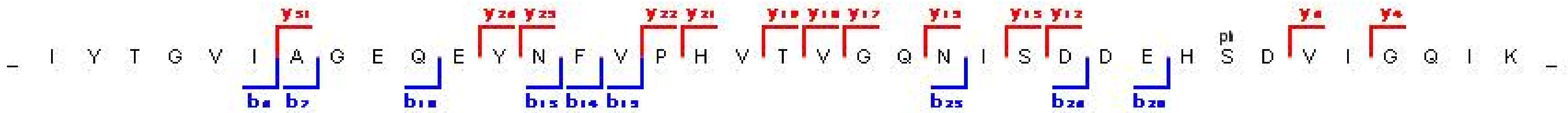
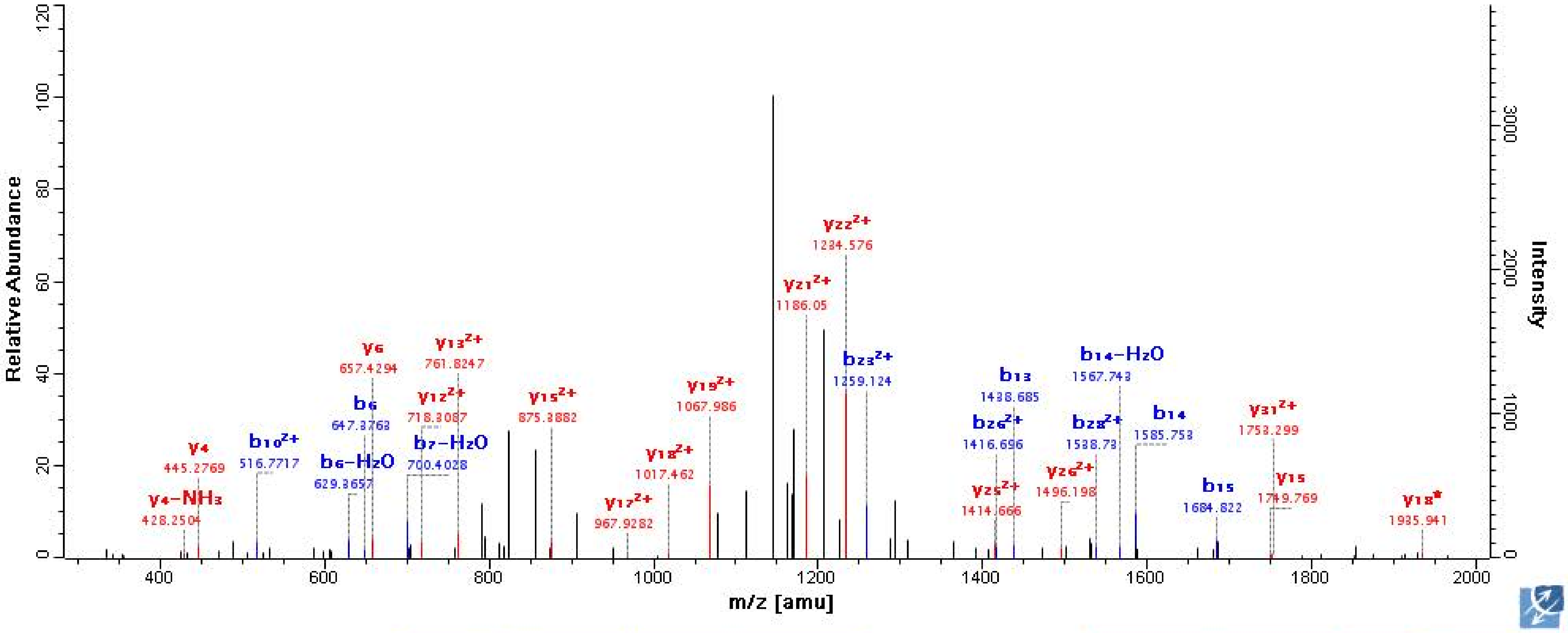
Source:	20120314_VR_TripleSILAC_pT1L1T2_F03
Scannumber:	10495
Protein:	BSU11850; yjcG
Peptide Score:	77.79
Method:	ITMS; CID; 3





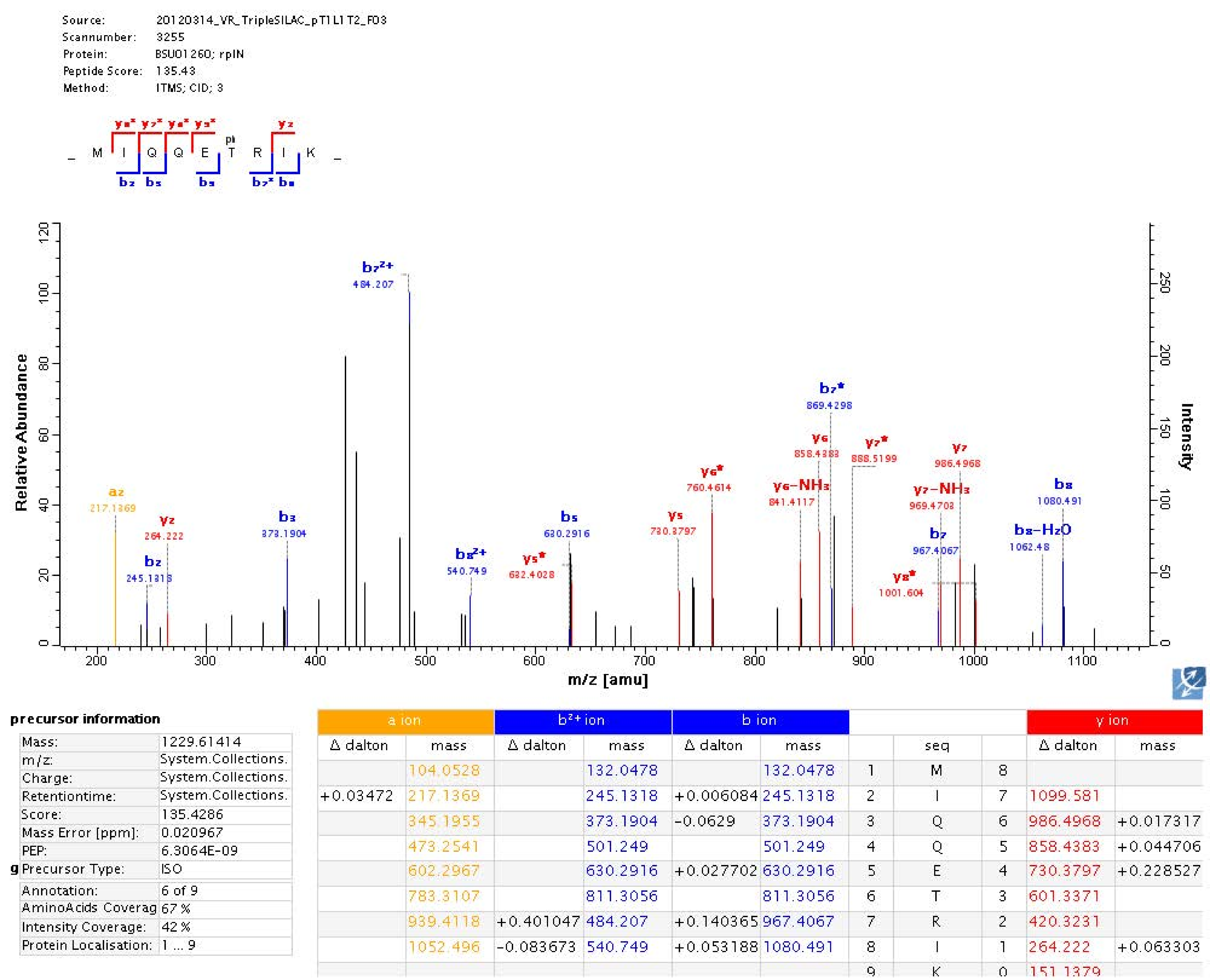
precursor information

Mass:	4150.95459
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	77.79086
Mass Error [ppm]:	0.50606
PEP:	5.0126E-17
Precursor Type:	ISO

general information

Annotation:	19 of 37
AminoAcids Coverag	51 %
Intensity Coverage:	26 %
Protein Localisation:	99 ... 135

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913		114.0913	1	I	36				
	277.1547		277.1547	2	Y	35	4038.876		4038.876	
	378.2023		378.2023	3	T	34	3875.812		3875.812	
	435.2238		435.2238	4	G	33	3774.765		3774.765	
	534.2922		534.2922	5	V	32	3717.743		3717.743	
	647.3763	+0.004753	647.3763	6	I	31	3618.675		3618.675	
	718.4134		718.4134	7	A	30	3505.591		1753.299	-0.210267
	775.4349		775.4349	8	G	29	3434.554		3434.554	
	904.4775		904.4775	9	E	28	3377.532		3377.532	
-0.398732	516.7717		1032.536	10	Q	27	3248.49		3248.49	
	1161.579		1161.579	11	E	26	3120.431		3120.431	
	1324.642		1324.642	12	Y	25	2991.388		1496.198	+0.157383
	1438.685	+0.138234	1438.685	13	N	24	2828.325		1414.666	+0.402182
	1585.753	-0.142338	1585.753	14	F	23	2714.282		2714.282	
	1684.822	-0.002622	1684.822	15	V	22	2567.214		2567.214	
	1781.874		1781.874	16	P	21	2468.145		1234.576	+0.118646
	1918.933		1918.933	17	H	20	2371.093		1186.05	-0.244498
	2018.002		2018.002	18	V	19	2234.034		2234.034	
	2119.049		2119.049	19	T	18	2134.965		1067.986	+0.242993
	2218.118		2218.118	20	V	17	2033.918		1017.462	+0.475695
	2275.139		2275.139	21	G	16	1934.849		967.9282	-0.01317
	2403.198		2403.198	22	Q	15	1877.828		1877.828	
-0.018846	1259.124		2517.241	23	N	14	1749.769	+0.410221	875.3882	+0.110469
	2630.325		2630.325	24	I	13	1635.726		1635.726	
	2717.357		2717.357	25	S	12	1522.642		761.8247	+0.181289
+0.273528	1416.696		2832.384	26	D	11	1435.61		718.3087	-0.028588
	2947.411		2947.411	27	D	10	1320.583		1320.583	
+0.10436	1538.73		3076.453	28	E	9	1205.556		1205.556	
	3213.512		3213.512	29	H	8	1076.514		1076.514	
	3380.511		3380.511	30	S	7	939.4547		939.4547	
	3495.538		3495.538	31	D	6	772.4563		772.4563	
	3594.606		3594.606	32	V	5	657.4294	+0.015498	657.4294	
	3707.69		3707.69	33	I	4	558.361		558.361	
	3764.712		3764.712	34	G	3	445.2769	+0.11573	445.2769	
	3892.77		3892.77	35	Q	2	388.2554		388.2554	
	4005.854		4005.854	36	I	1	260.1969		260.1969	
				37	K	0	147.1128		147.1128	

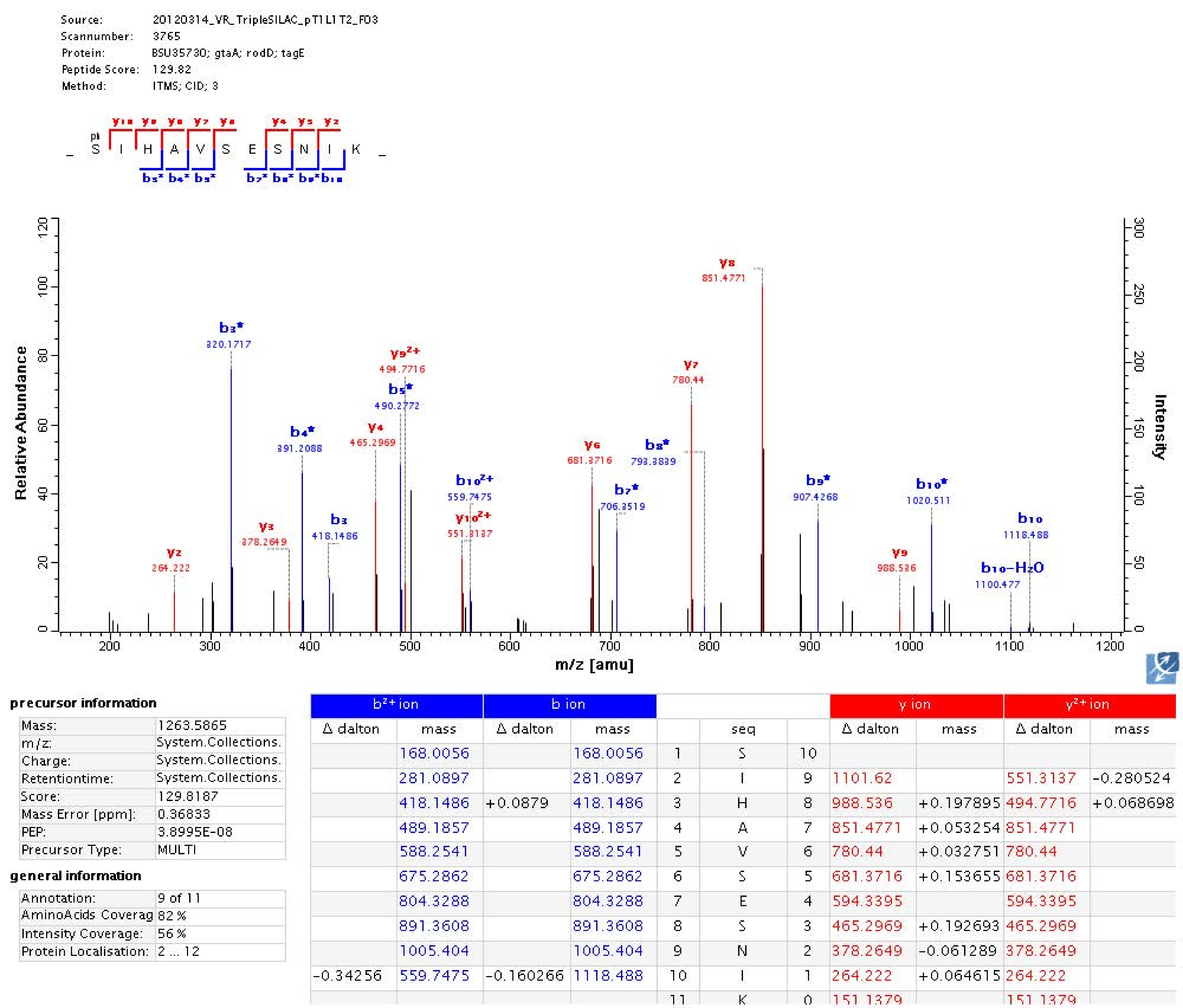


Source:	20120314_VR_TripleSILAC_pT1L1T2_F03
Scannumber:	3255
Protein:	BSU01260; rplN
Peptide Score:	135.43
Method:	ITMS; CID; 3

precursor information

Mass:	1229.61414
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	135.4286
Mass Error [ppm]:	0.020967
PEP:	6.3064E-09
Precursor Type:	ISO
Annotation:	6 of 9
AminoAcids Coverag	67 %
Intensity Coverage:	42 %
Protein Localisation:	1 ... 9

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	104.0528		132.0478		132.0478	1	M	8		
+0.03472	217.1369		245.1318	+0.006084	245.1318	2	I	7	1099.581	
	345.1955		373.1904	-0.0629	373.1904	3	Q	6	986.4968	+0.017317
	473.2541		501.249		501.249	4	Q	5	858.4383	+0.044706
	602.2967		630.2916	+0.027702	630.2916	5	E	4	730.3797	+0.228527
	783.3107		811.3056		811.3056	6	T	3	601.3371	
	939.4118	+0.401047	484.207	+0.140365	967.4067	7	R	2	420.3231	
	1052.496	-0.083673	540.749	+0.053188	1080.491	8	I	1	264.222	+0.063303
						9	K	0	151.1379	



