19	3	L	15	1827		914.01	+0.009
	425.28	-0.042	425.28	4	L	14	1713.9		857.46	+0.247
	540.3	+0.1816	540.3	5	D	13	1600.8		800.92	+0.2407
	655.33	+0.1099	655.33	6	D	12	1485.8		743.41	+0.222
	752.38		752.38	7	P	11	1370.8		685.9	+0.2727
-0.03	426.23		851.45	8	V	10	1273.7	-0.001	1273.7	
	998.52		998.52	9	F	9	1174.7	-0.011	587.83	+0.28
	1111.6	-0.085	1111.6	10	I	8	1027.6	-0.16	1027.6	
	1248.7	-0.052	1248.7	11	H	7	914.51	+0.1314	457.76	-0.043
	1345.7		1345.7	12	P	6	777.45	-0.003	777.45	
	1432.7		1432.7	13	S	5	680.4		680.4	
	1519.8		1519.8	14	S	4	593.37		593.37	
	1618.8		1618.8	15	V	3	506.33		506.33	
	1731.9		1731.9	16	L	2	407.27		407.27	
	1879		1879	17	F	1	294.18	-0.066	294.18	
				18	K	0	147.11		147.11	

Scan number	9113	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	142.39



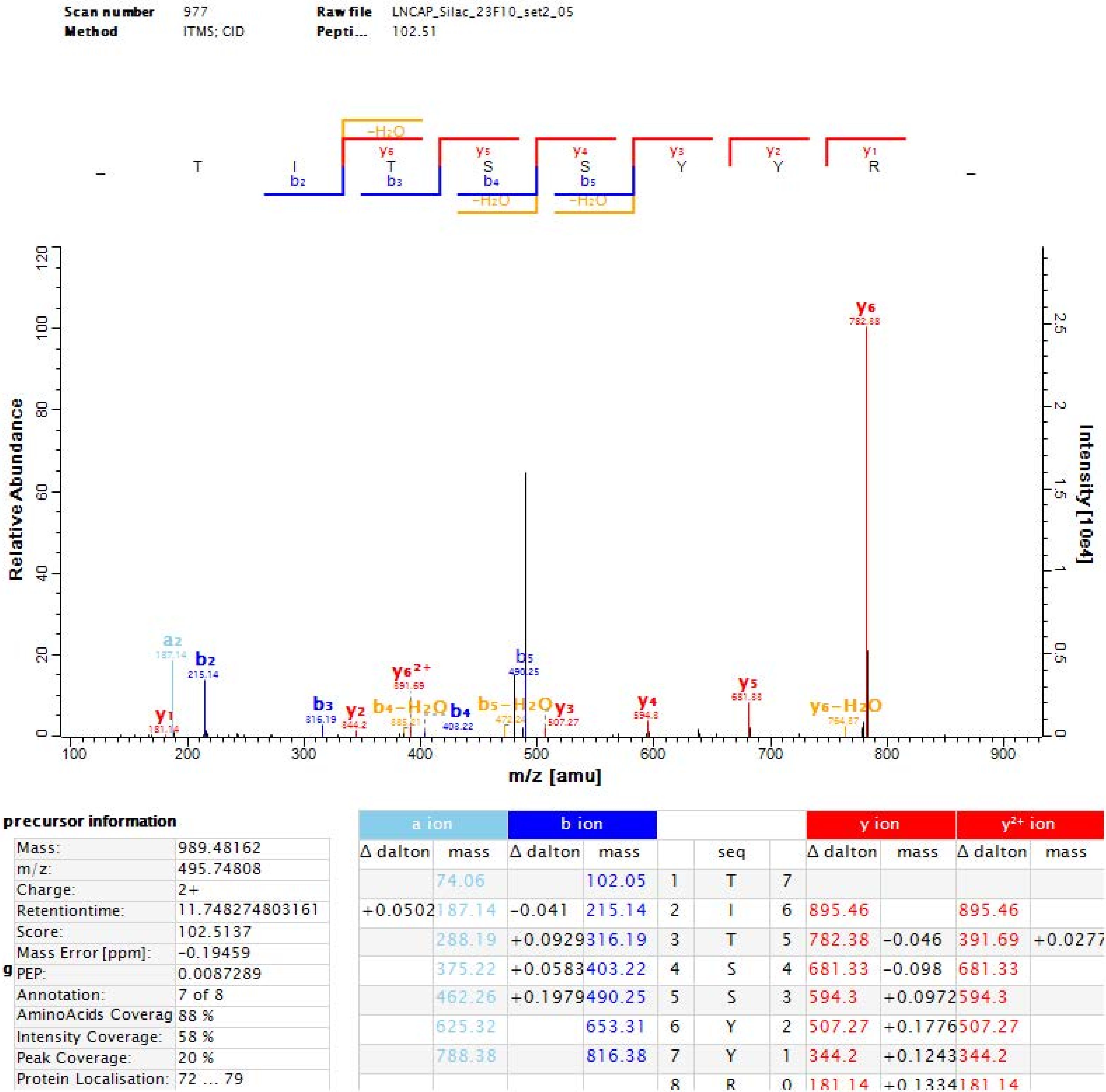
precursor information

Mass:	2468.18465
m/z:	823.73549
Charge:	3+
Retentiontime:	64.338180541992
Score:	142.3905
Mass Error [ppm]:	-0.27243
PEP:	8.3846E-21
Precursor Type:	MULTI

general information

Annotation:	16 of 22
AminoAcids Coverag	73 %
Intensity Coverage:	62 %
Peak Coverage:	37 %
Protein Localisation:	133 ... 154

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	21				
	231.1	+0.0917	231.1	2	T	20	2340.2		2340.2	
	344.18		344.18	3	I	19	2239.1		1120.1	+0.2272
	473.22		473.22	4	E	18	2126		1063.5	-0.168
	588.25	-0.144	588.25	5	D	17	1997		998.99	+0.1435
	687.32		687.32	6	V	16	1881.9		941.48	+0.0247
	816.36		816.36	7	E	15	1782.9		891.94	+0.0288
	945.4		945.4	8	E	14	1653.8		1653.8	
	1076.4		1076.4	9	M	13	1524.8		1524.8	
	1189.5	-0.291	1189.5	10	L	12	1393.8		697.38	+0.2273
	1303.6		1303.6	11	N	11	1280.7		640.84	+0.2264
	1417.6	-0.007	1417.6	12	N	10	1166.6		583.82	+0.0233
	1530.7		1530.7	13	L	9	1052.6		526.8	+0.0556
-0.217	814.38		1627.8	14	P	8	939.5	+0.0201	470.25	+0.266
	1684.8		1684.8	15	G	7	842.45		842.45	
+0.3013	892.42		1783.8	16	V	6	785.43		785.43	
	1884.9		1884.9	17	T	5	686.36	-0.003	343.68	+0.146
	1971.9		1971.9	18	S	4	585.31		585.31	
	2071		2071	19	V	3	498.28		498.28	
	2208		2208	20	H	2	399.21	+0.0093	399.21	
	2295.1		2295.1	21	S	1	262.15	+0.0586	262.15	
				22	R	0	175.12		175.12	



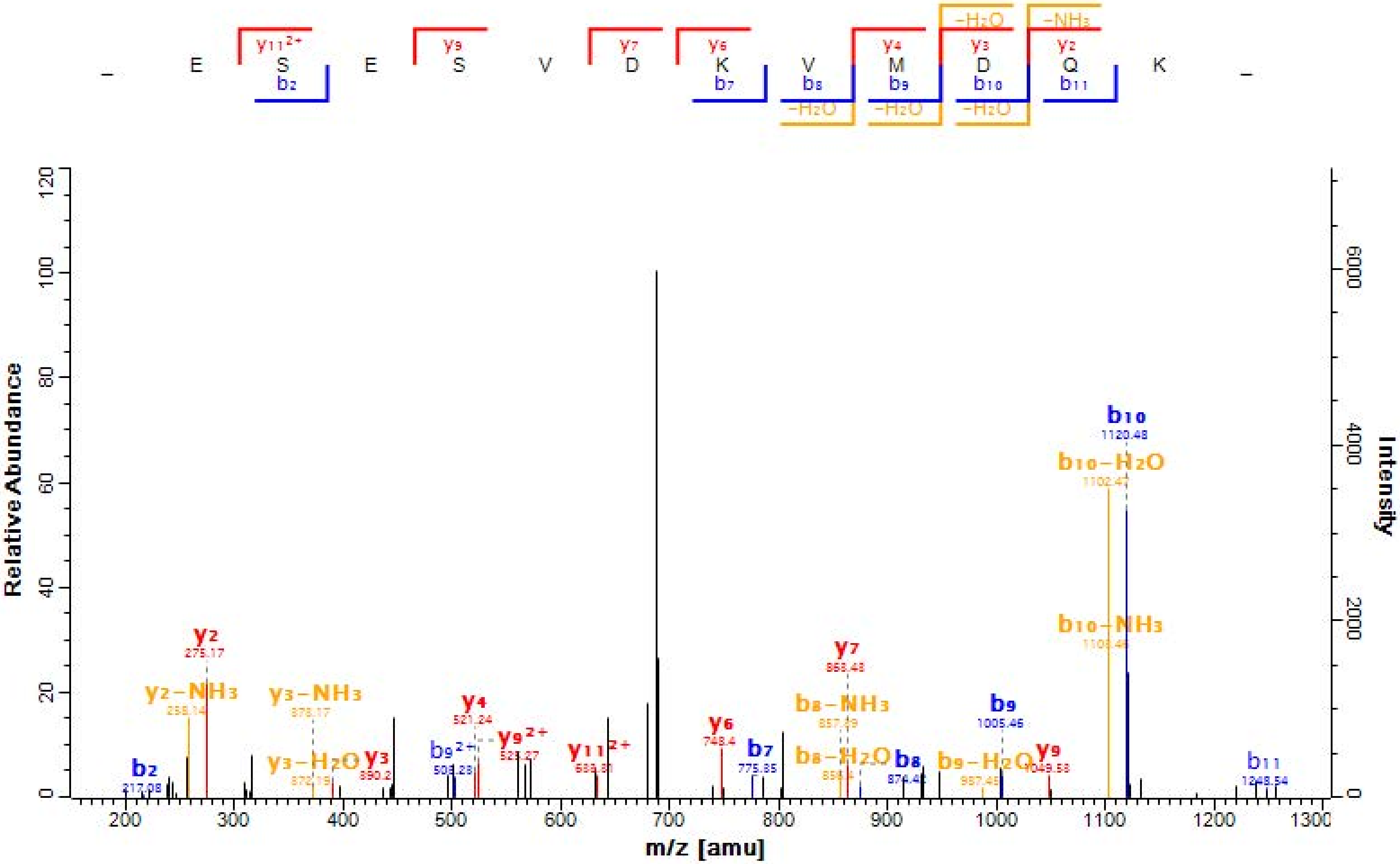
Scan number	977	**Raw file**	LNCAP_Silac_23F10_set2_05
Method	ITMS; CID	**Pepti...**	102.51

precursor information

Mass:	989.48162
m/z:	495.74808
Charge:	2+
Retentiontime:	11.748274803161
Score:	102.5137
Mass Error [ppm]:	-0.19459
PEP:	0.0087289
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	58 %
Peak Coverage:	20 %
Protein Localisation:	72 ... 79

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.05	1	T	7				
+0.0502	187.14	-0.041	215.14	2	I	6	895.46		895.46	
	288.19	+0.0929	316.19	3	T	5	782.38	-0.046	391.69	+0.0277
	375.22	+0.0583	403.22	4	S	4	681.33	-0.098	681.33	
	462.26	+0.1979	490.25	5	S	3	594.3	+0.0972	594.3	
	625.32		653.31	6	Y	2	507.27	+0.1776	507.27	
	788.38		816.38	7	Y	1	344.2	+0.1243	344.2	
				8	R	0	181.14	+0.1334	181.14	

Scan number	1005	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	140.14



precursor information

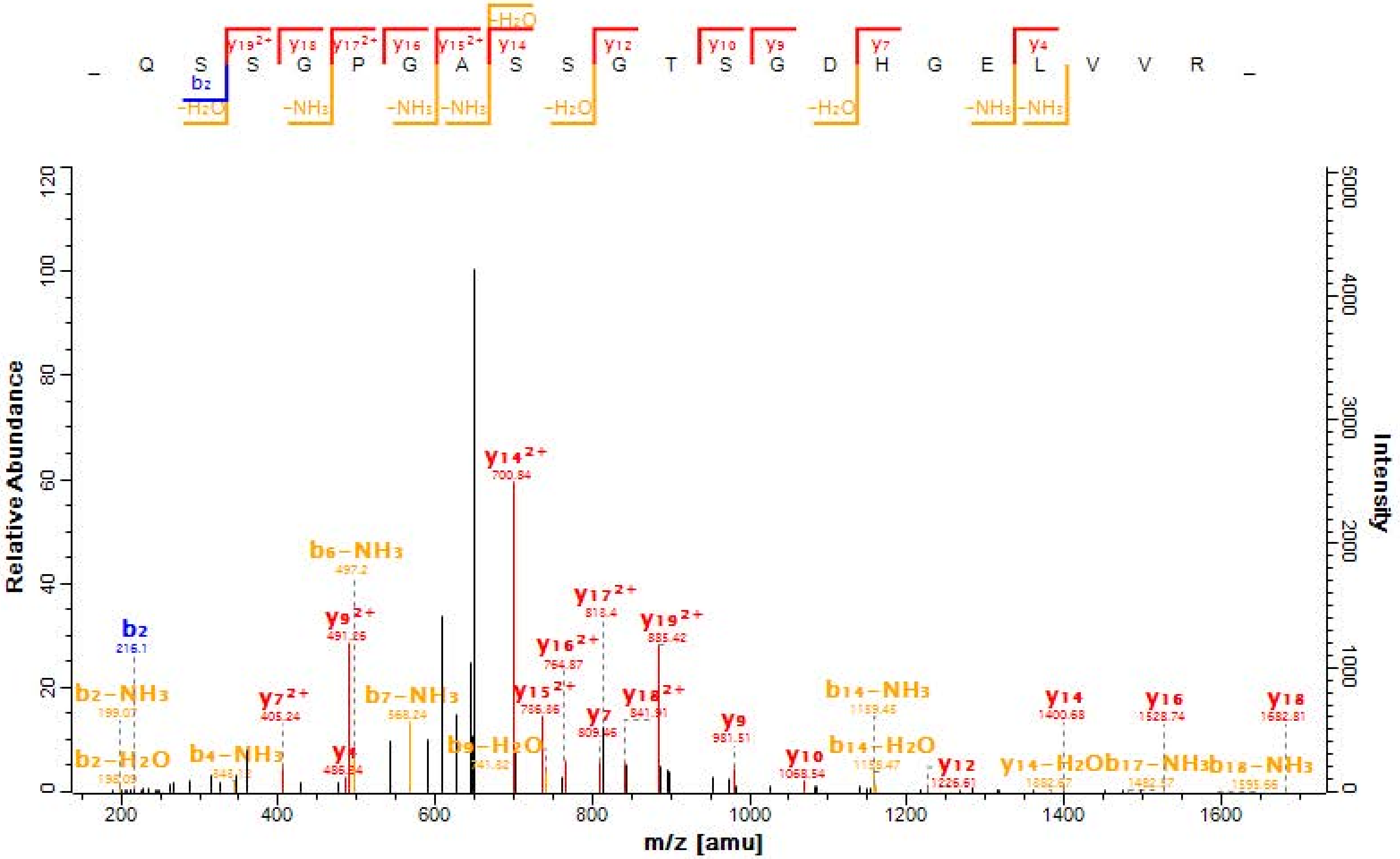
Mass:	1393.6397
m/z:	697.82713
Charge:	2+
Retentiontime:	11.145038604736
Score:	140.1416
Mass Error [ppm]:	0.13541
PEP:	1.5086E-05
Precursor Type:	MULTI

general information

Annotation:	8 of 12
AminoAcids Coverag	67 %
Intensity Coverage:	34 %
Peak Coverage:	28 %
Protein Localisation:	128 ... 139

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	11				
	217.08	+0.1281	217.08	2	S	10	1265.6		633.31	+0.1211
	346.12		346.12	3	E	9	1178.6		1178.6	
	433.16		433.16	4	S	8	1049.5	+0.0322	525.27	-0.001
	532.22		532.22	5	V	7	962.5		962.5	
	647.25		647.25	6	D	6	863.43	-0.032	863.43	
	775.35	+0.028	775.35	7	K	5	748.4	-0.034	748.4	
	874.42	+0.0814	874.42	8	V	4	620.31		620.31	
+0.0582	503.23	+0.0661	1005.5	9	M	3	521.24	+0.1505	521.24	
	1120.5	-0.017	1120.5	10	D	2	390.2	-0.004	390.2	
	1248.5	-0.067	1248.5	11	Q	1	275.17	+0.0095	275.17	
				12	K	0	147.11		147.11	

Scan number	1022	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	80.32



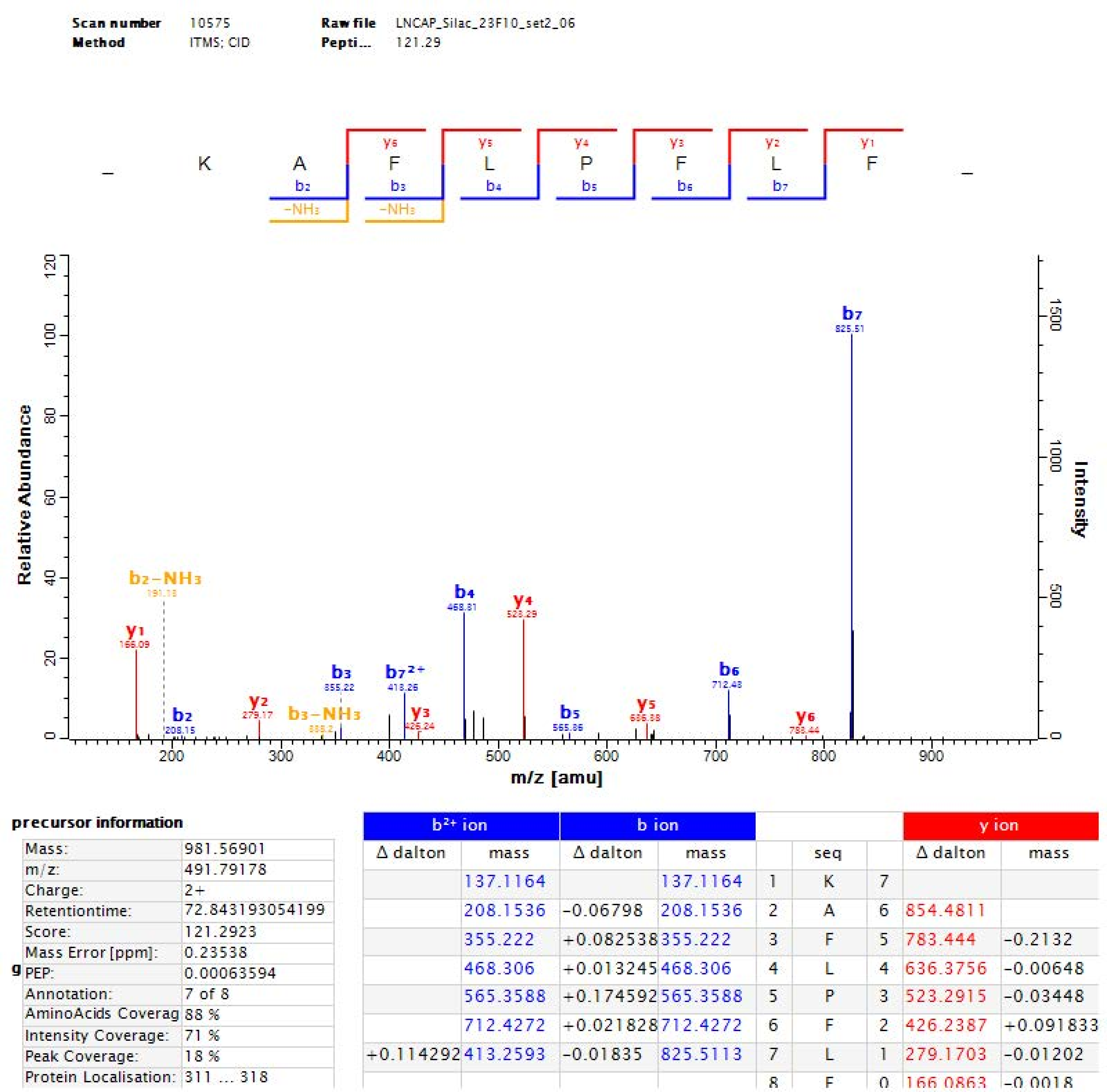
precursor information

Mass:	1983.92452
m/z:	662.31545
Charge:	3+
Retentiontime:	11.235930442810
Score:	80.31623
Mass Error [ppm]:	-0.044967
PEP:	0.00022135
Precursor Type:	MULTI

general information

Annotation:	15 of 21
AminoAcids Coverag	71 %
Intensity Coverage:	39 %
Peak Coverage:	27 %
Protein Localisation:	39 ... 59

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.0659	1	Q	20				
+0.426623	216.0979	2	S	19	1856.873		1856.873	
	303.1299	3	S	18	1769.841		885.4243	+0.259804
	360.1514	4	G	17	1682.809	+0.058058	841.9083	-0.08618
	457.2041	5	P	16	1625.788		813.3975	-0.0168
	514.2256	6	G	15	1528.735	-0.13029	764.8712	+0.222539
	585.2627	7	A	14	1471.714		736.3604	+0.322626
	672.2947	8	S	13	1400.676	+0.146429	700.8419	+0.243282
	759.3268	9	S	12	1313.644		1313.644	
	816.3482	10	G	11	1226.612	-0.09152	1226.612	
	917.3959	11	T	10	1169.591		1169.591	
	1004.428	12	S	9	1068.543	-0.06681	1068.543	
	1061.449	13	G	8	981.5112	+0.098339	491.2592	+0.150969
	1176.476	14	D	7	924.4898		924.4898	
	1313.535	15	H	6	809.4628	+0.056719	405.235	+0.145204
	1370.557	16	G	5	672.4039		672.4039	
	1499.599	17	E	4	615.3824		615.3824	
	1612.683	18	L	3	486.3398	+0.095337	486.3398	
	1711.752	19	V	2	373.2558		373.2558	
	1810.82	20	V	1	274.1874		274.1874	
		21	R	0	175.119		175.119	

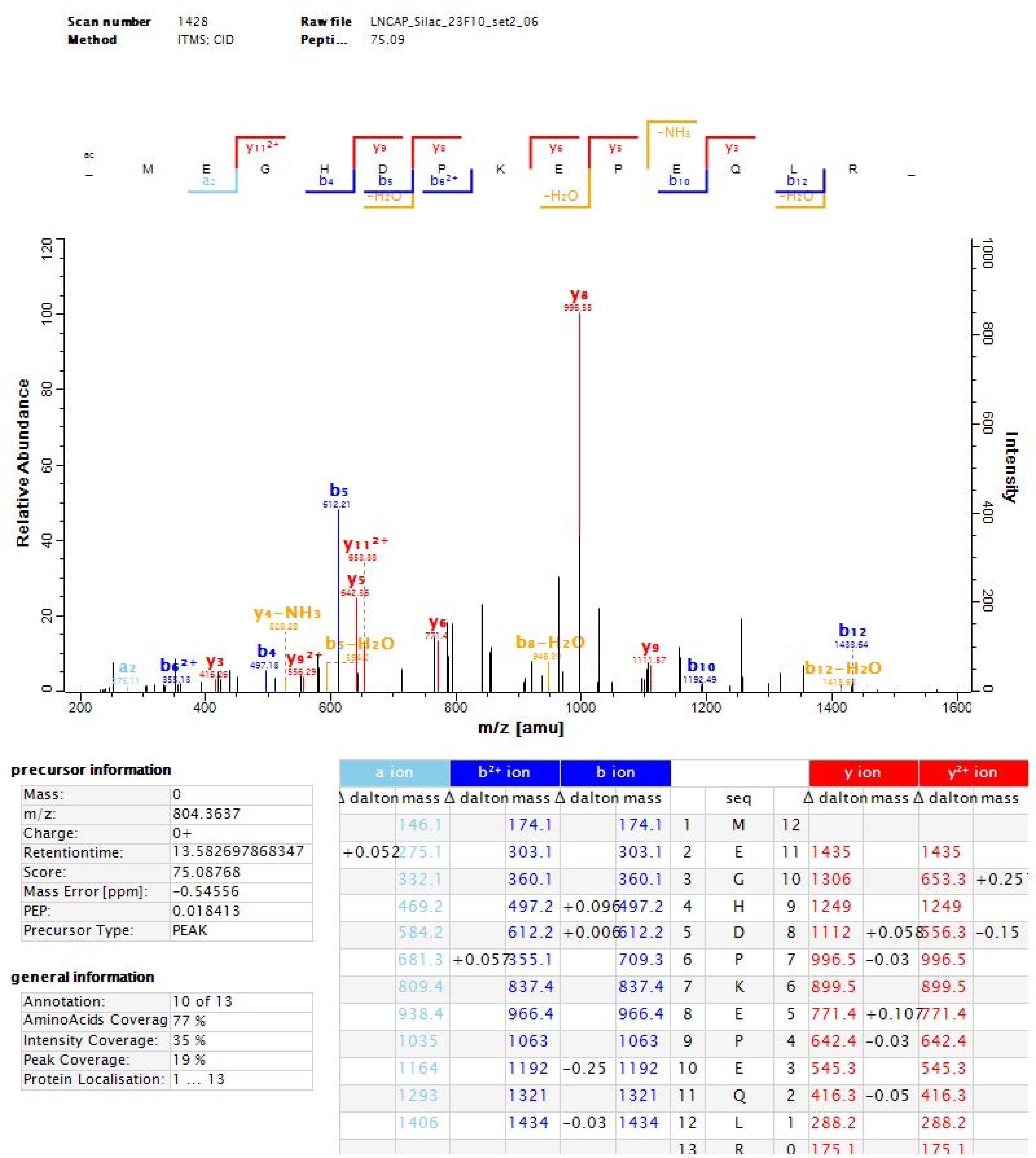


Scan number	10575	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	121.29

precursor information

Mass:	981.56901
m/z:	491.79178
Charge:	2+
Retentiontime:	72.843193054199
Score:	121.2923
Mass Error [ppm]:	0.23538
PEP:	0.00063594
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	71 %
Peak Coverage:	18 %
Protein Localisation:	311 ... 318

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	137.1164		137.1164	1	K	7		
	208.1536	-0.06798	208.1536	2	A	6	854.4811	
	355.222	+0.082538	355.222	3	F	5	783.444	-0.2132
	468.306	+0.013245	468.306	4	L	4	636.3756	-0.00648
	565.3588	+0.174592	565.3588	5	P	3	523.2915	-0.03448
	712.4272	+0.021828	712.4272	6	F	2	426.2387	+0.091833
+0.114292	413.2593	-0.01835	825.5113	7	L	1	279.1703	-0.01202
				8	F	0	166.0863	-0.0018



Scan number	1428	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	75.09

precursor information

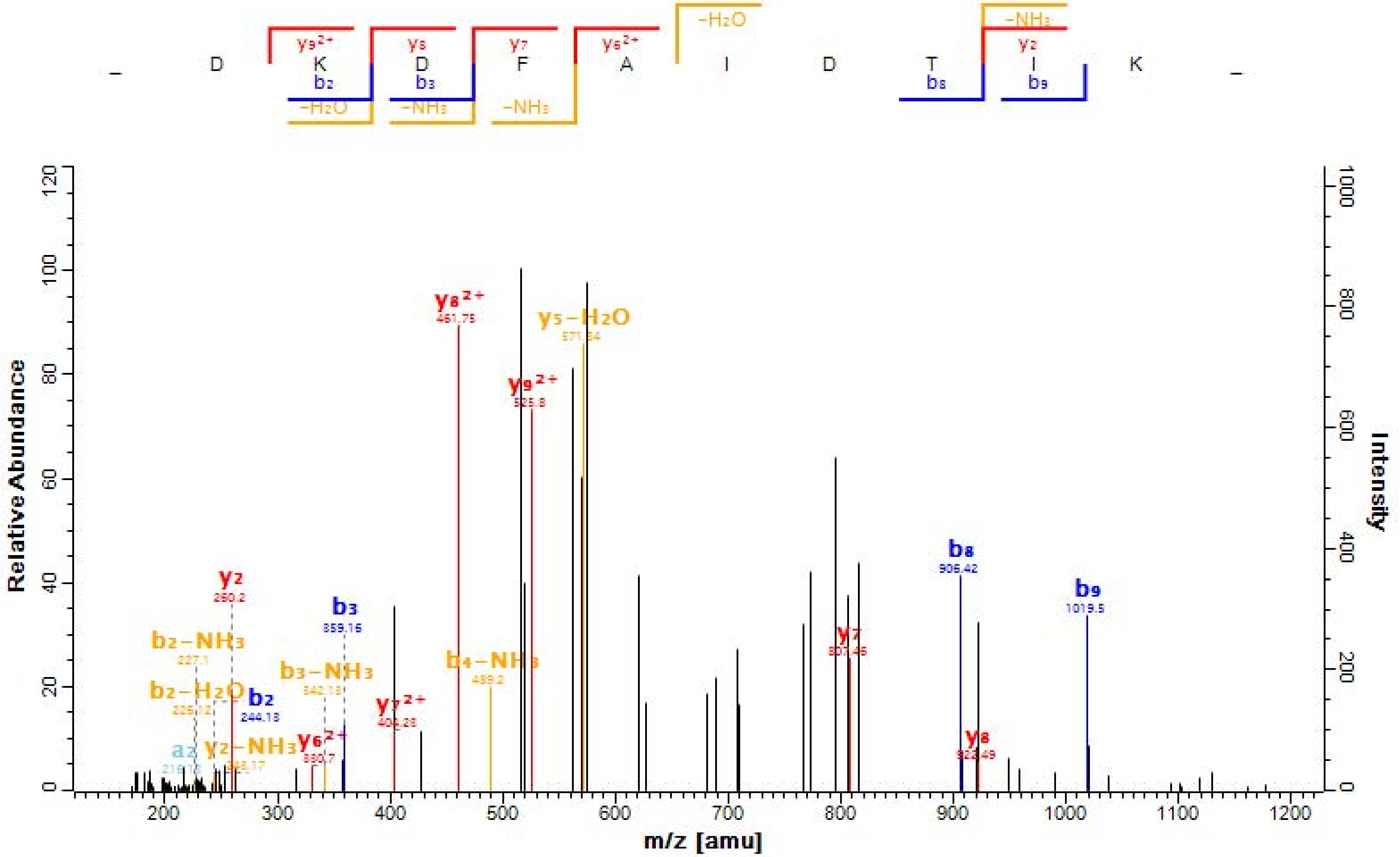
Mass:	0
m/z:	804.3637
Charge:	0+
Retentiontime:	13.582697868347
Score:	75.08768
Mass Error [ppm]:	-0.54556
PEP:	0.018413
Precursor Type:	PEAK

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	35 %
Peak Coverage:	19 %
Protein Localisation:	1 … 13

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	146.1		174.1		174.1	1	M	12				
+0.052	275.1		303.1		303.1	2	E	11	1435		1435	
	332.1		360.1		360.1	3	G	10	1306		653.3	+0.25
	469.2		497.2	+0.096	497.2	4	H	9	1249		1249	
	584.2		612.2	+0.006	612.2	5	D	8	1112	+0.058	556.3	-0.15
	681.3	+0.057	355.1		709.3	6	P	7	996.5	-0.03	996.5	
	809.4		837.4		837.4	7	K	6	899.5		899.5	
	938.4		966.4		966.4	8	E	5	771.4	+0.107	771.4	
	1035		1063		1063	9	P	4	642.4	-0.03	642.4	
	1164		1192	-0.25	1192	10	E	3	545.3		545.3	
	1293		1321		1321	11	Q	2	416.3	-0.05	416.3	
	1406		1434	-0.03	1434	12	L	1	288.2		288.2	
						13	R	0	175.1		175.1	

Scan number	1535	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	57.35



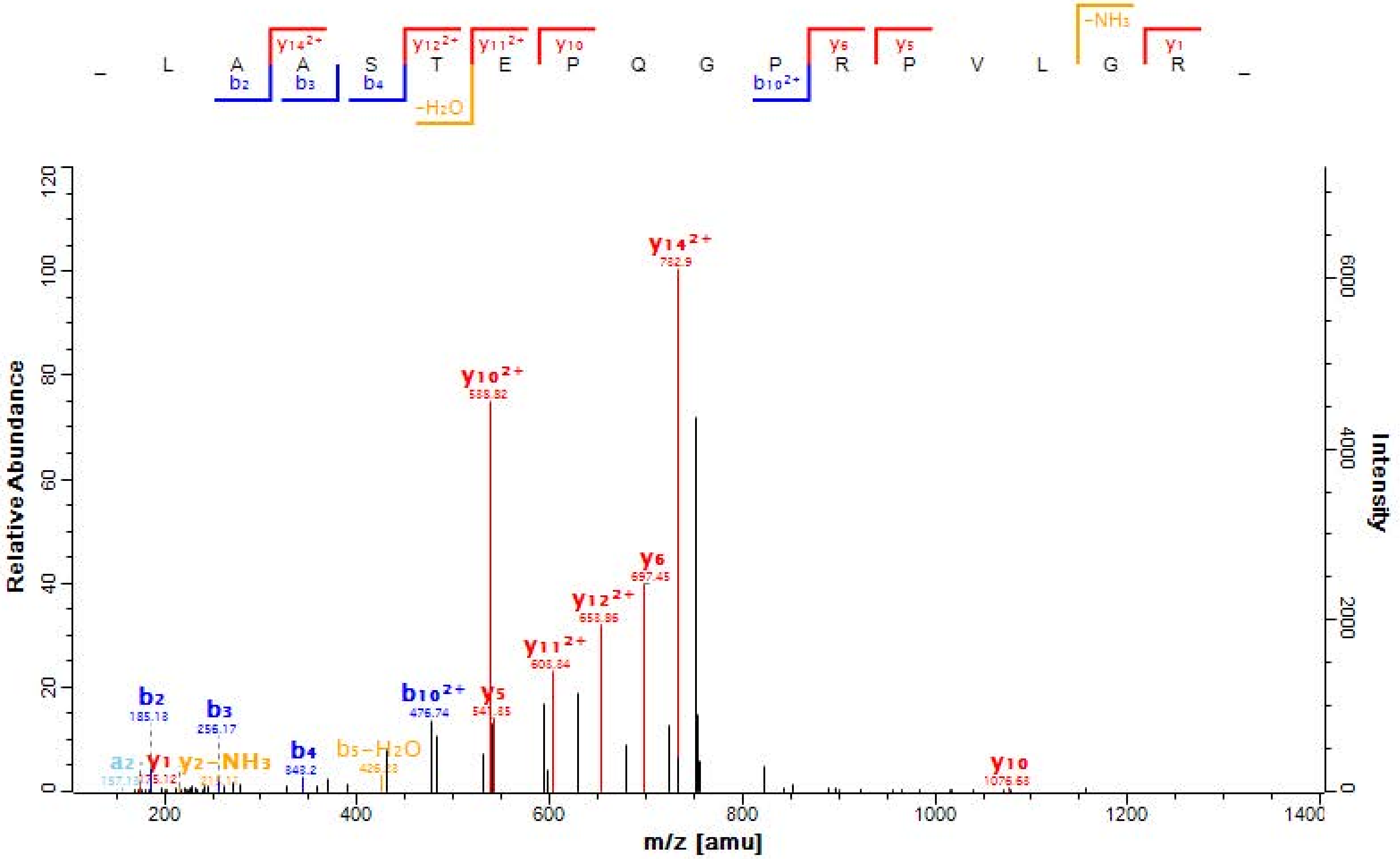
precursor information

Mass:	1164.60226
m/z:	583.30841
Charge:	2+
Retentiontime:	14.193103790283
Score:	57.3472
Mass Error [ppm]:	-0.33858
PEP:	0.019943
Precursor Type:	MULTI

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	30 %
Peak Coverage:	19 %
Protein Localisation:	154 ... 163

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	9				
+0.4106	216.13	+0.3153	244.13	2	K	8	1050.6		525.8	+0.291
	331.16	+0.0752	359.16	3	D	7	922.49	+0.1597	461.75	-0.351
	478.23		506.22	4	F	6	807.46	-0.064	404.23	+0.114
	549.27		577.26	5	A	5	660.39		330.7	-0.488
	662.35		690.35	6	I	4	589.36		589.36	
	777.38		805.37	7	D	3	476.27		476.27	
	878.43	-0.02	906.42	8	T	2	361.24		361.24	
	991.51	+0.0041	1019.5	9	I	1	260.2	-0.089	260.2	
				10	K	0	147.11		147.11	

Scan number	1612	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	90.93



precursor information

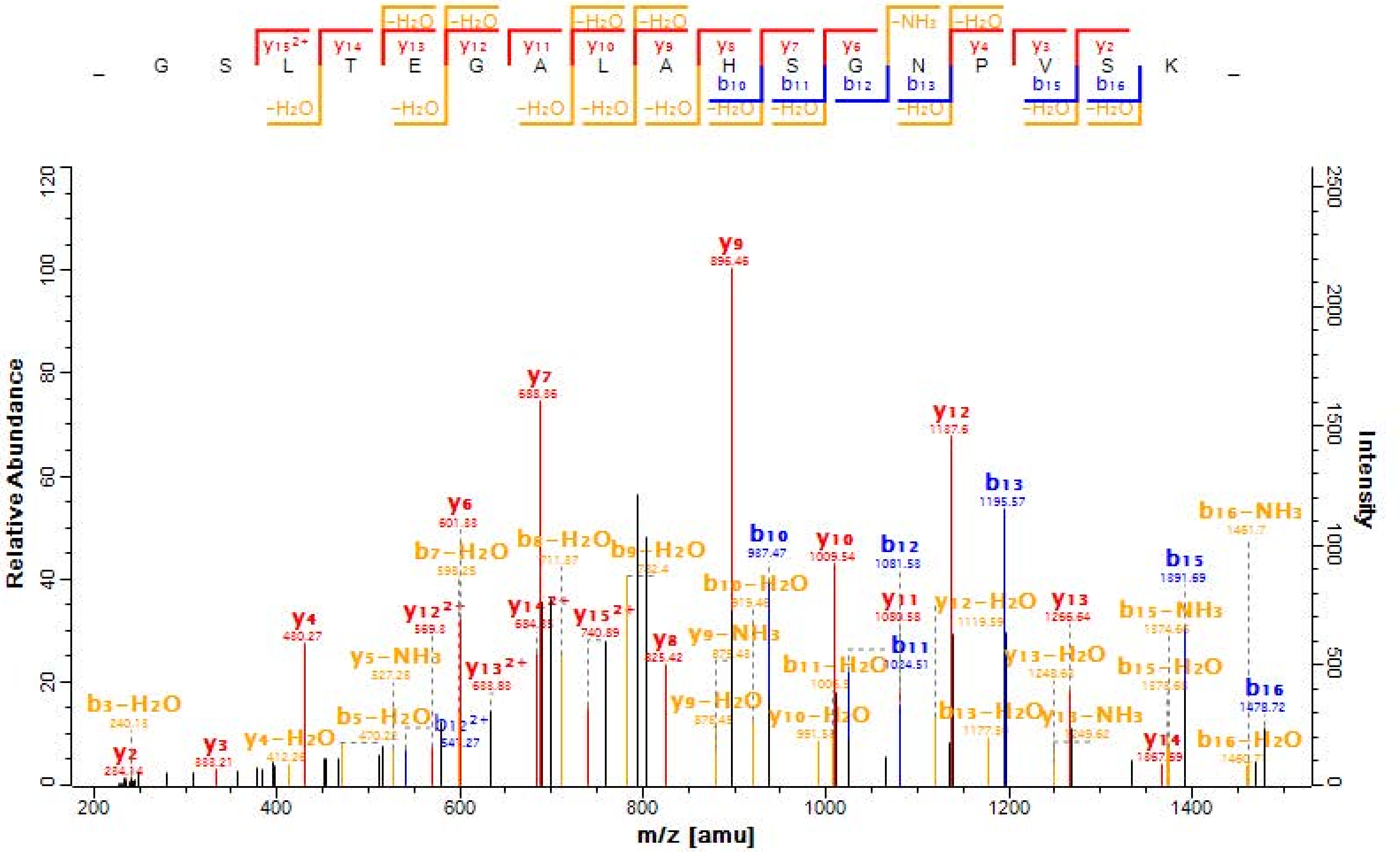
Mass:	1647.90545
m/z:	550.30909
Charge:	3+
Retentiontime:	14.611180305481
Score:	90.92576
Mass Error [ppm]:	-0.12569
PEP:	3.0455E-05
Precursor Type:	MULTI

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	54 %
Peak Coverage:	16 %
Protein Localisation:	4 ... 19

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	15				
-0.15	157.1		185.1	-0.08	185.1	2	A	14	1536		1536	
	228.2		256.2	-0.1	256.2	3	A	13	1465		732.9	+0.23
	315.2		343.2	-0.02	343.2	4	S	12	1394		1394	
	416.3		444.2		444.2	5	T	11	1307		653.9	+0.29
	545.3		573.3		573.3	6	E	10	1206		603.3	+0.18
	642.3		670.3		670.3	7	P	9	1077	+0.167	538.8	+0.01
	770.4		798.4		798.4	8	Q	8	979.6		979.6	
	827.4		855.4		855.4	9	G	7	851.5		851.5	
	924.5	-0.24	476.7		952.5	10	P	6	794.5		794.5	
	1081		1109		1109	11	R	5	697.4	+0.197	697.4	
	1178		1206		1206	12	P	4	541.3	+0.102	541.3	
	1277		1305		1305	13	V	3	444.3		444.3	
	1390		1418		1418	14	L	2	345.2		345.2	
	1447		1475		1475	15	G	1	232.1		232.1	
						16	R	0	175.1	+0.053	175.1	

Scan number	1755	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	233.78



precursor information

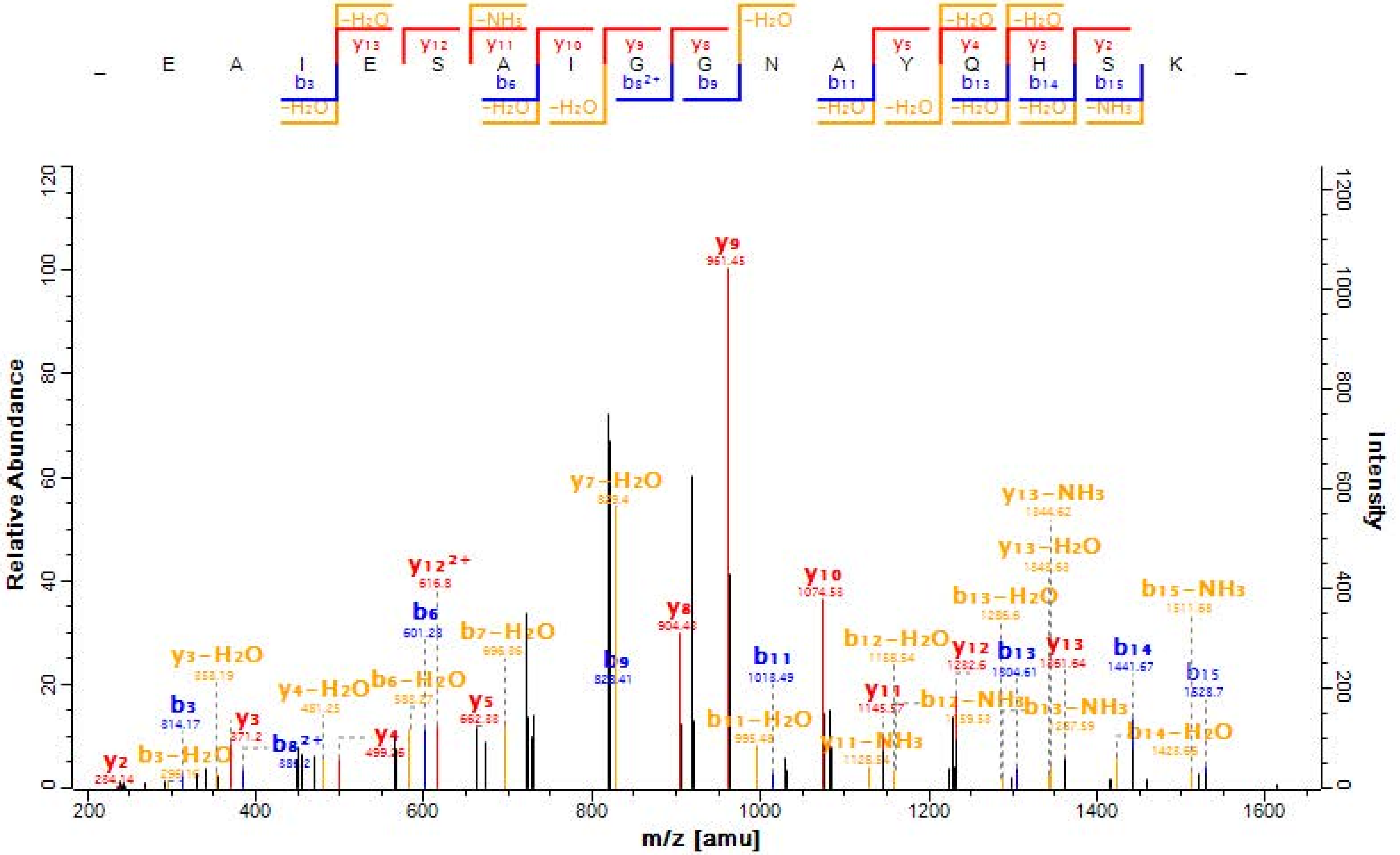
Mass:	1623.82178
m/z:	812.91817
Charge:	2+
Retentiontime:	15.384973526001
Score:	233.7795
Mass Error [ppm]:	0.081566
PEP:	6.174E-57
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	62 %
Peak Coverage:	48 %
Protein Localisation:	897 ... 913

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	16				
	145.06		145.06	2	S	15	1567.8		1567.8	
	258.14		258.14	3	L	14	1480.8		740.89	-0.146
	359.19		359.19	4	T	13	1367.7	-0.192	684.35	+0.2725
	488.24		488.24	5	E	12	1266.6	+0.0353	633.83	-0.089
	545.26		545.26	6	G	11	1137.6	+0.008	569.3	+0.115
	616.29		616.29	7	A	10	1080.6	+0.1173	1080.6	
	729.38		729.38	8	L	9	1009.5	-0.018	1009.5	
	800.41		800.41	9	A	8	896.46	-0.073	896.46	
	937.47	-0.016	937.47	10	H	7	825.42	-0.017	825.42	
	1024.5	+0.0748	1024.5	11	S	6	688.36	-0.008	688.36	
-0.173	541.27	+0.0025	1081.5	12	G	5	601.33	+0.1119	601.33	
	1195.6	-0.055	1195.6	13	N	4	544.31		544.31	
	1292.6		1292.6	14	P	3	430.27	+0.0942	430.27	
	1391.7	-0.08	1391.7	15	V	2	333.21	+0.1276	333.21	
	1478.7	-0.255	1478.7	16	S	1	234.14	+0.2078	234.14	
				17	K	0	147.11		147.11	

Scan number	1846	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	169.37



precursor information

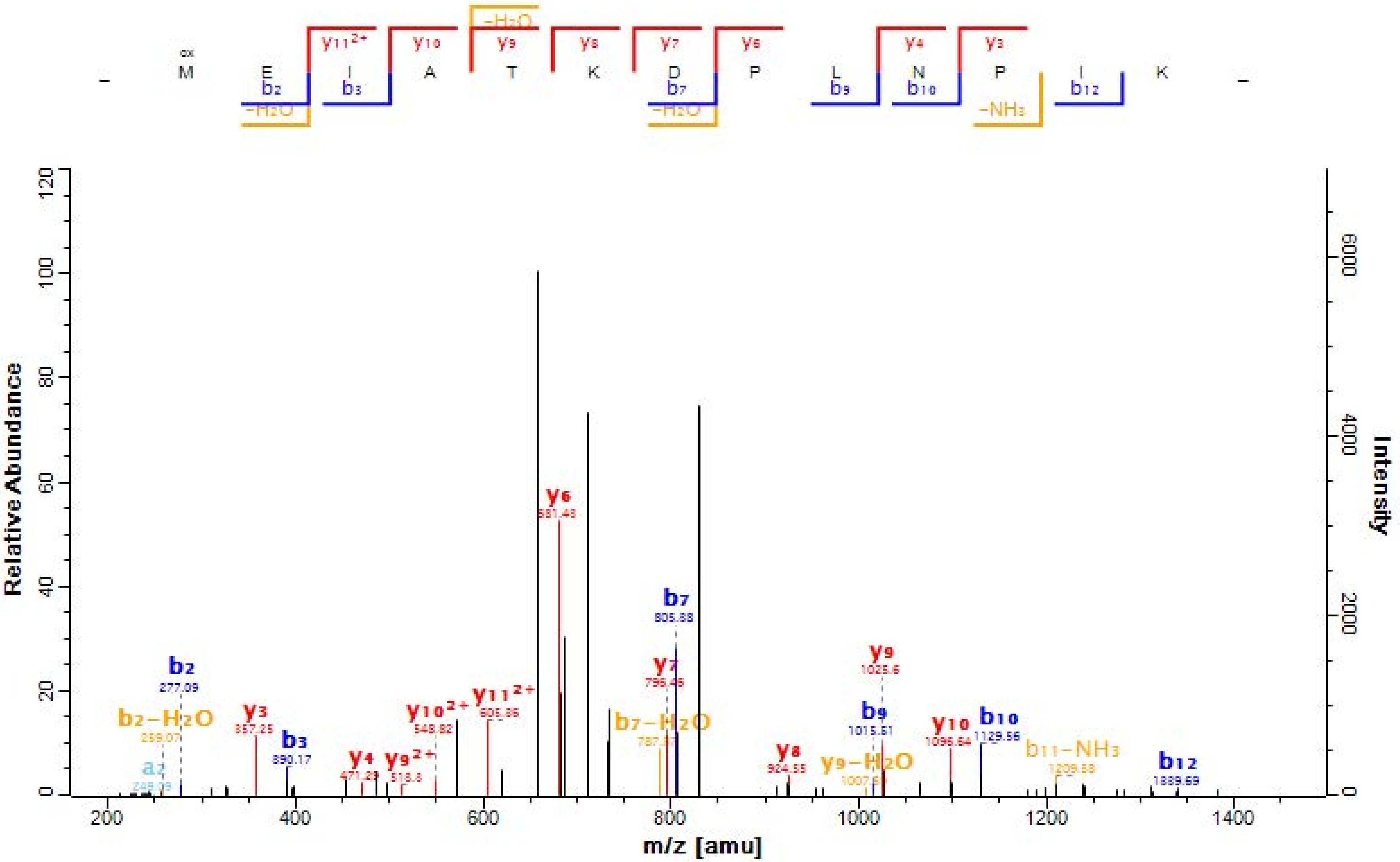
Mass:	1673.80083
m/z:	837.90769
Charge:	2+
Retentiontime:	15.880887031555
Score:	169.3689
Mass Error [ppm]:	-0.051203
PEP:	2.21E-14
Precursor Type:	ISO

general information

Annotation:	14 of 16
AminoAcids Coverag	88 %
Intensity Coverage:	42 %
Peak Coverage:	39 %
Protein Localisation:	23 ... 38

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	15				
	201.09		201.09	2	A	14	1545.8		1545.8	
	314.17	-0.034	314.17	3	I	13	1474.7		1474.7	
	443.21		443.21	4	E	12	1361.6	-0.114	1361.6	
	530.25		530.25	5	S	11	1232.6	-0.022	616.8	-0.071
	601.28	+0.0799	601.28	6	A	10	1145.6	+0.062	1145.6	
	714.37		714.37	7	I	9	1074.5	-0.036	1074.5	
-0.041	386.2		771.39	8	G	8	961.45	+0.0102	961.45	
	828.41	-0.473	828.41	9	G	7	904.43	-0.032	904.43	
	942.45		942.45	10	N	6	847.41		847.41	
	1013.5	+0.0688	1013.5	11	A	5	733.36		733.36	
	1176.6		1176.6	12	Y	4	662.33	+0.054	662.33	
	1304.6	-0.134	1304.6	13	Q	3	499.26	+0.0374	499.26	
	1441.7	-0.012	1441.7	14	H	2	371.2	+0.0321	371.2	
	1528.7	-0.226	1528.7	15	S	1	234.14	-0.269	234.14	
				16	K	0	147.11		147.11	

Scan number	2631	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	101.32



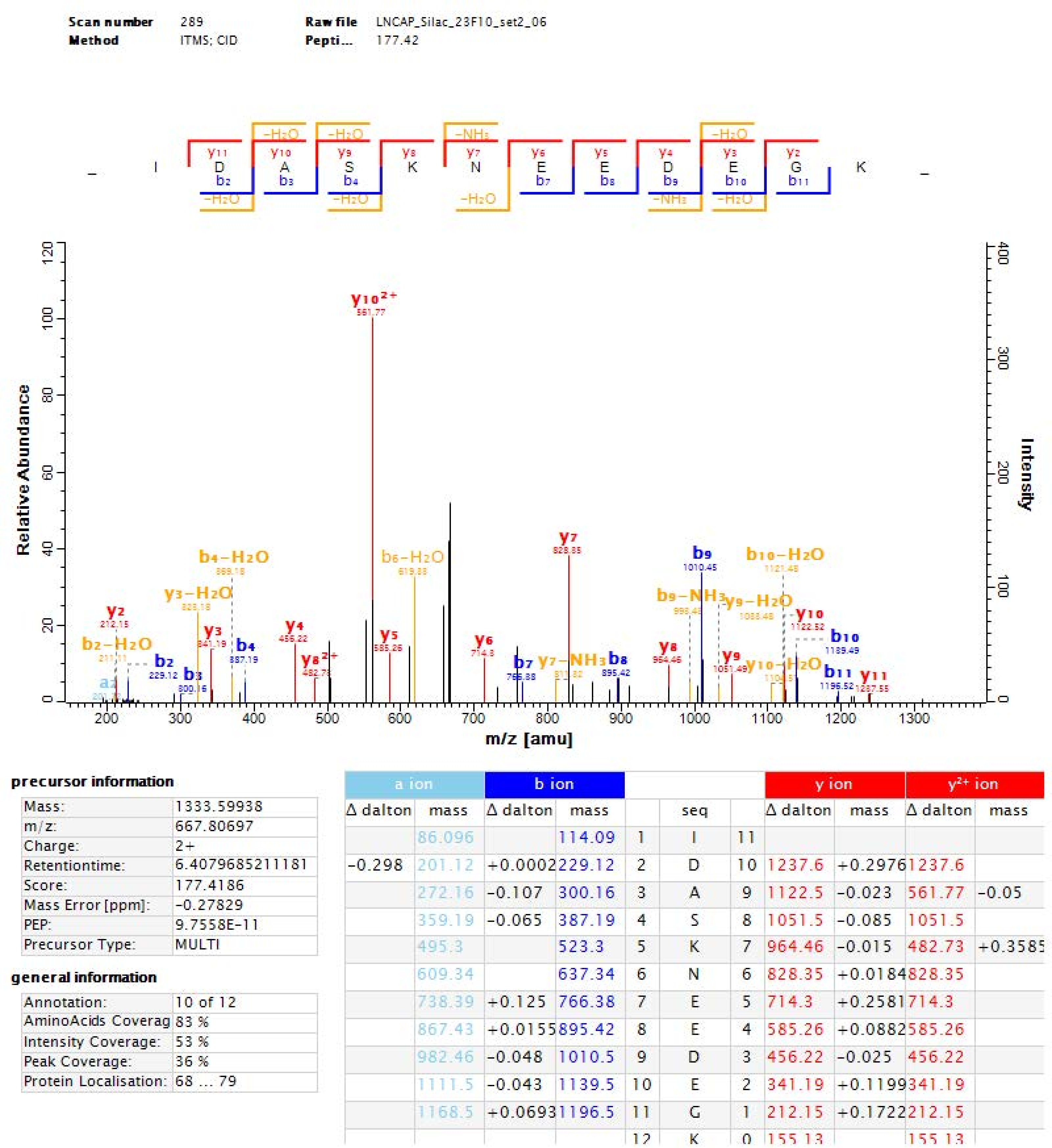
precursor information

Mass:	1484.78933
m/z:	743.40194
Charge:	2+
Retentiontime:	20.161993026733
Score:	101.3204
Mass Error [ppm]:	-1.0367
PEP:	0.00011169
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	26 %
Peak Coverage:	25 %
Protein Localisation:	58 ... 70

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.05		148.04	1	M	12				
+0.0616	249.09	+0.0887	277.09	2	E	11	1338.8		1338.8	
	362.17	+0.0669	390.17	3	I	10	1209.7		605.36	+0.2201
	433.21		461.21	4	A	9	1096.6	+0.0275	548.82	+0.0392
	534.26		562.25	5	T	8	1025.6	-0.075	513.3	+0.117
	662.35		690.35	6	K	7	924.55	+0.2172	924.55	
	777.38	+0.0381	805.38	7	D	6	796.46	+0.0323	796.46	
	874.43		902.43	8	P	5	681.43	+0.0309	681.43	
	987.52	+0.203	1015.5	9	L	4	584.38		584.38	
	1101.6	-0.009	1129.6	10	N	3	471.29	+0.1985	471.29	
	1198.6		1226.6	11	P	2	357.25	+0.1587	357.25	
	1311.7	-0.021	1339.7	12	I	1	260.2		260.2	
				13	K	0	147.11		147.11	



Scan number	289	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	177.42

precursor information

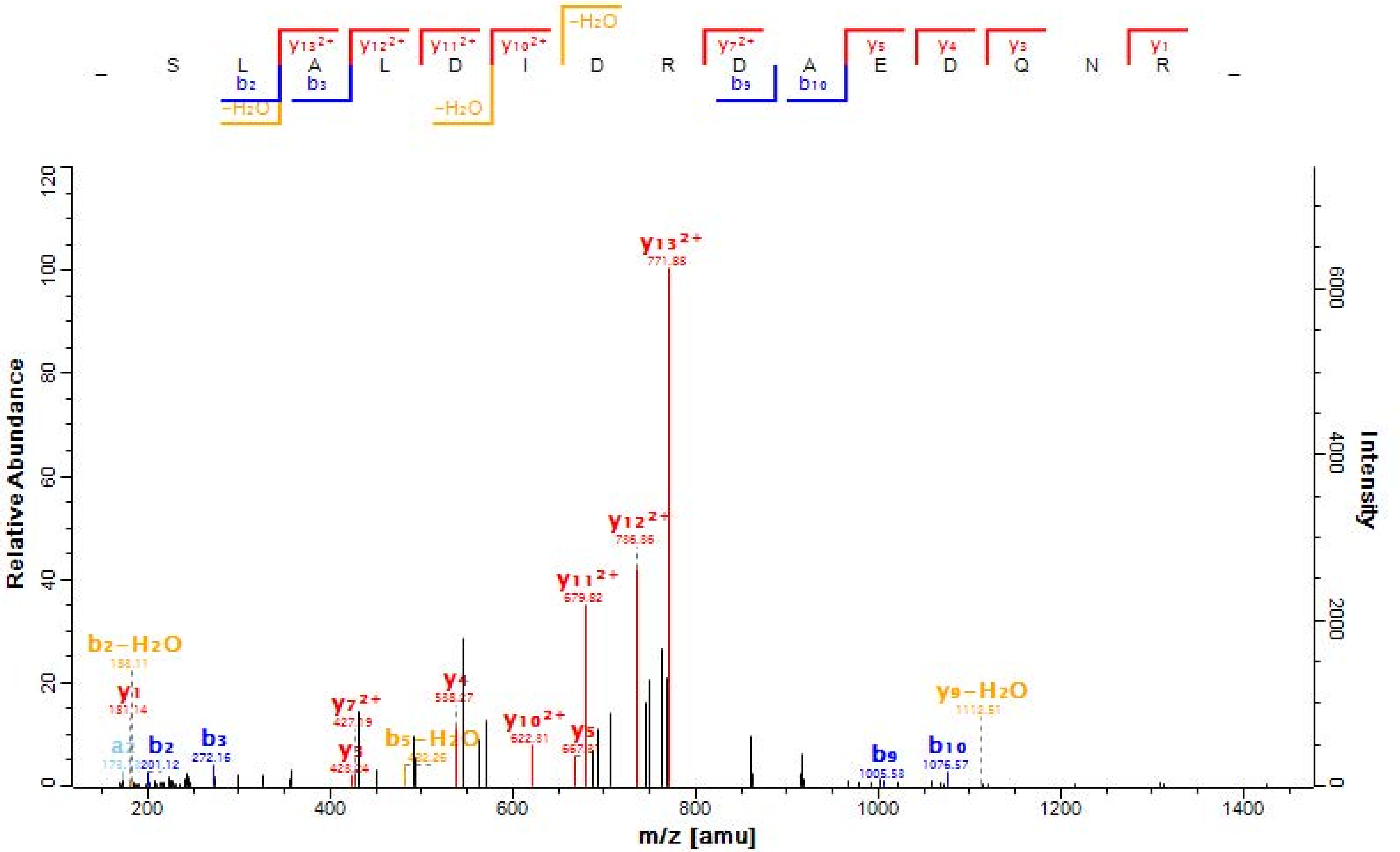
Mass:	1333.59938
m/z:	667.80697
Charge:	2+
Retentiontime:	6.4079685211181
Score:	177.4186
Mass Error [ppm]:	-0.27829
PEP:	9.7558E-11
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	53 %
Peak Coverage:	36 %
Protein Localisation:	68 ... 79

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	11				
-0.298	201.12	+0.0002	229.12	2	D	10	1237.6	+0.2976	1237.6	
	272.16	-0.107	300.16	3	A	9	1122.5	-0.023	561.77	-0.05
	359.19	-0.065	387.19	4	S	8	1051.5	-0.085	1051.5	
	495.3		523.3	5	K	7	964.46	-0.015	482.73	+0.3585
	609.34		637.34	6	N	6	828.35	+0.0184	828.35	
	738.39	+0.125	766.38	7	E	5	714.3	+0.2581	714.3	
	867.43	+0.0155	895.42	8	E	4	585.26	+0.0882	585.26	
	982.46	-0.048	1010.5	9	D	3	456.22	-0.025	456.22	
	1111.5	-0.043	1139.5	10	E	2	341.19	+0.1199	341.19	
	1168.5	+0.0693	1196.5	11	G	1	212.15	+0.1722	212.15	
				12	K	0	155.13		155.13	

Scan number	3210	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	56.48



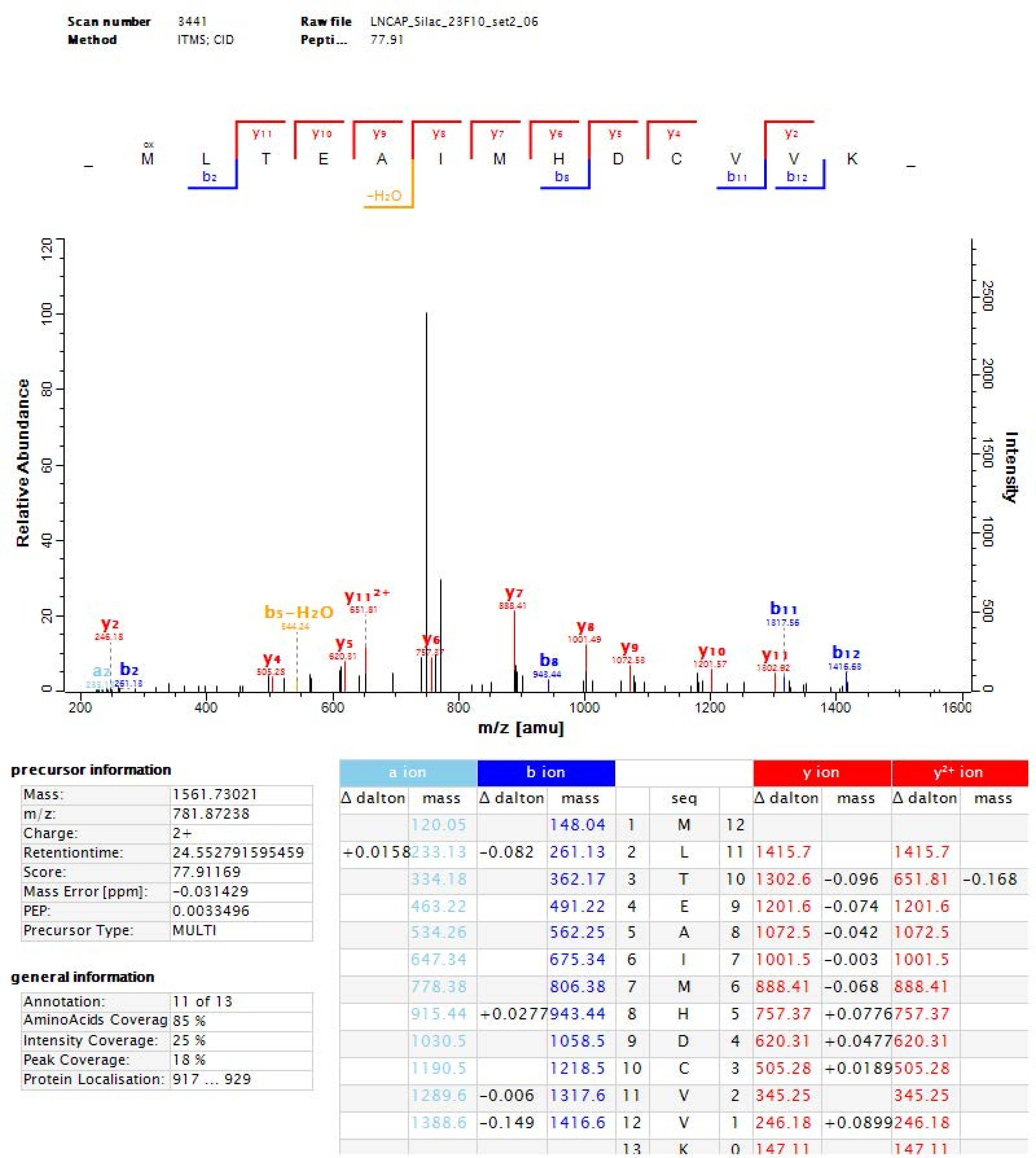
precursor information

Mass:	1729.82236
m/z:	577.61473
Charge:	3+
Retentiontime:	23.327249526977
Score:	56.48154
Mass Error [ppm]:	-0.42559
PEP:	0.0050493
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	44 %
Peak Coverage:	17 %
Protein Localisation:	37 ... 51

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	60.044		88.039	1	S	14				
+0.043	173.13	-0.048	201.12	2	L	13	1655.8		1655.8	
	244.17	-0.024	272.16	3	A	12	1542.8		771.88	+0.081
	357.25		385.24	4	L	11	1471.7		736.36	-0.118
	472.28		500.27	5	D	10	1358.6		679.82	+0.114
	585.36		613.36	6	I	9	1243.6		622.31	+0.0904
	700.39		728.38	7	D	8	1130.5		1130.5	
	862.51		890.5	8	R	7	1015.5		1015.5	
	977.54	+0.1026	1005.5	9	D	6	853.37		427.19	+0.044
	1048.6	+0.1057	1076.6	10	A	5	738.35		738.35	
	1177.6		1205.6	11	E	4	667.31	+0.1276	667.31	
	1292.6		1320.6	12	D	3	538.27	-0.142	538.27	
	1420.7		1448.7	13	Q	2	423.24	+0.0386	423.24	
	1534.7		1562.7	14	N	1	295.18		295.18	
				15	R	0	181.14	+0.045	181.14	



Scan number	3441	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	77.91

precursor information

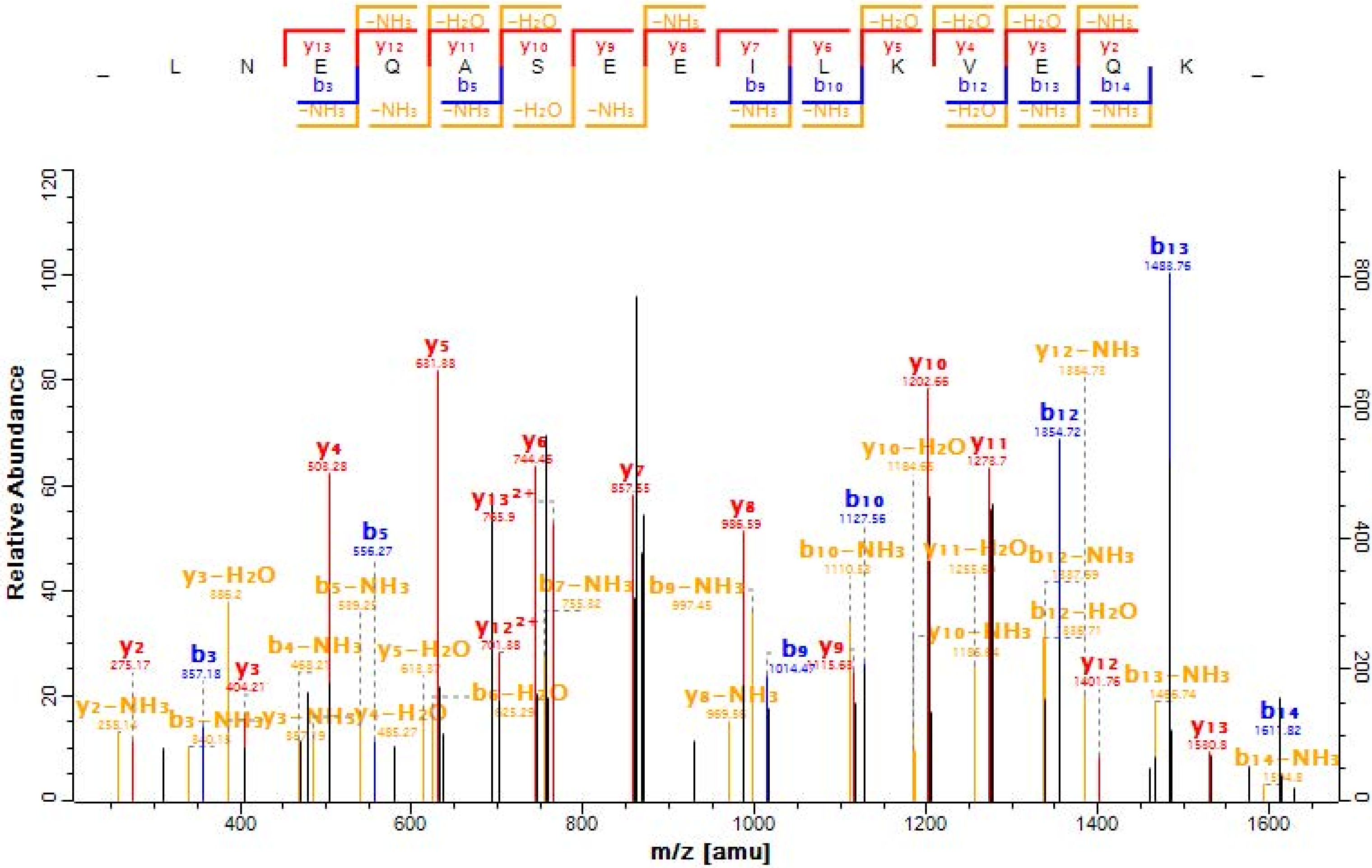
Mass:	1561.73021
m/z:	781.87238
Charge:	2+
Retentiontime:	24.552791595459
Score:	77.91169
Mass Error [ppm]:	-0.031429
PEP:	0.0033496
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	25 %
Peak Coverage:	18 %
Protein Localisation:	917 … 929

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.05		148.04	1	M	12				
+0.0158	233.13	-0.082	261.13	2	L	11	1415.7		1415.7	
	334.18		362.17	3	T	10	1302.6	-0.096	651.81	-0.168
	463.22		491.22	4	E	9	1201.6	-0.074	1201.6	
	534.26		562.25	5	A	8	1072.5	-0.042	1072.5	
	647.34		675.34	6	I	7	1001.5	-0.003	1001.5	
	778.38		806.38	7	M	6	888.41	-0.068	888.41	
	915.44	+0.0277	943.44	8	H	5	757.37	+0.0776	757.37	
	1030.5		1058.5	9	D	4	620.31	+0.0477	620.31	
	1190.5		1218.5	10	C	3	505.28	+0.0189	505.28	
	1289.6	-0.006	1317.6	11	V	2	345.25		345.25	
	1388.6	-0.149	1416.6	12	V	1	246.18	+0.0899	246.18	
				13	K	0	147.11		147.11	

Scan number	3497	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	256.8



precursor information

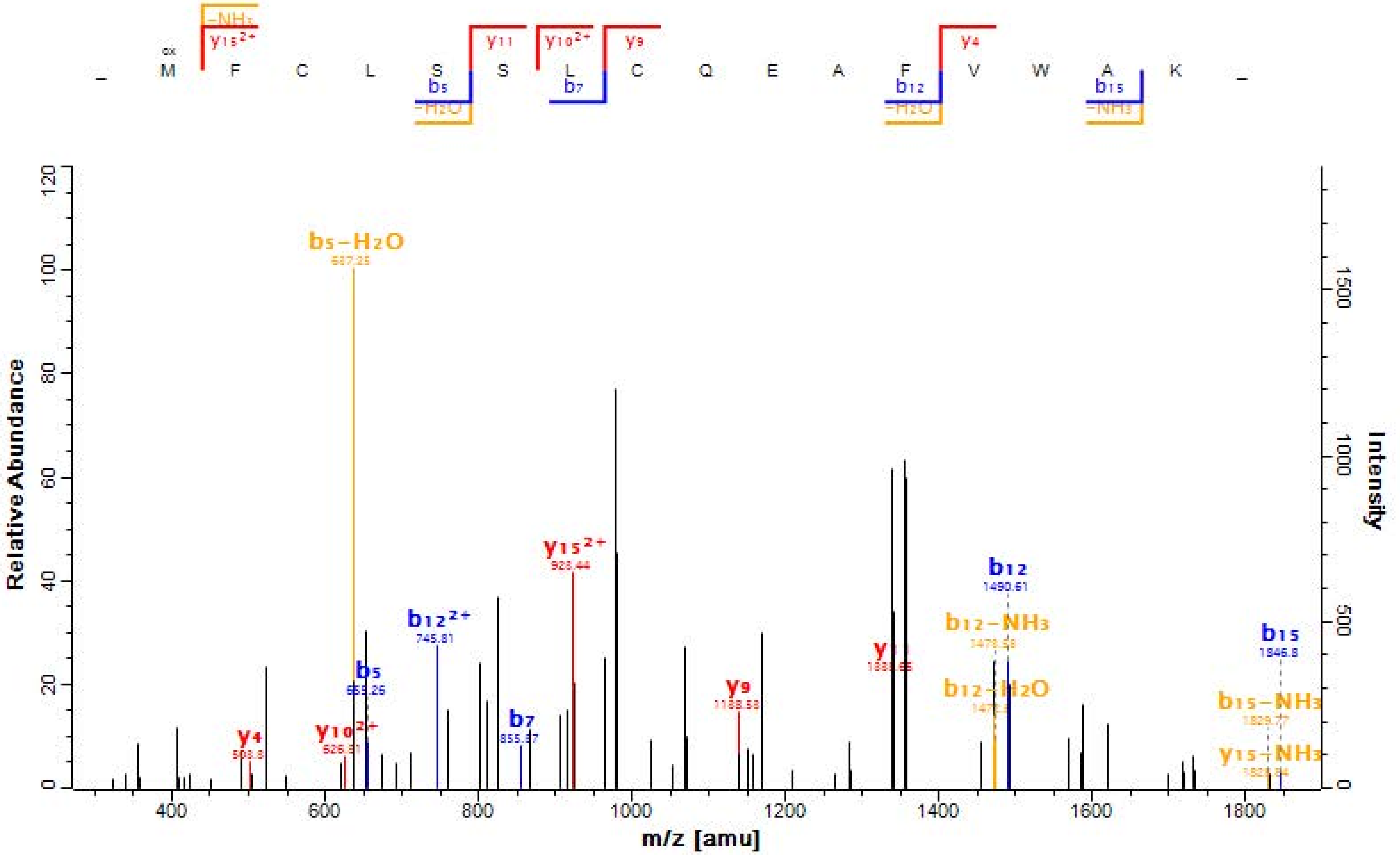
Mass:	1756.91989
m/z:	879.46722
Charge:	2+
Retentiontime:	24.839689254760
Score:	256.7987
Mass Error [ppm]:	-0.45577
PEP:	1.4237E-57
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	52 %
Peak Coverage:	49 %
Protein Localisation:	45 ... 59

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	14				
	228.1343	2	N	13	1644.844		1644.844	
+0.10329	357.1769	3	E	12	1530.801	-0.01277	765.9041	+0.250291
	485.2354	4	Q	11	1401.758	+0.011512	701.3828	+0.09013
+0.081085	556.2726	5	A	10	1273.7	-0.0333	1273.7	
	643.3046	6	S	9	1202.663	-0.14194	1202.663	
	772.3472	7	E	8	1115.631	-0.15716	1115.631	
	901.3898	8	E	7	986.5881	-0.04047	986.5881	
+0.046189	1014.474	9	I	6	857.5455	-0.15614	857.5455	
+0.216275	1127.558	10	L	5	744.4614	+0.110423	744.4614	
	1255.653	11	K	4	631.3774	+0.086149	631.3774	
+0.006633	1354.721	12	V	3	503.2824	-0.07871	503.2824	
-0.12532	1483.764	13	E	2	404.214	+0.077651	404.214	
-0.03838	1611.822	14	Q	1	275.1714	+0.056157	275.1714	
		15	K	0	147.1128		147.1128	

Scan number	3793	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	58.32



precursor information

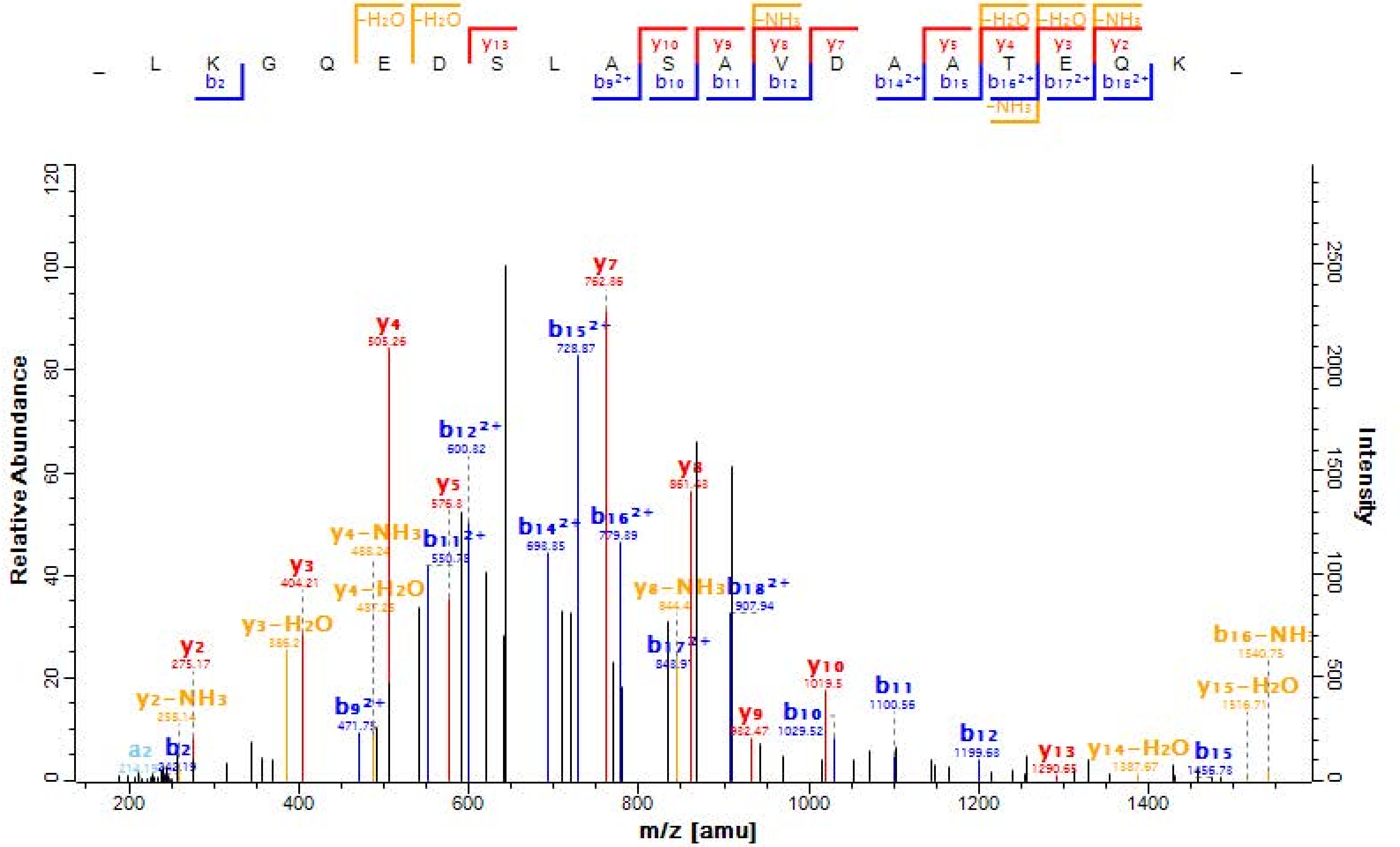
Mass:	1991.89388
m/z:	996.95421
Charge:	2+
Retentiontime:	26.41357421875
Score:	58.32032
Mass Error [ppm]:	-0.24354
PEP:	0.0099672
Precursor Type:	MULTI

general information

Annotation:	9 of 16
AminoAcids Coverag	56 %
Intensity Coverage:	23 %
Peak Coverage:	18 %
Protein Localisation:	1 ... 16

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.04		148.04	1	M	15				
	295.11		295.11	2	F	14	1845.9		923.44	+0.1799
	455.14		455.14	3	C	13	1698.8		1698.8	
	568.23		568.23	4	L	12	1538.8		1538.8	
	655.26	+0.178	655.26	5	S	11	1425.7		1425.7	
	742.29		742.29	6	S	10	1338.7	-0.043	1338.7	
	855.37	-0.097	855.37	7	L	9	1251.6		626.31	+0.0104
	1015.4		1015.4	8	C	8	1138.5	+0.1578	1138.5	
	1143.5		1143.5	9	Q	7	978.5		978.5	
	1272.5		1272.5	10	E	6	850.45		850.45	
	1343.5		1343.5	11	A	5	721.4		721.4	
+0.2314	745.81	-0.098	1490.6	12	F	4	650.37		650.37	
	1589.7		1589.7	13	V	3	503.3	+0.001	503.3	
	1775.8		1775.8	14	W	2	404.23		404.23	
	1846.8	+0.2188	1846.8	15	A	1	218.15		218.15	
				16	K	0	147.11		147.11	

Scan number	4229	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	112.01



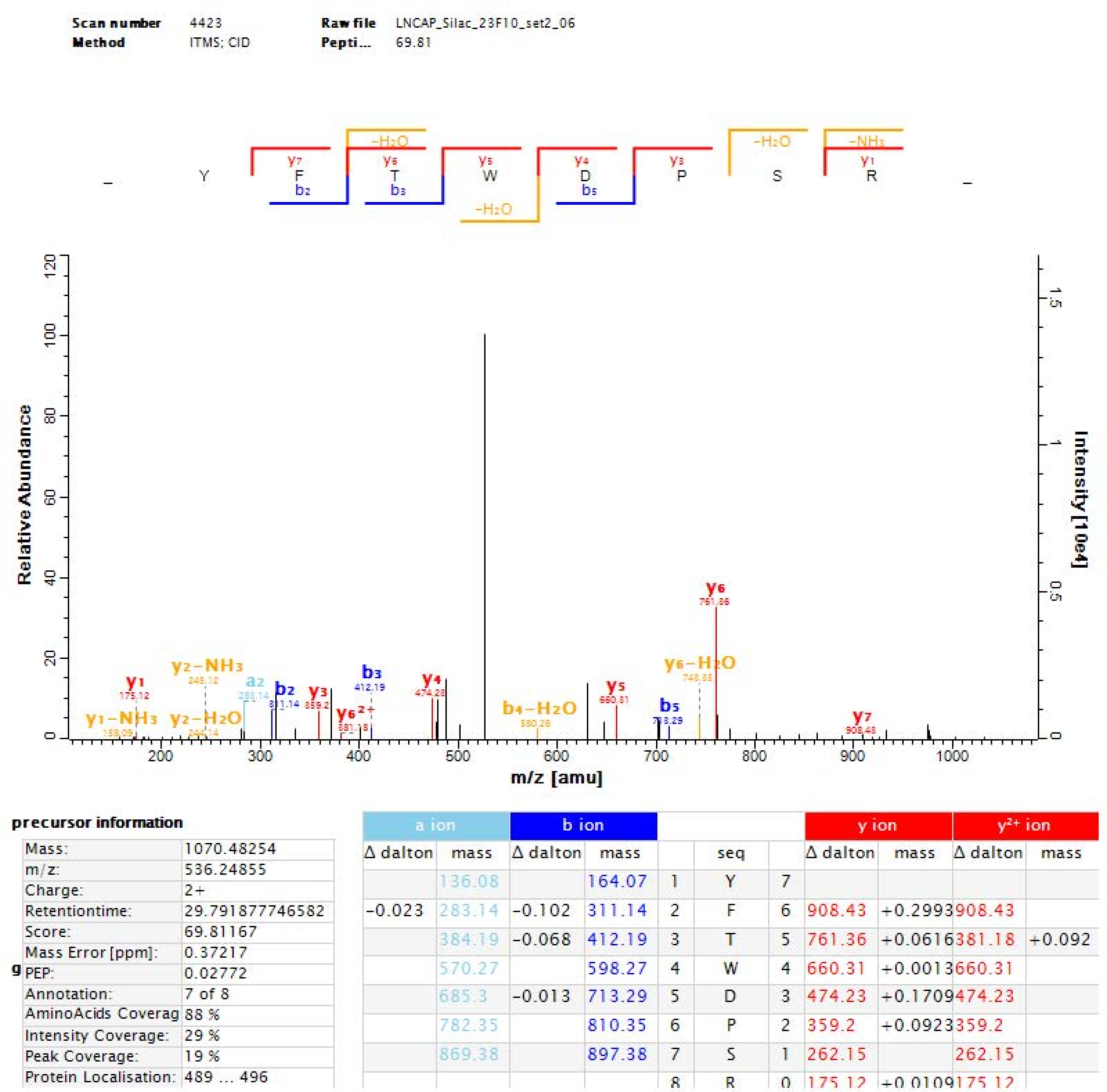
precursor information

Mass:	1959.97509
m/z:	654.33231
Charge:	3+
Retentiontime:	28.757925033569
Score:	112.0116
Mass Error [ppm]:	0.090444
PEP:	1.6366E-08
Precursor Type:	MULTI

general information

Annotation:	14 of 19
AminoAcids Coverag	74 %
Intensity Coverage:	51 %
Peak Coverage:	31 %
Protein Localisation:	156 ... 174

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	86.096		114.09		114.09	1	L	18		
+0.0319	214.19		242.19	+0.3233	242.19	2	K	17	1847.9	
	271.21		299.21		299.21	3	G	16	1719.8	
	399.27		427.27		427.27	4	Q	15	1662.8	
	528.31		556.31		556.31	5	E	14	1534.7	
	643.34		671.34		671.34	6	D	13	1405.7	
	730.37		758.37		758.37	7	S	12	1290.7	-0.032
	843.46		871.45		871.45	8	L	11	1203.6	
	914.49	+0.0708	471.75		942.49	9	A	10	1090.5	
	1001.5		1029.5	+0.0875	1029.5	10	S	9	1019.5	+0.0038
	1072.6	+0.1902	550.78	+0.1617	1100.6	11	A	8	932.47	-0.161
	1171.6	+0.1851	600.32	-0.111	1199.6	12	V	7	861.43	+0.0834
	1286.7		1314.7		1314.7	13	D	6	762.36	-0.012
	1357.7	+0.1717	693.35		1385.7	14	A	5	647.34	
	1428.7	+0.1424	728.87	+0.0497	1456.7	15	A	4	576.3	+0.0067
	1529.8	+0.0046	779.39		1557.8	16	T	3	505.26	+0.0537
	1658.8	+0.1039	843.91		1686.8	17	E	2	404.21	+0.017
	1786.9	-0.028	907.94		1814.9	18	Q	1	275.17	+0.0197
						19	K	0	147.11	

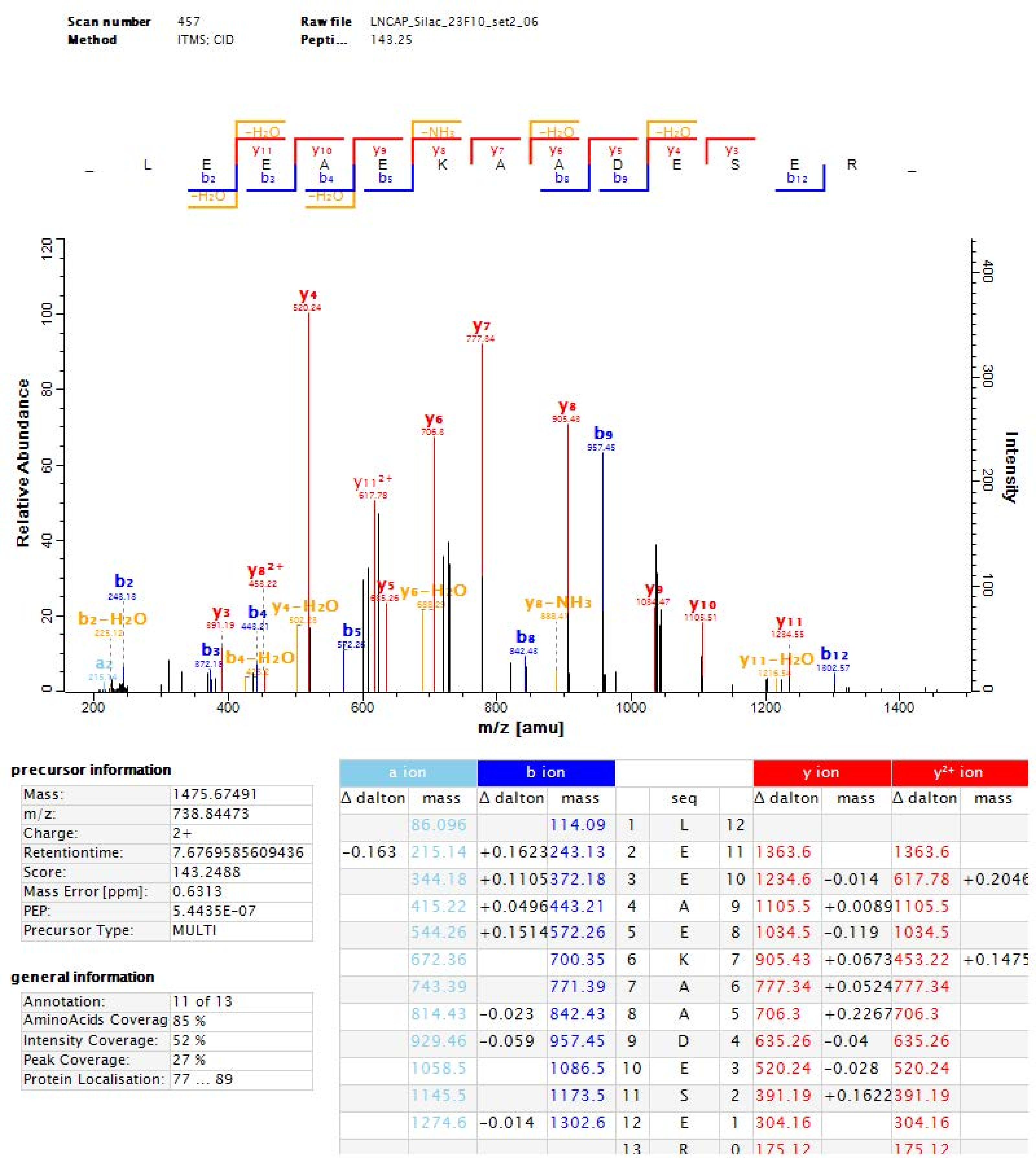


Scan number	4423	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	69.81

precursor information

Mass:	1070.48254
m/z:	536.24855
Charge:	2+
Retentiontime:	29.791877746582
Score:	69.81167
Mass Error [ppm]:	0.37217
PEP:	0.02772
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	29 %
Peak Coverage:	19 %
Protein Localisation:	489 ... 496

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.08		164.07	1	Y	7				
-0.023	283.14	-0.102	311.14	2	F	6	908.43	+0.2993	908.43	
	384.19	-0.068	412.19	3	T	5	761.36	+0.0616	381.18	+0.092
	570.27		598.27	4	W	4	660.31	+0.0013	660.31	
	685.3	-0.013	713.29	5	D	3	474.23	+0.1709	474.23	
	782.35		810.35	6	P	2	359.2	+0.0923	359.2	
	869.38		897.38	7	S	1	262.15		262.15	
				8	R	0	175.12	+0.0109	175.12	



Scan number	457	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	143.25

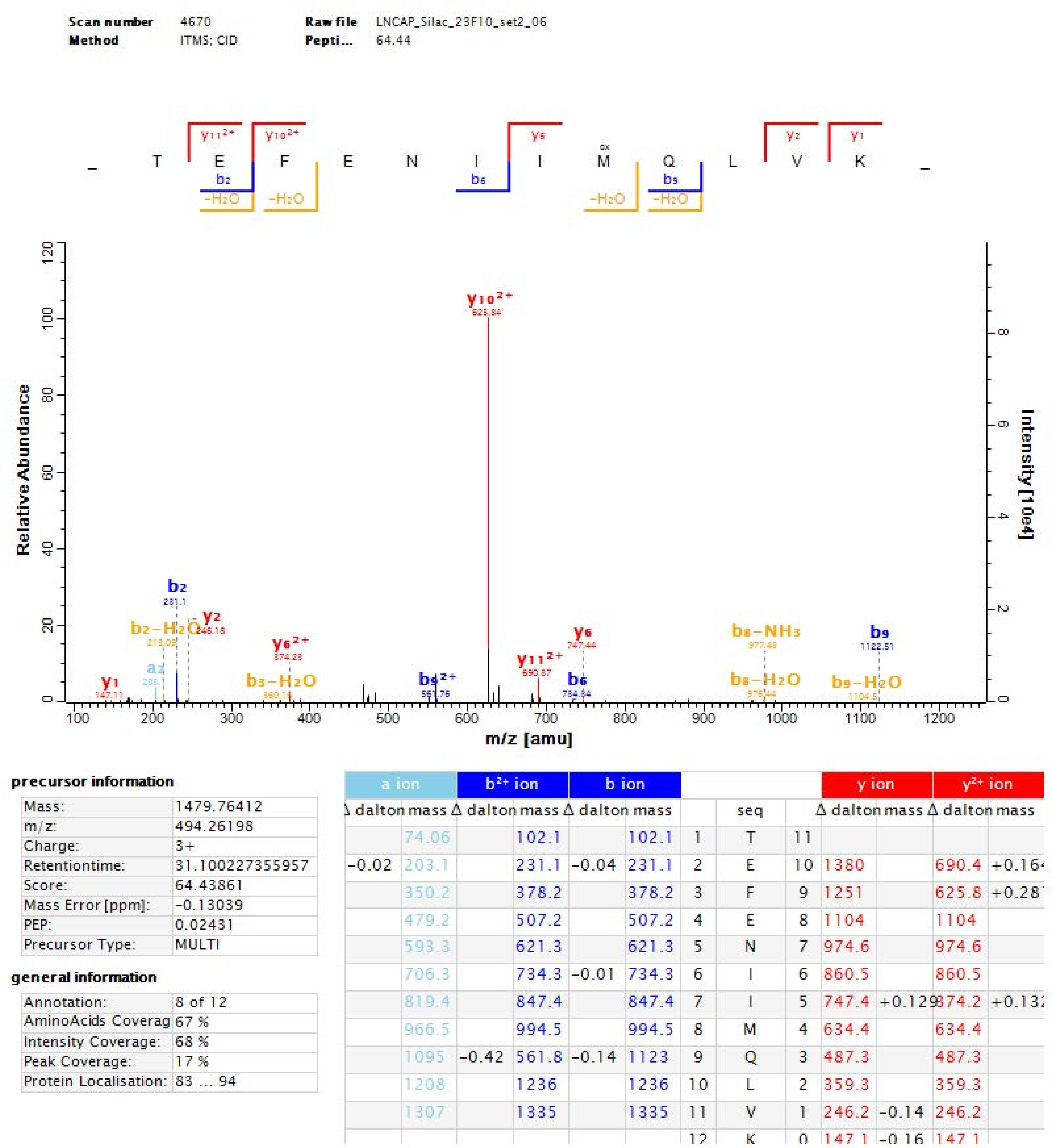
precursor information

Mass:	1475.67491
m/z:	738.84473
Charge:	2+
Retentiontime:	7.6769585609436
Score:	143.2488
Mass Error [ppm]:	0.6313
PEP:	5.4435E-07
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	52 %
Peak Coverage:	27 %
Protein Localisation:	77 ... 89

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	12				
-0.163	215.14	+0.1623	243.13	2	E	11	1363.6		1363.6	
	344.18	+0.1105	372.18	3	E	10	1234.6	-0.014	617.78	+0.2046
	415.22	+0.0496	443.21	4	A	9	1105.5	+0.0089	1105.5	
	544.26	+0.1514	572.26	5	E	8	1034.5	-0.119	1034.5	
	672.36		700.35	6	K	7	905.43	+0.0673	453.22	+0.1475
	743.39		771.39	7	A	6	777.34	+0.0524	777.34	
	814.43	-0.023	842.43	8	A	5	706.3	+0.2267	706.3	
	929.46	-0.059	957.45	9	D	4	635.26	-0.04	635.26	
	1058.5		1086.5	10	E	3	520.24	-0.028	520.24	
	1145.5		1173.5	11	S	2	391.19	+0.1622	391.19	
	1274.6	-0.014	1302.6	12	E	1	304.16		304.16	
				13	R	0	175.12		175.12	



Scan number	4670	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	64.44

precursor information

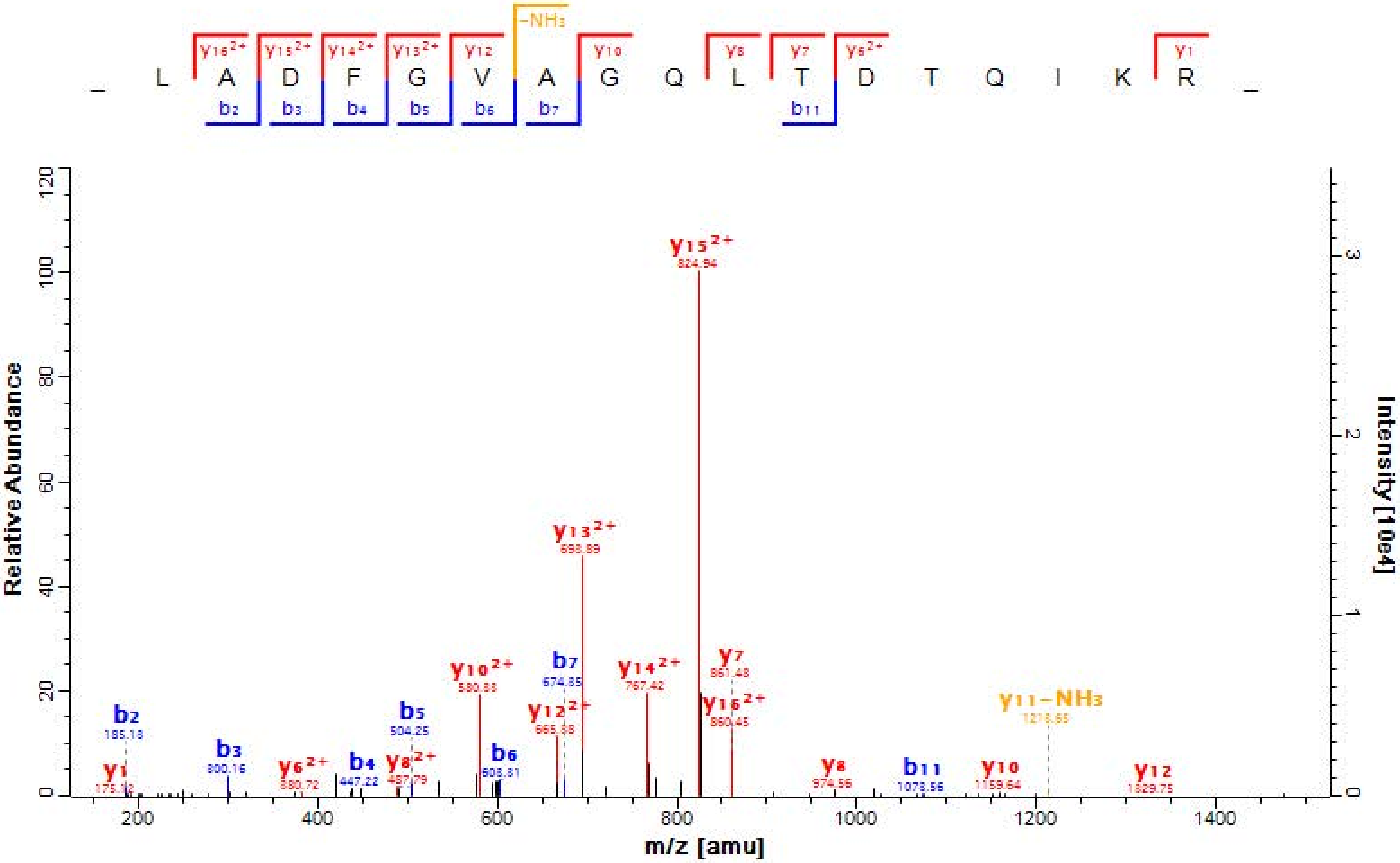
Mass:	1479.76412
m/z:	494.26198
Charge:	3+
Retentiontime:	31.100227355957
Score:	64.43861
Mass Error [ppm]:	-0.13039
PEP:	0.02431
Precursor Type:	MULTI

general information

Annotation:	8 of 12
AminoAcids Coverag	67 %
Intensity Coverage:	68 %
Peak Coverage:	17 %
Protein Localisation:	83 ... 94

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.1		102.1	1	T	11				
-0.02	203.1		231.1	-0.04	231.1	2	E	10	1380		690.4	+0.16
	350.2		378.2		378.2	3	F	9	1251		625.8	+0.28
	479.2		507.2		507.2	4	E	8	1104		1104	
	593.3		621.3		621.3	5	N	7	974.6		974.6	
	706.3		734.3	-0.01	734.3	6	I	6	860.5		860.5	
	819.4		847.4		847.4	7	I	5	747.4	+0.129	374.2	+0.13
	966.5		994.5		994.5	8	M	4	634.4		634.4	
	1095	-0.42	561.8	-0.14	1123	9	Q	3	487.3		487.3	
	1208		1236		1236	10	L	2	359.3		359.3	
	1307		1335		1335	11	V	1	246.2	-0.14	246.2	
						12	K	0	147.1	-0.16	147.1	

Scan number	5062	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	89.91



precursor information

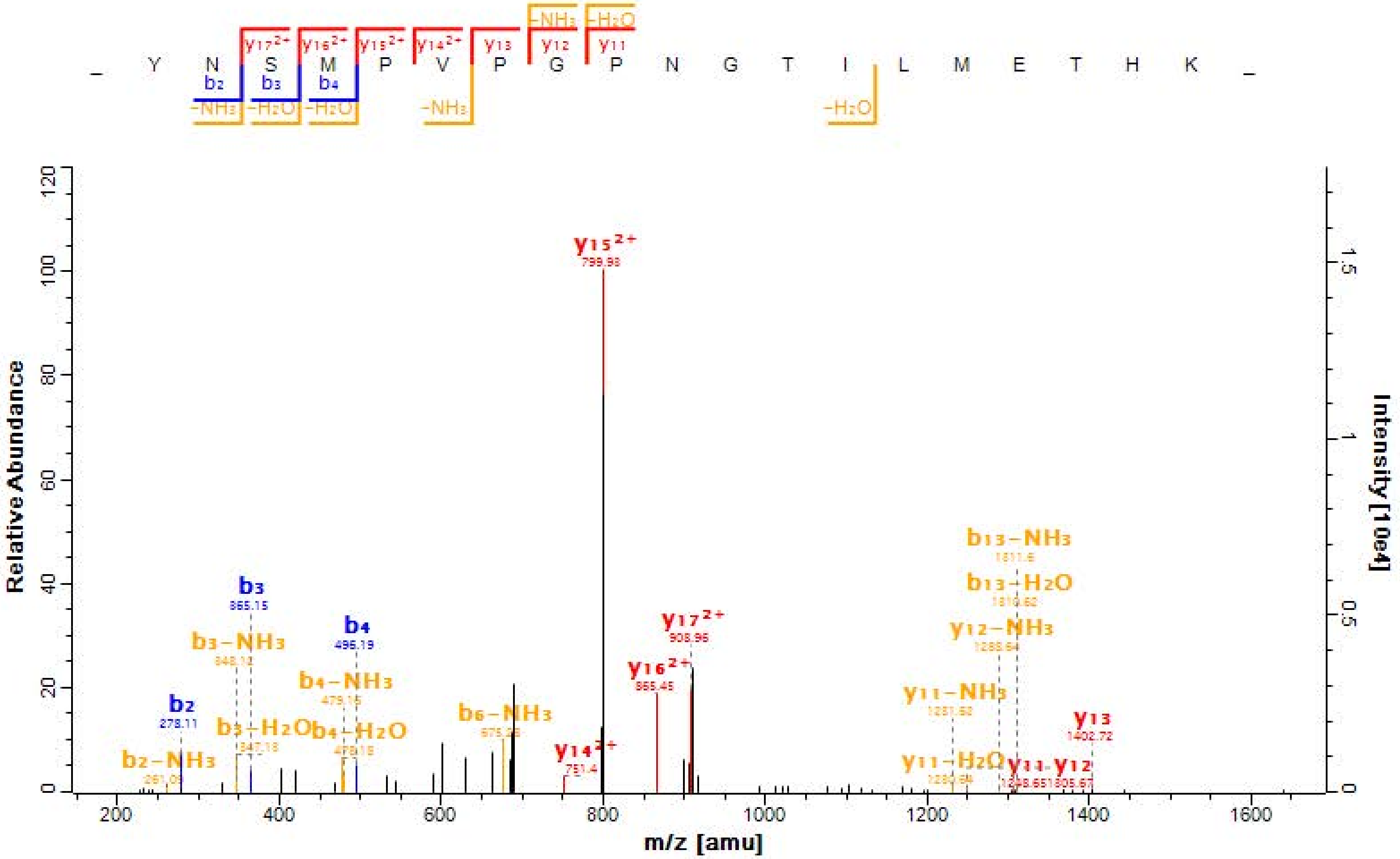
Mass:	1831.97953
m/z:	611.66712
Charge:	3+
Retentiontime:	33.179981231689
Score:	89.9108
Mass Error [ppm]:	0.17518
PEP:	5.2324E-06
Precursor Type:	MULTI

general information

Annotation:	11 of 17
AminoAcids Coverag	65 %
Intensity Coverage:	73 %
Peak Coverage:	23 %
Protein Localisation:	182 ... 198

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	16				
+0.010614	185.1285	2	A	15	1719.902		860.4549	+0.247542
-0.03247	300.1554	3	D	14	1648.865		824.9363	+0.236253
+0.18842	447.2238	4	F	13	1533.838		767.4228	+0.223479
+0.019679	504.2453	5	G	12	1386.77		693.8886	+0.222042
-0.39419	603.3137	6	V	11	1329.748	+0.232223	665.3779	+0.278062
+0.014615	674.3508	7	A	10	1230.68		1230.68	
	731.3723	8	G	9	1159.643	-0.19887	580.3251	+0.309952
	859.4308	9	Q	8	1102.621		1102.621	
	972.5149	10	L	7	974.5629	-0.00311	487.7851	+0.207272
+0.20255	1073.563	11	T	6	861.4789	+0.162196	861.4789	
	1188.59	12	D	5	760.4312		380.7192	+0.297069
	1289.637	13	T	4	645.4042		645.4042	
	1417.696	14	Q	3	544.3566		544.3566	
	1530.78	15	I	2	416.298		416.298	
	1658.875	16	K	1	303.2139		303.2139	
		17	R	0	175.119	-0.00395	175.119	

Scan number	5065	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	93.51



precursor information

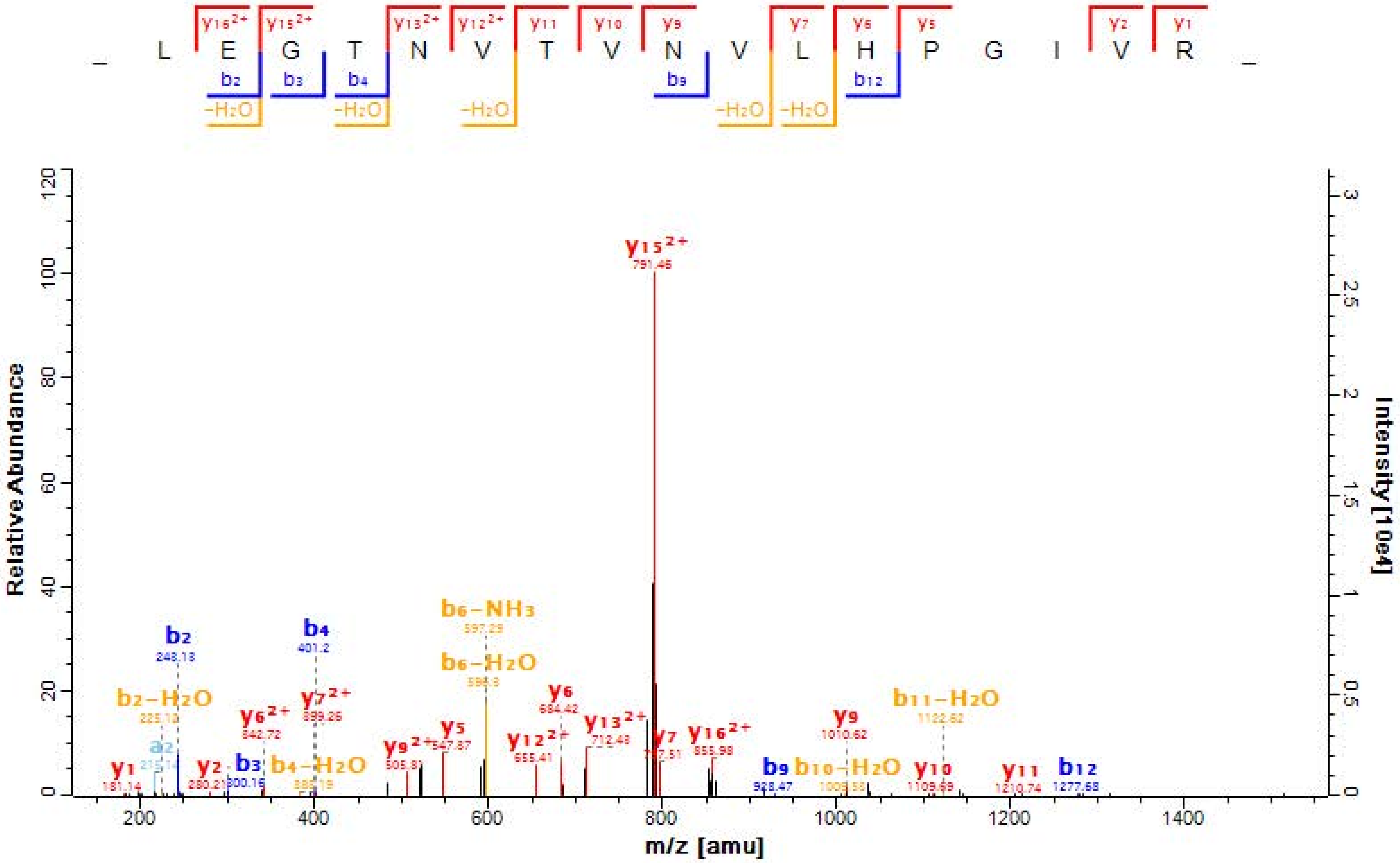
Mass:	2085.00126
m/z:	696.0077
Charge:	3+
Retentiontime:	33.194236755371
Score:	93.50977
Mass Error [ppm]:	-0.51143
PEP:	1.2536E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 19
AminoAcids Coverag	47 %
Intensity Coverage:	44 %
Peak Coverage:	24 %
Protein Localisation:	103 ... 121

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	164.0706	1	Y	18				
+0.058465	278.1135	2	N	17	1930.96		1930.96	
+0.042366	365.1456	3	S	16	1816.918		908.9624	+0.011524
-0.0088	496.186	4	M	15	1729.886		865.4464	+0.139355
	593.2388	5	P	14	1598.845		799.9262	-0.02729
	692.3072	6	V	13	1501.792		751.3998	+0.178411
	789.36	7	P	12	1402.724	-0.15269	1402.724	
	846.3815	8	G	11	1305.671	-0.38118	1305.671	
	943.4342	9	P	10	1248.65	-0.39121	1248.65	
	1057.477	10	N	9	1151.597		1151.597	
	1114.499	11	G	8	1037.554		1037.554	
	1215.546	12	T	7	980.5325		980.5325	
	1328.63	13	I	6	879.4848		879.4848	
	1441.714	14	L	5	766.4007		766.4007	
	1572.755	15	M	4	653.3167		653.3167	
	1701.797	16	E	3	522.2762		522.2762	
	1802.845	17	T	2	393.2336		393.2336	
	1939.904	18	H	1	292.1859		292.1859	
		19	K	0	155.127		155.127	

Scan number	5211	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	127.71



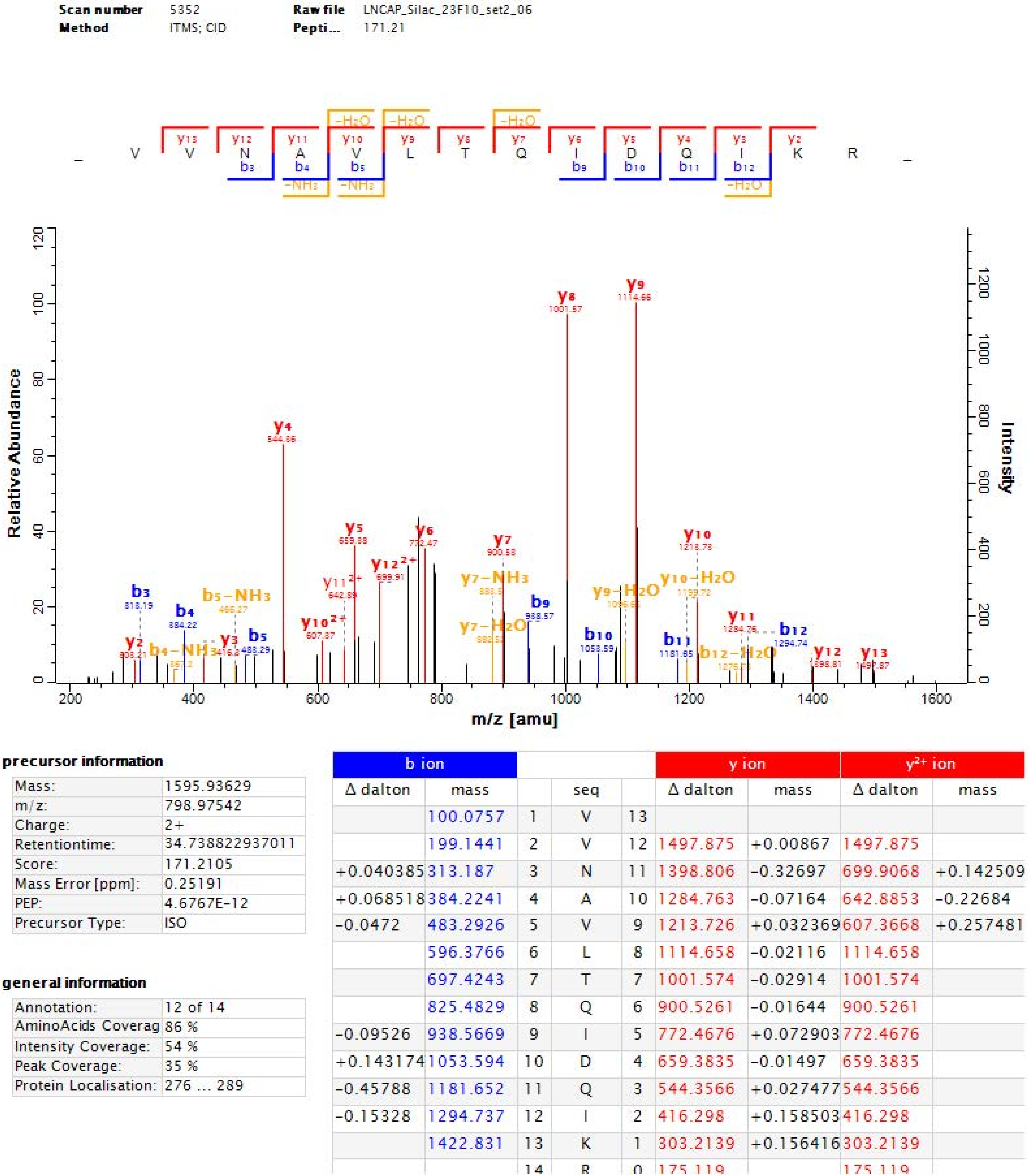
precursor information

Mass:	1817.01602
m/z:	606.67928
Charge:	3+
Retentiontime:	33.982402801513
Score:	127.712
Mass Error [ppm]:	0.046904
PEP:	3.697E-12
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	56 %
Peak Coverage:	27 %
Protein Localisation:	235 ... 251

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	16				
+0.0366	215.14	+0.0098	243.13	2	E	15	1711		855.98	+0.240
	272.16	+0.0966	300.16	3	G	14	1581.9		791.46	+0.179
	373.21	+0.1216	401.2	4	T	13	1524.9		1524.9	
	487.25		515.25	5	N	12	1423.8		712.43	+0.234
	586.32		614.31	6	V	11	1309.8		655.41	+0.239
	687.37		715.36	7	T	10	1210.7	-0.086	1210.7	
	786.44		814.43	8	V	9	1109.7	+0.3039	1109.7	
	900.48	-0.025	928.47	9	N	8	1010.6	+0.0474	505.81	+0.3561
	999.55		1027.5	10	V	7	896.58		896.58	
	1112.6		1140.6	11	L	6	797.51	-0.03	399.26	+0.128
	1249.7	-0.033	1277.7	12	H	5	684.42	+0.0655	342.72	-0.07
	1346.7		1374.7	13	P	4	547.37	-0.003	547.37	
	1403.8		1431.8	14	G	3	450.31		450.31	
	1516.8		1544.8	15	I	2	393.29		393.29	
	1615.9		1643.9	16	V	1	280.21	-0.166	280.21	
				17	R	0	181.14	-0.081	181.14	



Scan number 5352
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set2_06
Pepti... 171.21

precursor information

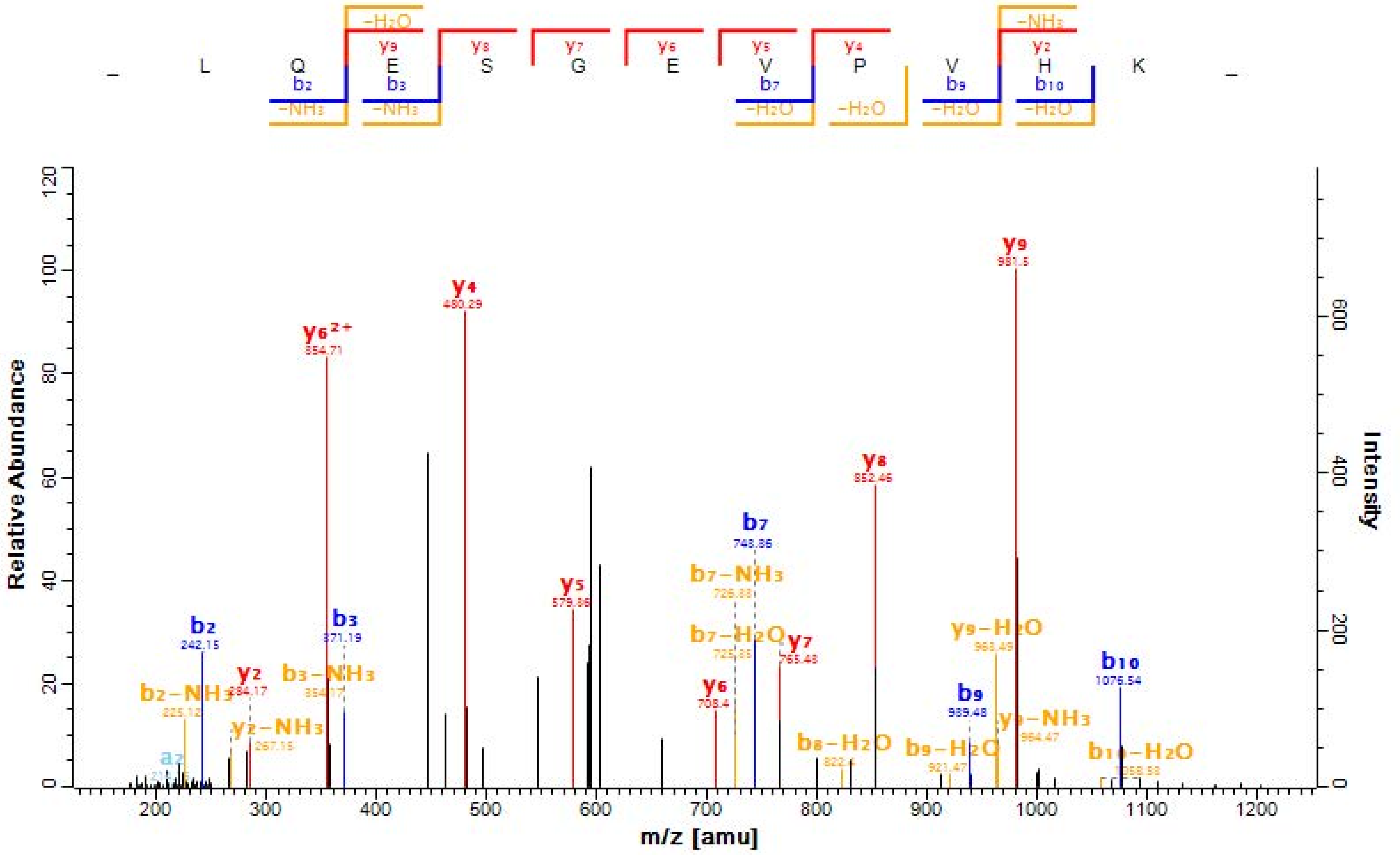
Mass:	1595.93629
m/z:	798.97542
Charge:	2+
Retentiontime:	34.738822937011
Score:	171.2105
Mass Error [ppm]:	0.25191
PEP:	4.6767E-12
Precursor Type:	ISO

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	54 %
Peak Coverage:	35 %
Protein Localisation:	276 ... 289

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	13				
	199.1441	2	V	12	1497.875	+0.00867	1497.875	
+0.040385	313.187	3	N	11	1398.806	-0.32697	699.9068	+0.142509
+0.068518	384.2241	4	A	10	1284.763	-0.07164	642.8853	-0.22684
-0.0472	483.2926	5	V	9	1213.726	+0.032369	607.3668	+0.257481
	596.3766	6	L	8	1114.658	-0.02116	1114.658	
	697.4243	7	T	7	1001.574	-0.02914	1001.574	
	825.4829	8	Q	6	900.5261	-0.01644	900.5261	
-0.09526	938.5669	9	I	5	772.4676	+0.072903	772.4676	
+0.143174	1053.594	10	D	4	659.3835	-0.01497	659.3835	
-0.45788	1181.652	11	Q	3	544.3566	+0.027477	544.3566	
-0.15328	1294.737	12	I	2	416.298	+0.158503	416.298	
	1422.831	13	K	1	303.2139	+0.156416	303.2139	
		14	R	0	175.119		175.119	
]

Scan number	567	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	141.08



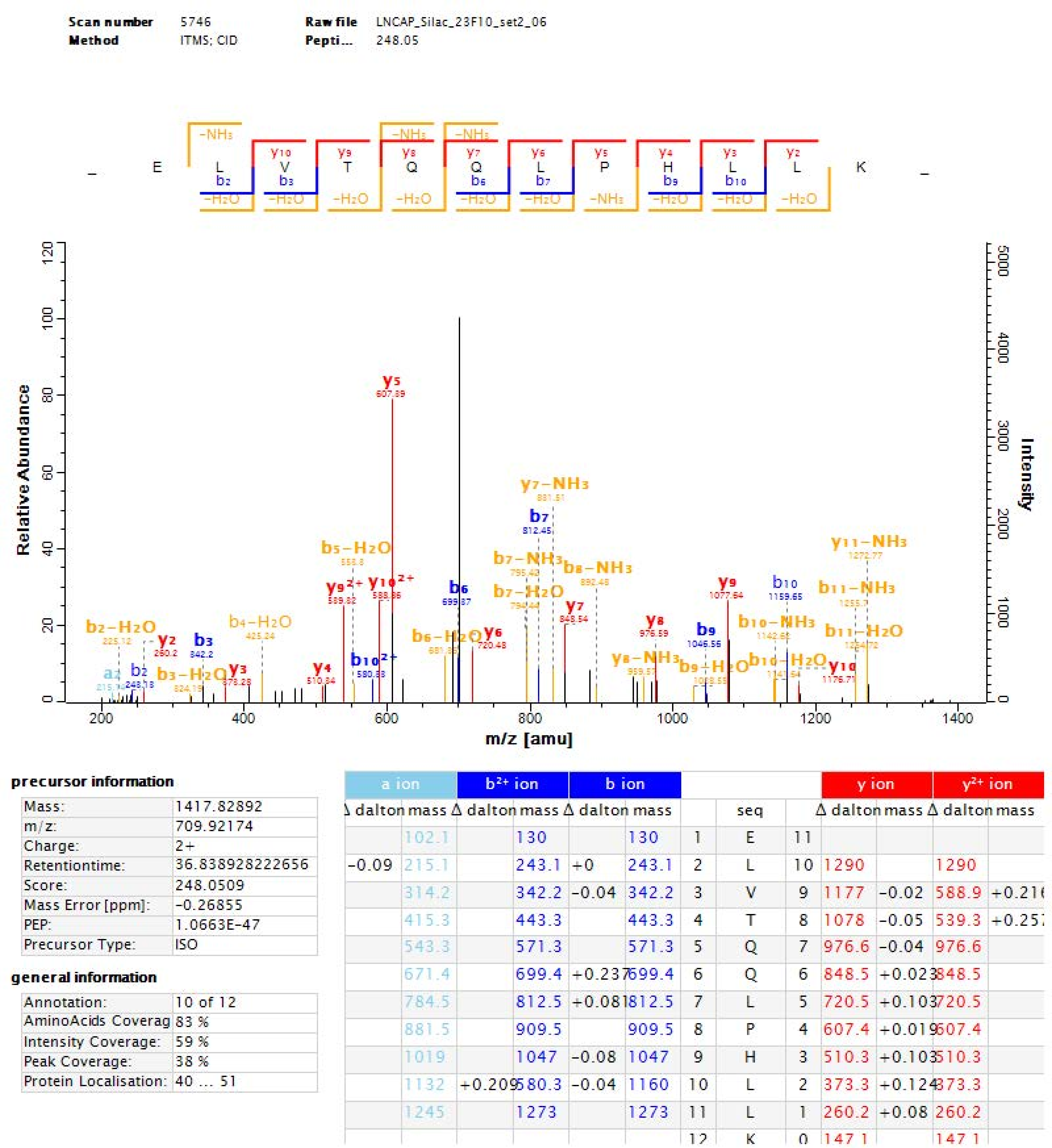
precursor information

Mass:	1221.63536
m/z:	611.82496
Charge:	2+
Retentiontime:	8.3789520263671
Score:	141.0841
Mass Error [ppm]:	0.0073032
PEP:	0.00011982
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	53 %
Peak Coverage:	23 %
Protein Localisation:	39 ... 49

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	10				
+0.1034	214.16	-0.01	242.15	2	Q	9	1109.6		1109.6	
	343.2	+0.0084	371.19	3	E	8	981.5	+0.0059	981.5	
	430.23		458.22	4	S	7	852.46	-0.019	852.46	
	487.25		515.25	5	G	6	765.43	-0.077	765.43	
	616.29		644.29	6	E	5	708.4	+0.0396	354.71	+0.3764
	715.36	+0.0171	743.36	7	V	4	579.36	+0.1118	579.36	
	812.41		840.41	8	P	3	480.29	+0.0386	480.29	
	911.48	+0.0291	939.48	9	V	2	383.24		383.24	
	1048.5	-0.078	1076.5	10	H	1	284.17	+0.1405	284.17	
				11	K	0	147.11		147.11	



Scan number	5746	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	248.05

precursor information

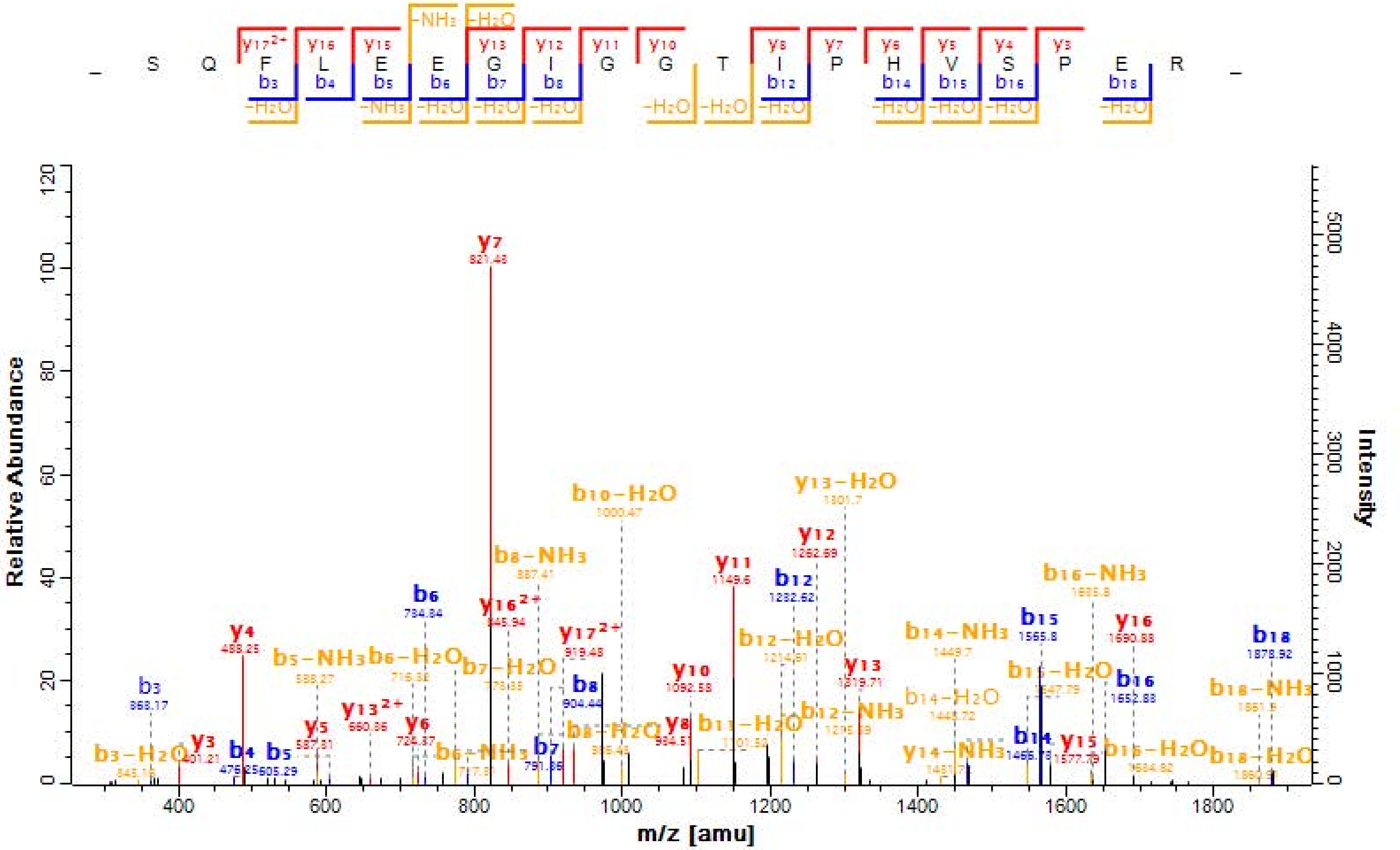
Mass:	1417.82892
m/z:	709.92174
Charge:	2+
Retentiontime:	36.838928222656
Score:	248.0509
Mass Error [ppm]:	-0.26855
PEP:	1.0663E-47
Precursor Type:	ISO

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	59 %
Peak Coverage:	38 %
Protein Localisation:	40 ... 51

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.1		130		130	1	E	11				
-0.09	215.1		243.1	+0	243.1	2	L	10	1290		1290	
	314.2		342.2	-0.04	342.2	3	V	9	1177	-0.02	588.9	+0.21
	415.3		443.3		443.3	4	T	8	1078	-0.05	539.3	+0.25
	543.3		571.3		571.3	5	Q	7	976.6	-0.04	976.6	
	671.4		699.4	+0.237	699.4	6	Q	6	848.5	+0.023	848.5	
	784.5		812.5	+0.081	812.5	7	L	5	720.5	+0.103	720.5	
	881.5		909.5		909.5	8	P	4	607.4	+0.019	607.4	
	1019		1047	-0.08	1047	9	H	3	510.3	+0.103	510.3	
	1132	+0.209	580.3	-0.04	1160	10	L	2	373.3	+0.124	373.3	
	1245		1273		1273	11	L	1	260.2	+0.08	260.2	
						12	K	0	147.1		147.1	

Scan number	5835	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	244.52



precursor information

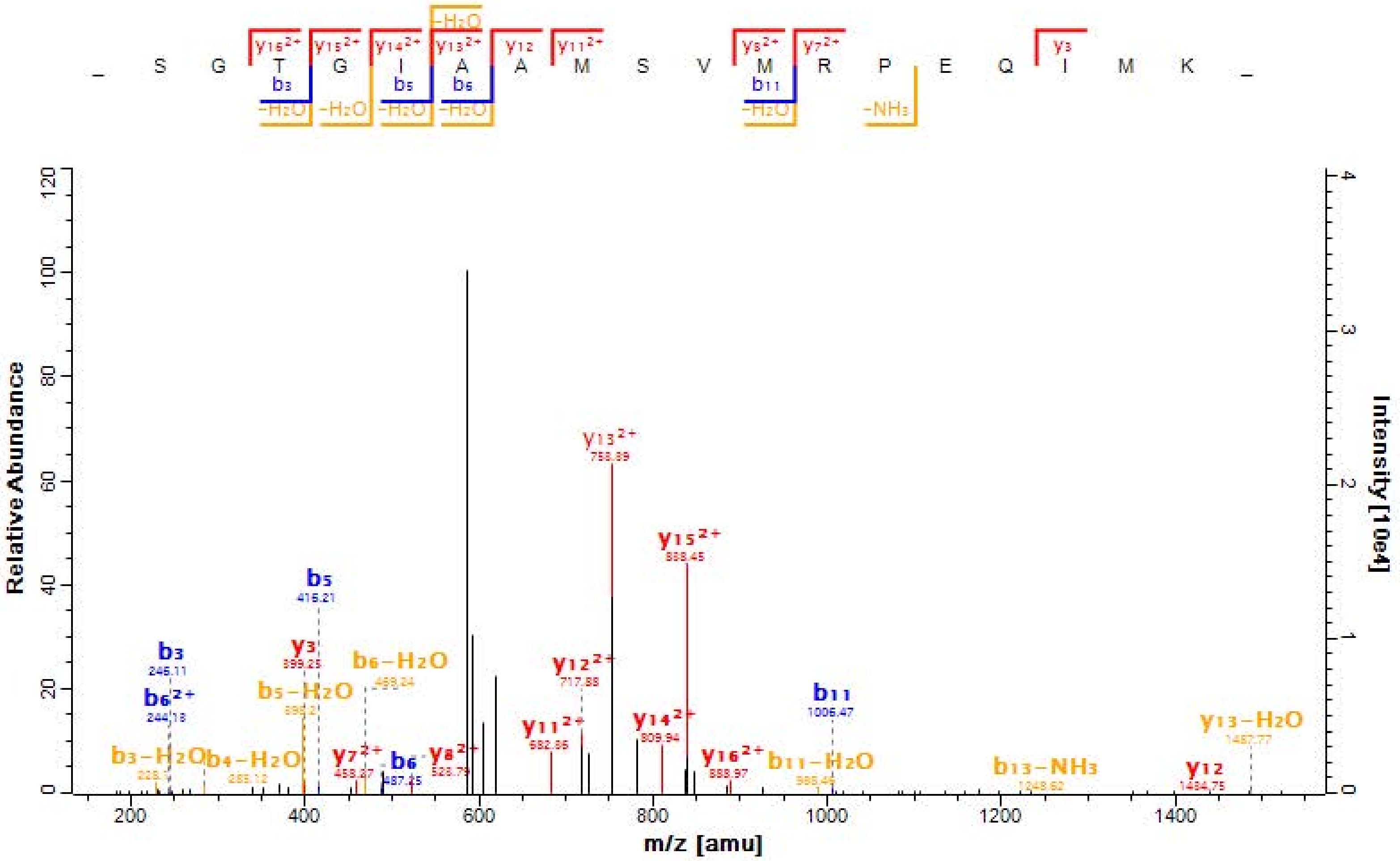
Mass:	2052.02703
m/z:	1027.02079
Charge:	2+
Retentiontime:	37.314022064209
Score:	244.5194
Mass Error [ppm]:	-0.28701
PEP:	6.4383E-66
Precursor Type:	MULTI

general information

Annotation:	16 of 19
AminoAcids Coverag	84 %
Intensity Coverage:	62 %
Peak Coverage:	46 %
Protein Localisation:	468 ... 486

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	18				
	216.0979	2	Q	17	1966.003		1966.003	
+0.006494	363.1663	3	F	16	1837.944		919.4758	+0.320238
-0.04635	476.2504	4	L	15	1690.876	+0.014506	845.9416	+0.304762
-0.06212	605.293	5	E	14	1577.792	-0.04901	1577.792	
-0.02518	734.3355	6	E	13	1448.749		1448.749	
-0.01717	791.357	7	G	12	1319.707	-0.07955	660.357	+0.145491
+0.021572	904.4411	8	I	11	1262.685	-0.00206	1262.685	
	961.4625	9	G	10	1149.601	+0.049294	1149.601	
	1018.484	10	G	9	1092.58	-0.07841	1092.58	
	1119.532	11	T	8	1035.558		1035.558	
+0.034769	1232.616	12	I	7	934.5105	+0.135993	934.5105	
	1329.669	13	P	6	821.4264	+0.046473	821.4264	
-0.03553	1466.727	14	H	5	724.3737	+0.11828	724.3737	
-0.0711	1565.796	15	V	4	587.3148	+0.079902	587.3148	
-0.00132	1652.828	16	S	3	488.2463	+0.036133	488.2463	
	1749.881	17	P	2	401.2143	+0.006272	401.2143	
-0.1106	1878.923	18	E	1	304.1615		304.1615	
		19	R	0	175.119		175.119	

Scan number	5927	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	79.81



precursor information

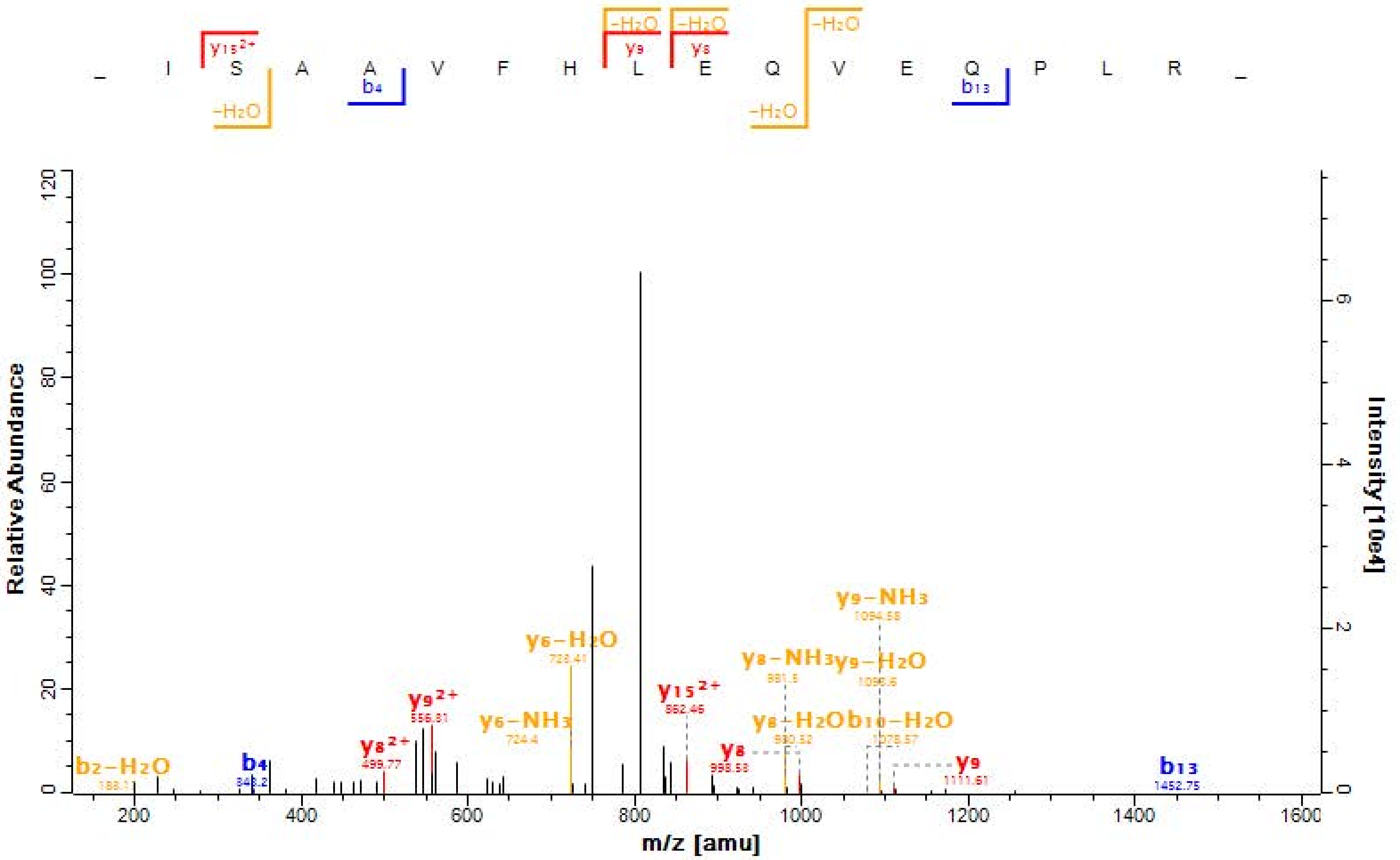
Mass:	1905.94687
m/z:	636.3229
Charge:	3+
Retentiontime:	37.812095642089
Score:	79.81033
Mass Error [ppm]:	−0.30509
PEP:	0.00014455
Precursor Type:	MULTI

general information

Annotation:	10 of 18
AminoAcids Coverag	56 %
Intensity Coverage:	37 %
Peak Coverage:	27 %
Protein Localisation:	37 ... 54

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	17				
	145.06		145.06	2	G	16	1834		1834	
	246.11	+0.0238	246.11	3	T	15	1776.9		888.97	+0.3521
	303.13		303.13	4	G	14	1675.9		838.45	+0.1621
	416.21	−0.025	416.21	5	I	13	1618.9		809.94	+0.1483
−0.072	244.13	+0.2487	487.25	6	A	12	1505.8		753.39	−0.005
	558.29		558.29	7	A	11	1434.7	−0.325	717.88	+0.1664
	689.33		689.33	8	M	10	1363.7		682.36	+0.1687
	776.36		776.36	9	S	9	1232.7		1232.7	
	875.43		875.43	10	V	8	1145.6		1145.6	
	1006.5	−0.091	1006.5	11	M	7	1046.6		523.79	−0.046
	1168.6		1168.6	12	R	6	915.53		458.27	−0.024
	1265.6		1265.6	13	P	5	753.41		753.41	
	1394.7		1394.7	14	E	4	656.35		656.35	
	1522.7		1522.7	15	Q	3	527.31		527.31	
	1635.8		1635.8	16	I	2	399.25	+0.058	399.25	
	1766.9		1766.9	17	M	1	286.17		286.17	
				18	K	0	155.13		155.13	

Scan number	5993	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	60.4



precursor information

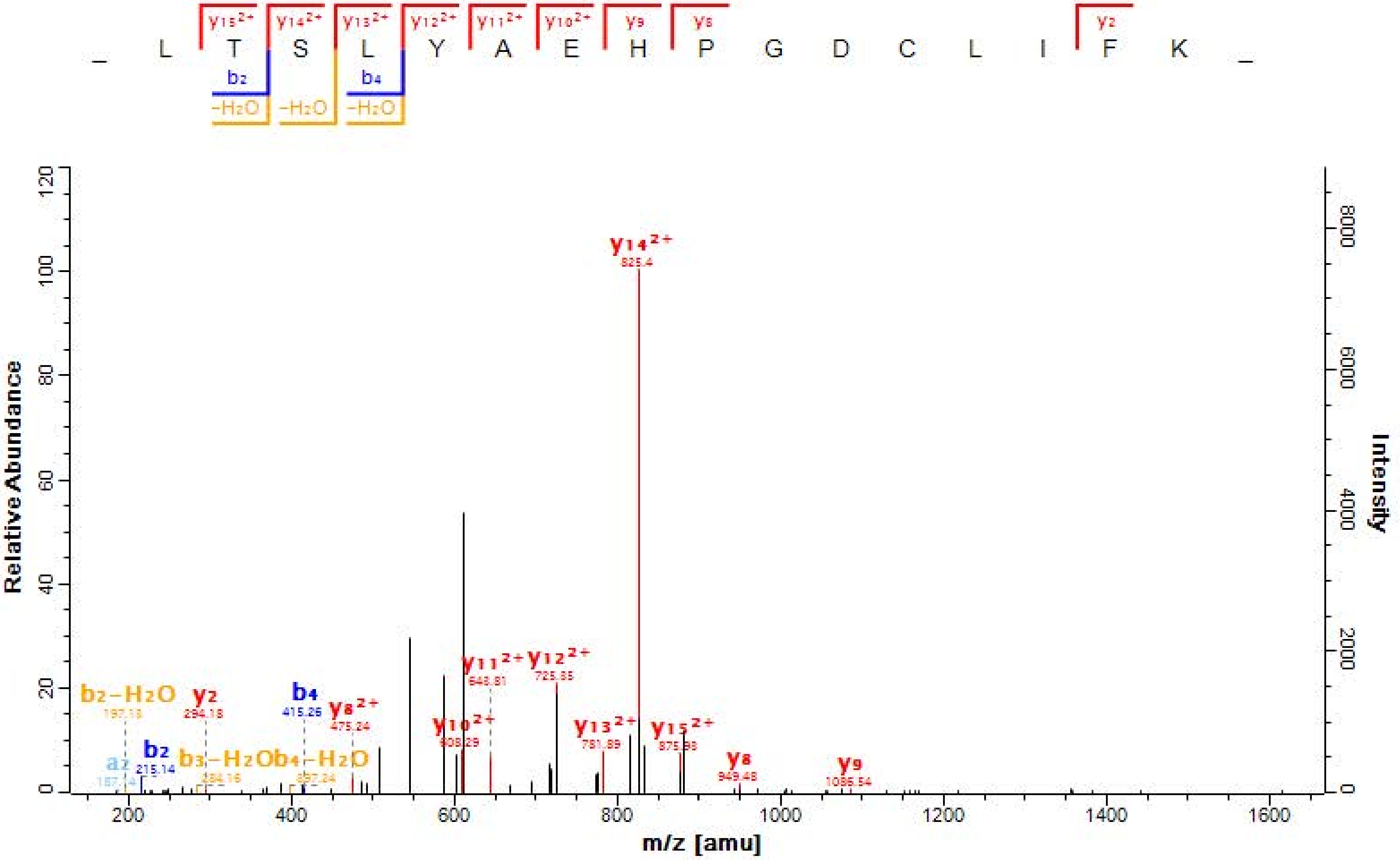
Mass:	1835.98991
m/z:	613.00391
Charge:	3+
Retentiontime:	38.176208496093
Score:	60.40071
Mass Error [ppm]:	0.28675
PEP:	0.0029715
Precursor Type:	MULTI

general information

Annotation:	7 of 16
AminoAcids Coverag	44 %
Intensity Coverage:	23 %
Peak Coverage:	16 %
Protein Localisation:	3454 ... 3469

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	I	15				
	201.1234	2	S	14	1723.913		862.4599	+0.297572
	272.1605	3	A	13	1636.881		1636.881	
+0.202428	343.1976	4	A	12	1565.843		1565.843	
	442.266	5	V	11	1494.806		1494.806	
	589.3344	6	F	10	1395.738		1395.738	
	726.3933	7	H	9	1248.67		1248.67	
	839.4774	8	L	8	1111.611	-0.10413	556.3089	+0.132407
	968.52	9	E	7	998.5265	-0.14543	499.7669	-0.25757
	1096.579	10	Q	6	869.4839		869.4839	
	1195.647	11	V	5	741.4254		741.4254	
	1324.69	12	E	4	642.357		642.357	
-0.04393	1452.748	13	Q	3	513.3144		513.3144	
	1549.801	14	P	2	385.2558		385.2558	
	1662.885	15	L	1	288.203		288.203	
		16	R	0	175.119		175.119	

Scan number	6224	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	70.44



precursor information

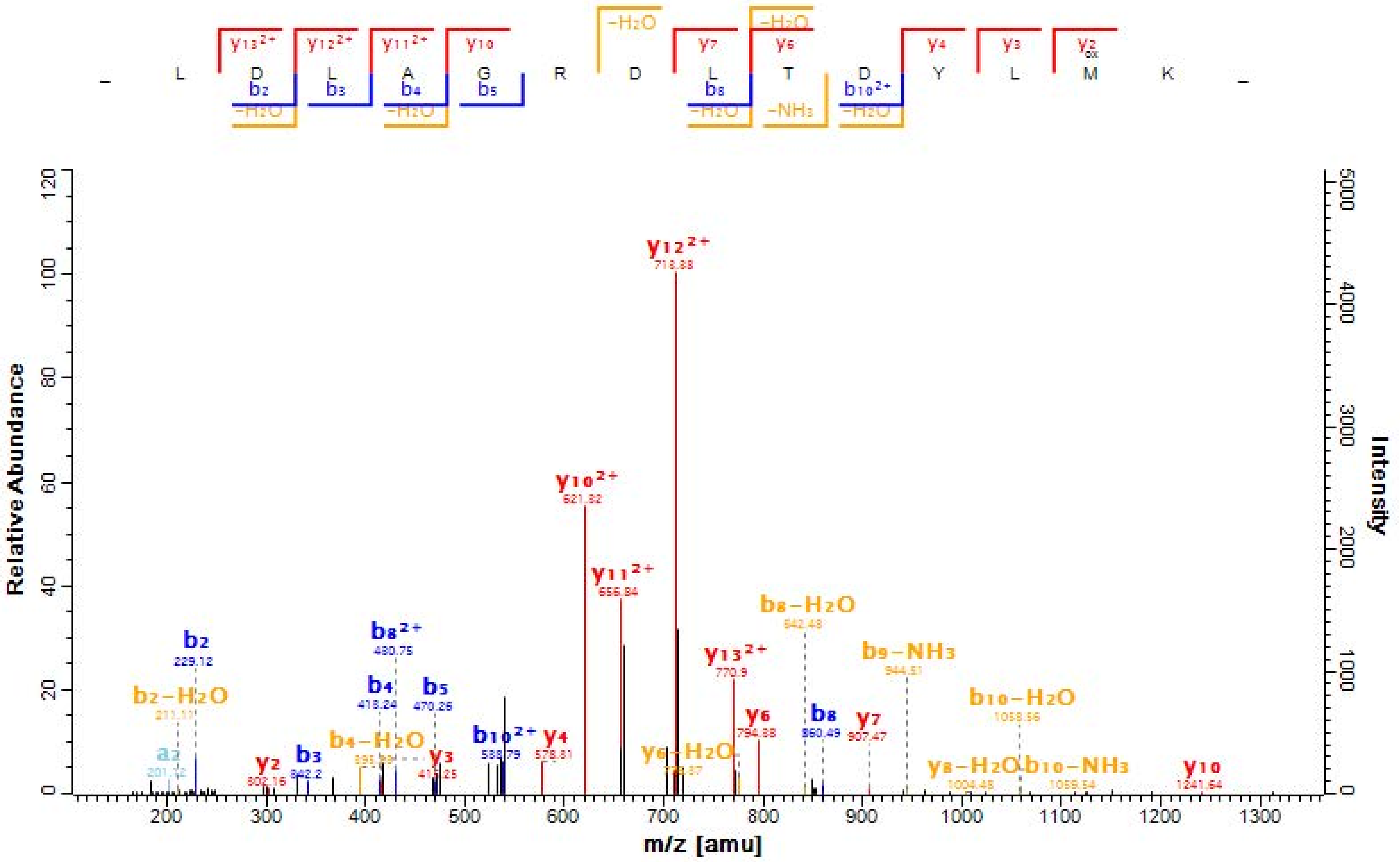
Mass:	1862.92442
m/z:	621.98208
Charge:	3+
Retentiontime:	39.497760772705
Score:	70.43787
Mass Error [ppm]:	0.39976
PEP:	0.00054339
Precursor Type:	MULTI

general information

Annotation:	9 of 16
AminoAcids Coverag	56 %
Intensity Coverage:	39 %
Peak Coverage:	14 %
Protein Localisation:	651 ... 666

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	15				
+0.0792	187.14	+0.0425	215.14	2	T	14	1750.8		875.93	+0.1925
	274.18		302.17	3	S	13	1649.8		825.4	+0.2187
	387.26	+0.175	415.26	4	L	12	1562.8		781.89	+0.3325
	550.32		578.32	5	Y	11	1449.7		725.35	+0.0272
	621.36		649.36	6	A	10	1286.6		643.81	+0.1191
	750.4		778.4	7	E	9	1215.6		608.29	+0.374
	887.46		915.46	8	H	8	1086.5	+0.3322	1086.5	
	984.51		1012.5	9	P	7	949.48	+0.0843	475.24	+0.0232
	1041.5		1069.5	10	G	6	852.43		852.43	
	1156.6		1184.6	11	D	5	795.41		795.41	
	1316.6		1344.6	12	C	4	680.38		680.38	
	1429.7		1457.7	13	L	3	520.35		520.35	
	1542.8		1570.8	14	I	2	407.27		407.27	
	1689.8		1717.8	15	F	1	294.18	-0.012	294.18	
				16	K	0	147.11		147.11	

Scan number	6473	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	117.2



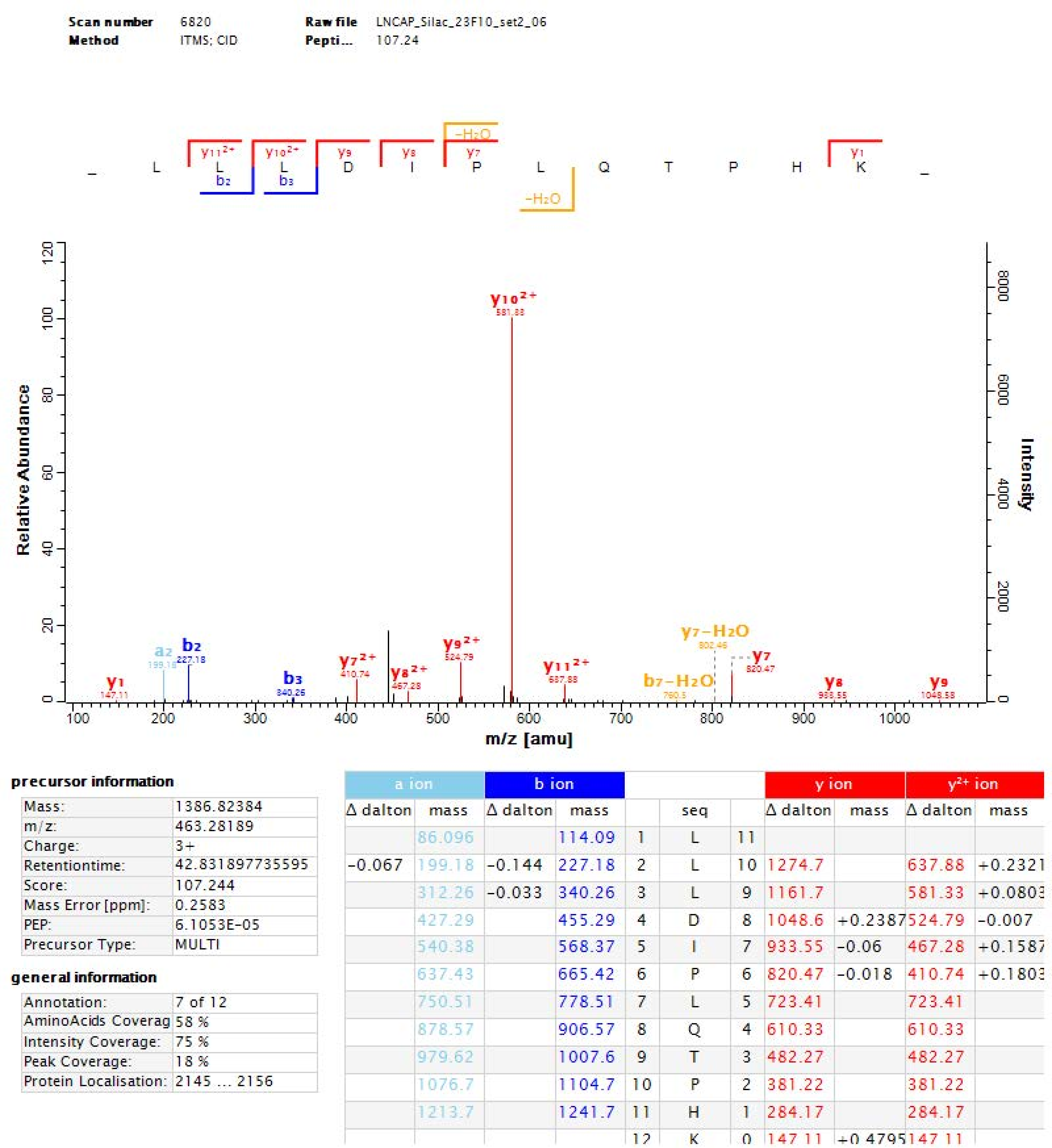
precursor information

Mass:	1638.82863
m/z:	547.28349
Charge:	3+
Retentiontime:	40.885448455810
Score:	117.2
Mass Error [ppm]:	-0.048372
PEP:	3.0564E-06
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	59 %
Peak Coverage:	23 %
Protein Localisation:	178 ... 191

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	13				
-0.01	201.1		229.1	-0.13	229.1	2	D	12	1541		770.9	+0.01
	314.2		342.2	-0.07	342.2	3	L	11	1426		713.4	-0.04
	385.2		413.2	+0.086	413.2	4	A	10	1313		656.8	-0.03
	442.3		470.3	-0.22	470.3	5	G	9	1242	+0.287	621.3	+0.13
	604.4		632.4		632.4	6	R	8	1185		1185	
	719.4		747.4		747.4	7	D	7	1022		1022	
	832.5	-0.05	430.8	+0.082	860.5	8	L	6	907.5	+0.079	907.5	
	933.5		961.5		961.5	9	T	5	794.4	-0.01	794.4	
	1049	-0.07	538.8		1077	10	D	4	693.3		693.3	
	1212		1240		1240	11	Y	3	578.3	+0.007	578.3	
	1325		1353		1353	12	L	2	415.2	+0.049	415.2	
	1472		1500		1500	13	M	1	302.2	+0	302.2	
						14	K	0	155.1		155.1	



Scan number	6820	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	107.24

precursor information

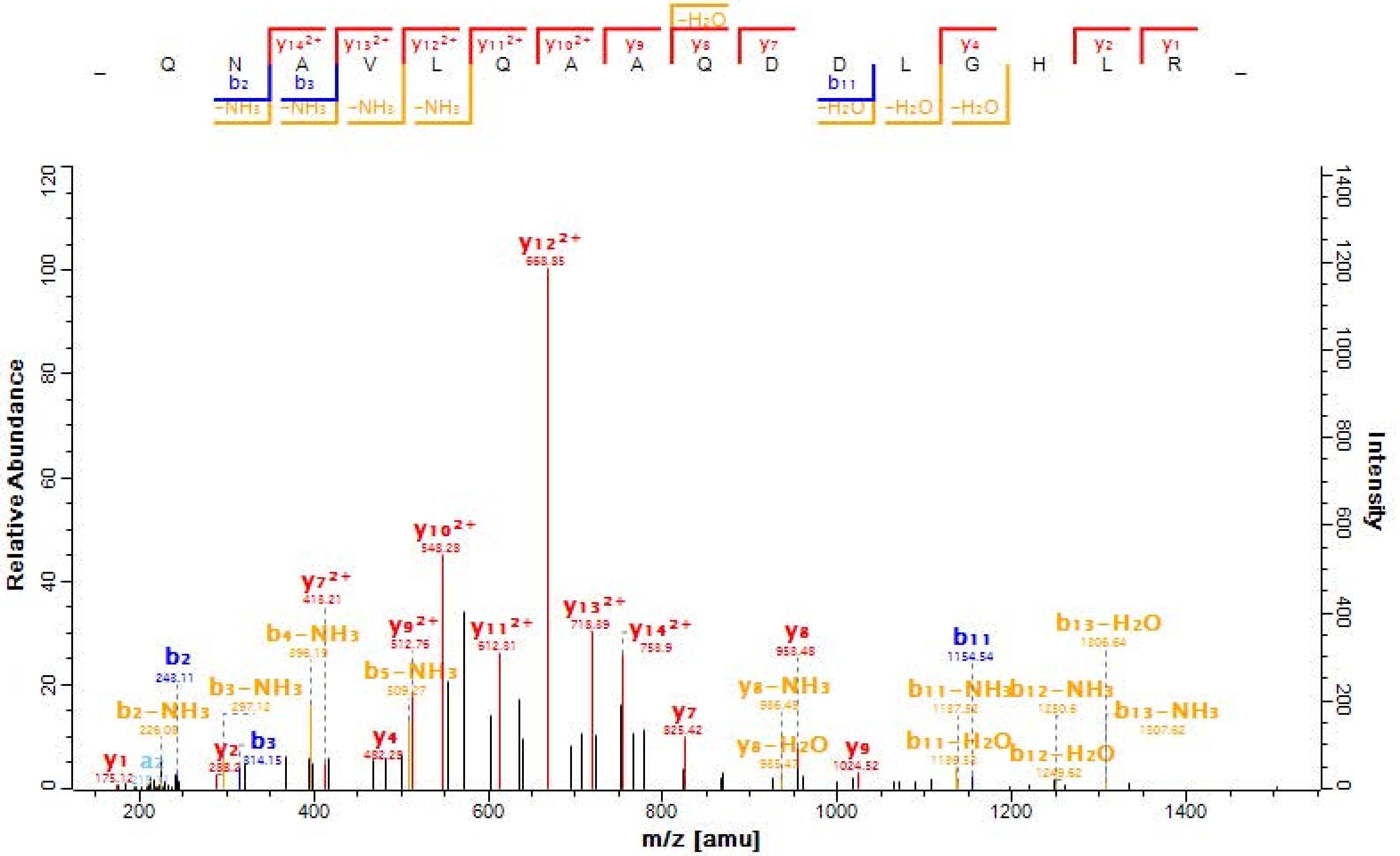
Mass:	1386.82384
m/z:	463.28189
Charge:	3+
Retentiontime:	42.831897735595
Score:	107.244
Mass Error [ppm]:	0.2583
PEP:	6.1053E-05
Precursor Type:	MULTI

general information

Annotation:	7 of 12
AminoAcids Coverag	58 %
Intensity Coverage:	75 %
Peak Coverage:	18 %
Protein Localisation:	2145 ... 2156

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	11				
-0.067	199.18	-0.144	227.18	2	L	10	1274.7		637.88	+0.2321
	312.26	-0.033	340.26	3	L	9	1161.7		581.33	+0.0803
	427.29		455.29	4	D	8	1048.6	+0.2387	524.79	-0.007
	540.38		568.37	5	I	7	933.55	-0.06	467.28	+0.1587
	637.43		665.42	6	P	6	820.47	-0.018	410.74	+0.1803
	750.51		778.51	7	L	5	723.41		723.41	
	878.57		906.57	8	Q	4	610.33		610.33	
	979.62		1007.6	9	T	3	482.27		482.27	
	1076.7		1104.7	10	P	2	381.22		381.22	
	1213.7		1241.7	11	H	1	284.17		284.17	
				12	K	0	147.11	+0.4795	147.11	

Scan number	7009	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	110.51



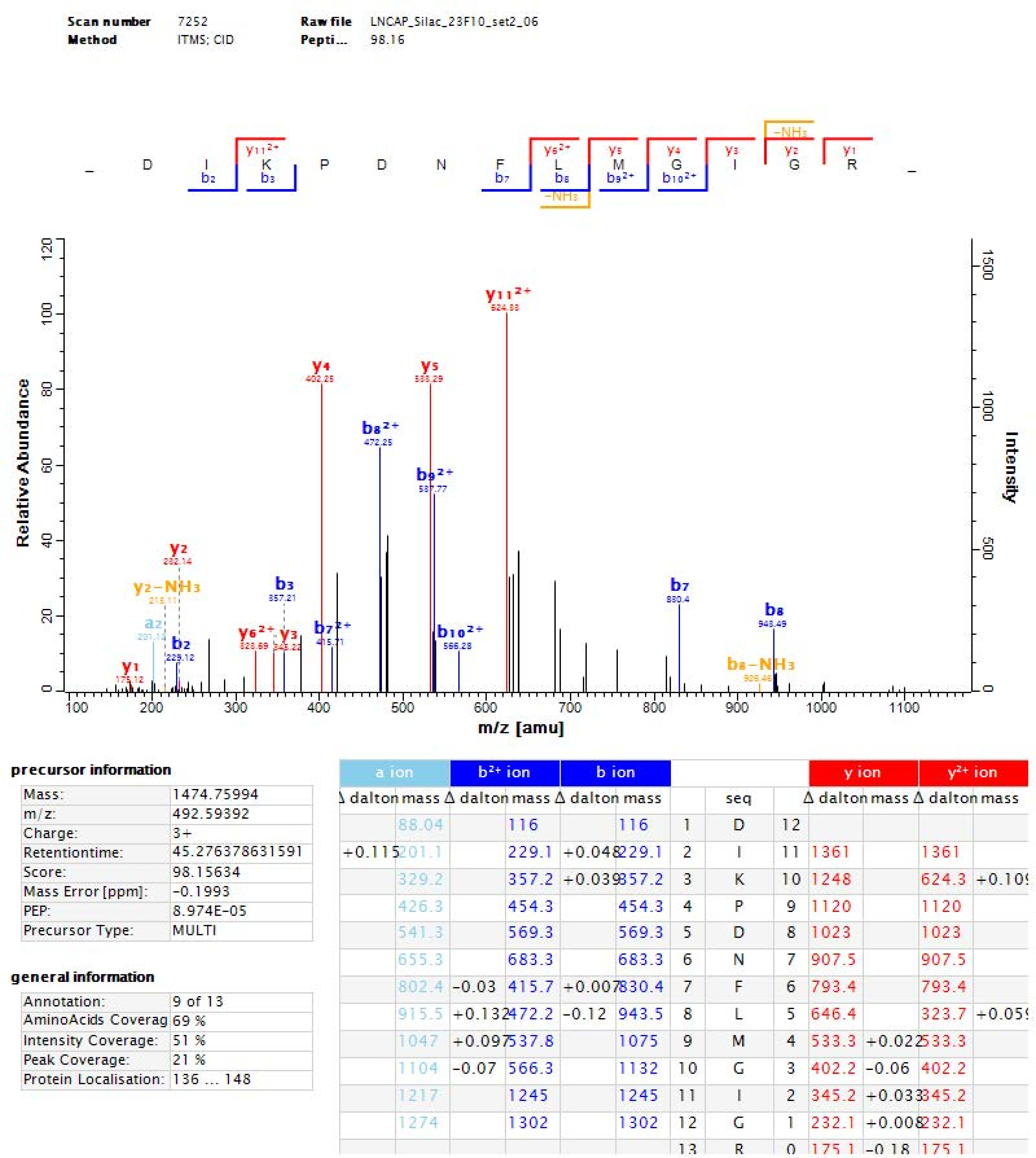
precursor information

Mass:	1747.89688
m/z:	583.63957
Charge:	3+
Retentiontime:	43.892982482910
Score:	110.5098
Mass Error [ppm]:	0.19267
PEP:	3.3823E-05
Precursor Type:	ISO

general information

Annotation:	14 of 16
AminoAcids Coverag	88 %
Intensity Coverage:	53 %
Peak Coverage:	31 %
Protein Localisation:	60 ... 75

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	101.07		129.07	1	Q	15				
-0.117	215.11	+0.2419	243.11	2	N	14	1620.8		1620.8	
	286.15	+0.0761	314.15	3	A	13	1506.8		753.9	+0.0719
	385.22		413.21	4	V	12	1435.8		718.39	+0.1041
	498.3		526.3	5	L	11	1336.7		668.85	+0.1672
	626.36		654.36	6	Q	10	1223.6		612.31	+0.0959
	697.4		725.39	7	A	9	1095.6		548.28	+0.1902
	768.44		796.43	8	A	8	1024.5	+0.0518	512.76	+0.0246
	896.49		924.49	9	Q	7	953.48	+0.1865	953.48	
	1011.5		1039.5	10	D	6	825.42	+0.0782	413.21	+0.1493
	1126.5	+0.366	1154.5	11	D	5	710.39		710.39	
	1239.6		1267.6	12	L	4	595.37		595.37	
	1296.7		1324.6	13	G	3	482.28	+0.0202	482.28	
	1433.7		1461.7	14	H	2	425.26		425.26	
	1546.8		1574.8	15	L	1	288.2	+0.1093	288.2	
				16	R	0	175.12	+0.0948	175.12	



Scan number	7252	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	98.16

precursor information

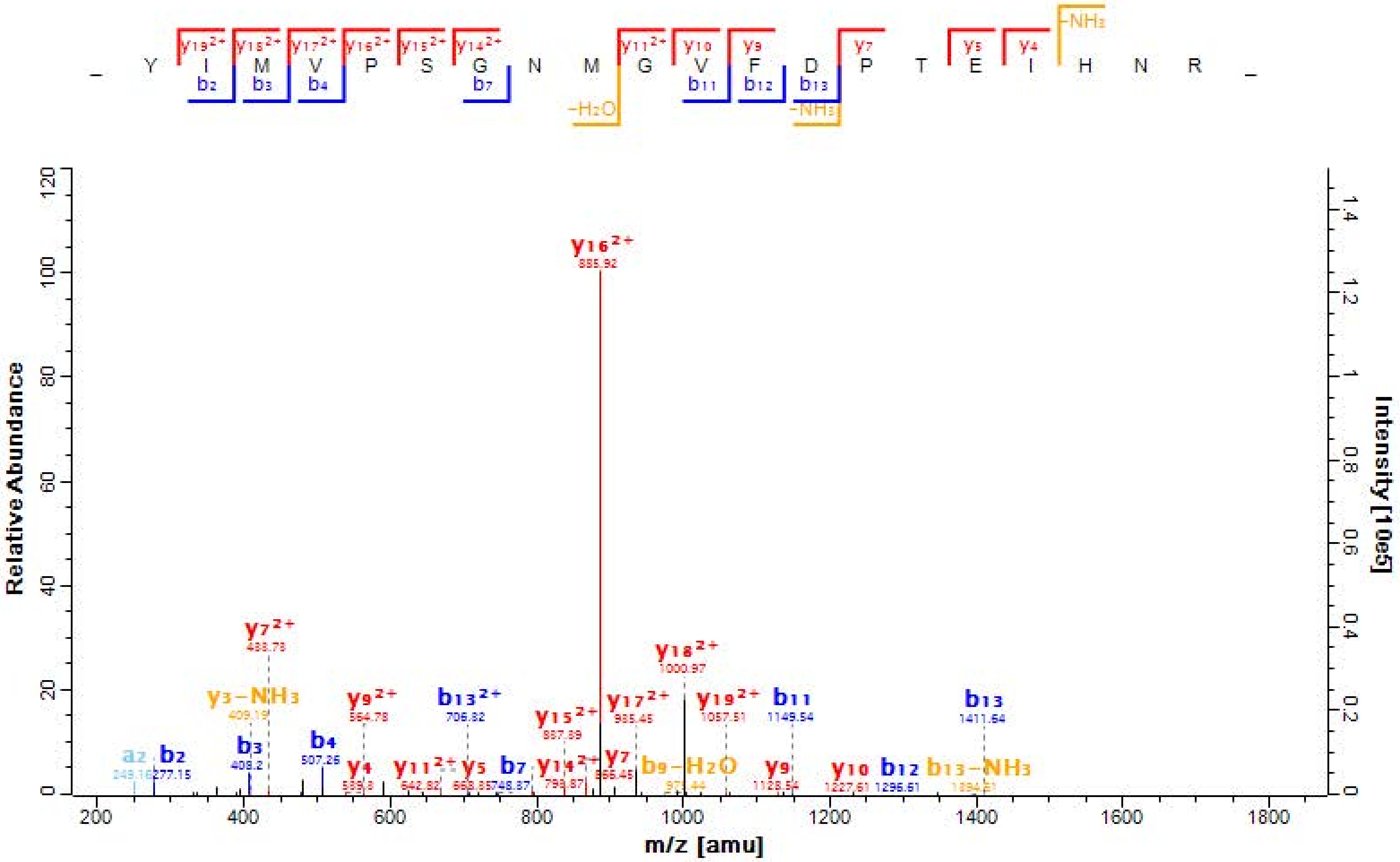
Mass:	1474.75994
m/z:	492.59392
Charge:	3+
Retentiontime:	45.276378631591
Score:	98.15634
Mass Error [ppm]:	-0.1993
PEP:	8.974E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	51 %
Peak Coverage:	21 %
Protein Localisation:	136 ... 148

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.04		116		116	1	D	12				
+0.115	201.1		229.1	+0.048	229.1	2	I	11	1361		1361	
	329.2		357.2	+0.039	357.2	3	K	10	1248		624.3	+0.10
	426.3		454.3		454.3	4	P	9	1120		1120	
	541.3		569.3		569.3	5	D	8	1023		1023	
	655.3		683.3		683.3	6	N	7	907.5		907.5	
	802.4	-0.03	415.7	+0.007	830.4	7	F	6	793.4		793.4	
	915.5	+0.132	472.2	-0.12	943.5	8	L	5	646.4		323.7	+0.05
	1047	+0.097	537.8		1075	9	M	4	533.3	+0.022	533.3	
	1104	-0.07	566.3		1132	10	G	3	402.2	-0.06	402.2	
	1217		1245		1245	11	I	2	345.2	+0.033	345.2	
	1274		1302		1302	12	G	1	232.1	+0.008	232.1	
						13	R	0	175.1	-0.18	175.1	

Scan number	7361	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	120.63



precursor information

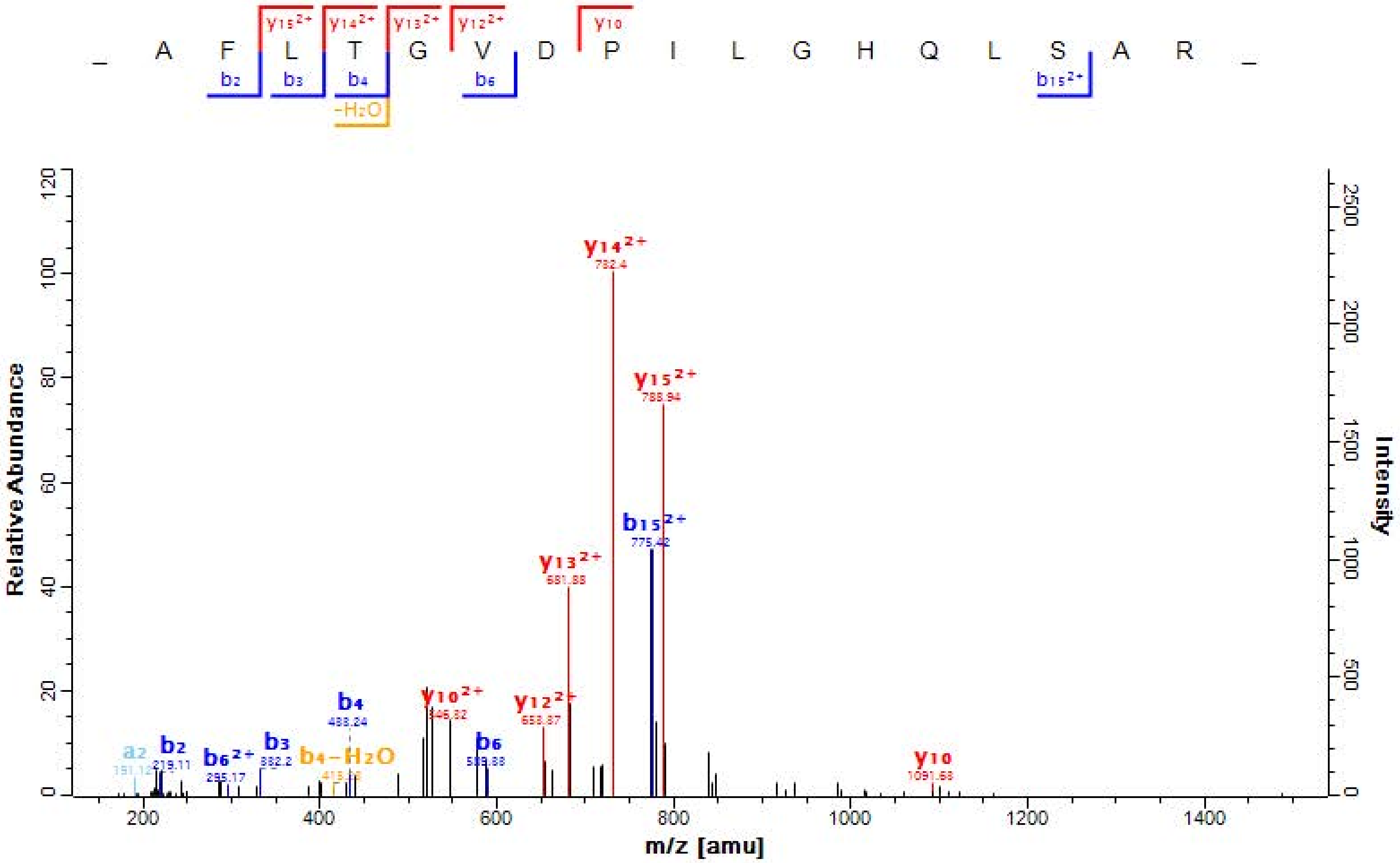
Mass:	2276.07187
m/z:	759.6979
Charge:	3+
Retentiontime:	45.876476287841
Score:	120.6271
Mass Error [ppm]:	0.02853
PEP:	9.4916E-13
Precursor Type:	MULTI

general information

Annotation:	15 of 20
AminoAcids Coverag	75 %
Intensity Coverage:	72 %
Peak Coverage:	31 %
Protein Localisation:	85 ... 104

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.1		164.1		164.1	1	Y	19				
+0.022	249.2		277.2	-0.02	277.2	2	I	18	2114		1058	+0.05
	380.2		408.2	-0.03	408.2	3	M	17	2001		1001	+0.02
	479.3		507.3	-0.05	507.3	4	V	16	1870		935.4	-0.04
	576.3		604.3		604.3	5	P	15	1771		885.9	+0.24
	663.4		691.3		691.3	6	S	14	1674		837.4	+0.31
	720.4		748.4	-0.29	748.4	7	G	13	1587		793.9	+0.24
	834.4		862.4		862.4	8	N	12	1530		1530	
	965.5		993.5		993.5	9	M	11	1416		1416	
	1022		1050		1050	10	G	10	1285		642.8	+0.44
	1122		1150	-0.04	1150	11	V	9	1228	-0.47	1228	
	1269		1297	+0.021	1297	12	F	8	1129	+0.099	564.8	+0.07
	1384	+0.415	706.3	-0.12	1412	13	D	7	981.5		981.5	
	1481		1509		1509	14	P	6	866.4	+0.082	433.7	+0.06
	1582		1610		1610	15	T	5	769.4		769.4	
	1711		1739		1739	16	E	4	668.3	+0.11	668.3	
	1824		1852		1852	17	I	3	539.3	+0.066	539.3	
	1961		1989		1989	18	H	2	426.2		426.2	
	2075		2103		2103	19	N	1	289.2		289.2	
						20	R	0	175.1		175.1	

Scan number	7412	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	55.72



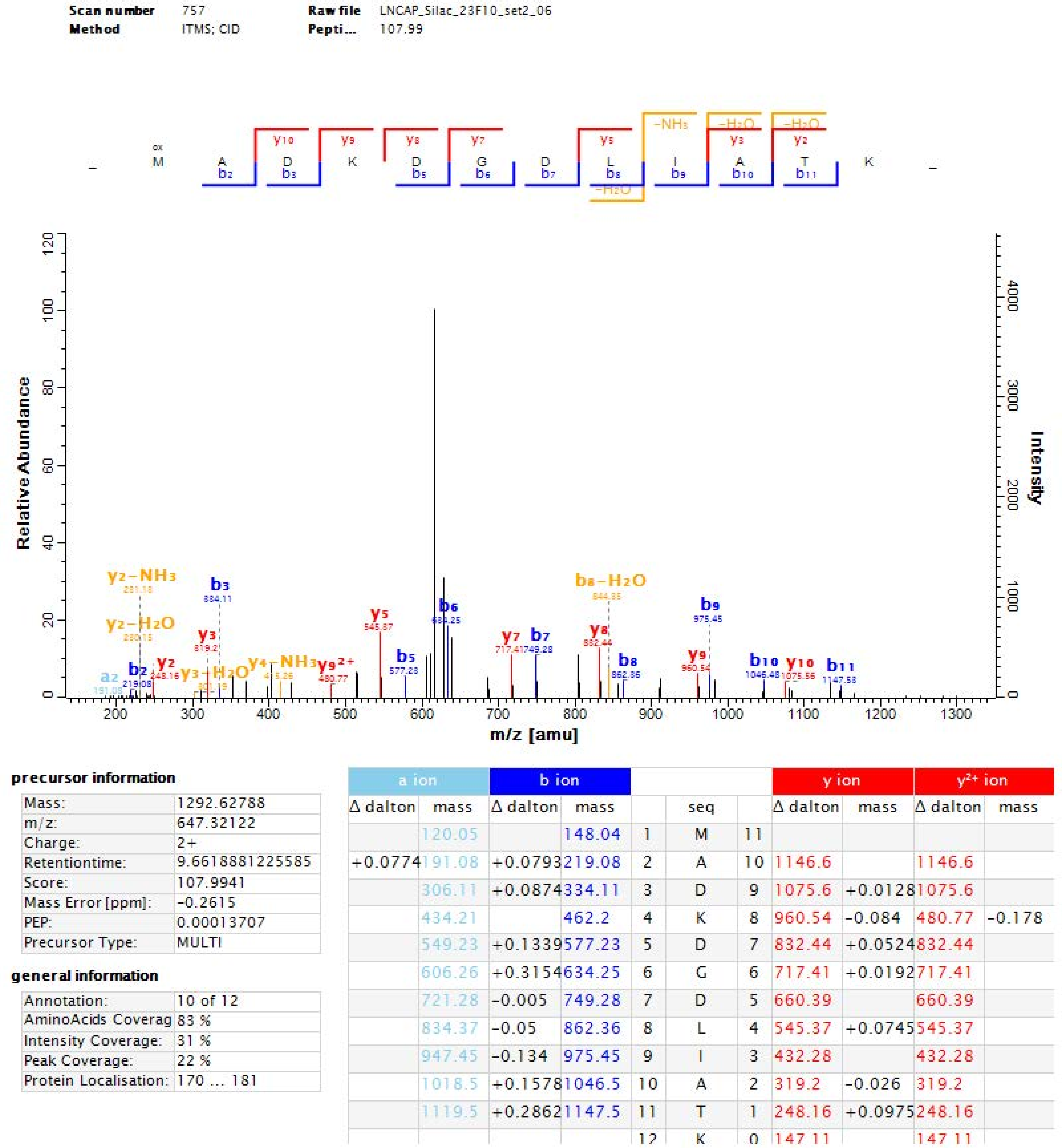
precursor information

Mass:	1793.97572
m/z:	598.99918
Charge:	3+
Retentiontime:	46.152130126953
Score:	55.72391
Mass Error [ppm]:	-1.7258
PEP:	0.0031535
Precursor Type:	MULTI

general information

Annotation:	7 of 17
AminoAcids Coverag	41 %
Intensity Coverage:	50 %
Peak Coverage:	17 %
Protein Localisation:	37 ... 53

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	44.05		72.04		72.04	1	A	16				
+0.01	191.1		219.1	-0.08	219.1	2	F	15	1724		1724	
	304.2		332.2	+0.077	332.2	3	L	14	1577		788.9	+0.20
	405.2		433.2	+0.091	433.2	4	T	13	1464		732.4	+0.21
	462.3		490.3		490.3	5	G	12	1363		681.9	+0
	561.3	-0.11	295.2	-0.29	589.3	6	V	11	1306		653.4	+0.12
	676.4		704.4		704.4	7	D	10	1207		1207	
	773.4		801.4		801.4	8	P	9	1092	+0	546.3	+0.01
	886.5		914.5		914.5	9	I	8	994.6		994.6	
	999.6		1028		1028	10	L	7	881.5		881.5	
	1057		1085		1085	11	G	6	768.4		768.4	
	1194		1222		1222	12	H	5	711.4		711.4	
	1322		1350		1350	13	Q	4	574.3		574.3	
	1435		1463		1463	14	L	3	446.3		446.3	
	1522	+0.269	775.4		1550	15	S	2	333.2		333.2	
	1593		1621		1621	16	A	1	246.2		246.2	
						17	R	0	175.1		175.1	



Scan number	757	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	107.99

precursor information

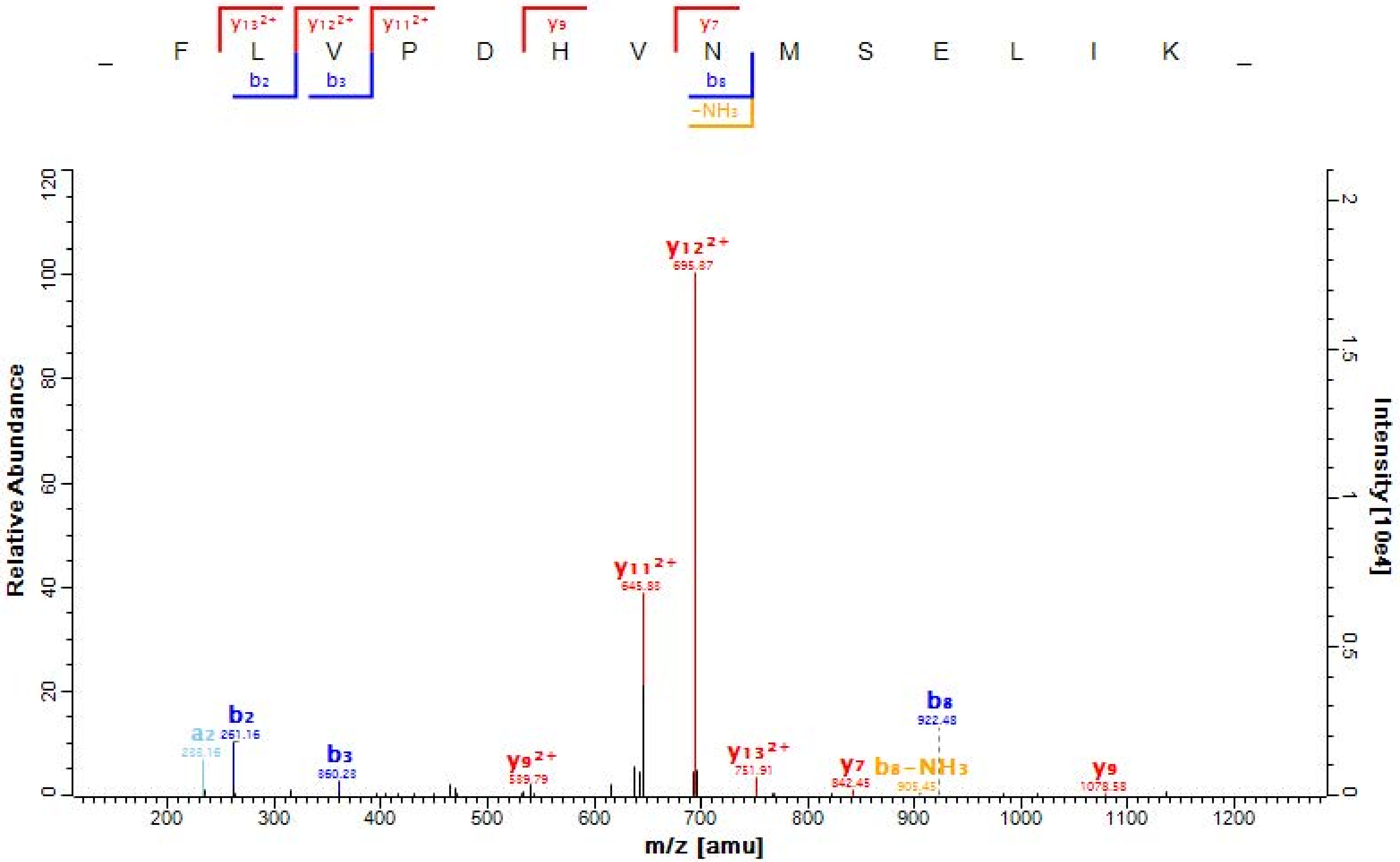
Mass:	1292.62788
m/z:	647.32122
Charge:	2+
Retentiontime:	9.6618881225585
Score:	107.9941
Mass Error [ppm]:	-0.2615
PEP:	0.00013707
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	31 %
Peak Coverage:	22 %
Protein Localisation:	170 ... 181

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.05		148.04	1	M	11				
+0.0774	191.08	+0.0793	219.08	2	A	10	1146.6		1146.6	
	306.11	+0.0874	334.11	3	D	9	1075.6	+0.0128	1075.6	
	434.21		462.2	4	K	8	960.54	-0.084	480.77	-0.178
	549.23	+0.1339	577.23	5	D	7	832.44	+0.0524	832.44	
	606.26	+0.3154	634.25	6	G	6	717.41	+0.0192	717.41	
	721.28	-0.005	749.28	7	D	5	660.39		660.39	
	834.37	-0.05	862.36	8	L	4	545.37	+0.0745	545.37	
	947.45	-0.134	975.45	9	I	3	432.28		432.28	
	1018.5	+0.1578	1046.5	10	A	2	319.2	-0.026	319.2	
	1119.5	+0.2862	1147.5	11	T	1	248.16	+0.0975	248.16	
				12	K	0	147.11		147.11	

Scan number	7757	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	86.31



precursor information

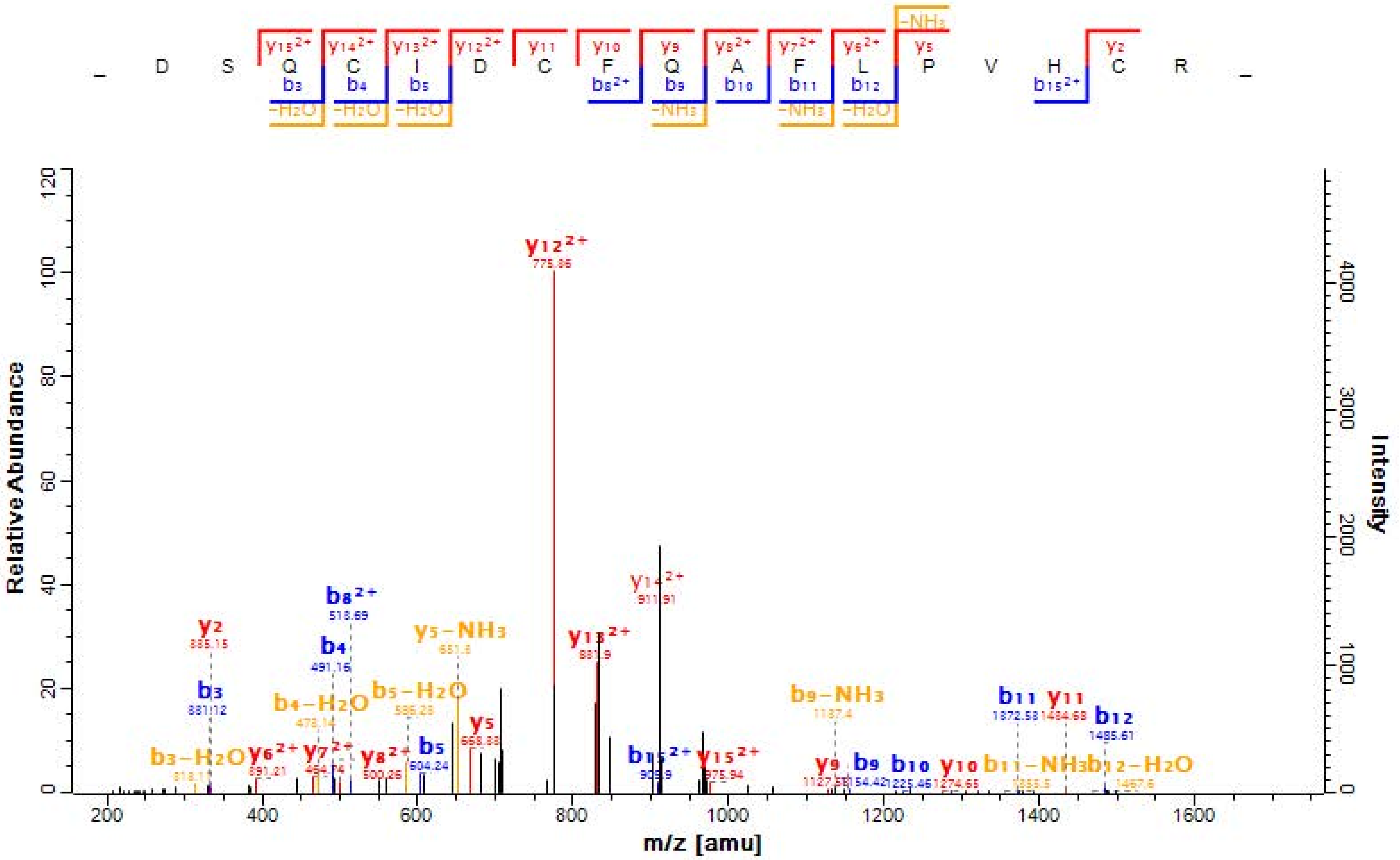
Mass:	1640.85956
m/z:	547.96046
Charge:	3+
Retentiontime:	48.122783660888
Score:	86.31258
Mass Error [ppm]:	-0.030261
PEP:	0.00044982
Precursor Type:	MULTI

general information

Annotation:	5 of 14
AminoAcids Coverag	36 %
Intensity Coverage:	73 %
Peak Coverage:	15 %
Protein Localisation:	52 ... 65

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08		148.08	1	F	13				
-0.048	233.16	-0.031	261.16	2	L	12	1502.8		751.91	+0.3291
	332.23	-0.026	360.23	3	V	11	1389.7		695.37	+0.184
	429.29		457.28	4	P	10	1290.7		645.83	+0.0381
	544.31		572.31	5	D	9	1193.6		1193.6	
	681.37		709.37	6	H	8	1078.6	-0.034	539.79	+0.0511
	780.44		808.44	7	V	7	941.52		941.52	
	894.48	+0.0062	922.48	8	N	6	842.45	-0.22	842.45	
	1025.5		1053.5	9	M	5	728.41		728.41	
	1112.6		1140.6	10	S	4	597.37		597.37	
	1241.6		1269.6	11	E	3	510.34		510.34	
	1354.7		1382.7	12	L	2	381.3		381.3	
	1467.8		1495.8	13	I	1	268.21		268.21	
				14	K	0	155.13		155.13	

Scan number	7877	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	152.88



precursor information

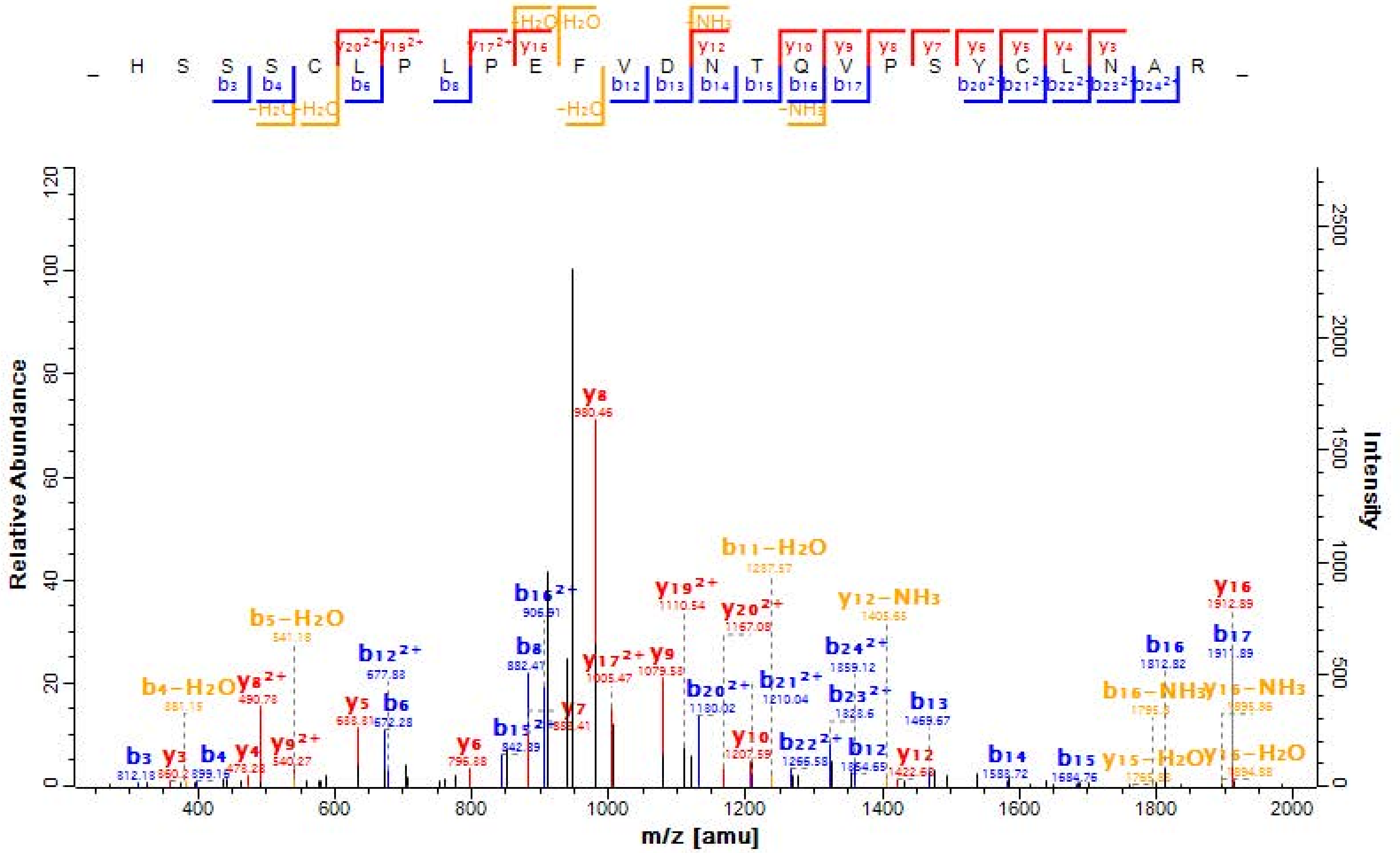
Mass:	2151.92885
m/z:	718.31689
Charge:	3+
Retentiontime:	48.826297760009
Score:	152.8763
Mass Error [ppm]:	0.002086
PEP:	1.5081E-22
Precursor Type:	MULTI

general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	45 %
Peak Coverage:	28 %
Protein Localisation:	135 ... 151

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	16				
	203.07		203.07	2	S	15	2037.9		2037.9	
	331.12	+0.0574	331.12	3	Q	14	1950.9		975.94	+0.3163
	491.16	+0.1213	491.16	4	C	13	1822.8		911.91	-0.051
	604.24	+0.1615	604.24	5	I	12	1662.8		831.9	+0.0213
	719.27		719.27	6	D	11	1549.7		775.36	+0.2536
	879.3		879.3	7	C	10	1434.7	+0.3105	1434.7	
-0.381	513.69		1026.4	8	F	9	1274.6	+0.2068	1274.6	
	1154.4	+0.2963	1154.4	9	Q	8	1127.6	+0.257	1127.6	
	1225.5	+0.0289	1225.5	10	A	7	999.52		500.26	+0.2215
	1372.5	+0.0051	1372.5	11	F	6	928.48		464.74	-0.158
	1485.6	-0.126	1485.6	12	L	5	781.41		391.21	+0.2861
	1582.7		1582.7	13	P	4	668.33	+0.1132	668.33	
	1681.7		1681.7	14	V	3	571.28		571.28	
+0.3253	909.9		1818.8	15	H	2	472.21		472.21	
	1978.8		1978.8	16	C	1	335.15	-0.168	335.15	
				17	R	0	175.12		175.12	

Scan number	7977	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	184.62



precursor information

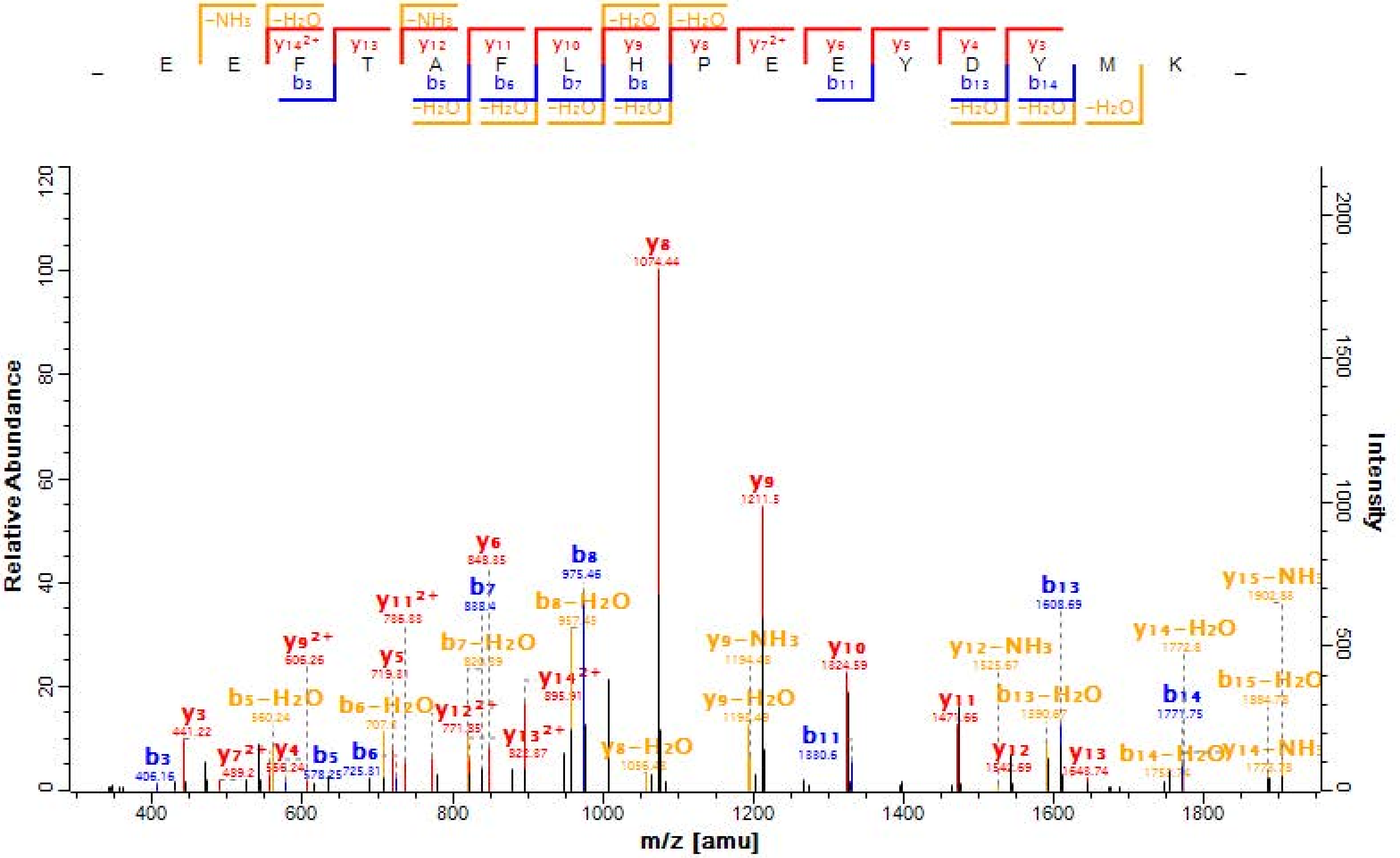
Mass:	2890.33626
m/z:	964.4527
Charge:	3+
Retentiontime:	49.434211730957
Score:	184.6166
Mass Error [ppm]:	-0.53641
PEP:	6.257E-52
Precursor Type:	MULTI

general information

Annotation:	22 of 25
AminoAcids Coverag	88 %
Intensity Coverage:	45 %
Peak Coverage:	42 %
Protein Localisation:	85 ... 109

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.07		138.07	1	H	24				
	225.1		225.1	2	S	23	2754.3		2754.3	
	312.13	-0.452	312.13	3	S	22	2667.3		2667.3	
	399.16	+0.1978	399.16	4	S	21	2580.2		2580.2	
	559.19		559.19	5	C	20	2493.2		2493.2	
	672.28	-0.051	672.28	6	L	19	2333.2		1167.1	+0.3568
	769.33		769.33	7	P	18	2220.1		1110.5	+0.3041
	882.41	+0.0637	882.41	8	L	17	2123		2123	
	979.47		979.47	9	P	16	2009.9		1005.5	-0.015
	1108.5		1108.5	10	E	15	1912.9	-0.14	1912.9	
	1255.6		1255.6	11	F	14	1783.8		1783.8	
+0.1597	677.83	-0.272	1354.6	12	V	13	1636.8		1636.8	
	1469.7	-0.229	1469.7	13	D	12	1537.7		1537.7	
	1583.7	+0	1583.7	14	N	11	1422.7	-0.068	1422.7	
+0.0561	842.89	+0.0615	1684.8	15	T	10	1308.6		1308.6	
+0.2777	906.91	-0.37	1812.8	16	Q	9	1207.6	-0.074	1207.6	
	1911.9	+0.0428	1911.9	17	V	8	1079.5	+0.0176	540.27	+0.2427
	2008.9		2008.9	18	P	7	980.46	-0.019	490.73	+0.2268
	2096		2096	19	S	6	883.41	+0.0651	883.41	
+0.2533	1130		2259	20	Y	5	796.38	+0.0174	796.38	
+0.3377	1210		2419.1	21	C	4	633.31	+0.0521	633.31	
-0.161	1266.6		2532.2	22	L	3	473.28	+0.1048	473.28	
+0.3888	1323.6		2646.2	23	N	2	360.2	+0.0131	360.2	
+0.4182	1359.1		2717.2	24	A	1	246.16		246.16	
				25	R	0	175.12		175.12	

Scan number	7989	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	227.47



precursor information

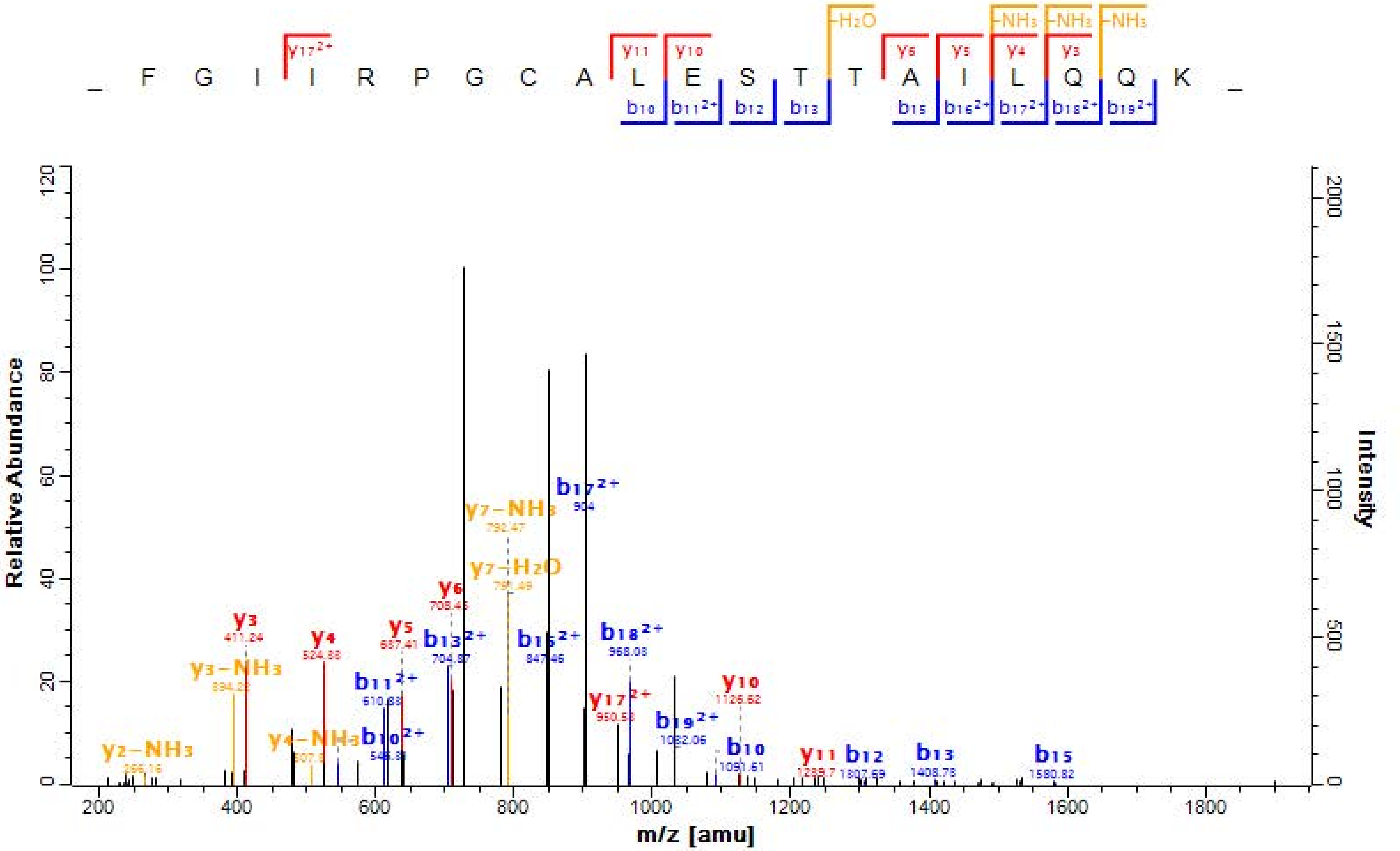
Mass:	2047.88718
m/z:	1024.95087
Charge:	2+
Retentiontime:	49.505222320556
Score:	227.4685
Mass Error [ppm]:	-0.079255
PEP:	2.2613E-41
Precursor Type:	MULTI

general information

Annotation:	14 of 16
AminoAcids Coverag	88 %
Intensity Coverage:	60 %
Peak Coverage:	39 %
Protein Localisation:	182 … 197

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	15				
	259.0925	2	E	14	1919.852		1919.852	
+0.248151	406.1609	3	F	13	1790.809		895.9084	+0.315521
	507.2086	4	T	12	1643.741	-0.10345	822.3741	+0.191647
+0.108457	578.2457	5	A	11	1542.693	-0.22227	771.8503	-0.19626
+0.047673	725.3141	6	F	10	1471.656	-0.06236	736.3318	+0.235264
-0.02302	838.3981	7	L	9	1324.588	-0.01042	1324.588	
-0.03933	975.4571	8	H	8	1211.504	-0.0477	606.2555	+0.162577
	1072.51	9	P	7	1074.445	+0.001084	1074.445	
	1201.552	10	E	6	977.3921		489.1997	+0.339936
-0.02726	1330.595	11	E	5	848.3495	-0.01892	848.3495	
	1493.658	12	Y	4	719.3069	-0.02088	719.3069	
-0.02476	1608.685	13	D	3	556.2436	+0.114594	556.2436	
-0.20344	1771.749	14	Y	2	441.2166	+0.060147	441.2166	
	1902.789	15	M	1	278.1533		278.1533	
		16	K	0	147.1128		147.1128	

Scan number	8080	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	80.54



precursor information

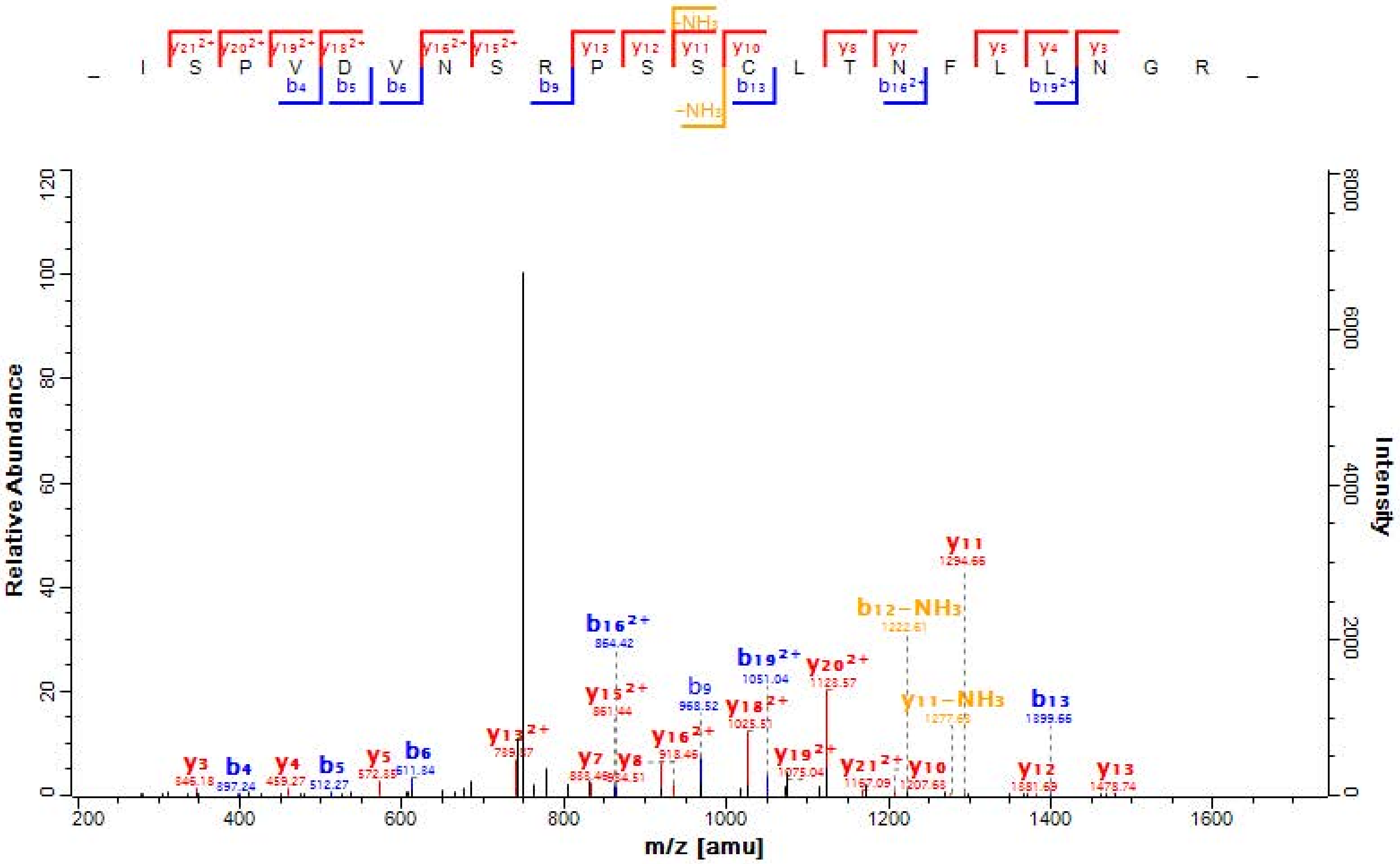
Mass:	2202.18318
m/z:	735.06834
Charge:	3+
Retentiontime:	50.078125
Score:	80.54491
Mass Error [ppm]:	0.046369
PEP:	8.5693E-05
Precursor Type:	MULTI

general information

Annotation:	11 of 20
AminoAcids Coverag	55 %
Intensity Coverage:	34 %
Peak Coverage:	25 %
Protein Localisation:	249 ... 268

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.08		148.08	1	F	19				
	205.1		205.1	2	G	18	2070.2		2070.2	
	318.18		318.18	3	I	17	2013.1		2013.1	
	431.27		431.27	4	I	16	1900.1		950.53	-0.224
	593.39		593.39	5	R	15	1787		1787	
	690.44		690.44	6	P	14	1624.8		1624.8	
	747.46		747.46	7	G	13	1527.8		1527.8	
	907.49		907.49	8	C	12	1470.8		1470.8	
	978.53		978.53	9	A	11	1310.7		1310.7	
+0.0638	546.31	-0.137	1091.6	10	L	10	1239.7	-0.191	1239.7	
+0.1426	610.83		1220.7	11	E	9	1126.6	-0.423	1126.6	
	1307.7	-0.025	1307.7	12	S	8	997.58		997.58	
+0.0293	704.87	+0.2765	1408.7	13	T	7	910.54		910.54	
	1509.8		1509.8	14	T	6	809.5		809.5	
	1580.8	-0.092	1580.8	15	A	5	708.45	+0.0398	708.45	
-0.083	847.46		1693.9	16	I	4	637.41	+0.014	637.41	
-0.101	904		1807	17	L	3	524.33	-0.01	524.33	
+0.291	968.03		1935	18	Q	2	411.24	+0.0915	411.24	
-0.234	1032.1		2063.1	19	Q	1	283.19		283.19	
				20	K	0	155.13		155.13	

Scan number	8331	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	96.39



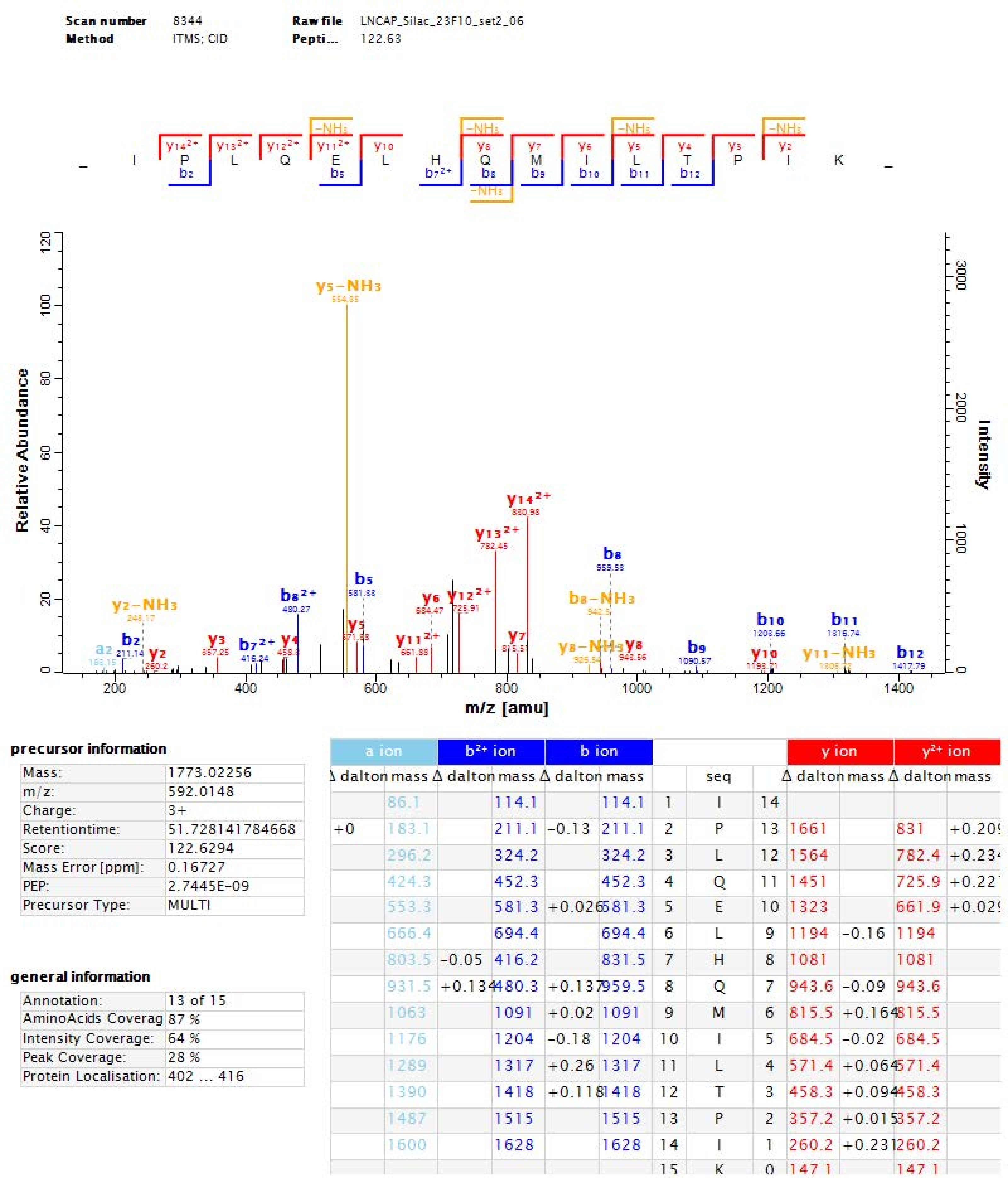
precursor information

Mass:	2445.24324
m/z:	816.08836
Charge:	3+
Retentiontime:	51.647369384765
Score:	96.39133
Mass Error [ppm]:	-0.08069
PEP:	2.0036E-06
Precursor Type:	MULTI

general information

Annotation:	17 of 22
AminoAcids Coverag	77 %
Intensity Coverage:	33 %
Peak Coverage:	30 %
Protein Localisation:	337 ... 358

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	I	21				
	201.12		201.12	2	S	20	2333.2		1167.1	+0.1625
	298.18		298.18	3	P	19	2246.1		1123.6	+0.1511
	397.24	+0.0648	397.24	4	V	18	2149.1		1075	-0.265
	512.27	-0.066	512.27	5	D	17	2050		1025.5	+0.1745
	611.34	+0.2203	611.34	6	V	16	1935		1935	
	725.38		725.38	7	N	15	1835.9		918.46	+0.4268
	812.41		812.41	8	S	14	1721.9		861.44	+0.1613
	968.52	-0.03	968.52	9	R	13	1634.8		1634.8	
	1065.6		1065.6	10	P	12	1478.7	+0.2002	739.87	+0.2463
	1152.6		1152.6	11	S	11	1381.7	+0.0627	1381.7	
	1239.6		1239.6	12	S	10	1294.7	-0.13	1294.7	
	1399.7	-0.008	1399.7	13	C	9	1207.6	+0.0433	1207.6	
	1512.7		1512.7	14	L	8	1047.6		1047.6	
	1613.8		1613.8	15	T	7	934.51	-0.035	934.51	
+0.4338	864.42		1727.8	16	N	6	833.46	-0.129	833.46	
	1874.9		1874.9	17	F	5	719.42		719.42	
	1988		1988	18	L	4	572.35	+0.0807	572.35	
+0.3445	1051		2101.1	19	L	3	459.27	+0.0275	459.27	
	2215.1		2215.1	20	N	2	346.18	+0.0123	346.18	
	2272.1		2272.1	21	G	1	232.14		232.14	
				22	R	0	175.12		175.12	



Scan number	8344	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	122.63

precursor information

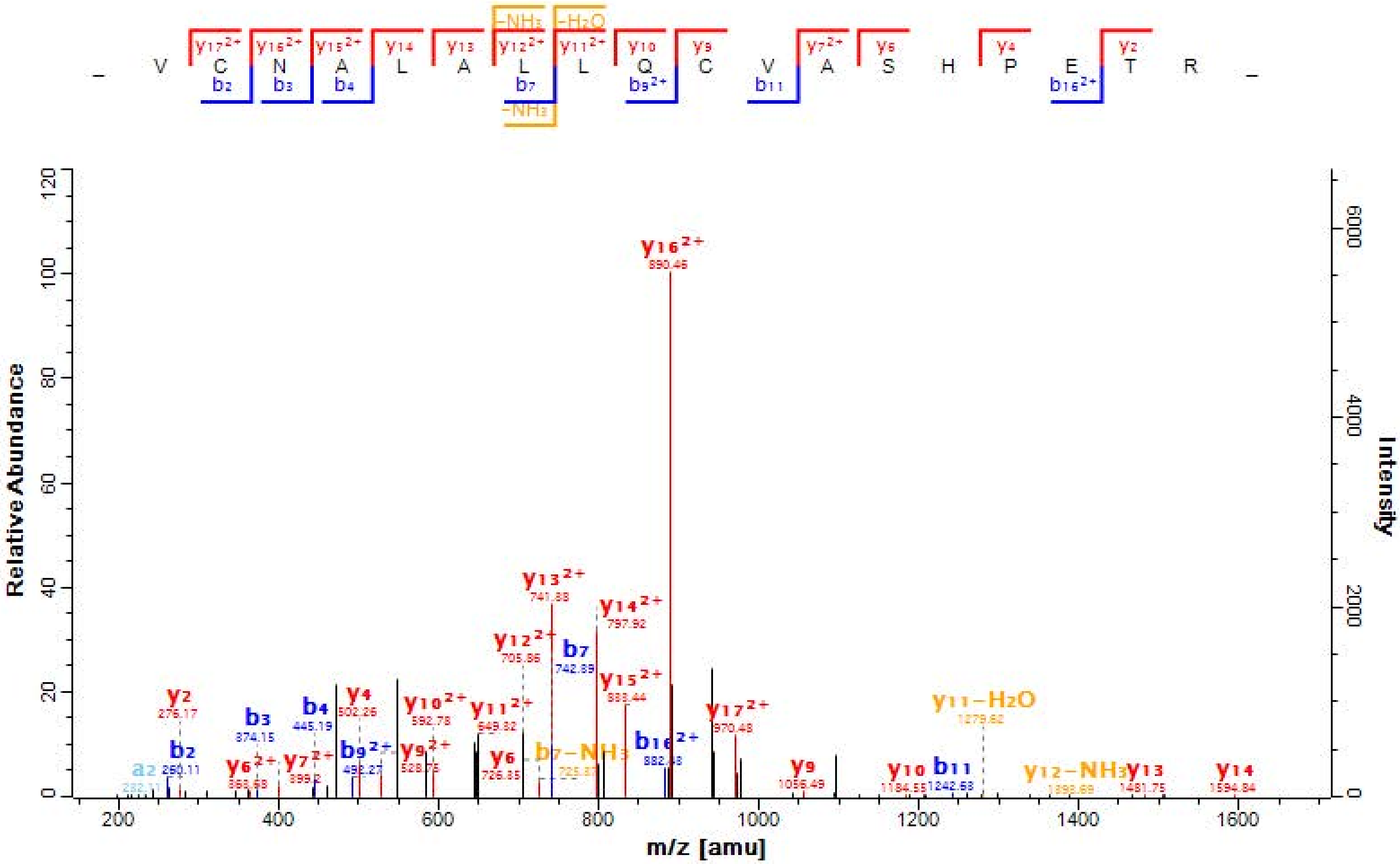
Mass:	1773.02256
m/z:	592.0148
Charge:	3+
Retentiontime:	51.728141784668
Score:	122.6294
Mass Error [ppm]:	0.16727
PEP:	2.7445E-09
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	64 %
Peak Coverage:	28 %
Protein Localisation:	402 ... 416

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	I	14				
+0	183.1		211.1	−0.13	211.1	2	P	13	1661		831	+0.20
	296.2		324.2		324.2	3	L	12	1564		782.4	+0.23
	424.3		452.3		452.3	4	Q	11	1451		725.9	+0.22
	553.3		581.3	+0.026	581.3	5	E	10	1323		661.9	+0.02
	666.4		694.4		694.4	6	L	9	1194	−0.16	1194	
	803.5	−0.05	416.2		831.5	7	H	8	1081		1081	
	931.5	+0.134	480.3	+0.137	959.5	8	Q	7	943.6	−0.09	943.6	
	1063		1091	+0.02	1091	9	M	6	815.5	+0.164	815.5	
	1176		1204	−0.18	1204	10	I	5	684.5	−0.02	684.5	
	1289		1317	+0.26	1317	11	L	4	571.4	+0.064	571.4	
	1390		1418	+0.118	1418	12	T	3	458.3	+0.094	458.3	
	1487		1515		1515	13	P	2	357.2	+0.015	357.2	
	1600		1628		1628	14	I	1	260.2	+0.231	260.2	
						15	K	0	147.1		147.1	

Scan number	8360	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	137.21



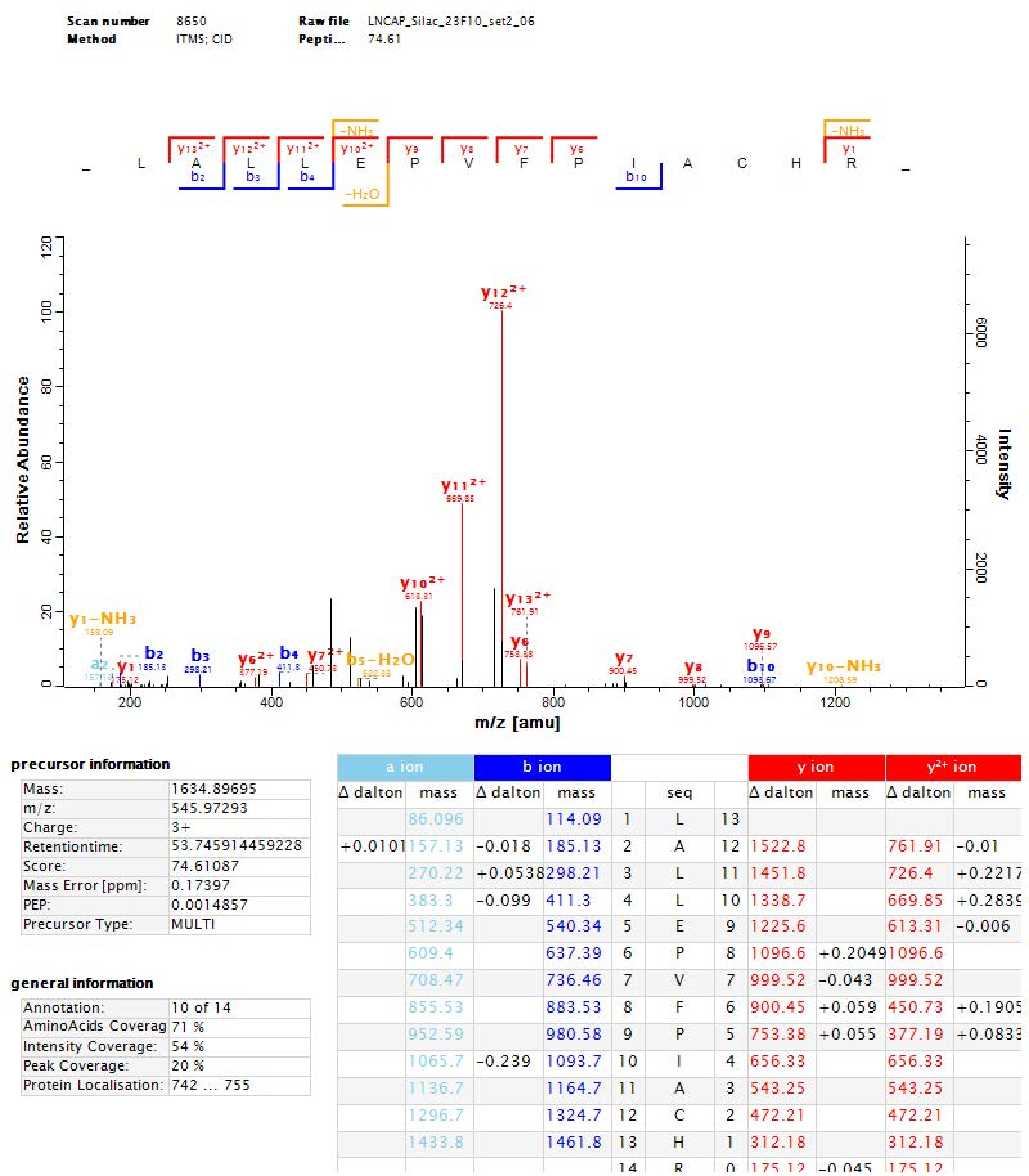
precursor information

Mass:	2038.00899
m/z:	680.34361
Charge:	3+
Retentiontime:	51.833724975585
Score:	137.207
Mass Error [ppm]:	0.084682
PEP:	3.4997E-17
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	52 %
Peak Coverage:	28 %
Protein Localisation:	90 ... 107

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.08		100.1		100.1	1	V	17				
+0	232.1		260.1	+0.088	260.1	2	C	16	1940		970.5	+0.19
	346.2		374.1	-0.01	374.1	3	N	15	1780		890.5	+0.34
	417.2		445.2	+0.002	445.2	4	A	14	1666		833.4	+0.21
	530.3		558.3		558.3	5	L	13	1595	+0.113	797.9	+0.19
	601.3		629.3		629.3	6	A	12	1482	+0.058	741.4	+0.25
	714.4		742.4	+0.215	742.4	7	L	11	1411		705.9	+0.05
	827.5		855.5		855.5	8	L	10	1298		649.3	+0.10
	955.5	-0.39	492.3		983.5	9	Q	9	1185	+0.129	592.8	+0.07
	1116		1144		1144	10	C	8	1056	+0.152	528.7	+0.18
	1215		1243	+0.017	1243	11	V	7	896.5		896.5	
	1286		1314		1314	12	A	6	797.4		399.2	+0.17
	1373		1401		1401	13	S	5	726.4	+0.094	363.7	+0.36
	1510		1538		1538	14	H	4	639.3		639.3	
	1607		1635		1635	15	P	3	502.3	-0.02	502.3	
	1736	-0.28	882.4		1764	16	E	2	405.2		405.2	
	1837		1865		1865	17	T	1	276.2	+0.101	276.2	
						18	R	0	175.1		175.1	



Scan number	8650	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	74.61

precursor information

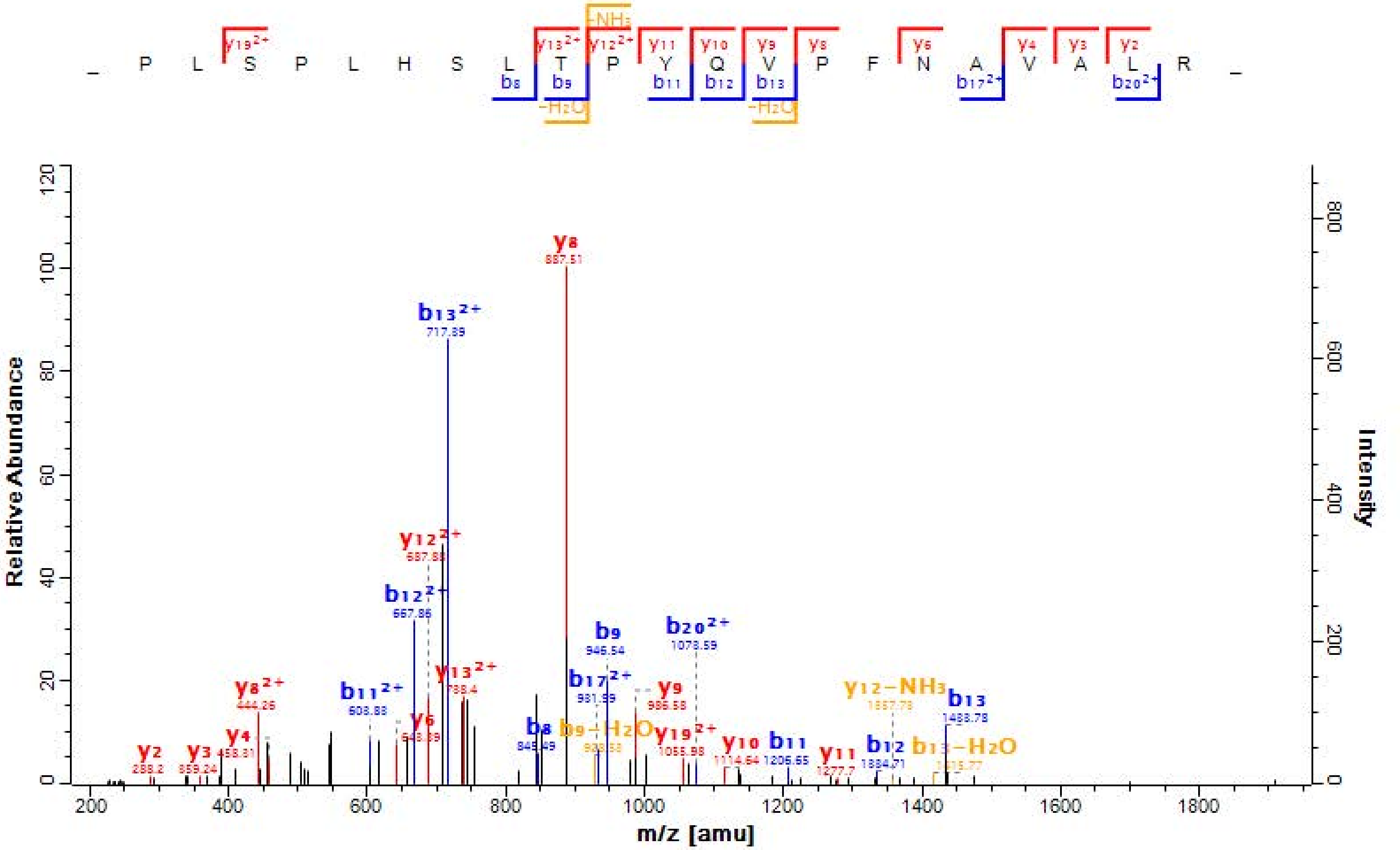
Mass:	1634.89695
m/z:	545.97293
Charge:	3+
Retentiontime:	53.745914459228
Score:	74.61087
Mass Error [ppm]:	0.17397
PEP:	0.0014857
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	54 %
Peak Coverage:	20 %
Protein Localisation:	742 ... 755

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	13				
+0.0101	157.13	-0.018	185.13	2	A	12	1522.8		761.91	-0.01
	270.22	+0.0538	298.21	3	L	11	1451.8		726.4	+0.2217
	383.3	-0.099	411.3	4	L	10	1338.7		669.85	+0.2839
	512.34		540.34	5	E	9	1225.6		613.31	-0.006
	609.4		637.39	6	P	8	1096.6	+0.2049	1096.6	
	708.47		736.46	7	V	7	999.52	-0.043	999.52	
	855.53		883.53	8	F	6	900.45	+0.059	450.73	+0.1905
	952.59		980.58	9	P	5	753.38	+0.055	377.19	+0.0833
	1065.7	-0.239	1093.7	10	I	4	656.33		656.33	
	1136.7		1164.7	11	A	3	543.25		543.25	
	1296.7		1324.7	12	C	2	472.21		472.21	
	1433.8		1461.8	13	H	1	312.18		312.18	
				14	R	0	175.12	-0.045	175.12	

Scan number	8915	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	107.03



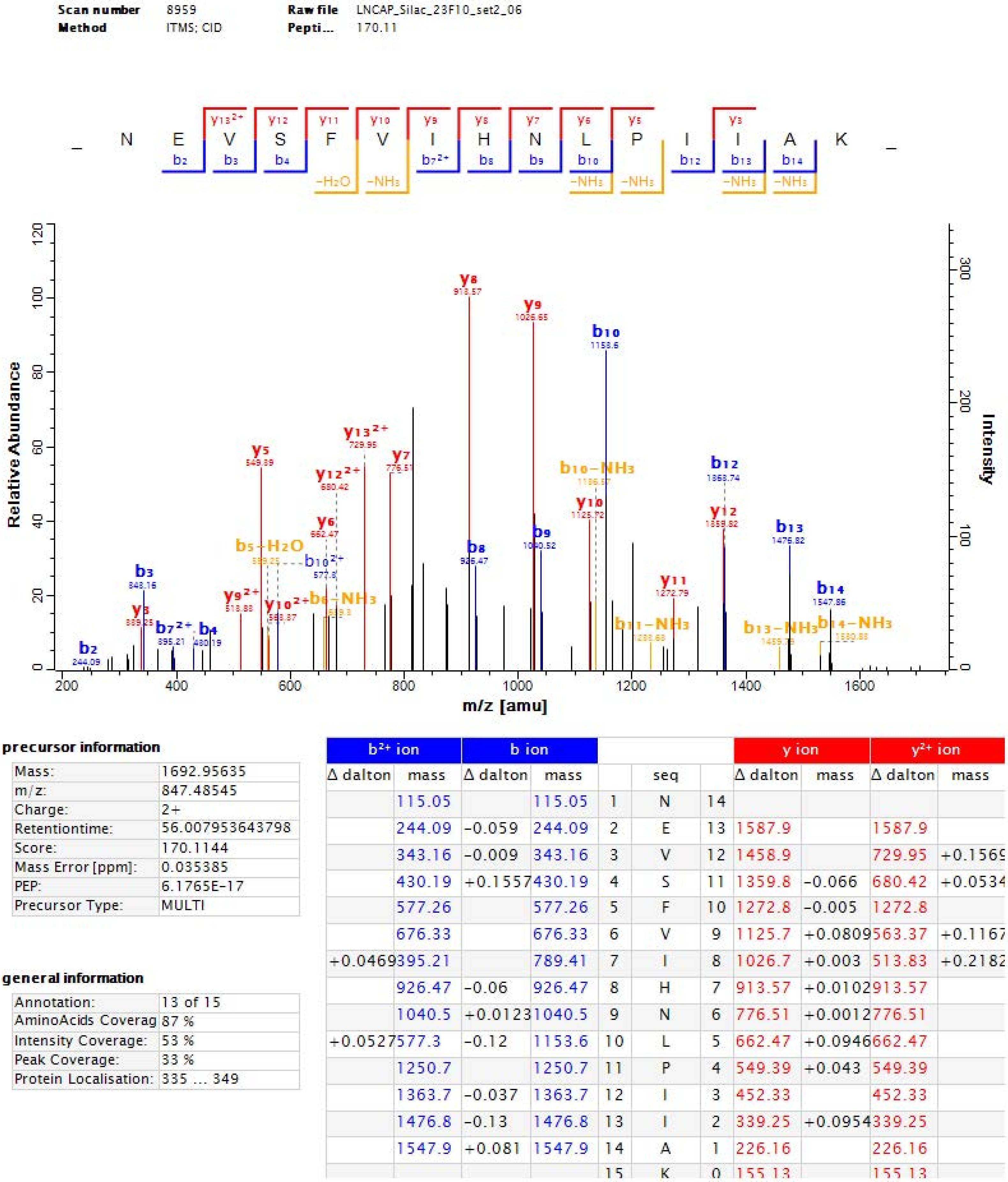
precursor information

Mass:	2319.27214
m/z:	774.09799
Charge:	3+
Retentiontime:	55.677364349365
Score:	107.0252
Mass Error [ppm]:	-0.77363
PEP:	2.3284E-06
Precursor Type:	ISO

general information

Annotation:	13 of 21
AminoAcids Coverag	62 %
Intensity Coverage:	57 %
Peak Coverage:	29 %
Protein Localisation:	538 ... 558

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	98.06		98.06	1	P	20				
	211.14		211.14	2	L	19	2223.2		2223.2	
	298.18		298.18	3	S	18	2110.1		1055.6	+0.4837
	395.23		395.23	4	P	17	2023.1		2023.1	
	508.31		508.31	5	L	16	1926.1		1926.1	
	645.37		645.37	6	H	15	1813		1813	
	732.4		732.4	7	S	14	1675.9		1675.9	
	845.49	+0.1327	845.49	8	L	13	1588.9		1588.9	
	946.54	-0.028	946.54	9	T	12	1475.8		738.4	+0.0631
	1043.6		1043.6	10	P	11	1374.8		687.88	+0.0028
+0.0664	603.83	+0.1228	1206.7	11	Y	10	1277.7	+0.1218	1277.7	
+0.205	667.86	-0.376	1334.7	12	Q	9	1114.6	-0.115	1114.6	
+0.1892	717.39	-0.027	1433.8	13	V	8	986.58	+0.0377	986.58	
	1530.8		1530.8	14	P	7	887.51	-0.025	444.26	+0.1534
	1677.9		1677.9	15	F	6	790.46		790.46	
	1791.9		1791.9	16	N	5	643.39	-0.004	643.39	
+0.4485	931.99		1863	17	A	4	529.35		529.35	
	1962		1962	18	V	3	458.31	-0.052	458.31	
	2033.1		2033.1	19	A	2	359.24	+0.0925	359.24	
+0.3056	1073.6		2146.2	20	L	1	288.2	+0.1096	288.2	
				21	R	0	175.12		175.12	



Scan number 8959
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set2_06
Pepti... 170.11

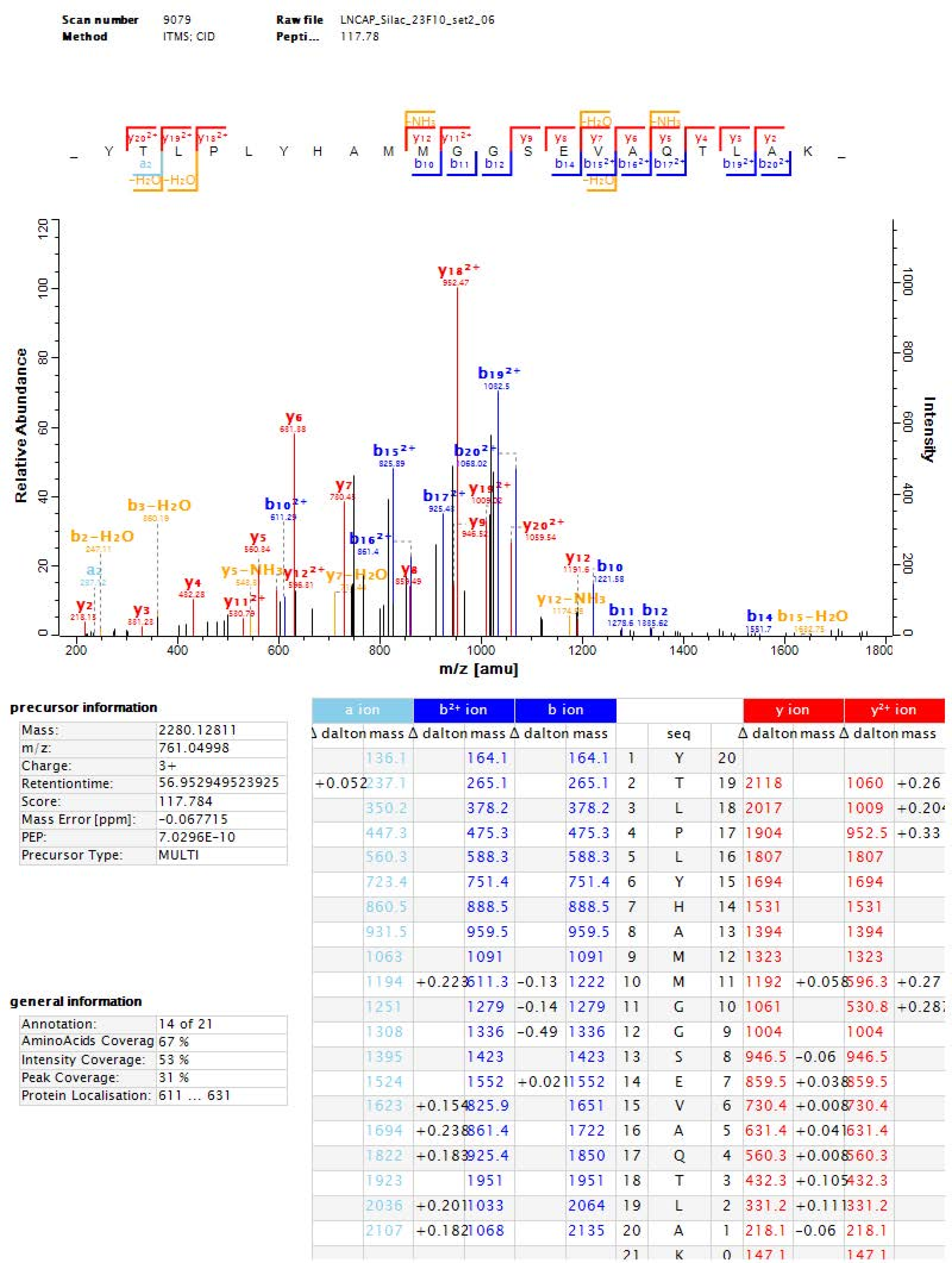
precursor information

Mass:	1692.95635
m/z:	847.48545
Charge:	2+
Retentiontime:	56.007953643798
Score:	170.1144
Mass Error [ppm]:	0.035385
PEP:	6.1765E-17
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	53 %
Peak Coverage:	33 %
Protein Localisation:	335 ... 349

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.05		115.05	1	N	14				
	244.09	-0.059	244.09	2	E	13	1587.9		1587.9	
	343.16	-0.009	343.16	3	V	12	1458.9		729.95	+0.1569
	430.19	+0.1557	430.19	4	S	11	1359.8	-0.066	680.42	+0.0534
	577.26		577.26	5	F	10	1272.8	-0.005	1272.8	
	676.33		676.33	6	V	9	1125.7	+0.0809	563.37	+0.1167
+0.0469	395.21		789.41	7	I	8	1026.7	+0.003	513.83	+0.2182
	926.47	-0.06	926.47	8	H	7	913.57	+0.0102	913.57	
	1040.5	+0.0123	1040.5	9	N	6	776.51	+0.0012	776.51	
+0.0527	577.3	-0.12	1153.6	10	L	5	662.47	+0.0946	662.47	
	1250.7		1250.7	11	P	4	549.39	+0.043	549.39	
	1363.7	-0.037	1363.7	12	I	3	452.33		452.33	
	1476.8	-0.13	1476.8	13	I	2	339.25	+0.0954	339.25	
	1547.9	+0.081	1547.9	14	A	1	226.16		226.16	
				15	K	0	155.13		155.13	



Scan number 9079 **Raw file** LNCAP_Silac_23F10_set2_06
Method ITMS; CID **Pepti...** 117.78

precursor information

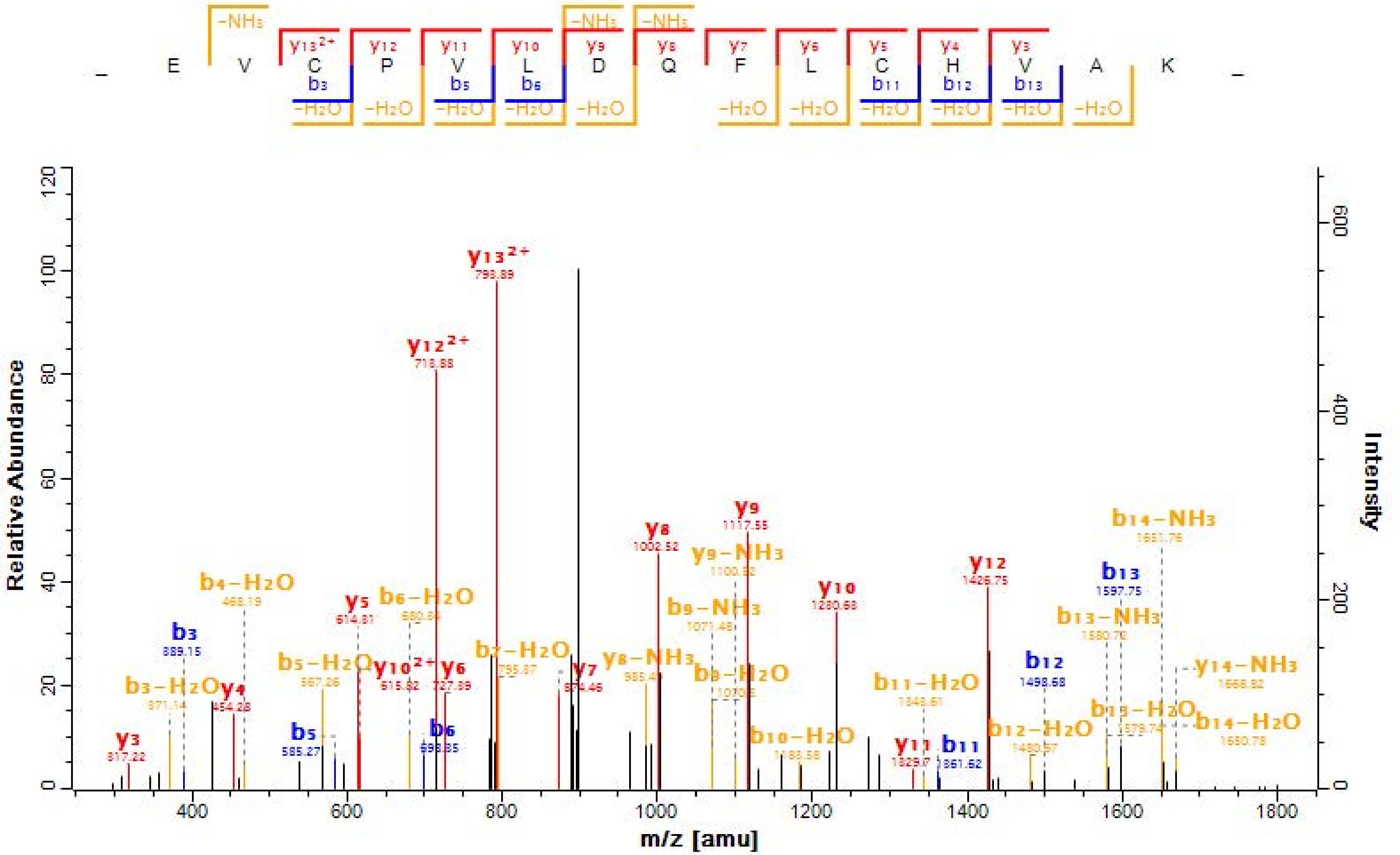
Mass:	2280.12811
m/z:	761.04998
Charge:	3+
Retentiontime:	56.952949523925
Score:	117.784
Mass Error [ppm]:	-0.067715
PEP:	7.0296E-10
Precursor Type:	MULTI

general information

Annotation:	14 of 21
AminoAcids Coverag	67 %
Intensity Coverage:	53 %
Peak Coverage:	31 %
Protein Localisation:	611 ... 631

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.1		164.1		164.1	1	Y	20				
+0.052	237.1		265.1		265.1	2	T	19	2118		1060	+0.26
	350.2		378.2		378.2	3	L	18	2017		1009	+0.20
	447.3		475.3		475.3	4	P	17	1904		952.5	+0.33
	560.3		588.3		588.3	5	L	16	1807		1807	
	723.4		751.4		751.4	6	Y	15	1694		1694	
	860.5		888.5		888.5	7	H	14	1531		1531	
	931.5		959.5		959.5	8	A	13	1394		1394	
	1063		1091		1091	9	M	12	1323		1323	
	1194	+0.223	611.3	-0.13	1222	10	M	11	1192	+0.058	596.3	+0.27
	1251		1279	-0.14	1279	11	G	10	1061		530.8	+0.28
	1308		1336	-0.49	1336	12	G	9	1004		1004	
	1395		1423		1423	13	S	8	946.5	-0.06	946.5	
	1524		1552	+0.021	1552	14	E	7	859.5	+0.038	859.5	
	1623	+0.154	825.9		1651	15	V	6	730.4	+0.008	730.4	
	1694	+0.238	861.4		1722	16	A	5	631.4	+0.041	631.4	
	1822	+0.183	925.4		1850	17	Q	4	560.3	+0.008	560.3	
	1923		1951		1951	18	T	3	432.3	+0.105	432.3	
	2036	+0.201	1033		2064	19	L	2	331.2	+0.111	331.2	
	2107	+0.182	1068		2135	20	A	1	218.1	-0.06	218.1	
						21	K	0	147.1		147.1	

Scan number	9169	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	202.13



precursor information

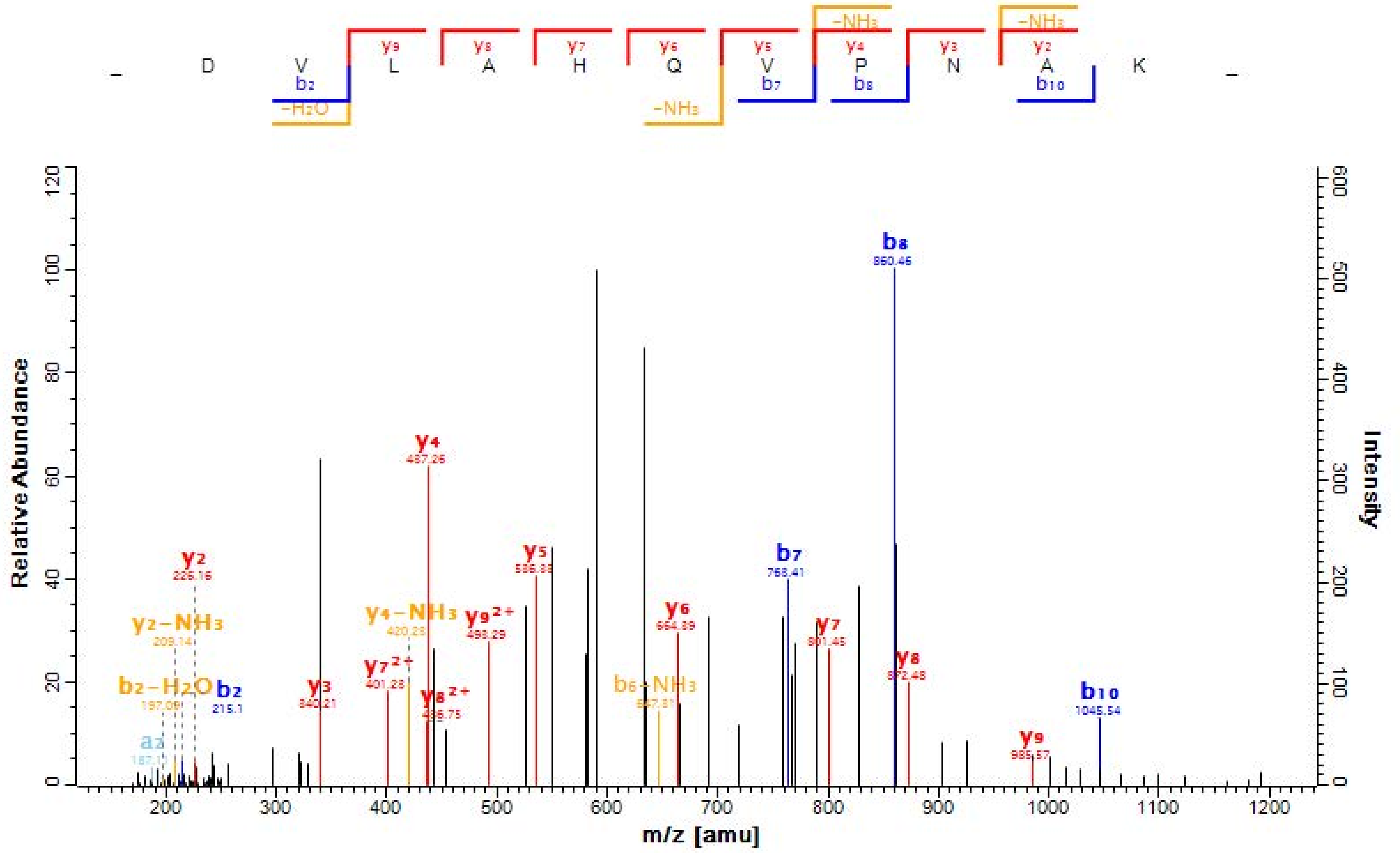
Mass:	1813.88539
m/z:	907.94997
Charge:	2+
Retentiontime:	57.741981506347
Score:	202.1269
Mass Error [ppm]:	-0.066605
PEP:	4.9227E-28
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	56 %
Peak Coverage:	40 %
Protein Localisation:	20 ... 34

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	14				
	229.1183	2	V	13	1685.85		1685.85	
-0.04731	389.1489	3	C	12	1586.782		793.8945	+0.24335
	486.2017	4	P	11	1426.751	-0.0391	713.8792	+0.28321
+0.130098	585.2701	5	V	10	1329.698	+0.026119	1329.698	
+0.017409	698.3542	6	L	9	1230.63	-0.08772	615.8186	-0.15742
	813.3811	7	D	8	1117.546	-0.12975	1117.546	
	941.4397	8	Q	7	1002.519	-0.03555	1002.519	
	1088.508	9	F	6	874.4604	-0.03642	874.4604	
	1201.592	10	L	5	727.392	+0.035229	727.392	
-0.17653	1361.623	11	C	4	614.3079	+0.066193	614.3079	
-0.06662	1498.682	12	H	3	454.2772	+0.000893	454.2772	
-0.08193	1597.75	13	V	2	317.2183	+0.015372	317.2183	
	1668.787	14	A	1	218.1499		218.1499	
		15	K	0	147.1128		147.1128	

Scan number	920	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	108.9



precursor information

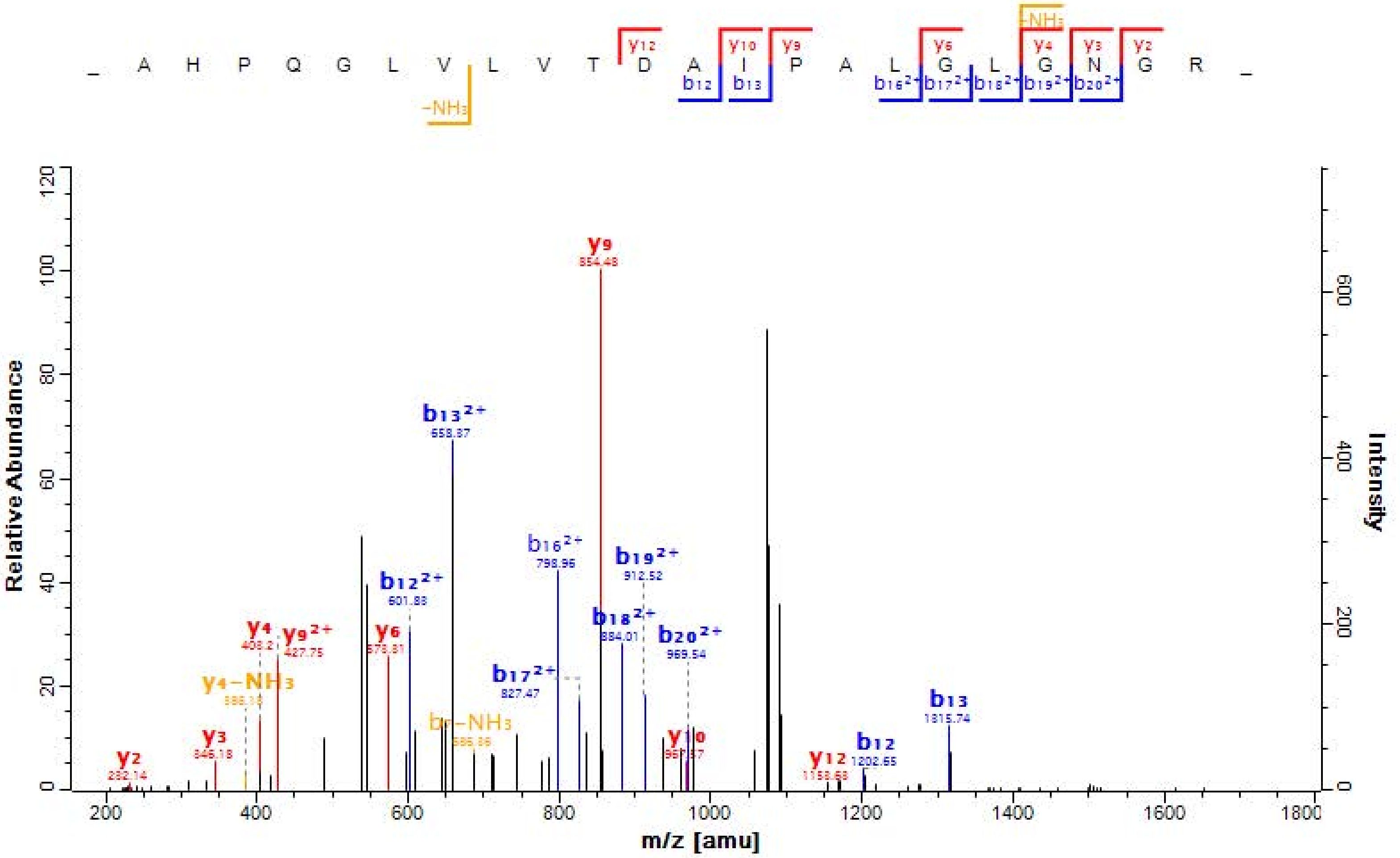
Mass:	1190.64067
m/z:	596.32761
Charge:	2+
Retentiontime:	10.652101516723
Score:	108.9032
Mass Error [ppm]:	-0.082709
PEP:	0.00028594
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	34 %
Peak Coverage:	20 %
Protein Localisation:	133 ... 143; 414 ...

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	10				
+0.011	187.11	-0.068	215.1	2	V	9	1084.6		1084.6	
	300.19		328.19	3	L	8	985.57	+0.036	493.29	+0.0101
	371.23		399.22	4	A	7	872.48	-0.06	436.75	-0.431
	508.29		536.28	5	H	6	801.45	+0.0512	401.23	+0.0516
	636.35		664.34	6	Q	5	664.39	-0.003	664.39	
	735.41	-0.022	763.41	7	V	4	536.33	+0.1386	536.33	
	832.47	+0.0773	860.46	8	P	3	437.26	-0.039	437.26	
	946.51		974.51	9	N	2	340.21	+0.0237	340.21	
	1017.5	+0.2327	1045.5	10	A	1	226.16	+0.1373	226.16	
				11	K	0	155.13		155.13	

Scan number	9328	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	67.43



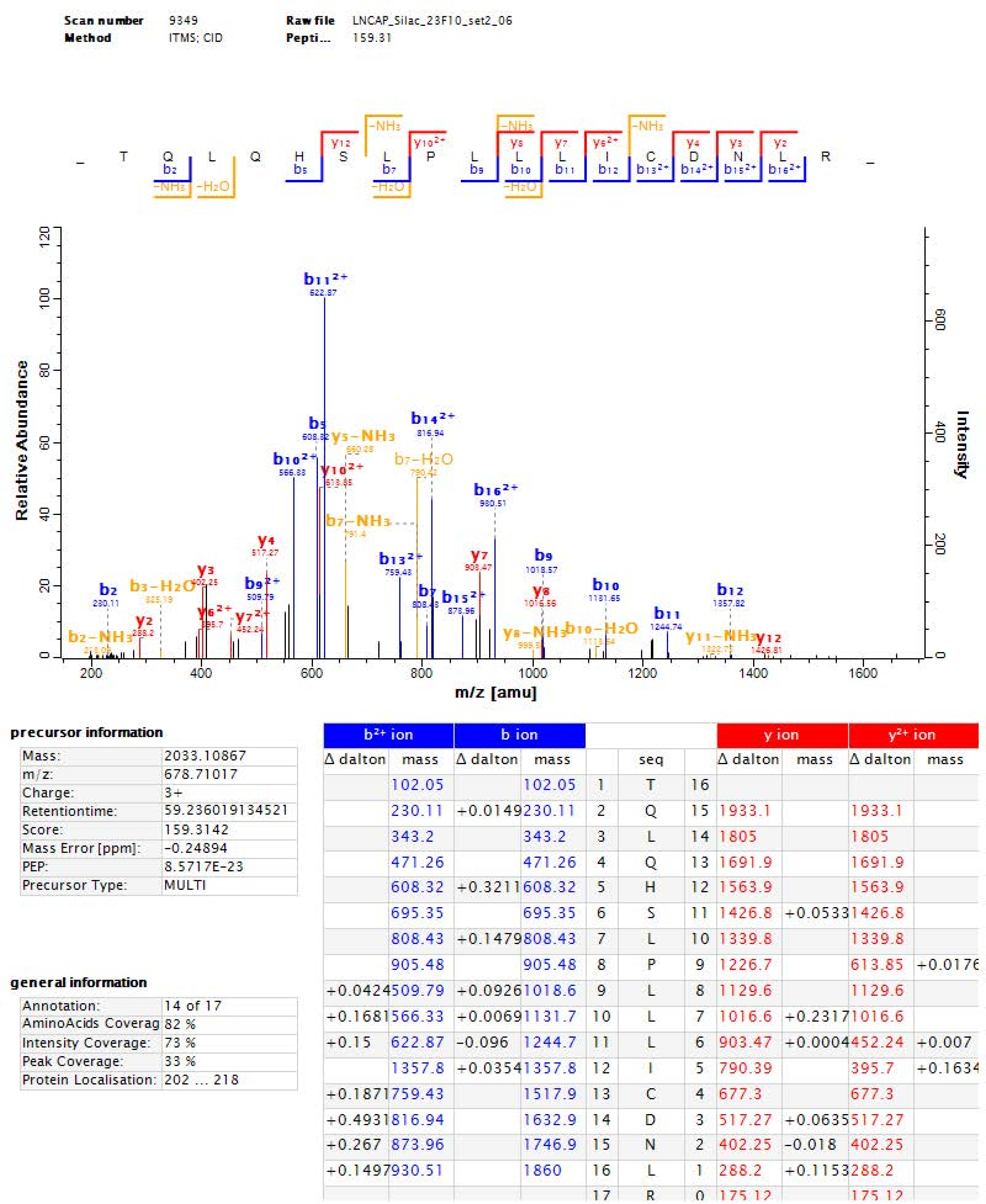
precursor information

Mass:	2168.20654
m/z:	723.74279
Charge:	3+
Retentiontime:	59.065235137939
Score:	67.43032
Mass Error [ppm]:	-0.021196
PEP:	0.00066329
Precursor Type:	MULTI

general information

Annotation:	12 of 22
AminoAcids Coverag	55 %
Intensity Coverage:	39 %
Peak Coverage:	20 %
Protein Localisation:	284 ... 305

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	21				
	209.1		209.1	2	H	20	2098.2		2098.2	
	306.16		306.16	3	P	19	1961.1		1961.1	
	434.21		434.21	4	Q	18	1864.1		1864.1	
	491.24		491.24	5	G	17	1736		1736	
	604.32		604.32	6	L	16	1679		1679	
	703.39		703.39	7	V	15	1565.9		1565.9	
	816.47		816.47	8	L	14	1466.8		1466.8	
	915.54		915.54	9	V	13	1353.7		1353.7	
	1016.6		1016.6	10	T	12	1254.7		1254.7	
	1131.6		1131.6	11	D	11	1153.6	+0.0241	1153.6	
+0.2246	601.83	-0.206	1202.7	12	A	10	1038.6		1038.6	
+0.0163	658.37	-0.074	1315.7	13	I	9	967.57	+0.1544	967.57	
	1412.8		1412.8	14	P	8	854.48	+0.019	427.75	+0.2116
	1483.8		1483.8	15	A	7	757.43		757.43	
+0.1939	798.96		1596.9	16	L	6	686.39		686.39	
+0.1644	827.47		1653.9	17	G	5	573.31	+0.0482	573.31	
+0.2455	884.01		1767	18	L	4	516.29		516.29	
+0.2551	912.52		1824	19	G	3	403.2	+0.0544	403.2	
+0.2474	969.54		1938.1	20	N	2	346.18	+0.022	346.18	
	1995.1		1995.1	21	G	1	232.14	+0.1263	232.14	
				22	R	0	175.12		175.12	



Scan number	9349	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	159.31

precursor information

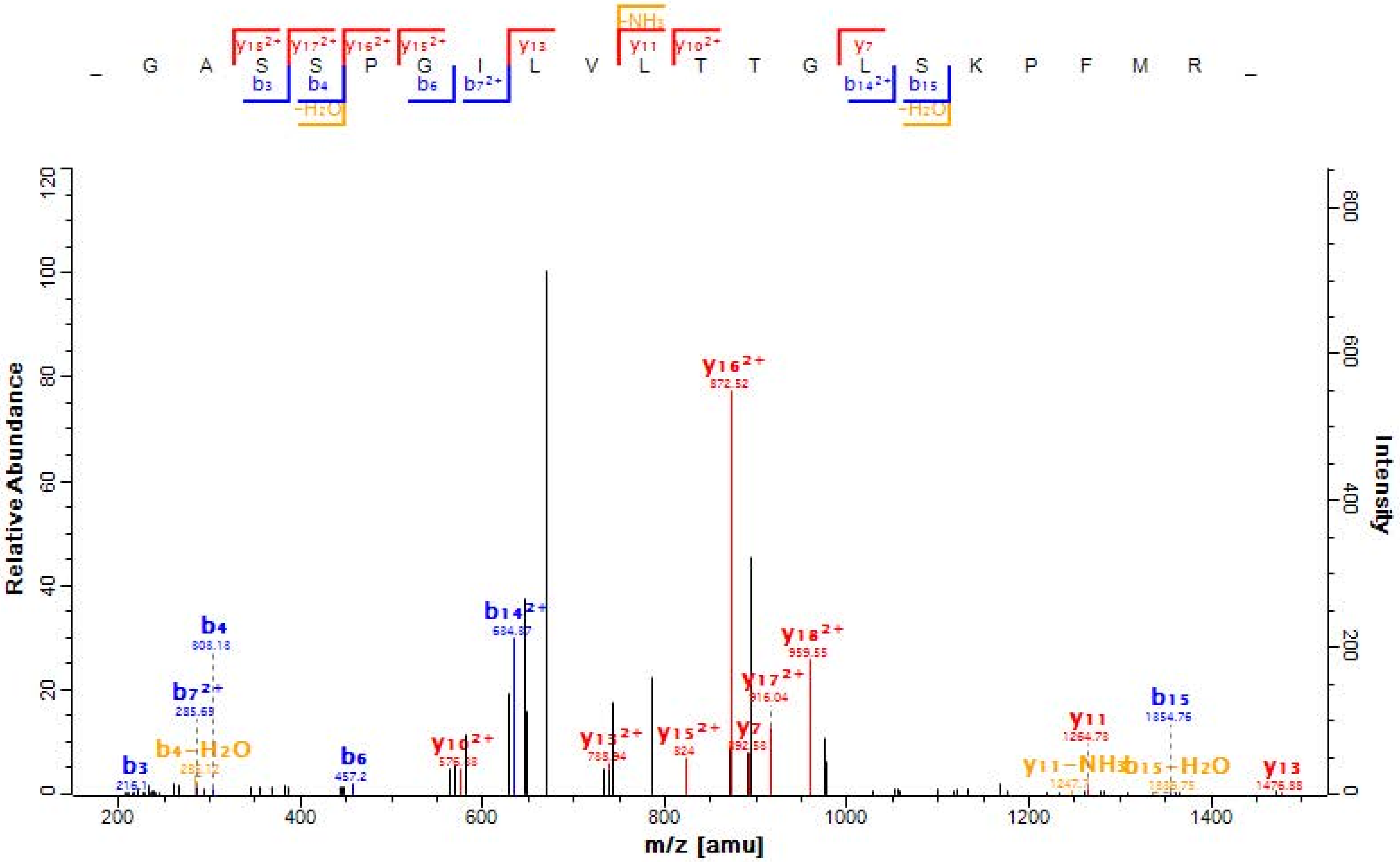
Mass:	2033.10867
m/z:	678.71017
Charge:	3+
Retentiontime:	59.236019134521
Score:	159.3142
Mass Error [ppm]:	-0.24894
PEP:	8.5717E-23
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	73 %
Peak Coverage:	33 %
Protein Localisation:	202 ... 218

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	16				
	230.11	+0.0149	230.11	2	Q	15	1933.1		1933.1	
	343.2		343.2	3	L	14	1805		1805	
	471.26		471.26	4	Q	13	1691.9		1691.9	
	608.32	+0.3211	608.32	5	H	12	1563.9		1563.9	
	695.35		695.35	6	S	11	1426.8	+0.0533	1426.8	
	808.43	+0.1479	808.43	7	L	10	1339.8		1339.8	
	905.48		905.48	8	P	9	1226.7		613.85	+0.0176
+0.0424	509.79	+0.0926	1018.6	9	L	8	1129.6		1129.6	
+0.1681	566.33	+0.0069	1131.7	10	L	7	1016.6	+0.2317	1016.6	
+0.15	622.87	-0.096	1244.7	11	L	6	903.47	+0.0004	452.24	+0.007
	1357.8	+0.0354	1357.8	12	I	5	790.39		395.7	+0.1634
+0.1871	759.43		1517.9	13	C	4	677.3		677.3	
+0.4931	816.94		1632.9	14	D	3	517.27	+0.0635	517.27	
+0.267	873.96		1746.9	15	N	2	402.25	-0.018	402.25	
+0.1497	930.51		1860	16	L	1	288.2	+0.1153	288.2	
				17	R	0	175.12		175.12	

Scan number	9469	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	60.31



precursor information

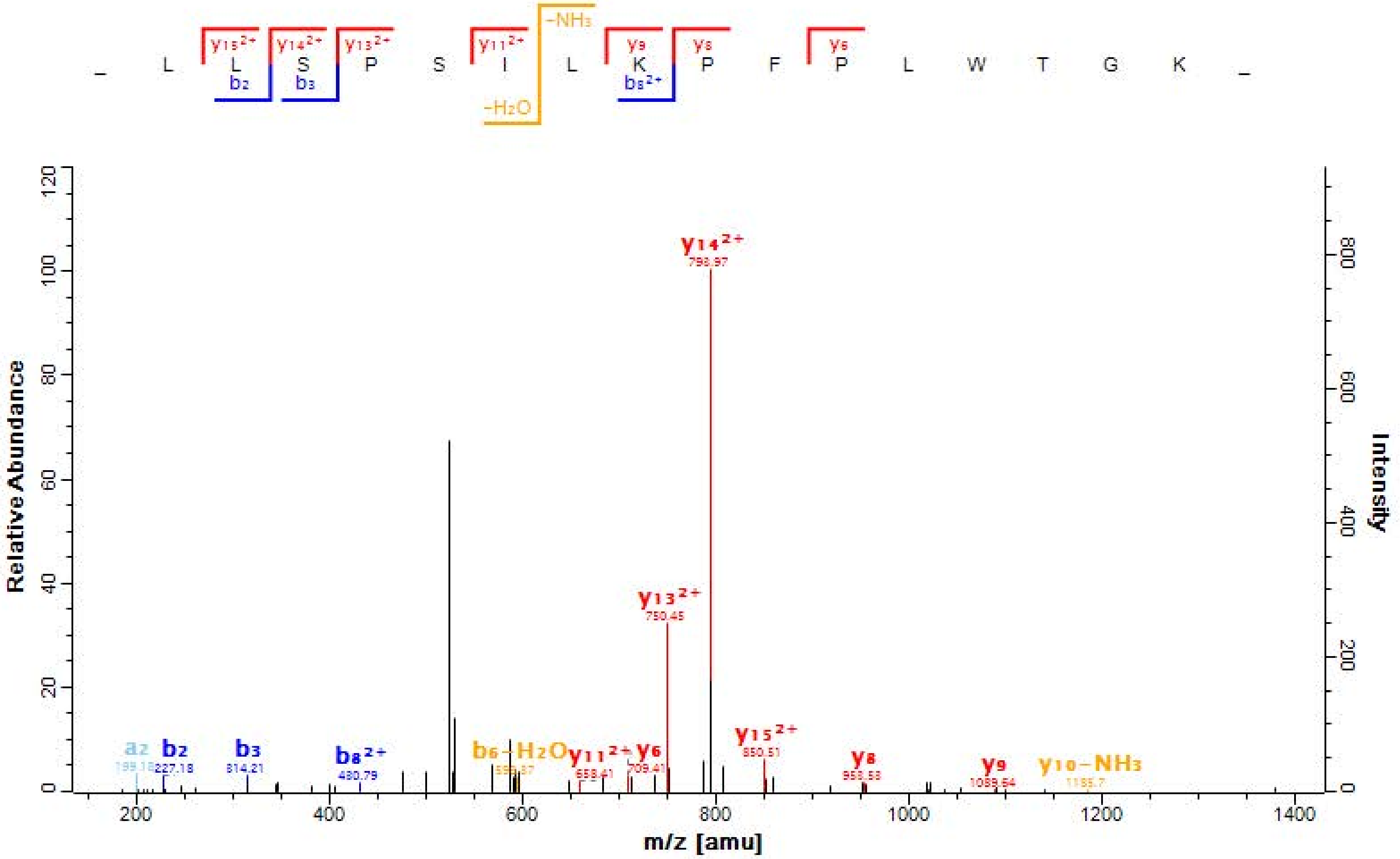
Mass:	2031.11766
m/z:	678.0465
Charge:	3+
Retentiontime:	60.232273101806
Score:	60.30704
Mass Error [ppm]:	-0.50137
PEP:	0.0011906
Precursor Type:	MULTI

general information

Annotation:	10 of 20
AminoAcids Coverag	50 %
Intensity Coverage:	32 %
Peak Coverage:	19 %
Protein Localisation:	390 ... 409

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	19				
	129.07		129.07	2	A	18	1989.1		1989.1	
	216.1	+0.1417	216.1	3	S	17	1918.1		959.55	+0.2413
	303.13	+0.0992	303.13	4	S	16	1831.1		916.04	-0.107
	400.18		400.18	5	P	15	1744		872.52	+0.199
	457.2	+0.4203	457.2	6	G	14	1647		824	+0.1519
+0.4695	285.65		570.29	7	I	13	1590		1590	
	683.37		683.37	8	L	12	1476.9	+0.0175	738.94	-0.037
	782.44		782.44	9	V	11	1363.8		1363.8	
	895.52		895.52	10	L	10	1264.7	-0.102	1264.7	
	996.57		996.57	11	T	9	1151.6		576.33	+0.2791
	1097.6		1097.6	12	T	8	1050.6		1050.6	
	1154.6		1154.6	13	G	7	949.55		949.55	
-0.073	634.37		1267.7	14	L	6	892.53	+0.2548	892.53	
	1354.8	+0.398	1354.8	15	S	5	779.44		779.44	
	1490.9		1490.9	16	K	4	692.41		692.41	
	1587.9		1587.9	17	P	3	556.3		556.3	
	1735		1735	18	F	2	459.25		459.25	
	1866		1866	19	M	1	312.18		312.18	
				20	R	0	181.14		181.14	

Scan number	9742	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	57.14



precursor information

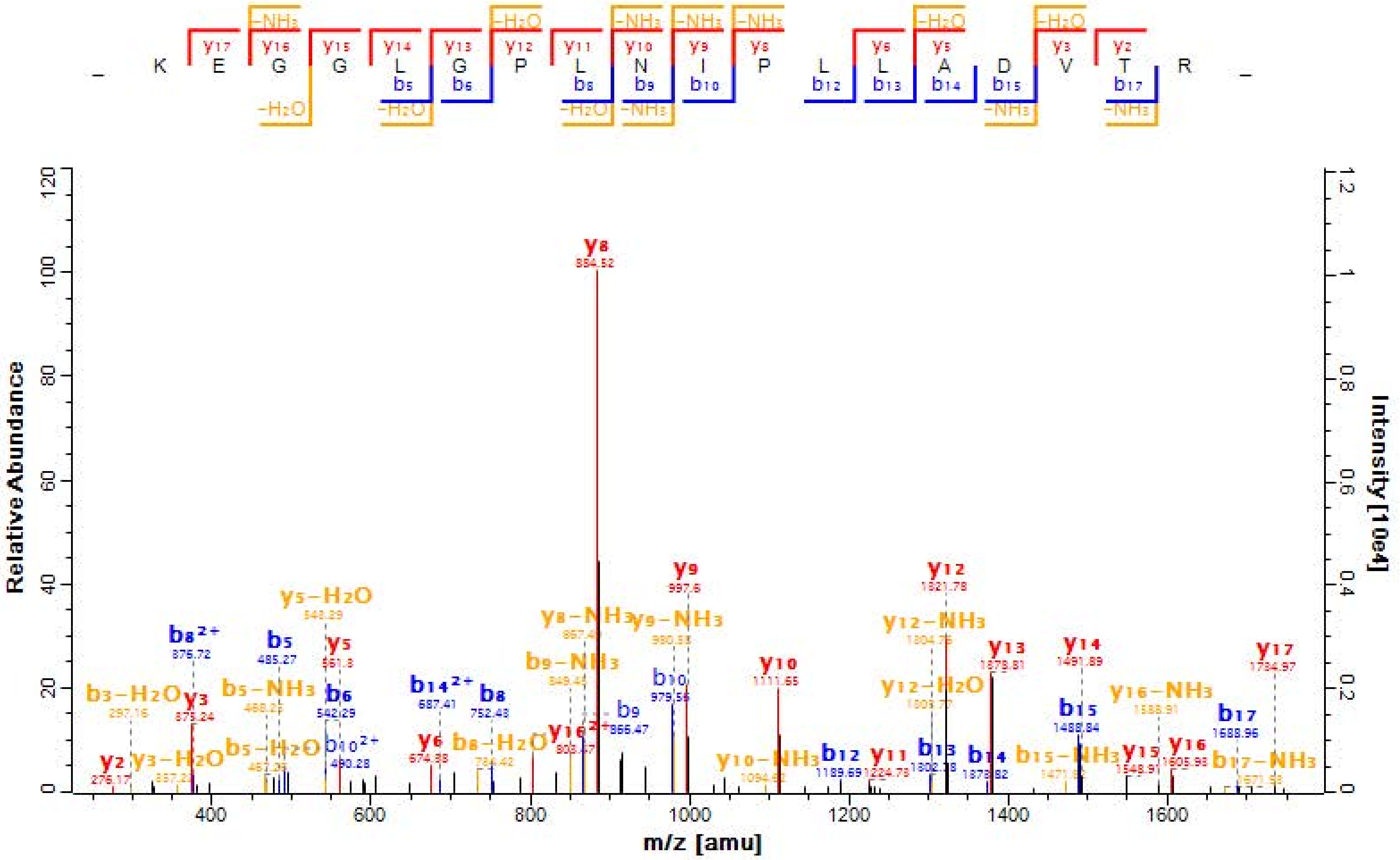
Mass:	1796.06087
m/z:	599.69423
Charge:	3+
Retentiontime:	62.742202758789
Score:	57.13573
Mass Error [ppm]:	0.4644
PEP:	0.0030732
Precursor Type:	MULTI

general information

Annotation:	10 of 16
AminoAcids Coverag	62 %
Intensity Coverage:	43 %
Peak Coverage:	18 %
Protein Localisation:	670 ... 685

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	15				
+0.069	199.2		227.2	+0.135	227.2	2	L	14	1700		850.5	+0.43
	286.2		314.2	+0.112	314.2	3	S	13	1587		794	+0.16
	383.3		411.3		411.3	4	P	12	1500		750.5	+0.18
	470.3		498.3		498.3	5	S	11	1403		1403	
	583.4		611.4		611.4	6	I	10	1316		658.4	+0.00
	696.5		724.5		724.5	7	L	9	1203		1203	
	832.6	-0.14	430.8		860.6	8	K	8	1090	+0.118	1090	
	929.6		957.6		957.6	9	P	7	953.5	-0.1	953.5	
	1077		1105		1105	10	F	6	856.5		856.5	
	1174		1202		1202	11	P	5	709.4	+0.002	709.4	
	1287		1315		1315	12	L	4	612.4		612.4	
	1473		1501		1501	13	W	3	499.3		499.3	
	1574		1602		1602	14	T	2	313.2		313.2	
	1631		1659		1659	15	G	1	212.1		212.1	
						16	K	0	155.1		155.1	

Scan number	9821	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	228.08



precursor information

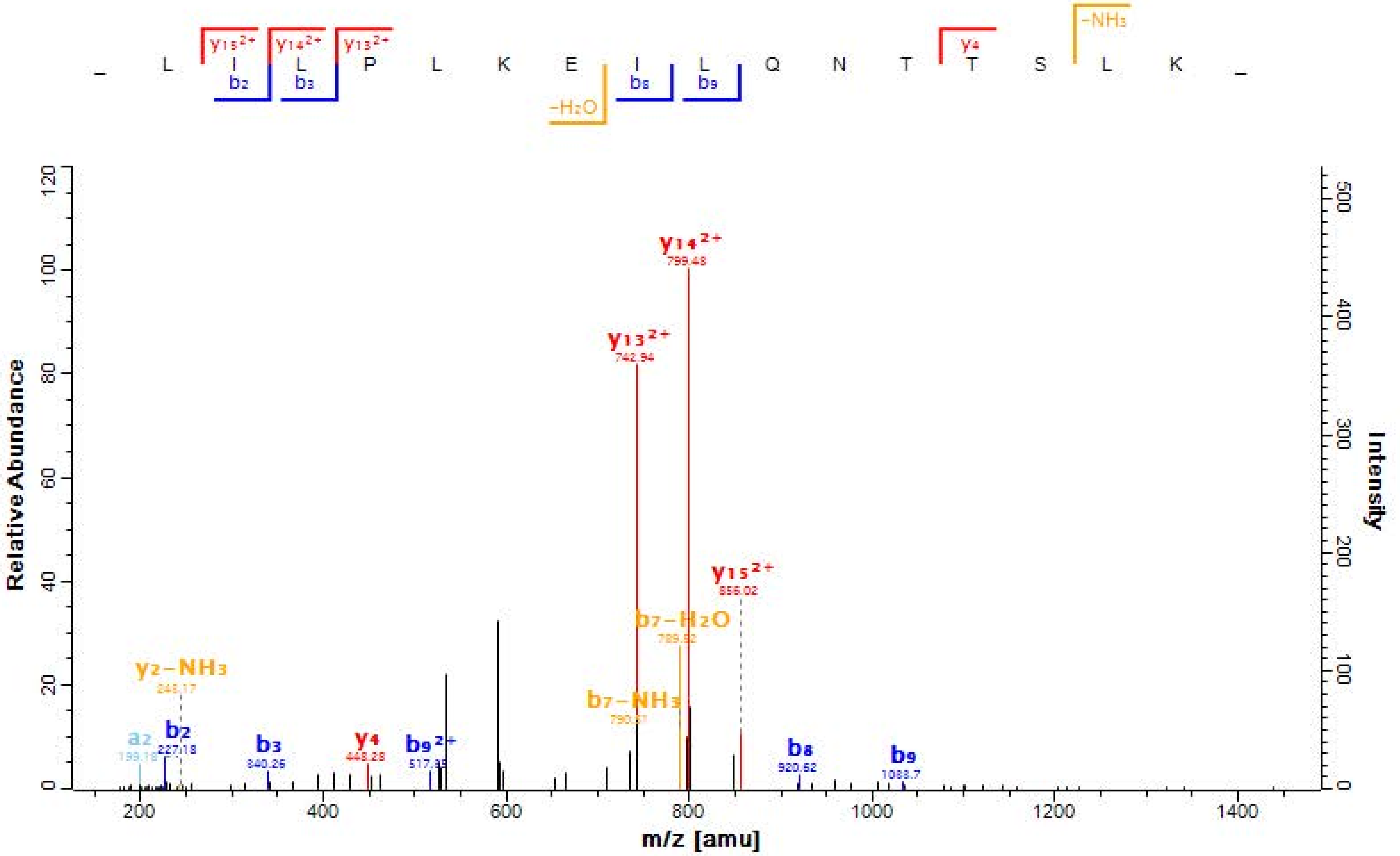
Mass:	1862.06275
m/z:	932.03865
Charge:	2+
Retentiontime:	63.498092651367
Score:	228.0807
Mass Error [ppm]:	0.10673
PEP:	4.5008E-49
Precursor Type:	MULTI

general information

Annotation:	16 of 18
AminoAcids Coverag	89 %
Intensity Coverage:	62 %
Peak Coverage:	47 %
Protein Localisation:	92 ... 109

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.1		129.1	1	K	17				
	258.14		258.14	2	E	16	1735	-0.139	1735	
	315.17		315.17	3	G	15	1605.9	-0.035	803.47	+0.0689
	372.19		372.19	4	G	14	1548.9	-0.12	1548.9	
	485.27	+0.0518	485.27	5	L	13	1491.9	-0.115	1491.9	
	542.29	-0.026	542.29	6	G	12	1378.8	-0.101	1378.8	
	639.35		639.35	7	P	11	1321.8	+0.0083	1321.8	
-0.334	376.72	-0.089	752.43	8	L	10	1224.7	-0.127	1224.7	
	866.47	+0.0058	866.47	9	N	9	1111.6	-0.067	1111.6	
+0.0458	490.28	-0.019	979.56	10	I	8	997.6	-0.018	997.6	
	1076.6		1076.6	11	P	7	884.52	+0.0043	884.52	
	1189.7	-0.115	1189.7	12	L	6	787.47		787.47	
	1302.8	+0.1055	1302.8	13	L	5	674.38	+0.1138	674.38	
+0.0257	687.41	+0.0466	1373.8	14	A	4	561.3	+0.0525	561.3	
	1488.8	-0.082	1488.8	15	D	3	490.26		490.26	
	1587.9		1587.9	16	V	2	375.24	+0.0087	375.24	
	1689	-0.026	1689	17	T	1	276.17	+0.0341	276.17	
				18	R	0	175.12		175.12	

Scan number	9917	**Raw file**	LNCAP_Silac_23F10_set2_06
Method	ITMS; CID	**Pepti...**	57.8



precursor information

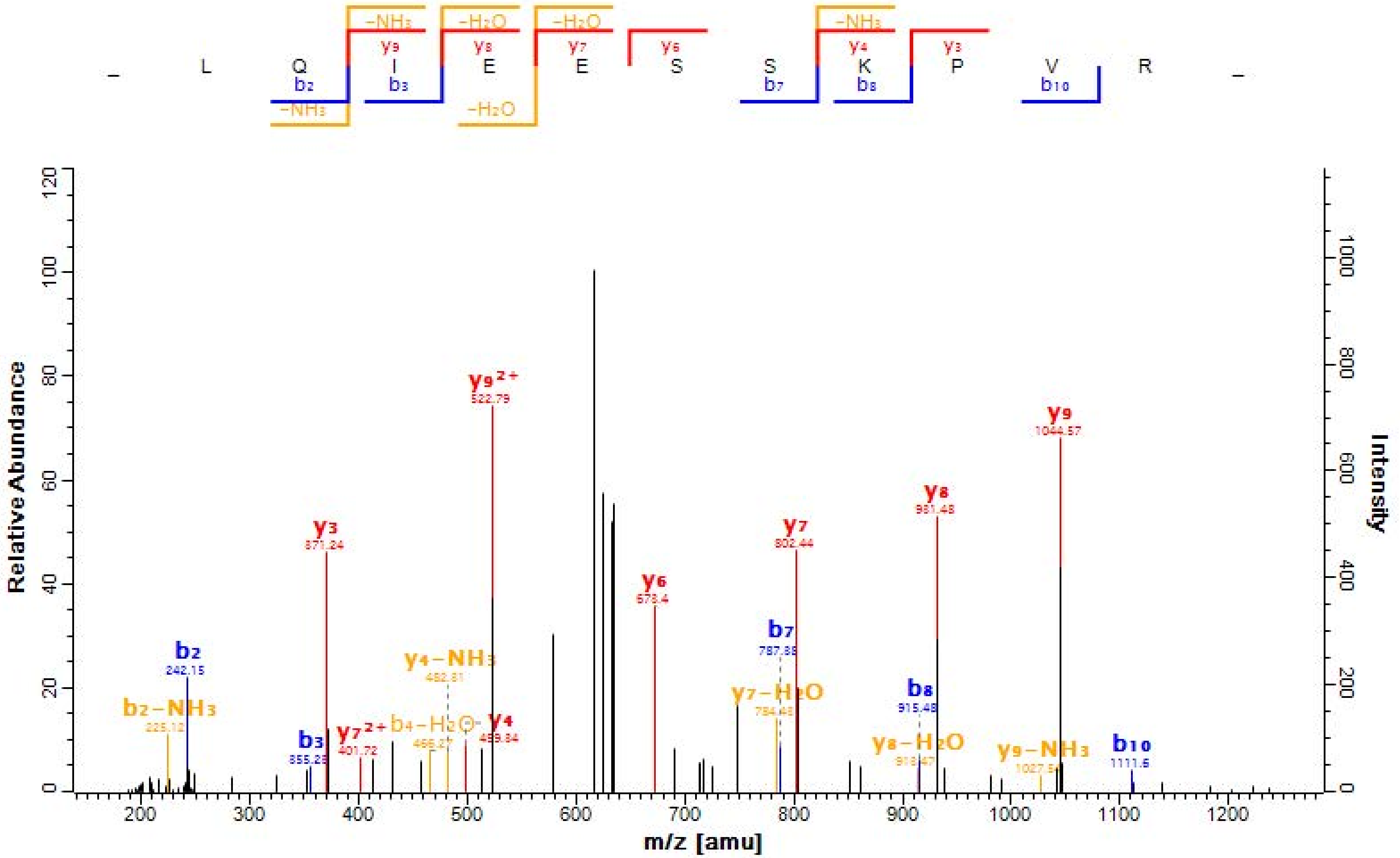
Mass:	1823.11383
m/z:	608.71189
Charge:	3+
Retentiontime:	64.391525268554
Score:	57.80392
Mass Error [ppm]:	0.35244
PEP:	0.0029412
Precursor Type:	MULTI

general information

Annotation:	9 of 16
AminoAcids Coverag	56 %
Intensity Coverage:	59 %
Peak Coverage:	15 %
Protein Localisation:	1980 ... 1995

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	15				
-0.05	199.2		227.2	-0.11	227.2	2	I	14	1711		856	+0.32
	312.3		340.3	-0.16	340.3	3	L	13	1598		799.5	+0.16
	409.3		437.3		437.3	4	P	12	1485		742.9	+0.30
	522.4		550.4		550.4	5	L	11	1388		1388	
	650.5		678.5		678.5	6	K	10	1275		1275	
	779.5		807.5		807.5	7	E	9	1147		1147	
	892.6		920.6	+0.115	920.6	8	I	8	1018		1018	
	1006	+0.168	517.4	+0.175	1034	9	L	7	904.5		904.5	
	1134		1162		1162	10	Q	6	791.4		791.4	
	1248		1276		1276	11	N	5	663.4		663.4	
	1349		1377		1377	12	T	4	549.3		549.3	
	1450		1478		1478	13	T	3	448.3	+0.038	448.3	
	1537		1565		1565	14	S	2	347.2		347.2	
	1650		1678		1678	15	L	1	260.2		260.2	
						16	K	0	147.1		147.1	

Scan number	1011	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	108.9



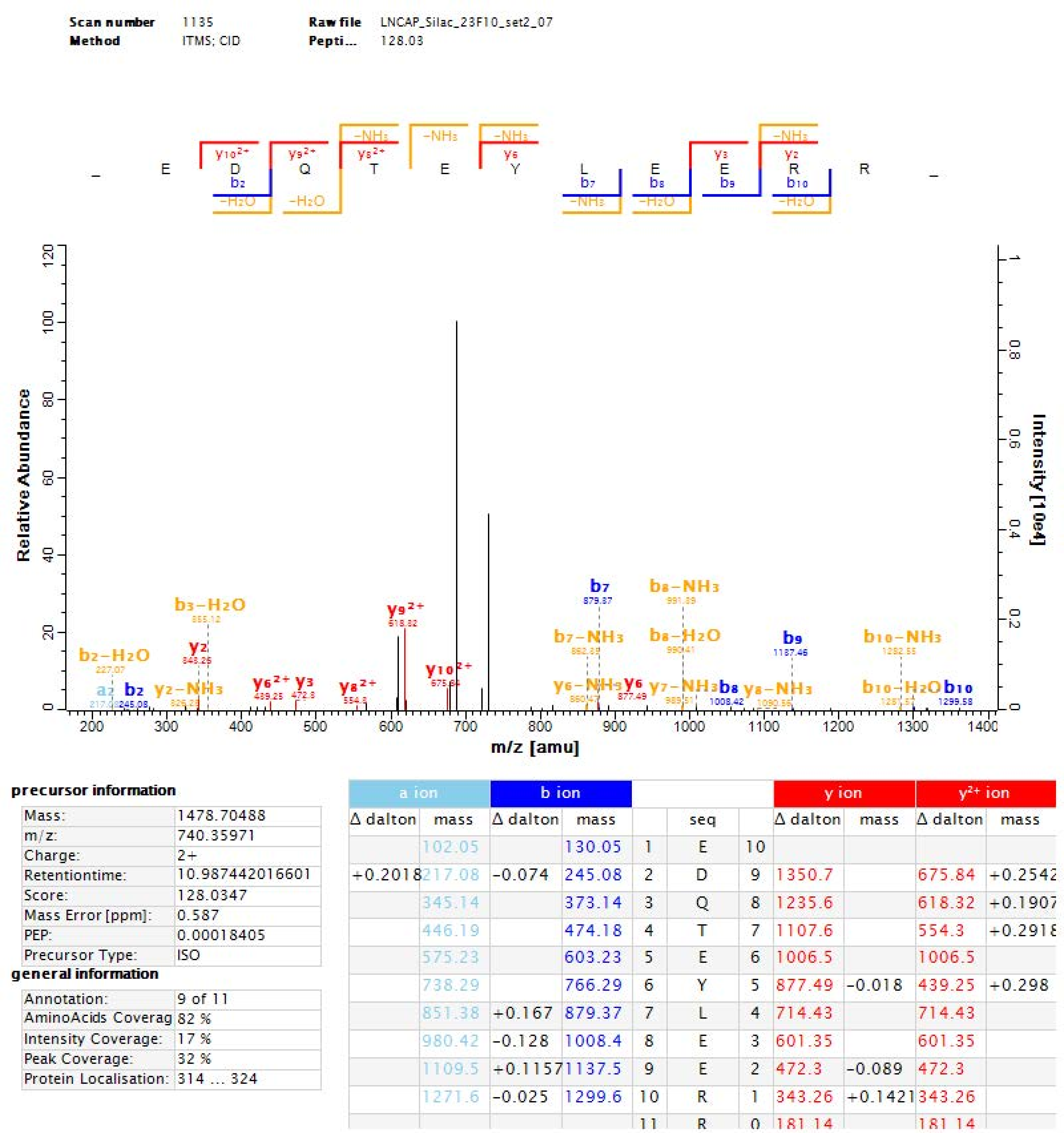
precursor information

Mass:	1284.70381
m/z:	643.35918
Charge:	2+
Retentiontime:	10.330109596252
Score:	108.9032
Mass Error [ppm]:	0.031402
PEP:	0.00023363
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	41 %
Peak Coverage:	22 %
Protein Localisation:	130 ... 140

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	10				
-0.01062	242.1499	2	Q	9	1172.627		1172.627	
+0.09866	355.234	3	I	8	1044.568	-0.02592	522.7878	+0.005741
	484.2766	4	E	7	931.4843	+0.010232	931.4843	
	613.3192	5	E	6	802.4417	-0.05106	401.7245	+0.152138
	700.3512	6	S	5	673.3991	-0.03709	673.3991	
-0.06169	787.3832	7	S	4	586.3671		586.3671	
+0.172264	915.4782	8	K	3	499.3351	-0.02174	499.3351	
	1012.531	9	P	2	371.2401	+0.006818	371.2401	
-0.09277	1111.599	10	V	1	274.1874		274.1874	
		11	R	0	175.119		175.119	



Scan number	1135	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	128.03

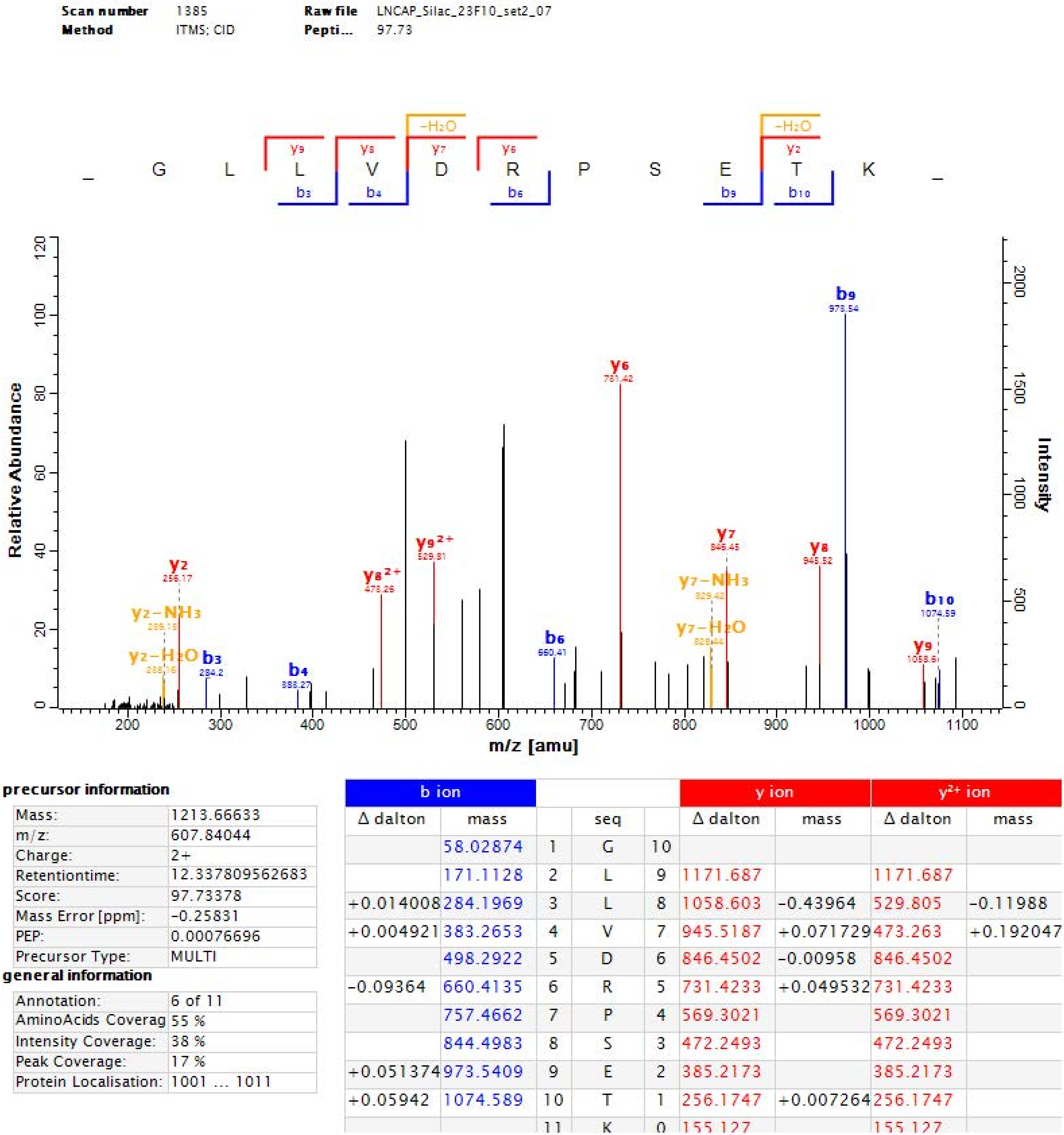
precursor information

Mass:	1478.70488
m/z:	740.35971
Charge:	2+
Retentiontime:	10.987442016601
Score:	128.0347
Mass Error [ppm]:	0.587
PEP:	0.00018405
Precursor Type:	ISO

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	17 %
Peak Coverage:	32 %
Protein Localisation:	314 ... 324

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	10				
+0.2018	217.08	-0.074	245.08	2	D	9	1350.7		675.84	+0.2542
	345.14		373.14	3	Q	8	1235.6		618.32	+0.1907
	446.19		474.18	4	T	7	1107.6		554.3	+0.2918
	575.23		603.23	5	E	6	1006.5		1006.5	
	738.29		766.29	6	Y	5	877.49	-0.018	439.25	+0.298
	851.38	+0.167	879.37	7	L	4	714.43		714.43	
	980.42	-0.128	1008.4	8	E	3	601.35		601.35	
	1109.5	+0.1157	1137.5	9	E	2	472.3	-0.089	472.3	
	1271.6	-0.025	1299.6	10	R	1	343.26	+0.1421	343.26	
				11	R	0	181.14		181.14	



Scan number	1385	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	97.73

precursor information

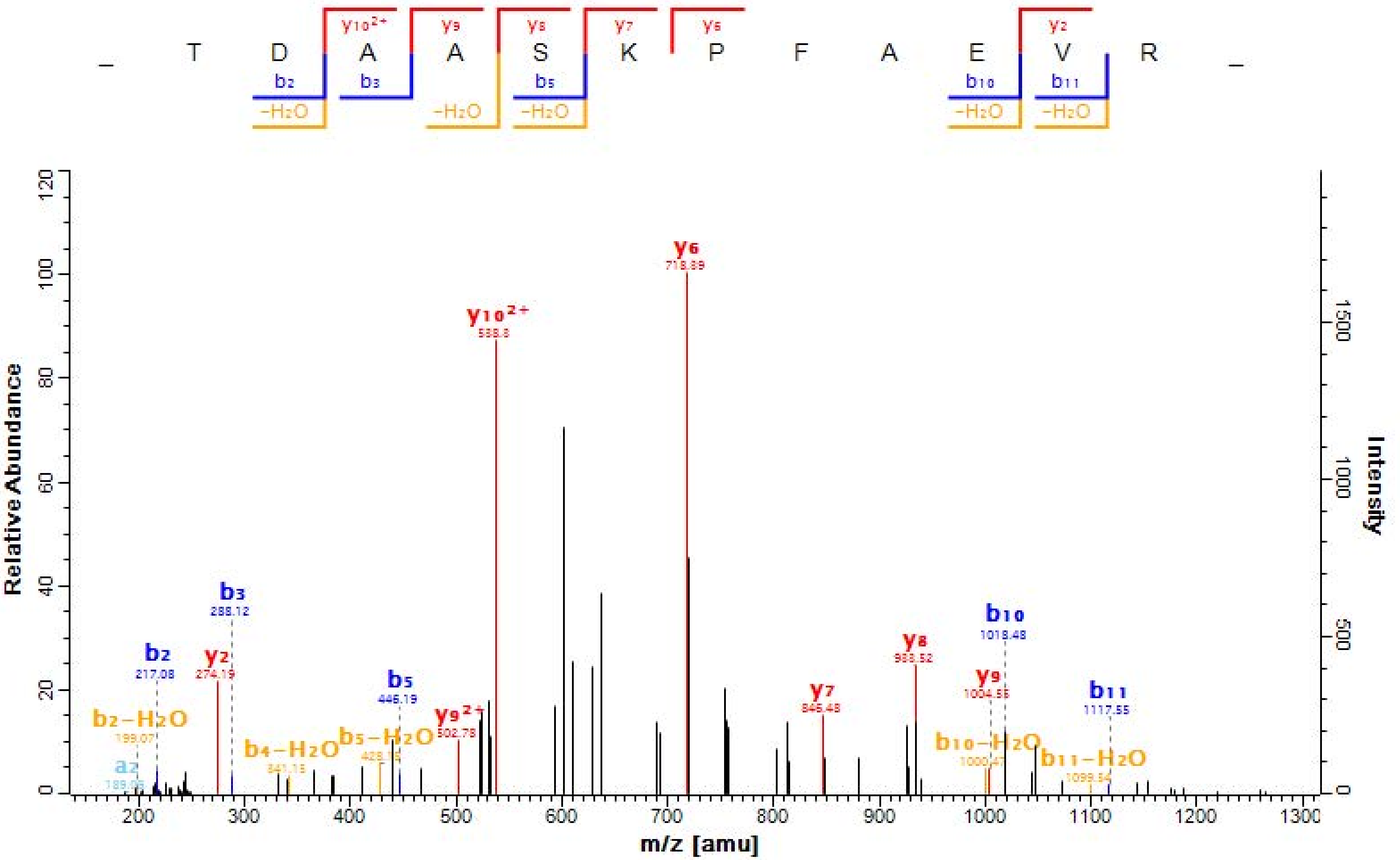
Mass:	1213.66633
m/z:	607.84044
Charge:	2+
Retentiontime:	12.337809562683
Score:	97.73378
Mass Error [ppm]:	-0.25831
PEP:	0.00076696
Precursor Type:	MULTI

general information

Annotation:	6 of 11
AminoAcids Coverag	55 %
Intensity Coverage:	38 %
Peak Coverage:	17 %
Protein Localisation:	1001 ... 1011

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	10				
	171.1128	2	L	9	1171.687		1171.687	
+0.014008	284.1969	3	L	8	1058.603	-0.43964	529.805	-0.11988
+0.004921	383.2653	4	V	7	945.5187	+0.071729	473.263	+0.192047
	498.2922	5	D	6	846.4502	-0.00958	846.4502	
-0.09364	660.4135	6	R	5	731.4233	+0.049532	731.4233	
	757.4662	7	P	4	569.3021		569.3021	
	844.4983	8	S	3	472.2493		472.2493	
+0.051374	973.5409	9	E	2	385.2173		385.2173	
+0.05942	1074.589	10	T	1	256.1747	+0.007264	256.1747	
		11	K	0	155.127		155.127	

Scan number	1387	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	69.86



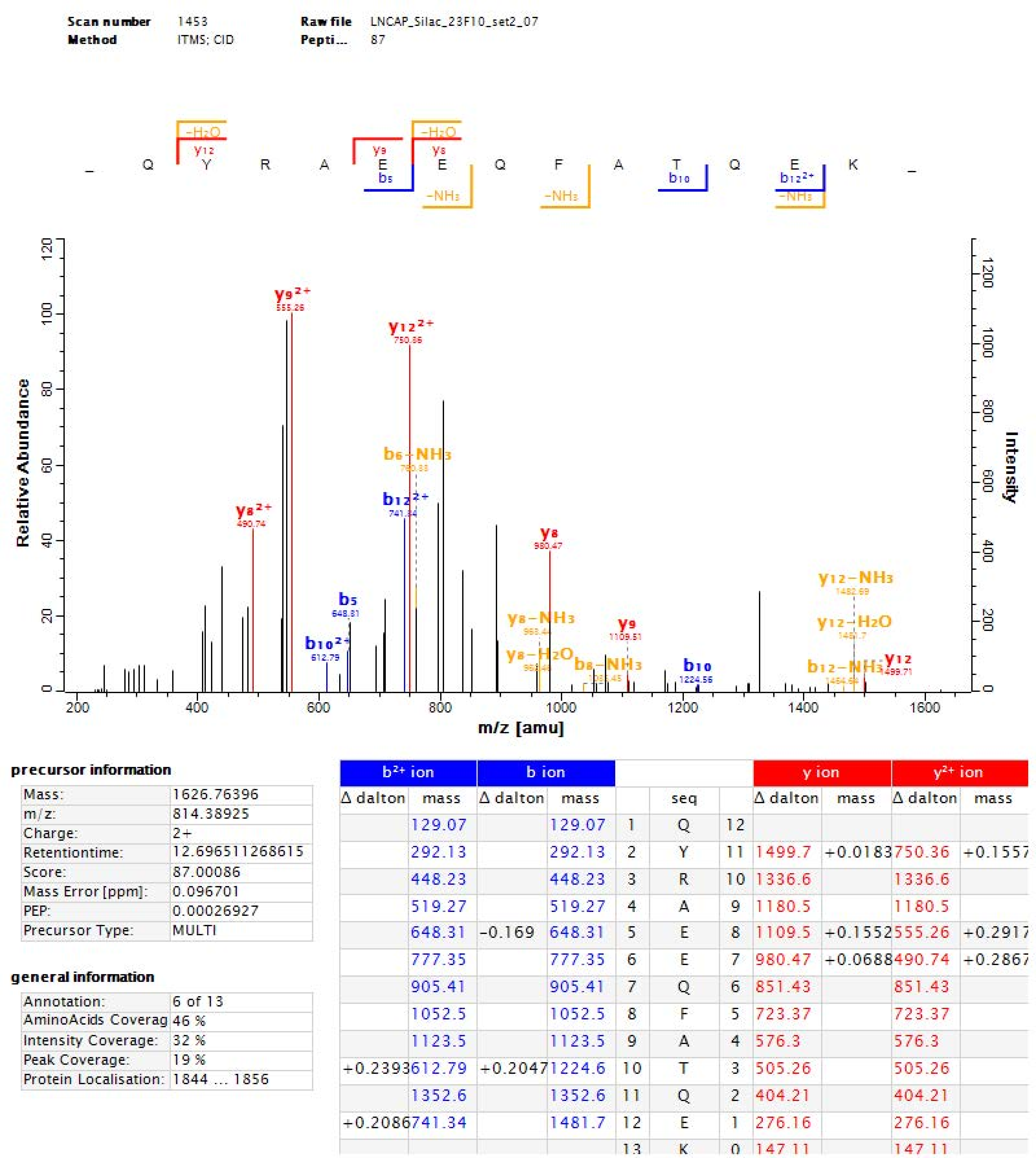
precursor information

Mass:	1290.65641
m/z:	646.33548
Charge:	2+
Retentiontime:	12.34792137146
Score:	69.86363
Mass Error [ppm]:	-0.31543
PEP:	0.003937
Precursor Type:	MULTI

general information

Annotation:	8 of 12
AminoAcids Coverag	67 %
Intensity Coverage:	35 %
Peak Coverage:	19 %
Protein Localisation:	159 ... 170

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.05	1	T	11				
-0.059	189.09	+0.1058	217.08	2	D	10	1190.6		1190.6	
	260.12	-0.058	288.12	3	A	9	1075.6		538.3	+0.1424
	331.16		359.16	4	A	8	1004.6	-0.144	502.78	-0.114
	418.19	+0.1498	446.19	5	S	7	933.52	+0.0695	933.52	
	546.29		574.28	6	K	6	846.48	-0.005	846.48	
	643.34		671.34	7	P	5	718.39	+0.0336	718.39	
	790.41		818.4	8	F	4	621.34		621.34	
	861.45		889.44	9	A	3	474.27		474.27	
	990.49	+0.025	1018.5	10	E	2	403.23		403.23	
	1089.6	-0.165	1117.6	11	V	1	274.19	+0.0226	274.19	
				12	R	0	175.12		175.12	



Scan number	1453	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	87

precursor information

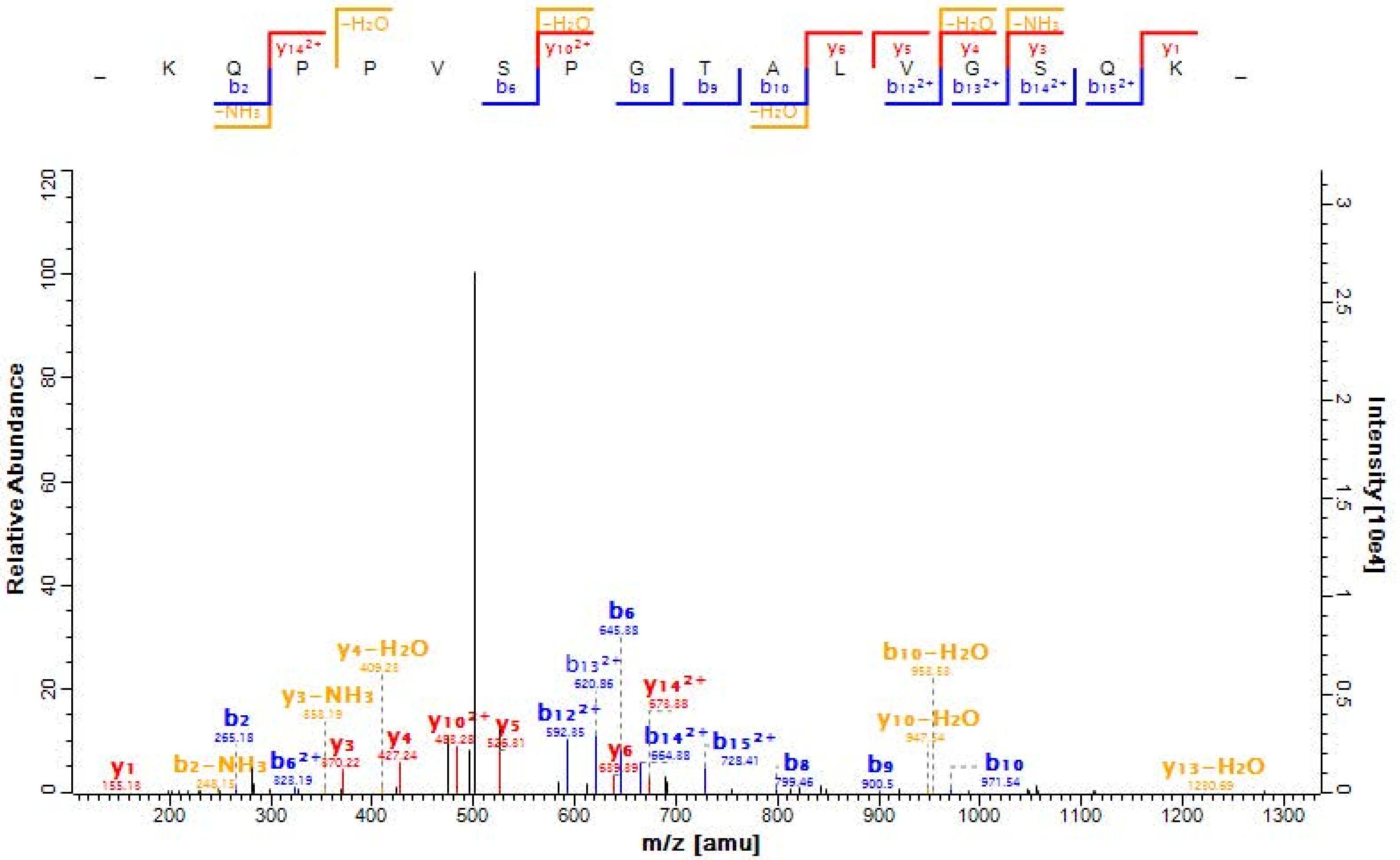
Mass:	1626.76396
m/z:	814.38925
Charge:	2+
Retentiontime:	12.696511268615
Score:	87.00086
Mass Error [ppm]:	0.096701
PEP:	0.00026927
Precursor Type:	MULTI

general information

Annotation:	6 of 13
AminoAcids Coverag	46 %
Intensity Coverage:	32 %
Peak Coverage:	19 %
Protein Localisation:	1844 ... 1856

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.07		129.07	1	Q	12				
	292.13		292.13	2	Y	11	1499.7	+0.0183	750.36	+0.1557
	448.23		448.23	3	R	10	1336.6		1336.6	
	519.27		519.27	4	A	9	1180.5		1180.5	
	648.31	−0.169	648.31	5	E	8	1109.5	+0.1552	555.26	+0.2917
	777.35		777.35	6	E	7	980.47	+0.0688	490.74	+0.2867
	905.41		905.41	7	Q	6	851.43		851.43	
	1052.5		1052.5	8	F	5	723.37		723.37	
	1123.5		1123.5	9	A	4	576.3		576.3	
+0.2393	612.79	+0.2047	1224.6	10	T	3	505.26		505.26	
	1352.6		1352.6	11	Q	2	404.21		404.21	
+0.2086	741.34		1481.7	12	E	1	276.16		276.16	
				13	K	0	147.11		147.11	

Scan number	1606	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	92.27



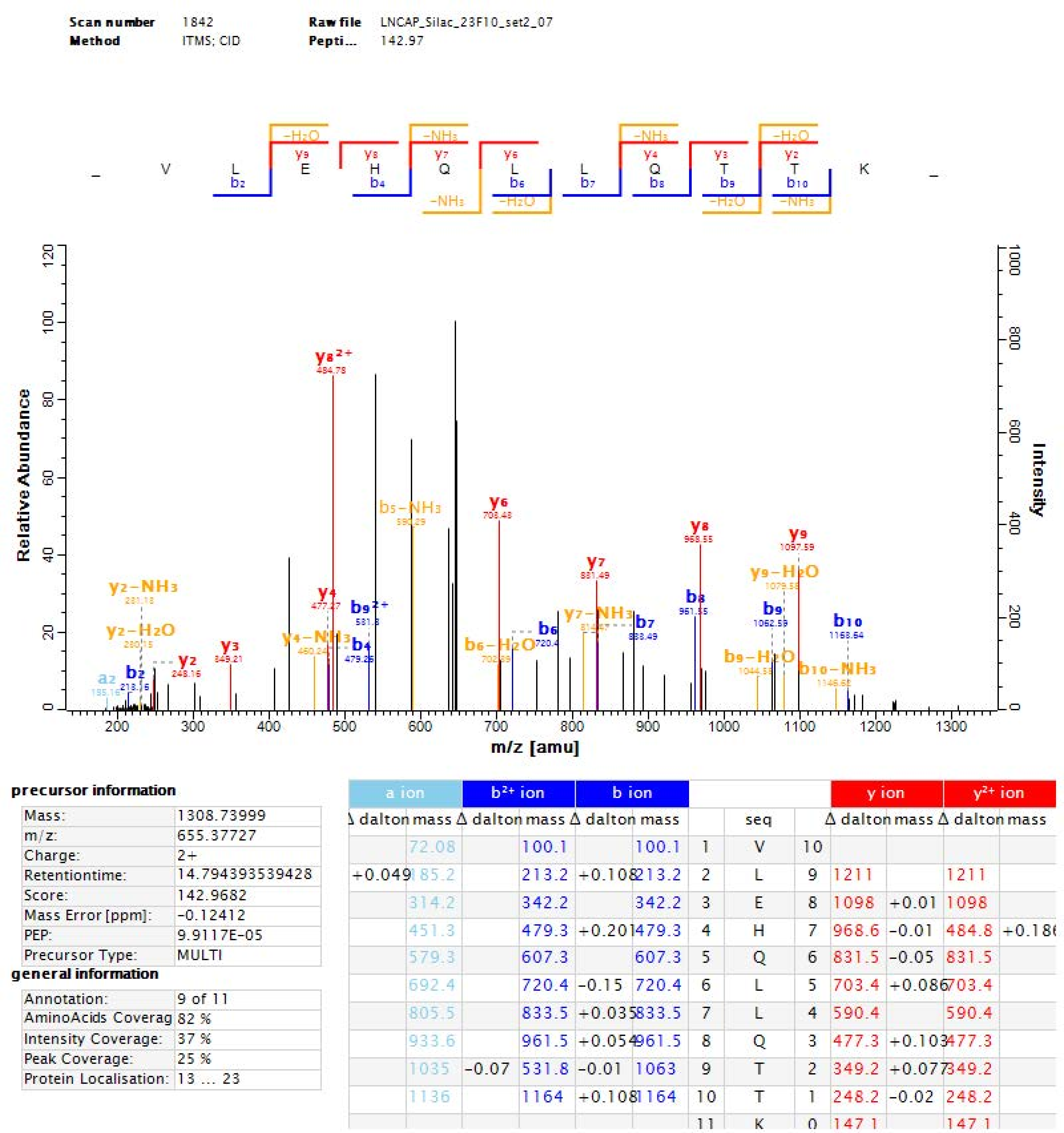
precursor information

Mass:	1592.88889
m/z:	531.97024
Charge:	3+
Retentiontime:	13.543733596801
Score:	92.26516
Mass Error [ppm]:	0.17801
PEP:	1.7081E-05
Precursor Type:	MULTI

general information

Annotation:	14 of 16
AminoAcids Coverag	88 %
Intensity Coverage:	33 %
Peak Coverage:	22 %
Protein Localisation:	31 ... 46

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	137.12		137.12	1	K	15				
	265.18	+0.145	265.18	2	Q	14	1473.8		1473.8	
	362.23		362.23	3	P	13	1345.8		673.38	+0.0687
	459.28		459.28	4	P	12	1248.7		1248.7	
	558.35		558.35	5	V	11	1151.7		1151.7	
+0.0266	323.19	+0.0706	645.38	6	S	10	1052.6		1052.6	
	742.43		742.43	7	P	9	965.55		483.28	+0.2133
	799.46	+0.0137	799.46	8	G	8	868.5		868.5	
	900.5	-0.095	900.5	9	T	7	811.48		811.48	
	971.54	+0.2647	971.54	10	A	6	710.43		710.43	
	1084.6		1084.6	11	L	5	639.39	-0.013	639.39	
+0.2442	592.35		1183.7	12	V	4	526.31	+0.0023	526.31	
+0.1797	620.86		1240.7	13	G	3	427.24	+0.0777	427.24	
+0.083	664.38		1327.7	14	S	2	370.22	+0.1866	370.22	
+0.1128	728.41		1455.8	15	Q	1	283.19		283.19	
				16	K	0	155.13	+0.0776	155.13	



Scan number	1842	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	142.97

precursor information

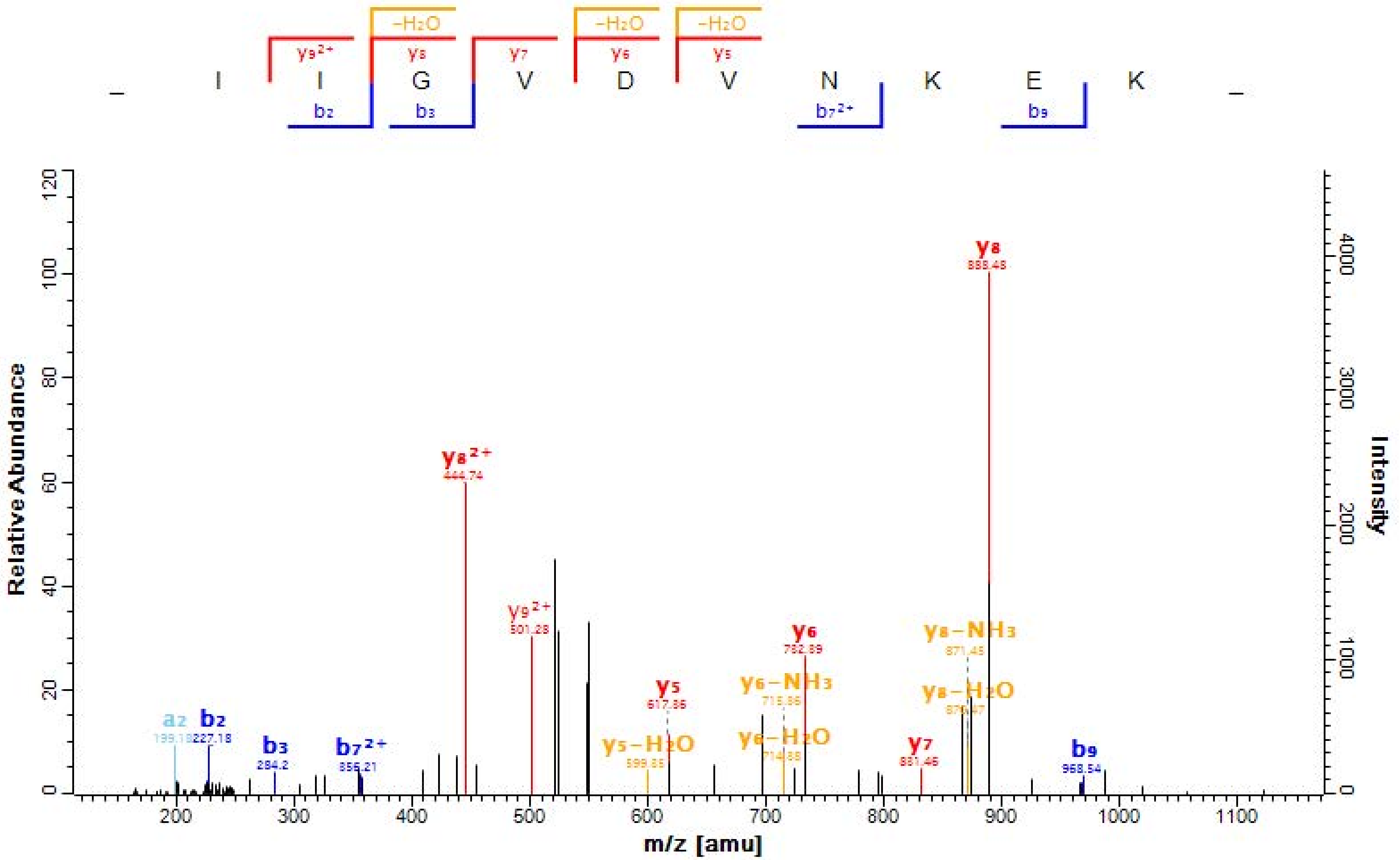
Mass:	1308.73999
m/z:	655.37727
Charge:	2+
Retentiontime:	14.794393539428
Score:	142.9682
Mass Error [ppm]:	-0.12412
PEP:	9.9117E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	37 %
Peak Coverage:	25 %
Protein Localisation:	13 ... 23

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.08		100.1		100.1	1	V	10				
+0.049	185.2		213.2	+0.108	213.2	2	L	9	1211		1211	
	314.2		342.2		342.2	3	E	8	1098	+0.01	1098	
	451.3		479.3	+0.201	479.3	4	H	7	968.6	-0.01	484.8	+0.186
	579.3		607.3		607.3	5	Q	6	831.5	-0.05	831.5	
	692.4		720.4	-0.15	720.4	6	L	5	703.4	+0.086	703.4	
	805.5		833.5	+0.035	833.5	7	L	4	590.4		590.4	
	933.6		961.5	+0.054	961.5	8	Q	3	477.3	+0.103	477.3	
	1035	-0.07	531.8	-0.01	1063	9	T	2	349.2	+0.077	349.2	
	1136		1164	+0.108	1164	10	T	1	248.2	-0.02	248.2	
						11	K	0	147.1		147.1	

Scan number	1847	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	102.07



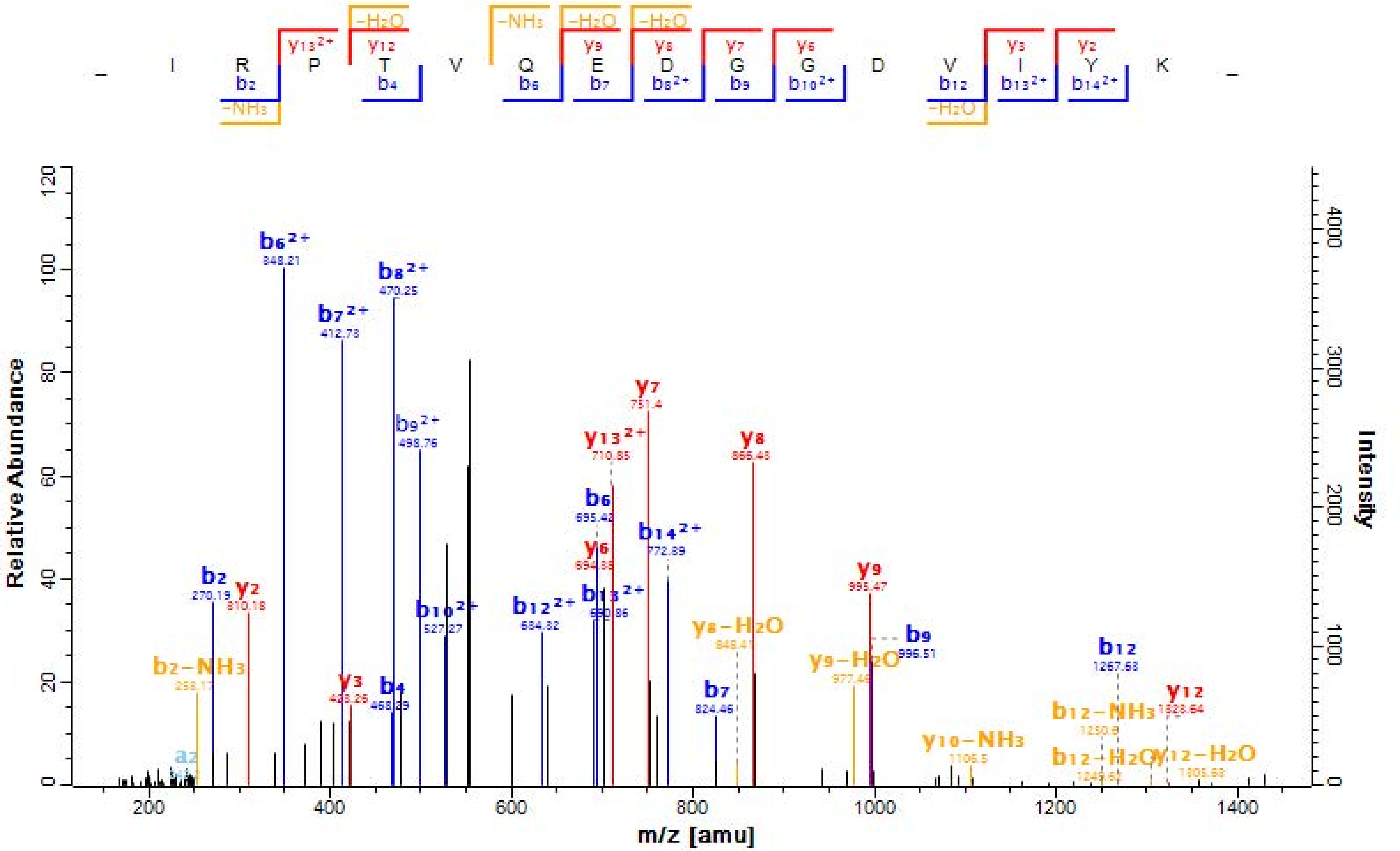
precursor information

Mass:	1113.63999
m/z:	557.82727
Charge:	2+
Retentiontime:	14.821597099304
Score:	102.0672
Mass Error [ppm]:	0.55137
PEP:	0.00065995
Precursor Type:	MULTI

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	44 %
Peak Coverage:	18 %
Protein Localisation:	220 ... 229

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	I	9				
+0.025	199.2		227.2	-0.02	227.2	2	I	8	1002		501.3	+0.25
	256.2		284.2	-0.09	284.2	3	G	7	888.5	+0.001	444.7	+0.13
	355.3		383.3		383.3	4	V	6	831.5	-0.03	831.5	
	470.3		498.3		498.3	5	D	5	732.4	-0.03	732.4	
	569.4		597.4		597.4	6	V	4	617.4	+0.117	617.4	
	683.4	+0.243	356.2		711.4	7	N	3	518.3		518.3	
	811.5		839.5		839.5	8	K	2	404.3		404.3	
	940.5		968.5	+0.076	968.5	9	E	1	276.2		276.2	
						10	K	0	147.1		147.1	

Scan number	2230	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	163.27



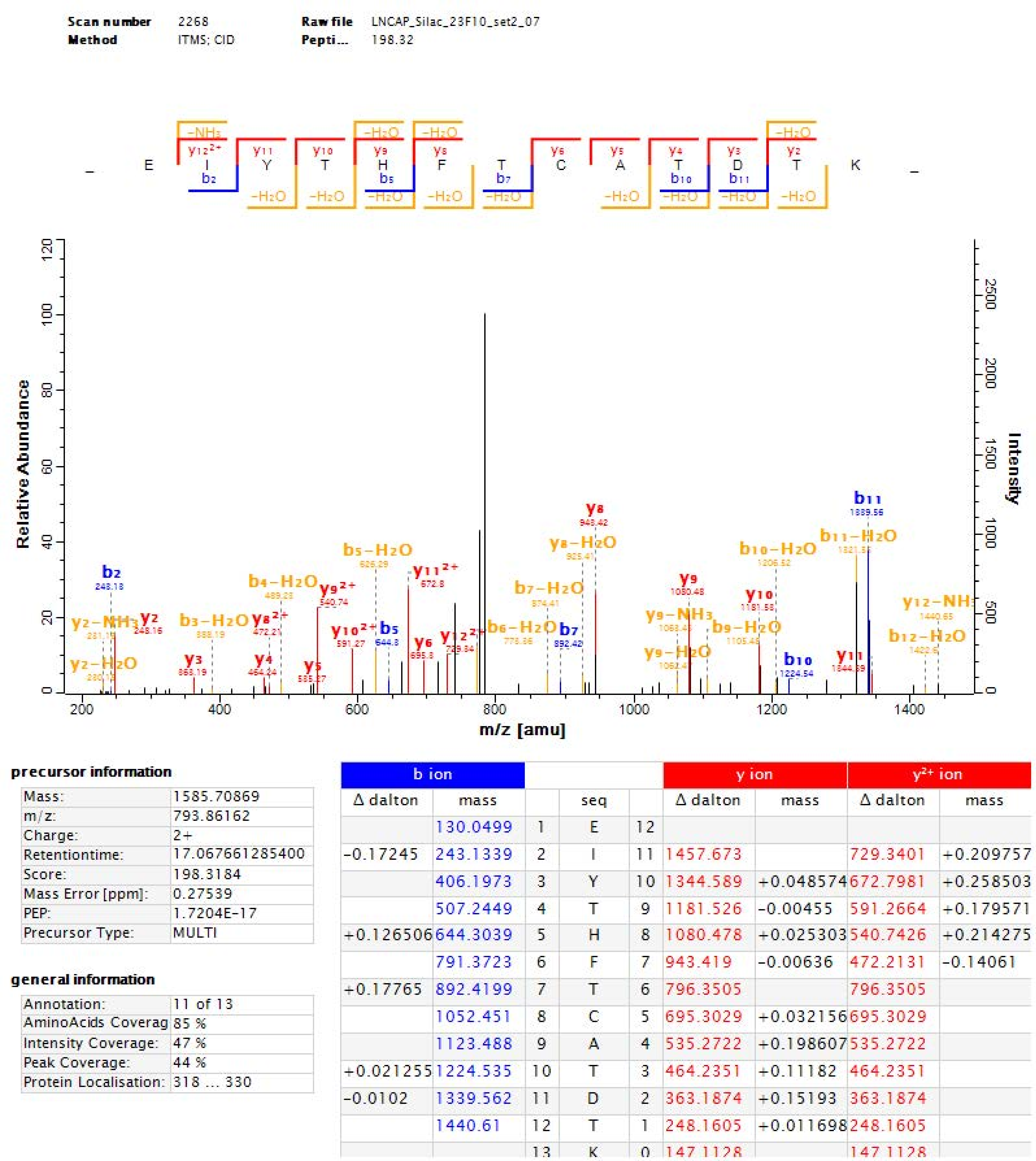
precursor information

Mass:	1688.87369
m/z:	563.96517
Charge:	3+
Retentiontime:	16.866405487060
Score:	163.2696
Mass Error [ppm]:	0.19973
PEP:	1.3154E-14
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	65 %
Peak Coverage:	29 %
Protein Localisation:	181 ... 195

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	I	14				
-0.03	242.2		270.2	+0.01	270.2	2	R	13	1577		1577	
	339.3		367.2		367.2	3	P	12	1421		710.9	+0.33
	440.3		468.3	+0.167	468.3	4	T	11	1324	+0.495	1324	
	539.4		567.4		567.4	5	V	10	1223		1223	
	667.4	+0.137	348.2	+0.003	695.4	6	Q	9	1124		1124	
	796.5	+0.156	412.7	-0.07	824.5	7	E	8	995.5	+0.02	995.5	
	911.5	+0.159	470.2		939.5	8	D	7	866.4	-0.01	866.4	
	968.5	-0.05	498.8	+0.064	996.5	9	G	6	751.4	-0.02	751.4	
	1026	+0	527.3		1054	10	G	5	694.4	-0.04	694.4	
	1141		1169		1169	11	D	4	637.4		637.4	
	1240	+0.139	634.3	+0.257	1268	12	V	3	522.3		522.3	
	1353	-0.04	690.9		1381	13	I	2	423.3	+0.044	423.3	
	1516	+0.338	772.4		1544	14	Y	1	310.2	+0.091	310.2	
						15	K	0	147.1		147.1	



Scan number 2268

Method ITMS; CID

Raw file LNCAP_Silac_23F10_set2_07

Pepti... 198.32

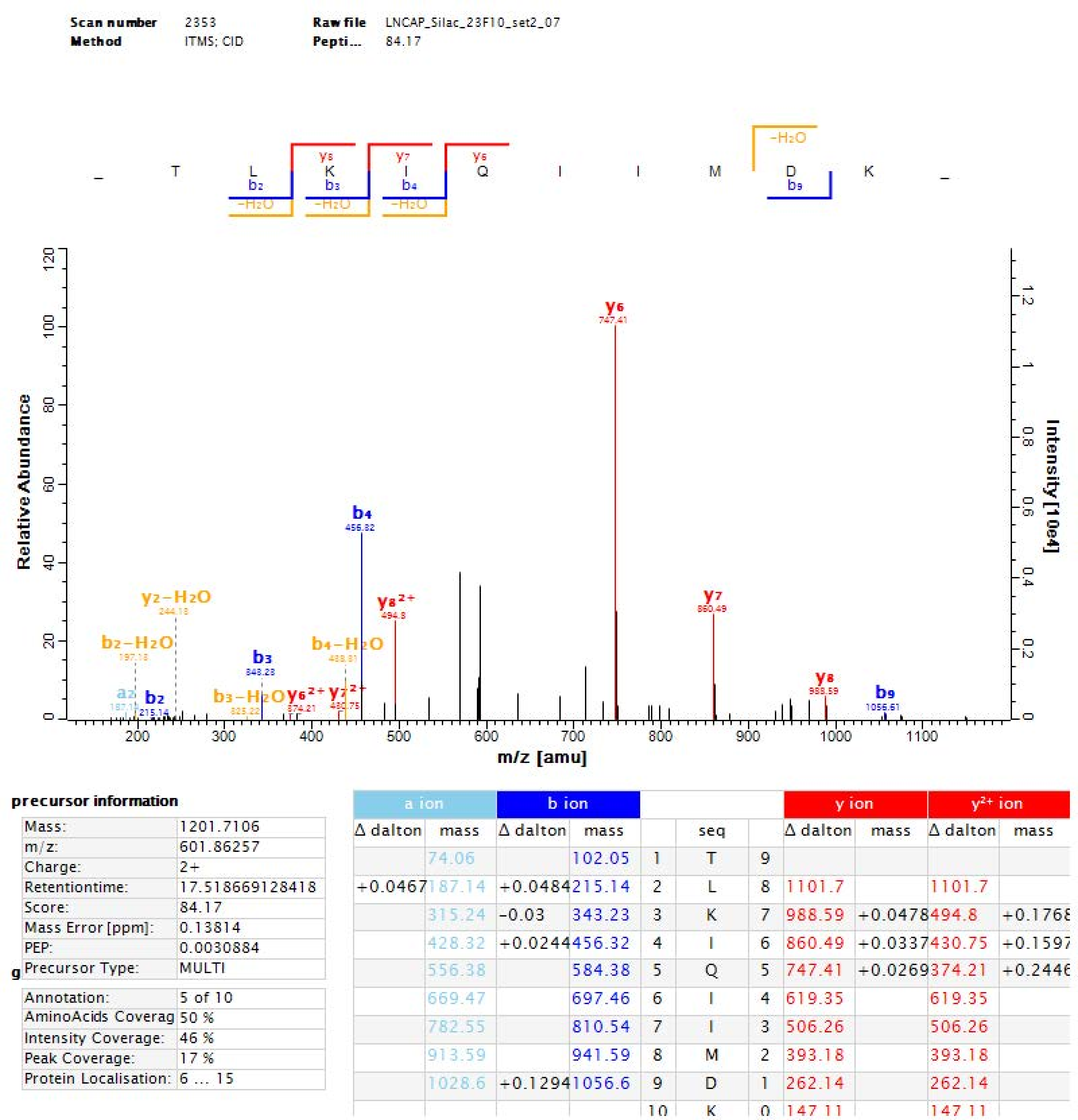
precursor information

Mass:	1585.70869
m/z:	793.86162
Charge:	2+
Retentiontime:	17.067661285400
Score:	198.3184
Mass Error [ppm]:	0.27539
PEP:	1.7204E-17
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	47 %
Peak Coverage:	44 %
Protein Localisation:	318 ... 330

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	12				
-0.17245	243.1339	2	I	11	1457.673		729.3401	+0.209757
	406.1973	3	Y	10	1344.589	+0.048574	672.7981	+0.258503
	507.2449	4	T	9	1181.526	-0.00455	591.2664	+0.179571
+0.126506	644.3039	5	H	8	1080.478	+0.025303	540.7426	+0.214275
	791.3723	6	F	7	943.419	-0.00636	472.2131	-0.14061
+0.17765	892.4199	7	T	6	796.3505		796.3505	
	1052.451	8	C	5	695.3029	+0.032156	695.3029	
	1123.488	9	A	4	535.2722	+0.198607	535.2722	
+0.021255	1224.535	10	T	3	464.2351	+0.11182	464.2351	
-0.0102	1339.562	11	D	2	363.1874	+0.15193	363.1874	
	1440.61	12	T	1	248.1605	+0.011698	248.1605	
		13	K	0	147.1128		147.1128	



Scan number 2353
Raw file LNCAP_Silac_23F10_set2_07
Method ITMS; CID
Pepti... 84.17

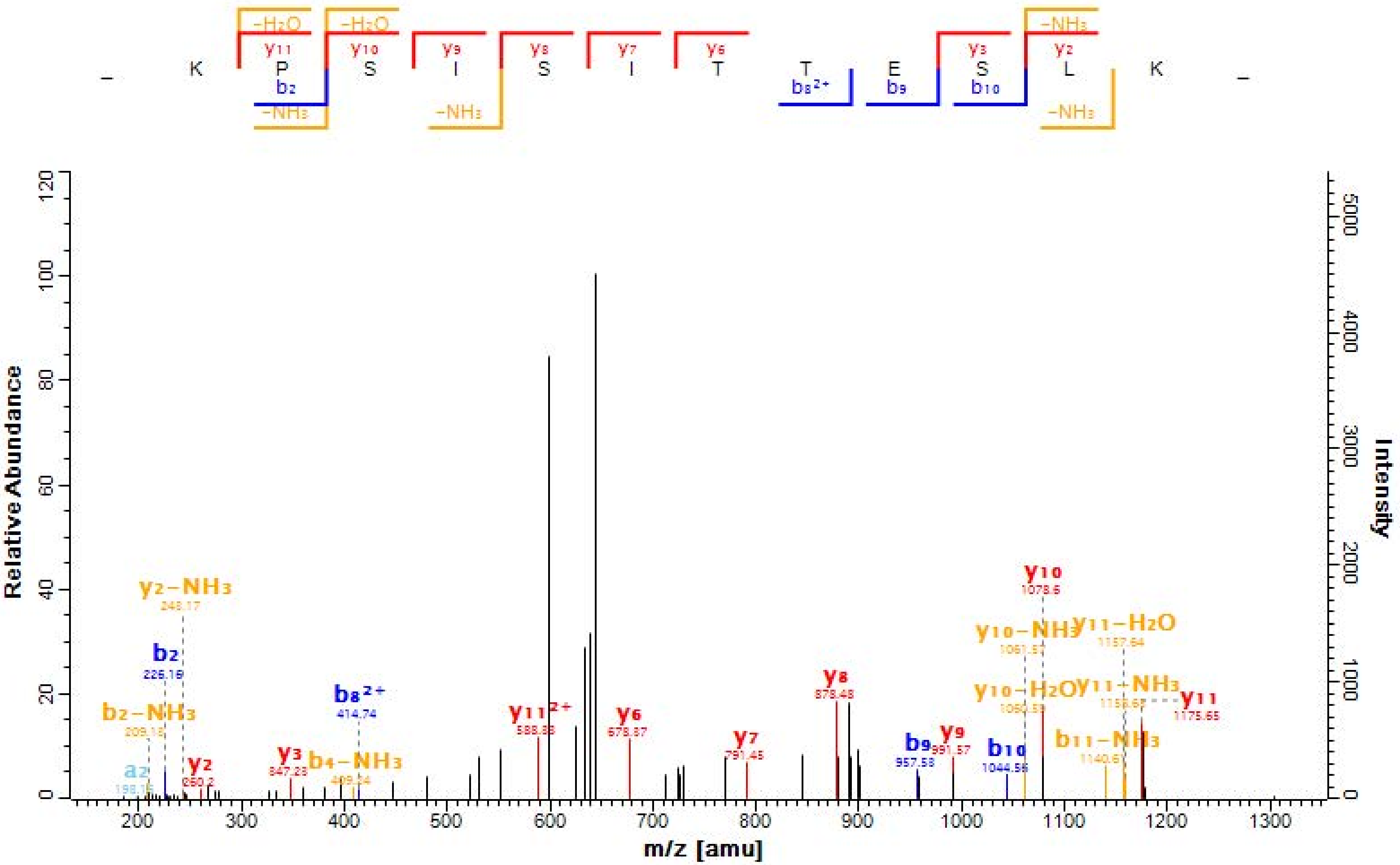
precursor information

Mass:	1201.7106
m/z:	601.86257
Charge:	2+
Retentiontime:	17.518669128418
Score:	84.17
Mass Error [ppm]:	0.13814
PEP:	0.0030884
Precursor Type:	MULTI

Annotation:	5 of 10
AminoAcids Coverag	50 %
Intensity Coverage:	46 %
Peak Coverage:	17 %
Protein Localisation:	6 ... 15

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.05	1	T	9				
+0.0467	187.14	+0.0484	215.14	2	L	8	1101.7		1101.7	
	315.24	-0.03	343.23	3	K	7	988.59	+0.0478	494.8	+0.176
	428.32	+0.0244	456.32	4	I	6	860.49	+0.0337	430.75	+0.159
	556.38		584.38	5	Q	5	747.41	+0.0269	374.21	+0.244
	669.47		697.46	6	I	4	619.35		619.35	
	782.55		810.54	7	I	3	506.26		506.26	
	913.59		941.59	8	M	2	393.18		393.18	
	1028.6	+0.1294	1056.6	9	D	1	262.14		262.14	
				10	K	0	147.11		147.11	

Scan number	2764	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	98.9



precursor information

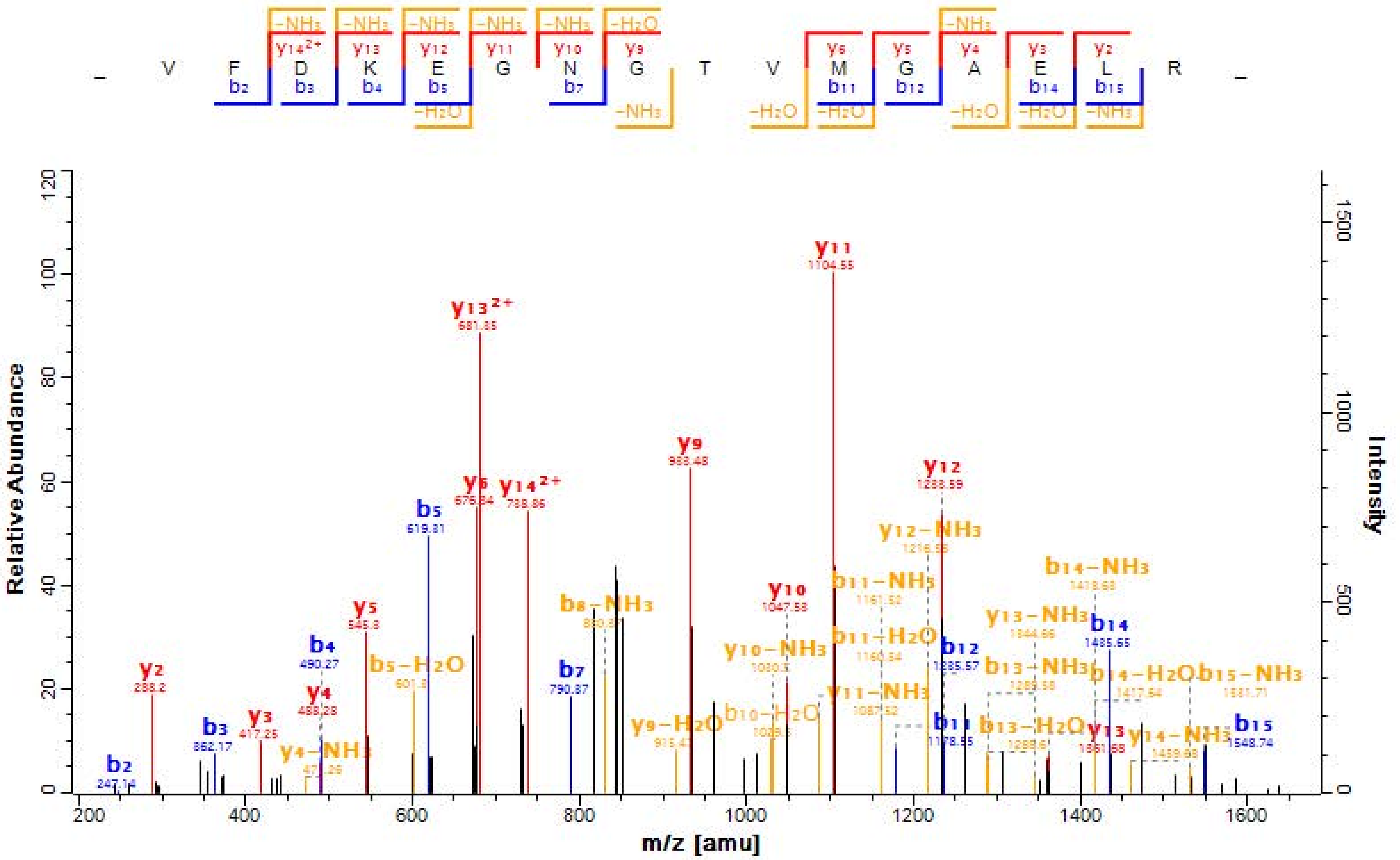
Mass:	1302.73986
m/z:	652.3772
Charge:	2+
Retentiontime:	19.657924652099
Score:	98.90169
Mass Error [ppm]:	0.28702
PEP:	0.00017949
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	24 %
Peak Coverage:	27 %
Protein Localisation:	765 ... 776

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	101.1		129.1		129.1	1	K	11				
+0.175	198.2		226.2	−0.05	226.2	2	P	10	1176	−0.08	588.3	−0.01
	285.2		313.2		313.2	3	S	9	1079	−0.06	1079	
	398.3		426.3		426.3	4	I	8	991.6	−0.23	991.6	
	485.3		513.3		513.3	5	S	7	878.5	+0.043	878.5	
	598.4		626.4		626.4	6	I	6	791.5	−0.01	791.5	
	699.4		727.4		727.4	7	T	5	678.4	−0.09	678.4	
	800.5	+0.101	414.7		828.5	8	T	4	577.3		577.3	
	929.5		957.5	+0.062	957.5	9	E	3	476.3		476.3	
	1017		1045	−0.17	1045	10	S	2	347.2	+0.035	347.2	
	1130		1158		1158	11	L	1	260.2	+0.108	260.2	
						12	K	0	147.1		147.1	

Scan number	2975	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	194.58



precursor information

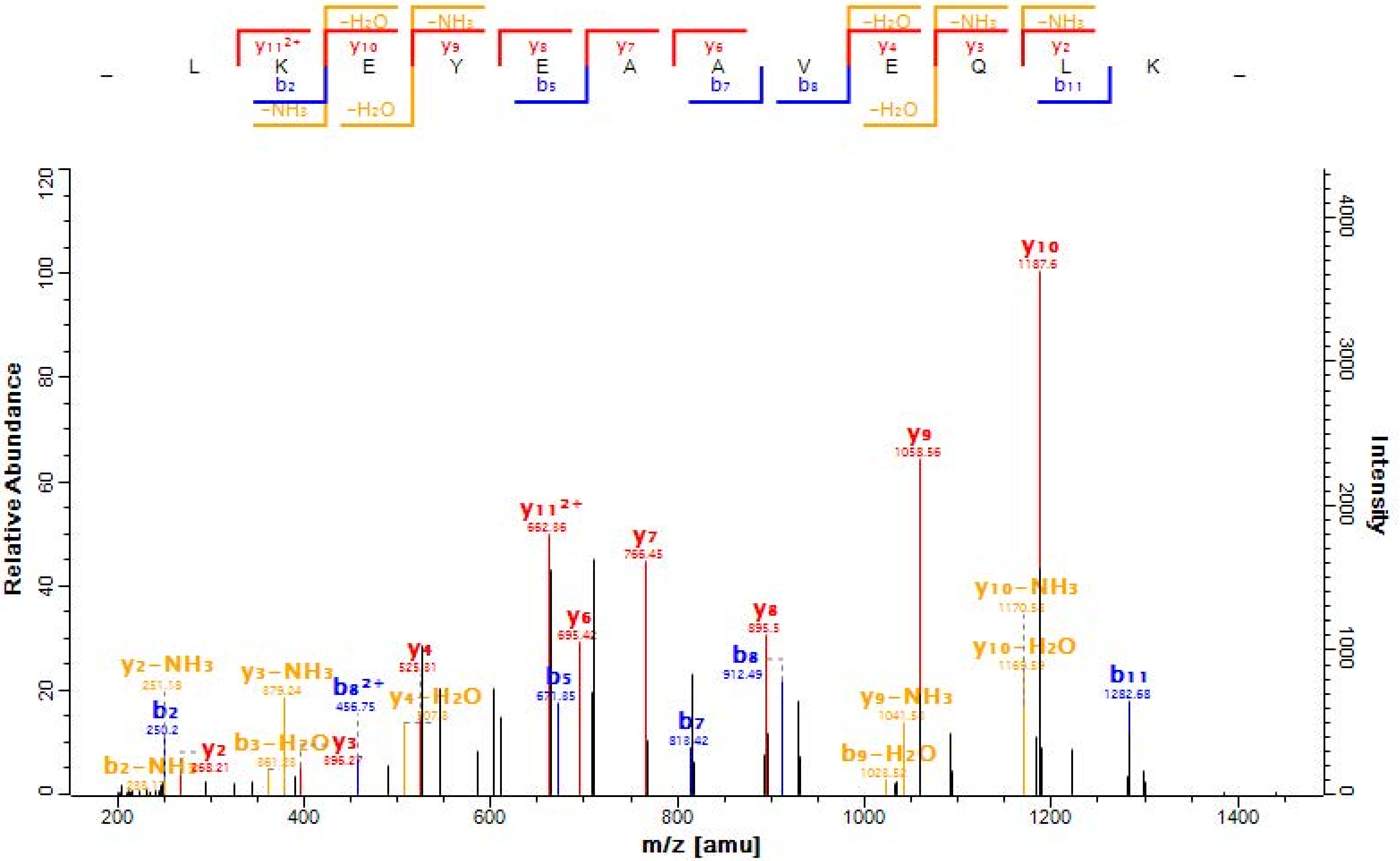
Mass:	0
m/z:	861.92711
Charge:	0+
Retentiontime:	20.775049209594
Score:	194.5789
Mass Error [ppm]:	-0.57936
PEP:	6.3596E-29
Precursor Type:	PEAK

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	58 %
Peak Coverage:	43 %
Protein Localisation:	139 ... 154

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	15				
-0.15097	247.1441	2	F	14	1623.78		1623.78	
+0.076328	362.171	3	D	13	1476.711		738.8592	+0.279047
+0.041302	490.266	4	K	12	1361.684	+0.006621	681.3457	+0.295998
+0.107839	619.3086	5	E	11	1233.589	+0.007712	1233.589	
	676.3301	6	G	10	1104.547	-0.10704	1104.547	
+0.02941	790.373	7	N	9	1047.525	+0.026481	1047.525	
	847.3945	8	G	8	933.4822	+0.037121	933.4822	
	948.4421	9	T	7	876.4608		876.4608	
	1047.511	10	V	6	775.4131		775.4131	
+0.068105	1178.551	11	M	5	676.3447	+0.040521	676.3447	
+0.087169	1235.572	12	G	4	545.3042	+0.085034	545.3042	
	1306.61	13	A	3	488.2827	+0.112541	488.2827	
-0.01756	1435.652	14	E	2	417.2456	+0.140682	417.2456	
-0.22418	1548.736	15	L	1	288.203	+0.003649	288.203	
		16	R	0	175.119		175.119	

Scan number	3120	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	147.26



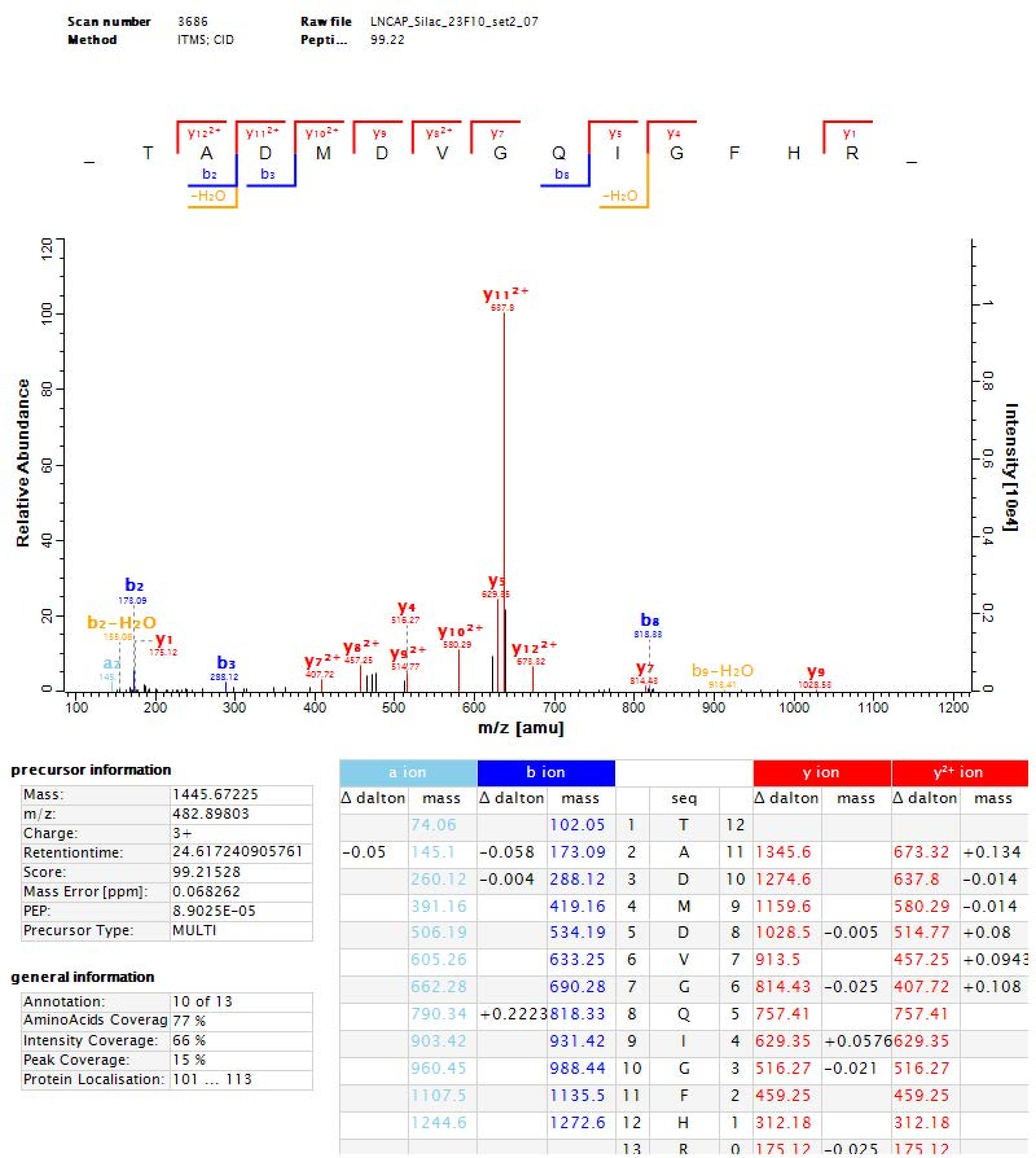
precursor information

Mass:	1419.7601
m/z:	710.88733
Charge:	2+
Retentiontime:	21.586795806884
Score:	147.2618
Mass Error [ppm]:	-0.58959
PEP:	6.0628E-06
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	52 %
Peak Coverage:	28 %
Protein Localisation:	93 ... 104

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	11				
	250.2	+0.0784	250.2	2	K	10	1323.7		662.36	-0.074
	379.24		379.24	3	E	9	1187.6	-0.025	1187.6	
	542.31		542.31	4	Y	8	1058.6	-0.036	1058.6	
	671.35	+0.0403	671.35	5	E	7	895.5	-0.003	895.5	
	742.39		742.39	6	A	6	766.45	+0.088	766.45	
	813.42	-0.063	813.42	7	A	5	695.42	+0.0149	695.42	
+0.4706	456.75	-0.043	912.49	8	V	4	624.38		624.38	
	1041.5		1041.5	9	E	3	525.31	+0.085	525.31	
	1169.6		1169.6	10	Q	2	396.27	-0.016	396.27	
	1282.7	-0.012	1282.7	11	L	1	268.21	-0.049	268.21	
				12	K	0	155.13		155.13	



Scan number	3686	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	99.22

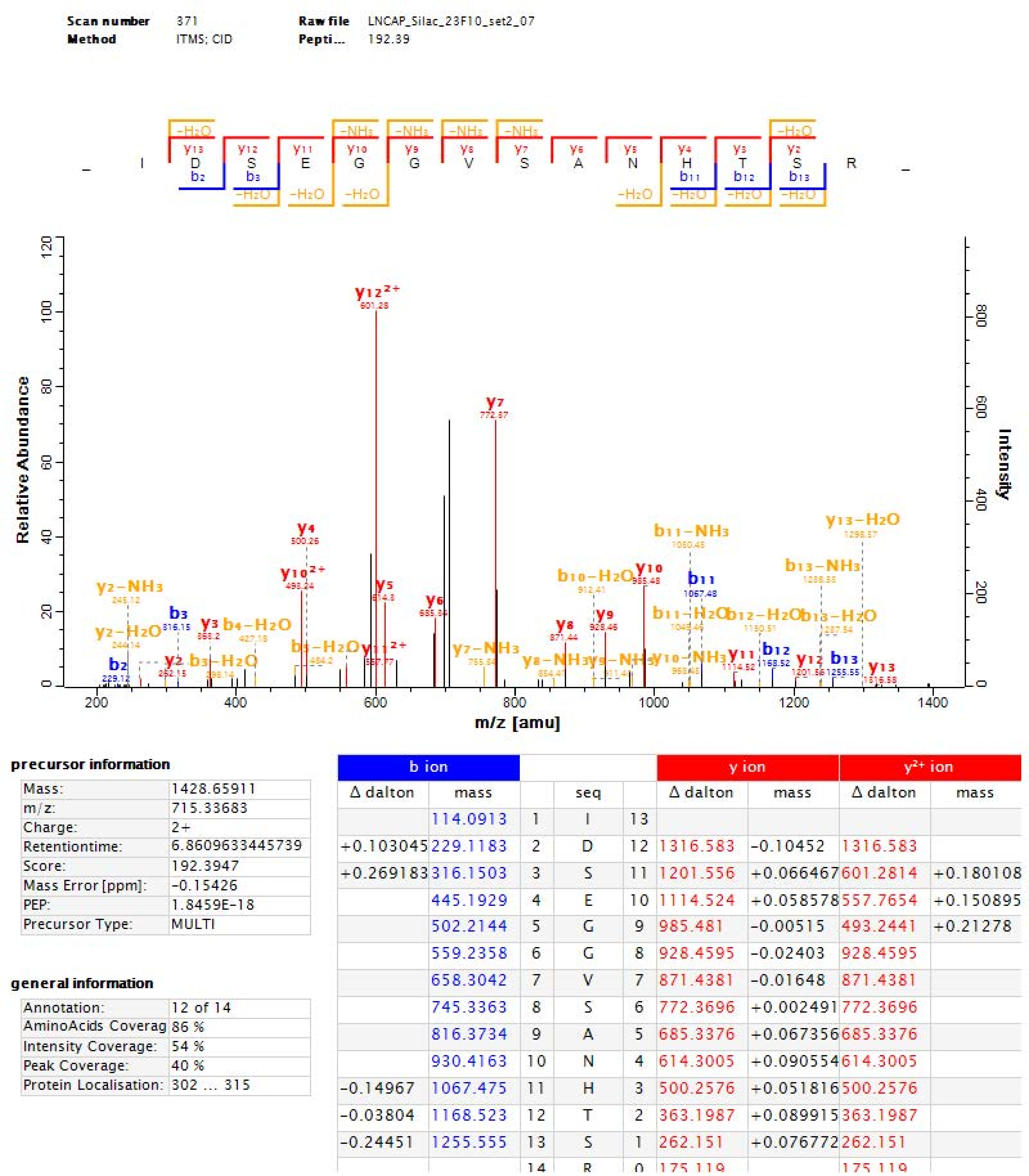
precursor information

Mass:	1445.67225
m/z:	482.89803
Charge:	3+
Retentiontime:	24.617240905761
Score:	99.21528
Mass Error [ppm]:	0.068262
PEP:	8.9025E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	66 %
Peak Coverage:	15 %
Protein Localisation:	101 ... 113

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.05	1	T	12				
-0.05	145.1	-0.058	173.09	2	A	11	1345.6		673.32	+0.134
	260.12	-0.004	288.12	3	D	10	1274.6		637.8	-0.014
	391.16		419.16	4	M	9	1159.6		580.29	-0.014
	506.19		534.19	5	D	8	1028.5	-0.005	514.77	+0.08
	605.26		633.25	6	V	7	913.5		457.25	+0.0943
	662.28		690.28	7	G	6	814.43	-0.025	407.72	+0.108
	790.34	+0.2223	818.33	8	Q	5	757.41		757.41	
	903.42		931.42	9	I	4	629.35	+0.0576	629.35	
	960.45		988.44	10	G	3	516.27	-0.021	516.27	
	1107.5		1135.5	11	F	2	459.25		459.25	
	1244.6		1272.6	12	H	1	312.18		312.18	
				13	R	0	175.12	-0.025	175.12	



Scan number 371
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set2_07
Pepti... 192.39

precursor information

Mass:	1428.65911
m/z:	715.33683
Charge:	2+
Retentiontime:	6.8609633445739
Score:	192.3947
Mass Error [ppm]:	-0.15426
PEP:	1.8459E-18
Precursor Type:	MULTI

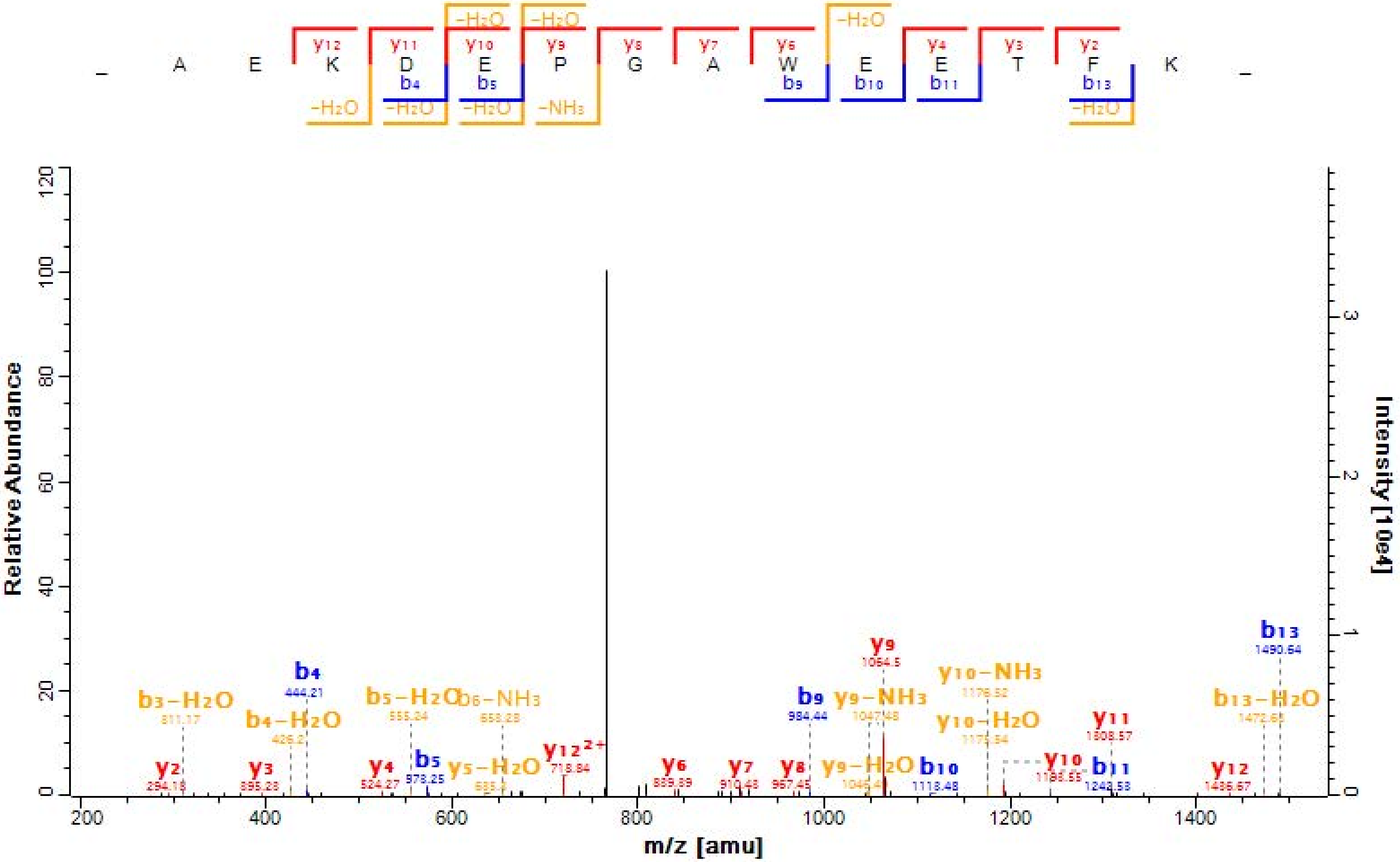
general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	54 %
Peak Coverage:	40 %
Protein Localisation:	302 ... 315

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	I	13				
+0.103045	229.1183	2	D	12	1316.583	-0.10452	1316.583	
+0.269183	316.1503	3	S	11	1201.556	+0.066467	601.2814	+0.180108
	445.1929	4	E	10	1114.524	+0.058578	557.7654	+0.150895
	502.2144	5	G	9	985.481	-0.00515	493.2441	+0.21278
	559.2358	6	G	8	928.4595	-0.02403	928.4595	
	658.3042	7	V	7	871.4381	-0.01648	871.4381	
	745.3363	8	S	6	772.3696	+0.002491	772.3696	
	816.3734	9	A	5	685.3376	+0.067356	685.3376	
	930.4163	10	N	4	614.3005	+0.090554	614.3005	
-0.14967	1067.475	11	H	3	500.2576	+0.051816	500.2576	
-0.03804	1168.523	12	T	2	363.1987	+0.089915	363.1987	
-0.24451	1255.555	13	S	1	262.151	+0.076772	262.151	
		14	R	0	175.119		175.119	

Scan number 3845
Method ITMS; CID

Raw file LNCAP_Silac_23F10_set2_07
Pepti... 139.58



precursor information

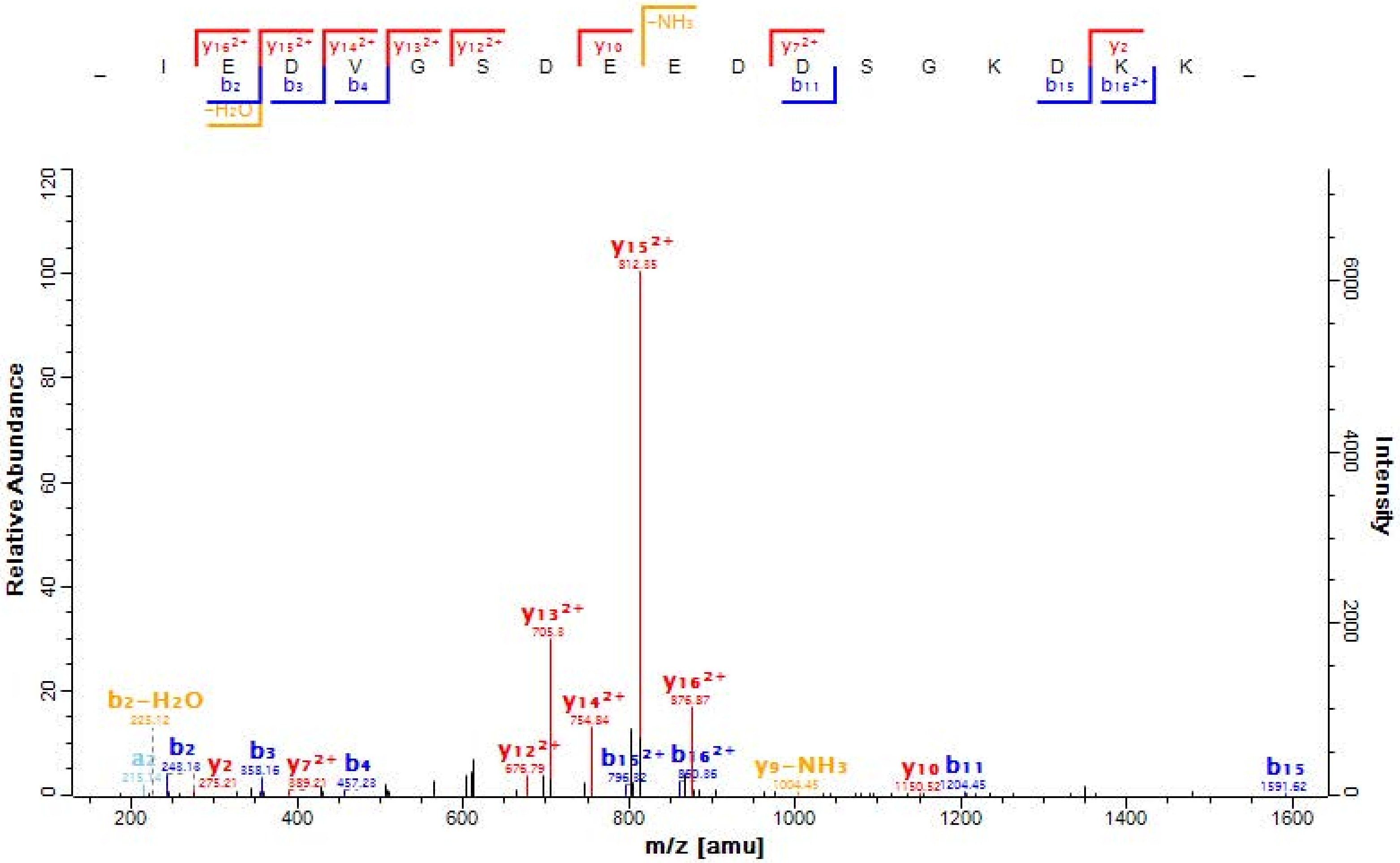
Mass:	1635.73721
m/z:	818.87588
Charge:	2+
Retentiontime:	25.477540969848
Score:	139.582
Mass Error [ppm]:	-2.7274
PEP:	5.7351E-09
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	18 %
Peak Coverage:	33 %
Protein Localisation:	269 ... 282

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	13				
	201.087	2	E	12	1565.712		1565.712	
	329.1819	3	K	11	1436.669	-0.45549	718.8383	+0.297669
+0.092685	444.2089	4	D	10	1308.574	-0.06365	1308.574	
+0.110578	573.2515	5	E	9	1193.547	-0.20797	1193.547	
	670.3042	6	P	8	1064.505	+0.025292	1064.505	
	727.3257	7	G	7	967.452	+0.042656	967.452	
	798.3628	8	A	6	910.4305	+0.214693	910.4305	
-0.01446	984.4421	9	W	5	839.3934	-0.03329	839.3934	
+0.301403	1113.485	10	E	4	653.3141		653.3141	
+0.324606	1242.527	11	E	3	524.2715	+0.071955	524.2715	
	1343.575	12	T	2	395.2289	+0.118149	395.2289	
-0.0991	1490.643	13	F	1	294.1812	+0.036952	294.1812	
		14	K	0	147.1128		147.1128	

Scan number	404	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	83.73



precursor information

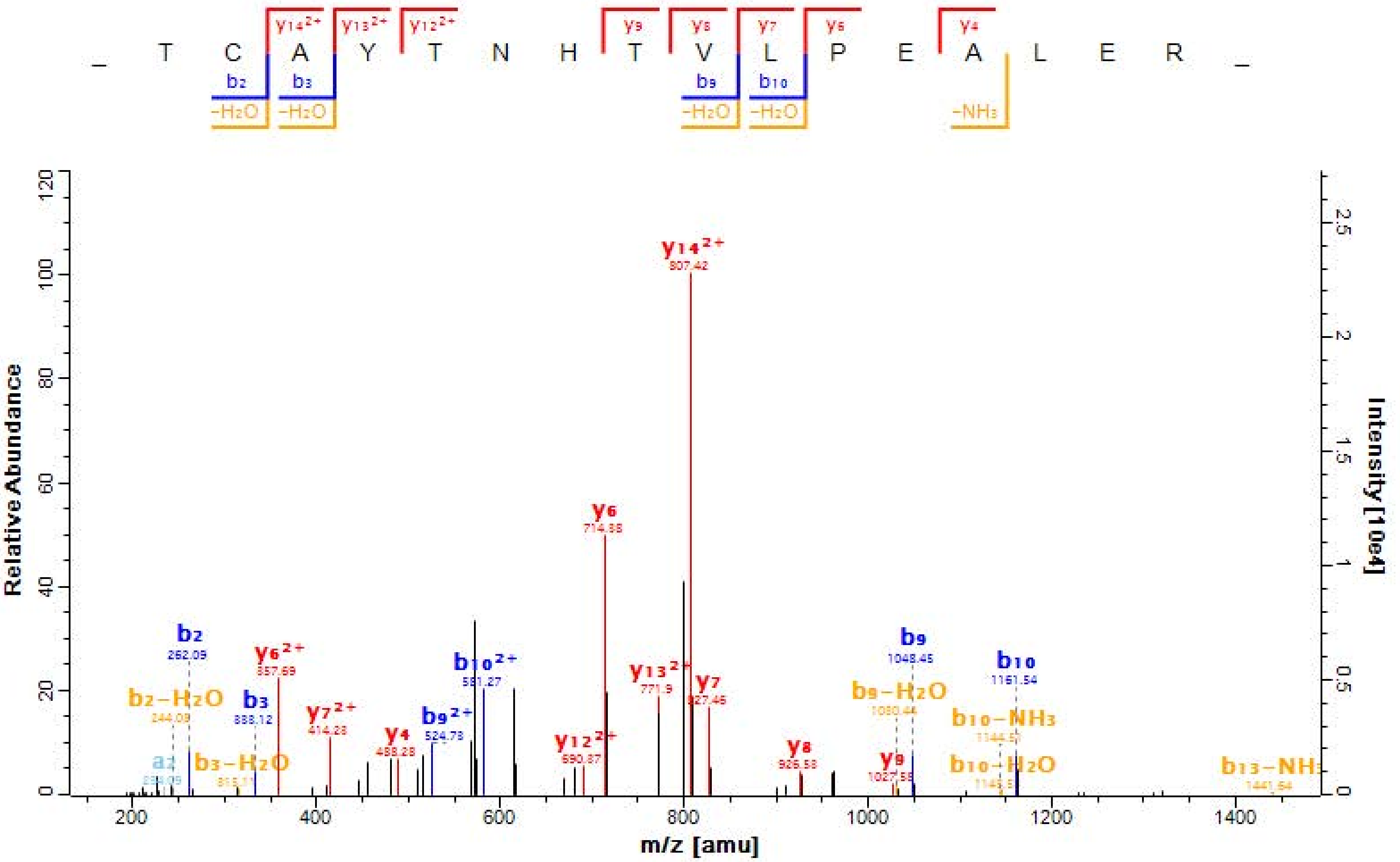
Mass:	1864.81802
m/z:	622.61328
Charge:	3+
Retentiontime:	7.0885548591613
Score:	83.729
Mass Error [ppm]:	0.32637
PEP:	4.292E-05
Precursor Type:	MULTI

general information

Annotation:	11 of 17
AminoAcids Coverag	65 %
Intensity Coverage:	66 %
Peak Coverage:	19 %
Protein Localisation:	250 ... 266

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	I	16				
+0.031	215.1		243.1	+0.041	243.1	2	E	15	1753		876.9	+0.20
	330.2		358.2	+0.162	358.2	3	D	14	1624		812.4	+0.26
	429.2		457.2	+0.094	457.2	4	V	13	1509		754.8	+0.25
	486.3		514.3		514.3	5	G	12	1410		705.3	+0.27
	573.3		601.3		601.3	6	S	11	1353		676.8	+0.19
	688.3		716.3		716.3	7	D	10	1266		1266	
	817.4		845.4		845.4	8	E	9	1151	-0.01	1151	
	946.4		974.4		974.4	9	E	8	1021		1021	
	1061		1089		1089	10	D	7	892.4		892.4	
	1176		1204	+0.014	1204	11	D	6	777.4		389.2	+0.06
	1263		1291		1291	12	S	5	662.4		662.4	
	1321		1349		1349	13	G	4	575.4		575.4	
	1449		1477		1477	14	K	3	518.3		518.3	
	1564	+0.279	796.3	-0.13	1592	15	D	2	390.2		390.2	
	1692	+0.213	860.4		1720	16	K	1	275.2	+0.183	275.2	
						17	K	0	147.1		147.1	

Scan number	4063	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	113.25



precursor information

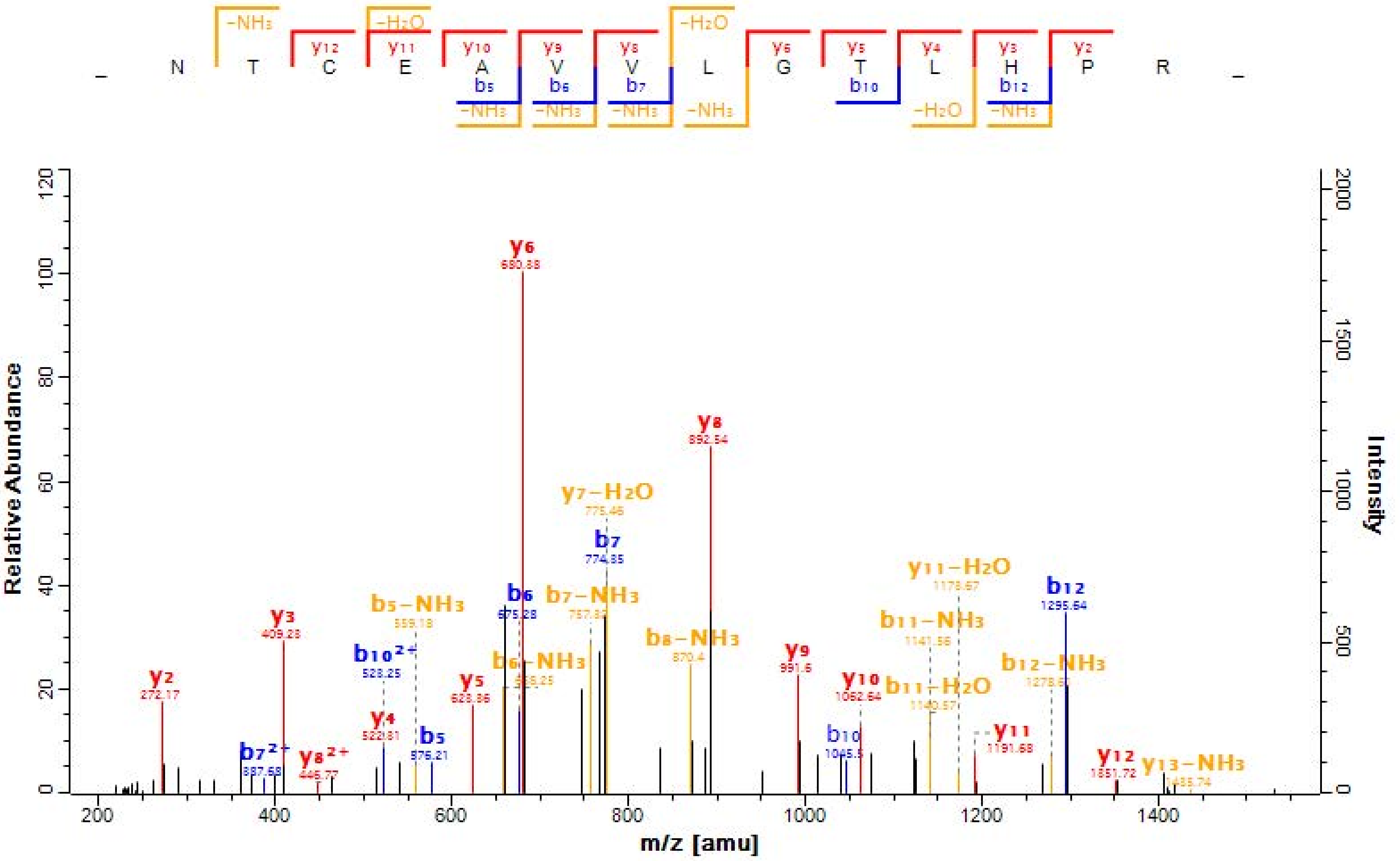
Mass:	1873.89879
m/z:	625.64021
Charge:	3+
Retentiontime:	26.631736755371
Score:	113.2528
Mass Error [ppm]:	-0.24121
PEP:	3.3815E-07
Precursor Type:	MULTI

general information

Annotation:	9 of 16
AminoAcids Coverag	56 %
Intensity Coverage:	53 %
Peak Coverage:	25 %
Protein Localisation:	372 ... 387

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.1		102.1	1	T	15				
+0.06	234.1		262.1	+0.088	262.1	2	C	14	1774		1774	
	305.1		333.1	-0.01	333.1	3	A	13	1614		807.4	+0.27
	468.2		496.2		496.2	4	Y	12	1543		771.9	-0.1
	569.2		597.2		597.2	5	T	11	1380		690.4	+0.22
	683.3		711.3		711.3	6	N	10	1279		1279	
	820.3		848.3		848.3	7	H	9	1165		1165	
	921.4		949.4		949.4	8	T	8	1028	+0.01	1028	
	1020	+0.163	524.7	+0.003	1048	9	V	7	926.5	-0.02	926.5	
	1134	+0.239	581.3	-0.11	1162	10	L	6	827.5	-0.02	414.2	+0.15
	1231		1259		1259	11	P	5	714.4	+0.021	357.7	+0.22
	1360		1388		1388	12	E	4	617.3		617.3	
	1431		1459		1459	13	A	3	488.3	+0.171	488.3	
	1544		1572		1572	14	L	2	417.2		417.2	
	1673		1701		1701	15	E	1	304.2		304.2	
						16	R	0	175.1		175.1	

Scan number	4358	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	112.02



precursor information

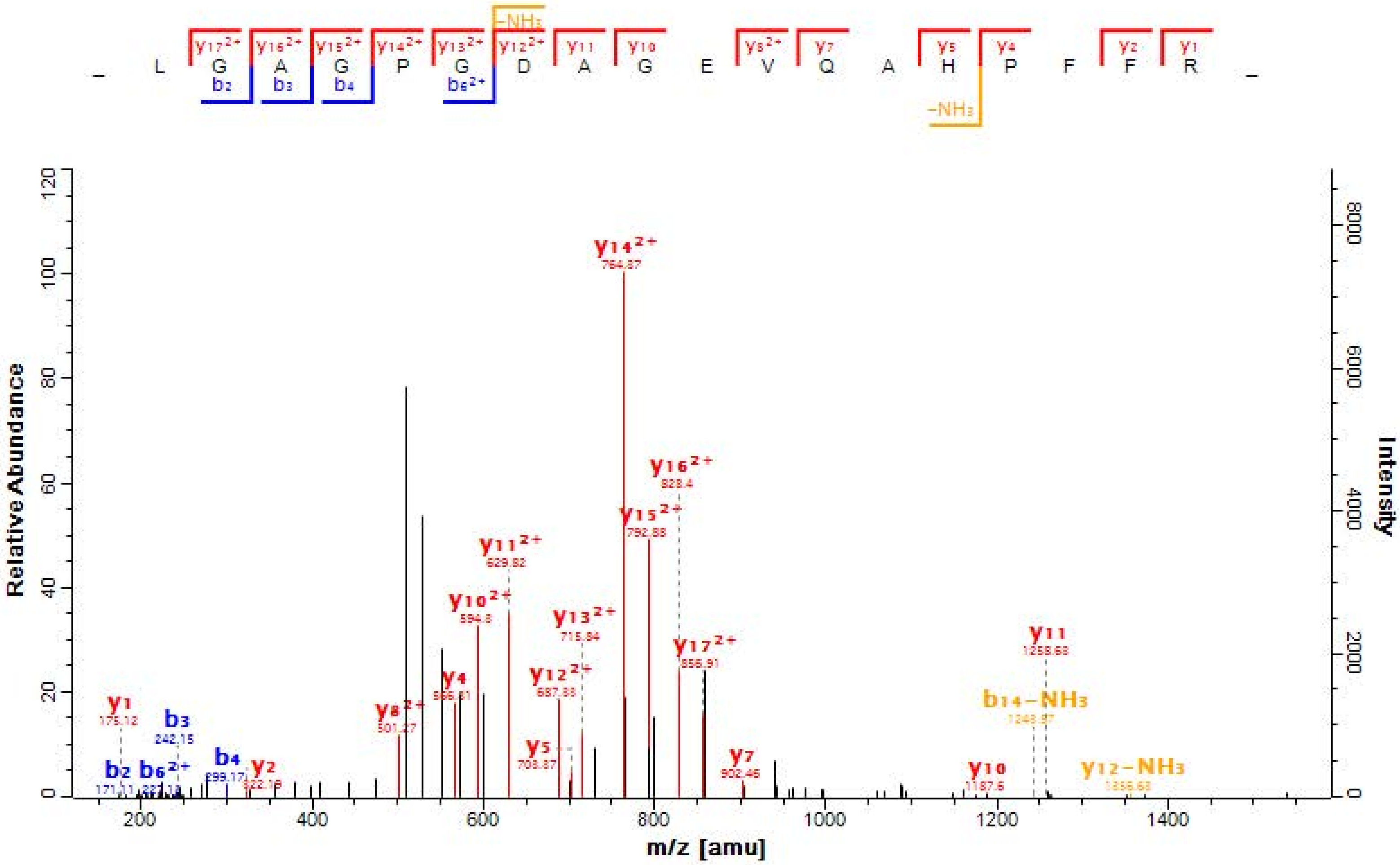
Mass:	1565.79856
m/z:	783.90655
Charge:	2+
Retentiontime:	28.219326019287
Score:	112.0222
Mass Error [ppm]:	0.092387
PEP:	4.4575E-06
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	58 %
Peak Coverage:	35 %
Protein Localisation:	133 ... 146

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.05		115.05	1	N	13				
	216.1		216.1	2	T	12	1452.8		1452.8	
	376.13		376.13	3	C	11	1351.7	+0.072	1351.7	
	505.17		505.17	4	E	10	1191.7	+0.0446	1191.7	
	576.21	+0.0603	576.21	5	A	9	1062.6	-0.064	1062.6	
	675.28	+0.0275	675.28	6	V	8	991.6	+0.0345	991.6	
-0.34	387.68	+0.4374	774.35	7	V	7	892.54	-0.068	446.77	+0.4231
	887.43		887.43	8	L	6	793.47		793.47	
	944.45		944.45	9	G	5	680.38	+0.0237	680.38	
+0.2279	523.25	-0.096	1045.5	10	T	4	623.36	+0.0605	623.36	
	1158.6		1158.6	11	L	3	522.31	+0.135	522.31	
	1295.6	-0.037	1295.6	12	H	2	409.23	+0.0412	409.23	
	1392.7		1392.7	13	P	1	272.17	-0.047	272.17	
				14	R	0	175.12		175.12	

Scan number	4427	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	60.55



precursor information

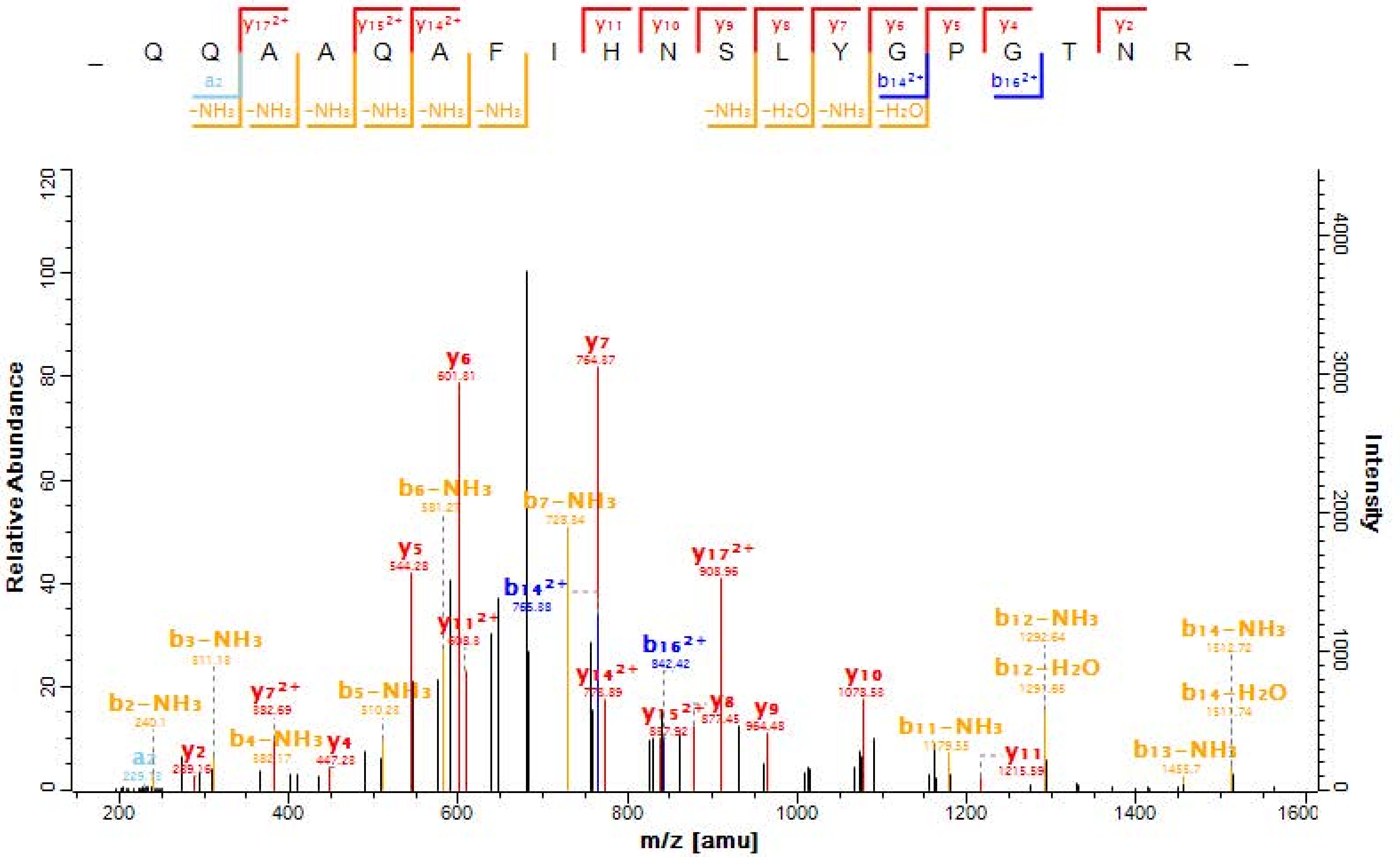
Mass:	1824.8903
m/z:	609.30404
Charge:	3+
Retentiontime:	28.580305099487
Score:	60.54892
Mass Error [ppm]:	-0.2378
PEP:	0.0018854
Precursor Type:	MULTI

general information

Annotation:	14 of 18
AminoAcids Coverag	78 %
Intensity Coverage:	48 %
Peak Coverage:	20 %
Protein Localisation:	336 ... 353

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	17				
	171.11	+0.2281	171.11	2	G	16	1712.8		856.91	+0.0481
	242.15	-0.059	242.15	3	A	15	1655.8		828.4	+0.2229
	299.17	+0.0117	299.17	4	G	14	1584.8		792.88	+0.1981
	396.22		396.22	5	P	13	1527.7		764.37	+0.3004
+0.162	227.13		453.25	6	G	12	1430.7		715.84	+0.1612
	568.27		568.27	7	D	11	1373.7		687.33	+0.1222
	639.31		639.31	8	A	10	1258.6	+0.0133	629.82	+0.2614
	696.33		696.33	9	G	9	1187.6	+0.1414	594.3	+0.2059
	825.37		825.37	10	E	8	1130.6		1130.6	
	924.44		924.44	11	V	7	1001.5		501.27	+0.2053
	1052.5		1052.5	12	Q	6	902.46	-0.118	902.46	
	1123.5		1123.5	13	A	5	774.4		774.4	
	1260.6		1260.6	14	H	4	703.37	+0.1173	703.37	
	1357.6		1357.6	15	P	3	566.31	+0.0383	566.31	
	1504.7		1504.7	16	F	2	469.26		469.26	
	1651.8		1651.8	17	F	1	322.19	-0.009	322.19	
				18	R	0	175.12	-0.062	175.12	

Scan number	4645	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	54.29



precursor information

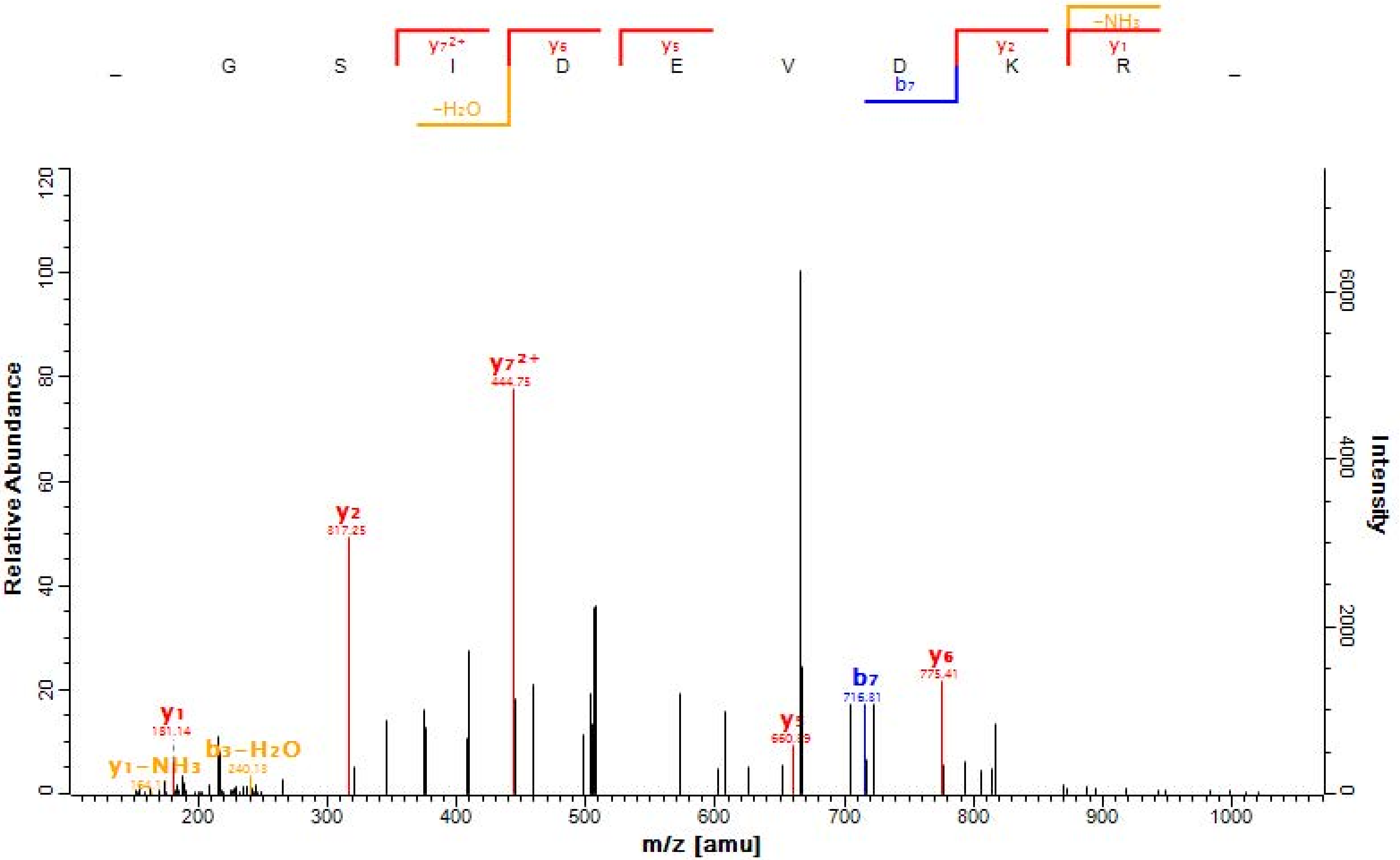
Mass:	2072.01913
m/z:	691.68032
Charge:	3+
Retentiontime:	29.740674972534
Score:	54.29184
Mass Error [ppm]:	0.16644
PEP:	0.0030981
Precursor Type:	MULTI

general information

Annotation:	15 of 19
AminoAcids Coverag	79 %
Intensity Coverage:	47 %
Peak Coverage:	27 %
Protein Localisation:	187 ... 205

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	101.1		129.1		129.1	1	Q	18				
+0.132	229.1		257.1		257.1	2	Q	17	1945		1945	
	300.2		328.2		328.2	3	A	16	1817		909	+0.37
	371.2		399.2		399.2	4	A	15	1746		1746	
	499.3		527.3		527.3	5	Q	14	1675		837.9	+0.41
	570.3		598.3		598.3	6	A	13	1547		773.9	+0.04
	717.4		745.4		745.4	7	F	12	1476		1476	
	830.5		858.4		858.4	8	I	11	1329		1329	
	967.5		995.5		995.5	9	H	10	1216	+0.113	608.3	+0.18
	1082		1110		1110	10	N	9	1079	+0.11	1079	
	1169		1197		1197	11	S	8	964.5	+0.104	964.5	
	1282		1310		1310	12	L	7	877.5	+0.018	877.5	
	1445		1473		1473	13	Y	6	764.4	+0.036	382.7	+0.32
	1502	+0.115	765.4		1530	14	G	5	601.3	+0.026	601.3	
	1599		1627		1627	15	P	4	544.3	+0.067	544.3	
	1656	+0.114	842.4		1684	16	G	3	447.2	-0.17	447.2	
	1757		1785		1785	17	T	2	390.2		390.2	
	1871		1899		1899	18	N	1	289.2	-0.06	289.2	
						19	R	0	175.1		175.1	

Scan number	497	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	30.56

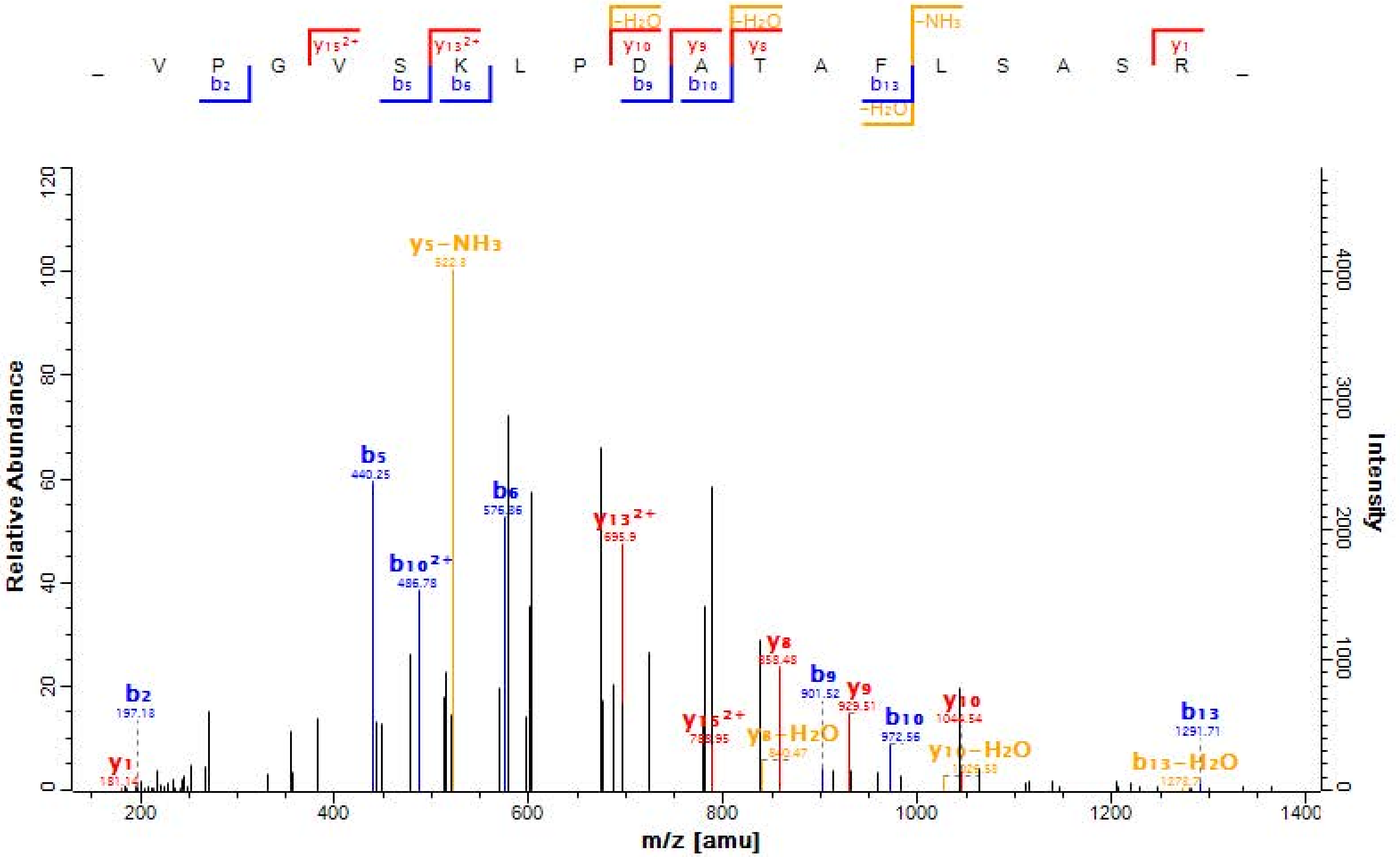


precursor information

Mass:	1017.50907
m/z:	509.76181
Charge:	2+
Retentiontime:	7.5844750404357
Score:	30.56388
Mass Error [ppm]:	-0.020829
PEP:	0.086726
Precursor Type:	MULTI
Annotation:	6 of 9
AminoAcids Coverag	67 %
Intensity Coverage:	24 %
Peak Coverage:	8 %
Protein Localisation:	322 ... 330