Source: 20120314_VR_TripleSILAC_pT1L1T2_F03
Scannumber: 3765
Protein: BSU35730; gtaA; rodD; tagE
Peptide Score: 129.82
Method: ITMS; CID; 3

precursor information

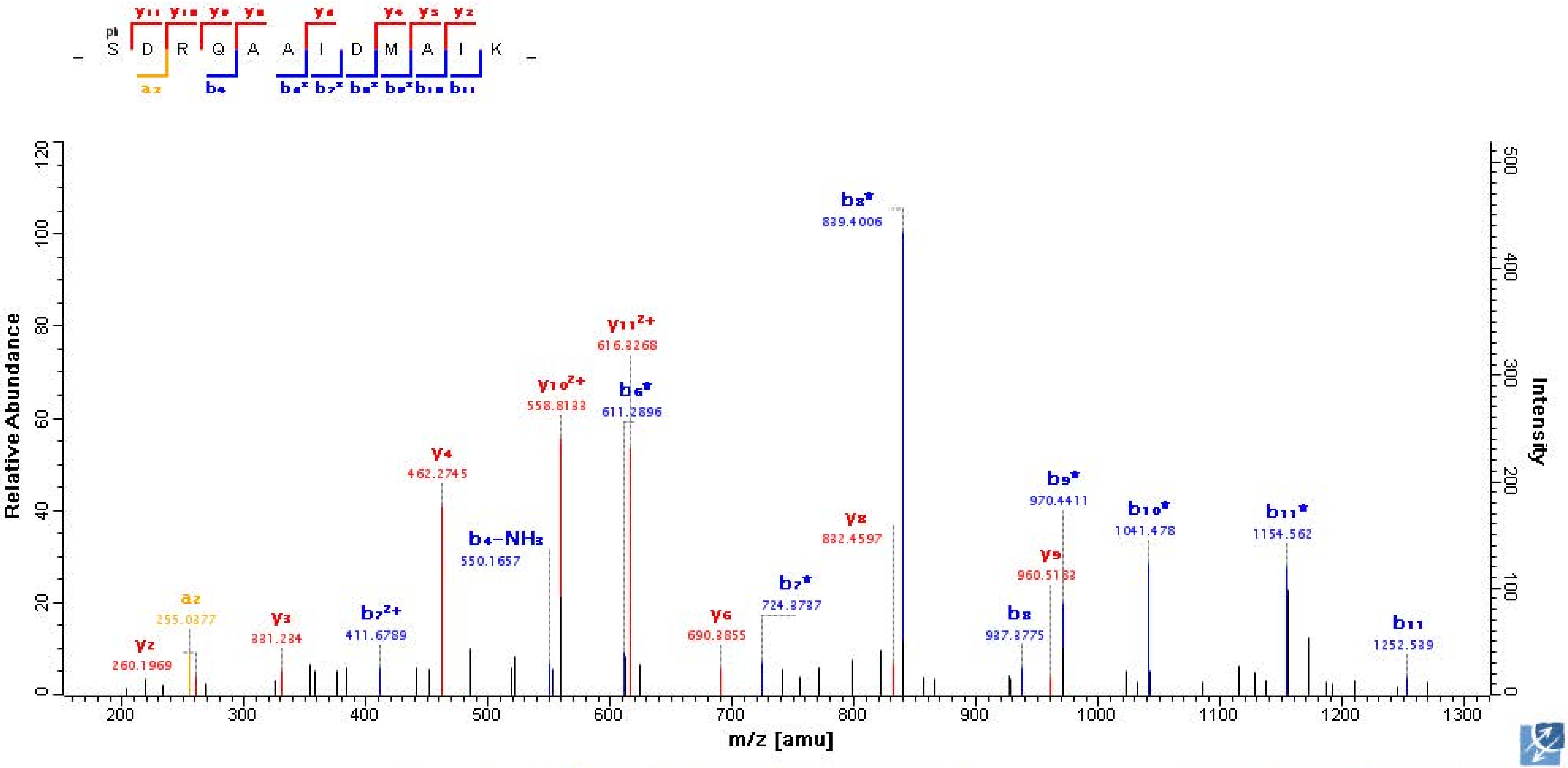
Mass:	1263.5865
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	129.8187
Mass Error [ppm]:	0.36833
PEP:	3.8995E-08
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	56 %
Protein Localisation:	2 ... 12

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.0056		168.0056	1	S	10				
	281.0897		281.0897	2	I	9	1101.62		551.3137	-0.280524
	418.1486	+0.0879	418.1486	3	H	8	988.536	+0.197895	494.7716	+0.068698
	489.1857		489.1857	4	A	7	851.4771	+0.053254	851.4771	
	588.2541		588.2541	5	V	6	780.44	+0.032751	780.44	
	675.2862		675.2862	6	S	5	681.3716	+0.153655	681.3716	
	804.3288		804.3288	7	E	4	594.3395		594.3395	
	891.3608		891.3608	8	S	3	465.2969	+0.192693	465.2969	
	1005.404		1005.404	9	N	2	378.2649	-0.061289	378.2649	
-0.34256	559.7475	-0.160266	1118.488	10	I	1	264.222	+0.064615	264.222	
				11	K	0	151.1379		151.1379	

Source:	20120314_VR_TripleSILAC_pT1L1T2_F03
Scannumber:	5982
Protein:	BSU16940; recA; recE
Peptide Score:	114.82
Method:	ITMS; CID; 3



precursor information

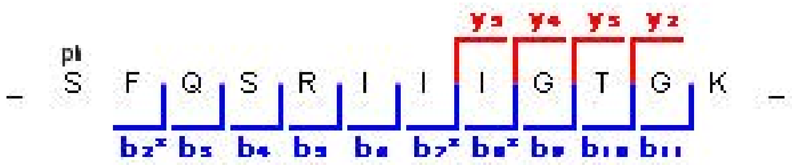
Mass:	1397.63817
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	114.8167
Mass Error [ppm]:	0.54315
PEP:	2.2616E-05
Precursor Type:	MULTI

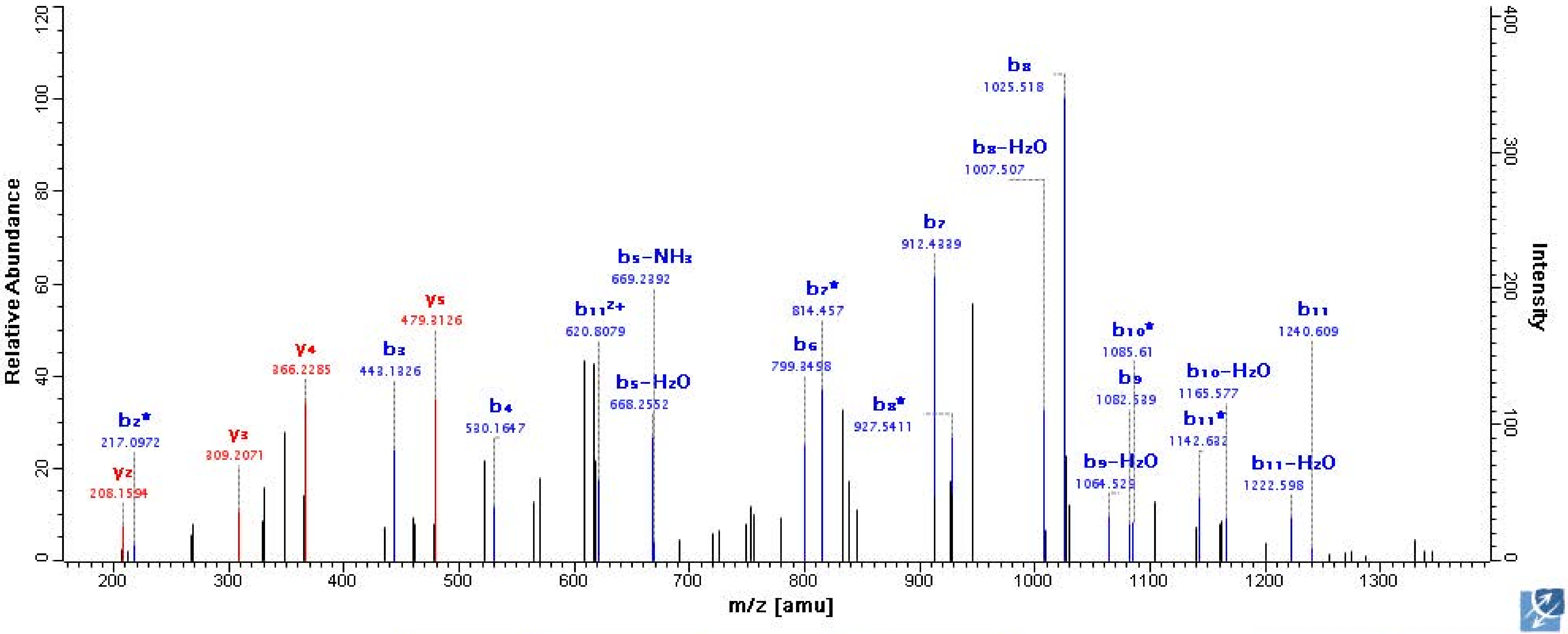
general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	60 %
Protein Localisation:	2 ... 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
	140.011		168.006		168.006	1	S	11				
+0.05146	255.038		283.033		283.033	2	D	10	1231.65		616.327	+0.2278
	411.139		439.134		439.134	3	R	9	1116.62		558.813	+0.0252
	539.197		567.192		567.192	4	Q	8	960.518	+0.09348	960.518	
	610.234		638.229		638.229	5	A	7	832.46	-0.1539	832.46	
	681.272		709.266		709.266	6	A	6	761.423		761.423	
	794.356	-0.1368	411.679		822.351	7	I	5	690.385	+0.14913	690.385	
	909.383		937.378	+0.11591	937.378	8	D	4	577.301		577.301	
	1040.42		1068.42		1068.42	9	M	3	462.274	+0.01966	462.274	
	1111.46		1139.46		1139.46	10	A	2	331.234	+0.06649	331.234	
	1224.54		1252.54	+0.12551	1252.54	11	I	1	260.197	+0.09439	260.197	
						12	K	0	147.113		147.113	

Source:	20120314_VR_TripleSILAC_pT1L1T2_F03
Scannumber:	7518
Protein:	BSU11690; thiG; yjbT
Peptide Score:	107.99
Method:	ITMS; CID; 3





precursor information

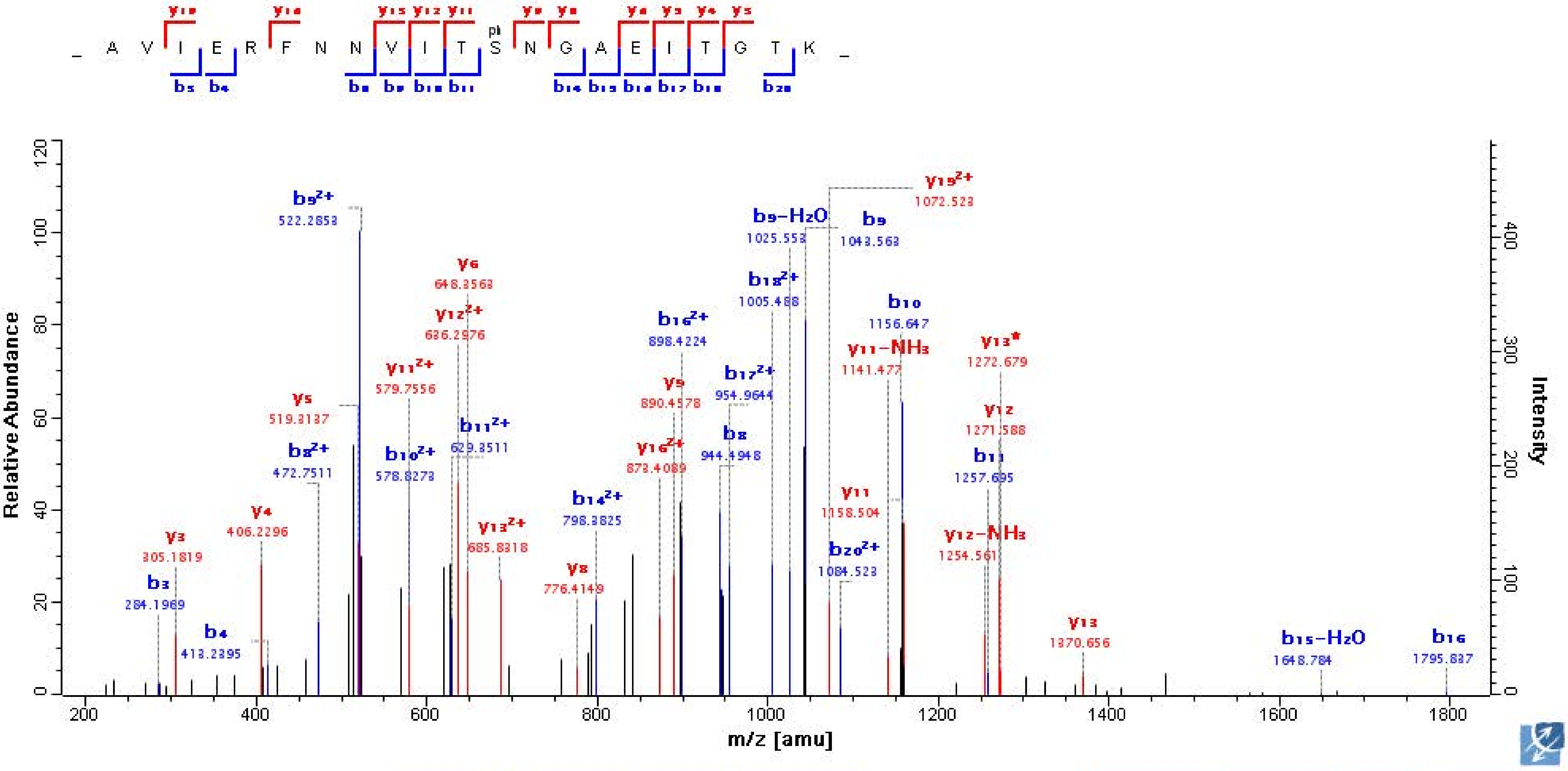
Mass:	1385.70607
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	107.9941
Mass Error [ppm]:	-0.5347
PEP:	0.0001056
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	45 %
Protein Localisation:	10 ... 21

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	168.00563528		168.00563528	1	S	11		
	315.0740492		315.0740492	2	F	10	1223.7408399	
	443.13262671	+0.0410793	443.13262671	3	Q	9	1076.672426	
	530.16465512	-0.350141	530.16465512	4	S	8	948.61384845	
	686.26576615		686.26576615	5	R	7	861.58182004	
	799.34983013	+0.0545278	799.34983013	6	I	6	705.48070902	
	912.43389411	-0.1201124	912.43389411	7	I	5	592.39664504	
	1025.5179581	-0.0106339	1025.5179581	8	I	4	479.31258106	+0.0099287
	1082.5394218	-0.1885917	1082.5394218	9	G	3	366.22851708	+0.018187
	1183.5871003		1183.5871003	10	T	2	309.20705335	-0.2433082
-0.1990335	620.80792024	-0.1177193	1240.608564	11	G	1	208.15937488	+0.0843538
				12	K	0	151.13791115	

Source:	20120314_VR_TripleSILAC_pT1L1T2_F03
Scannumber:	7867
Protein:	BSU40910; rpsF
Peptide Score:	171.78
Method:	ITMS; CID; 3



precursor information

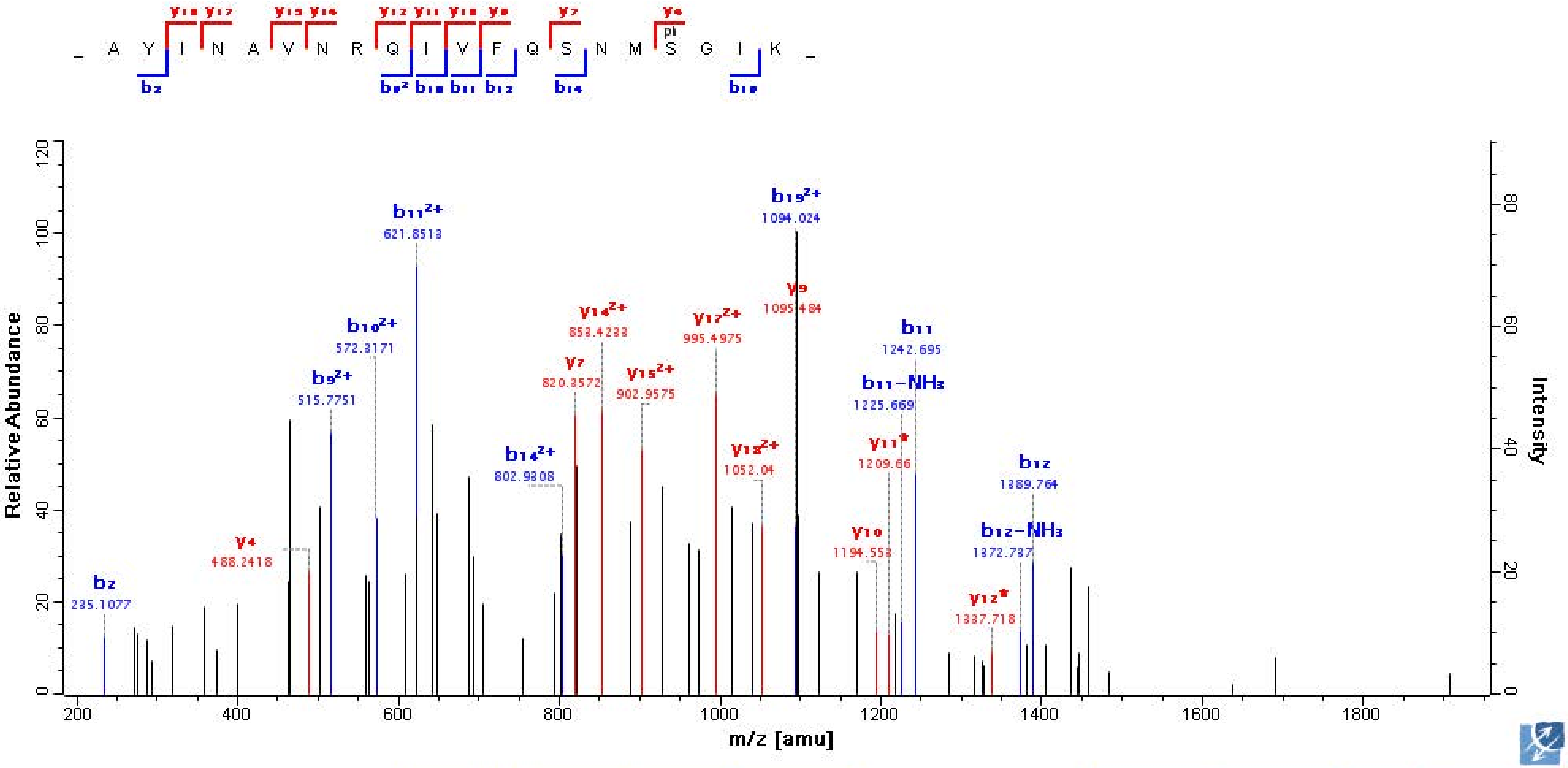
Mass:	2313.13811
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	171.7834
Mass Error [ppm]:	0.65874
PEP:	8.6057E-46
Precursor Type:	ISO

general information

Annotation:	15 of 21
AminoAcids Coverag	71 %
Intensity Coverage:	61 %
Protein Localisation:	21 ... 41

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439		72.04439	1	A	20				
	171.1128		171.1128	2	V	19	2243.107		2243.107	
	284.1969	+0.128266	284.1969	3	I	18	2144.038		1072.523	+0.242573
	413.2395	-0.066976	413.2395	4	E	17	2030.954		2030.954	
	569.3406		569.3406	5	R	16	1901.912		1901.912	
	716.409		716.409	6	F	15	1745.811		873.4089	+0.117138
	830.4519		830.4519	7	N	14	1598.742		1598.742	
+0.07432	472.7511	-0.012236	944.4948	8	N	13	1484.699		1484.699	
-0.363452	522.2853	+0.022682	1043.563	9	V	12	1370.656	-0.176077	685.8318	+0.155149
-0.107998	578.8273	+0.0873	1156.647	10	I	11	1271.588	-0.06384	636.2976	+0.109949
-0.07245	629.3511	-0.064748	1257.695	11	T	10	1158.504	+0.075522	579.7556	-0.270382
	1424.693		1424.693	12	S	9	1057.456		1057.456	
	1538.736		1538.736	13	N	8	890.4578	-0.150353	890.4578	
+0.351314	798.3825		1595.758	14	G	7	776.4149	-0.27222	776.4149	
	1666.795		1666.795	15	A	6	719.3934		719.3934	
+0.226133	898.4224	+0.376657	1795.837	16	E	5	648.3563	+0.038371	648.3563	
+0.13332	954.9644		1908.922	17	I	4	519.3137	+0.022859	519.3137	
+0.190169	1005.488		2009.969	18	T	3	406.2296	-0.021007	406.2296	
	2066.991		2066.991	19	G	2	305.1819	+0.075836	305.1819	
+0.114155	1084.523		2168.038	20	T	1	248.1605		248.1605	
				21	K	0	147.1128		147.1128	

Source:	20120314_VR_TripleSILAC_pT1L1T2_F03
Scannumber:	8656
Protein:	BSU28280; leuA
Peptide Score:	70.41
Method:	ITMS; CID; 3



precursor information

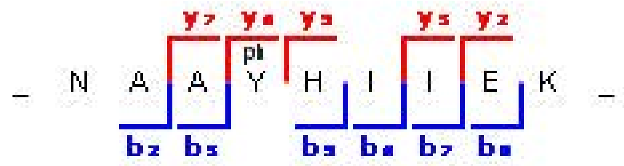
Mass:	2332.14105
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	70.41049
Mass Error [ppm]:	0.48951
PEP:	0.00014313
Precursor Type:	MULTI

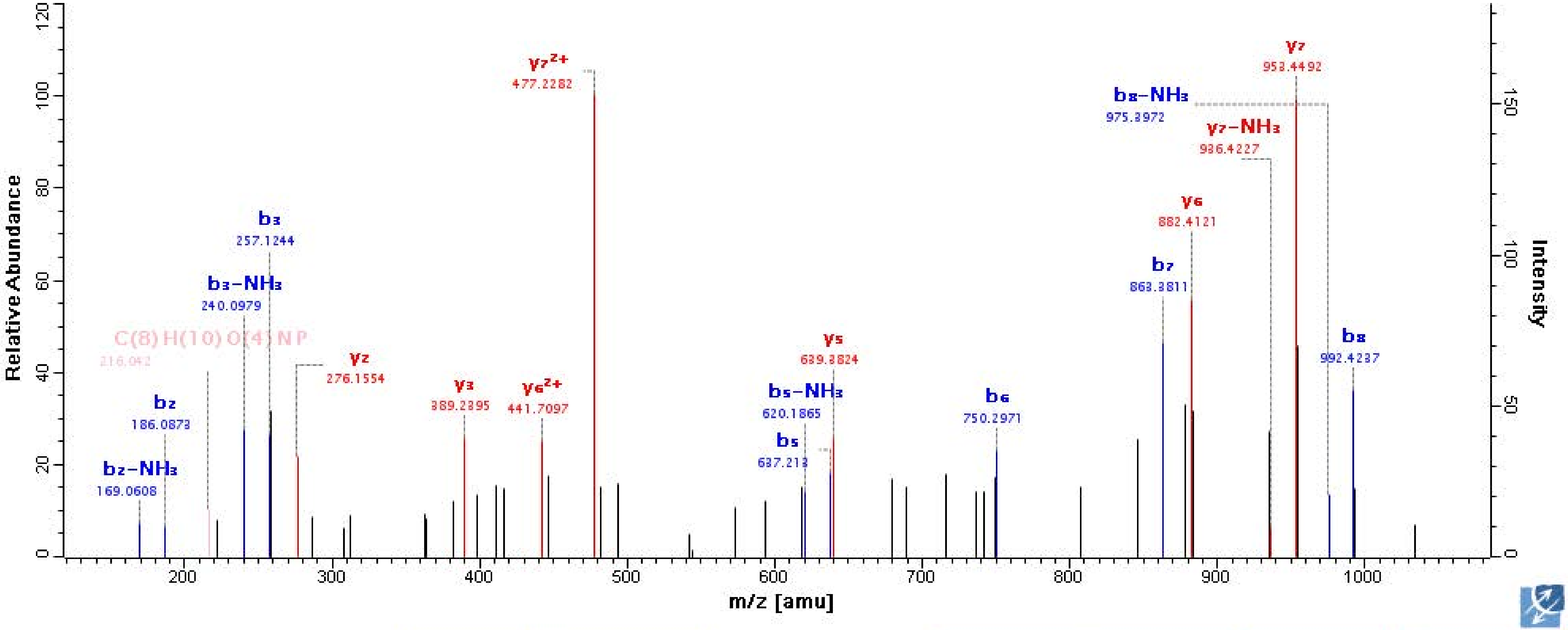
general information

Annotation:	14 of 20
AminoAcids Coverag	70 %
Intensity Coverage:	38 %
Protein Localisation:	492 ... 511

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439		72.04439	1	A	19				
	235.1077	+0.011086	235.1077	2	Y	18	2266.135		2266.135	
	348.1918		348.1918	3	I	17	2103.072		1052.04	+0.141959
	462.2347		462.2347	4	N	16	1989.988		995.4975	+0.014863
	533.2718		533.2718	5	A	15	1875.945		1875.945	
	632.3402		632.3402	6	V	14	1804.908		902.9575	-0.029284
	746.3832		746.3832	7	N	13	1705.839		853.4233	+0.011698
	902.4843		902.4843	8	R	12	1591.796		1591.796	
+0.326497	515.7751		1030.543	9	Q	11	1435.695		1435.695	
+0.248394	572.3171		1143.627	10	I	10	1307.637		1307.637	
+0.136123	621.8513	+0.099956	1242.695	11	V	9	1194.553	+0.332855	1194.553	
	1389.764	+0.009936	1389.764	12	F	8	1095.484	-0.359718	1095.484	
	1517.822		1517.822	13	Q	7	948.4158		948.4158	
+0.100802	802.9308		1604.854	14	S	6	820.3572	+0.036256	820.3572	
	1718.897		1718.897	15	N	5	733.3252		733.3252	
	1849.938		1849.938	16	M	4	619.2823		619.2823	
	2016.936		2016.936	17	S	3	488.2418	-0.431129	488.2418	
	2073.958		2073.958	18	G	2	321.2434		321.2434	
-0.067798	1094.024		2187.042	19	I	1	264.222		264.222	
				20	K	0	151.1379		151.1379	

Source: 20120314_VR_TripleSILAC_pT1L1T2_F05
Scannumber: 4748
Protein: BSU03050; lctE; ldh
Peptide Score: 144.09
Method: ITMS; CID; 3



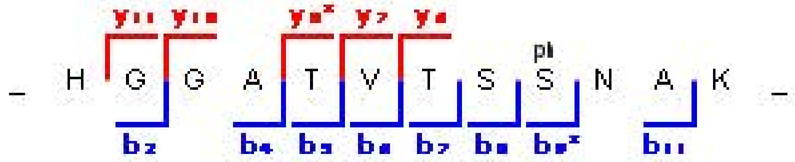


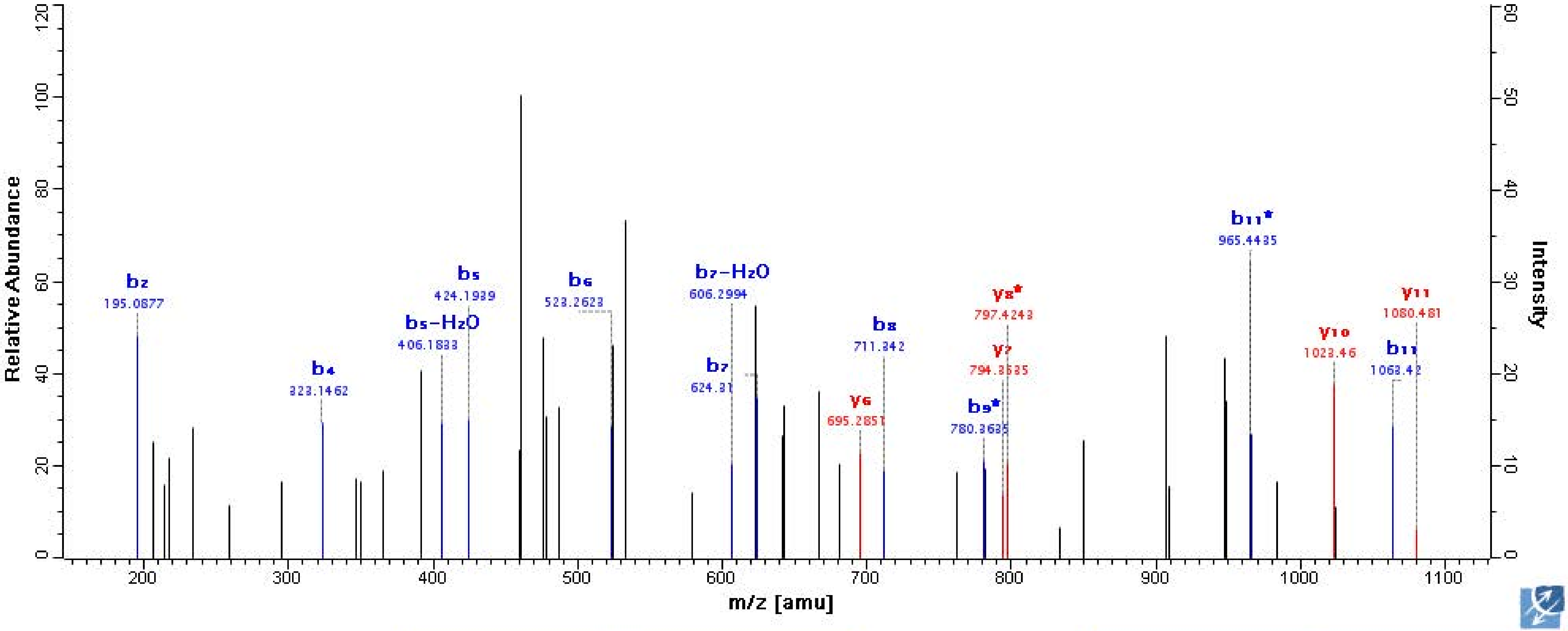
precursor information

Mass:	1137.52182
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	144.0888
Mass Error [ppm]:	-0.13383
PEP:	1.3877E-06
g Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	53 %
Protein Localisation:	220 ... 228

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.05020391	1	N	8				
-0.0208962	186.0873177	2	A	7	1024.4863236		1024.4863236	
+0.0168039	257.12443149	3	A	6	953.44920982	-0.0575472	477.22824315	+0.2170083
	500.15409044	4	Y	5	882.41209604	-0.0027332	441.70968625	-0.0452575
+0.072154	637.2130023	5	H	4	639.38243709	-0.0421661	639.38243709	
+0.043754	750.29706628	6	I	3	502.32352523		502.32352523	
-0.0029564	863.38113026	7	I	2	389.23946125	+0.0212809	389.23946125	
+0.035261	992.42372336	8	E	1	276.15539727	+0.112364	276.15539727	
		9	K	0	147.11280417		147.11280417	

Source: 20120314_VR_TripleSILAC_pT1L1T2_F07
Scannumber: 1391
Protein: BSU27850; nadA
Peptide Score: 72.7
Method: ITMS; CID; 3