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	8				
	145.0608	2	S	7	975.5292		975.5292	
	258.1448	3	I	6	888.4972		444.7522	-0.0612
	373.1718	4	D	5	775.4131	+0.026073	775.4131	
	502.2144	5	E	4	660.3862	+0.035743	660.3862	
	601.2828	6	V	3	531.3436		531.3436	
-0.05393	716.3097	7	D	2	432.2752		432.2752	
	852.4189	8	K	1	317.2482	+0.023241	317.2482	
		9	R	0	181.1391	+0.017169	181.1391	

Scan number	5794	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	56.85



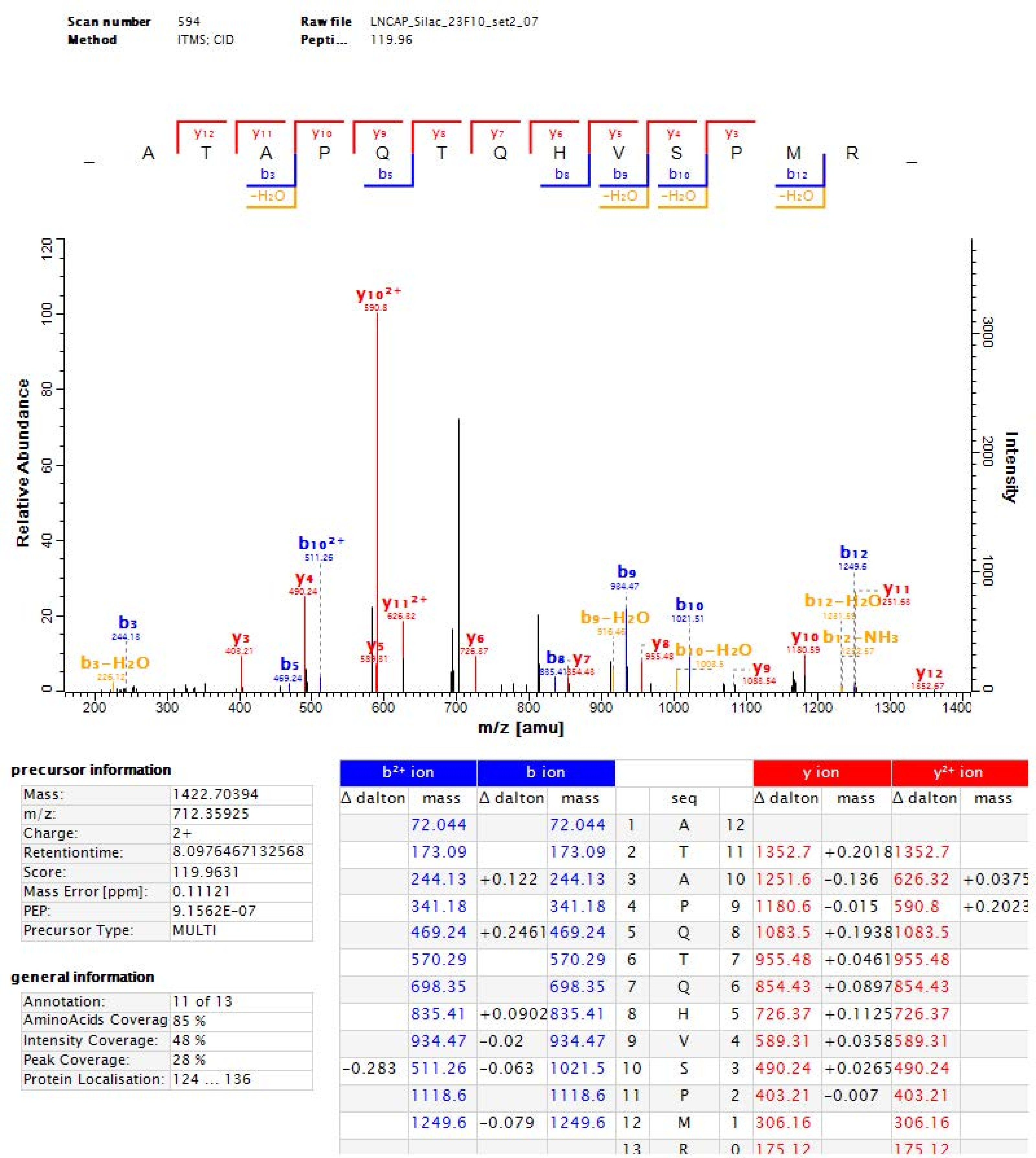
precursor information

Mass:	1814.98914
m/z:	606.00365
Charge:	3+
Retentiontime:	35.935310363769
Score:	56.85138
Mass Error [ppm]:	0.047697
PEP:	0.0019884
Precursor Type:	MULTI

general information

Annotation:	10 of 18
AminoAcids Coverag	56 %
Intensity Coverage:	34 %
Peak Coverage:	18 %
Protein Localisation:	2 ... 19

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	17				
	197.13	+0.0432	197.13	2	P	16	1731		1731	
	254.15		254.15	3	G	15	1633.9		1633.9	
	353.22		353.22	4	V	14	1576.9		788.95	−0.226
	440.25	+0.0031	440.25	5	S	13	1477.8		1477.8	
	576.36	−0.469	576.36	6	K	12	1390.8		695.9	−0.116
	689.44		689.44	7	L	11	1254.7		1254.7	
	786.5		786.5	8	P	10	1141.6		1141.6	
	901.52	+0.0346	901.52	9	D	9	1044.5	+0.1904	1044.5	
+0.0841	486.78	−0.111	972.56	10	A	8	929.51	+0.0147	929.51	
	1073.6		1073.6	11	T	7	858.48	+0.0073	858.48	
	1144.6		1144.6	12	A	6	757.43		757.43	
	1291.7	+0.2743	1291.7	13	F	5	686.39		686.39	
	1404.8		1404.8	14	L	4	539.32		539.32	
	1491.8		1491.8	15	S	3	426.24		426.24	
	1562.9		1562.9	16	A	2	339.21		339.21	
	1649.9		1649.9	17	S	1	268.17		268.17	
				18	R	0	181.14	+0.0224	181.14	



Scan number	594	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	119.96

precursor information

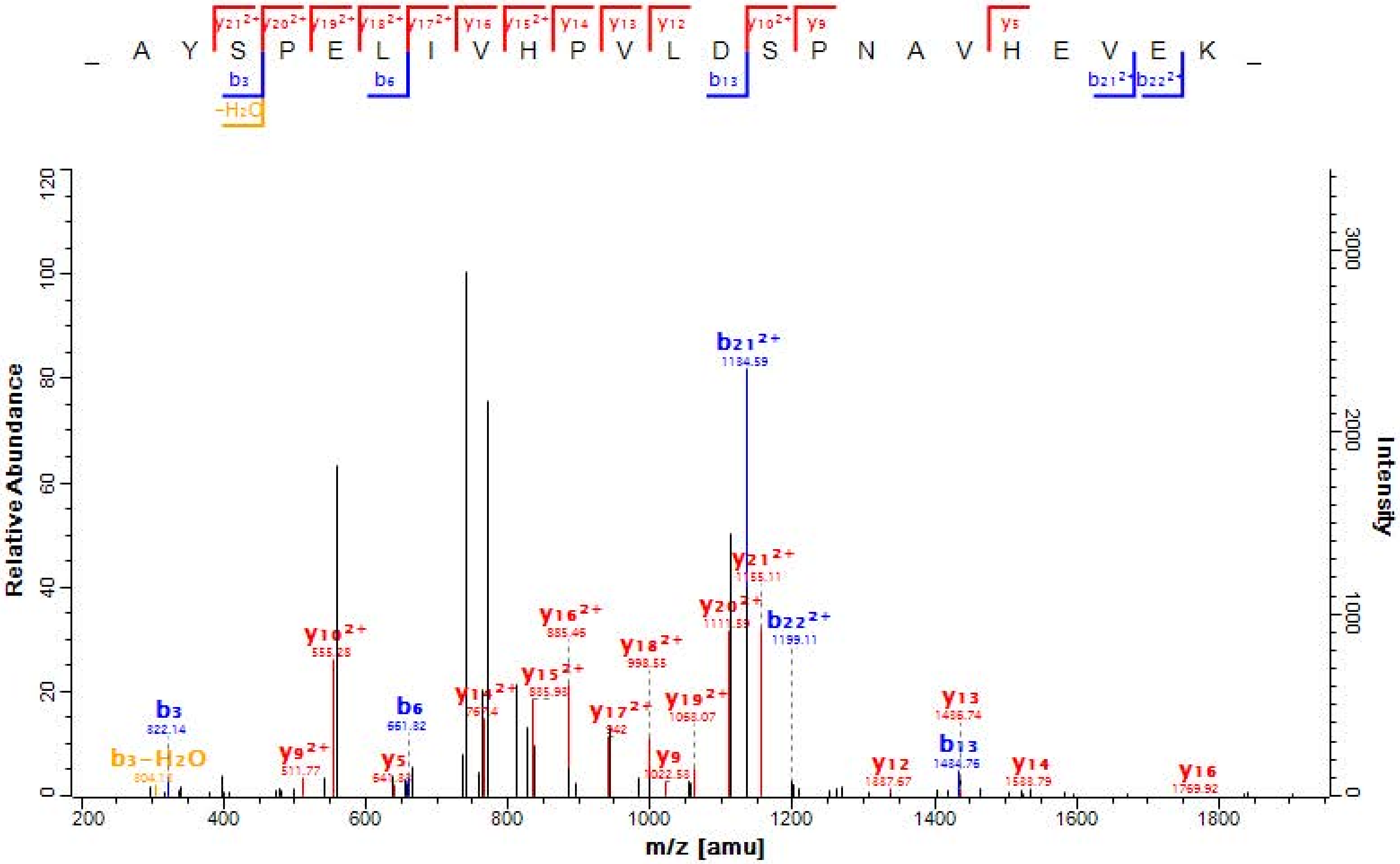
Mass:	1422.70394
m/z:	712.35925
Charge:	2+
Retentiontime:	8.0976467132568
Score:	119.9631
Mass Error [ppm]:	0.11121
PEP:	9.1562E-07
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	48 %
Peak Coverage:	28 %
Protein Localisation:	124 ... 136

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	12				
	173.09		173.09	2	T	11	1352.7	+0.2018	1352.7	
	244.13	+0.122	244.13	3	A	10	1251.6	-0.136	626.32	+0.0375
	341.18		341.18	4	P	9	1180.6	-0.015	590.8	+0.2023
	469.24	+0.2461	469.24	5	Q	8	1083.5	+0.1938	1083.5	
	570.29		570.29	6	T	7	955.48	+0.0461	955.48	
	698.35		698.35	7	Q	6	854.43	+0.0897	854.43	
	835.41	+0.0902	835.41	8	H	5	726.37	+0.1125	726.37	
	934.47	-0.02	934.47	9	V	4	589.31	+0.0358	589.31	
-0.283	511.26	-0.063	1021.5	10	S	3	490.24	+0.0265	490.24	
	1118.6		1118.6	11	P	2	403.21	-0.007	403.21	
	1249.6	-0.079	1249.6	12	M	1	306.16		306.16	
				13	R	0	175.12		175.12	

Scan number	6139	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	76.12



precursor information

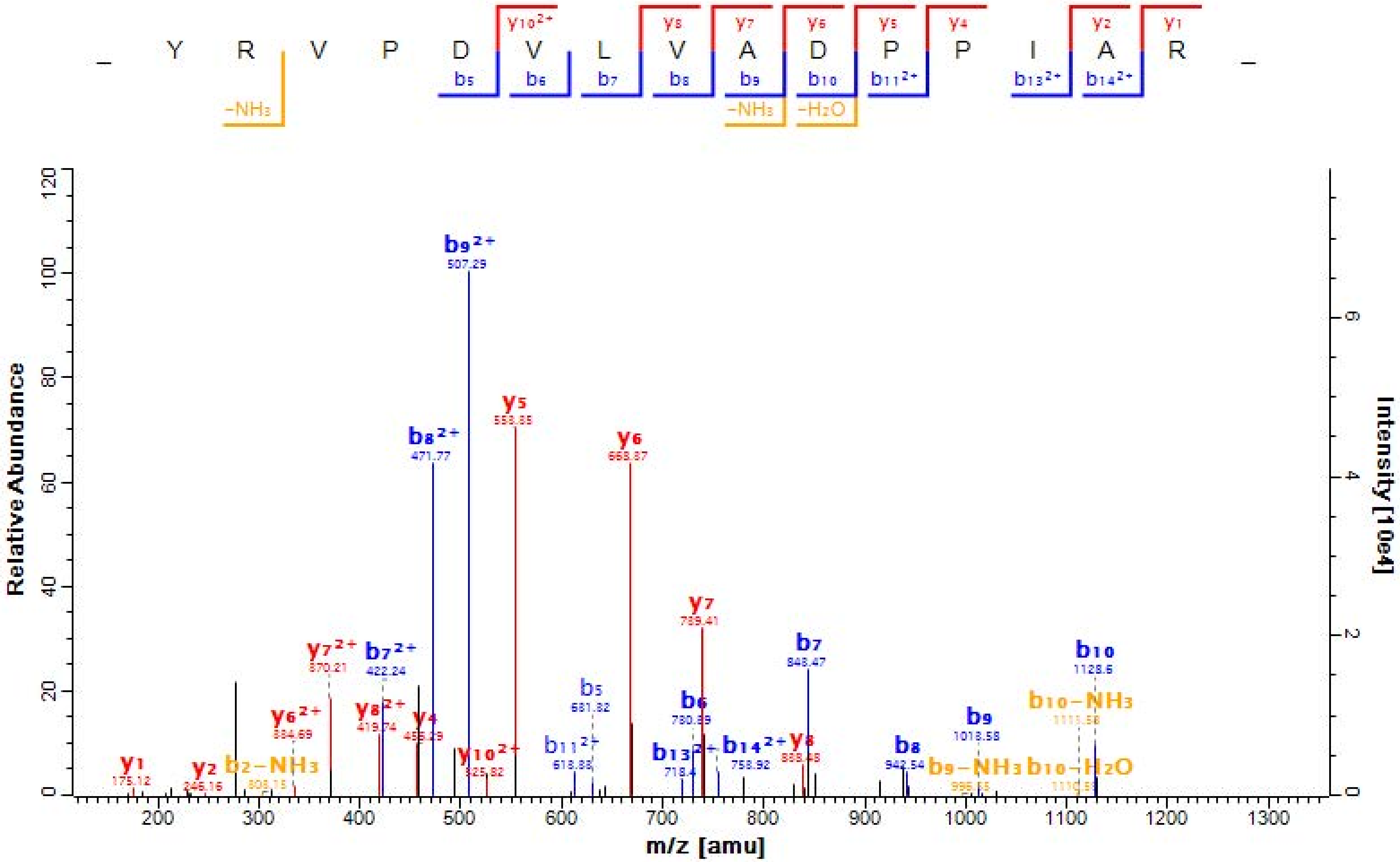
Mass:	2542.30623
m/z:	848.44269
Charge:	3+
Retentiontime:	37.895618438720
Score:	76.11842
Mass Error [ppm]:	-0.20611
PEP:	0.00010844
Precursor Type:	MULTI

general information

Annotation:	16 of 23
AminoAcids Coverag	70 %
Intensity Coverage:	34 %
Peak Coverage:	23 %
Protein Localisation:	118 ... 140

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	22				
	235.11		235.11	2	Y	21	2472.3		2472.3	
	322.14	+0.062	322.14	3	S	20	2309.2		1155.1	+0.3092
	419.19		419.19	4	P	19	2222.2		1111.6	-0.069
	548.24		548.24	5	E	18	2125.1		1063.1	+0.4043
	661.32	+0.0481	661.32	6	L	17	1996.1		998.55	+0.2818
	774.4		774.4	7	I	16	1883		942	-8E-06
	873.47		873.47	8	V	15	1769.9	-0.057	885.46	+0.097
	1010.5		1010.5	9	H	14	1670.8		835.93	+0.0692
	1107.6		1107.6	10	P	13	1533.8	-0.083	767.4	+0.174
	1206.7		1206.7	11	V	12	1436.7	-0.294	1436.7	
	1319.7		1319.7	12	L	11	1337.7	+0.1362	1337.7	
	1434.8	-0.142	1434.8	13	D	10	1224.6		1224.6	
	1521.8		1521.8	14	S	9	1109.6		555.28	+0.3143
	1618.8		1618.8	15	P	8	1022.5	-0.085	511.77	+0.463
	1732.9		1732.9	16	N	7	925.47		925.47	
	1803.9		1803.9	17	A	6	811.43		811.43	
	1903		1903	18	V	5	740.39		740.39	
	2040.1		2040.1	19	H	4	641.33	+0.1229	641.33	
	2169.1		2169.1	20	E	3	504.27		504.27	
-0.011	1134.6		2268.2	21	V	2	375.22		375.22	
+0.2123	1199.1		2397.2	22	E	1	276.16		276.16	
				23	K	0	147.11		147.11	

Scan number	6197	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	140.31



precursor information

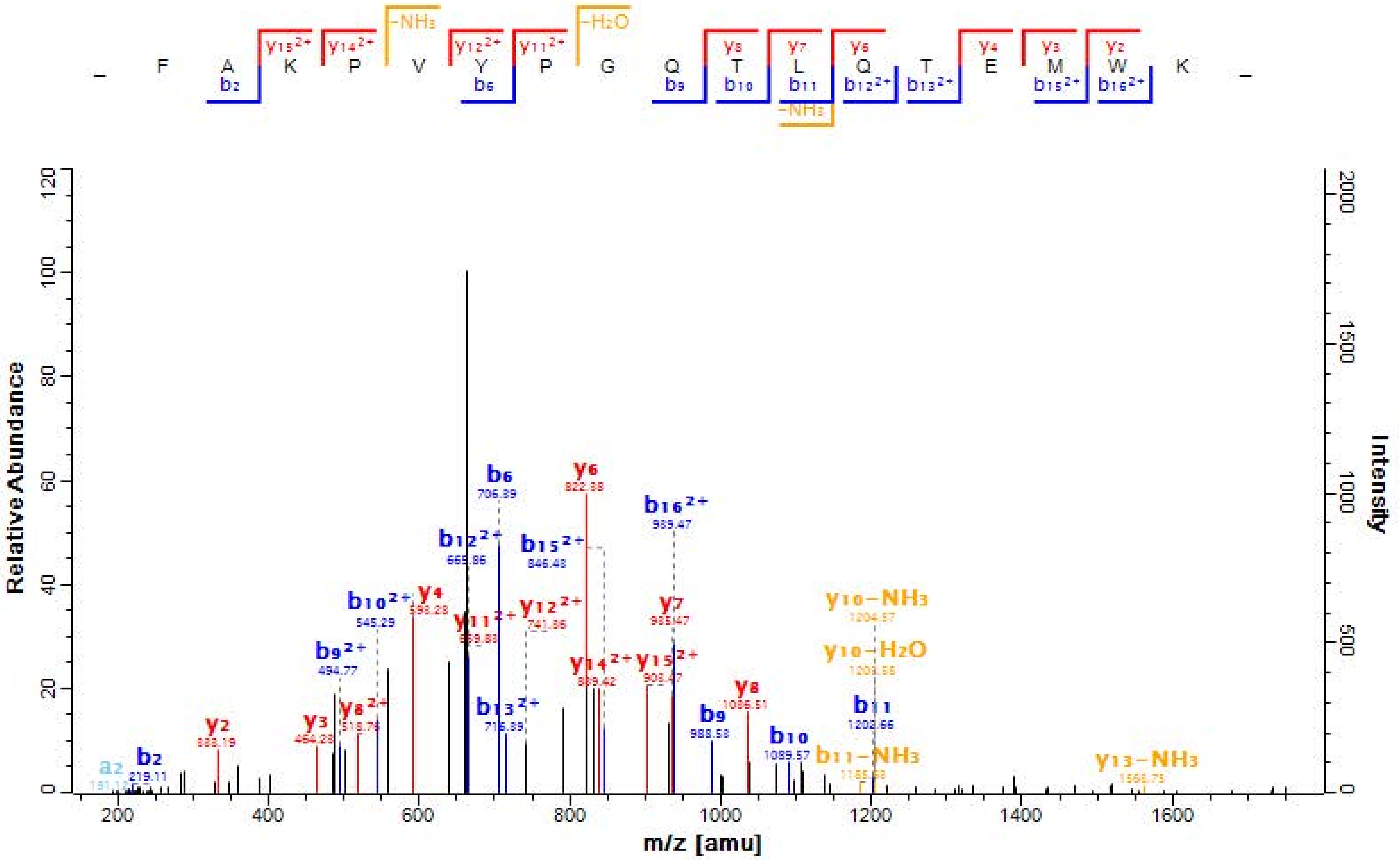
Mass:	1679.93597
m/z:	560.98593
Charge:	3+
Retentiontime:	38.237602233886
Score:	140.3079
Mass Error [ppm]:	0.044941
PEP:	3.1327E-07
Precursor Type:	ISO

general information

Annotation:	14 of 15
AminoAcids Coverag	93 %
Intensity Coverage:	76 %
Peak Coverage:	36 %
Protein Localisation:	164 ... 178

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	164.07		164.07	1	Y	14				
	320.17		320.17	2	R	13	1517.9		1517.9	
	419.24		419.24	3	V	12	1361.8		1361.8	
	516.29		516.29	4	P	11	1262.7		1262.7	
	631.32	+0.055	631.32	5	D	10	1165.7		1165.7	
	730.39	+0.0207	730.39	6	V	9	1050.6		525.82	+0.4693
+0.175	422.24	+0.0642	843.47	7	L	8	951.56		951.56	
+0.1633	471.77	-0.086	942.54	8	V	7	838.48	-0.003	419.74	-0.104
+0.1614	507.29	+0.0567	1013.6	9	A	6	739.41	+0.0249	370.21	+0.4836
	1128.6	-0.002	1128.6	10	D	5	668.37	+0.021	334.69	+0.1362
+0.0013	613.33		1225.7	11	P	4	553.35	+0.0327	553.35	
	1322.7		1322.7	12	P	3	456.29	+0.0444	456.29	
+0.3495	718.4		1435.8	13	I	2	359.24		359.24	
+0.356	753.92		1506.8	14	A	1	246.16	+0.0248	246.16	
				15	R	0	175.12	-0.003	175.12	

Scan number	6257	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	126.71



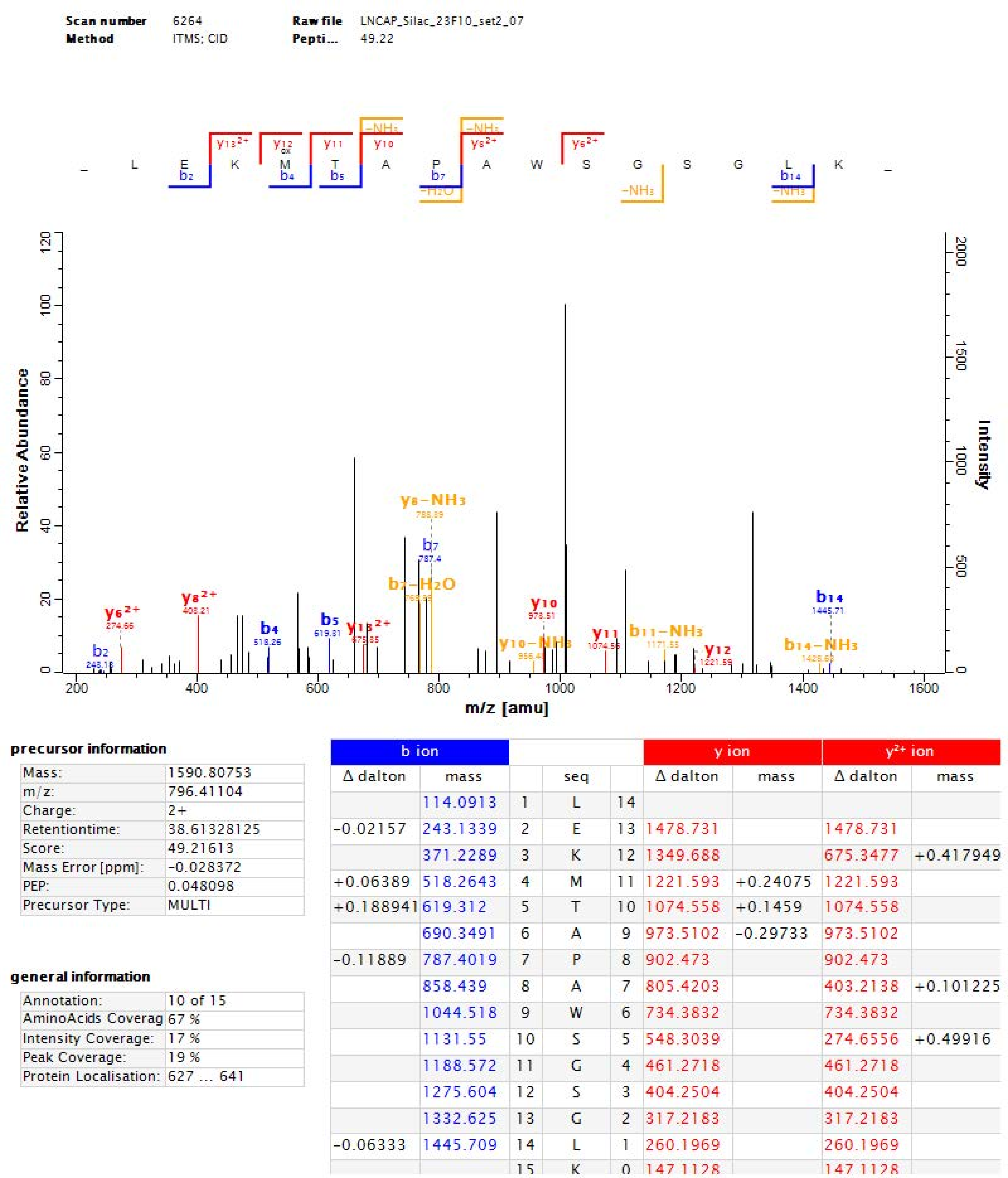
precursor information

Mass:	2023.0242
m/z:	675.34868
Charge:	3+
Retentiontime:	38.570861816406
Score:	126.7053
Mass Error [ppm]:	0.23901
PEP:	3.4121E-12
Precursor Type:	MULTI

general information

Annotation:	15 of 17
AminoAcids Coverag	88 %
Intensity Coverage:	50 %
Peak Coverage:	24 %
Protein Localisation:	563 ... 579

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.1		148.1		148.1	1	F	16				
+0.228	191.1		219.1	-0.03	219.1	2	A	15	1877		1877	
	319.2		347.2		347.2	3	K	14	1806		903.5	+0.23
	416.3		444.3		444.3	4	P	13	1678		839.4	+0.39
	515.3		543.3		543.3	5	V	12	1581		1581	
	678.4		706.4	+0.028	706.4	6	Y	11	1482		741.4	+0.14
	775.5		803.4		803.4	7	P	10	1319		659.8	+0.01
	832.5		860.5		860.5	8	G	9	1222		1222	
	960.5	+0.044	494.8	-0.01	988.5	9	Q	8	1165		1165	
	1062	+0.068	545.3	-0.02	1090	10	T	7	1037	-0.06	518.8	+0.15
	1175		1203	-0.22	1203	11	L	6	935.5	+0.032	935.5	
	1303	-0.24	665.9		1331	12	Q	5	822.4	-0.06	822.4	
	1404	+0.038	716.4		1432	13	T	4	694.3		694.3	
	1533		1561		1561	14	E	3	593.3	-0.08	593.3	
	1664	+0.18	846.4		1692	15	M	2	464.2	+0.062	464.2	
	1850	+0.173	939.5		1878	16	W	1	333.2	+0.194	333.2	
						17	K	0	147.1		147.1	



Scan number	6264	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	49.22

precursor information

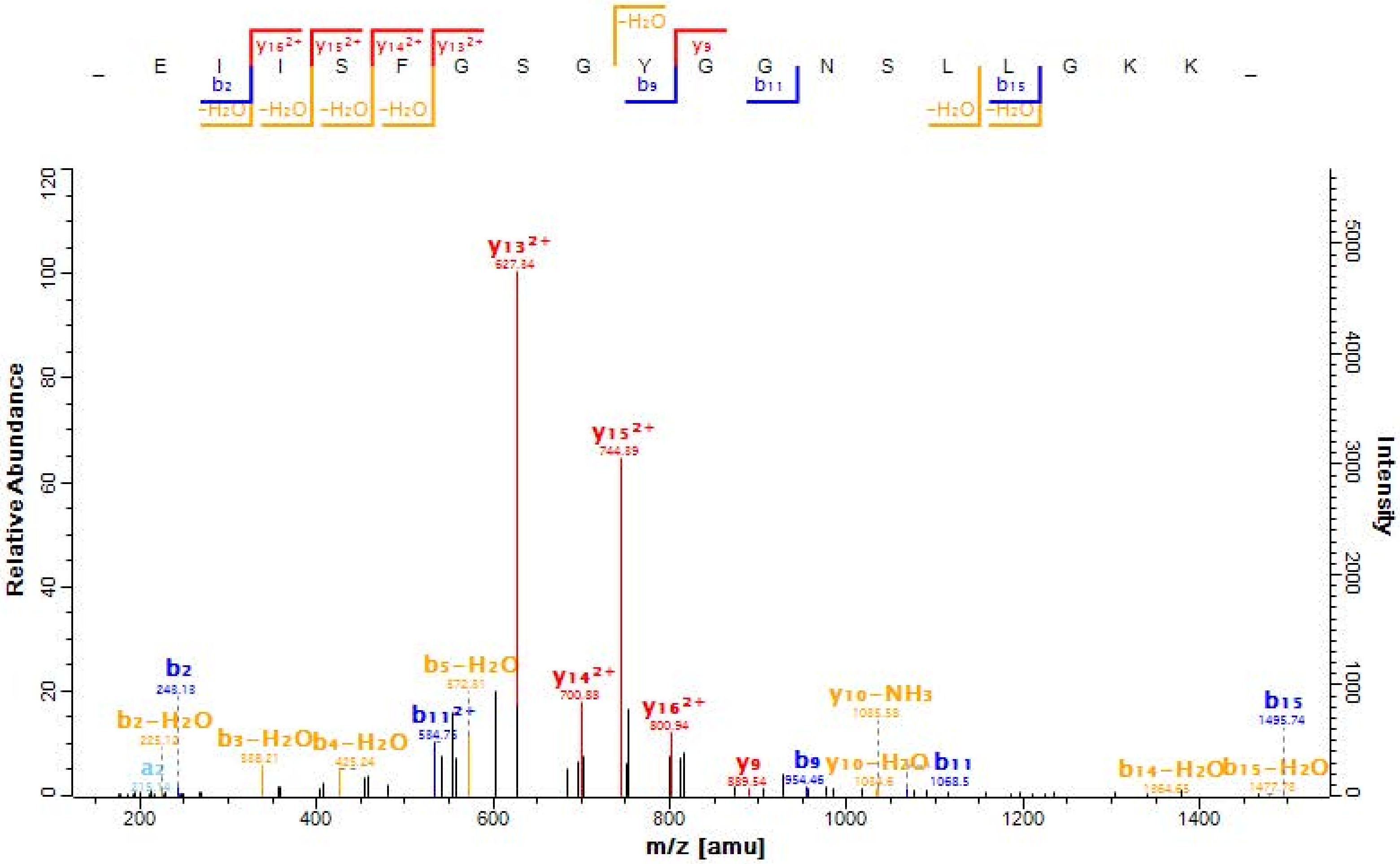
Mass:	1590.80753
m/z:	796.41104
Charge:	2+
Retentiontime:	38.61328125
Score:	49.21613
Mass Error [ppm]:	-0.028372
PEP:	0.048098
Precursor Type:	MULTI

general information

Annotation:	10 of 15
AminoAcids Coverag	67 %
Intensity Coverage:	17 %
Peak Coverage:	19 %
Protein Localisation:	627 ... 641

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	14				
-0.02157	243.1339	2	E	13	1478.731		1478.731	
	371.2289	3	K	12	1349.688		675.3477	+0.417949
+0.06389	518.2643	4	M	11	1221.593	+0.24075	1221.593	
+0.188941	619.312	5	T	10	1074.558	+0.1459	1074.558	
	690.3491	6	A	9	973.5102	-0.29733	973.5102	
-0.11889	787.4019	7	P	8	902.473		902.473	
	858.439	8	A	7	805.4203		403.2138	+0.101225
	1044.518	9	W	6	734.3832		734.3832	
	1131.55	10	S	5	548.3039		274.6556	+0.49916
	1188.572	11	G	4	461.2718		461.2718	
	1275.604	12	S	3	404.2504		404.2504	
	1332.625	13	G	2	317.2183		317.2183	
-0.06333	1445.709	14	L	1	260.1969		260.1969	
		15	K	0	147.1128		147.1128	

Scan number	6335	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	54.5



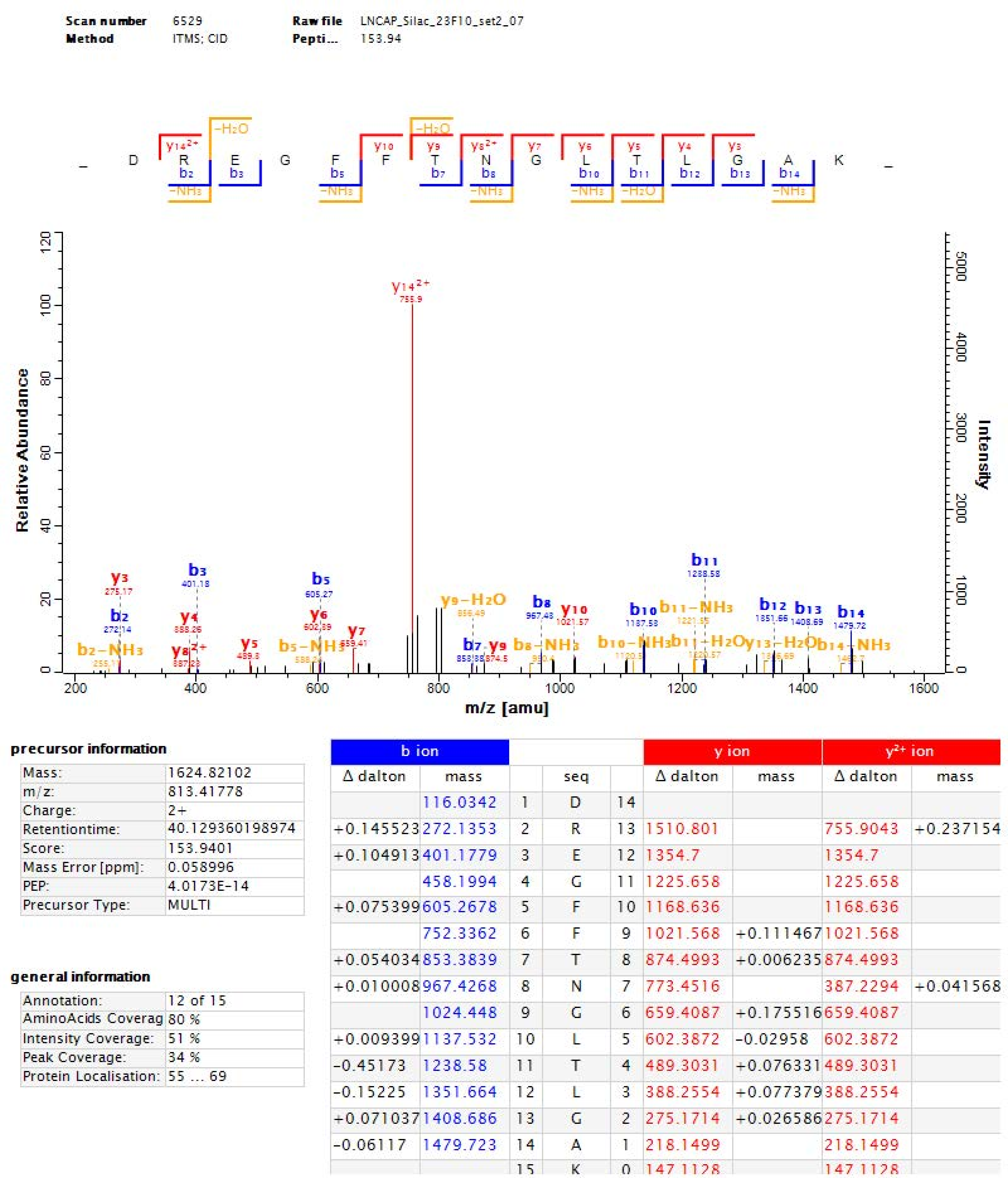
precursor information

Mass:	1825.95827
m/z:	609.66003
Charge:	3+
Retentiontime:	39.015834808349
Score:	54.50062
Mass Error [ppm]:	0.46492
PEP:	0.0016241
Precursor Type:	MULTI

general information

Annotation:	10 of 18
AminoAcids Coverag	56 %
Intensity Coverage:	56 %
Peak Coverage:	21 %
Protein Localisation:	245 ... 262

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.1		130		130	1	E	17				
-0.11	215.1		243.1	+0.078	243.1	2	I	16	1714		1714	
	328.2		356.2		356.2	3	I	15	1601		800.9	+0.11
	415.3		443.3		443.3	4	S	14	1488		744.4	+0.04
	562.3		590.3		590.3	5	F	13	1401		700.9	-0.05
	619.3		647.3		647.3	6	G	12	1254		627.3	-0.04
	706.4		734.4		734.4	7	S	11	1197		1197	
	763.4		791.4		791.4	8	G	10	1110		1110	
	926.5		954.5	-0.34	954.5	9	Y	9	1053		1053	
	983.5		1011		1011	10	G	8	889.5	+0	889.5	
	1041	-0.35	534.8	-0.08	1068	11	G	7	832.5		832.5	
	1155		1183		1183	12	N	6	775.5		775.5	
	1242		1270		1270	13	S	5	661.5		661.5	
	1355		1383		1383	14	L	4	574.4		574.4	
	1468		1496	+0.192	1496	15	L	3	461.3		461.3	
	1525		1553		1553	16	G	2	348.3		348.3	
	1661		1689		1689	17	K	1	291.2		291.2	
						18	K	0	155.1		155.1	



Scan number	6529	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	153.94

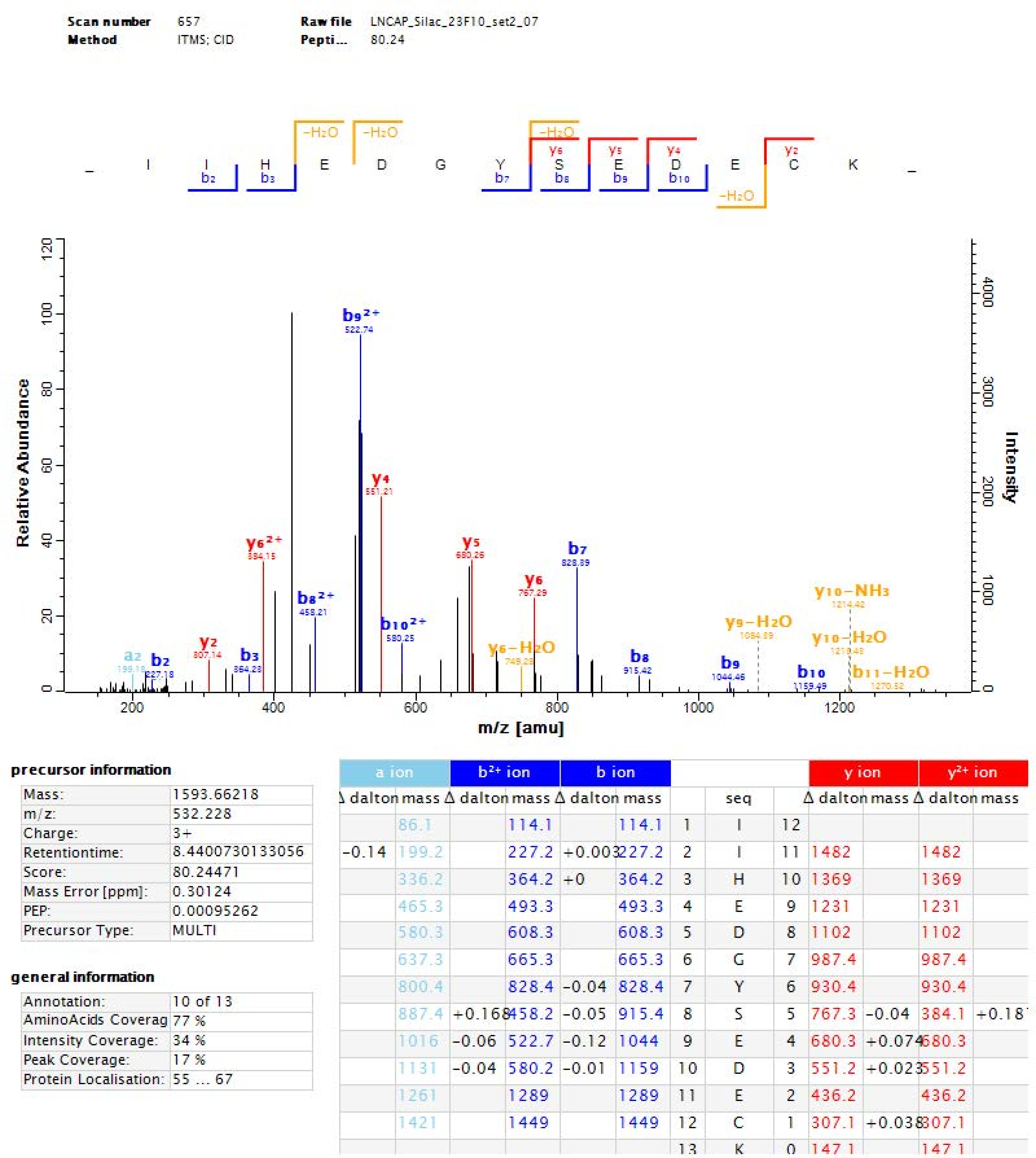
precursor information

Mass:	1624.82102
m/z:	813.41778
Charge:	2+
Retentiontime:	40.129360198974
Score:	153.9401
Mass Error [ppm]:	0.058996
PEP:	4.0173E-14
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	51 %
Peak Coverage:	34 %
Protein Localisation:	55 ... 69

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342	1	D	14				
+0.145523	272.1353	2	R	13	1510.801		755.9043	+0.237154
+0.104913	401.1779	3	E	12	1354.7		1354.7	
	458.1994	4	G	11	1225.658		1225.658	
+0.075399	605.2678	5	F	10	1168.636		1168.636	
	752.3362	6	F	9	1021.568	+0.111467	1021.568	
+0.054034	853.3839	7	T	8	874.4993	+0.006235	874.4993	
+0.010008	967.4268	8	N	7	773.4516		387.2294	+0.041568
	1024.448	9	G	6	659.4087	+0.175516	659.4087	
+0.009399	1137.532	10	L	5	602.3872	-0.02958	602.3872	
-0.45173	1238.58	11	T	4	489.3031	+0.076331	489.3031	
-0.15225	1351.664	12	L	3	388.2554	+0.077379	388.2554	
+0.071037	1408.686	13	G	2	275.1714	+0.026586	275.1714	
-0.06117	1479.723	14	A	1	218.1499		218.1499	
		15	K	0	147.1128		147.1128	



Scan number	657	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	80.24

precursor information

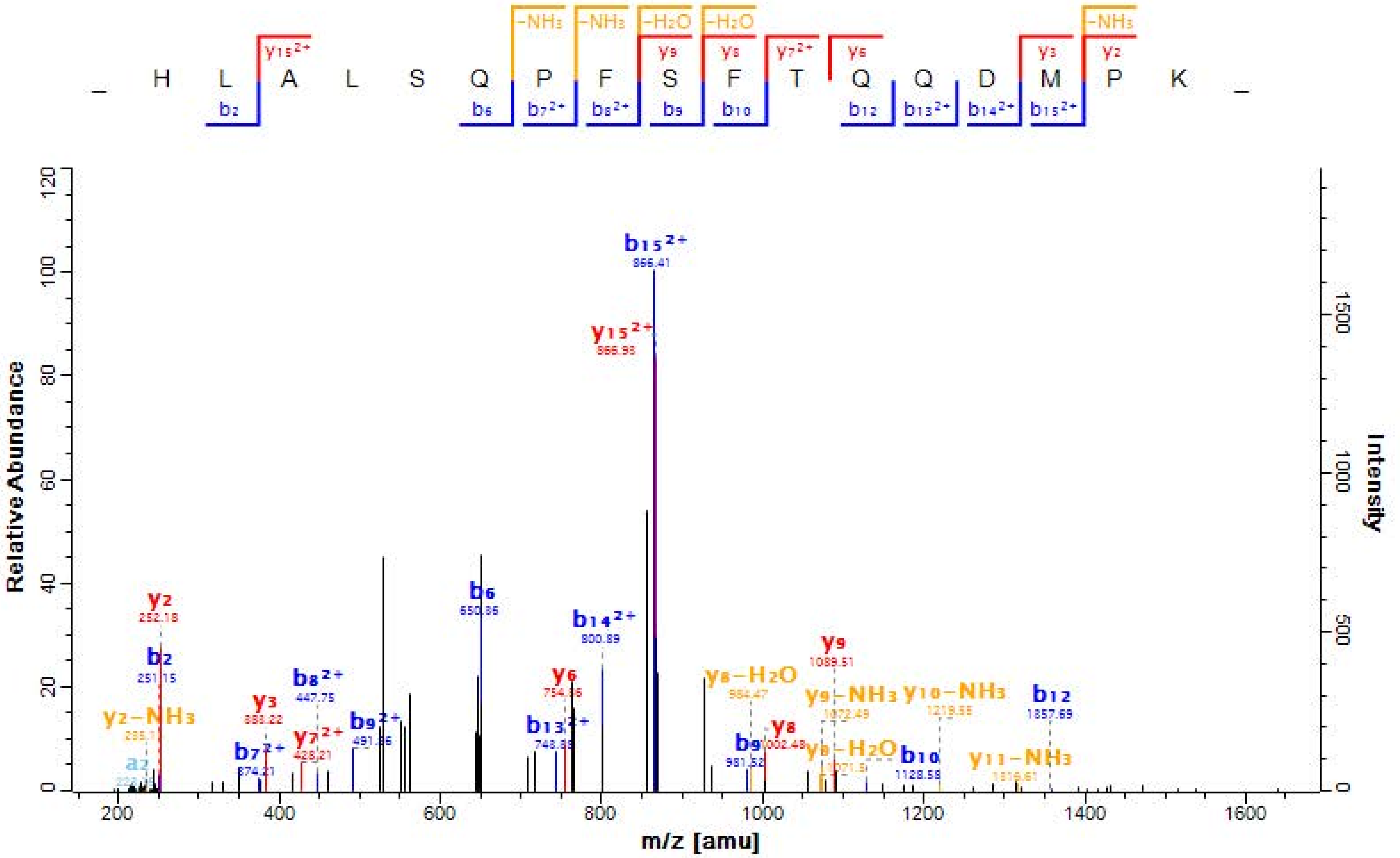
Mass:	1593.66218
m/z:	532.228
Charge:	3+
Retentiontime:	8.4400730133056
Score:	80.24471
Mass Error [ppm]:	0.30124
PEP:	0.00095262
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	34 %
Peak Coverage:	17 %
Protein Localisation:	55 … 67

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	I	12				
-0.14	199.2		227.2	+0.003	227.2	2	I	11	1482		1482	
	336.2		364.2	+0	364.2	3	H	10	1369		1369	
	465.3		493.3		493.3	4	E	9	1231		1231	
	580.3		608.3		608.3	5	D	8	1102		1102	
	637.3		665.3		665.3	6	G	7	987.4		987.4	
	800.4		828.4	-0.04	828.4	7	Y	6	930.4		930.4	
	887.4	+0.168	458.2	-0.05	915.4	8	S	5	767.3	-0.04	384.1	+0.18
	1016	-0.06	522.7	-0.12	1044	9	E	4	680.3	+0.074	680.3	
	1131	-0.04	580.2	-0.01	1159	10	D	3	551.2	+0.023	551.2	
	1261		1289		1289	11	E	2	436.2		436.2	
	1421		1449		1449	12	C	1	307.1	+0.038	307.1	
						13	K	0	147.1		147.1	

Scan number	6931	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	107.74



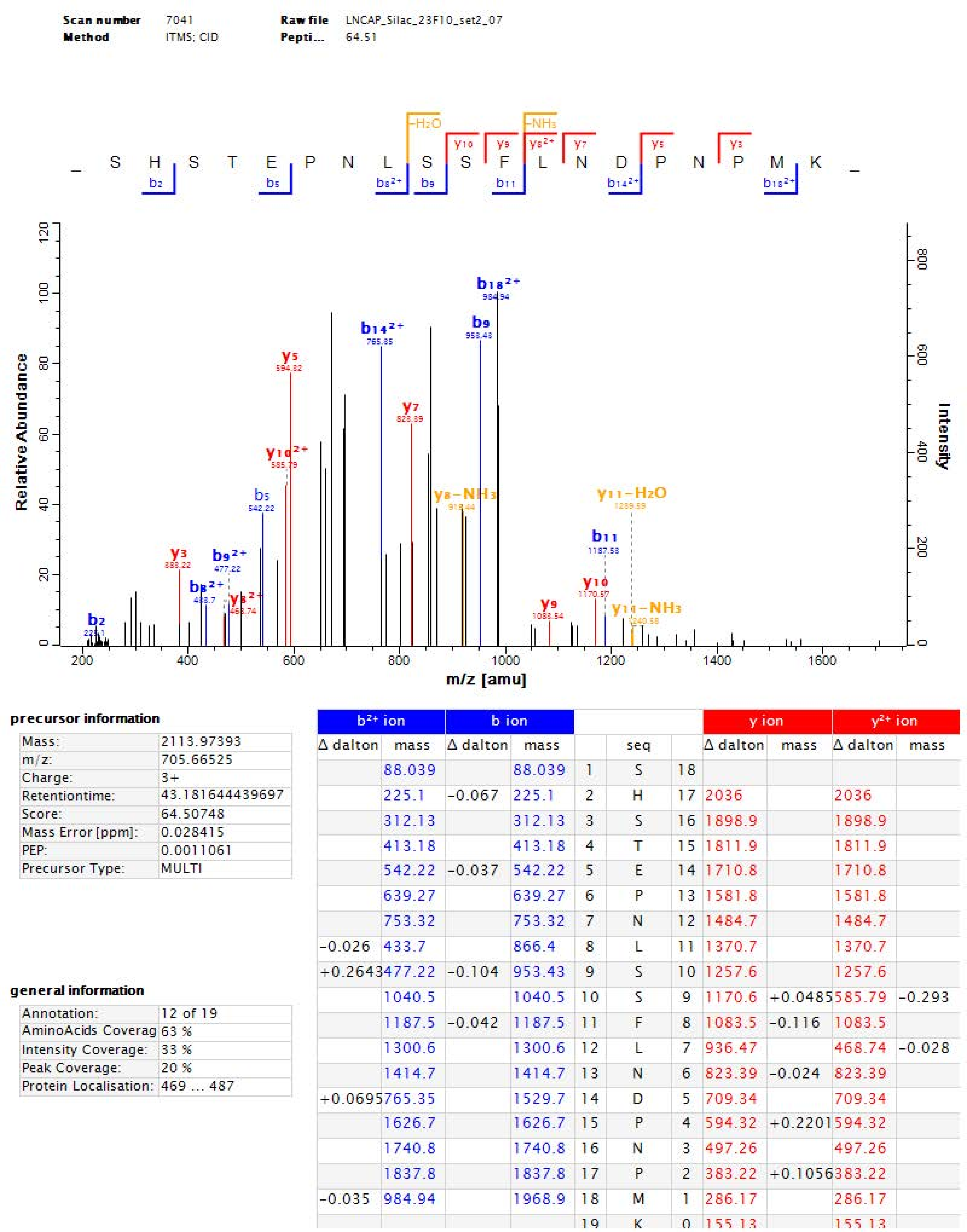
precursor information

Mass:	1973.96542
m/z:	658.99575
Charge:	3+
Retentiontime:	42.498817443847
Score:	107.7354
Mass Error [ppm]:	-0.76216
PEP:	2.1339E-08
Precursor Type:	MULTI

general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	41 %
Peak Coverage:	25 %
Protein Localisation:	542 ... 558

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	110.1		138.1		138.1	1	H	16				
+0.165	223.2		251.2	+0.052	251.2	2	L	15	1846		1846	
	294.2		322.2		322.2	3	A	14	1733		866.9	+0.08
	407.3		435.3		435.3	4	L	13	1662		1662	
	494.3		522.3		522.3	5	S	12	1549		1549	
	622.4		650.4	+0.079	650.4	6	Q	11	1462		1462	
	719.4	+0.311	374.2		747.4	7	P	10	1334		1334	
	866.5	+0.109	447.7		894.5	8	F	9	1237		1237	
	953.5	+0.166	491.3	-0.07	981.5	9	S	8	1090	-0.13	1090	
	1101		1129	+0.101	1129	10	F	7	1002	-0.02	1002	
	1202		1230		1230	11	T	6	855.4		428.2	+0.14
	1330		1358	+0.481	1358	12	Q	5	754.4	+0	754.4	
	1458	-0.07	743.4		1486	13	Q	4	626.3		626.3	
	1573	+0.234	800.9		1601	14	D	3	498.2		498.2	
	1704	-0.01	866.4		1732	15	M	2	383.2	+0.159	383.2	
	1801		1829		1829	16	P	1	252.2	+0.058	252.2	
						17	K	0	155.1		155.1	



Scan number	7041	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	64.51

precursor information

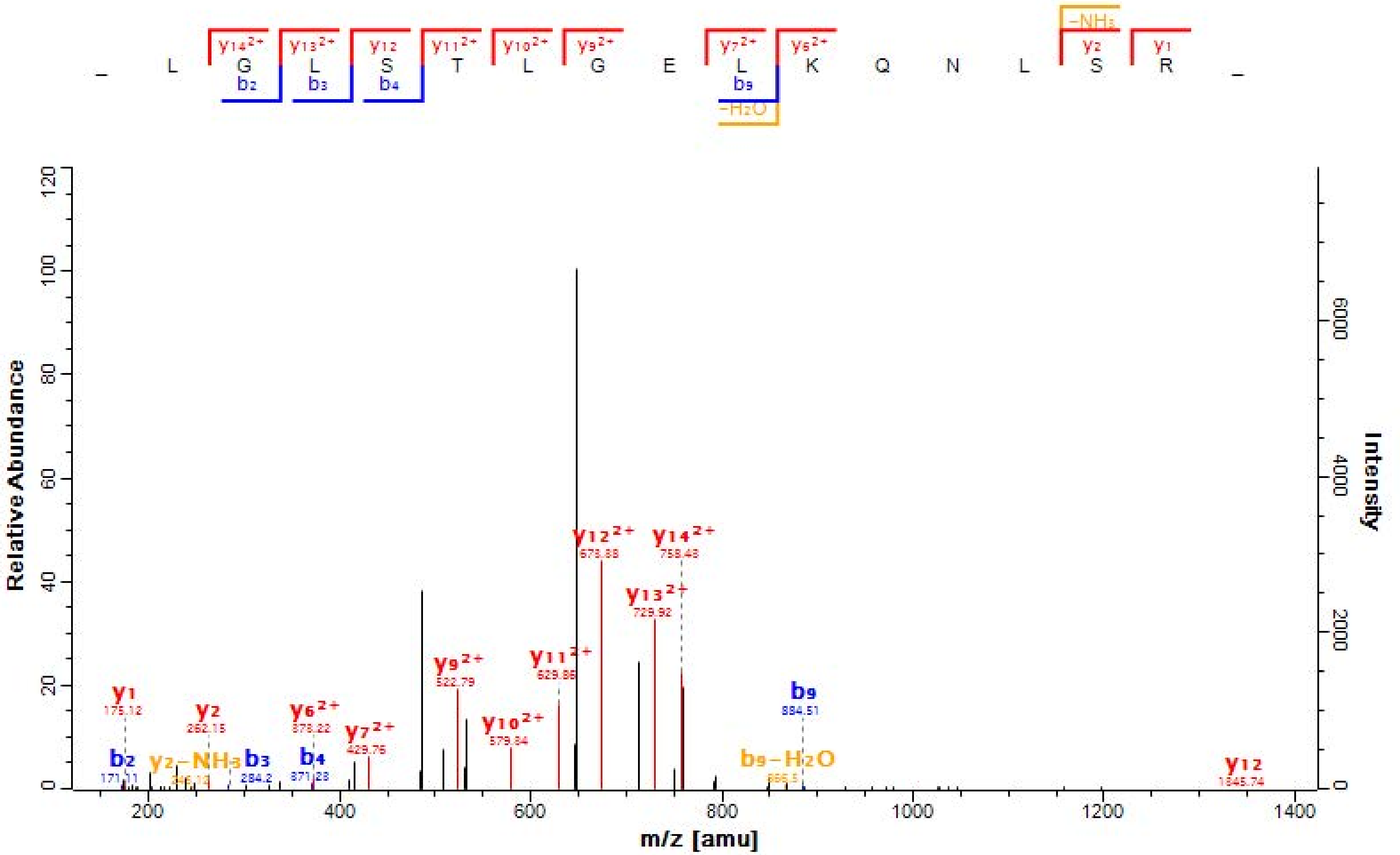
Mass:	2113.97393
m/z:	705.66525
Charge:	3+
Retentiontime:	43.181644439697
Score:	64.50748
Mass Error [ppm]:	0.028415
PEP:	0.0011061
Precursor Type:	MULTI

general information

Annotation:	12 of 19
AminoAcids Coverag	63 %
Intensity Coverage:	33 %
Peak Coverage:	20 %
Protein Localisation:	469 ... 487

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	18				
	225.1	−0.067	225.1	2	H	17	2036		2036	
	312.13		312.13	3	S	16	1898.9		1898.9	
	413.18		413.18	4	T	15	1811.9		1811.9	
	542.22	−0.037	542.22	5	E	14	1710.8		1710.8	
	639.27		639.27	6	P	13	1581.8		1581.8	
	753.32		753.32	7	N	12	1484.7		1484.7	
−0.026	433.7		866.4	8	L	11	1370.7		1370.7	
+0.2643	477.22	−0.104	953.43	9	S	10	1257.6		1257.6	
	1040.5		1040.5	10	S	9	1170.6	+0.0485	585.79	−0.293
	1187.5	−0.042	1187.5	11	F	8	1083.5	−0.116	1083.5	
	1300.6		1300.6	12	L	7	936.47		468.74	−0.028
	1414.7		1414.7	13	N	6	823.39	−0.024	823.39	
+0.0695	765.35		1529.7	14	D	5	709.34		709.34	
	1626.7		1626.7	15	P	4	594.32	+0.2201	594.32	
	1740.8		1740.8	16	N	3	497.26		497.26	
	1837.8		1837.8	17	P	2	383.22	+0.1056	383.22	
−0.035	984.94		1968.9	18	M	1	286.17		286.17	
				19	K	0	155.13		155.13	

Scan number	7087	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	73.08



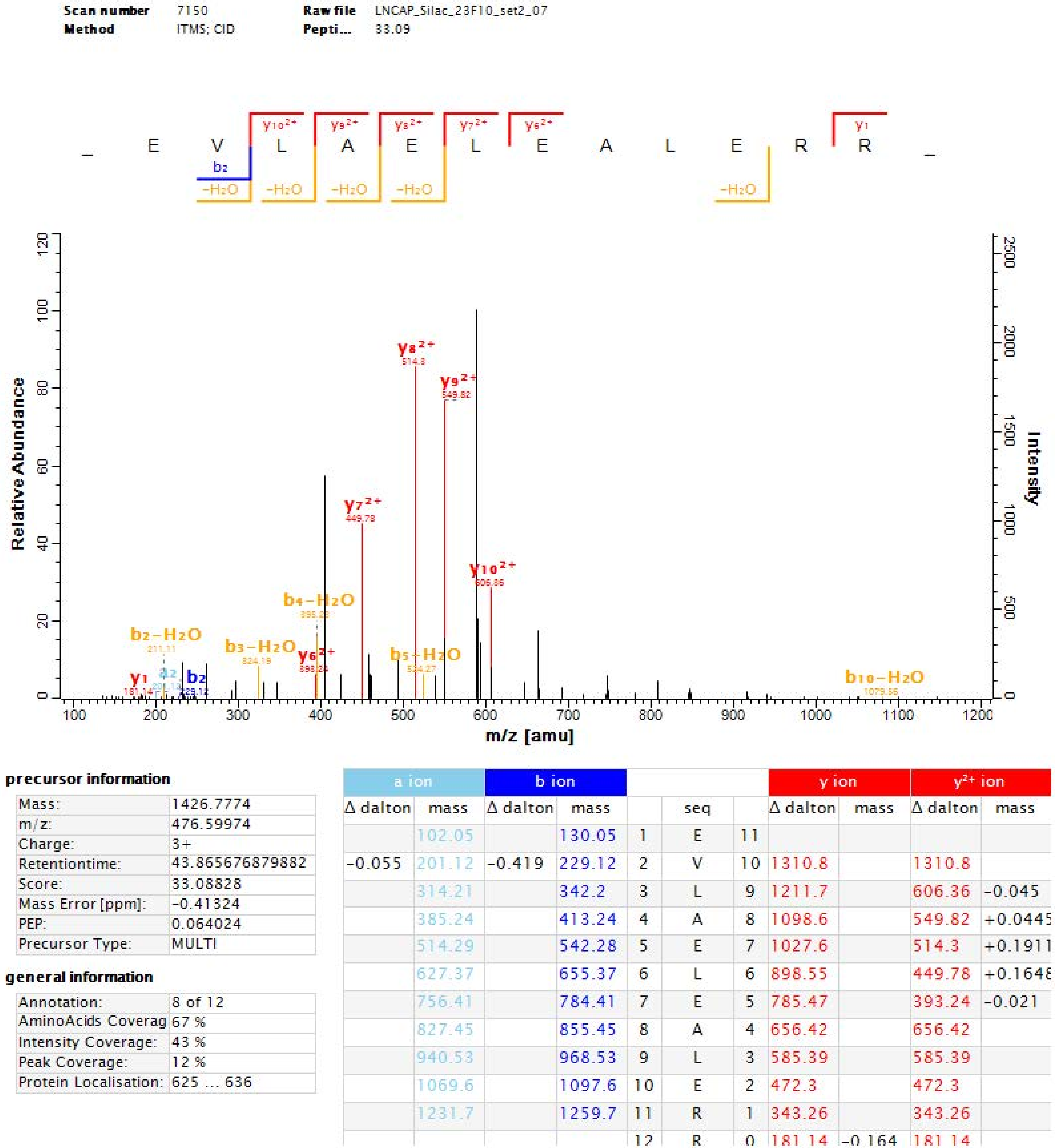
precursor information

Mass:	1627.92543
m/z:	543.64909
Charge:	3+
Retentiontime:	43.477947235107
Score:	73.082
Mass Error [ppm]:	-0.17948
PEP:	0.00076112
Precursor Type:	MULTI

general information

Annotation:	10 of 15
AminoAcids Coverag	67 %
Intensity Coverage:	32 %
Peak Coverage:	20 %
Protein Localisation:	81 ... 95

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	14				
+0.061543	171.1128	2	G	13	1515.849		758.4281	+0.015072
-0.12405	284.1969	3	L	12	1458.827		729.9174	+0.307603
+0.062241	371.2289	4	S	11	1345.743	+0.465458	673.3753	+0.284389
	472.2766	5	T	10	1258.711		629.8593	+0.127795
	585.3606	6	L	9	1157.664		579.3355	+0.279198
	642.3821	7	G	8	1044.58		522.7935	+0.197329
	771.4247	8	E	7	987.5582		987.5582	
+0.260588	884.5088	9	L	6	858.5156		429.7614	+0.313158
	1012.604	10	K	5	745.4315		373.2194	-0.02811
	1140.662	11	Q	4	617.3365		617.3365	
	1254.705	12	N	3	489.278		489.278	
	1367.789	13	L	2	375.235		375.235	
	1454.821	14	S	1	262.151	+0.033101	262.151	
		15	R	0	175.119	-0.10255	175.119	



Scan number	7150	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	33.09

precursor information

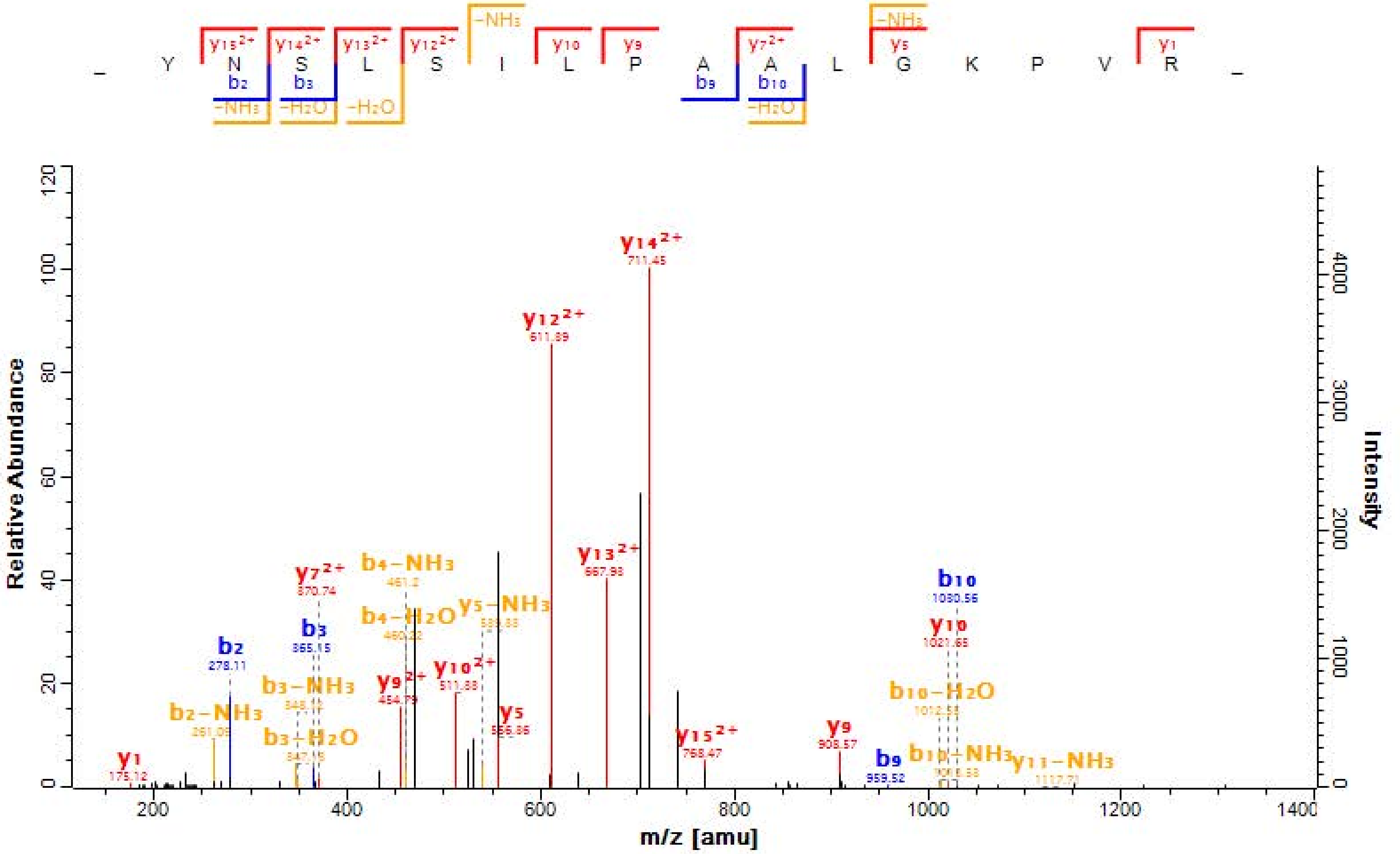
Mass:	1426.7774
m/z:	476.59974
Charge:	3+
Retentiontime:	43.865676879882
Score:	33.08828
Mass Error [ppm]:	-0.41324
PEP:	0.064024
Precursor Type:	MULTI

general information

Annotation:	8 of 12
AminoAcids Coverag	67 %
Intensity Coverage:	43 %
Peak Coverage:	12 %
Protein Localisation:	625 ... 636

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	11				
-0.055	201.12	-0.419	229.12	2	V	10	1310.8		1310.8	
	314.21		342.2	3	L	9	1211.7		606.36	-0.045
	385.24		413.24	4	A	8	1098.6		549.82	+0.0445
	514.29		542.28	5	E	7	1027.6		514.3	+0.1911
	627.37		655.37	6	L	6	898.55		449.78	+0.1648
	756.41		784.41	7	E	5	785.47		393.24	-0.021
	827.45		855.45	8	A	4	656.42		656.42	
	940.53		968.53	9	L	3	585.39		585.39	
	1069.6		1097.6	10	E	2	472.3		472.3	
	1231.7		1259.7	11	R	1	343.26		343.26	
				12	R	0	181.14	-0.164	181.14	

Scan number 7174 **Raw file** LNCAP_Silac_23F10_set2_07
Method ITMS; CID **Pepti...** 110.92



precursor information

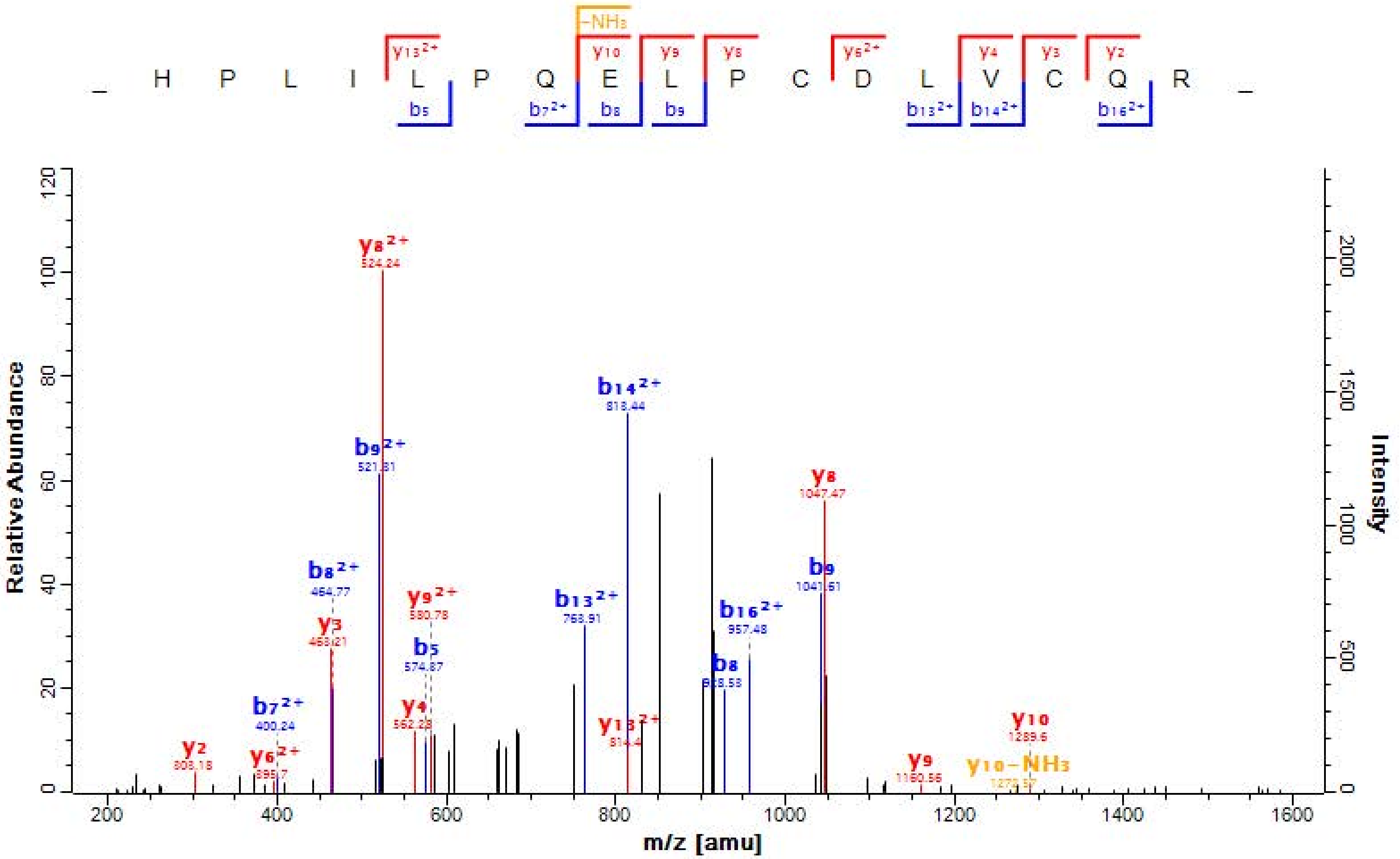
Mass:	1697.98273
m/z:	567.00152
Charge:	3+
Retentiontime:	44.008666992187
Score:	110.9227
Mass Error [ppm]:	-0.06524
PEP:	3.8208E-07
Precursor Type:	MULTI

general information

Annotation:	11 of 16
AminoAcids Coverag	69 %
Intensity Coverage:	59 %
Peak Coverage:	25 %
Protein Localisation:	138 ... 153

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	164.0706	1	Y	15				
-0.01014	278.1135	2	N	14	1535.927		768.467	-0.07818
+0.013314	365.1456	3	S	13	1421.884		711.4456	+0.236011
	478.2296	4	L	12	1334.852		667.9296	+0.238536
	565.2617	5	S	11	1221.768		611.3875	+0.194692
	678.3457	6	I	10	1134.736		1134.736	
	791.4298	7	L	9	1021.652	-0.12049	511.3295	+0.292411
	888.4825	8	P	8	908.5676	+0.090286	454.7874	-0.00174
-0.22602	959.5197	9	A	7	811.5148		811.5148	
-0.0951	1030.557	10	A	6	740.4777		370.7425	-0.03908
	1143.641	11	L	5	669.4406		669.4406	
	1200.662	12	G	4	556.3566	+0.196117	556.3566	
	1328.757	13	K	3	499.3351		499.3351	
	1425.81	14	P	2	371.2401		371.2401	
	1524.878	15	V	1	274.1874		274.1874	
		16	R	0	175.119	-0.00225	175.119	

Scan number	7306	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	88.71



precursor information

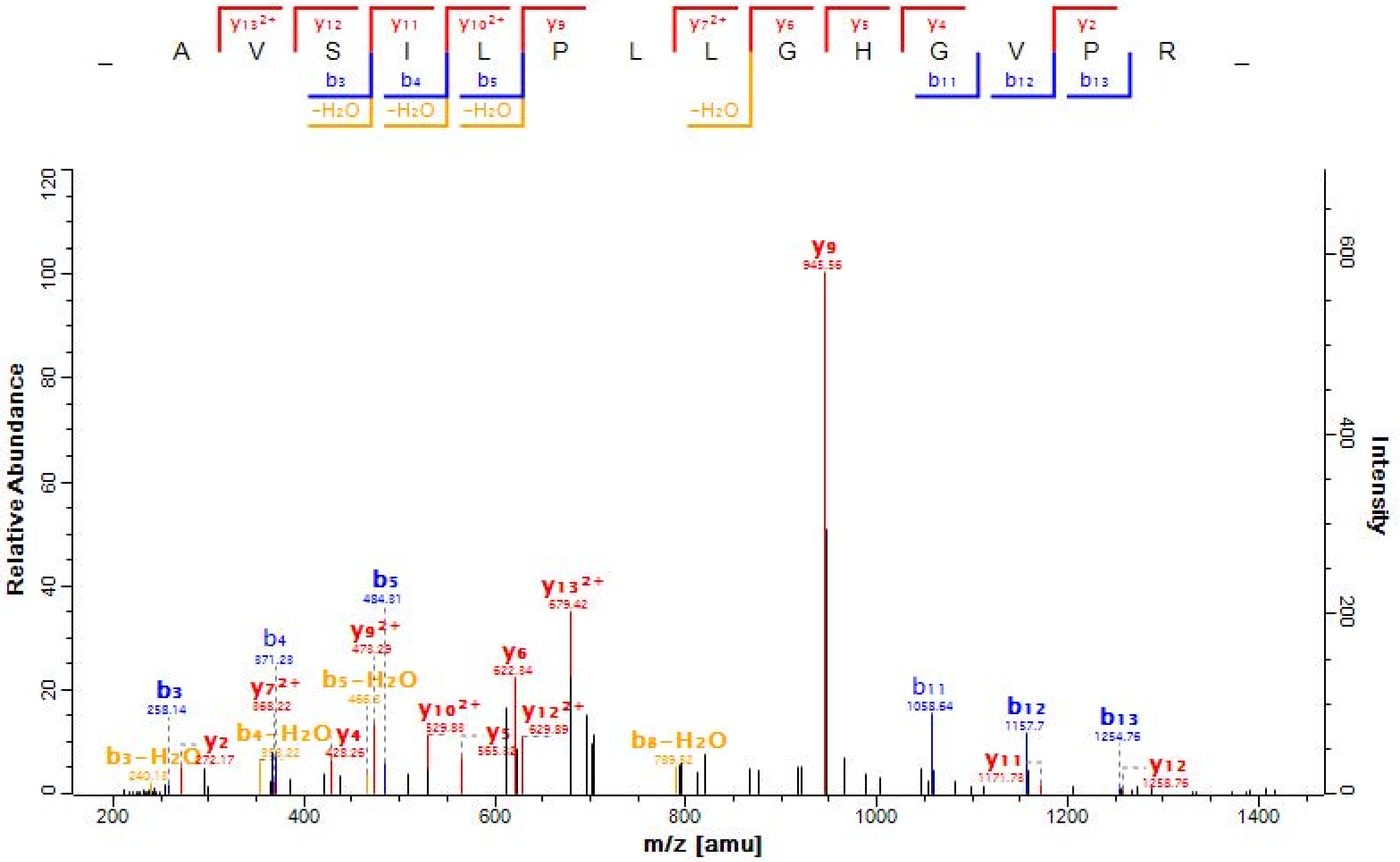
Mass:	2087.06502
m/z:	696.69561
Charge:	3+
Retentiontime:	44.817176818847
Score:	88.70626
Mass Error [ppm]:	-0.28044
PEP:	1.1123E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 17
AminoAcids Coverag	59 %
Intensity Coverage:	51 %
Peak Coverage:	22 %
Protein Localisation:	391 ... 407

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.07		138.07	1	H	16				
	235.12		235.12	2	P	15	1951		1951	
	348.2		348.2	3	L	14	1854		1854	
	461.29		461.29	4	I	13	1740.9		1740.9	
	574.37	-0.04	574.37	5	L	12	1627.8		814.4	+0.2715
	671.42		671.42	6	P	11	1514.7		1514.7	
+0.1604	400.24		799.48	7	Q	10	1417.7		1417.7	
+0.0182	464.77	+0.0049	928.53	8	E	9	1289.6	-0.397	1289.6	
+0.1124	521.31	-0.127	1041.6	9	L	8	1160.6	-0.073	580.78	+0.139
	1138.7		1138.7	10	P	7	1047.5	+0.0007	524.24	+0.222
	1298.7		1298.7	11	C	6	950.42		950.42	
	1413.7		1413.7	12	D	5	790.39		395.7	-0.133
+0.1275	763.91		1526.8	13	L	4	675.36		675.36	
+0.2089	813.44		1625.9	14	V	3	562.28	+0.122	562.28	
	1785.9		1785.9	15	C	2	463.21	+0.1815	463.21	
+0.2508	957.48		1914	16	Q	1	303.18	+0.0708	303.18	
				17	R	0	175.12		175.12	

Scan number	7826	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	115.57



precursor information

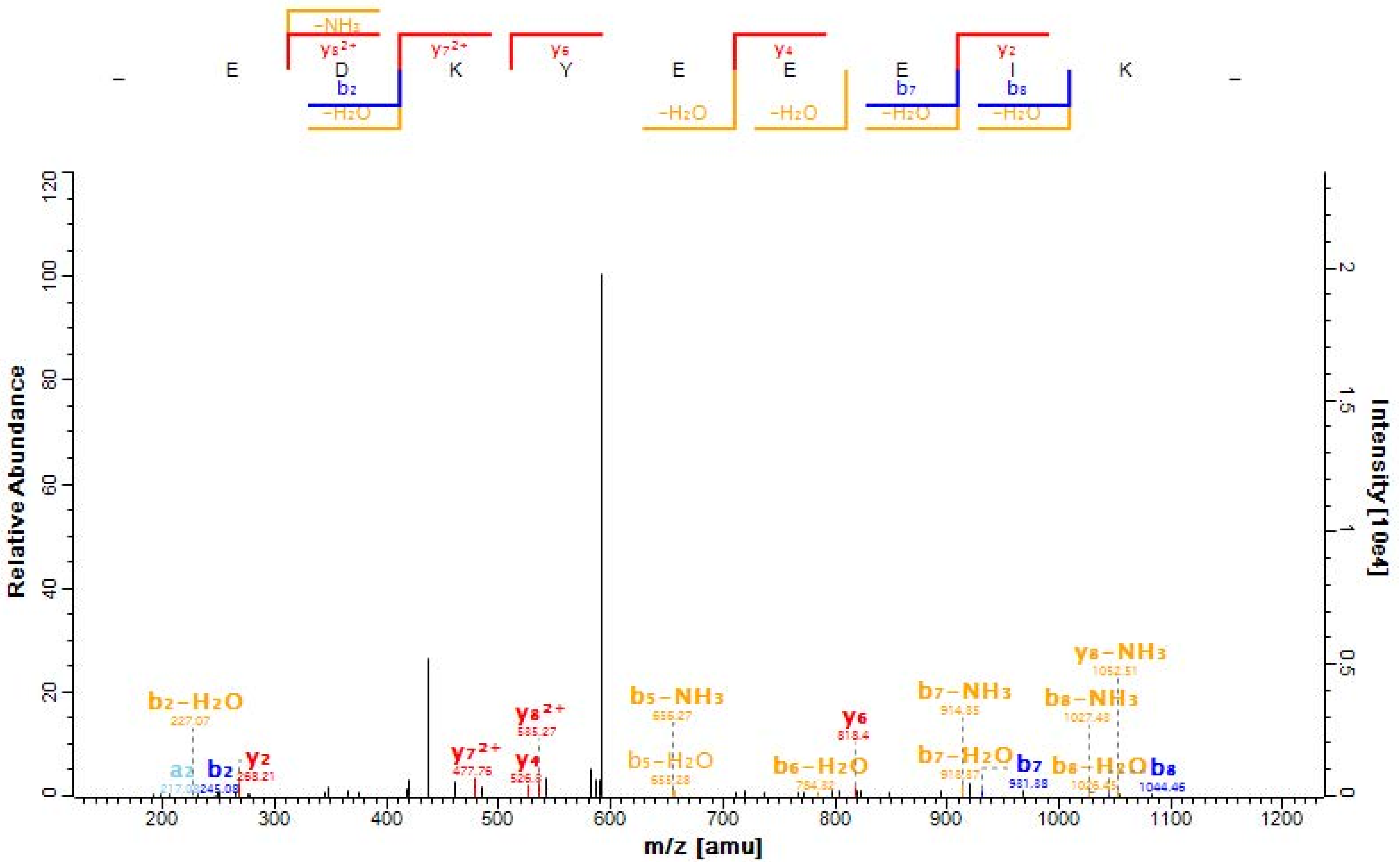
Mass:	1427.86208
m/z:	714.93832
Charge:	2+
Retentiontime:	48.214912414550
Score:	115.5744
Mass Error [ppm]:	0.56676
PEP:	0.00019376
Precursor Type:	ISO

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	49 %
Peak Coverage:	22 %
Protein Localisation:	179 ... 192

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	13				
	171.1128	2	V	12	1357.831		679.4194	-0.16429
-0.00463	258.1448	3	S	11	1258.763	-0.123	629.8851	-0.10536
+0.002793	371.2289	4	I	10	1171.731	+0.102385	1171.731	
-0.00986	484.313	5	L	9	1058.647		529.8271	+0.034166
	581.3657	6	P	8	945.5629	+0.012761	473.2851	+0.265163
	694.4498	7	L	7	848.5101		848.5101	
	807.5339	8	L	6	735.426		368.2167	+0.022969
	864.5553	9	G	5	622.342	+0.06129	622.342	
	1001.614	10	H	4	565.3205	+0.079092	565.3205	
-0.03779	1058.636	11	G	3	428.2616	+0.113528	428.2616	
-0.04871	1157.704	12	V	2	371.2401		371.2401	
-0.00431	1254.757	13	P	1	272.1717	+0.042395	272.1717	
		14	R	0	175.119		175.119	

Scan number	795	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	73.23

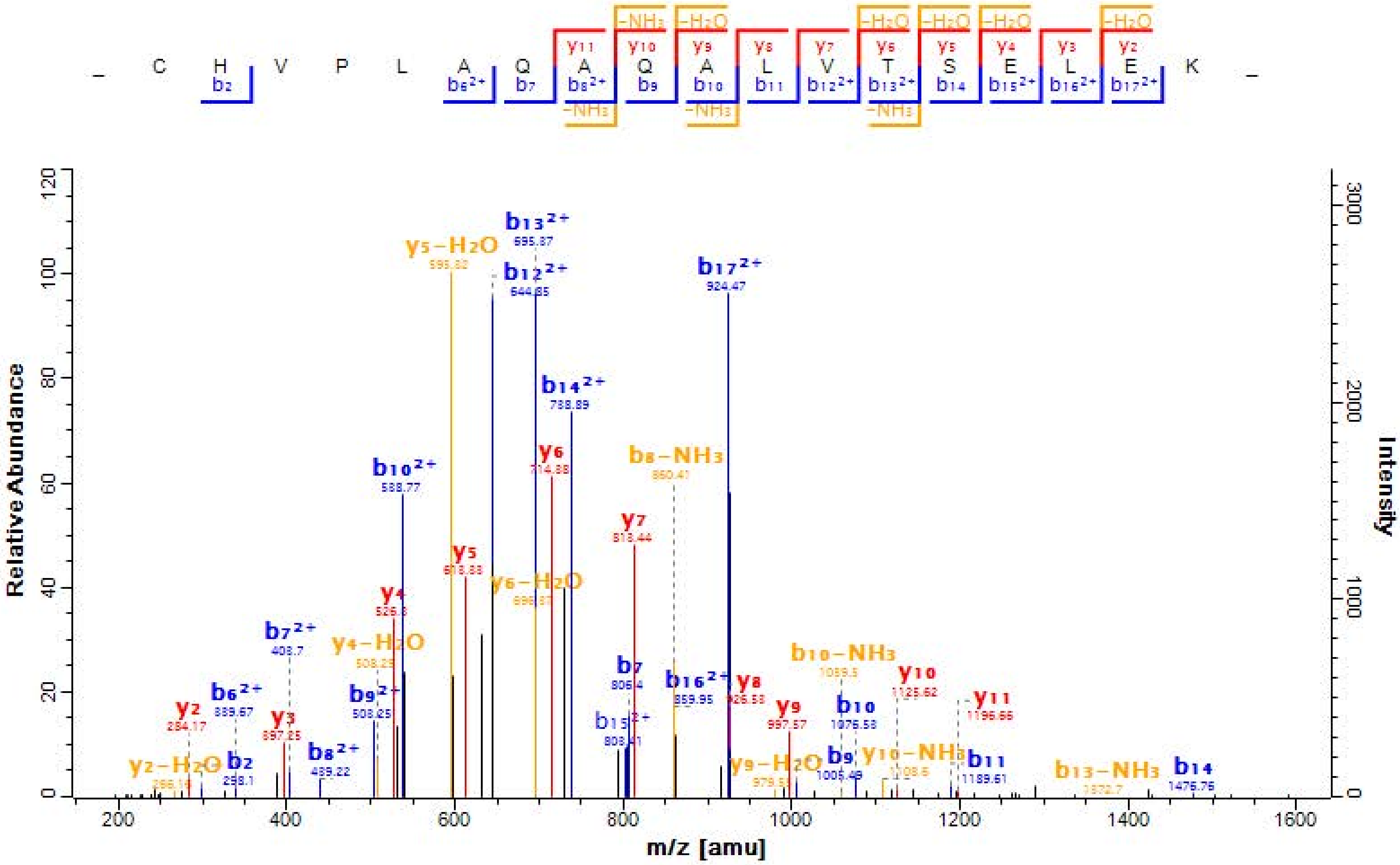


precursor information

Mass:	1181.54534
m/z:	591.77995
Charge:	2+
Retentiontime:	9.1939296722412
Score:	73.23321
Mass Error [ppm]:	0.11577
PEP:	0.010744
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	12 %
Peak Coverage:	18 %
Protein Localisation:	182 ... 190

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	8				
+0.0951	217.08	+0.2286	245.08	2	D	7	1069.5		535.27	−0.009
	353.19		381.19	3	K	6	954.51		477.76	+0.348
	516.25		544.25	4	Y	5	818.4	+0.0332	818.4	
	645.3		673.29	5	E	4	655.34		655.34	
	774.34		802.33	6	E	3	526.3	+0.0285	526.3	
	903.38	−0.184	931.38	7	E	2	397.25		397.25	
	1016.5	+0.1421	1044.5	8	I	1	268.21	+0.0069	268.21	
				9	K	0	155.13		155.13	

Scan number	7954	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	212.7



precursor information

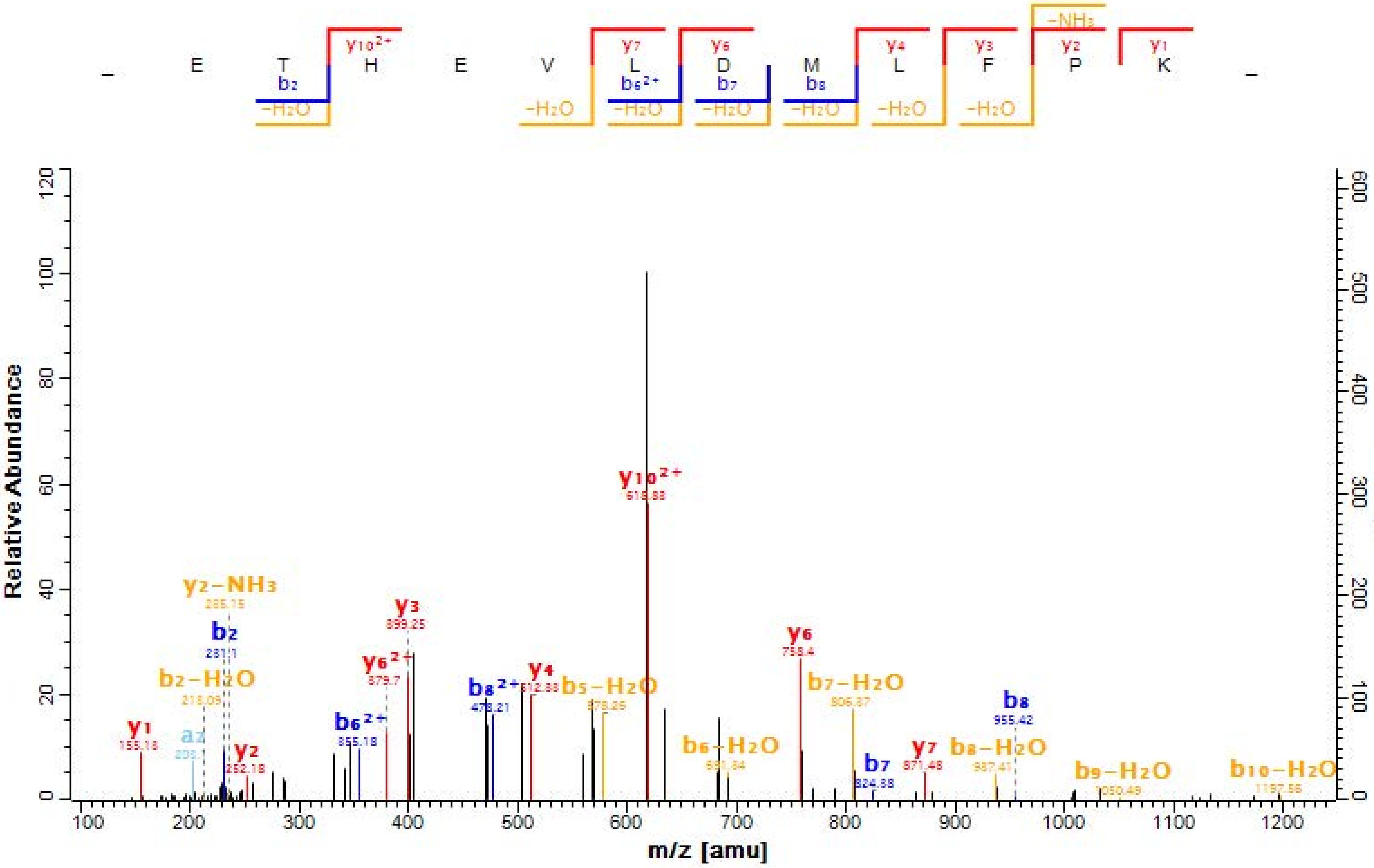
Mass:	1993.02971
m/z:	665.35051
Charge:	3+
Retentiontime:	49.154876708984
Score:	212.7039
Mass Error [ppm]:	-0.27652
PEP:	3.8098E-41
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	75 %
Peak Coverage:	40 %
Protein Localisation:	164 ... 181

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	161.0379		161.0379	1	C	17		
	298.0968	+0.035488	298.0968	2	H	16	1842.021	
	397.1653		397.1653	3	V	15	1704.962	
	494.218		494.218	4	P	14	1605.894	
	607.3021		607.3021	5	L	13	1508.841	
+0.14244	339.6732		678.3392	6	A	12	1395.757	
+0.246635	403.7025	-0.10273	806.3978	7	Q	11	1324.72	
-0.01173	439.2211		877.4349	8	A	10	1196.661	+0.250134
+0.243528	503.2504	+0.027962	1005.493	9	Q	9	1125.624	+0.127091
+0.034968	538.7689	+0.027775	1076.531	10	A	8	997.5656	+0.023865
	1189.615	+0.19835	1189.615	11	L	7	926.5284	+0.261784
+0.072682	644.8452		1288.683	12	V	6	813.4444	+0.029869
+0.2444	695.369		1389.731	13	T	5	714.376	+0.025285
+0.257865	738.885	-0.32343	1476.763	14	S	4	613.3283	+0.068325
-0.07843	803.4063		1605.805	15	E	3	526.2963	+0.203869
-0.10924	859.9483		1718.889	16	L	2	397.2537	+0.062258
+0.182884	924.4696		1847.932	17	E	1	284.1696	+0.00234
				18	K	0	155.127	

Scan number	8038	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	86.01



precursor information

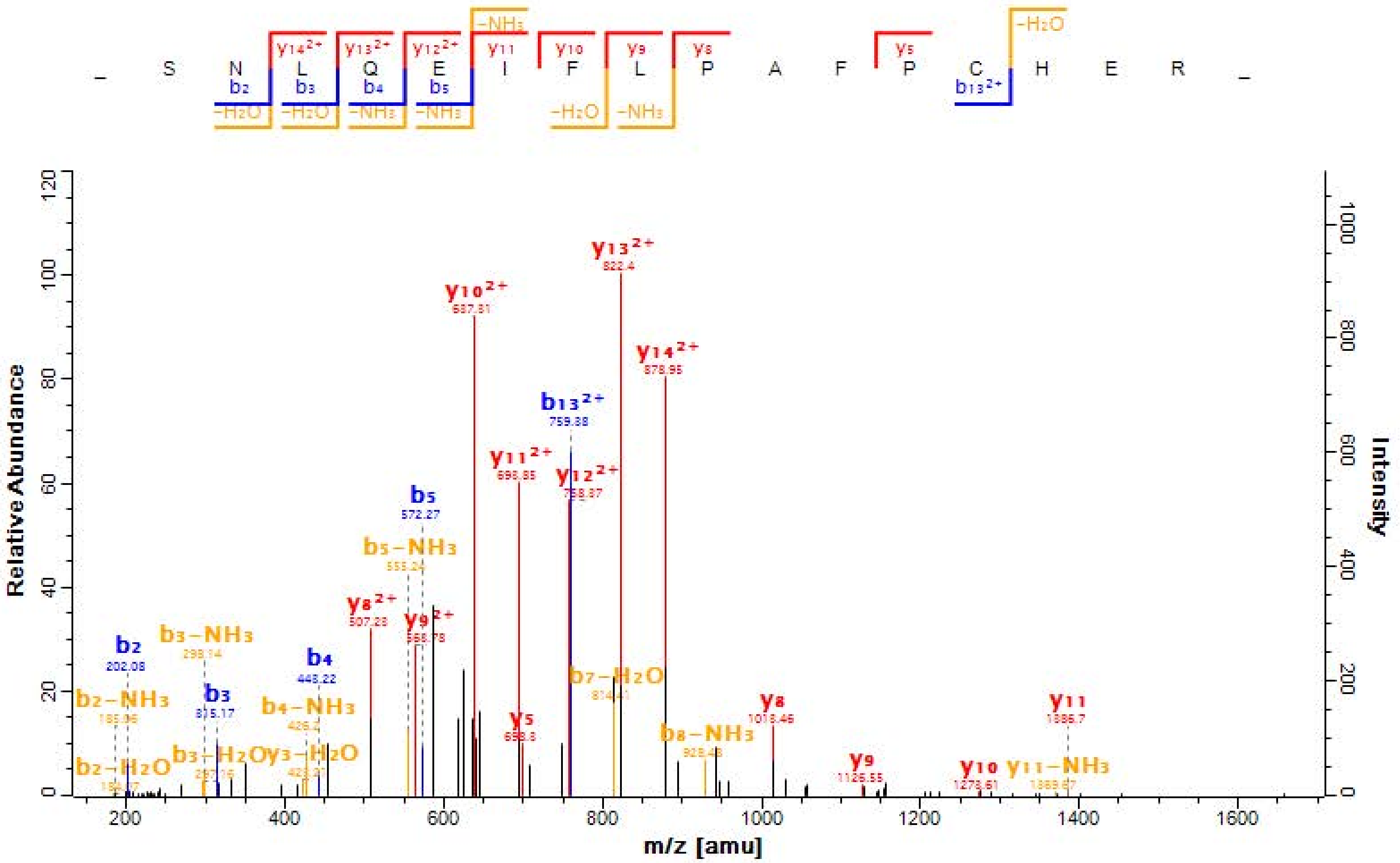
Mass:	1457.7216
m/z:	486.91448
Charge:	3+
Retentiontime:	49.722396850585
Score:	86.01421
Mass Error [ppm]:	-0.58173
PEP:	0.0013034
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	33 %
Peak Coverage:	22 %
Protein Localisation:	422 ... 433

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.1		130		130	1	E	11				
-0.04	203.1		231.1	+0.074	231.1	2	T	10	1338		1338	
	340.2		368.2		368.2	3	H	9	1237		618.8	+0.24
	469.2		497.2		497.2	4	E	8	1100		1100	
	568.3		596.3		596.3	5	V	7	970.6		970.6	
	681.4	-0.1	355.2		709.4	6	L	6	871.5	+0.11	871.5	
	796.4		824.4	-0.25	824.4	7	D	5	758.4	+0.03	379.7	+0.13
	927.4	-0.49	478.2	+0.2	955.4	8	M	4	643.4		643.4	
	1041		1069		1069	9	L	3	512.3	-0.02	512.3	
	1188		1216		1216	10	F	2	399.2	-0.08	399.2	
	1285		1313		1313	11	P	1	252.2	-0.03	252.2	
						12	K	0	155.1	-0.03	155.1	

Scan number	8396	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	130.24



precursor information

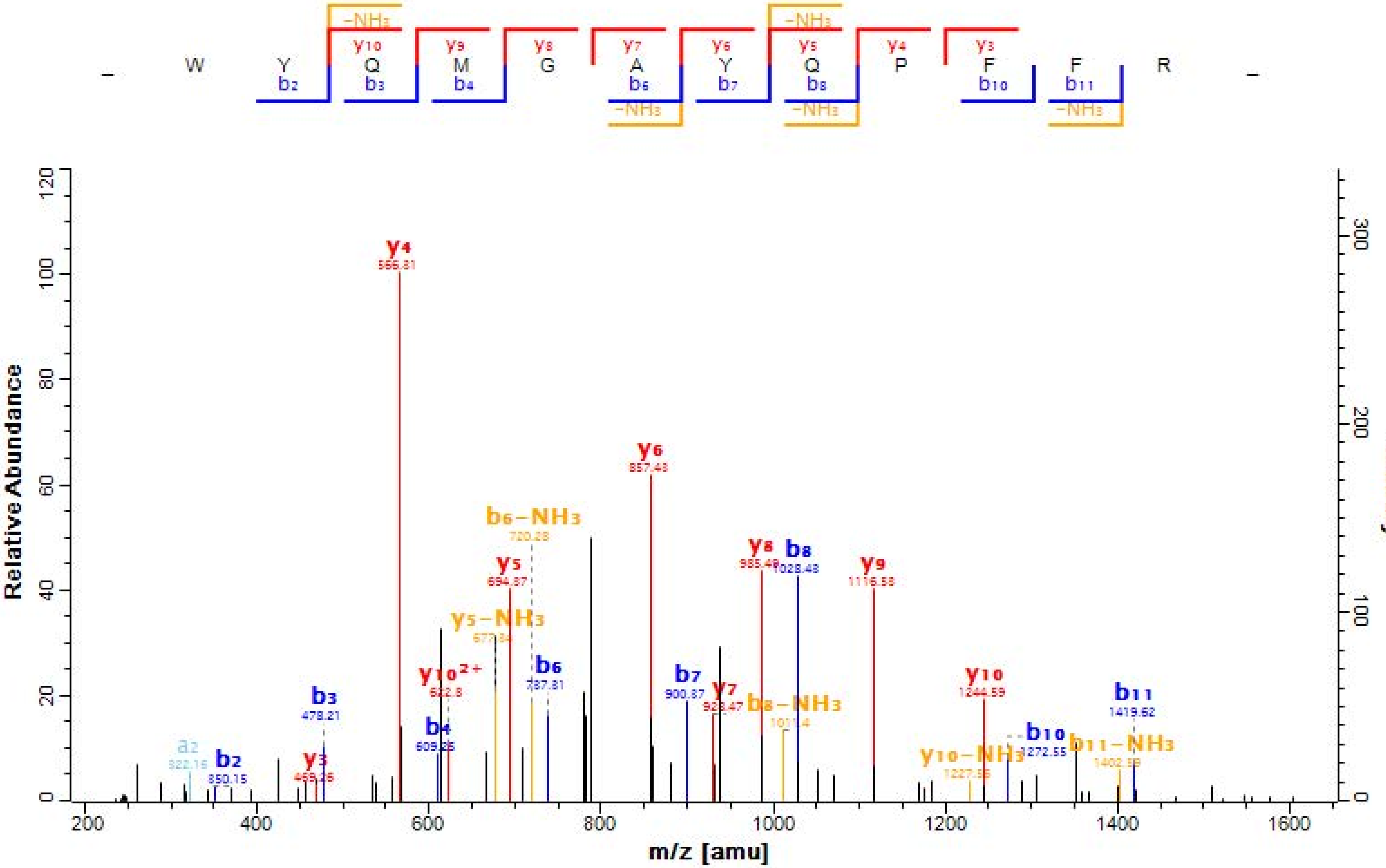
Mass:	1956.95115
m/z:	653.32433
Charge:	3+
Retentiontime:	52.377712249755
Score:	130.2359
Mass Error [ppm]:	-0.23628
PEP:	2.9685E-10
Precursor Type:	MULTI

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	66 %
Peak Coverage:	25 %
Protein Localisation:	325 ... 340

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	15				
	202.08	+0.0307	202.08	2	N	14	1870.9		1870.9	
	315.17	-0.037	315.17	3	L	13	1756.9		878.95	+0.2492
	443.22	+0.126	443.22	4	Q	12	1643.8		822.4	+0.1957
	572.27	+0.2064	572.27	5	E	11	1515.7		758.37	+0.0011
	685.35		685.35	6	I	10	1386.7	+0.1029	693.85	+0.2125
	832.42		832.42	7	F	9	1273.6	+0.1858	637.31	+0.244
	945.5		945.5	8	L	8	1126.5	+0.0628	563.78	+0.2132
	1042.6		1042.6	9	P	7	1013.5	+0.0185	507.23	+0.148
	1113.6		1113.6	10	A	6	916.41		916.41	
	1260.7		1260.7	11	F	5	845.37		845.37	
	1357.7		1357.7	12	P	4	698.3	+0.0585	698.3	
-0.262	759.38		1517.7	13	C	3	601.25		601.25	
	1654.8		1654.8	14	H	2	441.22		441.22	
	1783.8		1783.8	15	E	1	304.16		304.16	
				16	R	0	175.12		175.12	

Scan number	8462	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	164.65



precursor information

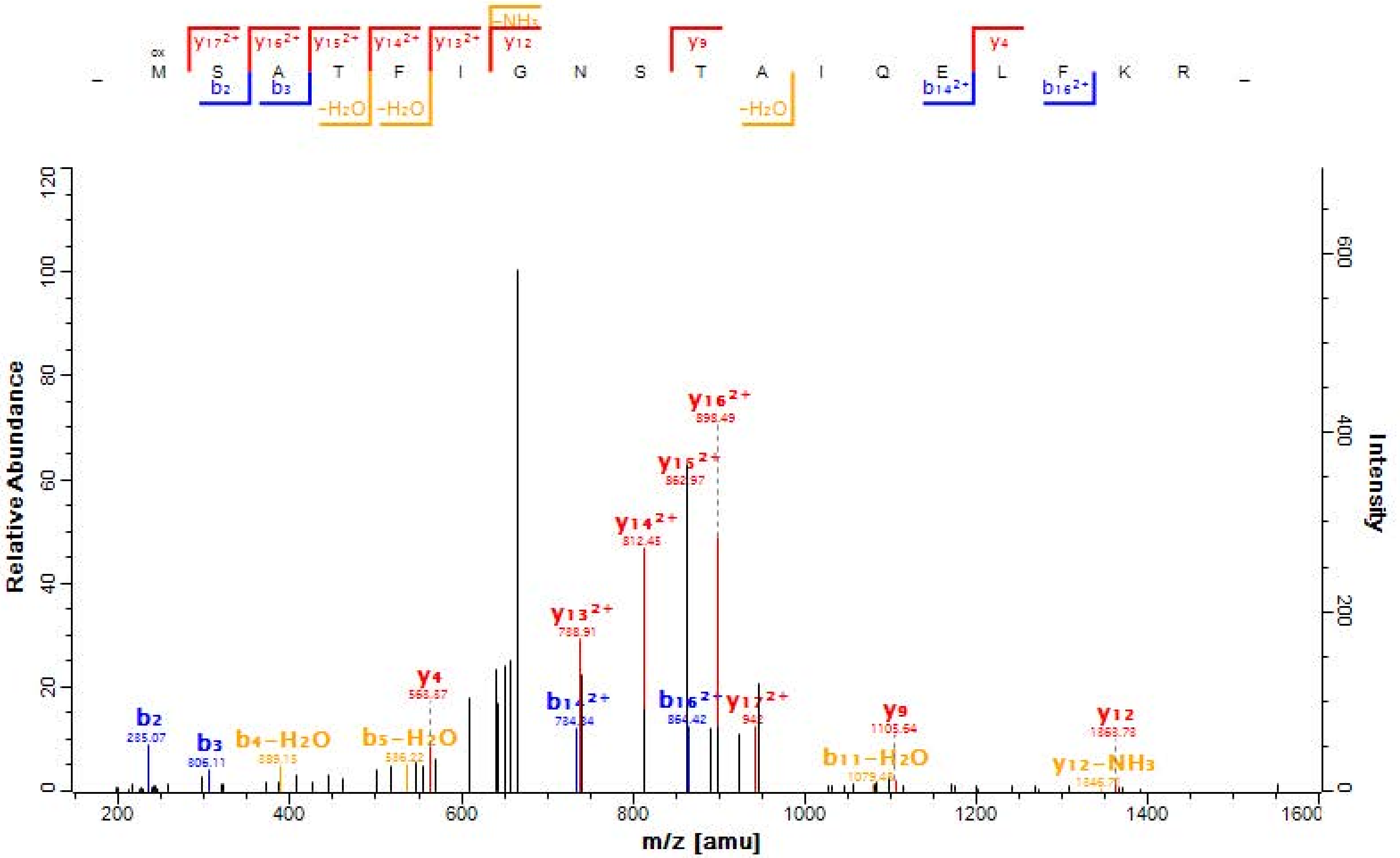
Mass:	1592.72393
m/z:	797.36924
Charge:	2+
Retentiontime:	52.932929992675
Score:	164.6517
Mass Error [ppm]:	0.30059
PEP:	1.2423E-07
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	53 %
Peak Coverage:	27 %
Protein Localisation:	714 ... 725

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	159.09		187.09	1	W	11				
-0.017	322.16	+0.2052	350.15	2	Y	10	1407.7		1407.7	
	450.21	+0.0954	478.21	3	Q	9	1244.6	+0.0728	622.8	-0.004
	581.25	+0.0965	609.25	4	M	8	1116.5	+0.0021	1116.5	
	638.28		666.27	5	G	7	985.49	-0.043	985.49	
	709.31	-0.09	737.31	6	A	6	928.47	+0.2032	928.47	
	872.38	-0.105	900.37	7	Y	5	857.43	+0.0036	857.43	
	1000.4	-0.073	1028.4	8	Q	4	694.37	+0.08	694.37	
	1097.5		1125.5	9	P	3	566.31	+0.0596	566.31	
	1244.6	-0.27	1272.6	10	F	2	469.26	+0.0204	469.26	
	1391.6	+0.3244	1419.6	11	F	1	322.19		322.19	
				12	R	0	175.12		175.12	

Scan number	8597	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	47.64



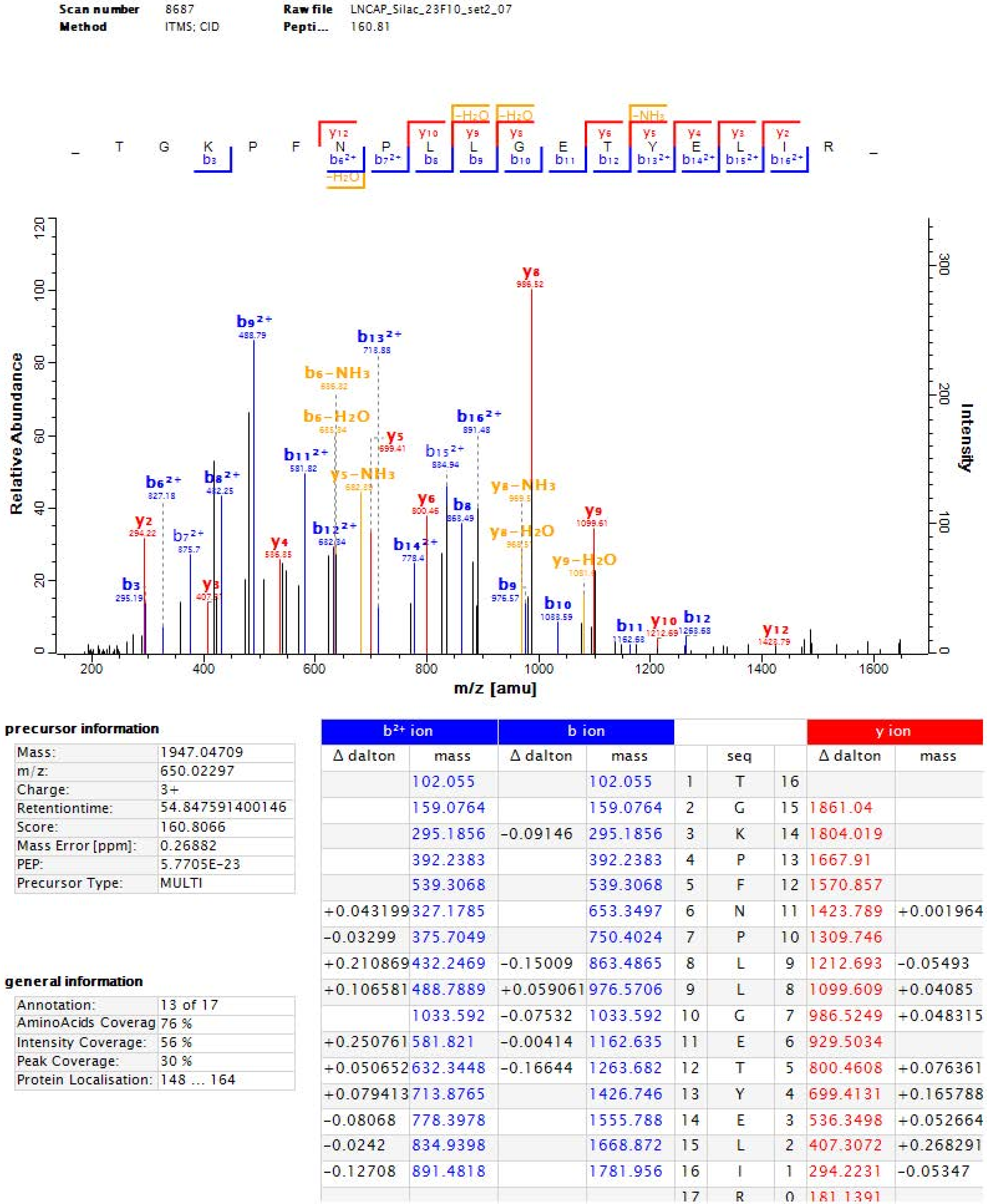
precursor information

Mass:	2029.0299
m/z:	677.35058
Charge:	3+
Retentiontime:	54.052192687988
Score:	47.63908
Mass Error [ppm]:	-0.17994
PEP:	0.026113
Precursor Type:	MULTI

general information

Annotation:	11 of 18
AminoAcids Coverag	61 %
Intensity Coverage:	36 %
Peak Coverage:	20 %
Protein Localisation:	363 ... 380

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.04		148.04	1	M	17				
	235.07	-0.025	235.07	2	S	16	1883		942	-0.006
	306.11	+0.0998	306.11	3	A	15	1796		898.49	+0.2603
	407.16		407.16	4	T	14	1724.9		862.97	-0.007
	554.23		554.23	5	F	13	1623.9		812.45	+0.2053
	667.31		667.31	6	I	12	1476.8		738.91	+0.0825
	724.33		724.33	7	G	11	1363.7	-0.026	1363.7	
	838.38		838.38	8	N	10	1306.7		1306.7	
	925.41		925.41	9	S	9	1192.7		1192.7	
	1026.5		1026.5	10	T	8	1105.6	+0.24	1105.6	
	1097.5		1097.5	11	A	7	1004.6		1004.6	
	1210.6		1210.6	12	I	6	933.55		933.55	
	1338.6		1338.6	13	Q	5	820.47		820.47	
-0.239	734.34		1467.7	14	E	4	692.41		692.41	
	1580.8		1580.8	15	L	3	563.37	-0.303	563.37	
+0.2584	864.42		1727.8	16	F	2	450.28		450.28	
	1855.9		1855.9	17	K	1	303.21		303.21	
				18	R	0	175.12		175.12	



Scan number	8687	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	160.81

precursor information

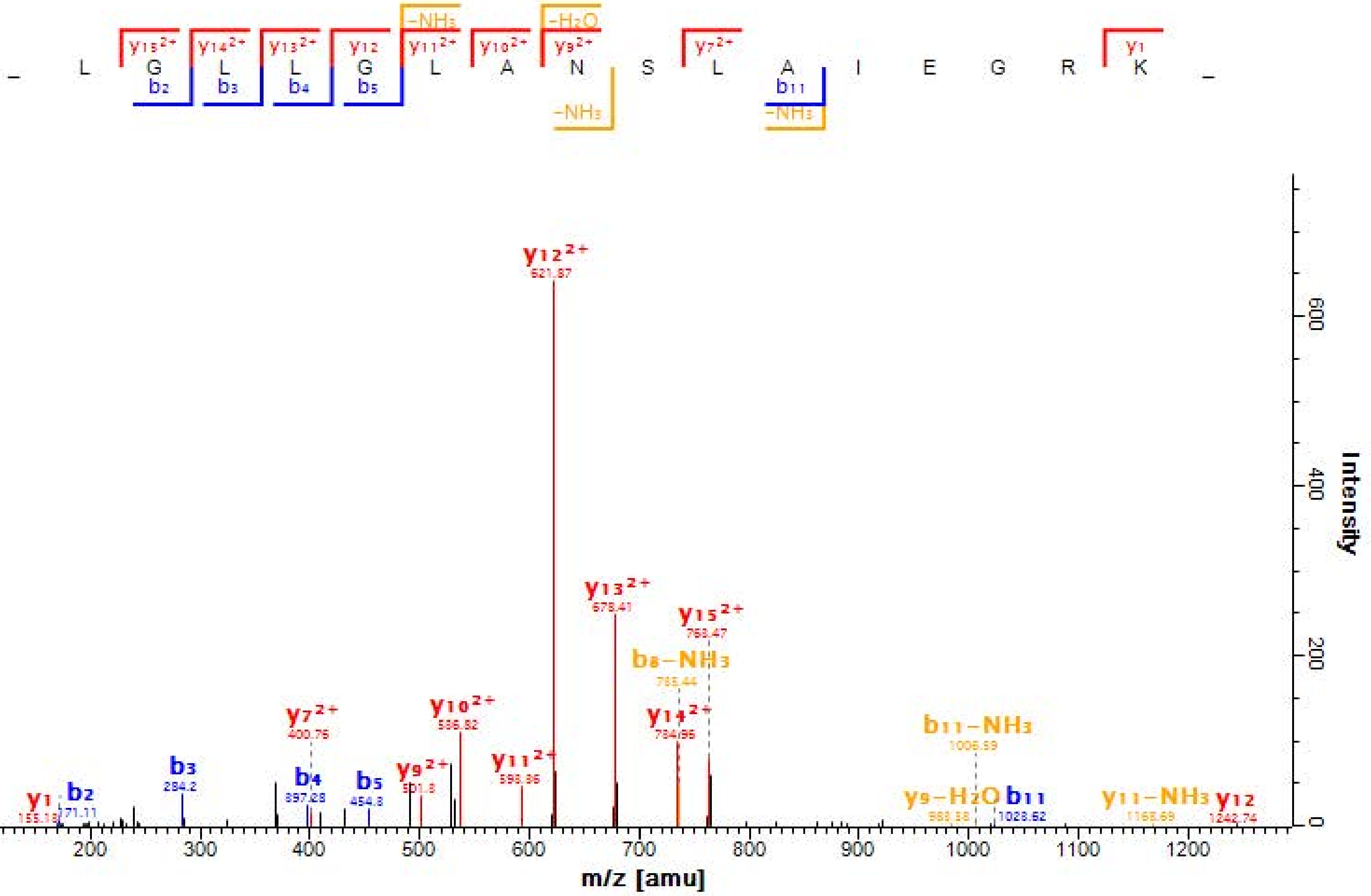
Mass:	1947.04709
m/z:	650.02297
Charge:	3+
Retentiontime:	54.847591400146
Score:	160.8066
Mass Error [ppm]:	0.26882
PEP:	5.7705E-23
Precursor Type:	MULTI

general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	56 %
Peak Coverage:	30 %
Protein Localisation:	148 ... 164

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	102.055		102.055	1	T	16		
	159.0764		159.0764	2	G	15	1861.04	
	295.1856	-0.09146	295.1856	3	K	14	1804.019	
	392.2383		392.2383	4	P	13	1667.91	
	539.3068		539.3068	5	F	12	1570.857	
+0.043199	327.1785		653.3497	6	N	11	1423.789	+0.001964
-0.03299	375.7049		750.4024	7	P	10	1309.746	
+0.210869	432.2469	-0.15009	863.4865	8	L	9	1212.693	-0.05493
+0.106581	488.7889	+0.059061	976.5706	9	L	8	1099.609	+0.04085
	1033.592	-0.07532	1033.592	10	G	7	986.5249	+0.048315
+0.250761	581.821	-0.00414	1162.635	11	E	6	929.5034	
+0.050652	632.3448	-0.16644	1263.682	12	T	5	800.4608	+0.076361
+0.079413	713.8765		1426.746	13	Y	4	699.4131	+0.165788
-0.08068	778.3978		1555.788	14	E	3	536.3498	+0.052664
-0.0242	834.9398		1668.872	15	L	2	407.3072	+0.268291
-0.12708	891.4818		1781.956	16	I	1	294.2231	-0.05347
				17	R	0	181.1391	

Scan number	8785	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	72.7



precursor information

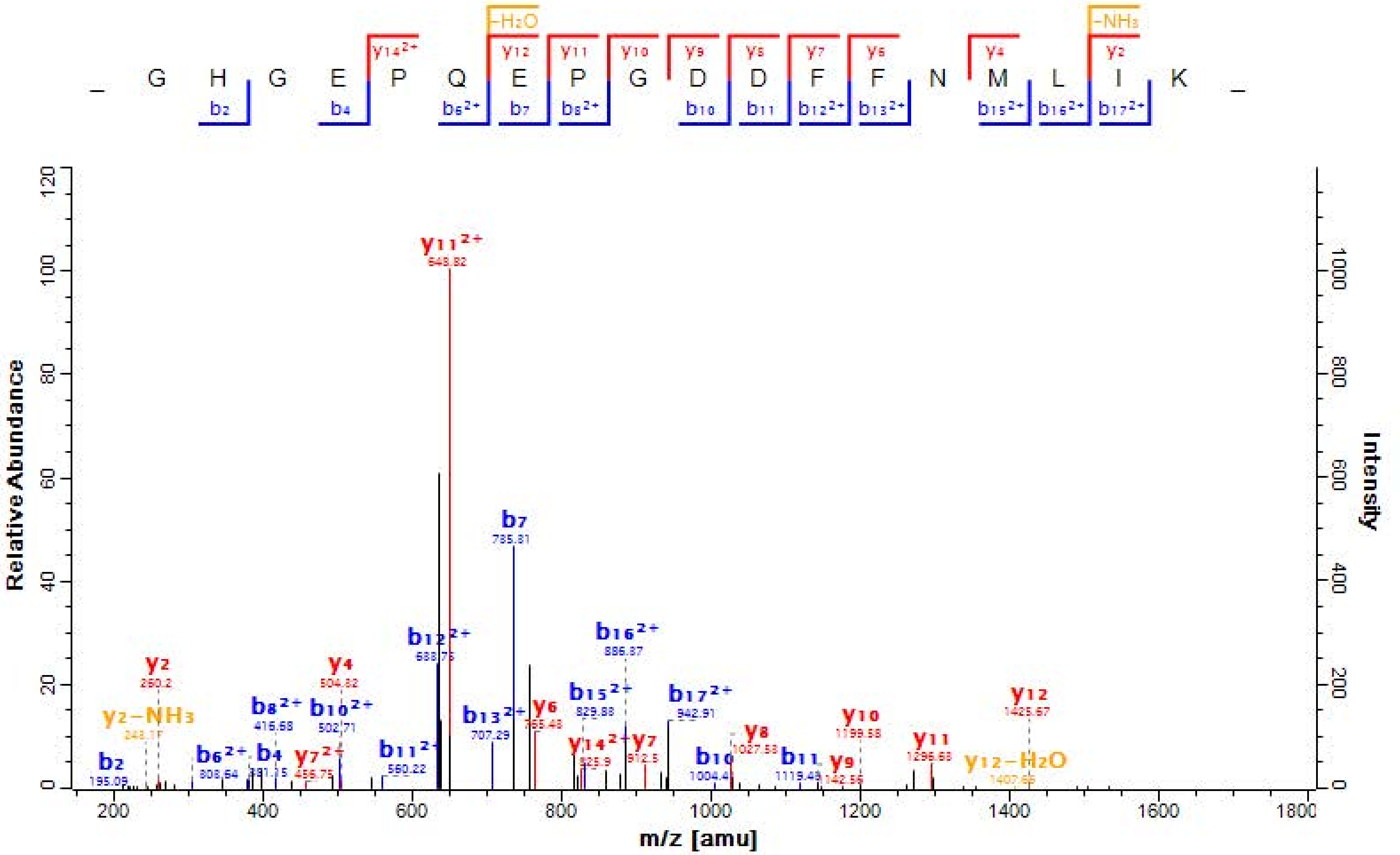
Mass:	1623.96667
m/z:	542.3295
Charge:	3+
Retentiontime:	55.767482757568
Score:	72.70486
Mass Error [ppm]:	-0.31511
PEP:	0.00020426
Precursor Type:	MULTI

general information

Annotation:	10 of 16
AminoAcids Coverag	62 %
Intensity Coverage:	68 %
Peak Coverage:	24 %
Protein Localisation:	169 ... 184

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	15				
+0.025822	171.1128	2	G	14	1525.925		763.466	-0.0025
-0.14682	284.1969	3	L	13	1468.903		734.9553	-0.14918
-0.04454	397.2809	4	L	12	1355.819		678.4132	+0.114409
-0.10037	454.3024	5	G	11	1242.735	+0.15805	621.8712	+0.176644
	567.3865	6	L	10	1185.714		593.3605	+0.08325
	638.4236	7	A	9	1072.63		536.8184	+0.115333
	752.4665	8	N	8	1001.592		501.2999	+0.0991
	839.4985	9	S	7	887.5496		887.5496	
	952.5826	10	L	6	800.5175		400.7624	-0.22084
+0.071943	1023.62	11	A	5	687.4335		687.4335	
	1136.704	12	I	4	616.3964		616.3964	
	1265.746	13	E	3	503.3123		503.3123	
	1322.768	14	G	2	374.2697		374.2697	
	1484.889	15	R	1	317.2482		317.2482	
		16	K	0	155.127	+0.194408	155.127	

Scan number	9017	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	132.81



precursor information

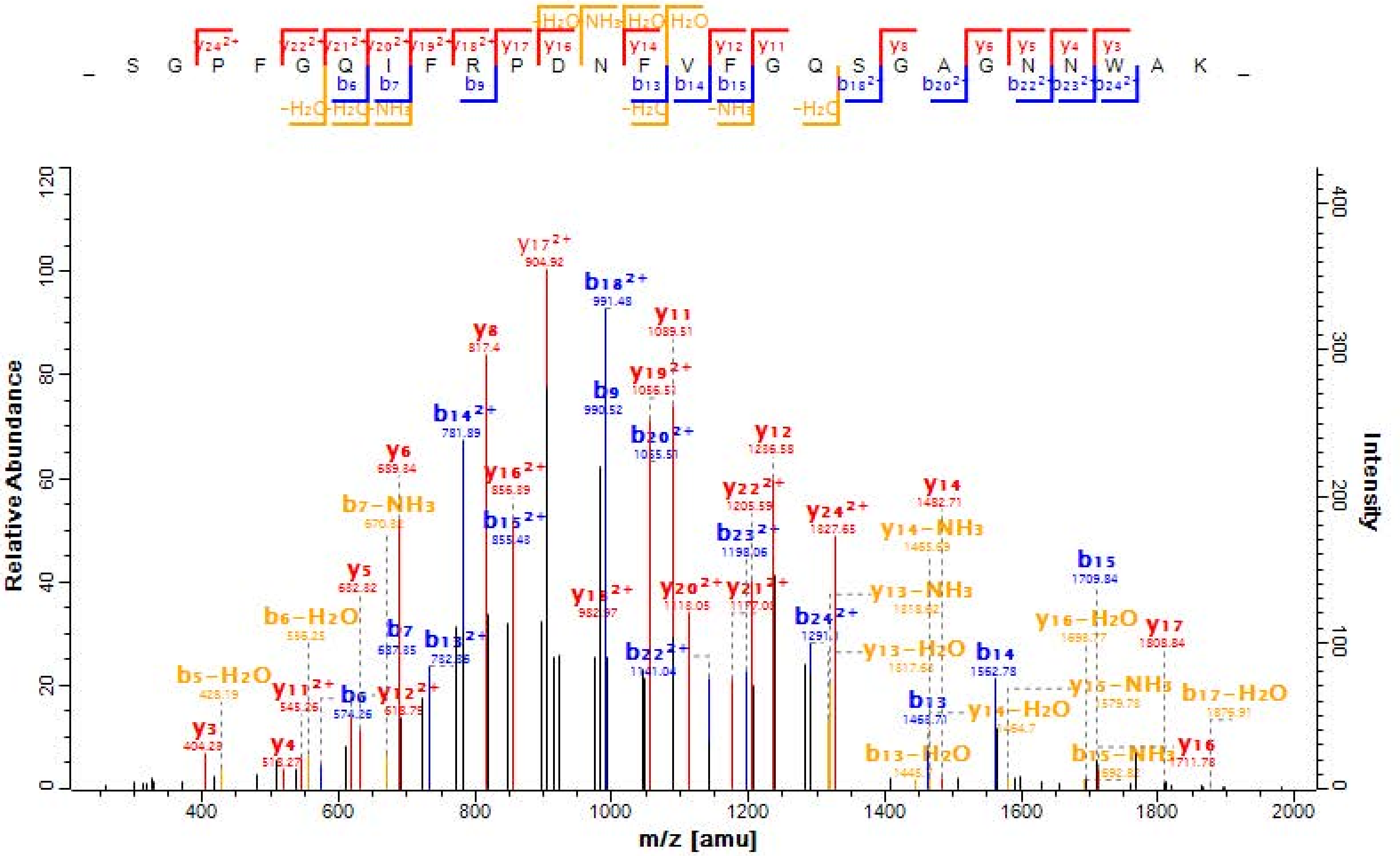
Mass:	2029.92042
m/z:	677.64742
Charge:	3+
Retentiontime:	58.129158020019
Score:	132.8108
Mass Error [ppm]:	0.021302
PEP:	5.3061E-13
Precursor Type:	MULTI

general information

Annotation:	14 of 18
AminoAcids Coverag	78 %
Intensity Coverage:	55 %
Peak Coverage:	27 %
Protein Localisation:	588 ... 605

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	17				
	195.09	+0.1876	195.09	2	H	16	1973.9		1973.9	
	252.11		252.11	3	G	15	1836.8		1836.8	
	381.15	+0.1283	381.15	4	E	14	1779.8		1779.8	
	478.2		478.2	5	P	13	1650.8		825.9	+0.1431
+0.0413	303.64		606.26	6	Q	12	1553.7		1553.7	
	735.31	-0.002	735.31	7	E	11	1425.7	-0.063	1425.7	
+0.0144	416.68		832.36	8	P	10	1296.6	-0.105	648.82	+0.255
	889.38		889.38	9	G	9	1199.6	-0.4	1199.6	
+0.1093	502.71	-0.143	1004.4	10	D	8	1142.6	-0.078	1142.6	
-0.073	560.22	+0.1641	1119.4	11	D	7	1027.5	-0.028	1027.5	
+0.1539	633.75		1266.5	12	F	6	912.5	-0.275	456.75	+0.1195
+0.1568	707.29		1413.6	13	F	5	765.43	-0.017	765.43	
	1527.6		1527.6	14	N	4	618.36		618.36	
+0.3064	829.83		1658.7	15	M	3	504.32	+0.3524	504.32	
-0.158	886.37		1771.7	16	L	2	373.28		373.28	
+0.011	942.91		1884.8	17	I	1	260.2	+0.0333	260.2	
				18	K	0	147.11		147.11	

Scan number	9180	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	218.72



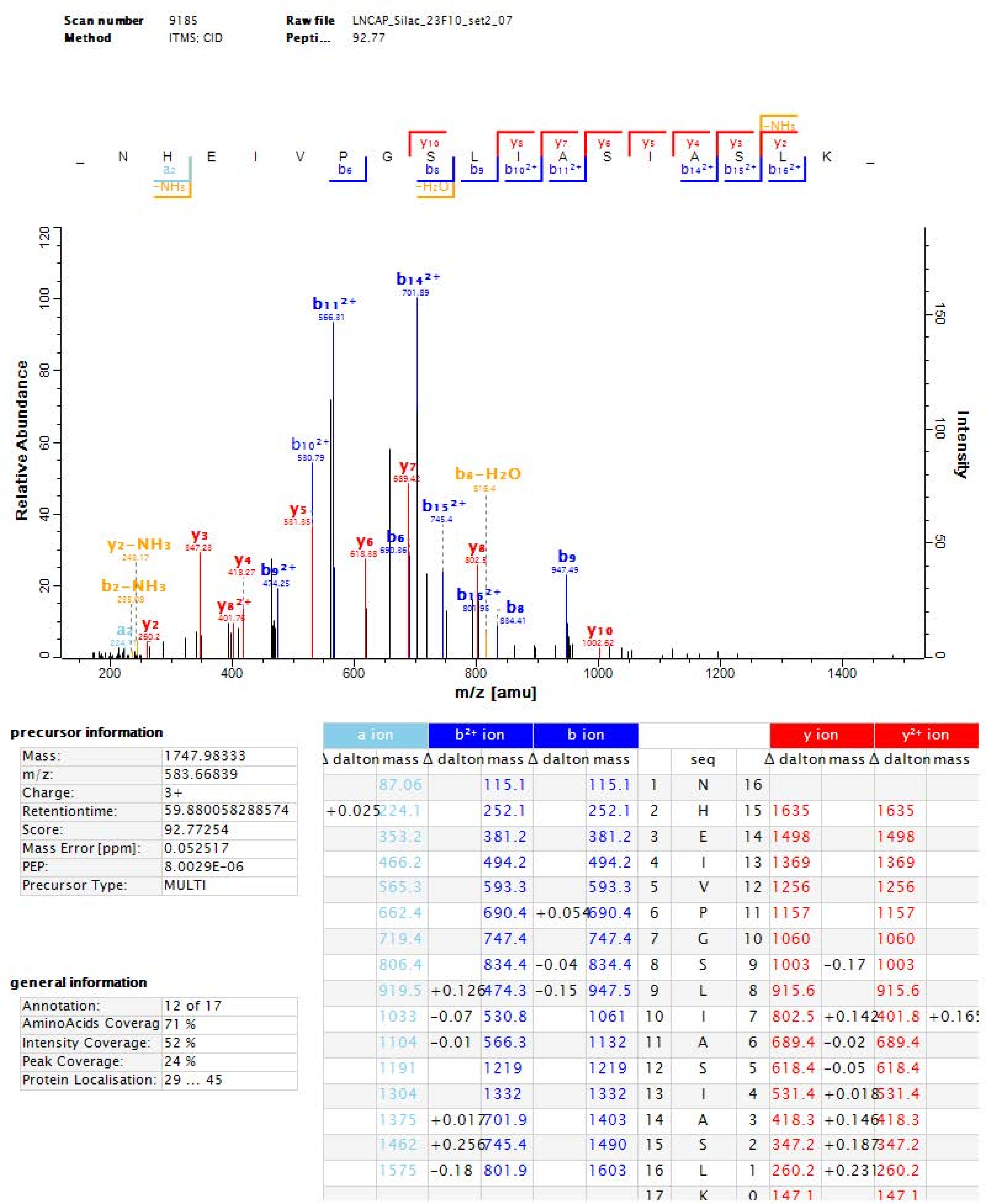
precursor information

Mass:	2797.33692
m/z:	933.45292
Charge:	3+
Retentiontime:	59.832431793212
Score:	218.7186
Mass Error [ppm]:	0.29545
PEP:	1.6655E-81
Precursor Type:	MULTI

general information

Annotation:	21 of 26
AminoAcids Coverag	81 %
Intensity Coverage:	64 %
Peak Coverage:	45 %
Protein Localisation:	78 ... 103

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	25				
	145.06		145.06	2	G	24	2711.3		2711.3	
	242.11		242.11	3	P	23	2654.3		1327.6	-0.379
	389.18		389.18	4	F	22	2557.2		2557.2	
	446.2		446.2	5	G	21	2410.2		1205.6	+0.2364
	574.26	+0.0356	574.26	6	Q	20	2353.1		1177.1	+0.2233
	687.35	-0.007	687.35	7	I	19	2225.1		1113	+0.2293
	834.41		834.41	8	F	18	2112		1056.5	+0.2951
	990.52	-0.032	990.52	9	R	17	1964.9		982.97	-0.097
	1087.6		1087.6	10	P	16	1808.8	+0.0568	904.92	-0.186
	1202.6		1202.6	11	D	15	1711.8	-0.06	856.39	-0.215
	1316.6		1316.6	12	N	14	1596.8		1596.8	
-0.004	732.36	+0.0313	1463.7	13	F	13	1482.7	-0.156	1482.7	
-0.007	781.89	-0.077	1562.8	14	V	12	1335.6		1335.6	
+0.0731	855.43	-0.034	1709.8	15	F	11	1236.6	-0.008	618.79	+0.1447
	1766.9		1766.9	16	G	10	1089.5	+0.0311	545.26	+0.1248
	1894.9		1894.9	17	Q	9	1032.5		1032.5	
+0.212	991.48		1982	18	S	8	904.43		904.43	
	2039		2039	19	G	7	817.4	+0.0863	817.4	
+0.2505	1055.5		2110	20	A	6	760.37		760.37	
	2167		2167	21	G	5	689.34	+0.0374	689.34	
+0.1263	1141		2281.1	22	N	4	632.32	+0.0751	632.32	
+0.1378	1198.1		2395.1	23	N	3	518.27	+0.0997	518.27	
+0.0013	1291.1		2581.2	24	W	2	404.23	+0.1458	404.23	
	2652.2		2652.2	25	A	1	218.15		218.15	
				26	K	0	147.11		147.11	



Scan number	9185
Method	ITMS; CID
Raw file	LNCAP_Silac_23F10_set2_07
Pepti...	92.77

precursor information

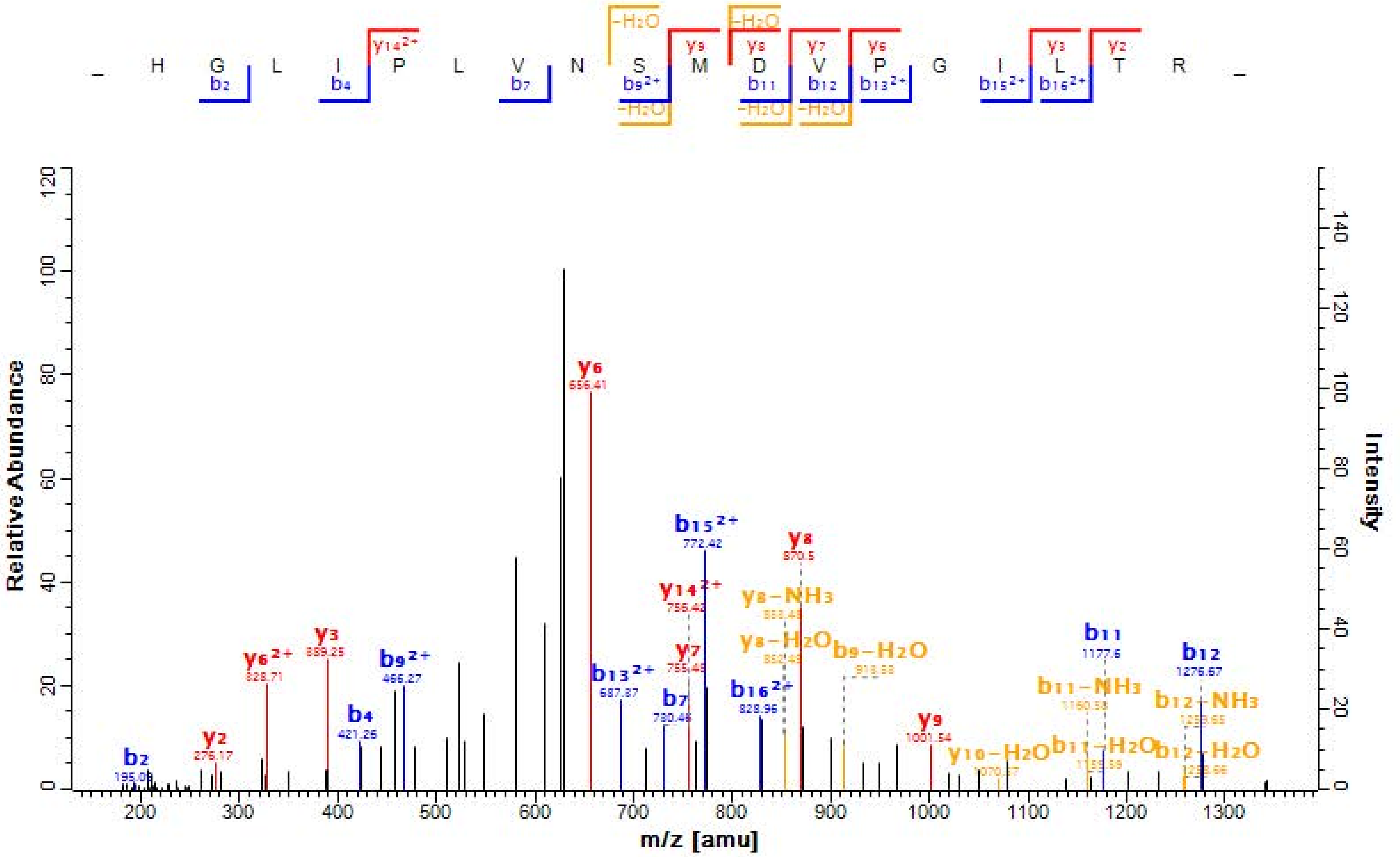
Mass:	1747.98333
m/z:	583.66839
Charge:	3+
Retentiontime:	59.880058288574
Score:	92.77254
Mass Error [ppm]:	0.052517
PEP:	8.0029E-06
Precursor Type:	MULTI

general information

Annotation:	12 of 17
AminoAcids Coverag	71 %
Intensity Coverage:	52 %
Peak Coverage:	24 %
Protein Localisation:	29 ... 45

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	87.06		115.1		115.1	1	N	16				
+0.025	224.1		252.1		252.1	2	H	15	1635		1635	
	353.2		381.2		381.2	3	E	14	1498		1498	
	466.2		494.2		494.2	4	I	13	1369		1369	
	565.3		593.3		593.3	5	V	12	1256		1256	
	662.4		690.4	+0.054	690.4	6	P	11	1157		1157	
	719.4		747.4		747.4	7	G	10	1060		1060	
	806.4		834.4	-0.04	834.4	8	S	9	1003	-0.17	1003	
	919.5	+0.126	474.3	-0.15	947.5	9	L	8	915.6		915.6	
	1033	-0.07	530.8		1061	10	I	7	802.5	+0.142	401.8	+0.16
	1104	-0.01	566.3		1132	11	A	6	689.4	-0.02	689.4	
	1191		1219		1219	12	S	5	618.4	-0.05	618.4	
	1304		1332		1332	13	I	4	531.4	+0.018	531.4	
	1375	+0.017	701.9		1403	14	A	3	418.3	+0.146	418.3	
	1462	+0.256	745.4		1490	15	S	2	347.2	+0.187	347.2	
	1575	-0.18	801.9		1603	16	L	1	260.2	+0.231	260.2	
						17	K	0	147.1		147.1	

Scan number	9209	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	102.64



precursor information

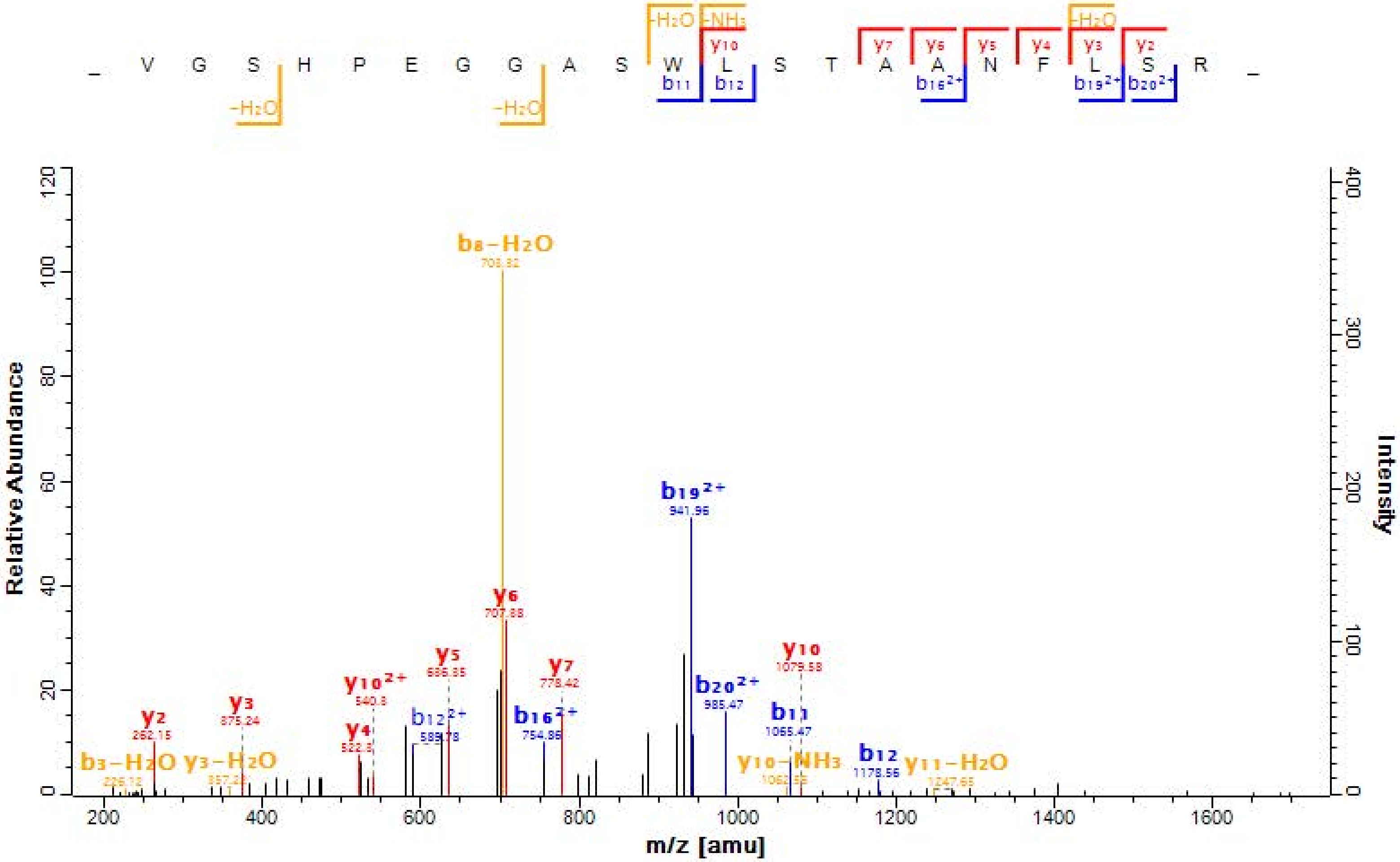
Mass:	1931.06647
m/z:	644.6961
Charge:	3+
Retentiontime:	60.115833282470
Score:	102.6366
Mass Error [ppm]:	0.11244
PEP:	1.0937E-06
Precursor Type:	MULTI

general information

Annotation:	12 of 18
AminoAcids Coverag	67 %
Intensity Coverage:	41 %
Peak Coverage:	27 %
Protein Localisation:	218 ... 235

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.07		138.07	1	H	17				
	195.09	+0.137	195.09	2	G	16	1795		1795	
	308.17		308.17	3	L	15	1738		1738	
	421.26	+0.0395	421.26	4	I	14	1624.9		1624.9	
	518.31		518.31	5	P	13	1511.8		756.42	+0.351
	631.39		631.39	6	L	12	1414.8		1414.8	
	730.46	-0.034	730.46	7	V	11	1301.7		1301.7	
	844.5		844.5	8	N	10	1202.6		1202.6	
+0.0879	466.27		931.54	9	S	9	1088.6		1088.6	
	1062.6		1062.6	10	M	8	1001.5	+0.1527	1001.5	
	1177.6	-0.283	1177.6	11	D	7	870.5	-0.084	870.5	
	1276.7	-0.121	1276.7	12	V	6	755.48	-0.29	755.48	
-0.166	687.37		1373.7	13	P	5	656.41	+0.0149	328.71	-0.058
	1430.7		1430.7	14	G	4	559.36		559.36	
-0.108	772.42		1543.8	15	I	3	502.33		502.33	
-0.202	828.96		1656.9	16	L	2	389.25	+0.0732	389.25	
	1758		1758	17	T	1	276.17	-0.057	276.17	
				18	R	0	175.12		175.12	

Scan number	9369	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	59



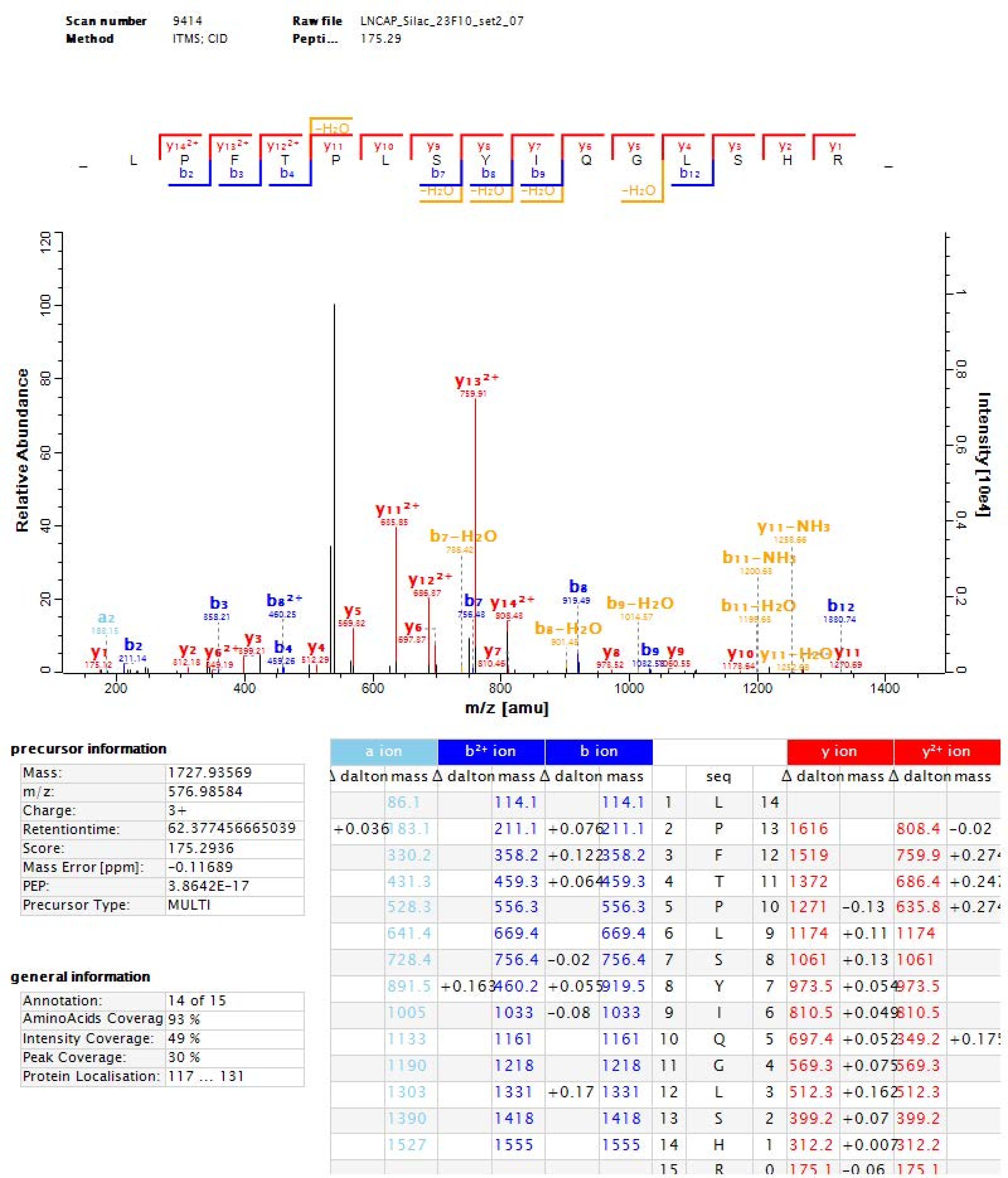
precursor information

Mass:	2143.04546
m/z:	715.35576
Charge:	3+
Retentiontime:	61.866130828857
Score:	58.99711
Mass Error [ppm]:	0.37044
PEP:	0.0015355
Precursor Type:	MULTI

general information

Annotation:	12 of 21
AminoAcids Coverag	57 %
Intensity Coverage:	53 %
Peak Coverage:	23 %
Protein Localisation:	258 ... 278

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	20				
	157.1		157.1	2	G	19	2045		2045	
	244.13		244.13	3	S	18	1988		1988	
	381.19		381.19	4	H	17	1900.9		1900.9	
	478.24		478.24	5	P	16	1763.9		1763.9	
	607.28		607.28	6	E	15	1666.8		1666.8	
	664.3		664.3	7	G	14	1537.8		1537.8	
	721.33		721.33	8	G	13	1480.8		1480.8	
	792.36		792.36	9	A	12	1423.7		1423.7	
	879.4		879.4	10	S	11	1352.7		1352.7	
	1065.5	+0.1154	1065.5	11	W	10	1265.7		1265.7	
-0.045	589.78	-0.019	1178.6	12	L	9	1079.6	-0.112	540.3	+0.2812
	1265.6		1265.6	13	S	8	966.5		966.5	
	1366.6		1366.6	14	T	7	879.47		879.47	
	1437.7		1437.7	15	A	6	778.42	-0.021	778.42	
-0.037	754.86		1508.7	16	A	5	707.38	-0.041	707.38	
	1622.8		1622.8	17	N	4	636.35	-0.145	636.35	
	1769.8		1769.8	18	F	3	522.3	+0.2229	522.3	
+0.2653	941.96		1882.9	19	L	2	375.24	+0.195	375.24	
+0.3206	985.47		1969.9	20	S	1	262.15	+0.0892	262.15	
				21	R	0	175.12		175.12	



Scan number	9414	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	175.29

precursor information

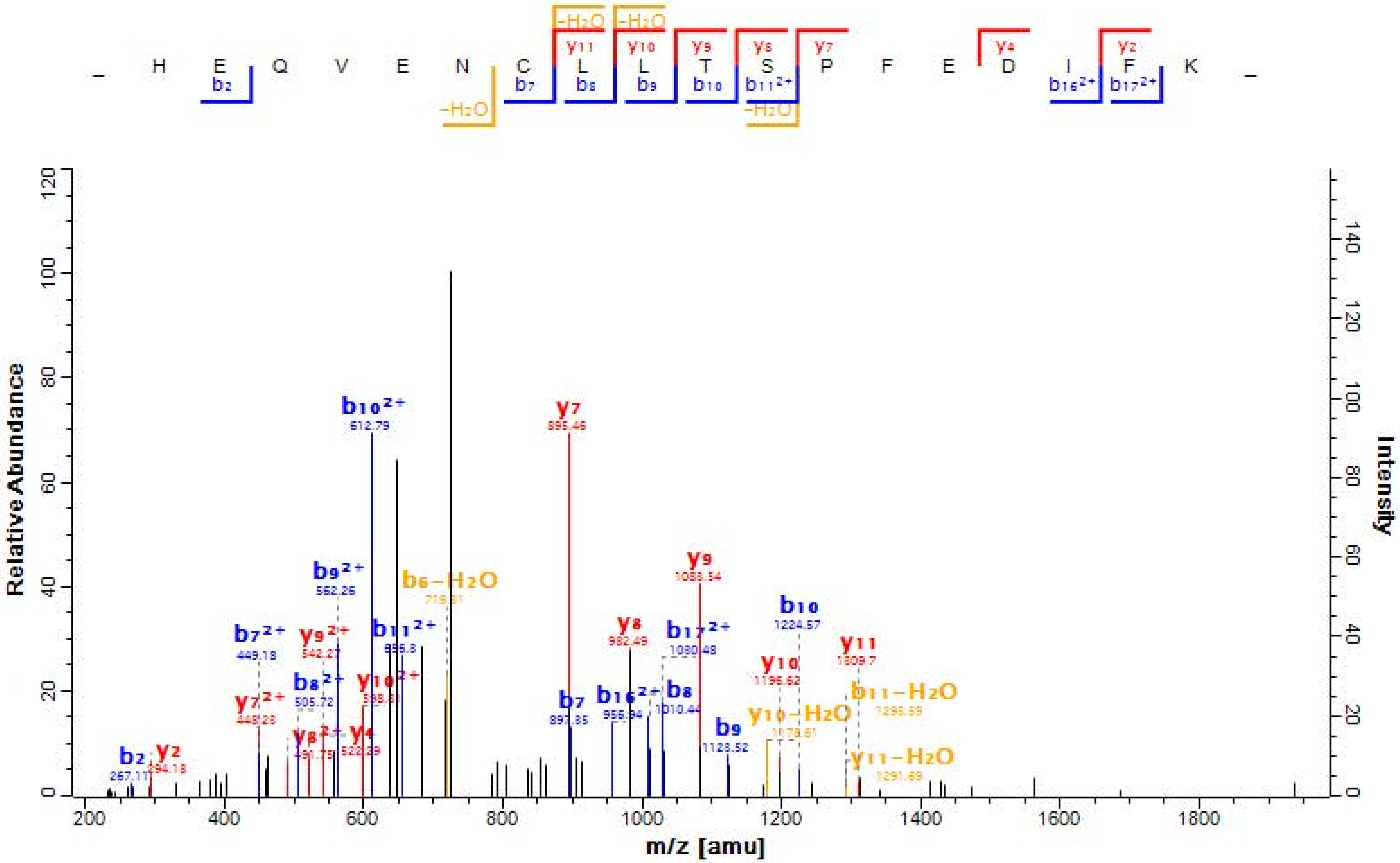
Mass:	1727.93569
m/z:	576.98584
Charge:	3+
Retentiontime:	62.377456665039
Score:	175.2936
Mass Error [ppm]:	-0.11689
PEP:	3.8642E-17
Precursor Type:	MULTI

general information

Annotation:	14 of 15
AminoAcids Coverag	93 %
Intensity Coverage:	49 %
Peak Coverage:	30 %
Protein Localisation:	117 ... 131

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	14				
+0.036	183.1		211.1	+0.076	211.1	2	P	13	1616		808.4	-0.02
	330.2		358.2	+0.122	358.2	3	F	12	1519		759.9	+0.27
	431.3		459.3	+0.064	459.3	4	T	11	1372		686.4	+0.24
	528.3		556.3		556.3	5	P	10	1271	-0.13	635.8	+0.27
	641.4		669.4		669.4	6	L	9	1174	+0.11	1174	
	728.4		756.4	-0.02	756.4	7	S	8	1061	+0.13	1061	
	891.5	+0.163	460.2	+0.055	919.5	8	Y	7	973.5	+0.054	973.5	
	1005		1033	-0.08	1033	9	I	6	810.5	+0.049	810.5	
	1133		1161		1161	10	Q	5	697.4	+0.052	349.2	+0.17
	1190		1218		1218	11	G	4	569.3	+0.075	569.3	
	1303		1331	+0.17	1331	12	L	3	512.3	+0.162	512.3	
	1390		1418		1418	13	S	2	399.2	+0.07	399.2	
	1527		1555		1555	14	H	1	312.2	+0.007	312.2	
						15	R	0	175.1	-0.06	175.1	

Scan number	9501	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	126.63



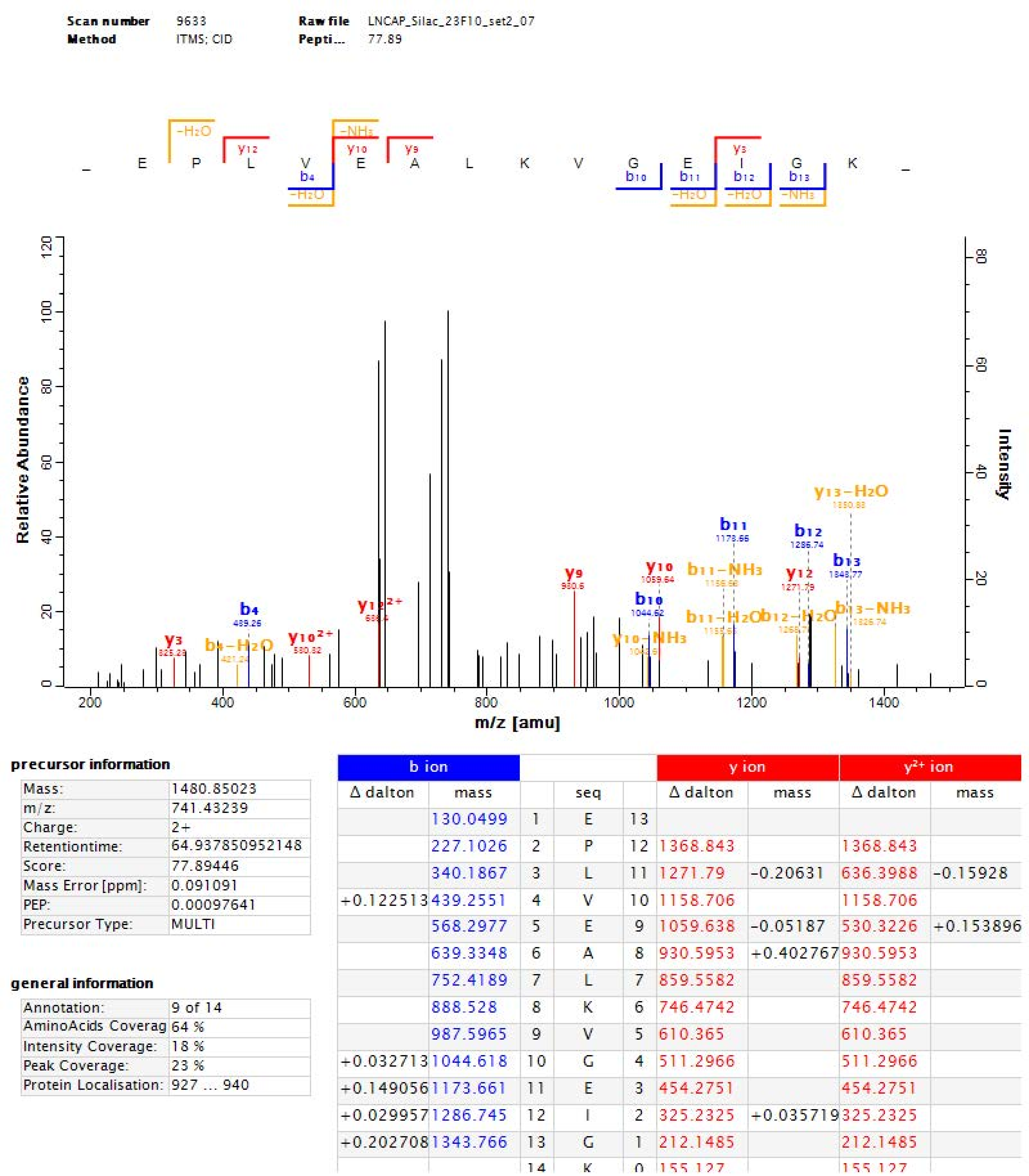
precursor information

Mass:	2205.04185
m/z:	736.02123
Charge:	3+
Retentiontime:	63.331623077392
Score:	126.6291
Mass Error [ppm]:	0.28398
PEP:	1.7603E-12
Precursor Type:	MULTI

general information

Annotation:	11 of 18
AminoAcids Coverag	61 %
Intensity Coverage:	48 %
Peak Coverage:	35 %
Protein Localisation:	386 ... 403

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.07		138.07	1	H	17				
	267.11	+0.2683	267.11	2	E	16	2069		2069	
	395.17		395.17	3	Q	15	1939.9		1939.9	
	494.24		494.24	4	V	14	1811.9		1811.9	
	623.28		623.28	5	E	13	1712.8		1712.8	
	737.32		737.32	6	N	12	1583.8		1583.8	
+0.2282	449.18	+0.0317	897.35	7	C	11	1469.7		1469.7	
+0.1088	505.72	-0.184	1010.4	8	L	10	1309.7	-0.161	1309.7	
+0.1653	562.26	-0.055	1123.5	9	L	9	1196.6	+0.1318	598.81	+0.3533
+0.2887	612.79	-0.236	1224.6	10	T	8	1083.5	+0.0422	542.27	+0.3411
+0.0514	656.3		1311.6	11	S	7	982.49	+0.0391	491.75	+0.2495
	1408.7		1408.7	12	P	6	895.46	+0.0098	448.23	+0.1283
	1555.7		1555.7	13	F	5	798.4		798.4	
	1684.8		1684.8	14	E	4	651.33		651.33	
	1799.8		1799.8	15	D	3	522.29	+0.2985	522.29	
+0.1671	956.94		1912.9	16	I	2	407.27		407.27	
+0.0338	1030.5		2059.9	17	F	1	294.18	-0.065	294.18	
				18	K	0	147.11		147.11	



Scan number 9633

Method ITMS; CID

Raw file LNCAP_Silac_23F10_set2_07

Pepti... 77.89

precursor information

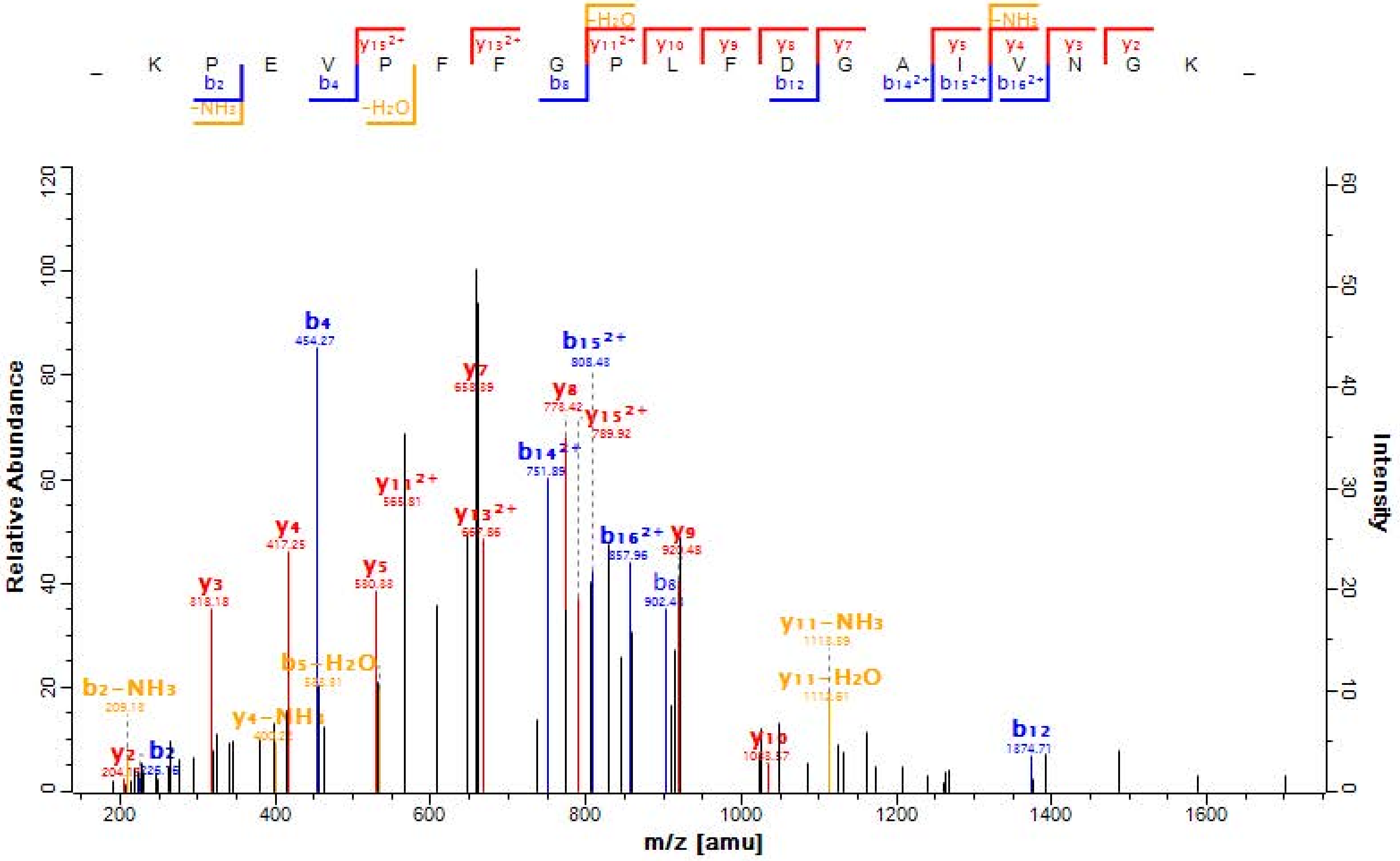
Mass:	1480.85023
m/z:	741.43239
Charge:	2+
Retentiontime:	64.937850952148
Score:	77.89446
Mass Error [ppm]:	0.091091
PEP:	0.00097641
Precursor Type:	MULTI

general information

Annotation:	9 of 14
AminoAcids Coverag	64 %
Intensity Coverage:	18 %
Peak Coverage:	23 %
Protein Localisation:	927 ... 940

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	13				
	227.1026	2	P	12	1368.843		1368.843	
	340.1867	3	L	11	1271.79	-0.20631	636.3988	-0.15928
+0.122513	439.2551	4	V	10	1158.706		1158.706	
	568.2977	5	E	9	1059.638	-0.05187	530.3226	+0.153896
	639.3348	6	A	8	930.5953	+0.402767	930.5953	
	752.4189	7	L	7	859.5582		859.5582	
	888.528	8	K	6	746.4742		746.4742	
	987.5965	9	V	5	610.365		610.365	
+0.032713	1044.618	10	G	4	511.2966		511.2966	
+0.149056	1173.661	11	E	3	454.2751		454.2751	
+0.029957	1286.745	12	I	2	325.2325	+0.035719	325.2325	
+0.202708	1343.766	13	G	1	212.1485		212.1485	
		14	K	0	155.127		155.127	

Scan number	9714	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	68.41



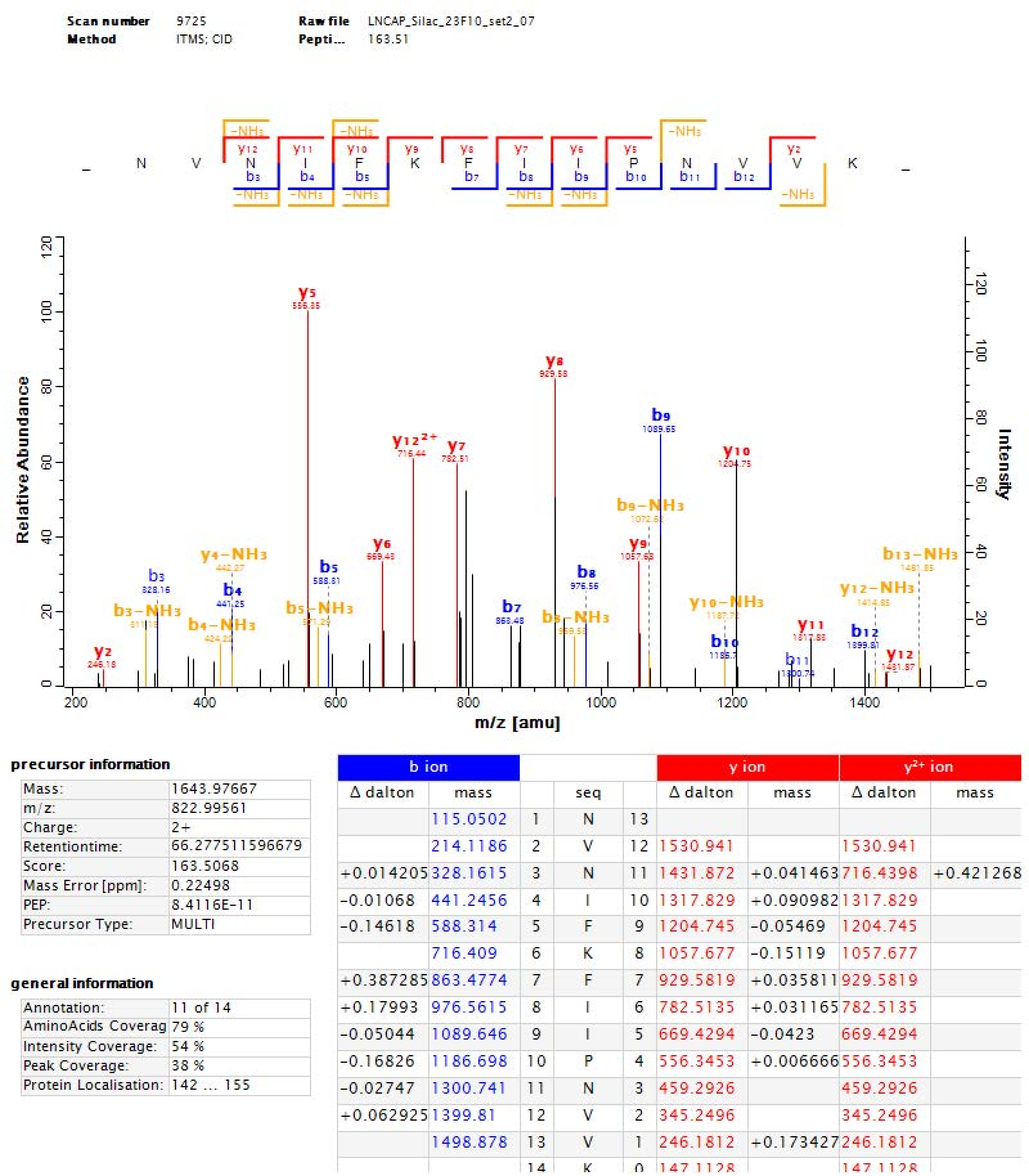
precursor information

Mass:	2031.08352
m/z:	678.03512
Charge:	3+
Retentiontime:	66.120849609375
Score:	68.41048
Mass Error [ppm]:	0.282
PEP:	0.000307
Precursor Type:	MULTI

general information

Annotation:	15 of 19
AminoAcids Coverag	79 %
Intensity Coverage:	45 %
Peak Coverage:	27 %
Protein Localisation:	1948 ... 1966

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.1		129.1	1	K	18				
	226.16	-0.165	226.16	2	P	17	1904		1904	
	355.2		355.2	3	E	16	1806.9		1806.9	
	454.27	+0.0003	454.27	4	V	15	1677.9		1677.9	
	551.32		551.32	5	P	14	1578.8		789.92	+0.0491
	698.39		698.39	6	F	13	1481.8		1481.8	
	845.46		845.46	7	F	12	1334.7		667.86	-0.483
	902.48	+0.0835	902.48	8	G	11	1187.6		1187.6	
	999.53		999.53	9	P	10	1130.6		565.81	+0.1077
	1112.6		1112.6	10	L	9	1033.6	+0.3009	1033.6	
	1259.7		1259.7	11	F	8	920.48	+0.0351	920.48	
	1374.7	+0.0191	1374.7	12	D	7	773.42	+0.0086	773.42	
	1431.7		1431.7	13	G	6	658.39	+0.0709	658.39	
+0.1519	751.89		1502.8	14	A	5	601.37		601.37	
+0.0438	808.43		1615.9	15	I	4	530.33	+0.1664	530.33	
+0.3147	857.96		1714.9	16	V	3	417.25	+0.1455	417.25	
	1829		1829	17	N	2	318.18	+0.1551	318.18	
	1886		1886	18	G	1	204.13	+0.1904	204.13	
				19	K	0	147.11		147.11	



Scan number	9725	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	163.51

precursor information

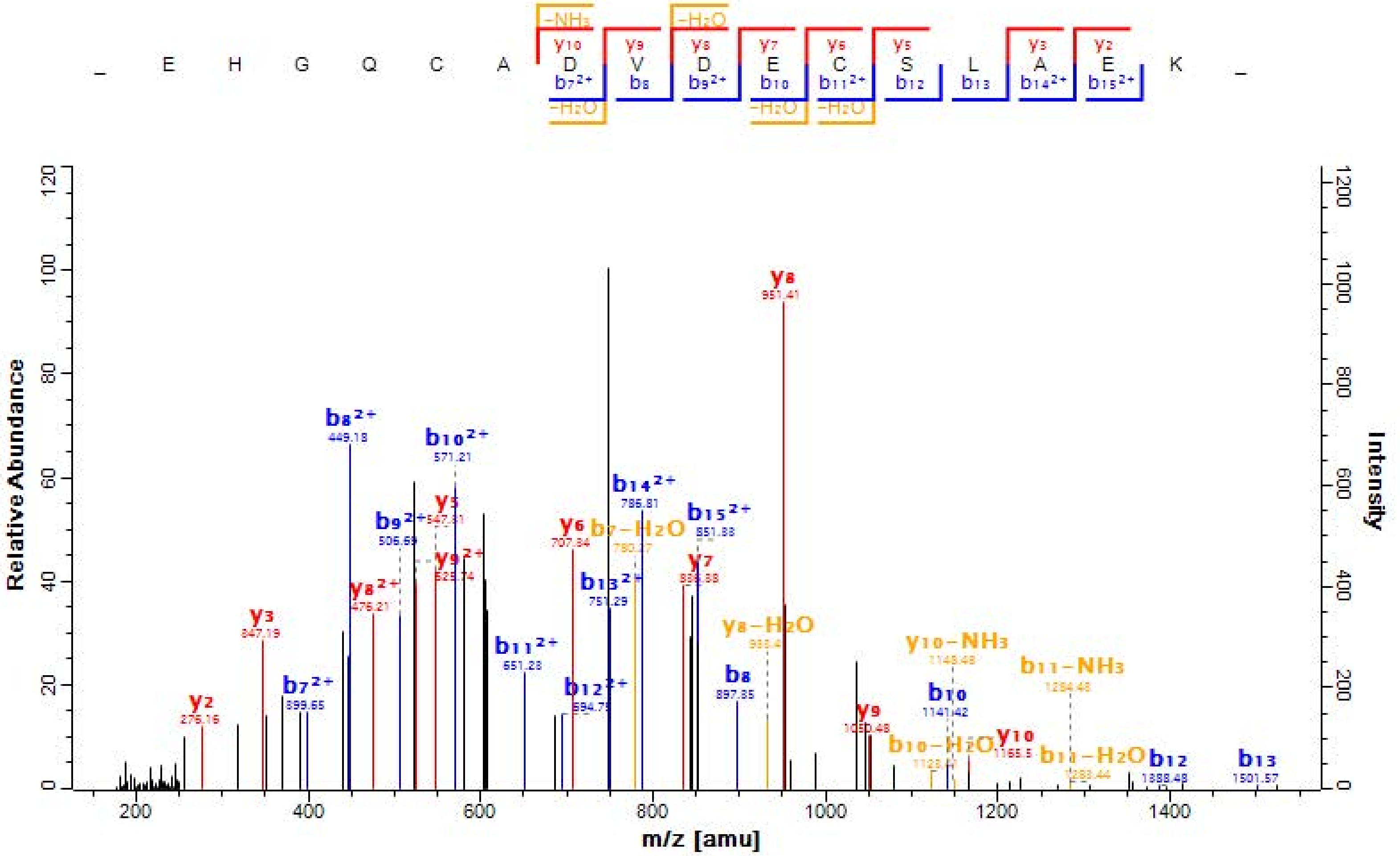
Mass:	1643.97667
m/z:	822.99561
Charge:	2+
Retentiontime:	66.277511596679
Score:	163.5068
Mass Error [ppm]:	0.22498
PEP:	8.4116E-11
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	54 %
Peak Coverage:	38 %
Protein Localisation:	142 ... 155

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502	1	N	13				
	214.1186	2	V	12	1530.941		1530.941	
+0.014205	328.1615	3	N	11	1431.872	+0.041463	716.4398	+0.421268
-0.01068	441.2456	4	I	10	1317.829	+0.090982	1317.829	
-0.14618	588.314	5	F	9	1204.745	-0.05469	1204.745	
	716.409	6	K	8	1057.677	-0.15119	1057.677	
+0.387285	863.4774	7	F	7	929.5819	+0.035811	929.5819	
+0.17993	976.5615	8	I	6	782.5135	+0.031165	782.5135	
-0.05044	1089.646	9	I	5	669.4294	-0.0423	669.4294	
-0.16826	1186.698	10	P	4	556.3453	+0.006666	556.3453	
-0.02747	1300.741	11	N	3	459.2926		459.2926	
+0.062925	1399.81	12	V	2	345.2496		345.2496	
	1498.878	13	V	1	246.1812	+0.173427	246.1812	
		14	K	0	147.1128		147.1128	

Scan number	976	**Raw file**	LNCAP_Silac_23F10_set2_07
Method	ITMS; CID	**Pepti...**	150.34



precursor information

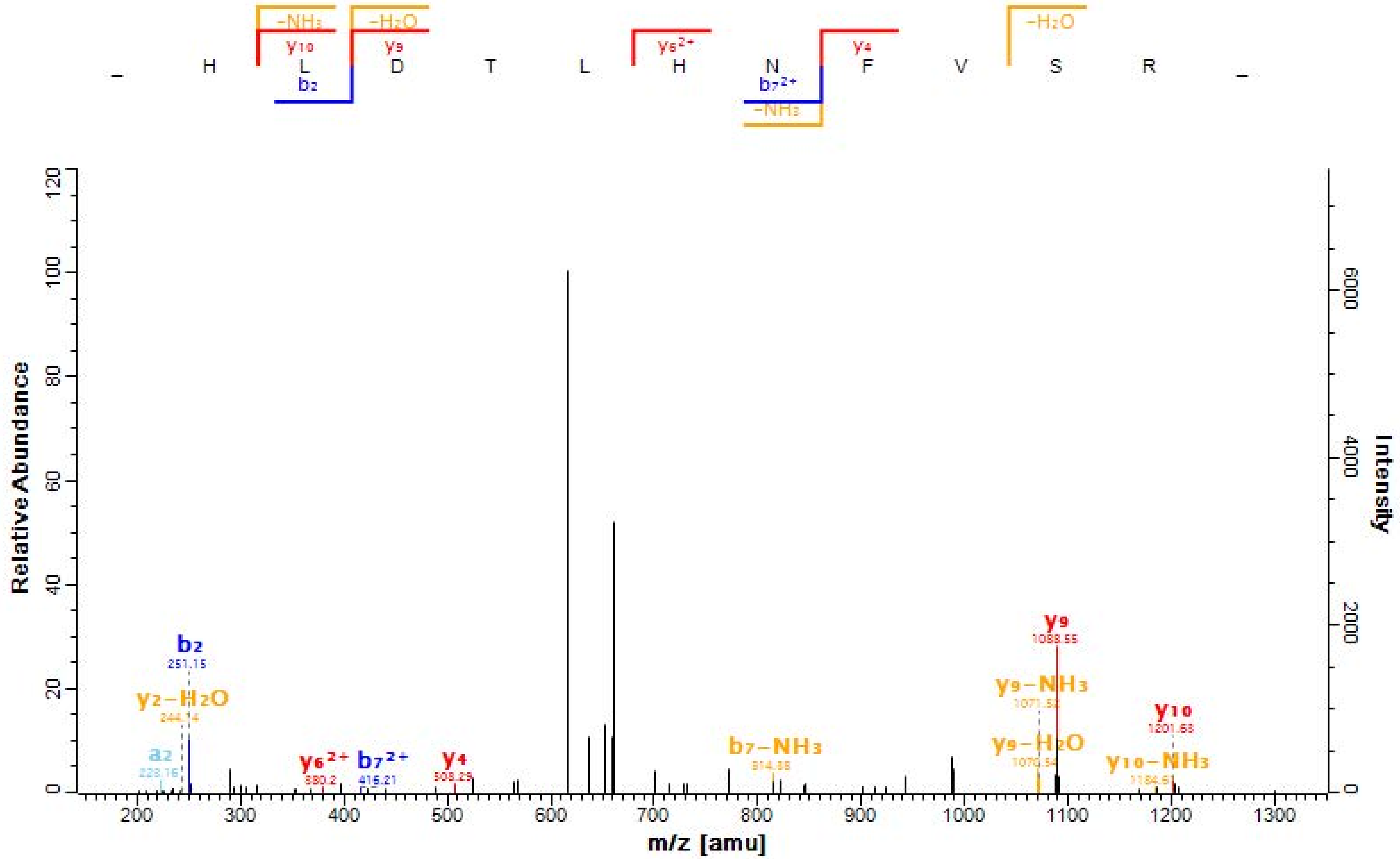
Mass:	1846.74687
m/z:	616.58957
Charge:	3+
Retentiontime:	10.150964736938
Score:	150.3361
Mass Error [ppm]:	0.37777
PEP:	1.6725E-15
Precursor Type:	MULTI

general information

Annotation:	9 of 16
AminoAcids Coverag	56 %
Intensity Coverage:	51 %
Peak Coverage:	26 %
Protein Localisation:	333 ... 348

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	15				
	267.11		267.11	2	H	14	1718.7		1718.7	
	324.13		324.13	3	G	13	1581.7		1581.7	
	452.19		452.19	4	Q	12	1524.6		1524.6	
	612.22		612.22	5	C	11	1396.6		1396.6	
	683.26		683.26	6	A	10	1236.5		1236.5	
+0.0295	399.65		798.28	7	D	9	1165.5	+0.1824	1165.5	
+0.2178	449.18	+0.1192	897.35	8	V	8	1050.5	-0.024	525.74	+0.1905
+0.0077	506.69		1012.4	9	D	7	951.41	-0.044	476.21	+0.0289
+0.2115	571.21	-0.15	1141.4	10	E	6	836.38	-0.089	836.38	
+0.0392	651.23		1301.5	11	C	5	707.34	+0.0599	707.34	
+0.0565	694.75	-0.16	1388.5	12	S	4	547.31	-0.001	547.31	
-0.027	751.29	+0.2456	1501.6	13	L	3	460.28		460.28	
-0.061	786.81		1572.6	14	A	2	347.19	+0.0759	347.19	
-0.032	851.33		1701.6	15	E	1	276.16	+0.0767	276.16	
				16	K	0	147.11		147.11	

Scan number	1149	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	60.52



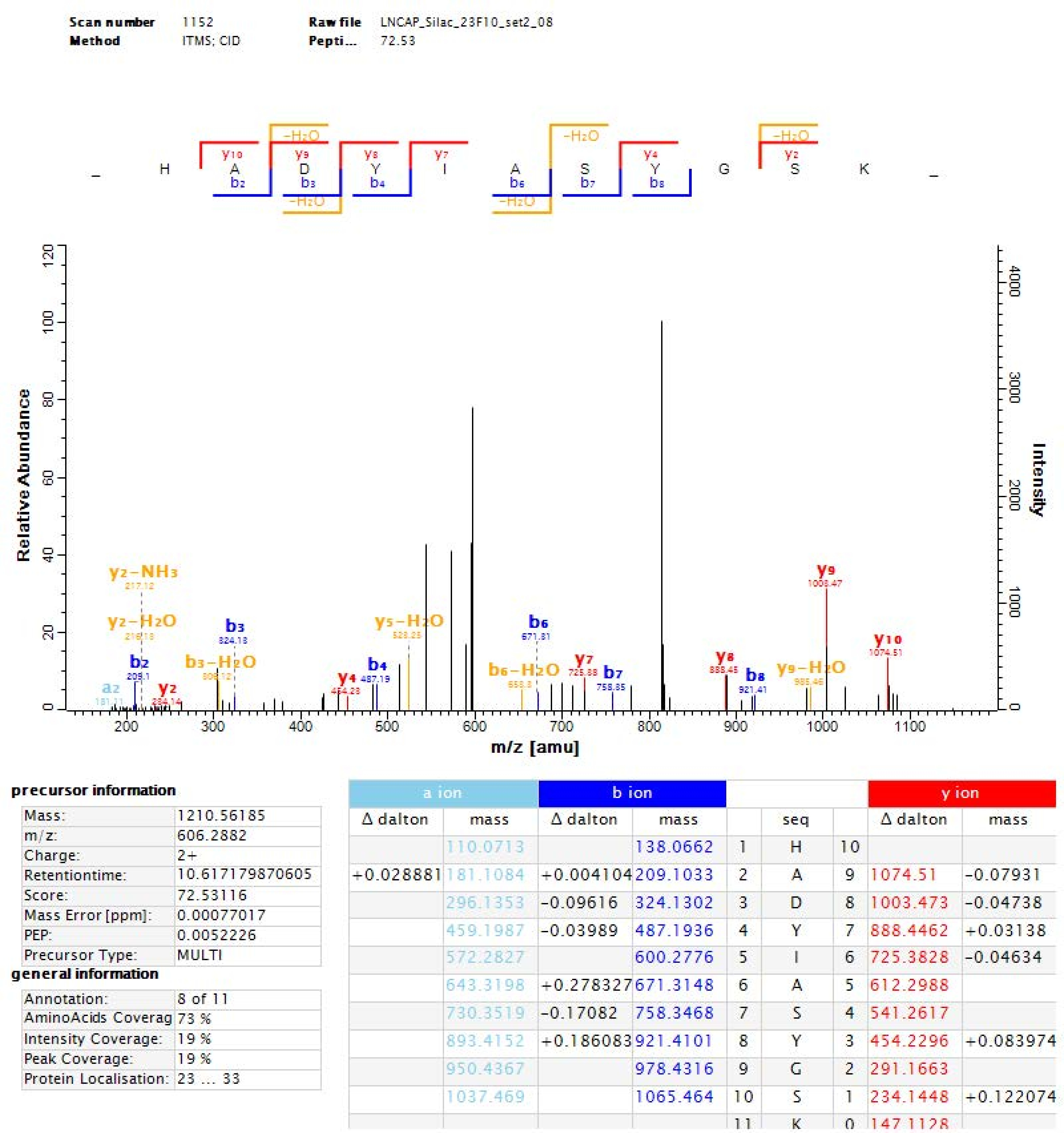
precursor information

Mass:	1337.68311
m/z:	669.84883
Charge:	2+
Retentiontime:	10.601613044738
Score:	60.51846
Mass Error [ppm]:	-0.68974
PEP:	0.01371
Precursor Type:	MULTI

general information

Annotation:	6 of 11
AminoAcids Coverag	55 %
Intensity Coverage:	17 %
Peak Coverage:	14 %
Protein Localisation:	702 ... 712

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	110.1		138.1		138.1	1	H	10				
+0.039	223.2		251.2	-0.05	251.2	2	L	9	1202	-0.11	1202	
	338.2		366.2		366.2	3	D	8	1089	-0.01	1089	
	439.2		467.2		467.2	4	T	7	973.5		973.5	
	552.3		580.3		580.3	5	L	6	872.5		872.5	
	689.4		717.4		717.4	6	H	5	759.4		380.2	+0.19
	803.4	+0.129	416.2		831.4	7	N	4	622.3		622.3	
	950.5		978.5		978.5	8	F	3	508.3	+0.111	508.3	
	1050		1078		1078	9	V	2	361.2		361.2	
	1137		1165		1165	10	S	1	262.2		262.2	
						11	R	0	175.1		175.1	



Scan number	1152	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	72.53

precursor information

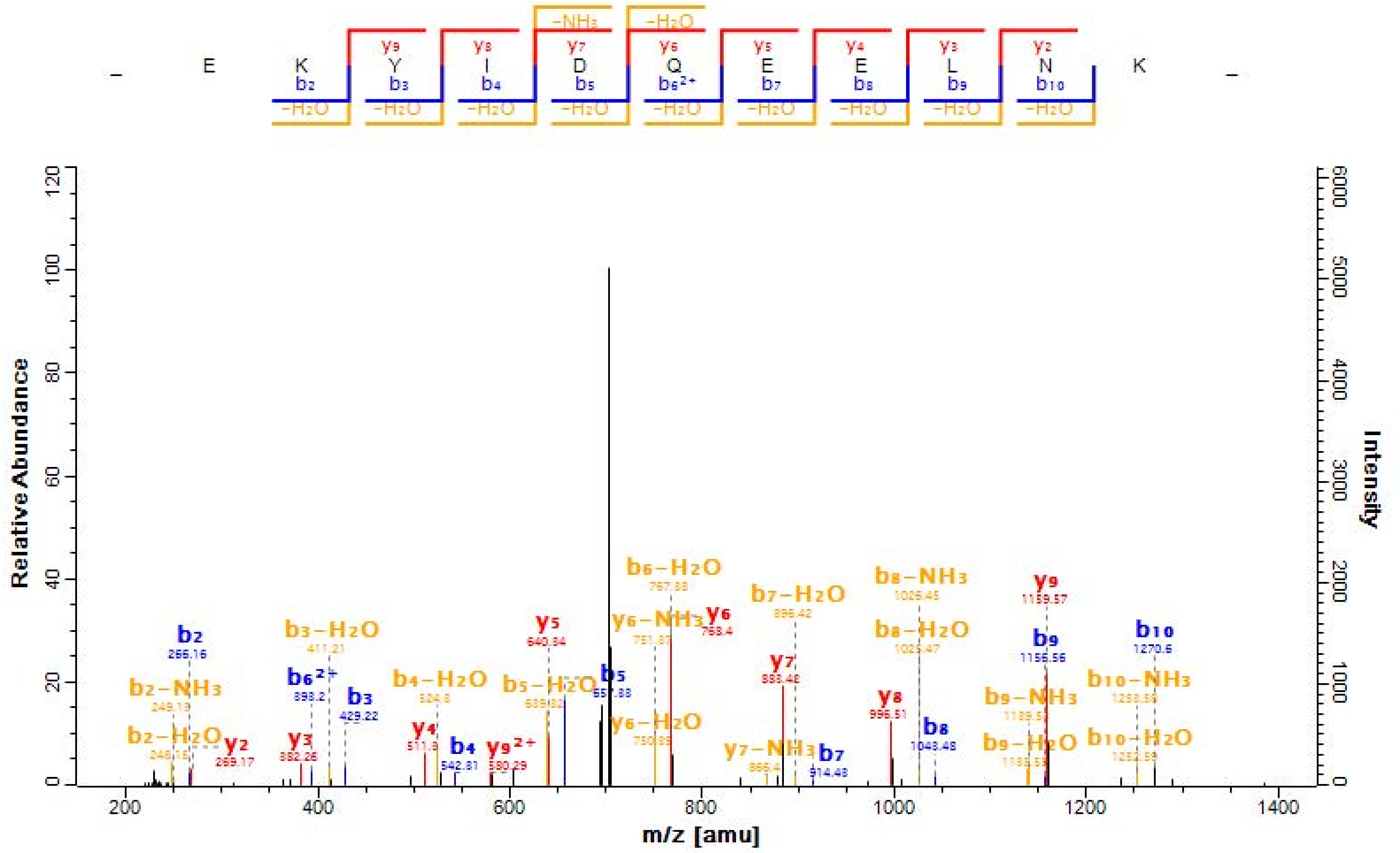
Mass:	1210.56185
m/z:	606.2882
Charge:	2+
Retentiontime:	10.617179870605
Score:	72.53116
Mass Error [ppm]:	0.00077017
PEP:	0.0052226
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	19 %
Peak Coverage:	19 %
Protein Localisation:	23 ... 33

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	110.0713		138.0662	1	H	10		
+0.028881	181.1084	+0.004104	209.1033	2	A	9	1074.51	-0.07931
	296.1353	-0.09616	324.1302	3	D	8	1003.473	-0.04738
	459.1987	-0.03989	487.1936	4	Y	7	888.4462	+0.03138
	572.2827		600.2776	5	I	6	725.3828	-0.04634
	643.3198	+0.278327	671.3148	6	A	5	612.2988	
	730.3519	-0.17082	758.3468	7	S	4	541.2617	
	893.4152	+0.186083	921.4101	8	Y	3	454.2296	+0.083974
	950.4367		978.4316	9	G	2	291.1663	
	1037.469		1065.464	10	S	1	234.1448	+0.122074
				11	K	0	147.1128	

Scan number	1295	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	228.12



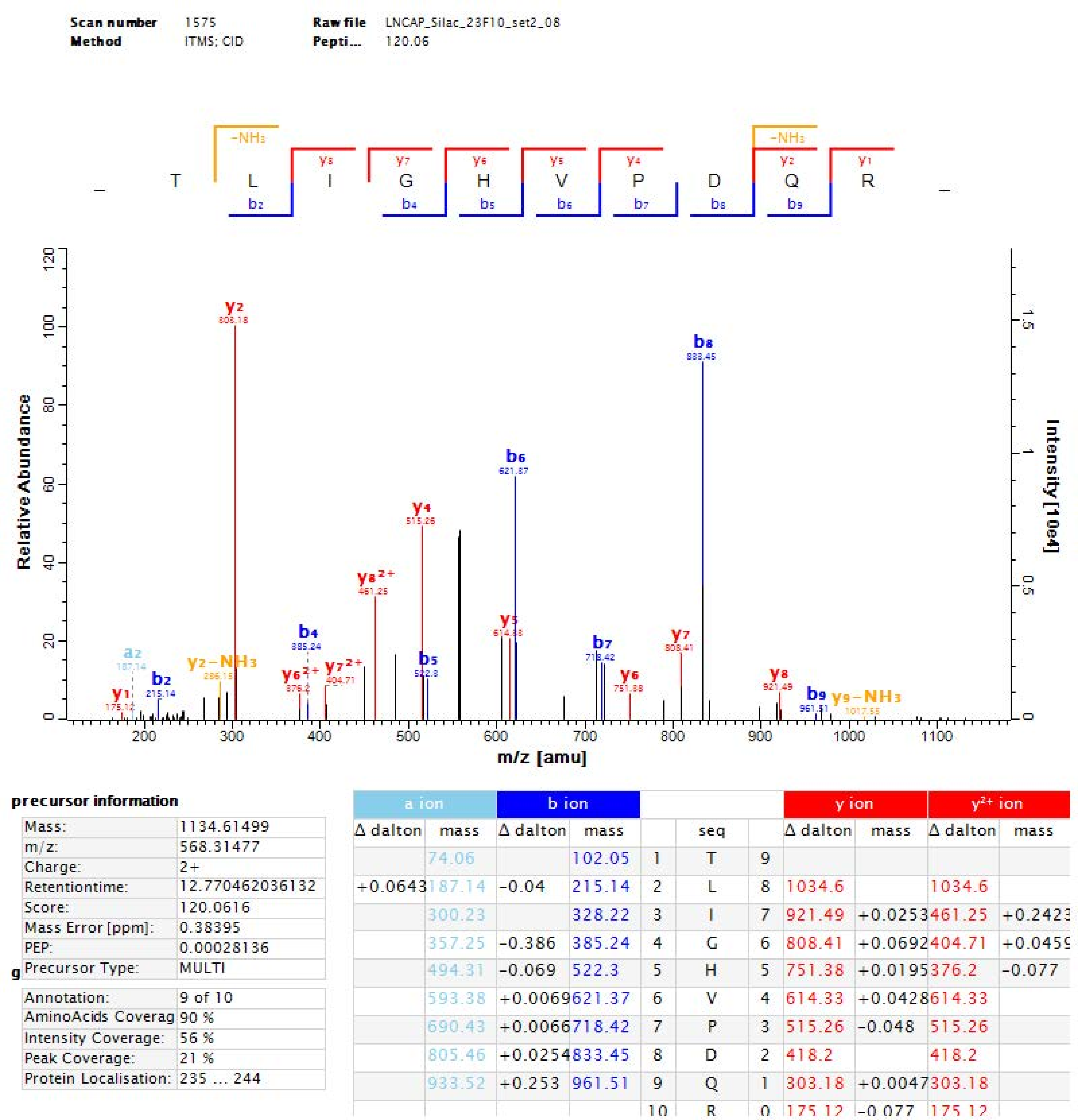
precursor information

Mass:	1407.6884
m/z:	704.85148
Charge:	2+
Retentiontime:	11.335071563720
Score:	228.1163
Mass Error [ppm]:	0.15904
PEP:	1.3525E-21
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	50 %
Peak Coverage:	38 %
Protein Localisation:	404 ... 414

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	10				
	266.16	-0.131	266.16	2	K	9	1295.7		1295.7	
	429.22	-0.096	429.22	3	Y	8	1159.6	-0.008	580.29	-0.061
	542.31	+0.1324	542.31	4	I	7	996.51	-0.088	996.51	
	657.33	+0.1165	657.33	5	D	6	883.42	-0.036	883.42	
+0.1048	393.2		785.39	6	Q	5	768.4	+0.0455	768.4	
	914.43	+0.1731	914.43	7	E	4	640.34	+0.0104	640.34	
	1043.5	-0.395	1043.5	8	E	3	511.3	+0.0702	511.3	
	1156.6	-0.078	1156.6	9	L	2	382.25	+0.0754	382.25	
	1270.6	+0.1049	1270.6	10	N	1	269.17	-0.165	269.17	
				11	K	0	155.13		155.13	



Scan number	1575	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	120.06

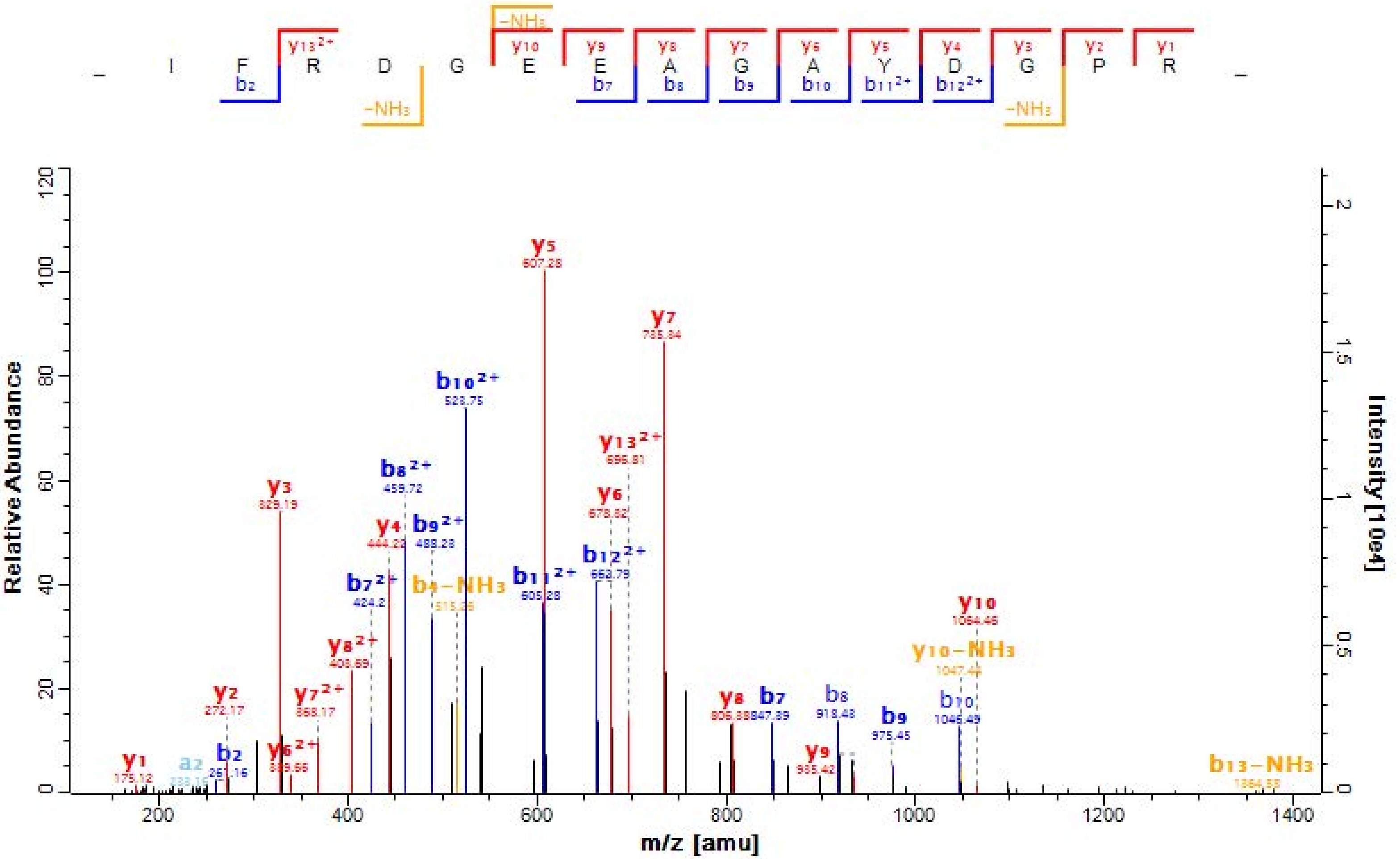
precursor information

Mass:	1134.61499
m/z:	568.31477
Charge:	2+
Retentiontime:	12.770462036132
Score:	120.0616
Mass Error [ppm]:	0.38395
PEP:	0.00028136
Precursor Type:	MULTI

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	56 %
Peak Coverage:	21 %
Protein Localisation:	235 ... 244

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.05	1	T	9				
+0.0643	187.14	-0.04	215.14	2	L	8	1034.6		1034.6	
	300.23		328.22	3	I	7	921.49	+0.0253	461.25	+0.2423
	357.25	-0.386	385.24	4	G	6	808.41	+0.0692	404.71	+0.0459
	494.31	-0.069	522.3	5	H	5	751.38	+0.0195	376.2	-0.077
	593.38	+0.0069	621.37	6	V	4	614.33	+0.0428	614.33	
	690.43	+0.0066	718.42	7	P	3	515.26	-0.048	515.26	
	805.46	+0.0254	833.45	8	D	2	418.2		418.2	
	933.52	+0.253	961.51	9	Q	1	303.18	+0.0047	303.18	
				10	R	0	175.12	-0.077	175.12	

Scan number	1706	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	155.43



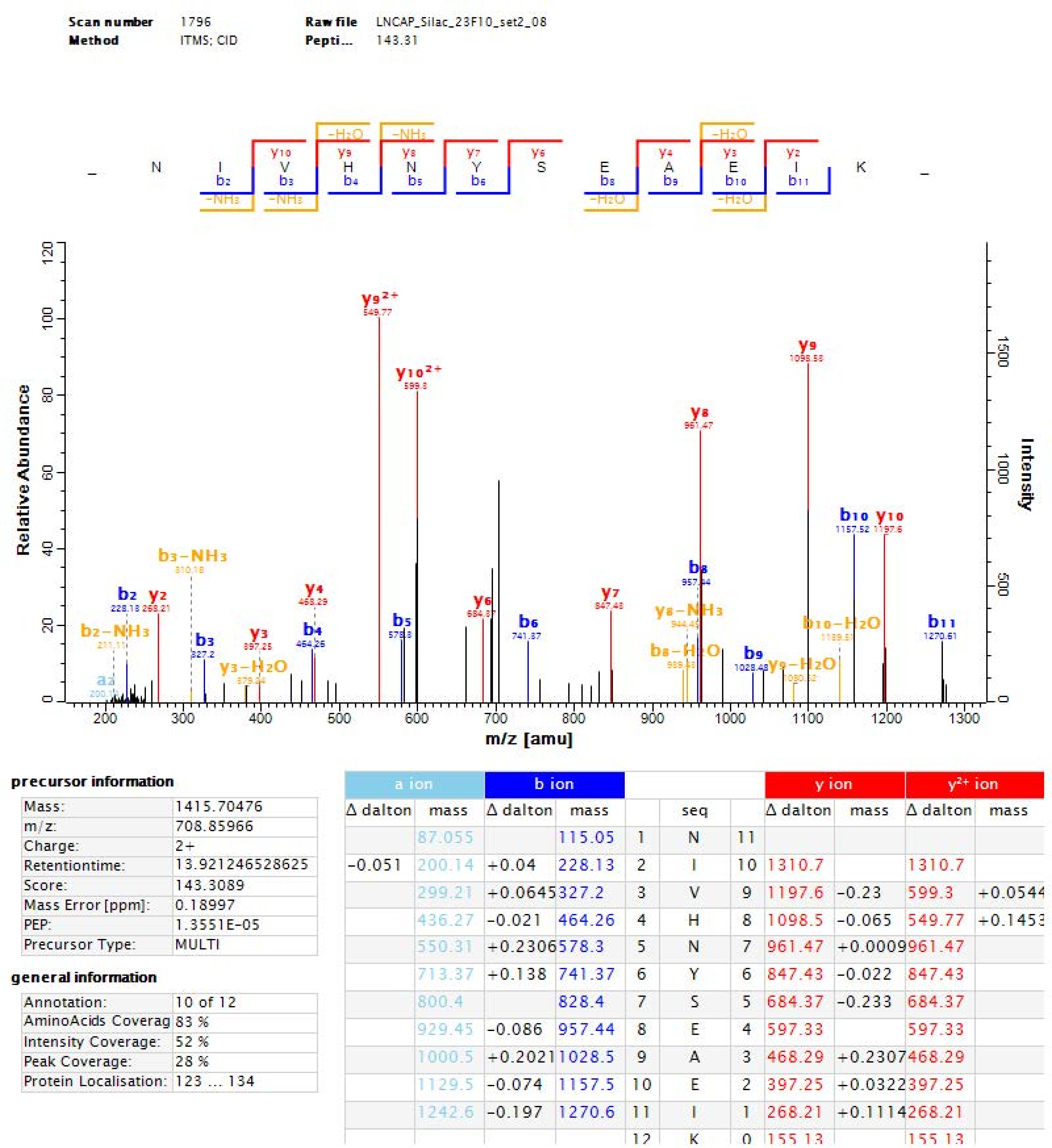
precursor information

Mass:	1651.75898
m/z:	551.5936
Charge:	3+
Retentiontime:	13.451230049133
Score:	155.4334
Mass Error [ppm]:	-0.044085
PEP:	4.8213E-09
Precursor Type:	ISO

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	70 %
Peak Coverage:	27 %
Protein Localisation:	105 ... 119

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	I	14				
-0.1	233.2		261.2	-0.15	261.2	2	F	13	1540		1540	
	389.3		417.3		417.3	3	R	12	1393		696.8	+0.26
	504.3		532.3		532.3	4	D	11	1237		1237	
	561.3		589.3		589.3	5	G	10	1121		1121	
	690.4		718.4		718.4	6	E	9	1064	-0.01	1064	
	819.4	+0.029	424.2	+0.018	847.4	7	E	8	935.4	+0.098	935.4	
	890.4	+0.088	459.7	+0	918.4	8	A	7	806.4	+0.084	403.7	+0.01
	947.5	+0.217	488.2	+0.191	975.5	9	G	6	735.3	+0.092	368.2	+0.11
	1018	+0.19	523.7	+0.008	1046	10	A	5	678.3	+0.046	339.7	+0.08
	1182	+0.165	605.3		1210	11	Y	4	607.3	-0.04	607.3	
	1297	+0.287	662.8		1325	12	D	3	444.2	-0.01	444.2	
	1354		1382		1382	13	G	2	329.2	-0.04	329.2	
	1451		1479		1479	14	P	1	272.2	+0.153	272.2	
						15	R	0	175.1	-0.07	175.1	



Scan number	1796	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	143.31

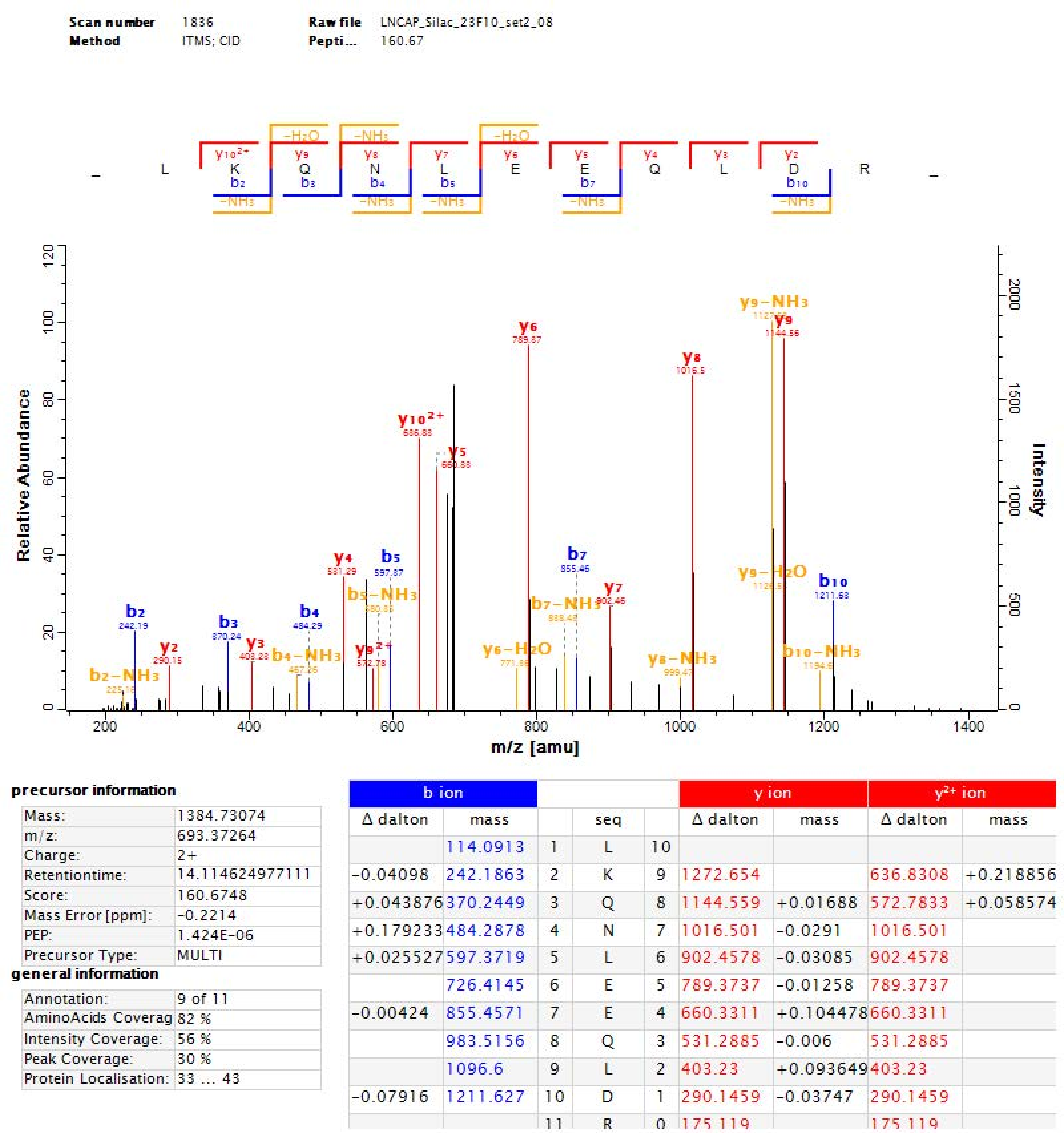
precursor information

Mass:	1415.70476
m/z:	708.85966
Charge:	2+
Retentiontime:	13.921246528625
Score:	143.3089
Mass Error [ppm]:	0.18997
PEP:	1.3551E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	52 %
Peak Coverage:	28 %
Protein Localisation:	123 ... 134

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	87.055		115.05	1	N	11				
-0.051	200.14	+0.04	228.13	2	I	10	1310.7		1310.7	
	299.21	+0.0645	327.2	3	V	9	1197.6	-0.23	599.3	+0.0544
	436.27	-0.021	464.26	4	H	8	1098.5	-0.065	549.77	+0.1453
	550.31	+0.2306	578.3	5	N	7	961.47	+0.0009	961.47	
	713.37	+0.138	741.37	6	Y	6	847.43	-0.022	847.43	
	800.4		828.4	7	S	5	684.37	-0.233	684.37	
	929.45	-0.086	957.44	8	E	4	597.33		597.33	
	1000.5	+0.2021	1028.5	9	A	3	468.29	+0.2307	468.29	
	1129.5	-0.074	1157.5	10	E	2	397.25	+0.0322	397.25	
	1242.6	-0.197	1270.6	11	I	1	268.21	+0.1114	268.21	
				12	K	0	155.13		155.13	



Scan number 1836 **Raw file** LNCAP_Silac_23F10_set2_08

Method ITMS; CID **Pepti...** 160.67

precursor information

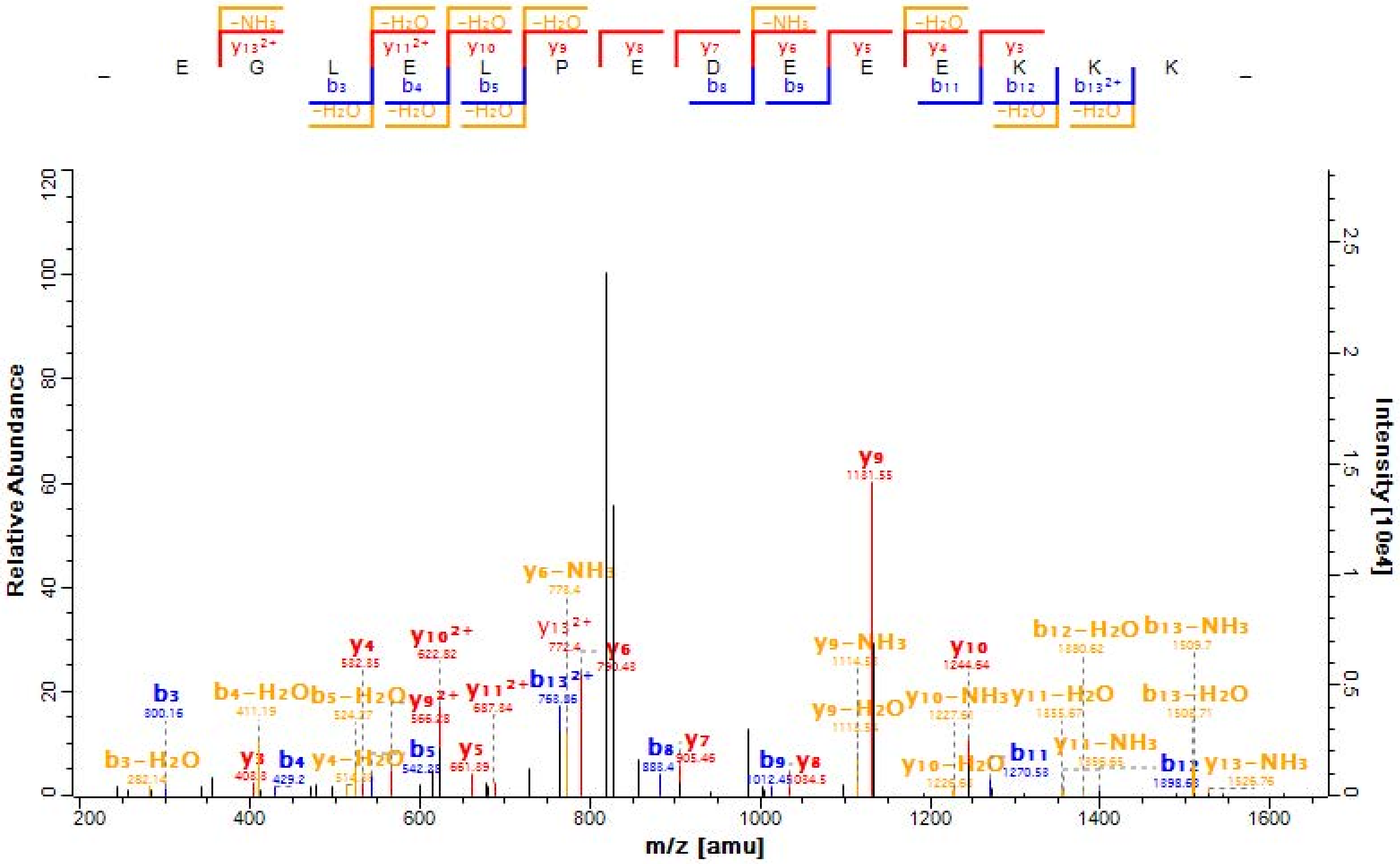
Mass:	1384.73074
m/z:	693.37264
Charge:	2+
Retentiontime:	14.114624977111
Score:	160.6748
Mass Error [ppm]:	-0.2214
PEP:	1.424E-06
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	56 %
Peak Coverage:	30 %
Protein Localisation:	33 ... 43

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	10				
-0.04098	242.1863	2	K	9	1272.654		636.8308	+0.218856
+0.043876	370.2449	3	Q	8	1144.559	+0.01688	572.7833	+0.058574
+0.179233	484.2878	4	N	7	1016.501	-0.0291	1016.501	
+0.025527	597.3719	5	L	6	902.4578	-0.03085	902.4578	
	726.4145	6	E	5	789.3737	-0.01258	789.3737	
-0.00424	855.4571	7	E	4	660.3311	+0.104478	660.3311	
	983.5156	8	Q	3	531.2885	-0.006	531.2885	
	1096.6	9	L	2	403.23	+0.093649	403.23	
-0.07916	1211.627	10	D	1	290.1459	-0.03747	290.1459	
		11	R	0	175.119		175.119	

Scan number	1854	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	220.53

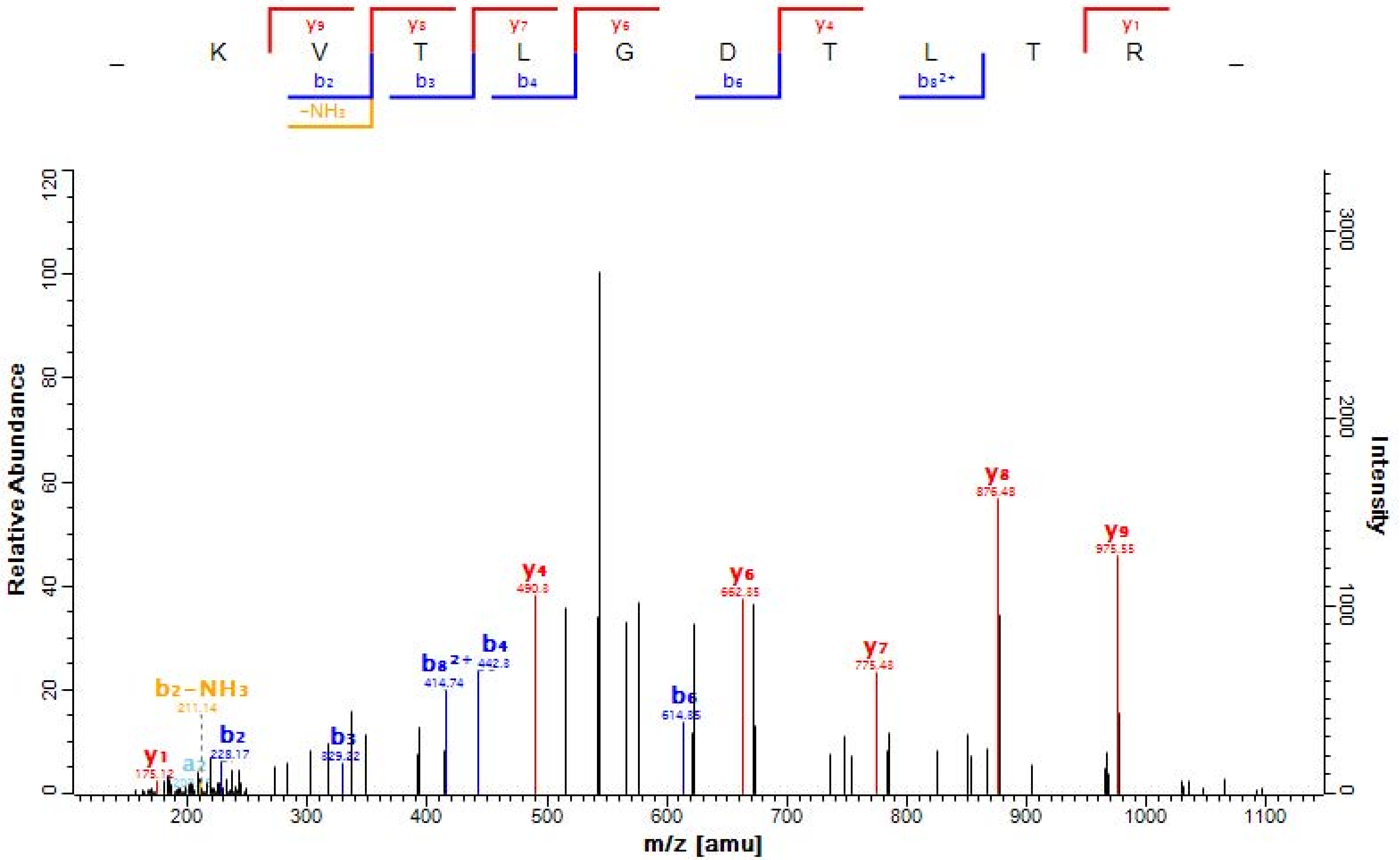


precursor information	
Mass:	1671.82032
m/z:	836.91744
Charge:	2+
Retentiontime:	14.204671859741
Score:	220.5303
Mass Error [ppm]:	0.0057468
PEP:	8.3924E-35
Precursor Type:	ISO

general information	
Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	46 %
Peak Coverage:	45 %
Protein Localisation:	669 ... 682

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	13				
	187.07		187.07	2	G	12	1543.8		772.4	+0.0099
	300.16	+0.0556	300.16	3	L	11	1486.8		1486.8	
	429.2	+0.0376	429.2	4	E	10	1373.7		687.34	+0.4359
	542.28	+0.066	542.28	5	L	9	1244.6	-0.113	622.82	+0.0321
	639.33		639.33	6	P	8	1131.6	+0.0051	566.28	+0.1762
	768.38		768.38	7	E	7	1034.5	+0.181	1034.5	
	883.4	-0.072	883.4	8	D	6	905.46	+0.1224	905.46	
	1012.4	+0.0654	1012.4	9	E	5	790.43	+0.0169	790.43	
	1141.5		1141.5	10	E	4	661.39	+0.112	661.39	
	1270.5	+0.0719	1270.5	11	E	3	532.35	+0.0716	532.35	
	1398.6	+0.1382	1398.6	12	K	2	403.3	+0.1024	403.3	
-0.046	763.86		1526.7	13	K	1	275.21		275.21	
				14	K	0	147.11		147.11	

Scan number	1873	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	56.23

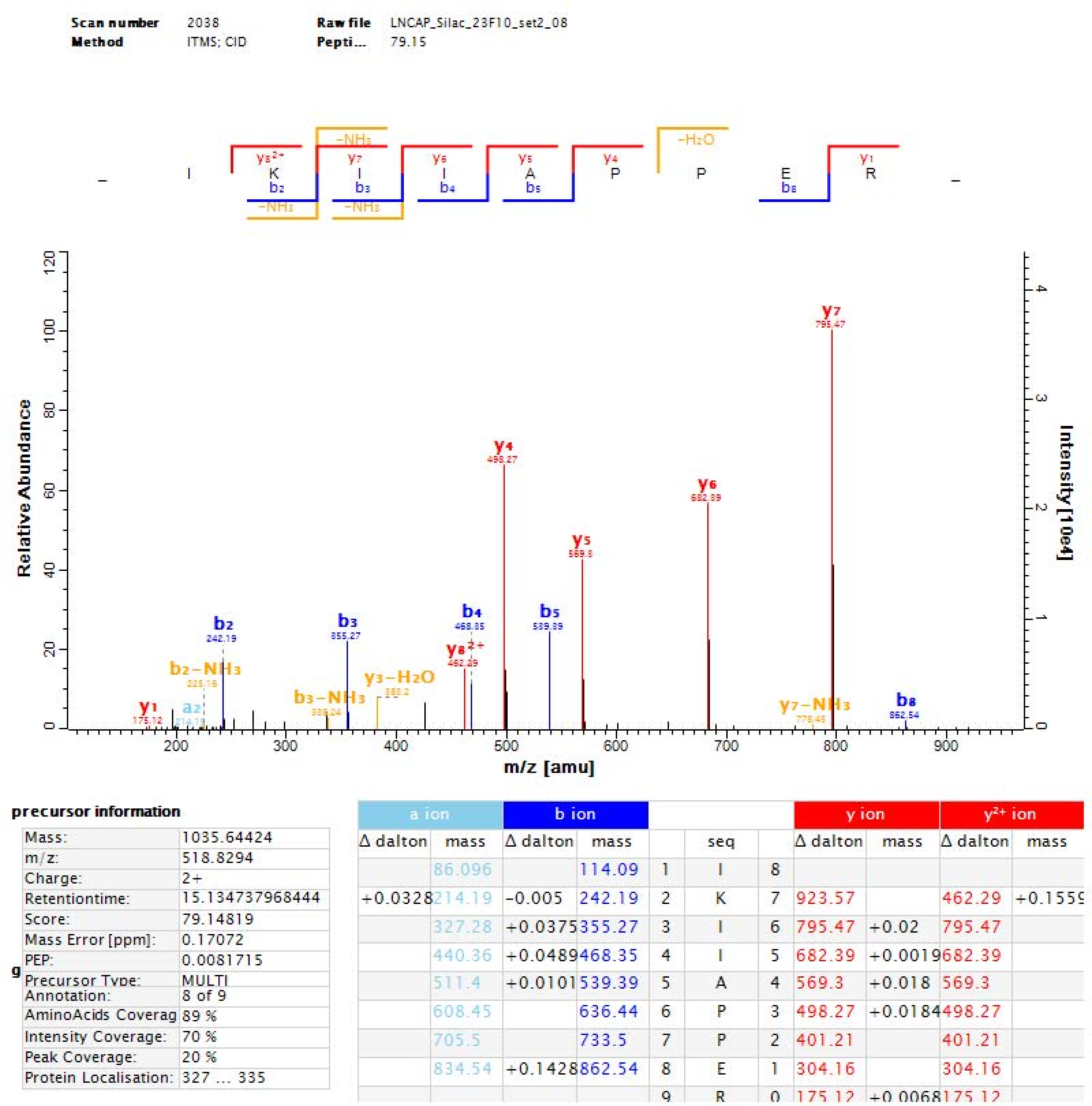


precursor information

Mass:	1102.6354
m/z:	552.32497
Charge:	2+
Retentiontime:	14.292401313781
Score:	56.22507
Mass Error [ppm]:	0.70203
PEP:	0.013158
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	27 %
Peak Coverage:	12 %
Protein Localisation:	874 ... 883

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	101.11		129.1		129.1	1	K	9		
-0.009	200.18		228.17	+0.0086	228.17	2	V	8	975.55	+0.0107
	301.22		329.22	+0.0002	329.22	3	T	7	876.48	+0.0102
	414.31		442.3	+0.4146	442.3	4	L	6	775.43	-0.093
	471.33		499.32		499.32	5	G	5	662.35	+0.0167
	586.36		614.35	-0.047	614.35	6	D	4	605.33	
	687.4		715.4		715.4	7	T	3	490.3	+0.0324
	800.49	+0.401	414.74		828.48	8	L	2	389.25	
	901.54		929.53		929.53	9	T	1	276.17	
						10	R	0	175.12	-0.004



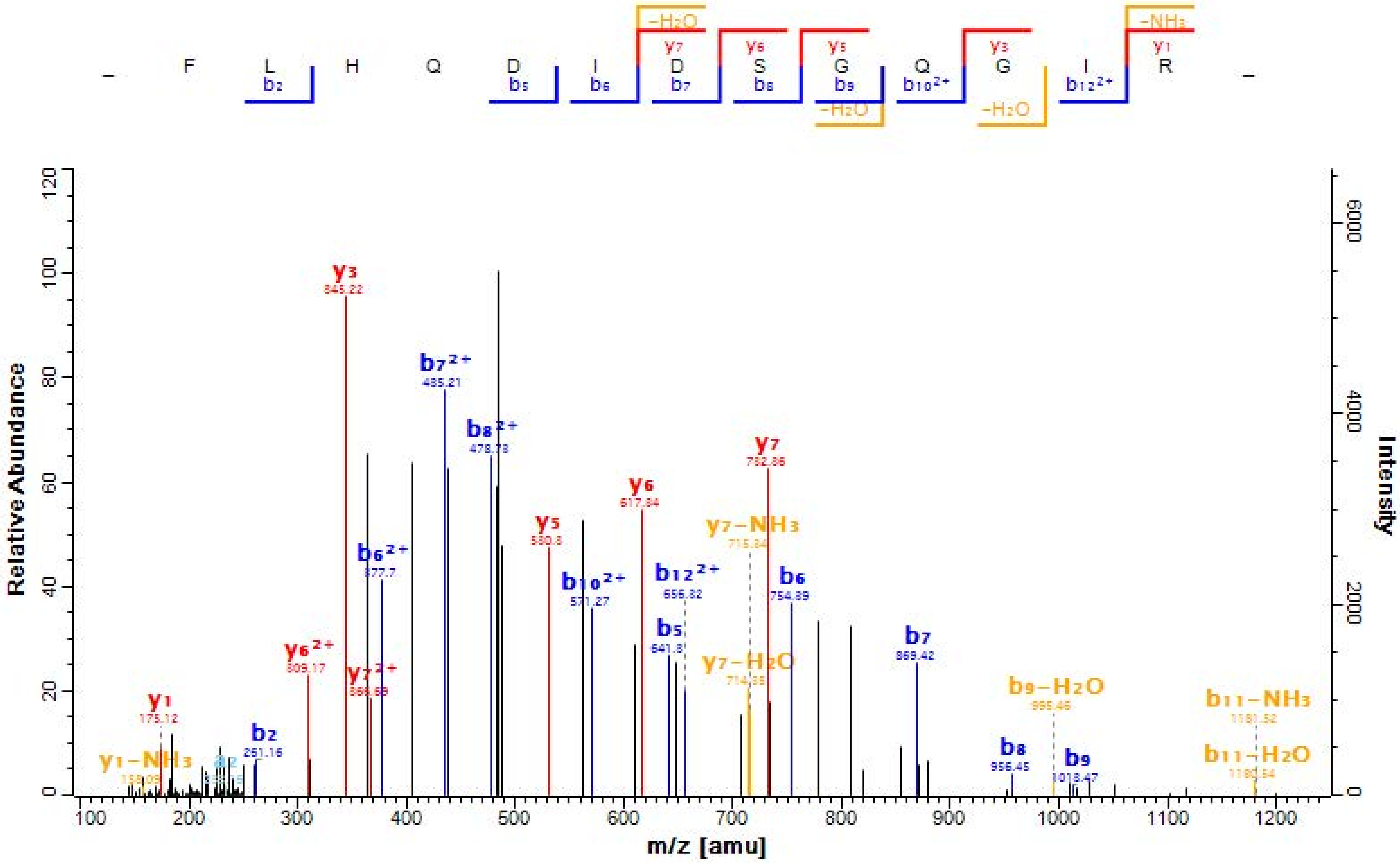
Scan number	2038	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	79.15

precursor information

Mass:	1035.64424
m/z:	518.8294
Charge:	2+
Retentiontime:	15.134737968444
Score:	79.14819
Mass Error [ppm]:	0.17072
PEP:	0.0081715
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	70 %
Peak Coverage:	20 %
Protein Localisation:	327 ... 335

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	8				
+0.0328	214.19	-0.005	242.19	2	K	7	923.57		462.29	+0.1559
	327.28	+0.0375	355.27	3	I	6	795.47	+0.02	795.47	
	440.36	+0.0489	468.35	4	I	5	682.39	+0.0019	682.39	
	511.4	+0.0101	539.39	5	A	4	569.3	+0.018	569.3	
	608.45		636.44	6	P	3	498.27	+0.0184	498.27	
	705.5		733.5	7	P	2	401.21		401.21	
	834.54	+0.1428	862.54	8	E	1	304.16		304.16	
				9	R	0	175.12	+0.0068	175.12	

Scan number	2072	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	120.57



precursor information

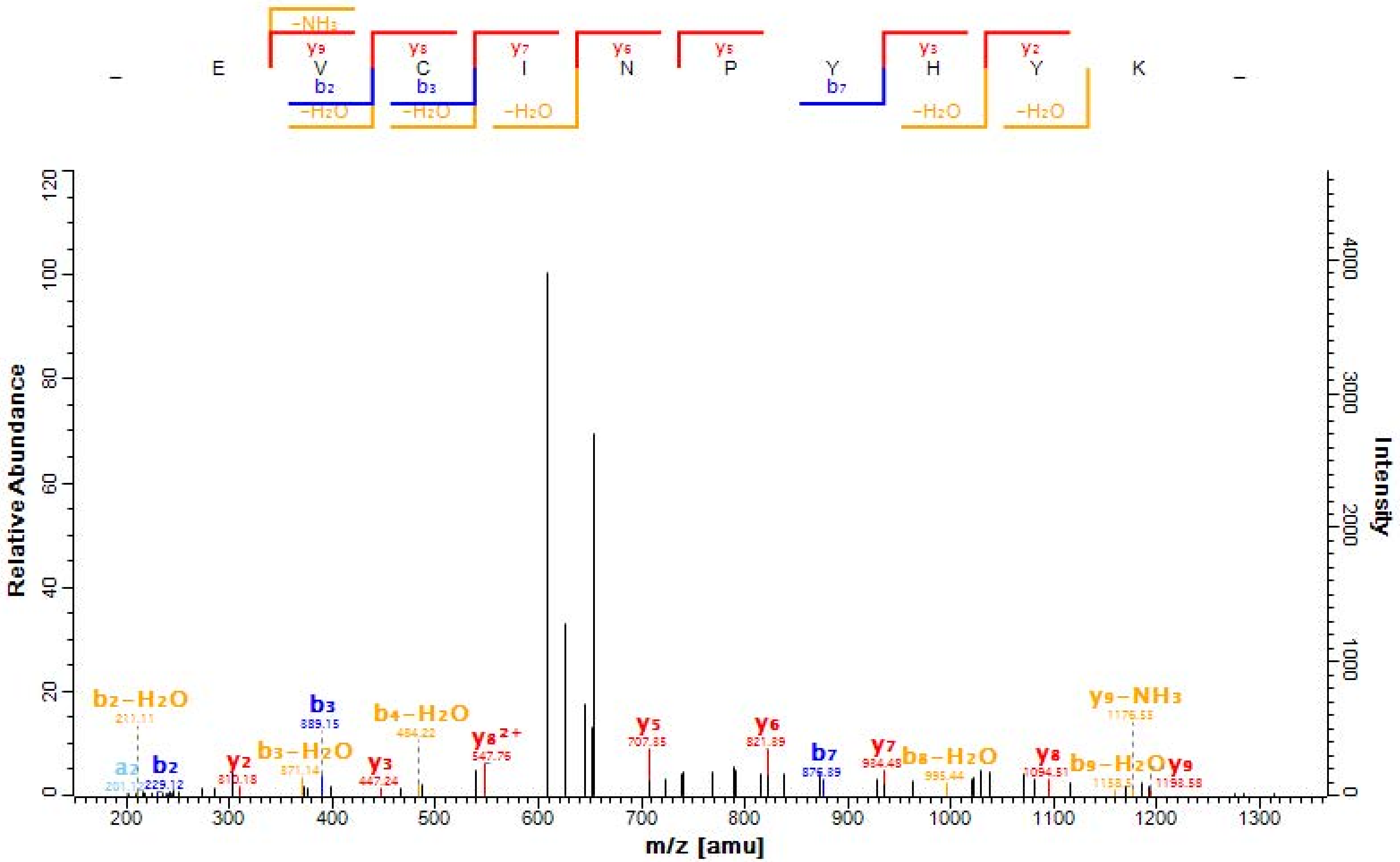
Mass:	1484.73688
m/z:	495.91957
Charge:	3+
Retentiontime:	15.308121681213
Score:	120.5736
Mass Error [ppm]:	-0.21229
PEP:	9.2888E-07
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	46 %
Peak Coverage:	22 %
Protein Localisation:	1053 ... 1065

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.1		148.1		148.1	1	F	12				
-0.05	233.2		261.2	+0.027	261.2	2	L	11	1339		1339	
	370.2		398.2		398.2	3	H	10	1226		1226	
	498.3		526.3		526.3	4	Q	9	1089		1089	
	613.3		641.3	+0.017	641.3	5	D	8	960.5		960.5	
	726.4	+0.155	377.7	-0.02	754.4	6	I	7	845.4		845.4	
	841.4	+0.18	435.2	+0.075	869.4	7	D	6	732.4	+0.047	366.7	+0.08
	928.5	-0.1	478.7	+0.17	956.4	8	S	5	617.3	+0	309.2	+0.13
	985.5		1013	+0.229	1013	9	G	4	530.3	+0.067	530.3	
	1114	+0.187	571.3		1142	10	Q	3	473.3		473.3	
	1171		1199		1199	11	G	2	345.2	+0.008	345.2	
	1284	+0.039	656.3		1312	12	I	1	288.2		288.2	
						13	R	0	175.1	-0.03	175.1	

Scan number	2619	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	75.51

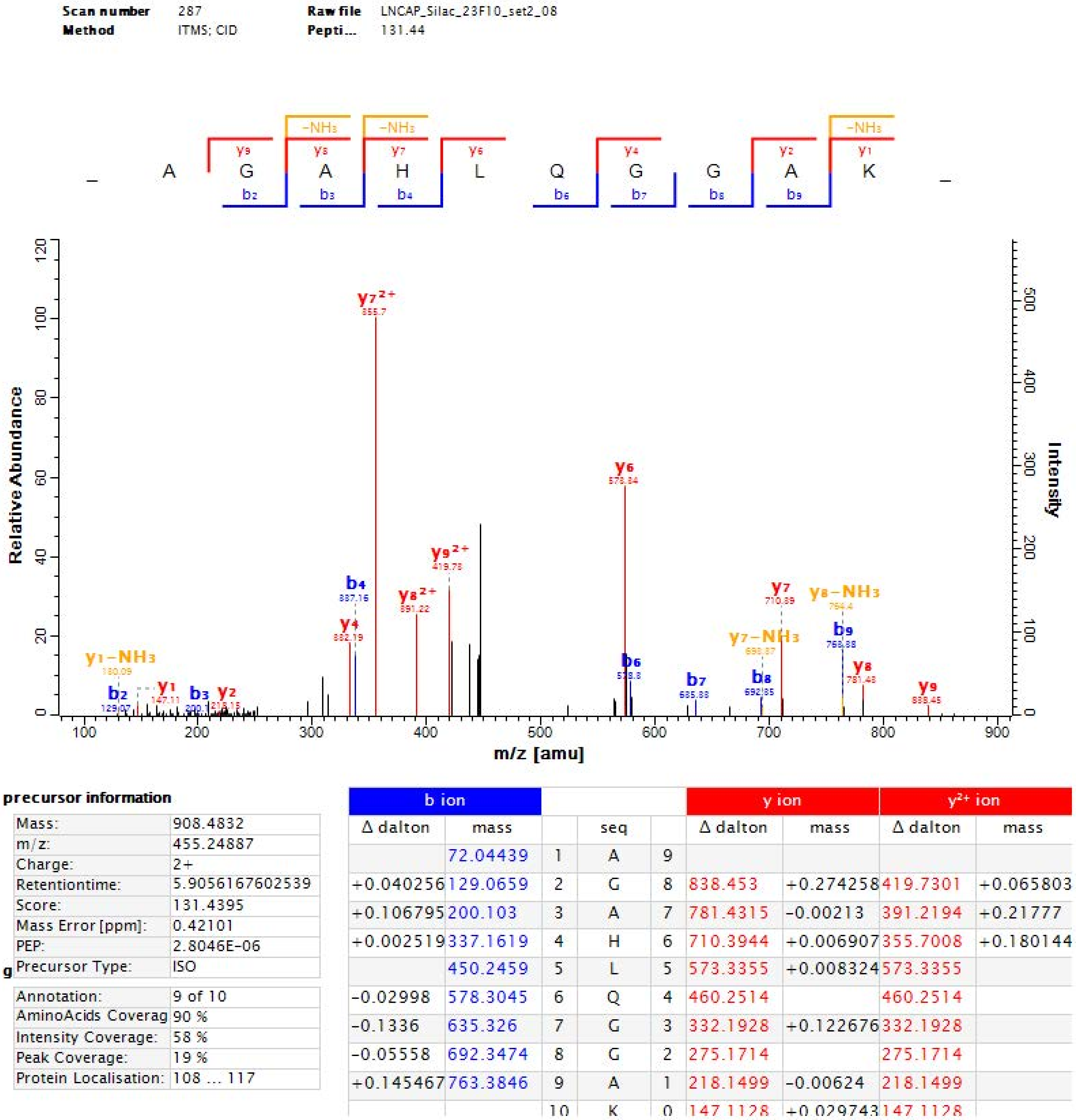


precursor information

Mass:	0
m/z:	661.81284
Charge:	0+
Retentiontime:	18.182144165039
Score:	75.50899
Mass Error [ppm]:	-1.0386
PEP:	0.020399
Precursor Type:	PEAK

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	12 %
Peak Coverage:	20 %
Protein Localisation:	120 ... 129

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	9				
+0.0274	201.12	+0.0094	229.12	2	V	8	1193.6	+0.0974	1193.6	
	361.15	+0.1442	389.15	3	C	7	1094.5	+0.1602	547.76	+0.1496
	474.24		502.23	4	I	6	934.48	+0.0629	934.48	
	588.28		616.28	5	N	5	821.39	+0.113	821.39	
	685.33		713.33	6	P	4	707.35	+0.1238	707.35	
	848.4	+0.1658	876.39	7	Y	3	610.3		610.3	
	985.46		1013.5	8	H	2	447.24	+0.0798	447.24	
	1148.5		1176.5	9	Y	1	310.18	+0.0974	310.18	
				10	K	0	147.11		147.11	



Scan number 287
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set2_08
Pepti... 131.44

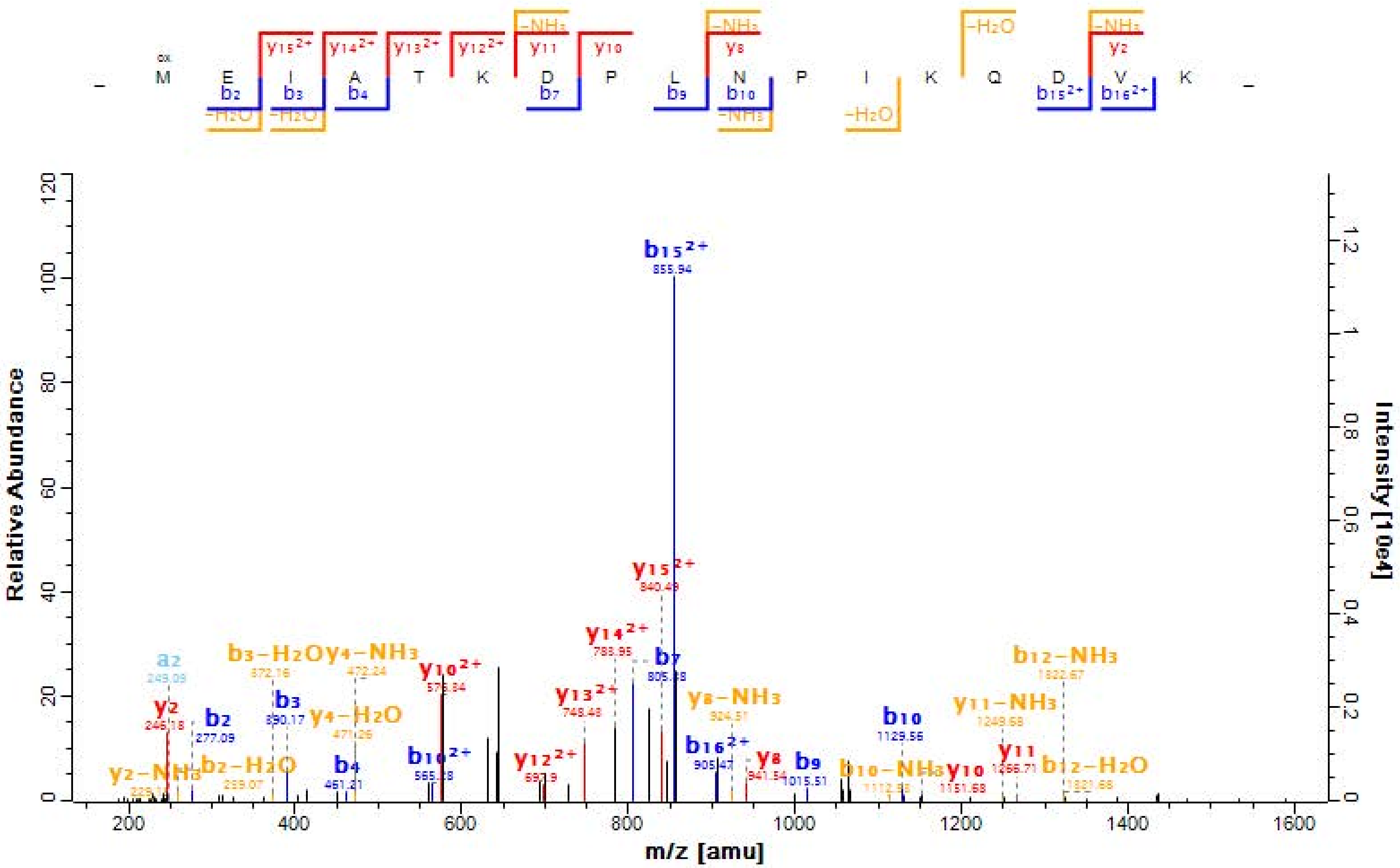
precursor information

Mass:	908.4832
m/z:	455.24887
Charge:	2+
Retentiontime:	5.9056167602539
Score:	131.4395
Mass Error [ppm]:	0.42101
PEP:	2.8046E-06
Precursor Type:	ISO

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	58 %
Peak Coverage:	19 %
Protein Localisation:	108 ... 117

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	9				
+0.040256	129.0659	2	G	8	838.453	+0.274258	419.7301	+0.065803
+0.106795	200.103	3	A	7	781.4315	-0.00213	391.2194	+0.21777
+0.002519	337.1619	4	H	6	710.3944	+0.006907	355.7008	+0.180144
	450.2459	5	L	5	573.3355	+0.008324	573.3355	
-0.02998	578.3045	6	Q	4	460.2514		460.2514	
-0.1336	635.326	7	G	3	332.1928	+0.122676	332.1928	
-0.05558	692.3474	8	G	2	275.1714		275.1714	
+0.145467	763.3846	9	A	1	218.1499	-0.00624	218.1499	
		10	K	0	147.1128	+0.029743	147.1128	

Scan number	2870	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	126.71



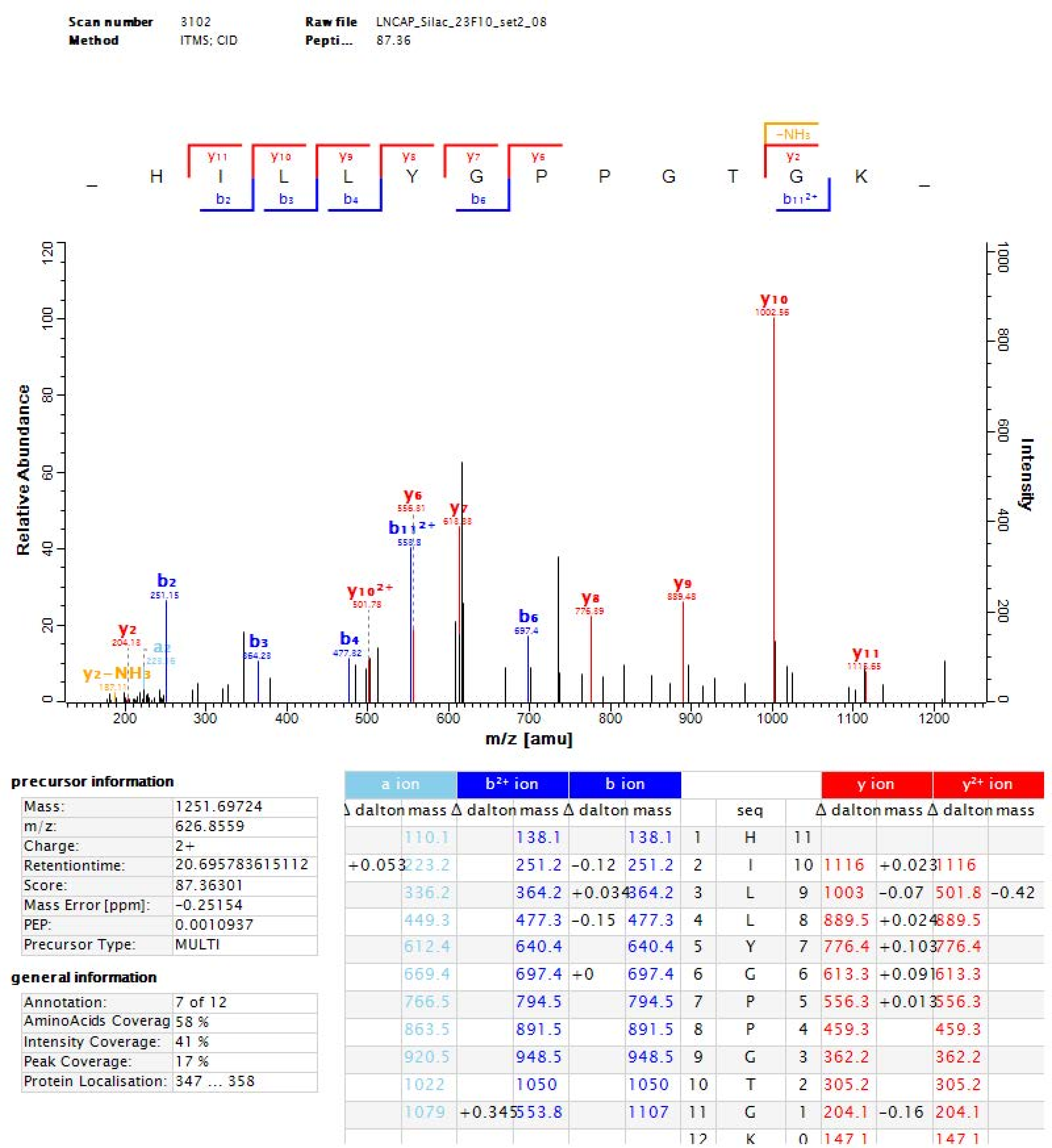
precursor information

Mass:	1955.03997
m/z:	652.68727
Charge:	3+
Retentiontime:	19.468547821044
Score:	126.7053
Mass Error [ppm]:	0.10777
PEP:	9.7106E-12
Precursor Type:	MULTI

general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	49 %
Peak Coverage:	26 %
Protein Localisation:	58 ... 74

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120		148		148	1	M	16				
-0.12	249.1		277.1	-0.05	277.1	2	E	15	1809		1809	
	362.2		390.2	+0.018	390.2	3	I	14	1680		840.5	+0.26
	433.2		461.2	+0.127	461.2	4	A	13	1567		783.9	+0
	534.3		562.3		562.3	5	T	12	1496		748.4	+0.22
	662.4		690.3		690.3	6	K	11	1395		697.9	-0.04
	777.4		805.4	-0.03	805.4	7	D	10	1267	-0.23	1267	
	874.4		902.4		902.4	8	P	9	1152	+0.298	576.3	+0
	987.5		1016	+0.001	1016	9	L	8	1055		1055	
	1102	+0.114	565.3	-0.02	1130	10	N	7	941.5	-0.11	941.5	
	1199		1227		1227	11	P	6	827.5		827.5	
	1312		1340		1340	12	I	5	730.4		730.4	
	1440		1468		1468	13	K	4	617.4		617.4	
	1568		1596		1596	14	Q	3	489.3		489.3	
	1683	+0.277	855.9		1711	15	D	2	361.2		361.2	
	1782	+0.335	905.5		1810	16	V	1	246.2	-0.06	246.2	
						17	K	0	147.1		147.1	



Scan number 3102 **Raw file** LNCAP_Silac_23F10_set2_08
Method ITMS; CID **Pepti...** 87.36

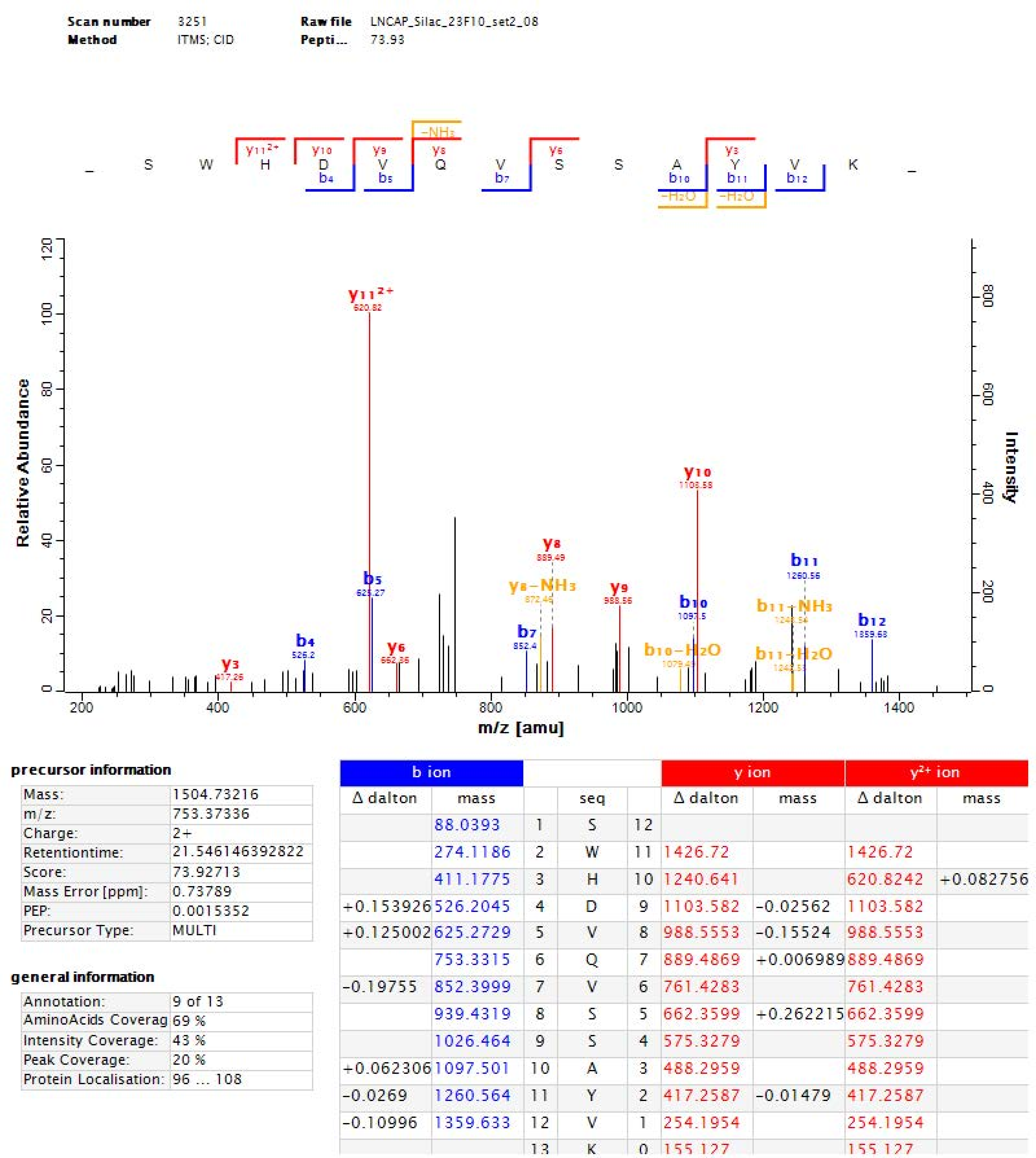
precursor information

Mass:	1251.69724
m/z:	626.8559
Charge:	2+
Retentiontime:	20.695783615112
Score:	87.36301
Mass Error [ppm]:	-0.25154
PEP:	0.0010937
Precursor Type:	MULTI

general information

Annotation:	7 of 12
AminoAcids Coverag	58 %
Intensity Coverage:	41 %
Peak Coverage:	17 %
Protein Localisation:	347 ... 358

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	110.1		138.1		138.1	1	H	11				
+0.053	223.2		251.2	-0.12	251.2	2	I	10	1116	+0.023	1116	
	336.2		364.2	+0.034	364.2	3	L	9	1003	-0.07	501.8	-0.42
	449.3		477.3	-0.15	477.3	4	L	8	889.5	+0.024	889.5	
	612.4		640.4		640.4	5	Y	7	776.4	+0.103	776.4	
	669.4		697.4	+0	697.4	6	G	6	613.3	+0.091	613.3	
	766.5		794.5		794.5	7	P	5	556.3	+0.013	556.3	
	863.5		891.5		891.5	8	P	4	459.3		459.3	
	920.5		948.5		948.5	9	G	3	362.2		362.2	
	1022		1050		1050	10	T	2	305.2		305.2	
	1079	+0.345	553.8		1107	11	G	1	204.1	-0.16	204.1	
						12	K	0	147.1		147.1	



Scan number	3251	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	73.93

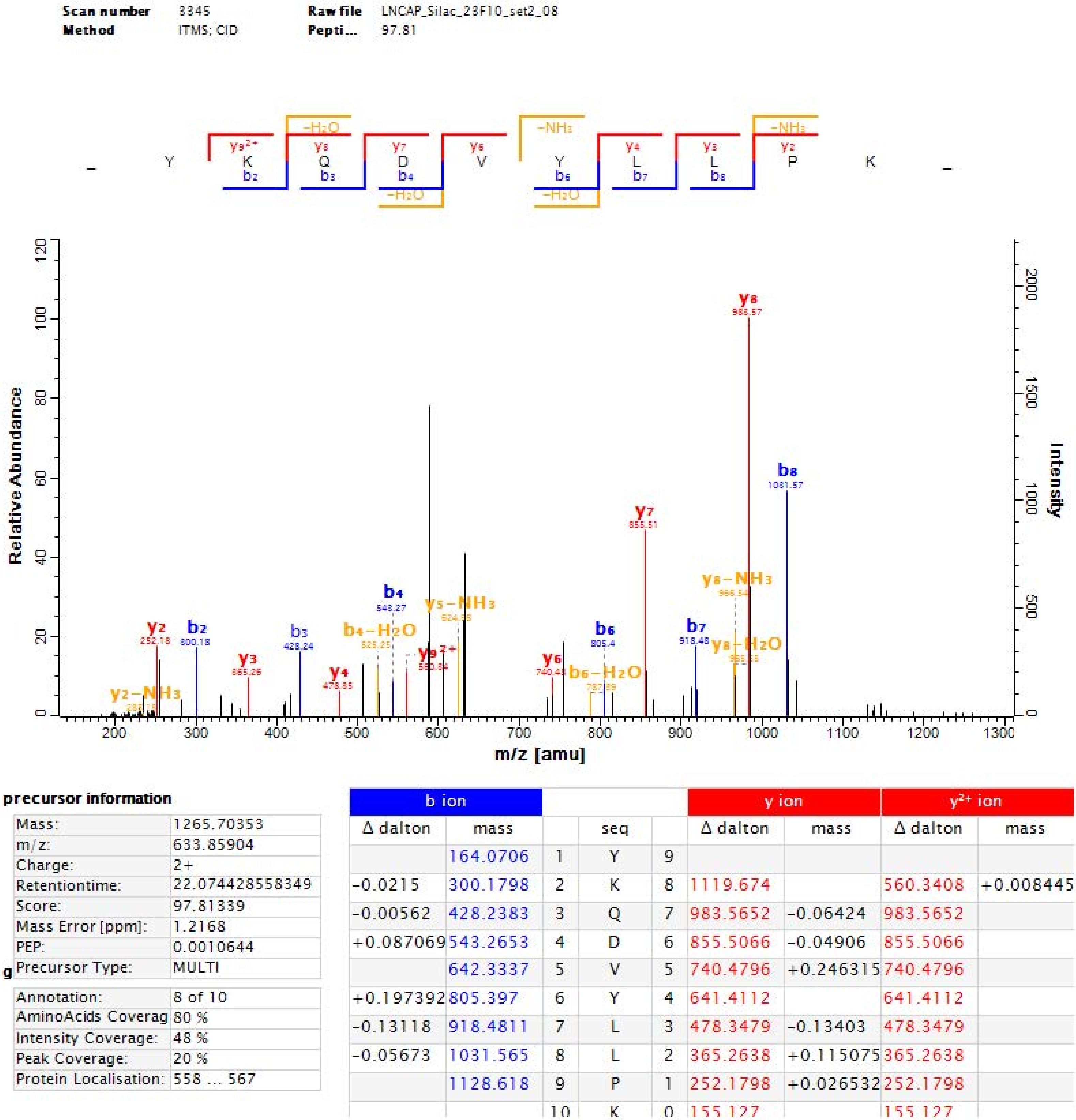
precursor information

Mass:	1504.73216
m/z:	753.37336
Charge:	2+
Retentiontime:	21.546146392822
Score:	73.92713
Mass Error [ppm]:	0.73789
PEP:	0.0015352
Precursor Type:	MULTI

general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	43 %
Peak Coverage:	20 %
Protein Localisation:	96 ... 108

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	12				
	274.1186	2	W	11	1426.72		1426.72	
	411.1775	3	H	10	1240.641		620.8242	+0.082756
+0.153926	526.2045	4	D	9	1103.582	-0.02562	1103.582	
+0.125002	625.2729	5	V	8	988.5553	-0.15524	988.5553	
	753.3315	6	Q	7	889.4869	+0.006989	889.4869	
-0.19755	852.3999	7	V	6	761.4283		761.4283	
	939.4319	8	S	5	662.3599	+0.262215	662.3599	
	1026.464	9	S	4	575.3279		575.3279	
+0.062306	1097.501	10	A	3	488.2959		488.2959	
-0.0269	1260.564	11	Y	2	417.2587	-0.01479	417.2587	
-0.10996	1359.633	12	V	1	254.1954		254.1954	
		13	K	0	155.127		155.127	



Scan number	3345	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	97.81

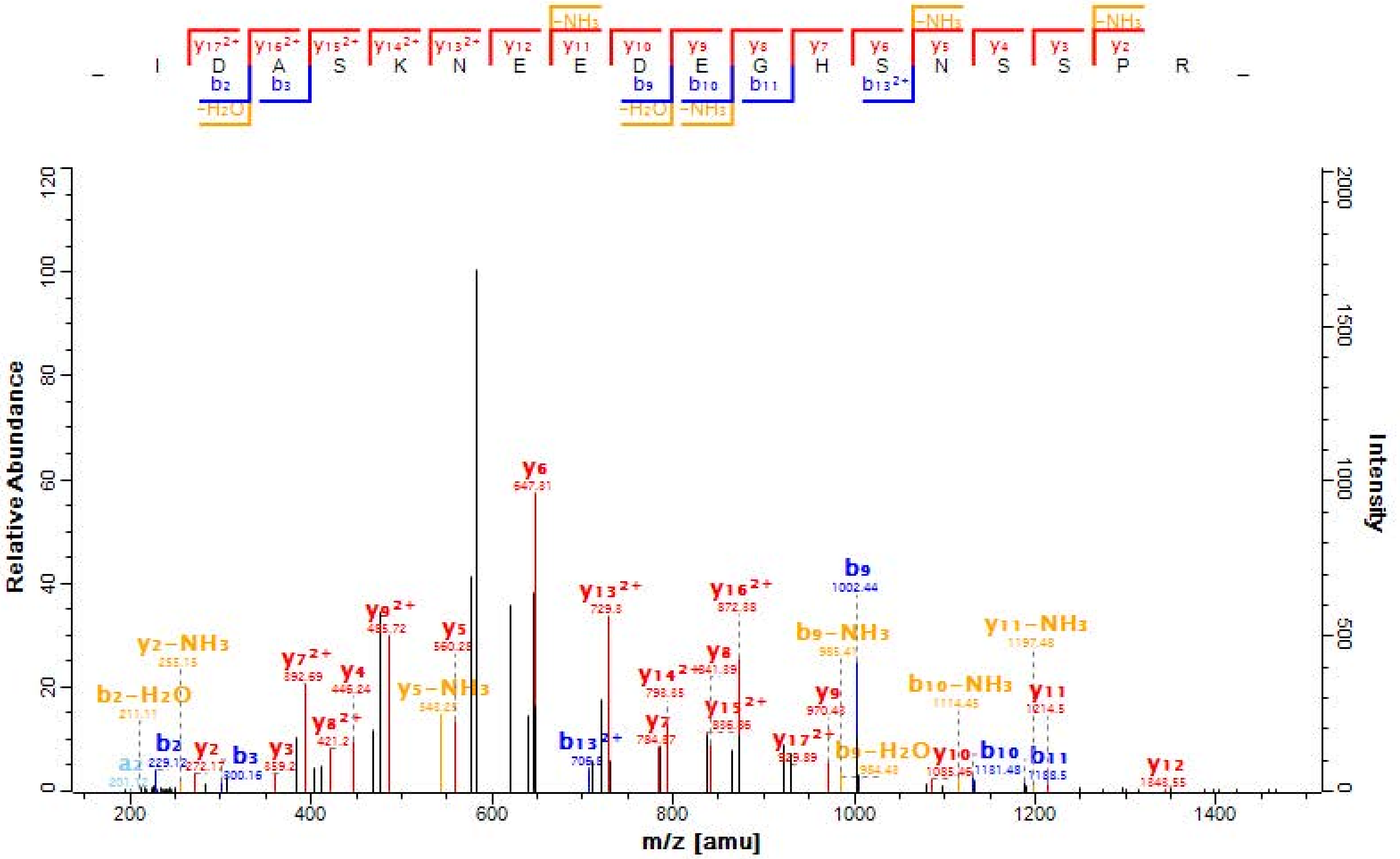
precursor information

Mass:	1265.70353
m/z:	633.85904
Charge:	2+
Retentiontime:	22.074428558349
Score:	97.81339
Mass Error [ppm]:	1.2168
PEP:	0.0010644
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	48 %
Peak Coverage:	20 %
Protein Localisation:	558 ... 567

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	164.0706	1	Y	9				
-0.0215	300.1798	2	K	8	1119.674		560.3408	+0.008445
-0.00562	428.2383	3	Q	7	983.5652	-0.06424	983.5652	
+0.087069	543.2653	4	D	6	855.5066	-0.04906	855.5066	
	642.3337	5	V	5	740.4796	+0.246315	740.4796	
+0.197392	805.397	6	Y	4	641.4112		641.4112	
-0.13118	918.4811	7	L	3	478.3479	-0.13403	478.3479	
-0.05673	1031.565	8	L	2	365.2638	+0.115075	365.2638	
	1128.618	9	P	1	252.1798	+0.026532	252.1798	
		10	K	0	155.127		155.127	

Scan number	343	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	157.74



precursor information

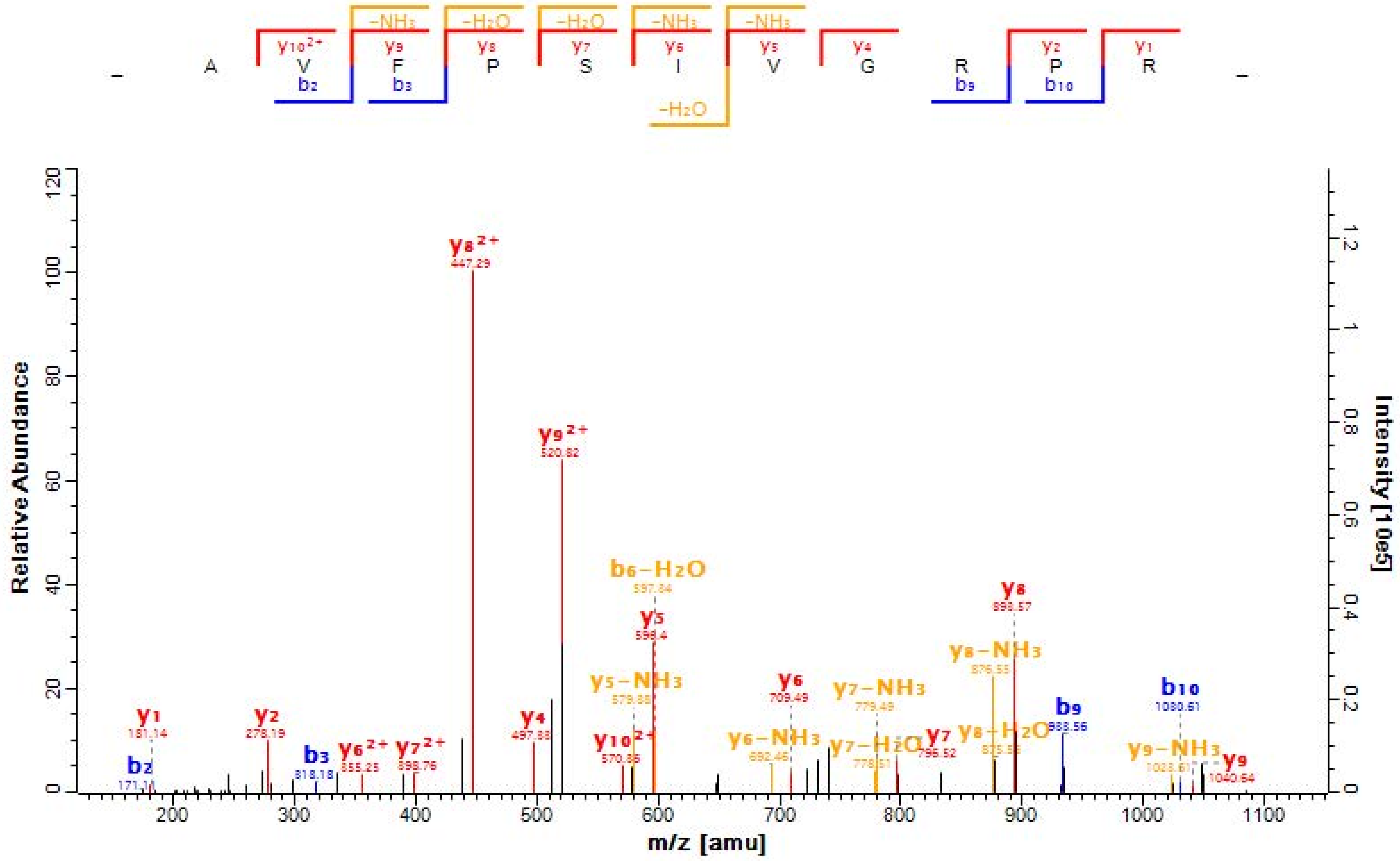
Mass:	1970.85799
m/z:	657.95994
Charge:	3+
Retentiontime:	6.4095482826232
Score:	157.741
Mass Error [ppm]:	0.71267
PEP:	1.3191E-23
Precursor Type:	MULTI

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	I	17				
+0.159	201.1		229.1	-0.05	229.1	2	D	16	1859		929.9	-0.02
	272.2		300.2	+0.12	300.2	3	A	15	1744		872.4	+0.26
	359.2		387.2		387.2	4	S	14	1673		836.9	+0.06
	487.3		515.3		515.3	5	K	13	1586		793.3	+0.15
	601.3		629.3		629.3	6	N	12	1458		729.3	+0.30
	730.4		758.4		758.4	7	E	11	1344	+0.086	1344	
	859.4		887.4		887.4	8	E	10	1215	+0.108	1215	
	974.4		1002	-0.05	1002	9	D	9	1085	+0.084	1085	
	1103		1131	-0.04	1131	10	E	8	970.4	+0.078	485.7	+0.16
	1161		1189	-0.38	1189	11	G	7	841.4	+0.147	421.2	+0.07
	1298		1326		1326	12	H	6	784.4	+0	392.7	+0.20
	1385	+0.171	706.8		1413	13	S	5	647.3	+0.037	647.3	
	1499		1527		1527	14	N	4	560.3	-0.02	560.3	
	1586		1614		1614	15	S	3	446.2	+0.031	446.2	
	1673		1701		1701	16	S	2	359.2	+0.029	359.2	
	1770		1798		1798	17	P	1	272.2	+0.067	272.2	
						18	R	0	175.1		175.1	

general information

Annotation:	16 of 18
AminoAcids Coverag	89 %
Intensity Coverage:	42 %
Peak Coverage:	29 %
Protein Localisation:	68 ... 85

Scan number	3854	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	160.53



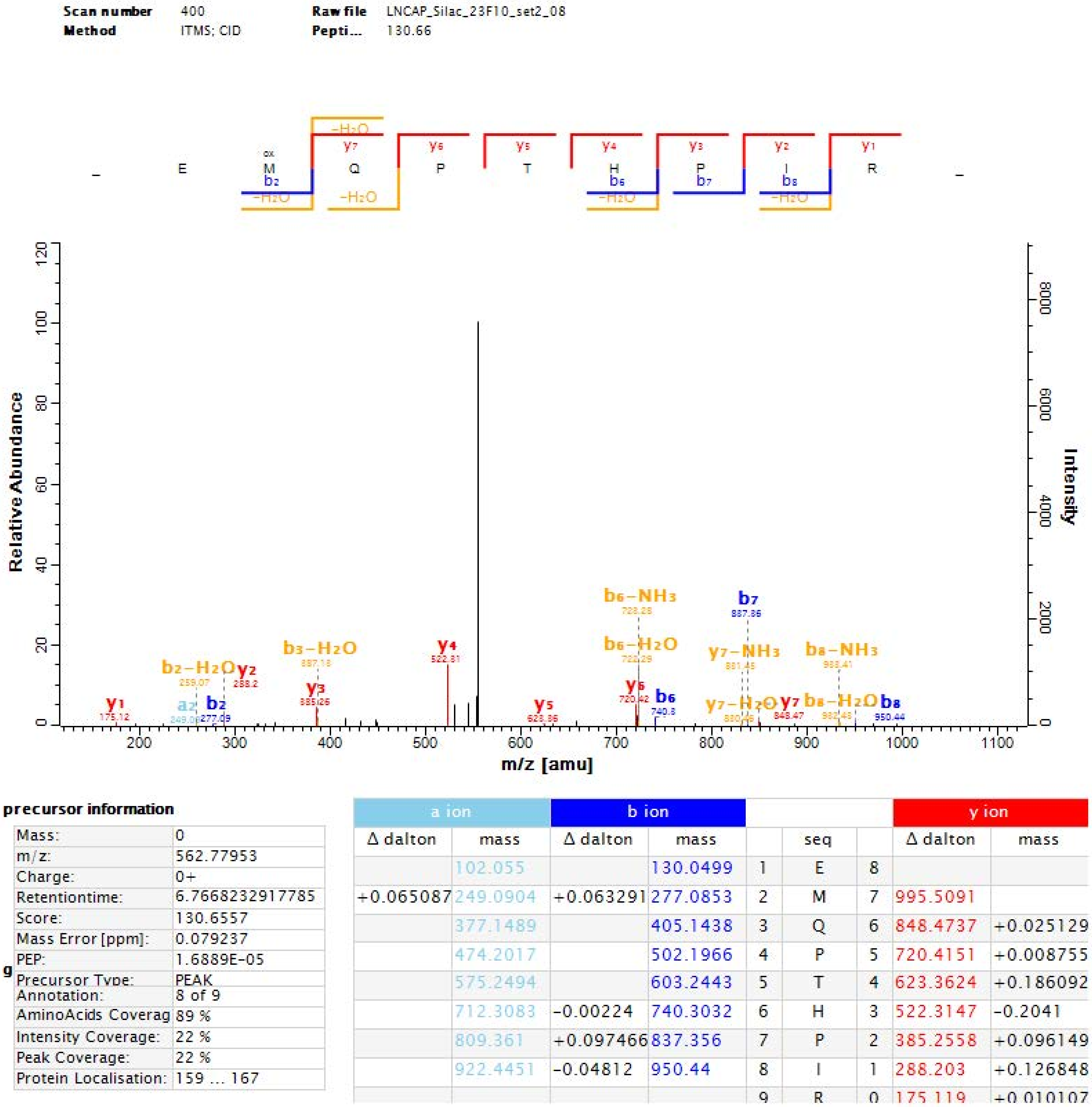
precursor information

Mass:	1197.69802
m/z:	599.85629
Charge:	2+
Retentiontime:	24.743335723877
Score:	160.5311
Mass Error [ppm]:	-0.17036
PEP:	1.4515E-06
Precursor Type:	MULTI

general information

Annotation:	10 of 11
AminoAcids Coverag	91 %
Intensity Coverage:	67 %
Peak Coverage:	30 %
Protein Localisation:	29 ... 39

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	10				
+0.304035	171.1128	2	V	9	1139.709		570.358	+0.06666
-0.03647	318.1812	3	F	8	1040.64	-0.05808	520.8238	+0.01261
	415.234	4	P	7	893.5718	+0.014851	447.2895	+0.142825
	502.266	5	S	6	796.5191	+0.039233	398.7632	+0.096942
	615.3501	6	I	5	709.487	+0.135715	355.2472	-0.00698
	714.4185	7	V	4	596.403	+0.218924	596.403	
	771.44	8	G	3	497.3345	+0.09819	497.3345	
-0.04093	933.5612	9	R	2	440.3131		440.3131	
+0.109677	1030.614	10	P	1	278.1918	-0.06422	278.1918	
		11	R	0	181.1391	-0.08714	181.1391	



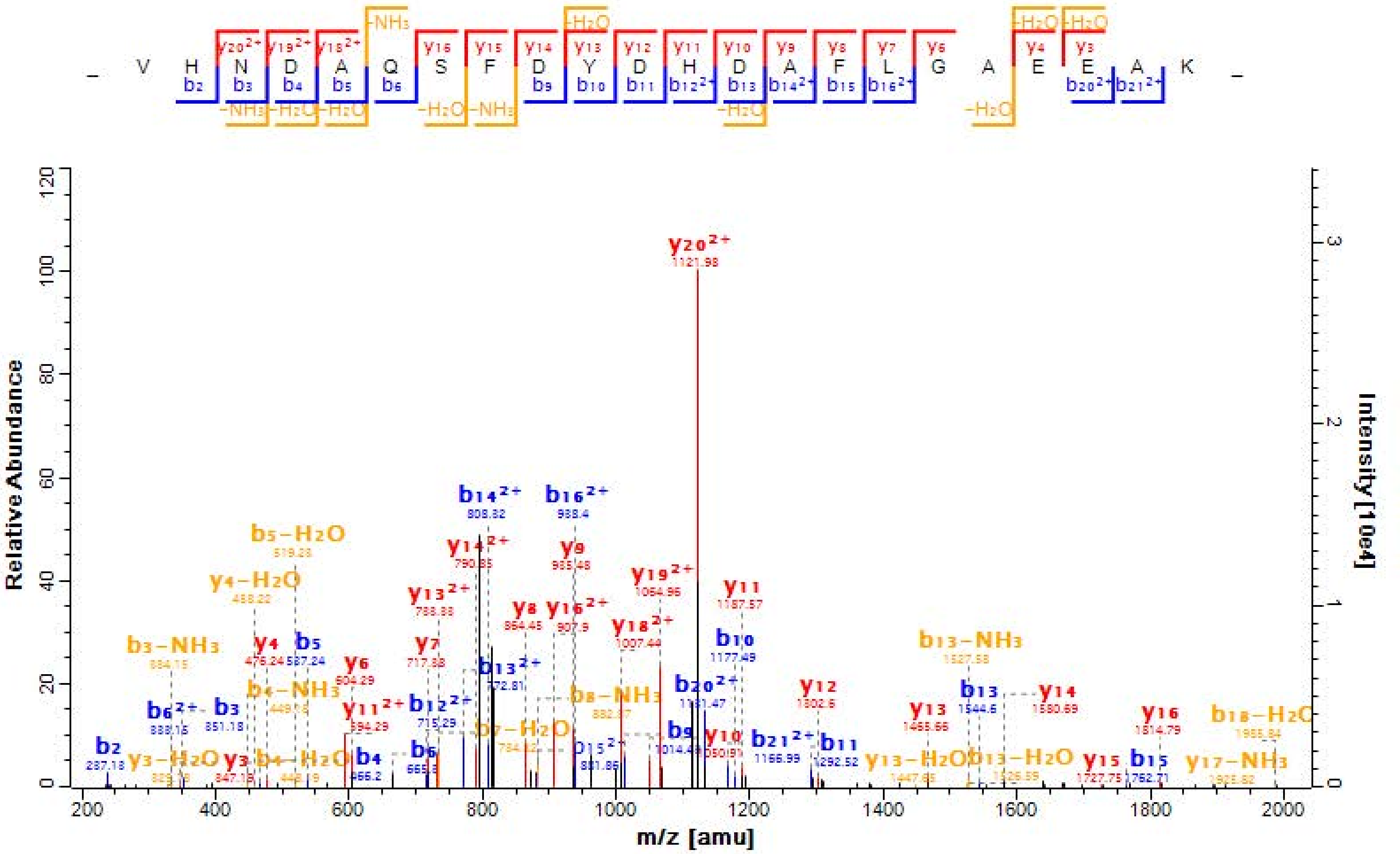
Scan number	400	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	130.66

precursor information

Mass:	0
m/z:	562.77953
Charge:	0+
Retentiontime:	6.7668232917785
Score:	130.6557
Mass Error [ppm]:	0.079237
PEP:	1.6889E-05
Precursor Type:	PEAK
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	22 %
Peak Coverage:	22 %
Protein Localisation:	159 ... 167

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	102.055		130.0499	1	E	8		
+0.065087	249.0904	+0.063291	277.0853	2	M	7	995.5091	
	377.1489		405.1438	3	Q	6	848.4737	+0.025129
	474.2017		502.1966	4	P	5	720.4151	+0.008755
	575.2494		603.2443	5	T	4	623.3624	+0.186092
	712.3083	−0.00224	740.3032	6	H	3	522.3147	−0.2041
	809.361	+0.097466	837.356	7	P	2	385.2558	+0.096149
	922.4451	−0.04812	950.44	8	I	1	288.203	+0.126848
				9	R	0	175.119	+0.010107

Scan number	4539	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	263.09



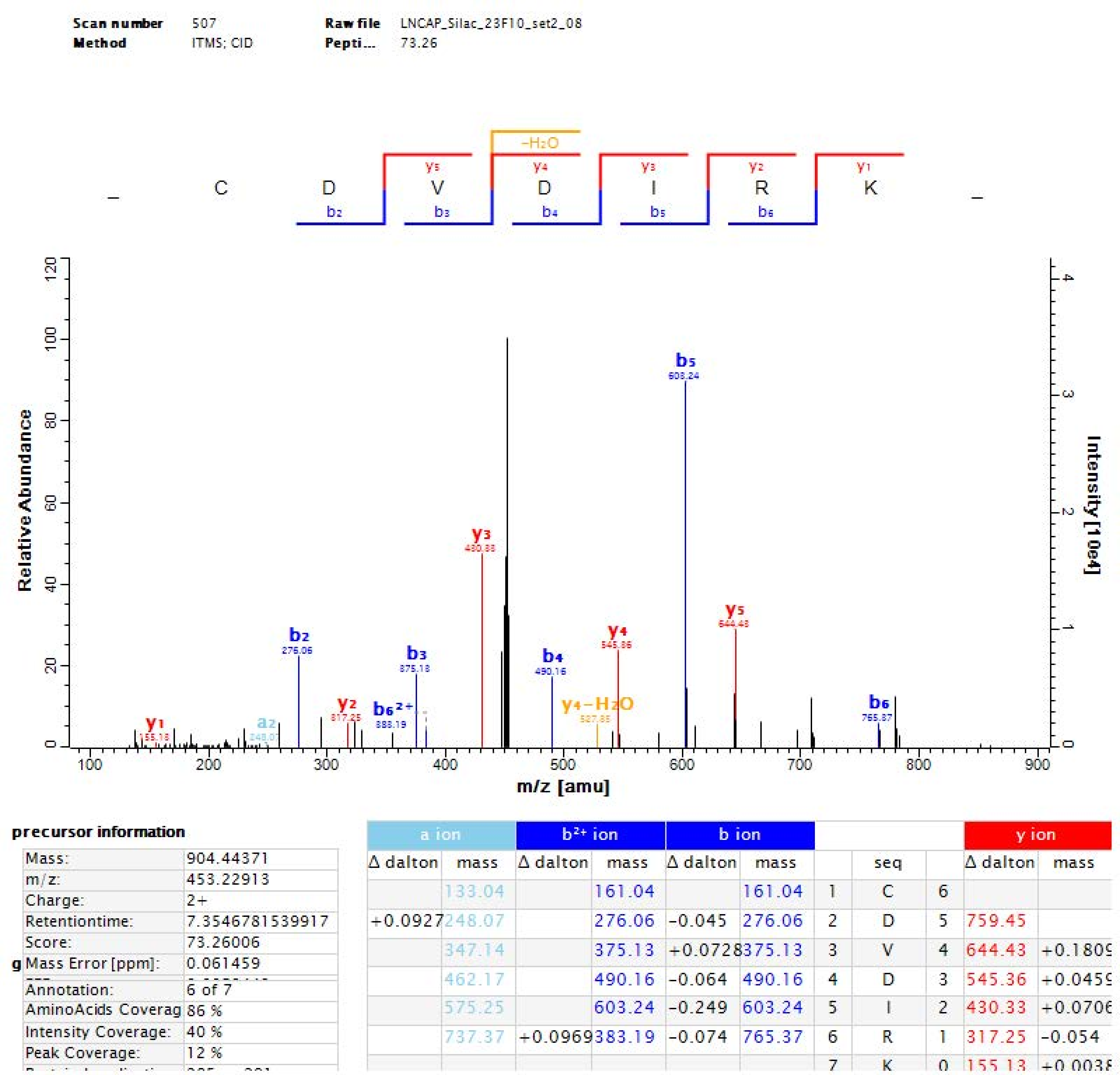
precursor information

Mass:	2478.07236
m/z:	827.0314
Charge:	3+
Retentiontime:	28.324234008789
Score:	263.09
Mass Error [ppm]:	-0.015279
PEP:	4.0271E-98
Precursor Type:	MULTI

general information

Annotation:	20 of 22
AminoAcids Coverag	91 %
Intensity Coverage:	59 %
Peak Coverage:	46 %
Protein Localisation:	46 ... 67

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	21				
	237.13	+0.0471	237.13	2	H	20	2380		2380	
	351.18	+0.1131	351.18	3	N	19	2243		1122	+0.268
	466.2	+0.0197	466.2	4	D	18	2128.9		1065	+0.277
	537.24	+0.0985	537.24	5	A	17	2013.9		1007.4	+0.321
+0.1867	333.15	+0.2139	665.3	6	Q	16	1942.8		1942.8	
	752.33		752.33	7	S	15	1814.8	+0.0561	907.9	+0.221
	899.4		899.4	8	F	14	1727.8	-0.077	1727.8	
	1014.4	-0.024	1014.4	9	D	13	1580.7	-0.46	790.85	+0.267
	1177.5	-0.196	1177.5	10	Y	12	1465.7	-0.047	733.33	-0.089
	1292.5	+0.0684	1292.5	11	D	11	1302.6	-0.235	1302.6	
+0.4704	715.29		1429.6	12	H	10	1187.6	-0.026	594.29	+0.307
+0.2191	772.81	+0.3017	1544.6	13	D	9	1050.5	+0.0146	1050.5	
+0.2564	808.32		1615.6	14	A	8	935.48	+0.036	935.48	
-0.163	881.86	+0.0009	1762.7	15	F	7	864.45	+0.0954	864.45	
+0.3285	938.4		1875.8	16	L	6	717.38	+0.0385	717.38	
	1932.8		1932.8	17	G	5	604.29	+0.0161	604.29	
	2003.9		2003.9	18	A	4	547.27		547.27	
	2132.9		2132.9	19	E	3	476.24	+0.1083	476.24	
+0.3228	1131.5		2261.9	20	E	2	347.19	+0.119	347.19	
+0.4133	1167		2333	21	A	1	218.15		218.15	
				22	K	0	147.11		147.11	



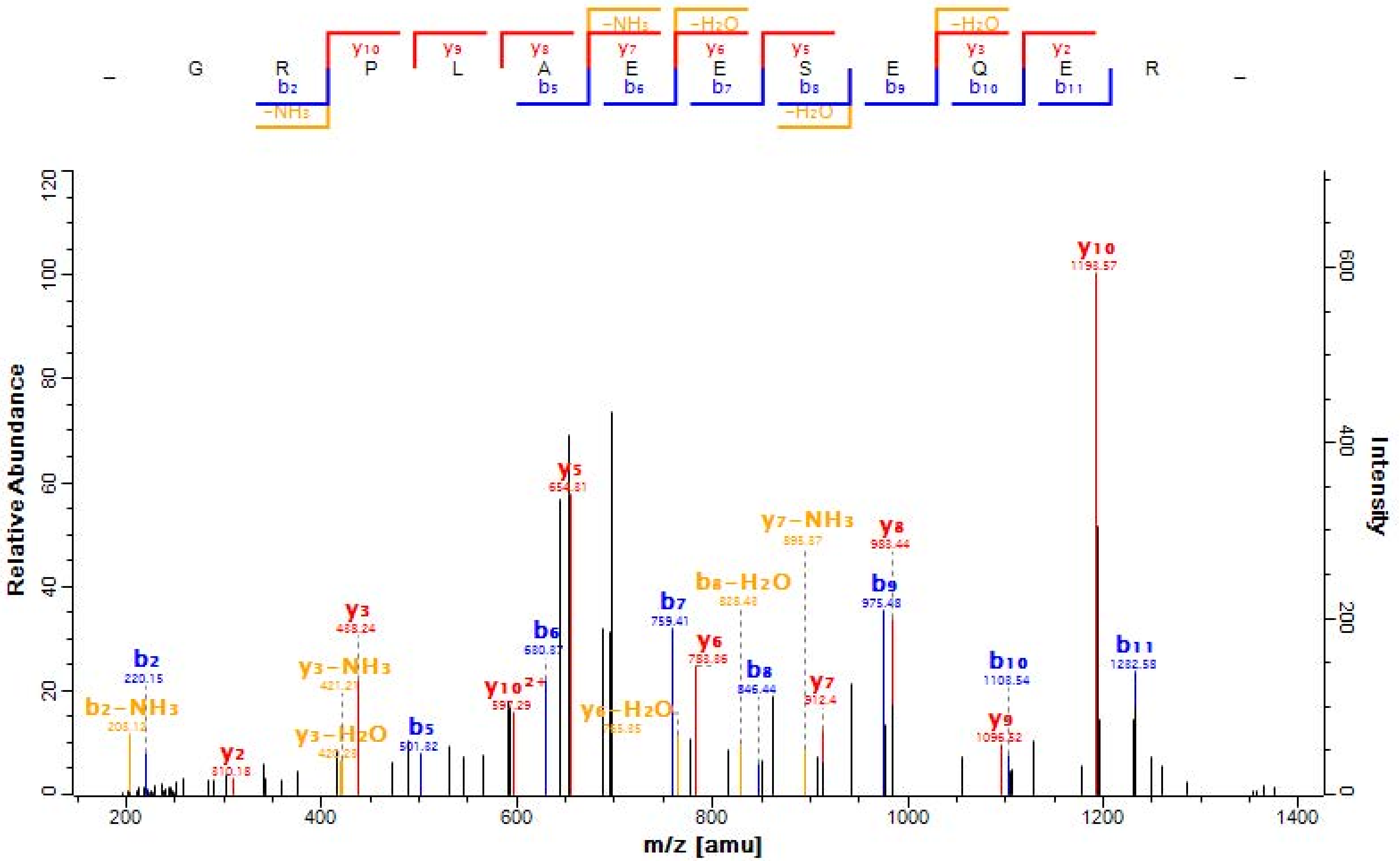
Scan number 507 **Raw file** LNCAP_Silac_23F10_set2_08
Method ITMS; CID **Pepti...** 73.26

precursor information

Mass:	904.44371
m/z:	453.22913
Charge:	2+
Retentiontime:	7.3546781539917
Score:	73.26006
Mass Error [ppm]:	0.061459
Annotation:	6 of 7
AminoAcids Coverag	86 %
Intensity Coverage:	40 %
Peak Coverage:	12 %

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	133.04		161.04		161.04	1	C	6		
+0.0927	248.07		276.06	-0.045	276.06	2	D	5	759.45	
	347.14		375.13	+0.0728	375.13	3	V	4	644.43	+0.180
	462.17		490.16	-0.064	490.16	4	D	3	545.36	+0.045
	575.25		603.24	-0.249	603.24	5	I	2	430.33	+0.070
	737.37	+0.0969	383.19	-0.074	765.37	6	R	1	317.25	-0.054
						7	K	0	155.13	+0.003

Scan number	519	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	134.68



precursor information

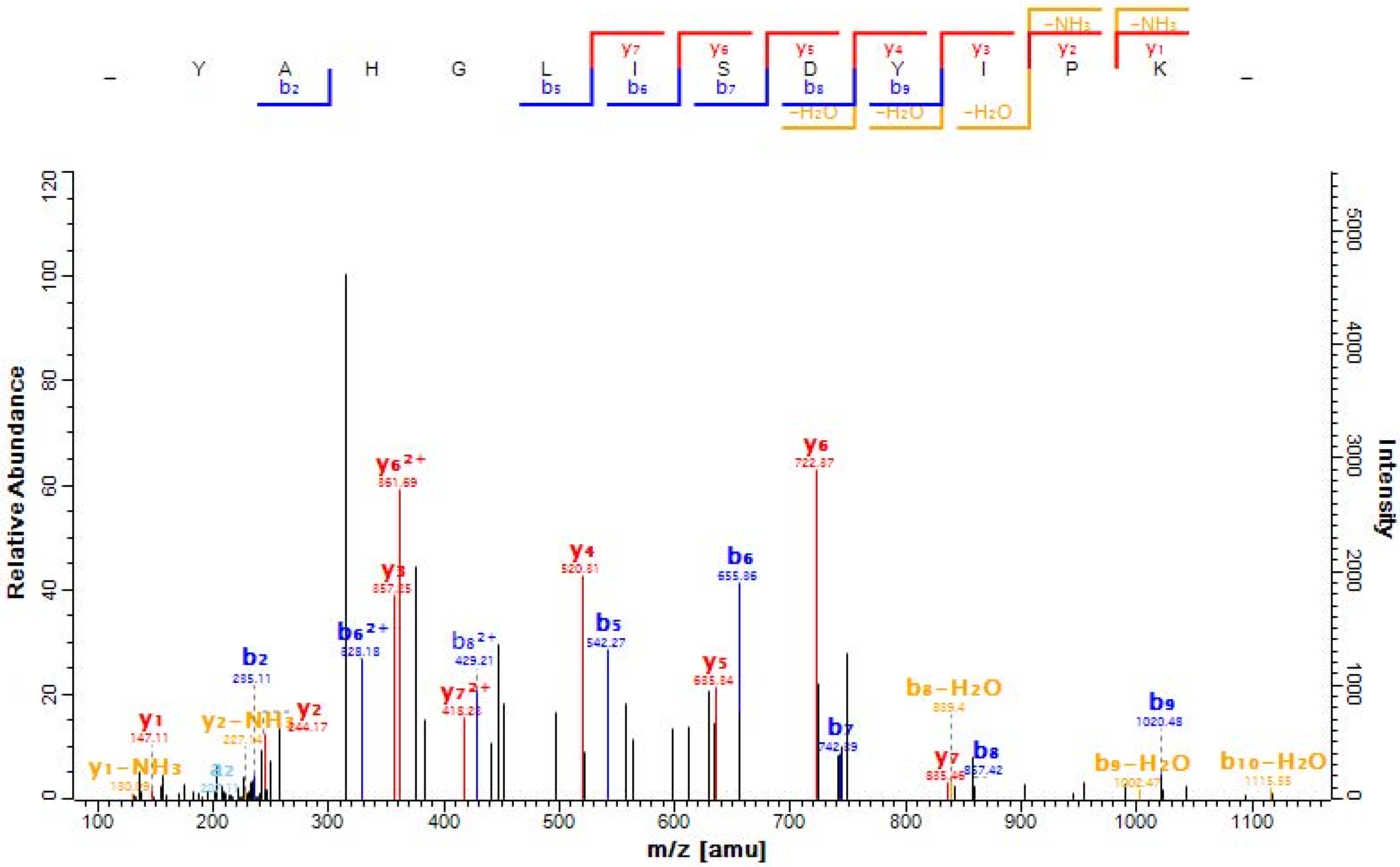
Mass:	1411.70846
m/z:	706.86151
Charge:	2+
Retentiontime:	7.4155917167663
Score:	134.6848
Mass Error [ppm]:	-0.6851
PEP:	0.00012298
Precursor Type:	ISO

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	40 %
Peak Coverage:	24 %
Protein Localisation:	347 ... 358

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	11				
+0.079237	220.15	2	R	10	1355.695		1355.695	
	317.2027	3	P	9	1193.574	-0.07425	597.2906	+0.273265
	430.2868	4	L	8	1096.521	+0.099246	1096.521	
+0.051688	501.3239	5	A	7	983.4372	-0.04331	983.4372	
-0.0755	630.3665	6	E	6	912.4001	+0.07632	912.4001	
+0.030894	759.4091	7	E	5	783.3575	-0.03465	783.3575	
+0.15243	846.4411	8	S	4	654.3149	+0.067268	654.3149	
+0.210057	975.4837	9	E	3	567.2828		567.2828	
-0.02265	1103.542	10	Q	2	438.2403	+0.084272	438.2403	
-0.03424	1232.585	11	E	1	310.1817	+0.091214	310.1817	
		12	R	0	181.1391		181.1391	

Scan number	5332	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	110.84



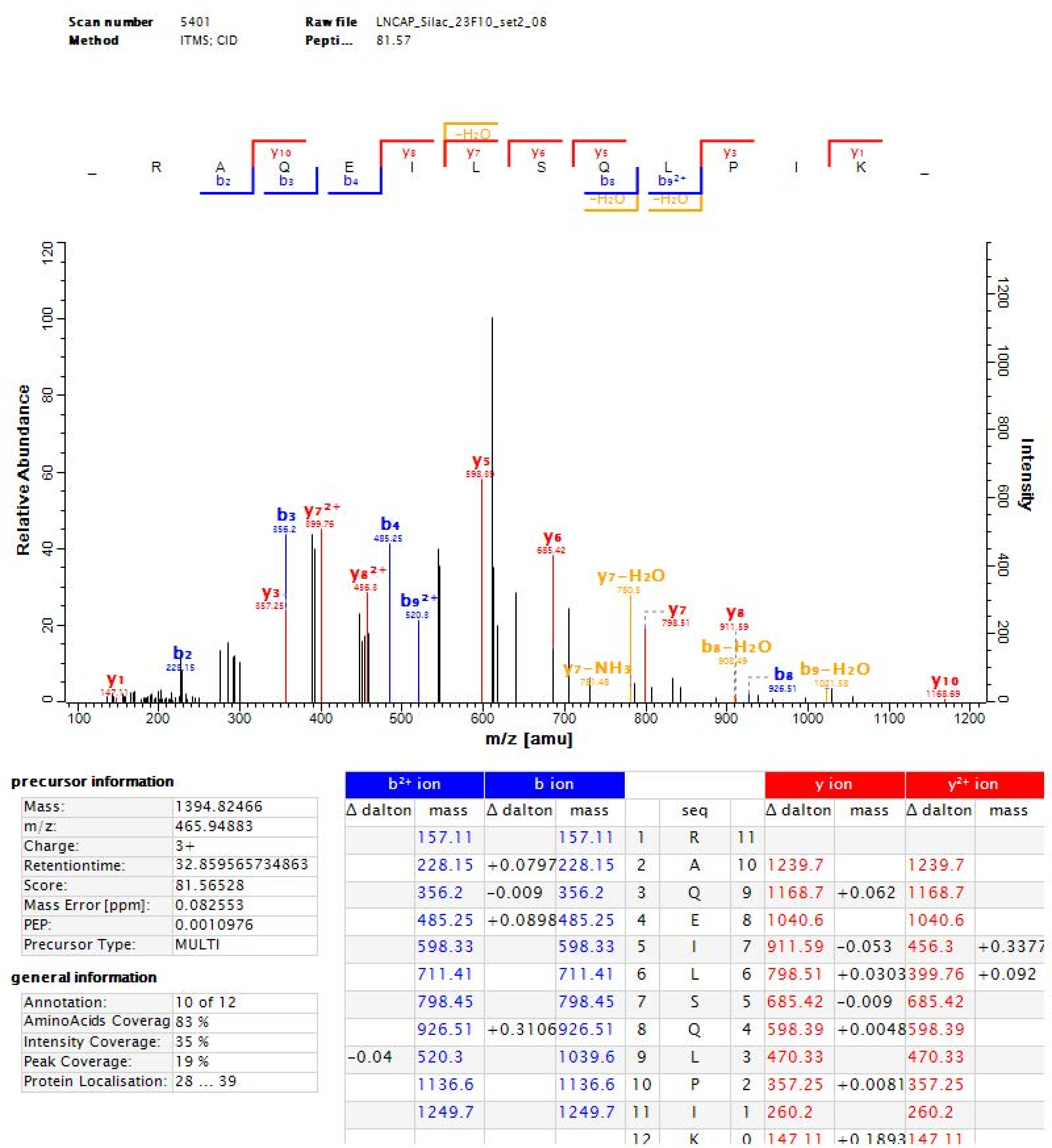
precursor information

Mass:	1375.71337
m/z:	459.5784
Charge:	3+
Retentiontime:	32.472579956054
Score:	110.8379
Mass Error [ppm]:	-0.16942
PEP:	4.8752E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	42 %
Peak Coverage:	23 %
Protein Localisation:	211 ... 222

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.1		164.1		164.1	1	Y	11				
-0.01	207.1		235.1	+0.119	235.1	2	A	10		1214		1214
	344.2		372.2		372.2	3	H	9		1143		1143
	401.2		429.2		429.2	4	G	8		1006		1006
	514.3		542.3	+0.114	542.3	5	L	7		948.5		948.5
	627.4	+0.052	328.2	-0.02	655.4	6	I	6	-0.03	835.5		418.2
	714.4		742.4	+0.234	742.4	7	S	5	-0.05	722.4		361.7
	829.4	+0.046	429.2	-0.01	857.4	8	D	4	+0	635.3		635.3
	992.5		1020	+0.018	1020	9	Y	3	+0.046	520.3		520.3
	1106		1134		1134	10	I	2	+0.163	357.2		357.2
	1203		1231		1231	11	P	1	+0.146	244.2		244.2
						12	K	0	-0.03	147.1		147.1



Scan number	5401	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	81.57

precursor information

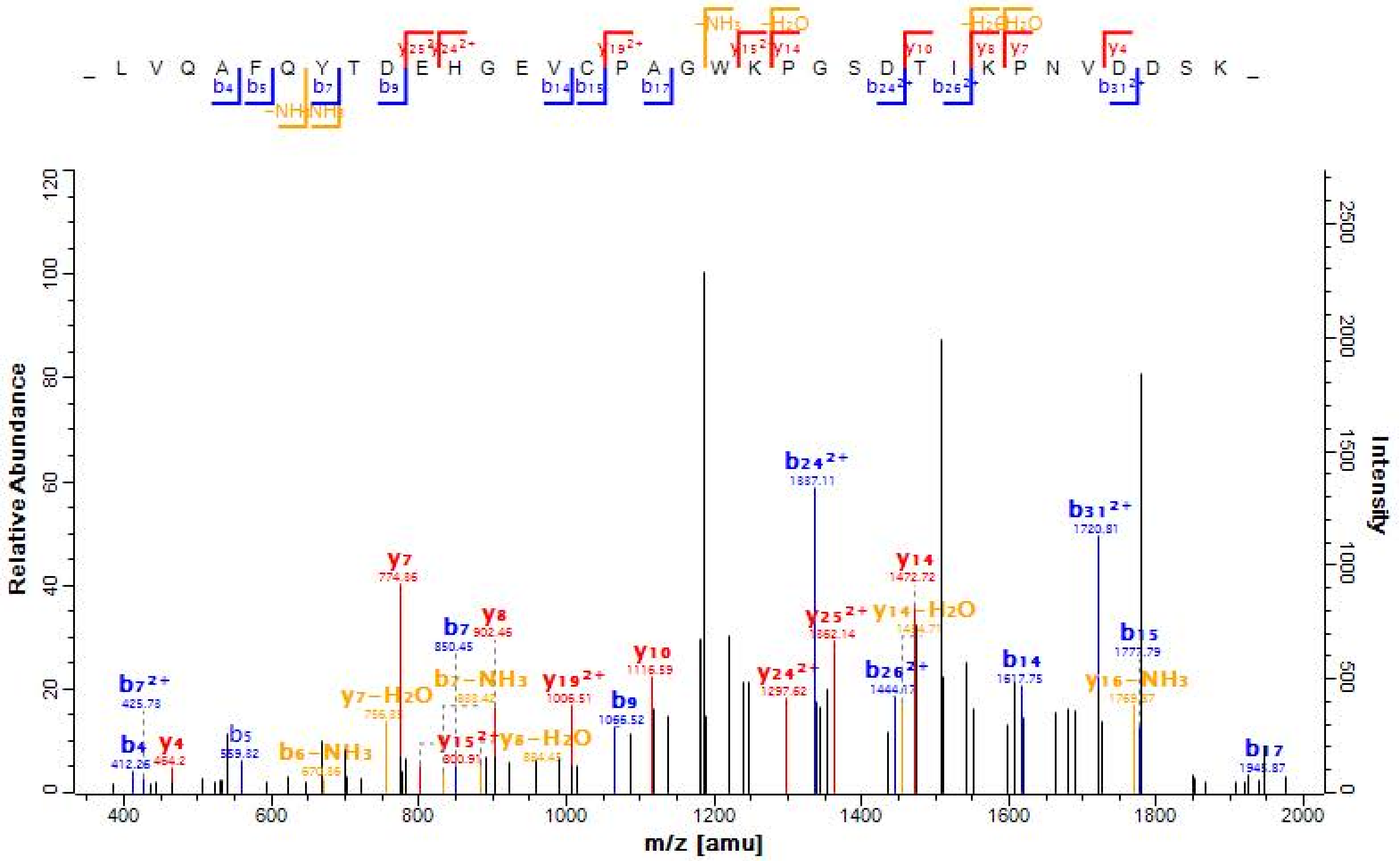
Mass:	1394.82466
m/z:	465.94883
Charge:	3+
Retentiontime:	32.859565734863
Score:	81.56528
Mass Error [ppm]:	0.082553
PEP:	0.0010976
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	35 %
Peak Coverage:	19 %
Protein Localisation:	28 ... 39

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	157.11		157.11	1	R	11				
	228.15	+0.0797	228.15	2	A	10	1239.7		1239.7	
	356.2	-0.009	356.2	3	Q	9	1168.7	+0.062	1168.7	
	485.25	+0.0898	485.25	4	E	8	1040.6		1040.6	
	598.33		598.33	5	I	7	911.59	-0.053	456.3	+0.3377
	711.41		711.41	6	L	6	798.51	+0.0303	399.76	+0.092
	798.45		798.45	7	S	5	685.42	-0.009	685.42	
	926.51	+0.3106	926.51	8	Q	4	598.39	+0.0048	598.39	
-0.04	520.3		1039.6	9	L	3	470.33		470.33	
	1136.6		1136.6	10	P	2	357.25	+0.0081	357.25	
	1249.7		1249.7	11	I	1	260.2		260.2	
				12	K	0	147.11	+0.1893	147.11	

Scan number	5417	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	71.67



precursor information

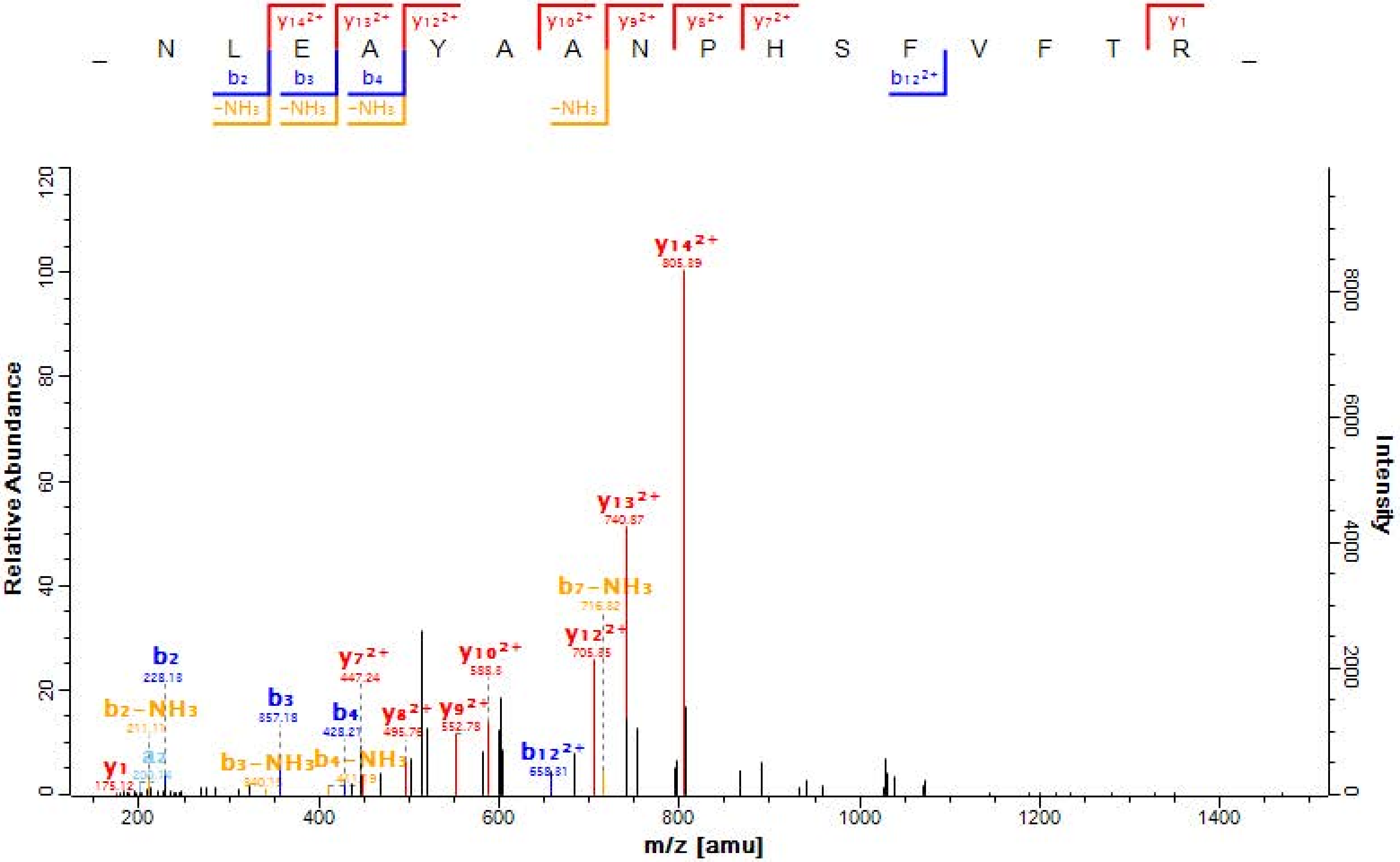
Mass:	3787.77992
m/z:	1263.60058
Charge:	3+
Retentiontime:	32.951045989990
Score:	71.66998
Mass Error [ppm]:	0.29401
PEP:	2.0039E-11
Precursor Type:	MULTI

general information

Annotation:	20 of 34
AminoAcids Coverag	59 %
Intensity Coverage:	31 %
Peak Coverage:	28 %
Protein Localisation:	158 ... 191

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	33				
	213.16		213.16	2	V	32	3675.7		3675.7	
	341.22		341.22	3	Q	31	3576.6		3576.6	
	412.26	+0.2721	412.26	4	A	30	3448.6		3448.6	
	559.32	-0.096	559.32	5	F	29	3377.5		3377.5	
	687.38		687.38	6	Q	28	3230.5		3230.5	
+0.4105	425.73	+0.1394	850.45	7	Y	27	3102.4		3102.4	
	951.49		951.49	8	T	26	2939.3		2939.3	
	1066.5	-0.085	1066.5	9	D	25	2838.3		2838.3	
	1195.6		1195.6	10	E	24	2723.3		1362.1	+0.4205
	1332.6		1332.6	11	H	23	2594.2		1297.6	+0.2757
	1389.6		1389.6	12	G	22	2457.2		2457.2	
	1518.7		1518.7	13	E	21	2400.2		2400.2	
	1617.8	-0.195	1617.8	14	V	20	2271.1		2271.1	
	1777.8	-0.026	1777.8	15	C	19	2172		2172	
	1874.8		1874.8	16	P	18	2012		1006.5	+0.3261
	1945.9	-0.222	1945.9	17	A	17	1915		1915	
	2002.9		2002.9	18	G	16	1843.9		1843.9	
	2189		2189	19	W	15	1786.9		1786.9	
	2317.1		2317.1	20	K	14	1600.8		800.91	+0.4375
	2414.1		2414.1	21	P	13	1472.7	-0.007	1472.7	
	2471.1		2471.1	22	G	12	1375.7		1375.7	
	2558.2		2558.2	23	S	11	1318.6		1318.6	
+0.4999	1337.1		2673.2	24	D	10	1231.6		1231.6	
	2774.3		2774.3	25	T	9	1116.6	+0.0715	1116.6	
+0.153	1444.2		2887.3	26	I	8	1015.5		1015.5	
	3015.4		3015.4	27	K	7	902.46	+0.0714	902.46	
	3112.5		3112.5	28	P	6	774.36	-0.009	774.36	
	3226.5		3226.5	29	N	5	677.31		677.31	
	3325.6		3325.6	30	V	4	563.27		563.27	
+0.4348	1720.8		3440.6	31	D	3	464.2	+0.0047	464.2	
	3555.6		3555.6	32	D	2	349.17		349.17	
	3642.7		3642.7	33	S	1	234.14		234.14	
				34	K	0	147.11		147.11	

Scan number	6292	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	63.18



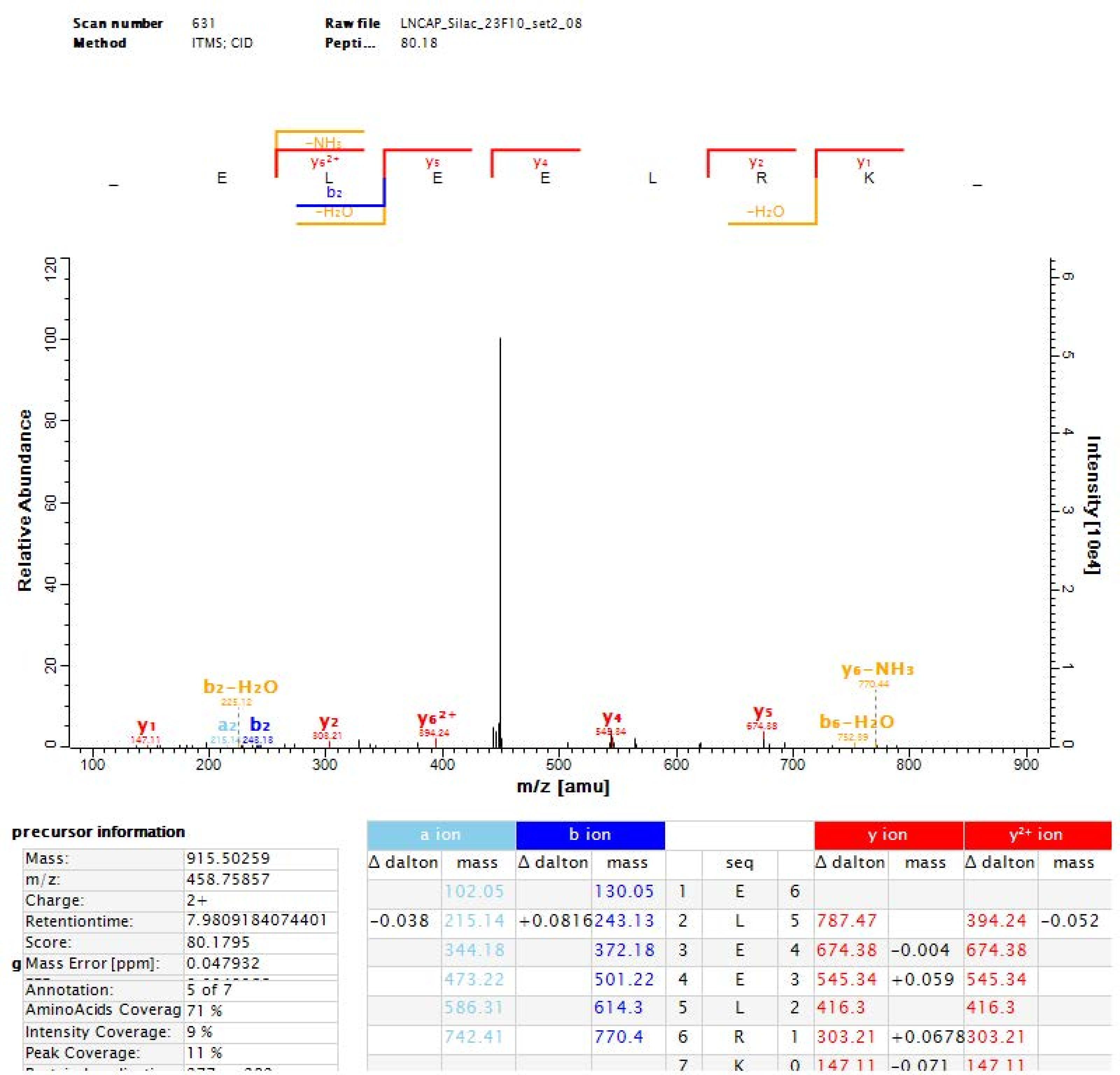
precursor information

Mass:	1835.89624
m/z:	612.97269
Charge:	3+
Retentiontime:	37.744781494140
Score:	63.18053
Mass Error [ppm]:	0.41269
PEP:	0.0022991
Precursor Type:	MULTI

general information

Annotation:	10 of 16
AminoAcids Coverag	62 %
Intensity Coverage:	49 %
Peak Coverage:	18 %
Protein Localisation:	21 ... 36

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	87.06		115.1		115.1	1	N	15				
+0.034	200.1		228.1	-0.05	228.1	2	L	14	1723		1723	
	329.2		357.2	+0.173	357.2	3	E	13	1610		805.4	+0.24
	400.2		428.2	-0.07	428.2	4	A	12	1481		740.9	+0.33
	563.3		591.3		591.3	5	Y	11	1410		705.4	+0.20
	634.3		662.3		662.3	6	A	10	1247		1247	
	705.4		733.4		733.4	7	A	9	1176		588.3	+0.04
	819.4		847.4		847.4	8	N	8	1105		552.8	+0.24
	916.5		944.4		944.4	9	P	7	990.5		495.8	+0.14
	1054		1082		1082	10	H	6	893.5		447.2	+0.32
	1141		1169		1169	11	S	5	756.4		756.4	
	1288	+0.301	658.3		1316	12	F	4	669.4		669.4	
	1387		1415		1415	13	V	3	522.3		522.3	
	1534		1562		1562	14	F	2	423.2		423.2	
	1635		1663		1663	15	T	1	276.2		276.2	
						16	R	0	175.1	+0.117	175.1	

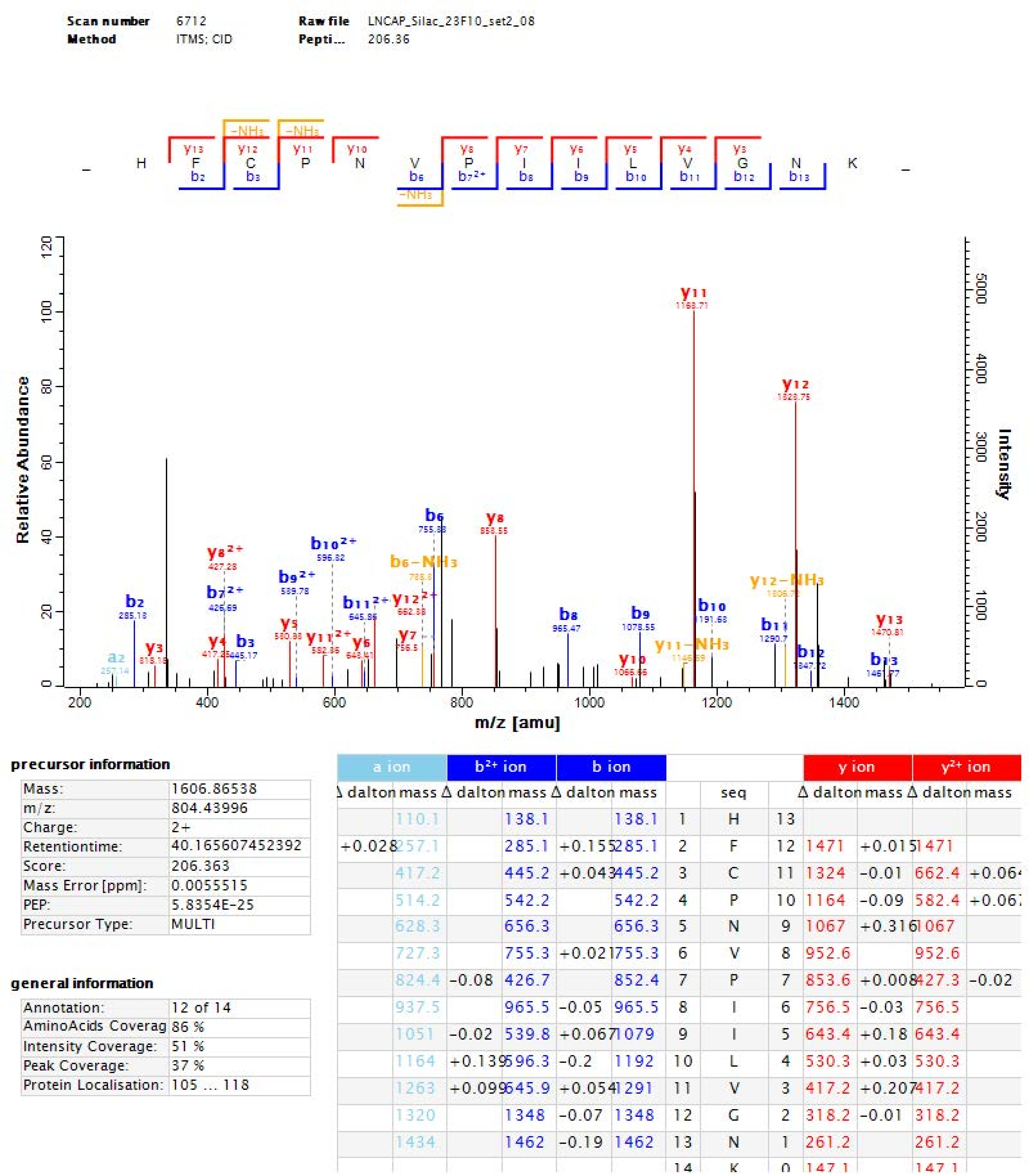


Scan number	631	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	80.18

precursor information

Mass:	915.50259
m/z:	458.75857
Charge:	2+
Retentiontime:	7.9809184074401
Score:	80.1795
Mass Error [ppm]:	0.047932
Annotation:	5 of 7
AminoAcids Coverag	71 %
Intensity Coverage:	9 %
Peak Coverage:	11 %

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	6				
-0.038	215.14	+0.0816	243.13	2	L	5	787.47		394.24	-0.052
	344.18		372.18	3	E	4	674.38	-0.004	674.38	
	473.22		501.22	4	E	3	545.34	+0.059	545.34	
	586.31		614.3	5	L	2	416.3		416.3	
	742.41		770.4	6	R	1	303.21	+0.0678	303.21	
				7	K	0	147.11	-0.071	147.11	



Scan number	6712	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	206.36

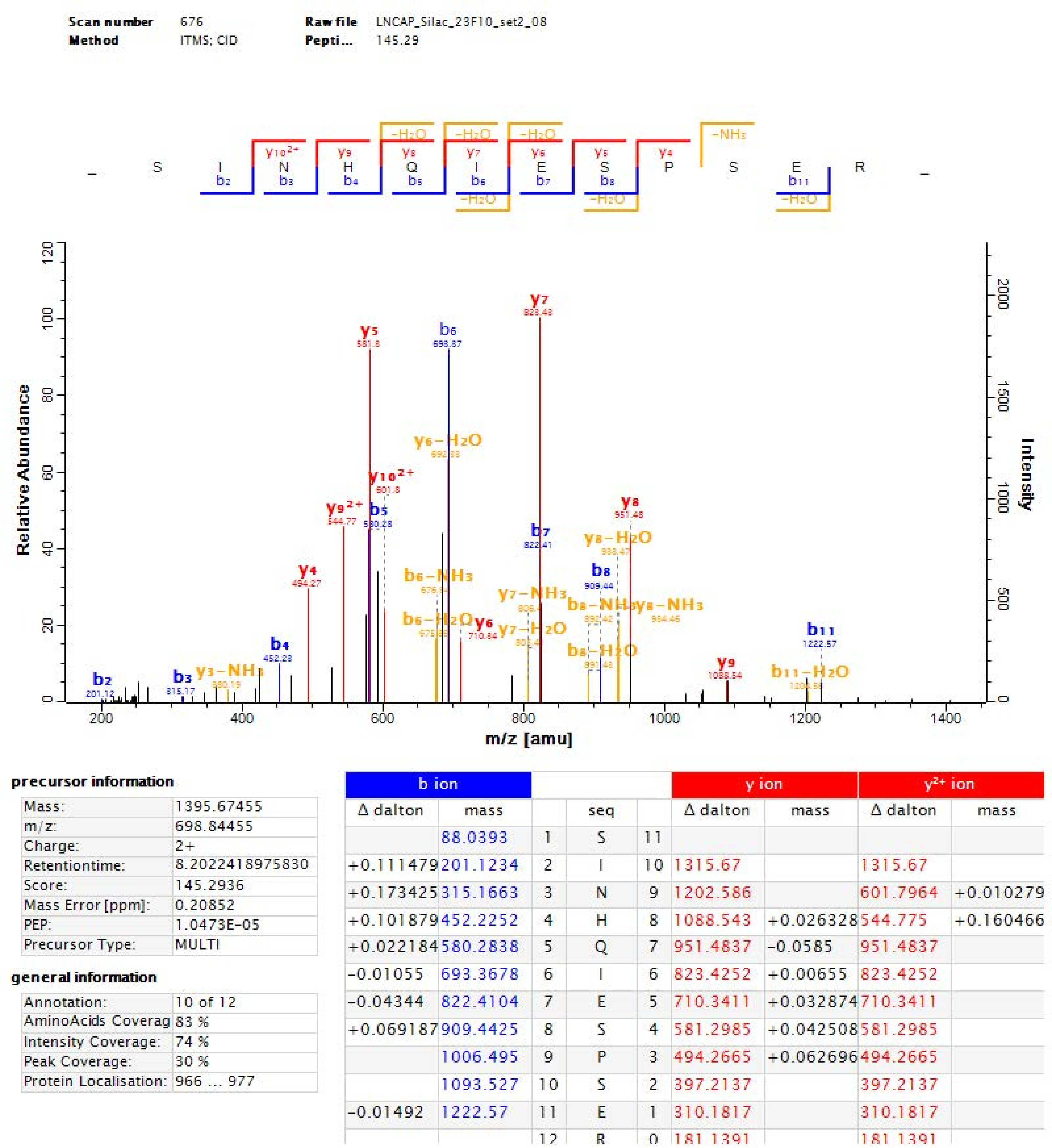
precursor information

Mass:	1606.86538
m/z:	804.43996
Charge:	2+
Retentiontime:	40.165607452392
Score:	206.363
Mass Error [ppm]:	0.0055515
PEP:	5.8354E-25
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	51 %
Peak Coverage:	37 %
Protein Localisation:	105 ... 118

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	110.1		138.1		138.1	1	H	13				
+0.028	257.1		285.1	+0.155	285.1	2	F	12	1471	+0.015	1471	
	417.2		445.2	+0.043	445.2	3	C	11	1324	-0.01	662.4	+0.06
	514.2		542.2		542.2	4	P	10	1164	-0.09	582.4	+0.06
	628.3		656.3		656.3	5	N	9	1067	+0.316	1067	
	727.3		755.3	+0.021	755.3	6	V	8	952.6		952.6	
	824.4	-0.08	426.7		852.4	7	P	7	853.6	+0.008	427.3	-0.02
	937.5		965.5	-0.05	965.5	8	I	6	756.5	-0.03	756.5	
	1051	-0.02	539.8	+0.067	1079	9	I	5	643.4	+0.18	643.4	
	1164	+0.139	596.3	-0.2	1192	10	L	4	530.3	+0.03	530.3	
	1263	+0.099	645.9	+0.054	1291	11	V	3	417.2	+0.207	417.2	
	1320		1348	-0.07	1348	12	G	2	318.2	-0.01	318.2	
	1434		1462	-0.19	1462	13	N	1	261.2		261.2	
						14	K	0	147.1		147.1	



Scan number	676	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	145.29

precursor information

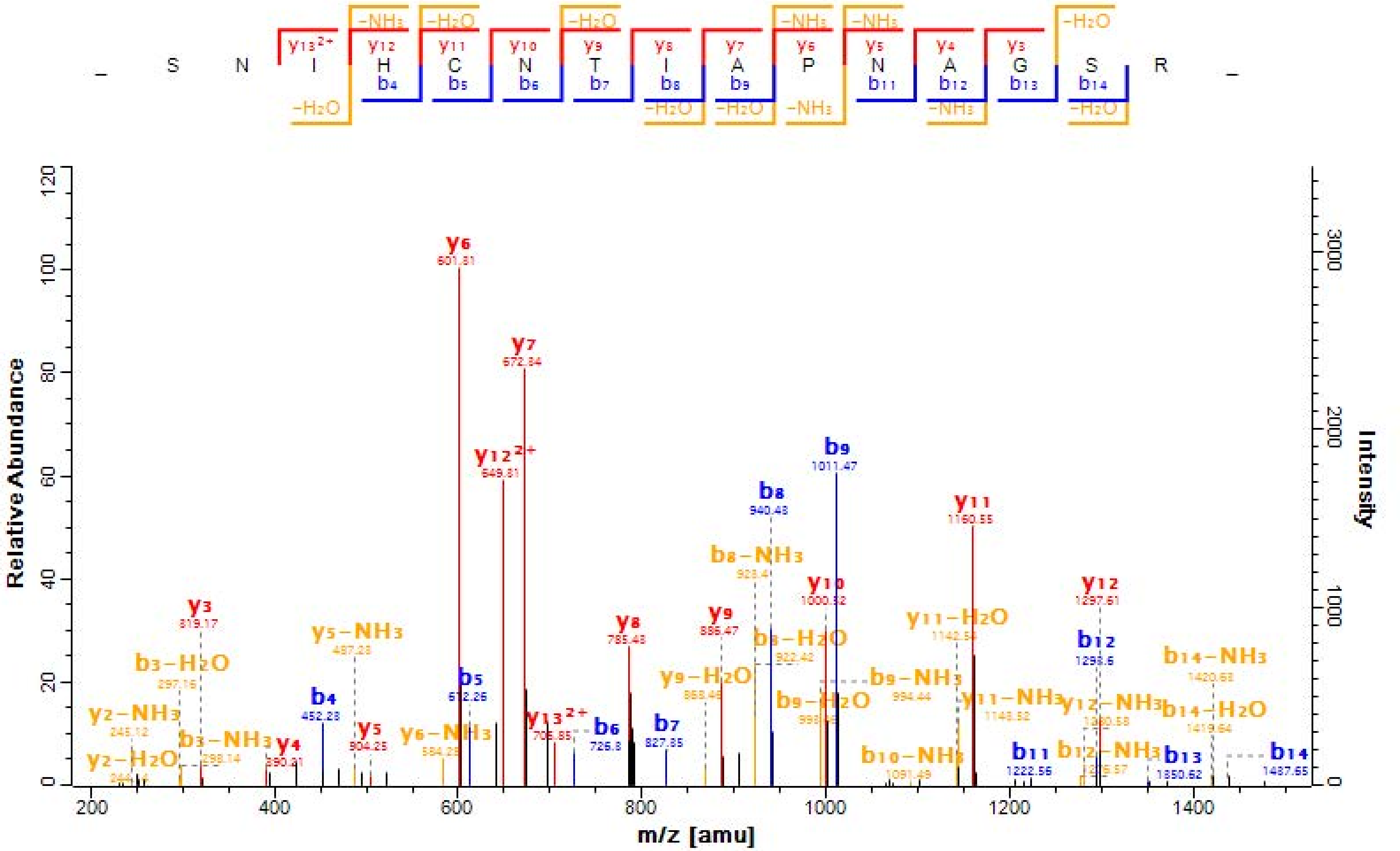
Mass:	1395.67455
m/z:	698.84455
Charge:	2+
Retentiontime:	8.2022418975830
Score:	145.2936
Mass Error [ppm]:	0.20852
PEP:	1.0473E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	74 %
Peak Coverage:	30 %
Protein Localisation:	966 ... 977

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	11				
+0.111479	201.1234	2	I	10	1315.67		1315.67	
+0.173425	315.1663	3	N	9	1202.586		601.7964	+0.010279
+0.101879	452.2252	4	H	8	1088.543	+0.026328	544.775	+0.160466
+0.022184	580.2838	5	Q	7	951.4837	-0.0585	951.4837	
-0.01055	693.3678	6	I	6	823.4252	+0.00655	823.4252	
-0.04344	822.4104	7	E	5	710.3411	+0.032874	710.3411	
+0.069187	909.4425	8	S	4	581.2985	+0.042508	581.2985	
	1006.495	9	P	3	494.2665	+0.062696	494.2665	
	1093.527	10	S	2	397.2137		397.2137	
-0.01492	1222.57	11	E	1	310.1817		310.1817	
		12	R	0	181.1391		181.1391	

Scan number	679	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	199.15



precursor information

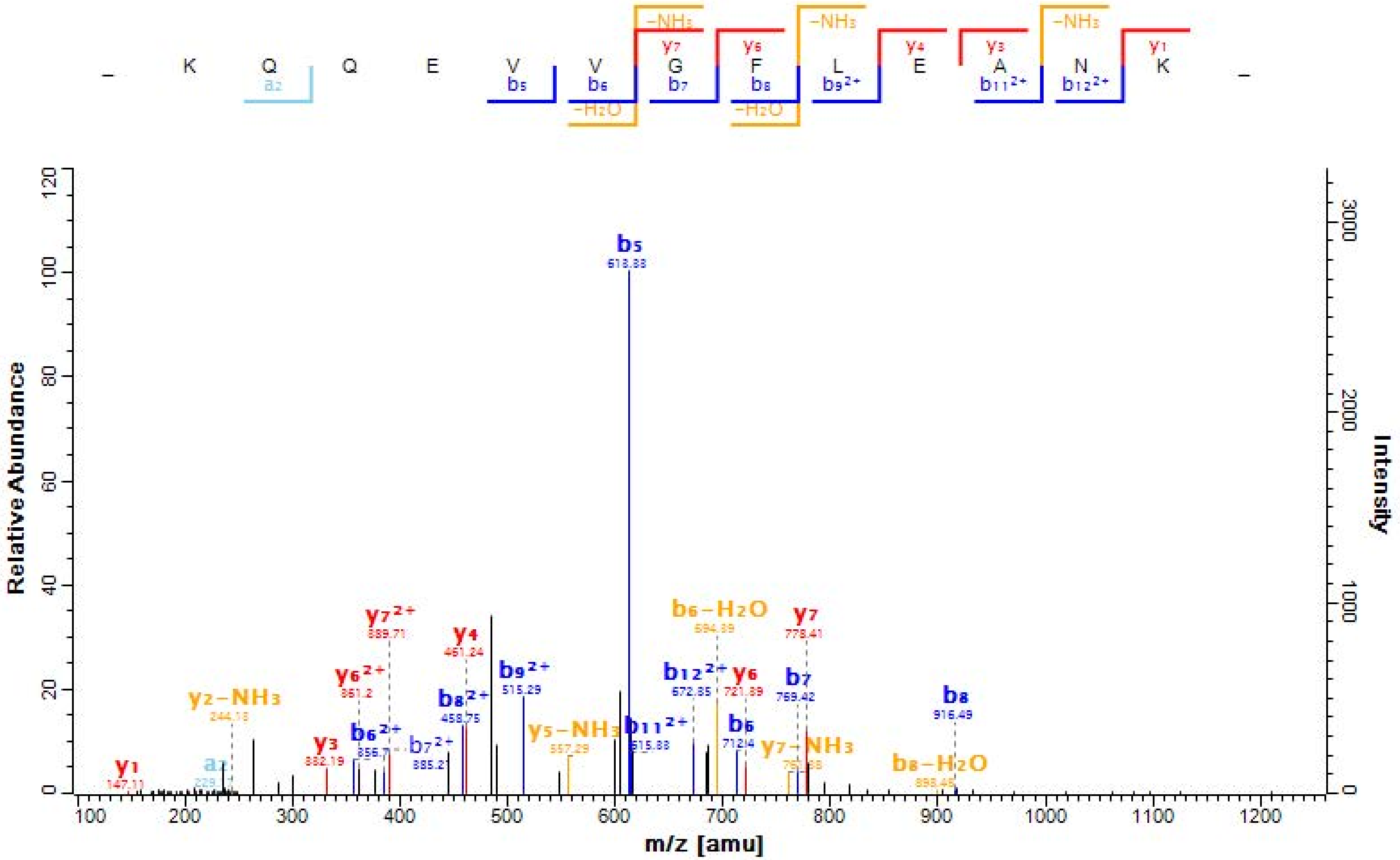
Mass:	1610.75813
m/z:	806.38634
Charge:	2+
Retentiontime:	8.2184896469116
Score:	199.1479
Mass Error [ppm]:	-0.12853
PEP:	8.7699E-23
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	73 %
Peak Coverage:	49 %
Protein Localisation:	185 ... 199

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	14				
	202.0822	2	N	13	1524.734		1524.734	
	315.1663	3	I	12	1410.691		705.849	+0.093233
+0.032177	452.2252	4	H	11	1297.607	-0.00161	649.3069	+0.287853
+0.040958	612.2559	5	C	10	1160.548	-0.04036	1160.548	
+0.085005	726.2988	6	N	9	1000.517	-0.00245	1000.517	
-0.04556	827.3465	7	T	8	886.4741	-0.09166	886.4741	
-0.06779	940.4305	8	I	7	785.4264	-0.02512	785.4264	
-0.02617	1011.468	9	A	6	672.3424	+0.004988	672.3424	
	1108.52	10	P	5	601.3052	+0.068835	601.3052	
+0.065087	1222.563	11	N	4	504.2525	-0.04808	504.2525	
-0.03978	1293.6	12	A	3	390.2096	+0.162817	390.2096	
+0.172159	1350.622	13	G	2	319.1724	+0.035869	319.1724	
+0.299798	1437.654	14	S	1	262.151		262.151	
		15	R	0	175.119		175.119	

Scan number	6804	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	106.26



precursor information

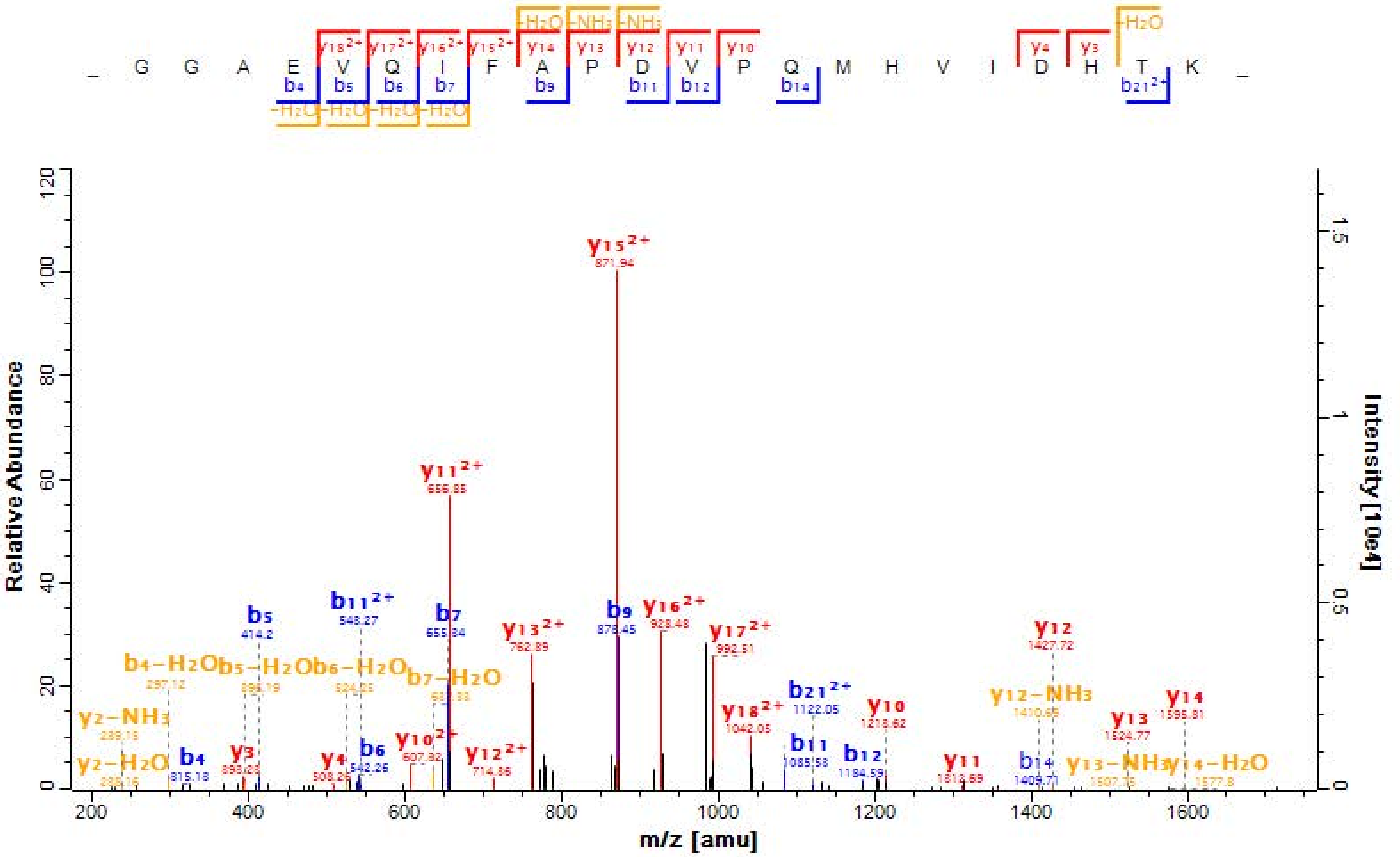
Mass:	1488.79435
m/z:	497.27206
Charge:	3+
Retentiontime:	40.698860168457
Score:	106.2576
Mass Error [ppm]:	0.47823
PEP:	0.003331
Precursor Type:	ISO

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	53 %
Peak Coverage:	21 %
Protein Localisation:	82 ... 94

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	101.1		129.1		129.1	1	K	12				
-0.11	229.2		257.2		257.2	2	Q	11	1362		1362	
	357.2		385.2		385.2	3	Q	10	1234		1234	
	486.3		514.3		514.3	4	E	9	1106		1106	
	585.3		613.3	-0.24	613.3	5	V	8	976.5		976.5	
	684.4	-0.1	356.7	+0.12	712.4	6	V	7	877.5		877.5	
	741.4	-0.05	385.2	-0.03	769.4	7	G	6	778.4	+0.02	389.7	+0.06
	888.5	-0.03	458.7	+0.026	916.5	8	F	5	721.4	+0.098	361.2	+0.01
	1002	+0.205	515.3		1030	9	L	4	574.3		574.3	
	1131		1159		1159	10	E	3	461.2	+0.22	461.2	
	1202	+0.006	615.3		1230	11	A	2	332.2	+0.084	332.2	
	1316	+0.25	672.4		1344	12	N	1	261.2		261.2	
						13	K	0	147.1	+0.135	147.1	

Scan number	6839	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	148.06



precursor information

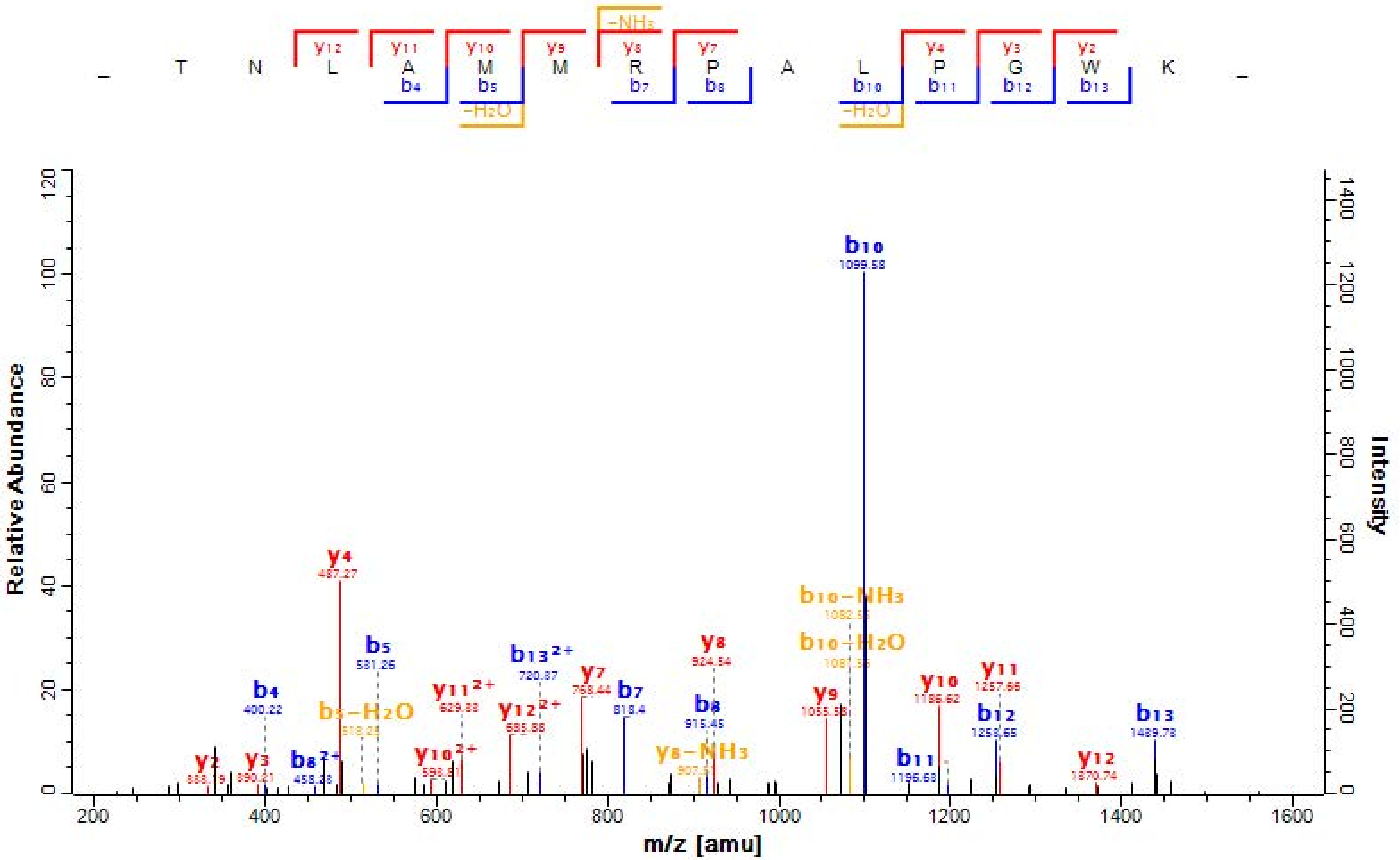
Mass:	2388.18913
m/z:	797.07032
Charge:	3+
Retentiontime:	40.897342681884
Score:	148.0627
Mass Error [ppm]:	-0.20248
PEP:	3.2399E-21
Precursor Type:	MULTI

general information

Annotation:	14 of 22
AminoAcids Coverag	64 %
Intensity Coverage:	65 %
Peak Coverage:	37 %
Protein Localisation:	73 ... 94

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	21				
	115.05		115.05	2	G	20	2340.2		2340.2	
	186.09		186.09	3	A	19	2283.2		2283.2	
	315.13	+0.0303	315.13	4	E	18	2212.1		2212.1	
	414.2	+0.0857	414.2	5	V	17	2083.1		1042	-0.023
	542.26	+0.0914	542.26	6	Q	16	1984		992.51	+0.291
	655.34	-0.127	655.34	7	I	15	1856		928.48	+0.1931
	802.41		802.41	8	F	14	1742.9		871.94	+0.249
	873.45	-0.253	873.45	9	A	13	1595.8	-0.197	1595.8	
	970.5		970.5	10	P	12	1524.8	+0.2582	762.89	-0.008
+0.0256	543.27	-0.11	1085.5	11	D	11	1427.7	+0.1477	714.36	-0.021
	1184.6	-0.098	1184.6	12	V	10	1312.7	-0.284	656.85	+0.170
	1281.6		1281.6	13	P	9	1213.6	+0.2386	607.32	+0.329
	1409.7	-0.04	1409.7	14	Q	8	1116.6		1116.6	
	1540.7		1540.7	15	M	7	988.51		988.51	
	1677.8		1677.8	16	H	6	857.47		857.47	
	1776.9		1776.9	17	V	5	720.41		720.41	
	1890		1890	18	I	4	621.34		621.34	
	2005		2005	19	D	3	508.26	+0.0707	508.26	
	2142		2142	20	H	2	393.23	-0.016	393.23	
+0.2164	1122		2243.1	21	T	1	256.17		256.17	
				22	K	0	155.13		155.13	

Scan number	7139	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	143.94



precursor information

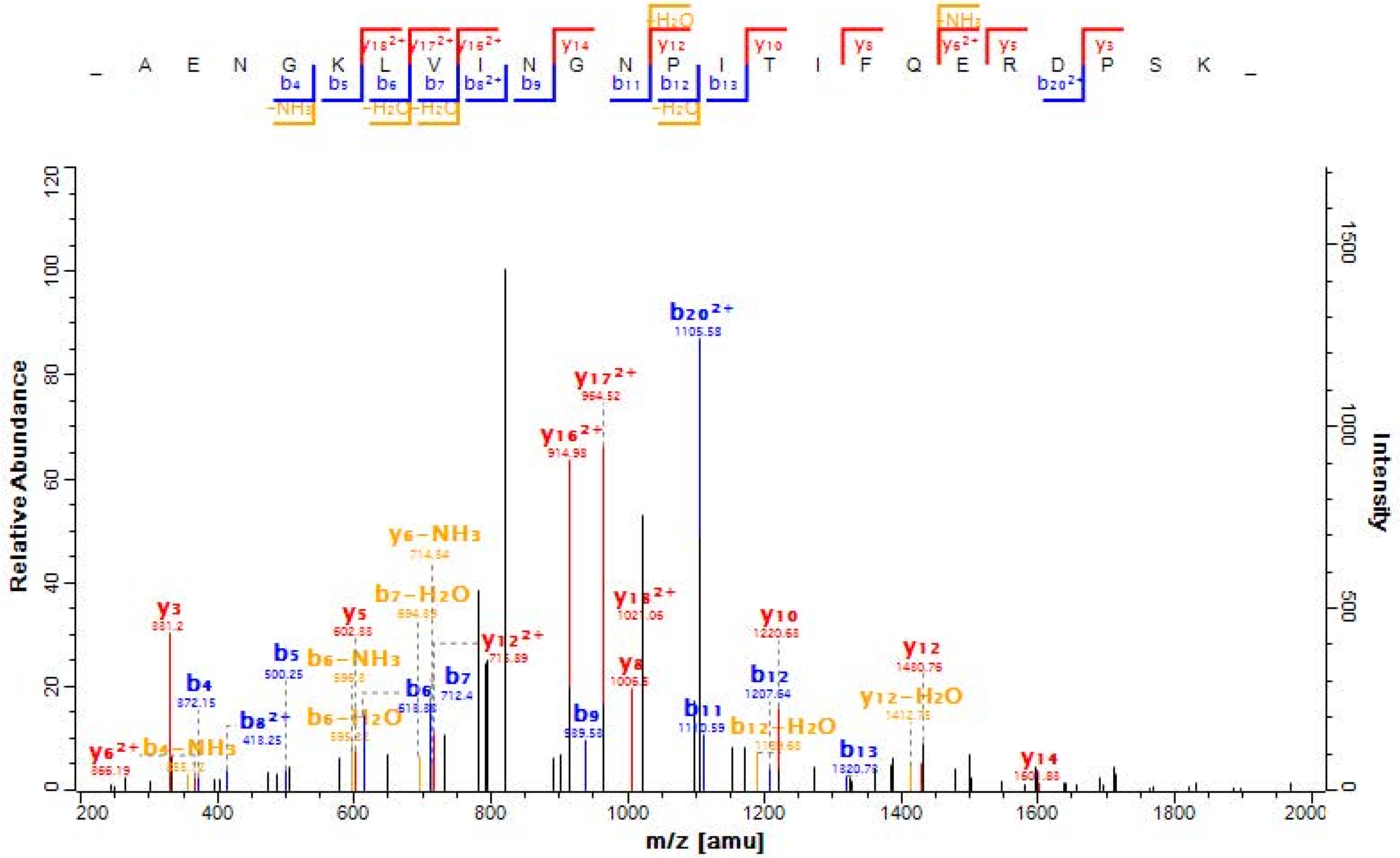
Mass:	1584.82686
m/z:	793.42071
Charge:	2+
Retentiontime:	42.646732330322
Score:	143.9394
Mass Error [ppm]:	-0.0067318
PEP:	3.7762E-09
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	60 %
Peak Coverage:	34 %
Protein Localisation:	309 ... 322

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	13				
	216.1		216.1	2	N	12	1484.8		1484.8	
	329.18		329.18	3	L	11	1370.7	+0.0427	685.88	+0.115
	400.22	+0.1563	400.22	4	A	10	1257.7	-0.034	629.33	-0.092
	531.26	+0.2129	531.26	5	M	9	1186.6	-0.013	593.81	+0.0425
	662.3		662.3	6	M	8	1055.6	+0.1693	1055.6	
	818.4	-0.128	818.4	7	R	7	924.54	+0.0157	924.54	
-0.068	458.23	+0.2746	915.45	8	P	6	768.44	-0.022	768.44	
	986.49		986.49	9	A	5	671.39		671.39	
	1099.6	-0.043	1099.6	10	L	4	600.35		600.35	
	1196.6	-0.241	1196.6	11	P	3	487.27	+0.1188	487.27	
	1253.6	-0.165	1253.6	12	G	2	390.21	+0.1665	390.21	
+0.0492	720.37	-0.226	1439.7	13	W	1	333.19	+0.0933	333.19	
				14	K	0	147.11		147.11	

Scan number	7169	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	101.48



precursor information

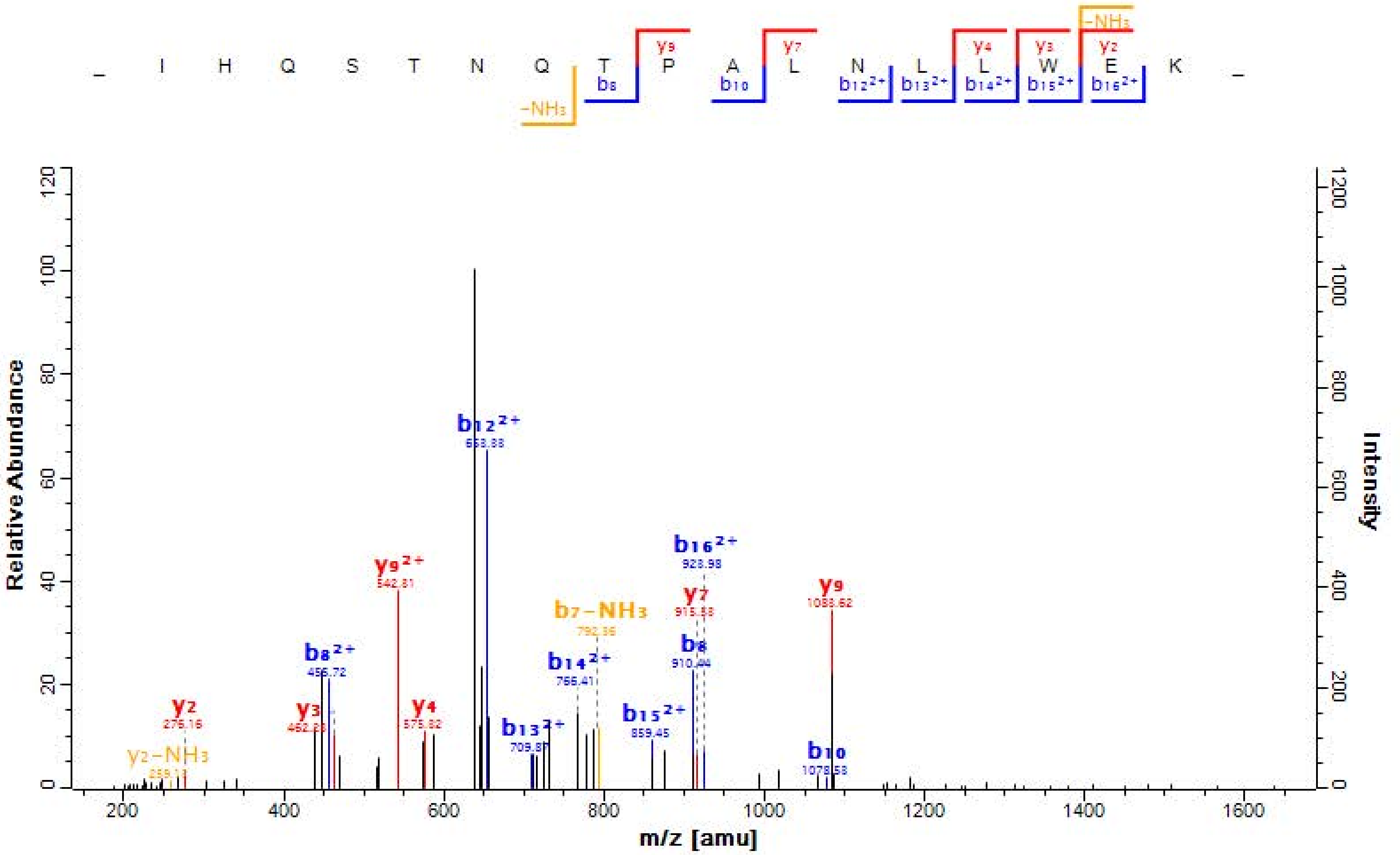
Mass:	2539.33991
m/z:	847.45391
Charge:	3+
Retentiontime:	42.822555541992
Score:	101.4772
Mass Error [ppm]:	0.18275
PEP:	7.0925E-06
Precursor Type:	ISO

general information

Annotation:	16 of 23
AminoAcids Coverag	70 %
Intensity Coverage:	41 %
Peak Coverage:	29 %
Protein Localisation:	62 ... 84

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	22				
	201.09		201.09	2	E	21	2469.3		2469.3	
	315.13		315.13	3	N	20	2340.3		2340.3	
	372.15	-0.034	372.15	4	G	19	2226.2		2226.2	
	500.25	+0.2278	500.25	5	K	18	2169.2		2169.2	
	613.33	+0.1907	613.33	6	L	17	2041.1		1021.1	-0.08
	712.4	+0.1773	712.4	7	V	16	1928		964.52	+0.311
+0.0141	413.25		825.48	8	I	15	1829		914.98	+0.236
	939.53	+0.1583	939.53	9	N	14	1715.9		1715.9	
	996.55		996.55	10	G	13	1601.8	+0.4543	1601.8	
	1110.6	-0.431	1110.6	11	N	12	1544.8		1544.8	
	1207.6	-0.118	1207.6	12	P	11	1430.8	-0.109	715.89	+0.2233
	1320.7	-0.124	1320.7	13	I	10	1333.7		1333.7	
	1421.8		1421.8	14	T	9	1220.6	+0.0293	1220.6	
	1534.9		1534.9	15	I	8	1119.6		1119.6	
	1681.9		1681.9	16	F	7	1006.5	-0.407	1006.5	
	1810		1810	17	Q	6	859.43		859.43	
	1939		1939	18	E	5	731.37		366.19	+0.2136
	2095.1		2095.1	19	R	4	602.33	-0.017	602.33	
+0.1602	1105.6		2210.2	20	D	3	446.22		446.22	
	2307.2		2307.2	21	P	2	331.2	+0.0912	331.2	
	2394.2		2394.2	22	S	1	234.14		234.14	
				23	K	0	147.11		147.11	

Scan number	7335	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	59.67



precursor information

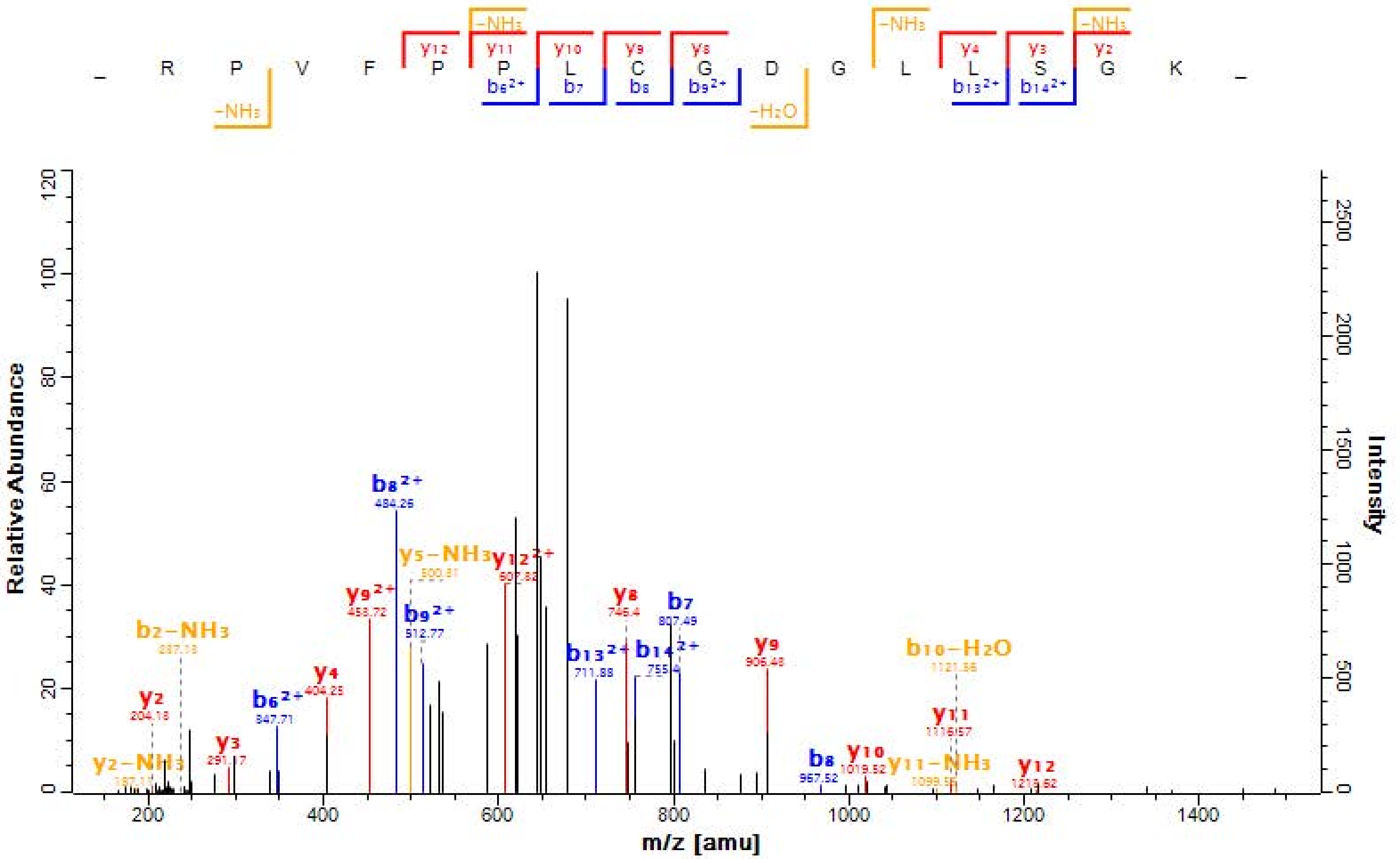
Mass:	1992.04387
m/z:	665.0219
Charge:	3+
Retentiontime:	43.857536315918
Score:	59.67264
Mass Error [ppm]:	0.49855
PEP:	0.0023857
Precursor Type:	MULTI

general information

Annotation:	10 of 17
AminoAcids Coverag	59 %
Intensity Coverage:	40 %
Peak Coverage:	19 %
Protein Localisation:	38 ... 54

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	I	16				
	251.15		251.15	2	H	15	1880		1880	
	379.21		379.21	3	Q	14	1742.9		1742.9	
	466.24		466.24	4	S	13	1614.8		1614.8	
	567.29		567.29	5	T	12	1527.8		1527.8	
	681.33		681.33	6	N	11	1426.8		1426.8	
	809.39		809.39	7	Q	10	1312.7		1312.7	
+0.047	455.72	+0.1013	910.44	8	T	9	1184.7		1184.7	
	1007.5		1007.5	9	P	8	1083.6	-0.074	542.31	+0.2867
	1078.5	+0.1658	1078.5	10	A	7	986.57		986.57	
	1191.6		1191.6	11	L	6	915.53	+0.0944	915.53	
+0.1825	653.33		1305.7	12	N	5	802.45		802.45	
-0.014	709.87		1418.7	13	L	4	688.4		688.4	
-0.009	766.41		1531.8	14	L	3	575.32	+0.1166	575.32	
-0.168	859.45		1717.9	15	W	2	462.23	+0.0786	462.23	
-0.114	923.98		1846.9	16	E	1	276.16	+0.0055	276.16	
				17	K	0	147.11		147.11	

Scan number	7391	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	98.94



precursor information

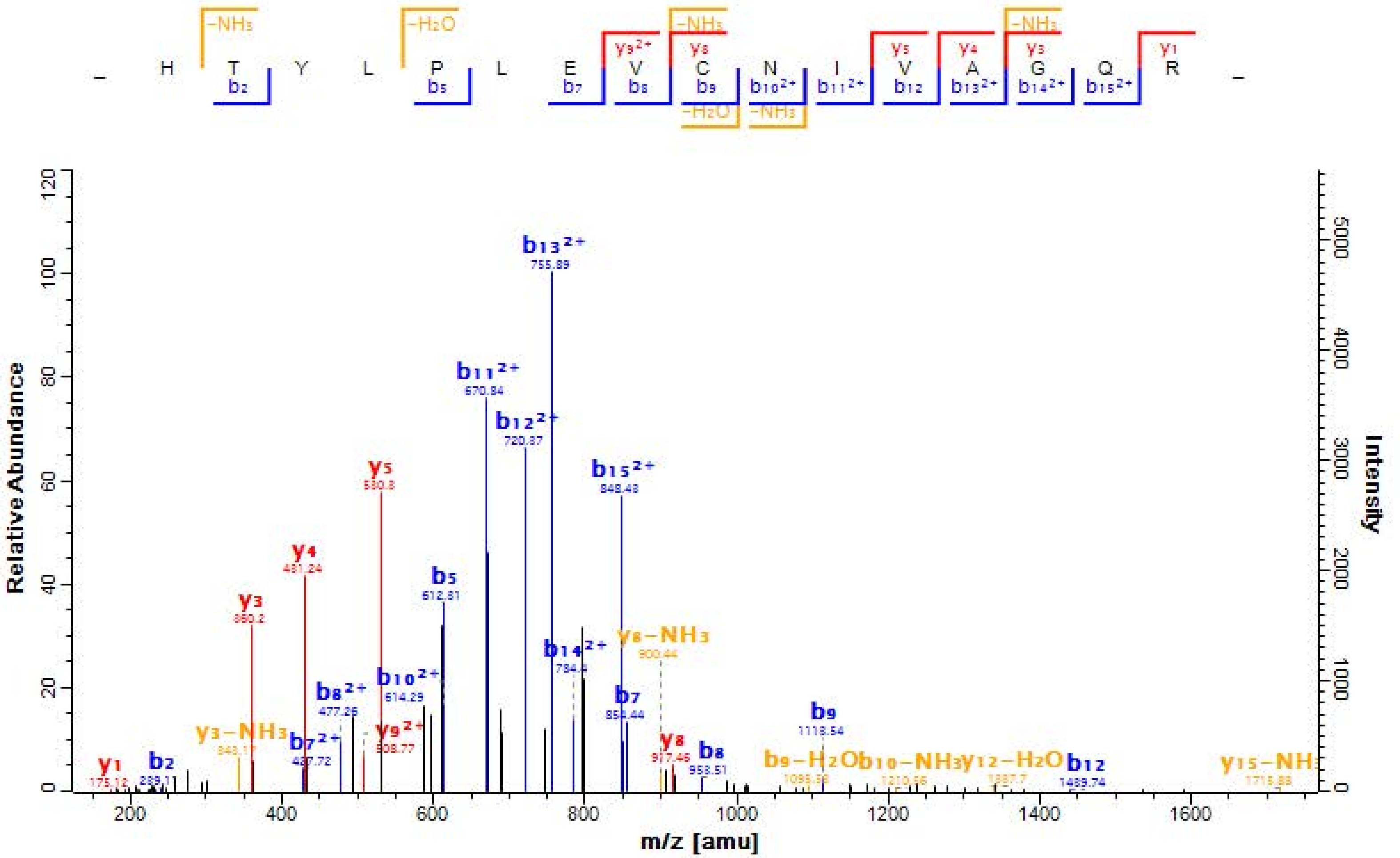
Mass:	1711.90787
m/z:	571.64323
Charge:	3+
Retentiontime:	44.221366882324
Score:	98.94319
Mass Error [ppm]:	-0.053582
PEP:	6.8983E-06
Precursor Type:	MULTI

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	36 %
Peak Coverage:	24 %
Protein Localisation:	57 ... 72

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	157.11		157.11	1	R	15				
	254.16		254.16	2	P	14	1556.8		1556.8	
	353.23		353.23	3	V	13	1459.8		1459.8	
	500.3		500.3	4	F	12	1360.7		1360.7	
	597.35		597.35	5	P	11	1213.6	+0.0069	607.32	+0.0997
-0.107	347.71		694.4	6	P	10	1116.6	-0.123	1116.6	
	807.49	-0.074	807.49	7	L	9	1019.5	-0.148	1019.5	
-0.022	484.26	+0.2731	967.52	8	C	8	906.43	-0.072	453.72	+0.0712
+0.2729	512.77		1024.5	9	G	7	746.4	+0.0441	746.4	
	1139.6		1139.6	10	D	6	689.38		689.38	
	1196.6		1196.6	11	G	5	574.36		574.36	
	1309.7		1309.7	12	L	4	517.33		517.33	
+0.2374	711.88		1422.8	13	L	3	404.25	+0.0018	404.25	
+0.1075	755.4		1509.8	14	S	2	291.17	+0.0948	291.17	
	1566.8		1566.8	15	G	1	204.13	+0.258	204.13	
				16	K	0	147.11		147.11	

Scan number	7455	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	119.25



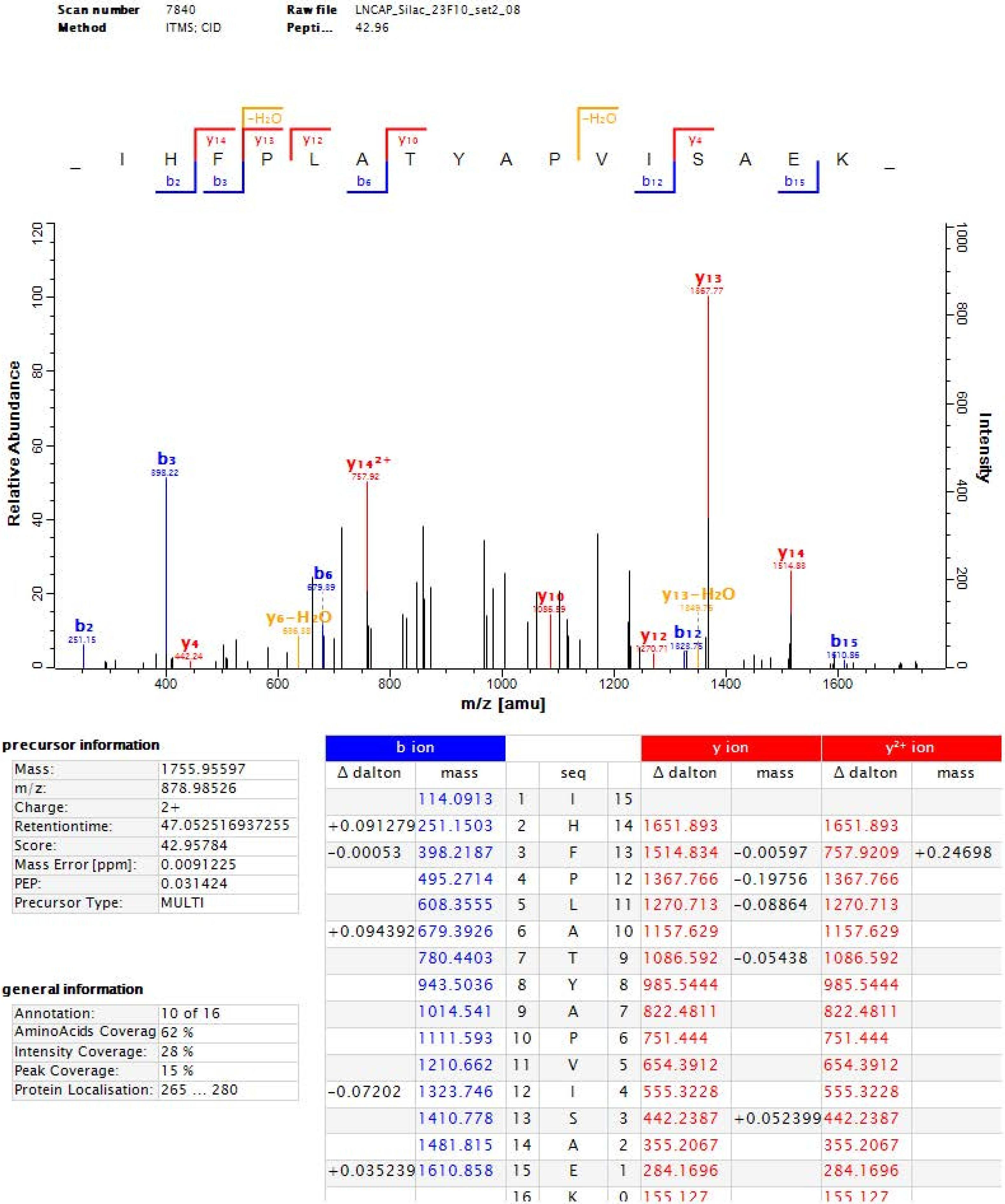
precursor information

Mass:	1868.95685
m/z:	623.99289
Charge:	3+
Retentiontime:	44.641334533691
Score:	119.2534
Mass Error [ppm]:	0.079795
PEP:	4.6907E-09
Precursor Type:	MULTI

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	62 %
Peak Coverage:	25 %
Protein Localisation:	326 ... 341

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.07		138.07	1	H	15				
	239.11	+0.1595	239.11	2	T	14	1732.9		1732.9	
	402.18		402.18	3	Y	13	1631.9		1631.9	
	515.26		515.26	4	L	12	1468.8		1468.8	
	612.31	+0.3514	612.31	5	P	11	1355.7		1355.7	
	725.4		725.4	6	L	10	1258.7		1258.7	
+0.0144	427.72	+0.0055	854.44	7	E	9	1145.6		1145.6	
+0.1086	477.26	+0.0386	953.51	8	V	8	1016.5		508.77	-0.066
	1113.5	+0.3309	1113.5	9	C	7	917.46	+0.0561	917.46	
+0.1635	614.29		1227.6	10	N	6	757.43		757.43	
+0.1045	670.84		1340.7	11	I	5	643.39		643.39	
+0.1902	720.37	-0.041	1439.7	12	V	4	530.3	+0.0135	530.3	
+0.1722	755.89		1510.8	13	A	3	431.24	+0.0524	431.24	
+0.1206	784.4		1567.8	14	G	2	360.2	+0.0063	360.2	
+0.2299	848.43		1695.9	15	Q	1	303.18		303.18	
				16	R	0	175.12	+0.1872	175.12	



Scan number	7840	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	42.96

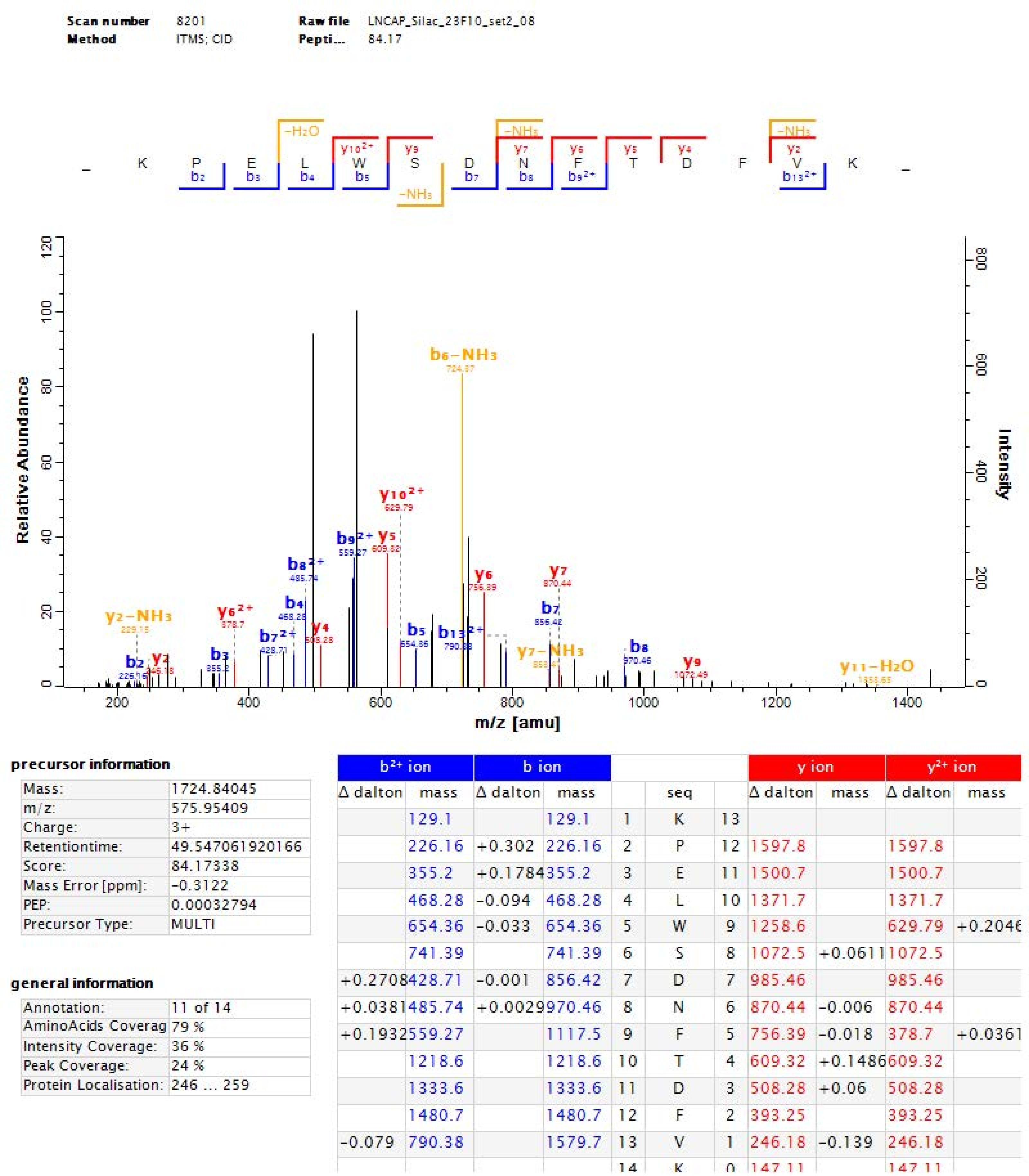
precursor information

Mass:	1755.95597
m/z:	878.98526
Charge:	2+
Retentiontime:	47.052516937255
Score:	42.95784
Mass Error [ppm]:	0.0091225
PEP:	0.031424
Precursor Type:	MULTI

general information

Annotation:	10 of 16
AminoAcids Coverag	62 %
Intensity Coverage:	28 %
Peak Coverage:	15 %
Protein Localisation:	265 ... 280

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	I	15				
+0.091279	251.1503	2	H	14	1651.893		1651.893	
-0.00053	398.2187	3	F	13	1514.834	-0.00597	757.9209	+0.24698
	495.2714	4	P	12	1367.766	-0.19756	1367.766	
	608.3555	5	L	11	1270.713	-0.08864	1270.713	
+0.094392	679.3926	6	A	10	1157.629		1157.629	
	780.4403	7	T	9	1086.592	-0.05438	1086.592	
	943.5036	8	Y	8	985.5444		985.5444	
	1014.541	9	A	7	822.4811		822.4811	
	1111.593	10	P	6	751.444		751.444	
	1210.662	11	V	5	654.3912		654.3912	
-0.07202	1323.746	12	I	4	555.3228		555.3228	
	1410.778	13	S	3	442.2387	+0.052399	442.2387	
	1481.815	14	A	2	355.2067		355.2067	
+0.035239	1610.858	15	E	1	284.1696		284.1696	
		16	K	0	155.127		155.127	



Scan number	8201	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	84.17

precursor information

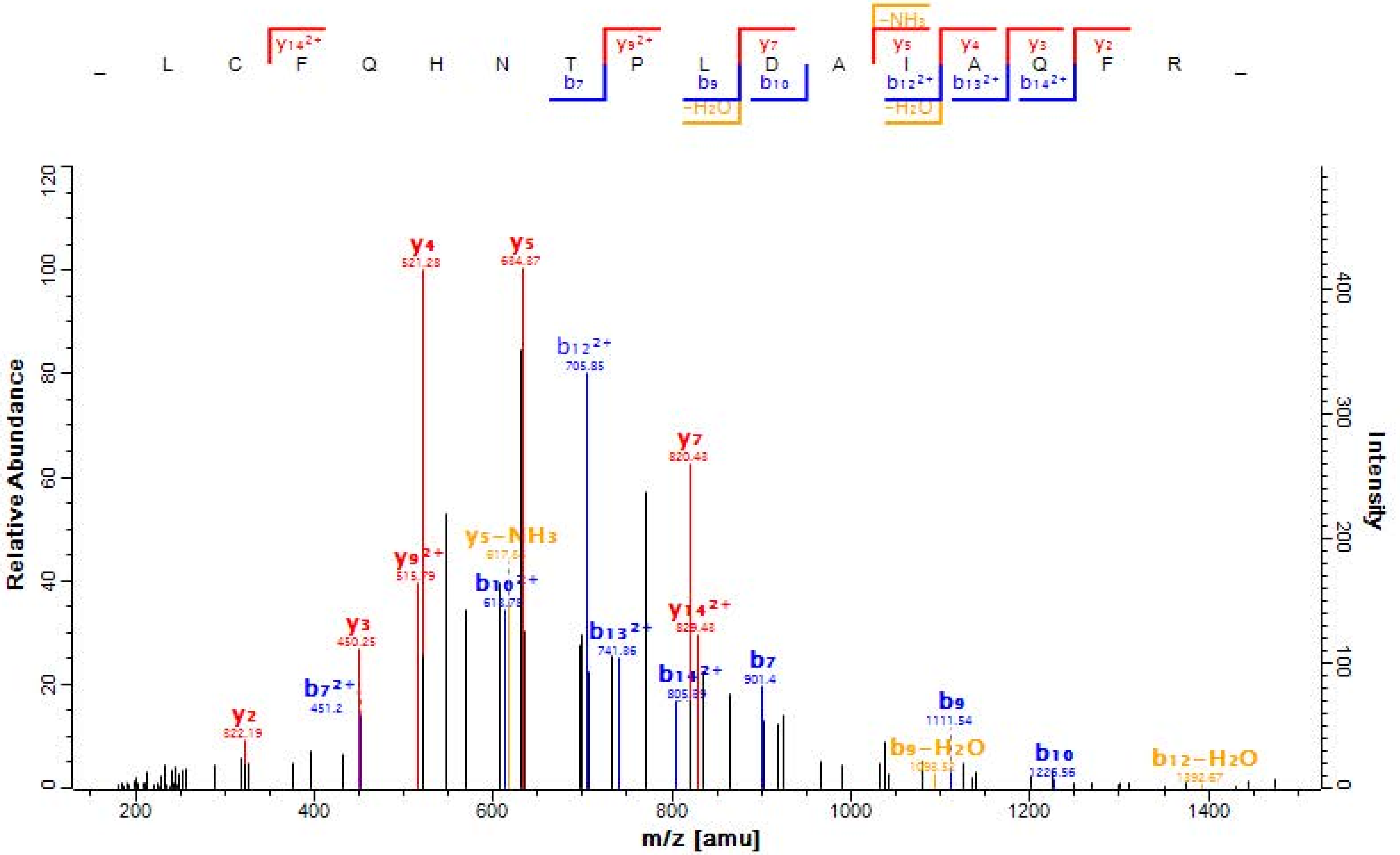
Mass:	1724.84045
m/z:	575.95409
Charge:	3+
Retentiontime:	49.547061920166
Score:	84.17338
Mass Error [ppm]:	-0.3122
PEP:	0.00032794
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	36 %
Peak Coverage:	24 %
Protein Localisation:	246 ... 259

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.1		129.1	1	K	13				
	226.16	+0.302	226.16	2	P	12	1597.8		1597.8	
	355.2	+0.1784	355.2	3	E	11	1500.7		1500.7	
	468.28	-0.094	468.28	4	L	10	1371.7		1371.7	
	654.36	-0.033	654.36	5	W	9	1258.6		629.79	+0.2046
	741.39		741.39	6	S	8	1072.5	+0.0611	1072.5	
+0.2708	428.71	-0.001	856.42	7	D	7	985.46		985.46	
+0.0381	485.74	+0.0029	970.46	8	N	6	870.44	-0.006	870.44	
+0.1932	559.27		1117.5	9	F	5	756.39	-0.018	378.7	+0.0361
	1218.6		1218.6	10	T	4	609.32	+0.1486	609.32	
	1333.6		1333.6	11	D	3	508.28	+0.06	508.28	
	1480.7		1480.7	12	F	2	393.25		393.25	
-0.079	790.38		1579.7	13	V	1	246.18	-0.139	246.18	
				14	K	0	147.11		147.11	

Scan number	8342	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	69.26



precursor information

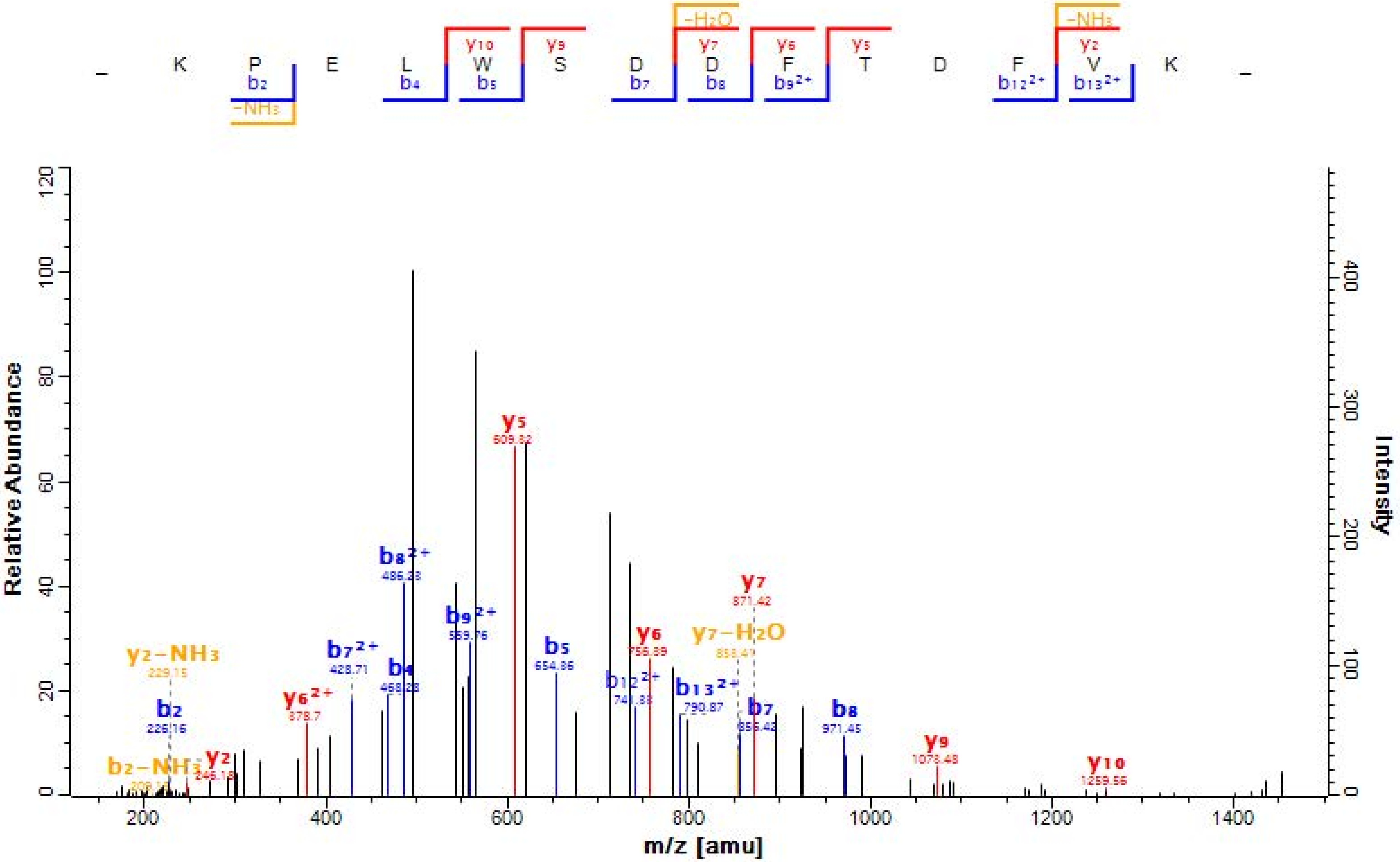
Mass:	1929.95243
m/z:	644.32475
Charge:	3+
Retentiontime:	50.679939270019
Score:	69.25761
Mass Error [ppm]:	0.24952
PEP:	0.00082891
Precursor Type:	MULTI

general information

Annotation:	10 of 16
AminoAcids Coverag	62 %
Intensity Coverage:	47 %
Peak Coverage:	19 %
Protein Localisation:	281 ... 296

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	15				
	274.12		274.12	2	C	14	1817.9		1817.9	
	421.19		421.19	3	F	13	1657.8		829.43	+0.2543
	549.25		549.25	4	Q	12	1510.8		1510.8	
	686.31		686.31	5	H	11	1382.7		1382.7	
	800.35		800.35	6	N	10	1245.7		1245.7	
+0.051	451.2	-0.04	901.4	7	T	9	1131.6		1131.6	
	998.45		998.45	8	P	8	1030.6		515.79	+0.0672
	1111.5	+0.2032	1111.5	9	L	7	933.52		933.52	
+0.0047	613.78	+0.2975	1226.6	10	D	6	820.43	-0.084	820.43	
	1297.6		1297.6	11	A	5	705.4		705.4	
-0.201	705.85		1410.7	12	I	4	634.37	-0.079	634.37	
+0.2487	741.36		1481.7	13	A	3	521.28	+0.0354	521.28	
+0.0501	805.39		1609.8	14	Q	2	450.25	-0.006	450.25	
	1756.8		1756.8	15	F	1	322.19	+0.1303	322.19	
				16	R	0	175.12		175.12	

Scan number	8399	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	88.28



precursor information

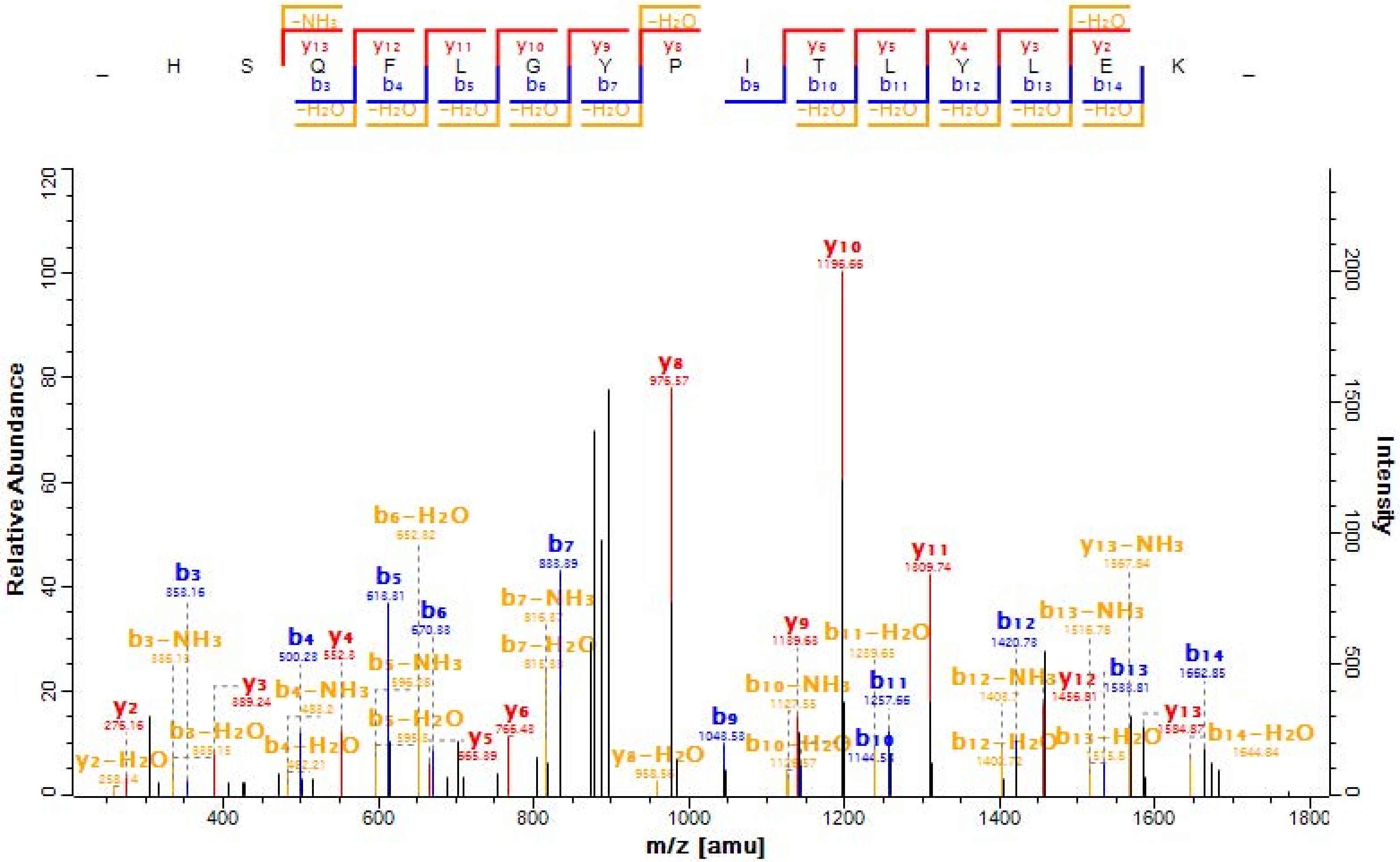
Mass:	1725.82602
m/z:	576.28262
Charge:	3+
Retentiontime:	51.162002563476
Score:	88.28183
Mass Error [ppm]:	0.59048
PEP:	0.00018389
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	31 %
Peak Coverage:	21 %
Protein Localisation:	271 ... 284

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.1		129.1	1	K	13				
	226.16	+0.046	226.16	2	P	12	1598.7		1598.7	
	355.2		355.2	3	E	11	1501.7		1501.7	
	468.28	-0.09	468.28	4	L	10	1372.6		1372.6	
	654.36	+0.0667	654.36	5	W	9	1259.6	+0.0697	1259.6	
	741.39		741.39	6	S	8	1073.5	+0.0982	1073.5	
+0.0128	428.71	+0.0551	856.42	7	D	7	986.45		986.45	
+0.2108	486.23	-0.098	971.45	8	D	6	871.42	+0.0994	871.42	
-0.098	559.76		1118.5	9	F	5	756.39	-0.114	378.7	+0.0723
	1219.6		1219.6	10	T	4	609.32	+0.0664	609.32	
	1334.6		1334.6	11	D	3	508.28		508.28	
-0.031	741.33		1481.7	12	F	2	393.25		393.25	
-0.079	790.87		1580.7	13	V	1	246.18	-0.074	246.18	
				14	K	0	147.11		147.11	

Scan number	8810	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	266.45



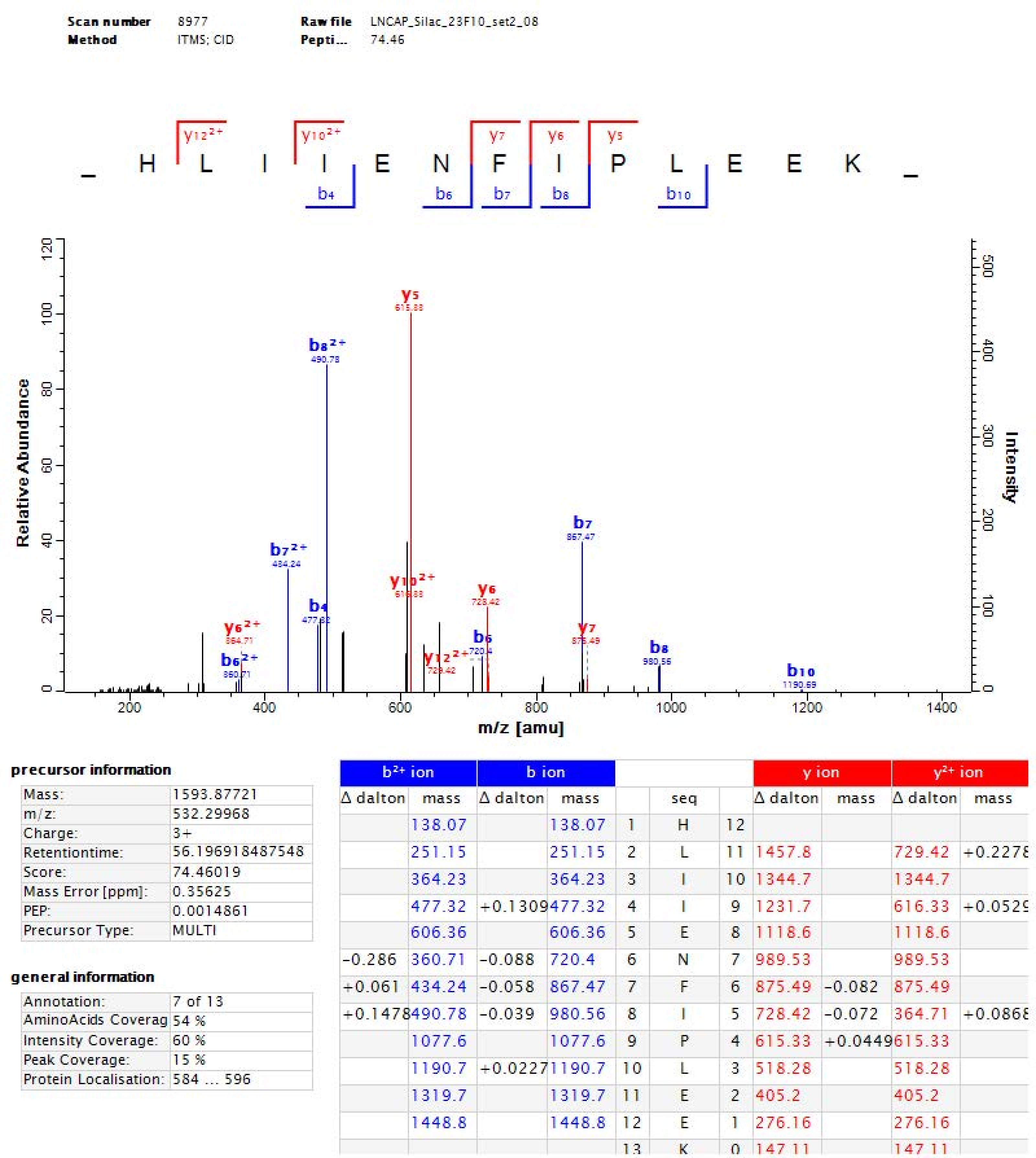
precursor information

Mass:	1807.95084
m/z:	904.9827
Charge:	2+
Retentiontime:	54.612751007080
Score:	266.4517
Mass Error [ppm]:	-0.018335
PEP:	6.5342E-68
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	48 %
Peak Coverage:	47 %
Protein Localisation:	168 ... 182

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	138.066188329	1	H	14		
	225.098216739	2	S	13	1671.89923615	
-0.0149485	353.15679425	3	Q	12	1584.86720774	-0.2007038
+0.0786248	500.225208166	4	F	11	1456.80863023	-0.1510375
-0.0013498	613.309272147	5	L	10	1309.74021631	-0.0440493
+0.1280654	670.330735871	6	G	9	1196.65615233	-0.0232178
-0.0093598	833.394064409	7	Y	8	1139.63468861	-0.1827843
	930.446828261	8	P	7	976.571360072	+0.0020652
-0.0609215	1043.53089224	9	I	6	879.51859622	
+0.0210387	1144.57857072	10	T	5	766.43453224	+0.1292495
-0.0658329	1257.6626347	11	L	4	665.386853766	+0.0237297
-0.1019398	1420.72596323	12	Y	3	552.302789786	+0.035406
+0.0433663	1533.81002721	13	L	2	389.239461247	+0.1287028
-0.1515705	1662.85262031	14	E	1	276.155397267	-1.8E-06
		15	K	0	147.112804171	



Scan number	8977
Method	ITMS; CID
Raw file	LNCAP_Silac_23F10_set2_08
Pepti...	74.46

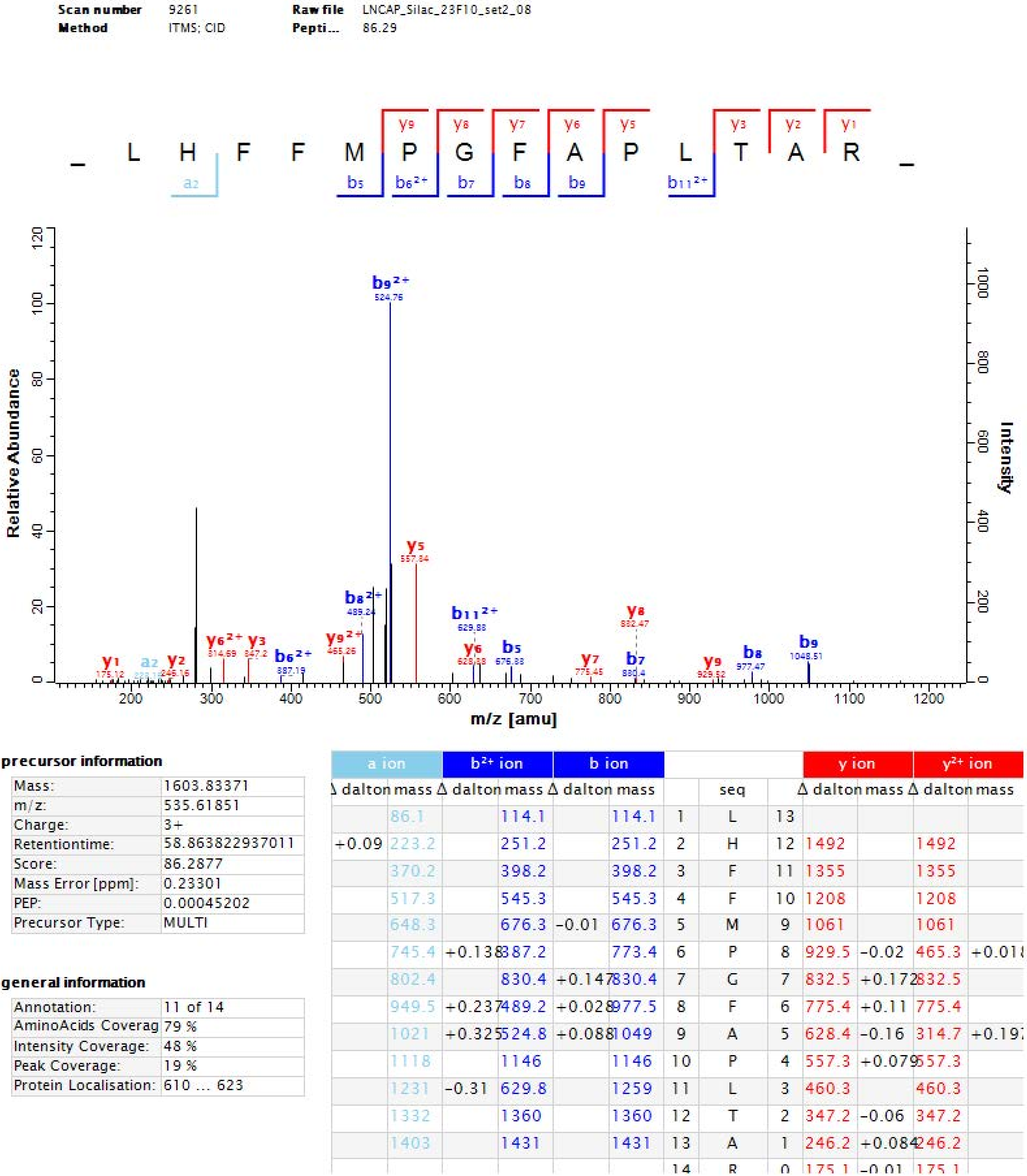
precursor information

Mass:	1593.87721
m/z:	532.29968
Charge:	3+
Retentiontime:	56.196918487548
Score:	74.46019
Mass Error [ppm]:	0.35625
PEP:	0.0014861
Precursor Type:	MULTI

general information

Annotation:	7 of 13
AminoAcids Coverag	54 %
Intensity Coverage:	60 %
Peak Coverage:	15 %
Protein Localisation:	584 ... 596

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.07		138.07	1	H	12				
	251.15		251.15	2	L	11	1457.8		729.42	+0.227
	364.23		364.23	3	I	10	1344.7		1344.7	
	477.32	+0.1309	477.32	4	I	9	1231.7		616.33	+0.052
	606.36		606.36	5	E	8	1118.6		1118.6	
-0.286	360.71	-0.088	720.4	6	N	7	989.53		989.53	
+0.061	434.24	-0.058	867.47	7	F	6	875.49	-0.082	875.49	
+0.1478	490.78	-0.039	980.56	8	I	5	728.42	-0.072	364.71	+0.086
	1077.6		1077.6	9	P	4	615.33	+0.0449	615.33	
	1190.7	+0.0227	1190.7	10	L	3	518.28		518.28	
	1319.7		1319.7	11	E	2	405.2		405.2	
	1448.8		1448.8	12	E	1	276.16		276.16	
				13	K	0	147.11		147.11	



Scan number	9261	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	86.29

precursor information

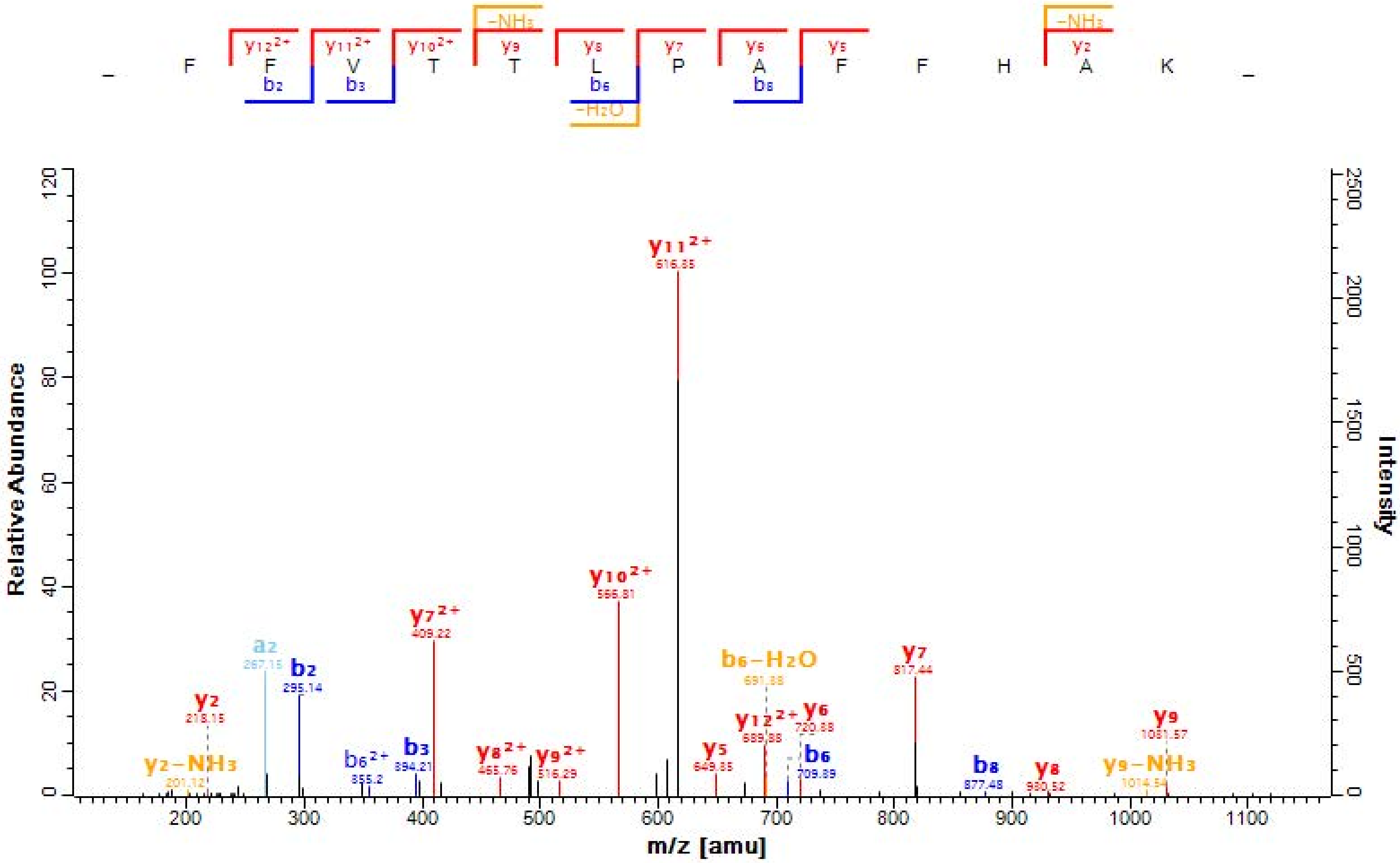
Mass:	1603.83371
m/z:	535.61851
Charge:	3+
Retentiontime:	58.863822937011
Score:	86.2877
Mass Error [ppm]:	0.23301
PEP:	0.00045202
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	48 %
Peak Coverage:	19 %
Protein Localisation:	610 ... 623