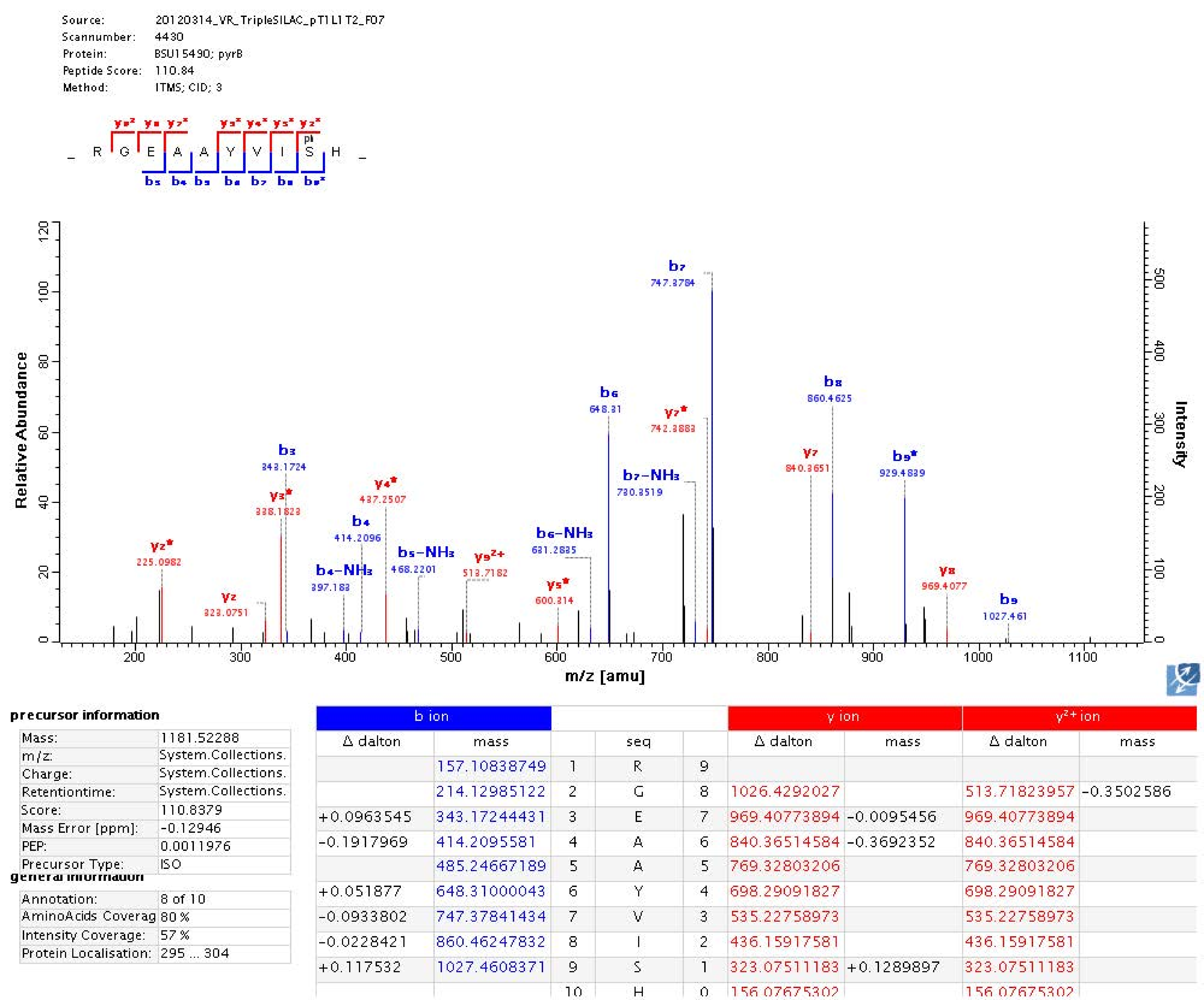
precursor information

Mass:	1208.51871
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	72.70486
Mass Error [ppm]:	0.021031
PEP:	0.01275
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	28 %
Protein Localisation:	155 ... 166

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	138.066188329	1	H	11		
-0.0397089	195.087652053	2	G	10	1080.481243546	+0.0984684
	252.109115776	3	G	9	1023.459779823	+0.1044292
+0.1350815	323.146229564	4	A	8	966.438316099	
+0.1069953	424.193908038	5	T	7	895.401202311	
+0.2281566	523.262321954	6	V	6	794.353523837	+0.0938028
+0.079709	624.310000428	7	T	5	695.285109921	+0.1769262
+0.05	711.342028838	8	S	4	594.237431447	
	878.340387657	9	S	3	507.205403037	
	992.383315104	10	N	2	340.207044219	
+0.140118	1063.420428892	11	A	1	226.164116772	
		12	K	0	155.127002984	



Source: 20120314_VR_TripleSILAC_pT1L1T2_F07
Scannumber: 4430
Protein: BSU15490; pyrB
Peptide Score: 110.84
Method: ITMS; CID; 3

precursor information

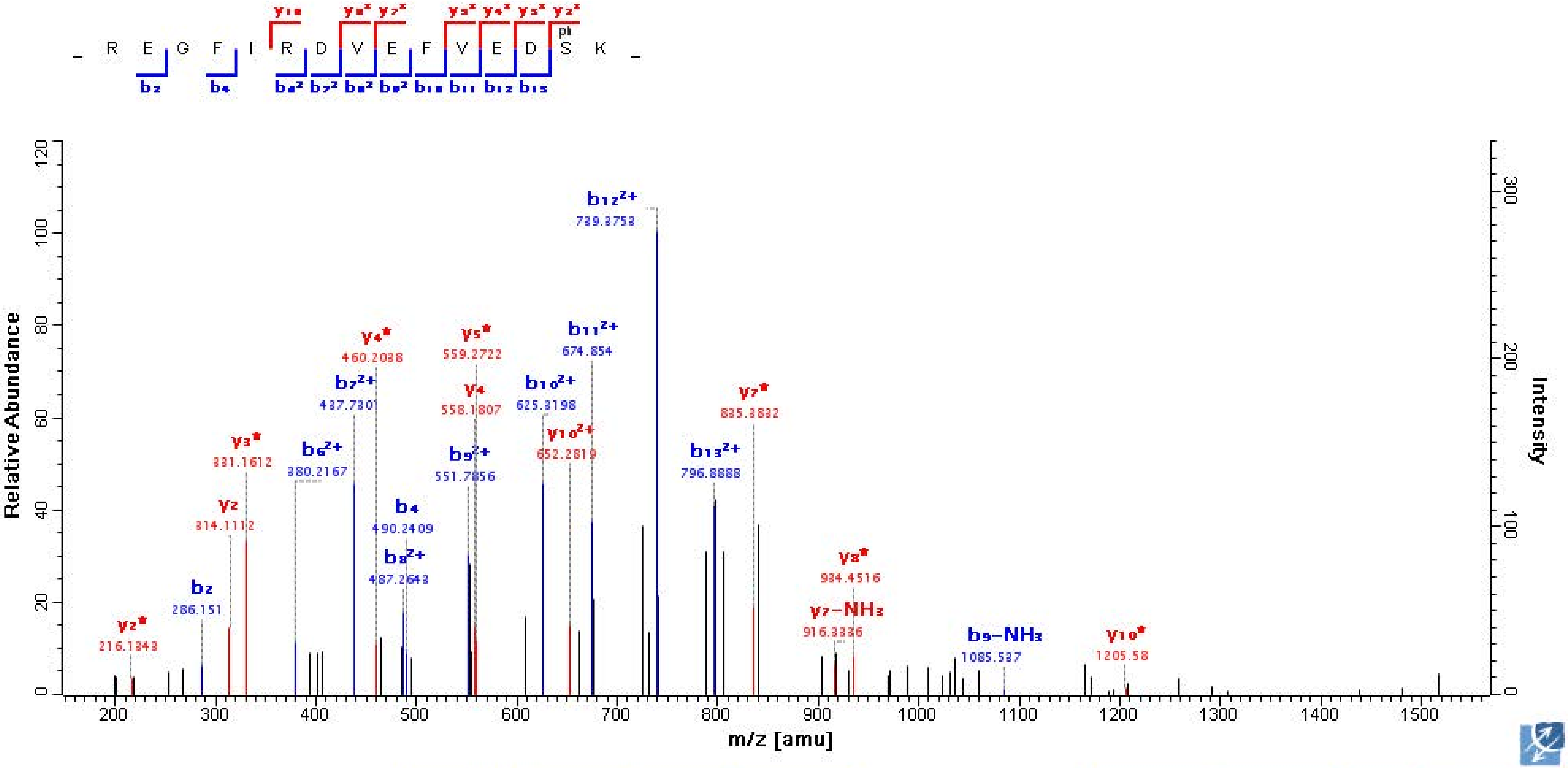
Mass:	1181.52288
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	110.8379
Mass Error [ppm]:	-0.12946
PEP:	0.0011976
Precursor Type:	ISO

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	57 %
Protein Localisation:	295 ... 304

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	157.10838749	1	R	9				
	214.12985122	2	G	8	1026.4292027		513.71823957	-0.3502586
+0.0963545	343.17244431	3	E	7	969.40773894	-0.0095456	969.40773894	
-0.1917969	414.2095581	4	A	6	840.36514584	-0.3692352	840.36514584	
	485.24667189	5	A	5	769.32803206		769.32803206	
+0.051877	648.31000043	6	Y	4	698.29091827		698.29091827	
-0.0933802	747.37841434	7	V	3	535.22758973		535.22758973	
-0.0228421	860.46247832	8	I	2	436.15917581		436.15917581	
+0.117532	1027.4608371	9	S	1	323.07511183	+0.1289897	323.07511183	
		10	H	0	156.07675302		156.07675302	

Source: 20120314_VR_TripleSILAC_pT1L1T2_F11
Scannumber: 8431
Protein: BSU01300; rpsH
Peptide Score: 94.72
Method: ITMS; CID; 3



precursor information

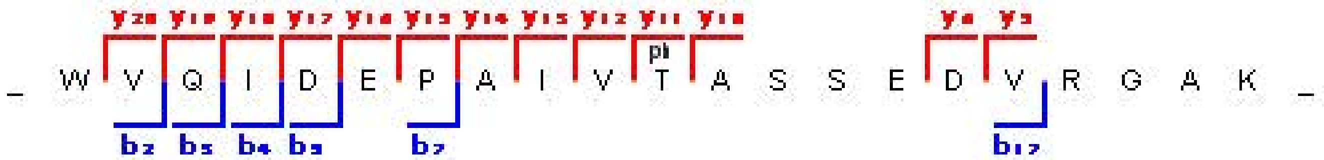
Mass:	1904.86717
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	94.71677
Mass Error [ppm]:	0.10994
PEP:	0.0070557
Precursor Type:	MULTI

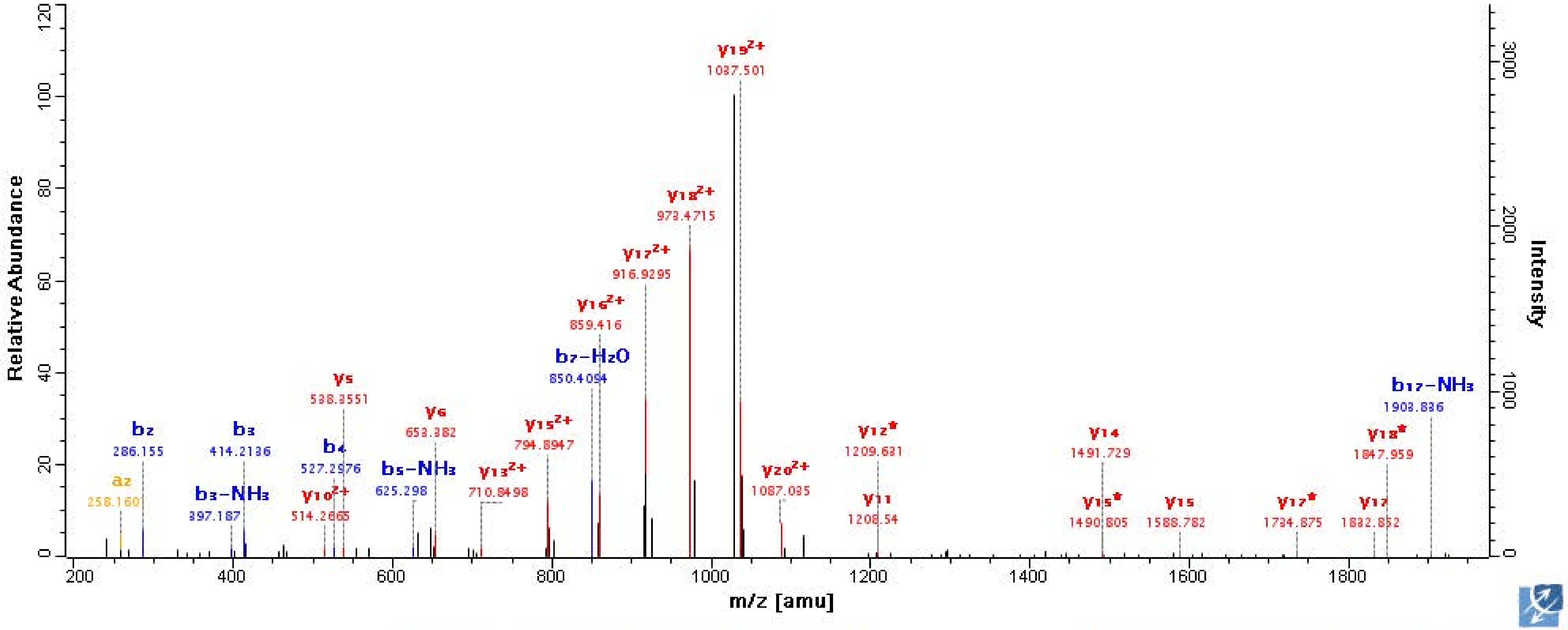
general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	50 %
Protein Localisation:	42 ... 56

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	157.1084		157.1084	1	R	14				
	286.151	-0.09376	286.151	2	E	13	1749.773		1749.773	
	343.1724		343.1724	3	G	12	1620.731		1620.731	
	490.2409	+0.094713	490.2409	4	F	11	1563.709		1563.709	
	603.3249		603.3249	5	I	10	1416.641		1416.641	
+0.038716	380.2167		759.426	6	R	9	1303.557		652.2819	+0.09734
+0.006141	437.7301		874.453	7	D	8	1147.455		1147.455	
-0.249014	487.2643		973.5214	8	V	7	1032.429		1032.429	
-0.083787	551.7856		1102.564	9	E	6	933.3601		933.3601	
+0.192675	625.3198		1249.632	10	F	5	804.3175		804.3175	
+0.13027	674.854		1348.701	11	V	4	657.2491		657.2491	
+0.043056	739.3753		1477.743	12	E	3	558.1807	-0.228856	558.1807	
-0.005816	796.8888		1592.77	13	D	2	429.1381		429.1381	
	1759.769		1759.769	14	S	1	314.1112	-0.054126	314.1112	
				15	K	0	147.1128		147.1128	

Source:	20120314_VR_TripleSILAC_pT1L1T2_F17
Scannumber:	10521
Protein:	BSU13180; metC; metE
Peptide Score:	107.33
Method:	ITMS; CID; 3





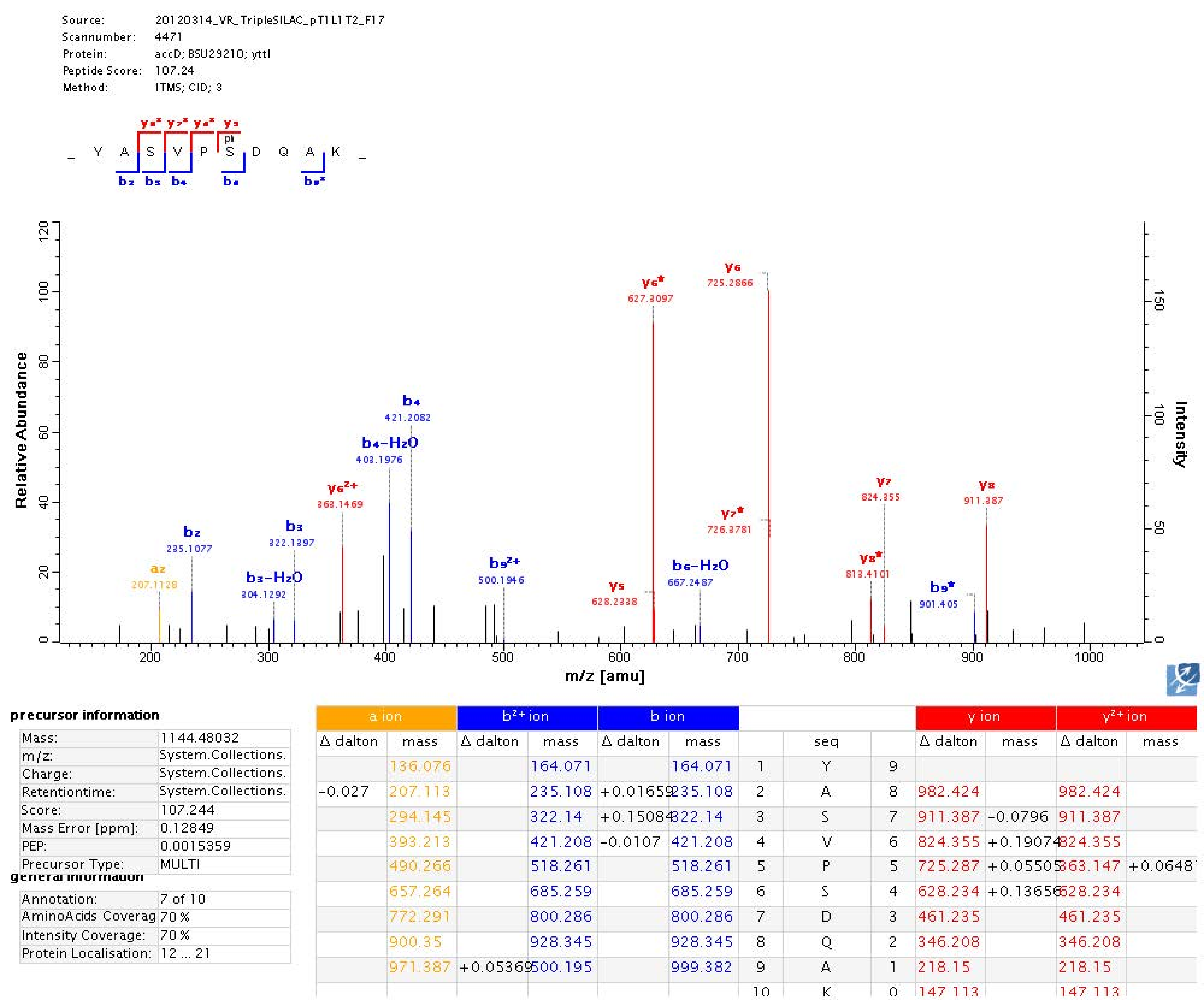
precursor information

Mass:	2350.11951
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	107.3267
Mass Error [ppm]:	-0.46524
PEP:	8.4282E-11
Precursor Type:	MULTI

general information

Annotation:	14 of 21
AminoAcids Coverag	67 %
Intensity Coverage:	41 %
Protein Localisation:	200 ... 220

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	159.0917		187.0866	1	W	20				
+0.007453	258.1601	+0.034267	286.155	2	V	19	2173.063		1087.035	+0.251721
	386.2187	-0.003315	414.2136	3	Q	18	2073.994		1037.501	-0.117026
	499.3027	-0.061256	527.2976	4	I	17	1945.936		973.4715	+0.202241
	614.3297		642.3246	5	D	16	1832.852	+0.343234	916.9295	-0.039907
	743.3723		771.3672	6	E	15	1717.825		859.416	+0.133843
	840.425		868.4199	7	P	14	1588.782	-0.370189	794.8947	-0.029431
	911.4621		939.4571	8	A	13	1491.729	+0.436847	1491.729	
	1024.546		1052.541	9	I	12	1420.692		710.8498	+0.079106
	1123.615		1151.61	10	V	11	1307.608		1307.608	
	1304.629		1332.624	11	T	10	1208.54	+0.006199	1208.54	
	1375.666		1403.661	12	A	9	1027.526		514.2665	-0.014164
	1462.698		1490.693	13	S	8	956.4887		956.4887	
	1549.73		1577.725	14	S	7	869.4567		869.4567	
	1678.772		1706.767	15	E	6	782.4246		782.4246	
	1793.799		1821.794	16	D	5	653.382	+0.171968	653.382	
	1892.868		1920.863	17	V	4	538.3551	-0.123233	538.3551	
	2048.969		2076.964	18	R	3	439.2867		439.2867	
	2105.99		2133.985	19	G	2	283.1856		283.1856	
	2177.027		2205.022	20	A	1	226.1641		226.1641	
				21	K	0	155.127		155.127	



Source: 20120314_VR_TripleSILAC_pT1L1T2_F17
Scannumber: 4471
Protein: accD; BSU29210; yttI
Peptide Score: 107.24
Method: ITMS; CID; 3

precursor information

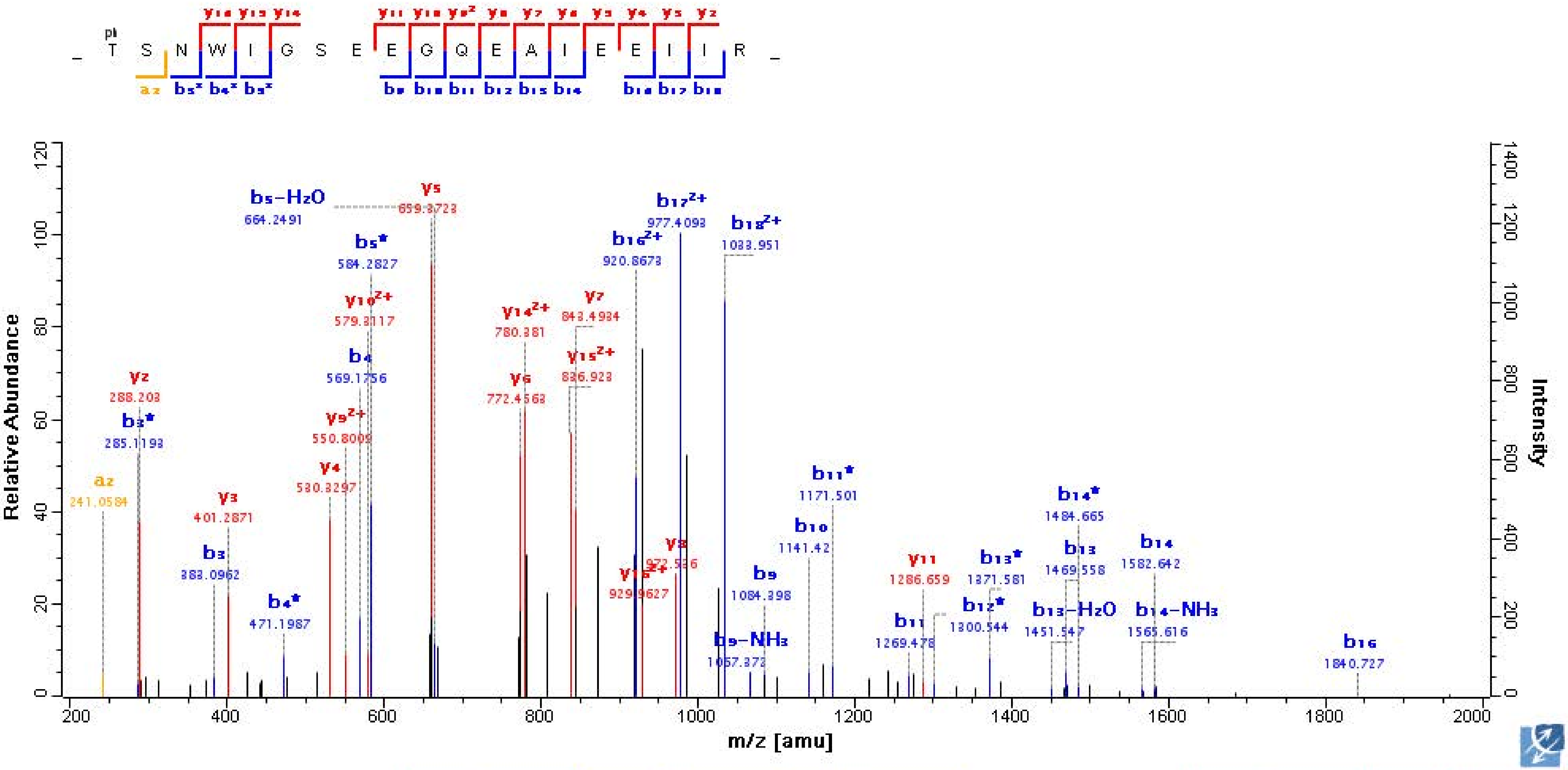
Mass:	1144.48032
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	107.244
Mass Error [ppm]:	0.12849
PEP:	0.0015359
Precursor Type:	MULTI

general information

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	70 %
Protein Localisation:	12 ... 21

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
	136.076		164.071		164.071	1	Y	9				
-0.027	207.113		235.108	+0.01659	235.108	2	A	8	982.424		982.424	
	294.145		322.14	+0.15084	322.14	3	S	7	911.387	-0.0796	911.387	
	393.213		421.208	-0.0107	421.208	4	V	6	824.355	+0.19074	824.355	
	490.266		518.261		518.261	5	P	5	725.287	+0.05505	363.147	+0.0648
	657.264		685.259		685.259	6	S	4	628.234	+0.13656	628.234	
	772.291		800.286		800.286	7	D	3	461.235		461.235	
	900.35		928.345		928.345	8	Q	2	346.208		346.208	
	971.387	+0.05369	500.195		999.382	9	A	1	218.15		218.15	
						10	K	0	147.113		147.113	

Source:	20120314_VR_TripleSILAC_pT1L1T2_F18
Scannumber:	13370
Protein:	BSU27660; yrzD
Peptide Score:	171.35
Method:	ITMS; CID; 3



precursor information

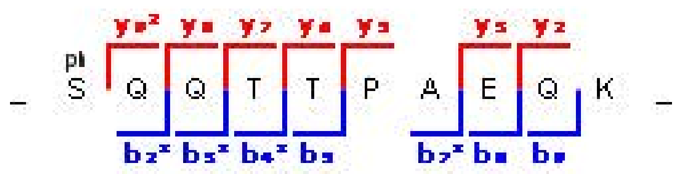
Mass:	2239.99994
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	171.3528
Mass Error [ppm]:	0.052471
PEP:	5.2603E-40
Precursor Type:	ISO

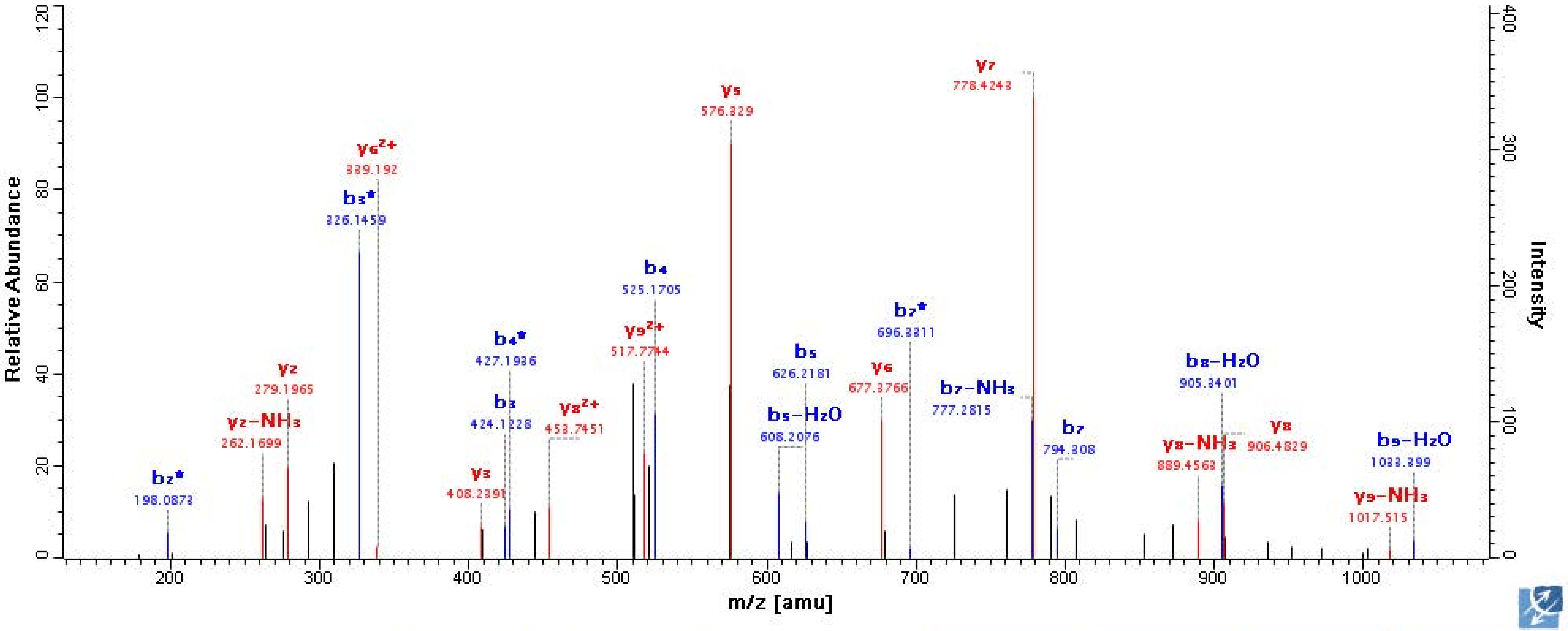
general information

Annotation:	15 of 19
AminoAcids Coverag	79 %
Intensity Coverage:	63 %
Protein Localisation:	80 ... 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
	154.026		182.021		182.021	1	T	18				
+0.01367	241.058		269.053		269.053	2	S	17	2059.99		2059.99	
	355.101		383.096	+0.03352	383.096	3	N	16	1972.96		1972.96	
	541.181		569.176	-0.0374	569.176	4	W	15	1858.92		929.963	-0.0052
	654.265		682.26		682.26	5	I	14	1672.84		836.923	+0.1917
	711.286		739.281		739.281	6	G	13	1559.75		780.381	+0.0200
	798.318		826.313		826.313	7	S	12	1502.73		1502.73	
	927.361		955.356		955.356	8	E	11	1415.7		1415.7	
	1056.4		1084.4	-0.3728	1084.4	9	E	10	1286.66	+0.03566	1286.66	
	1113.42		1141.42	+0.07328	1141.42	10	G	9	1157.62		579.312	+0.1904
	1241.48		1269.48	+0.09698	1269.48	11	Q	8	1100.59		550.801	+0.2758
	1370.53		1398.52		1398.52	12	E	7	972.536	-0.0573	972.536	
	1441.56		1469.56	-0.4205	1469.56	13	A	6	843.493	+0.04971	843.493	
	1554.65		1582.64	-0.3585	1582.64	14	I	5	772.456	-0.0663	772.456	
	1683.69		1711.68		1711.68	15	E	4	659.372	-0.023	659.372	
	1812.73	+0.1683	920.867	-0.3546	1840.73	16	E	3	530.33	+0.14872	530.33	
	1925.82	+0.15245	977.409		1953.81	17	I	2	401.287	+0.1066	401.287	
	2038.9	+0.28632	1033.95		2066.9	18	I	1	288.203	-0.0131	288.203	
						19	R	0	175.119		175.119	

Source: 20120314_VR_TripleSILAC_pT1L1T2_F18
Scannumber: 2189
Protein: BSU38960; N15NR; yxjG
Peptide Score: 131.83
Method: ITMS; CID; 3





precursor information

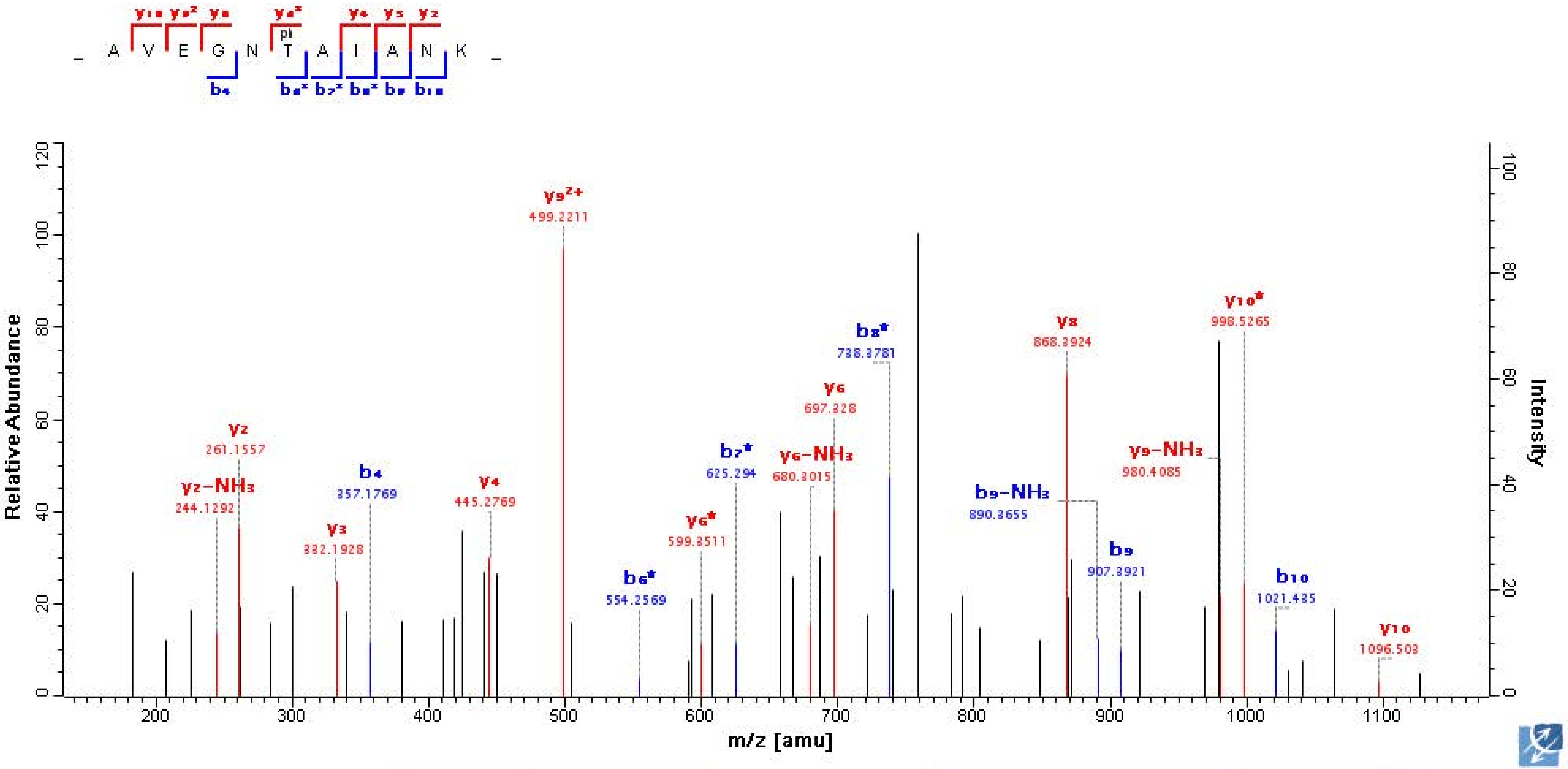
Mass:	1196.50655
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	131.8261
Mass Error [ppm]:	-0.75078
PEP:	1.0253E-05
Precursor Type:	MULTI