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	13				
+0.09	223.2		251.2		251.2	2	H	12	1492		1492	
	370.2		398.2		398.2	3	F	11	1355		1355	
	517.3		545.3		545.3	4	F	10	1208		1208	
	648.3		676.3	-0.01	676.3	5	M	9	1061		1061	
	745.4	+0.138	387.2		773.4	6	P	8	929.5	-0.02	465.3	+0.01
	802.4		830.4	+0.147	830.4	7	G	7	832.5	+0.172	832.5	
	949.5	+0.237	489.2	+0.028	977.5	8	F	6	775.4	+0.11	775.4	
	1021	+0.325	524.8	+0.088	1049	9	A	5	628.4	-0.16	314.7	+0.19
	1118		1146		1146	10	P	4	557.3	+0.079	557.3	
	1231	-0.31	629.8		1259	11	L	3	460.3		460.3	
	1332		1360		1360	12	T	2	347.2	-0.06	347.2	
	1403		1431		1431	13	A	1	246.2	+0.084	246.2	
						14	R	0	175.1	-0.01	175.1	

Scan number	9286	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	130.01



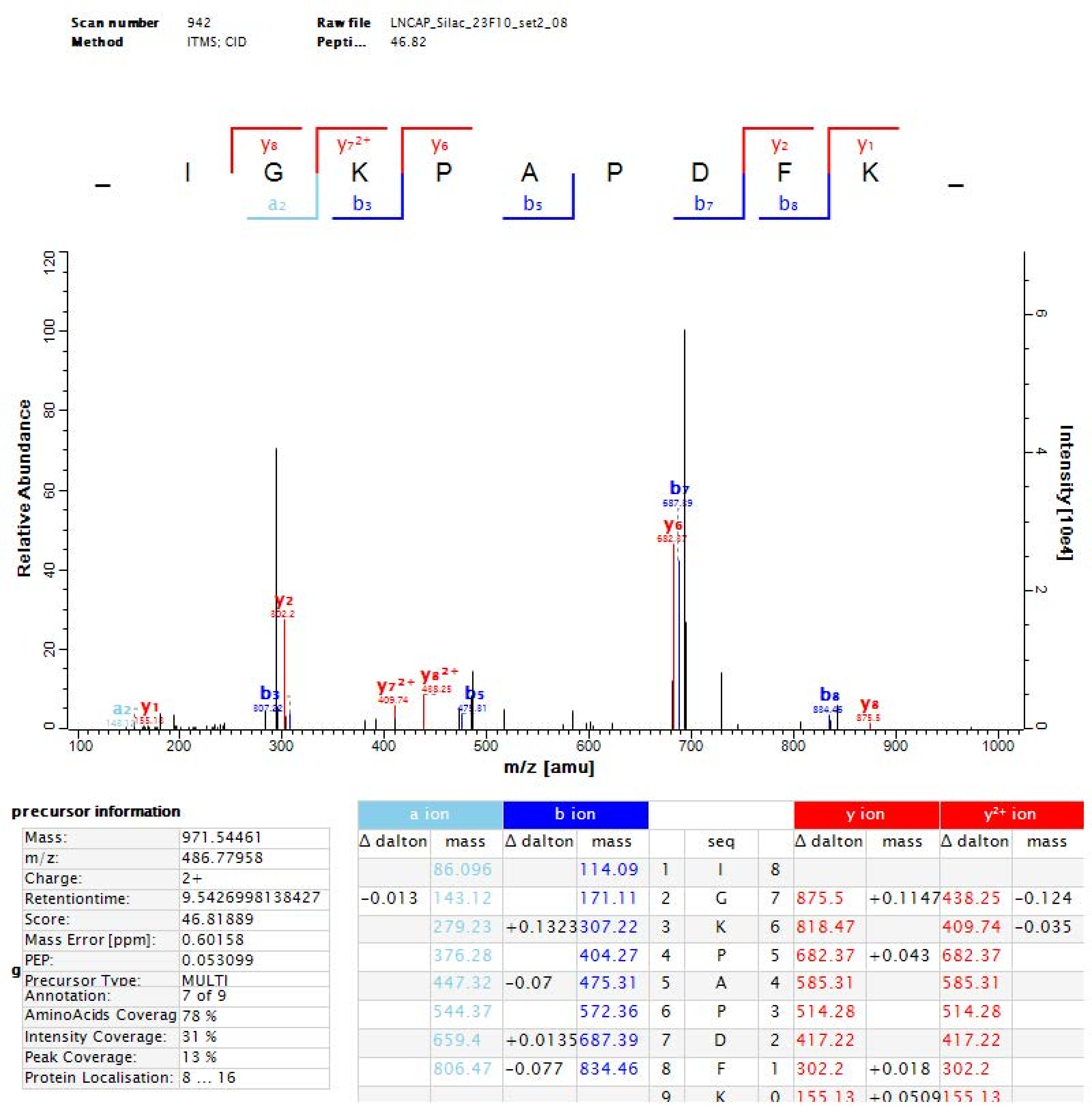
precursor information

Mass:	1524.81317
m/z:	509.27833
Charge:	3+
Retentiontime:	59.113864898681
Score:	130.006
Mass Error [ppm]:	0.16202
PEP:	1.1338E-06
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	63 %
Peak Coverage:	24 %
Protein Localisation:	103 ... 115

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.1		148.1		148.1	1	F	12				
+0.017	267.1		295.1	+0.018	295.1	2	F	11	1379		689.9	+0.16
	366.2		394.2	+0.085	394.2	3	V	10	1232		616.3	+0.03
	467.3		495.3		495.3	4	T	9	1133		566.8	+0.25
	568.3		596.3		596.3	5	T	8	1032	+0.259	516.3	+0.16
	681.4	-0.03	355.2	-0.03	709.4	6	L	7	930.5	+0.217	465.8	-0.02
	778.4		806.4		806.4	7	P	6	817.4	-0.01	409.2	+0.14
	849.5		877.5	-0.16	877.5	8	A	5	720.4	-0.04	720.4	
	996.6		1025		1025	9	F	4	649.3	+0.023	649.3	
	1144		1172		1172	10	F	3	502.3		502.3	
	1281		1309		1309	11	H	2	355.2		355.2	
	1352		1380		1380	12	A	1	218.1	-0.1	218.1	
						13	K	0	147.1		147.1	



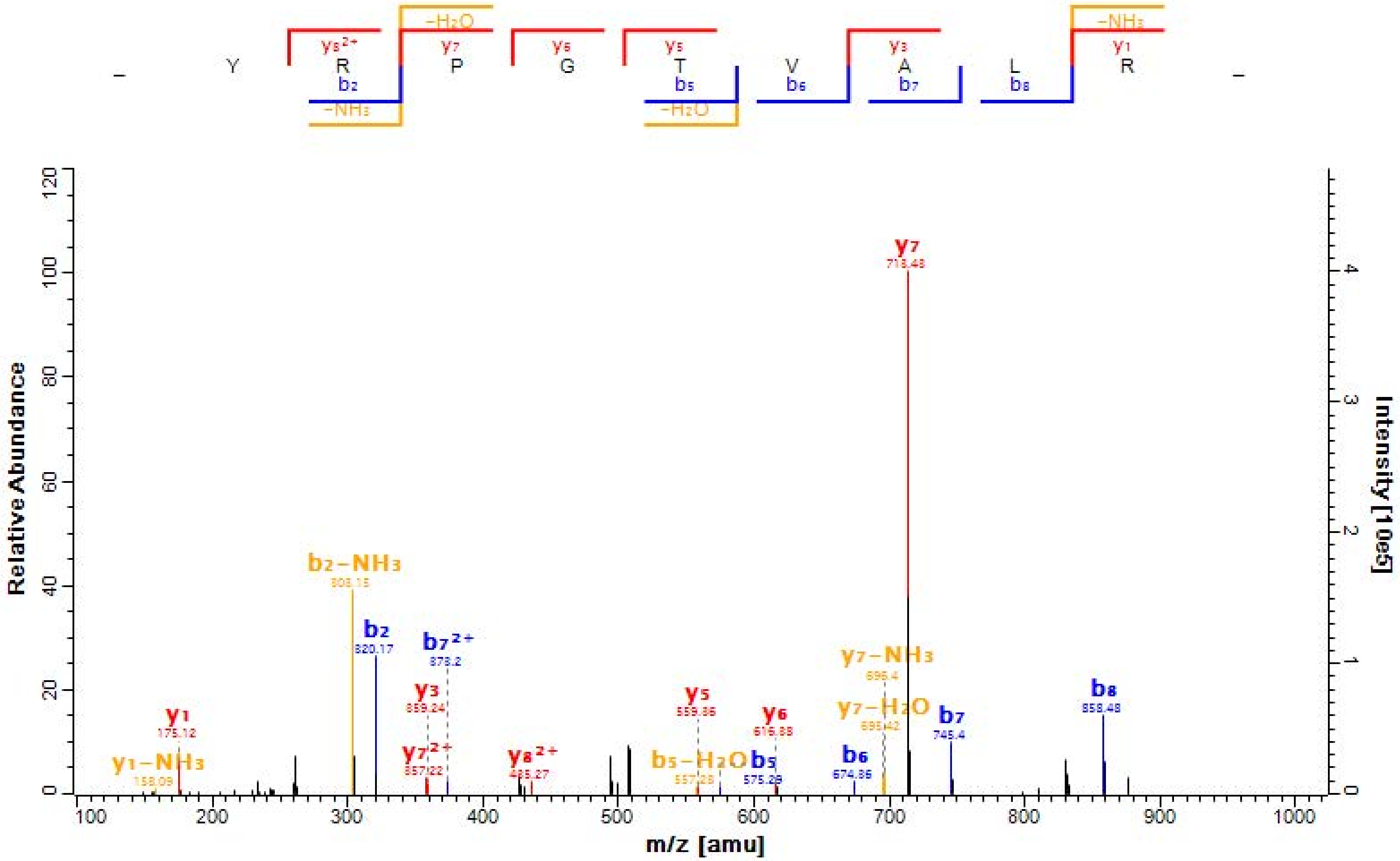
Scan number	942	**Raw file**	LNCAP_Silac_23F10_set2_08
Method	ITMS; CID	**Pepti...**	46.82

precursor information

Mass:	971.54461
m/z:	486.77958
Charge:	2+
Retentiontime:	9.5426998138427
Score:	46.81889
Mass Error [ppm]:	0.60158
PEP:	0.053099
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	31 %
Peak Coverage:	13 %
Protein Localisation:	8 ... 16

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	8				
-0.013	143.12		171.11	2	G	7	875.5	+0.1147	438.25	-0.124
	279.23	+0.1323	307.22	3	K	6	818.47		409.74	-0.035
	376.28		404.27	4	P	5	682.37	+0.043	682.37	
	447.32	-0.07	475.31	5	A	4	585.31		585.31	
	544.37		572.36	6	P	3	514.28		514.28	
	659.4	+0.0135	687.39	7	D	2	417.22		417.22	
	806.47	-0.077	834.46	8	F	1	302.2	+0.018	302.2	
				9	K	0	155.13	+0.0509	155.13	

Scan number	1104	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	117.31

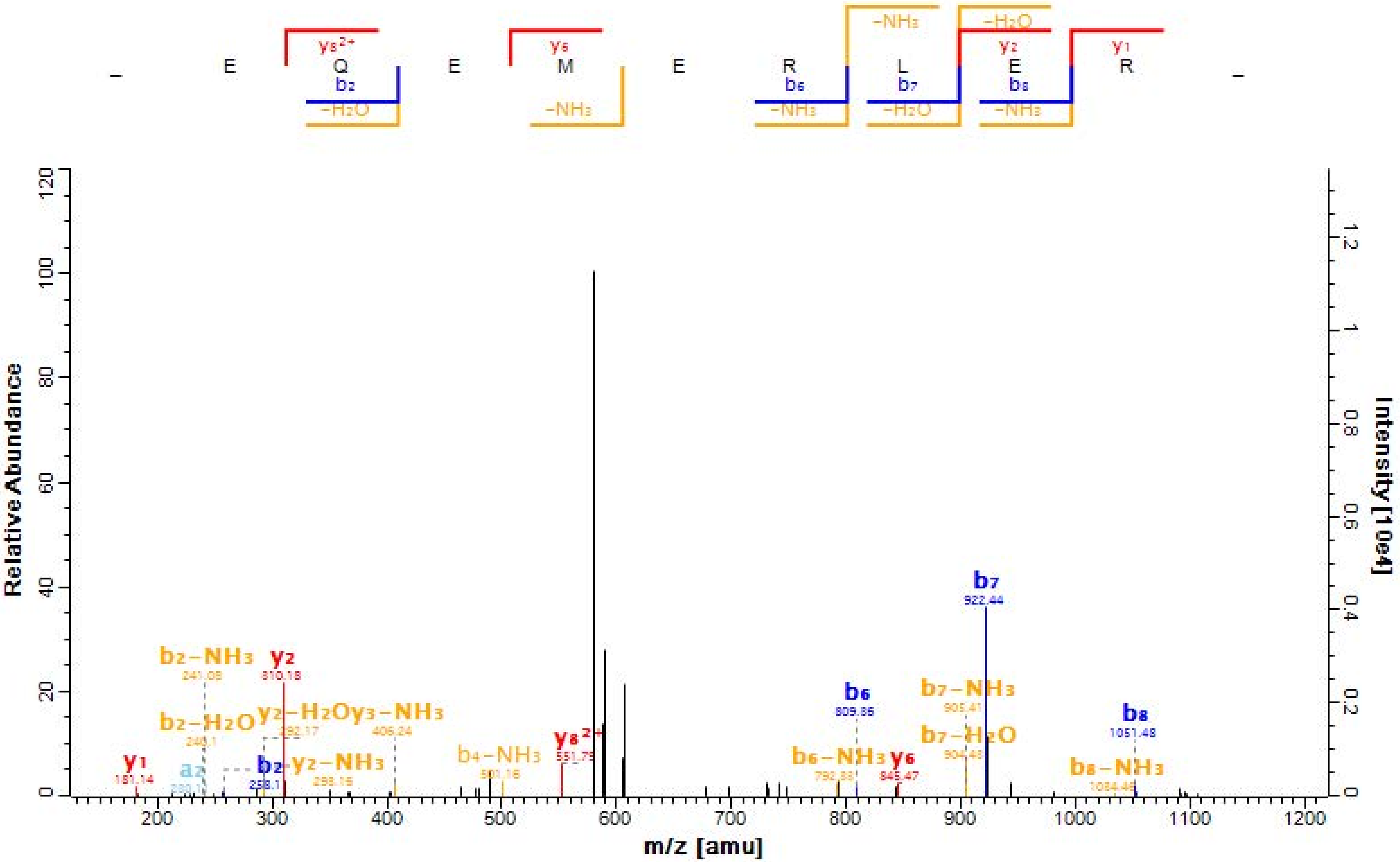


precursor information

Mass:	1031.5873
m/z:	516.80093
Charge:	2+
Retentiontime:	10.964016914367
Score:	117.3115
Mass Error [ppm]:	-0.30542
PEP:	0.00077121
Precursor Type:	ISO
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	61 %
Peak Coverage:	21 %
Protein Localisation:	42 ... 50

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	164.07		164.07	1	Y	8				
	320.17	+0.0226	320.17	2	R	7	869.53		435.27	+0.0834
	417.22		417.22	3	P	6	713.43	+0.0016	357.22	+0.1453
	474.25		474.25	4	G	5	616.38	-0.042	616.38	
	575.29	+0.0908	575.29	5	T	4	559.36	-0.025	559.36	
	674.36	+0.108	674.36	6	V	3	458.31		458.31	
+0.0481	373.2	+0.003	745.4	7	A	2	359.24	+0.0771	359.24	
	858.48	-0.003	858.48	8	L	1	288.2		288.2	
				9	R	0	175.12	+0.0287	175.12	

Scan number	1304	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	93.65



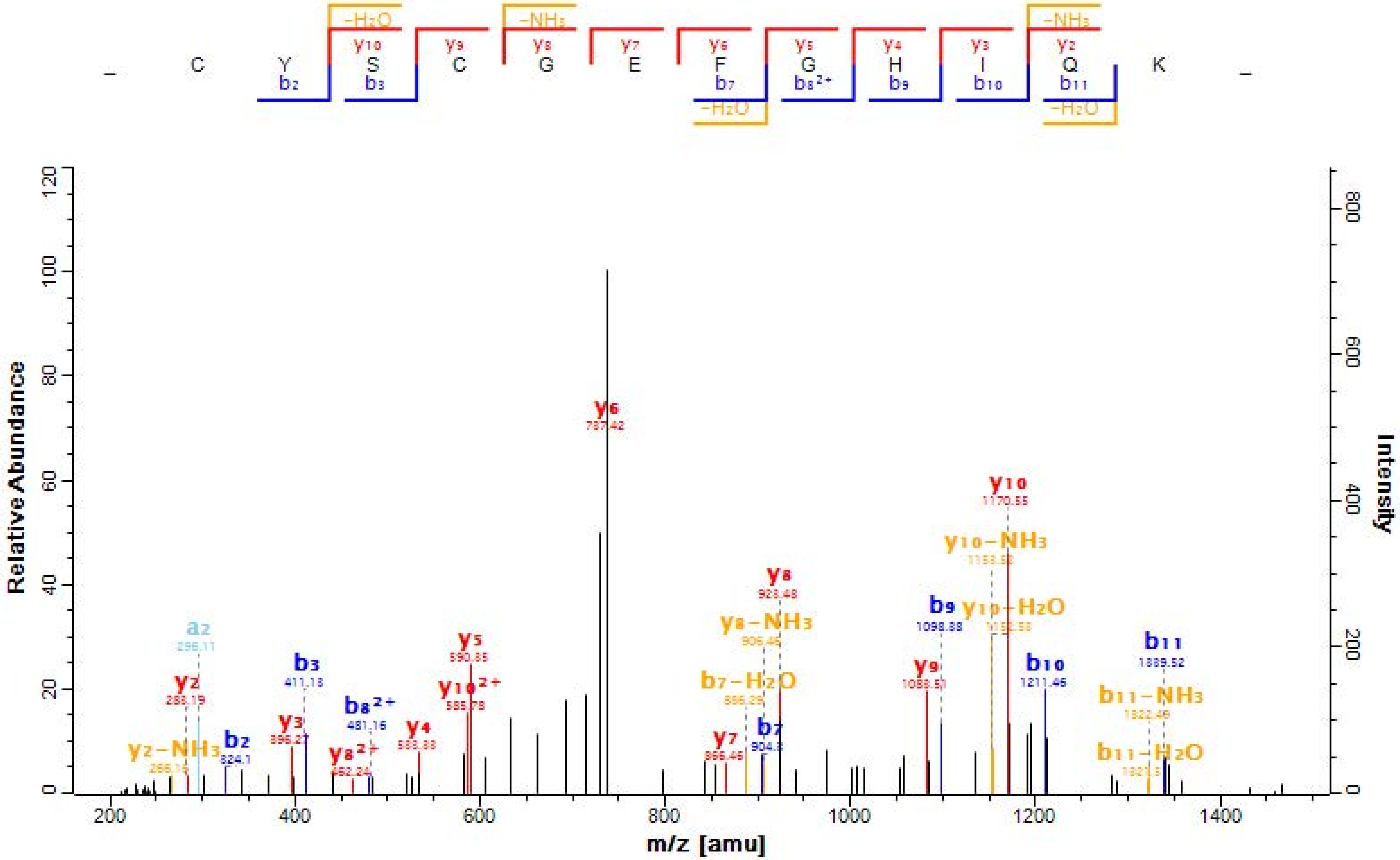
precursor information

g

Mass:	1218.56656
m/z:	610.29056
Charge:	2+
Retentiontime:	12.107703208923
Score:	93.64885
Mass Error [ppm]:	0.2218
PEP:	0.0037787
Precursor Type:	MULTI
Annotation:	6 of 9
AminoAcids Coverag	67 %
Intensity Coverage:	27 %
Peak Coverage:	20 %
Protein Localisation:	603 ... 611

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	8				
−0.02	230.11	+0.1025	258.11	2	Q	7	1102.6		551.79	+0.1735
	359.16		387.15	3	E	6	974.51		974.51	
	490.2		518.19	4	M	5	845.47	+0.1339	845.47	
	619.24		647.23	5	E	4	714.43		714.43	
	781.36	+0.1268	809.36	6	R	3	585.39		585.39	
	894.44	+0.0446	922.44	7	L	2	423.27		423.27	
	1023.5	−0.009	1051.5	8	E	1	310.18	+0.0344	310.18	
				9	R	0	181.14	+0.0385	181.14	

Scan number	1673	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	174.77



precursor information

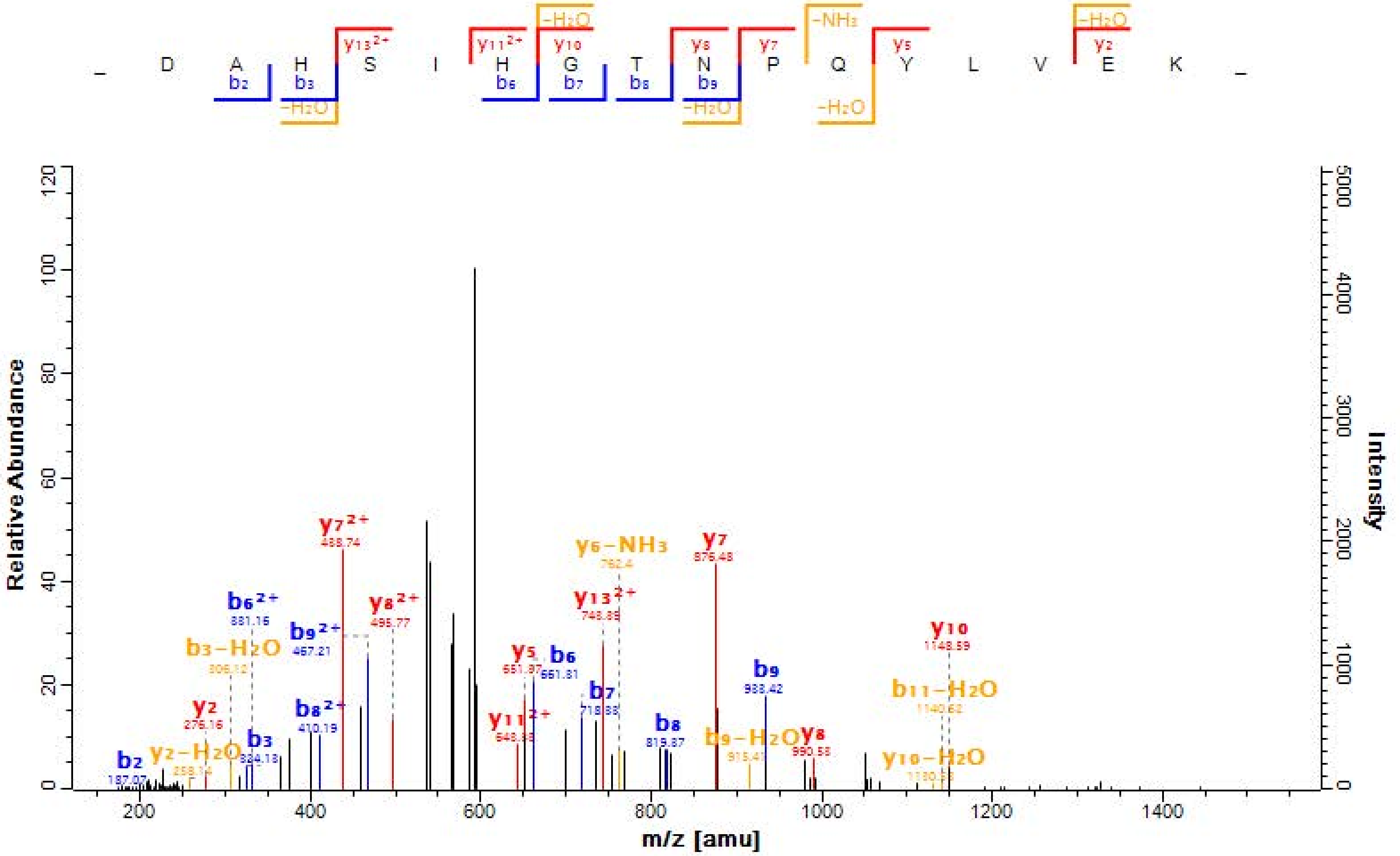
Mass:	1484.61754
m/z:	743.31605
Charge:	2+
Retentiontime:	14.207658767700
Score:	174.7679
Mass Error [ppm]:	-0.086735
PEP:	1.6786E-10
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	44 %
Peak Coverage:	30 %
Protein Localisation:	119 ... 130

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	133		161		161	1	C	11				
+0.021	296.1		324.1	+0.045	324.1	2	Y	10	1334		1334	
	383.1		411.1	+0.122	411.1	3	S	9	1171	-0.11	585.8	+0.00
	543.2		571.2		571.2	4	C	8	1084	-0.03	1084	
	600.2		628.2		628.2	5	G	7	923.5	+0.005	462.2	+0.10
	729.2		757.2		757.2	6	E	6	866.5	+0.055	866.5	
	876.3		904.3	-0.24	904.3	7	F	5	737.4	+0.196	737.4	
	933.3	-0.32	481.2		961.3	8	G	4	590.4	+0.122	590.4	
	1070		1098	-0.01	1098	9	H	3	533.3	+0.108	533.3	
	1183		1211	-0.09	1211	10	I	2	396.3	+0.013	396.3	
	1312		1340	+0	1340	11	Q	1	283.2	+0.048	283.2	
						12	K	0	155.1		155.1	

Scan number	1820	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	97.2



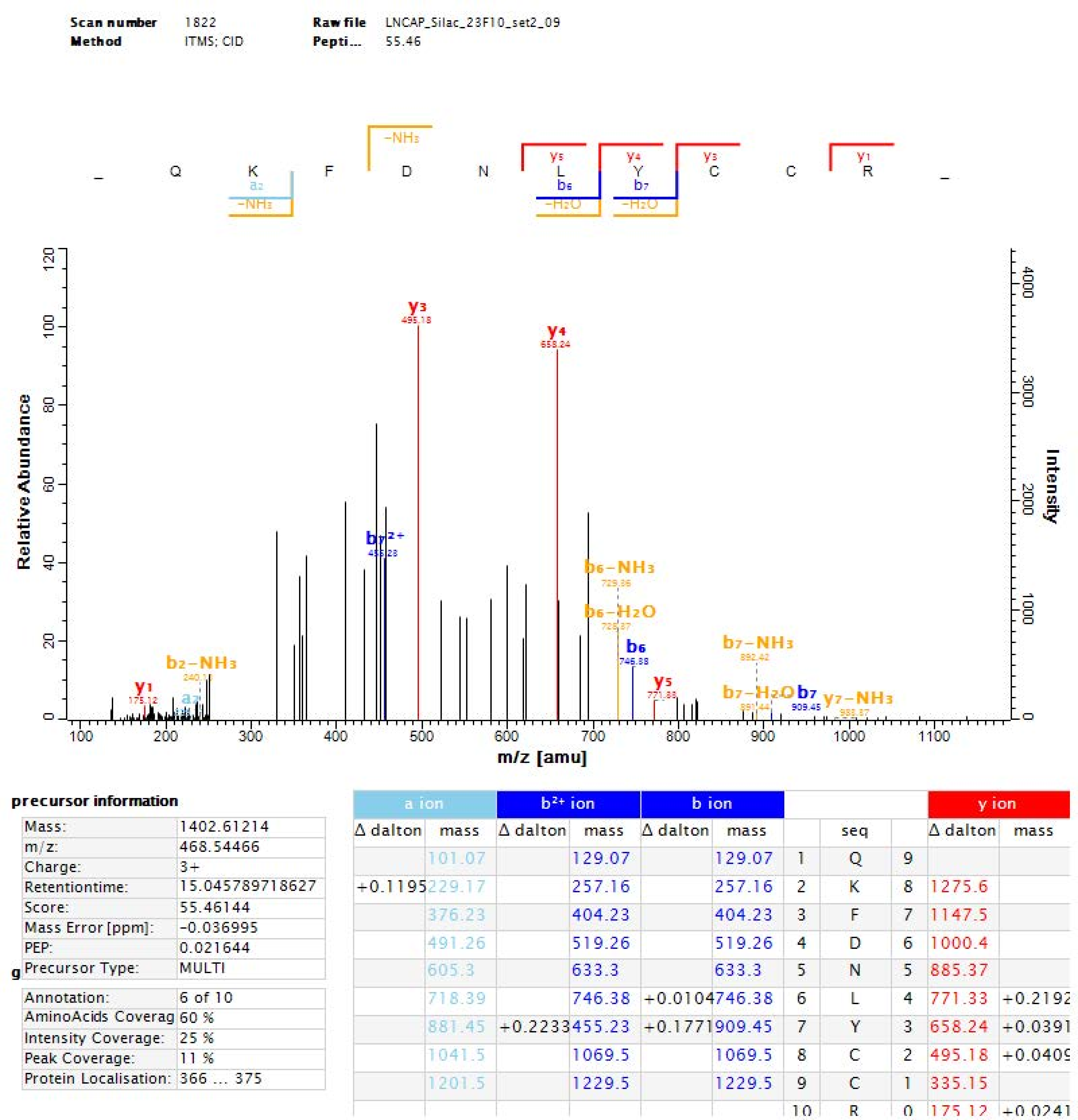
precursor information

Mass:	1807.88628
m/z:	603.63604
Charge:	3+
Retentiontime:	15.036221504211
Score:	97.20335
Mass Error [ppm]:	0.53823
PEP:	1.8617E-05
Precursor Type:	MULTI

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	35 %
Peak Coverage:	20 %
Protein Localisation:	8 ... 23

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	15				
	187.07	-0.075	187.07	2	A	14	1693.9		1693.9	
	324.13	+0.1259	324.13	3	H	13	1622.8		1622.8	
	411.16		411.16	4	S	12	1485.8		743.39	+0.2334
	524.25		524.25	5	I	11	1398.7		1398.7	
+0.1106	331.16	+0.2298	661.31	6	H	10	1285.7		643.33	+0.1422
	718.33	-0.218	718.33	7	G	9	1148.6	-0.027	1148.6	
+0.0215	410.19	+0.3141	819.37	8	T	8	1091.6		1091.6	
+0.3617	467.21	-0.15	933.42	9	N	7	990.53	-0.021	495.77	+0.3592
	1030.5		1030.5	10	P	6	876.48	+0.0475	438.74	+0.2464
	1158.5		1158.5	11	Q	5	779.43		779.43	
	1321.6		1321.6	12	Y	4	651.37	+0.0736	651.37	
	1434.7		1434.7	13	L	3	488.31		488.31	
	1533.7		1533.7	14	V	2	375.22		375.22	
	1662.8		1662.8	15	E	1	276.16	+0.0405	276.16	
				16	K	0	147.11		147.11	



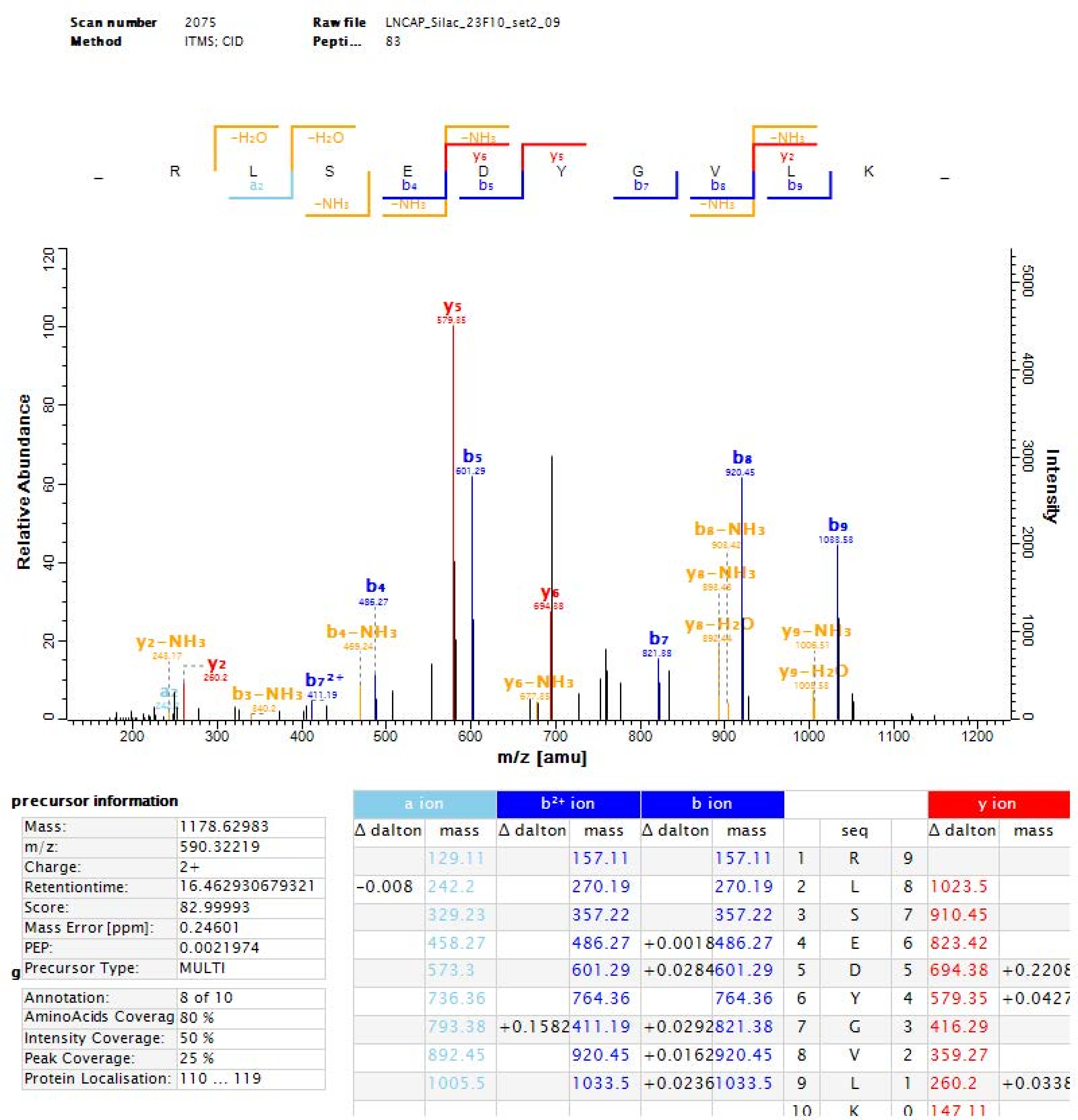
Scan number	1822	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	55.46

precursor information

Mass:	1402.61214
m/z:	468.54466
Charge:	3+
Retentiontime:	15.045789718627
Score:	55.46144
Mass Error [ppm]:	-0.036995
PEP:	0.021644
Precursor Type:	MULTI

Annotation:	6 of 10
AminoAcids Coverag	60 %
Intensity Coverage:	25 %
Peak Coverage:	11 %
Protein Localisation:	366 ... 375

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	101.07		129.07		129.07	1	Q	9		
+0.1195	229.17		257.16		257.16	2	K	8	1275.6	
	376.23		404.23		404.23	3	F	7	1147.5	
	491.26		519.26		519.26	4	D	6	1000.4	
	605.3		633.3		633.3	5	N	5	885.37	
	718.39		746.38	+0.0104	746.38	6	L	4	771.33	+0.2192
	881.45	+0.2233	455.23	+0.1771	909.45	7	Y	3	658.24	+0.0391
	1041.5		1069.5		1069.5	8	C	2	495.18	+0.040
	1201.5		1229.5		1229.5	9	C	1	335.15	
						10	R	0	175.12	+0.0241



Scan number	2075	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	83

precursor information

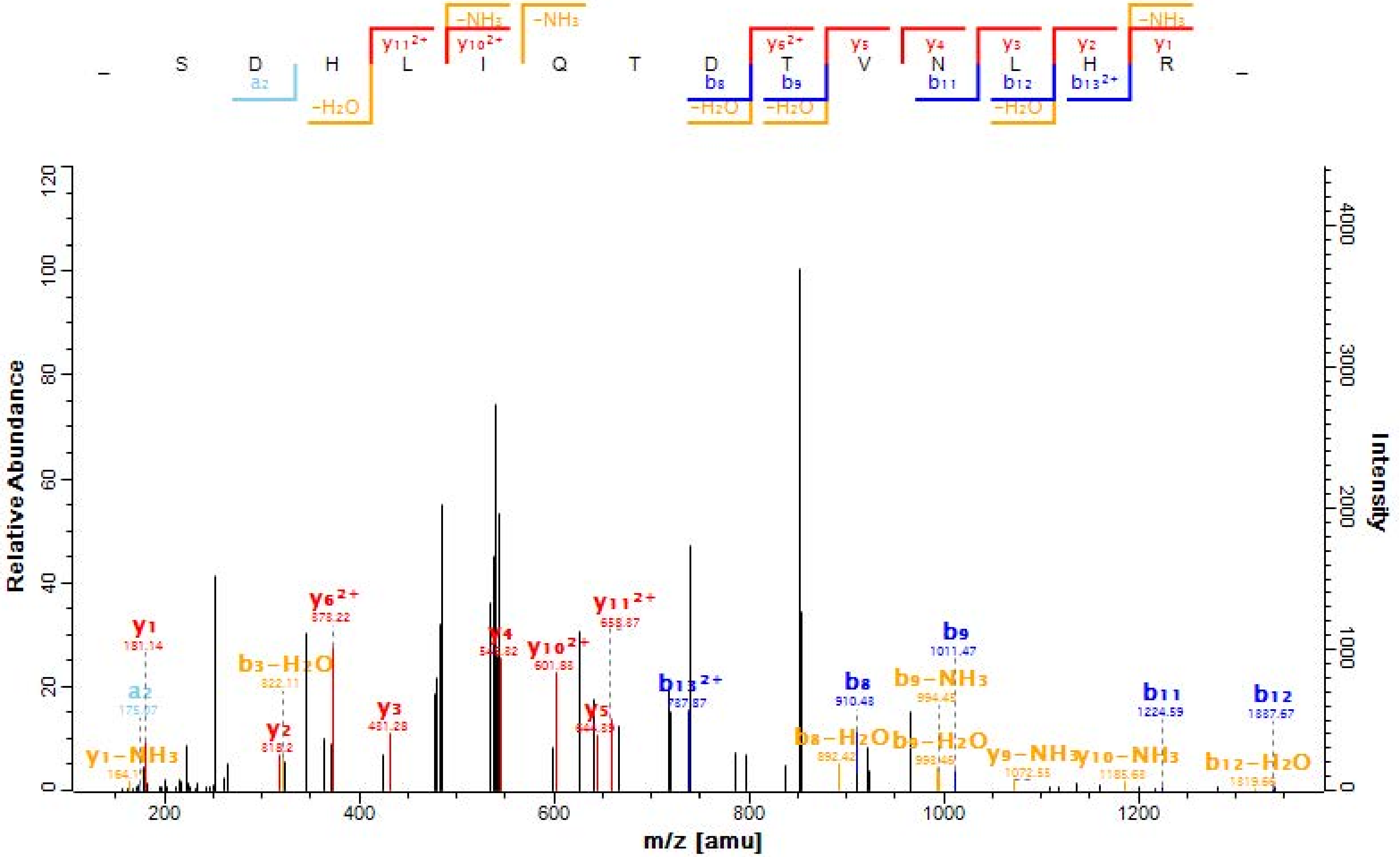
Mass:	1178.62983
m/z:	590.32219
Charge:	2+
Retentiontime:	16.462930679321
Score:	82.99993
Mass Error [ppm]:	0.24601
PEP:	0.0021974
Precursor Type:	MULTI

g

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	50 %
Peak Coverage:	25 %
Protein Localisation:	110 ... 119

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	129.11		157.11		157.11	1	R	9		
-0.008	242.2		270.19		270.19	2	L	8	1023.5	
	329.23		357.22		357.22	3	S	7	910.45	
	458.27		486.27	+0.0018	486.27	4	E	6	823.42	
	573.3		601.29	+0.0284	601.29	5	D	5	694.38	+0.2208
	736.36		764.36		764.36	6	Y	4	579.35	+0.0427
	793.38	+0.1582	411.19	+0.0292	821.38	7	G	3	416.29	
	892.45		920.45	+0.0162	920.45	8	V	2	359.27	
	1005.5		1033.5	+0.0236	1033.5	9	L	1	260.2	+0.0338
						10	K	0	147.11	

Scan number	2109	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	87.72



precursor information

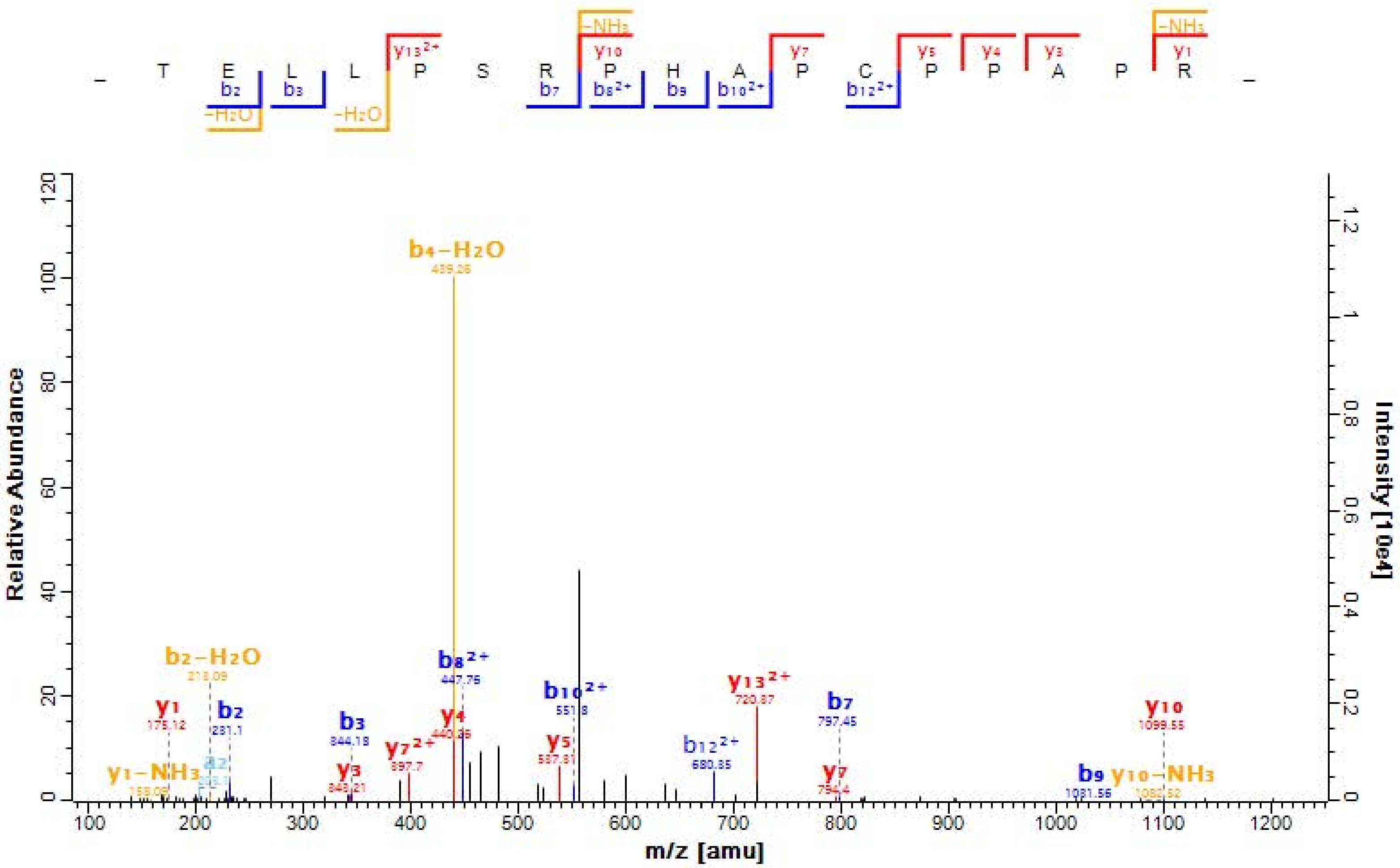
Mass:	1647.83276
m/z:	550.28486
Charge:	3+
Retentiontime:	16.647510528564
Score:	87.71938
Mass Error [ppm]:	-0.073216
PEP:	0.0003716
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	17 %
Peak Coverage:	23 %
Protein Localisation:	179 ... 192

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	60.04		88.04		88.04	1	S	13				
+0.229	175.1		203.1		203.1	2	D	12	1568		1568	
	312.1		340.1		340.1	3	H	11	1453		1453	
	425.2		453.2		453.2	4	L	10	1316		658.4	+0.20
	538.3		566.3		566.3	5	I	9	1203		601.8	+0.29
	666.4		694.4		694.4	6	Q	8	1090		1090	
	767.4		795.4		795.4	7	T	7	961.5		961.5	
	882.4		910.4	+0.148	910.4	8	D	6	860.5		860.5	
	983.5		1011	+0.014	1011	9	T	5	745.4		373.2	+0.11
	1083		1111		1111	10	V	4	644.4	-0.19	644.4	
	1197		1225	-0.02	1225	11	N	3	545.3	+0.124	545.3	
	1310		1338	+0.049	1338	12	L	2	431.3	+0.02	431.3	
	1447	+0.204	737.9		1475	13	H	1	318.2	+0.036	318.2	
						14	R	0	181.1	+0.018	181.1	

Scan number	2224	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	62.38



precursor information

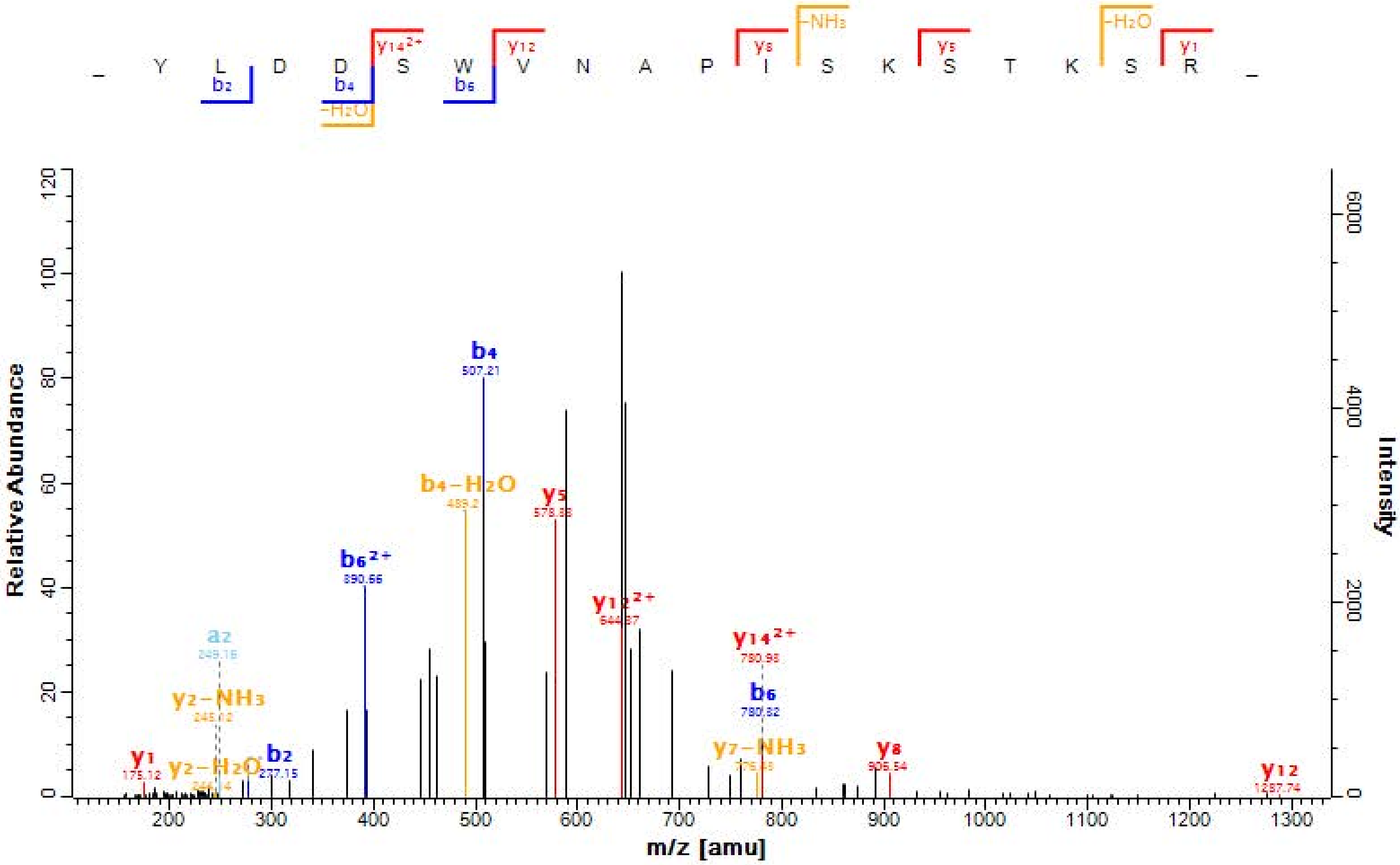
Mass:	1894.98337
m/z:	474.75312
Charge:	4+
Retentiontime:	17.275318145752
Score:	62.37733
Mass Error [ppm]:	-0.11588
PEP:	0.0015195
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	58 %
Peak Coverage:	18 %
Protein Localisation:	1863 ... 1879

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
∆ dalton	mass	∆ dalton	mass	∆ dalton	mass		seq		∆ dalton	mass	∆ dalton	mass
	74.06		102.1		102.1	1	T	16				
+0.11	203.1		231.1	+0.079	231.1	2	E	15	1795		1795	
	316.2		344.2	+0.148	344.2	3	L	14	1666		1666	
	429.3		457.3		457.3	4	L	13	1553		1553	
	526.3		554.3		554.3	5	P	12	1440		720.4	+0.12
	613.4		641.4		641.4	6	S	11	1343		1343	
	769.5		797.5	-0.01	797.5	7	R	10	1256		1256	
	866.5	+0.038	447.8		894.5	8	P	9	1100	+0.137	1100	
	1004		1032	-0.04	1032	9	H	8	1002		1002	
	1075	-0.23	551.8		1103	10	A	7	865.4		865.4	
	1172		1200		1200	11	P	6	794.4	+0.399	397.7	+0.06
	1332	+0.288	680.3		1360	12	C	5	697.3		697.3	
	1429		1457		1457	13	P	4	537.3	+0.044	537.3	
	1526		1554		1554	14	P	3	440.3	-0.04	440.3	
	1597		1625		1625	15	A	2	343.2	+0.047	343.2	
	1694		1722		1722	16	P	1	272.2		272.2	
						17	R	0	175.1	-0.06	175.1	

Scan number	2276	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	53.17



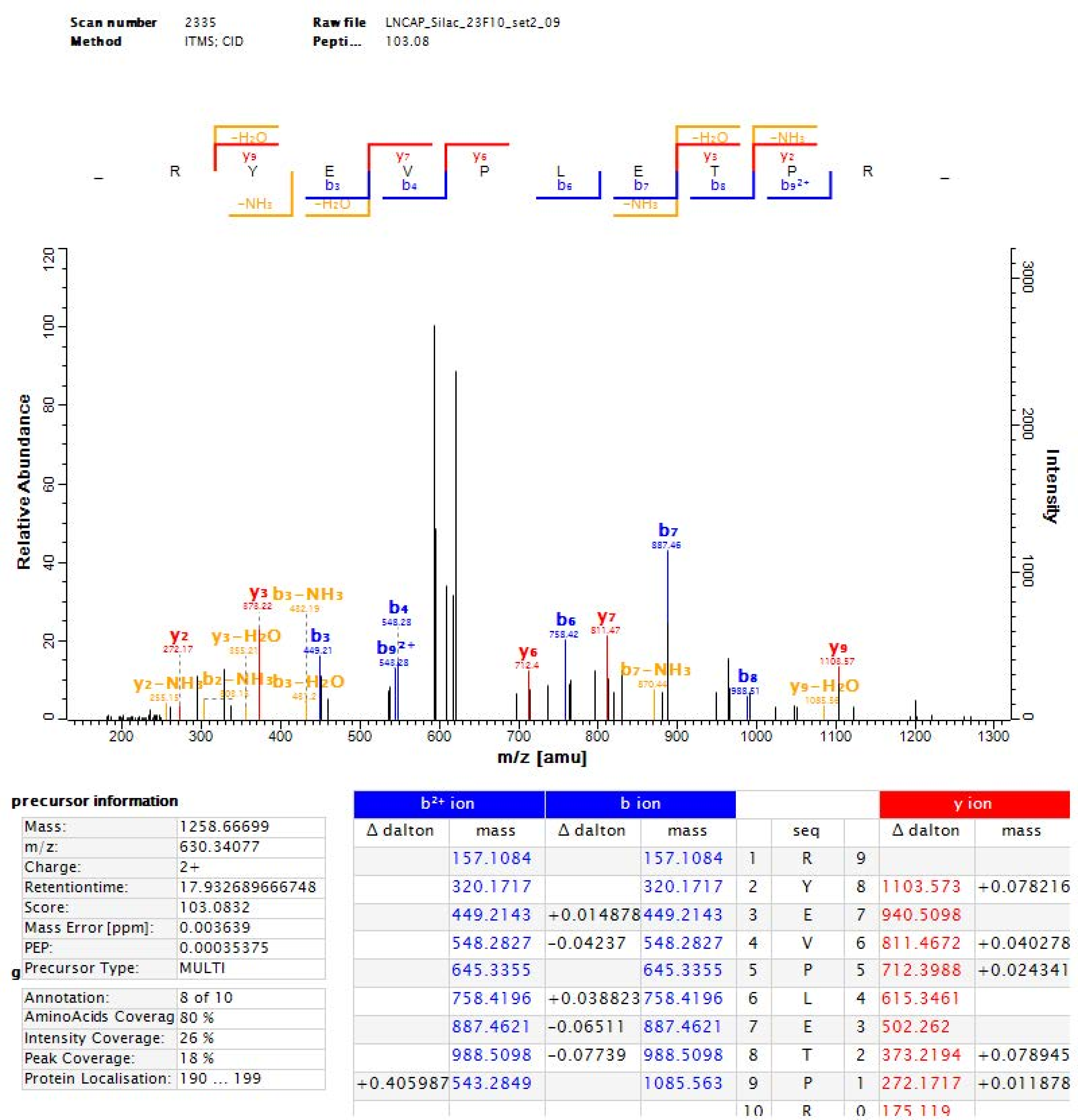
precursor information

Mass:	2066.04226
m/z:	517.51784
Charge:	4+
Retentiontime:	17.590311050415
Score:	53.16922
Mass Error [ppm]:	-0.48732
PEP:	0.0048592
Precursor Type:	MULTI

general information

Annotation:	10 of 18
AminoAcids Coverag	56 %
Intensity Coverage:	30 %
Peak Coverage:	14 %
Protein Localisation:	82 ... 99

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.1		164.1		164.1	1	Y	17				
+0.035	249.2		277.2	+0.136	277.2	2	L	16	1904		1904	
	364.2		392.2		392.2	3	D	15	1791		1791	
	479.2		507.2	+0.478	507.2	4	D	14	1676		1676	
	566.2		594.2		594.2	5	S	13	1561		780.9	+0.33
	752.3	+0.164	390.7	-0.05	780.3	6	W	12	1474		1474	
	851.4		879.4		879.4	7	V	11	1288	+0.061	644.4	-0.39
	965.4		993.4		993.4	8	N	10	1189		1189	
	1036		1064		1064	9	A	9	1075		1075	
	1134		1162		1162	10	P	8	1004		1004	
	1247		1275		1275	11	I	7	906.5	+0.091	906.5	
	1334		1362		1362	12	S	6	793.5		793.5	
	1462		1490		1490	13	K	5	706.4		706.4	
	1549		1577		1577	14	S	4	578.3	+0.258	578.3	
	1650		1678		1678	15	T	3	491.3		491.3	
	1778		1806		1806	16	K	2	390.2		390.2	
	1865		1893		1893	17	S	1	262.2		262.2	
						18	R	0	175.1	+0.162	175.1	



Scan number 2335
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set2_09
Pepti... 103.08

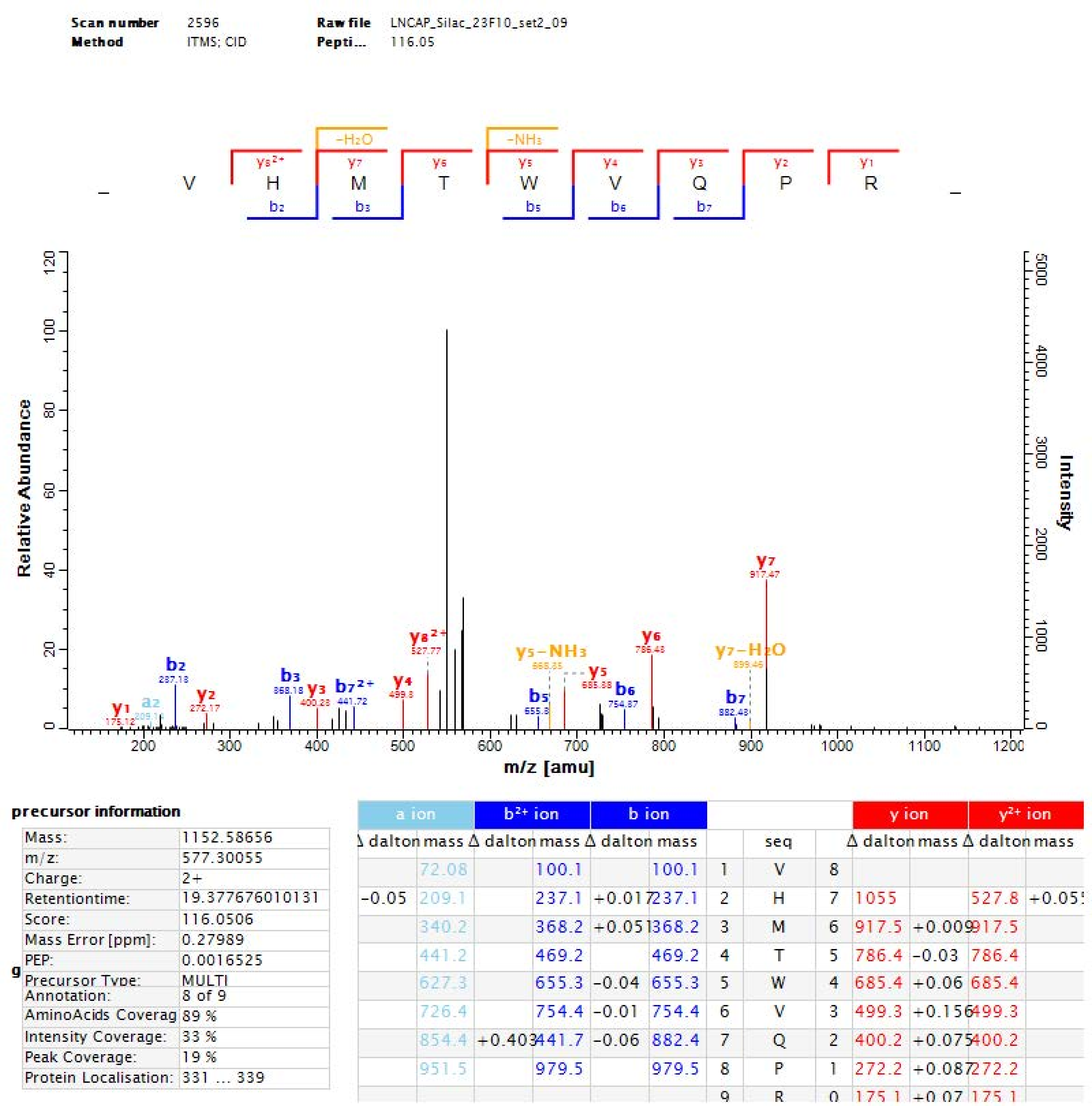
precursor information

Mass:	1258.66699
m/z:	630.34077
Charge:	2+
Retentiontime:	17.932689666748
Score:	103.0832
Mass Error [ppm]:	0.003639
PEP:	0.00035375
Precursor Type:	MULTI

g

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	26 %
Peak Coverage:	18 %
Protein Localisation:	190 ... 199

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	157.1084		157.1084	1	R	9		
	320.1717		320.1717	2	Y	8	1103.573	+0.078216
	449.2143	+0.014878	449.2143	3	E	7	940.5098	
	548.2827	-0.04237	548.2827	4	V	6	811.4672	+0.040278
	645.3355		645.3355	5	P	5	712.3988	+0.024341
	758.4196	+0.038823	758.4196	6	L	4	615.3461	
	887.4621	-0.06511	887.4621	7	E	3	502.262	
	988.5098	-0.07739	988.5098	8	T	2	373.2194	+0.078945
+0.405987	543.2849		1085.563	9	P	1	272.1717	+0.011878
				10	R	0	175.119	



Scan number 2596

Method ITMS; CID

Raw file LNCAP_Silac_23F10_set2_09

Pepti... 116.05

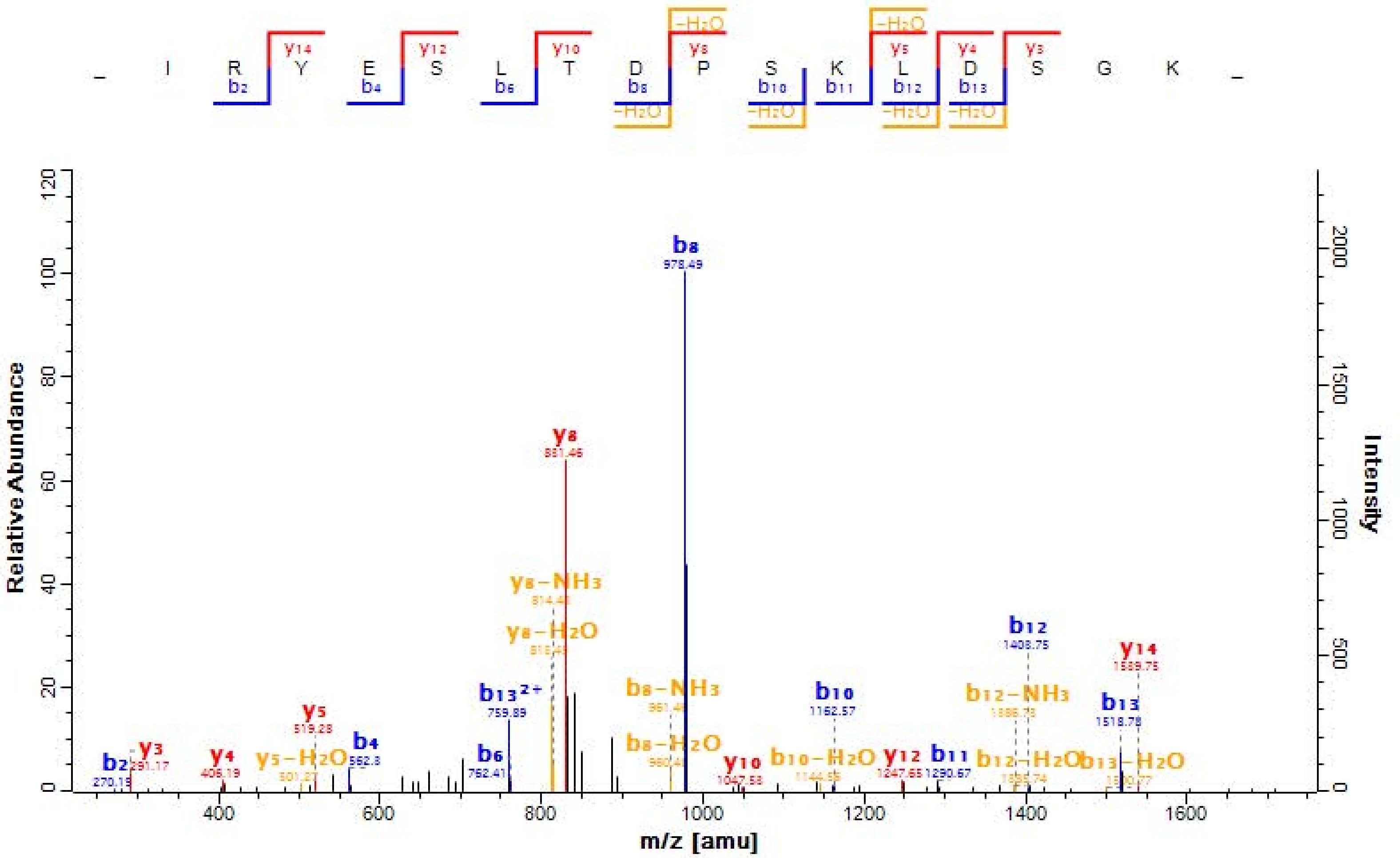
precursor information

Mass:	1152.58656
m/z:	577.30055
Charge:	2+
Retentiontime:	19.377676010131
Score:	116.0506
Mass Error [ppm]:	0.27989
PEP:	0.0016525
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	33 %
Peak Coverage:	19 %
Protein Localisation:	331 … 339

g

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.08		100.1		100.1	1	V	8				
-0.05	209.1		237.1	+0.017	237.1	2	H	7	1055		527.8	+0.05
	340.2		368.2	+0.051	368.2	3	M	6	917.5	+0.009	917.5	
	441.2		469.2		469.2	4	T	5	786.4	-0.03	786.4	
	627.3		655.3	-0.04	655.3	5	W	4	685.4	+0.06	685.4	
	726.4		754.4	-0.01	754.4	6	V	3	499.3	+0.156	499.3	
	854.4	+0.403	441.7	-0.06	882.4	7	Q	2	400.2	+0.075	400.2	
	951.5		979.5		979.5	8	P	1	272.2	+0.087	272.2	
						9	R	0	175.1	+0.07	175.1	

Scan number	2746	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	123.42



precursor information

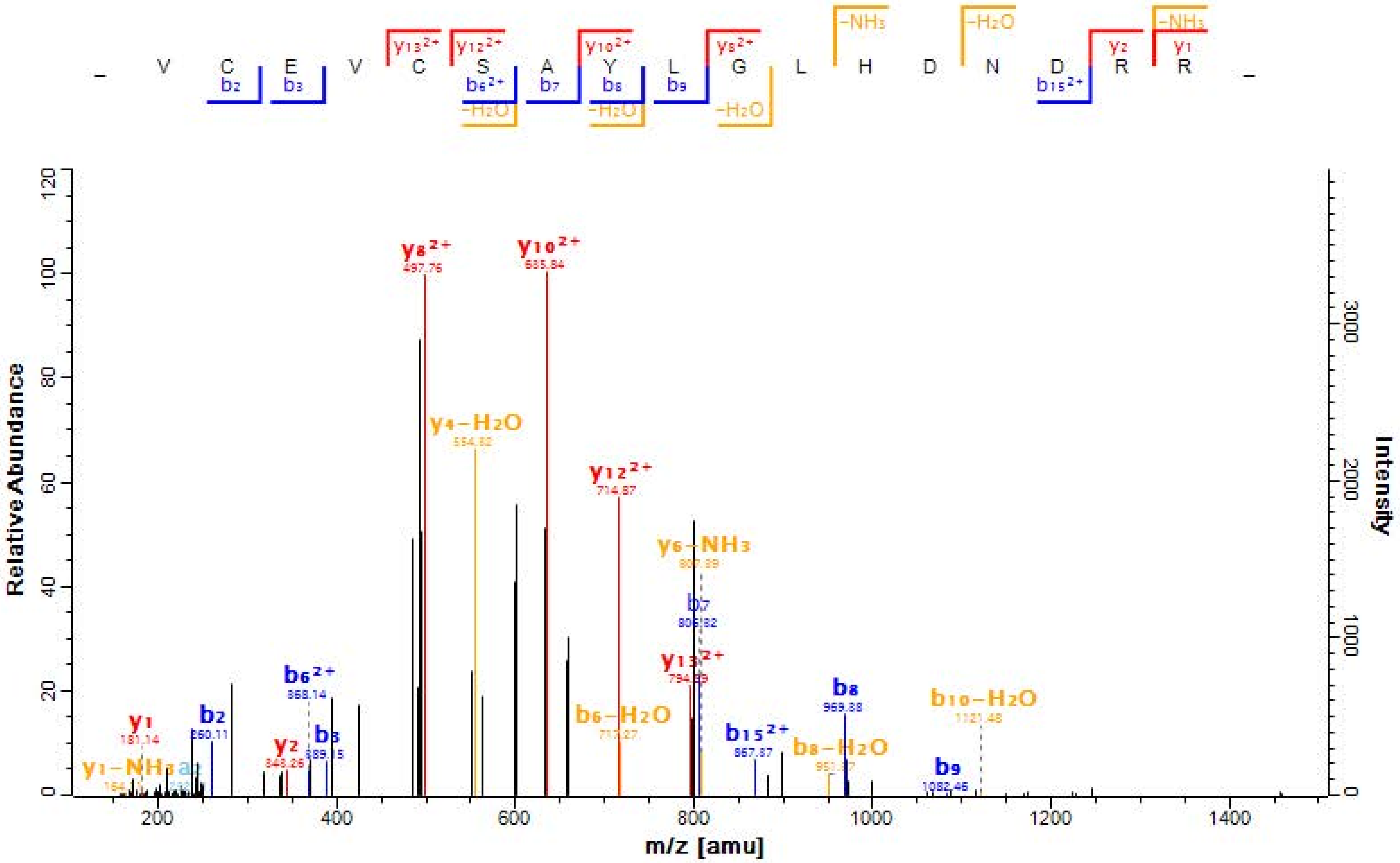
Mass:	1807.93163
m/z:	904.97309
Charge:	2+
Retentiontime:	20.22242546815
Score:	123.4163
Mass Error [ppm]:	0.023045
PEP:	5.5367E-10
Precursor Type:	MULTI

general information

Annotation:	14 of 16
AminoAcids Coverag	88 %
Intensity Coverage:	58 %
Peak Coverage:	32 %
Protein Localisation:	181 ... 196

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	114.0913		114.0913	1	I	15		
	270.1925	+0.136162	270.1925	2	R	14	1695.855	
	433.2558		433.2558	3	Y	13	1539.754	+0.162444
	562.2984	+0.003507	562.2984	4	E	12	1376.69	
	649.3304		649.3304	5	S	11	1247.648	-0.00568
	762.4145	+0.139062	762.4145	6	L	10	1160.616	
	863.4621		863.4621	7	T	9	1047.532	+0.067441
	978.4891	-0.0265	978.4891	8	D	8	946.484	
	1075.542		1075.542	9	P	7	831.4571	+0.042941
	1162.574	+0.284275	1162.574	10	S	6	734.4043	
	1290.669	-0.0635	1290.669	11	K	5	647.3723	
	1403.753	-0.1146	1403.753	12	L	4	519.2773	-0.01449
+0.197074	759.8936	-0.11518	1518.78	13	D	3	406.1932	+0.048765
	1605.812		1605.812	14	S	2	291.1663	-0.0015
	1662.833		1662.833	15	G	1	204.1343	
				16	K	0	147.1128	

Scan number	2795	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	58.07



precursor information

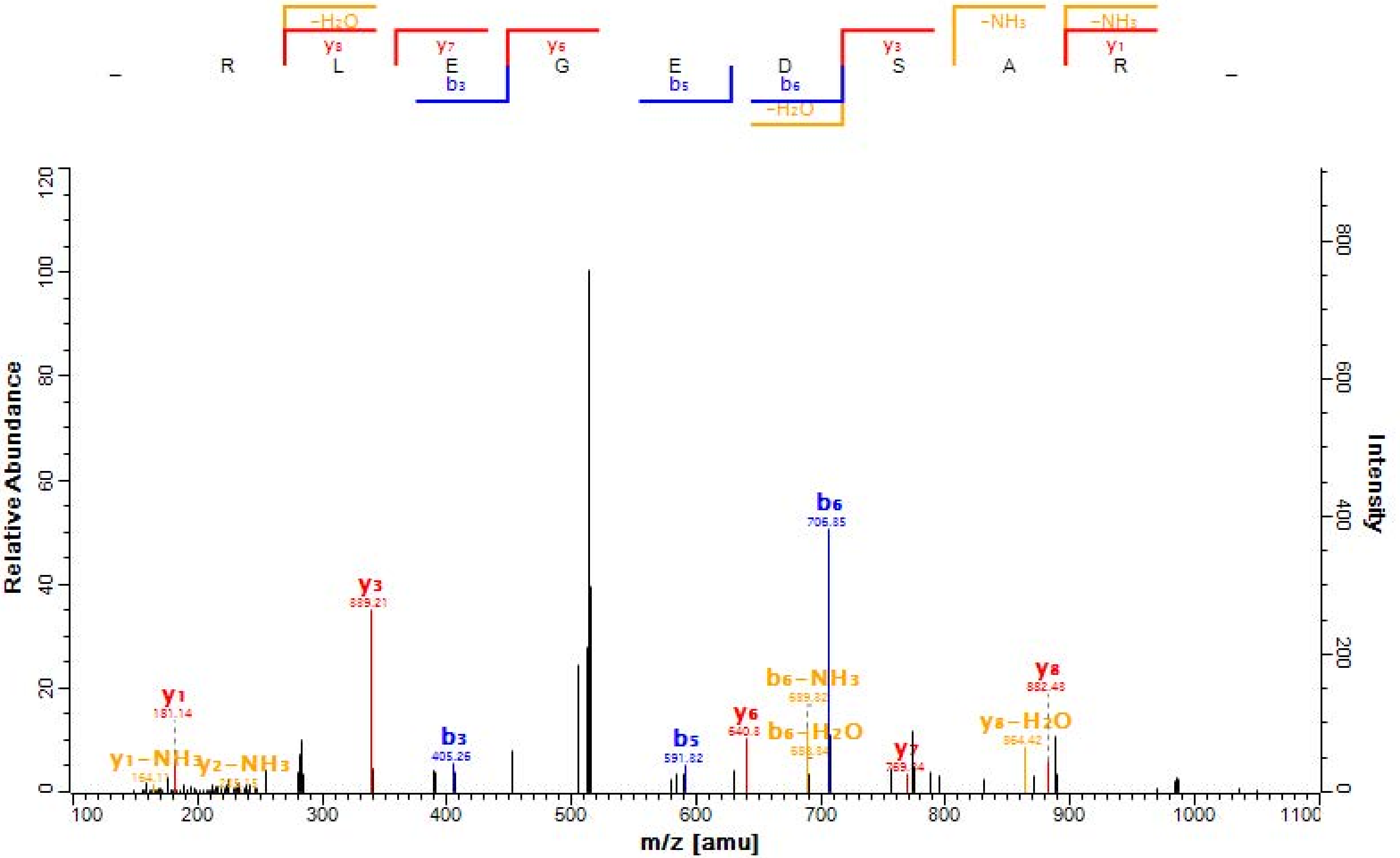
Mass:	2062.93068
m/z:	516.73995
Charge:	4+
Retentiontime:	20.508506774902
Score:	58.07133
Mass Error [ppm]:	-0.29391
PEP:	0.0013837
Precursor Type:	MULTI

general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	36 %
Peak Coverage:	17 %
Protein Localisation:	255 ... 271

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.08		100.1		100.1	1	V	16				
-0.01	232.1		260.1	+0.102	260.1	2	C	15	1977		1977	
	361.2		389.1	+0.036	389.1	3	E	14	1817		1817	
	460.2		488.2		488.2	4	V	13	1688		1688	
	620.3		648.2		648.2	5	C	12	1589		794.9	+0.33
	707.3	-0.09	368.1		735.3	6	S	11	1429		714.9	+0.27
	778.3		806.3	+0.023	806.3	7	A	10	1342		1342	
	941.4		969.4	-0.06	969.4	8	Y	9	1271		635.8	+0.22
	1054		1082	+0.133	1082	9	L	8	1108		1108	
	1111		1139		1139	10	G	7	994.5		497.8	+0.24
	1225		1253		1253	11	L	6	937.5		937.5	
	1362		1390		1390	12	H	5	824.4		824.4	
	1477		1505		1505	13	D	4	687.4		687.4	
	1591		1619		1619	14	N	3	572.3		572.3	
	1706	+0.273	867.4		1734	15	D	2	458.3		458.3	
	1868		1896		1896	16	R	1	343.3	+0.093	343.3	
						17	R	0	181.1	+0.011	181.1	

Scan number	308	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	65.72



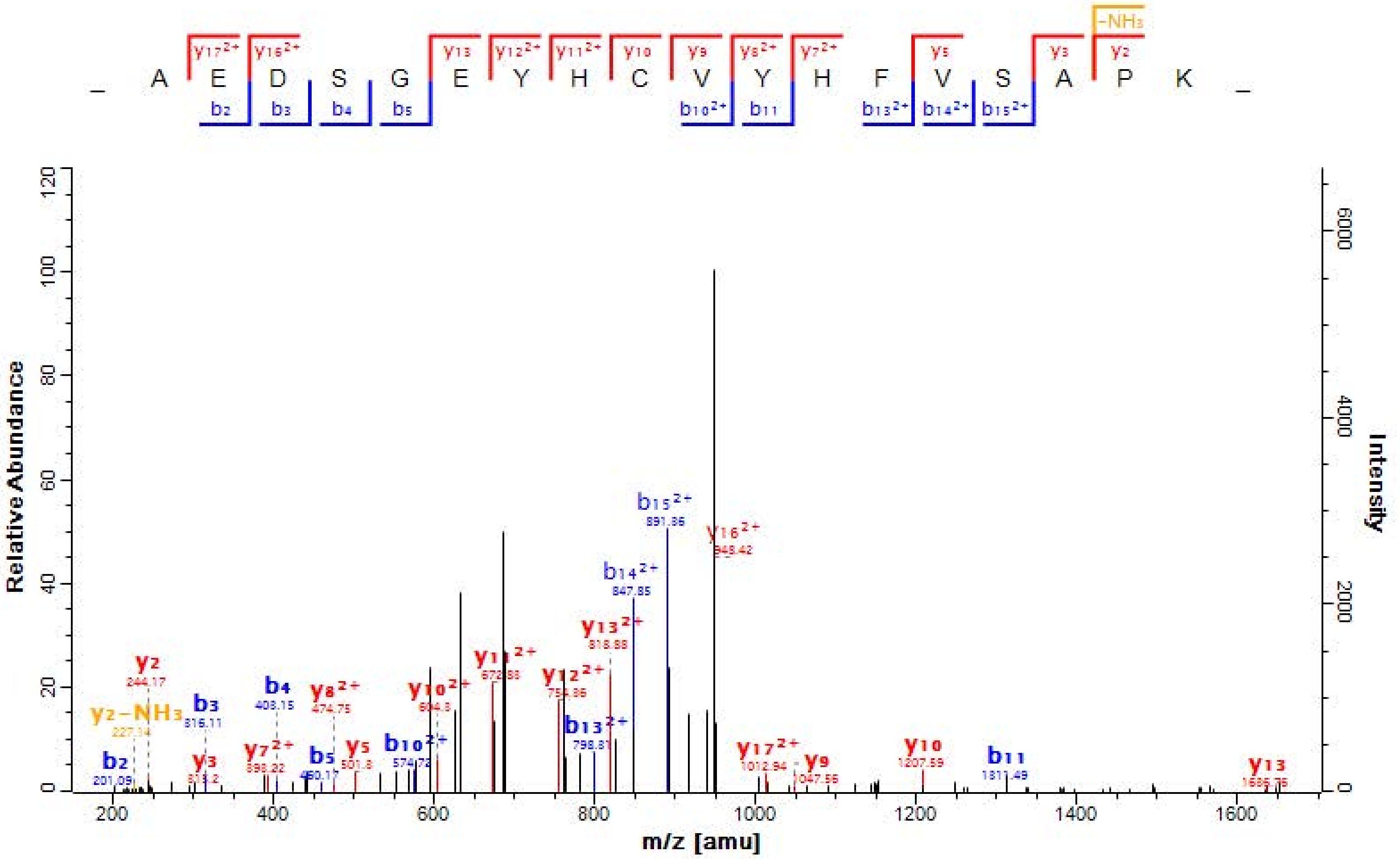
precursor information

g

Mass:	1031.50029
m/z:	516.75742
Charge:	2+
Retentiontime:	6.2934150695800
Score:	65.71947
Mass Error [ppm]:	0.67889
PEP:	0.010412
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	26 %
Peak Coverage:	11 %
Protein Localisation:	561 ... 569

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	163.128516522	1	R	8		
	276.212580502	2	L	7	882.425880334	+0.0558091
+0.1408225	405.255173598	3	E	6	769.341816354	-0.1303906
	462.276637322	4	G	5	640.299223257	+0.0341508
+0.1107012	591.319230418	5	E	4	583.277759534	
-0.0029728	706.34617345	6	D	3	454.235166438	
	793.37820186	7	S	2	339.208223406	-0.0549031
	864.415315648	8	A	1	252.176194996	
		9	R	0	181.139081208	+0.0077389

Scan number	3334	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	110.35



precursor information

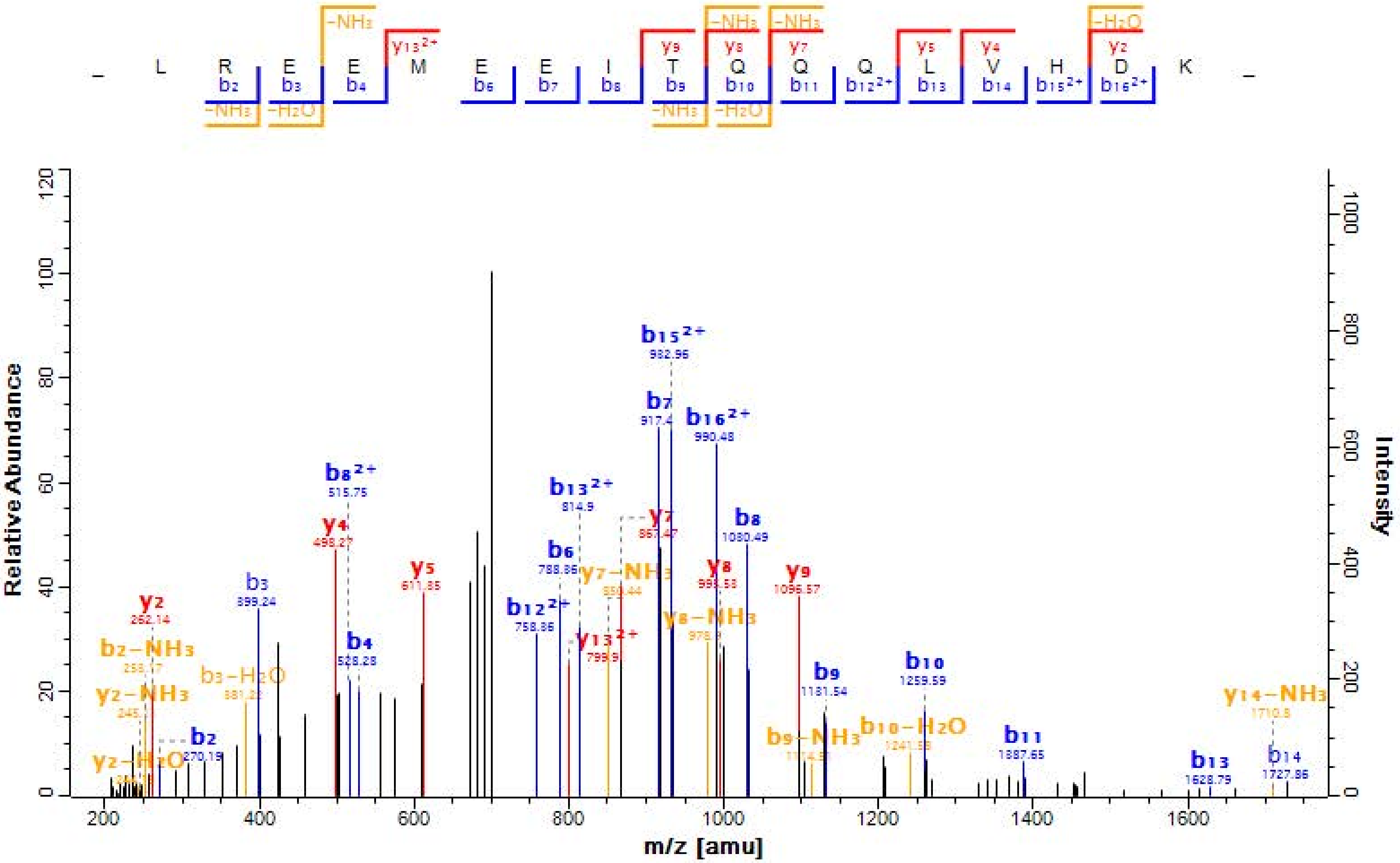
Mass:	2094.91089
m/z:	699.3109
Charge:	3+
Retentiontime:	23.586513519287
Score:	110.3472
Mass Error [ppm]:	0.165
PEP:	3.4605E-08
Precursor Type:	MULTI

general information

Annotation:	16 of 18
AminoAcids Coverag	89 %
Intensity Coverage:	34 %
Peak Coverage:	22 %
Protein Localisation:	210 ... 227

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	17				
	201.09	-0.072	201.09	2	E	16	2024.9		1012.9	-0.126
	316.11	-0.023	316.11	3	D	15	1895.8		948.42	-0.117
	403.15	+0.2575	403.15	4	S	14	1780.8		1780.8	
	460.17	-0.28	460.17	5	G	13	1693.8		1693.8	
	589.21		589.21	6	E	12	1636.8	-0.091	818.88	+0.3632
	752.27		752.27	7	Y	11	1507.7		754.36	+0.2801
	889.33		889.33	8	H	10	1344.7		672.83	+0.26
	1049.4		1049.4	9	C	9	1207.6	+0.1321	604.3	+0.3545
-0.195	574.72		1148.4	10	V	8	1047.6	-0.02	1047.6	
	1311.5	-0.1	1311.5	11	Y	7	948.49		474.75	+0.1294
	1448.6		1448.6	12	H	6	785.43		393.22	+0.1698
+0.1065	798.31		1595.6	13	F	5	648.37		648.37	
-0.198	847.85		1694.7	14	V	4	501.3	-0.011	501.3	
-0.196	891.36		1781.7	15	S	3	402.23		402.23	
	1852.8		1852.8	16	A	2	315.2	-0.086	315.2	
	1949.8		1949.8	17	P	1	244.17	-0.102	244.17	
				18	K	0	147.11		147.11	

Scan number	3534	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	158.45



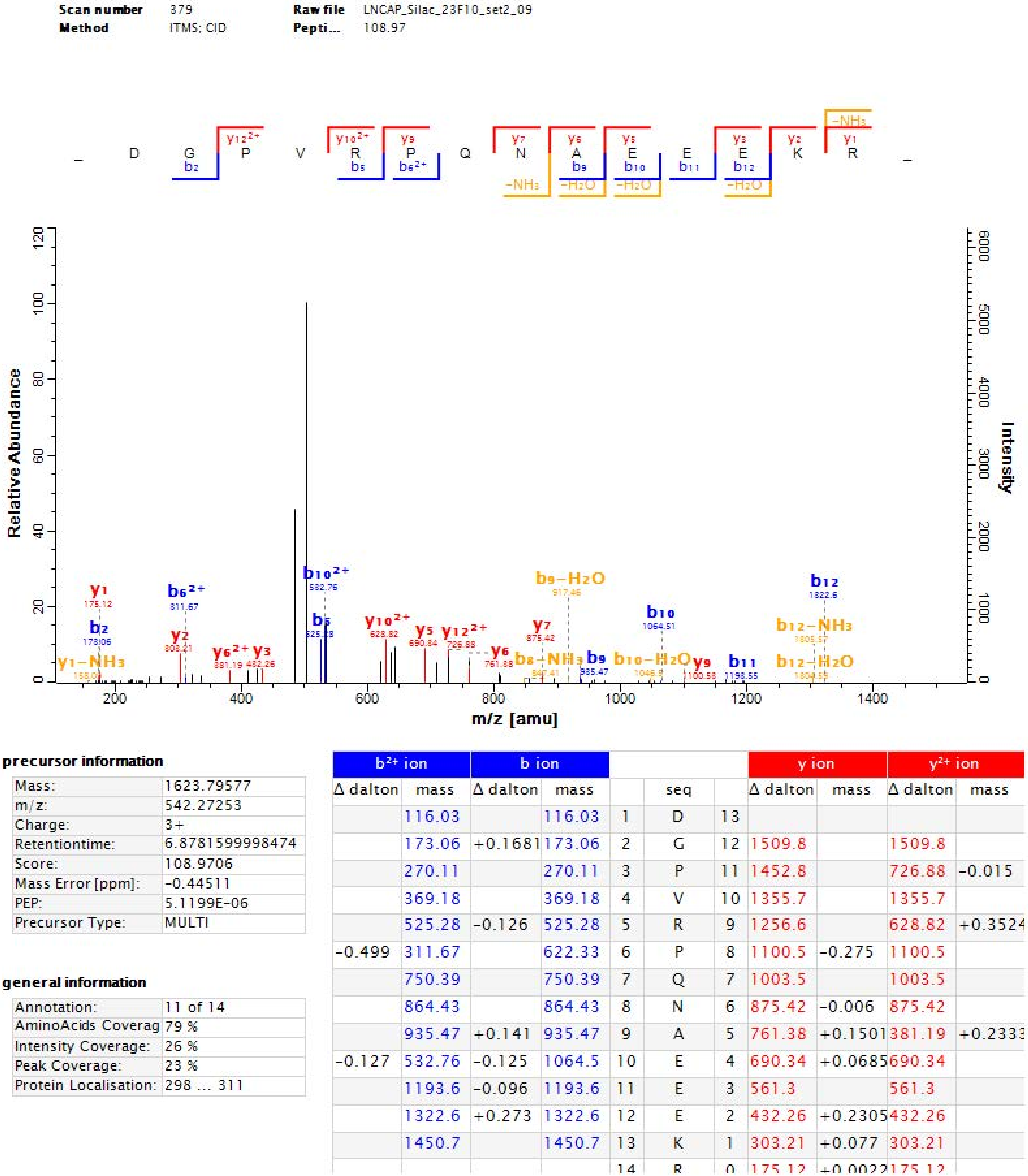
precursor information

Mass:	2125.04714
m/z:	709.35632
Charge:	3+
Retentiontime:	24.740625381469
Score:	158.4521
Mass Error [ppm]:	-0.10897
PEP:	7.7157E-23
Precursor Type:	MULTI

general information

Annotation:	15 of 17
AminoAcids Coverag	88 %
Intensity Coverage:	47 %
Peak Coverage:	29 %
Protein Localisation:	282 ... 298

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	16				
	270.19	+0.1082	270.19	2	R	15	2013		2013	
	399.24	+0.0473	399.24	3	E	14	1856.9		1856.9	
	528.28	+0.1455	528.28	4	E	13	1727.8		1727.8	
	659.32		659.32	5	M	12	1598.8		799.9	+0.4715
	788.36	-0.024	788.36	6	E	11	1467.7		1467.7	
	917.4	-0.037	917.4	7	E	10	1338.7		1338.7	
+0.2137	515.75	-0.035	1030.5	8	I	9	1209.7		1209.7	
	1131.5	+0.0043	1131.5	9	T	8	1096.6	+0.1343	1096.6	
	1259.6	+0.3427	1259.6	10	Q	7	995.53	-0.06	995.53	
	1387.7	-0.105	1387.7	11	Q	6	867.47	+0.0845	867.47	
+0.3774	758.36		1515.7	12	Q	5	739.41		739.41	
+0.166	814.9	-0.048	1628.8	13	L	4	611.35	+0.0328	611.35	
	1727.9	+0.1322	1727.9	14	V	3	498.27	+0.0226	498.27	
+0.2621	932.96		1864.9	15	H	2	399.2		399.2	
+0.2149	990.48		1979.9	16	D	1	262.14	+0.1571	262.14	
				17	K	0	147.11		147.11	



Scan number	379	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	108.97

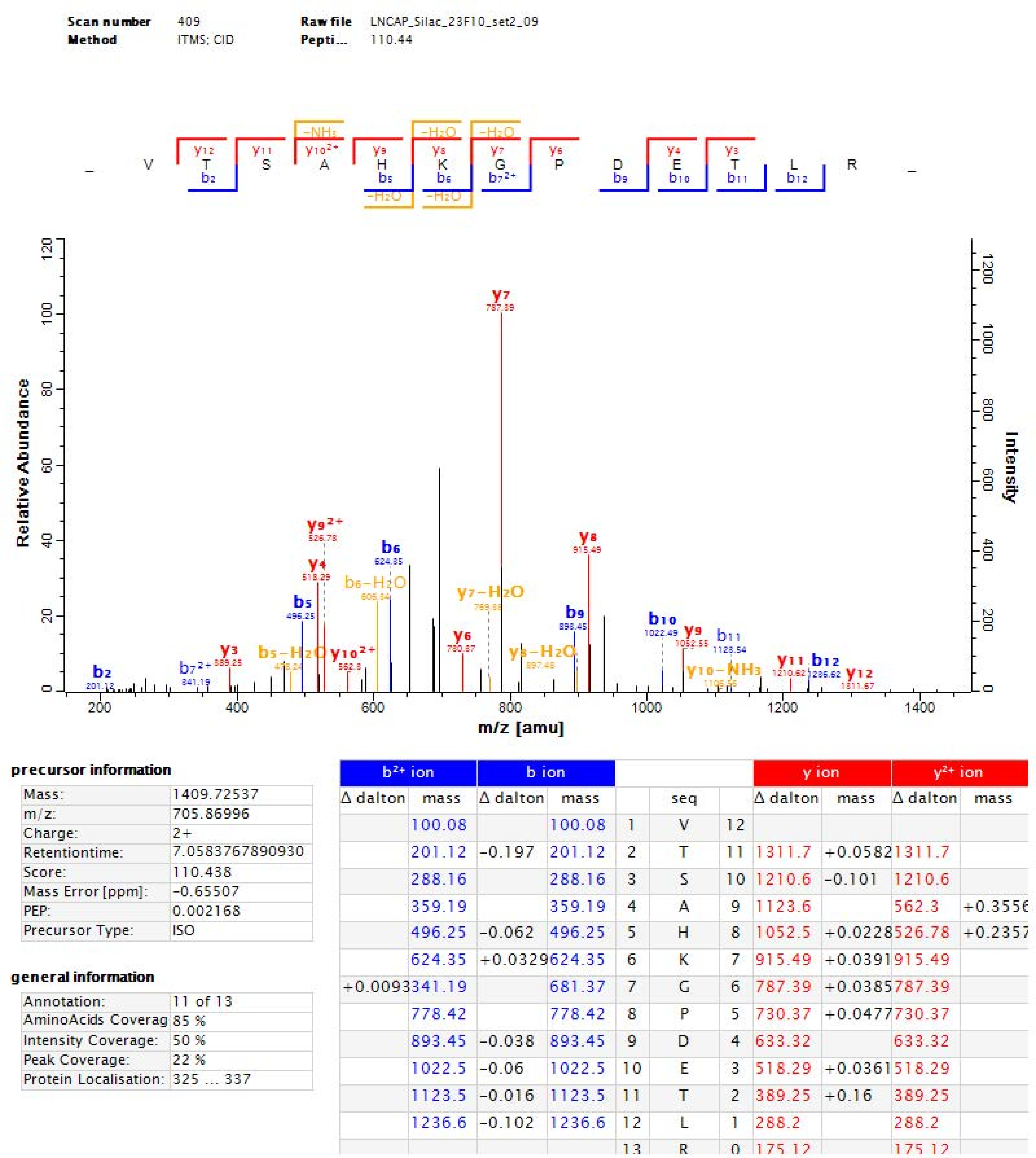
precursor information

Mass:	1623.79577
m/z:	542.27253
Charge:	3+
Retentiontime:	6.8781599998474
Score:	108.9706
Mass Error [ppm]:	-0.44511
PEP:	5.1199E-06
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	26 %
Peak Coverage:	23 %
Protein Localisation:	298 ... 311

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	13				
	173.06	+0.1681	173.06	2	G	12	1509.8		1509.8	
	270.11		270.11	3	P	11	1452.8		726.88	-0.015
	369.18		369.18	4	V	10	1355.7		1355.7	
	525.28	-0.126	525.28	5	R	9	1256.6		628.82	+0.3524
-0.499	311.67		622.33	6	P	8	1100.5	-0.275	1100.5	
	750.39		750.39	7	Q	7	1003.5		1003.5	
	864.43		864.43	8	N	6	875.42	-0.006	875.42	
	935.47	+0.141	935.47	9	A	5	761.38	+0.1501	381.19	+0.2333
-0.127	532.76	-0.125	1064.5	10	E	4	690.34	+0.0685	690.34	
	1193.6	-0.096	1193.6	11	E	3	561.3		561.3	
	1322.6	+0.273	1322.6	12	E	2	432.26	+0.2305	432.26	
	1450.7		1450.7	13	K	1	303.21	+0.077	303.21	
				14	R	0	175.12	+0.0022	175.12	



Scan number	409	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	110.44

precursor information

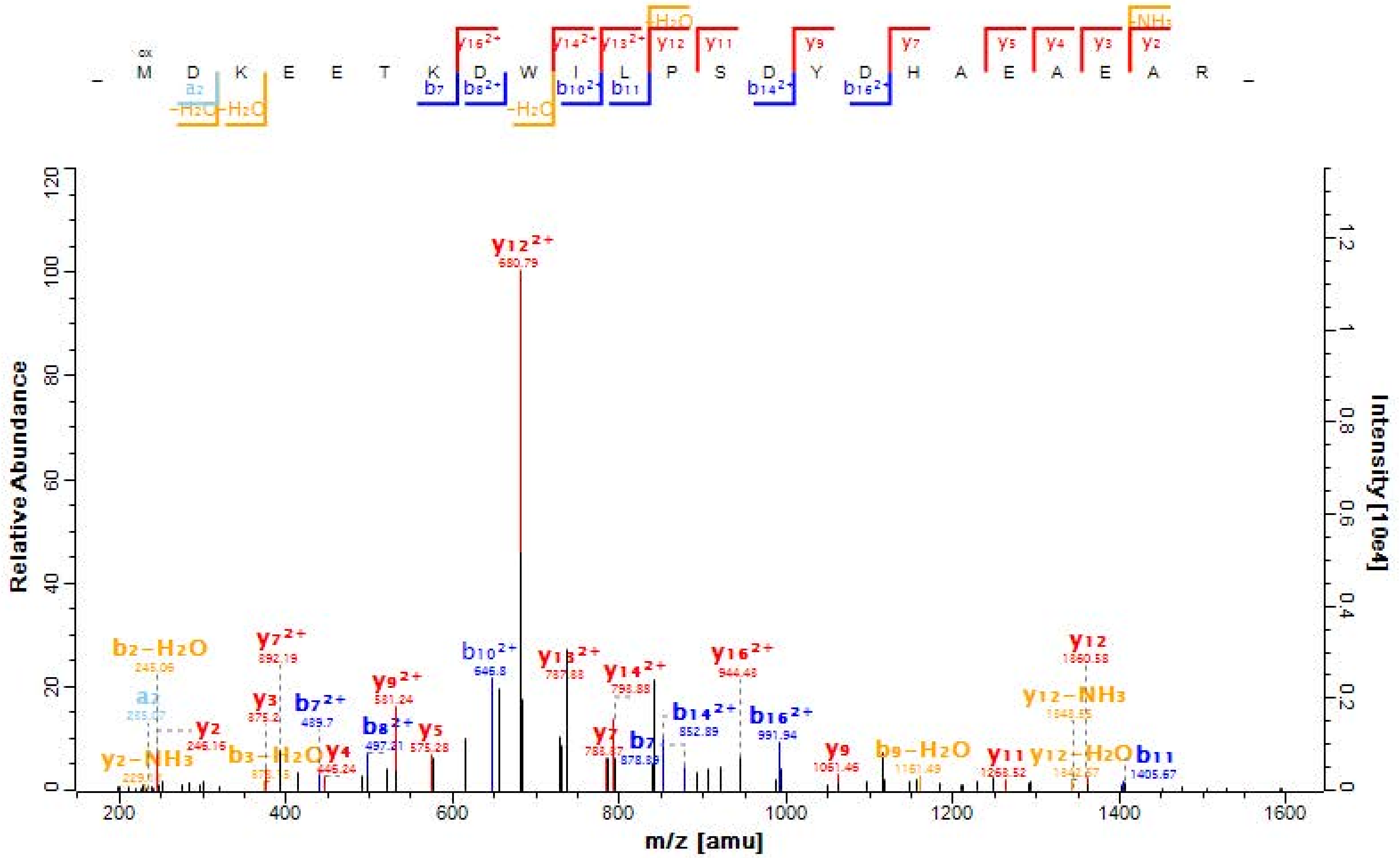
Mass:	1409.72537
m/z:	705.86996
Charge:	2+
Retentiontime:	7.0583767890930
Score:	110.438
Mass Error [ppm]:	-0.65507
PEP:	0.002168
Precursor Type:	ISO

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	50 %
Peak Coverage:	22 %
Protein Localisation:	325 ... 337

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	12				
	201.12	-0.197	201.12	2	T	11	1311.7	+0.0582	1311.7	
	288.16		288.16	3	S	10	1210.6	-0.101	1210.6	
	359.19		359.19	4	A	9	1123.6		562.3	+0.3556
	496.25	-0.062	496.25	5	H	8	1052.5	+0.0228	526.78	+0.2357
	624.35	+0.0329	624.35	6	K	7	915.49	+0.0391	915.49	
+0.0093	341.19		681.37	7	G	6	787.39	+0.0385	787.39	
	778.42		778.42	8	P	5	730.37	+0.0477	730.37	
	893.45	-0.038	893.45	9	D	4	633.32		633.32	
	1022.5	-0.06	1022.5	10	E	3	518.29	+0.0361	518.29	
	1123.5	-0.016	1123.5	11	T	2	389.25	+0.16	389.25	
	1236.6	-0.102	1236.6	12	L	1	288.2		288.2	
				13	R	0	175.12		175.12	

Scan number	4165	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	102.98



precursor information

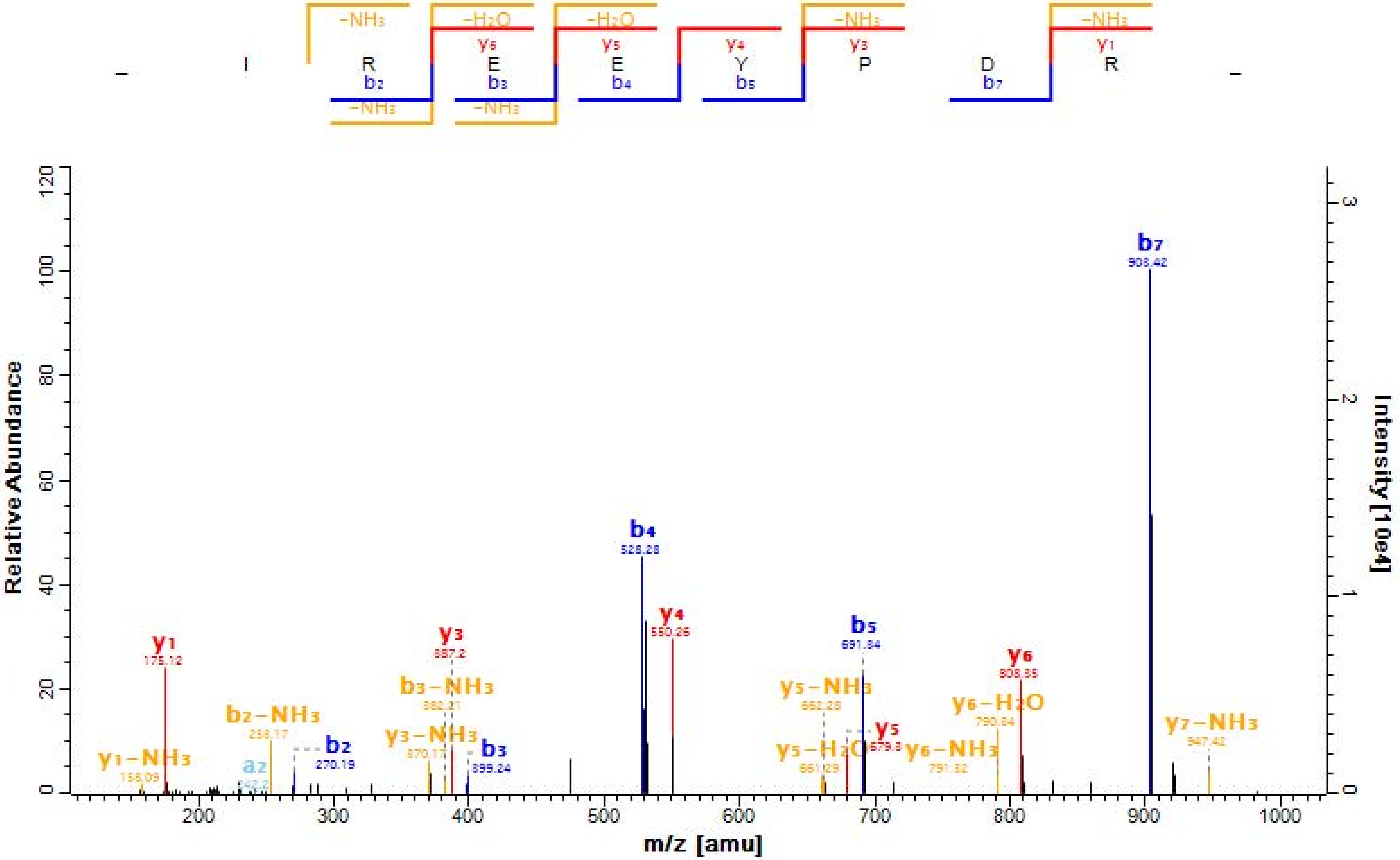
Mass:	2764.2275
m/z:	692.06415
Charge:	4+
Retentiontime:	28.246881484985
Score:	102.9783
Mass Error [ppm]:	-0.41351
PEP:	6.2035E-08
Precursor Type:	MULTI

general information

Annotation:	19 of 23
AminoAcids Coverag	83 %
Intensity Coverage:	46 %
Peak Coverage:	27 %
Protein Localisation:	257 ... 279

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120		148		148	1	M	22				
+0.396	235.1		263.1		263.1	2	D	21	2618		2618	
	363.2		391.2		391.2	3	K	20	2503		2503	
	492.2		520.2		520.2	4	E	19	2375		2375	
	621.3		649.2		649.2	5	E	18	2246		2246	
	722.3		750.3		750.3	6	T	17	2117		2117	
	850.4	+0.377	439.7	-0.14	878.4	7	K	16	2016		2016	
	965.4	+0.11	497.2		993.4	8	D	15	1888		944.4	-0.25
	1152		1179		1179	9	W	14	1773		1773	
	1265	-0.13	646.8		1293	10	I	13	1587		793.9	-0.08
	1378		1406	-0.3	1406	11	L	12	1474		737.3	+0.03
	1475		1503		1503	12	P	11	1361	+0.301	680.8	+0.26
	1562		1590		1590	13	S	10	1264	+0.165	1264	
	1677	+0.293	852.9		1705	14	D	9	1176		1176	
	1840		1868		1868	15	Y	8	1061	+0.122	531.2	+0.11
	1955	-0.02	991.9		1983	16	D	7	898.4		898.4	
	2092		2120		2120	17	H	6	783.4	+0.14	392.2	+0.04
	2163		2191		2191	18	A	5	646.3		646.3	
	2292		2320		2320	19	E	4	575.3	-0.01	575.3	
	2363		2391		2391	20	A	3	446.2	+0.276	446.2	
	2492		2520		2520	21	E	2	375.2	+0.134	375.2	
	2563		2591		2591	22	A	1	246.2	-0.07	246.2	
						23	R	0	175.1		175.1	

Scan number	507	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	138.4



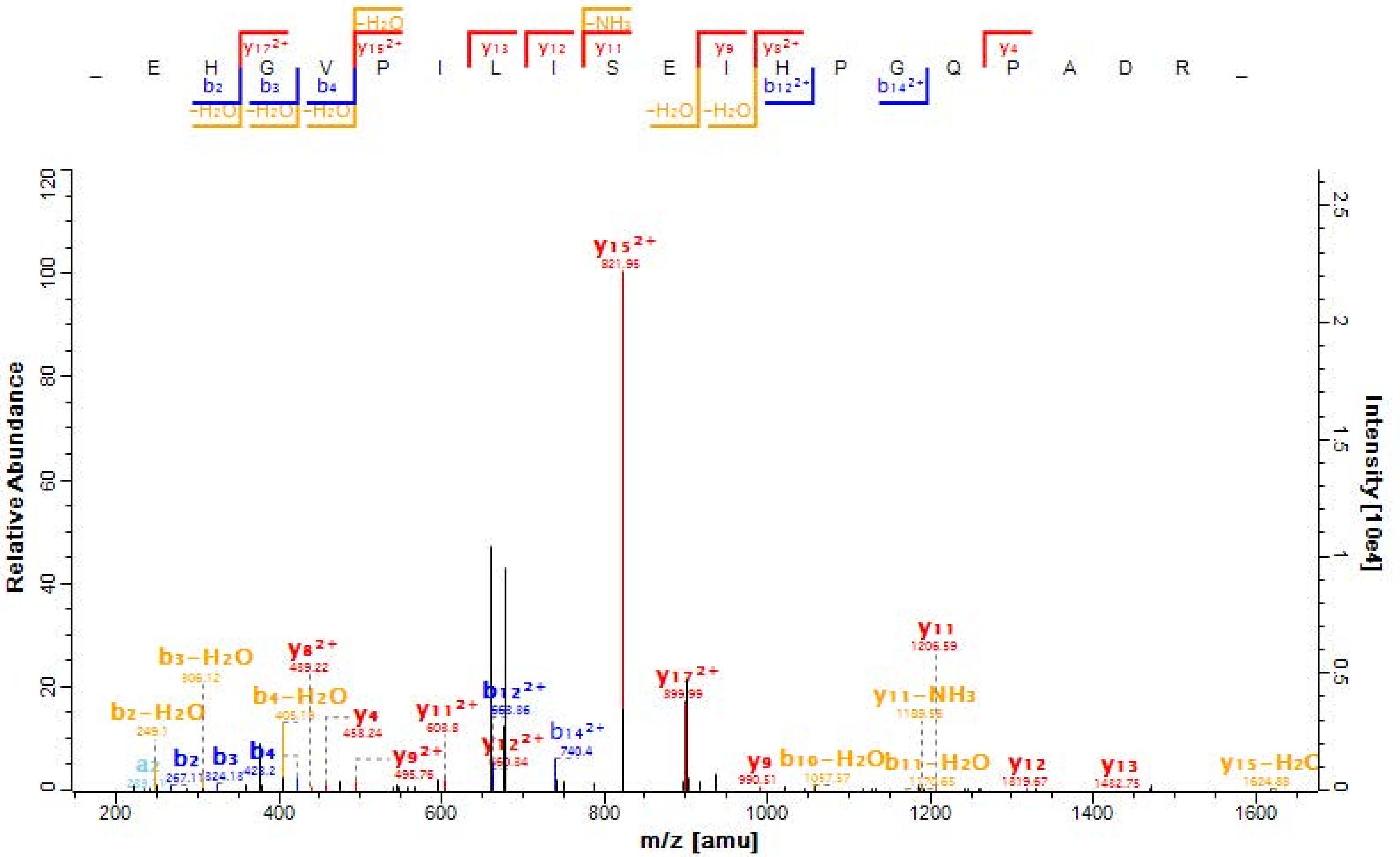
precursor information

Mass:	1076.52527
m/z:	539.26991
Charge:	2+
Retentiontime:	7.6463365554809
Score:	138.3957
Mass Error [ppm]:	0.18092
PEP:	3.8296E-06
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	60 %
Peak Coverage:	24 %
Protein Localisation:	155 ... 162

g

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	86.09643		114.0913	1	I	7		
-0.21817	242.1975	+0.082207	270.1925	2	R	6	964.4483	
	371.2401	-0.03723	399.235	3	E	5	808.3472	+0.022394
	500.2827	+0.033031	528.2776	4	E	4	679.3046	+0.046555
	663.3461	+0.049354	691.341	5	Y	3	550.262	+0.067419
	760.3988		788.3937	6	P	2	387.1987	-0.00841
	875.4258	-0.00032	903.4207	7	D	1	290.1459	
				8	R	0	175.119	-0.04565

Scan number	5168	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	77.19



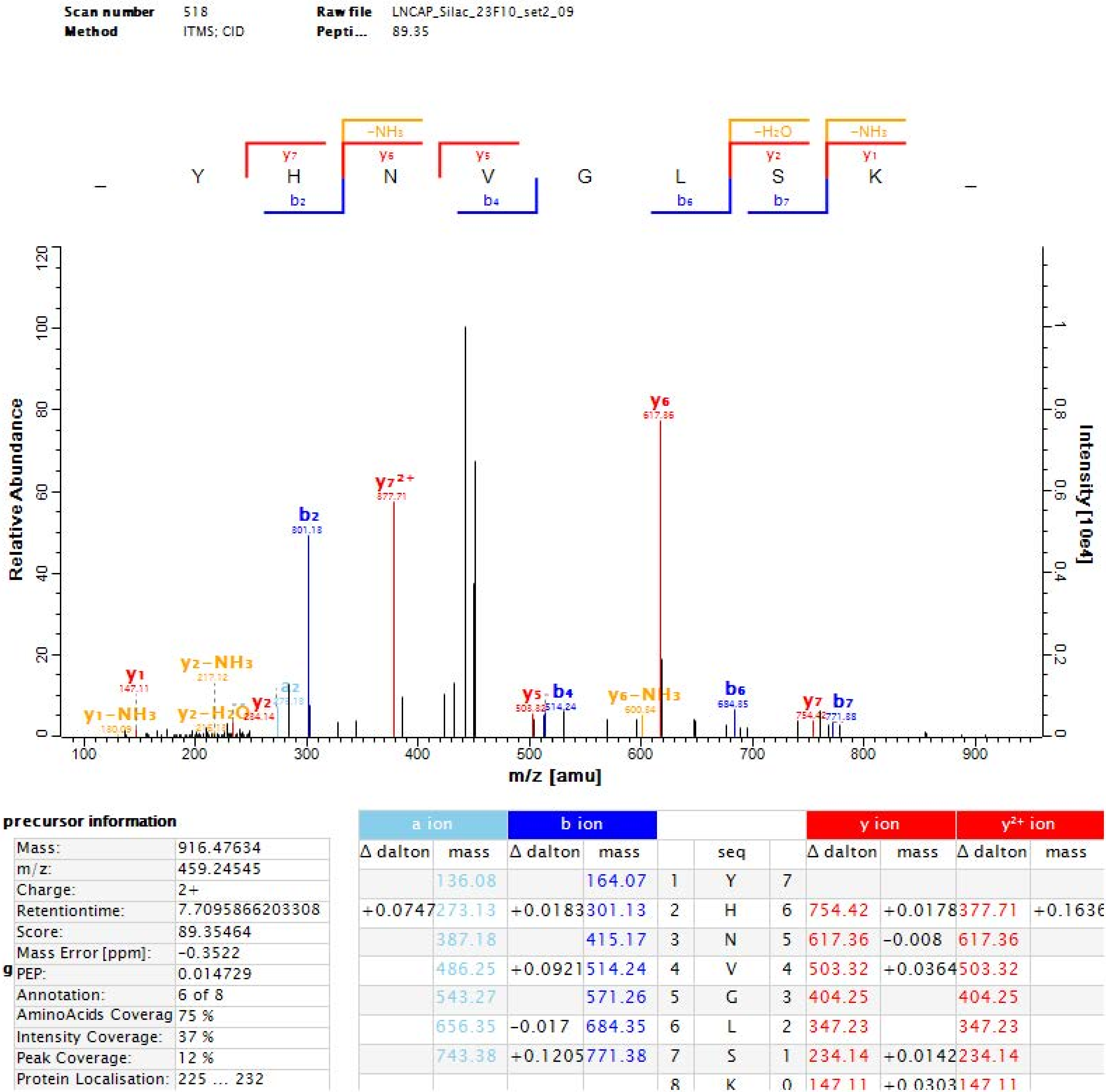
precursor information

Mass:	2064.0754
m/z:	689.03241
Charge:	3+
Retentiontime:	34.125946044921
Score:	77.19144
Mass Error [ppm]:	0.077372
PEP:	0.00017887
Precursor Type:	MULTI

general information

Annotation:	13 of 19
AminoAcids Coverag	68 %
Intensity Coverage:	47 %
Peak Coverage:	25 %
Protein Localisation:	308 ... 326

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.1		130		130	1	E	18				
+0.136	239.1		267.1	+0.105	267.1	2	H	17	1936		1936	
	296.1		324.1	+0.19	324.1	3	G	16	1799		900	−0.03
	395.2		423.2	+0.201	423.2	4	V	15	1742		1742	
	492.3		520.3		520.3	5	P	14	1643		821.9	+0.30
	605.3		633.3		633.3	6	I	13	1546		1546	
	718.4		746.4		746.4	7	L	12	1433	−0.41	1433	
	831.5		859.5		859.5	8	I	11	1320	−0.12	660.3	+0.31
	918.5		946.5		946.5	9	S	10	1207	+0.257	603.8	+0.20
	1048		1076		1076	10	E	9	1120		1120	
	1161		1189		1189	11	I	8	990.5	−0.09	495.8	+0.06
	1298	−0.25	663.4		1326	12	H	7	877.4		439.2	+0.15
	1395		1423		1423	13	P	6	740.4		740.4	
	1452	+0.045	740.4		1480	14	G	5	643.3		643.3	
	1580		1608		1608	15	Q	4	586.3		586.3	
	1677		1705		1705	16	P	3	458.2	+0.157	458.2	
	1748		1776		1776	17	A	2	361.2		361.2	
	1863		1891		1891	18	D	1	290.1		290.1	
						19	R	0	175.1		175.1	



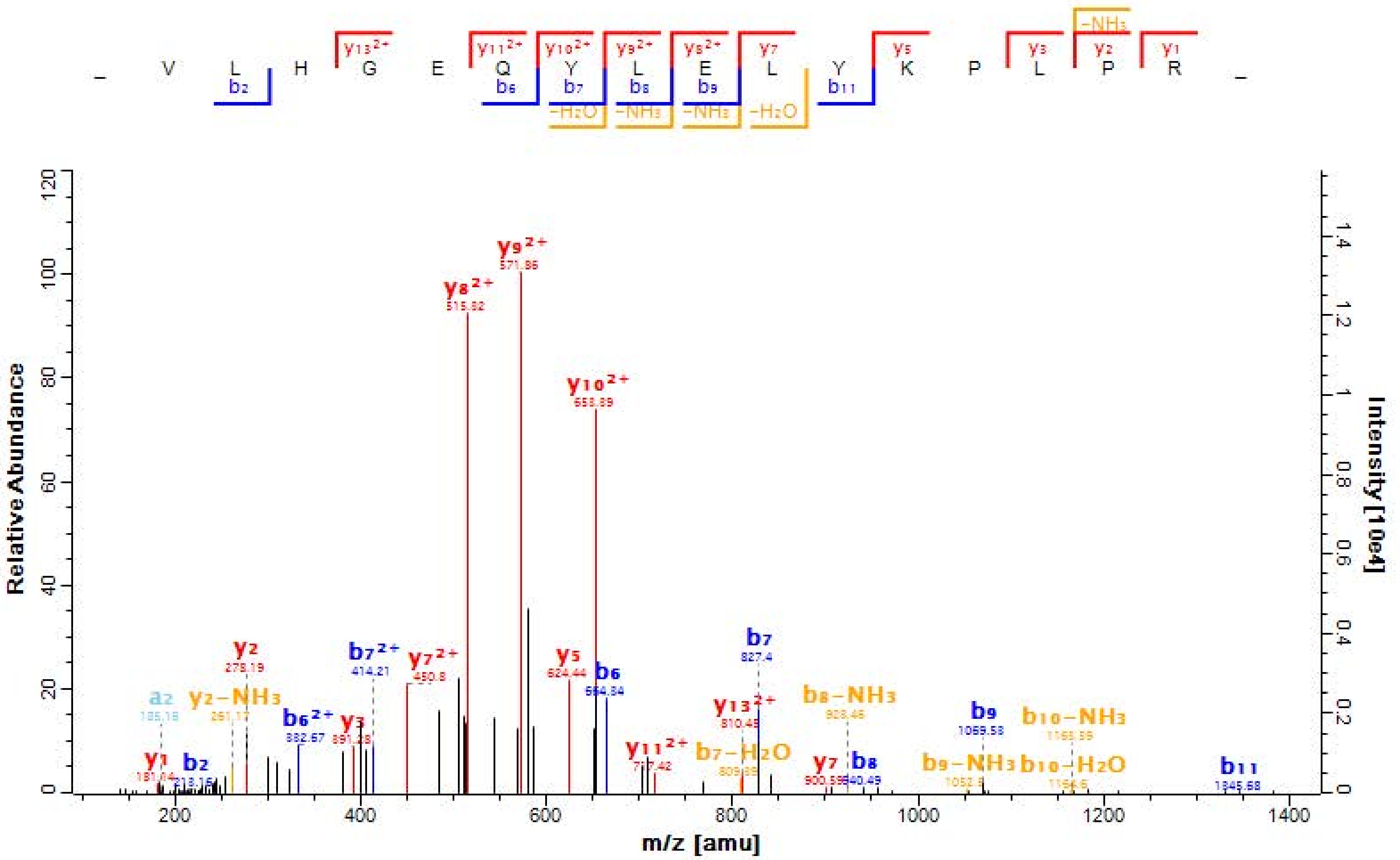
Scan number	518	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	89.35

precursor information

Mass:	916.47634
m/z:	459.24545
Charge:	2+
Retentiontime:	7.7095866203308
Score:	89.35464
Mass Error [ppm]:	-0.3522
PEP:	0.014729
Annotation:	6 of 8
AminoAcids Coverag	75 %
Intensity Coverage:	37 %
Peak Coverage:	12 %
Protein Localisation:	225 ... 232

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.08		164.07	1	Y	7				
+0.0747	273.13	+0.0183	301.13	2	H	6	754.42	+0.0178	377.71	+0.1636
	387.18		415.17	3	N	5	617.36	-0.008	617.36	
	486.25	+0.0921	514.24	4	V	4	503.32	+0.0364	503.32	
	543.27		571.26	5	G	3	404.25		404.25	
	656.35	-0.017	684.35	6	L	2	347.23		347.23	
	743.38	+0.1205	771.38	7	S	1	234.14	+0.0142	234.14	
				8	K	0	147.11	+0.0303	147.11	

Scan number	5255	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	124.51



precursor information

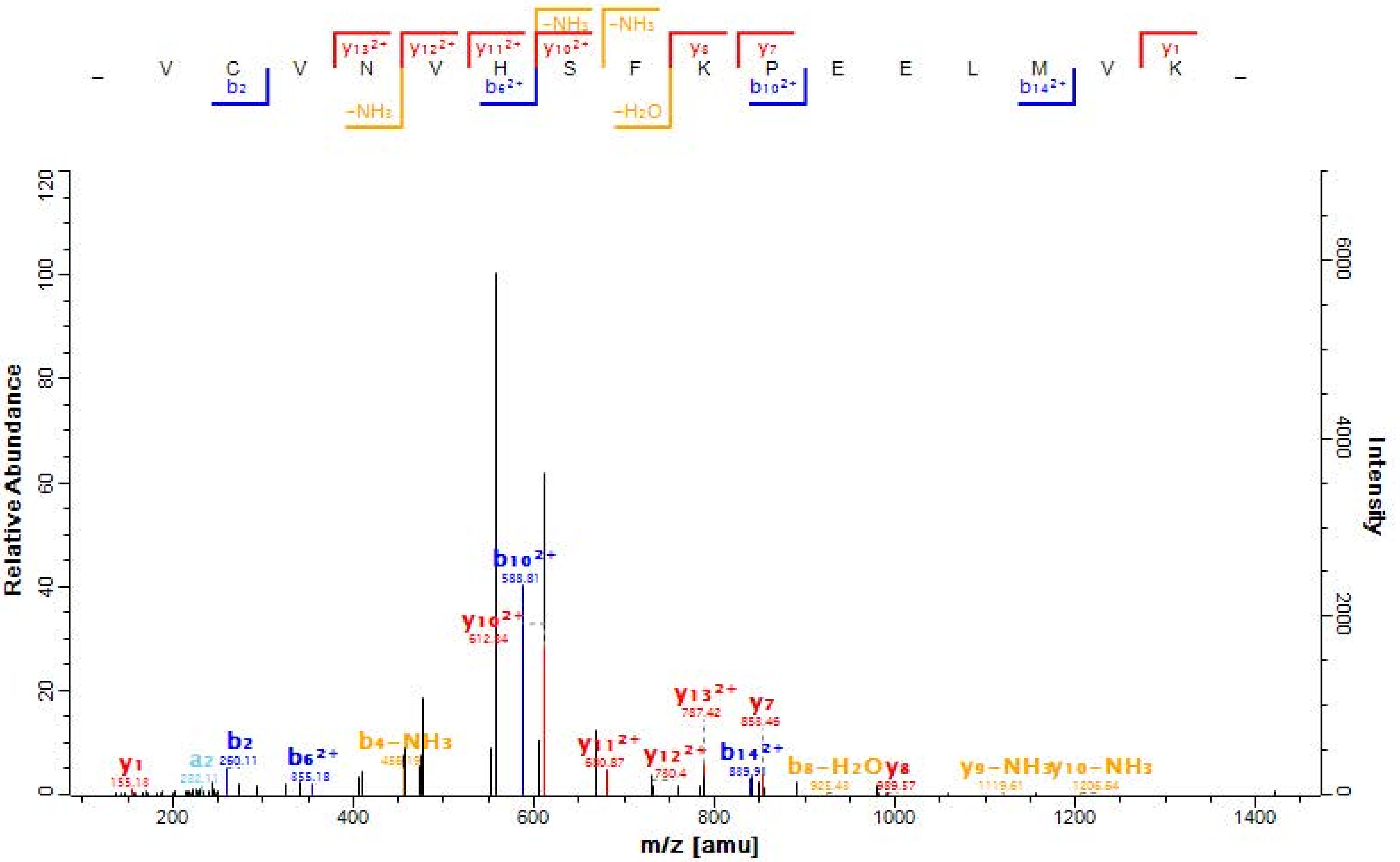
Mass:	1954.06768
m/z:	489.5242
Charge:	4+
Retentiontime:	34.666339874267
Score:	124.5147
Mass Error [ppm]:	0.024455
PEP:	5.0723E-10
Precursor Type:	MULTI

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	57 %
Peak Coverage:	24 %
Protein Localisation:	404 ... 419

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.08		100.1		100.1	1	V	15				
+0.013	185.2		213.2	+0.092	213.2	2	L	14	1870		1870	
	322.2		350.2		350.2	3	H	13	1757		1757	
	379.2		407.2		407.2	4	G	12	1620		810.5	+0.14
	508.3		536.3		536.3	5	E	11	1563		1563	
	636.3	+0.296	332.7	-0.03	664.3	6	Q	10	1434		717.4	+0.18
	799.4	+0.184	414.2	+0.052	827.4	7	Y	9	1306		653.4	+0.11
	912.5		940.5	+0.191	940.5	8	L	8	1143		571.9	+0.17
	1042		1070	-0.19	1070	9	E	7	1030		515.3	+0.10
	1155		1183		1183	10	L	6	900.6	-0.12	450.8	-0.04
	1318		1346	+0.161	1346	11	Y	5	787.5		787.5	
	1454		1482		1482	12	K	4	624.4	-0.12	624.4	
	1551		1579		1579	13	P	3	488.3		488.3	
	1664		1692		1692	14	L	2	391.3	+0.37	391.3	
	1761		1789		1789	15	P	1	278.2	+0.029	278.2	
						16	R	0	181.1	-0.02	181.1	

Scan number	5374	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	58.32



precursor information

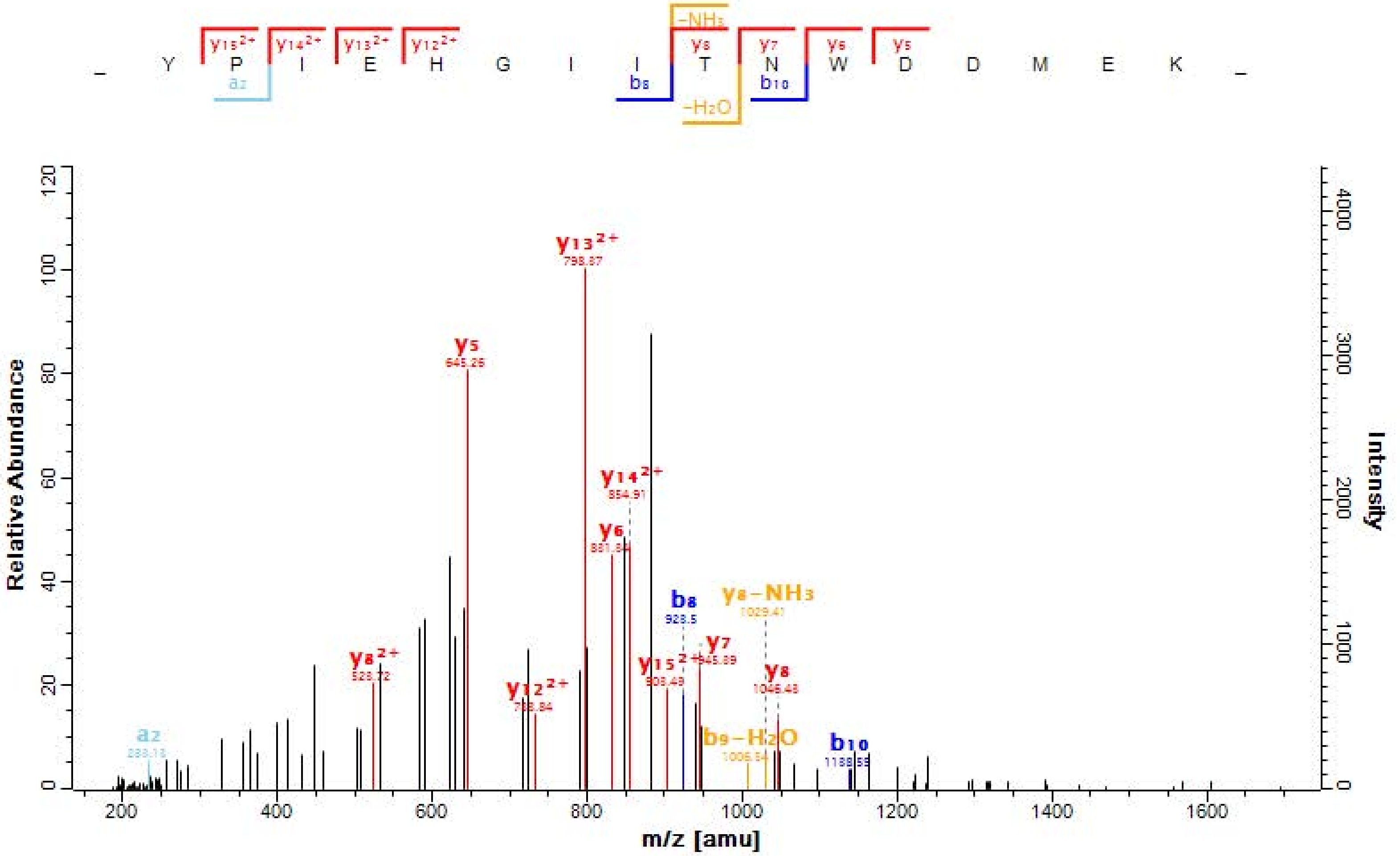
Mass:	1914.9687
m/z:	479.74945
Charge:	4+
Retentiontime:	35.390209197998
Score:	58.31998
Mass Error [ppm]:	-0.45428
PEP:	0.0028392
Precursor Type:	MULTI

general information

Annotation:	10 of 16
AminoAcids Coverag	62 %
Intensity Coverage:	25 %
Peak Coverage:	16 %
Protein Localisation:	98 ... 113

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.08		100.1		100.1	1	V	15				
+0.061	232.1		260.1	+0.104	260.1	2	C	14	1833		1833	
	331.2		359.2		359.2	3	V	13	1673		1673	
	445.2		473.2		473.2	4	N	12	1574		787.4	+0.08
	544.3		572.3		572.3	5	V	11	1460		730.4	-0.03
	681.4	+0.03	355.2		709.3	6	H	10	1361		680.9	+0.07
	768.4		796.4		796.4	7	S	9	1224		612.3	+0.30
	915.5		943.4		943.4	8	F	8	1137		1137	
	1052		1080		1080	9	K	7	989.6	-0.02	989.6	
	1149	-0.27	588.8		1177	10	P	6	853.5	-0.05	853.5	
	1278		1306		1306	11	E	5	756.4		756.4	
	1407		1435		1435	12	E	4	627.4		627.4	
	1520		1548		1548	13	L	3	498.3		498.3	
	1651	+0.053	839.9		1679	14	M	2	385.2		385.2	
	1750		1778		1778	15	V	1	254.2		254.2	
						16	K	0	155.1	-0.11	155.1	

Scan number	5793	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	50.81



precursor information

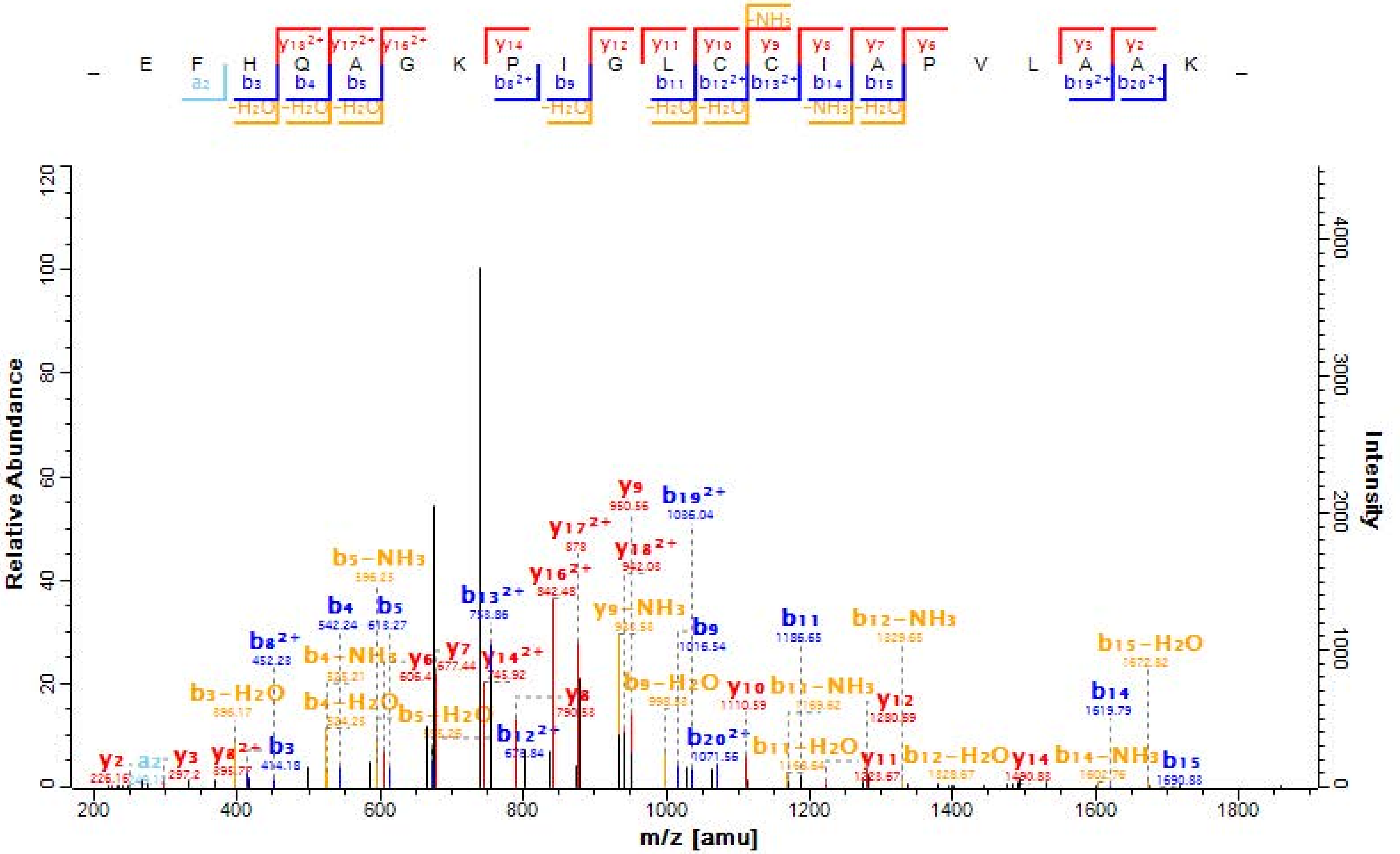
Mass:	1959.90377
m/z:	654.30853
Charge:	3+
Retentiontime:	38.006404876709
Score:	50.80611
Mass Error [ppm]:	0.053715
PEP:	0.013321
Precursor Type:	MULTI

general information

Annotation:	9 of 16
AminoAcids Coverag	56 %
Intensity Coverage:	34 %
Peak Coverage:	14 %
Protein Localisation:	71 ... 86

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.08		164.07	1	Y	15				
-0.097	233.13		261.12	2	P	14	1805.9		903.43	+0.4627
	346.21		374.21	3	I	13	1708.8		854.91	+0.2477
	475.26		503.25	4	E	12	1595.7		798.37	-0.168
	612.31		640.31	5	H	11	1466.7		733.84	+0.2896
	669.34		697.33	6	G	10	1329.6		1329.6	
	782.42		810.41	7	I	9	1272.6		1272.6	
	895.5	+0.0273	923.5	8	I	8	1159.5		1159.5	
	996.55		1024.5	9	T	7	1046.4	-0.023	523.72	+0.2644
	1110.6	-0.082	1138.6	10	N	6	945.39	+0.0127	945.39	
	1296.7		1324.7	11	W	5	831.34	+0.0216	831.34	
	1411.7		1439.7	12	D	4	645.26	+0.2378	645.26	
	1526.7		1554.7	13	D	3	530.24		530.24	
	1657.8		1685.8	14	M	2	415.21		415.21	
	1786.8		1814.8	15	E	1	284.17		284.17	
				16	K	0	155.13		155.13	

Scan number	6115	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	232.78



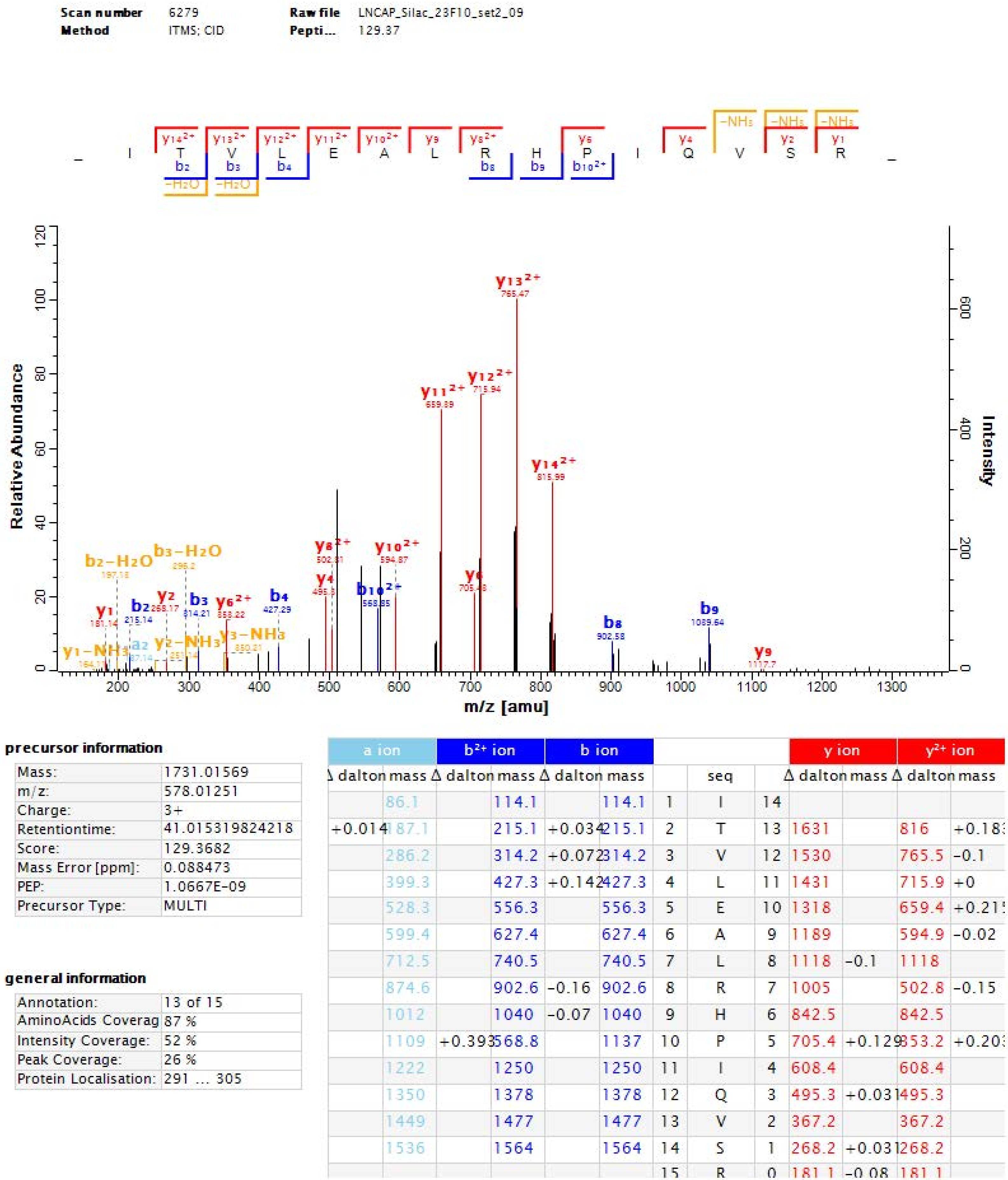
precursor information

Mass:	2279.19145
m/z:	760.73776
Charge:	3+
Retentiontime:	39.967727661132
Score:	232.7801
Mass Error [ppm]:	-0.18151
PEP:	1.503E-75
Precursor Type:	MULTI

general information

Annotation:	16 of 21
AminoAcids Coverag	76 %
Intensity Coverage:	50 %
Peak Coverage:	41 %
Protein Localisation:	165 ... 185

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.1		130		130	1	E	20				
+0.071	249.1		277.1		277.1	2	F	19	2167		2167	
	386.2		414.2	+0.057	414.2	3	H	18	2020		2020	
	514.2		542.2	-0.02	542.2	4	Q	17	1883		942	-0.05
	585.3		613.3	+0.196	613.3	5	A	16	1755		878	-0.04
	642.3		670.3		670.3	6	G	15	1684		842.5	+0.24
	778.4		806.4		806.4	7	K	14	1627		1627	
	875.5	+0.144	452.2		903.5	8	P	13	1491	-0.03	745.9	+0.11
	988.5		1017	-0.34	1017	9	I	12	1394		1394	
	1046		1074		1074	10	G	11	1281	-0.23	1281	
	1159		1187	-0.06	1187	11	L	10	1224	+0.033	1224	
	1319	-0.23	673.8		1347	12	C	9	1111	+0.019	1111	
	1479	+0.472	753.9		1507	13	C	8	950.6	+0.001	950.6	
	1592		1620	+0.38	1620	14	I	7	790.5	+0.038	395.8	-0.28
	1663		1691	+0.168	1691	15	A	6	677.4	-0.01	677.4	
	1760		1788		1788	16	P	5	606.4	+0.2	606.4	
	1859		1887		1887	17	V	4	509.4		509.4	
	1972		2000		2000	18	L	3	410.3		410.3	
	2043	+0.455	1036		2071	19	A	2	297.2	+0.077	297.2	
	2114	+0.106	1072		2142	20	A	1	226.2	-0.23	226.2	
						21	K	0	155.1		155.1	



Scan number	6279	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	129.37

precursor information

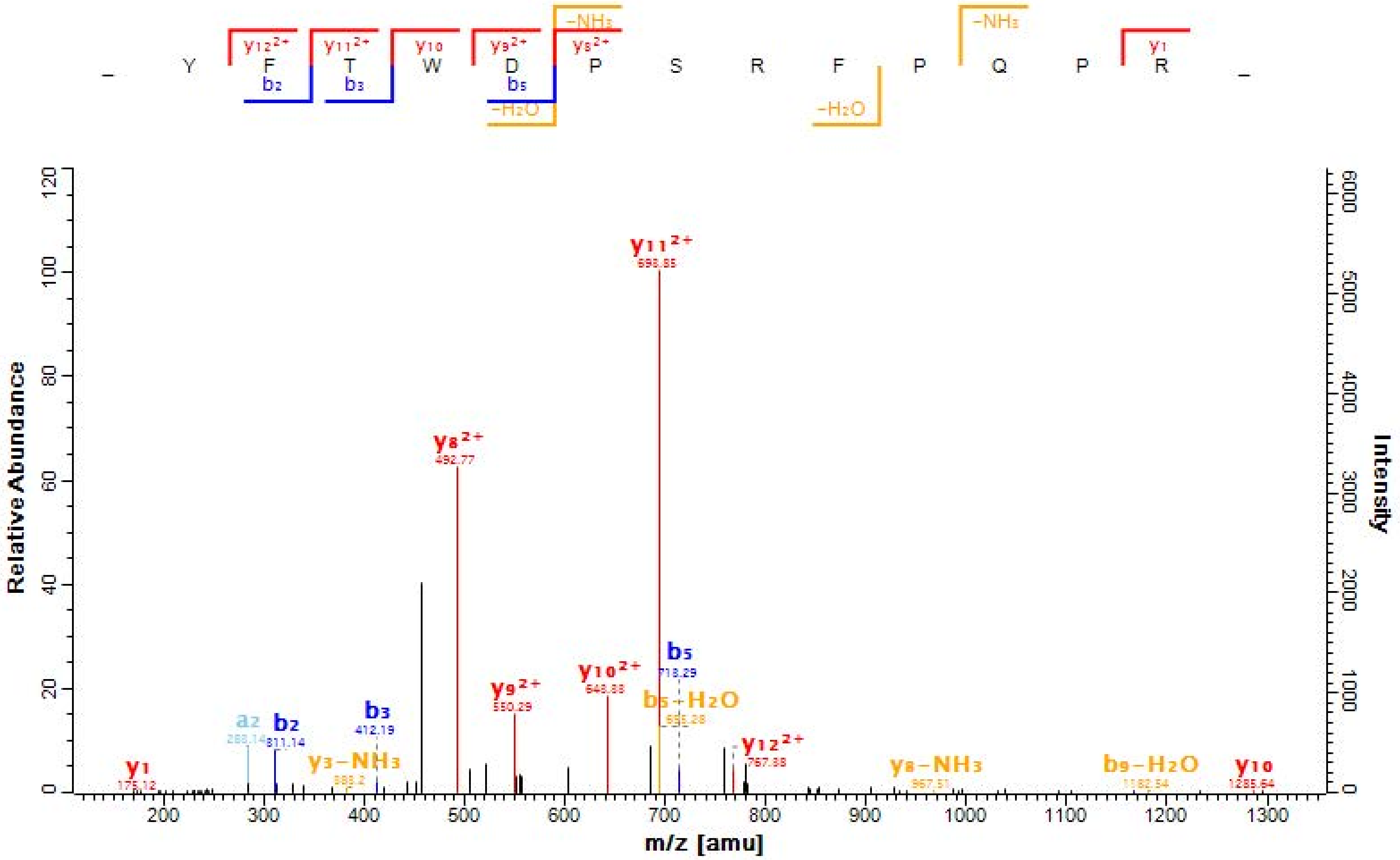
Mass:	1731.01569
m/z:	578.01251
Charge:	3+
Retentiontime:	41.015319824218
Score:	129.3682
Mass Error [ppm]:	0.088473
PEP:	1.0667E-09
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	52 %
Peak Coverage:	26 %
Protein Localisation:	291 ... 305

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	I	14				
+0.014	187.1		215.1	+0.034	215.1	2	T	13	1631		816	+0.18
	286.2		314.2	+0.072	314.2	3	V	12	1530		765.5	-0.1
	399.3		427.3	+0.142	427.3	4	L	11	1431		715.9	+0
	528.3		556.3		556.3	5	E	10	1318		659.4	+0.21
	599.4		627.4		627.4	6	A	9	1189		594.9	-0.02
	712.5		740.5		740.5	7	L	8	1118	-0.1	1118	
	874.6		902.6	-0.16	902.6	8	R	7	1005		502.8	-0.15
	1012		1040	-0.07	1040	9	H	6	842.5		842.5	
	1109	+0.393	568.8		1137	10	P	5	705.4	+0.129	353.2	+0.20
	1222		1250		1250	11	I	4	608.4		608.4	
	1350		1378		1378	12	Q	3	495.3	+0.031	495.3	
	1449		1477		1477	13	V	2	367.2		367.2	
	1536		1564		1564	14	S	1	268.2	+0.031	268.2	
						15	R	0	181.1	-0.08	181.1	

Scan number	6302	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	63.41



precursor information

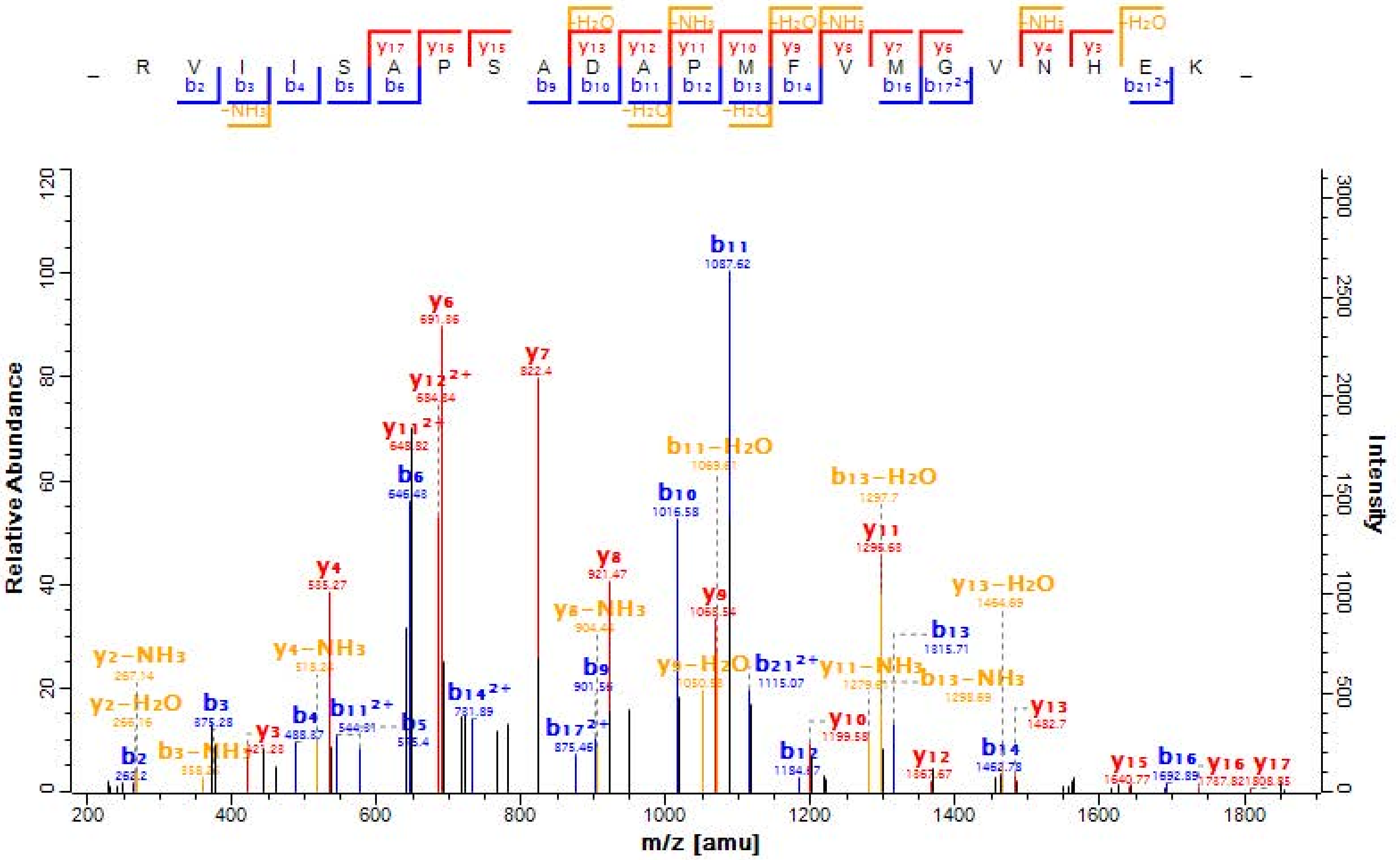
Mass:	1695.81601
m/z:	566.27928
Charge:	3+
Retentiontime:	41.151100158691
Score:	63.40819
Mass Error [ppm]:	0.1368
PEP:	0.0052532
Precursor Type:	MULTI

general information

Annotation:	8 of 13
AminoAcids Coverag	62 %
Intensity Coverage:	65 %
Peak Coverage:	16 %
Protein Localisation:	489 ... 501

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.08		164.07	1	Y	12				
+0.0693	283.14	-0.055	311.14	2	F	11	1533.8		767.38	+0.041
	384.19	-0.218	412.19	3	T	10	1386.7		693.85	+0.181
	570.27		598.27	4	W	9	1285.6	+0.044	643.33	+0.173
	685.3	-0.053	713.29	5	D	8	1099.6		550.29	+0.237
	782.35		810.35	6	P	7	984.54		492.77	+0.197
	869.38		897.38	7	S	6	887.48		887.48	
	1025.5		1053.5	8	R	5	800.45		800.45	
	1172.6		1200.5	9	F	4	644.35		644.35	
	1269.6		1297.6	10	P	3	497.28		497.28	
	1397.7		1425.7	11	Q	2	400.23		400.23	
	1494.7		1522.7	12	P	1	272.17		272.17	
				13	R	0	175.12	-0.067	175.12	

Scan number	6351	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	187.59



precursor information

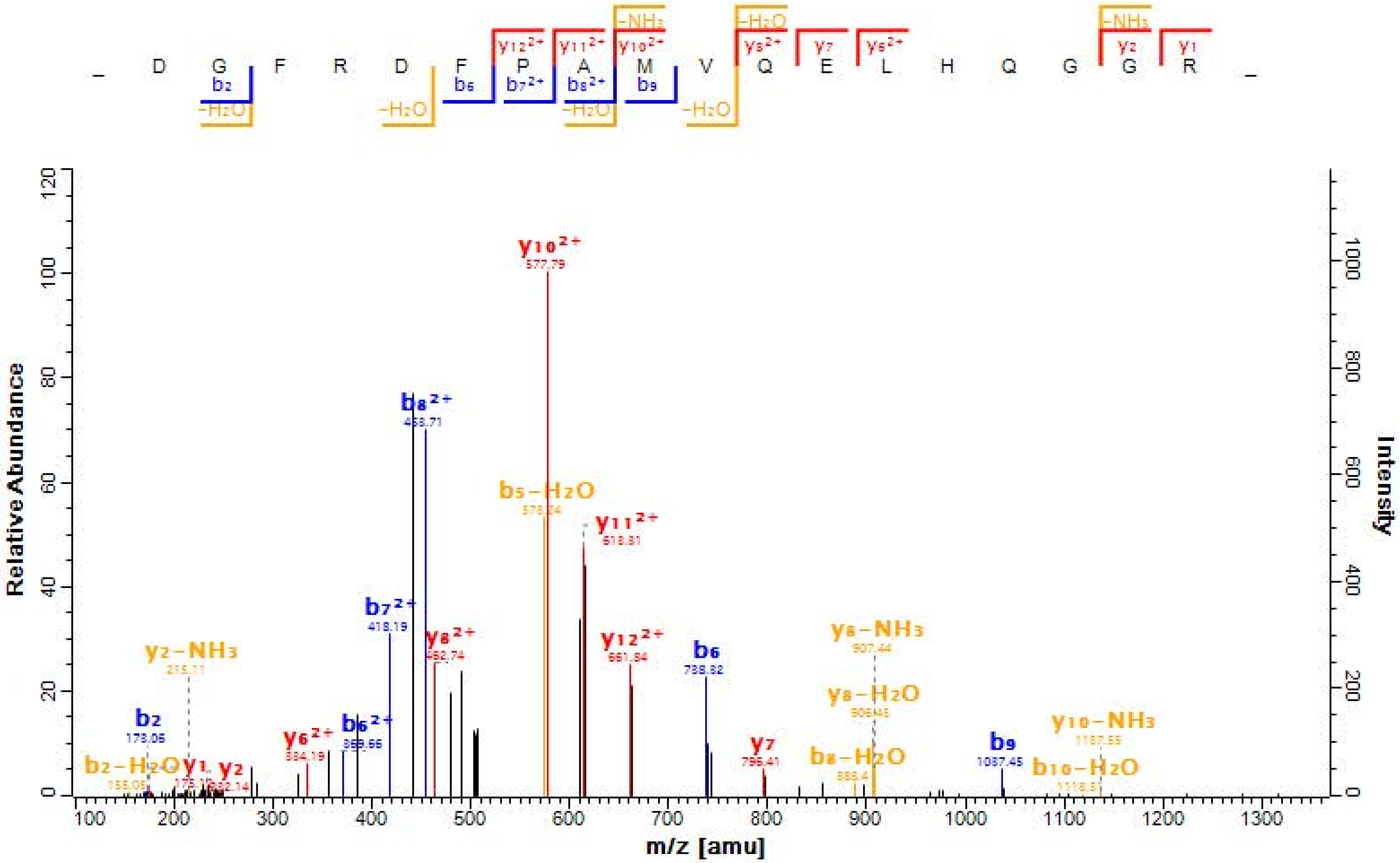
Mass:	2368.20213
m/z:	790.40799
Charge:	3+
Retentiontime:	41.454513549804
Score:	187.5905
Mass Error [ppm]:	-0.42991
PEP:	7.384E-49
Precursor Type:	MULTI

general information

Annotation:	19 of 22
AminoAcids Coverag	86 %
Intensity Coverage:	67 %
Peak Coverage:	47 %
Protein Localisation:	118 ... 139

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	163.13		163.13	1	R	21				
	262.2	+0.1838	262.2	2	V	20	2221.1		2221.1	
	375.28	+0.3042	375.28	3	I	19	2122.1		2122.1	
	488.37	+0.0362	488.37	4	I	18	2009		2009	
	575.4	+0.2109	575.4	5	S	17	1895.9		1895.9	
	646.43	-0.054	646.43	6	A	16	1808.9	+0.3772	1808.9	
	743.49		743.49	7	P	15	1737.8	-0.082	1737.8	
	830.52		830.52	8	S	14	1640.8	-0.046	1640.8	
	901.56	+0.0795	901.56	9	A	13	1553.7		1553.7	
	1016.6	+0.0443	1016.6	10	D	12	1482.7	-0.231	1482.7	
+0.0812	544.31	-0.019	1087.6	11	A	11	1367.7	-0.042	684.34	+0.1273
	1184.7	-0.14	1184.7	12	P	10	1296.6	-0.012	648.82	-0.047
	1315.7	-0.005	1315.7	13	M	9	1199.6	+0.4169	1199.6	
-0.133	731.89	+0.1057	1462.8	14	F	8	1068.5	+0.0131	1068.5	
	1561.9		1561.9	15	V	7	921.47	+0.064	921.47	
	1692.9	+0.2234	1692.9	16	M	6	822.4	-0.035	822.4	
+0.0687	875.46		1749.9	17	G	5	691.36	+0.046	691.36	
	1849		1849	18	V	4	634.34		634.34	
	1963		1963	19	N	3	535.27	-0.034	535.27	
	2100.1		2100.1	20	H	2	421.23	-0.082	421.23	
+0.1212	1115.1		2229.1	21	E	1	284.17		284.17	
				22	K	0	155.13		155.13	

Scan number	6649	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	71.08



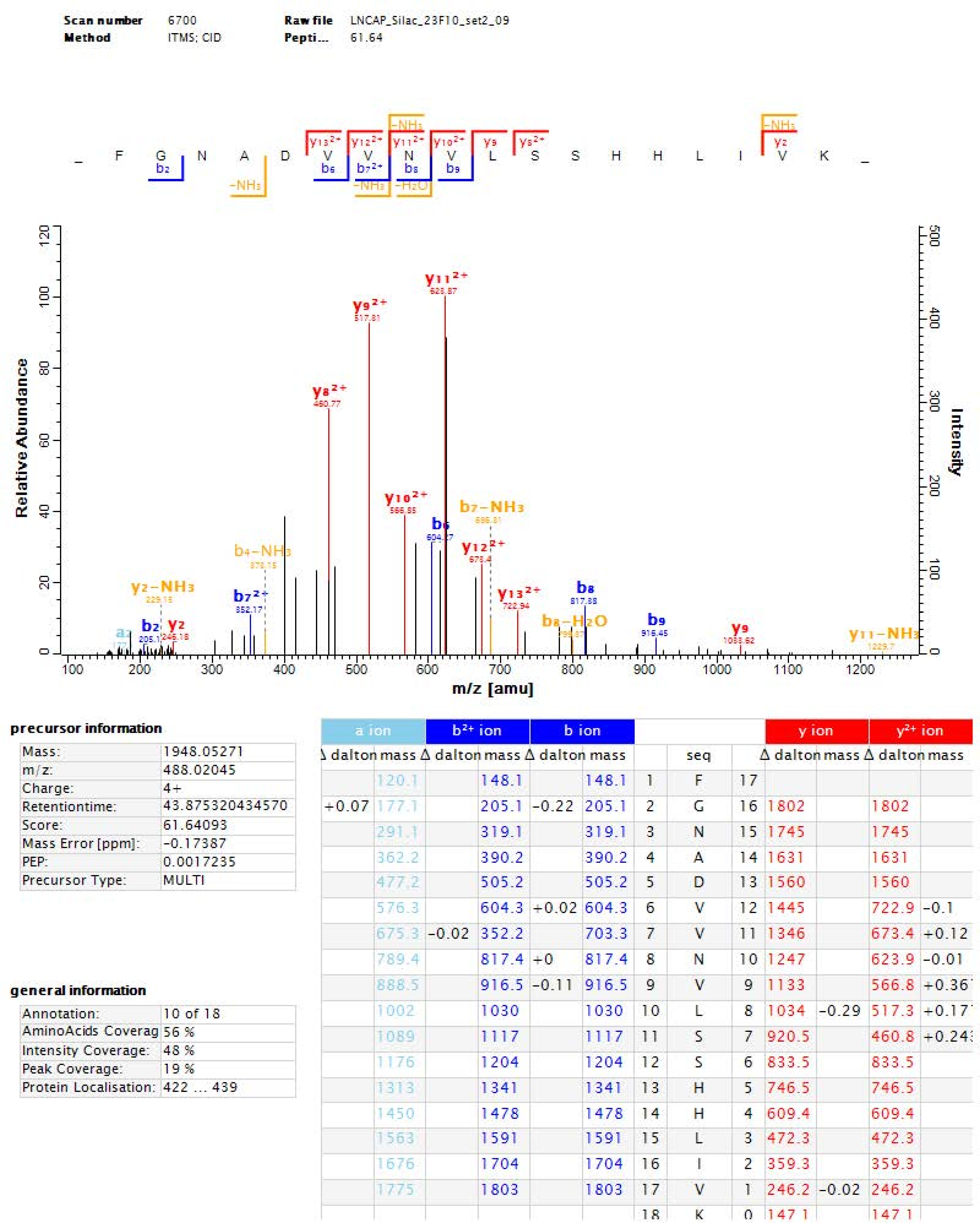
precursor information

Mass:	2058.96984
m/z:	515.74974
Charge:	4+
Retentiontime:	43.511604309082
Score:	71.07995
Mass Error [ppm]:	0.21646
PEP:	0.00028854
Precursor Type:	MULTI

general information

Annotation:	12 of 18
AminoAcids Coverag	67 %
Intensity Coverage:	54 %
Peak Coverage:	21 %
Protein Localisation:	419 ... 436

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	17				
	173.06	+0.1125	173.06	2	G	16	1944.9		1944.9	
	320.12		320.12	3	F	15	1887.9		1887.9	
	476.23		476.23	4	R	14	1740.9		1740.9	
	591.25		591.25	5	D	13	1584.8		1584.8	
+0.1215	369.66	-0.003	738.32	6	F	12	1469.7		1469.7	
+0.2508	418.19		835.37	7	P	11	1322.7		661.84	-0.027
+0.2495	453.71		906.41	8	A	10	1225.6		613.31	+0.255
	1037.5	+0.0757	1037.5	9	M	9	1154.6		577.79	+0.4405
	1136.5		1136.5	10	V	8	1023.5		1023.5	
	1264.6		1264.6	11	Q	7	924.46		462.74	+0.0321
	1393.6		1393.6	12	E	6	796.41	+0.0589	796.41	
	1506.7		1506.7	13	L	5	667.36		334.19	-0.073
	1643.8		1643.8	14	H	4	554.28		554.28	
	1771.8		1771.8	15	Q	3	417.22		417.22	
	1828.8		1828.8	16	G	2	289.16		289.16	
	1885.9		1885.9	17	G	1	232.14	-0.014	232.14	
				18	R	0	175.12	-0.019	175.12	



Scan number	6700	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	61.64

precursor information

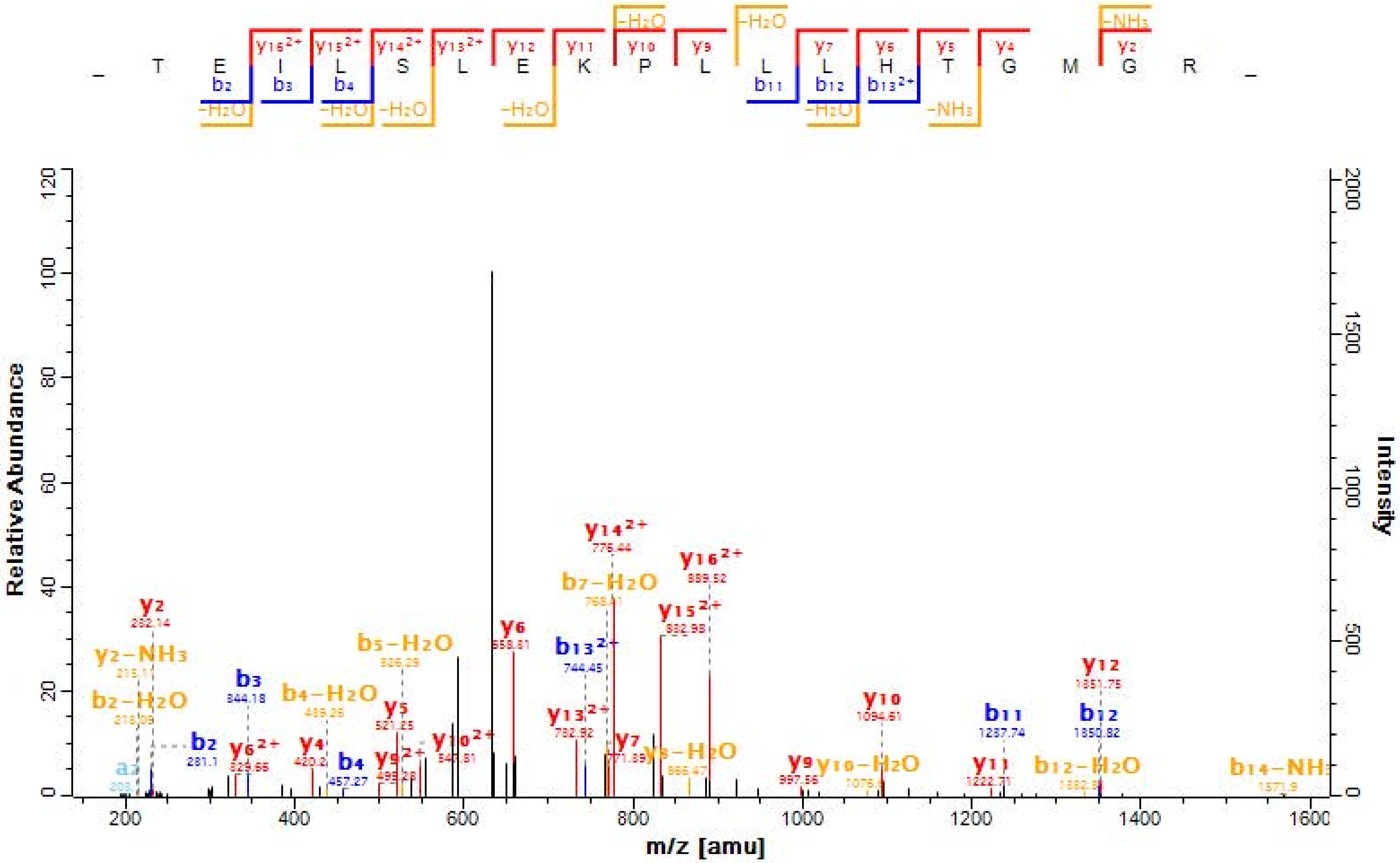
Mass:	1948.05271
m/z:	488.02045
Charge:	4+
Retentiontime:	43.875320434570
Score:	61.64093
Mass Error [ppm]:	-0.17387
PEP:	0.0017235
Precursor Type:	MULTI

general information

Annotation:	10 of 18
AminoAcids Coverag	56 %
Intensity Coverage:	48 %
Peak Coverage:	19 %
Protein Localisation:	422 ... 439

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.1		148.1		148.1	1	F	17				
+0.07	177.1		205.1	-0.22	205.1	2	G	16	1802		1802	
	291.1		319.1		319.1	3	N	15	1745		1745	
	362.2		390.2		390.2	4	A	14	1631		1631	
	477.2		505.2		505.2	5	D	13	1560		1560	
	576.3		604.3	+0.02	604.3	6	V	12	1445		722.9	-0.1
	675.3	-0.02	352.2		703.3	7	V	11	1346		673.4	+0.12
	789.4		817.4	+0	817.4	8	N	10	1247		623.9	-0.01
	888.5		916.5	-0.11	916.5	9	V	9	1133		566.8	+0.36
	1002		1030		1030	10	L	8	1034	-0.29	517.3	+0.17
	1089		1117		1117	11	S	7	920.5		460.8	+0.24
	1176		1204		1204	12	S	6	833.5		833.5	
	1313		1341		1341	13	H	5	746.5		746.5	
	1450		1478		1478	14	H	4	609.4		609.4	
	1563		1591		1591	15	L	3	472.3		472.3	
	1676		1704		1704	16	I	2	359.3		359.3	
	1775		1803		1803	17	V	1	246.2	-0.02	246.2	
						18	K	0	147.1		147.1	

Scan number	6940	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	120.77



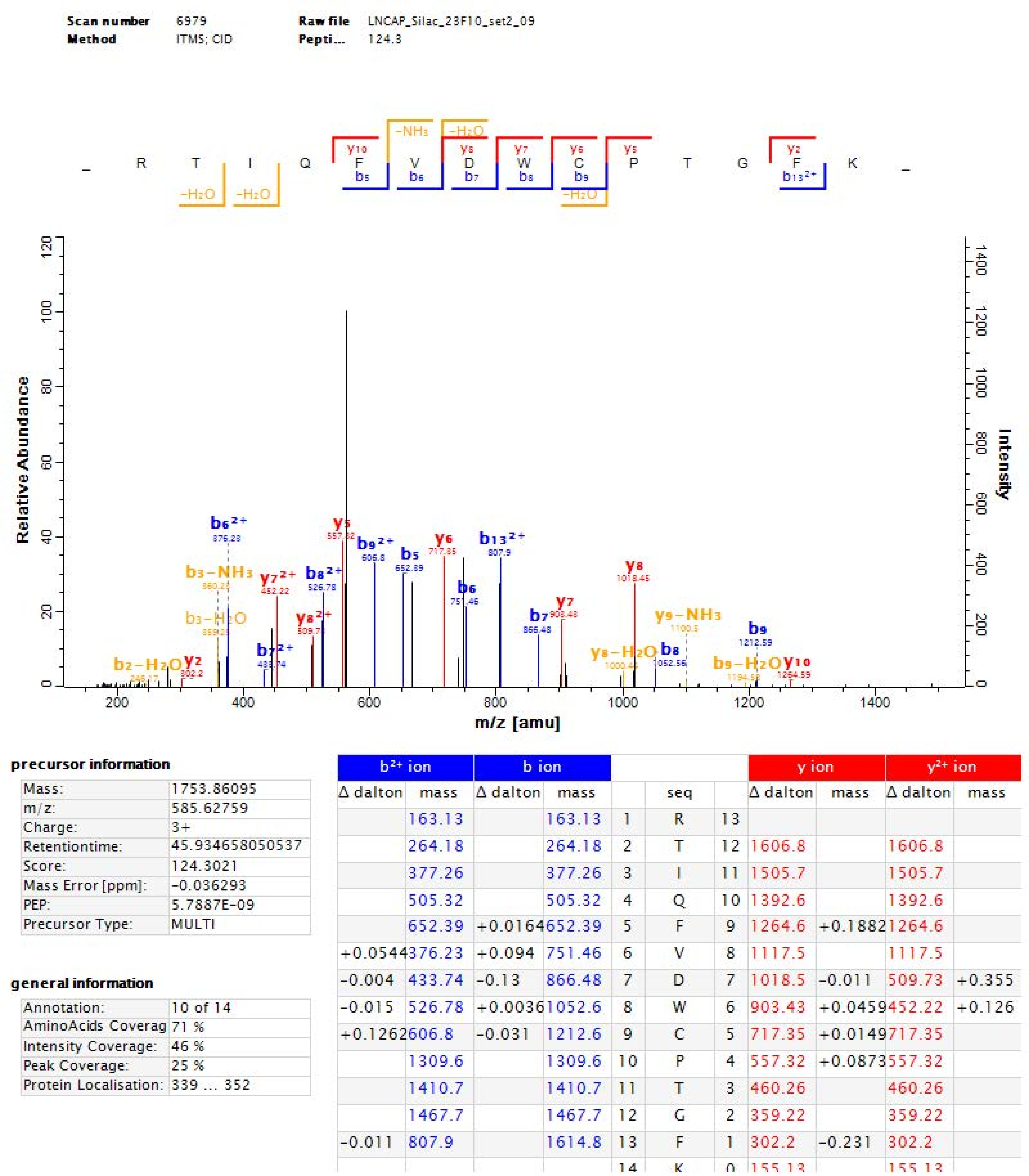
precursor information

Mass:	2007.11945
m/z:	670.04709
Charge:	3+
Retentiontime:	45.644332885742
Score:	120.7663
Mass Error [ppm]:	0.38081
PEP:	2.3911E-12
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	47 %
Peak Coverage:	32 %
Protein Localisation:	235 ... 252

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.1		102.1	1	T	17				
-0.26	203.1		231.1	-0.03	231.1	2	E	16	1907		1907	
	316.2		344.2	+0.04	344.2	3	I	15	1778		889.5	+0.19
	429.3		457.3	+0.123	457.3	4	L	14	1665		833	+0.28
	516.3		544.3		544.3	5	S	13	1552		776.4	+0.26
	629.4		657.4		657.4	6	L	12	1465		732.9	+0.23
	758.4		786.4		786.4	7	E	11	1352	+0.031	1352	
	886.5		914.5		914.5	8	K	10	1223	+0.024	1223	
	983.6		1012		1012	9	P	9	1095	-0.01	547.8	+0.21
	1097		1125		1125	10	L	8	997.6	+0.194	499.3	-0.11
	1210		1238	+0.235	1238	11	L	7	884.5		884.5	
	1323		1351	-0.1	1351	12	L	6	771.4	-0.09	771.4	
	1460	+0.186	744.4		1488	13	H	5	658.3	+0.067	329.7	+0.13
	1561		1589		1589	14	T	4	521.3	+0.029	521.3	
	1618		1646		1646	15	G	3	420.2	+0.067	420.2	
	1749		1777		1777	16	M	2	363.2		363.2	
	1806		1834		1834	17	G	1	232.1	+0.062	232.1	
						18	R	0	175.1		175.1	



Scan number	6979	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	124.3

precursor information

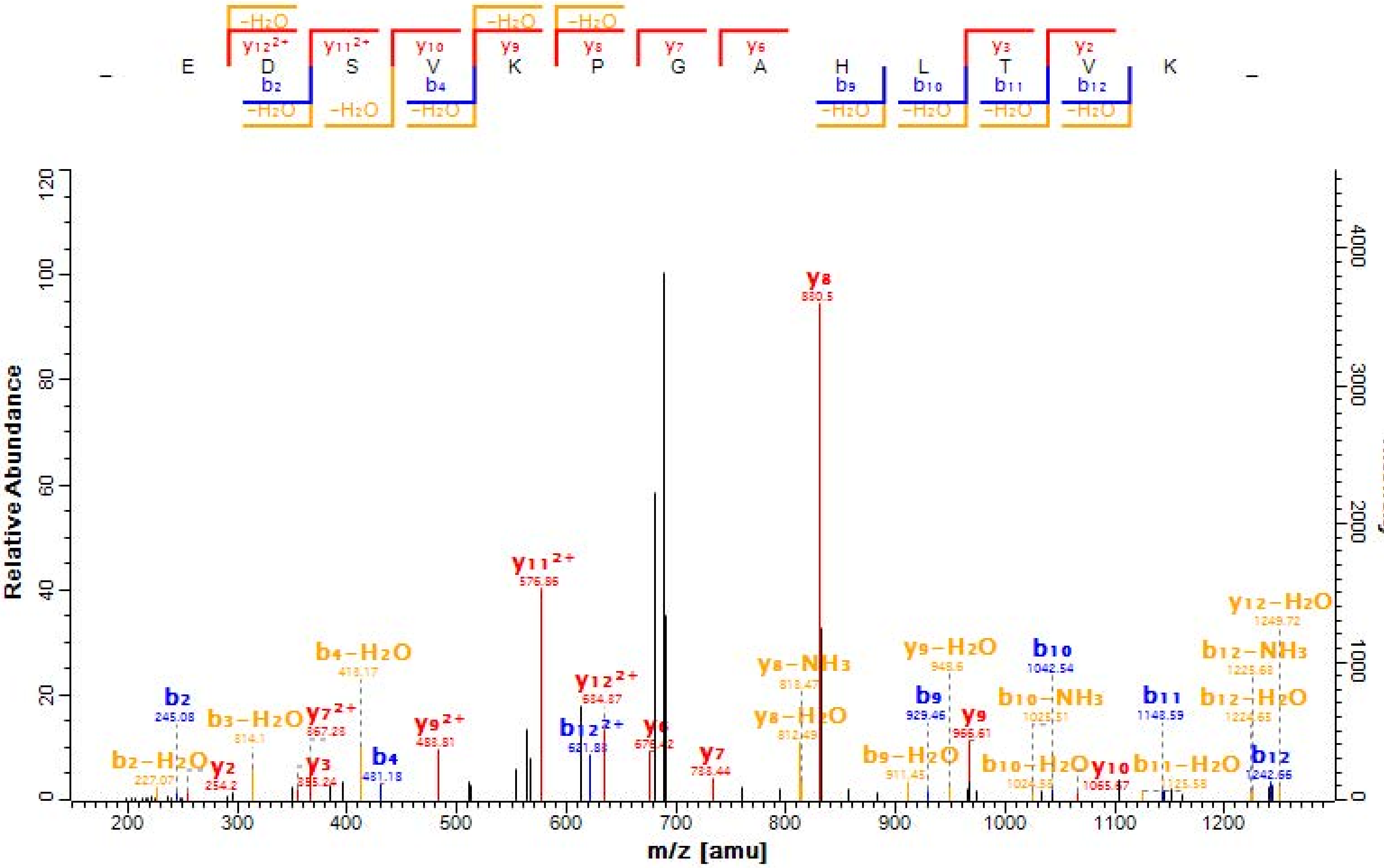
Mass:	1753.86095
m/z:	585.62759
Charge:	3+
Retentiontime:	45.934658050537
Score:	124.3021
Mass Error [ppm]:	-0.036293
PEP:	5.7887E-09
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	46 %
Peak Coverage:	25 %
Protein Localisation:	339 ... 352

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	163.13		163.13	1	R	13				
	264.18		264.18	2	T	12	1606.8		1606.8	
	377.26		377.26	3	I	11	1505.7		1505.7	
	505.32		505.32	4	Q	10	1392.6		1392.6	
	652.39	+0.0164	652.39	5	F	9	1264.6	+0.1882	1264.6	
+0.0544	376.23	+0.094	751.46	6	V	8	1117.5		1117.5	
-0.004	433.74	-0.13	866.48	7	D	7	1018.5	-0.011	509.73	+0.355
-0.015	526.78	+0.0036	1052.6	8	W	6	903.43	+0.0459	452.22	+0.126
+0.1262	606.8	-0.031	1212.6	9	C	5	717.35	+0.0149	717.35	
	1309.6		1309.6	10	P	4	557.32	+0.0873	557.32	
	1410.7		1410.7	11	T	3	460.26		460.26	
	1467.7		1467.7	12	G	2	359.22		359.22	
-0.011	807.9		1614.8	13	F	1	302.2	-0.231	302.2	
				14	K	0	155.13		155.13	

Scan number	709	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	189.24



precursor information

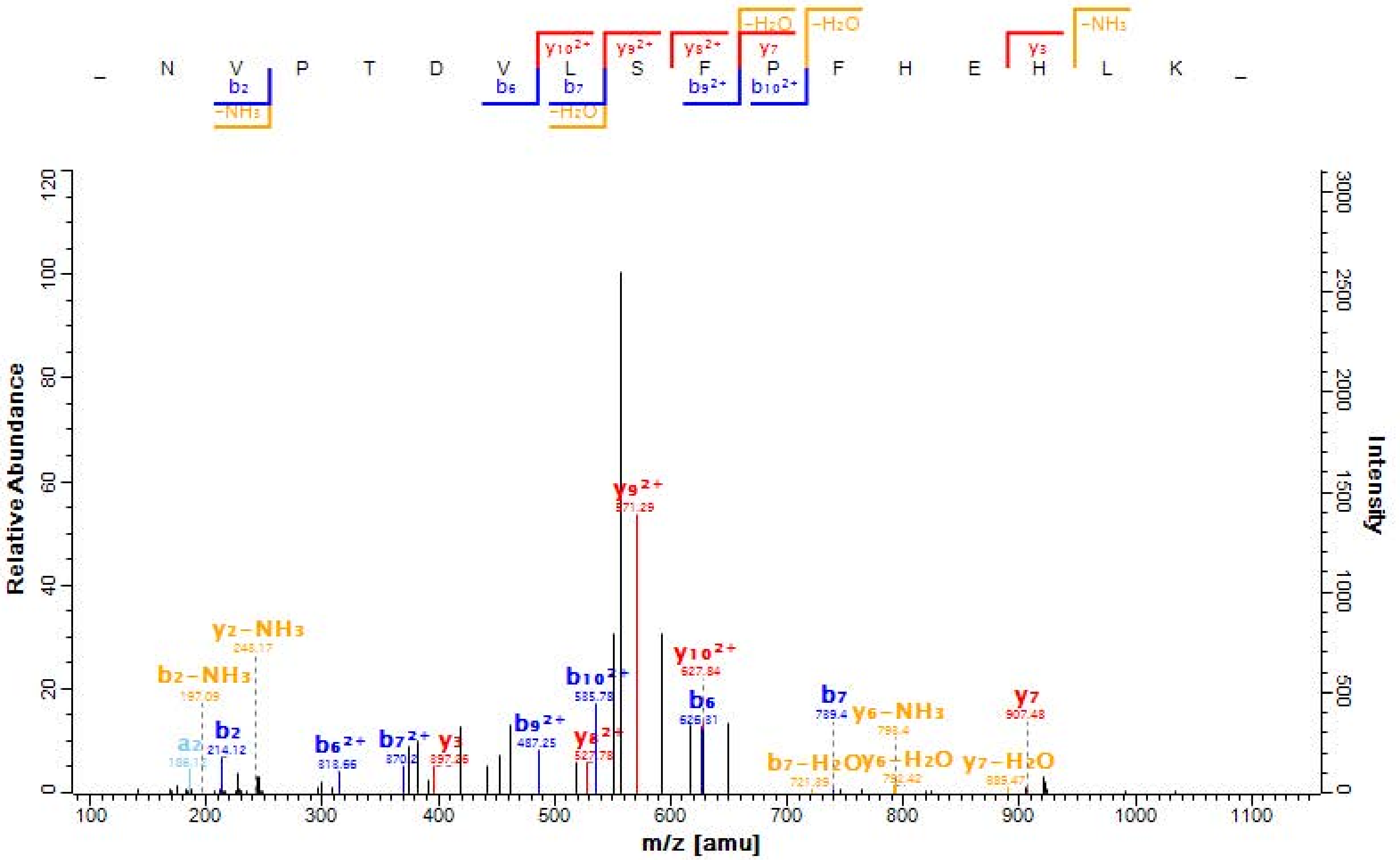
Mass:	1379.74097
m/z:	690.87776
Charge:	2+
Retentiontime:	8.7821149826049
Score:	189.2425
Mass Error [ppm]:	0.065055
PEP:	8.5468E-17
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	44 %
Peak Coverage:	39 %
Protein Localisation:	114 ... 126

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	12				
	245.08	+0.0718	245.08	2	D	11	1267.7		634.37	+0.2215
	332.11		332.11	3	S	10	1152.7		576.86	+0.1834
	431.18	+0.0101	431.18	4	V	9	1065.7	-0.006	1065.7	
	567.29		567.29	5	K	8	966.61	+0.0317	483.81	+0.1716
	664.34		664.34	6	P	7	830.5	-0.02	830.5	
	721.36		721.36	7	G	6	733.44	+0.0919	367.23	-0.059
	792.4		792.4	8	A	5	676.42	+0.0014	676.42	
	929.46	+0.0482	929.46	9	H	4	605.39		605.39	
	1042.5	+0.2625	1042.5	10	L	3	468.33		468.33	
	1143.6	+0.0344	1143.6	11	T	2	355.24	+0.0895	355.24	
-0.014	621.83	-0.086	1242.7	12	V	1	254.2	-0.131	254.2	
				13	K	0	155.13		155.13	

Scan number	7150	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	59.29



precursor information

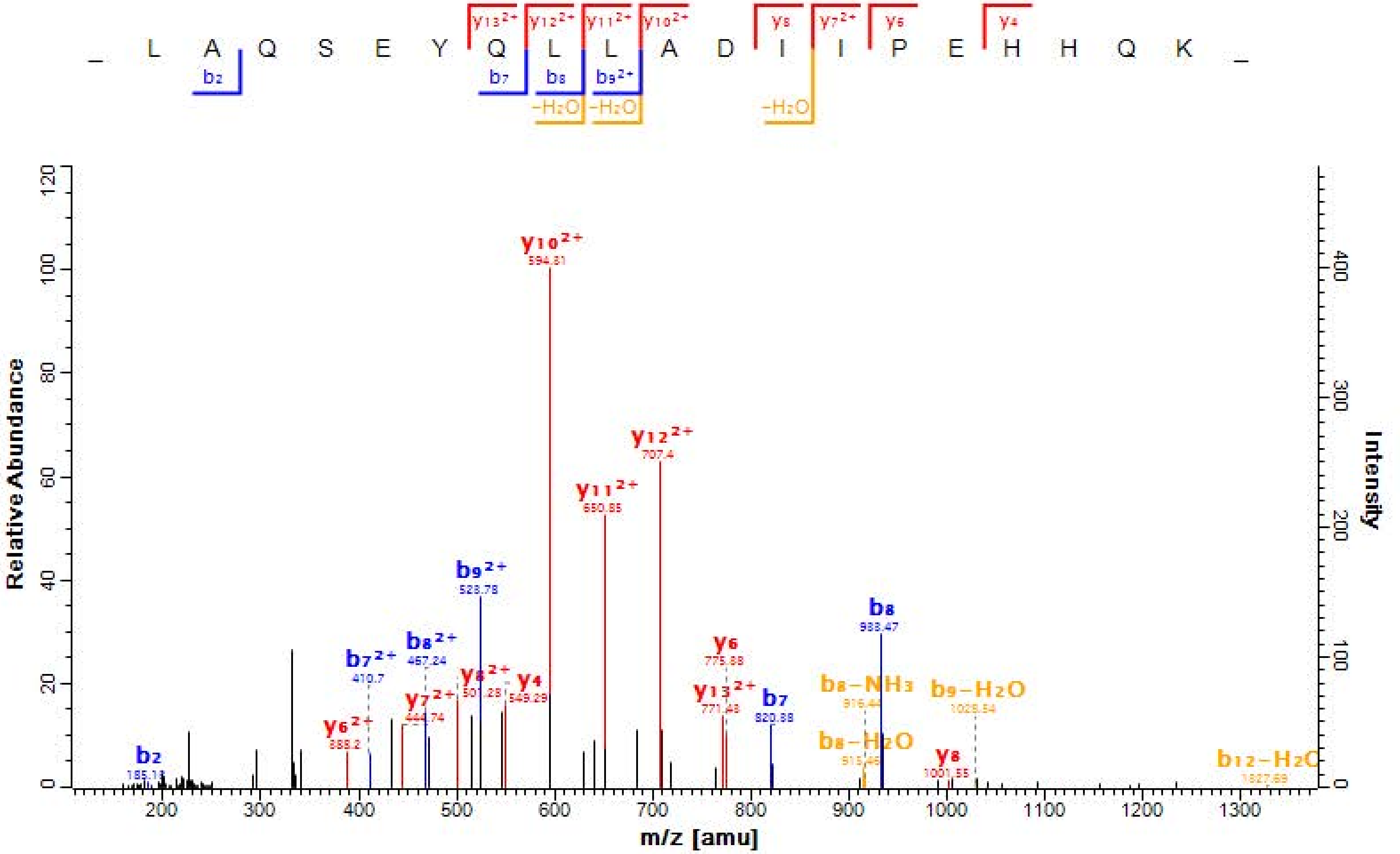
Mass:	1878.96304
m/z:	470.74804
Charge:	4+
Retentiontime:	47.253753662109
Score:	59.29396
Mass Error [ppm]:	0.11206
PEP:	0.0032393
Precursor Type:	MULTI

general information

Annotation:	9 of 16
AminoAcids Coverag	56 %
Intensity Coverage:	32 %
Peak Coverage:	17 %
Protein Localisation:	58 ... 73

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	87.06		115.1		115.1	1	N	15				
+0.05	186.1		214.1	+0.03	214.1	2	V	14	1766		1766	
	283.2		311.2		311.2	3	P	13	1667		1667	
	384.2		412.2		412.2	4	T	12	1570		1570	
	499.3		527.2		527.2	5	D	11	1469		1469	
	598.3	+0.425	313.7	-0.02	626.3	6	V	10	1354		1354	
	711.4	+0.071	370.2	-0.22	739.4	7	L	9	1255		627.8	-0.04
	798.4		826.4		826.4	8	S	8	1142		571.3	+0.18
	945.5	+0.059	487.3		973.5	9	F	7	1055		527.8	+0.22
	1043	-0.21	535.8		1071	10	P	6	907.5	+0.207	907.5	
	1190		1218		1218	11	F	5	810.4		810.4	
	1327		1355		1355	12	H	4	663.4		663.4	
	1456		1484		1484	13	E	3	526.3		526.3	
	1593		1621		1621	14	H	2	397.3	-0.48	397.3	
	1706		1734		1734	15	L	1	260.2		260.2	
						16	K	0	147.1		147.1	

Scan number	7577	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	69.33



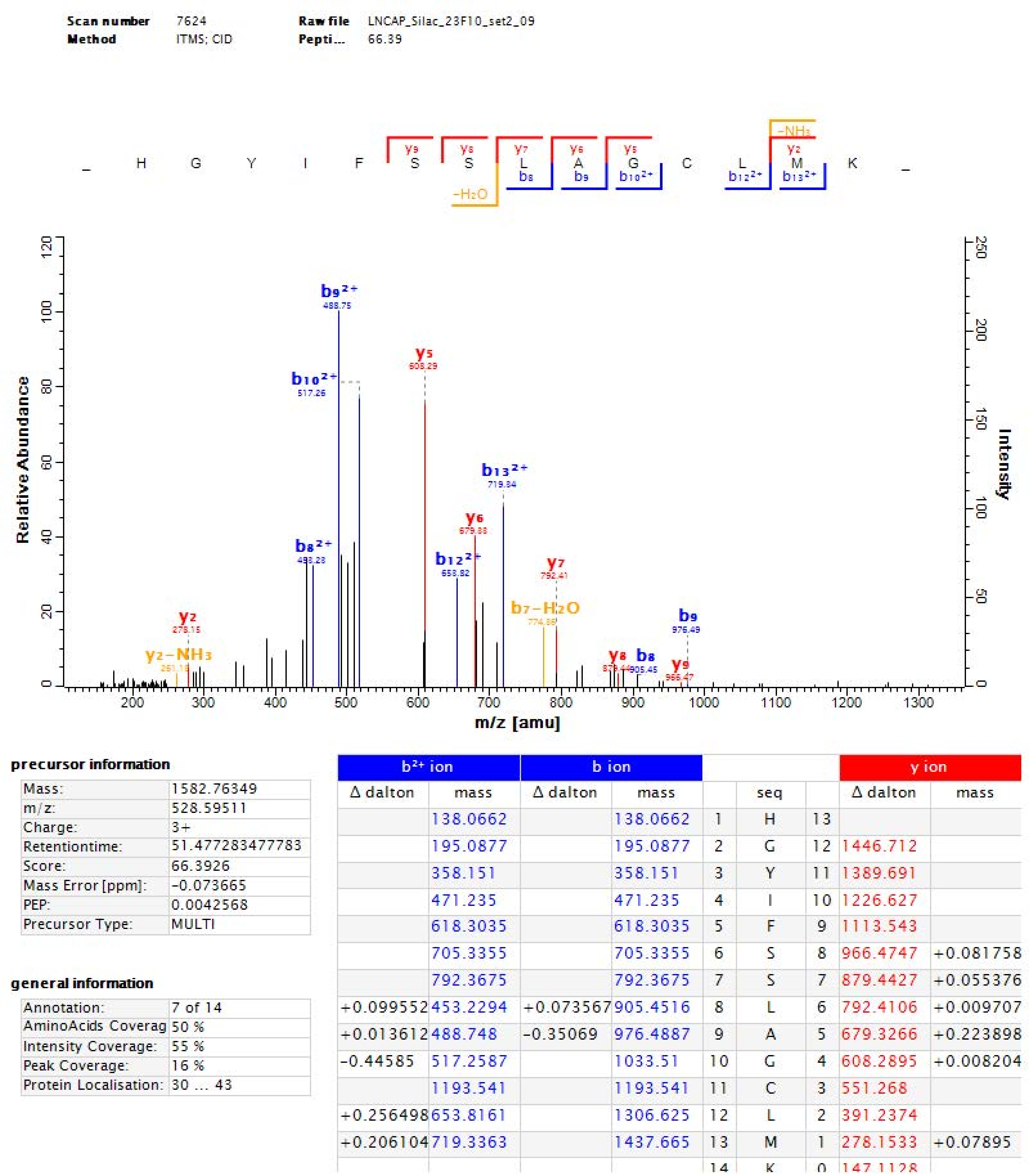
precursor information

Mass:	2232.15337
m/z:	559.04562
Charge:	4+
Retentiontime:	51.018989562988
Score:	69.33073
Mass Error [ppm]:	-0.22757
PEP:	0.00047866
Precursor Type:	MULTI

general information

Annotation:	9 of 19
AminoAcids Coverag	47 %
Intensity Coverage:	61 %
Peak Coverage:	20 %
Protein Localisation:	374 ... 392

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	18				
	185.13	-0.007	185.13	2	A	17	2120.1		2120.1	
	313.19		313.19	3	Q	16	2049		2049	
	400.22		400.22	4	S	15	1921		1921	
	529.26		529.26	5	E	14	1833.9		1833.9	
	692.32		692.32	6	Y	13	1704.9		1704.9	
+0.2724	410.7	+0.1164	820.38	7	Q	12	1541.8		771.43	+0.1736
+0.0422	467.24	-0.119	933.47	8	L	11	1413.8		707.4	+0.2674
-0.396	523.78		1046.6	9	L	10	1300.7		650.85	+0.2241
	1117.6		1117.6	10	A	9	1187.6		594.31	+0.2151
	1232.6		1232.6	11	D	8	1116.6		1116.6	
	1345.7		1345.7	12	I	7	1001.6	+0.0151	501.28	+0.1357
	1458.8		1458.8	13	I	6	888.47		444.74	+0.1164
	1555.8		1555.8	14	P	5	775.38	-0.133	388.2	+0.1135
	1684.9		1684.9	15	E	4	678.33		678.33	
	1821.9		1821.9	16	H	3	549.29	-0.198	549.29	
	1959		1959	17	H	2	412.23		412.23	
	2087.1		2087.1	18	Q	1	275.17		275.17	
				19	K	0	147.11		147.11	



Scan number	7624	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	66.39

precursor information

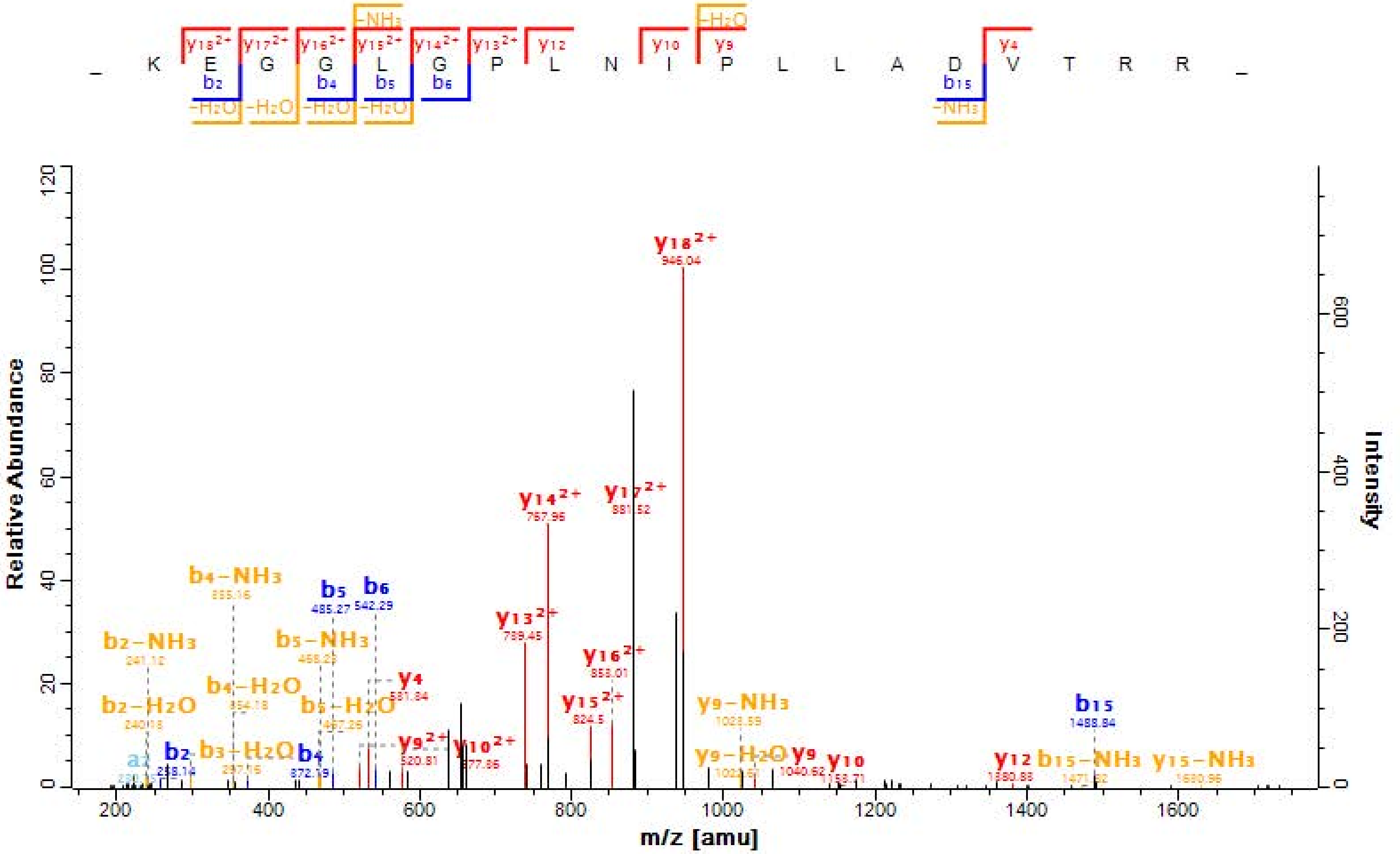
Mass:	1582.76349
m/z:	528.59511
Charge:	3+
Retentiontime:	51.477283477783
Score:	66.3926
Mass Error [ppm]:	-0.073665
PEP:	0.0042568
Precursor Type:	MULTI

general information

Annotation:	7 of 14
AminoAcids Coverag	50 %
Intensity Coverage:	55 %
Peak Coverage:	16 %
Protein Localisation:	30 ... 43

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	138.0662		138.0662	1	H	13		
	195.0877		195.0877	2	G	12	1446.712	
	358.151		358.151	3	Y	11	1389.691	
	471.235		471.235	4	I	10	1226.627	
	618.3035		618.3035	5	F	9	1113.543	
	705.3355		705.3355	6	S	8	966.4747	+0.081758
	792.3675		792.3675	7	S	7	879.4427	+0.055376
+0.099552	453.2294	+0.073567	905.4516	8	L	6	792.4106	+0.009707
+0.013612	488.748	-0.35069	976.4887	9	A	5	679.3266	+0.223898
-0.44585	517.2587		1033.51	10	G	4	608.2895	+0.008204
	1193.541		1193.541	11	C	3	551.268	
+0.256498	653.8161		1306.625	12	L	2	391.2374	
+0.206104	719.3363		1437.665	13	M	1	278.1533	+0.07895
				14	K	0	147.1128	

Scan number	8210	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	122.75



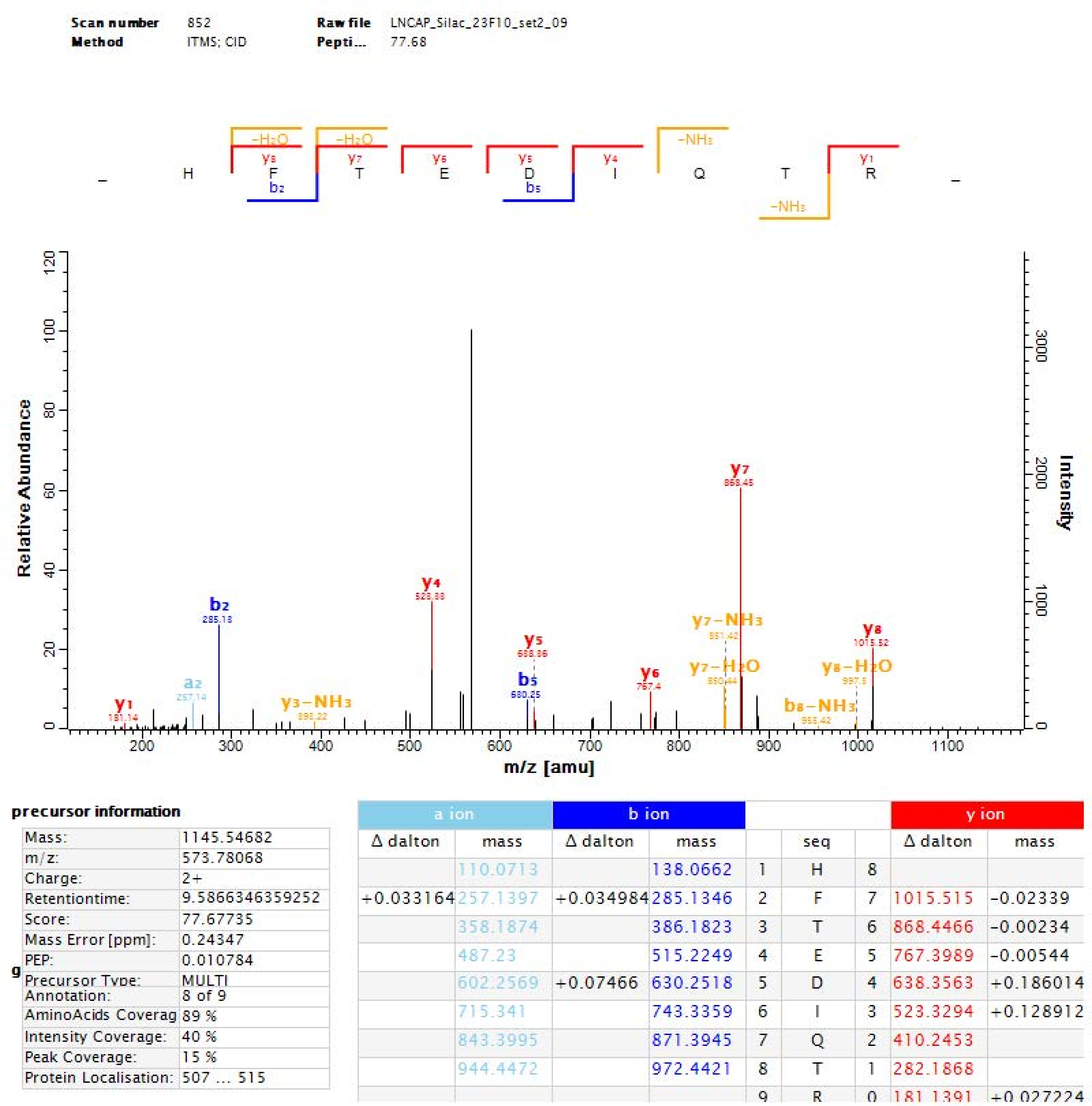
precursor information

Mass:	2018.16333
m/z:	673.72839
Charge:	3+
Retentiontime:	58.070903778076
Score:	122.7454
Mass Error [ppm]:	-0.16396
PEP:	7.9443E-06
Precursor Type:	ISO

general information

Annotation:	11 of 19
AminoAcids Coverag	58 %
Intensity Coverage:	50 %
Peak Coverage:	27 %
Protein Localisation:	92 ... 110

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	101.11		129.1	1	K	18				
-0.099	230.15	+0.0553	258.14	2	E	17	1891.1		946.04	+0.2949
	287.17		315.17	3	G	16	1762		881.52	+0.0227
	344.19	+0.3707	372.19	4	G	15	1705		853.01	+0.2832
	457.28	+0.2024	485.27	5	L	14	1648		824.5	+0.1888
	514.3	-0.222	542.29	6	G	13	1534.9		767.96	+0.2352
	611.35		639.35	7	P	12	1477.9		739.45	+0.2544
	724.44		752.43	8	L	11	1380.8	+0.1451	1380.8	
	838.48		866.47	9	N	10	1267.7		1267.7	
	951.56		979.56	10	I	9	1153.7	+0.0426	577.36	+0.0766
	1048.6		1076.6	11	P	8	1040.6	-0.105	520.81	+0.1986
	1161.7		1189.7	12	L	7	943.57		943.57	
	1274.8		1302.8	13	L	6	830.48		830.48	
	1345.8		1373.8	14	A	5	717.4		717.4	
	1460.8	+0.0605	1488.8	15	D	4	646.36		646.36	
	1559.9		1587.9	16	V	3	531.34	+0.1052	531.34	
	1661		1689	17	T	2	432.27		432.27	
	1817.1		1845.1	18	R	1	331.22		331.22	
				19	R	0	175.12		175.12	

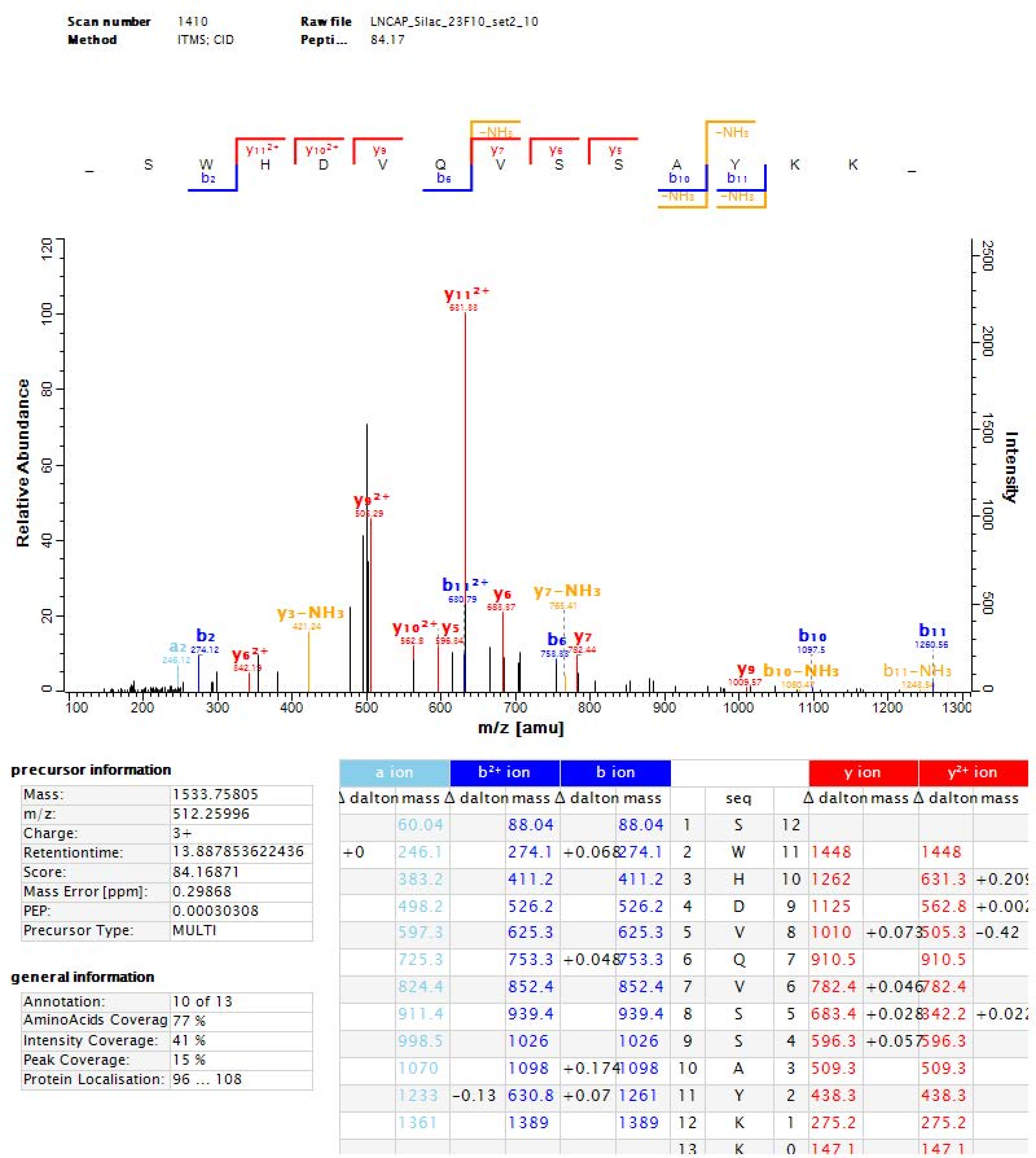


Scan number	852	**Raw file**	LNCAP_Silac_23F10_set2_09
Method	ITMS; CID	**Pepti...**	77.68

precursor information

Mass:	1145.54682
m/z:	573.78068
Charge:	2+
Retentiontime:	9.5866346359252
Score:	77.67735
Mass Error [ppm]:	0.24347
PEP:	0.010784
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	40 %
Peak Coverage:	15 %
Protein Localisation:	507 ... 515

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	110.0713		138.0662	1	H	8		
+0.033164	257.1397	+0.034984	285.1346	2	F	7	1015.515	-0.02339
	358.1874		386.1823	3	T	6	868.4466	-0.00234
	487.23		515.2249	4	E	5	767.3989	-0.00544
	602.2569	+0.07466	630.2518	5	D	4	638.3563	+0.186014
	715.341		743.3359	6	I	3	523.3294	+0.128912
	843.3995		871.3945	7	Q	2	410.2453	
	944.4472		972.4421	8	T	1	282.1868	
				9	R	0	181.1391	+0.027224



Scan number 1410
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set2_10
Pepti... 84.17

precursor information

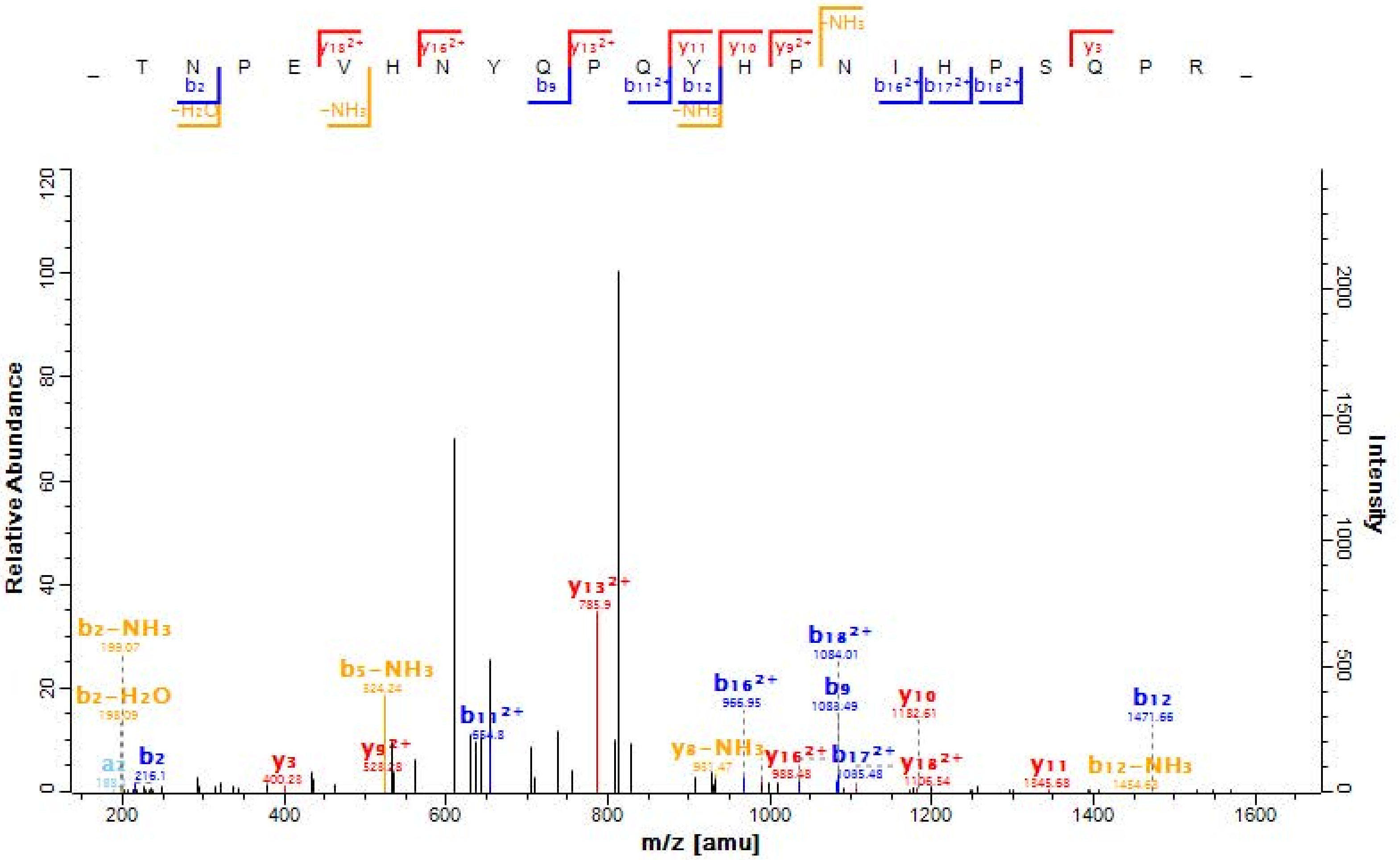
Mass:	1533.75805
m/z:	512.25996
Charge:	3+
Retentiontime:	13.887853622436
Score:	84.16871
Mass Error [ppm]:	0.29868
PEP:	0.00030308
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	41 %
Peak Coverage:	15 %
Protein Localisation:	96 ... 108

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	60.04		88.04		88.04	1	S	12				
+0	246.1		274.1	+0.068	274.1	2	W	11	1448		1448	
	383.2		411.2		411.2	3	H	10	1262		631.3	+0.20
	498.2		526.2		526.2	4	D	9	1125		562.8	+0.00
	597.3		625.3		625.3	5	V	8	1010	+0.073	505.3	-0.42
	725.3		753.3	+0.048	753.3	6	Q	7	910.5		910.5	
	824.4		852.4		852.4	7	V	6	782.4	+0.046	782.4	
	911.4		939.4		939.4	8	S	5	683.4	+0.028	342.2	+0.02
	998.5		1026		1026	9	S	4	596.3	+0.057	596.3	
	1070		1098	+0.174	1098	10	A	3	509.3		509.3	
	1233	-0.13	630.8	+0.07	1261	11	Y	2	438.3		438.3	
	1361		1389		1389	12	K	1	275.2		275.2	
						13	K	0	147.1		147.1	

Scan number	1479	**Raw file**	LNCAP_Silac_23F10_set2_10
Method	ITMS; CID	**Pepti...**	53.55



precursor information

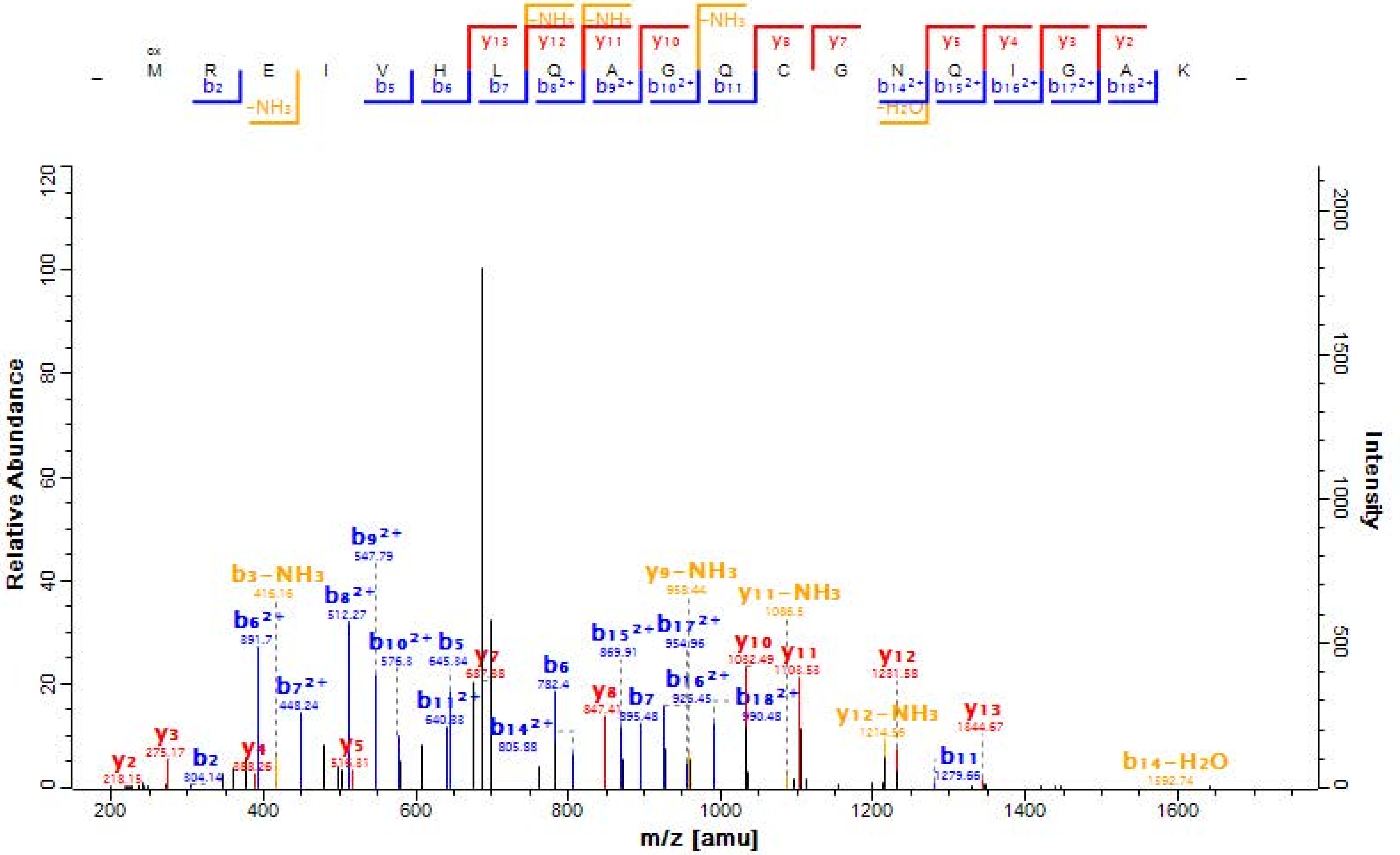
Mass:	2652.25731
m/z:	664.0716
Charge:	4+
Retentiontime:	14.328432083129
Score:	53.55374
Mass Error [ppm]:	-0.32803
PEP:	0.0022534
Precursor Type:	MULTI

general information

Annotation:	15 of 22
AminoAcids Coverag	68 %
Intensity Coverage:	18 %
Peak Coverage:	20 %
Protein Localisation:	440 ... 461

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.1		102.1	1	T	21				
+0.22	188.1		216.1	+0.11	216.1	2	N	20	2552		2552	
	285.2		313.2		313.2	3	P	19	2438		2438	
	414.2		442.2		442.2	4	E	18	2341		2341	
	513.3		541.3		541.3	5	V	17	2212		1107	+0.44
	650.3		678.3		678.3	6	H	16	2113		2113	
	764.4		792.4		792.4	7	N	15	1976		988.5	+0.25
	927.4		955.4		955.4	8	Y	14	1862		1862	
	1055		1083	-0.29	1083	9	Q	13	1699		1699	
	1153		1181		1181	10	P	12	1571		785.9	+0.21
	1281	+0.199	654.8		1309	11	Q	11	1474		1474	
	1444		1472	-0.17	1472	12	Y	10	1346	-0.08	1346	
	1581		1609		1609	13	H	9	1183	-0.09	1183	
	1678		1706		1706	14	P	8	1046		523.3	+0.10
	1792		1820		1820	15	N	7	948.5		948.5	
	1905	+0.22	1967		1933	16	I	6	834.5		834.5	
	2042	+0.269	1035		2070	17	H	5	721.4		721.4	
	2139	+0.39	1084		2167	18	P	4	584.3		584.3	
	2226		2254		2254	19	S	3	487.3		487.3	
	2354		2382		2382	20	Q	2	400.2	+0.107	400.2	
	2451		2479		2479	21	P	1	272.2		272.2	
						22	R	0	175.1		175.1	

Scan number	1489	**Raw file**	LNCAP_Silac_23F10_set2_10
Method	ITMS; CID	**Pepti...**	141.55



precursor information

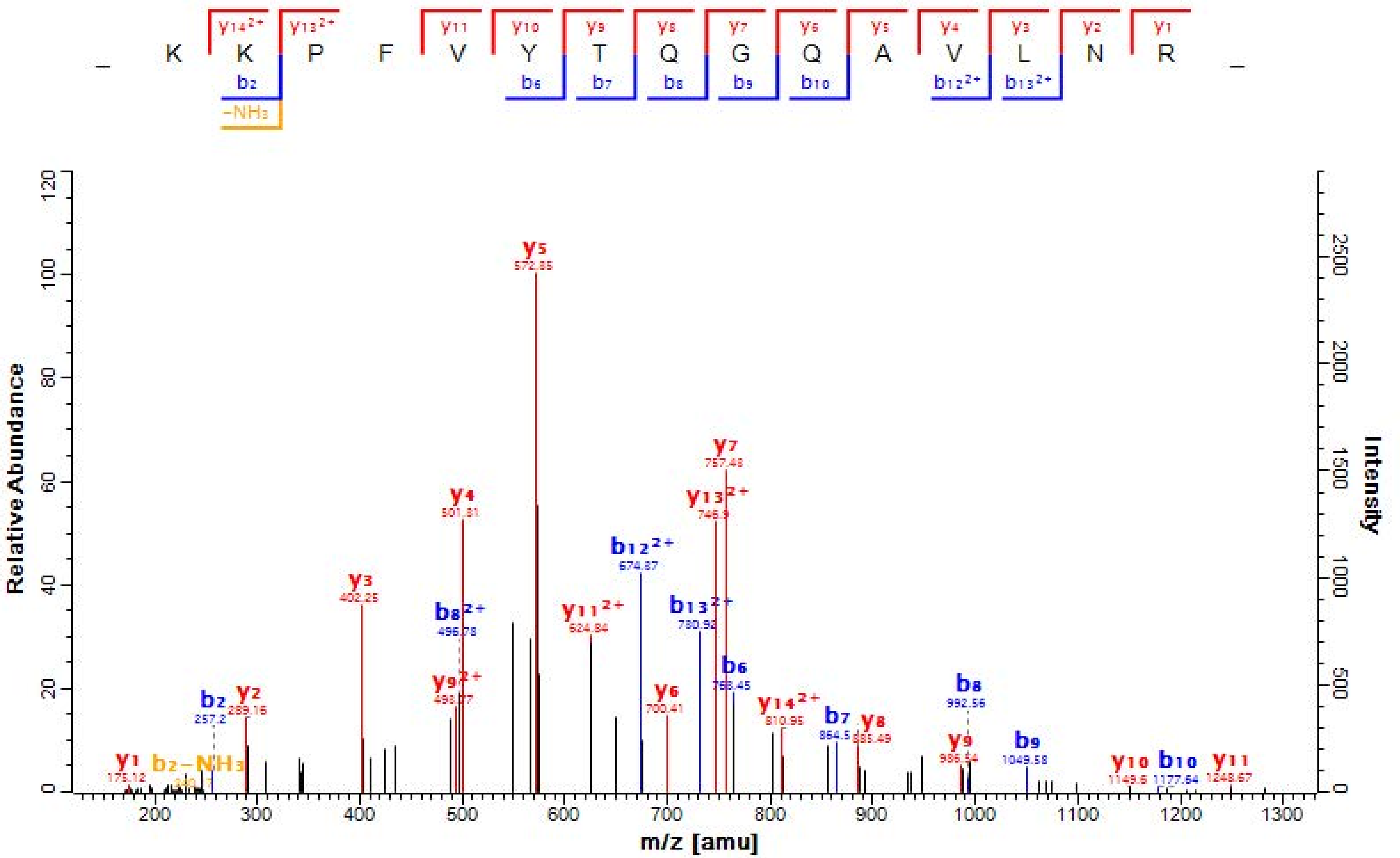
Mass:	2125.05169
m/z:	709.35784
Charge:	3+
Retentiontime:	14.391808509826
Score:	141.5524
Mass Error [ppm]:	-0.18155
PEP:	1.9537E-18
Precursor Type:	MULTI

general information

Annotation:	17 of 19
AminoAcids Coverag	89 %
Intensity Coverage:	52 %
Peak Coverage:	30 %
Protein Localisation:	1 ... 19

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	148.0427		148.0427	1	M	18		
	304.1438	+0.244946	304.1438	2	R	17	1979.024	
	433.1864		433.1864	3	E	16	1822.923	
	546.2704		546.2704	4	I	15	1693.88	
	645.3389	-0.00115	645.3389	5	V	14	1580.796	
+0.217277	391.7025	-0.03162	782.3978	6	H	13	1481.728	
+0.152418	448.2446	+0.054299	895.4818	7	L	12	1344.669	-0.08573
+0.265097	512.2738		1023.54	8	Q	11	1231.585	-0.06893
+0.208759	547.7924		1094.578	9	A	10	1103.526	-0.05381
+0.245451	576.3031		1151.599	10	G	9	1032.489	-0.0112
+0.055091	640.3324	-0.15049	1279.658	11	Q	8	975.4676	
	1439.688		1439.688	12	C	7	847.4091	-0.00715
	1496.71		1496.71	13	G	6	687.3784	+0.087711
+0.492679	805.8799		1610.753	14	N	5	630.357	
+0.251354	869.9092		1738.811	15	Q	4	516.314	-0.4906
+0.037569	926.4513		1851.895	16	I	3	388.2554	+0.116197
+0.224591	954.962		1908.917	17	G	2	275.1714	-0.05661
+0.187418	990.4806		1979.954	18	A	1	218.1499	-0.092
				19	K	0	147.1128	

Scan number	2236	**Raw file**	LNCAP_Silac_23F10_set2_10
Method	ITMS; CID	**Pepti...**	142.45



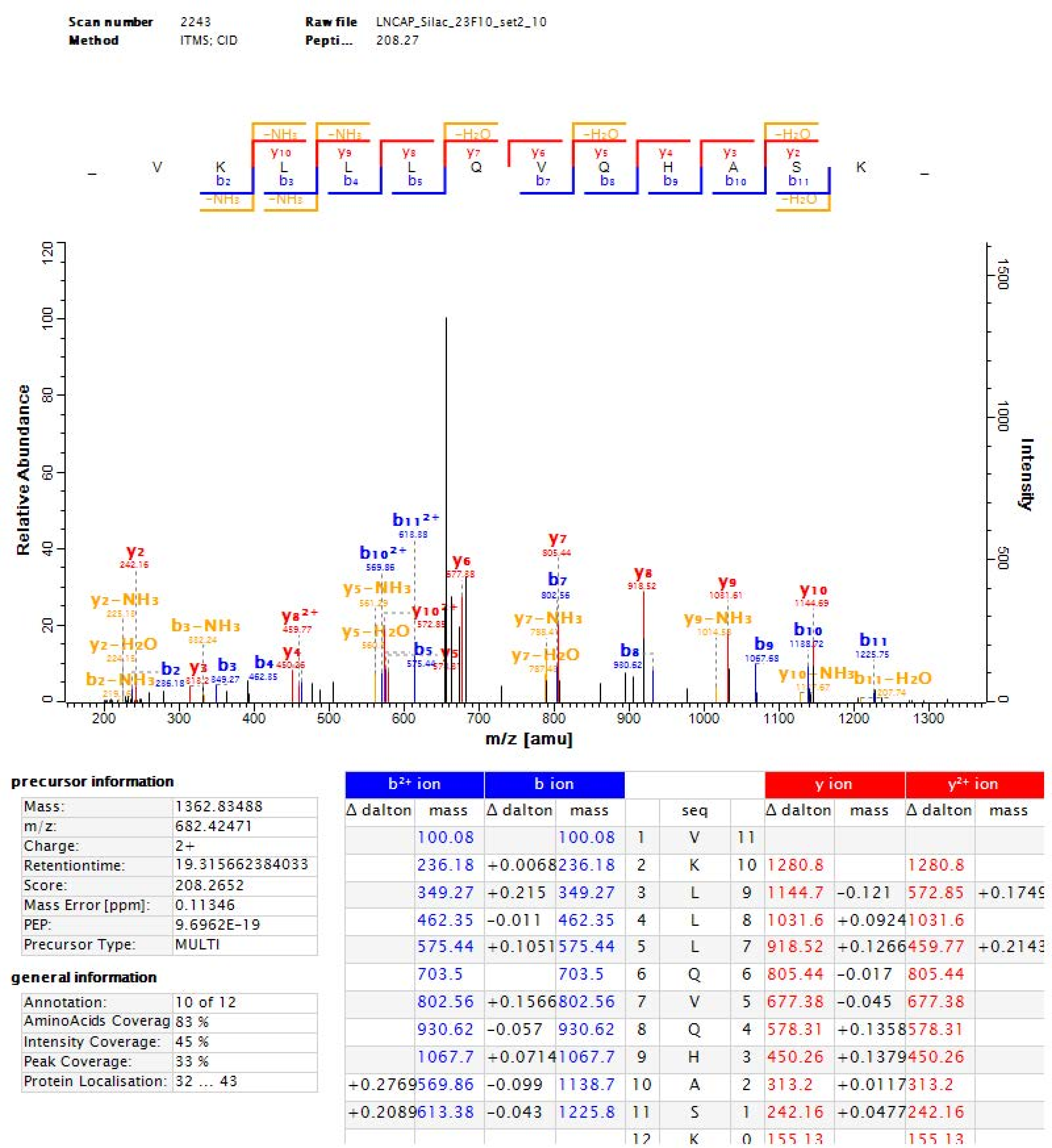
precursor information

Mass:	1747.97402
m/z:	583.66528
Charge:	3+
Retentiontime:	19.275974273681
Score:	142.451
Mass Error [ppm]:	0.38951
PEP:	4.2745E-13
Precursor Type:	MULTI

general information

Annotation:	14 of 15
AminoAcids Coverag	93 %
Intensity Coverage:	55 %
Peak Coverage:	26 %
Protein Localisation:	170 ... 184

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.1		129.1	1	K	14				
	257.2	-0.101	257.2	2	K	13	1620.9		810.95	+0.3534
	354.25		354.25	3	P	12	1492.8		746.9	+0.2791
	501.32		501.32	4	F	11	1395.7		1395.7	
	600.39		600.39	5	V	10	1248.7	-0.09	624.84	-0.064
	763.45	-0.056	763.45	6	Y	9	1149.6	+0.0724	1149.6	
	864.5	+0.0166	864.5	7	T	8	986.54	-0.052	493.77	+0.3231
-0.088	496.78	-0.116	992.56	8	Q	7	885.49	+0.1079	885.49	
	1049.6	+0.0663	1049.6	9	G	6	757.43	+0.1049	757.43	
	1177.6	+0.1635	1177.6	10	Q	5	700.41	-0.022	700.41	
	1248.7		1248.7	11	A	4	572.35	+0.1624	572.35	
+0.1297	674.37		1347.7	12	V	3	501.31	-0.019	501.31	
+0.2138	730.92		1460.8	13	L	2	402.25	+0.1284	402.25	
	1574.9		1574.9	14	N	1	289.16	+0.0737	289.16	
				15	R	0	175.12	+0.0517	175.12	



Scan number 2243
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set2_10
Pepti... 208.27

precursor information

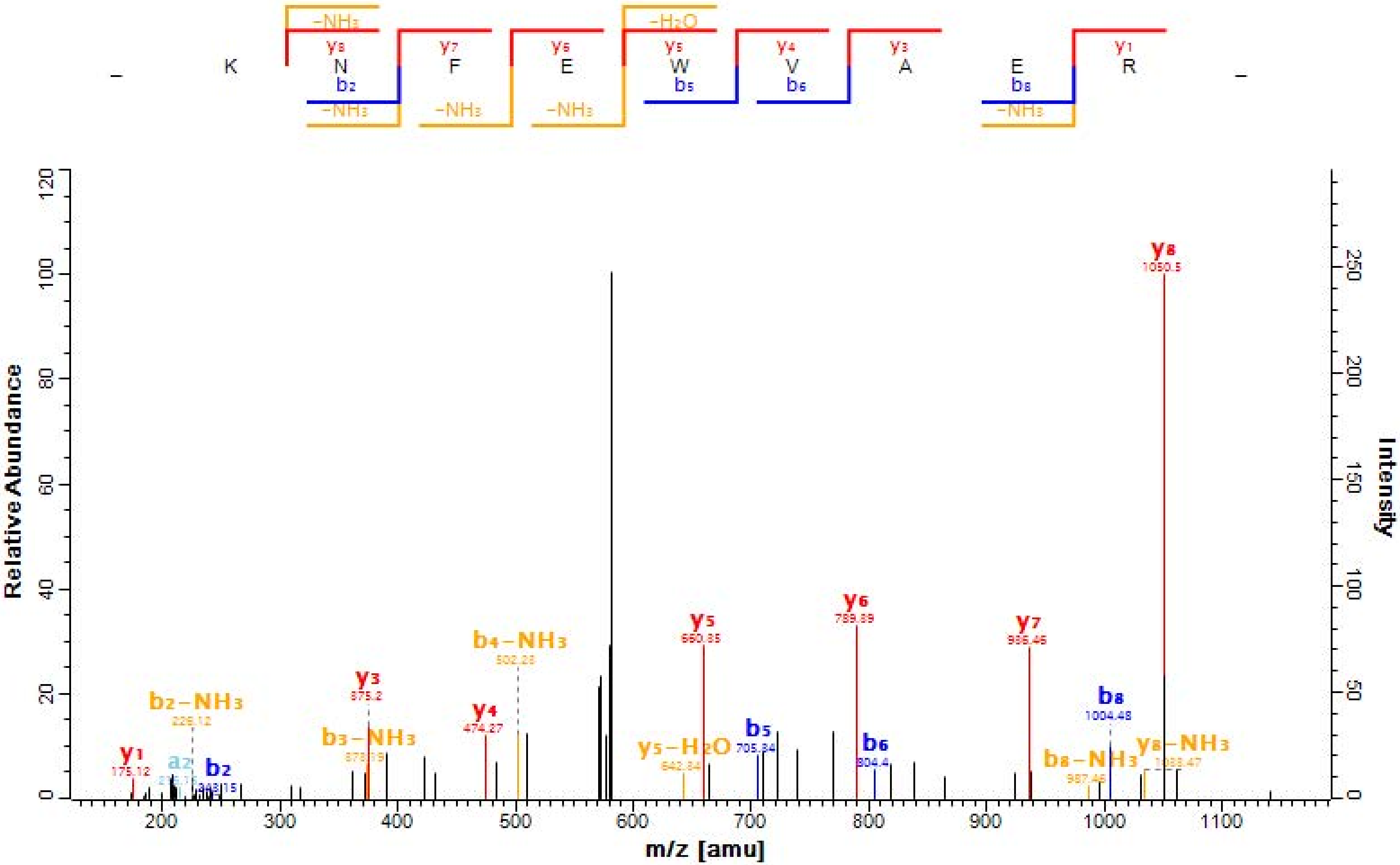
Mass:	1362.83488
m/z:	682.42471
Charge:	2+
Retentiontime:	19.315662384033
Score:	208.2652
Mass Error [ppm]:	0.11346
PEP:	9.6962E-19
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	45 %
Peak Coverage:	33 %
Protein Localisation:	32 ... 43

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	11				
	236.18	+0.0068	236.18	2	K	10	1280.8		1280.8	
	349.27	+0.215	349.27	3	L	9	1144.7	-0.121	572.85	+0.1749
	462.35	-0.011	462.35	4	L	8	1031.6	+0.0924	1031.6	
	575.44	+0.1051	575.44	5	L	7	918.52	+0.1266	459.77	+0.2143
	703.5		703.5	6	Q	6	805.44	-0.017	805.44	
	802.56	+0.1566	802.56	7	V	5	677.38	-0.045	677.38	
	930.62	-0.057	930.62	8	Q	4	578.31	+0.1358	578.31	
	1067.7	+0.0714	1067.7	9	H	3	450.26	+0.1379	450.26	
+0.2769	569.86	-0.099	1138.7	10	A	2	313.2	+0.0117	313.2	
+0.2089	613.38	-0.043	1225.8	11	S	1	242.16	+0.0477	242.16	
				12	K	0	155.13		155.13	

Scan number	2593	**Raw file**	LNCAP_Silac_23F10_set2_10
Method	ITMS; CID	**Pepti...**	71.03

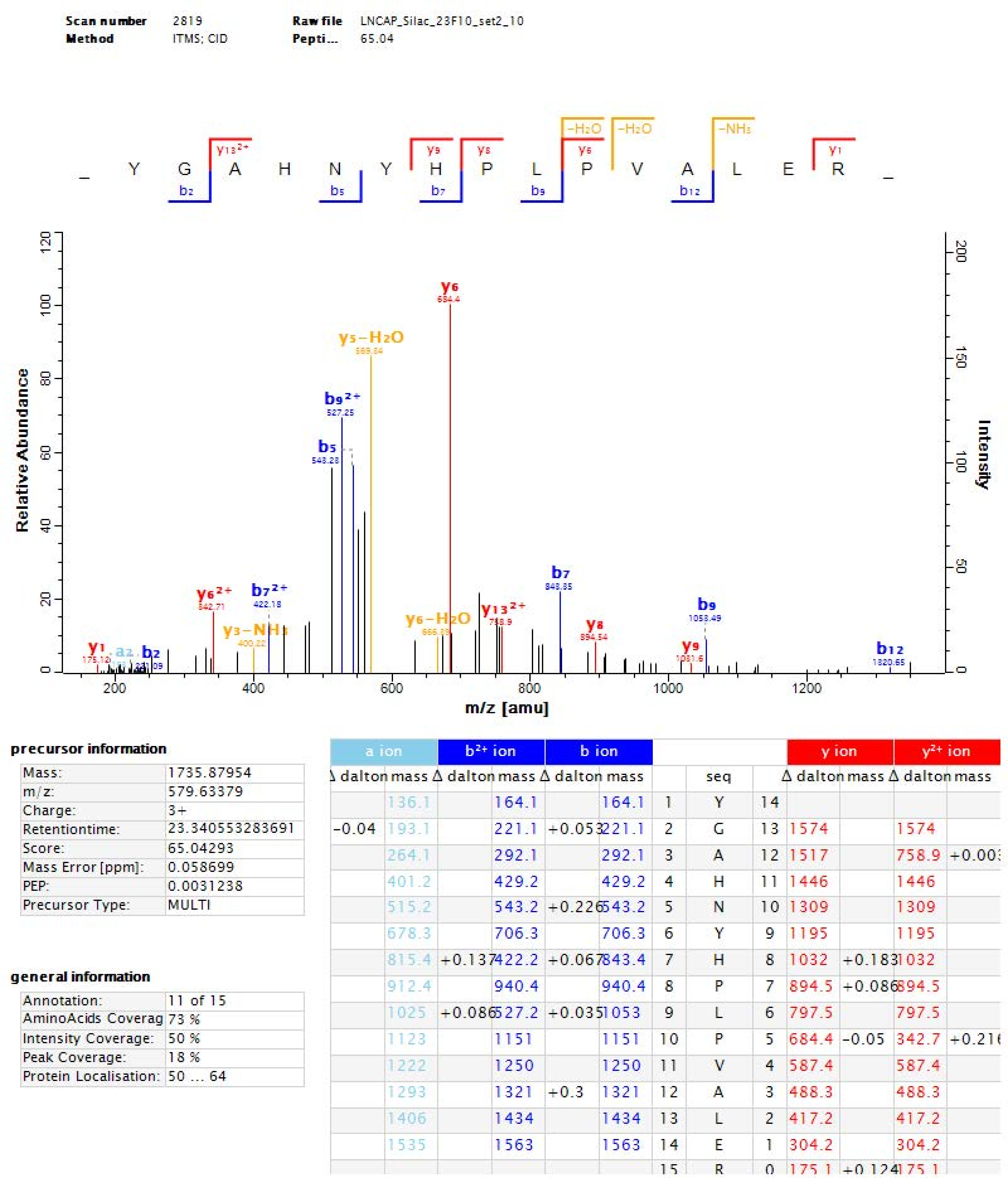


precursor information

g

Mass:	1177.58786
m/z:	589.80121
Charge:	2+
Retentiontime:	21.734296798706
Score:	71.03031
Mass Error [ppm]:	-0.12427
PEP:	0.0073479
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	39 %
Peak Coverage:	24 %
Protein Localisation:	273 ... 281

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	101.1073		129.1022	1	K	8		
+0.111497	215.1503	-0.16842	243.1452	2	N	7	1050.5	+0.023605
	362.2187		390.2136	3	F	6	936.4574	+0.141728
	491.2613		519.2562	4	E	5	789.389	-0.18433
	677.3406	-0.28941	705.3355	5	W	4	660.3464	-0.04841
	776.409	-0.12961	804.4039	6	V	3	474.2671	+0.177324
	847.4461		875.441	7	A	2	375.1987	-0.01818
	976.4887	+0.095494	1004.484	8	E	1	304.1615	
				9	R	0	175.119	+0.010488



Scan number	2819	**Raw file**	LNCAP_Silac_23F10_set2_10
Method	ITMS; CID	**Pepti...**	65.04

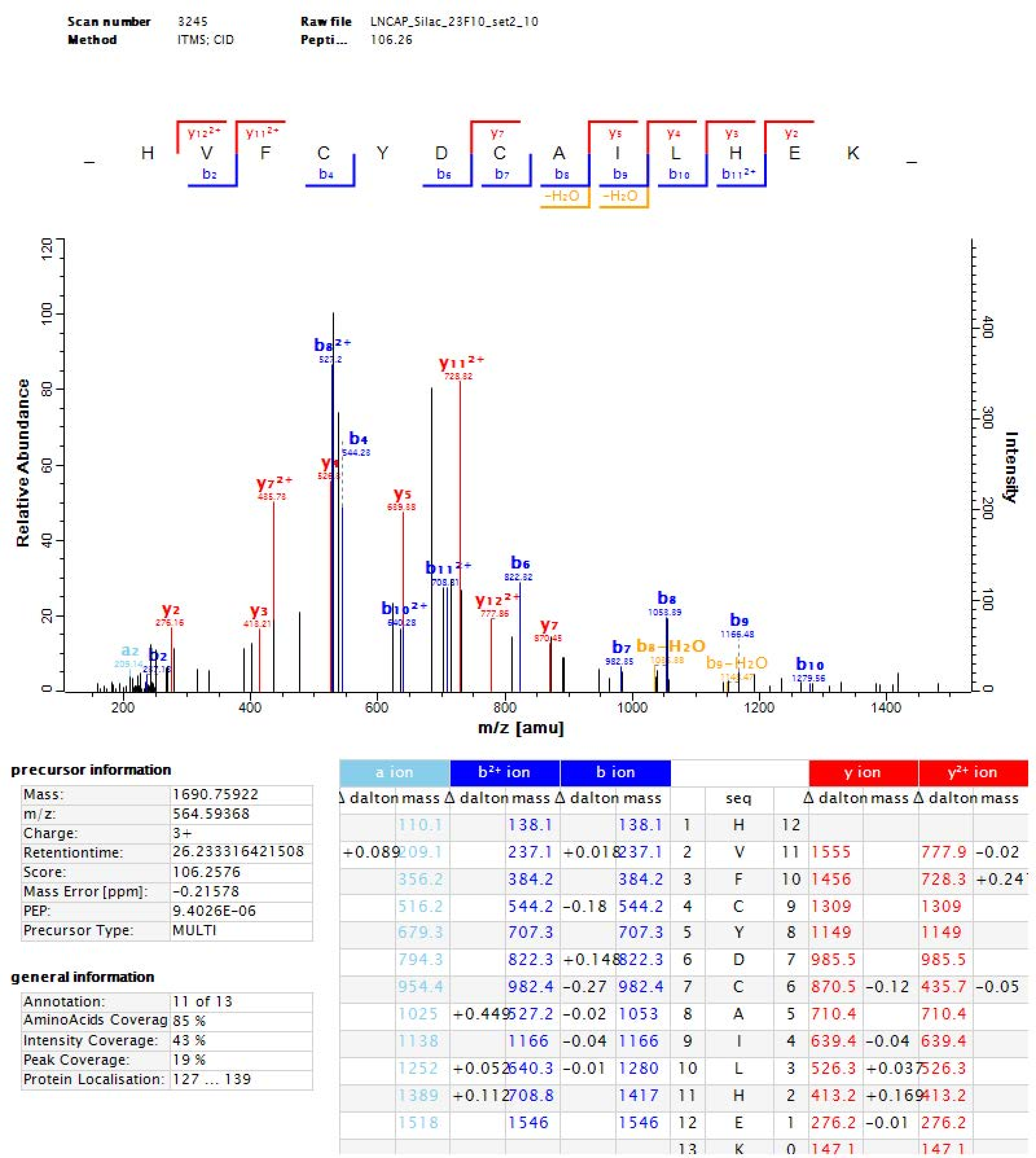
precursor information

Mass:	1735.87954
m/z:	579.63379
Charge:	3+
Retentiontime:	23.340553283691
Score:	65.04293
Mass Error [ppm]:	0.058699
PEP:	0.0031238
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	50 %
Peak Coverage:	18 %
Protein Localisation:	50 ... 64

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.1		164.1		164.1	1	Y	14				
−0.04	193.1		221.1	+0.053	221.1	2	G	13	1574		1574	
	264.1		292.1		292.1	3	A	12	1517		758.9	+0.00
	401.2		429.2		429.2	4	H	11	1446		1446	
	515.2		543.2	+0.226	543.2	5	N	10	1309		1309	
	678.3		706.3		706.3	6	Y	9	1195		1195	
	815.4	+0.137	422.2	+0.067	843.4	7	H	8	1032	+0.183	1032	
	912.4		940.4		940.4	8	P	7	894.5	+0.086	894.5	
	1025	+0.086	527.2	+0.035	1053	9	L	6	797.5		797.5	
	1123		1151		1151	10	P	5	684.4	−0.05	342.7	+0.21
	1222		1250		1250	11	V	4	587.4		587.4	
	1293		1321	+0.3	1321	12	A	3	488.3		488.3	
	1406		1434		1434	13	L	2	417.2		417.2	
	1535		1563		1563	14	E	1	304.2		304.2	
						15	R	0	175.1	+0.124	175.1	



Scan number	3245	**Raw file**	LNCAP_Silac_23F10_set2_10
Method	ITMS; CID	**Pepti...**	106.26

precursor information

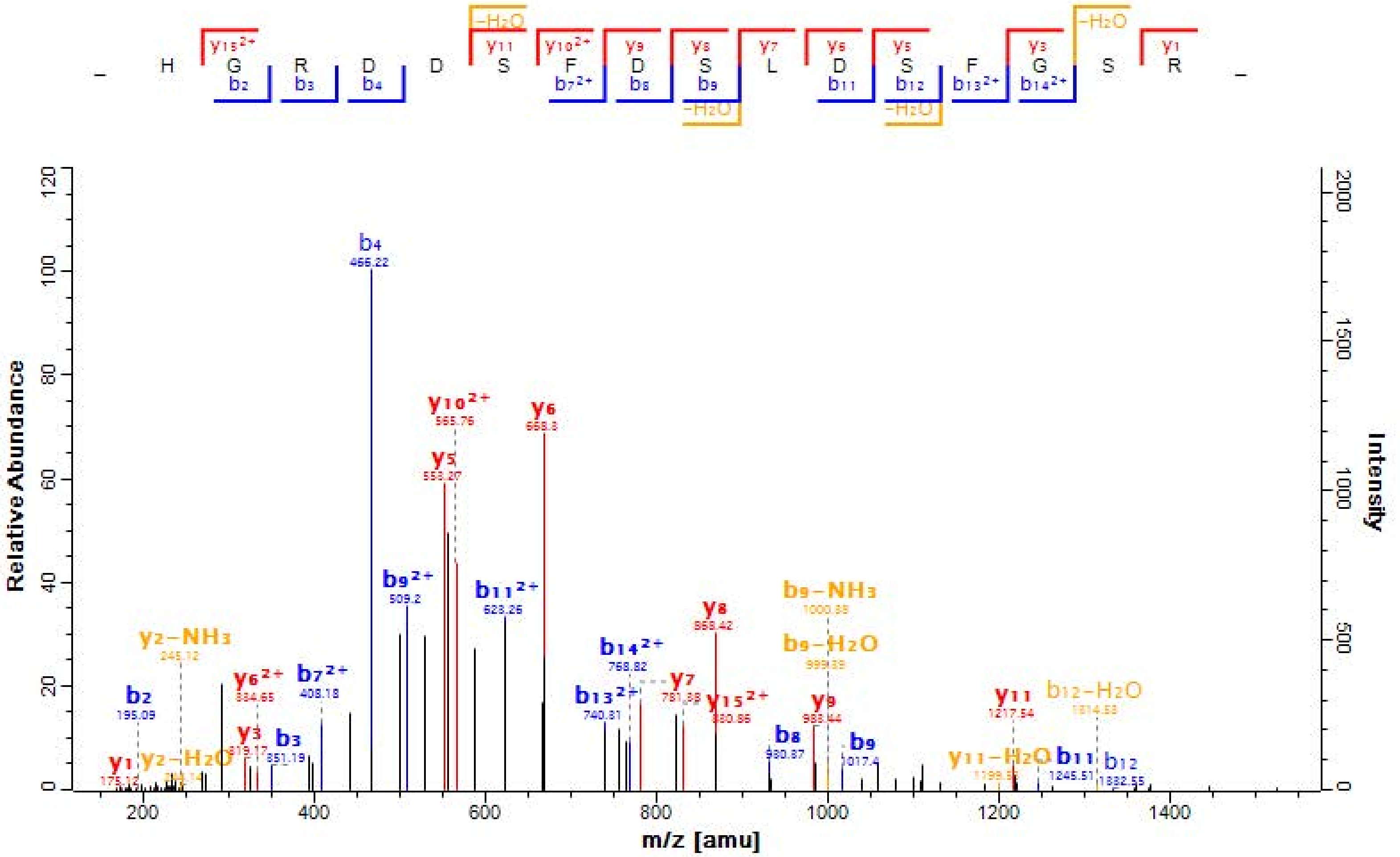
Mass:	1690.75922
m/z:	564.59368
Charge:	3+
Retentiontime:	26.233316421508
Score:	106.2576
Mass Error [ppm]:	-0.21578
PEP:	9.4026E-06
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	43 %
Peak Coverage:	19 %
Protein Localisation:	127 ... 139

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	110.1		138.1		138.1	1	H	12				
+0.089	209.1		237.1	+0.018	237.1	2	V	11	1555		777.9	-0.02
	356.2		384.2		384.2	3	F	10	1456		728.3	+0.24
	516.2		544.2	-0.18	544.2	4	C	9	1309		1309	
	679.3		707.3		707.3	5	Y	8	1149		1149	
	794.3		822.3	+0.148	822.3	6	D	7	985.5		985.5	
	954.4		982.4	-0.27	982.4	7	C	6	870.5	-0.12	435.7	-0.05
	1025	+0.449	527.2	-0.02	1053	8	A	5	710.4		710.4	
	1138		1166	-0.04	1166	9	I	4	639.4	-0.04	639.4	
	1252	+0.052	640.3	-0.01	1280	10	L	3	526.3	+0.037	526.3	
	1389	+0.112	708.8		1417	11	H	2	413.2	+0.169	413.2	
	1518		1546		1546	12	E	1	276.2	-0.01	276.2	
						13	K	0	147.1		147.1	

Scan number	3385	**Raw file**	LNCAP_Silac_23F10_set2_10
Method	ITMS; CID	**Pepti...**	119.47



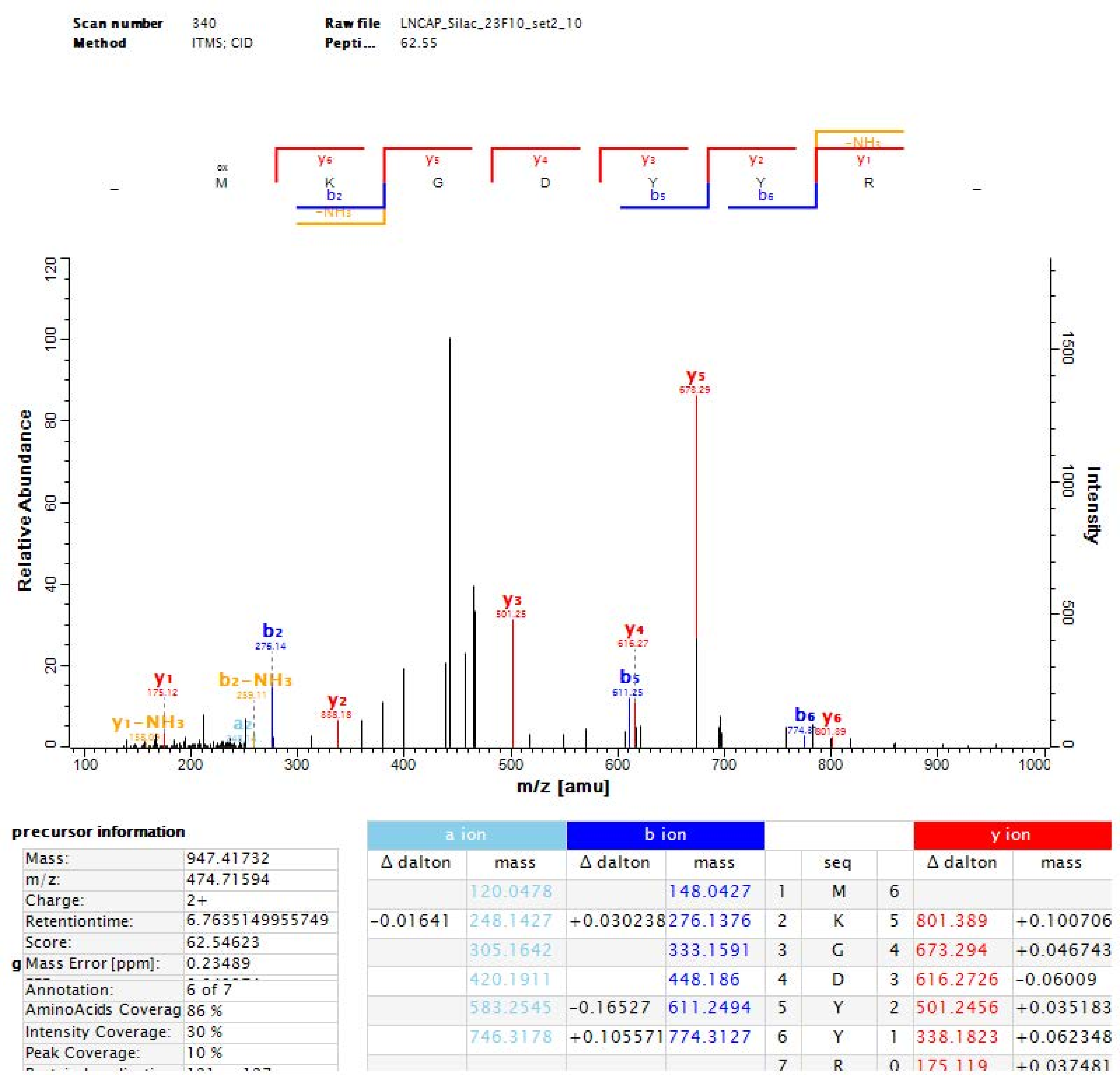
precursor information

Mass:	1796.77152
m/z:	599.93112
Charge:	3+
Retentiontime:	27.224260330200
Score:	119.4749
Mass Error [ppm]:	0.064874
PEP:	2.257E-05
Precursor Type:	ISO

general information

Annotation:	15 of 16
AminoAcids Coverag	94 %
Intensity Coverage:	55 %
Peak Coverage:	27 %
Protein Localisation:	196 ... 211

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.07		138.07	1	H	15				
	195.09	+0.1251	195.09	2	G	14	1660.7		830.86	+0.2094
	351.19	+0.1928	351.19	3	R	13	1603.7		1603.7	
	466.22	-0.209	466.22	4	D	12	1447.6		1447.6	
	581.24		581.24	5	D	11	1332.6		1332.6	
	668.27		668.27	6	S	10	1217.5	-0.17	1217.5	
+0.3342	408.18		815.34	7	F	9	1130.5		565.76	+0.271
	930.37	-0.088	930.37	8	D	8	983.44	+0.0354	983.44	
+0.1642	509.2	+0.1859	1017.4	9	S	7	868.42	-0.026	868.42	
	1130.5		1130.5	10	L	6	781.38	+0.1084	781.38	
+0.0848	623.26	+0.1926	1245.5	11	D	5	668.3	+0.13	334.65	+0.041
	1332.5	-0.045	1332.5	12	S	4	553.27	+0.0118	553.27	
-0.148	740.31		1479.6	13	F	3	466.24		466.24	
+0.1164	768.82		1536.6	14	G	2	319.17	+0.0792	319.17	
	1623.7		1623.7	15	S	1	262.15		262.15	
				16	R	0	175.12	+0.0238	175.12	

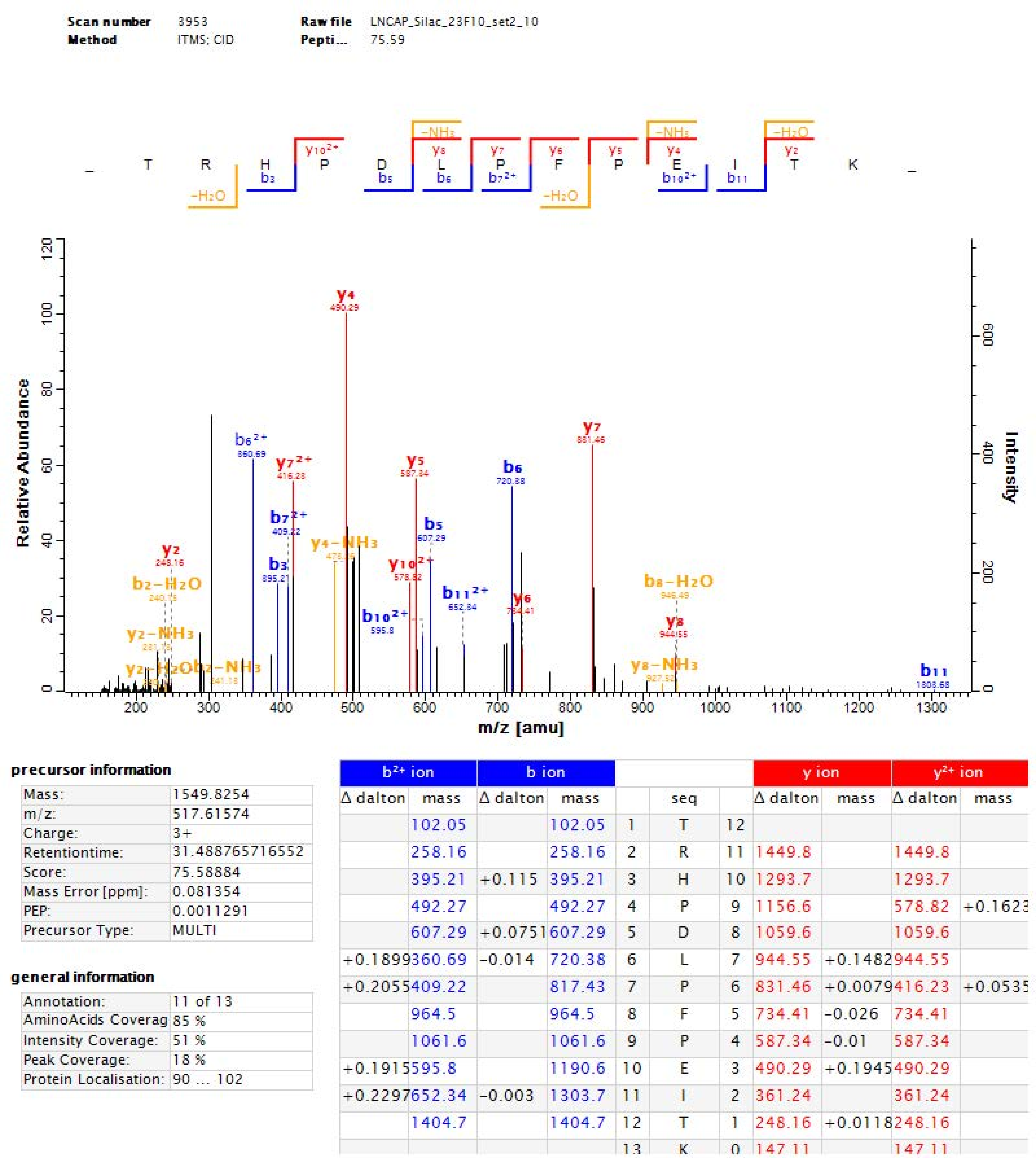


Scan number	340	**Raw file**	LNCAP_Silac_23F10_set2_10
Method	ITMS; CID	**Pepti...**	62.55

precursor information

Mass:	947.41732
m/z:	474.71594
Charge:	2+
Retentiontime:	6.7635149955749
Score:	62.54623
Mass Error [ppm]:	0.23489
Annotation:	6 of 7
AminoAcids Coverag	86 %
Intensity Coverage:	30 %
Peak Coverage:	10 %

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	120.0478		148.0427	1	M	6		
-0.01641	248.1427	+0.030238	276.1376	2	K	5	801.389	+0.100706
	305.1642		333.1591	3	G	4	673.294	+0.046743
	420.1911		448.186	4	D	3	616.2726	-0.06009
	583.2545	-0.16527	611.2494	5	Y	2	501.2456	+0.035183
	746.3178	+0.105571	774.3127	6	Y	1	338.1823	+0.062348
				7	R	0	175.119	+0.037481



Scan number	3953	**Raw file**	LNCAP_Silac_23F10_set2_10
Method	ITMS; CID	**Pepti...**	75.59

precursor information

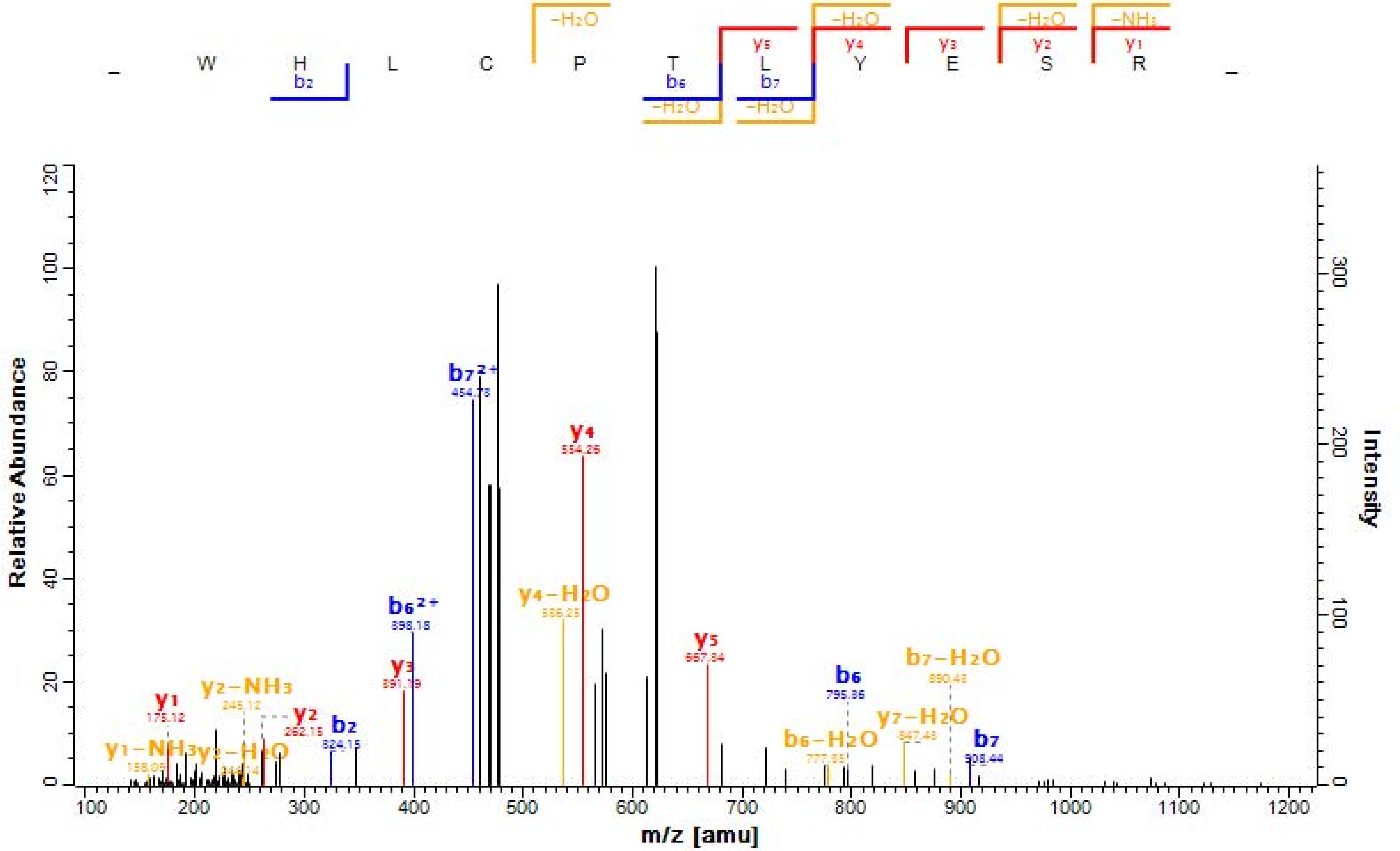
Mass:	1549.8254
m/z:	517.61574
Charge:	3+
Retentiontime:	31.488765716552
Score:	75.58884
Mass Error [ppm]:	0.081354
PEP:	0.0011291
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	51 %
Peak Coverage:	18 %
Protein Localisation:	90 ... 102

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	12				
	258.16		258.16	2	R	11	1449.8		1449.8	
	395.21	+0.115	395.21	3	H	10	1293.7		1293.7	
	492.27		492.27	4	P	9	1156.6		578.82	+0.1623
	607.29	+0.0751	607.29	5	D	8	1059.6		1059.6	
+0.1899	360.69	-0.014	720.38	6	L	7	944.55	+0.1482	944.55	
+0.2055	409.22		817.43	7	P	6	831.46	+0.0079	416.23	+0.0535
	964.5		964.5	8	F	5	734.41	-0.026	734.41	
	1061.6		1061.6	9	P	4	587.34	-0.01	587.34	
+0.1915	595.8		1190.6	10	E	3	490.29	+0.1945	490.29	
+0.2297	652.34	-0.003	1303.7	11	I	2	361.24		361.24	
	1404.7		1404.7	12	T	1	248.16	+0.0118	248.16	
				13	K	0	147.11		147.11	

Scan number	4149	**Raw file**	LNCAP_Silac_23F10_set2_10
Method	ITMS; CID	**Pepti...**	76.14



precursor information

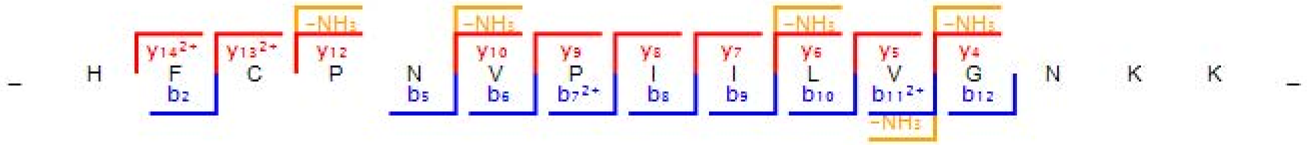
Mass:	1460.68706
m/z:	487.90296
Charge:	3+
Retentiontime:	33.103023529052
Score:	76.14272
Mass Error [ppm]:	-0.0088681
PEP:	0.0044509
Precursor Type:	MULTI

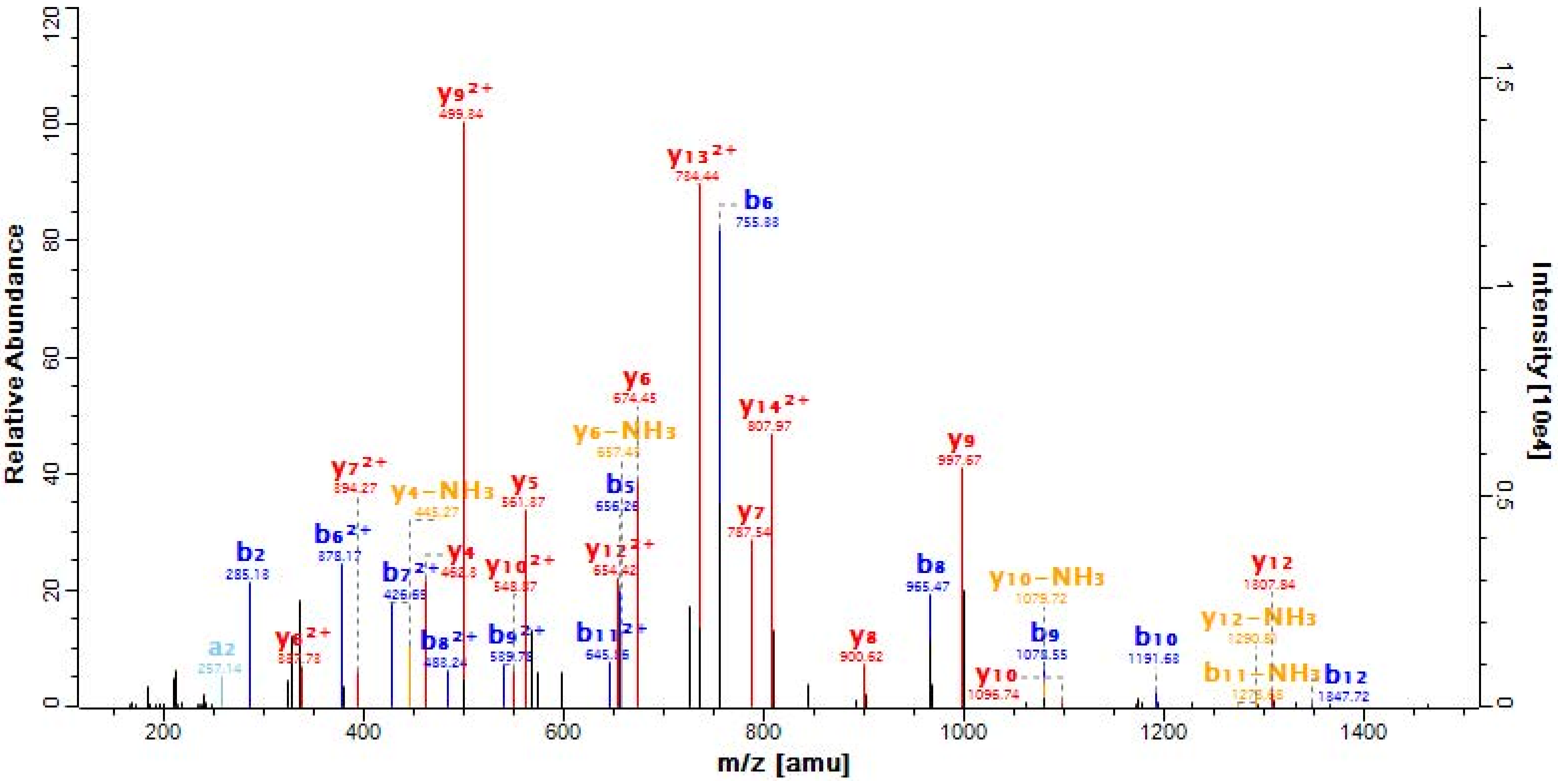
general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	27 %
Peak Coverage:	14 %
Protein Localisation:	261 ... 271

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	187.0866		187.0866	1	W	10		
	324.1455	+0.046363	324.1455	2	H	9	1275.615	
	437.2296		437.2296	3	L	8	1138.556	
	597.2602		597.2602	4	C	7	1025.472	
	694.313		694.313	5	P	6	865.4414	
+0.17074	398.184	+0.10193	795.3607	6	T	5	768.3886	
-0.03163	454.726	+0.285749	908.4447	7	L	4	667.341	-0.00118
	1071.508		1071.508	8	Y	3	554.2569	-0.01343
	1200.551		1200.551	9	E	2	391.1936	+0.088012
	1287.583		1287.583	10	S	1	262.151	+0.109884
				11	R	0	175.119	+0.052511

Scan number	4411	**Raw file**	LNCAP_Silac_23F10_set2_10
Method	ITMS; CID	**Pepti...**	251.03





precursor information

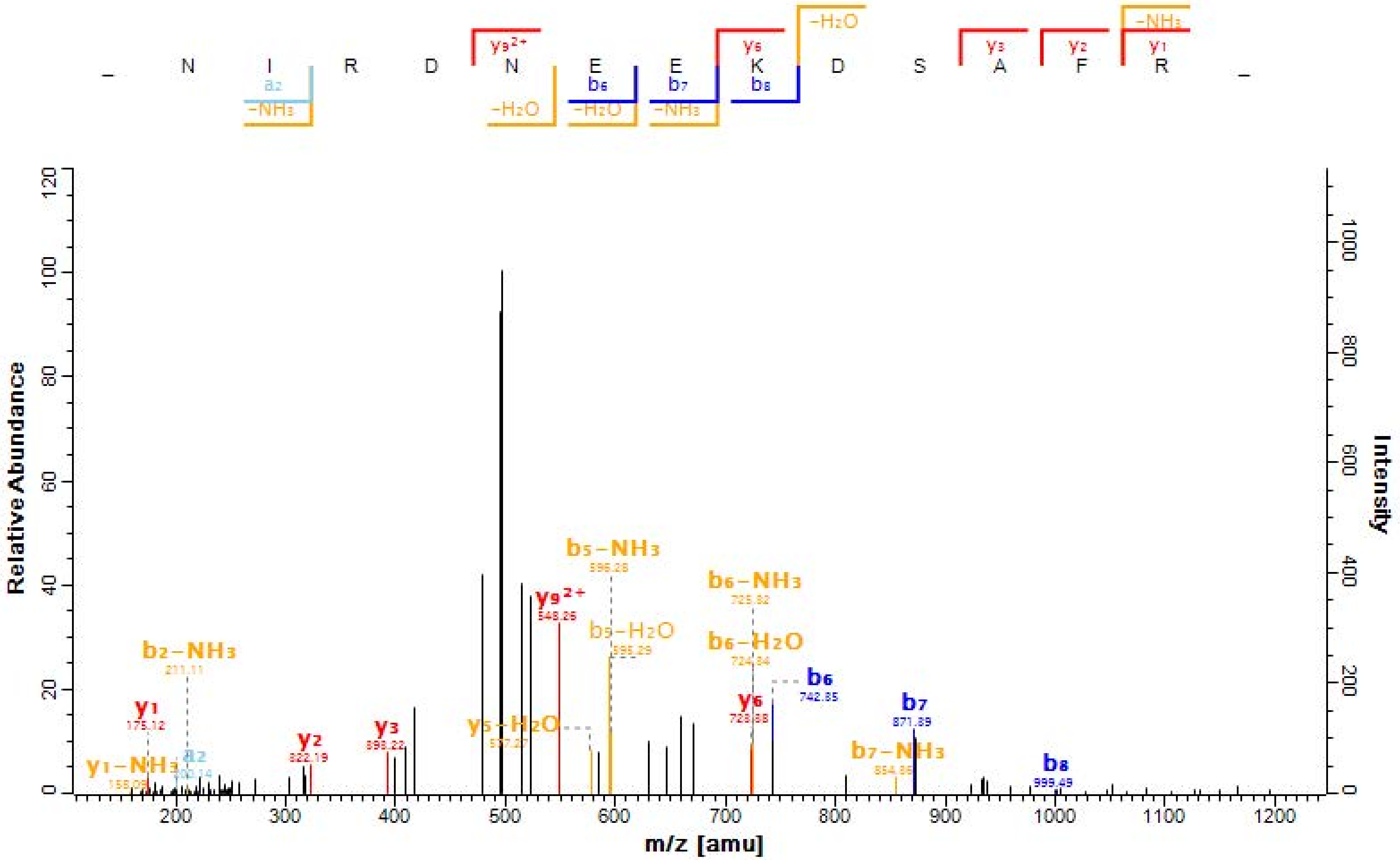
Mass:	1734.96002
m/z:	579.32728
Charge:	3+
Retentiontime:	35.338375091552
Score:	251.0254
Mass Error [ppm]:	-0.17804
PEP:	1.5446E-57
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	74 %
Peak Coverage:	35 %
Protein Localisation:	105 ... 119

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	110.1		138.1		138.1	1	H	14				
+0.005	257.1		285.1	+0.059	285.1	2	F	13	1615		808	+0.29
	417.2		445.2		445.2	3	C	12	1468		734.4	+0.31
	514.2		542.2		542.2	4	P	11	1308	+0.198	654.4	-0.06
	628.3		656.3	+0.002	656.3	5	N	10	1211		1211	
	727.3	+0.174	378.2	-0.01	755.3	6	V	9	1097	-0.07	548.9	+0.19
	824.4	+0.242	426.7		852.4	7	P	8	997.7	-0.03	499.3	+0.12
	937.5	+0.023	483.2	+0.016	965.5	8	I	7	900.6	-0.04	900.6	
	1051	+0.178	539.8	+0	1079	9	I	6	787.5	-0.02	394.3	-0.06
	1164		1192	+0.026	1192	10	L	5	674.5	+0.005	337.7	-0.44
	1263	+0.197	645.9		1291	11	V	4	561.4	+0.041	561.4	
	1320		1348	+0.014	1348	12	G	3	462.3	+0.031	462.3	
	1434		1462		1462	13	N	2	405.3		405.3	
	1570		1598		1598	14	K	1	291.2		291.2	
						15	K	0	155.1		155.1	

Scan number	615	**Raw file**	LNCAP_Silac_23F10_set2_10
Method	ITMS; CID	**Pepti...**	62.09



precursor information

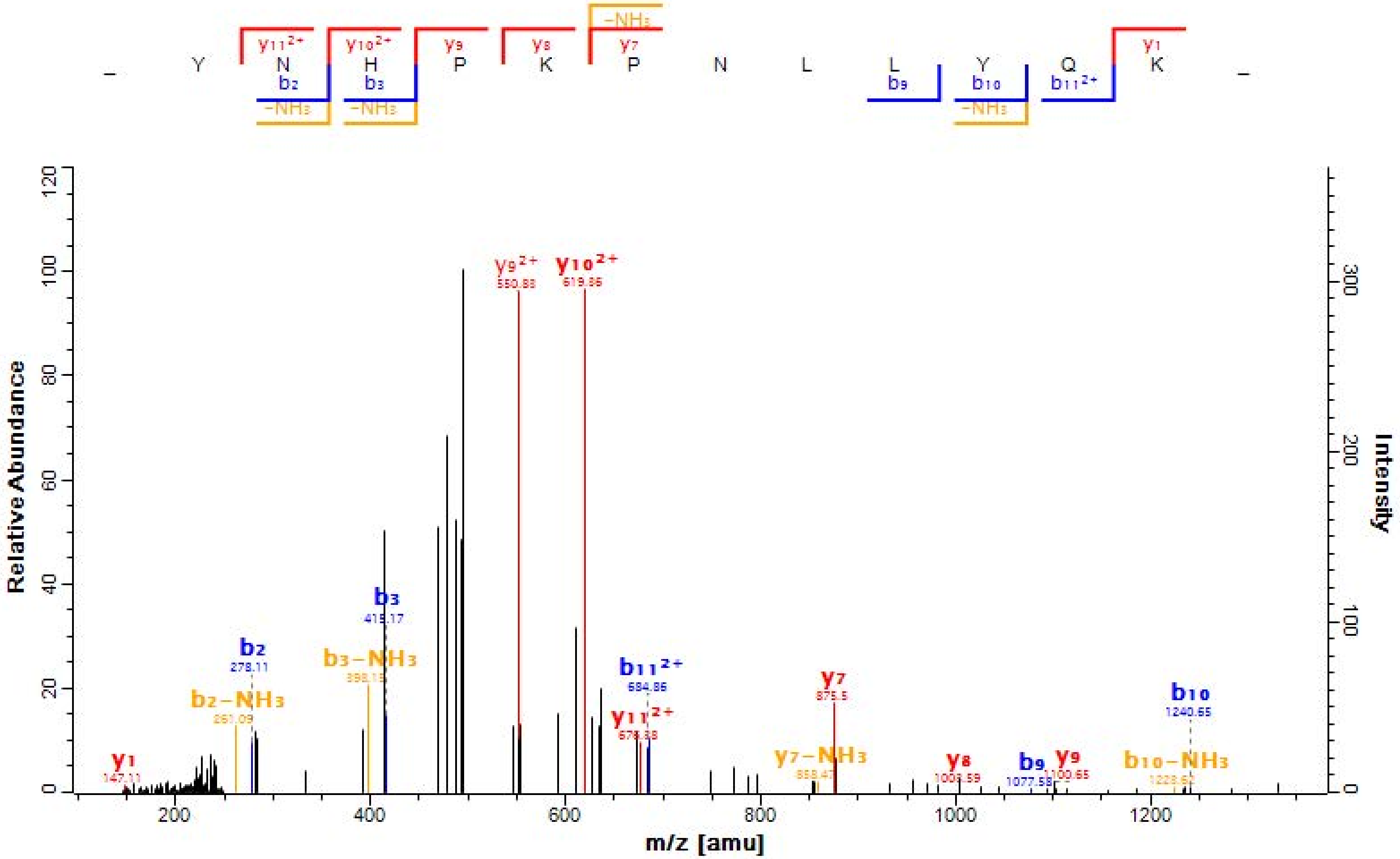
Mass:	1592.75547
m/z:	531.92577
Charge:	3+
Retentiontime:	8.6735286712646
Score:	62.08793
Mass Error [ppm]:	0.73799
PEP:	0.0058749
Precursor Type:	MULTI

general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	24 %
Peak Coverage:	16 %
Protein Localisation:	811 ... 823

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	87.055		115.05	1	N	12				
+0.0123	200.14		228.13	2	I	11	1479.7		1479.7	
	356.24		384.24	3	R	10	1366.6		1366.6	
	471.27		499.26	4	D	9	1210.5		1210.5	
	585.31		613.31	5	N	8	1095.5		548.26	+0.121
	714.35	+0.0472	742.35	6	E	7	981.46		981.46	
	843.4	+0.0961	871.39	7	E	6	852.42		852.42	
	971.49	+0.1747	999.49	8	K	5	723.38	+0.2387	723.38	
	1086.5		1114.5	9	D	4	595.28		595.28	
	1173.5		1201.5	10	S	3	480.26		480.26	
	1244.6		1272.6	11	A	2	393.22	+0.0313	393.22	
	1391.7		1419.6	12	F	1	322.19	+0.0645	322.19	
				13	R	0	175.12	+0.1565	175.12	

Scan number	1045	**Raw file**	LNCAP_Silac_23F10_set2_11
Method	ITMS; CID	**Pepti...**	79.2



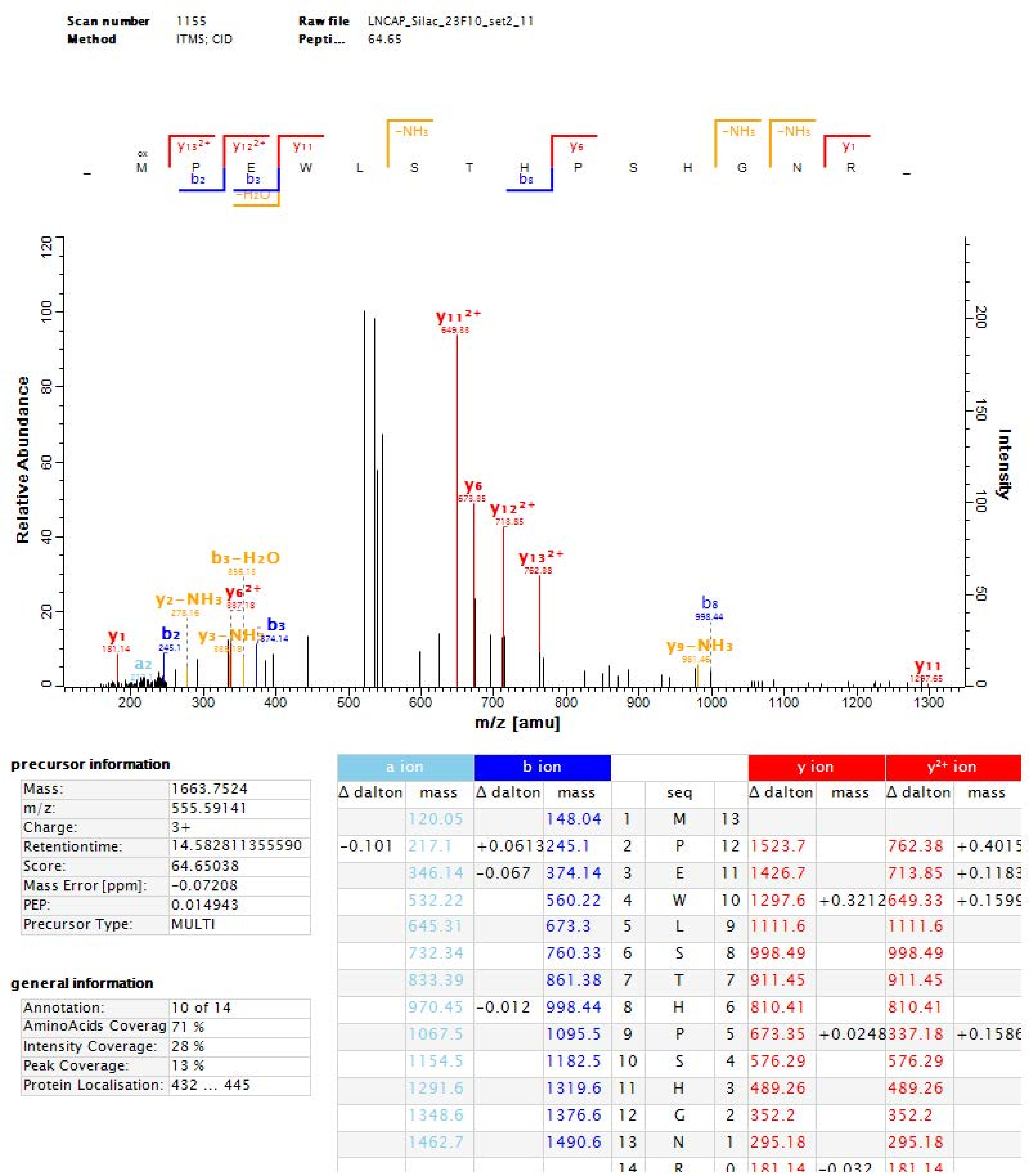
precursor information

Mass:	1513.80479
m/z:	505.60887
Charge:	3+
Retentiontime:	13.427463531494
Score:	79.20142
Mass Error [ppm]:	0.42661
PEP:	0.002111
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	27 %
Peak Coverage:	11 %
Protein Localisation:	97 ... 108

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	164.07		164.07	1	Y	11				
	278.11	+0.0319	278.11	2	N	10	1351.7		676.38	+0.1514
	415.17	+0.093	415.17	3	H	9	1237.7		619.36	+0.3721
	512.23		512.23	4	P	8	1100.6	+0.0001	550.83	+0.238
	640.32		640.32	5	K	7	1003.6	+0.013	1003.6	
	737.37		737.37	6	P	6	875.5	-0.069	875.5	
	851.42		851.42	7	N	5	778.45		778.45	
	964.5		964.5	8	L	4	664.4		664.4	
	1077.6	+0.1583	1077.6	9	L	3	551.32		551.32	
	1240.6	+0.1184	1240.6	10	Y	2	438.23		438.23	
+0.3673	684.86		1368.7	11	Q	1	275.17		275.17	
				12	K	0	147.11	+0.1878	147.11	



Scan number 1155
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set2_11
Pepti... 64.65

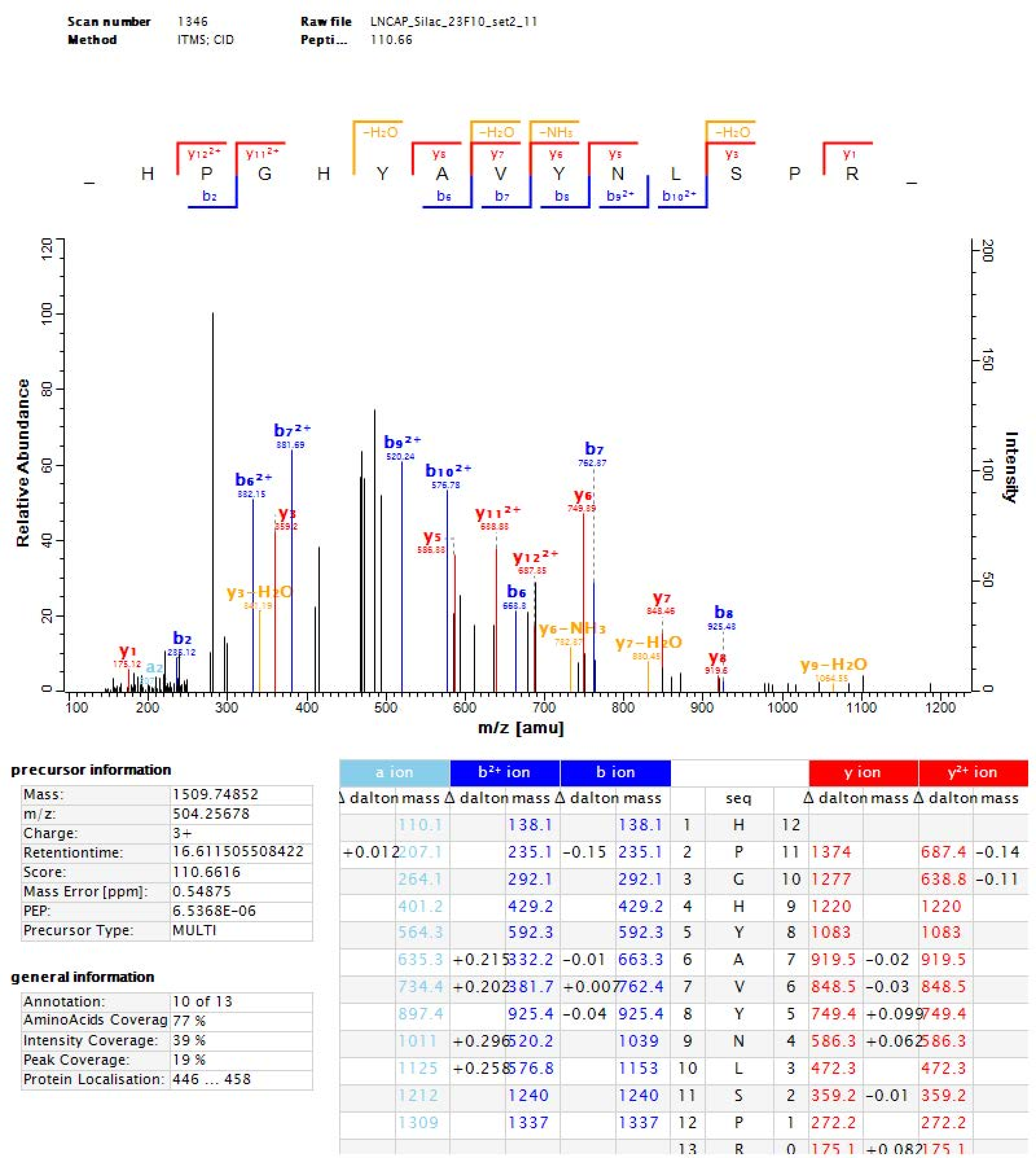
precursor information

Mass:	1663.7524
m/z:	555.59141
Charge:	3+
Retentiontime:	14.582811355590
Score:	64.65038
Mass Error [ppm]:	-0.07208
PEP:	0.014943
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	28 %
Peak Coverage:	13 %
Protein Localisation:	432 ... 445

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.05		148.04	1	M	13				
-0.101	217.1	+0.0613	245.1	2	P	12	1523.7		762.38	+0.4015
	346.14	-0.067	374.14	3	E	11	1426.7		713.85	+0.1183
	532.22		560.22	4	W	10	1297.6	+0.3212	649.33	+0.1599
	645.31		673.3	5	L	9	1111.6		1111.6	
	732.34		760.33	6	S	8	998.49		998.49	
	833.39		861.38	7	T	7	911.45		911.45	
	970.45	-0.012	998.44	8	H	6	810.41		810.41	
	1067.5		1095.5	9	P	5	673.35	+0.0248	337.18	+0.1586
	1154.5		1182.5	10	S	4	576.29		576.29	
	1291.6		1319.6	11	H	3	489.26		489.26	
	1348.6		1376.6	12	G	2	352.2		352.2	
	1462.7		1490.6	13	N	1	295.18		295.18	
				14	R	0	181.14	-0.032	181.14	



Scan number 1346 **Raw file** LNCAP_Silac_23F10_set2_11
Method ITMS; CID **Pepti...** 110.66

precursor information

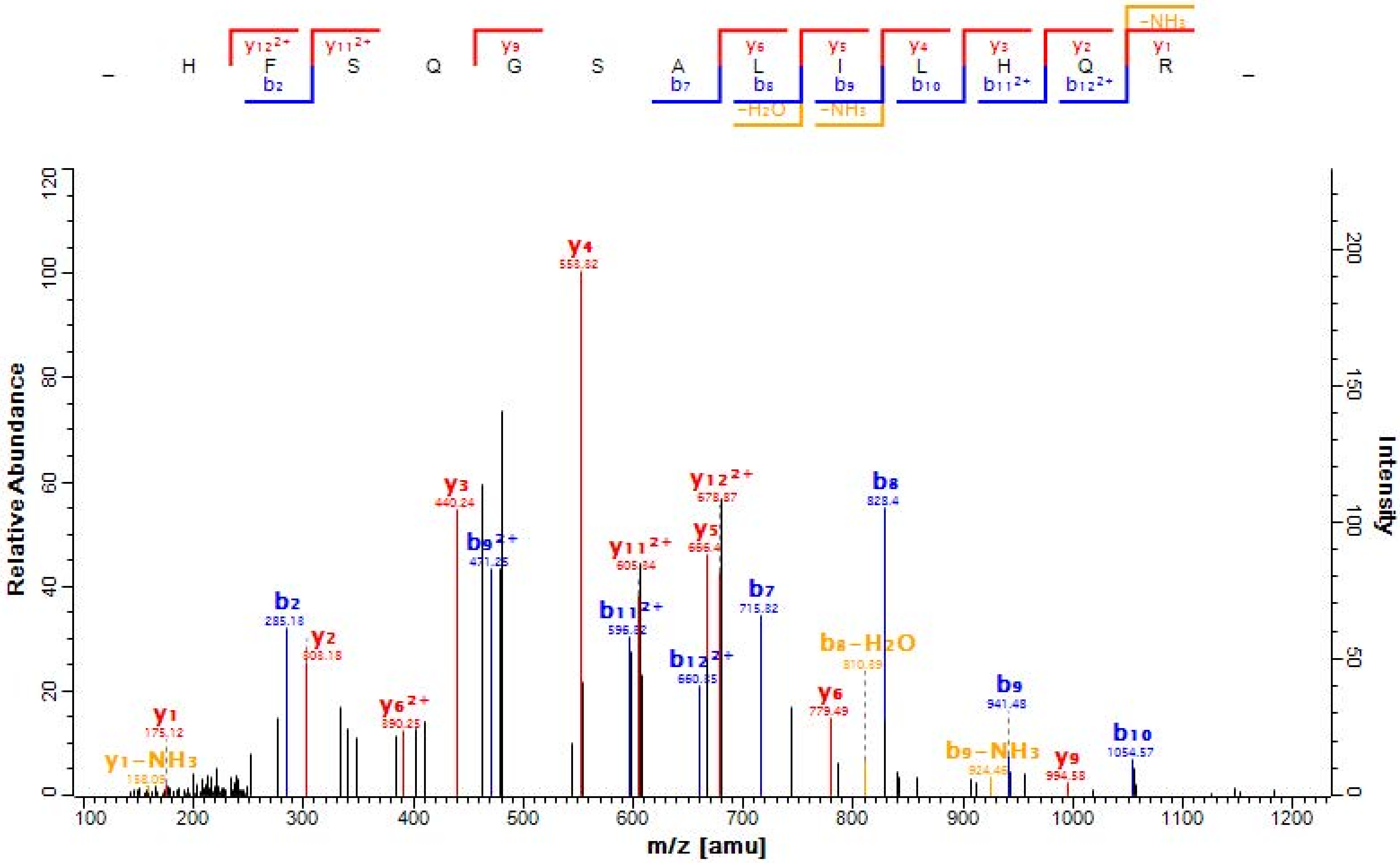
Mass:	1509.74852
m/z:	504.25678
Charge:	3+
Retentiontime:	16.611505508422
Score:	110.6616
Mass Error [ppm]:	0.54875
PEP:	6.5368E-06
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	39 %
Peak Coverage:	19 %
Protein Localisation:	446 ... 458

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	110.1		138.1		138.1	1	H	12				
+0.012	207.1		235.1	-0.15	235.1	2	P	11	1374		687.4	-0.14
	264.1		292.1		292.1	3	G	10	1277		638.8	-0.11
	401.2		429.2		429.2	4	H	9	1220		1220	
	564.3		592.3		592.3	5	Y	8	1083		1083	
	635.3	+0.215	332.2	-0.01	663.3	6	A	7	919.5	-0.02	919.5	
	734.4	+0.202	381.7	+0.007	762.4	7	V	6	848.5	-0.03	848.5	
	897.4		925.4	-0.04	925.4	8	Y	5	749.4	+0.099	749.4	
	1011	+0.296	520.2		1039	9	N	4	586.3	+0.062	586.3	
	1125	+0.258	576.8		1153	10	L	3	472.3		472.3	
	1212		1240		1240	11	S	2	359.2	-0.01	359.2	
	1309		1337		1337	12	P	1	272.2		272.2	
						13	R	0	175.1	+0.082	175.1	

Scan number	1413	**Raw file**	LNCAP_Silac_23F10_set2_11
Method	ITMS; CID	**Pepti...**	107.97



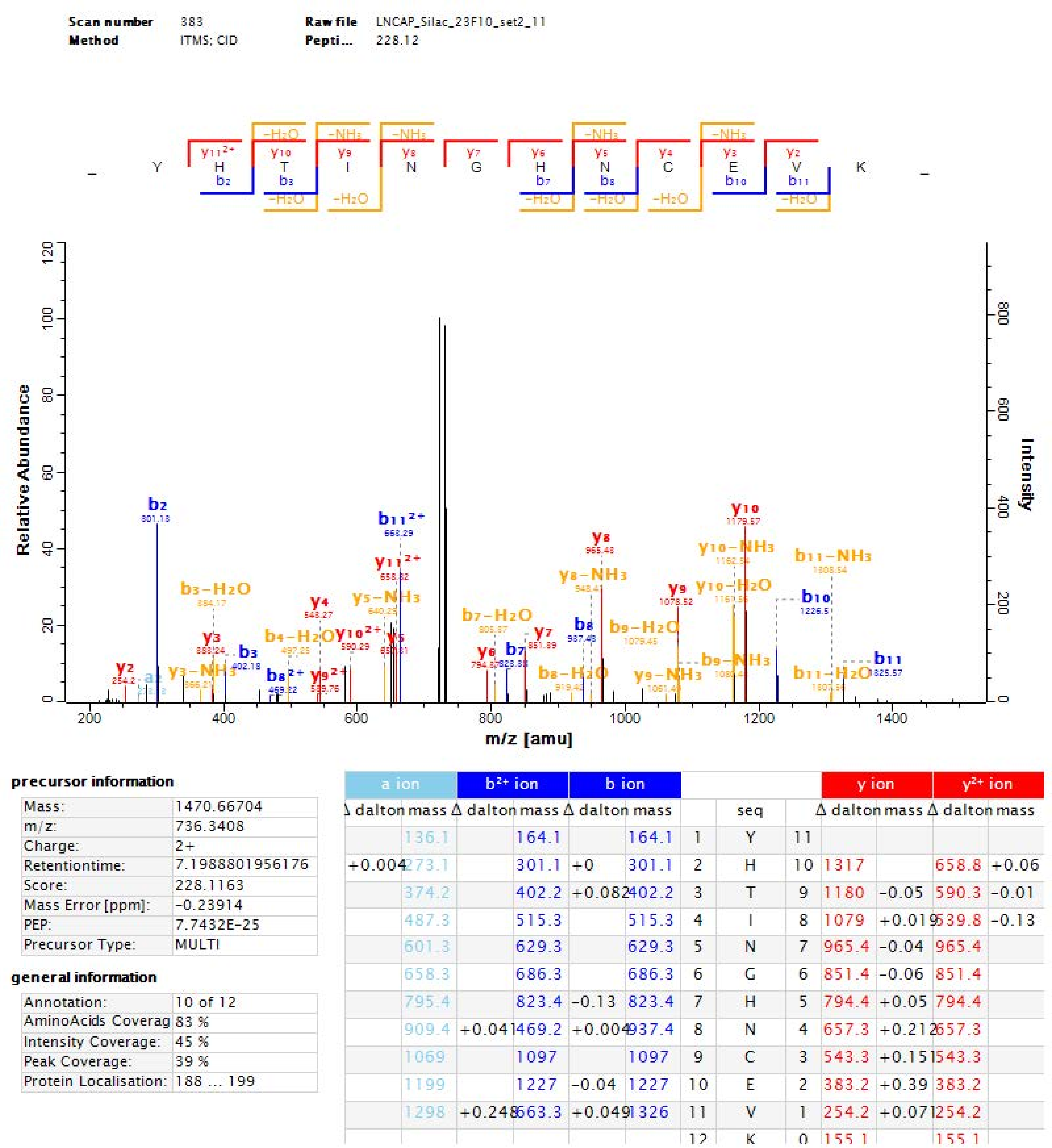
precursor information

Mass:	1492.78992
m/z:	498.60392
Charge:	3+
Retentiontime:	17.313058853149
Score:	107.9664
Mass Error [ppm]:	0.018299
PEP:	8.2906E-06
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	45 %
Peak Coverage:	18 %
Protein Localisation:	259 ... 271

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.07		138.07	1	H	12				
	285.13	+0.0037	285.13	2	F	11	1356.7		678.87	-0.058
	372.17		372.17	3	S	10	1209.7		605.34	-0.059
	500.23		500.23	4	Q	9	1122.6		1122.6	
	557.25		557.25	5	G	8	994.58	+0.1332	994.58	
	644.28		644.28	6	S	7	937.56		937.56	
	715.32	+0.1386	715.32	7	A	6	850.53		850.53	
	828.4	-0.03	828.4	8	L	5	779.49	-0.051	390.25	+0.0698
+0.1695	471.25	+0.0223	941.48	9	I	4	666.4	+0.131	666.4	
	1054.6	+0.0389	1054.6	10	L	3	553.32	-0.041	553.32	
+0.2558	596.32		1191.6	11	H	2	440.24	+0.04	440.24	
+0.1817	660.35		1319.7	12	Q	1	303.18	+0.0182	303.18	
				13	R	0	175.12	+0.0683	175.12	



Scan number	383	**Raw file**	LNCAP_Silac_23F10_set2_11
Method	ITMS; CID	**Pepti...**	228.12

precursor information

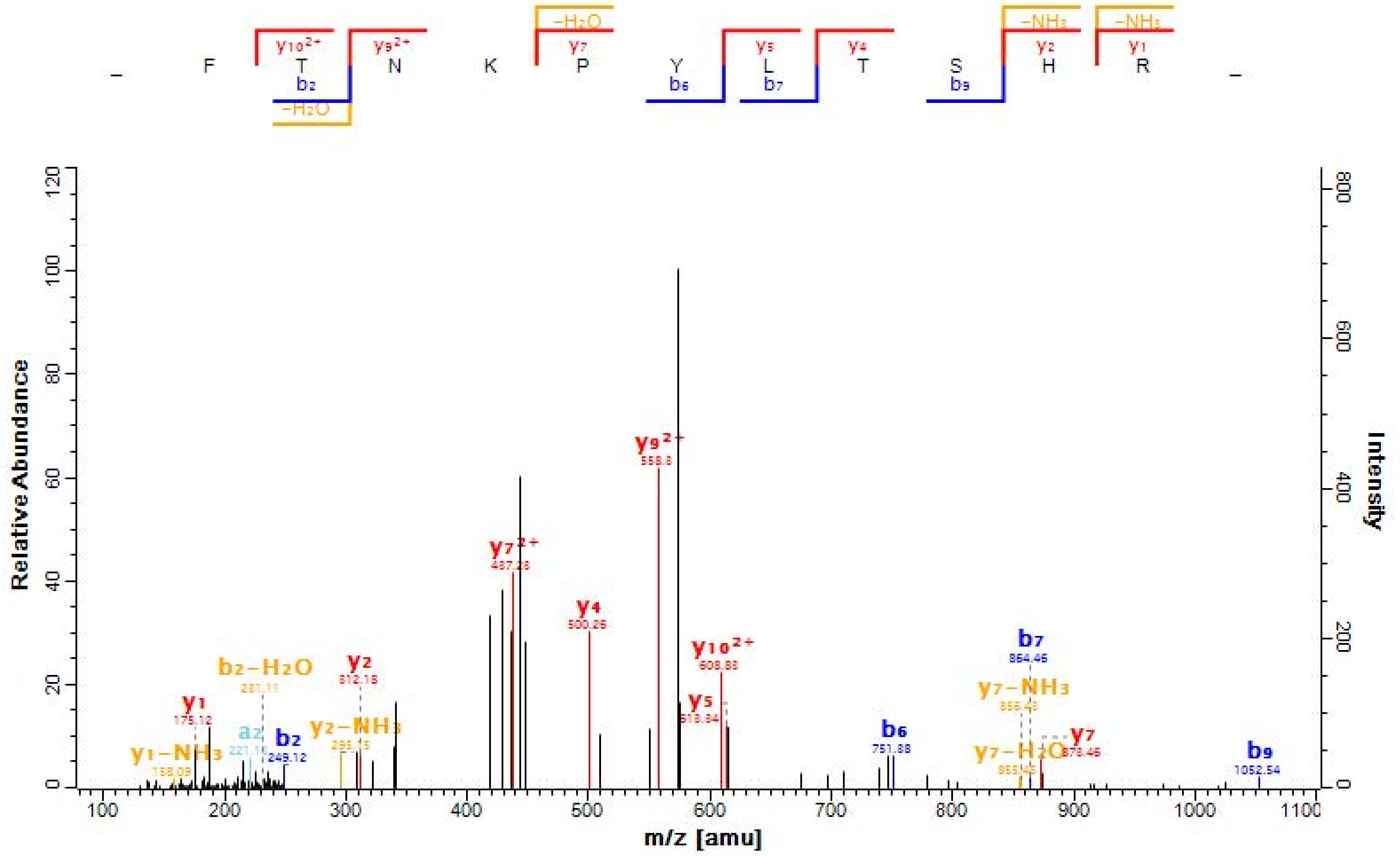
Mass:	1470.66704
m/z:	736.3408
Charge:	2+
Retentiontime:	7.1988801956176
Score:	228.1163
Mass Error [ppm]:	-0.23914
PEP:	7.7432E-25
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	45 %
Peak Coverage:	39 %
Protein Localisation:	188 ... 199

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.1		164.1		164.1	1	Y	11				
+0.004	273.1		301.1	+0	301.1	2	H	10	1317		658.8	+0.06
	374.2		402.2	+0.082	402.2	3	T	9	1180	-0.05	590.3	-0.01
	487.3		515.3		515.3	4	I	8	1079	+0.019	539.8	-0.13
	601.3		629.3		629.3	5	N	7	965.4	-0.04	965.4	
	658.3		686.3		686.3	6	G	6	851.4	-0.06	851.4	
	795.4		823.4	-0.13	823.4	7	H	5	794.4	+0.05	794.4	
	909.4	+0.041	469.2	+0.004	937.4	8	N	4	657.3	+0.212	657.3	
	1069		1097		1097	9	C	3	543.3	+0.151	543.3	
	1199		1227	-0.04	1227	10	E	2	383.2	+0.39	383.2	
	1298	+0.248	663.3	+0.049	1326	11	V	1	254.2	+0.071	254.2	
						12	K	0	155.1		155.1	

Scan number	633	**Raw file**	LNCAP_Silac_23F10_set2_11
Method	ITMS; CID	**Pepti...**	96.11



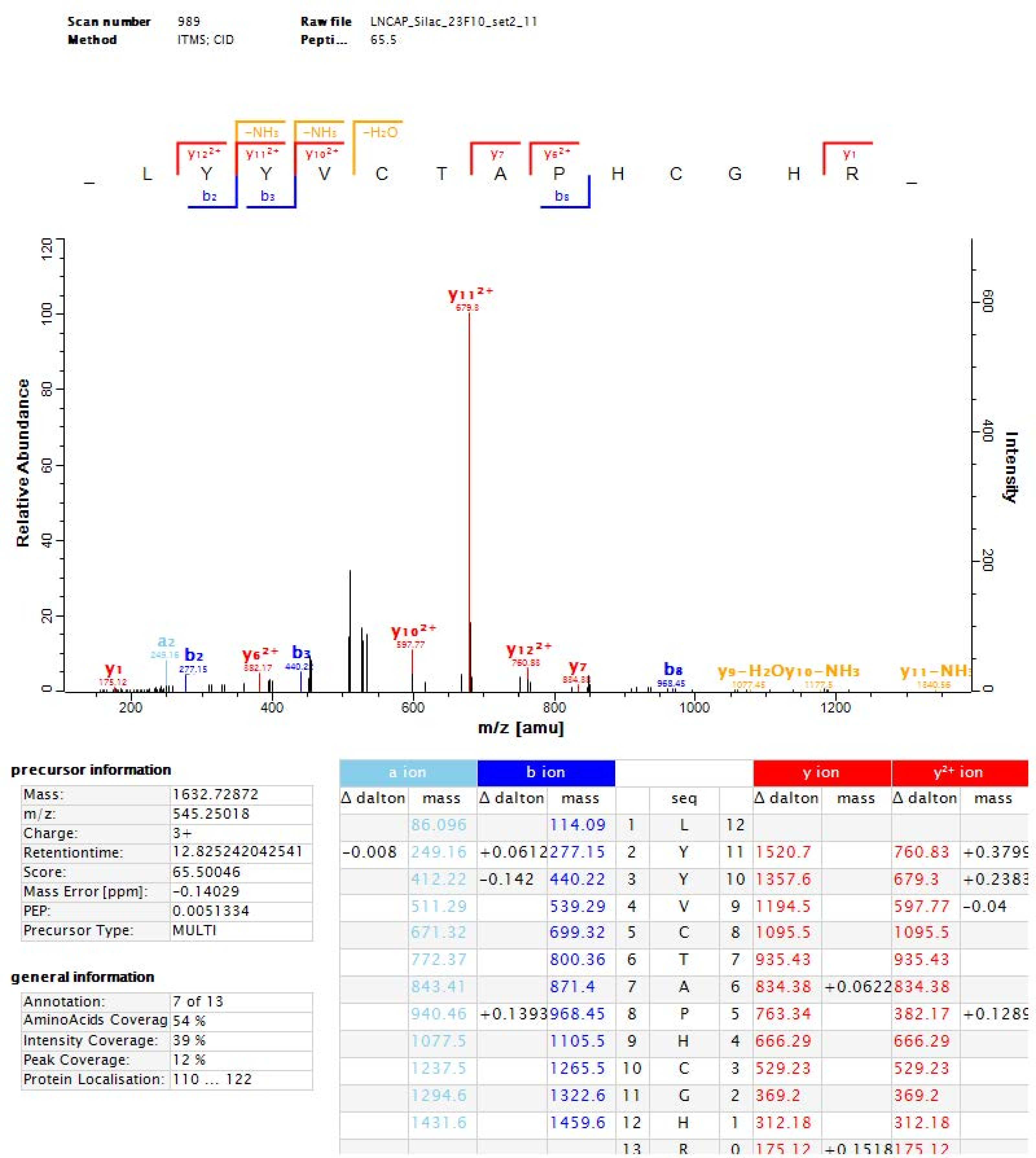
precursor information

Mass:	1362.70472
m/z:	455.24218
Charge:	3+
Retentiontime:	9.4482250213623
Score:	96.11349
Mass Error [ppm]:	0.20821
PEP:	0.00091392
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	30 %
Peak Coverage:	13 %
Protein Localisation:	330 ... 340

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08		148.08	1	F	10				
+0.1105	221.13	+0.1044	249.12	2	T	9	1216.6		608.83	+0.2213
	335.17		363.17	3	N	8	1115.6		558.3	+0.2662
	463.27		491.26	4	K	7	1001.6		1001.6	
	560.32		588.31	5	P	6	873.46	-0.082	437.23	+0.347
	723.38	+0.0419	751.38	6	Y	5	776.4		776.4	
	836.47	-0.025	864.46	7	L	4	613.34	+0.4825	613.34	
	937.51		965.51	8	T	3	500.26	+0.0184	500.26	
	1024.5	-0.005	1052.5	9	S	2	399.21		399.21	
	1161.6		1189.6	10	H	1	312.18	+0.0541	312.18	
				11	R	0	175.12	-0.003	175.12	



Scan number	989	**Raw file**	LNCAP_Silac_23F10_set2_11
Method	ITMS; CID	**Pepti...**	65.5

precursor information

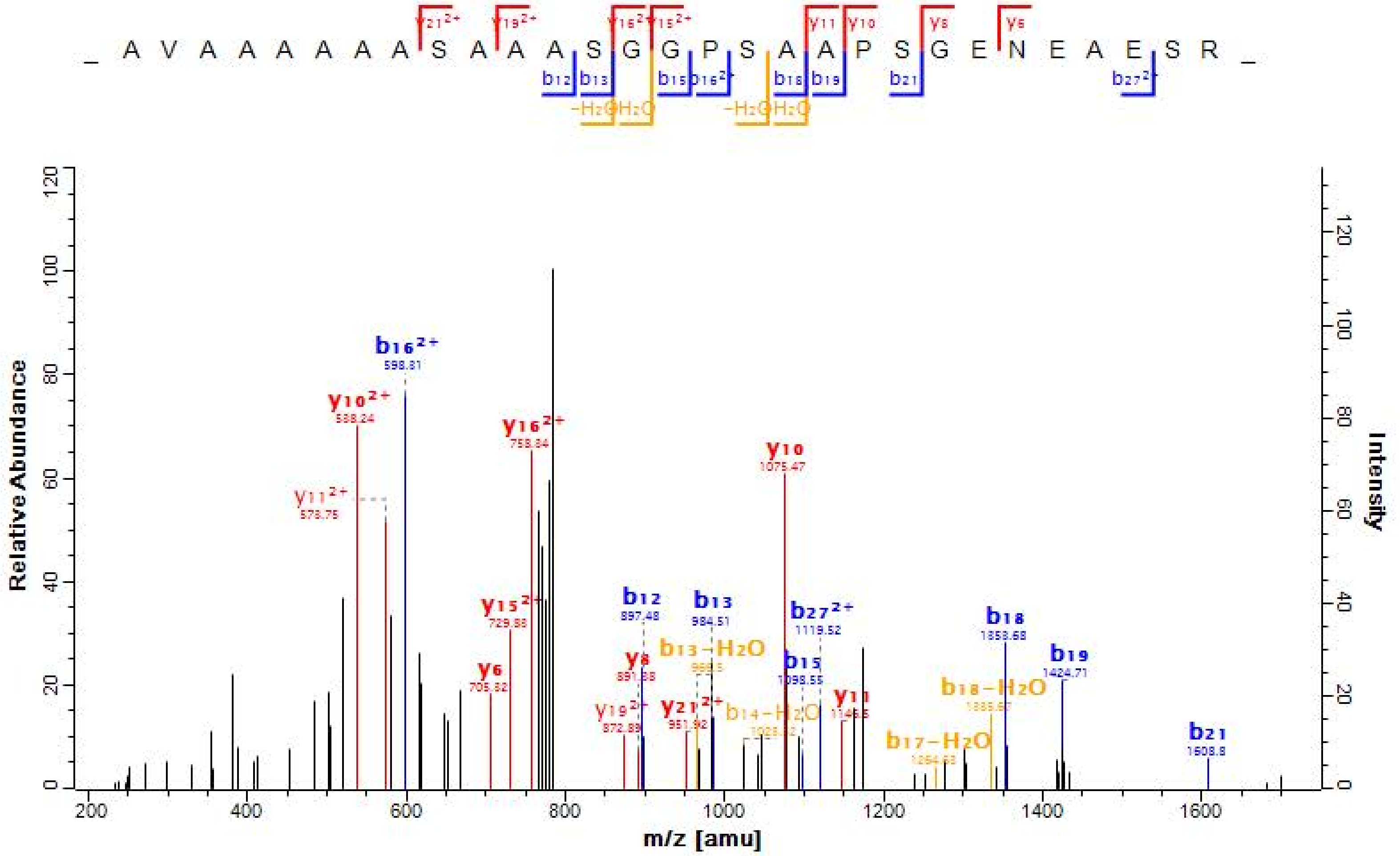
Mass:	1632.72872
m/z:	545.25018
Charge:	3+
Retentiontime:	12.825242042541
Score:	65.50046
Mass Error [ppm]:	-0.14029
PEP:	0.0051334
Precursor Type:	MULTI

general information

Annotation:	7 of 13
AminoAcids Coverag	54 %
Intensity Coverage:	39 %
Peak Coverage:	12 %
Protein Localisation:	110 ... 122

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	12				
-0.008	249.16	+0.0612	277.15	2	Y	11	1520.7		760.83	+0.3799
	412.22	-0.142	440.22	3	Y	10	1357.6		679.3	+0.2383
	511.29		539.29	4	V	9	1194.5		597.77	-0.04
	671.32		699.32	5	C	8	1095.5		1095.5	
	772.37		800.36	6	T	7	935.43		935.43	
	843.41		871.4	7	A	6	834.38	+0.0622	834.38	
	940.46	+0.1393	968.45	8	P	5	763.34		382.17	+0.1289
	1077.5		1105.5	9	H	4	666.29		666.29	
	1237.5		1265.5	10	C	3	529.23		529.23	
	1294.6		1322.6	11	G	2	369.2		369.2	
	1431.6		1459.6	12	H	1	312.18		312.18	
				13	R	0	175.12	+0.1518	175.12	

Scan number	1068	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	67.22



precursor information

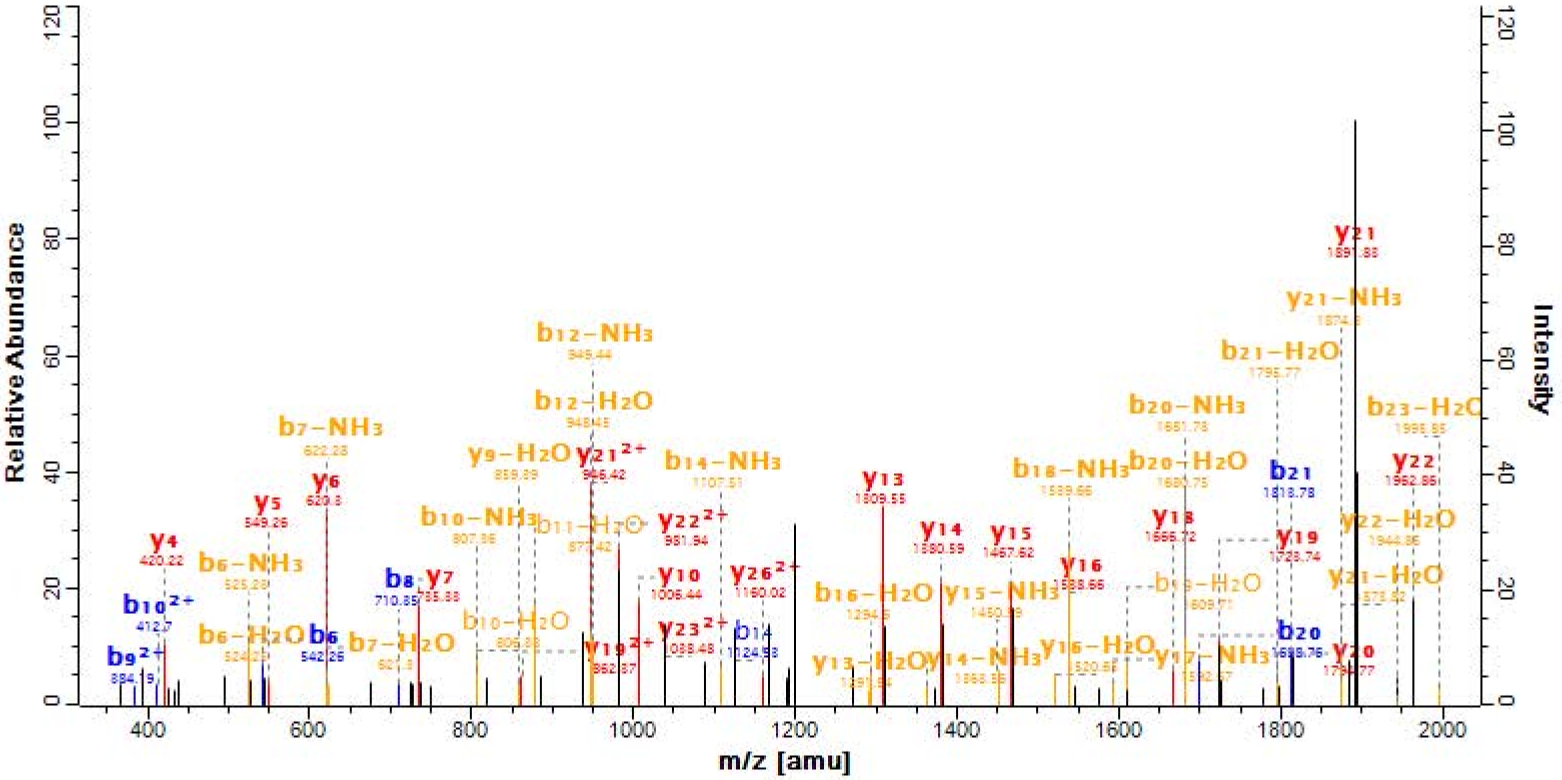
Mass:	2498.1631
m/z:	833.72831
Charge:	3+
Retentiontime:	15.868140220642
Score:	67.21661
Mass Error [ppm]:	-0.096028
PEP:	5.1628E-06
Precursor Type:	MULTI

general information

Annotation:	17 of 29
AminoAcids Coverag	59 %
Intensity Coverage:	41 %
Peak Coverage:	28 %
Protein Localisation:	8 ... 36

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	28				
	171.11		171.11	2	V	27	2428.1		2428.1	
	242.15		242.15	3	A	26	2329.1		2329.1	
	313.19		313.19	4	A	25	2258		2258	
	384.22		384.22	5	A	24	2187		2187	
	455.26		455.26	6	A	23	2116		2116	
	526.3		526.3	7	A	22	2044.9		2044.9	
	597.34		597.34	8	A	21	1973.9		1973.9	
	684.37		684.37	9	S	20	1902.8		951.92	-0.119
	755.4		755.4	10	A	19	1815.8		1815.8	
	826.44		826.44	11	A	18	1744.8		872.89	+0.185
	897.48	-0.188	897.48	12	A	17	1673.7		1673.7	
	984.51	+0.2032	984.51	13	S	16	1602.7		1602.7	
	1041.5		1041.5	14	G	15	1515.7		758.34	-0.02
	1098.6	+0.0192	1098.6	15	G	14	1458.6		729.83	+0.013
-0.217	598.31		1195.6	16	P	13	1401.6		1401.6	
	1282.6		1282.6	17	S	12	1304.6		1304.6	
	1353.7	-0.03	1353.7	18	A	11	1217.5		1217.5	
	1424.7	-0.172	1424.7	19	A	10	1146.5	+0.0513	573.75	+0.101
	1521.8		1521.8	20	P	9	1075.5	-0.056	538.24	+0.237
	1608.8	-0.071	1608.8	21	S	8	978.41		978.41	
	1665.8		1665.8	22	G	7	891.38	-0.213	891.38	
	1794.9		1794.9	23	E	6	834.36		834.36	
	1908.9		1908.9	24	N	5	705.32	+0.2407	705.32	
	2037.9		2037.9	25	E	4	591.27		591.27	
	2109		2109	26	A	3	462.23		462.23	
+0.3379	1119.5		2238	27	E	2	391.19		391.19	
	2325.1		2325.1	28	S	1	262.15		262.15	
				29	R	0	175.12		175.12	

Scan number	1144	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	198.47



precursor information

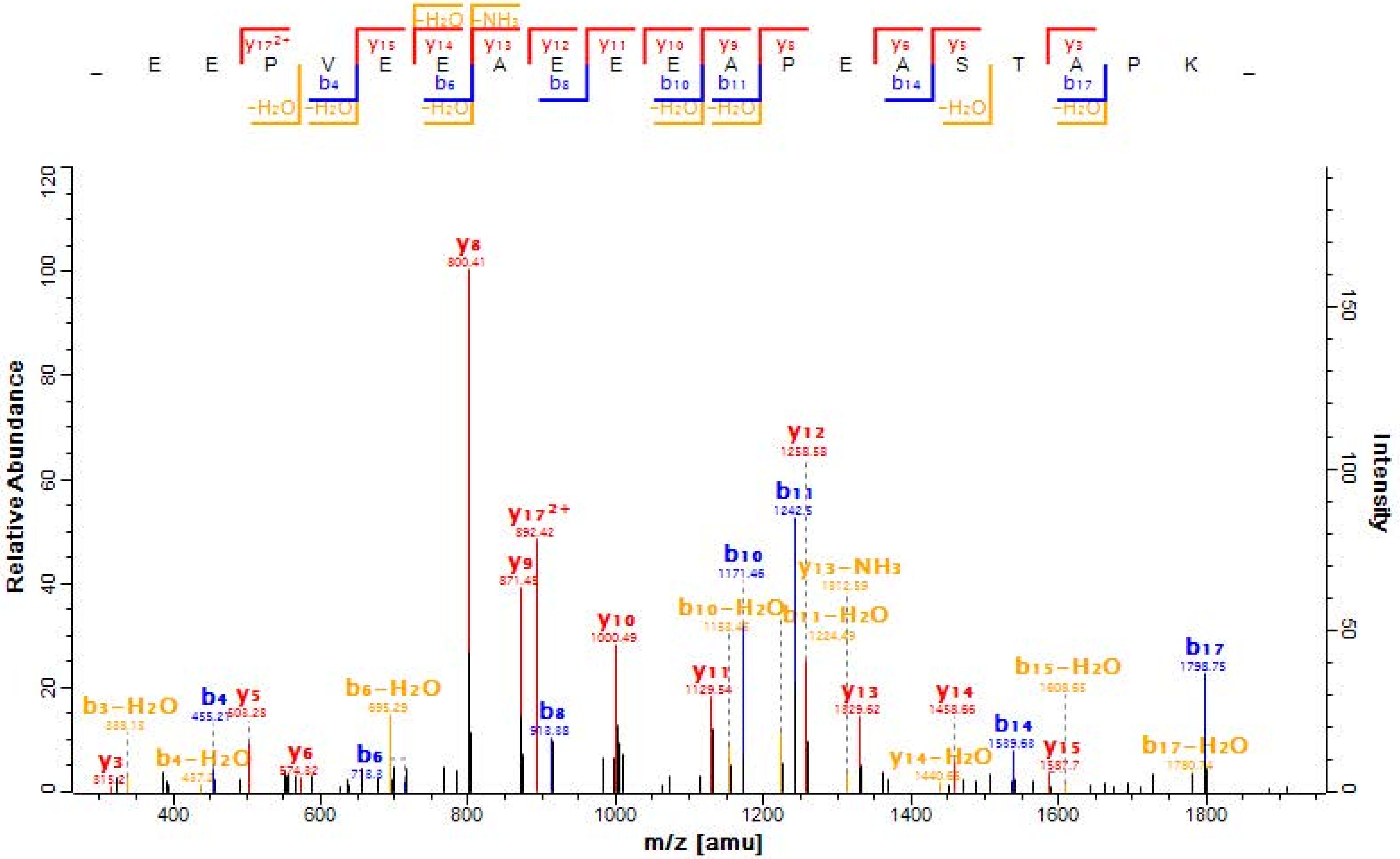
Mass:	2432.06897
m/z:	1217.04176
Charge:	2+
Retentiontime:	16.664182662963
Score:	198.4651
Mass Error [ppm]:	0.08317
PEP:	4.9819E-56
Precursor Type:	MULTI

general information

Annotation:	21 of 27
AminoAcids Coverag	78 %
Intensity Coverage:	57 %
Peak Coverage:	53 %
Protein Localisation:	42 ... 68

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.05		115.05	1	N	26				
	186.09		186.09	2	A	25	2319		1160	+0.4431
	243.11		243.11	3	G	24	2248		2248	
	358.14		358.14	4	D	23	2191		2191	
	471.22		471.22	5	L	22	2075.9		1038.5	-0.141
	542.26	+0.0823	542.26	6	A	21	1962.9	-0.139	981.94	+0.0569
	639.31		639.31	7	P	20	1891.8	-0.153	946.42	+0.4042
	710.35	-0.053	710.35	8	A	19	1794.8	-0.017	1794.8	
-0.078	384.19		767.37	9	G	18	1723.7	+0.0835	862.37	-0.111
-0.44	412.7		824.39	10	G	17	1666.7	+0.2174	1666.7	
	895.43		895.43	11	A	16	1609.7		1609.7	
	966.46		966.46	12	A	15	1538.7	-0.186	1538.7	
	1053.5		1053.5	13	S	14	1467.6	-0.093	1467.6	
	1124.5	+0.078	1124.5	14	A	13	1380.6	-0.031	1380.6	
	1211.6		1211.6	15	S	12	1309.6	-0.173	1309.6	
	1312.6		1312.6	16	T	11	1222.5		1222.5	
	1427.6		1427.6	17	D	10	1121.5		1121.5	
	1556.7		1556.7	18	E	9	1006.4	-0.157	1006.4	
	1627.7		1627.7	19	A	8	877.4		877.4	
	1698.8	-0.12	1698.8	20	A	7	806.36		806.36	
	1813.8	-0.16	1813.8	21	D	6	735.33	+0.0774	735.33	
	1884.8		1884.8	22	A	5	620.3	+0.1289	620.3	
	2013.9		2013.9	23	E	4	549.26	+0.1465	549.26	
	2100.9		2100.9	24	S	3	420.22	+0.0996	420.22	
	2157.9		2157.9	25	G	2	333.19		333.19	
	2259		2259	26	T	1	276.17		276.17	
				27	R	0	175.12		175.12	

Scan number	1465	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	120.9



precursor information

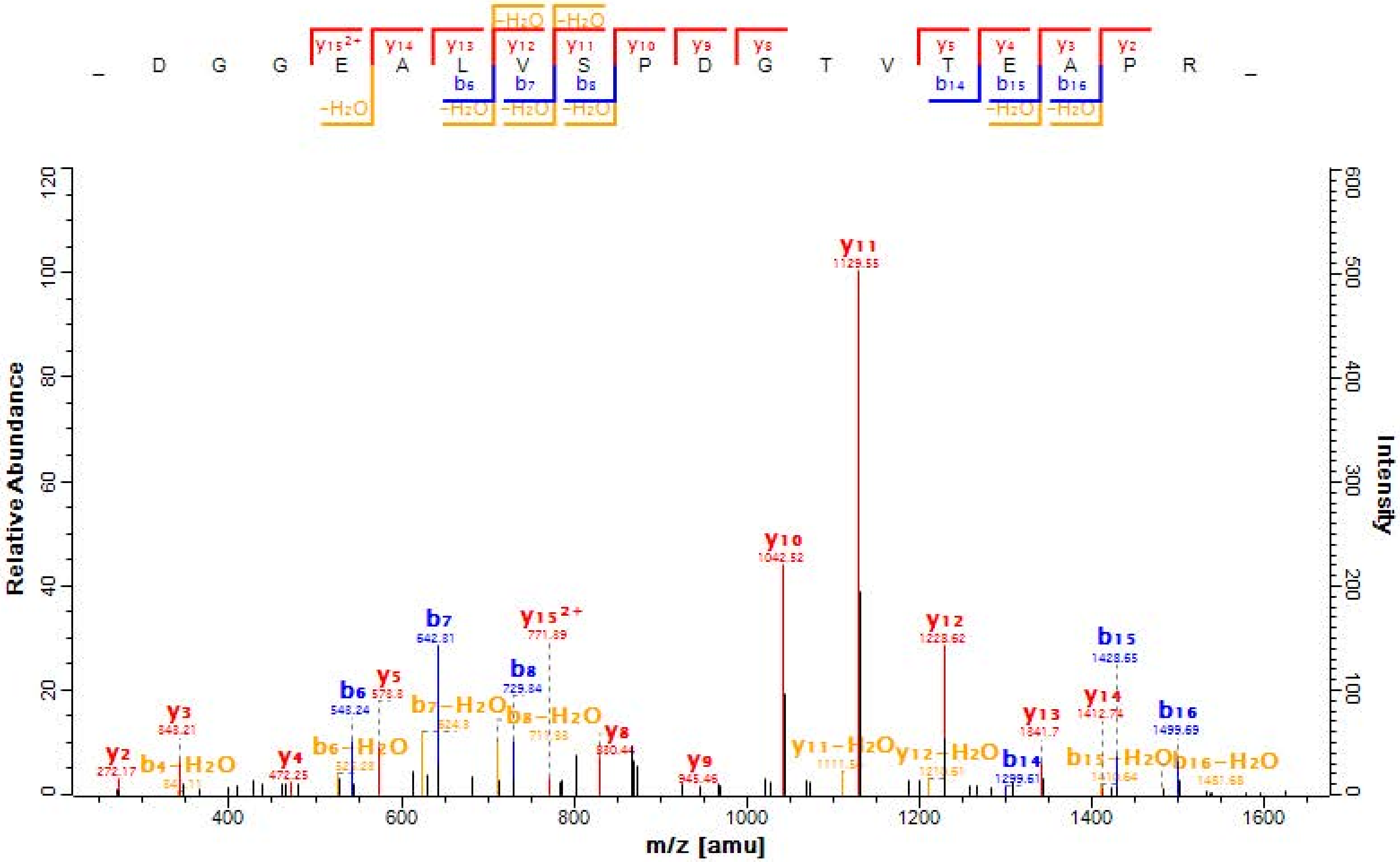
Mass:	2040.90257
m/z:	1021.45856
Charge:	2+
Retentiontime:	19.856170654296
Score:	120.8965
Mass Error [ppm]:	0.70243
PEP:	1.5871E-12
Precursor Type:	MULTI

general information

Annotation:	13 of 19
AminoAcids Coverag	68 %
Intensity Coverage:	61 %
Peak Coverage:	30 %
Protein Localisation:	880 ... 898

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	18				
	259.0925	2	E	17	1912.866		1912.866	
	356.1452	3	P	16	1783.823		892.4153	+0.288604
+0.088331	455.2136	4	V	15	1686.77		1686.77	
	584.2562	5	E	14	1587.702	-0.0502	1587.702	
+0.123903	713.2988	6	E	13	1458.659	-0.21842	1458.659	
	784.3359	7	A	12	1329.617	-0.05119	1329.617	
+0.139411	913.3785	8	E	11	1258.58	-0.03483	1258.58	
	1042.421	9	E	10	1129.537	+0.020824	1129.537	
+0.014308	1171.464	10	E	9	1000.495	+0.115053	1000.495	
-0.14121	1242.501	11	A	8	871.452	+0.084038	871.452	
	1339.554	12	P	7	800.4149	+0.029599	800.4149	
	1468.596	13	E	6	703.3621		703.3621	
-0.16614	1539.633	14	A	5	574.3195	+0.134843	574.3195	
	1626.665	15	S	4	503.2824	+0.198141	503.2824	
	1727.713	16	T	3	416.2504		416.2504	
+0.066159	1798.75	17	A	2	315.2027	-0.05	315.2027	
	1895.803	18	P	1	244.1656		244.1656	
		19	K	0	147.1128		147.1128	

Scan number	1590	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	143.14



precursor information

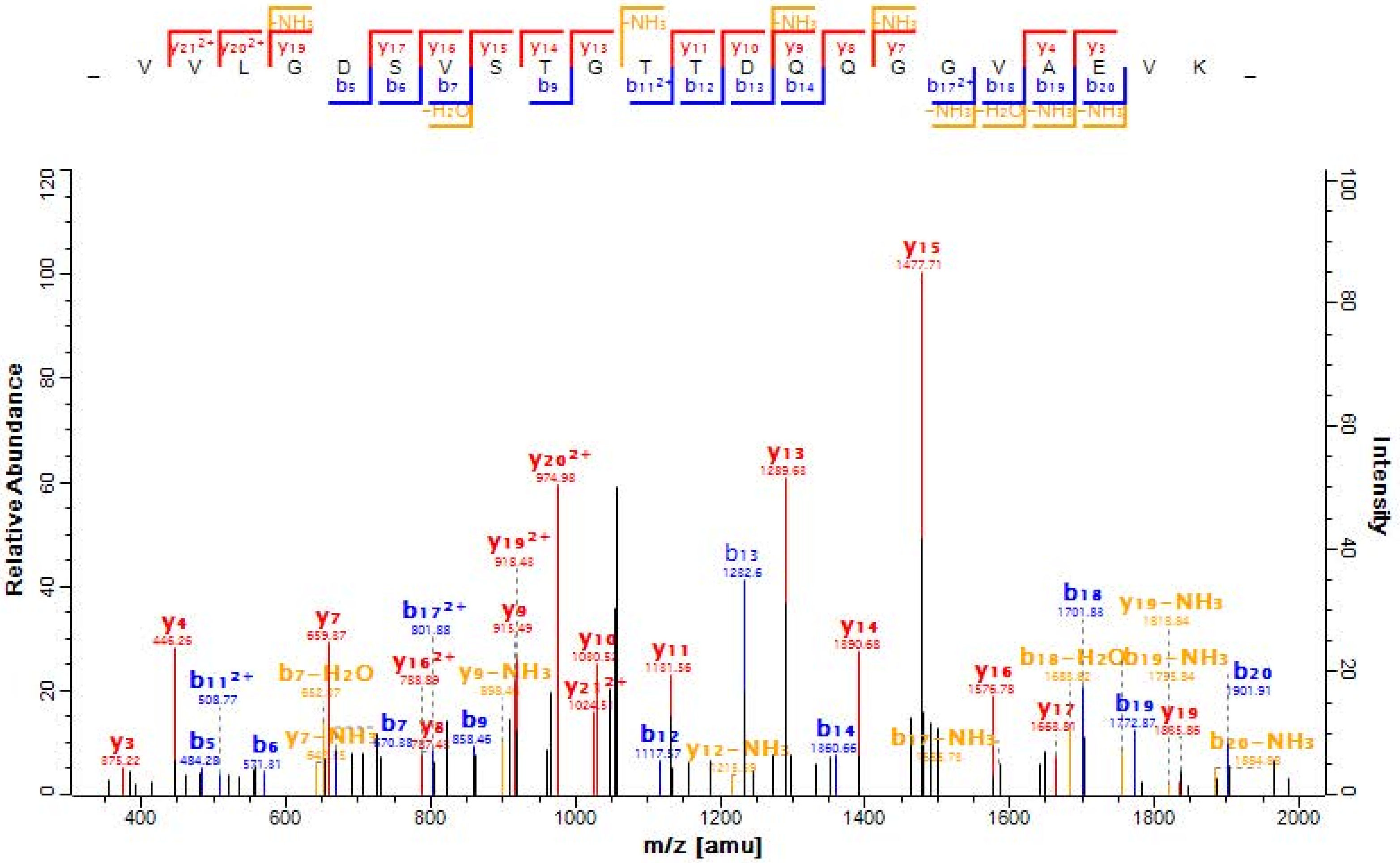
Mass:	1769.84328
m/z:	885.92892
Charge:	2+
Retentiontime:	21.088050842285
Score:	143.1416
Mass Error [ppm]:	0.06162
PEP:	2.0602E-17
Precursor Type:	MULTI

general information

Annotation:	12 of 18
AminoAcids Coverag	67 %
Intensity Coverage:	61 %
Peak Coverage:	31 %
Protein Localisation:	100 ... 117

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342	1	D	17				
	173.0557	2	G	16	1655.824		1655.824	
	230.0771	3	G	15	1598.802		1598.802	
	359.1197	4	E	14	1541.781		771.3939	-0.17939
	430.1569	5	A	13	1412.738	-0.12397	1412.738	
-0.03865	543.2409	6	L	12	1341.701	-0.08991	1341.701	
-0.04999	642.3093	7	V	11	1228.617	-0.06505	1228.617	
-0.0067	729.3414	8	S	10	1129.548	+0.000313	1129.548	
	826.3941	9	P	9	1042.516	+0.021233	1042.516	
	941.4211	10	D	8	945.4636	+0.227317	945.4636	
	998.4425	11	G	7	830.4367	-0.10933	830.4367	
	1099.49	12	T	6	773.4152		773.4152	
	1198.559	13	V	5	672.3675		672.3675	
+0.08132	1299.606	14	T	4	573.2991	+0.052156	573.2991	
-0.2662	1428.649	15	E	3	472.2514	-0.09127	472.2514	
-0.09153	1499.686	16	A	2	343.2088	+0.08127	343.2088	
	1596.739	17	P	1	272.1717	+0.090918	272.1717	
		18	R	0	175.119		175.119	

Scan number	1662	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	166.91



precursor information

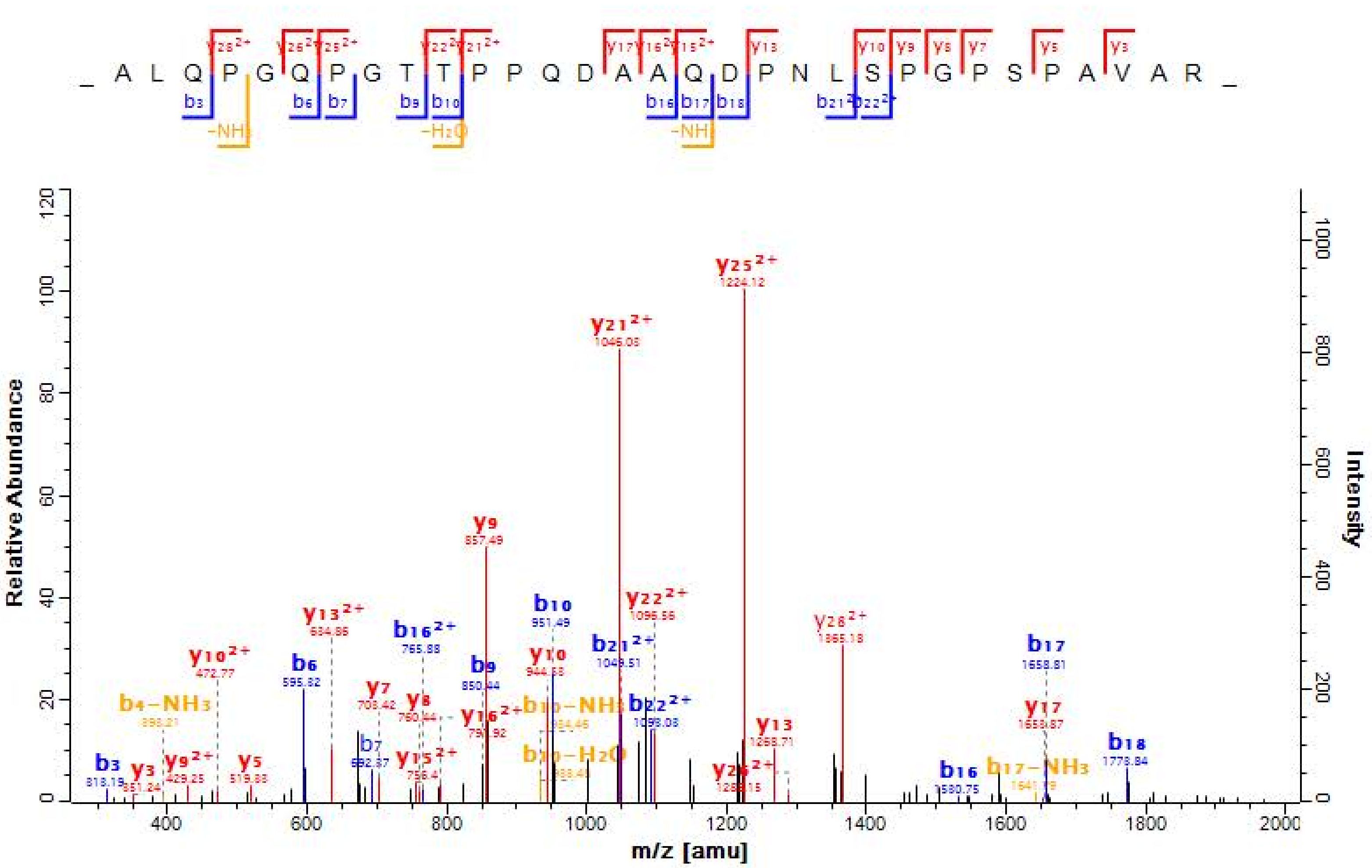
Mass:	2146.0766
m/z:	1074.04557
Charge:	2+
Retentiontime:	21.804317474365
Score:	166.9057
Mass Error [ppm]:	0.57769
PEP:	2.2294E-29
Precursor Type:	MULTI

general information

Annotation:	19 of 22
AminoAcids Coverag	86 %
Intensity Coverage:	52 %
Peak Coverage:	38 %
Protein Localisation:	85 ... 106

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	21				
	199.14		199.14	2	V	20	2048		1024.5	+0.3085
	312.23		312.23	3	L	19	1948.9		974.98	+0.3172
	369.25		369.25	4	G	18	1835.9	-0.339	918.43	+0.1701
	484.28	+0.1919	484.28	5	D	17	1778.8		1778.8	
	571.31	+0.0148	571.31	6	S	16	1663.8	-0.067	1663.8	
	670.38	-0.004	670.38	7	V	15	1576.8	-0.034	788.89	-0.38
	757.41		757.41	8	S	14	1477.7	-0.057	1477.7	
	858.46	+0.0051	858.46	9	T	13	1390.7	+0.1122	1390.7	
	915.48		915.48	10	G	12	1289.6	-0.104	1289.6	
-0.288	508.77		1016.5	11	T	11	1232.6		1232.6	
	1117.6	-0.056	1117.6	12	T	10	1131.6	-0.205	1131.6	
	1232.6	-0.09	1232.6	13	D	9	1030.5	+0.1338	1030.5	
	1360.7	-0.042	1360.7	14	Q	8	915.49	+0.0601	915.49	
	1488.7		1488.7	15	Q	7	787.43	+0.1367	787.43	
	1545.7		1545.7	16	G	6	659.37	-0.008	659.37	
-0.024	801.88		1602.8	17	G	5	602.35		602.35	
	1701.8	+0.1854	1701.8	18	V	4	545.33		545.33	
	1772.9	+0.3354	1772.9	19	A	3	446.26	+0.1282	446.26	
	1901.9	-0.109	1901.9	20	E	2	375.22	+0.0623	375.22	
	2001		2001	21	V	1	246.18		246.18	
				22	K	0	147.11		147.11	

Scan number	1817	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	119.45



precursor information

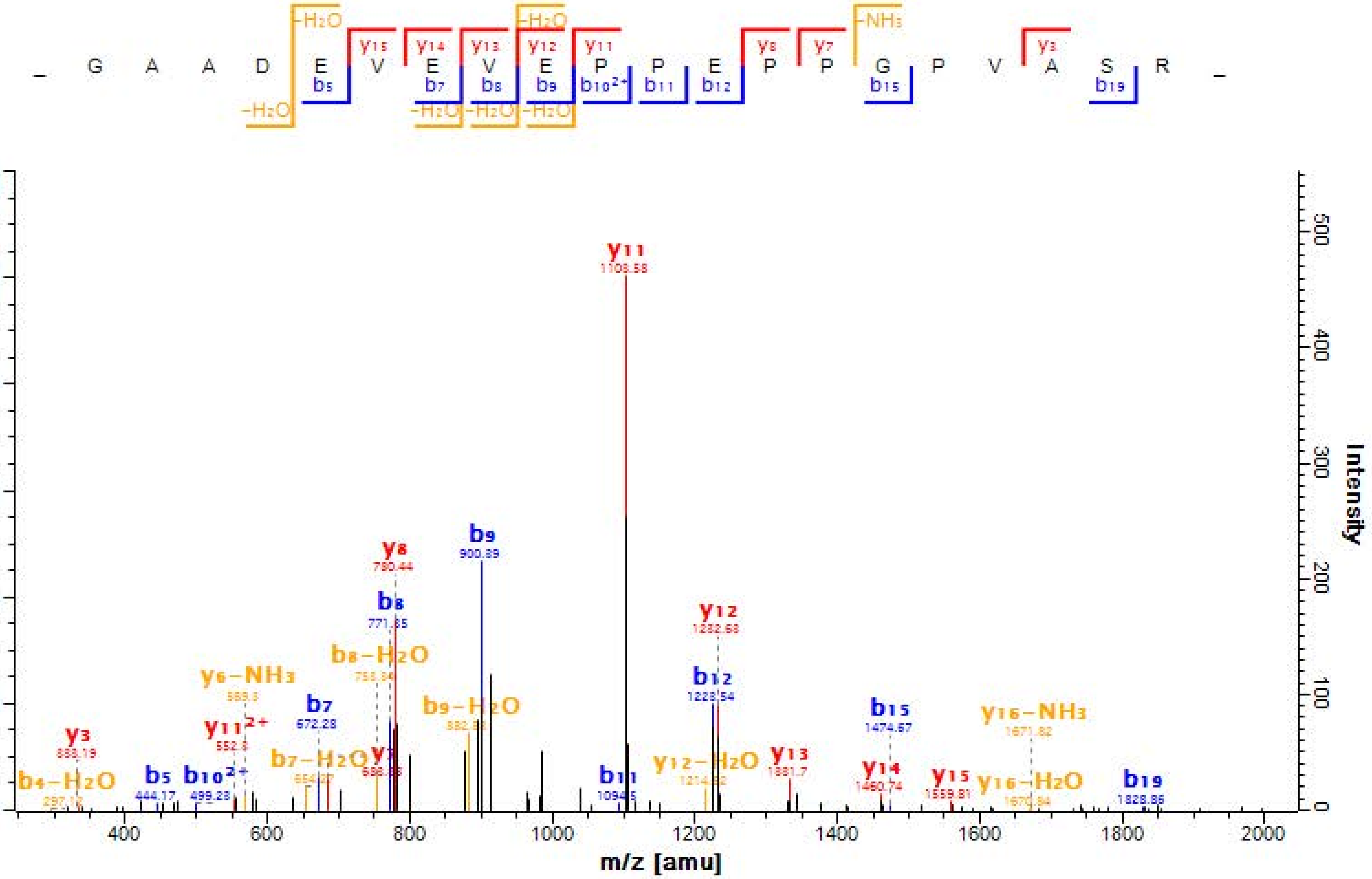
Mass:	3040.53007
m/z:	1014.5173
Charge:	3+
Retentiontime:	23.297088623046
Score:	119.4498
Mass Error [ppm]:	-0.28973
PEP:	6.6281E-14
Precursor Type:	ISO

general information

Annotation:	19 of 31
AminoAcids Coverag	61 %
Intensity Coverage:	63 %
Peak Coverage:	33 %
Protein Localisation:	375 ... 405

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	30				
	185.13		185.13	2	L	29	2970.5		2970.5	
	313.19	+0.1069	313.19	3	Q	28	2857.4		2857.4	
	410.24		410.24	4	P	27	2729.4		1365.2	+0.108
	467.26		467.26	5	G	26	2632.3		2632.3	
	595.32	-0.005	595.32	6	Q	25	2575.3		1288.1	-0.013
	692.37	+0.2989	692.37	7	P	24	2447.2		1224.1	+0.1992
	749.39		749.39	8	G	23	2350.2		2350.2	
	850.44	+0.029	850.44	9	T	22	2293.2		2293.2	
	951.49	-0.046	951.49	10	T	21	2192.1		1096.6	+0.204
	1048.5		1048.5	11	P	20	2091.1		1046	+0.257
	1145.6		1145.6	12	P	19	1994		1994	
	1273.7		1273.7	13	Q	18	1897		1897	
	1388.7		1388.7	14	D	17	1768.9		1768.9	
	1459.7		1459.7	15	A	16	1653.9	-0.126	1653.9	
+0.2185	765.88	+0.0152	1530.8	16	A	15	1582.8		791.92	+0.0361
	1658.8	-0.152	1658.8	17	Q	14	1511.8		756.4	+0.017
	1773.8	+0.0808	1773.8	18	D	13	1383.7		1383.7	
	1870.9		1870.9	19	P	12	1268.7	-0.043	634.86	-0.098
	1984.9		1984.9	20	N	11	1171.7		1171.7	
+0.0973	1049.5		2098	21	L	10	1057.6		1057.6	
+0.1422	1093		2185.1	22	S	9	944.53	+0.0489	472.77	-0.031
	2282.1		2282.1	23	P	8	857.49	-0.143	429.25	-0.135
	2339.1		2339.1	24	G	7	760.44	+0.0303	760.44	
	2436.2		2436.2	25	P	6	703.42	+0.1571	703.42	
	2523.2		2523.2	26	S	5	606.37		606.37	
	2620.3		2620.3	27	P	4	519.33	+0.0173	519.33	
	2691.3		2691.3	28	A	3	422.28		422.28	
	2790.4		2790.4	29	V	2	351.24	+0.1334	351.24	
	2861.4		2861.4	30	A	1	252.18		252.18	
				31	R	0	181.14		181.14	

Scan number	2034	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	87.49



precursor information

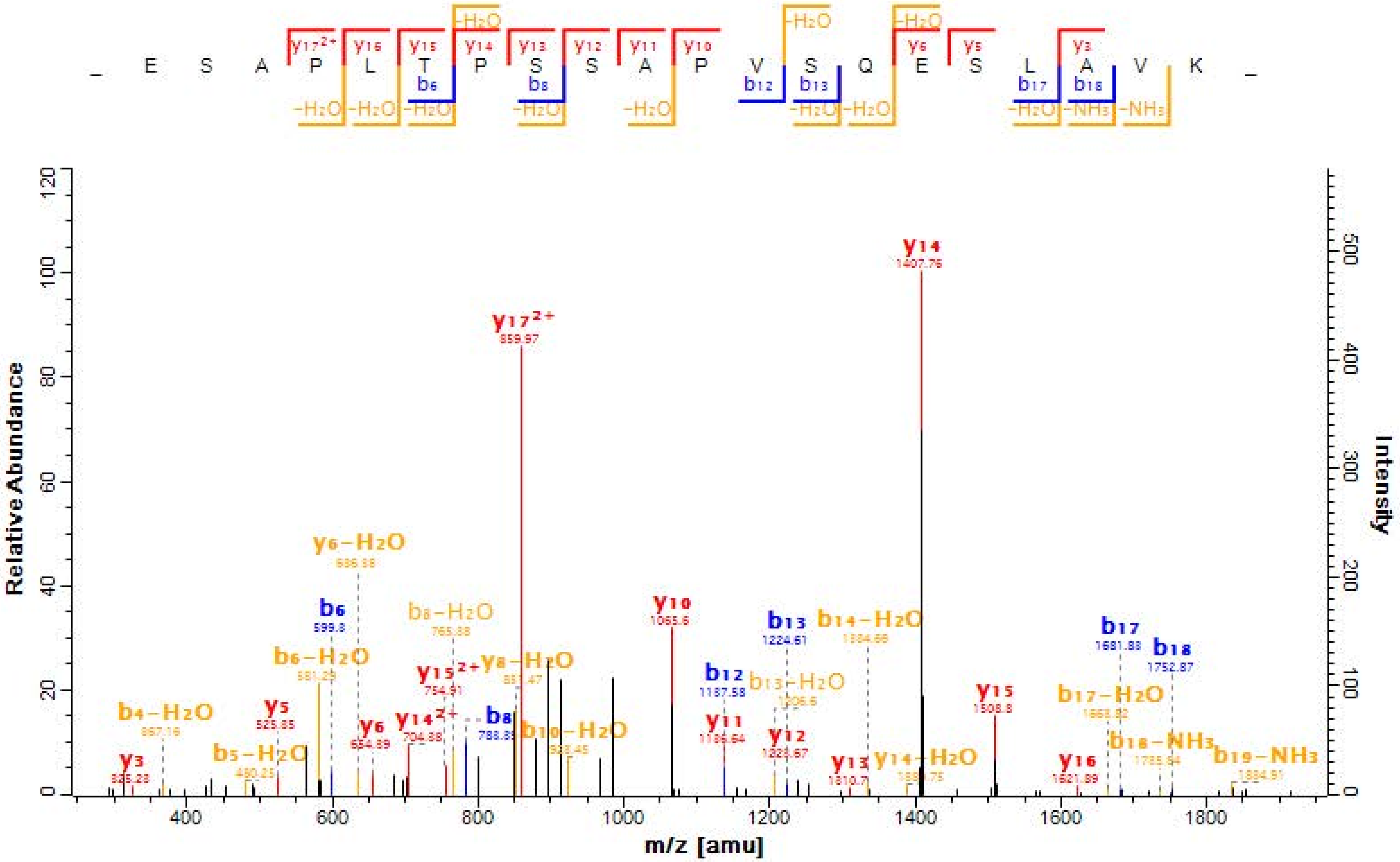
Mass:	2001.96474
m/z:	1001.98965
Charge:	2+
Retentiontime:	25.189147949218
Score:	87.48995
Mass Error [ppm]:	0.19745
PEP:	7.6184E-06
Precursor Type:	MULTI

general information

Annotation:	15 of 20
AminoAcids Coverag	75 %
Intensity Coverage:	51 %
Peak Coverage:	28 %
Protein Localisation:	66 ... 85

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	19				
	129.07		129.07	2	A	18	1946		1946	
	200.1		200.1	3	A	17	1874.9		1874.9	
	315.13		315.13	4	D	16	1803.9		1803.9	
	444.17	-0.096	444.17	5	E	15	1688.8		1688.8	
	543.24		543.24	6	V	14	1559.8	-0.109	1559.8	
	672.28	+0.0008	672.28	7	E	13	1460.7	-0.064	1460.7	
	771.35	+0.0941	771.35	8	V	12	1331.7	+0.1088	1331.7	
	900.39	-0.001	900.39	9	E	11	1232.6	+0.024	1232.6	
+0.1758	499.23		997.45	10	P	10	1103.6	-0.051	552.3	+0.1071
	1094.5	-0.204	1094.5	11	P	9	1006.5		1006.5	
	1223.5	-0.039	1223.5	12	E	8	909.48		909.48	
	1320.6		1320.6	13	P	7	780.44	-0.01	780.44	
	1417.6		1417.6	14	P	6	683.38	+0.0578	683.38	
	1474.7	-0.142	1474.7	15	G	5	586.33		586.33	
	1571.7		1571.7	16	P	4	529.31		529.31	
	1670.8		1670.8	17	V	3	432.26		432.26	
	1741.8		1741.8	18	A	2	333.19	+0.2794	333.19	
	1828.9	-0.269	1828.9	19	S	1	262.15		262.15	
				20	R	0	175.12		175.12	

Scan number	2231	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	136.26



precursor information

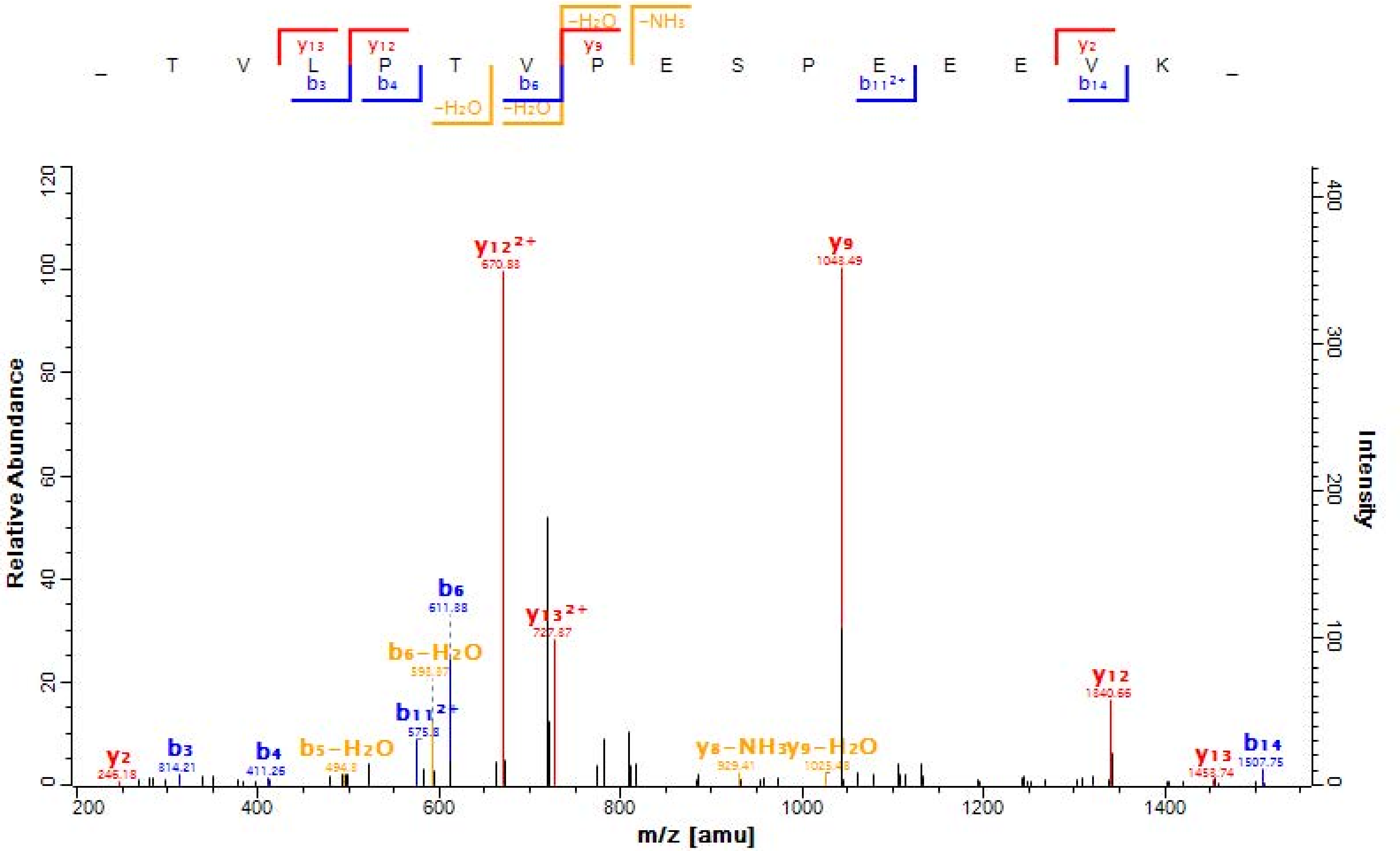
Mass:	1997.03197
m/z:	999.52326
Charge:	2+
Retentiontime:	26.961641311645
Score:	136.2613
Mass Error [ppm]:	0.13208
PEP:	9.7524E-19
Precursor Type:	MULTI

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	19				
	217.0819	2	S	18	1877.011		1877.011	
	288.119	3	A	17	1789.979		1789.979	
	385.1718	4	P	16	1718.941		859.9744	+0.3357
	498.2558	5	L	15	1621.889	+0.007686	1621.889	
+0.167673	599.3035	6	T	14	1508.805	-0.1646	754.9059	+0.21637
	696.3563	7	P	13	1407.757	-0.05015	704.3821	+0.030981
-0.06104	783.3883	8	S	12	1310.704	+0.097831	1310.704	
	870.4203	9	S	11	1223.672	+0.322487	1223.672	
	941.4575	10	A	10	1136.64	-0.02879	1136.64	
	1038.51	11	P	9	1065.603	-0.03488	1065.603	
+0.214949	1137.579	12	V	8	968.5502		968.5502	
+0.146666	1224.611	13	S	7	869.4818		869.4818	
	1352.669	14	Q	6	782.4498		782.4498	
	1481.712	15	E	5	654.3912	+0.097248	654.3912	
	1568.744	16	S	4	525.3486	+0.068369	525.3486	
+0.078695	1681.828	17	L	3	438.3166		438.3166	
-0.23015	1752.865	18	A	2	325.2325	+0.038954	325.2325	
	1851.933	19	V	1	254.1954		254.1954	
		20	K	0	155.127		155.127	

general information

Annotation:	16 of 20
AminoAcids Coverag	80 %
Intensity Coverage:	51 %
Peak Coverage:	33 %
Protein Localisation:	2402 ... 2421

Scan number	2505	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	69.72



precursor information

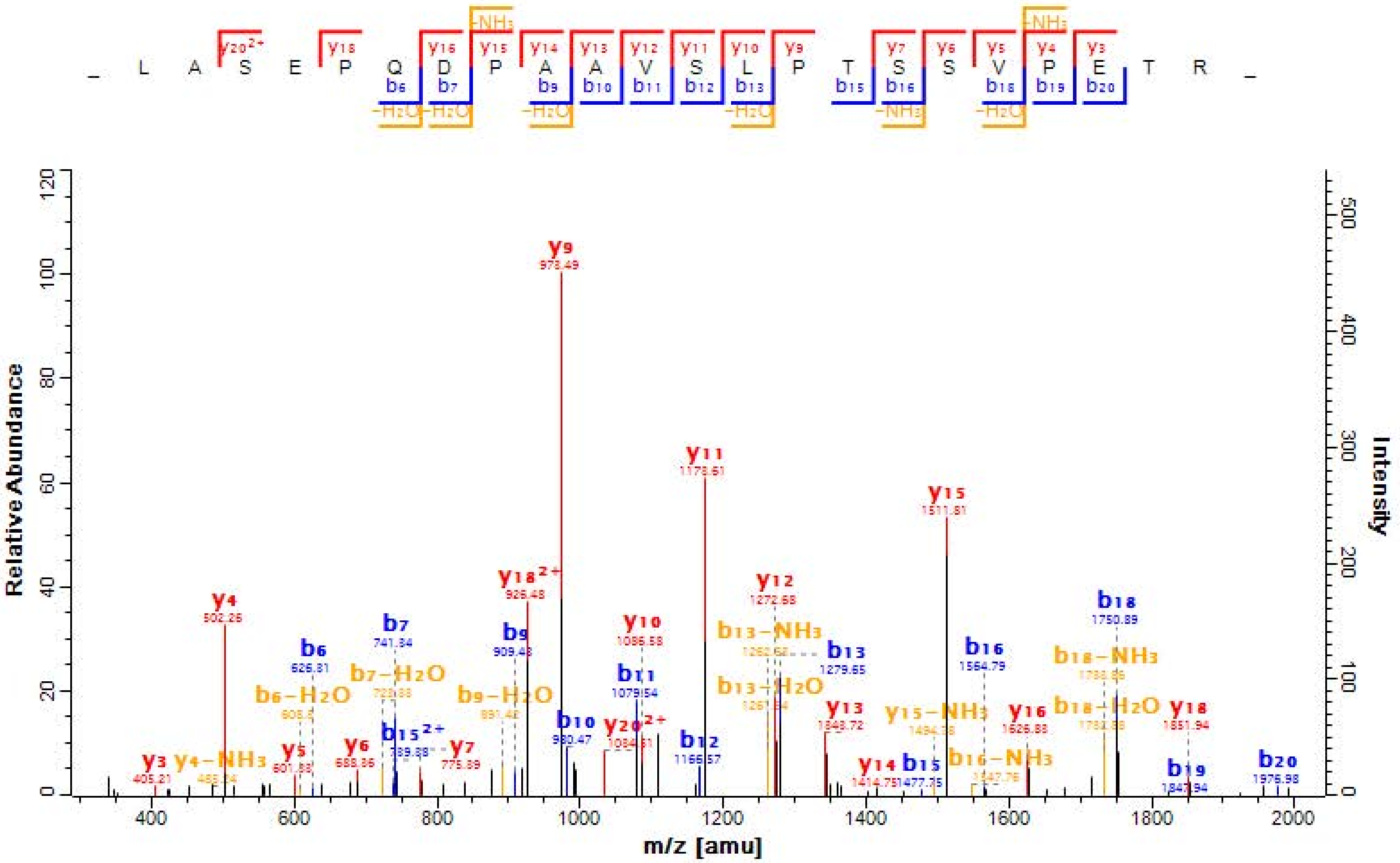
Mass:	1652.85091
m/z:	827.43273
Charge:	2+
Retentiontime:	29.349010467529
Score:	69.71599
Mass Error [ppm]:	0.015123
PEP:	0.0014557
Precursor Type:	MULTI

general information

Annotation:	8 of 15
AminoAcids Coverag	53 %
Intensity Coverage:	56 %
Peak Coverage:	19 %
Protein Localisation:	100 ... 114

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	14				
	201.12		201.12	2	V	13	1552.8		1552.8	
	314.21	-0.044	314.21	3	L	12	1453.7	-0.075	727.37	+0.1156
	411.26	+0.0958	411.26	4	P	11	1340.7	-0.036	670.83	+0.1252
	512.31		512.31	5	T	10	1243.6		1243.6	
	611.38	-0.01	611.38	6	V	9	1142.6		1142.6	
	708.43		708.43	7	P	8	1043.5	-0.038	1043.5	
	837.47		837.47	8	E	7	946.44		946.44	
	924.5		924.5	9	S	6	817.39		817.39	
	1021.6		1021.6	10	P	5	730.36		730.36	
-0.444	575.8		1150.6	11	E	4	633.31		633.31	
	1279.6		1279.6	12	E	3	504.27		504.27	
	1408.7		1408.7	13	E	2	375.22		375.22	
	1507.8	-0.165	1507.8	14	V	1	246.18	+0.1012	246.18	
				15	K	0	147.11		147.11	

Scan number	2535	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	171.84



precursor information

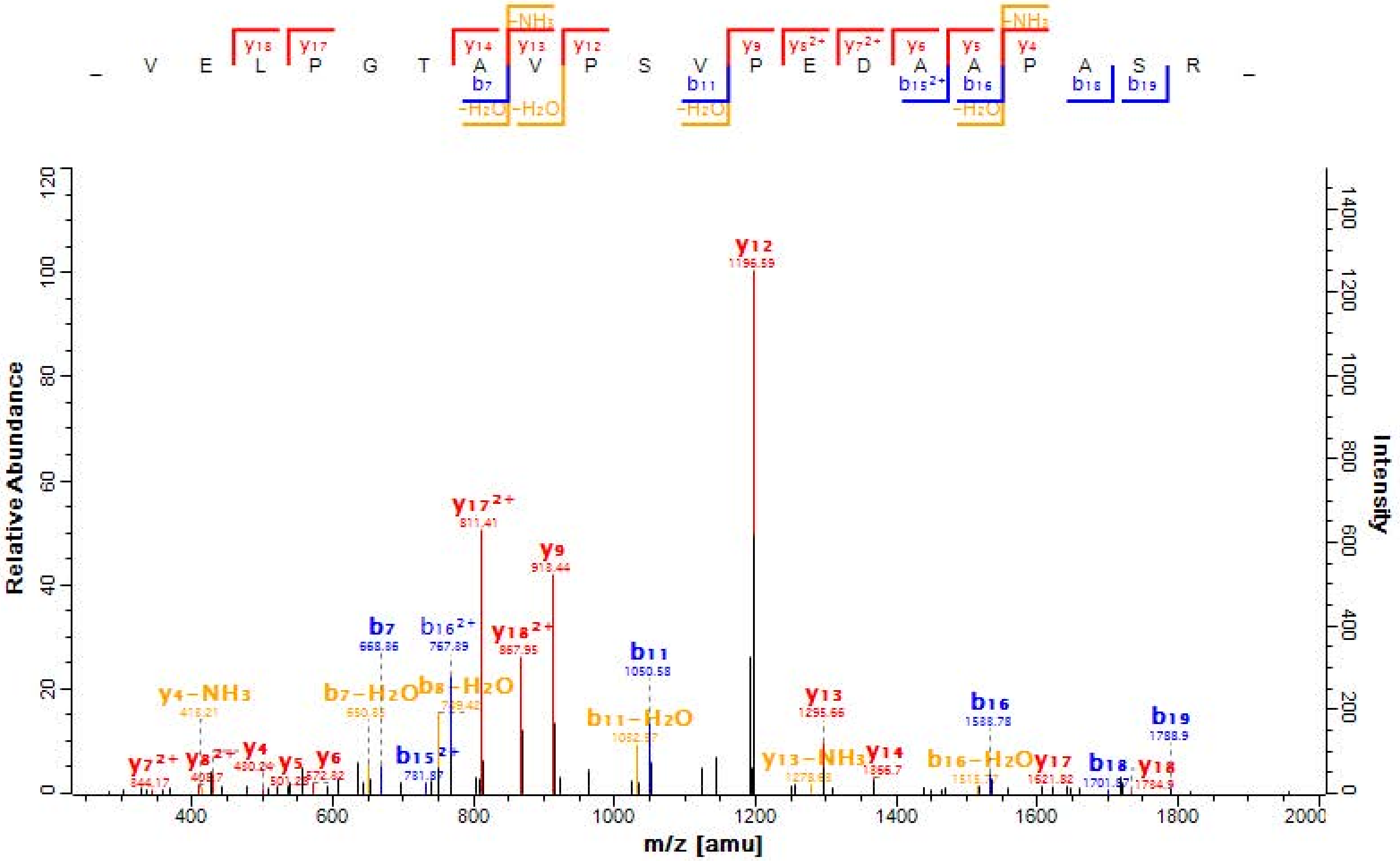
Mass:	2251.13308
m/z:	1126.57382
Charge:	2+
Retentiontime:	29.629743576049
Score:	171.8372
Mass Error [ppm]:	-0.053905
PEP:	1.5322E-37
Precursor Type:	MULTI

general information

Annotation:	17 of 22
AminoAcids Coverag	77 %
Intensity Coverage:	60 %
Peak Coverage:	39 %
Protein Localisation:	94 ... 115

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	21				
	185.13		185.13	2	A	20	2139.1		2139.1	
	272.16		272.16	3	S	19	2068		1034.5	+0.1851
	401.2		401.2	4	E	18	1981		1981	
	498.26		498.26	5	P	17	1851.9	+0.0585	926.48	+0.0123
	626.31	+0.1845	626.31	6	Q	16	1754.9		1754.9	
	741.34	-0.057	741.34	7	D	15	1626.8	-0.103	1626.8	
	838.39		838.39	8	P	14	1511.8	-0.051	1511.8	
	909.43	-0.118	909.43	9	A	13	1414.8	+0.0226	1414.8	
	980.47	+0.0473	980.47	10	A	12	1343.7	-0.122	1343.7	
	1079.5	+0.0616	1079.5	11	V	11	1272.7	-0.098	1272.7	
	1166.6	-0.096	1166.6	12	S	10	1173.6	-0.055	1173.6	
	1279.7	-0.028	1279.7	13	L	9	1086.6	-0.013	1086.6	
	1376.7		1376.7	14	P	8	973.49	+0.0229	973.49	
+0.1558	739.38	-0.082	1477.8	15	T	7	876.44		876.44	
	1564.8	+0.236	1564.8	16	S	6	775.39	-0.032	775.39	
	1651.8		1651.8	17	S	5	688.36	+0.0602	688.36	
	1750.9	-0.121	1750.9	18	V	4	601.33	+0.0918	601.33	
	1847.9	+0.1688	1847.9	19	P	3	502.26	+0.0792	502.26	
	1977	-0.242	1977	20	E	2	405.21	+0.2194	405.21	
	2078		2078	21	T	1	276.17		276.17	
				22	R	0	175.12		175.12	

Scan number	2650	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	111.77



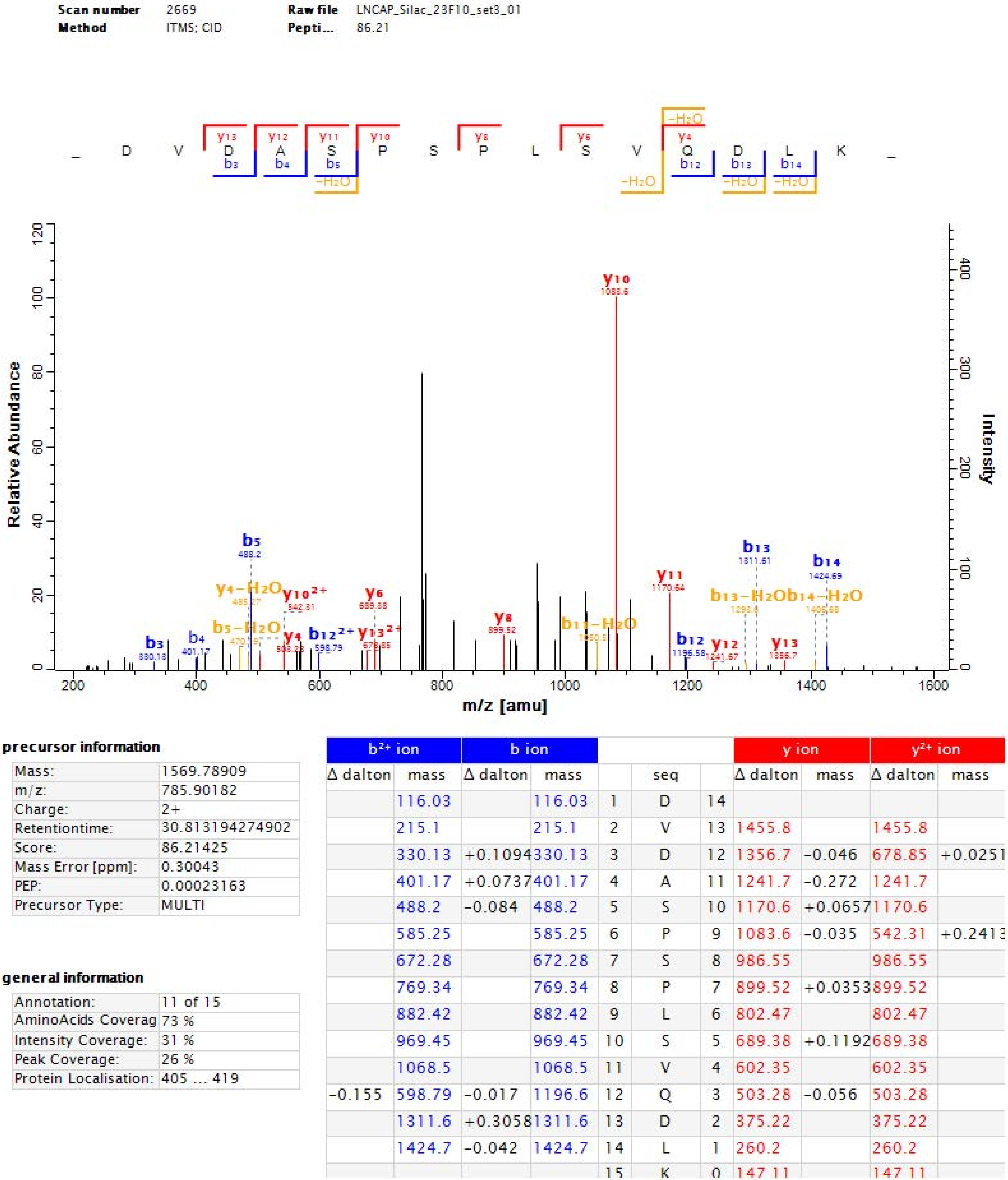
precursor information

Mass:	1962.00612
m/z:	982.01034
Charge:	2+
Retentiontime:	30.642309188842
Score:	111.769
Mass Error [ppm]:	0.15532
PEP:	9.0244E-09
Precursor Type:	MULTI

general information

Annotation:	14 of 20
AminoAcids Coverag	70 %
Intensity Coverage:	54 %
Peak Coverage:	27 %
Protein Localisation:	32 ... 51

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	19				
	229.12		229.12	2	E	18	1863.9		1863.9	
	342.2		342.2	3	L	17	1734.9	-0.389	867.95	-0.145
	439.26		439.26	4	P	16	1621.8	+0.0415	811.41	+0.2206
	496.28		496.28	5	G	15	1524.8		1524.8	
	597.32		597.32	6	T	14	1467.7		1467.7	
	668.36	+0.1723	668.36	7	A	13	1366.7	+0.0364	1366.7	
	767.43		767.43	8	V	12	1295.7	-0.03	1295.7	
	864.48		864.48	9	P	11	1196.6	-0.023	1196.6	
	951.51		951.51	10	S	10	1099.5		1099.5	
	1050.6	-0.1	1050.6	11	V	9	1012.5		1012.5	
	1147.6		1147.6	12	P	8	913.44	+0.0005	913.44	
	1276.7		1276.7	13	E	7	816.38		408.7	-0.343
	1391.7		1391.7	14	D	6	687.34		344.17	-0.034
-0.429	731.87		1462.7	15	A	5	572.32	-0.034	572.32	
-0.001	767.39	-0.073	1533.8	16	A	4	501.28	+0.1972	501.28	
	1630.8		1630.8	17	P	3	430.24	-0.003	430.24	
	1701.9	+0.0586	1701.9	18	A	2	333.19		333.19	
	1788.9	+0.0882	1788.9	19	S	1	262.15		262.15	
				20	R	0	175.12		175.12	



Scan number	2669	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	86.21

precursor information

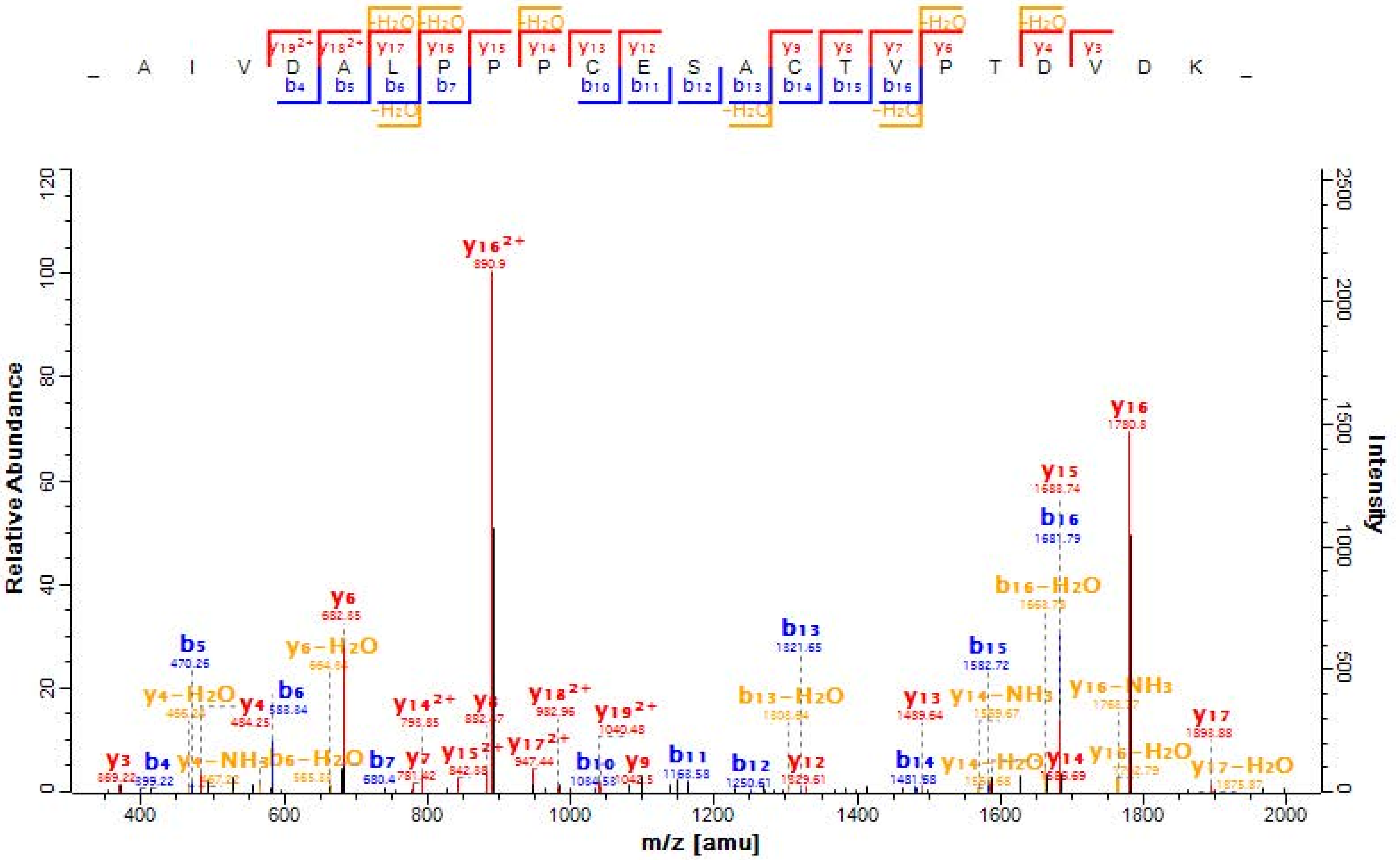
Mass:	1569.78909
m/z:	785.90182
Charge:	2+
Retentiontime:	30.813194274902
Score:	86.21425
Mass Error [ppm]:	0.30043
PEP:	0.00023163
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	31 %
Peak Coverage:	26 %
Protein Localisation:	405 … 419

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	14				
	215.1		215.1	2	V	13	1455.8		1455.8	
	330.13	+0.1094	330.13	3	D	12	1356.7	-0.046	678.85	+0.0251
	401.17	+0.0737	401.17	4	A	11	1241.7	-0.272	1241.7	
	488.2	-0.084	488.2	5	S	10	1170.6	+0.0657	1170.6	
	585.25		585.25	6	P	9	1083.6	-0.035	542.31	+0.2413
	672.28		672.28	7	S	8	986.55		986.55	
	769.34		769.34	8	P	7	899.52	+0.0353	899.52	
	882.42		882.42	9	L	6	802.47		802.47	
	969.45		969.45	10	S	5	689.38	+0.1192	689.38	
	1068.5		1068.5	11	V	4	602.35		602.35	
-0.155	598.79	-0.017	1196.6	12	Q	3	503.28	-0.056	503.28	
	1311.6	+0.3058	1311.6	13	D	2	375.22		375.22	
	1424.7	-0.042	1424.7	14	L	1	260.2		260.2	
				15	K	0	147.11		147.11	

Scan number	2811	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	206.64



precursor information

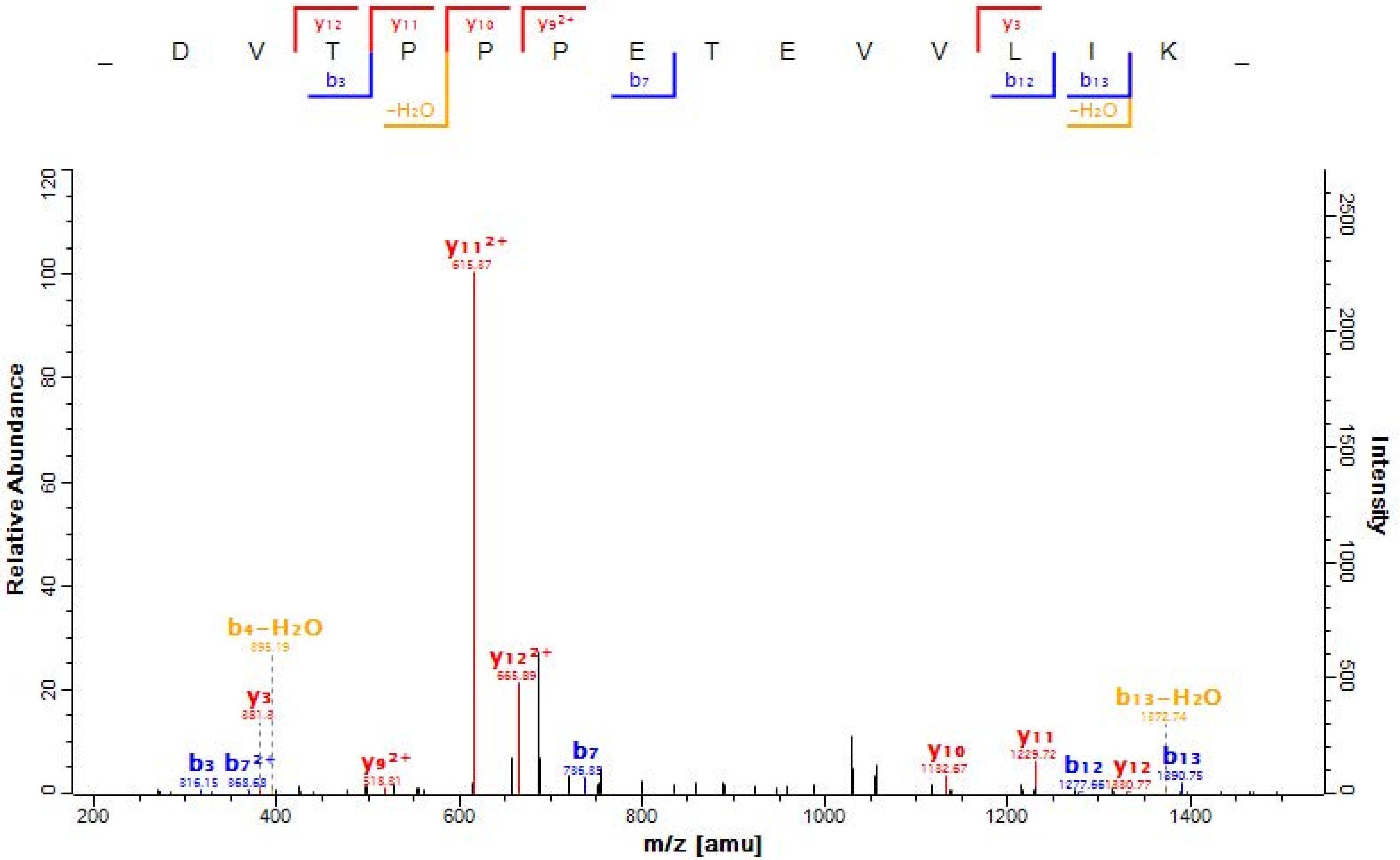
Mass:	2354.1134
m/z:	1178.06398
Charge:	2+
Retentiontime:	32.022045135498
Score:	206.6444
Mass Error [ppm]:	0.00075178
PEP:	2.0971E-61
Precursor Type:	MULTI

general information

Annotation:	16 of 22
AminoAcids Coverag	73 %
Intensity Coverage:	59 %
Peak Coverage:	40 %
Protein Localisation:	261 … 282

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	21				
	185.1285	2	I	20	2292.098		2292.098	
	284.1969	3	V	19	2179.014		2179.014	
+0.170659	399.2238	4	D	18	2079.945		1040.476	+0.166543
-0.02124	470.2609	5	A	17	1964.918		982.9628	-0.26579
-0.03224	583.345	6	L	16	1893.881	+0.385987	947.4443	+0.171472
-0.04711	680.3978	7	P	15	1780.797	-0.04264	890.9022	-0.01745
	777.4505	8	P	14	1683.744	+0.014514	842.3758	+0.184832
	874.5033	9	P	13	1586.692	-0.09593	793.8495	+0.058016
-0.04089	1034.534	10	C	12	1489.639	-0.00764	1489.639	
-0.09154	1163.577	11	E	11	1329.608	+0.226862	1329.608	
+0.259003	1250.609	12	S	10	1200.566		1200.566	
-0.23136	1321.646	13	A	9	1113.534		1113.534	
-0.15959	1481.676	14	C	8	1042.496	+0.058934	1042.496	
-0.04711	1582.724	15	T	7	882.4658	-0.18349	882.4658	
-0.16264	1681.792	16	V	6	781.4182	-0.3592	781.4182	
	1778.845	17	P	5	682.3497	+0.105577	682.3497	
	1879.893	18	T	4	585.297		585.297	
	1994.92	19	D	3	484.2493	+0.106135	484.2493	
	2093.988	20	V	2	369.2224	+0.055014	369.2224	
	2209.015	21	D	1	270.1539		270.1539	
		22	K	0	155.127		155.127	

Scan number	3287	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	54.52



precursor information

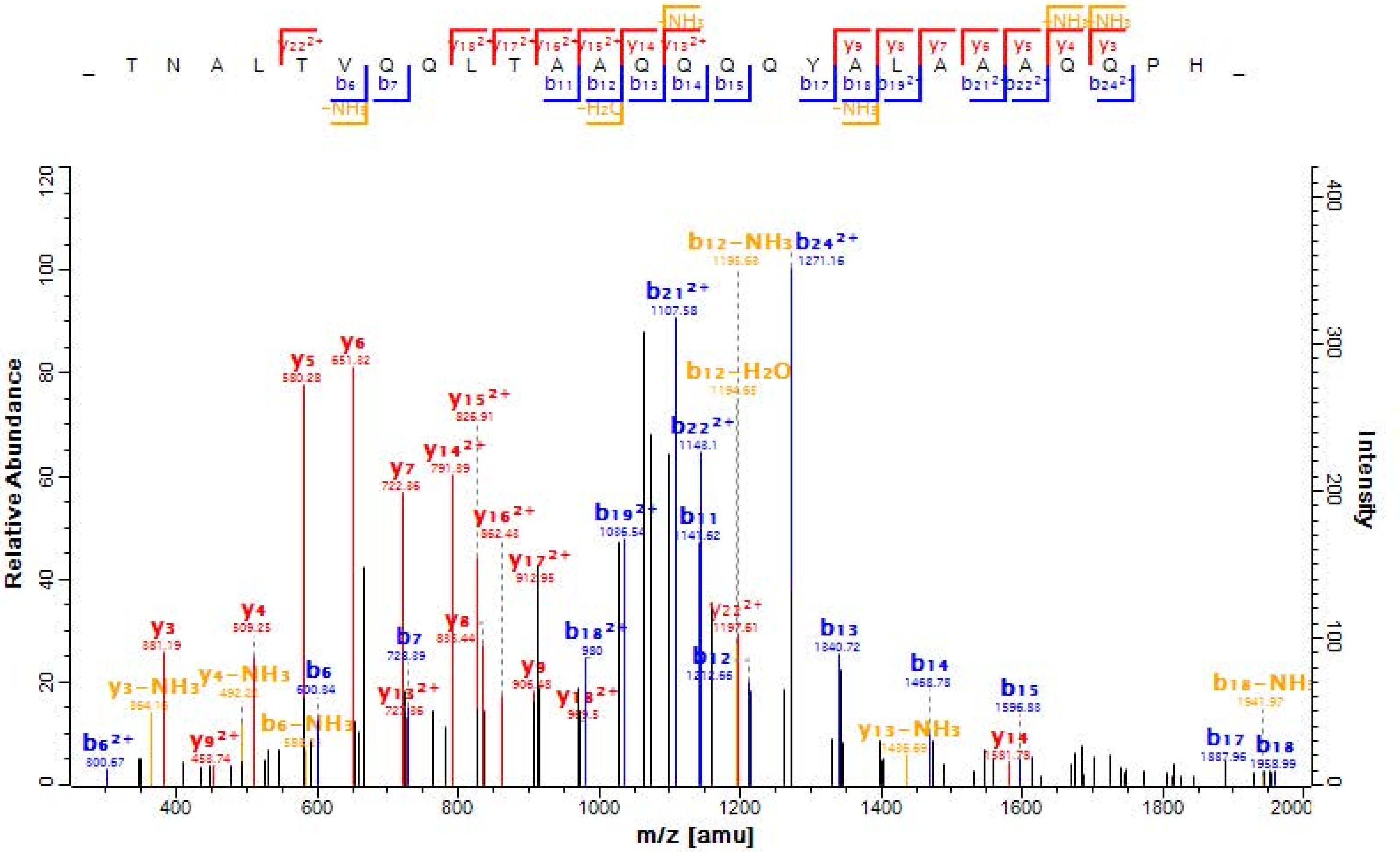
Mass:	1535.84473
m/z:	768.92964
Charge:	2+
Retentiontime:	36.102569580078
Score:	54.52445
Mass Error [ppm]:	0.034579
PEP:	0.011168
Precursor Type:	MULTI

general information

Annotation:	7 of 14
AminoAcids Coverag	50 %
Intensity Coverage:	51 %
Peak Coverage:	16 %
Protein Localisation:	519 ... 532

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	13				
	215.1		215.1	2	V	12	1429.8		1429.8	
	316.15	+0.1036	316.15	3	T	11	1330.8	+0.1152	665.89	-0.073
	413.2		413.2	4	P	10	1229.7	-0.025	615.37	+0.0477
	510.26		510.26	5	P	9	1132.7	+0.1026	1132.7	
	607.31		607.31	6	P	8	1035.6		518.31	+0.156
+0.2562	368.68	+0.3443	736.35	7	E	7	938.56		938.56	
	837.4		837.4	8	T	6	809.52		809.52	
	966.44		966.44	9	E	5	708.47		708.47	
	1065.5		1065.5	10	V	4	579.43		579.43	
	1164.6		1164.6	11	V	3	480.36		480.36	
	1277.7	-0.212	1277.7	12	L	2	381.3	+0.1588	381.3	
	1390.7	-0.034	1390.7	13	I	1	268.21		268.21	
				14	K	0	155.13		155.13	

Scan number	3386	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	172.24



precursor information

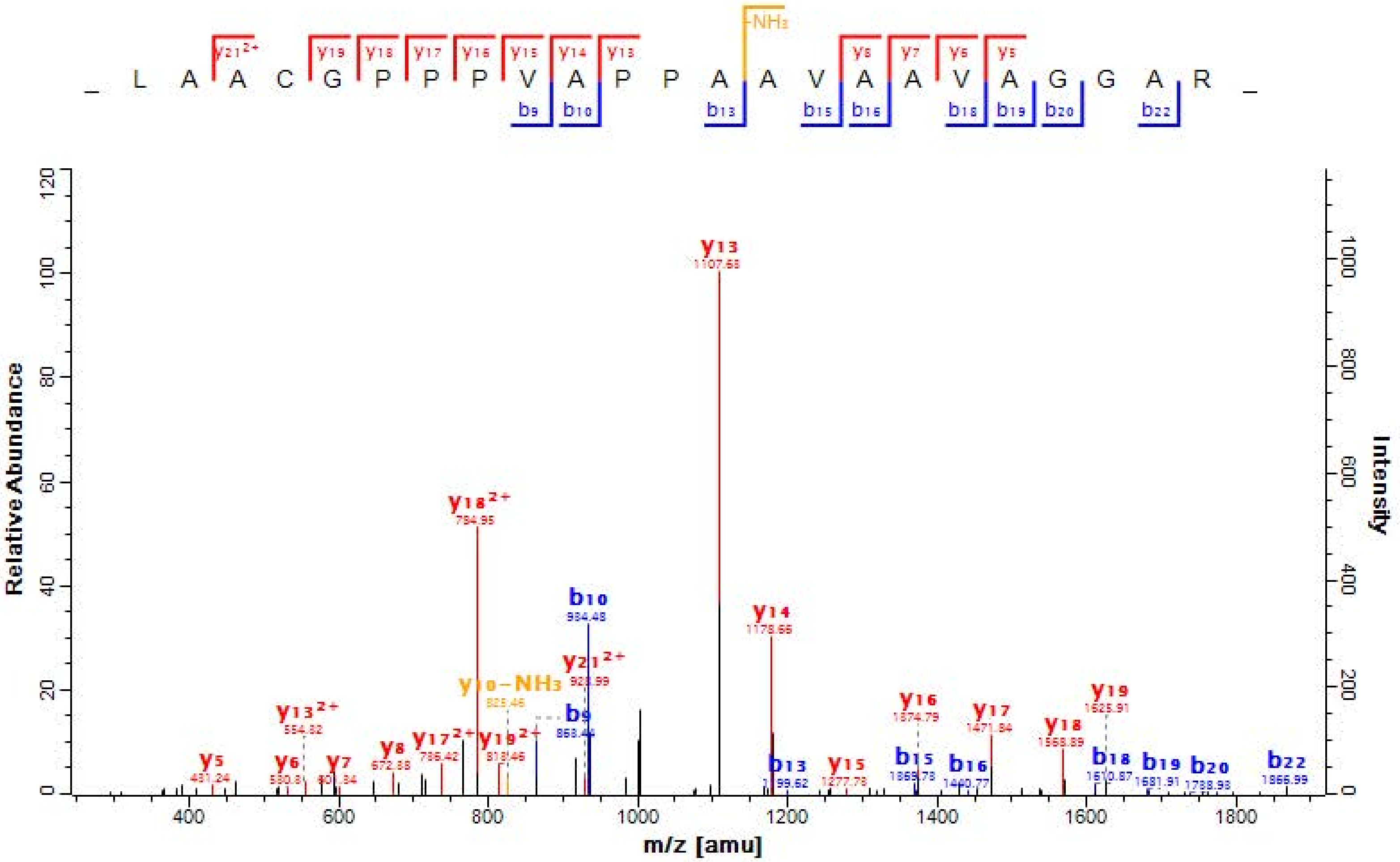
Mass:	2792.42236
m/z:	931.81473
Charge:	3+
Retentiontime:	36.843063354492
Score:	172.2399
Mass Error [ppm]:	0.64587
PEP:	5.5198E-27
Precursor Type:	ISO

general information

Annotation:	19 of 26
AminoAcids Coverag	73 %
Intensity Coverage:	54 %
Peak Coverage:	34 %
Protein Localisation:	268 ... 293

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	25				
	216.1		216.1	2	N	24	2692.4		2692.4	
	287.13		287.13	3	A	23	2578.3		2578.3	
	400.22		400.22	4	L	22	2507.3		2507.3	
	501.27		501.27	5	T	21	2394.2		1197.6	+0.4777
+0.2915	300.67	+0.003	600.34	6	V	20	2293.2		2293.2	
	728.39	-0.068	728.39	7	Q	19	2194.1		2194.1	
	856.45		856.45	8	Q	18	2066		2066	
	969.54		969.54	9	L	17	1938		969.5	-0.002
	1070.6		1070.6	10	T	16	1824.9		912.95	-0.158
	1141.6	-0.165	1141.6	11	A	15	1723.9		862.43	+0.133
	1212.7	+0.0025	1212.7	12	A	14	1652.8		826.91	+0.0439
	1340.7	-0.112	1340.7	13	Q	13	1581.8	-0.348	791.39	+0.2045
	1468.8	+0.4334	1468.8	14	Q	12	1453.7		727.36	-0.118
	1596.8	-0.171	1596.8	15	Q	11	1325.7		1325.7	
	1724.9		1724.9	16	Q	10	1197.6		1197.6	
	1888	-0.185	1888	17	Y	9	1069.5		1069.5	
+0.097	980	+0.4457	1959	18	A	8	906.48	-0.119	453.74	-0.268
+0.1251	1036.5		2072.1	19	L	7	835.44	+0.0843	835.44	
	2143.1		2143.1	20	A	6	722.36	+0.0976	722.36	
+0.176	1107.6		2214.2	21	A	5	651.32	-0.038	651.32	
+0.3868	1143.1		2285.2	22	A	4	580.28	+0.0866	580.28	
	2413.2		2413.2	23	Q	3	509.25	+0.0362	509.25	
+0.2529	1271.2		2541.3	24	Q	2	381.19	+0.1402	381.19	
	2638.4		2638.4	25	P	1	253.13		253.13	
				26	H	0	156.08		156.08	

Scan number	3465	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	102.69



precursor information

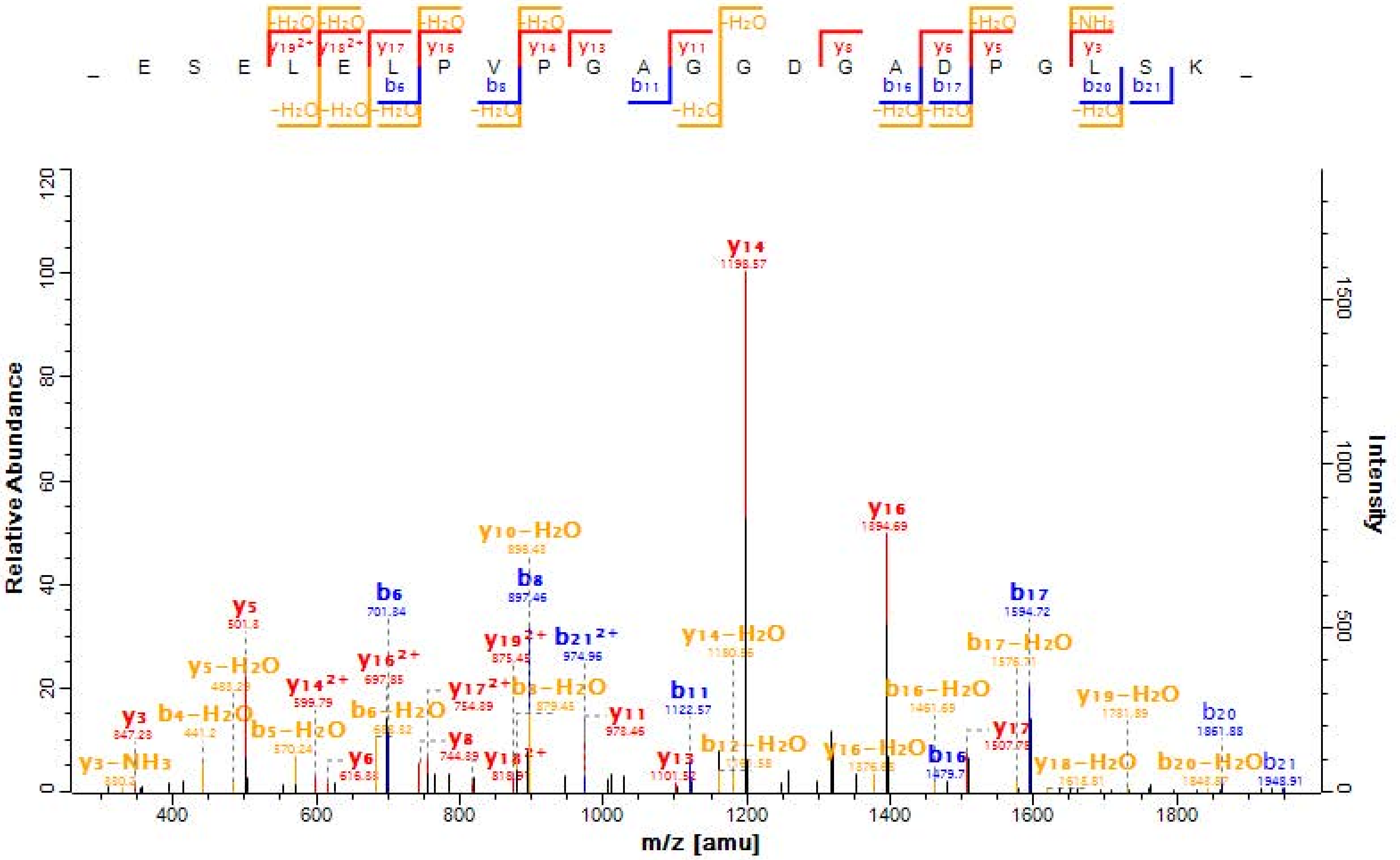
Mass:	2040.09185
m/z:	1021.0532
Charge:	2+
Retentiontime:	37.550273895263
Score:	102.6893
Mass Error [ppm]:	-0.98494
PEP:	6.7029E-08
Precursor Type:	MULTI

general information

Annotation:	17 of 23
AminoAcids Coverag	74 %
Intensity Coverage:	58 %
Peak Coverage:	27 %
Protein Localisation:	53 ... 75

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	22				
	185.1285	2	A	21	1928.017		1928.017	
	256.1656	3	A	20	1856.98		928.9936	+0.159701
	416.1962	4	C	19	1785.943		1785.943	
	473.2177	5	G	18	1625.912	-0.11105	813.4597	+0.369363
	570.2704	6	P	17	1568.891	+0.035777	784.949	+0.301726
	667.3232	7	P	16	1471.838	-0.02657	736.4226	+0.082258
	764.376	8	P	15	1374.785	-0.13348	1374.785	
+0.025341	863.4444	9	V	14	1277.732	-0.1155	1277.732	
-0.02715	934.4815	10	A	13	1178.664	-0.02536	1178.664	
	1031.534	11	P	12	1107.627	-0.00839	554.3171	+0.201213
	1128.587	12	P	11	1010.574		1010.574	
-0.38391	1199.624	13	A	10	913.5214		913.5214	
	1270.661	14	A	9	842.4843		842.4843	
+0.002387	1369.73	15	V	8	771.4472		771.4472	
-0.30072	1440.767	16	A	7	672.3787	-0.00863	672.3787	
	1511.804	17	A	6	601.3416	+0.078348	601.3416	
-0.05114	1610.872	18	V	5	530.3045	+0.460982	530.3045	
+0.093628	1681.909	19	A	4	431.2361	+0.147621	431.2361	
+0.287618	1738.931	20	G	3	360.199		360.199	
	1795.952	21	G	2	303.1775		303.1775	
-0.15438	1866.989	22	A	1	246.1561		246.1561	
		23	R	0	175.119		175.119	

Scan number	3572	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	139.81



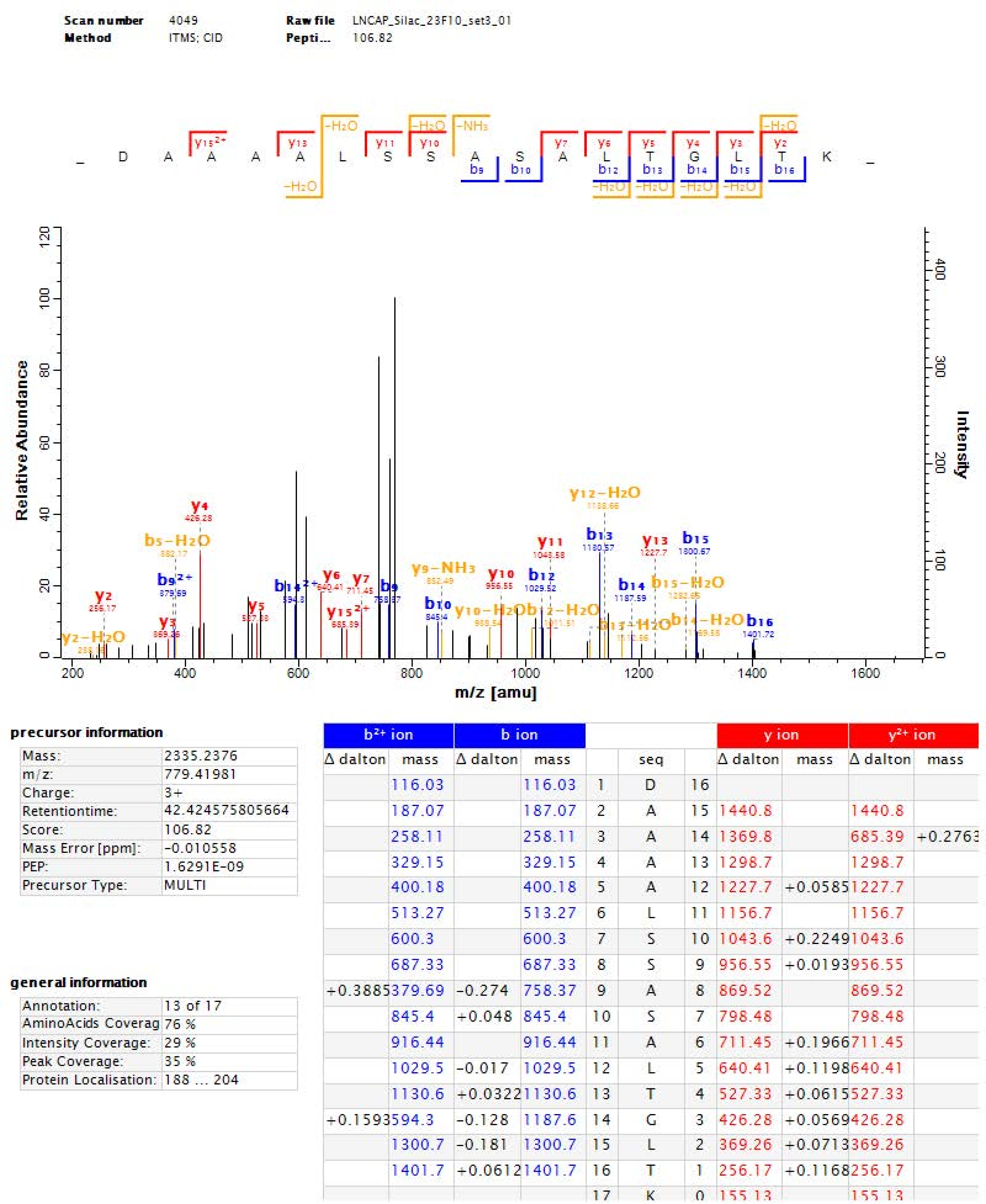
precursor information

Mass:	2094.01136
m/z:	1048.01296
Charge:	2+
Retentiontime:	38.418273925781
Score:	139.8125
Mass Error [ppm]:	-0.15692
PEP:	1.0723E-20
Precursor Type:	MULTI

general information

Annotation:	18 of 22
AminoAcids Coverag	82 %
Intensity Coverage:	57 %
Peak Coverage:	38 %
Protein Localisation:	25 ... 46