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	65 %
Protein Localisation:	2 ... 11

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.00563528	1	S	9				
	296.0642128	2	Q	8	1034.5414714		517.77437392	-0.2890834
+0.1915407	424.12279031	3	Q	7	906.48289386	-0.0564412	453.74508516	+0.1524978
+0.2156396	525.17046878	4	T	6	778.42431635	+0.0578614	778.42431635	
+0.0812912	626.21814726	5	T	5	677.37663788	+0.048533	339.19195717	-0.4479997
	723.27091111	6	P	4	576.3289594	+0.0644122	576.3289594	
+0.2513623	794.3080249	7	A	3	479.27619555		479.27619555	
	923.35061799	8	E	2	408.23908176	+0.1202322	408.23908176	
	1051.4091955	9	Q	1	279.19648867	+0.0975787	279.19648867	
		10	K	0	151.13791115		151.13791115	

Source:	20120314_VR_TripleSILAC_pT1L1T2_F18
Scannumber:	4338
Protein:	BSU25020; sodA; yqgD
Peptide Score:	93.84
Method:	ITMS; CID; 3



precursor information

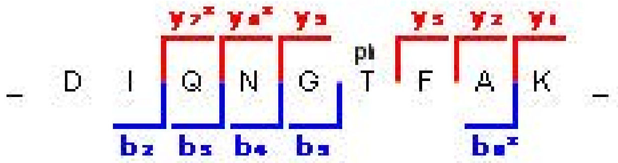
Mass:	1166.5343
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	93.83924
Mass Error [ppm]:	0.88744
PEP:	0.001563
Precursor Type:	MULTI

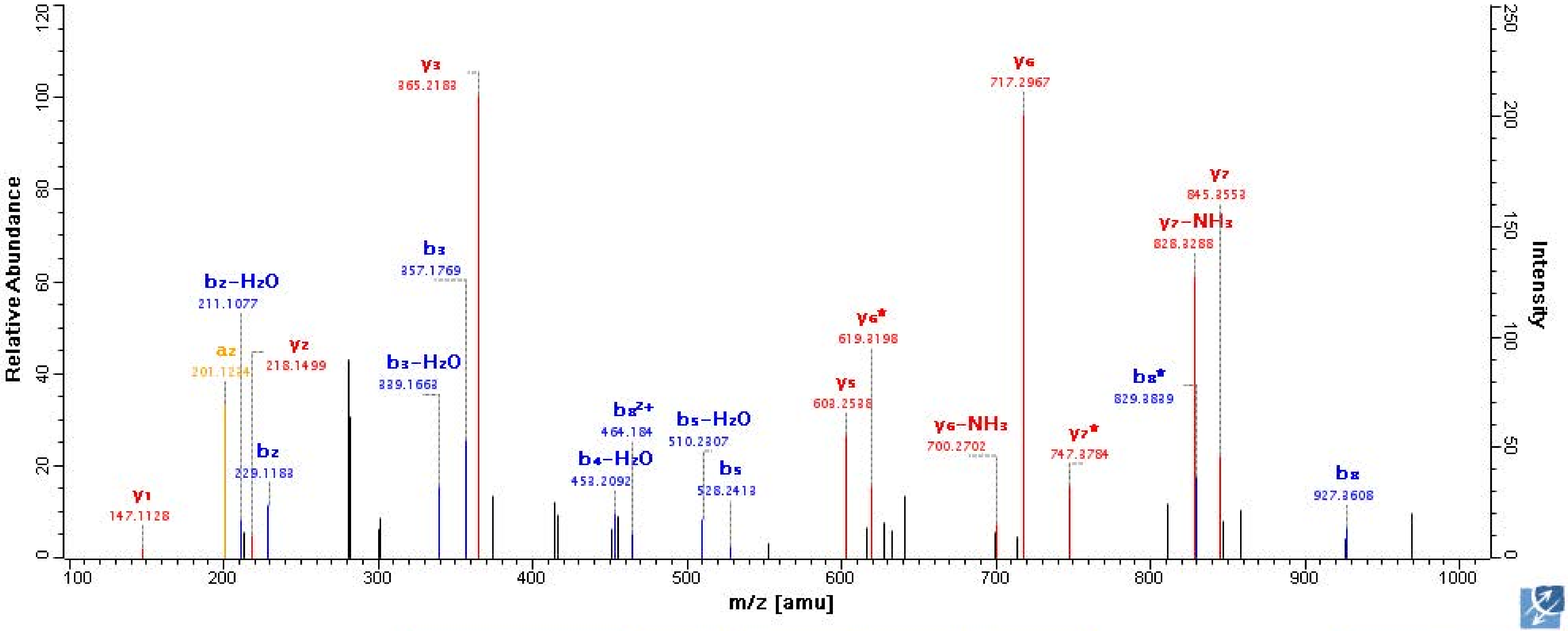
general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	36 %
Protein Localisation:	42 ... 52

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	10				
	171.11280417	2	V	9	1096.5034302	-0.0969361	1096.5034302	
	300.15539727	3	E	8	997.43501632		499.22114639	+0.0401451
-0.194256	357.17686099	4	G	7	868.39242323	+0.1076378	868.39242323	
	471.21978844	5	N	6	811.3709595		811.3709595	
	652.23379732	6	T	5	697.32803206	-0.1106859	697.32803206	
	723.27091111	7	A	4	516.31402317		516.31402317	
	836.35497509	8	I	3	445.27690939	-0.3929372	445.27690939	
-0.0859365	907.39208888	9	A	2	332.19284541	+0.20724	332.19284541	
-0.099323	1021.4350163	10	N	1	261.15573162	-0.0046086	261.15573162	
		11	K	0	147.11280417		147.11280417	

Source:	20120314_VR_TripleSILAC_pT1L1T2_F18
Scannumber:	6077
Protein:	BSU28290; ilvC
Peptide Score:	159.4
Method:	ITMS; CID; 3



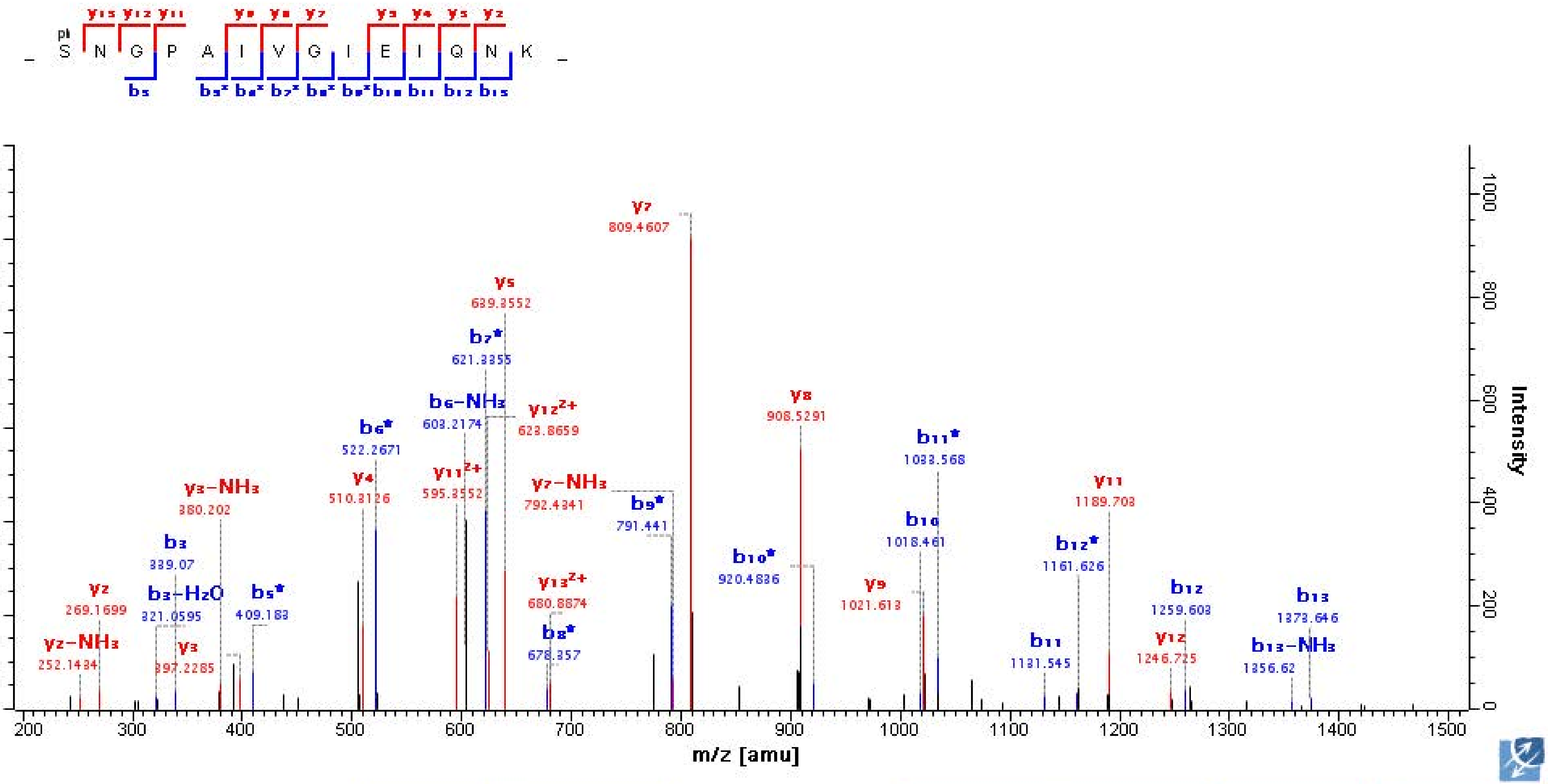


precursor information

Mass:	1072.459
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	159.4039
Mass Error [ppm]:	-0.034267
PEP:	2.1185E-10
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	68 %
Protein Localisation:	280 ... 288

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	88.0393		116.0342		116.0342	1	D	8		
-0.022676	201.1234		229.1183	-0.153653	229.1183	2	I	7	958.4394	
	329.1819		357.1769	-0.076458	357.1769	3	Q	6	845.3553	+0.068519
	443.2249		471.2198		471.2198	4	N	5	717.2967	+0.105795
	500.2463		528.2413	+0.155904	528.2413	5	G	4	603.2538	-0.158651
	681.2603		709.2553		709.2553	6	T	3	546.2323	
	828.3288		856.3237		856.3237	7	F	2	365.2183	+0.218436
	899.3659	+0.175342	464.184	-0.292429	927.3608	8	A	1	218.1499	+0.072174
						9	K	0	147.1128	+0.12978

Source: 20120314_VR_TripleSILAC_pT1L1T2_F18
Scannumber: 9124
Protein: BSU21770; ilvA
Peptide Score: 173.44
Method: ITMS; CID; 3



precursor information

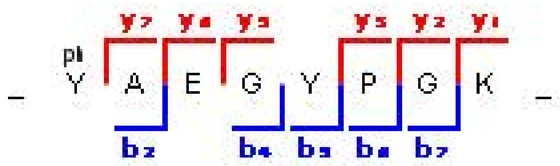
Mass:	1518.74377
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	173.4413
Mass Error [ppm]:	-0.36251
PEP:	4.0347E-25
Precursor Type:	MULTI

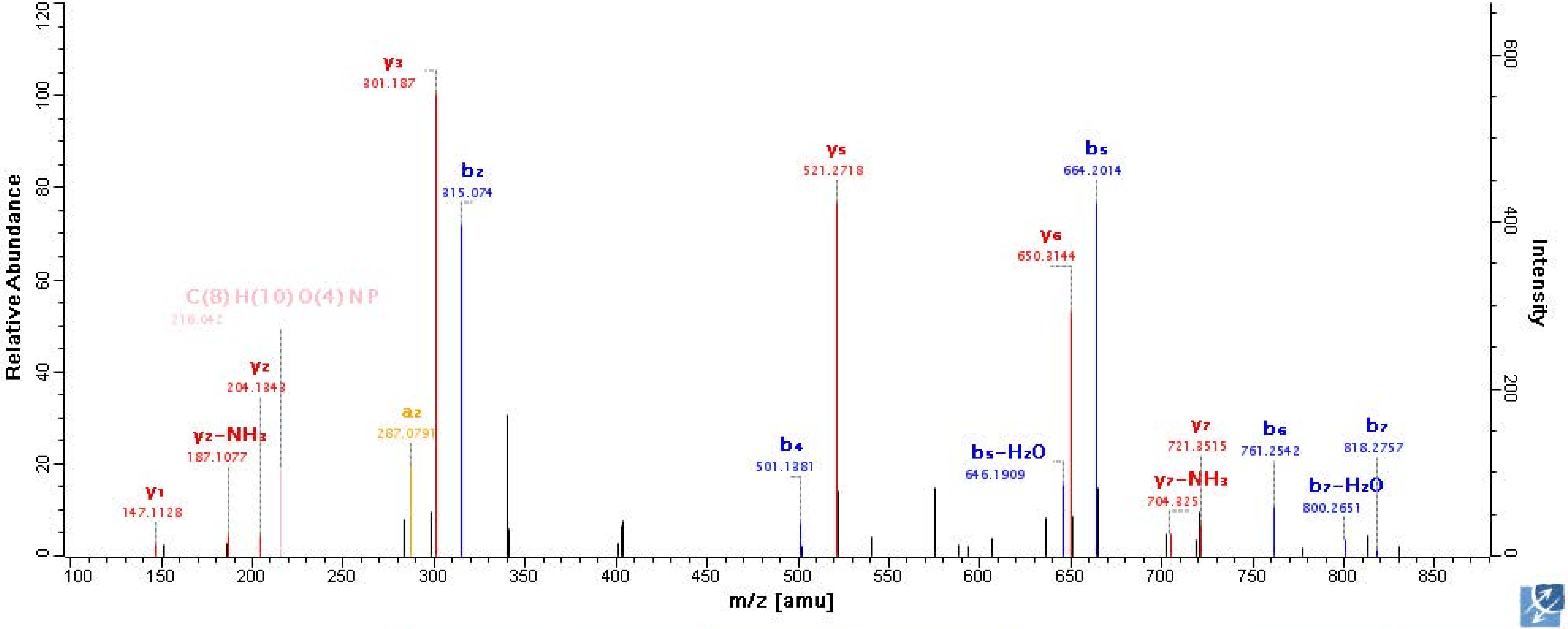
general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	66 %
Protein Localisation:	378 ... 391

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.00563528	1	S	13				
	282.04856273	2	N	12	1360.7674394		680.88735795	-0.0606978
+0.0414237	339.07002646	3	G	11	1246.724512	+0.1269284	623.86589422	+0.3413201
	436.12279031	4	P	10	1189.7030483	-0.0048061	595.35516236	+0.2661755
	507.1599041	5	A	9	1092.6502844		1092.6502844	
	620.24396808	6	I	8	1021.6131706	-0.1443596	1021.6131706	
	719.31238199	7	V	7	908.52910664	+0.013618	908.52910664	
	776.33384572	8	G	6	809.46069272	-0.0029901	809.46069272	
	889.4179097	9	I	5	752.439229		752.439229	
-0.0266649	1018.4605028	10	E	4	639.35516502	+0.1514878	639.35516502	
-0.100475	1131.5445668	11	I	3	510.31257192	-0.0675768	510.31257192	
+0.3054251	1259.6031443	12	Q	2	397.22850794	+0.0413285	397.22850794	
+0.0371558	1373.6460717	13	N	1	269.16993043	+0.0746374	269.16993043	
		14	K	0	155.12700298		155.12700298	