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	21				
	217.08		217.08	2	S	20	1966		1966	
	346.12		346.12	3	E	19	1878.9		1878.9	
	459.21		459.21	4	L	18	1749.9		875.45	+0.3834
	588.25		588.25	5	E	17	1636.8		818.91	-0.312
	701.34	+0.0461	701.34	6	L	16	1507.8	-0.192	754.39	-0.07
	798.39		798.39	7	P	15	1394.7	-0.124	697.85	-0.151
	897.46	-0.085	897.46	8	V	14	1297.6		1297.6	
	994.51		994.51	9	P	13	1198.6	-0.056	599.79	+0.0442
	1051.5		1051.5	10	G	12	1101.5	+0.097	1101.5	
	1122.6	-0.146	1122.6	11	A	11	1044.5		1044.5	
	1179.6		1179.6	12	G	10	973.46	+0.0119	973.46	
	1236.6		1236.6	13	G	9	916.44		916.44	
	1351.6		1351.6	14	D	8	859.42		859.42	
	1408.7		1408.7	15	G	7	744.39	-0.075	744.39	
	1479.7	-0.228	1479.7	16	A	6	687.37		687.37	
	1594.7	-0.168	1594.7	17	D	5	616.33	+0.1101	616.33	
	1691.8		1691.8	18	P	4	501.3	+0.0107	501.3	
	1748.8		1748.8	19	G	3	404.25		404.25	
	1861.9	-0.093	1861.9	20	L	2	347.23	+0.0144	347.23	
-0.472	974.96	-0.331	1948.9	21	S	1	234.14		234.14	
				22	K	0	147.11		147.11	



Scan number	4049	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	106.82

precursor information

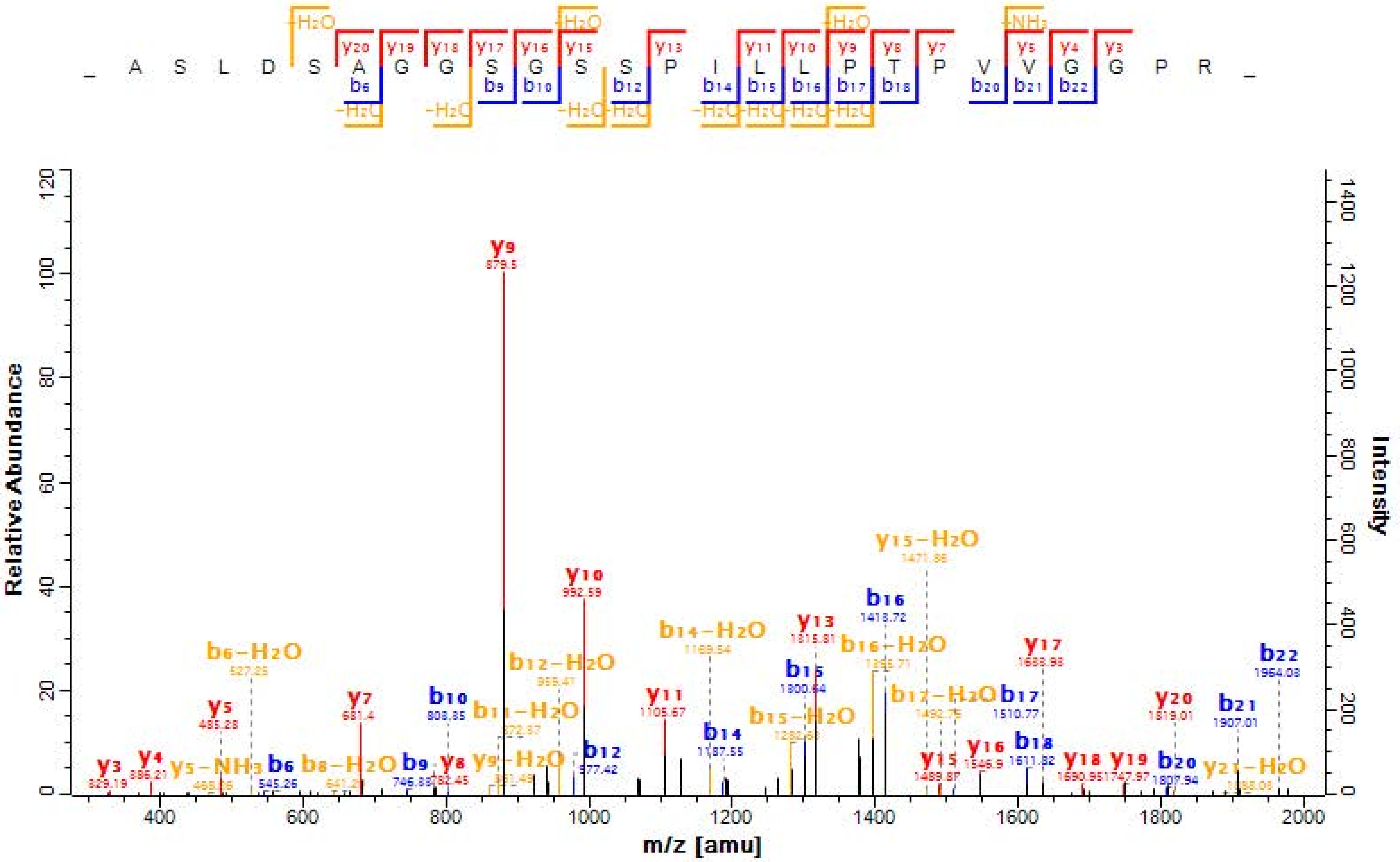
Mass:	2335.2376
m/z:	779.41981
Charge:	3+
Retentiontime:	42.424575805664
Score:	106.82
Mass Error [ppm]:	-0.010558
PEP:	1.6291E-09
Precursor Type:	MULTI

general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	29 %
Peak Coverage:	35 %
Protein Localisation:	188 ... 204

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	16				
	187.07		187.07	2	A	15	1440.8		1440.8	
	258.11		258.11	3	A	14	1369.8		685.39	+0.2763
	329.15		329.15	4	A	13	1298.7		1298.7	
	400.18		400.18	5	A	12	1227.7	+0.0585	1227.7	
	513.27		513.27	6	L	11	1156.7		1156.7	
	600.3		600.3	7	S	10	1043.6	+0.2249	1043.6	
	687.33		687.33	8	S	9	956.55	+0.0193	956.55	
+0.3885	379.69	-0.274	758.37	9	A	8	869.52		869.52	
	845.4	+0.048	845.4	10	S	7	798.48		798.48	
	916.44		916.44	11	A	6	711.45	+0.1966	711.45	
	1029.5	-0.017	1029.5	12	L	5	640.41	+0.1198	640.41	
	1130.6	+0.0322	1130.6	13	T	4	527.33	+0.0615	527.33	
+0.1593	594.3	-0.128	1187.6	14	G	3	426.28	+0.0569	426.28	
	1300.7	-0.181	1300.7	15	L	2	369.26	+0.0713	369.26	
	1401.7	+0.0612	1401.7	16	T	1	256.17	+0.1168	256.17	
				17	K	0	155.13		155.13	

Scan number	4243	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	165.13



precursor information

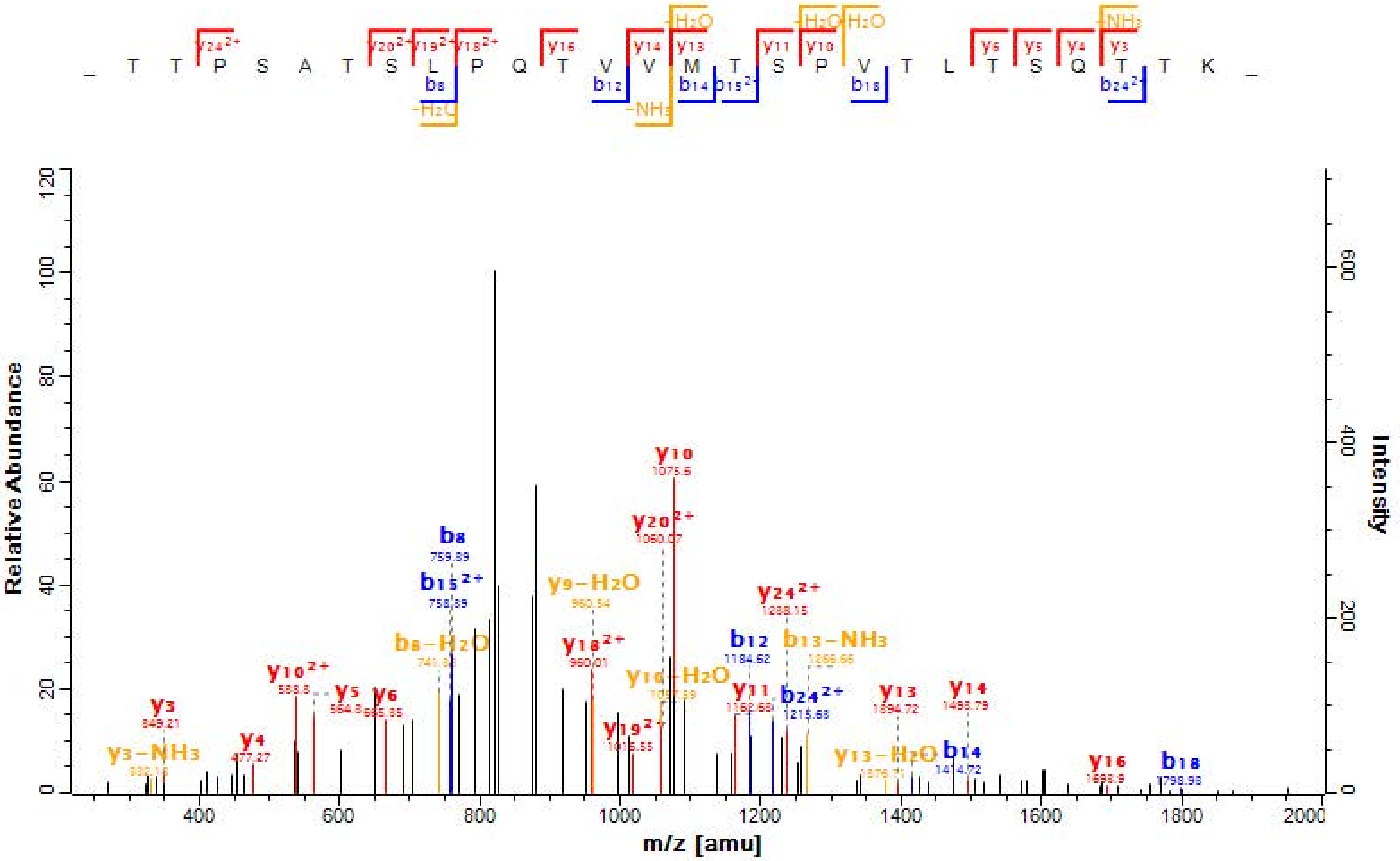
Mass:	2291.21166
m/z:	1146.61311
Charge:	2+
Retentiontime:	44.072620391845
Score:	165.1253
Mass Error [ppm]:	-0.20392
PEP:	3.4462E-32
Precursor Type:	MULTI

general information

Annotation:	19 of 25
AminoAcids Coverag	76 %
Intensity Coverage:	59 %
Peak Coverage:	38 %
Protein Localisation:	235 ... 259

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	72.044390254	1	A	24		
	159.076418664	2	S	23	2221.1822873	
	272.160482645	3	L	22	2134.15025889	
	387.187425677	4	D	21	2021.06619491	
	474.219454087	5	S	20	1906.03925188	
+0.0377436	545.256567874	6	A	19	1819.00722347	-0.4448455
	602.278031598	7	G	18	1747.97010968	-0.2194993
	659.299495322	8	G	17	1690.94864596	-0.0371469
+0.0780222	746.331523732	9	S	16	1633.92718224	-0.1575289
-0.1267912	803.352987455	10	G	15	1546.89515383	-0.0630005
	890.385015865	11	S	14	1489.8736901	-0.0569176
-0.0283724	977.417044275	12	S	13	1402.84166169	
	1074.46980813	13	P	12	1315.80963328	-0.0106831
-0.0648584	1187.55387211	14	I	11	1218.75686943	
-0.0803189	1300.63793609	15	L	10	1105.67280545	-0.0429226
-0.1615753	1413.72200007	16	L	9	992.588741471	-0.0329553
-0.1678303	1510.77476392	17	P	8	879.504677491	+0.0381692
-0.0931943	1611.82244239	18	T	7	782.451913639	+0.0615751
	1708.87520625	19	P	6	681.404235165	+0.0239875
-0.0820479	1807.94362016	20	V	5	584.351471313	
-0.1309306	1907.01203408	21	V	4	485.283057396	+0.1637199
+0.1338606	1964.0334978	22	G	3	386.21464348	+0.1621265
	2021.05496153	23	G	2	329.193179757	+0.1557887
	2118.10772538	24	P	1	272.171716033	
		25	R	0	175.118952181	

Scan number	4280	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	86.18



precursor information

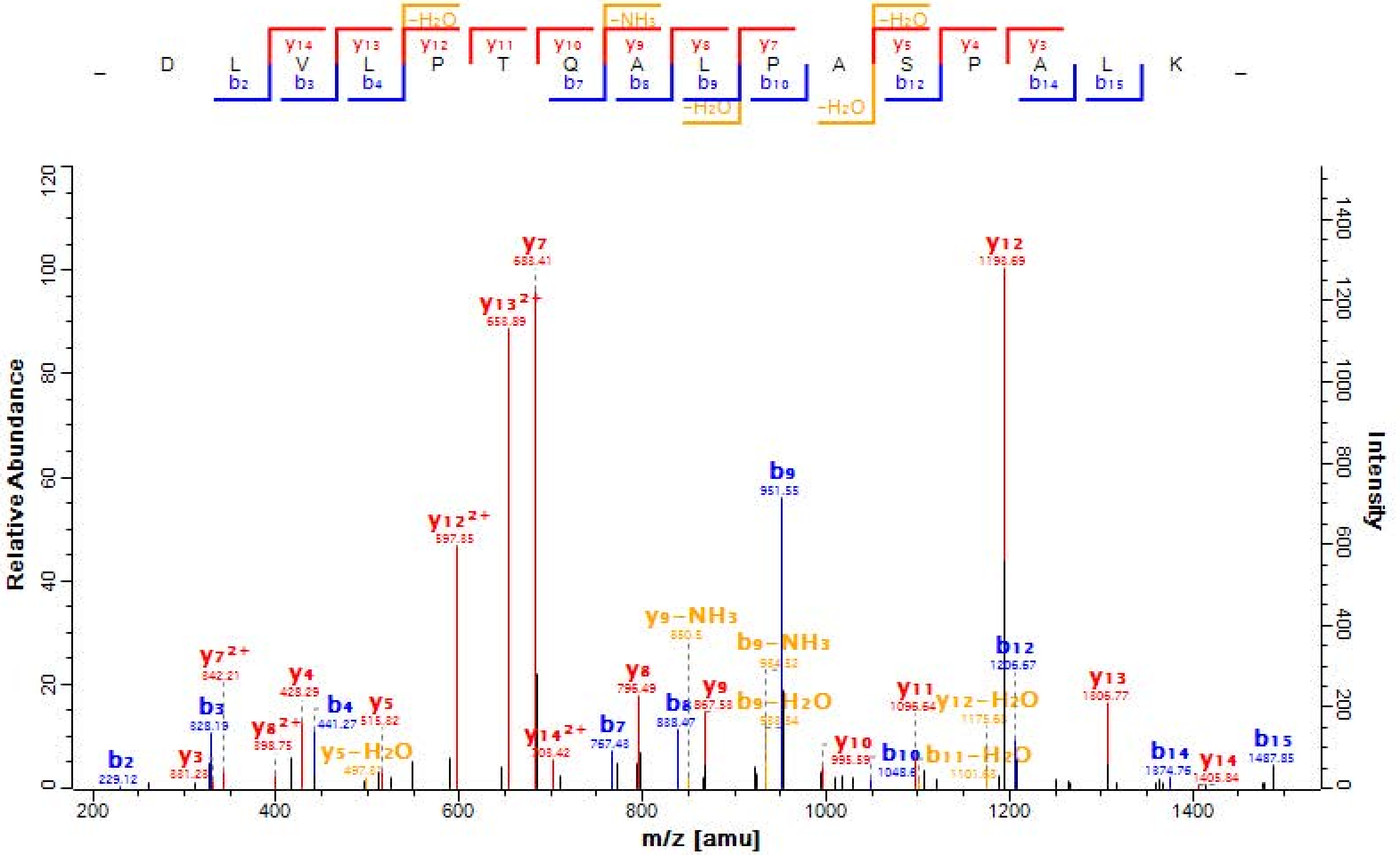
Mass:	2676.38721
m/z:	893.13635
Charge:	3+
Retentiontime:	44.411331176757
Score:	86.18197
Mass Error [ppm]:	-0.72944
PEP:	9.2533E-09
Precursor Type:	MULTI

general information

Annotation:	17 of 26
AminoAcids Coverag	65 %
Intensity Coverage:	32 %
Peak Coverage:	28 %
Protein Localisation:	183 ... 208

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	25				
	203.1		203.1	2	T	24	2576.3		2576.3	
	300.16		300.16	3	P	23	2475.3		1238.2	+0.272
	387.19		387.19	4	S	22	2378.2		2378.2	
	458.22		458.22	5	A	21	2291.2		2291.2	
	559.27		559.27	6	T	20	2220.2		2220.2	
	646.3		646.3	7	S	19	2119.1		1060.1	-0.234
	759.39	-0.025	759.39	8	L	18	2032.1		1016.6	+0.259
	856.44		856.44	9	P	17	1919		960.01	-0.097
	984.5		984.5	10	Q	16	1822		1822	
	1085.5		1085.5	11	T	15	1693.9	-0.148	1693.9	
	1184.6	+0.1487	1184.6	12	V	14	1592.9		1592.9	
	1283.7		1283.7	13	V	13	1493.8	+0.4995	1493.8	
	1414.7	+0.0376	1414.7	14	M	12	1394.7	+0.2999	1394.7	
-0.145	758.39		1515.8	15	T	11	1263.7		1263.7	
	1602.8		1602.8	16	S	10	1162.6	-0.062	1162.6	
	1699.9		1699.9	17	P	9	1075.6	-0.005	538.3	+0.256
	1798.9	-0.053	1798.9	18	V	8	978.55		978.55	
	1900		1900	19	T	7	879.48		879.48	
	2013.1		2013.1	20	L	6	778.43		778.43	
	2114.1		2114.1	21	T	5	665.35	+0.0988	665.35	
	2201.1		2201.1	22	S	4	564.3	+0.0434	564.3	
	2329.2		2329.2	23	Q	3	477.27	+0.0814	477.27	
+0.0491	1215.6		2430.2	24	T	2	349.21	+0.0939	349.21	
	2531.3		2531.3	25	T	1	248.16		248.16	
				26	K	0	147.11		147.11	

Scan number	4377	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	169.64



precursor information

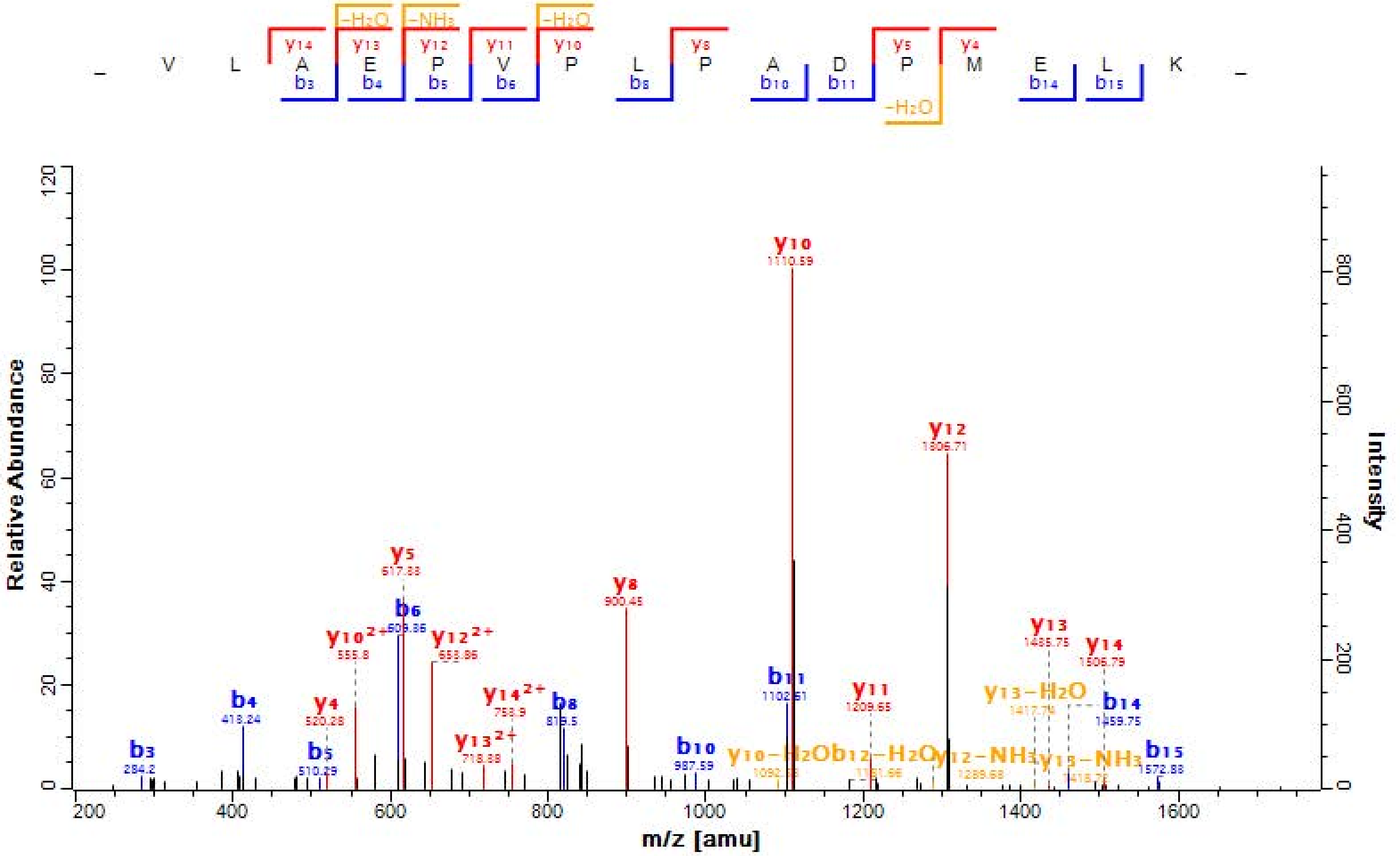
Mass:	1632.94611
m/z:	817.48033
Charge:	2+
Retentiontime:	45.258213043212
Score:	169.6427
Mass Error [ppm]:	0.64564
PEP:	2.6452E-22
Precursor Type:	MULTI

general information

Annotation:	14 of 16
AminoAcids Coverag	88 %
Intensity Coverage:	73 %
Peak Coverage:	41 %
Protein Localisation:	312 ... 327

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342	1	D	15				
+0.209567	229.1183	2	L	14	1518.925		1518.925	
+0.100046	328.1867	3	V	13	1405.841	-0.24623	703.4243	-0.03789
-0.00215	441.2708	4	L	12	1306.773	+0.030675	653.8901	+0.074932
	538.3235	5	P	11	1193.689	-0.09193	597.3481	+0.223592
	639.3712	6	T	10	1096.636	+0.080345	1096.636	
-0.21103	767.4298	7	Q	9	995.5884	-0.09457	995.5884	
-0.12345	838.4669	8	A	8	867.5298	+0.033464	867.5298	
-0.12182	951.551	9	L	7	796.4927	+0.125875	398.75	+0.457096
-0.08273	1048.604	10	P	6	683.4087	+0.015115	342.208	+0.123396
	1119.641	11	A	5	586.3559		586.3559	
-0.13551	1206.673	12	S	4	515.3188	+0.125196	515.3188	
	1303.726	13	P	3	428.2867	+0.052243	428.2867	
-0.22136	1374.763	14	A	2	331.234	-0.06552	331.234	
+0.103511	1487.847	15	L	1	260.1969		260.1969	
		16	K	0	147.1128		147.1128	

Scan number	4824	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	144.68



precursor information

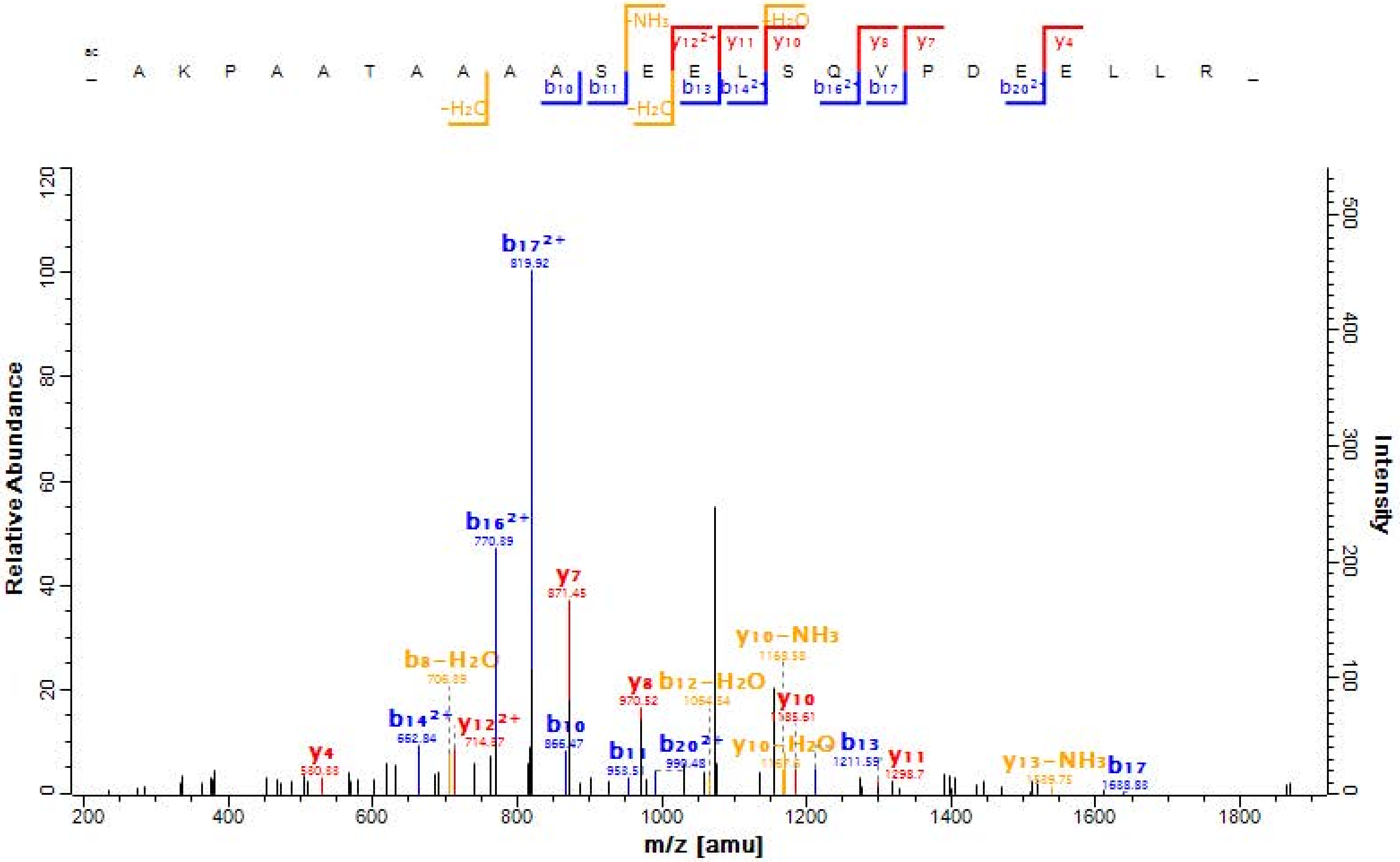
Mass:	1717.93327
m/z:	859.97391
Charge:	2+
Retentiontime:	48.895057678222
Score:	144.6781
Mass Error [ppm]:	0.47852
PEP:	5.4148E-10
Precursor Type:	ISO

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	59 %
Peak Coverage:	29 %
Protein Localisation:	98 ... 113

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	15				
	213.1598	2	L	14	1619.871		1619.871	
+0.09961	284.1969	3	A	13	1506.787	-0.15333	753.8973	+0.021075
-0.01943	413.2395	4	E	12	1435.75	+0.055413	718.3787	+0.190633
+0.120495	510.2922	5	P	11	1306.708	-0.07863	653.8574	+0.162918
-0.00822	609.3606	6	V	10	1209.655	+0.165296	1209.655	
	706.4134	7	P	9	1110.586	-0.08978	555.7968	+0.082089
-0.00449	819.4975	8	L	8	1013.534		1013.534	
	916.5502	9	P	7	900.4495	-0.02155	900.4495	
+0.043454	987.5873	10	A	6	803.3968		803.3968	
-0.11648	1102.614	11	D	5	732.3597		732.3597	
	1199.667	12	P	4	617.3327	+0.095452	617.3327	
	1330.708	13	M	3	520.2799	+0.065269	520.2799	
-0.21485	1459.75	14	E	2	389.2395		389.2395	
-0.07077	1572.834	15	L	1	260.1969		260.1969	
		16	K	0	147.1128		147.1128	

Scan number	4918	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	55.13



precursor information

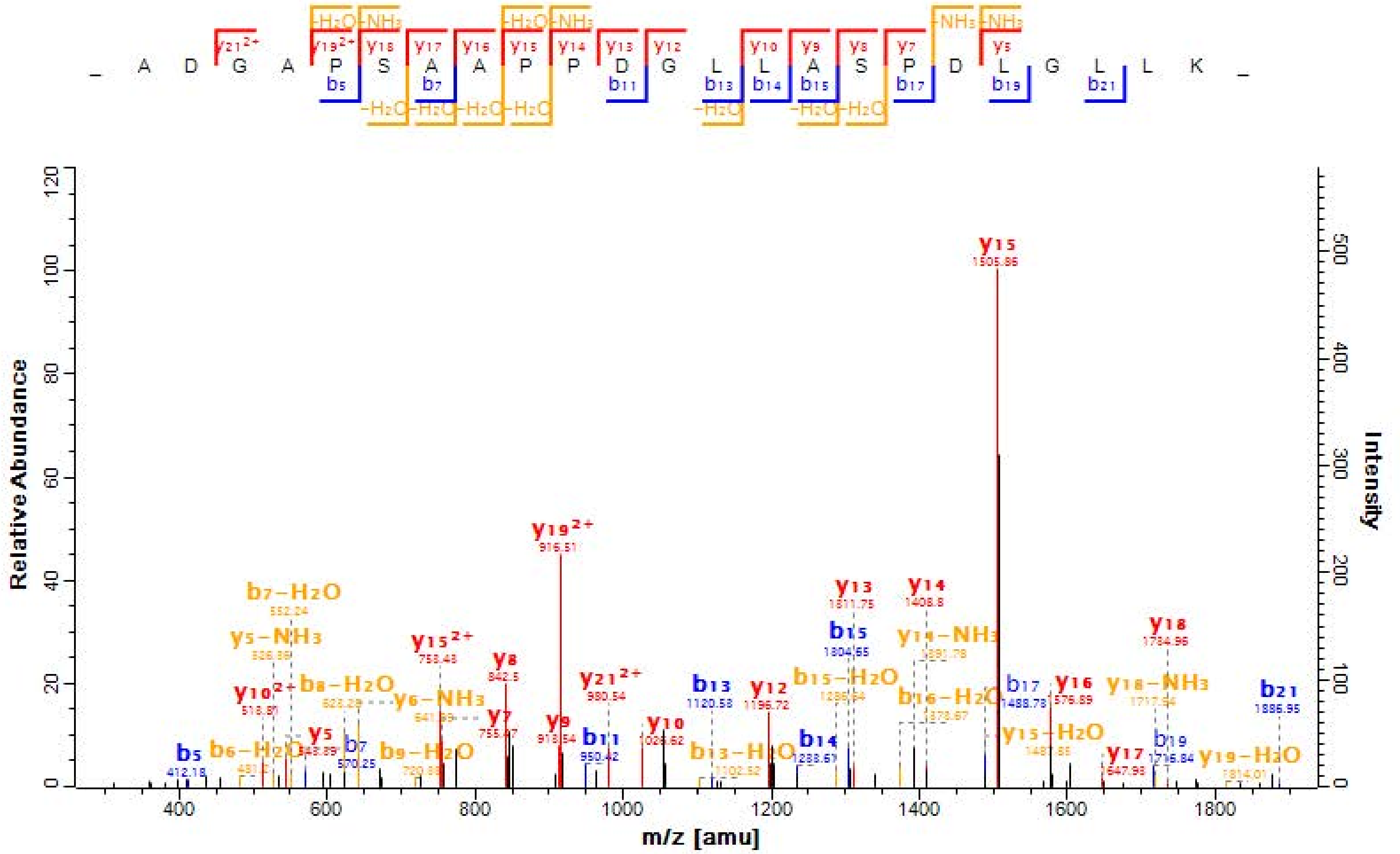
Mass:	2508.27128
m/z:	837.0977
Charge:	3+
Retentiontime:	49.723083496093
Score:	55.12832
Mass Error [ppm]:	0.2075
PEP:	0.00044905
Precursor Type:	MULTI

general information

Annotation:	12 of 24
AminoAcids Coverag	50 %
Intensity Coverage:	47 %
Peak Coverage:	24 %
Protein Localisation:	2 ... 25

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.05		114.05	1	A	23				
	242.15		242.15	2	K	22	2396.2		2396.2	
	339.2		339.2	3	P	21	2268.1		2268.1	
	410.24		410.24	4	A	20	2171.1		2171.1	
	481.28		481.28	5	A	19	2100		2100	
	582.32		582.32	6	T	18	2029		2029	
	653.36		653.36	7	A	17	1928		1928	
	724.4		724.4	8	A	16	1856.9		1856.9	
	795.44		795.44	9	A	15	1785.9		1785.9	
	866.47	+0.0102	866.47	10	A	14	1714.8		1714.8	
	953.51	+0.495	953.51	11	S	13	1643.8		1643.8	
	1082.5		1082.5	12	E	12	1556.8		1556.8	
	1211.6	+0.0017	1211.6	13	E	11	1427.7		714.37	-0.132
-0.042	662.84		1324.7	14	L	10	1298.7	-0.046	1298.7	
	1411.7		1411.7	15	S	9	1185.6	+0.0484	1185.6	
+0.215	770.39		1539.8	16	Q	8	1098.6		1098.6	
-0.012	819.92	-0.162	1638.8	17	V	7	970.52	+0.0138	970.52	
	1735.9		1735.9	18	P	6	871.45	+0.0596	871.45	
	1850.9		1850.9	19	D	5	774.4		774.4	
+0.3842	990.48		1980	20	E	4	659.37		659.37	
	2109		2109	21	E	3	530.33	+0.2856	530.33	
	2222.1		2222.1	22	L	2	401.29		401.29	
	2335.2		2335.2	23	L	1	288.2		288.2	
				24	R	0	175.12		175.12	

Scan number	5394	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	162.32



precursor information

Mass:	2145.13257
m/z:	1073.57356
Charge:	2+
Retentiontime:	53.860843658447
Score:	162.3238
Mass Error [ppm]:	0.38337
PEP:	3.4155E-29
Precursor Type:	MULTI

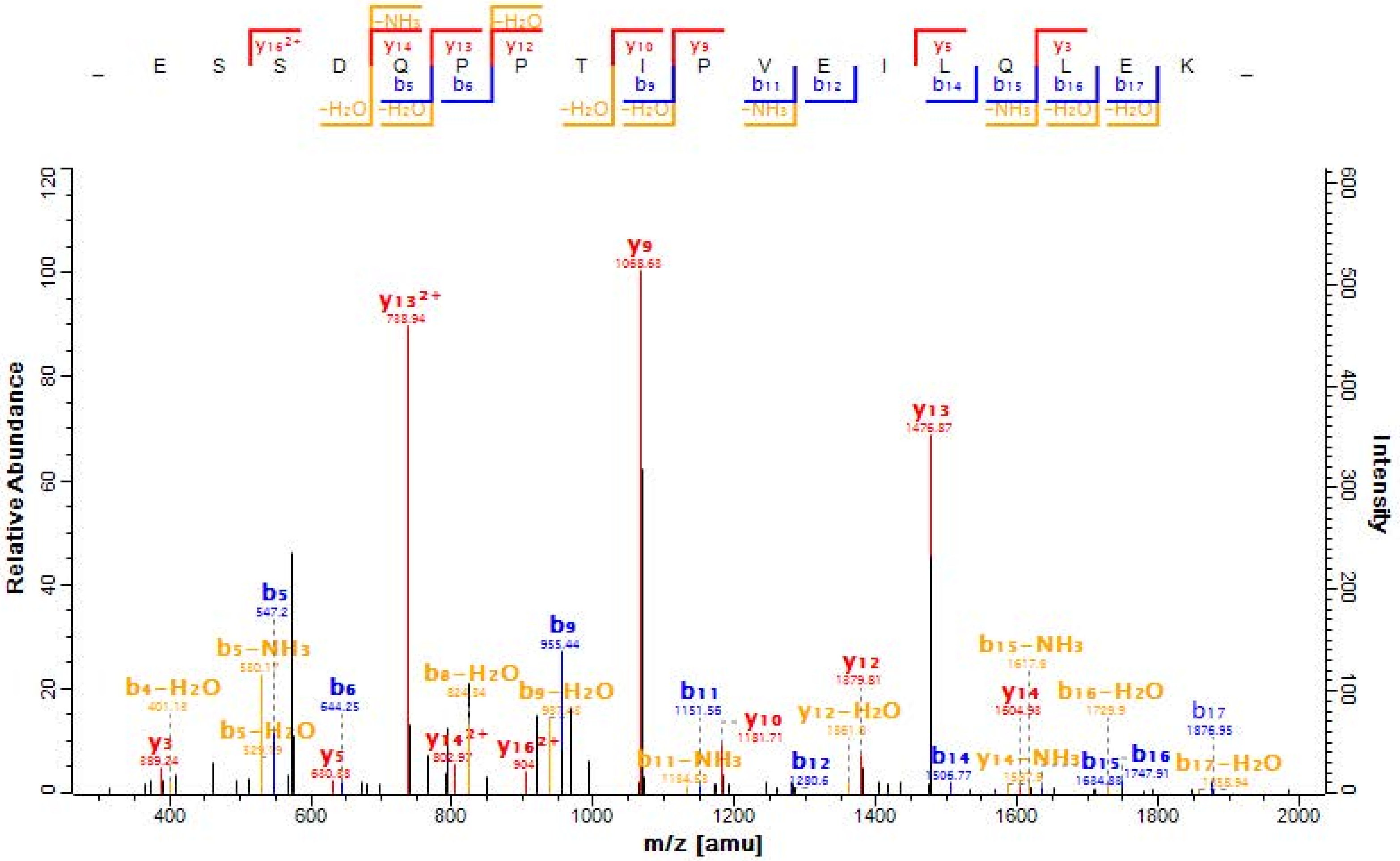
general information

Annotation:	17 of 23
AminoAcids Coverag	74 %
Intensity Coverage:	58 %
Peak Coverage:	40 %
Protein Localisation:	75 ... 97

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	22				
	187.0713	2	D	21	2075.102		2075.102	
	244.0928	3	G	20	1960.075		980.5411	+0.369522
	315.1299	4	A	19	1903.054		1903.054	
+0.119175	412.1827	5	P	18	1832.016		916.5118	+0.211921
	499.2147	6	S	17	1734.964	-0.14124	1734.964	
+0.042739	570.2518	7	A	16	1647.932	-0.15328	1647.932	
	641.2889	8	A	15	1576.894	-0.14192	1576.894	
	738.3417	9	P	14	1505.857	-0.10627	753.4323	+0.170337
	835.3945	10	P	13	1408.805	+0.009724	1408.805	
-0.12453	950.4214	11	D	12	1311.752	-0.00929	1311.752	
	1007.443	12	G	11	1196.725	+0.068312	1196.725	
+0.212817	1120.527	13	L	10	1139.703		1139.703	
-0.09244	1233.611	14	L	9	1026.619	+0.049572	513.8133	-0.42014
-0.09354	1304.648	15	A	8	913.5353	+0.030121	913.5353	
	1391.68	16	S	7	842.4982	-0.04446	842.4982	
+0.046886	1488.733	17	P	6	755.4662	+0.018636	755.4662	
	1603.76	18	D	5	658.4134		658.4134	
-0.15909	1716.844	19	L	4	543.3865	+0.109024	543.3865	
	1773.865	20	G	3	430.3024		430.3024	
+0.061919	1886.949	21	L	2	373.2809		373.2809	
	2000.033	22	L	1	260.1969		260.1969	
		23	K	0	147.1128		147.1128	

Scan number	5466
Method	ITMS; CID

Raw file	LNCAP_Silac_23F10_set3_01
Pepti...	126.25



precursor information

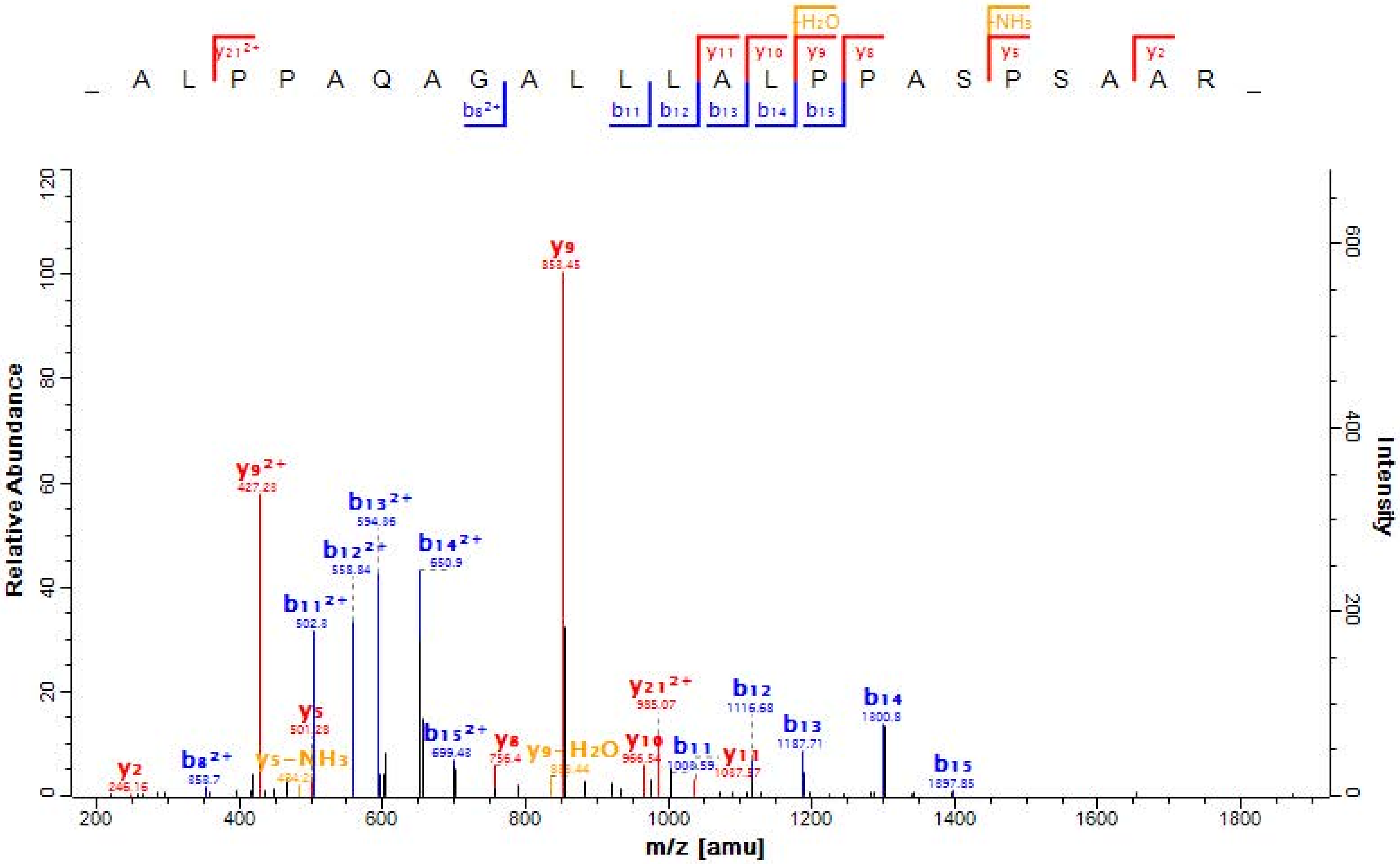
Mass:	2022.05187
m/z:	1012.03321
Charge:	2+
Retentiontime:	54.518241882324
Score:	126.2474
Mass Error [ppm]:	-0.11534
PEP:	1.8362E-12
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	51 %
Peak Coverage:	32 %
Protein Localisation:	164 ... 181

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	17				
	217.0819	2	S	16	1894.017		1894.017	
	304.1139	3	S	15	1806.985		903.996	+0.361772
	419.1409	4	D	14	1719.953		1719.953	
+0.06569	547.1994	5	Q	13	1604.926	+0.015621	802.9665	+0.29116
+0.216112	644.2522	6	P	12	1476.867	-0.1017	738.9372	+0.203993
	741.305	7	P	11	1379.814	-0.17809	1379.814	
	842.3527	8	T	10	1282.762		1282.762	
-0.0893	955.4367	9	I	9	1181.714	-0.04628	1181.714	
	1052.489	10	P	8	1068.63	-0.02557	1068.63	
-0.06522	1151.558	11	V	7	971.5772		971.5772	
-0.2405	1280.6	12	E	6	872.5088		872.5088	
	1393.685	13	I	5	743.4662		743.4662	
+0.055725	1506.769	14	L	4	630.3821	+0.117592	630.3821	
-0.14677	1634.827	15	Q	3	517.298		517.298	
+0.063108	1747.911	16	L	2	389.2395	+0.047343	389.2395	
-0.08093	1876.954	17	E	1	276.1554		276.1554	
		18	K	0	147.1128		147.1128	

Scan number	5511	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	90.72



precursor information

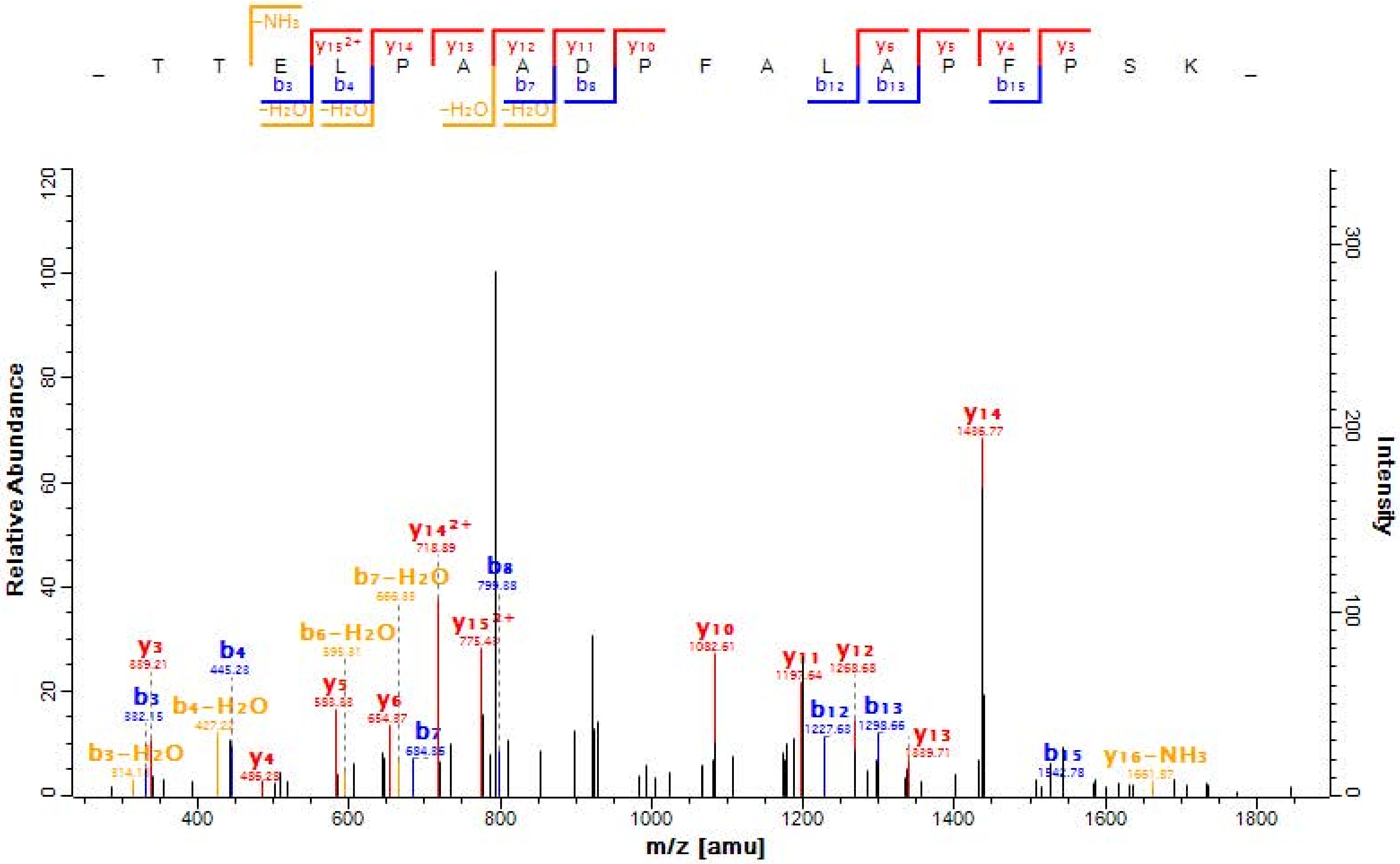
Mass:	2152.23644
m/z:	718.41942
Charge:	3+
Retentiontime:	54.905693054199
Score:	90.7179
Mass Error [ppm]:	-0.17781
PEP:	1.7385E-06
Precursor Type:	MULTI

general information

Annotation:	10 of 23
AminoAcids Coverag	43 %
Intensity Coverage:	69 %
Peak Coverage:	30 %
Protein Localisation:	449 ... 471

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	22				
	185.13		185.13	2	L	21	2082.2		2082.2	
	282.18		282.18	3	P	20	1969.1		985.07	+0.3627
	379.23		379.23	4	P	19	1872.1		1872.1	
	450.27		450.27	5	A	18	1775		1775	
	578.33		578.33	6	Q	17	1704		1704	
	649.37		649.37	7	A	16	1575.9		1575.9	
-0.425	353.7		706.39	8	G	15	1504.9		1504.9	
	777.43		777.43	9	A	14	1447.9		1447.9	
	890.51		890.51	10	L	13	1376.8		1376.8	
+0.1897	502.3	+0.1262	1003.6	11	L	12	1263.7		1263.7	
+0.0998	558.84	-0.024	1116.7	12	L	11	1150.7		1150.7	
+0.1077	594.36	-0.19	1187.7	13	A	10	1037.6	-0.141	1037.6	
-0.117	650.9	-0.128	1300.8	14	L	9	966.54	+0.0563	966.54	
+0.0589	699.43	-0.398	1397.9	15	P	8	853.45	+0.0036	427.23	+0.1384
	1494.9		1494.9	16	P	7	756.4	+0.2324	756.4	
	1565.9		1565.9	17	A	6	659.35		659.35	
	1653		1653	18	S	5	588.31		588.31	
	1750		1750	19	P	4	501.28	+0.0693	501.28	
	1837.1		1837.1	20	S	3	404.23		404.23	
	1908.1		1908.1	21	A	2	317.19		317.19	
	1979.1		1979.1	22	A	1	246.16	+0.0739	246.16	
				23	R	0	175.12		175.12	

Scan number	5650	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	84.38



precursor information

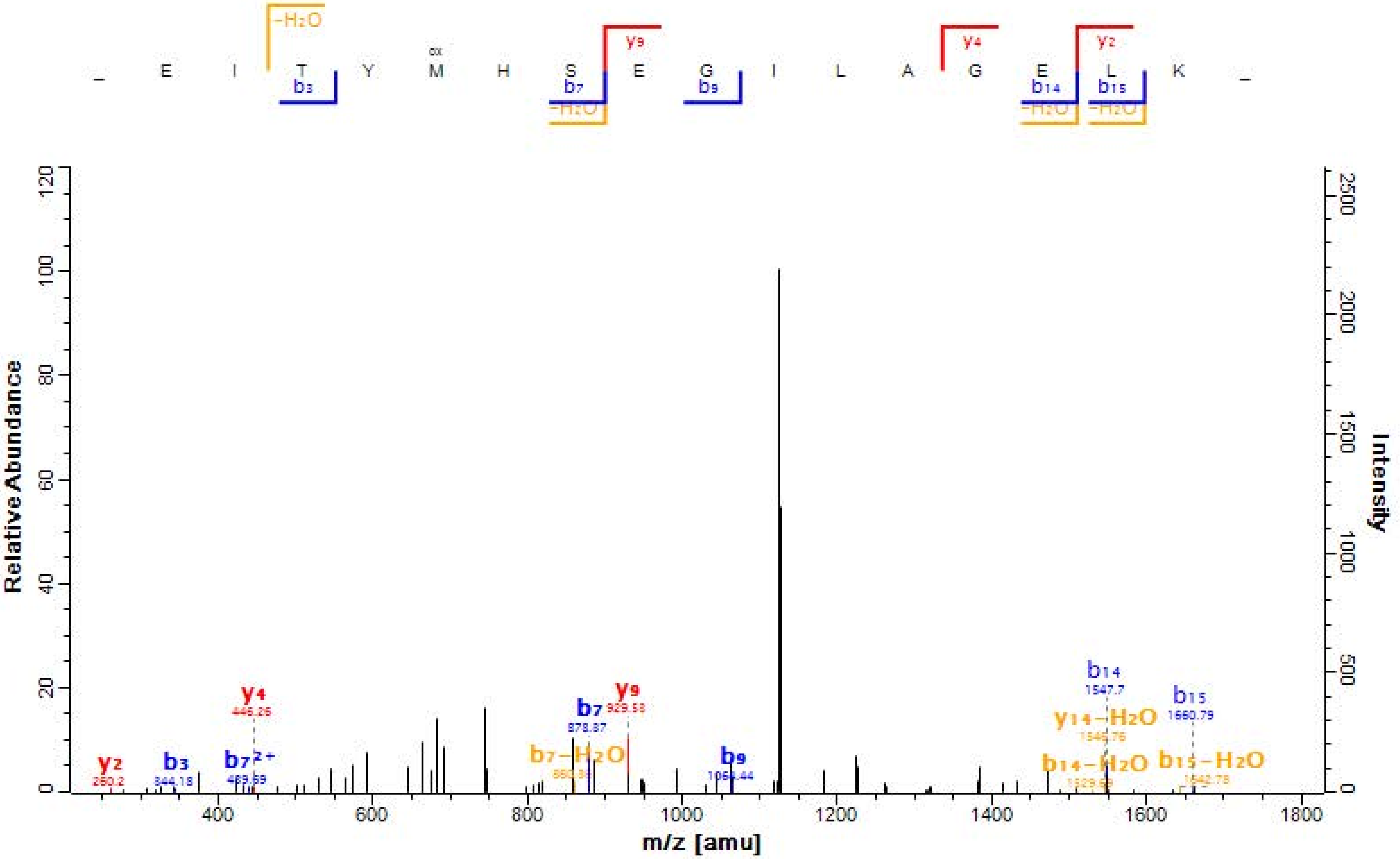
Mass:	1871.9672
m/z:	936.99087
Charge:	2+
Retentiontime:	56.219230651855
Score:	84.37524
Mass Error [ppm]:	0.14921
PEP:	8.4764E-05
Precursor Type:	MULTI

general information

Annotation:	12 of 18
AminoAcids Coverag	67 %
Intensity Coverage:	35 %
Peak Coverage:	25 %
Protein Localisation:	333 ... 350

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055	1	T	17				
	203.1026	2	T	16	1779.941		1779.941	
+0.211982	332.1452	3	E	15	1678.893		1678.893	
+0.054096	445.2293	4	L	14	1549.85		775.4289	+0.129796
	542.2821	5	P	13	1436.766	-0.05947	718.8868	+0.369094
	613.3192	6	A	12	1339.714	+0.111949	1339.714	
-0.10054	684.3563	7	A	11	1268.676	+0.018569	1268.676	
+0.356094	799.3832	8	D	10	1197.639	+0.003437	1197.639	
	896.436	9	P	9	1082.612	+0.04161	1082.612	
	1043.504	10	F	8	985.5597		985.5597	
	1114.542	11	A	7	838.4913		838.4913	
-0.10141	1227.626	12	L	6	767.4542		767.4542	
+0.210475	1298.663	13	A	5	654.3701	+0.018036	654.3701	
	1395.715	14	P	4	583.333	+0.074803	583.333	
-0.12066	1542.784	15	F	3	486.2802	+0.121707	486.2802	
	1639.837	16	P	2	339.2118	-0.03681	339.2118	
	1726.869	17	S	1	242.159		242.159	
		18	K	0	155.127		155.127	

Scan number	5660	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	44.44



precursor information

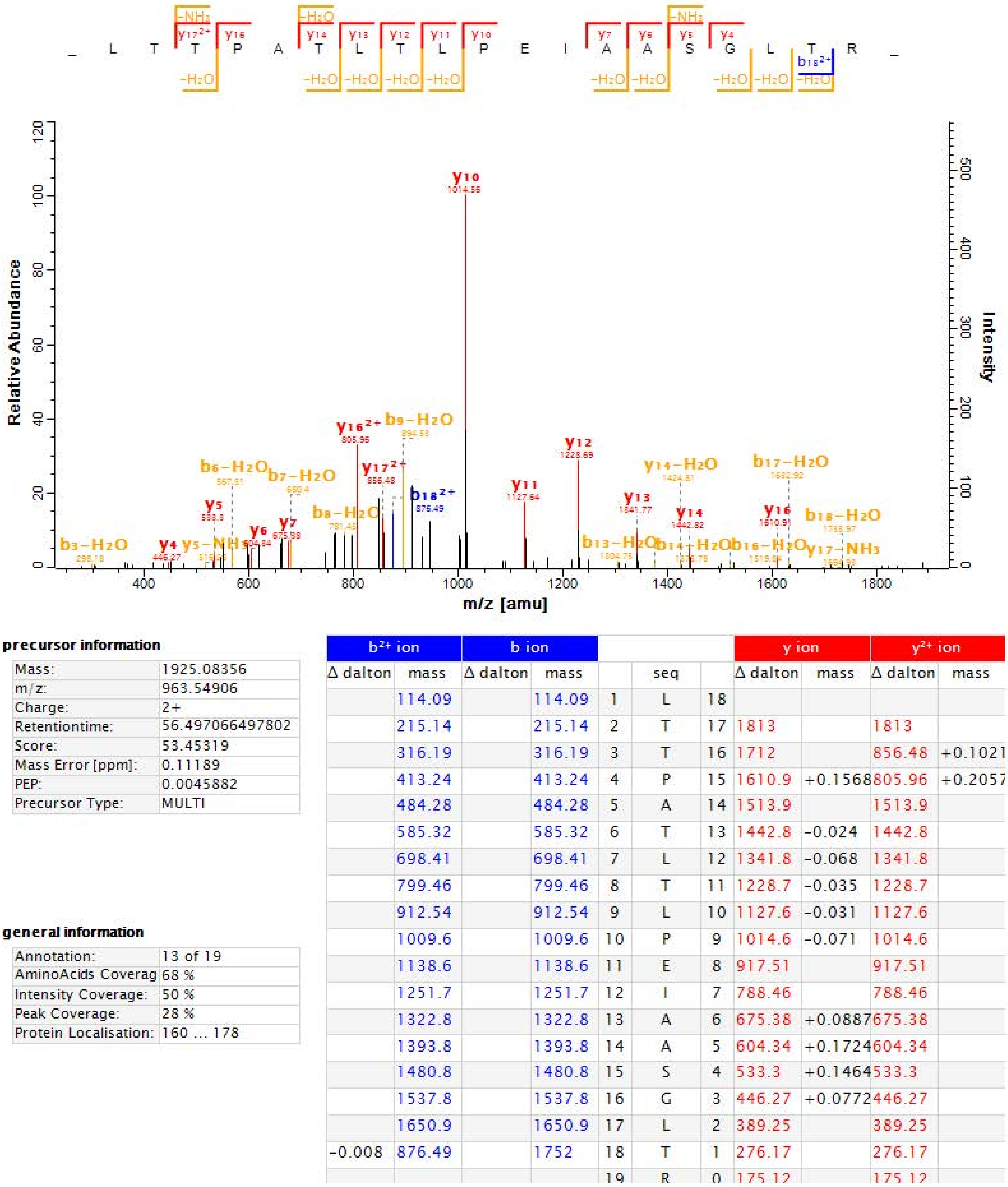
Mass:	1805.88696
m/z:	903.95076
Charge:	2+
Retentiontime:	56.318492889404
Score:	44.43975
Mass Error [ppm]:	0.003855
PEP:	0.080332
Precursor Type:	MULTI

general information

Annotation:	8 of 16
AminoAcids Coverag	50 %
Intensity Coverage:	8 %
Peak Coverage:	14 %
Protein Localisation:	579 ... 594

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	130.0499		130.0499	1	E	15		
	243.1339		243.1339	2	I	14	1677.852	
	344.1816	+0.096891	344.1816	3	T	13	1564.768	
	507.2449		507.2449	4	Y	12	1463.72	
	654.2803		654.2803	5	M	11	1300.657	
	791.3393		791.3393	6	H	10	1153.621	
+0.44744	439.6893	-0.21039	878.3713	7	S	9	1016.562	
	1007.414		1007.414	8	E	8	929.5302	-0.04994
	1064.435	-0.09146	1064.435	9	G	7	800.4876	
	1177.519		1177.519	10	I	6	743.4662	
	1290.603		1290.603	11	L	5	630.3821	
	1361.641		1361.641	12	A	4	517.298	
	1418.662		1418.662	13	G	3	446.2609	+0.045594
	1547.705	+0.003494	1547.705	14	E	2	389.2395	
	1660.789	-0.01319	1660.789	15	L	1	260.1969	-0.30533
				16	K	0	147.1128	

Scan number	5678	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	53.45



precursor information

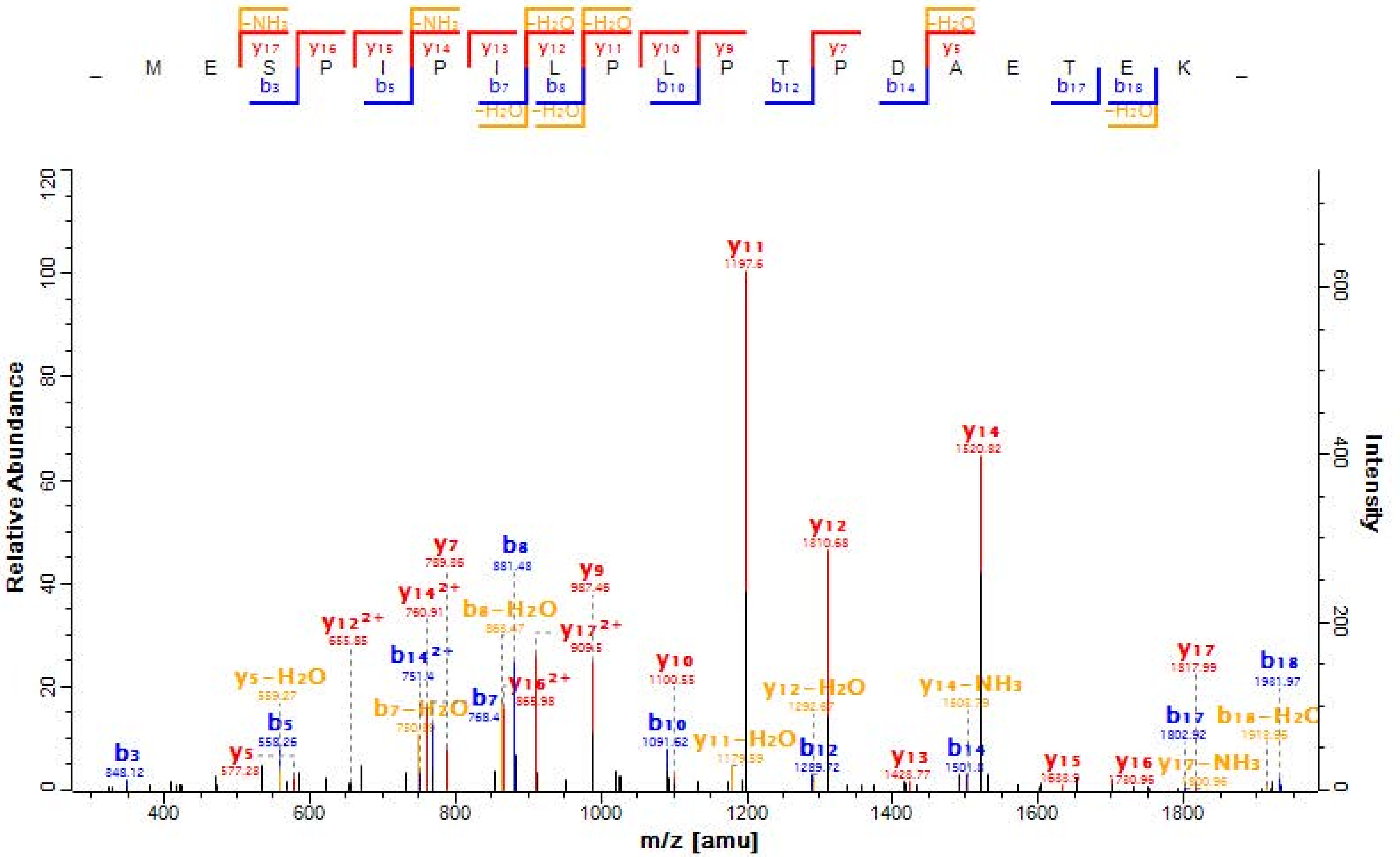
Mass:	1925.08356
m/z:	963.54906
Charge:	2+
Retentiontime:	56.497066497802
Score:	53.45319
Mass Error [ppm]:	0.11189
PEP:	0.0045882
Precursor Type:	MULTI

general information

Annotation:	13 of 19
AminoAcids Coverag	68 %
Intensity Coverage:	50 %
Peak Coverage:	28 %
Protein Localisation:	160 ... 178

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	18				
	215.14		215.14	2	T	17	1813		1813	
	316.19		316.19	3	T	16	1712		856.48	+0.1021
	413.24		413.24	4	P	15	1610.9	+0.1568	805.96	+0.2057
	484.28		484.28	5	A	14	1513.9		1513.9	
	585.32		585.32	6	T	13	1442.8	-0.024	1442.8	
	698.41		698.41	7	L	12	1341.8	-0.068	1341.8	
	799.46		799.46	8	T	11	1228.7	-0.035	1228.7	
	912.54		912.54	9	L	10	1127.6	-0.031	1127.6	
	1009.6		1009.6	10	P	9	1014.6	-0.071	1014.6	
	1138.6		1138.6	11	E	8	917.51		917.51	
	1251.7		1251.7	12	I	7	788.46		788.46	
	1322.8		1322.8	13	A	6	675.38	+0.0887	675.38	
	1393.8		1393.8	14	A	5	604.34	+0.1724	604.34	
	1480.8		1480.8	15	S	4	533.3	+0.1464	533.3	
	1537.8		1537.8	16	G	3	446.27	+0.0772	446.27	
	1650.9		1650.9	17	L	2	389.25		389.25	
-0.008	876.49		1752	18	T	1	276.17		276.17	
				19	R	0	175.12		175.12	

Scan number	5741	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	170.16



precursor information

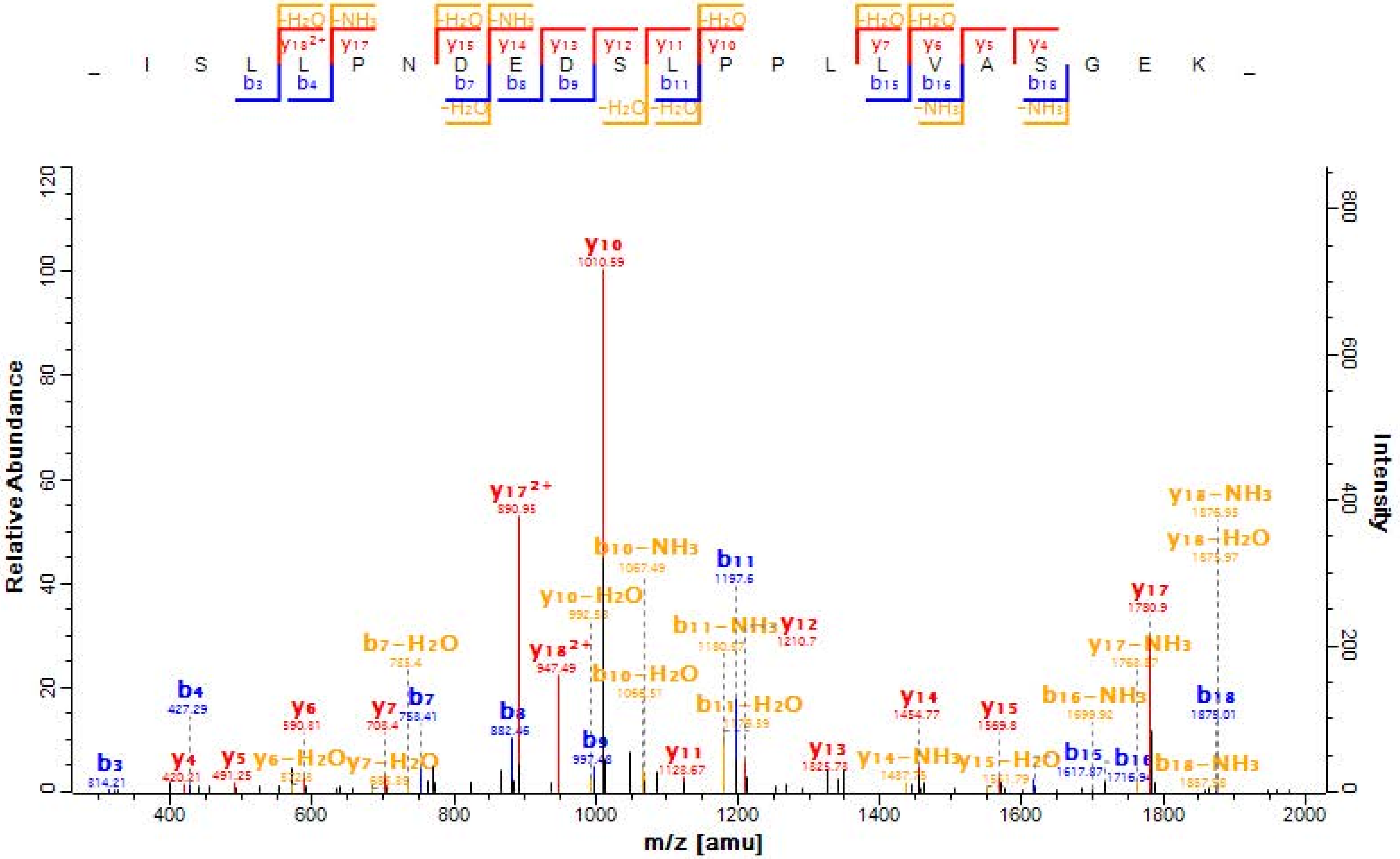
Mass:	2077.06555
m/z:	1039.54005
Charge:	2+
Retentiontime:	57.116527557373
Score:	170.1628
Mass Error [ppm]:	0.11633
PEP:	4.2254E-34
Precursor Type:	MULTI

general information

Annotation:	15 of 19
AminoAcids Coverag	79 %
Intensity Coverage:	66 %
Peak Coverage:	34 %
Protein Localisation:	373 ... 391

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	132.05		132.05	1	M	18				
	261.09		261.09	2	E	17	1947		1947	
	348.12	+0.0417	348.12	3	S	16	1818	-0.154	909.5	+0.1415
	445.18		445.18	4	P	15	1731	-0.086	865.98	+0.1351
	558.26	+0.082	558.26	5	I	14	1633.9	-0.031	1633.9	
	655.31		655.31	6	P	13	1520.8	-0.129	760.91	+0.1006
	768.4	-0.077	768.4	7	I	12	1423.8	+0.1456	1423.8	
	881.48	-0.072	881.48	8	L	11	1310.7	-0.144	655.85	+0.0354
	978.53		978.53	9	P	10	1197.6	-0.065	1197.6	
	1091.6	-0.201	1091.6	10	L	9	1100.5	+0.1122	1100.5	
	1188.7		1188.7	11	P	8	987.46	+0.0158	987.46	
	1289.7	-0.076	1289.7	12	T	7	890.41		890.41	
	1386.8		1386.8	13	P	6	789.36	+0.0628	789.36	
+0.2641	751.4	-0.108	1501.8	14	D	5	692.31		692.31	
	1572.8		1572.8	15	A	4	577.28	-0.324	577.28	
	1701.9		1701.9	16	E	3	506.25		506.25	
	1802.9	+0.0953	1802.9	17	T	2	377.2		377.2	
	1932	-0.066	1932	18	E	1	276.16		276.16	
				19	K	0	147.11		147.11	

Scan number	6039	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	158.44



precursor information

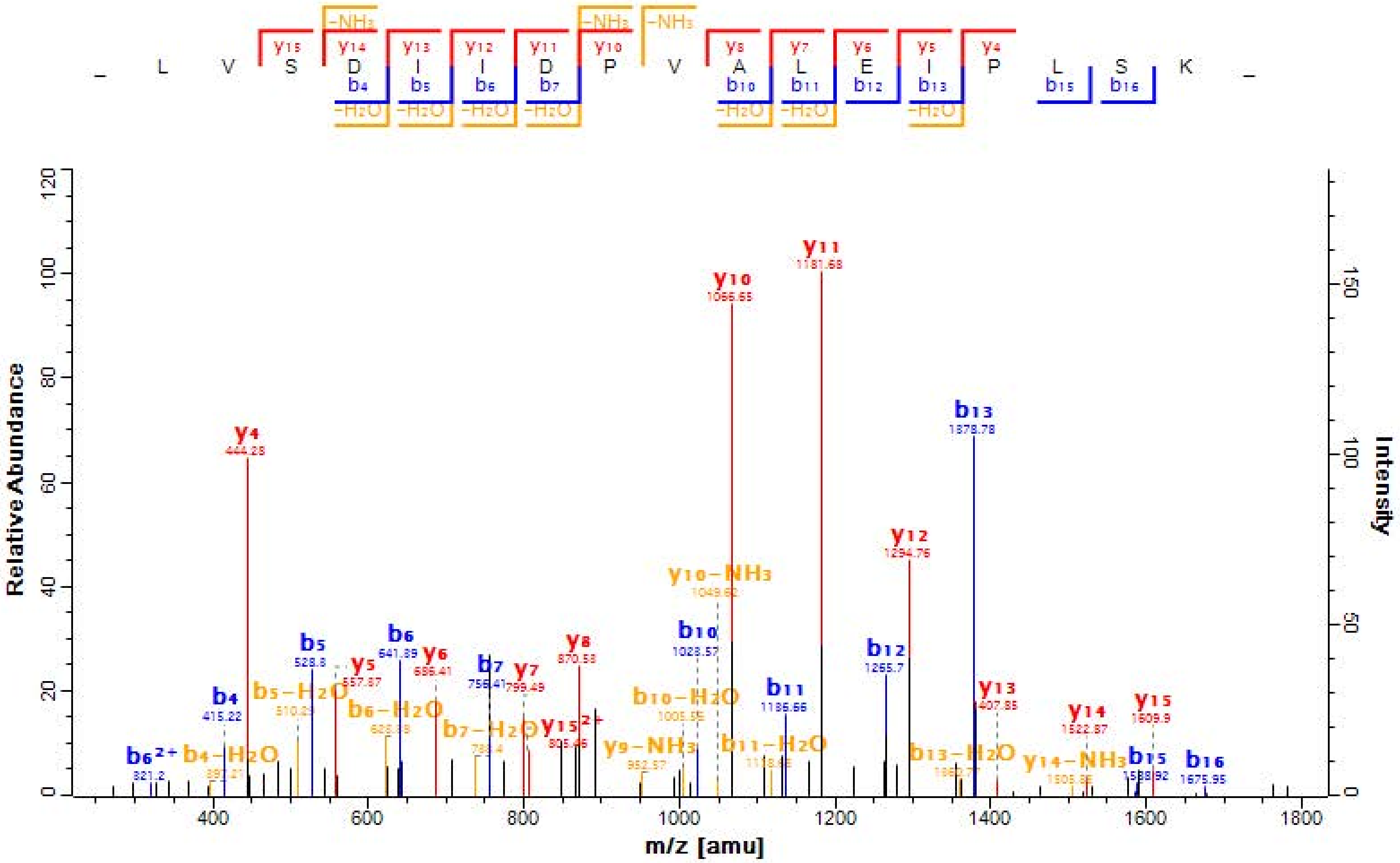
Mass:	2206.17386
m/z:	1104.09421
Charge:	2+
Retentiontime:	60.035194396972
Score:	158.4369
Mass Error [ppm]:	0.26387
PEP:	3.3087E-27
Precursor Type:	MULTI

general information

Annotation:	14 of 21
AminoAcids Coverag	67 %
Intensity Coverage:	65 %
Peak Coverage:	35 %
Protein Localisation:	1012 ... 1032

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	I	20				
	201.1234	2	S	19	2094.096		2094.096	
+0.108027	314.2074	3	L	18	2007.064		2007.064	
-0.06371	427.2915	4	L	17	1893.98		947.4938	+0.191587
	524.3443	5	P	16	1780.896	+0.082302	890.9518	+0.32688
	638.3872	6	N	15	1683.844		1683.844	
-0.08717	753.4141	7	D	14	1569.801	-0.14525	1569.801	
-0.17206	882.4567	8	E	13	1454.774	-0.14248	1454.774	
+0.023291	997.4837	9	D	12	1325.731	+0.001436	1325.731	
	1084.516	10	S	11	1210.704	+0.042783	1210.704	
-0.10953	1197.6	11	L	10	1123.672	+0.08885	1123.672	
	1294.653	12	P	9	1010.588	-0.01105	1010.588	
	1391.705	13	P	8	913.5353		913.5353	
	1504.789	14	L	7	816.4825		816.4825	
-0.15137	1617.873	15	L	6	703.3985	+0.008257	703.3985	
-0.05328	1716.942	16	V	5	590.3144	+0.033361	590.3144	
	1787.979	17	A	4	491.246	+0.020202	491.246	
-0.22948	1875.011	18	S	3	420.2089	+0.148594	420.2089	
	1932.032	19	G	2	333.1769		333.1769	
	2061.075	20	E	1	276.1554		276.1554	
		21	K	0	147.1128		147.1128	

Scan number 6266 **Raw file** LNCAP_Silac_23F10_set3_01
Method ITMS; CID **Pepti...** 190.19



precursor information

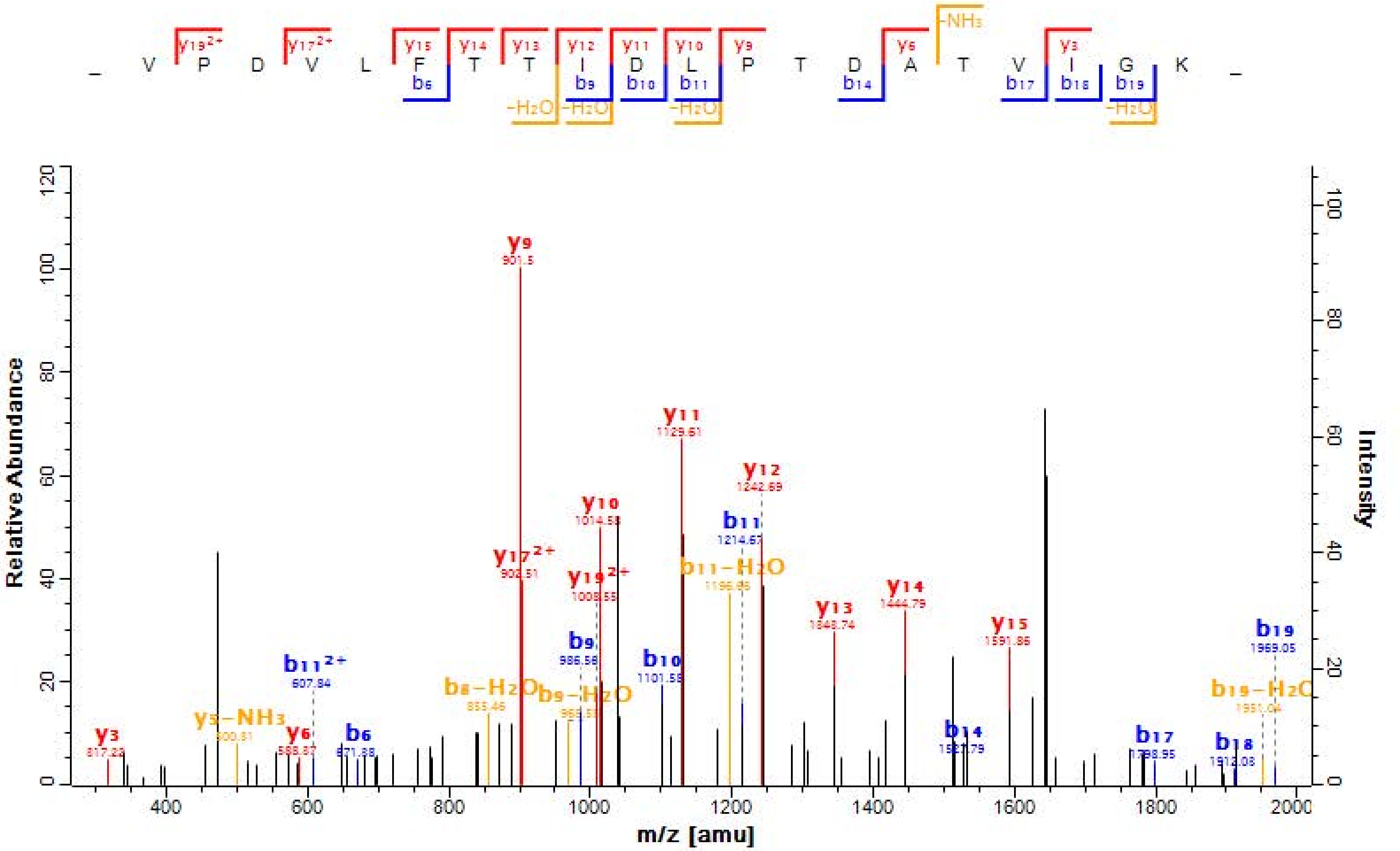
Mass:	1821.04932
m/z:	911.53194
Charge:	2+
Retentiontime:	62.294456481933
Score:	190.1851
Mass Error [ppm]:	-0.32756
PEP:	6.6563E-34
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	64 %
Peak Coverage:	38 %
Protein Localisation:	2399 ... 2415

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	16				
	213.16		213.16	2	V	15	1709		1709	
	300.19		300.19	3	S	14	1609.9	+0.0784	805.46	+0.423
	415.22	-0.01	415.22	4	D	13	1522.9	+0.1604	1522.9	
	528.3	+0.0632	528.3	5	I	12	1407.8	-0.038	1407.8	
+0.0661	321.2	-0.094	641.39	6	I	11	1294.8	-0.053	1294.8	
	756.41	+0.2902	756.41	7	D	10	1181.7	-0.085	1181.7	
	853.47		853.47	8	P	9	1066.7	-0.085	1066.7	
	952.53		952.53	9	V	8	969.6		969.6	
	1023.6	-0.084	1023.6	10	A	7	870.53	-0.035	870.53	
	1136.7	-0.07	1136.7	11	L	6	799.49	+0.0314	799.49	
	1265.7	-0.286	1265.7	12	E	5	686.41	-0.016	686.41	
	1378.8	-0.055	1378.8	13	I	4	557.37	+0.2072	557.37	
	1475.8		1475.8	14	P	3	444.28	-0.005	444.28	
	1588.9	-0.263	1588.9	15	L	2	347.23		347.23	
	1676	-0.002	1676	16	S	1	234.14		234.14	
				17	K	0	147.11		147.11	

Scan number 6410 **Raw file** LNCAP_Silac_23F10_set3_01
Method ITMS; CID **Pepti...** 85.2



precursor information

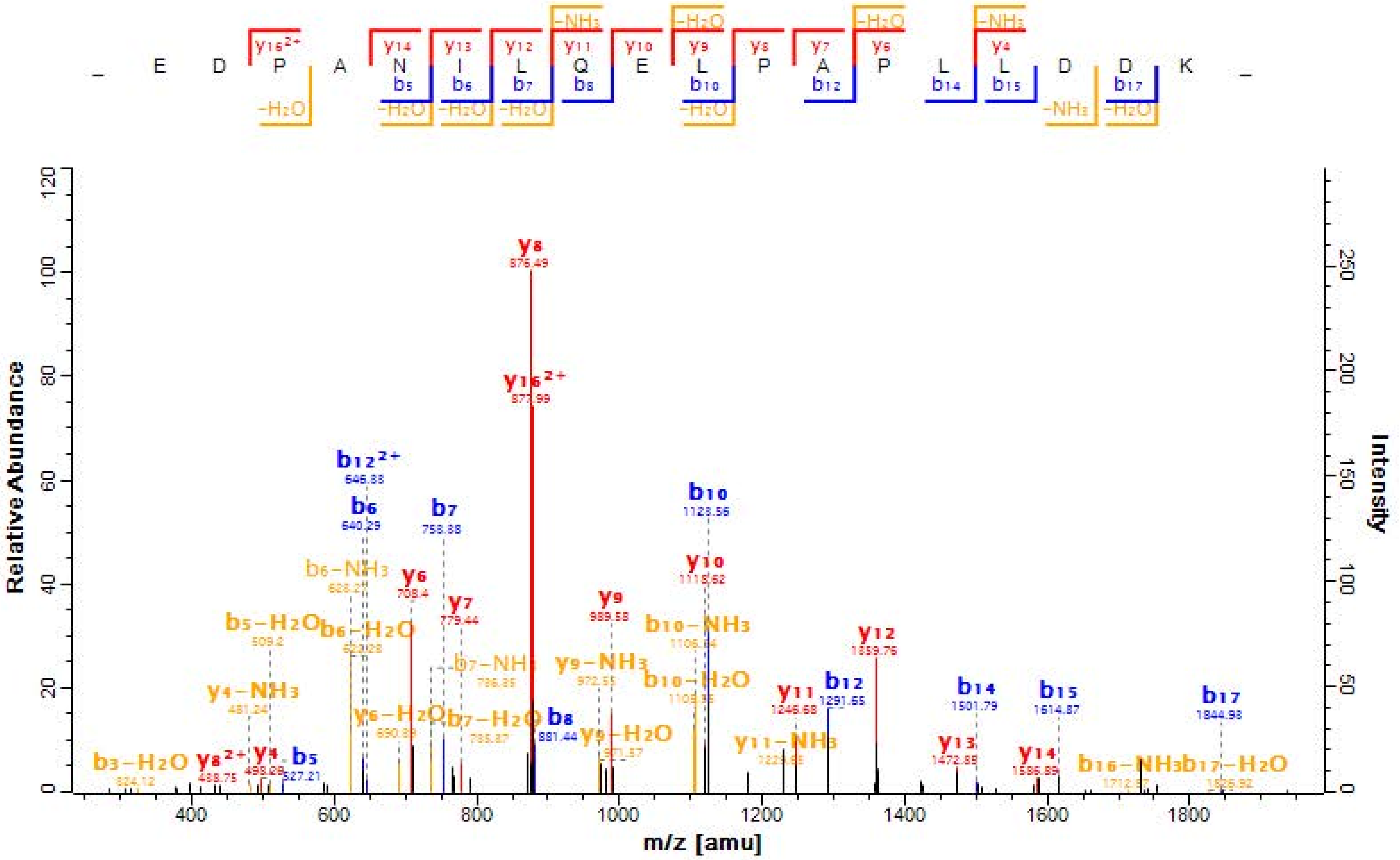
Mass:	2114.15103
m/z:	1058.08279
Charge:	2+
Retentiontime:	63.560852050781
Score:	85.20261
Mass Error [ppm]:	-0.027589
PEP:	3.4955E-05
Precursor Type:	MULTI

general information

Annotation:	15 of 20
AminoAcids Coverag	75 %
Intensity Coverage:	38 %
Peak Coverage:	24 %
Protein Localisation:	540 ... 559

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	19				
	197.13		197.13	2	P	18	2016.1		1008.5	-0.114
	312.16		312.16	3	D	17	1919		1919	
	411.22		411.22	4	V	16	1804		902.51	+0.0254
	524.31		524.31	5	L	15	1704.9		1704.9	
	671.38	+0.0861	671.38	6	F	14	1591.9	+0.0281	1591.9	
	772.42		772.42	7	T	13	1444.8	+0.1235	1444.8	
	873.47		873.47	8	T	12	1343.7	+0.0716	1343.7	
	986.56	-0.193	986.56	9	I	11	1242.7	-0.047	1242.7	
	1101.6	-0.091	1101.6	10	D	10	1129.6	-0.041	1129.6	
-0.251	607.84	+0.0297	1214.7	11	L	9	1014.6	-0.039	1014.6	
	1311.7		1311.7	12	P	8	901.5	-0.045	901.5	
	1412.8		1412.8	13	T	7	804.45		804.45	
	1527.8	+0.3757	1527.8	14	D	6	703.4		703.4	
	1598.8		1598.8	15	A	5	588.37	+0.1498	588.37	
	1699.9		1699.9	16	T	4	517.33		517.33	
	1798.9	-0.096	1798.9	17	V	3	416.29		416.29	
	1912	-0.087	1912	18	I	2	317.22	-0.166	317.22	
	1969.1	+0.0832	1969.1	19	G	1	204.13		204.13	
				20	K	0	147.11		147.11	

Scan number	6547	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	185.33



precursor information

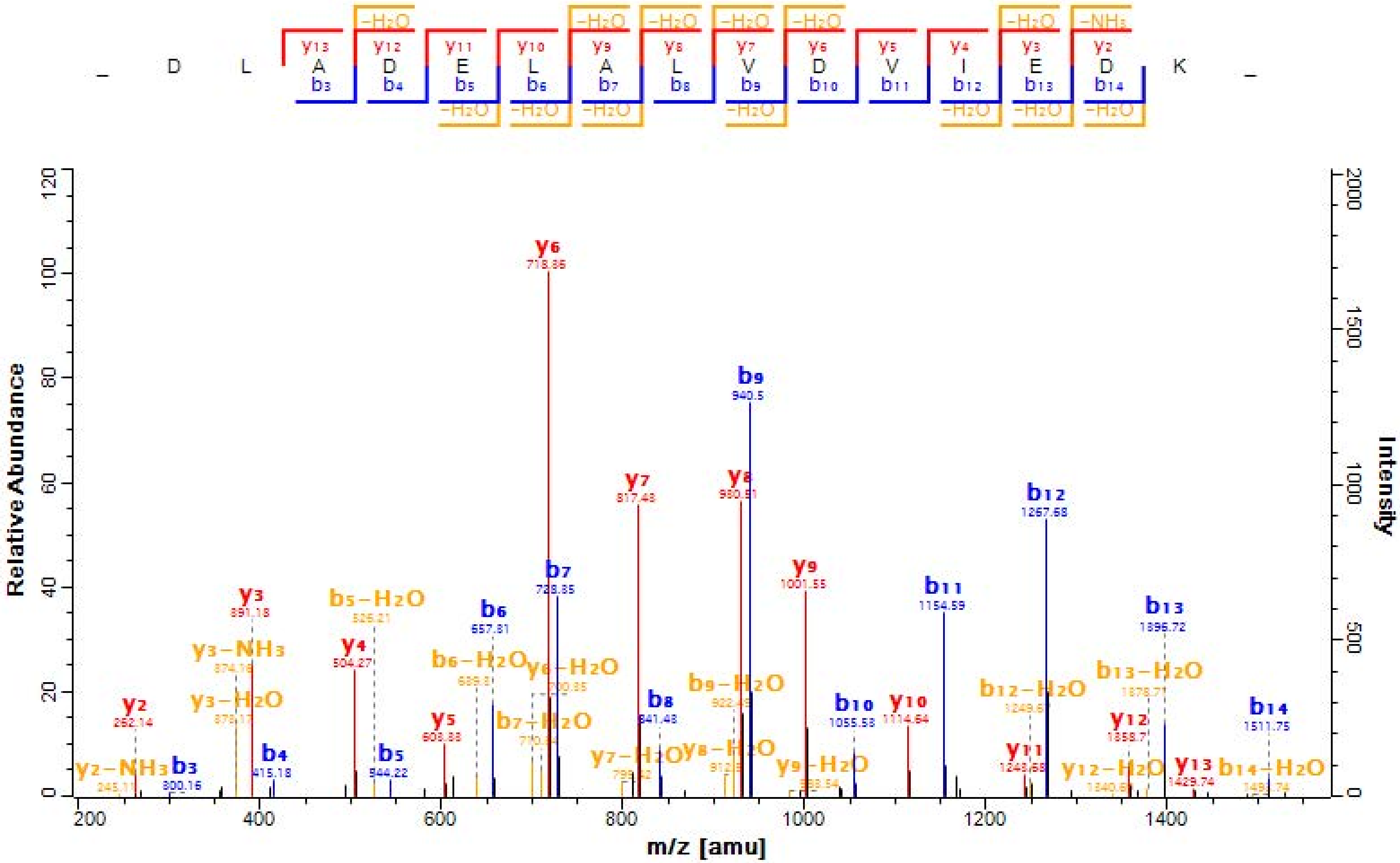
Mass:	1990.0254
m/z:	996.01998
Charge:	2+
Retentiontime:	64.993896484375
Score:	185.3261
Mass Error [ppm]:	-0.24154
PEP:	1.572E-34
Precursor Type:	MULTI

general information

Annotation:	14 of 18
AminoAcids Coverag	78 %
Intensity Coverage:	71 %
Peak Coverage:	40 %
Protein Localisation:	120 ... 137

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	17				
	245.08		245.08	2	D	16	1870		1870	
	342.13		342.13	3	P	15	1755		877.99	-0.298
	413.17		413.17	4	A	14	1657.9		1657.9	
	527.21	+0.2661	527.21	5	N	13	1586.9	+0.0416	1586.9	
	640.29	+0.0399	640.29	6	I	12	1472.8	-0.24	1472.8	
	753.38	-0.07	753.38	7	L	11	1359.8	-0.102	1359.8	
	881.44	+0.0376	881.44	8	Q	10	1246.7	+0.0753	1246.7	
	1010.5		1010.5	9	E	9	1118.6	-0.001	1118.6	
	1123.6	-0.136	1123.6	10	L	8	989.58	-0.03	989.58	
	1220.6		1220.6	11	P	7	876.49	-0.073	438.75	+0.3736
+0.2994	646.33	-0.107	1291.7	12	A	6	779.44	-0.035	779.44	
	1388.7		1388.7	13	P	5	708.4	+0.1065	708.4	
	1501.8	-0.201	1501.8	14	L	4	611.35		611.35	
	1614.9	+0.257	1614.9	15	L	3	498.26	+0.1115	498.26	
	1729.9		1729.9	16	D	2	385.18		385.18	
	1844.9	-0.451	1844.9	17	D	1	270.15		270.15	
				18	K	0	155.13		155.13	

Scan number	6580	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	251.91



precursor information

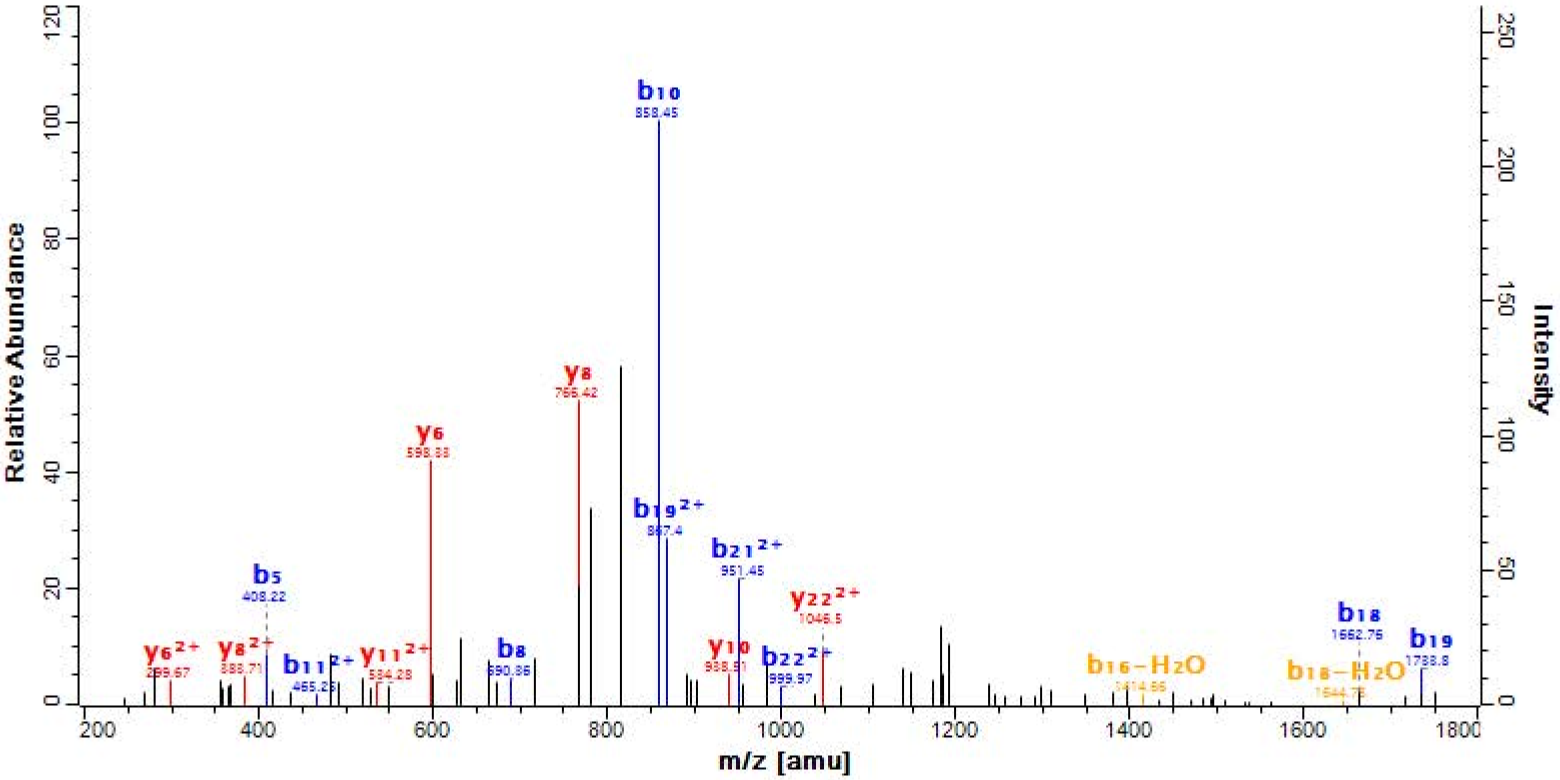
Mass:	1656.84525
m/z:	829.4299
Charge:	2+
Retentiontime:	65.344779968261
Score:	251.9055
Mass Error [ppm]:	-0.32964
PEP:	2.8174E-57
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	78 %
Peak Coverage:	48 %
Protein Localisation:	72 ... 86

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	116.034219499	1	D	14		
	229.118283479	2	L	13	1542.82613079	
-0.1030291	300.155397267	3	A	12	1429.74206681	-0.0185561
+0.1435264	415.182340299	4	D	11	1358.70495302	-0.0463837
+0.2278864	544.224933395	5	E	10	1243.67800999	-0.0250559
+0.0194328	657.308997375	6	L	9	1114.63541689	-0.0541181
+0.0246164	728.346111163	7	A	8	1001.55135291	+0.0003439
-0.0546258	841.430175144	8	L	7	930.514239124	-0.0582455
-0.0319753	940.49858906	9	V	6	817.430175144	-0.0118402
-0.134663	1055.52553209	10	D	5	718.361761227	+0.041376
-0.0652595	1154.59394601	11	V	4	603.334818195	+0.0934655
-0.1952219	1267.67800999	12	I	3	504.266404279	+0.0094136
-0.1938697	1396.72060308	13	E	2	391.182340299	+0.0358604
+0.0190554	1511.74754612	14	D	1	262.139747203	+0.0718922
		15	K	0	147.112804171	

Scan number	845	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	61.52



precursor information

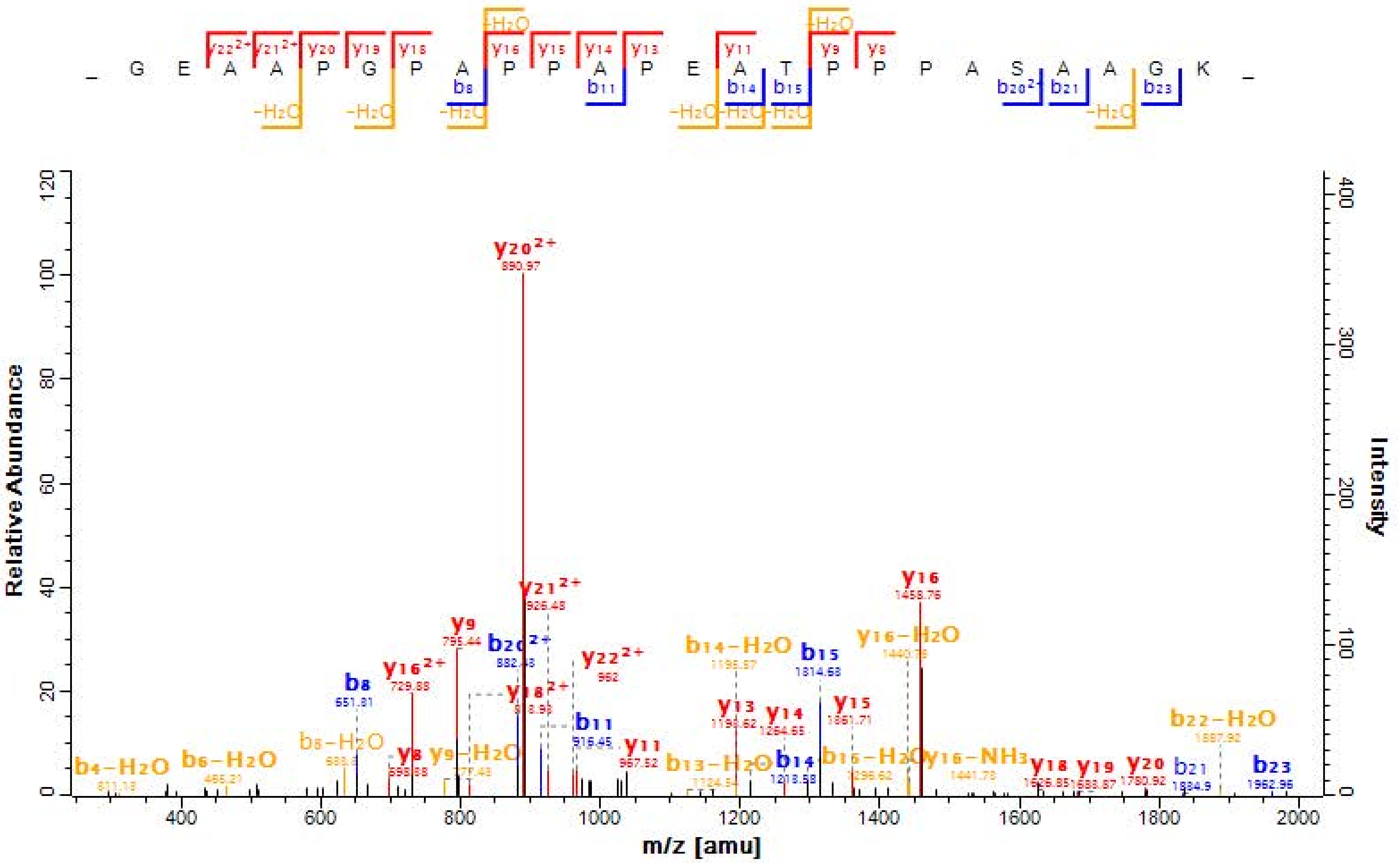
Mass:	2498.20407
m/z:	833.74196
Charge:	3+
Retentiontime:	13.538198471069
Score:	61.52413
Mass Error [ppm]:	0.12841
PEP:	4.2098E-05
Precursor Type:	MULTI

general information

Annotation:	12 of 27
AminoAcids Coverag	44 %
Intensity Coverage:	46 %
Peak Coverage:	21 %
Protein Localisation:	170 ... 196

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	26				
	143.08		143.08	2	A	25	2428.2		2428.2	
	240.13		240.13	3	P	24	2357.1		2357.1	
	337.19		337.19	4	P	23	2260.1		2260.1	
	408.22	+0.0415	408.22	5	A	22	2163		2163	
	505.28		505.28	6	P	21	2092		1046.5	+0.0541
	619.32		619.32	7	N	20	1994.9		1994.9	
	690.36	-0.121	690.36	8	A	19	1880.9		1880.9	
	787.41		787.41	9	P	18	1809.9		1809.9	
	858.45	+0.1561	858.45	10	A	17	1712.8		1712.8	
+0.1451	465.25		929.48	11	A	16	1641.8		1641.8	
	986.51		986.51	12	G	15	1570.7		1570.7	
	1115.5		1115.5	13	E	14	1513.7		1513.7	
	1230.6		1230.6	14	D	13	1384.7		1384.7	
	1331.6		1331.6	15	T	12	1269.6		1269.6	
	1432.7		1432.7	16	T	11	1168.6		1168.6	
	1561.7		1561.7	17	E	10	1067.5		534.28	+0.3457
	1662.8	-0.066	1662.8	18	T	9	938.51	+0.499	938.51	
-0.057	867.4	+0.019	1733.8	19	A	8	837.46		837.46	
	1830.9		1830.9	20	P	7	766.42	-0.05	383.71	+0.0517
+0.3365	951.45		1901.9	21	A	6	669.37		669.37	
-0.093	999.97		1998.9	22	P	5	598.33	-0.039	299.67	-0.351
	2056		2056	23	G	4	501.28		501.28	
	2157		2157	24	T	3	444.26		444.26	
	2254.1		2254.1	25	P	2	343.21		343.21	
	2325.1		2325.1	26	A	1	246.16		246.16	
				27	R	0	175.12		175.12	

Scan number	886	**Raw file**	LNCAP_Silac_23F10_set3_01
Method	ITMS; CID	**Pepti...**	107.39



precursor information

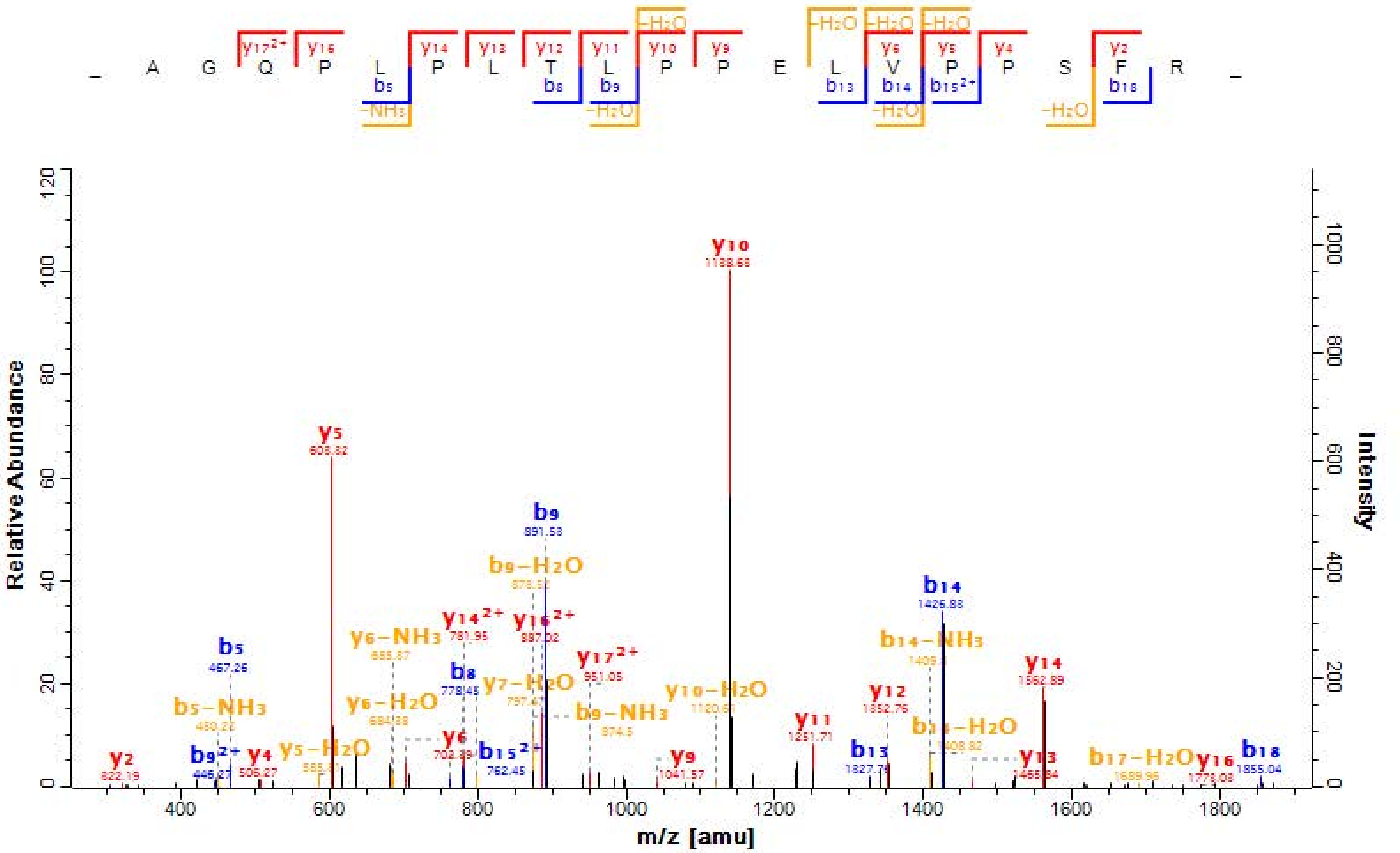
Mass:	2108.05479
m/z:	1055.03467
Charge:	2+
Retentiontime:	13.956355094909
Score:	107.3907
Mass Error [ppm]:	0.45378
PEP:	1.9791E-10
Precursor Type:	MULTI

general information

Annotation:	19 of 24
AminoAcids Coverag	79 %
Intensity Coverage:	63 %
Peak Coverage:	33 %
Protein Localisation:	20 ... 43

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	23				
	187.07		187.07	2	E	22	2052		2052	
	258.11		258.11	3	A	21	1923		962	-0.212
	329.15		329.15	4	A	20	1852		926.48	+0.2491
	426.2		426.2	5	P	19	1780.9	-0.16	890.97	+0.165
	483.22		483.22	6	G	18	1683.9	+0.2756	1683.9	
	580.27		580.27	7	P	17	1626.8	-0.063	813.93	+0.0989
	651.31	+0.0191	651.31	8	A	16	1529.8		1529.8	
	748.36		748.36	9	P	15	1458.8	-0.107	729.88	+0.2234
	845.42		845.42	10	P	14	1361.7	-0.024	1361.7	
	916.45	-0.004	916.45	11	A	13	1264.7	+0.0813	1264.7	
	1013.5		1013.5	12	P	12	1193.6	-0.067	1193.6	
	1142.5		1142.5	13	E	11	1096.6		1096.6	
	1213.6	+0.0869	1213.6	14	A	10	967.52	-0.179	967.52	
	1314.6	-0.192	1314.6	15	T	9	896.48		896.48	
	1411.7		1411.7	16	P	8	795.44	-0.089	795.44	
	1508.7		1508.7	17	P	7	698.38	+0.0121	698.38	
	1605.8		1605.8	18	P	6	601.33		601.33	
	1676.8		1676.8	19	A	5	504.28		504.28	
-0.271	882.43		1763.9	20	S	4	433.24		433.24	
	1834.9	-0.273	1834.9	21	A	3	346.21		346.21	
	1905.9		1905.9	22	A	2	275.17		275.17	
	1963	-0.177	1963	23	G	1	204.13		204.13	
				24	K	0	147.11		147.11	

Scan number	10120	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	158.98



precursor information

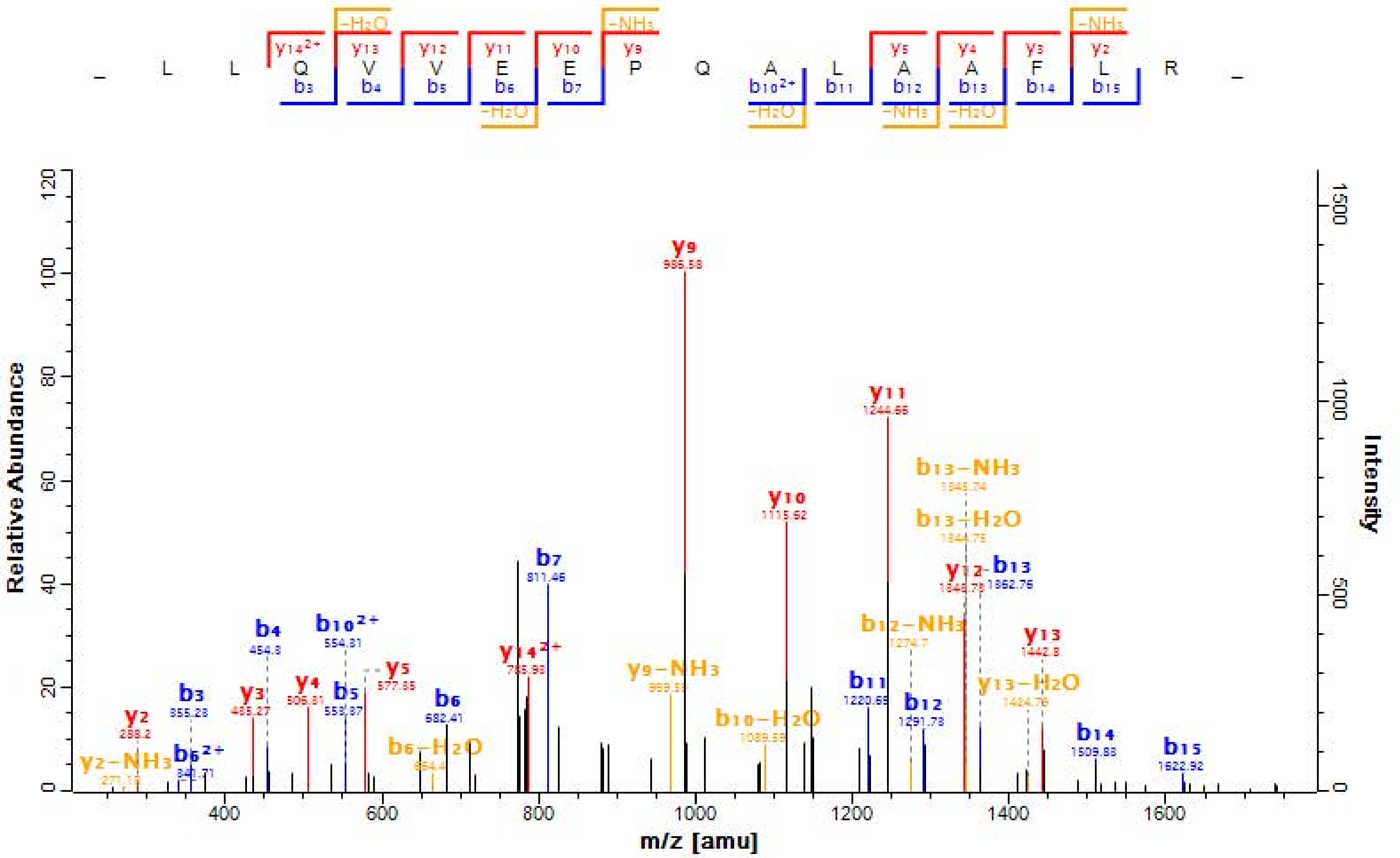
Mass:	2028.14062
m/z:	1015.07759
Charge:	2+
Retentiontime:	66.273178100585
Score:	158.9763
Mass Error [ppm]:	-0.088328
PEP:	2.3122E-26
Precursor Type:	MULTI

general information

Annotation:	15 of 19
AminoAcids Coverag	79 %
Intensity Coverage:	59 %
Peak Coverage:	35 %
Protein Localisation:	314 ... 332

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	18				
	129.07		129.07	2	G	17	1958.1		1958.1	
	257.12		257.12	3	Q	16	1901.1		951.05	-0.27
	354.18		354.18	4	P	15	1773	+0.0006	887.02	+0.2554
	467.26	+0.0576	467.26	5	L	14	1676		1676	
	564.31		564.31	6	P	13	1562.9	-0.154	781.95	-0.15
	677.4		677.4	7	L	12	1465.8	+0.0991	1465.8	
	778.45	+0.0308	778.45	8	T	11	1352.8	+0.006	1352.8	
+0.0968	446.27	-0.042	891.53	9	L	10	1251.7	-0.143	1251.7	
	988.58		988.58	10	P	9	1138.6	+0.0036	1138.6	
	1085.6		1085.6	11	P	8	1041.6	+0.064	1041.6	
	1214.7		1214.7	12	E	7	944.52		944.52	
	1327.8	-0.02	1327.8	13	L	6	815.48		815.48	
	1426.8	-0.154	1426.8	14	V	5	702.39	-0.031	702.39	
-0.053	762.45		1523.9	15	P	4	603.32	+0.0294	603.32	
	1620.9		1620.9	16	P	3	506.27	+0.1	506.27	
	1708		1708	17	S	2	409.22		409.22	
	1855	-0.249	1855	18	F	1	322.19	-0.071	322.19	
				19	R	0	175.12		175.12	

Scan number	10205	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	171.08



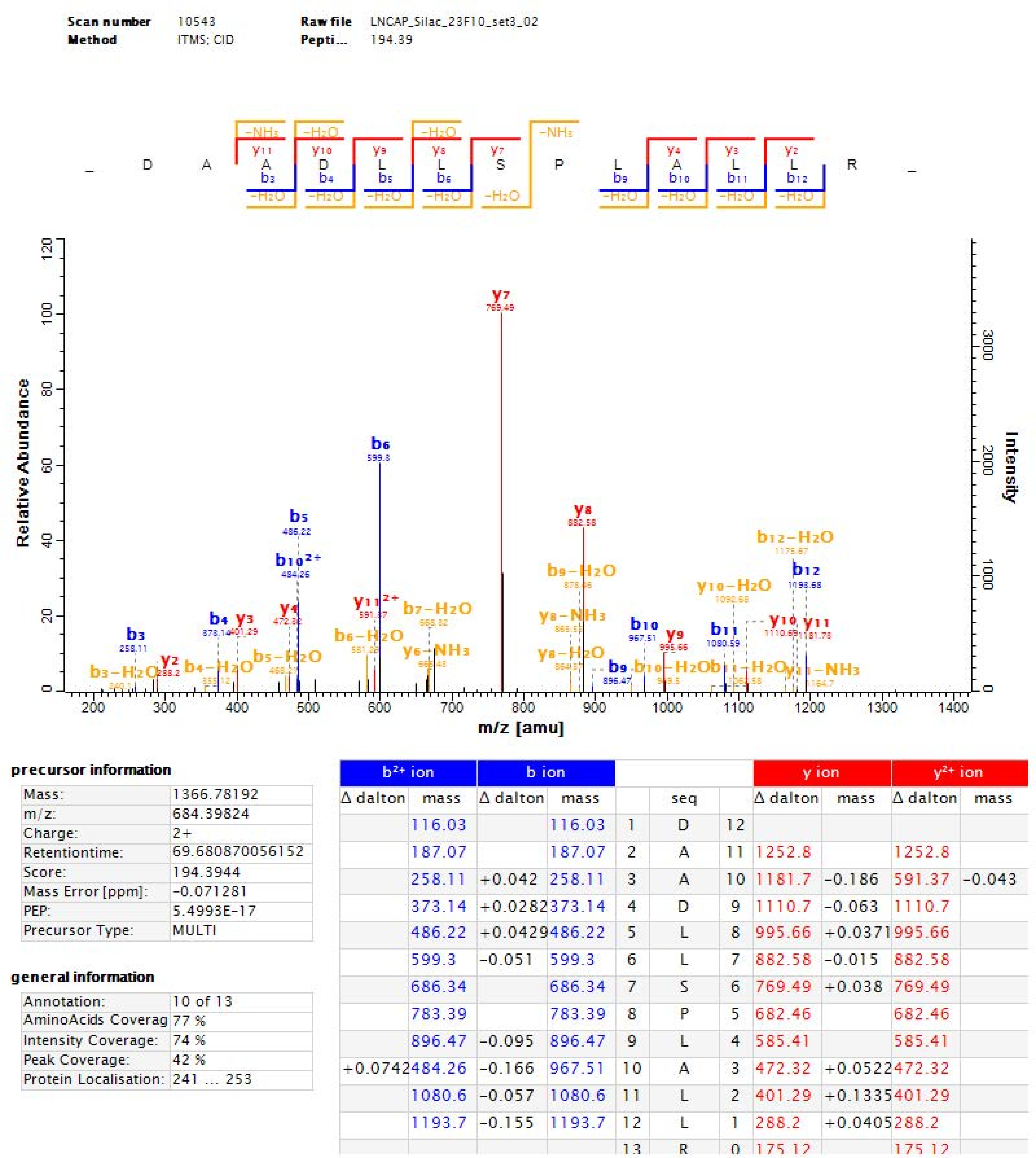
precursor information

Mass:	1796.01889
m/z:	899.01672
Charge:	2+
Retentiontime:	66.891716003418
Score:	171.0793
Mass Error [ppm]:	-0.40434
PEP:	2.3795E-22
Precursor Type:	MULTI

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	54 %
Peak Coverage:	34 %
Protein Localisation:	183 ... 198

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	15				
	227.18		227.18	2	L	14	1683.9		1683.9	
	355.23	+0.0279	355.23	3	Q	13	1570.9		785.93	+0.181
	454.3	+0.1034	454.3	4	V	12	1442.8	-0.002	1442.8	
	553.37	-0.041	553.37	5	V	11	1343.7	-0.092	1343.7	
-0.435	341.71	-0.007	682.41	6	E	10	1244.7	-0.033	1244.7	
	811.46	-0.02	811.46	7	E	9	1115.6	-0.011	1115.6	
	908.51		908.51	8	P	8	986.58	+0.0134	986.58	
	1036.6		1036.6	9	Q	7	889.53		889.53	
+0.0198	554.31		1107.6	10	A	6	761.47		761.47	
	1220.7	+0.1256	1220.7	11	L	5	690.43		690.43	
	1291.7	-0.134	1291.7	12	A	4	577.35	+0.1175	577.35	
	1362.8	-0.085	1362.8	13	A	3	506.31	+0.0032	506.31	
	1509.8	-0.215	1509.8	14	F	2	435.27	+0.1742	435.27	
	1622.9	-0.326	1622.9	15	L	1	288.2	+0.0959	288.2	
				16	R	0	175.12		175.12	



Scan number	10543	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	194.39

precursor information

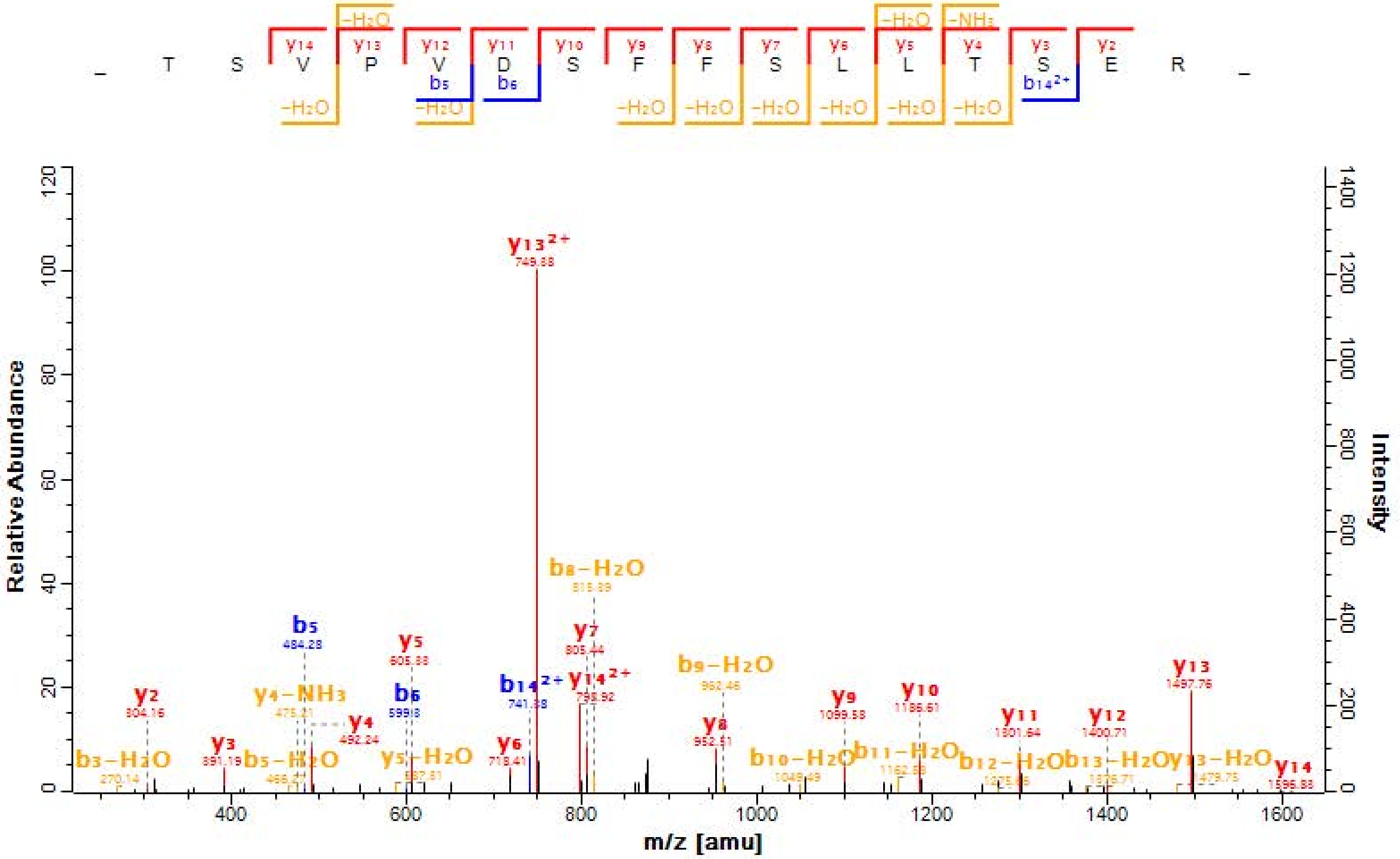
Mass:	1366.78192
m/z:	684.39824
Charge:	2+
Retentiontime:	69.680870056152
Score:	194.3944
Mass Error [ppm]:	-0.071281
PEP:	5.4993E-17
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	74 %
Peak Coverage:	42 %
Protein Localisation:	241 ... 253

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	12				
	187.07		187.07	2	A	11	1252.8		1252.8	
	258.11	+0.042	258.11	3	A	10	1181.7	-0.186	591.37	-0.043
	373.14	+0.0282	373.14	4	D	9	1110.7	-0.063	1110.7	
	486.22	+0.0429	486.22	5	L	8	995.66	+0.0371	995.66	
	599.3	-0.051	599.3	6	L	7	882.58	-0.015	882.58	
	686.34		686.34	7	S	6	769.49	+0.038	769.49	
	783.39		783.39	8	P	5	682.46		682.46	
	896.47	-0.095	896.47	9	L	4	585.41		585.41	
+0.0742	484.26	-0.166	967.51	10	A	3	472.32	+0.0522	472.32	
	1080.6	-0.057	1080.6	11	L	2	401.29	+0.1335	401.29	
	1193.7	-0.155	1193.7	12	L	1	288.2	+0.0405	288.2	
				13	R	0	175.12		175.12	

Scan number	10712	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	106.6



precursor information

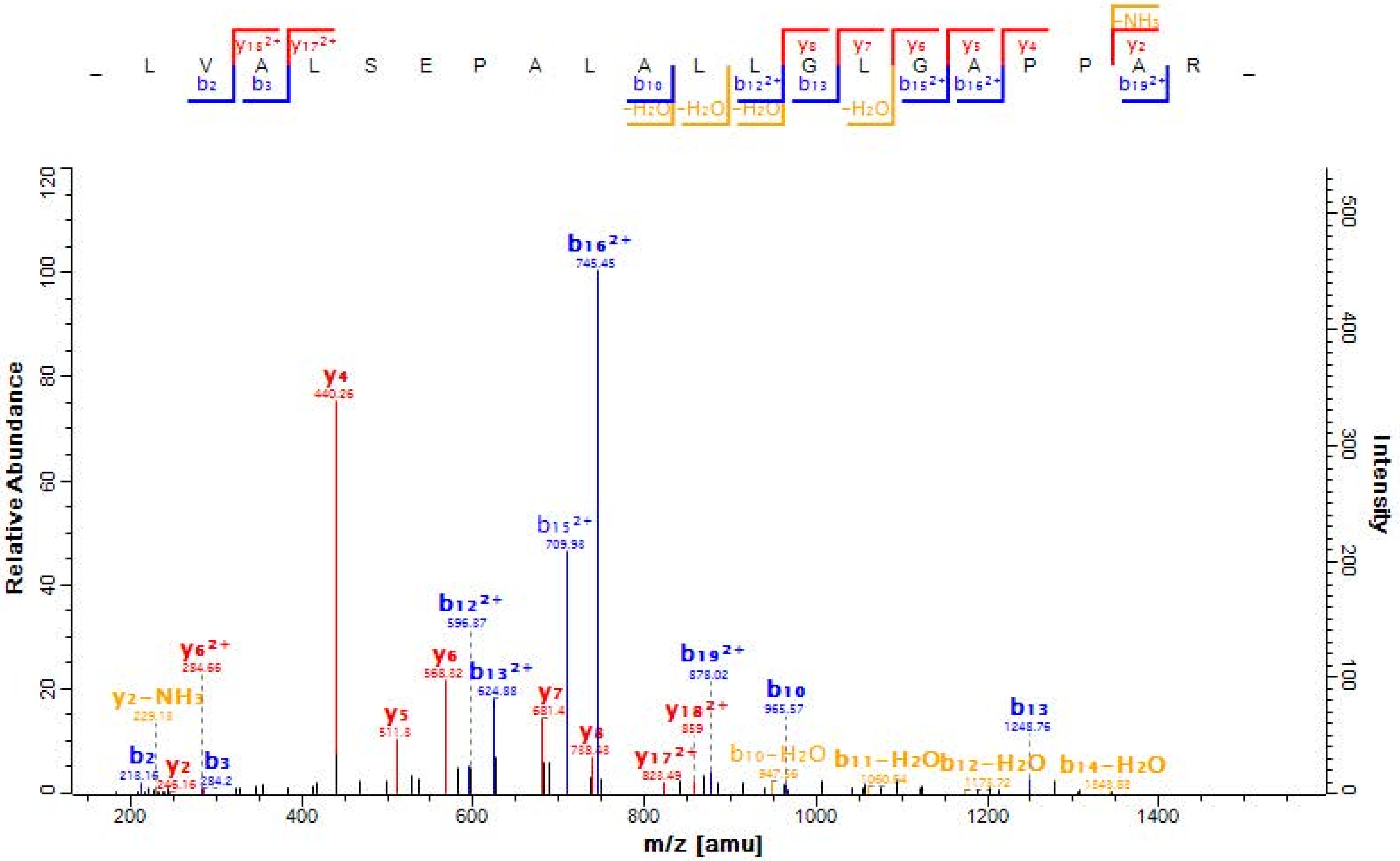
Mass:	1783.90071
m/z:	892.95763
Charge:	2+
Retentiontime:	71.217323303222
Score:	106.5974
Mass Error [ppm]:	0.83087
PEP:	7.08E-07
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	69 %
Peak Coverage:	35 %
Protein Localisation:	115 ... 130

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	15				
	189.09		189.09	2	S	14	1683.9		1683.9	
	288.16		288.16	3	V	13	1596.8	+0.2956	798.92	+0.1774
	385.21		385.21	4	P	12	1497.8	-0.084	749.38	+0.2231
	484.28	+0.107	484.28	5	V	11	1400.7	+0.0947	1400.7	
	599.3	+0.1914	599.3	6	D	10	1301.6	-0.073	1301.6	
	686.34		686.34	7	S	9	1186.6	-0.084	1186.6	
	833.4		833.4	8	F	8	1099.6	-0.026	1099.6	
	980.47		980.47	9	F	7	952.51	-0.029	952.51	
	1067.5		1067.5	10	S	6	805.44	+0.0567	805.44	
	1180.6		1180.6	11	L	5	718.41	+0.0122	718.41	
	1293.7		1293.7	12	L	4	605.33	+0.0173	605.33	
	1394.7		1394.7	13	T	3	492.24	+0.0112	492.24	
-0.266	741.38		1481.8	14	S	2	391.19	+0.0981	391.19	
	1610.8		1610.8	15	E	1	304.16	+0.0736	304.16	
				16	R	0	175.12		175.12	

Scan number	10734	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	91.66



precursor information

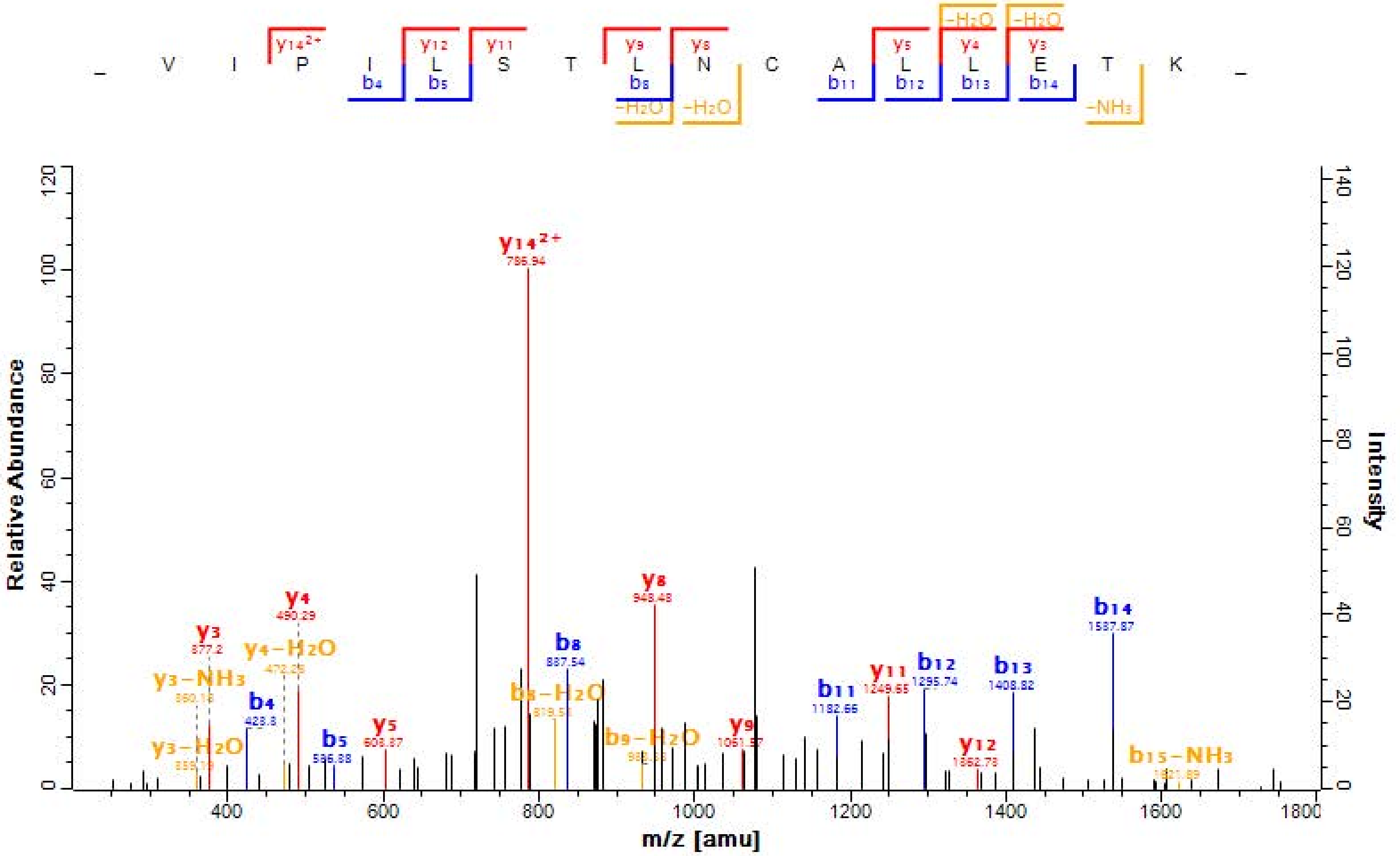
Mass:	1928.14608
m/z:	643.72264
Charge:	3+
Retentiontime:	71.413688659668
Score:	91.65682
Mass Error [ppm]:	0.10348
PEP:	5.5983E-06
Precursor Type:	MULTI

general information

Annotation:	13 of 20
AminoAcids Coverag	65 %
Intensity Coverage:	75 %
Peak Coverage:	28 %
Protein Localisation:	95 ... 114

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	19				
	213.16	-0.132	213.16	2	V	18	1816.1		1816.1	
	284.2	-0.087	284.2	3	A	17	1717		859	+0.0607
	397.28		397.28	4	L	16	1646		823.49	+0.188
	484.31		484.31	5	S	15	1532.9		1532.9	
	613.36		613.36	6	E	14	1445.8		1445.8	
	710.41		710.41	7	P	13	1316.8		1316.8	
	781.45		781.45	8	A	12	1219.8		1219.8	
	894.53		894.53	9	L	11	1148.7		1148.7	
	965.57	-0.145	965.57	10	A	10	1035.6		1035.6	
	1078.7		1078.7	11	L	9	964.59		964.59	
-0.383	596.37		1191.7	12	L	8	851.51		851.51	
+0.1919	624.88	-0.319	1248.8	13	G	7	738.43	+0.1016	738.43	
	1361.8		1361.8	14	L	6	681.4	-0.042	681.4	
+0.1274	709.93		1418.9	15	G	5	568.32	+0.0166	284.66	+0.421
+0.0385	745.45		1489.9	16	A	4	511.3	+0.0876	511.3	
	1587		1587	17	P	3	440.26	+0.0467	440.26	
	1684		1684	18	P	2	343.21		343.21	
-0.309	878.02		1755	19	A	1	246.16	+0.1215	246.16	
				20	R	0	175.12		175.12	

Scan number	10847	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	86.55



precursor information

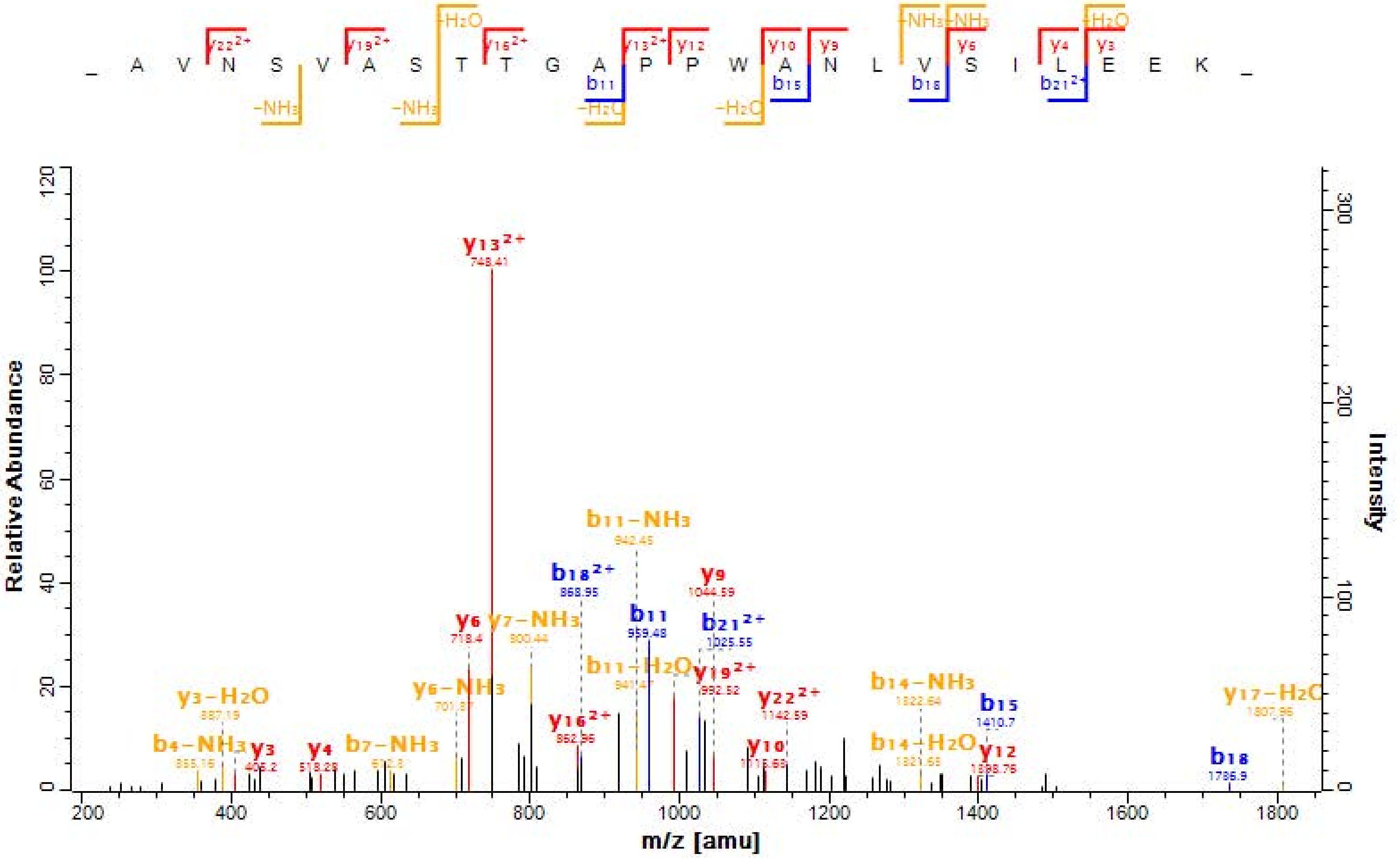
Mass:	1784.01323
m/z:	893.01389
Charge:	2+
Retentiontime:	72.470031738281
Score:	86.54771
Mass Error [ppm]:	0.82484
PEP:	0.0034891
Precursor Type:	ISO

general information

Annotation:	11 of 16
AminoAcids Coverag	69 %
Intensity Coverage:	40 %
Peak Coverage:	23 %
Protein Localisation:	177 ... 192

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	15				
	213.1598	2	I	14	1685.951		1685.951	
	310.2125	3	P	13	1572.867		786.9369	+0.011997
-0.0019	423.2966	4	I	12	1475.814		1475.814	
-0.28635	536.3806	5	L	11	1362.73	-0.05041	1362.73	
	623.4127	6	S	10	1249.646	-0.32853	1249.646	
	724.4604	7	T	9	1162.614		1162.614	
-0.20555	837.5444	8	L	8	1061.566	+0.085166	1061.566	
	951.5873	9	N	7	948.4819	+0.037455	948.4819	
	1111.618	10	C	6	834.439		834.439	
+0.066817	1182.655	11	A	5	674.4083		674.4083	
-0.22648	1295.739	12	L	4	603.3712	+0.149548	603.3712	
+0.133431	1408.823	13	L	3	490.2871	+0.223297	490.2871	
+0.012957	1537.866	14	E	2	377.2031	+0.023914	377.2031	
	1638.914	15	T	1	248.1605		248.1605	
		16	K	0	147.1128		147.1128	

Scan number	11230	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	63



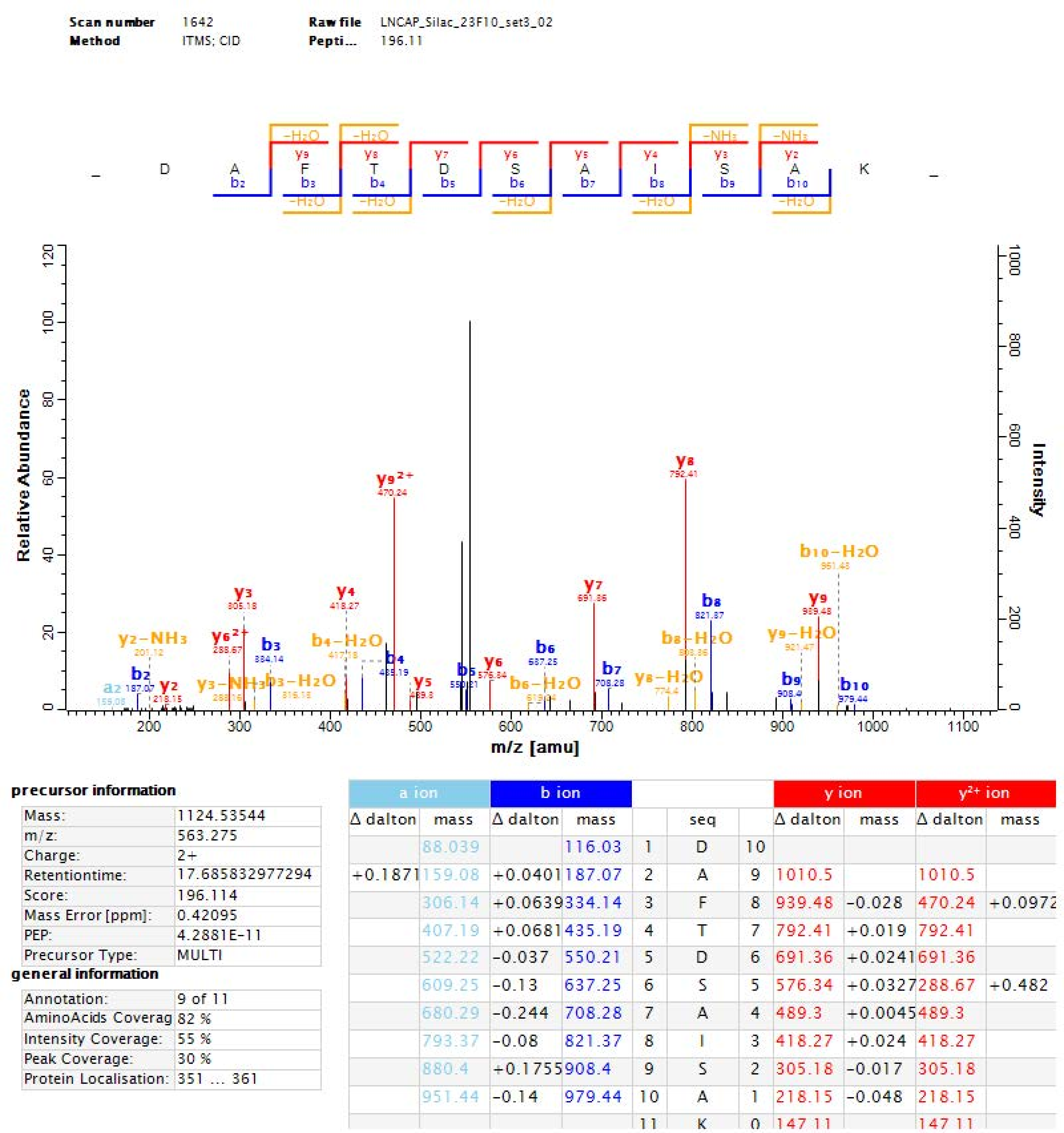
precursor information

Mass:	2453.27902
m/z:	818.76695
Charge:	3+
Retentiontime:	76.333229064941
Score:	62.99929
Mass Error [ppm]:	-0.48312
PEP:	0.00011563
Precursor Type:	MULTI

general information

Annotation:	16 of 24
AminoAcids Coverag	67 %
Intensity Coverage:	54 %
Peak Coverage:	31 %
Protein Localisation:	243 ... 266

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	23				
	171.11		171.11	2	V	22	2383.3		2383.3	
	285.16		285.16	3	N	21	2284.2		1142.6	+0.027
	372.19		372.19	4	S	20	2170.1		2170.1	
	471.26		471.26	5	V	19	2083.1		2083.1	
	542.29		542.29	6	A	18	1984		992.52	+0.1204
	629.33		629.33	7	S	17	1913		1913	
	730.37		730.37	8	T	16	1826		1826	
	831.42		831.42	9	T	15	1724.9		862.96	+0.1604
	888.44		888.44	10	G	14	1623.9		1623.9	
	959.48	-0.177	959.48	11	A	13	1566.9		1566.9	
	1056.5		1056.5	12	P	12	1495.8		748.41	+0.1765
	1153.6		1153.6	13	P	11	1398.8	+0.0625	1398.8	
	1339.7		1339.7	14	W	10	1301.7		1301.7	
	1410.7	-0.028	1410.7	15	A	9	1115.6	+0.0377	1115.6	
	1524.7		1524.7	16	N	8	1044.6	-0.13	1044.6	
	1637.8		1637.8	17	L	7	930.55		930.55	
-0.048	868.95	-0.125	1736.9	18	V	6	817.47		817.47	
	1823.9		1823.9	19	S	5	718.4	+0.0509	718.4	
	1937		1937	20	I	4	631.37		631.37	
+0.3235	1025.6		2050.1	21	L	3	518.28	+0.1558	518.28	
	2179.1		2179.1	22	E	2	405.2	+0.0704	405.2	
	2308.2		2308.2	23	E	1	276.16		276.16	
				24	K	0	147.11		147.11	



Scan number	1642	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	196.11

precursor information

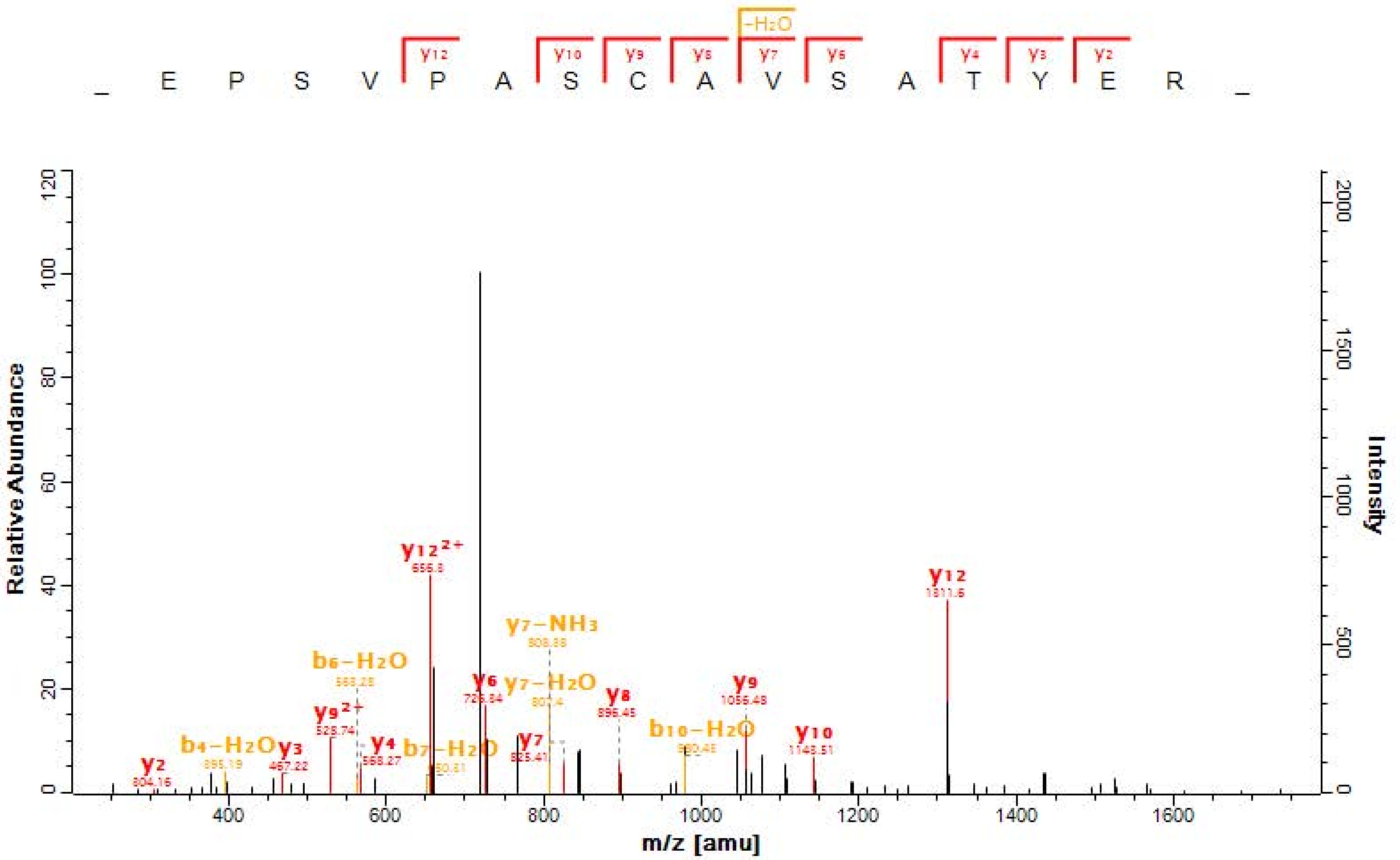
Mass:	1124.53544
m/z:	563.275
Charge:	2+
Retentiontime:	17.685832977294
Score:	196.114
Mass Error [ppm]:	0.42095
PEP:	4.2881E-11
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	55 %
Peak Coverage:	30 %
Protein Localisation:	351 ... 361

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	10				
+0.1871	159.08	+0.0401	187.07	2	A	9	1010.5		1010.5	
	306.14	+0.0639	334.14	3	F	8	939.48	-0.028	470.24	+0.0972
	407.19	+0.0681	435.19	4	T	7	792.41	+0.019	792.41	
	522.22	-0.037	550.21	5	D	6	691.36	+0.0241	691.36	
	609.25	-0.13	637.25	6	S	5	576.34	+0.0327	288.67	+0.482
	680.29	-0.244	708.28	7	A	4	489.3	+0.0045	489.3	
	793.37	-0.08	821.37	8	I	3	418.27	+0.024	418.27	
	880.4	+0.1755	908.4	9	S	2	305.18	-0.017	305.18	
	951.44	-0.14	979.44	10	A	1	218.15	-0.048	218.15	
				11	K	0	147.11		147.11	

Scan number	1927	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	50.61



precursor information

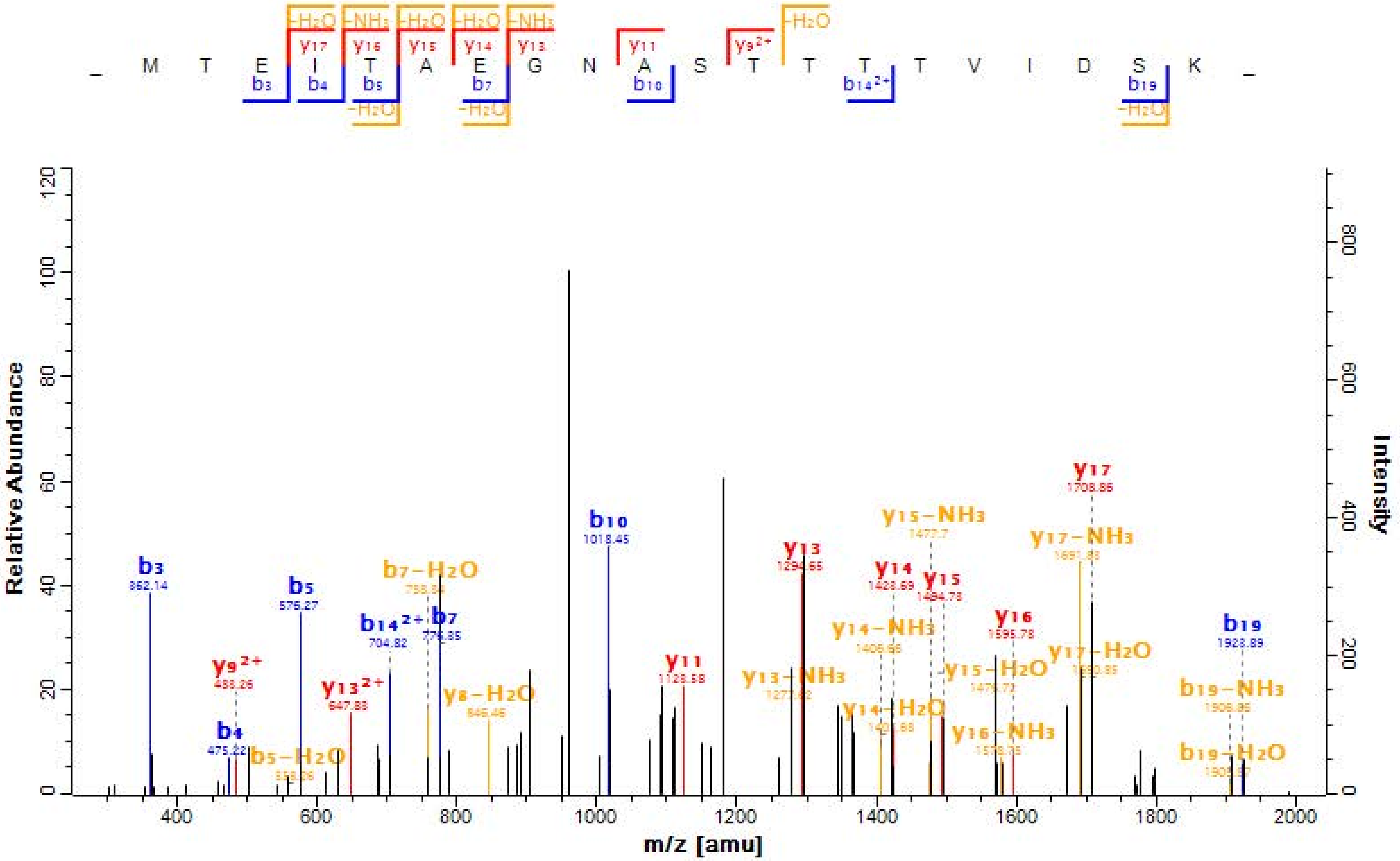
Mass:	1722.78938
m/z:	862.40197
Charge:	2+
Retentiontime:	19.540180206298
Score:	50.60823
Mass Error [ppm]:	0.62872
PEP:	0.013777
Precursor Type:	MULTI

general information

Annotation:	11 of 16
AminoAcids Coverag	69 %
Intensity Coverage:	36 %
Peak Coverage:	22 %
Protein Localisation:	588 ... 603

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	15				
	227.1026	2	P	14	1594.753		1594.753	
	314.1347	3	S	13	1497.7		1497.7	
	413.2031	4	V	12	1410.668		1410.668	
	510.2558	5	P	11	1311.6	-0.0479	656.3035	+0.266664
	581.293	6	A	10	1214.547		1214.547	
	668.325	7	S	9	1143.51	-0.05165	1143.51	
	828.3556	8	C	8	1056.478	-0.08859	528.7426	+0.217449
	899.3927	9	A	7	896.4472	+0.008527	896.4472	
	998.4612	10	V	6	825.4101	-0.00502	825.4101	
	1085.493	11	S	5	726.3417	-0.08199	726.3417	
	1156.53	12	A	4	639.3097		639.3097	
	1257.578	13	T	3	568.2726	+0.153534	568.2726	
	1420.641	14	Y	2	467.2249	-0.04665	467.2249	
	1549.684	15	E	1	304.1615	+0.135574	304.1615	
		16	R	0	175.119		175.119	

Scan number	2072	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	123.4



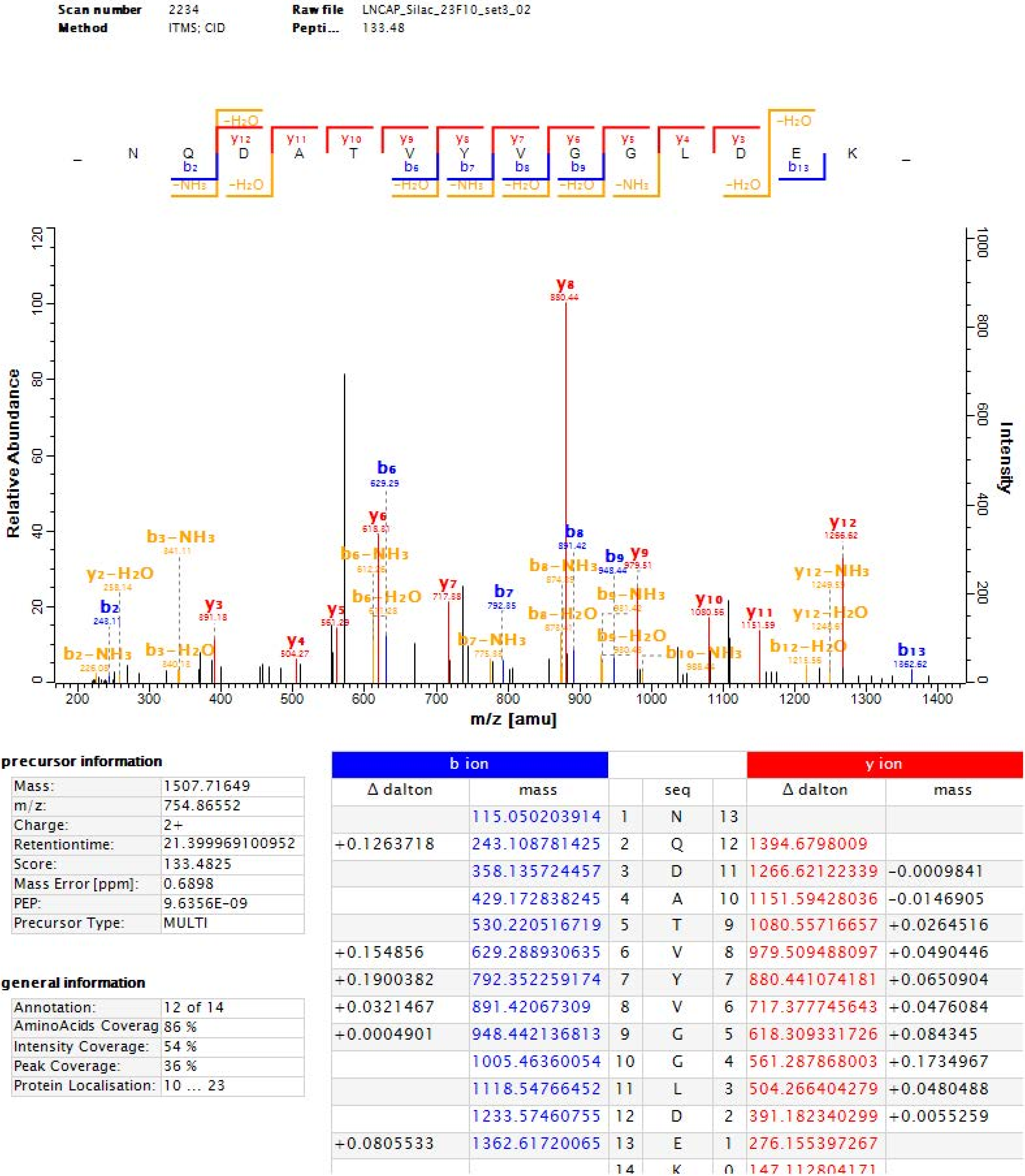
precursor information

Mass:	2068.98322
m/z:	1035.49889
Charge:	2+
Retentiontime:	20.466842651367
Score:	123.3966
Mass Error [ppm]:	-0.099652
PEP:	7.7215E-13
Precursor Type:	MULTI

general information

Annotation:	11 of 20
AminoAcids Coverag	55 %
Intensity Coverage:	34 %
Peak Coverage:	27 %
Protein Localisation:	1 ... 20

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	132.05		132.05	1	M	19				
	233.1		233.1	2	T	18	1939		1939	
	362.14	+0.0368	362.14	3	E	17	1837.9		1837.9	
	475.22	+0.1544	475.22	4	I	16	1708.9	-0.018	1708.9	
	576.27	+0.0544	576.27	5	T	15	1595.8	-0.223	1595.8	
	647.31		647.31	6	A	14	1494.7	-0.275	1494.7	
	776.35	+0.1075	776.35	7	E	13	1423.7	+0.0672	1423.7	
	833.37		833.37	8	G	12	1294.6	-0.028	647.83	+0.345
	947.41		947.41	9	N	11	1237.6		1237.6	
	1018.5	-0.237	1018.5	10	A	10	1123.6	-0.042	1123.6	
	1105.5		1105.5	11	S	9	1052.5		1052.5	
	1206.5		1206.5	12	T	8	965.51		483.26	+0.0722
	1307.6		1307.6	13	T	7	864.47		864.47	
-0.292	704.82		1408.6	14	T	6	763.42		763.42	
	1509.7		1509.7	15	T	5	662.37		662.37	
	1608.7		1608.7	16	V	4	561.32		561.32	
	1721.8		1721.8	17	I	3	462.26		462.26	
	1836.9		1836.9	18	D	2	349.17		349.17	
	1923.9	+0.1077	1923.9	19	S	1	234.14		234.14	
				20	K	0	147.11		147.11	



Scan number 2234

Method ITMS; CID

Raw file LNCAP_Silac_23F10_set3_02

Pepti... 133.48

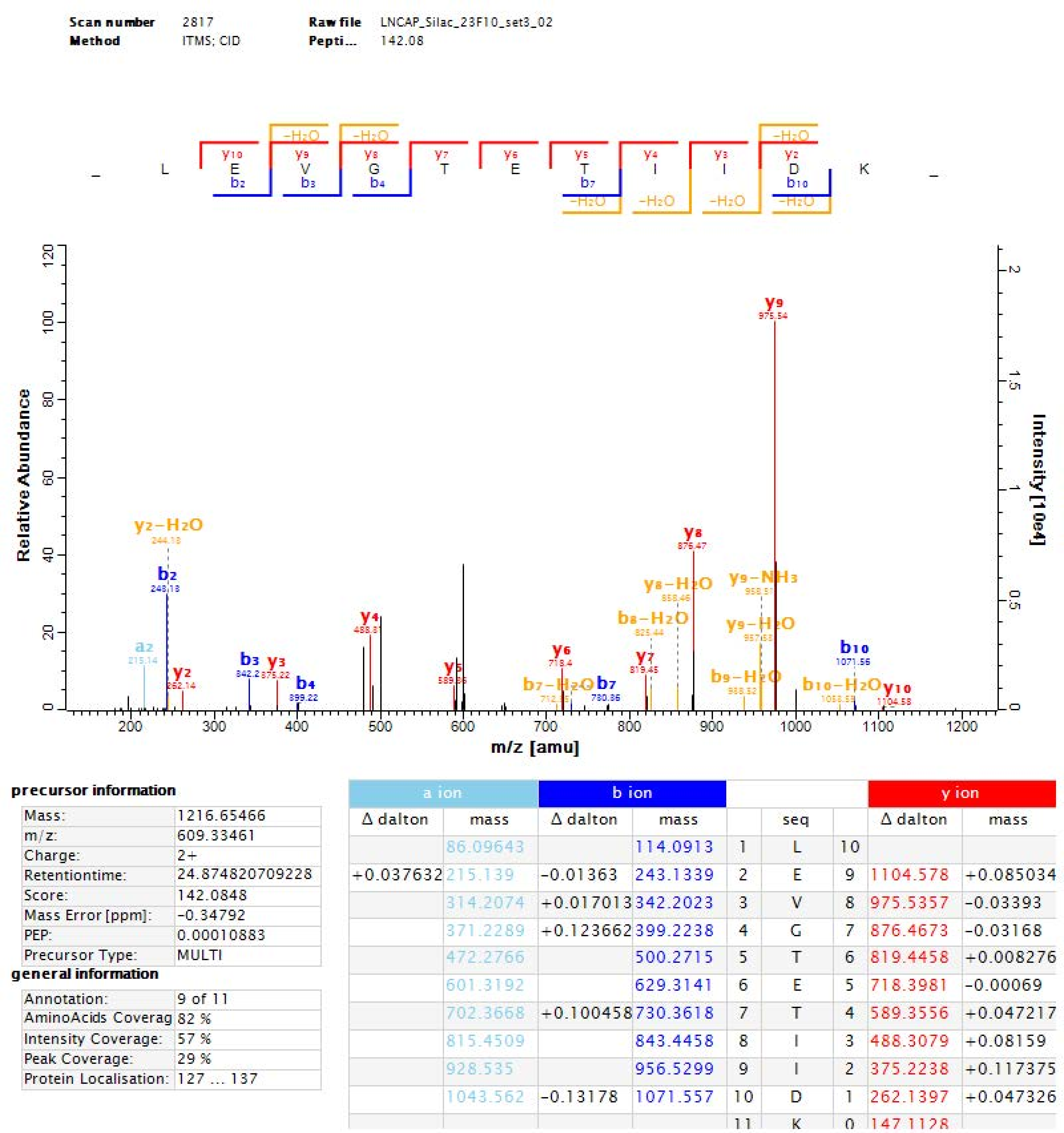
precursor information

Mass:	1507.71649
m/z:	754.86552
Charge:	2+
Retentiontime:	21.399969100952
Score:	133.4825
Mass Error [ppm]:	0.6898
PEP:	9.6356E-09
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	54 %
Peak Coverage:	36 %
Protein Localisation:	10 ... 23

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	115.050203914	1	N	13		
+0.1263718	243.108781425	2	Q	12	1394.6798009	
	358.135724457	3	D	11	1266.62122339	−0.0009841
	429.172838245	4	A	10	1151.59428036	−0.0146905
	530.220516719	5	T	9	1080.55716657	+0.0264516
+0.154856	629.288930635	6	V	8	979.509488097	+0.0490446
+0.1900382	792.352259174	7	Y	7	880.441074181	+0.0650904
+0.0321467	891.42067309	8	V	6	717.377745643	+0.0476084
+0.0004901	948.442136813	9	G	5	618.309331726	+0.084345
	1005.46360054	10	G	4	561.287868003	+0.1734967
	1118.54766452	11	L	3	504.266404279	+0.0480488
	1233.57460755	12	D	2	391.182340299	+0.0055259
+0.0805533	1362.61720065	13	E	1	276.155397267	
		14	K	0	147.112804171	



Scan number	2817	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	142.08

precursor information

Mass:	1216.65466
m/z:	609.33461
Charge:	2+
Retentiontime:	24.874820709228
Score:	142.0848
Mass Error [ppm]:	-0.34792
PEP:	0.00010883
Precursor Type:	MULTI

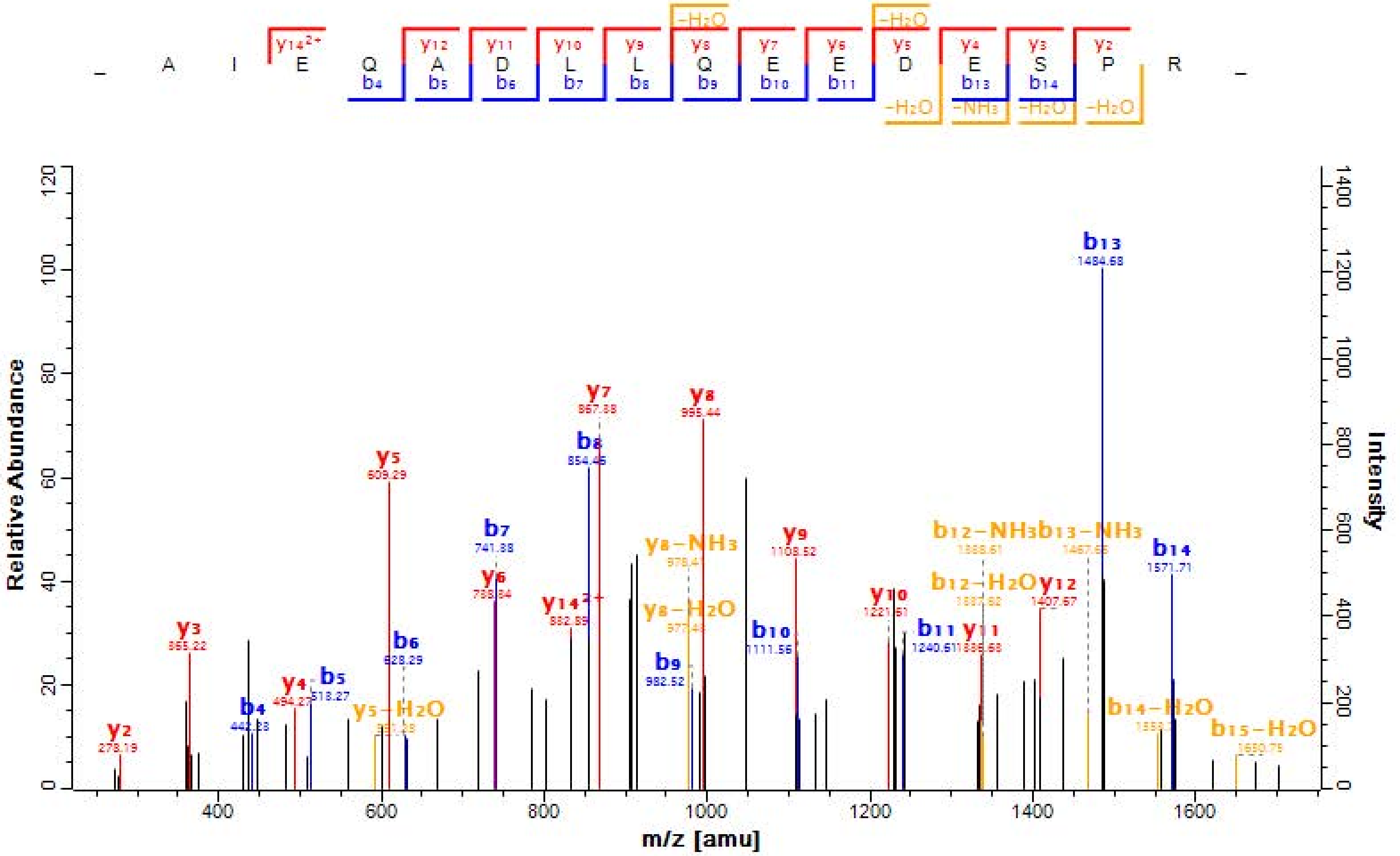
general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	57 %
Peak Coverage:	29 %
Protein Localisation:	127 ... 137

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	86.09643		114.0913	1	L	10		
+0.037632	215.139	-0.01363	243.1339	2	E	9	1104.578	+0.085034
	314.2074	+0.017013	342.2023	3	V	8	975.5357	-0.03393
	371.2289	+0.123662	399.2238	4	G	7	876.4673	-0.03168
	472.2766		500.2715	5	T	6	819.4458	+0.008276
	601.3192		629.3141	6	E	5	718.3981	-0.00069
	702.3668	+0.100458	730.3618	7	T	4	589.3556	+0.047217
	815.4509		843.4458	8	I	3	488.3079	+0.08159
	928.535		956.5299	9	I	2	375.2238	+0.117375
	1043.562	-0.13178	1071.557	10	D	1	262.1397	+0.047326
				11	K	0	147.1128	

Scan number 2904 **Raw file** LNCAP_Silac_23F10_set3_02

Method ITMS; CID **Pepti...** 116.51



precursor information

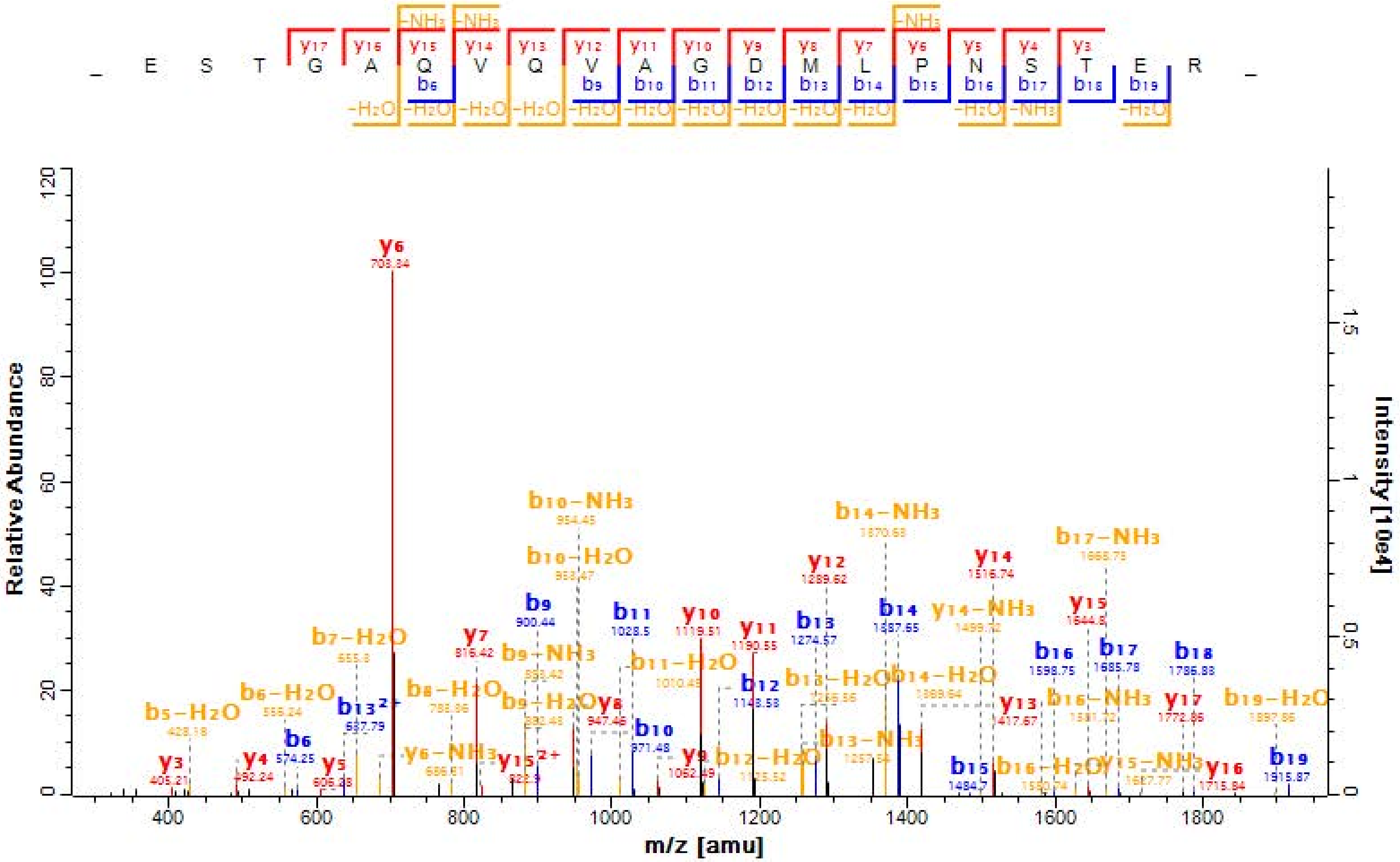
Mass:	1841.86359
m/z:	921.93907
Charge:	2+
Retentiontime:	25.346410751342
Score:	116.5128
Mass Error [ppm]:	-0.38629
PEP:	1.5699E-07
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	45 %
Peak Coverage:	34 %
Protein Localisation:	176 ... 191

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	15				
	185.1285	2	I	14	1777.855		1777.855	
	314.171	3	E	13	1664.771		832.8889	-0.00383
-0.44801	442.2296	4	Q	12	1535.728		1535.728	
-7.6E-05	513.2667	5	A	11	1407.669	+0.264236	1407.669	
+0.078083	628.2937	6	D	10	1336.632	-0.12931	1336.632	
+0.072877	741.3777	7	L	9	1221.605	+0.162033	1221.605	
+0.027814	854.4618	8	L	8	1108.521	+0.069705	1108.521	
+0.203307	982.5204	9	Q	7	995.4372	-0.01017	995.4372	
+0.02491	1111.563	10	E	6	867.3786	+0.01148	867.3786	
-0.0648	1240.606	11	E	5	738.336	-0.01197	738.336	
	1355.633	12	D	4	609.2934	+0.12401	609.2934	
-0.16608	1484.675	13	E	3	494.2665	+0.001905	494.2665	
-0.06566	1571.707	14	S	2	365.2239	+0.115146	365.2239	
	1668.76	15	P	1	278.1918	+0.059132	278.1918	
		16	R	0	181.1391		181.1391	

Scan number	3076	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	278.93



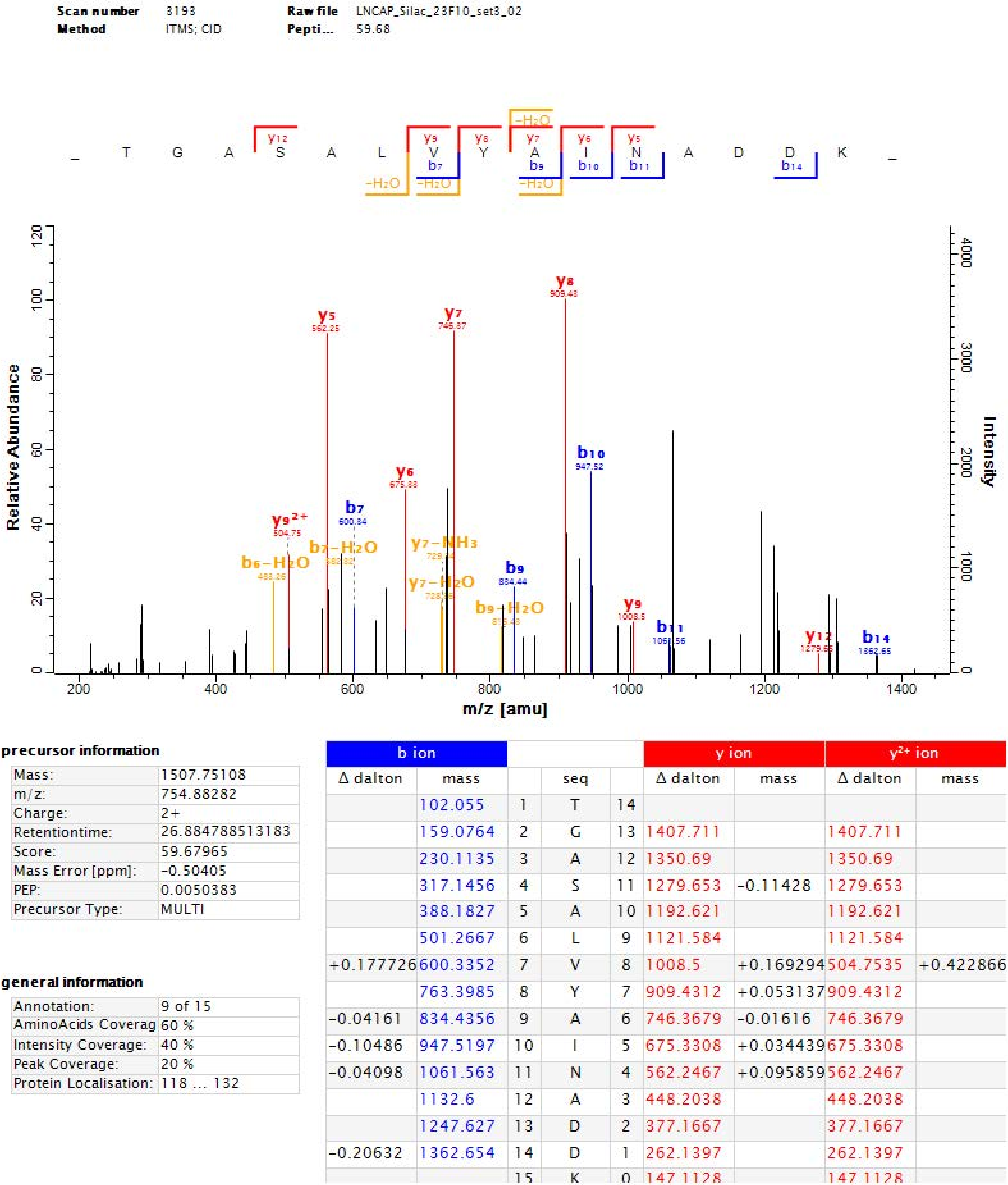
precursor information

Mass:	2088.97451
m/z:	1045.49453
Charge:	2+
Retentiontime:	26.265327453613
Score:	278.9311
Mass Error [ppm]:	-0.041109
PEP:	2.9186E-99
Precursor Type:	MULTI

general information

Annotation:	16 of 20
AminoAcids Coverag	80 %
Intensity Coverage:	72 %
Peak Coverage:	52 %
Protein Localisation:	125 ... 144

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	19				
	217.08		217.08	2	S	18	1960.9		1960.9	
	318.13		318.13	3	T	17	1873.9		1873.9	
	375.15		375.15	4	G	16	1772.9	-0.377	1772.9	
	446.19		446.19	5	A	15	1715.8	-0.127	1715.8	
	574.25	-0.003	574.25	6	Q	14	1644.8	+0.0177	822.9	+0.4483
	673.32		673.32	7	V	13	1516.7	+0.0232	1516.7	
	801.37		801.37	8	Q	12	1417.7	-0.072	1417.7	
	900.44	-0.018	900.44	9	V	11	1289.6	-0.009	1289.6	
	971.48	+0.0366	971.48	10	A	10	1190.5	-0.039	1190.5	
	1028.5	-0.227	1028.5	11	G	9	1119.5	-0.004	1119.5	
	1143.5	-0.167	1143.5	12	D	8	1062.5	+0.0384	1062.5	
+0.45	637.79	-0.126	1274.6	13	M	7	947.46	+0.0134	947.46	
	1387.7	-0.074	1387.7	14	L	6	816.42	+0.007	816.42	
	1484.7	-0.035	1484.7	15	P	5	703.34	+0.0199	703.34	
	1598.7	-0.015	1598.7	16	N	4	606.28	+0.0444	606.28	
	1685.8	-0.042	1685.8	17	S	3	492.24	+0.0748	492.24	
	1786.8	+0.0257	1786.8	18	T	2	405.21	+0.0306	405.21	
	1915.9	-0.039	1915.9	19	E	1	304.16		304.16	
				20	R	0	175.12		175.12	



Scan number	3193	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	59.68

precursor information

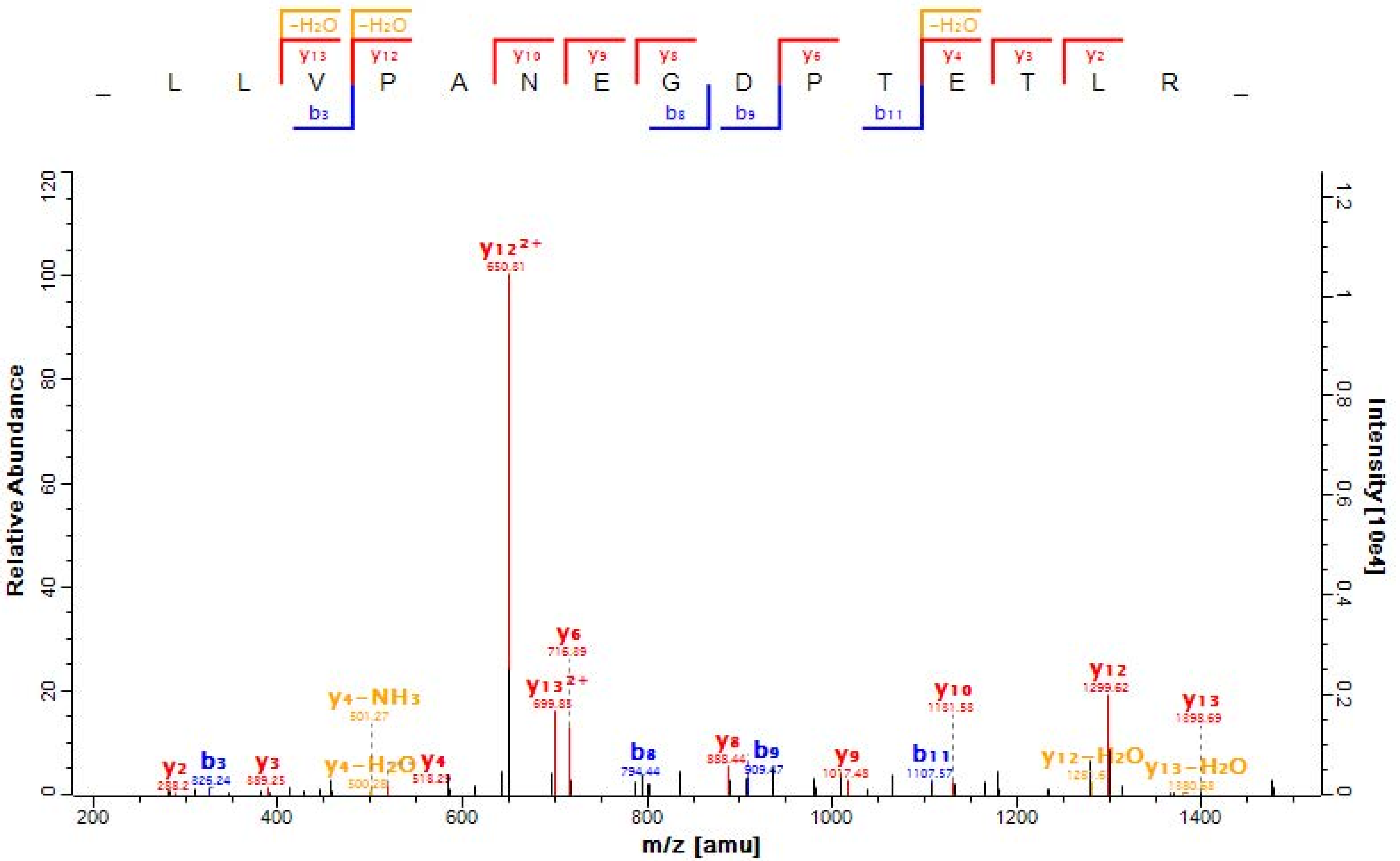
Mass:	1507.75108
m/z:	754.88282
Charge:	2+
Retentiontime:	26.884788513183
Score:	59.67965
Mass Error [ppm]:	-0.50405
PEP:	0.0050383
Precursor Type:	MULTI

general information

Annotation:	9 of 15
AminoAcids Coverag	60 %
Intensity Coverage:	40 %
Peak Coverage:	20 %
Protein Localisation:	118 ... 132

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055	1	T	14				
	159.0764	2	G	13	1407.711		1407.711	
	230.1135	3	A	12	1350.69		1350.69	
	317.1456	4	S	11	1279.653	-0.11428	1279.653	
	388.1827	5	A	10	1192.621		1192.621	
	501.2667	6	L	9	1121.584		1121.584	
+0.177726	600.3352	7	V	8	1008.5	+0.169294	504.7535	+0.422866
	763.3985	8	Y	7	909.4312	+0.053137	909.4312	
-0.04161	834.4356	9	A	6	746.3679	-0.01616	746.3679	
-0.10486	947.5197	10	I	5	675.3308	+0.034439	675.3308	
-0.04098	1061.563	11	N	4	562.2467	+0.095859	562.2467	
	1132.6	12	A	3	448.2038		448.2038	
	1247.627	13	D	2	377.1667		377.1667	
-0.20632	1362.654	14	D	1	262.1397		262.1397	
		15	K	0	147.1128		147.1128	

Scan number	3408	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	91.08



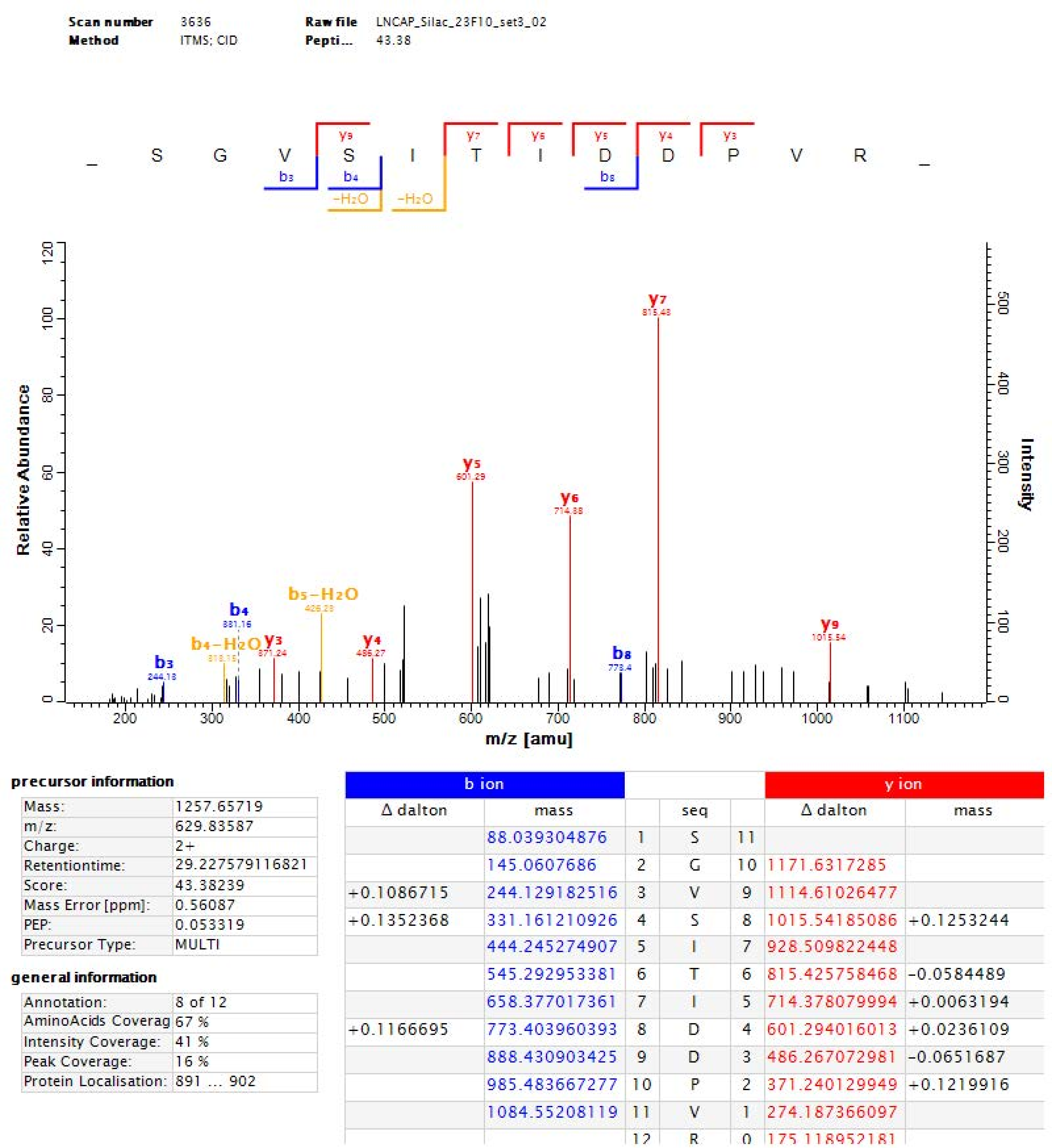
precursor information

Mass:	1623.84616
m/z:	812.93036
Charge:	2+
Retentiontime:	28.019496917724
Score:	91.07624
Mass Error [ppm]:	-0.3918
PEP:	0.00014277
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	55 %
Peak Coverage:	24 %
Protein Localisation:	325 ... 339

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	14				
	227.1754	2	L	13	1511.77		1511.77	
+0.04915	326.2438	3	V	12	1398.686	+0.134852	699.8466	+0.240607
	423.2966	4	P	11	1299.618	-0.04612	650.3124	+0.092379
	494.3337	5	A	10	1202.565		1202.565	
	608.3766	6	N	9	1131.528	-0.01191	1131.528	
	737.4192	7	E	8	1017.485	-0.05962	1017.485	
-0.2046	794.4407	8	G	7	888.4421	+0.005007	888.4421	
-0.04581	909.4676	9	D	6	831.4207		831.4207	
	1006.52	10	P	5	716.3937	-0.00634	716.3937	
-0.02412	1107.568	11	T	4	619.341		619.341	
	1236.611	12	E	3	518.2933	+0.065721	518.2933	
	1337.658	13	T	2	389.2507	-0.05367	389.2507	
	1450.742	14	L	1	288.203	+0.111406	288.203	
		15	R	0	175.119		175.119	



Scan number	3636	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	43.38

precursor information

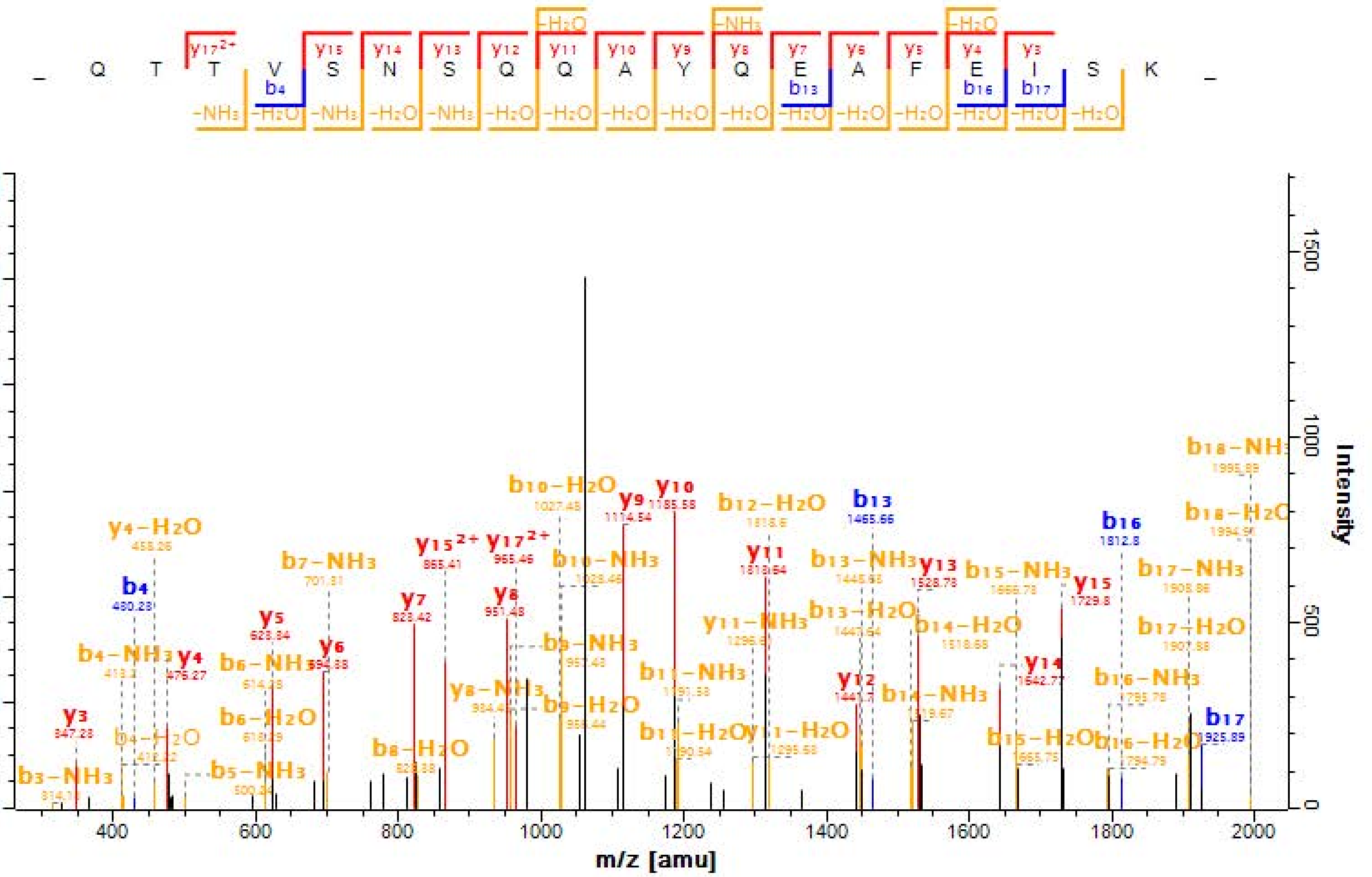
Mass:	1257.65719
m/z:	629.83587
Charge:	2+
Retentiontime:	29.227579116821
Score:	43.38239
Mass Error [ppm]:	0.56087
PEP:	0.053319
Precursor Type:	MULTI

general information

Annotation:	8 of 12
AminoAcids Coverag	67 %
Intensity Coverage:	41 %
Peak Coverage:	16 %
Protein Localisation:	891 ... 902

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	88.039304876	1	S	11		
	145.0607686	2	G	10	1171.6317285	
+0.1086715	244.129182516	3	V	9	1114.61026477	
+0.1352368	331.161210926	4	S	8	1015.54185086	+0.1253244
	444.245274907	5	I	7	928.509822448	
	545.292953381	6	T	6	815.425758468	-0.0584489
	658.377017361	7	I	5	714.378079994	+0.0063194
+0.1166695	773.403960393	8	D	4	601.294016013	+0.0236109
	888.430903425	9	D	3	486.267072981	-0.0651687
	985.483667277	10	P	2	371.240129949	+0.1219916
	1084.55208119	11	V	1	274.187366097	
		12	R	0	175.118952181	

Scan number	3915	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	151.95



precursor information

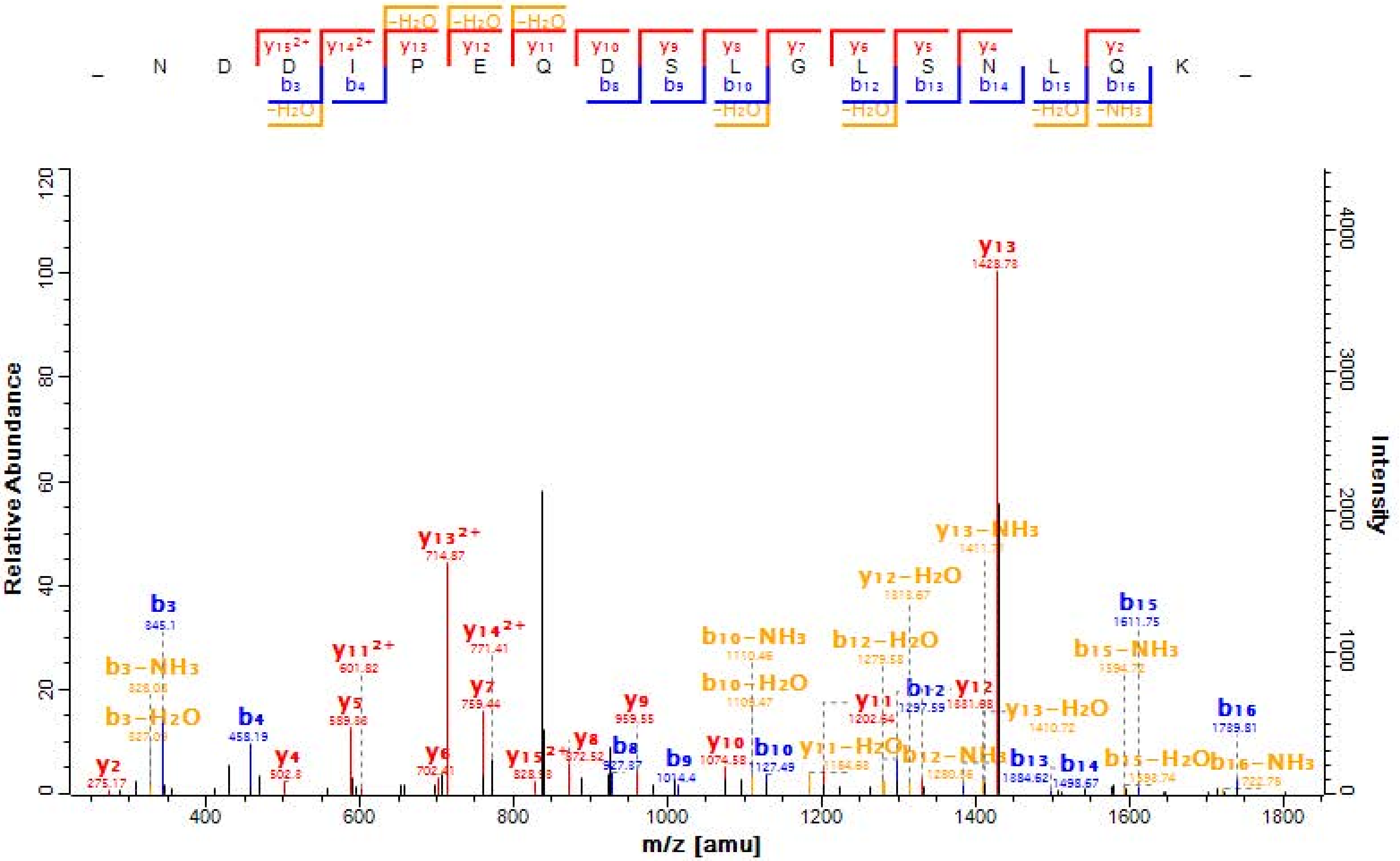
Mass:	2158.01552
m/z:	1080.01504
Charge:	2+
Retentiontime:	30.702781677246
Score:	151.948
Mass Error [ppm]:	-1.0756
PEP:	3.7589E-13
Precursor Type:	ISO

general information

Annotation:	16 of 19
AminoAcids Coverag	84 %
Intensity Coverage:	59 %
Peak Coverage:	53 %
Protein Localisation:	141 ... 159

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.0659	1	Q	18				
	230.1135	2	T	17	2030.967		2030.967	
	331.1612	3	T	16	1929.919		965.4631	+0.372624
+0.166249	430.2296	4	V	15	1828.871		1828.871	
	517.2617	5	S	14	1729.803	-0.16471	865.405	+0.153327
	631.3046	6	N	13	1642.771	-0.09923	1642.771	
	718.3366	7	S	12	1528.728	-0.11832	1528.728	
	846.3952	8	Q	11	1441.696	-0.21226	1441.696	
	974.4538	9	Q	10	1313.637	-0.09168	1313.637	
	1045.491	10	A	9	1185.579	+0.016218	1185.579	
	1208.554	11	Y	8	1114.542	+0.006945	1114.542	
	1336.613	12	Q	7	951.4782	-0.02091	951.4782	
-0.30919	1465.655	13	E	6	823.4196	+0.042426	823.4196	
	1536.692	14	A	5	694.377	+0.081357	694.377	
	1683.761	15	F	4	623.3399	+0.06476	623.3399	
-0.04288	1812.803	16	E	3	476.2715	+0.059992	476.2715	
+0.184826	1925.888	17	I	2	347.2289	+0.130784	347.2289	
	2012.92	18	S	1	234.1448		234.1448	
		19	K	0	147.1128		147.1128	

Scan number	4083	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	210.39



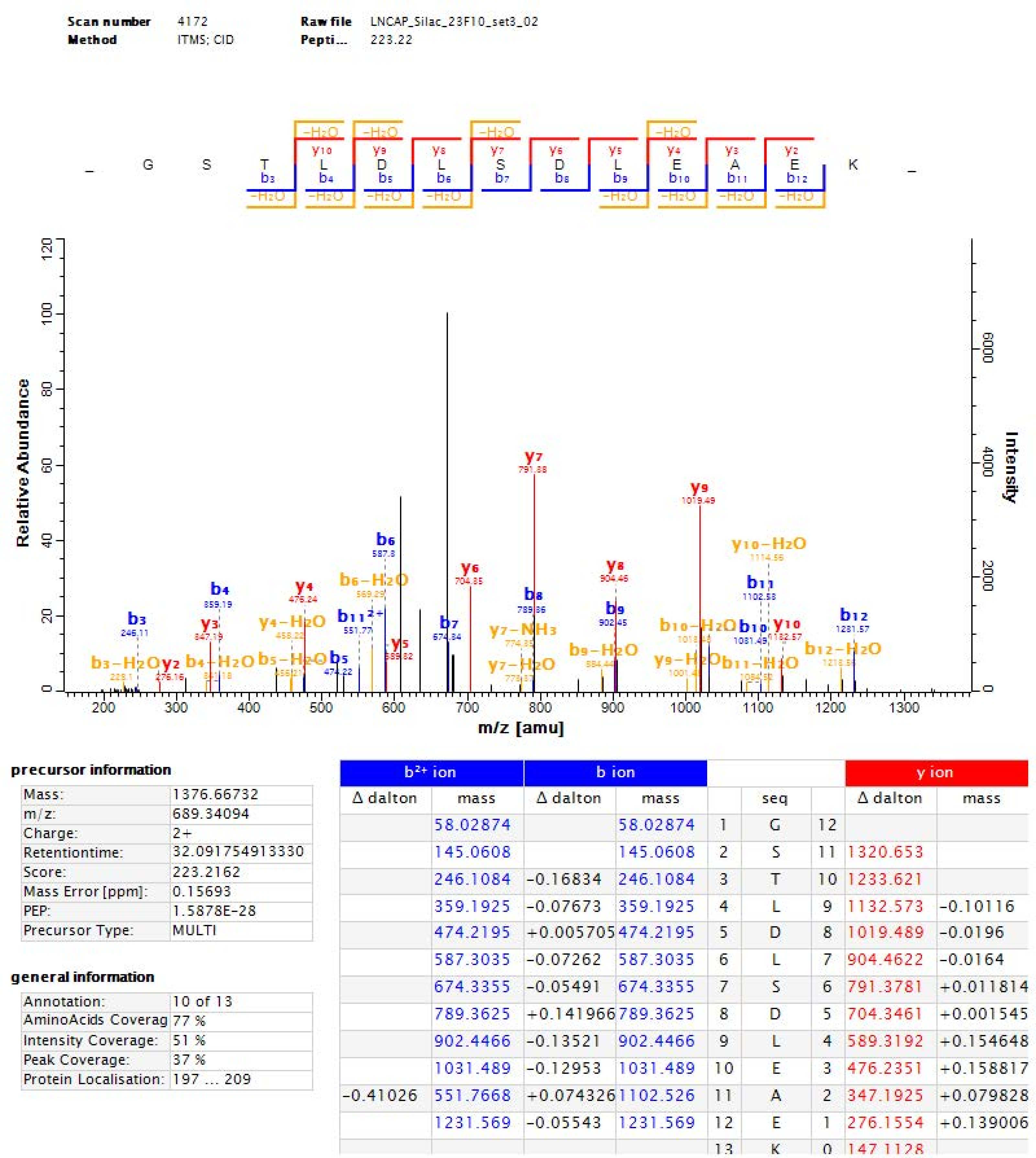
precursor information

Mass:	1884.90622
m/z:	943.46039
Charge:	2+
Retentiontime:	31.613727569580
Score:	210.3904
Mass Error [ppm]:	-0.14945
PEP:	3.9663E-40
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	55 %
Peak Coverage:	43 %
Protein Localisation:	41 ... 57

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502	1	N	16				
	230.0771	2	D	15	1771.871		1771.871	
+0.005316	345.1041	3	D	14	1656.844		828.9256	+0.13111
+0.006914	458.1882	4	I	13	1541.817		771.4121	-0.07197
	555.2409	5	P	12	1428.733	-0.09667	714.8701	+0.183318
	684.2835	6	E	11	1331.68	-0.08504	1331.68	
	812.3421	7	Q	10	1202.638	-0.01852	601.8224	+0.065347
-0.09968	927.369	8	D	9	1074.579	-0.07591	1074.579	
+0.063723	1014.401	9	S	8	959.552	+0.156169	959.552	
-0.05007	1127.485	10	L	7	872.52	+0.115078	872.52	
	1184.507	11	G	6	759.4359	+0.038436	759.4359	
-0.06514	1297.591	12	L	5	702.4145	-0.00187	702.4145	
-0.1355	1384.623	13	S	4	589.3304	+0.02403	589.3304	
-0.02657	1498.666	14	N	3	502.2984	+0.170926	502.2984	
-0.07963	1611.75	15	L	2	388.2554		388.2554	
-0.05459	1739.808	16	Q	1	275.1714	+0.129766	275.1714	
		17	K	0	147.1128		147.1128	



Scan number 4172
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set3_02
Pepti... 223.22

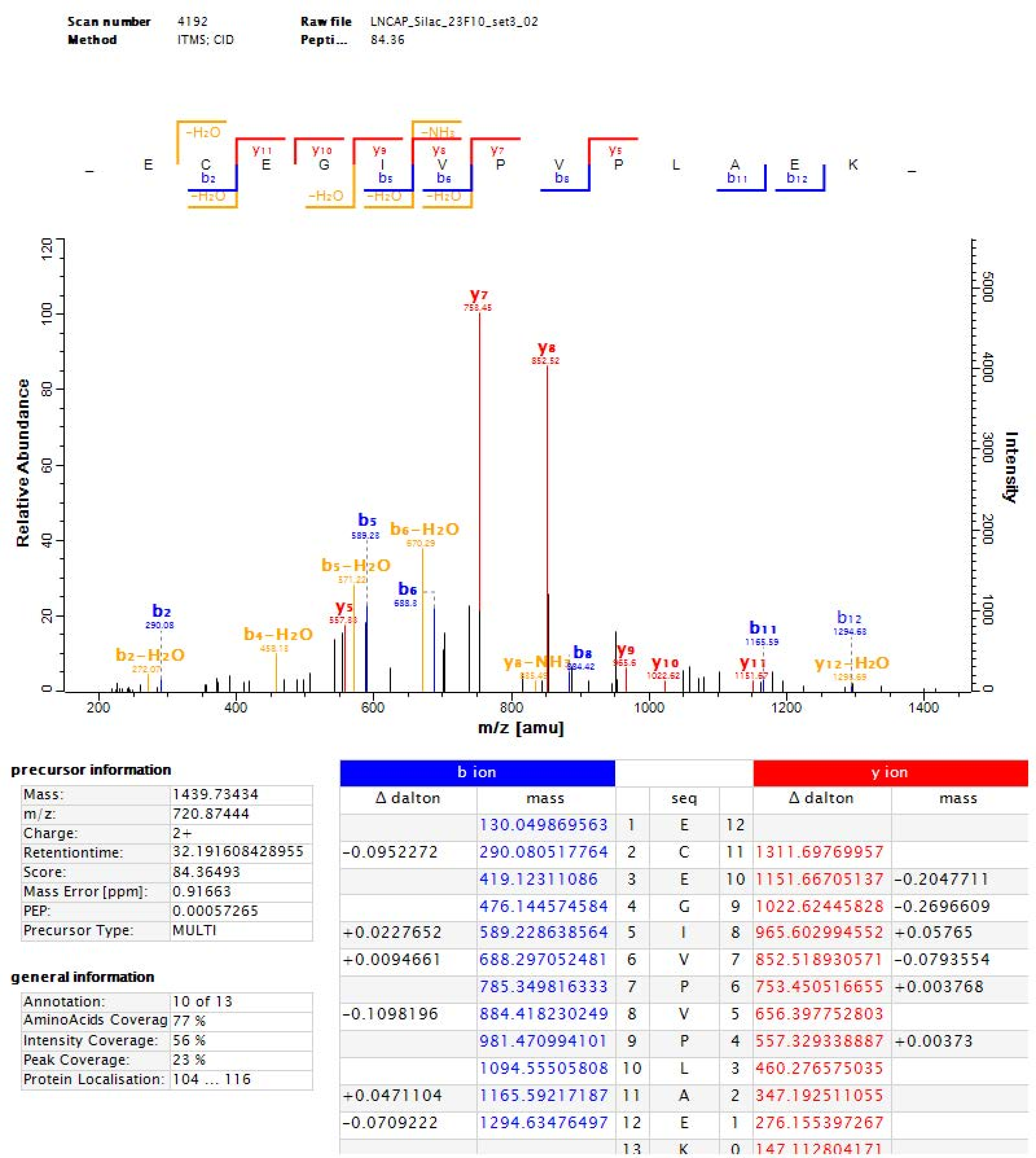
precursor information

Mass:	1376.66732
m/z:	689.34094
Charge:	2+
Retentiontime:	32.091754913330
Score:	223.2162
Mass Error [ppm]:	0.15693
PEP:	1.5878E-28
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	51 %
Peak Coverage:	37 %
Protein Localisation:	197 ... 209

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	58.02874		58.02874	1	G	12		
	145.0608		145.0608	2	S	11	1320.653	
	246.1084	-0.16834	246.1084	3	T	10	1233.621	
	359.1925	-0.07673	359.1925	4	L	9	1132.573	-0.10116
	474.2195	+0.005705	474.2195	5	D	8	1019.489	-0.0196
	587.3035	-0.07262	587.3035	6	L	7	904.4622	-0.0164
	674.3355	-0.05491	674.3355	7	S	6	791.3781	+0.011814
	789.3625	+0.141966	789.3625	8	D	5	704.3461	+0.001545
	902.4466	-0.13521	902.4466	9	L	4	589.3192	+0.154648
	1031.489	-0.12953	1031.489	10	E	3	476.2351	+0.158817
-0.41026	551.7668	+0.074326	1102.526	11	A	2	347.1925	+0.079828
	1231.569	-0.05543	1231.569	12	E	1	276.1554	+0.139006
				13	K	0	147.1128	



Scan number	4192	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	84.36

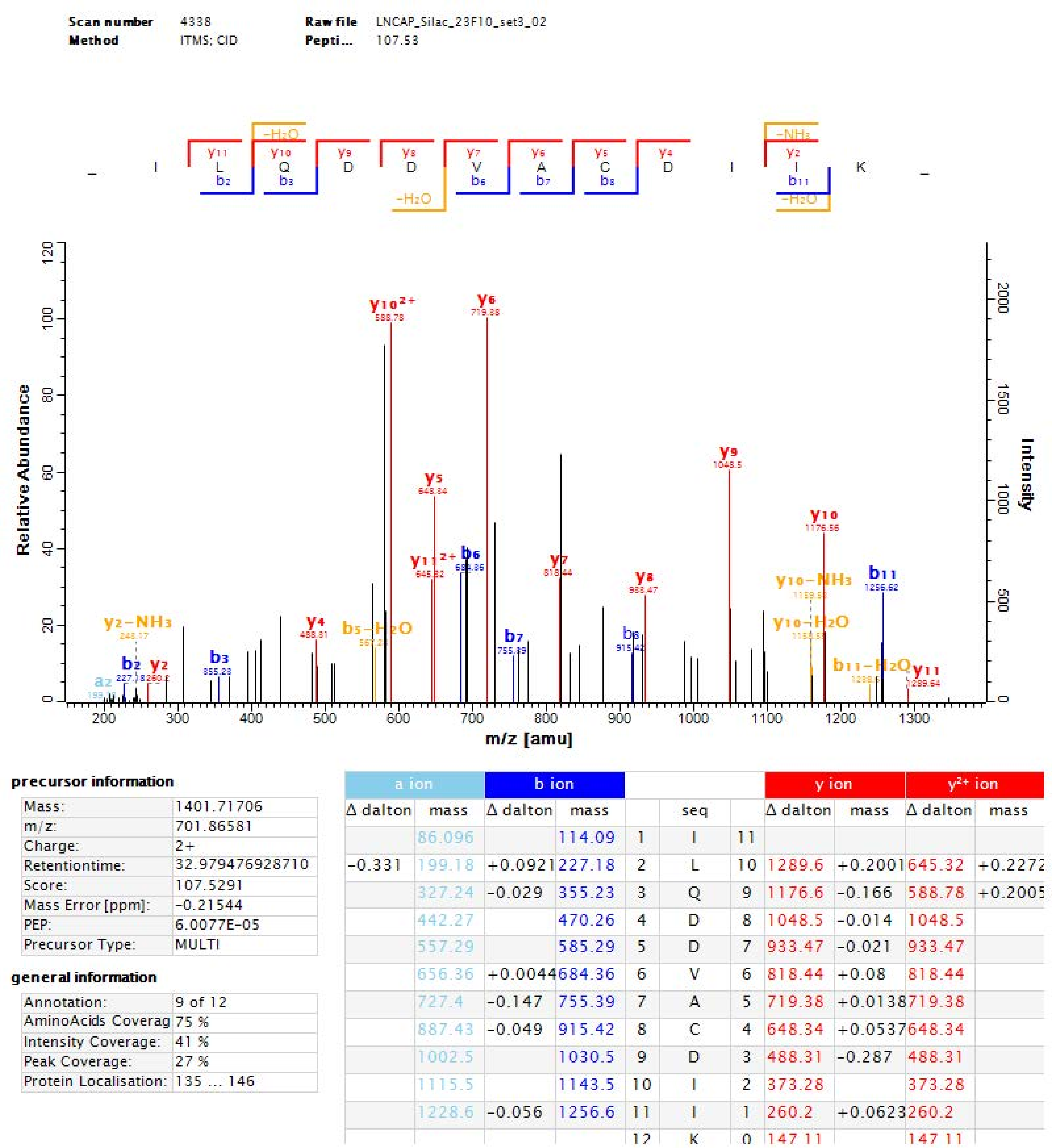
precursor information

Mass:	1439.73434
m/z:	720.87444
Charge:	2+
Retentiontime:	32.191608428955
Score:	84.36493
Mass Error [ppm]:	0.91663
PEP:	0.00057265
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	56 %
Peak Coverage:	23 %
Protein Localisation:	104 ... 116

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	130.049869563	1	E	12		
-0.0952272	290.080517764	2	C	11	1311.69769957	
	419.12311086	3	E	10	1151.66705137	-0.2047711
	476.144574584	4	G	9	1022.62445828	-0.2696609
+0.0227652	589.228638564	5	I	8	965.602994552	+0.05765
+0.0094661	688.297052481	6	V	7	852.518930571	-0.0793554
	785.349816333	7	P	6	753.450516655	+0.003768
-0.1098196	884.418230249	8	V	5	656.397752803	
	981.470994101	9	P	4	557.329338887	+0.00373
	1094.55505808	10	L	3	460.276575035	
+0.0471104	1165.59217187	11	A	2	347.192511055	
-0.0709222	1294.63476497	12	E	1	276.155397267	
		13	K	0	147.112804171	



Scan number	4338	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	107.53

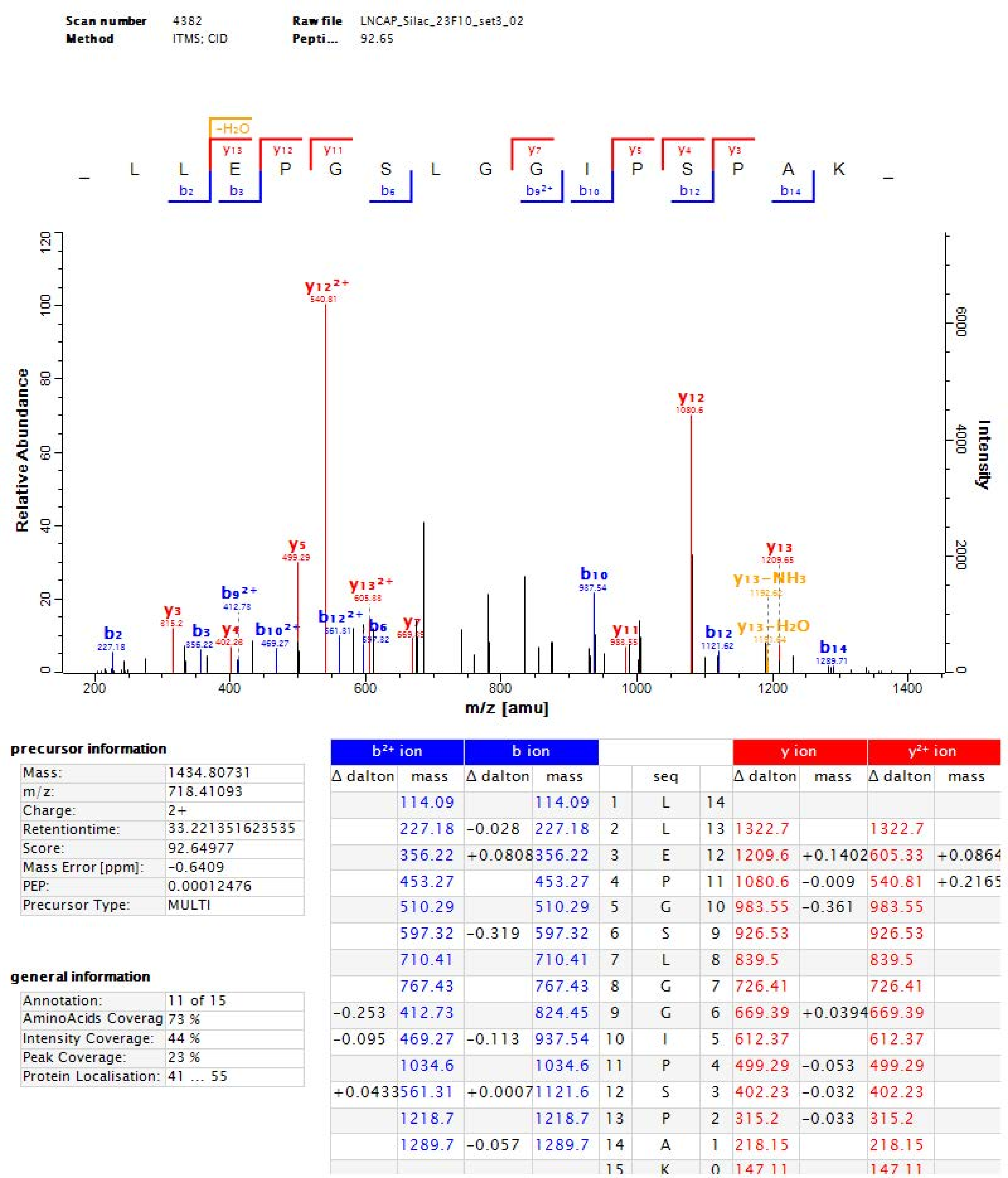
precursor information

Mass:	1401.71706
m/z:	701.86581
Charge:	2+
Retentiontime:	32.979476928710
Score:	107.5291
Mass Error [ppm]:	-0.21544
PEP:	6.0077E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	41 %
Peak Coverage:	27 %
Protein Localisation:	135 ... 146

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	11				
-0.331	199.18	+0.0921	227.18	2	L	10	1289.6	+0.2001	645.32	+0.2272
	327.24	-0.029	355.23	3	Q	9	1176.6	-0.166	588.78	+0.2005
	442.27		470.26	4	D	8	1048.5	-0.014	1048.5	
	557.29		585.29	5	D	7	933.47	-0.021	933.47	
	656.36	+0.0044	684.36	6	V	6	818.44	+0.08	818.44	
	727.4	-0.147	755.39	7	A	5	719.38	+0.0138	719.38	
	887.43	-0.049	915.42	8	C	4	648.34	+0.0537	648.34	
	1002.5		1030.5	9	D	3	488.31	-0.287	488.31	
	1115.5		1143.5	10	I	2	373.28		373.28	
	1228.6	-0.056	1256.6	11	I	1	260.2	+0.0623	260.2	
				12	K	0	147.11		147.11	



Scan number	4382	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	92.65

precursor information

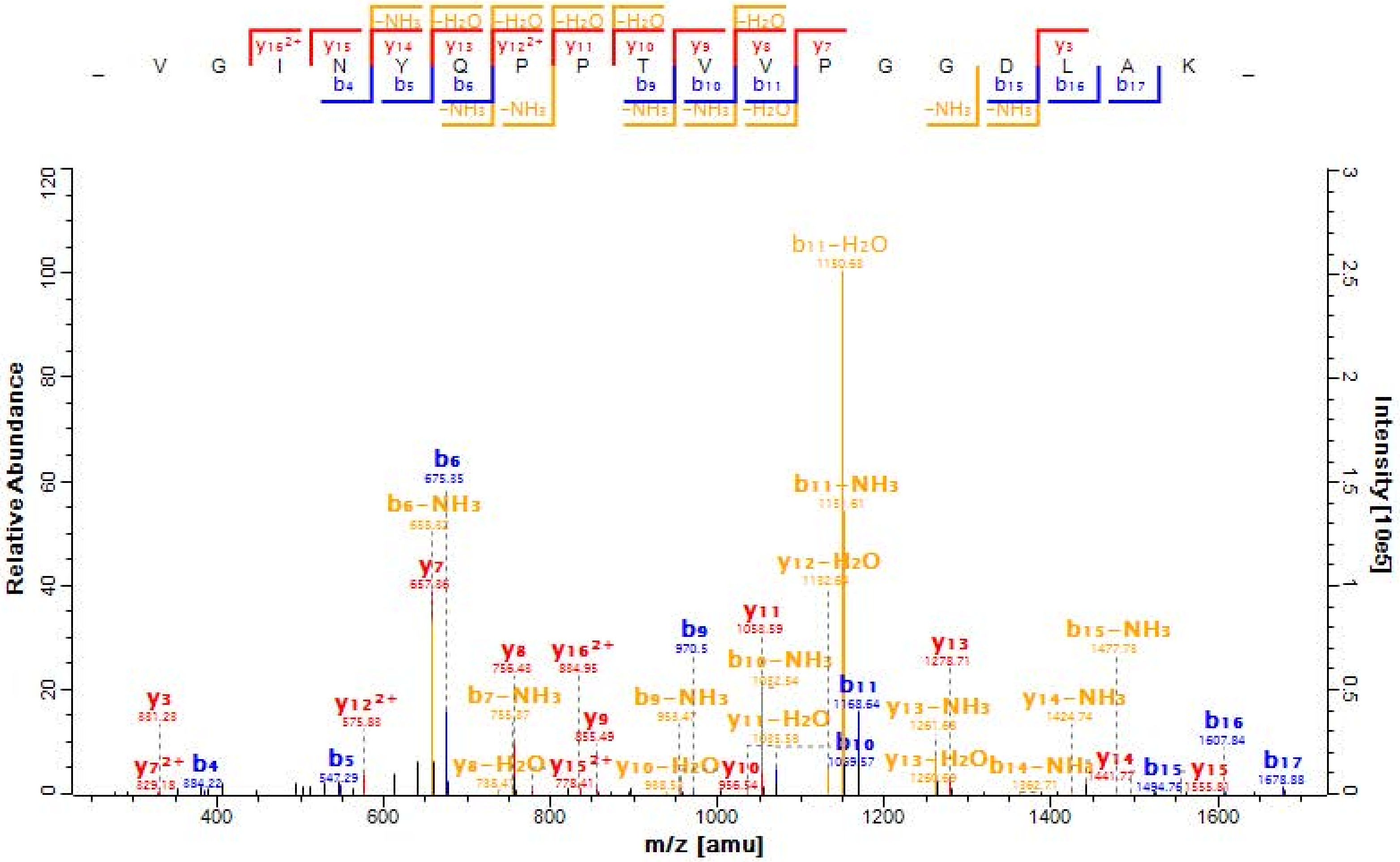
Mass:	1434.80731
m/z:	718.41093
Charge:	2+
Retentiontime:	33.221351623535
Score:	92.64977
Mass Error [ppm]:	-0.6409
PEP:	0.00012476
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	44 %
Peak Coverage:	23 %
Protein Localisation:	41 ... 55

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	14				
	227.18	-0.028	227.18	2	L	13	1322.7		1322.7	
	356.22	+0.0808	356.22	3	E	12	1209.6	+0.1402	605.33	+0.0864
	453.27		453.27	4	P	11	1080.6	-0.009	540.81	+0.2165
	510.29		510.29	5	G	10	983.55	-0.361	983.55	
	597.32	-0.319	597.32	6	S	9	926.53		926.53	
	710.41		710.41	7	L	8	839.5		839.5	
	767.43		767.43	8	G	7	726.41		726.41	
-0.253	412.73		824.45	9	G	6	669.39	+0.0394	669.39	
-0.095	469.27	-0.113	937.54	10	I	5	612.37		612.37	
	1034.6		1034.6	11	P	4	499.29	-0.053	499.29	
+0.0433	561.31	+0.0007	1121.6	12	S	3	402.23	-0.032	402.23	
	1218.7		1218.7	13	P	2	315.2	-0.033	315.2	
	1289.7	-0.057	1289.7	14	A	1	218.15		218.15	
				15	K	0	147.11		147.11	

Scan number	4583	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	187.78



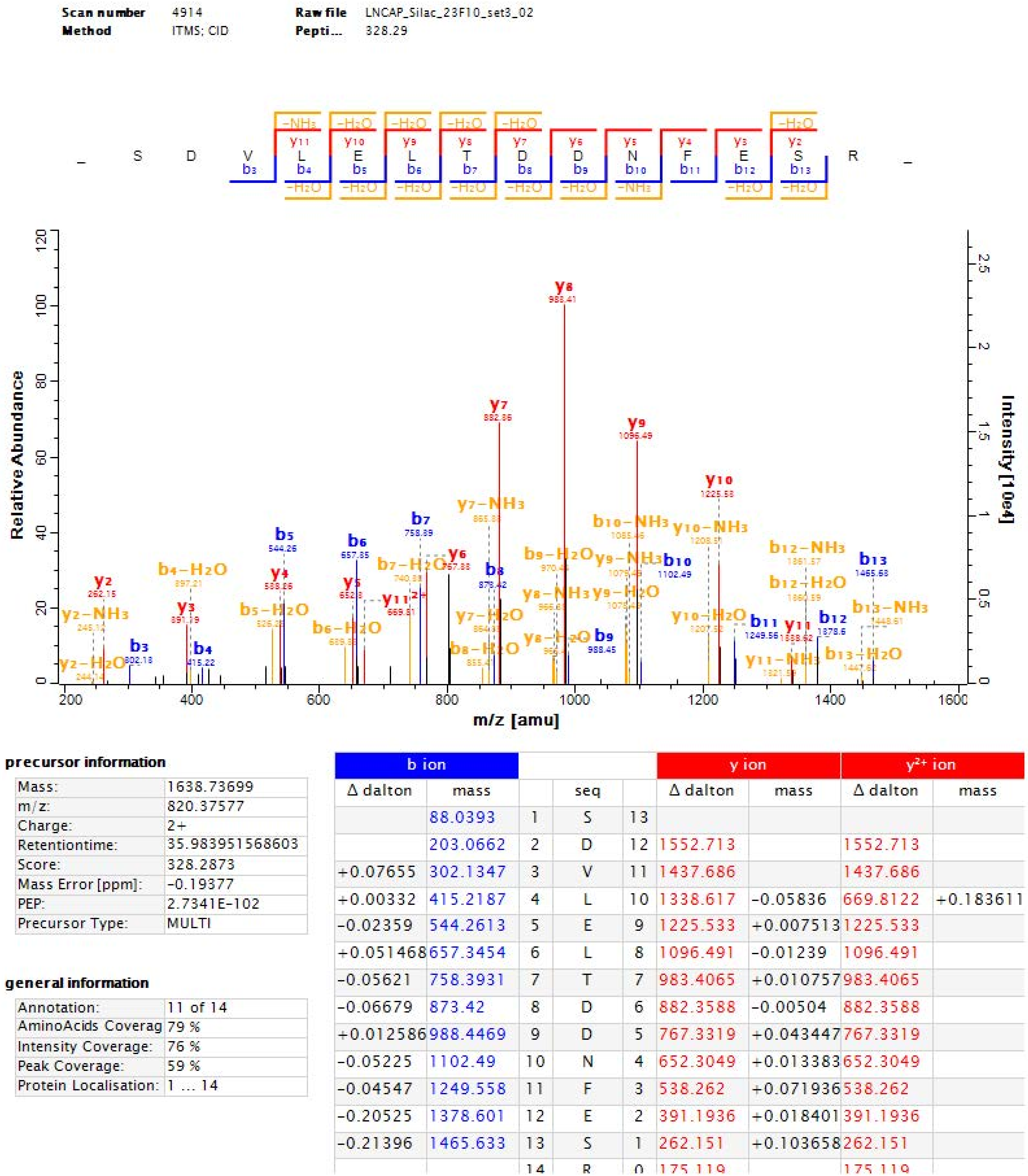
precursor information

Mass:	1823.97804
m/z:	912.9963
Charge:	2+
Retentiontime:	34.262466430664
Score:	187.776
Mass Error [ppm]:	-0.058609
PEP:	1.3114E-34
Precursor Type:	MULTI

general information

Annotation:	14 of 18
AminoAcids Coverag	78 %
Intensity Coverage:	82 %
Peak Coverage:	43 %
Protein Localisation:	353 ... 370

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	17				
	157.0972	2	G	16	1725.917		1725.917	
	270.1812	3	I	15	1668.896		834.9514	+0.129582
+0.09281	384.2241	4	N	14	1555.811	+0.04838	778.4094	+0.290632
+0.060915	547.2875	5	Y	13	1441.769	-0.06726	1441.769	
+0.009112	675.3461	6	Q	12	1278.705	-0.05752	1278.705	
	772.3988	7	P	11	1150.647		575.827	+0.324648
	869.4516	8	P	10	1053.594	+0.029405	1053.594	
-0.03393	970.4993	9	T	9	956.5411	+0.024734	956.5411	
-0.002	1069.568	10	V	8	855.4934	+0.079981	855.4934	
-0.09068	1168.636	11	V	7	756.425	-0.03959	756.425	
	1265.689	12	P	6	657.3566	-0.02086	329.1819	+0.056396
	1322.71	13	G	5	560.3039		560.3039	
	1379.732	14	G	4	503.2824		503.2824	
-0.1159	1494.759	15	D	3	446.2609		446.2609	
+0.082753	1607.843	16	L	2	331.234	+0.122341	331.234	
-0.04323	1678.88	17	A	1	218.1499		218.1499	
		18	K	0	147.1128		147.1128	



Scan number	4914	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	328.29

precursor information

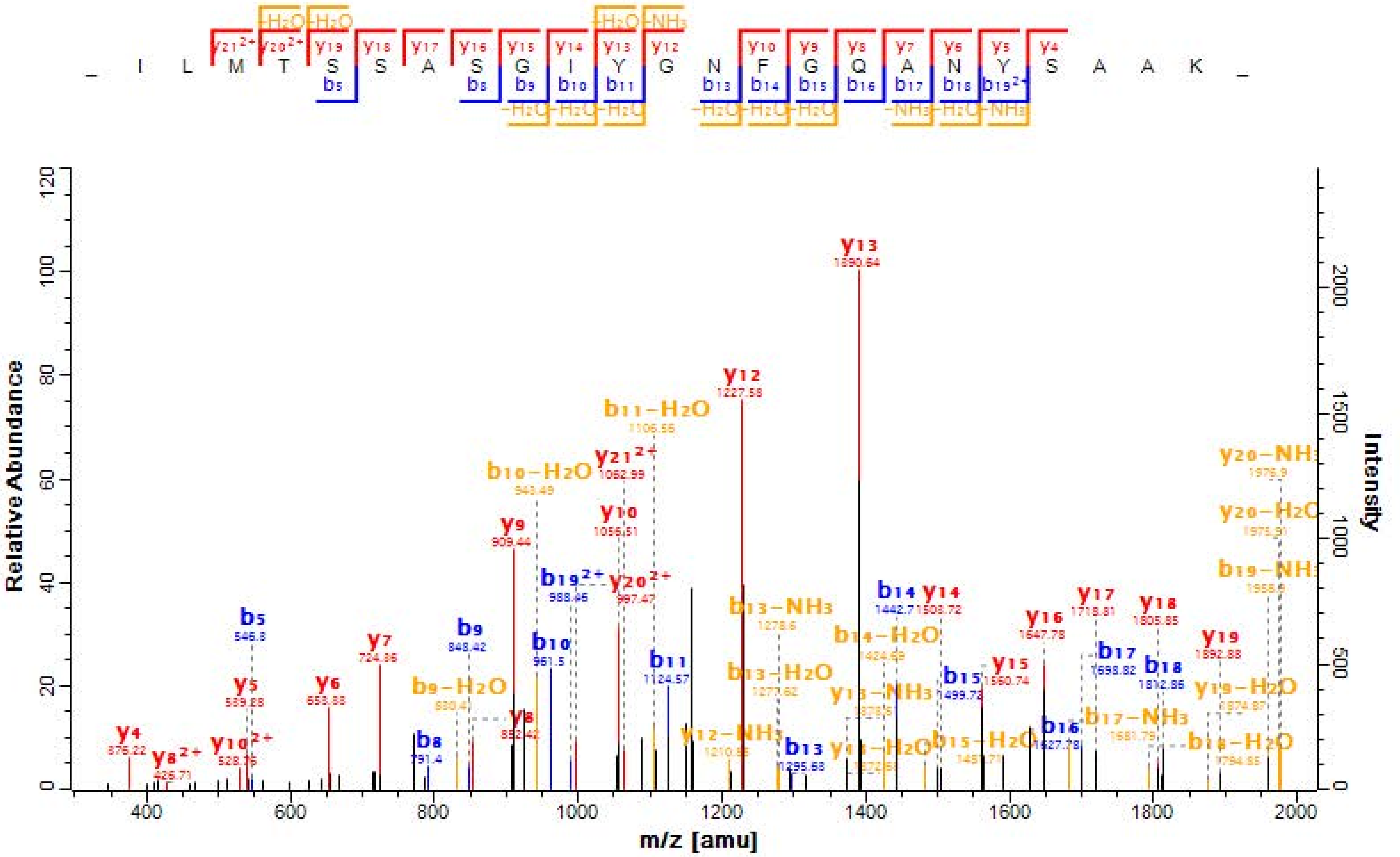
Mass:	1638.73699
m/z:	820.37577
Charge:	2+
Retentiontime:	35.983951568603
Score:	328.2873
Mass Error [ppm]:	-0.19377
PEP:	2.7341E-102
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	76 %
Peak Coverage:	59 %
Protein Localisation:	1 ... 14

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	13				
	203.0662	2	D	12	1552.713		1552.713	
+0.07655	302.1347	3	V	11	1437.686		1437.686	
+0.00332	415.2187	4	L	10	1338.617	-0.05836	669.8122	+0.183611
-0.02359	544.2613	5	E	9	1225.533	+0.007513	1225.533	
+0.051468	657.3454	6	L	8	1096.491	-0.01239	1096.491	
-0.05621	758.3931	7	T	7	983.4065	+0.010757	983.4065	
-0.06679	873.42	8	D	6	882.3588	-0.00504	882.3588	
+0.012586	988.4469	9	D	5	767.3319	+0.043447	767.3319	
-0.05225	1102.49	10	N	4	652.3049	+0.013383	652.3049	
-0.04547	1249.558	11	F	3	538.262	+0.071936	538.262	
-0.20525	1378.601	12	E	2	391.1936	+0.018401	391.1936	
-0.21396	1465.633	13	S	1	262.151	+0.103658	262.151	
		14	R	0	175.119		175.119	

Scan number	5113	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	235.92



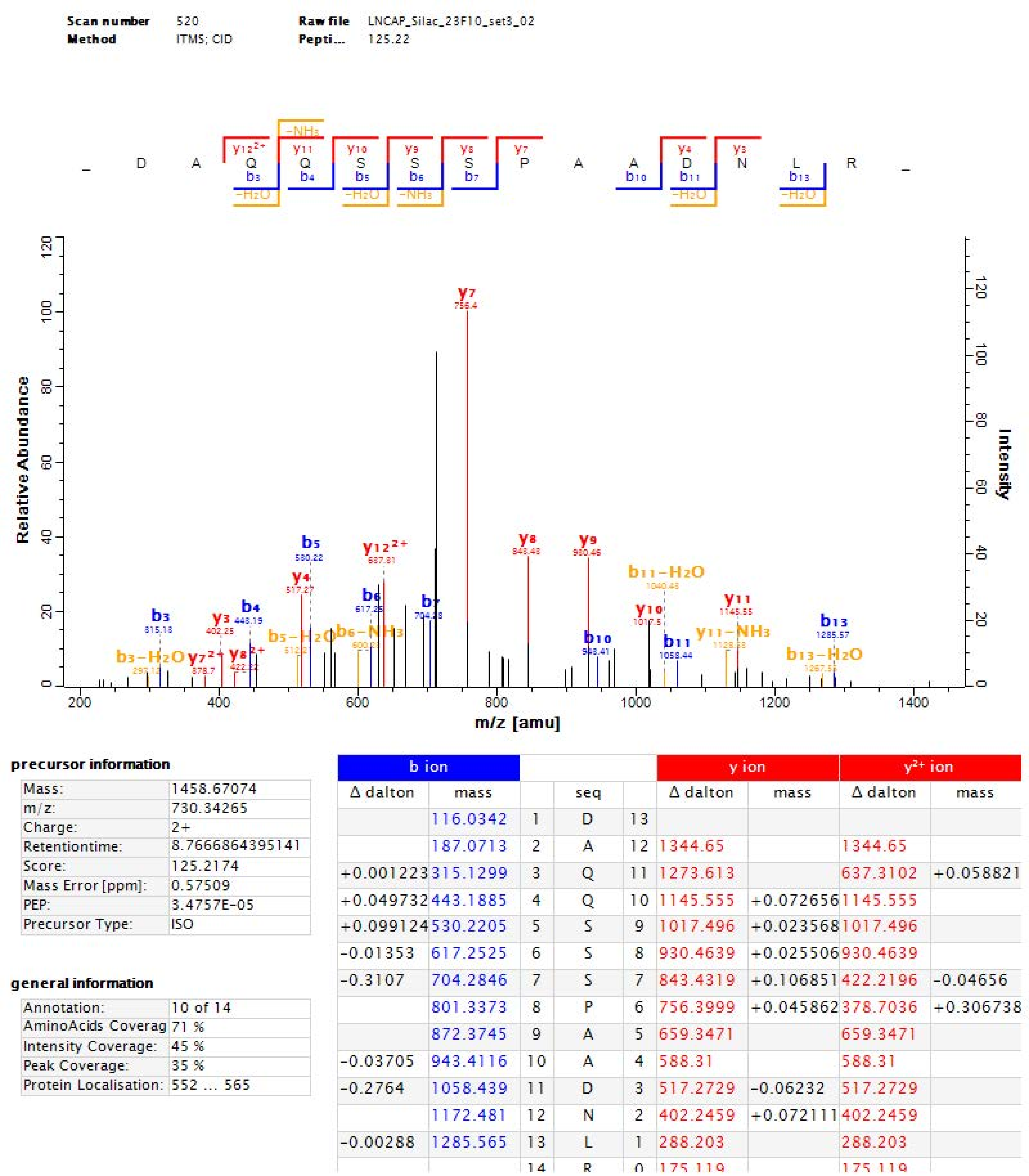
precursor information

Mass:	2350.12735
m/z:	1176.07095
Charge:	2+
Retentiontime:	37.039775848388
Score:	235.9228
Mass Error [ppm]:	0.42642
PEP:	2.9125E-87
Precursor Type:	MULTI

general information

Annotation:	18 of 23
AminoAcids Coverag	78 %
Intensity Coverage:	57 %
Peak Coverage:	46 %
Protein Localisation:	9 ... 31

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	I	22				
	227.18		227.18	2	L	21	2238		2238	
	358.22		358.22	3	M	20	2125		1063	-0.079
	459.26		459.26	4	T	19	1993.9		997.47	+0.3539
	546.3	-0.045	546.3	5	S	18	1892.9	-0.017	1892.9	
	633.33		633.33	6	S	17	1805.8	-0.104	1805.8	
	704.36		704.36	7	A	16	1718.8	-0.191	1718.8	
	791.4	-0.012	791.4	8	S	15	1647.8	-0.059	1647.8	
	848.42	-0.067	848.42	9	G	14	1560.7	-0.021	1560.7	
	961.5	-0.105	961.5	10	I	13	1503.7	+0.0133	1503.7	
	1124.6	+0.0478	1124.6	11	Y	12	1390.6	-0.029	1390.6	
	1181.6		1181.6	12	G	11	1227.6	-0.081	1227.6	
	1295.6	+0.0046	1295.6	13	N	10	1170.6		1170.6	
	1442.7	-0.066	1442.7	14	F	9	1056.5	-0.084	528.76	+0.4353
	1499.7	-0.179	1499.7	15	G	8	909.44	+0.0559	909.44	
	1627.8	-0.241	1627.8	16	Q	7	852.42	+0.0047	426.71	-0.391
	1698.8	+0.0539	1698.8	17	A	6	724.36	+0.082	724.36	
	1812.9	+0.1389	1812.9	18	N	5	653.33	-0.002	653.33	
+0.0628	988.46		1975.9	19	Y	4	539.28	+0.2222	539.28	
	2063		2063	20	S	3	376.22	+0.051	376.22	
	2134		2134	21	A	2	289.19		289.19	
	2205		2205	22	A	1	218.15		218.15	
				23	K	0	147.11		147.11	



Scan number	520	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	125.22

precursor information

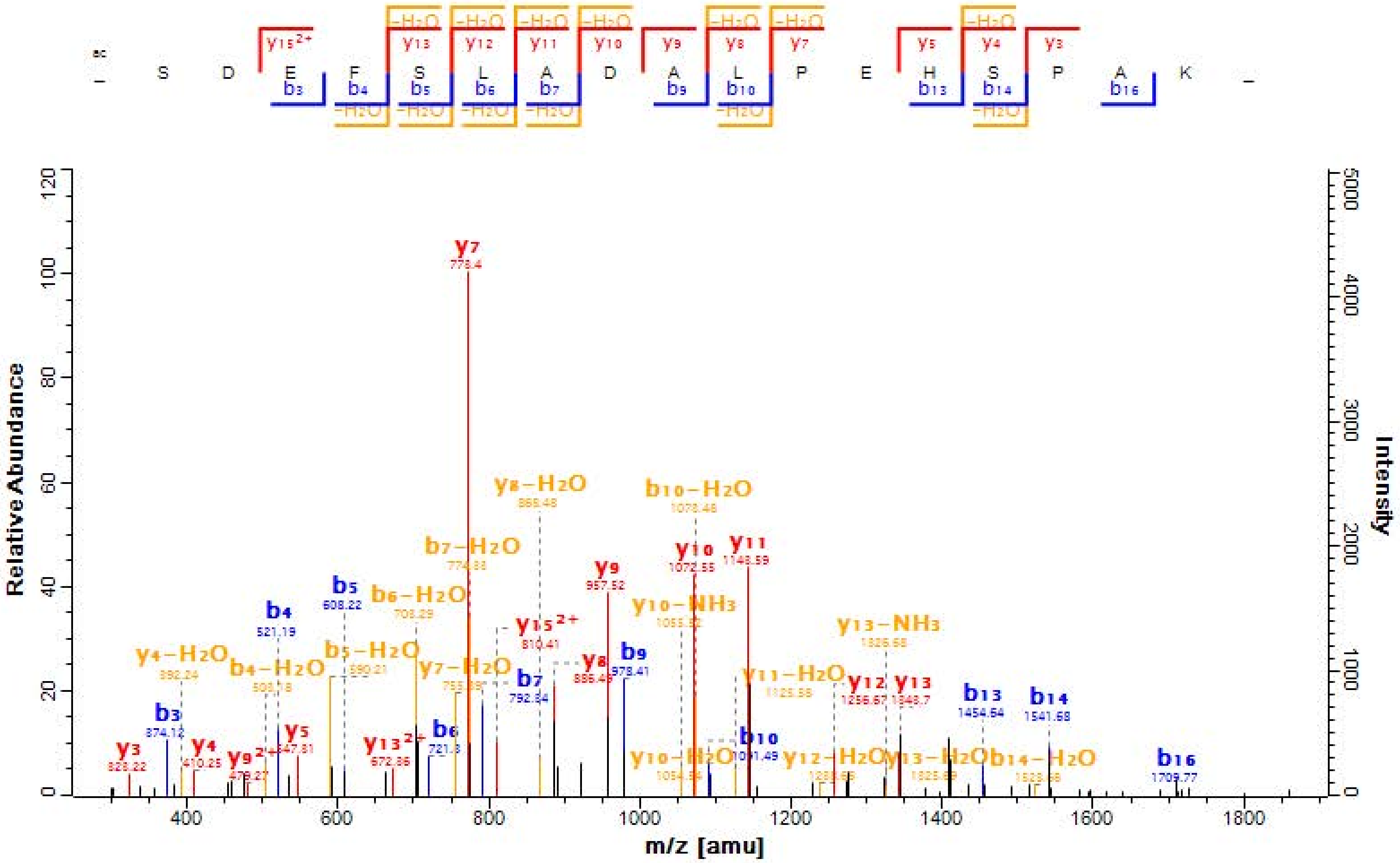
Mass:	1458.67074
m/z:	730.34265
Charge:	2+
Retentiontime:	8.7666864395141
Score:	125.2174
Mass Error [ppm]:	0.57509
PEP:	3.4757E-05
Precursor Type:	ISO

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	45 %
Peak Coverage:	35 %
Protein Localisation:	552 ... 565

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342	1	D	13				
	187.0713	2	A	12	1344.65		1344.65	
+0.001223	315.1299	3	Q	11	1273.613		637.3102	+0.058821
+0.049732	443.1885	4	Q	10	1145.555	+0.072656	1145.555	
+0.099124	530.2205	5	S	9	1017.496	+0.023568	1017.496	
-0.01353	617.2525	6	S	8	930.4639	+0.025506	930.4639	
-0.3107	704.2846	7	S	7	843.4319	+0.106851	422.2196	-0.04656
	801.3373	8	P	6	756.3999	+0.045862	378.7036	+0.306738
	872.3745	9	A	5	659.3471		659.3471	
-0.03705	943.4116	10	A	4	588.31		588.31	
-0.2764	1058.439	11	D	3	517.2729	-0.06232	517.2729	
	1172.481	12	N	2	402.2459	+0.072111	402.2459	
-0.00288	1285.565	13	L	1	288.203		288.203	
		14	R	0	175.119		175.119	

Scan number	6010	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	238.07



precursor information

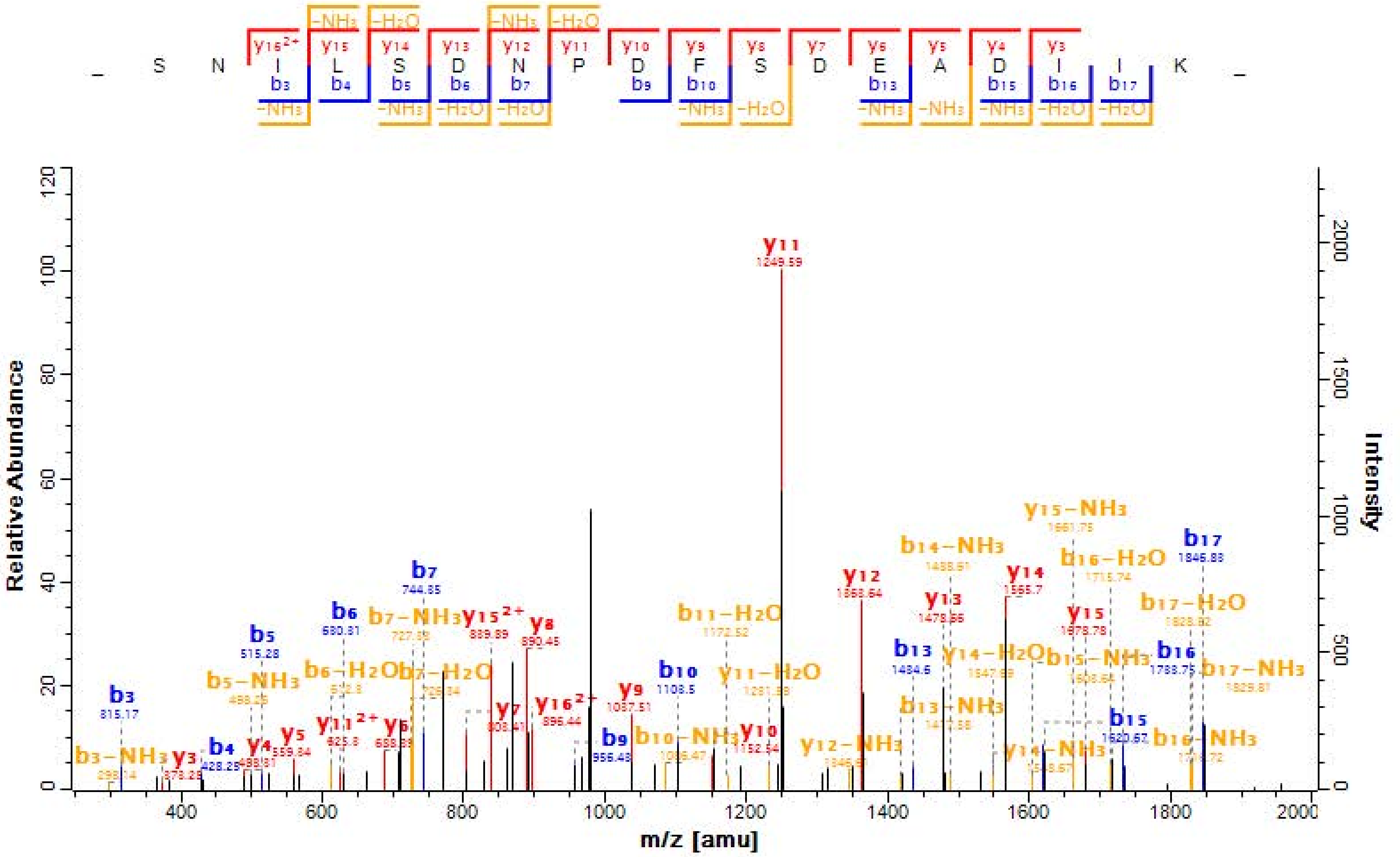
Mass:	1854.86361
m/z:	928.43908
Charge:	2+
Retentiontime:	41.785461425781
Score:	238.0663
Mass Error [ppm]:	0.021304
PEP:	1.2402E-56
Precursor Type:	MULTI

general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	70 %
Peak Coverage:	42 %
Protein Localisation:	2 ... 18

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	S	16				
	245.0768	2	D	15	1734.842		1734.842	
-0.02816	374.1194	3	E	14	1619.816		810.4114	+0.047773
+0.045457	521.1878	4	F	13	1490.773		1490.773	
+0.12671	608.2198	5	S	12	1343.705	-0.29374	672.3559	+0.003912
-0.09218	721.3039	6	L	11	1256.672	+0.033578	1256.672	
-0.0685	792.341	7	A	10	1143.588	-0.0784	1143.588	
	907.368	8	D	9	1072.551	-0.10904	1072.551	
-0.07549	978.4051	9	A	8	957.5244	-0.04138	479.2658	+0.12902
-0.25025	1091.489	10	L	7	886.4872	+0.033571	886.4872	
	1188.542	11	P	6	773.4032	+0.059774	773.4032	
	1317.585	12	E	5	676.3504		676.3504	
-0.15831	1454.643	13	H	4	547.3078	+0.079874	547.3078	
-0.14358	1541.675	14	S	3	410.2489	+0.058891	410.2489	
	1638.728	15	P	2	323.2169	+0.050453	323.2169	
-0.04108	1709.765	16	A	1	226.1641		226.1641	
		17	K	0	155.127		155.127	

Scan number	6103	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	254.58



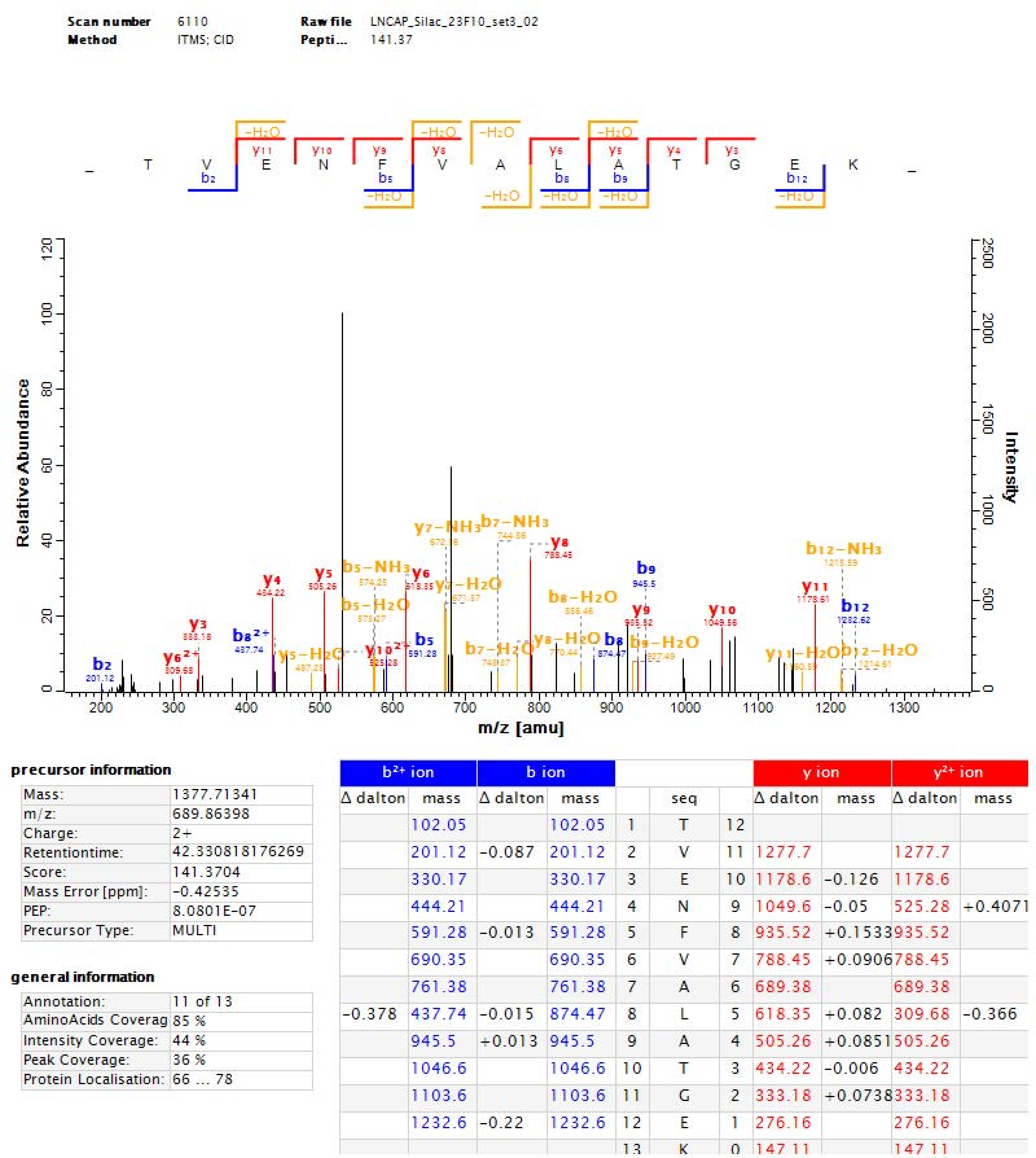
precursor information

Mass:	1991.93164
m/z:	996.9731
Charge:	2+
Retentiontime:	42.294292449951
Score:	254.5751
Mass Error [ppm]:	-0.37059
PEP:	1.9278E-63
Precursor Type:	ISO

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	50 %
Peak Coverage:	45 %
Protein Localisation:	1031 ... 1048

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	17				
	202.0822	2	N	16	1905.908		1905.908	
-0.0113	315.1663	3	I	15	1791.865		896.436	+0.024338
+0.050451	428.2504	4	L	14	1678.781	-0.08056	839.894	+0.26327
+0.312033	515.2824	5	S	13	1565.697	-0.11271	1565.697	
+0.127863	630.3093	6	D	12	1478.665	-0.32653	1478.665	
-0.03414	744.3523	7	N	11	1363.638	-0.06753	1363.638	
	841.405	8	P	10	1249.595	-0.11372	625.301	+0.115956
-0.04635	956.432	9	D	9	1152.542	-0.11296	1152.542	
-0.06508	1103.5	10	F	8	1037.515	-0.00911	1037.515	
	1190.532	11	S	7	890.4466	+0.063822	890.4466	
	1305.559	12	D	6	803.4145	-0.03562	803.4145	
-0.21498	1434.602	13	E	5	688.3876	+0.036002	688.3876	
	1505.639	14	A	4	559.345	-0.04463	559.345	
-0.20982	1620.666	15	D	3	488.3079	+0.098253	488.3079	
-0.22748	1733.75	16	I	2	373.2809	+0.067396	373.2809	
-0.1177	1846.834	17	I	1	260.1969		260.1969	
		18	K	0	147.1128		147.1128	



Scan number	6110	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	141.37

precursor information

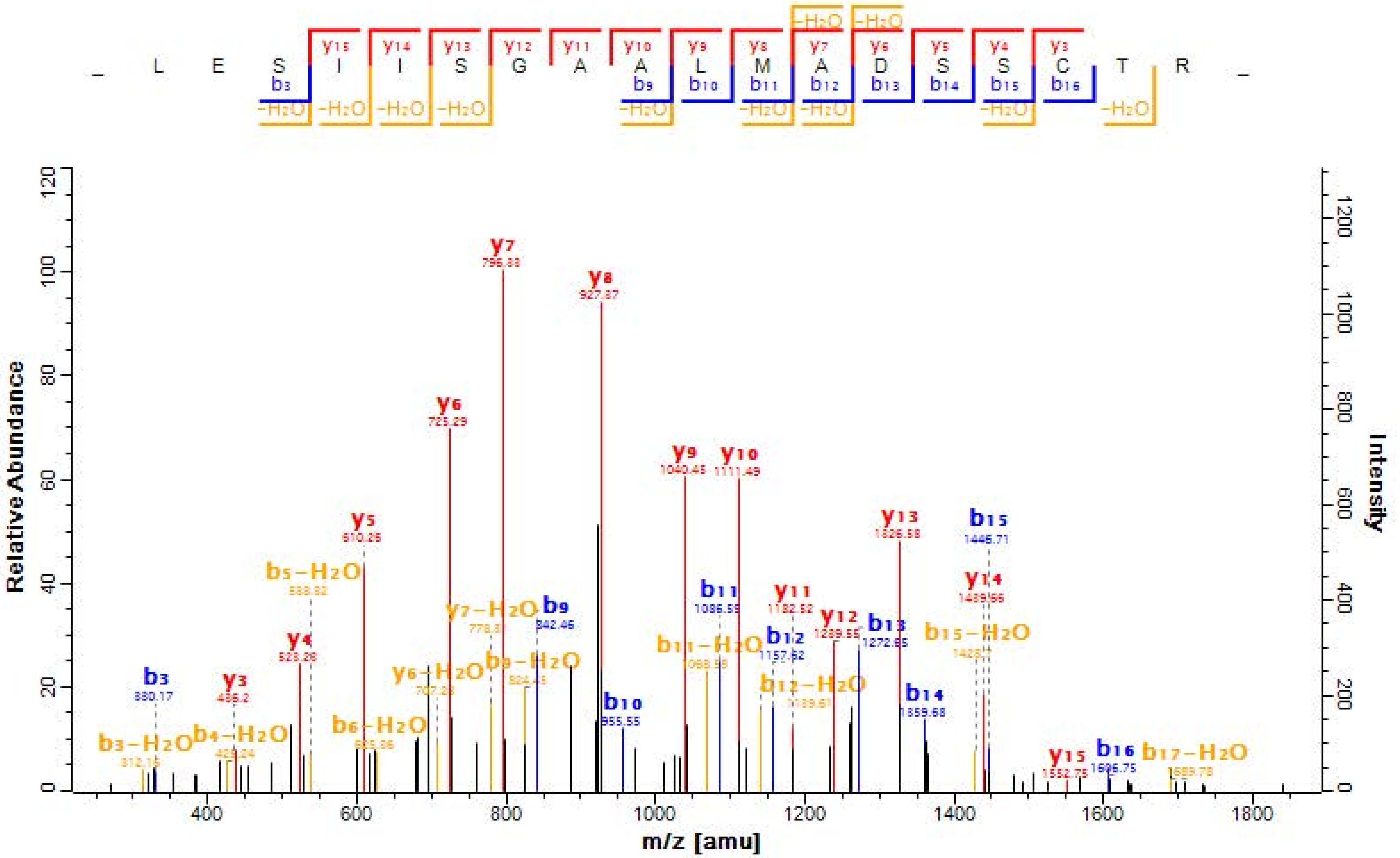
Mass:	1377.71341
m/z:	689.86398
Charge:	2+
Retentiontime:	42.330818176269
Score:	141.3704
Mass Error [ppm]:	-0.42535
PEP:	8.0801E-07
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	44 %
Peak Coverage:	36 %
Protein Localisation:	66 ... 78

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	12				
	201.12	-0.087	201.12	2	V	11	1277.7		1277.7	
	330.17		330.17	3	E	10	1178.6	-0.126	1178.6	
	444.21		444.21	4	N	9	1049.6	-0.05	525.28	+0.4071
	591.28	-0.013	591.28	5	F	8	935.52	+0.1533	935.52	
	690.35		690.35	6	V	7	788.45	+0.0906	788.45	
	761.38		761.38	7	A	6	689.38		689.38	
-0.378	437.74	-0.015	874.47	8	L	5	618.35	+0.082	309.68	-0.366
	945.5	+0.013	945.5	9	A	4	505.26	+0.0851	505.26	
	1046.6		1046.6	10	T	3	434.22	-0.006	434.22	
	1103.6		1103.6	11	G	2	333.18	+0.0738	333.18	
	1232.6	-0.22	1232.6	12	E	1	276.16		276.16	
				13	K	0	147.11		147.11	

Scan number	6326	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	175.51



precursor information

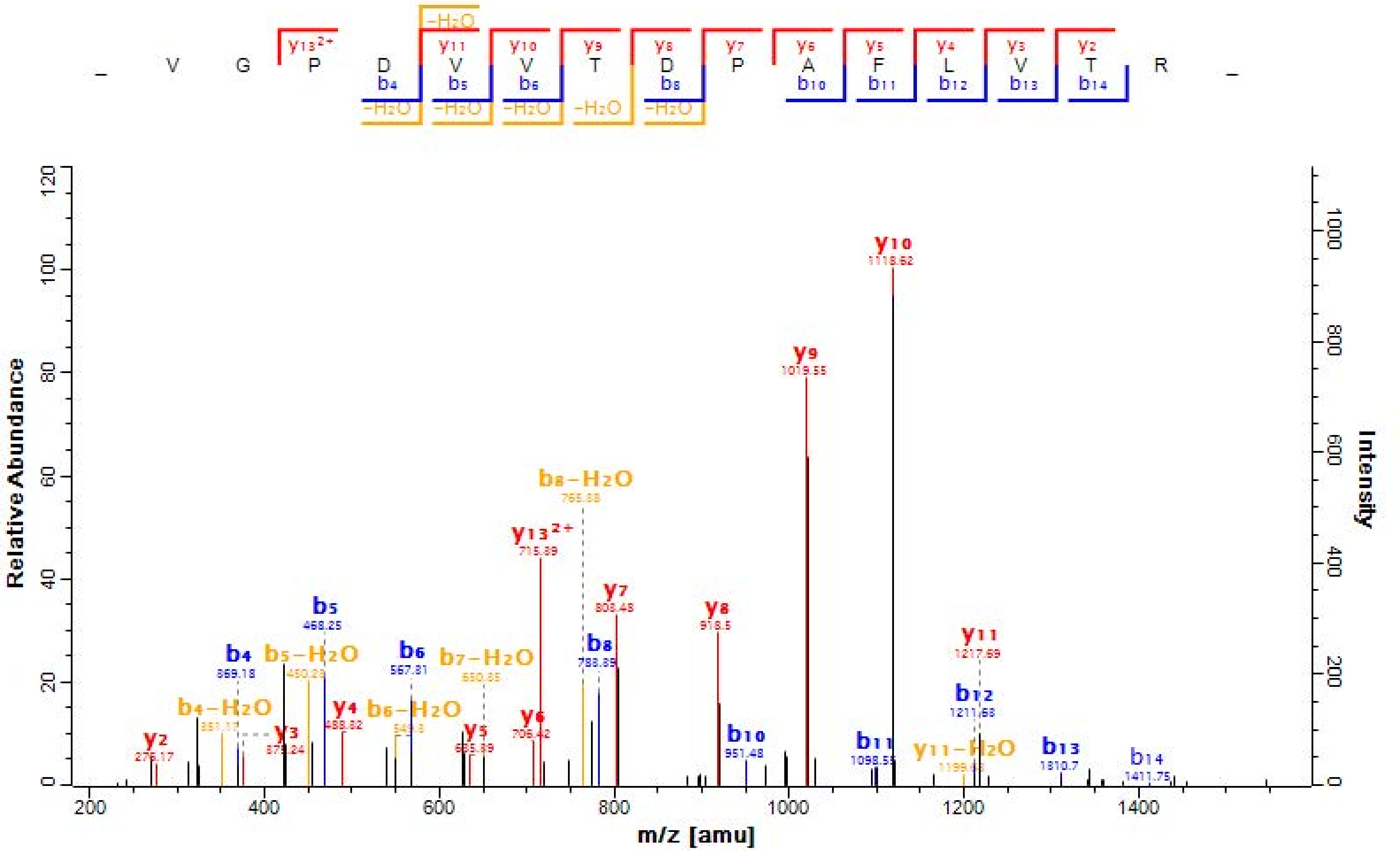
Mass:	1880.89686
m/z:	941.45571
Charge:	2+
Retentiontime:	43.462425231933
Score:	175.5093
Mass Error [ppm]:	-0.17853
PEP:	1.824E-30
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	62 %
Peak Coverage:	34 %
Protein Localisation:	309 ... 326

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	114.091340447	1	L	17		
	243.133933543	2	E	16	1768.82041026	
-0.1105115	330.165961953	3	S	15	1639.77781716	
	443.250025933	4	I	14	1552.74578875	-0.1730348
	556.334089914	5	I	13	1439.66172477	+0.0002625
	643.366118324	6	S	12	1326.57766079	-0.1078122
	700.387582047	7	G	11	1239.54563238	-0.0164576
	771.424695835	8	A	10	1182.52416866	-0.0390612
+0.0283027	842.461809623	9	A	9	1111.48705487	-0.0418644
-0.0997676	955.545873603	10	L	8	1040.44994108	+0.0500589
-0.1552059	1086.58635821	11	M	7	927.365877102	+0.0499554
-0.2334573	1157.623472	12	A	6	796.325392496	-0.0059345
-0.1617676	1272.65041503	13	D	5	725.288278708	+0.0108546
-0.24238	1359.68244344	14	S	4	610.261335676	+0.111345
-0.2000676	1446.71447185	15	S	3	523.229307266	-0.0683576
+0.2700167	1606.74512005	16	C	2	436.197278856	+0.1588002
	1707.79279852	17	T	1	276.166630655	
		18	R	0	175.118952181	

Scan number	6448	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	129.01



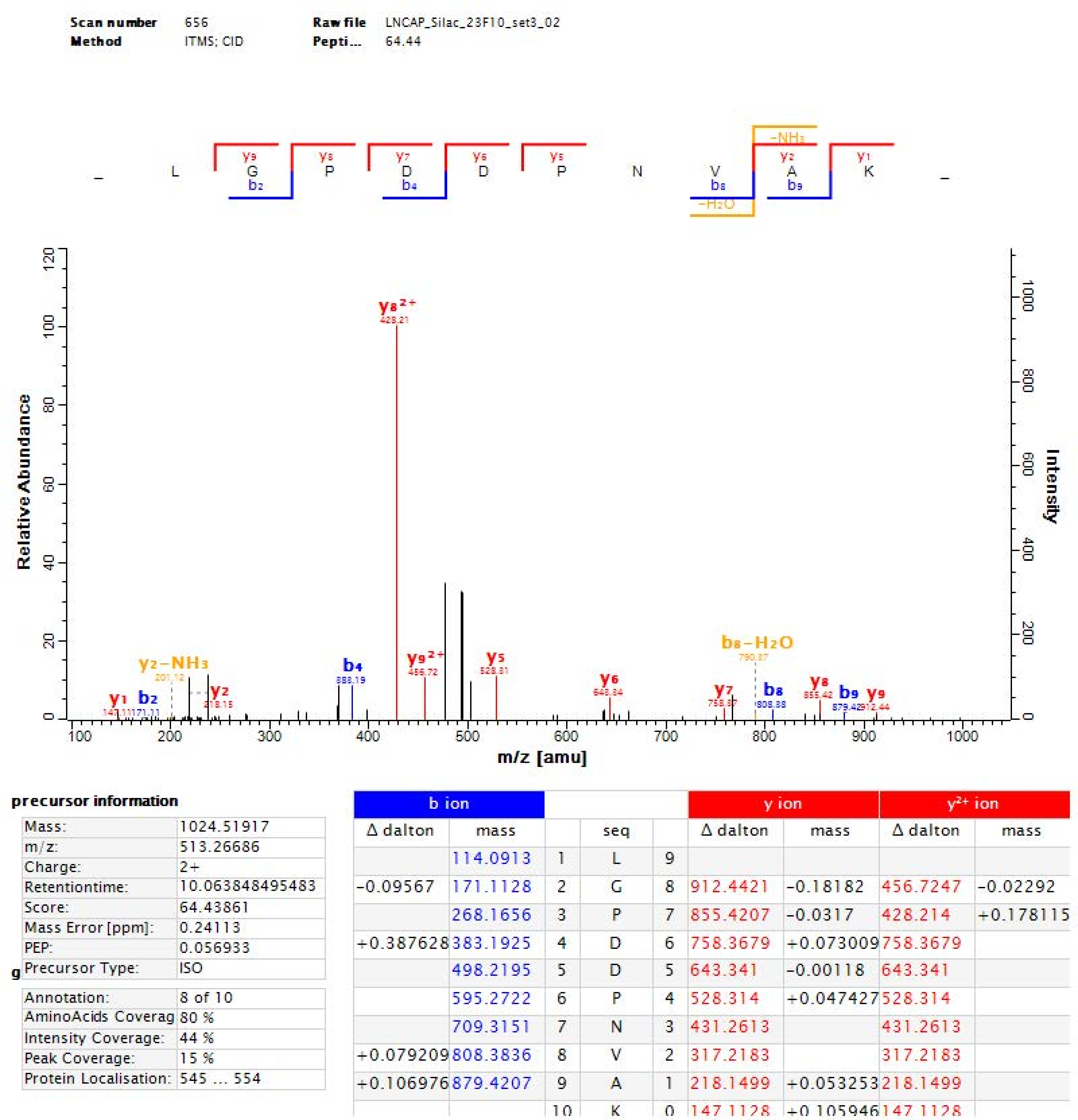
precursor information

Mass:	1584.85185
m/z:	793.4332
Charge:	2+
Retentiontime:	44.131961822509
Score:	129.0058
Mass Error [ppm]:	0.4339
PEP:	1.8274E-06
Precursor Type:	ISO

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	54 %
Peak Coverage:	35 %
Protein Localisation:	138 ... 152

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	14				
	157.0972	2	G	13	1486.79		1486.79	
	254.1499	3	P	12	1429.769		715.3879	+0.271691
+0.097736	369.1769	4	D	11	1332.716		1332.716	
−0.00278	468.2453	5	V	10	1217.689	−0.15467	1217.689	
+0.0701	567.3137	6	V	9	1118.62	−0.0533	1118.62	
	668.3614	7	T	8	1019.552	−0.01864	1019.552	
−0.01416	783.3883	8	D	7	918.5043	+0.012808	918.5043	
	880.4411	9	P	6	803.4774	+0.103349	803.4774	
−0.14347	951.4782	10	A	5	706.4246	+0.248765	706.4246	
−0.03183	1098.547	11	F	4	635.3875	+0.003957	635.3875	
−0.17925	1211.631	12	L	3	488.3191	+0.201338	488.3191	
−0.25413	1310.699	13	V	2	375.235	+0.078524	375.235	
−0.2597	1411.747	14	T	1	276.1666	+0.092799	276.1666	
		15	R	0	175.119		175.119	



Scan number	656	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	64.44

precursor information

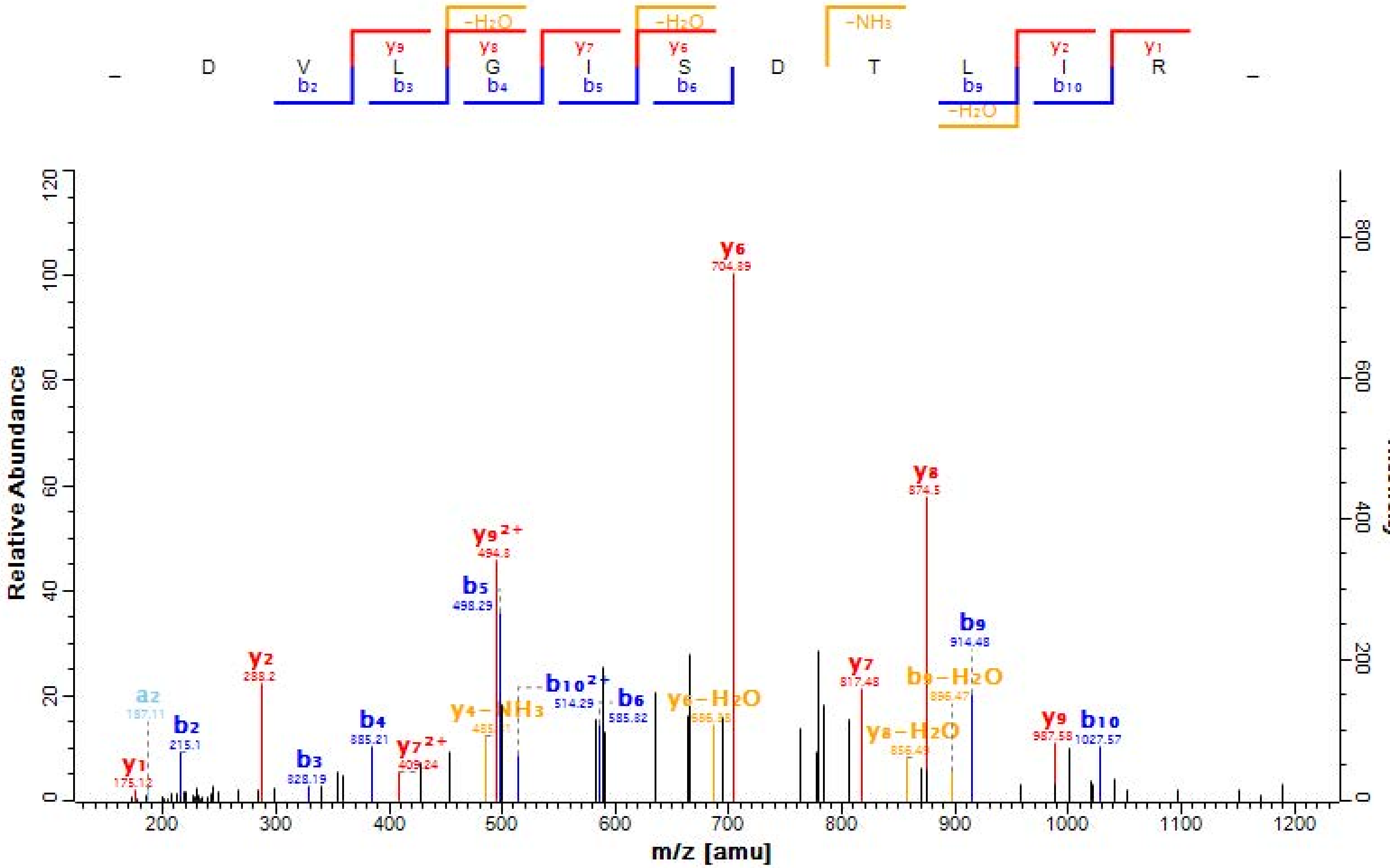
Mass:	1024.51917
m/z:	513.26686
Charge:	2+
Retentiontime:	10.063848495483
Score:	64.43861
Mass Error [ppm]:	0.24113
PEP:	0.056933
Precursor Type:	ISO

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	44 %
Peak Coverage:	15 %
Protein Localisation:	545 ... 554

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	9				
-0.09567	171.1128	2	G	8	912.4421	-0.18182	456.7247	-0.02292
	268.1656	3	P	7	855.4207	-0.0317	428.214	+0.178115
+0.387628	383.1925	4	D	6	758.3679	+0.073009	758.3679	
	498.2195	5	D	5	643.341	-0.00118	643.341	
	595.2722	6	P	4	528.314	+0.047427	528.314	
	709.3151	7	N	3	431.2613		431.2613	
+0.079209	808.3836	8	V	2	317.2183		317.2183	
+0.106976	879.4207	9	A	1	218.1499	+0.053253	218.1499	
		10	K	0	147.1128	+0.105946	147.1128	

Scan number 6593 **Raw file** LNCAP_Silac_23F10_set3_02

Method ITMS; CID **Pepti...** 121.36



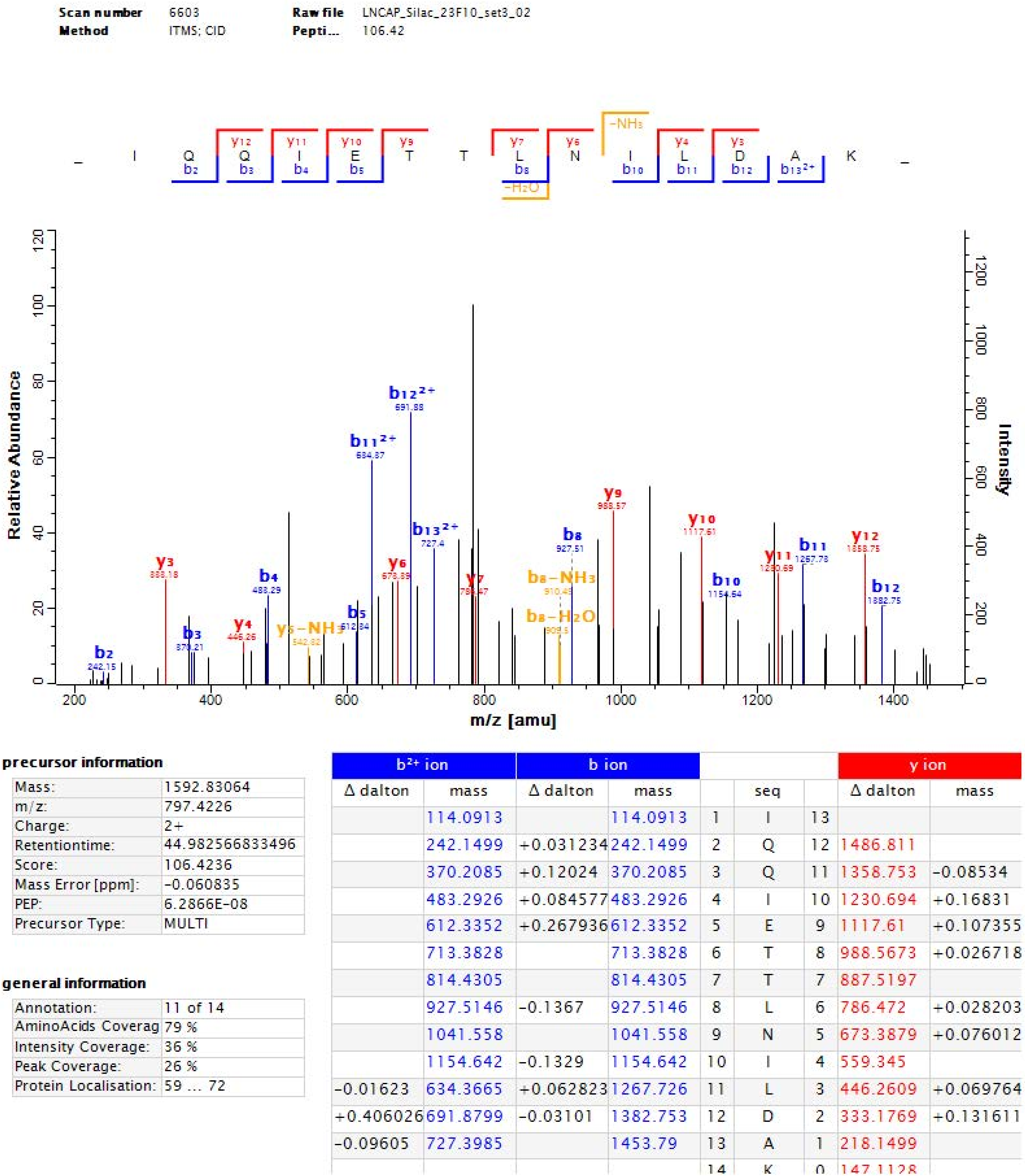
precursor information

Mass:	1200.67131
m/z:	601.34293
Charge:	2+
Retentiontime:	44.922489166259
Score:	121.3605
Mass Error [ppm]:	-0.075775
PEP:	0.00019356
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	53 %
Peak Coverage:	25 %
Protein Localisation:	365 ... 375

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.04		116		116	1	D	10				
-0.04	187.1		215.1	-0.02	215.1	2	V	9	1087		1087	
	300.2		328.2	+0.149	328.2	3	L	8	987.6	-0.1	494.3	+0.09
	357.2		385.2	-0.07	385.2	4	G	7	874.5	-0.02	874.5	
	470.3		498.3	+0.11	498.3	5	I	6	817.5	+0.045	409.2	+0.18
	557.3		585.3	+0.026	585.3	6	S	5	704.4	+0.075	704.4	
	672.4		700.4		700.4	7	D	4	617.4		617.4	
	773.4		801.4		801.4	8	T	3	502.3		502.3	
	886.5		914.5	-0.12	914.5	9	L	2	401.3		401.3	
	999.6	+0.354	514.3	-0.17	1028	10	I	1	288.2	-0.06	288.2	
						11	R	0	175.1	+0	175.1	



Scan number	6603	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	106.42

precursor information

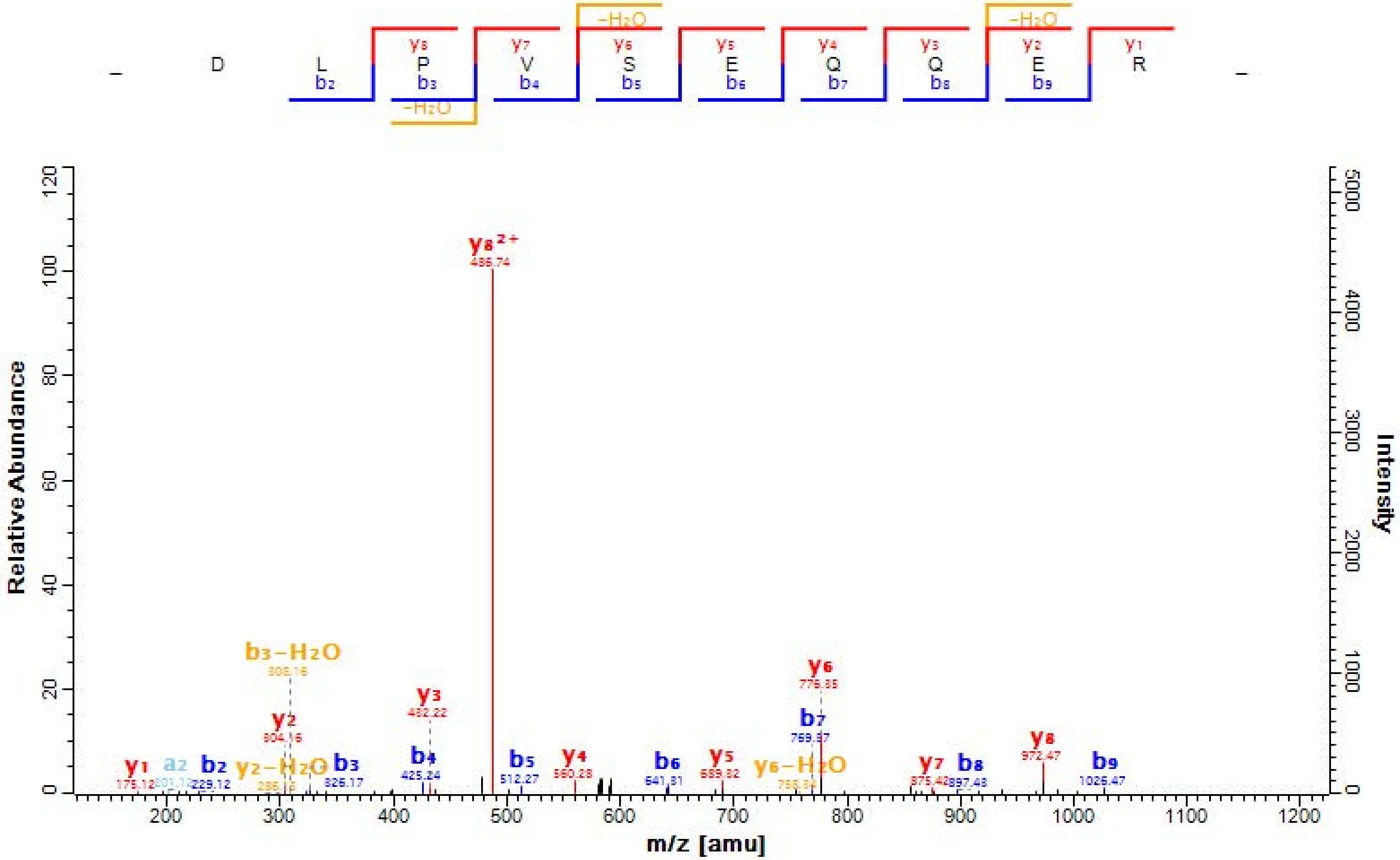
Mass:	1592.83064
m/z:	797.4226
Charge:	2+
Retentiontime:	44.982566833496
Score:	106.4236
Mass Error [ppm]:	-0.060835
PEP:	6.2866E-08
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	36 %
Peak Coverage:	26 %
Protein Localisation:	59 ... 72

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	114.0913		114.0913	1	I	13		
	242.1499	+0.031234	242.1499	2	Q	12	1486.811	
	370.2085	+0.12024	370.2085	3	Q	11	1358.753	-0.08534
	483.2926	+0.084577	483.2926	4	I	10	1230.694	+0.16831
	612.3352	+0.267936	612.3352	5	E	9	1117.61	+0.107355
	713.3828		713.3828	6	T	8	988.5673	+0.026718
	814.4305		814.4305	7	T	7	887.5197	
	927.5146	-0.1367	927.5146	8	L	6	786.472	+0.028203
	1041.558		1041.558	9	N	5	673.3879	+0.076012
	1154.642	-0.1329	1154.642	10	I	4	559.345	
-0.01623	634.3665	+0.062823	1267.726	11	L	3	446.2609	+0.069764
+0.406026	691.8799	-0.03101	1382.753	12	D	2	333.1769	+0.131611
-0.09605	727.3985		1453.79	13	A	1	218.1499	
				14	K	0	147.1128	

Scan number 668 **Raw file** LNCAP_Silac_23F10_set3_02
Method ITMS; CID **Pepti...** 132.32



precursor information

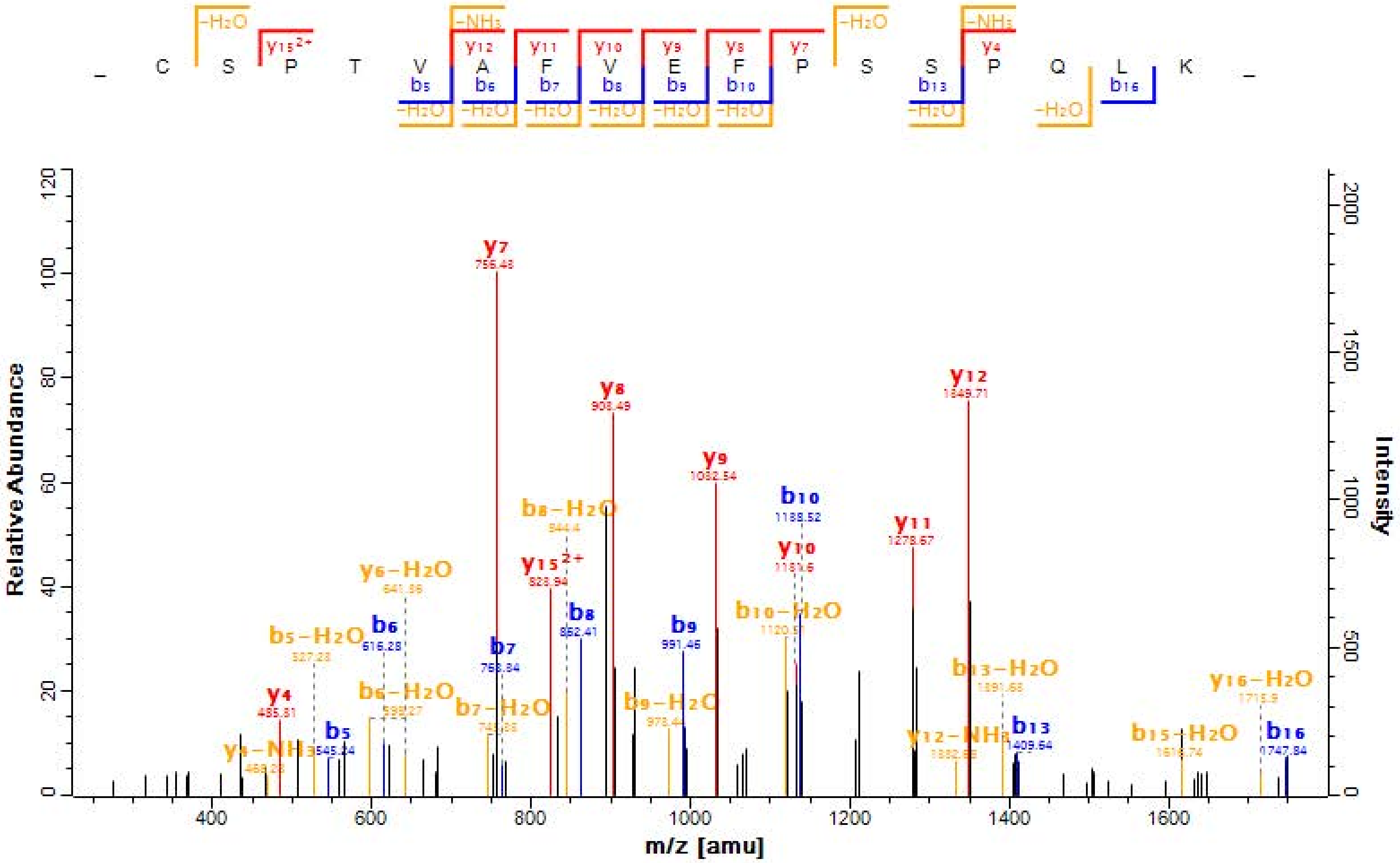
Mass:	1199.57817
m/z:	600.79636
Charge:	2+
Retentiontime:	10.179546356201
Score:	132.3229
Mass Error [ppm]:	-0.046437
PEP:	0.00023643
Precursor Type:	MULTI

g

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	80 %
Peak Coverage:	25 %
Protein Localisation:	187 ... 196

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	9				
+0.0695	201.12	-0.141	229.12	2	L	8	1085.6		1085.6	
	298.18	-0.028	326.17	3	P	7	972.47	+0.024	486.74	+0.1404
	397.24	-0.058	425.24	4	V	6	875.42	+0.2089	875.42	
	484.28	+0.0519	512.27	5	S	5	776.35	+0.0133	776.35	
	613.32	-0.028	641.31	6	E	4	689.32	+0.0214	689.32	
	741.38	+0.0017	769.37	7	Q	3	560.28	+0.0572	560.28	
	869.44	+0.0484	897.43	8	Q	2	432.22	+0.1359	432.22	
	998.48	-0.175	1026.5	9	E	1	304.16	+0.039	304.16	
				10	R	0	175.12	+0.0138	175.12	

Scan number	6700	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	138.19



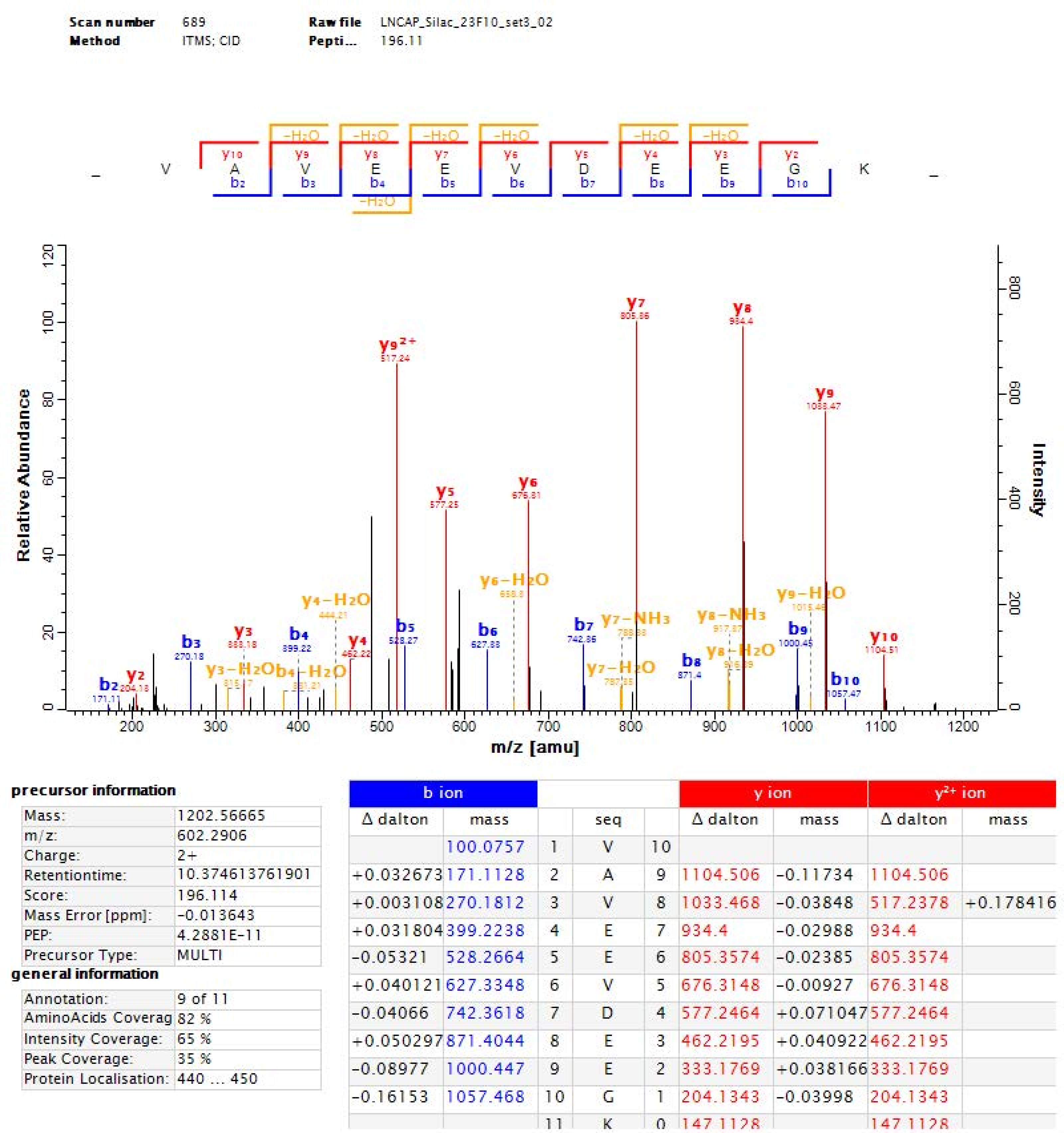
precursor information

Mass:	1892.93449
m/z:	947.47452
Charge:	2+
Retentiontime:	45.509956359863
Score:	138.1857
Mass Error [ppm]:	0.13387
PEP:	1.9919E-16
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	50 %
Peak Coverage:	31 %
Protein Localisation:	669 ... 685

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	161.0379	1	C	16				
	248.07	2	S	15	1733.911		1733.911	
	345.1227	3	P	14	1646.879		823.9431	+0.152647
	446.1704	4	T	13	1549.826		1549.826	
+0.19985	545.2388	5	V	12	1448.778		1448.778	
+0.025041	616.2759	6	A	11	1349.71	-0.03261	1349.71	
+0.022301	763.3443	7	F	10	1278.673	-0.06056	1278.673	
+0.065948	862.4128	8	V	9	1131.604	+0.117961	1131.604	
+0.043924	991.4553	9	E	8	1032.536	-0.03811	1032.536	
-0.1097	1138.524	10	F	7	903.4934	-0.07859	903.4934	
	1235.577	11	P	6	756.425	+0.010089	756.425	
	1322.609	12	S	5	659.3723		659.3723	
-0.45784	1409.641	13	S	4	572.3402		572.3402	
	1506.693	14	P	3	485.3082	-0.01597	485.3082	
	1634.752	15	Q	2	388.2554		388.2554	
-0.14787	1747.836	16	L	1	260.1969		260.1969	
		17	K	0	147.1128		147.1128	



Scan number 689
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set3_02
Pepti... 196.11

precursor information

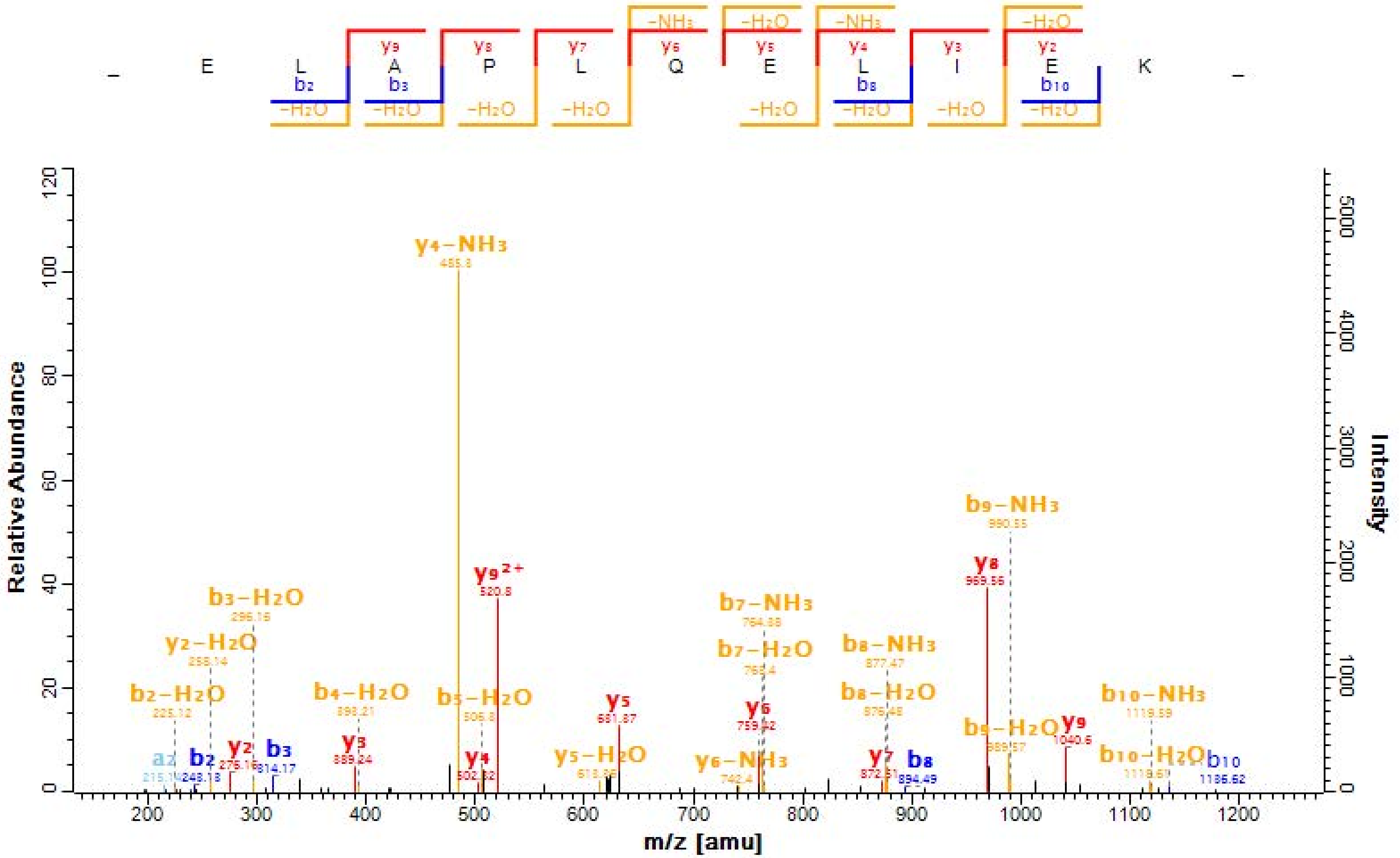
Mass:	1202.56665
m/z:	602.2906
Charge:	2+
Retentiontime:	10.374613761901
Score:	196.114
Mass Error [ppm]:	-0.013643
PEP:	4.2881E-11
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	65 %
Peak Coverage:	35 %
Protein Localisation:	440 ... 450

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	10				
+0.032673	171.1128	2	A	9	1104.506	-0.11734	1104.506	
+0.003108	270.1812	3	V	8	1033.468	-0.03848	517.2378	+0.178416
+0.031804	399.2238	4	E	7	934.4	-0.02988	934.4	
-0.05321	528.2664	5	E	6	805.3574	-0.02385	805.3574	
+0.040121	627.3348	6	V	5	676.3148	-0.00927	676.3148	
-0.04066	742.3618	7	D	4	577.2464	+0.071047	577.2464	
+0.050297	871.4044	8	E	3	462.2195	+0.040922	462.2195	
-0.08977	1000.447	9	E	2	333.1769	+0.038166	333.1769	
-0.16153	1057.468	10	G	1	204.1343	-0.03998	204.1343	
		11	K	0	147.1128		147.1128	

Scan number	7153	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti…**	154.15



precursor information

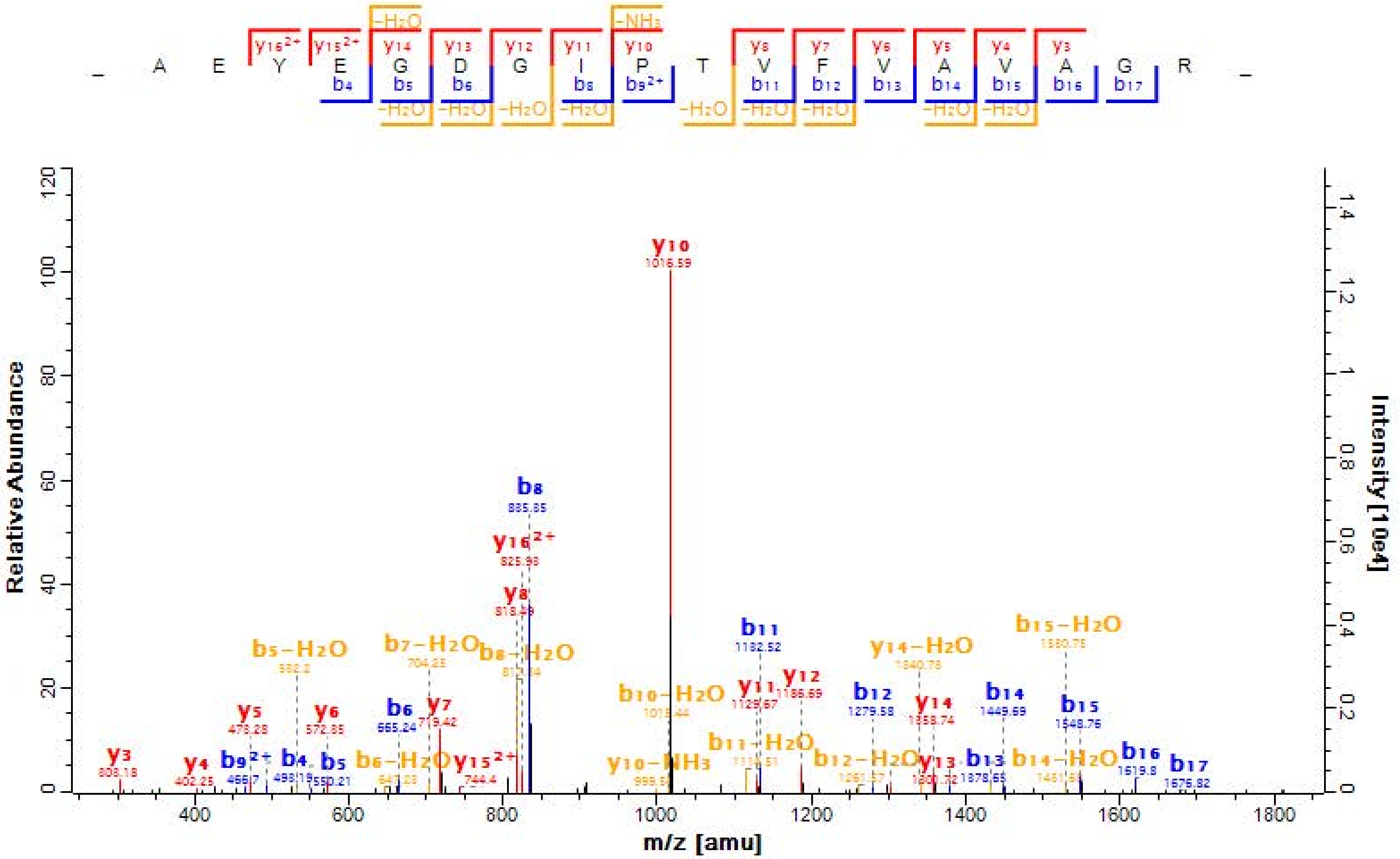
Mass:	1281.7182
m/z:	641.86638
Charge:	2+
Retentiontime:	48.031192779541
Score:	154.1496
Mass Error [ppm]:	0.13981
PEP:	3.2726E-06
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	83 %
Peak Coverage:	38 %
Protein Localisation:	205 … 215

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	10				
+0.0066	215.14	+0.0494	243.13	2	L	9	1153.7		1153.7	
	286.18	+0.0616	314.17	3	A	8	1040.6	-0.074	520.8	+0.1045
	383.23		411.22	4	P	7	969.56	+0.0059	969.56	
	496.31		524.31	5	L	6	872.51	-0.041	872.51	
	624.37		652.37	6	Q	5	759.42	-0.051	759.42	
	753.41		781.41	7	E	4	631.37	+0.0792	631.37	
	866.5	-0.04	894.49	8	L	3	502.32	+0.1301	502.32	
	979.58		1007.6	9	I	2	389.24	-0.021	389.24	
	1108.6	-0.302	1136.6	10	E	1	276.16	+0.0653	276.16	
				11	K	0	147.11		147.11	

Scan number	7358	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	210.9



precursor information

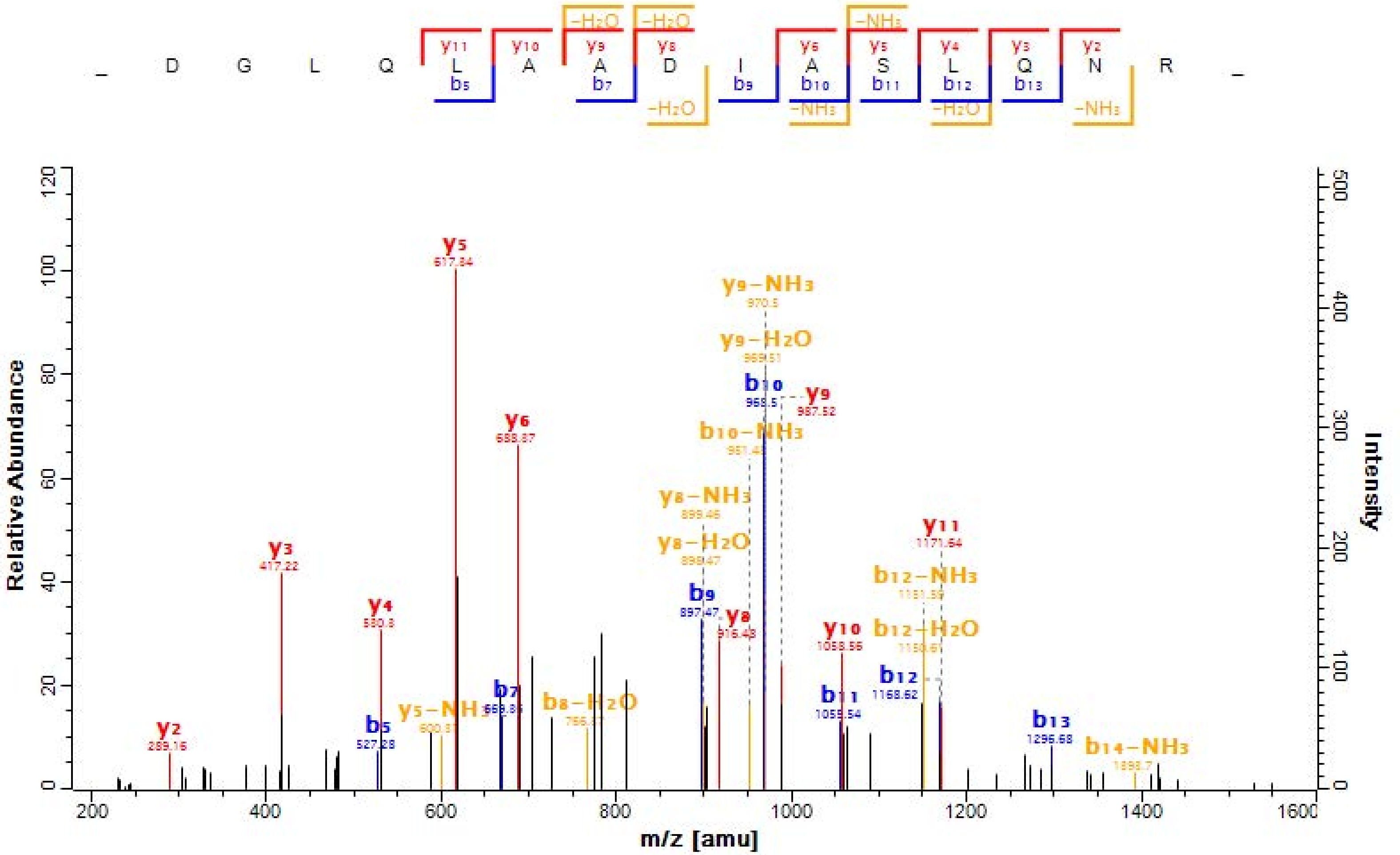
Mass:	1849.92136
m/z:	925.96796
Charge:	2+
Retentiontime:	49.148559570312
Score:	210.9049
Mass Error [ppm]:	0.17805
PEP:	5.7362E-41
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	71 %
Peak Coverage:	40 %
Protein Localisation:	340 … 357

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	17				
	201.09		201.09	2	E	16	1779.9		1779.9	
	364.15		364.15	3	Y	15	1650.8		825.93	+0.1782
	493.19	-0.058	493.19	4	E	14	1487.8		744.4	+0.2851
	550.21	+0.1158	550.21	5	G	13	1358.7	-0.036	1358.7	
	665.24	-0.048	665.24	6	D	12	1301.7	-0.151	1301.7	
	722.26		722.26	7	G	11	1186.7	-0.066	1186.7	
	835.35	-0.004	835.35	8	I	10	1129.7	-0.035	1129.7	
-0.286	466.7		932.4	9	P	9	1016.6	+0.0311	1016.6	
	1033.4		1033.4	10	T	8	919.54		919.54	
	1132.5	+0.0075	1132.5	11	V	7	818.49	-0.205	818.49	
	1279.6	+0.2036	1279.6	12	F	6	719.42	-0.021	719.42	
	1378.7	-0.169	1378.7	13	V	5	572.35	+0.0312	572.35	
	1449.7	+0.1081	1449.7	14	A	4	473.28	+0.0451	473.28	
	1548.8	+0.0685	1548.8	15	V	3	402.25	-0.024	402.25	
	1619.8	-0.036	1619.8	16	A	2	303.18	+0.1458	303.18	
	1676.8	+0.4121	1676.8	17	G	1	232.14		232.14	
				18	R	0	175.12		175.12	

Scan number	7505	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	112.24



precursor information

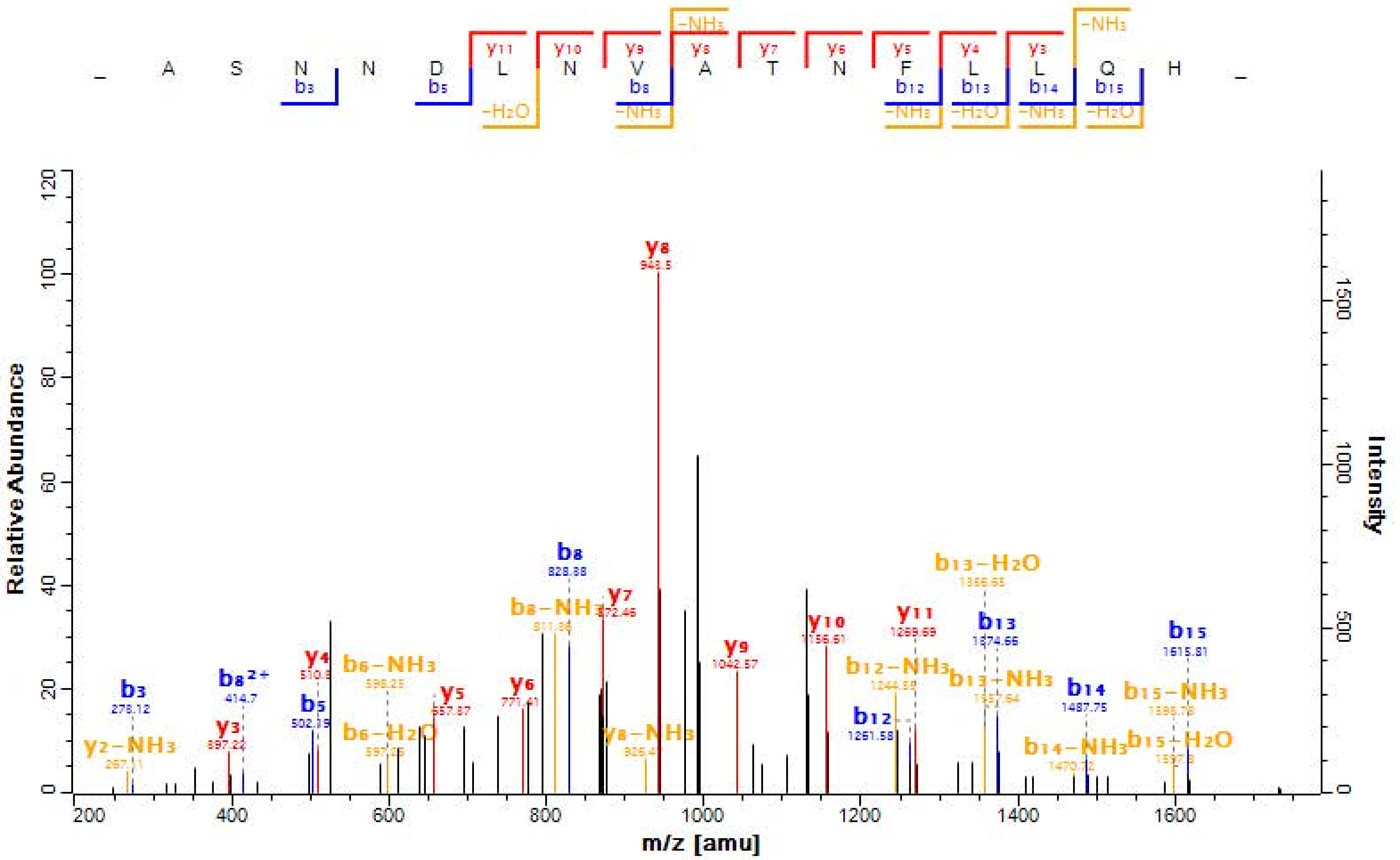
Mass:	1583.82749
m/z:	792.92102
Charge:	2+
Retentiontime:	49.966335296630
Score:	112.2354
Mass Error [ppm]:	0.48028
PEP:	1.9414E-06
Precursor Type:	MULTI

general information

Annotation:	10 of 15
AminoAcids Coverag	67 %
Intensity Coverage:	59 %
Peak Coverage:	32 %
Protein Localisation:	143 ... 157

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	116.034219499	1	D	14		
	173.055683222	2	G	13	1469.8070671	
	286.139747203	3	L	12	1412.78560338	
	414.198324714	4	Q	11	1299.7015394	
+0.0383511	527.282388694	5	L	10	1171.64296189	-0.0254082
	598.319502482	6	A	9	1058.55889791	-0.0198354
-0.0004761	669.35661627	7	A	8	987.521784118	+0.0643975
	784.383559302	8	D	7	916.48467033	+0.0050147
-0.0007654	897.467623282	9	I	6	801.457727298	
+0.016259	968.50473707	10	A	5	688.373663318	+0.1384827
-0.0296854	1055.53676548	11	S	4	617.33654953	+0.0336287
-0.0502728	1168.62082946	12	L	3	530.30452112	+0.0103593
+0.0680296	1296.67940697	13	Q	2	417.22045714	+0.154787
	1410.72233442	14	N	1	289.161879628	-0.0621177
		15	R	0	175.118952181	

Scan number	7597	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	156.17



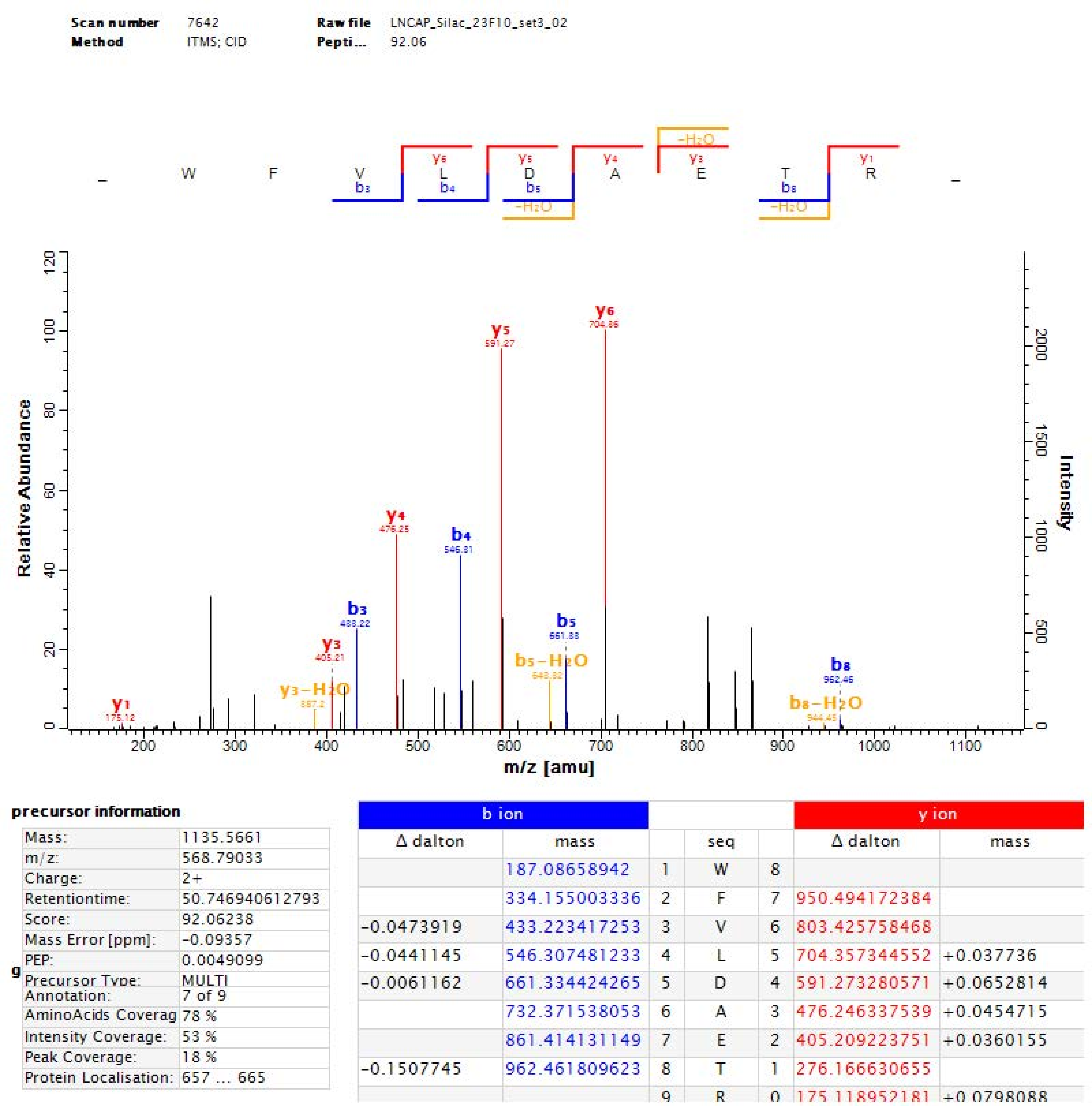
precursor information

Mass:	1769.87078
m/z:	885.94267
Charge:	2+
Retentiontime:	50.497425079345
Score:	156.1734
Mass Error [ppm]:	0.63145
PEP:	1.1038E-10
Precursor Type:	ISO

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	40 %
Peak Coverage:	33 %
Protein Localisation:	329 ... 344

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	72.04439		72.04439	1	A	15		
	159.0764		159.0764	2	S	14	1699.84	
	273.1193	+0.2006	273.1193	3	N	13	1612.808	
	387.1623		387.1623	4	N	12	1498.765	
	502.1892	+0.0523	502.1892	5	D	11	1384.722	
	615.2733		615.2733	6	L	10	1269.695	+0.110789
	729.3162		729.3162	7	N	9	1156.611	-0.07443
-0.30593	414.6959	-0.10148	828.3846	8	V	8	1042.568	+0.099474
	899.4217		899.4217	9	A	7	943.4996	-0.12117
	1000.469		1000.469	10	T	6	872.4625	-0.03236
	1114.512		1114.512	11	N	5	771.4148	-0.07502
	1261.581	+0.008478	1261.581	12	F	4	657.3719	-0.00792
	1374.665	-0.04617	1374.665	13	L	3	510.3035	-0.00957
	1487.749	-0.15513	1487.749	14	L	2	397.2194	+0.088162
	1615.807	-0.20236	1615.807	15	Q	1	284.1353	
				16	H	0	156.0768	

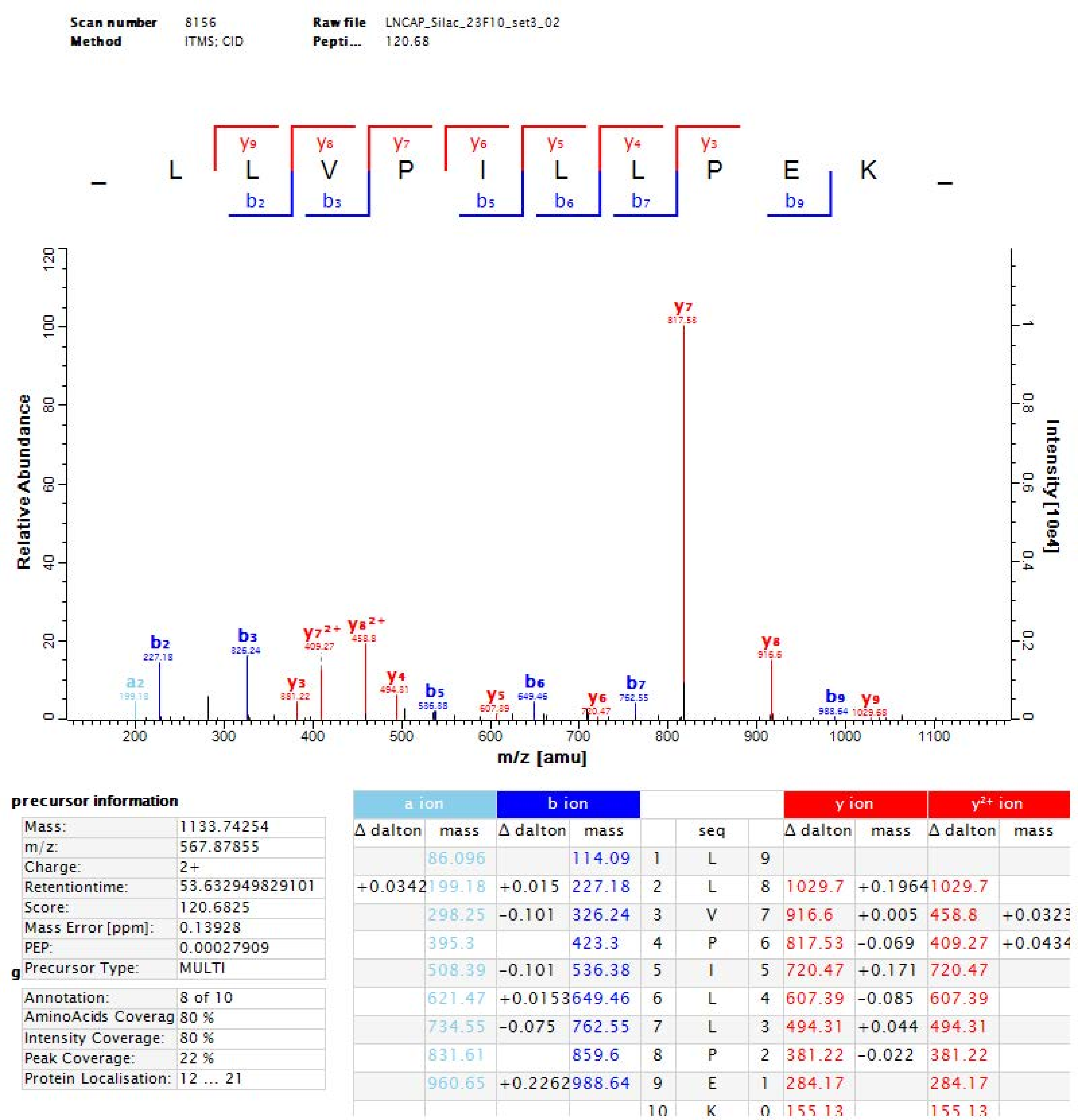


Scan number	7642	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	92.06

precursor information

Mass:	1135.5661
m/z:	568.79033
Charge:	2+
Retentiontime:	50.746940612793
Score:	92.06238
Mass Error [ppm]:	-0.09357
PEP:	0.0049099
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	53 %
Peak Coverage:	18 %
Protein Localisation:	657 ... 665

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	187.08658942	1	W	8		
	334.155003336	2	F	7	950.494172384	
−0.0473919	433.223417253	3	V	6	803.425758468	
−0.0441145	546.307481233	4	L	5	704.357344552	+0.037736
−0.0061162	661.334424265	5	D	4	591.273280571	+0.0652814
	732.371538053	6	A	3	476.246337539	+0.0454715
	861.414131149	7	E	2	405.209223751	+0.0360155
−0.1507745	962.461809623	8	T	1	276.166630655	
		9	R	0	175.118952181	+0.0798088



Scan number	8156	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	120.68

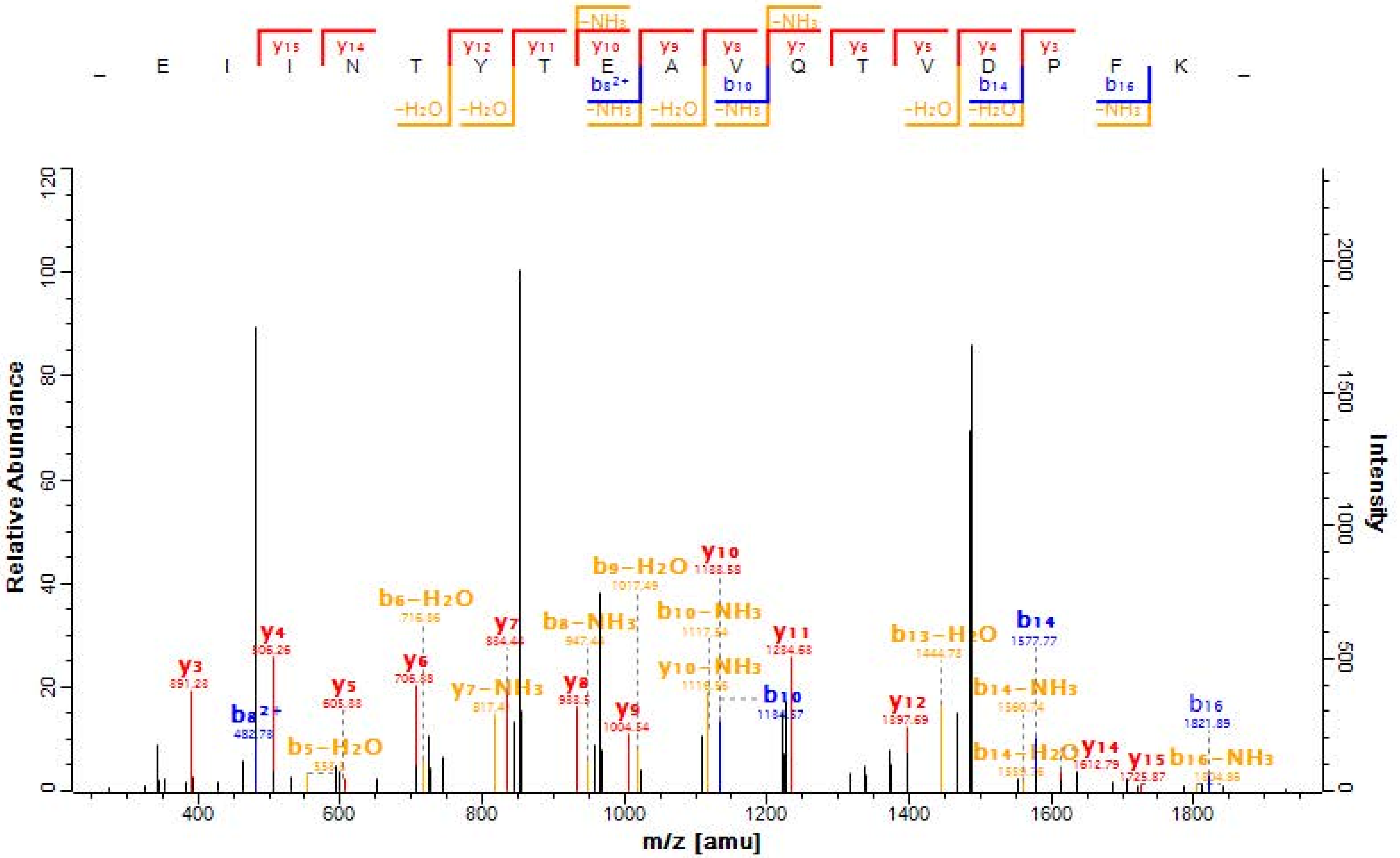
precursor information

Mass:	1133.74254
m/z:	567.87855
Charge:	2+
Retentiontime:	53.632949829101
Score:	120.6825
Mass Error [ppm]:	0.13928
PEP:	0.00027909
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	80 %
Peak Coverage:	22 %
Protein Localisation:	12 ... 21

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	9				
+0.0342	199.18	+0.015	227.18	2	L	8	1029.7	+0.1964	1029.7	
	298.25	-0.101	326.24	3	V	7	916.6	+0.005	458.8	+0.0323
	395.3		423.3	4	P	6	817.53	-0.069	409.27	+0.0434
	508.39	-0.101	536.38	5	I	5	720.47	+0.171	720.47	
	621.47	+0.0153	649.46	6	L	4	607.39	-0.085	607.39	
	734.55	-0.075	762.55	7	L	3	494.31	+0.044	494.31	
	831.61		859.6	8	P	2	381.22	-0.022	381.22	
	960.65	+0.2262	988.64	9	E	1	284.17		284.17	
				10	K	0	155.13		155.13	

Scan number	8388		**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID		**Pepti...**	101.05



precursor information

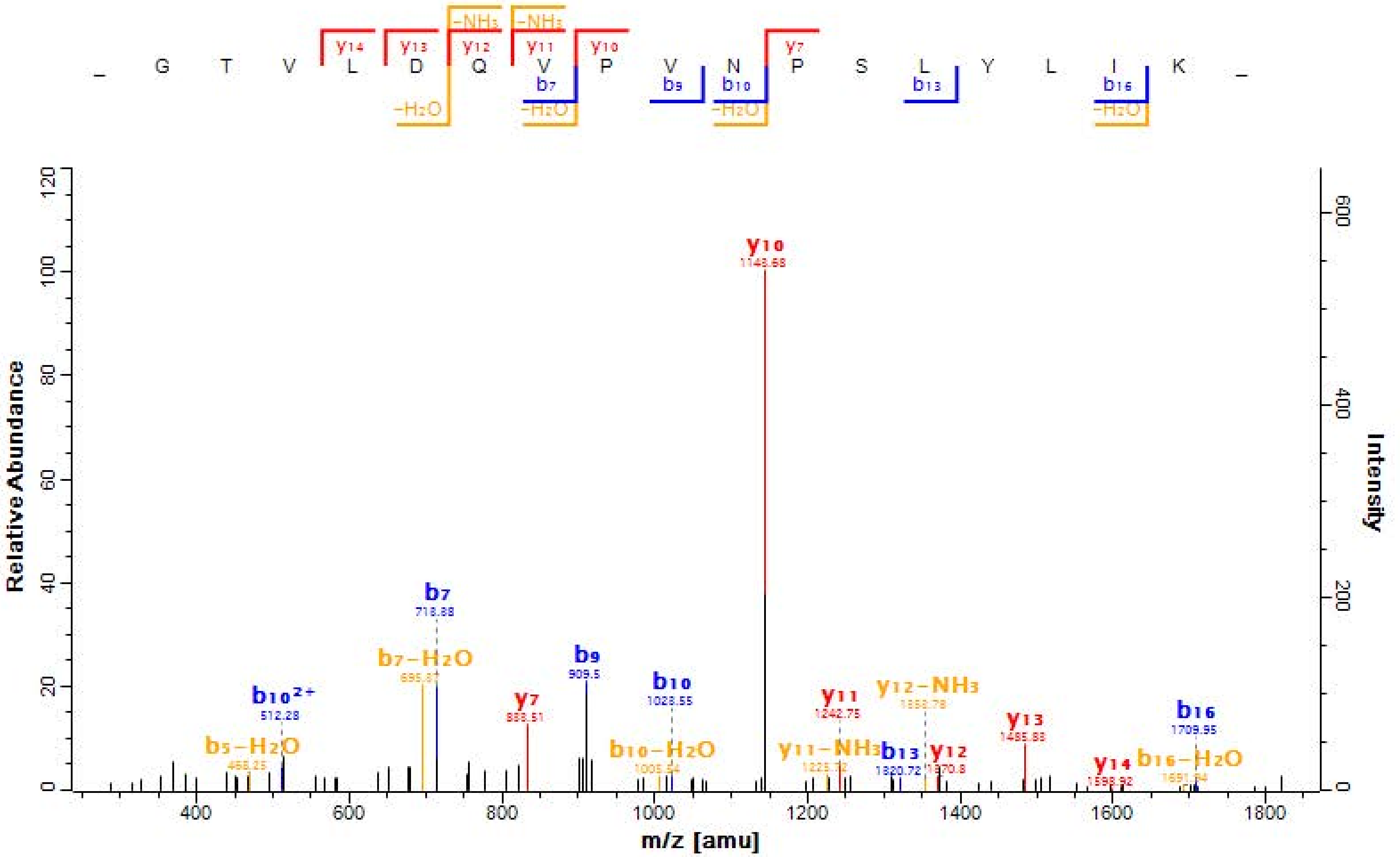
Mass:	1966.98856
m/z:	984.50156
Charge:	2+
Retentiontime:	54.931945800781
Score:	101.055
Mass Error [ppm]:	-0.10881
PEP:	0.00065698
Precursor Type:	ISO

general information

Annotation:	15 of 17
AminoAcids Coverag	88 %
Intensity Coverage:	27 %
Peak Coverage:	30 %
Protein Localisation:	373 ... 389

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	130.0499		130.0499	1	E	16		
	243.1339		243.1339	2	I	15	1838.953	
	356.218		356.218	3	I	14	1725.869	-0.07142
	470.2609		470.2609	4	N	13	1612.785	-0.14898
	571.3086		571.3086	5	T	12	1498.742	
	734.3719		734.3719	6	Y	11	1397.695	-0.10195
	835.4196		835.4196	7	T	10	1234.631	-0.06804
-0.42731	482.7347		964.4622	8	E	9	1133.584	+0.127832
	1035.499		1035.499	9	A	8	1004.541	+0.211563
	1134.568	+0.003802	1134.568	10	V	7	933.504	+0.008076
	1262.626		1262.626	11	Q	6	834.4356	-0.00493
	1363.674		1363.674	12	T	5	706.377	-0.01728
	1462.742		1462.742	13	V	4	605.3293	+0.143317
	1577.769	+0.020817	1577.769	14	D	3	506.2609	+0.052948
	1674.822		1674.822	15	P	2	391.234	+0.067288
	1821.891	-0.0696	1821.891	16	F	1	294.1812	
				17	K	0	147.1128	

Scan number	8503	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	84.14



precursor information

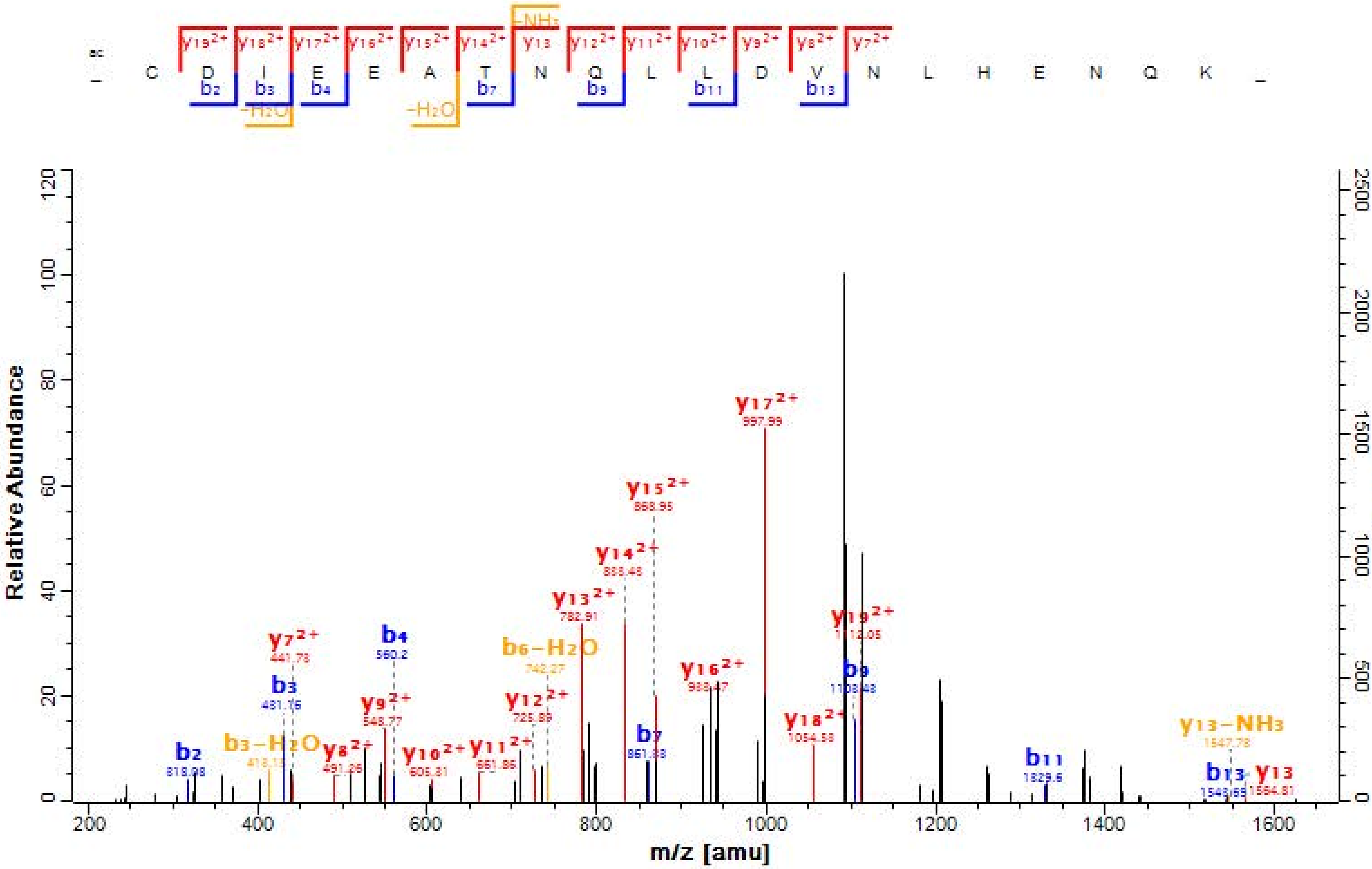
Mass:	1855.04504
m/z:	928.52979
Charge:	2+
Retentiontime:	55.631446838378
Score:	84.13975
Mass Error [ppm]:	-0.25067
PEP:	4.787E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 17
AminoAcids Coverag	59 %
Intensity Coverage:	46 %
Peak Coverage:	20 %
Protein Localisation:	74 ... 90

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	58.02874		58.02874	1	G	16		
	159.0764		159.0764	2	T	15	1799.031	
	258.1448		258.1448	3	V	14	1697.984	
	371.2289		371.2289	4	L	13	1598.915	-0.32941
	486.2558		486.2558	5	D	12	1485.831	-0.15489
	614.3144		614.3144	6	Q	11	1370.804	+0.195786
	713.3828	+0.052716	713.3828	7	V	10	1242.746	-0.00845
	810.4356		810.4356	8	P	9	1143.677	-0.00144
	909.504	+0.150105	909.504	9	V	8	1046.624	
-0.10285	512.2771	-0.01324	1023.547	10	N	7	947.556	
	1120.6		1120.6	11	P	6	833.5131	-0.04785
	1207.632		1207.632	12	S	5	736.4604	
	1320.716	-0.077	1320.716	13	L	4	649.4283	
	1483.779		1483.779	14	Y	3	536.3443	
	1596.863		1596.863	15	L	2	373.2809	
	1709.947	-0.03783	1709.947	16	I	1	260.1969	
				17	K	0	147.1128	

Scan number	8643	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	106.6



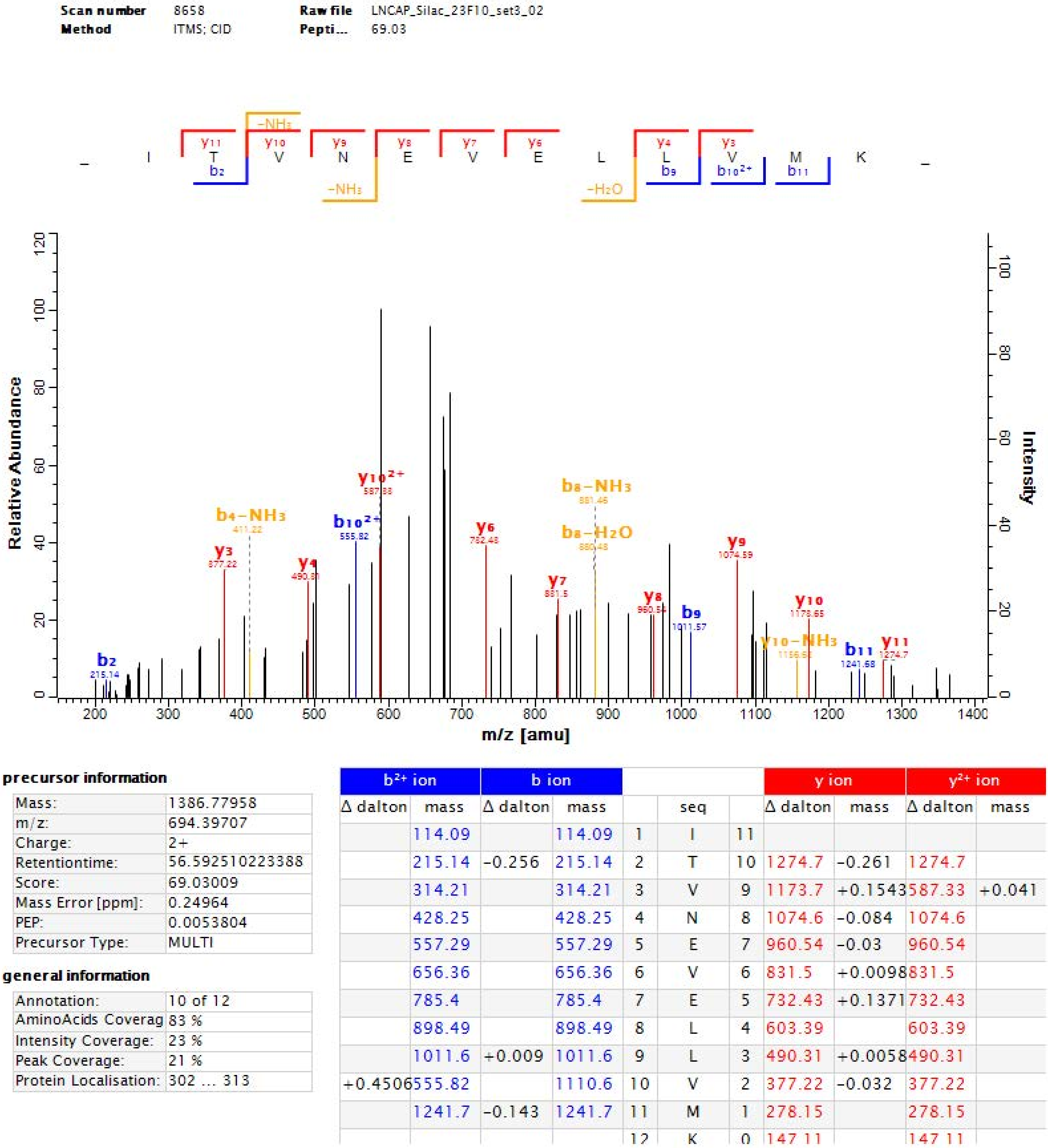
precursor information

Mass:	1616.96155
m/z:	809.48805
Charge:	2+
Retentiontime:	56.500843048095
Score:	106.5974
Mass Error [ppm]:	-0.35392
PEP:	1.3221E-11
Precursor Type:	MULTI

general information

Annotation:	13 of 20
AminoAcids Coverag	65 %
Intensity Coverage:	36 %
Peak Coverage:	28 %
Protein Localisation:	2 ... 21

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	203.0485	1	C	19				
-0.1021	318.0754	2	D	18	2223.089		1112.048	+0.018011
-0.0782	431.1595	3	I	17	2108.062		1054.535	+0.330433
-0.02832	560.2021	4	E	16	1994.978		997.9925	+0.222502
	689.2447	5	E	15	1865.935		933.4712	-0.05619
	760.2818	6	A	14	1736.893		868.9499	+0.242512
-0.04511	861.3295	7	T	13	1665.855		833.4314	+0.217978
	975.3724	8	N	12	1564.808	+0.425969	782.9075	+0.303707
+0.456471	1103.431	9	Q	11	1450.765		725.8861	+0.332495
	1216.515	10	L	10	1322.706		661.8568	+0.099332
-0.2379	1329.599	11	L	9	1209.622		605.3148	+0.097175
	1444.626	12	D	8	1096.538		548.7727	+0.30864
-0.27174	1543.694	13	V	7	981.5112		491.2592	+0.073455
	1657.737	14	N	6	882.4428		441.725	+0.006526
	1770.821	15	L	5	768.3999		768.3999	
	1907.88	16	H	4	655.3158		655.3158	
	2036.923	17	E	3	518.2569		518.2569	
	2150.966	18	N	2	389.2143		389.2143	
	2279.024	19	Q	1	275.1714		275.1714	
		20	K	0	147.1128		147.1128	



Scan number	8658
Method	ITMS; CID
Raw file	LNCAP_Silac_23F10_set3_02
Pepti...	69.03

precursor information

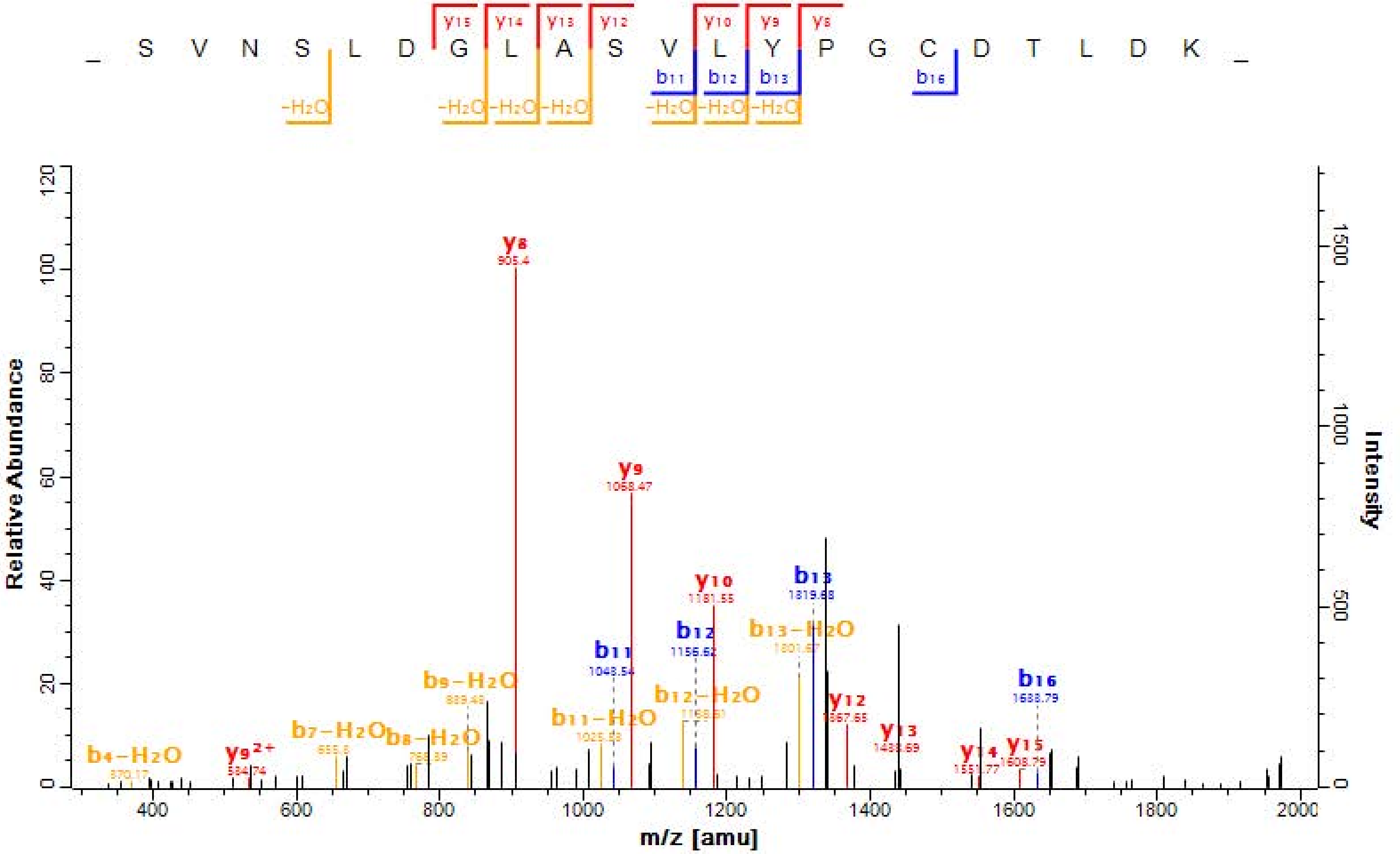
Mass:	1386.77958
m/z:	694.39707
Charge:	2+
Retentiontime:	56.592510223388
Score:	69.03009
Mass Error [ppm]:	0.24964
PEP:	0.0053804
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	23 %
Peak Coverage:	21 %
Protein Localisation:	302 ... 313

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	I	11				
	215.14	-0.256	215.14	2	T	10	1274.7	-0.261	1274.7	
	314.21		314.21	3	V	9	1173.7	+0.1543	587.33	+0.041
	428.25		428.25	4	N	8	1074.6	-0.084	1074.6	
	557.29		557.29	5	E	7	960.54	-0.03	960.54	
	656.36		656.36	6	V	6	831.5	+0.0098	831.5	
	785.4		785.4	7	E	5	732.43	+0.1371	732.43	
	898.49		898.49	8	L	4	603.39		603.39	
	1011.6	+0.009	1011.6	9	L	3	490.31	+0.0058	490.31	
+0.4506	555.82		1110.6	10	V	2	377.22	-0.032	377.22	
	1241.7	-0.143	1241.7	11	M	1	278.15		278.15	
				12	K	0	147.11		147.11	

Scan number	8741	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	37.17



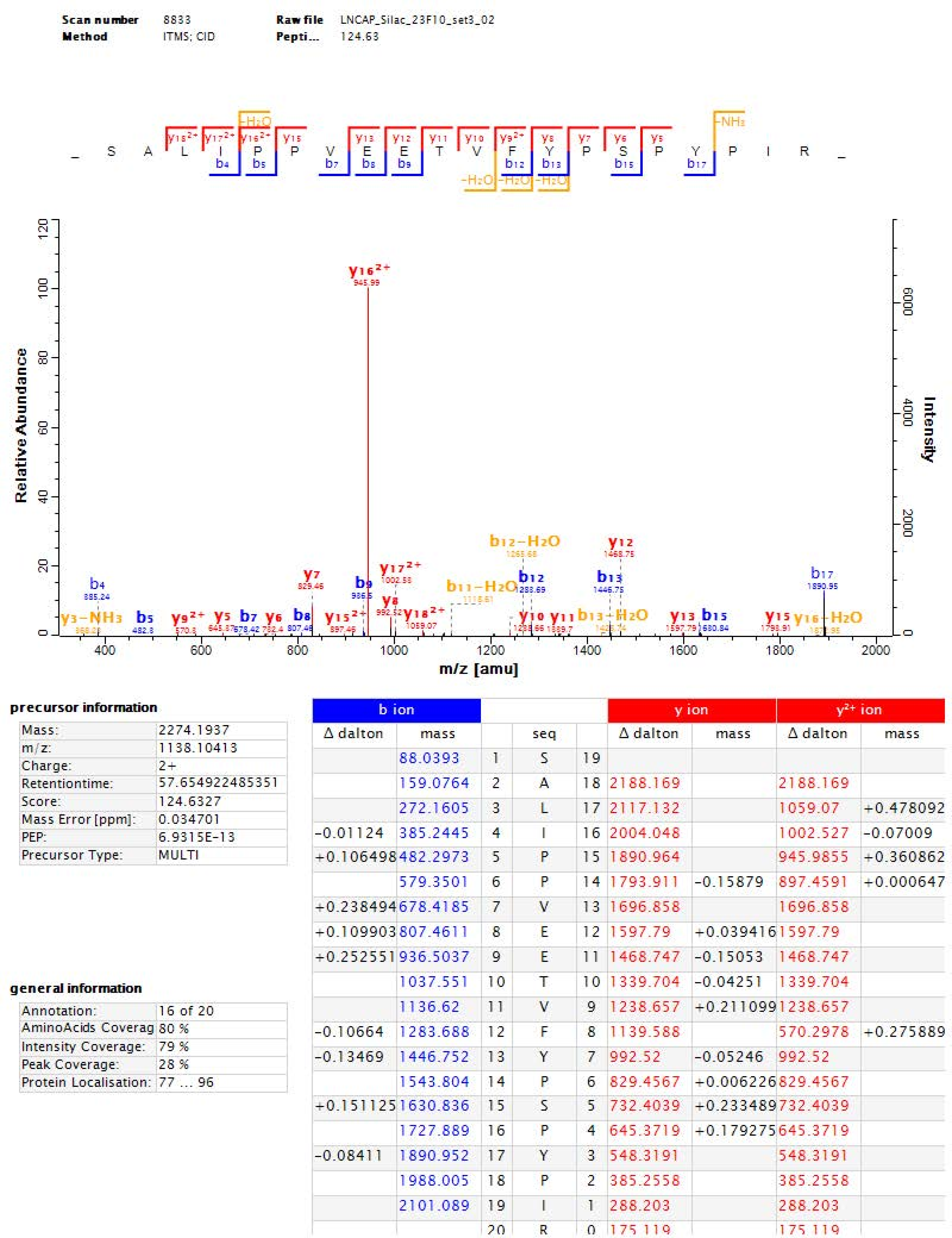
precursor information

Mass:	2223.07274
m/z:	1112.54365
Charge:	2+
Retentiontime:	57.101764678955
Score:	37.16883
Mass Error [ppm]:	-0.077351
PEP:	0.030031
Precursor Type:	MULTI

general information

Annotation:	10 of 21
AminoAcids Coverag	48 %
Intensity Coverage:	45 %
Peak Coverage:	20 %
Protein Localisation:	70 ... 90

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	20				
	187.1077	2	V	19	2137.048		2137.048	
	301.1506	3	N	18	2037.98		2037.98	
	388.1827	4	S	17	1923.937		1923.937	
	501.2667	5	L	16	1836.905		1836.905	
	616.2937	6	D	15	1723.821		1723.821	
	673.3151	7	G	14	1608.794	-0.04183	1608.794	
	786.3992	8	L	13	1551.772	-0.14464	1551.772	
	857.4363	9	A	12	1438.688	-0.15933	1438.688	
	944.4684	10	S	11	1367.651	+0.009379	1367.651	
+0.013527	1043.537	11	V	10	1280.619		1280.619	
-0.20201	1156.621	12	L	9	1181.551	-0.09025	1181.551	
-0.23116	1319.684	13	Y	8	1068.467	-0.06673	534.737	-0.05068
	1416.737	14	P	7	905.4033	-0.01024	905.4033	
	1473.758	15	G	6	808.3505		808.3505	
-0.19528	1633.789	16	C	5	751.3291		751.3291	
	1748.816	17	D	4	591.2984		591.2984	
	1849.864	18	T	3	476.2715		476.2715	
	1962.948	19	L	2	375.2238		375.2238	
	2077.975	20	D	1	262.1397		262.1397	
		21	K	0	147.1128		147.1128	



Scan number	8833	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	124.63

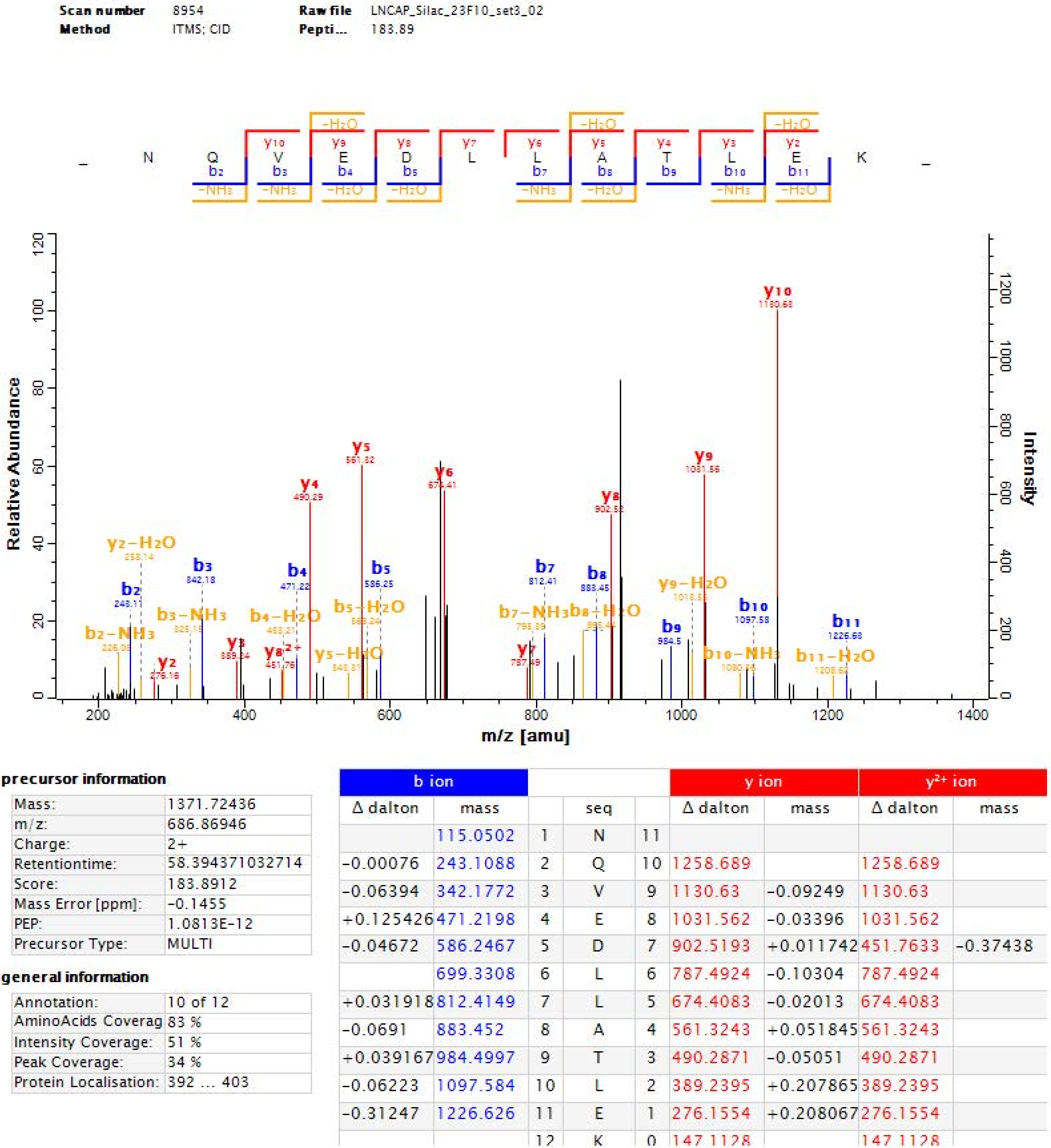
precursor information

Mass:	2274.1937
m/z:	1138.10413
Charge:	2+
Retentiontime:	57.654922485351
Score:	124.6327
Mass Error [ppm]:	0.034701
PEP:	6.9315E-13
Precursor Type:	MULTI

general information

Annotation:	16 of 20
AminoAcids Coverag	80 %
Intensity Coverage:	79 %
Peak Coverage:	28 %
Protein Localisation:	77 ... 96

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	19				
	159.0764	2	A	18	2188.169		2188.169	
	272.1605	3	L	17	2117.132		1059.07	+0.478092
-0.01124	385.2445	4	I	16	2004.048		1002.527	-0.07009
+0.106498	482.2973	5	P	15	1890.964		945.9855	+0.360862
	579.3501	6	P	14	1793.911	-0.15879	897.4591	+0.000647
+0.238494	678.4185	7	V	13	1696.858		1696.858	
+0.109903	807.4611	8	E	12	1597.79	+0.039416	1597.79	
+0.252551	936.5037	9	E	11	1468.747	-0.15053	1468.747	
	1037.551	10	T	10	1339.704	-0.04251	1339.704	
	1136.62	11	V	9	1238.657	+0.211099	1238.657	
-0.10664	1283.688	12	F	8	1139.588		570.2978	+0.275889
-0.13469	1446.752	13	Y	7	992.52	-0.05246	992.52	
	1543.804	14	P	6	829.4567	+0.006226	829.4567	
+0.151125	1630.836	15	S	5	732.4039	+0.233489	732.4039	
	1727.889	16	P	4	645.3719	+0.179275	645.3719	
-0.08411	1890.952	17	Y	3	548.3191		548.3191	
	1988.005	18	P	2	385.2558		385.2558	
	2101.089	19	I	1	288.203		288.203	
		20	R	0	175.119		175.119	



Scan number	8954	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	183.89

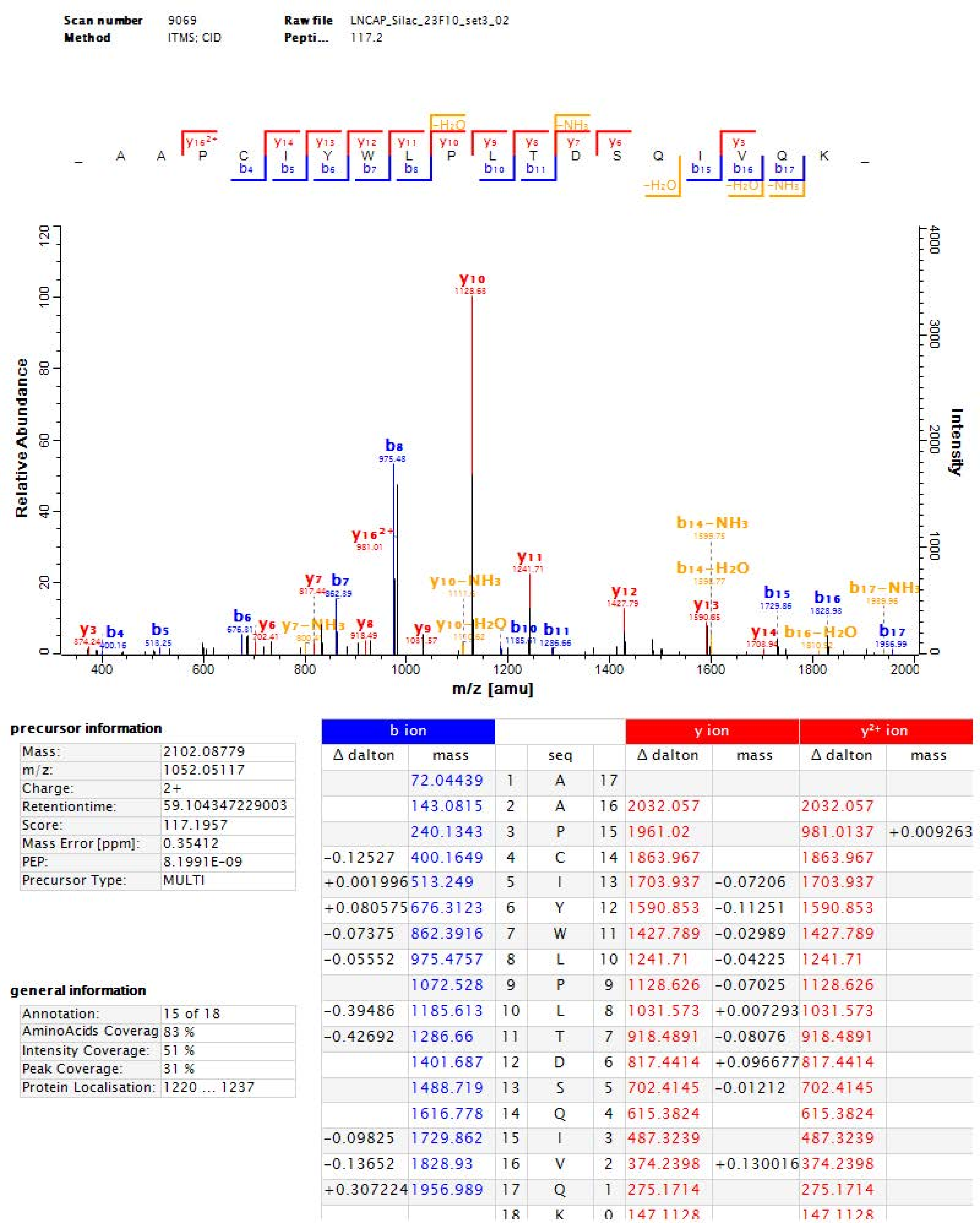
precursor information

Mass:	1371.72436
m/z:	686.86946
Charge:	2+
Retentiontime:	58.394371032714
Score:	183.8912
Mass Error [ppm]:	-0.1455
PEP:	1.0813E-12
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	51 %
Peak Coverage:	34 %
Protein Localisation:	392 ... 403

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502	1	N	11				
-0.00076	243.1088	2	Q	10	1258.689		1258.689	
-0.06394	342.1772	3	V	9	1130.63	-0.09249	1130.63	
+0.125426	471.2198	4	E	8	1031.562	-0.03396	1031.562	
-0.04672	586.2467	5	D	7	902.5193	+0.011742	451.7633	-0.37438
	699.3308	6	L	6	787.4924	-0.10304	787.4924	
+0.031918	812.4149	7	L	5	674.4083	-0.02013	674.4083	
-0.0691	883.452	8	A	4	561.3243	+0.051845	561.3243	
+0.039167	984.4997	9	T	3	490.2871	-0.05051	490.2871	
-0.06223	1097.584	10	L	2	389.2395	+0.207865	389.2395	
-0.31247	1226.626	11	E	1	276.1554	+0.208067	276.1554	
		12	K	0	147.1128		147.1128	



Scan number	9069	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	117.2

precursor information

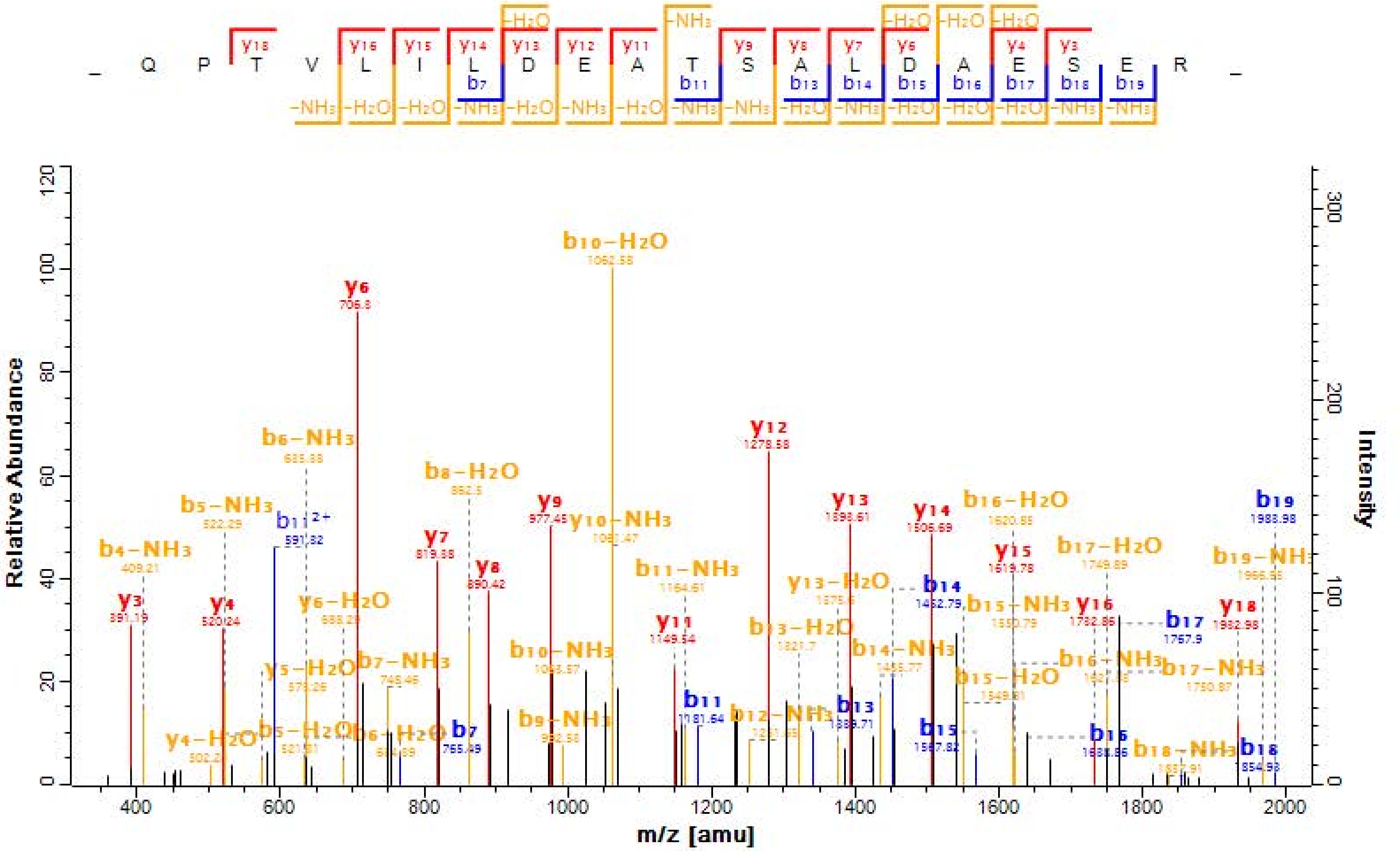
Mass:	2102.08779
m/z:	1052.05117
Charge:	2+
Retentiontime:	59.104347229003
Score:	117.1957
Mass Error [ppm]:	0.35412
PEP:	8.1991E-09
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	51 %
Peak Coverage:	31 %
Protein Localisation:	1220 ... 1237

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	17				
	143.0815	2	A	16	2032.057		2032.057	
	240.1343	3	P	15	1961.02		981.0137	+0.009263
-0.12527	400.1649	4	C	14	1863.967		1863.967	
+0.001996	513.249	5	I	13	1703.937	-0.07206	1703.937	
+0.080575	676.3123	6	Y	12	1590.853	-0.11251	1590.853	
-0.07375	862.3916	7	W	11	1427.789	-0.02989	1427.789	
-0.05552	975.4757	8	L	10	1241.71	-0.04225	1241.71	
	1072.528	9	P	9	1128.626	-0.07025	1128.626	
-0.39486	1185.613	10	L	8	1031.573	+0.007293	1031.573	
-0.42692	1286.66	11	T	7	918.4891	-0.08076	918.4891	
	1401.687	12	D	6	817.4414	+0.096677	817.4414	
	1488.719	13	S	5	702.4145	-0.01212	702.4145	
	1616.778	14	Q	4	615.3824		615.3824	
-0.09825	1729.862	15	I	3	487.3239		487.3239	
-0.13652	1828.93	16	V	2	374.2398	+0.130016	374.2398	
+0.307224	1956.989	17	Q	1	275.1714		275.1714	
		18	K	0	147.1128		147.1128	

Scan number	9225	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	209.85



precursor information

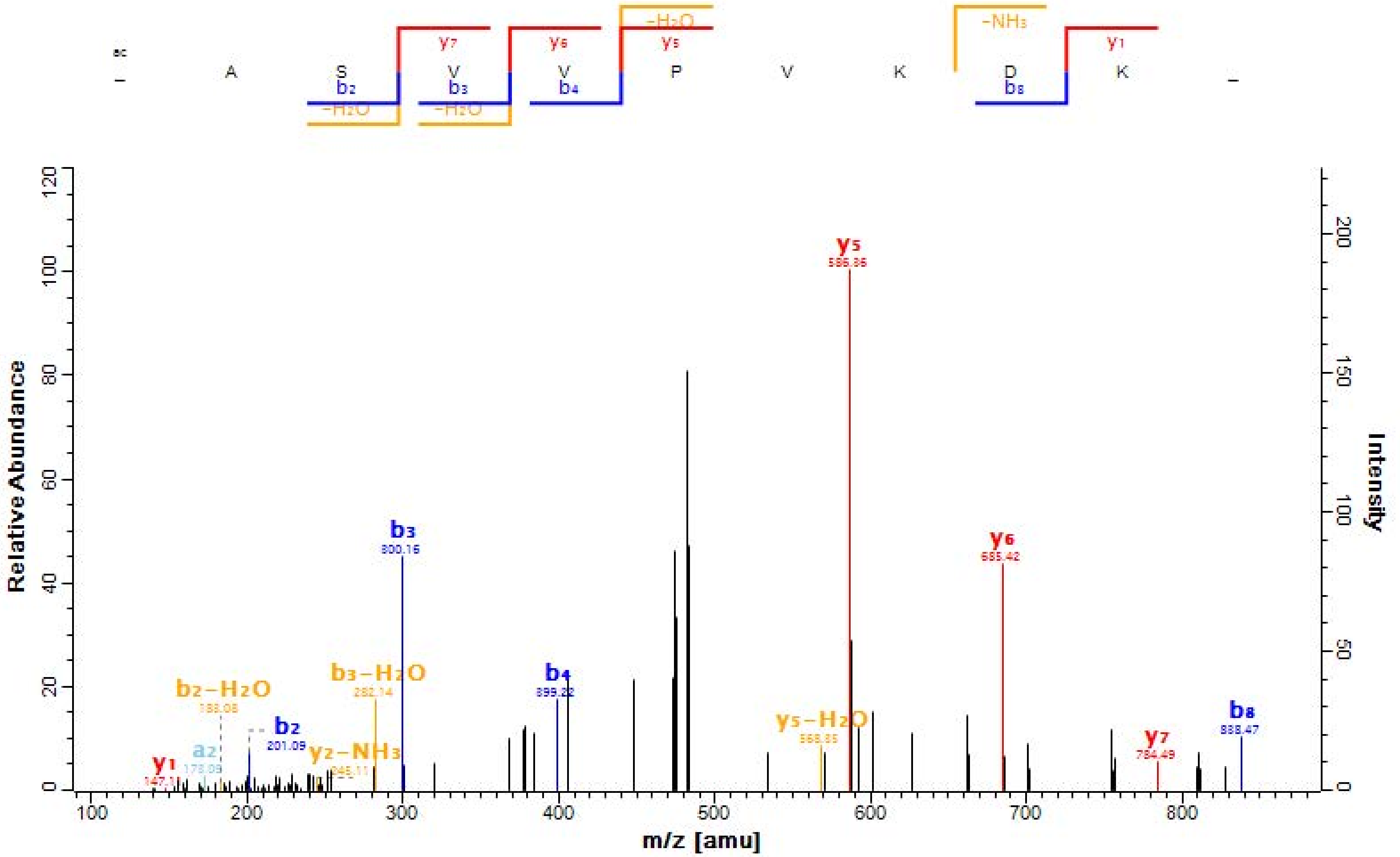
Mass:	2157.07982
m/z:	1079.54719
Charge:	2+
Retentiontime:	60.069854736328
Score:	209.8471
Mass Error [ppm]:	-0.13192
PEP:	6.9487E-59
Precursor Type:	MULTI

general information

Annotation:	17 of 20
AminoAcids Coverag	85 %
Intensity Coverage:	67 %
Peak Coverage:	50 %
Protein Localisation:	629 ... 648

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	129.0659		129.0659	1	Q	19		
	226.1186		226.1186	2	P	18	2030.029	
	327.1663		327.1663	3	T	17	1932.976	-0.24789
	426.2347		426.2347	4	V	16	1831.928	
	539.3188		539.3188	5	L	15	1732.86	-0.17721
	652.4028		652.4028	6	I	14	1619.776	-0.14906
	765.4869	-0.02609	765.4869	7	L	13	1506.692	-0.14751
	880.5138		880.5138	8	D	12	1393.608	-0.0549
	1009.556		1009.556	9	E	11	1278.581	-0.01453
	1080.594		1080.594	10	A	10	1149.538	-0.00331
-0.01273	591.3243	-0.2019	1181.641	11	T	9	1078.501	
	1268.673		1268.673	12	S	8	977.4534	-0.06757
	1339.71	+0.211014	1339.71	13	A	7	890.4214	+0.153672
	1452.794	-0.19568	1452.794	14	L	6	819.3843	+0.008291
	1567.821	-0.38327	1567.821	15	D	5	706.3002	+0.055794
	1638.858	-0.28537	1638.858	16	A	4	591.2733	
	1767.901	-0.25631	1767.901	17	E	3	520.2362	+0.065408
	1854.933	-0.45436	1854.933	18	S	2	391.1936	-0.01614
	1983.976	+0.000244	1983.976	19	E	1	304.1615	
				20	R	0	175.119	

Scan number 923 **Raw file** LNCAP_Silac_23F10_set3_02
Method ITMS; CID **Pepti...** 53.75

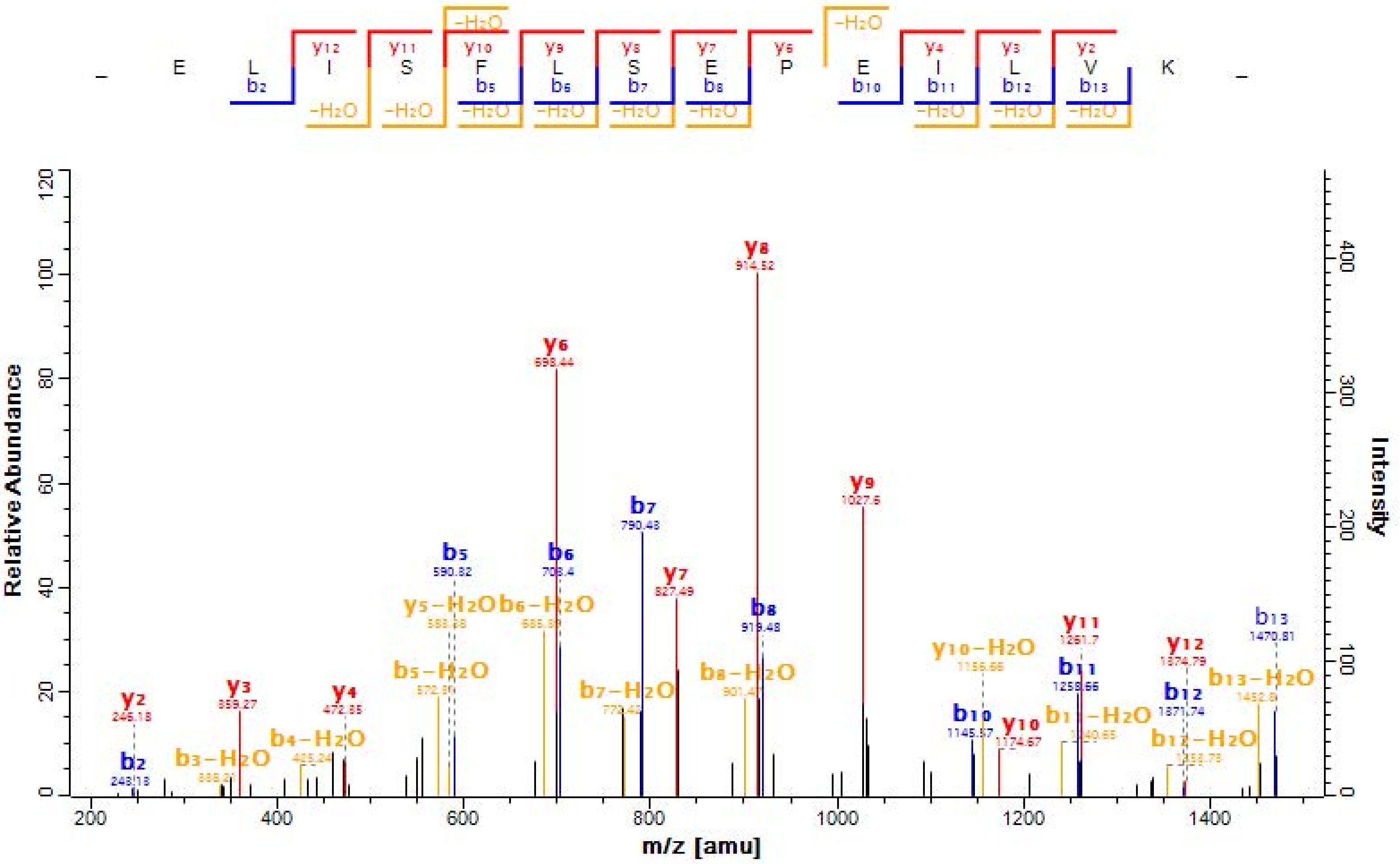


precursor information

Mass:	983.56533
m/z:	492.78994
Charge:	2+
Retentiontime:	12.477801322937
Score:	53.75107
Mass Error [ppm]:	0.18282
PEP:	0.084946
Precursor Type:	MULTI
Annotation:	6 of 9
AminoAcids Coverag	67 %
Intensity Coverage:	32 %
Peak Coverage:	14 %
Protein Localisation:	2 ... 10

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	86.06004		114.055	1	A	8		
-0.01906	173.0921	+0.014213	201.087	2	S	7	871.5247	
	272.1605	+0.000456	300.1554	3	V	6	784.4927	+0.010519
	371.2289	-0.15304	399.2238	4	V	5	685.4243	+0.049697
	468.2817		496.2766	5	P	4	586.3559	+0.1222
	567.3501		595.345	6	V	3	489.3031	
	695.445		723.44	7	K	2	390.2347	
	810.472	-0.03483	838.4669	8	D	1	262.1397	
				9	K	0	147.1128	+0.149616

Scan number	9704	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	176.91



precursor information

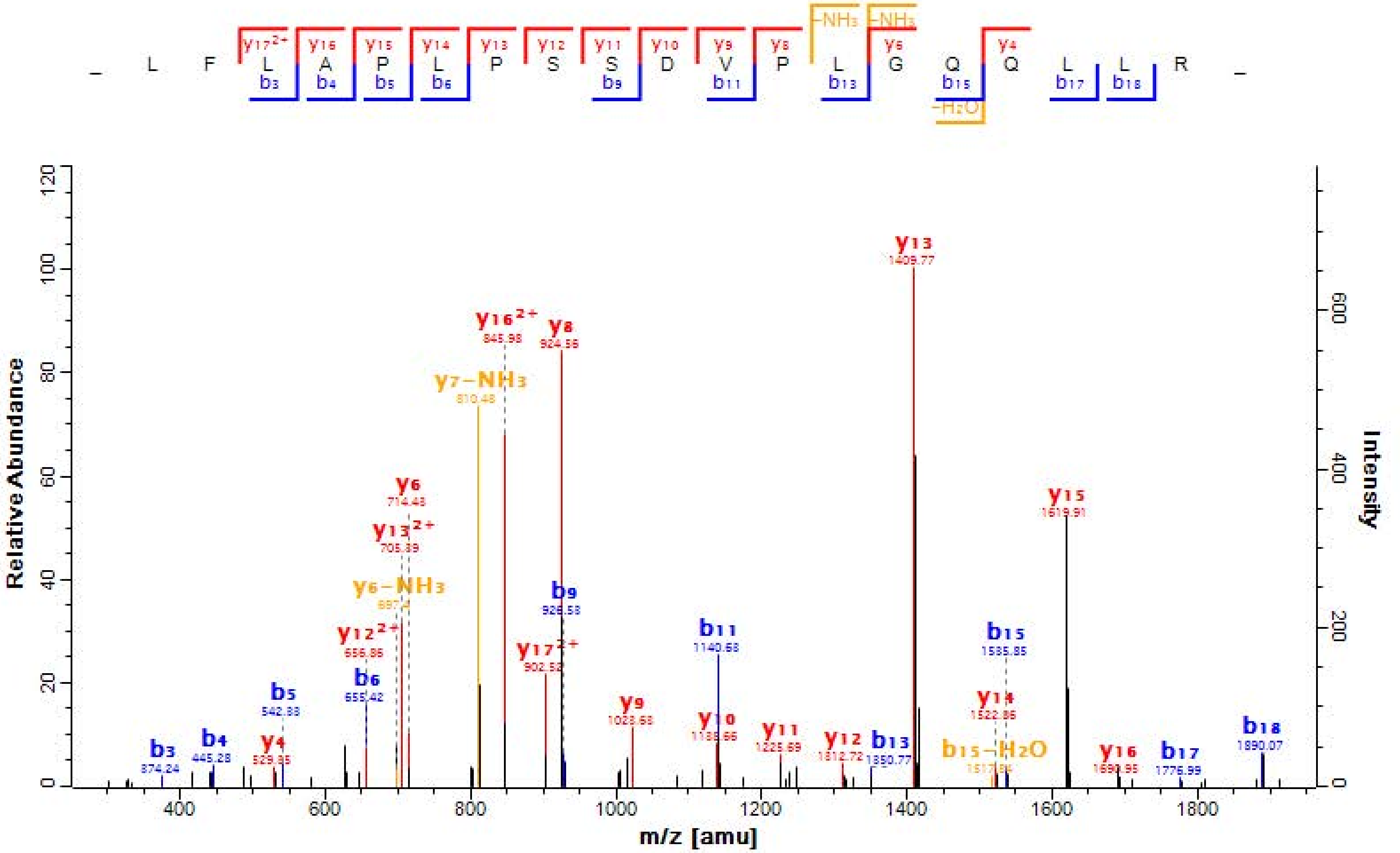
Mass:	1615.90752
m/z:	808.96104
Charge:	2+
Retentiontime:	63.231220245361
Score:	176.9149
Mass Error [ppm]:	0.15061
PEP:	1.2347E-13
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	68 %
Peak Coverage:	39 %
Protein Localisation:	98 ... 111

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	130.049869563	1	E	13		
+0.0604329	243.133933543	2	L	12	1487.87195877	
	356.217997524	3	I	11	1374.78789479	-0.1057659
	443.250025934	4	S	10	1261.70383081	+0.0012473
-0.0049633	590.31843985	5	F	9	1174.6718024	-0.0931891
-0.0077895	703.40250383	6	L	8	1027.60338848	-0.0497996
+0.1662368	790.43453224	7	S	7	914.519324502	+0.0199821
-0.0083753	919.477125336	8	E	6	827.487296092	-0.016654
	1016.52988919	9	P	5	698.444702996	+0.0072623
+0.0732697	1145.57248228	10	E	4	601.391939144	
-0.1366488	1258.65654626	11	I	3	472.349346048	+0.1240426
-0.2136327	1371.74061025	12	L	2	359.265282067	-0.0987782
-0.1948884	1470.80902416	13	V	1	246.181218087	+0.136592
		14	K	0	147.112804171	

Scan number	9766	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	173.34



precursor information

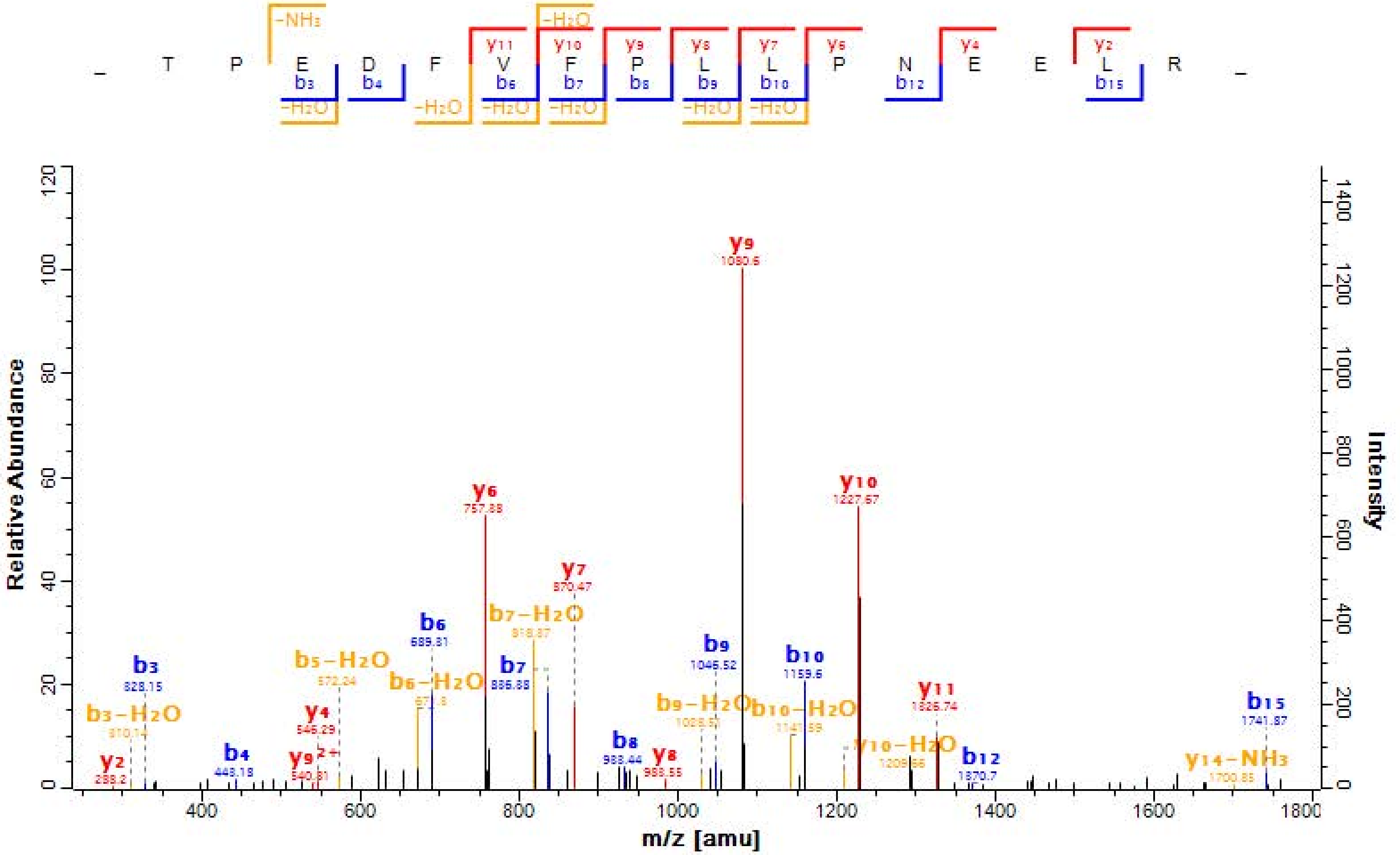
Mass:	2063.17847
m/z:	1032.59651
Charge:	2+
Retentiontime:	63.686180114746
Score:	173.3369
Mass Error [ppm]:	0.27299
PEP:	3.2525E-34
Precursor Type:	MULTI

general information

Annotation:	16 of 19
AminoAcids Coverag	84 %
Intensity Coverage:	57 %
Peak Coverage:	29 %
Protein Localisation:	773 ... 791

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	18				
	261.1598	2	F	17	1951.101		1951.101	
-0.04021	374.2438	3	L	16	1804.033		902.52	+0.3334
+0.091749	445.2809	4	A	15	1690.949	-0.29154	845.978	+0.214055
+0.036177	542.3337	5	P	14	1619.912	-0.0026	1619.912	
-0.04703	655.4178	6	L	13	1522.859	-0.11963	1522.859	
	752.4705	7	P	12	1409.775	-0.0778	705.391	+0.235597
	839.5026	8	S	11	1312.722	-0.0768	656.8646	-0.38377
+0.056972	926.5346	9	S	10	1225.69	-0.00205	1225.69	
	1041.562	10	D	9	1138.658	+0.009841	1138.658	
+0.073676	1140.63	11	V	8	1023.631	-0.03084	1023.631	
	1237.683	12	P	7	924.5625	+0.069309	924.5625	
-0.06962	1350.767	13	L	6	827.5098		827.5098	
	1407.788	14	G	5	714.4257	+0.009604	714.4257	
+0.185786	1535.847	15	Q	4	657.4042		657.4042	
	1663.905	16	Q	3	529.3457	+0.066879	529.3457	
-0.09113	1776.989	17	L	2	401.2871		401.2871	
-0.4252	1890.074	18	L	1	288.203		288.203	
		19	R	0	175.119		175.119	

Scan number	9767	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	110.84



precursor information

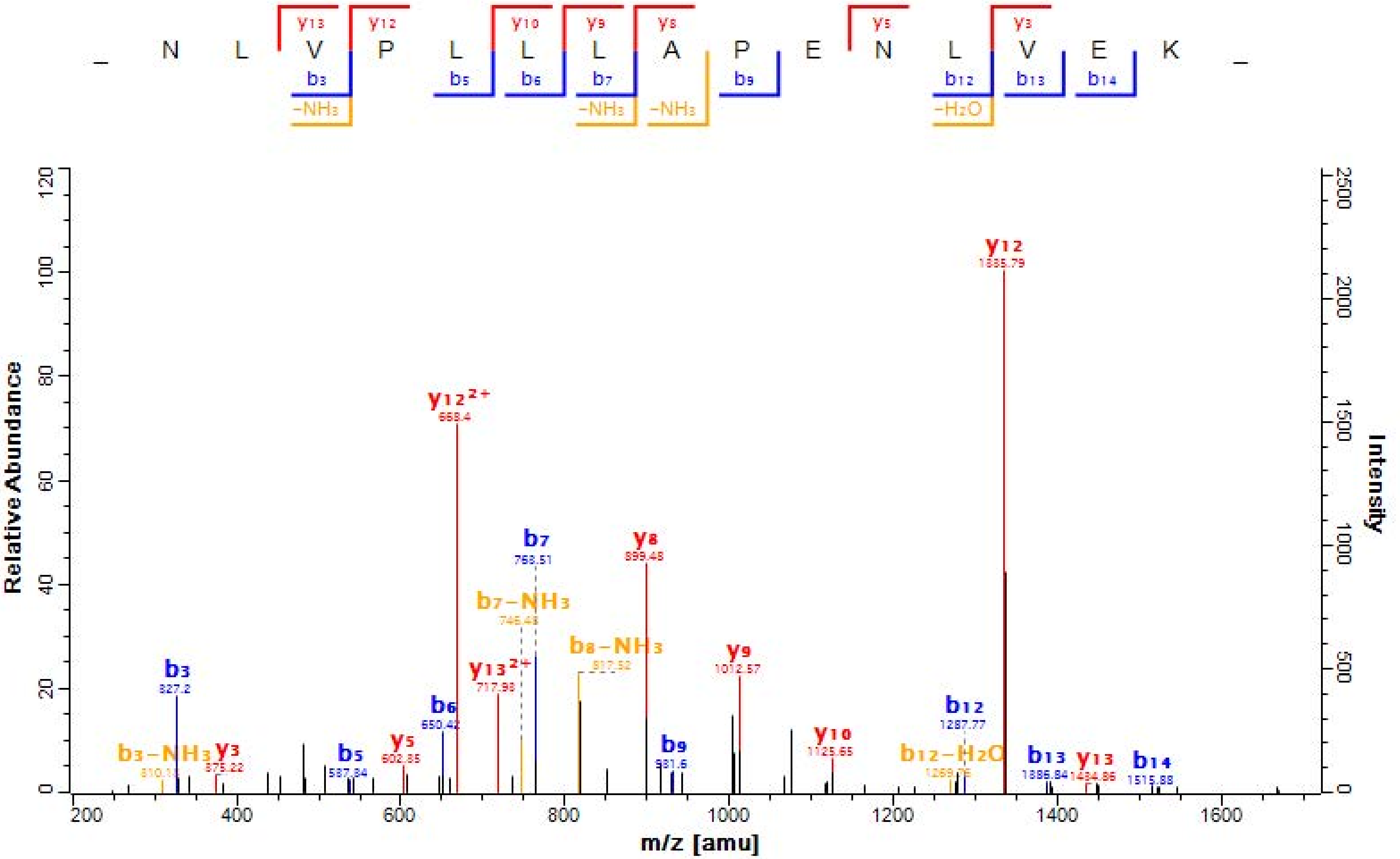
Mass:	1914.97331
m/z:	958.49393
Charge:	2+
Retentiontime:	63.695320129394
Score:	110.8435
Mass Error [ppm]:	0.30215
PEP:	4.7204E-07
Precursor Type:	MULTI

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	56 %
Peak Coverage:	29 %
Protein Localisation:	192 ... 207

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055	1	T	15				
	199.1077	2	P	14	1814.932		1814.932	
+0.175555	328.1503	3	E	13	1717.88		1717.88	
+0.121512	443.1773	4	D	12	1588.837		1588.837	
	590.2457	5	F	11	1473.81		1473.81	
+0.103947	689.3141	6	V	10	1326.742	+0.020594	1326.742	
-0.0902	836.3825	7	F	9	1227.673	-0.00181	1227.673	
-0.3022	933.4353	8	P	8	1080.605	-0.07024	540.806	-0.49121
+0.068322	1046.519	9	L	7	983.552	-0.06148	983.552	
-0.15441	1159.603	10	L	6	870.468	-0.00305	870.468	
	1256.656	11	P	5	757.3839	-0.00908	757.3839	
+0.012956	1370.699	12	N	4	660.3311		660.3311	
	1499.742	13	E	3	546.2882	-0.16747	546.2882	
	1628.784	14	E	2	417.2456		417.2456	
+0.132402	1741.868	15	L	1	288.203	+0.108202	288.203	
		16	R	0	175.119		175.119	

Scan number	9777	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	104.95



precursor information

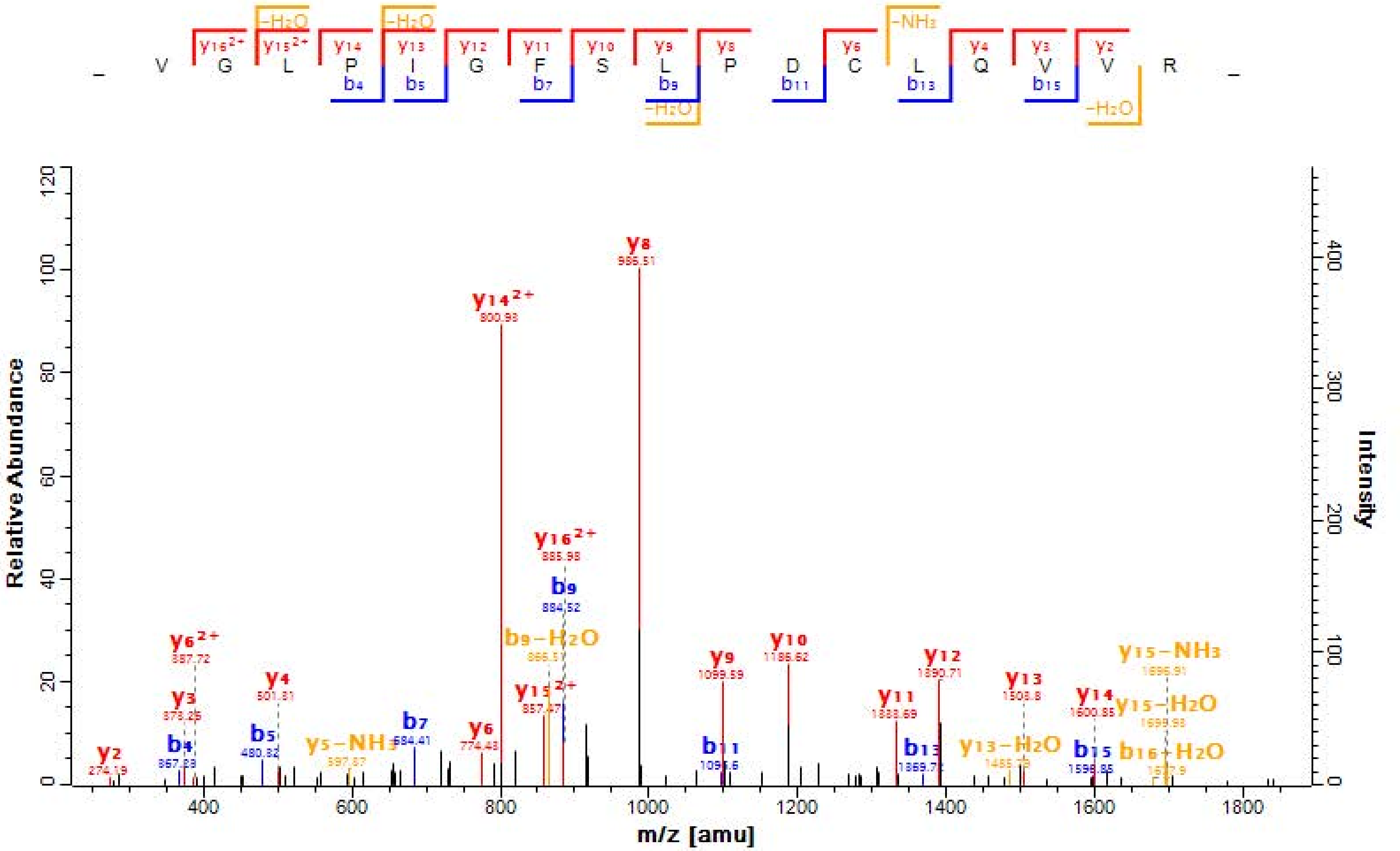
Mass:	1660.97683
m/z:	831.49569
Charge:	2+
Retentiontime:	63.760334014892
Score:	104.9545
Mass Error [ppm]:	0.28338
PEP:	3.9326E-06
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	58 %
Peak Coverage:	26 %
Protein Localisation:	326 ... 340

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502	1	N	14				
	228.1343	2	L	13	1547.941		1547.941	
+0.028825	327.2027	3	V	12	1434.857	-0.17171	717.932	+0.293443
	424.2554	4	P	11	1335.788	-0.03615	668.3978	+0.250318
-0.2103	537.3395	5	L	10	1238.735		1238.735	
+0.052317	650.4236	6	L	9	1125.651	+0.010952	1125.651	
-0.02589	763.5076	7	L	8	1012.567	+0.000351	1012.567	
	834.5448	8	A	7	899.4833	-0.00518	899.4833	
-0.03263	931.5975	9	P	6	828.4462		828.4462	
	1060.64	10	E	5	731.3934		731.3934	
	1174.683	11	N	4	602.3508	+0.061307	602.3508	
-0.02137	1287.767	12	L	3	488.3079		488.3079	
+0.12994	1386.836	13	V	2	375.2238	+0.160893	375.2238	
-0.34869	1515.878	14	E	1	276.1554		276.1554	
		15	K	0	147.1128		147.1128	

Scan number	9923	**Raw file**	LNCAP_Silac_23F10_set3_02
Method	ITMS; CID	**Pepti...**	127.75



precursor information

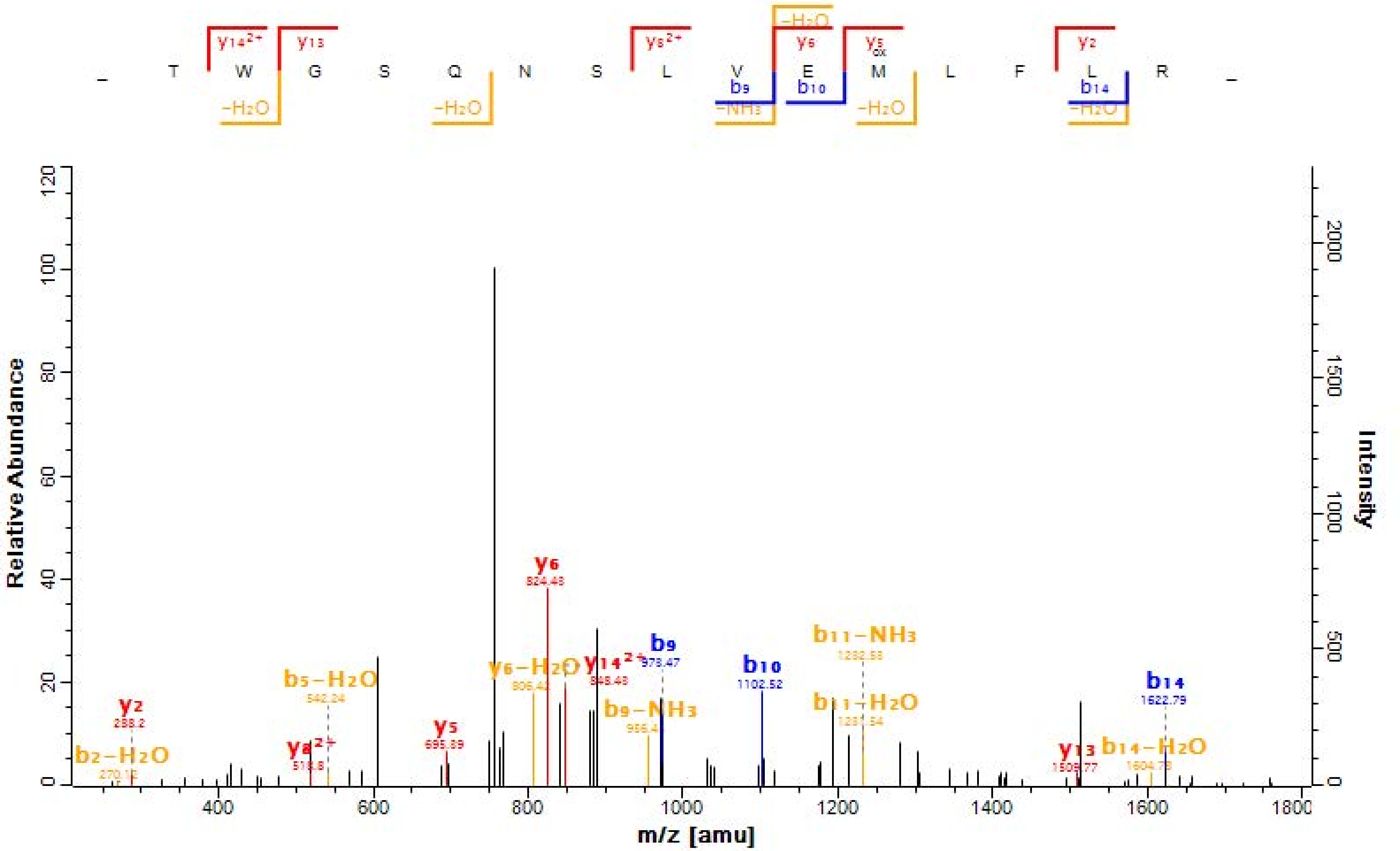
Mass:	1869.01824
m/z:	935.5164
Charge:	2+
Retentiontime:	64.845825195312
Score:	127.7531
Mass Error [ppm]:	0.0020786
PEP:	3.6774E-12
Precursor Type:	MULTI

general information

Annotation:	15 of 17
AminoAcids Coverag	88 %
Intensity Coverage:	63 %
Peak Coverage:	30 %
Protein Localisation:	98 ... 114

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	16				
	157.0972	2	G	15	1770.957		885.9822	-0.3766
	270.1812	3	L	14	1713.936		857.4715	+0.135903
-0.15946	367.234	4	P	13	1600.852	+0.00011	800.9294	+0.203692
-0.04662	480.318	5	I	12	1503.799	+0.168597	1503.799	
	537.3395	6	G	11	1390.715	-0.11233	1390.715	
-0.06326	684.4079	7	F	10	1333.693	-0.08647	1333.693	
	771.44	8	S	9	1186.625	+0.023691	1186.625	
+0.163728	884.524	9	L	8	1099.593	+0.061212	1099.593	
	981.5768	10	P	7	986.5088	-0.03099	986.5088	
-0.25289	1096.604	11	D	6	889.456		889.456	
	1256.634	12	C	5	774.4291	+0.059639	387.7182	-0.45584
+0.045603	1369.718	13	L	4	614.3984		614.3984	
	1497.777	14	Q	3	501.3144	+0.160252	501.3144	
-0.306	1596.845	15	V	2	373.2558	+0.010761	373.2558	
	1695.914	16	V	1	274.1874	+0.049572	274.1874	
		17	R	0	175.119		175.119	

Scan number	10008	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti…**	61.41



precursor information

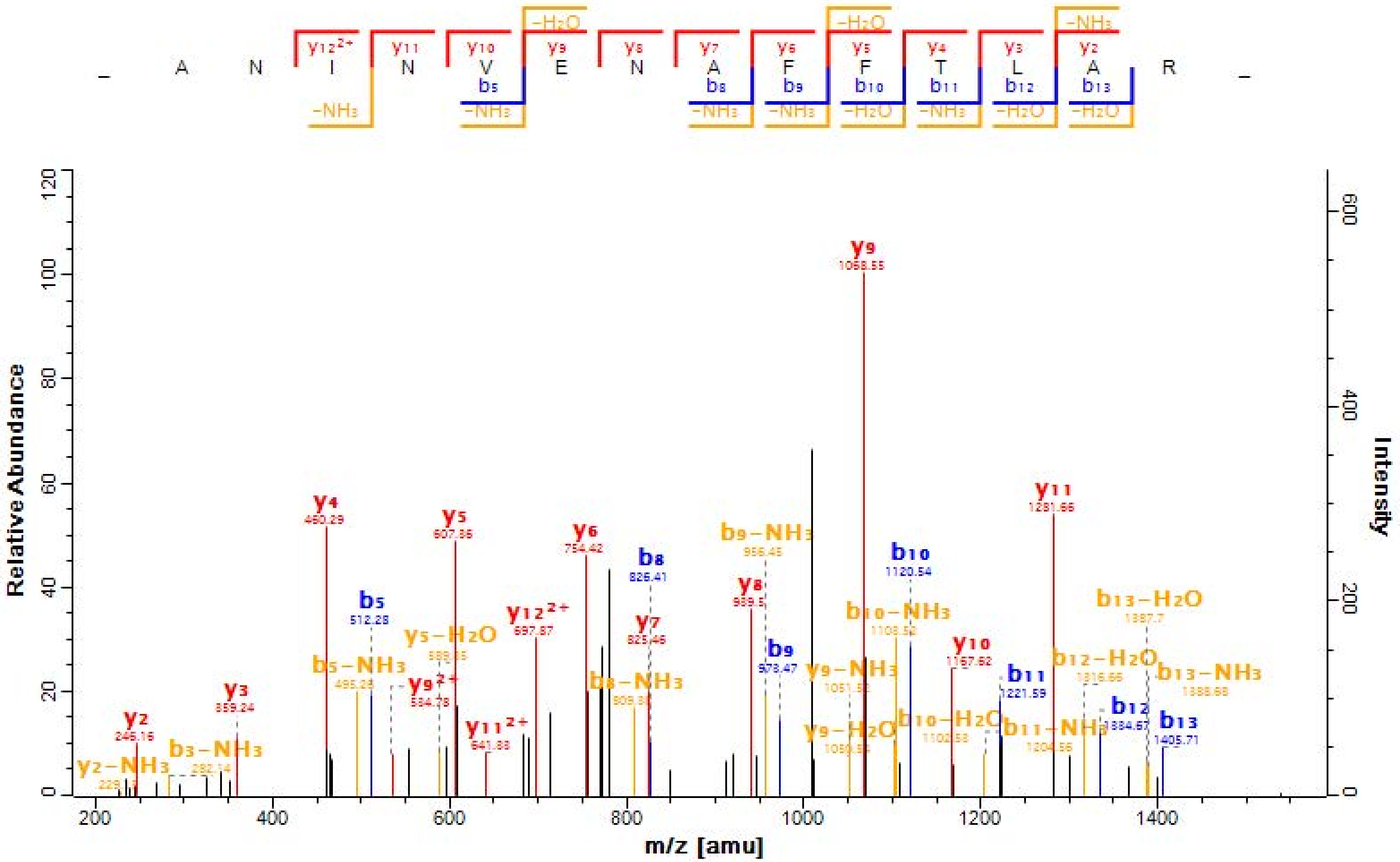
Mass:	1795.89199
m/z:	898.95327
Charge:	2+
Retentiontime:	57.198043823242
Score:	61.40926
Mass Error [ppm]:	-0.39931
PEP:	0.012681
Precursor Type:	MULTI

general information

Annotation:	9 of 15
AminoAcids Coverag	60 %
Intensity Coverage:	25 %
Peak Coverage:	18 %
Protein Localisation:	1275 … 1289

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055	1	T	14				
	288.1343	2	W	13	1695.852		848.4298	+0.300435
	345.1557	3	G	12	1509.773	+0.137899	1509.773	
	432.1878	4	S	11	1452.752		1452.752	
	560.2463	5	Q	10	1365.719		1365.719	
	674.2893	6	N	9	1237.661		1237.661	
	761.3213	7	S	8	1123.618		1123.618	
	874.4054	8	L	7	1036.586		518.7966	-0.36614
-0.0309	973.4738	9	V	6	923.5019		923.5019	
+0.062249	1102.516	10	E	5	824.4335	-0.03133	824.4335	
	1249.552	11	M	4	695.3909	-0.00131	695.3909	
	1362.636	12	L	3	548.3555		548.3555	
	1509.704	13	F	2	435.2714		435.2714	
-0.22544	1622.788	14	L	1	288.203	+0.0497	288.203	
		15	R	0	175.119		175.119	

Scan number	10077	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	191.06



precursor information

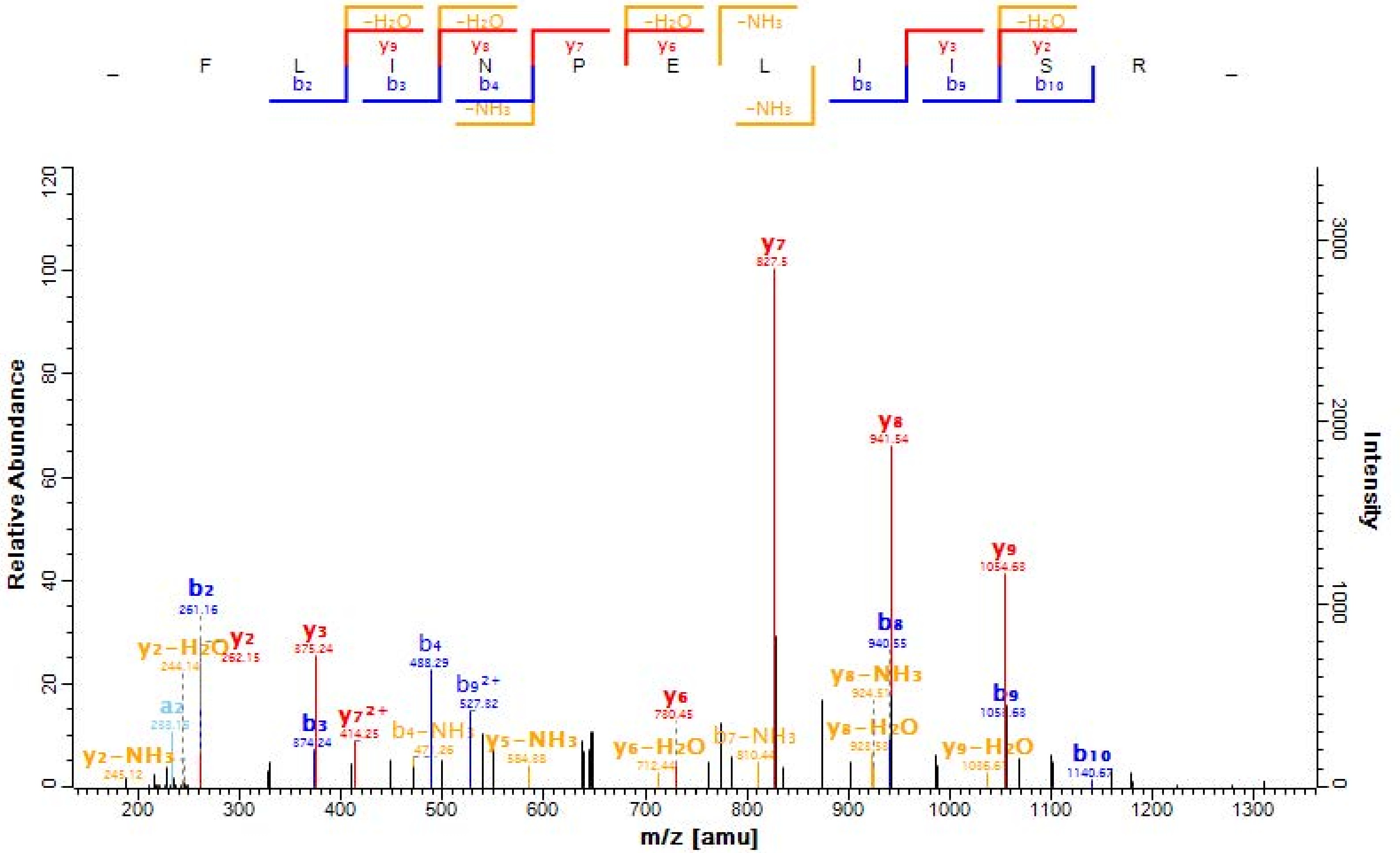
Mass:	1578.81498
m/z:	790.41477
Charge:	2+
Retentiontime:	57.632118225097
Score:	191.0584
Mass Error [ppm]:	-0.28931
PEP:	2.1658E-18
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	61 %
Peak Coverage:	44 %
Protein Localisation:	154 ... 167

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	13				
	186.0873	2	N	12	1508.786		1508.786	
	299.1714	3	I	11	1394.743		697.875	+0.260339
	413.2143	4	N	10	1281.659	-0.08036	641.3329	+0.165225
+0.067008	512.2827	5	V	9	1167.616	+0.102577	1167.616	
	641.3253	6	E	8	1068.547	+0.010102	534.7773	+0.455026
	755.3682	7	N	7	939.5047	+0.027	939.5047	
+0.029762	826.4054	8	A	6	825.4618	-0.04842	825.4618	
+0.046431	973.4738	9	F	5	754.4246	+0.092515	754.4246	
-0.16889	1120.542	10	F	4	607.3562	+0.060709	607.3562	
-0.24392	1221.59	11	T	3	460.2878	+0.151706	460.2878	
-0.07688	1334.674	12	L	2	359.2401	+0.09416	359.2401	
-0.19896	1405.711	13	A	1	246.1561	-0.04692	246.1561	
		14	R	0	175.119		175.119	

Scan number	10142	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	128.08



precursor information

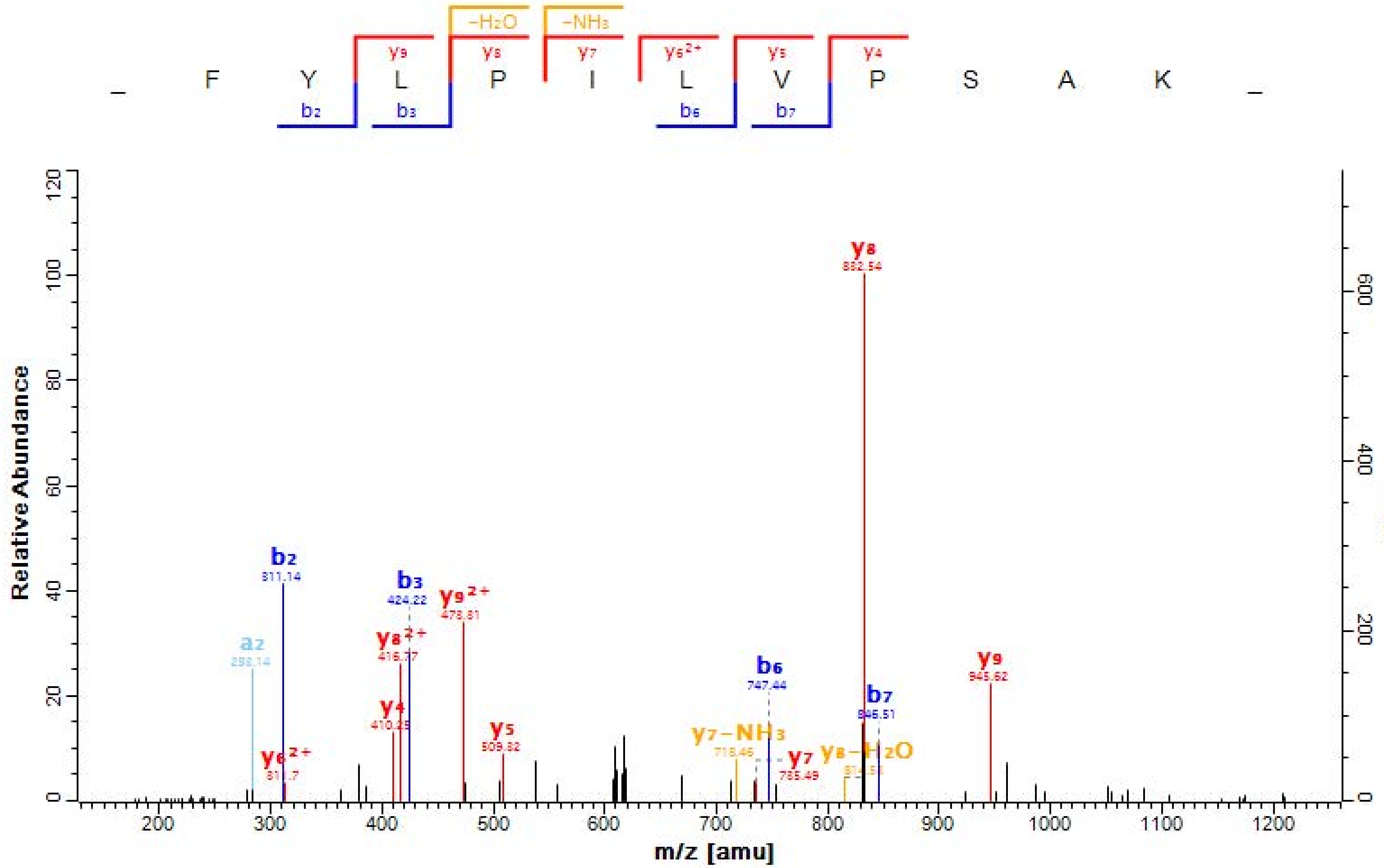
Mass:	1313.77077
m/z:	657.89266
Charge:	2+
Retentiontime:	58.059024810791
Score:	128.081
Mass Error [ppm]:	0.03978
PEP:	0.00018779
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	57 %
Peak Coverage:	27 %
Protein Localisation:	759 ... 769

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.1		148.1		148.1	1	F	10				
-0.01	233.2		261.2	-0.01	261.2	2	L	9	1168		1168	
	346.2		374.2	-0.01	374.2	3	I	8	1055	-0.03	1055	
	460.3		488.3	-0.05	488.3	4	N	7	941.5	-0.02	941.5	
	557.3		585.3		585.3	5	P	6	827.5	+0.014	414.3	+0.03
	686.4		714.4		714.4	6	E	5	730.4	-0.15	730.4	
	799.5		827.5		827.5	7	L	4	601.4		601.4	
	912.6		940.6	-0.26	940.6	8	I	3	488.3		488.3	
	1026	+0.091	527.3	-0.15	1054	9	I	2	375.2	+0.13	375.2	
	1113		1141	+0.075	1141	10	S	1	262.2	-0.05	262.2	
						11	R	0	175.1		175.1	

Scan number	10195	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	100.48



precursor information

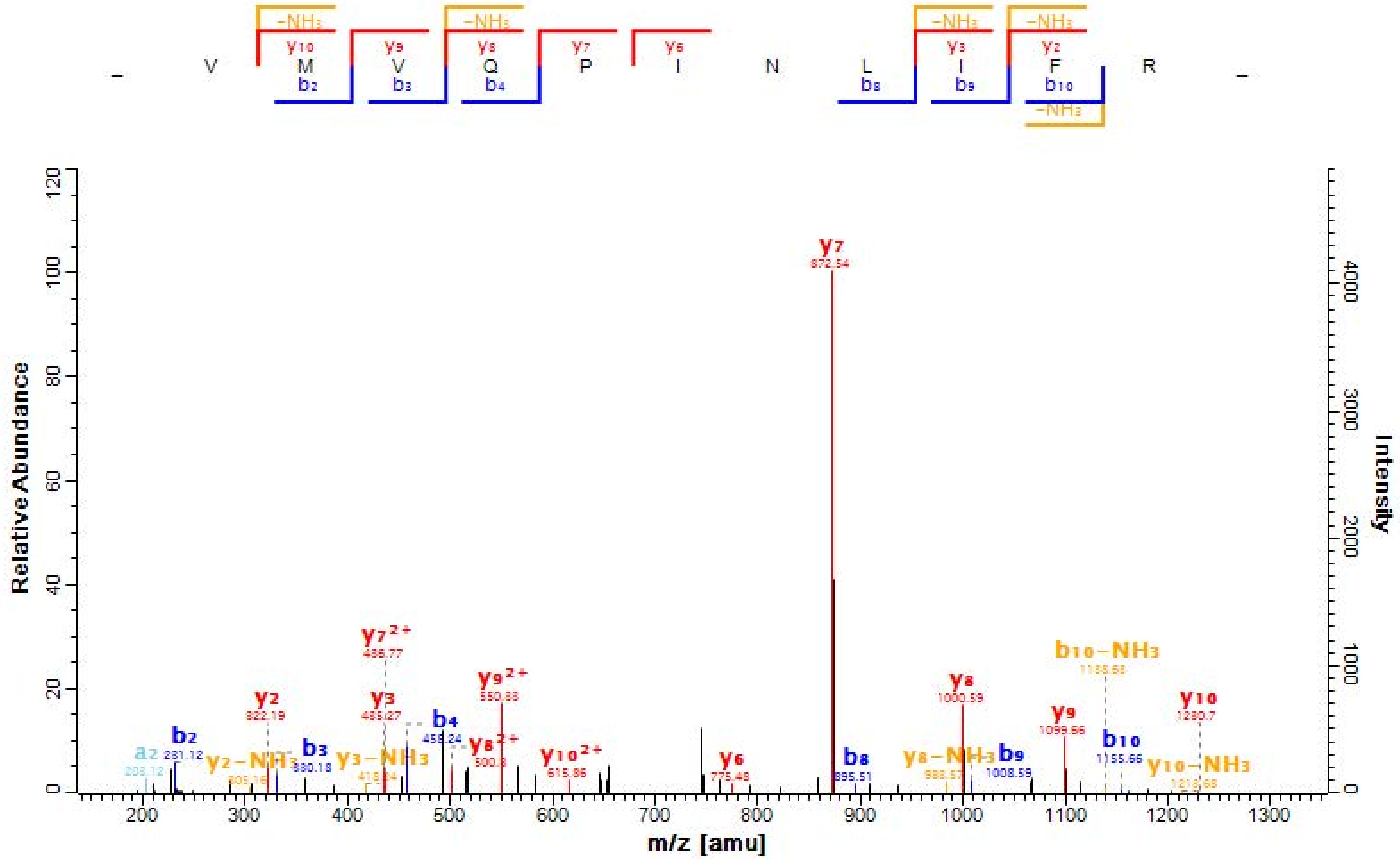
Mass:	1246.73294
m/z:	624.37375
Charge:	2+
Retentiontime:	58.376426696777
Score:	100.4767
Mass Error [ppm]:	0.31606
PEP:	0.00063423
Precursor Type:	MULTI

general information

Annotation:	7 of 11
AminoAcids Coverag	64 %
Intensity Coverage:	67 %
Peak Coverage:	19 %
Protein Localisation:	155 ... 165

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08		148.08	1	F	10				
+0.0027	283.14	+0.0185	311.14	2	Y	9	1108.7		1108.7	
	396.23	-0.045	424.22	3	L	8	945.62	+0.005	473.31	-0.028
	493.28		521.28	4	P	7	832.54	+0.0237	416.77	+0.0803
	606.36		634.36	5	I	6	735.49	-0.169	735.49	
	719.45	+0.0093	747.44	6	L	5	622.4		311.7	+0.3946
	818.52	-0.061	846.51	7	V	4	509.32	+0.0101	509.32	
	915.57		943.57	8	P	3	410.25	+0.0873	410.25	
	1002.6		1030.6	9	S	2	313.2		313.2	
	1073.6		1101.6	10	A	1	226.16		226.16	
				11	K	0	155.13		155.13	

Scan number	10249	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	190.02



precursor information

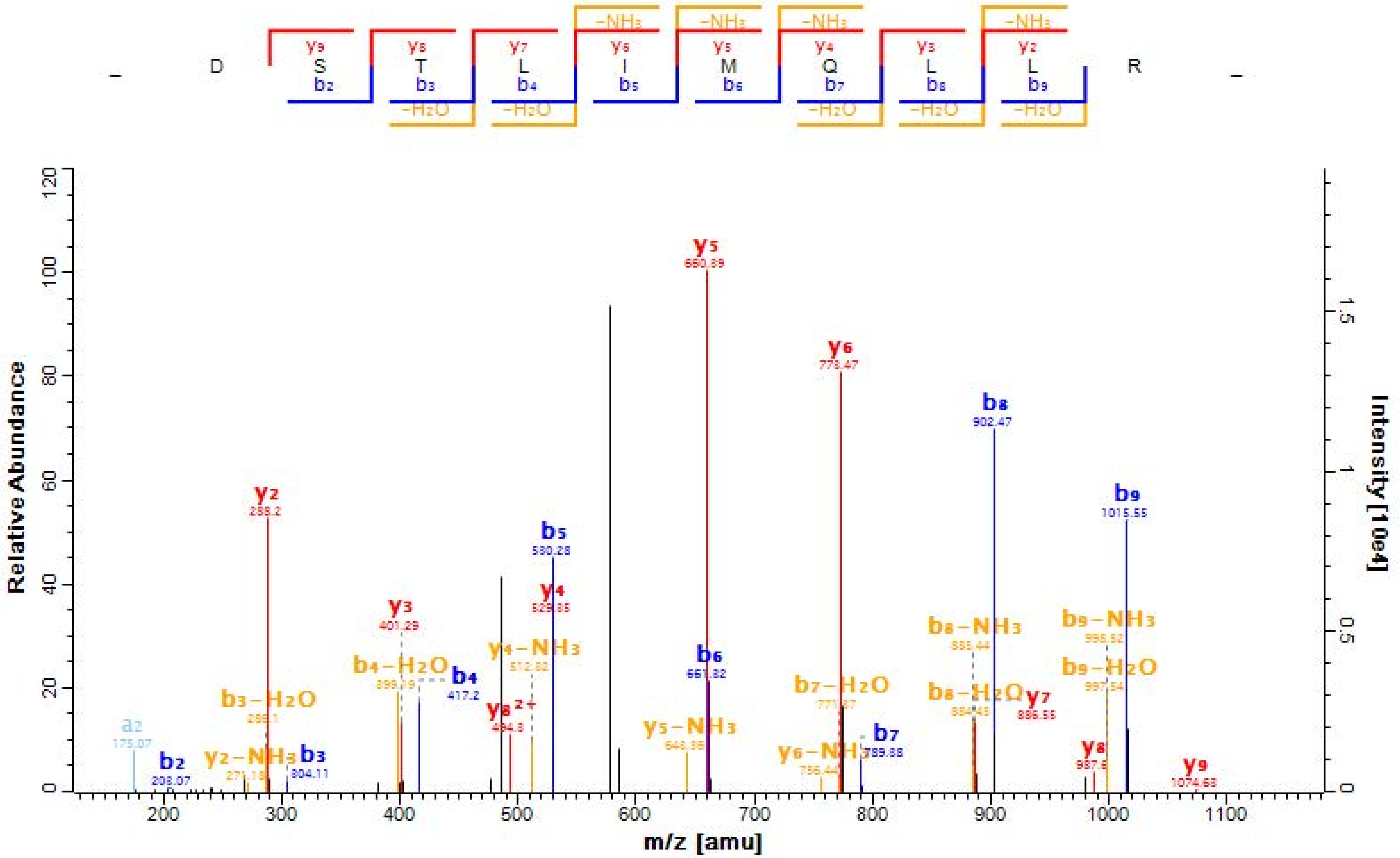
Mass:	1328.76425
m/z:	665.3894
Charge:	2+
Retentiontime:	58.705665588378
Score:	190.0165
Mass Error [ppm]:	0.29169
PEP:	1.0839E-10
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	55 %
Peak Coverage:	26 %
Protein Localisation:	13 ... 23

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.081		100.08	1	V	10				
+0.0267	203.12	-0.027	231.12	2	M	9	1230.7	-0.059	615.86	-0.035
	302.19	-0.165	330.18	3	V	8	1099.7	-0.017	550.33	+0.2161
	430.25	-0.048	458.24	4	Q	7	1000.6	+0.0097	500.8	+0.0677
	527.3		555.3	5	P	6	872.54	-0.04	436.77	-0.08
	640.39		668.38	6	I	5	775.48	+0.1992	775.48	
	754.43		782.42	7	N	4	662.4		662.4	
	867.51	+0.1004	895.51	8	L	3	548.36		548.36	
	980.6	-0.196	1008.6	9	I	2	435.27	+0.0803	435.27	
	1127.7	-0.179	1155.7	10	F	1	322.19	+0.1355	322.19	
				11	R	0	175.12		175.12	

Scan number	10406	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	236.35



precursor information

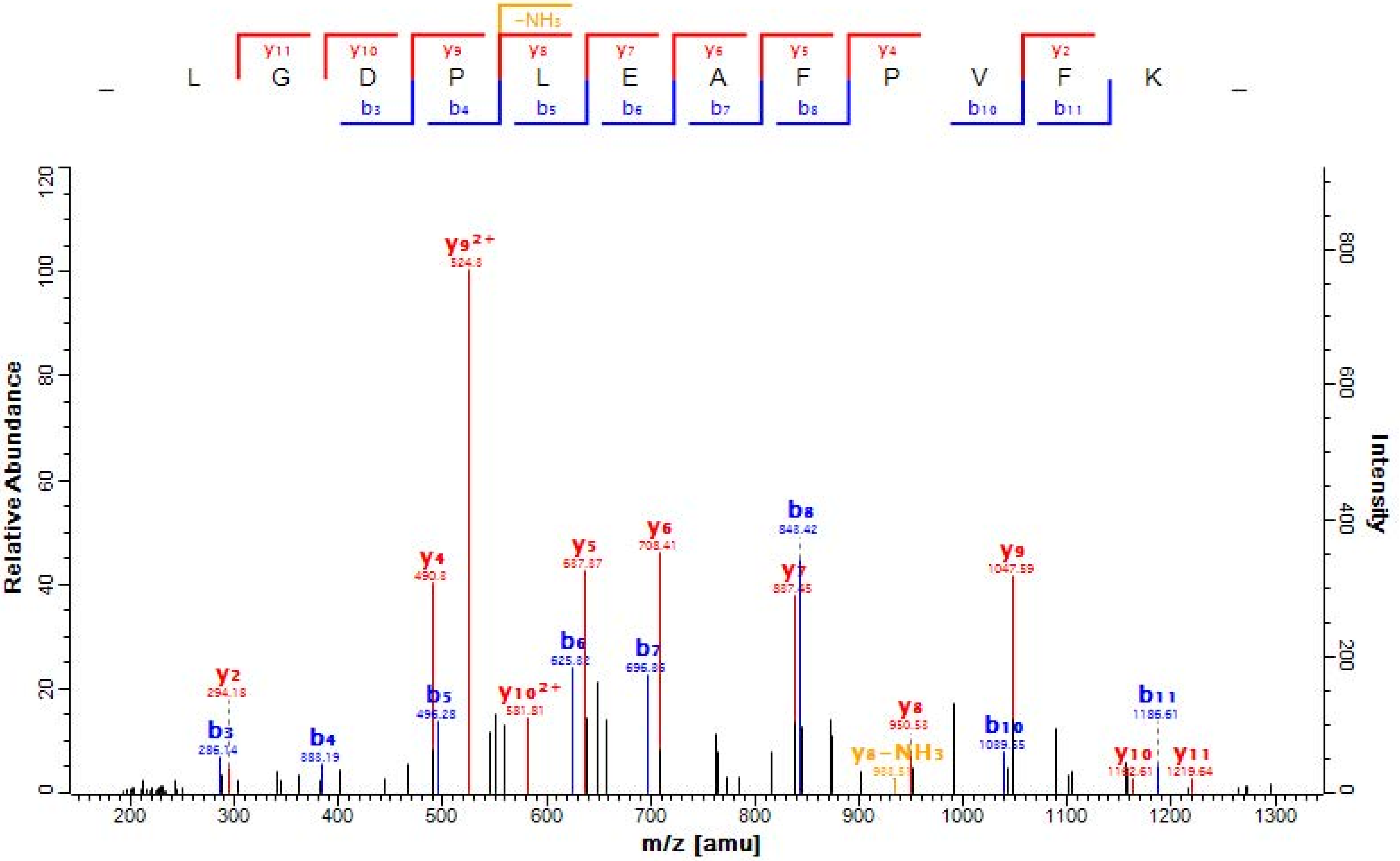
Mass:	1188.6533
m/z:	595.33393
Charge:	2+
Retentiontime:	59.699569702148
Score:	236.3472
Mass Error [ppm]:	-0.28835
PEP:	3.4842E-27
Precursor Type:	MULTI

g

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	74 %
Peak Coverage:	47 %
Protein Localisation:	216 ... 225

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	9				
-0.018	175.07	-0.055	203.07	2	S	8	1074.6	-0.416	1074.6	
	276.12	+0.1329	304.11	3	T	7	987.6	+0.0853	494.3	-0.012
	389.2	-0.096	417.2	4	L	6	886.55	-0.001	886.55	
	502.29	+0.0293	530.28	5	I	5	773.47	+0.0228	773.47	
	633.33	+0.0843	661.32	6	M	4	660.39	+0.0229	660.39	
	761.39	-0.021	789.38	7	Q	3	529.35	+0.0594	529.35	
	874.47	-0.079	902.47	8	L	2	401.29	+0.0722	401.29	
	987.55	-0.158	1015.5	9	L	1	288.2	-0.008	288.2	
				10	R	0	175.12		175.12	

Scan number	10465	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	126.1



precursor information

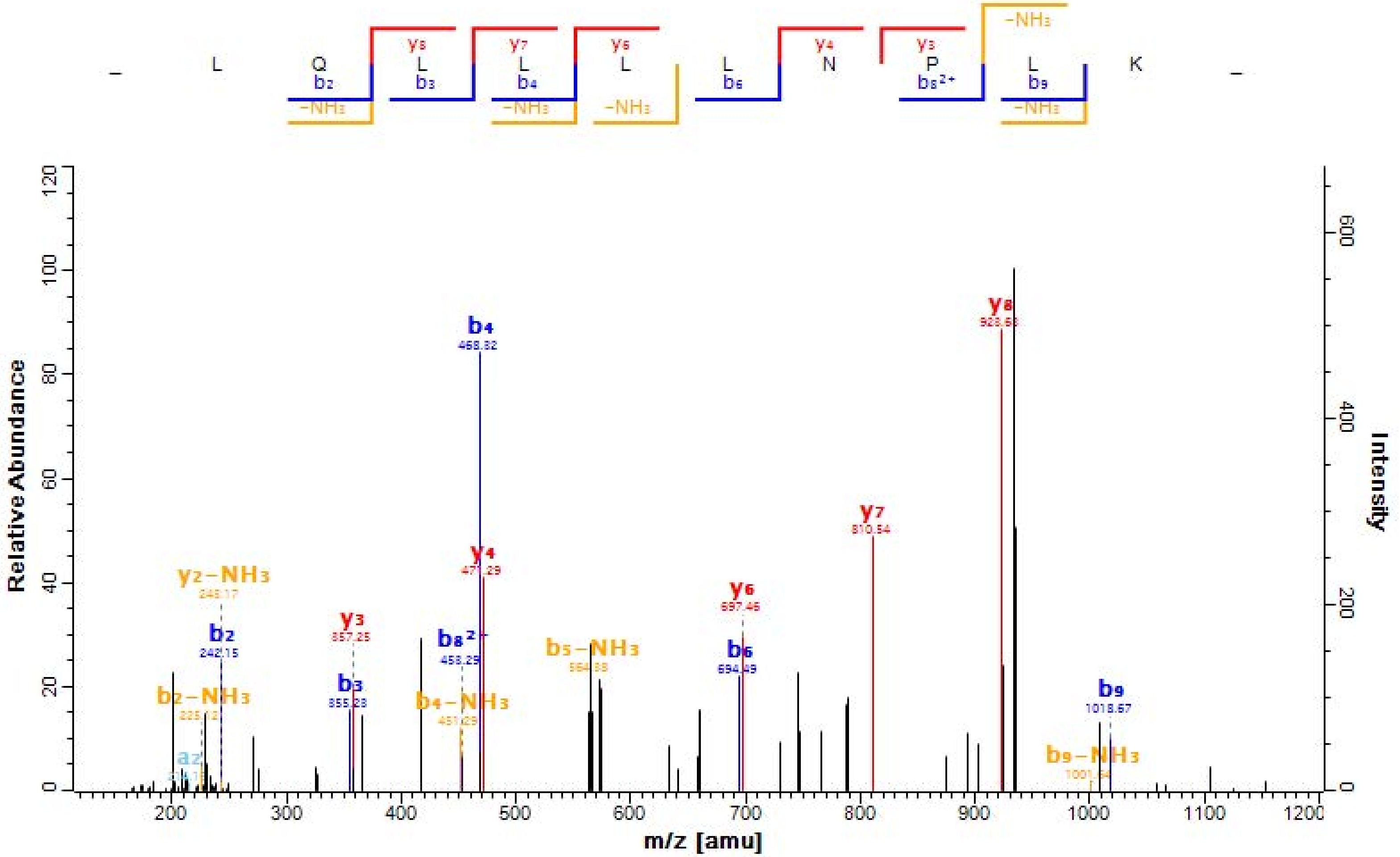
Mass:	1331.713
m/z:	666.86378
Charge:	2+
Retentiontime:	60.100566864013
Score:	126.1012
Mass Error [ppm]:	0.3449
PEP:	2.2225E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	58 %
Peak Coverage:	22 %
Protein Localisation:	35 ... 46

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	11				
	171.1128	2	G	10	1219.636	-0.18372	1219.636	
-0.02479	286.1397	3	D	9	1162.614	+0.066621	581.8108	-0.03521
+0.151849	383.1925	4	P	8	1047.587	+0.039364	524.2973	+0.178153
+0.036718	496.2766	5	L	7	950.5346	+0.097438	950.5346	
-0.03798	625.3192	6	E	6	837.4505	-0.02406	837.4505	
-0.02999	696.3563	7	A	5	708.4079	+0.012792	708.4079	
-0.01991	843.4247	8	F	4	637.3708	+0.081033	637.3708	
	940.4775	9	P	3	490.3024	+0.048251	490.3024	
+0.281885	1039.546	10	V	2	393.2496		393.2496	
-0.13834	1186.614	11	F	1	294.1812	+0.059352	294.1812	
		12	K	0	147.1128		147.1128	

Scan number	10479	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	87.91



precursor information

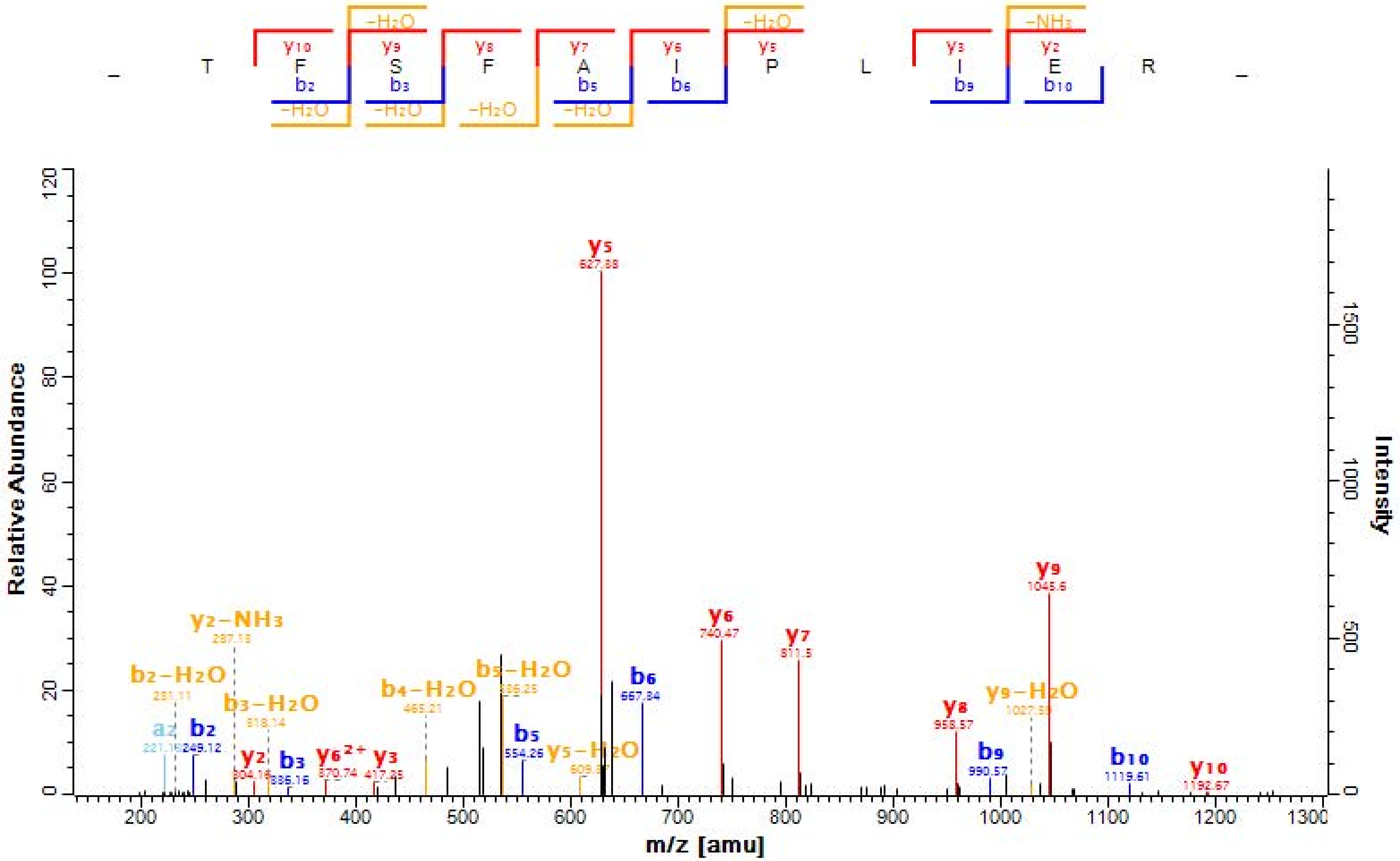
Mass:	1163.76405
m/z:	582.8893
Charge:	2+
Retentiontime:	60.200618743896
Score:	87.91328
Mass Error [ppm]:	-0.10977
PEP:	0.0024547
Precursor Type:	MULTI

g

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	42 %
Peak Coverage:	20 %
Protein Localisation:	862 ... 871

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	86.096		114.09		114.09	1	L	9		
-0.104	214.16		242.15	+0.0387	242.15	2	Q	8	1051.7	
	327.24		355.23	+0.076	355.23	3	L	7	923.63	-0.081
	440.32		468.32	-0.417	468.32	4	L	6	810.54	-0.035
	553.41		581.4		581.4	5	L	5	697.46	+0.1655
	666.49		694.49	-0.059	694.49	6	L	4	584.38	
	780.53		808.53		808.53	7	N	3	471.29	+0.0546
	877.59	+0.0894	453.29		905.58	8	P	2	357.25	-0.013
	990.67		1018.7	-0.115	1018.7	9	L	1	260.2	
						10	K	0	147.11	

Scan number	10556	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	121.68



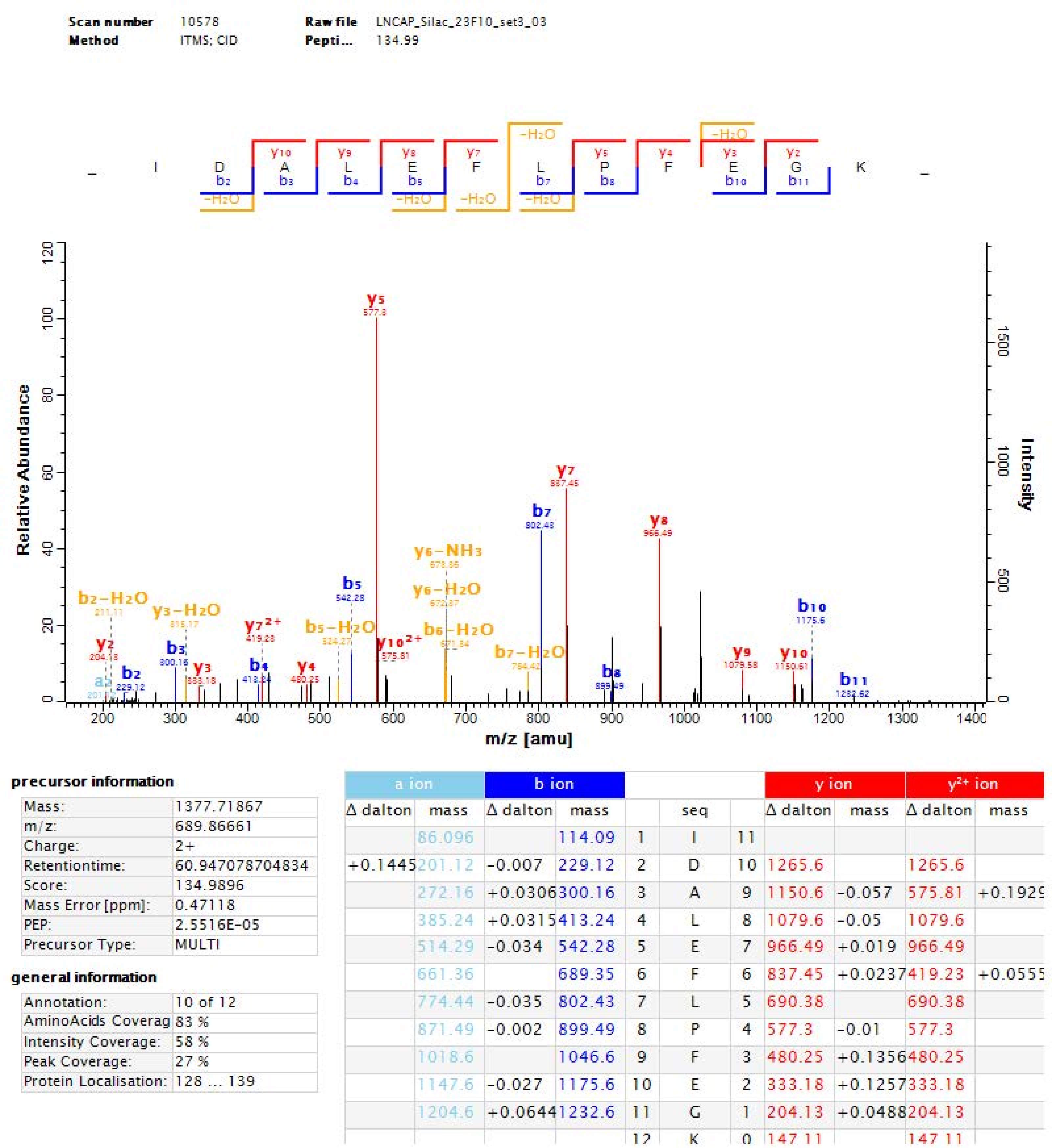
precursor information

Mass:	1292.71322
m/z:	647.36389
Charge:	2+
Retentiontime:	60.795761108398
Score:	121.6796
Mass Error [ppm]:	0.26924
PEP:	0.00019329
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	62 %
Peak Coverage:	27 %
Protein Localisation:	188 ... 198

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.05	1	T	10				
-0.058	221.13	-0.071	249.12	2	F	9	1192.7	+0.4339	1192.7	
	308.16	+0.2049	336.16	3	S	8	1045.6	-0.021	1045.6	
	455.23		483.22	4	F	7	958.57	-0.065	958.57	
	526.27	-0.05	554.26	5	A	6	811.5	+0.016	811.5	
	639.35	-0.068	667.34	6	I	5	740.47	-0.054	370.74	+0.4089
	736.4		764.4	7	P	4	627.38	+0.0761	627.38	
	849.49		877.48	8	L	3	530.33		530.33	
	962.57	+0.0699	990.57	9	I	2	417.25	+0.0654	417.25	
	1091.6	-0.252	1119.6	10	E	1	304.16	+0.1026	304.16	
				11	R	0	175.12		175.12	



Scan number	10578	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	134.99

precursor information

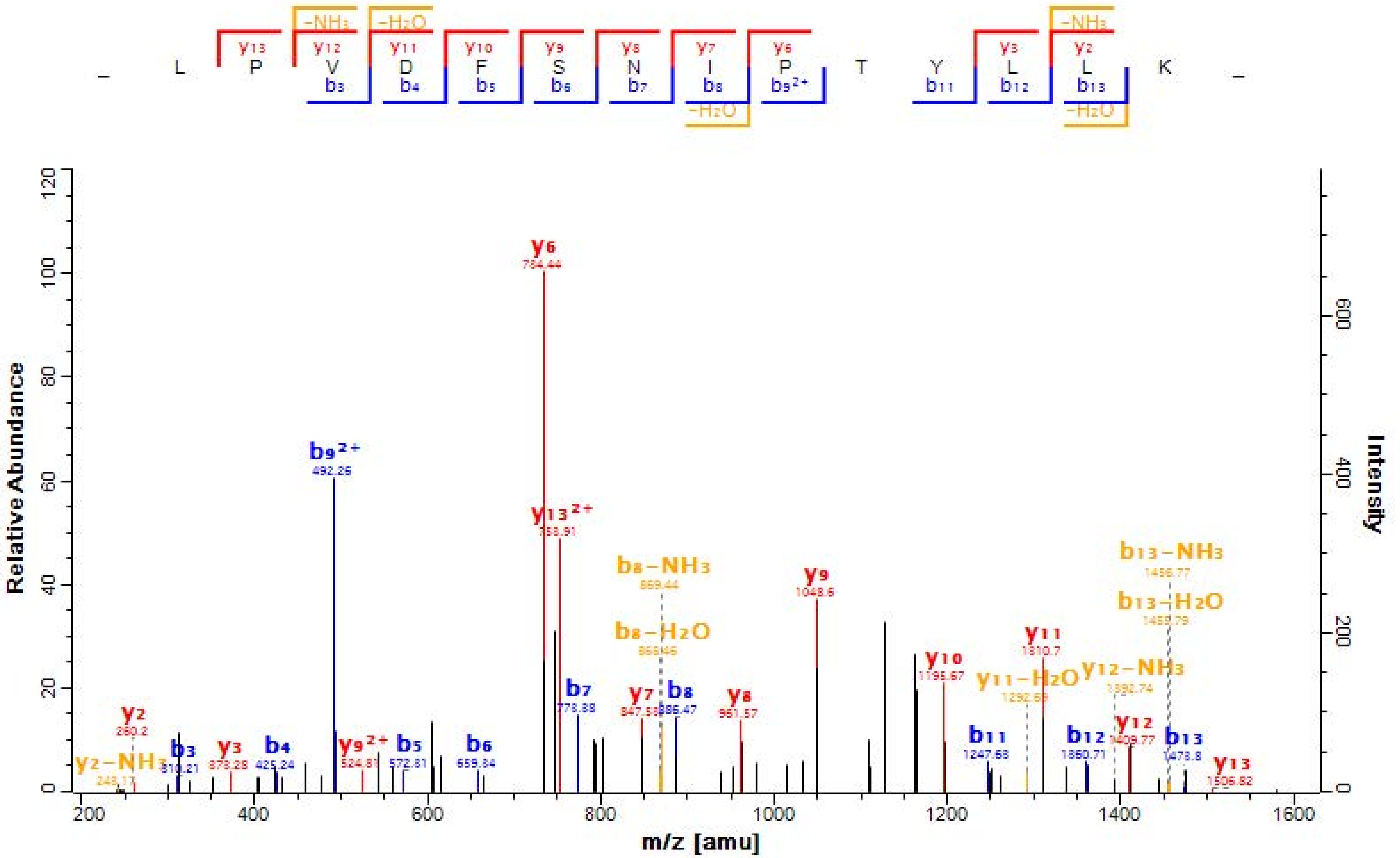
Mass:	1377.71867
m/z:	689.86661
Charge:	2+
Retentiontime:	60.947078704834
Score:	134.9896
Mass Error [ppm]:	0.47118
PEP:	2.5516E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	58 %
Peak Coverage:	27 %
Protein Localisation:	128 ... 139

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	11				
+0.1445	201.12	-0.007	229.12	2	D	10	1265.6		1265.6	
	272.16	+0.0306	300.16	3	A	9	1150.6	-0.057	575.81	+0.192
	385.24	+0.0315	413.24	4	L	8	1079.6	-0.05	1079.6	
	514.29	-0.034	542.28	5	E	7	966.49	+0.019	966.49	
	661.36		689.35	6	F	6	837.45	+0.0237	419.23	+0.0555
	774.44	-0.035	802.43	7	L	5	690.38		690.38	
	871.49	-0.002	899.49	8	P	4	577.3	-0.01	577.3	
	1018.6		1046.6	9	F	3	480.25	+0.1356	480.25	
	1147.6	-0.027	1175.6	10	E	2	333.18	+0.1257	333.18	
	1204.6	+0.0644	1232.6	11	G	1	204.13	+0.0488	204.13	
				12	K	0	147.11		147.11	

Scan number	10627	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	162.94



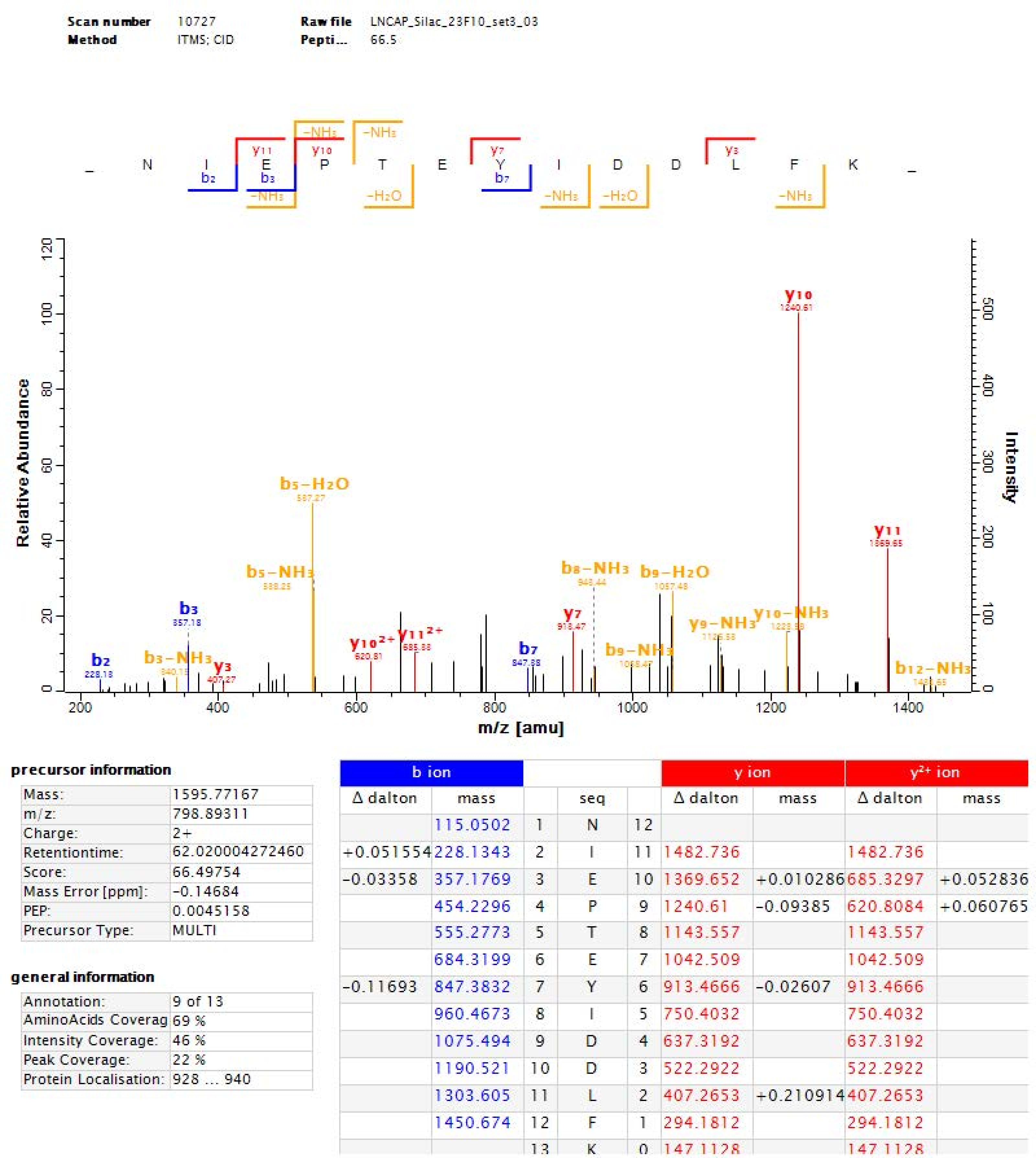
precursor information

Mass:	1618.89684
m/z:	810.4557
Charge:	2+
Retentiontime:	61.266548156738
Score:	162.9437
Mass Error [ppm]:	-0.12701
PEP:	1.1644E-10
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	50 %
Peak Coverage:	33 %
Protein Localisation:	177 ... 190

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	13				
	211.14		211.14	2	P	12	1506.8	-0.207	753.91	+0.223
	310.21	+0.1879	310.21	3	V	11	1409.8	+0.0015	1409.8	
	425.24	+0.1858	425.24	4	D	10	1310.7	-0.032	1310.7	
	572.31	+0.106	572.31	5	F	9	1195.7	-0.066	1195.7	
	659.34	+0.0642	659.34	6	S	8	1048.6	-0.115	524.81	+0.0745
	773.38	+0.0938	773.38	7	N	7	961.57	+0.0006	961.57	
	886.47	+0.0235	886.47	8	I	6	847.53	+0.0377	847.53	
+0.0852	492.26		983.52	9	P	5	734.44	-0.024	734.44	
	1084.6		1084.6	10	T	4	637.39		637.39	
	1247.6	+0.0386	1247.6	11	Y	3	536.34		536.34	
	1360.7	-0.006	1360.7	12	L	2	373.28	+0.0433	373.28	
	1473.8	-0.199	1473.8	13	L	1	260.2	+0.1498	260.2	
				14	K	0	147.11		147.11	



Scan number	10727	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	66.5

precursor information

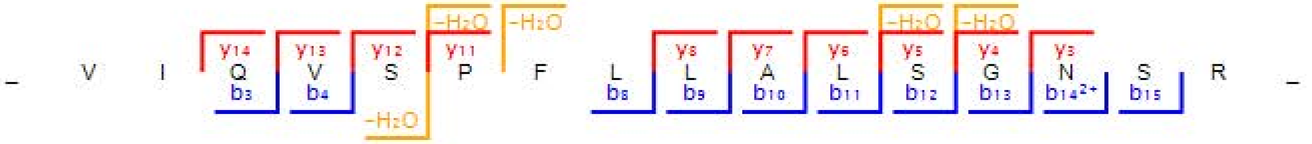
Mass:	1595.77167
m/z:	798.89311
Charge:	2+
Retentiontime:	62.020004272460
Score:	66.49754
Mass Error [ppm]:	-0.14684
PEP:	0.0045158
Precursor Type:	MULTI

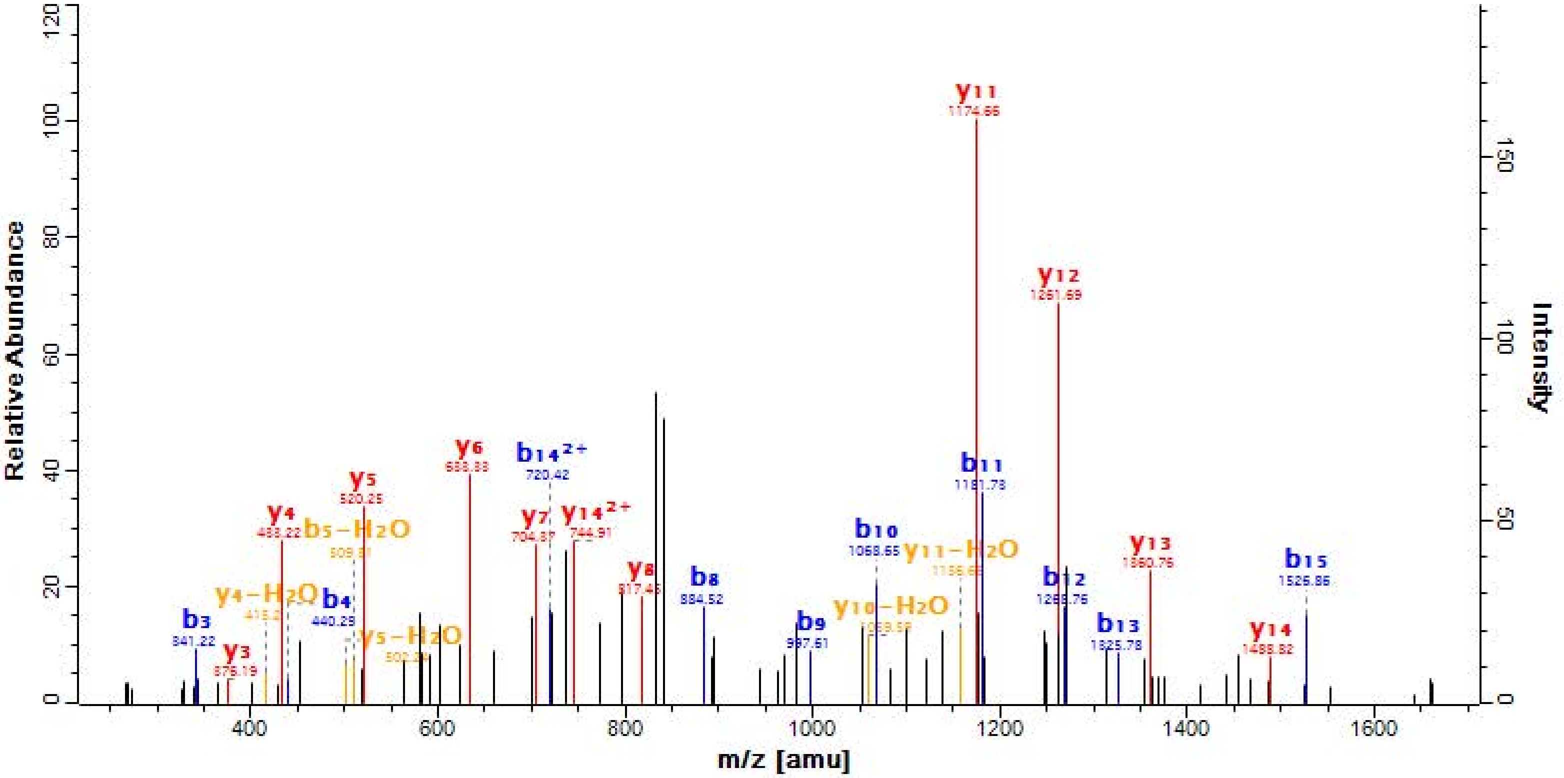
general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	46 %
Peak Coverage:	22 %
Protein Localisation:	928 ... 940

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502	1	N	12				
+0.051554	228.1343	2	I	11	1482.736		1482.736	
-0.03358	357.1769	3	E	10	1369.652	+0.010286	685.3297	+0.052836
	454.2296	4	P	9	1240.61	-0.09385	620.8084	+0.060765
	555.2773	5	T	8	1143.557		1143.557	
	684.3199	6	E	7	1042.509		1042.509	
-0.11693	847.3832	7	Y	6	913.4666	-0.02607	913.4666	
	960.4673	8	I	5	750.4032		750.4032	
	1075.494	9	D	4	637.3192		637.3192	
	1190.521	10	D	3	522.2922		522.2922	
	1303.605	11	L	2	407.2653	+0.210914	407.2653	
	1450.674	12	F	1	294.1812		294.1812	
		13	K	0	147.1128		147.1128	

Scan number	10760	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	125.45





precursor information

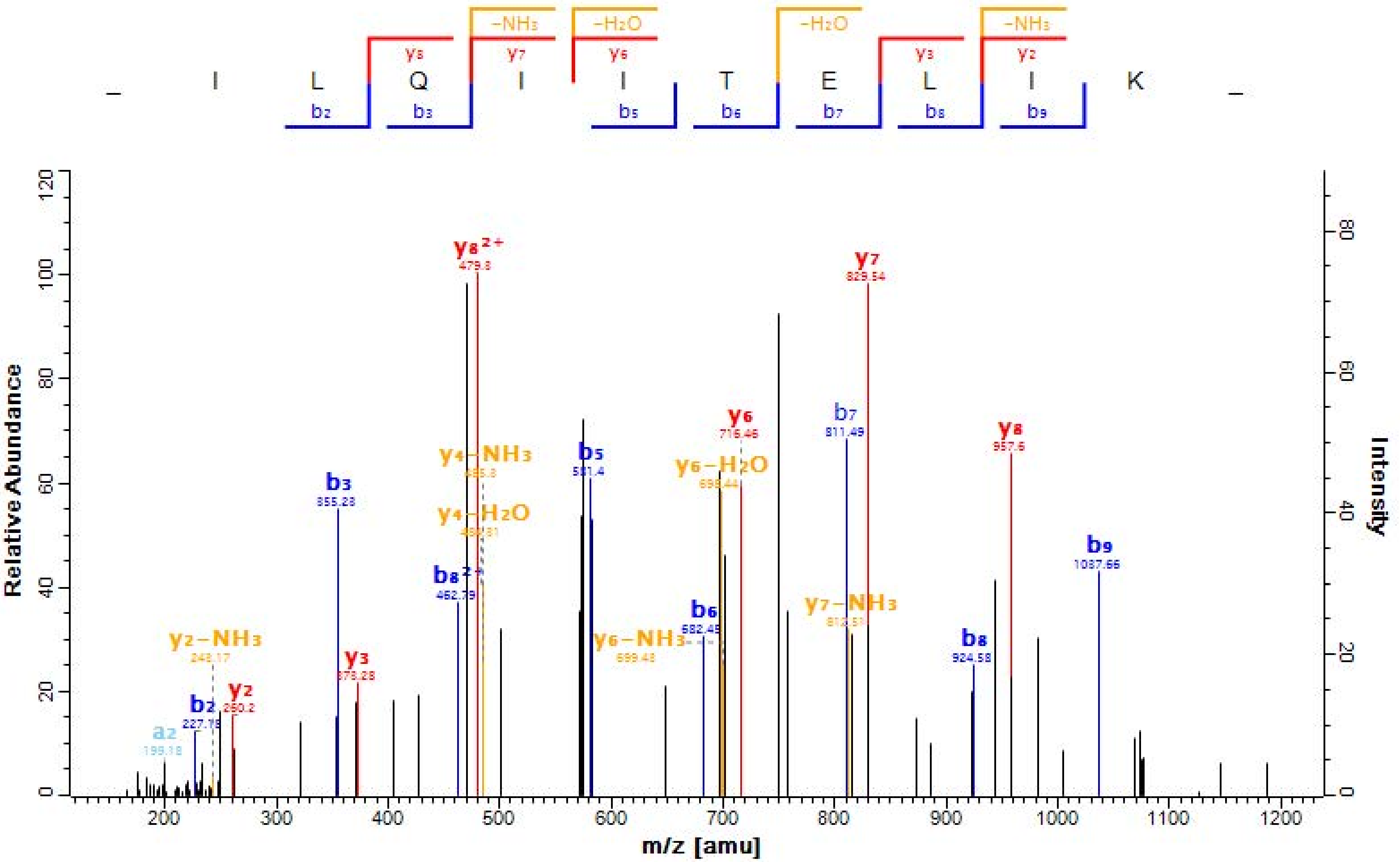
Mass:	1699.96206
m/z:	850.98831
Charge:	2+
Retentiontime:	62.236579895019
Score:	125.4501
Mass Error [ppm]:	-0.023611
PEP:	5.6784E-10
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	48 %
Peak Coverage:	30 %
Protein Localisation:	104 ... 119

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	15				
	213.16		213.16	2	I	14	1601.9		1601.9	
	341.22	+0.0875	341.22	3	Q	13	1488.8	-0.089	744.91	+0.0677
	440.29	-0.197	440.29	4	V	12	1360.8	-0.055	1360.8	
	527.32		527.32	5	S	11	1261.7	+0.0008	1261.7	
	624.37		624.37	6	P	10	1174.7	+0.101	1174.7	
	771.44		771.44	7	F	9	1077.6		1077.6	
	884.52	+0.0942	884.52	8	L	8	930.54		930.54	
	997.61	+0.0269	997.61	9	L	7	817.45	+0.0349	817.45	
	1068.6	-0.005	1068.6	10	A	6	704.37	+0.109	704.37	
	1181.7	-0.198	1181.7	11	L	5	633.33	+0.1305	633.33	
	1268.8	-0.231	1268.8	12	S	4	520.25	+0.1647	520.25	
	1325.8	-0.269	1325.8	13	G	3	433.22	+0.1017	433.22	
-0.033	720.42		1439.8	14	N	2	376.19	+0.061	376.19	
	1526.9	-0.499	1526.9	15	S	1	262.15		262.15	
				16	R	0	175.12		175.12	

Scan number	11030	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	108.47



precursor information

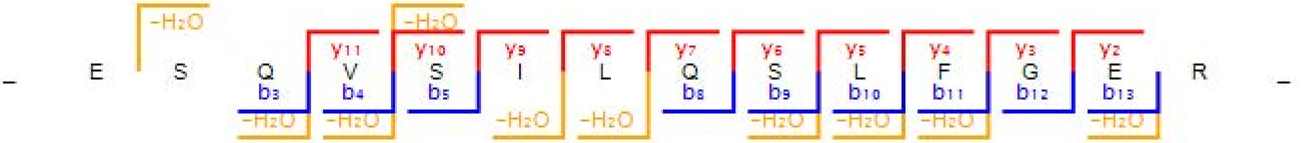
Mass:	1182.75848
m/z:	592.38652
Charge:	2+
Retentiontime:	64.230033874511
Score:	108.4698
Mass Error [ppm]:	-0.2331
PEP:	0.00058166
Precursor Type:	ISO

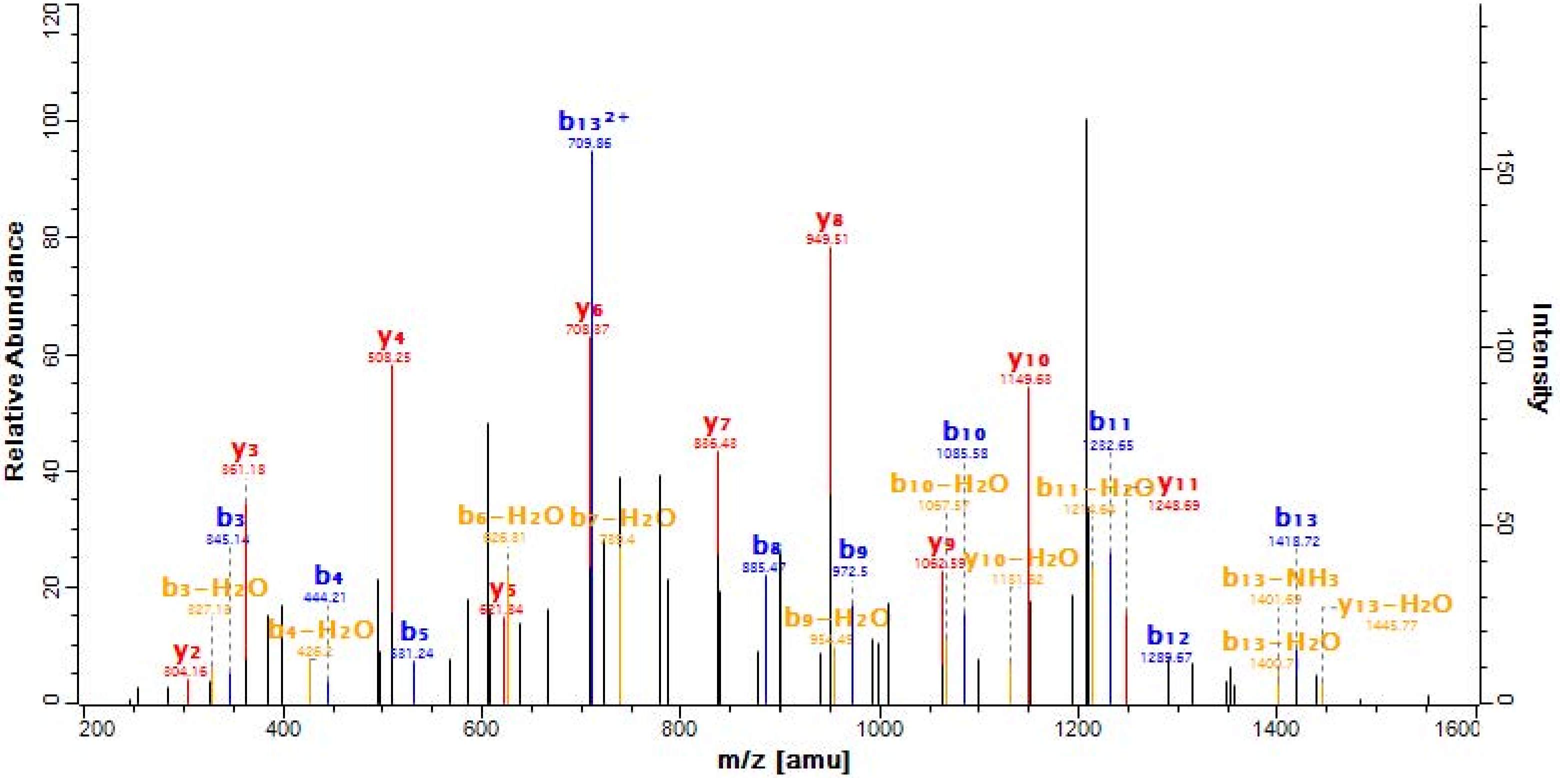
g

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	43 %
Peak Coverage:	23 %
Protein Localisation:	1356 ... 1365

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	I	9				
+0.218	199.2		227.2	+0.029	227.2	2	L	8	1071		1071	
	327.2		355.2	+0.172	355.2	3	Q	7	957.6	+0.015	479.3	+0.23
	440.3		468.3		468.3	4	I	6	829.5	-0.09	829.5	
	553.4		581.4	+0.002	581.4	5	I	5	716.5	+0.125	716.5	
	654.5		682.4	+0.005	682.4	6	T	4	603.4		603.4	
	783.5		811.5	-0.04	811.5	7	E	3	502.3		502.3	
	896.6	+0.379	462.8	+0.017	924.6	8	L	2	373.3	+0.138	373.3	
	1010		1038	-0.15	1038	9	I	1	260.2	+0.153	260.2	
						10	K	0	147.1		147.1	

Scan number	11084	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	140.93





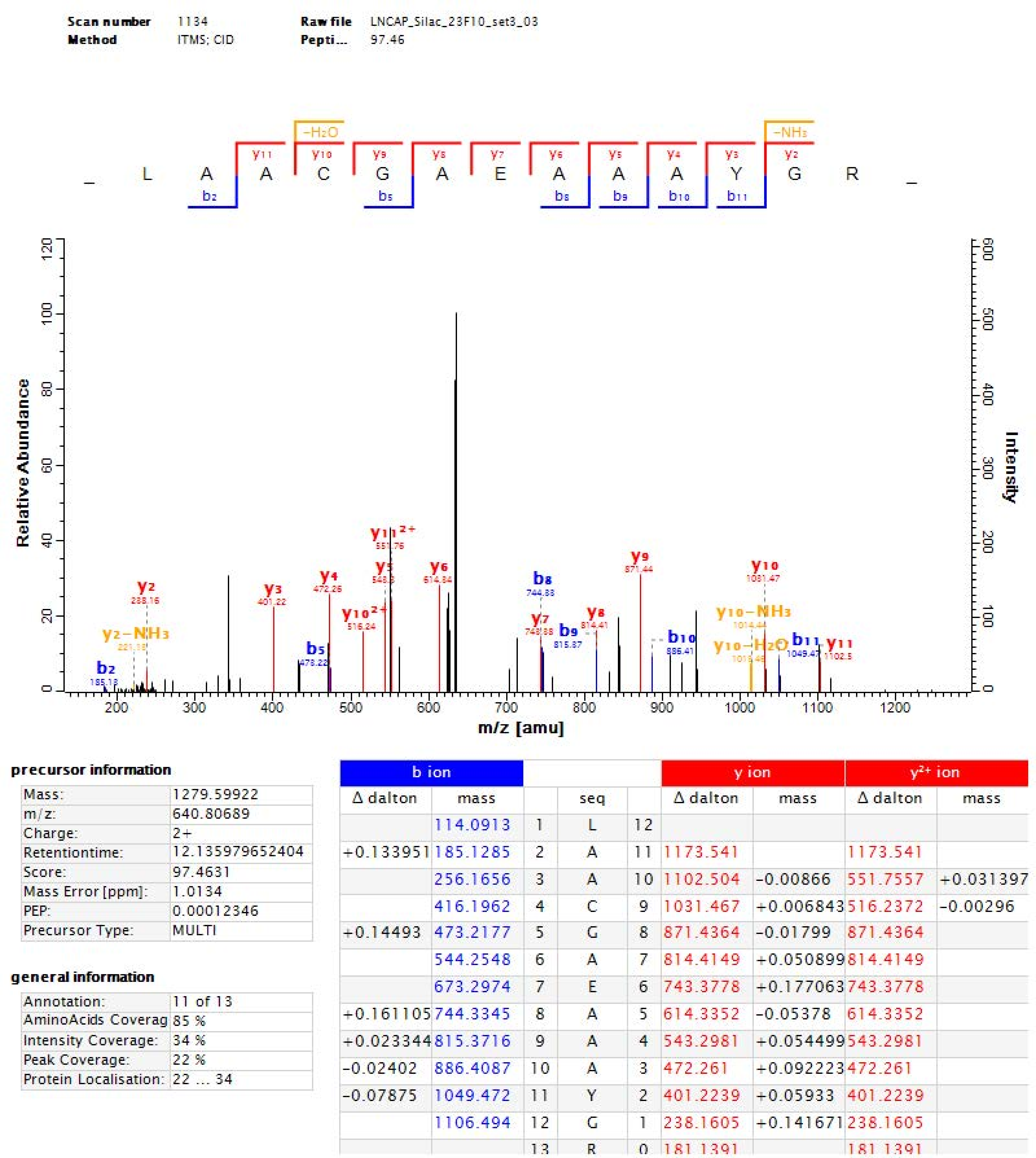
precursor information

Mass:	1591.82115
m/z:	796.91785
Charge:	2+
Retentiontime:	64.720687866210
Score:	140.9276
Mass Error [ppm]:	0.35365
PEP:	6.279E-09
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	48 %
Peak Coverage:	40 %
Protein Localisation:	12 ... 25

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	130.0499		130.0499	1	E	13		
	217.0819		217.0819	2	S	12	1463.785	
	345.1405	-0.0748	345.1405	3	Q	11	1376.753	
	444.2089	+0.131443	444.2089	4	V	10	1248.695	-0.04769
	531.2409	+0.053577	531.2409	5	S	9	1149.626	-0.09817
	644.325		644.325	6	I	8	1062.594	-0.01536
	757.409		757.409	7	L	7	949.5102	-0.00997
	885.4676	-0.01505	885.4676	8	Q	6	836.4261	+0.08056
	972.4997	+0.113202	972.4997	9	S	5	708.3675	-0.01492
	1085.584	+0.262598	1085.584	10	L	4	621.3355	+0.028588
	1232.652	-0.13748	1232.652	11	F	3	508.2514	-0.00203
	1289.674	-0.21852	1289.674	12	G	2	361.183	-0.02255
+0.346215	709.8617	+0.114258	1418.716	13	E	1	304.1615	+0.001907
				14	R	0	175.119	



Scan number	1134	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	97.46

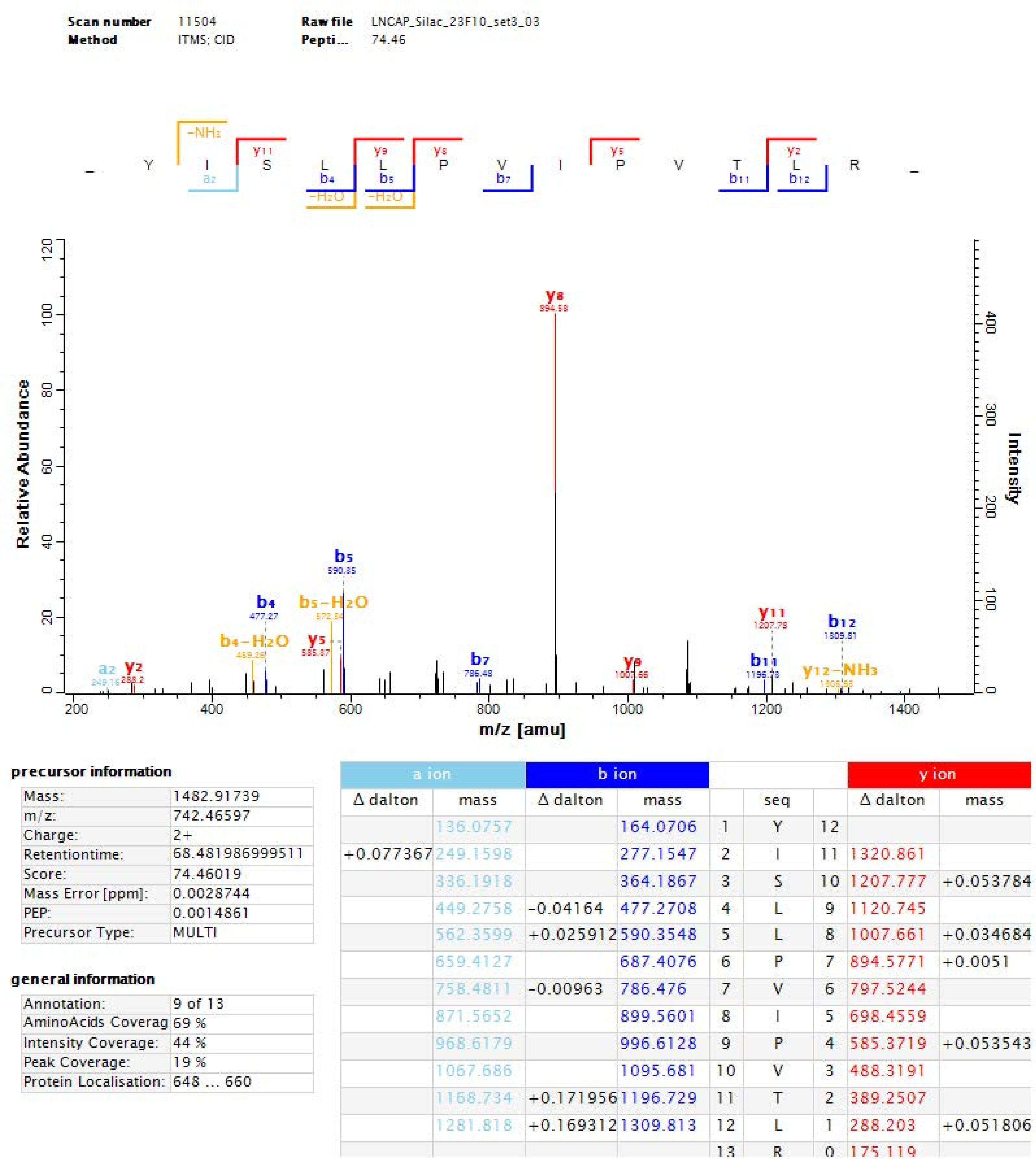
precursor information

Mass:	1279.59922
m/z:	640.80689
Charge:	2+
Retentiontime:	12.135979652404
Score:	97.4631
Mass Error [ppm]:	1.0134
PEP:	0.00012346
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	34 %
Peak Coverage:	22 %
Protein Localisation:	22 ... 34

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	12				
+0.133951	185.1285	2	A	11	1173.541		1173.541	
	256.1656	3	A	10	1102.504	-0.00866	551.7557	+0.031397
	416.1962	4	C	9	1031.467	+0.006843	516.2372	-0.00296
+0.14493	473.2177	5	G	8	871.4364	-0.01799	871.4364	
	544.2548	6	A	7	814.4149	+0.050899	814.4149	
	673.2974	7	E	6	743.3778	+0.177063	743.3778	
+0.161105	744.3345	8	A	5	614.3352	-0.05378	614.3352	
+0.023344	815.3716	9	A	4	543.2981	+0.054499	543.2981	
-0.02402	886.4087	10	A	3	472.261	+0.092223	472.261	
-0.07875	1049.472	11	Y	2	401.2239	+0.05933	401.2239	
	1106.494	12	G	1	238.1605	+0.141671	238.1605	
		13	R	0	181.1391		181.1391	



Scan number	11504	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	74.46

precursor information

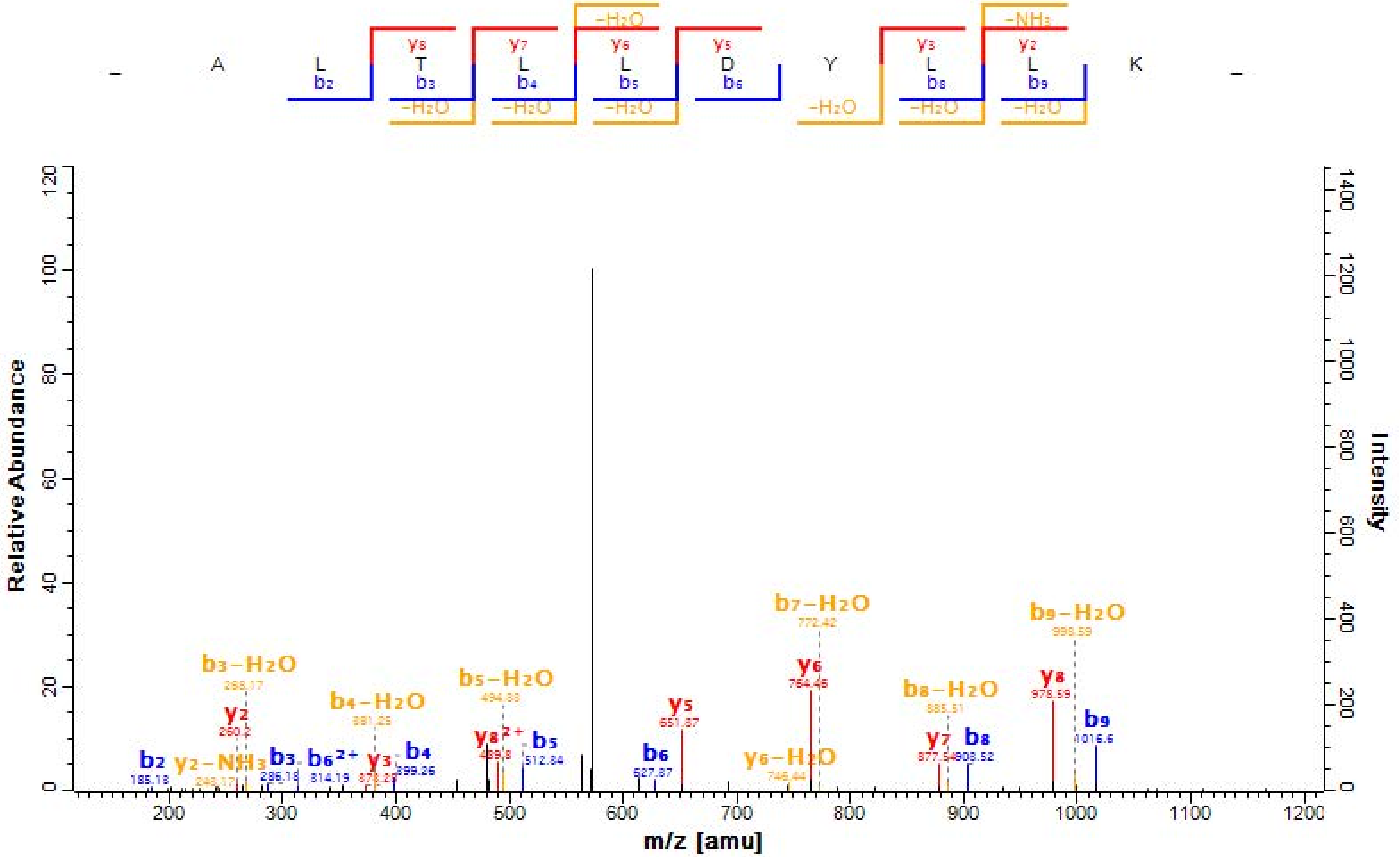
Mass:	1482.91739
m/z:	742.46597
Charge:	2+
Retentiontime:	68.481986999511
Score:	74.46019
Mass Error [ppm]:	0.0028744
PEP:	0.0014861
Precursor Type:	MULTI

general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	44 %
Peak Coverage:	19 %
Protein Localisation:	648 ... 660

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	136.0757		164.0706	1	Y	12		
+0.077367	249.1598		277.1547	2	I	11	1320.861	
	336.1918		364.1867	3	S	10	1207.777	+0.053784
	449.2758	-0.04164	477.2708	4	L	9	1120.745	
	562.3599	+0.025912	590.3548	5	L	8	1007.661	+0.034684
	659.4127		687.4076	6	P	7	894.5771	+0.0051
	758.4811	-0.00963	786.476	7	V	6	797.5244	
	871.5652		899.5601	8	I	5	698.4559	
	968.6179		996.6128	9	P	4	585.3719	+0.053543
	1067.686		1095.681	10	V	3	488.3191	
	1168.734	+0.171956	1196.729	11	T	2	389.2507	
	1281.818	+0.169312	1309.813	12	L	1	288.203	+0.051806
				13	R	0	175.119	

Scan number	11580	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	179.8



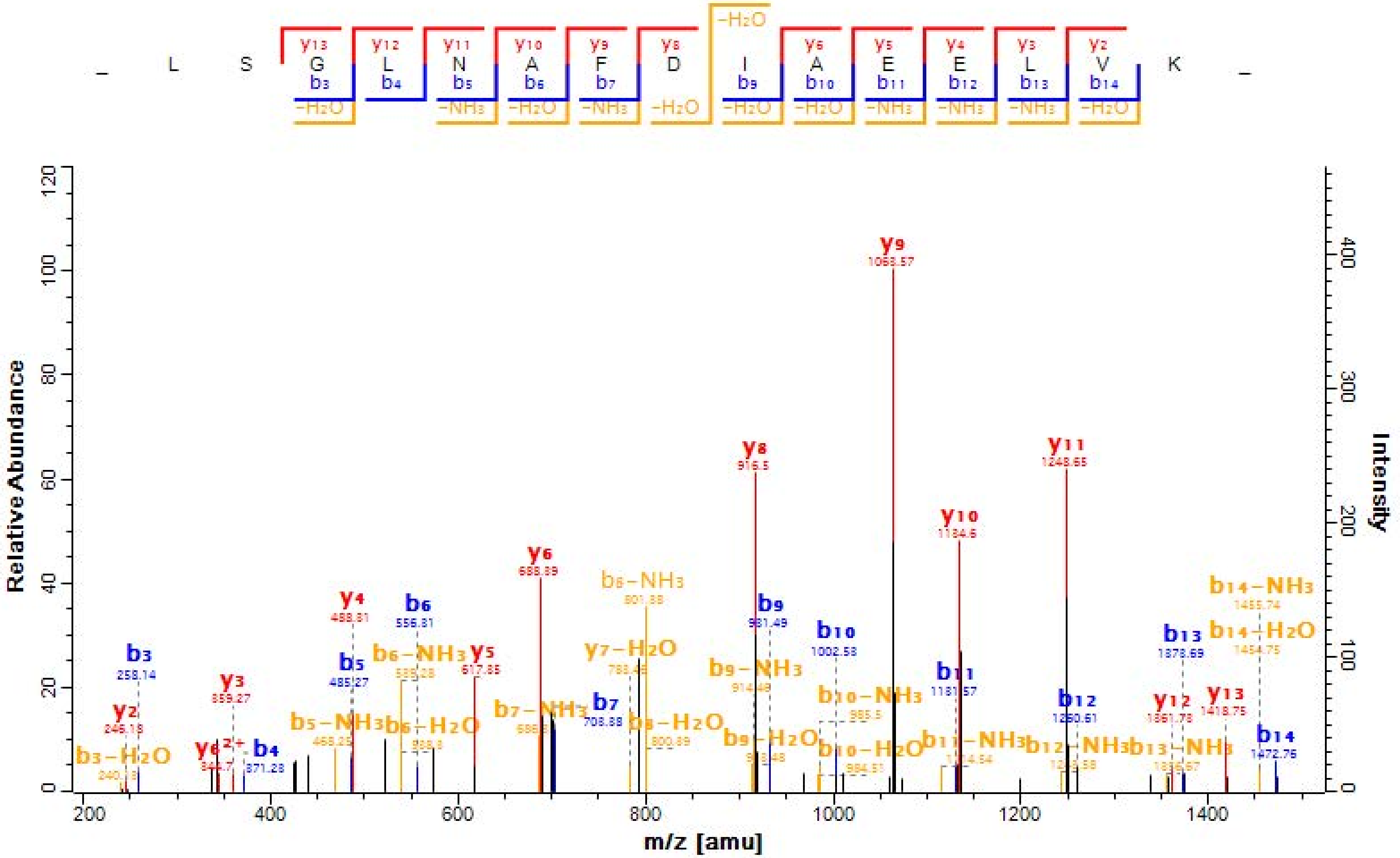
precursor information

Mass:	1161.70082
m/z:	581.85769
Charge:	2+
Retentiontime:	69.236152648925
Score:	179.8049
Mass Error [ppm]:	-0.079965
PEP:	3.1255E-06
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	38 %
Peak Coverage:	26 %
Protein Localisation:	77 ... 86

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	9				
	185.13	-0.124	185.13	2	L	8	1091.7		1091.7	
	286.18	+0.1387	286.18	3	T	7	978.59	-0.05	489.8	-0.029
	399.26	-0.227	399.26	4	L	6	877.54	+0.021	877.54	
	512.34	-0.001	512.34	5	L	5	764.46	-0.04	764.46	
-0.16	314.19	+0.1582	627.37	6	D	4	651.37	+0.0092	651.37	
	790.43		790.43	7	Y	3	536.34		536.34	
	903.52	-0.094	903.52	8	L	2	373.28	-0.123	373.28	
	1016.6	-0.135	1016.6	9	L	1	260.2	+0.0148	260.2	
				10	K	0	147.11		147.11	

Scan number	11674	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	237.59



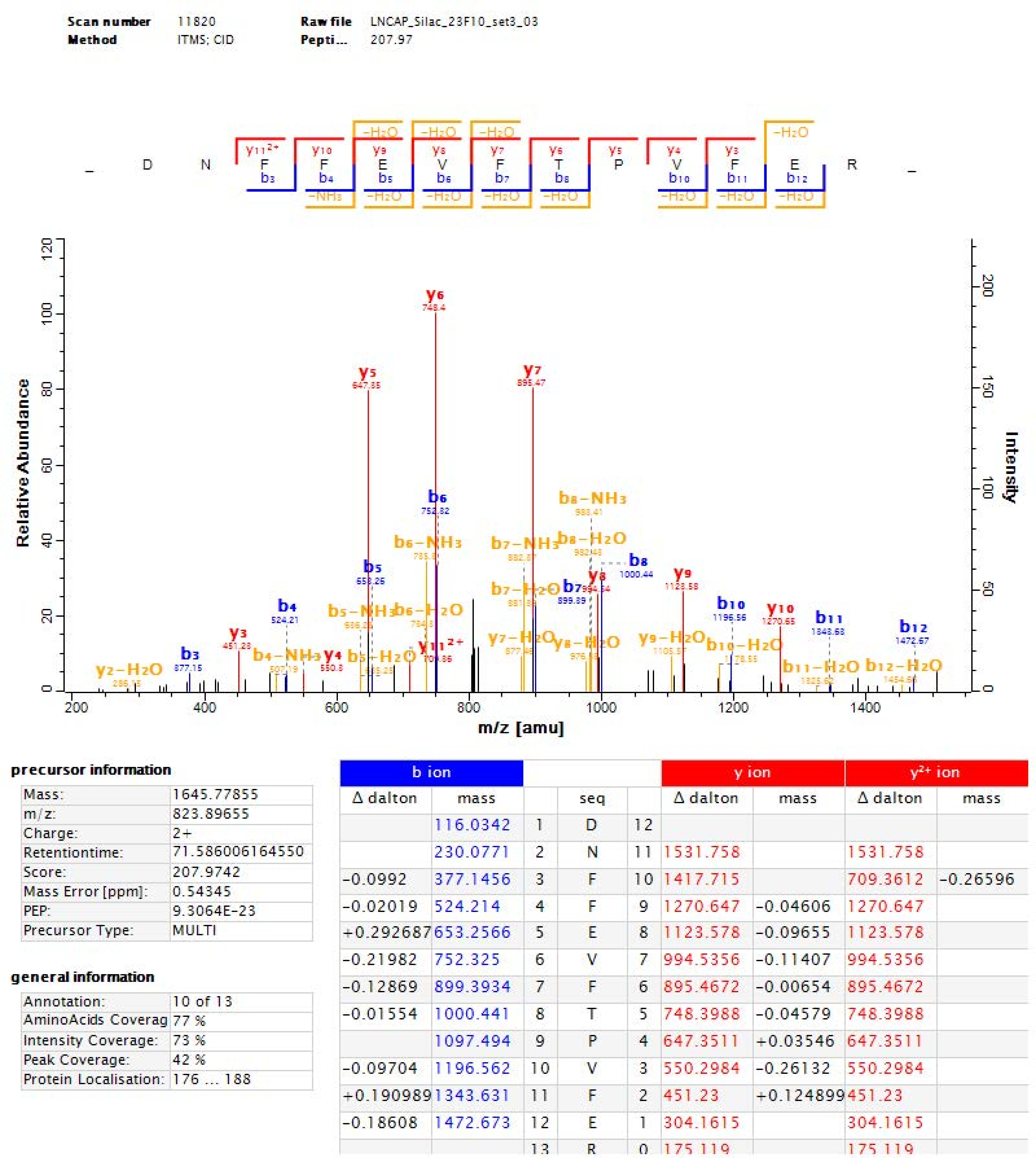
precursor information

Mass:	1617.86109
m/z:	809.93782
Charge:	2+
Retentiontime:	70.100860595703
Score:	237.59
Mass Error [ppm]:	-0.18535
PEP:	3.2577E-46
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	62 %
Peak Coverage:	51 %
Protein Localisation:	143 ... 157

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	14				
	201.1234	2	S	13	1505.785		1505.785	
-0.09613	258.1448	3	G	12	1418.753	-0.09669	1418.753	
+0.12584	371.2289	4	L	11	1361.731	-0.29422	1361.731	
+0.100674	485.2718	5	N	10	1248.647	-0.12031	1248.647	
+0.144798	556.3089	6	A	9	1134.604	-0.06908	1134.604	
-0.05844	703.3774	7	F	8	1063.567	-0.08898	1063.567	
	818.4043	8	D	7	916.4986	-0.08379	916.4986	
-0.06972	931.4884	9	I	6	801.4716		801.4716	
+0.058817	1002.525	10	A	5	688.3876	-0.00605	344.6974	-0.3144
-0.17427	1131.568	11	E	4	617.3505	+0.016597	617.3505	
-0.27143	1260.611	12	E	3	488.3079	-0.03895	488.3079	
-0.07265	1373.695	13	L	2	359.2653	+0.003395	359.2653	
-0.07246	1472.763	14	V	1	246.1812	+0.032649	246.1812	
		15	K	0	147.1128		147.1128	



Scan number	11820	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	207.97

precursor information

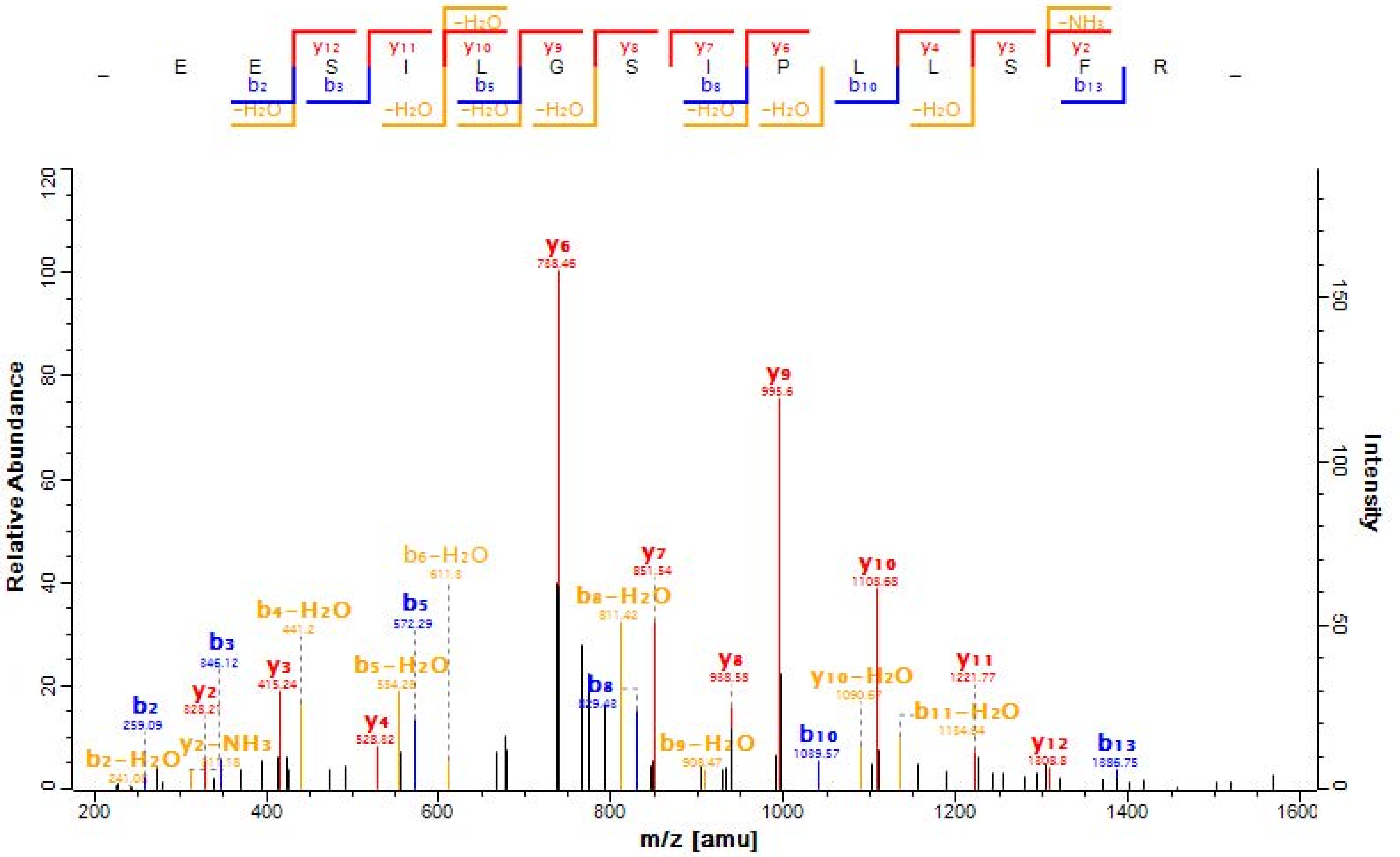
Mass:	1645.77855
m/z:	823.89655
Charge:	2+
Retentiontime:	71.586006164550
Score:	207.9742
Mass Error [ppm]:	0.54345
PEP:	9.3064E-23
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	73 %
Peak Coverage:	42 %
Protein Localisation:	176 ... 188

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342	1	D	12				
	230.0771	2	N	11	1531.758		1531.758	
-0.0992	377.1456	3	F	10	1417.715		709.3612	-0.26596
-0.02019	524.214	4	F	9	1270.647	-0.04606	1270.647	
+0.292687	653.2566	5	E	8	1123.578	-0.09655	1123.578	
-0.21982	752.325	6	V	7	994.5356	-0.11407	994.5356	
-0.12869	899.3934	7	F	6	895.4672	-0.00654	895.4672	
-0.01554	1000.441	8	T	5	748.3988	-0.04579	748.3988	
	1097.494	9	P	4	647.3511	+0.03546	647.3511	
-0.09704	1196.562	10	V	3	550.2984	-0.26132	550.2984	
+0.190989	1343.631	11	F	2	451.23	+0.124899	451.23	
-0.18608	1472.673	12	E	1	304.1615		304.1615	
		13	R	0	175.119		175.119	

Scan number	11926	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	125.53



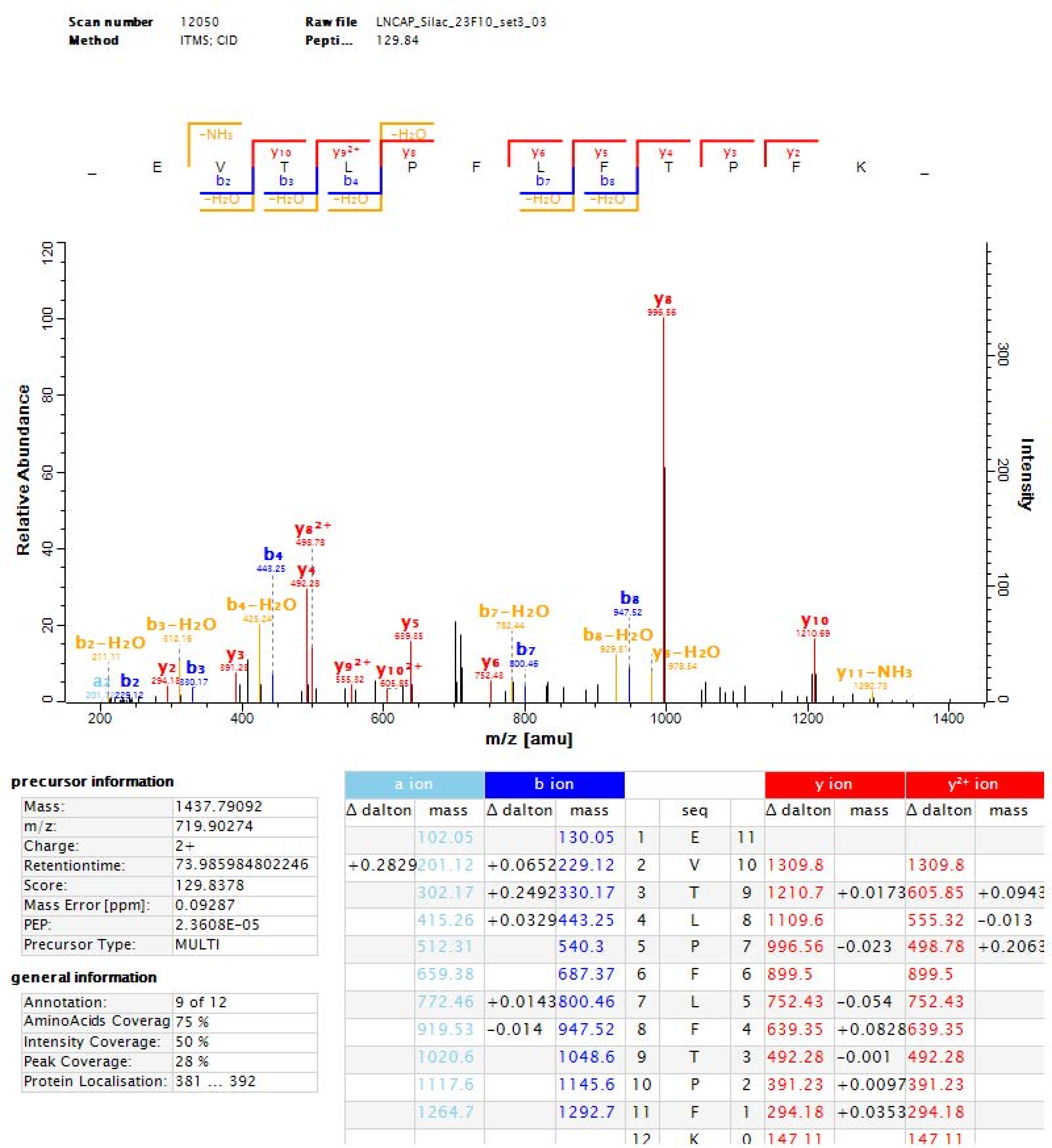
precursor information

Mass:	1559.85583
m/z:	780.93519
Charge:	2+
Retentiontime:	72.676673889160
Score:	125.53
Mass Error [ppm]:	-0.049209
PEP:	1.1063E-08
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	54 %
Peak Coverage:	31 %
Protein Localisation:	97 ... 110

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	130.049869563	1	E	13		
+0.1252192	259.092462659	2	E	12	1437.84072093	
+0.2282616	346.124491069	3	S	11	1308.79812783	-0.0193192
	459.208555049	4	I	10	1221.76609942	+0.3025041
+0.0825641	572.29261903	5	L	9	1108.68203544	-0.0453167
	629.314082753	6	G	8	995.597971461	+0.0196433
	716.346111163	7	S	7	938.576507737	-0.0356752
+0.0339972	829.430175144	8	I	6	851.544479327	+0.0147858
	926.482938996	9	P	5	738.460415347	+0.0455051
-0.2054307	1039.56700298	10	L	4	641.407651495	
	1152.65106696	11	L	3	528.323587514	-0.0243321
	1239.68309537	12	S	2	415.239523534	+0.1359037
-0.0804888	1386.75150928	13	F	1	328.207495124	-0.0260986
		14	R	0	181.139081208	



Scan number	12050	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	129.84

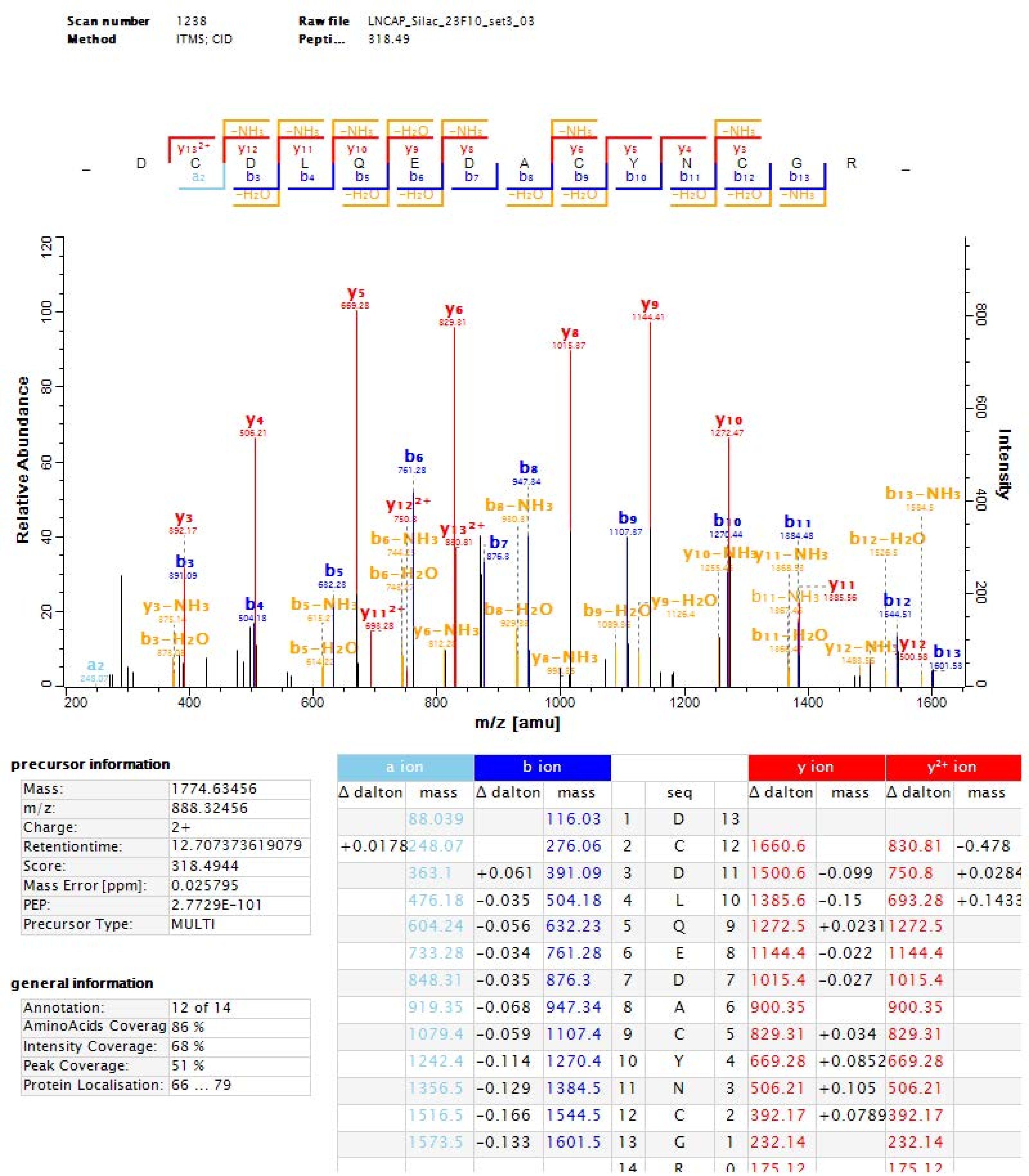
precursor information

Mass:	1437.79092
m/z:	719.90274
Charge:	2+
Retentiontime:	73.985984802246
Score:	129.8378
Mass Error [ppm]:	0.09287
PEP:	2.3608E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	50 %
Peak Coverage:	28 %
Protein Localisation:	381 ... 392

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	11				
+0.2829	201.12	+0.0652	229.12	2	V	10	1309.8		1309.8	
	302.17	+0.2492	330.17	3	T	9	1210.7	+0.0173	605.85	+0.0943
	415.26	+0.0329	443.25	4	L	8	1109.6		555.32	-0.013
	512.31		540.3	5	P	7	996.56	-0.023	498.78	+0.2063
	659.38		687.37	6	F	6	899.5		899.5	
	772.46	+0.0143	800.46	7	L	5	752.43	-0.054	752.43	
	919.53	-0.014	947.52	8	F	4	639.35	+0.0828	639.35	
	1020.6		1048.6	9	T	3	492.28	-0.001	492.28	
	1117.6		1145.6	10	P	2	391.23	+0.0097	391.23	
	1264.7		1292.7	11	F	1	294.18	+0.0353	294.18	
				12	K	0	147.11		147.11	



Scan number	1238	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	318.49

precursor information

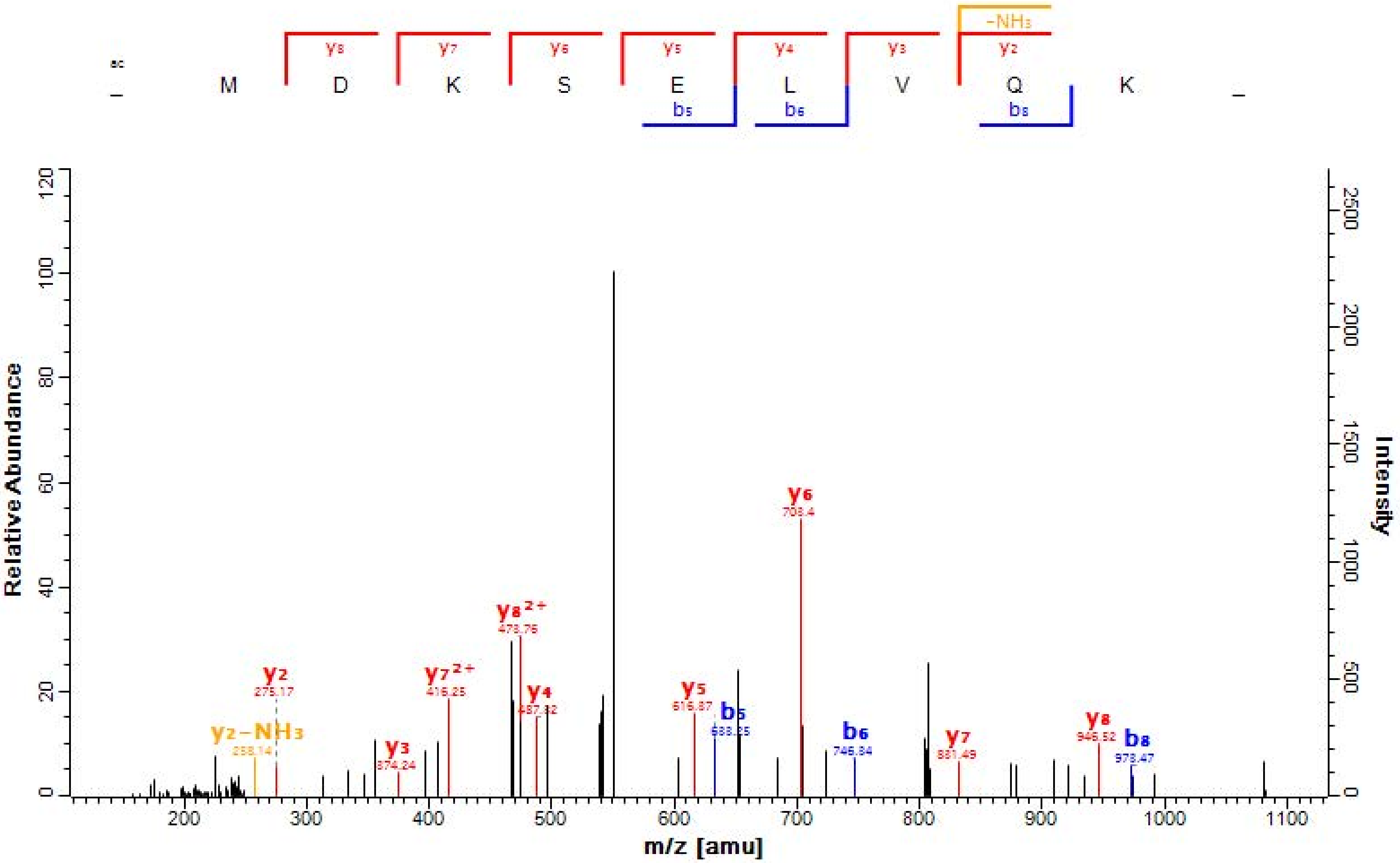
Mass:	1774.63456
m/z:	888.32456
Charge:	2+
Retentiontime:	12.707373619079
Score:	318.4944
Mass Error [ppm]:	0.025795
PEP:	2.7729E-101
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	68 %
Peak Coverage:	51 %
Protein Localisation:	66 ... 79

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	13				
+0.0178	248.07		276.06	2	C	12	1660.6		830.81	-0.478
	363.1	+0.061	391.09	3	D	11	1500.6	-0.099	750.8	+0.0284
	476.18	-0.035	504.18	4	L	10	1385.6	-0.15	693.28	+0.1433
	604.24	-0.056	632.23	5	Q	9	1272.5	+0.0231	1272.5	
	733.28	-0.034	761.28	6	E	8	1144.4	-0.022	1144.4	
	848.31	-0.035	876.3	7	D	7	1015.4	-0.027	1015.4	
	919.35	-0.068	947.34	8	A	6	900.35		900.35	
	1079.4	-0.059	1107.4	9	C	5	829.31	+0.034	829.31	
	1242.4	-0.114	1270.4	10	Y	4	669.28	+0.0852	669.28	
	1356.5	-0.129	1384.5	11	N	3	506.21	+0.105	506.21	
	1516.5	-0.166	1544.5	12	C	2	392.17	+0.0789	392.17	
	1573.5	-0.133	1601.5	13	G	1	232.14		232.14	
				14	R	0	175.12		175.12	

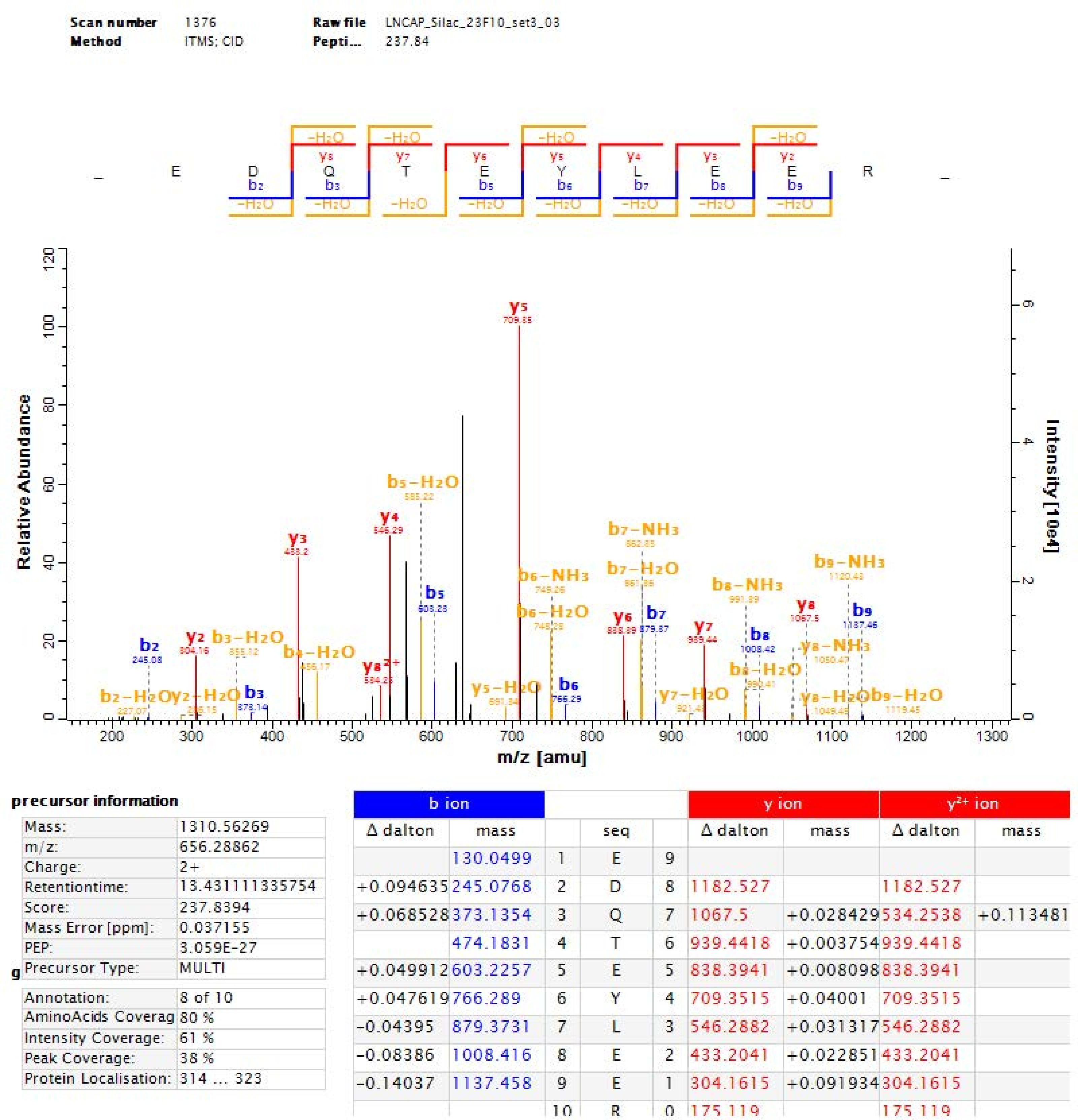
Scan number 1337 **Raw file** LNCAP_Silac_23F10_set3_03
Method ITMS; CID **Pepti...** 66.19



precursor information

Mass:	1118.56426
m/z:	560.28941
Charge:	2+
Retentiontime:	13.228949546814
Score:	66.18996
Mass Error [ppm]:	0.0933
PEP:	0.045649
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	27 %
Peak Coverage:	13 %
Protein Localisation:	1 ... 9

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	174.0583	1	M	8				
	289.0853	2	D	7	946.5204	-0.01428	473.7638	+0.29226
	417.1802	3	K	6	831.4934	+0.056422	416.2504	+0.170843
	504.2123	4	S	5	703.3985	-0.00609	703.3985	
+0.132354	633.2549	5	E	4	616.3665	+0.00342	616.3665	
+0.180187	746.3389	6	L	3	487.3239	+0.15783	487.3239	
	845.4073	7	V	2	374.2398	-0.00145	374.2398	
-0.1788	973.4659	8	Q	1	275.1714	+0.016423	275.1714	
		9	K	0	147.1128		147.1128	



Scan number	1376	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	237.84

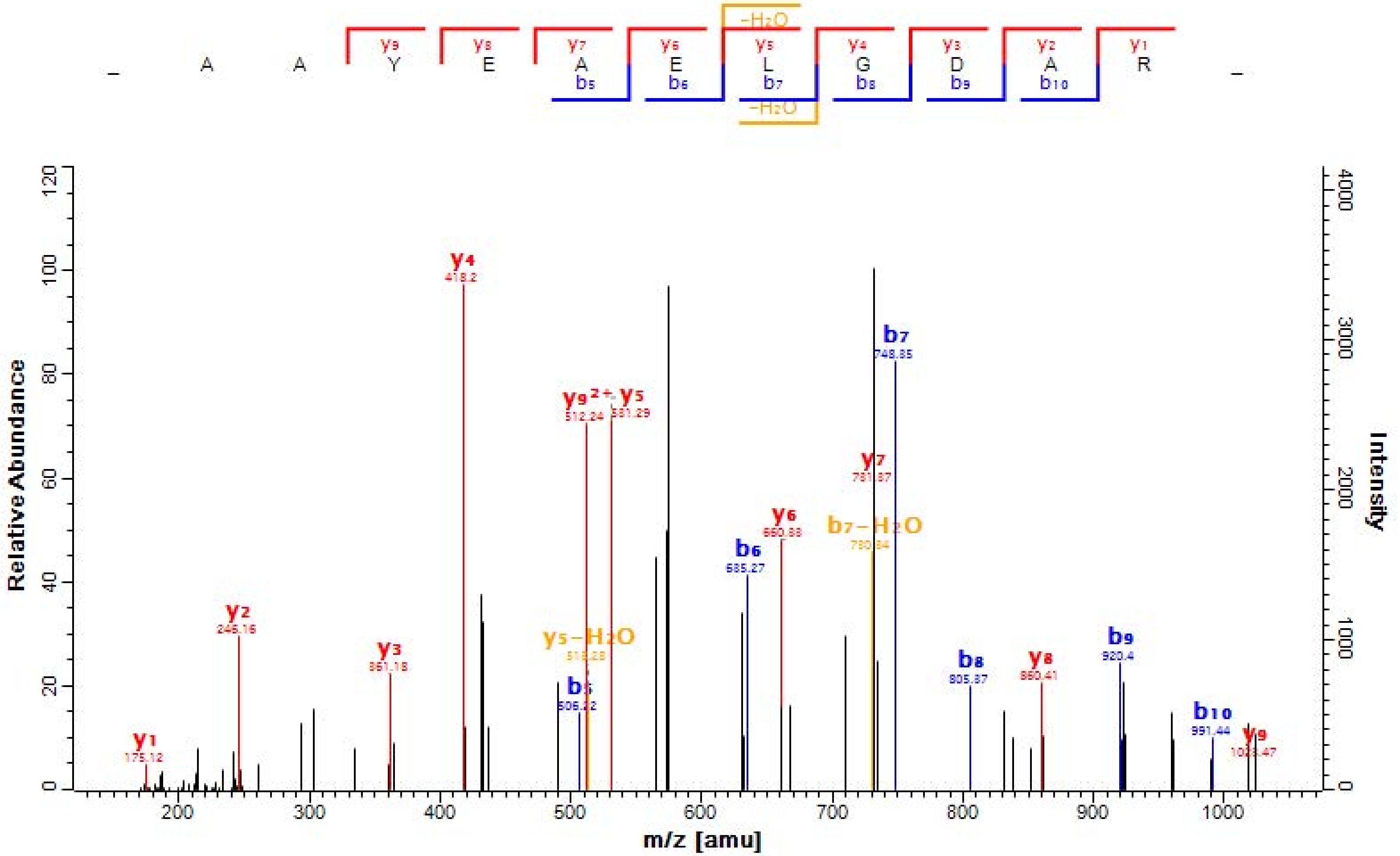
precursor information

Mass:	1310.56269
m/z:	656.28862
Charge:	2+
Retentiontime:	13.431111335754
Score:	237.8394
Mass Error [ppm]:	0.037155
PEP:	3.059E-27
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	61 %
Peak Coverage:	38 %
Protein Localisation:	314 ... 323

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	9				
+0.094635	245.0768	2	D	8	1182.527		1182.527	
+0.068528	373.1354	3	Q	7	1067.5	+0.028429	534.2538	+0.113481
	474.1831	4	T	6	939.4418	+0.003754	939.4418	
+0.049912	603.2257	5	E	5	838.3941	+0.008098	838.3941	
+0.047619	766.289	6	Y	4	709.3515	+0.04001	709.3515	
-0.04395	879.3731	7	L	3	546.2882	+0.031317	546.2882	
-0.08386	1008.416	8	E	2	433.2041	+0.022851	433.2041	
-0.14037	1137.458	9	E	1	304.1615	+0.091934	304.1615	
		10	R	0	175.119		175.119	

Scan number	1508	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	105.03



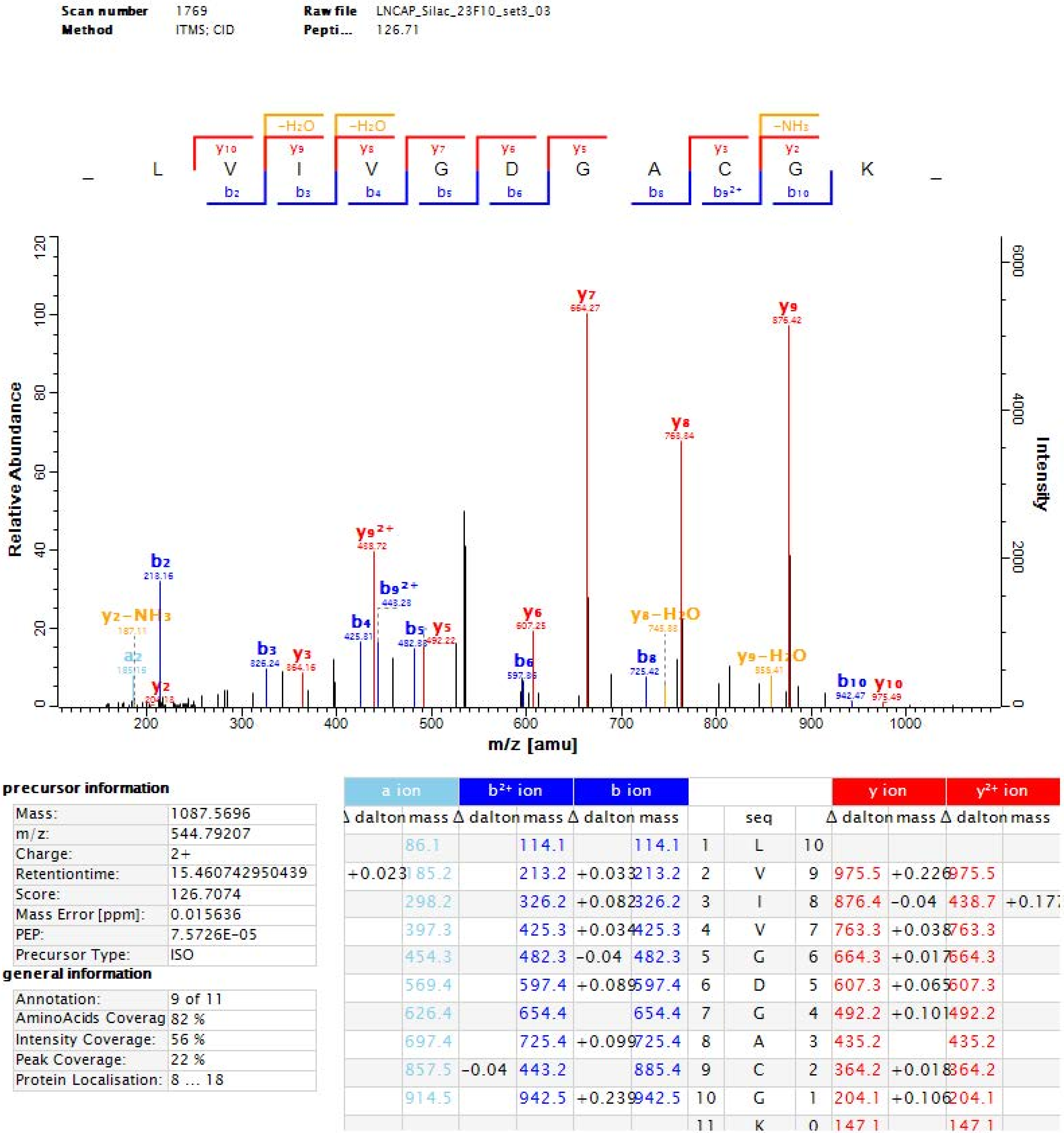
precursor information

Mass:	1164.5402
m/z:	583.27738
Charge:	2+
Retentiontime:	14.106860160827
Score:	105.0319
Mass Error [ppm]:	-0.7849
PEP:	0.00031962
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	45 %
Peak Coverage:	21 %
Protein Localisation:	79 ... 89

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	10				
	143.0815	2	A	9	1094.511		1094.511	
	306.1448	3	Y	8	1023.474	+0.049577	512.2407	-0.00146
	435.1874	4	E	7	860.4108	+0.032767	860.4108	
+0.020273	506.2245	5	A	6	731.3682	+0.00816	731.3682	
+0.005267	635.2671	6	E	5	660.3311	+0.011705	660.3311	
-0.01129	748.3512	7	L	4	531.2885	-0.10507	531.2885	
+0.069539	805.3727	8	G	3	418.2045	+0.029109	418.2045	
-0.05982	920.3996	9	D	2	361.183	+0.116979	361.183	
+0.038381	991.4367	10	A	1	246.1561	-0.00711	246.1561	
		11	R	0	175.119	+0.040105	175.119	



Scan number 1769 **Raw file** LNCAP_Silac_23F10_set3_03
Method ITMS; CID **Pepti...** 126.71

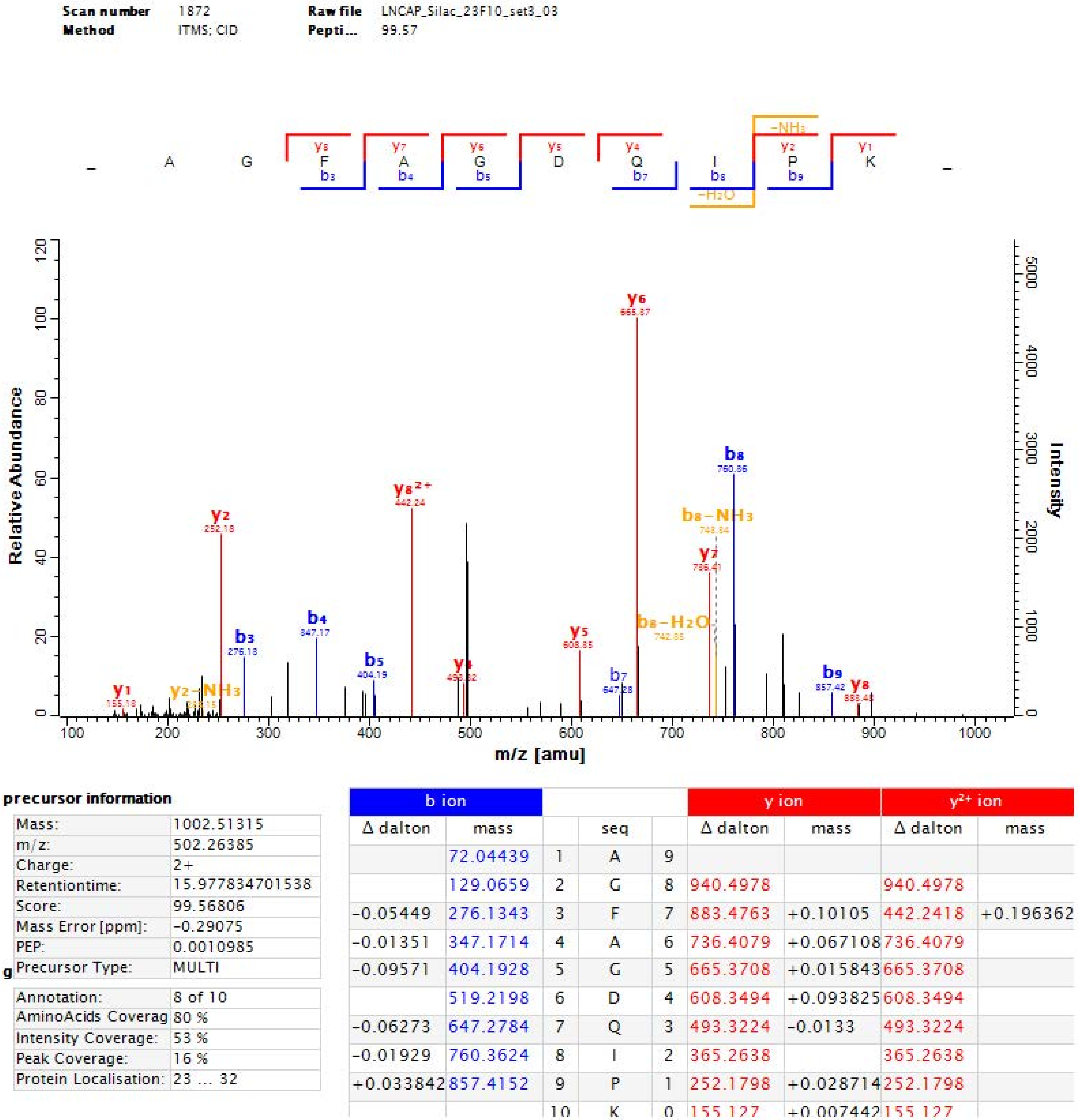
precursor information

Mass:	1087.5696
m/z:	544.79207
Charge:	2+
Retentiontime:	15.460742950439
Score:	126.7074
Mass Error [ppm]:	0.015636
PEP:	7.5726E-05
Precursor Type:	ISO

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	56 %
Peak Coverage:	22 %
Protein Localisation:	8 ... 18

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	10				
+0.023	185.2		213.2	+0.033	213.2	2	V	9	975.5	+0.226	975.5	
	298.2		326.2	+0.082	326.2	3	I	8	876.4	-0.04	438.7	+0.17
	397.3		425.3	+0.034	425.3	4	V	7	763.3	+0.038	763.3	
	454.3		482.3	-0.04	482.3	5	G	6	664.3	+0.017	664.3	
	569.4		597.4	+0.089	597.4	6	D	5	607.3	+0.065	607.3	
	626.4		654.4		654.4	7	G	4	492.2	+0.101	492.2	
	697.4		725.4	+0.099	725.4	8	A	3	435.2		435.2	
	857.5	-0.04	443.2		885.4	9	C	2	364.2	+0.018	364.2	
	914.5		942.5	+0.239	942.5	10	G	1	204.1	+0.106	204.1	
						11	K	0	147.1		147.1	



Scan number	1872	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	99.57

precursor information

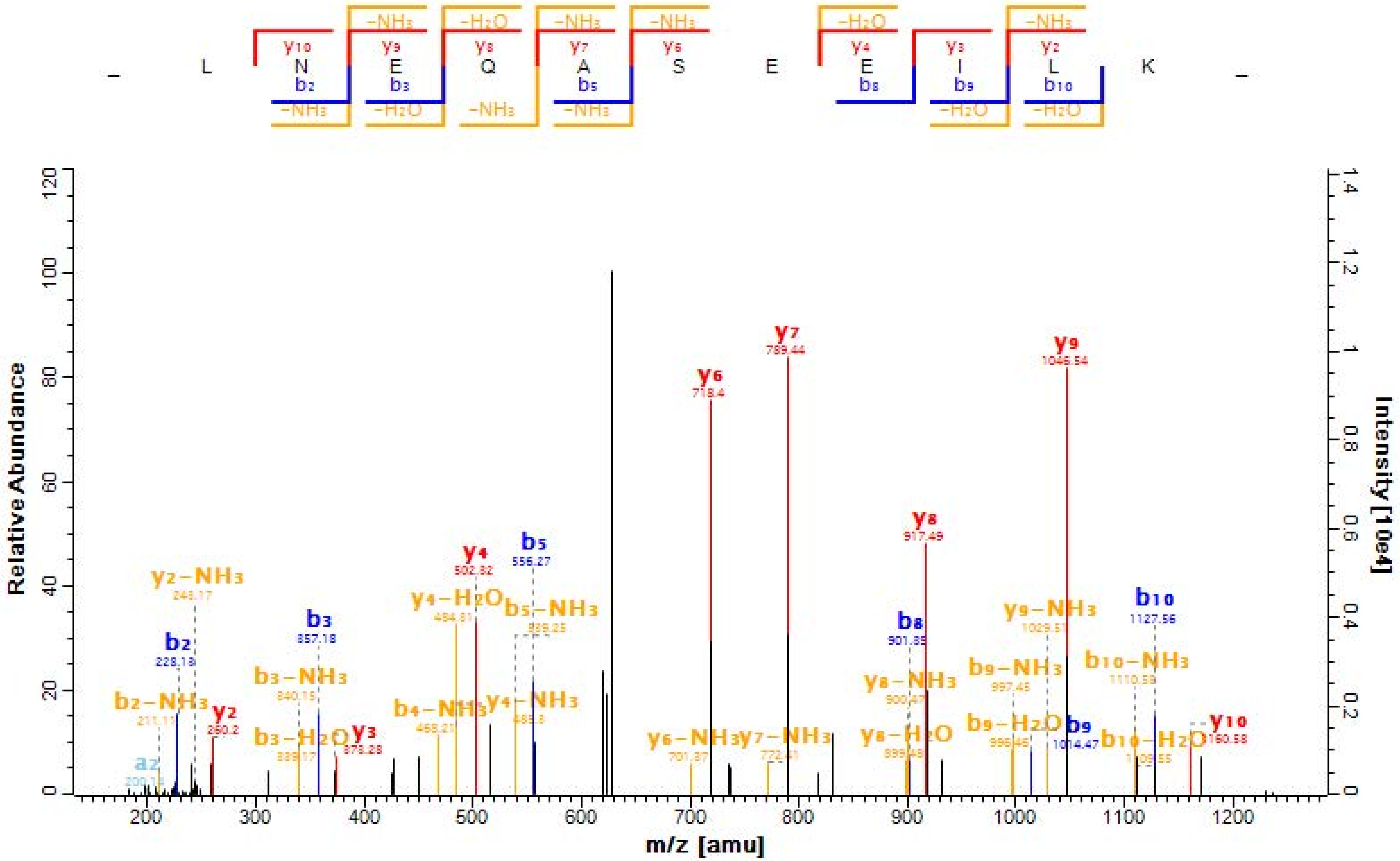
Mass:	1002.51315
m/z:	502.26385
Charge:	2+
Retentiontime:	15.977834701538
Score:	99.56806
Mass Error [ppm]:	-0.29075
PEP:	0.0010985
Precursor Type:	MULTI

g

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	53 %
Peak Coverage:	16 %
Protein Localisation:	23 ... 32

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	9				
	129.0659	2	G	8	940.4978		940.4978	
-0.05449	276.1343	3	F	7	883.4763	+0.10105	442.2418	+0.196362
-0.01351	347.1714	4	A	6	736.4079	+0.067108	736.4079	
-0.09571	404.1928	5	G	5	665.3708	+0.015843	665.3708	
	519.2198	6	D	4	608.3494	+0.093825	608.3494	
-0.06273	647.2784	7	Q	3	493.3224	-0.0133	493.3224	
-0.01929	760.3624	8	I	2	365.2638		365.2638	
+0.033842	857.4152	9	P	1	252.1798	+0.028714	252.1798	
		10	K	0	155.127	+0.007442	155.127	

Scan number	2395	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	216.03



precursor information

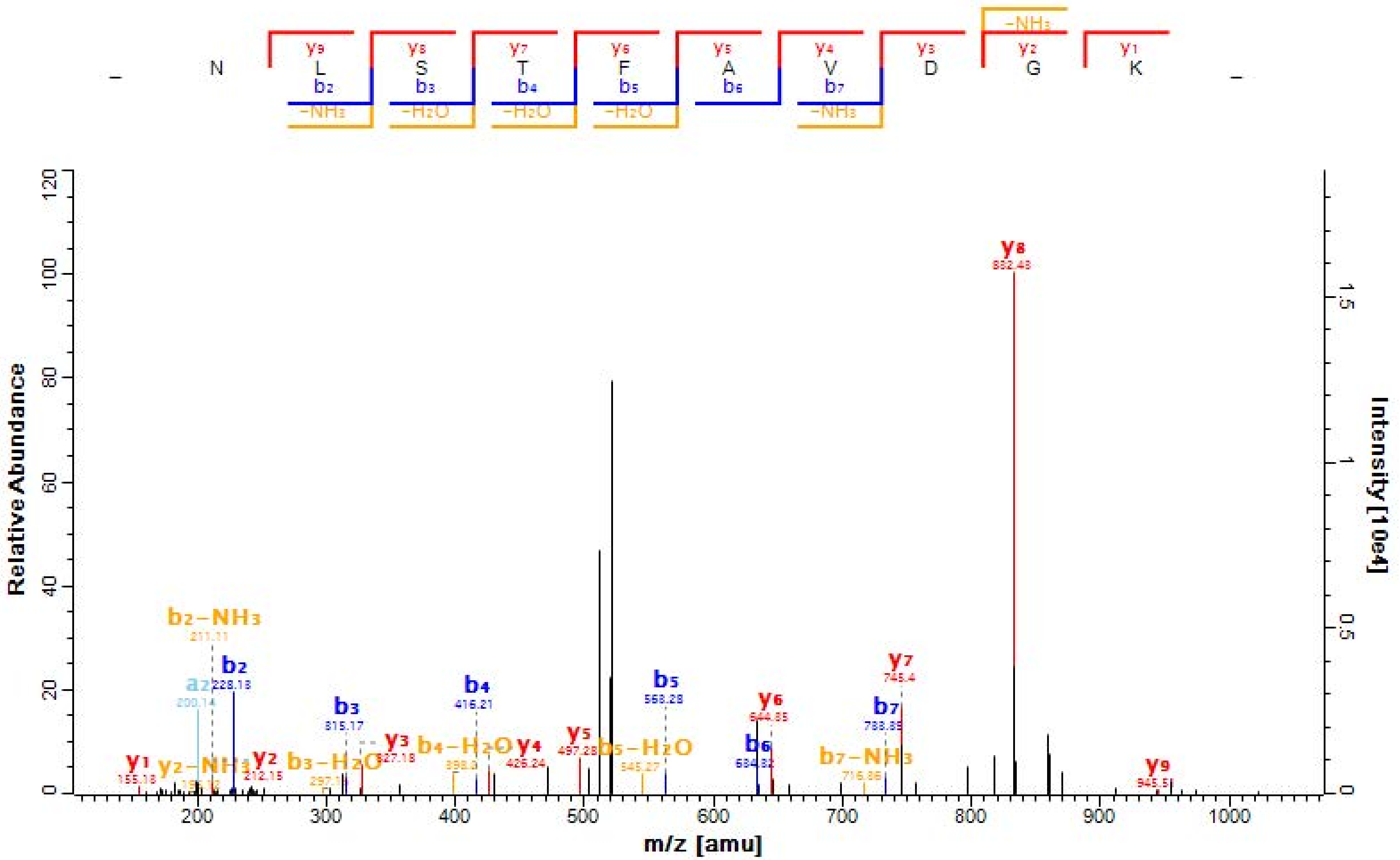
Mass:	1272.65531
m/z:	637.33493
Charge:	2+
Retentiontime:	18.573080062866
Score:	216.0294
Mass Error [ppm]:	-0.65374
PEP:	1.0532E-16
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	56 %
Peak Coverage:	34 %
Protein Localisation:	45 ... 55

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	86.09643		114.0913	1	L	10		
-0.30558	200.1394	-0.07796	228.1343	2	N	9	1160.579	-0.17384
	329.1819	+0.056721	357.1769	3	E	8	1046.536	-0.00164
	457.2405		485.2354	4	Q	7	917.4938	-0.04871
	528.2776	-0.09769	556.2726	5	A	6	789.4353	-0.03627
	615.3097		643.3046	6	S	5	718.3981	-0.0052
	744.3523		772.3472	7	E	4	631.3661	
	873.3949	+0.31171	901.3898	8	E	3	502.3235	+0.030723
	986.4789	-0.39552	1014.474	9	I	2	373.2809	+0.04292
	1099.563	-0.04325	1127.558	10	L	1	260.1969	-0.11362
				11	K	0	147.1128	

Scan number	2670	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	119.74



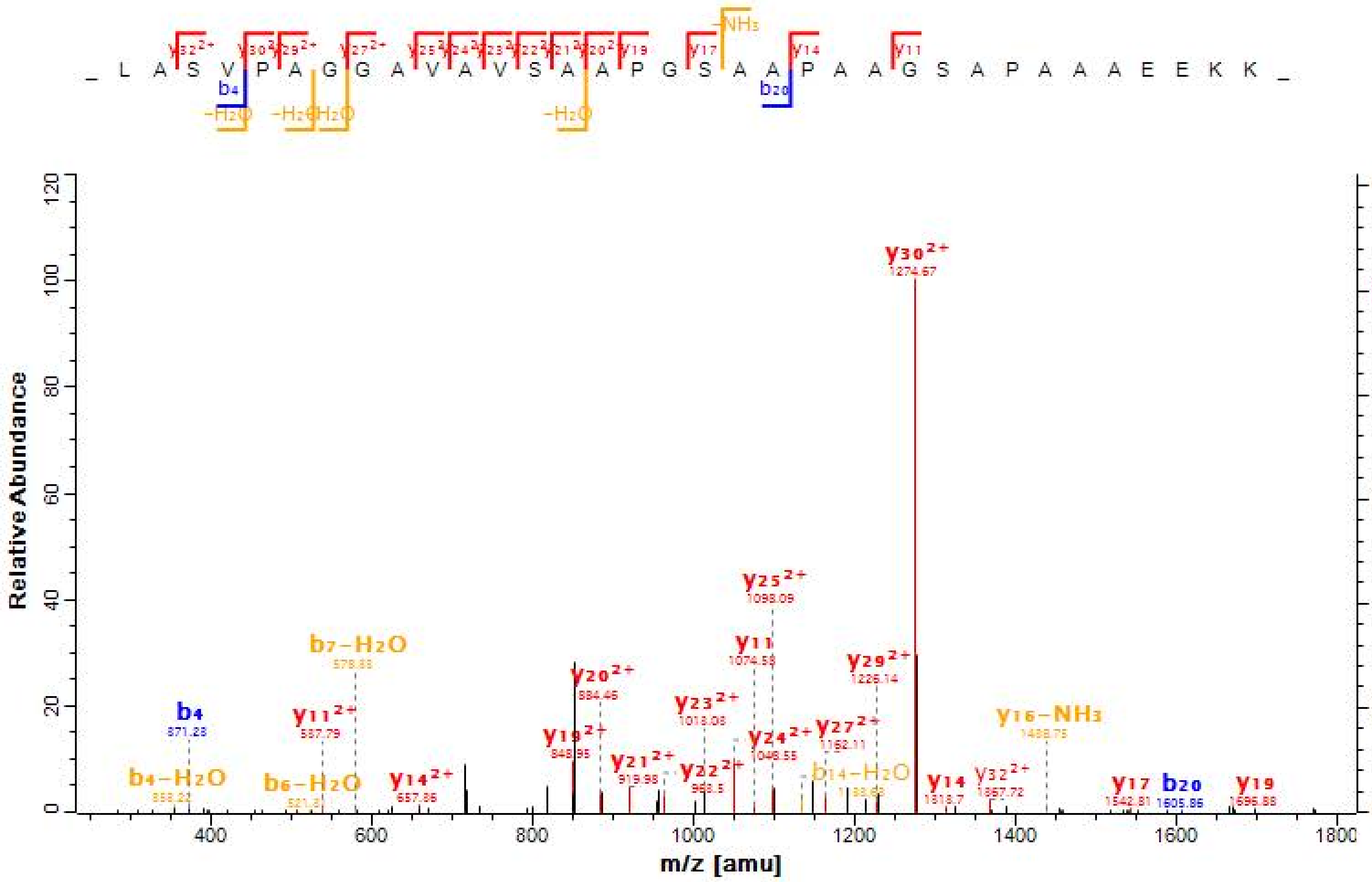
precursor information

Mass:	1050.53466
m/z:	526.27461
Charge:	2+
Retentiontime:	19.887544631958
Score:	119.7433
Mass Error [ppm]:	0.083
PEP:	0.00028253
Precursor Type:	MULTI

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	41 %
Peak Coverage:	22 %
Protein Localisation:	142 ... 151

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	87.05529		115.0502	1	N	9		
-0.0214	200.1394	-0.09946	228.1343	2	L	8	945.5131	+0.111573
	287.1714	+0.082239	315.1663	3	S	7	832.4291	-0.03306
	388.2191	-0.44115	416.214	4	T	6	745.397	+0.045048
	535.2875	+0.058554	563.2824	5	F	5	644.3494	+0.013136
	606.3246	-0.02006	634.3195	6	A	4	497.2809	-0.1961
	705.393	-0.1345	733.3879	7	V	3	426.2438	+0.017041
	820.4199		848.4149	8	D	2	327.1754	+0.136053
	877.4414		905.4363	9	G	1	212.1485	-0.017
				10	K	0	155.127	-0.02852

Scan number	2817	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	52.25



precursor information

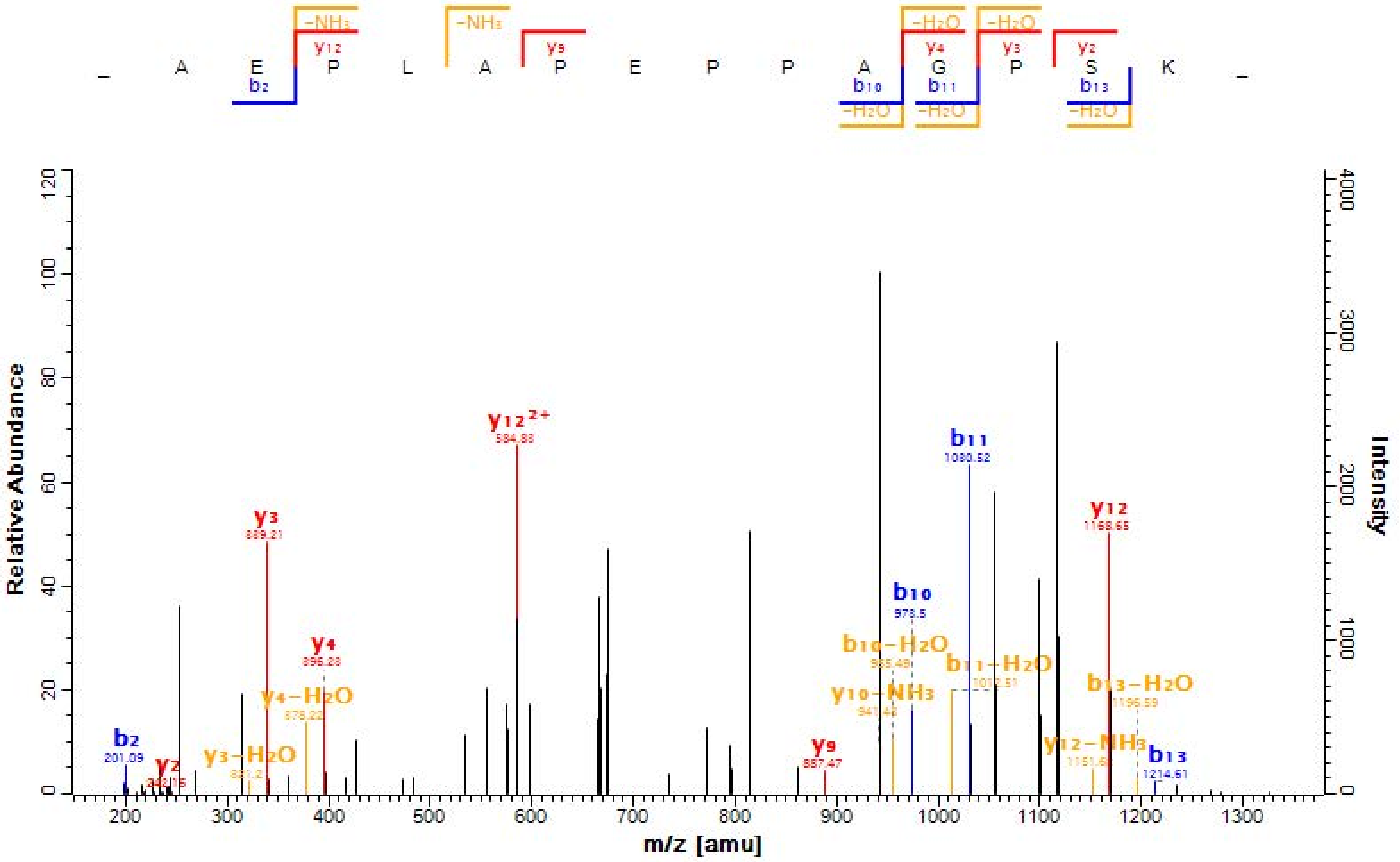
Mass:	2901.51998
m/z:	968.1806
Charge:	3+
Retentiontime:	20.566749572753
Score:	52.24911
Mass Error [ppm]:	0.13019
PEP:	5.6141E-05
Precursor Type:	MULTI

general information

Annotation:	19 of 34
AminoAcids Coverag	56 %
Intensity Coverage:	52 %
Peak Coverage:	27 %
Protein Localisation:	62 ... 95

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	33				
	185.1285	2	A	32	2805.471		2805.471	
	272.1605	3	S	31	2734.434		1367.721	+0.40883
-0.10228	371.2289	4	V	30	2647.402		2647.402	
	468.2817	5	P	29	2548.334		1274.67	+0.197577
	539.3188	6	A	28	2451.281		1226.144	+0.0212
	596.3402	7	G	27	2380.244		2380.244	
	653.3617	8	G	26	2323.222		1162.115	+0.241285
	724.3988	9	A	25	2266.201		2266.201	
	823.4672	10	V	24	2195.164		1098.086	-0.00201
	894.5043	11	A	23	2096.095		1048.551	+0.221651
	993.5728	12	V	22	2025.058		1013.033	-0.20462
	1080.605	13	S	21	1925.99		963.4985	+0.195008
	1151.642	14	A	20	1838.958		919.9825	-0.02683
	1222.679	15	A	19	1767.921		884.464	-0.08024
	1319.732	16	P	18	1696.884	+0.031868	848.9454	+0.19589
	1376.753	17	G	17	1599.831		1599.831	
	1463.785	18	S	16	1542.809	-0.15391	1542.809	
	1534.822	19	A	15	1455.777		1455.777	
+0.141236	1605.859	20	A	14	1384.74		1384.74	
	1702.912	21	P	13	1313.703	-0.2636	657.3552	-0.09747
	1773.949	22	A	12	1216.65		1216.65	
	1844.986	23	A	11	1145.613		1145.613	
	1902.008	24	G	10	1074.576	+0.010486	537.7917	-0.28563
	1989.04	25	S	9	1017.555		1017.555	
	2060.077	26	A	8	930.5226		930.5226	
	2157.13	27	P	7	859.4855		859.4855	
	2228.167	28	A	6	762.4327		762.4327	
	2299.204	29	A	5	691.3956		691.3956	
	2370.241	30	A	4	620.3585		620.3585	
	2499.284	31	E	3	549.3214		549.3214	
	2628.326	32	E	2	420.2788		420.2788	
	2764.436	33	K	1	291.2362		291.2362	
		34	K	0	155.127		155.127	

Scan number	2893	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	71.56



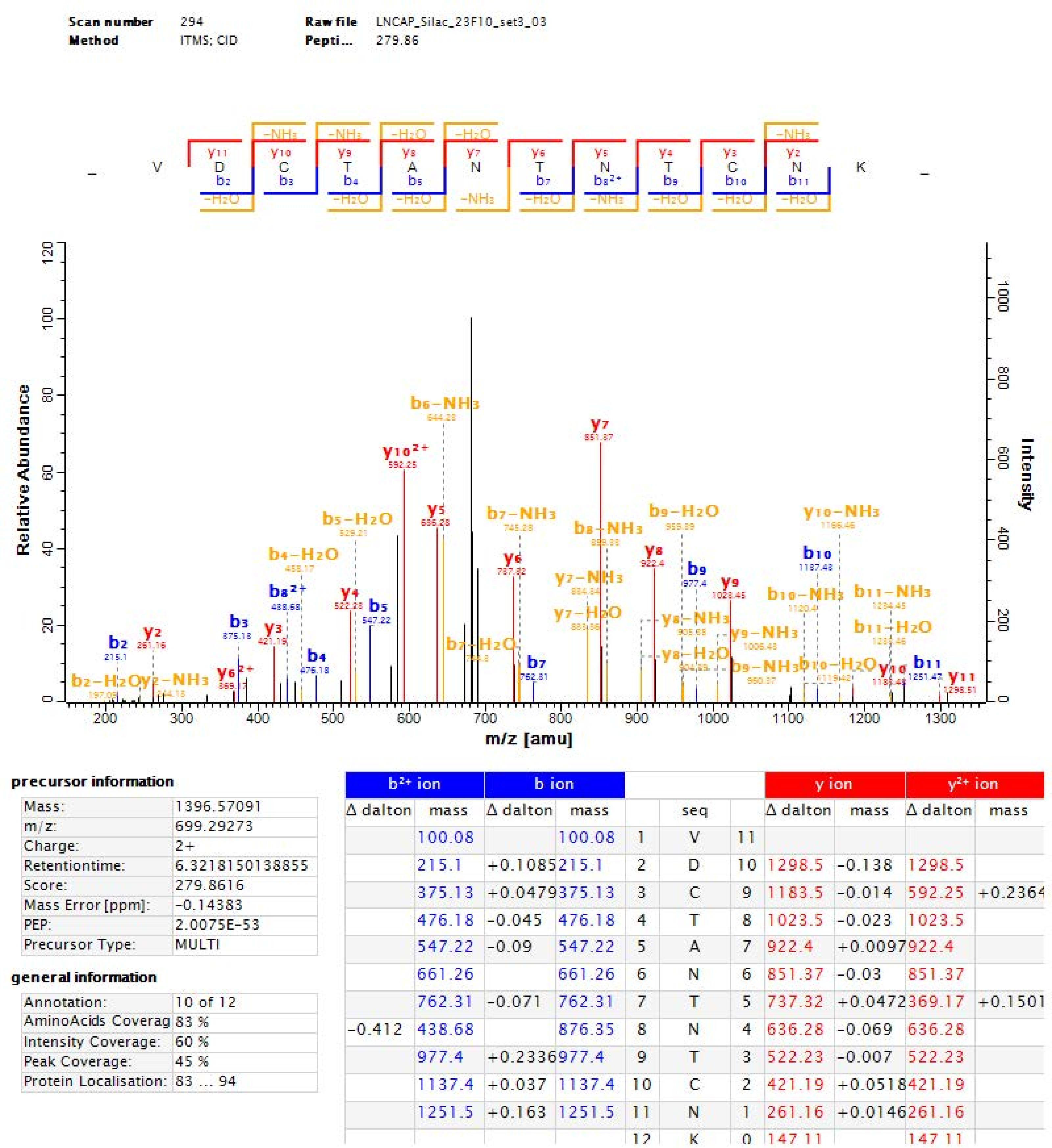
precursor information

Mass:	1359.70337
m/z:	680.85896
Charge:	2+
Retentiontime:	20.924814224243
Score:	71.5575
Mass Error [ppm]:	-0.043823
PEP:	0.001756
Precursor Type:	MULTI

general information

Annotation:	8 of 14
AminoAcids Coverag	57 %
Intensity Coverage:	28 %
Peak Coverage:	22 %
Protein Localisation:	1 ... 14

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	13				
+0.049613	201.087	2	E	12	1297.688		1297.688	
	298.1397	3	P	11	1168.645	-0.0346	584.8262	-0.02906
	411.2238	4	L	10	1071.592		1071.592	
	482.2609	5	A	9	958.5084		958.5084	
	579.3137	6	P	8	887.4713	+0.09936	887.4713	
	708.3563	7	E	7	790.4185		790.4185	
	805.409	8	P	6	661.3759		661.3759	
	902.4618	9	P	5	564.3231		564.3231	
-0.09542	973.4989	10	A	4	467.2704		467.2704	
-0.08264	1030.52	11	G	3	396.2333	+0.042986	396.2333	
	1127.573	12	P	2	339.2118	+0.032254	339.2118	
-0.24446	1214.605	13	S	1	242.159	-0.04056	242.159	
		14	K	0	155.127		155.127	



Scan number	294	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	279.86

precursor information

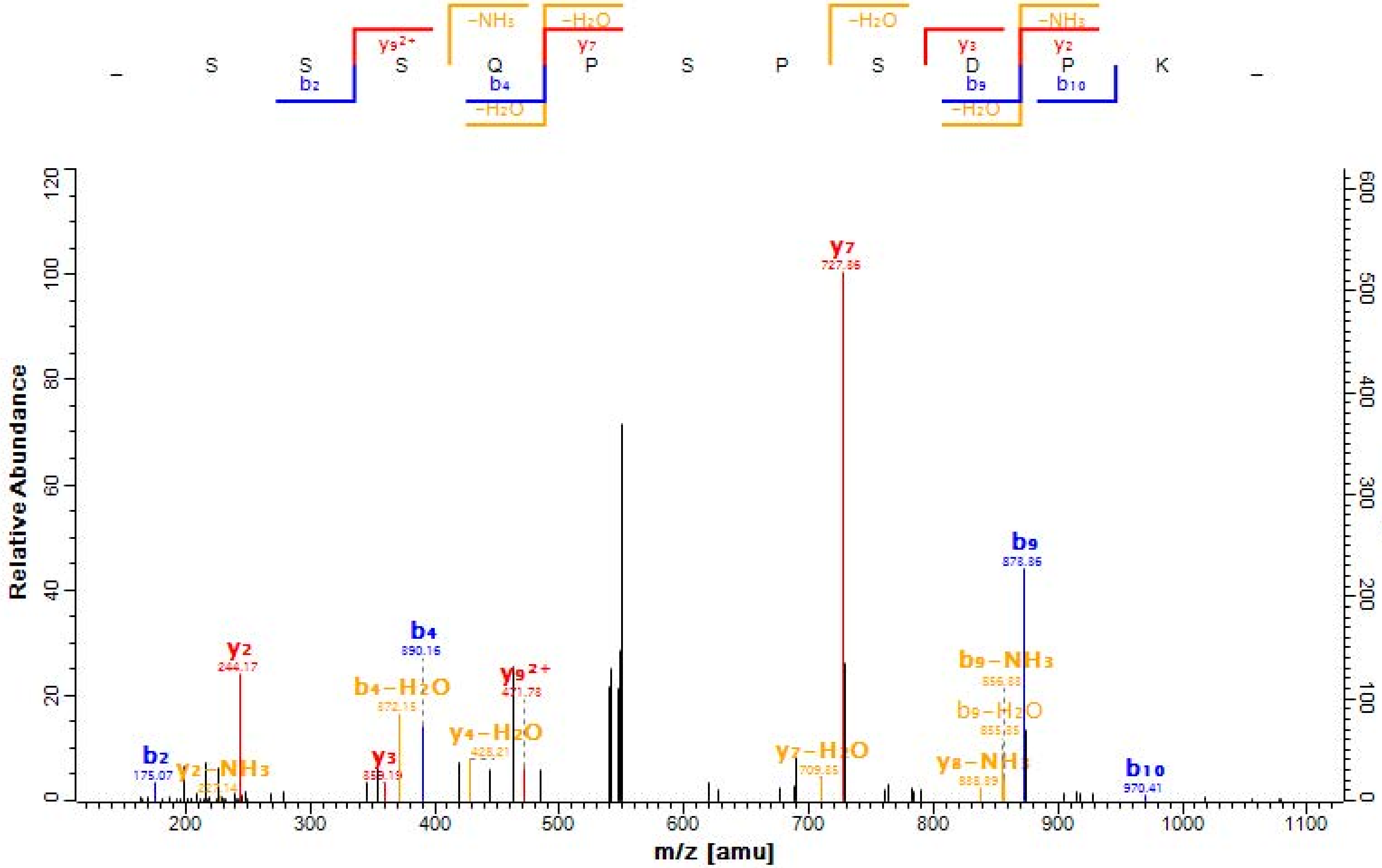
Mass:	1396.57091
m/z:	699.29273
Charge:	2+
Retentiontime:	6.3218150138855
Score:	279.8616
Mass Error [ppm]:	-0.14383
PEP:	2.0075E-53
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	60 %
Peak Coverage:	45 %
Protein Localisation:	83 ... 94

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	11				
	215.1	+0.1085	215.1	2	D	10	1298.5	-0.138	1298.5	
	375.13	+0.0479	375.13	3	C	9	1183.5	-0.014	592.25	+0.2364
	476.18	-0.045	476.18	4	T	8	1023.5	-0.023	1023.5	
	547.22	-0.09	547.22	5	A	7	922.4	+0.0097	922.4	
	661.26		661.26	6	N	6	851.37	-0.03	851.37	
	762.31	-0.071	762.31	7	T	5	737.32	+0.0472	369.17	+0.1501
-0.412	438.68		876.35	8	N	4	636.28	-0.069	636.28	
	977.4	+0.2336	977.4	9	T	3	522.23	-0.007	522.23	
	1137.4	+0.037	1137.4	10	C	2	421.19	+0.0518	421.19	
	1251.5	+0.163	1251.5	11	N	1	261.16	+0.0146	261.16	
				12	K	0	147.11		147.11	

Scan number	308	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	77.74



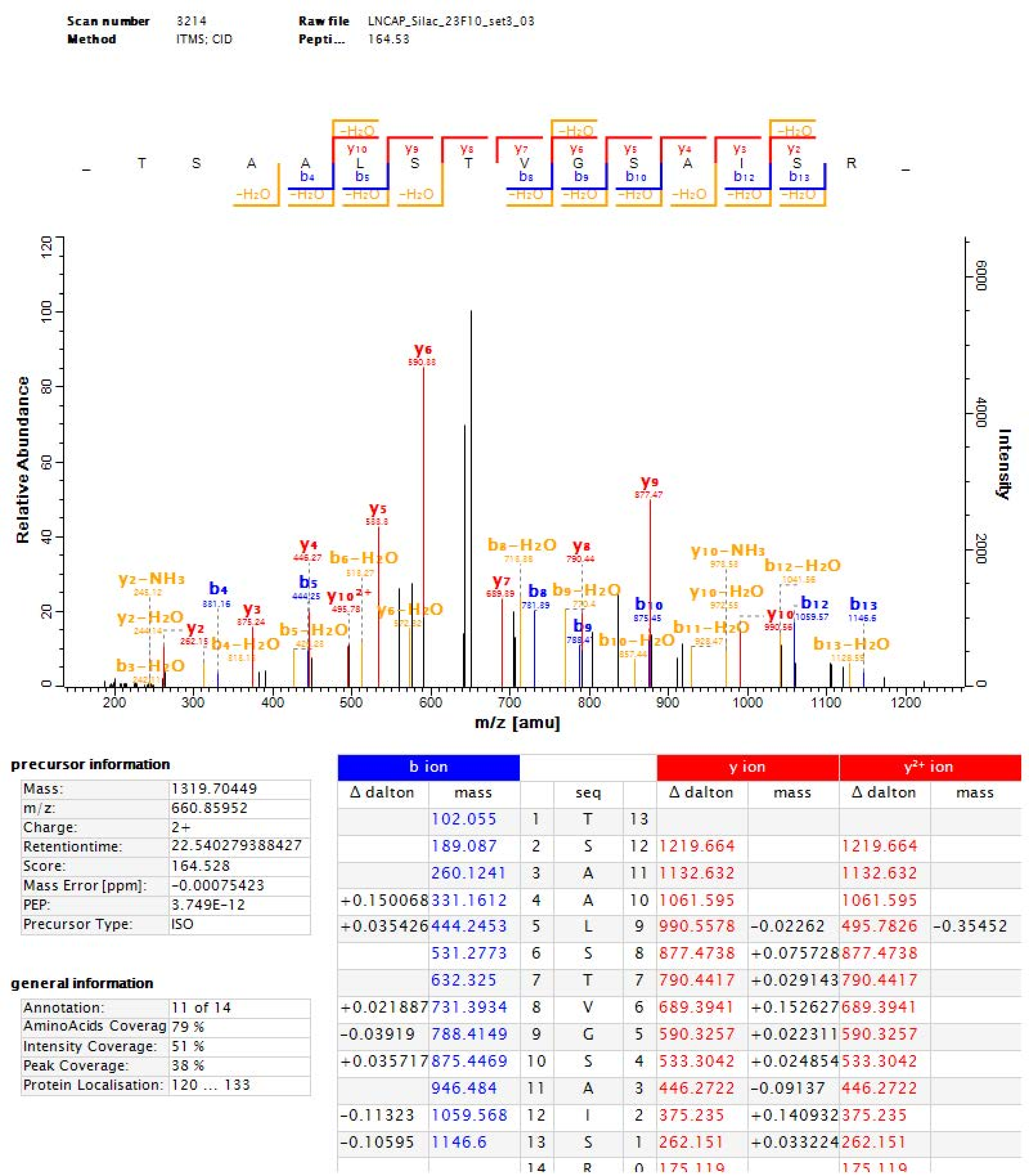
precursor information

Mass:	1115.51014
m/z:	558.76235
Charge:	2+
Retentiontime:	6.4584732055664
Score:	77.74419
Mass Error [ppm]:	0.58877
PEP:	0.0041087
Precursor Type:	MULTI

general information

Annotation:	7 of 11
AminoAcids Coverag	64 %
Intensity Coverage:	40 %
Peak Coverage:	17 %
Protein Localisation:	22 ... 32

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	10				
-0.11012	175.0713	2	S	9	1029.485		1029.485	
	262.1034	3	S	8	942.4527		471.73	-0.11427
+0.061633	390.1619	4	Q	7	855.4207		855.4207	
	487.2147	5	P	6	727.3621	-0.02732	727.3621	
	574.2467	6	S	5	630.3093		630.3093	
	671.2995	7	P	4	543.2773		543.2773	
	758.3315	8	S	3	446.2245		446.2245	
-0.04432	873.3585	9	D	2	359.1925	+0.048334	359.1925	
+0.224328	970.4112	10	P	1	244.1656	-0.0359	244.1656	
		11	K	0	147.1128		147.1128	



Scan number	3214	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	164.53

precursor information

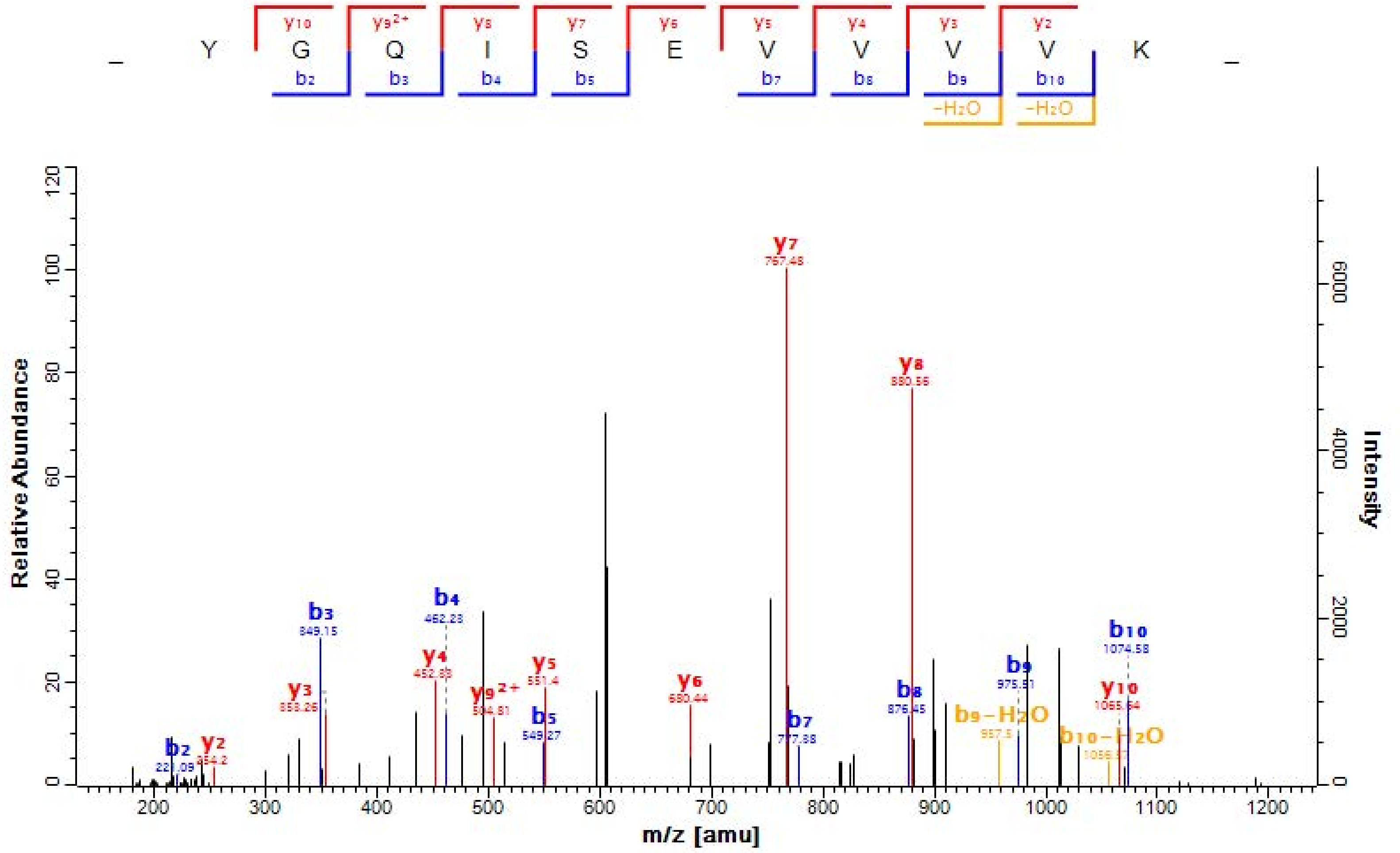
Mass:	1319.70449
m/z:	660.85952
Charge:	2+
Retentiontime:	22.540279388427
Score:	164.528
Mass Error [ppm]:	-0.00075423
PEP:	3.749E-12
Precursor Type:	ISO

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	51 %
Peak Coverage:	38 %
Protein Localisation:	120 ... 133

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055	1	T	13				
	189.087	2	S	12	1219.664		1219.664	
	260.1241	3	A	11	1132.632		1132.632	
+0.150068	331.1612	4	A	10	1061.595		1061.595	
+0.035426	444.2453	5	L	9	990.5578	-0.02262	495.7826	-0.35452
	531.2773	6	S	8	877.4738	+0.075728	877.4738	
	632.325	7	T	7	790.4417	+0.029143	790.4417	
+0.021887	731.3934	8	V	6	689.3941	+0.152627	689.3941	
-0.03919	788.4149	9	G	5	590.3257	+0.022311	590.3257	
+0.035717	875.4469	10	S	4	533.3042	+0.024854	533.3042	
	946.484	11	A	3	446.2722	-0.09137	446.2722	
-0.11323	1059.568	12	I	2	375.235	+0.140932	375.235	
-0.10595	1146.6	13	S	1	262.151	+0.033224	262.151	
		14	R	0	175.119		175.119	

Scan number	3587	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	98.41



precursor information

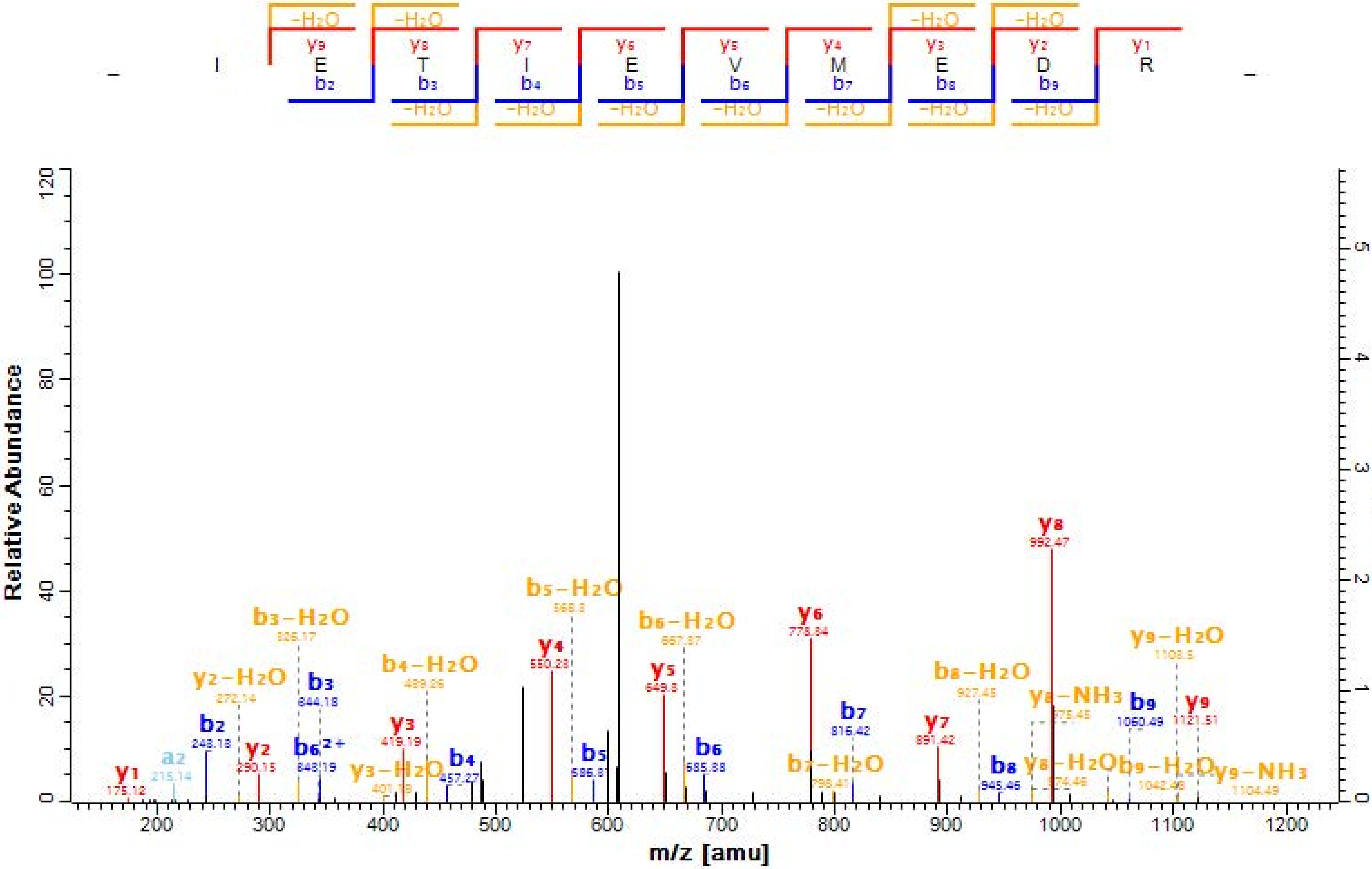
Mass:	1227.69539
m/z:	614.85497
Charge:	2+
Retentiontime:	24.346303939819
Score:	98.40717
Mass Error [ppm]:	-0.041932
PEP:	0.0042087
Precursor Type:	ISO

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	41 %
Peak Coverage:	21 %
Protein Localisation:	29 ... 39

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	164.0706	1	Y	10				
-0.09561	221.0921	2	G	9	1065.639	-0.04759	1065.639	
+0.061756	349.1506	3	Q	8	1008.618		504.8126	-0.1005
+0.000153	462.2347	4	I	7	880.5593	-0.07497	880.5593	
+0.11406	549.2667	5	S	6	767.4753	-0.03546	767.4753	
	678.3093	6	E	5	680.4433	+0.043626	680.4433	
+0.062562	777.3777	7	V	4	551.4007	+0.132789	551.4007	
+0.035774	876.4462	8	V	3	452.3322	+0.071503	452.3322	
-0.17943	975.5146	9	V	2	353.2638	+0.026758	353.2638	
+0.005147	1074.583	10	V	1	254.1954	-0.03398	254.1954	
		11	K	0	155.127		155.127	

Scan number	3600	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	259.08

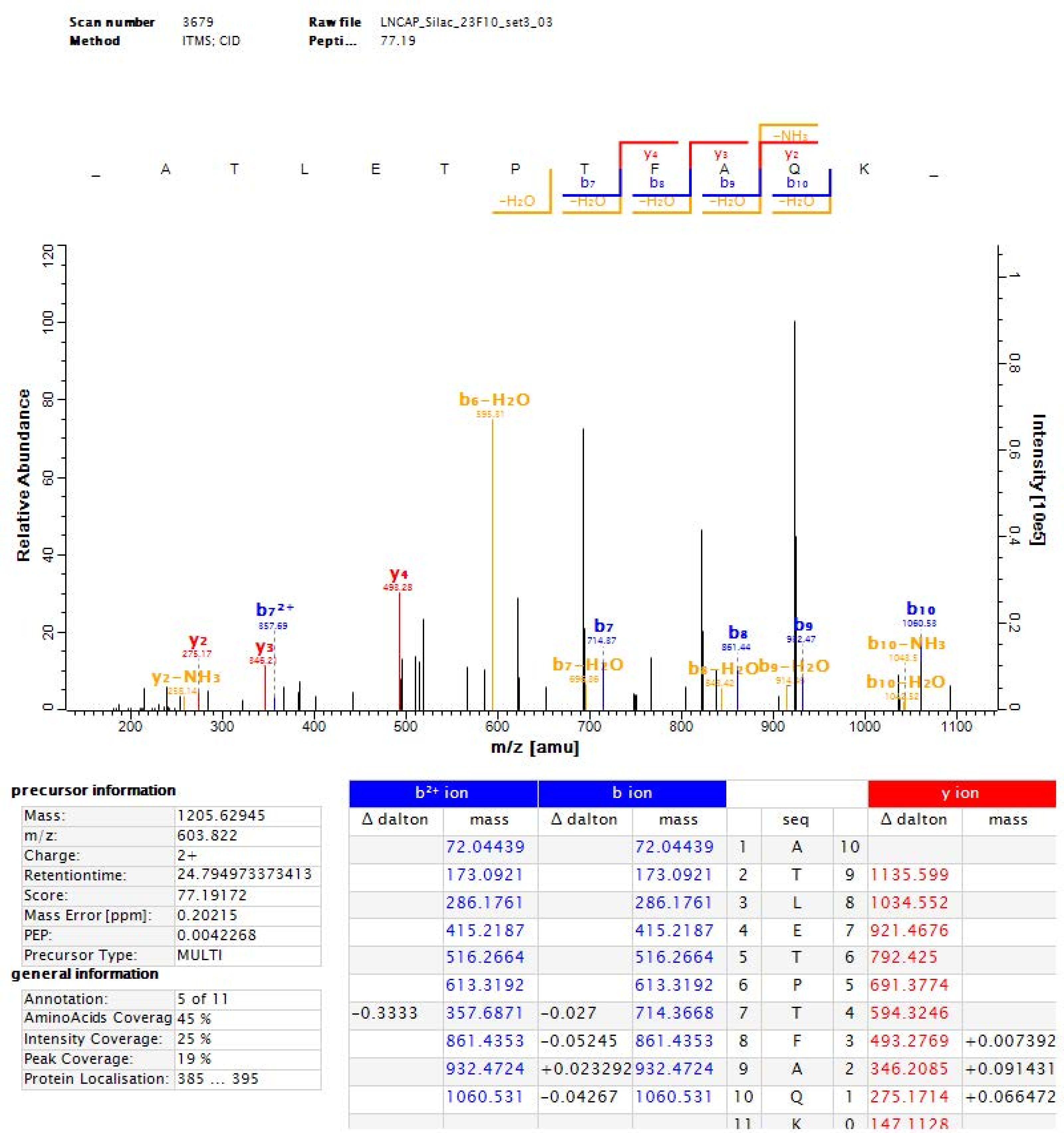


precursor information

Mass:	1233.5912
m/z:	617.80288
Charge:	2+
Retentiontime:	24.407228469848
Score:	259.0814
Mass Error [ppm]:	0.082384
PEP:	4.3859E-37
Precursor Type:	MULTI

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	51 %
Peak Coverage:	42 %
Protein Localisation:	152 ... 161

a ion		b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	86.096		114.09		114.09	1	I	9		
+0.042	215.14		243.13	-0.001	243.13	2	E	8	1121.5	-0.051
	316.19		344.18	+0.044	344.18	3	T	7	992.47	+0.017
	429.27		457.27	+0.0192	457.27	4	I	6	891.42	-0.023
	558.31		586.31	+0.1289	586.31	5	E	5	778.34	+0.069
	657.38	+0.1828	343.19	-0.067	685.38	6	V	4	649.3	+0.0032
	788.42		816.42	-0.104	816.42	7	M	3	550.23	+0.0362
	917.46		945.46	-0.186	945.46	8	E	2	419.19	+0.0134
	1032.5		1060.5	+0.0563	1060.5	9	D	1	290.15	+0.0979
						10	R	0	175.12	-0.088



Scan number	3679	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	77.19

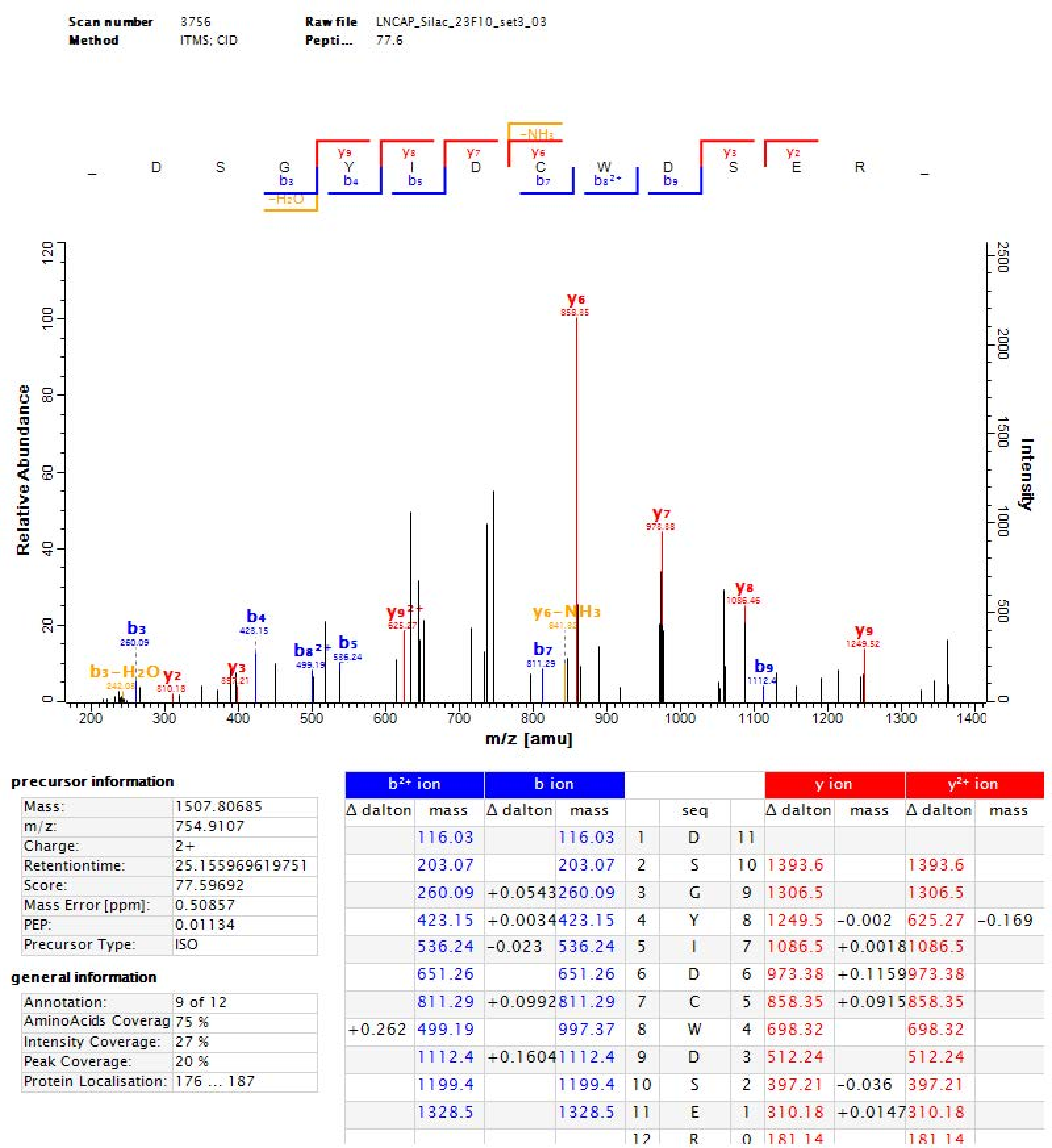
precursor information

Mass:	1205.62945
m/z:	603.822
Charge:	2+
Retentiontime:	24.794973373413
Score:	77.19172
Mass Error [ppm]:	0.20215
PEP:	0.0042268
Precursor Type:	MULTI

general information

Annotation:	5 of 11
AminoAcids Coverag	45 %
Intensity Coverage:	25 %
Peak Coverage:	19 %
Protein Localisation:	385 ... 395

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	72.04439		72.04439	1	A	10		
	173.0921		173.0921	2	T	9	1135.599	
	286.1761		286.1761	3	L	8	1034.552	
	415.2187		415.2187	4	E	7	921.4676	
	516.2664		516.2664	5	T	6	792.425	
	613.3192		613.3192	6	P	5	691.3774	
-0.3333	357.6871	-0.027	714.3668	7	T	4	594.3246	
	861.4353	-0.05245	861.4353	8	F	3	493.2769	+0.007392
	932.4724	+0.023292	932.4724	9	A	2	346.2085	+0.091431
	1060.531	-0.04267	1060.531	10	Q	1	275.1714	+0.066472
				11	K	0	147.1128	



Scan number	3756	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	77.6

precursor information

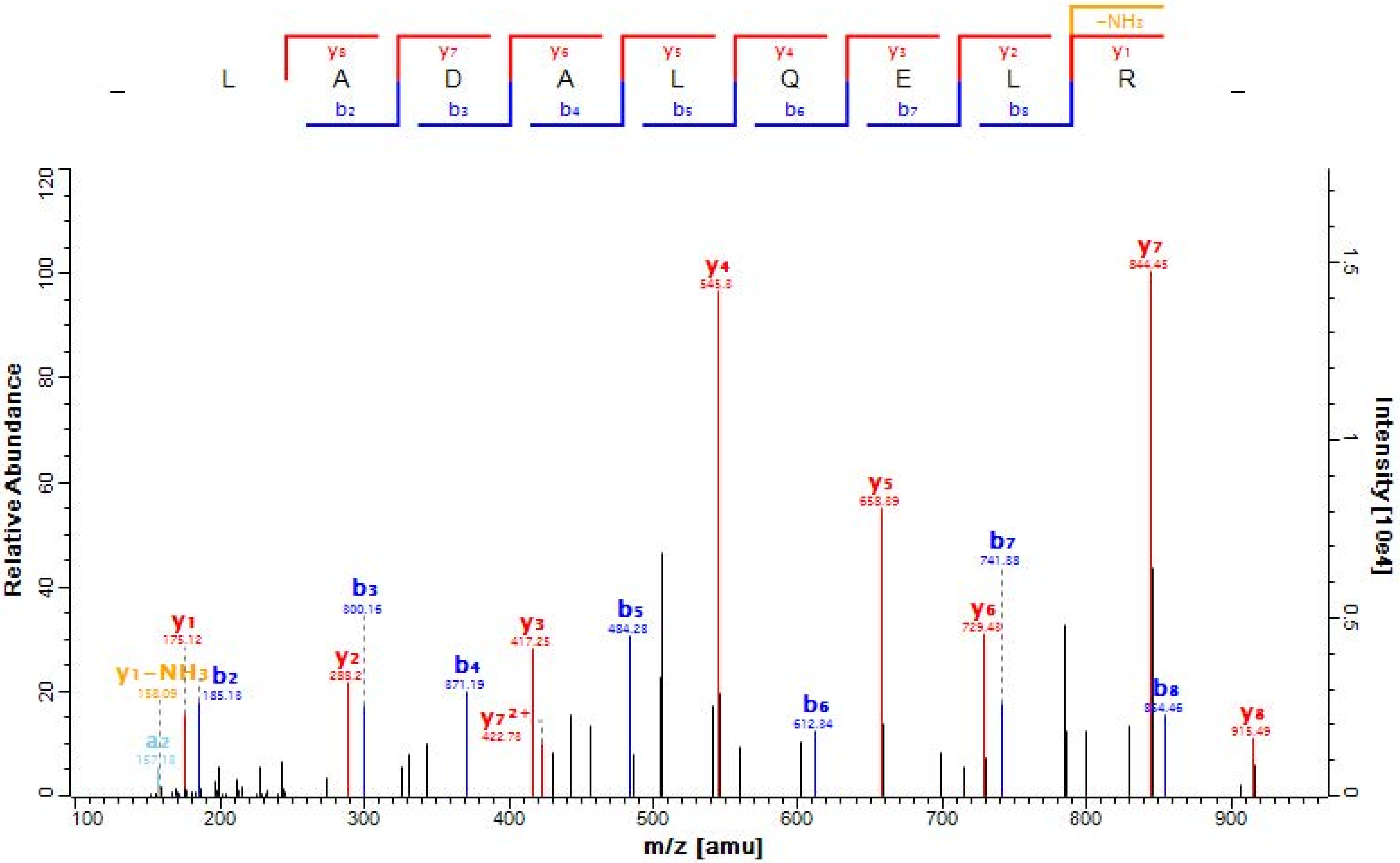
Mass:	1507.80685
m/z:	754.9107
Charge:	2+
Retentiontime:	25.155969619751
Score:	77.59692
Mass Error [ppm]:	0.50857
PEP:	0.01134
Precursor Type:	ISO

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	27 %
Peak Coverage:	20 %
Protein Localisation:	176 ... 187

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	11				
	203.07		203.07	2	S	10	1393.6		1393.6	
	260.09	+0.0543	260.09	3	G	9	1306.5		1306.5	
	423.15	+0.0034	423.15	4	Y	8	1249.5	-0.002	625.27	-0.169
	536.24	-0.023	536.24	5	I	7	1086.5	+0.0018	1086.5	
	651.26		651.26	6	D	6	973.38	+0.1159	973.38	
	811.29	+0.0992	811.29	7	C	5	858.35	+0.0915	858.35	
+0.262	499.19		997.37	8	W	4	698.32		698.32	
	1112.4	+0.1604	1112.4	9	D	3	512.24		512.24	
	1199.4		1199.4	10	S	2	397.21	-0.036	397.21	
	1328.5		1328.5	11	E	1	310.18	+0.0147	310.18	
				12	R	0	181.14		181.14	

Scan number	3871	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	121.9

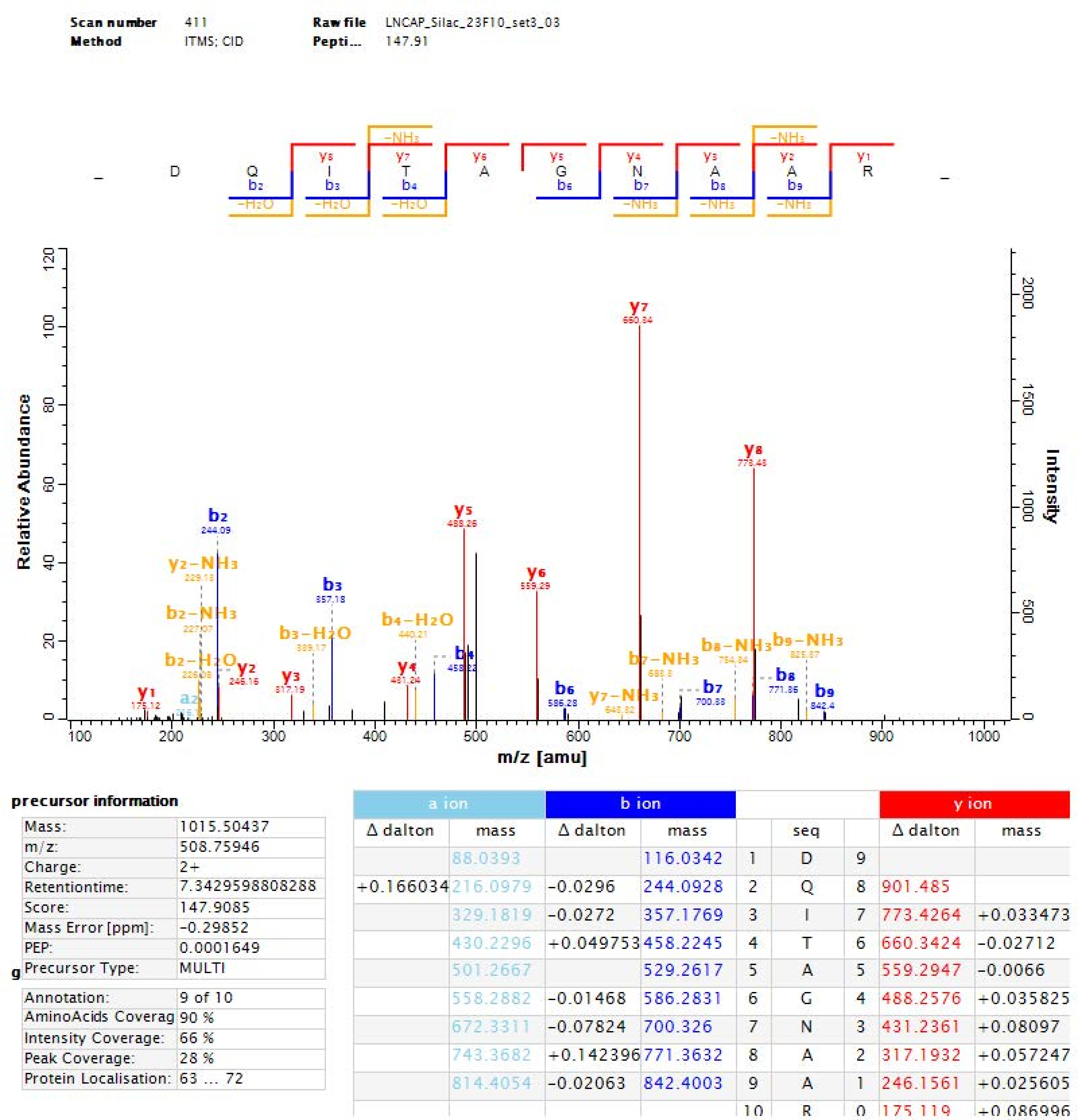


precursor information

g

Mass:	1027.56618
m/z:	514.79037
Charge:	2+
Retentiontime:	25.721845626831
Score:	121.8986
Mass Error [ppm]:	-0.029856
PEP:	0.0012825
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	56 %
Peak Coverage:	23 %
Protein Localisation:	241 ... 249

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	8				
+0.0685	157.13	-0.018	185.13	2	A	7	915.49	+0.0249	915.49	
	272.16	+0.0021	300.16	3	D	6	844.45	+0.0098	422.73	+0.1155
	343.2	+0.0602	371.19	4	A	5	729.43	-0.005	729.43	
	456.28	-0.06	484.28	5	L	4	658.39	+0.0463	658.39	
	584.34	-0.029	612.34	6	Q	3	545.3	+0.0227	545.3	
	713.38	+0.0391	741.38	7	E	2	417.25	+0.053	417.25	
	826.47	-0.121	854.46	8	L	1	288.2	-0.035	288.2	
				9	R	0	175.12	+0.0366	175.12	



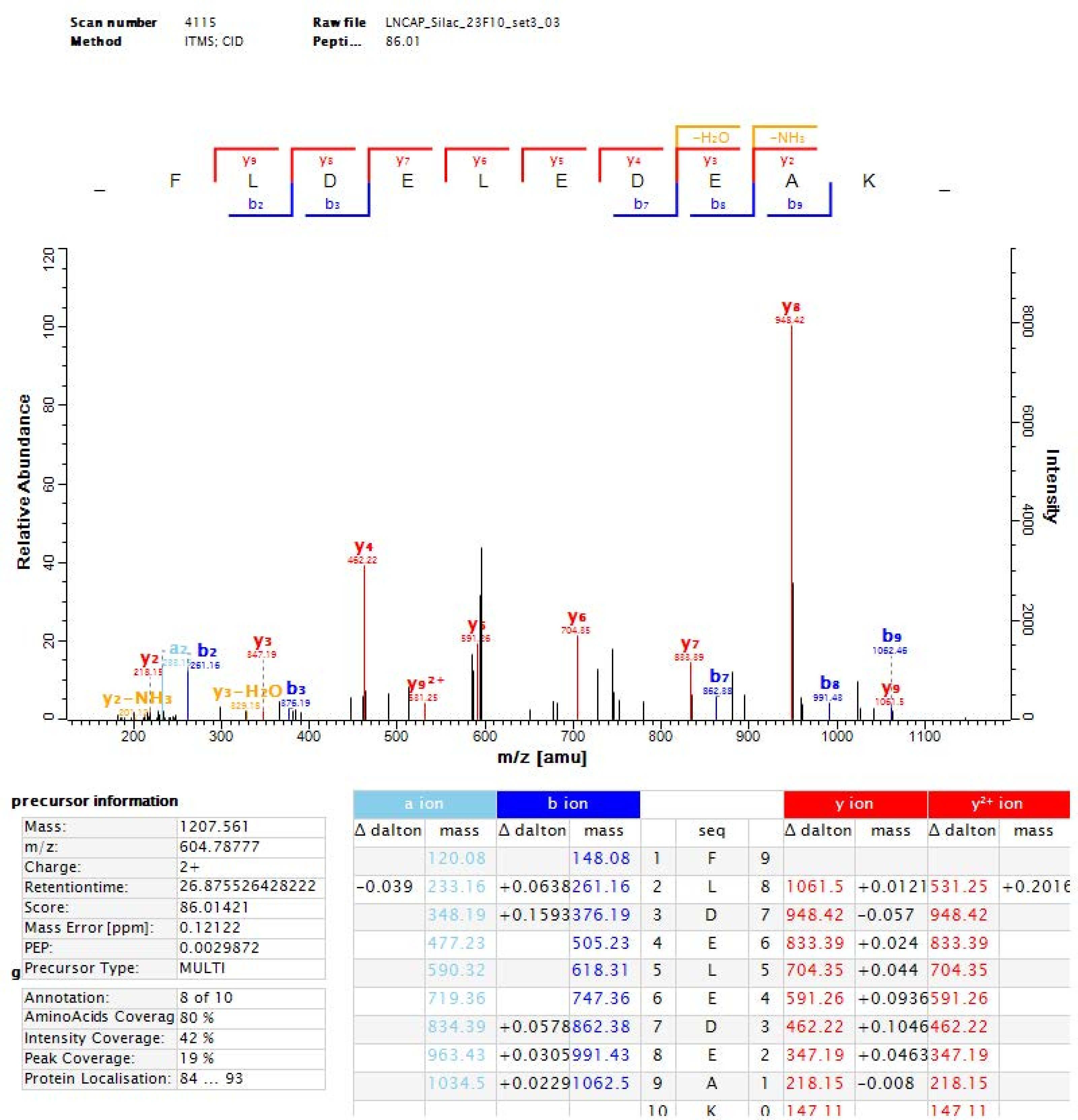
Scan number	411	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	147.91

precursor information

Mass:	1015.50437
m/z:	508.75946
Charge:	2+
Retentiontime:	7.3429598808288
Score:	147.9085
Mass Error [ppm]:	-0.29852
PEP:	0.0001649
Precursor Type:	MULTI

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	66 %
Peak Coverage:	28 %
Protein Localisation:	63 ... 72

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	88.0393		116.0342	1	D	9		
+0.166034	216.0979	-0.0296	244.0928	2	Q	8	901.485	
	329.1819	-0.0272	357.1769	3	I	7	773.4264	+0.033473
	430.2296	+0.049753	458.2245	4	T	6	660.3424	-0.02712
	501.2667		529.2617	5	A	5	559.2947	-0.0066
	558.2882	-0.01468	586.2831	6	G	4	488.2576	+0.035825
	672.3311	-0.07824	700.326	7	N	3	431.2361	+0.08097
	743.3682	+0.142396	771.3632	8	A	2	317.1932	+0.057247
	814.4054	-0.02063	842.4003	9	A	1	246.1561	+0.025605
				10	R	0	175.119	+0.086996



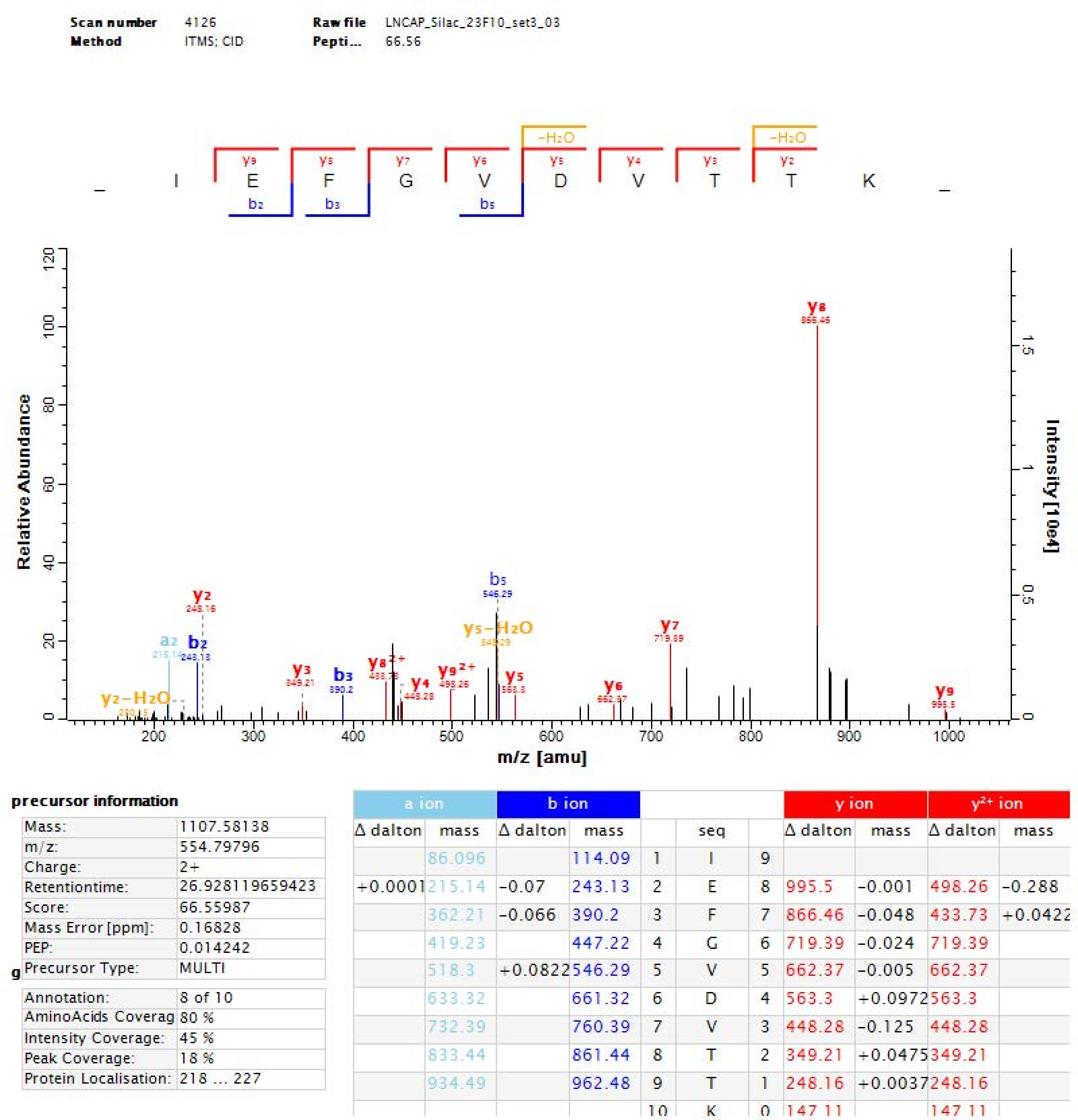
Scan number 4115
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set3_03
Pepti... 86.01

precursor information

Mass:	1207.561
m/z:	604.78777
Charge:	2+
Retentiontime:	26.875526428222
Score:	86.01421
Mass Error [ppm]:	0.12122
PEP:	0.0029872
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	42 %
Peak Coverage:	19 %
Protein Localisation:	84 ... 93

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08		148.08	1	F	9				
-0.039	233.16	+0.0638	261.16	2	L	8	1061.5	+0.0121	531.25	+0.2016
	348.19	+0.1593	376.19	3	D	7	948.42	-0.057	948.42	
	477.23		505.23	4	E	6	833.39	+0.024	833.39	
	590.32		618.31	5	L	5	704.35	+0.044	704.35	
	719.36		747.36	6	E	4	591.26	+0.0936	591.26	
	834.39	+0.0578	862.38	7	D	3	462.22	+0.1046	462.22	
	963.43	+0.0305	991.43	8	E	2	347.19	+0.0463	347.19	
	1034.5	+0.0229	1062.5	9	A	1	218.15	-0.008	218.15	
				10	K	0	147.11		147.11	



Scan number	4126	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti…**	66.56

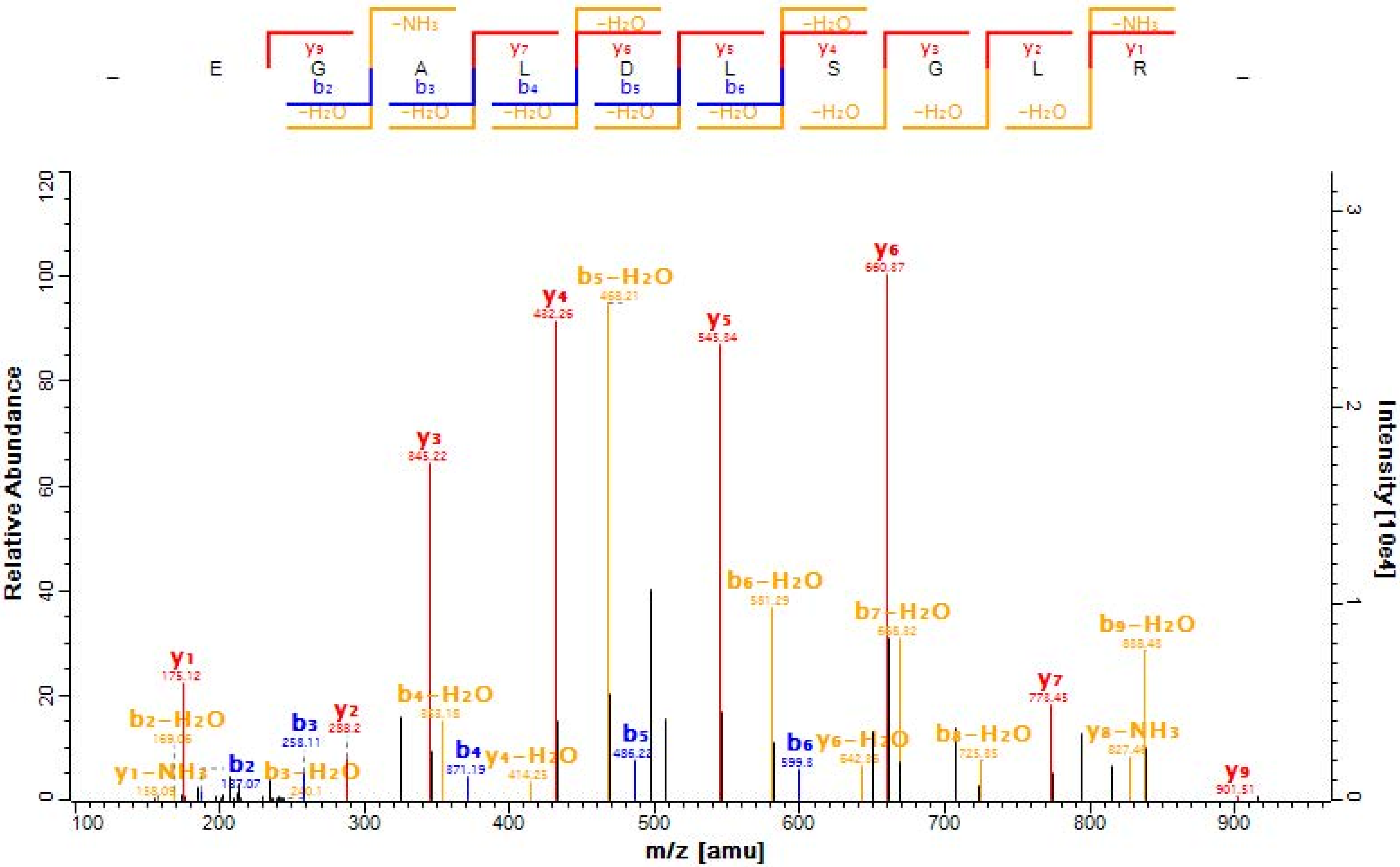
precursor information

Mass:	1107.58138
m/z:	554.79796
Charge:	2+
Retentiontime:	26.928119659423
Score:	66.55987
Mass Error [ppm]:	0.16828
PEP:	0.014242
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	45 %
Peak Coverage:	18 %
Protein Localisation:	218 … 227

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	9				
+0.0001	215.14	-0.07	243.13	2	E	8	995.5	-0.001	498.26	-0.288
	362.21	-0.066	390.2	3	F	7	866.46	-0.048	433.73	+0.0422
	419.23		447.22	4	G	6	719.39	-0.024	719.39	
	518.3	+0.0822	546.29	5	V	5	662.37	-0.005	662.37	
	633.32		661.32	6	D	4	563.3	+0.0972	563.3	
	732.39		760.39	7	V	3	448.28	-0.125	448.28	
	833.44		861.44	8	T	2	349.21	+0.0475	349.21	
	934.49		962.48	9	T	1	248.16	+0.0037	248.16	
				10	K	0	147.11		147.11	

Scan number	4344	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	117.02

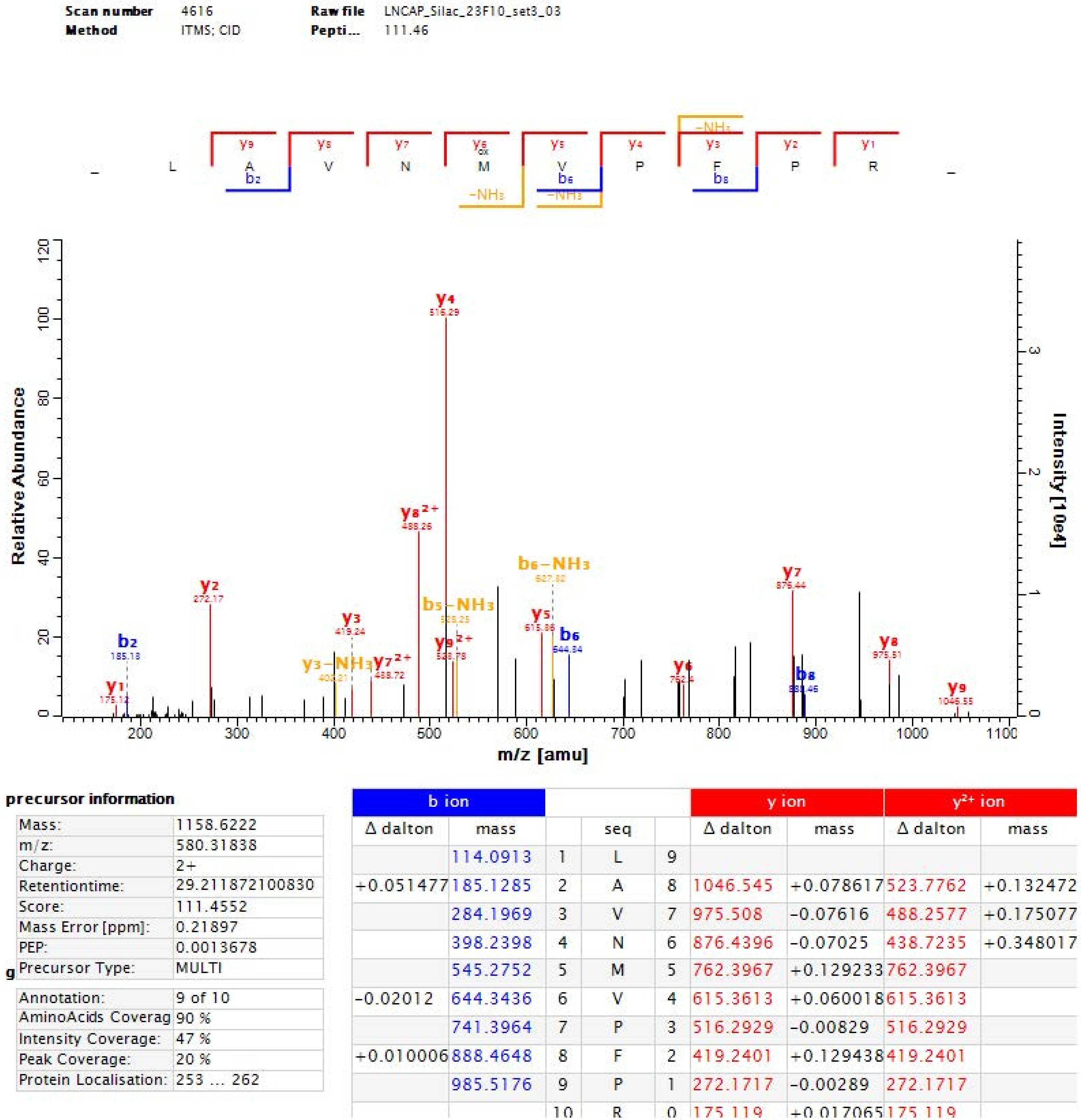


precursor information

Mass:	1029.54534
m/z:	515.77994
Charge:	2+
Retentiontime:	27.947154998779
Score:	117.0223
Mass Error [ppm]:	-0.13262
PEP:	0.00034042
Precursor Type:	MULTI

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	71 %
Peak Coverage:	36 %
Protein Localisation:	579 ... 588

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	130.049869563	1	E	9		
+0.0566574	187.071333286	2	G	8	901.510156799	+0.0374506
-0.1877623	258.108447074	3	A	7	844.488693075	
+0.0897765	371.192511055	4	L	6	773.451579288	+0.0251663
+0.027189	486.219454087	5	D	5	660.367515307	+0.0732806
+0.0813696	599.303518067	6	L	4	545.340572275	+0.010563
	686.335546477	7	S	3	432.256508295	+0.0243755
	743.357010201	8	G	2	345.224479885	+0.0446852
	856.441074181	9	L	1	288.203016161	+0.1246816
		10	R	0	175.118952181	+0.0386711



Scan number 4616
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set3_03
Pepti... 111.46

precursor information

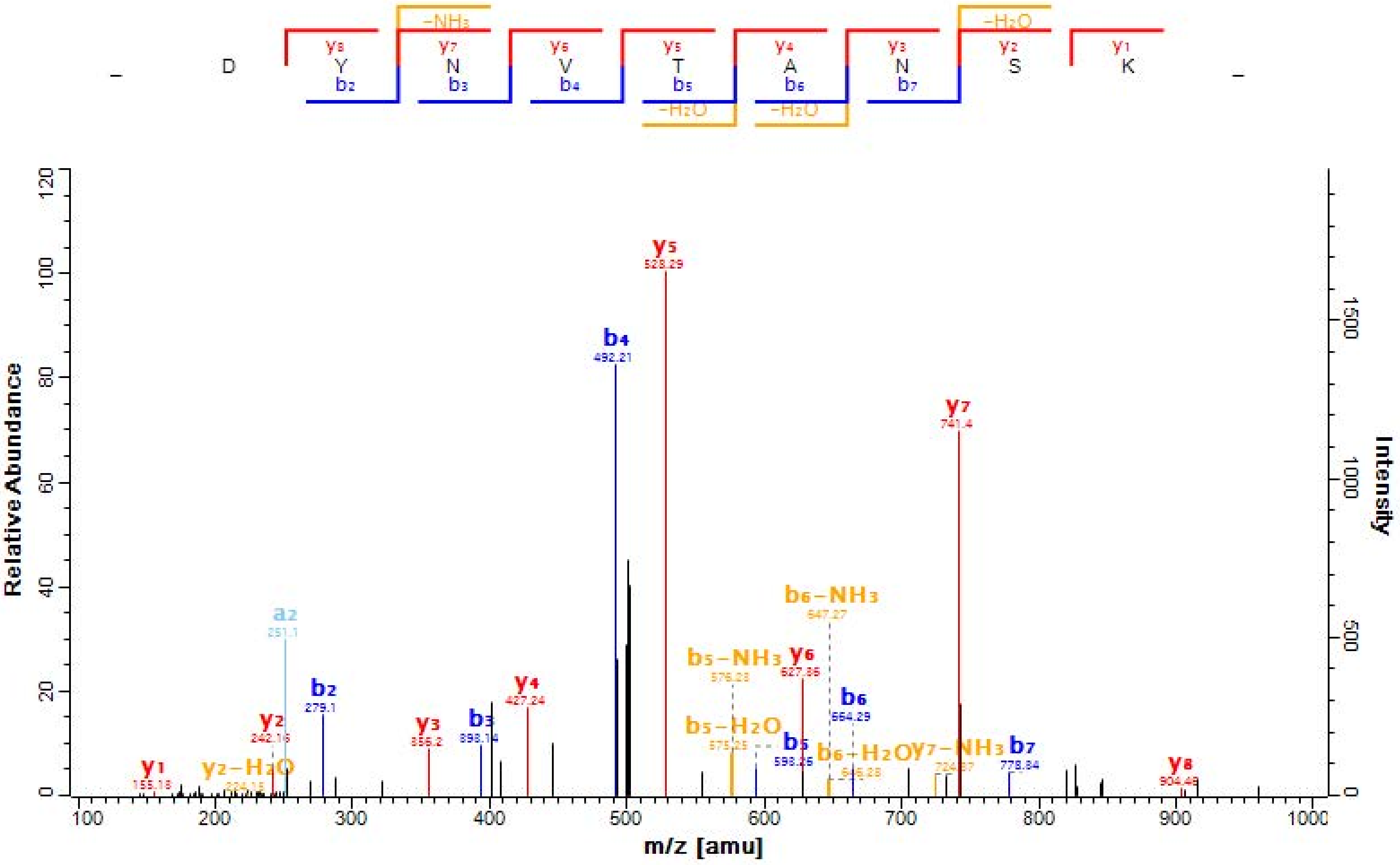
Mass:	1158.6222
m/z:	580.31838
Charge:	2+
Retentiontime:	29.211872100830
Score:	111.4552
Mass Error [ppm]:	0.21897
PEP:	0.0013678
Precursor Type:	MULTI

g

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	47 %
Peak Coverage:	20 %
Protein Localisation:	253 ... 262

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	9				
+0.051477	185.1285	2	A	8	1046.545	+0.078617	523.7762	+0.132472
	284.1969	3	V	7	975.508	−0.07616	488.2577	+0.175077
	398.2398	4	N	6	876.4396	−0.07025	438.7235	+0.348017
	545.2752	5	M	5	762.3967	+0.129233	762.3967	
−0.02012	644.3436	6	V	4	615.3613	+0.060018	615.3613	
	741.3964	7	P	3	516.2929	−0.00829	516.2929	
+0.010006	888.4648	8	F	2	419.2401	+0.129438	419.2401	
	985.5176	9	P	1	272.1717	−0.00289	272.1717	
		10	R	0	175.119	+0.017065	175.119	

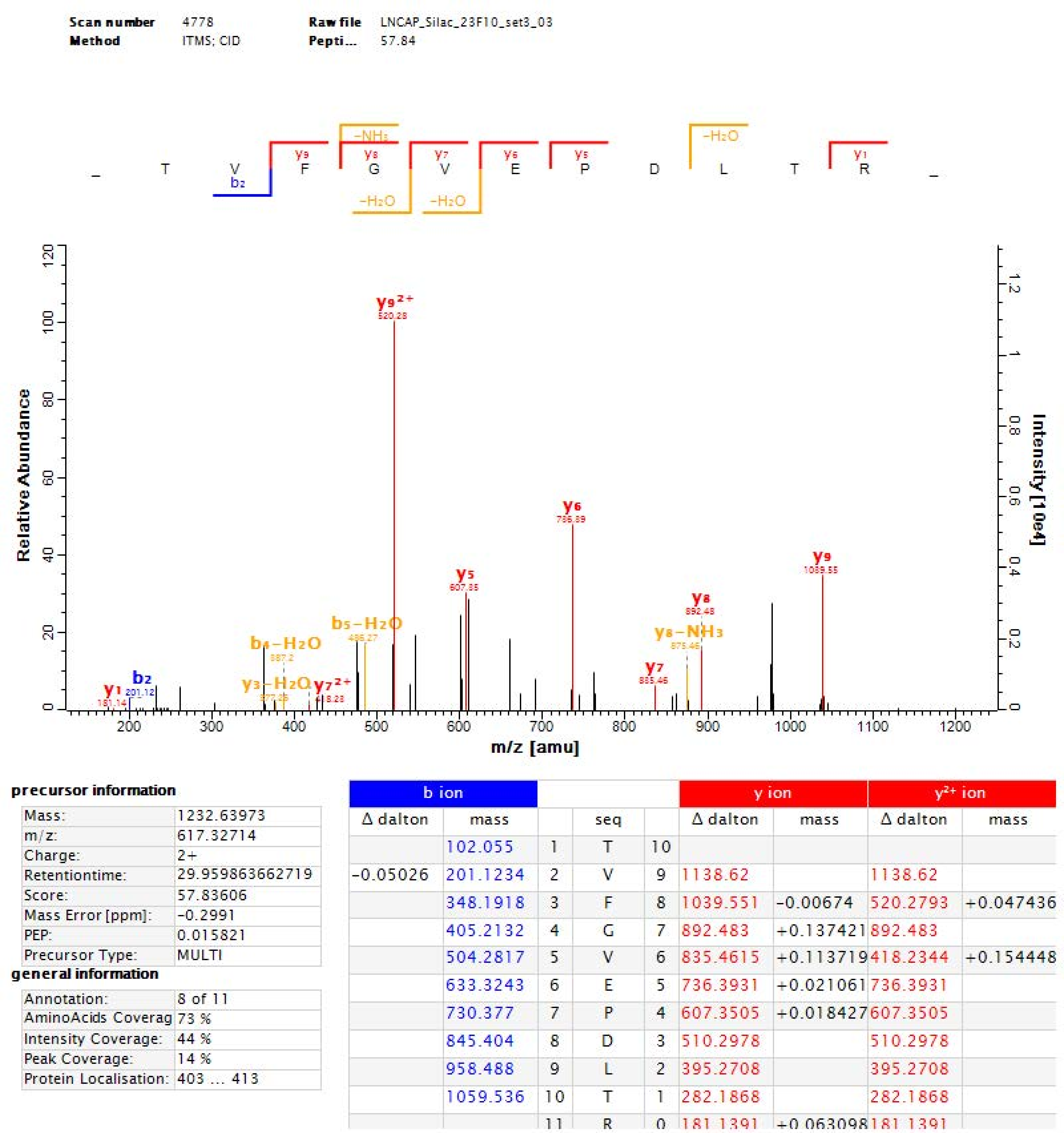
Scan number	477	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	133.89



precursor information

Mass:	1010.46697
m/z:	506.24076
Charge:	2+
Retentiontime:	7.8696284294128
Score:	133.8929
Mass Error [ppm]:	0.08114
PEP:	0.0010521
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	59 %
Peak Coverage:	22 %
Protein Localisation:	111 ... 119

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	88.0393		116.0342	1	D	8		
+0.11192	251.1026	-0.02217	279.0975	2	Y	7	904.4614	-0.17791
	365.1456	+0.114224	393.1405	3	N	6	741.3981	-0.04183
	464.214	-0.08401	492.2089	4	V	5	627.3552	-0.05823
	565.2617	+0.019738	593.2566	5	T	4	528.2868	-0.02699
	636.2988	+0.073689	664.2937	6	A	3	427.2391	+0.075625
	750.3417	+0.001953	778.3366	7	N	2	356.202	+0.063666
	837.3737		865.3686	8	S	1	242.159	+0.083019
				9	K	0	155.127	+0.007198



Scan number	4778	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	57.84

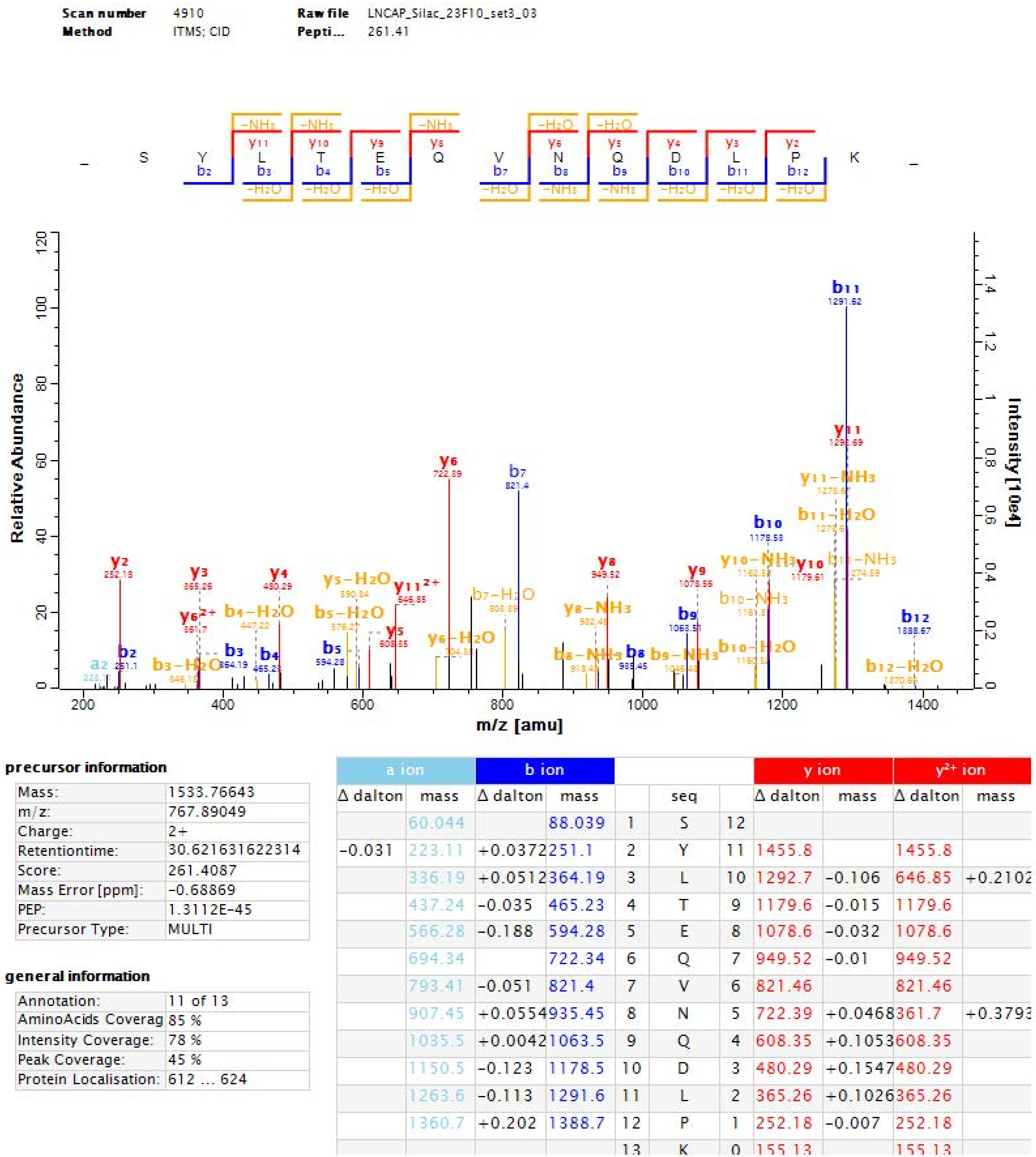
precursor information

Mass:	1232.63973
m/z:	617.32714
Charge:	2+
Retentiontime:	29.959863662719
Score:	57.83606
Mass Error [ppm]:	−0.2991
PEP:	0.015821
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	44 %
Peak Coverage:	14 %
Protein Localisation:	403 ... 413

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055	1	T	10				
−0.05026	201.1234	2	V	9	1138.62		1138.62	
	348.1918	3	F	8	1039.551	−0.00674	520.2793	+0.047436
	405.2132	4	G	7	892.483	+0.137421	892.483	
	504.2817	5	V	6	835.4615	+0.113719	418.2344	+0.154448
	633.3243	6	E	5	736.3931	+0.021061	736.3931	
	730.377	7	P	4	607.3505	+0.018427	607.3505	
	845.404	8	D	3	510.2978		510.2978	
	958.488	9	L	2	395.2708		395.2708	
	1059.536	10	T	1	282.1868		282.1868	
		11	R	0	181.1391	+0.063098	181.1391	



Scan number	4910	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	261.41

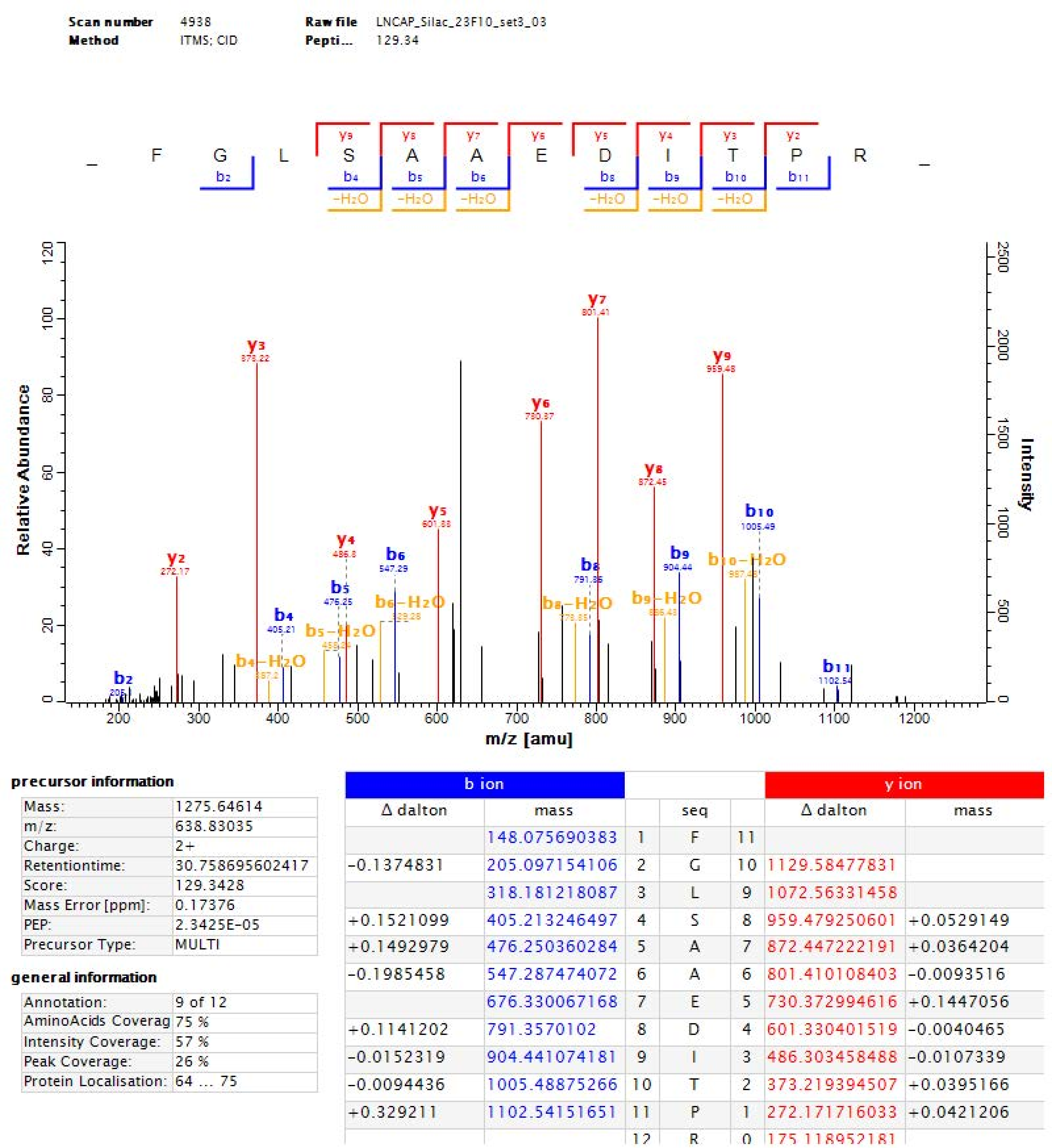
precursor information

Mass:	1533.76643
m/z:	767.89049
Charge:	2+
Retentiontime:	30.621631622314
Score:	261.4087
Mass Error [ppm]:	-0.68869
PEP:	1.3112E-45
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	78 %
Peak Coverage:	45 %
Protein Localisation:	612 ... 624

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	60.044		88.039	1	S	12				
-0.031	223.11	+0.0372	251.1	2	Y	11	1455.8		1455.8	
	336.19	+0.0512	364.19	3	L	10	1292.7	-0.106	646.85	+0.2102
	437.24	-0.035	465.23	4	T	9	1179.6	-0.015	1179.6	
	566.28	-0.188	594.28	5	E	8	1078.6	-0.032	1078.6	
	694.34		722.34	6	Q	7	949.52	-0.01	949.52	
	793.41	-0.051	821.4	7	V	6	821.46		821.46	
	907.45	+0.0554	935.45	8	N	5	722.39	+0.0468	361.7	+0.3793
	1035.5	+0.0042	1063.5	9	Q	4	608.35	+0.1053	608.35	
	1150.5	-0.123	1178.5	10	D	3	480.29	+0.1547	480.29	
	1263.6	-0.113	1291.6	11	L	2	365.26	+0.1026	365.26	
	1360.7	+0.202	1388.7	12	P	1	252.18	-0.007	252.18	
				13	K	0	155.13		155.13	



Scan number	4938	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	129.34

precursor information

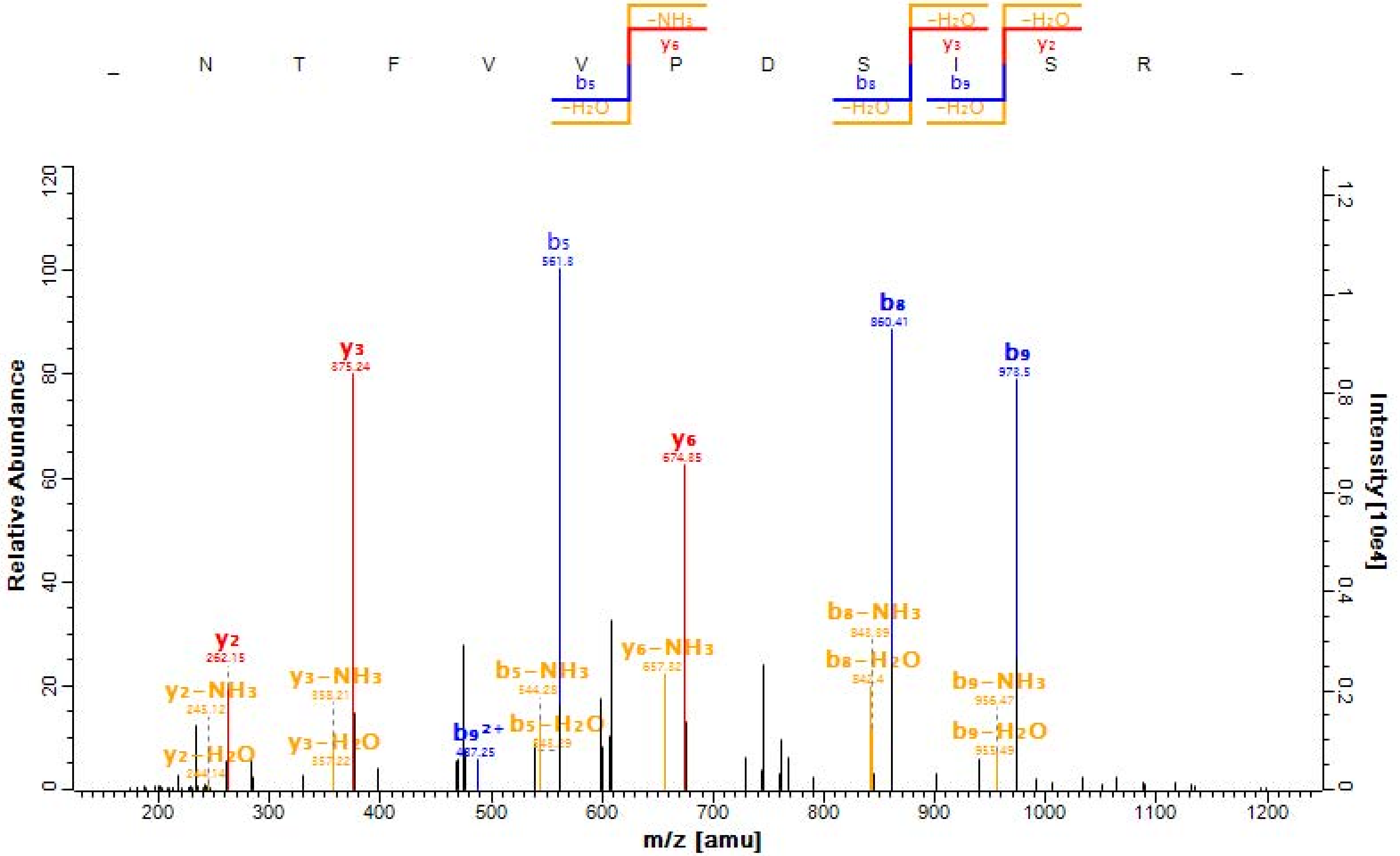
Mass:	1275.64614
m/z:	638.83035
Charge:	2+
Retentiontime:	30.758695602417
Score:	129.3428
Mass Error [ppm]:	0.17376
PEP:	2.3425E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	57 %
Peak Coverage:	26 %
Protein Localisation:	64 ... 75

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	148.075690383	1	F	11		
-0.1374831	205.097154106	2	G	10	1129.58477831	
	318.181218087	3	L	9	1072.56331458	
+0.1521099	405.213246497	4	S	8	959.479250601	+0.0529149
+0.1492979	476.250360284	5	A	7	872.447222191	+0.0364204
-0.1985458	547.287474072	6	A	6	801.410108403	-0.0093516
	676.330067168	7	E	5	730.372994616	+0.1447056
+0.1141202	791.3570102	8	D	4	601.330401519	-0.0040465
-0.0152319	904.441074181	9	I	3	486.303458488	-0.0107339
-0.0094436	1005.48875266	10	T	2	373.219394507	+0.0395166
+0.329211	1102.54151651	11	P	1	272.171716033	+0.0421206
		12	R	0	175.118952181	

Scan number	4967	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	101.38



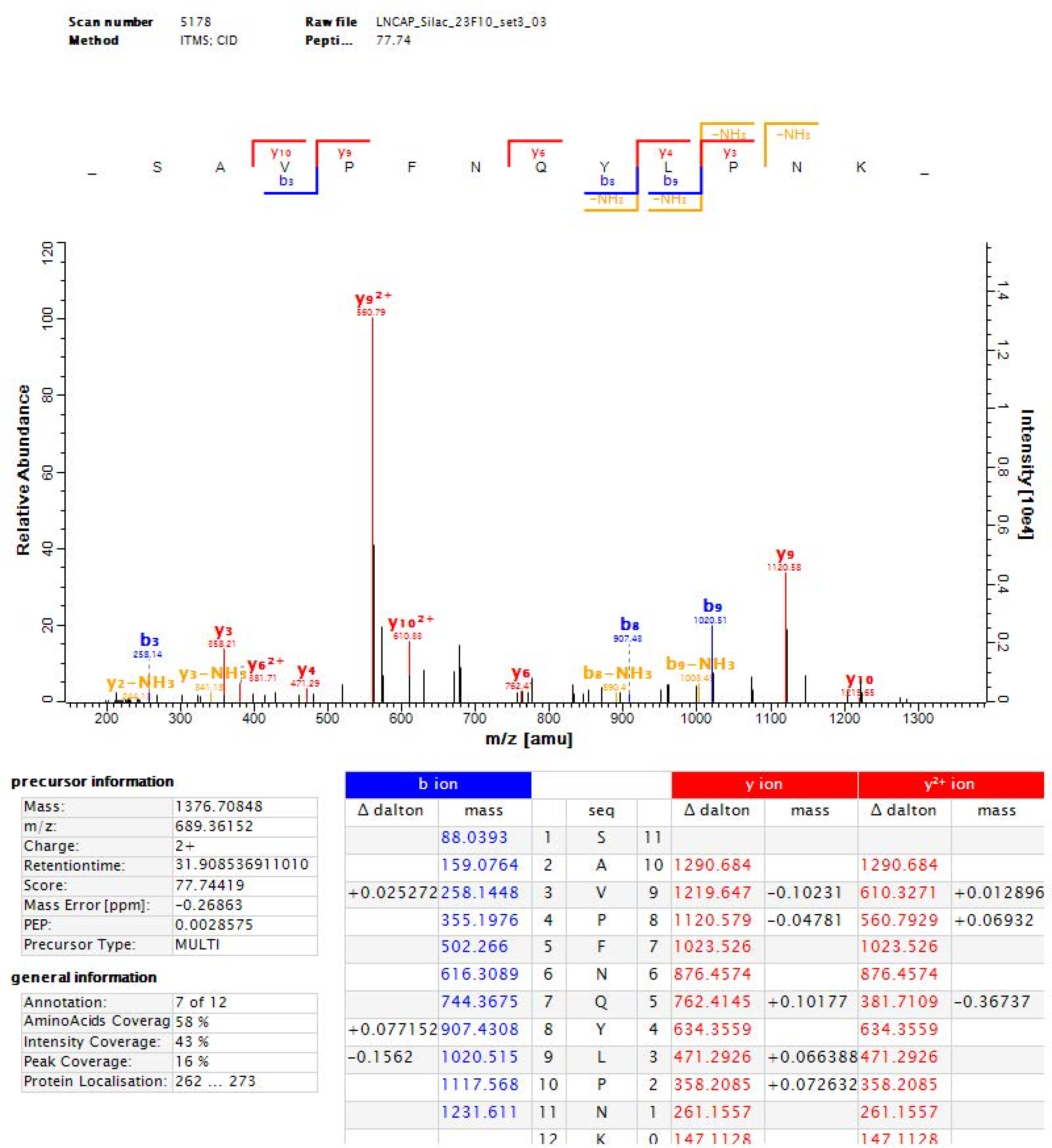
precursor information

Mass:	1233.63485
m/z:	617.8247
Charge:	2+
Retentiontime:	30.89404296875
Score:	101.3808
Mass Error [ppm]:	-0.40556
PEP:	0.0030244
Precursor Type:	ISO

general information

Annotation:	6 of 11
AminoAcids Coverag	55 %
Intensity Coverage:	61 %
Peak Coverage:	20 %
Protein Localisation:	99 ... 109

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	115.0502		115.0502	1	N	10		
	216.0979		216.0979	2	T	9	1120.6	
	363.1663		363.1663	3	F	8	1019.552	
	462.2347		462.2347	4	V	7	872.4836	
	561.3031	-0.04623	561.3031	5	V	6	773.4152	
	658.3559		658.3559	6	P	5	674.3468	+0.006919
	773.3828		773.3828	7	D	4	577.294	
	860.4149	+0.023861	860.4149	8	S	3	462.2671	
+0.209119	487.2531	-0.02822	973.4989	9	I	2	375.235	-0.0246
	1060.531		1060.531	10	S	1	262.151	+0.015066
				11	R	0	175.119	



Scan number	5178	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	77.74

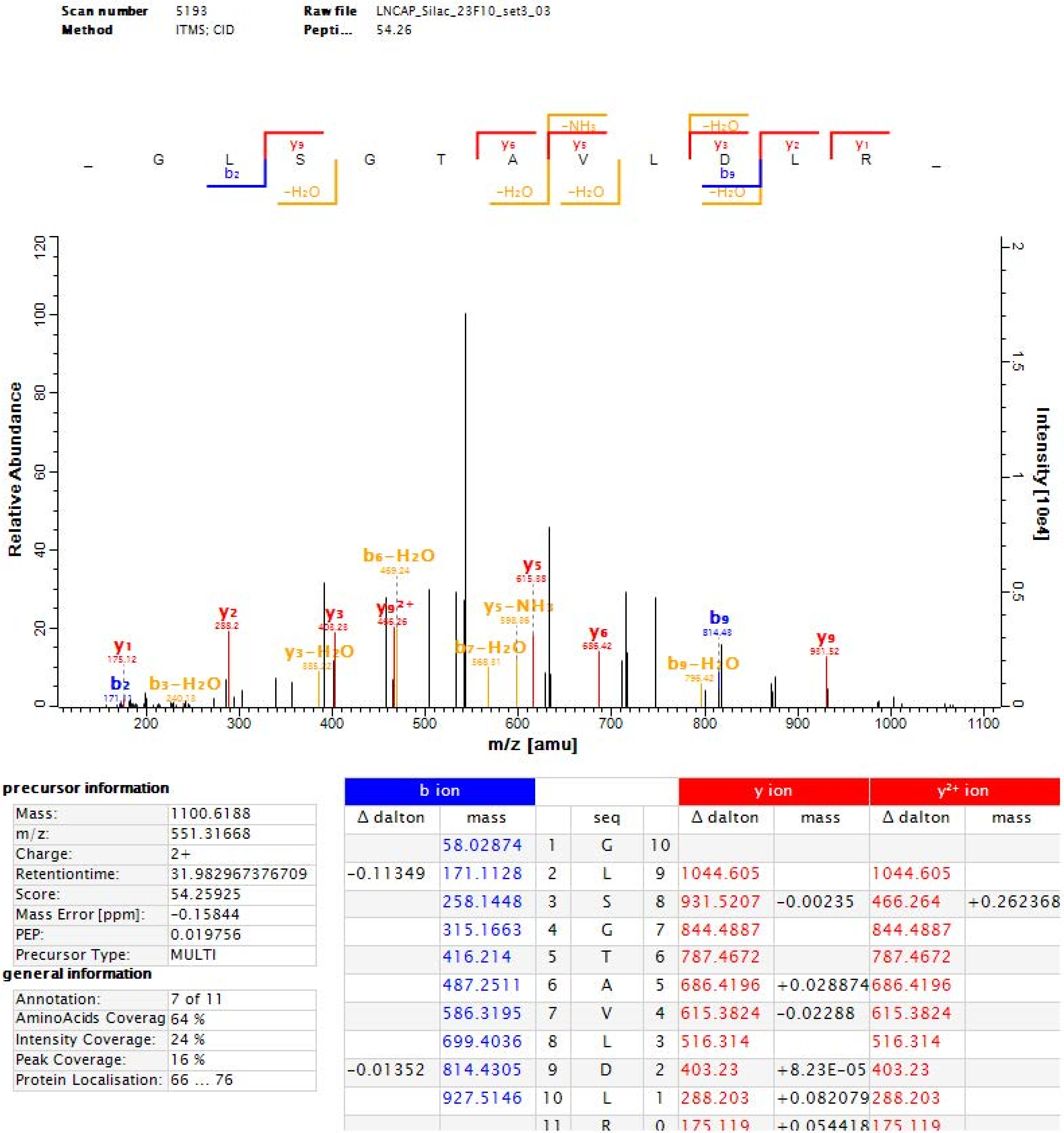
precursor information

Mass:	1376.70848
m/z:	689.36152
Charge:	2+
Retentiontime:	31.908536911010
Score:	77.74419
Mass Error [ppm]:	-0.26863
PEP:	0.0028575
Precursor Type:	MULTI

general information

Annotation:	7 of 12
AminoAcids Coverag	58 %
Intensity Coverage:	43 %
Peak Coverage:	16 %
Protein Localisation:	262 ... 273

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	11				
	159.0764	2	A	10	1290.684		1290.684	
+0.025272	258.1448	3	V	9	1219.647	-0.10231	610.3271	+0.012896
	355.1976	4	P	8	1120.579	-0.04781	560.7929	+0.06932
	502.266	5	F	7	1023.526		1023.526	
	616.3089	6	N	6	876.4574		876.4574	
	744.3675	7	Q	5	762.4145	+0.10177	381.7109	-0.36737
+0.077152	907.4308	8	Y	4	634.3559		634.3559	
-0.1562	1020.515	9	L	3	471.2926	+0.066388	471.2926	
	1117.568	10	P	2	358.2085	+0.072632	358.2085	
	1231.611	11	N	1	261.1557		261.1557	
		12	K	0	147.1128		147.1128	



Scan number 5193
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set3_03
Pepti... 54.26

precursor information

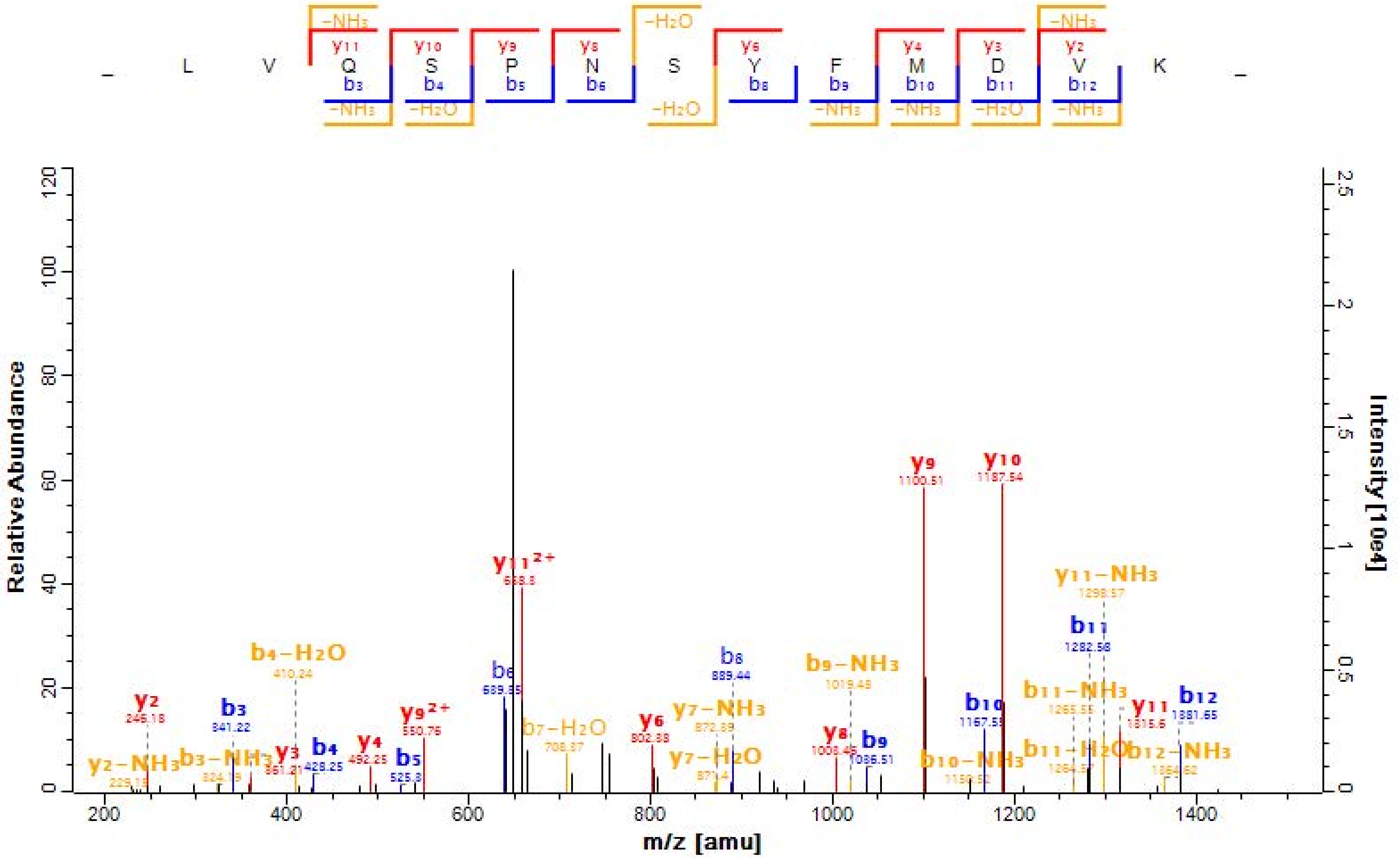
Mass:	1100.6188
m/z:	551.31668
Charge:	2+
Retentiontime:	31.982967376709
Score:	54.25925
Mass Error [ppm]:	-0.15844
PEP:	0.019756
Precursor Type:	MULTI

general information

Annotation:	7 of 11
AminoAcids Coverag	64 %
Intensity Coverage:	24 %
Peak Coverage:	16 %
Protein Localisation:	66 ... 76

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	10				
-0.11349	171.1128	2	L	9	1044.605		1044.605	
	258.1448	3	S	8	931.5207	-0.00235	466.264	+0.262368
	315.1663	4	G	7	844.4887		844.4887	
	416.214	5	T	6	787.4672		787.4672	
	487.2511	6	A	5	686.4196	+0.028874	686.4196	
	586.3195	7	V	4	615.3824	-0.02288	615.3824	
	699.4036	8	L	3	516.314		516.314	
-0.01352	814.4305	9	D	2	403.23	+8.23E-05	403.23	
	927.5146	10	L	1	288.203	+0.082079	288.203	
		11	R	0	175.119	+0.054418	175.119	

Scan number	5522	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	181.71



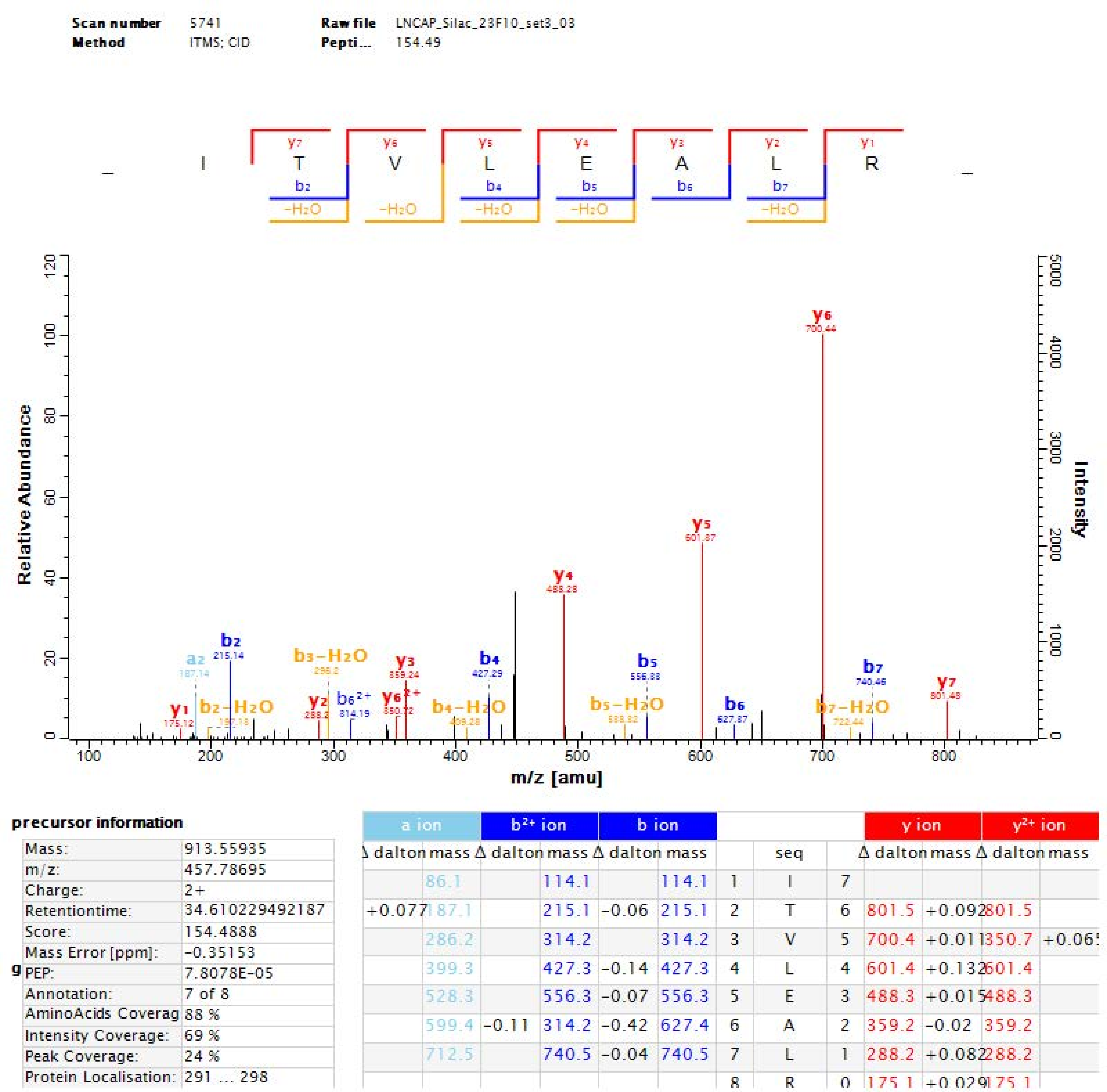
precursor information

Mass:	1526.7436
m/z:	764.37908
Charge:	2+
Retentiontime:	33.554782867431
Score:	181.7068
Mass Error [ppm]:	-0.20582
PEP:	2.2267E-12
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	54 %
Peak Coverage:	42 %
Protein Localisation:	24 ... 36

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	12				
	213.1598	2	V	11	1414.667		1414.667	
+0.022208	341.2183	3	Q	10	1315.599	+0.062541	658.303	+0.018965
+0.137396	428.2504	4	S	9	1187.54	-0.04746	1187.54	
-0.18148	525.3031	5	P	8	1100.508	-0.07549	550.7577	+0.137877
+0.03377	639.3461	6	N	7	1003.455	+0.107644	1003.455	
	726.3781	7	S	6	889.4124		889.4124	
+0.051267	889.4414	8	Y	5	802.3804	-0.03536	802.3804	
+0.108586	1036.51	9	F	4	639.3171		639.3171	
-0.04628	1167.55	10	M	3	492.2486	+0.099133	492.2486	
-0.23362	1282.577	11	D	2	361.2082	+0.050811	361.2082	
+0.115322	1381.646	12	V	1	246.1812	+0.027858	246.1812	
		13	K	0	147.1128		147.1128	



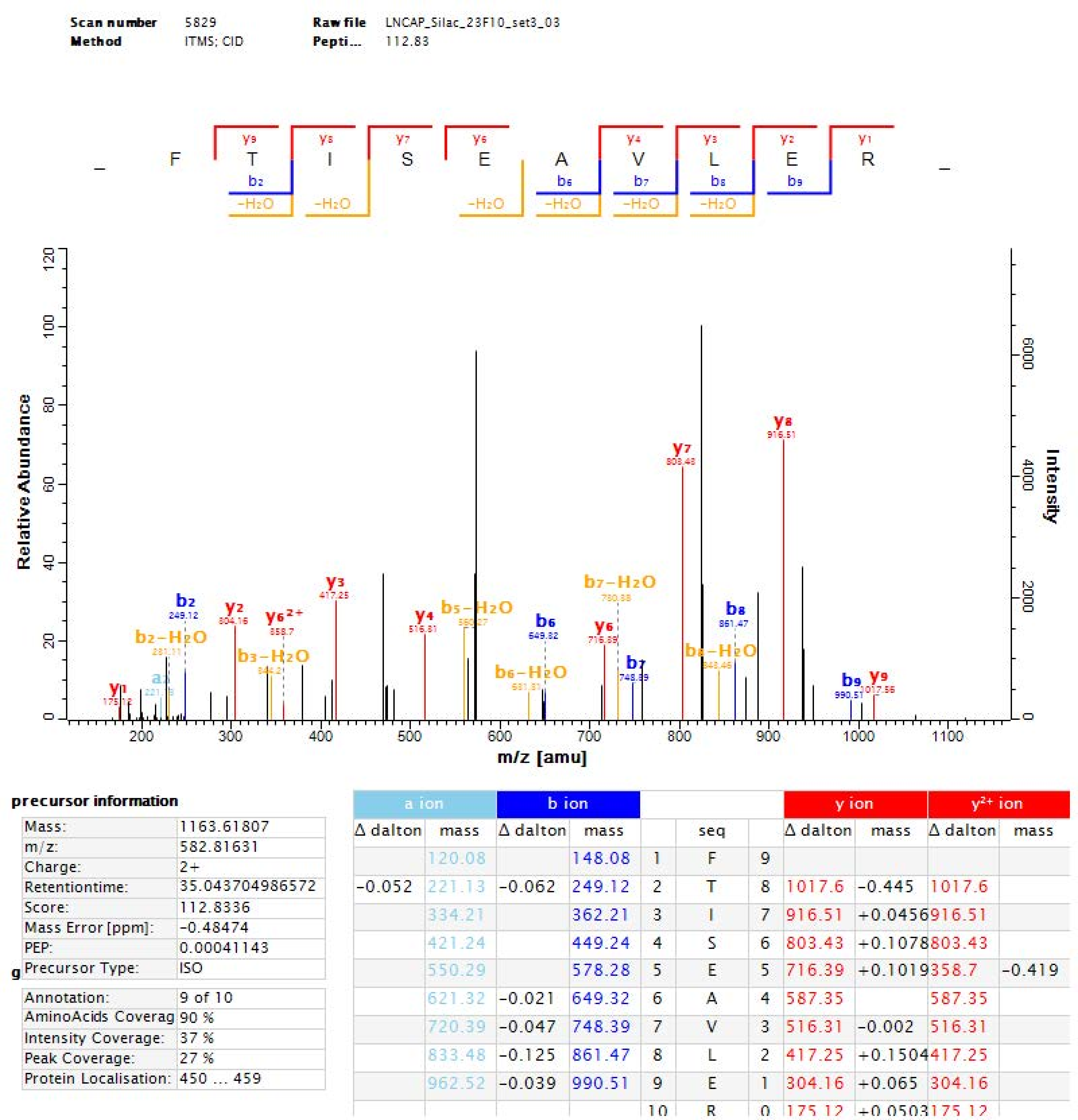
Scan number	5741	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	154.49

g

precursor information

Mass:	913.55935
m/z:	457.78695
Charge:	2+
Retentiontime:	34.610229492187
Score:	154.4888
Mass Error [ppm]:	-0.35153
PEP:	7.8078E-05
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	69 %
Peak Coverage:	24 %
Protein Localisation:	291 ... 298

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	I	7				
+0.077	187.1		215.1	-0.06	215.1	2	T	6	801.5	+0.092	801.5	
	286.2		314.2		314.2	3	V	5	700.4	+0.011	350.7	+0.06
	399.3		427.3	-0.14	427.3	4	L	4	601.4	+0.132	601.4	
	528.3		556.3	-0.07	556.3	5	E	3	488.3	+0.015	488.3	
	599.4	-0.11	314.2	-0.42	627.4	6	A	2	359.2	-0.02	359.2	
	712.5		740.5	-0.04	740.5	7	L	1	288.2	+0.082	288.2	
						8	R	0	175.1	+0.029	175.1	



Scan number 5829 **Raw file** LNCAP_Silac_23F10_set3_03
Method ITMS; CID **Pepti…** 112.83

precursor information

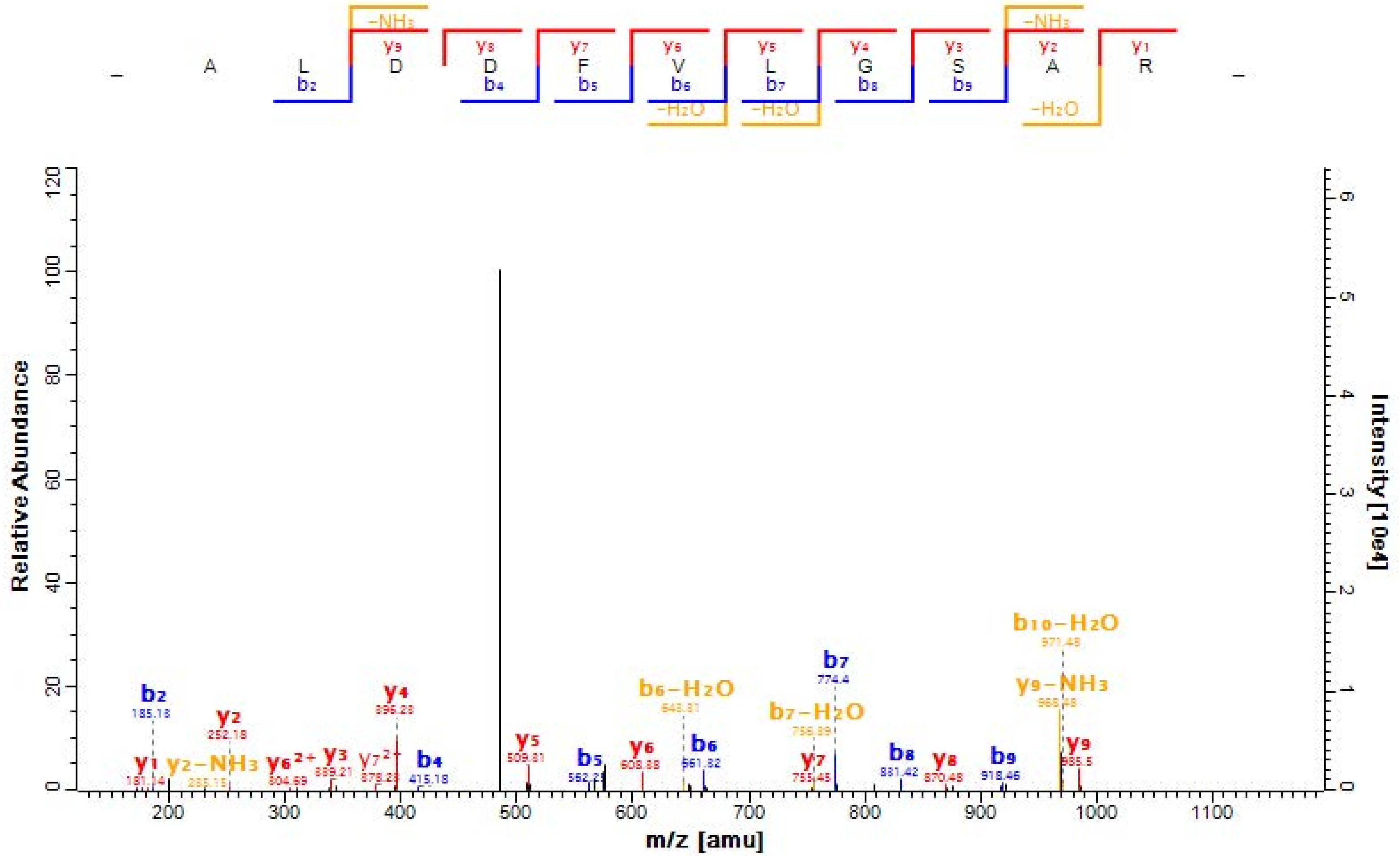
Mass:	1163.61807
m/z:	582.81631
Charge:	2+
Retentiontime:	35.043704986572
Score:	112.8336
Mass Error [ppm]:	-0.48474
PEP:	0.00041143
Precursor Type:	ISO

g

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	37 %
Peak Coverage:	27 %
Protein Localisation:	450 … 459

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08		148.08	1	F	9				
-0.052	221.13	-0.062	249.12	2	T	8	1017.6	-0.445	1017.6	
	334.21		362.21	3	I	7	916.51	+0.0456	916.51	
	421.24		449.24	4	S	6	803.43	+0.1078	803.43	
	550.29		578.28	5	E	5	716.39	+0.1019	358.7	-0.419
	621.32	-0.021	649.32	6	A	4	587.35		587.35	
	720.39	-0.047	748.39	7	V	3	516.31	-0.002	516.31	
	833.48	-0.125	861.47	8	L	2	417.25	+0.1504	417.25	
	962.52	-0.039	990.51	9	E	1	304.16	+0.065	304.16	
				10	R	0	175.12	+0.0503	175.12	

Scan number	5915	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	142.07



precursor information

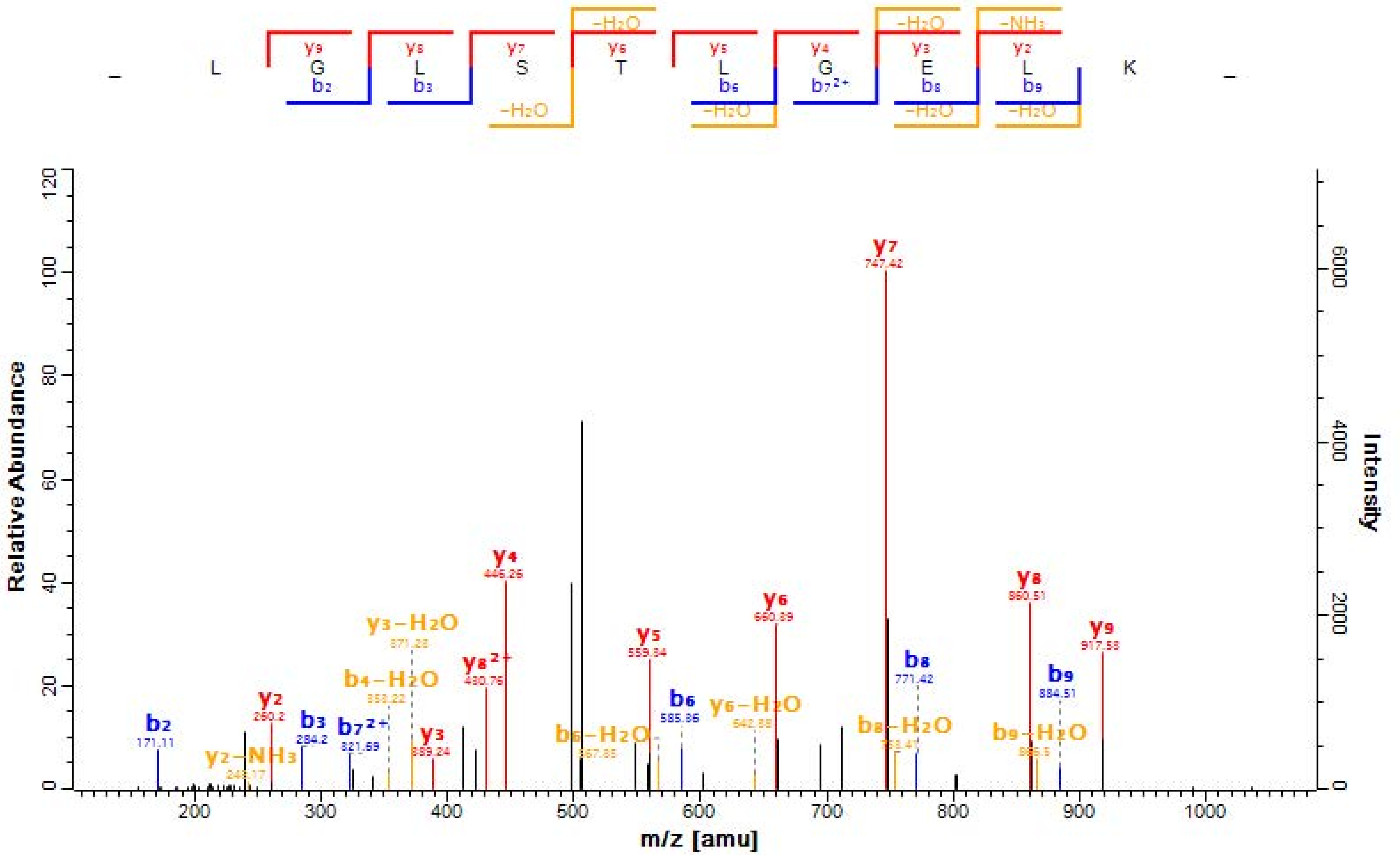
Mass:	0
m/z:	585.31634
Charge:	0+
Retentiontime:	35.460304260253
Score:	142.0682
Mass Error [ppm]:	-0.19801
PEP:	3.0592E-06
Precursor Type:	PEAK

general information

Annotation:	10 of 11
AminoAcids Coverag	91 %
Intensity Coverage:	30 %
Peak Coverage:	28 %
Protein Localisation:	11 ... 21

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	10				
-0.01974	185.1285	2	L	9	1098.589		1098.589	
	300.1554	3	D	8	985.5045	-0.06739	985.5045	
-0.04294	415.1823	4	D	7	870.4775	+0.098406	870.4775	
+0.222451	562.2508	5	F	6	755.4506	+0.035993	378.2289	+0.080765
-0.02956	661.3192	6	V	5	608.3822	+0.06504	304.6947	-0.44619
-0.05698	774.4032	7	L	4	509.3138	+0.082428	509.3138	
+0.015551	831.4247	8	G	3	396.2297	+0.005603	396.2297	
-0.03869	918.4567	9	S	2	339.2082	+0.103422	339.2082	
	989.4938	10	A	1	252.1762	+0.016539	252.1762	
		11	R	0	181.1391	-0.08032	181.1391	

Scan number	5926	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	145.99



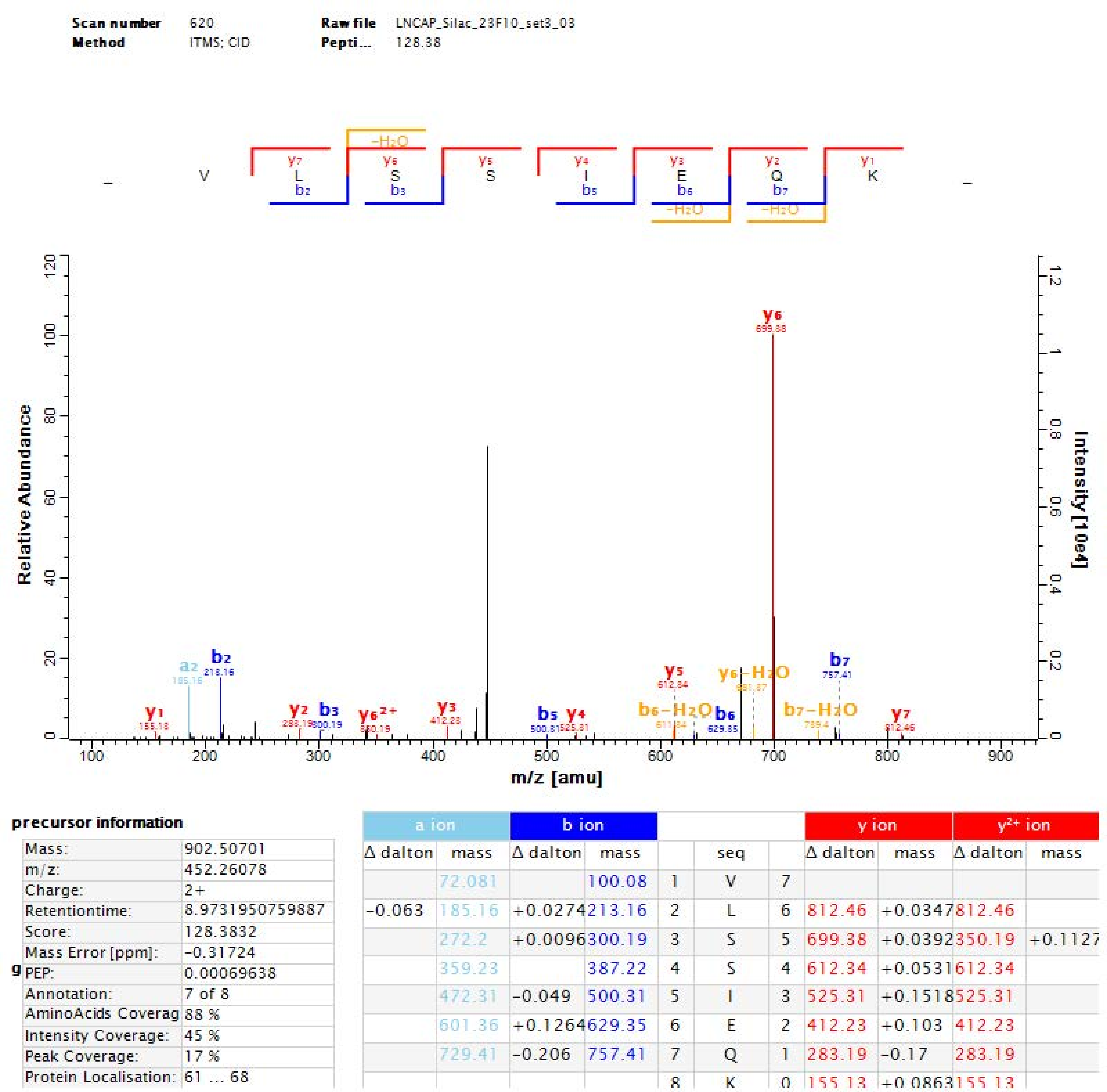
precursor information

Mass:	1029.607
m/z:	515.81078
Charge:	2+
Retentiontime:	35.512763977050
Score:	145.9875
Mass Error [ppm]:	-0.009931
PEP:	0.00017417
Precursor Type:	MULTI

g

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	56 %
Peak Coverage:	28 %
Protein Localisation:	81 ... 90

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	9				
	171.11	+0.0285	171.11	2	G	8	917.53	+0.0201	917.53	
	284.2	-0.049	284.2	3	L	7	860.51	-0.013	430.76	+0.1884
	371.23		371.23	4	S	6	747.42	+0.0054	747.42	
	472.28		472.28	5	T	5	660.39	-0.039	660.39	
	585.36	-0.023	585.36	6	L	4	559.34	+0.1371	559.34	
+0.2933	321.69		642.38	7	G	3	446.26	+0.0547	446.26	
	771.42	-0.123	771.42	8	E	2	389.24	+0.0618	389.24	
	884.51	-0.135	884.51	9	L	1	260.2	+0.0319	260.2	
				10	K	0	147.11		147.11	

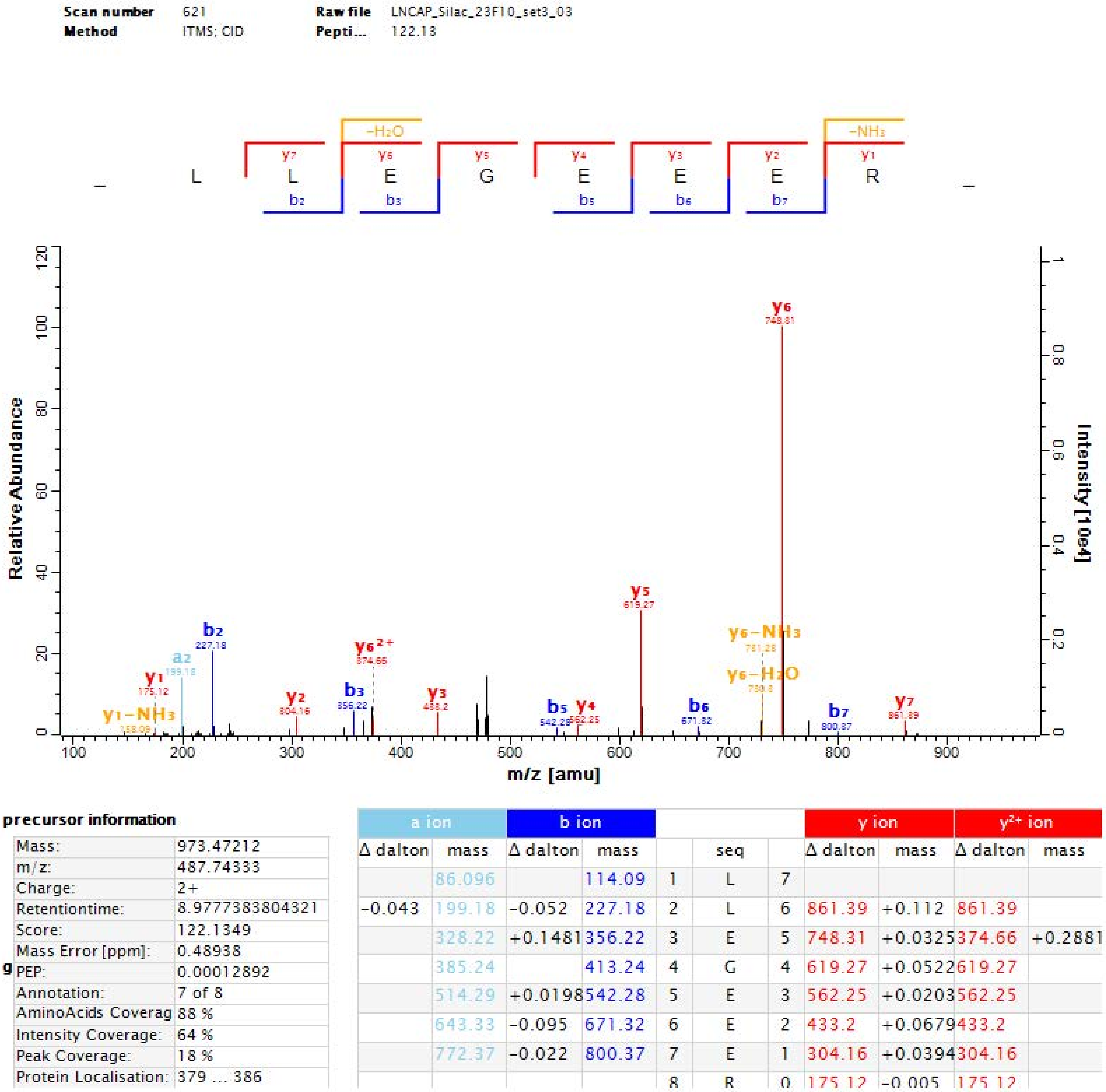


Scan number	620	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	128.38

precursor information

Mass:	902.50701
m/z:	452.26078
Charge:	2+
Retentiontime:	8.9731950759887
Score:	128.3832
Mass Error [ppm]:	-0.31724
PEP:	0.00069638
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	45 %
Peak Coverage:	17 %
Protein Localisation:	61 ... 68

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.081		100.08	1	V	7				
-0.063	185.16	+0.0274	213.16	2	L	6	812.46	+0.0347	812.46	
	272.2	+0.0096	300.19	3	S	5	699.38	+0.0392	350.19	+0.1127
	359.23		387.22	4	S	4	612.34	+0.0531	612.34	
	472.31	-0.049	500.31	5	I	3	525.31	+0.1518	525.31	
	601.36	+0.1264	629.35	6	E	2	412.23	+0.103	412.23	
	729.41	-0.206	757.41	7	Q	1	283.19	-0.17	283.19	
				8	K	0	155.13	+0.0863	155.13	

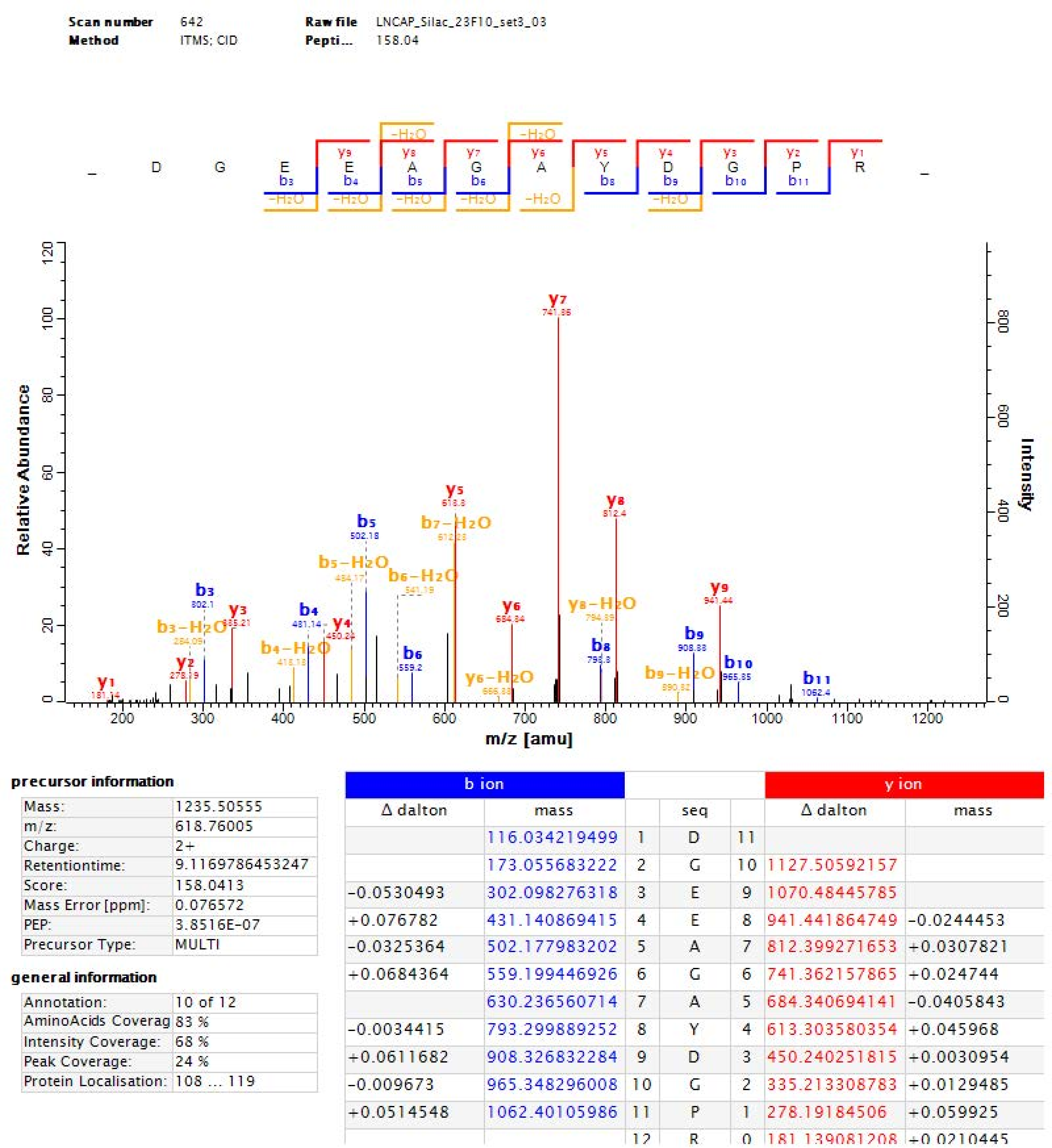


Scan number	621	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	122.13

precursor information

Mass:	973.47212
m/z:	487.74333
Charge:	2+
Retentiontime:	8.9777383804321
Score:	122.1349
Mass Error [ppm]:	0.48938
PEP:	0.00012892
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	64 %
Peak Coverage:	18 %
Protein Localisation:	379 ... 386

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	7				
-0.043	199.18	-0.052	227.18	2	L	6	861.39	+0.112	861.39	
	328.22	+0.1481	356.22	3	E	5	748.31	+0.0325	374.66	+0.2881
	385.24		413.24	4	G	4	619.27	+0.0522	619.27	
	514.29	+0.0198	542.28	5	E	3	562.25	+0.0203	562.25	
	643.33	-0.095	671.32	6	E	2	433.2	+0.0679	433.2	
	772.37	-0.022	800.37	7	E	1	304.16	+0.0394	304.16	
				8	R	0	175.12	-0.005	175.12	



Scan number	642	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	158.04

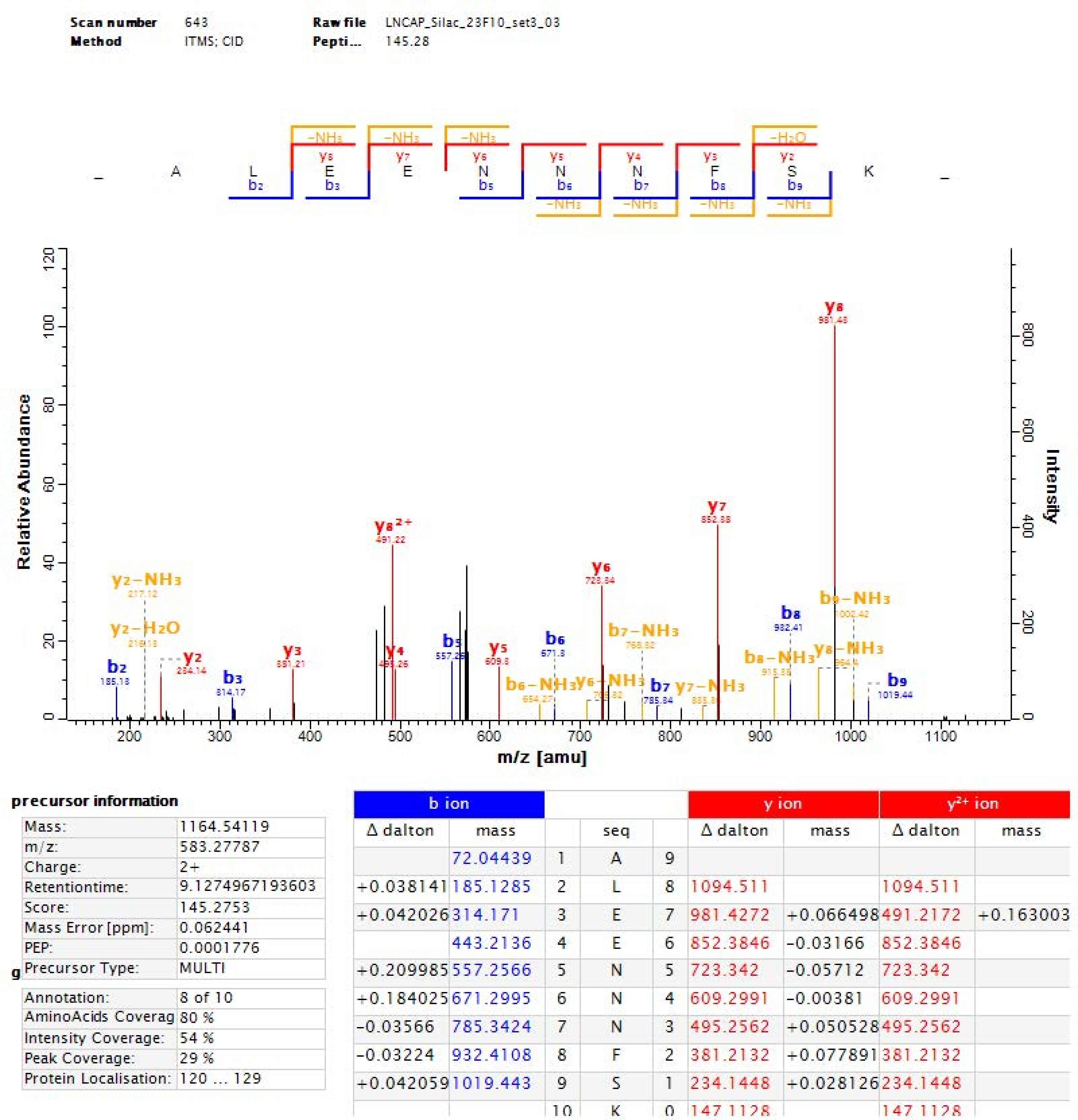
precursor information

Mass:	1235.50555
m/z:	618.76005
Charge:	2+
Retentiontime:	9.1169786453247
Score:	158.0413
Mass Error [ppm]:	0.076572
PEP:	3.8516E-07
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	68 %
Peak Coverage:	24 %
Protein Localisation:	108 ... 119

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	116.034219499	1	D	11		
	173.055683222	2	G	10	1127.50592157	
-0.0530493	302.098276318	3	E	9	1070.48445785	
+0.076782	431.140869415	4	E	8	941.441864749	-0.0244453
-0.0325364	502.177983202	5	A	7	812.399271653	+0.0307821
+0.0684364	559.199446926	6	G	6	741.362157865	+0.024744
	630.236560714	7	A	5	684.340694141	-0.0405843
-0.0034415	793.299889252	8	Y	4	613.303580354	+0.045968
+0.0611682	908.326832284	9	D	3	450.240251815	+0.0030954
-0.009673	965.348296008	10	G	2	335.213308783	+0.0129485
+0.0514548	1062.40105986	11	P	1	278.19184506	+0.059925
		12	R	0	181.139081208	+0.0210445



Scan number 643 **Raw file** LNCAP_Silac_23F10_set3_03

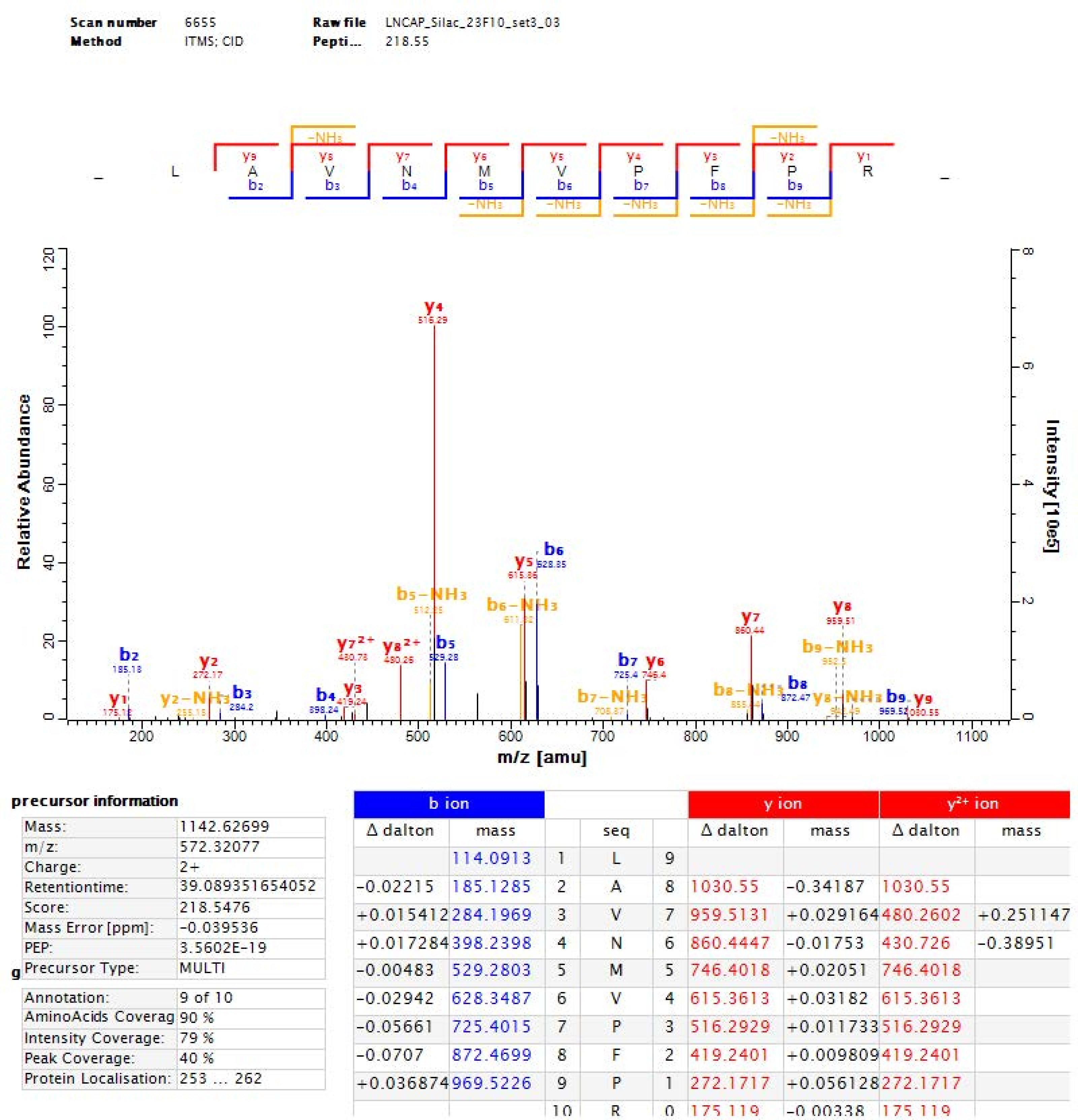
Method ITMS; CID **Pepti...** 145.28

precursor information

Mass:	1164.54119
m/z:	583.27787
Charge:	2+
Retentiontime:	9.1274967193603
Score:	145.2753
Mass Error [ppm]:	0.062441
PEP:	0.0001776
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	54 %
Peak Coverage:	29 %
Protein Localisation:	120 ... 129

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	9				
+0.038141	185.1285	2	L	8	1094.511		1094.511	
+0.042026	314.171	3	E	7	981.4272	+0.066498	491.2172	+0.163003
	443.2136	4	E	6	852.3846	-0.03166	852.3846	
+0.209985	557.2566	5	N	5	723.342	-0.05712	723.342	
+0.184025	671.2995	6	N	4	609.2991	-0.00381	609.2991	
-0.03566	785.3424	7	N	3	495.2562	+0.050528	495.2562	
-0.03224	932.4108	8	F	2	381.2132	+0.077891	381.2132	
+0.042059	1019.443	9	S	1	234.1448	+0.028126	234.1448	
		10	K	0	147.1128		147.1128	



Scan number	6655	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	218.55

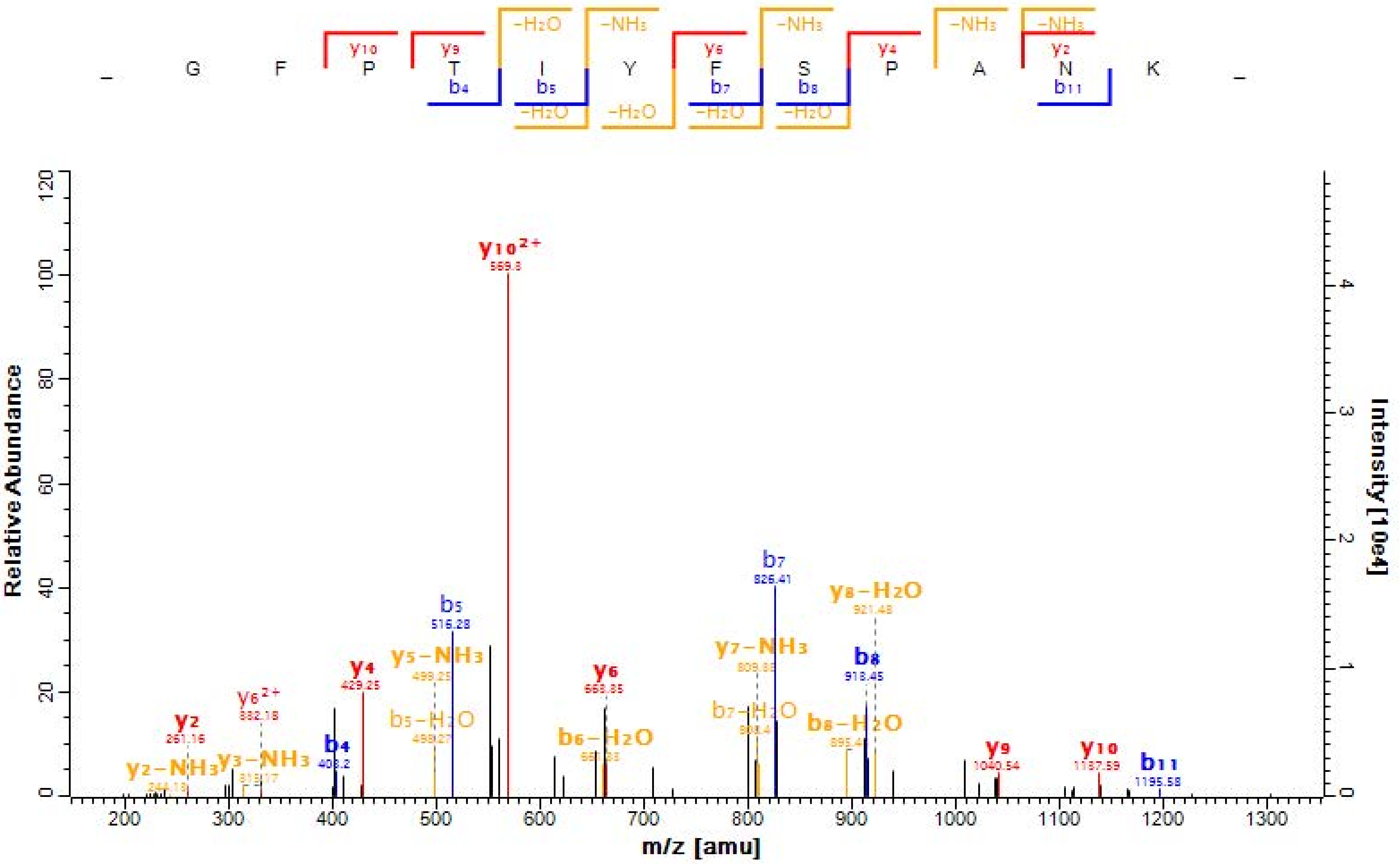
precursor information

Mass:	1142.62699
m/z:	572.32077
Charge:	2+
Retentiontime:	39.089351654052
Score:	218.5476
Mass Error [ppm]:	-0.039536
PEP:	3.5602E-19
Precursor Type:	MULTI

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	79 %
Peak Coverage:	40 %
Protein Localisation:	253 ... 262

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	9				
-0.02215	185.1285	2	A	8	1030.55	-0.34187	1030.55	
+0.015412	284.1969	3	V	7	959.5131	+0.029164	480.2602	+0.251147
+0.017284	398.2398	4	N	6	860.4447	-0.01753	430.726	-0.38951
-0.00483	529.2803	5	M	5	746.4018	+0.02051	746.4018	
-0.02942	628.3487	6	V	4	615.3613	+0.03182	615.3613	
-0.05661	725.4015	7	P	3	516.2929	+0.011733	516.2929	
-0.0707	872.4699	8	F	2	419.2401	+0.009809	419.2401	
+0.036874	969.5226	9	P	1	272.1717	+0.056128	272.1717	
		10	R	0	175.119	-0.00338	175.119	

Scan number	6854	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	100.04



precursor information

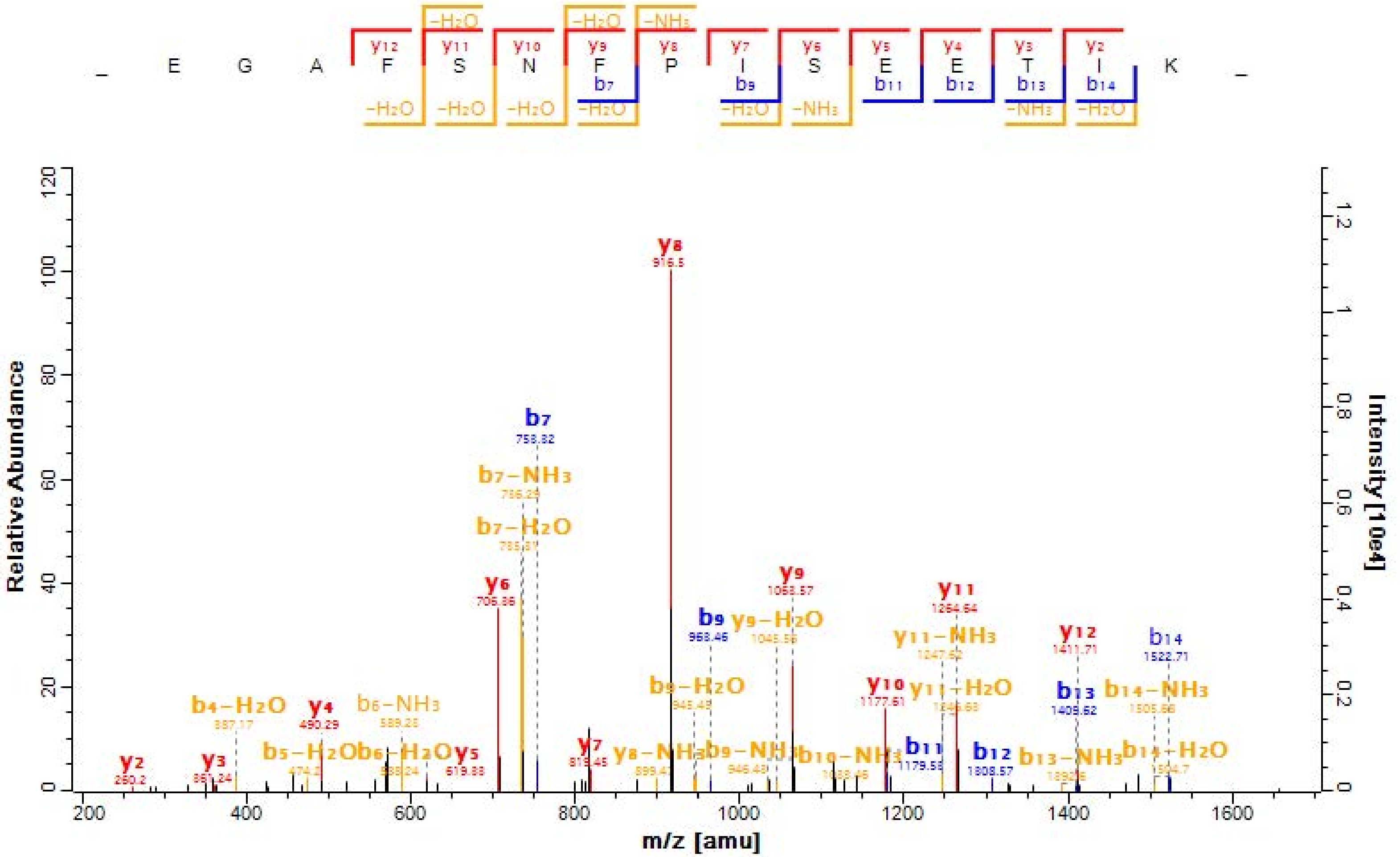
Mass:	1340.67604
m/z:	671.3453
Charge:	2+
Retentiontime:	40.038631439209
Score:	100.037
Mass Error [ppm]:	-0.33175
PEP:	0.00027665
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	53 %
Peak Coverage:	26 %
Protein Localisation:	449 ... 460

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	11				
	205.0972	2	F	10	1284.662		1284.662	
	302.1499	3	P	9	1137.594	-0.07313	569.3006	+0.229387
+0.099401	403.1976	4	T	8	1040.541	-0.00401	1040.541	
+0.083513	516.2817	5	I	7	939.4934		939.4934	
	679.345	6	Y	6	826.4094		826.4094	
+0.009449	826.4134	7	F	5	663.3461	+0.083453	332.1767	-0.00265
+0.03046	913.4454	8	S	4	516.2776		516.2776	
	1010.498	9	P	3	429.2456	+0.034359	429.2456	
	1081.535	10	A	2	332.1928		332.1928	
-0.07787	1195.578	11	N	1	261.1557	+0.269653	261.1557	
		12	K	0	147.1128		147.1128	

Scan number	6929	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	152.07



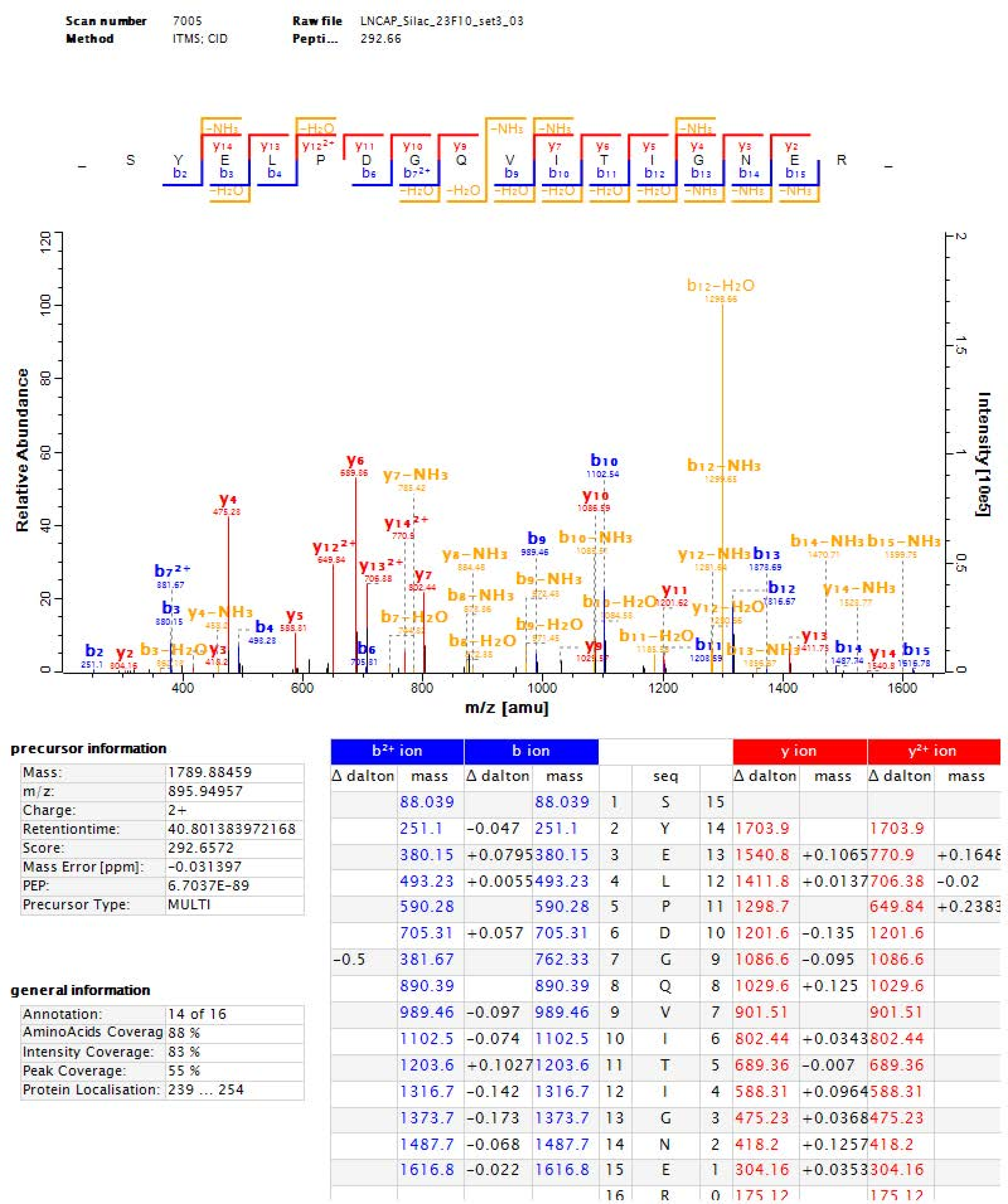
precursor information

Mass:	1667.80435
m/z:	834.90945
Charge:	2+
Retentiontime:	40.412994384765
Score:	152.0666
Mass Error [ppm]:	0.047337
PEP:	4.1526E-09
Precursor Type:	ISO

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	63 %
Peak Coverage:	39 %
Protein Localisation:	185 ... 199

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	130.049869563	1	E	14		
	187.071333286	2	G	13	1539.76895026	
	258.108447074	3	A	12	1482.74748654	
	405.17686099	4	F	11	1411.71037275	-0.0630339
	492.2088894	5	S	10	1264.64195883	-0.0749422
	606.251816848	6	N	9	1177.60993042	-0.0777039
+0.0348107	753.320230764	7	F	8	1063.56700298	-0.0231797
	850.372994616	8	P	7	916.49858906	-0.0023122
+0.1023286	963.457058596	9	I	6	819.445825208	+0.0013794
	1050.48908701	10	S	5	706.361761227	+0.0288638
-0.1891508	1179.5316801	11	E	4	619.329732818	+0.027628
-0.348321	1308.5742732	12	E	3	490.287139721	-0.0578917
-0.1036411	1409.62195167	13	T	2	361.244546625	+0.1982329
-0.2284766	1522.70601565	14	I	1	260.196868151	-0.0816643
		15	K	0	147.112804171	



Scan number	7005	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	292.66

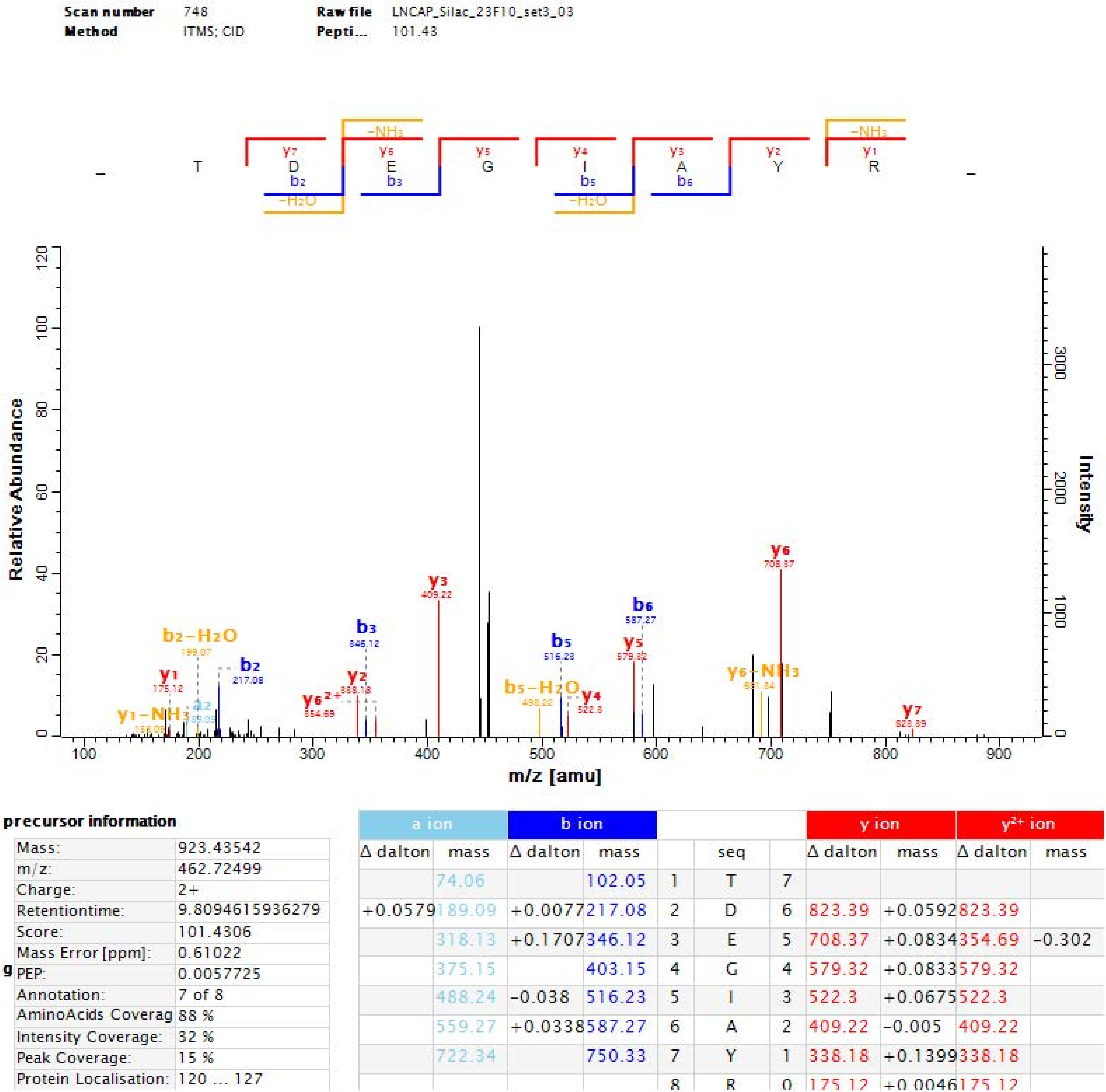
precursor information

Mass:	1789.88459
m/z:	895.94957
Charge:	2+
Retentiontime:	40.801383972168
Score:	292.6572
Mass Error [ppm]:	-0.031397
PEP:	6.7037E-89
Precursor Type:	MULTI

general information

Annotation:	14 of 16
AminoAcids Coverag	88 %
Intensity Coverage:	83 %
Peak Coverage:	55 %
Protein Localisation:	239 ... 254

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	15				
	251.1	-0.047	251.1	2	Y	14	1703.9		1703.9	
	380.15	+0.0795	380.15	3	E	13	1540.8	+0.1065	770.9	+0.1648
	493.23	+0.0055	493.23	4	L	12	1411.8	+0.0137	706.38	-0.02
	590.28		590.28	5	P	11	1298.7		649.84	+0.2383
	705.31	+0.057	705.31	6	D	10	1201.6	-0.135	1201.6	
-0.5	381.67		762.33	7	G	9	1086.6	-0.095	1086.6	
	890.39		890.39	8	Q	8	1029.6	+0.125	1029.6	
	989.46	-0.097	989.46	9	V	7	901.51		901.51	
	1102.5	-0.074	1102.5	10	I	6	802.44	+0.0343	802.44	
	1203.6	+0.1027	1203.6	11	T	5	689.36	-0.007	689.36	
	1316.7	-0.142	1316.7	12	I	4	588.31	+0.0964	588.31	
	1373.7	-0.173	1373.7	13	G	3	475.23	+0.0368	475.23	
	1487.7	-0.068	1487.7	14	N	2	418.2	+0.1257	418.2	
	1616.8	-0.022	1616.8	15	E	1	304.16	+0.0353	304.16	
				16	R	0	175.12		175.12	



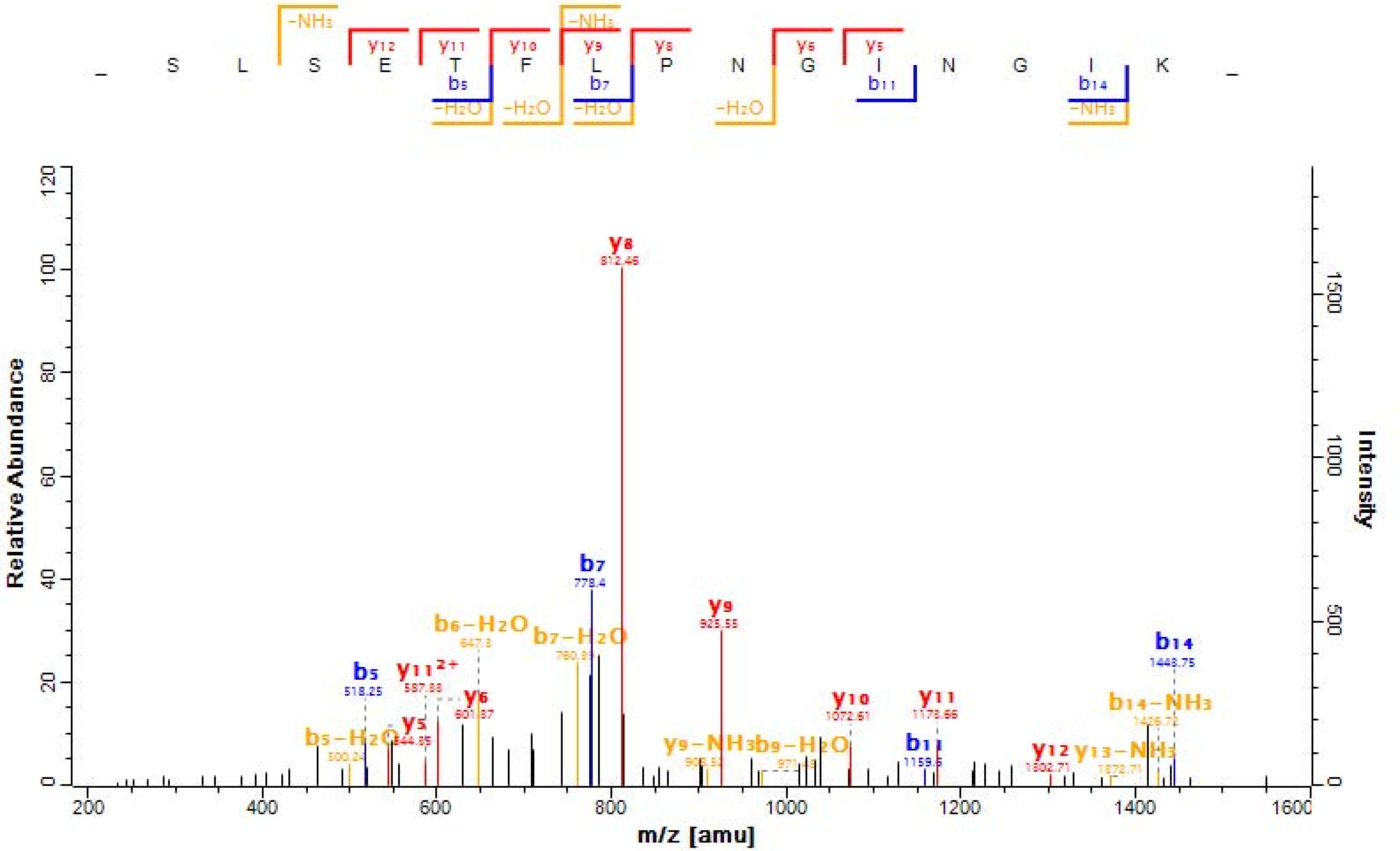
Scan number	748	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	101.43

precursor information

Mass:	923.43542
m/z:	462.72499
Charge:	2+
Retentiontime:	9.8094615936279
Score:	101.4306
Mass Error [ppm]:	0.61022
PEP:	0.0057725
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	32 %
Peak Coverage:	15 %
Protein Localisation:	120 ... 127

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.05	1	T	7				
+0.0579	189.09	+0.0077	217.08	2	D	6	823.39	+0.0592	823.39	
	318.13	+0.1707	346.12	3	E	5	708.37	+0.0834	354.69	-0.302
	375.15		403.15	4	G	4	579.32	+0.0833	579.32	
	488.24	-0.038	516.23	5	I	3	522.3	+0.0675	522.3	
	559.27	+0.0338	587.27	6	A	2	409.22	-0.005	409.22	
	722.34		750.33	7	Y	1	338.18	+0.1399	338.18	
				8	R	0	175.12	+0.0046	175.12	

Scan number	7494	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	74.48



precursor information

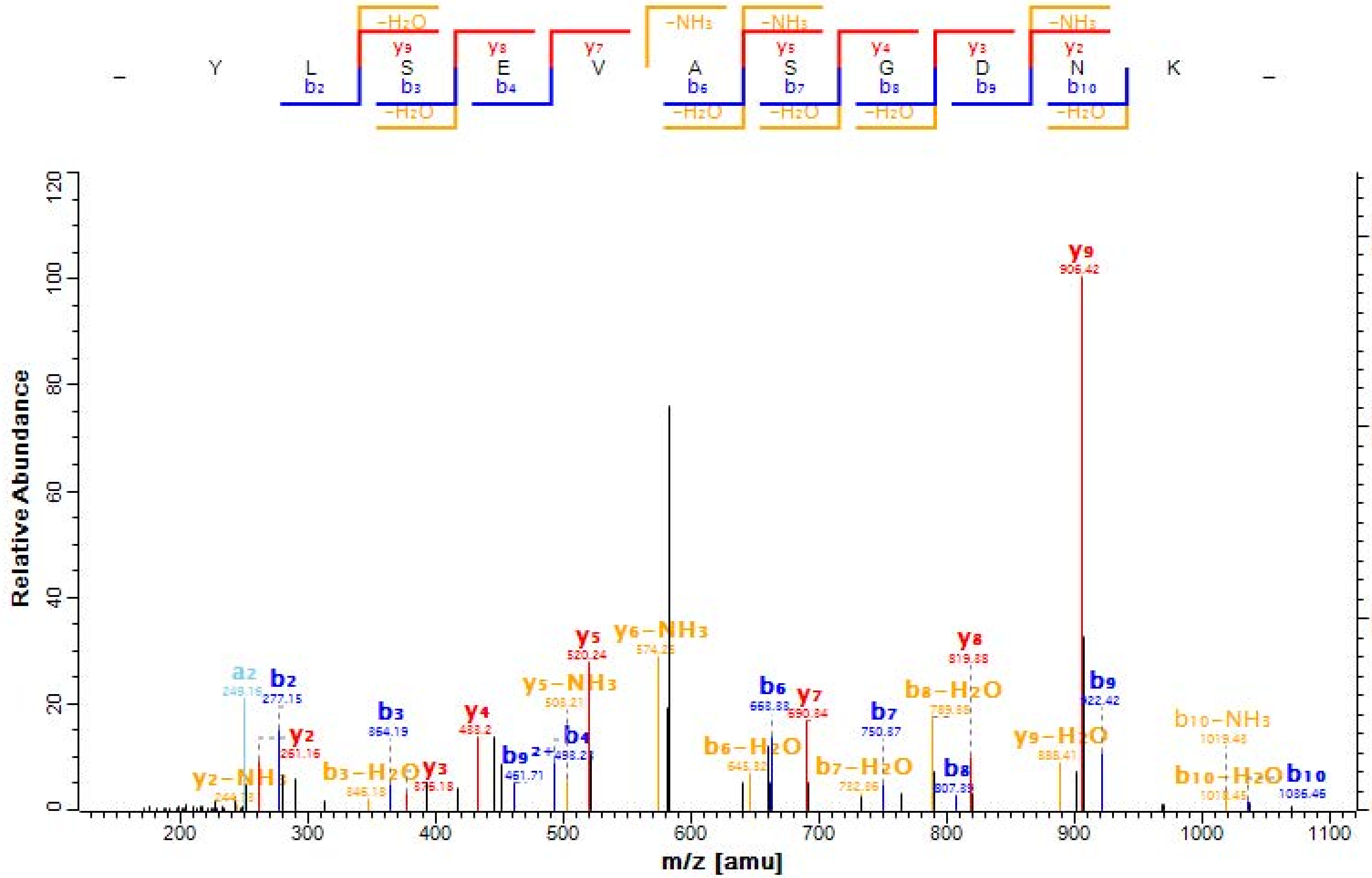
Mass:	1588.84597
m/z:	795.43026
Charge:	2+
Retentiontime:	43.301300048828
Score:	74.47521
Mass Error [ppm]:	-0.06218
PEP:	0.00085729
Precursor Type:	MULTI

general information

Annotation:	10 of 15
AminoAcids Coverag	67 %
Intensity Coverage:	49 %
Peak Coverage:	23 %
Protein Localisation:	12 ... 26

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	14				
	201.1234	2	L	13	1502.821		1502.821	
	288.1554	3	S	12	1389.737		1389.737	
	417.198	4	E	11	1302.705	-0.09341	1302.705	
+0.00543	518.2457	5	T	10	1173.663	+0.02633	587.335	+0.098821
	665.3141	6	F	9	1072.615	+0.027134	1072.615	
-0.16395	778.3981	7	L	8	925.5465	+0.15701	925.5465	
	875.4509	8	P	7	812.4625	-0.00636	812.4625	
	989.4938	9	N	6	715.4097		715.4097	
	1046.515	10	G	5	601.3668	+0.085239	601.3668	
+0.062133	1159.599	11	I	4	544.3453	+0.31526	544.3453	
	1273.642	12	N	3	431.2613		431.2613	
	1330.664	13	G	2	317.2183		317.2183	
+0.254987	1443.748	14	I	1	260.1969		260.1969	
		15	K	0	147.1128		147.1128	

Scan number	759	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	166.14



precursor information

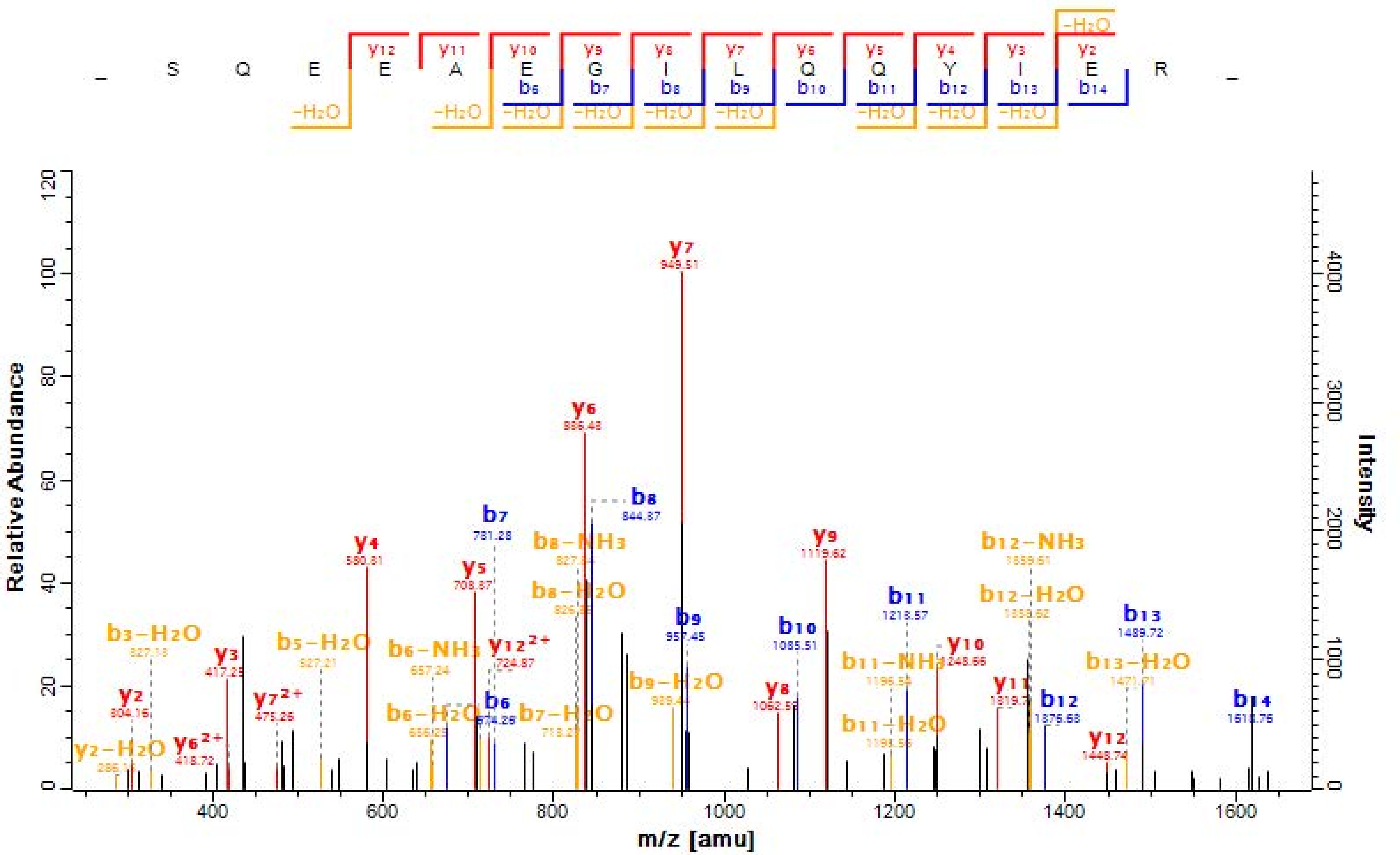
Mass:	1181.55685
m/z:	591.7857
Charge:	2+
Retentiontime:	9.874436378479
Score:	166.1414
Mass Error [ppm]:	0.35005
PEP:	4.6127E-07
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	54 %
Peak Coverage:	28 %
Protein Localisation:	130 ... 140

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	136.08		164.07		164.07	1	Y	10		
+0.0443	249.16		277.15	+0.0208	277.15	2	L	9	1019.5	
	336.19		364.19	-0.089	364.19	3	S	8	906.42	-0.029
	465.23		493.23	-0.072	493.23	4	E	7	819.38	+0.0444
	564.3		592.3		592.3	5	V	6	690.34	+0.0425
	635.34		663.33	-0.049	663.33	6	A	5	591.27	
	722.37		750.37	-0.008	750.37	7	S	4	520.24	-0.007
	779.39		807.39	-0.052	807.39	8	G	3	433.2	+0.0387
	894.42	-0.496	461.71	-0.044	922.42	9	D	2	376.18	+0.1
	1008.5		1036.5	-0.049	1036.5	10	N	1	261.16	+0.0598
						11	K	0	147.11	

Scan number	7686	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	199.15



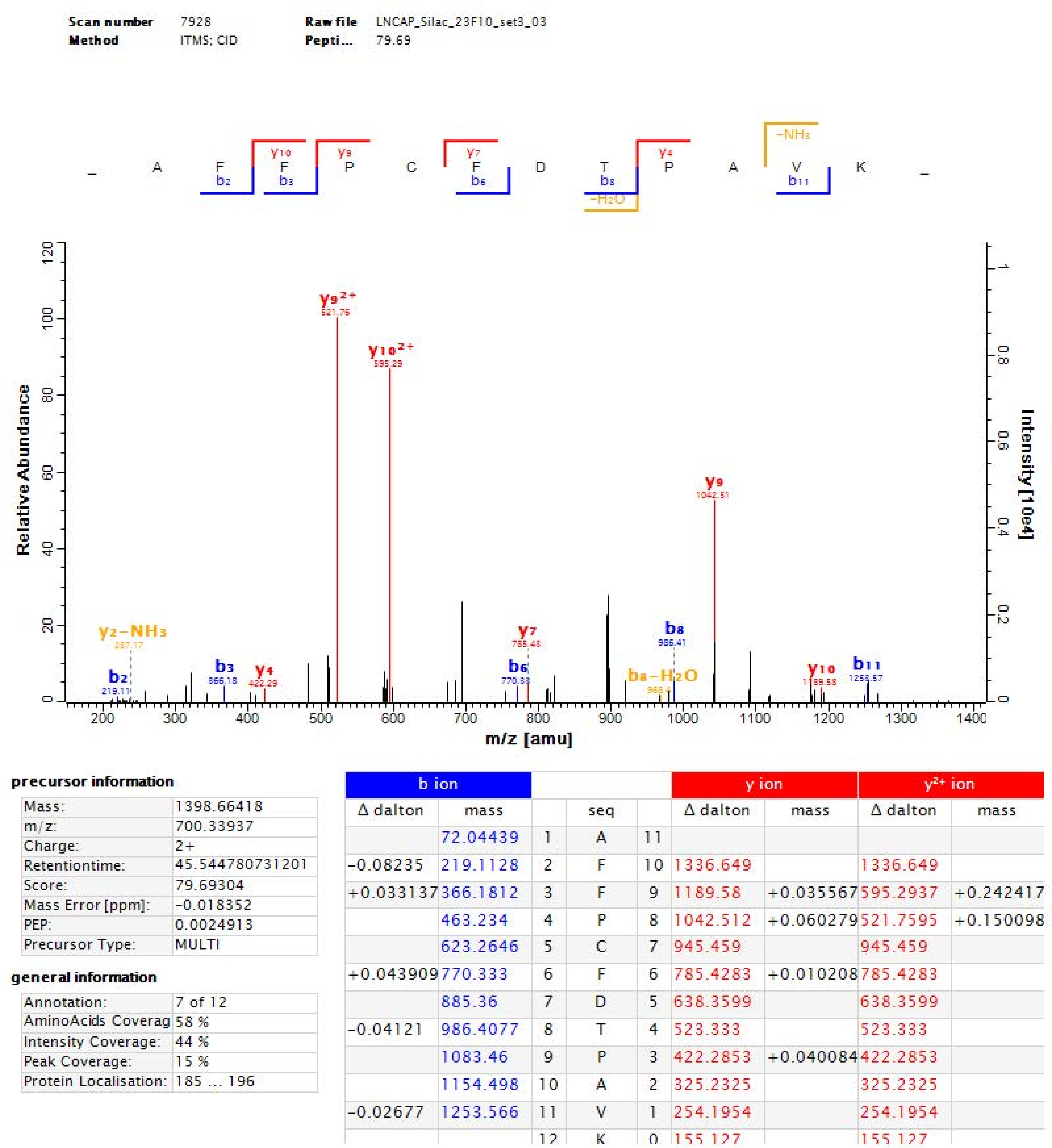
precursor information

Mass:	1791.86514
m/z:	896.93985
Charge:	2+
Retentiontime:	44.289180755615
Score:	199.1479
Mass Error [ppm]:	0.69034
PEP:	1.6975E-26
Precursor Type:	ISO

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	56 %
Peak Coverage:	43 %
Protein Localisation:	435 ... 449

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	14				
	216.0979	2	Q	13	1705.839		1705.839	
	345.1405	3	E	12	1577.781		1577.781	
	474.1831	4	E	11	1448.738	+0.016898	724.8726	-0.27217
	545.2202	5	A	10	1319.695	-0.07942	1319.695	
-0.0121	674.2628	6	E	9	1248.658	-0.05452	1248.658	
-0.20288	731.2842	7	G	8	1119.616	+0.001869	1119.616	
+0.016401	844.3683	8	I	7	1062.594	-0.01976	1062.594	
-0.01291	957.4524	9	L	6	949.5102	+0.042272	475.2587	-0.06853
+0.100139	1085.511	10	Q	5	836.4261	+0.017694	418.7167	-0.41877
+0.048642	1213.57	11	Q	4	708.3675	+0.01725	708.3675	
-0.28458	1376.633	12	Y	3	580.3089	+0.066795	580.3089	
-0.10986	1489.717	13	I	2	417.2456	+0.10284	417.2456	
-0.15587	1618.76	14	E	1	304.1615	+0.081283	304.1615	
		15	R	0	175.119		175.119	



Scan number	7928	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	79.69

precursor information

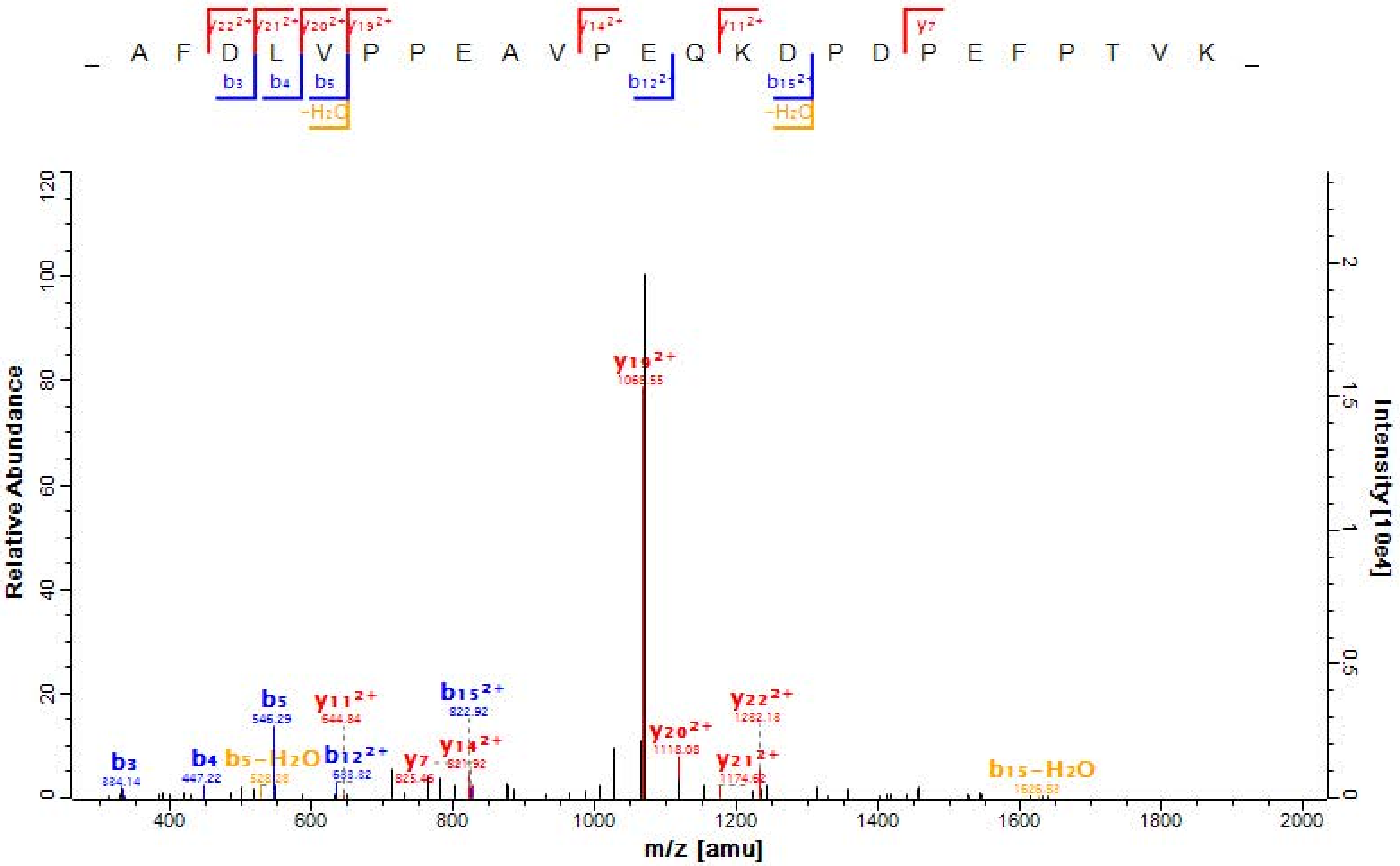
Mass:	1398.66418
m/z:	700.33937
Charge:	2+
Retentiontime:	45.544780731201
Score:	79.69304
Mass Error [ppm]:	-0.018352
PEP:	0.0024913
Precursor Type:	MULTI

general information

Annotation:	7 of 12
AminoAcids Coverag	58 %
Intensity Coverage:	44 %
Peak Coverage:	15 %
Protein Localisation:	185 ... 196

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	11				
-0.08235	219.1128	2	F	10	1336.649		1336.649	
+0.033137	366.1812	3	F	9	1189.58	+0.035567	595.2937	+0.242417
	463.234	4	P	8	1042.512	+0.060279	521.7595	+0.150098
	623.2646	5	C	7	945.459		945.459	
+0.043909	770.333	6	F	6	785.4283	+0.010208	785.4283	
	885.36	7	D	5	638.3599		638.3599	
-0.04121	986.4077	8	T	4	523.333		523.333	
	1083.46	9	P	3	422.2853	+0.040084	422.2853	
	1154.498	10	A	2	325.2325		325.2325	
-0.02677	1253.566	11	V	1	254.1954		254.1954	
		12	K	0	155.127		155.127	

Scan number	7944	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	37.4



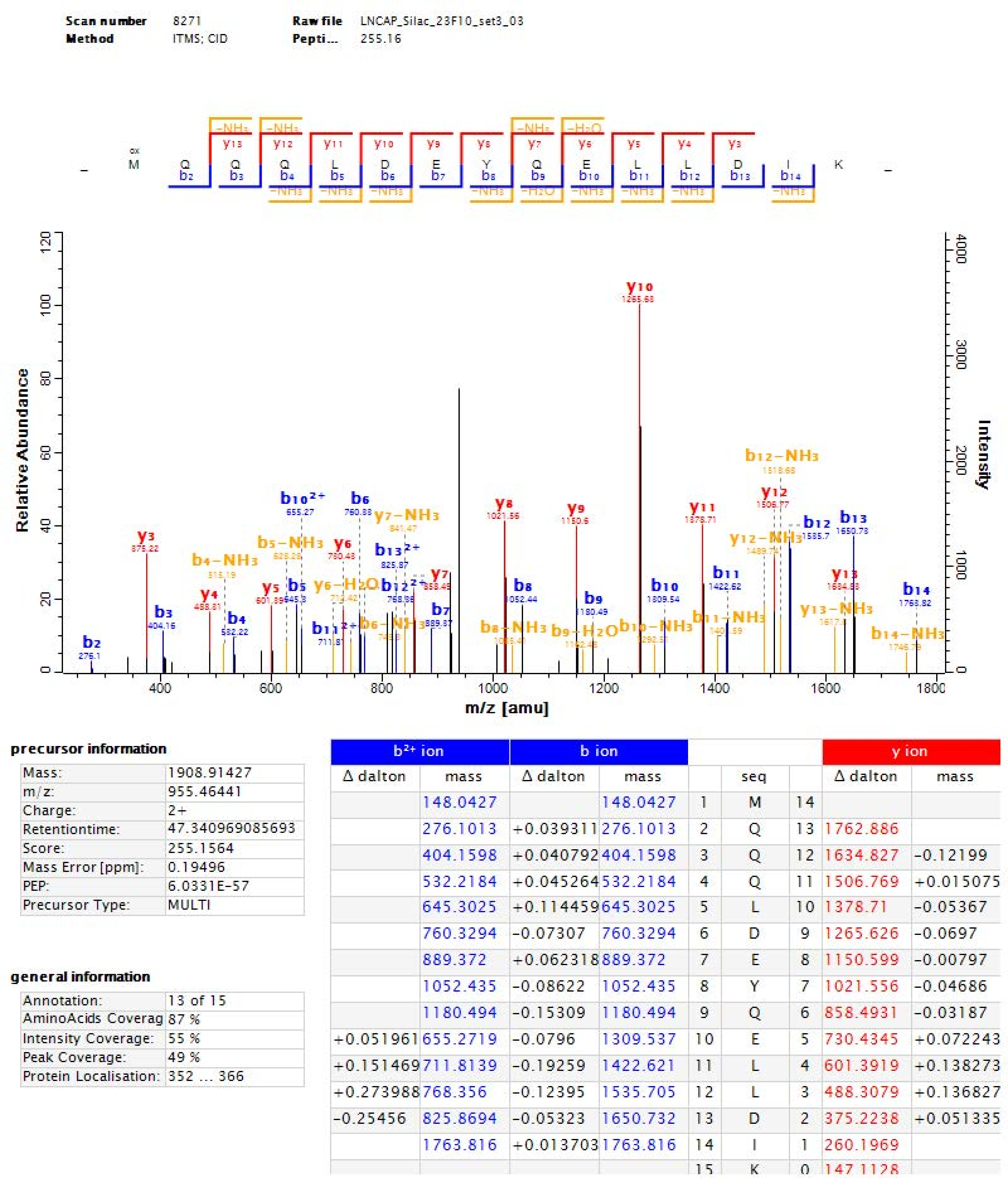
precursor information

Mass:	2664.33301
m/z:	889.11828
Charge:	3+
Retentiontime:	45.624668121337
Score:	37.39959
Mass Error [ppm]:	0.26359
PEP:	0.018085
Precursor Type:	MULTI

general information

Annotation:	9 of 24
AminoAcids Coverag	38 %
Intensity Coverage:	38 %
Peak Coverage:	17 %
Protein Localisation:	269 ... 292

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	23				
	219.11		219.11	2	F	22	2610.3		2610.3	
	334.14	+0.1922	334.14	3	D	21	2463.3		1232.1	+0.2204
	447.22	+0.1106	447.22	4	L	20	2348.2		1174.6	+0.3088
	546.29	-0.088	546.29	5	V	19	2235.2		1118.1	+0.2305
	643.34		643.34	6	P	18	2136.1		1068.5	-0.091
	740.4		740.4	7	P	17	2039		2039	
	869.44		869.44	8	E	16	1942		1942	
	940.48		940.48	9	A	15	1812.9		1812.9	
	1039.5		1039.5	10	V	14	1741.9		1741.9	
	1136.6		1136.6	11	P	13	1642.8		821.92	+0.1591
+0.0724	633.32		1265.6	12	E	12	1545.8		1545.8	
	1393.7		1393.7	13	Q	11	1416.7		1416.7	
	1529.8		1529.8	14	K	10	1288.7		644.84	+0.09
+0.174	822.92		1644.8	15	D	9	1152.6		1152.6	
	1741.9		1741.9	16	P	8	1037.5		1037.5	
	1856.9		1856.9	17	D	7	940.49		940.49	
	1954		1954	18	P	6	825.46	+0.1492	825.46	
	2083		2083	19	E	5	728.41		728.41	
	2230.1		2230.1	20	F	4	599.36		599.36	
	2327.1		2327.1	21	P	3	452.3		452.3	
	2428.2		2428.2	22	T	2	355.24		355.24	
	2527.2		2527.2	23	V	1	254.2		254.2	
				24	K	0	155.13		155.13	



Scan number	8271	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	255.16

precursor information

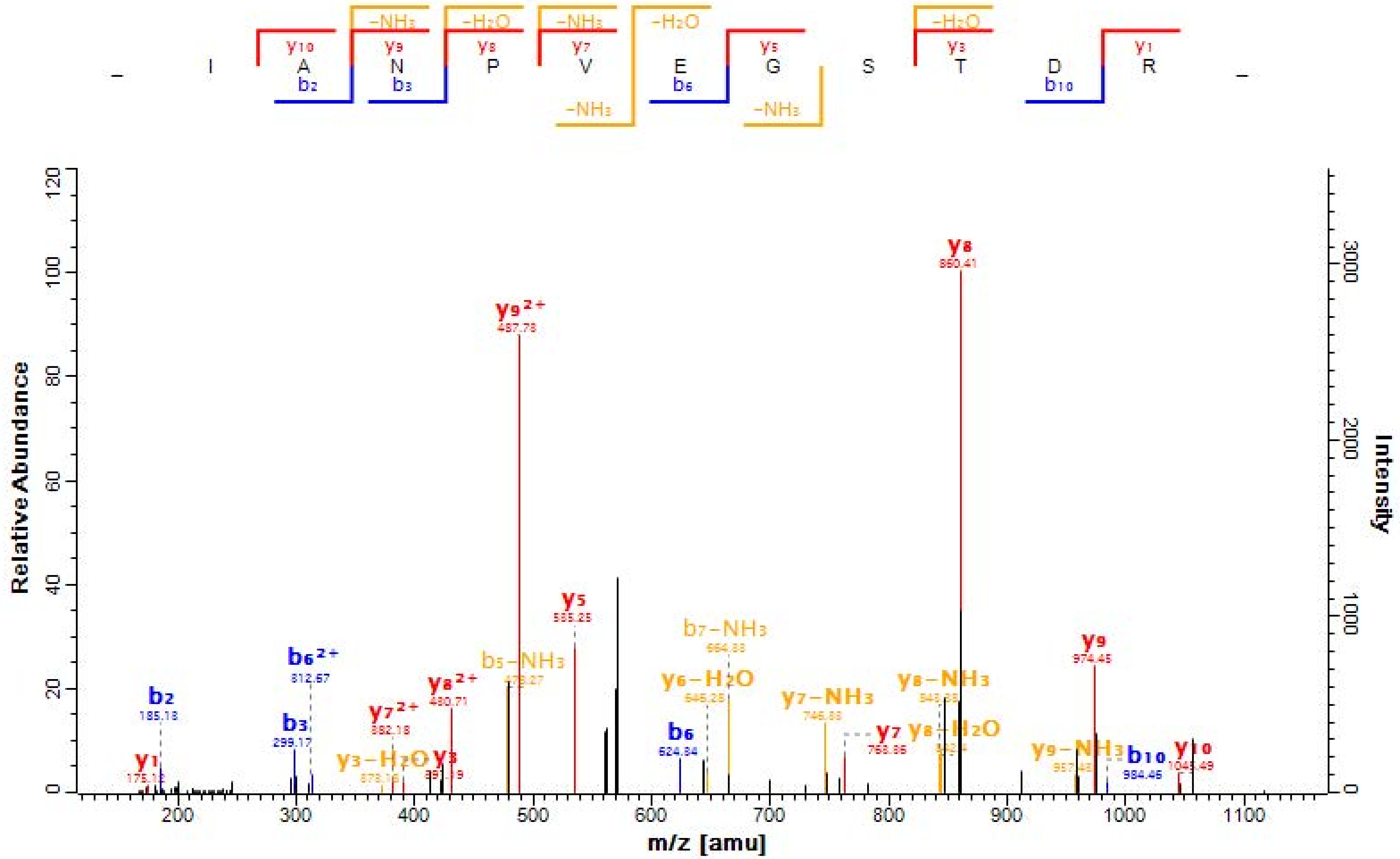
Mass:	1908.91427
m/z:	955.46441
Charge:	2+
Retentiontime:	47.340969085693
Score:	255.1564
Mass Error [ppm]:	0.19496
PEP:	6.0331E-57
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	55 %
Peak Coverage:	49 %
Protein Localisation:	352 … 366

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	148.0427		148.0427	1	M	14		
	276.1013	+0.039311	276.1013	2	Q	13	1762.886	
	404.1598	+0.040792	404.1598	3	Q	12	1634.827	-0.12199
	532.2184	+0.045264	532.2184	4	Q	11	1506.769	+0.015075
	645.3025	+0.114459	645.3025	5	L	10	1378.71	-0.05367
	760.3294	-0.07307	760.3294	6	D	9	1265.626	-0.0697
	889.372	+0.062318	889.372	7	E	8	1150.599	-0.00797
	1052.435	-0.08622	1052.435	8	Y	7	1021.556	-0.04686
	1180.494	-0.15309	1180.494	9	Q	6	858.4931	-0.03187
+0.051961	655.2719	-0.0796	1309.537	10	E	5	730.4345	+0.072243
+0.151469	711.8139	-0.19259	1422.621	11	L	4	601.3919	+0.138273
+0.273988	768.356	-0.12395	1535.705	12	L	3	488.3079	+0.136827
-0.25456	825.8694	-0.05323	1650.732	13	D	2	375.2238	+0.051335
	1763.816	+0.013703	1763.816	14	I	1	260.1969	
				15	K	0	147.1128	

Scan number	842	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	143



precursor information

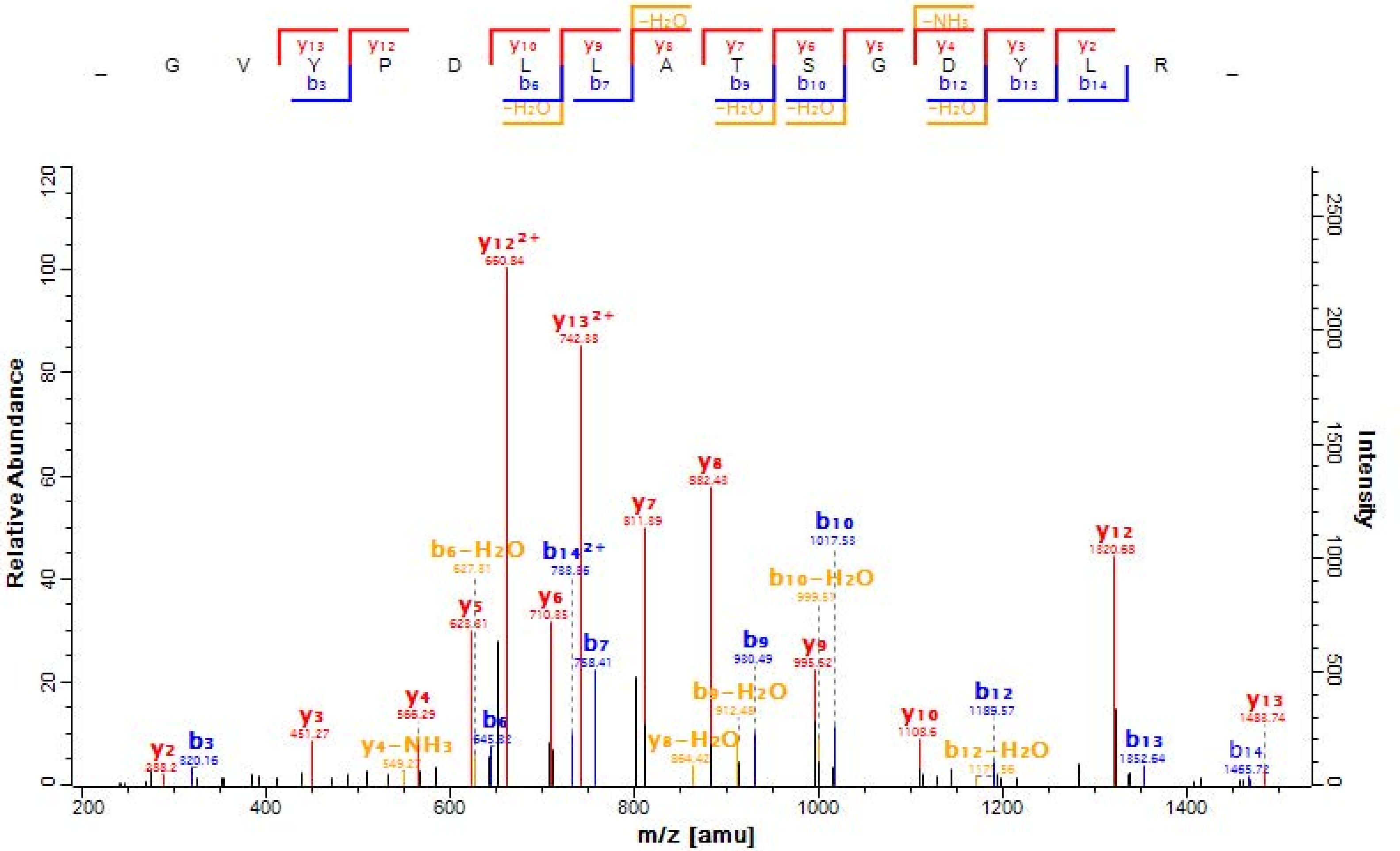
Mass:	1157.56726
m/z:	579.79091
Charge:	2+
Retentiontime:	10.389933586120
Score:	142.9956
Mass Error [ppm]:	-0.34912
PEP:	9.8815E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 11
AminoAcids Coverag	91 %
Intensity Coverage:	55 %
Peak Coverage:	22 %
Protein Localisation:	324 ... 334

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	I	10				
	185.13	-0.038	185.13	2	A	9	1045.5	-0.078	1045.5	
	299.17	+0.0271	299.17	3	N	8	974.45	+0.0066	487.73	+0.1544
	396.22		396.22	4	P	7	860.41	+0.0118	430.71	+0.0574
	495.29		495.29	5	V	6	763.36	+0.0525	382.18	+0.1749
+0.4797	312.67	+0.1868	624.34	6	E	5	664.29		664.29	
	681.36		681.36	7	G	4	535.25	+0.0004	535.25	
	768.39		768.39	8	S	3	478.23		478.23	
	869.44		869.44	9	T	2	391.19	+0.0677	391.19	
	984.46	+0.1746	984.46	10	D	1	290.15		290.15	
				11	R	0	175.12	+0.0171	175.12	

Scan number	8485	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	173.06



precursor information

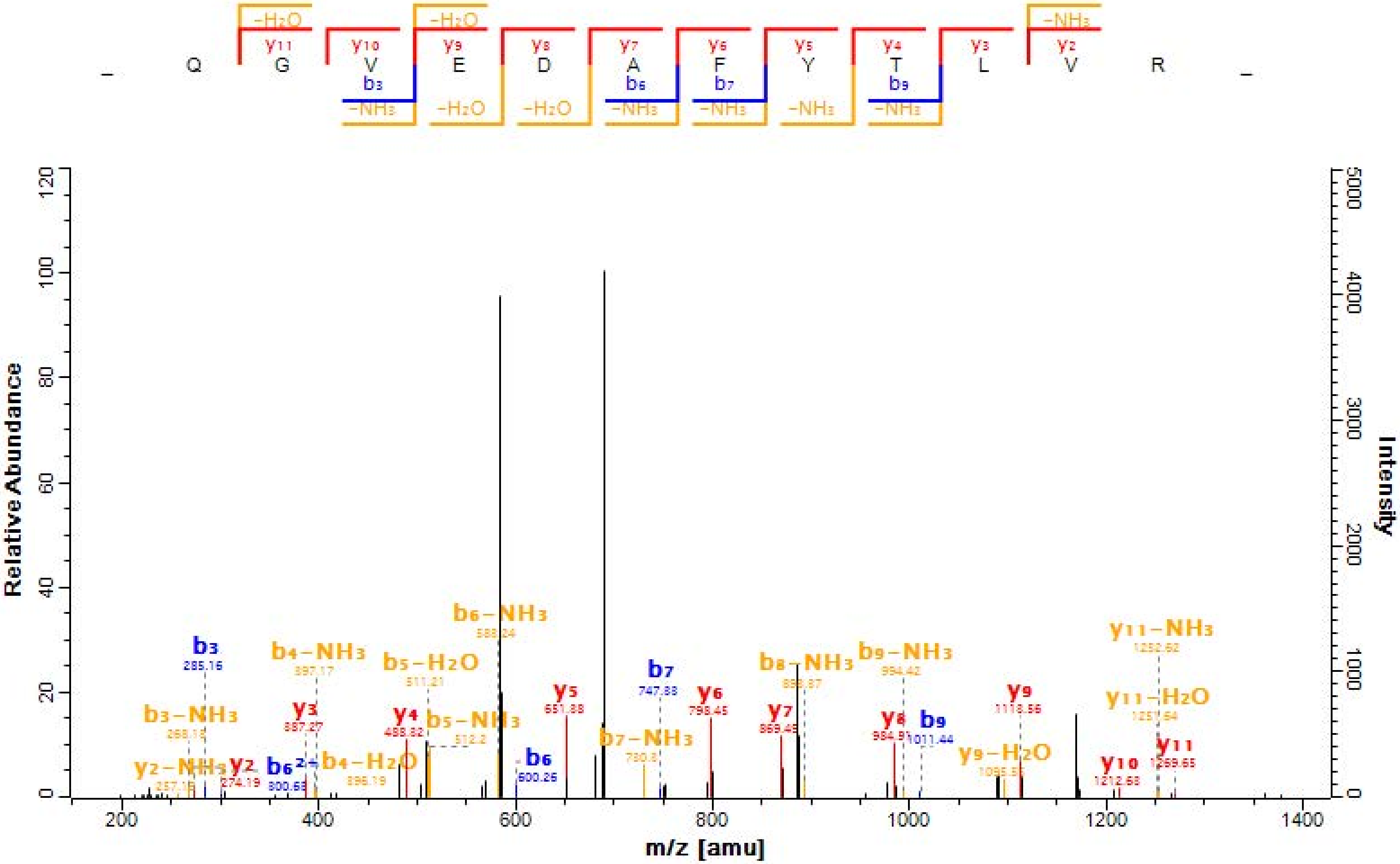
Mass:	1638.82562
m/z:	820.42008
Charge:	2+
Retentiontime:	48.497200012207
Score:	173.061
Mass Error [ppm]:	0.17094
PEP:	4.861E-17
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	74 %
Peak Coverage:	36 %
Protein Localisation:	82 ... 96

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	14				
	157.1		157.1	2	V	13	1582.8		1582.8	
	320.16	+0.055	320.16	3	Y	12	1483.7	+0.0307	742.38	+0.2487
	417.21		417.21	4	P	11	1320.7	-0.03	660.84	+0.2209
	532.24		532.24	5	D	10	1223.6		1223.6	
	645.32	+0.0471	645.32	6	L	9	1108.6	-0.164	1108.6	
	758.41	-0.072	758.41	7	L	8	995.52	+0.0043	995.52	
	829.45		829.45	8	A	7	882.43	-0.016	882.43	
	930.49	-0.02	930.49	9	T	6	811.39	-0.04	811.39	
	1017.5	+0.0542	1017.5	10	S	5	710.35	-0.034	710.35	
	1074.5		1074.5	11	G	4	623.31	+0.033	623.31	
	1189.6	-0.104	1189.6	12	D	3	566.29	+0.0386	566.29	
	1352.6	-0.123	1352.6	13	Y	2	451.27	+0.0115	451.27	
+0.3073	733.36	-0.064	1465.7	14	L	1	288.2	+0.0776	288.2	
				15	R	0	175.12		175.12	

Scan number	8516	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	128.68



precursor information

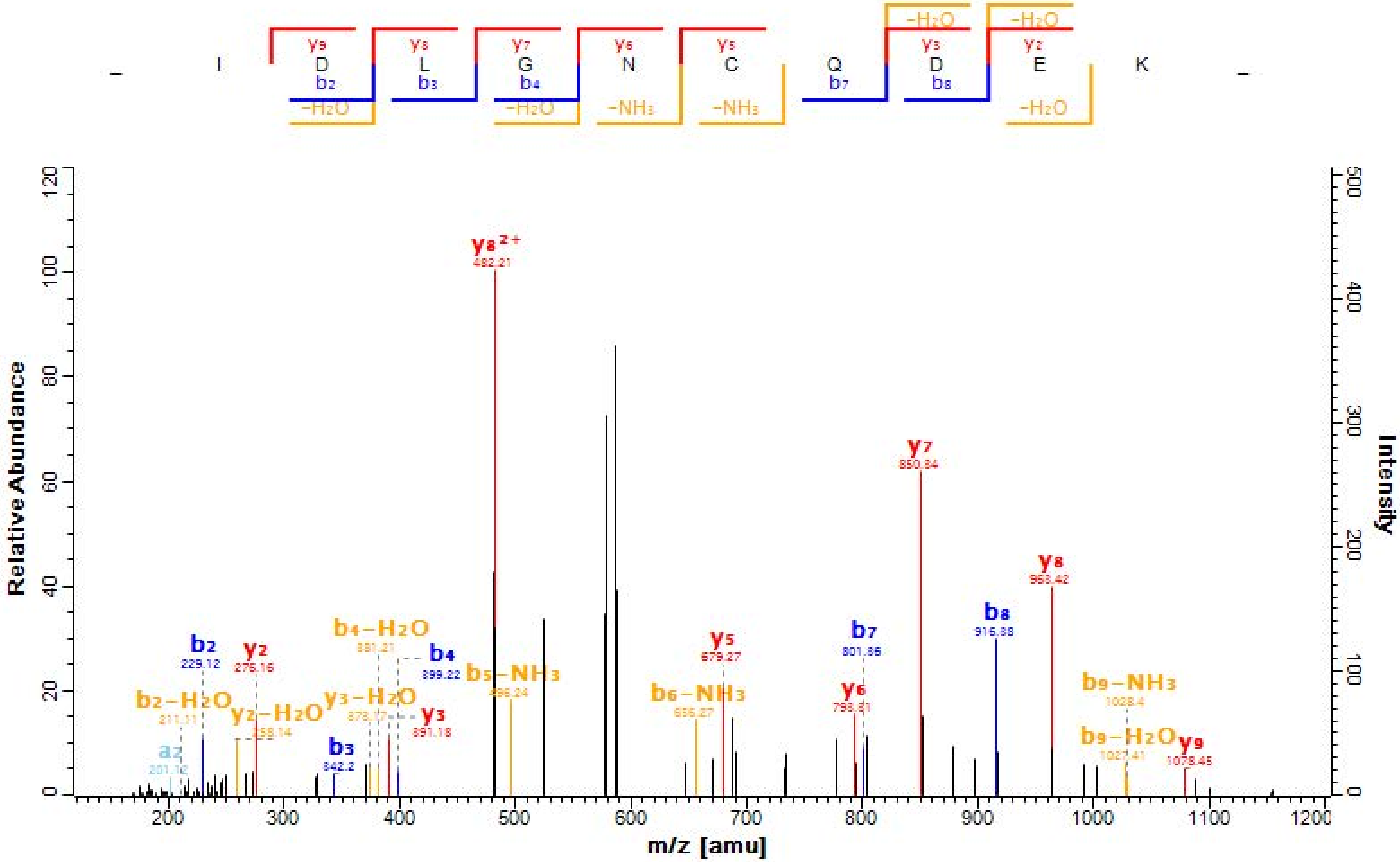
Mass:	1396.69989
m/z:	699.35722
Charge:	2+
Retentiontime:	48.662555694580
Score:	128.6753
Mass Error [ppm]:	0.86932
PEP:	2.3178E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	26 %
Peak Coverage:	30 %
Protein Localisation:	150 ... 161

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	129.0659		129.0659	1	Q	11		
	186.0873		186.0873	2	G	10	1269.647	-0.12882
	285.1557	+0.008239	285.1557	3	V	9	1212.626	+0.099061
	414.1983		414.1983	4	E	8	1113.558	-0.01722
	529.2253		529.2253	5	D	7	984.5149	-0.03938
-0.43076	300.6348	-0.06994	600.2624	6	A	6	869.488	+0.01057
	747.3308	+0.121658	747.3308	7	F	5	798.4509	+0.032608
	910.3941		910.3941	8	Y	4	651.3824	+0.065073
	1011.442	-0.38443	1011.442	9	T	3	488.3191	+0.128279
	1124.526		1124.526	10	L	2	387.2714	+0.004388
	1223.594		1223.594	11	V	1	274.1874	+0.021984
				12	R	0	175.119	

Scan number	858	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	92.87



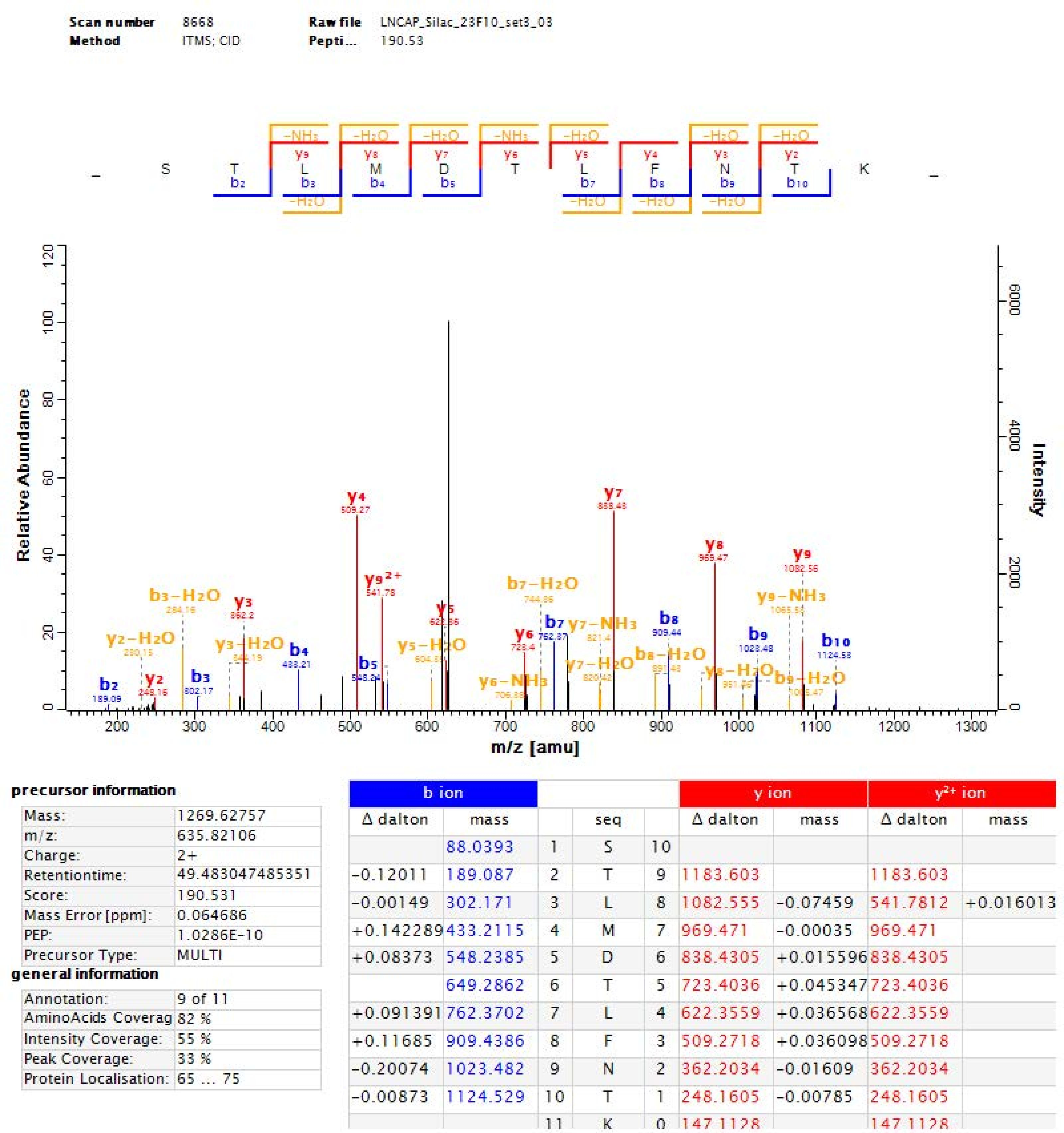
precursor information

Mass:	1190.52333
m/z:	596.26894
Charge:	2+
Retentiontime:	10.486499786377
Score:	92.86611
Mass Error [ppm]:	-0.3525
PEP:	0.0018784
Precursor Type:	MULTI

g

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	37 %
Peak Coverage:	23 %
Protein Localisation:	858 ... 867

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	9				
+0.0255	201.12	+0.0053	229.12	2	D	8	1078.4	+0.404	1078.4	
	314.21	+0.1773	342.2	3	L	7	963.42	+0.0222	482.21	+0.0512
	371.23	+0.0396	399.22	4	G	6	850.34	-0.038	850.34	
	485.27		513.27	5	N	5	793.31	+0.1421	793.31	
	645.3		673.3	6	C	4	679.27	+0.0403	679.27	
	773.36	-0.2	801.36	7	Q	3	519.24		519.24	
	888.39	-0.063	916.38	8	D	2	391.18	-0.061	391.18	
	1017.4		1045.4	9	E	1	276.16	+0.0618	276.16	
				10	K	0	147.11		147.11	



Scan number	8668	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	190.53

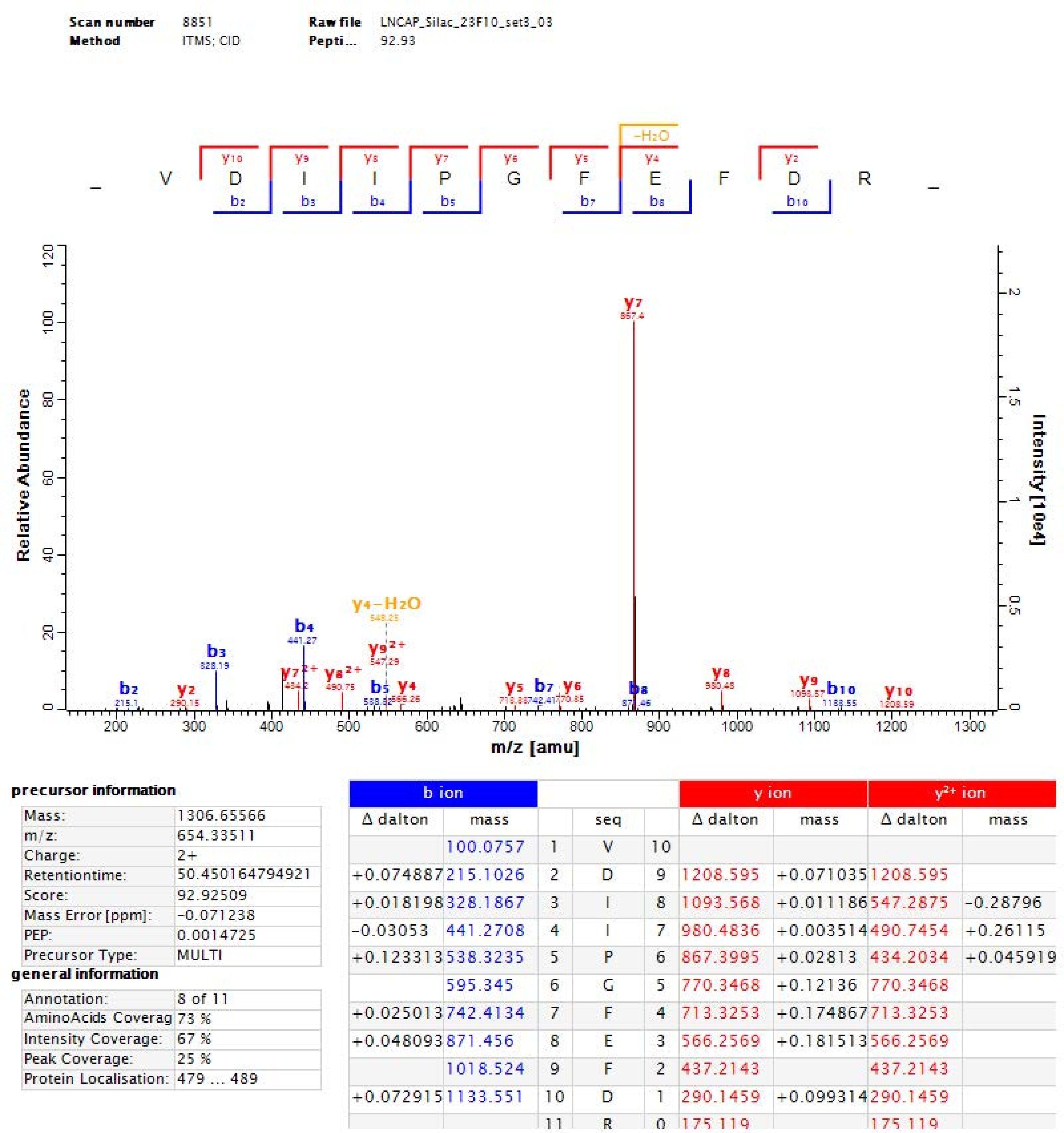
precursor information

Mass:	1269.62757
m/z:	635.82106
Charge:	2+
Retentiontime:	49.483047485351
Score:	190.531
Mass Error [ppm]:	0.064686
PEP:	1.0286E-10
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	55 %
Peak Coverage:	33 %
Protein Localisation:	65 ... 75

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	10				
-0.12011	189.087	2	T	9	1183.603		1183.603	
-0.00149	302.171	3	L	8	1082.555	-0.07459	541.7812	+0.016013
+0.142289	433.2115	4	M	7	969.471	-0.00035	969.471	
+0.08373	548.2385	5	D	6	838.4305	+0.015596	838.4305	
	649.2862	6	T	5	723.4036	+0.045347	723.4036	
+0.091391	762.3702	7	L	4	622.3559	+0.036568	622.3559	
+0.11685	909.4386	8	F	3	509.2718	+0.036098	509.2718	
-0.20074	1023.482	9	N	2	362.2034	-0.01609	362.2034	
-0.00873	1124.529	10	T	1	248.1605	-0.00785	248.1605	
		11	K	0	147.1128		147.1128	



Scan number	8851	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	92.93

precursor information

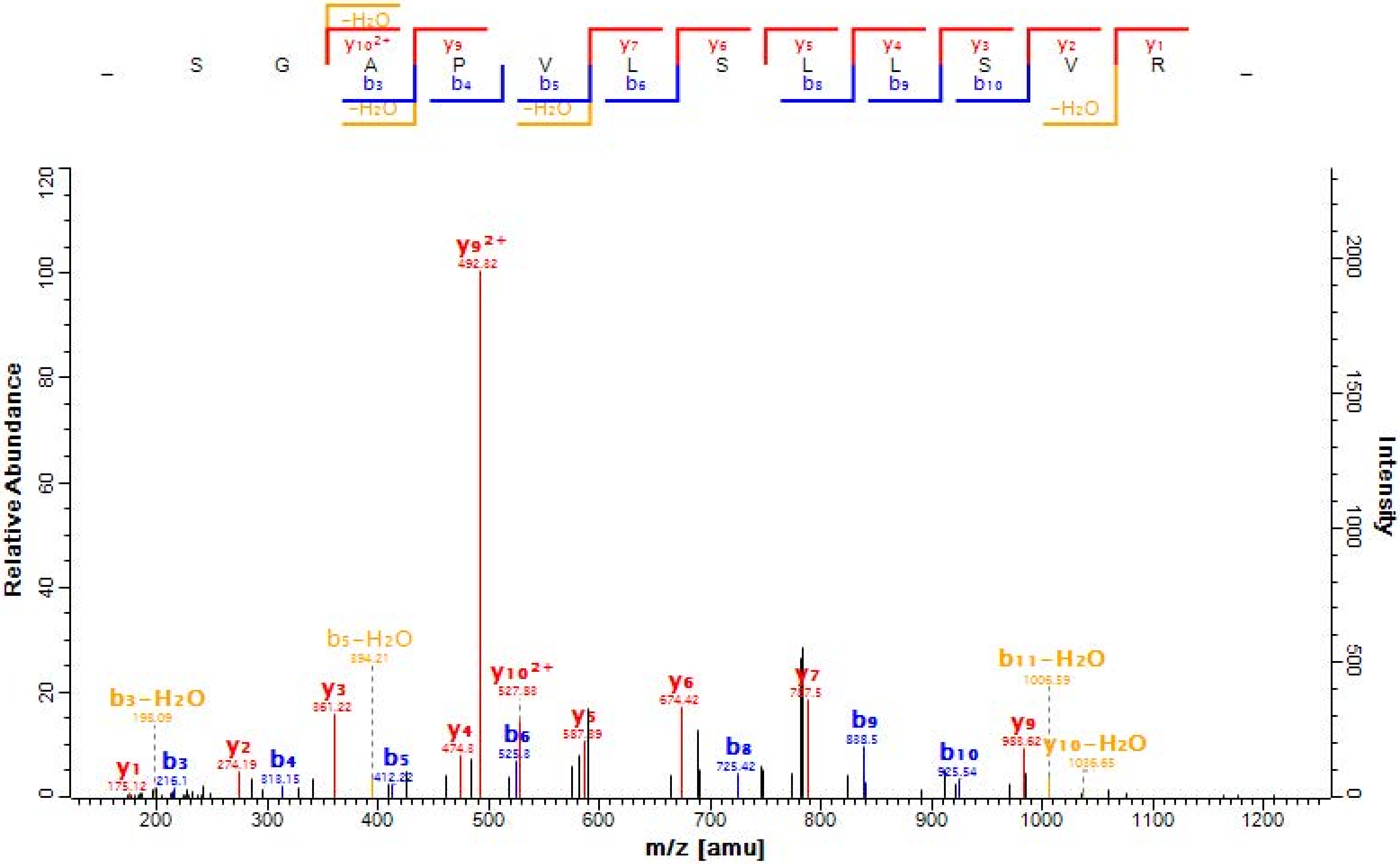
Mass:	1306.65566
m/z:	654.33511
Charge:	2+
Retentiontime:	50.450164794921
Score:	92.92509
Mass Error [ppm]:	-0.071238
PEP:	0.0014725
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	67 %
Peak Coverage:	25 %
Protein Localisation:	479 ... 489

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	10				
+0.074887	215.1026	2	D	9	1208.595	+0.071035	1208.595	
+0.018198	328.1867	3	I	8	1093.568	+0.011186	547.2875	-0.28796
-0.03053	441.2708	4	I	7	980.4836	+0.003514	490.7454	+0.26115
+0.123313	538.3235	5	P	6	867.3995	+0.02813	434.2034	+0.045919
	595.345	6	G	5	770.3468	+0.12136	770.3468	
+0.025013	742.4134	7	F	4	713.3253	+0.174867	713.3253	
+0.048093	871.456	8	E	3	566.2569	+0.181513	566.2569	
	1018.524	9	F	2	437.2143		437.2143	
+0.072915	1133.551	10	D	1	290.1459	+0.099314	290.1459	
		11	R	0	175.119		175.119	

Scan number 9081 **Raw file** LNCAP_Silac_23F10_set3_03
Method ITMS; CID **Pepti...** 81.57



precursor information

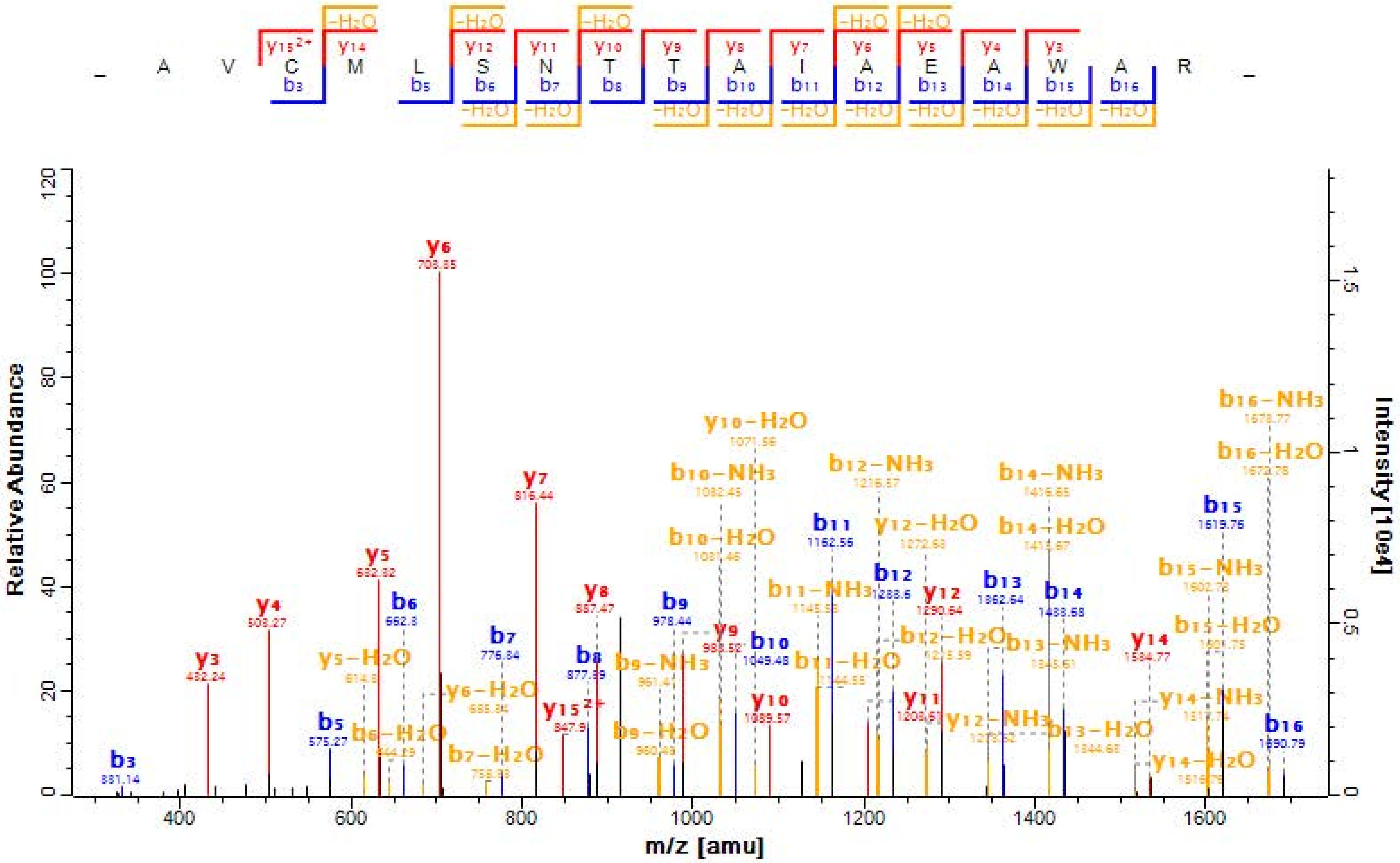
Mass:	1197.70845
m/z:	599.8615
Charge:	2+
Retentiontime:	51.713199615478
Score:	81.56528
Mass Error [ppm]:	0.27007
PEP:	0.0021394
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	54 %
Peak Coverage:	26 %
Protein Localisation:	321 ... 332

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	11				
	145.0608	2	G	10	1111.683		1111.683	
-0.06419	216.0979	3	A	9	1054.662		527.8346	+0.0293
+0.159107	313.1506	4	P	8	983.6248	+0.15249	492.316	+0.04566
+0.0097	412.2191	5	V	7	886.572		886.572	
+0.028419	525.3031	6	L	6	787.5036	+0.068651	787.5036	
	612.3352	7	S	5	674.4196	+0.103948	674.4196	
+0.004673	725.4192	8	L	4	587.3875	-0.05091	587.3875	
-0.07451	838.5033	9	L	3	474.3035	+0.128976	474.3035	
-0.03793	925.5353	10	S	2	361.2194	+0.075772	361.2194	
	1024.604	11	V	1	274.1874	+0.168225	274.1874	
		12	R	0	175.119	+0.039724	175.119	

Scan number	9412	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	372.64



precursor information

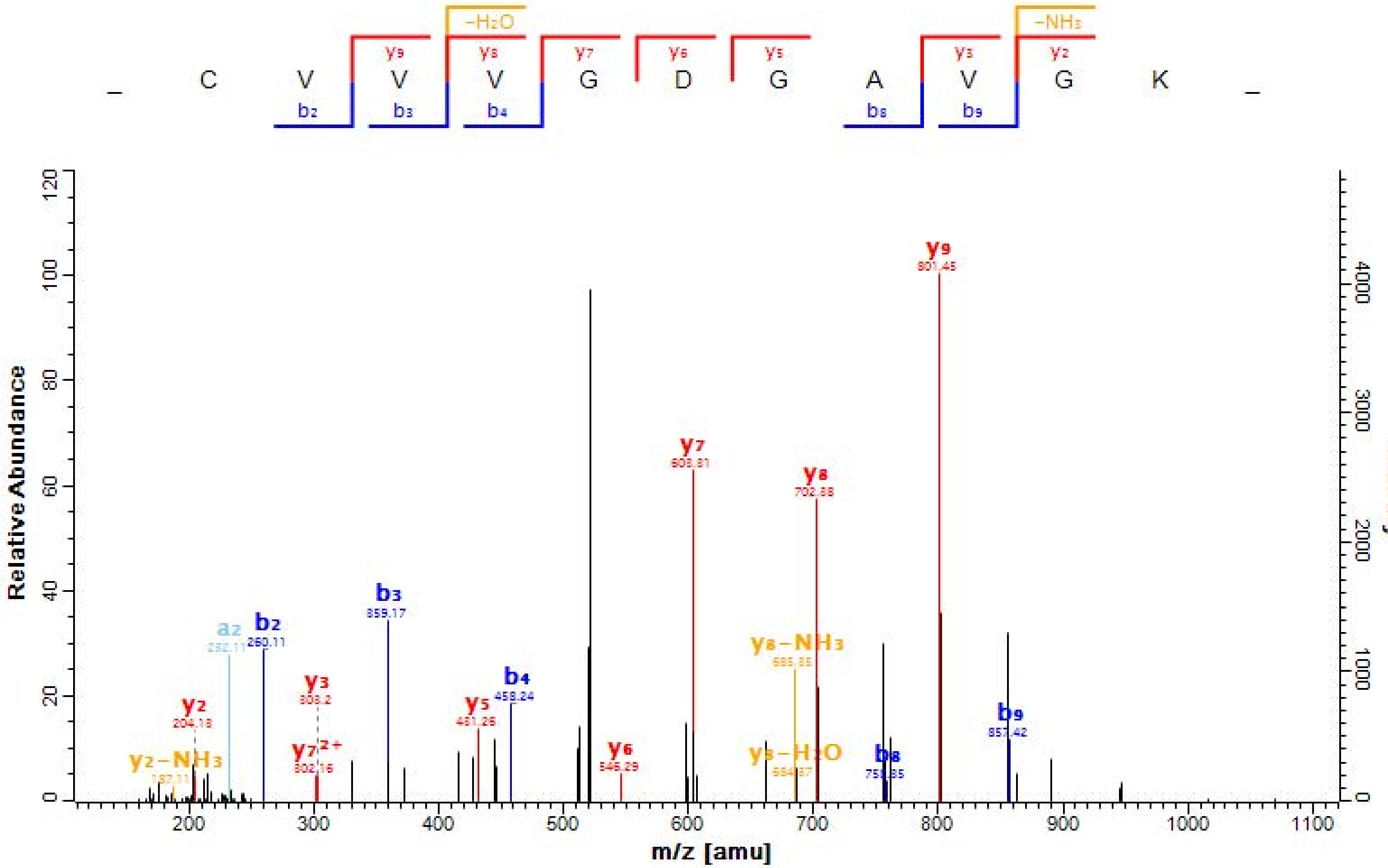
Mass:	1863.89687
m/z:	932.95571
Charge:	2+
Retentiontime:	53.617969512939
Score:	372.6425
Mass Error [ppm]:	-0.14195
PEP:	7.5303E-178
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	79 %
Peak Coverage:	60 %
Protein Localisation:	374 ... 390

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	16				
	171.1128	2	V	15	1793.867		1793.867	
-0.07302	331.1435	3	C	14	1694.799		847.9031	-0.0196
	462.1839	4	M	13	1534.768	-0.15349	1534.768	
-0.06451	575.268	5	L	12	1403.728		1403.728	
+0.009236	662.3	6	S	11	1290.644	+0.013414	1290.644	
+0.115173	776.343	7	N	10	1203.612	+0.050203	1203.612	
+0.004811	877.3906	8	T	9	1089.569	+0.016959	1089.569	
-0.06704	978.4383	9	T	8	988.5211	-0.00244	988.5211	
-0.04733	1049.475	10	A	7	887.4734	-0.00493	887.4734	
-0.04997	1162.559	11	I	6	816.4363	-0.01591	816.4363	
-0.05571	1233.597	12	A	5	703.3522	+0.025425	703.3522	
-0.06535	1362.639	13	E	4	632.3151	+0.028603	632.3151	
-0.17448	1433.676	14	A	3	503.2725	-0.01096	503.2725	
-0.22352	1619.756	15	W	2	432.2354	+0.140415	432.2354	
+0.127915	1690.793	16	A	1	246.1561		246.1561	
		17	R	0	175.119		175.119	

Scan number	948	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	88.06



precursor information

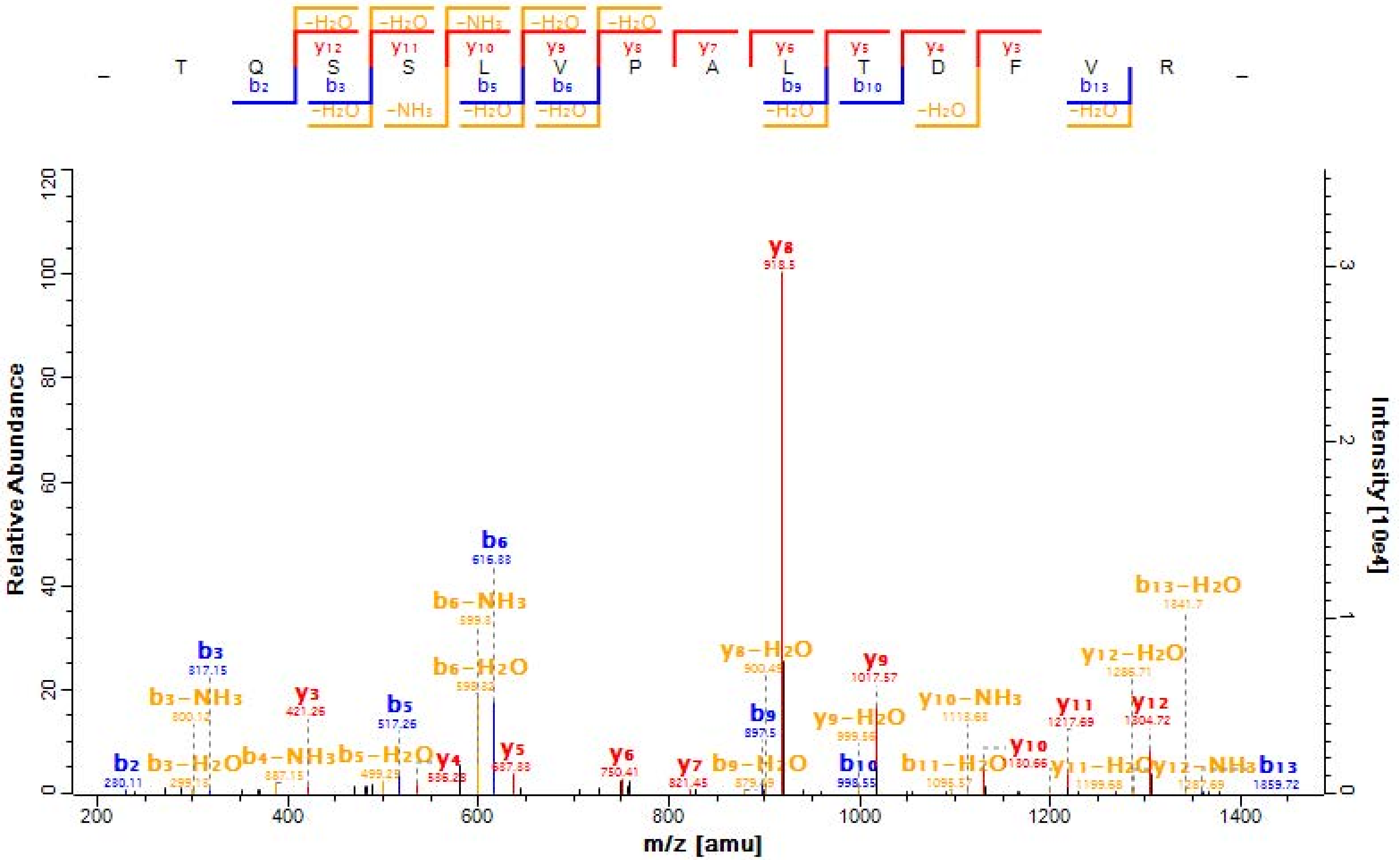
Mass:	1059.53817
m/z:	530.77636
Charge:	2+
Retentiontime:	11.045905113220
Score:	88.05646
Mass Error [ppm]:	-0.10722
PEP:	0.0020129
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	44 %
Peak Coverage:	18 %
Protein Localisation:	6 ... 16

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	133.04		161.04	1	C	10				
-0.025	232.11	-0.069	260.11	2	V	9	900.51		900.51	
	331.18	-0.06	359.17	3	V	8	801.45	-0.011	801.45	
	430.25	-0.056	458.24	4	V	7	702.38	+0.0174	702.38	
	487.27		515.26	5	G	6	603.31	+0.0016	302.16	+0.0151
	602.3		630.29	6	D	5	546.29	+0.0331	546.29	
	659.32		687.31	7	G	4	431.26	+0.0801	431.26	
	730.36	+0.0687	758.35	8	A	3	374.24		374.24	
	829.42	-0.003	857.42	9	V	2	303.2	+0.0371	303.2	
	886.45		914.44	10	G	1	204.13	+0.0775	204.13	
				11	K	0	147.11		147.11	

Scan number	9587	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	176.4



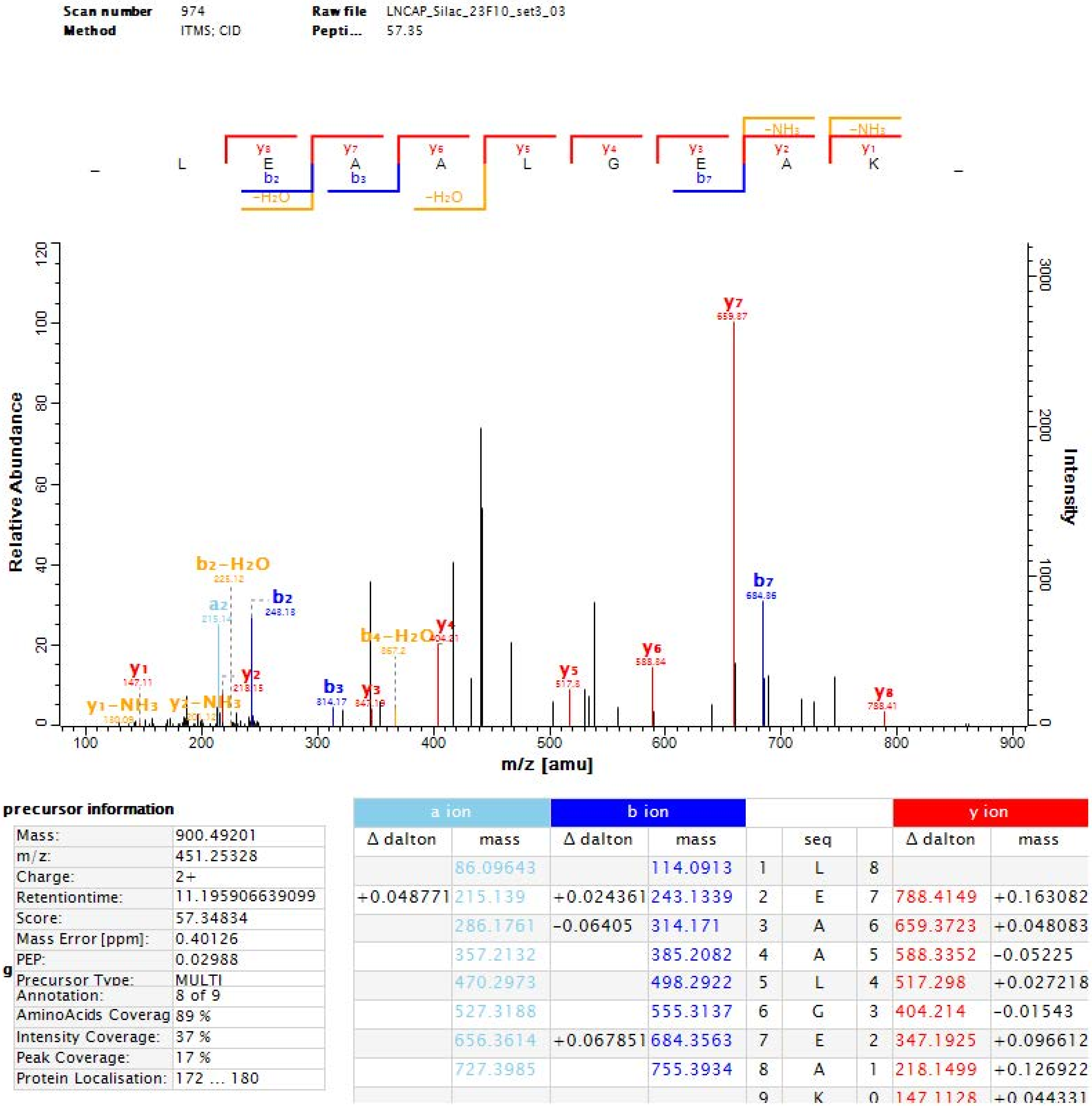
precursor information

Mass:	1532.82028
m/z:	767.41742
Charge:	2+
Retentiontime:	54.630268096923
Score:	176.3965
Mass Error [ppm]:	0.27766
PEP:	1.9534E-13
Precursor Type:	ISO

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	73 %
Peak Coverage:	40 %
Protein Localisation:	144 ... 157

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	102.054954941	1	T	13		
-0.0087351	230.113532452	2	Q	12	1432.77945537	
+0.010445	317.145560862	3	S	11	1304.72087786	-0.0151894
	404.177589272	4	S	10	1217.68884945	-0.0524969
+0.1087081	517.261653252	5	L	9	1130.65682104	+0.0309231
-0.0038343	616.330067169	6	V	8	1017.57275706	-0.0189851
	713.382831021	7	P	7	918.50434314	+0.0007838
	784.419944808	8	A	6	821.451579288	+0.231221
+0.0058179	897.504008789	9	L	5	750.4144655	+0.0411009
-0.0709133	998.551687263	10	T	4	637.33040152	+0.0674867
	1113.57863029	11	D	3	536.282723045	+0.0603556
	1260.64704421	12	F	2	421.255780013	+0.1567566
-0.1279337	1359.71545813	13	V	1	274.187366097	
		14	R	0	175.118952181	



Scan number 974 **Raw file** LNCAP_Silac_23F10_set3_03

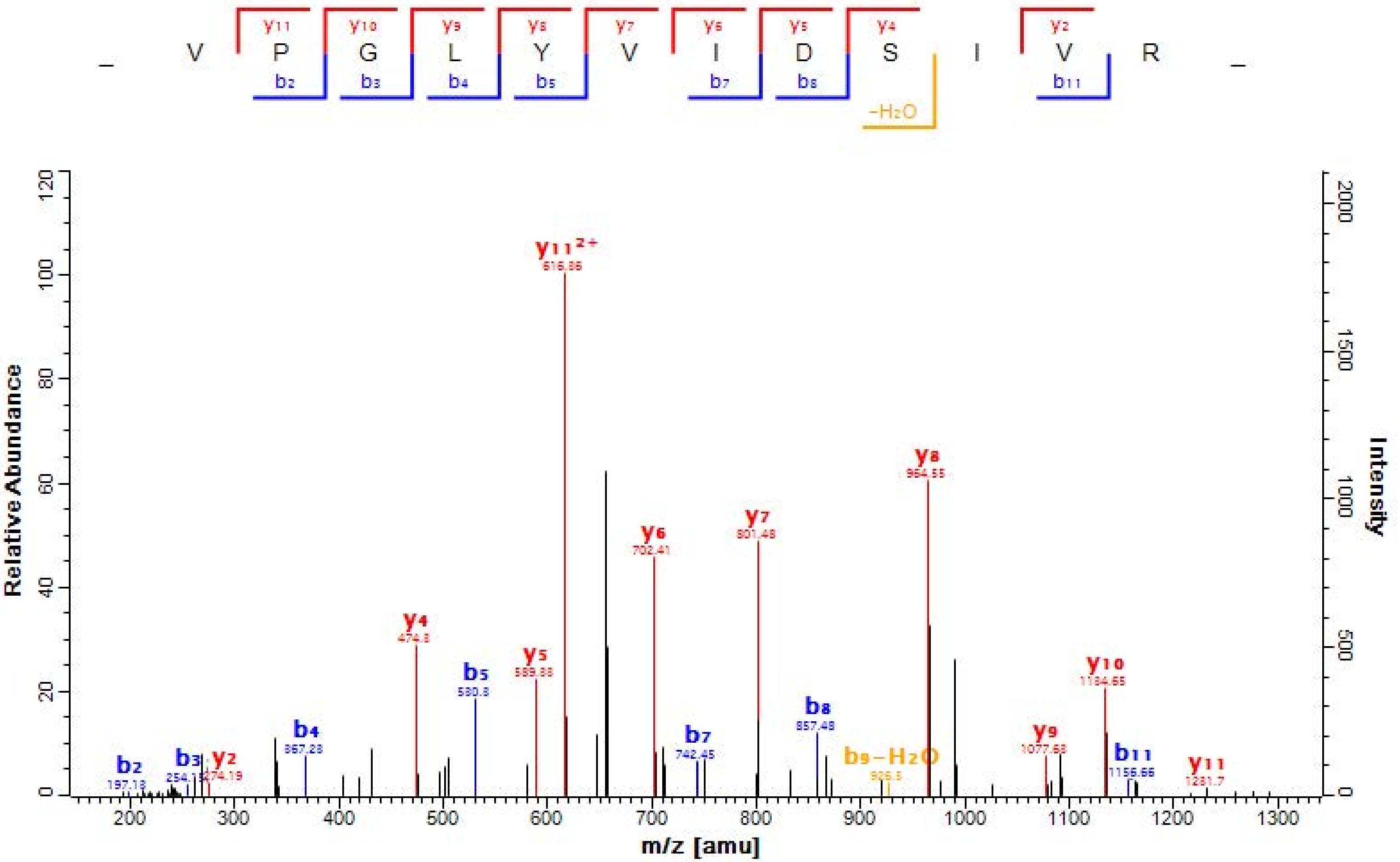
Method ITMS; CID **Pepti...** 57.35

precursor information

Mass:	900.49201
m/z:	451.25328
Charge:	2+
Retentiontime:	11.195906639099
Score:	57.34834
Mass Error [ppm]:	0.40126
PEP:	0.02988
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	37 %
Peak Coverage:	17 %
Protein Localisation:	172 ... 180

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	86.09643		114.0913	1	L	8		
+0.048771	215.139	+0.024361	243.1339	2	E	7	788.4149	+0.163082
	286.1761	-0.06405	314.171	3	A	6	659.3723	+0.048083
	357.2132		385.2082	4	A	5	588.3352	-0.05225
	470.2973		498.2922	5	L	4	517.298	+0.027218
	527.3188		555.3137	6	G	3	404.214	-0.01543
	656.3614	+0.067851	684.3563	7	E	2	347.1925	+0.096612
	727.3985		755.3934	8	A	1	218.1499	+0.126922
				9	K	0	147.1128	+0.044331

Scan number	9815	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	94.19



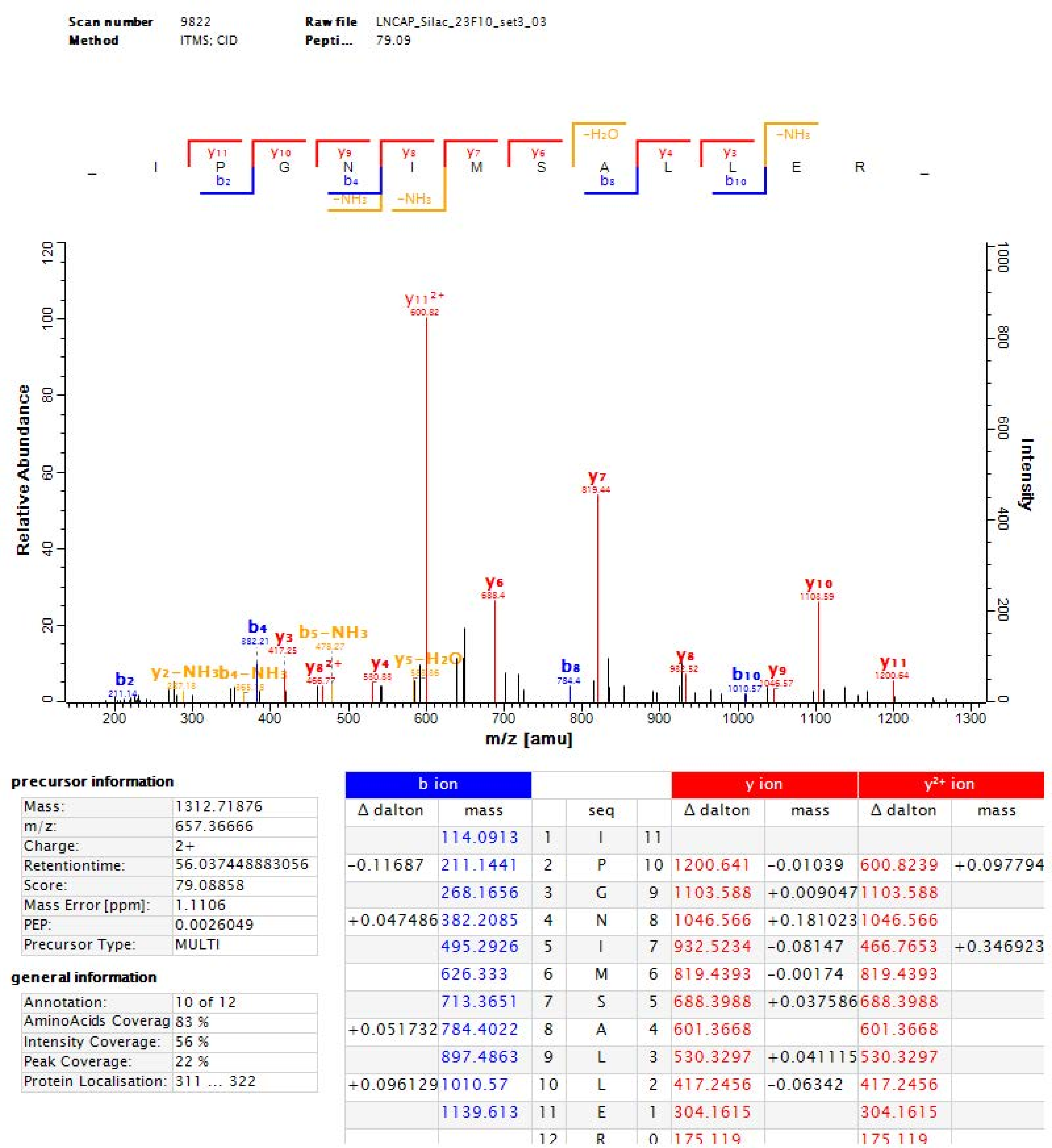
precursor information

Mass:	1329.76491
m/z:	665.88973
Charge:	2+
Retentiontime:	55.996360778808
Score:	94.19147
Mass Error [ppm]:	-0.54798
PEP:	0.0006535
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	50 %
Peak Coverage:	20 %
Protein Localisation:	60 ... 71

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	11				
+0.046167	197.1285	2	P	10	1231.704	-0.06937	616.3559	+0.247322
-0.05426	254.1499	3	G	9	1134.652	+0.082639	1134.652	
+0.061123	367.234	4	L	8	1077.63	+0.052223	1077.63	
+0.002067	530.2973	5	Y	7	964.5462	+0.019466	964.5462	
	629.3657	6	V	6	801.4829	+0.049225	801.4829	
+0.142314	742.4498	7	I	5	702.4145	+0.027124	702.4145	
-0.1281	857.4767	8	D	4	589.3304	+0.125104	589.3304	
	944.5088	9	S	3	474.3035	+0.038644	474.3035	
	1057.593	10	I	2	387.2714		387.2714	
-0.06053	1156.661	11	V	1	274.1874	+0.152783	274.1874	
		12	R	0	175.119		175.119	



Scan number	9822	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	79.09

precursor information

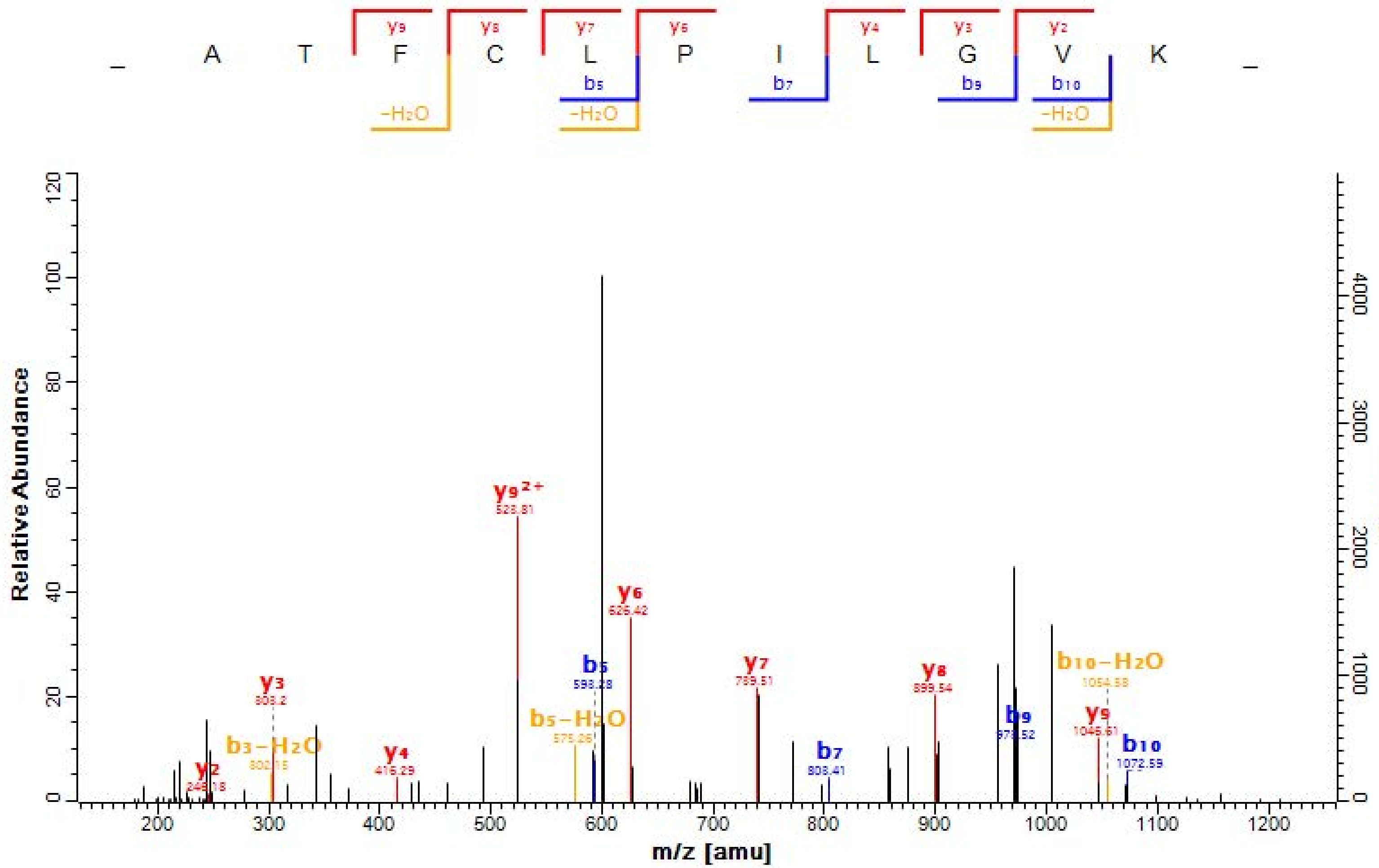
Mass:	1312.71876
m/z:	657.36666
Charge:	2+
Retentiontime:	56.037448883056
Score:	79.08858
Mass Error [ppm]:	1.1106
PEP:	0.0026049
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	56 %
Peak Coverage:	22 %
Protein Localisation:	311 ... 322

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	I	11				
-0.11687	211.1441	2	P	10	1200.641	-0.01039	600.8239	+0.097794
	268.1656	3	G	9	1103.588	+0.009047	1103.588	
+0.047486	382.2085	4	N	8	1046.566	+0.181023	1046.566	
	495.2926	5	I	7	932.5234	-0.08147	466.7653	+0.346923
	626.333	6	M	6	819.4393	-0.00174	819.4393	
	713.3651	7	S	5	688.3988	+0.037586	688.3988	
+0.051732	784.4022	8	A	4	601.3668		601.3668	
	897.4863	9	L	3	530.3297	+0.041115	530.3297	
+0.096129	1010.57	10	L	2	417.2456	-0.06342	417.2456	
	1139.613	11	E	1	304.1615		304.1615	
		12	R	0	175.119		175.119	

Scan number	9925	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	76.14



precursor information

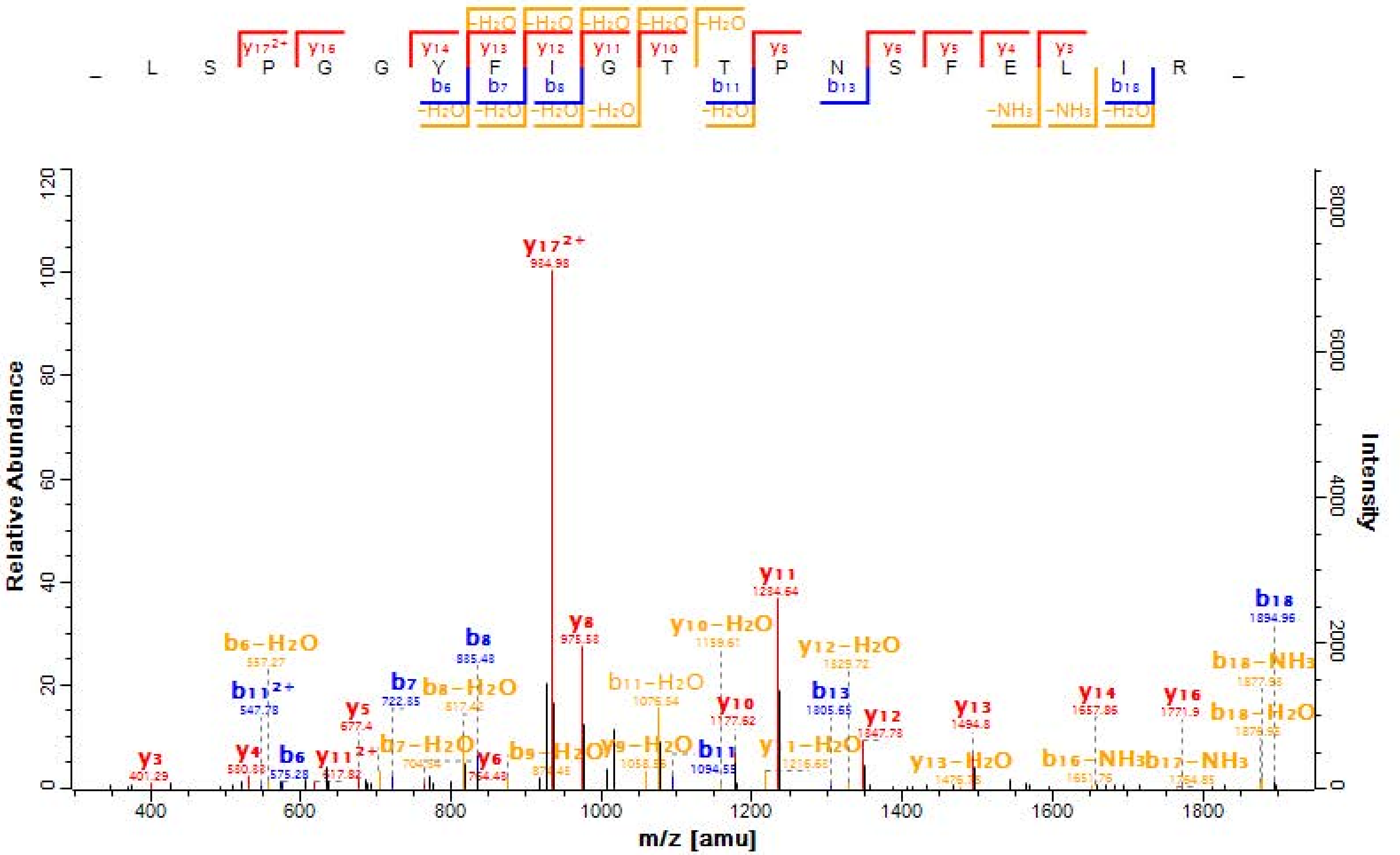
Mass:	1217.6843
m/z:	609.84943
Charge:	2+
Retentiontime:	56.675773620605
Score:	76.14272
Mass Error [ppm]:	0.071669
PEP:	0.0044509
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	28 %
Peak Coverage:	16 %
Protein Localisation:	190 ... 200

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	10				
	173.0921	2	T	9	1147.654		1147.654	
	320.1605	3	F	8	1046.607	-0.07972	523.807	+0.030048
	480.1911	4	C	7	899.5383	-0.02632	899.5383	
+0.046277	593.2752	5	L	6	739.5076	+0.065788	739.5076	
	690.328	6	P	5	626.4236	+0.009837	626.4236	
-0.10239	803.412	7	I	4	529.3708		529.3708	
	916.4961	8	L	3	416.2867	+0.0556	416.2867	
+0.341092	973.5176	9	G	2	303.2027	+0.08516	303.2027	
+0.123386	1072.586	10	V	1	246.1812	+0.0769	246.1812	
		11	K	0	147.1128		147.1128	

Scan number	9973	**Raw file**	LNCAP_Silac_23F10_set3_03
Method	ITMS; CID	**Pepti...**	148.36



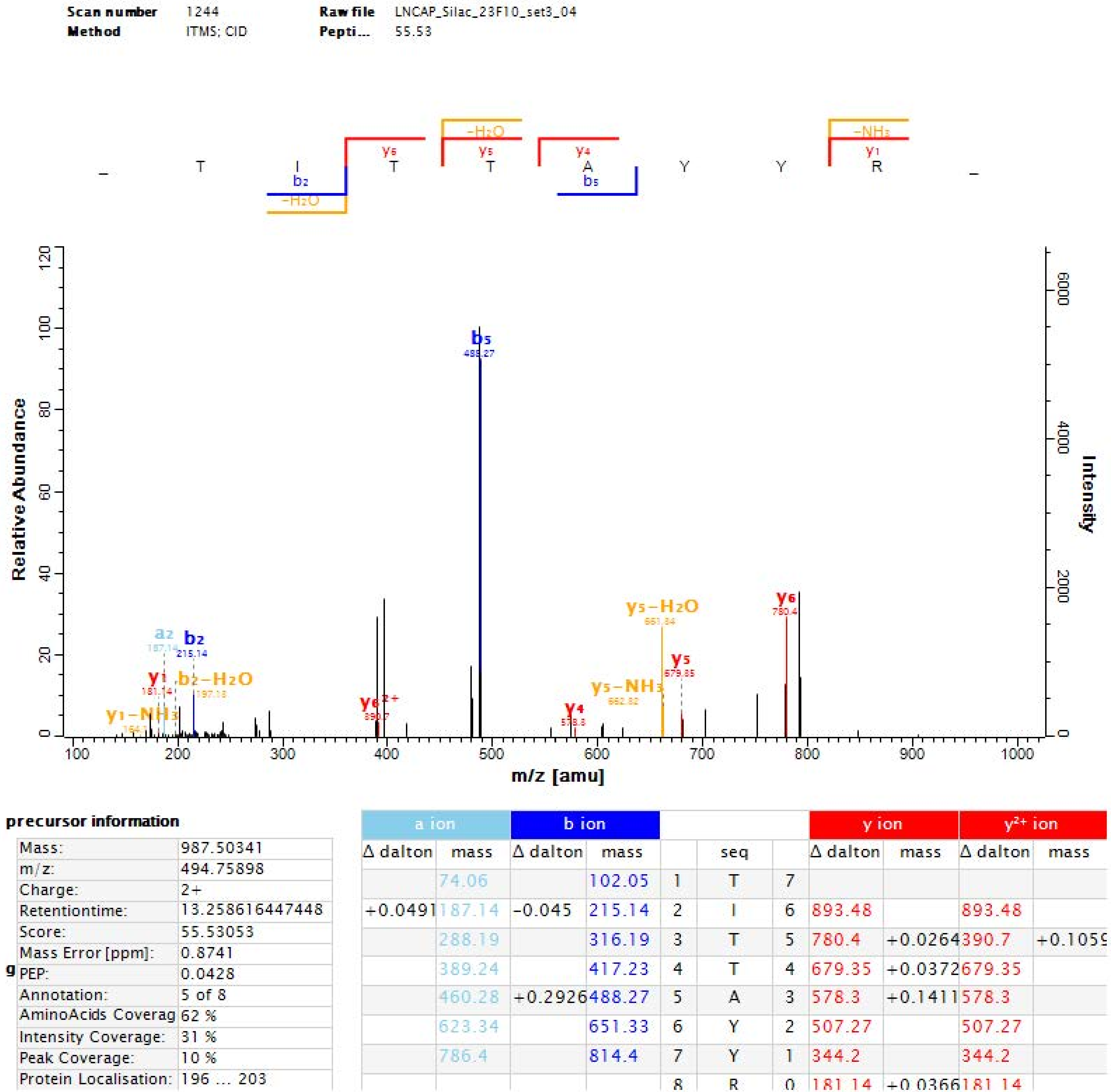
precursor information

Mass:	2068.06299
m/z:	1035.03877
Charge:	2+
Retentiontime:	56.967273712158
Score:	148.3611
Mass Error [ppm]:	0.023279
PEP:	2.7067E-19
Precursor Type:	MULTI

general information

Annotation:	15 of 19
AminoAcids Coverag	79 %
Intensity Coverage:	60 %
Peak Coverage:	37 %
Protein Localisation:	308 ... 326

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	18				
	201.12		201.12	2	S	17	1956		1956	
	298.18		298.18	3	P	16	1869		934.98	+0.2488
	355.2		355.2	4	G	15	1771.9	-0.172	1771.9	
	412.22		412.22	5	G	14	1714.9		1714.9	
	575.28	-0.059	575.28	6	Y	13	1657.9	+0.1978	1657.9	
	722.35	-0.025	722.35	7	F	12	1494.8	-0.066	1494.8	
	835.43	-0.012	835.43	8	I	11	1347.7	-0.042	1347.7	
	892.46		892.46	9	G	10	1234.6	-0.013	617.82	-0.418
	993.5		993.5	10	T	9	1177.6	-0.024	1177.6	
-0.458	547.78	-0.117	1094.6	11	T	8	1076.6		1076.6	
	1191.6		1191.6	12	P	7	975.53	-0.01	975.53	
	1305.6	+0.0275	1305.6	13	N	6	878.47		878.47	
	1392.7		1392.7	14	S	5	764.43	+0.3166	764.43	
	1539.7		1539.7	15	F	4	677.4	-0.126	677.4	
	1668.8		1668.8	16	E	3	530.33	-0.06	530.33	
	1781.9		1781.9	17	L	2	401.29	-0.004	401.29	
	1895	+0.0743	1895	18	I	1	288.2		288.2	
				19	R	0	175.12		175.12	



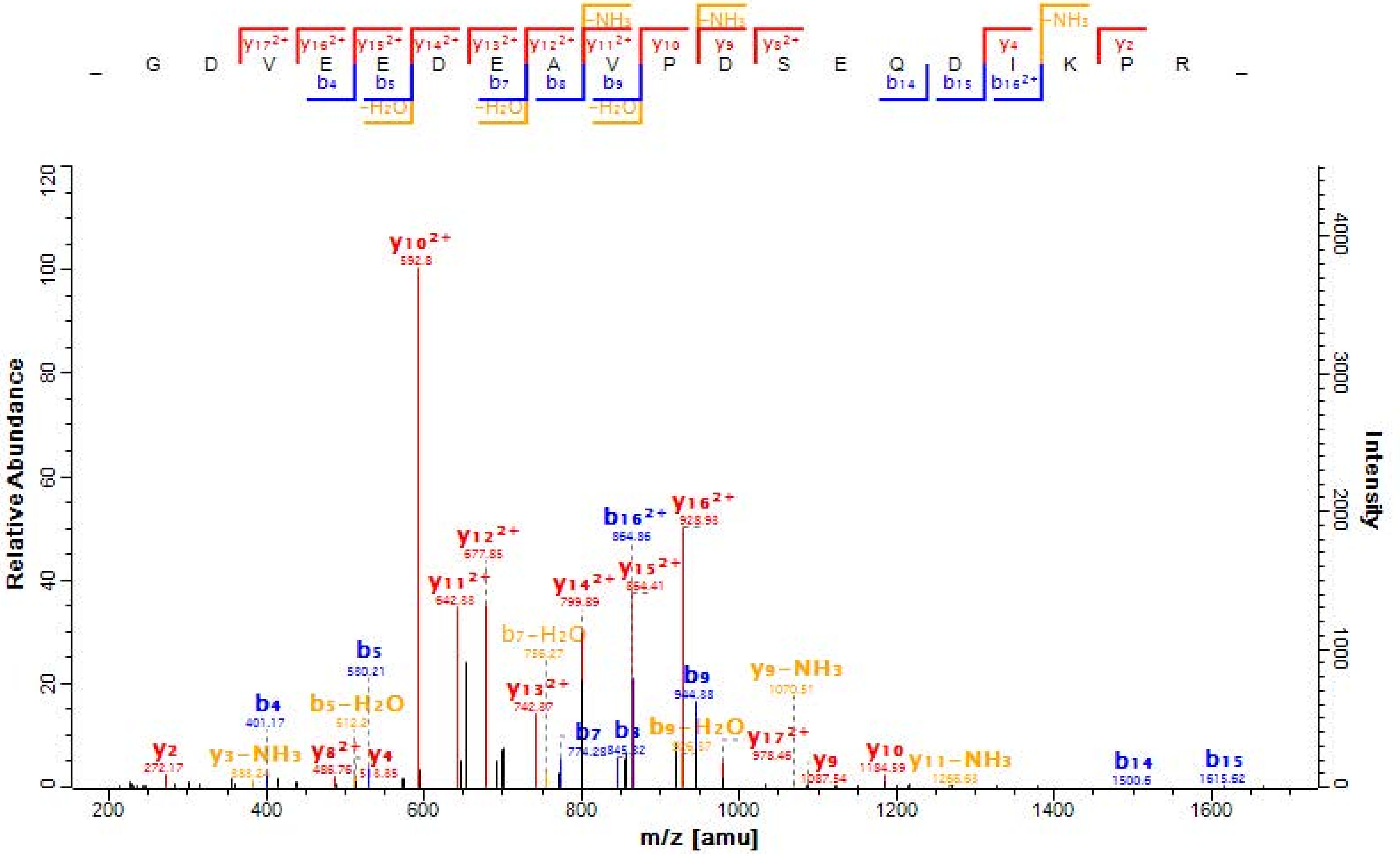
Scan number	1244	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	55.53

precursor information

Mass:	987.50341
m/z:	494.75898
Charge:	2+
Retentiontime:	13.258616447448
Score:	55.53053
Mass Error [ppm]:	0.8741
PEP:	0.0428
Annotation:	5 of 8
AminoAcids Coverag	62 %
Intensity Coverage:	31 %
Peak Coverage:	10 %
Protein Localisation:	196 ... 203

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.05	1	T	7				
+0.0491	187.14	−0.045	215.14	2	I	6	893.48		893.48	
	288.19		316.19	3	T	5	780.4	+0.0264	390.7	+0.1059
	389.24		417.23	4	T	4	679.35	+0.0372	679.35	
	460.28	+0.2926	488.27	5	A	3	578.3	+0.1411	578.3	
	623.34		651.33	6	Y	2	507.27		507.27	
	786.4		814.4	7	Y	1	344.2		344.2	
				8	R	0	181.14	+0.0366	181.14	

Scan number	1605	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	131.4



precursor information

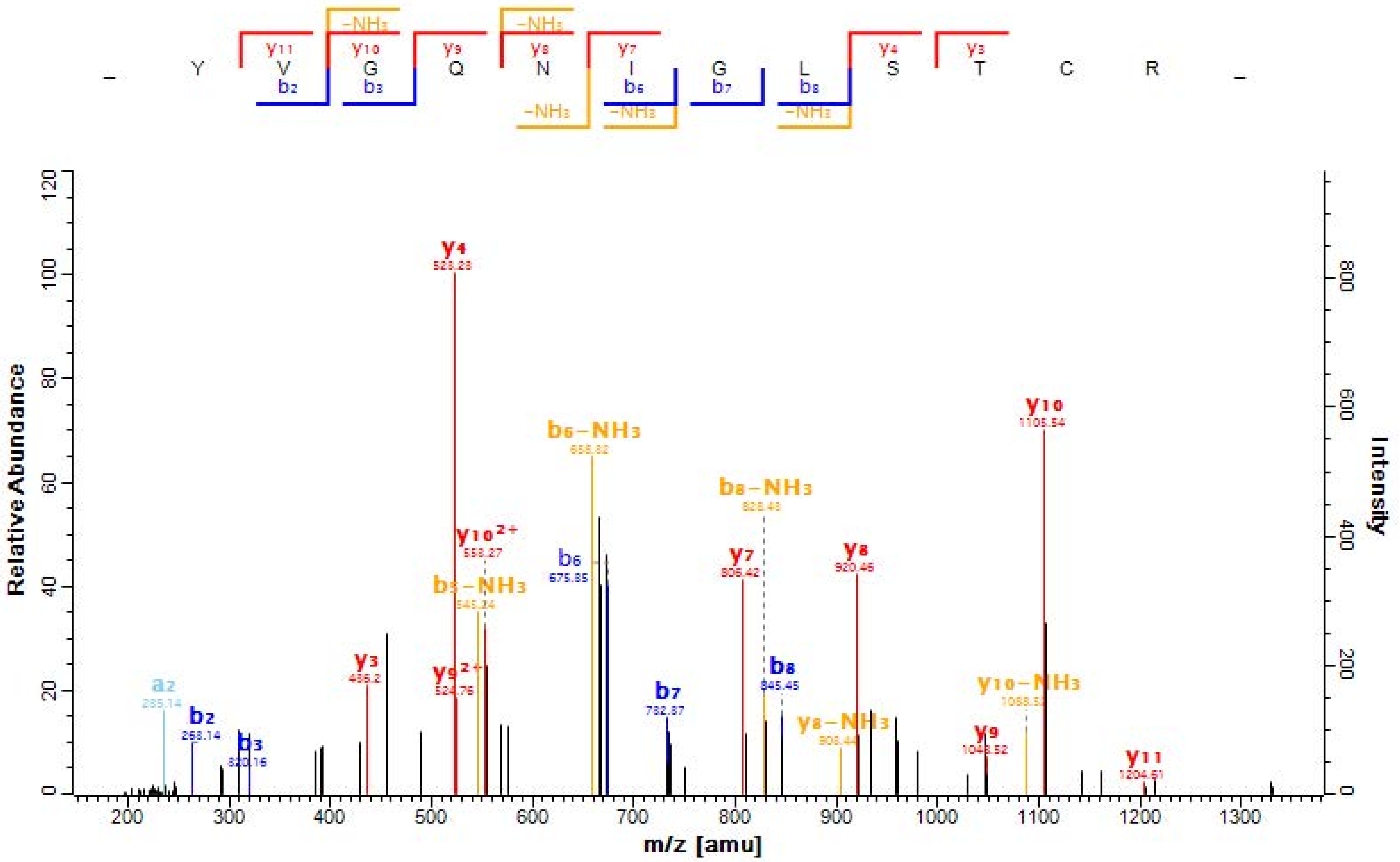
Mass:	2126.96054
m/z:	709.99412
Charge:	3+
Retentiontime:	15.437981605529
Score:	131.3965
Mass Error [ppm]:	0.07068
PEP:	3.6296E-13
Precursor Type:	MULTI

general information

Annotation:	15 of 19
AminoAcids Coverag	79 %
Intensity Coverage:	75 %
Peak Coverage:	29 %
Protein Localisation:	318 ... 336

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	18				
	173.06		173.06	2	D	17	2070.9		2070.9	
	272.12		272.12	3	V	16	1955.9		978.46	+0.0997
	401.17	+0.0076	401.17	4	E	15	1856.9		928.93	+0.2494
	530.21	+0.0712	530.21	5	E	14	1727.8		864.41	+0.05
	645.24		645.24	6	D	13	1598.8		799.89	+0.015
	774.28	-0.086	774.28	7	E	12	1483.7		742.37	+0.257
	845.32	+0.032	845.32	8	A	11	1354.7		677.85	+0.188
	944.38	-0.047	944.38	9	V	10	1283.7		642.33	+0.167
	1041.4		1041.4	10	P	9	1184.6	-0.068	592.8	+0.225
	1156.5		1156.5	11	D	8	1087.5	-0.06	1087.5	
	1243.5		1243.5	12	S	7	972.51		486.76	-0.093
	1372.5		1372.5	13	E	6	885.48		885.48	
	1500.6	-0.258	1500.6	14	Q	5	756.44		756.44	
	1615.6	-0.107	1615.6	15	D	4	628.38		628.38	
+0.215	864.86		1728.7	16	I	3	513.35	+0.0515	513.35	
	1856.8		1856.8	17	K	2	400.27		400.27	
	1953.9		1953.9	18	P	1	272.17	+0.0096	272.17	
				19	R	0	175.12		175.12	

Scan number	2244	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	117.09



precursor information

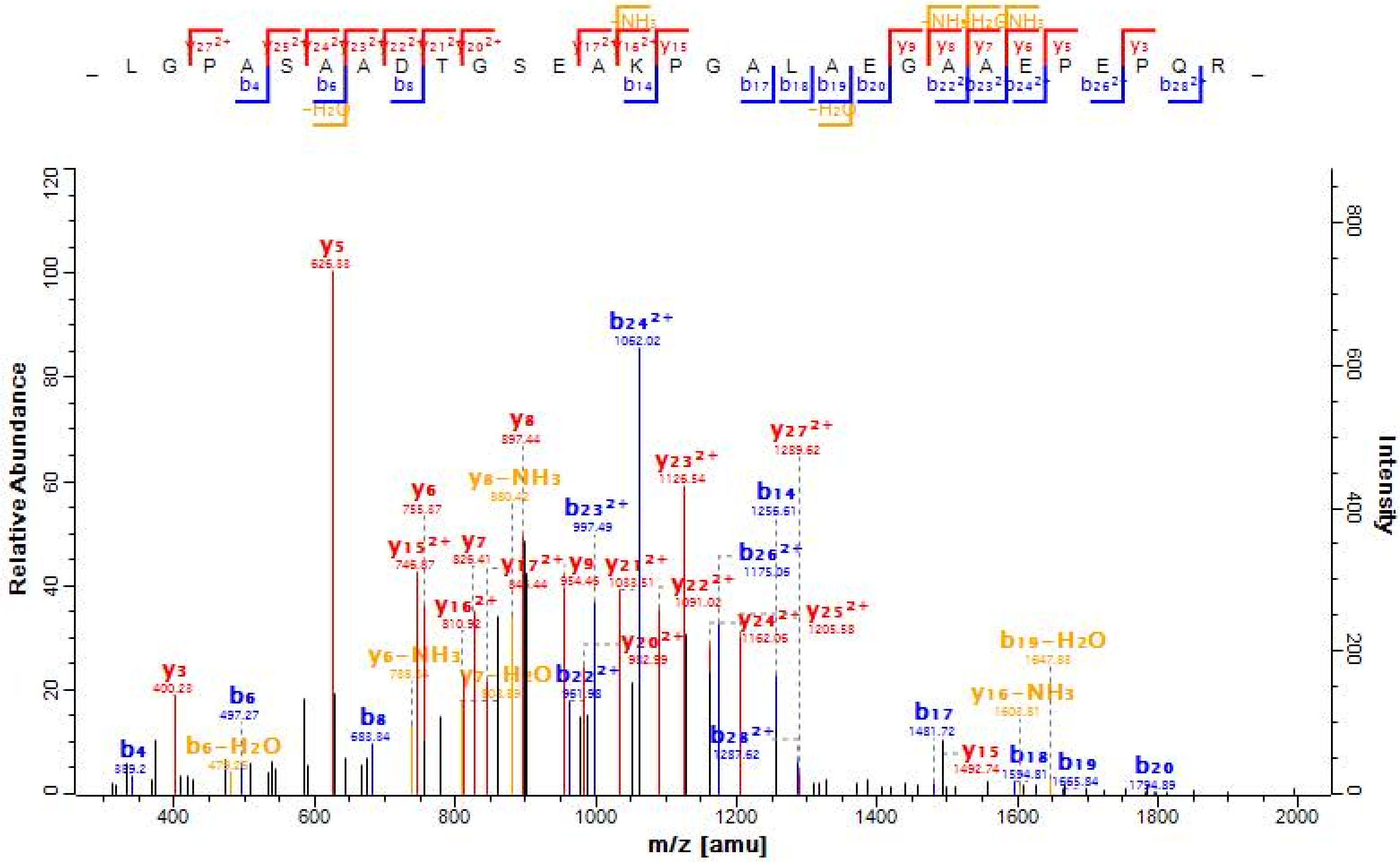
Mass:	1366.66655
m/z:	684.34055
Charge:	2+
Retentiontime:	18.934509277343
Score:	117.0911
Mass Error [ppm]:	0.15984
PEP:	2.7349E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	50 %
Peak Coverage:	23 %
Protein Localisation:	243 ... 254

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.08		164.07	1	Y	11				
+0.0022	235.14	+0.0009	263.14	2	V	10	1204.6	+0.0711	1204.6	
	292.17	+0.0228	320.16	3	G	9	1105.5	+0.0032	553.27	-0.061
	420.22		448.22	4	Q	8	1048.5	+0.1844	524.76	-0.392
	534.27		562.26	5	N	7	920.46	-0.004	920.46	
	647.35	+0.1353	675.35	6	I	6	806.42	+0.0444	806.42	
	704.37	-0.1	732.37	7	G	5	693.33		693.33	
	817.46	-0.051	845.45	8	L	4	636.31		636.31	
	904.49		932.48	9	S	3	523.23	-0.041	523.23	
	1005.5		1033.5	10	T	2	436.2	+0.0716	436.2	
	1165.6		1193.6	11	C	1	335.15		335.15	
				12	R	0	175.12		175.12	

Scan number	2259	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	163.18



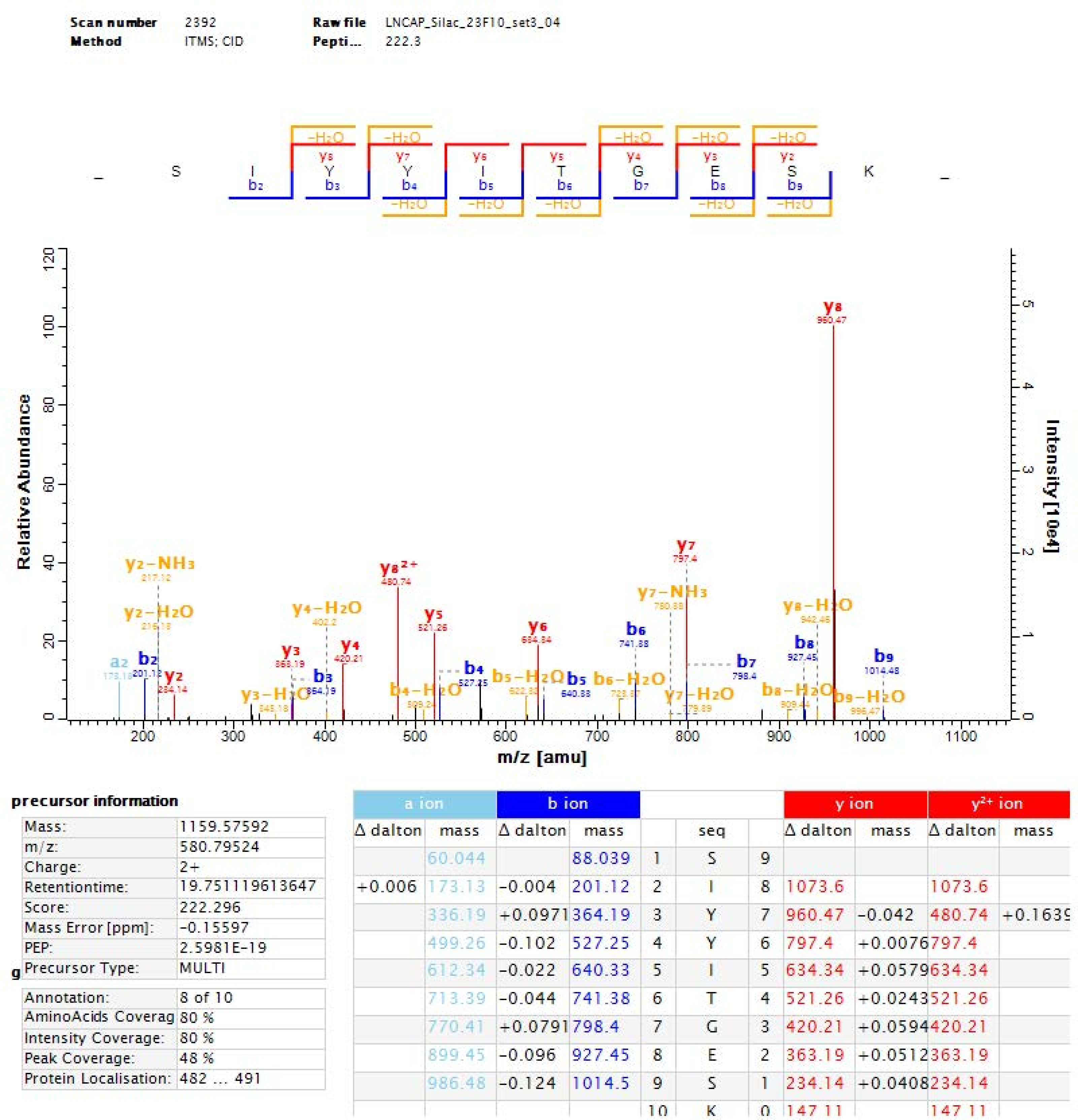
precursor information

Mass:	2747.33534
m/z:	916.78572
Charge:	3+
Retentiontime:	19.017257690429
Score:	163.1846
Mass Error [ppm]:	-0.31699
PEP:	5.013E-32
Precursor Type:	ISO

general information

Annotation:	24 of 29
AminoAcids Coverag	83 %
Intensity Coverage:	65 %
Peak Coverage:	38 %
Protein Localisation:	101 ... 129

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	28				
	171.11		171.11	2	G	27	2635.3		2635.3	
	268.17		268.17	3	P	26	2578.2		1289.6	-0.265
	339.2	+0.1034	339.2	4	A	25	2481.2		2481.2	
	426.23		426.23	5	S	24	2410.1		1205.6	+0.2463
	497.27	-0.093	497.27	6	A	23	2323.1		1162.1	+0.1565
	568.31		568.31	7	A	22	2252.1		1126.5	+0.2605
	683.34	-0.156	683.34	8	D	21	2181		1091	+0.3128
	784.38		784.38	9	T	20	2066		1033.5	+0.2241
	841.41		841.41	10	G	19	1965		982.99	+0.2778
	928.44		928.44	11	S	18	1907.9		1907.9	
	1057.5		1057.5	12	E	17	1820.9		1820.9	
	1128.5		1128.5	13	A	16	1691.9		846.44	+0.2775
	1256.6	-0.05	1256.6	14	K	15	1620.8		810.92	+0.2475
	1353.7		1353.7	15	P	14	1492.7	-0.101	746.87	+0.1887
	1410.7		1410.7	16	G	13	1395.7		1395.7	
	1481.7	-0.189	1481.7	17	A	12	1338.7		1338.7	
	1594.8	+0.1049	1594.8	18	L	11	1267.6		1267.6	
	1665.8	-0.438	1665.8	19	A	10	1154.5		1154.5	
	1794.9	-0.336	1794.9	20	E	9	1083.5		1083.5	
	1851.9		1851.9	21	G	8	954.46	+0.006	954.46	
+0.2242	961.98		1922.9	22	A	7	897.44	-0.06	897.44	
+0.234	997.49		1994	23	A	6	826.41	+0.0575	826.41	
+0.2904	1062		2123	24	E	5	755.37	+0.0739	755.37	
	2220.1		2220.1	25	P	4	626.33	+0.003	626.33	
+0.2365	1175.1		2349.1	26	E	3	529.27		529.27	
	2446.2		2446.2	27	P	2	400.23	+0.089	400.23	
+0.1883	1287.6		2574.2	28	Q	1	303.18		303.18	
				29	R	0	175.12		175.12	



Scan number	2392	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	222.3

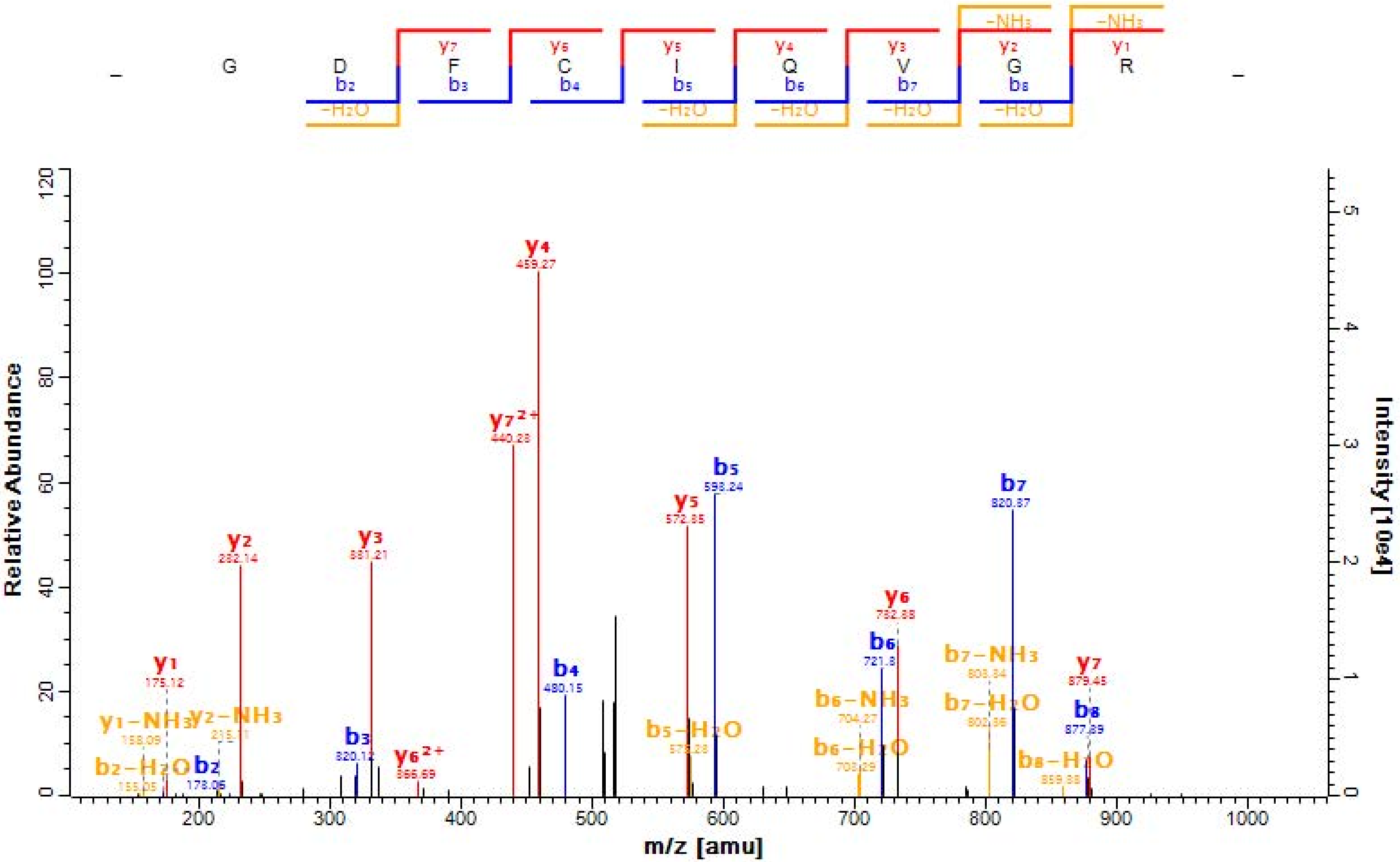
precursor information

Mass:	1159.57592
m/z:	580.79524
Charge:	2+
Retentiontime:	19.751119613647
Score:	222.296
Mass Error [ppm]:	-0.15597
PEP:	2.5981E-19
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	80 %
Peak Coverage:	48 %
Protein Localisation:	482 ... 491

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	60.044		88.039	1	S	9				
+0.006	173.13	-0.004	201.12	2	I	8	1073.6		1073.6	
	336.19	+0.0971	364.19	3	Y	7	960.47	-0.042	480.74	+0.1639
	499.26	-0.102	527.25	4	Y	6	797.4	+0.0076	797.4	
	612.34	-0.022	640.33	5	I	5	634.34	+0.0579	634.34	
	713.39	-0.044	741.38	6	T	4	521.26	+0.0243	521.26	
	770.41	+0.0791	798.4	7	G	3	420.21	+0.0594	420.21	
	899.45	-0.096	927.45	8	E	2	363.19	+0.0512	363.19	
	986.48	-0.124	1014.5	9	S	1	234.14	+0.0408	234.14	
				10	K	0	147.11		147.11	

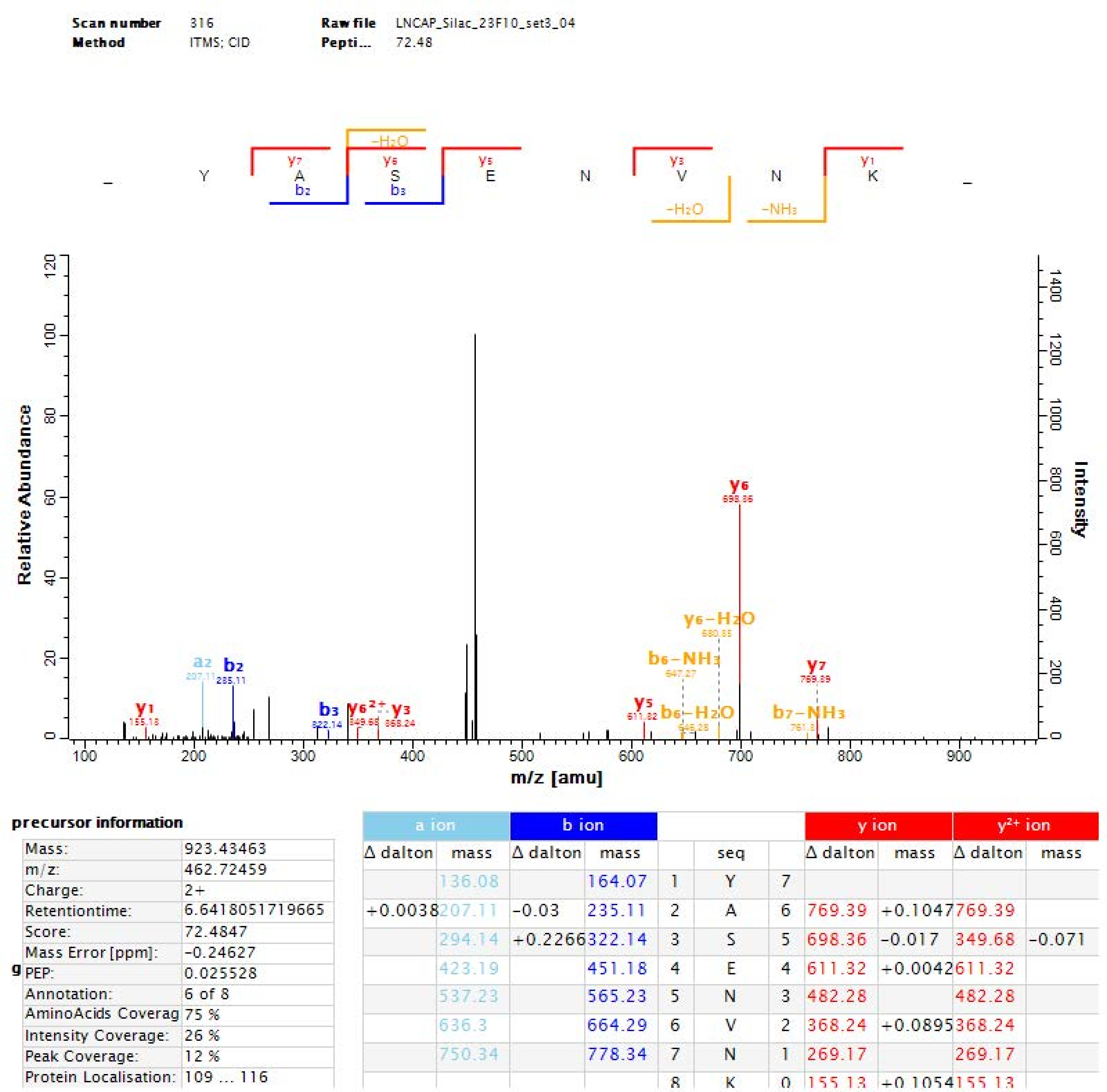
Scan number	3059	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	207.29



precursor information

Mass:	1050.49156
m/z:	526.25306
Charge:	2+
Retentiontime:	23.451385498046
Score:	207.2877
Mass Error [ppm]:	-0.10007
PEP:	1.0455E-12
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	73 %
Peak Coverage:	35 %
Protein Localisation:	131 ... 139; 246 ...