Source:	20120314_VR_TripleSILAC_pT1L1T2_F21
Scannumber:	3087
Protein:	BSU36900; glyA; glyC; ipc-34d
Peptide Score:	151.27
Method:	ITMS; CID; 3



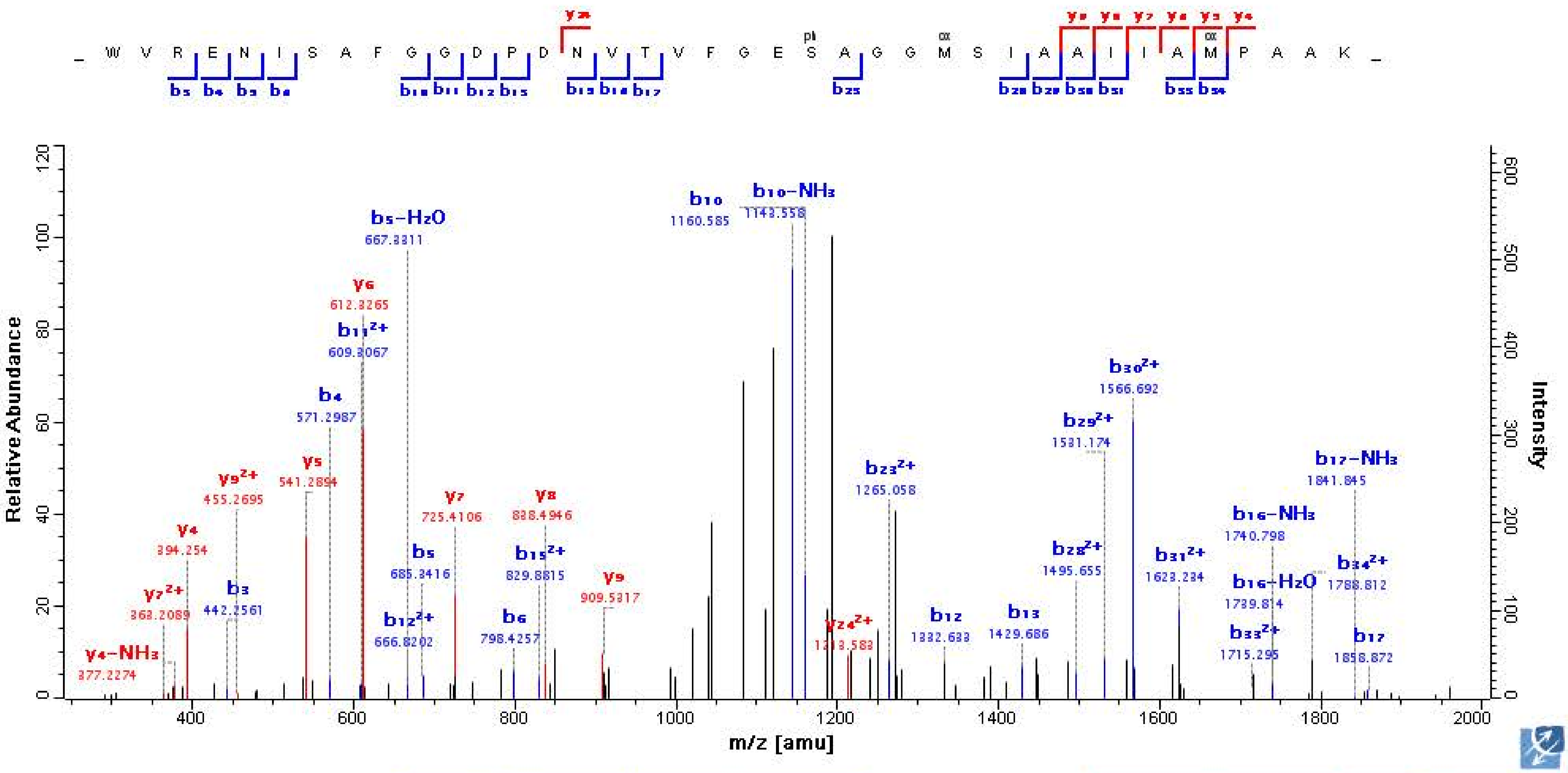


precursor information

Mass:	963.37422
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	151.2687
Mass Error [ppm]:	0.31991
PEP:	1.3404E-08
Precursor Type:	MULTI
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	73 %
Protein Localisation:	51 ... 58

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	216.04202079		244.03693541	1	Y	7		
+0.0427831	287.07913458	+0.0183885	315.0740492	2	A	6	721.35153089	+0.0376903
	416.12172768		444.1166423	3	E	5	650.3144171	+0.0348871
	473.1431914	+0.0918134	501.13810602	4	G	4	521.27182401	-0.0037576
	636.20651994	+0.0370908	664.20143456	5	Y	3	464.25036028	
	733.25928379	+0.1136605	761.25419841	6	P	2	301.18703175	-0.0253496
	790.28074751	-0.0088164	818.27566213	7	G	1	204.13426789	-0.0035611
				8	K	0	147.11280417	+0.1506846

Source:	20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F03
Scannumber:	11810
Protein:	BSU34390; estB; pnbA
Peptide Score:	94.5
Method:	ITMS; CID; 3



precursor information

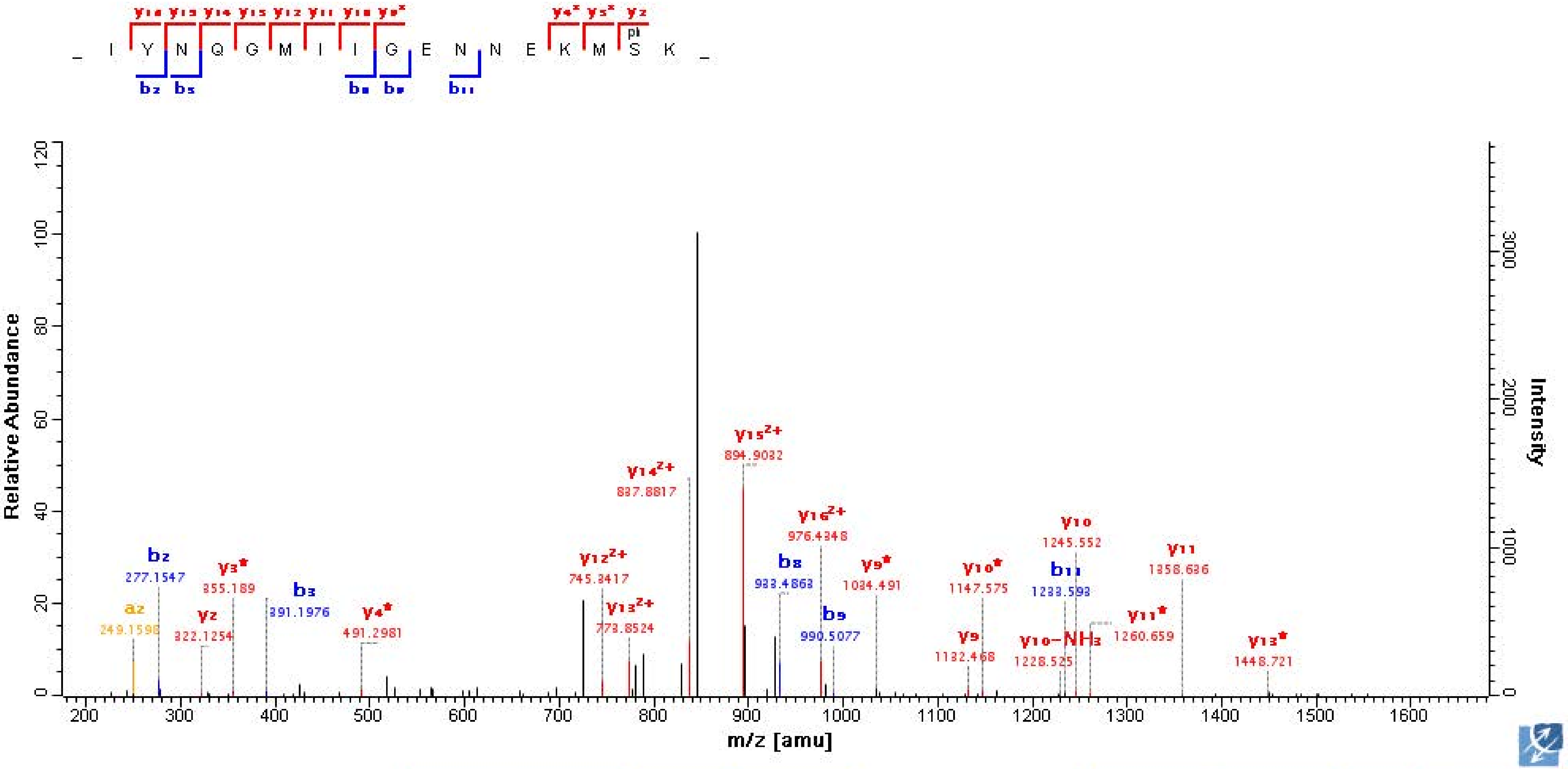
Mass:	3968.85527
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	94.49538
Mass Error [ppm]:	-0.42109
PEP:	9.3982E-26
Precursor Type:	ISO

general information

Annotation:	20 of 38
AminoAcids Coverag	53 %
Intensity Coverage:	40 %
Protein Localisation:	168 ... 205

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	187.0866		187.0866	1	W	37				
	286.155		286.155	2	V	36	3783.785		3783.785	
	442.2561	+0.09087	442.2561	3	R	35	3684.716		3684.716	
	571.2987	+0.030699	571.2987	4	E	34	3528.615		3528.615	
	685.3416	+0.07255	685.3416	5	N	33	3399.573		3399.573	
	798.4257	-0.007608	798.4257	6	I	32	3285.53		3285.53	
	885.4577		885.4577	7	S	31	3172.446		3172.446	
	956.4948		956.4948	8	A	30	3085.414		3085.414	
	1103.563		1103.563	9	F	29	3014.377		3014.377	
	1160.585	-0.022951	1160.585	10	G	28	2867.308		2867.308	
+0.051181	609.3067		1217.606	11	G	27	2810.287		2810.287	
-0.008617	666.8202	+0.188774	1332.633	12	D	26	2753.265		2753.265	
	1429.686	+0.456078	1429.686	13	P	25	2638.238		2638.238	
	1544.713		1544.713	14	D	24	2541.186		2541.186	
+0.47334	829.8815		1658.756	15	N	23	2426.159		1213.583	+0.207071
	1757.824		1757.824	16	V	22	2312.116		2312.116	
	1858.872	-0.406886	1858.872	17	T	21	2213.047		2213.047	
	1957.94		1957.94	18	V	20	2112		2112	
	2105.009		2105.009	19	F	19	2012.931		2012.931	
	2162.03		2162.03	20	G	18	1865.863		1865.863	
	2291.073		2291.073	21	E	17	1808.841		1808.841	
	2458.071		2458.071	22	S	16	1679.799		1679.799	
-0.468387	1265.058		2529.108	23	A	15	1512.8		1512.8	
	2586.13		2586.13	24	G	14	1441.763		1441.763	
	2643.151		2643.151	25	G	13	1384.742		1384.742	
	2790.187		2790.187	26	M	12	1327.72		1327.72	
	2877.219		2877.219	27	S	11	1180.685		1180.685	
+0.323563	1495.655		2990.303	28	I	10	1093.653		1093.653	
+0.495436	1531.174		3061.34	29	A	9	980.5689		980.5689	
+0.305492	1566.692		3132.377	30	A	8	909.5317	-0.158824	455.2695	+0.38512
-0.037565	1623.234		3245.461	31	I	7	838.4946	+0.057	838.4946	
	3358.545		3358.545	32	I	6	725.4106	-0.031787	363.2089	-0.044282
+0.086783	1715.295		3429.582	33	A	5	612.3265	-0.016693	612.3265	
-0.173105	1788.812		3576.617	34	M	4	541.2894	-0.032741	541.2894	
	3673.67		3673.67	35	P	3	394.254	-0.073361	394.254	
	3744.707		3744.707	36	A	2	297.2012		297.2012	
	3815.744		3815.744	37	A	1	226.1641		226.1641	
				38	K	0	155.127		155.127	

Source: 20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F03
Scannumber: 6692
Protein: BSU30320; leuS
Peptide Score: 105.39
Method: ITMS; CID; 3



precursor information

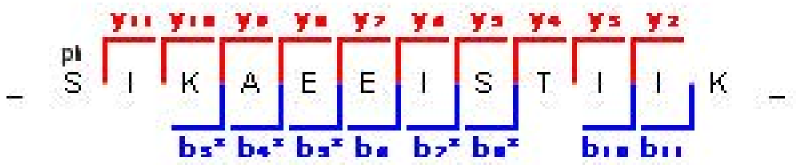
Mass:	2047.91142
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	105.3914
Mass Error [ppm]:	0.29273
PEP:	0.00012039
Precursor Type:	MULTI

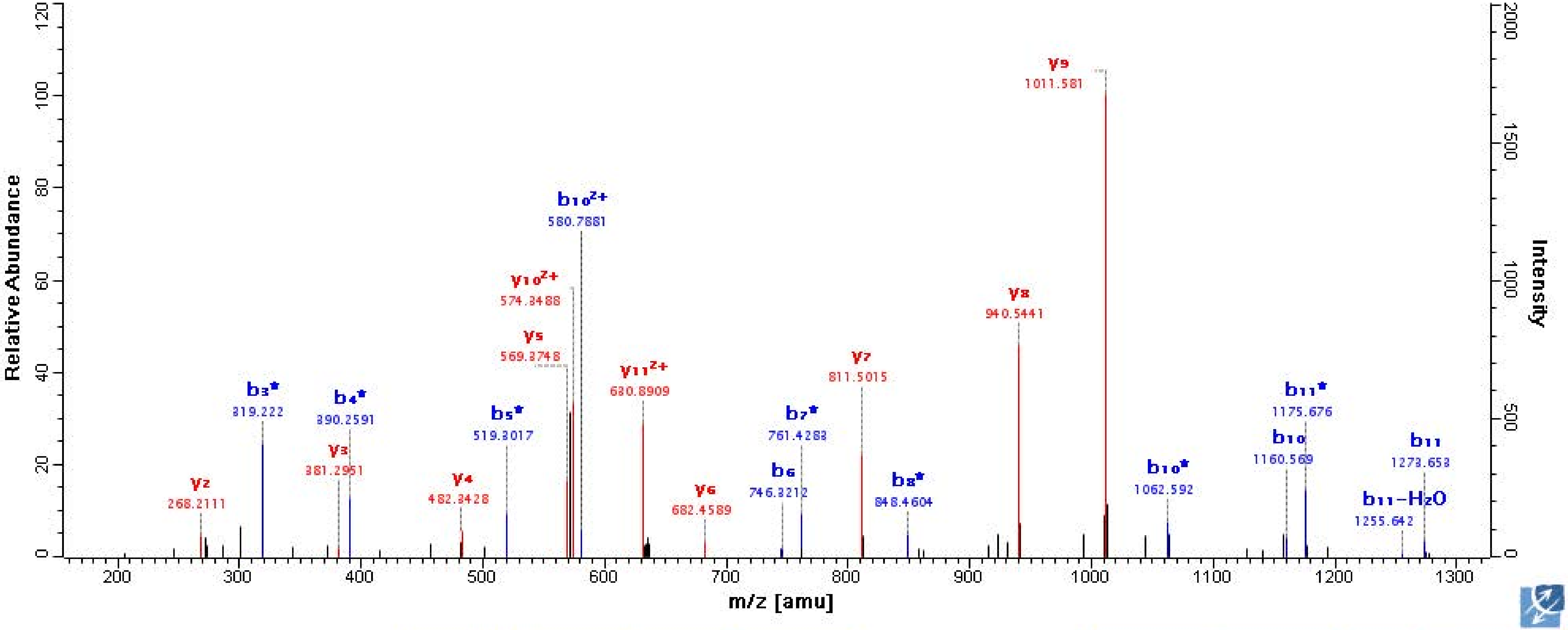
general information

Annotation:	12 of 17
AminoAcids Coverag	71 %
Intensity Coverage:	32 %
Protein Localisation:	563 ... 579