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	8				
-0.07035	173.0557	2	D	7	994.4775		994.4775	
+0.01958	320.1241	3	F	6	879.4505	-0.08194	440.2289	+0.203407
-0.01467	480.1547	4	C	5	732.3821	+0.030173	366.6947	+0.191716
+0.005759	593.2388	5	I	4	572.3515	+0.056976	572.3515	
-0.07284	721.2974	6	Q	3	459.2674	+0.022082	459.2674	
-0.0436	820.3658	7	V	2	331.2088	+0.02762	331.2088	
-0.07452	877.3873	8	G	1	232.1404	+0.009303	232.1404	
		9	R	0	175.119	+0.074834	175.119	



Scan number	316	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	72.48

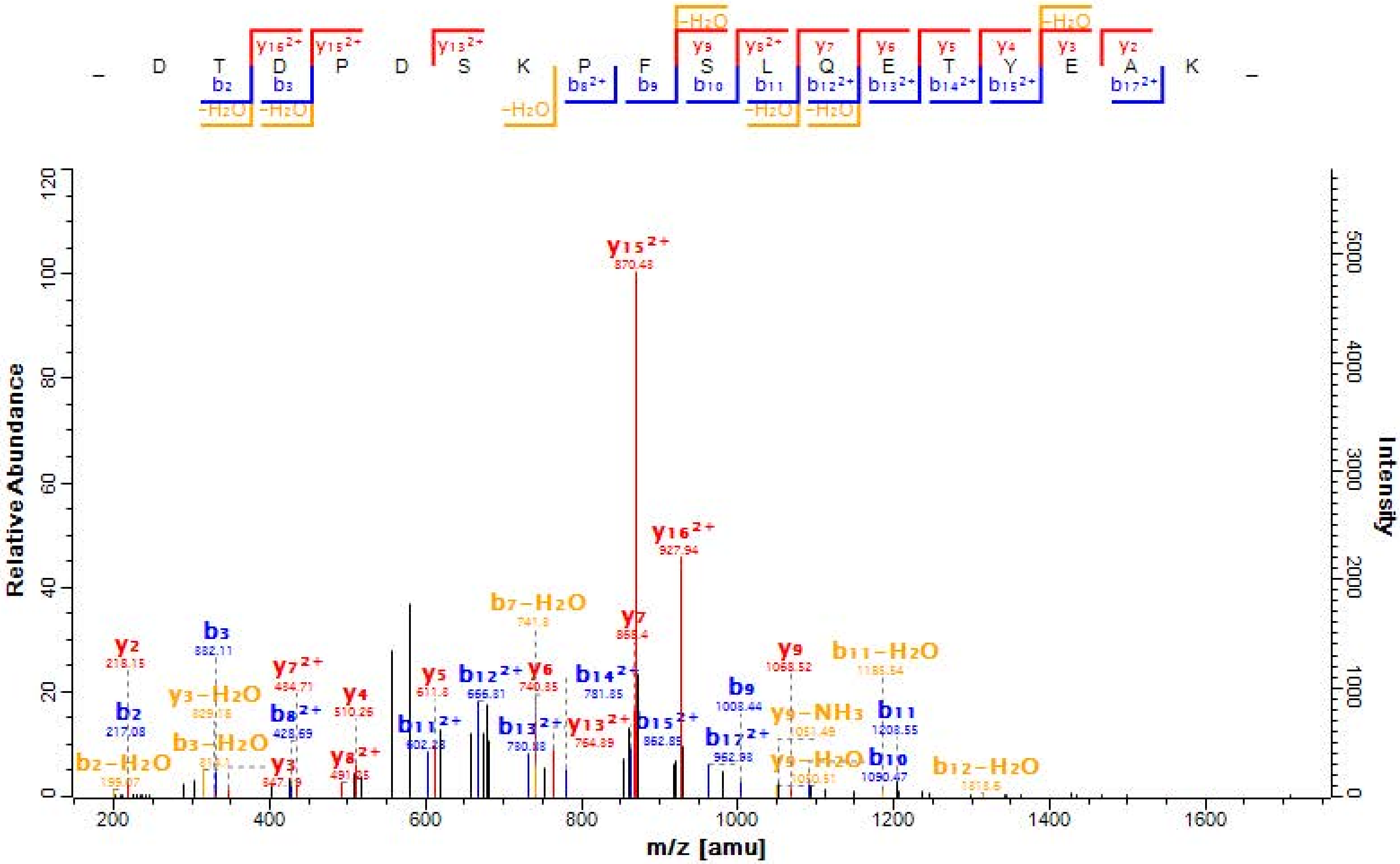
precursor information

g

Mass:	923.43463
m/z:	462.72459
Charge:	2+
Retentiontime:	6.6418051719665
Score:	72.4847
Mass Error [ppm]:	-0.24627
PEP:	0.025528
Annotation:	6 of 8
AminoAcids Coverag	75 %
Intensity Coverage:	26 %
Peak Coverage:	12 %
Protein Localisation:	109 ... 116

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.08		164.07	1	Y	7				
+0.0038	207.11	-0.03	235.11	2	A	6	769.39	+0.1047	769.39	
	294.14	+0.2266	322.14	3	S	5	698.36	-0.017	349.68	-0.071
	423.19		451.18	4	E	4	611.32	+0.0042	611.32	
	537.23		565.23	5	N	3	482.28		482.28	
	636.3		664.29	6	V	2	368.24	+0.0895	368.24	
	750.34		778.34	7	N	1	269.17		269.17	
				8	K	0	155.13	+0.1054	155.13	

Scan number	3320	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	161.82



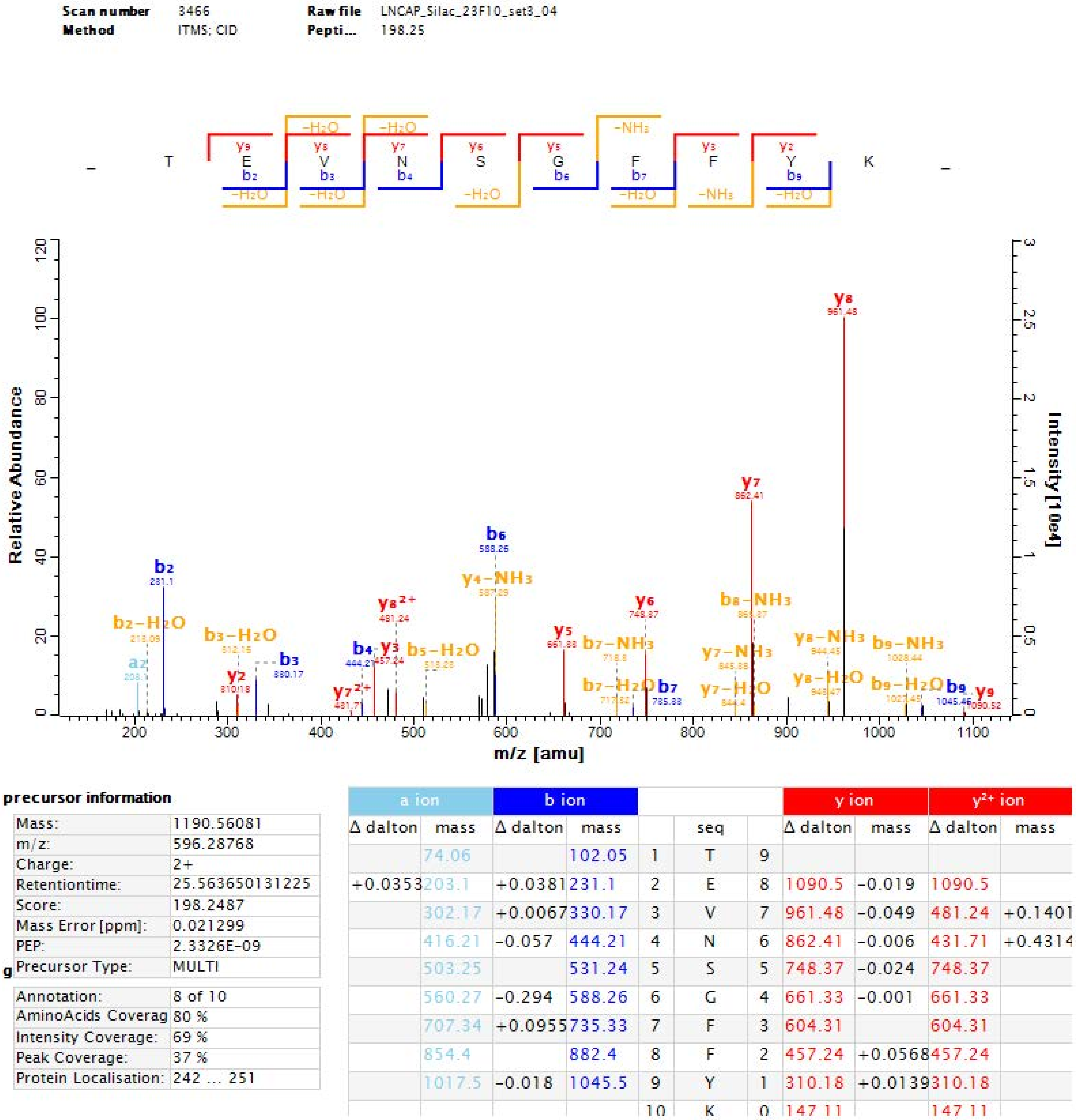
precursor information

Mass:	2069.94318
m/z:	690.98834
Charge:	3+
Retentiontime:	24.827289581298
Score:	161.8241
Mass Error [ppm]:	0.11533
PEP:	7.8318E-24
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	53 %
Peak Coverage:	32 %
Protein Localisation:	319 ... 336

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	17				
	217.08	+0.0454	217.08	2	T	16	1955.9		1955.9	
	332.11	-0.017	332.11	3	D	15	1854.9		927.94	+0.2448
	429.16		429.16	4	P	14	1739.8		870.43	+0.2122
	544.19		544.19	5	D	13	1642.8		1642.8	
	631.22		631.22	6	S	12	1527.8		764.39	+0.4164
	759.32		759.32	7	K	11	1440.7		1440.7	
-0.352	428.69		856.37	8	P	10	1312.6		1312.6	
	1003.4	-0.031	1003.4	9	F	9	1215.6		1215.6	
	1090.5	-0.036	1090.5	10	S	8	1068.5	+0.4738	1068.5	
+0.1527	602.28	-0.162	1203.6	11	L	7	981.49		491.25	+0.3494
+0.2404	666.31		1331.6	12	Q	6	868.4	-0.024	434.71	-0.171
+0.3241	730.83		1460.7	13	E	5	740.35	+0.0174	740.35	
+0.0342	781.35		1561.7	14	T	4	611.3	+0.0401	611.3	
-0.274	862.89		1724.8	15	Y	3	510.26	+0.093	510.26	
	1853.8		1853.8	16	E	2	347.19	+0.1154	347.19	
-0.096	962.93		1924.8	17	A	1	218.15	+0.062	218.15	
				18	K	0	147.11		147.11	



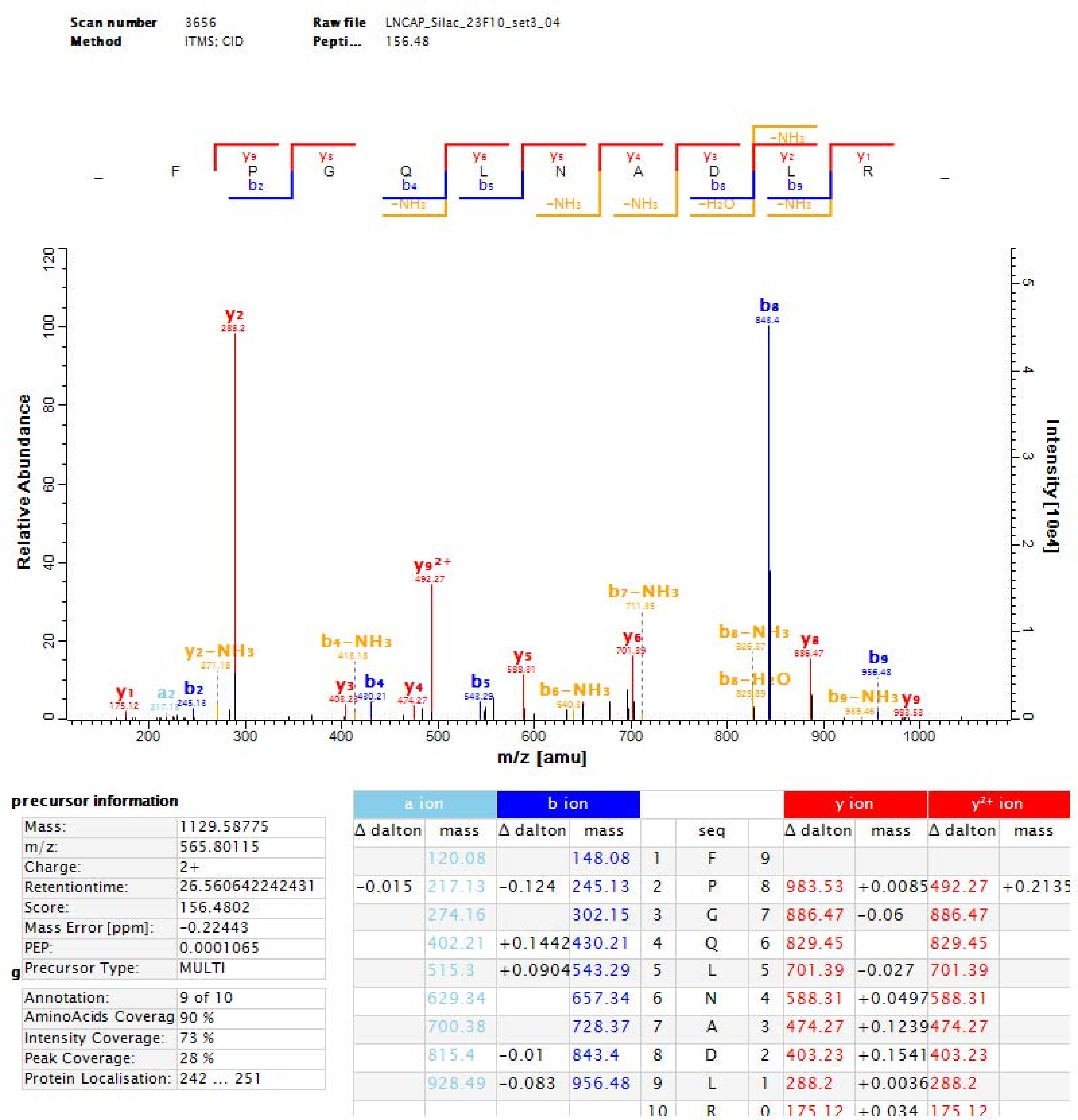
Scan number 3466 **Raw file** LNCAP_Silac_23F10_set3_04
Method ITMS; CID **Pepti...** 198.25

precursor information

Mass:	1190.56081
m/z:	596.28768
Charge:	2+
Retentiontime:	25.563650131225
Score:	198.2487
Mass Error [ppm]:	0.021299
PEP:	2.3326E-09
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	69 %
Peak Coverage:	37 %
Protein Localisation:	242 ... 251

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.05	1	T	9				
+0.0353	203.1	+0.0381	231.1	2	E	8	1090.5	-0.019	1090.5	
	302.17	+0.0067	330.17	3	V	7	961.48	-0.049	481.24	+0.1401
	416.21	-0.057	444.21	4	N	6	862.41	-0.006	431.71	+0.4314
	503.25		531.24	5	S	5	748.37	-0.024	748.37	
	560.27	-0.294	588.26	6	G	4	661.33	-0.001	661.33	
	707.34	+0.0955	735.33	7	F	3	604.31		604.31	
	854.4		882.4	8	F	2	457.24	+0.0568	457.24	
	1017.5	-0.018	1045.5	9	Y	1	310.18	+0.0139	310.18	
				10	K	0	147.11		147.11	



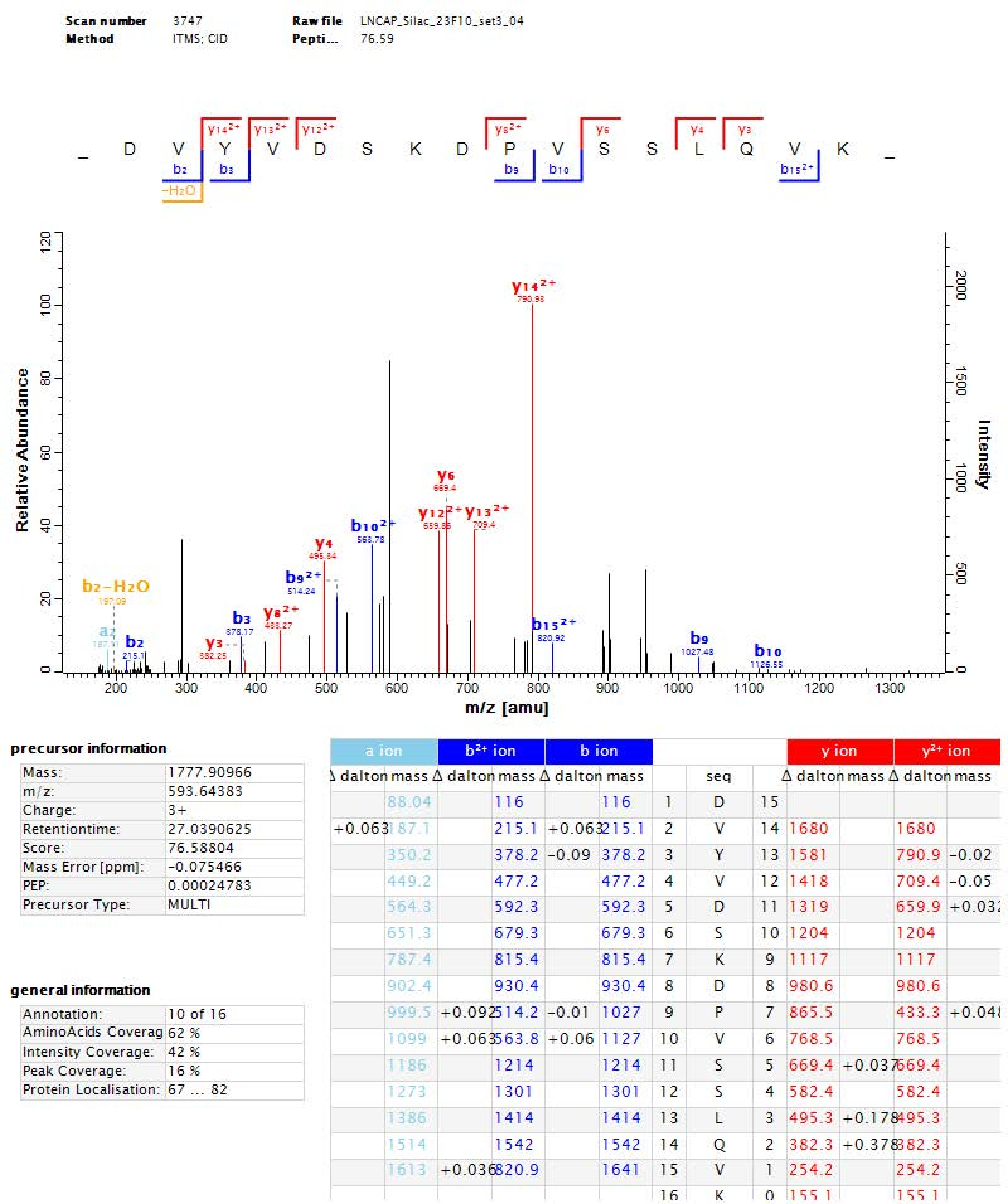
Scan number	3656	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	156.48

precursor information

Mass:	1129.58775
m/z:	565.80115
Charge:	2+
Retentiontime:	26.560642242431
Score:	156.4802
Mass Error [ppm]:	-0.22443
PEP:	0.0001065
Precursor Type:	MULTI

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	73 %
Peak Coverage:	28 %
Protein Localisation:	242 ... 251

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08		148.08	1	F	9				
-0.015	217.13	-0.124	245.13	2	P	8	983.53	+0.0085	492.27	+0.2135
	274.16		302.15	3	G	7	886.47	-0.06	886.47	
	402.21	+0.1442	430.21	4	Q	6	829.45		829.45	
	515.3	+0.0904	543.29	5	L	5	701.39	-0.027	701.39	
	629.34		657.34	6	N	4	588.31	+0.0497	588.31	
	700.38		728.37	7	A	3	474.27	+0.1239	474.27	
	815.4	-0.01	843.4	8	D	2	403.23	+0.1541	403.23	
	928.49	-0.083	956.48	9	L	1	288.2	+0.0036	288.2	
				10	R	0	175.12	+0.034	175.12	



Scan number	3747	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	76.59

precursor information

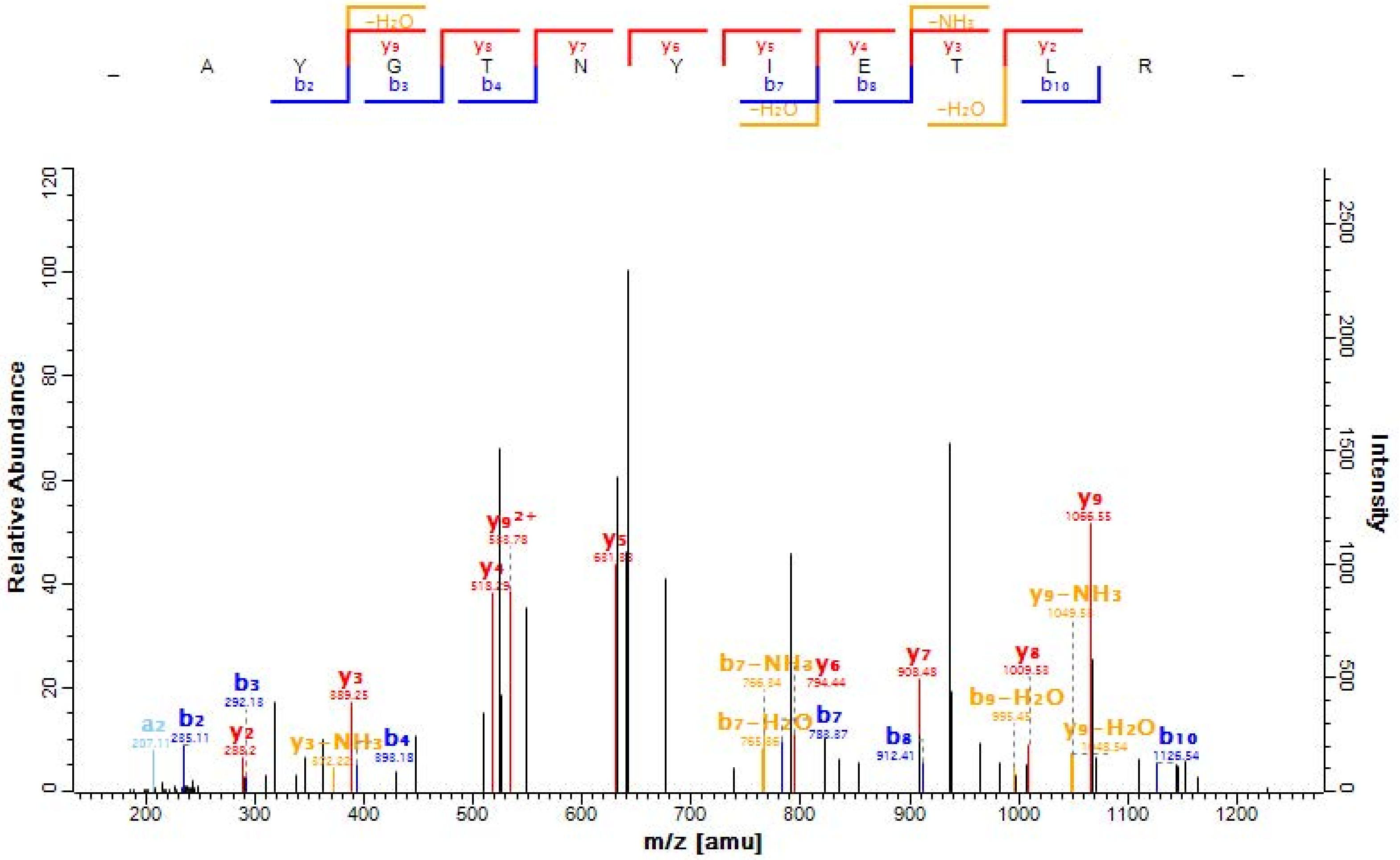
Mass:	1777.90966
m/z:	593.64383
Charge:	3+
Retentiontime:	27.0390625
Score:	76.58804
Mass Error [ppm]:	-0.075466
PEP:	0.00024783
Precursor Type:	MULTI

general information

Annotation:	10 of 16
AminoAcids Coverag	62 %
Intensity Coverage:	42 %
Peak Coverage:	16 %
Protein Localisation:	67 ... 82

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.04		116		116	1	D	15				
+0.063	187.1		215.1	+0.063	215.1	2	V	14	1680		1680	
	350.2		378.2	-0.09	378.2	3	Y	13	1581		790.9	-0.02
	449.2		477.2		477.2	4	V	12	1418		709.4	-0.05
	564.3		592.3		592.3	5	D	11	1319		659.9	+0.03
	651.3		679.3		679.3	6	S	10	1204		1204	
	787.4		815.4		815.4	7	K	9	1117		1117	
	902.4		930.4		930.4	8	D	8	980.6		980.6	
	999.5	+0.092	514.2	-0.01	1027	9	P	7	865.5		433.3	+0.04
	1099	+0.063	563.8	+0.06	1127	10	V	6	768.5		768.5	
	1186		1214		1214	11	S	5	669.4	+0.037	669.4	
	1273		1301		1301	12	S	4	582.4		582.4	
	1386		1414		1414	13	L	3	495.3	+0.178	495.3	
	1514		1542		1542	14	Q	2	382.3	+0.378	382.3	
	1613	+0.036	820.9		1641	15	V	1	254.2		254.2	
						16	K	0	155.1		155.1	

Scan number	4164	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	121.68



precursor information

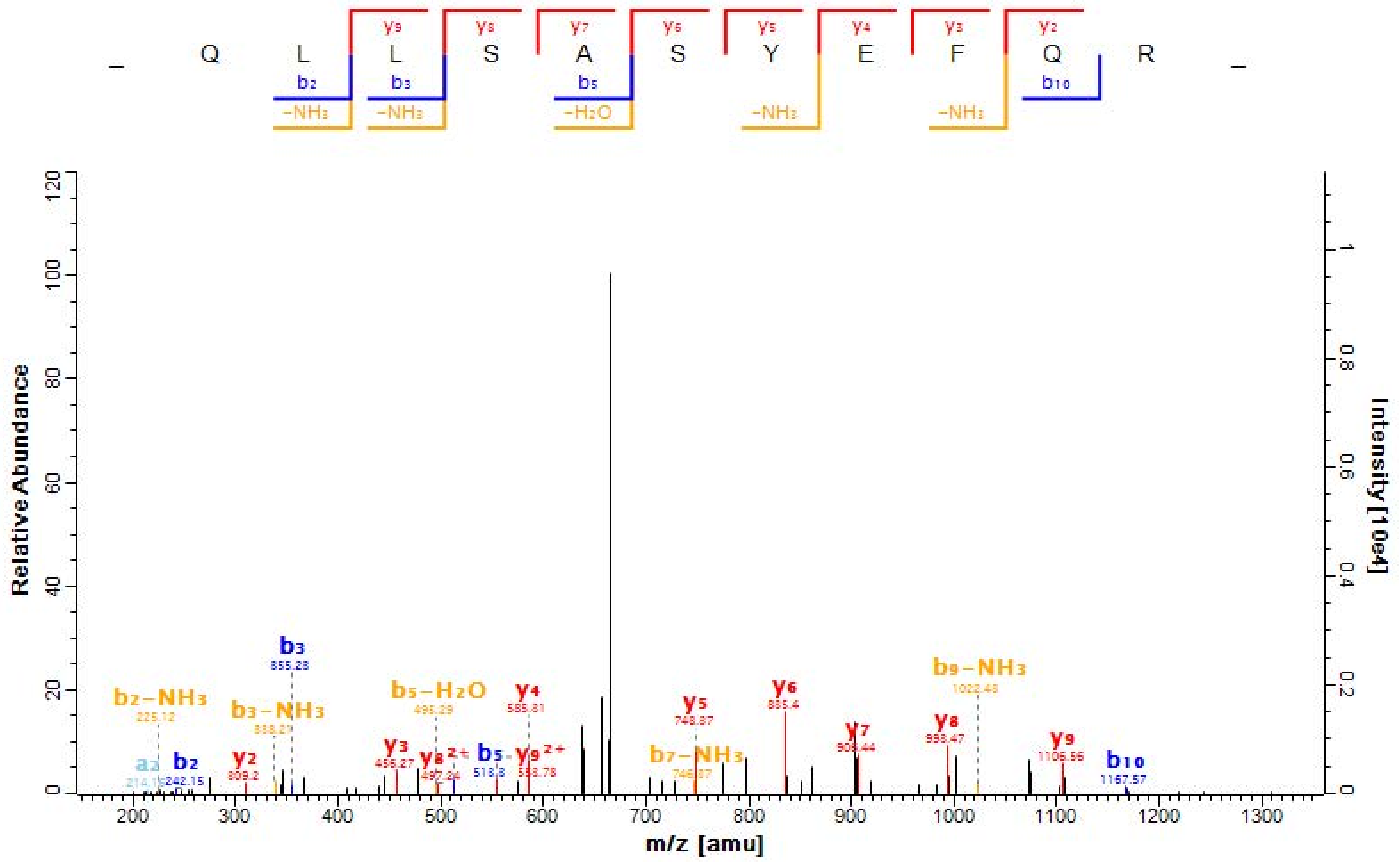
Mass:	1299.64733
m/z:	650.83094
Charge:	2+
Retentiontime:	29.189712524414
Score:	121.6796
Mass Error [ppm]:	1.0862
PEP:	0.00021309
Precursor Type:	ISO

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	30 %
Peak Coverage:	25 %
Protein Localisation:	143 ... 153

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	44.049		72.044	1	A	10				
+0.0839	207.11	-0.03	235.11	2	Y	9	1229.6		1229.6	
	264.13	+0.0926	292.13	3	G	8	1066.6	+0.0221	533.78	-0.252
	365.18	+0.0961	393.18	4	T	7	1009.5	-0.046	1009.5	
	479.22		507.22	5	N	6	908.48	-0.019	908.48	
	642.29		670.28	6	Y	5	794.44	+0.0624	794.44	
	755.37	+0.0009	783.37	7	I	4	631.38	+0.0746	631.38	
	884.41	+0	912.41	8	E	3	518.29	+0.0254	518.29	
	985.46		1013.5	9	T	2	389.25	+0.1442	389.25	
	1098.5	-0.021	1126.5	10	L	1	288.2	-0.068	288.2	
				11	R	0	175.12		175.12	

Scan number	4179	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	98.16



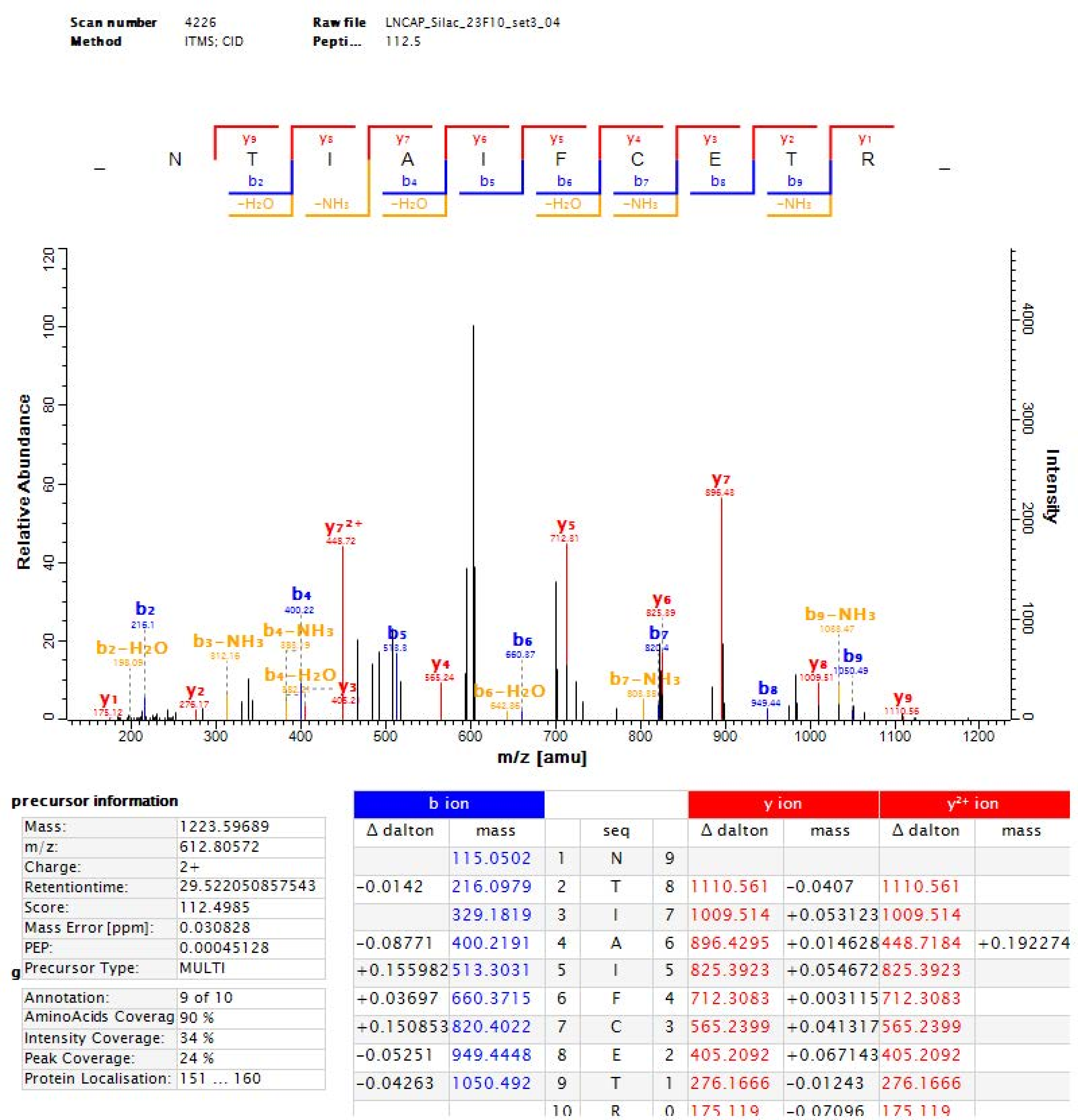
precursor information

Mass:	1340.6719
m/z:	671.34323
Charge:	2+
Retentiontime:	29.275884628295
Score:	98.15634
Mass Error [ppm]:	-0.4182
PEP:	0.0008918
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	22 %
Peak Coverage:	22 %
Protein Localisation:	259 ... 269

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	101.07		129.07	1	Q	10				
+0.0706	214.16	+0.3139	242.15	2	L	9	1219.6		1219.6	
	327.24	+0.0251	355.23	3	L	8	1106.6	+0.3034	553.78	+0.3081
	414.27		442.27	4	S	7	993.47	+0.049	497.24	+0.2509
	485.31	+0.08	513.3	5	A	6	906.44	-0.073	906.44	
	572.34		600.34	6	S	5	835.4	+0.0131	835.4	
	735.4		763.4	7	Y	4	748.37	+0.0641	748.37	
	864.45		892.44	8	E	3	585.31	+0.1186	585.31	
	1011.5		1039.5	9	F	2	456.27	+0.0594	456.27	
	1139.6	-0.143	1167.6	10	Q	1	309.2	+0.0442	309.2	
				11	R	0	181.14		181.14	



Scan number	4226	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	112.5

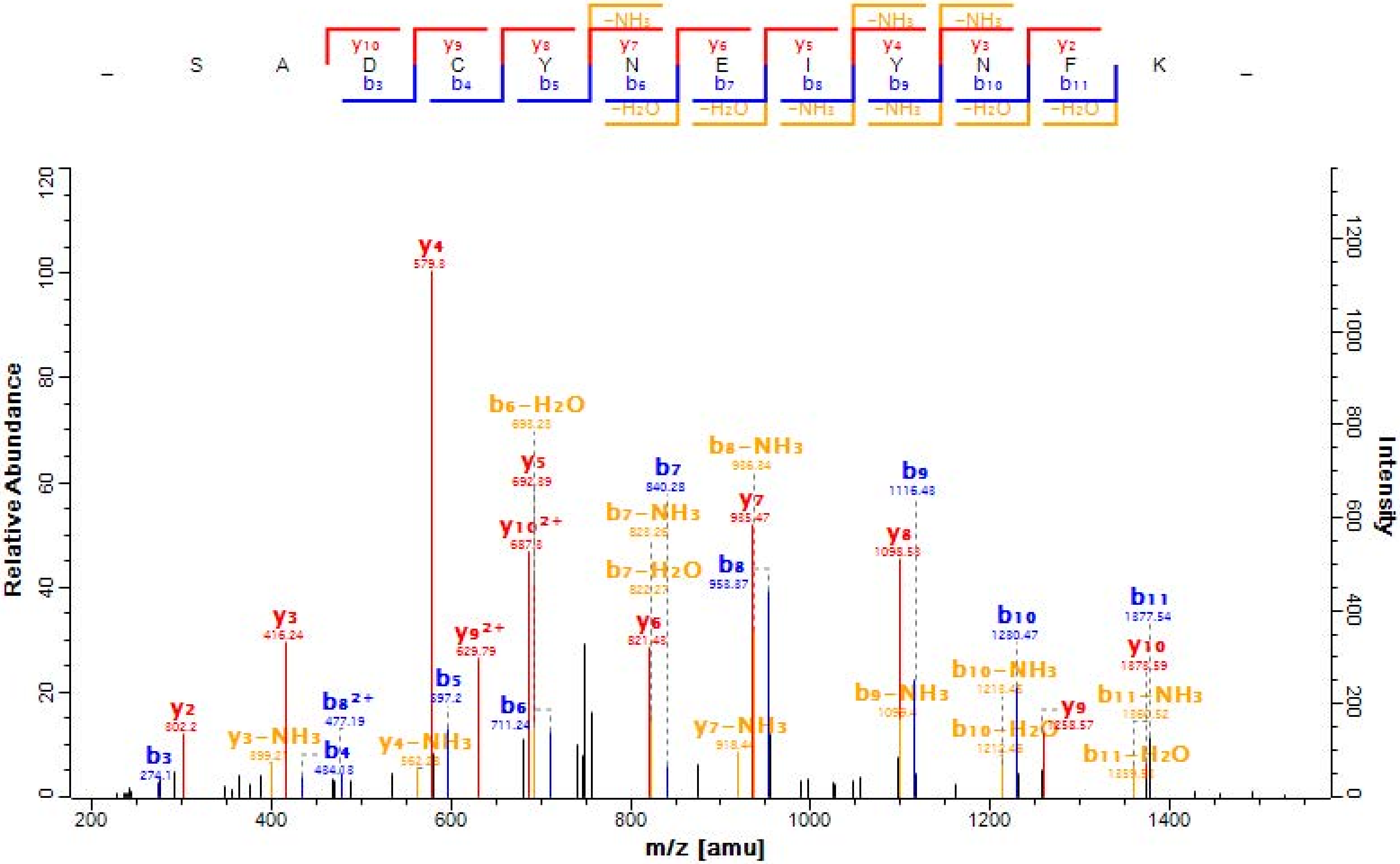
precursor information

Mass:	1223.59689
m/z:	612.80572
Charge:	2+
Retentiontime:	29.522050857543
Score:	112.4985
Mass Error [ppm]:	0.030828
PEP:	0.00045128
Precursor Type:	MULTI

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	34 %
Peak Coverage:	24 %
Protein Localisation:	151 ... 160

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502	1	N	9				
-0.0142	216.0979	2	T	8	1110.561	-0.0407	1110.561	
	329.1819	3	I	7	1009.514	+0.053123	1009.514	
-0.08771	400.2191	4	A	6	896.4295	+0.014628	448.7184	+0.192274
+0.155982	513.3031	5	I	5	825.3923	+0.054672	825.3923	
+0.03697	660.3715	6	F	4	712.3083	+0.003115	712.3083	
+0.150853	820.4022	7	C	3	565.2399	+0.041317	565.2399	
-0.05251	949.4448	8	E	2	405.2092	+0.067143	405.2092	
-0.04263	1050.492	9	T	1	276.1666	-0.01243	276.1666	
		10	R	0	175.119	-0.07096	175.119	

Scan number	4228	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	231.67



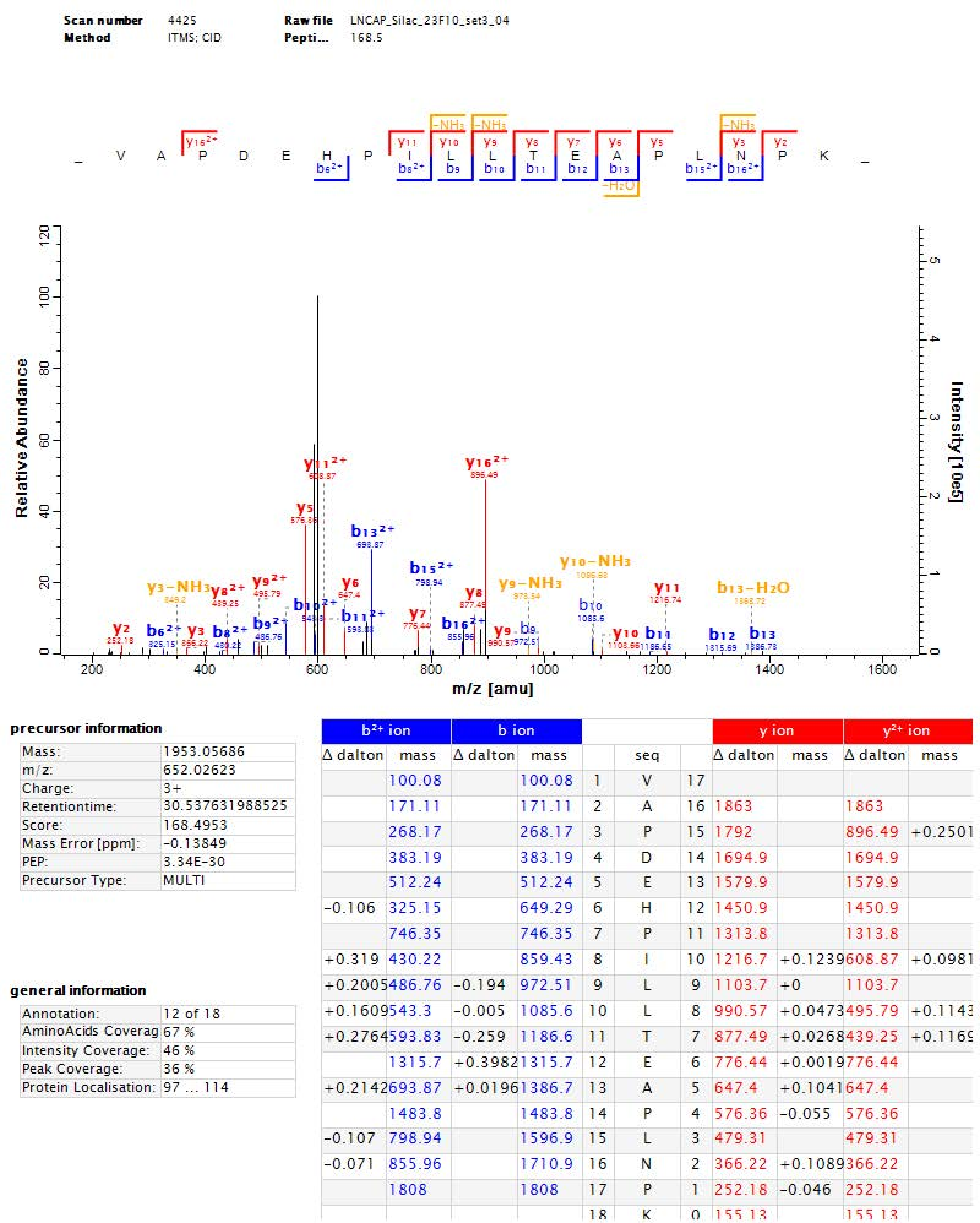
precursor information

Mass:	1522.64009
m/z:	762.32732
Charge:	2+
Retentiontime:	29.531682968139
Score:	231.672
Mass Error [ppm]:	0.16261
PEP:	1.3432E-25
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	74 %
Peak Coverage:	40 %
Protein Localisation:	86 ... 97

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	11				
	159.08		159.08	2	A	10	1444.6		1444.6	
	274.1	-0.021	274.1	3	D	9	1373.6	-0.066	687.3	+0.0302
	434.13	+0.1345	434.13	4	C	8	1258.6	+0.0432	629.79	-0.119
	597.2	+0.0418	597.2	5	Y	7	1098.5	-0.033	1098.5	
	711.24	+0.0002	711.24	6	N	6	935.47	-0.038	935.47	
	840.28	+0.0235	840.28	7	E	5	821.43	+0.0676	821.43	
+0.3042	477.19	-0.089	953.37	8	I	4	692.39	-0.101	692.39	
	1116.4	-0.098	1116.4	9	Y	3	579.3	-0.009	579.3	
	1230.5	+0.0103	1230.5	10	N	2	416.24	+0.0958	416.24	
	1377.5	-0.162	1377.5	11	F	1	302.2	+0.0561	302.2	
				12	K	0	155.13		155.13	



Scan number	4425	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	168.5

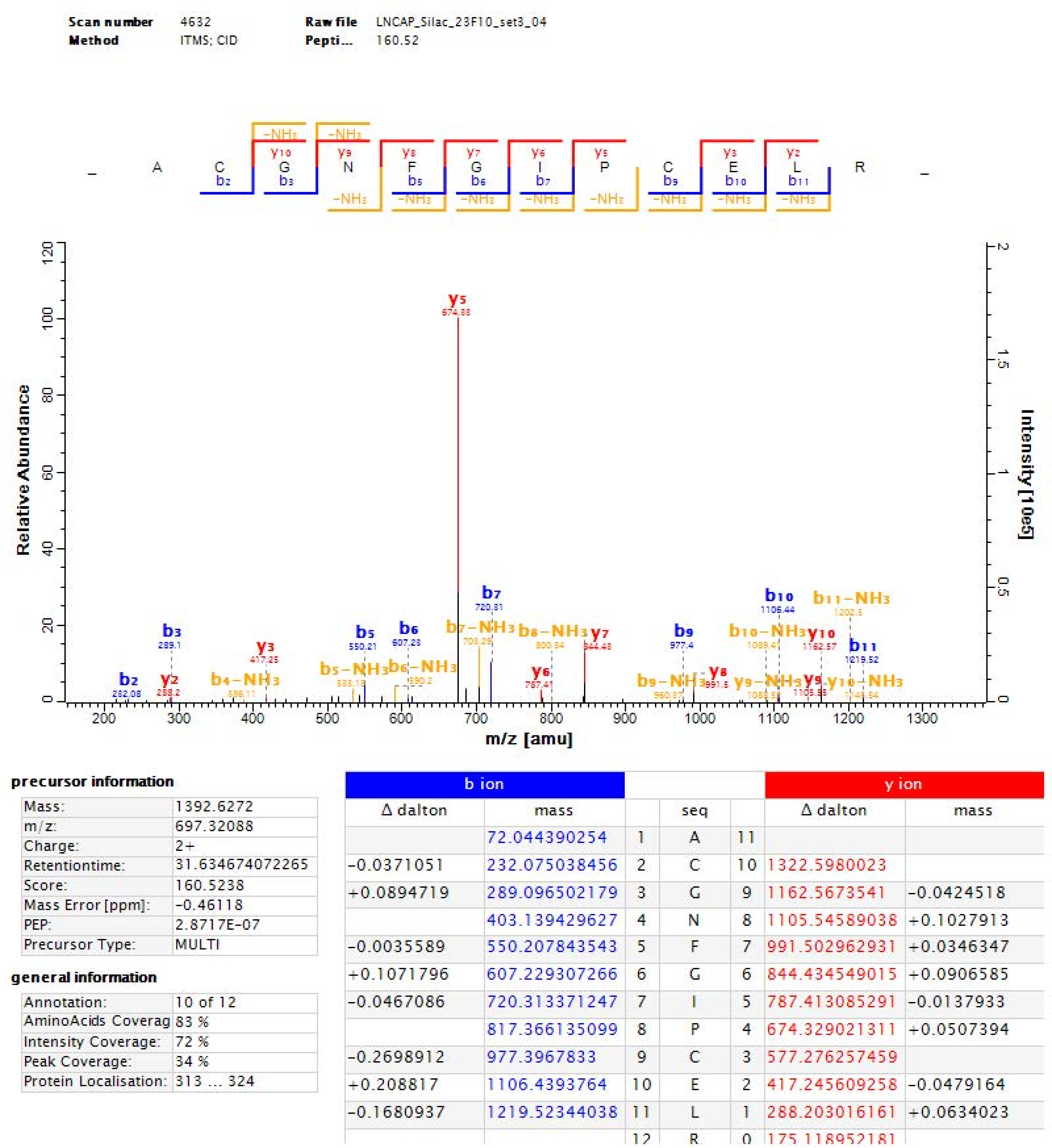
precursor information

Mass:	1953.05686
m/z:	652.02623
Charge:	3+
Retentiontime:	30.537631988525
Score:	168.4953
Mass Error [ppm]:	-0.13849
PEP:	3.34E-30
Precursor Type:	MULTI

general information

Annotation:	12 of 18
AminoAcids Coverag	67 %
Intensity Coverage:	46 %
Peak Coverage:	36 %
Protein Localisation:	97 ... 114

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	17				
	171.11		171.11	2	A	16	1863		1863	
	268.17		268.17	3	P	15	1792		896.49	+0.2501
	383.19		383.19	4	D	14	1694.9		1694.9	
	512.24		512.24	5	E	13	1579.9		1579.9	
-0.106	325.15		649.29	6	H	12	1450.9		1450.9	
	746.35		746.35	7	P	11	1313.8		1313.8	
+0.319	430.22		859.43	8	I	10	1216.7	+0.1239	608.87	+0.0981
+0.2005	486.76	-0.194	972.51	9	L	9	1103.7	+0	1103.7	
+0.1609	543.3	-0.005	1085.6	10	L	8	990.57	+0.0473	495.79	+0.1143
+0.2764	593.83	-0.259	1186.6	11	T	7	877.49	+0.0268	439.25	+0.1169
	1315.7	+0.3982	1315.7	12	E	6	776.44	+0.0019	776.44	
+0.2142	693.87	+0.0196	1386.7	13	A	5	647.4	+0.1041	647.4	
	1483.8		1483.8	14	P	4	576.36	-0.055	576.36	
-0.107	798.94		1596.9	15	L	3	479.31		479.31	
-0.071	855.96		1710.9	16	N	2	366.22	+0.1089	366.22	
	1808		1808	17	P	1	252.18	-0.046	252.18	
				18	K	0	155.13		155.13	



Scan number	4632	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	160.52

precursor information

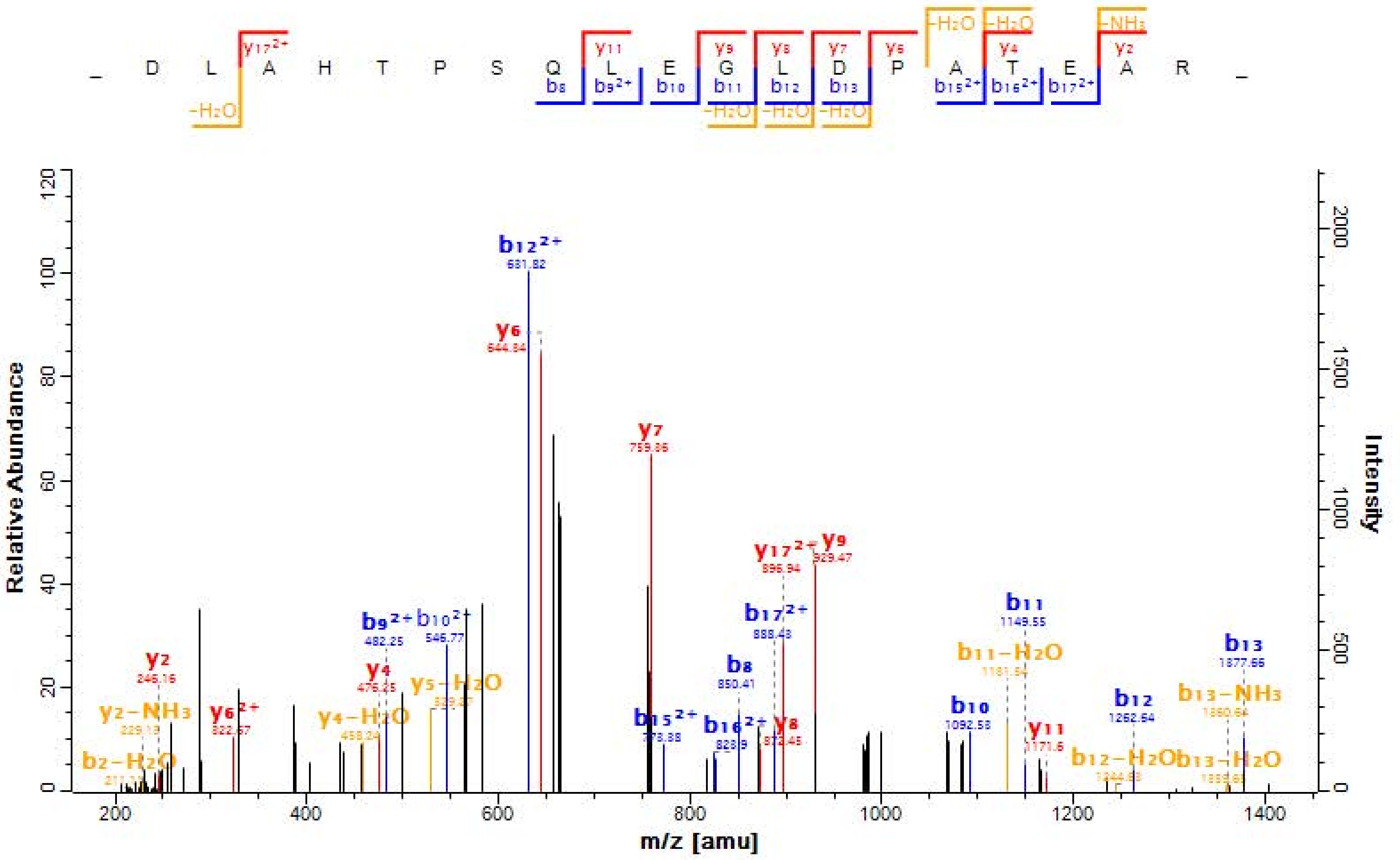
Mass:	1392.6272
m/z:	697.32088
Charge:	2+
Retentiontime:	31.634674072265
Score:	160.5238
Mass Error [ppm]:	-0.46118
PEP:	2.8717E-07
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	72 %
Peak Coverage:	34 %
Protein Localisation:	313 ... 324

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	72.044390254	1	A	11		
-0.0371051	232.075038456	2	C	10	1322.5980023	
+0.0894719	289.096502179	3	G	9	1162.5673541	-0.0424518
	403.139429627	4	N	8	1105.54589038	+0.1027913
-0.0035589	550.207843543	5	F	7	991.502962931	+0.0346347
+0.1071796	607.229307266	6	G	6	844.434549015	+0.0906585
-0.0467086	720.313371247	7	I	5	787.413085291	-0.0137933
	817.366135099	8	P	4	674.329021311	+0.0507394
-0.2698912	977.3967833	9	C	3	577.276257459	
+0.208817	1106.4393764	10	E	2	417.245609258	-0.0479164
-0.1680937	1219.52344038	11	L	1	288.203016161	+0.0634023
		12	R	0	175.118952181	

Scan number	4672	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	103.87



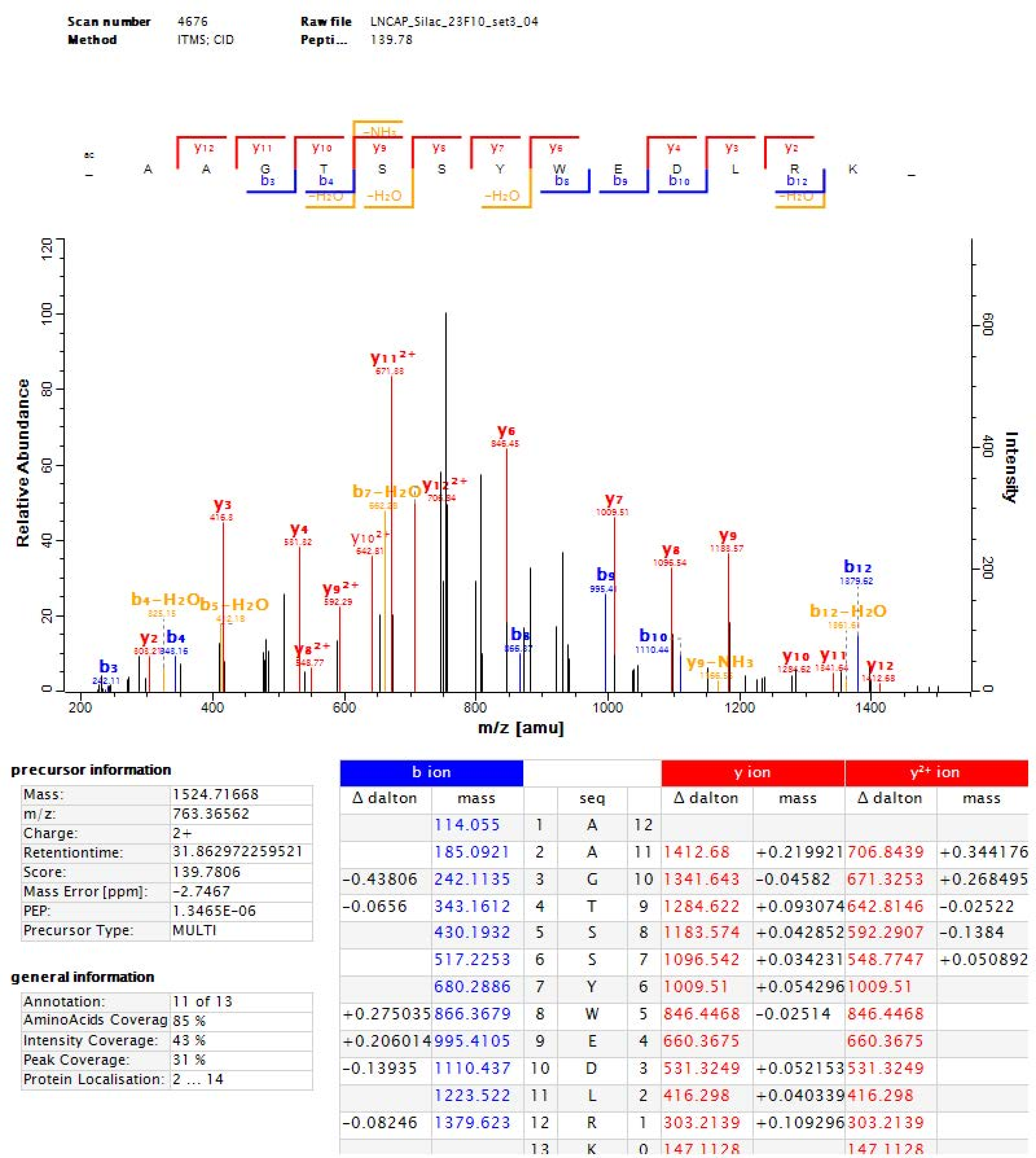
precursor information

Mass:	2019.98669
m/z:	674.33617
Charge:	3+
Retentiontime:	31.840959548950
Score:	103.8651
Mass Error [ppm]:	0.26935
PEP:	4.2353E-08
Precursor Type:	MULTI

general information

Annotation:	13 of 19
AminoAcids Coverag	68 %
Intensity Coverage:	41 %
Peak Coverage:	28 %
Protein Localisation:	30 ... 48

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	18				
	229.12		229.12	2	L	17	1906		1906	
	300.16		300.16	3	A	16	1792.9		896.94	-0.095
	437.21		437.21	4	H	15	1721.8		1721.8	
	538.26		538.26	5	T	14	1584.8		1584.8	
	635.31		635.31	6	P	13	1483.7		1483.7	
	722.35		722.35	7	S	12	1386.7		1386.7	
	850.41	-0.017	850.41	8	Q	11	1299.7		1299.7	
+0.0433	482.25		963.49	9	L	10	1171.6	+0.0184	1171.6	
+0.1055	546.77	-0.001	1092.5	10	E	9	1058.5		1058.5	
	1149.6	-0.012	1149.6	11	G	8	929.47	+0.118	929.47	
+0.1164	631.82	+0.1509	1262.6	12	L	7	872.45	+0.0555	872.45	
	1377.7	-0.042	1377.7	13	D	6	759.36	+0.0413	759.36	
	1474.7		1474.7	14	P	5	644.34	-0.042	322.67	+0.0867
+0.1067	773.38		1545.8	15	A	4	547.28		547.28	
-0.052	823.9		1646.8	16	T	3	476.25	+0.2738	476.25	
-0.086	888.43		1775.8	17	E	2	375.2		375.2	
	1846.9		1846.9	18	A	1	246.16	+0.1747	246.16	
				19	R	0	175.12		175.12	



Scan number	4676	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	139.78

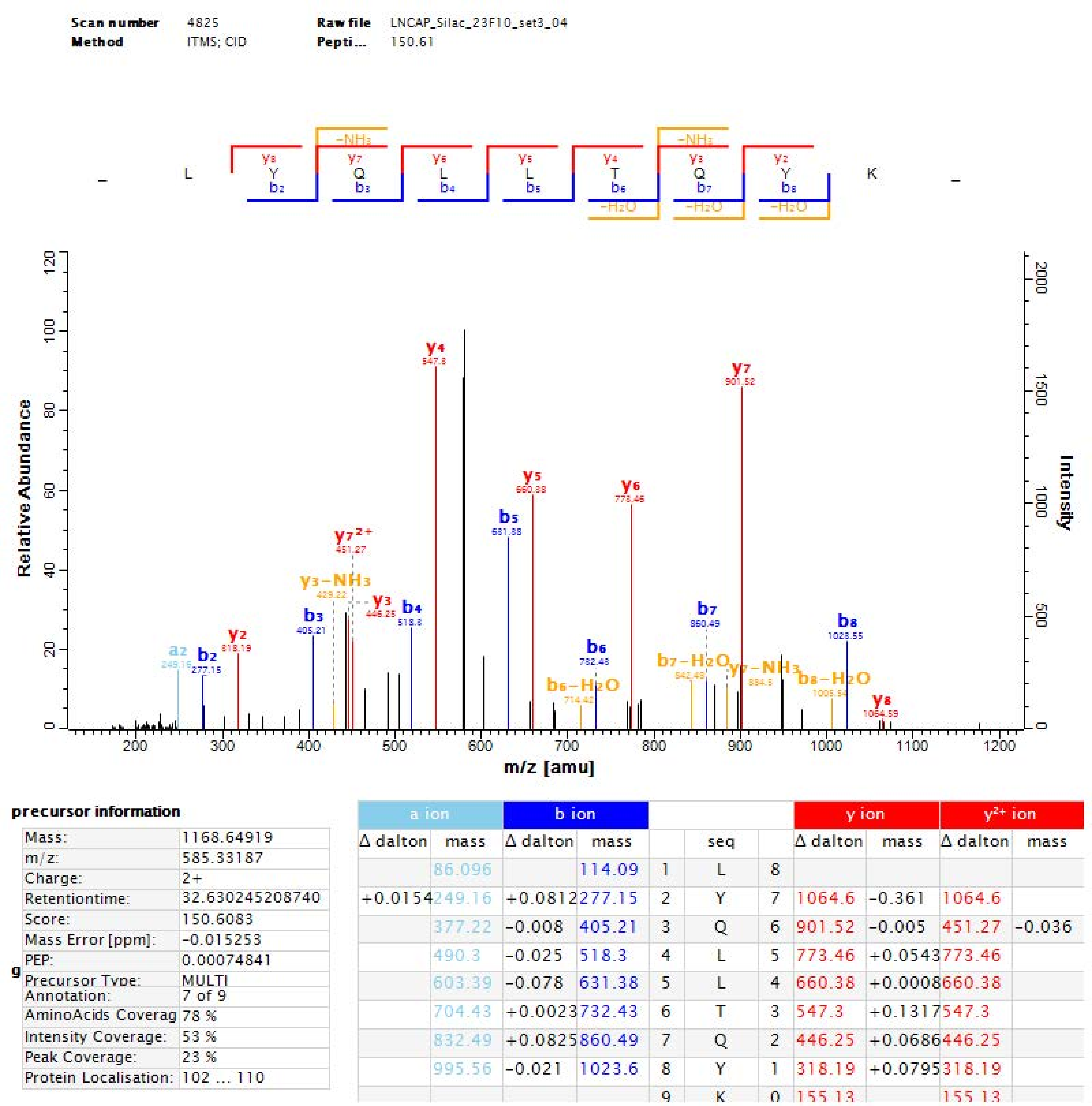
precursor information

Mass:	1524.71668
m/z:	763.36562
Charge:	2+
Retentiontime:	31.862972259521
Score:	139.7806
Mass Error [ppm]:	-2.7467
PEP:	1.3465E-06
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	43 %
Peak Coverage:	31 %
Protein Localisation:	2 ... 14

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.055	1	A	12				
	185.0921	2	A	11	1412.68	+0.219921	706.8439	+0.344176
-0.43806	242.1135	3	G	10	1341.643	-0.04582	671.3253	+0.268495
-0.0656	343.1612	4	T	9	1284.622	+0.093074	642.8146	-0.02522
	430.1932	5	S	8	1183.574	+0.042852	592.2907	-0.1384
	517.2253	6	S	7	1096.542	+0.034231	548.7747	+0.050892
	680.2886	7	Y	6	1009.51	+0.054296	1009.51	
+0.275035	866.3679	8	W	5	846.4468	-0.02514	846.4468	
+0.206014	995.4105	9	E	4	660.3675		660.3675	
-0.13935	1110.437	10	D	3	531.3249	+0.052153	531.3249	
	1223.522	11	L	2	416.298	+0.040339	416.298	
-0.08246	1379.623	12	R	1	303.2139	+0.109296	303.2139	
		13	K	0	147.1128		147.1128	

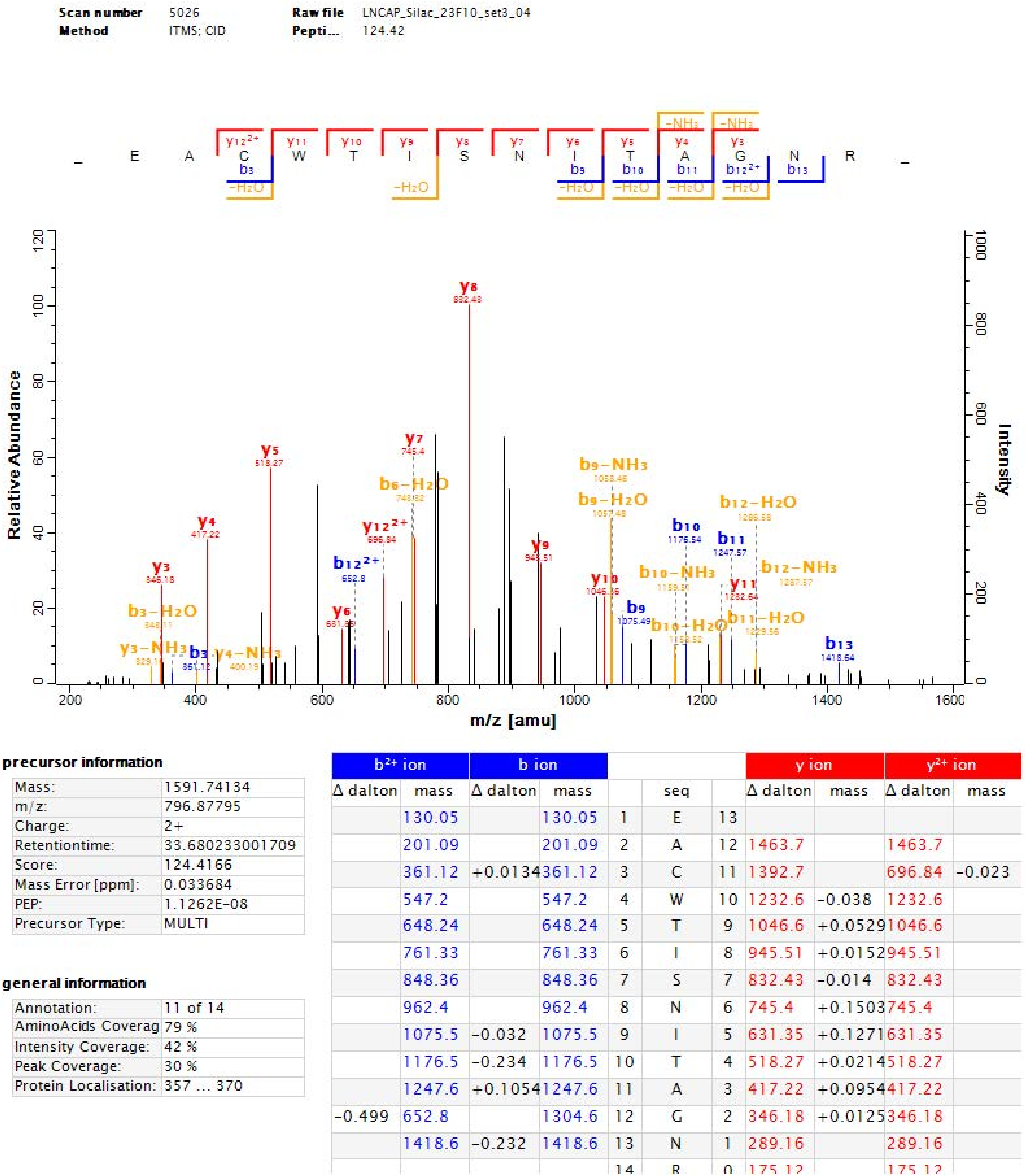


Scan number 4825 **Raw file** LNCAP_Silac_23F10_set3_04
Method ITMS; CID **Pepti...** 150.61

precursor information

Mass:	1168.64919
m/z:	585.33187
Charge:	2+
Retentiontime:	32.630245208740
Score:	150.6083
Mass Error [ppm]:	-0.015253
PEP:	0.00074841
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	53 %
Peak Coverage:	23 %
Protein Localisation:	102 ... 110

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	8				
+0.0154	249.16	+0.0812	277.15	2	Y	7	1064.6	-0.361	1064.6	
	377.22	-0.008	405.21	3	Q	6	901.52	-0.005	451.27	-0.036
	490.3	-0.025	518.3	4	L	5	773.46	+0.0543	773.46	
	603.39	-0.078	631.38	5	L	4	660.38	+0.0008	660.38	
	704.43	+0.0023	732.43	6	T	3	547.3	+0.1317	547.3	
	832.49	+0.0825	860.49	7	Q	2	446.25	+0.0686	446.25	
	995.56	-0.021	1023.6	8	Y	1	318.19	+0.0795	318.19	
				9	K	0	155.13		155.13	



Scan number	5026	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	124.42

precursor information

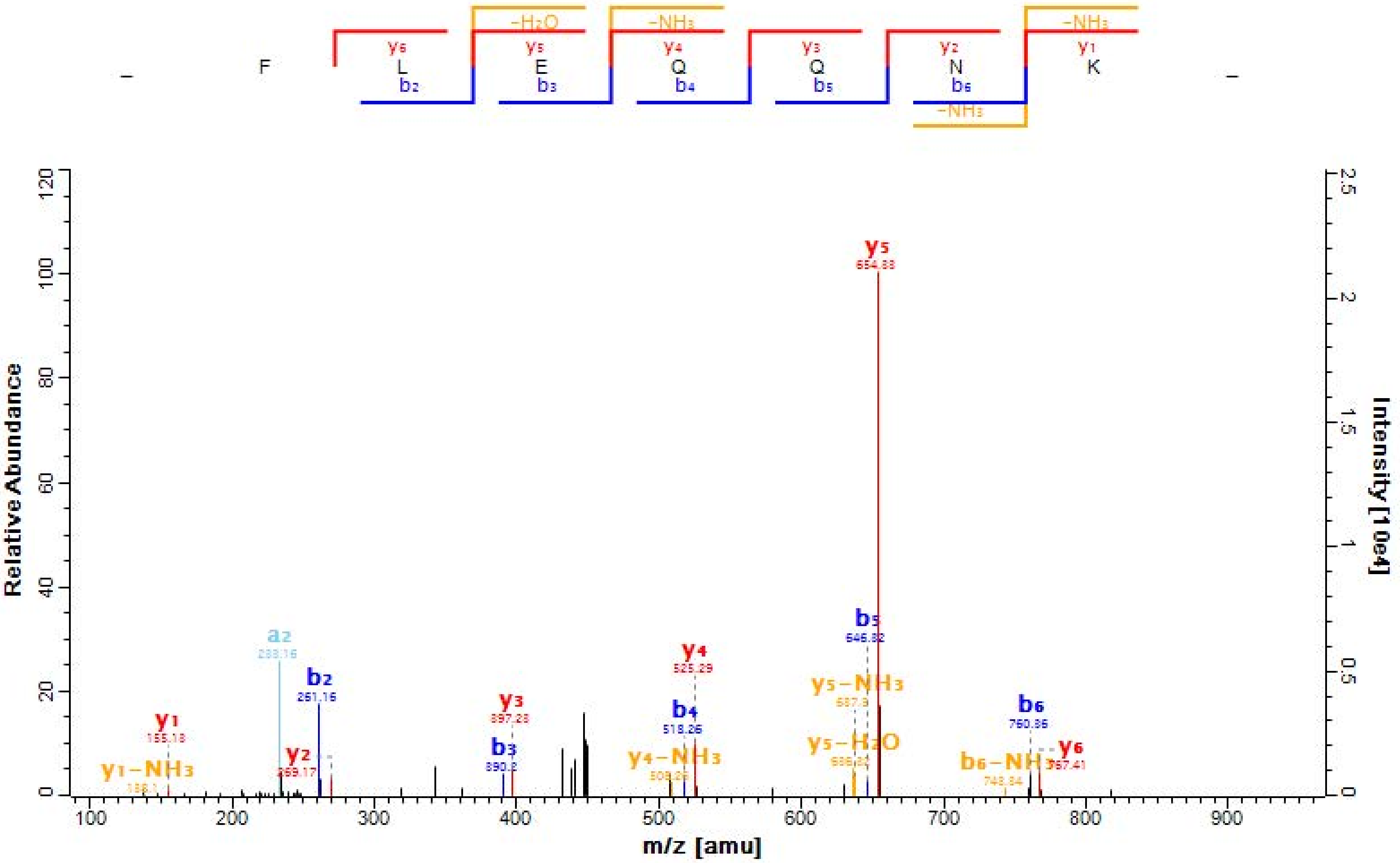
Mass:	1591.74134
m/z:	796.87795
Charge:	2+
Retentiontime:	33.680233001709
Score:	124.4166
Mass Error [ppm]:	0.033684
PEP:	1.1262E-08
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	42 %
Peak Coverage:	30 %
Protein Localisation:	357 ... 370

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	13				
	201.09		201.09	2	A	12	1463.7		1463.7	
	361.12	+0.0134	361.12	3	C	11	1392.7		696.84	-0.023
	547.2		547.2	4	W	10	1232.6	-0.038	1232.6	
	648.24		648.24	5	T	9	1046.6	+0.0529	1046.6	
	761.33		761.33	6	I	8	945.51	+0.0152	945.51	
	848.36		848.36	7	S	7	832.43	-0.014	832.43	
	962.4		962.4	8	N	6	745.4	+0.1503	745.4	
	1075.5	-0.032	1075.5	9	I	5	631.35	+0.1271	631.35	
	1176.5	-0.234	1176.5	10	T	4	518.27	+0.0214	518.27	
	1247.6	+0.1054	1247.6	11	A	3	417.22	+0.0954	417.22	
-0.499	652.8		1304.6	12	G	2	346.18	+0.0125	346.18	
	1418.6	-0.232	1418.6	13	N	1	289.16		289.16	
				14	R	0	175.12		175.12	

Scan number	505	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti…**	132.57

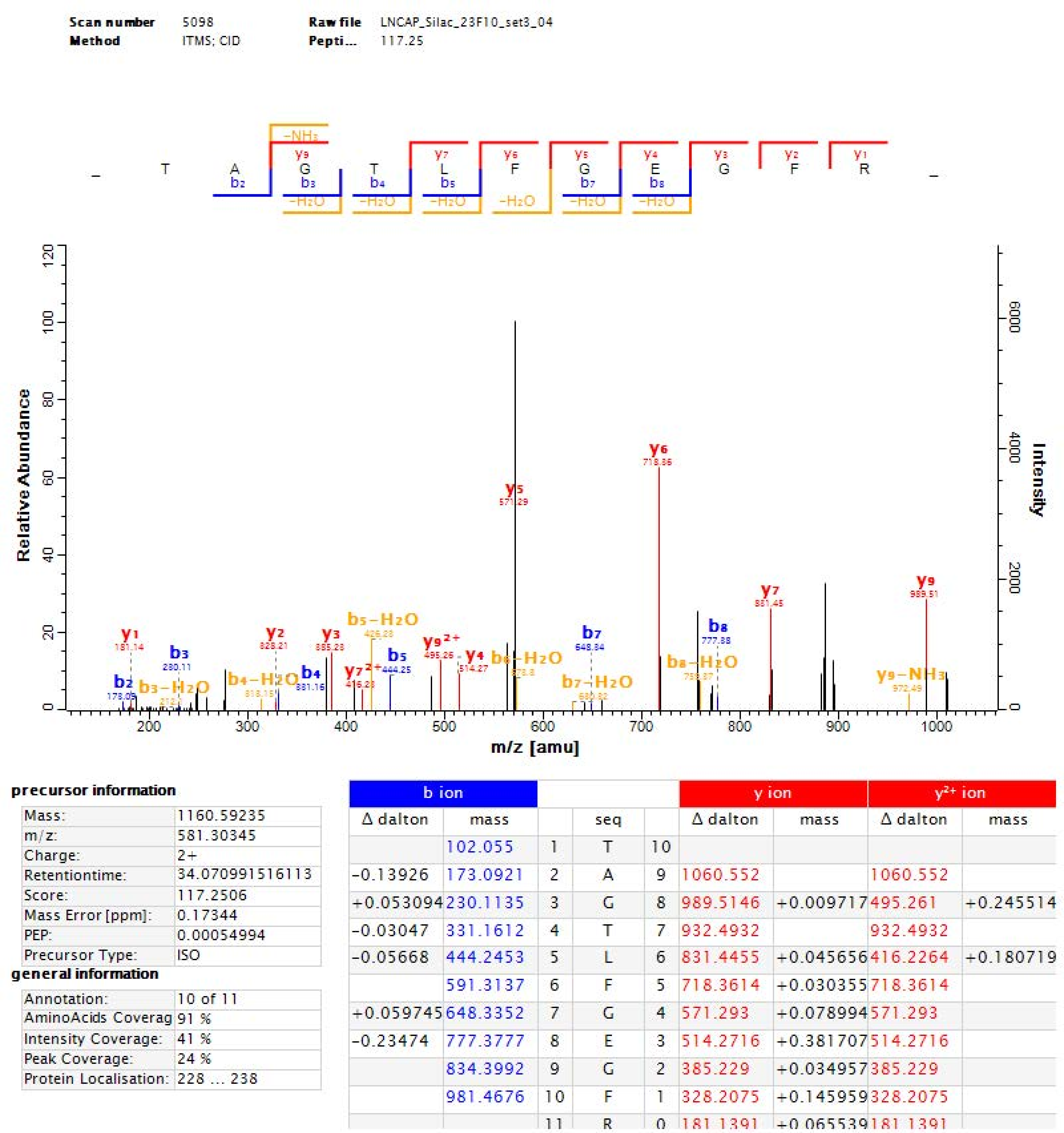


precursor information

g

Mass:	905.46051
m/z:	453.73753
Charge:	2+
Retentiontime:	8.2565469741821
Score:	132.5669
Mass Error [ppm]:	-0.19279
Annotation:	6 of 7
AminoAcids Coverag	86 %
Intensity Coverage:	62 %
Peak Coverage:	19 %

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	120.0808		148.0757	1	F	6		
+0.051347	233.1648	-0.05233	261.1598	2	L	5	767.4137	-0.06682
	362.2074	+0.012771	390.2023	3	E	4	654.3297	-0.04886
	490.266	+0.05365	518.2609	4	Q	3	525.2871	+0.00686
	618.3246	-0.13353	646.3195	5	Q	2	397.2285	-0.01681
	732.3675	+0.057553	760.3624	6	N	1	269.1699	+0.049186
				7	K	0	155.127	+0.001873



Scan number	5098	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	117.25

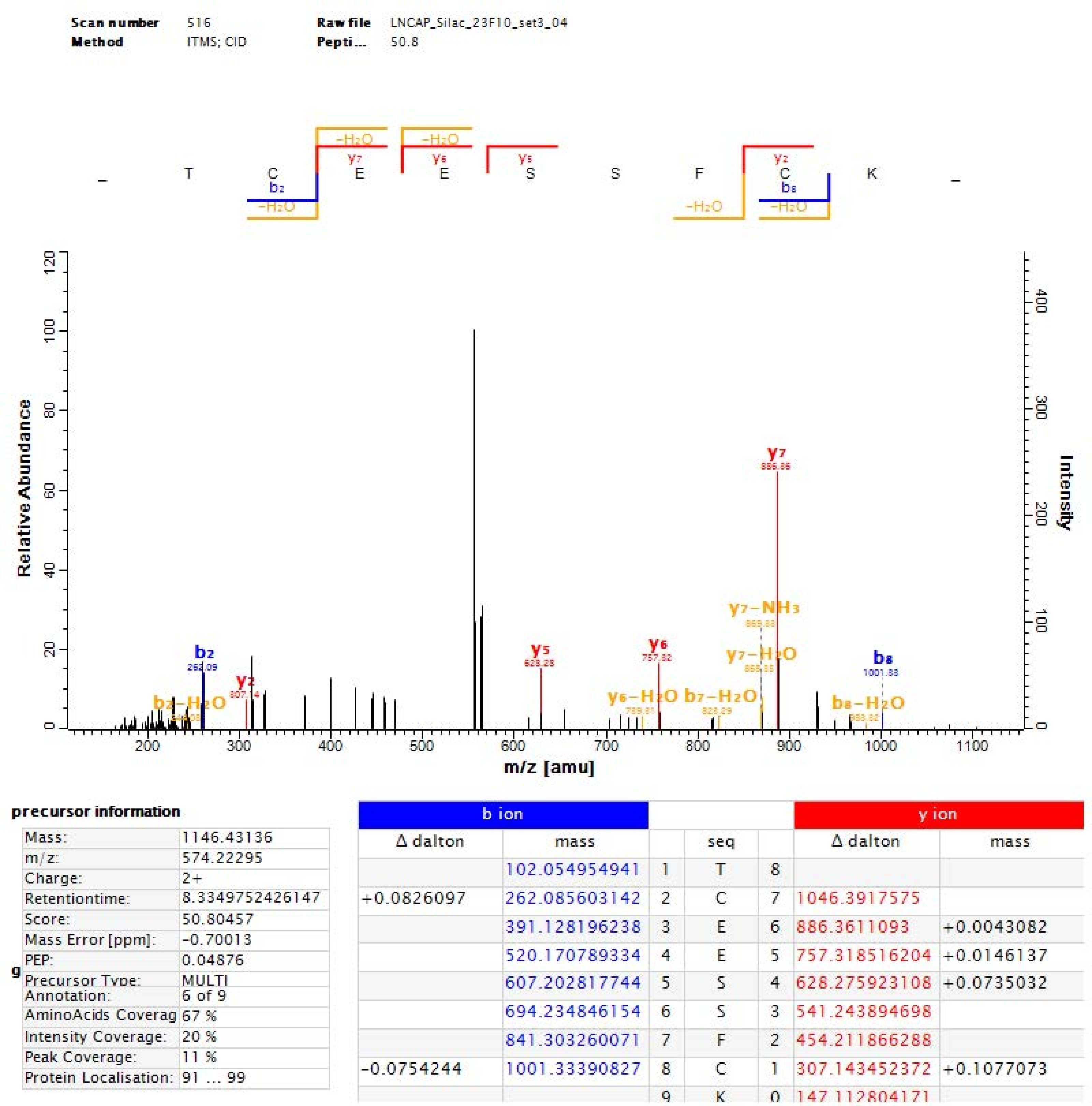
precursor information

Mass:	1160.59235
m/z:	581.30345
Charge:	2+
Retentiontime:	34.070991516113
Score:	117.2506
Mass Error [ppm]:	0.17344
PEP:	0.00054994
Precursor Type:	ISO

general information

Annotation:	10 of 11
AminoAcids Coverag	91 %
Intensity Coverage:	41 %
Peak Coverage:	24 %
Protein Localisation:	228 ... 238

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055	1	T	10				
-0.13926	173.0921	2	A	9	1060.552		1060.552	
+0.053094	230.1135	3	G	8	989.5146	+0.009717	495.261	+0.245514
-0.03047	331.1612	4	T	7	932.4932		932.4932	
-0.05668	444.2453	5	L	6	831.4455	+0.045656	416.2264	+0.180719
	591.3137	6	F	5	718.3614	+0.030355	718.3614	
+0.059745	648.3352	7	G	4	571.293	+0.078994	571.293	
-0.23474	777.3777	8	E	3	514.2716	+0.381707	514.2716	
	834.3992	9	G	2	385.229	+0.034957	385.229	
	981.4676	10	F	1	328.2075	+0.145959	328.2075	
		11	R	0	181.1391	+0.065539	181.1391	



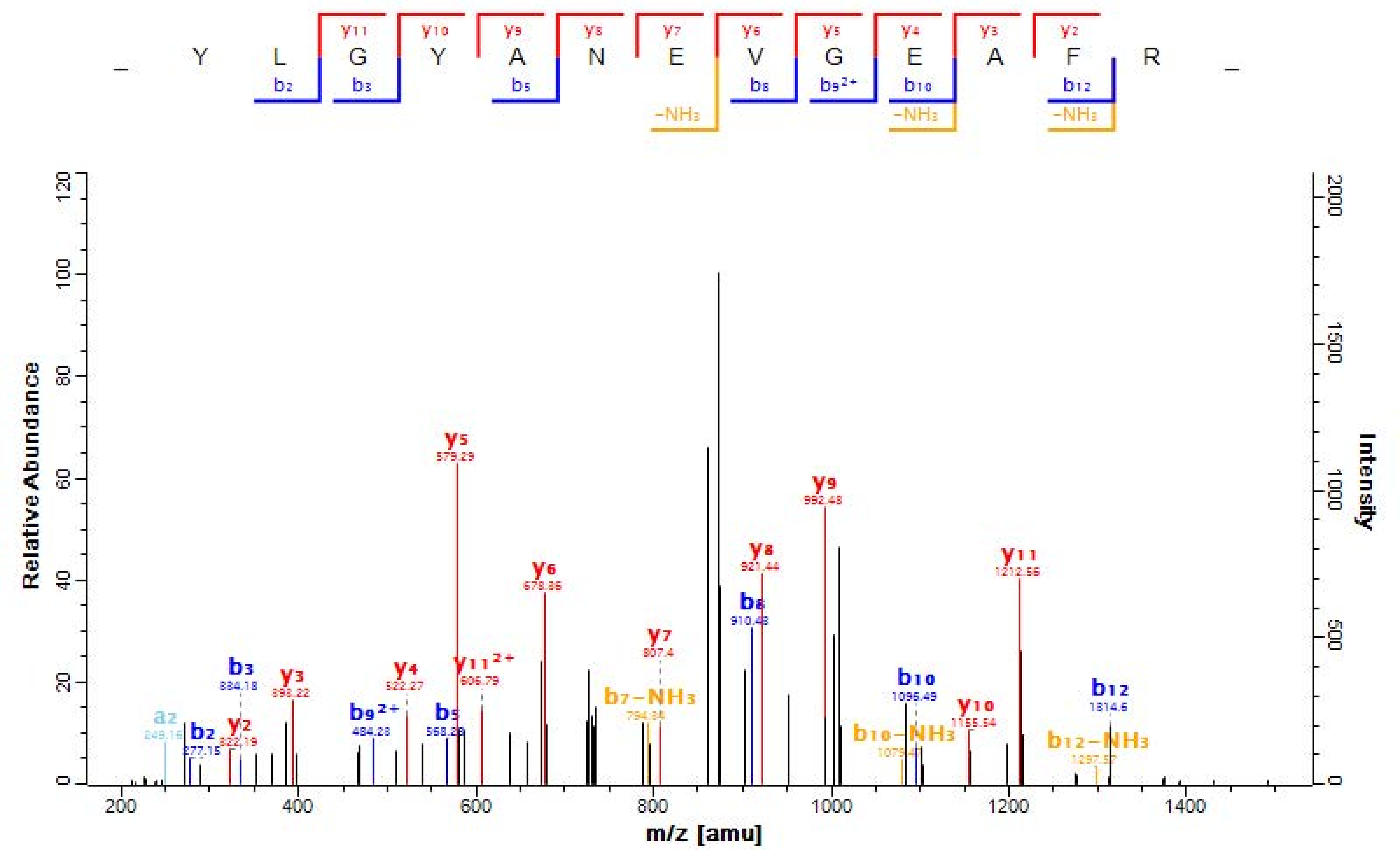
Scan number	516	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	50.8

precursor information

Mass:	1146.43136
m/z:	574.22295
Charge:	2+
Retentiontime:	8.3349752426147
Score:	50.80457
Mass Error [ppm]:	-0.70013
PEP:	0.04876
Precursor Type:	MULTI
Annotation:	6 of 9
AminoAcids Coverag	67 %
Intensity Coverage:	20 %
Peak Coverage:	11 %
Protein Localisation:	91 ... 99

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	102.054954941	1	T	8		
+0.0826097	262.085603142	2	C	7	1046.3917575	
	391.128196238	3	E	6	886.3611093	+0.0043082
	520.170789334	4	E	5	757.318516204	+0.0146137
	607.202817744	5	S	4	628.275923108	+0.0735032
	694.234846154	6	S	3	541.243894698	
	841.303260071	7	F	2	454.211866288	
-0.0754244	1001.33390827	8	C	1	307.143452372	+0.1077073
		9	K	0	147.112804171	

Scan number	5724	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	109.44



precursor information

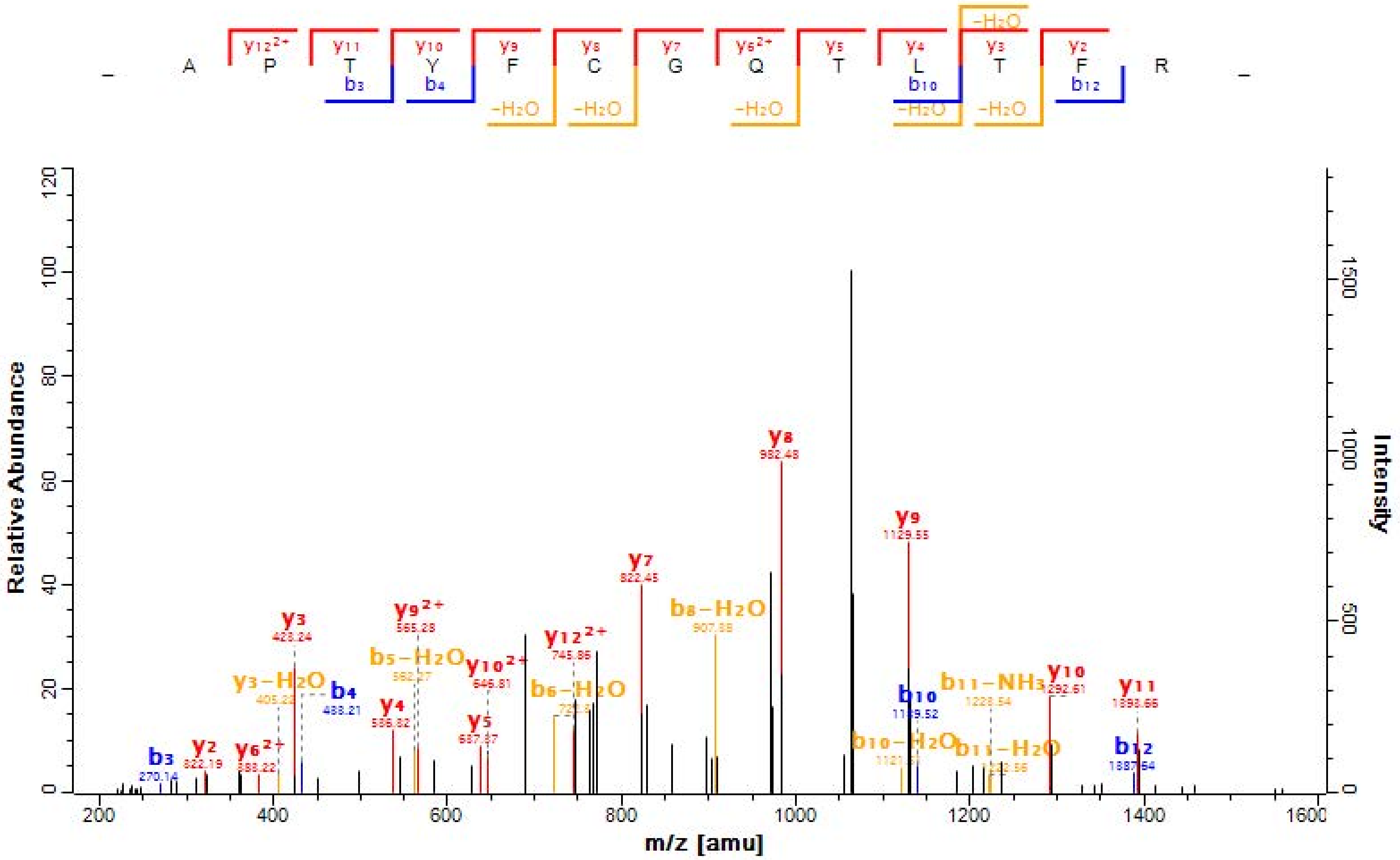
Mass:	1487.70549
m/z:	744.86002
Charge:	2+
Retentiontime:	37.451843261718
Score:	109.4421
Mass Error [ppm]:	0.669
PEP:	7.3304E-06
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	36 %
Peak Coverage:	27 %
Protein Localisation:	21 ... 33

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.1		164.1		164.1	1	Y	12				
+0.012	249.2		277.2	+0.084	277.2	2	L	11	1326		1326	
	306.2		334.2	+0.156	334.2	3	G	10	1213	-0.06	606.8	-0.12
	469.2		497.2		497.2	4	Y	9	1156	+0.104	1156	
	540.3		568.3	-0.11	568.3	5	A	8	992.5	+0	992.5	
	654.3		682.3		682.3	6	N	7	921.4	+0	921.4	
	783.4		811.4		811.4	7	E	6	807.4	+0.156	807.4	
	882.4		910.4	+0.39	910.4	8	V	5	678.4	-0.01	678.4	
	939.5	-0.07	484.2		967.5	9	G	4	579.3	+0.106	579.3	
	1068		1096	+0.035	1096	10	E	3	522.3	+0.029	522.3	
	1140		1168		1168	11	A	2	393.2	+0.123	393.2	
	1287		1315	-0.26	1315	12	F	1	322.2	+0.074	322.2	
						13	R	0	175.1		175.1	

Scan number	5879	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	88.09



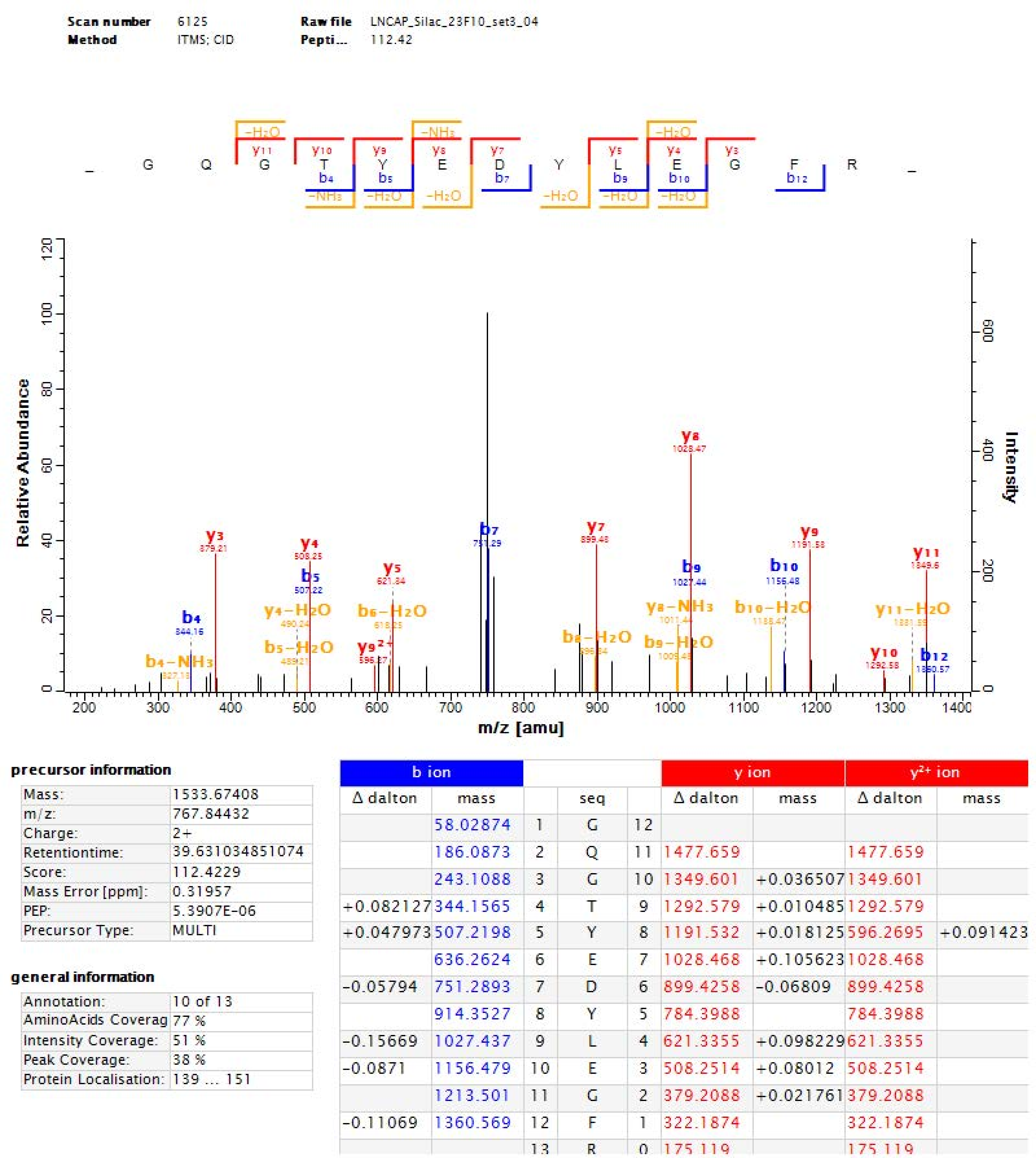
precursor information

Mass:	1560.74063
m/z:	781.37759
Charge:	2+
Retentiontime:	38.270416259765
Score:	88.09225
Mass Error [ppm]:	0.72451
PEP:	0.00030761
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	37 %
Peak Coverage:	28 %
Protein Localisation:	308 ... 320

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	12				
	169.0972	2	P	11	1490.71		745.8585	-0.09992
+0.057041	270.1448	3	T	10	1393.657	-0.00883	1393.657	
+0.042022	433.2082	4	Y	9	1292.609	-0.03549	646.8082	-0.31319
	580.2766	5	F	8	1129.546	+0.023568	565.2766	+0.057584
	740.3072	6	C	7	982.4775	+0.013429	982.4775	
	797.3287	7	G	6	822.4468	-0.09887	822.4468	
	925.3873	8	Q	5	765.4254		383.2163	+0.192615
	1026.435	9	T	4	637.3668	+0.100193	637.3668	
+0.160925	1139.519	10	L	3	536.3191	+0.020125	536.3191	
	1240.567	11	T	2	423.235	-0.0003	423.235	
+0.044466	1387.635	12	F	1	322.1874	+0.105236	322.1874	
		13	R	0	175.119		175.119	



Scan number	6125	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	112.42

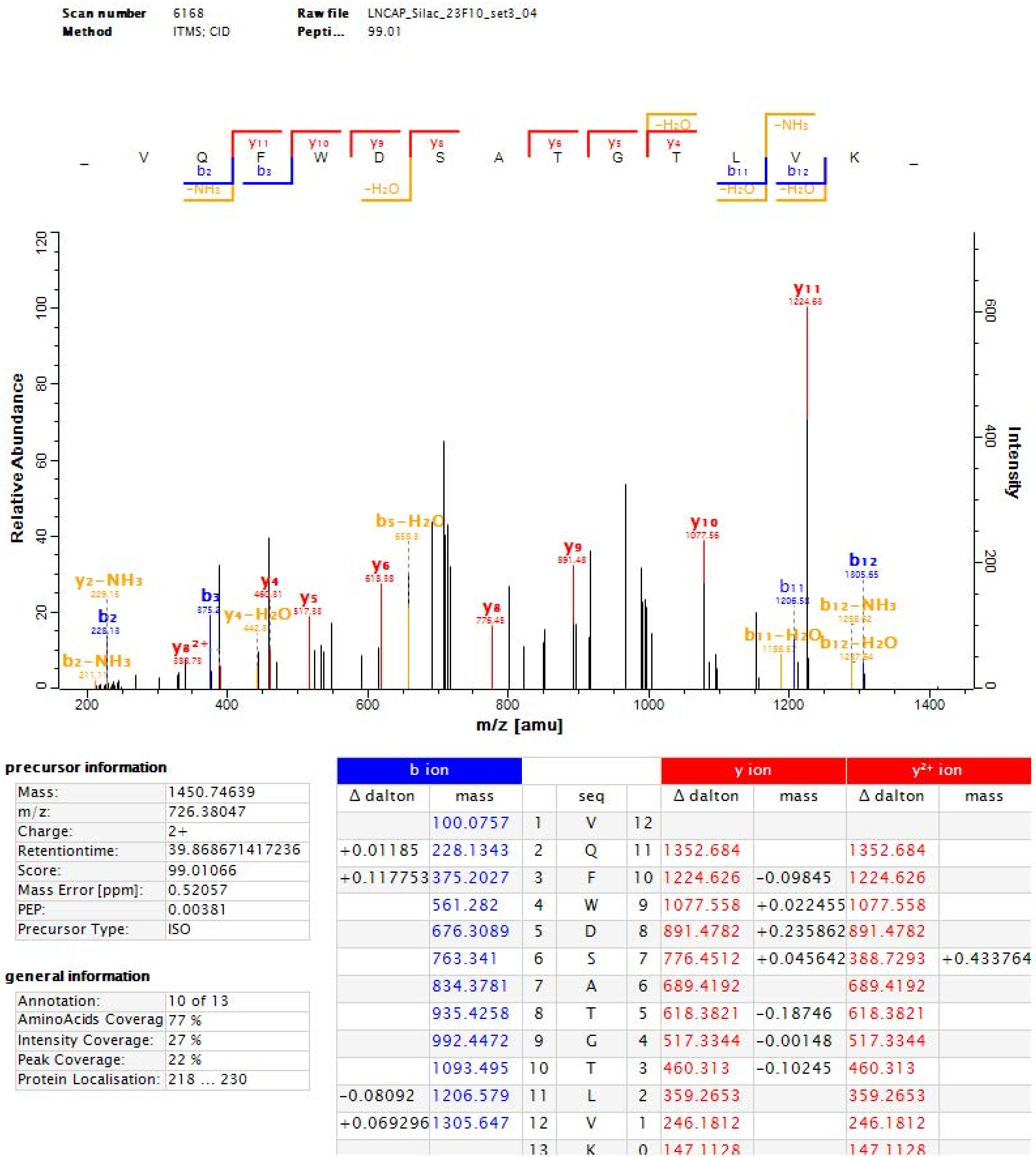
precursor information

Mass:	1533.67408
m/z:	767.84432
Charge:	2+
Retentiontime:	39.631034851074
Score:	112.4229
Mass Error [ppm]:	0.31957
PEP:	5.3907E-06
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	51 %
Peak Coverage:	38 %
Protein Localisation:	139 ... 151

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	12				
	186.0873	2	Q	11	1477.659		1477.659	
	243.1088	3	G	10	1349.601	+0.036507	1349.601	
+0.082127	344.1565	4	T	9	1292.579	+0.010485	1292.579	
+0.047973	507.2198	5	Y	8	1191.532	+0.018125	596.2695	+0.091423
	636.2624	6	E	7	1028.468	+0.105623	1028.468	
-0.05794	751.2893	7	D	6	899.4258	-0.06809	899.4258	
	914.3527	8	Y	5	784.3988		784.3988	
-0.15669	1027.437	9	L	4	621.3355	+0.098229	621.3355	
-0.0871	1156.479	10	E	3	508.2514	+0.08012	508.2514	
	1213.501	11	G	2	379.2088	+0.021761	379.2088	
-0.11069	1360.569	12	F	1	322.1874		322.1874	
		13	R	0	175.119		175.119	



Scan number 6168 **Raw file** LNCAP_Silac_23F10_set3_04

Method ITMS; CID **Pepti...** 99.01

precursor information

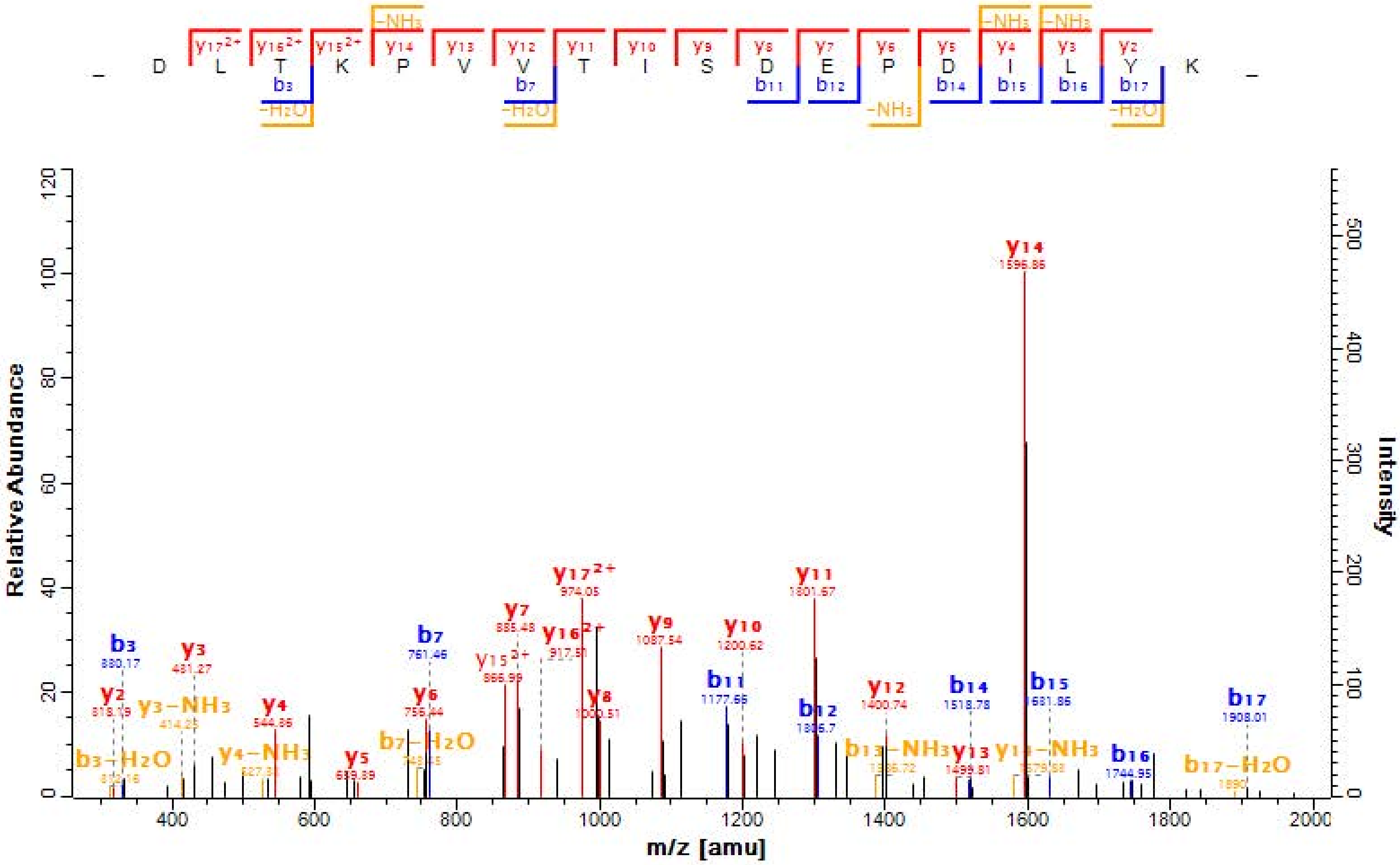
Mass:	1450.74639
m/z:	726.38047
Charge:	2+
Retentiontime:	39.868671417236
Score:	99.01066
Mass Error [ppm]:	0.52057
PEP:	0.00381
Precursor Type:	ISO

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	27 %
Peak Coverage:	22 %
Protein Localisation:	218 ... 230

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	12				
+0.01185	228.1343	2	Q	11	1352.684		1352.684	
+0.117753	375.2027	3	F	10	1224.626	-0.09845	1224.626	
	561.282	4	W	9	1077.558	+0.022455	1077.558	
	676.3089	5	D	8	891.4782	+0.235862	891.4782	
	763.341	6	S	7	776.4512	+0.045642	388.7293	+0.433764
	834.3781	7	A	6	689.4192		689.4192	
	935.4258	8	T	5	618.3821	-0.18746	618.3821	
	992.4472	9	G	4	517.3344	-0.00148	517.3344	
	1093.495	10	T	3	460.313	-0.10245	460.313	
-0.08092	1206.579	11	L	2	359.2653		359.2653	
+0.069296	1305.647	12	V	1	246.1812		246.1812	
		13	K	0	147.1128		147.1128	

Scan number	6567	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	156.13



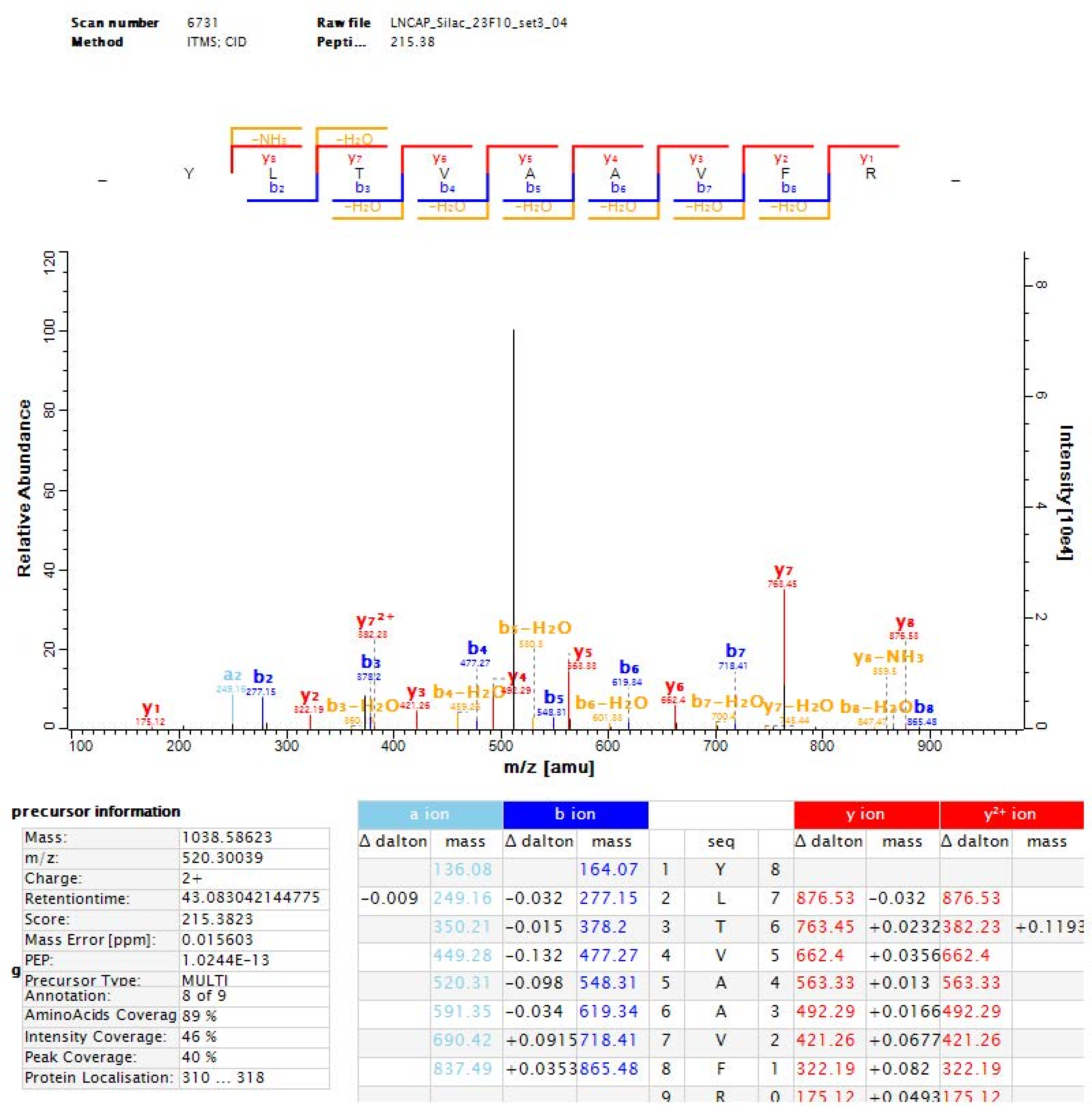
precursor information

Mass:	2045.09355
m/z:	1023.55405
Charge:	2+
Retentiontime:	42.148601531982
Score:	156.13
Mass Error [ppm]:	0.15258
PEP:	1.5305E-23
Precursor Type:	MULTI

general information

Annotation:	16 of 18
AminoAcids Coverag	89 %
Intensity Coverage:	44 %
Peak Coverage:	33 %
Protein Localisation:	57 ... 74

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342	1	D	17				
	229.1183	2	L	16	1947.102		974.0546	+0.249698
+0.067314	330.166	3	T	15	1834.018		917.5126	-0.16469
	466.2751	4	K	14	1732.97		866.9888	+0.088641
	563.3279	5	P	13	1596.861	-0.18028	1596.861	
	662.3963	6	V	12	1499.808	+0.052661	1499.808	
+0.127081	761.4647	7	V	11	1400.74	-0.20852	1400.74	
	862.5124	8	T	10	1301.671	-0.11129	1301.671	
	975.5965	9	I	9	1200.624	+0.161239	1200.624	
	1062.628	10	S	8	1087.54	-0.00811	1087.54	
+0.062344	1177.655	11	D	7	1000.508	-0.05189	1000.508	
-0.05361	1306.698	12	E	6	885.4808	+0.045974	885.4808	
	1403.751	13	P	5	756.4382	+0.090764	756.4382	
-0.25905	1518.778	14	D	4	659.3854	+0.080784	659.3854	
-0.41795	1631.862	15	I	3	544.3585	+0.04248	544.3585	
-0.18695	1744.946	16	L	2	431.2744	+0.002552	431.2744	
-0.42874	1908.009	17	Y	1	318.1903	+0.019843	318.1903	
		18	K	0	155.127		155.127	



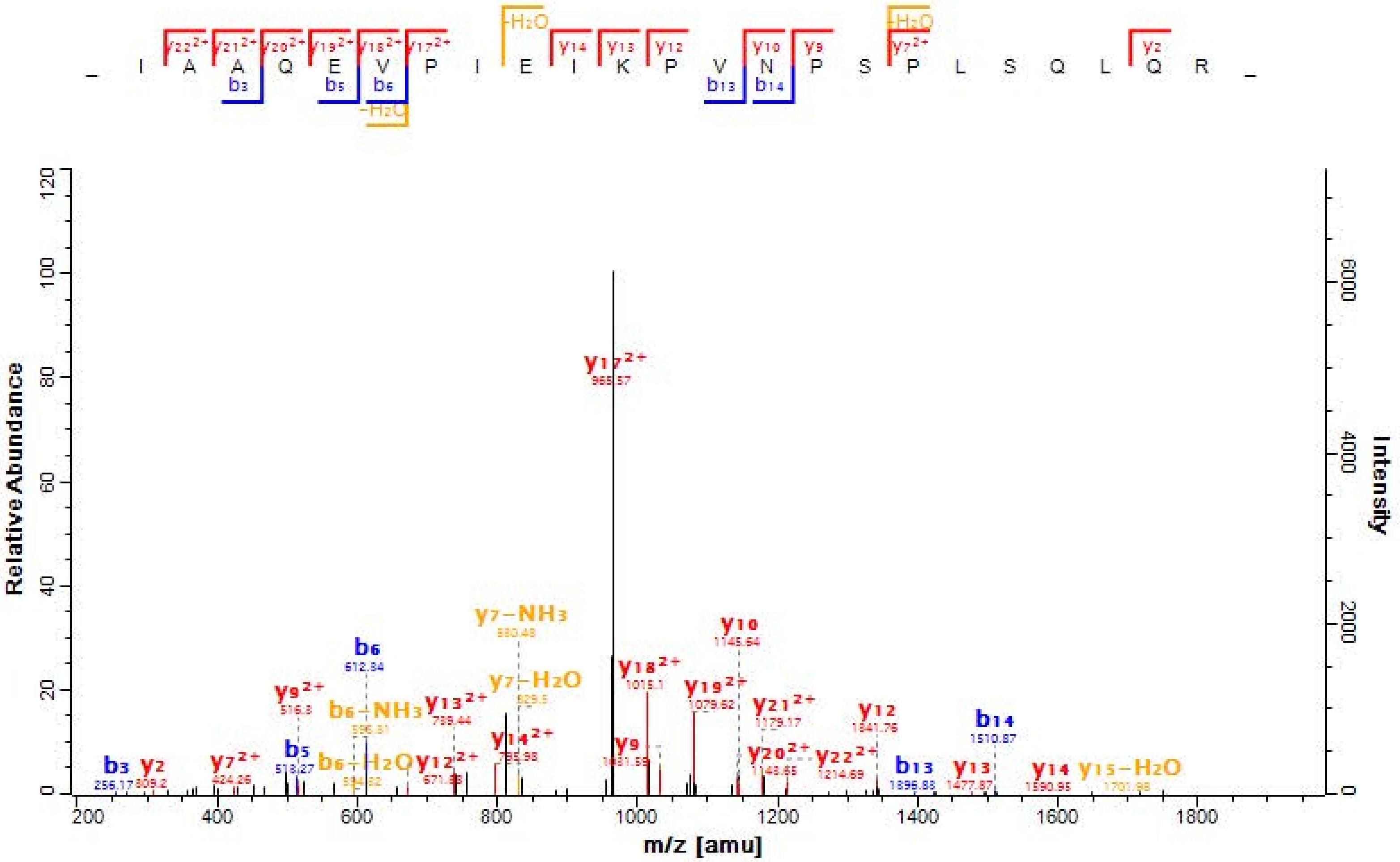
Scan number	6731	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	215.38

precursor information

Mass:	1038.58623
m/z:	520.30039
Charge:	2+
Retentiontime:	43.083042144775
Score:	215.3823
Mass Error [ppm]:	0.015603
PEP:	1.0244E-13
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	46 %
Peak Coverage:	40 %
Protein Localisation:	310 ... 318

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.08		164.07	1	Y	8				
-0.009	249.16	-0.032	277.15	2	L	7	876.53	-0.032	876.53	
	350.21	-0.015	378.2	3	T	6	763.45	+0.0232	382.23	+0.1193
	449.28	-0.132	477.27	4	V	5	662.4	+0.0356	662.4	
	520.31	-0.098	548.31	5	A	4	563.33	+0.013	563.33	
	591.35	-0.034	619.34	6	A	3	492.29	+0.0166	492.29	
	690.42	+0.0915	718.41	7	V	2	421.26	+0.0677	421.26	
	837.49	+0.0353	865.48	8	F	1	322.19	+0.082	322.19	
				9	R	0	175.12	+0.0493	175.12	

Scan number	6760	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	102.39



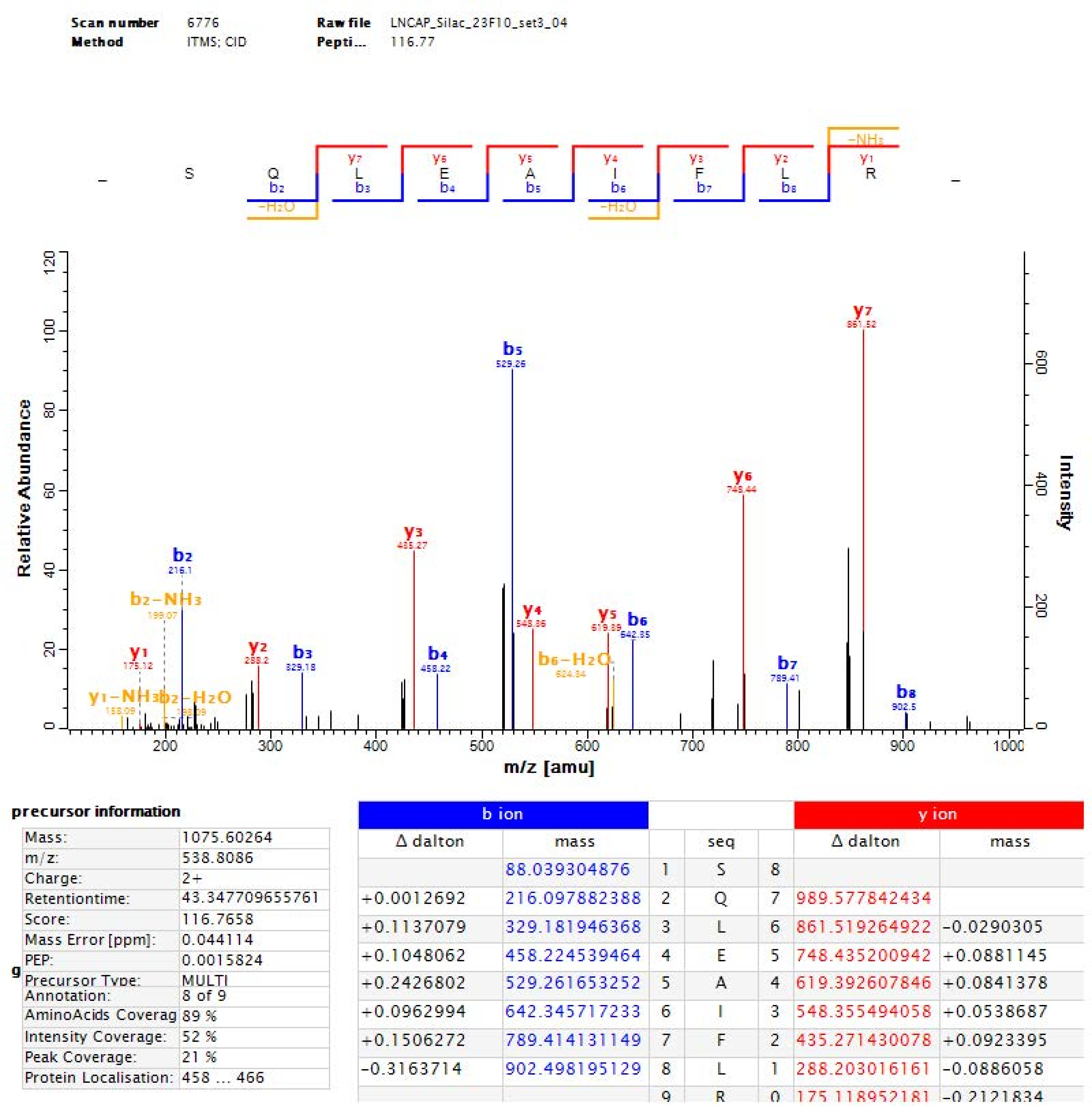
precursor information

Mass:	2526.41744
m/z:	843.14642
Charge:	3+
Retentiontime:	43.252574920654
Score:	102.3903
Mass Error [ppm]:	0.18485
PEP:	8.8874E-08
Precursor Type:	MULTI

general information

Annotation:	15 of 23
AminoAcids Coverag	65 %
Intensity Coverage:	42 %
Peak Coverage:	31 %
Protein Localisation:	178 ... 200

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	I	22				
	185.1285	2	A	21	2428.375		1214.691	+0.325219
-0.00984	256.1656	3	A	20	2357.337		1179.172	-0.0676
	384.2241	4	Q	19	2286.3		1143.654	-0.14487
+0.050034	513.2667	5	E	18	2158.242		1079.624	+0.281758
+0.009147	612.3352	6	V	17	2029.199		1015.103	+0.302871
	709.3879	7	P	16	1930.131		965.569	-0.01229
	822.472	8	I	15	1833.078		1833.078	
	951.5146	9	E	14	1719.994		1719.994	
	1064.599	10	I	13	1590.951	-0.02391	795.9793	+0.192048
	1200.708	11	K	12	1477.867	-0.13052	739.4372	+0.03425
	1297.761	12	P	11	1341.758	+0.005008	671.3827	+0.343104
-0.08752	1396.829	13	V	10	1244.705		1244.705	
-0.04878	1510.872	14	N	9	1145.637	+0.175013	1145.637	
	1607.925	15	P	8	1031.594	-0.09798	516.3006	+0.203111
	1694.957	16	S	7	934.5412		934.5412	
	1792.009	17	P	6	847.5092		424.2582	+0.048912
	1905.094	18	L	5	750.4564		750.4564	
	1992.126	19	S	4	637.3723		637.3723	
	2120.184	20	Q	3	550.3403		550.3403	
	2233.268	21	L	2	422.2817		422.2817	
	2361.327	22	Q	1	309.1977	+0.196995	309.1977	
		23	R	0	181.1391		181.1391	

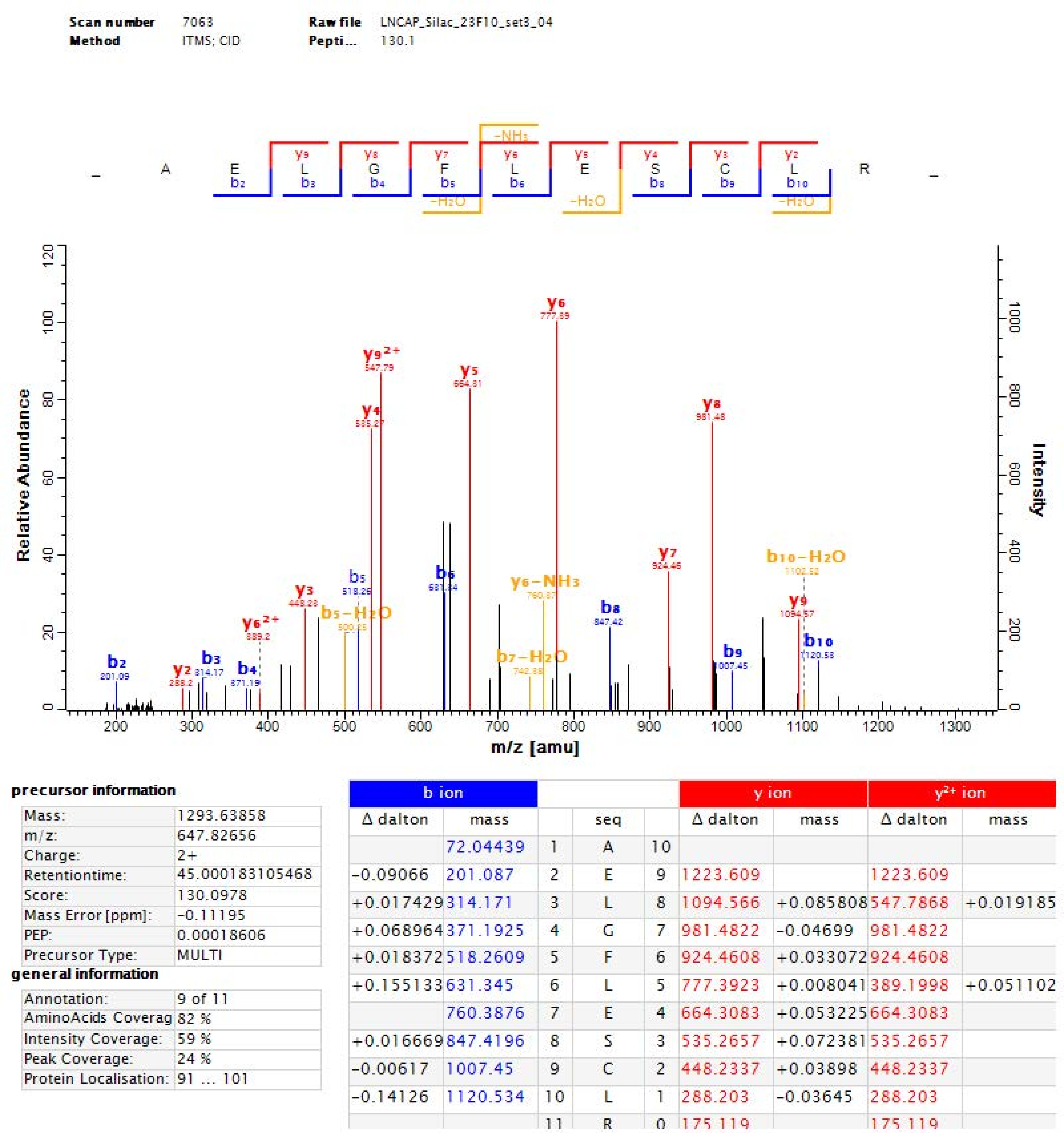


Scan number	6776	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	116.77

precursor information

Mass:	1075.60264
m/z:	538.8086
Charge:	2+
Retentiontime:	43.347709655761
Score:	116.7658
Mass Error [ppm]:	0.044114
PEP:	0.0015824
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	52 %
Peak Coverage:	21 %
Protein Localisation:	458 ... 466

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	88.039304876	1	S	8		
+0.0012692	216.097882388	2	Q	7	989.577842434	
+0.1137079	329.181946368	3	L	6	861.519264922	-0.0290305
+0.1048062	458.224539464	4	E	5	748.435200942	+0.0881145
+0.2426802	529.261653252	5	A	4	619.392607846	+0.0841378
+0.0962994	642.345717233	6	I	3	548.355494058	+0.0538687
+0.1506272	789.414131149	7	F	2	435.271430078	+0.0923395
-0.3163714	902.498195129	8	L	1	288.203016161	-0.0886058
		9	R	0	175.118952181	-0.2121834



Scan number 7063
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set3_04
Pepti... 130.1

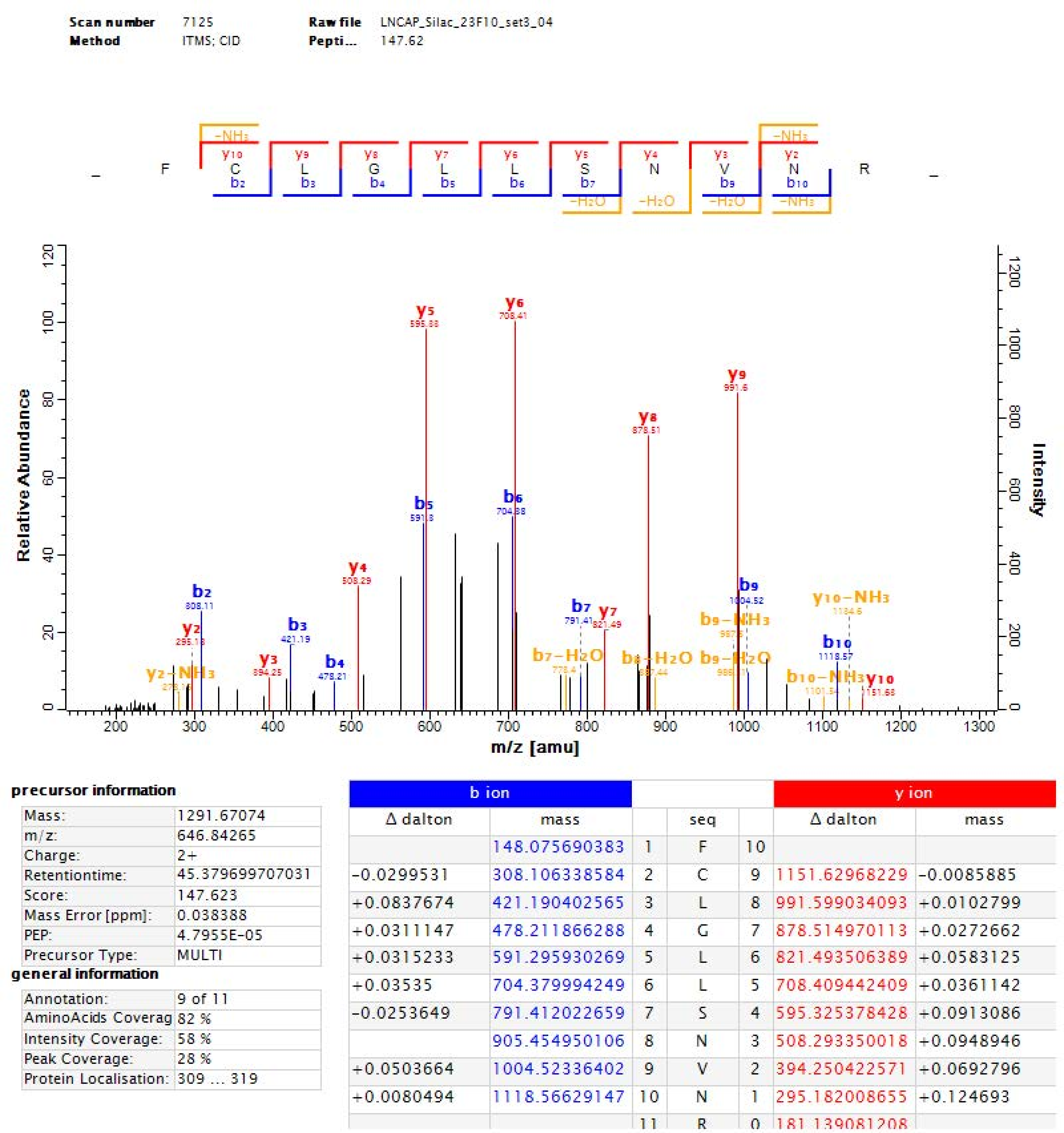
precursor information

Mass:	1293.63858
m/z:	647.82656
Charge:	2+
Retentiontime:	45.000183105468
Score:	130.0978
Mass Error [ppm]:	-0.11195
PEP:	0.00018606
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	59 %
Peak Coverage:	24 %
Protein Localisation:	91 ... 101

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	10				
-0.09066	201.087	2	E	9	1223.609		1223.609	
+0.017429	314.171	3	L	8	1094.566	+0.085808	547.7868	+0.019185
+0.068964	371.1925	4	G	7	981.4822	-0.04699	981.4822	
+0.018372	518.2609	5	F	6	924.4608	+0.033072	924.4608	
+0.155133	631.345	6	L	5	777.3923	+0.008041	389.1998	+0.051102
	760.3876	7	E	4	664.3083	+0.053225	664.3083	
+0.016669	847.4196	8	S	3	535.2657	+0.072381	535.2657	
-0.00617	1007.45	9	C	2	448.2337	+0.03898	448.2337	
-0.14126	1120.534	10	L	1	288.203	-0.03645	288.203	
		11	R	0	175.119		175.119	



Scan number	7125	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	147.62

precursor information

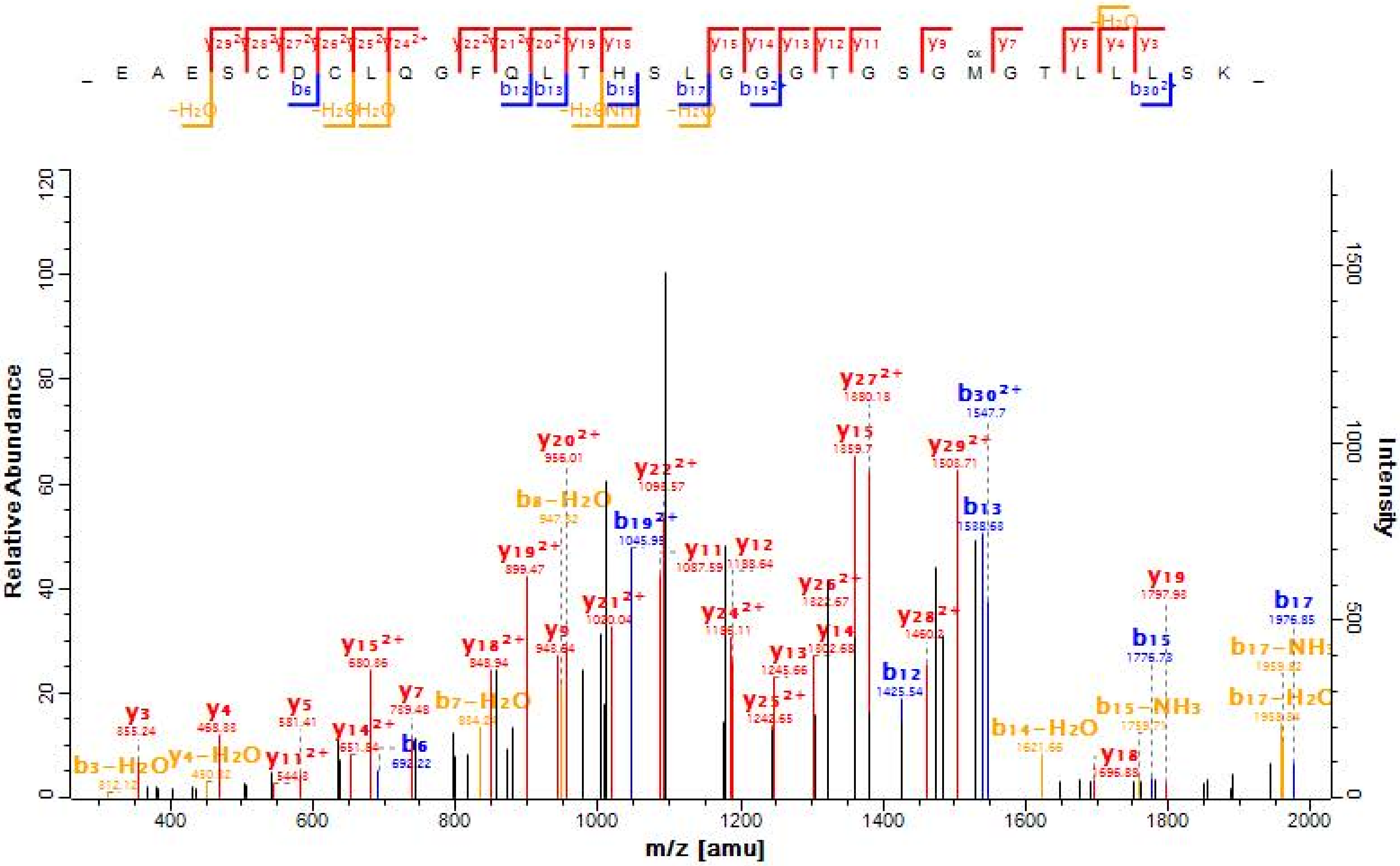
Mass:	1291.67074
m/z:	646.84265
Charge:	2+
Retentiontime:	45.379699707031
Score:	147.623
Mass Error [ppm]:	0.038388
PEP:	4.7955E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	58 %
Peak Coverage:	28 %
Protein Localisation:	309 ... 319

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	148.075690383	1	F	10		
-0.0299531	308.106338584	2	C	9	1151.62968229	-0.0085885
+0.0837674	421.190402565	3	L	8	991.599034093	+0.0102799
+0.0311147	478.211866288	4	G	7	878.514970113	+0.0272662
+0.0315233	591.295930269	5	L	6	821.493506389	+0.0583125
+0.03535	704.379994249	6	L	5	708.409442409	+0.0361142
-0.0253649	791.412022659	7	S	4	595.325378428	+0.0913086
	905.454950106	8	N	3	508.293350018	+0.0948946
+0.0503664	1004.52336402	9	V	2	394.250422571	+0.0692796
+0.0080494	1118.56629147	10	N	1	295.182008655	+0.124693
		11	R	0	181.139081208	

Scan number	7129	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	158.61



precursor information

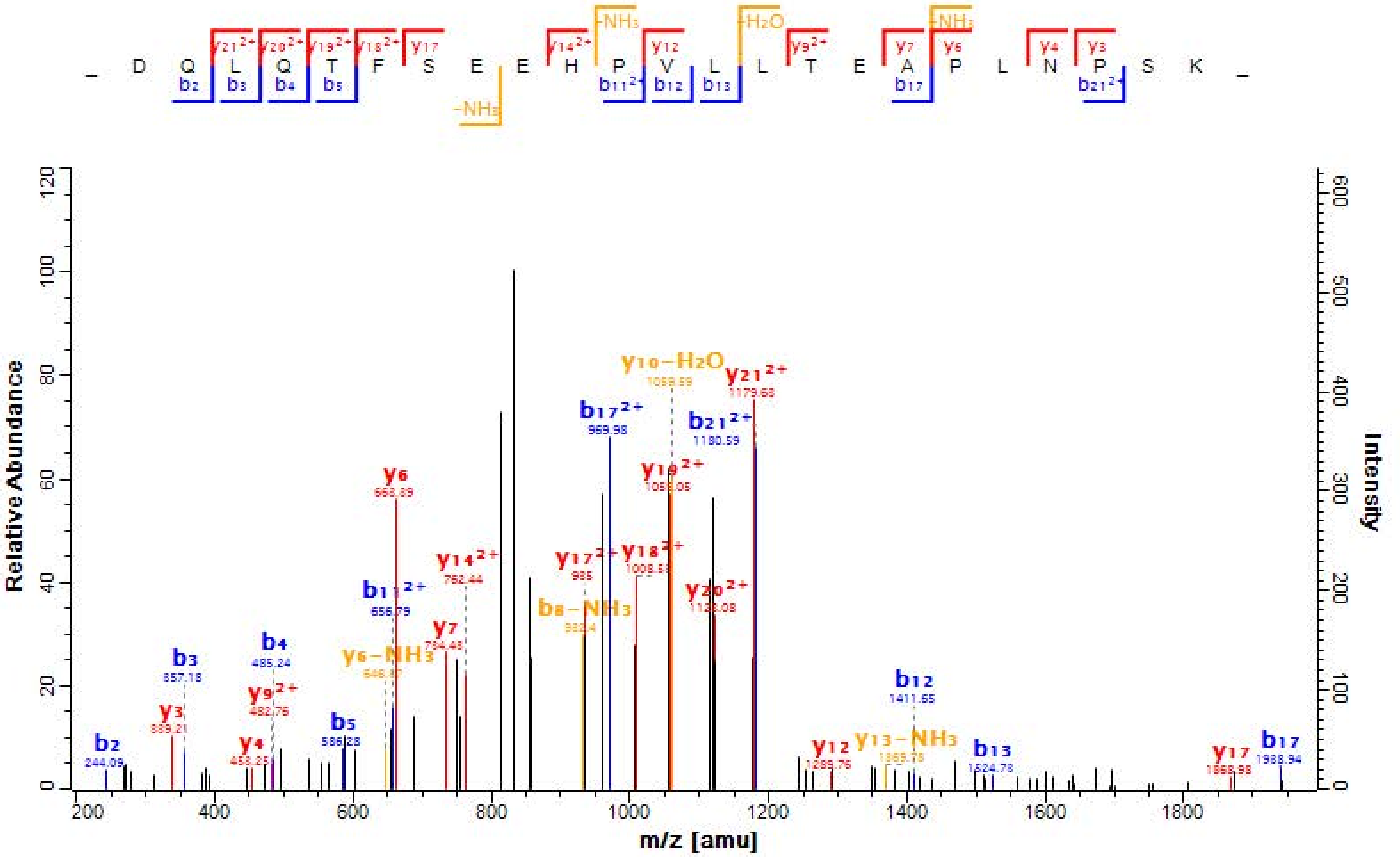
Mass:	3326.52019
m/z:	1109.84734
Charge:	3+
Retentiontime:	45.403121948242
Score:	158.6072
Mass Error [ppm]:	-0.45967
PEP:	2.3205E-41
Precursor Type:	MULTI

general information

Annotation:	23 of 32
AminoAcids Coverag	72 %
Intensity Coverage:	52 %
Peak Coverage:	44 %
Protein Localisation:	123 ... 154

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	31				
	201.09		201.09	2	A	30	3206.5		3206.5	
	330.13		330.13	3	E	29	3135.5		3135.5	
	417.16		417.16	4	S	28	3006.4		1503.7	+0.1942
	577.19		577.19	5	C	27	2919.4		1460.2	+0.167
	692.22	-0.072	692.22	6	D	26	2759.4		1380.2	+0.3251
	852.25		852.25	7	C	25	2644.3		1322.7	-0.083
	965.33		965.33	8	L	24	2484.3		1242.7	-0.028
	1093.4		1093.4	9	Q	23	2371.2		1186.1	+0.1199
	1150.4		1150.4	10	G	22	2243.2		2243.2	
	1297.5		1297.5	11	F	21	2186.1		1093.6	-0.074
	1425.5	+0.0516	1425.5	12	Q	20	2039.1		1020	+0.1504
	1538.6	+0.4663	1538.6	13	L	19	1911		956.01	-0.01
	1639.7		1639.7	14	T	18	1797.9	+0.0068	899.47	+0.1149
	1776.7	+0.317	1776.7	15	H	17	1696.9	+0.021	848.94	+0.2584
	1863.8		1863.8	16	S	16	1559.8		1559.8	
	1976.8	-0.293	1976.8	17	L	15	1472.8		1472.8	
	2033.9		2033.9	18	G	14	1359.7	+0.0395	680.36	+0.1498
+0.2965	1045.9		2090.9	19	G	13	1302.7	+0.0068	651.84	+0.02
	2147.9		2147.9	20	G	12	1245.7	-0.044	1245.7	
	2249		2249	21	T	11	1188.6	-0.295	1188.6	
	2306		2306	22	G	10	1087.6	+0.0746	544.3	+0.1784
	2393		2393	23	S	9	1030.6		1030.6	
	2450		2450	24	G	8	943.54	+0.0306	943.54	
	2597.1		2597.1	25	M	7	886.52		886.52	
	2654.1		2654.1	26	G	6	739.48	+0.0028	739.48	
	2755.1		2755.1	27	T	5	682.46		682.46	
	2868.2		2868.2	28	L	4	581.41	+0.1116	581.41	
	2981.3		2981.3	29	L	3	468.33	+0.1519	468.33	
+0.2749	1547.7		3094.4	30	L	2	355.24	+0.0918	355.24	
	3181.4		3181.4	31	S	1	242.16		242.16	
				32	K	0	155.13		155.13	

Scan number	7215	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	95.21



precursor information

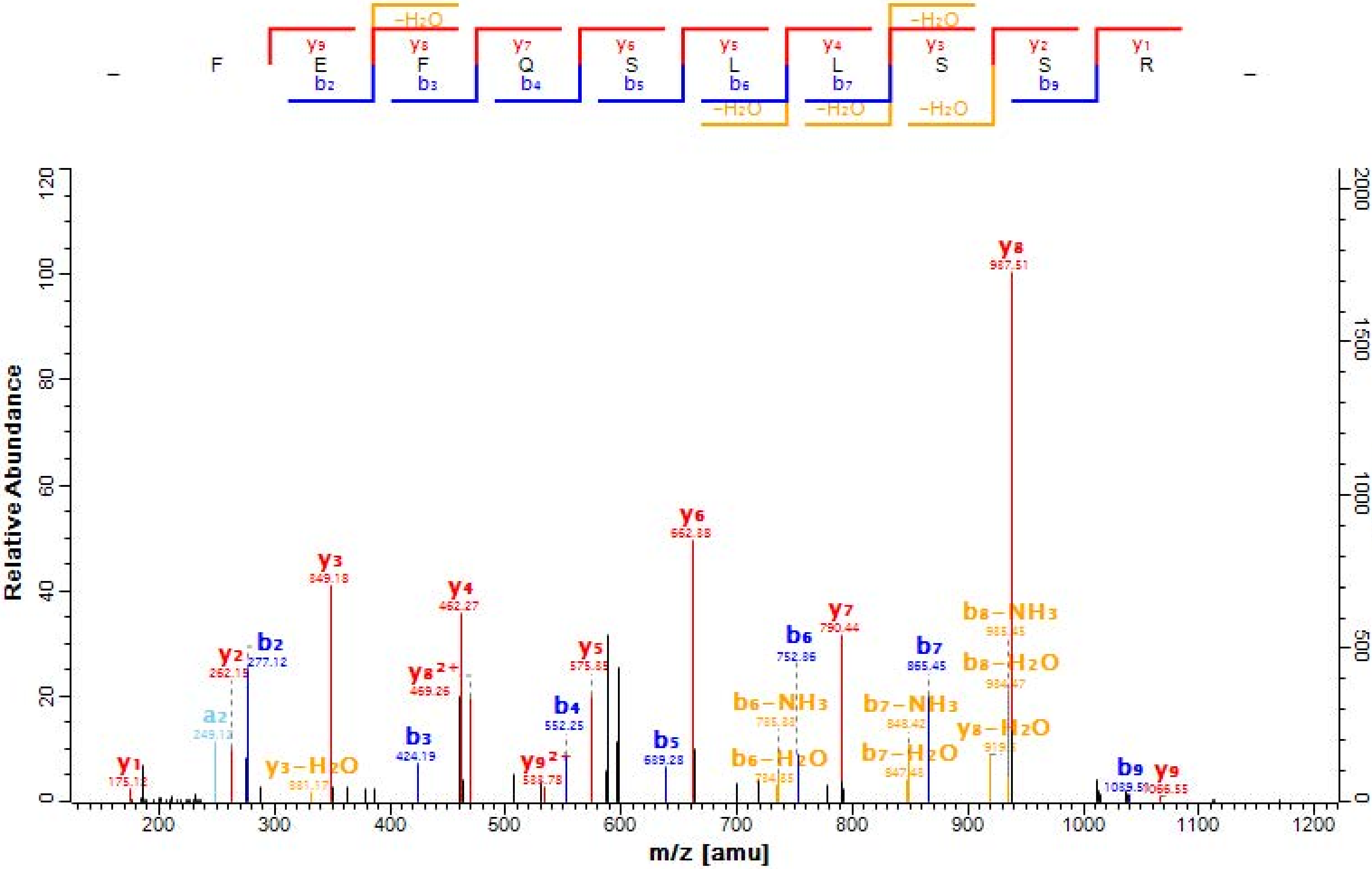
Mass:	2592.30766
m/z:	865.10983
Charge:	3+
Retentiontime:	45.896591186523
Score:	95.20565
Mass Error [ppm]:	0.19907
PEP:	1.1119E-06
Precursor Type:	MULTI

general information

Annotation:	17 of 23
AminoAcids Coverag	74 %
Intensity Coverage:	42 %
Peak Coverage:	28 %
Protein Localisation:	97 ... 119

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	22				
	244.09	+0.0414	244.09	2	Q	21	2486.3		2486.3	
	357.18	+0.0591	357.18	3	L	20	2358.2		1179.6	-0.087
	485.24	-0.014	485.24	4	Q	19	2245.2		1123.1	-0.073
	586.28	-0.086	586.28	5	T	18	2117.1		1059.1	-0.159
	733.35		733.35	6	F	17	2016.1		1008.5	+0.0554
	820.38		820.38	7	S	16	1869	+0.3246	935	-0.003
	949.43		949.43	8	E	15	1782		1782	
	1078.5		1078.5	9	E	14	1652.9		1652.9	
	1215.5		1215.5	10	H	13	1523.9		762.44	+0.1692
-0.458	656.79		1312.6	11	P	12	1386.8		1386.8	
	1411.6	-0.047	1411.6	12	V	11	1289.8	-0.006	1289.8	
	1524.7	-0.051	1524.7	13	L	10	1190.7		1190.7	
	1637.8		1637.8	14	L	9	1077.6		1077.6	
	1738.9		1738.9	15	T	8	964.52		482.76	+0.344
	1867.9		1867.9	16	E	7	863.47		863.47	
+0.3432	969.98	+0.0422	1938.9	17	A	6	734.43	-0.002	734.43	
	2036		2036	18	P	5	663.39	+0.0162	663.39	
	2149.1		2149.1	19	L	4	566.34		566.34	
	2263.1		2263.1	20	N	3	453.25	+0.482	453.25	
-0.225	1180.6		2360.2	21	P	2	339.21	+0.0099	339.21	
	2447.2		2447.2	22	S	1	242.16		242.16	
				23	K	0	155.13		155.13	

Scan number	7503	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	158.3



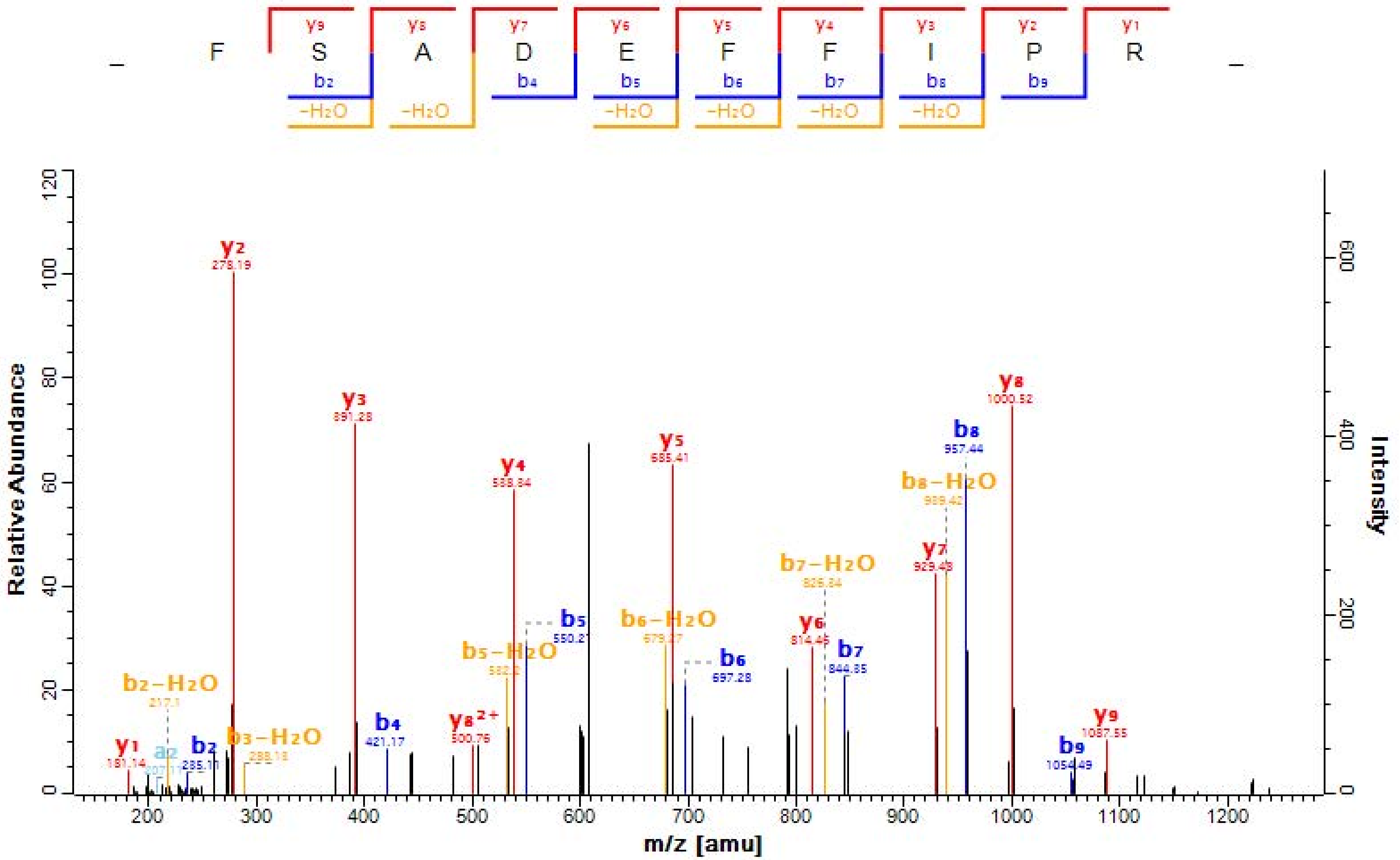
precursor information

Mass:	1212.61404
m/z:	607.3143
Charge:	2+
Retentiontime:	47.549579620361
Score:	158.2997
Mass Error [ppm]:	0.12996
PEP:	9.132E-05
Precursor Type:	MULTI

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	69 %
Peak Coverage:	34 %
Protein Localisation:	38 ... 47

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08		148.08	1	F	9				
+0.0191	249.12	+0.0365	277.12	2	E	8	1066.6	-0.451	533.78	-0.262
	396.19	+0.147	424.19	3	F	7	937.51	-0.033	469.26	+0.1327
	524.25	-0.048	552.25	4	Q	6	790.44	+0.0009	790.44	
	611.28	+0.1373	639.28	5	S	5	662.38	-0.012	662.38	
	724.37	+0.06	752.36	6	L	4	575.35	-0.014	575.35	
	837.45	+0.0209	865.45	7	L	3	462.27	+0.0239	462.27	
	924.48		952.48	8	S	2	349.18	+0.1198	349.18	
	1011.5	+0.0782	1039.5	9	S	1	262.15	+0.0454	262.15	
				10	R	0	175.12	-0.068	175.12	

Scan number	7666	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	156.48

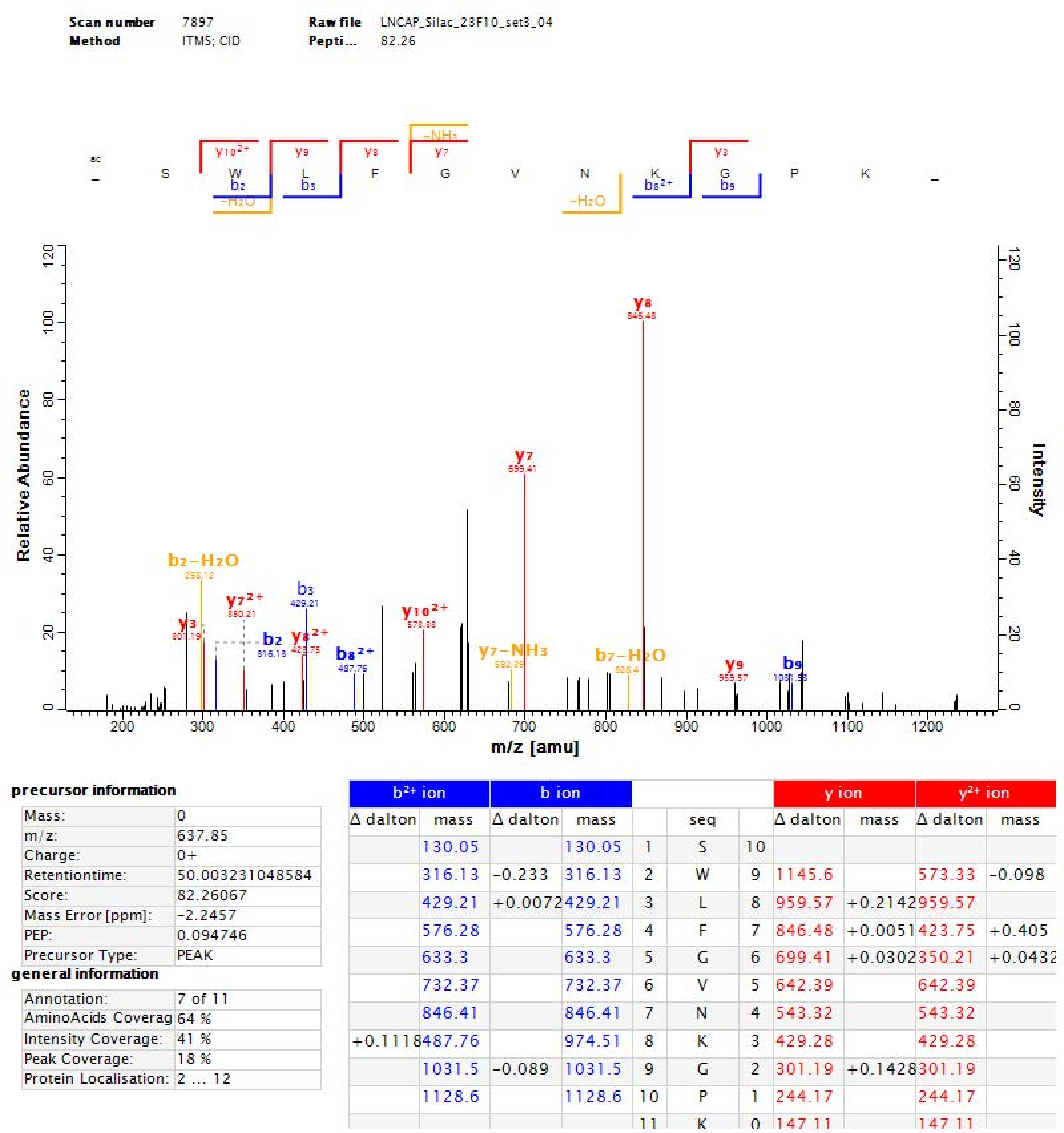


precursor information

Mass:	1227.59254
m/z:	614.80355
Charge:	2+
Retentiontime:	48.540802001953
Score:	156.4802
Mass Error [ppm]:	0.093502
PEP:	0.0001065
Precursor Type:	MULTI

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	57 %
Peak Coverage:	25 %
Protein Localisation:	112 ... 121

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08		148.08	1	F	9				
+0.0103	207.11	+0.0304	235.11	2	S	8	1087.6	+0.0753	1087.6	
	278.15		306.14	3	A	7	1000.5	+0.0127	500.76	-0.229
	393.18	-0.032	421.17	4	D	6	929.48	-0.003	929.48	
	522.22	-0.01	550.21	5	E	5	814.46	-0.041	814.46	
	669.29	-0.093	697.28	6	F	4	685.41	-0.098	685.41	
	816.36	-0.185	844.35	7	F	3	538.34	+0.0757	538.34	
	929.44	-0.074	957.44	8	I	2	391.28	+0.0808	391.28	
	1026.5	-0.015	1054.5	9	P	1	278.19	+0.0297	278.19	
				10	R	0	181.14	+0.1728	181.14	



Scan number	7897	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	82.26

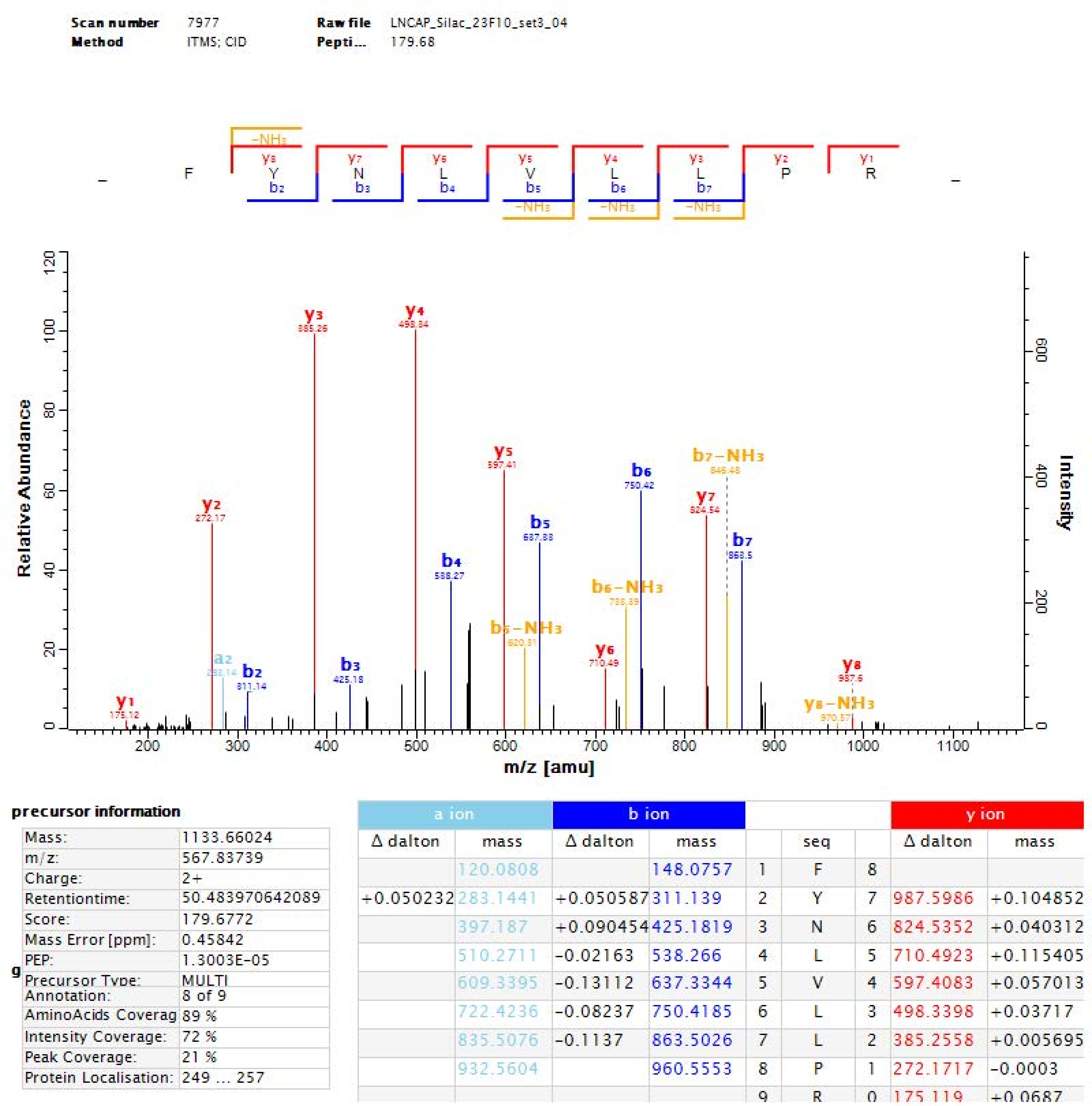
precursor information

Mass:	0
m/z:	637.85
Charge:	0+
Retentiontime:	50.003231048584
Score:	82.26067
Mass Error [ppm]:	-2.2457
PEP:	0.094746
Precursor Type:	PEAK

general information

Annotation:	7 of 11
AminoAcids Coverag	64 %
Intensity Coverage:	41 %
Peak Coverage:	18 %
Protein Localisation:	2 ... 12

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	S	10				
	316.13	-0.233	316.13	2	W	9	1145.6		573.33	-0.098
	429.21	+0.0072	429.21	3	L	8	959.57	+0.2142	959.57	
	576.28		576.28	4	F	7	846.48	+0.0051	423.75	+0.405
	633.3		633.3	5	G	6	699.41	+0.0302	350.21	+0.0432
	732.37		732.37	6	V	5	642.39		642.39	
	846.41		846.41	7	N	4	543.32		543.32	
+0.1118	487.76		974.51	8	K	3	429.28		429.28	
	1031.5	-0.089	1031.5	9	G	2	301.19	+0.1428	301.19	
	1128.6		1128.6	10	P	1	244.17		244.17	
				11	K	0	147.11		147.11	

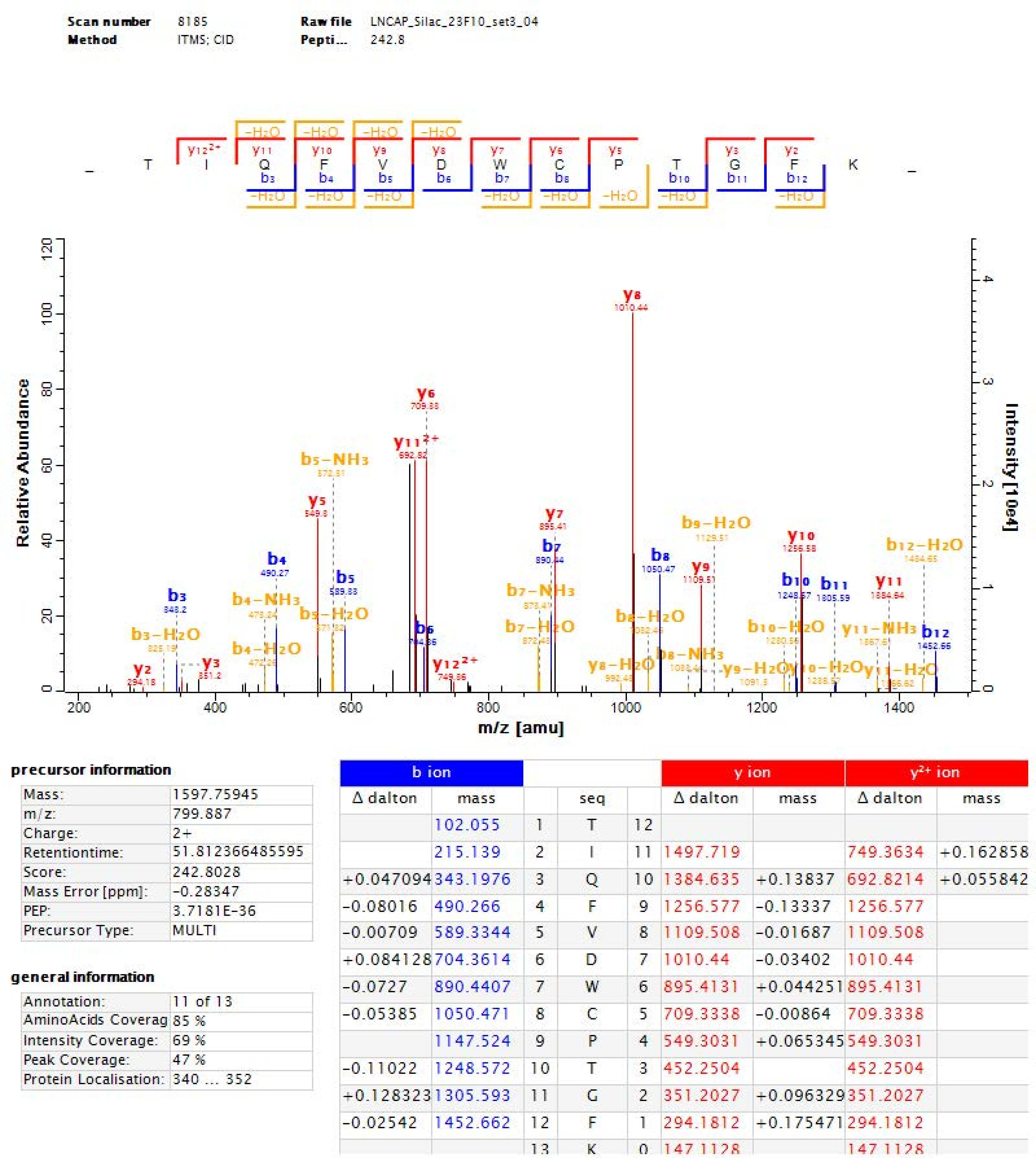


Scan number	7977	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti…**	179.68

precursor information

Mass:	1133.66024
m/z:	567.83739
Charge:	2+
Retentiontime:	50.483970642089
Score:	179.6772
Mass Error [ppm]:	0.45842
PEP:	1.3003E-05
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	72 %
Peak Coverage:	21 %
Protein Localisation:	249 … 257

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	120.0808		148.0757	1	F	8		
+0.050232	283.1441	+0.050587	311.139	2	Y	7	987.5986	+0.104852
	397.187	+0.090454	425.1819	3	N	6	824.5352	+0.040312
	510.2711	-0.02163	538.266	4	L	5	710.4923	+0.115405
	609.3395	-0.13112	637.3344	5	V	4	597.4083	+0.057013
	722.4236	-0.08237	750.4185	6	L	3	498.3398	+0.03717
	835.5076	-0.1137	863.5026	7	L	2	385.2558	+0.005695
	932.5604		960.5553	8	P	1	272.1717	-0.0003
				9	R	0	175.119	+0.0687



Scan number 8185

Method ITMS; CID

Raw file LNCAP_Silac_23F10_set3_04

Pepti... 242.8

precursor information

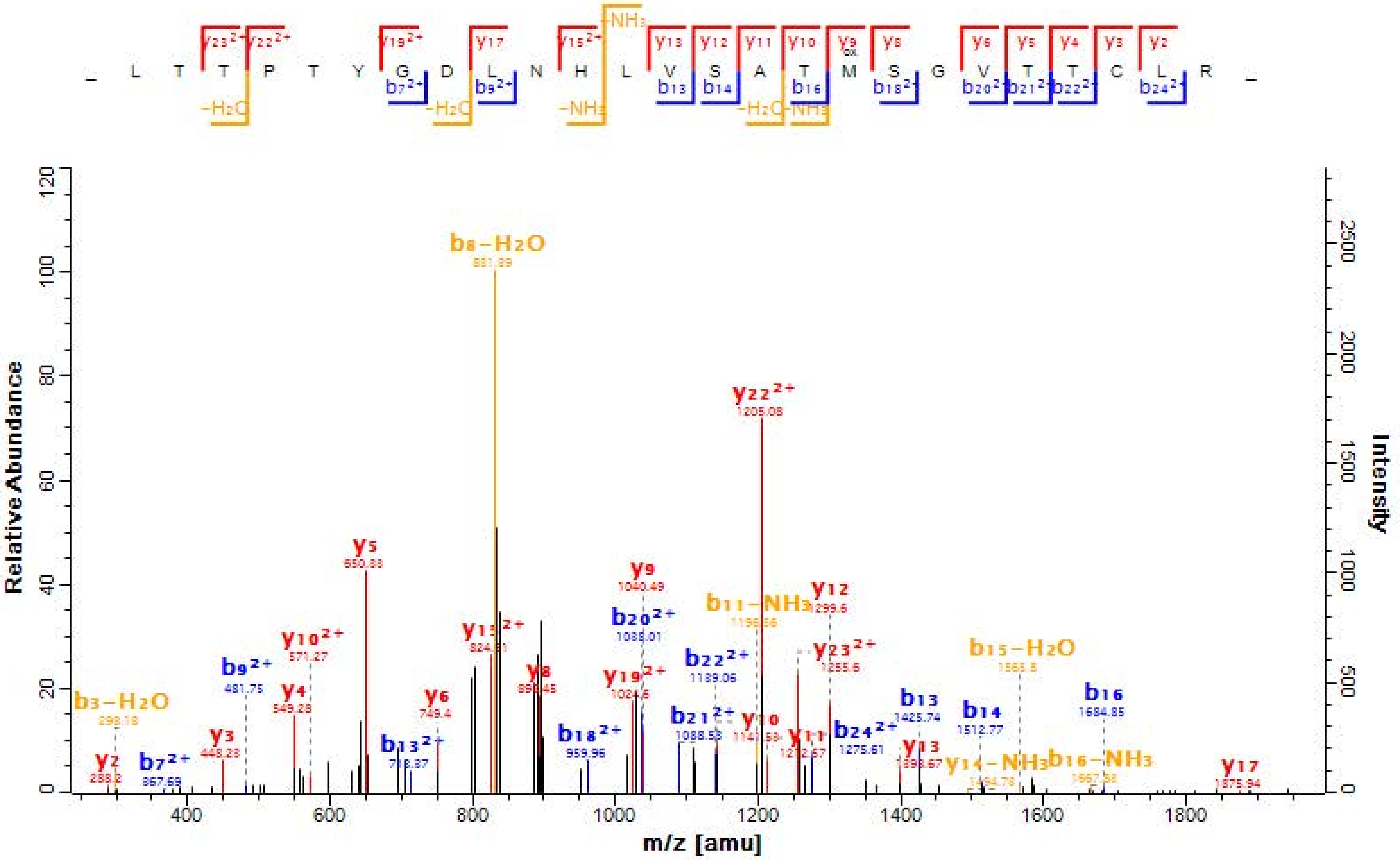
Mass:	1597.75945
m/z:	799.887
Charge:	2+
Retentiontime:	51.812366485595
Score:	242.8028
Mass Error [ppm]:	-0.28347
PEP:	3.7181E-36
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	69 %
Peak Coverage:	47 %
Protein Localisation:	340 ... 352

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055	1	T	12				
	215.139	2	I	11	1497.719		749.3634	+0.162858
+0.047094	343.1976	3	Q	10	1384.635	+0.13837	692.8214	+0.055842
-0.08016	490.266	4	F	9	1256.577	-0.13337	1256.577	
-0.00709	589.3344	5	V	8	1109.508	-0.01687	1109.508	
+0.084128	704.3614	6	D	7	1010.44	-0.03402	1010.44	
-0.0727	890.4407	7	W	6	895.4131	+0.044251	895.4131	
-0.05385	1050.471	8	C	5	709.3338	-0.00864	709.3338	
	1147.524	9	P	4	549.3031	+0.065345	549.3031	
-0.11022	1248.572	10	T	3	452.2504		452.2504	
+0.128323	1305.593	11	G	2	351.2027	+0.096329	351.2027	
-0.02542	1452.662	12	F	1	294.1812	+0.175471	294.1812	
		13	K	0	147.1128		147.1128	

Scan number	8227	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	125.45



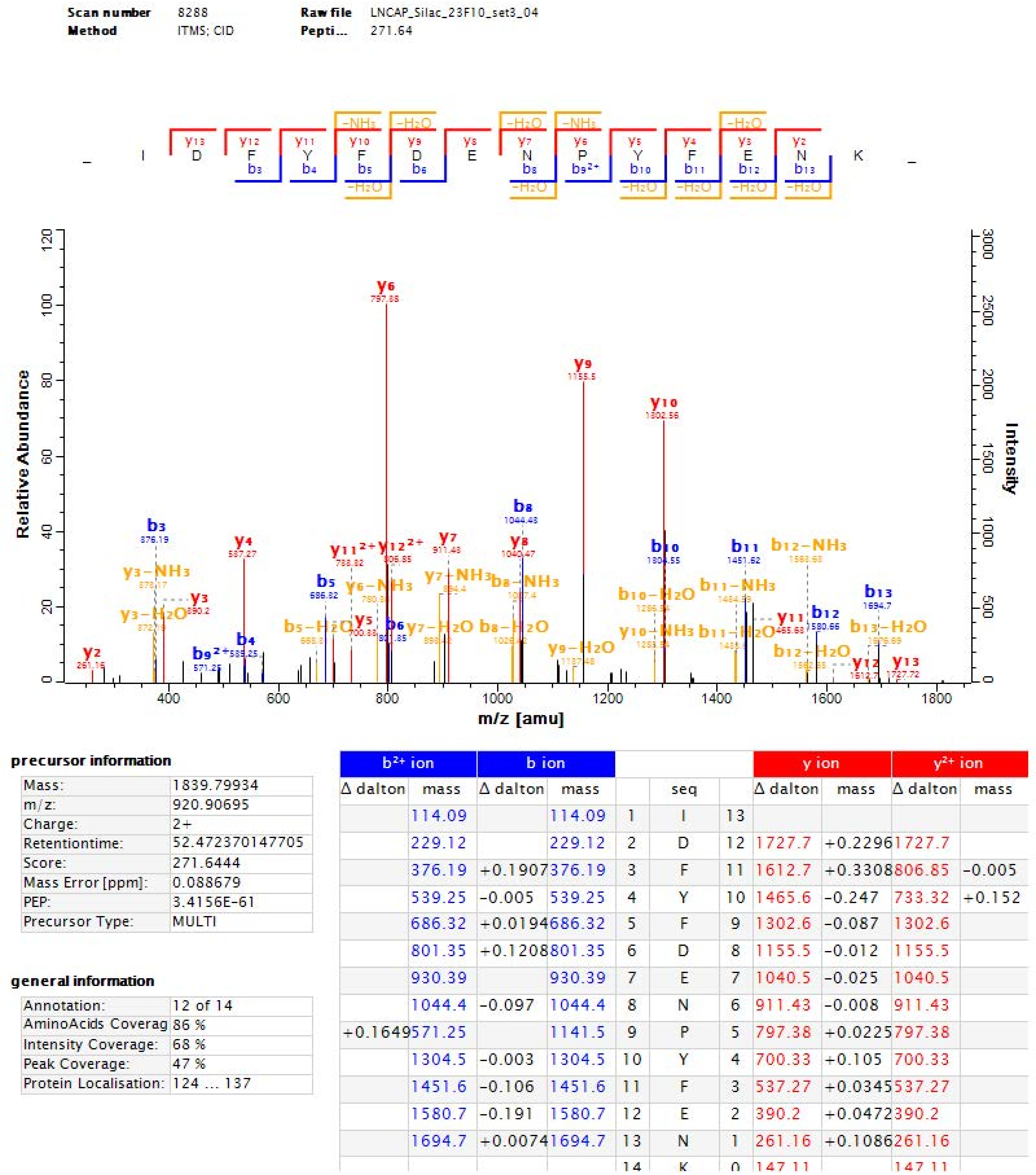
precursor information

Mass:	2723.32644
m/z:	908.78276
Charge:	3+
Retentiontime:	52.062042236328
Score:	125.447
Mass Error [ppm]:	0.21532
PEP:	9.0452E-16
Precursor Type:	MULTI

general information

Annotation:	18 of 25
AminoAcids Coverag	72 %
Intensity Coverage:	51 %
Peak Coverage:	32 %
Protein Localisation:	217 ... 241

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	24				
	215.14		215.14	2	T	23	2611.2		2611.2	
	316.19		316.19	3	T	22	2510.2		1255.6	+0.2222
	413.24		413.24	4	P	21	2409.2		1205.1	+0.3511
	514.29		514.29	5	T	20	2312.1		2312.1	
	677.35		677.35	6	Y	19	2211.1		2211.1	
-0.449	367.69		734.37	7	G	18	2048		1024.5	+0.1824
	849.4		849.4	8	D	17	1991		1991	
-0.383	481.75		962.48	9	L	16	1875.9	+0.3867	1875.9	
	1076.5		1076.5	10	N	15	1762.9		1762.9	
	1213.6		1213.6	11	H	14	1648.8		824.91	+0.4991
	1326.7		1326.7	12	L	13	1511.8		1511.8	
-0.219	713.37	-0.076	1425.7	13	V	12	1398.7	-0.126	1398.7	
	1512.8	+0.2213	1512.8	14	S	11	1299.6	-0.046	1299.6	
	1583.8		1583.8	15	A	10	1212.6	-0.084	1212.6	
	1684.9	-0.145	1684.9	16	T	9	1141.5	-0.063	571.27	+0.2804
	1831.9		1831.9	17	M	8	1040.5	-0.023	1040.5	
+0.331	959.96		1918.9	18	S	7	893.45	+0.0879	893.45	
	1975.9		1975.9	19	G	6	806.42		806.42	
+0.0676	1038		2075	20	V	5	749.4	+0.0694	749.4	
+0.2193	1088.5		2176.1	21	T	4	650.33	+0.0069	650.33	
+0.2203	1139.1		2277.1	22	T	3	549.28	+0.1001	549.28	
	2437.1		2437.1	23	C	2	448.23	-0.028	448.23	
+0.2923	1275.6		2550.2	24	L	1	288.2	+0.0491	288.2	
				25	R	0	175.12		175.12	



Scan number	8288	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	271.64

precursor information

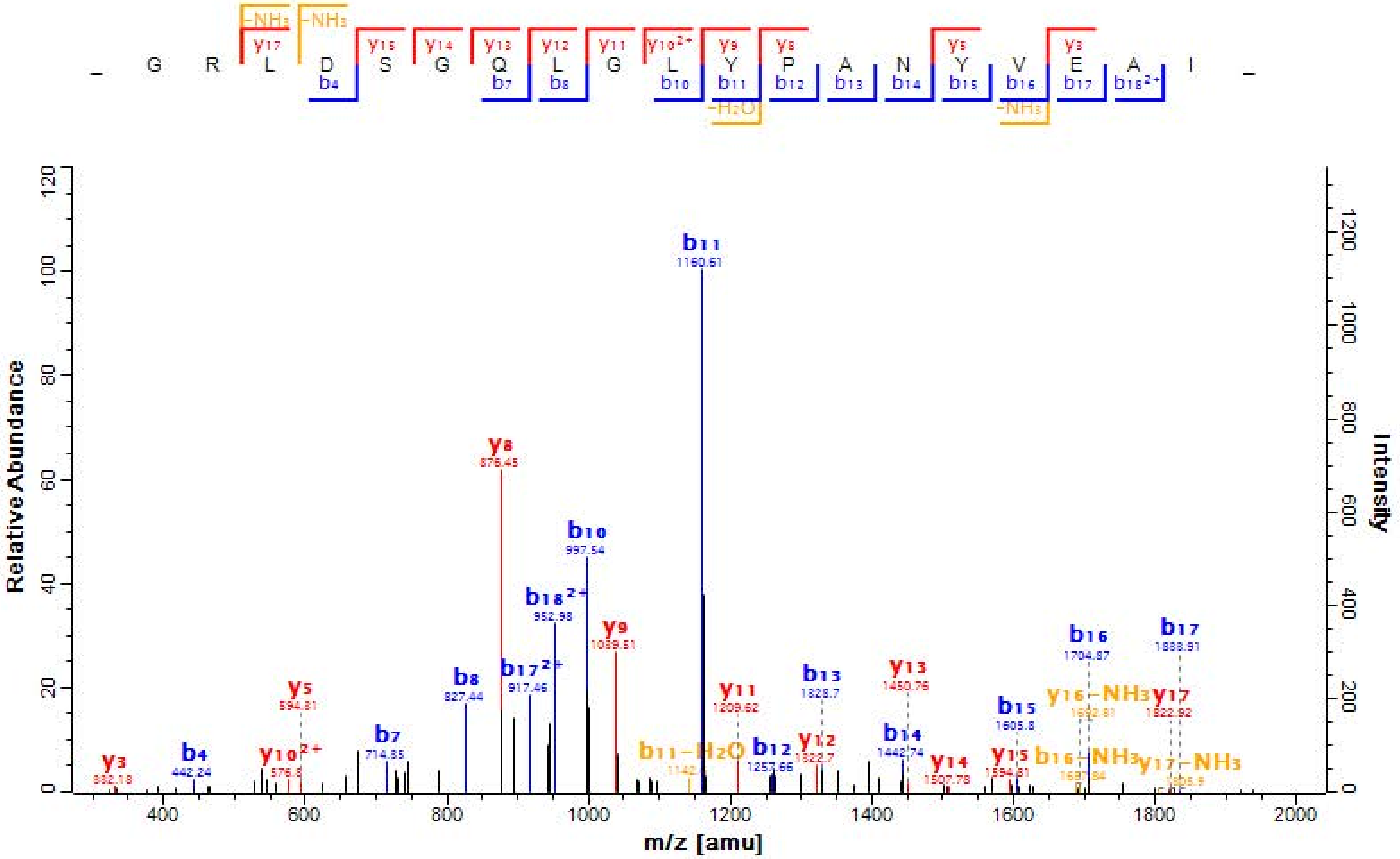
Mass:	1839.79934
m/z:	920.90695
Charge:	2+
Retentiontime:	52.472370147705
Score:	271.6444
Mass Error [ppm]:	0.088679
PEP:	3.4156E-61
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	68 %
Peak Coverage:	47 %
Protein Localisation:	124 ... 137

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	I	13				
	229.12		229.12	2	D	12	1727.7	+0.2296	1727.7	
	376.19	+0.1907	376.19	3	F	11	1612.7	+0.3308	806.85	-0.005
	539.25	-0.005	539.25	4	Y	10	1465.6	-0.247	733.32	+0.152
	686.32	+0.0194	686.32	5	F	9	1302.6	-0.087	1302.6	
	801.35	+0.1208	801.35	6	D	8	1155.5	-0.012	1155.5	
	930.39		930.39	7	E	7	1040.5	-0.025	1040.5	
	1044.4	-0.097	1044.4	8	N	6	911.43	-0.008	911.43	
+0.1649	571.25		1141.5	9	P	5	797.38	+0.0225	797.38	
	1304.5	-0.003	1304.5	10	Y	4	700.33	+0.105	700.33	
	1451.6	-0.106	1451.6	11	F	3	537.27	+0.0345	537.27	
	1580.7	-0.191	1580.7	12	E	2	390.2	+0.0472	390.2	
	1694.7	+0.0074	1694.7	13	N	1	261.16	+0.1086	261.16	
				14	K	0	147.11		147.11	

Scan number	8425	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	144.01



precursor information

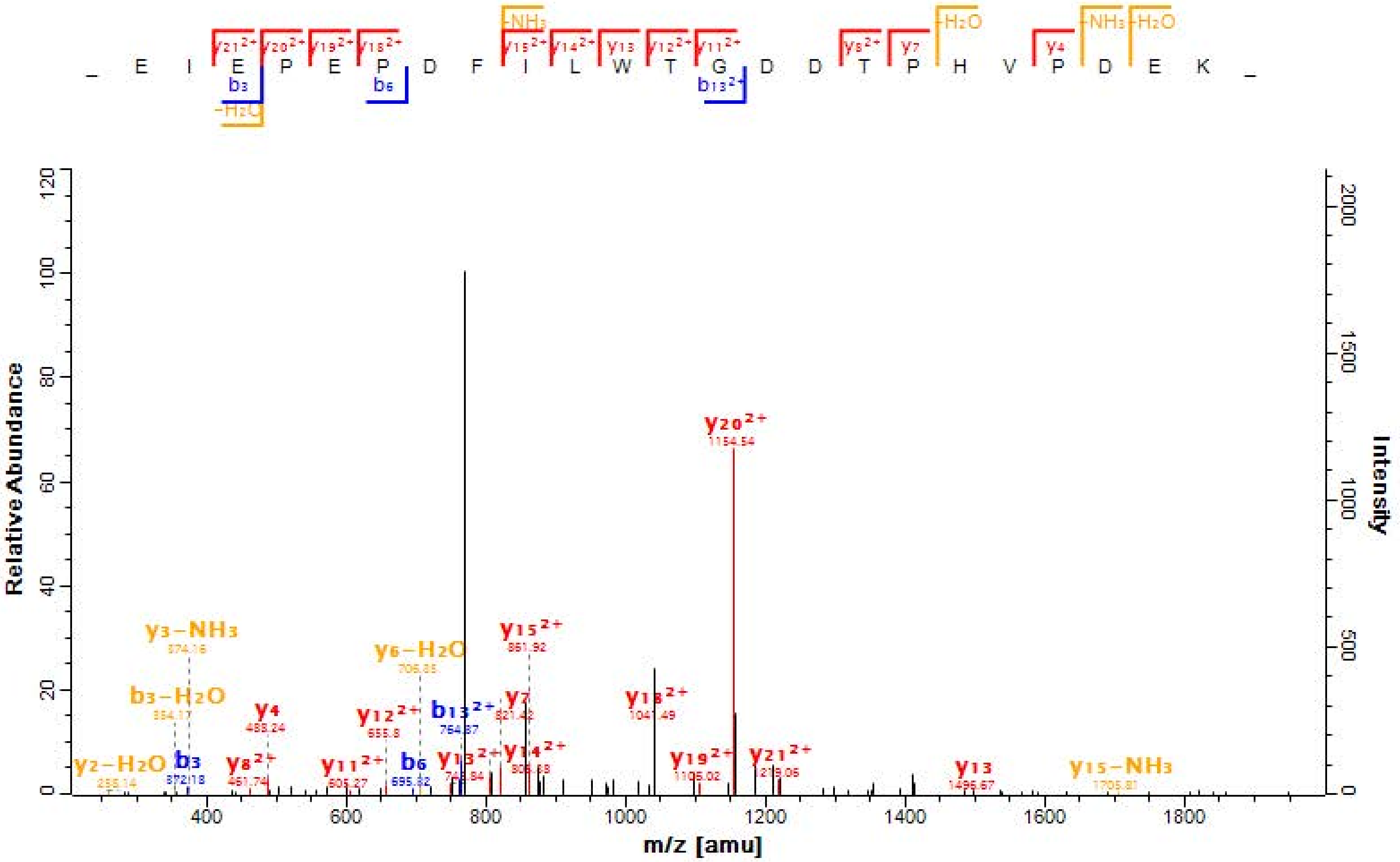
Mass:	2035.03868
m/z:	1018.52662
Charge:	2+
Retentiontime:	53.388240814209
Score:	144.0086
Mass Error [ppm]:	0.60397
PEP:	5.1518E-19
Precursor Type:	MULTI

general information

Annotation:	16 of 19
AminoAcids Coverag	84 %
Intensity Coverage:	56 %
Peak Coverage:	29 %
Protein Localisation:	426 ... 444

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	18				
	214.13		214.13	2	R	17	1979		1979	
	327.21		327.21	3	L	16	1822.9	-0.048	1822.9	
	442.24	+0.1327	442.24	4	D	15	1709.8		1709.8	
	529.27		529.27	5	S	14	1594.8	-0.175	1594.8	
	586.29		586.29	6	G	13	1507.8	+0.3265	1507.8	
	714.35	-0.012	714.35	7	Q	12	1450.8	+0.2251	1450.8	
	827.44	-0.094	827.44	8	L	11	1322.7	-0.16	1322.7	
	884.46		884.46	9	G	10	1209.6	+0.0425	1209.6	
	997.54	+0	997.54	10	L	9	1152.6		576.8	+0.0361
	1160.6	-0.018	1160.6	11	Y	8	1039.5	-0.053	1039.5	
	1257.7	+0.0786	1257.7	12	P	7	876.45	-0.008	876.45	
	1328.7	-0.127	1328.7	13	A	6	779.39		779.39	
	1442.7	+0.0425	1442.7	14	N	5	708.36		708.36	
	1605.8	+0.0391	1605.8	15	Y	4	594.31	-0.121	594.31	
	1704.9	+0.0675	1704.9	16	V	3	431.25		431.25	
+0.059	917.46	-0.011	1833.9	17	E	2	332.18	-0.007	332.18	
+0.2738	952.98		1905	18	A	1	203.14		203.14	
				19	I	0	132.1		132.1	

Scan number	8565	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	49.07



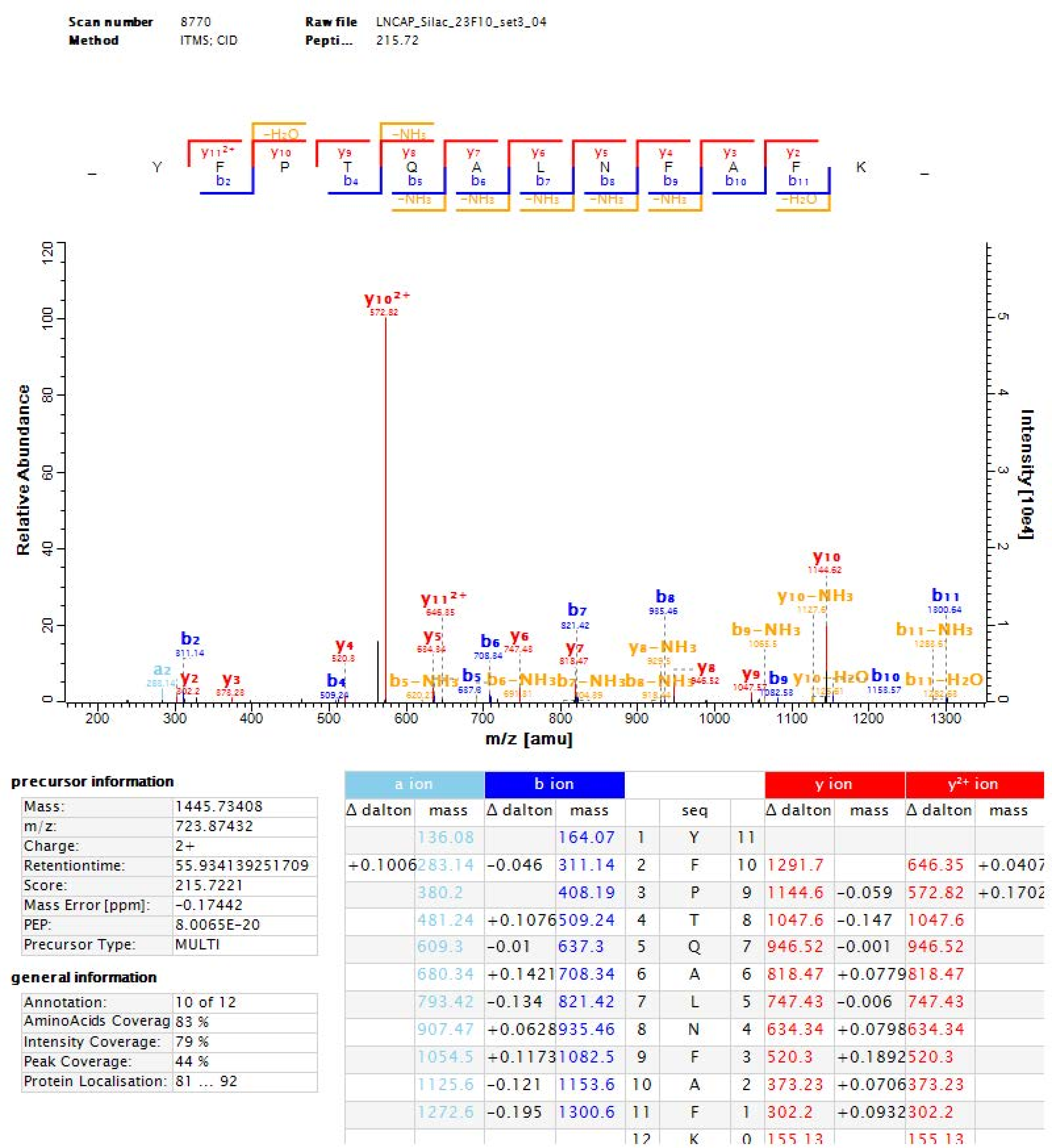
precursor information

Mass:	2678.23936
m/z:	893.75373
Charge:	3+
Retentiontime:	54.421859741210
Score:	49.06598
Mass Error [ppm]:	0.21076
PEP:	0.0049228
Precursor Type:	MULTI

general information

Annotation:	16 of 23
AminoAcids Coverag	70 %
Intensity Coverage:	32 %
Peak Coverage:	22 %
Protein Localisation:	80 ... 102

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	22				
	243.13		243.13	2	I	21	2550.2		2550.2	
	372.18	-0.2	372.18	3	E	20	2437.1		1219.1	+0.064
	469.23		469.23	4	P	19	2308.1		1154.5	+0.265
	598.27		598.27	5	E	18	2211		1106	+0.466
	695.32	-0.256	695.32	6	P	17	2082		1041.5	-0.054
	810.35		810.35	7	D	16	1984.9		1984.9	
	957.42		957.42	8	F	15	1869.9		1869.9	
	1070.5		1070.5	9	I	14	1722.8		861.92	+0.469
	1183.6		1183.6	10	L	13	1609.7		805.38	+0.164
	1369.7		1369.7	11	W	12	1496.7	+0.1717	748.84	+0.285
	1470.7		1470.7	12	T	11	1310.6		655.8	-0.011
-0.269	764.37		1527.7	13	G	10	1209.5		605.27	+0.393
	1642.8		1642.8	14	D	9	1152.5		1152.5	
	1757.8		1757.8	15	D	8	1037.5		1037.5	
	1858.8		1858.8	16	T	7	922.46		461.74	+0.339
	1955.9		1955.9	17	P	6	821.42	+0.0467	821.42	
	2092.9		2092.9	18	H	5	724.36		724.36	
	2192		2192	19	V	4	587.3		587.3	
	2289.1		2289.1	20	P	3	488.24	+0.0535	488.24	
	2404.1		2404.1	21	D	2	391.18		391.18	
	2533.1		2533.1	22	E	1	276.16		276.16	
				23	K	0	147.11		147.11	



Scan number	8770	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	215.72

precursor information

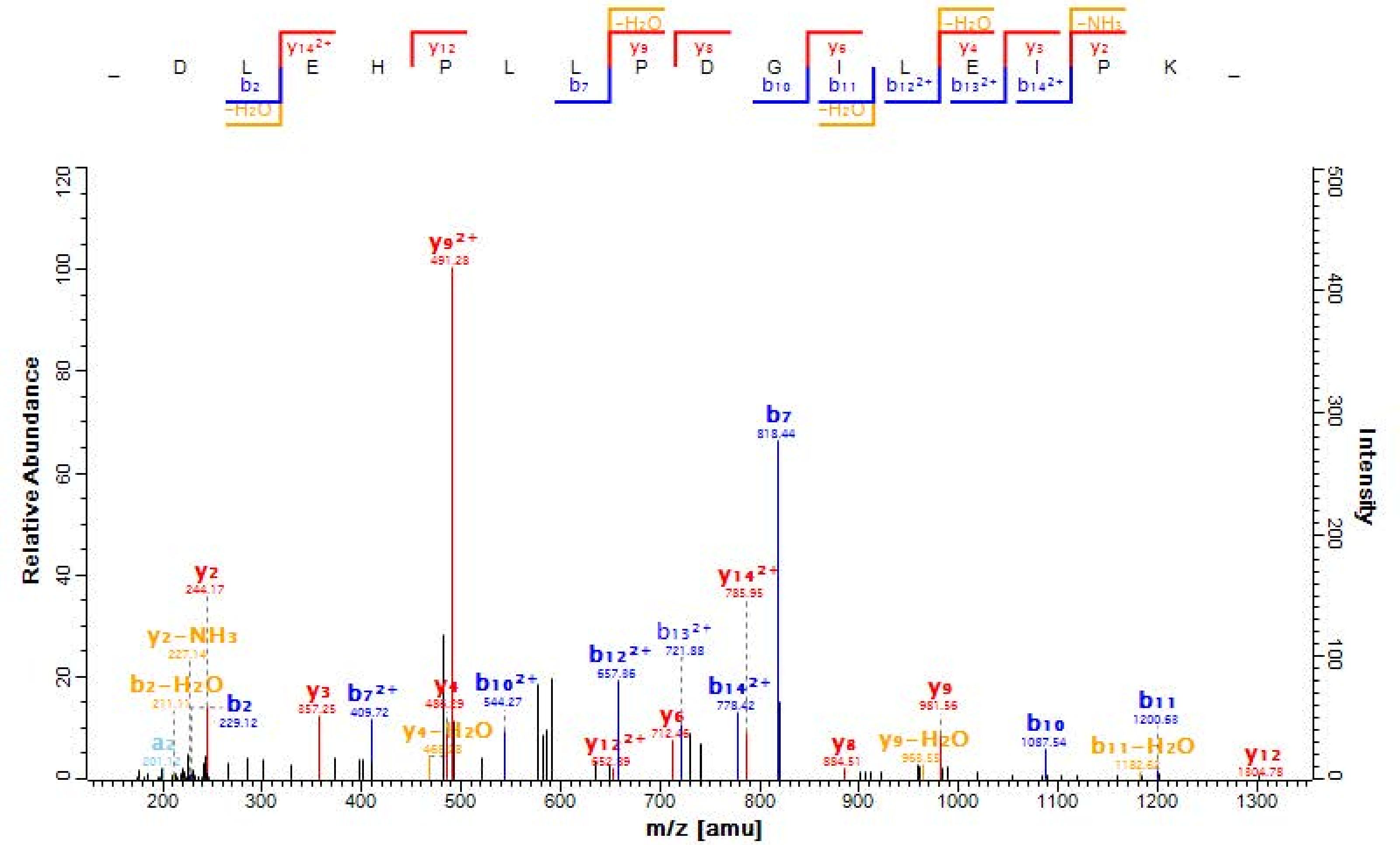
Mass:	1445.73408
m/z:	723.87432
Charge:	2+
Retentiontime:	55.934139251709
Score:	215.7221
Mass Error [ppm]:	-0.17442
PEP:	8.0065E-20
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	79 %
Peak Coverage:	44 %
Protein Localisation:	81 … 92

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.08		164.07	1	Y	11				
+0.1006	283.14	-0.046	311.14	2	F	10	1291.7		646.35	+0.0407
	380.2		408.19	3	P	9	1144.6	-0.059	572.82	+0.1702
	481.24	+0.1076	509.24	4	T	8	1047.6	-0.147	1047.6	
	609.3	-0.01	637.3	5	Q	7	946.52	-0.001	946.52	
	680.34	+0.1421	708.34	6	A	6	818.47	+0.0779	818.47	
	793.42	-0.134	821.42	7	L	5	747.43	-0.006	747.43	
	907.47	+0.0628	935.46	8	N	4	634.34	+0.0798	634.34	
	1054.5	+0.1173	1082.5	9	F	3	520.3	+0.1892	520.3	
	1125.6	-0.121	1153.6	10	A	2	373.23	+0.0706	373.23	
	1272.6	-0.195	1300.6	11	F	1	302.2	+0.0932	302.2	
				12	K	0	155.13		155.13	

Scan number	8887	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	113.25



precursor information

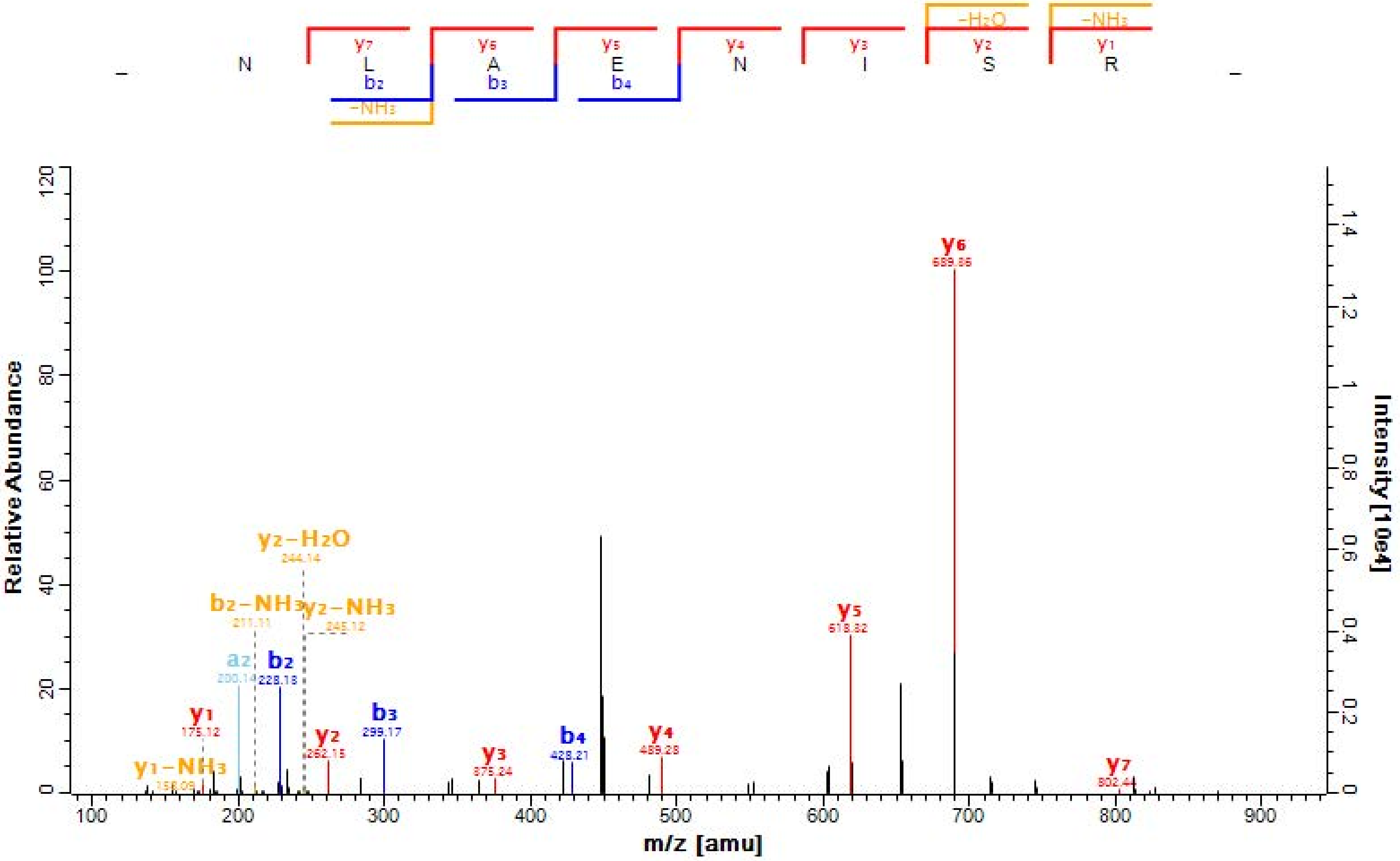
Mass:	1797.98804
m/z:	600.33662
Charge:	3+
Retentiontime:	56.831237792968
Score:	113.2528
Mass Error [ppm]:	0.21734
PEP:	3.3815E-07
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	57 %
Peak Coverage:	25 %
Protein Localisation:	63 ... 78

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.04		116		116	1	D	15				
+0.15	201.1		229.1	-0.04	229.1	2	L	14	1684		1684	
	330.2		358.2		358.2	3	E	13	1571		785.9	+0.09
	467.2		495.2		495.2	4	H	12	1442		1442	
	564.3		592.3		592.3	5	P	11	1305	+0.011	652.9	-0.22
	677.4		705.4		705.4	6	L	10	1208		1208	
	790.4	-0.03	409.7	+0	818.4	7	L	9	1095		1095	
	887.5		915.5		915.5	8	P	8	981.6	+0.026	491.3	+0.14
	1003		1031		1031	9	D	7	884.5	+0.039	884.5	
	1060	+0.212	544.3	+0.015	1088	10	G	6	769.5		769.5	
	1173		1201	-0.01	1201	11	I	5	712.5	+0.344	712.5	
	1286	+0.197	657.4		1314	12	L	4	599.4		599.4	
	1415	-0.1	721.9		1443	13	E	3	486.3	+0	486.3	
	1528	+0.191	778.4		1556	14	I	2	357.2	-0.19	357.2	
	1625		1653		1653	15	P	1	244.2	+0.109	244.2	
						16	K	0	147.1		147.1	

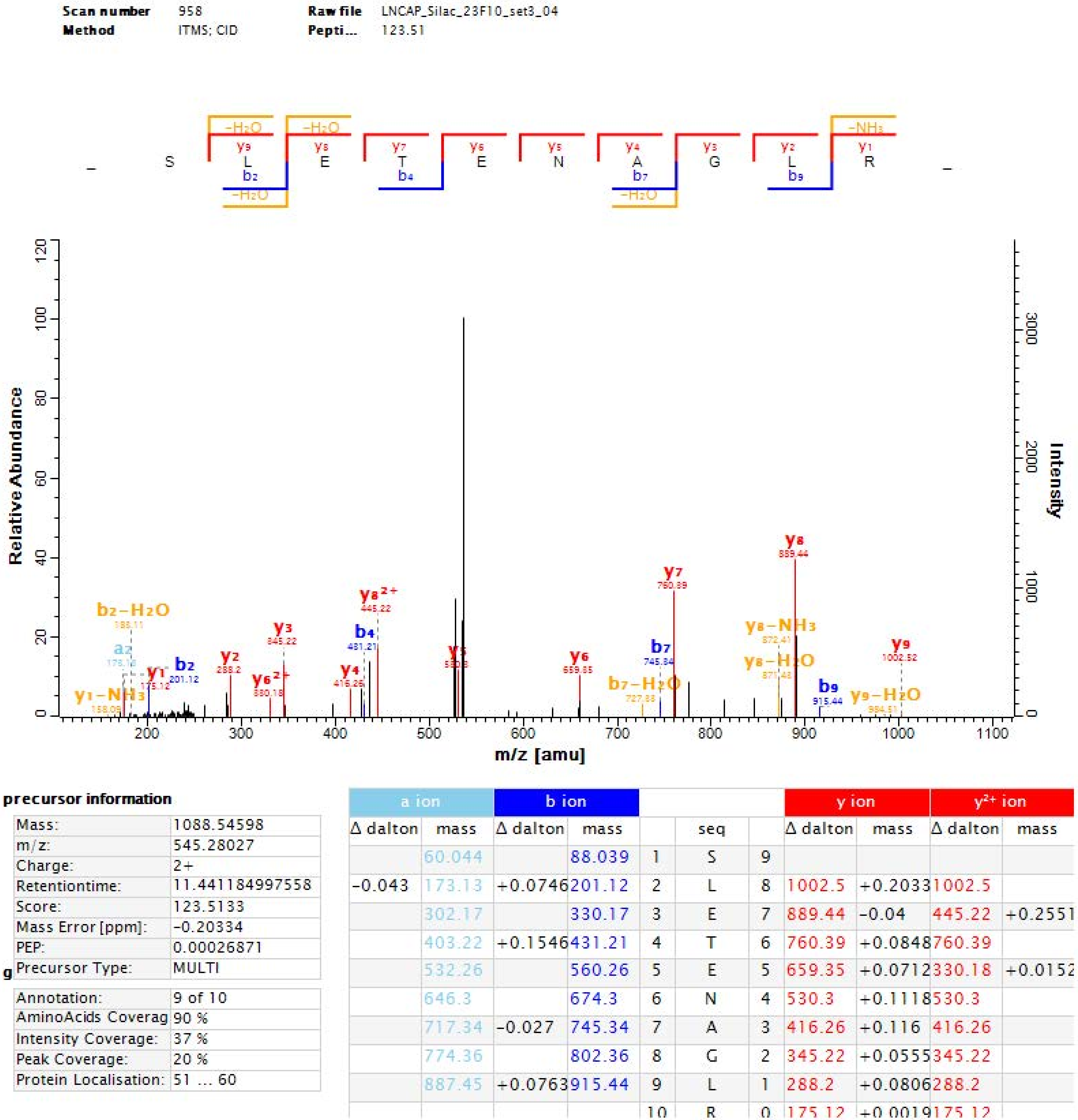
Scan number	927	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	61.78



precursor information

Mass:	915.47788
m/z:	458.74622
Charge:	2+
Retentiontime:	11.259828567504
Score:	61.77951
Mass Error [ppm]:	0.53012
PEP:	0.036201
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	48 %
Peak Coverage:	14 %
Protein Localisation:	271 ... 278

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	87.05529		115.0502	1	N	7		
-0.02856	200.1394	-0.03704	228.1343	2	L	6	802.4417	+0.019134
	271.1765	-0.03103	299.1714	3	A	5	689.3577	-0.00514
	400.2191	-0.08128	428.214	4	E	4	618.3206	+0.010856
	514.262		542.2569	5	N	3	489.278	+0.007611
	627.3461		655.341	6	I	2	375.235	+0.146547
	714.3781		742.373	7	S	1	262.151	+0.005453
				8	R	0	175.119	-0.01977



Scan number	958	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	123.51

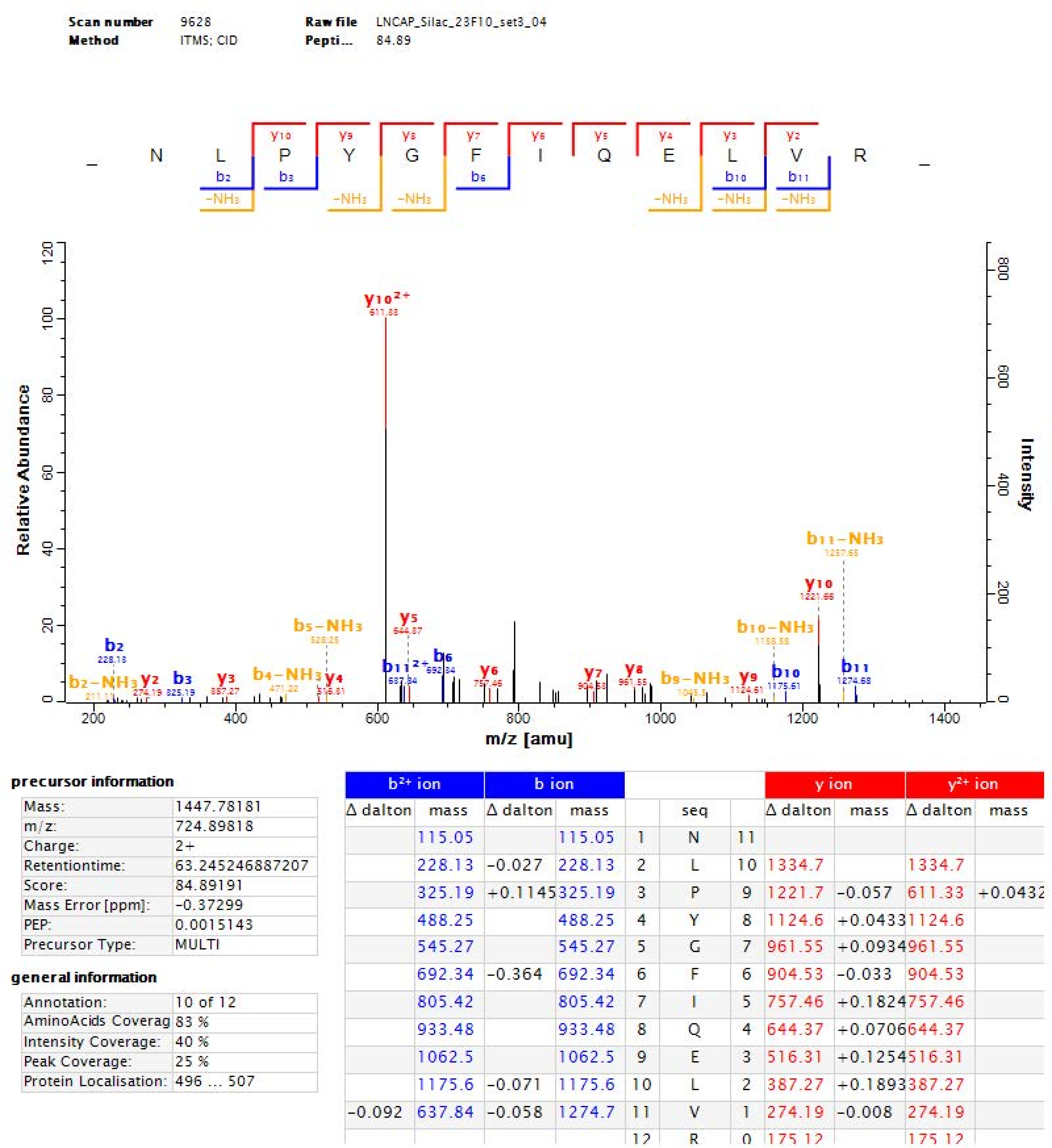
precursor information

Mass:	1088.54598
m/z:	545.28027
Charge:	2+
Retentiontime:	11.441184997558
Score:	123.5133
Mass Error [ppm]:	-0.20334
PEP:	0.00026871
Precursor Type:	MULTI

g

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	37 %
Peak Coverage:	20 %
Protein Localisation:	51 ... 60

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	60.044		88.039	1	S	9				
-0.043	173.13	+0.0746	201.12	2	L	8	1002.5	+0.2033	1002.5	
	302.17		330.17	3	E	7	889.44	-0.04	445.22	+0.2551
	403.22	+0.1546	431.21	4	T	6	760.39	+0.0848	760.39	
	532.26		560.26	5	E	5	659.35	+0.0712	330.18	+0.0152
	646.3		674.3	6	N	4	530.3	+0.1118	530.3	
	717.34	-0.027	745.34	7	A	3	416.26	+0.116	416.26	
	774.36		802.36	8	G	2	345.22	+0.0555	345.22	
	887.45	+0.0763	915.44	9	L	1	288.2	+0.0806	288.2	
				10	R	0	175.12	+0.0019	175.12	



Scan number	9628	**Raw file**	LNCAP_Silac_23F10_set3_04
Method	ITMS; CID	**Pepti...**	84.89

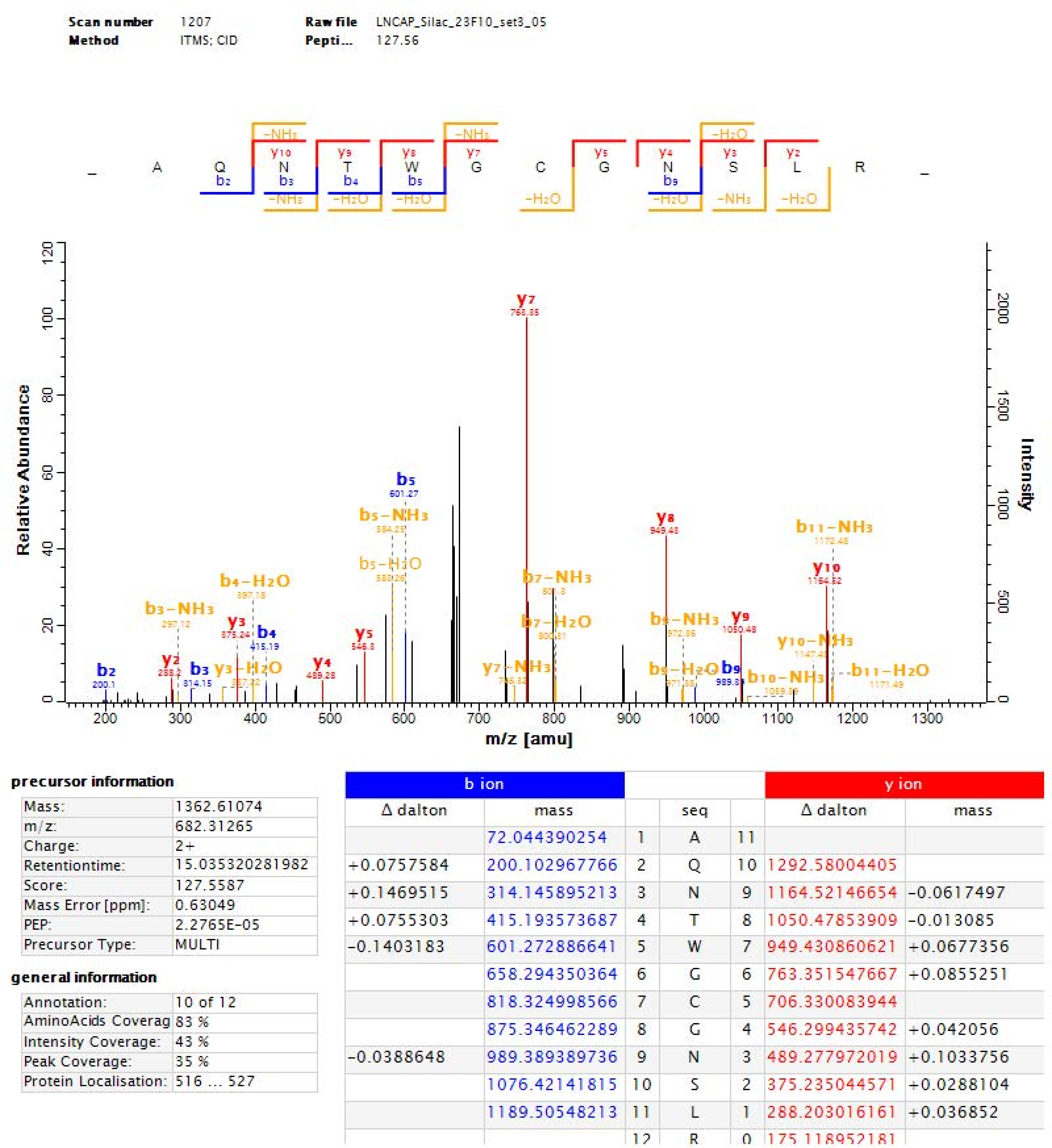
precursor information

Mass:	1447.78181
m/z:	724.89818
Charge:	2+
Retentiontime:	63.245246887207
Score:	84.89191
Mass Error [ppm]:	-0.37299
PEP:	0.0015143
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	40 %
Peak Coverage:	25 %
Protein Localisation:	496 ... 507

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.05		115.05	1	N	11				
	228.13	-0.027	228.13	2	L	10	1334.7		1334.7	
	325.19	+0.1145	325.19	3	P	9	1221.7	-0.057	611.33	+0.0432
	488.25		488.25	4	Y	8	1124.6	+0.0433	1124.6	
	545.27		545.27	5	G	7	961.55	+0.0934	961.55	
	692.34	-0.364	692.34	6	F	6	904.53	-0.033	904.53	
	805.42		805.42	7	I	5	757.46	+0.1824	757.46	
	933.48		933.48	8	Q	4	644.37	+0.0706	644.37	
	1062.5		1062.5	9	E	3	516.31	+0.1254	516.31	
	1175.6	-0.071	1175.6	10	L	2	387.27	+0.1893	387.27	
-0.092	637.84	-0.058	1274.7	11	V	1	274.19	-0.008	274.19	
				12	R	0	175.12		175.12	



Scan number	1207	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	127.56

precursor information

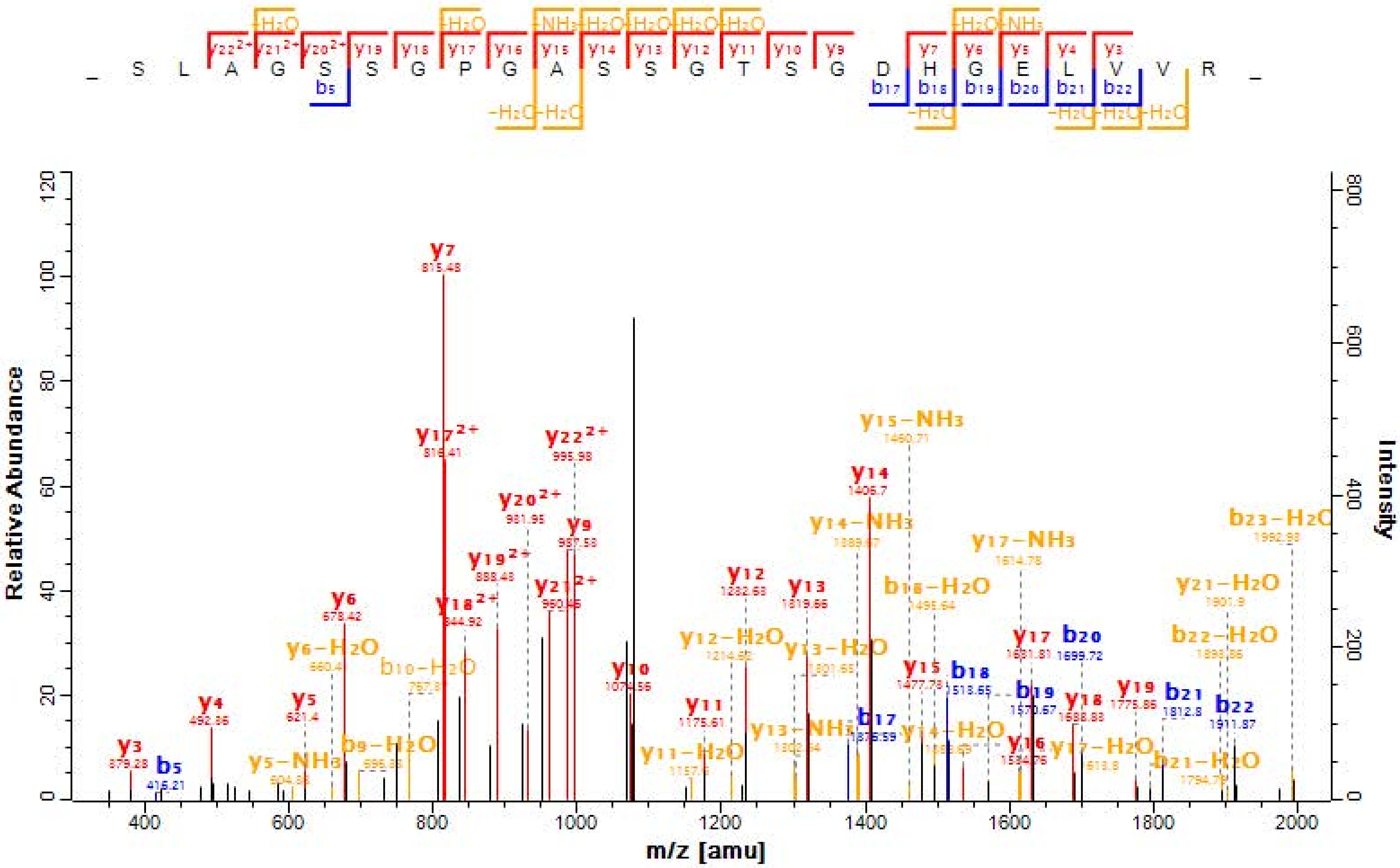
Mass:	1362.61074
m/z:	682.31265
Charge:	2+
Retentiontime:	15.035320281982
Score:	127.5587
Mass Error [ppm]:	0.63049
PEP:	2.2765E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	43 %
Peak Coverage:	35 %
Protein Localisation:	516 ... 527

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	72.044390254	1	A	11		
+0.0757584	200.102967766	2	Q	10	1292.58004405	
+0.1469515	314.145895213	3	N	9	1164.52146654	-0.0617497
+0.0755303	415.193573687	4	T	8	1050.47853909	-0.013085
-0.1403183	601.272886641	5	W	7	949.430860621	+0.0677356
	658.294350364	6	G	6	763.351547667	+0.0855251
	818.324998566	7	C	5	706.330083944	
	875.346462289	8	G	4	546.299435742	+0.042056
-0.0388648	989.389389736	9	N	3	489.277972019	+0.1033756
	1076.42141815	10	S	2	375.235044571	+0.0288104
	1189.50548213	11	L	1	288.203016161	+0.036852
		12	R	0	175.118952181	

Scan number	1301	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	238.79



precursor information

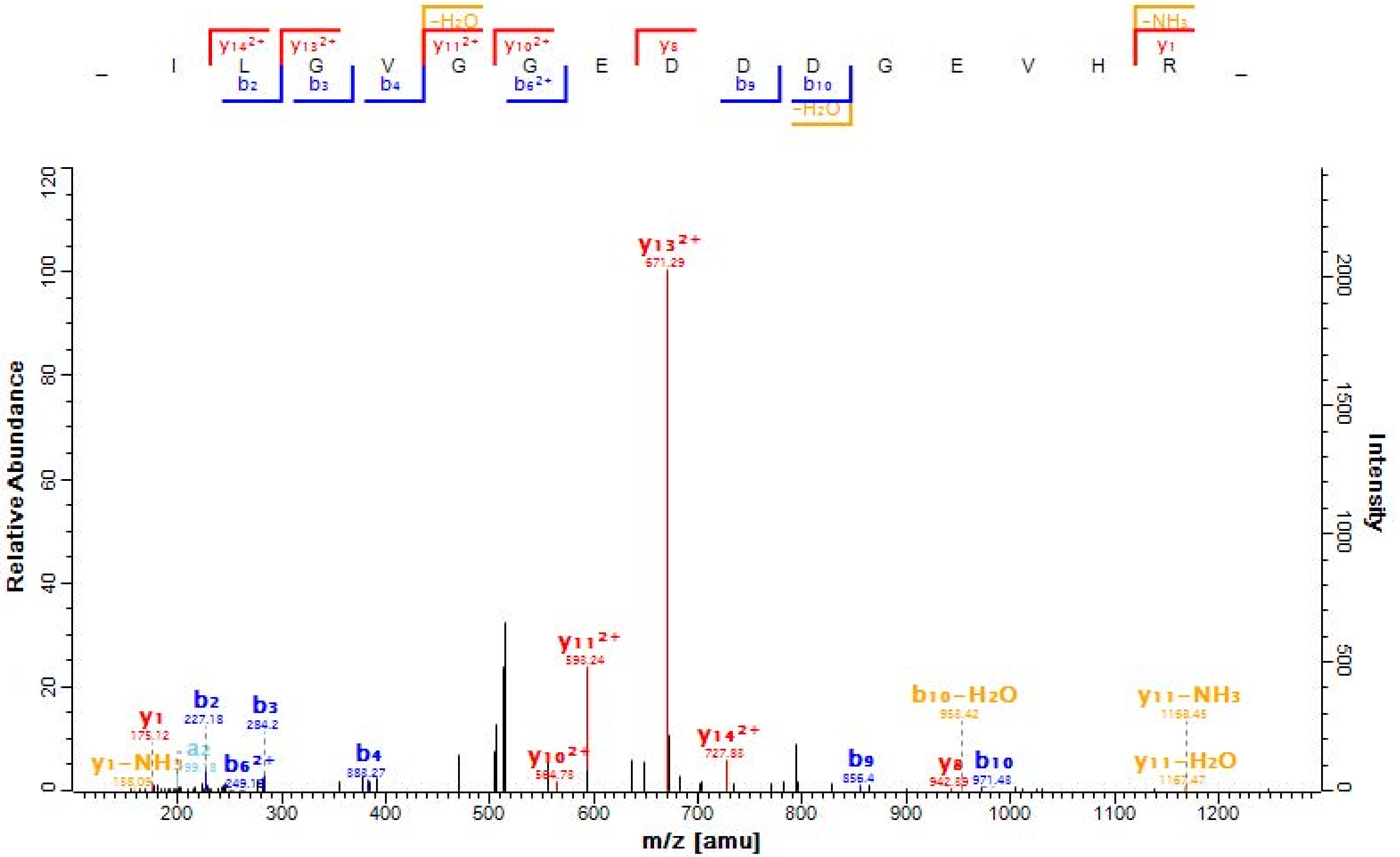
Mass:	2184.03976
m/z:	1093.02716
Charge:	2+
Retentiontime:	15.715456962585
Score:	238.791
Mass Error [ppm]:	-0.42906
PEP:	5.1872E-92
Precursor Type:	MULTI

general information

Annotation:	21 of 24
AminoAcids Coverag	88 %
Intensity Coverage:	58 %
Peak Coverage:	47 %
Protein Localisation:	60 ... 83

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393	1	S	23				
	201.1234	2	L	22	2104.036		2104.036	
	272.1605	3	A	21	1990.952		995.9796	+0.227141
	329.1819	4	G	20	1919.915		960.4611	+0.278291
+0.11354	416.214	5	S	19	1862.893		931.9504	-0.19682
	503.246	6	S	18	1775.861	+0.291179	888.4343	+0.147322
	560.2675	7	G	17	1688.829	+0.046351	844.9183	+0.296149
	657.3202	8	P	16	1631.808	-0.19708	816.4076	+0.278072
	714.3417	9	G	15	1534.755	+0.151585	1534.755	
	785.3788	10	A	14	1477.734	-0.11101	1477.734	
	872.4108	11	S	13	1406.697	-0.12687	1406.697	
	959.4429	12	S	12	1319.665	-0.02258	1319.665	
	1016.464	13	G	11	1232.633	-0.07283	1232.633	
	1117.512	14	T	10	1175.611	-0.05429	1175.611	
	1204.544	15	S	9	1074.563	-0.00454	1074.563	
	1261.565	16	G	8	987.5313	-0.19614	987.5313	
-0.07938	1376.592	17	D	7	930.5099		930.5099	
-0.02062	1513.651	18	H	6	815.4829	+0.029265	815.4829	
-0.08334	1570.673	19	G	5	678.424	+0.038128	678.424	
-0.12032	1699.715	20	E	4	621.4026	+0.060447	621.4026	
+0.144006	1812.799	21	L	3	492.36	+0.156445	492.36	
-0.09409	1911.868	22	V	2	379.2759	-0.04385	379.2759	
	2010.936	23	V	1	280.2075		280.2075	
		24	R	0	181.1391		181.1391	

Scan number	1400	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	62.09



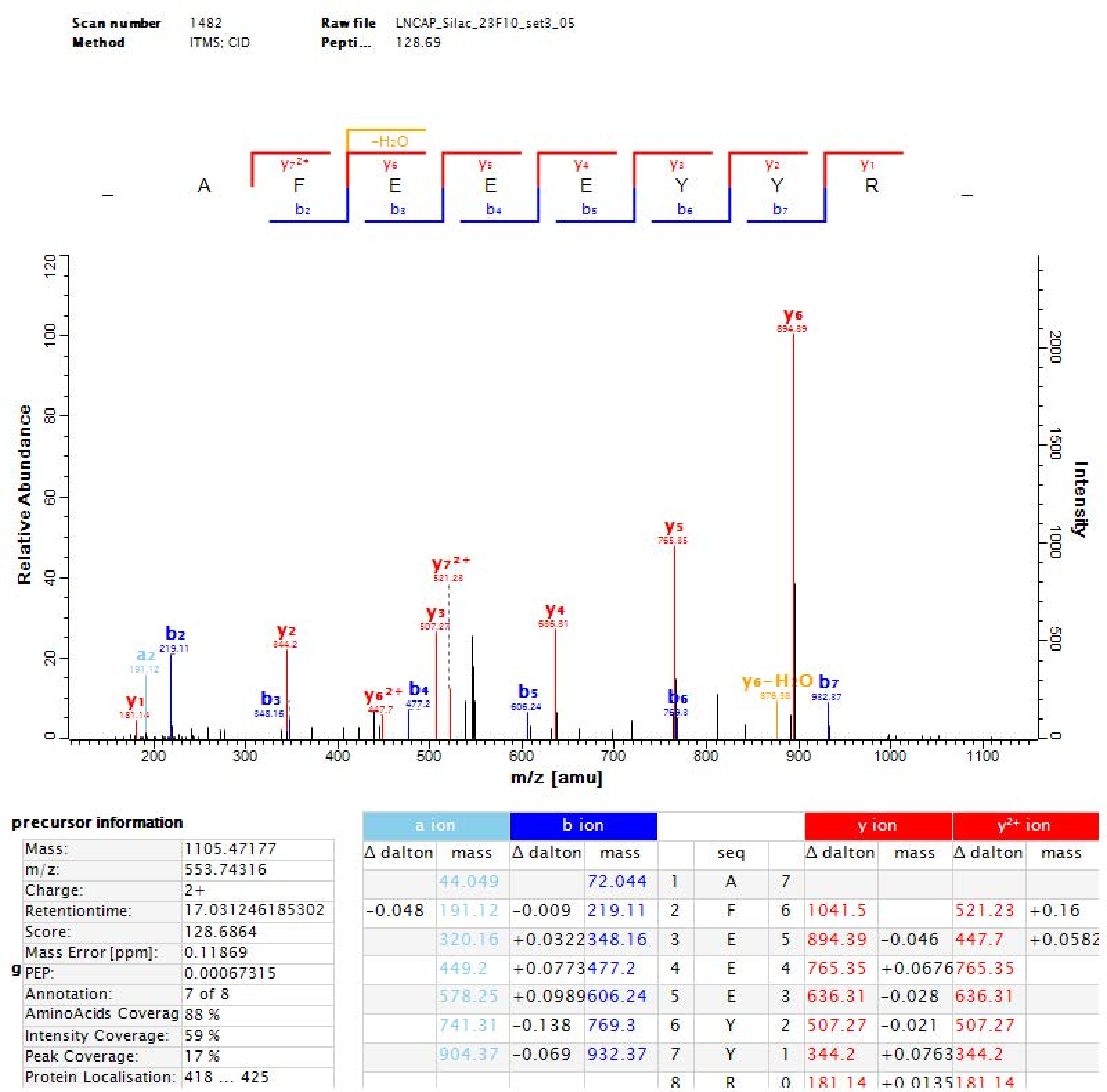
precursor information

Mass:	1566.72722
m/z:	523.24968
Charge:	3+
Retentiontime:	16.439025878906
Score:	62.08793
Mass Error [ppm]:	-0.12484
PEP:	0.0041787
Precursor Type:	MULTI

general information

Annotation:	9 of 15
AminoAcids Coverag	60 %
Intensity Coverage:	44 %
Peak Coverage:	14 %
Protein Localisation:	175 ... 189

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	I	14				
-0.05	199.2		227.2	-0.1	227.2	2	L	13	1455		727.8	+0.28
	256.2		284.2	-0.01	284.2	3	G	12	1342		671.3	+0.23
	355.3		383.3	-0.11	383.3	4	V	11	1285		1285	
	412.3		440.3		440.3	5	G	10	1185		593.2	+0.23
	469.3	+0.075	249.2		497.3	6	G	9	1128		564.7	+0
	598.4		626.4		626.4	7	E	8	1071		1071	
	713.4		741.4		741.4	8	D	7	942.4	+0.402	942.4	
	828.4		856.4	+0.053	856.4	9	D	6	827.4		827.4	
	943.4		971.4	+0.319	971.4	10	D	5	712.3		712.3	
	1000		1028		1028	11	G	4	597.3		597.3	
	1130		1157		1157	12	E	3	540.3		540.3	
	1229		1257		1257	13	V	2	411.2		411.2	
	1366		1394		1394	14	H	1	312.2		312.2	
						15	R	0	175.1	-0.05	175.1	



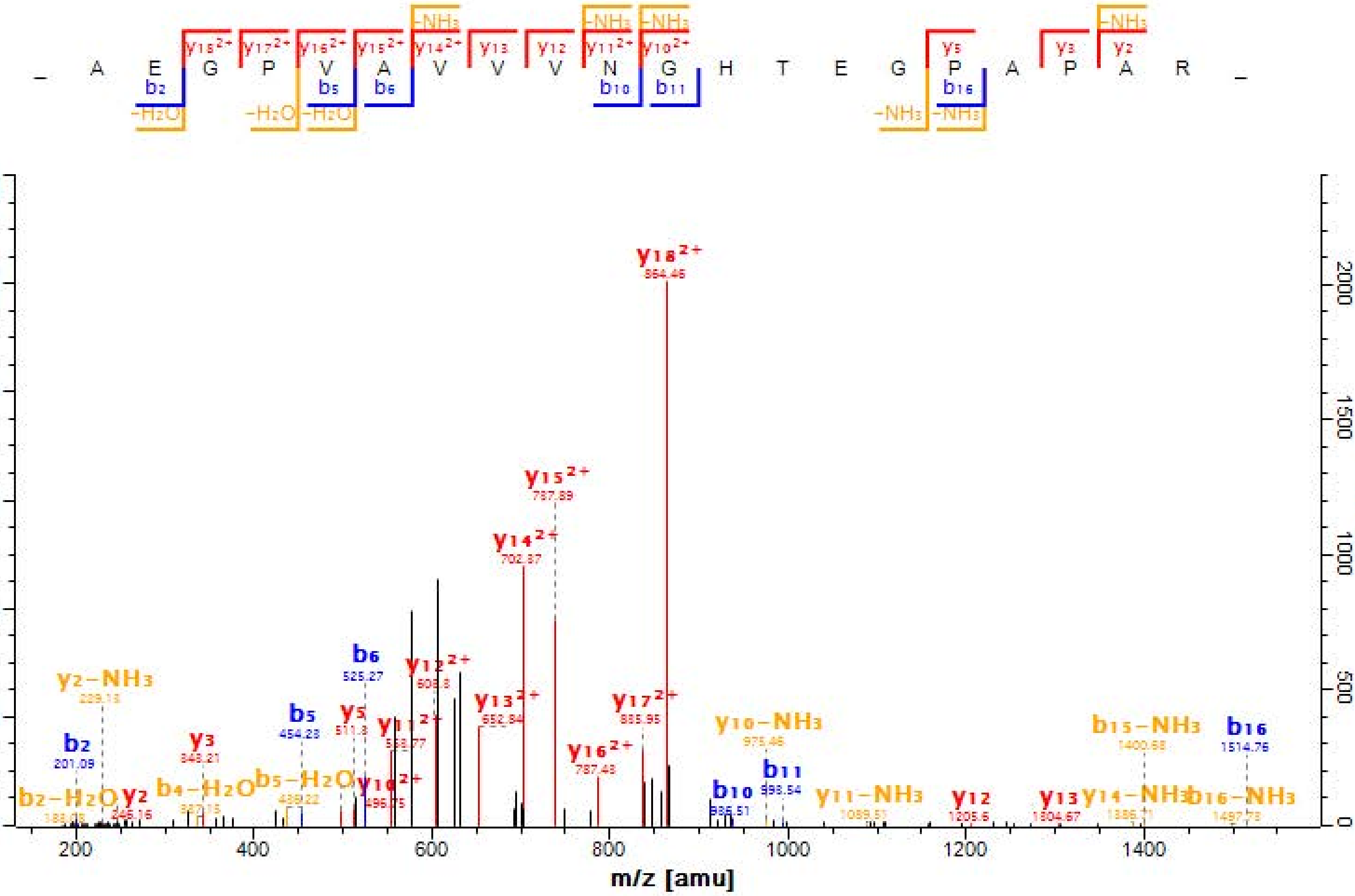
Scan number	1482	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	128.69

precursor information

Mass:	1105.47177
m/z:	553.74316
Charge:	2+
Retentiontime:	17.031246185302
Score:	128.6864
Mass Error [ppm]:	0.11869
PEP:	0.00067315
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	59 %
Peak Coverage:	17 %
Protein Localisation:	418 ... 425

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	44.049		72.044	1	A	7				
-0.048	191.12	-0.009	219.11	2	F	6	1041.5		521.23	+0.16
	320.16	+0.0322	348.16	3	E	5	894.39	-0.046	447.7	+0.0582
	449.2	+0.0773	477.2	4	E	4	765.35	+0.0676	765.35	
	578.25	+0.0989	606.24	5	E	3	636.31	-0.028	636.31	
	741.31	-0.138	769.3	6	Y	2	507.27	-0.021	507.27	
	904.37	-0.069	932.37	7	Y	1	344.2	+0.0763	344.2	
				8	R	0	181.14	+0.0135	181.14	

Scan number	1991	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	93.5



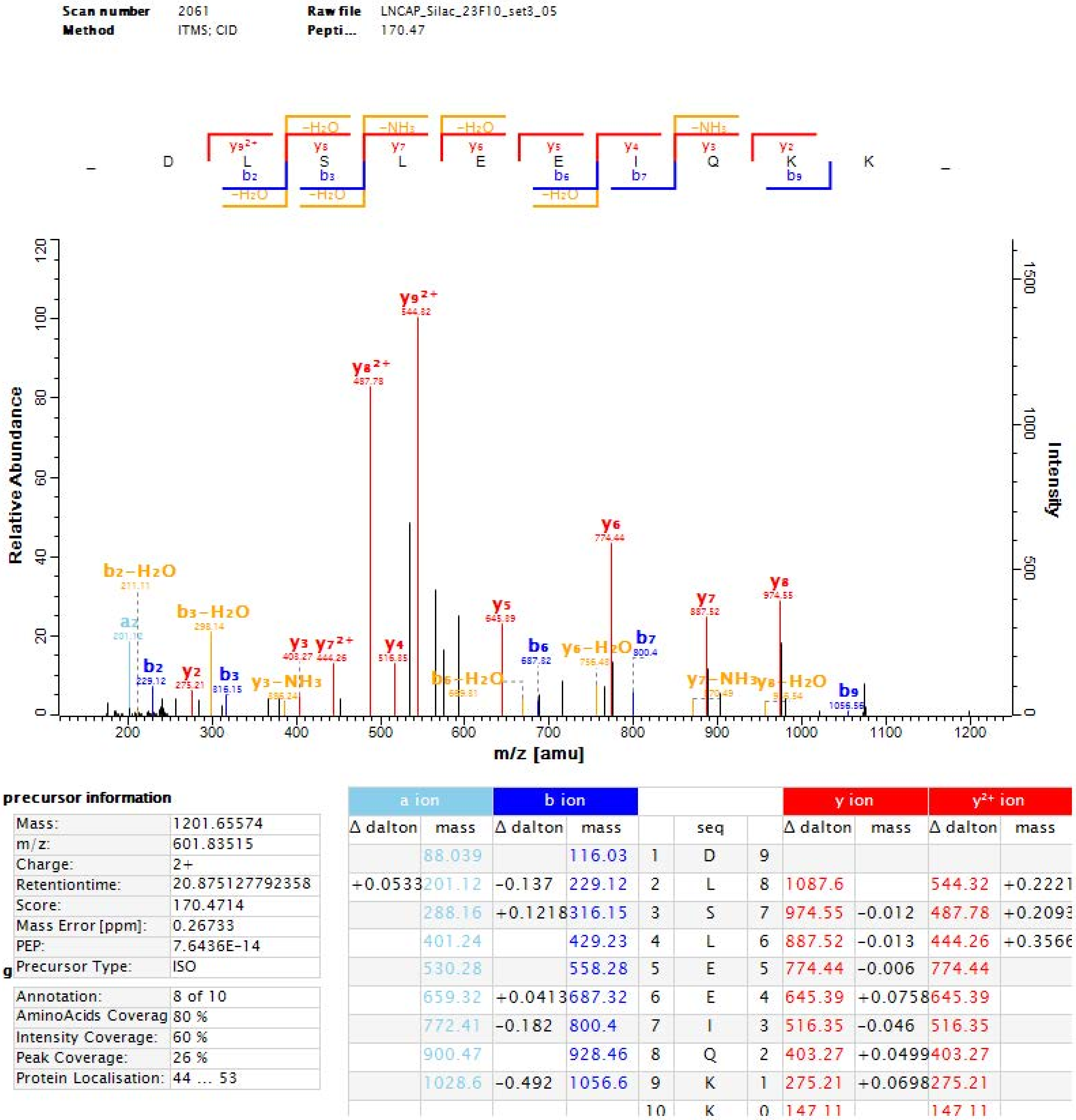
precursor information

Mass:	1926.99212
m/z:	643.33798
Charge:	3+
Retentiontime:	20.428529739379
Score:	93.49528
Mass Error [ppm]:	0.49096
PEP:	4.707E-06
Precursor Type:	MULTI

general information

Annotation:	14 of 20
AminoAcids Coverag	70 %
Intensity Coverage:	52 %
Peak Coverage:	24 %
Protein Localisation:	625 ... 644

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	19				
-0.02982	201.087	2	E	18	1856.961		1856.961	
	258.1084	3	G	17	1727.919		864.463	+0.269229
	355.1612	4	P	16	1670.897		835.9523	+0.322075
+0.003896	454.2296	5	V	15	1573.845		787.4259	+0.103706
+0.140793	525.2667	6	A	14	1474.776		737.8917	+0.251561
	624.3352	7	V	13	1403.739		702.3731	+0.259619
	723.4036	8	V	12	1304.671	+0.134724	652.8389	+0.264041
	822.472	9	V	11	1205.602	-0.29173	603.3047	+0.285797
+0.0681	936.5149	10	N	10	1106.534		553.7705	+0.216366
+0.144476	993.5364	11	G	9	992.4908		496.749	-0.02761
	1130.595	12	H	8	935.4694		935.4694	
	1231.643	13	T	7	798.4104		798.4104	
	1360.686	14	E	6	697.3628		697.3628	
	1417.707	15	G	5	568.3202		568.3202	
+0.332381	1514.76	16	P	4	511.2987	-0.02997	511.2987	
	1585.797	17	A	3	414.2459		414.2459	
	1682.85	18	P	2	343.2088	-0.11819	343.2088	
	1753.887	19	A	1	246.1561	+0.134919	246.1561	
		20	R	0	175.119		175.119	



Scan number	2061	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	170.47

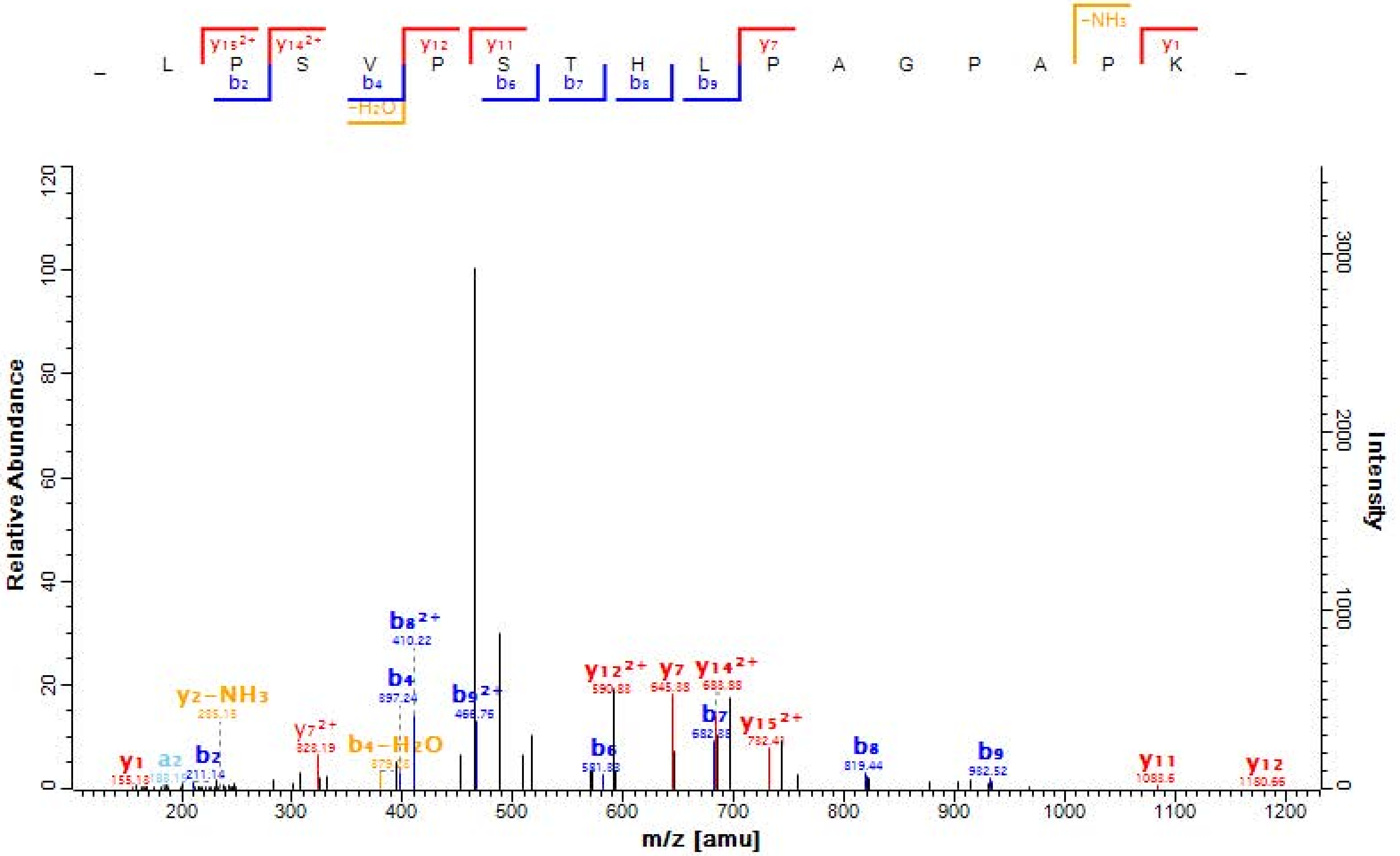
precursor information

Mass:	1201.65574
m/z:	601.83515
Charge:	2+
Retentiontime:	20.875127792358
Score:	170.4714
Mass Error [ppm]:	0.26733
PEP:	7.6436E-14
Precursor Type:	ISO

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	60 %
Peak Coverage:	26 %
Protein Localisation:	44 ... 53

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	9				
+0.0533	201.12	-0.137	229.12	2	L	8	1087.6		544.32	+0.2221
	288.16	+0.1218	316.15	3	S	7	974.55	-0.012	487.78	+0.2093
	401.24		429.23	4	L	6	887.52	-0.013	444.26	+0.3566
	530.28		558.28	5	E	5	774.44	-0.006	774.44	
	659.32	+0.0413	687.32	6	E	4	645.39	+0.0758	645.39	
	772.41	-0.182	800.4	7	I	3	516.35	-0.046	516.35	
	900.47		928.46	8	Q	2	403.27	+0.0499	403.27	
	1028.6	-0.492	1056.6	9	K	1	275.21	+0.0698	275.21	
				10	K	0	147.11		147.11	

Scan number	2481	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	70.37



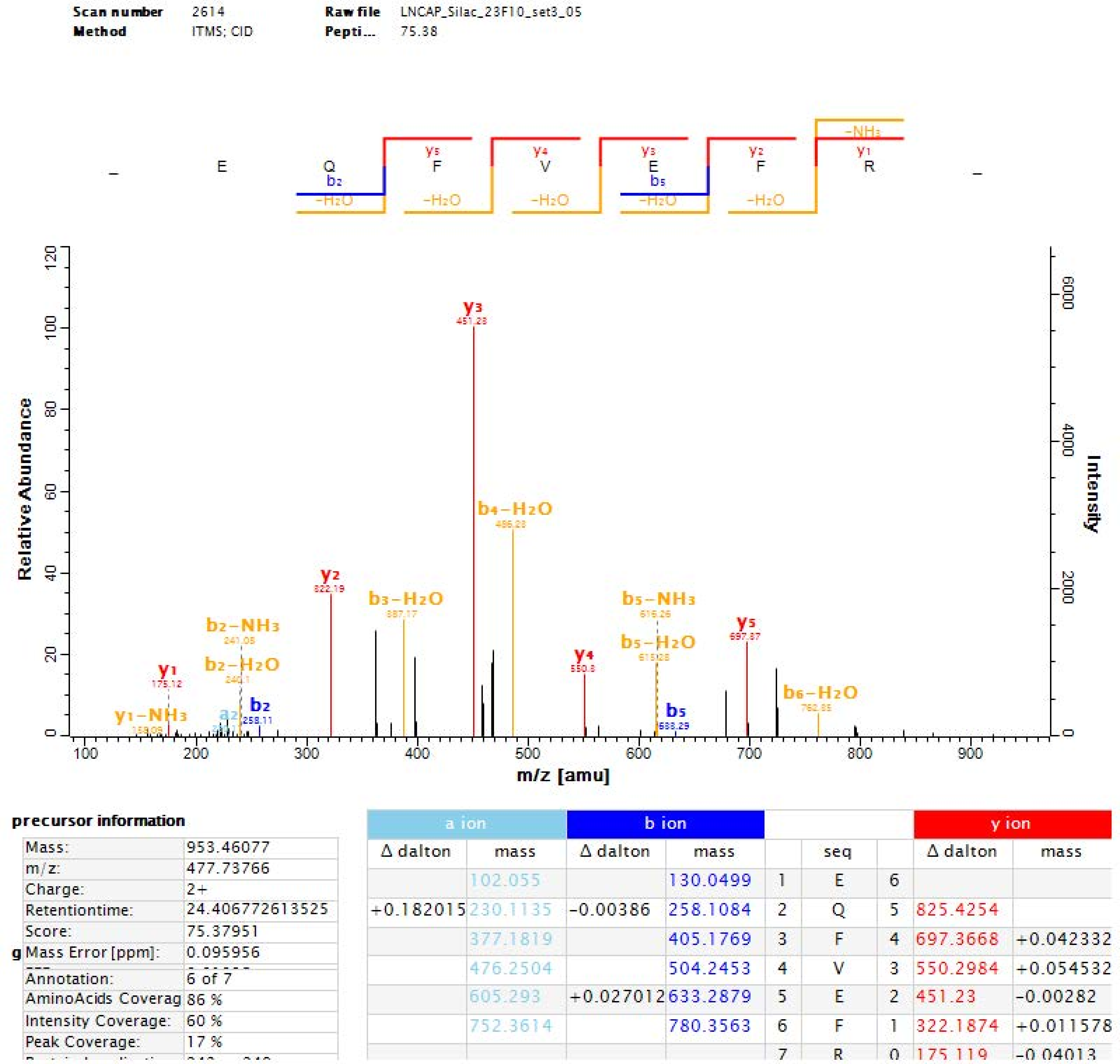
precursor information

Mass:	1567.87148
m/z:	523.6311
Charge:	3+
Retentiontime:	23.590467453002
Score:	70.37257
Mass Error [ppm]:	-0.47536
PEP:	0.00055919
Precursor Type:	MULTI

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	28 %
Peak Coverage:	19 %
Protein Localisation:	234 ... 249

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	15				
−0.02	183.1		211.1	−0.03	211.1	2	P	14	1464		732.4	+0.05
	270.2		298.2		298.2	3	S	13	1367		683.9	−0.14
	369.2		397.2	+0.049	397.2	4	V	12	1280		1280	
	466.3		494.3		494.3	5	P	11	1181	−0.02	590.8	−0.02
	553.3		581.3	+0.283	581.3	6	S	10	1084	−0.14	1084	
	654.4		682.4	+0	682.4	7	T	9	996.6		996.6	
	791.4	+0.158	410.2	+0.084	819.4	8	H	8	895.5		895.5	
	904.5	+0.213	466.8	−0.03	932.5	9	L	7	758.5		758.5	
	1002		1030		1030	10	P	6	645.4	+0.041	323.2	+0.00
	1073		1101		1101	11	A	5	548.3		548.3	
	1130		1158		1158	12	G	4	477.3		477.3	
	1227		1255		1255	13	P	3	420.3		420.3	
	1298		1326		1326	14	A	2	323.2		323.2	
	1395		1423		1423	15	P	1	252.2		252.2	
						16	K	0	155.1	−0.03	155.1	



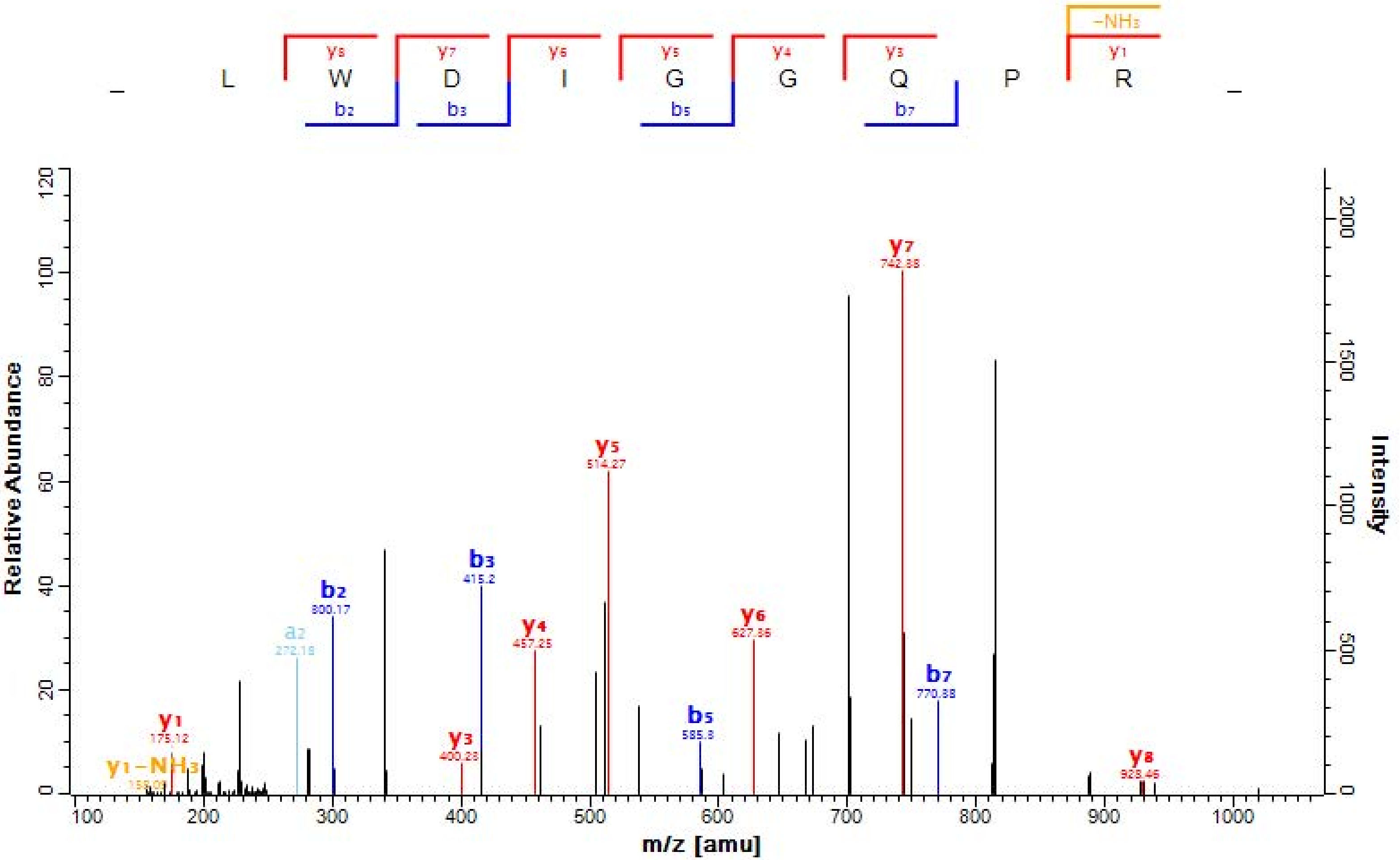
Scan number	2614	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	75.38

precursor information

Mass:	953.46077
m/z:	477.73766
Charge:	2+
Retentiontime:	24.406772613525
Score:	75.37951
Mass Error [ppm]:	0.095956
Annotation:	6 of 7
AminoAcids Coverag	86 %
Intensity Coverage:	60 %
Peak Coverage:	17 %

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	102.055		130.0499	1	E	6		
+0.182015	230.1135	-0.00386	258.1084	2	Q	5	825.4254	
	377.1819		405.1769	3	F	4	697.3668	+0.042332
	476.2504		504.2453	4	V	3	550.2984	+0.054532
	605.293	+0.027012	633.2879	5	E	2	451.23	-0.00282
	752.3614		780.3563	6	F	1	322.1874	+0.011578
				7	R	0	175.119	-0.04013

Scan number	3116	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	82.75



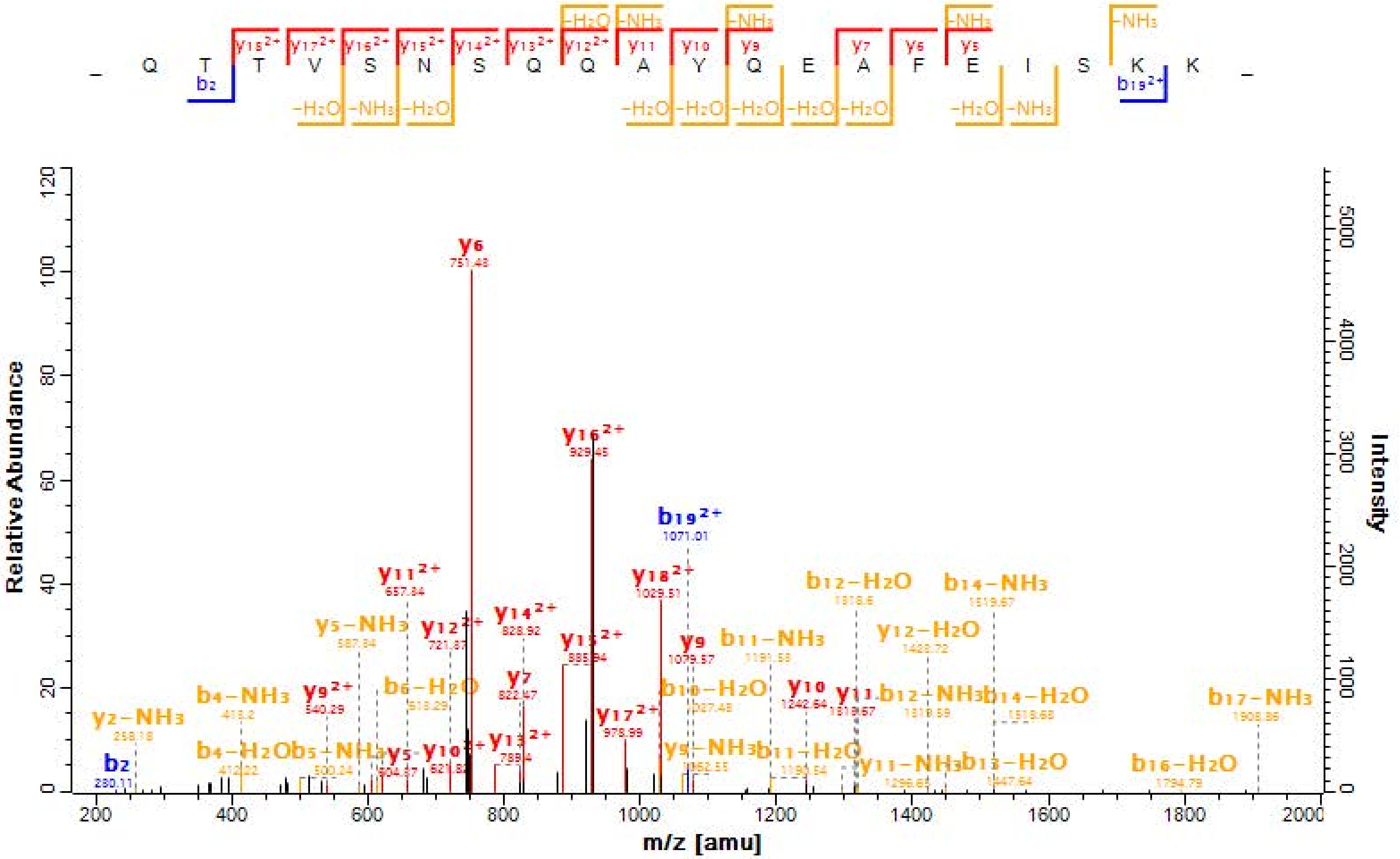
precursor information

g

Mass:	1040.54203
m/z:	521.27829
Charge:	2+
Retentiontime:	27.332010269165
Score:	82.74943
Mass Error [ppm]:	1.6349
PEP:	0.0080846
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	36 %
Peak Coverage:	13 %
Protein Localisation:	69 ... 77

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	86.09643		114.0913	1	L	8		
+0.038922	272.1757	+0.03235	300.1707	2	W	7	928.4635	+0.301779
	387.2027	-0.04422	415.1976	3	D	6	742.3842	-0.01045
	500.2867		528.2817	4	I	5	627.3573	+0.110427
	557.3082	+0.056678	585.3031	5	G	4	514.2732	+0.011691
	614.3297		642.3246	6	G	3	457.2518	+0.04347
	742.3883	-0.00469	770.3832	7	Q	2	400.2303	+0.032036
	839.441		867.4359	8	P	1	272.1717	
				9	R	0	175.119	+0.012212

Scan number	3120	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	81.59



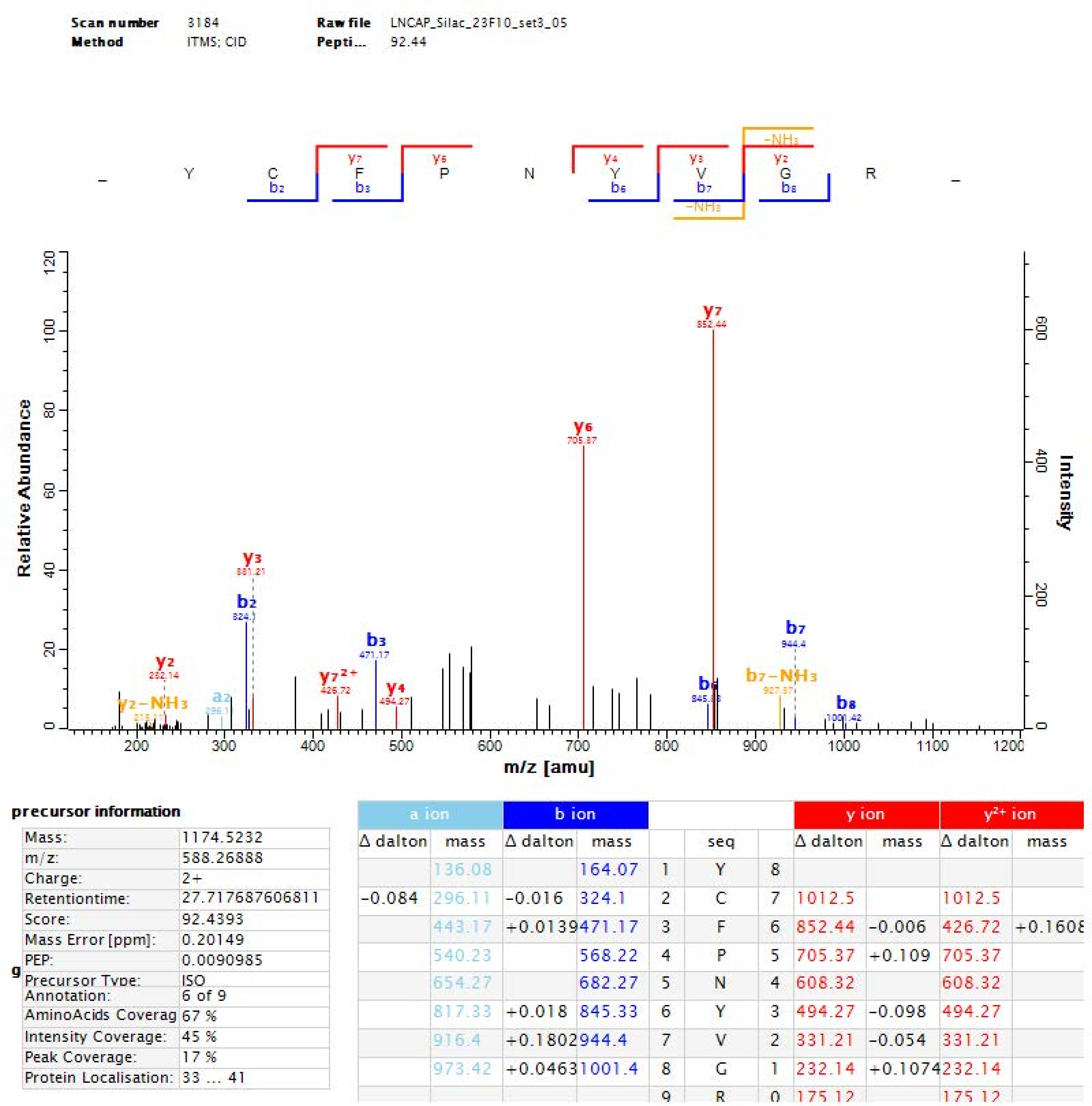
precursor information

Mass:	2286.11289
m/z:	763.04491
Charge:	3+
Retentiontime:	27.353302001953
Score:	81.59438
Mass Error [ppm]:	0.038834
PEP:	4.5726E-05
Precursor Type:	MULTI

general information

Annotation:	17 of 20
AminoAcids Coverag	85 %
Intensity Coverage:	61 %
Peak Coverage:	39 %
Protein Localisation:	141 ... 160

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.07		129.07	1	Q	19				
	230.11	+0.104	230.11	2	T	18	2159.1		2159.1	
	331.16		331.16	3	T	17	2058		1029.5	+0.3535
	430.23		430.23	4	V	16	1957		978.99	+0.1248
	517.26		517.26	5	S	15	1857.9		929.45	+0.0189
	631.3		631.3	6	N	14	1770.9		885.94	+0.3394
	718.34		718.34	7	S	13	1656.8		828.92	+0.1331
	846.4		846.4	8	Q	12	1569.8		785.4	+0.2861
	974.45		974.45	9	Q	11	1441.7		721.37	+0.297
	1045.5		1045.5	10	A	10	1313.7	+0.0343	657.34	+0.4359
	1208.6		1208.6	11	Y	9	1242.6	+0.0348	621.82	+0.1323
	1336.6		1336.6	12	Q	8	1079.6	+0.0178	540.29	+0.1818
	1465.7		1465.7	13	E	7	951.51		951.51	
	1536.7		1536.7	14	A	6	822.47	+0.2333	822.47	
	1683.8		1683.8	15	F	5	751.43	+0.0543	751.43	
	1812.8		1812.8	16	E	4	604.37	+0.1943	604.37	
	1925.9		1925.9	17	I	3	475.32		475.32	
	2012.9		2012.9	18	S	2	362.24		362.24	
+0.3107	1071		2141	19	K	1	275.21		275.21	
				20	K	0	147.11		147.11	



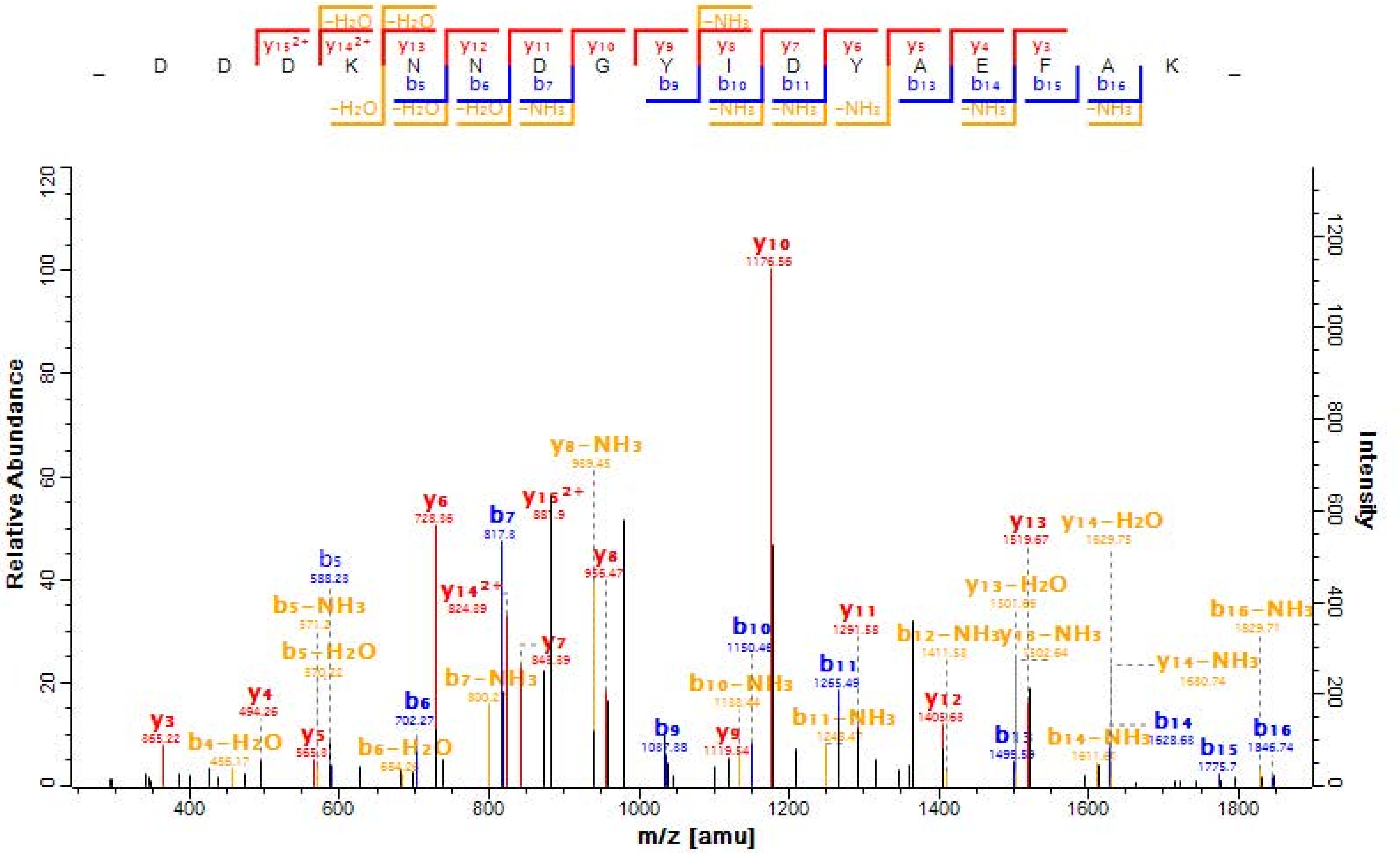
Scan number	3184	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	92.44

precursor information

Mass:	1174.5232
m/z:	588.26888
Charge:	2+
Retentiontime:	27.717687606811
Score:	92.4393
Mass Error [ppm]:	0.20149
PEP:	0.0090985
Precursor Type:	ISO
Annotation:	6 of 9
AminoAcids Coverag	67 %
Intensity Coverage:	45 %
Peak Coverage:	17 %
Protein Localisation:	33 ... 41

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.08		164.07	1	Y	8				
-0.084	296.11	-0.016	324.1	2	C	7	1012.5		1012.5	
	443.17	+0.0139	471.17	3	F	6	852.44	-0.006	426.72	+0.160
	540.23		568.22	4	P	5	705.37	+0.109	705.37	
	654.27		682.27	5	N	4	608.32		608.32	
	817.33	+0.018	845.33	6	Y	3	494.27	-0.098	494.27	
	916.4	+0.1802	944.4	7	V	2	331.21	-0.054	331.21	
	973.42	+0.0463	1001.4	8	G	1	232.14	+0.1074	232.14	
				9	R	0	175.12		175.12	

Scan number	3700	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	176.94



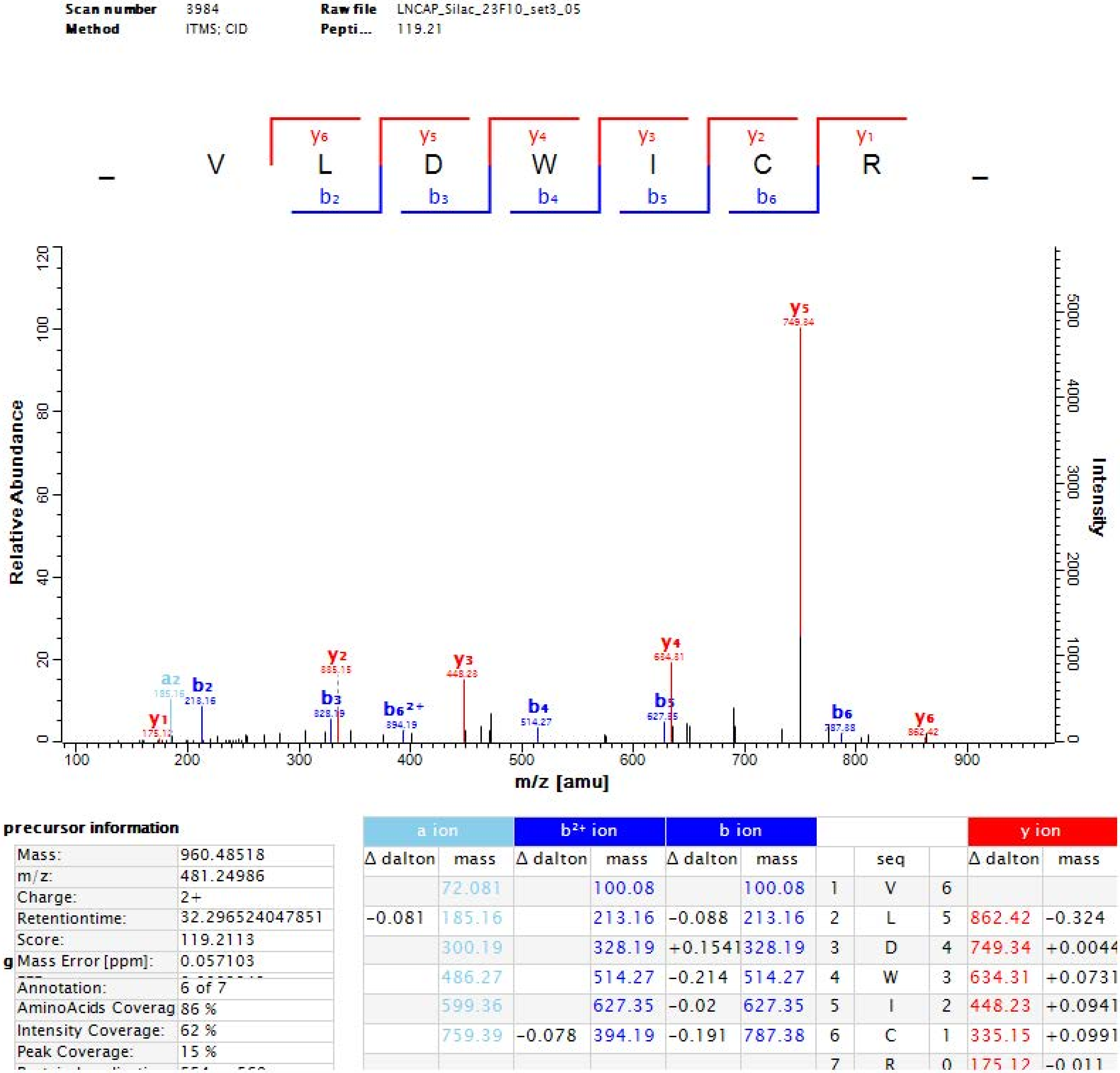
precursor information

Mass:	1991.83917
m/z:	996.92686
Charge:	2+
Retentiontime:	30.656839370727
Score:	176.9393
Mass Error [ppm]:	0.34828
PEP:	7.8068E-30
Precursor Type:	MULTI

general information

Annotation:	15 of 17
AminoAcids Coverag	88 %
Intensity Coverage:	54 %
Peak Coverage:	42 %
Protein Localisation:	127 ... 143

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342	1	D	16				
	231.0612	2	D	15	1877.819		1877.819	
	346.0881	3	D	14	1762.792		881.8996	+0.020104
	474.1831	4	K	13	1647.765		824.3861	+0.343756
+0.175615	588.226	5	N	12	1519.67	-0.16118	1519.67	
-0.22809	702.2689	6	N	11	1405.627	-0.1086	1405.627	
-0.03927	817.2959	7	D	10	1291.584	-0.12647	1291.584	
	874.3173	8	G	9	1176.557	-0.06791	1176.557	
-0.33256	1037.381	9	Y	8	1119.536	-0.09894	1119.536	
-0.07178	1150.465	10	I	7	956.4724	-0.04842	956.4724	
-0.13376	1265.492	11	D	6	843.3883	+0.027583	843.3883	
	1428.555	12	Y	5	728.3614	+0.055808	728.3614	
-0.20051	1499.592	13	A	4	565.298	+0.159237	565.298	
-0.02594	1628.635	14	E	3	494.2609	+0.105469	494.2609	
+0.016245	1775.703	15	F	2	365.2183	+0.062735	365.2183	
+0.166876	1846.74	16	A	1	218.1499		218.1499	
		17	K	0	147.1128		147.1128	



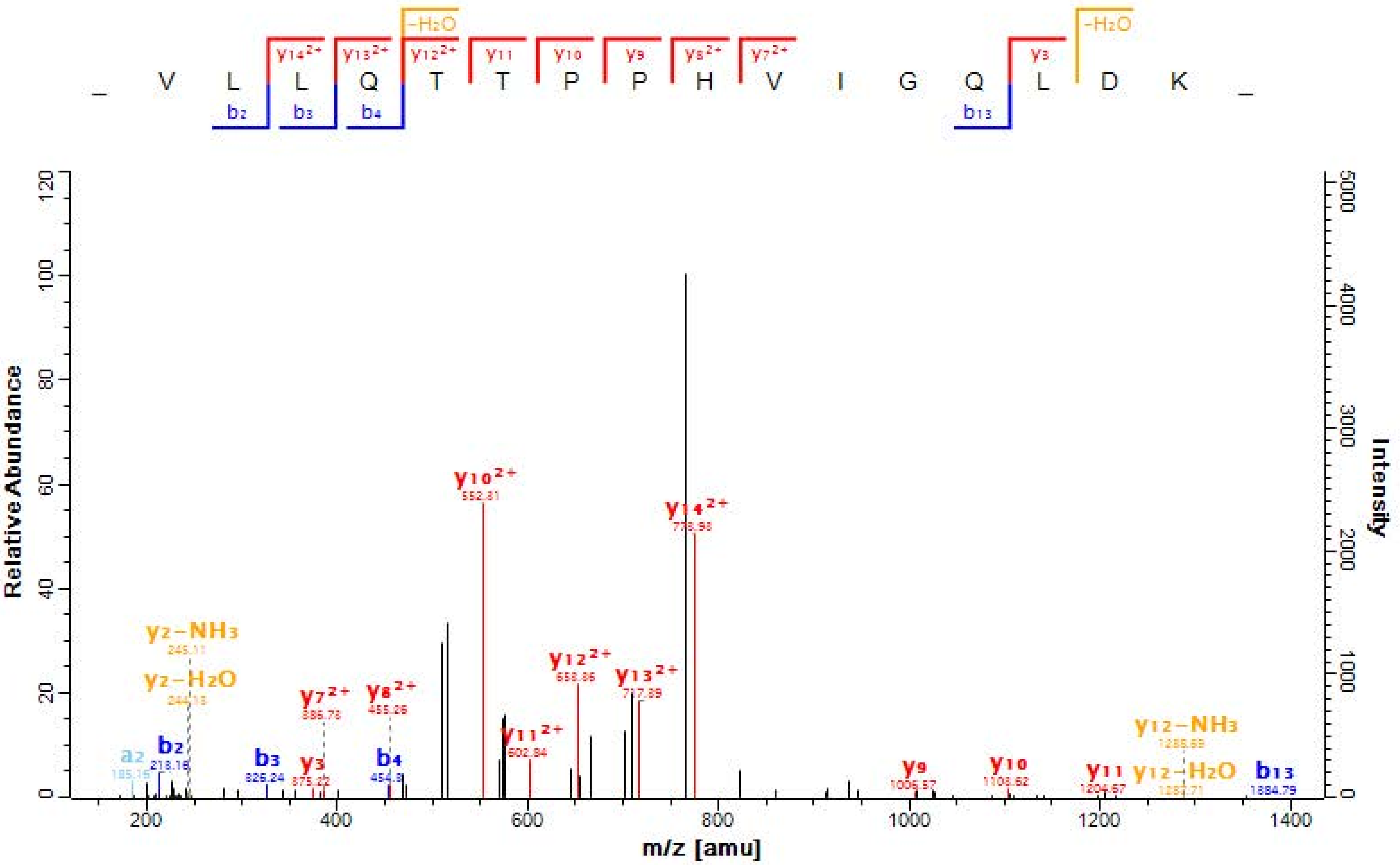
Scan number	3984	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	119.21

precursor information

Mass:	960.48518
m/z:	481.24986
Charge:	2+
Retentiontime:	32.296524047851
Score:	119.2113
Mass Error [ppm]:	0.057103
Annotation:	6 of 7
AminoAcids Coverag	86 %
Intensity Coverage:	62 %
Peak Coverage:	15 %

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	72.081		100.08		100.08	1	V	6		
-0.081	185.16		213.16	-0.088	213.16	2	L	5	862.42	-0.324
	300.19		328.19	+0.1541	328.19	3	D	4	749.34	+0.0044
	486.27		514.27	-0.214	514.27	4	W	3	634.31	+0.0731
	599.36		627.35	-0.02	627.35	5	I	2	448.23	+0.0941
	759.39	-0.078	394.19	-0.191	787.38	6	C	1	335.15	+0.0991
						7	R	0	175.12	-0.011

Scan number	4141	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	78.81



precursor information

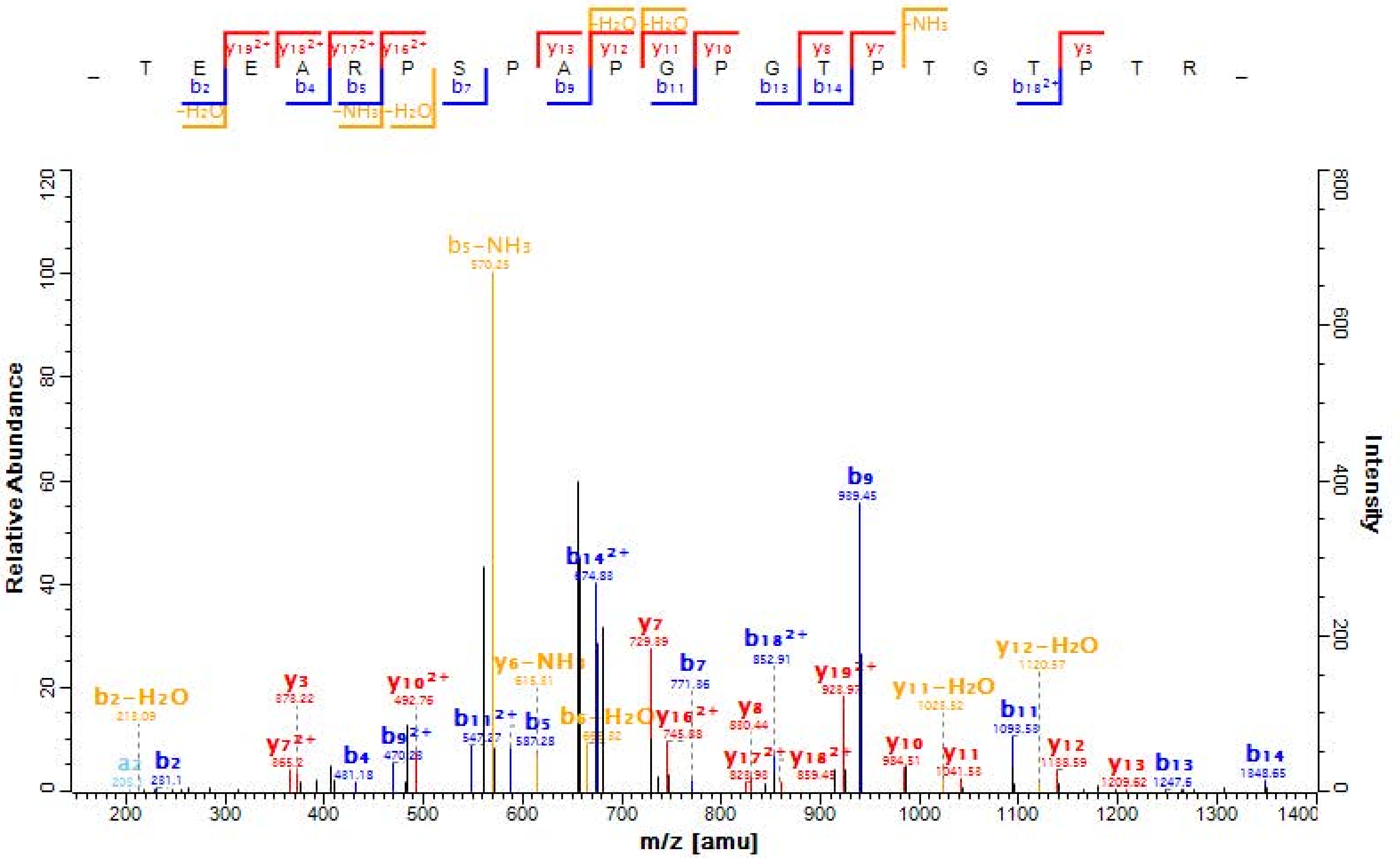
Mass:	1758.00369
m/z:	587.00851
Charge:	3+
Retentiontime:	33.220573425293
Score:	78.81388
Mass Error [ppm]:	-0.15909
PEP:	0.00024898
Precursor Type:	MULTI

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	33 %
Peak Coverage:	22 %
Protein Localisation:	293 ... 308

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.081		100.08	1	V	15				
-0.108	185.16	-0.018	213.16	2	L	14	1659.9		1659.9	
	298.25	+0.1398	326.24	3	L	13	1546.9		773.93	+0.3046
	426.31	-0.29	454.3	4	Q	12	1433.8		717.39	+0.2363
	527.36		555.35	5	T	11	1305.7		653.36	+0.1957
	628.4		656.4	6	T	10	1204.7	+0.018	602.84	+0.2931
	725.46		753.45	7	P	9	1103.6	+0.1043	552.31	+0.1947
	822.51		850.5	8	P	8	1006.6	-0.131	1006.6	
	959.57		987.56	9	H	7	909.52		455.26	+0.0554
	1058.6		1086.6	10	V	6	772.46		386.73	+0.2712
	1171.7		1199.7	11	I	5	673.39		673.39	
	1228.7		1256.7	12	G	4	560.3		560.3	
	1356.8	-0.053	1384.8	13	Q	3	503.28		503.28	
	1469.9		1497.9	14	L	2	375.22	+0.0123	375.22	
	1584.9		1612.9	15	D	1	262.14		262.14	
				16	K	0	147.11		147.11	

Scan number	497	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	126.4



precursor information

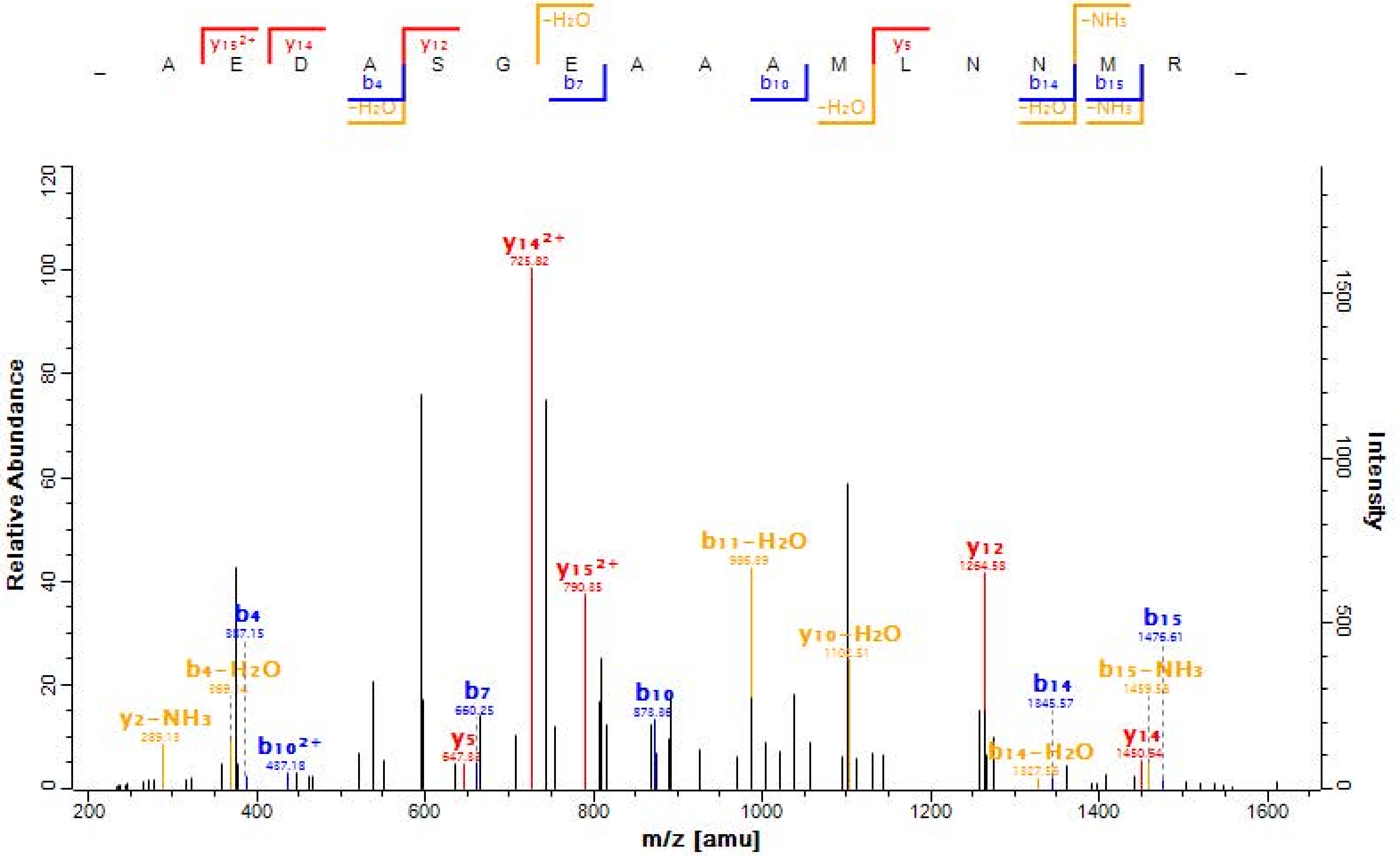
Mass:	2076.02282
m/z:	693.01488
Charge:	3+
Retentiontime:	8.8006095886230
Score:	126.3998
Mass Error [ppm]:	-0.37342
PEP:	1.5587E-13
Precursor Type:	MULTI

general information

Annotation:	16 of 21
AminoAcids Coverag	76 %
Intensity Coverage:	52 %
Peak Coverage:	40 %
Protein Localisation:	135 ... 155

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.1		102.1	1	T	20				
-0.03	203.1		231.1	-0.02	231.1	2	E	19	1976		1976	
	332.1		360.1		360.1	3	E	18	1847		924	+0.35
	403.2		431.2	-0.06	431.2	4	A	17	1718		859.5	+0.31
	559.3		587.3	+0.136	587.3	5	R	16	1647		823.9	+0.04
	656.3		684.3		684.3	6	P	15	1491		745.9	+0.30
	743.4		771.4	-0.31	771.4	7	S	14	1394		1394	
	840.4		868.4		868.4	8	P	13	1307		1307	
	911.5	-0.03	470.2	-0.06	939.5	9	A	12	1210	-0.12	1210	
	1009		1037		1037	10	P	11	1139	+0.086	1139	
	1066	+0.247	547.3	+0.107	1094	11	G	10	1042	+0.122	1042	
	1163		1191		1191	12	P	9	984.5	+0.008	492.8	+0.22
	1220		1248	+0.26	1248	13	G	8	887.5		887.5	
	1321	-0.16	674.8	-0.03	1349	14	T	7	830.4	+0.004	830.4	
	1418		1446		1446	15	P	6	729.4	+0	365.2	+0.26
	1519		1547		1547	16	T	5	632.3		632.3	
	1576		1604		1604	17	G	4	531.3		531.3	
	1677	+0.205	852.9		1705	18	T	3	474.3		474.3	
	1774		1802		1802	19	P	2	373.2	+0.014	373.2	
	1875		1903		1903	20	T	1	276.2		276.2	
						21	R	0	175.1		175.1	

Scan number	4989	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	56.6



precursor information

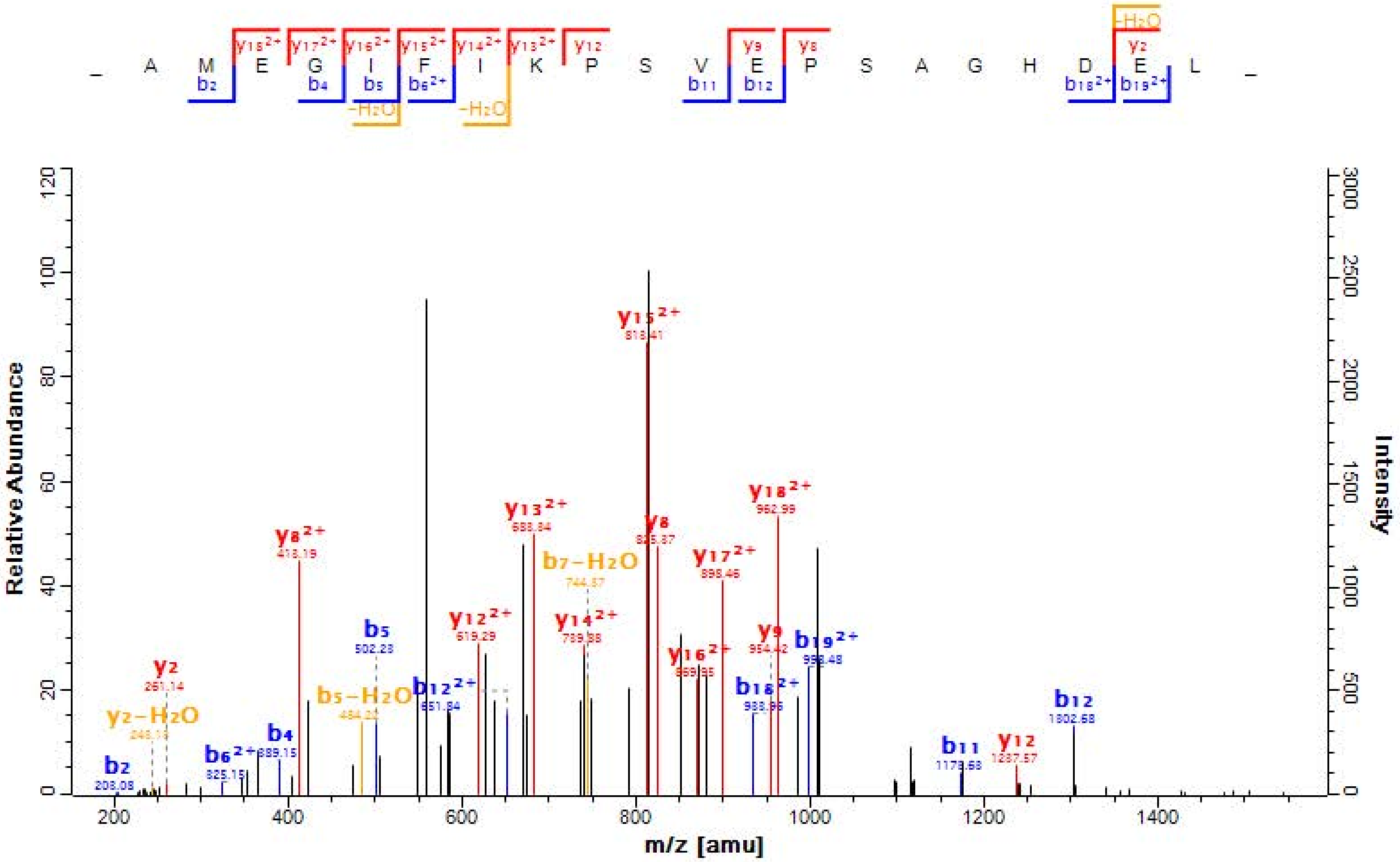
Mass:	1649.71311
m/z:	825.86383
Charge:	2+
Retentiontime:	38.082763671875
Score:	56.59909
Mass Error [ppm]:	-0.3885
PEP:	0.0038912
Precursor Type:	MULTI

general information

Annotation:	10 of 16
AminoAcids Coverag	62 %
Intensity Coverage:	30 %
Peak Coverage:	20 %
Protein Localisation:	239 ... 254

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	15				
	201.09		201.09	2	E	14	1579.7		790.35	+0.2701
	316.11		316.11	3	D	13	1450.6	-0.266	725.82	+0.2313
	387.15	+0.0879	387.15	4	A	12	1335.6		1335.6	
	474.18		474.18	5	S	11	1264.6	-0.039	1264.6	
	531.2		531.2	6	G	10	1177.5		1177.5	
	660.25	+0.0619	660.25	7	E	9	1120.5		1120.5	
	731.28		731.28	8	A	8	991.48		991.48	
	802.32		802.32	9	A	7	920.44		920.44	
-0.239	437.18	-0.048	873.36	10	A	6	849.41		849.41	
	1004.4		1004.4	11	M	5	778.37		778.37	
	1117.5		1117.5	12	L	4	647.33	+0.0848	647.33	
	1231.5		1231.5	13	N	3	534.25		534.25	
	1345.6	-0.095	1345.6	14	N	2	420.2		420.2	
	1476.6	-0.011	1476.6	15	M	1	306.16		306.16	
				16	R	0	175.12		175.12	

Scan number	5413	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	108.63



precursor information

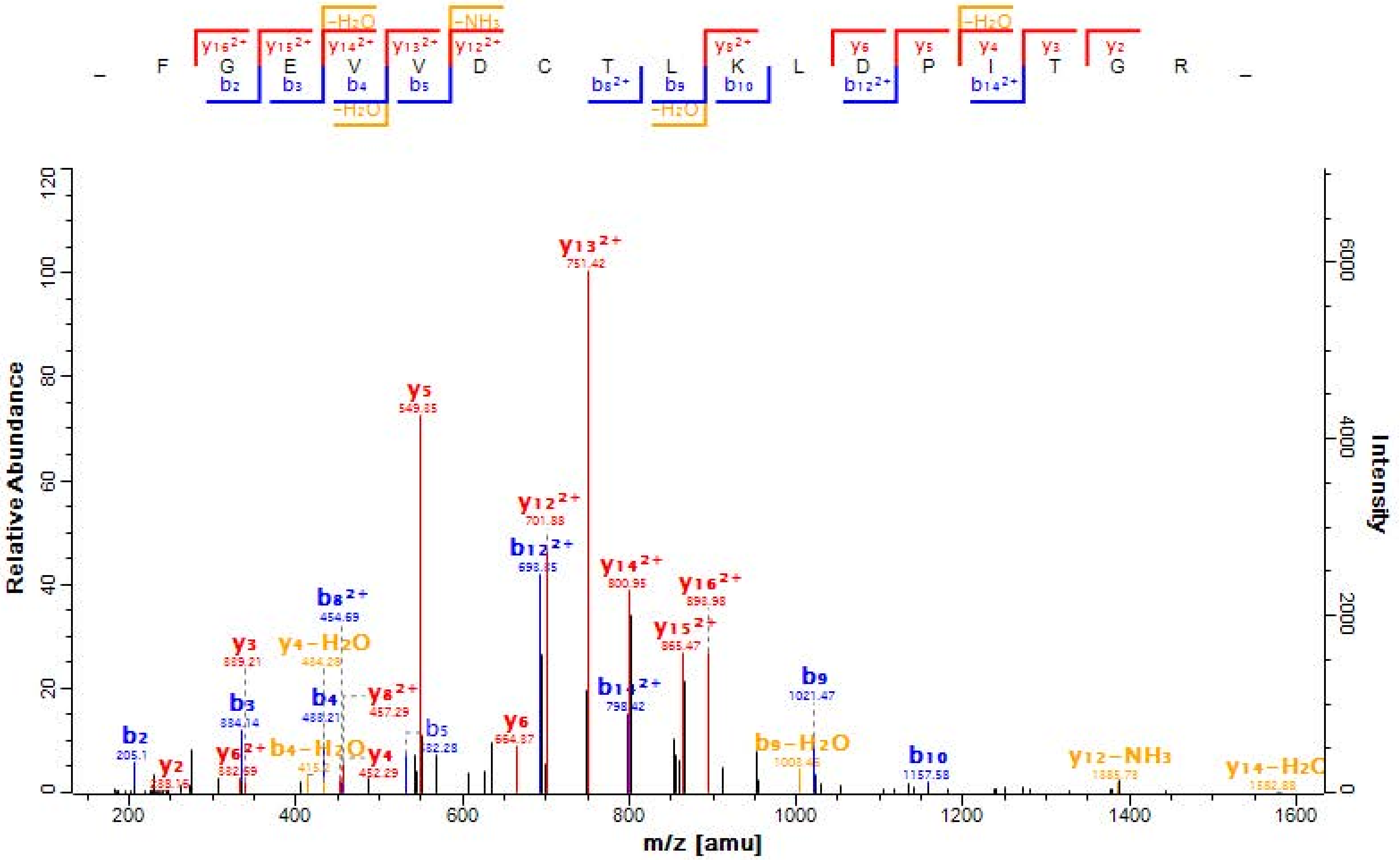
Mass:	2126.03657
m/z:	709.68613
Charge:	3+
Retentiontime:	40.523056030273
Score:	108.6344
Mass Error [ppm]:	0.54766
PEP:	1.0433E-08
Precursor Type:	MULTI

general information

Annotation:	13 of 20
AminoAcids Coverag	65 %
Intensity Coverage:	42 %
Peak Coverage:	26 %
Protein Localisation:	600 ... 619

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	19				
	203.08	+0.0923	203.08	2	M	18	2056		2056	
	332.13		332.13	3	E	17	1925		962.99	+0.1927
	389.15	+0.1204	389.15	4	G	16	1795.9		898.46	+0.1775
	502.23	-0.029	502.23	5	I	15	1738.9		869.95	+0.3717
-0.068	325.15		649.3	6	F	14	1625.8		813.41	-0.016
	762.39		762.39	7	I	13	1478.7		739.88	-0.044
	890.48		890.48	8	K	12	1365.7		683.34	+0.1819
	987.53		987.53	9	P	11	1237.6	+0.1017	619.29	+0.0657
	1074.6		1074.6	10	S	10	1140.5		1140.5	
	1173.6	+0.0199	1173.6	11	V	9	1053.5		1053.5	
+0.0524	651.84	-0.043	1302.7	12	E	8	954.42	-0.349	954.42	
	1399.7		1399.7	13	P	7	825.37	+0.0345	413.19	+0.184
	1486.8		1486.8	14	S	6	728.32		728.32	
	1557.8		1557.8	15	A	5	641.29		641.29	
	1614.8		1614.8	16	G	4	570.25		570.25	
	1751.9		1751.9	17	H	3	513.23		513.23	
+0.2729	933.96		1866.9	18	D	2	376.17		376.17	
+0.2598	998.48		1995.9	19	E	1	261.14	+0.1141	261.14	
				20	L	0	132.1		132.1	

Scan number	5875	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	118.08



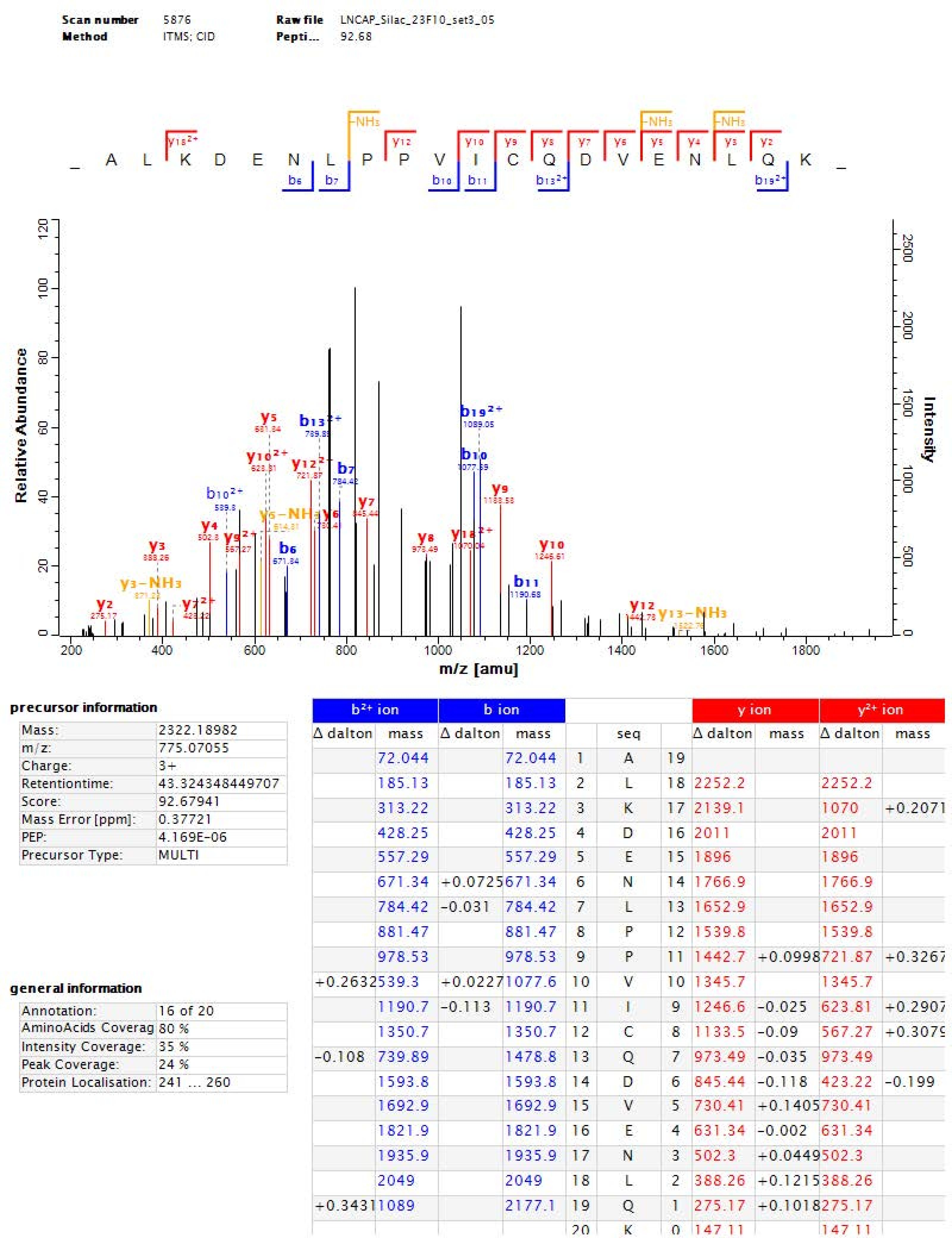
precursor information

Mass:	1918.98175
m/z:	640.66786
Charge:	3+
Retentiontime:	43.319118499755
Score:	118.0802
Mass Error [ppm]:	-0.25736
PEP:	1.8733E-09
Precursor Type:	MULTI

general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	62 %
Peak Coverage:	25 %
Protein Localisation:	101 ... 117

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.08		148.08	1	F	16				
	205.1	+0.0418	205.1	2	G	15	1787		893.98	+0.14
	334.14	+0.0897	334.14	3	E	14	1729.9		865.47	-0.122
	433.21	+0.0285	433.21	4	V	13	1600.9		800.95	-0.006
	532.28	+0.0122	532.28	5	V	12	1501.8		751.42	+0.2738
	647.3		647.3	6	D	11	1402.8		701.88	+0.1179
	807.33		807.33	7	C	10	1287.7		1287.7	
+0.2568	454.69		908.38	8	T	9	1127.7		1127.7	
	1021.5	-0.072	1021.5	9	L	8	1026.6		1026.6	
	1157.6	-0.064	1157.6	10	K	7	913.57		457.29	+0.0153
	1270.7		1270.7	11	L	6	777.46		777.46	
+0.0349	693.35		1385.7	12	D	5	664.37	+0.1136	332.69	+0.211
	1482.7		1482.7	13	P	4	549.35	-0.021	549.35	
-0.092	798.42		1595.8	14	I	3	452.29	+0.0395	452.29	
	1696.9		1696.9	15	T	2	339.21	+0.1026	339.21	
	1753.9		1753.9	16	G	1	238.16	+0.1954	238.16	
				17	R	0	181.14		181.14	



Scan number	5876	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	92.68

precursor information

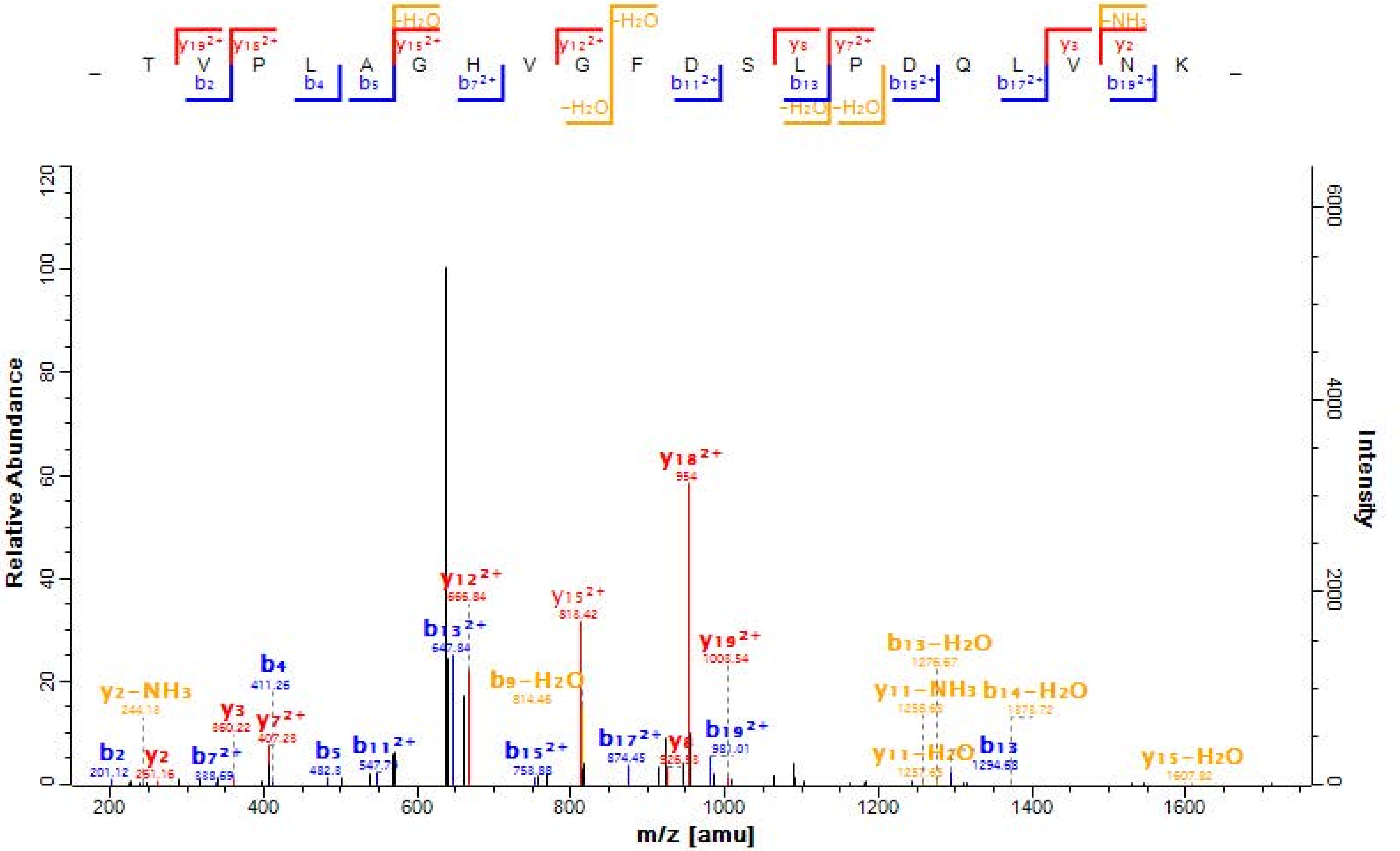
Mass:	2322.18982
m/z:	775.07055
Charge:	3+
Retentiontime:	43.324348449707
Score:	92.67941
Mass Error [ppm]:	0.37721
PEP:	4.169E-06
Precursor Type:	MULTI

general information

Annotation:	16 of 20
AminoAcids Coverag	80 %
Intensity Coverage:	35 %
Peak Coverage:	24 %
Protein Localisation:	241 ... 260

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	19				
	185.13		185.13	2	L	18	2252.2		2252.2	
	313.22		313.22	3	K	17	2139.1		1070	+0.2071
	428.25		428.25	4	D	16	2011		2011	
	557.29		557.29	5	E	15	1896		1896	
	671.34	+0.0725	671.34	6	N	14	1766.9		1766.9	
	784.42	-0.031	784.42	7	L	13	1652.9		1652.9	
	881.47		881.47	8	P	12	1539.8		1539.8	
	978.53		978.53	9	P	11	1442.7	+0.0998	721.87	+0.3267
+0.2632	539.3	+0.0227	1077.6	10	V	10	1345.7		1345.7	
	1190.7	-0.113	1190.7	11	I	9	1246.6	-0.025	623.81	+0.2907
	1350.7		1350.7	12	C	8	1133.5	-0.09	567.27	+0.3079
-0.108	739.89		1478.8	13	Q	7	973.49	-0.035	973.49	
	1593.8		1593.8	14	D	6	845.44	-0.118	423.22	-0.199
	1692.9		1692.9	15	V	5	730.41	+0.1405	730.41	
	1821.9		1821.9	16	E	4	631.34	-0.002	631.34	
	1935.9		1935.9	17	N	3	502.3	+0.0449	502.3	
	2049		2049	18	L	2	388.26	+0.1215	388.26	
+0.3431	1089		2177.1	19	Q	1	275.17	+0.1018	275.17	
				20	K	0	147.11		147.11	

Scan number	5960	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	70.78



precursor information

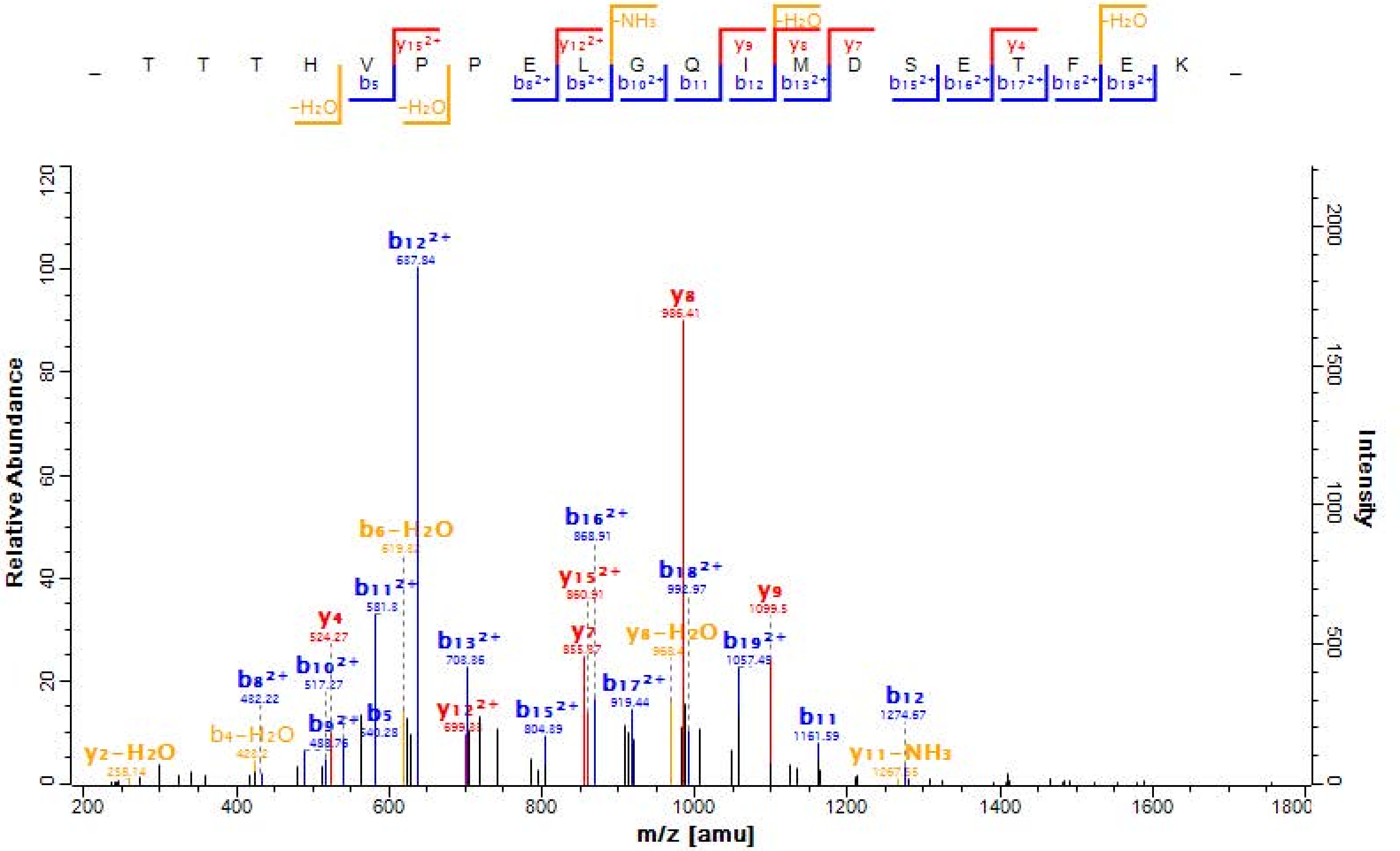
Mass:	2106.11088
m/z:	703.04424
Charge:	3+
Retentiontime:	43.853218078613
Score:	70.78362
Mass Error [ppm]:	-0.034338
PEP:	0.00025815
Precursor Type:	MULTI

general information

Annotation:	15 of 20
AminoAcids Coverag	75 %
Intensity Coverage:	44 %
Peak Coverage:	30 %
Protein Localisation:	46 ... 65

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	19				
	201.12	+0.0139	201.12	2	V	18	2006.1		1003.5	-0.364
	298.18		298.18	3	P	17	1907		954	+0.2772
	411.26	+0.428	411.26	4	L	16	1809.9		1809.9	
	482.3	+0.0305	482.3	5	A	15	1696.9		1696.9	
	539.32		539.32	6	G	14	1625.8		813.42	-0.01
-0.323	338.69		676.38	7	H	13	1568.8		1568.8	
	775.45		775.45	8	V	12	1431.7		1431.7	
	832.47		832.47	9	G	11	1332.7		666.84	+0.4505
	979.54		979.54	10	F	10	1275.7		1275.7	
+0.2469	547.79		1094.6	11	D	9	1128.6		1128.6	
	1181.6		1181.6	12	S	8	1013.6		1013.6	
+0.1176	647.84	+0.0314	1294.7	13	L	7	926.53	-0.307	926.53	
	1391.7		1391.7	14	P	6	813.45		407.23	+0.0208
+0.162	753.88		1506.8	15	D	5	716.39		716.39	
	1634.8		1634.8	16	Q	4	601.37		601.37	
+0.3842	874.45		1747.9	17	L	3	473.31		473.31	
	1847		1847	18	V	2	360.22	-0.037	360.22	
+0.4069	981.01		1961	19	N	1	261.16	+0.1556	261.16	
				20	K	0	147.11		147.11	

Scan number	5961	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	111.92



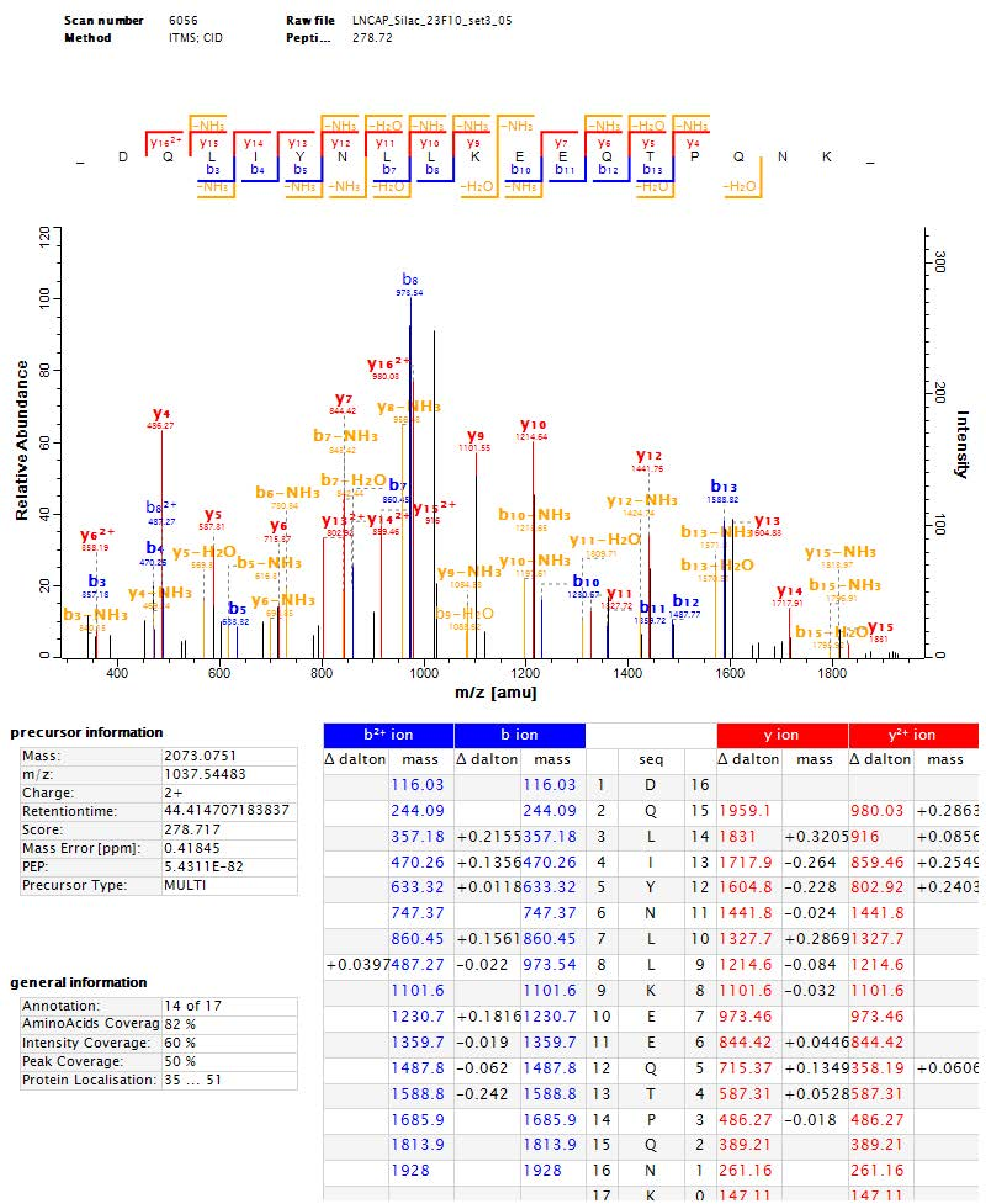
precursor information

Mass:	2259.07296
m/z:	754.0316
Charge:	3+
Retentiontime:	43.859085083007
Score:	111.9249
Mass Error [ppm]:	0.022007
PEP:	8.8382E-09
Precursor Type:	MULTI

general information

Annotation:	15 of 20
AminoAcids Coverag	75 %
Intensity Coverage:	65 %
Peak Coverage:	29 %
Protein Localisation:	47 ... 66

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	19				
	203.1		203.1	2	T	18	2159		2159	
	304.15		304.15	3	T	17	2058		2058	
	441.21		441.21	4	H	16	1956.9		1956.9	
	540.28	+0.0218	540.28	5	V	15	1819.9		1819.9	
	637.33		637.33	6	P	14	1720.8		860.91	+0.3499
	734.38		734.38	7	P	13	1623.8		1623.8	
+0.1505	432.22		863.43	8	E	12	1526.7		1526.7	
+0.0211	488.76		976.51	9	L	11	1397.7		699.33	-0.002
+0.0448	517.27		1033.5	10	G	10	1284.6		1284.6	
+0.2301	581.3	+0.0349	1161.6	11	Q	9	1227.6		1227.6	
+0.1527	637.84	+0.136	1274.7	12	I	8	1099.5	-0.047	1099.5	
+0.0549	703.36		1405.7	13	M	7	986.41	-0.065	986.41	
	1520.7		1520.7	14	D	6	855.37	+0.0307	855.37	
+0.2777	804.39		1607.8	15	S	5	740.35		740.35	
+0.0079	868.91		1736.8	16	E	4	653.31		653.31	
+0.0631	919.44		1837.9	17	T	3	524.27	+0.0276	524.27	
+0.2025	992.97		1984.9	18	F	2	423.22		423.22	
+0.038	1057.5		2114	19	E	1	276.16		276.16	
				20	K	0	147.11		147.11	



Scan number	6056	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	278.72

precursor information

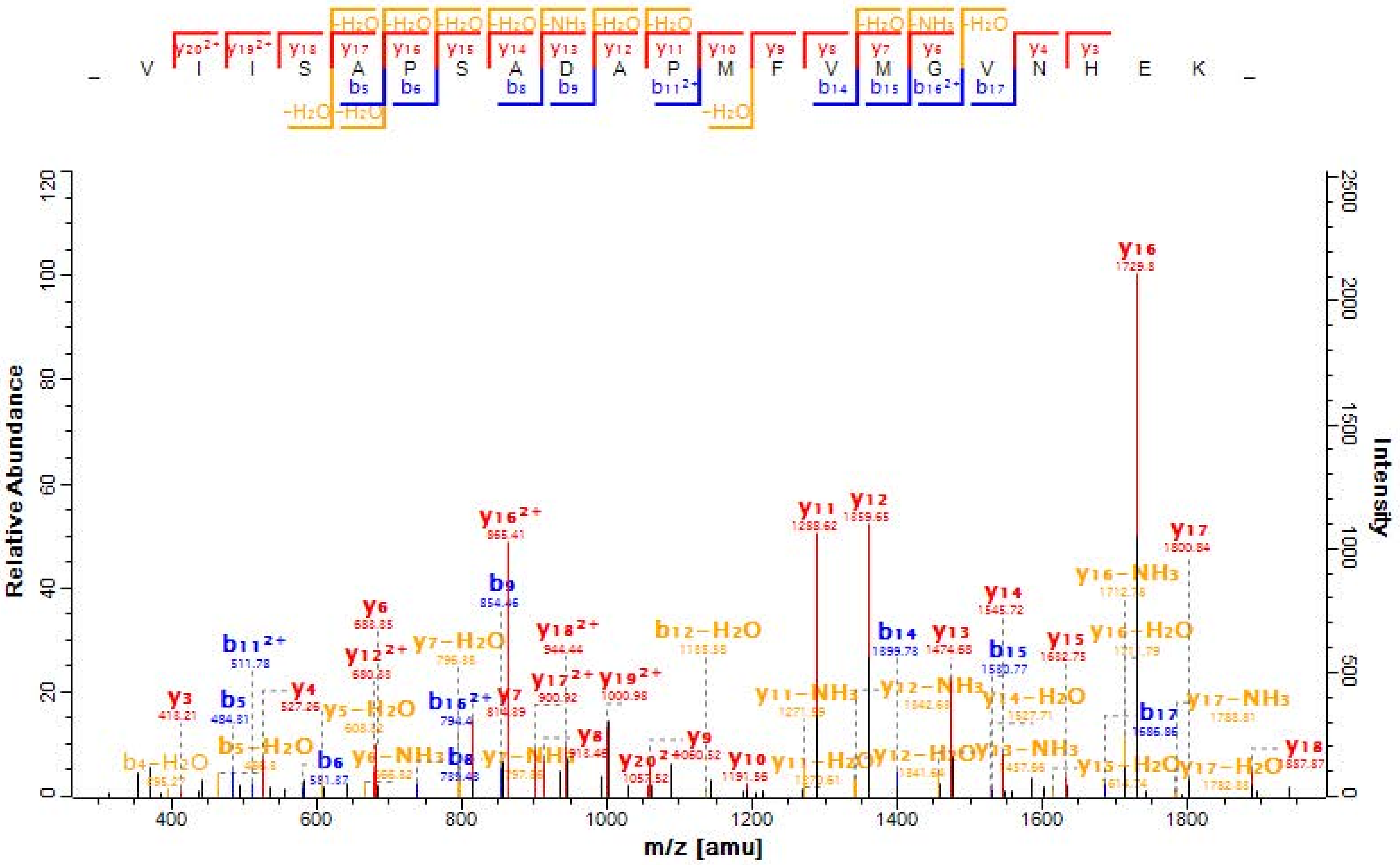
Mass:	2073.0751
m/z:	1037.54483
Charge:	2+
Retentiontime:	44.414707183837
Score:	278.717
Mass Error [ppm]:	0.41845
PEP:	5.4311E-82
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	60 %
Peak Coverage:	50 %
Protein Localisation:	35 ... 51

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	16				
	244.09		244.09	2	Q	15	1959.1		980.03	+0.2863
	357.18	+0.2155	357.18	3	L	14	1831	+0.3205	916	+0.085
	470.26	+0.1356	470.26	4	I	13	1717.9	-0.264	859.46	+0.254
	633.32	+0.0118	633.32	5	Y	12	1604.8	-0.228	802.92	+0.2403
	747.37		747.37	6	N	11	1441.8	-0.024	1441.8	
	860.45	+0.1561	860.45	7	L	10	1327.7	+0.2869	1327.7	
+0.0397	487.27	-0.022	973.54	8	L	9	1214.6	-0.084	1214.6	
	1101.6		1101.6	9	K	8	1101.6	-0.032	1101.6	
	1230.7	+0.1816	1230.7	10	E	7	973.46		973.46	
	1359.7	-0.019	1359.7	11	E	6	844.42	+0.0446	844.42	
	1487.8	-0.062	1487.8	12	Q	5	715.37	+0.1349	358.19	+0.060
	1588.8	-0.242	1588.8	13	T	4	587.31	+0.0528	587.31	
	1685.9		1685.9	14	P	3	486.27	-0.018	486.27	
	1813.9		1813.9	15	Q	2	389.21		389.21	
	1928		1928	16	N	1	261.16		261.16	
				17	K	0	147.11		147.11	

Scan number	6063	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	287.54



precursor information

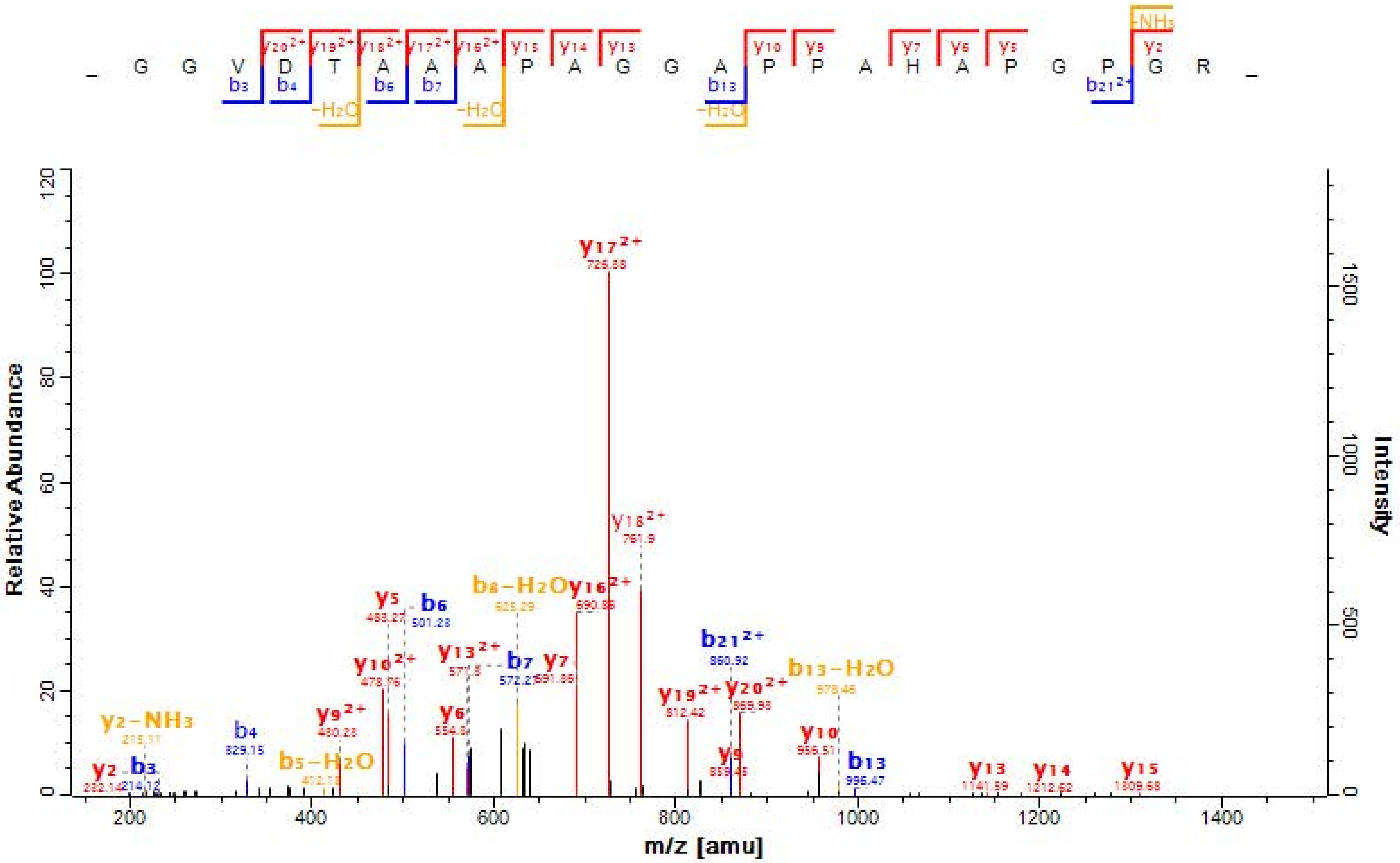
Mass:	2212.10126
m/z:	1107.05791
Charge:	2+
Retentiontime:	44.461170196533
Score:	287.5408
Mass Error [ppm]:	-0.35457
PEP:	1.2747E-112
Precursor Type:	MULTI

general information

Annotation:	18 of 21
AminoAcids Coverag	86 %
Intensity Coverage:	67 %
Peak Coverage:	47 %
Protein Localisation:	119 ... 139

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	20				
	213.16		213.16	2	I	19	2114		1057.5	+0.2019
	326.24		326.24	3	I	18	2001		1001	-0.077
	413.28		413.28	4	S	17	1887.9	-0.031	944.44	+0.0005
	484.31	-0.005	484.31	5	A	16	1800.8	-0.116	900.92	-0.007
	581.37	-0.039	581.37	6	P	15	1729.8	-0.111	865.41	+0.2451
	668.4		668.4	7	S	14	1632.8	-0.087	1632.8	
	739.43	+0.002	739.43	8	A	13	1545.7	-0.2	1545.7	
	854.46	-0.027	854.46	9	D	12	1474.7	-0.117	1474.7	
	925.5		925.5	10	A	11	1359.7	-0.086	680.33	+0.1878
-0.4	511.78		1022.6	11	P	10	1288.6	-0.085	1288.6	
	1153.6		1153.6	12	M	9	1191.6	-0.028	1191.6	
	1300.7		1300.7	13	F	8	1060.5	+0.0495	1060.5	
	1399.7	-0.324	1399.7	14	V	7	913.46	+0.034	913.46	
	1530.8	-0.231	1530.8	15	M	6	814.39	-0.039	814.39	
+0.0527	794.4		1587.8	16	G	5	683.35	-0.063	683.35	
	1686.9	-0.057	1686.9	17	V	4	626.33		626.33	
	1800.9		1800.9	18	N	3	527.26	+0.0669	527.26	
	1938		1938	19	H	2	413.21	-0.004	413.21	
	2067		2067	20	E	1	276.16		276.16	
				21	K	0	147.11		147.11	

Scan number	615	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	107.72



precursor information

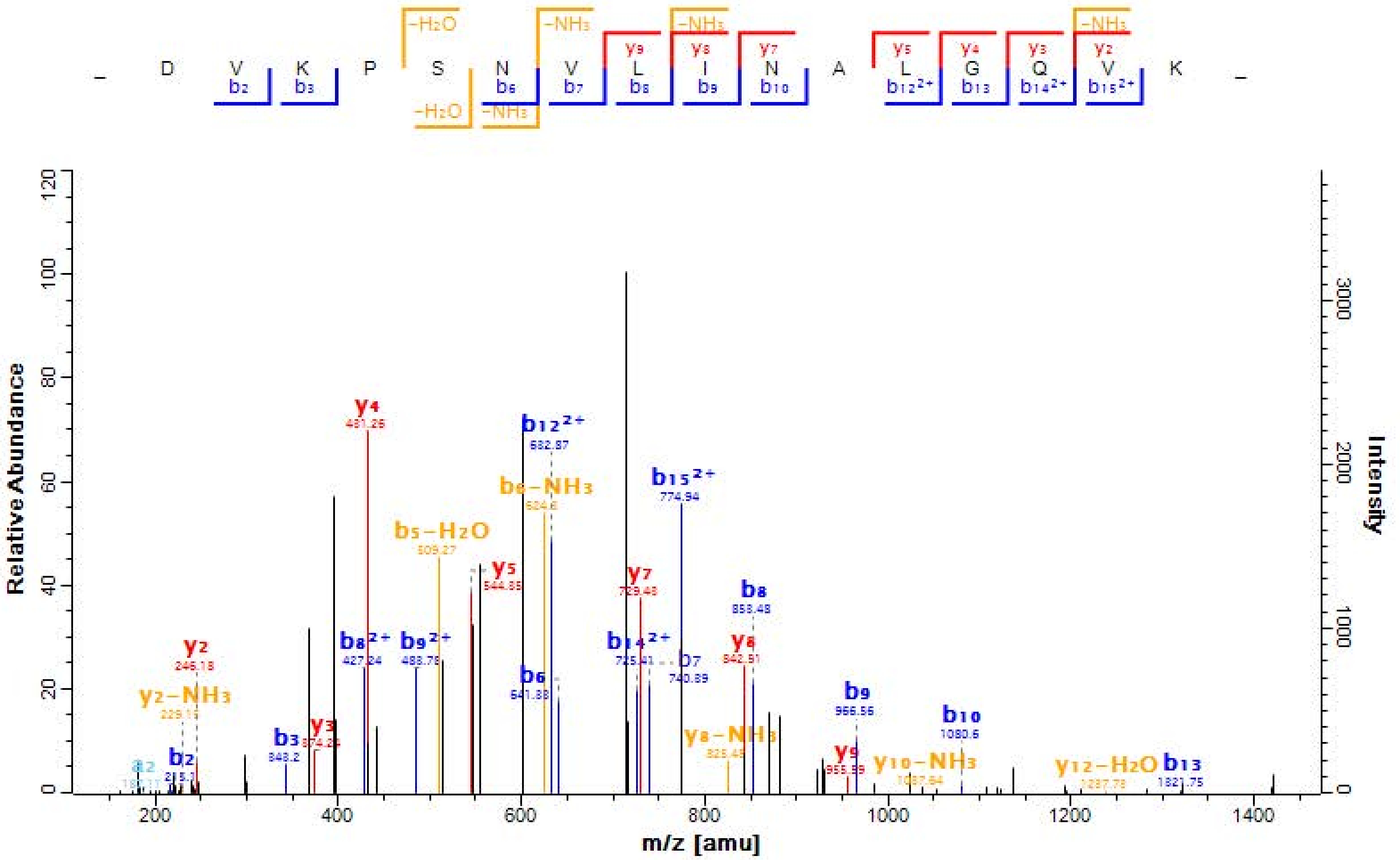
Mass:	1950.96595
m/z:	651.32926
Charge:	3+
Retentiontime:	9.9336528778076
Score:	107.7236
Mass Error [ppm]:	-0.034698
PEP:	4.753E-10
Precursor Type:	MULTI

general information

Annotation:	19 of 23
AminoAcids Coverag	83 %
Intensity Coverage:	78 %
Peak Coverage:	25 %
Protein Localisation:	25 ... 47

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	22				
	115.05		115.05	2	G	21	1895		1895	
	214.12	+0.1818	214.12	3	V	20	1837.9		1837.9	
	329.15	+0.013	329.15	4	D	19	1738.9		869.93	+0.2426
	430.19		430.19	5	T	18	1623.8		812.42	+0.2523
	501.23	+0.0586	501.23	6	A	17	1522.8		761.9	+0.2021
	572.27	-0.005	572.27	7	A	16	1451.8		726.38	+0.2094
	643.3		643.3	8	A	15	1380.7		690.86	+0.0189
	740.36		740.36	9	P	14	1309.7	-0.155	1309.7	
	811.39		811.39	10	A	13	1212.6	+0.3063	1212.6	
	868.42		868.42	11	G	12	1141.6	+0.045	571.3	+0.194
	925.44		925.44	12	G	11	1084.6		1084.6	
	996.47	+0.2442	996.47	13	A	10	1027.5		1027.5	
	1093.5		1093.5	14	P	9	956.51	-0.027	478.76	+0.2076
	1190.6		1190.6	15	P	8	859.45	+0.0618	430.23	+0.0904
	1261.6		1261.6	16	A	7	762.4		762.4	
	1398.7		1398.7	17	H	6	691.36	+0.1396	691.36	
	1469.7		1469.7	18	A	5	554.3	+0.0102	554.3	
	1566.8		1566.8	19	P	4	483.27	+0.0102	483.27	
	1623.8		1623.8	20	G	3	386.21		386.21	
+0.1979	860.92		1720.8	21	P	2	329.19		329.19	
	1777.9		1777.9	22	G	1	232.14	+0.0667	232.14	
				23	R	0	175.12		175.12	

Scan number	6466	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	99.07



precursor information

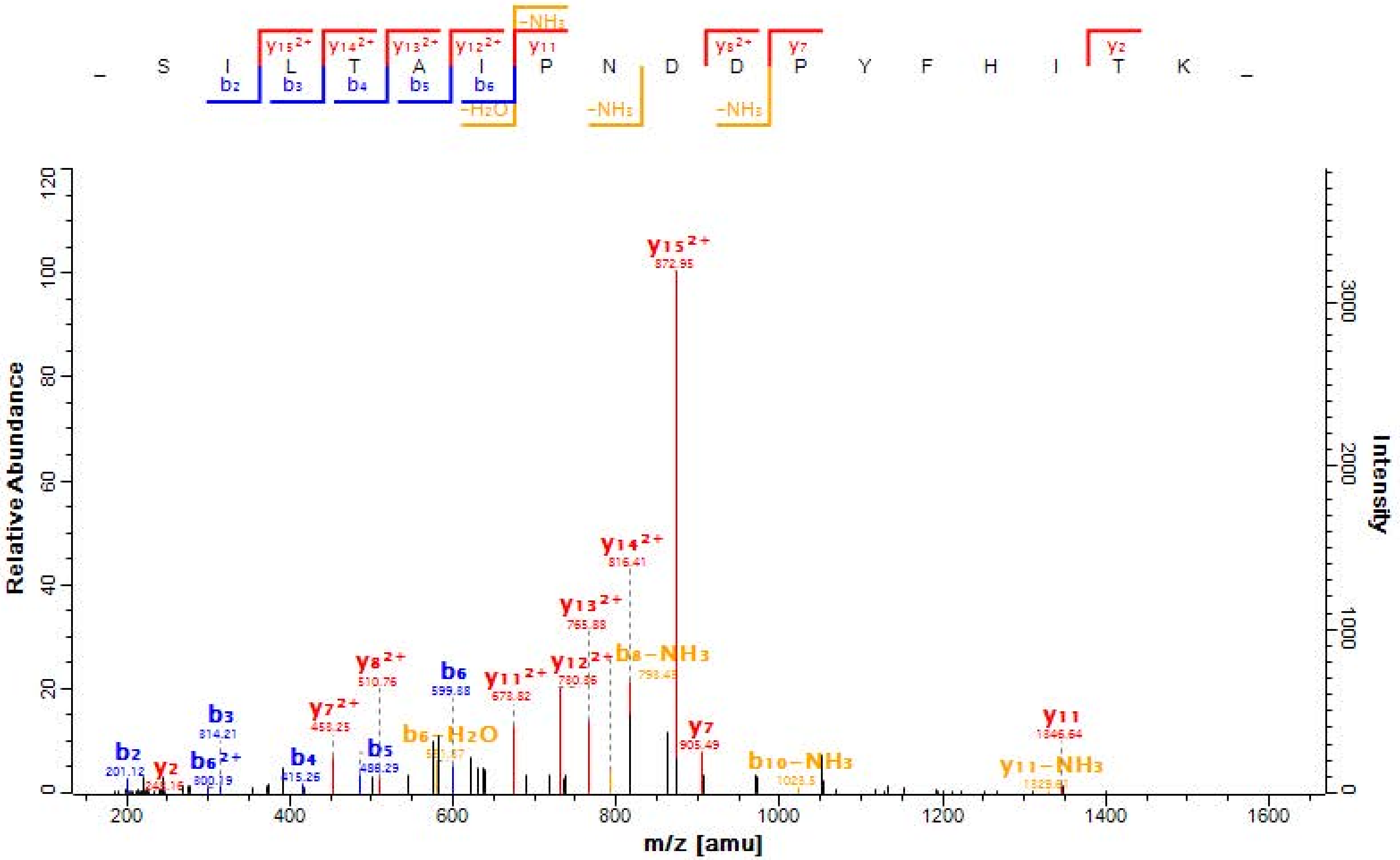
Mass:	1693.97277
m/z:	565.66487
Charge:	3+
Retentiontime:	46.996128082275
Score:	99.06912
Mass Error [ppm]:	0.061771
PEP:	0.0020067
Precursor Type:	ISO

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	45 %
Peak Coverage:	27 %
Protein Localisation:	179 ... 194

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	88.039		116.03		116.03	1	D	15		
+0.1189	187.11		215.1	+0.0462	215.1	2	V	14	1580	
	315.2		343.2	+0.0425	343.2	3	K	13	1480.9	
	412.26		440.25		440.25	4	P	12	1352.8	
	499.29		527.28		527.28	5	S	11	1255.7	
	613.33		641.33	-0.106	641.33	6	N	10	1168.7	
	712.4		740.39	+0.0797	740.39	7	V	9	1054.7	
	825.48	+0.197	427.24	+0.0015	853.48	8	L	8	955.59	-0.052
	938.57	+0.1679	483.78	-0.028	966.56	9	I	7	842.51	-0.001
	1052.6		1080.6	+0.1687	1080.6	10	N	6	729.43	+0.069
	1123.6		1151.6		1151.6	11	A	5	615.38	
	1236.7	+0.1966	632.87		1264.7	12	L	4	544.35	-0.031
	1293.8		1321.7	-0.222	1321.7	13	G	3	431.26	+0.034
	1421.8	+0.0132	725.41		1449.8	14	Q	2	374.24	+0.068
	1520.9	-0.01	774.94		1548.9	15	V	1	246.18	+0.065
						16	K	0	147.11	

Scan number	6577	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	70.26



precursor information

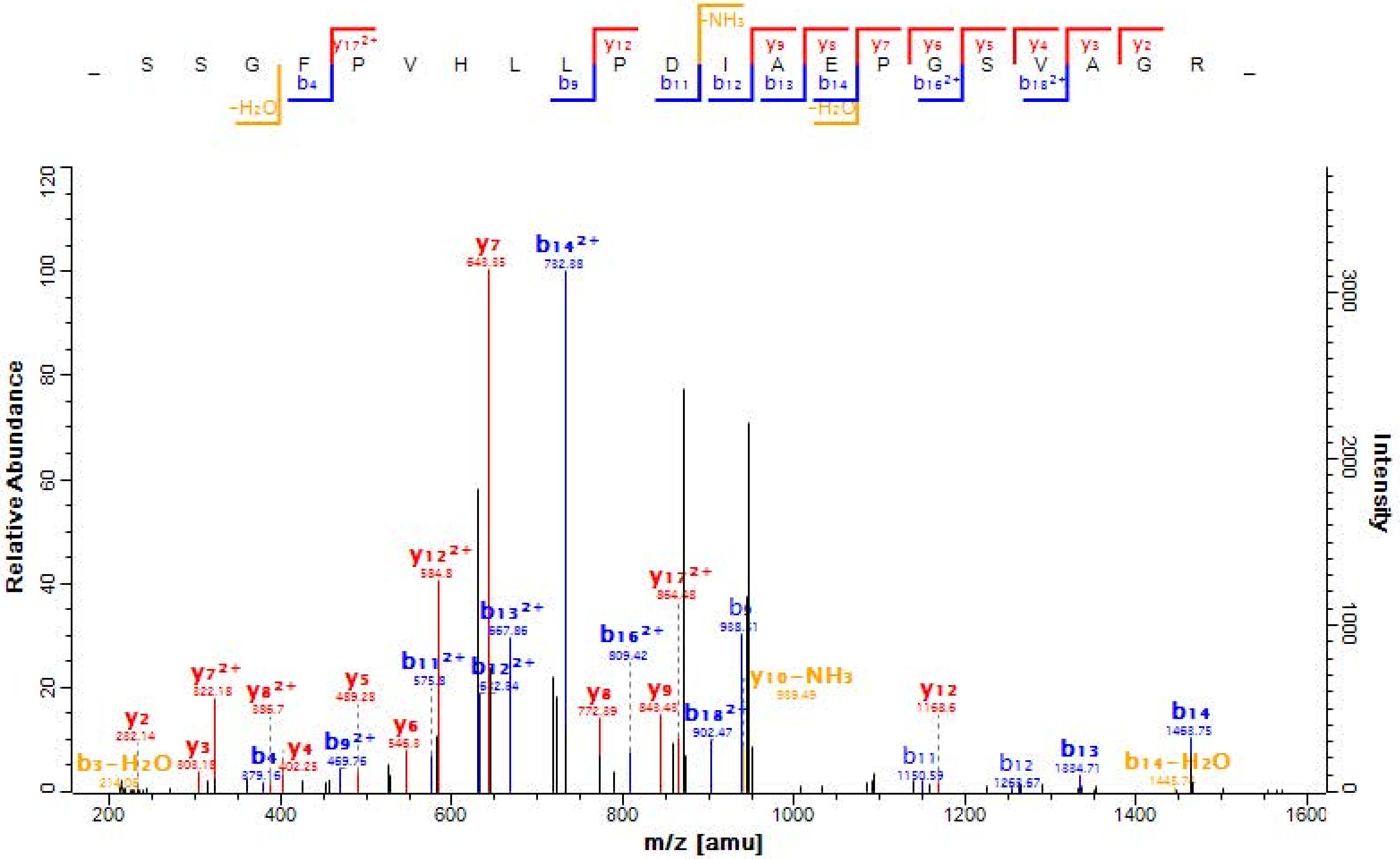
Mass:	1943.99997
m/z:	649.00727
Charge:	3+
Retentiontime:	47.725654602050
Score:	70.25957
Mass Error [ppm]:	0.35478
PEP:	0.00032713
Precursor Type:	MULTI

general information

Annotation:	10 of 17
AminoAcids Coverag	59 %
Intensity Coverage:	58 %
Peak Coverage:	21 %
Protein Localisation:	284 ... 300

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	16				
	201.12	-0.079	201.12	2	I	15	1858		1858	
	314.21	+0.0761	314.21	3	L	14	1744.9		872.95	+0.2464
	415.26	+0.1031	415.26	4	T	13	1631.8		816.41	-0.061
	486.29	+0.214	486.29	5	A	12	1530.8		765.88	+0.331
+0.1258	300.19	+0.0745	599.38	6	I	11	1459.7		730.36	+0.237
	696.43		696.43	7	P	10	1346.6	-0.107	673.82	+0.26
	810.47		810.47	8	N	9	1249.6		1249.6	
	925.5		925.5	9	D	8	1135.5		1135.5	
	1040.5		1040.5	10	D	7	1020.5		510.76	+0.2321
	1137.6		1137.6	11	P	6	905.49	-0.086	453.25	+0.308
	1300.6		1300.6	12	Y	5	808.44		808.44	
	1447.7		1447.7	13	F	4	645.37		645.37	
	1584.8		1584.8	14	H	3	498.3		498.3	
	1697.9		1697.9	15	I	2	361.24		361.24	
	1798.9		1798.9	16	T	1	248.16	+0.0589	248.16	
				17	K	0	147.11		147.11	

Scan number	6903	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	118.72



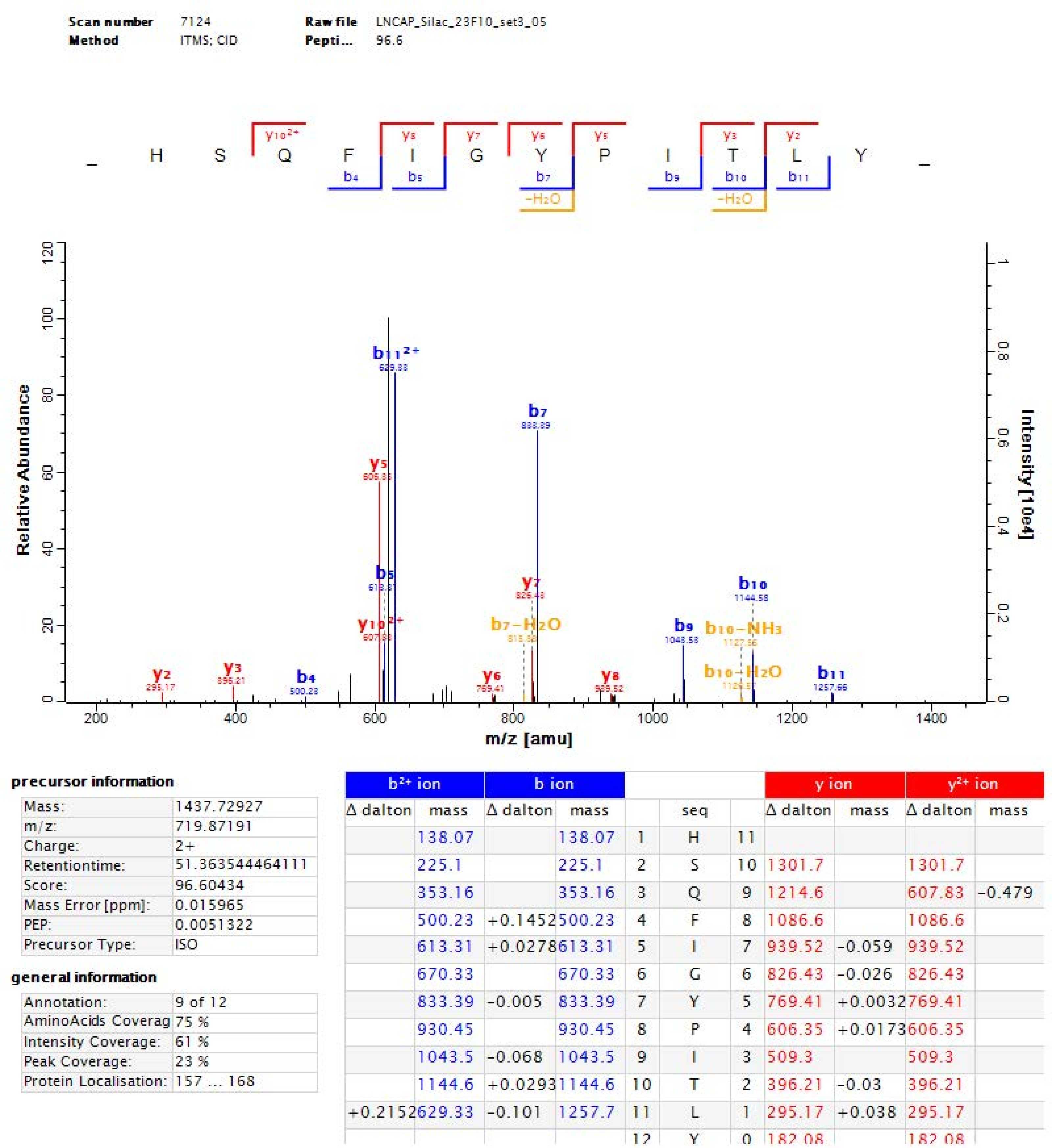
precursor information

Mass:	2105.09017
m/z:	702.704
Charge:	3+
Retentiontime:	49.827587127685
Score:	118.7195
Mass Error [ppm]:	-0.18292
PEP:	2.754E-10
Precursor Type:	MULTI

general information

Annotation:	15 of 21
AminoAcids Coverag	71 %
Intensity Coverage:	51 %
Peak Coverage:	31 %
Protein Localisation:	219 ... 239

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	20				
	175.07		175.07	2	S	19	2019.1		2019.1	
	232.09		232.09	3	G	18	1932		1932	
	379.16	+0.0296	379.16	4	F	17	1875		1875	
	476.21		476.21	5	P	16	1727.9		864.48	+0.1491
	575.28		575.28	6	V	15	1630.9		1630.9	
	712.34		712.34	7	H	14	1531.8		1531.8	
	825.43		825.43	8	L	13	1394.8		1394.8	
-0.026	469.76	+0.0291	938.51	9	L	12	1281.7		1281.7	
	1035.6		1035.6	10	P	11	1168.6	-0.463	584.8	+0.1804
+0.1471	575.8	+0.2619	1150.6	11	D	10	1071.5		1071.5	
-0.003	632.34	+0.2659	1263.7	12	I	9	956.52		956.52	
+0.2529	667.86	+0.1387	1334.7	13	A	8	843.43	+0.1053	843.43	
+0.2442	732.38	+0.0402	1463.8	14	E	7	772.39	+0.0746	386.7	+0.3671
	1560.8		1560.8	15	P	6	643.35	+0.0653	322.18	+0.2222
+0.0567	809.42		1617.8	16	G	5	546.3	+0.0521	546.3	
	1704.9		1704.9	17	S	4	489.28	+0.2227	489.28	
+0.2874	902.47		1803.9	18	V	3	402.25	+0.0803	402.25	
	1875		1875	19	A	2	303.18	+0.1813	303.18	
	1932		1932	20	G	1	232.14	+0.0824	232.14	
				21	R	0	175.12		175.12	



Scan number	7124	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	96.6

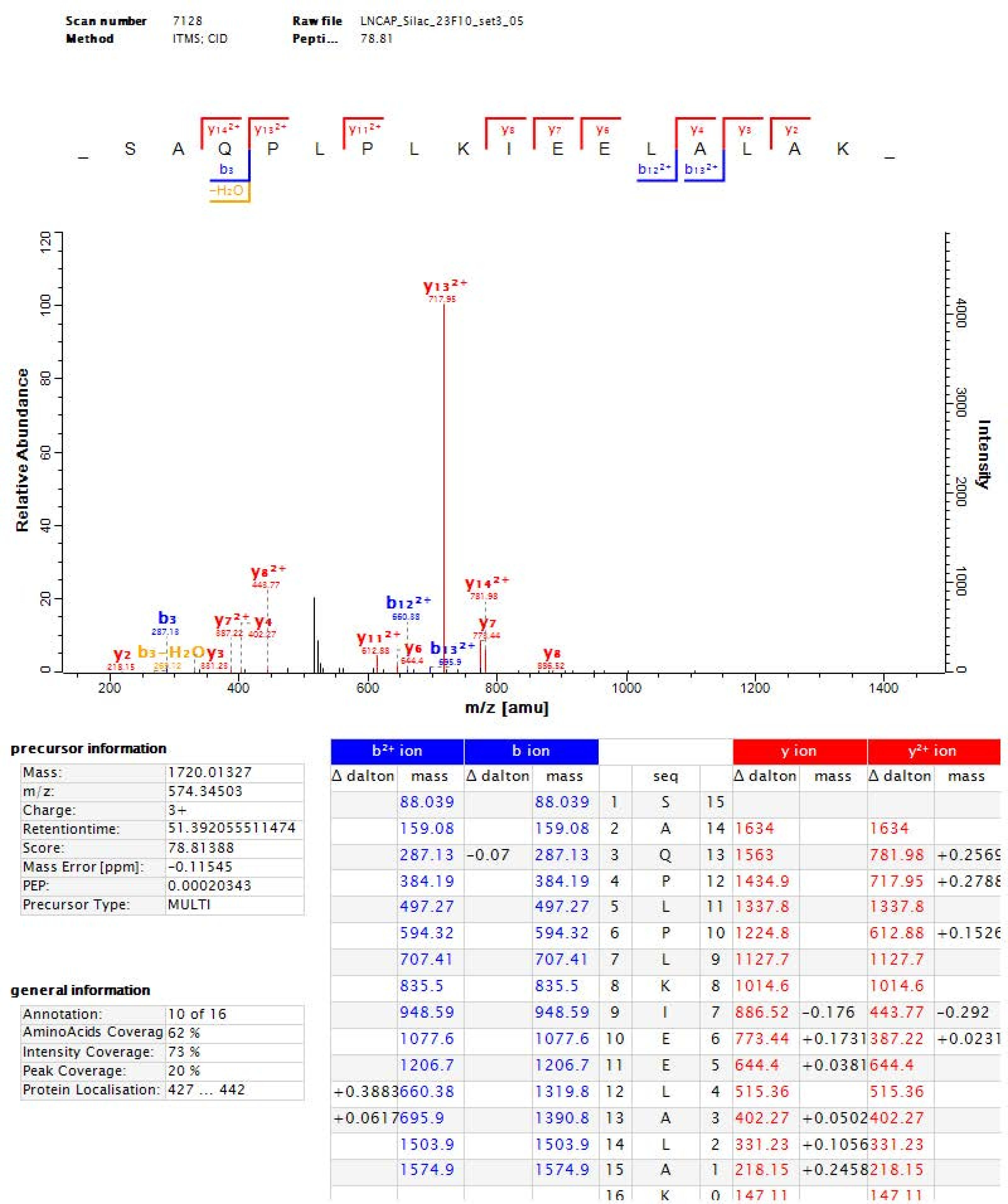
precursor information

Mass:	1437.72927
m/z:	719.87191
Charge:	2+
Retentiontime:	51.363544464111
Score:	96.60434
Mass Error [ppm]:	0.015965
PEP:	0.0051322
Precursor Type:	ISO

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	61 %
Peak Coverage:	23 %
Protein Localisation:	157 ... 168

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.07		138.07	1	H	11				
	225.1		225.1	2	S	10	1301.7		1301.7	
	353.16		353.16	3	Q	9	1214.6		607.83	-0.479
	500.23	+0.1452	500.23	4	F	8	1086.6		1086.6	
	613.31	+0.0278	613.31	5	I	7	939.52	-0.059	939.52	
	670.33		670.33	6	G	6	826.43	-0.026	826.43	
	833.39	-0.005	833.39	7	Y	5	769.41	+0.0032	769.41	
	930.45		930.45	8	P	4	606.35	+0.0173	606.35	
	1043.5	-0.068	1043.5	9	I	3	509.3		509.3	
	1144.6	+0.0293	1144.6	10	T	2	396.21	-0.03	396.21	
+0.2152	629.33	-0.101	1257.7	11	L	1	295.17	+0.038	295.17	
				12	Y	0	182.08		182.08	



Scan number	7128	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	78.81

precursor information

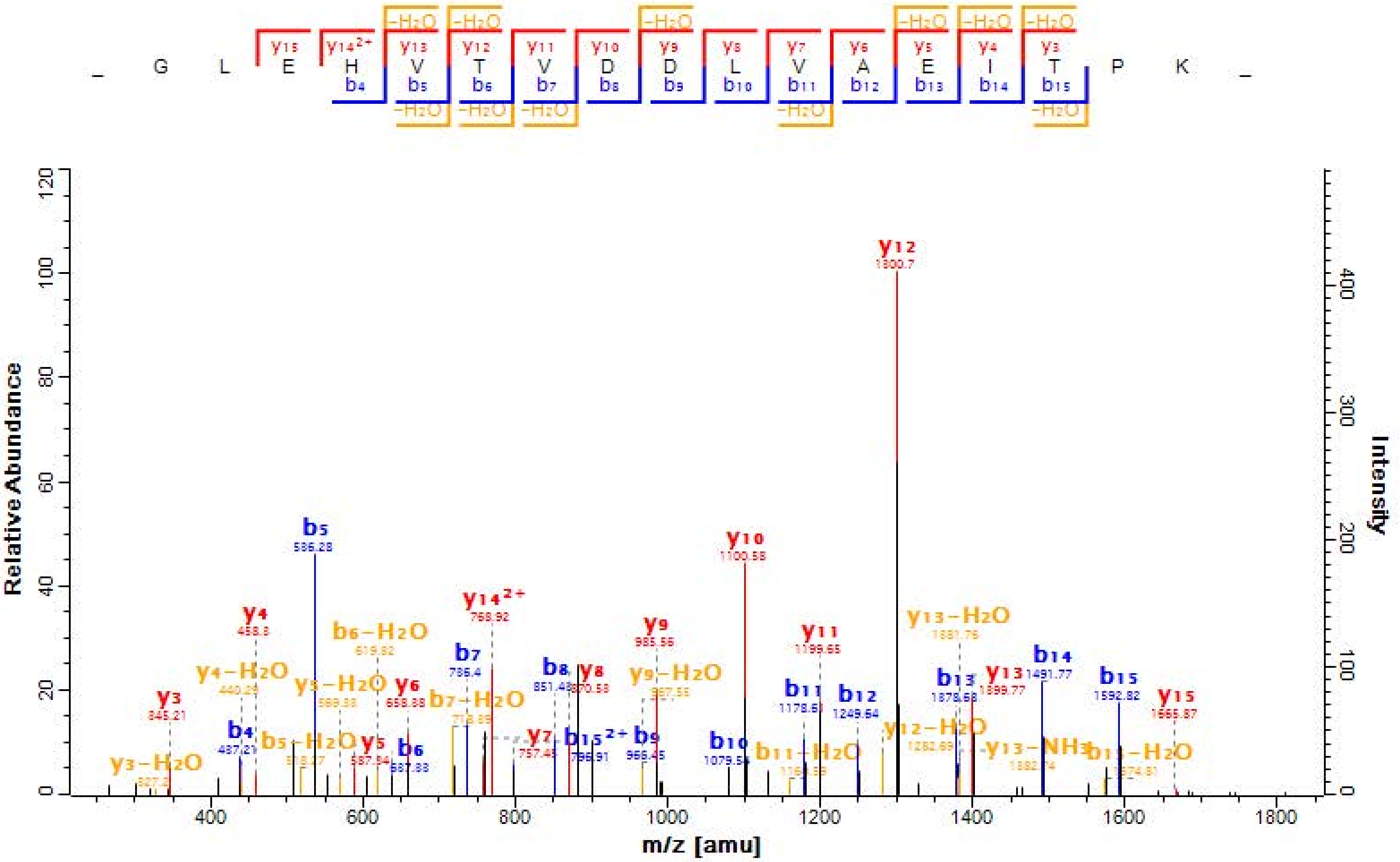
Mass:	1720.01327
m/z:	574.34503
Charge:	3+
Retentiontime:	51.392055511474
Score:	78.81388
Mass Error [ppm]:	-0.11545
PEP:	0.00020343
Precursor Type:	MULTI

general information

Annotation:	10 of 16
AminoAcids Coverag	62 %
Intensity Coverage:	73 %
Peak Coverage:	20 %
Protein Localisation:	427 ... 442

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	15				
	159.08		159.08	2	A	14	1634		1634	
	287.13	-0.07	287.13	3	Q	13	1563		781.98	+0.2569
	384.19		384.19	4	P	12	1434.9		717.95	+0.2788
	497.27		497.27	5	L	11	1337.8		1337.8	
	594.32		594.32	6	P	10	1224.8		612.88	+0.1526
	707.41		707.41	7	L	9	1127.7		1127.7	
	835.5		835.5	8	K	8	1014.6		1014.6	
	948.59		948.59	9	I	7	886.52	-0.176	443.77	-0.292
	1077.6		1077.6	10	E	6	773.44	+0.1731	387.22	+0.0231
	1206.7		1206.7	11	E	5	644.4	+0.0381	644.4	
+0.3883	660.38		1319.8	12	L	4	515.36		515.36	
+0.0617	695.9		1390.8	13	A	3	402.27	+0.0502	402.27	
	1503.9		1503.9	14	L	2	331.23	+0.1056	331.23	
	1574.9		1574.9	15	A	1	218.15	+0.2458	218.15	
				16	K	0	147.11		147.11	

Scan number	7750	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	222.42



precursor information

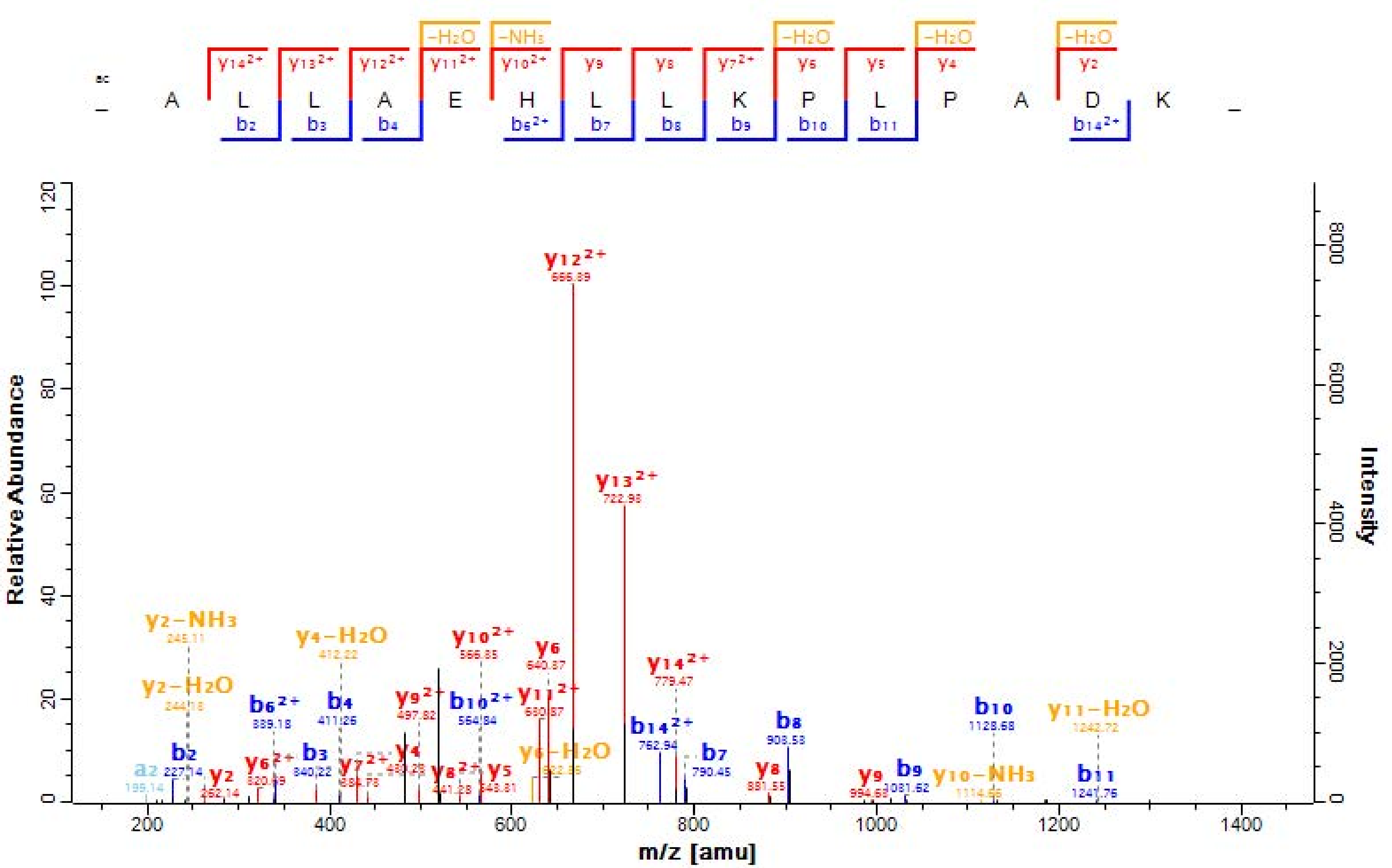
Mass:	1834.96776
m/z:	918.49116
Charge:	2+
Retentiontime:	56.428783416748
Score:	222.4237
Mass Error [ppm]:	0.06307
PEP:	1.2752E-47
Precursor Type:	MULTI

general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	58 %
Peak Coverage:	42 %
Protein Localisation:	58 ... 74

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	16				
	171.11		171.11	2	L	15	1779		1779	
	300.16		300.16	3	E	14	1665.9	+0.3536	1665.9	
	437.21	+0.0522	437.21	4	H	13	1536.8		768.92	+0.3753
	536.28	+0.0465	536.28	5	V	12	1399.8	-0.063	1399.8	
	637.33	-0.05	637.33	6	T	11	1300.7	-0.038	1300.7	
	736.4	+0.1014	736.4	7	V	10	1199.7	-0.038	1199.7	
	851.43	+0.0119	851.43	8	D	9	1100.6	-0.014	1100.6	
	966.45	+0.0114	966.45	9	D	8	985.56	+0.0055	985.56	
	1079.5	+0.0161	1079.5	10	L	7	870.53	-0.077	870.53	
	1178.6	-0.116	1178.6	11	V	6	757.45	+0.1158	757.45	
	1249.6	-0.031	1249.6	12	A	5	658.38	+0.0859	658.38	
	1378.7	+0.0131	1378.7	13	E	4	587.34	+0.1381	587.34	
	1491.8	+0.0489	1491.8	14	I	3	458.3	+0.1036	458.3	
-0.137	796.91	-0.056	1592.8	15	T	2	345.21	+0.1789	345.21	
	1689.9		1689.9	16	P	1	244.17		244.17	
				17	K	0	147.11		147.11	

Scan number	7762	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	177.42



precursor information

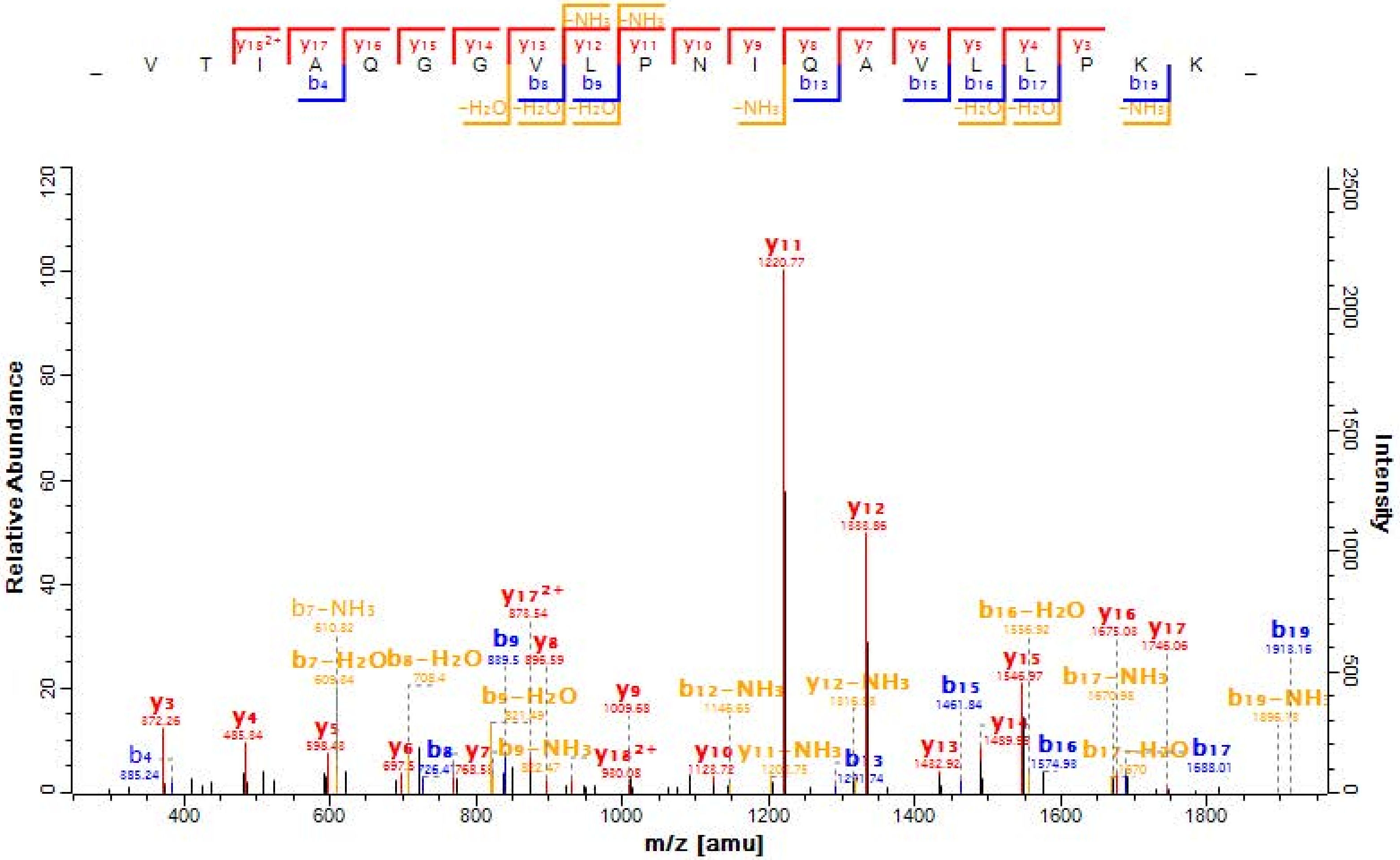
Mass:	1669.97667
m/z:	557.66617
Charge:	3+
Retentiontime:	56.539184570312
Score:	177.4186
Mass Error [ppm]:	-0.010924
PEP:	6.7368E-17
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	72 %
Peak Coverage:	35 %
Protein Localisation:	2 ... 16

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.06		114.1		114.1	1	A	14				
-0.01	199.1		227.1	-0.01	227.1	2	L	13	1558		779.5	+0.17
	312.2		340.2	-0.05	340.2	3	L	12	1445		722.9	+0.25
	383.3		411.3	-0.04	411.3	4	A	11	1332		666.4	+0.28
	512.3		540.3		540.3	5	E	10	1261		630.9	+0.23
	649.4	-0.03	339.2		677.4	6	H	9	1132		566.3	+0.30
	762.5		790.4	-0.02	790.4	7	L	8	994.6	-0.01	497.8	+0.18
	875.5		903.5	+0.023	903.5	8	L	7	881.5	+0.017	441.3	+0.15
	1004		1032	+0.153	1032	9	K	6	768.5		384.7	+0.25
	1101	-0.48	564.8	-0.36	1129	10	P	5	640.4	+0	320.7	+0.13
	1214		1242	-0.36	1242	11	L	4	543.3	+0.359	543.3	
	1311		1339		1339	12	P	3	430.2	+0.072	430.2	
	1382		1410		1410	13	A	2	333.2		333.2	
	1497	+0.257	762.9		1525	14	D	1	262.1	+0.109	262.1	
						15	K	0	147.1		147.1	

Scan number	7869	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	185.33



precursor information

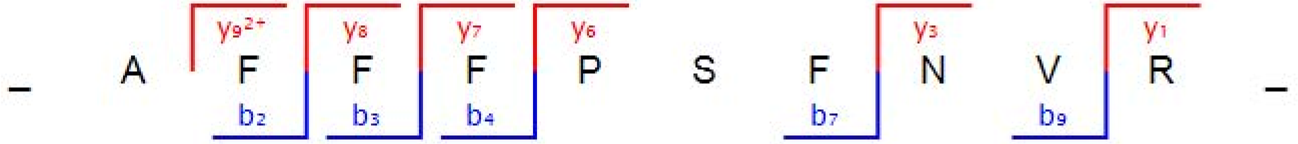
Mass:	2058.25563
m/z:	1030.13509
Charge:	2+
Retentiontime:	57.477954864502
Score:	185.3261
Mass Error [ppm]:	-0.4193
PEP:	1.8556E-26
Precursor Type:	ISO

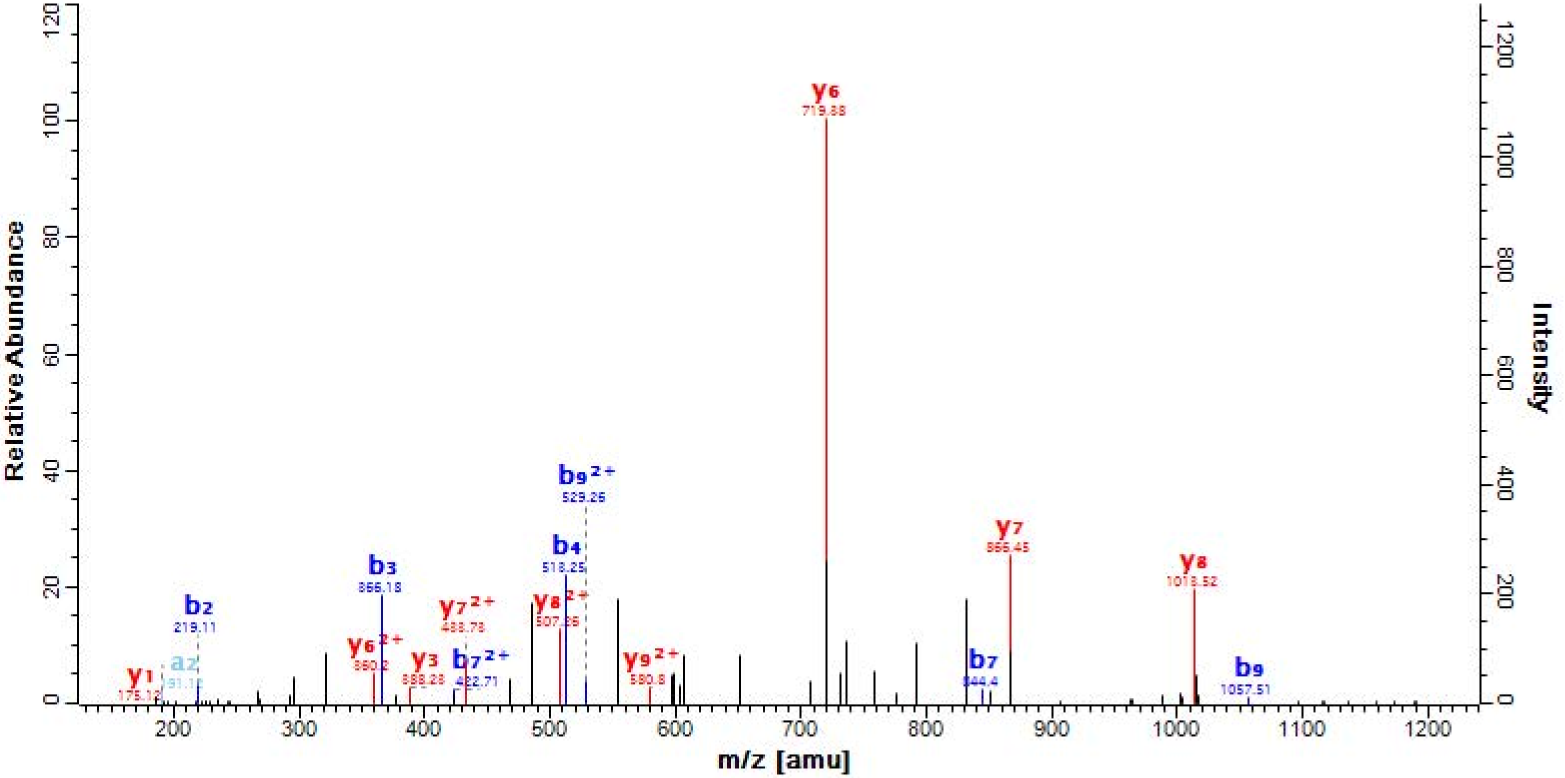
general information

Annotation:	17 of 20
AminoAcids Coverag	85 %
Intensity Coverage:	56 %
Peak Coverage:	40 %
Protein Localisation:	101 ... 120

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	19				
	201.1234	2	T	18	1960.195		1960.195	
	314.2074	3	I	17	1859.148		930.0775	+0.152136
+0.002707	385.2445	4	A	16	1746.064	+0.017316	873.5354	+0.105545
	513.3031	5	Q	15	1675.027	+0.343493	1675.027	
	570.3246	6	G	14	1546.968	-0.09012	1546.968	
	627.3461	7	G	13	1489.946	-0.05095	1489.946	
+0.028345	726.4145	8	V	12	1432.925	-0.16706	1432.925	
-0.08959	839.4985	9	L	11	1333.857	-0.07106	1333.857	
	936.5513	10	P	10	1220.773	-0.01593	1220.773	
	1050.594	11	N	9	1123.72	-0.01053	1123.72	
	1163.678	12	I	8	1009.677	-0.0561	1009.677	
-0.19975	1291.737	13	Q	7	896.5928	-0.08996	896.5928	
	1362.774	14	A	6	768.5342	+0.229607	768.5342	
-0.06956	1461.842	15	V	5	697.4971	-0.04395	697.4971	
-0.15326	1574.926	16	L	4	598.4287	-0.07032	598.4287	
-0.15822	1688.011	17	L	3	485.3446	+0.075785	485.3446	
	1785.063	18	P	2	372.2605	+0.092222	372.2605	
-0.02616	1913.158	19	K	1	275.2078		275.2078	
		20	K	0	147.1128		147.1128	

Scan number	8128	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	100.02





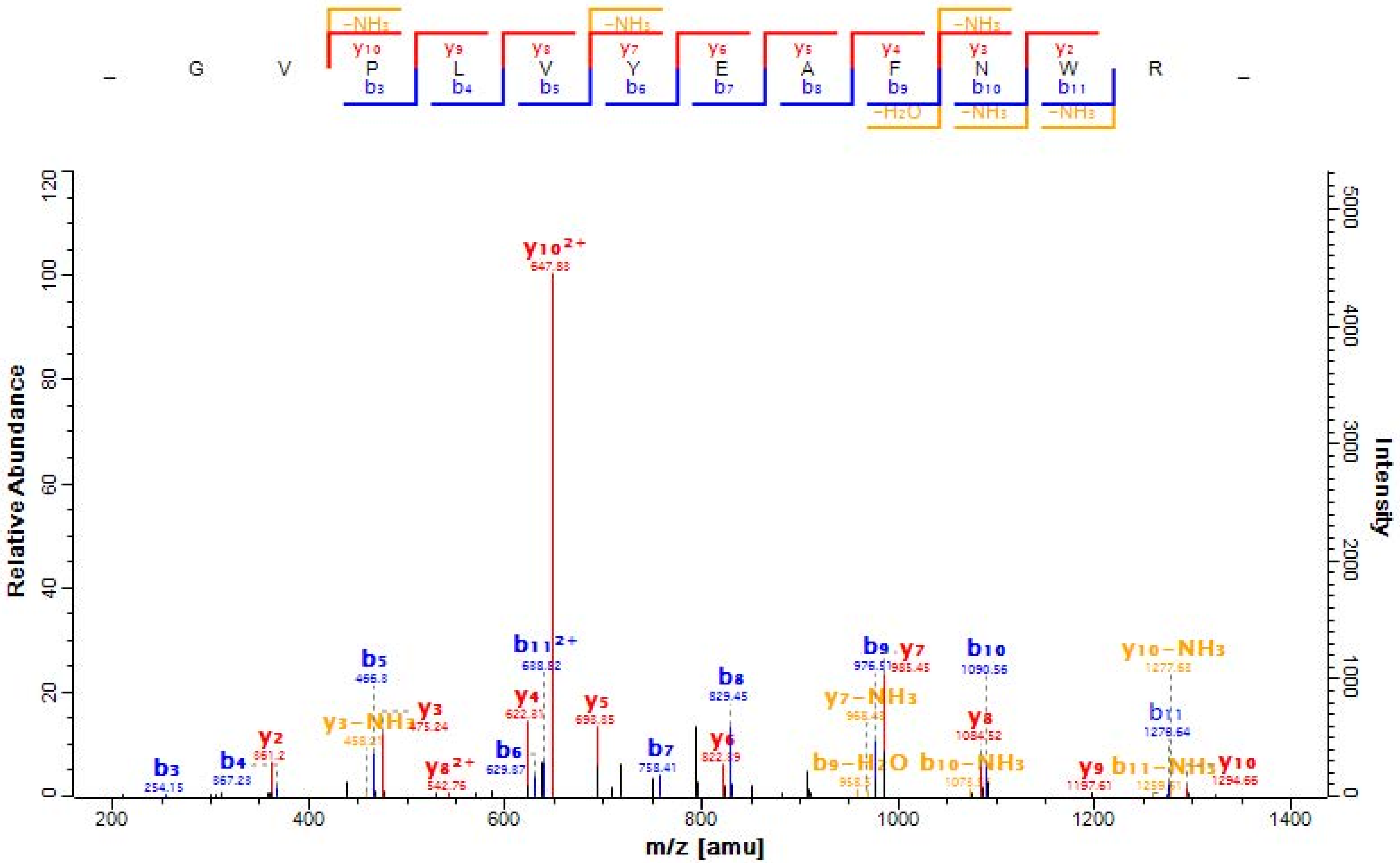
precursor information

Mass:	1230.61876
m/z:	616.31666
Charge:	2+
Retentiontime:	59.794971466064
Score:	100.017
Mass Error [ppm]:	0.14509
PEP:	0.0010463
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	51 %
Peak Coverage:	19 %
Protein Localisation:	193 ... 202

a ion		b2+ ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	44.05		72.04		72.04	1	A	9				
+0.012	191.1		219.1	-0.07	219.1	2	F	8	1161		580.8	-0.44
	338.2		366.2	-0.02	366.2	3	F	7	1014	+0.061	507.3	+0.13
	485.3		513.2	-0.08	513.2	4	F	6	866.5	-0.06	433.7	+0.04
	582.3		610.3		610.3	5	P	5	719.4	+0.005	360.2	-0.06
	669.3		697.3		697.3	6	S	4	622.3		622.3	
	816.4	+0.04	422.7	-0.06	844.4	7	F	3	535.3		535.3	
	930.5		958.4		958.4	8	N	2	388.2	+0.169	388.2	
	1030	-0.37	529.3	-0.15	1058	9	V	1	274.2		274.2	
						10	R	0	175.1	-0.04	175.1	

Scan number	8208	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	181.31



precursor information

Mass:	1449.74097
m/z:	725.87776
Charge:	2+
Retentiontime:	60.588134765625
Score:	181.3127
Mass Error [ppm]:	0.33318
PEP:	4.8217E-11
Precursor Type:	MULTI

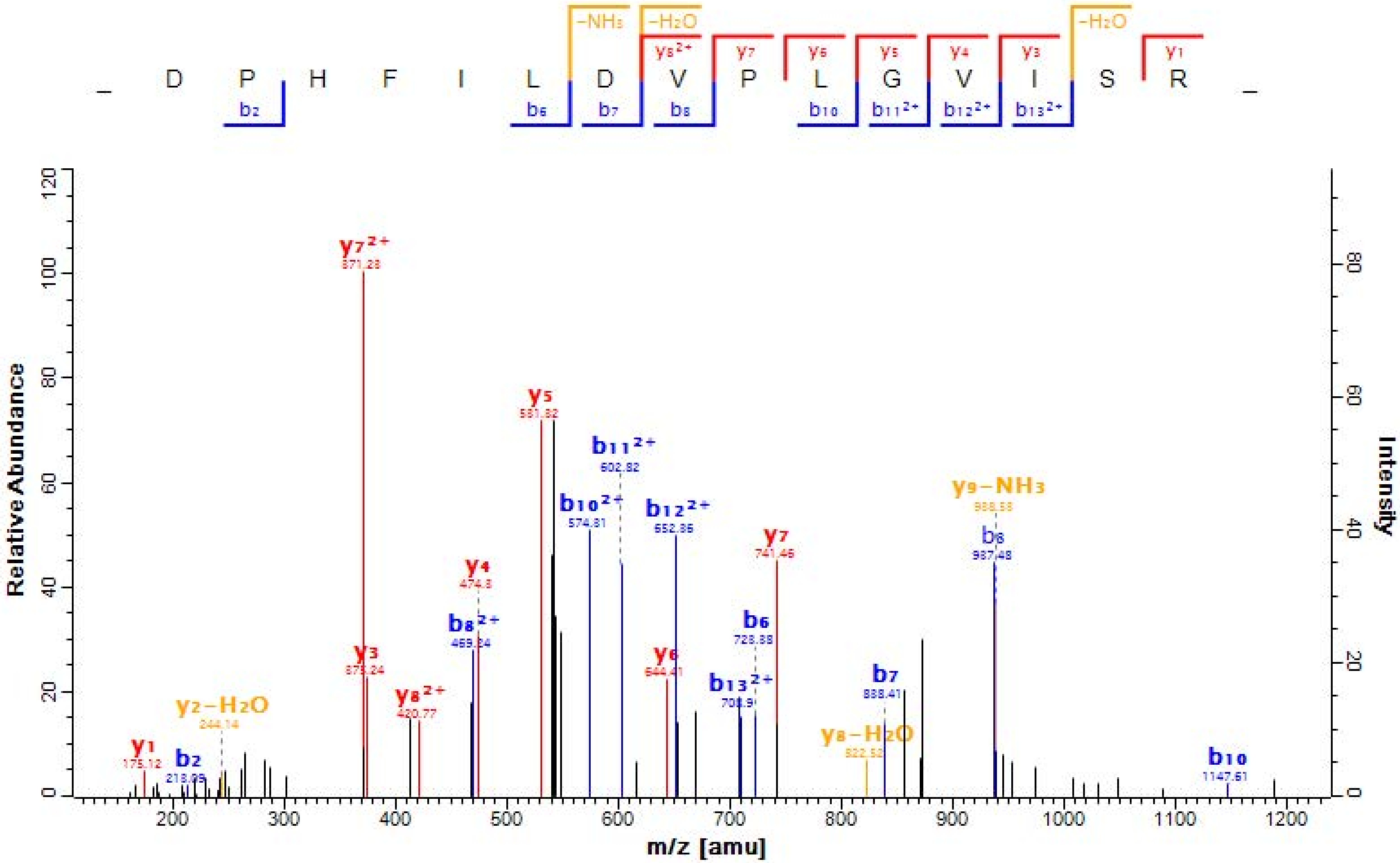
general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	73 %
Peak Coverage:	33 %
Protein Localisation:	458 ... 469

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	11				
	157.1		157.1	2	V	10	1393.7		1393.7	
	254.15	+0.0249	254.15	3	P	9	1294.7	+0.1145	647.83	+0.2214
	367.23	-0.007	367.23	4	L	8	1197.6	+0.0043	1197.6	
	466.3	+0.0543	466.3	5	V	7	1084.5	-0.005	542.76	-0.003
	629.37	+0.0423	629.37	6	Y	6	985.45	+0.0027	985.45	
	758.41	+0.0598	758.41	7	E	5	822.39	+0.0618	822.39	
	829.45	-0.059	829.45	8	A	4	693.35	+0.2185	693.35	
	976.51	-0.105	976.51	9	F	3	622.31	+0.0033	622.31	
	1090.6	-0.045	1090.6	10	N	2	475.24	+0.0329	475.24	
+0.4786	638.82	-0.019	1276.6	11	W	1	361.2	+0.0956	361.2	
				12	R	0	175.12		175.12	

Scan number 8241 **Raw file** LNCAP_Silac_23F10_set3_05

Method ITMS; CID **Pepti...** 86.94



precursor information

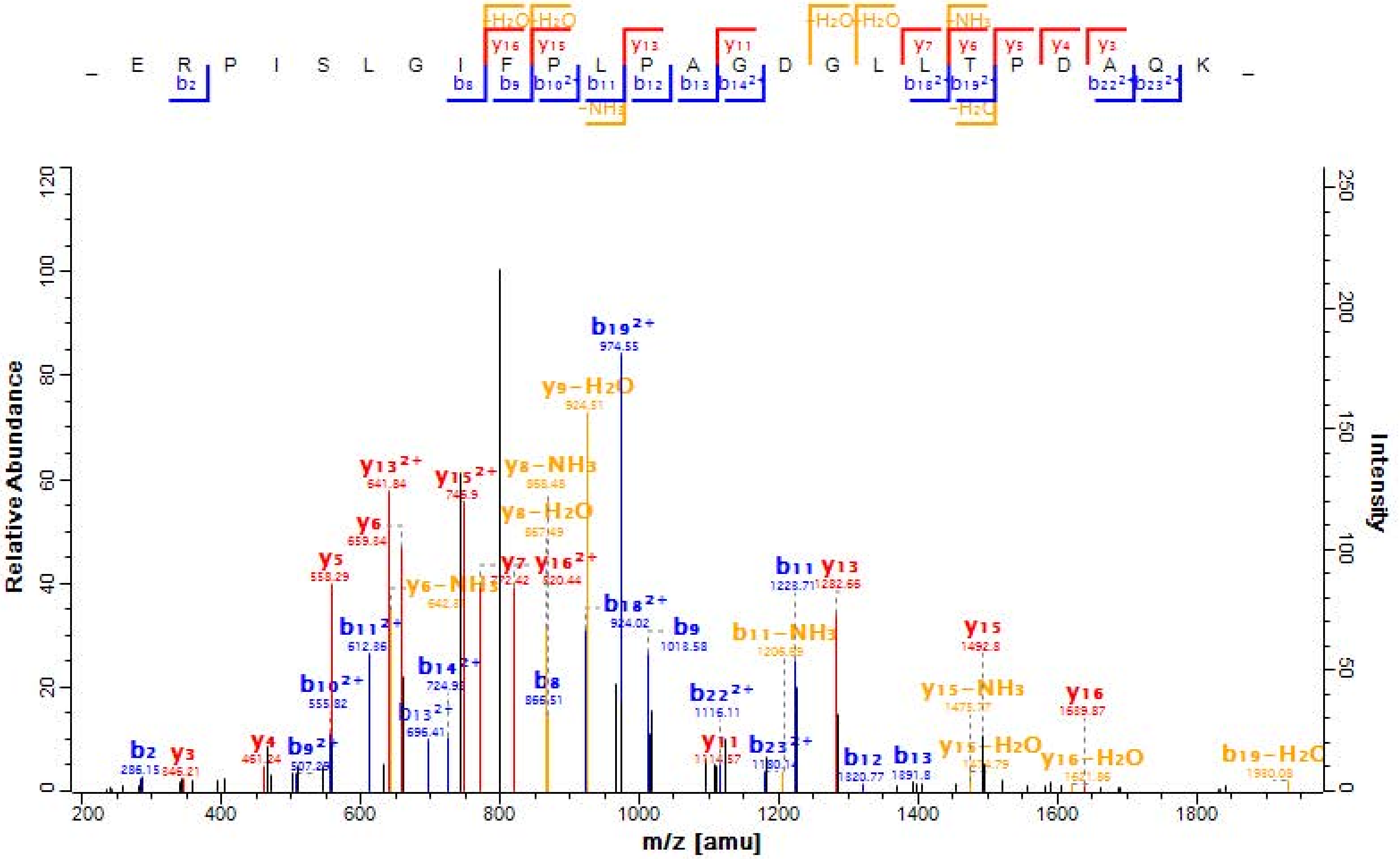
Mass:	1676.92571
m/z:	559.98251
Charge:	3+
Retentiontime:	60.888778686523
Score:	86.94421
Mass Error [ppm]:	0.42757
PEP:	0.00019272
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	56 %
Peak Coverage:	29 %
Protein Localisation:	142 ... 156

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	14				
	213.09	-0.009	213.09	2	P	13	1562.9		1562.9	
	350.15		350.15	3	H	12	1465.9		1465.9	
	497.21		497.21	4	F	11	1328.8		1328.8	
	610.3		610.3	5	I	10	1181.7		1181.7	
	723.38	-0.46	723.38	6	L	9	1068.6		1068.6	
	838.41	-0.146	838.41	7	D	8	955.56		955.56	
+0.0854	469.24	+0.0136	937.48	8	V	7	840.53		420.77	+0.3909
	1034.5		1034.5	9	P	6	741.46	+0.034	371.23	+0.0967
+0.2976	574.31	-0.064	1147.6	10	L	5	644.41	+0.0076	644.41	
+0.0757	602.82		1204.6	11	G	4	531.32	+0.0658	531.32	
+0.293	652.36		1303.7	12	V	3	474.3	+0.0177	474.3	
-0.181	708.9		1416.8	13	I	2	375.24	-0.031	375.24	
	1503.8		1503.8	14	S	1	262.15		262.15	
				15	R	0	175.12	+0.0187	175.12	

Scan number	8384	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	138.46



precursor information

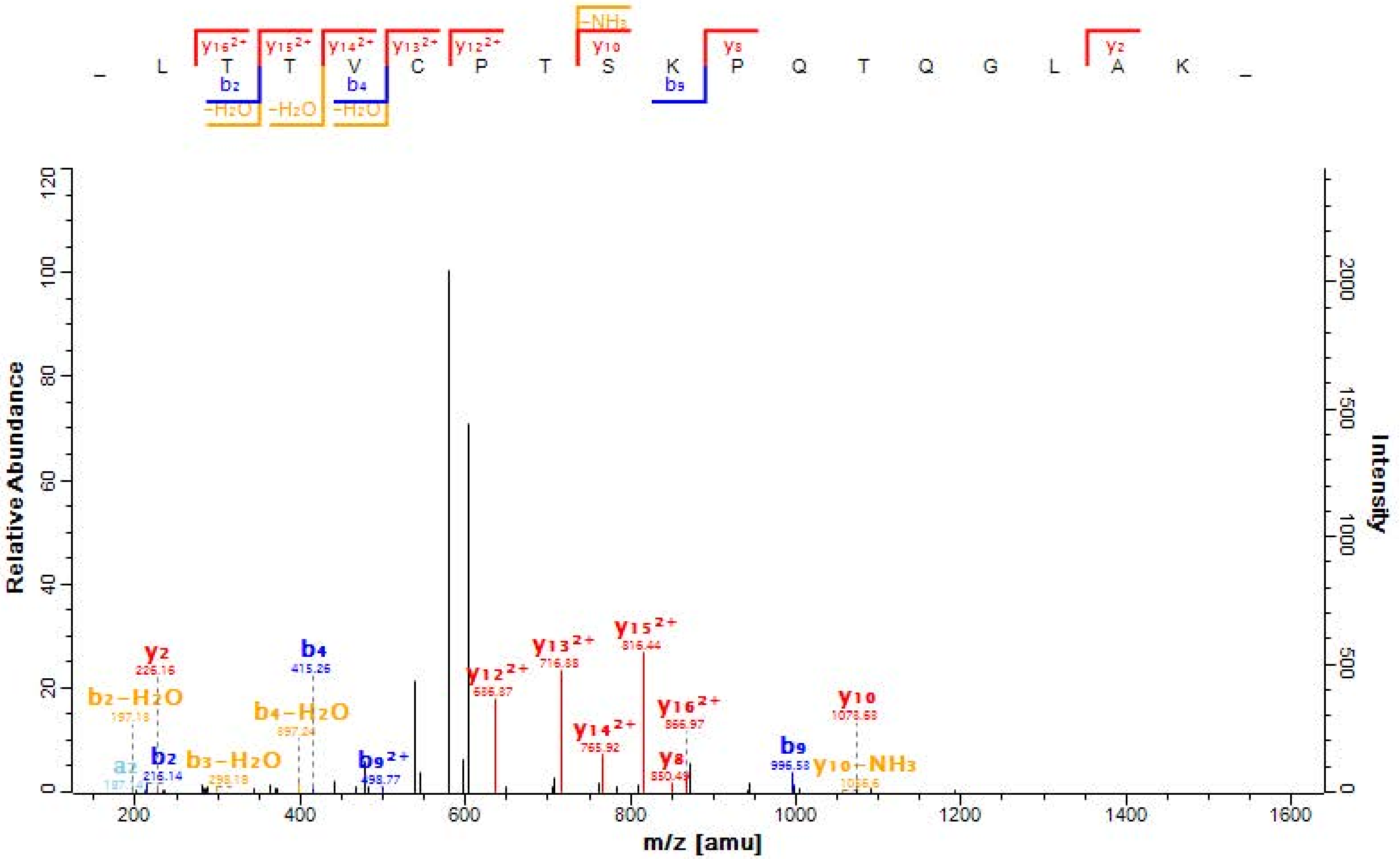
Mass:	2504.36448
m/z:	835.79544
Charge:	3+
Retentiontime:	62.261711120605
Score:	138.4552
Mass Error [ppm]:	0.24283
PEP:	1.6789E-22
Precursor Type:	MULTI

general information

Annotation:	17 of 24
AminoAcids Coverag	71 %
Intensity Coverage:	60 %
Peak Coverage:	39 %
Protein Localisation:	199 ... 222

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	23				
	286.15	-0.145	286.15	2	R	22	2376.3		2376.3	
	383.2		383.2	3	P	21	2220.2		2220.2	
	496.29		496.29	4	I	20	2123.2		2123.2	
	583.32		583.32	5	S	19	2010.1		2010.1	
	696.4		696.4	6	L	18	1923.1		1923.1	
	753.43		753.43	7	G	17	1810		1810	
	866.51	+0.1163	866.51	8	I	16	1753		1753	
+0.0918	507.29	-0.004	1013.6	9	F	15	1639.9	-0.006	820.44	+0.1734
+0.0772	555.82		1110.6	10	P	14	1492.8	-0.205	746.9	+0.2944
+0.3887	612.36	-0.079	1223.7	11	L	13	1395.7		1395.7	
	1320.8	+0.1771	1320.8	12	P	12	1282.7	-0.008	641.84	+0.0024
+0.0464	696.41	+0.1376	1391.8	13	A	11	1185.6		1185.6	
+0.2189	724.92		1448.8	14	G	10	1114.6	-0.04	1114.6	
	1563.9		1563.9	15	D	9	1057.6		1057.6	
	1620.9		1620.9	16	G	8	942.53		942.53	
	1734		1734	17	L	7	885.5		885.5	
-0.086	924.02		1847	18	L	6	772.42	-0.023	772.42	
+0.2044	974.55		1948.1	19	T	5	659.34	+0.0475	659.34	
	2045.1		2045.1	20	P	4	558.29	+0.0228	558.29	
	2160.2		2160.2	21	D	3	461.24	+0.1675	461.24	
+0.3422	1116.1		2231.2	22	A	2	346.21	+0.1056	346.21	
+0.0424	1180.1		2359.3	23	Q	1	275.17		275.17	
				24	K	0	147.11		147.11	

Scan number	894	**Raw file**	LNCAP_Silac_23F10_set3_05
Method	ITMS; CID	**Pepti...**	49.19



precursor information

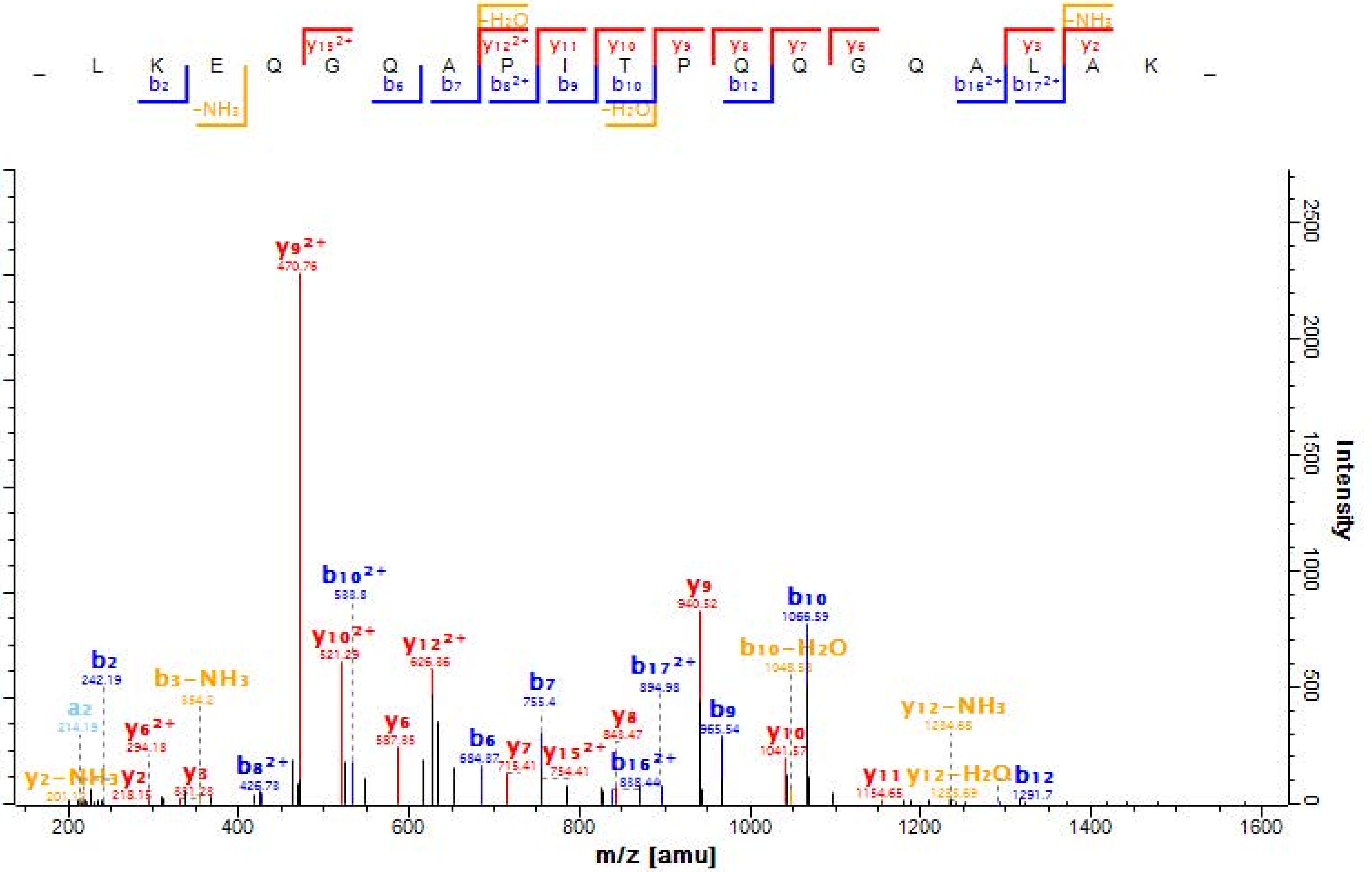
Mass:	1828.97207
m/z:	610.66463
Charge:	3+
Retentiontime:	12.447854995727
Score:	49.1875
Mass Error [ppm]:	0.20973
PEP:	0.01301
Precursor Type:	MULTI

general information

Annotation:	9 of 17
AminoAcids Coverag	53 %
Intensity Coverage:	26 %
Peak Coverage:	22 %
Protein Localisation:	250 ... 266

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	16				
-0.01	187.1		215.1	+0.017	215.1	2	T	15		1733		867	+0.27
	288.2		316.2		316.2	3	T	14		1632		816.4	+0.15
	387.3		415.3	-0.01	415.3	4	V	13		1531		765.9	+0.09
	547.3		575.3		575.3	5	C	12		1432		716.4	+0.12
	644.3		672.3		672.3	6	P	11		1272		636.4	+0.15
	745.4		773.4		773.4	7	T	10		1175		1175	
	832.4		860.4		860.4	8	S	9		1074	+0.201	1074	
	968.5	+0.174	498.8	-0.08	996.5	9	K	8		986.6		986.6	
	1066		1094		1094	10	P	7		850.5	+0.02	850.5	
	1194		1222		1222	11	Q	6		753.4		753.4	
	1295		1323		1323	12	T	5		625.4		625.4	
	1423		1451		1451	13	Q	4		524.3		524.3	
	1480		1508		1508	14	G	3		396.3		396.3	
	1593		1621		1621	15	L	2		339.2		339.2	
	1664		1692		1692	16	A	1		226.2	+0.064	226.2	
						17	K	0		155.1		155.1	

Scan number	1238	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	86



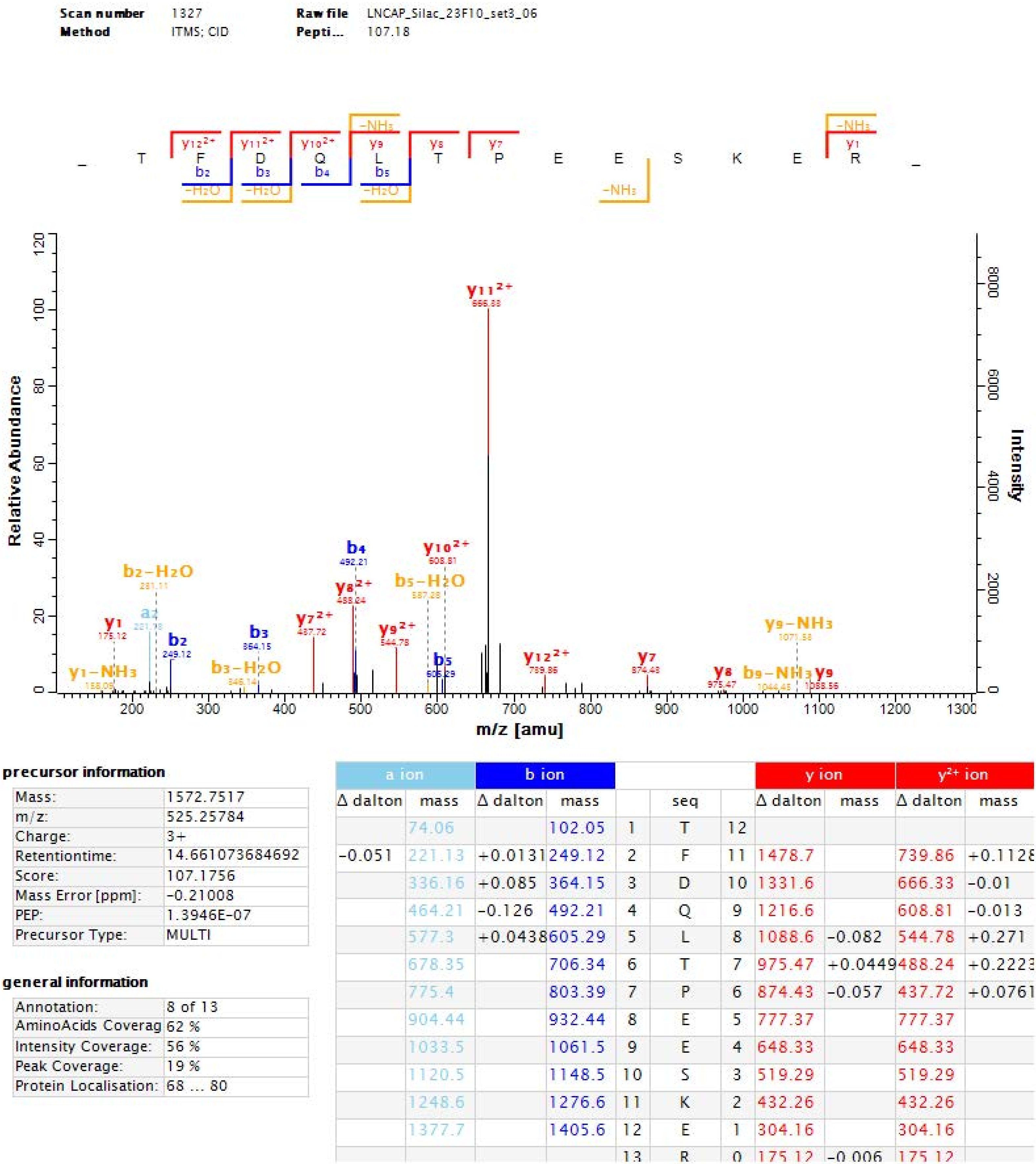
precursor information

Mass:	2005.0955
m/z:	669.37244
Charge:	3+
Retentiontime:	14.080313682556
Score:	86.00483
Mass Error [ppm]:	-0.071276
PEP:	3.03E-05
Precursor Type:	MULTI

general information

Annotation:	15 of 19
AminoAcids Coverag	79 %
Intensity Coverage:	63 %
Peak Coverage:	28 %
Protein Localisation:	129 ... 147

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	18				
+0.094	214.2		242.2	+0.187	242.2	2	K	17	1893		1893	
	343.2		371.2		371.2	3	E	16	1765		1765	
	471.3		499.3		499.3	4	Q	15	1636		1636	
	528.3		556.3		556.3	5	G	14	1508		754.4	+0.41
	656.4		684.4	-0.27	684.4	6	Q	13	1451		1451	
	727.4		755.4	+0.081	755.4	7	A	12	1323		1323	
	824.5	-0.31	426.7		852.5	8	P	11	1252		626.4	+0.03
	937.5		965.5	-0.01	965.5	9	I	10	1155	+0.06	1155	
	1039	+0.153	533.8	-0.05	1067	10	T	9	1042	+0	521.3	+0.22
	1136		1164		1164	11	P	8	940.5	-0.04	470.8	+0.20
	1264		1292	+0.163	1292	12	Q	7	843.5	+0.095	843.5	
	1392		1420		1420	13	Q	6	715.4	-0.05	715.4	
	1449		1477		1477	14	G	5	587.4	+0.086	294.2	+0.11
	1577		1605		1605	15	Q	4	530.3		530.3	
	1648	+0.261	838.4		1676	16	A	3	402.3		402.3	
	1761	+0.166	895		1789	17	L	2	331.2	+0.097	331.2	
	1832		1860		1860	18	A	1	218.1	+0.093	218.1	
						19	K	0	147.1		147.1	



Scan number	1327	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	107.18

precursor information

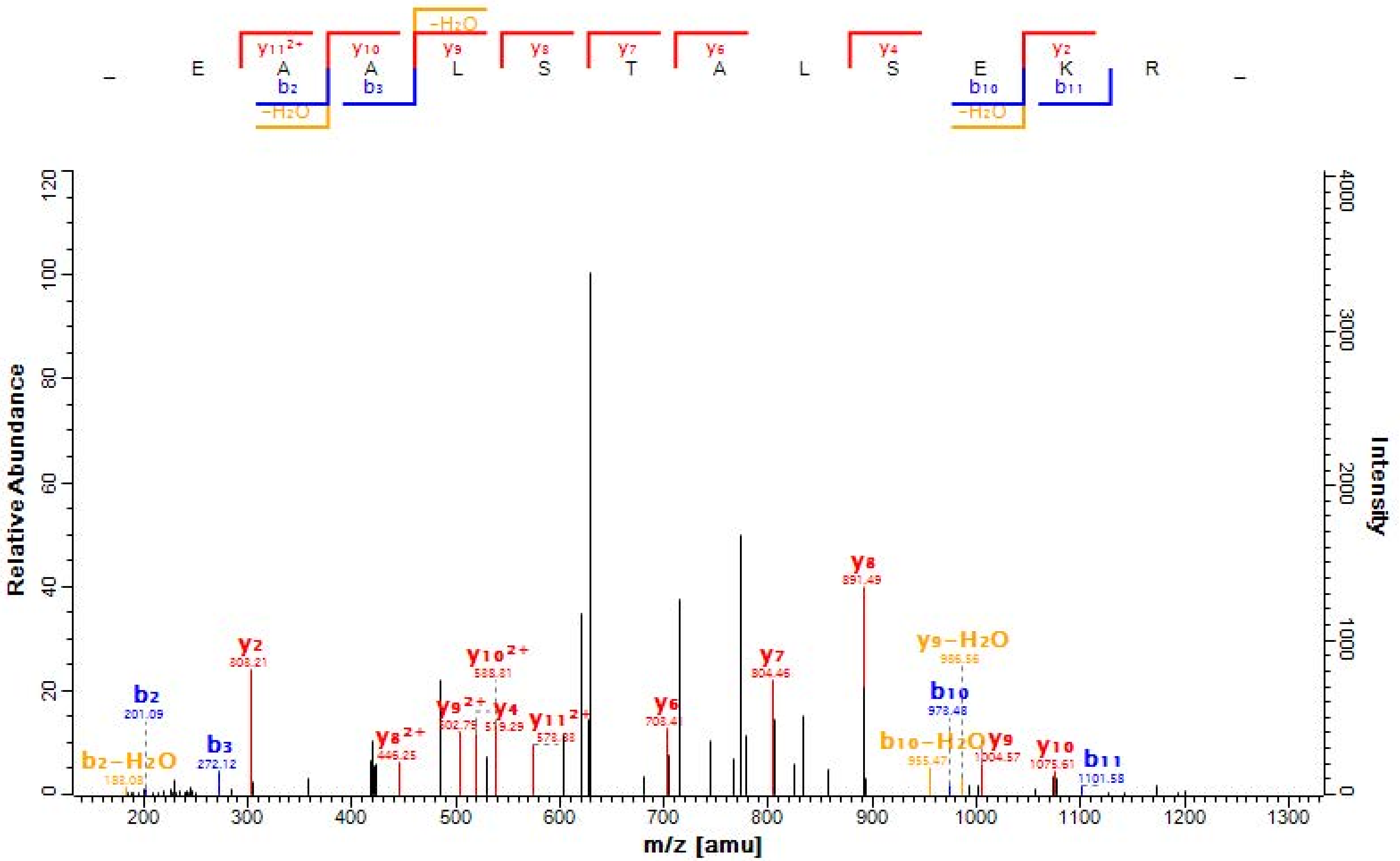
Mass:	1572.7517
m/z:	525.25784
Charge:	3+
Retentiontime:	14.661073684692
Score:	107.1756
Mass Error [ppm]:	-0.21008
PEP:	1.3946E-07
Precursor Type:	MULTI

general information

Annotation:	8 of 13
AminoAcids Coverag	62 %
Intensity Coverage:	56 %
Peak Coverage:	19 %
Protein Localisation:	68 ... 80

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.05	1	T	12				
-0.051	221.13	+0.0131	249.12	2	F	11	1478.7		739.86	+0.1128
	336.16	+0.085	364.15	3	D	10	1331.6		666.33	-0.01
	464.21	-0.126	492.21	4	Q	9	1216.6		608.81	-0.013
	577.3	+0.0438	605.29	5	L	8	1088.6	-0.082	544.78	+0.271
	678.35		706.34	6	T	7	975.47	+0.0449	488.24	+0.2223
	775.4		803.39	7	P	6	874.43	-0.057	437.72	+0.0761
	904.44		932.44	8	E	5	777.37		777.37	
	1033.5		1061.5	9	E	4	648.33		648.33	
	1120.5		1148.5	10	S	3	519.29		519.29	
	1248.6		1276.6	11	K	2	432.26		432.26	
	1377.7		1405.6	12	E	1	304.16		304.16	
				13	R	0	175.12	-0.006	175.12	

Scan number	1385	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	110.08



precursor information

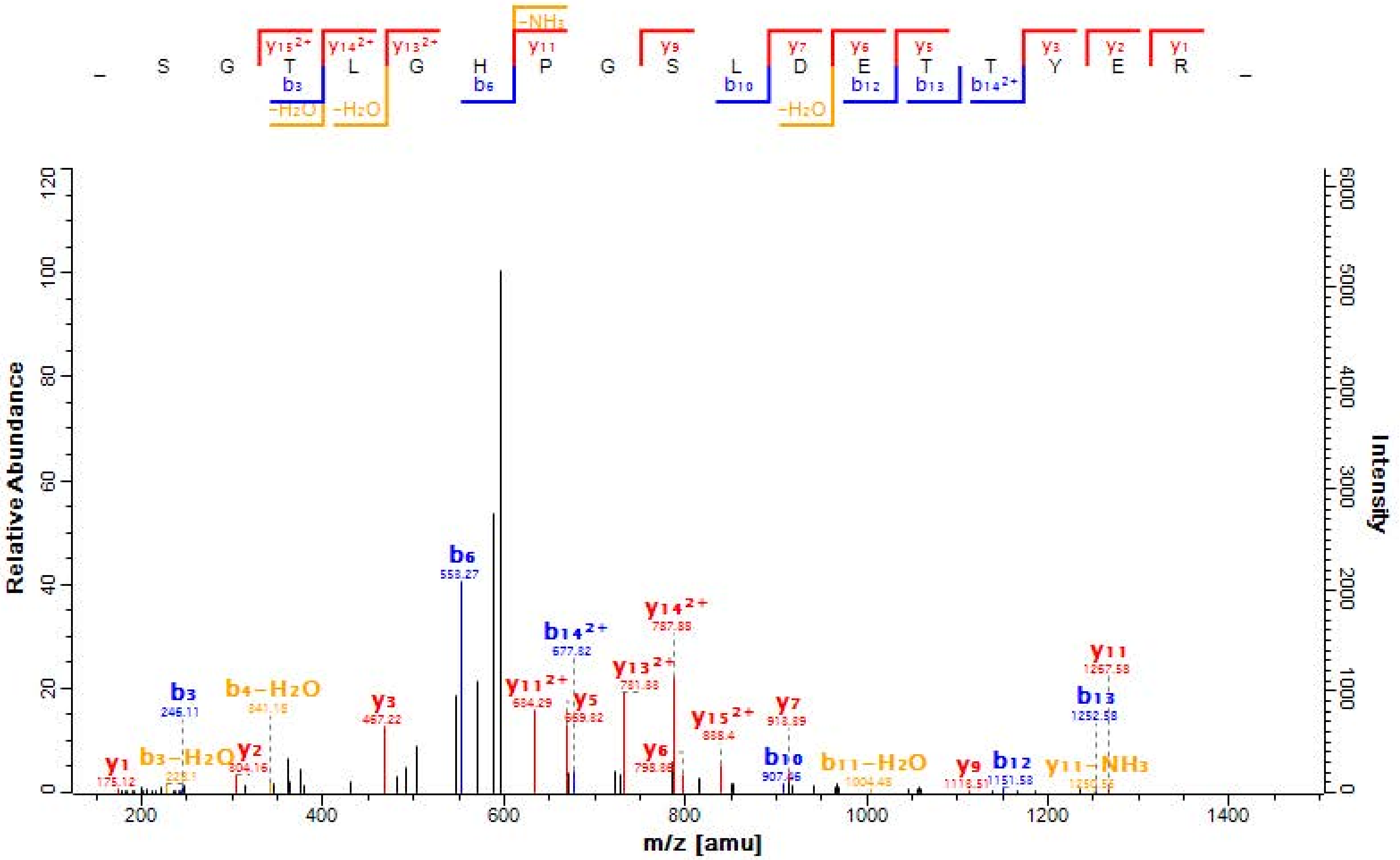
Mass:	1274.68305
m/z:	638.3488
Charge:	2+
Retentiontime:	15.021142005920
Score:	110.0771
Mass Error [ppm]:	0.017246
PEP:	2.6348E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	25 %
Peak Coverage:	20 %
Protein Localisation:	145 ... 156

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	11				
+0.165855	201.087	2	A	10	1146.648		573.8275	+0.444417
-0.05272	272.1241	3	A	9	1075.611	+0.000485	538.3089	+0.226951
	385.2082	4	L	8	1004.573	-0.00873	502.7904	+0.398584
	472.2402	5	S	7	891.4894	+0.035176	446.2483	+0.020633
	573.2879	6	T	6	804.4574	-0.07763	804.4574	
	644.325	7	A	5	703.4097	-0.05333	703.4097	
	757.409	8	L	4	632.3726		632.3726	
	844.4411	9	S	3	519.2885	+0.127418	519.2885	
-0.03103	973.4837	10	E	2	432.2565		432.2565	
-0.02333	1101.579	11	K	1	303.2139	+0.061048	303.2139	
		12	R	0	175.119		175.119	

Scan number	1474	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	110.97



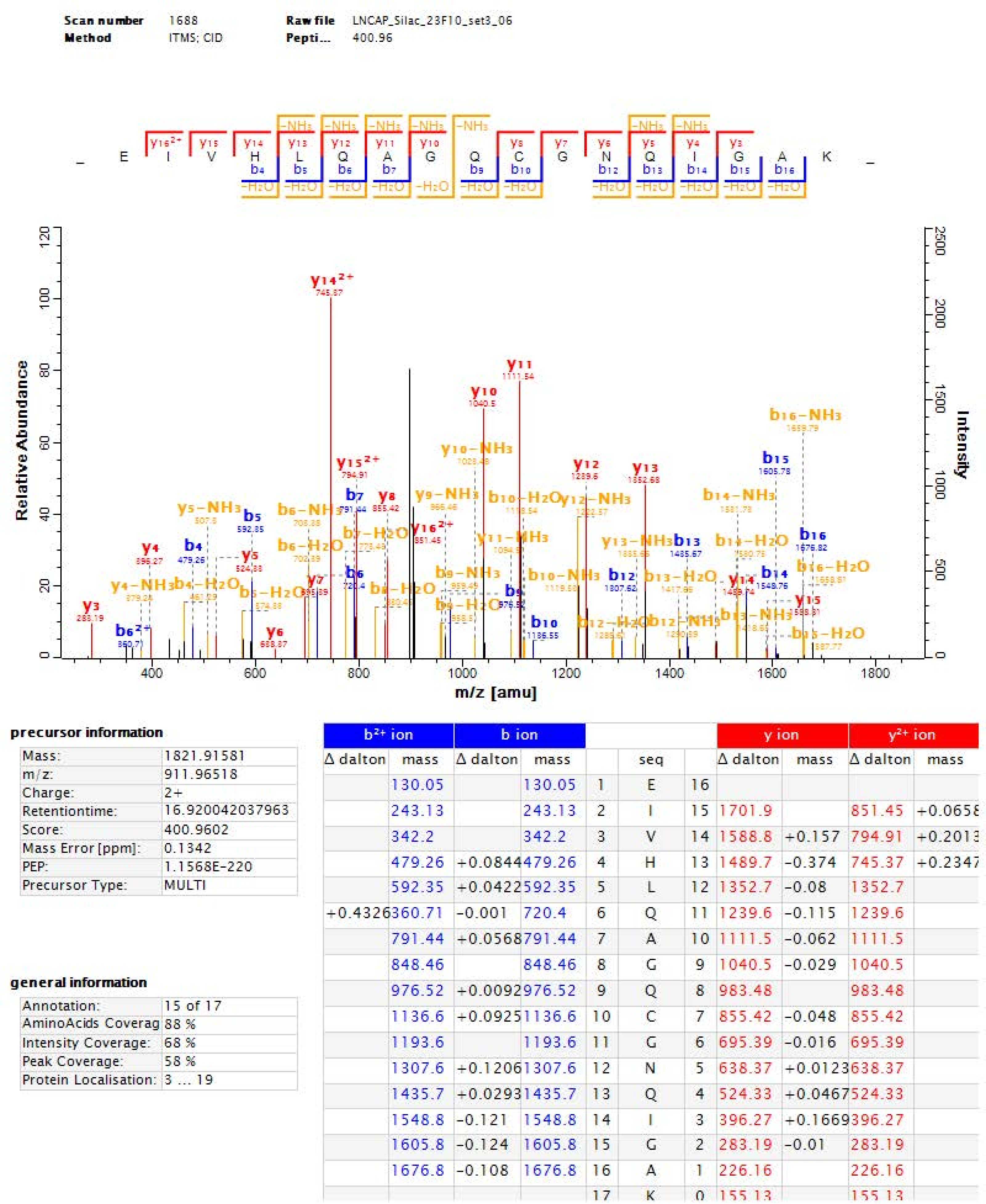
precursor information

Mass:	1818.83808
m/z:	607.28664
Charge:	3+
Retentiontime:	15.554471969604
Score:	110.9721
Mass Error [ppm]:	-0.18575
PEP:	1.5379E-08
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	35 %
Peak Coverage:	21 %
Protein Localisation:	81 ... 97

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		88.039	1	S	16				
	145.06		145.06	2	G	15	1732.8		1732.8	
	246.11	-0.016	246.11	3	T	14	1675.8		838.4	+0.125
	359.19		359.19	4	L	13	1574.7		787.88	+0.208
	416.21		416.21	5	G	12	1461.7		731.33	+0.145
	553.27	+0.1627	553.27	6	H	11	1404.6		1404.6	
	650.33		650.33	7	P	10	1267.6	+0.0406	634.29	+0.237
	707.35		707.35	8	G	9	1170.5		1170.5	
	794.38		794.38	9	S	8	1113.5	-0.084	1113.5	
	907.46	+0.156	907.46	10	L	7	1026.5		1026.5	
	1022.5		1022.5	11	D	6	913.39	+0.1253	913.39	
	1151.5	+0.0121	1151.5	12	E	5	798.36	-0.025	798.36	
	1252.6	+0.1575	1252.6	13	T	4	669.32	-0.017	669.32	
+0.2028	677.32		1353.6	14	T	3	568.27		568.27	
	1516.7		1516.7	15	Y	2	467.22	-0.048	467.22	
	1645.7		1645.7	16	E	1	304.16	+0.0873	304.16	
				17	R	0	175.12	-0.218	175.12	



Scan number	1688	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	400.96

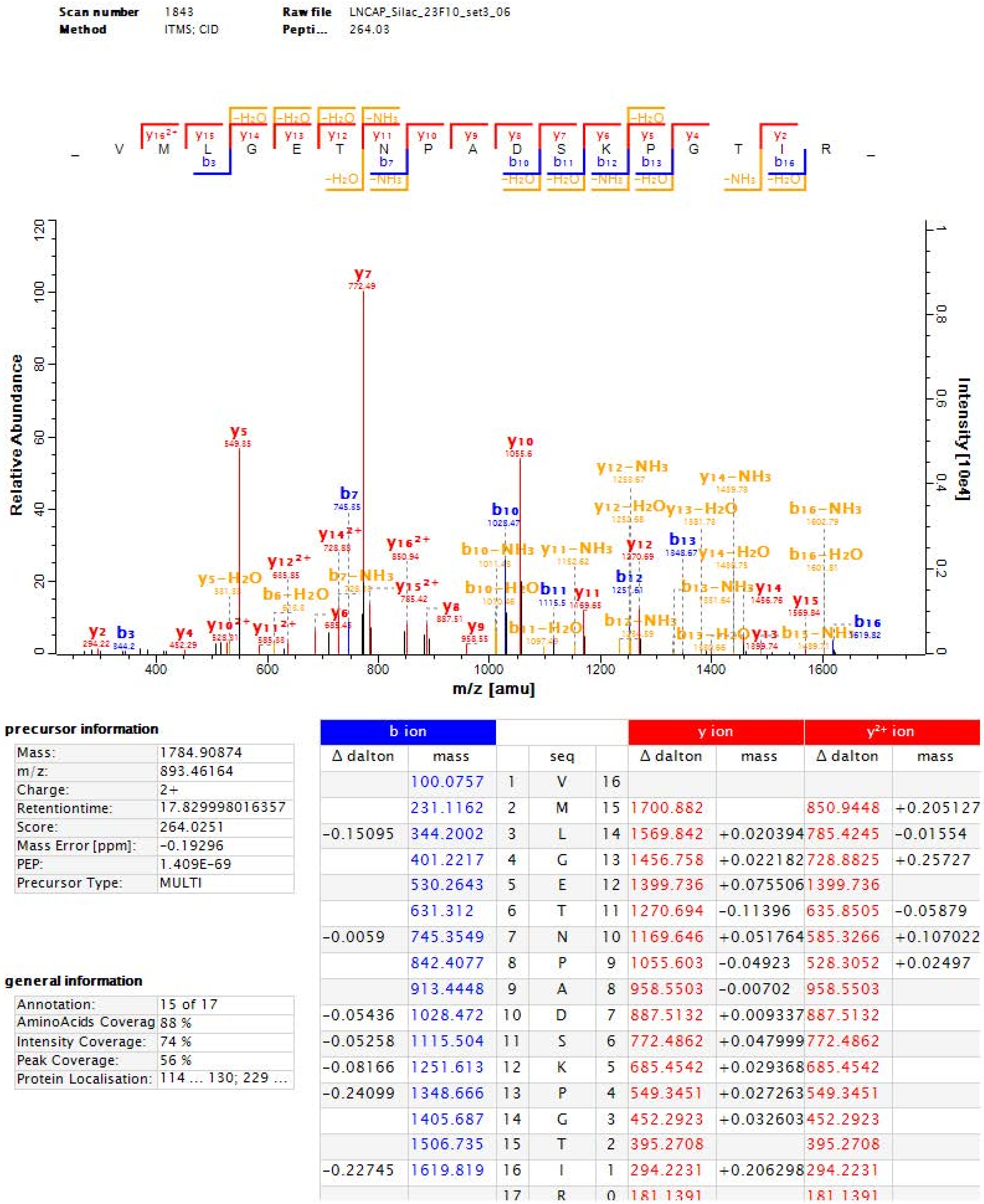
precursor information

Mass:	1821.91581
m/z:	911.96518
Charge:	2+
Retentiontime:	16.920042037963
Score:	400.9602
Mass Error [ppm]:	0.1342
PEP:	1.1568E-220
Precursor Type:	MULTI

general information

Annotation:	15 of 17
AminoAcids Coverag	88 %
Intensity Coverage:	68 %
Peak Coverage:	58 %
Protein Localisation:	3 ... 19

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	16				
	243.13		243.13	2	I	15	1701.9		851.45	+0.0658
	342.2		342.2	3	V	14	1588.8	+0.157	794.91	+0.2013
	479.26	+0.0844	479.26	4	H	13	1489.7	-0.374	745.37	+0.2347
	592.35	+0.0422	592.35	5	L	12	1352.7	-0.08	1352.7	
+0.4326	360.71	-0.001	720.4	6	Q	11	1239.6	-0.115	1239.6	
	791.44	+0.0568	791.44	7	A	10	1111.5	-0.062	1111.5	
	848.46		848.46	8	G	9	1040.5	-0.029	1040.5	
	976.52	+0.0092	976.52	9	Q	8	983.48		983.48	
	1136.6	+0.0925	1136.6	10	C	7	855.42	-0.048	855.42	
	1193.6		1193.6	11	G	6	695.39	-0.016	695.39	
	1307.6	+0.1206	1307.6	12	N	5	638.37	+0.0123	638.37	
	1435.7	+0.0293	1435.7	13	Q	4	524.33	+0.0467	524.33	
	1548.8	-0.121	1548.8	14	I	3	396.27	+0.1669	396.27	
	1605.8	-0.124	1605.8	15	G	2	283.19	-0.01	283.19	
	1676.8	-0.108	1676.8	16	A	1	226.16		226.16	
				17	K	0	155.13		155.13	



Scan number	1843	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	264.03

precursor information

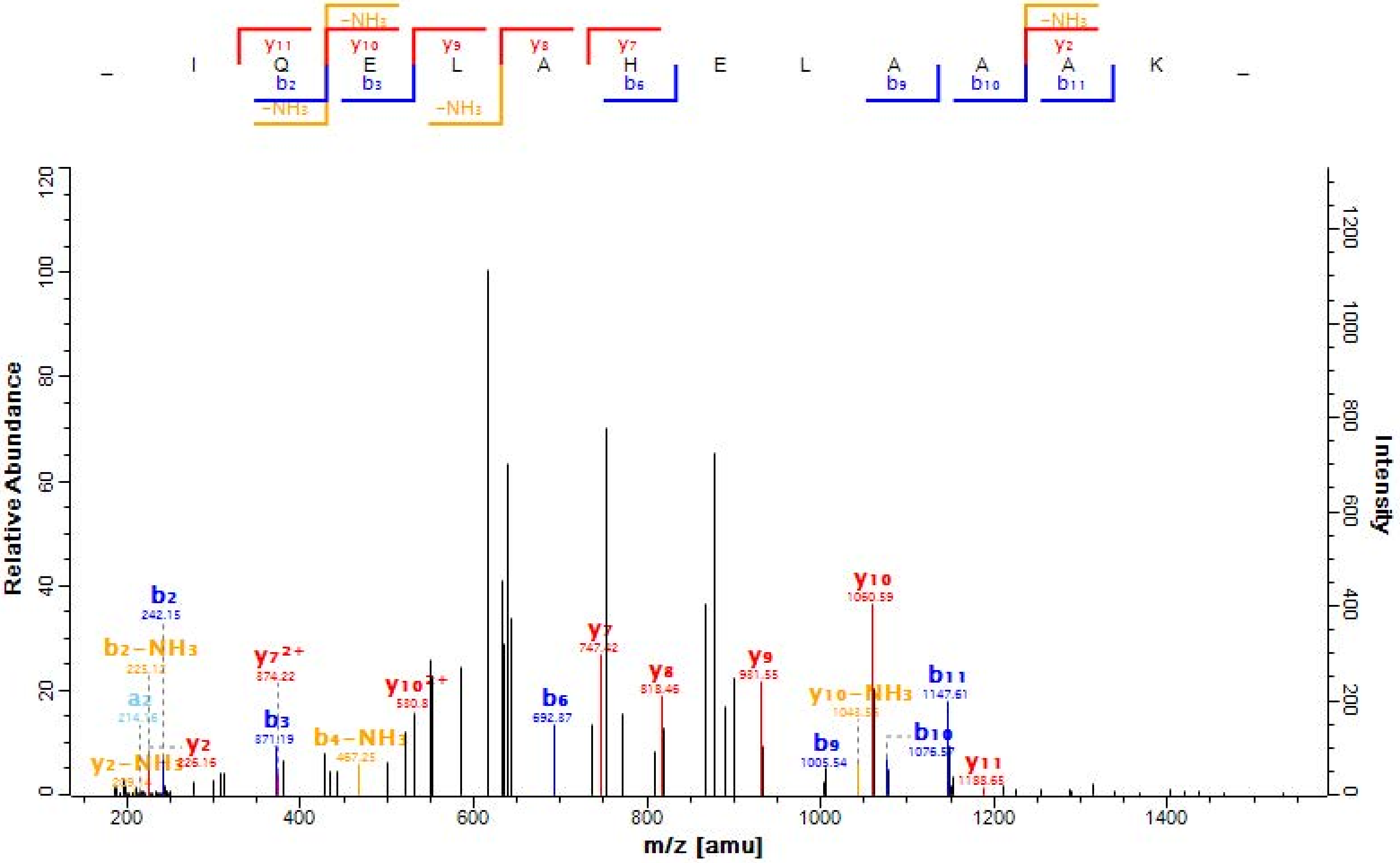
Mass:	1784.90874
m/z:	893.46164
Charge:	2+
Retentiontime:	17.829998016357
Score:	264.0251
Mass Error [ppm]:	-0.19296
PEP:	1.409E-69
Precursor Type:	MULTI

general information

Annotation:	15 of 17
AminoAcids Coverag	88 %
Intensity Coverage:	74 %
Peak Coverage:	56 %
Protein Localisation:	114 ... 130; 229 ...

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	16				
	231.1162	2	M	15	1700.882		850.9448	+0.205127
-0.15095	344.2002	3	L	14	1569.842	+0.020394	785.4245	-0.01554
	401.2217	4	G	13	1456.758	+0.022182	728.8825	+0.25727
	530.2643	5	E	12	1399.736	+0.075506	1399.736	
	631.312	6	T	11	1270.694	-0.11396	635.8505	-0.05879
-0.0059	745.3549	7	N	10	1169.646	+0.051764	585.3266	+0.107022
	842.4077	8	P	9	1055.603	-0.04923	528.3052	+0.02497
	913.4448	9	A	8	958.5503	-0.00702	958.5503	
-0.05436	1028.472	10	D	7	887.5132	+0.009337	887.5132	
-0.05258	1115.504	11	S	6	772.4862	+0.047999	772.4862	
-0.08166	1251.613	12	K	5	685.4542	+0.029368	685.4542	
-0.24099	1348.666	13	P	4	549.3451	+0.027263	549.3451	
	1405.687	14	G	3	452.2923	+0.032603	452.2923	
	1506.735	15	T	2	395.2708		395.2708	
-0.22745	1619.819	16	I	1	294.2231	+0.206298	294.2231	
		17	R	0	181.1391		181.1391	

Scan number	2179	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	90.73



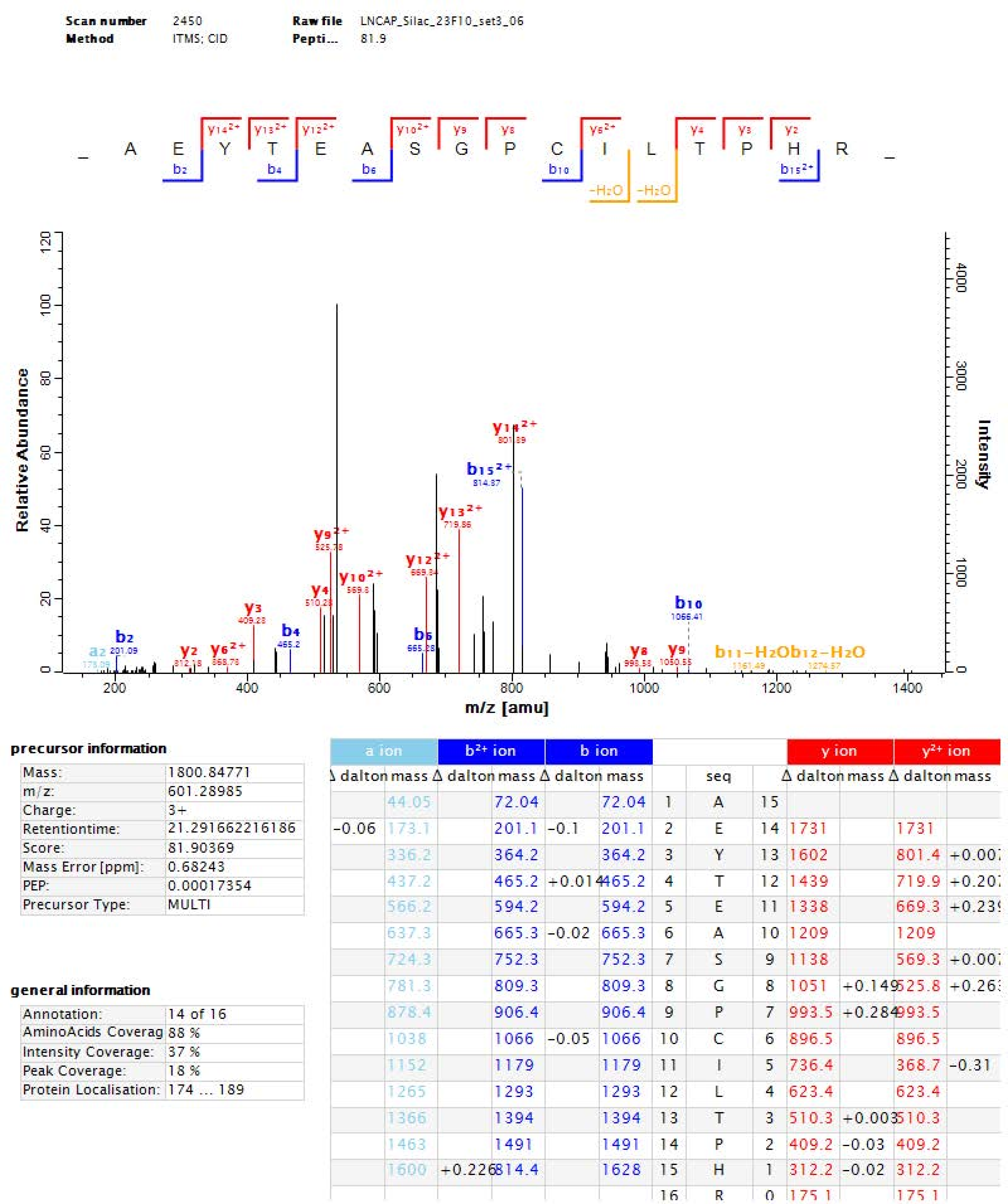
precursor information

Mass:	1955.00332
m/z:	652.67505
Charge:	3+
Retentiontime:	19.741809844970
Score:	90.73092
Mass Error [ppm]:	-0.24509
PEP:	0.0029921
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	18 %
Peak Coverage:	18 %
Protein Localisation:	184 ... 195

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	11				
+0.2848	214.16	+0.0089	242.15	2	Q	10	1188.6	+0.04	1188.6	
	343.2	+0.1565	371.19	3	E	9	1060.6	-0.091	530.8	-0.037
	456.28		484.28	4	L	8	931.55	+0.0791	931.55	
	527.32		555.31	5	A	7	818.46	+0.0573	818.46	
	664.38	+0.0249	692.37	6	H	6	747.42	+0.0808	374.22	-0.483
	793.42		821.42	7	E	5	610.37		610.37	
	906.5		934.5	8	L	4	481.32		481.32	
	977.54	+0.1397	1005.5	9	A	3	368.24		368.24	
	1048.6	-0.162	1076.6	10	A	2	297.2		297.2	
	1119.6	+0.0067	1147.6	11	A	1	226.16	-0.02	226.16	
				12	K	0	155.13		155.13	



Scan number	2450	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	81.9

precursor information

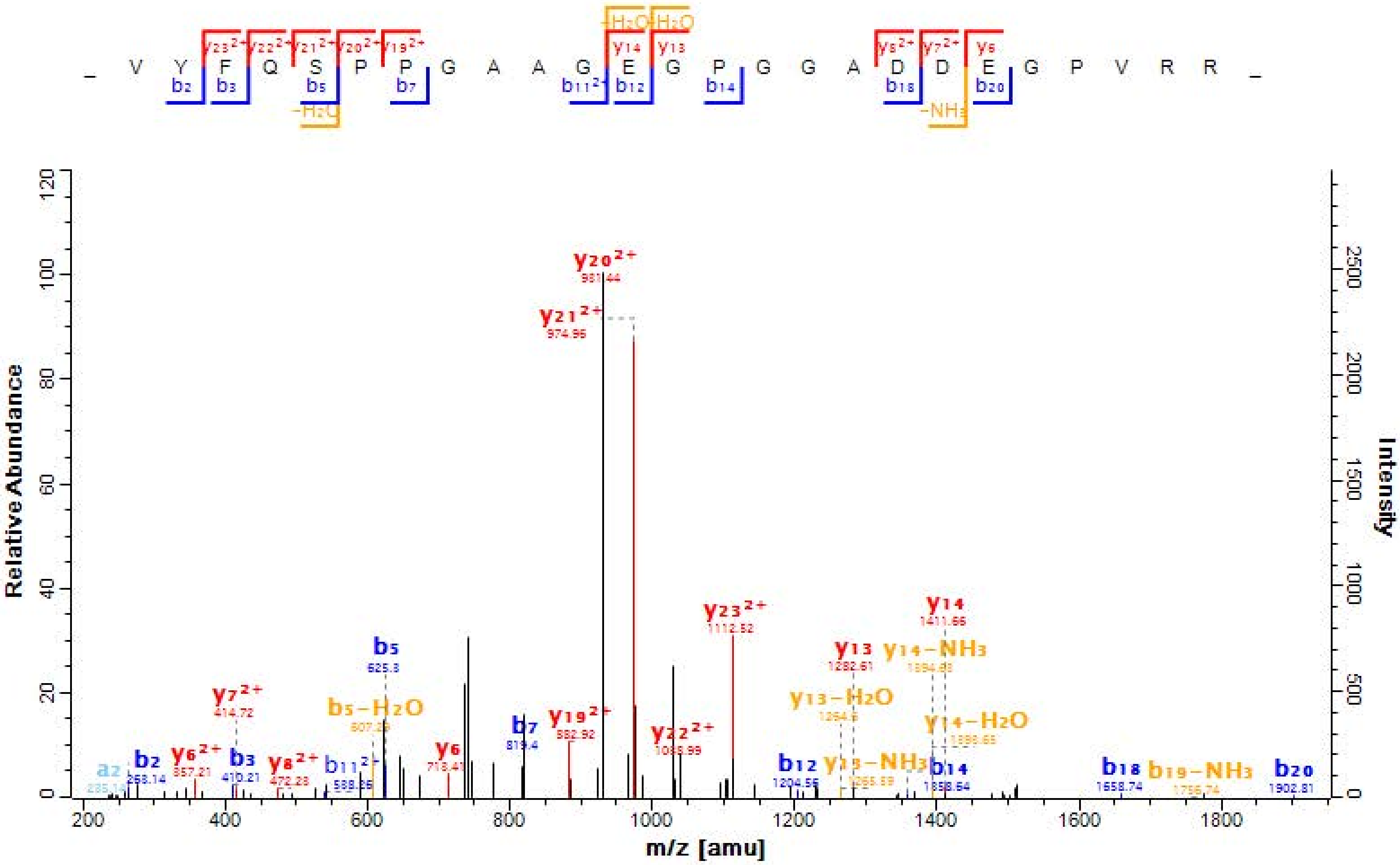
Mass:	1800.84771
m/z:	601.28985
Charge:	3+
Retentiontime:	21.291662216186
Score:	81.90369
Mass Error [ppm]:	0.68243
PEP:	0.00017354
Precursor Type:	MULTI

general information

Annotation:	14 of 16
AminoAcids Coverag	88 %
Intensity Coverage:	37 %
Peak Coverage:	18 %
Protein Localisation:	174 ... 189

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	44.05		72.04		72.04	1	A	15				
−0.06	173.1		201.1	−0.1	201.1	2	E	14	1731		1731	
	336.2		364.2		364.2	3	Y	13	1602		801.4	+0.00
	437.2		465.2	+0.014	465.2	4	T	12	1439		719.9	+0.20
	566.2		594.2		594.2	5	E	11	1338		669.3	+0.23
	637.3		665.3	−0.02	665.3	6	A	10	1209		1209	
	724.3		752.3		752.3	7	S	9	1138		569.3	+0.00
	781.3		809.3		809.3	8	G	8	1051	+0.149	525.8	+0.26
	878.4		906.4		906.4	9	P	7	993.5	+0.284	993.5	
	1038		1066	−0.05	1066	10	C	6	896.5		896.5	
	1152		1179		1179	11	I	5	736.4		368.7	−0.31
	1265		1293		1293	12	L	4	623.4		623.4	
	1366		1394		1394	13	T	3	510.3	+0.003	510.3	
	1463		1491		1491	14	P	2	409.2	−0.03	409.2	
	1600	+0.226	814.4		1628	15	H	1	312.2	−0.02	312.2	
						16	R	0	175.1		175.1	

Scan number	2460	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	97.69



precursor information

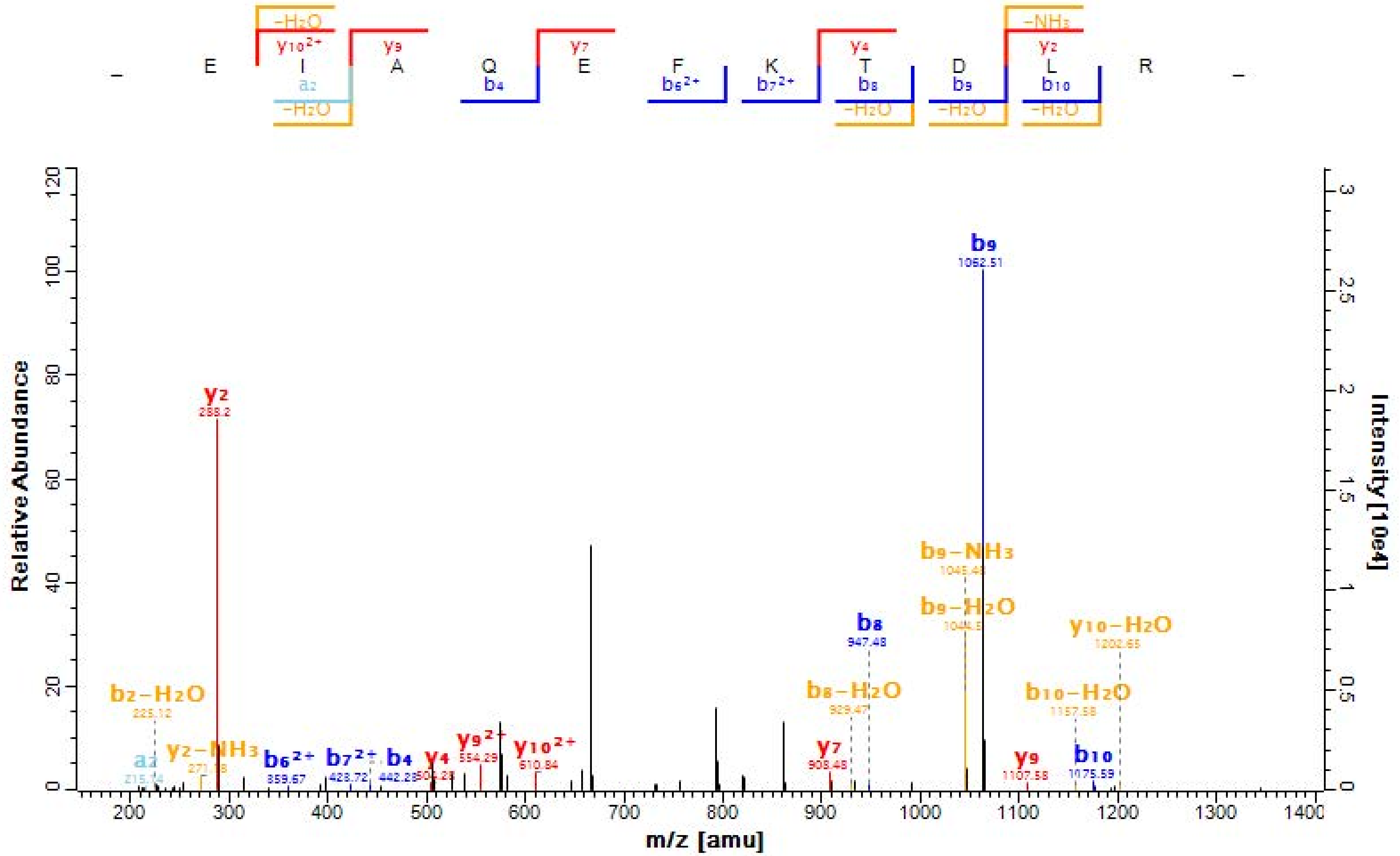
Mass:	2485.16186
m/z:	829.39456
Charge:	3+
Retentiontime:	21.352262496948
Score:	97.68987
Mass Error [ppm]:	-0.14271
PEP:	3.2518E-08
Precursor Type:	MULTI

general information

Annotation:	13 of 25
AminoAcids Coverag	52 %
Intensity Coverage:	44 %
Peak Coverage:	28 %
Protein Localisation:	80 ... 104

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.08		100.1		100.1	1	V	24				
+0.107	235.1		263.1	-0.05	263.1	2	Y	23	2387		2387	
	382.2		410.2	+0.104	410.2	3	F	22	2224		1113	+0.19
	510.3		538.3		538.3	4	Q	21	2077		1039	-0.01
	597.3		625.3	+0.178	625.3	5	S	20	1949		975	+0.25
	694.4		722.4		722.4	6	P	19	1862		931.4	+0.06
	791.4		819.4	-0.09	819.4	7	P	18	1765		882.9	+0.21
	848.4		876.4		876.4	8	G	17	1668		1668	
	919.5		947.5		947.5	9	A	16	1611		1611	
	990.5		1018		1018	10	A	15	1540		1540	
	1048	-0.14	538.3		1076	11	G	14	1469		1469	
	1177		1205	-0.1	1205	12	E	13	1412	+0.015	1412	
	1234		1262		1262	13	G	12	1283	-0.08	1283	
	1331		1359	+0.114	1359	14	P	11	1226		1226	
	1388		1416		1416	15	G	10	1129		1129	
	1445		1473		1473	16	G	9	1072		1072	
	1516		1544		1544	17	A	8	1014		1014	
	1631		1659	+0.009	1659	18	D	7	943.5		472.2	+0.23
	1746		1774		1774	19	D	6	828.4		414.7	+0.08
	1875		1903	-0.35	1903	20	E	5	713.4	+0.113	357.2	+0.22
	1932		1960		1960	21	G	4	584.4		584.4	
	2029		2057		2057	22	P	3	527.3		527.3	
	2128		2156		2156	23	V	2	430.3		430.3	
	2284		2312		2312	24	R	1	331.2		331.2	
						25	R	0	175.1		175.1	

Scan number	2553	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	106.62



precursor information

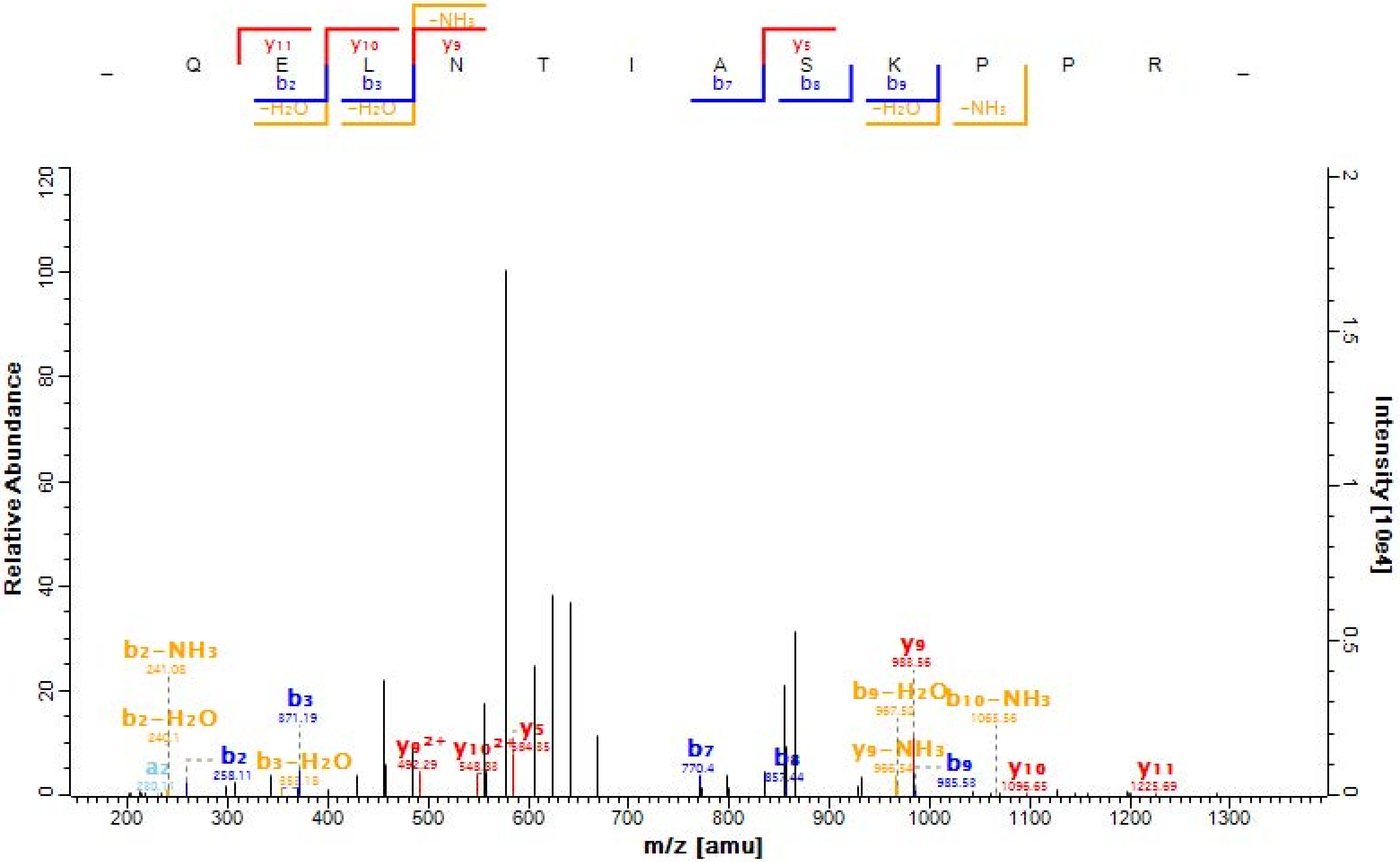
Mass:	1348.6988
m/z:	675.35667
Charge:	2+
Retentiontime:	21.871187210083
Score:	106.6184
Mass Error [ppm]:	0.086268
PEP:	0.00024987
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	52 %
Peak Coverage:	24 %
Protein Localisation:	74 ... 84

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.1		130		130	1	E	10				
+0.054	215.1		243.1		243.1	2	I	9	1221		610.8	+0.2
	286.2		314.2		314.2	3	A	8	1108	-0.05	554.3	+0.24
	414.2		442.2	+0.212	442.2	4	Q	7	1037		1037	
	543.3		571.3		571.3	5	E	6	908.5	+0.029	908.5	
	690.3	-0.45	359.7		718.3	6	F	5	779.4		779.4	
	818.4	-0.5	423.7		846.4	7	K	4	632.4		632.4	
	919.5		947.5	-0.13	947.5	8	T	3	504.3	-0.03	504.3	
	1035		1063	+0.026	1063	9	D	2	403.2		403.2	
	1148		1176	+0.139	1176	10	L	1	288.2	-0.01	288.2	
						11	R	0	175.1		175.1	

Scan number	2719	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	74.39



precursor information

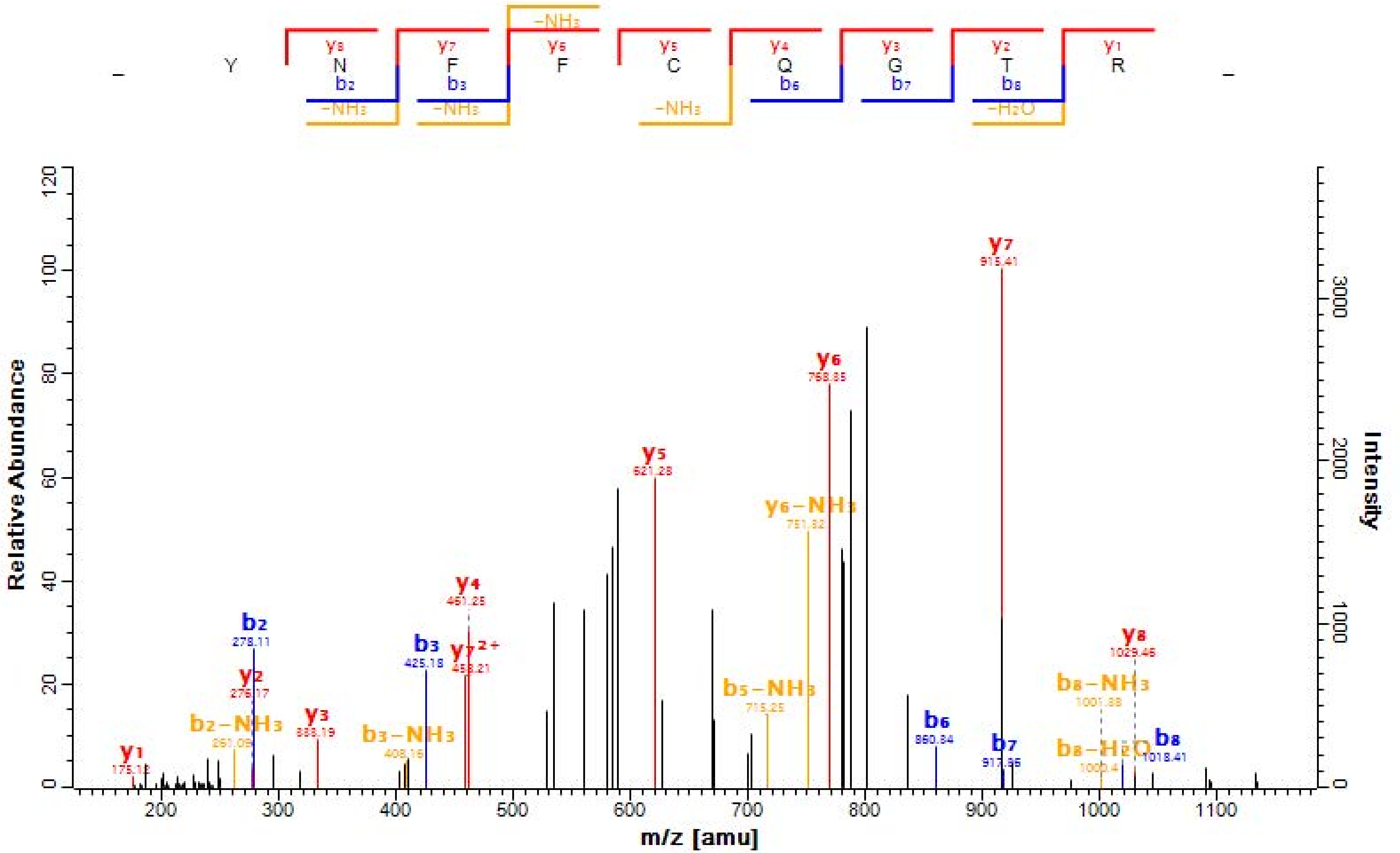
Mass:	1352.74119
m/z:	677.37787
Charge:	2+
Retentiontime:	22.845481872558
Score:	74.39246
Mass Error [ppm]:	-0.015371
PEP:	0.0028494
Precursor Type:	MULTI

general information

Annotation:	7 of 12
AminoAcids Coverag	58 %
Intensity Coverage:	11 %
Peak Coverage:	22 %
Protein Localisation:	298 ... 309

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	101.07		129.07	1	Q	11				
+0.048	230.11	-0.131	258.11	2	E	10	1225.7	+0.3671	1225.7	
	343.2	+0.0935	371.19	3	L	9	1096.6	+0.109	548.83	+0.3424
	457.24		485.24	4	N	8	983.56	+0.0736	492.29	+0.0091
	558.29		586.28	5	T	7	869.52		869.52	
	671.37		699.37	6	I	6	768.47		768.47	
	742.41	-0.13	770.4	7	A	5	655.39		655.39	
	829.44	+0.03	857.44	8	S	4	584.35	+0.0953	584.35	
	957.54	+0.1173	985.53	9	K	3	497.32		497.32	
	1054.6		1082.6	10	P	2	369.22		369.22	
	1151.6		1179.6	11	P	1	272.17		272.17	
				12	R	0	175.12		175.12	

Scan number	3673	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	125.75

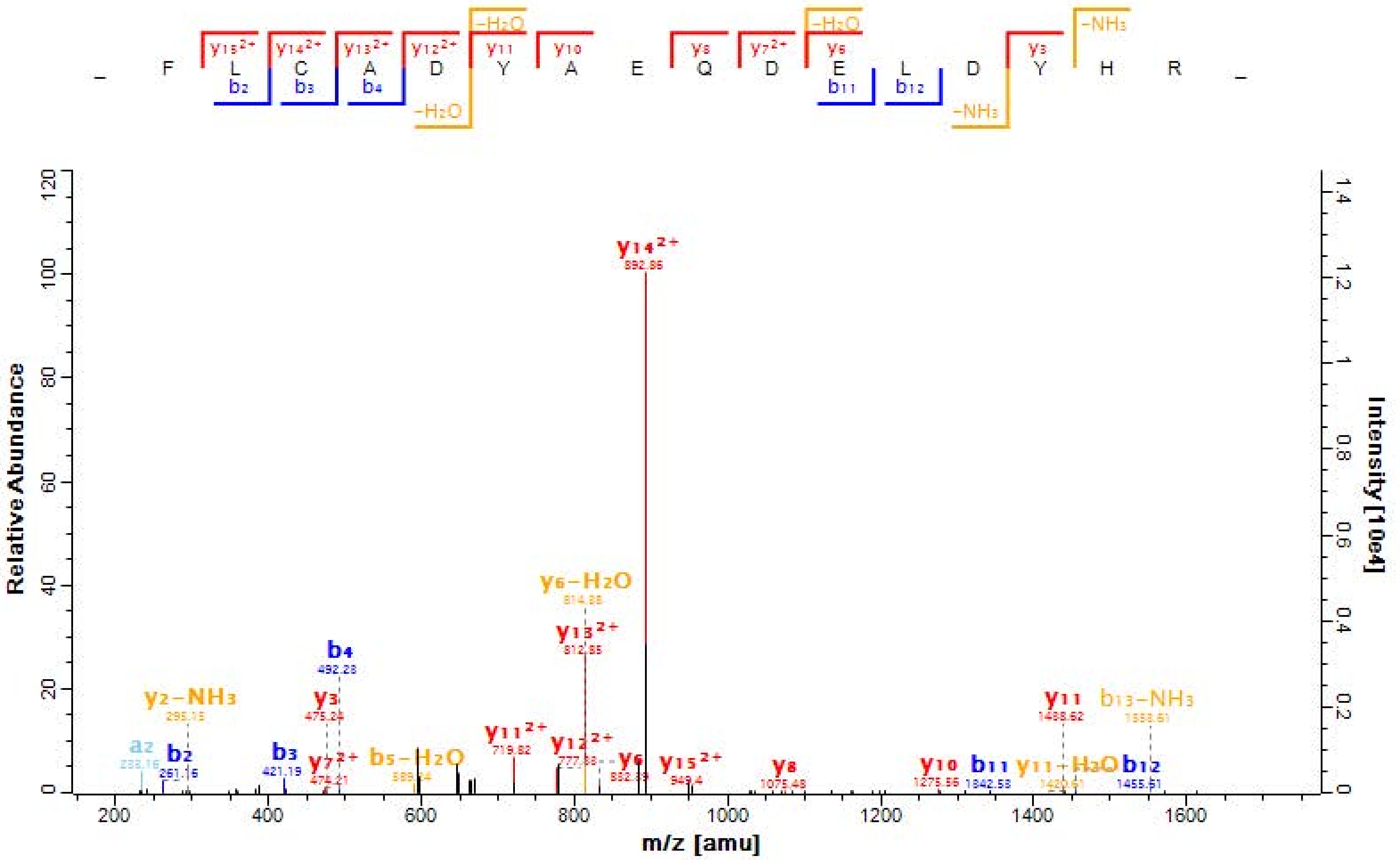


precursor information

Mass:	1191.51312
m/z:	596.76384
Charge:	2+
Retentiontime:	28.098049163818
Score:	125.7467
Mass Error [ppm]:	-0.0022455
PEP:	0.0012086
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	39 %
Peak Coverage:	23 %
Protein Localisation:	119 ... 127

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	164.0706	1	Y	8				
-0.01063	278.1135	2	N	7	1029.457	+0.053789	1029.457	
-0.11304	425.1819	3	F	6	915.4141	-0.0198	458.2107	+0.113751
	572.2504	4	F	5	768.3457	+0.082428	768.3457	
	732.281	5	C	4	621.2773	+0.007958	621.2773	
-0.13671	860.3396	6	Q	3	461.2467	+0.020845	461.2467	
+0.029087	917.361	7	G	2	333.1881	-0.00743	333.1881	
-0.03037	1018.409	8	T	1	276.1666	+0.031428	276.1666	
		9	R	0	175.119	+0.010442	175.119	

Scan number	3716	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	122.64



precursor information

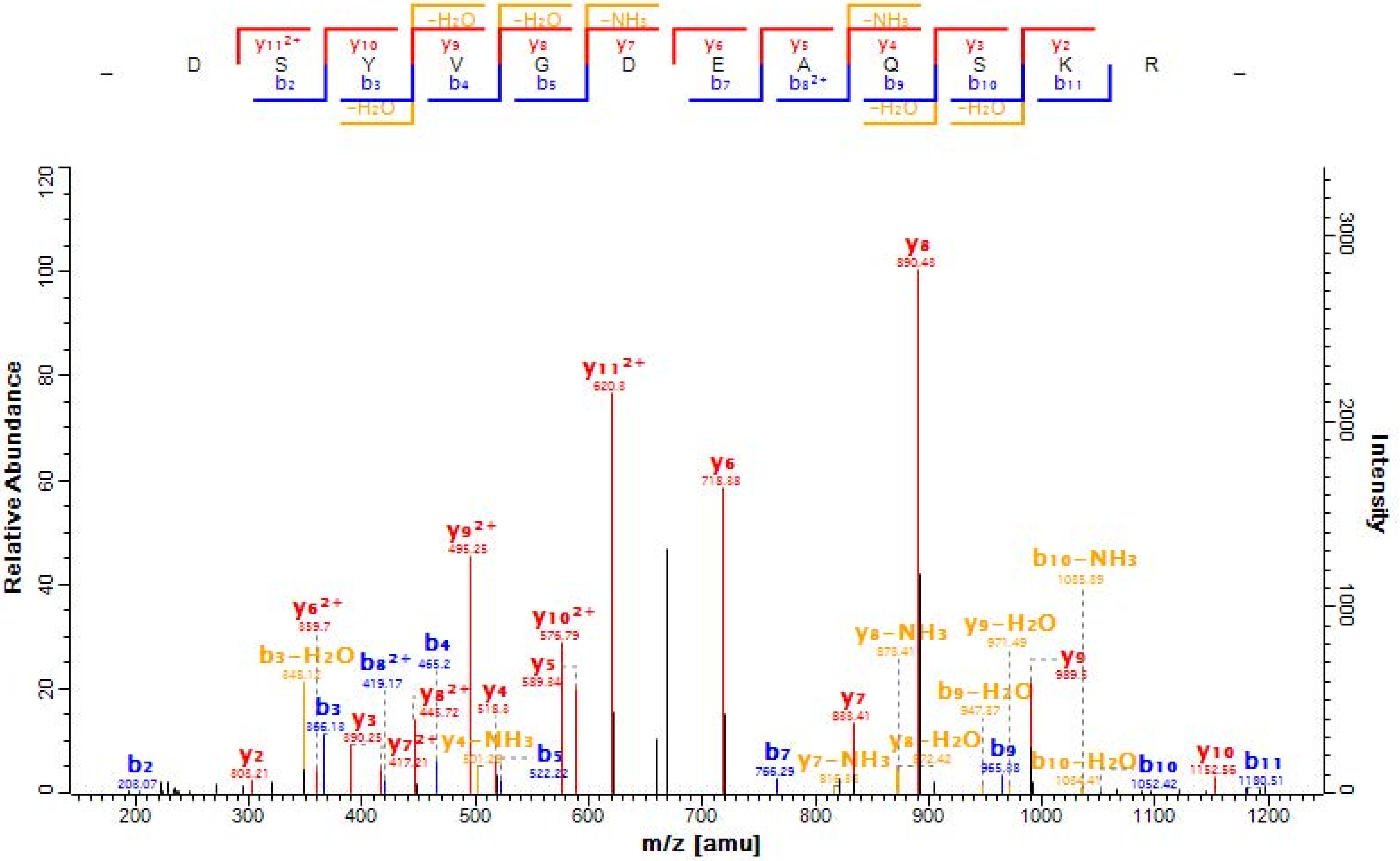
Mass:	2043.86304
m/z:	682.29496
Charge:	3+
Retentiontime:	28.339681625366
Score:	122.6385
Mass Error [ppm]:	-0.1059
PEP:	7.2704E-10
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	61 %
Peak Coverage:	19 %
Protein Localisation:	985 ... 1000

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08		148.08	1	F	15				
+0.074	233.16	+0.0591	261.16	2	L	14	1897.8		949.4	-0.073
	393.2	+0.0271	421.19	3	C	13	1784.7		892.86	+0.2736
	464.23	-0.076	492.23	4	A	12	1624.7		812.85	+0.2819
	579.26		607.25	5	D	11	1553.7		777.33	+0.0374
	742.32		770.32	6	Y	10	1438.6	+0.476	719.82	+0.1366
	813.36		841.35	7	A	9	1275.6	-0.149	1275.6	
	942.4		970.4	8	E	8	1204.5		1204.5	
	1070.5		1098.5	9	Q	7	1075.5	+0.476	1075.5	
	1185.5		1213.5	10	D	6	947.42		474.21	+0.0745
	1314.5	+0.1205	1342.5	11	E	5	832.39	-0.148	832.39	
	1427.6	+0.0909	1455.6	12	L	4	703.35		703.35	
	1542.6		1570.6	13	D	3	590.27		590.27	
	1705.7		1733.7	14	Y	2	475.24	+0.2198	475.24	
	1842.8		1870.8	15	H	1	312.18		312.18	
				16	R	0	175.12		175.12	

Scan number	380	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	222.25



precursor information

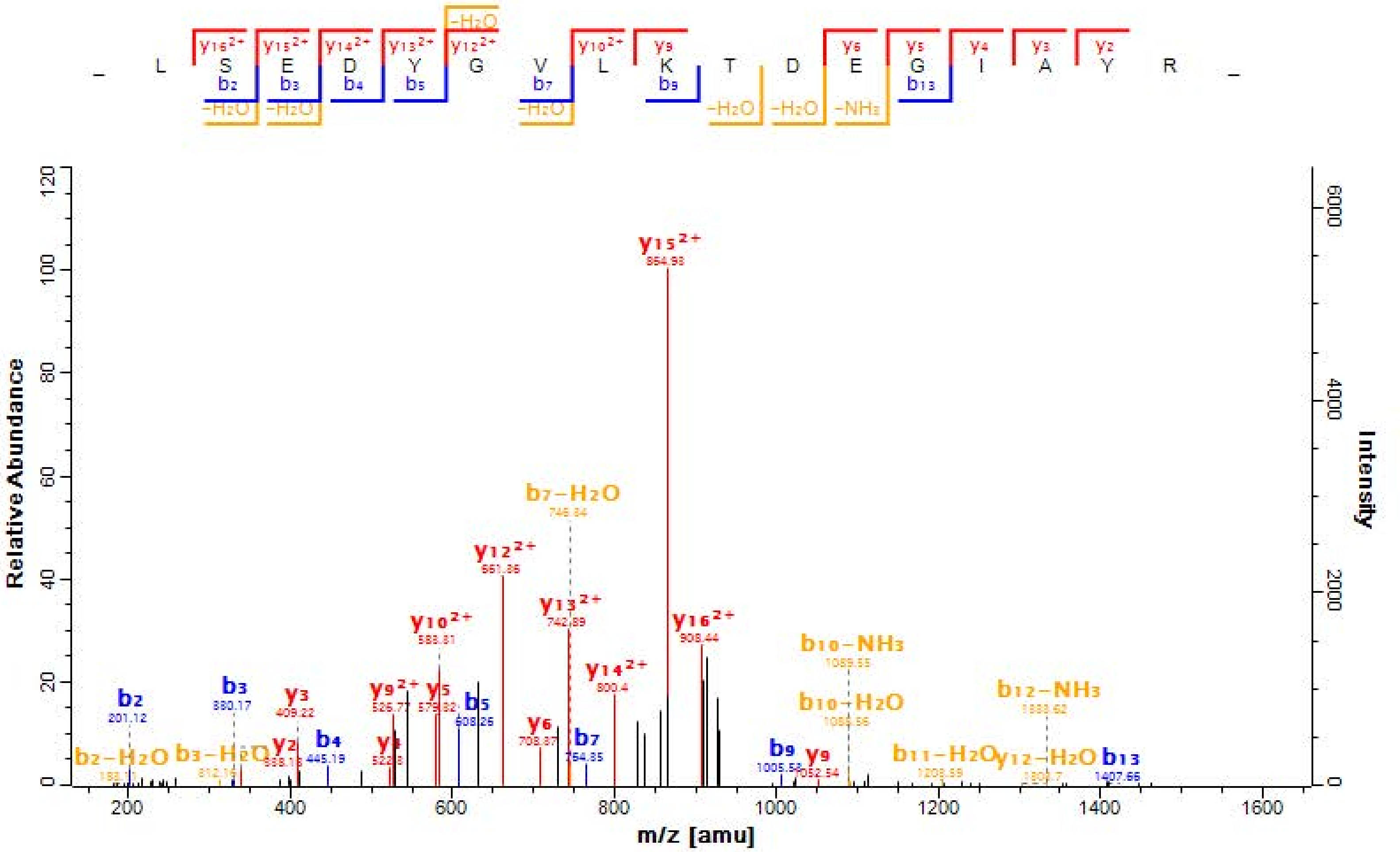
Mass:	1353.61554
m/z:	677.81505
Charge:	2+
Retentiontime:	7.3903751373291
Score:	222.254
Mass Error [ppm]:	-0.39196
PEP:	9.3862E-25
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	71 %
Peak Coverage:	44 %
Protein Localisation:	51 ... 62

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	11				
	203.07	+0.2396	203.07	2	S	10	1239.6		620.3	+0.2322
	366.13	+0.0369	366.13	3	Y	9	1152.6	+0.0559	576.79	+0.1909
	465.2	+0.0756	465.2	4	V	8	989.5	+0.0311	495.25	+0.2283
	522.22	-0.092	522.22	5	G	7	890.43	+0.0055	445.72	+0.1901
	637.25		637.25	6	D	6	833.41	+0.1234	417.21	+0.2007
	766.29	+0.0563	766.29	7	E	5	718.38	+0.1132	359.7	+0.2591
+0.1593	419.17		837.33	8	A	4	589.34	+0.0473	589.34	
	965.38	-0.013	965.38	9	Q	3	518.3	+0.0002	518.3	
	1052.4	+0.1438	1052.4	10	S	2	390.25	+0.091	390.25	
	1180.5	-0.043	1180.5	11	K	1	303.21	-0.106	303.21	
				12	R	0	175.12		175.12	

Scan number	3888	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	124.62



precursor information

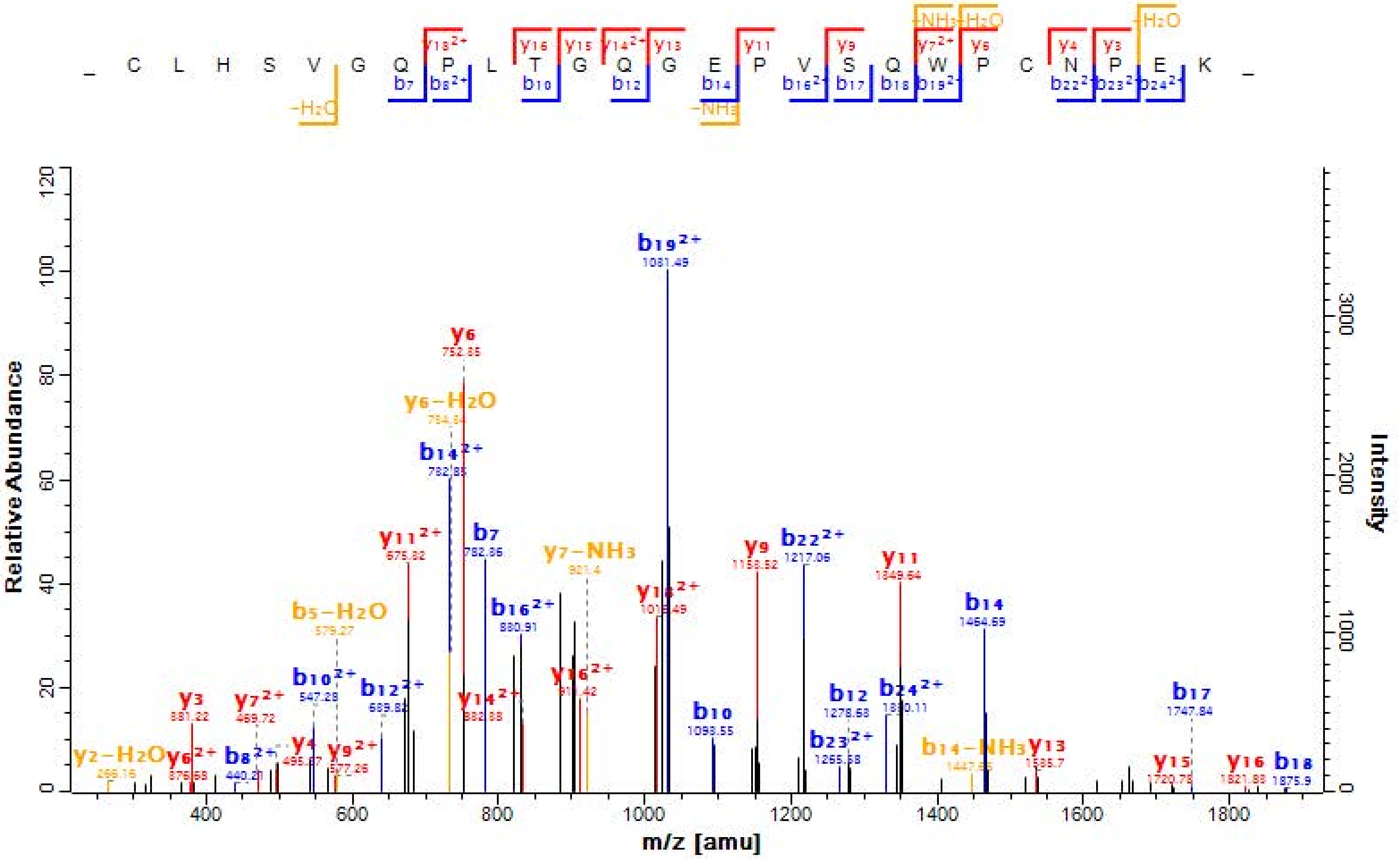
Mass:	1927.95135
m/z:	643.65773
Charge:	3+
Retentiontime:	29.257268905639
Score:	124.6202
Mass Error [ppm]:	-0.71315
PEP:	4.2231E-12
Precursor Type:	MULTI

general information

Annotation:	15 of 17
AminoAcids Coverag	88 %
Intensity Coverage:	58 %
Peak Coverage:	27 %
Protein Localisation:	111 ... 127

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	16				
-0.04872	201.1234	2	S	15	1815.876		908.4416	-0.00288
+0.163506	330.166	3	E	14	1728.844		864.9256	+0.217475
+0.051907	445.1929	4	D	13	1599.801		800.4043	+0.233523
+0.097587	608.2562	5	Y	12	1484.774		742.8908	+0.205551
	665.2777	6	G	11	1321.711		661.3592	+0.220858
+0.038105	764.3461	7	V	10	1264.69		1264.69	
	877.4302	8	L	9	1165.621		583.3142	+0.181996
-0.12279	1005.525	9	K	8	1052.537	-0.05785	526.7722	+0.311674
	1106.573	10	T	7	924.4421		924.4421	
	1221.6	11	D	6	823.3945		823.3945	
	1350.642	12	E	5	708.3675	+0.113259	708.3675	
-0.13318	1407.664	13	G	4	579.3249	+0.02011	579.3249	
	1520.748	14	I	3	522.3035	+0.034005	522.3035	
	1591.785	15	A	2	409.2194	+0.015347	409.2194	
	1754.848	16	Y	1	338.1823	+0.146272	338.1823	
		17	R	0	175.119		175.119	

Scan number	3912	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	133.74



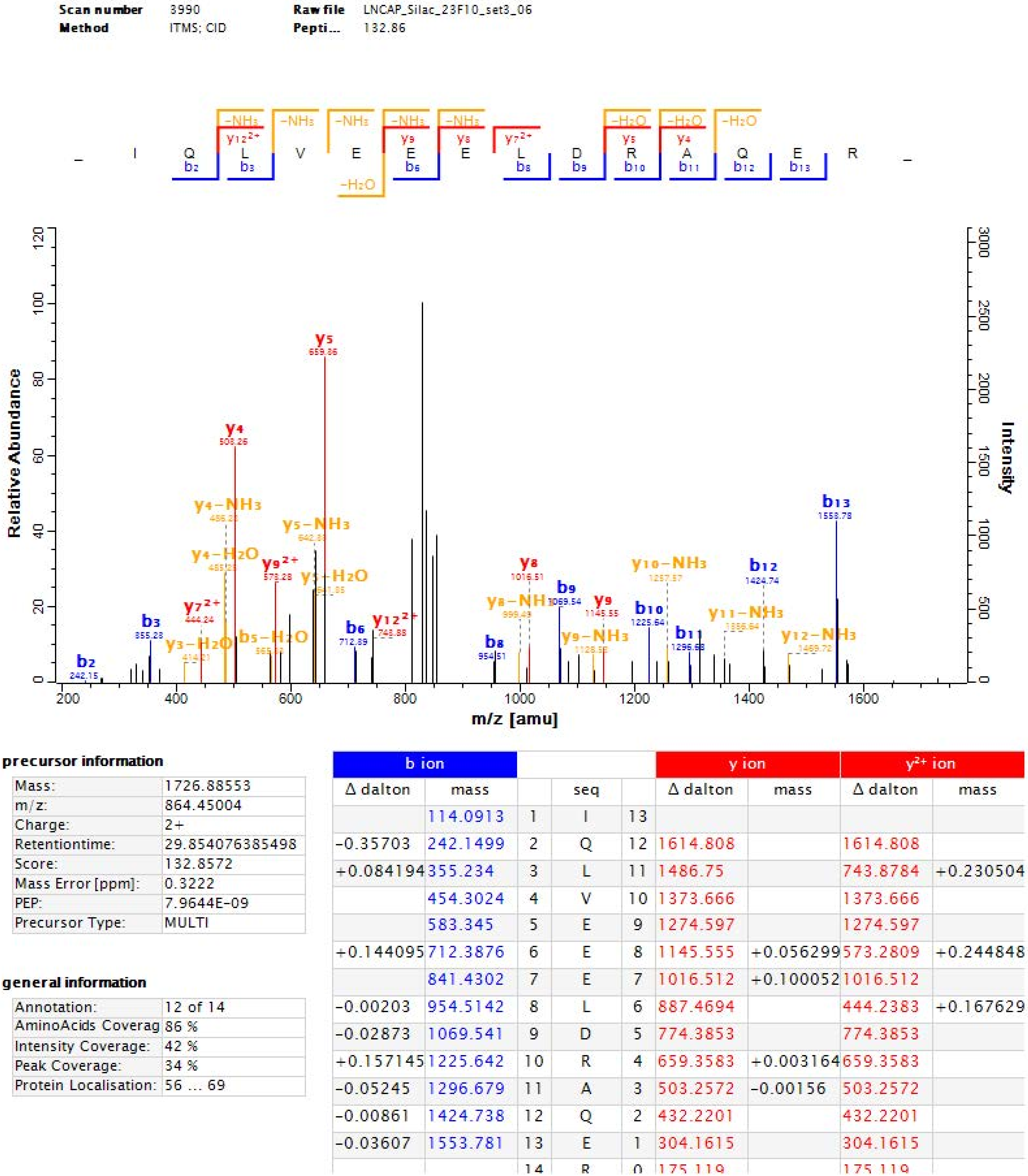
precursor information

Mass:	2804.2998
m/z:	935.77388
Charge:	3+
Retentiontime:	29.384754180908
Score:	133.744
Mass Error [ppm]:	-0.4393
PEP:	5.4512E-17
Precursor Type:	MULTI

general information

Annotation:	17 of 25
AminoAcids Coverag	68 %
Intensity Coverage:	51 %
Peak Coverage:	36 %
Protein Localisation:	210 ... 234

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	161.04		161.04	1	C	24				
	274.12		274.12	2	L	23	2653.3		2653.3	
	411.18		411.18	3	H	22	2540.2		2540.2	
	498.21		498.21	4	S	21	2403.1		2403.1	
	597.28		597.28	5	V	20	2316.1		2316.1	
	654.3		654.3	6	G	19	2217		2217	
	782.36	+0.0402	782.36	7	Q	18	2160		2160	
+0.1226	440.21		879.41	8	P	17	2032		1016.5	+0.3963
	992.5		992.5	9	L	16	1934.9		1934.9	
+0.2245	547.28	+0.031	1093.5	10	T	15	1821.8	+0.072	911.42	+0.262
	1150.6		1150.6	11	G	14	1720.8	+0.0768	1720.8	
+0.4844	639.82	+0.0302	1278.6	12	Q	13	1663.8		832.38	+0.2815
	1335.6		1335.6	13	G	12	1535.7	+0.2922	1535.7	
+0.3243	732.85	-0.043	1464.7	14	E	11	1478.7		1478.7	
	1561.7		1561.7	15	P	10	1349.6	-0.025	675.32	+0.027
+0.0633	830.91		1660.8	16	V	9	1252.6		1252.6	
	1747.8	-0.182	1747.8	17	S	8	1153.5	-0.128	577.26	+0.1806
	1875.9	-0.054	1875.9	18	Q	7	1066.5		1066.5	
+0.2419	1031.5		2062	19	W	6	938.43		469.72	+0.4473
	2159		2159	20	P	5	752.35	+0.0224	376.68	+0.3275
	2319.1		2319.1	21	C	4	655.3		655.3	
+0.3239	1217.1		2433.1	22	N	3	495.27	+0.1302	495.27	
-0.053	1265.6		2530.2	23	P	2	381.22	+0.0333	381.22	
+0.2851	1330.1		2659.2	24	E	1	284.17		284.17	
				25	K	0	155.13		155.13	



Scan number	3990	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	132.86

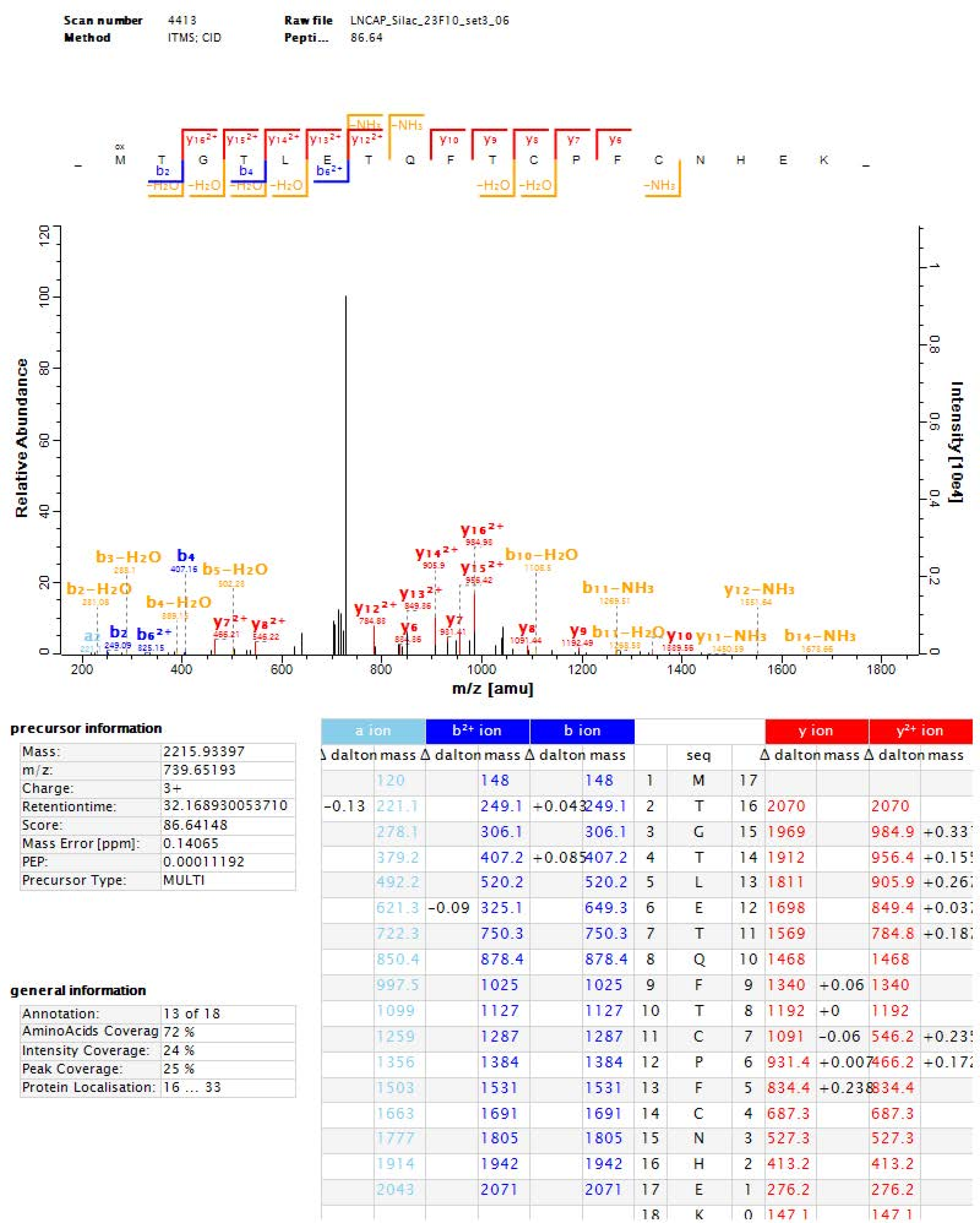
precursor information

Mass:	1726.88553
m/z:	864.45004
Charge:	2+
Retentiontime:	29.854076385498
Score:	132.8572
Mass Error [ppm]:	0.3222
PEP:	7.9644E-09
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	42 %
Peak Coverage:	34 %
Protein Localisation:	56 ... 69

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	I	13				
-0.35703	242.1499	2	Q	12	1614.808		1614.808	
+0.084194	355.234	3	L	11	1486.75		743.8784	+0.230504
	454.3024	4	V	10	1373.666		1373.666	
	583.345	5	E	9	1274.597		1274.597	
+0.144095	712.3876	6	E	8	1145.555	+0.056299	573.2809	+0.244848
	841.4302	7	E	7	1016.512	+0.100052	1016.512	
-0.00203	954.5142	8	L	6	887.4694		444.2383	+0.167629
-0.02873	1069.541	9	D	5	774.3853		774.3853	
+0.157145	1225.642	10	R	4	659.3583	+0.003164	659.3583	
-0.05245	1296.679	11	A	3	503.2572	-0.00156	503.2572	
-0.00861	1424.738	12	Q	2	432.2201		432.2201	
-0.03607	1553.781	13	E	1	304.1615		304.1615	
		14	R	0	175.119		175.119	



Scan number	4413	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	86.64

precursor information

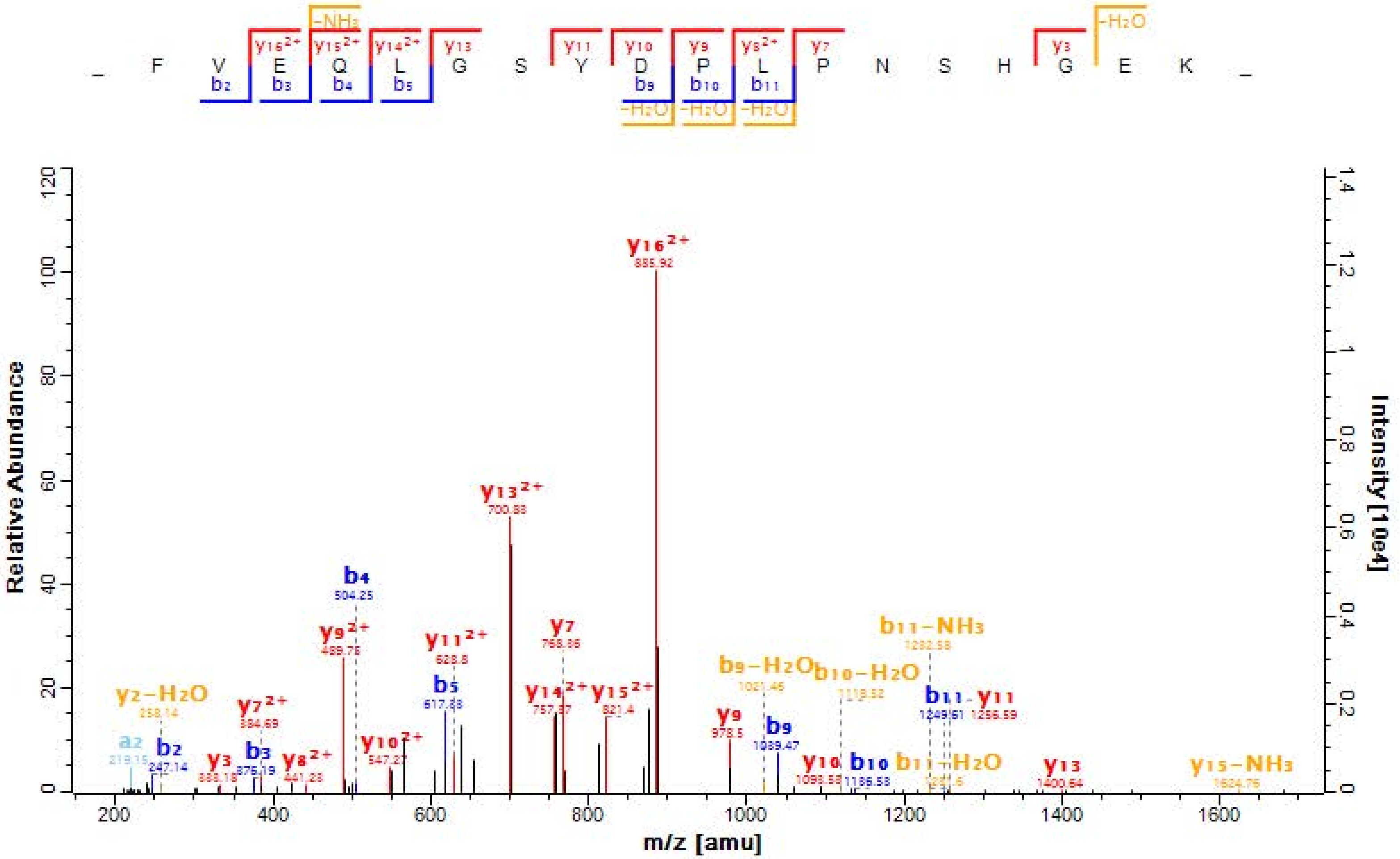
Mass:	2215.93397
m/z:	739.65193
Charge:	3+
Retentiontime:	32.168930053710
Score:	86.64148
Mass Error [ppm]:	0.14065
PEP:	0.00011192
Precursor Type:	MULTI

general information

Annotation:	13 of 18
AminoAcids Coverag	72 %
Intensity Coverage:	24 %
Peak Coverage:	25 %
Protein Localisation:	16 ... 33

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120		148		148	1	M	17				
−0.13	221.1		249.1	+0.043	249.1	2	T	16	2070		2070	
	278.1		306.1		306.1	3	G	15	1969		984.9	+0.33
	379.2		407.2	+0.085	407.2	4	T	14	1912		956.4	+0.15
	492.2		520.2		520.2	5	L	13	1811		905.9	+0.26
	621.3	−0.09	325.1		649.3	6	E	12	1698		849.4	+0.03
	722.3		750.3		750.3	7	T	11	1569		784.8	+0.18
	850.4		878.4		878.4	8	Q	10	1468		1468	
	997.5		1025		1025	9	F	9	1340	+0.06	1340	
	1099		1127		1127	10	T	8	1192	+0	1192	
	1259		1287		1287	11	C	7	1091	−0.06	546.2	+0.23
	1356		1384		1384	12	P	6	931.4	+0.007	466.2	+0.17
	1503		1531		1531	13	F	5	834.4	+0.238	834.4	
	1663		1691		1691	14	C	4	687.3		687.3	
	1777		1805		1805	15	N	3	527.3		527.3	
	1914		1942		1942	16	H	2	413.2		413.2	
	2043		2071		2071	17	E	1	276.2		276.2	
						18	K	0	147.1		147.1	

Scan number	4416	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	136.01



precursor information

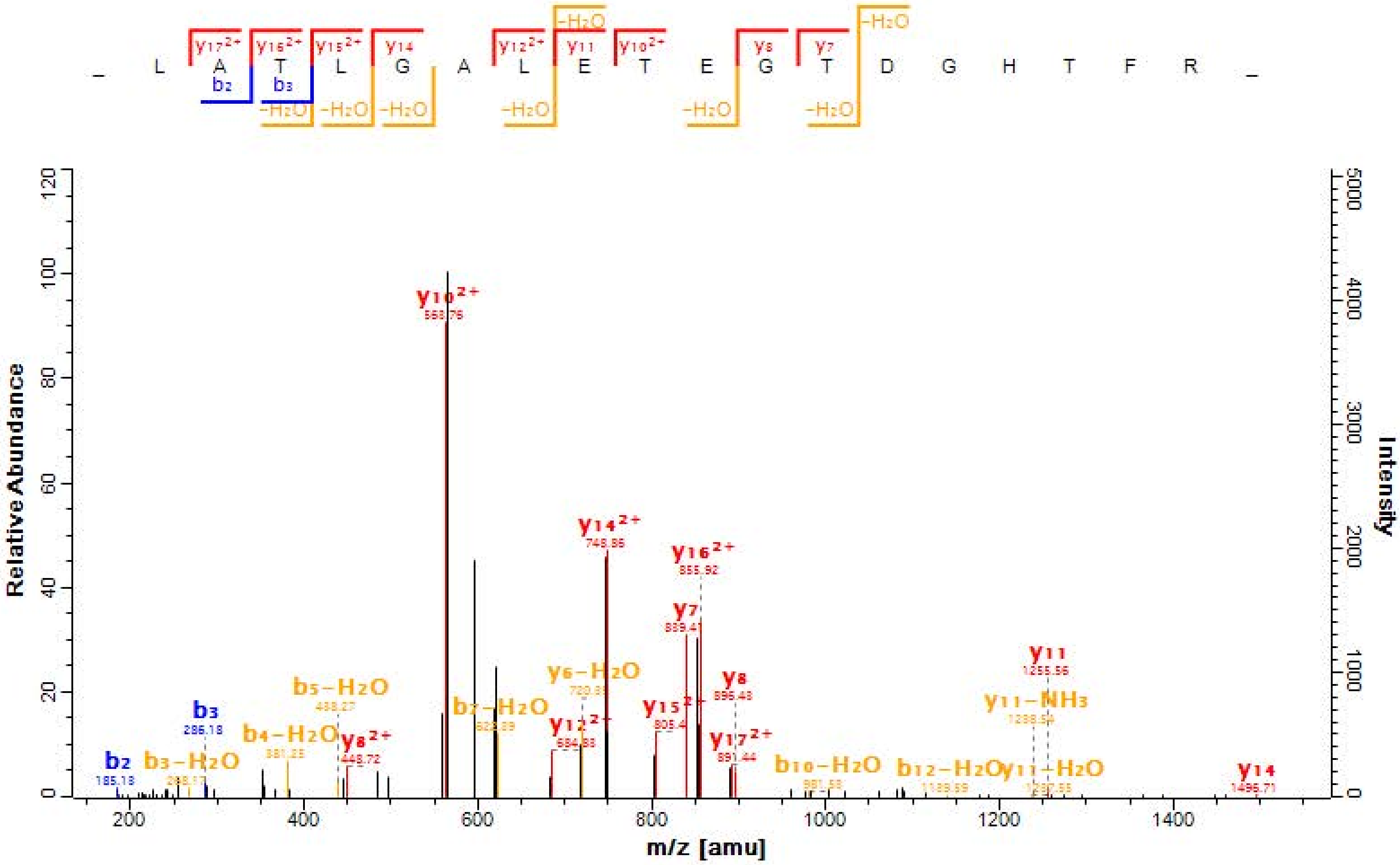
Mass:	2015.9589
m/z:	672.99358
Charge:	3+
Retentiontime:	32.186531066894
Score:	136.014
Mass Error [ppm]:	0.016002
PEP:	3.7891E-17
Precursor Type:	MULTI

general information

Annotation:	12 of 18
AminoAcids Coverag	67 %
Intensity Coverage:	56 %
Peak Coverage:	27 %
Protein Localisation:	47 ... 64

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08		148.08	1	F	17				
-0.049	219.15	-0.09	247.14	2	V	16	1869.9		1869.9	
	348.19	+0.1086	376.19	3	E	15	1770.8		885.92	+0.2406
	476.25	+0.0122	504.25	4	Q	14	1641.8		821.4	+0.3283
	589.33	-0.031	617.33	5	L	13	1513.7		757.37	+0.0296
	646.36		674.35	6	G	12	1400.6	-0.061	700.83	+0.0442
	733.39		761.38	7	S	11	1343.6		1343.6	
	896.45		924.45	8	Y	10	1256.6	+0.0455	628.8	-0.053
	1011.5	-0.074	1039.5	9	D	9	1093.5	-0.048	547.27	+0.1973
	1108.5	+0.111	1136.5	10	P	8	978.5	+0.0072	489.75	+0.2116
	1221.6	+0.4118	1249.6	11	L	7	881.45		441.23	+0.2413
	1318.7		1346.7	12	P	6	768.36	+0.0284	384.69	+0.0064
	1432.7		1460.7	13	N	5	671.31		671.31	
	1519.7		1547.7	14	S	4	557.27		557.27	
	1656.8		1684.8	15	H	3	470.24		470.24	
	1713.8		1741.8	16	G	2	333.18	+0.0444	333.18	
	1842.9		1870.9	17	E	1	276.16		276.16	
				18	K	0	147.11		147.11	

Scan number	4594	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	81.63



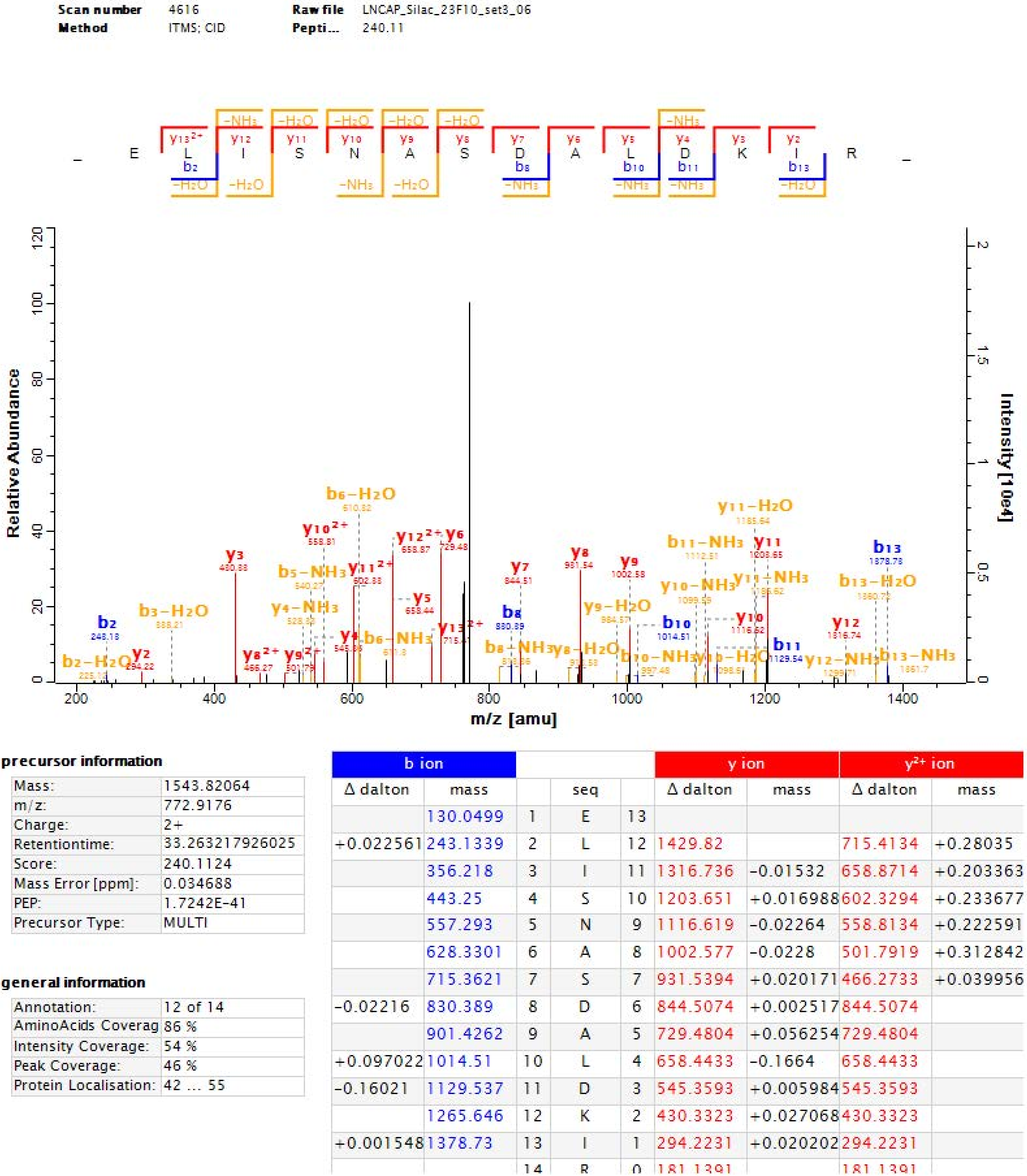
precursor information

Mass:	1887.93028
m/z:	630.31737
Charge:	3+
Retentiontime:	33.140731811523
Score:	81.63164
Mass Error [ppm]:	-1.2529
PEP:	0.00014015
Precursor Type:	MULTI

general information

Annotation:	12 of 18
AminoAcids Coverag	67 %
Intensity Coverage:	39 %
Peak Coverage:	23 %
Protein Localisation:	252 ... 269

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	17				
+0.01829	185.1285	2	A	16	1781.876		891.4416	-0.03935
-0.22807	286.1761	3	T	15	1710.839		855.9231	+0.259965
	399.2602	4	L	14	1609.791		805.3992	-0.042
	456.2817	5	G	13	1496.707	-0.33031	748.8572	-0.01547
	527.3188	6	A	12	1439.686		1439.686	
	640.4028	7	L	11	1368.649		684.8279	+0.010154
	769.4454	8	E	10	1255.564	-0.00566	1255.564	
	870.4931	9	T	9	1126.522		563.7646	-0.25562
	999.5357	10	E	8	1025.474		1025.474	
	1056.557	11	G	7	896.4316	-0.23614	448.7195	+0.277493
	1157.605	12	T	6	839.4102	+0.097154	839.4102	
	1272.632	13	D	5	738.3625		738.3625	
	1329.653	14	G	4	623.3355		623.3355	
	1466.712	15	H	3	566.3141		566.3141	
	1567.76	16	T	2	429.2552		429.2552	
	1714.828	17	F	1	328.2075		328.2075	
		18	R	0	181.1391		181.1391	



Scan number 4616 **Raw file** LNCAP_Silac_23F10_set3_06

Method ITMS; CID **Pepti...** 240.11

precursor information

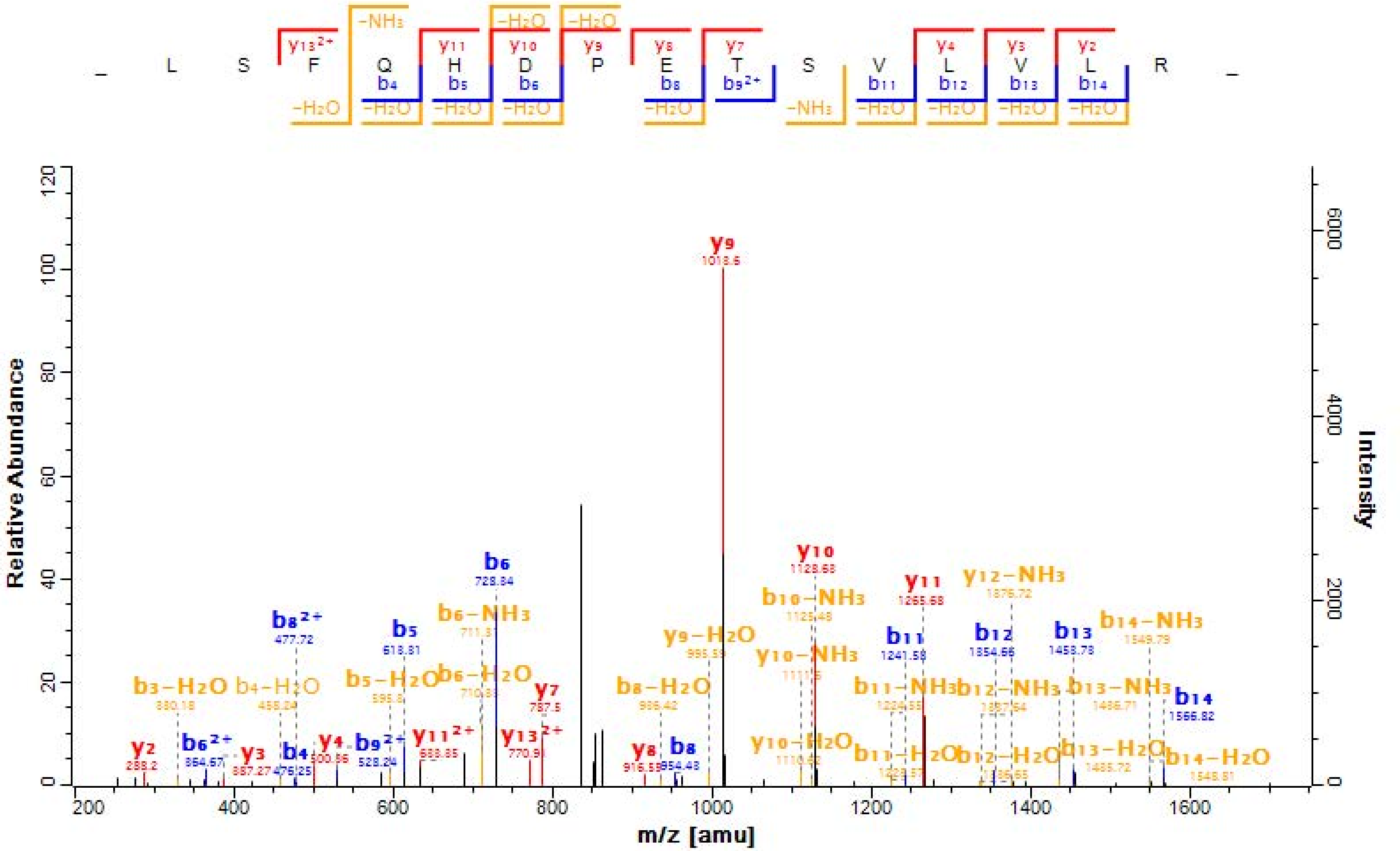
Mass:	1543.82064
m/z:	772.9176
Charge:	2+
Retentiontime:	33.263217926025
Score:	240.1124
Mass Error [ppm]:	0.034688
PEP:	1.7242E-41
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	54 %
Peak Coverage:	46 %
Protein Localisation:	42 ... 55

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	13				
+0.022561	243.1339	2	L	12	1429.82		715.4134	+0.28035
	356.218	3	I	11	1316.736	-0.01532	658.8714	+0.203363
	443.25	4	S	10	1203.651	+0.016988	602.3294	+0.233677
	557.293	5	N	9	1116.619	-0.02264	558.8134	+0.222591
	628.3301	6	A	8	1002.577	-0.0228	501.7919	+0.312842
	715.3621	7	S	7	931.5394	+0.020171	466.2733	+0.039956
-0.02216	830.389	8	D	6	844.5074	+0.002517	844.5074	
	901.4262	9	A	5	729.4804	+0.056254	729.4804	
+0.097022	1014.51	10	L	4	658.4433	-0.1664	658.4433	
-0.16021	1129.537	11	D	3	545.3593	+0.005984	545.3593	
	1265.646	12	K	2	430.3323	+0.027068	430.3323	
+0.001548	1378.73	13	I	1	294.2231	+0.020202	294.2231	
		14	R	0	181.1391		181.1391	

Scan number	5485	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	249.32



precursor information

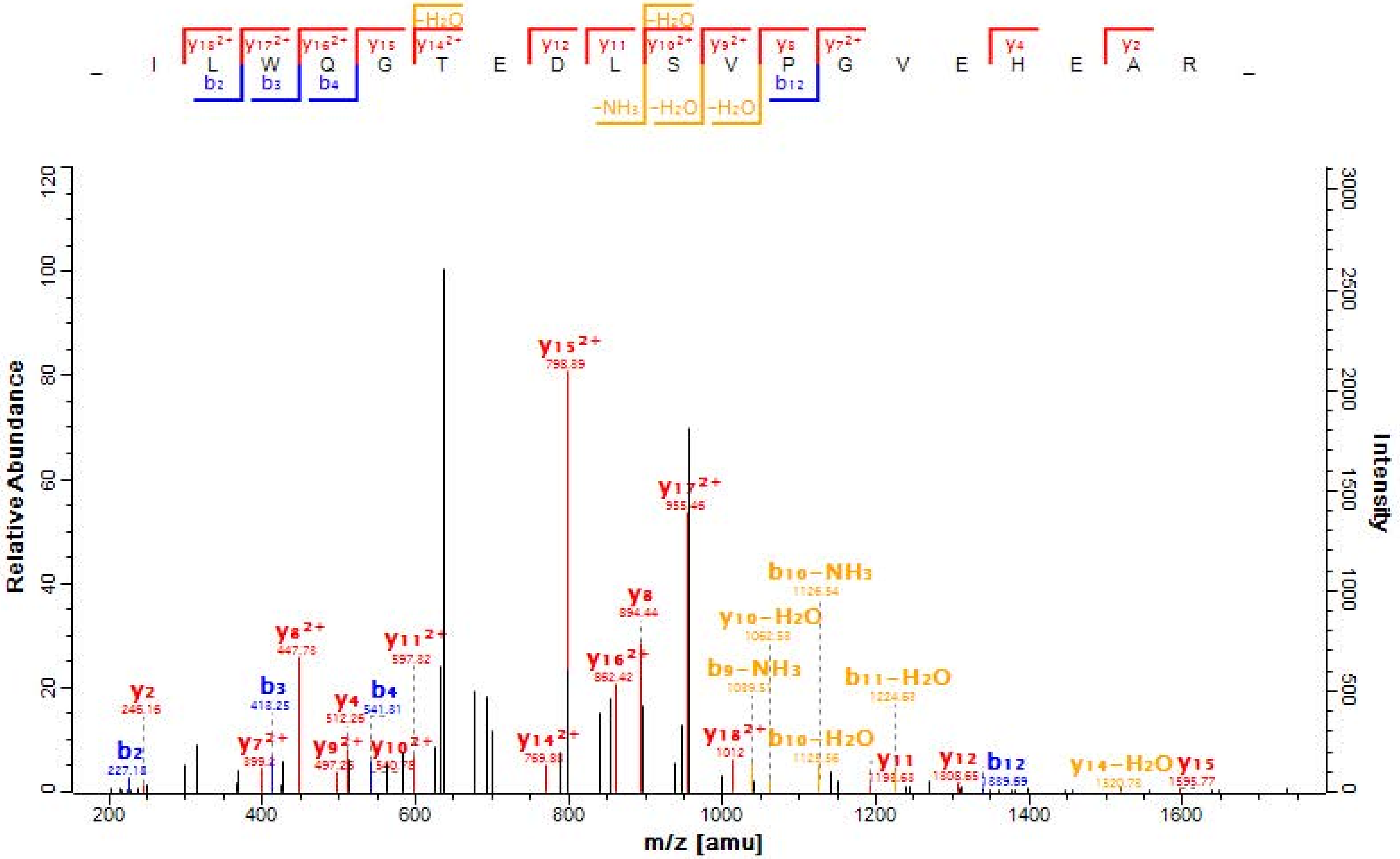
Mass:	1739.92073
m/z:	870.96764
Charge:	2+
Retentiontime:	38.070663452148
Score:	249.3229
Mass Error [ppm]:	0.055479
PEP:	3.3846E-57
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	56 %
Peak Coverage:	49 %
Protein Localisation:	966 ... 980

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	14				
	201.12		201.12	2	S	13	1627.8		1627.8	
	348.19		348.19	3	F	12	1540.8		770.91	+0.2651
	476.25	+0.1681	476.25	4	Q	11	1393.7		1393.7	
	613.31	+0.124	613.31	5	H	10	1265.7	-0.035	633.35	+0.0758
-0.394	364.67	+0.039	728.34	6	D	9	1128.6	-0.077	1128.6	
	825.39		825.39	7	P	8	1013.6	-0.018	1013.6	
-0.408	477.72	+0.0432	954.43	8	E	7	916.55	+0.1969	916.55	
+0.0005	528.24		1055.5	9	T	6	787.5	-0.006	787.5	
	1142.5		1142.5	10	S	5	686.46		686.46	
	1241.6	+0.0556	1241.6	11	V	4	599.42		599.42	
	1354.7	-0.08	1354.7	12	L	3	500.36	+0.0163	500.36	
	1453.7	-0.1	1453.7	13	V	2	387.27	+0.1696	387.27	
	1566.8	-0.074	1566.8	14	L	1	288.2	-0.078	288.2	
				15	R	0	175.12		175.12	

Scan number	6108	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	78.24



precursor information

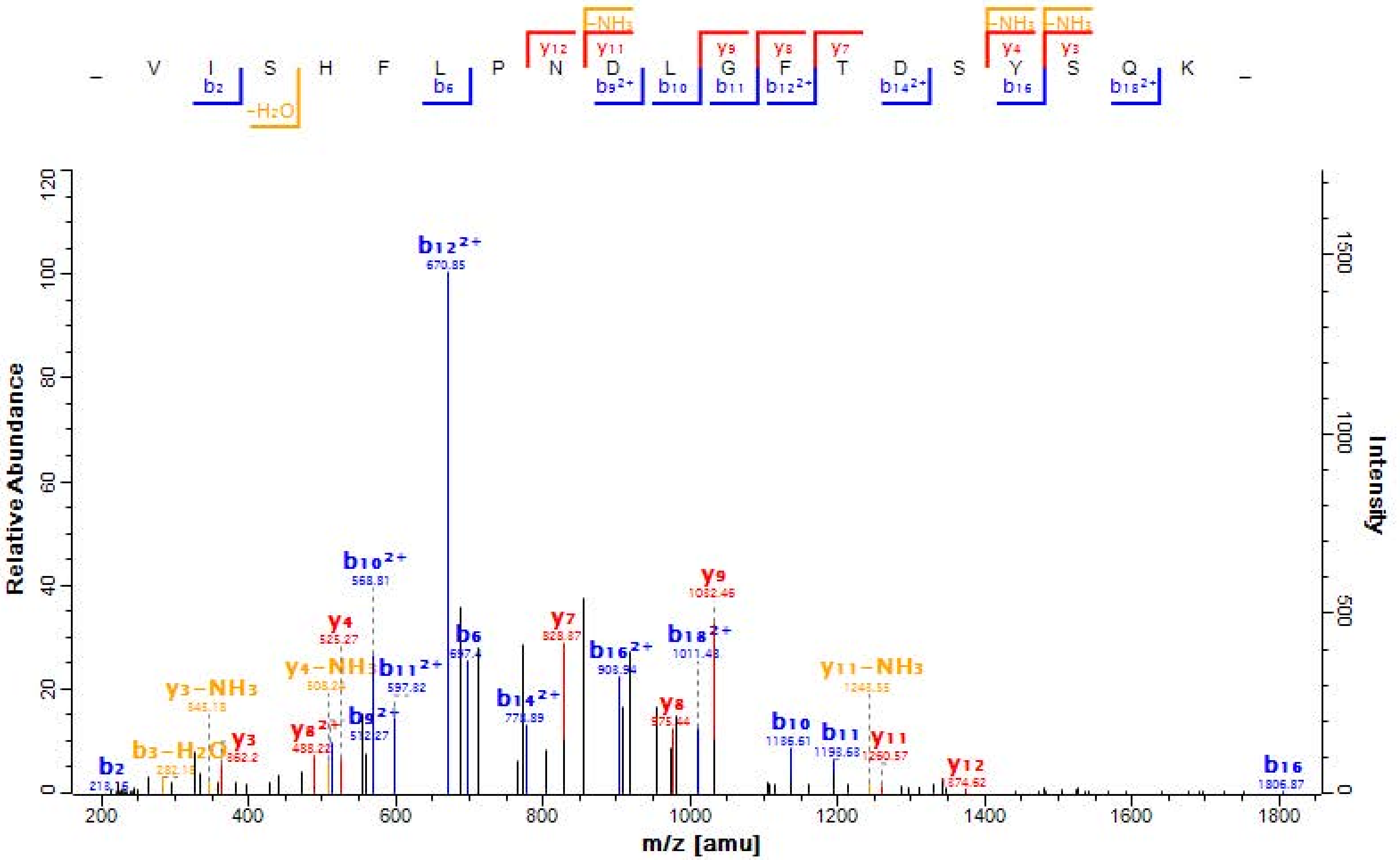
Mass:	2135.06561
m/z:	712.69581
Charge:	3+
Retentiontime:	41.637187957763
Score:	78.24441
Mass Error [ppm]:	0.4099
PEP:	0.00016193
Precursor Type:	MULTI

general information

Annotation:	13 of 19
AminoAcids Coverag	68 %
Intensity Coverage:	37 %
Peak Coverage:	27 %
Protein Localisation:	30 ... 48

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	I	18				
-0.03388	227.1754	2	L	17	2022.988		1011.998	+0.289682
+0.306623	413.2547	3	W	16	1909.904		955.4556	+0.025623
+0.117796	541.3133	4	Q	15	1723.825		862.4159	+0.151827
	598.3348	5	G	14	1595.766	-0.02893	798.3866	+0.309412
	699.3824	6	T	13	1538.745		769.8759	+0.085891
	828.425	7	E	12	1437.697		1437.697	
	943.452	8	D	11	1308.654	-0.30941	1308.654	
	1056.536	9	L	10	1193.627	+0.145027	597.3173	+0.234158
	1143.568	10	S	9	1080.543		540.7753	-0.06243
	1242.636	11	V	8	993.5112		497.2592	-0.00552
+0.007412	1339.689	12	P	7	894.4428	+0.055974	447.725	+0.231502
	1396.711	13	G	6	797.39		399.1987	+0.069468
	1495.779	14	V	5	740.3686		740.3686	
	1624.822	15	E	4	641.3002		641.3002	
	1761.881	16	H	3	512.2576	+0.030149	512.2576	
	1890.923	17	E	2	375.1987		375.1987	
	1961.96	18	A	1	246.1561	+0.137361	246.1561	
		19	R	0	175.119		175.119	

Scan number	6710	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	86



precursor information

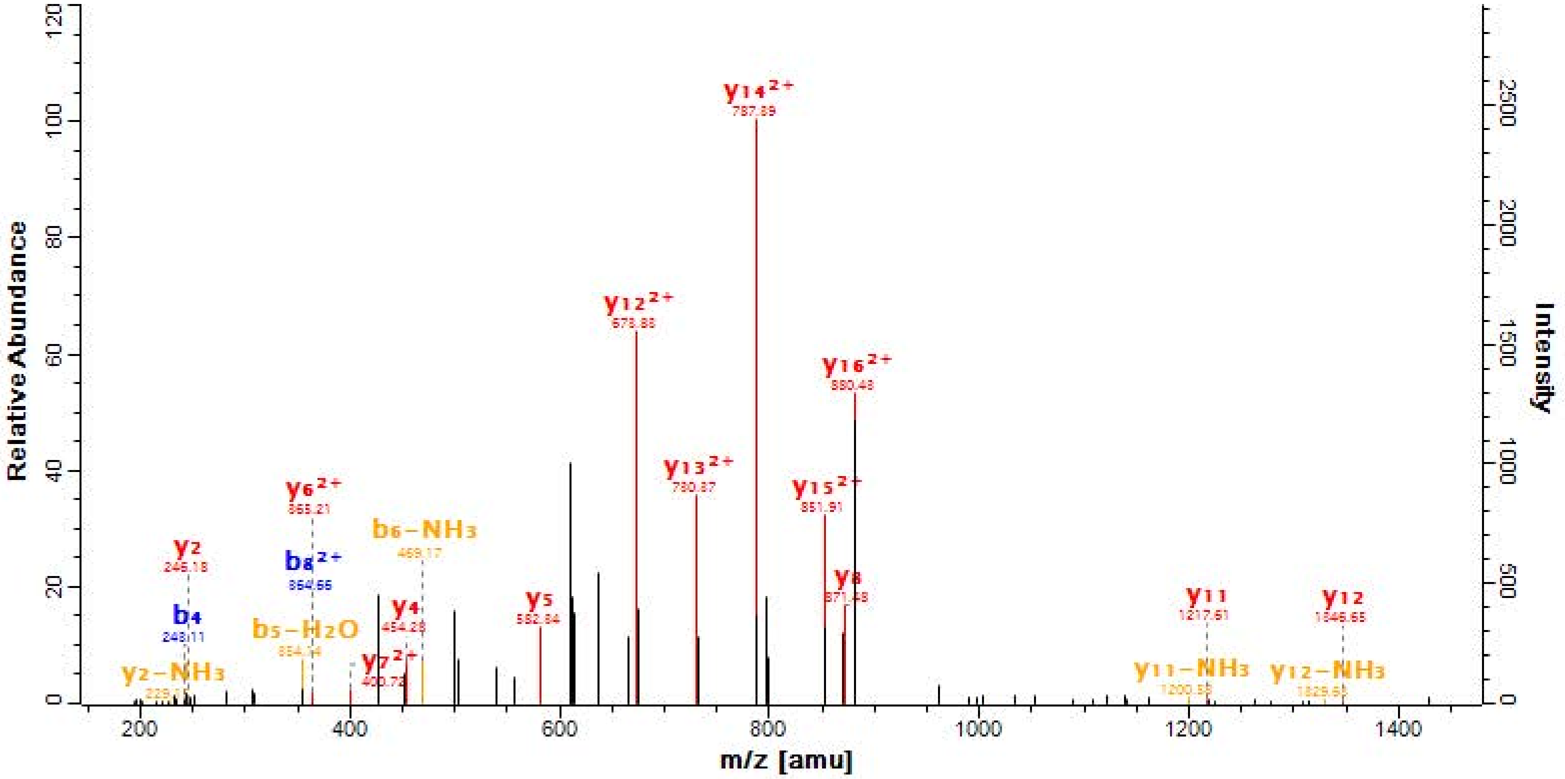
Mass:	2167.06013
m/z:	723.36065
Charge:	3+
Retentiontime:	45.106575012207
Score:	86.00483
Mass Error [ppm]:	0.71218
PEP:	3.7085E-05
Precursor Type:	MULTI

general information

Annotation:	13 of 19
AminoAcids Coverag	68 %
Intensity Coverage:	45 %
Peak Coverage:	22 %
Protein Localisation:	156 ... 174

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	18				
	213.16	-0.017	213.16	2	I	17	2069		2069	
	300.19		300.19	3	S	16	1955.9		1955.9	
	437.25		437.25	4	H	15	1868.9		1868.9	
	584.32		584.32	5	F	14	1731.8		1731.8	
	697.4	-0.075	697.4	6	L	13	1584.8		1584.8	
	794.46		794.46	7	P	12	1471.7		1471.7	
	908.5		908.5	8	N	11	1374.6	+0.0616	1374.6	
+0.1878	512.27		1023.5	9	D	10	1260.6	-0.208	1260.6	
+0.1334	568.81	-0.045	1136.6	10	L	9	1145.5		1145.5	
+0.178	597.32	+0.0309	1193.6	11	G	8	1032.5	+0.0513	1032.5	
+0.2211	670.85		1340.7	12	F	7	975.44	-0.052	488.22	+0.293
	1441.7		1441.7	13	T	6	828.37	-0.057	828.37	
-0.007	778.89		1556.8	14	D	5	727.33		727.33	
	1643.8		1643.8	15	S	4	612.3		612.3	
+0.232	903.94	-0.216	1806.9	16	Y	3	525.27	+0.1414	525.27	
	1893.9		1893.9	17	S	2	362.2	+0.1366	362.2	
-0.028	1011.5		2022	18	Q	1	275.17		275.17	
				19	K	0	147.11		147.11	

Scan number	6946	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	65.47



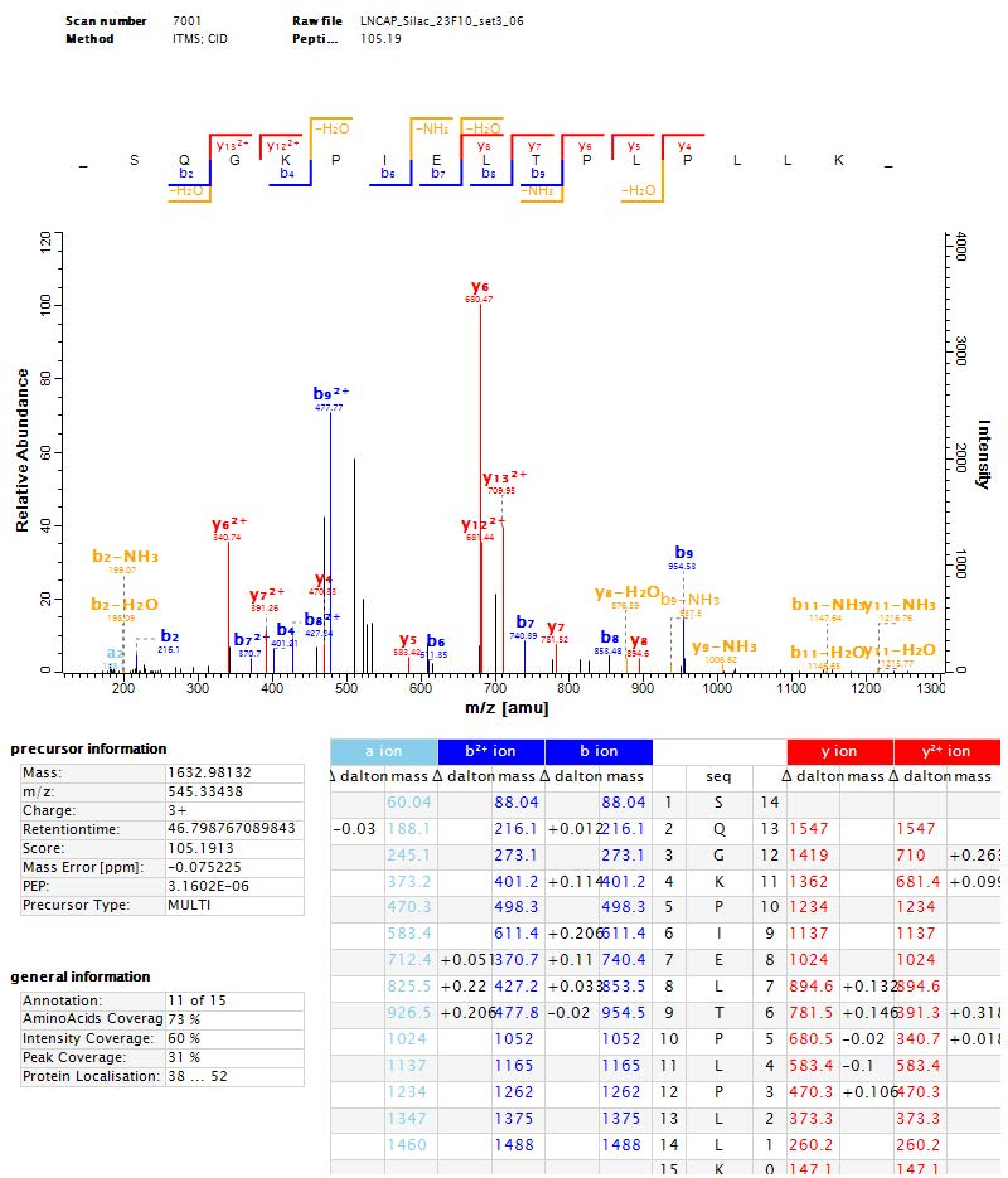
precursor information

Mass:	1943.916
m/z:	648.97928
Charge:	3+
Retentiontime:	46.484432220459
Score:	65.467
Mass Error [ppm]:	0.022735
PEP:	0.00098128
Precursor Type:	MULTI

general information

Annotation:	12 of 19
AminoAcids Coverag	63 %
Intensity Coverage:	49 %
Peak Coverage:	24 %
Protein Localisation:	47 ... 65

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	18				
	115.05		115.05	2	G	17	1887.9		1887.9	
	186.09		186.09	3	A	16	1830.9		1830.9	
	243.11	+0.1355	243.11	4	G	15	1759.8		880.43	+0.0093
	372.15		372.15	5	E	14	1702.8		851.91	+0.2669
	486.19		486.19	6	N	13	1573.8		787.39	+0.2636
	599.28		599.28	7	L	12	1459.7		730.37	+0.2536
-0.118	364.66		728.32	8	E	11	1346.7	+0.3287	673.83	+0.1813
	842.36		842.36	9	N	10	1217.6	-0.041	1217.6	
	943.41		943.41	10	T	9	1103.6		1103.6	
	1074.5		1074.5	11	M	8	1002.5		1002.5	
	1145.5		1145.5	12	A	7	871.48	+0.1188	871.48	
	1216.5		1216.5	13	A	6	800.44		400.72	-0.463
	1363.6		1363.6	14	F	5	729.4		365.21	-0.01
	1491.7		1491.7	15	Q	4	582.34	-0.034	582.34	
	1628.7		1628.7	16	H	3	454.28	+0.0512	454.28	
	1699.7		1699.7	17	A	2	317.22		317.22	
	1798.8		1798.8	18	V	1	246.18	+0.0829	246.18	
				19	K	0	147.11		147.11	



Scan number	7001	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	105.19

precursor information

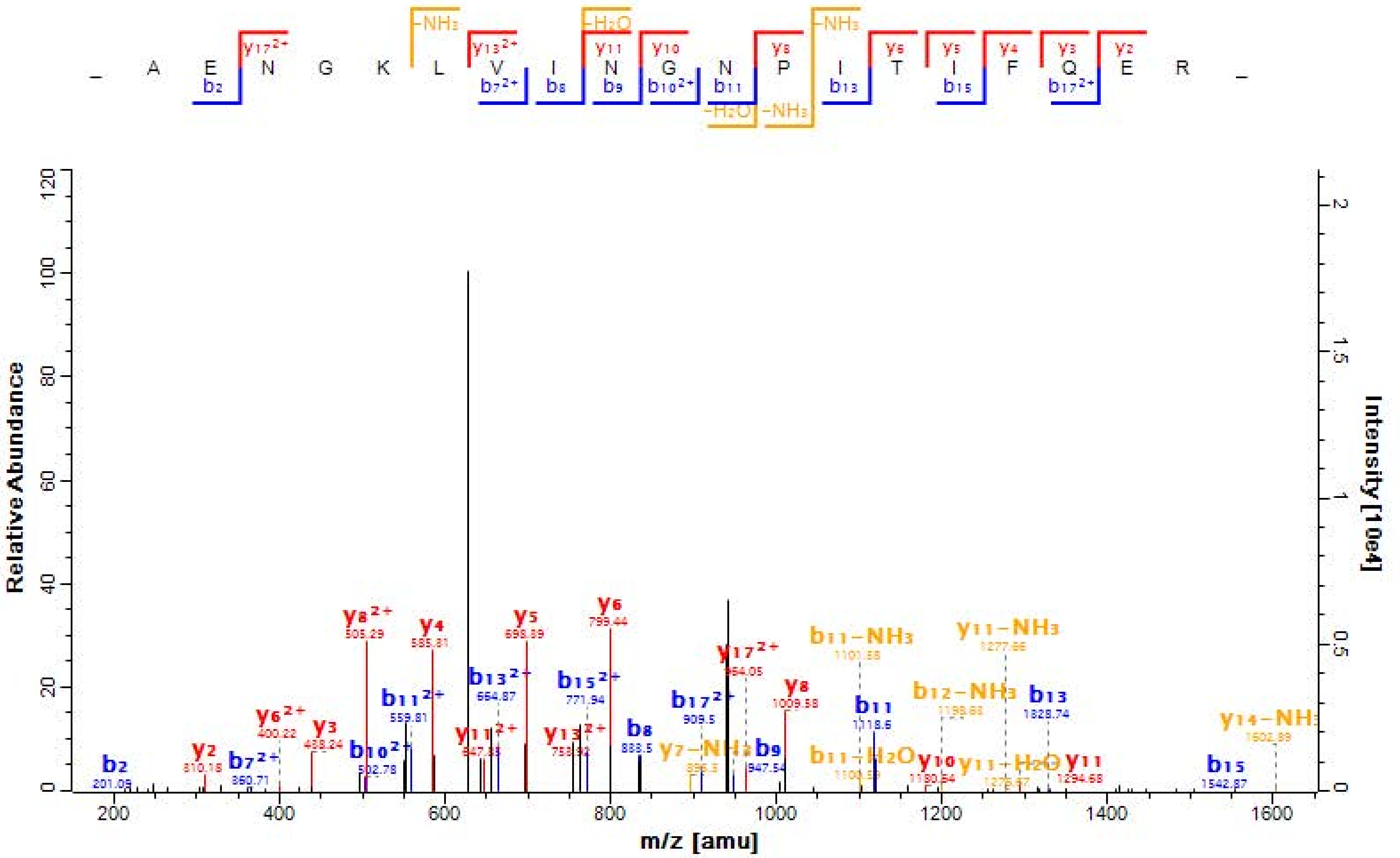
Mass:	1632.98132
m/z:	545.33438
Charge:	3+
Retentiontime:	46.798767089843
Score:	105.1913
Mass Error [ppm]:	-0.075225
PEP:	3.1602E-06
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	60 %
Peak Coverage:	31 %
Protein Localisation:	38 ... 52

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	60.04		88.04		88.04	1	S	14				
-0.03	188.1		216.1	+0.012	216.1	2	Q	13	1547		1547	
	245.1		273.1		273.1	3	G	12	1419		710	+0.26
	373.2		401.2	+0.114	401.2	4	K	11	1362		681.4	+0.09
	470.3		498.3		498.3	5	P	10	1234		1234	
	583.4		611.4	+0.206	611.4	6	I	9	1137		1137	
	712.4	+0.051	370.7	+0.11	740.4	7	E	8	1024		1024	
	825.5	+0.22	427.2	+0.033	853.5	8	L	7	894.6	+0.132	894.6	
	926.5	+0.206	477.8	-0.02	954.5	9	T	6	781.5	+0.146	391.3	+0.31
	1024		1052		1052	10	P	5	680.5	-0.02	340.7	+0.01
	1137		1165		1165	11	L	4	583.4	-0.1	583.4	
	1234		1262		1262	12	P	3	470.3	+0.106	470.3	
	1347		1375		1375	13	L	2	373.3		373.3	
	1460		1488		1488	14	L	1	260.2		260.2	
						15	K	0	147.1		147.1	

Scan number	7034	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	127.61



precursor information

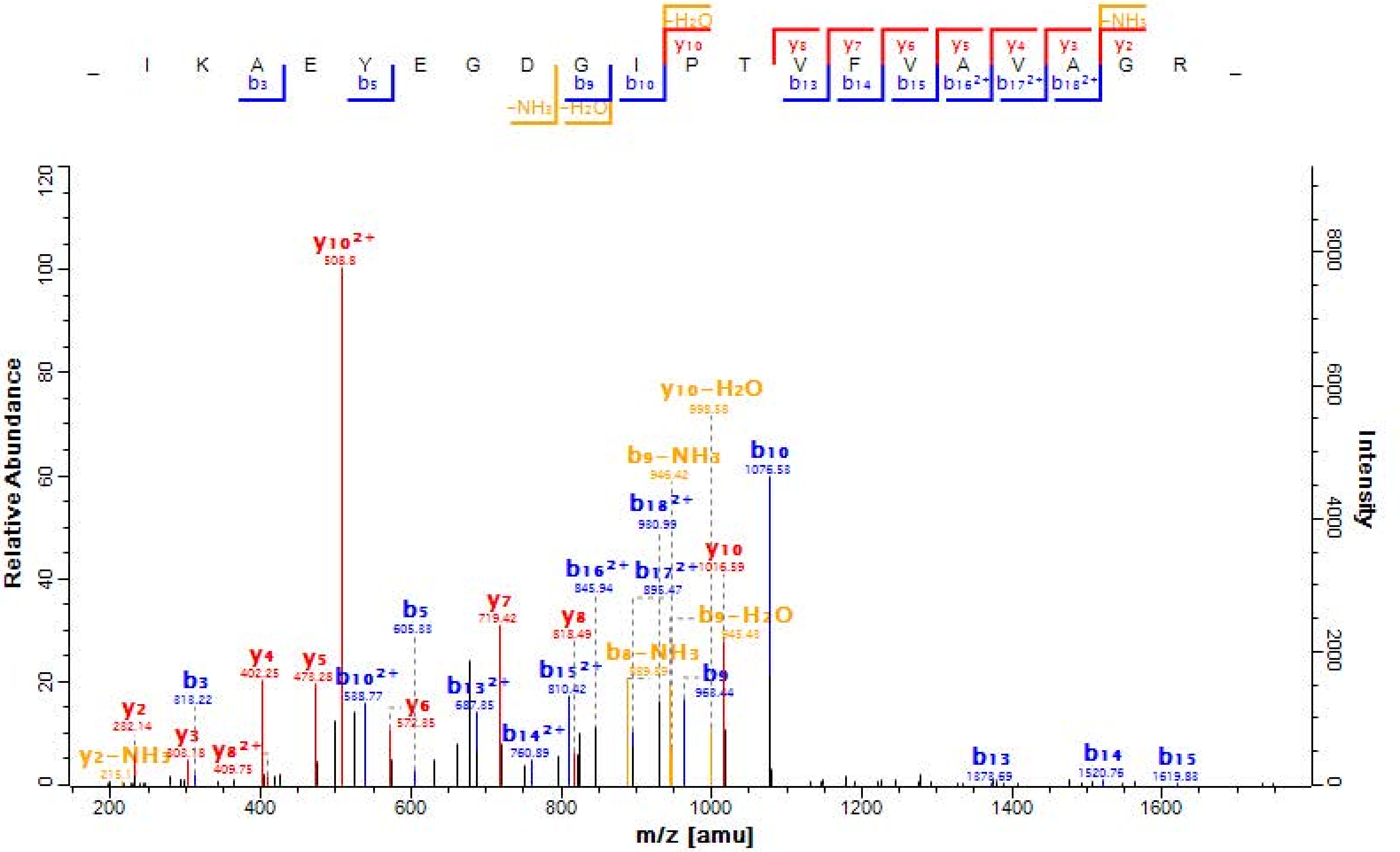
Mass:	2112.13236
m/z:	705.0514
Charge:	3+
Retentiontime:	46.980216979980
Score:	127.608
Mass Error [ppm]:	-0.18314
PEP:	6.9986E-13
Precursor Type:	MULTI

general information

Annotation:	15 of 19
AminoAcids Coverag	79 %
Intensity Coverage:	41 %
Peak Coverage:	34 %
Protein Localisation:	62 ... 80

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	18				
	201.09	-0.325	201.09	2	E	17	2056.1		2056.1	
	315.13		315.13	3	N	16	1927.1		964.05	+0.0842
	372.15		372.15	4	G	15	1813.1		1813.1	
	508.26		508.26	5	K	14	1756		1756	
	621.34		621.34	6	L	13	1619.9		1619.9	
-0.359	360.71		720.41	7	V	12	1506.8		753.92	-0.133
	833.5	+0.2211	833.5	8	I	11	1407.8		1407.8	
	947.54	-0.055	947.54	9	N	10	1294.7	-0.346	647.85	-0.022
+0.4361	502.78		1004.6	10	G	9	1180.6	-0.057	1180.6	
+0.1888	559.81	-0.036	1118.6	11	N	8	1123.6		1123.6	
	1215.7		1215.7	12	P	7	1009.6	-0.039	505.29	+0.2425
+0.0404	664.87	-0.011	1328.7	13	I	6	912.52		912.52	
	1429.8		1429.8	14	T	5	799.44	+0.0291	400.22	+0.0648
+0.1621	771.94	-0.197	1542.9	15	I	4	698.39	+0.2581	698.39	
	1689.9		1689.9	16	F	3	585.31	+0.1062	585.31	
-0.203	909.5		1818	17	Q	2	438.24	+0.0657	438.24	
	1947		1947	18	E	1	310.18	+0.0915	310.18	
				19	R	0	181.14		181.14	

Scan number	7083	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	128.99



precursor information

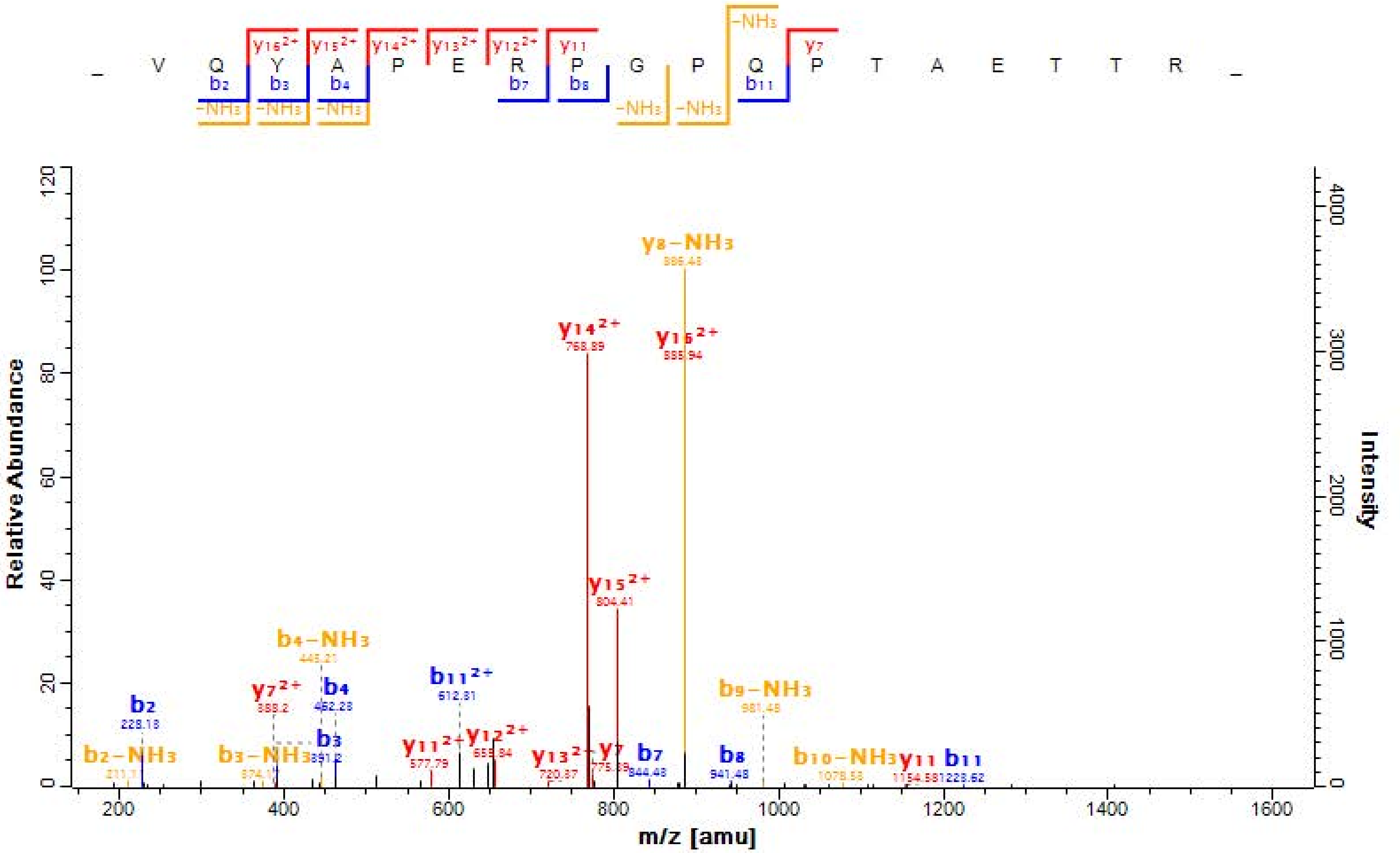
Mass:	2091.09994
m/z:	698.04059
Charge:	3+
Retentiontime:	47.259059906005
Score:	128.9908
Mass Error [ppm]:	-0.052805
PEP:	1.9369E-08
Precursor Type:	ISO

general information

Annotation:	13 of 20
AminoAcids Coverag	65 %
Intensity Coverage:	66 %
Peak Coverage:	28 %
Protein Localisation:	338 ... 357

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	I	19				
	242.19		242.19	2	K	18	1979		1979	
	313.22	+0.1939	313.22	3	A	17	1850.9		1850.9	
	442.27		442.27	4	E	16	1779.9		1779.9	
	605.33	+0.0729	605.33	5	Y	15	1650.8		1650.8	
	734.37		734.37	6	E	14	1487.8		1487.8	
	791.39		791.39	7	G	13	1358.7		1358.7	
	906.42		906.42	8	D	12	1301.7		1301.7	
	963.44	-0.016	963.44	9	G	11	1186.7		1186.7	
+0.2672	538.77	-0.038	1076.5	10	I	10	1129.7		1129.7	
	1173.6		1173.6	11	P	9	1016.6	+0.0267	508.8	+0.195
	1274.6		1274.6	12	T	8	919.54		919.54	
+0.004	687.35	-0.24	1373.7	13	V	7	818.49	+0.0591	409.75	+0.0913
+0.2204	760.89	-0.221	1520.8	14	F	6	719.42	+0.026	719.42	
+0.1982	810.42	-0.113	1619.8	15	V	5	572.35	+0.0816	572.35	
-0.077	845.94		1690.9	16	A	4	473.28	-0.037	473.28	
+0.3575	895.47		1789.9	17	V	3	402.25	-0.02	402.25	
-0.208	930.99		1861	18	A	2	303.18	+0.025	303.18	
	1918		1918	19	G	1	232.14	+0.0028	232.14	
				20	R	0	175.12		175.12	

Scan number	779	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	85.73



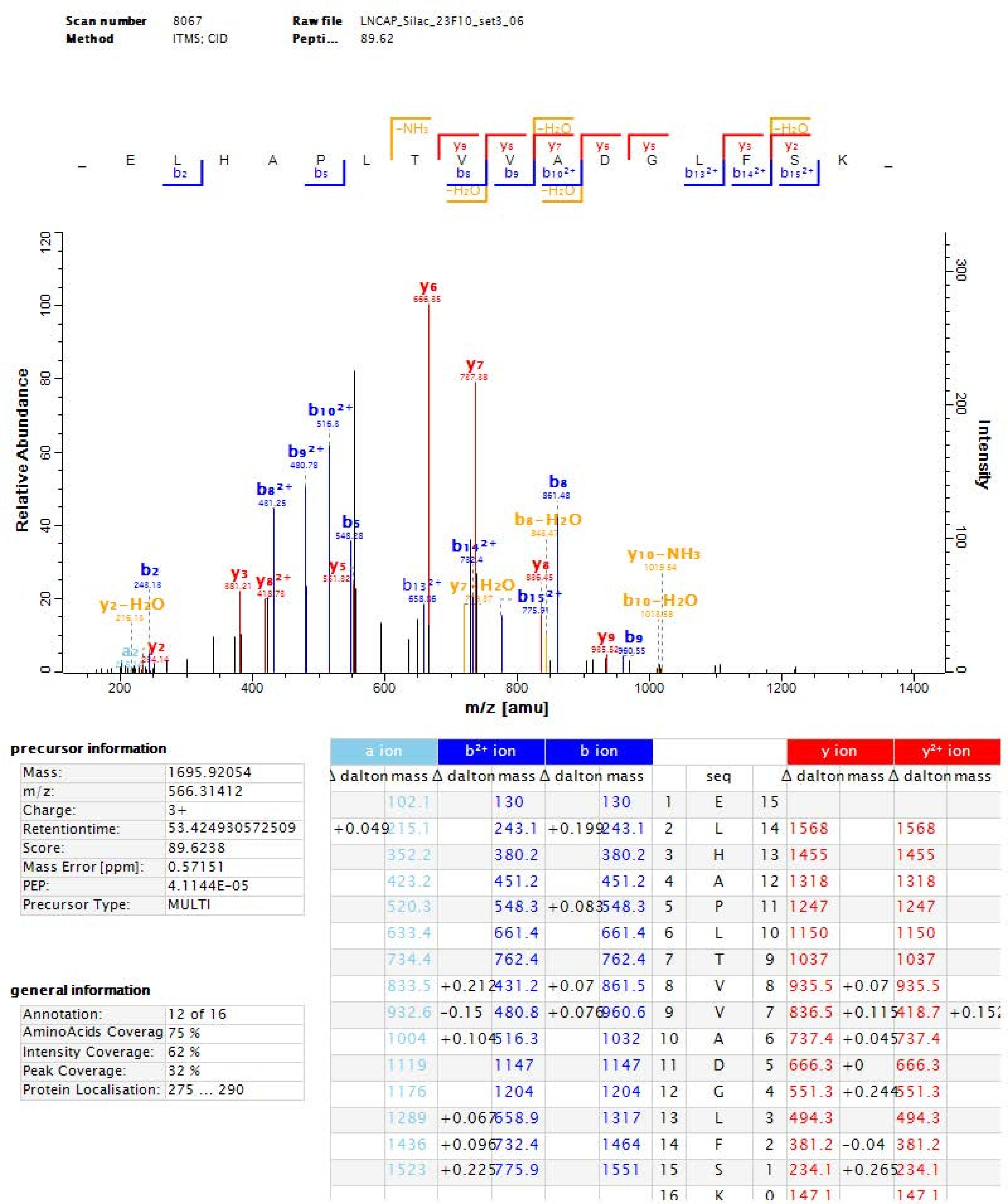
precursor information

Mass:	1996.99709
m/z:	666.67297
Charge:	3+
Retentiontime:	10.823862075805
Score:	85.73382
Mass Error [ppm]:	0.22078
PEP:	4.6849E-05
Precursor Type:	MULTI

general information

Annotation:	11 of 18
AminoAcids Coverag	61 %
Intensity Coverage:	82 %
Peak Coverage:	27 %
Protein Localisation:	171 ... 188

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	17				
	228.13	-0.079	228.13	2	Q	16	1898.9		1898.9	
	391.2	-0.019	391.2	3	Y	15	1770.9		885.94	+0.0385
	462.23	-0.091	462.23	4	A	14	1607.8		804.41	+0.2202
	559.29		559.29	5	P	13	1536.8		768.89	+0.3115
	688.33		688.33	6	E	12	1439.7		720.37	-0.1
	844.43	+0.0577	844.43	7	R	11	1310.7		655.84	+0.4083
	941.48	+0.2947	941.48	8	P	10	1154.6	+0.0543	577.79	+0.1821
	998.51		998.51	9	G	9	1057.5		1057.5	
	1095.6		1095.6	10	P	8	1000.5		1000.5	
+0.2061	612.31	+0.236	1223.6	11	Q	7	903.45		903.45	
	1320.7		1320.7	12	P	6	775.39	+0.1473	388.2	+0.3508
	1421.7		1421.7	13	T	5	678.34		678.34	
	1492.8		1492.8	14	A	4	577.29		577.29	
	1621.8		1621.8	15	E	3	506.26		506.26	
	1722.8		1722.8	16	T	2	377.21		377.21	
	1823.9		1823.9	17	T	1	276.17		276.17	
				18	R	0	175.12		175.12	



Scan number 8067
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set3_06
Pepti... 89.62

precursor information

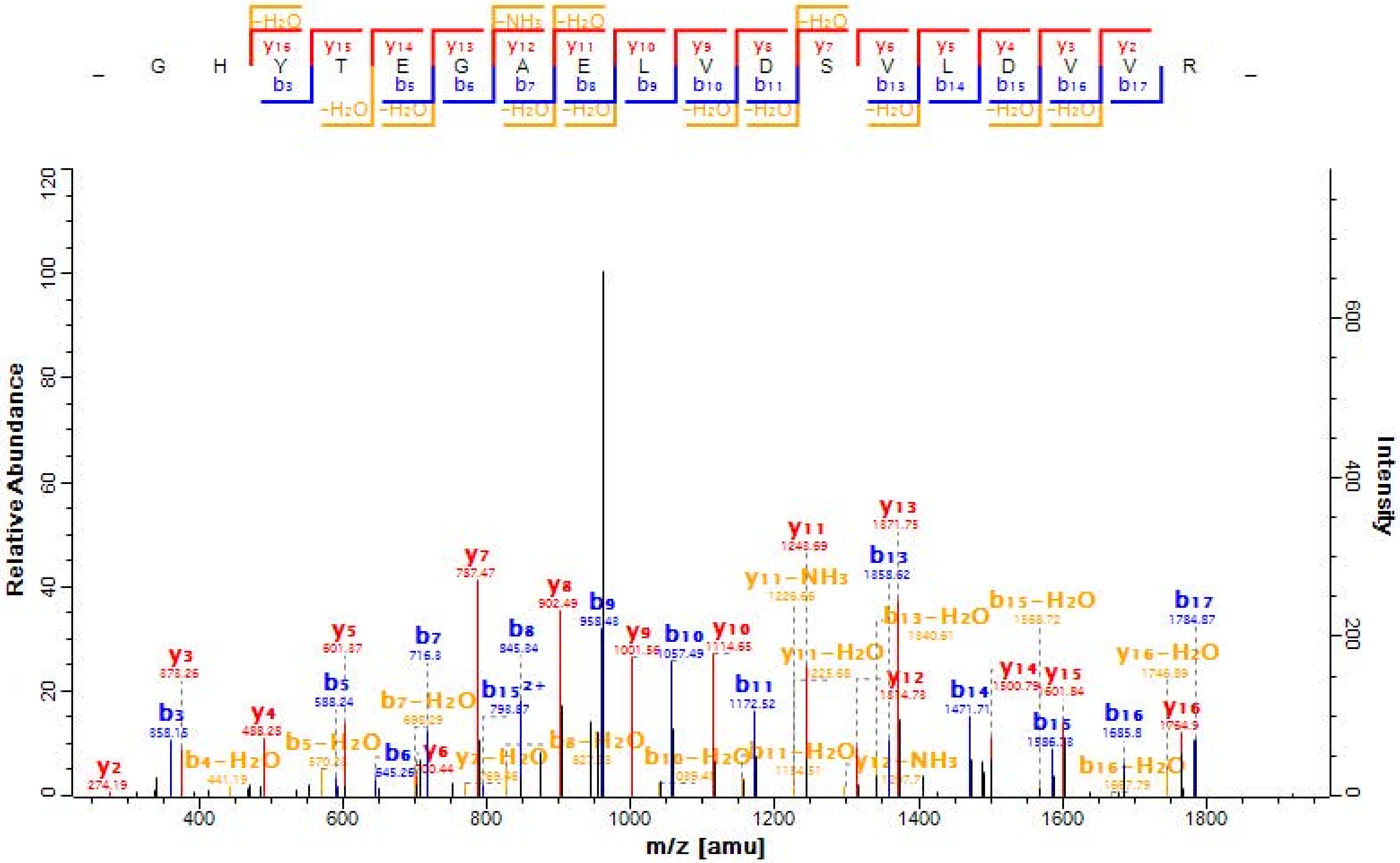
Mass:	1695.92054
m/z:	566.31412
Charge:	3+
Retentiontime:	53.424930572509
Score:	89.6238
Mass Error [ppm]:	0.57151
PEP:	4.1144E-05
Precursor Type:	MULTI

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	62 %
Peak Coverage:	32 %
Protein Localisation:	275 ... 290

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.1		130		130	1	E	15				
+0.049	215.1		243.1	+0.199	243.1	2	L	14	1568		1568	
	352.2		380.2		380.2	3	H	13	1455		1455	
	423.2		451.2		451.2	4	A	12	1318		1318	
	520.3		548.3	+0.083	548.3	5	P	11	1247		1247	
	633.4		661.4		661.4	6	L	10	1150		1150	
	734.4		762.4		762.4	7	T	9	1037		1037	
	833.5	+0.212	431.2	+0.07	861.5	8	V	8	935.5	+0.07	935.5	
	932.6	-0.15	480.8	+0.076	960.6	9	V	7	836.5	+0.115	418.7	+0.15
	1004	+0.104	516.3		1032	10	A	6	737.4	+0.045	737.4	
	1119		1147		1147	11	D	5	666.3	+0	666.3	
	1176		1204		1204	12	G	4	551.3	+0.244	551.3	
	1289	+0.067	658.9		1317	13	L	3	494.3		494.3	
	1436	+0.096	732.4		1464	14	F	2	381.2	-0.04	381.2	
	1523	+0.225	775.9		1551	15	S	1	234.1	+0.265	234.1	
						16	K	0	147.1		147.1	

Scan number	9228	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	267.38



precursor information

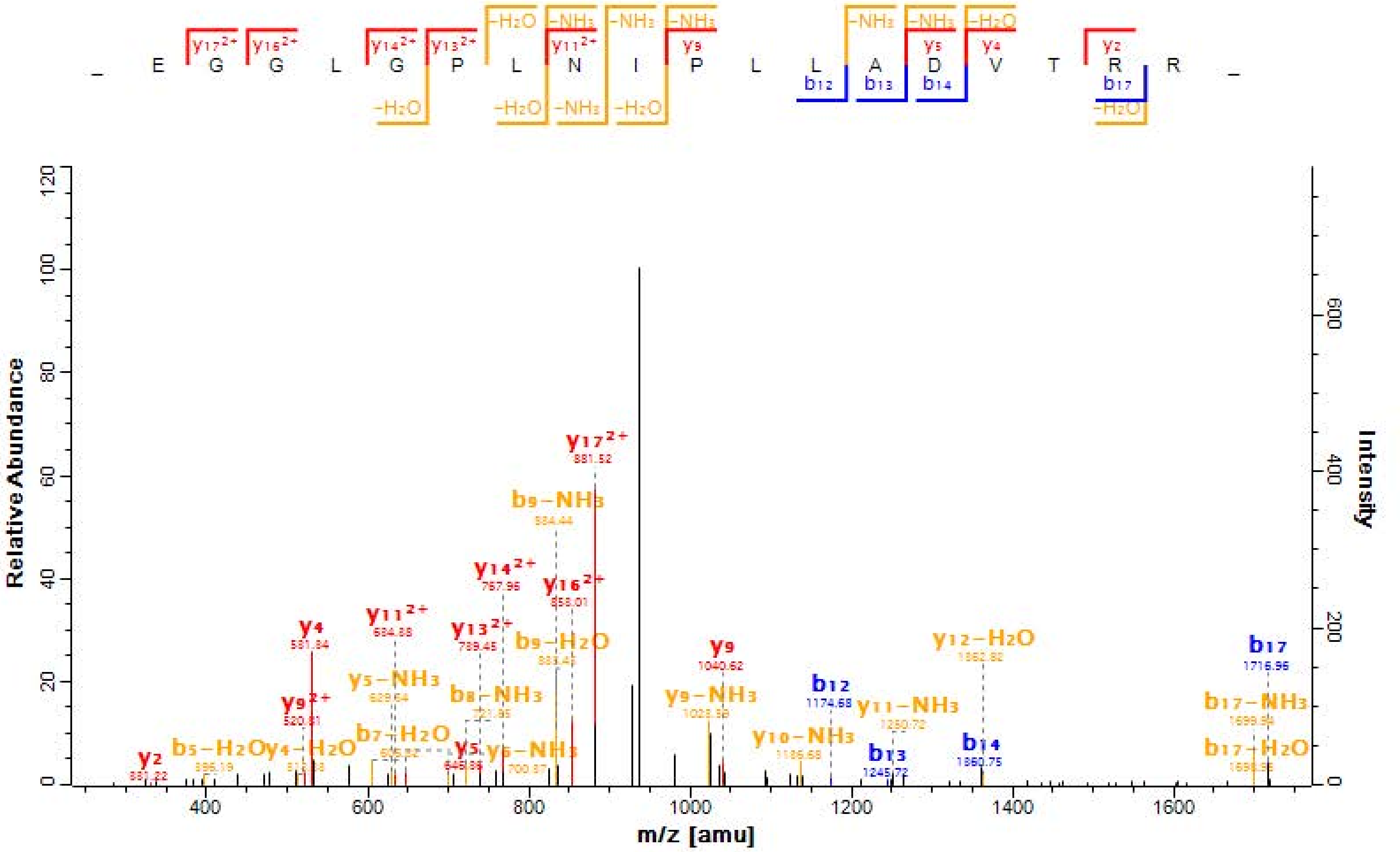
Mass:	1957.9748
m/z:	979.99467
Charge:	2+
Retentiontime:	62.787651062011
Score:	267.3771
Mass Error [ppm]:	0.14144
PEP:	6.5565E-82
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	59 %
Peak Coverage:	45 %
Protein Localisation:	104 ... 121

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	58.02874		58.02874	1	G	17		
	195.0877		195.0877	2	H	16	1901.96	
	358.151	+0.065328	358.151	3	Y	15	1764.901	-0.03338
	459.1987		459.1987	4	T	14	1601.838	-0.14901
	588.2413	-0.06205	588.2413	5	E	13	1500.79	-0.04334
	645.2627	+0.001933	645.2627	6	G	12	1371.748	-0.13625
	716.2998	+0.141821	716.2998	7	A	11	1314.726	-0.08732
	845.3424	+0.016708	845.3424	8	E	10	1243.689	-0.03739
	958.4265	-0.05057	958.4265	9	L	9	1114.647	-0.02702
	1057.495	-0.01785	1057.495	10	V	8	1001.563	+0.05454
	1172.522	-0.05627	1172.522	11	D	7	902.4942	-0.00546
	1259.554		1259.554	12	S	6	787.4672	+0.057368
	1358.622	+0.00662	1358.622	13	V	5	700.4352	+0.03184
	1471.706	-0.0844	1471.706	14	L	4	601.3668	+0.001072
+0.461808	793.8703	+0.192122	1586.733	15	D	3	488.2827	+0.021537
	1685.802	+0.034963	1685.802	16	V	2	373.2558	+0.121051
	1784.87	-0.1261	1784.87	17	V	1	274.1874	+0.046246
				18	R	0	175.119	

Scan number	9411	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	93.42



precursor information

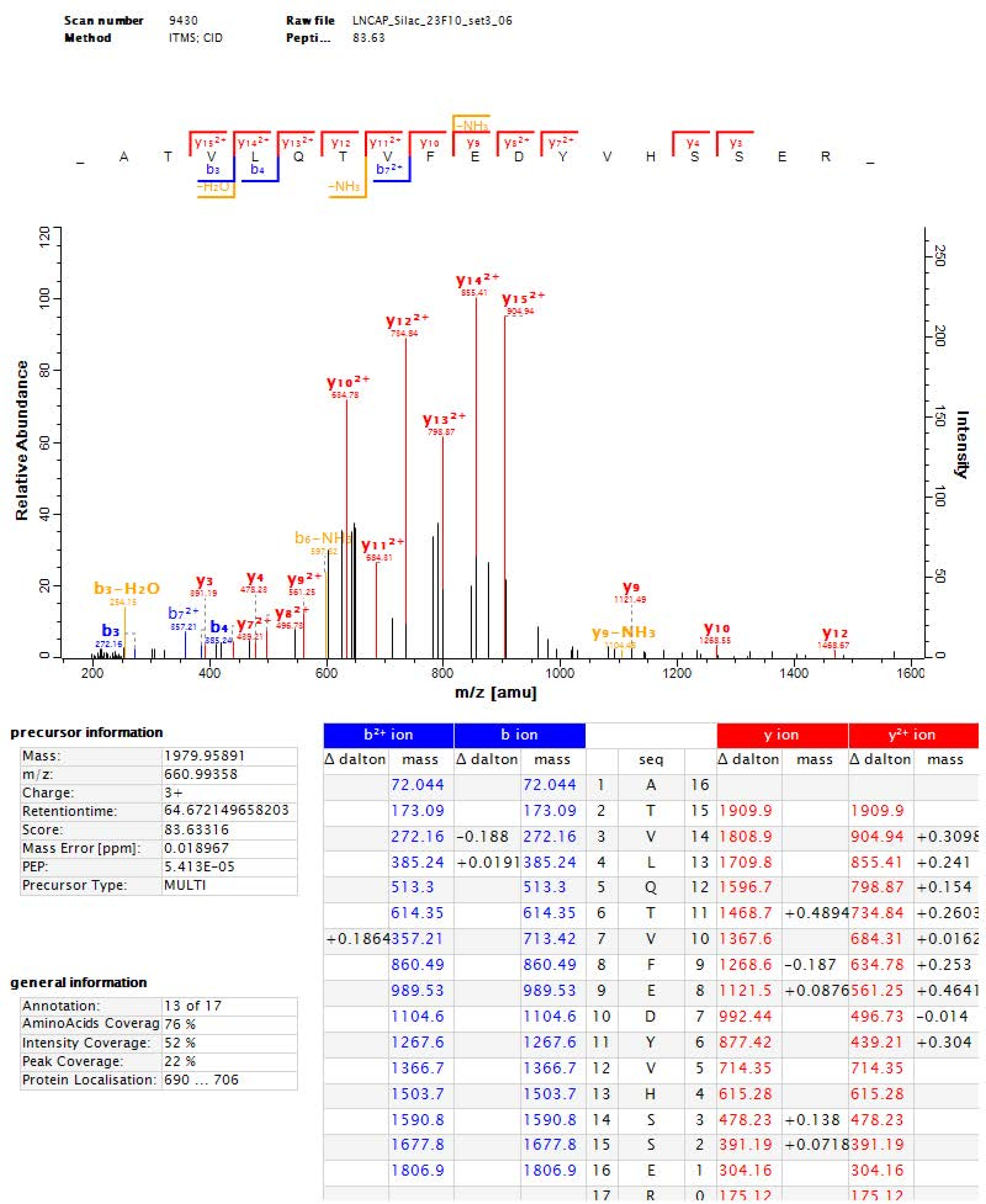
Mass:	1890.06858
m/z:	946.04156
Charge:	2+
Retentiontime:	64.485786437988
Score:	93.42417
Mass Error [ppm]:	-0.062872
PEP:	9.7928E-06
Precursor Type:	MULTI

general information

Annotation:	14 of 18
AminoAcids Coverag	78 %
Intensity Coverage:	38 %
Peak Coverage:	32 %
Protein Localisation:	93 ... 110

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	17				
	187.0713	2	G	16	1762.033		881.5203	+0.260678
	244.0928	3	G	15	1705.012		853.0096	+0.190539
	357.1769	4	L	14	1647.99		1647.99	
	414.1983	5	G	13	1534.906		767.9568	+0.406694
	511.2511	6	P	12	1477.885		739.4461	+0.16944
	624.3352	7	L	11	1380.832		1380.832	
	738.3781	8	N	10	1267.748		634.3777	+0.203918
	851.4621	9	I	9	1153.705		1153.705	
	948.5149	10	P	8	1040.621	-0.0713	520.8142	+0.118976
	1061.599	11	L	7	943.5683		943.5683	
-0.04607	1174.683	12	L	6	830.4843		830.4843	
+0.030217	1245.72	13	A	5	717.4002		717.4002	
-0.19887	1360.747	14	D	4	646.3631	+0.016174	646.3631	
	1459.816	15	V	3	531.3362	+0.021327	531.3362	
	1560.863	16	T	2	432.2677		432.2677	
+0.025084	1716.964	17	R	1	331.2201	+0.220733	331.2201	
		18	R	0	175.119		175.119	

Scan number	9430	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	83.63



precursor information

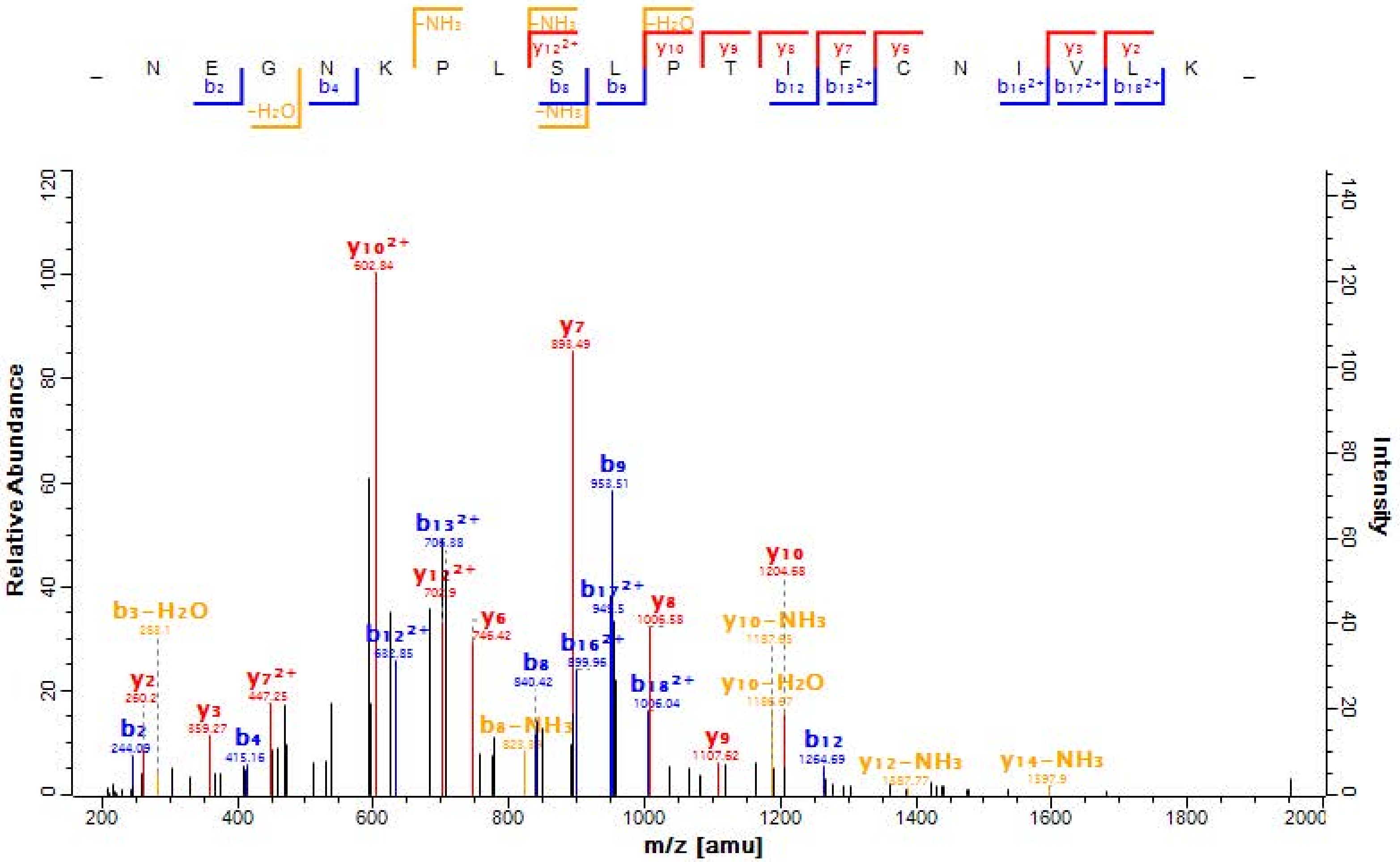
Mass:	1979.95891
m/z:	660.99358
Charge:	3+
Retentiontime:	64.672149658203
Score:	83.63316
Mass Error [ppm]:	0.018967
PEP:	5.413E-05
Precursor Type:	MULTI

general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	52 %
Peak Coverage:	22 %
Protein Localisation:	690 ... 706

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	16				
	173.09		173.09	2	T	15	1909.9		1909.9	
	272.16	-0.188	272.16	3	V	14	1808.9		904.94	+0.3098
	385.24	+0.0191	385.24	4	L	13	1709.8		855.41	+0.241
	513.3		513.3	5	Q	12	1596.7		798.87	+0.154
	614.35		614.35	6	T	11	1468.7	+0.4894	734.84	+0.2603
+0.1864	357.21		713.42	7	V	10	1367.6		684.31	+0.0162
	860.49		860.49	8	F	9	1268.6	-0.187	634.78	+0.253
	989.53		989.53	9	E	8	1121.5	+0.0876	561.25	+0.4641
	1104.6		1104.6	10	D	7	992.44		496.73	-0.014
	1267.6		1267.6	11	Y	6	877.42		439.21	+0.304
	1366.7		1366.7	12	V	5	714.35		714.35	
	1503.7		1503.7	13	H	4	615.28		615.28	
	1590.8		1590.8	14	S	3	478.23	+0.138	478.23	
	1677.8		1677.8	15	S	2	391.19	+0.0718	391.19	
	1806.9		1806.9	16	E	1	304.16		304.16	
				17	R	0	175.12		175.12	

Scan number	9563	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	111.78



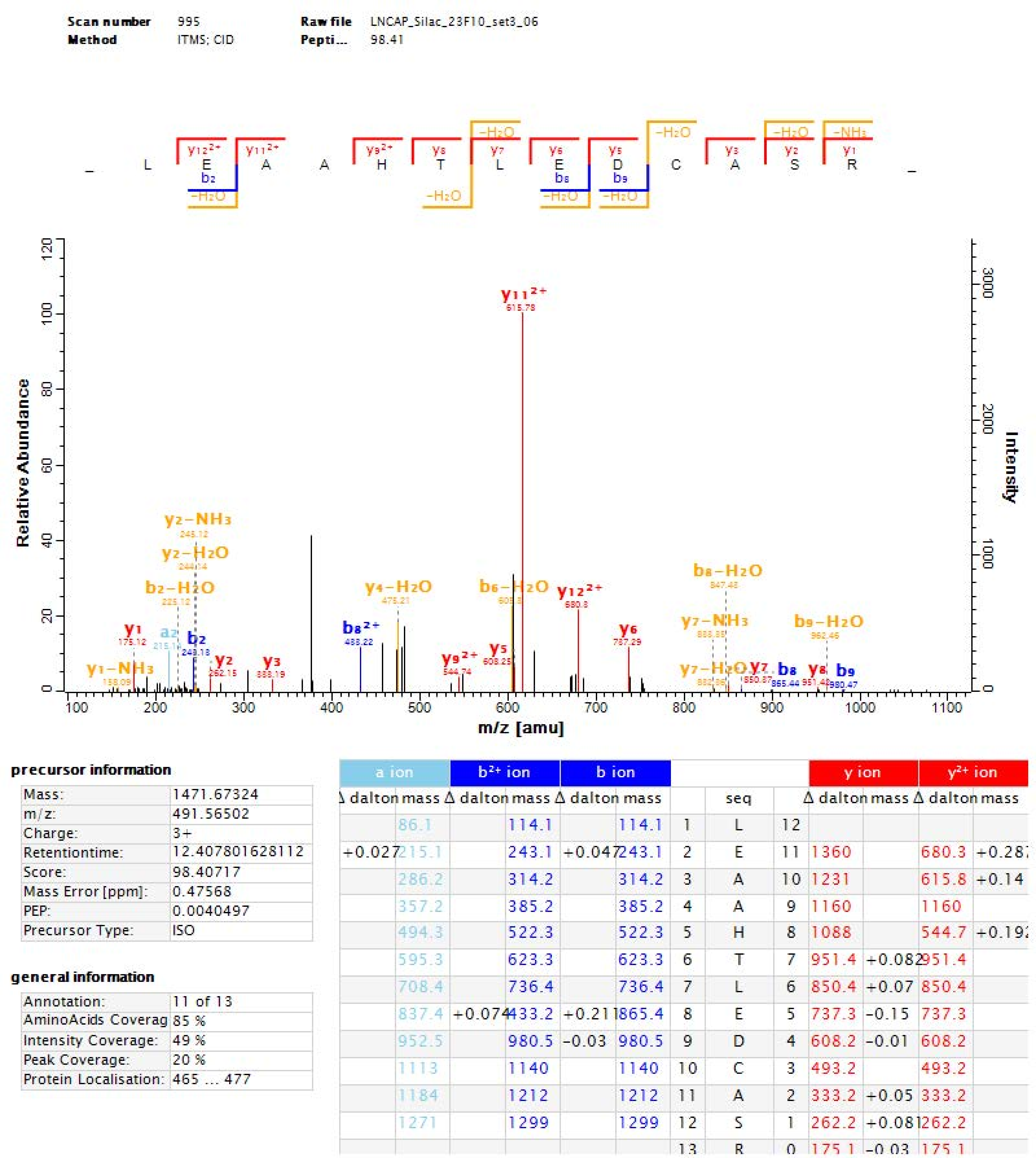
precursor information

Mass:	2156.16717
m/z:	719.72967
Charge:	3+
Retentiontime:	66.051361083984
Score:	111.776
Mass Error [ppm]:	0.37441
PEP:	1.6894E-08
Precursor Type:	MULTI

general information

Annotation:	14 of 19
AminoAcids Coverag	74 %
Intensity Coverage:	50 %
Peak Coverage:	29 %
Protein Localisation:	803 ... 821

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.05		115.05	1	N	18				
	244.09	+0.1597	244.09	2	E	17	2043.1		2043.1	
	301.11		301.11	3	G	16	1914.1		1914.1	
	415.16	+0.1904	415.16	4	N	15	1857.1		1857.1	
	543.25		543.25	5	K	14	1743		1743	
	640.3		640.3	6	P	13	1614.9		1614.9	
	753.39		753.39	7	L	12	1517.9		1517.9	
	840.42	-0.049	840.42	8	S	11	1404.8		702.9	-0.305
	953.51	-0.021	953.51	9	L	10	1317.8		1317.8	
	1050.6		1050.6	10	P	9	1204.7	-0.028	602.84	+0.1667
	1151.6		1151.6	11	T	8	1107.6	+0.0796	1107.6	
+0.3245	632.85	+0.1475	1264.7	12	I	7	1006.6	+0.2724	1006.6	
+0.2004	706.38		1411.8	13	F	6	893.49	-0.069	447.25	+0.2061
	1571.8		1571.8	14	C	5	746.42	+0.1984	746.42	
	1685.8		1685.8	15	N	4	586.39		586.39	
+0.463	899.96		1798.9	16	I	3	472.35		472.35	
+0.3666	949.5		1898	17	V	2	359.27	+0.1366	359.27	
-0.032	1006		2011.1	18	L	1	260.2	+0.0993	260.2	
				19	K	0	147.11		147.11	



Scan number	995	**Raw file**	LNCAP_Silac_23F10_set3_06
Method	ITMS; CID	**Pepti...**	98.41

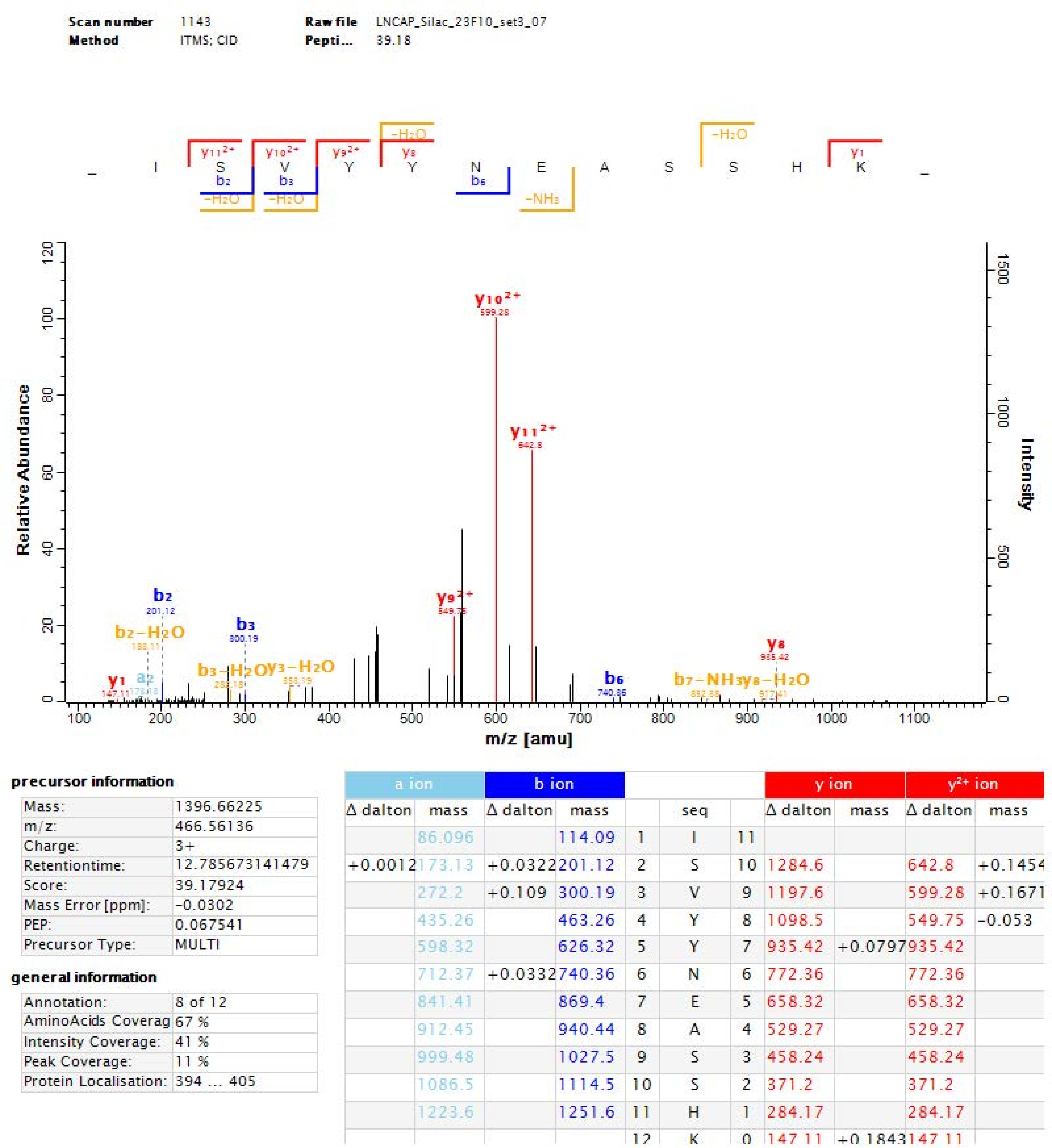
precursor information

Mass:	1471.67324
m/z:	491.56502
Charge:	3+
Retentiontime:	12.407801628112
Score:	98.40717
Mass Error [ppm]:	0.47568
PEP:	0.0040497
Precursor Type:	ISO

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	49 %
Peak Coverage:	20 %
Protein Localisation:	465 ... 477

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	12				
+0.027	215.1		243.1	+0.047	243.1	2	E	11	1360		680.3	+0.28
	286.2		314.2		314.2	3	A	10	1231		615.8	+0.14
	357.2		385.2		385.2	4	A	9	1160		1160	
	494.3		522.3		522.3	5	H	8	1088		544.7	+0.19
	595.3		623.3		623.3	6	T	7	951.4	+0.082	951.4	
	708.4		736.4		736.4	7	L	6	850.4	+0.07	850.4	
	837.4	+0.074	433.2	+0.211	865.4	8	E	5	737.3	-0.15	737.3	
	952.5		980.5	-0.03	980.5	9	D	4	608.2	-0.01	608.2	
	1113		1140		1140	10	C	3	493.2		493.2	
	1184		1212		1212	11	A	2	333.2	+0.05	333.2	
	1271		1299		1299	12	S	1	262.2	+0.081	262.2	
						13	R	0	175.1	-0.03	175.1	



Scan number	1143	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	39.18

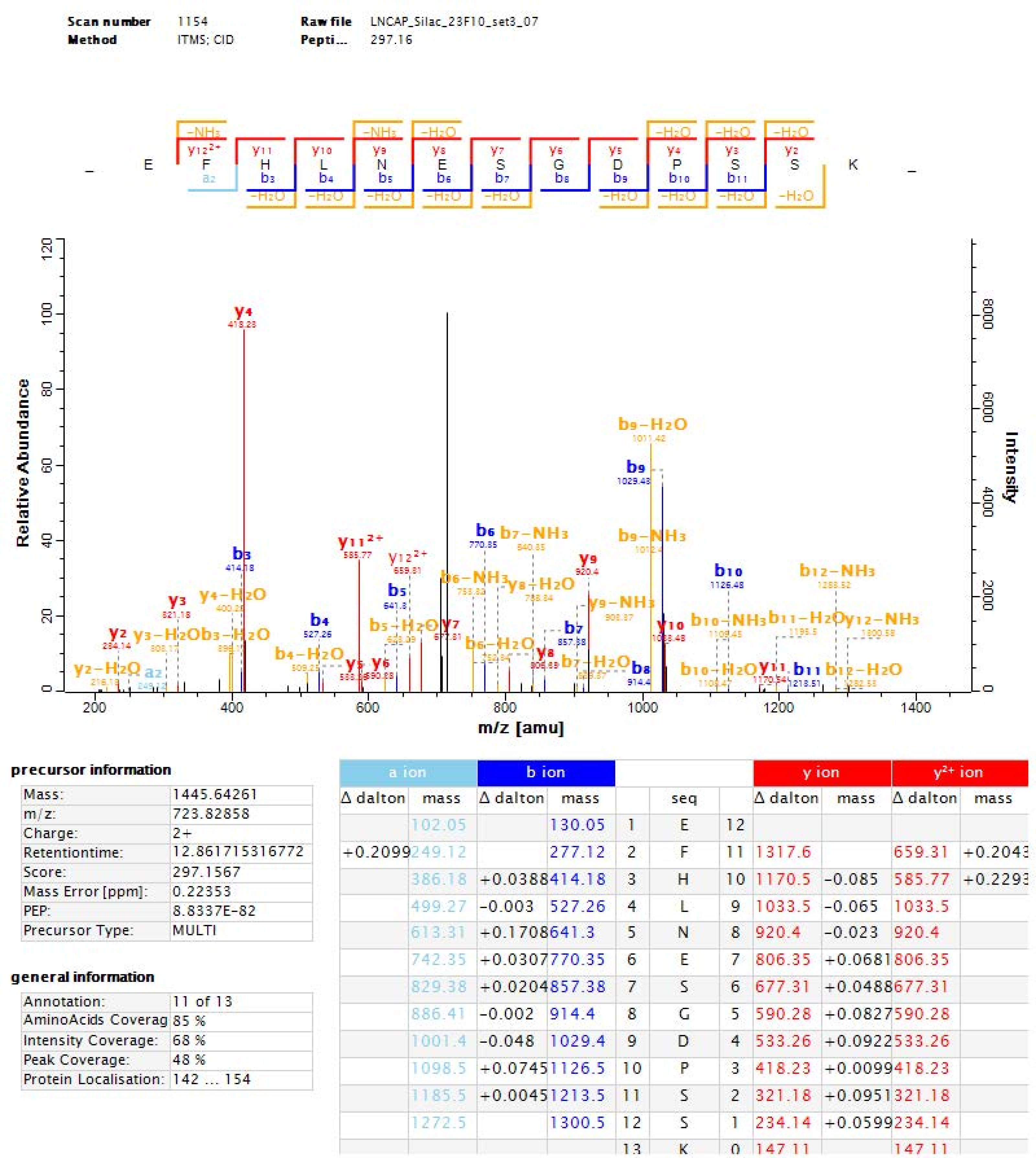
precursor information

Mass:	1396.66225
m/z:	466.56136
Charge:	3+
Retentiontime:	12.785673141479
Score:	39.17924
Mass Error [ppm]:	-0.0302
PEP:	0.067541
Precursor Type:	MULTI

general information

Annotation:	8 of 12
AminoAcids Coverag	67 %
Intensity Coverage:	41 %
Peak Coverage:	11 %
Protein Localisation:	394 ... 405

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	11				
+0.0012	173.13	+0.0322	201.12	2	S	10	1284.6		642.8	+0.1454
	272.2	+0.109	300.19	3	V	9	1197.6		599.28	+0.1671
	435.26		463.26	4	Y	8	1098.5		549.75	-0.053
	598.32		626.32	5	Y	7	935.42	+0.0797	935.42	
	712.37	+0.0332	740.36	6	N	6	772.36		772.36	
	841.41		869.4	7	E	5	658.32		658.32	
	912.45		940.44	8	A	4	529.27		529.27	
	999.48		1027.5	9	S	3	458.24		458.24	
	1086.5		1114.5	10	S	2	371.2		371.2	
	1223.6		1251.6	11	H	1	284.17		284.17	
				12	K	0	147.11	+0.1843	147.11	



Scan number	1154	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	297.16

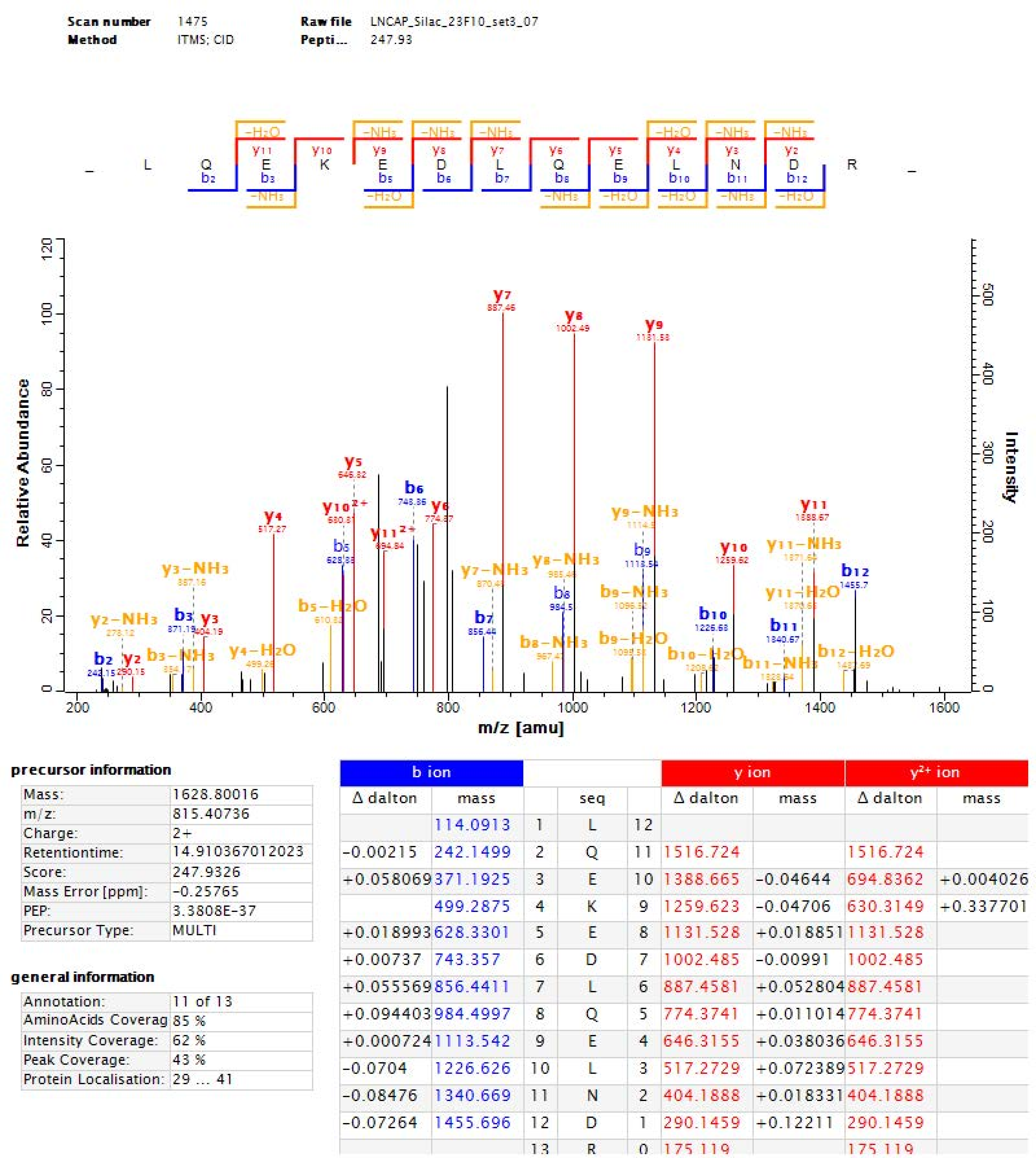
precursor information

Mass:	1445.64261
m/z:	723.82858
Charge:	2+
Retentiontime:	12.861715316772
Score:	297.1567
Mass Error [ppm]:	0.22353
PEP:	8.8337E-82
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	68 %
Peak Coverage:	48 %
Protein Localisation:	142 ... 154

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	12				
+0.2099	249.12		277.12	2	F	11	1317.6		659.31	+0.2043
	386.18	+0.0388	414.18	3	H	10	1170.5	-0.085	585.77	+0.2293
	499.27	-0.003	527.26	4	L	9	1033.5	-0.065	1033.5	
	613.31	+0.1708	641.3	5	N	8	920.4	-0.023	920.4	
	742.35	+0.0307	770.35	6	E	7	806.35	+0.0681	806.35	
	829.38	+0.0204	857.38	7	S	6	677.31	+0.0488	677.31	
	886.41	-0.002	914.4	8	G	5	590.28	+0.0827	590.28	
	1001.4	-0.048	1029.4	9	D	4	533.26	+0.0922	533.26	
	1098.5	+0.0745	1126.5	10	P	3	418.23	+0.0099	418.23	
	1185.5	+0.0045	1213.5	11	S	2	321.18	+0.0951	321.18	
	1272.5		1300.5	12	S	1	234.14	+0.0599	234.14	
				13	K	0	147.11		147.11	



Scan number	1475	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	247.93

precursor information

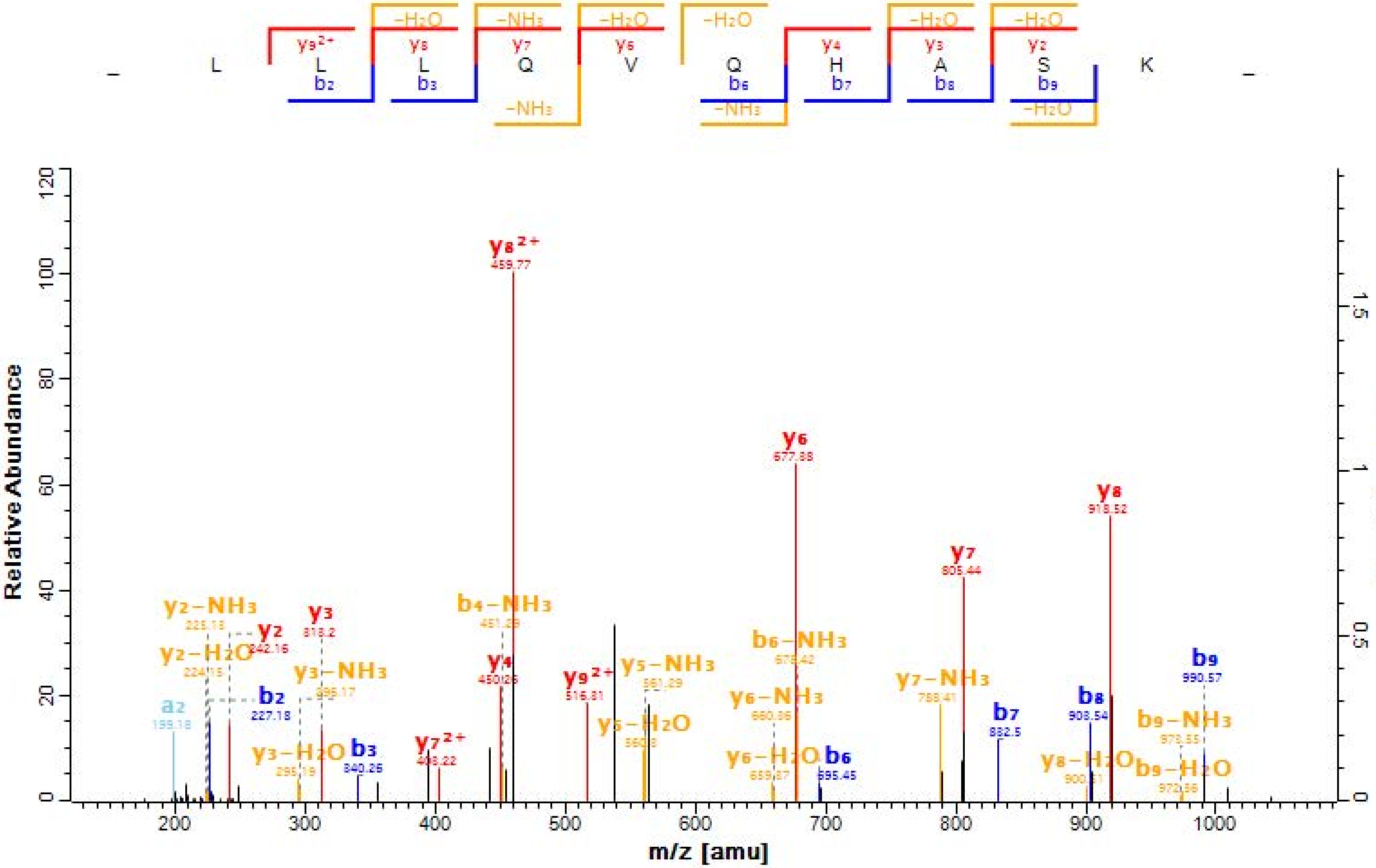
Mass:	1628.80016
m/z:	815.40736
Charge:	2+
Retentiontime:	14.910367012023
Score:	247.9326
Mass Error [ppm]:	-0.25765
PEP:	3.3808E-37
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	62 %
Peak Coverage:	43 %
Protein Localisation:	29 … 41

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	12				
-0.00215	242.1499	2	Q	11	1516.724		1516.724	
+0.058069	371.1925	3	E	10	1388.665	-0.04644	694.8362	+0.004026
	499.2875	4	K	9	1259.623	-0.04706	630.3149	+0.337701
+0.018993	628.3301	5	E	8	1131.528	+0.018851	1131.528	
+0.00737	743.357	6	D	7	1002.485	-0.00991	1002.485	
+0.055569	856.4411	7	L	6	887.4581	+0.052804	887.4581	
+0.094403	984.4997	8	Q	5	774.3741	+0.011014	774.3741	
+0.000724	1113.542	9	E	4	646.3155	+0.038036	646.3155	
-0.0704	1226.626	10	L	3	517.2729	+0.072389	517.2729	
-0.08476	1340.669	11	N	2	404.1888	+0.018331	404.1888	
-0.07264	1455.696	12	D	1	290.1459	+0.12211	290.1459	
		13	R	0	175.119		175.119	

Scan number	1656	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	205.83

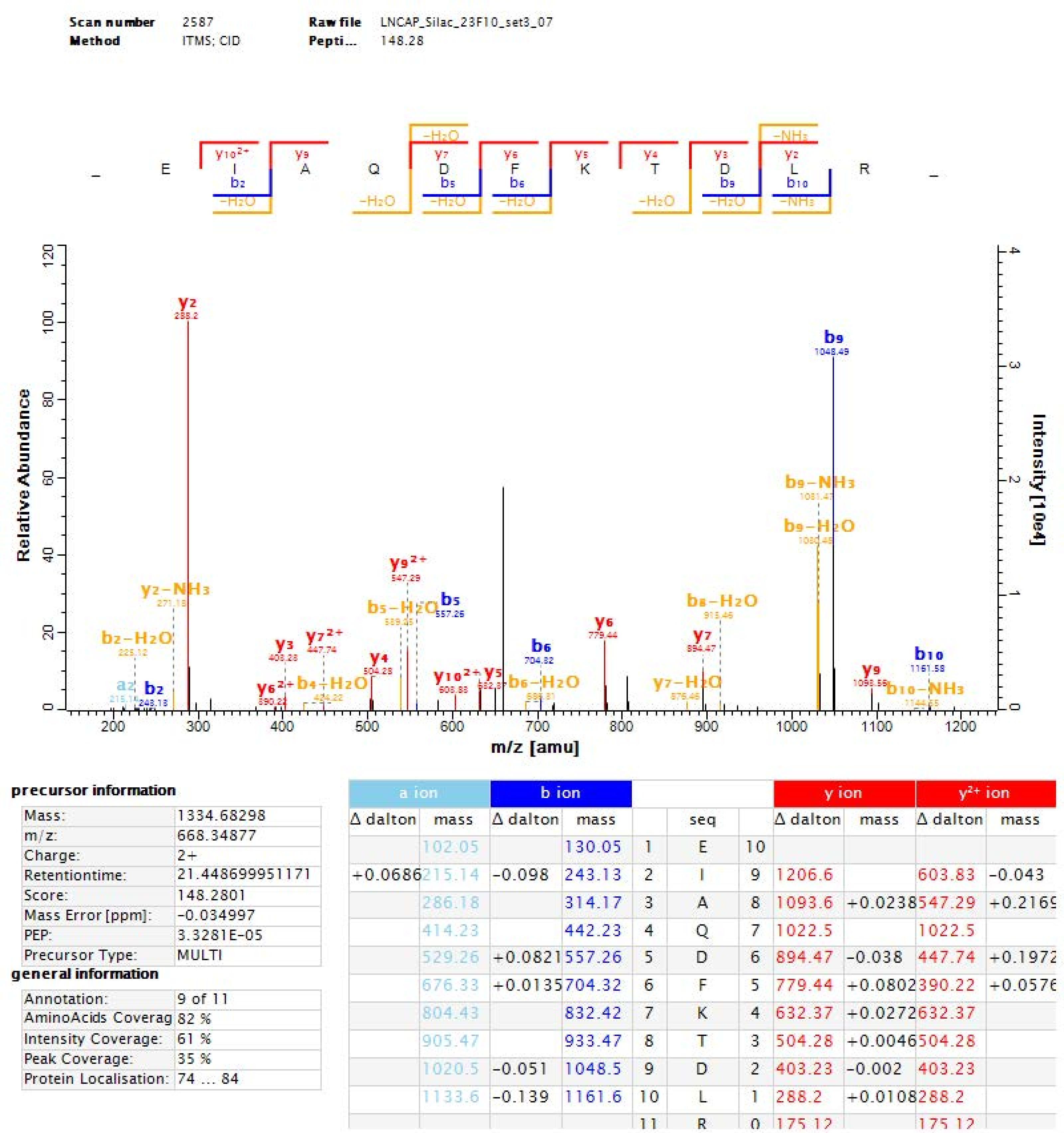


precursor information

Mass:	1135.67131
m/z:	568.84293
Charge:	2+
Retentiontime:	16.003427505493
Score:	205.8269
Mass Error [ppm]:	-0.026876
PEP:	4.1172E-13
Precursor Type:	MULTI

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	70 %
Peak Coverage:	37 %
Protein Localisation:	34 ... 43

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	9				
-0.03	199.18	-0.066	227.18	2	L	8	1031.6		516.31	+0.2605
	312.26	-0.047	340.26	3	L	7	918.52	-0.046	459.77	+0.0496
	440.32		468.32	4	Q	6	805.44	+0.0279	403.22	+0.1588
	539.39		567.39	5	V	5	677.38	-0.056	677.38	
	667.45	-0.179	695.45	6	Q	4	578.31		578.31	
	804.51	+0.111	832.5	7	H	3	450.26	+0.181	450.26	
	875.55	-0.019	903.54	8	A	2	313.2	-0.004	313.2	
	962.58	-0.059	990.57	9	S	1	242.16	+0.1233	242.16	
				10	K	0	155.13		155.13	



Scan number	2587	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	148.28

precursor information

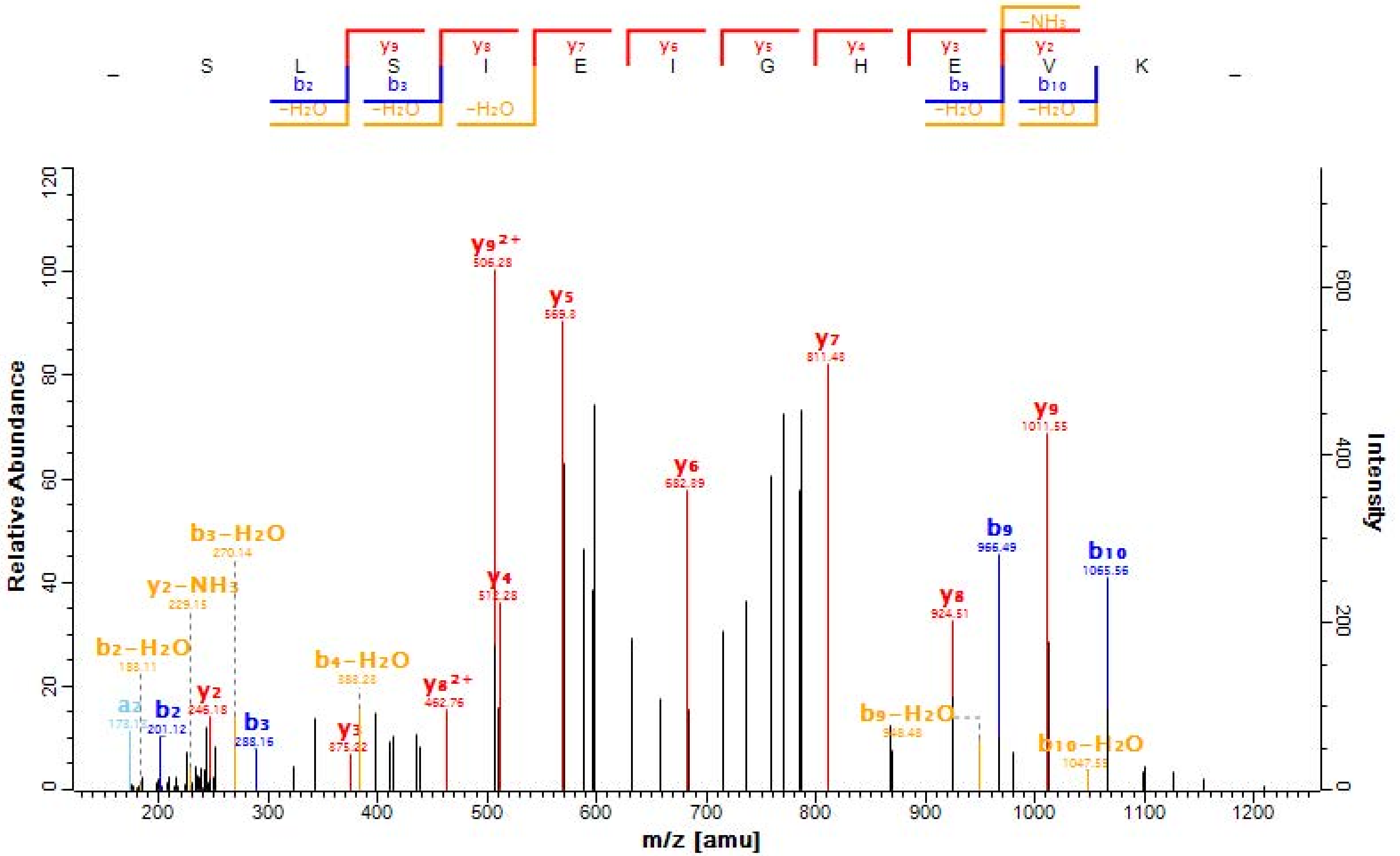
Mass:	1334.68298
m/z:	668.34877
Charge:	2+
Retentiontime:	21.448699951171
Score:	148.2801
Mass Error [ppm]:	-0.034997
PEP:	3.3281E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	61 %
Peak Coverage:	35 %
Protein Localisation:	74 ... 84

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	10				
+0.0686	215.14	-0.098	243.13	2	I	9	1206.6		603.83	-0.043
	286.18		314.17	3	A	8	1093.6	+0.0238	547.29	+0.2169
	414.23		442.23	4	Q	7	1022.5		1022.5	
	529.26	+0.0821	557.26	5	D	6	894.47	-0.038	447.74	+0.1972
	676.33	+0.0135	704.32	6	F	5	779.44	+0.0802	390.22	+0.0576
	804.43		832.42	7	K	4	632.37	+0.0272	632.37	
	905.47		933.47	8	T	3	504.28	+0.0046	504.28	
	1020.5	-0.051	1048.5	9	D	2	403.23	-0.002	403.23	
	1133.6	-0.139	1161.6	10	L	1	288.2	+0.0108	288.2	
				11	R	0	175.12		175.12	

Scan number	2870	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	99.75



precursor information

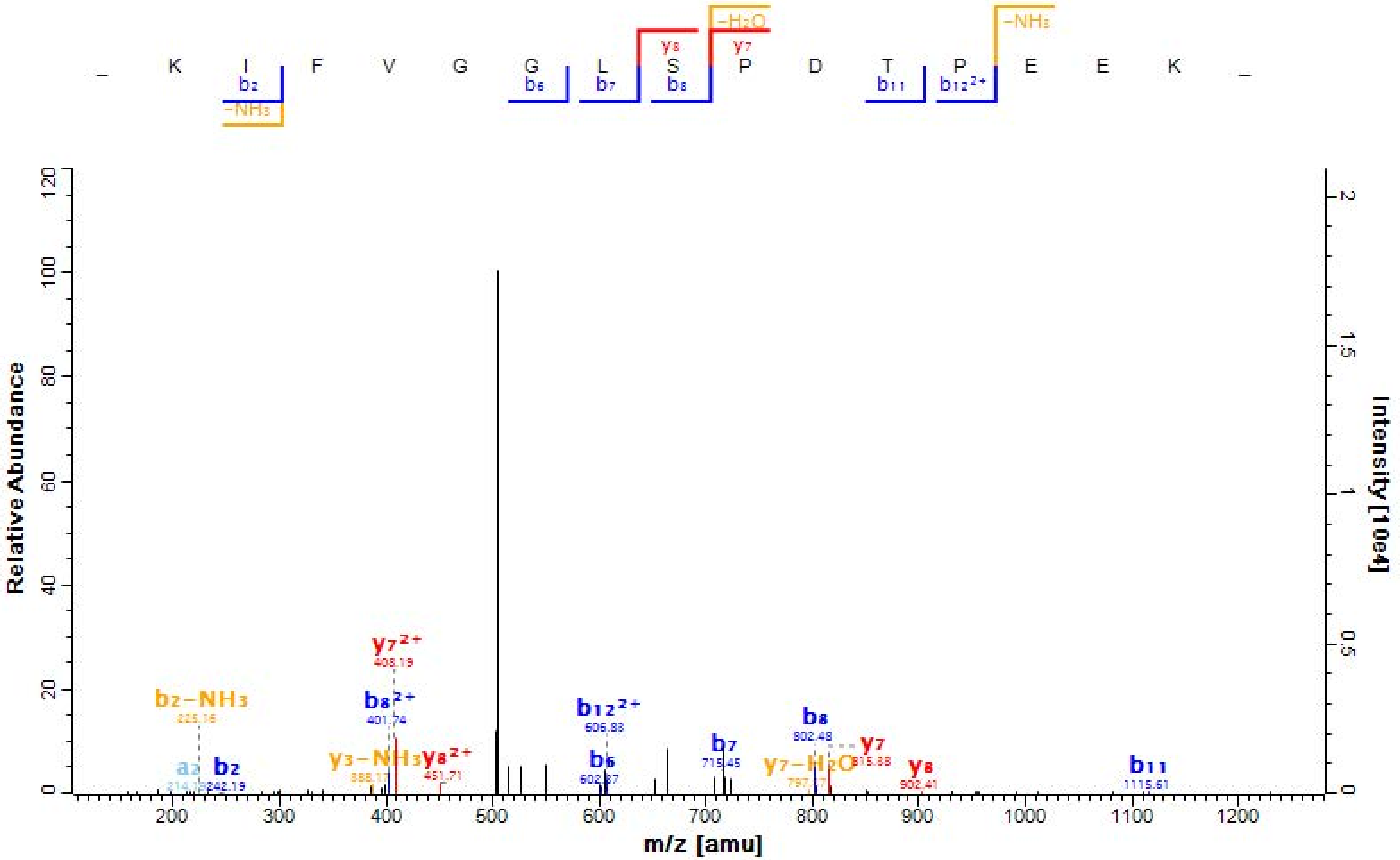
Mass:	1210.65543
m/z:	606.33499
Charge:	2+
Retentiontime:	23.167114257812
Score:	99.75196
Mass Error [ppm]:	-0.26229
PEP:	0.00071468
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	40 %
Peak Coverage:	23 %
Protein Localisation:	63 ... 73

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	60.044		88.039	1	S	10				
+0.0204	173.13	-0.032	201.12	2	L	9	1124.6		1124.6	
	260.16	+0.0609	288.16	3	S	8	1011.5	-0.065	506.28	-0.013
	373.24		401.24	4	I	7	924.51	-0.036	462.76	+0.1942
	502.29		530.28	5	E	6	811.43	+0.0162	811.43	
	615.37		643.37	6	I	5	682.39	+0.2076	682.39	
	672.39		700.39	7	G	4	569.3	+0.1816	569.3	
	809.45		837.45	8	H	3	512.28	+0.0292	512.28	
	938.49	-0.047	966.49	9	E	2	375.22	-0.051	375.22	
	1037.6	+0.0677	1065.6	10	V	1	246.18	-0.128	246.18	
				11	K	0	147.11		147.11	

Scan number	3010	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	47.53



precursor information

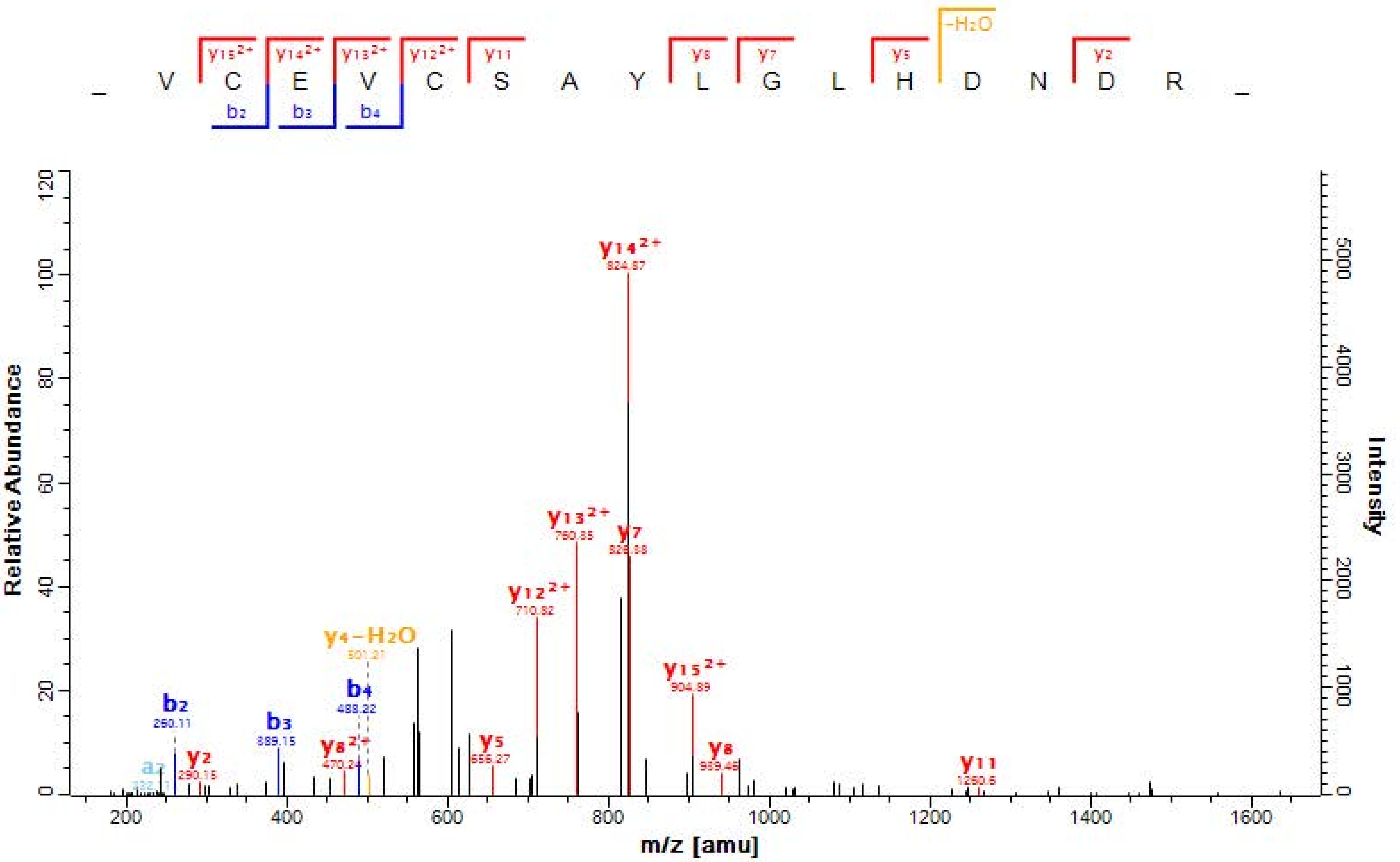
Mass:	1615.76894
m/z:	539.59692
Charge:	3+
Retentiontime:	23.954595565795
Score:	47.53175
Mass Error [ppm]:	-0.92079
PEP:	0.03475
Precursor Type:	MULTI

general information

Annotation:	8 of 15
AminoAcids Coverag	53 %
Intensity Coverage:	17 %
Peak Coverage:	16 %
Protein Localisation:	164 ... 178

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	101.1		129.1		129.1	1	K	14				
+0.097	214.2		242.2	+0.051	242.2	2	I	13	1489		1489	
	361.3		389.3		389.3	3	F	12	1376		1376	
	460.3		488.3		488.3	4	V	11	1229		1229	
	517.3		545.3		545.3	5	G	10	1130		1130	
	574.4		602.4	+0.037	602.4	6	G	9	1073		1073	
	687.5		715.5	+0.239	715.5	7	L	8	1015		1015	
	774.5	+0.101	401.7	+0.061	802.5	8	S	7	902.4	+0.224	451.7	+0.24
	871.5		899.5		899.5	9	P	6	815.4	+0.11	408.2	+0.19
	986.6		1015		1015	10	D	5	718.3		718.3	
	1088		1116	+0.269	1116	11	T	4	603.3		603.3	
	1185	+0.03	606.8		1213	12	P	3	502.3		502.3	
	1314		1342		1342	13	E	2	405.2		405.2	
	1443		1471		1471	14	E	1	276.2		276.2	
						15	K	0	147.1		147.1	

Scan number	3055	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	65.47



precursor information

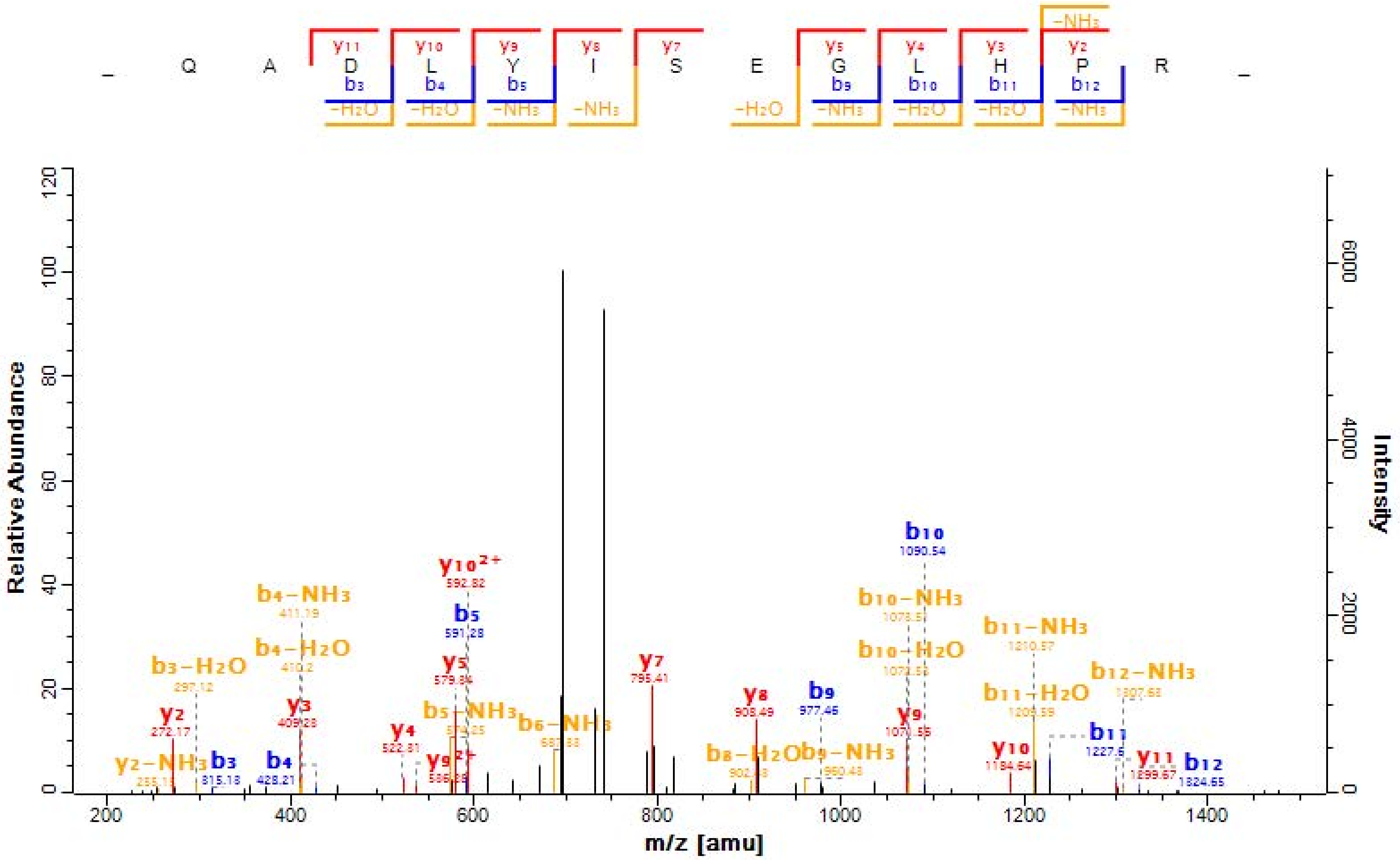
Mass:	1906.82915
m/z:	636.61699
Charge:	3+
Retentiontime:	24.199304580688
Score:	65.47156
Mass Error [ppm]:	-0.53903
PEP:	0.0017448
Precursor Type:	MULTI

general information

Annotation:	10 of 16
AminoAcids Coverag	62 %
Intensity Coverage:	43 %
Peak Coverage:	16 %
Protein Localisation:	255 ... 270

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.081		100.08	1	V	15				
+0.1795	232.11	-0.002	260.11	2	C	14	1808.8		904.89	+0.2452
	361.15	+0.0283	389.15	3	E	13	1648.7		824.87	-0.013
	460.22	+0.1885	488.22	4	V	12	1519.7		760.35	+0.2235
	620.25		648.25	5	C	11	1420.6		710.82	+0.2602
	707.29		735.28	6	S	10	1260.6	-0.066	1260.6	
	778.32		806.32	7	A	9	1173.6		1173.6	
	941.39		969.38	8	Y	8	1102.5		1102.5	
	1054.5		1082.5	9	L	7	939.46	+0.1338	470.24	+0.353
	1111.5		1139.5	10	G	6	826.38	-0.222	826.38	
	1224.6		1252.6	11	L	5	769.36		769.36	
	1361.6		1389.6	12	H	4	656.27	-0.017	656.27	
	1476.7		1504.7	13	D	3	519.22		519.22	
	1590.7		1618.7	14	N	2	404.19		404.19	
	1705.7		1733.7	15	D	1	290.15	-0.01	290.15	
				16	R	0	175.12		175.12	

Scan number	3142	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	198.74



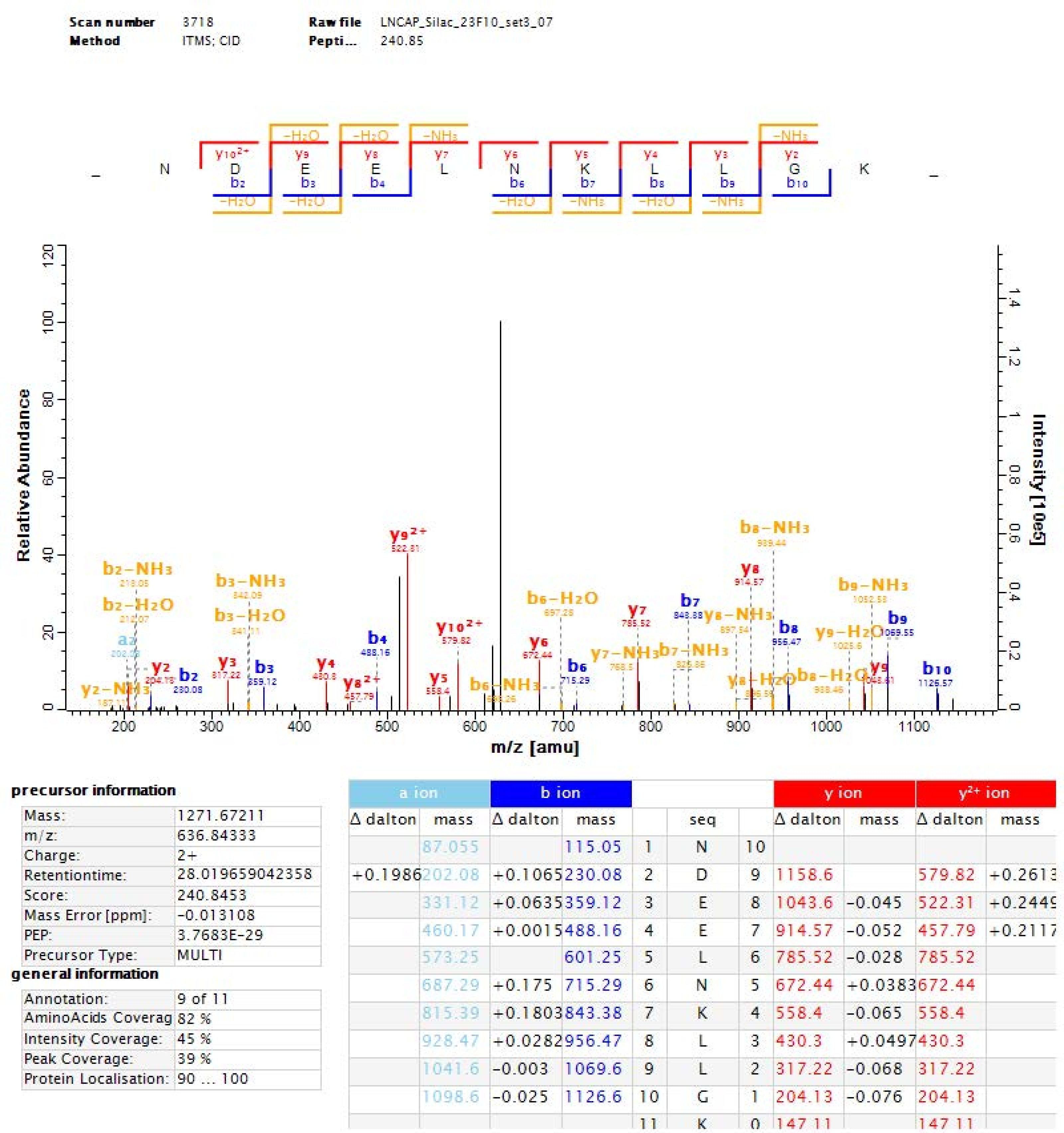
precursor information

Mass:	1497.75747
m/z:	749.88601
Charge:	2+
Retentiontime:	24.717082977294
Score:	198.7447
Mass Error [ppm]:	-0.082134
PEP:	1.3099E-17
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	36 %
Peak Coverage:	38 %
Protein Localisation:	105 ... 117

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.0659	1	Q	12				
	200.103	2	A	11	1370.706		1370.706	
+0.00986	315.1299	3	D	10	1299.669	+0.010023	1299.669	
+0.117995	428.214	4	L	9	1184.642	+0.011941	592.8248	-0.04149
-0.11135	591.2773	5	Y	8	1071.558	+0.051938	536.2827	+0.215141
	704.3614	6	I	7	908.4948	+0.018159	908.4948	
	791.3934	7	S	6	795.4108	-0.00239	795.4108	
	920.436	8	E	5	708.3787		708.3787	
-0.07171	977.4575	9	G	4	579.3362	+0.052577	579.3362	
+0.093371	1090.542	10	L	3	522.3147	+0.048284	522.3147	
-0.10299	1227.6	11	H	2	409.2306	+0.097497	409.2306	
+0.028693	1324.653	12	P	1	272.1717	+0.018164	272.1717	
		13	R	0	175.119		175.119	



Scan number 3718
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set3_07
Pepti... 240.85

precursor information

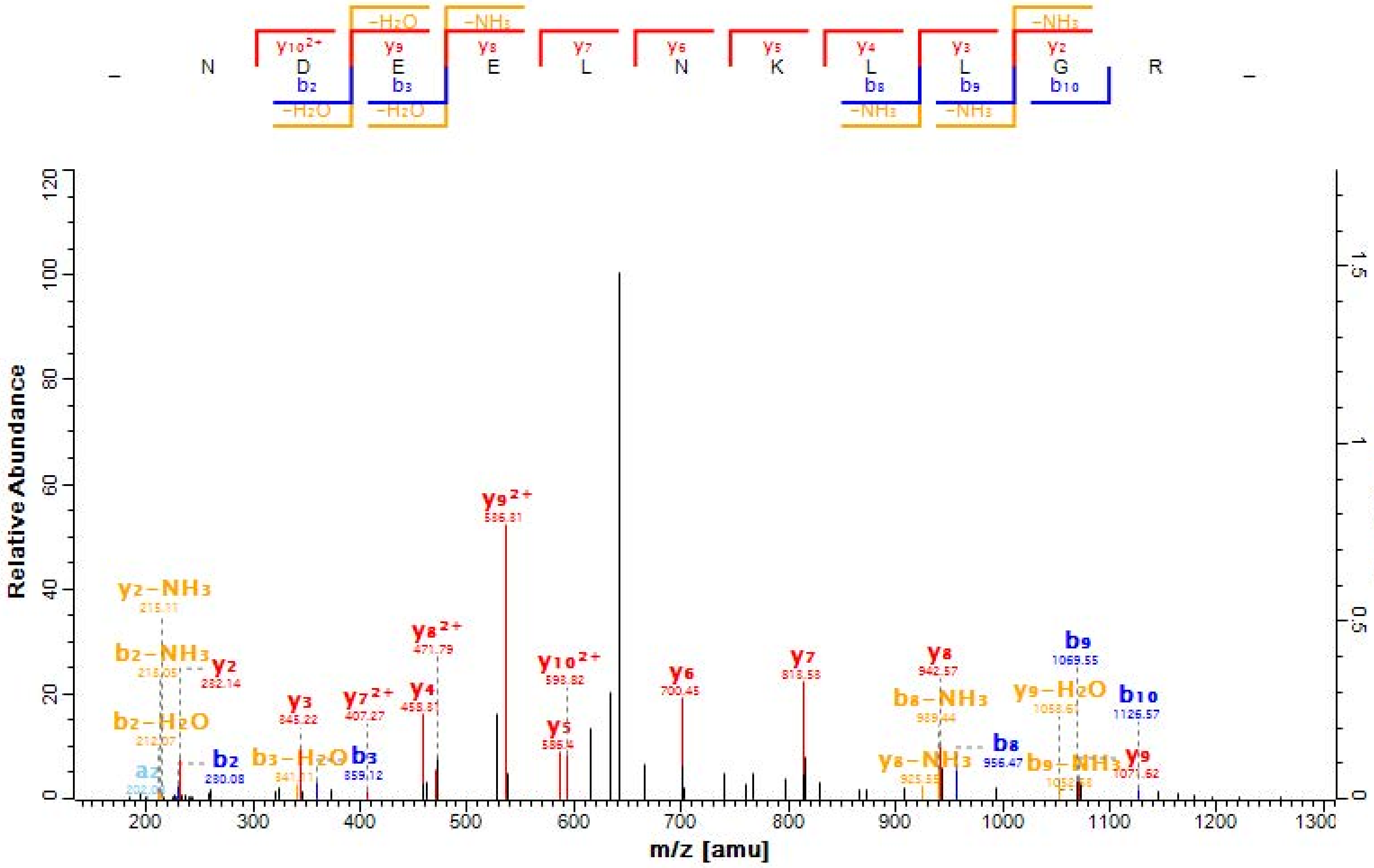
Mass:	1271.67211
m/z:	636.84333
Charge:	2+
Retentiontime:	28.019659042358
Score:	240.8453
Mass Error [ppm]:	-0.013108
PEP:	3.7683E-29
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	45 %
Peak Coverage:	39 %
Protein Localisation:	90 ... 100

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	87.055		115.05	1	N	10				
+0.1986	202.08	+0.1065	230.08	2	D	9	1158.6		579.82	+0.2613
	331.12	+0.0635	359.12	3	E	8	1043.6	-0.045	522.31	+0.2449
	460.17	+0.0015	488.16	4	E	7	914.57	-0.052	457.79	+0.2117
	573.25		601.25	5	L	6	785.52	-0.028	785.52	
	687.29	+0.175	715.29	6	N	5	672.44	+0.0383	672.44	
	815.39	+0.1803	843.38	7	K	4	558.4	-0.065	558.4	
	928.47	+0.0282	956.47	8	L	3	430.3	+0.0497	430.3	
	1041.6	-0.003	1069.6	9	L	2	317.22	-0.068	317.22	
	1098.6	-0.025	1126.6	10	G	1	204.13	-0.076	204.13	
				11	K	0	147.11		147.11	

Scan number 4127 **Raw file** LNCAP_Silac_23F10_set3_07
Method ITMS; CID **Pepti…** 147.62



precursor information

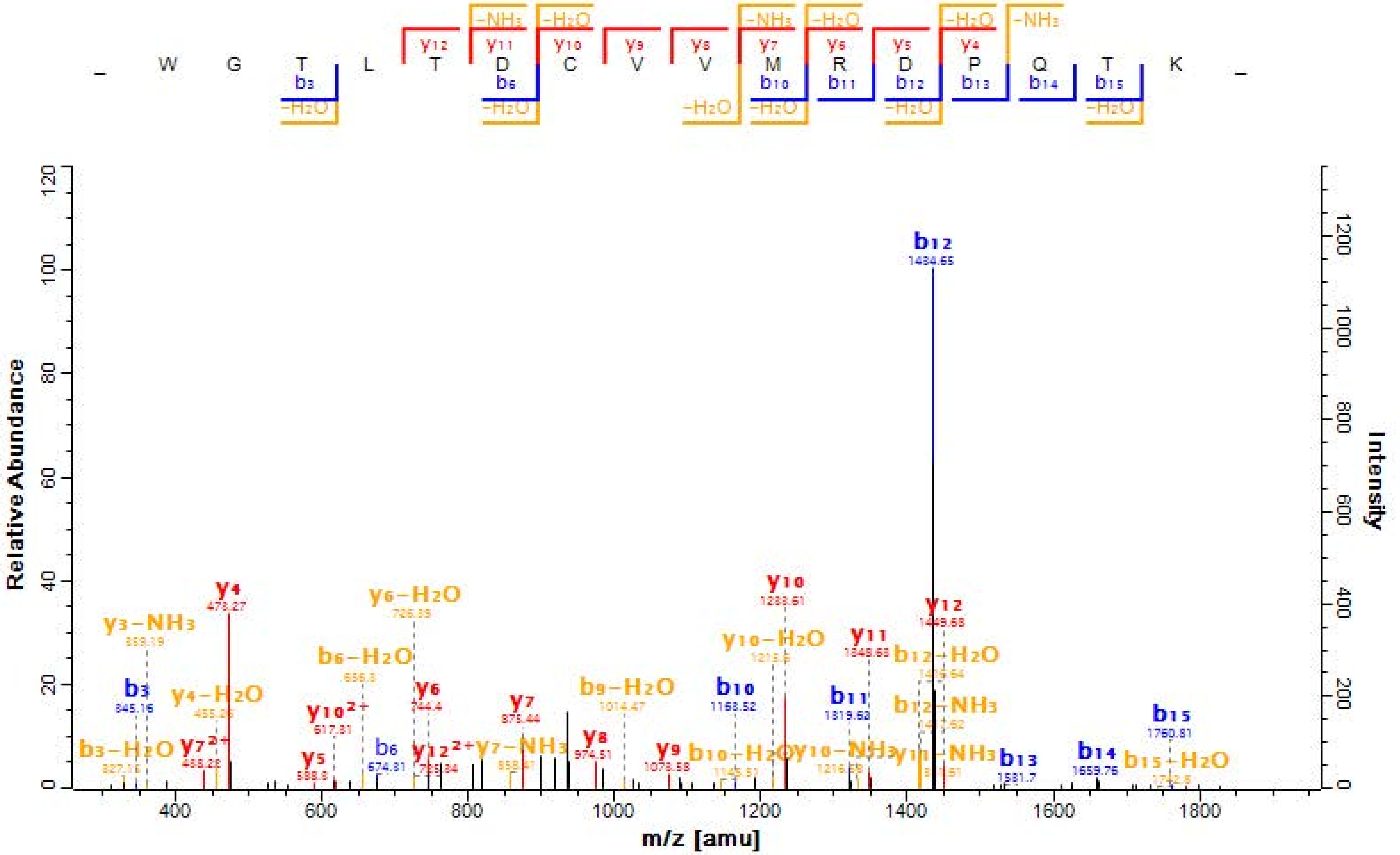
Mass:	1299.67815
m/z:	650.84635
Charge:	2+
Retentiontime:	30.375572204589
Score:	147.623
Mass Error [ppm]:	-0.097025
PEP:	3.9182E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	42 %
Peak Coverage:	31 %
Protein Localisation:	90 … 100

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	87.055		115.05	1	N	10				
+0.0367	202.08	-0.028	230.08	2	D	9	1186.6		593.82	-0.015
	331.12	+0.0957	359.12	3	E	8	1071.6	-0.064	536.31	+0.2532
	460.17		488.16	4	E	7	942.57	-0.012	471.79	-0.325
	573.25		601.25	5	L	6	813.53	-0.036	407.27	+0.0415
	687.29		715.29	6	N	5	700.45	+0.0694	700.45	
	815.39		843.38	7	K	4	586.4	+0.0581	586.4	
	928.47	+0.0128	956.47	8	L	3	458.31	+0.0625	458.31	
	1041.6	+0.0122	1069.6	9	L	2	345.22	+0.0368	345.22	
	1098.6	+0.0902	1126.6	10	G	1	232.14	+0.0125	232.14	
				11	R	0	175.12		175.12	

Scan number	4277	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	178.14



precursor information

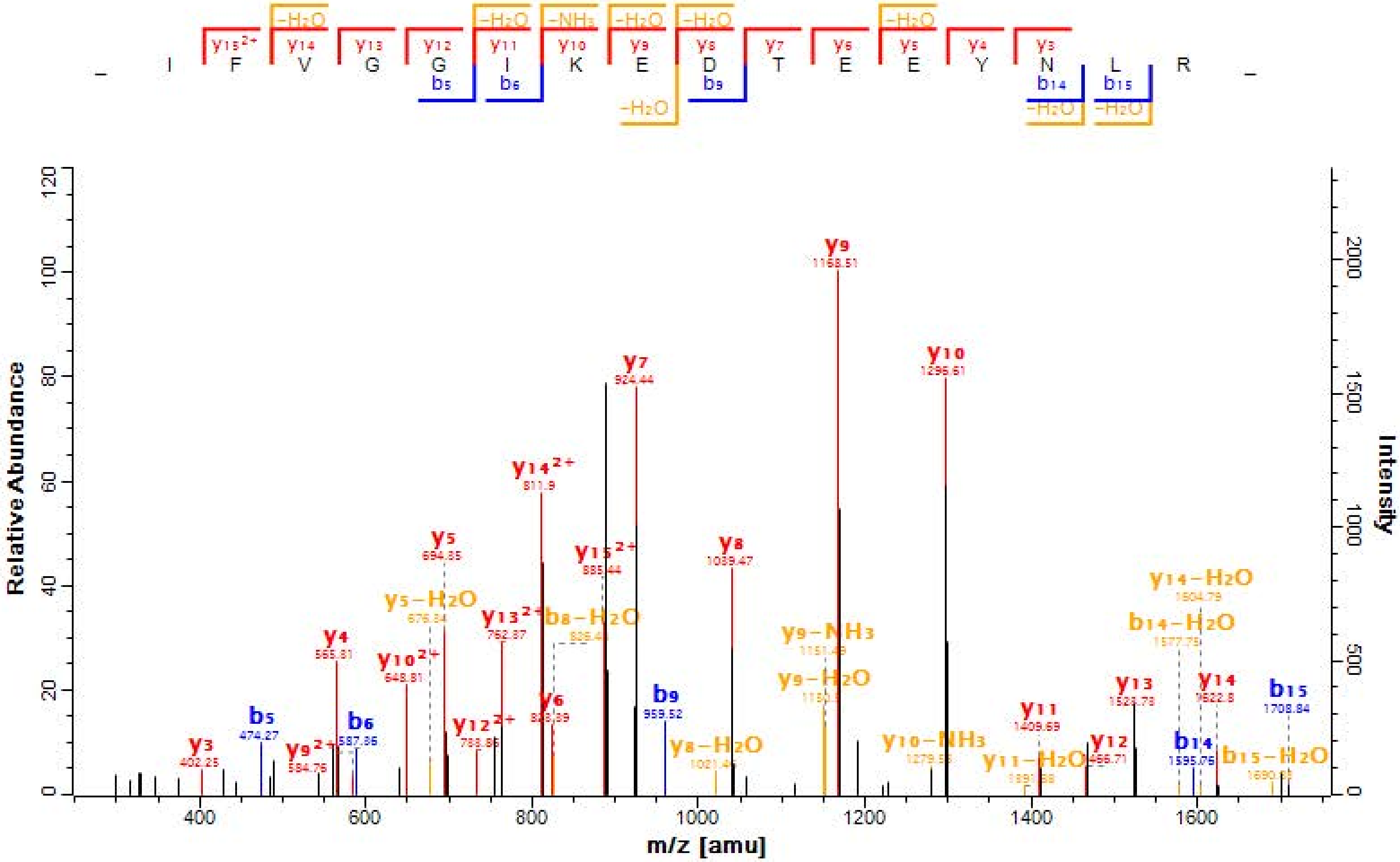
Mass:	1905.90812
m/z:	953.96134
Charge:	2+
Retentiontime:	31.224948883056
Score:	178.1395
Mass Error [ppm]:	0.21739
PEP:	1.2807E-19
Precursor Type:	ISO

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	54 %
Peak Coverage:	38 %
Protein Localisation:	58 ... 73

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	187.0866	1	W	15				
	244.1081	2	G	14	1720.836		1720.836	
+0.234741	345.1557	3	T	13	1663.814		1663.814	
	458.2398	4	L	12	1562.767		1562.767	
	559.2875	5	T	11	1449.682	+0.023717	725.3449	-0.06673
+0.162817	674.3144	6	D	10	1348.635	+0.053695	1348.635	
	834.3451	7	C	9	1233.608	-0.03313	617.3076	+0.260985
	933.4135	8	V	8	1073.577	+0.047809	1073.577	
	1032.482	9	V	7	974.5088	-0.06298	974.5088	
+0.3348	1163.522	10	M	6	875.4404	-0.11022	438.2238	+0.074337
-0.00642	1319.623	11	R	5	744.3999	-0.08451	744.3999	
-0.05973	1434.65	12	D	4	588.2988	+0.286682	588.2988	
+0.115042	1531.703	13	P	3	473.2718	+0.013149	473.2718	
-0.15179	1659.762	14	Q	2	376.2191		376.2191	
+0.230465	1760.809	15	T	1	248.1605		248.1605	
		16	K	0	147.1128		147.1128	

Scan number	4310	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	184.02



precursor information

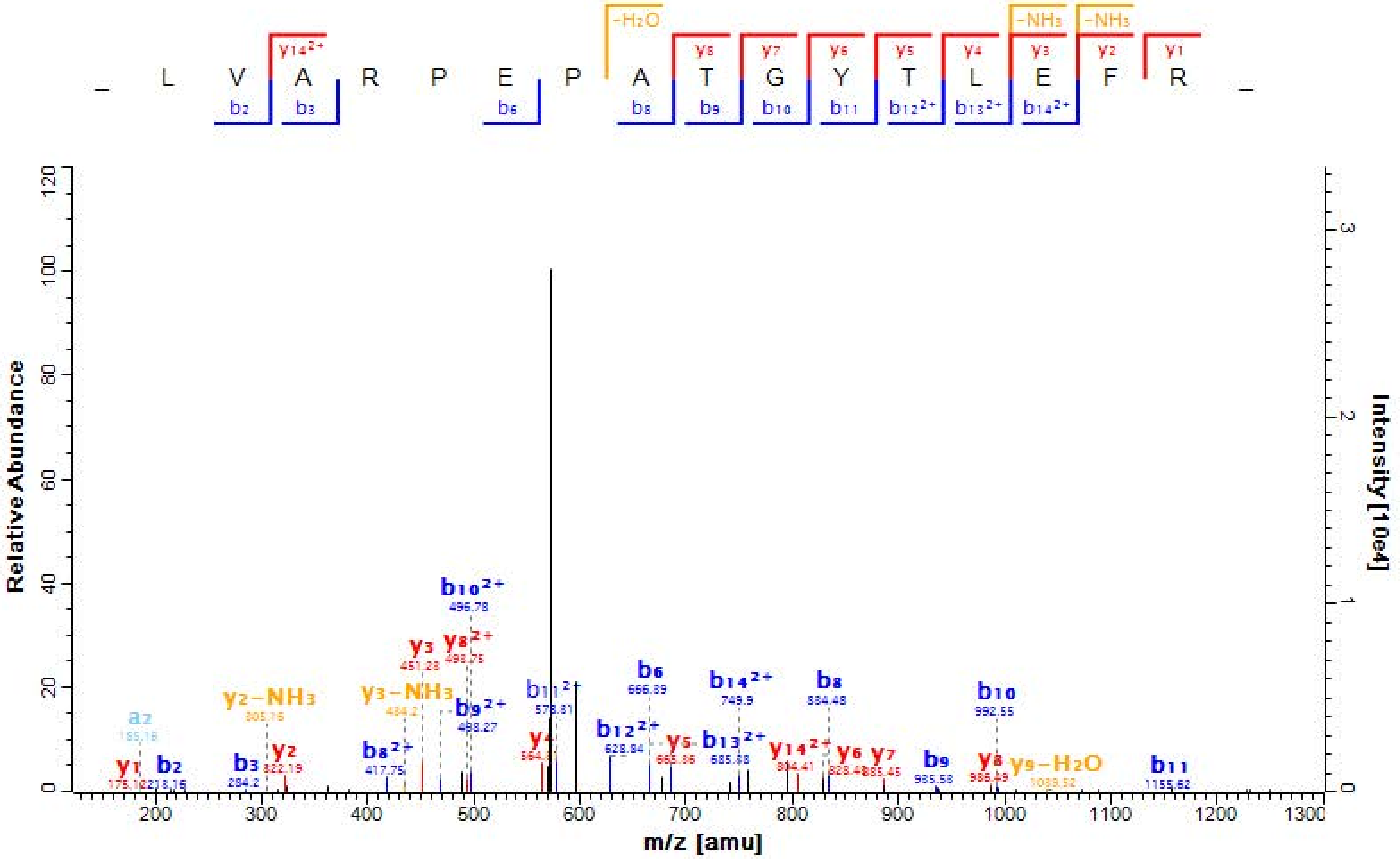
Mass:	1881.94716
m/z:	941.98086
Charge:	2+
Retentiontime:	31.413152694702
Score:	184.0175
Mass Error [ppm]:	-0.042843
PEP:	8.3374E-20
Precursor Type:	ISO

general information

Annotation:	14 of 16
AminoAcids Coverag	88 %
Intensity Coverage:	52 %
Peak Coverage:	41 %
Protein Localisation:	128 ... 143

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	I	15				
	261.1598	2	F	14	1769.87		885.4389	+0.168983
	360.2282	3	V	13	1622.802	+0.016196	811.9047	+0.03394
	417.2496	4	G	12	1523.734	-0.12706	762.3705	+0.247895
-0.00022	474.2711	5	G	11	1466.712	-0.19703	733.8597	-0.23966
+0.081425	587.3552	6	I	10	1409.691	-0.1138	1409.691	
	715.4501	7	K	9	1296.607	-0.04694	648.807	+0.209706
	844.4927	8	E	8	1168.512	-0.00349	584.7595	+0.474412
-0.12678	959.5197	9	D	7	1039.469	+0.005041	1039.469	
	1060.567	10	T	6	924.4421	+0.093325	924.4421	
	1189.61	11	E	5	823.3945	+0.001111	823.3945	
	1318.653	12	E	4	694.3519	+0.046755	694.3519	
	1481.716	13	Y	3	565.3093	-0.03815	565.3093	
-0.03478	1595.759	14	N	2	402.2459	+0.034818	402.2459	
-0.20637	1708.843	15	L	1	288.203		288.203	
		16	R	0	175.119		175.119	

Scan number	4411	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	140.27



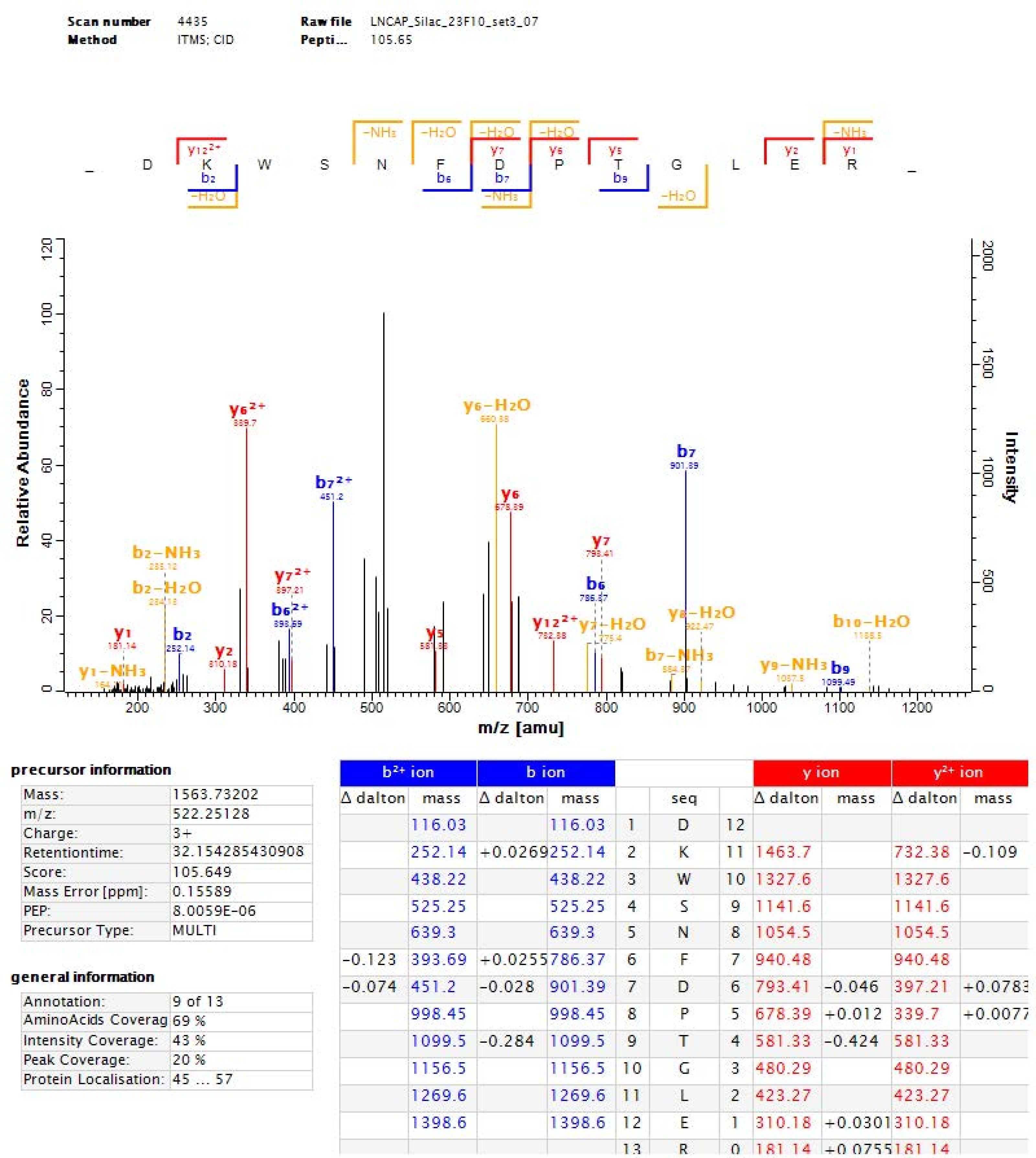
precursor information

Mass:	1812.85396
m/z:	605.29193
Charge:	3+
Retentiontime:	32.023139953613
Score:	140.2742
Mass Error [ppm]:	0.42768
PEP:	6.047E-32
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	30 %
Peak Coverage:	37 %
Protein Localisation:	209 ... 224

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	15				
+0.097	185.2		213.2	+0.065	213.2	2	V	14	1707		1707	
	256.2		284.2	-0.03	284.2	3	A	13	1608		804.4	+0.12
	412.3		440.3		440.3	4	R	12	1537		1537	
	509.4		537.4		537.4	5	P	11	1381		1381	
	638.4		666.4	-0.04	666.4	6	E	10	1284		1284	
	735.5		763.4		763.4	7	P	9	1155		1155	
	806.5	+0.287	417.7	+0.046	834.5	8	A	8	1058		1058	
	907.5	-0.01	468.3	+0.319	935.5	9	T	7	986.5	+0.077	493.8	-0.01
	964.6	+0.146	496.8	+0.043	992.6	10	G	6	885.4	+0	885.4	
	1128	-0.13	578.3	-0.14	1156	11	Y	5	828.4	+0.113	828.4	
	1229	+0.296	628.8		1257	12	T	4	665.4	+0.091	665.4	
	1342	+0.199	685.4		1370	13	L	3	564.3	+0.047	564.3	
	1471	+0.153	749.9		1499	14	E	2	451.2	+0.103	451.2	
	1618		1646		1646	15	F	1	322.2	+0.126	322.2	
						16	R	0	175.1	-0.05	175.1	



Scan number	4435	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	105.65

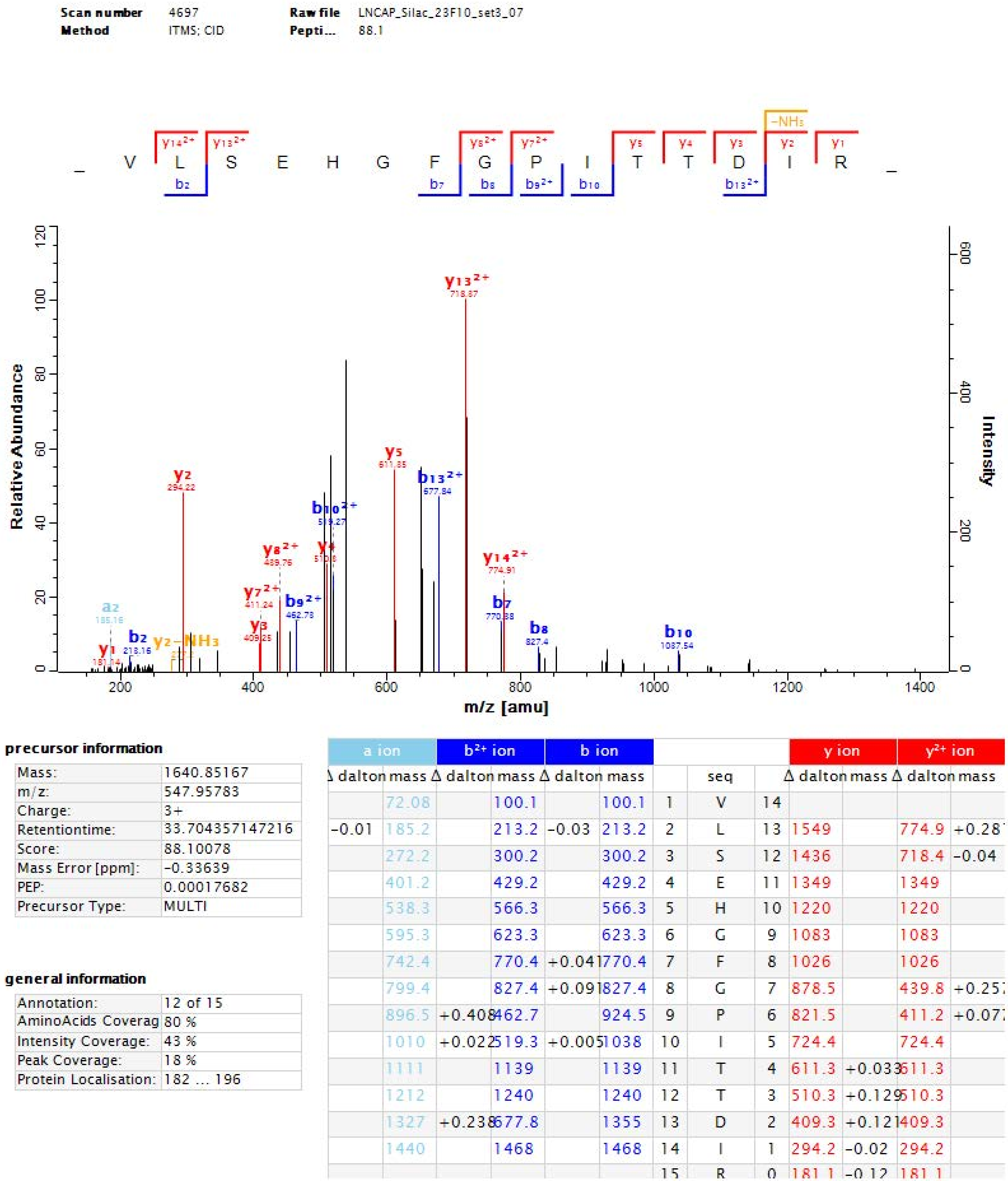
precursor information

Mass:	1563.73202
m/z:	522.25128
Charge:	3+
Retentiontime:	32.154285430908
Score:	105.649
Mass Error [ppm]:	0.15589
PEP:	8.0059E-06
Precursor Type:	MULTI

general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	43 %
Peak Coverage:	20 %
Protein Localisation:	45 ... 57

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	12				
	252.14	+0.0269	252.14	2	K	11	1463.7		732.38	-0.109
	438.22		438.22	3	W	10	1327.6		1327.6	
	525.25		525.25	4	S	9	1141.6		1141.6	
	639.3		639.3	5	N	8	1054.5		1054.5	
-0.123	393.69	+0.0255	786.37	6	F	7	940.48		940.48	
-0.074	451.2	-0.028	901.39	7	D	6	793.41	-0.046	397.21	+0.0783
	998.45		998.45	8	P	5	678.39	+0.012	339.7	+0.0077
	1099.5	-0.284	1099.5	9	T	4	581.33	-0.424	581.33	
	1156.5		1156.5	10	G	3	480.29		480.29	
	1269.6		1269.6	11	L	2	423.27		423.27	
	1398.6		1398.6	12	E	1	310.18	+0.0301	310.18	
				13	R	0	181.14	+0.0755	181.14	



Scan number	4697	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	88.1

precursor information

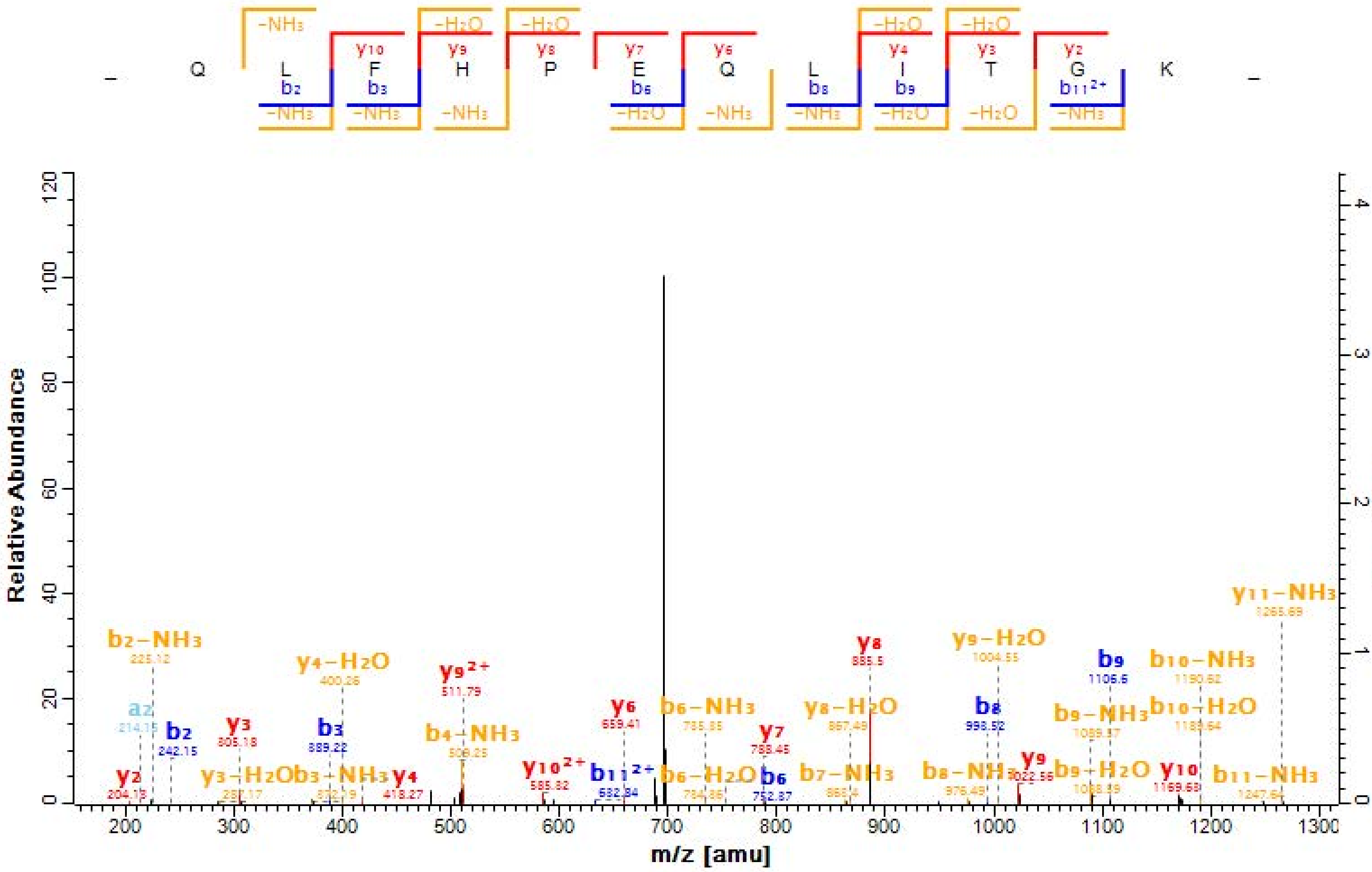
Mass:	1640.85167
m/z:	547.95783
Charge:	3+
Retentiontime:	33.704357147216
Score:	88.10078
Mass Error [ppm]:	-0.33639
PEP:	0.00017682
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	43 %
Peak Coverage:	18 %
Protein Localisation:	182 ... 196

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.08		100.1		100.1	1	V	14				
-0.01	185.2		213.2	-0.03	213.2	2	L	13	1549		774.9	+0.28
	272.2		300.2		300.2	3	S	12	1436		718.4	-0.04
	401.2		429.2		429.2	4	E	11	1349		1349	
	538.3		566.3		566.3	5	H	10	1220		1220	
	595.3		623.3		623.3	6	G	9	1083		1083	
	742.4		770.4	+0.041	770.4	7	F	8	1026		1026	
	799.4		827.4	+0.091	827.4	8	G	7	878.5		439.8	+0.25
	896.5	+0.408	462.7		924.5	9	P	6	821.5		411.2	+0.07
	1010	+0.022	519.3	+0.005	1038	10	I	5	724.4		724.4	
	1111		1139		1139	11	T	4	611.3	+0.033	611.3	
	1212		1240		1240	12	T	3	510.3	+0.129	510.3	
	1327	+0.238	677.8		1355	13	D	2	409.3	+0.121	409.3	
	1440		1468		1468	14	I	1	294.2	-0.02	294.2	
						15	R	0	181.1	-0.12	181.1	

Scan number	4884	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	187.85



precursor information

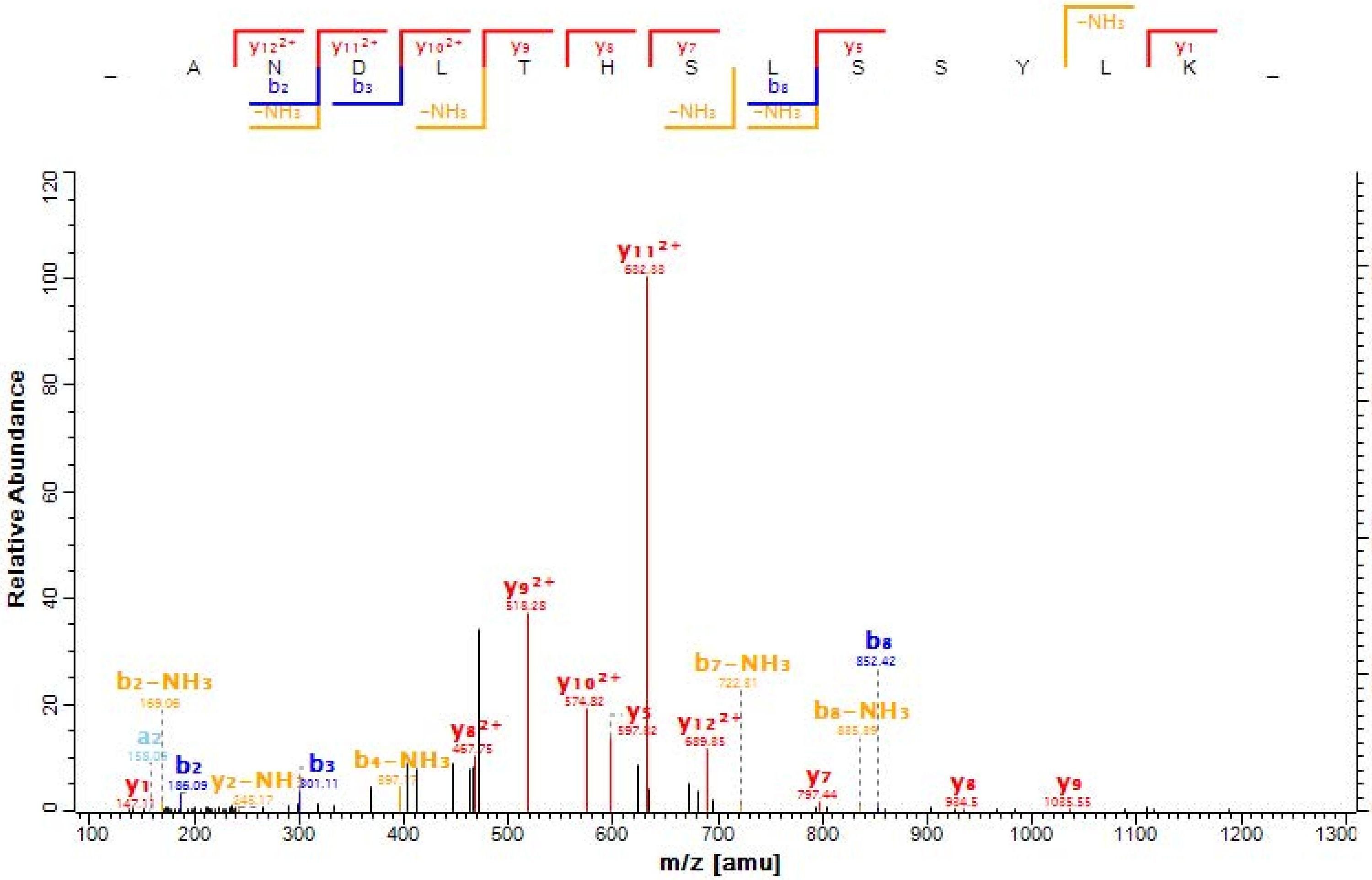
Mass:	1409.76672
m/z:	705.89064
Charge:	2+
Retentiontime:	34.824890136718
Score:	187.8548
Mass Error [ppm]:	0.016647
PEP:	3.0301E-14
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	27 %
Peak Coverage:	49 %
Protein Localisation:	85 ... 96

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	101.1		129.1		129.1	1	Q	11				
+0.125	214.2		242.1	+0.132	242.1	2	L	10	1283		1283	
	361.2		389.2	+0.094	389.2	3	F	9	1170	−0.08	585.3	+0.18
	498.3		526.3		526.3	4	H	8	1023	−0.05	511.8	+0.22
	595.3		623.3		623.3	5	P	7	885.5	+0	885.5	
	724.4		752.4	−0.2	752.4	6	E	6	788.5	−0.05	788.5	
	852.4		880.4		880.4	7	Q	5	659.4	+0.036	659.4	
	965.5		993.5	−0.04	993.5	8	L	4	531.4		531.4	
	1079		1107	+0.01	1107	9	I	3	418.3	+0.181	418.3	
	1180		1208		1208	10	T	2	305.2	−0.05	305.2	
	1237	−0.05	632.8		1265	11	G	1	204.1	+0.121	204.1	
						12	K	0	147.1		147.1	

Scan number	5035	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	84.72



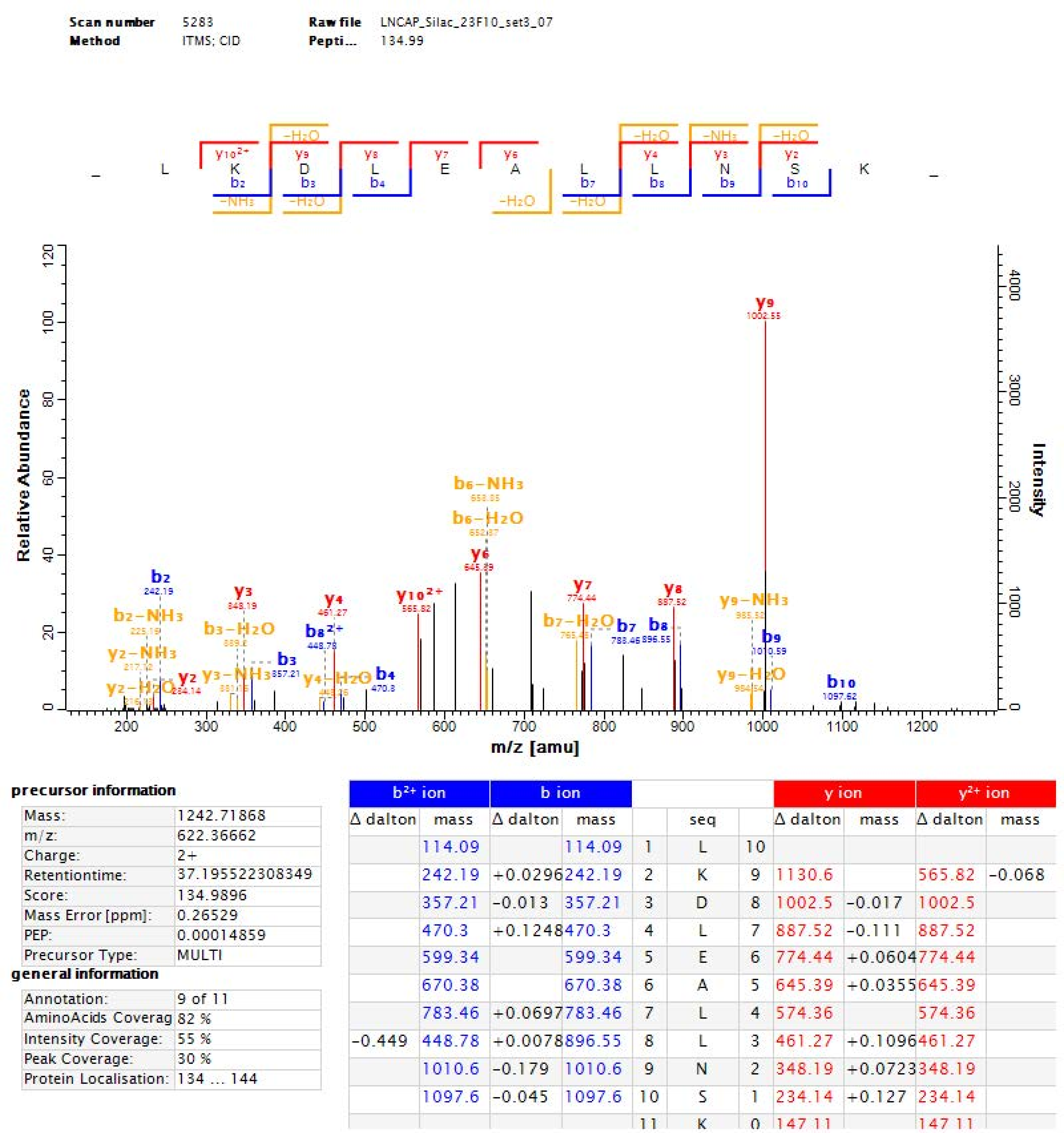
precursor information

Mass:	1447.731
m/z:	483.58428
Charge:	3+
Retentiontime:	35.715412139892
Score:	84.71755
Mass Error [ppm]:	0.20492
PEP:	0.00054013
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	59 %
Peak Coverage:	18 %
Protein Localisation:	125 ... 137

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	44.049		72.044	1	A	12				
-0.119	158.09	+0.0234	186.09	2	N	11	1377.7		689.35	+0.1996
	273.12	+0.0683	301.11	3	D	10	1263.7		632.33	+0.2665
	386.2		414.2	4	L	9	1148.6		574.82	+0.2467
	487.25		515.25	5	T	8	1035.5	+0.0761	518.28	+0.1961
	624.31		652.3	6	H	7	934.5	-0.092	467.75	+0.2926
	711.34		739.34	7	S	6	797.44	+0.0911	797.44	
	824.43	-0.344	852.42	8	L	5	710.41		710.41	
	911.46		939.45	9	S	4	597.32	+0.0143	597.32	
	998.49		1026.5	10	S	3	510.29		510.29	
	1161.6		1189.5	11	Y	2	423.26		423.26	
	1274.6		1302.6	12	L	1	260.2		260.2	
				13	K	0	147.11	+0.2174	147.11	



Scan number	5283	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	134.99

precursor information

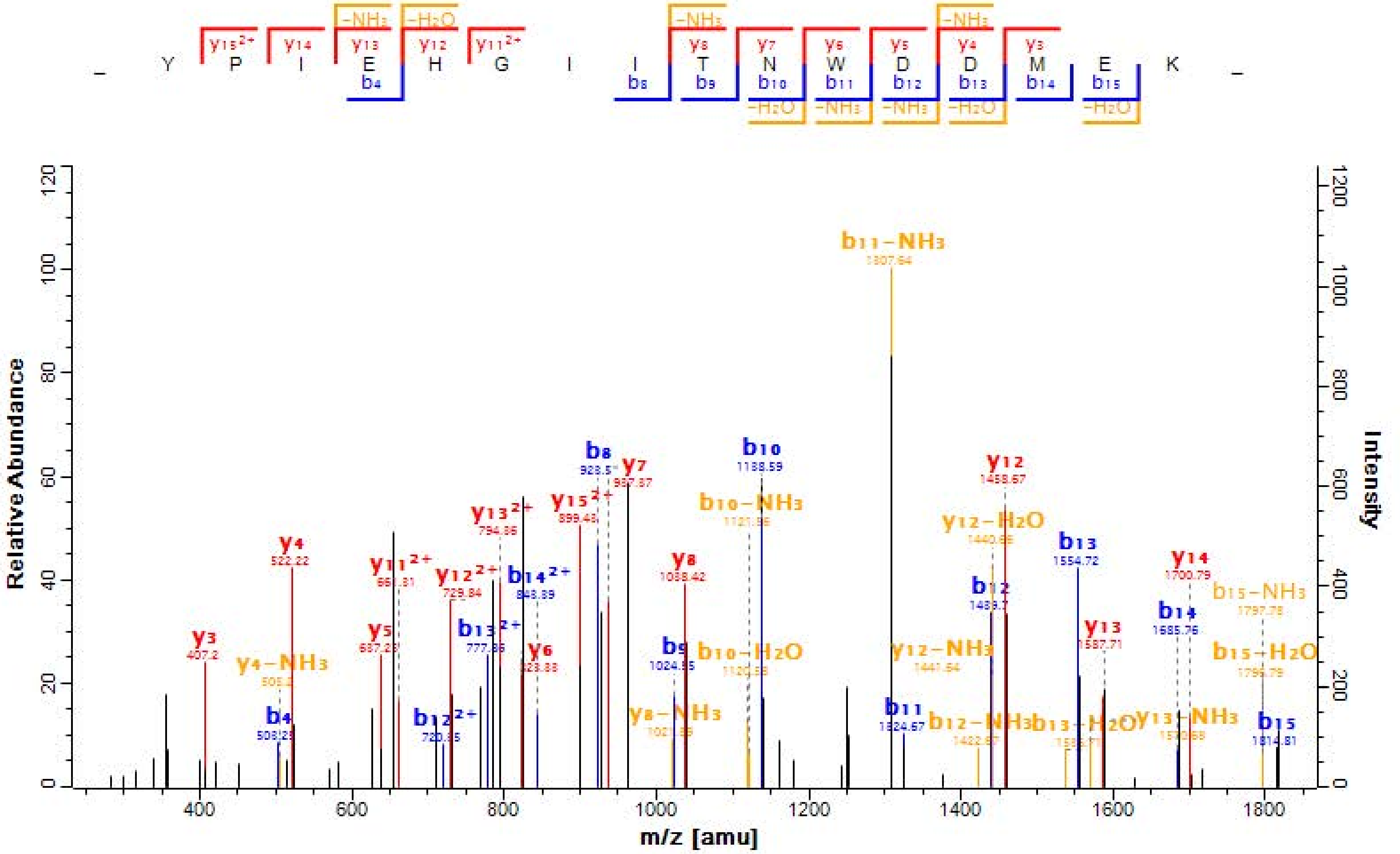
Mass:	1242.71868
m/z:	622.36662
Charge:	2+
Retentiontime:	37.195522308349
Score:	134.9896
Mass Error [ppm]:	0.26529
PEP:	0.00014859
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	55 %
Peak Coverage:	30 %
Protein Localisation:	134 ... 144

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	10				
	242.19	+0.0296	242.19	2	K	9	1130.6		565.82	-0.068
	357.21	-0.013	357.21	3	D	8	1002.5	-0.017	1002.5	
	470.3	+0.1248	470.3	4	L	7	887.52	-0.111	887.52	
	599.34		599.34	5	E	6	774.44	+0.0604	774.44	
	670.38		670.38	6	A	5	645.39	+0.0355	645.39	
	783.46	+0.0697	783.46	7	L	4	574.36		574.36	
-0.449	448.78	+0.0078	896.55	8	L	3	461.27	+0.1096	461.27	
	1010.6	-0.179	1010.6	9	N	2	348.19	+0.0723	348.19	
	1097.6	-0.045	1097.6	10	S	1	234.14	+0.127	234.14	
				11	K	0	147.11		147.11	

Scan number	5344	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	222.45



precursor information

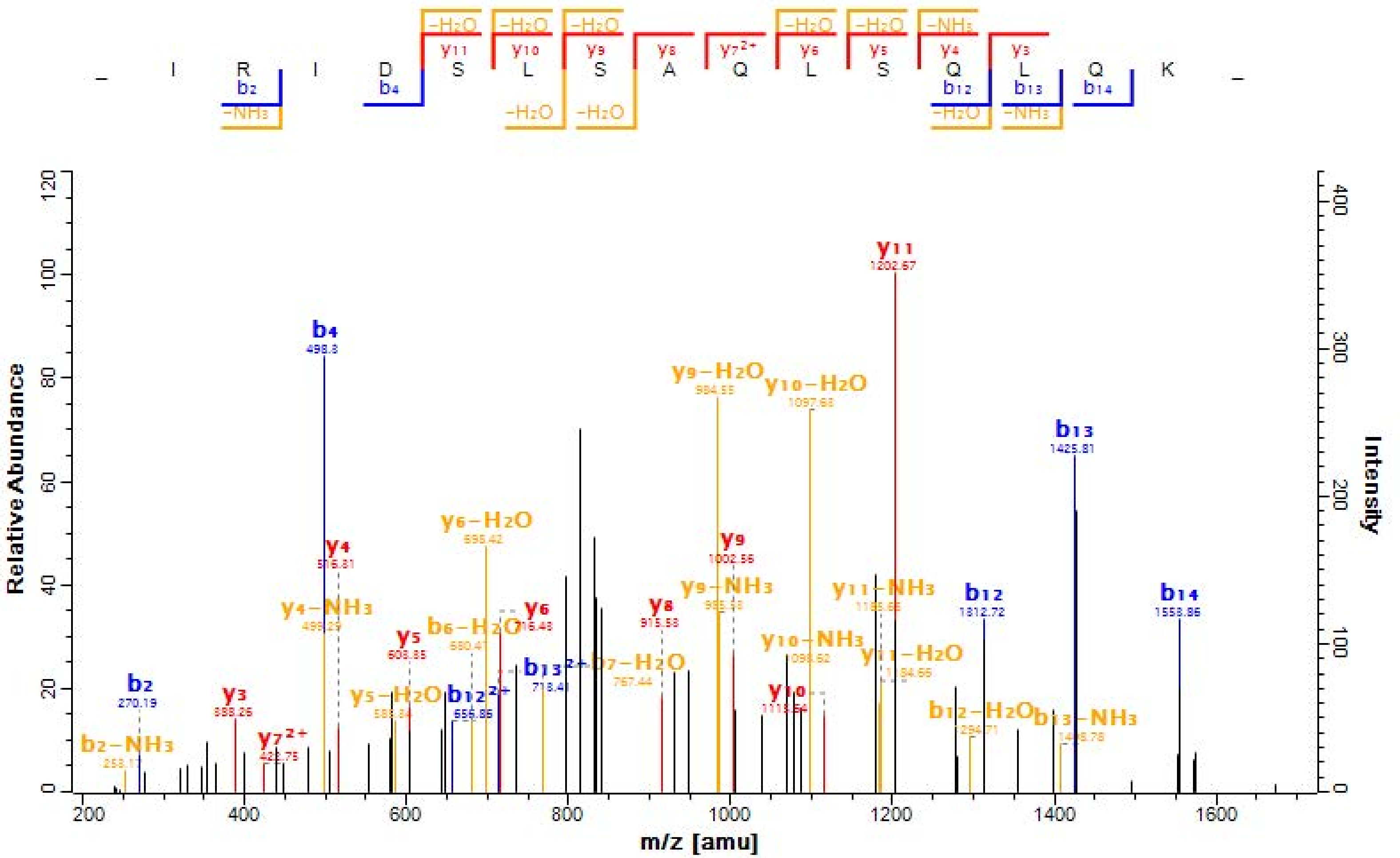
Mass:	1959.9031
m/z:	980.95883
Charge:	2+
Retentiontime:	37.576763153076
Score:	222.4475
Mass Error [ppm]:	-0.28629
PEP:	4.5551E-41
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	51 %
Peak Coverage:	42 %
Protein Localisation:	71 ... 86

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	164.07		164.07	1	Y	15				
	261.12		261.12	2	P	14	1797.8		899.43	-0.022
	374.21		374.21	3	I	13	1700.8	-0.027	1700.8	
	503.25	+0.3636	503.25	4	E	12	1587.7	-0.071	794.36	+0.0537
	640.31		640.31	5	H	11	1458.7	-0.112	729.84	+0.1781
	697.33		697.33	6	G	10	1321.6		661.31	+0.1123
	810.41		810.41	7	I	9	1264.6		1264.6	
	923.5	-0.042	923.5	8	I	8	1151.5		1151.5	
	1024.5	+0.0381	1024.5	9	T	7	1038.4	-0.02	1038.4	
	1138.6	-0.085	1138.6	10	N	6	937.37	-0.036	937.37	
	1324.7	-0.019	1324.7	11	W	5	823.33	+0.0676	823.33	
-0.332	720.35	-0.122	1439.7	12	D	4	637.25	+0.0832	637.25	
-0.168	777.86	-0.146	1554.7	13	D	3	522.22	+0.0151	522.22	
-0.126	843.39	-0.168	1685.8	14	M	2	407.2	+0.0787	407.2	
	1814.8	+0.0375	1814.8	15	E	1	276.16		276.16	
				16	K	0	147.11		147.11	

Scan number	5879	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	152.34



precursor information

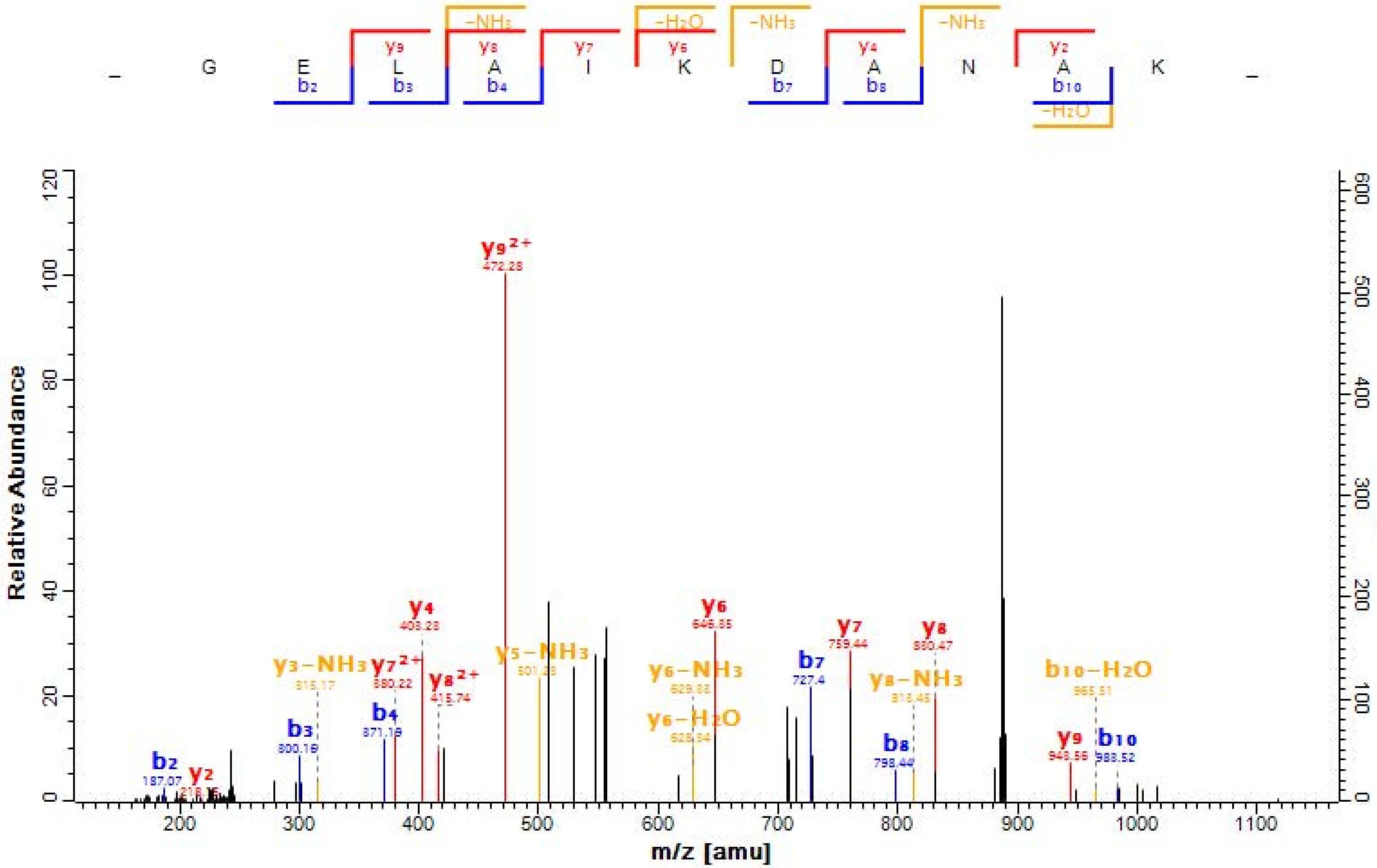
Mass:	1698.9625
m/z:	850.48852
Charge:	2+
Retentiontime:	40.909805297851
Score:	152.3377
Mass Error [ppm]:	-0.19878
PEP:	4.4813E-14
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	48 %
Peak Coverage:	35 %
Protein Localisation:	297 ... 311

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	I	14				
	270.19	+0.1479	270.19	2	R	13	1586.9		1586.9	
	383.28		383.28	3	I	12	1430.8		1430.8	
	498.3	+0.0798	498.3	4	D	11	1317.7		1317.7	
	585.34		585.34	5	S	10	1202.7	+0.1286	1202.7	
	698.42		698.42	6	L	9	1115.6	+0.0286	1115.6	
	785.45		785.45	7	S	8	1002.6	-0.075	1002.6	
	856.49		856.49	8	A	7	915.53	+0.158	915.53	
	984.55		984.55	9	Q	6	844.49		422.75	+0.4171
	1097.6		1097.6	10	L	5	716.43	-0.016	716.43	
	1184.7		1184.7	11	S	4	603.35	+0.0865	603.35	
+0.1387	656.86	-0.202	1312.7	12	Q	3	516.31	+0.069	516.31	
+0.0821	713.41	-0.128	1425.8	13	L	2	388.26	+0.0229	388.26	
	1553.9	+0.0594	1553.9	14	Q	1	275.17		275.17	
				15	K	0	147.11		147.11	

Scan number	629	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	103.91



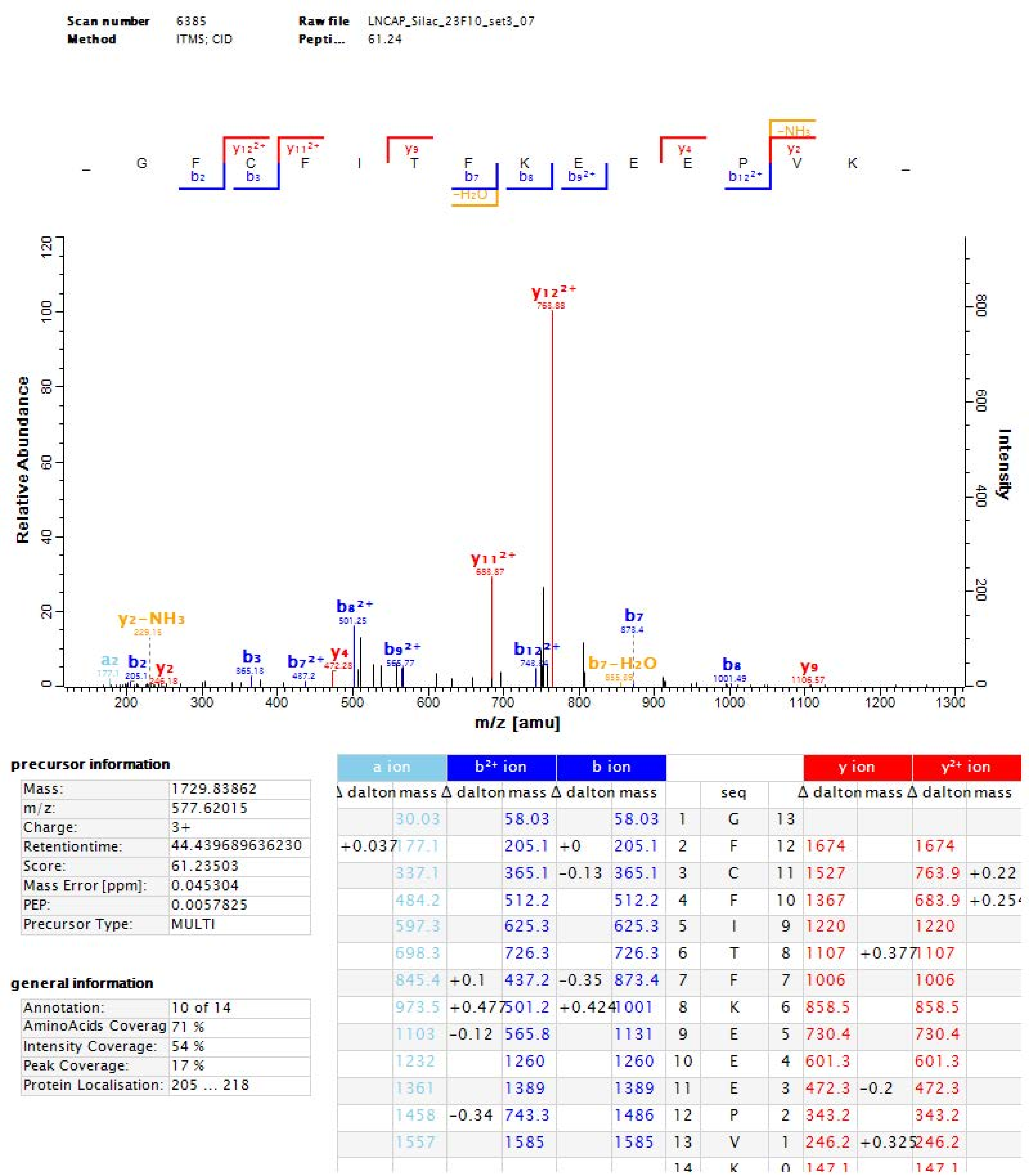
precursor information

Mass:	1128.61446
m/z:	565.31451
Charge:	2+
Retentiontime:	9.1914329528808
Score:	103.9094
Mass Error [ppm]:	0.50687
PEP:	0.00026912
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	40 %
Peak Coverage:	21 %
Protein Localisation:	342 ... 352

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874	1	G	10				
+0.023332	187.0713	2	E	9	1072.6		1072.6	
-0.06629	300.1554	3	L	8	943.5571	+0.119102	472.2822	+0.272984
+0.01452	371.1925	4	A	7	830.473	+0.018473	415.7402	-0.06041
	484.2766	5	I	6	759.4359	+0.022872	380.2216	+0.370743
	612.3715	6	K	5	646.3519	+0.109744	646.3519	
+0.024432	727.3985	7	D	4	518.2569		518.2569	
+0.072462	798.4356	8	A	3	403.23	-0.00877	403.23	
	912.4785	9	N	2	332.1928		332.1928	
-0.08442	983.5156	10	A	1	218.1499	+0.217331	218.1499	
		11	K	0	147.1128		147.1128	



Scan number	6385	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	61.24

precursor information

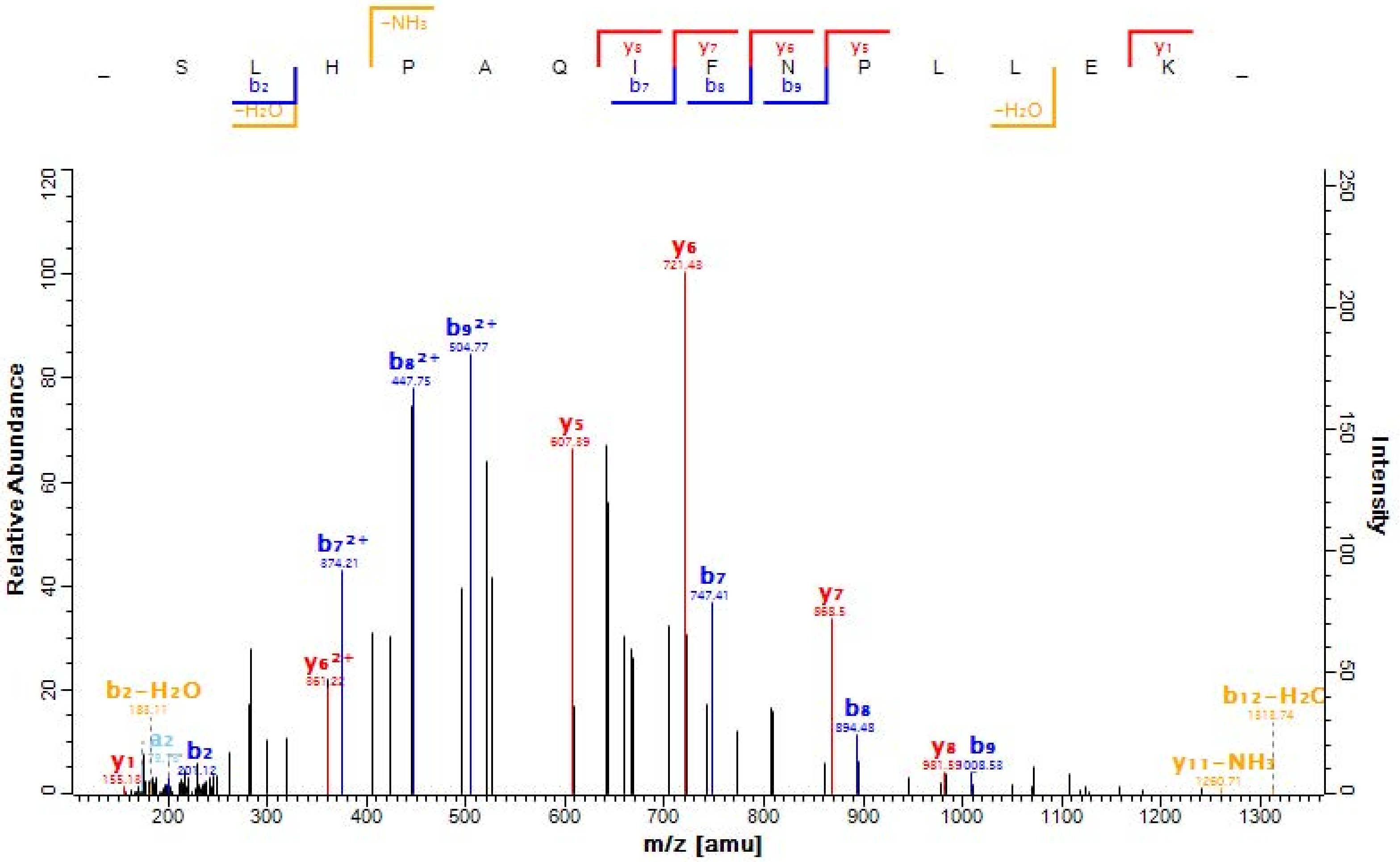
Mass:	1729.83862
m/z:	577.62015
Charge:	3+
Retentiontime:	44.439689636230
Score:	61.23503
Mass Error [ppm]:	0.045304
PEP:	0.0057825
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	54 %
Peak Coverage:	17 %
Protein Localisation:	205 ... 218

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	30.03		58.03		58.03	1	G	13				
+0.037	177.1		205.1	+0	205.1	2	F	12	1674		1674	
	337.1		365.1	-0.13	365.1	3	C	11	1527		763.9	+0.22
	484.2		512.2		512.2	4	F	10	1367		683.9	+0.25
	597.3		625.3		625.3	5	I	9	1220		1220	
	698.3		726.3		726.3	6	T	8	1107	+0.377	1107	
	845.4	+0.1	437.2	-0.35	873.4	7	F	7	1006		1006	
	973.5	+0.477	501.2	+0.424	1001	8	K	6	858.5		858.5	
	1103	-0.12	565.8		1131	9	E	5	730.4		730.4	
	1232		1260		1260	10	E	4	601.3		601.3	
	1361		1389		1389	11	E	3	472.3	-0.2	472.3	
	1458	-0.34	743.3		1486	12	P	2	343.2		343.2	
	1557		1585		1585	13	V	1	246.2	+0.325	246.2	
						14	K	0	147.1		147.1	

Scan number	6430	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	77.08



precursor information

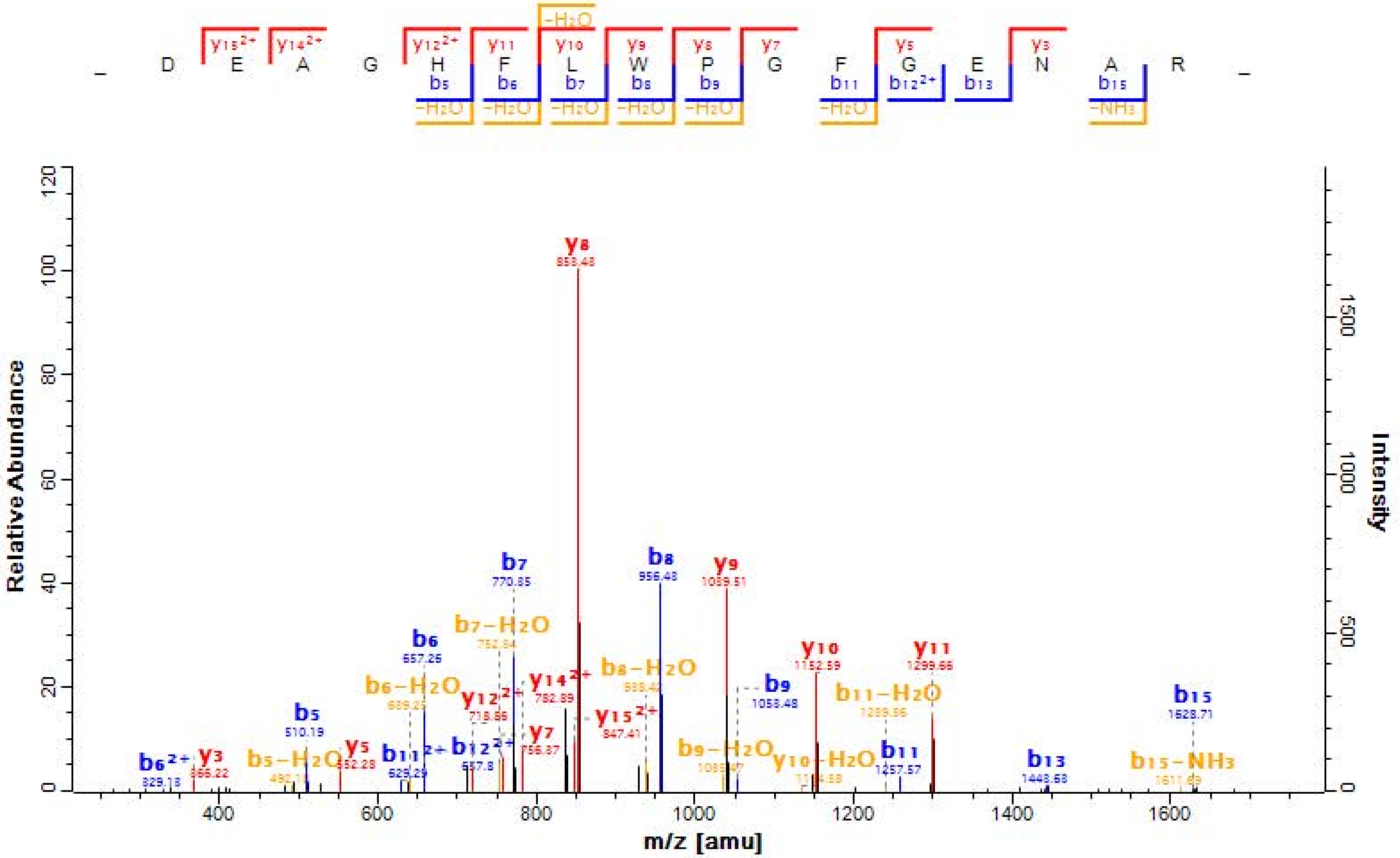
Mass:	1605.88844
m/z:	536.30342
Charge:	3+
Retentiontime:	44.774169921875
Score:	77.07824
Mass Error [ppm]:	0.34816
PEP:	0.0012673
Precursor Type:	MULTI

general information

Annotation:	8 of 14
AminoAcids Coverag	57 %
Intensity Coverage:	35 %
Peak Coverage:	15 %
Protein Localisation:	425 ... 438

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	60.04		88.04		88.04	1	S	13				
+0.032	173.1		201.1	+0.079	201.1	2	L	12	1528		1528	
	310.2		338.2		338.2	3	H	11	1415		1415	
	407.2		435.2		435.2	4	P	10	1278		1278	
	478.3		506.3		506.3	5	A	9	1181		1181	
	606.3		634.3		634.3	6	Q	8	1110		1110	
	719.4	+0.159	374.2	-0.01	747.4	7	I	7	981.6	+0.011	981.6	
	866.5	+0.17	447.7	-0.09	894.5	8	F	6	868.5	-0.12	868.5	
	980.5	+0.273	504.8	-0.08	1009	9	N	5	721.4	-0.01	361.2	+0.13
	1078		1106		1106	10	P	4	607.4	-0.02	607.4	
	1191		1219		1219	11	L	3	510.3		510.3	
	1304		1332		1332	12	L	2	397.3		397.3	
	1433		1461		1461	13	E	1	284.2		284.2	
						14	K	0	155.1	-0.13	155.1	

Scan number	6781	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	164.88



precursor information

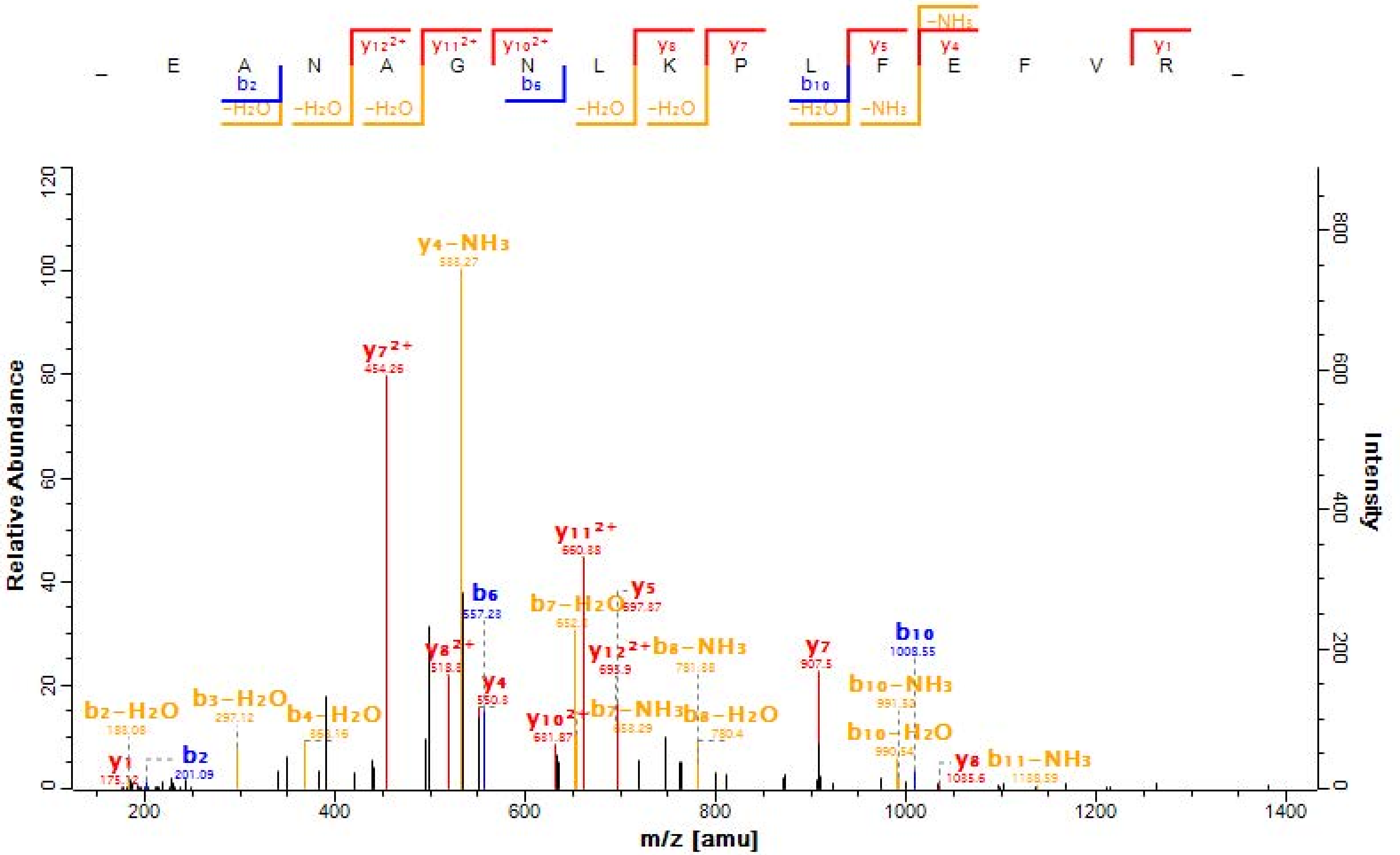
Mass:	1801.81692
m/z:	901.91574
Charge:	2+
Retentiontime:	47.266506195068
Score:	164.8837
Mass Error [ppm]:	-0.17092
PEP:	2.723E-20
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	60 %
Peak Coverage:	35 %
Protein Localisation:	538 ... 553

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.03		116.03	1	D	15				
	245.08		245.08	2	E	14	1693.8		847.41	+0.1131
	316.11		316.11	3	A	13	1564.8		782.89	+0.2092
	373.14		373.14	4	G	12	1493.7		1493.7	
	510.19	+0.0828	510.19	5	H	11	1436.7		718.86	+0.2194
+0.4924	329.13	+0.0177	657.26	6	F	10	1299.7	+0.0256	1299.7	
	770.35	+0.0024	770.35	7	L	9	1152.6	+0.0336	1152.6	
	956.43	-0.04	956.43	8	W	8	1039.5	+0.0378	1039.5	
	1053.5	+0.0458	1053.5	9	P	7	853.43	-0.038	853.43	
	1110.5		1110.5	10	G	6	756.37	+0.1537	756.37	
+0.1604	629.29	+0.1044	1257.6	11	F	5	699.35		699.35	
+0.4782	657.8		1314.6	12	G	4	552.28	-0.069	552.28	
	1443.6	-0.047	1443.6	13	E	3	495.26		495.26	
	1557.7		1557.7	14	N	2	366.22	+0.1392	366.22	
	1628.7	-0.272	1628.7	15	A	1	252.18		252.18	
				16	R	0	181.14		181.14	

Scan number	7142	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	67.23



precursor information

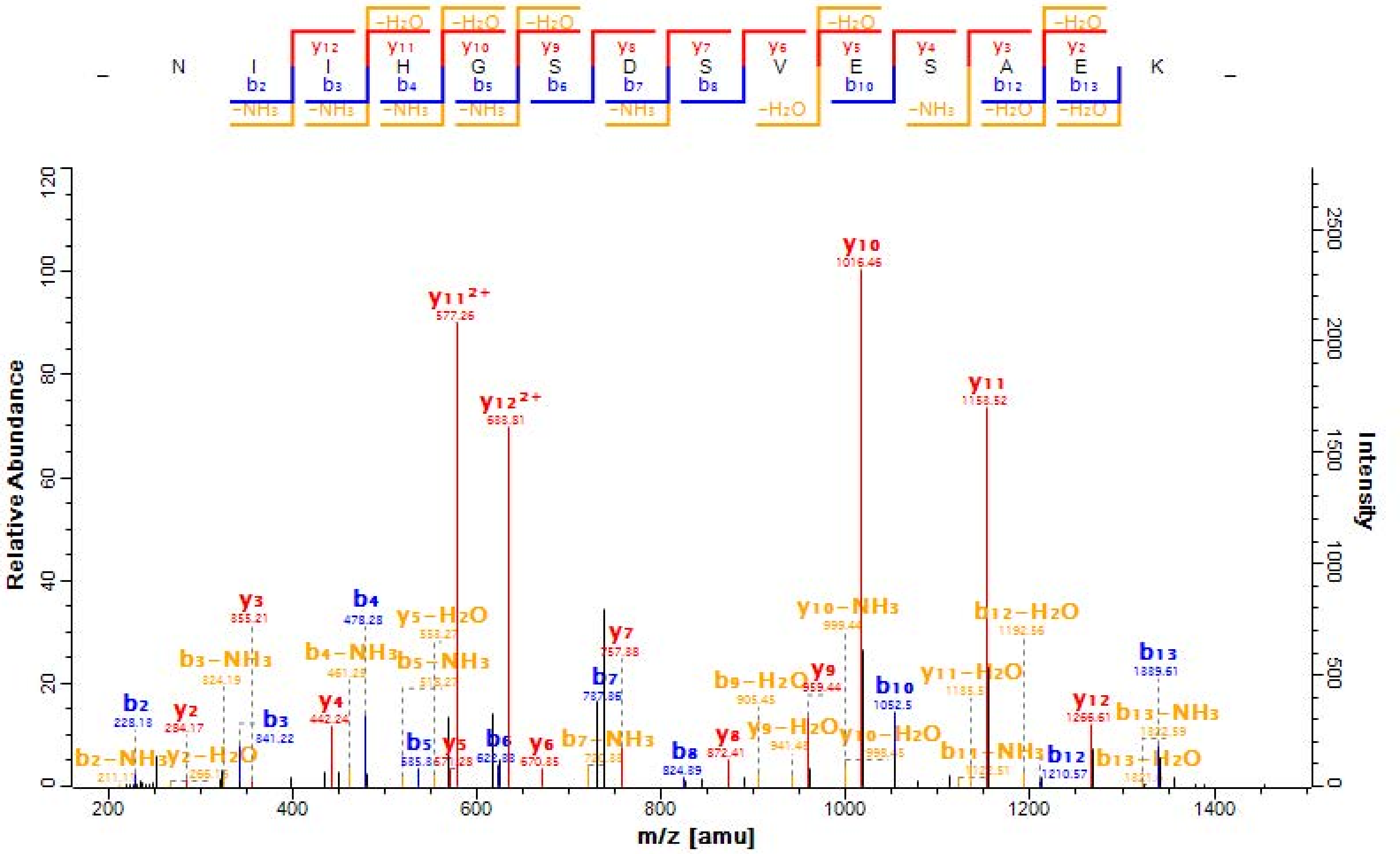
Mass:	1703.89943
m/z:	568.97375
Charge:	3+
Retentiontime:	50.279209136962
Score:	67.23447
Mass Error [ppm]:	-0.043067
PEP:	0.0019131
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	65 %
Peak Coverage:	28 %
Protein Localisation:	109 ... 123

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499	1	E	14				
-0.04905	201.087	2	A	13	1575.864		1575.864	
	315.1299	3	N	12	1504.827		1504.827	
	386.167	4	A	11	1390.784		695.8957	+0.207194
	443.1885	5	G	10	1319.747		660.3772	+0.199933
-0.00174	557.2314	6	N	9	1262.726		631.8664	-0.01004
	670.3155	7	L	8	1148.683		1148.683	
	798.4104	8	K	7	1035.599	+0.080255	518.3029	+0.251882
	895.4632	9	P	6	907.5036	-0.03029	454.2554	+0.234423
-0.08407	1008.547	10	L	5	810.4509		810.4509	
	1155.616	11	F	4	697.3668	+0.003879	697.3668	
	1284.658	12	E	3	550.2984	+0.023648	550.2984	
	1431.727	13	F	2	421.2558		421.2558	
	1530.795	14	V	1	274.1874		274.1874	
		15	R	0	175.119	-0.007	175.119	

Scan number	754	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	222.75



precursor information

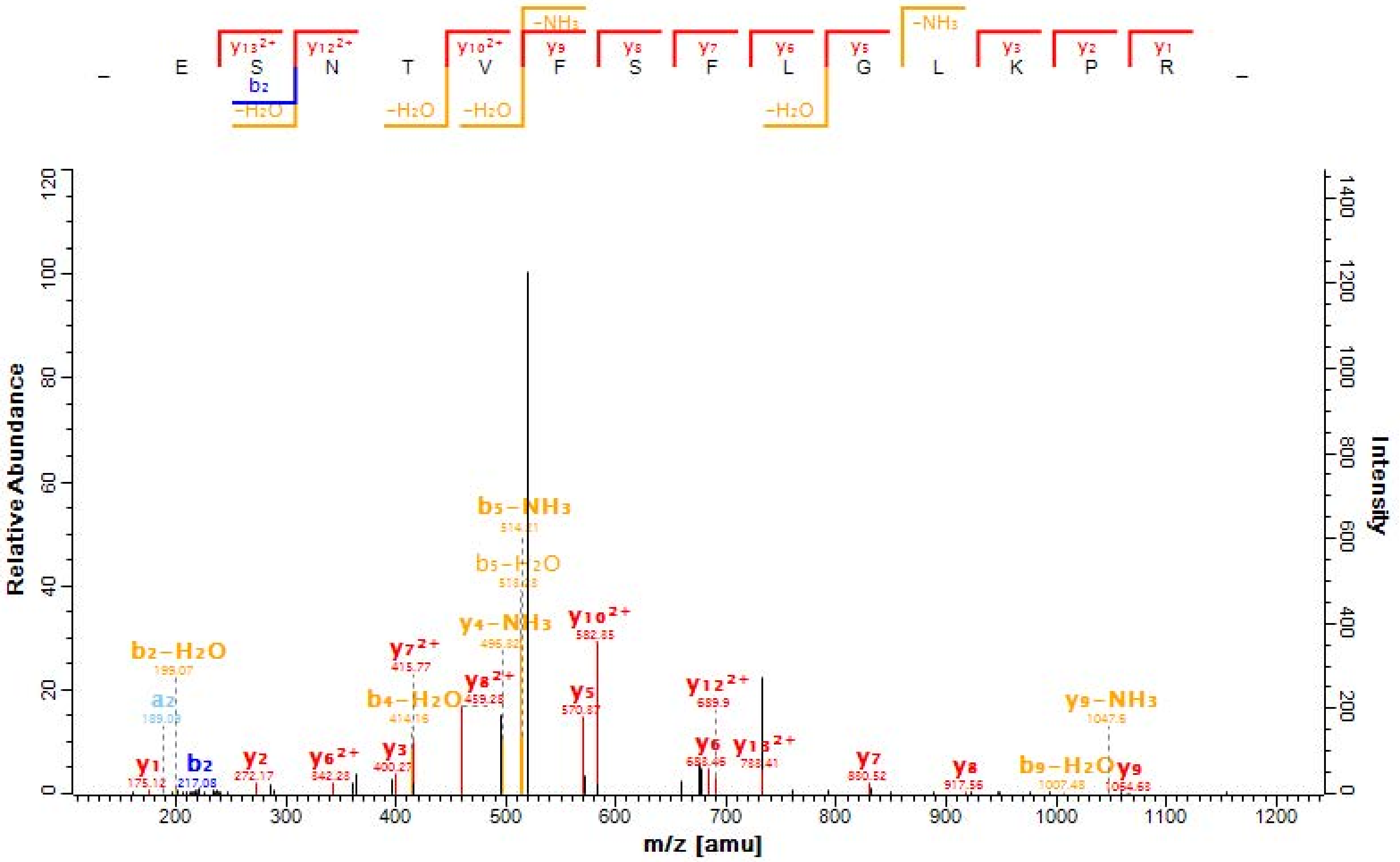
Mass:	1484.71035
m/z:	743.36245
Charge:	2+
Retentiontime:	10.085885047912
Score:	222.7519
Mass Error [ppm]:	-0.23789
PEP:	2.9996E-33
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	70 %
Peak Coverage:	42 %
Protein Localisation:	140 ... 153

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502	1	N	13				
-0.02607	228.1343	2	I	12	1379.689		1379.689	
+0.067374	341.2183	3	I	11	1266.605	+0.025064	633.8062	+0.15904
+0.045937	478.2772	4	H	10	1153.521	-0.02698	577.2642	+0.111839
-0.008	535.2987	5	G	9	1016.462	-0.04833	1016.462	
-0.01781	622.3307	6	S	8	959.4407	+0.098989	959.4407	
-0.02467	737.3577	7	D	7	872.4087	-0.08541	872.4087	
+0.104006	824.3897	8	S	6	757.3818	+0.198915	757.3818	
	923.4581	9	V	5	670.3497	+0.00432	670.3497	
-0.05943	1052.501	10	E	4	571.2813	+0.081034	571.2813	
	1139.533	11	S	3	442.2387	+0.106782	442.2387	
+0.168181	1210.57	12	A	2	355.2067	+0.068009	355.2067	
-0.02248	1339.612	13	E	1	284.1696	+0.185842	284.1696	
		14	K	0	155.127		155.127	

Scan number	7663	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	98.41



precursor information

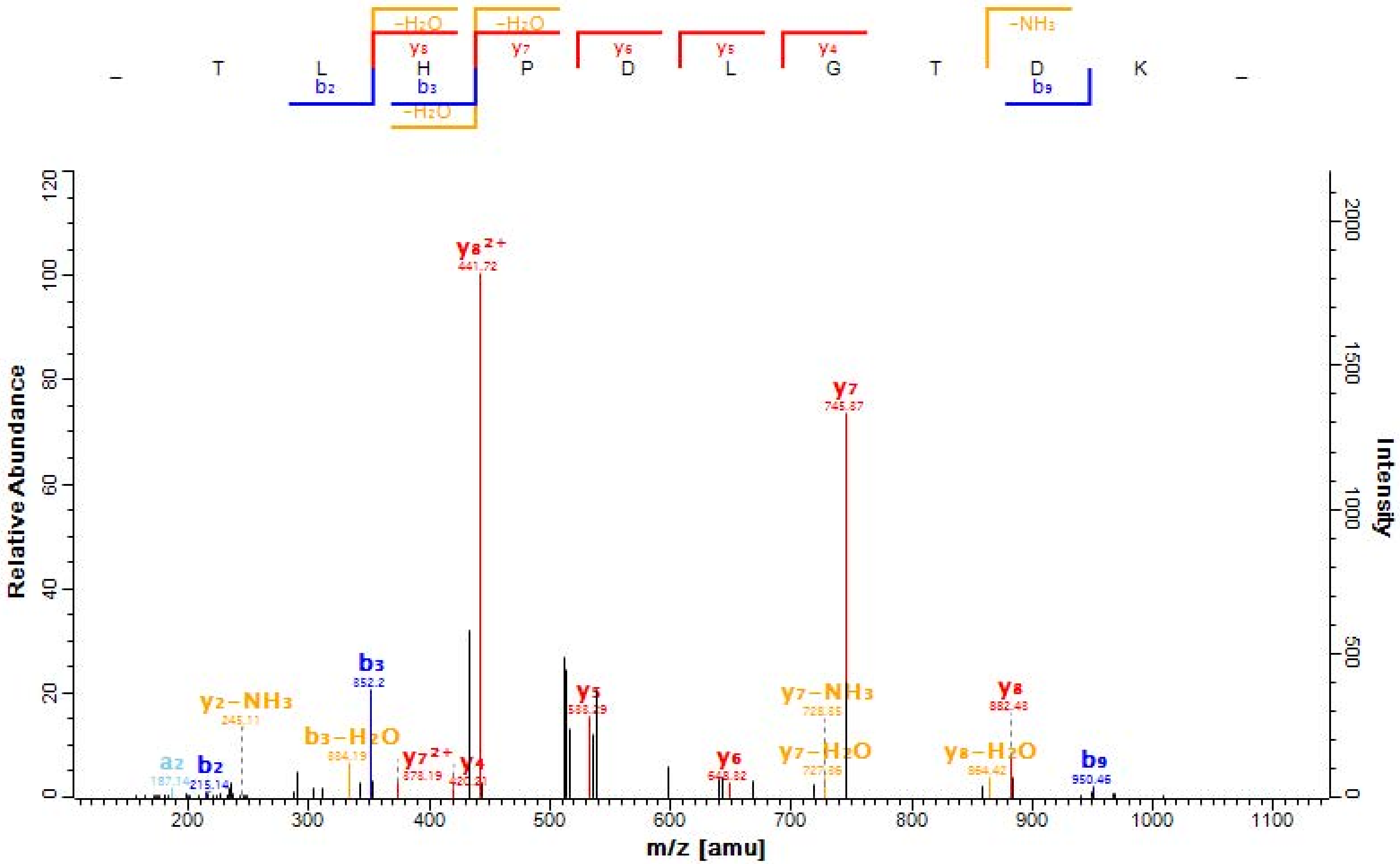
Mass:	1593.8518
m/z:	532.29121
Charge:	3+
Retentiontime:	55.265190124511
Score:	98.40717
Mass Error [ppm]:	0.19023
PEP:	9.9089E-05
Precursor Type:	MULTI

general information

Annotation:	13 of 14
AminoAcids Coverag	93 %
Intensity Coverage:	45 %
Peak Coverage:	23 %
Protein Localisation:	87 ... 100

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		130.05	1	E	13				
-0.091	189.09	+0	217.08	2	S	12	1465.8		733.41	-0.427
	303.13		331.12	3	N	11	1378.8		689.9	+0.1951
	404.18		432.17	4	T	10	1264.7		1264.7	
	503.25		531.24	5	V	9	1163.7		582.35	+0.1979
	650.31		678.31	6	F	8	1064.6	-0.018	1064.6	
	737.35		765.34	7	S	7	917.56	+0.0427	459.28	+0.2321
	884.41		912.41	8	F	6	830.52	+0.2951	415.77	-0.052
	997.5		1025.5	9	L	5	683.46	+0.0409	342.23	+0.1145
	1054.5		1082.5	10	G	4	570.37	+0.0788	570.37	
	1167.6		1195.6	11	L	3	513.35		513.35	
	1295.7		1323.7	12	K	2	400.27	+0.0096	400.27	
	1392.8		1420.7	13	P	1	272.17	+0.0832	272.17	
				14	R	0	175.12	+0.1385	175.12	

Scan number	776	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	96.14



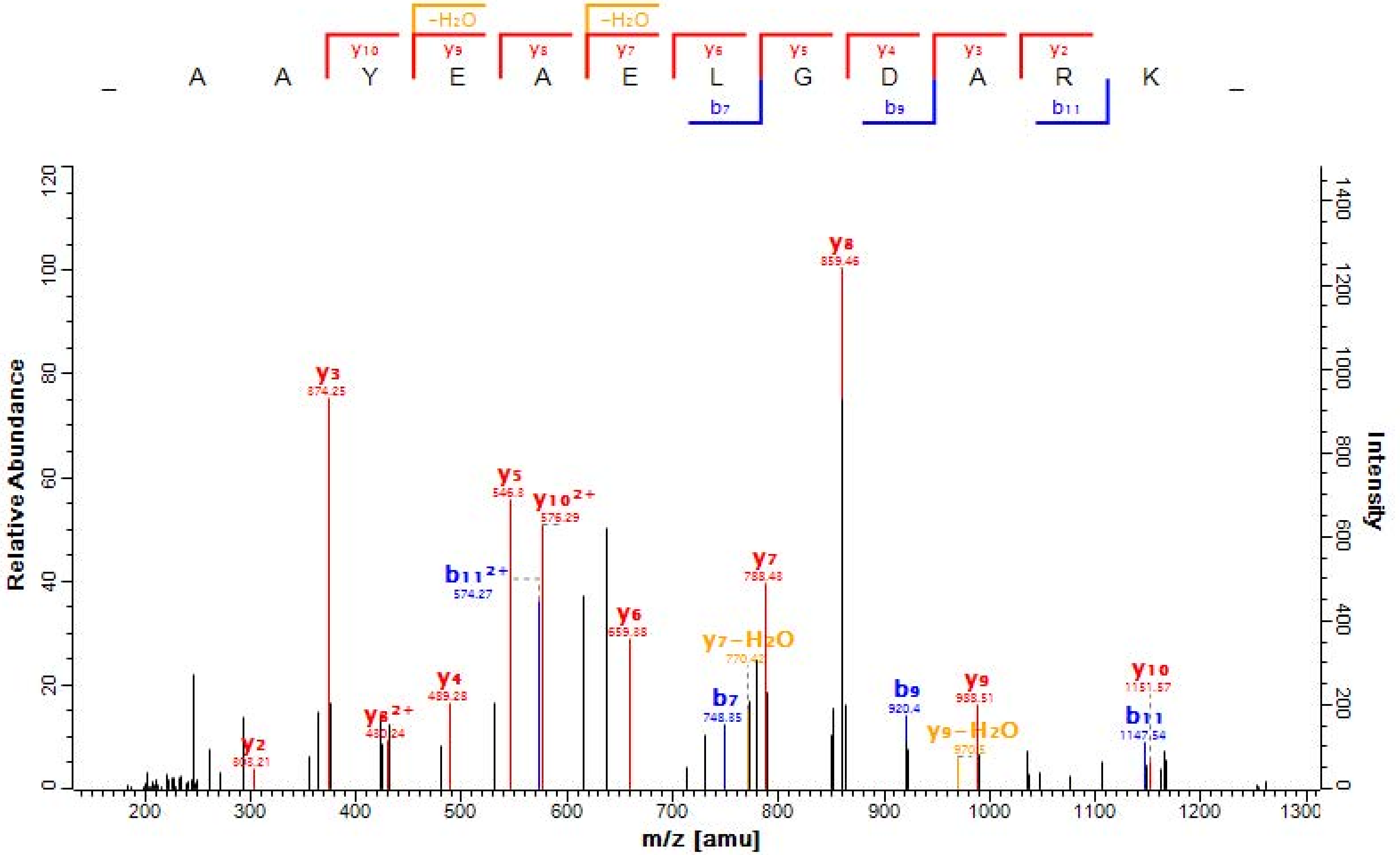
precursor information

Mass:	1095.55636
m/z:	548.78546
Charge:	2+
Retentiontime:	10.25439453125
Score:	96.14293
Mass Error [ppm]:	0.29198
PEP:	0.0014971
Precursor Type:	MULTI

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	53 %
Peak Coverage:	17 %
Protein Localisation:	242 ... 251

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.05	1	T	9				
+0.0432	187.14	+0.051	215.14	2	L	8	995.52		995.52	
	324.2	+0.0165	352.2	3	H	7	882.43	+0.0239	441.72	+0.197
	421.26		449.25	4	P	6	745.37	+0.0122	373.19	+0.294
	536.28		564.28	5	D	5	648.32	+0.1146	648.32	
	649.37		677.36	6	L	4	533.29	+0.0693	533.29	
	706.39		734.38	7	G	3	420.21	+0.2087	420.21	
	807.44		835.43	8	T	2	363.19		363.19	
	922.46	+0.0485	950.46	9	D	1	262.14		262.14	
				10	K	0	147.11		147.11	

Scan number	936	**Raw file**	LNCAP_Silac_23F10_set3_07
Method	ITMS; CID	**Pepti...**	82.85



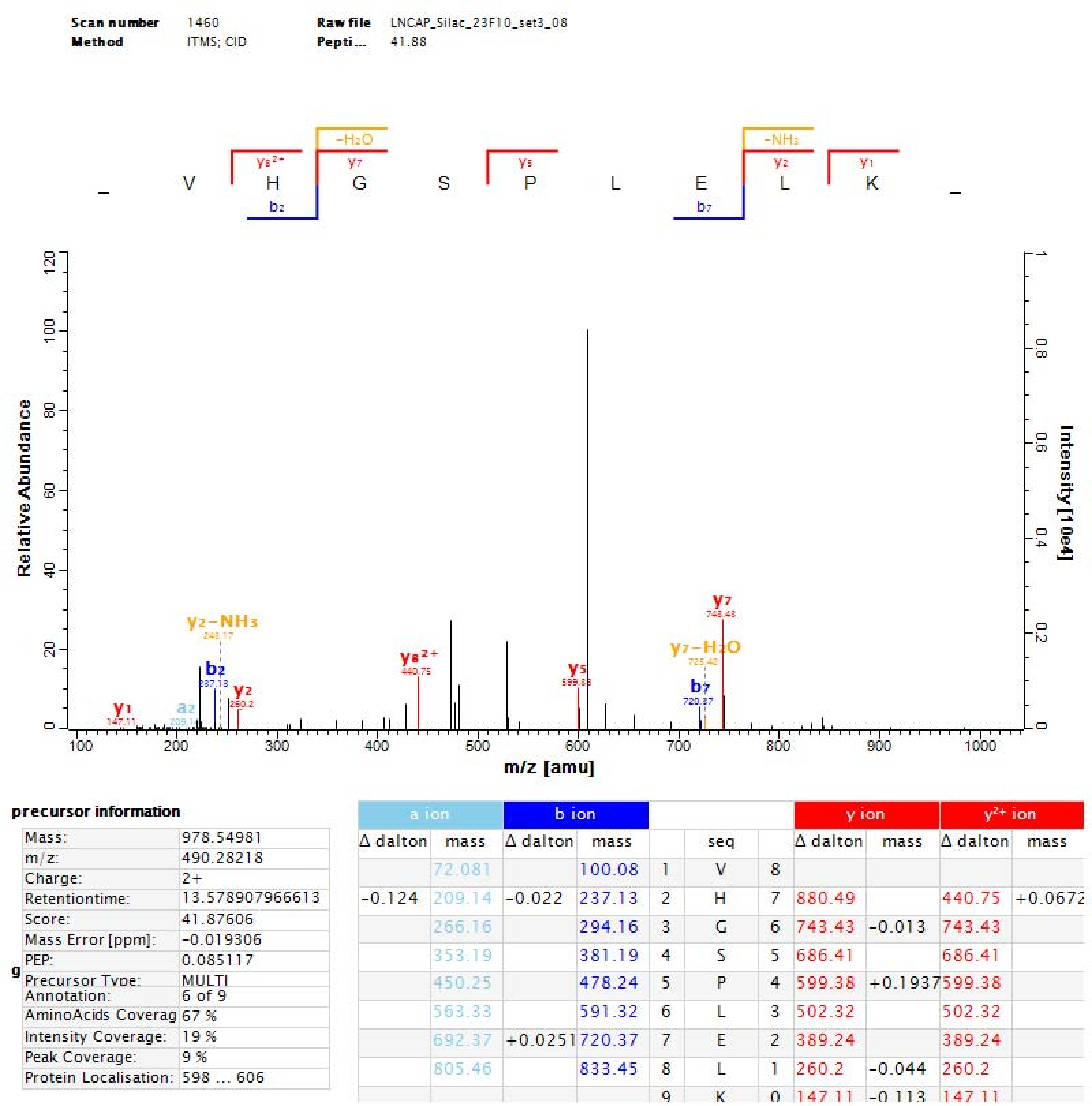
precursor information

Mass:	1292.63602
m/z:	647.32529
Charge:	2+
Retentiontime:	11.385793685913
Score:	82.85046
Mass Error [ppm]:	-0.043404
PEP:	0.00097373
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	47 %
Peak Coverage:	20 %
Protein Localisation:	79 ... 90

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	11				
	143.08		143.08	2	A	10	1222.6		1222.6	
	306.14		306.14	3	Y	9	1151.6	+0.0554	576.29	-0.006
	435.19		435.19	4	E	8	988.51	+0.0828	988.51	
	506.22		506.22	5	A	7	859.46	+0.2298	430.24	+0.069
	635.27		635.27	6	E	6	788.43	-0.062	788.43	
	748.35	+0.0552	748.35	7	L	5	659.38	+0.1677	659.38	
	805.37		805.37	8	G	4	546.3	+0.0806	546.3	
	920.4	+0.002	920.4	9	D	3	489.28	+0.0907	489.28	
	991.44		991.44	10	A	2	374.25	+0.1403	374.25	
-0.485	574.27	-0.021	1147.5	11	R	1	303.21	+0.1673	303.21	
				12	K	0	147.11		147.11	



Scan number	1460	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	41.88

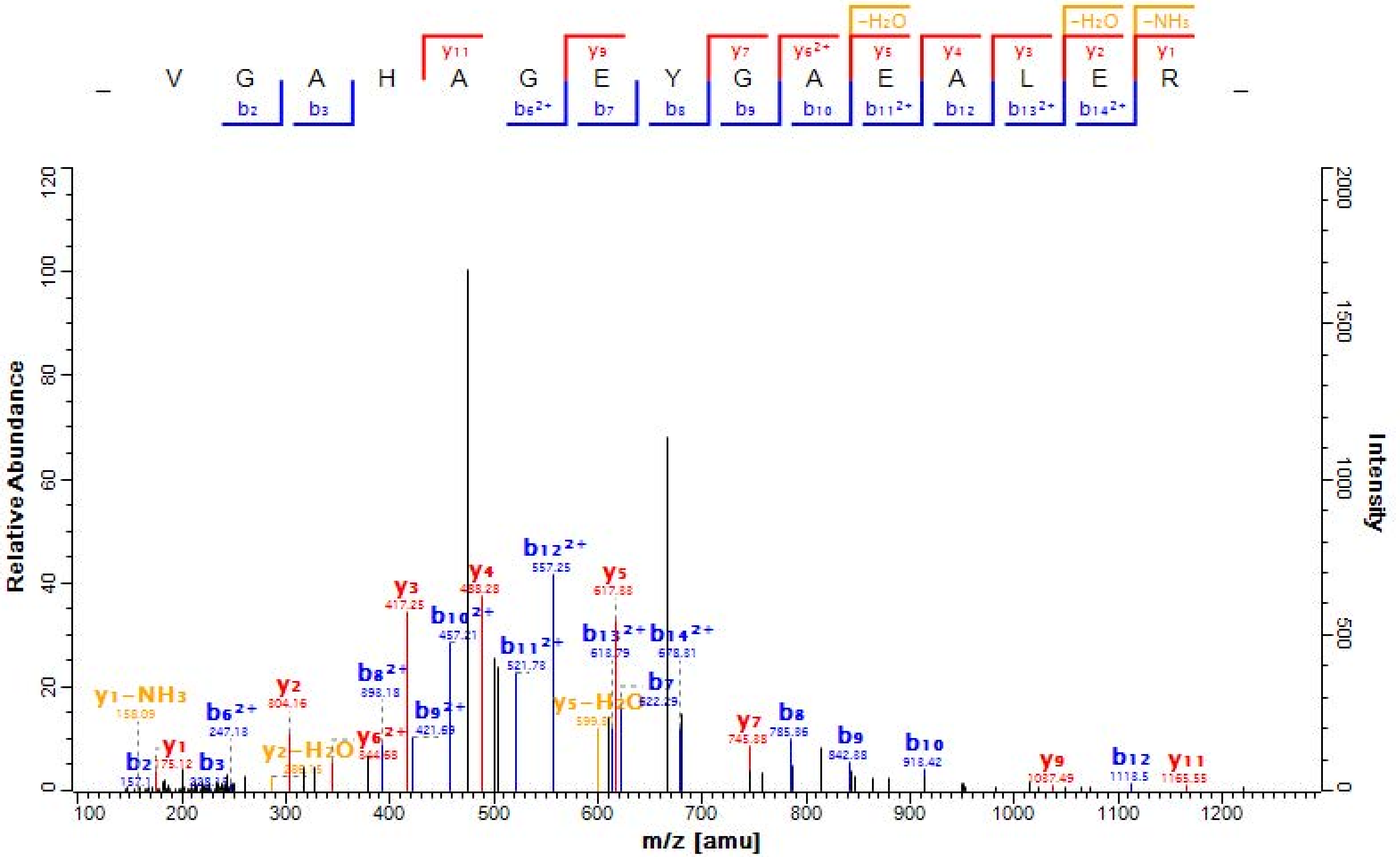
precursor information

g

Mass:	978.54981
m/z:	490.28218
Charge:	2+
Retentiontime:	13.578907966613
Score:	41.87606
Mass Error [ppm]:	-0.019306
PEP:	0.085117
Precursor Type:	MULTI
Annotation:	6 of 9
AminoAcids Coverag	67 %
Intensity Coverage:	19 %
Peak Coverage:	9 %
Protein Localisation:	598 ... 606

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.081		100.08	1	V	8				
-0.124	209.14	-0.022	237.13	2	H	7	880.49		440.75	+0.0672
	266.16		294.16	3	G	6	743.43	-0.013	743.43	
	353.19		381.19	4	S	5	686.41		686.41	
	450.25		478.24	5	P	4	599.38	+0.1937	599.38	
	563.33		591.32	6	L	3	502.32		502.32	
	692.37	+0.0251	720.37	7	E	2	389.24		389.24	
	805.46		833.45	8	L	1	260.2	-0.044	260.2	
				9	K	0	147.11	-0.113	147.11	

Scan number	1763	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	122.97



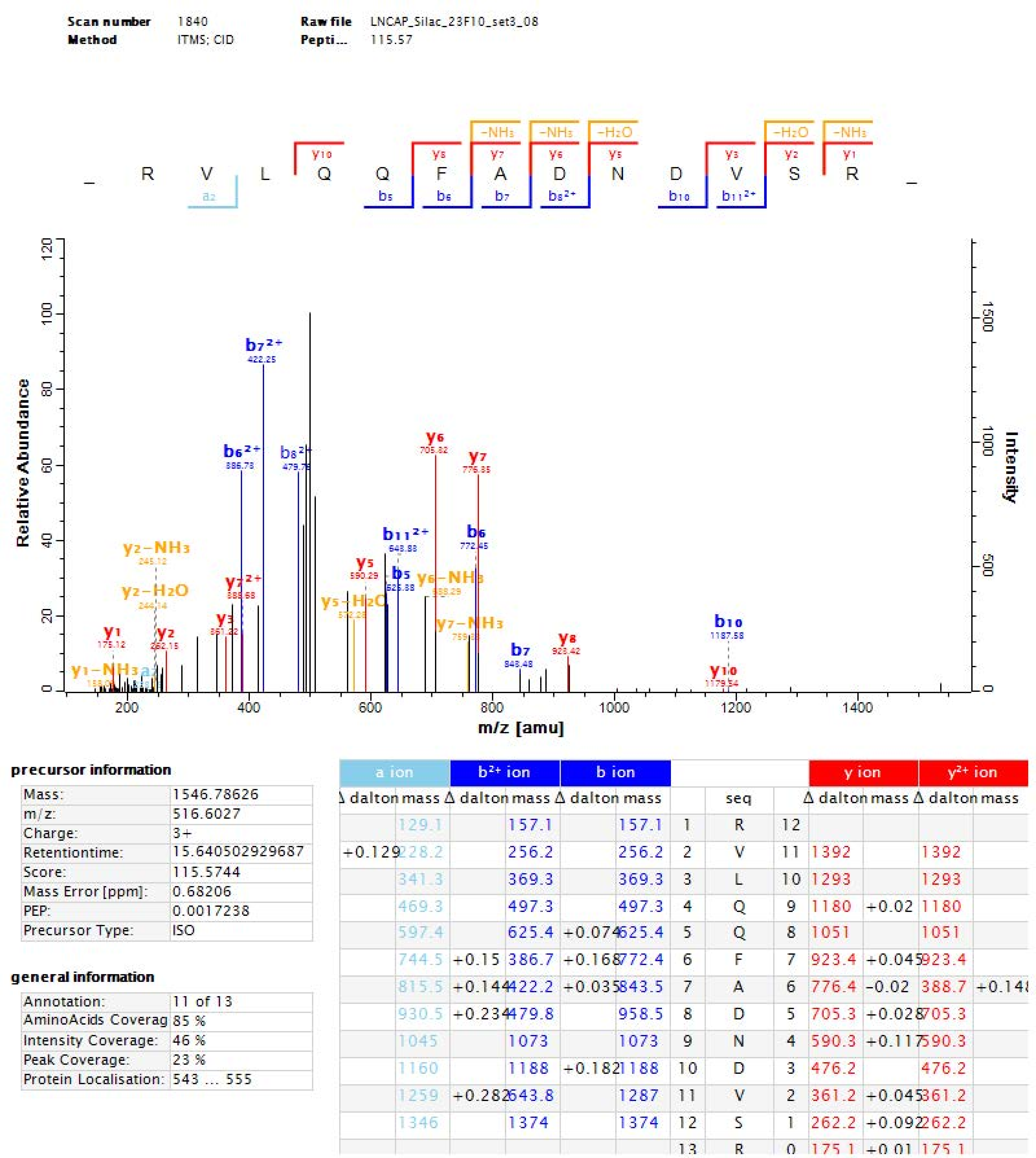
precursor information

Mass:	1528.72693
m/z:	510.58292
Charge:	3+
Retentiontime:	15.215983390808
Score:	122.9656
Mass Error [ppm]:	-0.057327
PEP:	4.0364E-06
Precursor Type:	ISO

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	47 %
Peak Coverage:	21 %
Protein Localisation:	18 ... 32

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	14				
	157.1	+0.0255	157.1	2	G	13	1430.7		1430.7	
	228.13	+0.0149	228.13	3	A	12	1373.6		1373.6	
	365.19		365.19	4	H	11	1302.6		1302.6	
	436.23		436.23	5	A	10	1165.5	-0.011	1165.5	
+0.1155	247.13		493.25	6	G	9	1094.5		1094.5	
	622.29	-0.17	622.29	7	E	8	1037.5	-0.451	1037.5	
-0.057	393.18	+0.0339	785.36	8	Y	7	908.45		908.45	
+0.0667	421.69	-0.04	842.38	9	G	6	745.38	+0.1093	745.38	
-0.111	457.21	+0.1563	913.42	10	A	5	688.36		344.68	+0.0908
+0.0799	521.73		1042.5	11	E	4	617.33	+0.0175	617.33	
+0.2249	557.25	-0.026	1113.5	12	A	3	488.28	+0.0848	488.28	
-0.081	613.79		1226.6	13	L	2	417.25	-0.056	417.25	
+0.1773	678.31		1355.6	14	E	1	304.16	+0.0509	304.16	
				15	R	0	175.12	+0.127	175.12	



Scan number 1840
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set3_08
Pepti... 115.57

precursor information

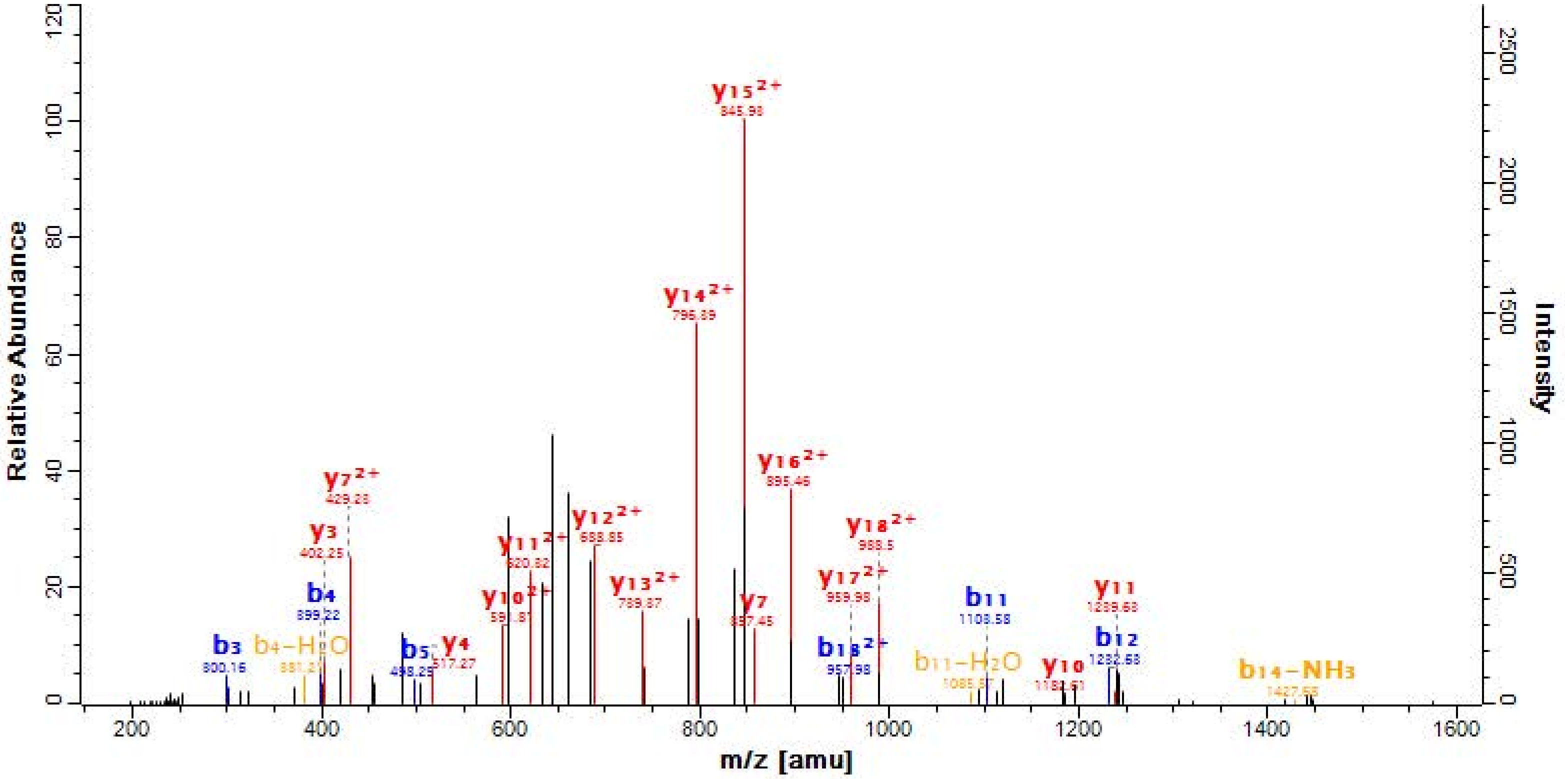
Mass:	1546.78626
m/z:	516.6027
Charge:	3+
Retentiontime:	15.640502929687
Score:	115.5744
Mass Error [ppm]:	0.68206
PEP:	0.0017238
Precursor Type:	ISO

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	46 %
Peak Coverage:	23 %
Protein Localisation:	543 … 555

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.1		157.1		157.1	1	R	12				
+0.129	228.2		256.2		256.2	2	V	11	1392		1392	
	341.3		369.3		369.3	3	L	10	1293		1293	
	469.3		497.3		497.3	4	Q	9	1180	+0.02	1180	
	597.4		625.4	+0.074	625.4	5	Q	8	1051		1051	
	744.5	+0.15	386.7	+0.168	772.4	6	F	7	923.4	+0.045	923.4	
	815.5	+0.144	422.2	+0.035	843.5	7	A	6	776.4	-0.02	388.7	+0.14
	930.5	+0.234	479.8		958.5	8	D	5	705.3	+0.028	705.3	
	1045		1073		1073	9	N	4	590.3	+0.117	590.3	
	1160		1188	+0.182	1188	10	D	3	476.2		476.2	
	1259	+0.282	643.8		1287	11	V	2	361.2	+0.045	361.2	
	1346		1374		1374	12	S	1	262.2	+0.092	262.2	
						13	R	0	175.1	+0.01	175.1	

Scan number	1869	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	113.01



precursor information

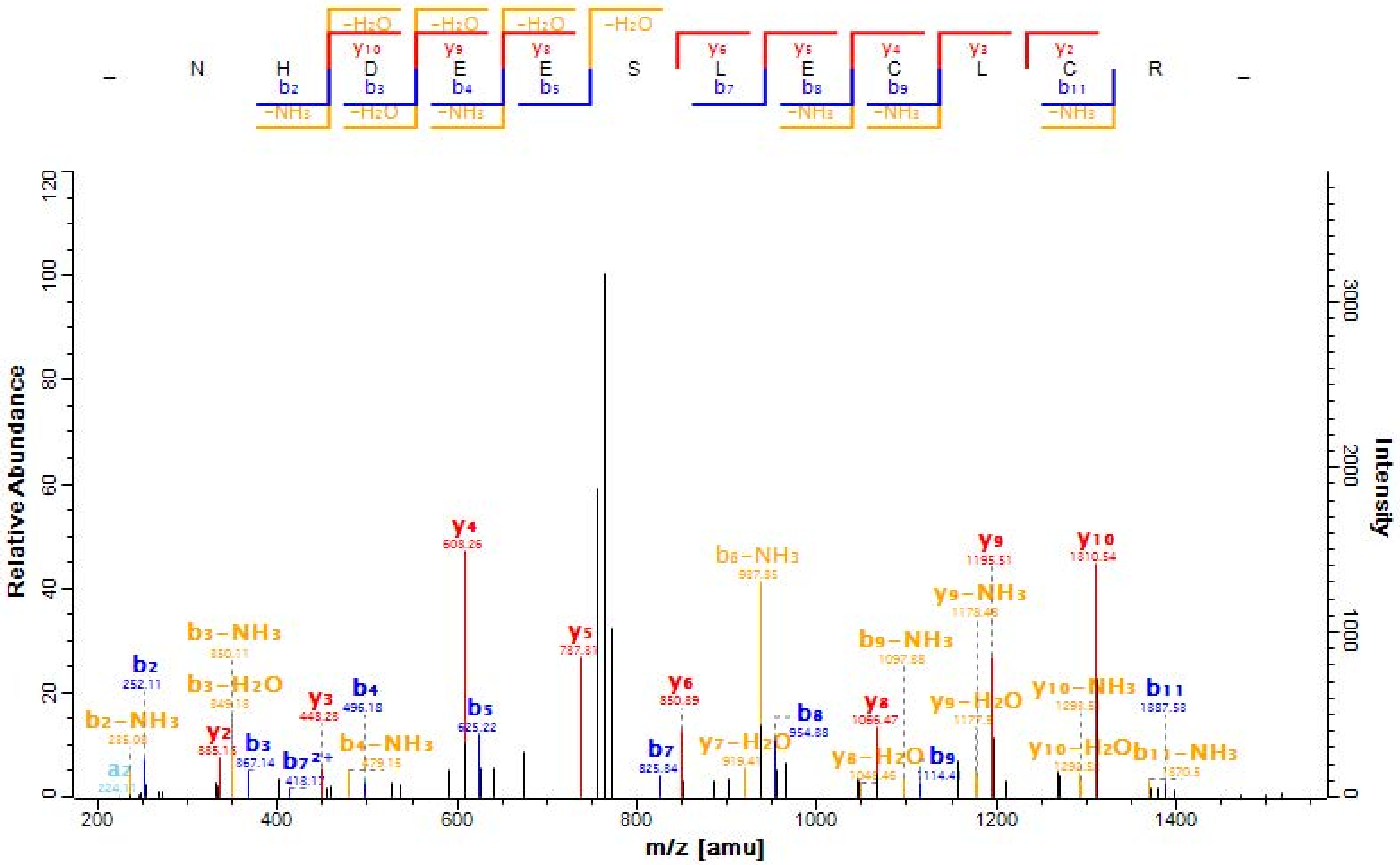
Mass:	2088.05961
m/z:	697.02715
Charge:	3+
Retentiontime:	15.808485031127
Score:	113.0145
Mass Error [ppm]:	-0.1793
PEP:	1.4121E-08
Precursor Type:	MULTI

general information

Annotation:	16 of 19
AminoAcids Coverag	84 %
Intensity Coverage:	49 %
Peak Coverage:	26 %
Protein Localisation:	128 ... 146

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	L	18				
	171.11		171.11	2	G	17	1976		988.5	+0.2354
	300.16	-0.221	300.16	3	E	16	1919		959.98	+0.2504
	399.22	+0.0694	399.22	4	V	15	1789.9		895.46	+0.1613
	498.29	-0.173	498.29	5	V	14	1690.9		845.93	+0.174
	612.34		612.34	6	N	13	1591.8		796.39	+0.23
	713.38		713.38	7	T	12	1477.7		739.37	+0.2068
	850.44		850.44	8	H	11	1376.7		688.85	-0.026
	907.46		907.46	9	G	10	1239.6	-0.285	620.32	+0.2057
	1004.5		1004.5	10	P	9	1182.6	-0.127	591.81	-0.241
	1103.6	+0.0096	1103.6	11	V	8	1085.6		1085.6	
	1232.6	-0.24	1232.6	12	E	7	986.49		986.49	
	1329.7		1329.7	13	P	6	857.45	+0.3096	429.23	+0.2687
	1444.7		1444.7	14	D	5	760.39		760.39	
	1572.8		1572.8	15	K	4	645.37		645.37	
	1687.8		1687.8	16	D	3	517.27	+0.0797	517.27	
	1801.9		1801.9	17	N	2	402.25	+0.0851	402.25	
+0.4461	957.98		1915	18	I	1	288.2		288.2	
				19	R	0	175.12		175.12	

Scan number	1886	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	193.28



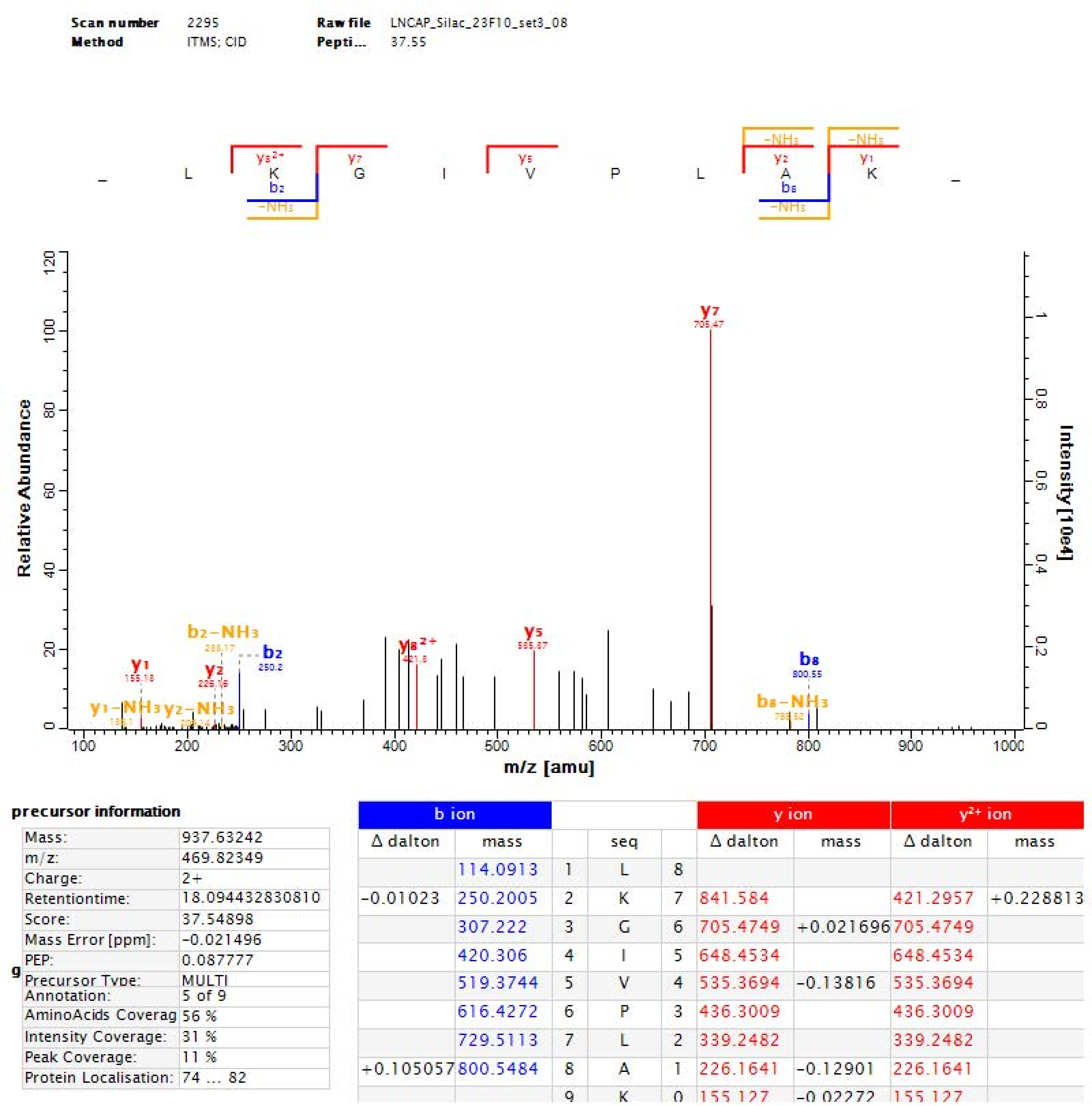
precursor information

Mass:	1560.62915
m/z:	781.32185
Charge:	2+
Retentiontime:	15.905056953430
Score:	193.2815
Mass Error [ppm]:	-0.34753
PEP:	1.6879E-14
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	43 %
Peak Coverage:	39 %
Protein Localisation:	933 ... 944

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	87.055		115.05		115.05	1	N	11		
-0.045	224.11		252.11	+0.0412	252.11	2	H	10	1447.6	
	339.14		367.14	+0.1189	367.14	3	D	9	1310.5	-0.044
	468.18		496.18	+0.1062	496.18	4	E	8	1195.5	-0.024
	597.23		625.22	+0.1076	625.22	5	E	7	1066.5	-0.043
	684.26		712.25		712.25	6	S	6	937.42	
	797.34	+0.2039	413.17	-0.008	825.34	7	L	5	850.39	+0.0805
	926.39		954.38	-0.021	954.38	8	E	4	737.31	-0.025
	1086.4		1114.4	-0.149	1114.4	9	C	3	608.26	+0.0415
	1199.5		1227.5		1227.5	10	L	2	448.23	+0.0921
	1359.5		1387.5	-0.066	1387.5	11	C	1	335.15	+0.0436
						12	R	0	175.12	

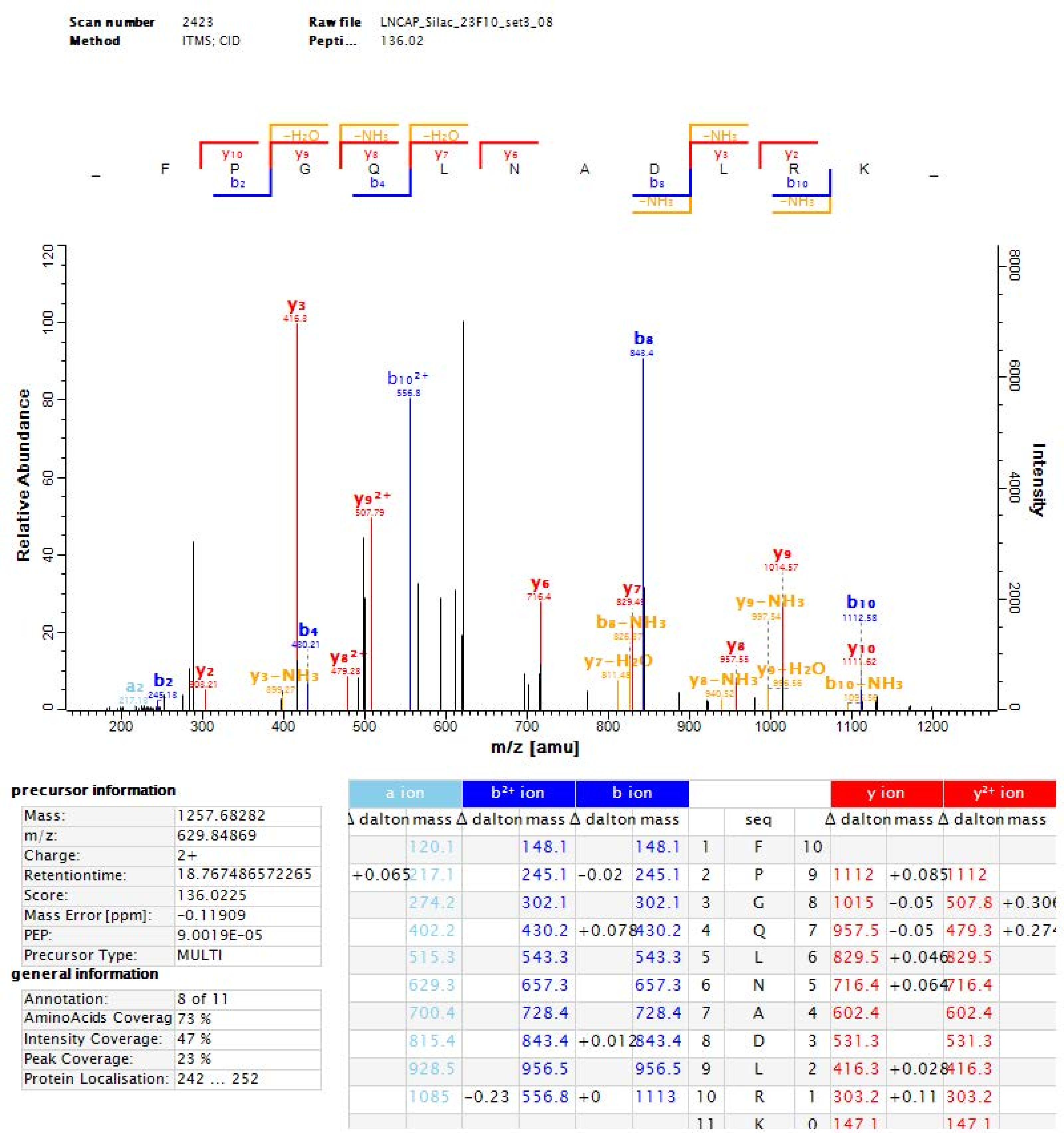


Scan number	2295	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	37.55

precursor information

Mass:	937.63242
m/z:	469.82349
Charge:	2+
Retentiontime:	18.094432830810
Score:	37.54898
Mass Error [ppm]:	-0.021496
PEP:	0.087777
Precursor Type:	MULTI
Annotation:	5 of 9
AminoAcids Coverag	56 %
Intensity Coverage:	31 %
Peak Coverage:	11 %
Protein Localisation:	74 ... 82

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	8				
-0.01023	250.2005	2	K	7	841.584		421.2957	+0.228813
	307.222	3	G	6	705.4749	+0.021696	705.4749	
	420.306	4	I	5	648.4534		648.4534	
	519.3744	5	V	4	535.3694	-0.13816	535.3694	
	616.4272	6	P	3	436.3009		436.3009	
	729.5113	7	L	2	339.2482		339.2482	
+0.105057	800.5484	8	A	1	226.1641	-0.12901	226.1641	
		9	K	0	155.127	-0.02272	155.127	



Scan number	2423	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	136.02

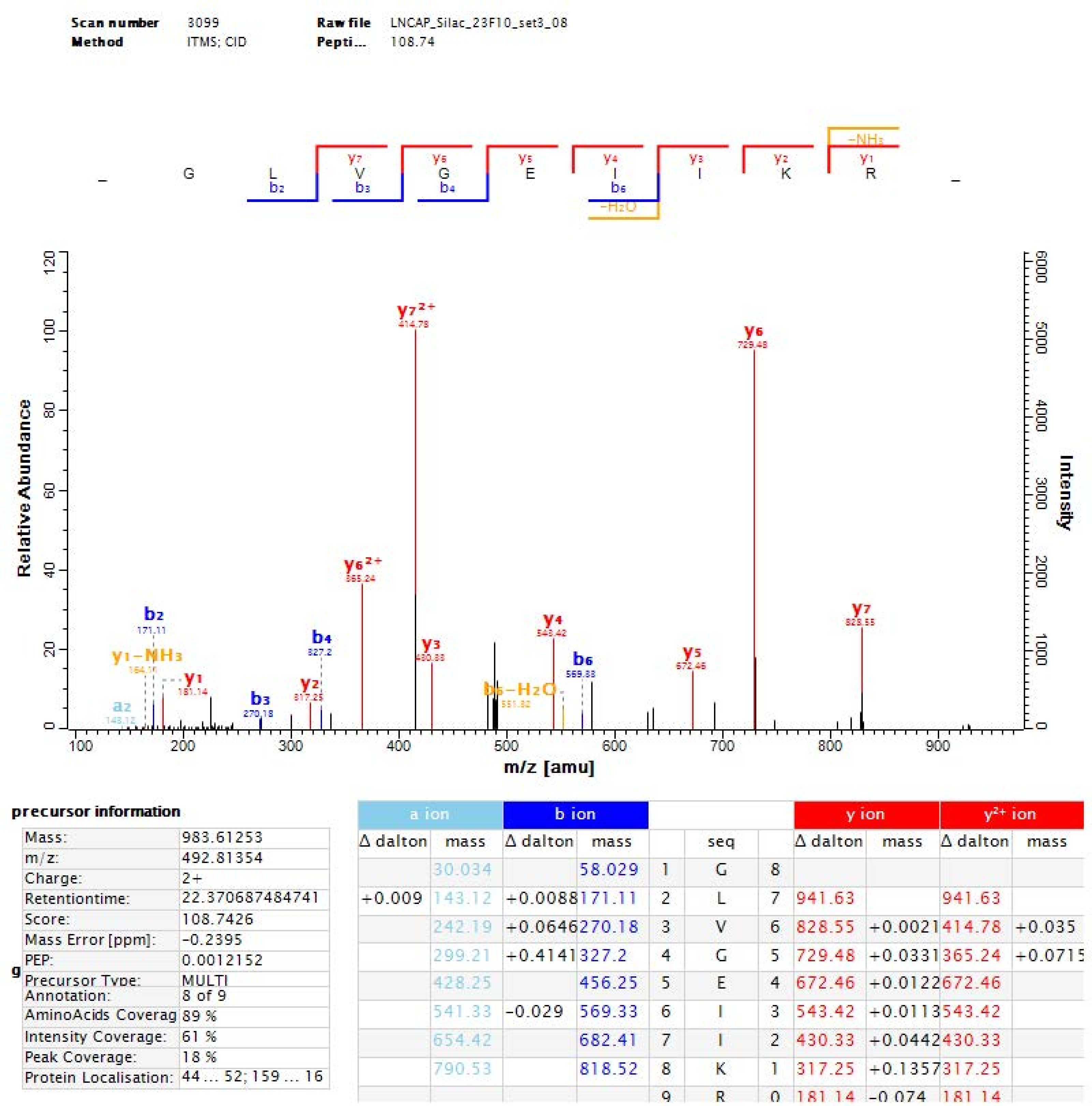
precursor information

Mass:	1257.68282
m/z:	629.84869
Charge:	2+
Retentiontime:	18.767486572265
Score:	136.0225
Mass Error [ppm]:	-0.11909
PEP:	9.0019E-05
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	47 %
Peak Coverage:	23 %
Protein Localisation:	242 ... 252

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.1		148.1		148.1	1	F	10				
+0.065	217.1		245.1	-0.02	245.1	2	P	9	1112	+0.085	1112	
	274.2		302.1		302.1	3	G	8	1015	-0.05	507.8	+0.30
	402.2		430.2	+0.078	430.2	4	Q	7	957.5	-0.05	479.3	+0.27
	515.3		543.3		543.3	5	L	6	829.5	+0.046	829.5	
	629.3		657.3		657.3	6	N	5	716.4	+0.064	716.4	
	700.4		728.4		728.4	7	A	4	602.4		602.4	
	815.4		843.4	+0.012	843.4	8	D	3	531.3		531.3	
	928.5		956.5		956.5	9	L	2	416.3	+0.028	416.3	
	1085	-0.23	556.8	+0	1113	10	R	1	303.2	+0.11	303.2	
						11	K	0	147.1		147.1	

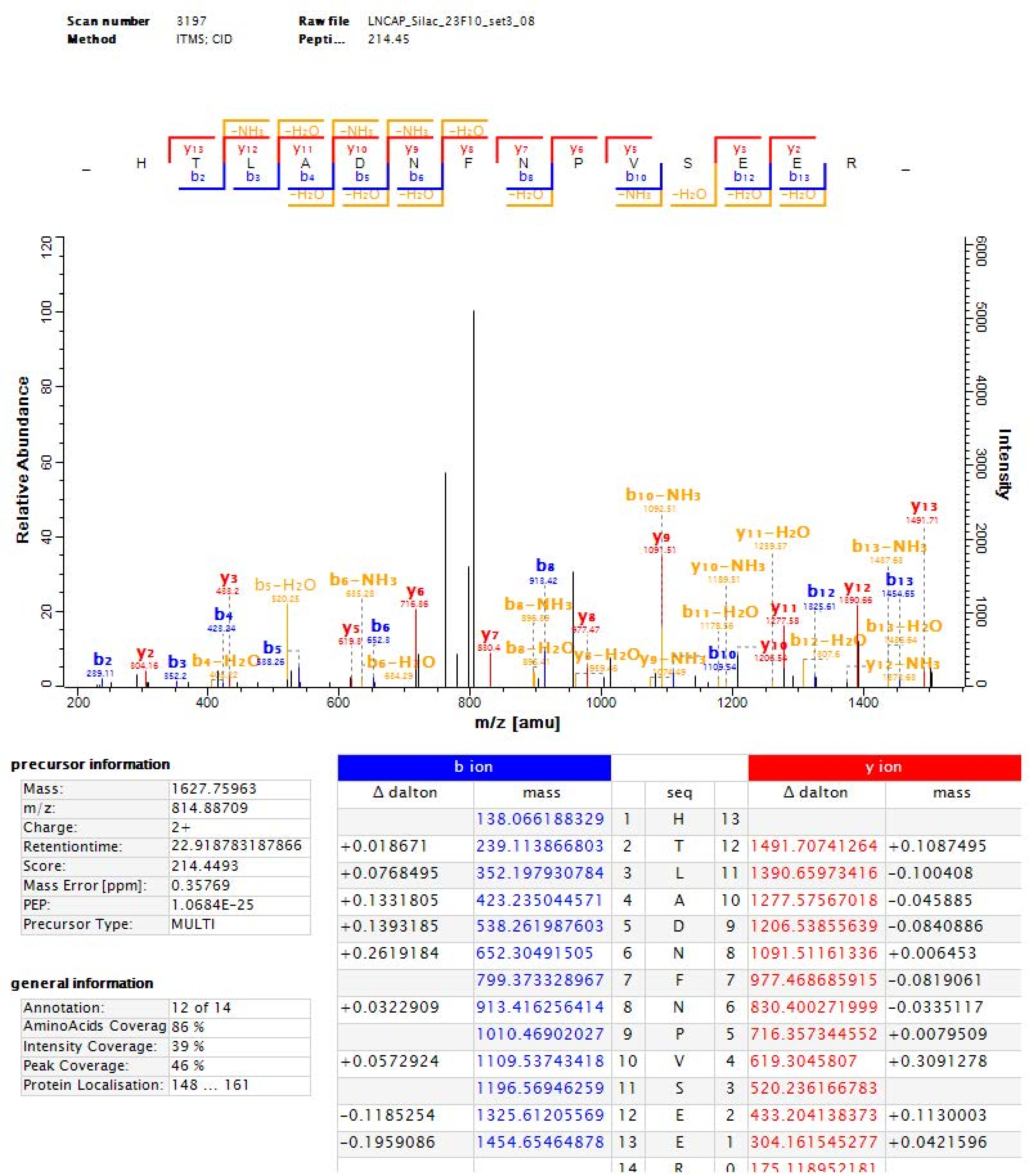


Scan number	3099	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	108.74

precursor information

Mass:	983.61253
m/z:	492.81354
Charge:	2+
Retentiontime:	22.370687484741
Score:	108.7426
Mass Error [ppm]:	-0.2395
PEP:	0.0012152
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	61 %
Peak Coverage:	18 %
Protein Localisation:	44 ... 52; 159 ... 16

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	30.034		58.029	1	G	8				
+0.009	143.12	+0.0088	171.11	2	L	7	941.63		941.63	
	242.19	+0.0646	270.18	3	V	6	828.55	+0.0021	414.78	+0.035
	299.21	+0.4141	327.2	4	G	5	729.48	+0.0331	365.24	+0.0715
	428.25		456.25	5	E	4	672.46	+0.0122	672.46	
	541.33	-0.029	569.33	6	I	3	543.42	+0.0113	543.42	
	654.42		682.41	7	I	2	430.33	+0.0442	430.33	
	790.53		818.52	8	K	1	317.25	+0.1357	317.25	
				9	R	0	181.14	-0.074	181.14	



Scan number	3197	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	214.45

precursor information

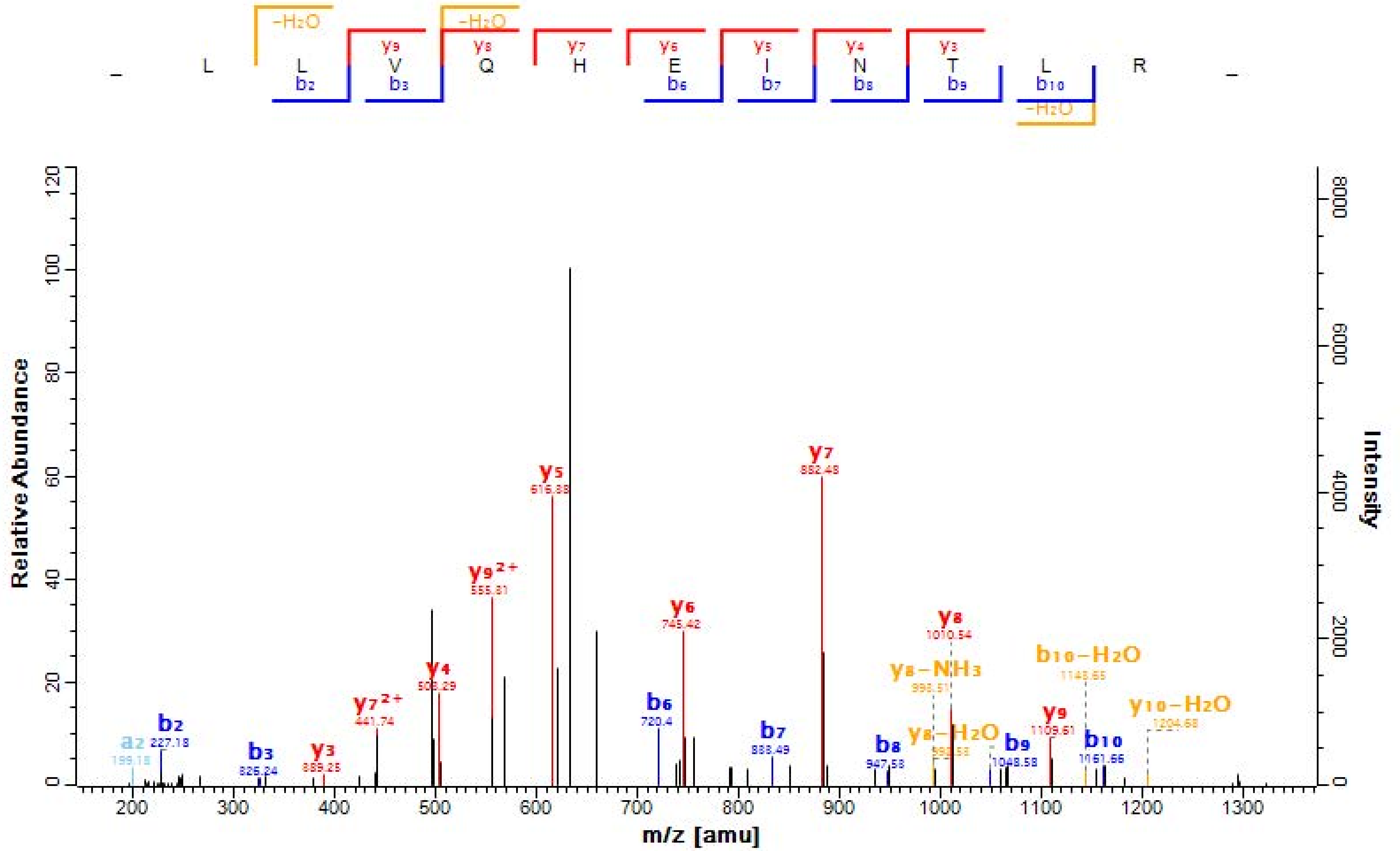
Mass:	1627.75963
m/z:	814.88709
Charge:	2+
Retentiontime:	22.918783187866
Score:	214.4493
Mass Error [ppm]:	0.35769
PEP:	1.0684E-25
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	39 %
Peak Coverage:	46 %
Protein Localisation:	148 ... 161

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	138.066188329	1	H	13		
+0.018671	239.113866803	2	T	12	1491.70741264	+0.1087495
+0.0768495	352.197930784	3	L	11	1390.65973416	-0.100408
+0.1331805	423.235044571	4	A	10	1277.57567018	-0.045885
+0.1393185	538.261987603	5	D	9	1206.53855639	-0.0840886
+0.2619184	652.30491505	6	N	8	1091.51161336	+0.006453
	799.373328967	7	F	7	977.468685915	-0.0819061
+0.0322909	913.416256414	8	N	6	830.400271999	-0.0335117
	1010.46902027	9	P	5	716.357344552	+0.0079509
+0.0572924	1109.53743418	10	V	4	619.3045807	+0.3091278
	1196.56946259	11	S	3	520.236166783	
-0.1185254	1325.61205569	12	E	2	433.204138373	+0.1130003
-0.1959086	1454.65464878	13	E	1	304.161545277	+0.0421596
		14	R	0	175.118952181	

Scan number	3236	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	128.67



precursor information

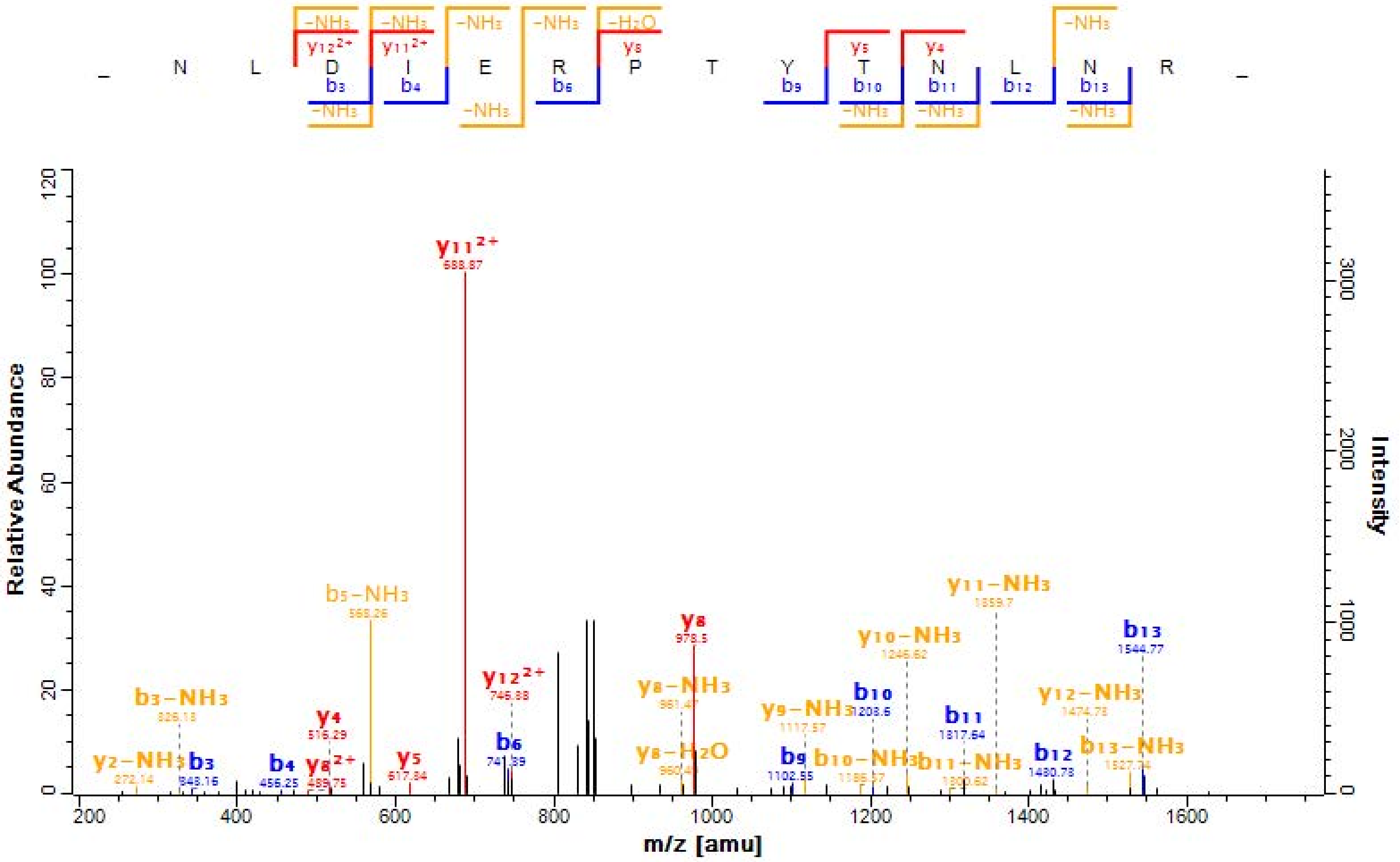
Mass:	1334.76714
m/z:	668.39085
Charge:	2+
Retentiontime:	23.130344390869
Score:	128.6744
Mass Error [ppm]:	0.08281
PEP:	0.00018728
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	38 %
Peak Coverage:	23 %
Protein Localisation:	553 ... 563

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	L	10				
-0.079	199.18	-0.006	227.18	2	L	9	1222.7		1222.7	
	298.25	-0.226	326.24	3	V	8	1109.6	-0.019	555.31	+0.0405
	426.31		454.3	4	Q	7	1010.5	-0.047	1010.5	
	563.37		591.36	5	H	6	882.48	-0.015	441.74	+0.032
	692.41	-0.09	720.4	6	E	5	745.42	+0.0275	745.42	
	805.49	-0.032	833.49	7	I	4	616.38	-0.231	616.38	
	919.54	-0.089	947.53	8	N	3	503.29	+0.0734	503.29	
	1020.6	-0.047	1048.6	9	T	2	389.25	+0.0983	389.25	
	1133.7	-0.08	1161.7	10	L	1	288.2		288.2	
				11	R	0	175.12		175.12	

Scan number	3283	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	125.61



precursor information

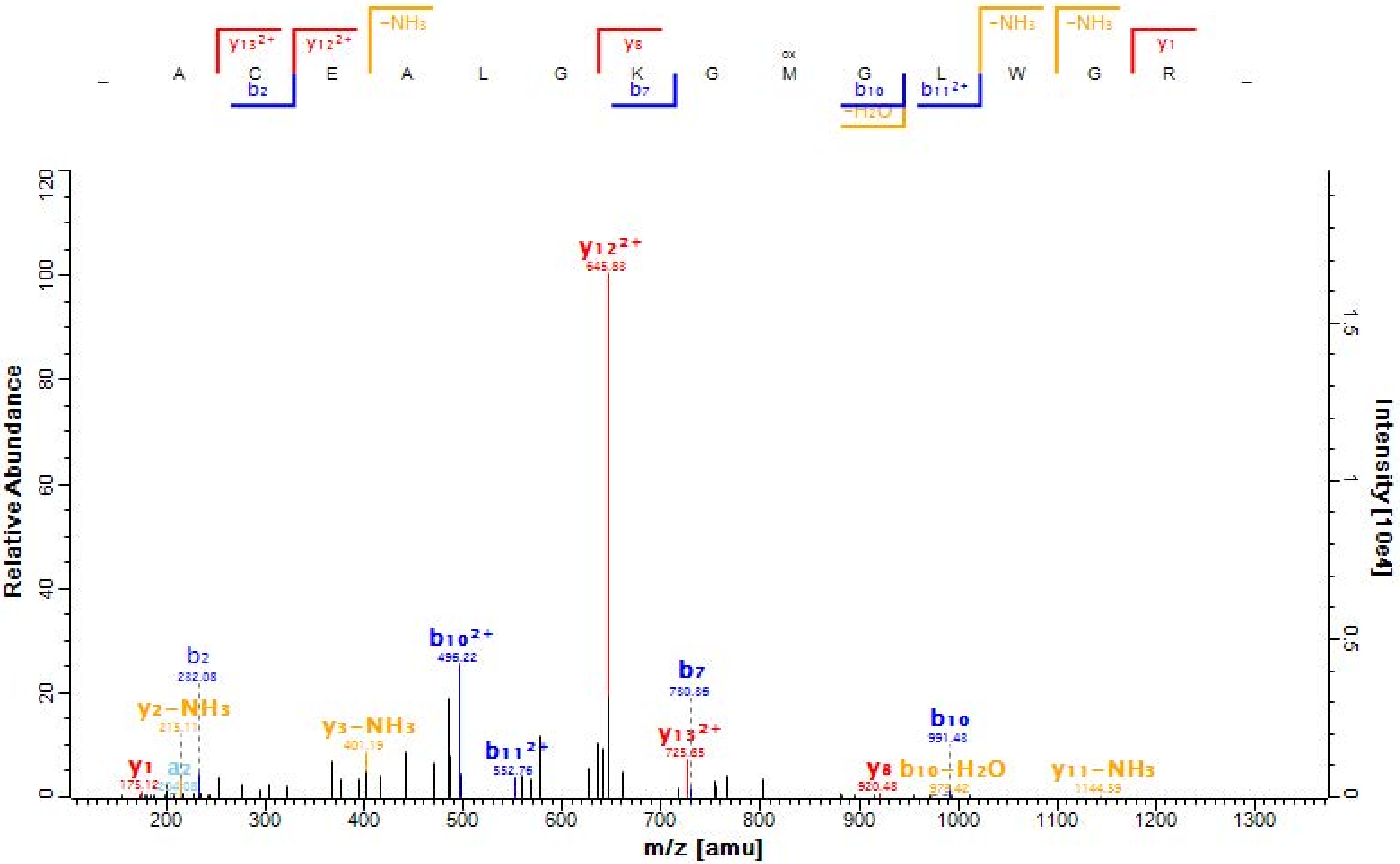
Mass:	1717.87424
m/z:	859.9444
Charge:	2+
Retentiontime:	23.378295898437
Score:	125.6116
Mass Error [ppm]:	-0.29594
PEP:	9.0267E-09
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	48 %
Peak Coverage:	31 %
Protein Localisation:	216 ... 229

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502	1	N	13				
	228.1343	2	L	12	1604.839		1604.839	
+0.113295	343.1612	3	D	11	1491.755		746.3812	+0.008678
+0.005885	456.2453	4	I	10	1376.728		688.8677	+0.245721
	585.2879	5	E	9	1263.644		1263.644	
-0.03357	741.389	6	R	8	1134.601		1134.601	
	838.4417	7	P	7	978.5003	-0.0547	489.7538	+0.271653
	939.4894	8	T	6	881.4476		881.4476	
+0.100815	1102.553	9	Y	5	780.3999		780.3999	
-0.1379	1203.6	10	T	4	617.3365	+0.03076	617.3365	
-0.22368	1317.643	11	N	3	516.2889	+0.157723	516.2889	
+0.112546	1430.727	12	L	2	402.2459		402.2459	
-0.23251	1544.77	13	N	1	289.1619		289.1619	
		14	R	0	175.119		175.119	

Scan number	3461	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	57.8



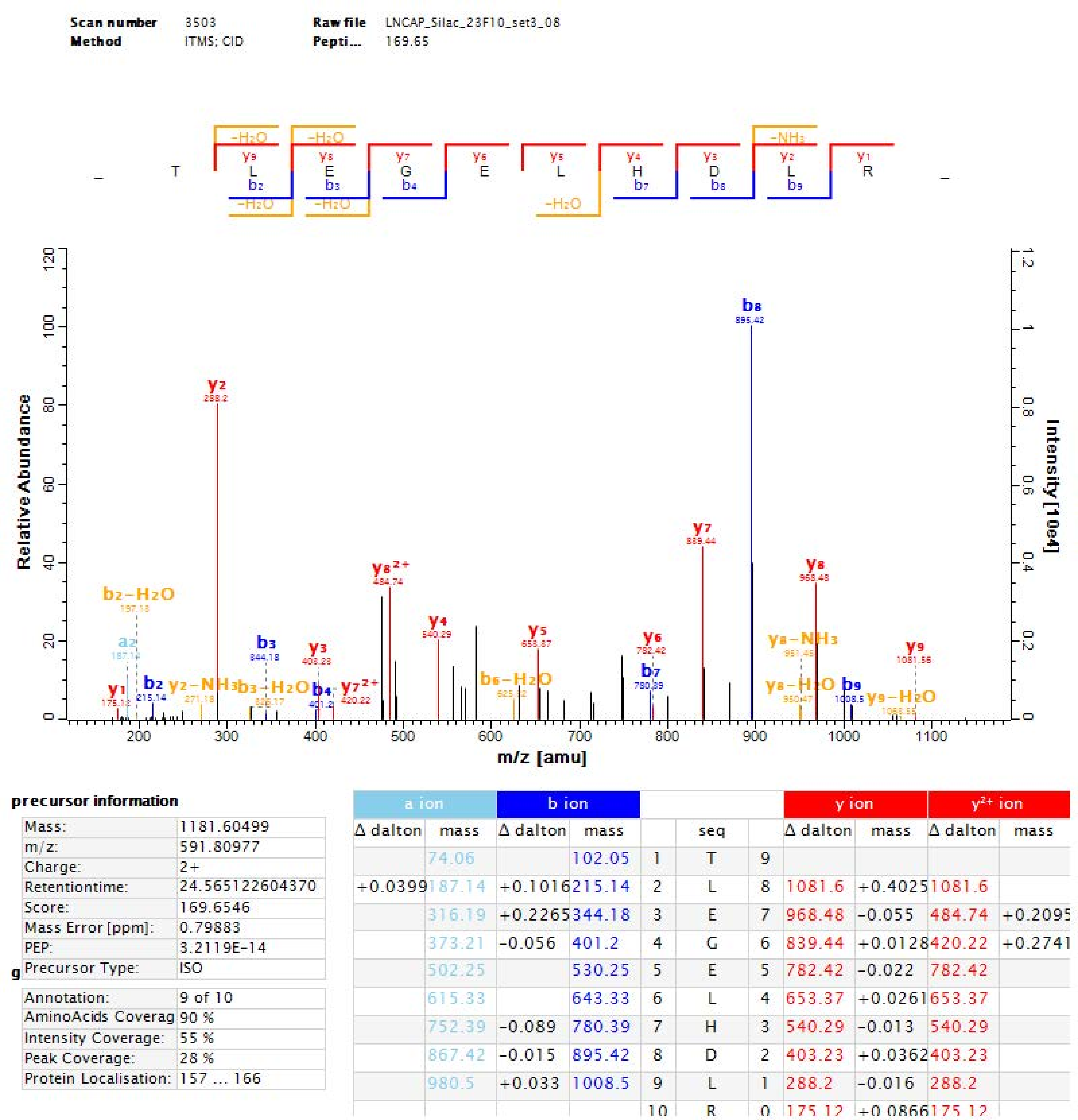
precursor information

Mass:	1520.72223
m/z:	507.91469
Charge:	3+
Retentiontime:	24.332654953002
Score:	57.80165
Mass Error [ppm]:	-0.37625
PEP:	0.020987
Precursor Type:	MULTI

general information

Annotation:	9 of 14
AminoAcids Coverag	64 %
Intensity Coverage:	46 %
Peak Coverage:	14 %
Protein Localisation:	73 ... 86

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
∆ dalton	mass	∆ dalton	mass	∆ dalton	mass		seq		∆ dalton	mass	∆ dalton	mass
	44.05		72.04		72.04	1	A	13				
+0.012	204.1		232.1	-0.01	232.1	2	C	12	1451		725.9	+0.16
	333.1		361.1		361.1	3	E	11	1291		645.8	+0.26
	404.2		432.2		432.2	4	A	10	1162		1162	
	517.2		545.2		545.2	5	L	9	1091		1091	
	574.3		602.3		602.3	6	G	8	977.5		977.5	
	702.4		730.4	+0.222	730.4	7	K	7	920.5	+0.039	920.5	
	759.4		787.4		787.4	8	G	6	792.4		792.4	
	906.4		934.4		934.4	9	M	5	735.4		735.4	
	963.4	+0.017	496.2	+0.291	991.4	10	G	4	588.3		588.3	
	1077	+0.062	552.8		1105	11	L	3	531.3		531.3	
	1263		1291		1291	12	W	2	418.2		418.2	
	1320		1348		1348	13	G	1	232.1		232.1	
						14	R	0	175.1	+0.017	175.1	



Scan number	3503	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	169.65

precursor information

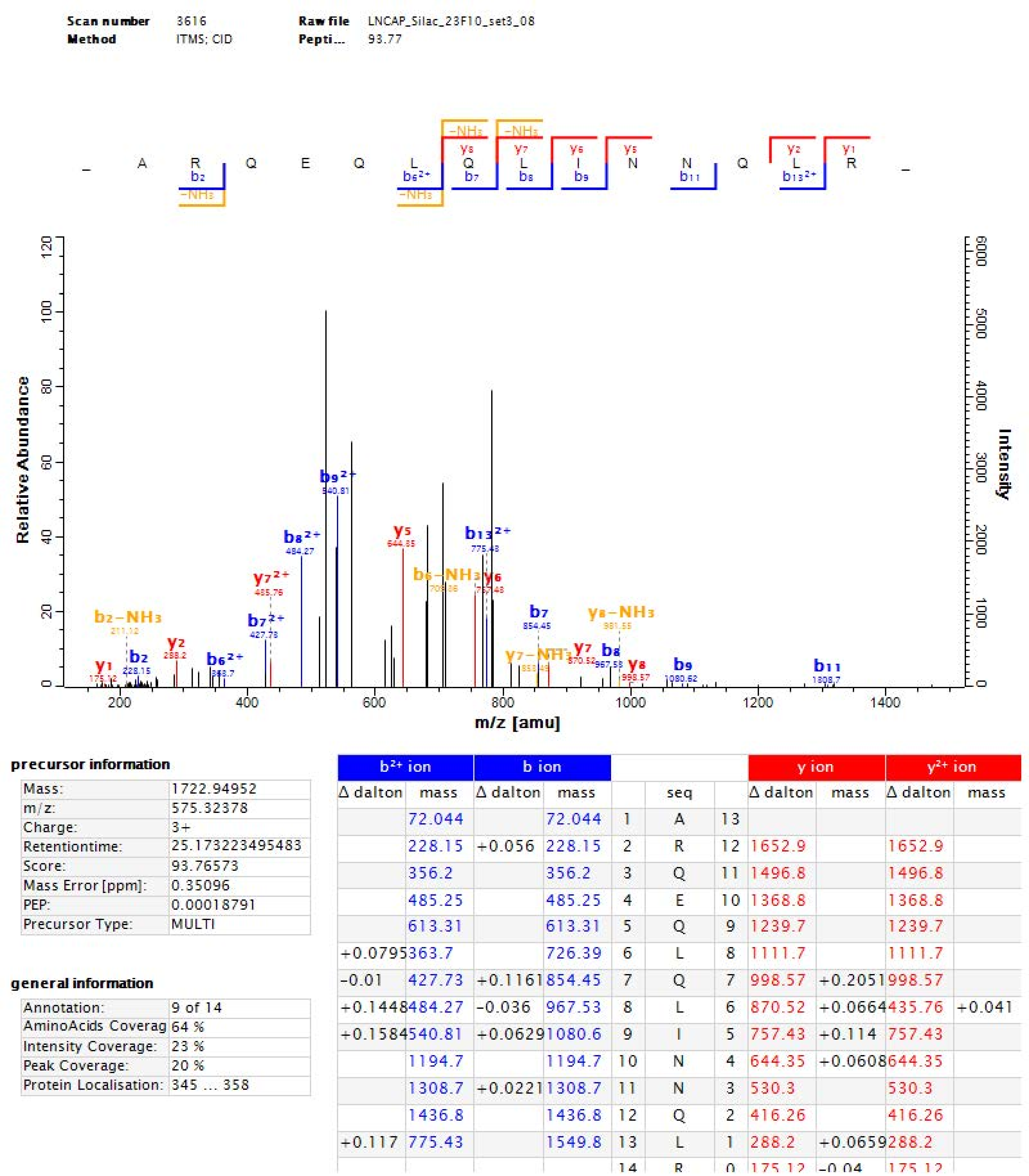
Mass:	1181.60499
m/z:	591.80977
Charge:	2+
Retentiontime:	24.565122604370
Score:	169.6546
Mass Error [ppm]:	0.79883
PEP:	3.2119E-14
Precursor Type:	ISO

g

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	55 %
Peak Coverage:	28 %
Protein Localisation:	157 ... 166

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.05	1	T	9				
+0.0399	187.14	+0.1016	215.14	2	L	8	1081.6	+0.4025	1081.6	
	316.19	+0.2265	344.18	3	E	7	968.48	-0.055	484.74	+0.2095
	373.21	-0.056	401.2	4	G	6	839.44	+0.0128	420.22	+0.2741
	502.25		530.25	5	E	5	782.42	-0.022	782.42	
	615.33		643.33	6	L	4	653.37	+0.0261	653.37	
	752.39	-0.089	780.39	7	H	3	540.29	-0.013	540.29	
	867.42	-0.015	895.42	8	D	2	403.23	+0.0362	403.23	
	980.5	+0.033	1008.5	9	L	1	288.2	-0.016	288.2	
				10	R	0	175.12	+0.0866	175.12	

Scan number 3616 **Raw file** LNCAP_Silac_23F10_set3_08
Method ITMS; CID **Pepti...** 93.77



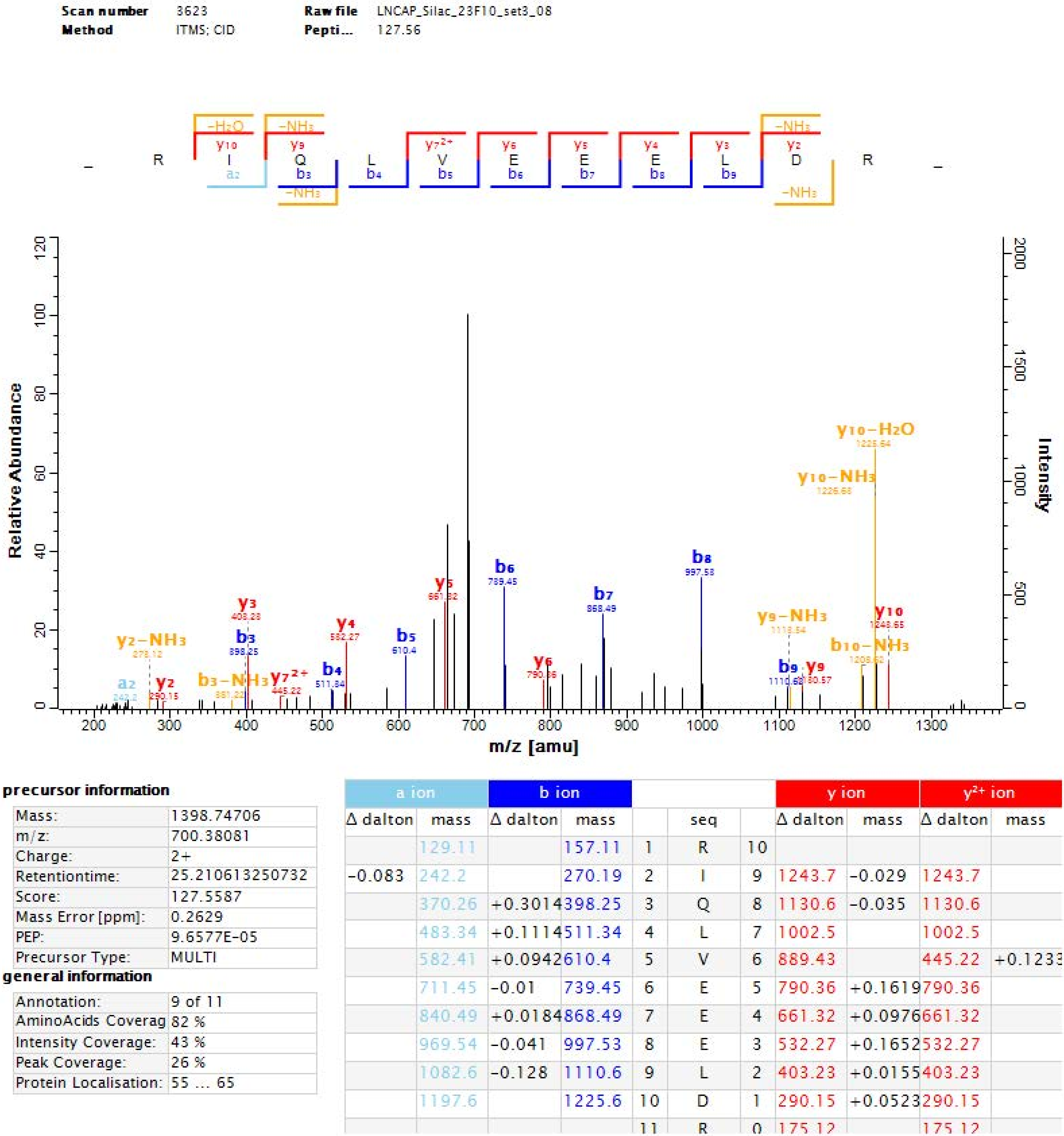
precursor information

Mass:	1722.94952
m/z:	575.32378
Charge:	3+
Retentiontime:	25.173223495483
Score:	93.76573
Mass Error [ppm]:	0.35096
PEP:	0.00018791
Precursor Type:	MULTI

general information

Annotation:	9 of 14
AminoAcids Coverag	64 %
Intensity Coverage:	23 %
Peak Coverage:	20 %
Protein Localisation:	345 ... 358

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	13				
	228.15	+0.056	228.15	2	R	12	1652.9		1652.9	
	356.2		356.2	3	Q	11	1496.8		1496.8	
	485.25		485.25	4	E	10	1368.8		1368.8	
	613.31		613.31	5	Q	9	1239.7		1239.7	
+0.0795	363.7		726.39	6	L	8	1111.7		1111.7	
-0.01	427.73	+0.1161	854.45	7	Q	7	998.57	+0.2051	998.57	
+0.1448	484.27	-0.036	967.53	8	L	6	870.52	+0.0664	435.76	+0.041
+0.1584	540.81	+0.0629	1080.6	9	I	5	757.43	+0.114	757.43	
	1194.7		1194.7	10	N	4	644.35	+0.0608	644.35	
	1308.7	+0.0221	1308.7	11	N	3	530.3		530.3	
	1436.8		1436.8	12	Q	2	416.26		416.26	
+0.117	775.43		1549.8	13	L	1	288.2	+0.0659	288.2	
				14	R	0	175.12	-0.04	175.12	



Scan number	3623	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	127.56

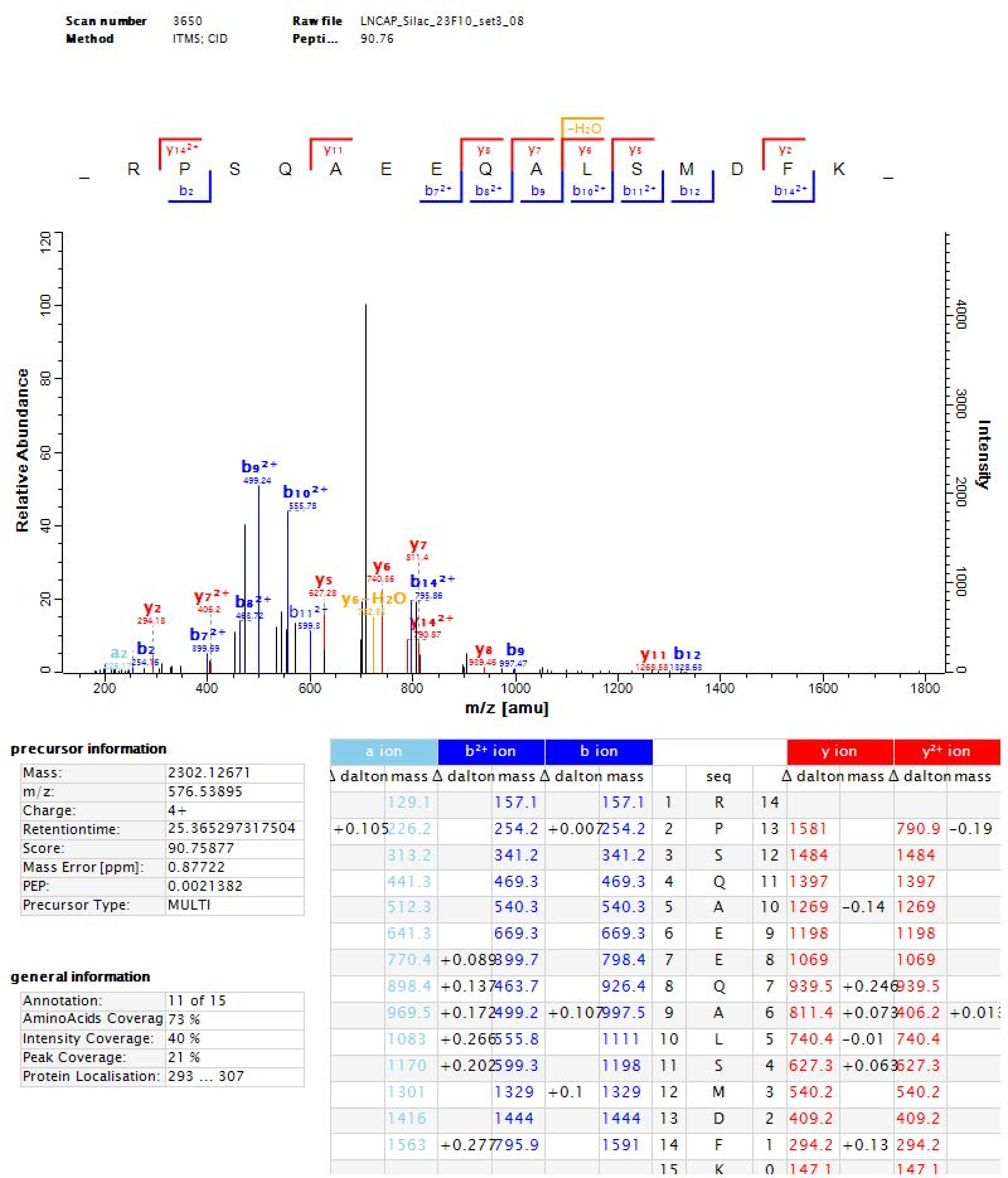
precursor information

Mass:	1398.74706
m/z:	700.38081
Charge:	2+
Retentiontime:	25.210613250732
Score:	127.5587
Mass Error [ppm]:	0.2629
PEP:	9.6577E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	43 %
Peak Coverage:	26 %
Protein Localisation:	55 ... 65

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.11		157.11	1	R	10				
-0.083	242.2		270.19	2	I	9	1243.7	-0.029	1243.7	
	370.26	+0.3014	398.25	3	Q	8	1130.6	-0.035	1130.6	
	483.34	+0.1114	511.34	4	L	7	1002.5		1002.5	
	582.41	+0.0942	610.4	5	V	6	889.43		445.22	+0.1233
	711.45	-0.01	739.45	6	E	5	790.36	+0.1619	790.36	
	840.49	+0.0184	868.49	7	E	4	661.32	+0.0976	661.32	
	969.54	-0.041	997.53	8	E	3	532.27	+0.1652	532.27	
	1082.6	-0.128	1110.6	9	L	2	403.23	+0.0155	403.23	
	1197.6		1225.6	10	D	1	290.15	+0.0523	290.15	
				11	R	0	175.12		175.12	



Scan number	3650	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	90.76

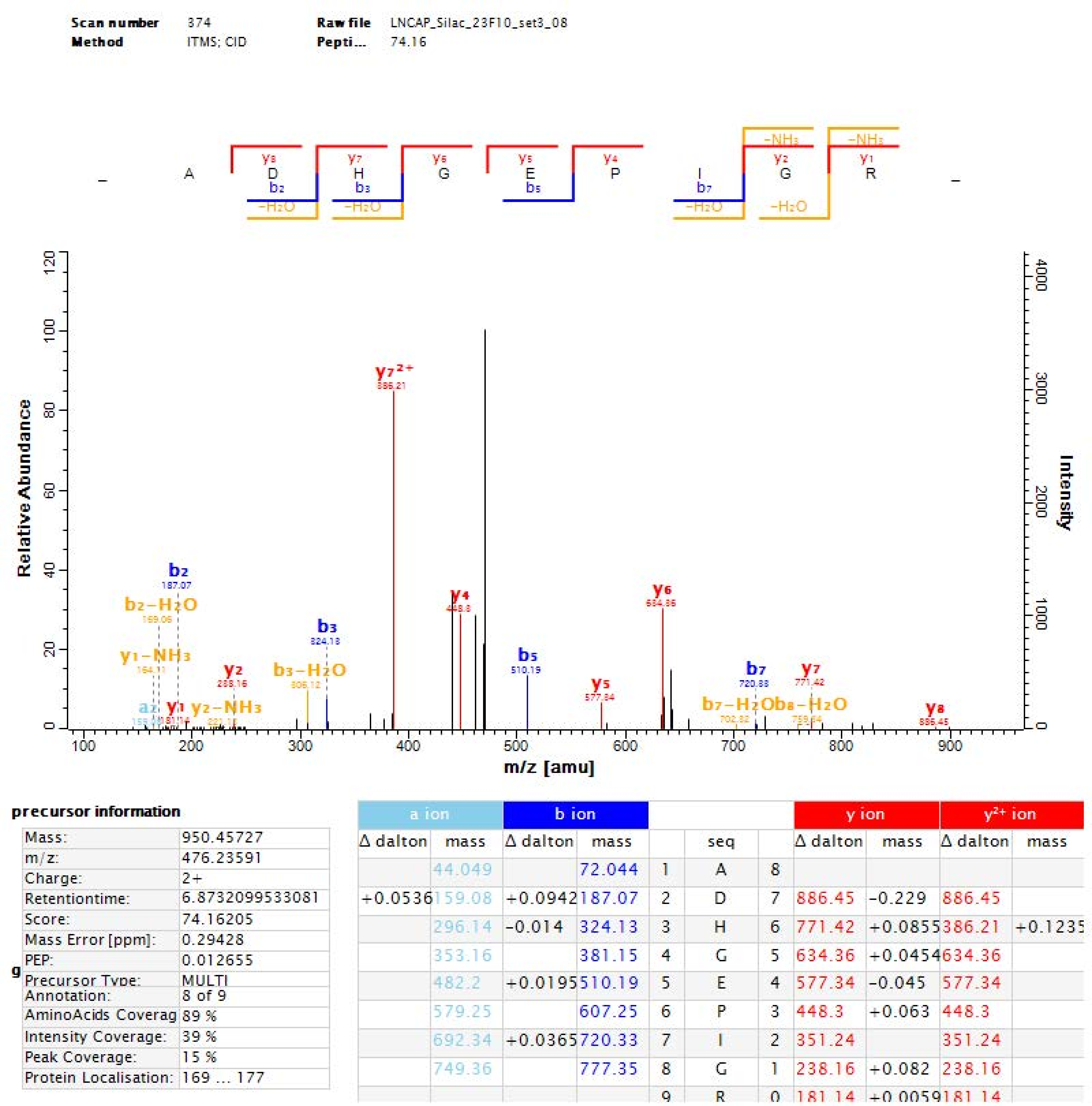
precursor information

Mass:	2302.12671
m/z:	576.53895
Charge:	4+
Retentiontime:	25.365297317504
Score:	90.75877
Mass Error [ppm]:	0.87722
PEP:	0.0021382
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	40 %
Peak Coverage:	21 %
Protein Localisation:	293 ... 307

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.1		157.1		157.1	1	R	14				
+0.105	226.2		254.2	+0.007	254.2	2	P	13	1581		790.9	-0.19
	313.2		341.2		341.2	3	S	12	1484		1484	
	441.3		469.3		469.3	4	Q	11	1397		1397	
	512.3		540.3		540.3	5	A	10	1269	-0.14	1269	
	641.3		669.3		669.3	6	E	9	1198		1198	
	770.4	+0.089	399.7		798.4	7	E	8	1069		1069	
	898.4	+0.137	463.7		926.4	8	Q	7	939.5	+0.246	939.5	
	969.5	+0.172	499.2	+0.107	997.5	9	A	6	811.4	+0.073	406.2	+0.01
	1083	+0.266	555.8		1111	10	L	5	740.4	-0.01	740.4	
	1170	+0.202	599.3		1198	11	S	4	627.3	+0.063	627.3	
	1301		1329	+0.1	1329	12	M	3	540.2		540.2	
	1416		1444		1444	13	D	2	409.2		409.2	
	1563	+0.277	795.9		1591	14	F	1	294.2	+0.13	294.2	
						15	K	0	147.1		147.1	



Scan number	374	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	74.16

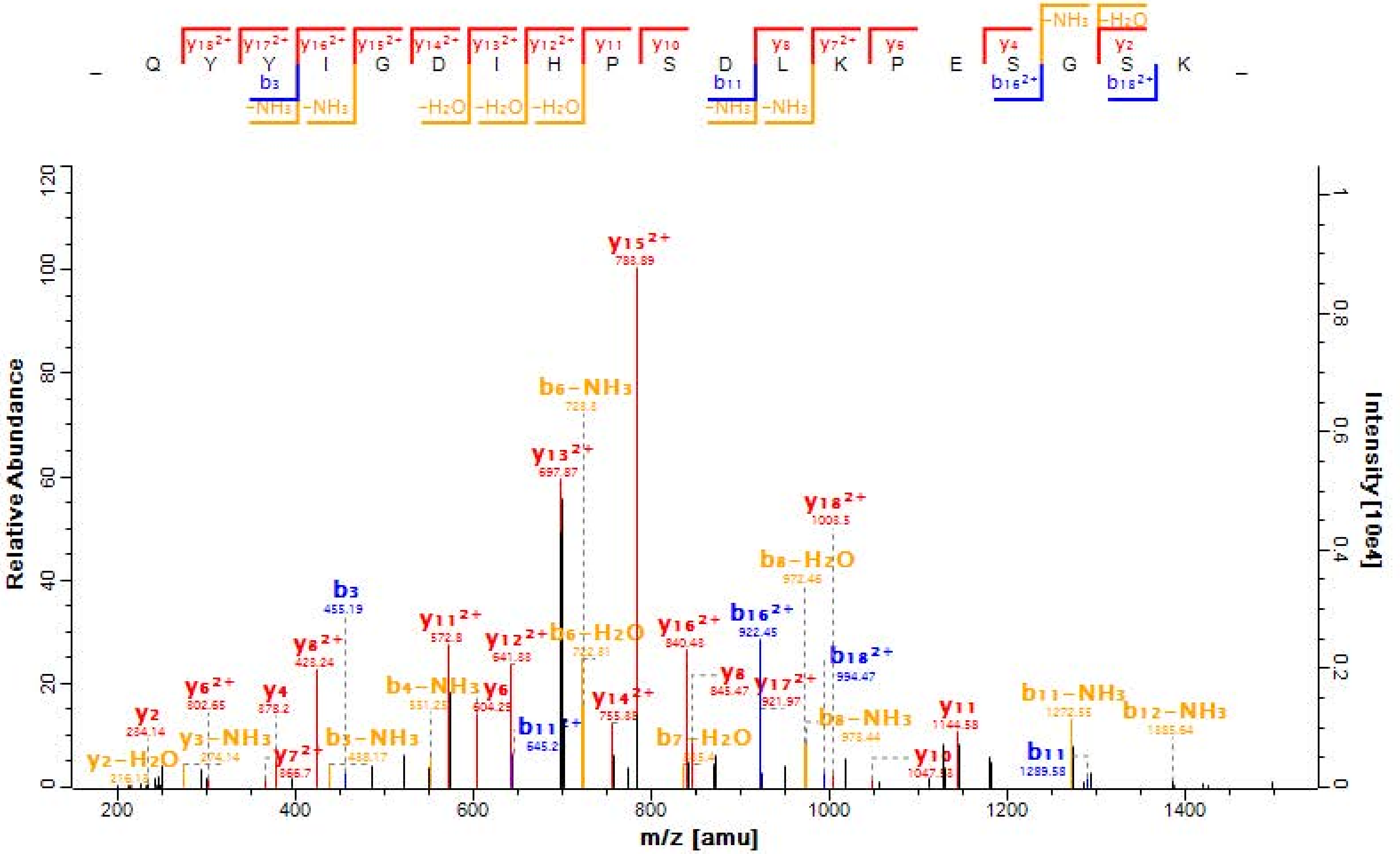
precursor information

g

Mass:	950.45727
m/z:	476.23591
Charge:	2+
Retentiontime:	6.8732099533081
Score:	74.16205
Mass Error [ppm]:	0.29428
PEP:	0.012655
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	39 %
Peak Coverage:	15 %
Protein Localisation:	169 ... 177

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	44.049		72.044	1	A	8				
+0.0536	159.08	+0.0942	187.07	2	D	7	886.45	-0.229	886.45	
	296.14	-0.014	324.13	3	H	6	771.42	+0.0855	386.21	+0.1235
	353.16		381.15	4	G	5	634.36	+0.0454	634.36	
	482.2	+0.0195	510.19	5	E	4	577.34	-0.045	577.34	
	579.25		607.25	6	P	3	448.3	+0.063	448.3	
	692.34	+0.0365	720.33	7	I	2	351.24		351.24	
	749.36		777.35	8	G	1	238.16	+0.082	238.16	
				9	R	0	181.14	+0.0059	181.14	

Scan number	3849	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	116.86



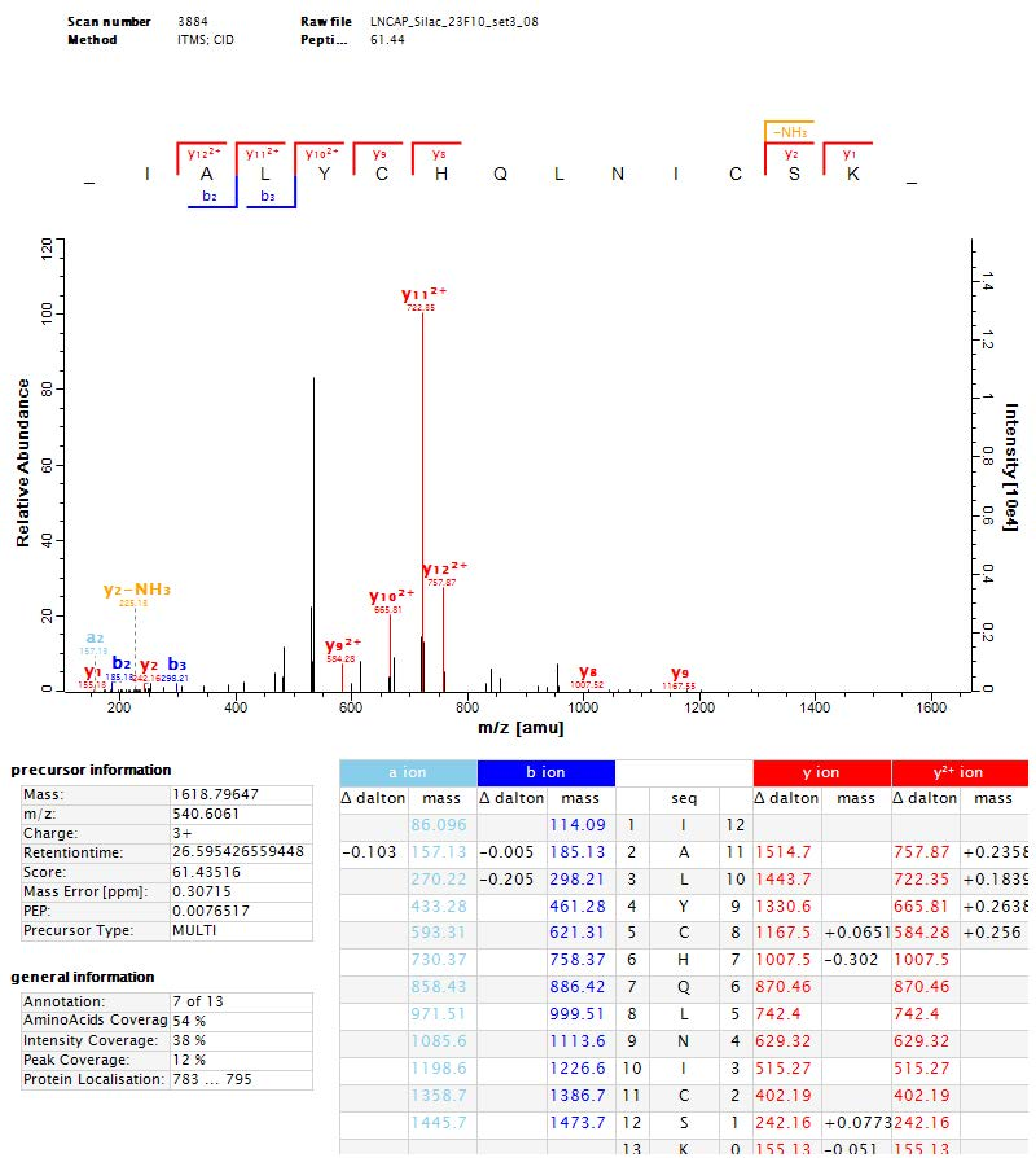
precursor information

Mass:	2133.03804
m/z:	712.01996
Charge:	3+
Retentiontime:	26.416809082031
Score:	116.8621
Mass Error [ppm]:	0.091643
PEP:	5.5071E-09
Precursor Type:	MULTI

general information

Annotation:	16 of 19
AminoAcids Coverag	84 %
Intensity Coverage:	62 %
Peak Coverage:	37 %
Protein Localisation:	93 ... 111

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.07		129.07	1	Q	18				
	292.13		292.13	2	Y	17	2006		1003.5	-0.009
	455.19	+0.1167	455.19	3	Y	16	1842.9		921.97	-0.062
	568.28		568.28	4	I	15	1679.9		840.43	+0.3264
	625.3		625.3	5	G	14	1566.8		783.89	+0.249
	740.32		740.32	6	D	13	1509.8		755.38	+0.349
	853.41		853.41	7	I	12	1394.7		697.87	+0.050
	990.47		990.47	8	H	11	1281.6		641.33	+0.231
	1087.5		1087.5	9	P	10	1144.6	-0.029	572.8	-0.025
	1174.6		1174.6	10	S	9	1047.5	-0.018	1047.5	
-0.191	645.29	-0.272	1289.6	11	D	8	960.5		960.5	
	1402.7		1402.7	12	L	7	845.47	-0.119	423.24	+0.270
	1530.8		1530.8	13	K	6	732.39		366.7	+0.014
	1627.8		1627.8	14	P	5	604.29	-0.017	302.65	+0.343
	1756.9		1756.9	15	E	4	507.24		507.24	
+0.1659	922.45		1843.9	16	S	3	378.2	-0.054	378.2	
	1900.9		1900.9	17	G	2	291.17		291.17	
-0.008	994.47		1987.9	18	S	1	234.14	-0.077	234.14	
				19	K	0	147.11		147.11	



Scan number	3884	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	61.44

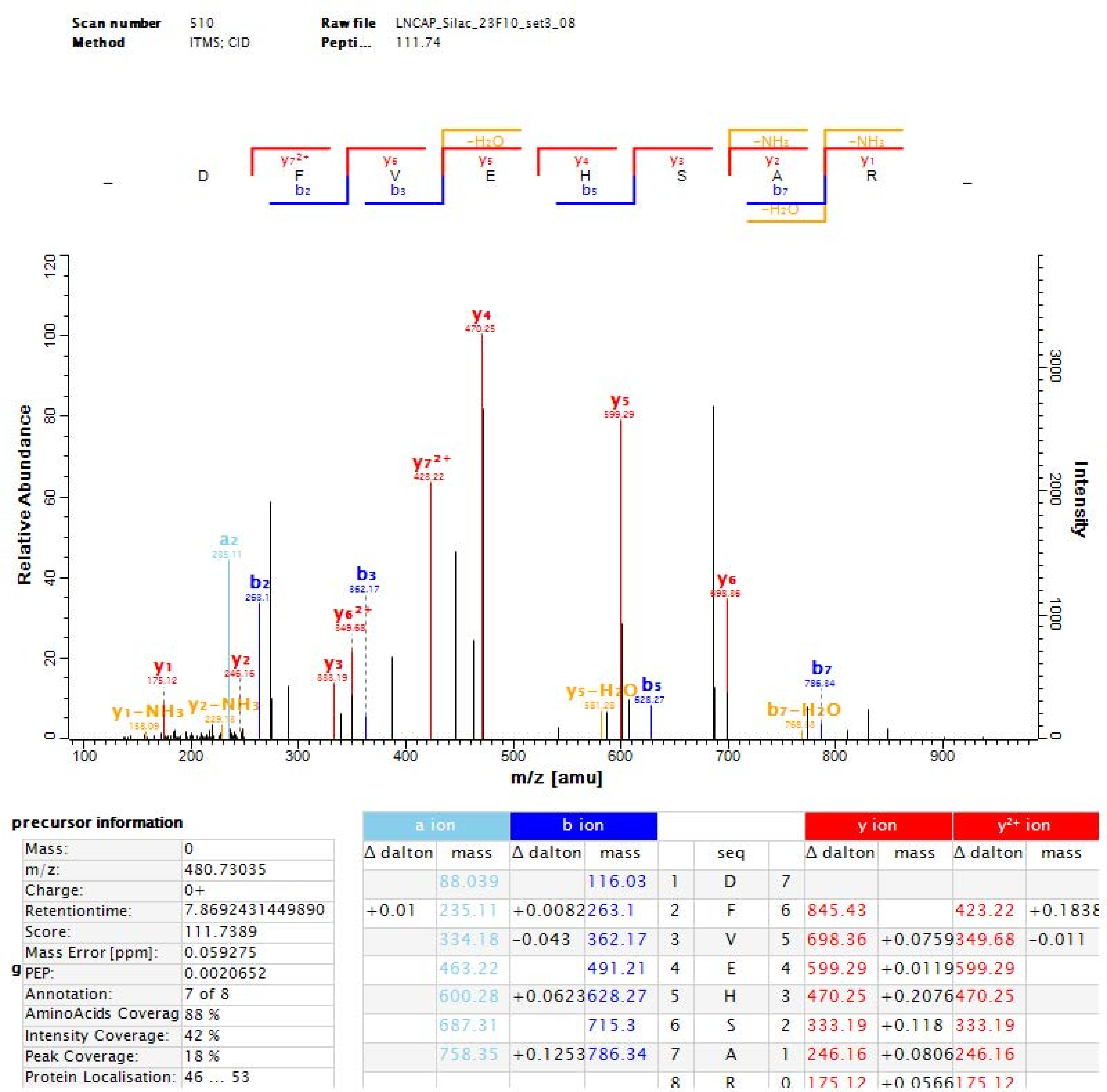
precursor information

Mass:	1618.79647
m/z:	540.6061
Charge:	3+
Retentiontime:	26.595426559448
Score:	61.43516
Mass Error [ppm]:	0.30715
PEP:	0.0076517
Precursor Type:	MULTI

general information

Annotation:	7 of 13
AminoAcids Coverag	54 %
Intensity Coverage:	38 %
Peak Coverage:	12 %
Protein Localisation:	783 ... 795

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	12				
-0.103	157.13	-0.005	185.13	2	A	11	1514.7		757.87	+0.2358
	270.22	-0.205	298.21	3	L	10	1443.7		722.35	+0.1839
	433.28		461.28	4	Y	9	1330.6		665.81	+0.2638
	593.31		621.31	5	C	8	1167.5	+0.0651	584.28	+0.256
	730.37		758.37	6	H	7	1007.5	-0.302	1007.5	
	858.43		886.42	7	Q	6	870.46		870.46	
	971.51		999.51	8	L	5	742.4		742.4	
	1085.6		1113.6	9	N	4	629.32		629.32	
	1198.6		1226.6	10	I	3	515.27		515.27	
	1358.7		1386.7	11	C	2	402.19		402.19	
	1445.7		1473.7	12	S	1	242.16	+0.0773	242.16	
				13	K	0	155.13	-0.051	155.13	

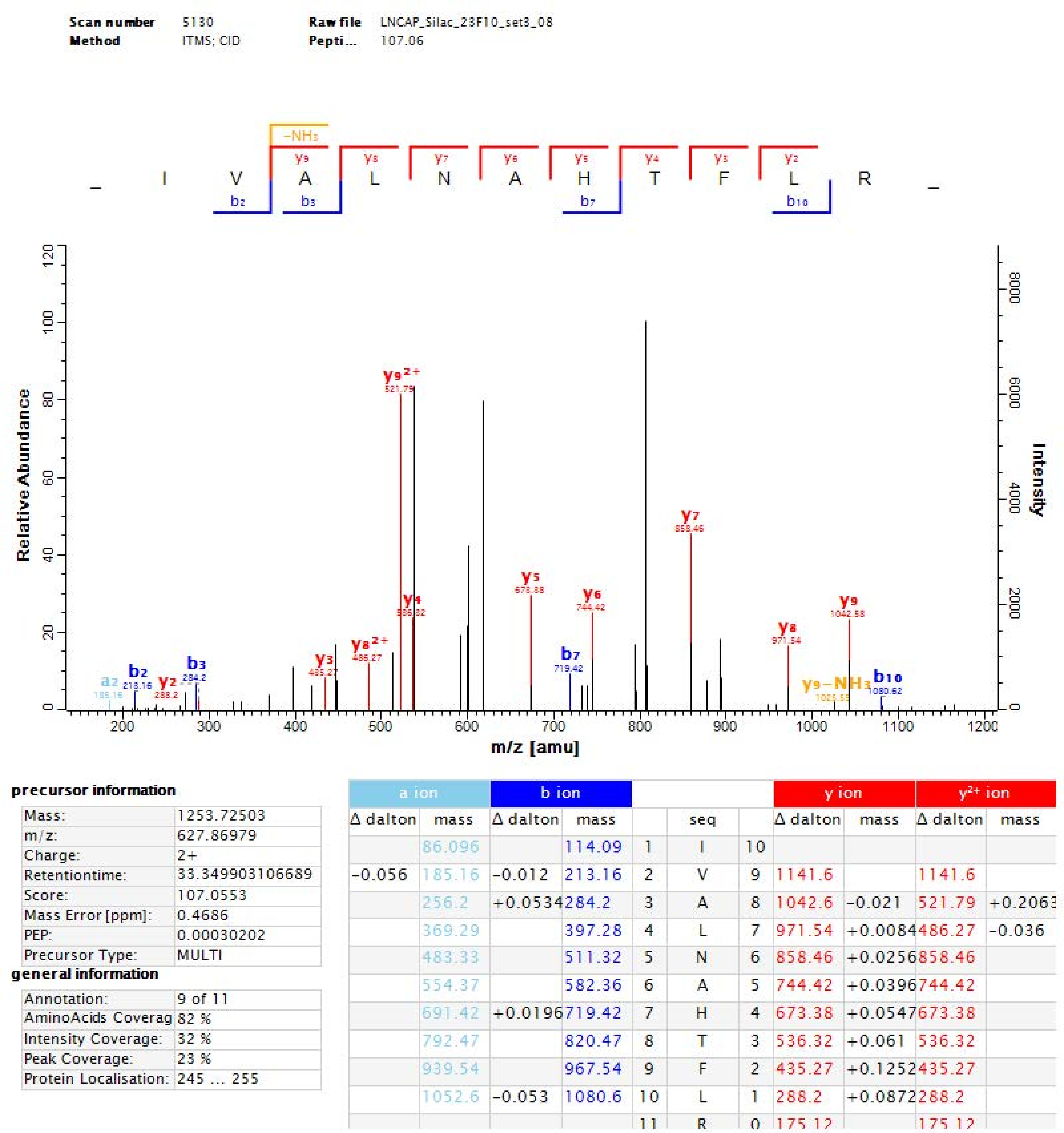


Scan number	510	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	111.74

precursor information

Mass:	0
m/z:	480.73035
Charge:	0+
Retentiontime:	7.8692431449890
Score:	111.7389
Mass Error [ppm]:	0.059275
PEP:	0.0020652
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	42 %
Peak Coverage:	18 %
Protein Localisation:	46 ... 53

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	7				
+0.01	235.11	+0.0082	263.1	2	F	6	845.43		423.22	+0.1838
	334.18	-0.043	362.17	3	V	5	698.36	+0.0759	349.68	-0.011
	463.22		491.21	4	E	4	599.29	+0.0119	599.29	
	600.28	+0.0623	628.27	5	H	3	470.25	+0.2076	470.25	
	687.31		715.3	6	S	2	333.19	+0.118	333.19	
	758.35	+0.1253	786.34	7	A	1	246.16	+0.0806	246.16	
				8	R	0	175.12	+0.0566	175.12	



Scan number	5130	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	107.06

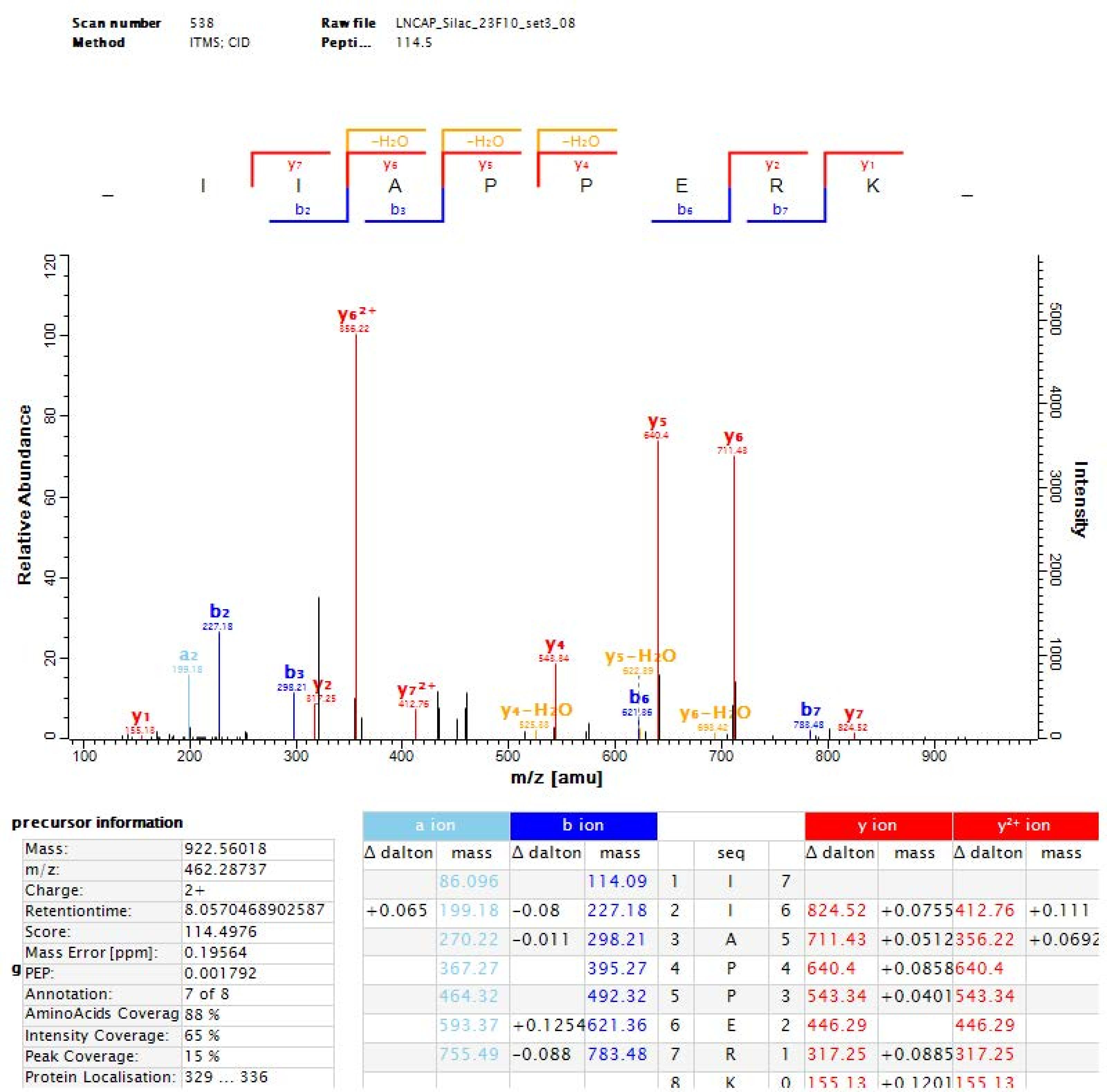
precursor information

Mass:	1253.72503
m/z:	627.86979
Charge:	2+
Retentiontime:	33.349903106689
Score:	107.0553
Mass Error [ppm]:	0.4686
PEP:	0.00030202
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	32 %
Peak Coverage:	23 %
Protein Localisation:	245 ... 255

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	10				
-0.056	185.16	-0.012	213.16	2	V	9	1141.6		1141.6	
	256.2	+0.0534	284.2	3	A	8	1042.6	-0.021	521.79	+0.2063
	369.29		397.28	4	L	7	971.54	+0.0084	486.27	-0.036
	483.33		511.32	5	N	6	858.46	+0.0256	858.46	
	554.37		582.36	6	A	5	744.42	+0.0396	744.42	
	691.42	+0.0196	719.42	7	H	4	673.38	+0.0547	673.38	
	792.47		820.47	8	T	3	536.32	+0.061	536.32	
	939.54		967.54	9	F	2	435.27	+0.1252	435.27	
	1052.6	-0.053	1080.6	10	L	1	288.2	+0.0872	288.2	
				11	R	0	175.12		175.12	

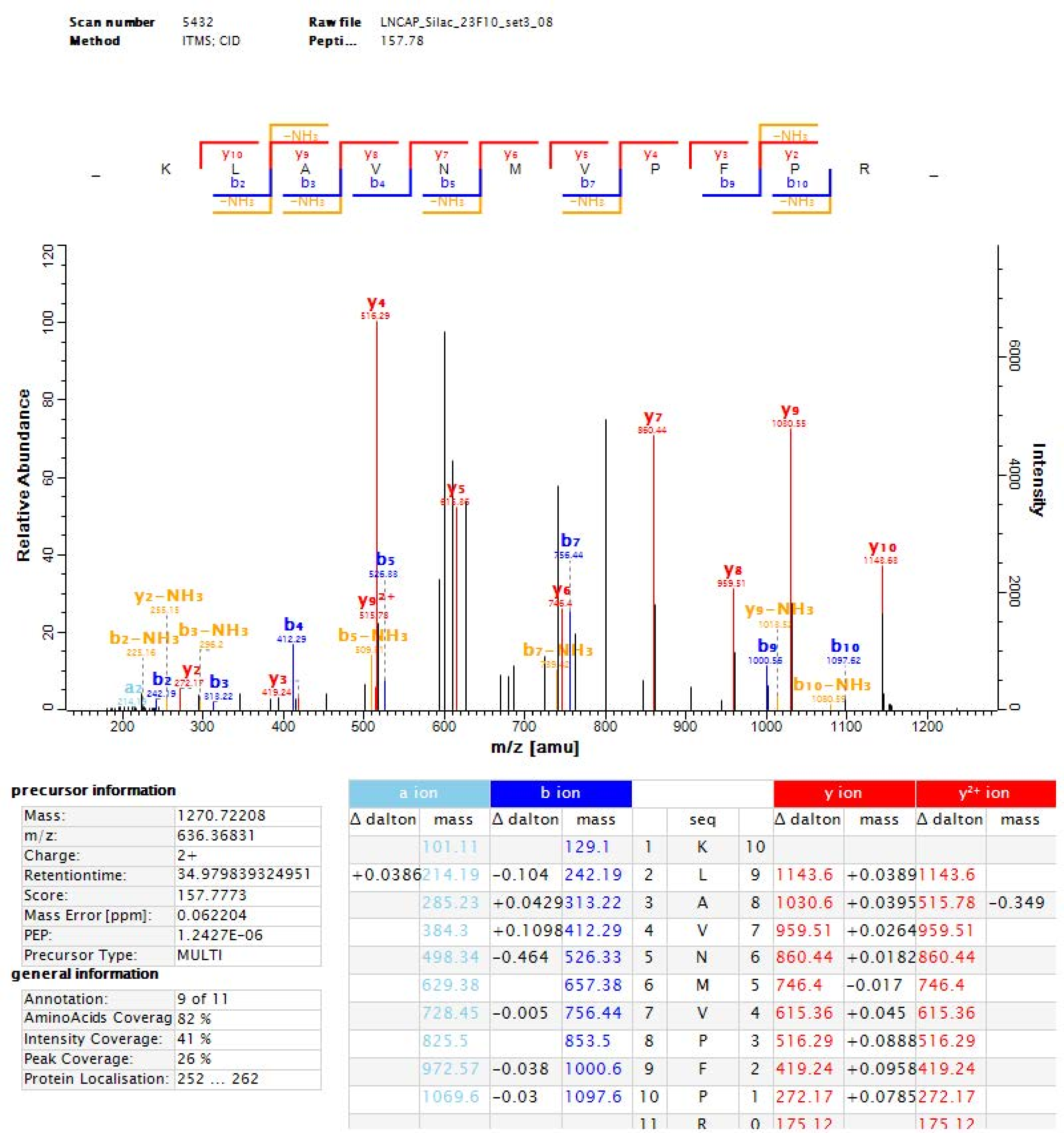


Scan number	538	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	114.5

precursor information

Mass:	922.56018
m/z:	462.28737
Charge:	2+
Retentiontime:	8.0570468902587
Score:	114.4976
Mass Error [ppm]:	0.19564
PEP:	0.001792
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	65 %
Peak Coverage:	15 %
Protein Localisation:	329 ... 336

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	7				
+0.065	199.18	-0.08	227.18	2	I	6	824.52	+0.0755	412.76	+0.111
	270.22	-0.011	298.21	3	A	5	711.43	+0.0512	356.22	+0.0692
	367.27		395.27	4	P	4	640.4	+0.0858	640.4	
	464.32		492.32	5	P	3	543.34	+0.0401	543.34	
	593.37	+0.1254	621.36	6	E	2	446.29		446.29	
	755.49	-0.088	783.48	7	R	1	317.25	+0.0885	317.25	
				8	K	0	155.13	+0.1201	155.13	



Scan number	5432	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	157.78

precursor information

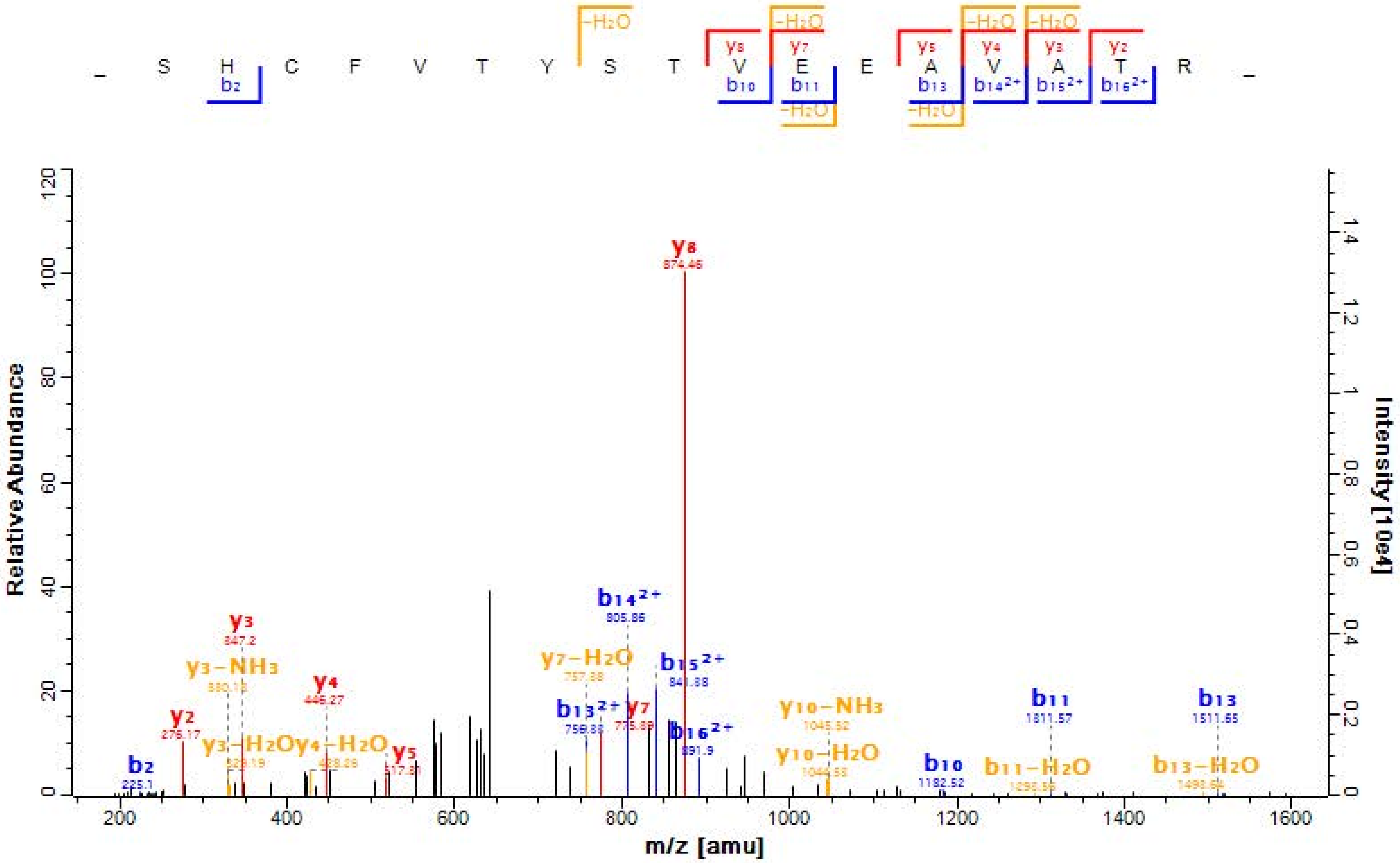
Mass:	1270.72208
m/z:	636.36831
Charge:	2+
Retentiontime:	34.979839324951
Score:	157.7773
Mass Error [ppm]:	0.062204
PEP:	1.2427E-06
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	41 %
Peak Coverage:	26 %
Protein Localisation:	252 ... 262

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	101.11		129.1	1	K	10				
+0.0386	214.19	-0.104	242.19	2	L	9	1143.6	+0.0389	1143.6	
	285.23	+0.0429	313.22	3	A	8	1030.6	+0.0395	515.78	-0.349
	384.3	+0.1098	412.29	4	V	7	959.51	+0.0264	959.51	
	498.34	-0.464	526.33	5	N	6	860.44	+0.0182	860.44	
	629.38		657.38	6	M	5	746.4	-0.017	746.4	
	728.45	-0.005	756.44	7	V	4	615.36	+0.045	615.36	
	825.5		853.5	8	P	3	516.29	+0.0888	516.29	
	972.57	-0.038	1000.6	9	F	2	419.24	+0.0958	419.24	
	1069.6	-0.03	1097.6	10	P	1	272.17	+0.0785	272.17	
				11	R	0	175.12		175.12	

Scan number	5524	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	98.68



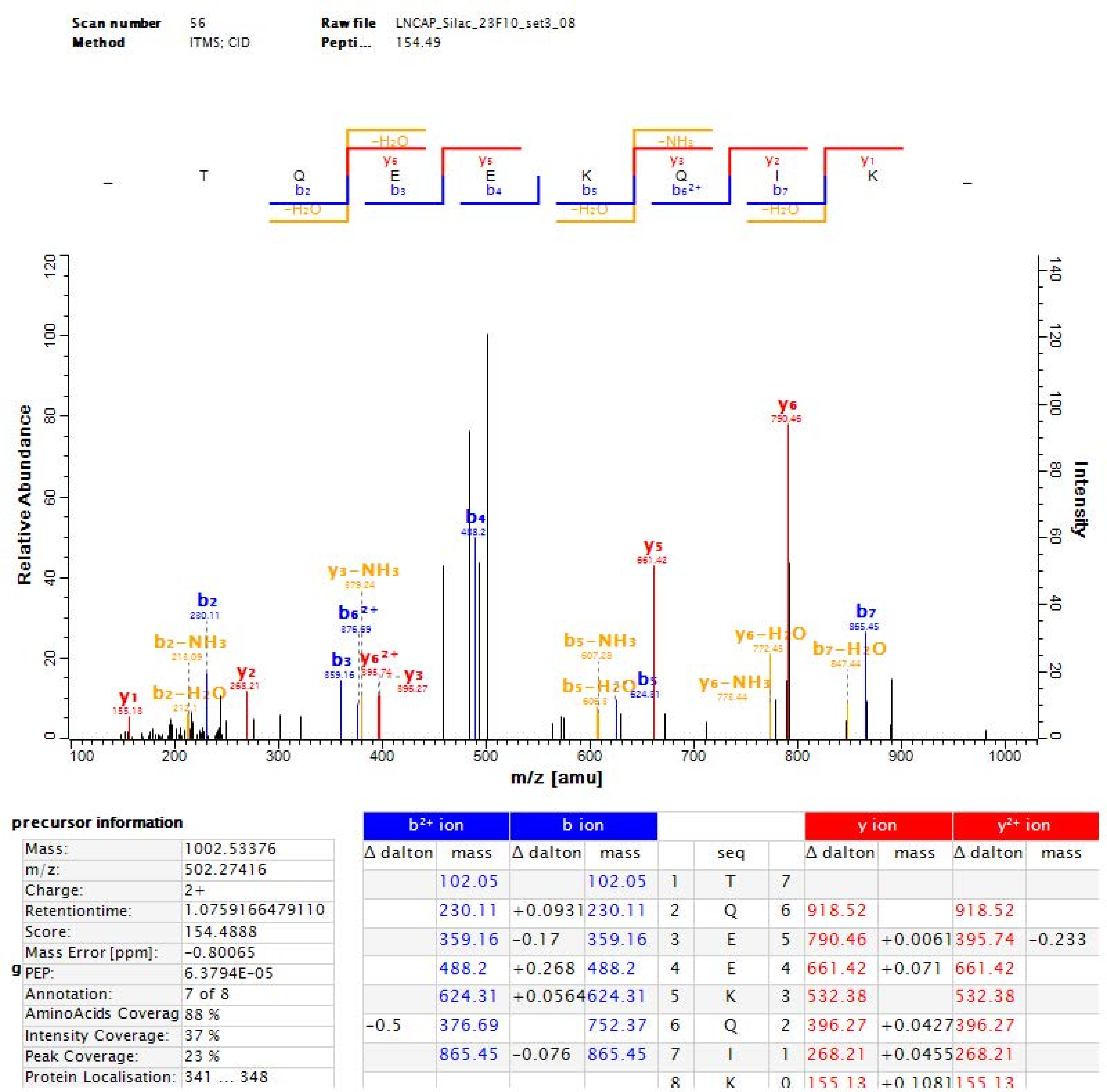
precursor information

Mass:	1955.90571
m/z:	652.97585
Charge:	3+
Retentiontime:	35.472053527832
Score:	98.67624
Mass Error [ppm]:	0.50153
PEP:	3.4734E-06
Precursor Type:	MULTI

general information

Annotation:	8 of 17
AminoAcids Coverag	47 %
Intensity Coverage:	46 %
Peak Coverage:	21 %
Protein Localisation:	954 ... 970

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	88.0393		88.0393	1	S	16		
	225.0982	+0.178593	225.0982	2	H	15	1869.88	
	385.1289		385.1289	3	C	14	1732.821	
	532.1973		532.1973	4	F	13	1572.79	
	631.2657		631.2657	5	V	12	1425.722	
	732.3134		732.3134	6	T	11	1326.654	
	895.3767		895.3767	7	Y	10	1225.606	
	982.4087		982.4087	8	S	9	1062.543	
	1083.456		1083.456	9	T	8	975.5106	
	1182.525	+0.131185	1182.525	10	V	7	874.4629	-0.0562
	1311.567	+0.231292	1311.567	11	E	6	775.3945	-0.01818
	1440.61		1440.61	12	E	5	646.3519	
+0.16444	756.3272	-0.13797	1511.647	13	A	4	517.3093	-0.04108
+0.237044	805.8614		1610.716	14	V	3	446.2722	+0.146238
+0.276898	841.38		1681.753	15	A	2	347.2037	+0.1043
+0.259101	891.9038		1782.8	16	T	1	276.1666	+0.013972
				17	R	0	175.119	



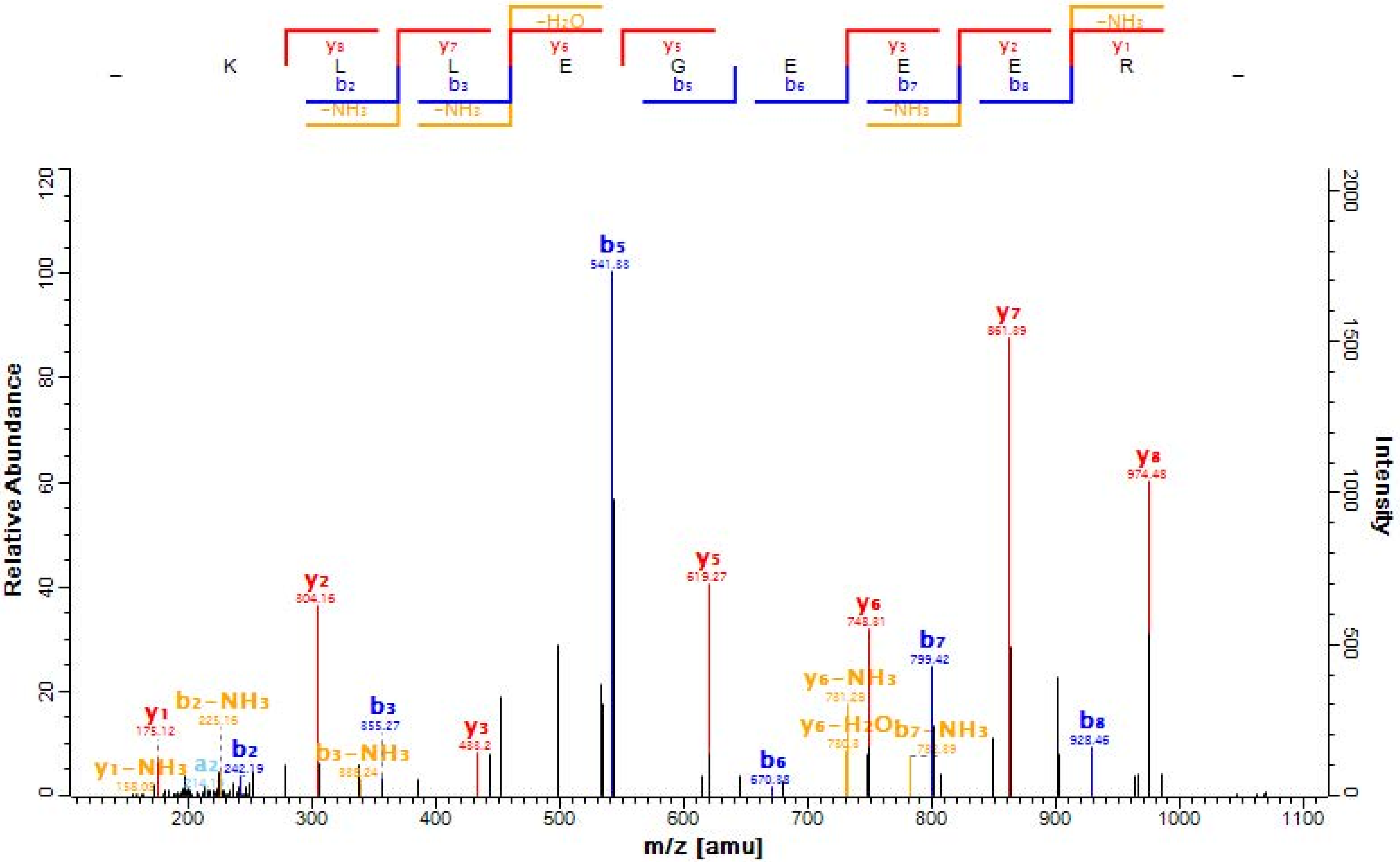
Scan number	56	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	154.49

precursor information

Mass:	1002.53376
m/z:	502.27416
Charge:	2+
Retentiontime:	1.0759166479110
Score:	154.4888
Mass Error [ppm]:	-0.80065
PEP:	6.3794E-05
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	37 %
Peak Coverage:	23 %
Protein Localisation:	341 ... 348

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	7				
	230.11	+0.0931	230.11	2	Q	6	918.52		918.52	
	359.16	-0.17	359.16	3	E	5	790.46	+0.0061	395.74	-0.233
	488.2	+0.268	488.2	4	E	4	661.42	+0.071	661.42	
	624.31	+0.0564	624.31	5	K	3	532.38		532.38	
-0.5	376.69		752.37	6	Q	2	396.27	+0.0427	396.27	
	865.45	-0.076	865.45	7	I	1	268.21	+0.0455	268.21	
				8	K	0	155.13	+0.1081	155.13	

Scan number	605	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	104.43

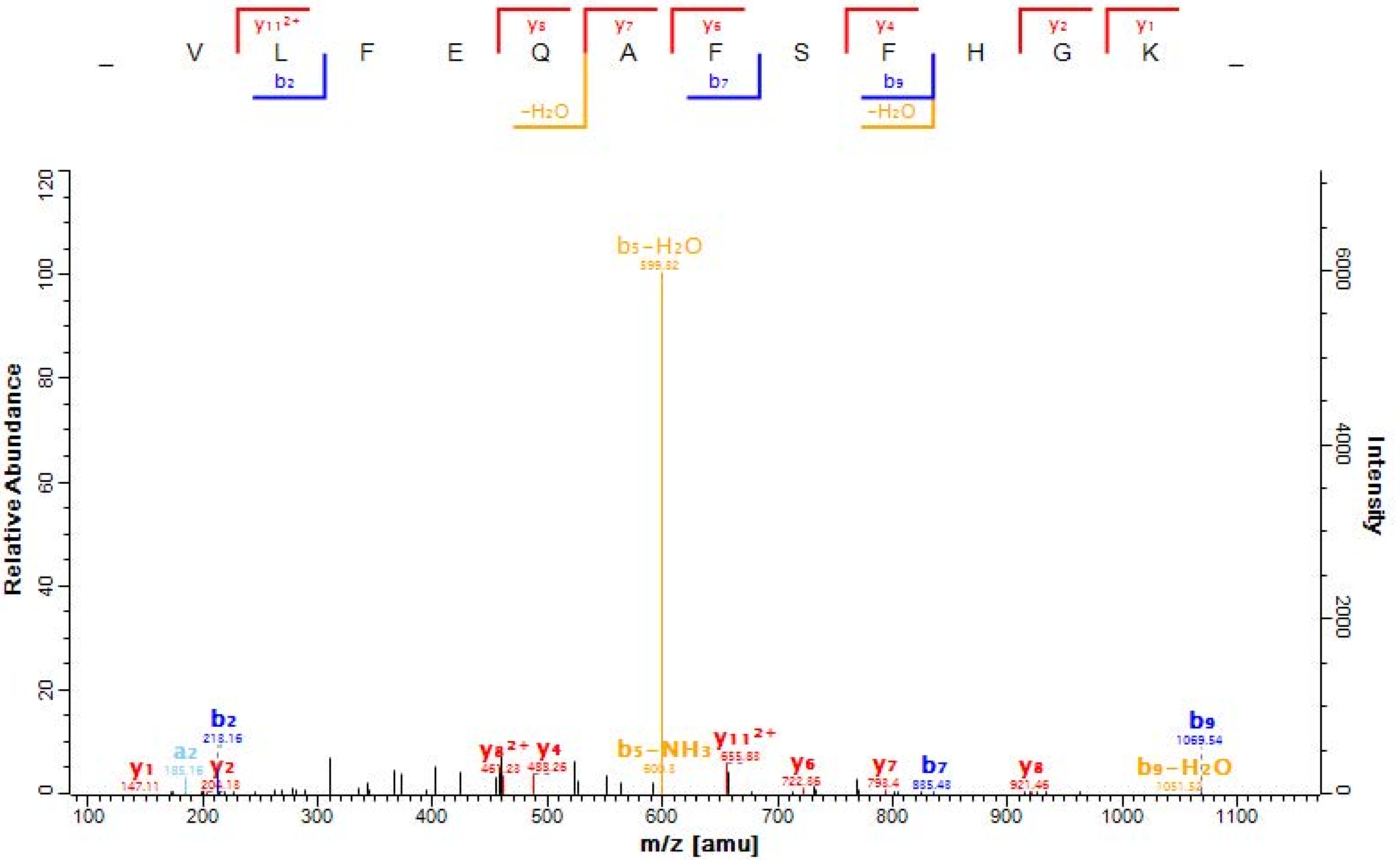


precursor information

Mass:	1101.5669
m/z:	551.79073
Charge:	2+
Retentiontime:	8.4634513854980
Score:	104.434
Mass Error [ppm]:	0.27011
PEP:	0.0042484
Precursor Type:	ISO
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	51 %
Peak Coverage:	17 %
Protein Localisation:	378 ... 386

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	101.1073		129.1022	1	K	8		
-0.22856	214.1914	-0.06793	242.1863	2	L	7	974.4789	-0.02976
	327.2755	+0.092487	355.2704	3	L	6	861.3949	+0.000106
	456.318		484.313	4	E	5	748.3108	+0.07294
	513.3395	+0.249133	541.3344	5	G	4	619.2682	+0.041192
	642.3821	+0.117184	670.377	6	E	3	562.2467	
	771.4247	-0.02978	799.4196	7	E	2	433.2041	+0.095239
	900.4673	+0.032669	928.4622	8	E	1	304.1615	+0.024978
				9	R	0	175.119	+0.034917

Scan number	6637	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	56.09



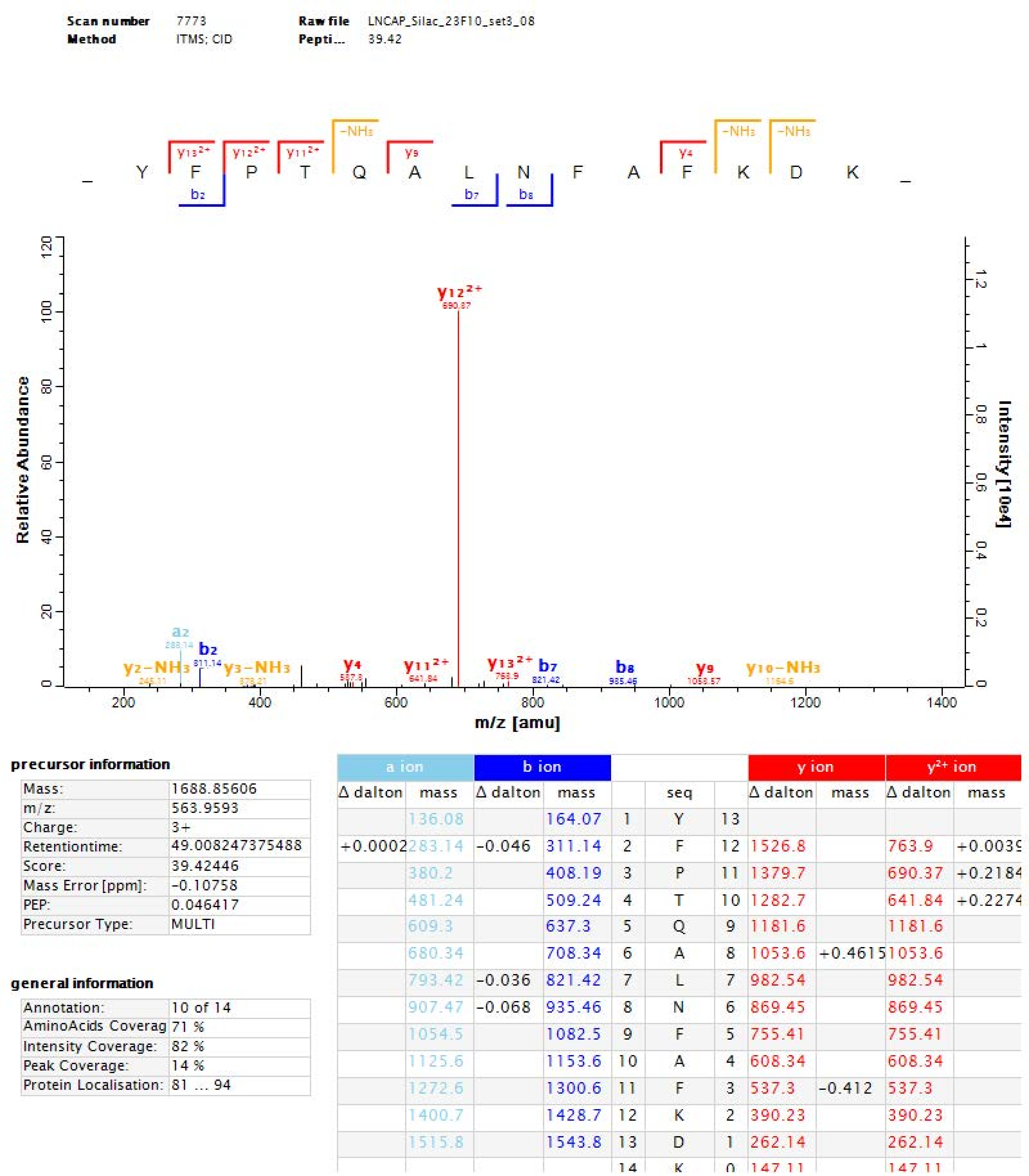
precursor information

Mass:	1408.71365
m/z:	470.57849
Charge:	3+
Retentiontime:	41.769187927246
Score:	56.08672
Mass Error [ppm]:	-0.20207
PEP:	0.014105
Precursor Type:	MULTI

general information

Annotation:	8 of 12
AminoAcids Coverag	67 %
Intensity Coverage:	60 %
Peak Coverage:	16 %
Protein Localisation:	198 ... 209

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.081		100.08	1	V	11				
+0.0388	185.16	+0.0126	213.16	2	L	10	1310.7		655.83	+0.0296
	332.23		360.23	3	F	9	1197.6		1197.6	
	461.28		489.27	4	E	8	1050.5		1050.5	
	589.33		617.33	5	Q	7	921.46	+0.0891	461.23	-0.206
	660.37		688.37	6	A	6	793.4	-0.003	793.4	
	807.44	+0.0521	835.43	7	F	5	722.36	-0.049	722.36	
	894.47		922.47	8	S	4	575.29		575.29	
	1041.5	-0.065	1069.5	9	F	3	488.26	+0.0204	488.26	
	1178.6		1206.6	10	H	2	341.19		341.19	
	1235.6		1263.6	11	G	1	204.13	-0.109	204.13	
				12	K	0	147.11	+0.0289	147.11	



Scan number 7773
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set3_08
Pepti... 39.42

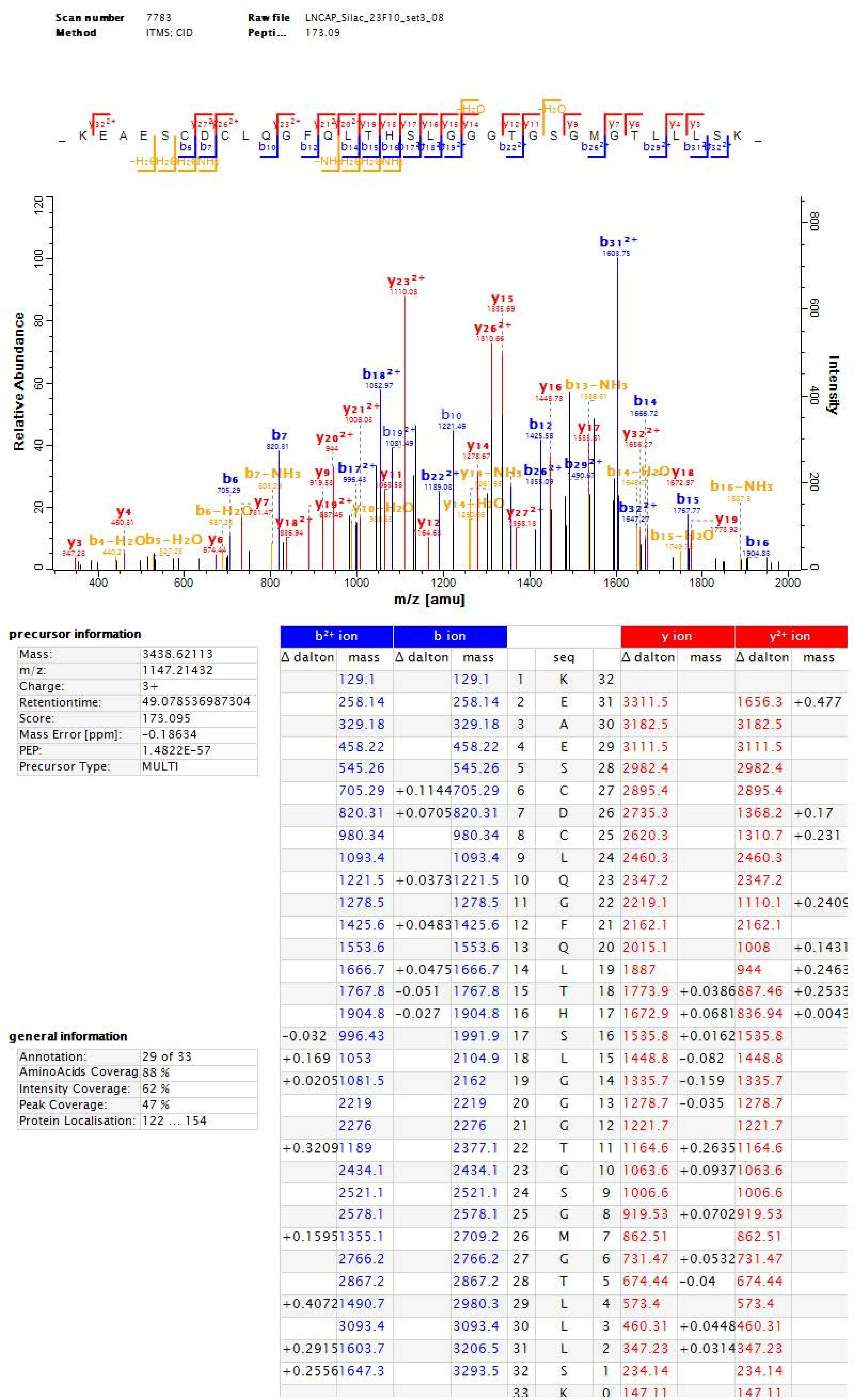
precursor information

Mass:	1688.85606
m/z:	563.9593
Charge:	3+
Retentiontime:	49.008247375488
Score:	39.42446
Mass Error [ppm]:	-0.10758
PEP:	0.046417
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	82 %
Peak Coverage:	14 %
Protein Localisation:	81 ... 94

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.08		164.07	1	Y	13				
+0.0002	283.14	-0.046	311.14	2	F	12	1526.8		763.9	+0.0039
	380.2		408.19	3	P	11	1379.7		690.37	+0.2184
	481.24		509.24	4	T	10	1282.7		641.84	+0.2274
	609.3		637.3	5	Q	9	1181.6		1181.6	
	680.34		708.34	6	A	8	1053.6	+0.4615	1053.6	
	793.42	-0.036	821.42	7	L	7	982.54		982.54	
	907.47	-0.068	935.46	8	N	6	869.45		869.45	
	1054.5		1082.5	9	F	5	755.41		755.41	
	1125.6		1153.6	10	A	4	608.34		608.34	
	1272.6		1300.6	11	F	3	537.3	-0.412	537.3	
	1400.7		1428.7	12	K	2	390.23		390.23	
	1515.8		1543.8	13	D	1	262.14		262.14	
				14	K	0	147.11		147.11	



Scan number	7783	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	173.09

precursor information

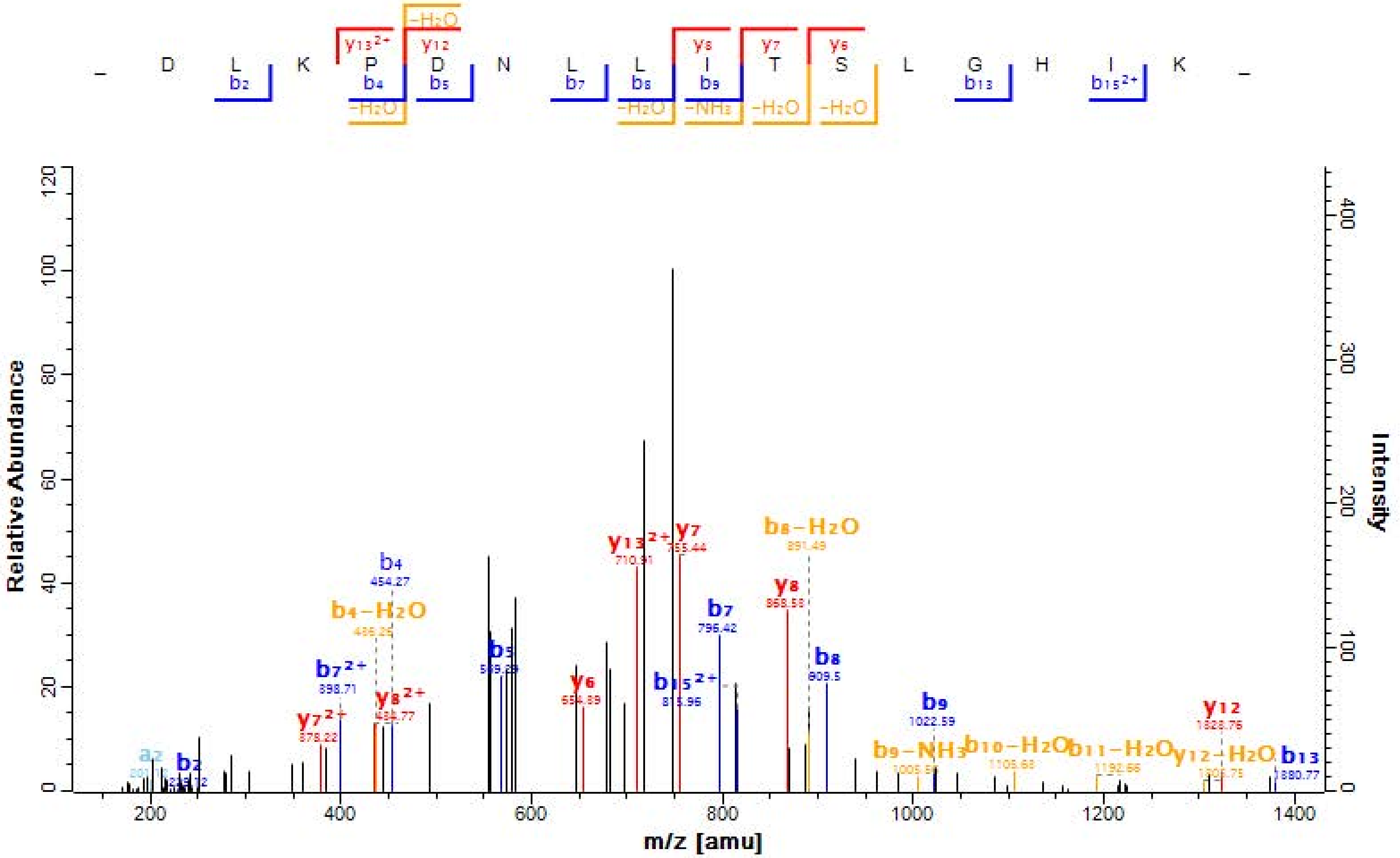
Mass:	3438.62113
m/z:	1147.21432
Charge:	3+
Retentiontime:	49.078536987304
Score:	173.095
Mass Error [ppm]:	-0.18634
PEP:	1.4822E-57
Precursor Type:	MULTI

general information

Annotation:	29 of 33
AminoAcids Coverag	88 %
Intensity Coverage:	62 %
Peak Coverage:	47 %
Protein Localisation:	122 ... 154

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.1		129.1	1	K	32				
	258.14		258.14	2	E	31	3311.5		1656.3	+0.477
	329.18		329.18	3	A	30	3182.5		3182.5	
	458.22		458.22	4	E	29	3111.5		3111.5	
	545.26		545.26	5	S	28	2982.4		2982.4	
	705.29	+0.1144	705.29	6	C	27	2895.4		2895.4	
	820.31	+0.0705	820.31	7	D	26	2735.3		1368.2	+0.17
	980.34		980.34	8	C	25	2620.3		1310.7	+0.231
	1093.4		1093.4	9	L	24	2460.3		2460.3	
	1221.5	+0.0373	1221.5	10	Q	23	2347.2		2347.2	
	1278.5		1278.5	11	G	22	2219.1		1110.1	+0.2409
	1425.6	+0.0483	1425.6	12	F	21	2162.1		2162.1	
	1553.6		1553.6	13	Q	20	2015.1		1008	+0.1431
	1666.7	+0.0475	1666.7	14	L	19	1887		944	+0.2463
	1767.8	-0.051	1767.8	15	T	18	1773.9	+0.0386	887.46	+0.2533
	1904.8	-0.027	1904.8	16	H	17	1672.9	+0.0681	836.94	+0.0043
-0.032	996.43		1991.9	17	S	16	1535.8	+0.0162	1535.8	
+0.169	1053		2104.9	18	L	15	1448.8	-0.082	1448.8	
+0.0205	1081.5		2162	19	G	14	1335.7	-0.159	1335.7	
	2219		2219	20	G	13	1278.7	-0.035	1278.7	
	2276		2276	21	G	12	1221.7		1221.7	
+0.3209	1189		2377.1	22	T	11	1164.6	+0.2635	1164.6	
	2434.1		2434.1	23	G	10	1063.6	+0.0937	1063.6	
	2521.1		2521.1	24	S	9	1006.6		1006.6	
	2578.1		2578.1	25	G	8	919.53	+0.0702	919.53	
+0.1595	1355.1		2709.2	26	M	7	862.51		862.51	
	2766.2		2766.2	27	G	6	731.47	+0.0532	731.47	
	2867.2		2867.2	28	T	5	674.44	-0.04	674.44	
+0.4072	1490.7		2980.3	29	L	4	573.4		573.4	
	3093.4		3093.4	30	L	3	460.31	+0.0448	460.31	
+0.2915	1603.7		3206.5	31	L	2	347.23	+0.0314	347.23	
+0.2556	1647.3		3293.5	32	S	1	234.14		234.14	
				33	K	0	147.11		147.11	

Scan number	7838	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	72.8



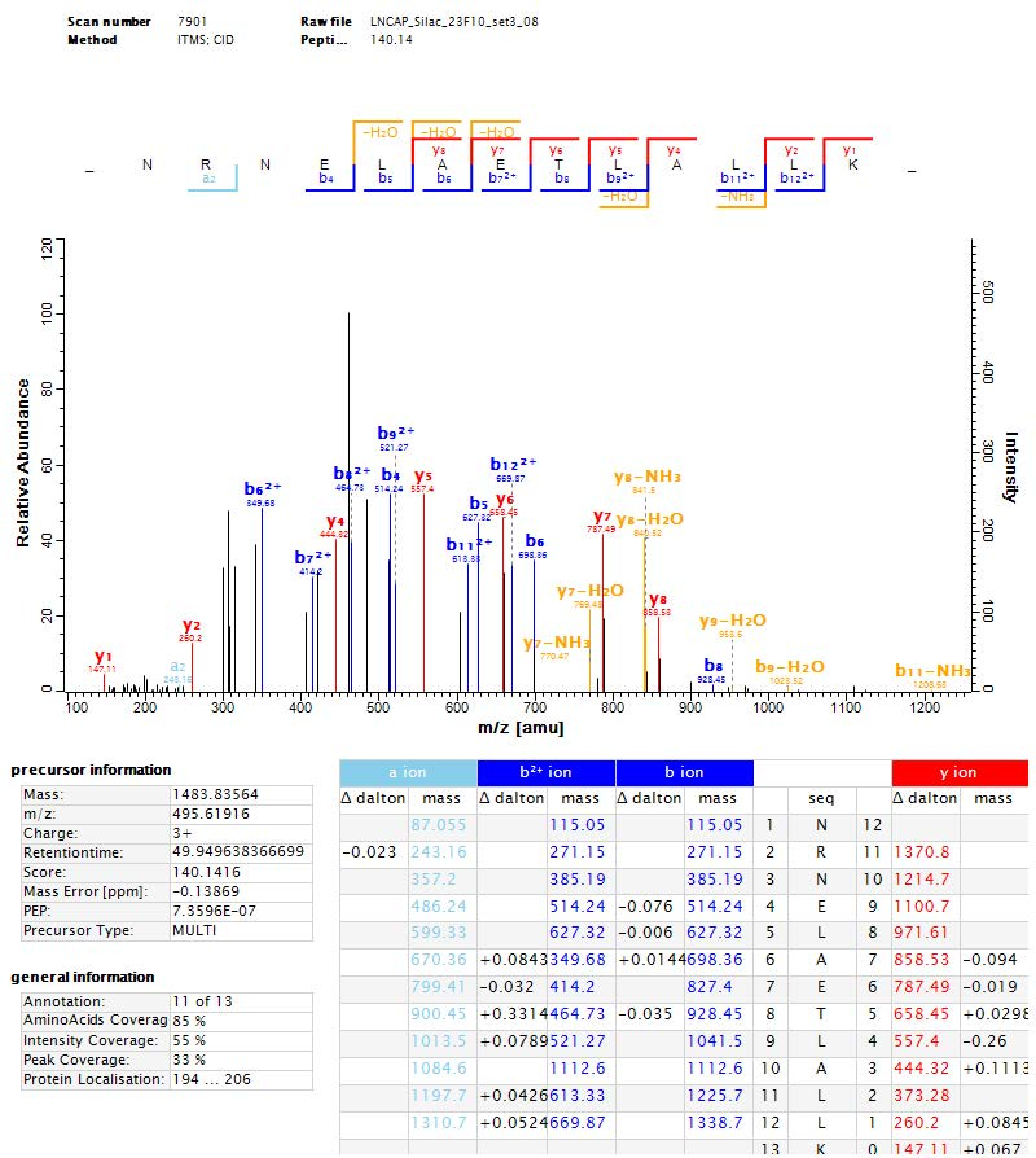
precursor information

Mass:	1776.01523
m/z:	593.01235
Charge:	3+
Retentiontime:	49.462863922119
Score:	72.79709
Mass Error [ppm]:	0.39179
PEP:	0.00032345
Precursor Type:	MULTI

general information

Annotation:	11 of 16
AminoAcids Coverag	69 %
Intensity Coverage:	33 %
Peak Coverage:	25 %
Protein Localisation:	490 ... 505

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.04		116		116	1	D	15				
+0.134	201.1		229.1	-0.46	229.1	2	L	14	1662		1662	
	329.2		357.2		357.2	3	K	13	1549		1549	
	426.3		454.3	-0.01	454.3	4	P	12	1421		710.9	+0.14
	541.3		569.3	-0.33	569.3	5	D	11	1324	+0.206	1324	
	655.3		683.3		683.3	6	N	10	1209		1209	
	768.4	+0.257	398.7	-0.08	796.4	7	L	9	1095		1095	
	881.5		909.5	+0.01	909.5	8	L	8	981.6		981.6	
	994.6		1023	-0.09	1023	9	I	7	868.5	+0.004	434.8	+0.06
	1096		1124		1124	10	T	6	755.4	+0.192	378.2	+0.23
	1183		1211		1211	11	S	5	654.4	+0.041	654.4	
	1296		1324		1324	12	L	4	567.4		567.4	
	1353		1381	+0.15	1381	13	G	3	454.3		454.3	
	1490		1518		1518	14	H	2	397.3		397.3	
	1603	+0.258	816		1631	15	I	1	260.2		260.2	
						16	K	0	147.1		147.1	



Scan number	7901	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	140.14

precursor information

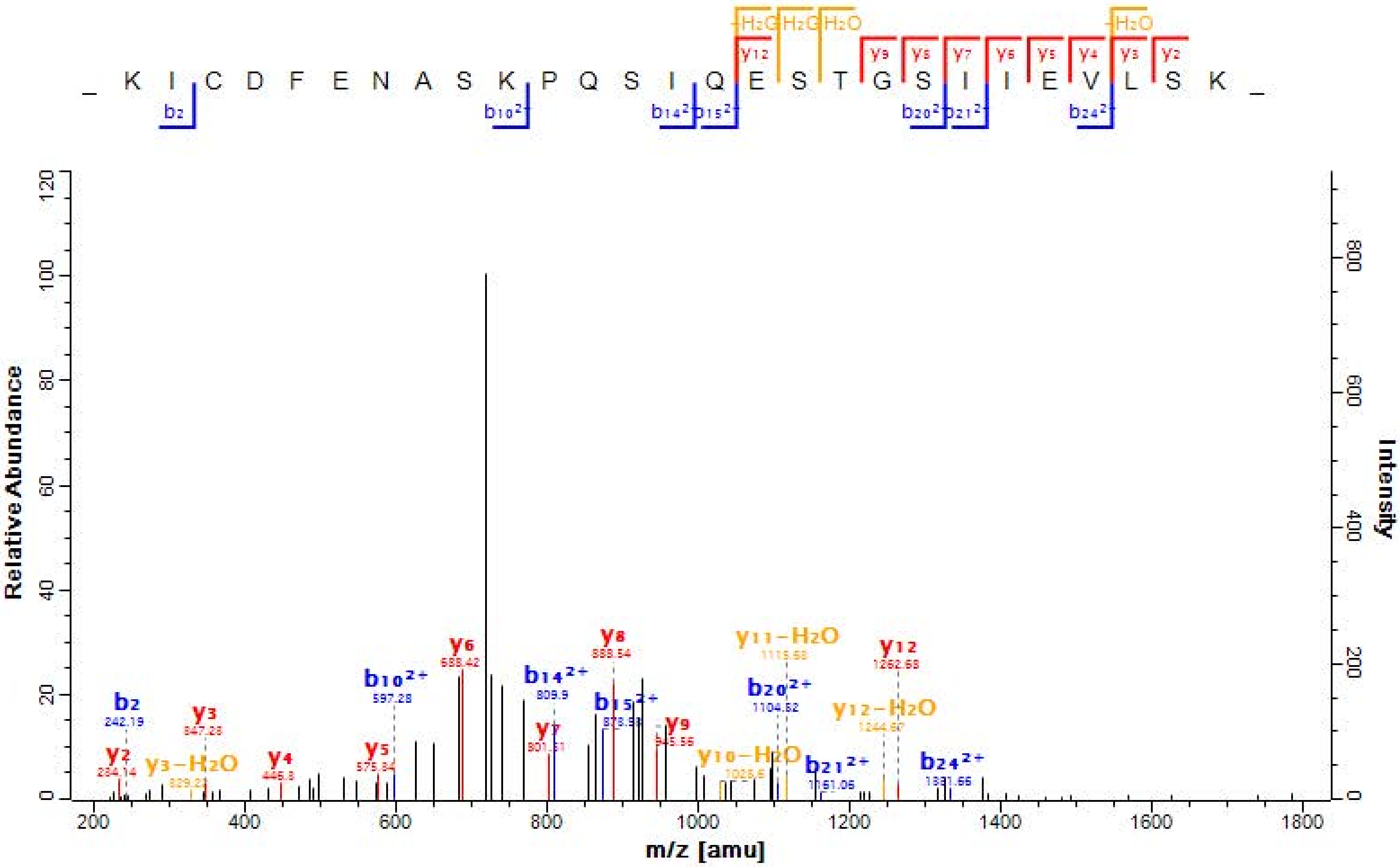
Mass:	1483.83564
m/z:	495.61916
Charge:	3+
Retentiontime:	49.949638366699
Score:	140.1416
Mass Error [ppm]:	-0.13869
PEP:	7.3596E-07
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	55 %
Peak Coverage:	33 %
Protein Localisation:	194 ... 206

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	87.055		115.05		115.05	1	N	12		
-0.023	243.16		271.15		271.15	2	R	11	1370.8	
	357.2		385.19		385.19	3	N	10	1214.7	
	486.24		514.24	-0.076	514.24	4	E	9	1100.7	
	599.33		627.32	-0.006	627.32	5	L	8	971.61	
	670.36	+0.0843	349.68	+0.0144	698.36	6	A	7	858.53	-0.094
	799.41	-0.032	414.2		827.4	7	E	6	787.49	-0.019
	900.45	+0.3314	464.73	-0.035	928.45	8	T	5	658.45	+0.0298
	1013.5	+0.0789	521.27		1041.5	9	L	4	557.4	-0.26
	1084.6		1112.6		1112.6	10	A	3	444.32	+0.1113
	1197.7	+0.0426	613.33		1225.7	11	L	2	373.28	
	1310.7	+0.0524	669.87		1338.7	12	L	1	260.2	+0.0845
						13	K	0	147.11	+0.067

Scan number	8003	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	44.3



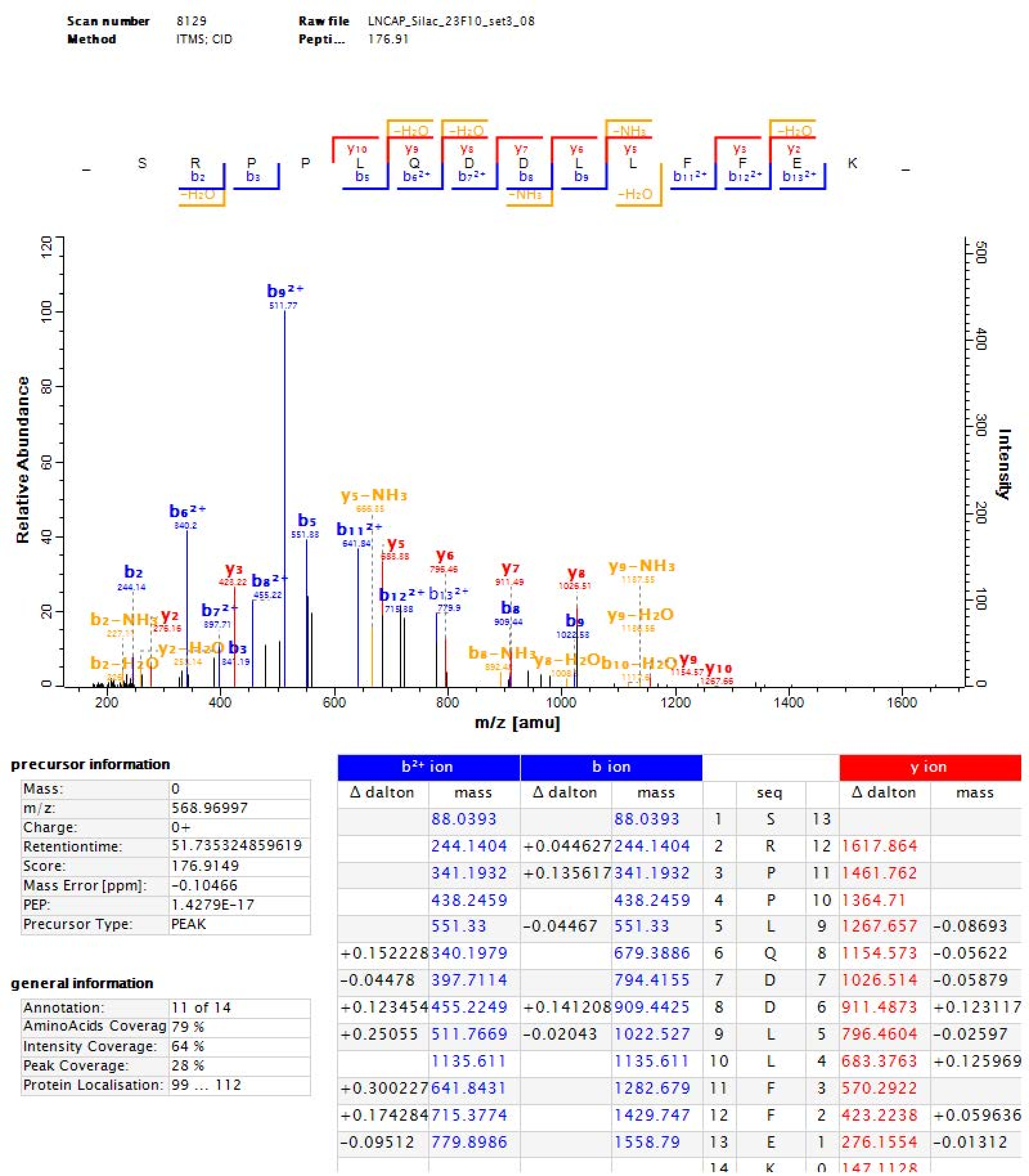
precursor information

Mass:	3007.51589
m/z:	752.88625
Charge:	4+
Retentiontime:	50.728397369384
Score:	44.30027
Mass Error [ppm]:	-0.44125
PEP:	0.0046183
Precursor Type:	MULTI

general information

Annotation:	15 of 27
AminoAcids Coverag	56 %
Intensity Coverage:	23 %
Peak Coverage:	24 %
Protein Localisation:	275 ... 301

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	129.1022		129.1022	1	K	26		
	242.1863	+0.302924	242.1863	2	I	25	2880.43	
	402.217		402.217	3	C	24	2767.345	
	517.2439		517.2439	4	D	23	2607.315	
	664.3123		664.3123	5	F	22	2492.288	
	793.3549		793.3549	6	E	21	2345.219	
	907.3978		907.3978	7	N	20	2216.177	
	978.4349		978.4349	8	A	19	2102.134	
	1065.467		1065.467	9	S	18	2031.097	
+0.338136	597.2846		1193.562	10	K	17	1944.065	
	1290.615		1290.615	11	P	16	1815.97	
	1418.673		1418.673	12	Q	15	1718.917	
	1505.705		1505.705	13	S	14	1590.858	
+0.054375	809.8983		1618.789	14	I	13	1503.826	
+0.240541	873.9276		1746.848	15	Q	12	1390.742	
	1875.891		1875.891	16	E	11	1262.684	-0.3015
	1962.923		1962.923	17	S	10	1133.641	
	2063.97		2063.97	18	T	9	1046.609	
	2120.992		2120.992	19	G	8	945.5615	-0.08105
+0.261715	1104.516		2208.024	20	S	7	888.5401	-0.24001
-0.36198	1161.058		2321.108	21	I	6	801.508	+0.29867
	2434.192		2434.192	22	I	5	688.424	+0.018965
	2563.234		2563.234	23	E	4	575.3399	-0.05347
-0.09343	1331.655		2662.303	24	V	3	446.2973	+0.077873
	2775.387		2775.387	25	L	2	347.2289	-0.01579
	2862.419		2862.419	26	S	1	234.1448	-0.06532
				27	K	0	147.1128	



Scan number	8129	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti…**	176.91

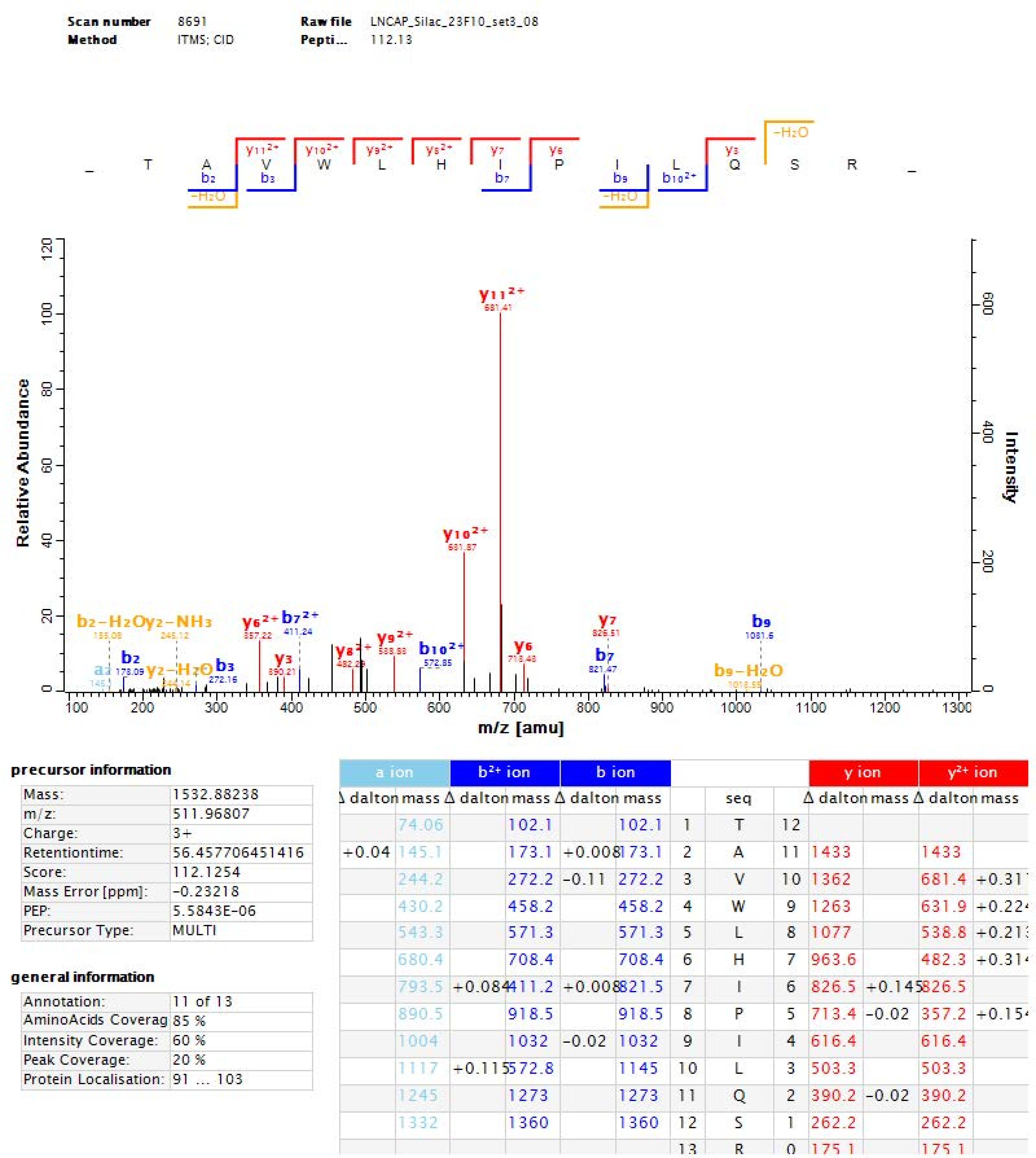
precursor information

Mass:	0
m/z:	568.96997
Charge:	0+
Retentiontime:	51.735324859619
Score:	176.9149
Mass Error [ppm]:	-0.10466
PEP:	1.4279E-17
Precursor Type:	PEAK

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	64 %
Peak Coverage:	28 %
Protein Localisation:	99 … 112

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	88.0393		88.0393	1	S	13		
	244.1404	+0.044627	244.1404	2	R	12	1617.864	
	341.1932	+0.135617	341.1932	3	P	11	1461.762	
	438.2459		438.2459	4	P	10	1364.71	
	551.33	-0.04467	551.33	5	L	9	1267.657	-0.08693
+0.152228	340.1979		679.3886	6	Q	8	1154.573	-0.05622
-0.04478	397.7114		794.4155	7	D	7	1026.514	-0.05879
+0.123454	455.2249	+0.141208	909.4425	8	D	6	911.4873	+0.123117
+0.25055	511.7669	-0.02043	1022.527	9	L	5	796.4604	-0.02597
	1135.611		1135.611	10	L	4	683.3763	+0.125969
+0.300227	641.8431		1282.679	11	F	3	570.2922	
+0.174284	715.3774		1429.747	12	F	2	423.2238	+0.059636
-0.09512	779.8986		1558.79	13	E	1	276.1554	-0.01312
				14	K	0	147.1128	



Scan number	8691
Method	ITMS; CID
Raw file	LNCAP_Silac_23F10_set3_08
Pepti...	112.13

precursor information

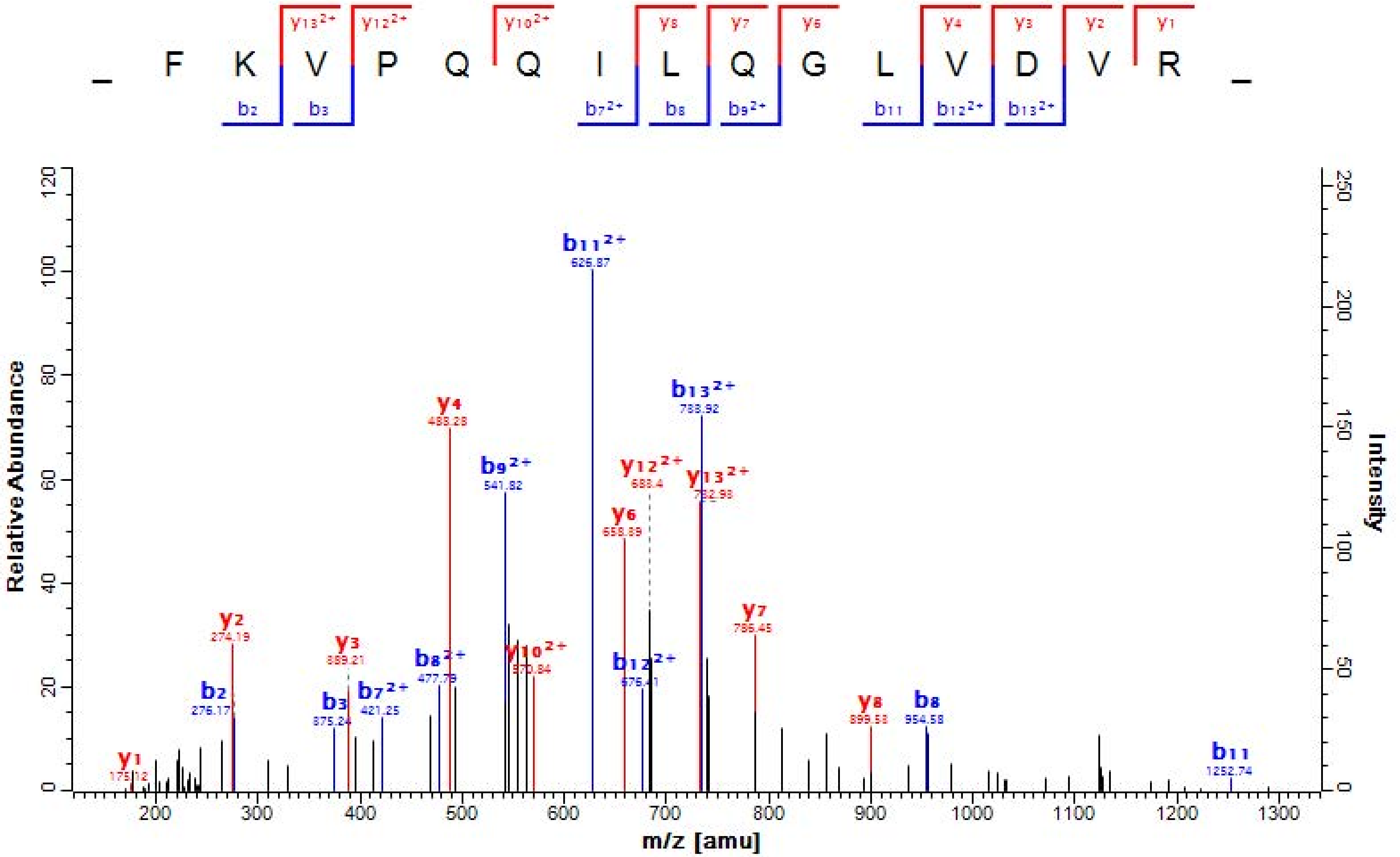
Mass:	1532.88238
m/z:	511.96807
Charge:	3+
Retentiontime:	56.457706451416
Score:	112.1254
Mass Error [ppm]:	-0.23218
PEP:	5.5843E-06
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	60 %
Peak Coverage:	20 %
Protein Localisation:	91 ... 103

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.1		102.1	1	T	12				
+0.04	145.1		173.1	+0.008	173.1	2	A	11	1433		1433	
	244.2		272.2	-0.11	272.2	3	V	10	1362		681.4	+0.31
	430.2		458.2		458.2	4	W	9	1263		631.9	+0.22
	543.3		571.3		571.3	5	L	8	1077		538.8	+0.21
	680.4		708.4		708.4	6	H	7	963.6		482.3	+0.31
	793.5	+0.084	411.2	+0.008	821.5	7	I	6	826.5	+0.145	826.5	
	890.5		918.5		918.5	8	P	5	713.4	-0.02	357.2	+0.15
	1004		1032	-0.02	1032	9	I	4	616.4		616.4	
	1117	+0.115	572.8		1145	10	L	3	503.3		503.3	
	1245		1273		1273	11	Q	2	390.2	-0.02	390.2	
	1332		1360		1360	12	S	1	262.2		262.2	
						13	R	0	175.1		175.1	

Scan number	8695	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	107.14



precursor information

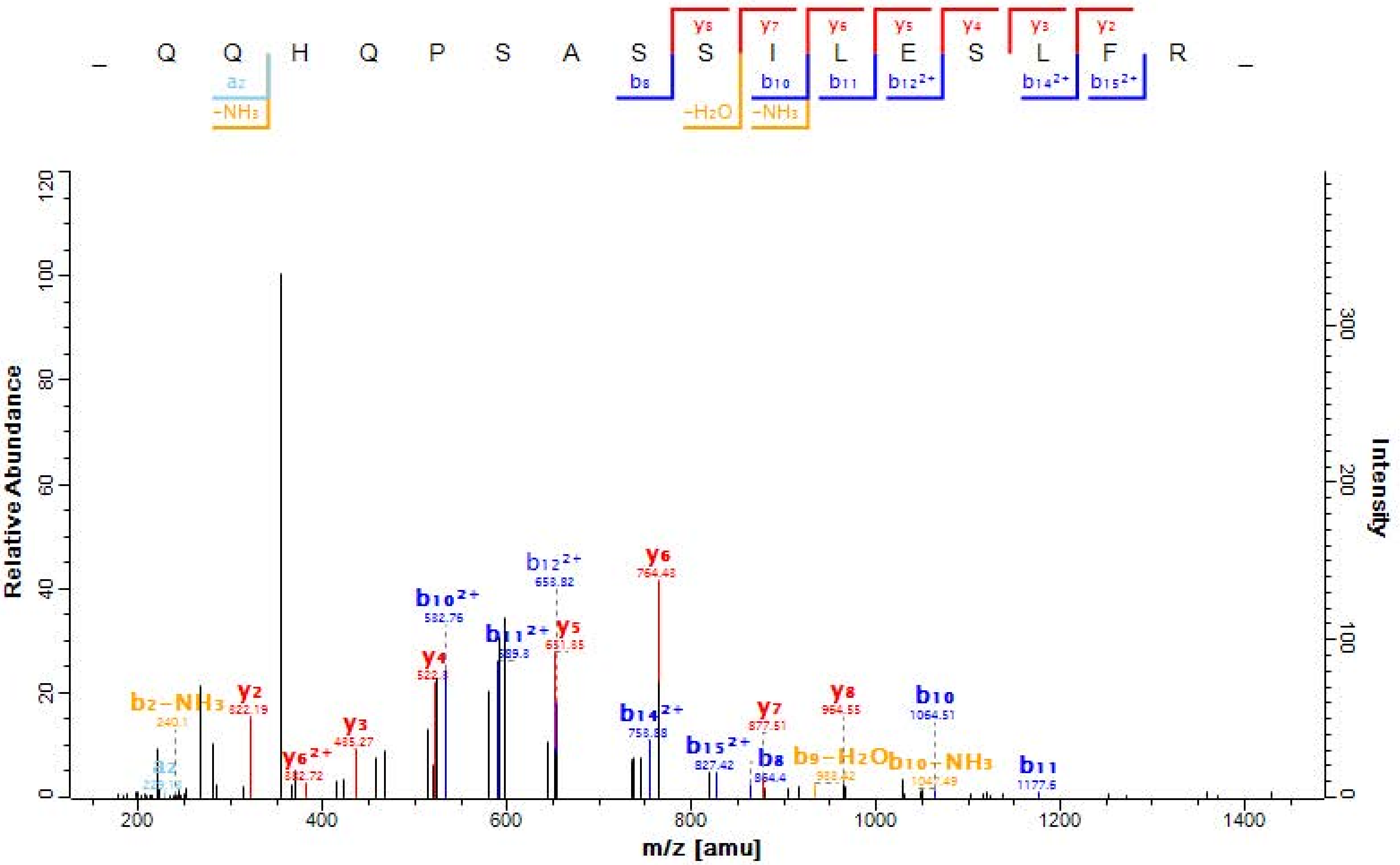
Mass:	1739.00914
m/z:	580.67699
Charge:	3+
Retentiontime:	56.498989105224
Score:	107.1399
Mass Error [ppm]:	-0.14308
PEP:	2.7248E-06
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	58 %
Peak Coverage:	24 %
Protein Localisation:	222 ... 236

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.08		148.08	1	F	14				
	276.17	-0.078	276.17	2	K	13	1592.9		1592.9	
	375.24	-0.114	375.24	3	V	12	1464.9		732.93	+0.2897
	472.29		472.29	4	P	11	1365.8		683.4	-0.067
	600.35		600.35	5	Q	10	1268.7		1268.7	
	728.41		728.41	6	Q	9	1140.7		570.84	-0.141
+0.1733	421.25		841.49	7	I	8	1012.6		1012.6	
-0.076	477.79	+0.0267	954.58	8	L	7	899.53	+0.0414	899.53	
+0.1968	541.82		1082.6	9	Q	6	786.45	+0.0748	786.45	
	1139.7		1139.7	10	G	5	658.39	+0.0656	658.39	
+0.1937	626.87	+0.1825	1252.7	11	L	4	601.37		601.37	
+0.341	676.41		1351.8	12	V	3	488.28	+0.0125	488.28	
+0.1688	733.92		1466.8	13	D	2	389.21	+0.0236	389.21	
	1565.9		1565.9	14	V	1	274.19	+0.0994	274.19	
				15	R	0	175.12	-0.051	175.12	

Scan number	9302	**Raw file**	LNCAP_Silac_23F10_set3_08
Method	ITMS; CID	**Pepti...**	79.65



precursor information

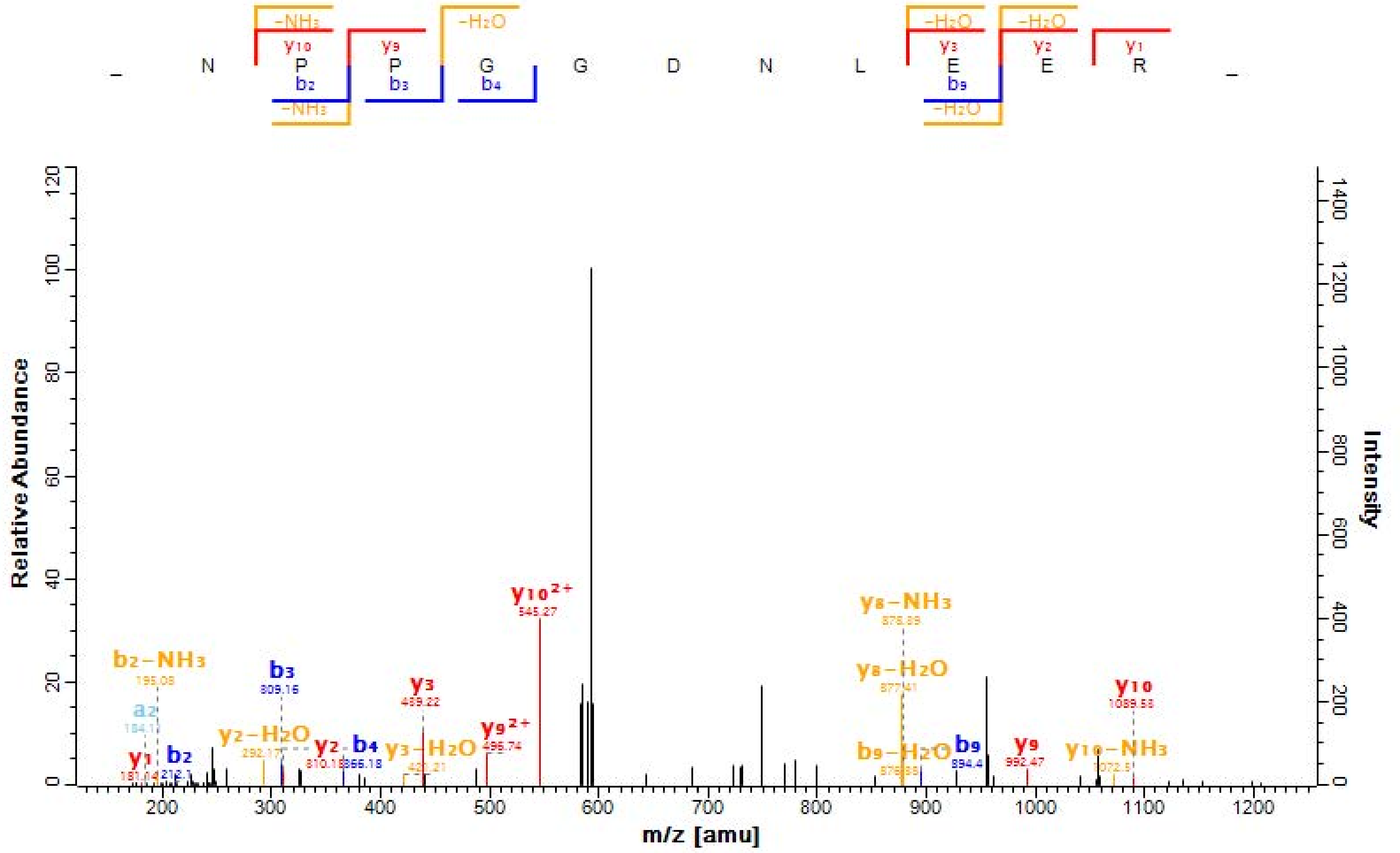
Mass:	1826.92761
m/z:	609.98315
Charge:	3+
Retentiontime:	62.701122283935
Score:	79.65154
Mass Error [ppm]:	0.054299
PEP:	0.00022853
Precursor Type:	MULTI

general information

Annotation:	11 of 16
AminoAcids Coverag	69 %
Intensity Coverage:	32 %
Peak Coverage:	21 %
Protein Localisation:	1148 ... 1163

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	101.1		129.1		129.1	1	Q	15				
+0.16	229.1		257.1		257.1	2	Q	14	1700		1700	
	366.2		394.2		394.2	3	H	13	1572		1572	
	494.2		522.2		522.2	4	Q	12	1435		1435	
	591.3		619.3		619.3	5	P	11	1307		1307	
	678.3		706.3		706.3	6	S	10	1210		1210	
	749.4		777.4		777.4	7	A	9	1123		1123	
	836.4		864.4	-0.01	864.4	8	S	8	1052		1052	
	923.4		951.4		951.4	9	S	7	964.5	+0.109	964.5	
	1037	+0.236	532.8	-0.07	1065	10	I	6	877.5	+0.201	877.5	
	1150	+0.082	589.3	-0.32	1178	11	L	5	764.4	-0.03	382.7	+0.12
	1279	-0.1	653.8		1307	12	E	4	651.3	+0.08	651.3	
	1366		1394		1394	13	S	3	522.3	+0.029	522.3	
	1479	+0.469	753.9		1507	14	L	2	435.3	+0.138	435.3	
	1626	+0.323	827.4		1654	15	F	1	322.2	+0.102	322.2	
						16	R	0	175.1		175.1	

Scan number	1130	**Raw file**	LNCAP_Silac_23F10_set3_09
Method	ITMS; CID	**Pepti...**	97.81



precursor information

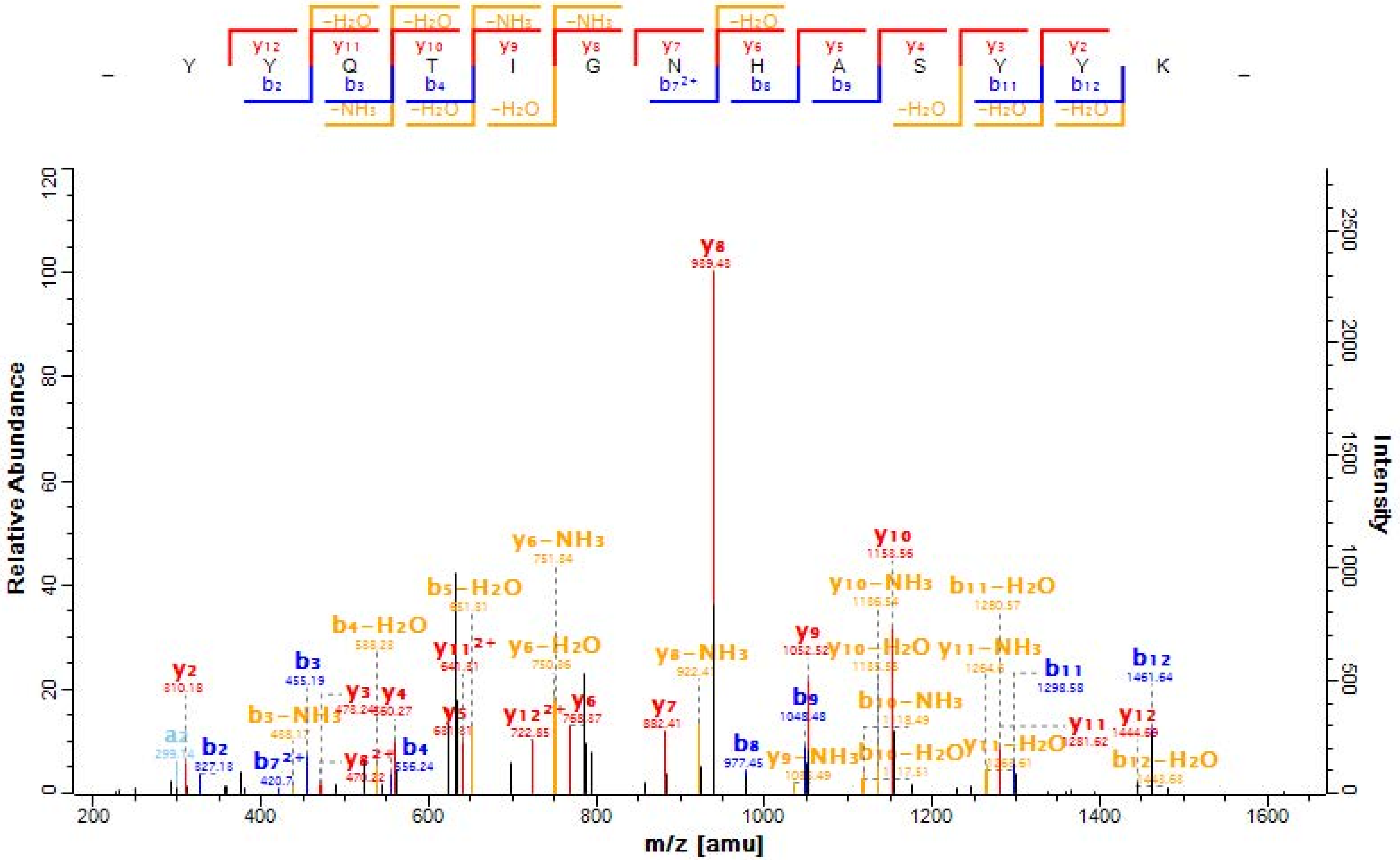
Mass:	1202.56139
m/z:	602.28797
Charge:	2+
Retentiontime:	11.826787948608
Score:	97.81339
Mass Error [ppm]:	-0.76308
PEP:	0.0044452
Precursor Type:	ISO

general information

Annotation:	6 of 11
AminoAcids Coverag	55 %
Intensity Coverage:	24 %
Peak Coverage:	21 %
Protein Localisation:	216 ... 226

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	87.055		115.05	1	N	10				
-0.041	184.11	+0.0797	212.1	2	P	9	1089.5	-0.137	545.27	+0.1405
	281.16	+0.0637	309.16	3	P	8	992.47	-0.046	496.74	+0.0805
	338.18	+0.1727	366.18	4	G	7	895.42		895.42	
	395.2		423.2	5	G	6	838.4		838.4	
	510.23		538.23	6	D	5	781.38		781.38	
	624.27		652.27	7	N	4	666.35		666.35	
	737.36		765.35	8	L	3	552.31		552.31	
	866.4	+0.0015	894.4	9	E	2	439.22	+0.086	439.22	
	995.44		1023.4	10	E	1	310.18	+0.2119	310.18	
				11	R	0	181.14	-0.01	181.14	

Scan number	1484	**Raw file**	LNCAP_Silac_23F10_set3_09
Method	ITMS; CID	**Pepti...**	259.7



precursor information

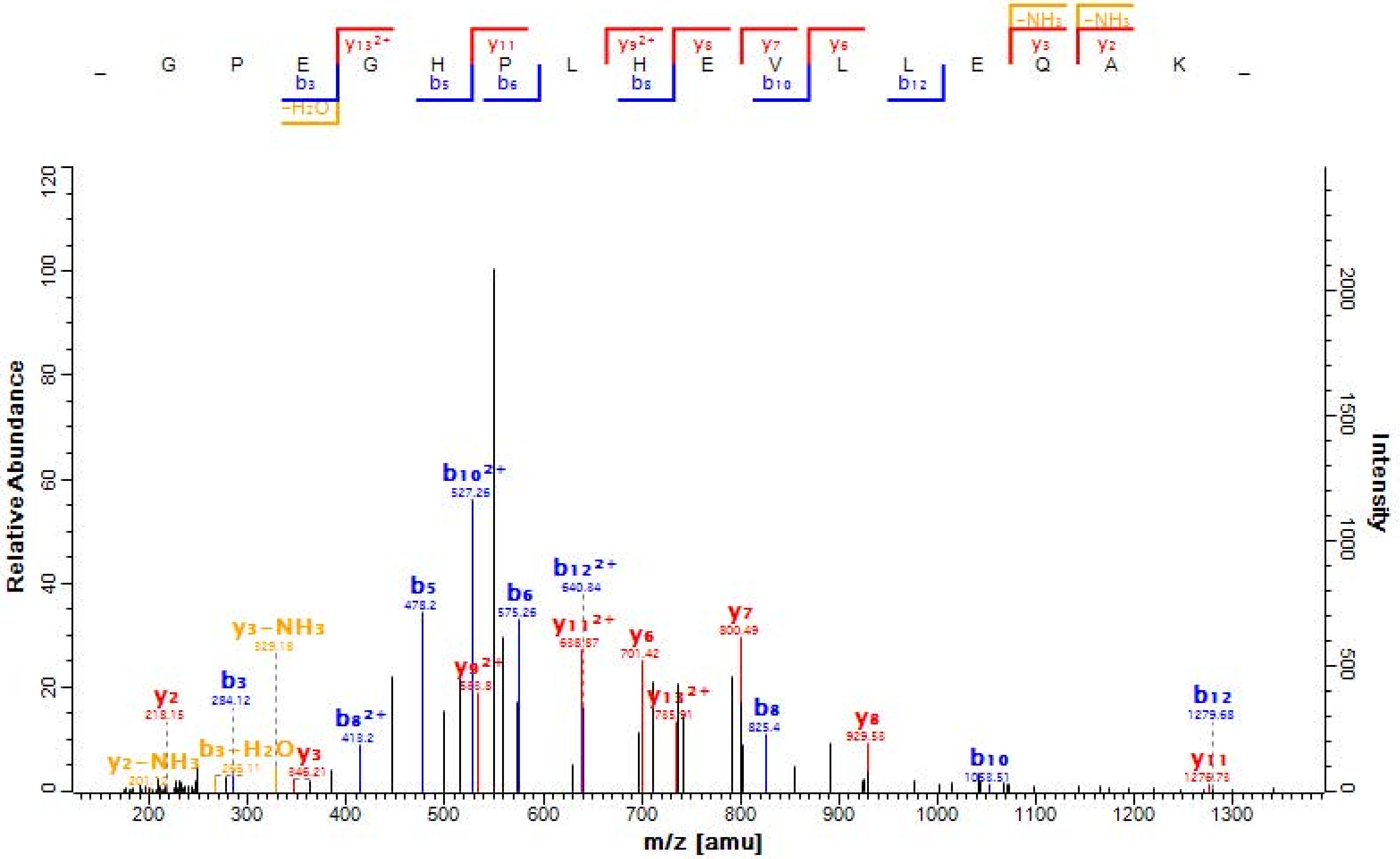
Mass:	1606.74188
m/z:	804.37822
Charge:	2+
Retentiontime:	13.941345214843
Score:	259.697
Mass Error [ppm]:	0.16983
PEP:	1.3598E-59
Precursor Type:	ISO

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	61 %
Peak Coverage:	45 %
Protein Localisation:	162 ... 174

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.1		164.1		164.1	1	Y	12				
+0.047	299.1		327.1	+0.117	327.1	2	Y	11	1445	+0.021	722.8	+0.24
	427.2		455.2	-0.06	455.2	3	Q	10	1282	-0.01	641.3	+0.18
	528.2		556.2	-0.05	556.2	4	T	9	1154	-0.04	1154	
	641.3		669.3		669.3	5	I	8	1053	-0.01	1053	
	698.4		726.3		726.3	6	G	7	939.4	-0.04	470.2	+0.18
	812.4	-0.38	420.7		840.4	7	N	6	882.4	-0.02	882.4	
	949.5		977.4	-0.06	977.4	8	H	5	768.4	+0.087	768.4	
	1020		1048	+0.031	1048	9	A	4	631.3	-0.13	631.3	
	1108		1136		1136	10	S	3	560.3	-0.03	560.3	
	1271		1299	-0.13	1299	11	Y	2	473.2	+0.015	473.2	
	1434		1462	-0.01	1462	12	Y	1	310.2	+0.151	310.2	
						13	K	0	147.1		147.1	

Scan number	2412	**Raw file**	LNCAP_Silac_23F10_set3_09
Method	ITMS; CID	**Pepti...**	85.91



precursor information

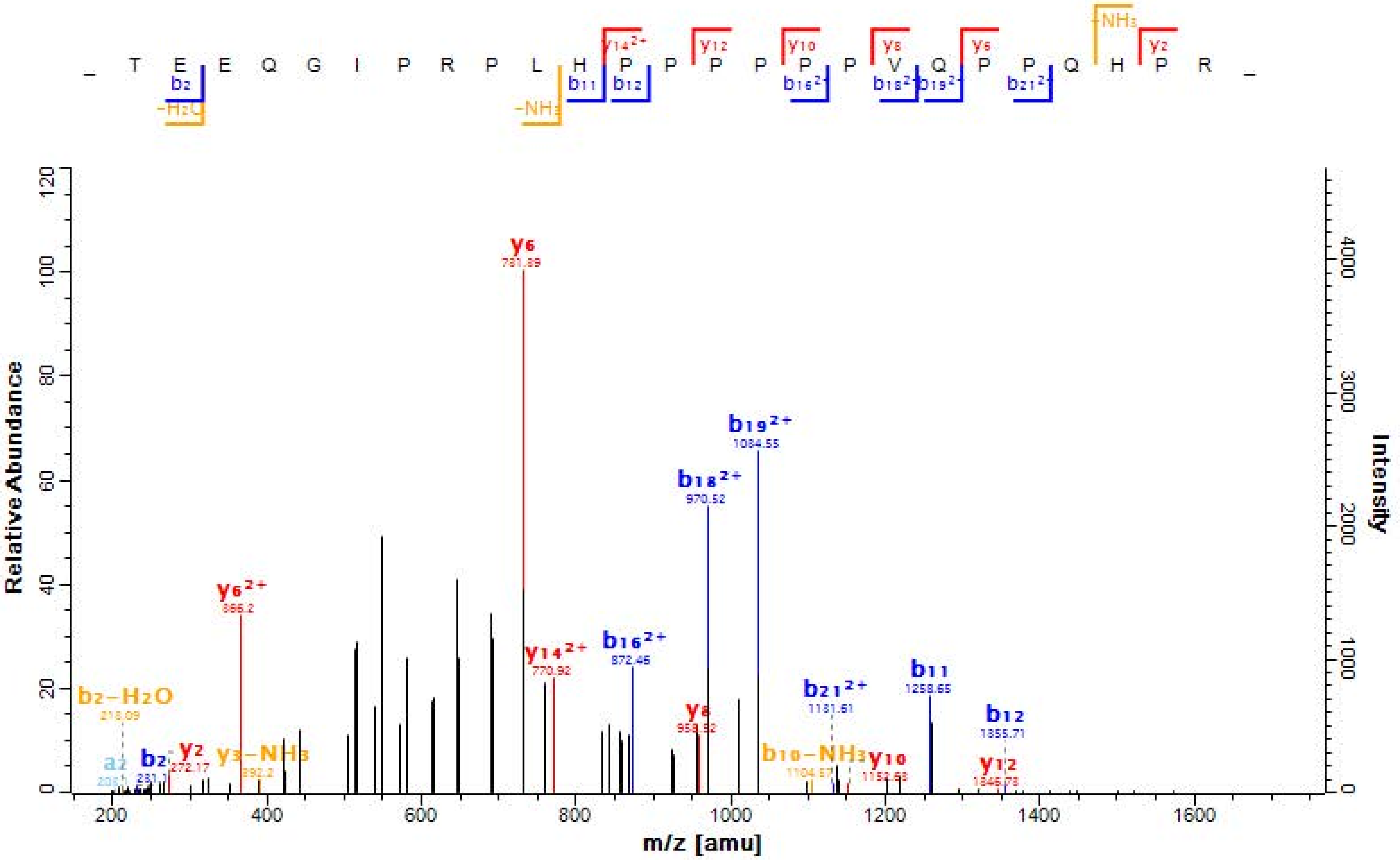
Mass:	1752.91584
m/z:	585.31256
Charge:	3+
Retentiontime:	19.308992385864
Score:	85.90907
Mass Error [ppm]:	-0.024343
PEP:	7.5748E-05
Precursor Type:	MULTI

general information

Annotation:	11 of 16
AminoAcids Coverag	69 %
Intensity Coverage:	42 %
Peak Coverage:	21 %
Protein Localisation:	107 ... 122

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	15				
	155.08		155.08	2	P	14	1696.9		1696.9	
	284.12	+0.1111	284.12	3	E	13	1599.8		1599.8	
	341.15		341.15	4	G	12	1470.8		735.91	-0.117
	478.2	-0.197	478.2	5	H	11	1413.8		1413.8	
	575.26	-0.204	575.26	6	P	10	1276.7	+0.2985	638.87	+0.24
	688.34		688.34	7	L	9	1179.7		1179.7	
+0.0977	413.2	+0.0507	825.4	8	H	8	1066.6		533.8	+0.3812
	954.44		954.44	9	E	7	929.53	-0.042	929.53	
+0.2327	527.26	-0.073	1053.5	10	V	6	800.49	+0.0205	800.49	
	1166.6		1166.6	11	L	5	701.42	-0.019	701.42	
+0.2672	640.34	-0.378	1279.7	12	L	4	588.34		588.34	
	1408.7		1408.7	13	E	3	475.25		475.25	
	1536.8		1536.8	14	Q	2	346.21	+0.0157	346.21	
	1607.8		1607.8	15	A	1	218.15	-0.252	218.15	
				16	K	0	147.11		147.11	

Scan number	2667	**Raw file**	LNCAP_Silac_23F10_set3_09
Method	ITMS; CID	**Pepti...**	38.58



precursor information

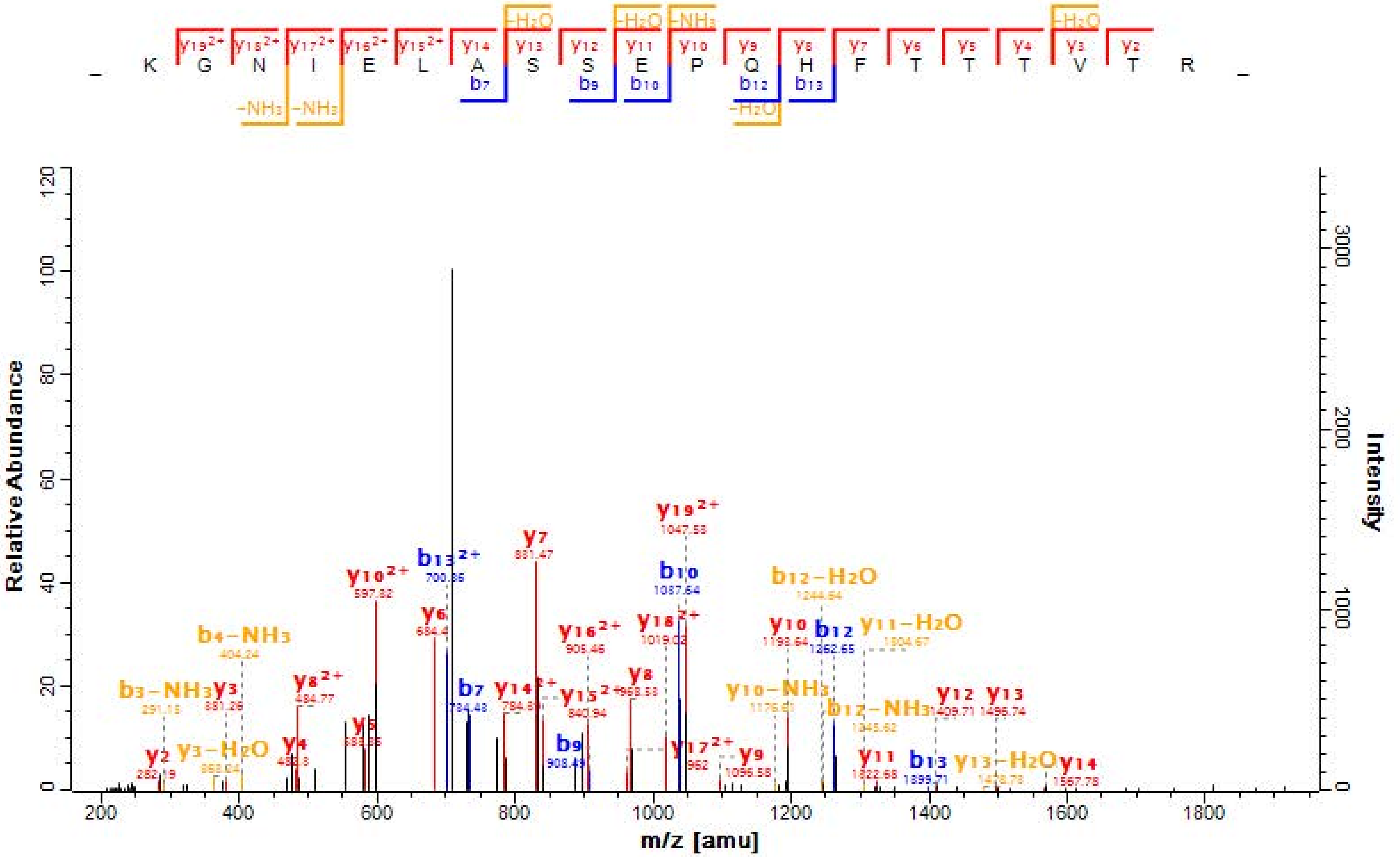
Mass:	2797.47722
m/z:	700.37658
Charge:	4+
Retentiontime:	20.763109207153
Score:	38.58278
Mass Error [ppm]:	-0.14274
PEP:	0.0099003
Precursor Type:	MULTI

general information

Annotation:	12 of 25
AminoAcids Coverag	48 %
Intensity Coverage:	35 %
Peak Coverage:	17 %
Protein Localisation:	1012 ... 1036

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.1		102.1	1	T	24				
+0	203.1		231.1	-0.03	231.1	2	E	23	2697		2697	
	332.1		360.1		360.1	3	E	22	2568		2568	
	460.2		488.2		488.2	4	Q	21	2439		2439	
	517.2		545.2		545.2	5	G	20	2311		2311	
	630.3		658.3		658.3	6	I	19	2254		2254	
	727.4		755.4		755.4	7	P	18	2141		2141	
	883.5		911.5		911.5	8	R	17	2044		2044	
	980.5		1009		1009	9	P	16	1888		1888	
	1094		1122		1122	10	L	15	1791		1791	
	1231		1259	-0.02	1259	11	H	14	1678		1678	
	1328		1356	-0.2	1356	12	P	13	1541		770.9	+0.44
	1425		1453		1453	13	P	12	1444		1444	
	1522		1550		1550	14	P	11	1347	-0.28	1347	
	1619		1647		1647	15	P	10	1250		1250	
	1716	+0.109	872.5		1744	16	P	9	1153	-0.16	1153	
	1813		1841		1841	17	P	8	1056		1056	
	1912	+0.197	970.5		1940	18	V	7	958.5	-0.12	958.5	
	2040	+0.366	1035		2068	19	Q	6	859.5		859.5	
	2137		2165		2165	20	P	5	731.4	+0.026	366.2	+0.25
	2234	+0.23	1132		2262	21	P	4	634.3		634.3	
	2362		2390		2390	22	Q	3	537.3		537.3	
	2499		2527		2527	23	H	2	409.2		409.2	
	2596		2624		2624	24	P	1	272.2	+0.065	272.2	
						25	R	0	175.1		175.1	

Scan number 2750 **Raw file** LNCAP_Silac_23F10_set3_09
Method ITMS; CID **Pepti...** 157.22



precursor information

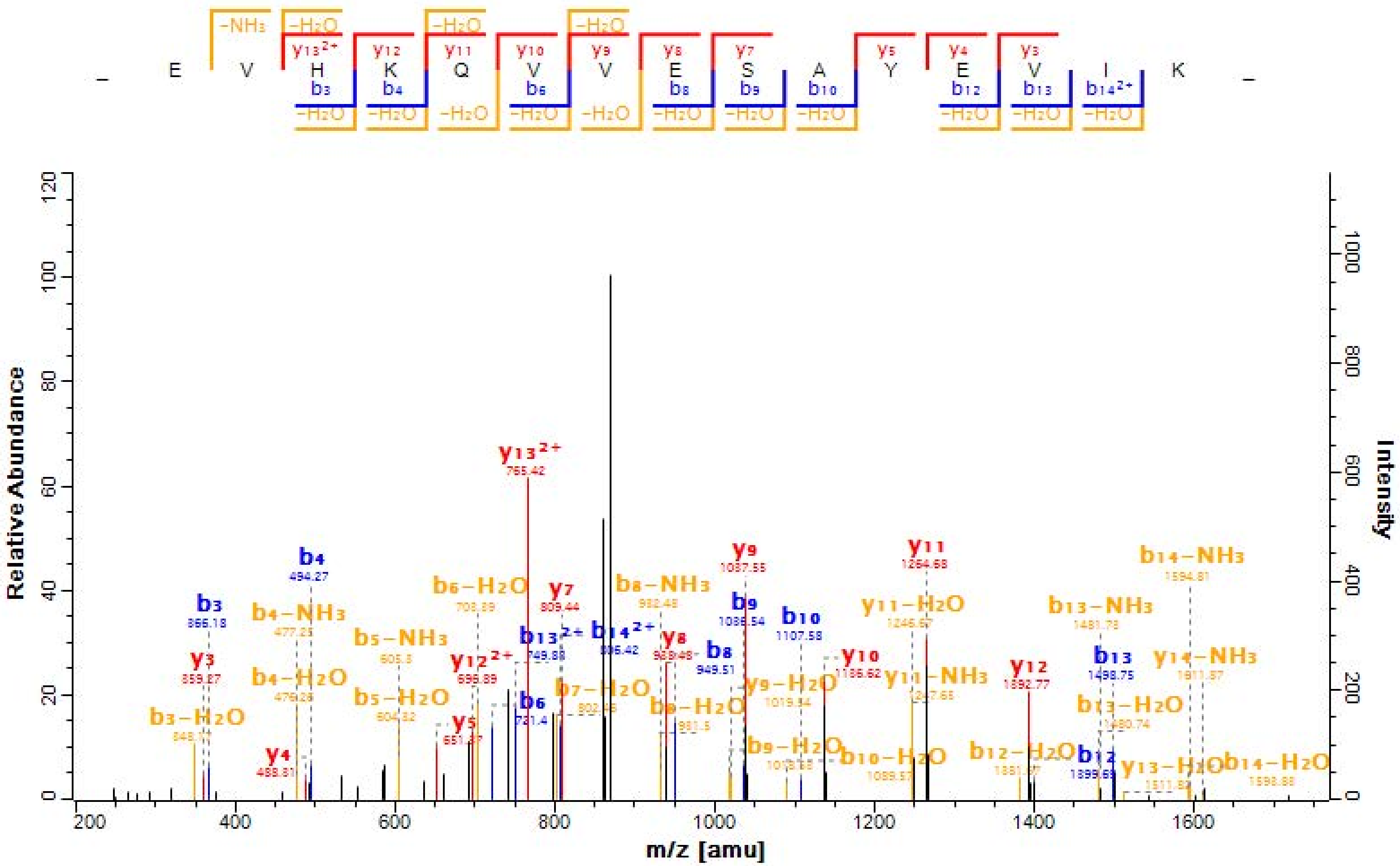
Mass:	2215.12308
m/z:	739.38163
Charge:	3+
Retentiontime:	21.227899551391
Score:	157.2171
Mass Error [ppm]:	-0.10505
PEP:	5.6593E-27
Precursor Type:	MULTI

general information

Annotation:	18 of 20
AminoAcids Coverag	90 %
Intensity Coverage:	49 %
Peak Coverage:	30 %
Protein Localisation:	649 ... 668

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	137.12		137.12	1	K	19				
	194.14		194.14	2	G	18	2094.1		1047.5	+0.1304
	308.18		308.18	3	N	17	2037		1019	+0.2195
	421.26		421.26	4	I	16	1923		962	+0.3253
	550.31		550.31	5	E	15	1809.9		905.46	+0.4265
	663.39		663.39	6	L	14	1680.9		840.94	+0.0886
	734.43	-0.222	734.43	7	A	13	1567.8	-0.134	784.39	+0.1095
	821.46		821.46	8	S	12	1496.7	+0.0723	1496.7	
	908.49	+0.1051	908.49	9	S	11	1409.7	+0.1561	1409.7	
	1037.5	-0.066	1037.5	10	E	10	1322.7	-0.118	1322.7	
	1134.6		1134.6	11	P	9	1193.6	-0.07	597.32	-0.016
	1262.6	-0.046	1262.6	12	Q	8	1096.6	+0.2139	1096.6	
+0.1933	700.36	+0.0702	1399.7	13	H	7	968.53	+0.0454	484.77	+0.1185
	1546.8		1546.8	14	F	6	831.47	+0.0099	831.47	
	1647.8		1647.8	15	T	5	684.4	+0.0249	684.4	
	1748.9		1748.9	16	T	4	583.35	+0.0865	583.35	
	1849.9		1849.9	17	T	3	482.3	+0.1925	482.3	
	1949		1949	18	V	2	381.26	+0.0577	381.26	
	2050		2050	19	T	1	282.19	+0.1092	282.19	
				20	R	0	181.14		181.14	

Scan number	2780	**Raw file**	LNCAP_Silac_23F10_set3_09
Method	ITMS; CID	**Pepti...**	245.4



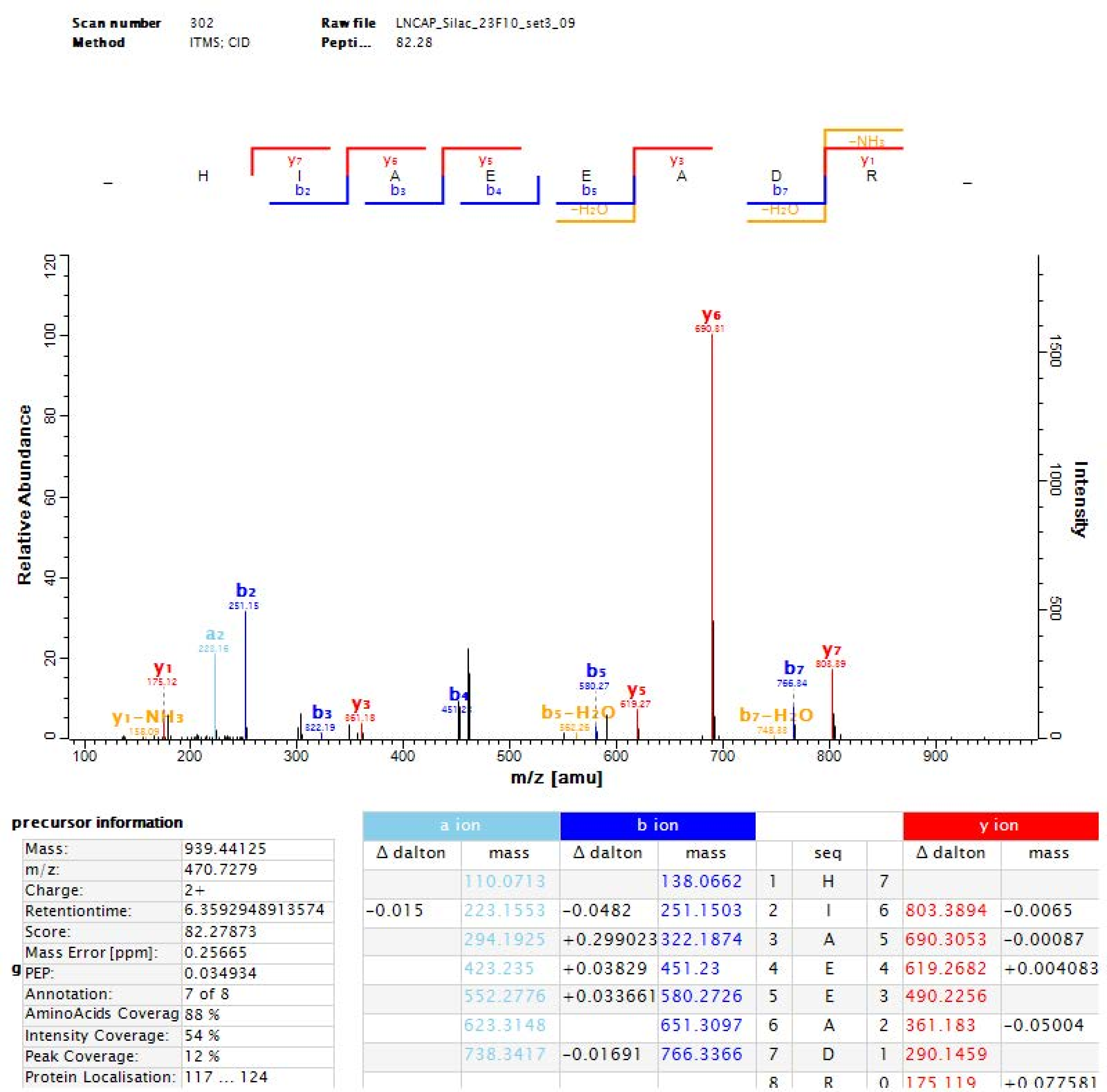
precursor information

Mass:	1756.93671
m/z:	879.47563
Charge:	2+
Retentiontime:	21.404933929443
Score:	245.3954
Mass Error [ppm]:	0.43032
PEP:	7.7043E-47
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	57 %
Peak Coverage:	51 %
Protein Localisation:	258 ... 272

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.05		130.05	1	E	14				
	229.12		229.12	2	V	13	1628.9		1628.9	
	366.18	+0.1182	366.18	3	H	12	1529.8		765.42	+0.271
	494.27	+0.1857	494.27	4	K	11	1392.8	-0.097	696.89	+0.0147
	622.33		622.33	5	Q	10	1264.7	-0.048	1264.7	
	721.4	-0.001	721.4	6	V	9	1136.6	-0.03	1136.6	
	820.47		820.47	7	V	8	1037.6	+0.0299	1037.6	
	949.51	+0.0282	949.51	8	E	7	938.48	+0.0191	938.48	
	1036.5	+0.3545	1036.5	9	S	6	809.44	+0.0177	809.44	
	1107.6	-0.002	1107.6	10	A	5	722.41		722.41	
	1270.6		1270.6	11	Y	4	651.37	+0.048	651.37	
	1399.7	+0.1439	1399.7	12	E	3	488.31	+0.2004	488.31	
+0.2436	749.88	-0.078	1498.8	13	V	2	359.27	+0.0157	359.27	
-0.122	806.42		1611.8	14	I	1	260.2		260.2	
				15	K	0	147.11		147.11	



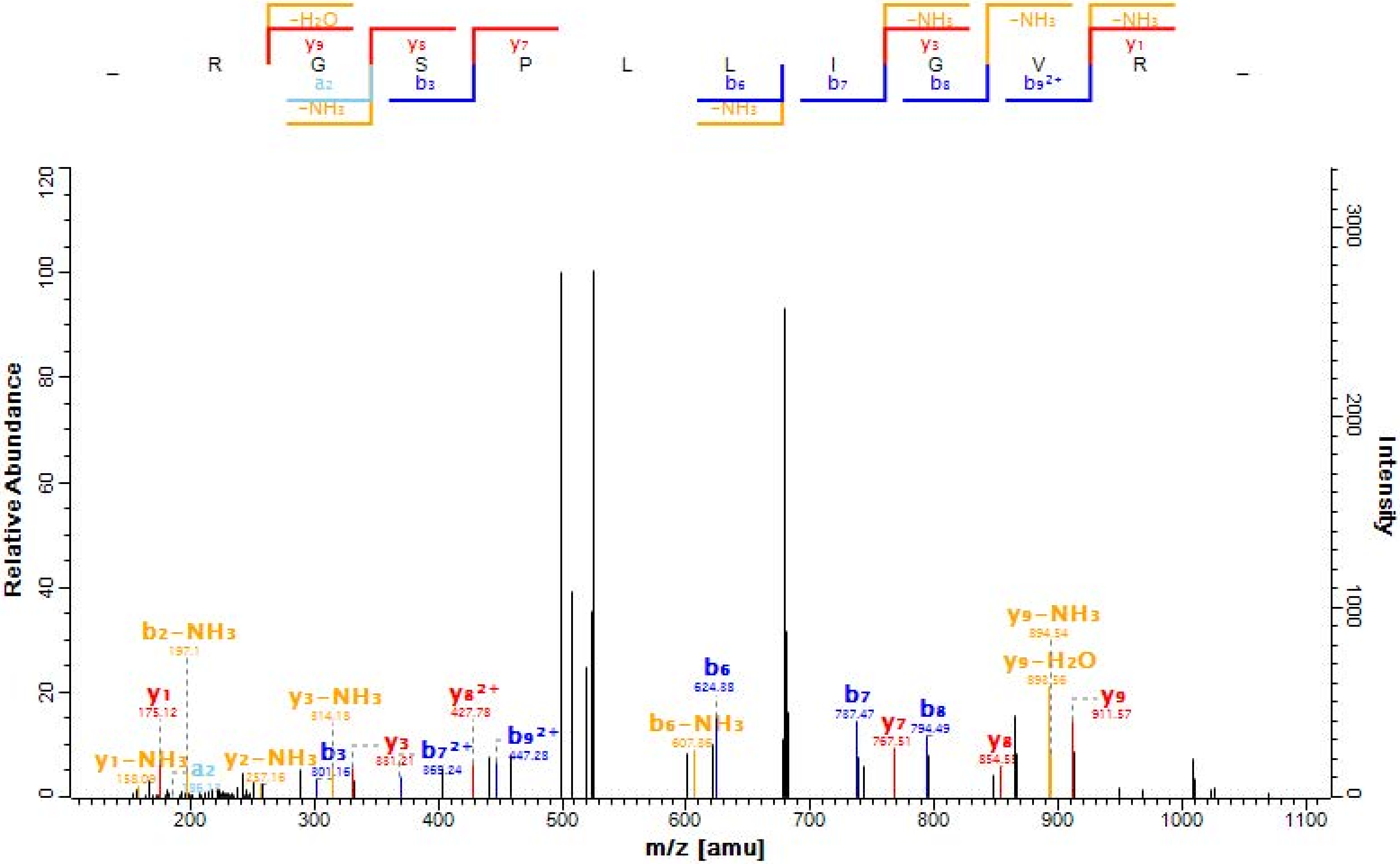
Scan number	302	**Raw file**	LNCAP_Silac_23F10_set3_09
Method	ITMS; CID	**Pepti...**	82.28

precursor information

Mass:	939.44125
m/z:	470.7279
Charge:	2+
Retentiontime:	6.3592948913574
Score:	82.27873
Mass Error [ppm]:	0.25665
PEP:	0.034934
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	54 %
Peak Coverage:	12 %
Protein Localisation:	117 ... 124

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	110.0713		138.0662	1	H	7		
-0.015	223.1553	-0.0482	251.1503	2	I	6	803.3894	-0.0065
	294.1925	+0.299023	322.1874	3	A	5	690.3053	-0.00087
	423.235	+0.03829	451.23	4	E	4	619.2682	+0.004083
	552.2776	+0.033661	580.2726	5	E	3	490.2256	
	623.3148		651.3097	6	A	2	361.183	-0.05004
	738.3417	-0.01691	766.3366	7	D	1	290.1459	
				8	R	0	175.119	+0.077581

Scan number	3084	**Raw file**	LNCAP_Silac_23F10_set3_09
Method	ITMS; CID	**Pepti...**	102.52



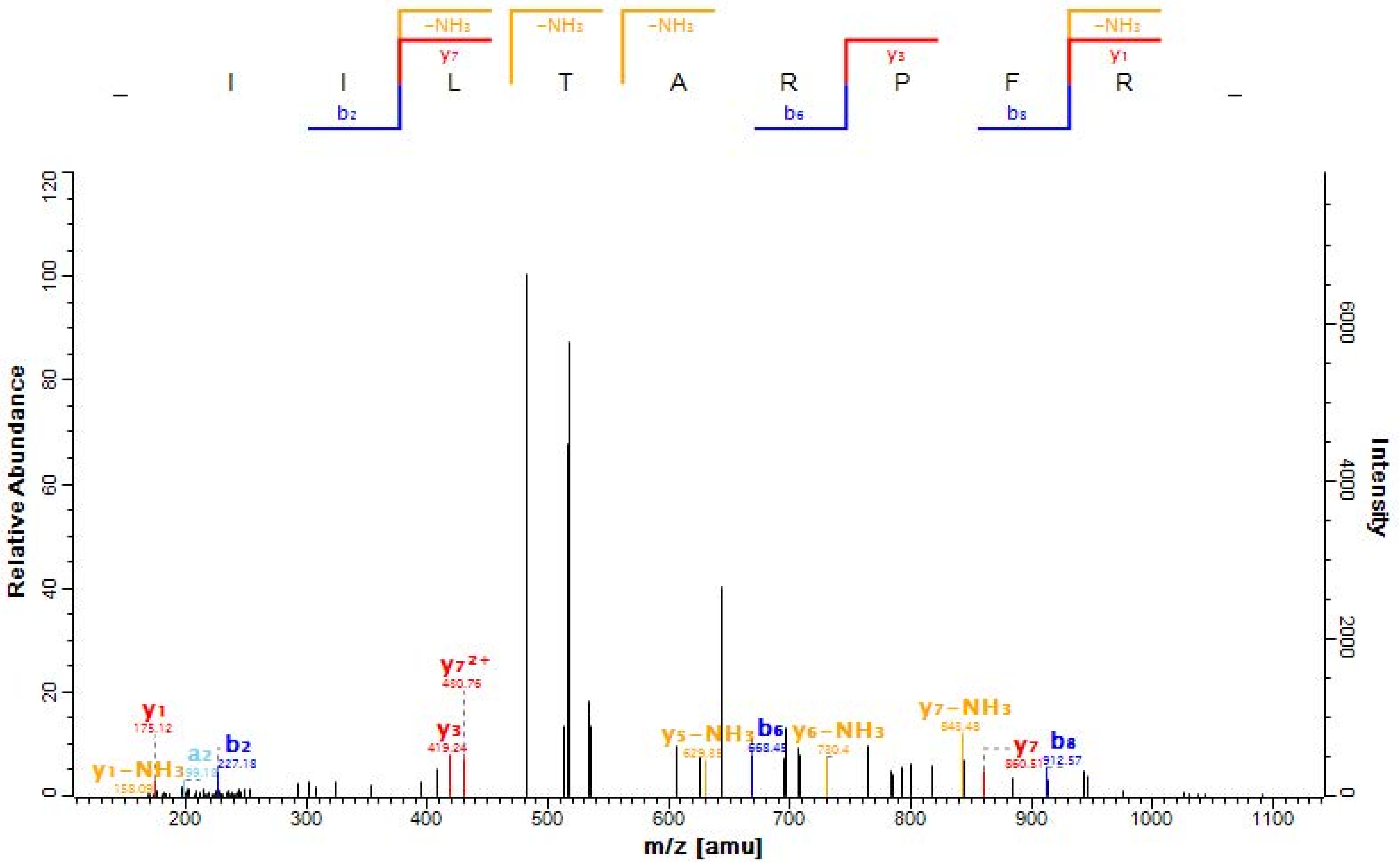
precursor information

Mass:	1066.66144
m/z:	534.338
Charge:	2+
Retentiontime:	23.273738861084
Score:	102.5236
Mass Error [ppm]:	0.30453
PEP:	0.0055249
Precursor Type:	ISO

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	19 %
Peak Coverage:	20 %
Protein Localisation:	203 ... 212

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.1		157.1		157.1	1	R	9				
-0.22	186.1		214.1		214.1	2	G	8	911.6	+0	911.6	
	273.2		301.2	+0.023	301.2	3	S	7	854.5	-0.18	427.8	+0.33
	370.2		398.2		398.2	4	P	6	767.5	+0.054	767.5	
	483.3		511.3		511.3	5	L	5	670.5		670.5	
	596.4		624.4	+0.09	624.4	6	L	4	557.4		557.4	
	709.5	+0.15	369.2	-0.01	737.5	7	I	3	444.3		444.3	
	766.5		794.5	-0.01	794.5	8	G	2	331.2	+0.109	331.2	
	865.6	-0.09	447.3		893.6	9	V	1	274.2		274.2	
						10	R	0	175.1	+0.011	175.1	

Scan number	3318	**Raw file**	LNCAP_Silac_23F10_set3_09
Method	ITMS; CID	**Pepti...**	49.72

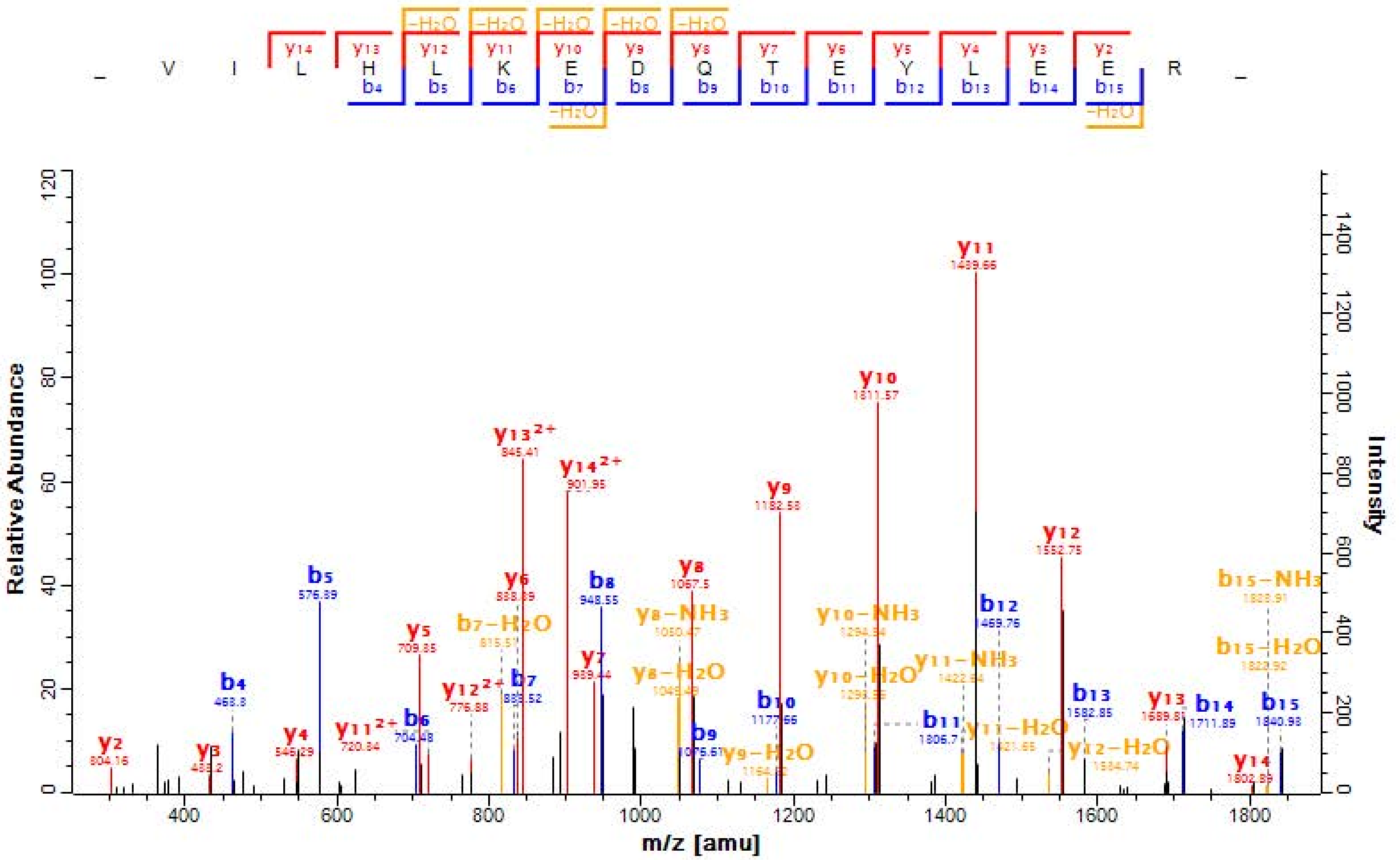


precursor information

Mass:	1085.67102
m/z:	543.84279
Charge:	2+
Retentiontime:	24.581544876098
Score:	49.71508
Mass Error [ppm]:	0.069325
PEP:	0.043464
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	12 %
Peak Coverage:	12 %
Protein Localisation:	200 ... 208

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096		114.09	1	I	8				
-0.184	199.18	-0.059	227.18	2	I	7	973.59		973.59	
	312.26		340.26	3	L	6	860.51	+0.0804	430.76	+0.358
	413.31		441.31	4	T	5	747.43		747.43	
	484.35		512.34	5	A	4	646.38		646.38	
	640.45	-0.094	668.45	6	R	3	575.34		575.34	
	737.5		765.5	7	P	2	419.24	+0.0348	419.24	
	884.57	-0.085	912.57	8	F	1	322.19		322.19	
				9	R	0	175.12	+0.0374	175.12	

Scan number	3598	**Raw file**	LNCAP_Silac_23F10_set3_09
Method	ITMS; CID	**Pepti...**	233.14



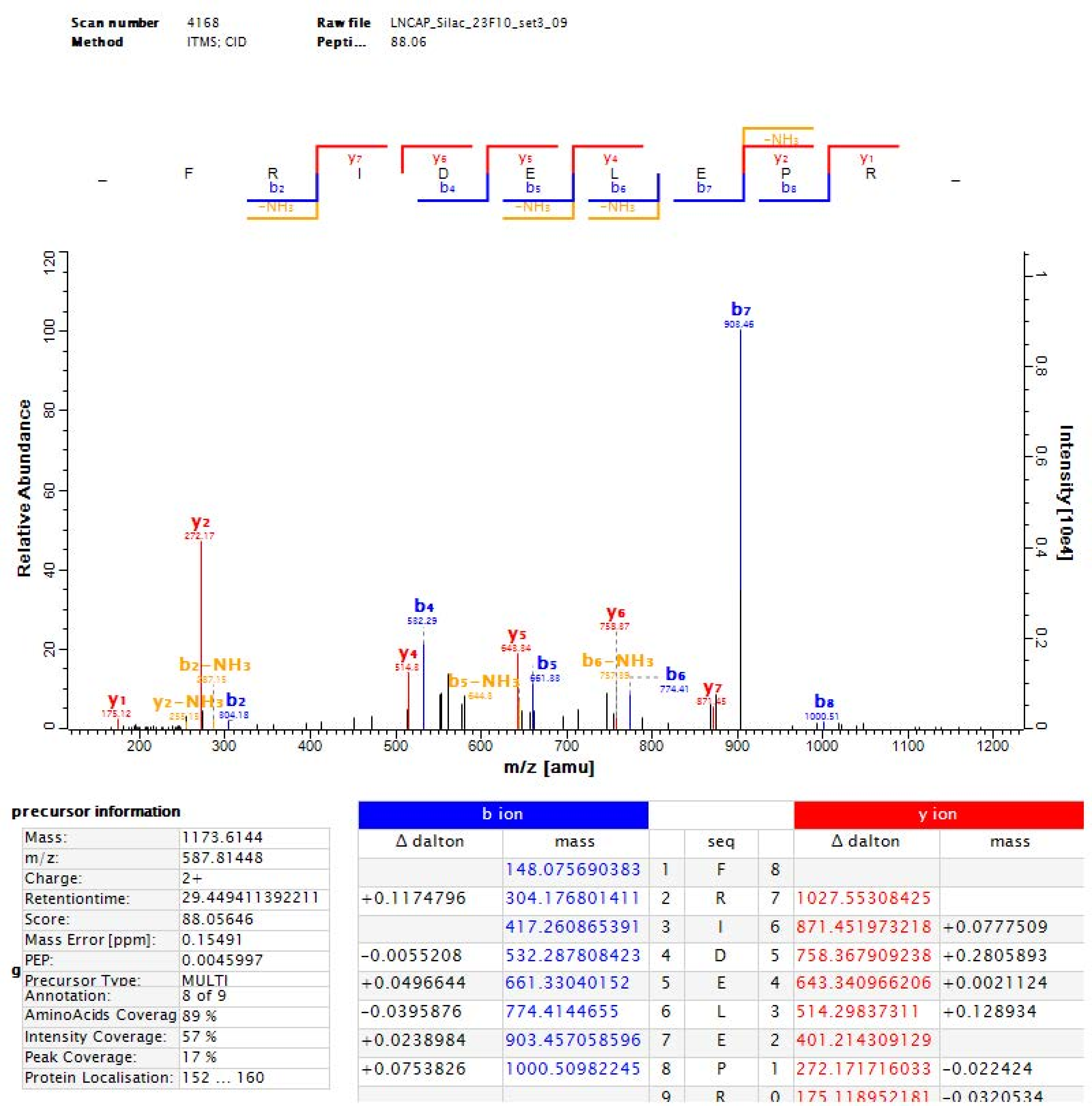
precursor information

Mass:	2014.03627
m/z:	1008.02541
Charge:	2+
Retentiontime:	26.207149505615
Score:	233.1442
Mass Error [ppm]:	-0.42035
PEP:	1.0938E-50
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	66 %
Peak Coverage:	40 %
Protein Localisation:	308 ... 323

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757	1	V	15				
	213.1598	2	I	14	1915.976		1915.976	
	326.2438	3	L	13	1802.892	+0.068164	901.9496	+0.264636
+0.131779	463.3027	4	H	12	1689.808	-0.08996	845.4076	+0.197293
+0.042039	576.3868	5	L	11	1552.749	-0.0048	776.8781	+0.043704
+0.091363	704.4818	6	K	10	1439.665	-0.01962	720.3361	-0.13845
+0.084903	833.5244	7	E	9	1311.57	-0.00339	1311.57	
-0.04189	948.5513	8	D	8	1182.527	-0.02586	1182.527	
-0.09132	1076.61	9	Q	7	1067.5	-0.03383	1067.5	
+0.060712	1177.658	10	T	6	939.4418	-0.03116	939.4418	
-0.04438	1306.7	11	E	5	838.3941	-0.06563	838.3941	
-0.01005	1469.763	12	Y	4	709.3515	+0.095613	709.3515	
-0.03821	1582.848	13	L	3	546.2882	+0.128668	546.2882	
-0.14623	1711.89	14	E	2	433.2041	+0.086023	433.2041	
-0.27684	1840.933	15	E	1	304.1615	-0.002	304.1615	
		16	R	0	175.119		175.119	



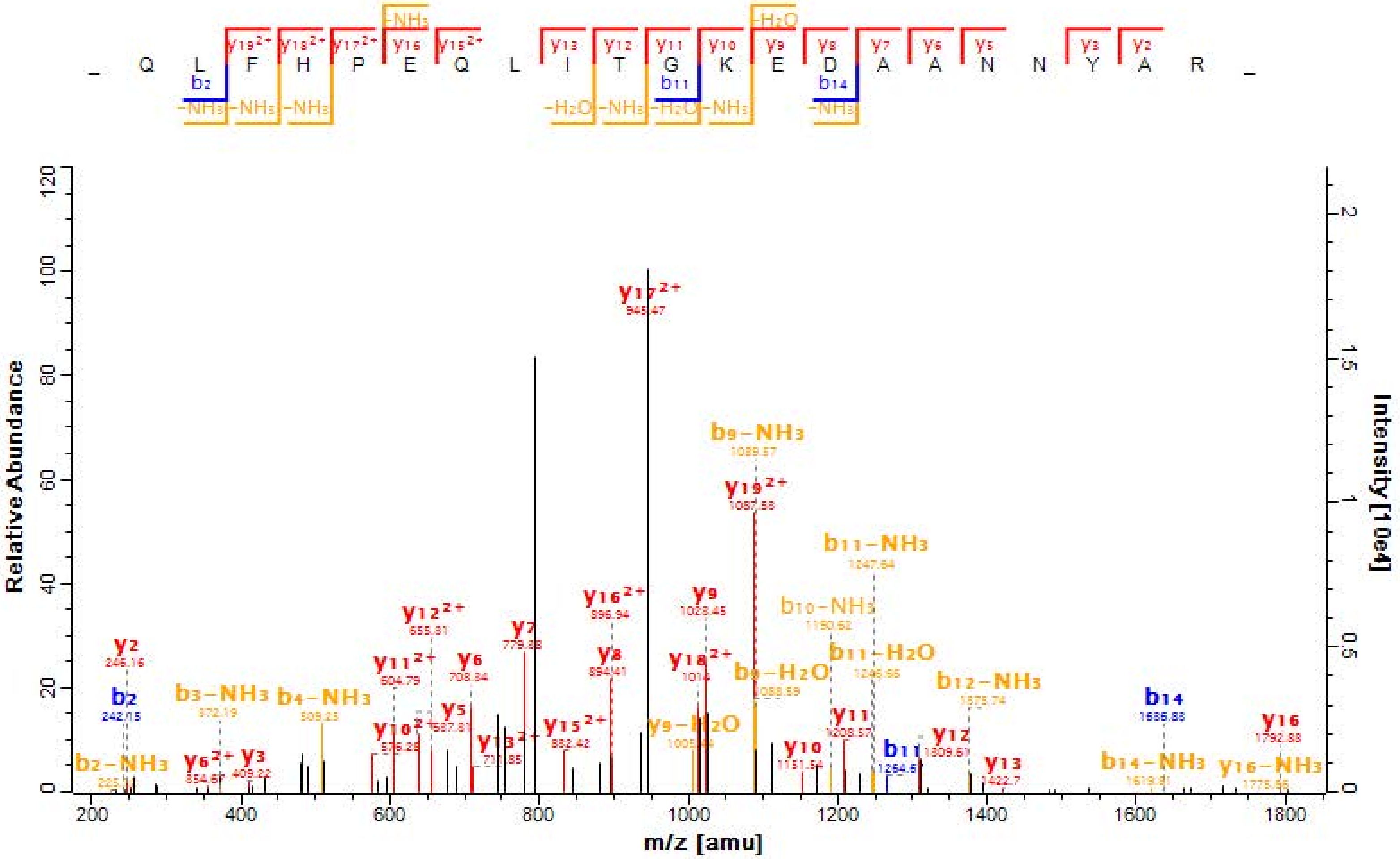
Scan number	4168	**Raw file**	LNCAP_Silac_23F10_set3_09
Method	ITMS; CID	**Pepti...**	88.06

precursor information

Mass:	1173.6144
m/z:	587.81448
Charge:	2+
Retentiontime:	29.449411392211
Score:	88.05646
Mass Error [ppm]:	0.15491
PEP:	0.0045997
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	57 %
Peak Coverage:	17 %
Protein Localisation:	152 ... 160

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	148.075690383	1	F	8		
+0.1174796	304.176801411	2	R	7	1027.55308425	
	417.260865391	3	I	6	871.451973218	+0.0777509
-0.0055208	532.287808423	4	D	5	758.367909238	+0.2805893
+0.0496644	661.33040152	5	E	4	643.340966206	+0.0021124
-0.0395876	774.4144655	6	L	3	514.29837311	+0.128934
+0.0238984	903.457058596	7	E	2	401.214309129	
+0.0753826	1000.50982245	8	P	1	272.171716033	-0.022424
		9	R	0	175.118952181	-0.0320534

Scan number	4792	**Raw file**	LNCAP_Silac_23F10_set3_09
Method	ITMS; CID	**Pepti...**	149.52



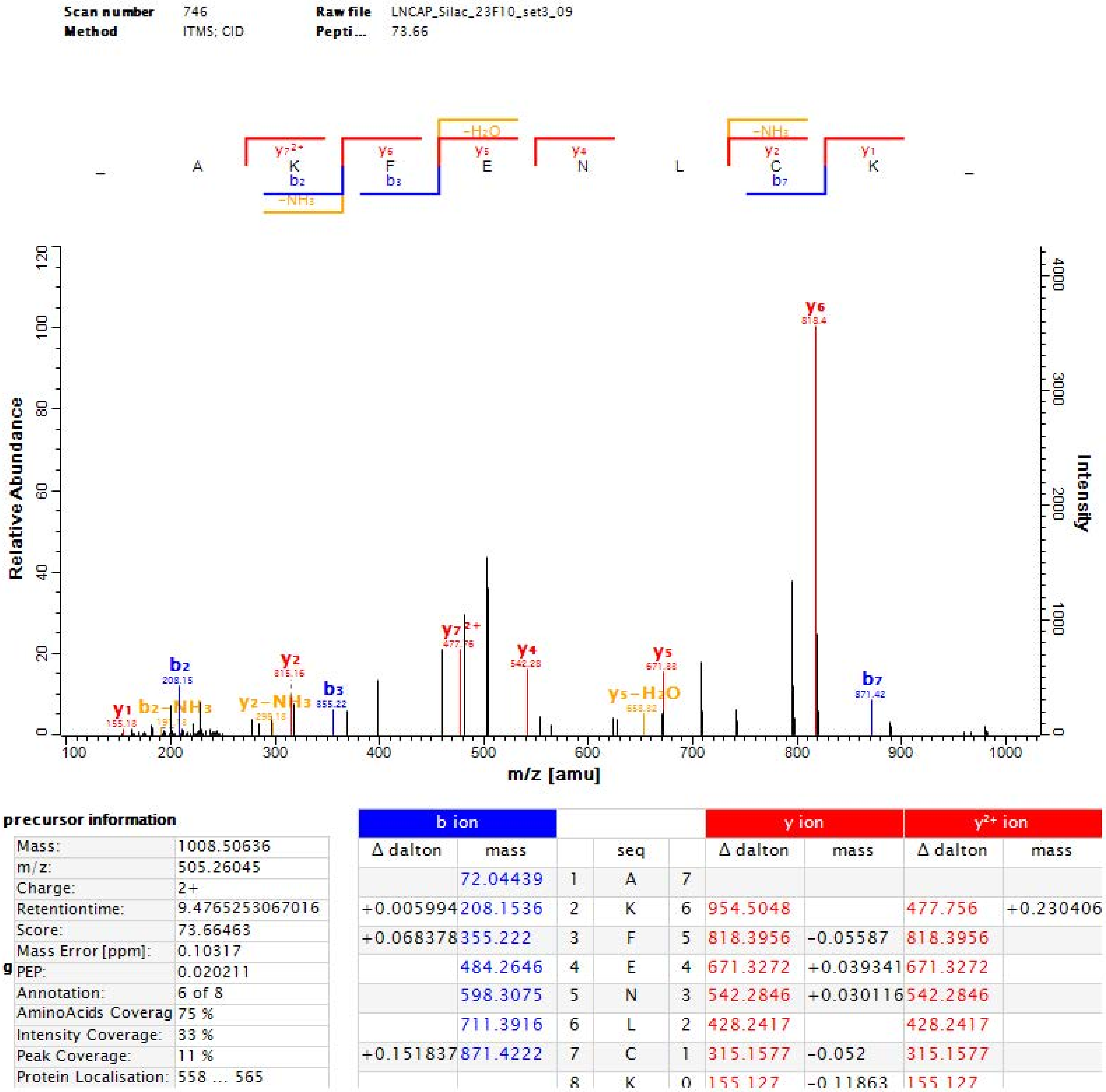
precursor information

Mass:	2414.19793
m/z:	805.73992
Charge:	3+
Retentiontime:	33.147140502929
Score:	149.5208
Mass Error [ppm]:	0.022607
PEP:	3.6106E-20
Precursor Type:	MULTI

general information

Annotation:	17 of 21
AminoAcids Coverag	81 %
Intensity Coverage:	49 %
Peak Coverage:	39 %
Protein Localisation:	85 … 105

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.0659	1	Q	20				
+0.298919	242.1499	2	L	19	2287.147		2287.147	
	389.2183	3	F	18	2174.063		1087.535	+0.34963
	526.2772	4	H	17	2026.994		1014.001	-0.09059
	623.33	5	P	16	1889.935		945.4712	+0.053491
	752.3726	6	E	15	1792.882	-0.10031	896.9448	+0.14872
	880.4312	7	Q	14	1663.84		832.4236	+0.349216
	993.5152	8	L	13	1535.781		1535.781	
	1106.599	9	I	12	1422.697	-0.25785	711.8522	-0.16918
	1207.647	10	T	11	1309.613	-0.08761	655.3102	+0.1071
+0.077279	1264.668	11	G	10	1208.565	-0.15943	604.7864	+0.243915
	1392.763	12	K	9	1151.544	-0.01309	576.2756	+0.161202
	1521.806	13	E	8	1023.449	+0.019066	1023.449	
-0.34442	1636.833	14	D	7	894.4064	+0.037733	894.4064	
	1707.87	15	A	6	779.3795	+0.085306	779.3795	
	1778.907	16	A	5	708.3424	+0.09593	354.6748	+0.103256
	1892.95	17	N	4	637.3052	+0.170581	637.3052	
	2006.993	18	N	3	523.2623		523.2623	
	2170.056	19	Y	2	409.2194	+0.117459	409.2194	
	2241.093	20	A	1	246.1561	+0.098176	246.1561	
		21	R	0	175.119		175.119	



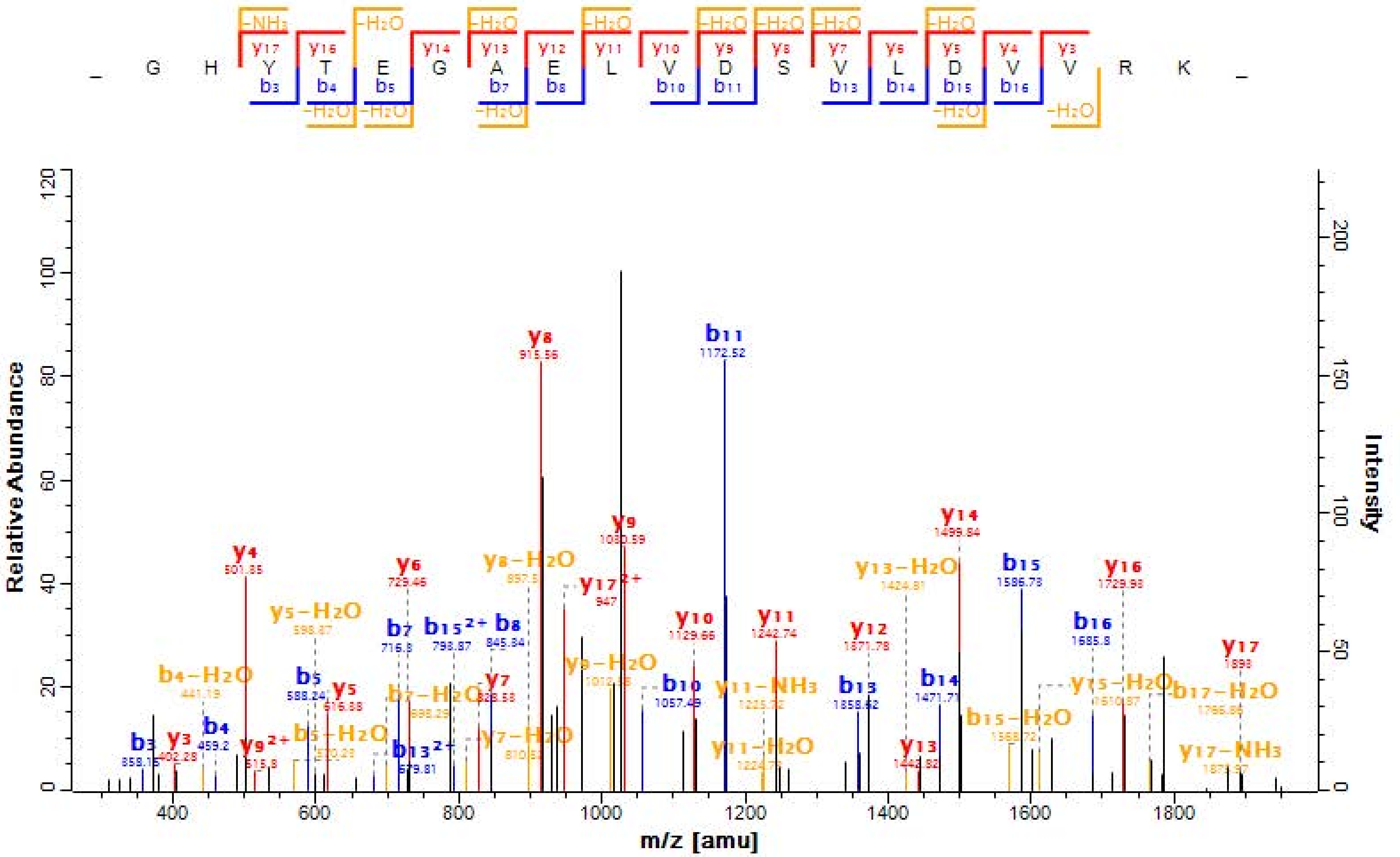
Scan number	746	**Raw file**	LNCAP_Silac_23F10_set3_09
Method	ITMS; CID	**Pepti...**	73.66

precursor information

Mass:	1008.50636
m/z:	505.26045
Charge:	2+
Retentiontime:	9.4765253067016
Score:	73.66463
Mass Error [ppm]:	0.10317
PEP:	0.020211
Annotation:	6 of 8
AminoAcids Coverag	75 %
Intensity Coverage:	33 %
Peak Coverage:	11 %
Protein Localisation:	558 ... 565

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439	1	A	7				
+0.005994	208.1536	2	K	6	954.5048		477.756	+0.230406
+0.068378	355.222	3	F	5	818.3956	−0.05587	818.3956	
	484.2646	4	E	4	671.3272	+0.039341	671.3272	
	598.3075	5	N	3	542.2846	+0.030116	542.2846	
	711.3916	6	L	2	428.2417		428.2417	
+0.151837	871.4222	7	C	1	315.1577	−0.052	315.1577	
		8	K	0	155.127	−0.11863	155.127	

Scan number	8166	**Raw file**	LNCAP_Silac_23F10_set3_09
Method	ITMS; CID	**Pepti...**	237.46



precursor information

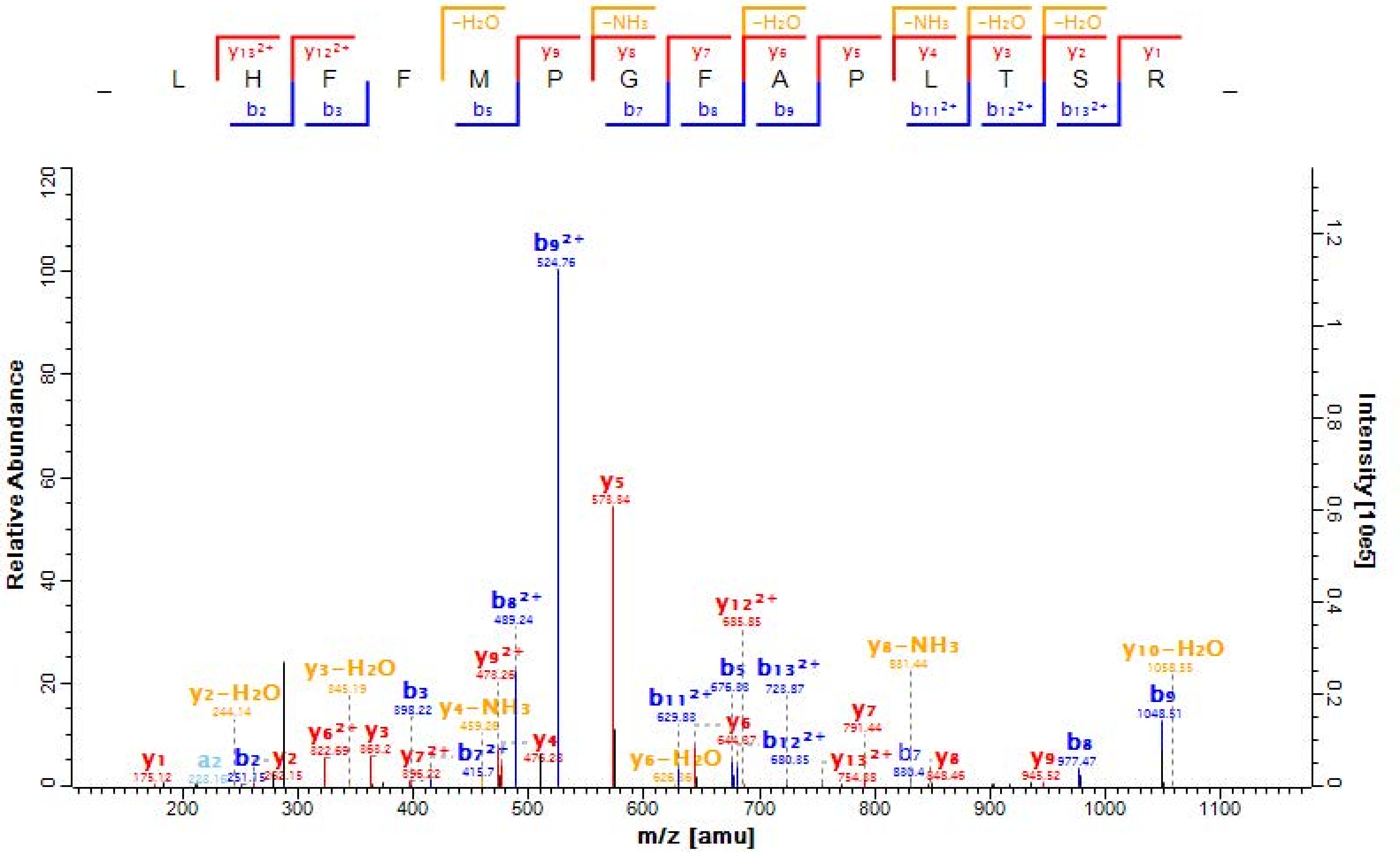
Mass:	2086.06961
m/z:	1044.04208
Charge:	2+
Retentiontime:	57.943073272705
Score:	237.4612
Mass Error [ppm]:	0.059993
PEP:	9.0519E-66
Precursor Type:	MULTI

general information

Annotation:	15 of 19
AminoAcids Coverag	79 %
Intensity Coverage:	52 %
Peak Coverage:	44 %
Protein Localisation:	104 ... 122

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.029		58.029	1	G	18				
	195.09		195.09	2	H	17	2030.1		2030.1	
	358.15	-0.141	358.15	3	Y	16	1893	-0.33	947	+0.1067
	459.2	+0.0435	459.2	4	T	15	1729.9	-0.112	1729.9	
	588.24	+0.0799	588.24	5	E	14	1628.9		1628.9	
	645.26		645.26	6	G	13	1499.8	-0.004	1499.8	
	716.3	-0.007	716.3	7	A	12	1442.8	-0.119	1442.8	
	845.34	-0.054	845.34	8	E	11	1371.8	-0.066	1371.8	
	958.43		958.43	9	L	10	1242.7	+0.0124	1242.7	
	1057.5	+0.0186	1057.5	10	V	9	1129.7	-0.127	1129.7	
	1172.5	-0.09	1172.5	11	D	8	1030.6	+0.1842	515.8	-0.411
	1259.6		1259.6	12	S	7	915.56	-0.016	915.56	
+0.3538	679.81	-0.023	1358.6	13	V	6	828.53	-0.109	828.53	
	1471.7	-0.017	1471.7	14	L	5	729.46	+0.0998	729.46	
-0.257	793.87	-0.01	1586.7	15	D	4	616.38	-0.119	616.38	
	1685.8	-0.035	1685.8	16	V	3	501.35	+0.0542	501.35	
	1784.9		1784.9	17	V	2	402.28	+0.2242	402.28	
	1941		1941	18	R	1	303.21		303.21	
				19	K	0	147.11		147.11	

Scan number	8170	**Raw file**	LNCAP_Silac_23F10_set3_09
Method	ITMS; CID	**Pepti...**	206.36



precursor information

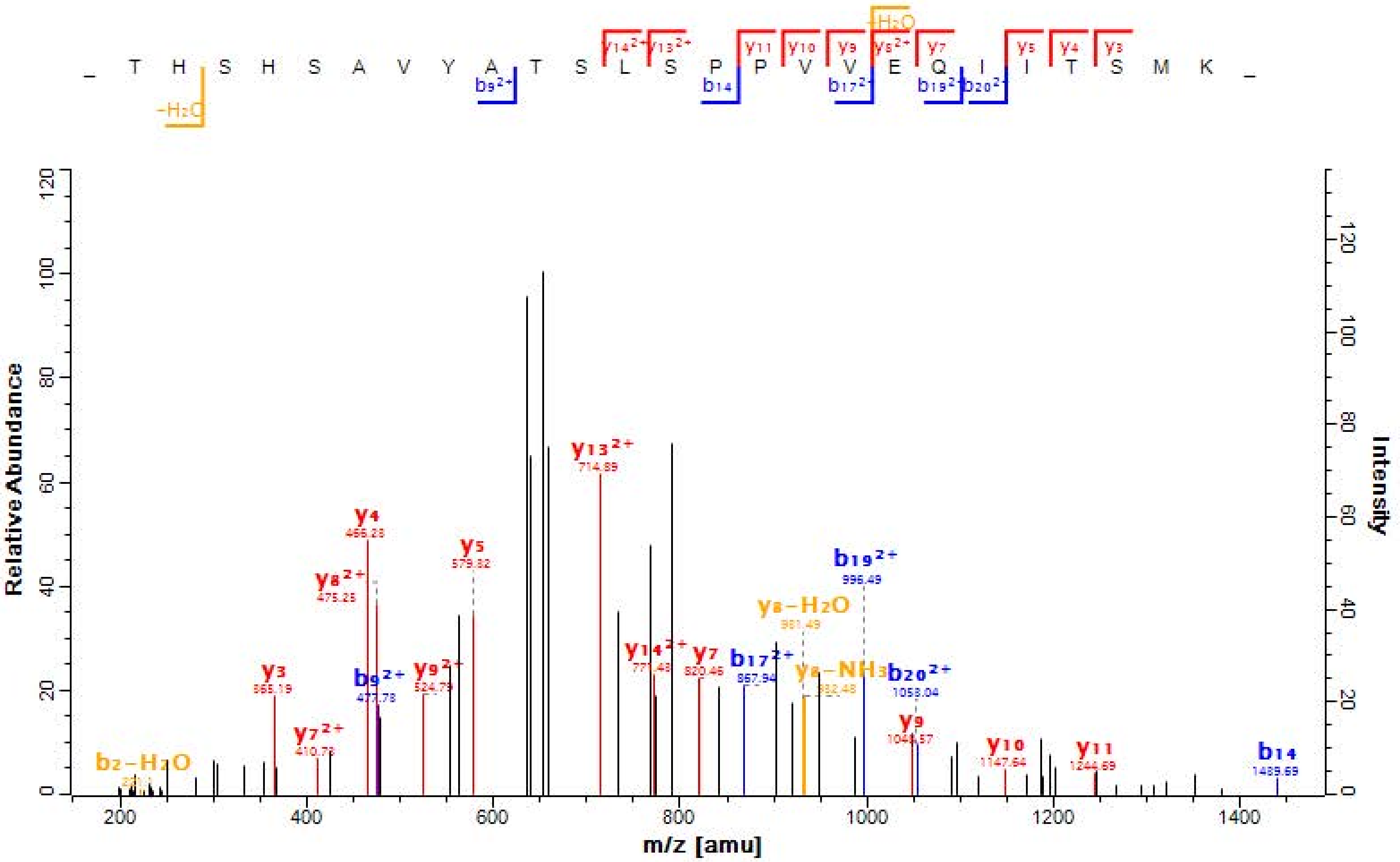
Mass:	1619.82835
m/z:	540.95006
Charge:	3+
Retentiontime:	57.980754852294
Score:	206.363
Mass Error [ppm]:	0.056618
PEP:	5.8354E-25
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	79 %
Peak Coverage:	43 %
Protein Localisation:	263 ... 276

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	13				
+0.179	223.2		251.2	+0.054	251.2	2	H	12	1508		754.4	-0.24
	370.2		398.2	+0.097	398.2	3	F	11	1371		685.8	+0.37
	517.3		545.3		545.3	4	F	10	1224		1224	
	648.3		676.3	+0.025	676.3	5	M	9	1077		1077	
	745.4		773.4		773.4	6	P	8	945.5	-0.11	473.3	+0.13
	802.4	+0.071	415.7	+0.01	830.4	7	G	7	848.5	+0.224	848.5	
	949.5	+0.205	489.2	-0.05	977.5	8	F	6	791.4	-0.07	396.2	+0.13
	1021	+0.226	524.8	-0.01	1049	9	A	5	644.4	+0.056	322.7	+0.13
	1118		1146		1146	10	P	4	573.3	+0.05	573.3	
	1231	+0.279	629.8		1259	11	L	3	476.3	+0.192	476.3	
	1332	+0.247	680.3		1360	12	T	2	363.2	+0.029	363.2	
	1419	+0.213	723.9		1447	13	S	1	262.2	+0.033	262.2	
						14	R	0	175.1	+0.221	175.1	

Scan number	8419	**Raw file**	LNCAP_Silac_23F10_set3_09
Method	ITMS; CID	**Pepti...**	69.77



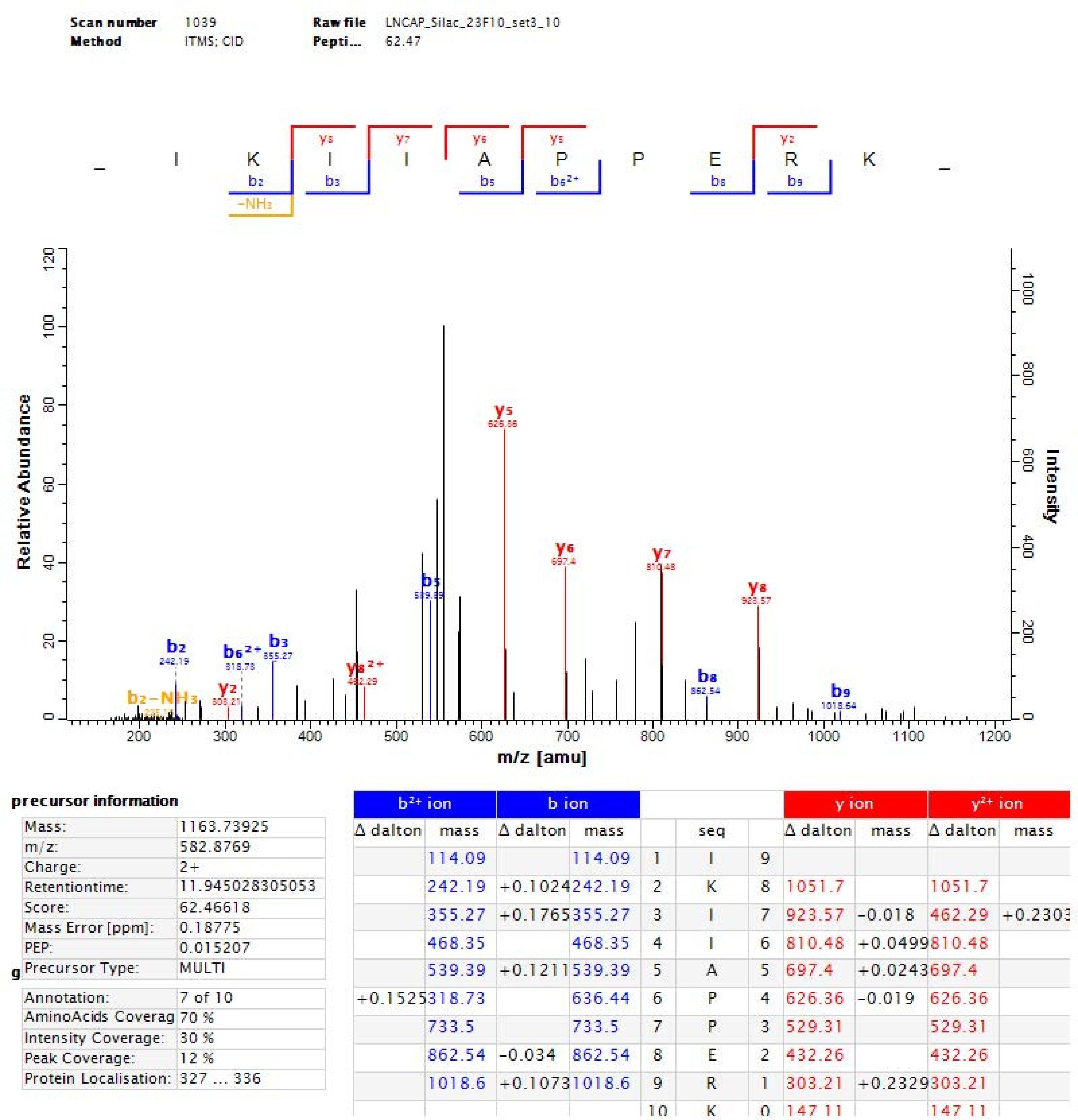
precursor information

Mass:	2682.3689
m/z:	671.5995
Charge:	4+
Retentiontime:	60.558139801025
Score:	69.76527
Mass Error [ppm]:	0.074235
PEP:	1.9491E-05
Precursor Type:	MULTI

general information

Annotation:	14 of 25
AminoAcids Coverag	56 %
Intensity Coverage:	29 %
Peak Coverage:	25 %
Protein Localisation:	400 ... 424

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	24				
	239.11		239.11	2	H	23	2582.3		2582.3	
	326.15		326.15	3	S	22	2445.3		2445.3	
	463.2		463.2	4	H	21	2358.2		2358.2	
	550.24		550.24	5	S	20	2221.2		2221.2	
	621.27		621.27	6	A	19	2134.1		2134.1	
	720.34		720.34	7	V	18	2063.1		2063.1	
	883.41		883.41	8	Y	17	1964		1964	
-0.05	477.73		954.44	9	A	16	1801		1801	
	1055.5		1055.5	10	T	15	1729.9		1729.9	
	1142.5		1142.5	11	S	14	1628.9		1628.9	
	1255.6		1255.6	12	L	13	1541.9		771.43	+0.376
	1342.6		1342.6	13	S	12	1428.8		714.89	+0.2558
	1439.7	-0.194	1439.7	14	P	11	1341.7		1341.7	
	1536.7		1536.7	15	P	10	1244.7	+0.0162	1244.7	
	1635.8		1635.8	16	V	9	1147.6	+0.2117	1147.6	
+0.2282	867.94		1734.9	17	V	8	1048.6	+0.1815	524.79	-0.391
	1863.9		1863.9	18	E	7	949.5		475.25	-0.227
-0.139	996.49		1992	19	Q	6	820.46	+0.4533	410.73	+0.4014
+0.4635	1053		2105.1	20	I	5	692.4		692.4	
	2218.2		2218.2	21	I	4	579.32	-0.036	579.32	
	2319.2		2319.2	22	T	3	466.23	-0.026	466.23	
	2406.2		2406.2	23	S	2	365.19	+0.1493	365.19	
	2537.3		2537.3	24	M	1	278.15		278.15	
				25	K	0	147.11		147.11	



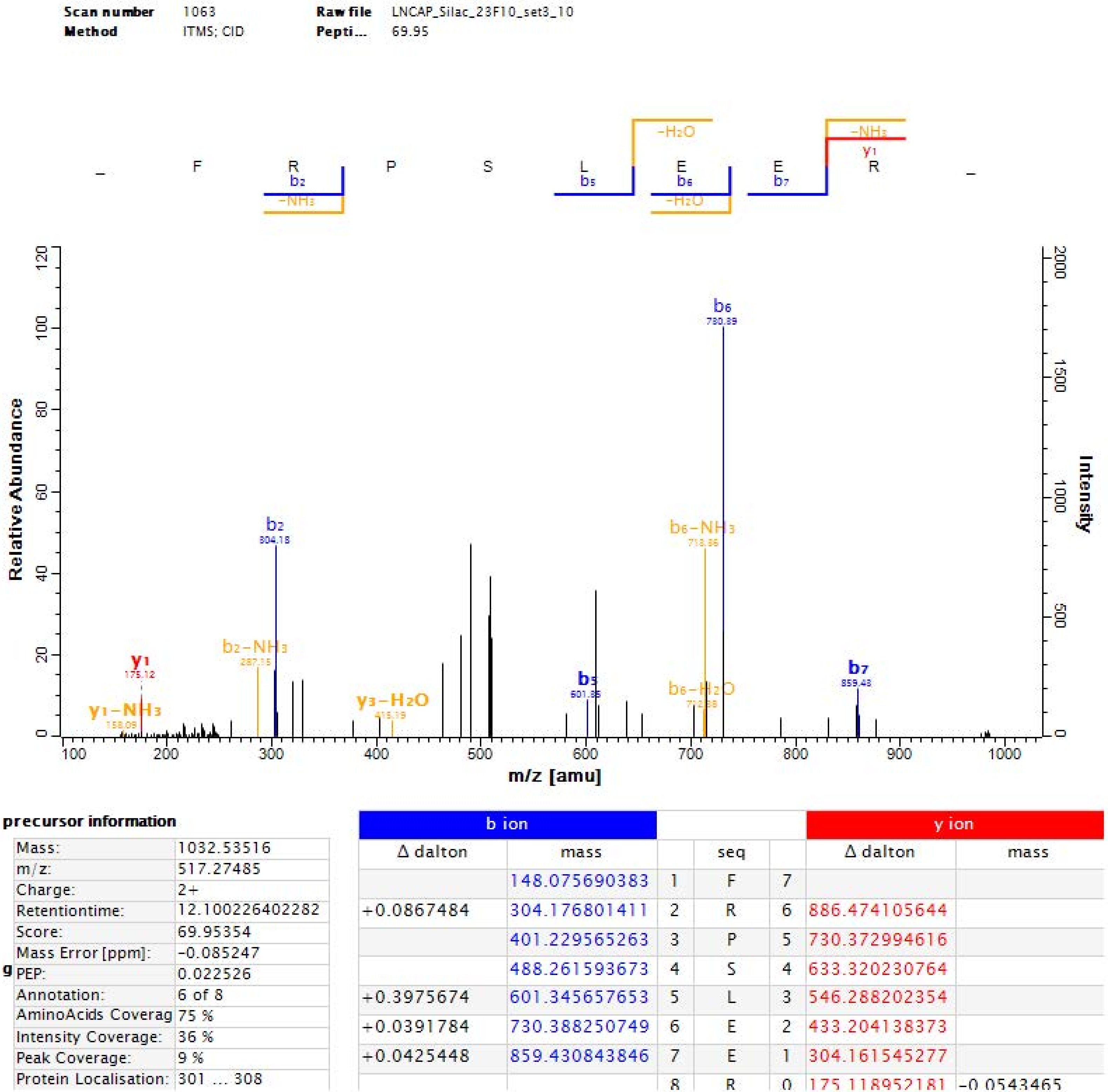
Scan number	1039	**Raw file**	LNCAP_Silac_23F10_set3_10
Method	ITMS; CID	**Pepti...**	62.47

precursor information

Mass:	1163.73925
m/z:	582.8769
Charge:	2+
Retentiontime:	11.945028305053
Score:	62.46618
Mass Error [ppm]:	0.18775
PEP:	0.015207
Precursor Type:	MULTI

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	30 %
Peak Coverage:	12 %
Protein Localisation:	327 ... 336

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09		114.09	1	I	9				
	242.19	+0.1024	242.19	2	K	8	1051.7		1051.7	
	355.27	+0.1765	355.27	3	I	7	923.57	-0.018	462.29	+0.2303
	468.35		468.35	4	I	6	810.48	+0.0499	810.48	
	539.39	+0.1211	539.39	5	A	5	697.4	+0.0243	697.4	
+0.1525	318.73		636.44	6	P	4	626.36	-0.019	626.36	
	733.5		733.5	7	P	3	529.31		529.31	
	862.54	-0.034	862.54	8	E	2	432.26		432.26	
	1018.6	+0.1073	1018.6	9	R	1	303.21	+0.2329	303.21	
				10	K	0	147.11		147.11	



Scan number	1063	**Raw file**	LNCAP_Silac_23F10_set3_10
Method	ITMS; CID	**Pepti...**	69.95

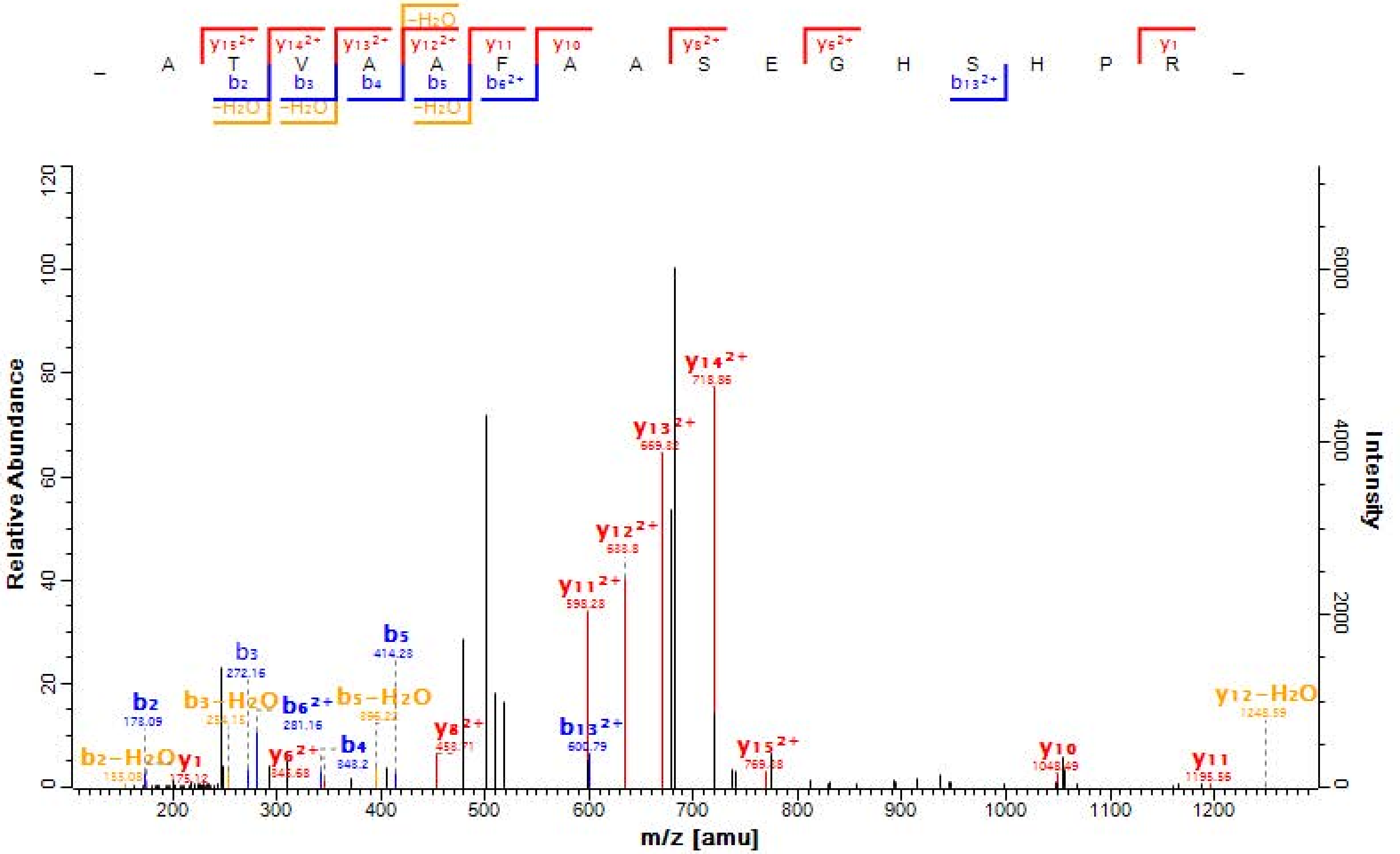
precursor information

g

Mass:	1032.53516
m/z:	517.27485
Charge:	2+
Retentiontime:	12.100226402282
Score:	69.95354
Mass Error [ppm]:	-0.085247
PEP:	0.022526
Annotation:	6 of 8
AminoAcids Coverag	75 %
Intensity Coverage:	36 %
Peak Coverage:	9 %
Protein Localisation:	301 ... 308

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	148.075690383	1	F	7		
+0.0867484	304.176801411	2	R	6	886.474105644	
	401.229565263	3	P	5	730.372994616	
	488.261593673	4	S	4	633.320230764	
+0.3975674	601.345657653	5	L	3	546.28802354	
+0.0391784	730.388250749	6	E	2	433.204138373	
+0.0425448	859.430843846	7	E	1	304.161545277	
		8	R	0	175.118952181	-0.0543465

Scan number	1081	**Raw file**	LNCAP_Silac_23F10_set3_10
Method	ITMS; CID	**Pepti...**	80.91



precursor information

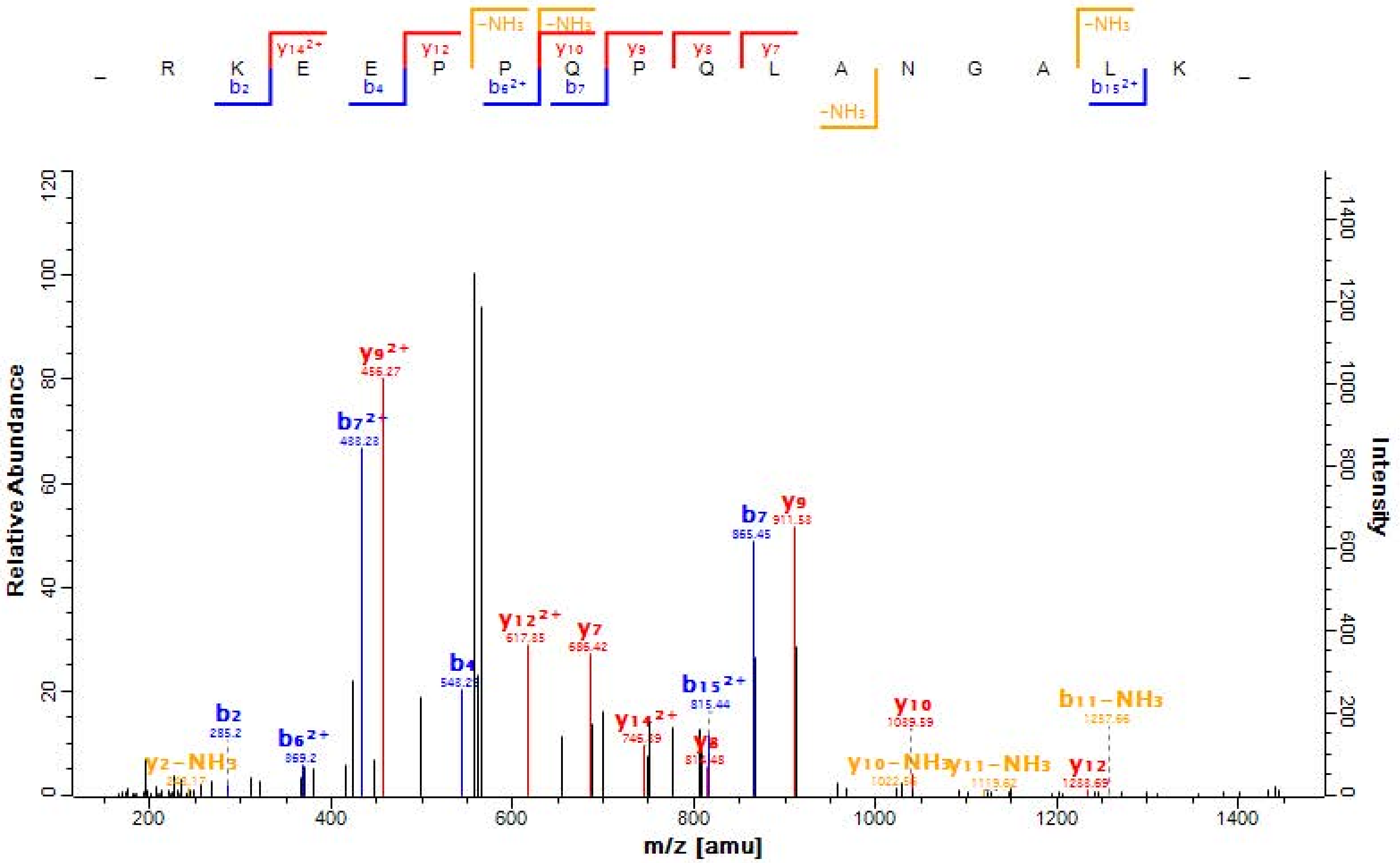
Mass:	1607.7803
m/z:	536.93404
Charge:	3+
Retentiontime:	12.210351943969
Score:	80.90513
Mass Error [ppm]:	-0.097665
PEP:	0.00019792
Precursor Type:	MULTI

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	35 %
Peak Coverage:	20 %
Protein Localisation:	92 ... 107

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044		72.044	1	A	15				
	173.09	+0.0783	173.09	2	T	14	1537.8		769.38	+0.2456
	272.16	-0.053	272.16	3	V	13	1436.7		718.86	+0.221
	343.2	-0.002	343.2	4	A	12	1337.6		669.32	+0.2852
	414.23	+0.0038	414.23	5	A	11	1266.6		633.8	+0.273
-0.099	281.16		561.3	6	F	10	1195.6	-0.029	598.28	+0.2749
	632.34		632.34	7	A	9	1048.5	+0.3792	1048.5	
	703.38		703.38	8	A	8	977.45		977.45	
	790.41		790.41	9	S	7	906.42		453.71	+0.1842
	919.45		919.45	10	E	6	819.39		819.39	
	976.47		976.47	11	G	5	690.34		345.68	+0.3847
	1113.5		1113.5	12	H	4	633.32		633.32	
-0.069	600.79		1200.6	13	S	3	496.26		496.26	
	1337.6		1337.6	14	H	2	409.23		409.23	
	1434.7		1434.7	15	P	1	272.17		272.17	
				16	R	0	175.12	+0.1215	175.12	

Scan number	1214	**Raw file**	LNCAP_Silac_23F10_set3_10
Method	ITMS; CID	**Pepti...**	62.29



precursor information

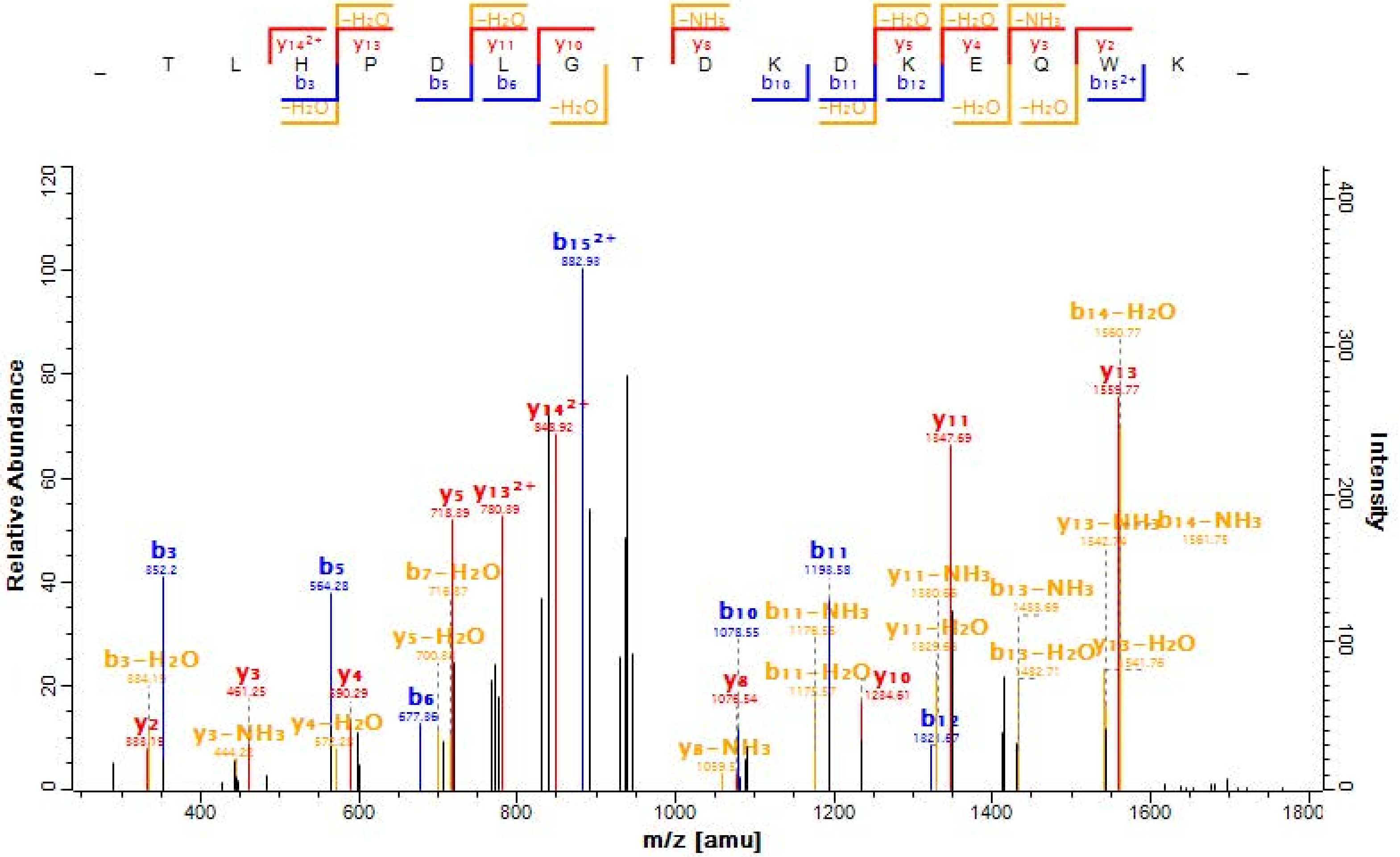
Mass:	1774.96952
m/z:	592.66378
Charge:	3+
Retentiontime:	13.100241661071
Score:	62.2875
Mass Error [ppm]:	0.30523
PEP:	0.0020388
Precursor Type:	MULTI

general information

Annotation:	11 of 16
AminoAcids Coverag	69 %
Intensity Coverage:	38 %
Peak Coverage:	17 %
Protein Localisation:	6 ... 21

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	157.11		157.11	1	R	15				
	285.2	−0.048	285.2	2	K	14	1619.9		1619.9	
	414.25		414.25	3	E	13	1491.8		746.39	−0.3
	543.29	−0.023	543.29	4	E	12	1362.7		1362.7	
	640.34		640.34	5	P	11	1233.7	−0.198	617.35	−0.049
−0.273	369.2		737.39	6	P	10	1136.6		1136.6	
+0.2138	433.23	+0.0225	865.45	7	Q	9	1039.6	+0.3875	1039.6	
	962.51		962.51	8	P	8	911.53	−0.038	456.27	+0.1162
	1090.6		1090.6	9	Q	7	814.48	+0.0195	814.48	
	1203.6		1203.6	10	L	6	686.42	−0.08	686.42	
	1274.7		1274.7	11	A	5	573.34		573.34	
	1388.7		1388.7	12	N	4	502.3		502.3	
	1445.7		1445.7	13	G	3	388.26		388.26	
	1516.8		1516.8	14	A	2	331.23		331.23	
+0.3717	815.44		1629.9	15	L	1	260.2		260.2	
				16	K	0	147.11		147.11	

Scan number	1364	**Raw file**	LNCAP_Silac_23F10_set3_10
Method	ITMS; CID	**Pepti...**	162.41



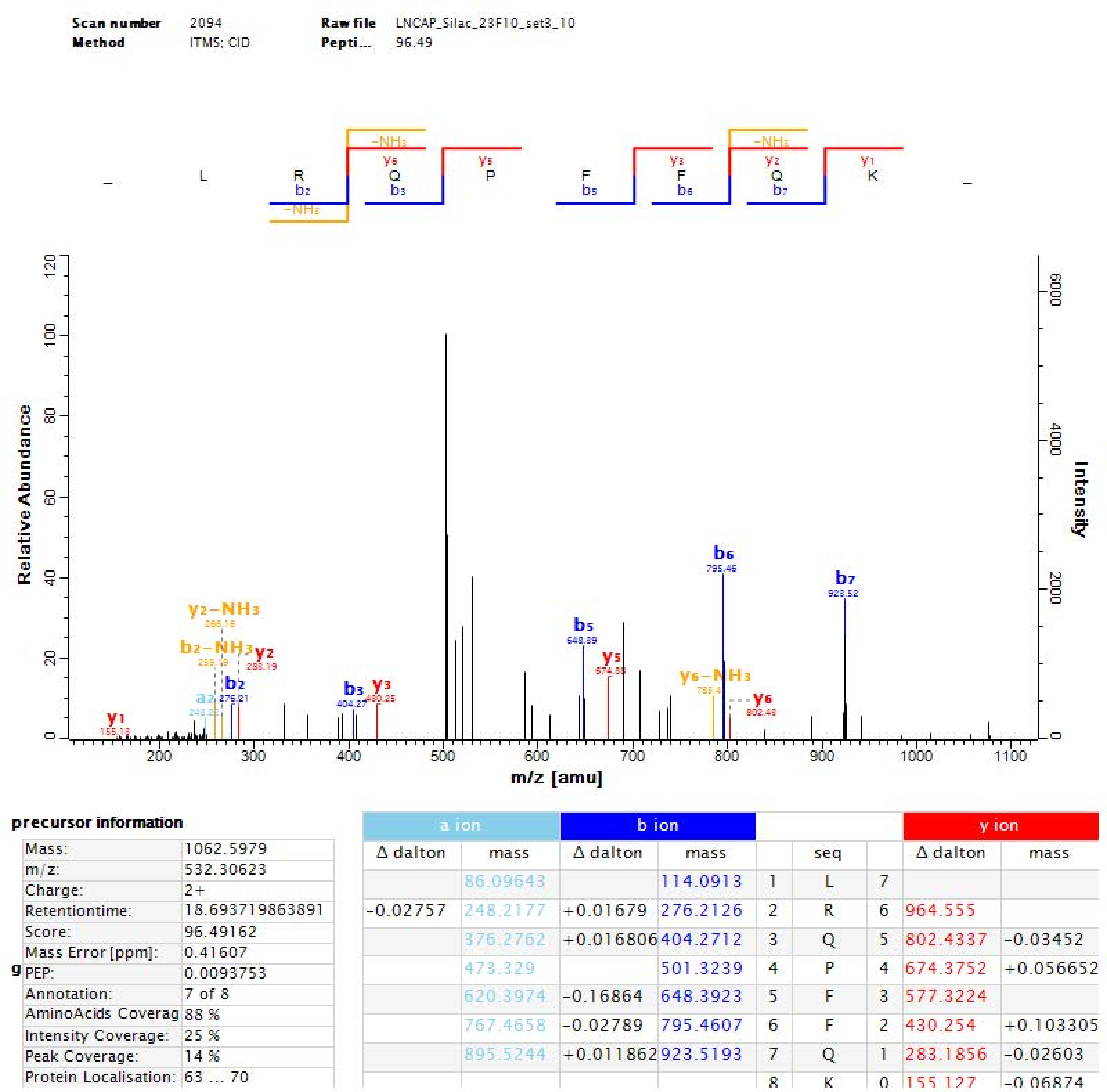
precursor information

Mass:	1909.95409
m/z:	955.98432
Charge:	2+
Retentiontime:	14.063008308410
Score:	162.407
Mass Error [ppm]:	0.3645
PEP:	4.0669E-20
Precursor Type:	MULTI

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	56 %
Peak Coverage:	42 %
Protein Localisation:	242 ... 257

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05		102.05	1	T	15				
	215.14		215.14	2	L	14	1809.9		1809.9	
	352.2	+0.0063	352.2	3	H	13	1696.8		848.92	+0.2777
	449.25		449.25	4	P	12	1559.8	−0.096	780.39	+0.2415
	564.28	−0.016	564.28	5	D	11	1462.7		1462.7	
	677.36	+0.1	677.36	6	L	10	1347.7	+0.0006	1347.7	
	734.38		734.38	7	G	9	1234.6	+0.0898	1234.6	
	835.43		835.43	8	T	8	1177.6		1177.6	
	950.46		950.46	9	D	7	1076.5	+0.1585	1076.5	
	1078.6	+0.1196	1078.6	10	K	6	961.51		961.51	
	1193.6	−0.093	1193.6	11	D	5	833.42		833.42	
	1321.7	+0.1291	1321.7	12	K	4	718.39	+0.0065	718.39	
	1450.7		1450.7	13	E	3	590.29	−0.018	590.29	
	1578.8		1578.8	14	Q	2	461.25	+0.0816	461.25	
+0.2894	882.93		1764.9	15	W	1	333.19	+0.035	333.19	
				16	K	0	147.11		147.11	



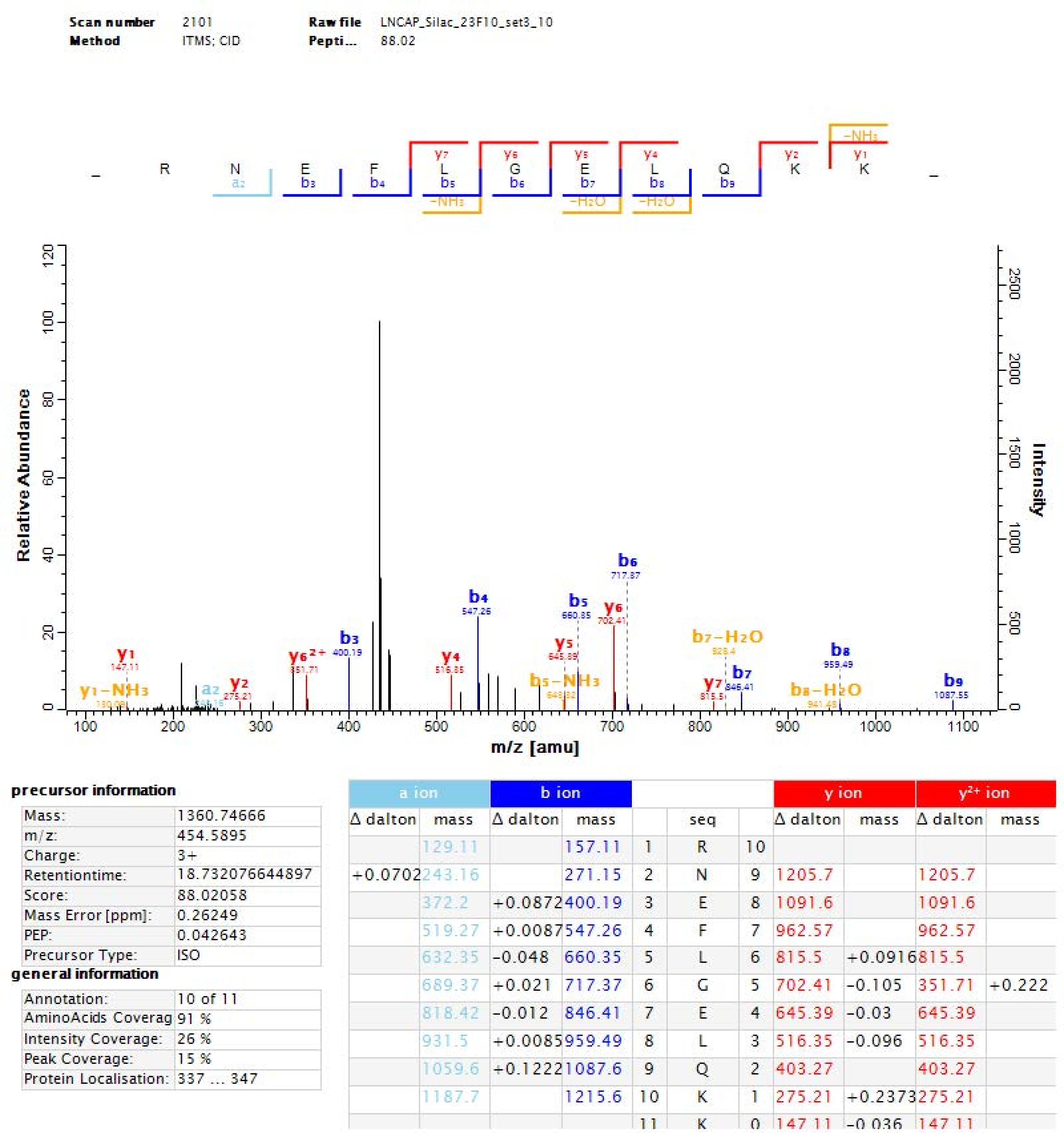
Scan number	2094	**Raw file**	LNCAP_Silac_23F10_set3_10
Method	ITMS; CID	**Pepti...**	96.49

precursor information

Mass:	1062.5979
m/z:	532.30623
Charge:	2+
Retentiontime:	18.693719863891
Score:	96.49162
Mass Error [ppm]:	0.41607
PEP:	0.0093753
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	25 %
Peak Coverage:	14 %
Protein Localisation:	63 ... 70

g

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	86.09643		114.0913	1	L	7		
-0.02757	248.2177	+0.01679	276.2126	2	R	6	964.555	
	376.2762	+0.016806	404.2712	3	Q	5	802.4337	-0.03452
	473.329		501.3239	4	P	4	674.3752	+0.056652
	620.3974	-0.16864	648.3923	5	F	3	577.3224	
	767.4658	-0.02789	795.4607	6	F	2	430.254	+0.103305
	895.5244	+0.011862	923.5193	7	Q	1	283.1856	-0.02603
				8	K	0	155.127	-0.06874



Scan number 2101

Raw file LNCAP_Silac_23F10_set3_10

Method ITMS; CID

Pepti... 88.02

precursor information

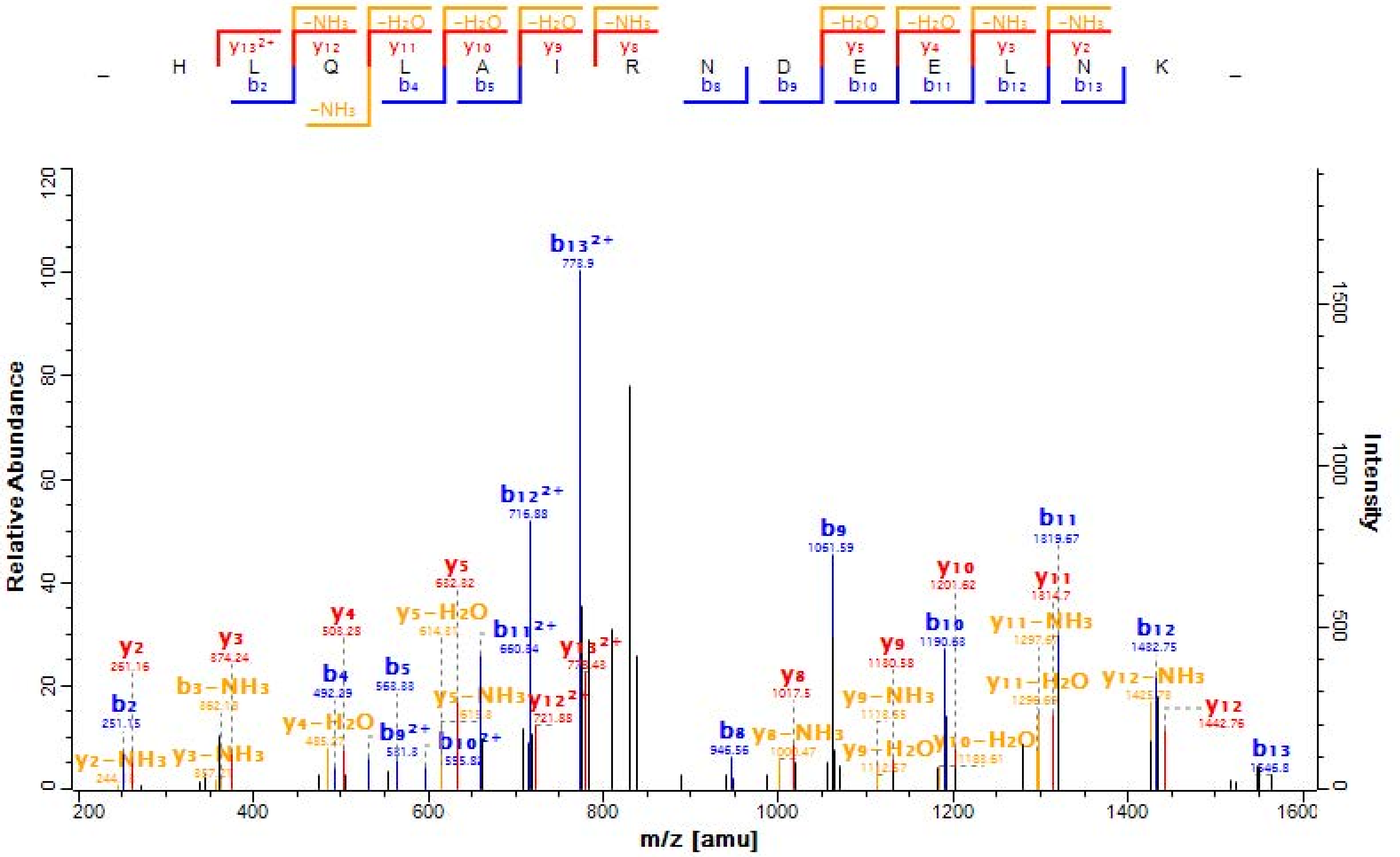
Mass:	1360.74666
m/z:	454.5895
Charge:	3+
Retentiontime:	18.732076644897
Score:	88.02058
Mass Error [ppm]:	0.26249
PEP:	0.042643
Precursor Type:	ISO

general information

Annotation:	10 of 11
AminoAcids Coverag	91 %
Intensity Coverage:	26 %
Peak Coverage:	15 %
Protein Localisation:	337 ... 347

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.11		157.11	1	R	10				
+0.0702	243.16		271.15	2	N	9	1205.7		1205.7	
	372.2	+0.0872	400.19	3	E	8	1091.6		1091.6	
	519.27	+0.0087	547.26	4	F	7	962.57		962.57	
	632.35	-0.048	660.35	5	L	6	815.5	+0.0916	815.5	
	689.37	+0.021	717.37	6	G	5	702.41	-0.105	351.71	+0.222
	818.42	-0.012	846.41	7	E	4	645.39	-0.03	645.39	
	931.5	+0.0085	959.49	8	L	3	516.35	-0.096	516.35	
	1059.6	+0.1222	1087.6	9	Q	2	403.27		403.27	
	1187.7		1215.6	10	K	1	275.21	+0.2373	275.21	
				11	K	0	147.11	-0.036	147.11	

Scan number	2135	**Raw file**	LNCAP_Silac_23F10_set3_10
Method	ITMS; CID	**Pepti...**	259.7



precursor information

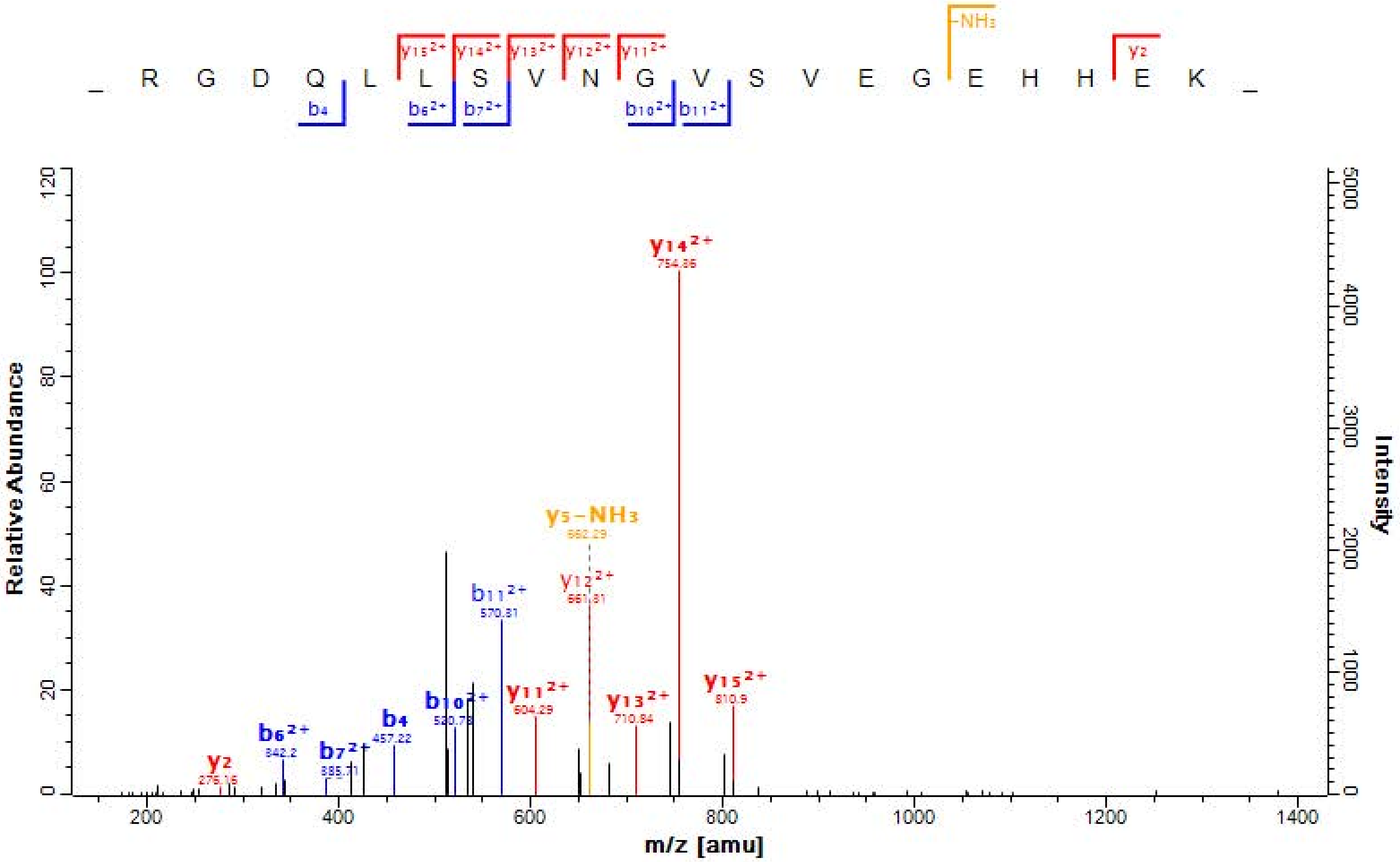
Mass:	1691.89588
m/z:	846.95522
Charge:	2+
Retentiontime:	18.953710556030
Score:	259.697
Mass Error [ppm]:	0.23573
PEP:	8.791E-51
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	55 %
Peak Coverage:	49 %
Protein Localisation:	83 ... 96

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.07		138.07	1	H	13				
	251.15	-0.015	251.15	2	L	12	1555.8		778.43	+0.3359
	379.21		379.21	3	Q	11	1442.8	-0.122	721.88	-0.023
	492.29	+0.0283	492.29	4	L	10	1314.7	-0.058	1314.7	
	563.33	+0.0551	563.33	5	A	9	1201.6	+0.0284	1201.6	
	676.41		676.41	6	I	8	1130.6	+0.0977	1130.6	
	832.52		832.52	7	R	7	1017.5	-0.157	1017.5	
	946.56	-0.059	946.56	8	N	6	861.39		861.39	
+0.2722	531.3	+0.0103	1061.6	9	D	5	747.35		747.35	
+0.4642	595.82	+0.01	1190.6	10	E	4	632.32	+0.1076	632.32	
+0.1435	660.34	-0.049	1319.7	11	E	3	503.28	+0.1653	503.28	
+0.2025	716.88	+0.0285	1432.8	12	L	2	374.24	+0.043	374.24	
+0.3262	773.9	+0.2241	1546.8	13	N	1	261.16	+0.0824	261.16	
				14	K	0	147.11		147.11	

Scan number	2272	**Raw file**	LNCAP_Silac_23F10_set3_10
Method	ITMS; CID	**Pepti...**	32.18



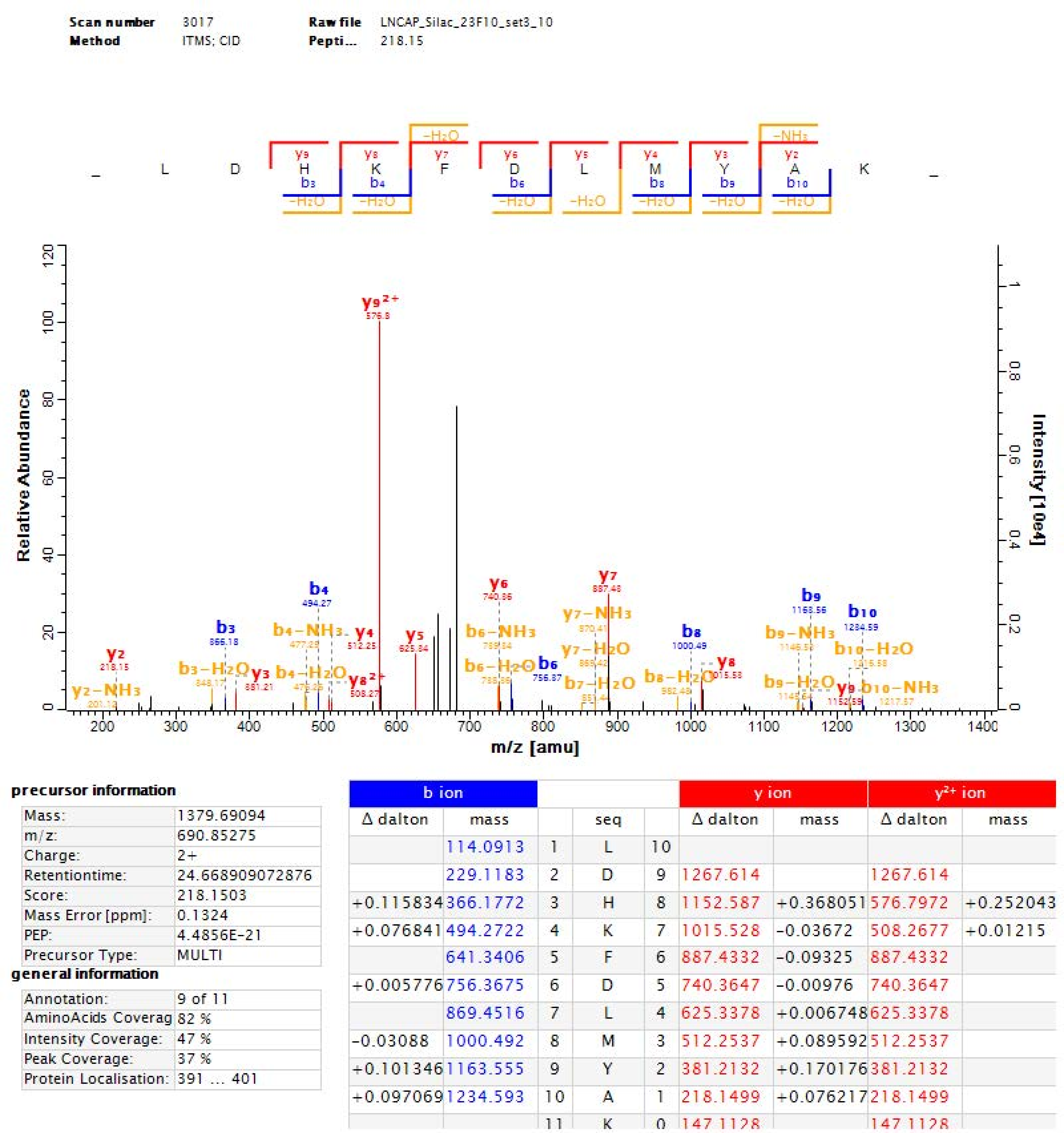
precursor information

Mass:	2189.08319
m/z:	548.27808
Charge:	4+
Retentiontime:	19.793272018432
Score:	32.18085
Mass Error [ppm]:	0.31389
PEP:	0.044459
Precursor Type:	MULTI

general information

Annotation:	10 of 20
AminoAcids Coverag	50 %
Intensity Coverage:	57 %
Peak Coverage:	16 %
Protein Localisation:	151 ... 170

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	157.11		157.11	1	R	19				
	214.13		214.13	2	G	18	2034		2034	
	329.16		329.16	3	D	17	1977		1977	
	457.22	+0.177	457.22	4	Q	16	1861.9		1861.9	
	570.3		570.3	5	L	15	1733.9		1733.9	
+0.0085	342.2		683.38	6	L	14	1620.8		810.9	+0.1767
+0.0381	385.71		770.42	7	S	13	1507.7		754.36	+0.2164
	869.48		869.48	8	V	12	1420.7		710.84	-0.003
	983.53		983.53	9	N	11	1321.6		661.31	+0.0002
+0.2232	520.78		1040.5	10	G	10	1207.6		604.29	+0.3679
+0.0318	570.31		1139.6	11	V	9	1150.5		1150.5	
	1226.6		1226.6	12	S	8	1051.5		1051.5	
	1325.7		1325.7	13	V	7	964.45		964.45	
	1454.8		1454.8	14	E	6	865.38		865.38	
	1511.8		1511.8	15	G	5	736.34		736.34	
	1640.8		1640.8	16	E	4	679.32		679.32	
	1777.9		1777.9	17	H	3	550.27		550.27	
	1914.9		1914.9	18	H	2	413.21		413.21	
	2044		2044	19	E	1	276.16	+0.006	276.16	
				20	K	0	147.11		147.11	



Scan number	3017	**Raw file**	LNCAP_Silac_23F10_set3_10
Method	ITMS; CID	**Pepti...**	218.15

precursor information

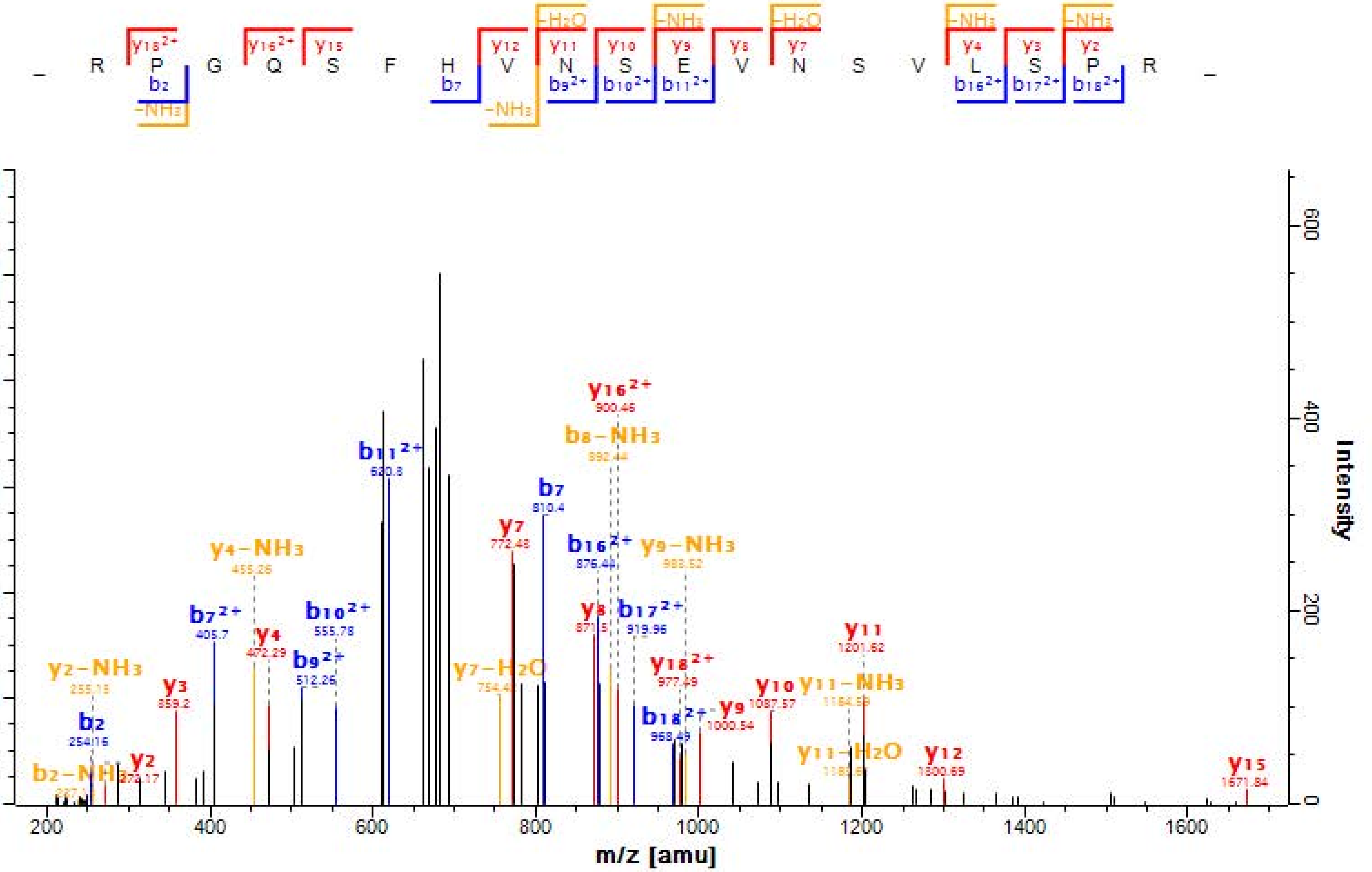
Mass:	1379.69094
m/z:	690.85275
Charge:	2+
Retentiontime:	24.668909072876
Score:	218.1503
Mass Error [ppm]:	0.1324
PEP:	4.4856E-21
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	47 %
Peak Coverage:	37 %
Protein Localisation:	391 ... 401

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913	1	L	10				
	229.1183	2	D	9	1267.614		1267.614	
+0.115834	366.1772	3	H	8	1152.587	+0.368051	576.7972	+0.252043
+0.076841	494.2722	4	K	7	1015.528	-0.03672	508.2677	+0.01215
	641.3406	5	F	6	887.4332	-0.09325	887.4332	
+0.005776	756.3675	6	D	5	740.3647	-0.00976	740.3647	
	869.4516	7	L	4	625.3378	+0.006748	625.3378	
-0.03088	1000.492	8	M	3	512.2537	+0.089592	512.2537	
+0.101346	1163.555	9	Y	2	381.2132	+0.170176	381.2132	
+0.097069	1234.593	10	A	1	218.1499	+0.076217	218.1499	
		11	K	0	147.1128		147.1128	

Scan number	3451	**Raw file**	LNCAP_Silac_23F10_set3_10
Method	ITMS; CID	**Pepti...**	125.86



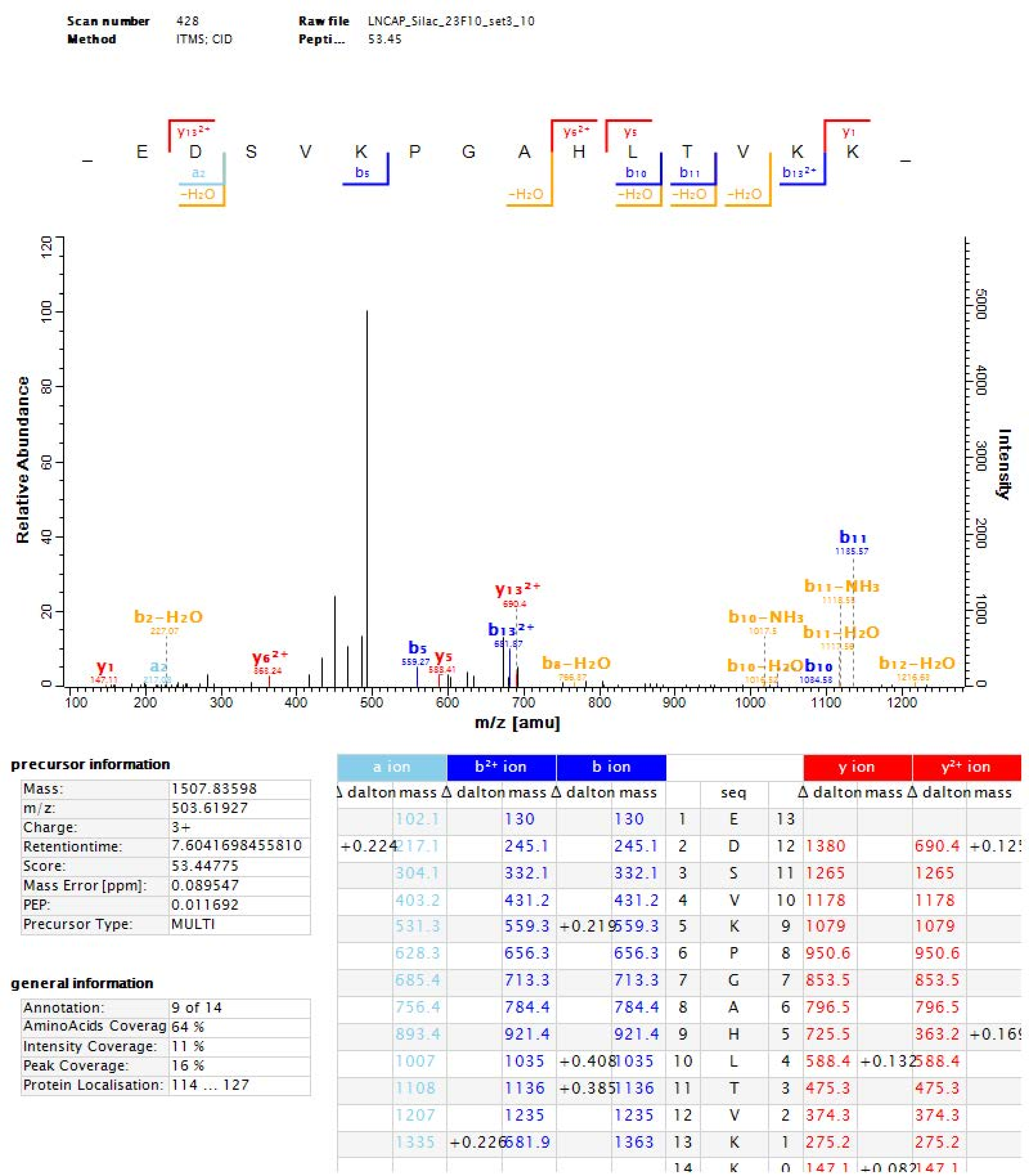
precursor information

Mass:	2109.07027
m/z:	704.0307
Charge:	3+
Retentiontime:	27.437892913818
Score:	125.8601
Mass Error [ppm]:	-0.60685
PEP:	1.1866E-07
Precursor Type:	ISO

general information

Annotation:	13 of 19
AminoAcids Coverag	68 %
Intensity Coverage:	37 %
Peak Coverage:	32 %
Protein Localisation:	229 ... 247

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	157.11		157.11	1	R	18				
	254.16	-0.059	254.16	2	P	17	1954		977.49	-0.024
	311.18		311.18	3	G	16	1856.9		1856.9	
	439.24		439.24	4	Q	15	1799.9		900.46	+0.2952
	526.27		526.27	5	S	14	1671.8	-0.04	1671.8	
	673.34		673.34	6	F	13	1584.8		1584.8	
+0.0115	405.7	-0.016	810.4	7	H	12	1437.7		1437.7	
	909.47		909.47	8	V	11	1300.7	-0.086	1300.7	
+0.0851	512.26		1023.5	9	N	10	1201.6	-0.069	1201.6	
+0.1706	555.78		1110.5	10	S	9	1087.6	-0.06	1087.6	
+0.1669	620.3		1239.6	11	E	8	1000.5	-0.13	1000.5	
	1338.7		1338.7	12	V	7	871.5	-0.066	871.5	
	1452.7		1452.7	13	N	6	772.43	+0.0089	772.43	
	1539.7		1539.7	14	S	5	658.39		658.39	
	1638.8		1638.8	15	V	4	571.36		571.36	
+0.104	876.44		1751.9	16	L	3	472.29	+0.1419	472.29	
+0.3248	919.96		1838.9	17	S	2	359.2	+0.0908	359.2	
+0.2157	968.49		1936	18	P	1	272.17	+0.0165	272.17	
				19	R	0	175.12		175.12	



Scan number	428	**Raw file**	LNCAP_Silac_23F10_set3_10
Method	ITMS; CID	**Pepti...**	53.45

precursor information

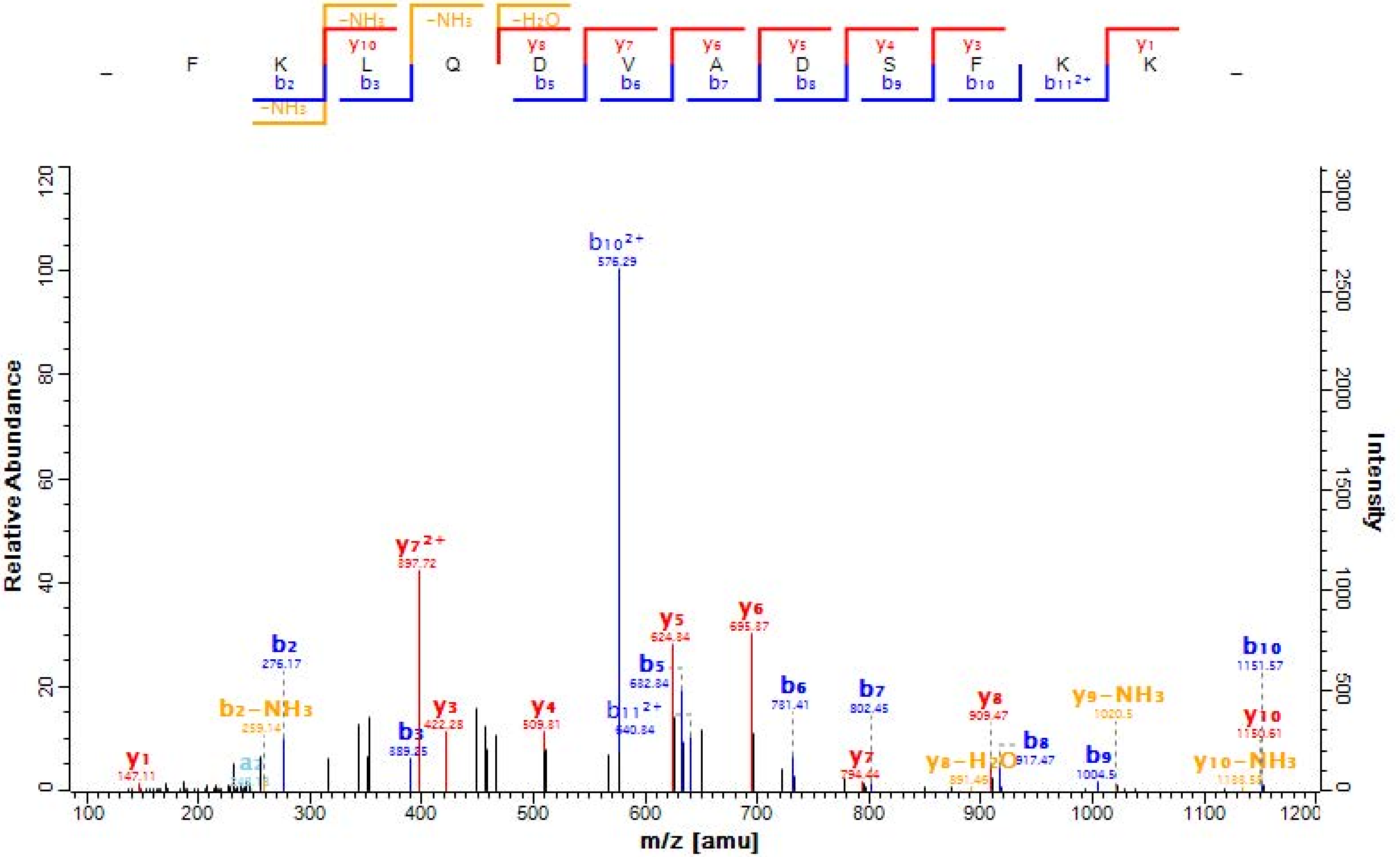
Mass:	1507.83598
m/z:	503.61927
Charge:	3+
Retentiontime:	7.6041698455810
Score:	53.44775
Mass Error [ppm]:	0.089547
PEP:	0.011692
Precursor Type:	MULTI

general information

Annotation:	9 of 14
AminoAcids Coverag	64 %
Intensity Coverage:	11 %
Peak Coverage:	16 %
Protein Localisation:	114 ... 127

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.1		130		130	1	E	13				
+0.224	217.1		245.1		245.1	2	D	12	1380		690.4	+0.12
	304.1		332.1		332.1	3	S	11	1265		1265	
	403.2		431.2		431.2	4	V	10	1178		1178	
	531.3		559.3	+0.219	559.3	5	K	9	1079		1079	
	628.3		656.3		656.3	6	P	8	950.6		950.6	
	685.4		713.3		713.3	7	G	7	853.5		853.5	
	756.4		784.4		784.4	8	A	6	796.5		796.5	
	893.4		921.4		921.4	9	H	5	725.5		363.2	+0.16
	1007		1035	+0.408	1035	10	L	4	588.4	+0.132	588.4	
	1108		1136	+0.385	1136	11	T	3	475.3		475.3	
	1207		1235		1235	12	V	2	374.3		374.3	
	1335	+0.226	681.9		1363	13	K	1	275.2		275.2	
						14	K	0	147.1	+0.082	147.1	

Scan number	4426	**Raw file**	LNCAP_Silac_23F10_set3_10
Method	ITMS; CID	**Pepti...**	127.02



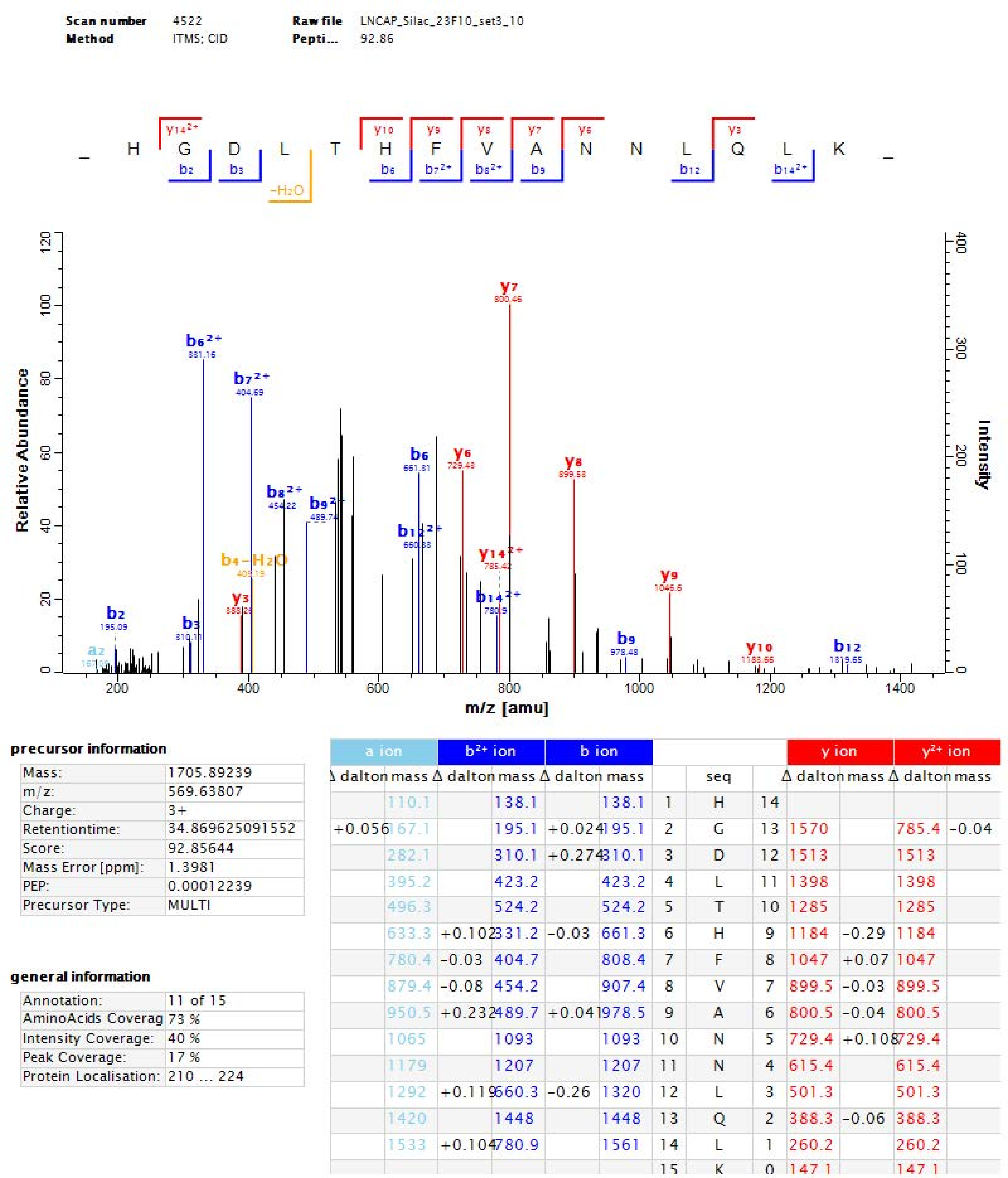
precursor information

Mass:	1424.76596
m/z:	475.92926
Charge:	3+
Retentiontime:	34.167804718017
Score:	127.0177
Mass Error [ppm]:	-0.2831
PEP:	1.8291E-05
Precursor Type:	MULTI

general information

Annotation:	11 of 12
AminoAcids Coverag	92 %
Intensity Coverage:	57 %
Peak Coverage:	19 %
Protein Localisation:	2423 ... 2434

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.1		148.1		148.1	1	F	11				
-0.05	248.2		276.2	+0.07	276.2	2	K	10	1279		1279	
	361.3		389.3	-0.11	389.3	3	L	9	1151	+0.387	1151	
	489.3		517.3		517.3	4	Q	8	1038		1038	
	604.3		632.3	+0.058	632.3	5	D	7	909.5	-0.09	909.5	
	703.4		731.4	+0.001	731.4	6	V	6	794.4	+0.125	397.7	+0.16
	774.5		802.4	+0.172	802.4	7	A	5	695.4	+0.004	695.4	
	889.5		917.5	-0.01	917.5	8	D	4	624.3	+0.053	624.3	
	976.5		1005	-0.04	1005	9	S	3	509.3	+0.057	509.3	
	1124	-0.23	576.3	+0.346	1152	10	F	2	422.3	+0.007	422.3	
	1252	-0.18	640.3		1280	11	K	1	275.2		275.2	
						12	K	0	147.1	+0.047	147.1	



Scan number	4522	**Raw file**	LNCAP_Silac_23F10_set3_10
Method	ITMS; CID	**Pepti...**	92.86

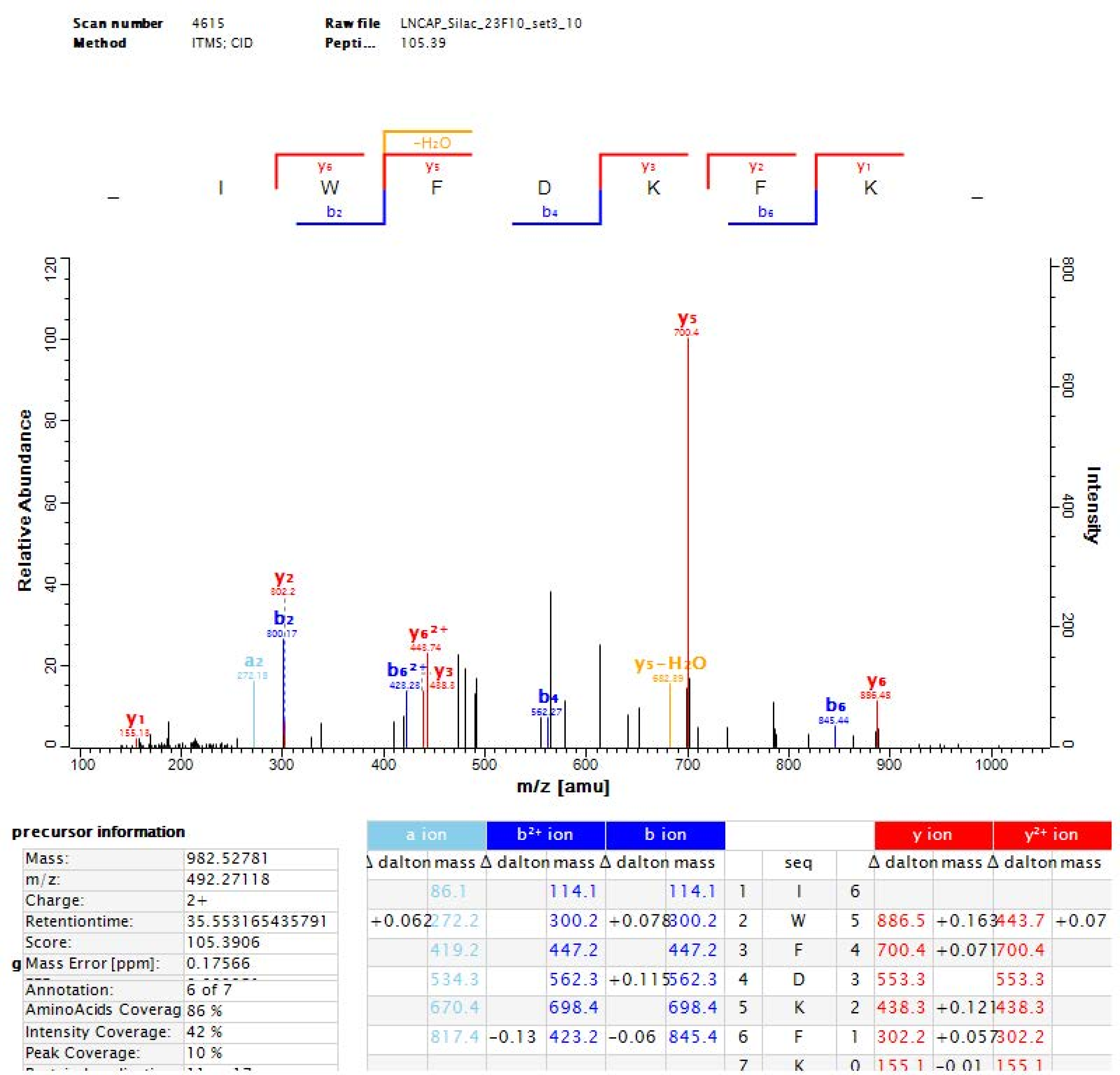
precursor information

Mass:	1705.89239
m/z:	569.63807
Charge:	3+
Retentiontime:	34.869625091552
Score:	92.85644
Mass Error [ppm]:	1.3981
PEP:	0.00012239
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	40 %
Peak Coverage:	17 %
Protein Localisation:	210 ... 224

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	110.1		138.1		138.1	1	H	14				
+0.056	167.1		195.1	+0.024	195.1	2	G	13	1570		785.4	-0.04
	282.1		310.1	+0.274	310.1	3	D	12	1513		1513	
	395.2		423.2		423.2	4	L	11	1398		1398	
	496.3		524.2		524.2	5	T	10	1285		1285	
	633.3	+0.102	331.2	-0.03	661.3	6	H	9	1184	-0.29	1184	
	780.4	-0.03	404.7		808.4	7	F	8	1047	+0.07	1047	
	879.4	-0.08	454.2		907.4	8	V	7	899.5	-0.03	899.5	
	950.5	+0.232	489.7	+0.041	978.5	9	A	6	800.5	-0.04	800.5	
	1065		1093		1093	10	N	5	729.4	+0.108	729.4	
	1179		1207		1207	11	N	4	615.4		615.4	
	1292	+0.119	660.3	-0.26	1320	12	L	3	501.3		501.3	
	1420		1448		1448	13	Q	2	388.3	-0.06	388.3	
	1533	+0.104	780.9		1561	14	L	1	260.2		260.2	
						15	K	0	147.1		147.1	



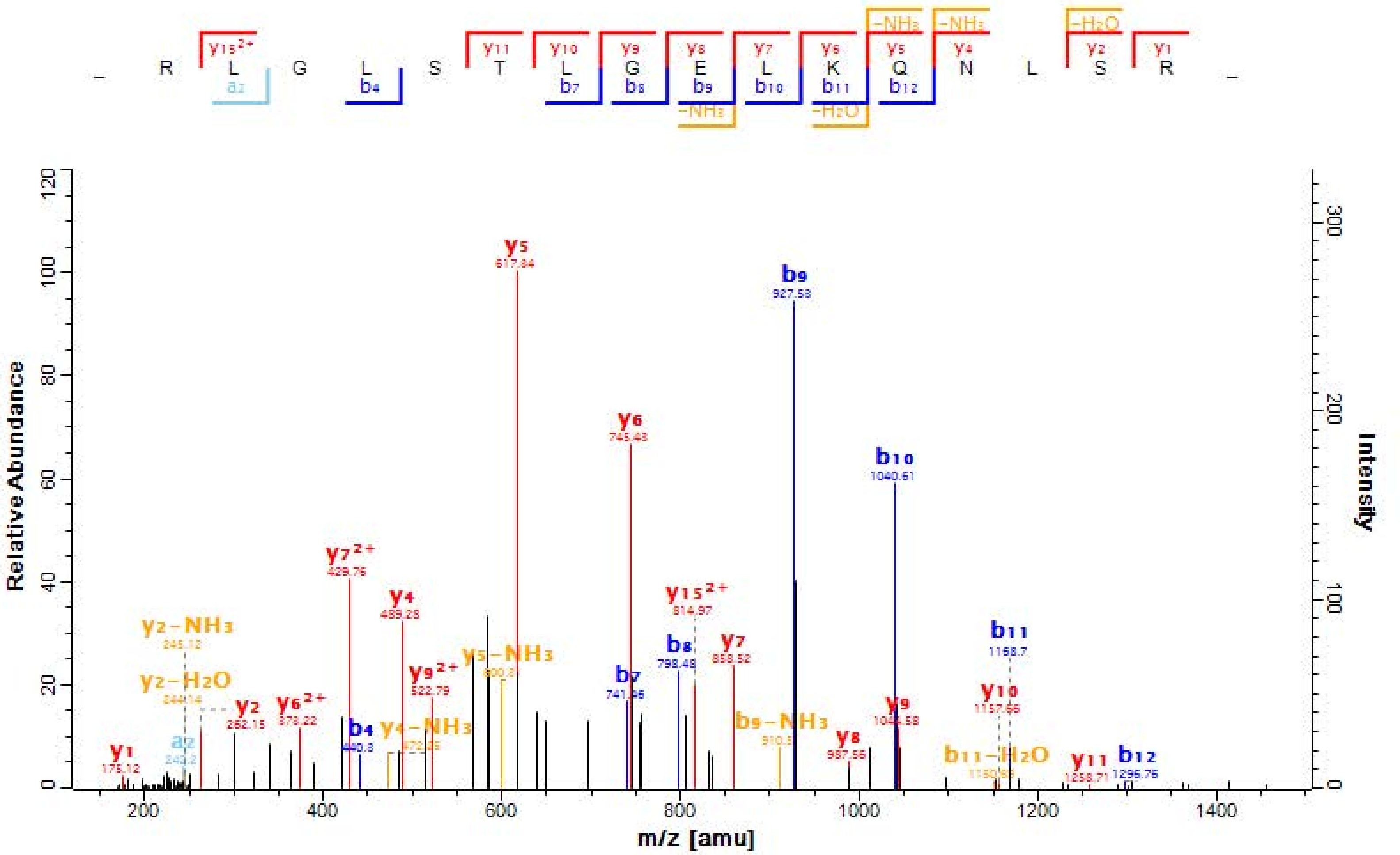
Scan number	4615	**Raw file**	LNCAP_Silac_23F10_set3_10
Method	ITMS; CID	**Pepti...**	105.39

precursor information

Mass:	982.52781
m/z:	492.27118
Charge:	2+
Retentiontime:	35.553165435791
Score:	105.3906
g Mass Error [ppm]:	0.17566
Annotation:	6 of 7
AminoAcids Coverag	86 %
Intensity Coverage:	42 %
Peak Coverage:	10 %

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	I	6				
+0.062	272.2		300.2	+0.078	300.2	2	W	5	886.5	+0.163	443.7	+0.07
	419.2		447.2		447.2	3	F	4	700.4	+0.071	700.4	
	534.3		562.3	+0.115	562.3	4	D	3	553.3		553.3	
	670.4		698.4		698.4	5	K	2	438.3	+0.121	438.3	
	817.4	-0.13	423.2	-0.06	845.4	6	F	1	302.2	+0.057	302.2	
						7	K	0	155.1	-0.01	155.1	

Scan number	5032	**Raw file**	LNCAP_Silac_23F10_set3_10
Method	ITMS; CID	**Pepti...**	128.74



precursor information

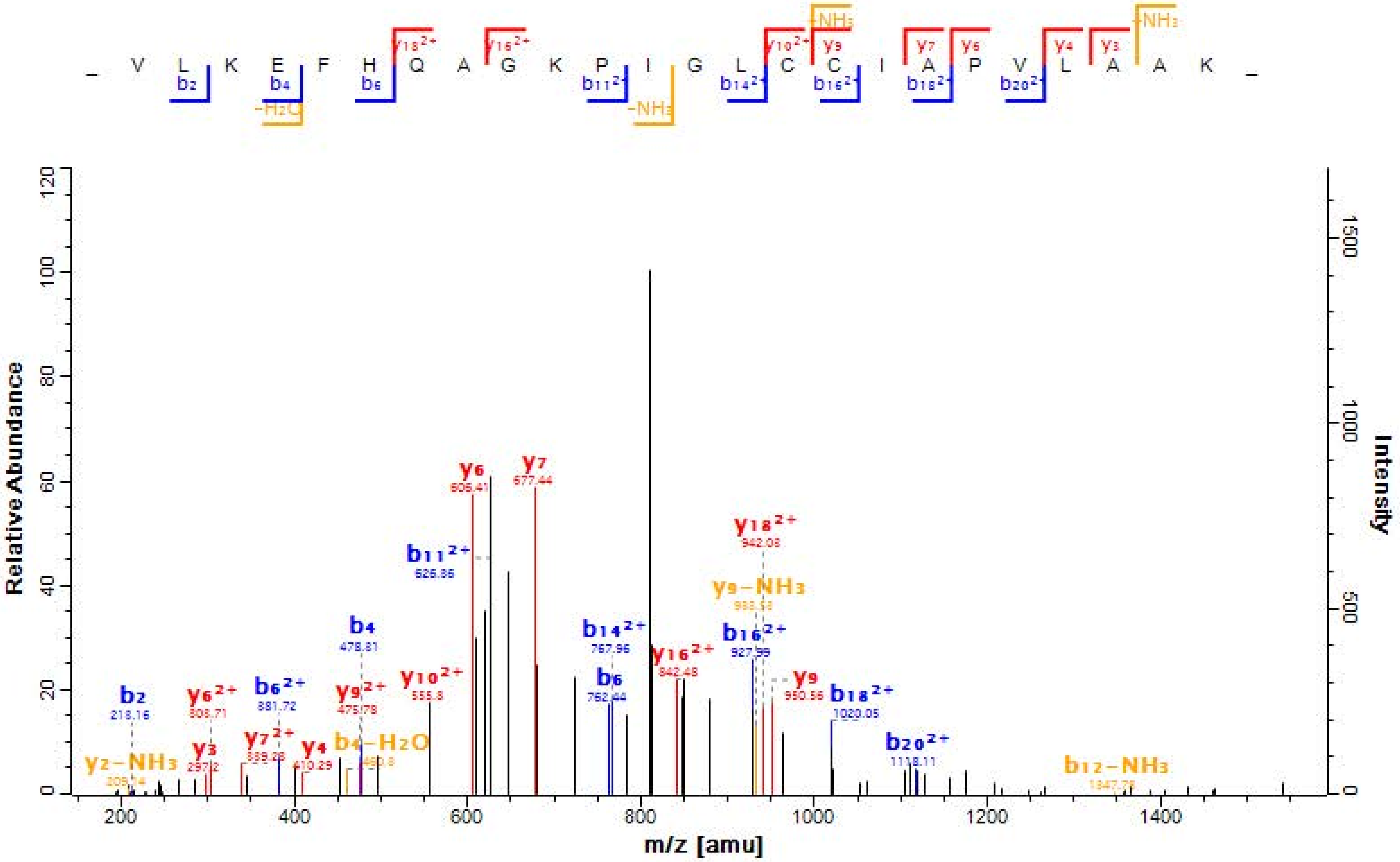
Mass:	1784.02692
m/z:	595.68292
Charge:	3+
Retentiontime:	38.840103149414
Score:	128.7379
Mass Error [ppm]:	0.051681
PEP:	3.094E-10
Precursor Type:	MULTI

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	57 %
Peak Coverage:	25 %
Protein Localisation:	80 ... 95

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.11		157.11	1	R	15				
+0.0364	242.2		270.19	2	L	14	1628.9		814.97	+0.0965
	299.22		327.21	3	G	13	1515.8		1515.8	
	412.3	+0.0137	440.3	4	L	12	1458.8		1458.8	
	499.34		527.33	5	S	11	1345.7		1345.7	
	600.38		628.38	6	T	10	1258.7	-0.062	1258.7	
	713.47	-0.034	741.46	7	L	9	1157.7	-0.096	1157.7	
	770.49	+0.0831	798.48	8	G	8	1044.6	-0.2	522.79	+0.1102
	899.53	+0.0272	927.53	9	E	7	987.56	+0.1171	987.56	
	1012.6	-0.051	1040.6	10	L	6	858.52	+0.0779	429.76	+0.1053
	1140.7	+0.027	1168.7	11	K	5	745.43	+0.0245	373.22	+0.2069
	1268.8	-0.029	1296.8	12	Q	4	617.34	+0.0538	617.34	
	1382.8		1410.8	13	N	3	489.28	-0.095	489.28	
	1495.9		1523.9	14	L	2	375.24		375.24	
	1582.9		1610.9	15	S	1	262.15	+0.0329	262.15	
				16	R	0	175.12	-0.154	175.12	

Scan number	5180	**Raw file**	LNCAP_Silac_23F10_set3_10
Method	ITMS; CID	**Pepti...**	92.39



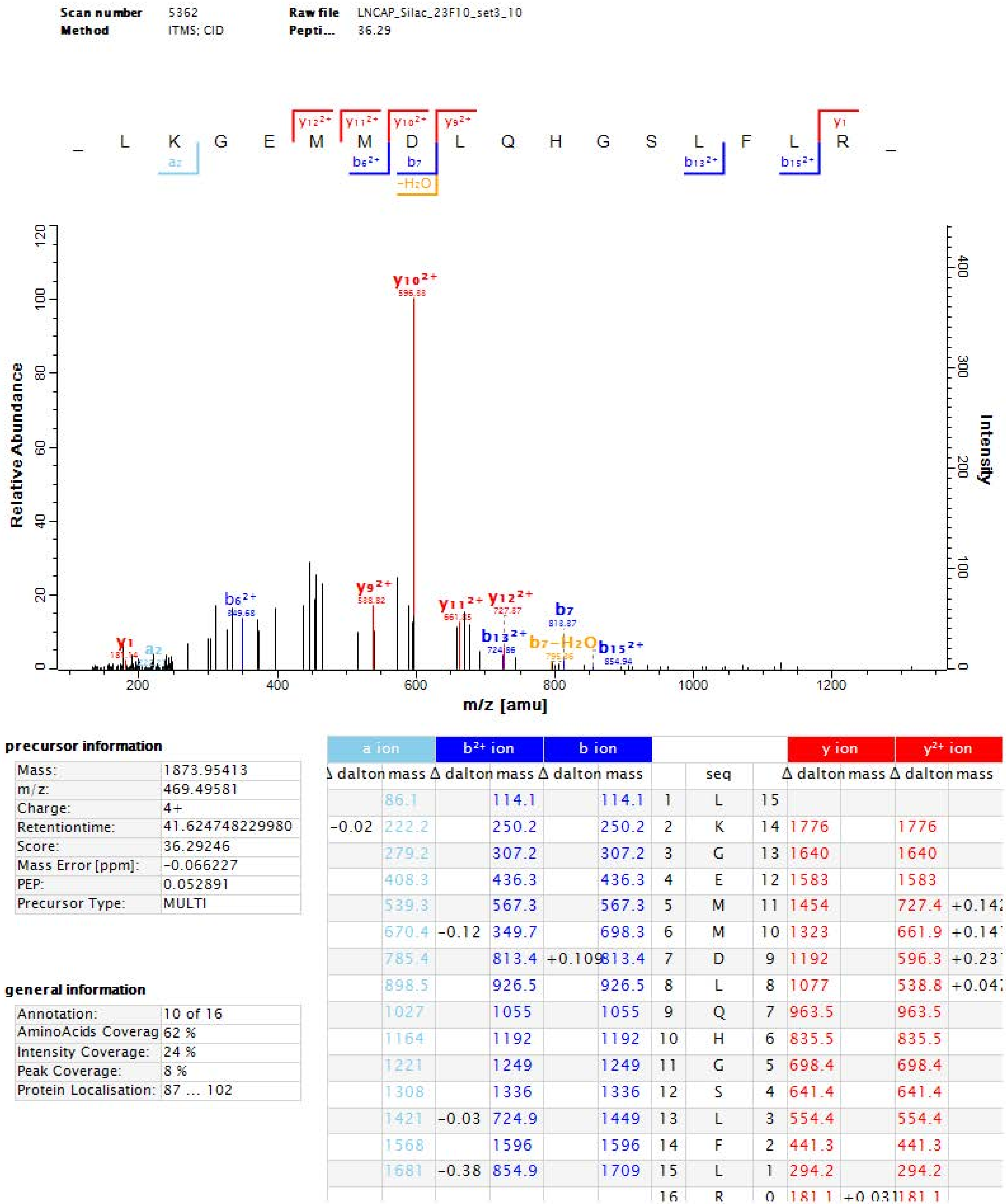
precursor information

Mass:	2619.4384
m/z:	655.86688
Charge:	4+
Retentiontime:	39.992404937744
Score:	92.39011
Mass Error [ppm]:	-0.34277
PEP:	3.8864E-07
Precursor Type:	MULTI

general information

Annotation:	16 of 24
AminoAcids Coverag	67 %
Intensity Coverage:	40 %
Peak Coverage:	29 %
Protein Localisation:	162 ... 185

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.08		100.08	1	V	23				
	213.16	-0.071	213.16	2	L	22	2545.4		2545.4	
	349.27		349.27	3	K	21	2432.3		2432.3	
	478.31	+0.0962	478.31	4	E	20	2296.2		2296.2	
	625.38		625.38	5	F	19	2167.2		2167.2	
-0.497	381.72	+0.1357	762.44	6	H	18	2020.1		2020.1	
	890.5		890.5	7	Q	17	1883.1		942.03	+0.034
	961.53		961.53	8	A	16	1755		1755	
	1018.6		1018.6	9	G	15	1684		842.48	+0.171
	1154.7		1154.7	10	K	14	1626.9		1626.9	
+0.0018	626.36		1251.7	11	P	13	1490.8		1490.8	
	1364.8		1364.8	12	I	12	1393.8		1393.8	
	1421.8		1421.8	13	G	11	1280.7		1280.7	
-0.161	767.96		1534.9	14	L	10	1223.7		1223.7	
	1694.9		1694.9	15	C	9	1110.6		555.8	+0.0771
-0.066	927.99		1855	16	C	8	950.56	+0.2001	475.78	+0.0241
	1968.1		1968.1	17	I	7	790.53		790.53	
+0.0325	1020		2039.1	18	A	6	677.44	-0.031	339.23	+0.2154
	2136.1		2136.1	19	P	5	606.41	+0.0189	303.71	+0.0747
-0.172	1118.1		2235.2	20	V	4	509.35		509.35	
	2348.3		2348.3	21	L	3	410.29	-0.369	410.29	
	2419.3		2419.3	22	A	2	297.2	+0.0694	297.2	
	2490.4		2490.4	23	A	1	226.16		226.16	
				24	K	0	155.13		155.13	



Scan number	5362	**Raw file**	LNCAP_Silac_23F10_set3_10
Method	ITMS; CID	**Pepti...**	36.29

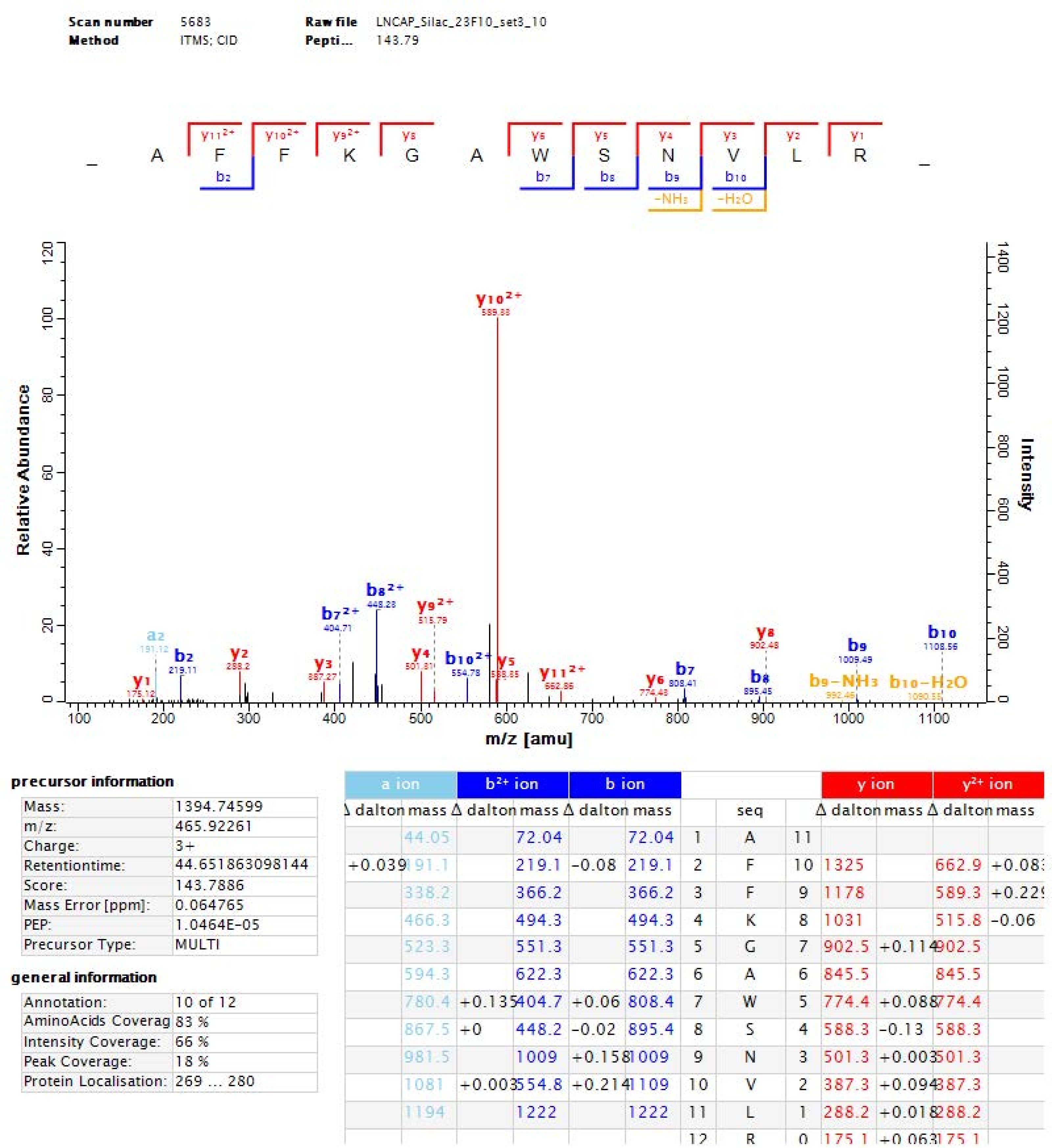
precursor information

Mass:	1873.95413
m/z:	469.49581
Charge:	4+
Retentiontime:	41.624748229980
Score:	36.29246
Mass Error [ppm]:	-0.066227
PEP:	0.052891
Precursor Type:	MULTI

general information

Annotation:	10 of 16
AminoAcids Coverag	62 %
Intensity Coverage:	24 %
Peak Coverage:	8 %
Protein Localisation:	87 ... 102

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.1		114.1		114.1	1	L	15				
-0.02	222.2		250.2		250.2	2	K	14	1776		1776	
	279.2		307.2		307.2	3	G	13	1640		1640	
	408.3		436.3		436.3	4	E	12	1583		1583	
	539.3		567.3		567.3	5	M	11	1454		727.4	+0.14
	670.4	-0.12	349.7		698.3	6	M	10	1323		661.9	+0.14
	785.4		813.4	+0.109	813.4	7	D	9	1192		596.3	+0.23
	898.5		926.5		926.5	8	L	8	1077		538.8	+0.04
	1027		1055		1055	9	Q	7	963.5		963.5	
	1164		1192		1192	10	H	6	835.5		835.5	
	1221		1249		1249	11	G	5	698.4		698.4	
	1308		1336		1336	12	S	4	641.4		641.4	
	1421	-0.03	724.9		1449	13	L	3	554.4		554.4	
	1568		1596		1596	14	F	2	441.3		441.3	
	1681	-0.38	854.9		1709	15	L	1	294.2		294.2	
						16	R	0	181.1	+0.031	181.1	



Scan number	5683	**Raw file**	LNCAP_Silac_23F10_set3_10
Method	ITMS; CID	**Pepti...**	143.79

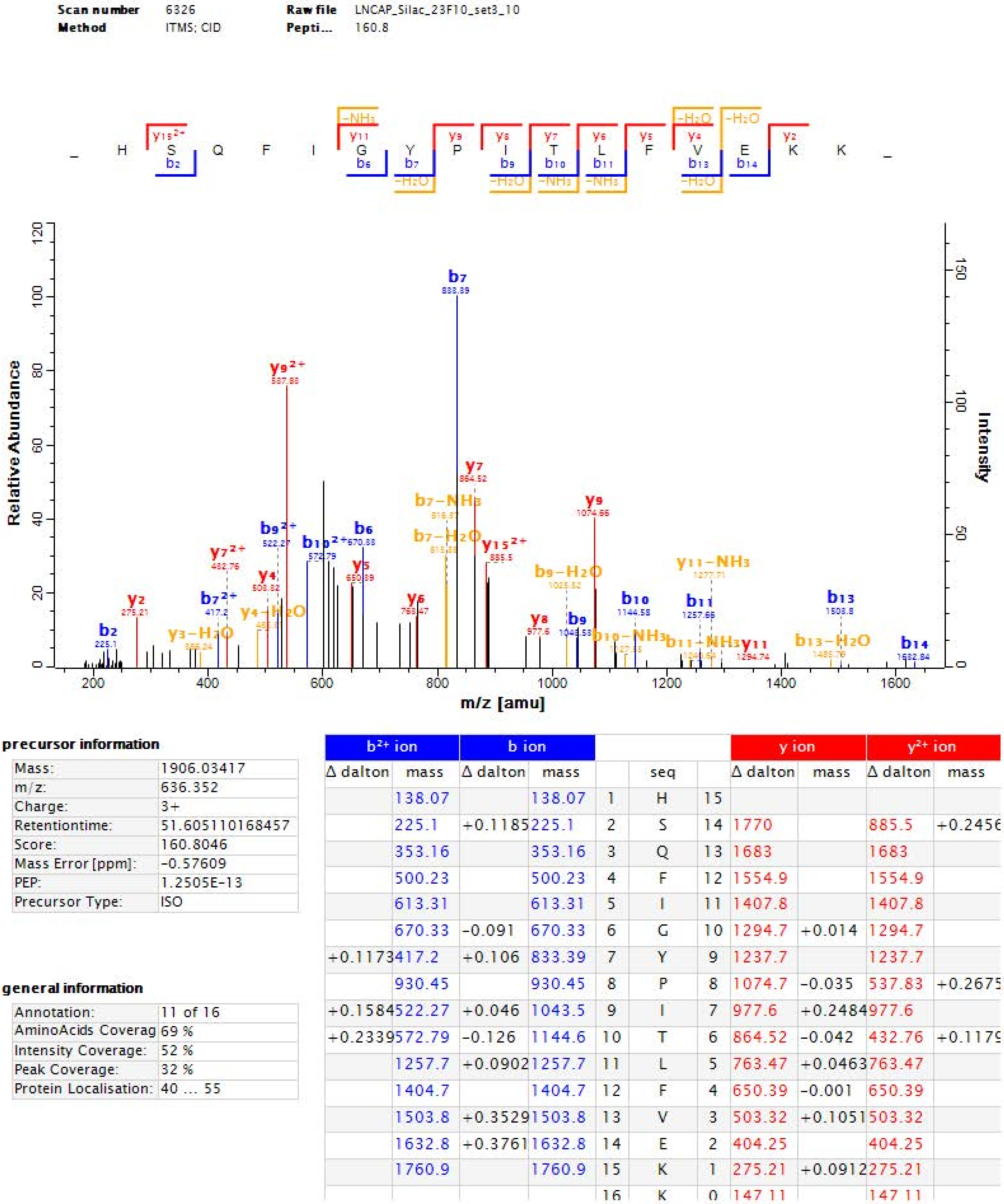
precursor information

Mass:	1394.74599
m/z:	465.92261
Charge:	3+
Retentiontime:	44.651863098144
Score:	143.7886
Mass Error [ppm]:	0.064765
PEP:	1.0464E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	66 %
Peak Coverage:	18 %
Protein Localisation:	269 ... 280

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	44.05		72.04		72.04	1	A	11				
+0.039	191.1		219.1	-0.08	219.1	2	F	10	1325		662.9	+0.08
	338.2		366.2		366.2	3	F	9	1178		589.3	+0.22
	466.3		494.3		494.3	4	K	8	1031		515.8	-0.06
	523.3		551.3		551.3	5	G	7	902.5	+0.114	902.5	
	594.3		622.3		622.3	6	A	6	845.5		845.5	
	780.4	+0.135	404.7	+0.06	808.4	7	W	5	774.4	+0.088	774.4	
	867.5	+0	448.2	-0.02	895.4	8	S	4	588.3	-0.13	588.3	
	981.5		1009	+0.158	1009	9	N	3	501.3	+0.003	501.3	
	1081	+0.003	554.8	+0.214	1109	10	V	2	387.3	+0.094	387.3	
	1194		1222		1222	11	L	1	288.2	+0.018	288.2	
						12	R	0	175.1	+0.063	175.1	



Scan number 6326

Method ITMS; CID

Raw file LNCAP_Silac_23F10_set3_10

Pepti... 160.8

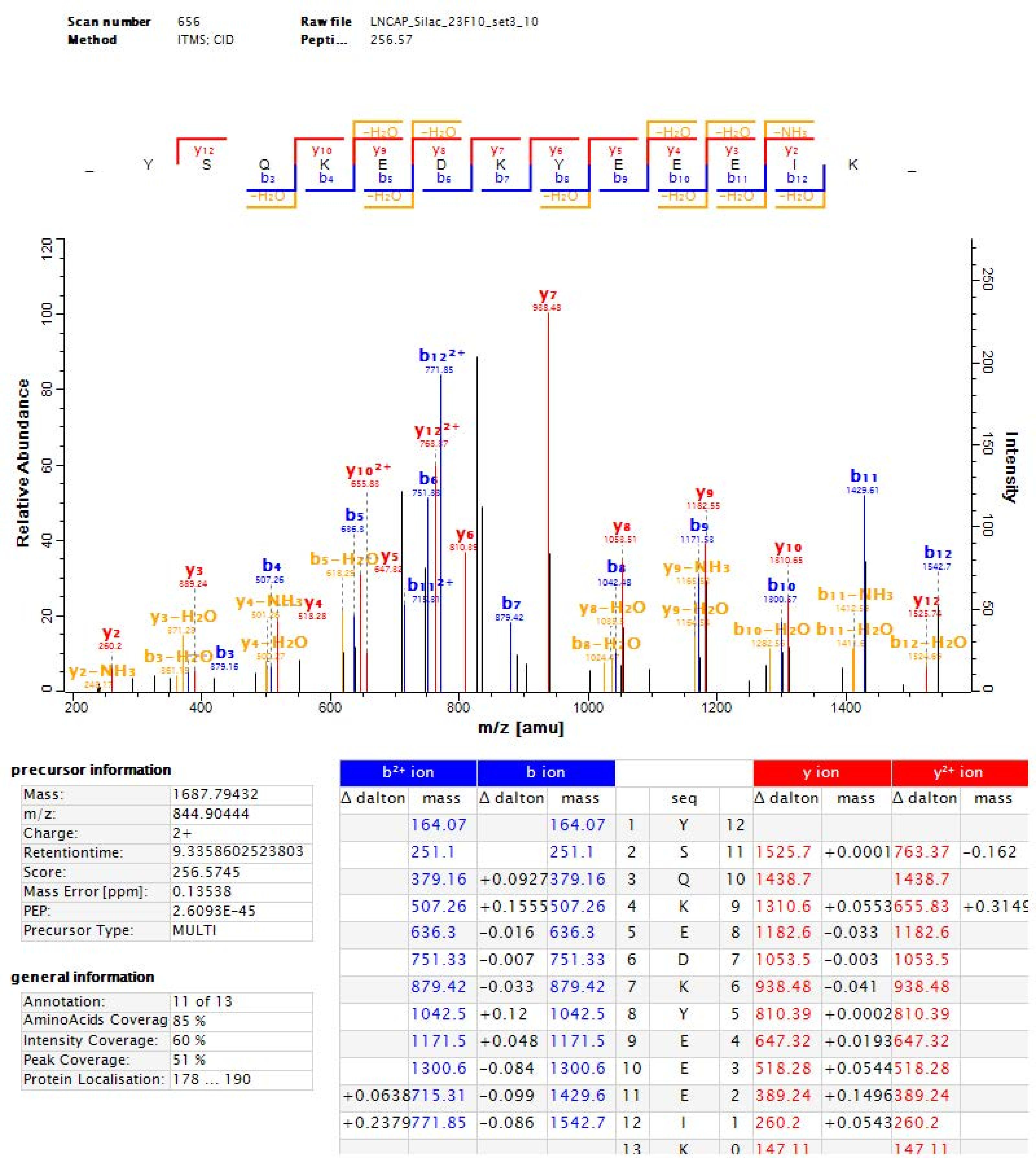
precursor information

Mass:	1906.03417
m/z:	636.352
Charge:	3+
Retentiontime:	51.605110168457
Score:	160.8046
Mass Error [ppm]:	-0.57609
PEP:	1.2505E-13
Precursor Type:	ISO

general information

Annotation:	11 of 16
AminoAcids Coverag	69 %
Intensity Coverage:	52 %
Peak Coverage:	32 %
Protein Localisation:	40 ... 55

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.07		138.07	1	H	15				
	225.1	+0.1185	225.1	2	S	14	1770		885.5	+0.2456
	353.16		353.16	3	Q	13	1683		1683	
	500.23		500.23	4	F	12	1554.9		1554.9	
	613.31		613.31	5	I	11	1407.8		1407.8	
	670.33	-0.091	670.33	6	G	10	1294.7	+0.014	1294.7	
+0.1173	417.2	+0.106	833.39	7	Y	9	1237.7		1237.7	
	930.45		930.45	8	P	8	1074.7	-0.035	537.83	+0.2675
+0.1584	522.27	+0.046	1043.5	9	I	7	977.6	+0.2484	977.6	
+0.2339	572.79	-0.126	1144.6	10	T	6	864.52	-0.042	432.76	+0.1179
	1257.7	+0.0902	1257.7	11	L	5	763.47	+0.0463	763.47	
	1404.7		1404.7	12	F	4	650.39	-0.001	650.39	
	1503.8	+0.3529	1503.8	13	V	3	503.32	+0.1051	503.32	
	1632.8	+0.3761	1632.8	14	E	2	404.25		404.25	
	1760.9		1760.9	15	K	1	275.21	+0.0912	275.21	
				16	K	0	147.11		147.11	



Scan number	656	**Raw file**	LNCAP_Silac_23F10_set3_10
Method	ITMS; CID	**Pepti...**	256.57

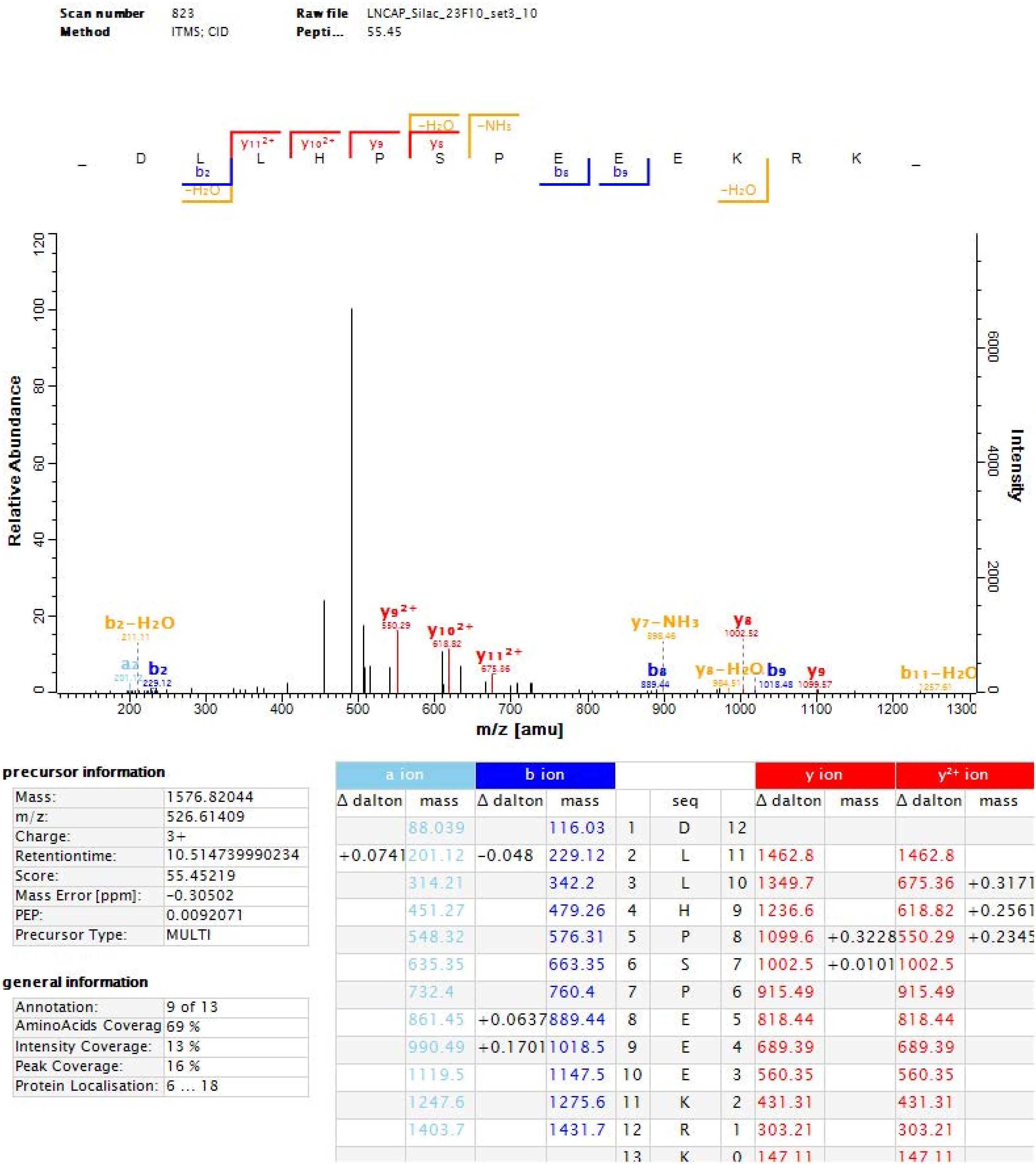
precursor information

Mass:	1687.79432
m/z:	844.90444
Charge:	2+
Retentiontime:	9.3358602523803
Score:	256.5745
Mass Error [ppm]:	0.13538
PEP:	2.6093E-45
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	60 %
Peak Coverage:	51 %
Protein Localisation:	178 ... 190

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	164.07		164.07	1	Y	12				
	251.1		251.1	2	S	11	1525.7	+0.0001	763.37	-0.162
	379.16	+0.0927	379.16	3	Q	10	1438.7		1438.7	
	507.26	+0.1555	507.26	4	K	9	1310.6	+0.0553	655.83	+0.3149
	636.3	-0.016	636.3	5	E	8	1182.6	-0.033	1182.6	
	751.33	-0.007	751.33	6	D	7	1053.5	-0.003	1053.5	
	879.42	-0.033	879.42	7	K	6	938.48	-0.041	938.48	
	1042.5	+0.12	1042.5	8	Y	5	810.39	+0.0002	810.39	
	1171.5	+0.048	1171.5	9	E	4	647.32	+0.0193	647.32	
	1300.6	-0.084	1300.6	10	E	3	518.28	+0.0544	518.28	
+0.0638	715.31	-0.099	1429.6	11	E	2	389.24	+0.1496	389.24	
+0.2379	771.85	-0.086	1542.7	12	I	1	260.2	+0.0543	260.2	
				13	K	0	147.11		147.11	



Scan number	823	**Raw file**	LNCAP_Silac_23F10_set3_10
Method	ITMS; CID	**Pepti...**	55.45

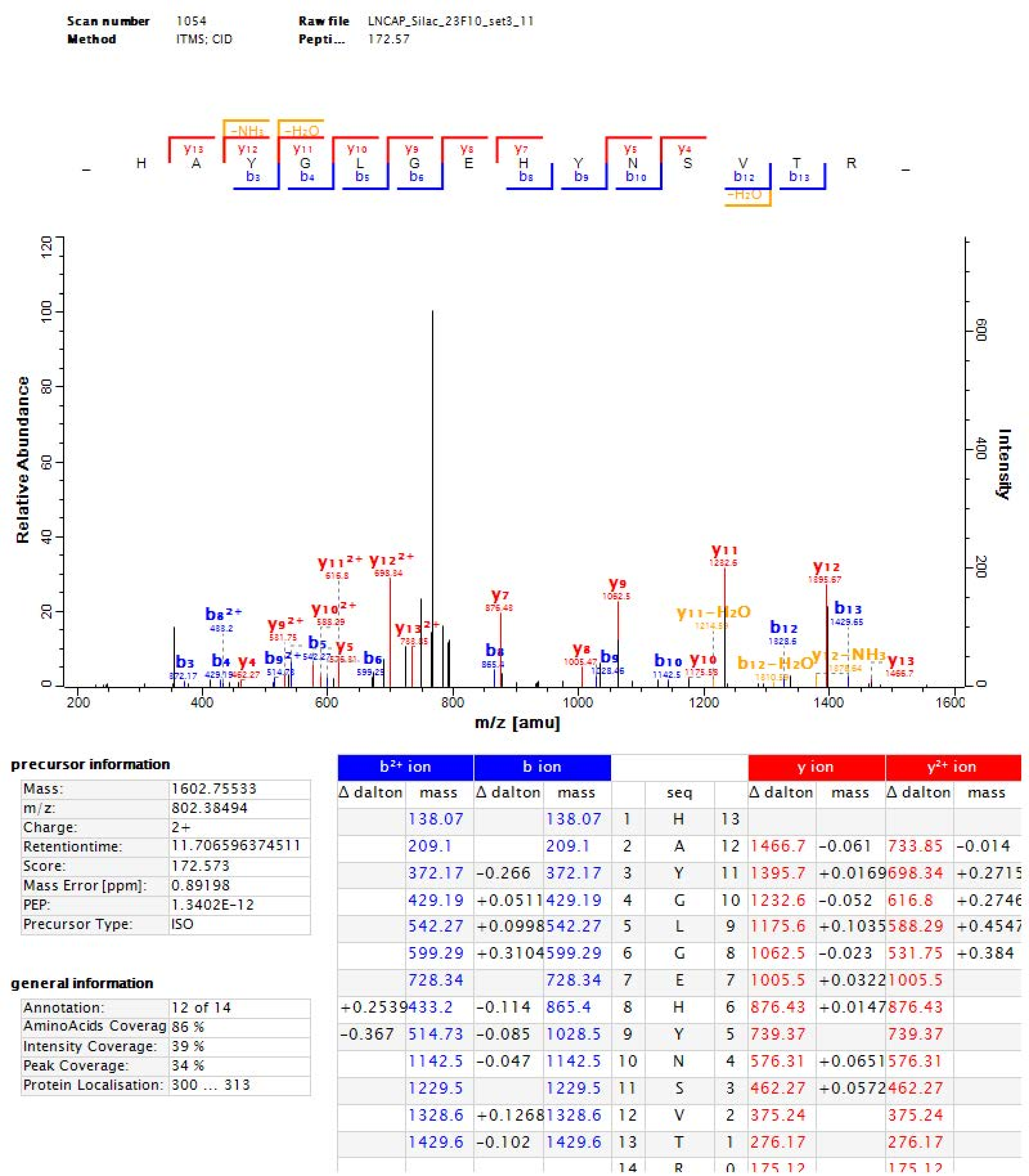
precursor information

Mass:	1576.82044
m/z:	526.61409
Charge:	3+
Retentiontime:	10.514739990234
Score:	55.45219
Mass Error [ppm]:	-0.30502
PEP:	0.0092071
Precursor Type:	MULTI

general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	13 %
Peak Coverage:	16 %
Protein Localisation:	6 … 18

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039		116.03	1	D	12				
+0.0741	201.12	-0.048	229.12	2	L	11	1462.8		1462.8	
	314.21		342.2	3	L	10	1349.7		675.36	+0.3171
	451.27		479.26	4	H	9	1236.6		618.82	+0.2561
	548.32		576.31	5	P	8	1099.6	+0.3228	550.29	+0.2345
	635.35		663.35	6	S	7	1002.5	+0.0101	1002.5	
	732.4		760.4	7	P	6	915.49		915.49	
	861.45	+0.0637	889.44	8	E	5	818.44		818.44	
	990.49	+0.1701	1018.5	9	E	4	689.39		689.39	
	1119.5		1147.5	10	E	3	560.35		560.35	
	1247.6		1275.6	11	K	2	431.31		431.31	
	1403.7		1431.7	12	R	1	303.21		303.21	
				13	K	0	147.11		147.11	



Scan number 1054
Method ITMS; CID
Raw file LNCAP_Silac_23F10_set3_11
Pepti... 172.57

precursor information

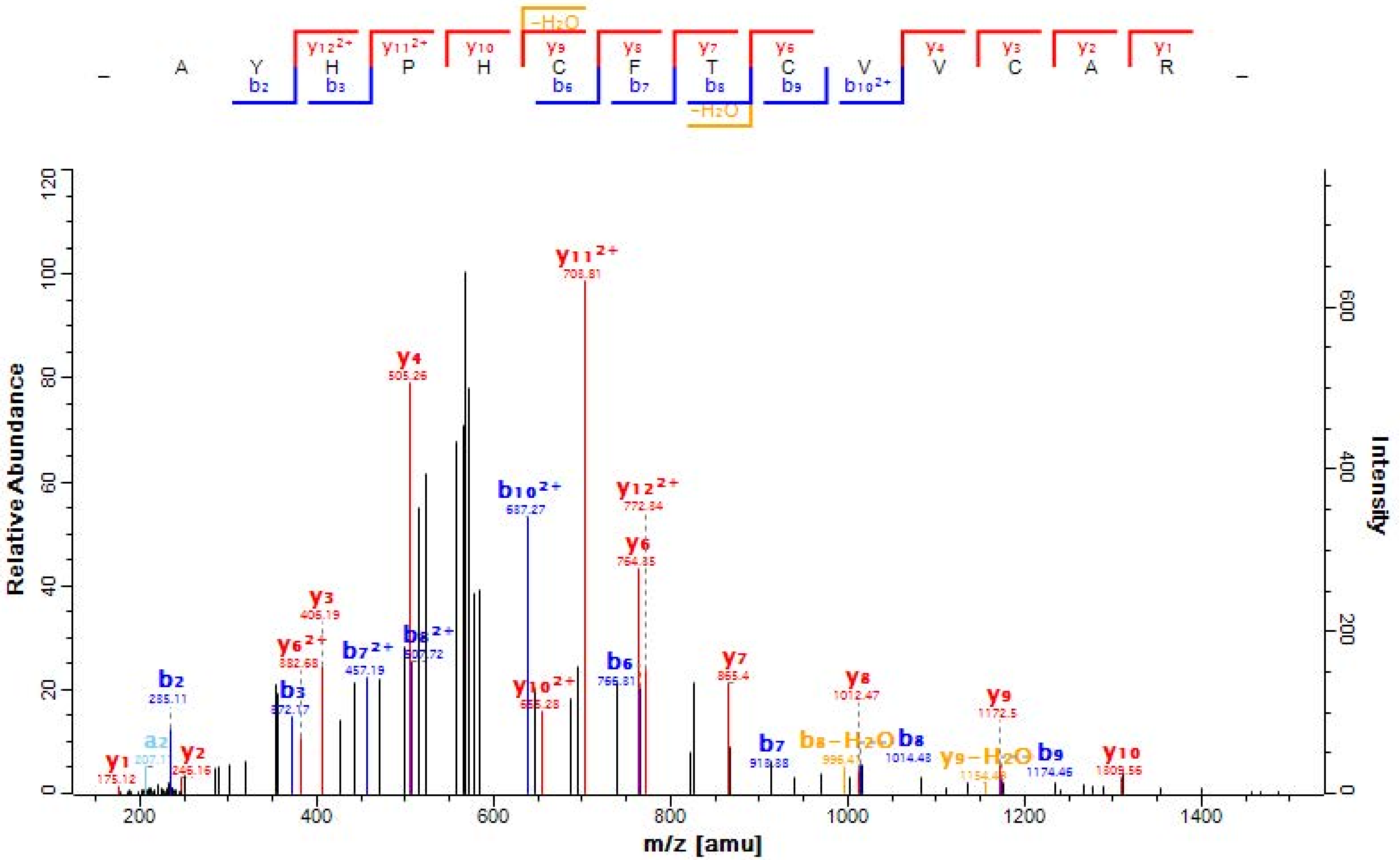
Mass:	1602.75533
m/z:	802.38494
Charge:	2+
Retentiontime:	11.706596374511
Score:	172.573
Mass Error [ppm]:	0.89198
PEP:	1.3402E-12
Precursor Type:	ISO

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	39 %
Peak Coverage:	34 %
Protein Localisation:	300 ... 313

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.07		138.07	1	H	13				
	209.1		209.1	2	A	12	1466.7	-0.061	733.85	-0.014
	372.17	-0.266	372.17	3	Y	11	1395.7	+0.0169	698.34	+0.2715
	429.19	+0.0511	429.19	4	G	10	1232.6	-0.052	616.8	+0.2746
	542.27	+0.0998	542.27	5	L	9	1175.6	+0.1035	588.29	+0.4547
	599.29	+0.3104	599.29	6	G	8	1062.5	-0.023	531.75	+0.384
	728.34		728.34	7	E	7	1005.5	+0.0322	1005.5	
+0.2539	433.2	-0.114	865.4	8	H	6	876.43	+0.0147	876.43	
-0.367	514.73	-0.085	1028.5	9	Y	5	739.37		739.37	
	1142.5	-0.047	1142.5	10	N	4	576.31	+0.0651	576.31	
	1229.5		1229.5	11	S	3	462.27	+0.0572	462.27	
	1328.6	+0.1268	1328.6	12	V	2	375.24		375.24	
	1429.6	-0.102	1429.6	13	T	1	276.17		276.17	
				14	R	0	175.12		175.12	

Scan number	1856	**Raw file**	LNCAP_Silac_23F10_set3_11
Method	ITMS; CID	**Pepti...**	153.74



precursor information

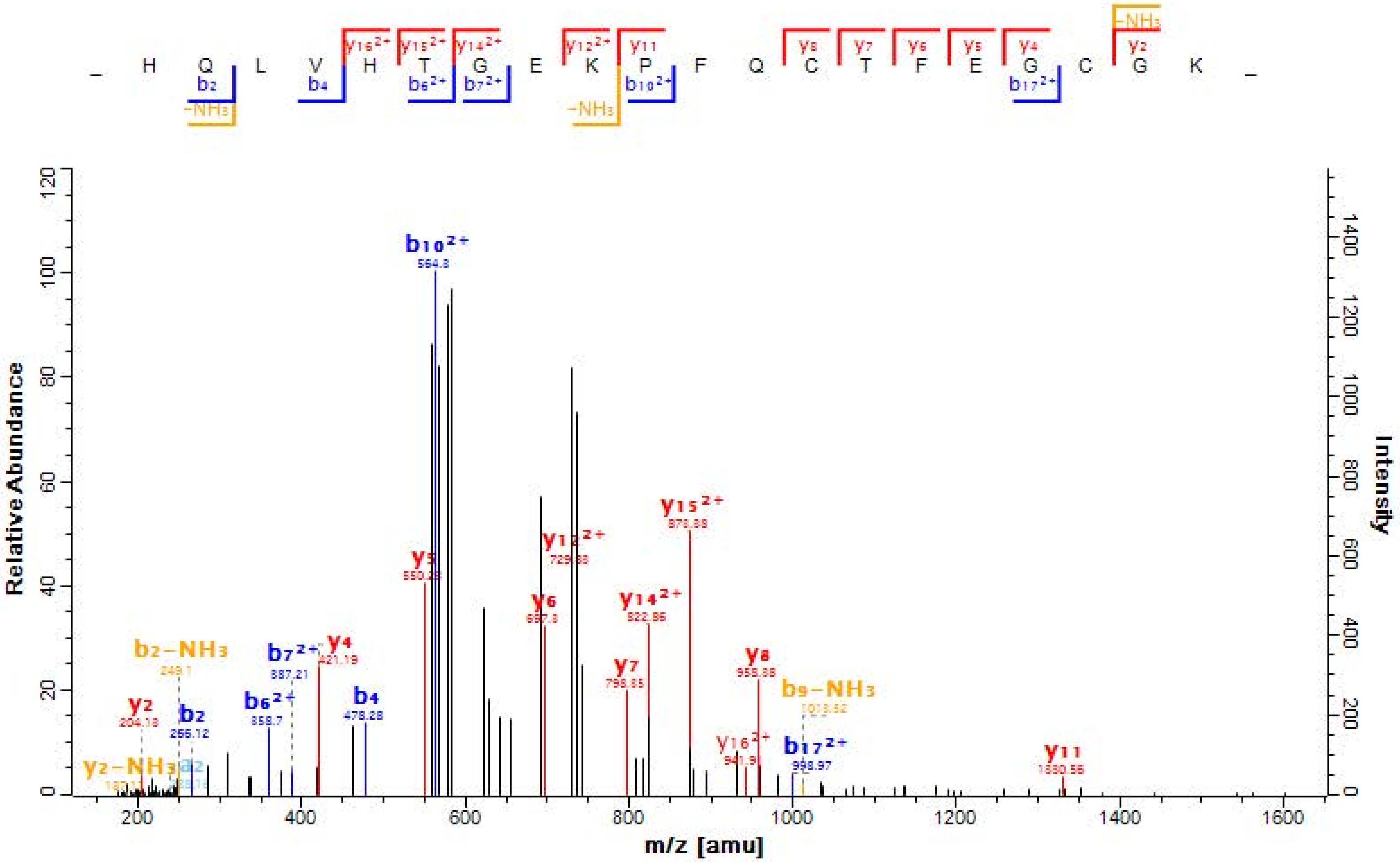
Mass:	1776.76486
m/z:	593.26223
Charge:	3+
Retentiontime:	17.599239349365
Score:	153.7388
Mass Error [ppm]:	0.097427
PEP:	3.3701E-10
Precursor Type:	MULTI

general information

Annotation:	13 of 14
AminoAcids Coverag	93 %
Intensity Coverage:	37 %
Peak Coverage:	23 %
Protein Localisation:	471 ... 484

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	44.05		72.04		72.04	1	A	13				
-0.1	207.1		235.1	+0.032	235.1	2	Y	12	1707		1707	
	344.2		372.2	-0.03	372.2	3	H	11	1544		772.3	+0.17
	441.2		469.2		469.2	4	P	10	1407		703.8	+0.28
	578.3		606.3		606.3	5	H	9	1310	+0.012	655.3	-0.09
	738.3		766.3	+0.096	766.3	6	C	8	1173	-0.01	1173	
	885.4	+0.089	457.2	-0.18	913.4	7	F	7	1012	-0.04	1012	
	986.4	-0.11	507.7	+0.2	1014	8	T	6	865.4	-0.02	865.4	
	1146		1174	-0.03	1174	9	C	5	764.4	+0.029	382.7	+0.08
	1246	+0.301	637.3		1274	10	V	4	604.3		604.3	
	1345		1373		1373	11	V	3	505.3	+0.009	505.3	
	1505		1533		1533	12	C	2	406.2	+0.05	406.2	
	1576		1604		1604	13	A	1	246.2	+0	246.2	
						14	R	0	175.1	+0.131	175.1	

Scan number	2023	**Raw file**	LNCAP_Silac_23F10_set3_11
Method	ITMS; CID	**Pepti...**	69.98



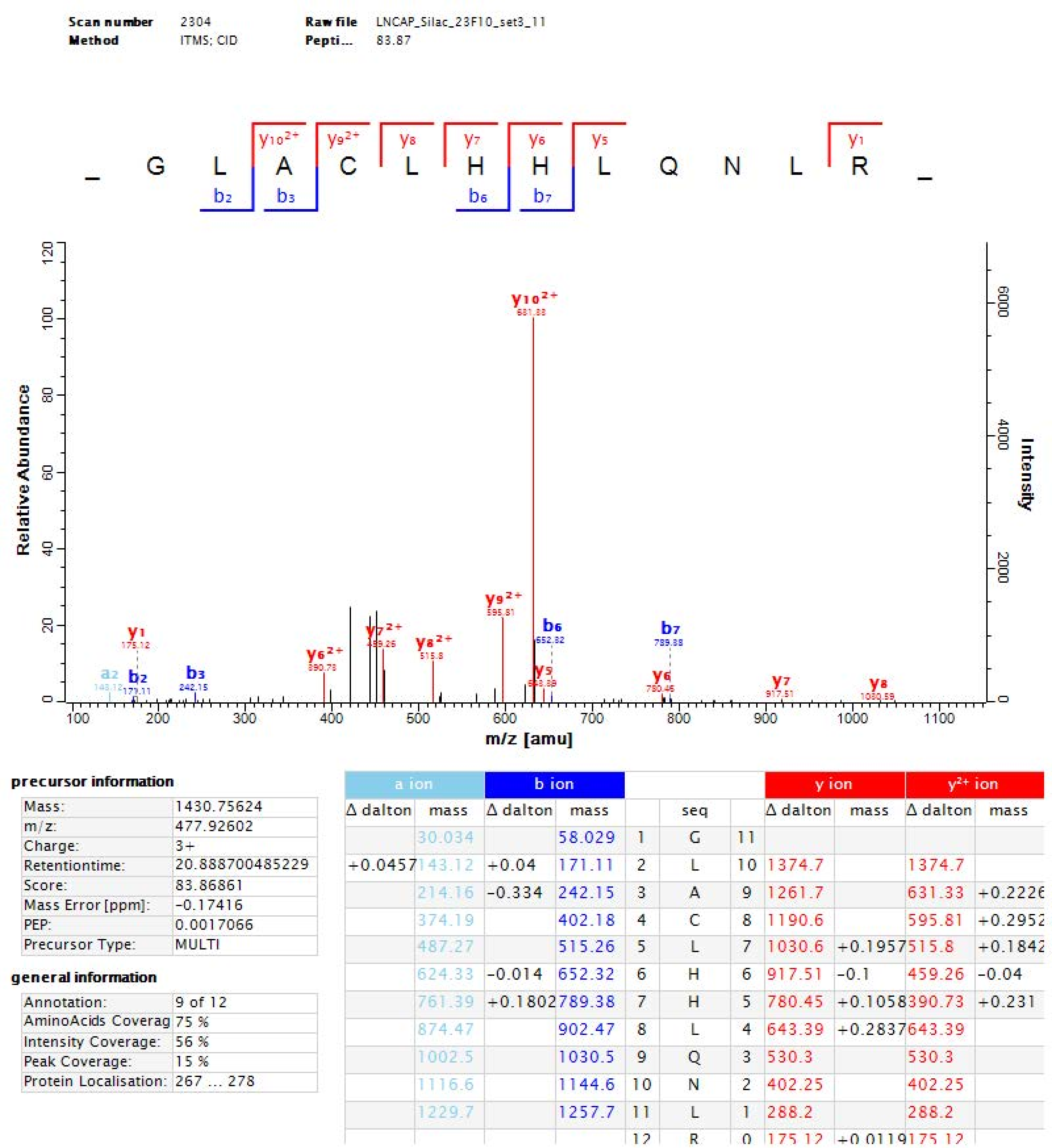
precursor information

Mass:	2359.08434
m/z:	590.77836
Charge:	4+
Retentiontime:	18.786092758178
Score:	69.97897
Mass Error [ppm]:	0.2433
PEP:	0.00028617
Precursor Type:	MULTI

general information

Annotation:	13 of 20
AminoAcids Coverag	65 %
Intensity Coverage:	33 %
Peak Coverage:	18 %
Protein Localisation:	503 ... 522

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	110.1		138.1		138.1	1	H	19				
+0.086	238.1		266.1	+0.089	266.1	2	Q	18	2223		2223	
	351.2		379.2		379.2	3	L	17	2095		2095	
	450.3		478.3	+0.132	478.3	4	V	16	1982		1982	
	587.3		615.3		615.3	5	H	15	1883		941.9	-0.12
	688.4	+0.25	358.7		716.4	6	T	14	1746		873.4	+0.20
	745.4	+0.347	387.2		773.4	7	G	13	1645		822.9	+0.31
	874.5		902.4		902.4	8	E	12	1588		1588	
	1003		1031		1031	9	K	11	1459		729.8	-0.22
	1100	-0.47	564.3		1128	10	P	10	1331	-0.09	1331	
	1247		1275		1275	11	F	9	1234		1234	
	1375		1403		1403	12	Q	8	1086		1086	
	1535		1563		1563	13	C	7	958.4	-0.05	958.4	
	1636		1664		1664	14	T	6	798.3	+0.017	798.3	
	1783		1811		1811	15	F	5	697.3	+0.119	697.3	
	1912		1940		1940	16	E	4	550.2	-0.11	550.2	
	1969	+0.365	999		1997	17	G	3	421.2	+0.002	421.2	
	2129		2157		2157	18	C	2	364.2		364.2	
	2186		2214		2214	19	G	1	204.1	+0.048	204.1	
						20	K	0	147.1		147.1	



Scan number 2304 **Raw file** LNCAP_Silac_23F10_set3_11
Method ITMS; CID **Pepti...** 83.87

precursor information

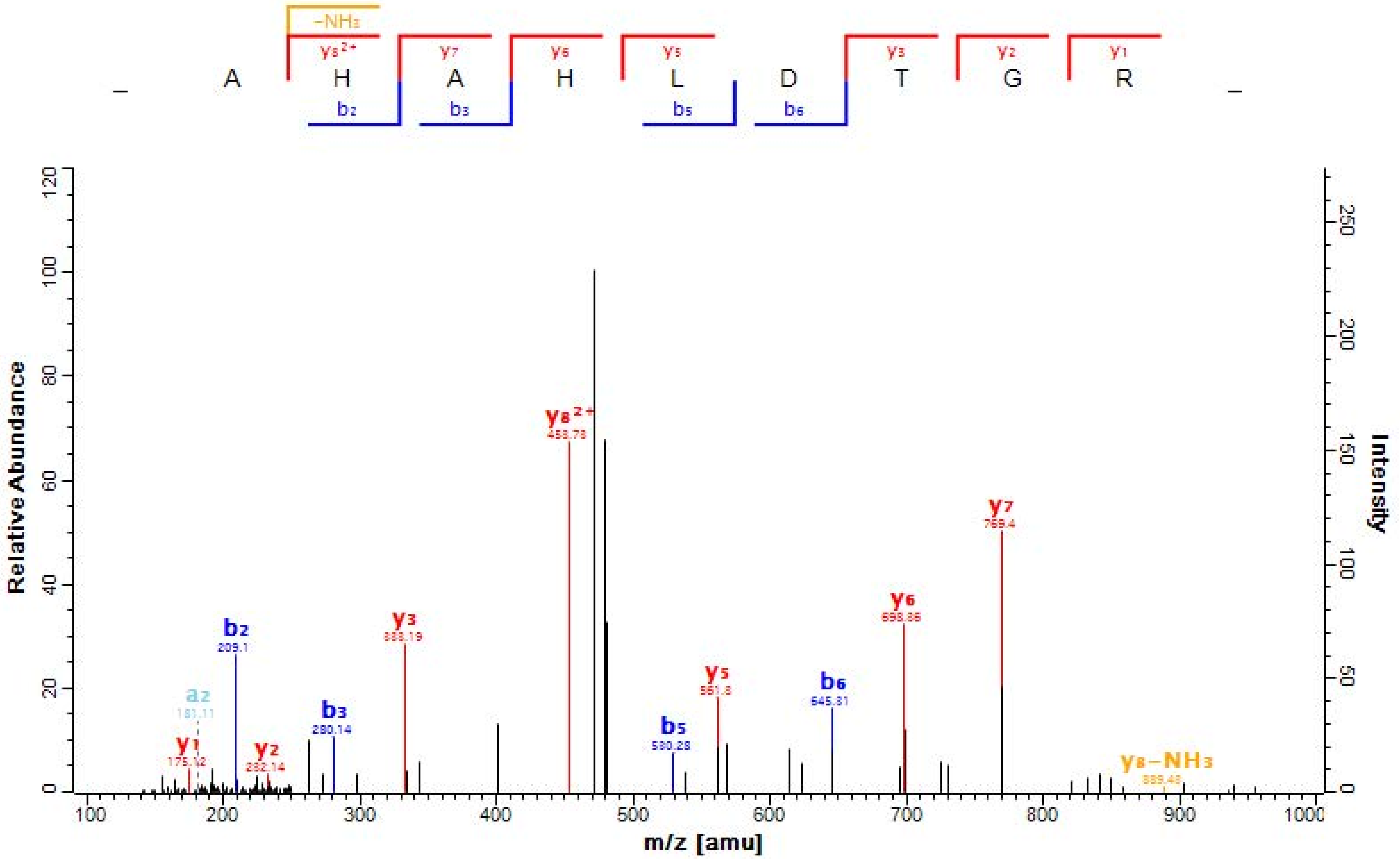
Mass:	1430.75624
m/z:	477.92602
Charge:	3+
Retentiontime:	20.888700485229
Score:	83.86861
Mass Error [ppm]:	-0.17416
PEP:	0.0017066
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	56 %
Peak Coverage:	15 %
Protein Localisation:	267 ... 278

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	30.034		58.029	1	G	11				
+0.0457	143.12	+0.04	171.11	2	L	10	1374.7		1374.7	
	214.16	-0.334	242.15	3	A	9	1261.7		631.33	+0.2226
	374.19		402.18	4	C	8	1190.6		595.81	+0.2952
	487.27		515.26	5	L	7	1030.6	+0.1957	515.8	+0.1842
	624.33	-0.014	652.32	6	H	6	917.51	-0.1	459.26	-0.04
	761.39	+0.1802	789.38	7	H	5	780.45	+0.1058	390.73	+0.231
	874.47		902.47	8	L	4	643.39	+0.2837	643.39	
	1002.5		1030.5	9	Q	3	530.3		530.3	
	1116.6		1144.6	10	N	2	402.25		402.25	
	1229.7		1257.7	11	L	1	288.2		288.2	
				12	R	0	175.12	+0.0119	175.12	

Scan number	291	**Raw file**	LNCAP_Silac_23F10_set3_11
Method	ITMS; CID	**Pepti...**	66.43



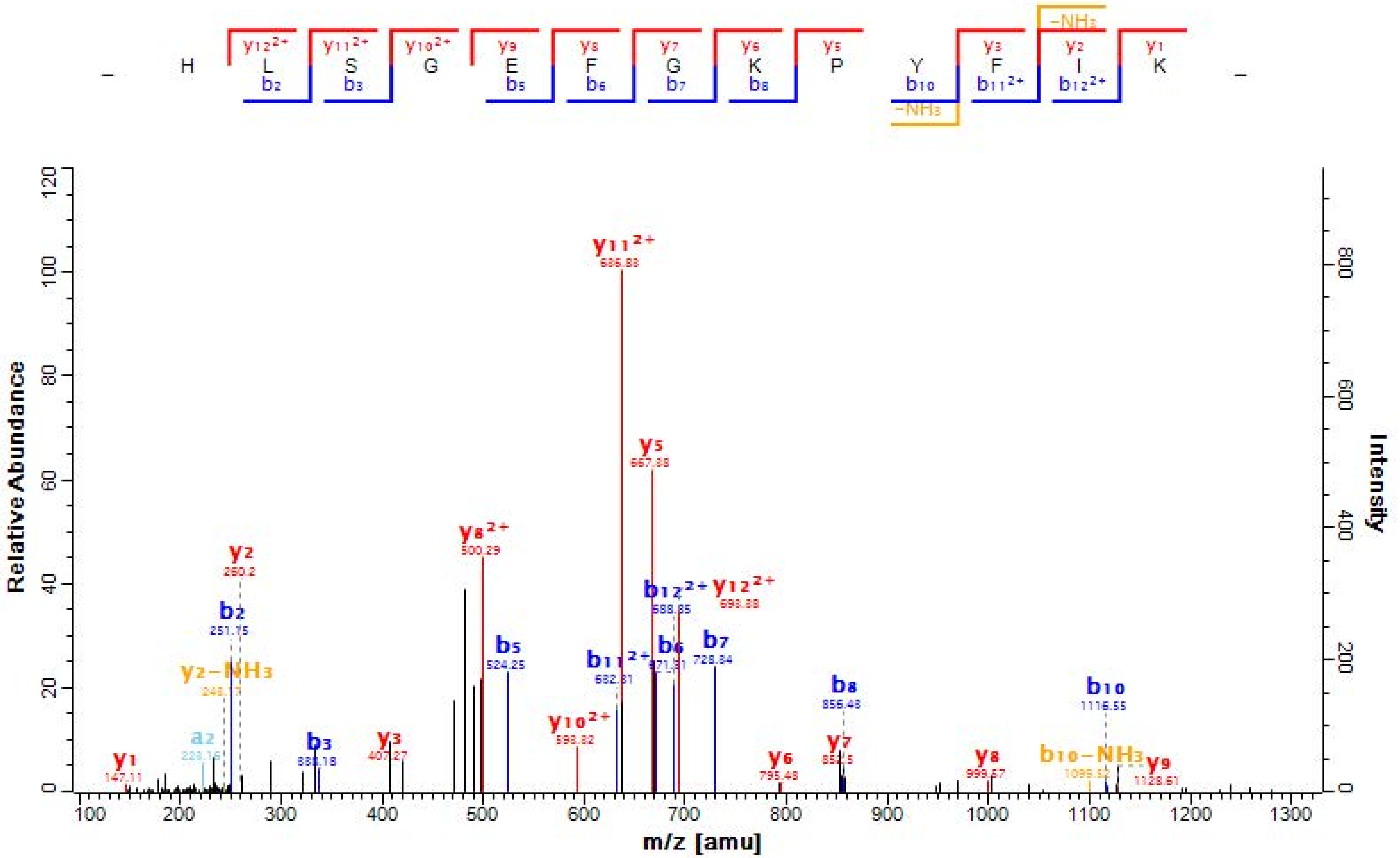
precursor information

g

Mass:	976.4847
m/z:	489.24963
Charge:	2+
Retentiontime:	6.2669634819030
Score:	66.43451
Mass Error [ppm]:	0.84401
PEP:	0.059064
Precursor Type:	ISO
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	36 %
Peak Coverage:	12 %
Protein Localisation:	726 ... 734

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	44.049		72.044	1	A	8				
+0.0507	181.11	+0.0154	209.1	2	H	7	906.45		453.73	+0.002
	252.15	+0.1193	280.14	3	A	6	769.4	-0.047	769.4	
	389.2		417.2	4	H	5	698.36	+0.0503	698.36	
	502.29	-0.45	530.28	5	L	4	561.3	+0.0929	561.3	
	617.32	+0.0249	645.31	6	D	3	448.22		448.22	
	718.36		746.36	7	T	2	333.19	+0.0798	333.19	
	775.38		803.38	8	G	1	232.14	+0.1105	232.14	
				9	R	0	175.12	+0.0475	175.12	

Scan number	3282	**Raw file**	LNCAP_Silac_23F10_set3_11
Method	ITMS; CID	**Pepti...**	136.53



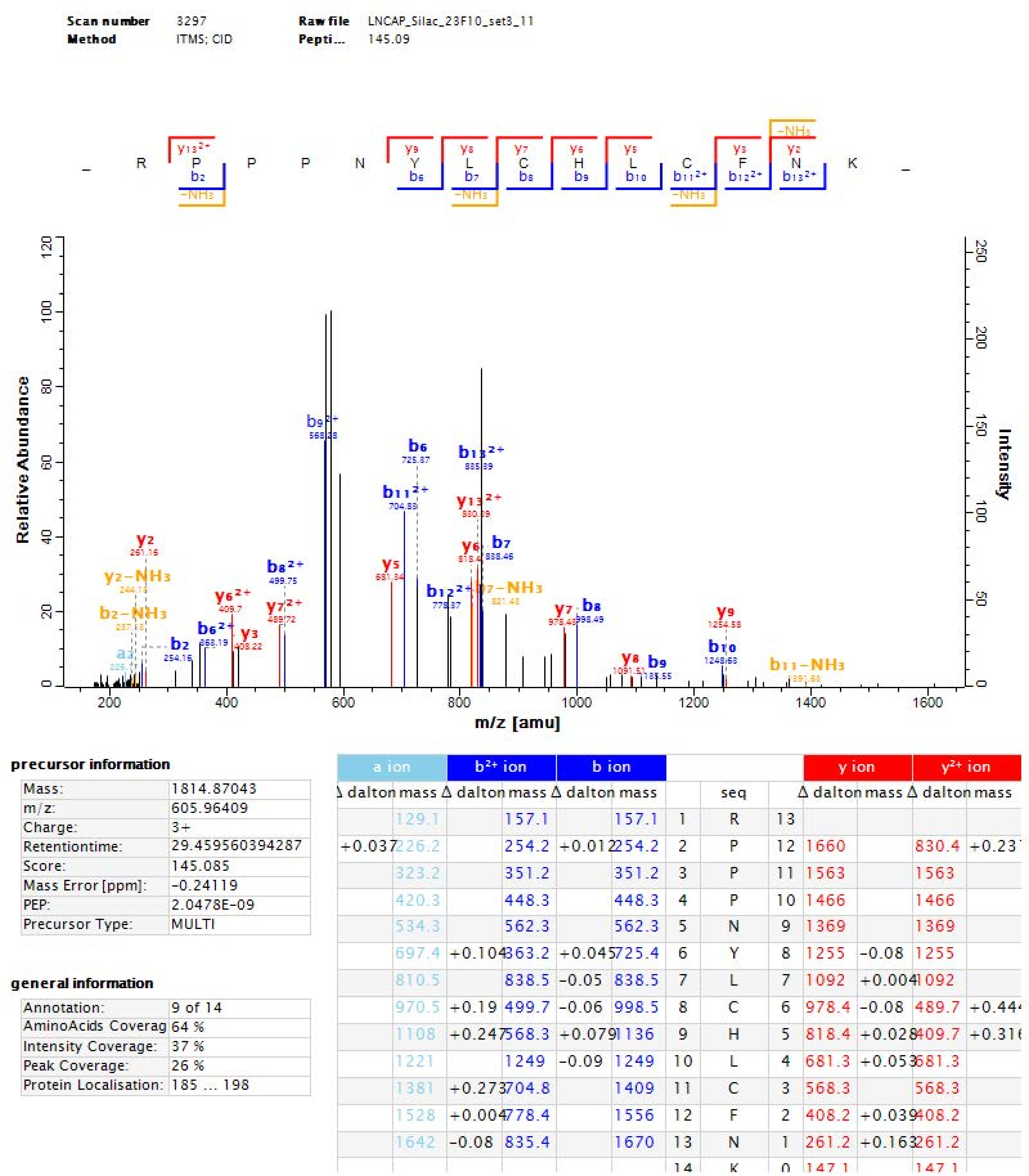
precursor information

Mass:	1521.7982
m/z:	508.27334
Charge:	3+
Retentiontime:	29.334287643432
Score:	136.5304
Mass Error [ppm]:	0.13222
PEP:	9.5866E-07
Precursor Type:	MULTI

general information

Annotation:	12 of 13
AminoAcids Coverag	92 %
Intensity Coverage:	61 %
Peak Coverage:	19 %
Protein Localisation:	101 ... 113

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	110.1		138.1		138.1	1	H	12				
+0	223.2		251.2	-0.04	251.2	2	L	11	1386		693.4	+0.29
	310.2		338.2	-0.2	338.2	3	S	10	1273		636.8	+0.21
	367.2		395.2		395.2	4	G	9	1186		593.3	+0.12
	496.3		524.2	-0.03	524.2	5	E	8	1129	-0.07	1129	
	643.3		671.3	+0.021	671.3	6	F	7	999.6	-0.02	500.3	+0.02
	700.3		728.3	+0.016	728.3	7	G	6	852.5	-0.03	852.5	
	828.4		856.4	+0.258	856.4	8	K	5	795.5	-0.06	795.5	
	925.5		953.5		953.5	9	P	4	667.4	+0.038	667.4	
	1089		1117	+0.262	1117	10	Y	3	570.3		570.3	
	1236	+0.285	632.3		1264	11	F	2	407.3	+0.14	407.3	
	1349	+0.11	688.9		1377	12	I	1	260.2	+0.139	260.2	
						13	K	0	147.1	+0.001	147.1	



Scan number	3297	**Raw file**	LNCAP_Silac_23F10_set3_11
Method	ITMS; CID	**Pepti...**	145.09

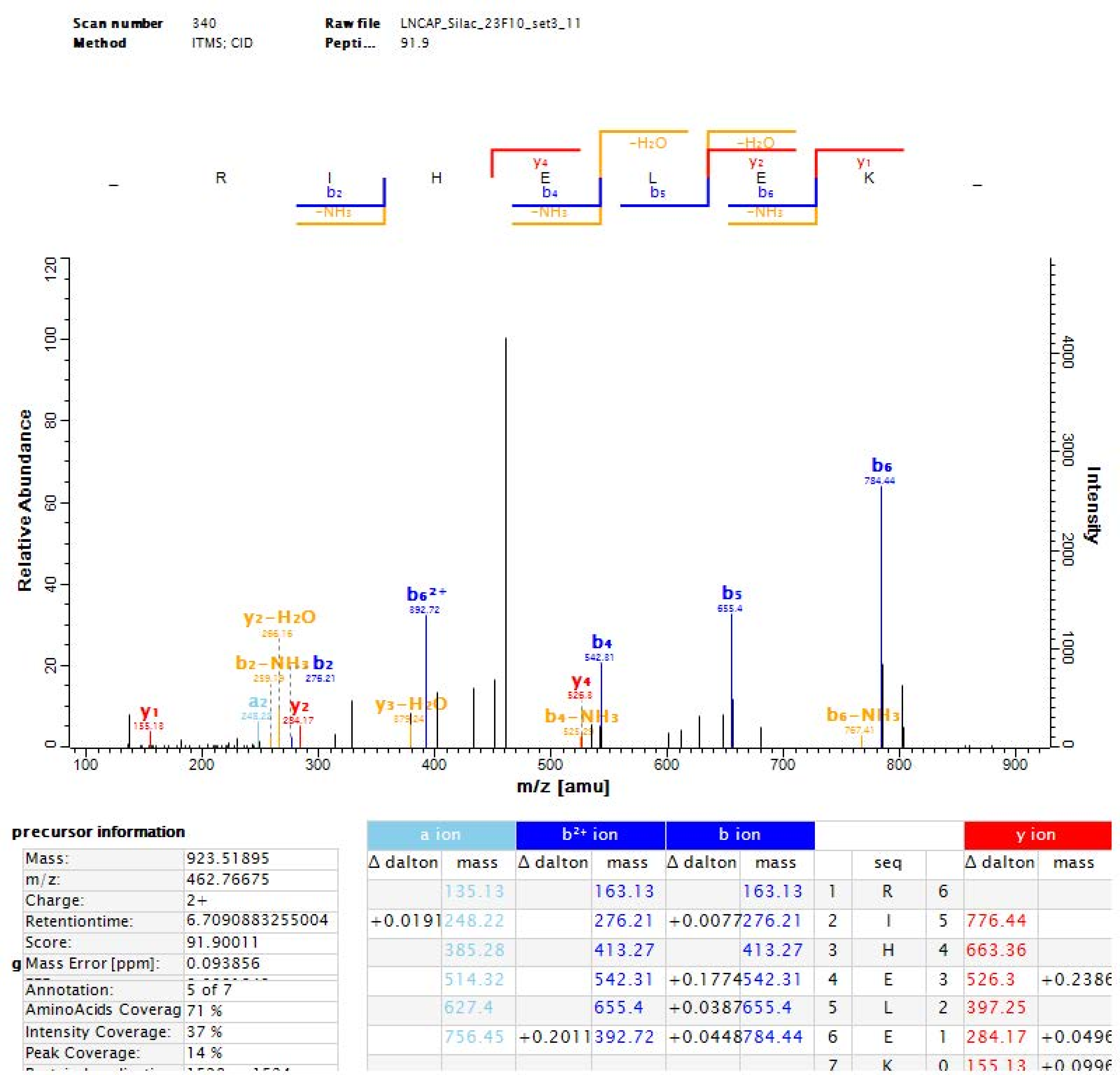
precursor information

Mass:	1814.87043
m/z:	605.96409
Charge:	3+
Retentiontime:	29.459560394287
Score:	145.085
Mass Error [ppm]:	-0.24119
PEP:	2.0478E-09
Precursor Type:	MULTI

general information

Annotation:	9 of 14
AminoAcids Coverag	64 %
Intensity Coverage:	37 %
Peak Coverage:	26 %
Protein Localisation:	185 ... 198

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.1		157.1		157.1	1	R	13				
+0.037	226.2		254.2	+0.012	254.2	2	P	12	1660		830.4	+0.23
	323.2		351.2		351.2	3	P	11	1563		1563	
	420.3		448.3		448.3	4	P	10	1466		1466	
	534.3		562.3		562.3	5	N	9	1369		1369	
	697.4	+0.104	363.2	+0.045	725.4	6	Y	8	1255	-0.08	1255	
	810.5		838.5	-0.05	838.5	7	L	7	1092	+0.004	1092	
	970.5	+0.19	499.7	-0.06	998.5	8	C	6	978.4	-0.08	489.7	+0.44
	1108	+0.247	568.3	+0.079	1136	9	H	5	818.4	+0.028	409.7	+0.31
	1221		1249	-0.09	1249	10	L	4	681.3	+0.053	681.3	
	1381	+0.273	704.8		1409	11	C	3	568.3		568.3	
	1528	+0.004	778.4		1556	12	F	2	408.2	+0.039	408.2	
	1642	-0.08	835.4		1670	13	N	1	261.2	+0.163	261.2	
						14	K	0	147.1		147.1	



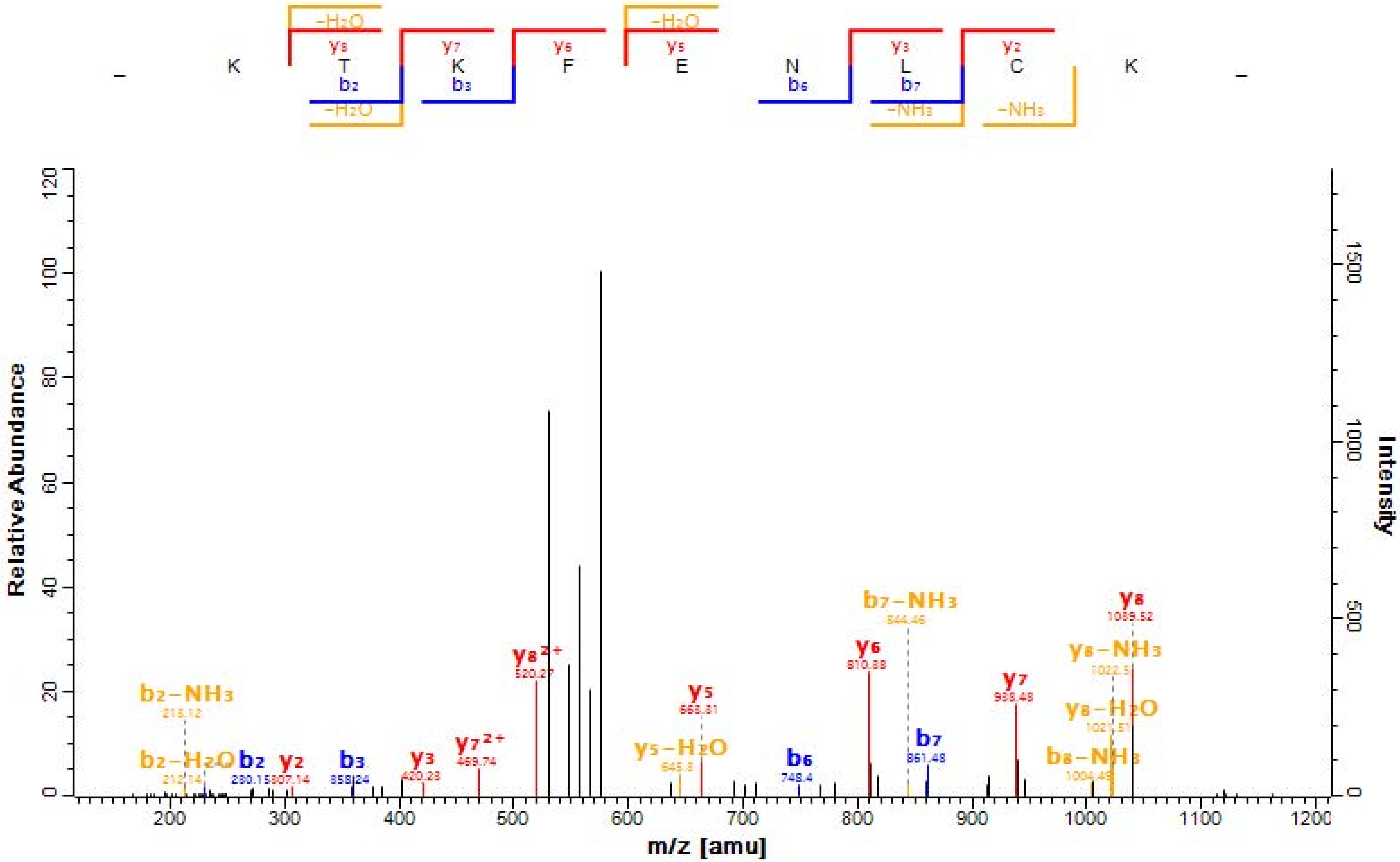
Scan number	340	**Raw file**	LNCAP_Silac_23F10_set3_11
Method	ITMS; CID	**Pepti...**	91.9

precursor information

Mass:	923.51895
m/z:	462.76675
Charge:	2+
Retentiontime:	6.7090883255004
Score:	91.90011
Mass Error [ppm]:	0.093856
Annotation:	5 of 7
AminoAcids Coverag	71 %
Intensity Coverage:	37 %
Peak Coverage:	14 %

a ion		b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	135.13		163.13		163.13	1	R	6		
+0.0191	248.22		276.21	+0.0077	276.21	2	I	5	776.44	
	385.28		413.27		413.27	3	H	4	663.36	
	514.32		542.31	+0.1774	542.31	4	E	3	526.3	+0.2386
	627.4		655.4	+0.0387	655.4	5	L	2	397.25	
	756.45	+0.2011	392.72	+0.0448	784.44	6	E	1	284.17	+0.0496
						7	K	0	155.13	+0.0996

Scan number	558	**Raw file**	LNCAP_Silac_23F10_set3_11
Method	ITMS; CID	**Pepti...**	121.5



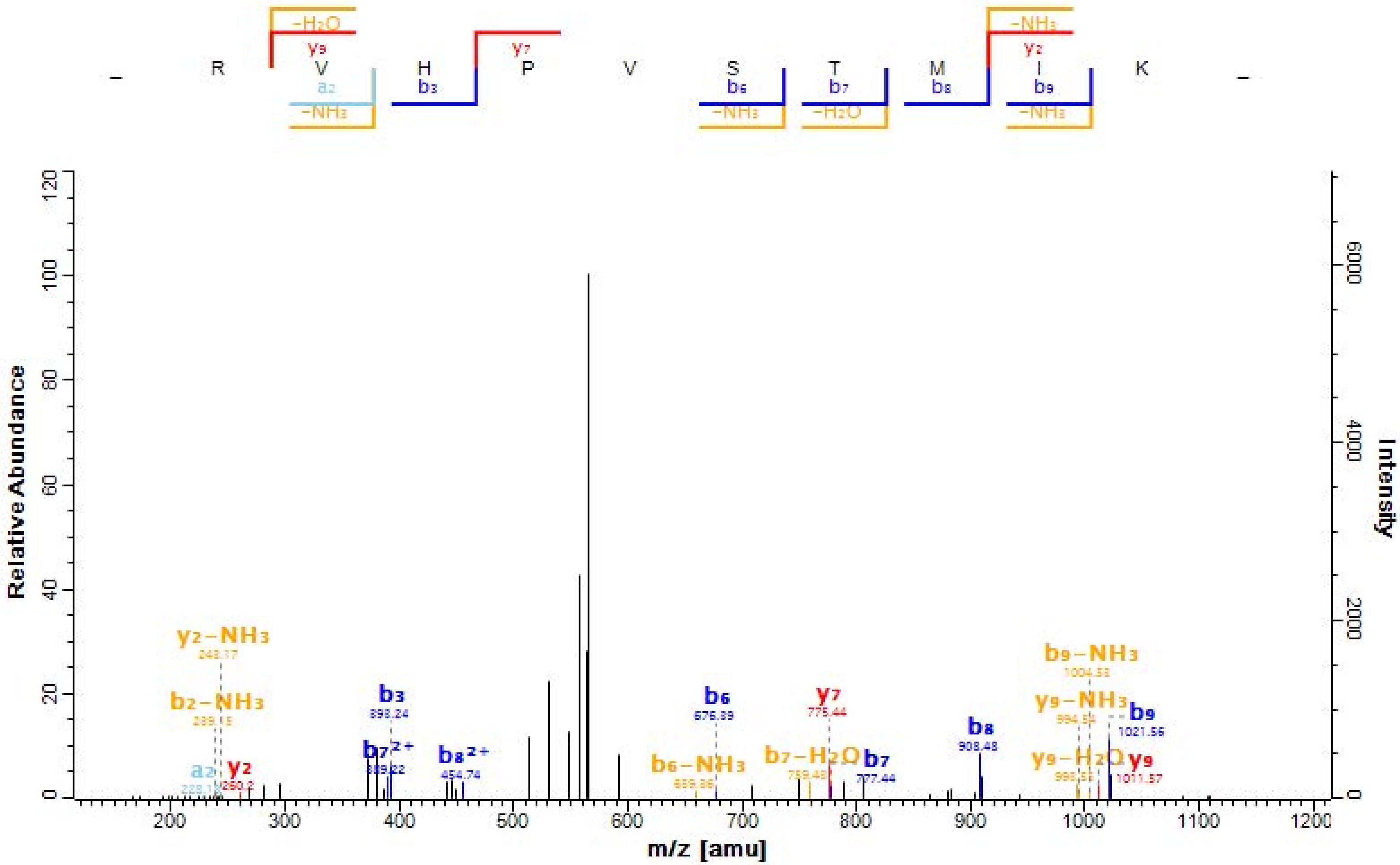
precursor information

g

Mass:	1166.61184
m/z:	584.3132
Charge:	2+
Retentiontime:	8.1826333999633
Score:	121.5022
Mass Error [ppm]:	0.051785
PEP:	0.0010458
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	29 %
Peak Coverage:	22 %
Protein Localisation:	687 ... 695

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.1022	1	K	8				
+0.077621	230.1499	2	T	7	1039.524	−0.05815	520.2657	+0.182192
+0.293815	358.2449	3	K	6	938.4764	+0.00497	469.7418	−0.02273
	505.3133	4	F	5	810.3815	+0.001789	810.3815	
	634.3559	5	E	4	663.313	+0.075818	663.313	
−0.16969	748.3988	6	N	3	534.2704		534.2704	
+0.036896	861.4829	7	L	2	420.2275	+0.142784	420.2275	
	1021.514	8	C	1	307.1435	−0.10415	307.1435	
		9	K	0	147.1128		147.1128	

Scan number	757	**Raw file**	LNCAP_Silac_23F10_set3_11
Method	ITMS; CID	**Pepti...**	83.5

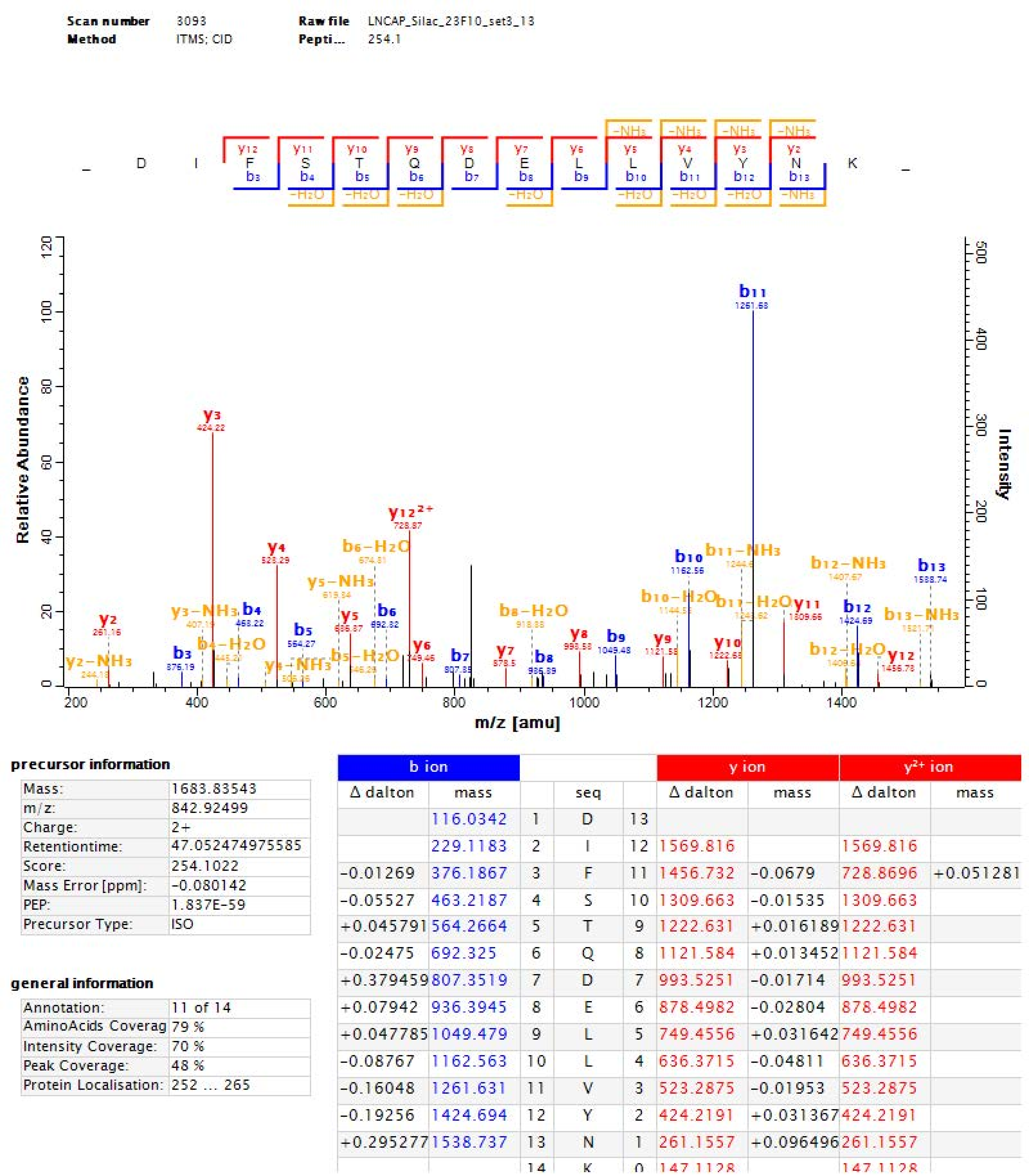


precursor information

Mass:	1166.65962
m/z:	584.33709
Charge:	2+
Retentiontime:	9.5763950347900
Score:	83.49903
Mass Error [ppm]:	0.18859
PEP:	0.0020873
Precursor Type:	MULTI

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	16 %
Peak Coverage:	20 %
Protein Localisation:	298 ... 307

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	129.11		157.11		157.11	1	R	9		
−0.013	228.18		256.18		256.18	2	V	8	1011.6	−0.066
	365.24		393.24	−0.083	393.24	3	H	7	912.5	
	462.29		490.29		490.29	4	P	6	775.44	−0.034
	561.36		589.36		589.36	5	V	5	678.39	
	648.39		676.39	+0.2062	676.39	6	S	4	579.32	
	749.44	+0.1501	389.22	+0.0327	777.44	7	T	3	492.29	
	880.48	−0.039	454.74	+0.0766	908.48	8	M	2	391.24	
	993.57		1021.6	−0.058	1021.6	9	I	1	260.2	+0.0301
						10	K	0	147.11	



Scan number	3093	**Raw file**	LNCAP_Silac_23F10_set3_13
Method	ITMS; CID	**Pepti...**	254.1

precursor information

Mass:	1683.83543
m/z:	842.92499
Charge:	2+
Retentiontime:	47.052474975585
Score:	254.1022
Mass Error [ppm]:	-0.080142
PEP:	1.837E-59
Precursor Type:	ISO

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	70 %
Peak Coverage:	48 %
Protein Localisation:	252 ... 265

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342	1	D	13				
	229.1183	2	I	12	1569.816		1569.816	
-0.01269	376.1867	3	F	11	1456.732	-0.0679	728.8696	+0.051281
-0.05527	463.2187	4	S	10	1309.663	-0.01535	1309.663	
+0.045791	564.2664	5	T	9	1222.631	+0.016189	1222.631	
-0.02475	692.325	6	Q	8	1121.584	+0.013452	1121.584	
+0.379459	807.3519	7	D	7	993.5251	-0.01714	993.5251	
+0.07942	936.3945	8	E	6	878.4982	-0.02804	878.4982	
+0.047785	1049.479	9	L	5	749.4556	+0.031642	749.4556	
-0.08767	1162.563	10	L	4	636.3715	-0.04811	636.3715	
-0.16048	1261.631	11	V	3	523.2875	-0.01953	523.2875	
-0.19256	1424.694	12	Y	2	424.2191	+0.031367	424.2191	
+0.295277	1538.737	13	N	1	261.1557	+0.096496	261.1557	
		14	K	0	147.1128		147.1128	