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.09643		114.0913	1	I	16				
-0.004893	249.1598	+0.093103	277.1547	2	Y	15	1951.862		976.4348	+0.232936
	363.2027	-0.006801	391.1976	3	N	14	1788.799		894.9032	-0.054064
	491.2613		519.2562	4	Q	13	1674.756		837.8817	-0.430123
	548.2827		576.2776	5	G	12	1546.698		773.8524	+0.116927
	679.3232		707.3181	6	M	11	1489.676		745.3417	-0.000392
	792.4073		820.4022	7	I	10	1358.636	-0.118429	1358.636	
	905.4913	-0.345869	933.4863	8	I	9	1245.552	+0.202451	1245.552	
	962.5128	-0.216149	990.5077	9	G	8	1132.468	+0.053727	1132.468	
	1091.555		1119.55	10	E	7	1075.446		1075.446	
	1205.598	+0.168728	1233.593	11	N	6	946.4035		946.4035	
	1319.641		1347.636	12	N	5	832.3605		832.3605	
	1448.684		1476.679	13	E	4	718.3176		718.3176	
	1584.793		1612.788	14	K	3	589.275		589.275	
	1715.833		1743.828	15	M	2	453.1658		453.1658	
	1882.832		1910.827	16	S	1	322.1254	-0.136135	322.1254	
				17	K	0	155.127		155.127	

Source:	20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F03
Scannumber:	8024
Protein:	atpA; BSU36830
Peptide Score:	147.87
Method:	ITMS; CID; 3





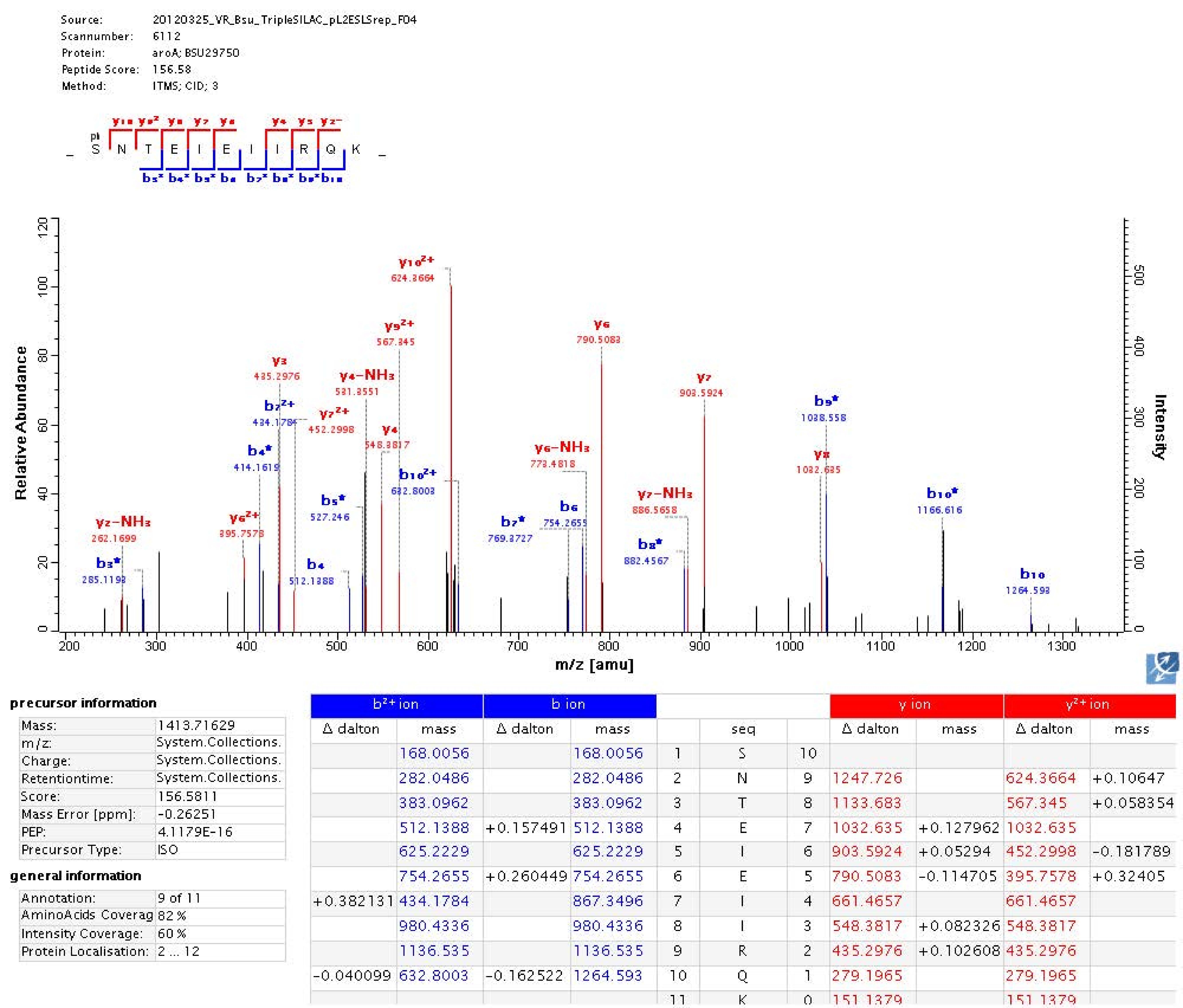
precursor information

Mass:	1410.73634
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	147.8661
Mass Error [ppm]:	-0.54427
PEP:	7.9429E-13
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	62 %
Protein Localisation:	2 ... 13

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.0056		168.0056	1	S	11				
	281.0897		281.0897	2	I	10	1260.774		630.8909	+0.015398
	417.1989		417.1989	3	K	9	1147.69		574.3488	+0.028438
	488.236		488.236	4	A	8	1011.581	-0.030848	1011.581	
	617.2786		617.2786	5	E	7	940.5441	-0.053671	940.5441	
	746.3212	+0.195868	746.3212	6	E	6	811.5015	-0.041351	811.5015	
	859.4052		859.4052	7	I	5	682.4589	+0.267722	682.4589	
	946.4373		946.4373	8	S	4	569.3748	+0.150797	569.3748	
	1047.485		1047.485	9	T	3	482.3428	+0.161341	482.3428	
+0.194713	580.7881	-0.266017	1160.569	10	I	2	381.2951	+0.03037	381.2951	
	1273.653	+0.066056	1273.653	11	I	1	268.2111	+0.073357	268.2111	
				12	K	0	155.127		155.127	



Source:	20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F04
Scannumber:	6112
Protein:	aroA; BSU29750
Peptide Score:	156.58
Method:	ITMS; CID; 3

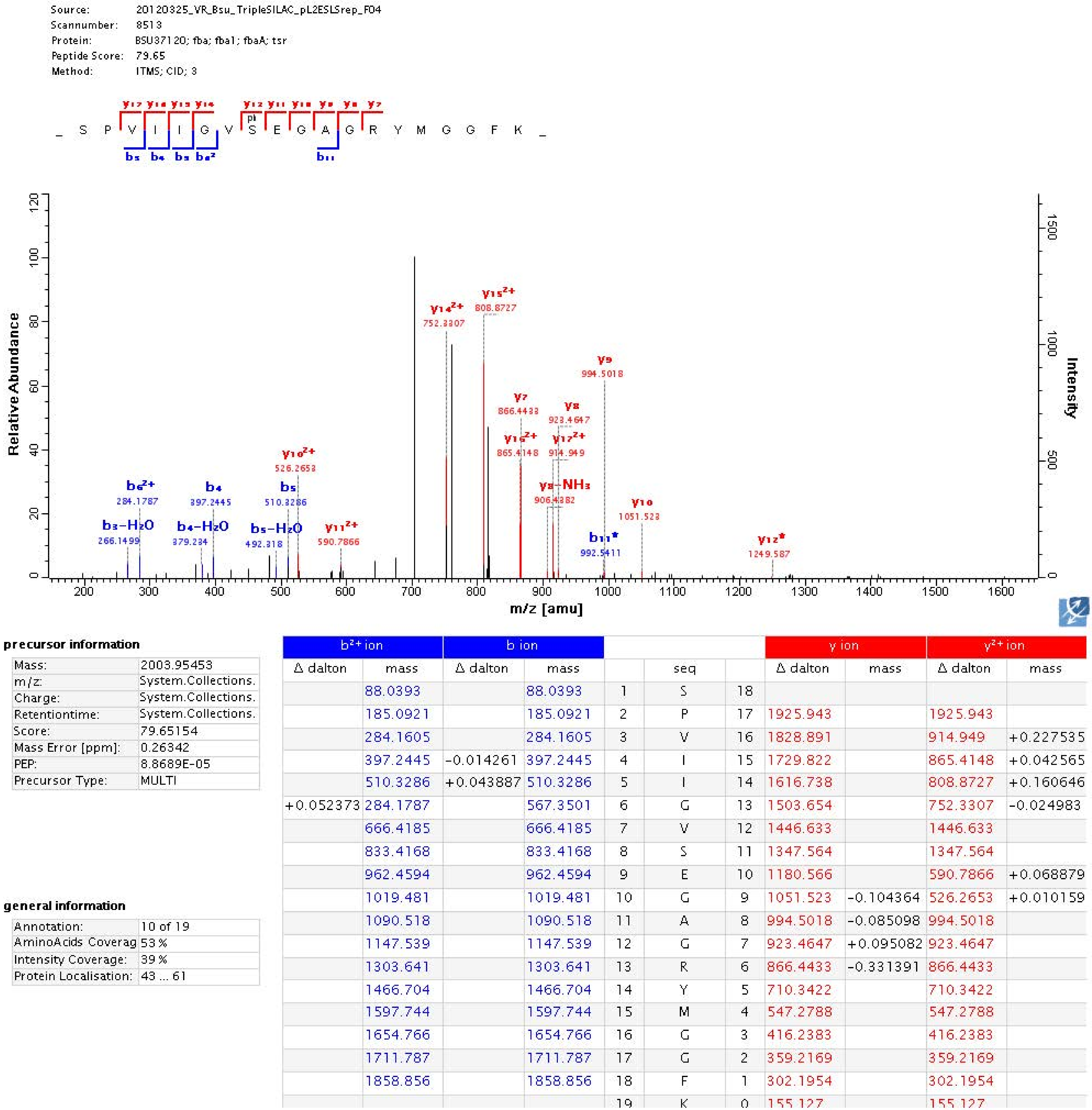
precursor information

Mass:	1413.71629
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	156.5811
Mass Error [ppm]:	-0.26251
PEP:	4.1179E-16
Precursor Type:	ISO

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	60 %
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
	168.0056		168.0056	1	S	10				
	282.0486		282.0486	2	N	9	1247.726		624.3664	+0.10647
	383.0962		383.0962	3	T	8	1133.683		567.345	+0.058354
	512.1388	+0.157491	512.1388	4	E	7	1032.635	+0.127962	1032.635	
	625.2229		625.2229	5	I	6	903.5924	+0.05294	452.2998	-0.181789
	754.2655	+0.260449	754.2655	6	E	5	790.5083	-0.114705	395.7578	+0.32405
+0.382131	434.1784		867.3496	7	I	4	661.4657		661.4657	
	980.4336		980.4336	8	I	3	548.3817	+0.082326	548.3817	
	1136.535		1136.535	9	R	2	435.2976	+0.102608	435.2976	
-0.040099	632.8003	-0.162522	1264.593	10	Q	1	279.1965		279.1965	
				11	K	0	151.1379		151.1379	



Source: 20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F04
Scannumber: 8513
Protein: BSU37120; fba; fba1; fbaA; tsr
Peptide Score: 79.65
Method: ITMS; CID; 3

precursor information

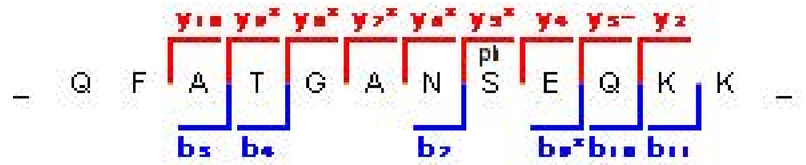
Mass:	2003.95453
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	79.65154
Mass Error [ppm]:	0.26342
PEP:	8.8689E-05
Precursor Type:	MULTI

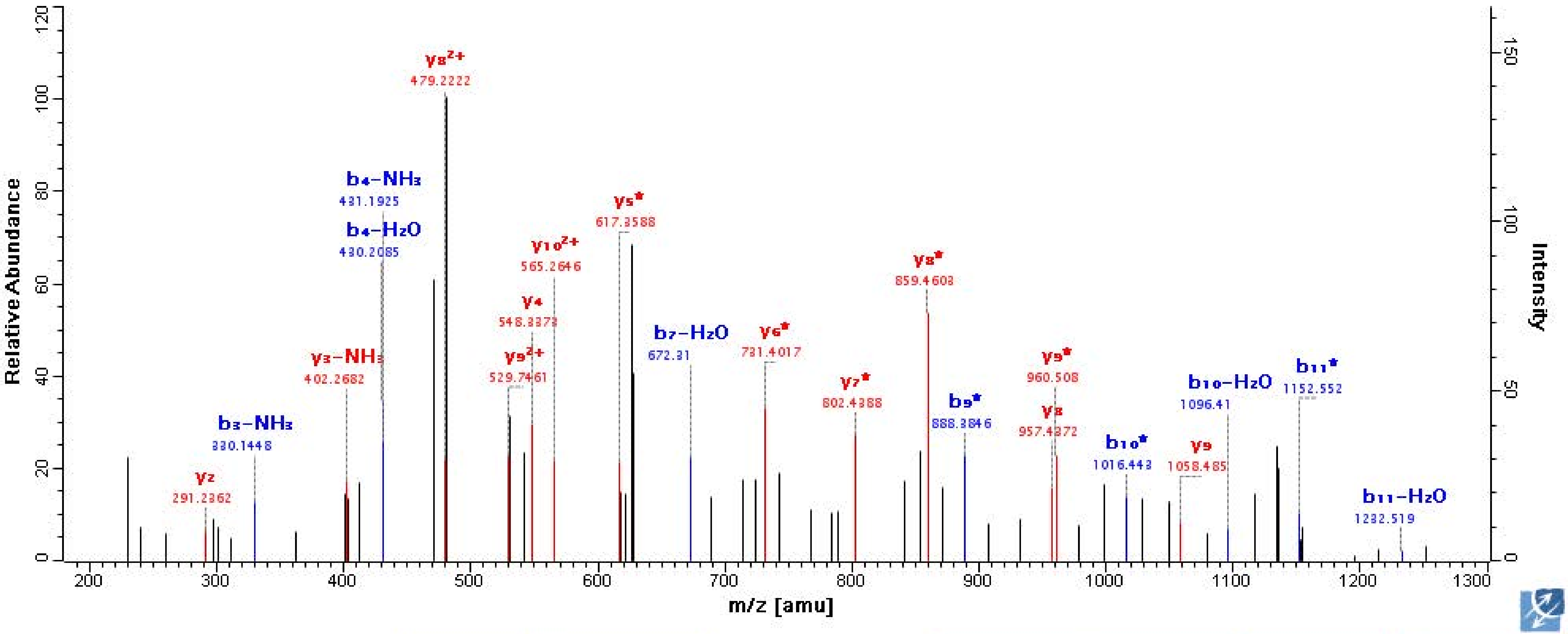
general information

Annotation:	10 of 19
AminoAcids Coverag	53 %
Intensity Coverage:	39 %
Protein Localisation:	43 ... 61

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393		88.0393	1	S	18				
	185.0921		185.0921	2	P	17	1925.943		1925.943	
	284.1605		284.1605	3	V	16	1828.891		914.949	+0.227535
	397.2445	-0.014261	397.2445	4	I	15	1729.822		865.4148	+0.042565
	510.3286	+0.043887	510.3286	5	I	14	1616.738		808.8727	+0.160646
+0.052373	284.1787		567.3501	6	G	13	1503.654		752.3307	-0.024983
	666.4185		666.4185	7	V	12	1446.633		1446.633	
	833.4168		833.4168	8	S	11	1347.564		1347.564	
	962.4594		962.4594	9	E	10	1180.566		590.7866	+0.068879
	1019.481		1019.481	10	G	9	1051.523	-0.104364	526.2653	+0.010159
	1090.518		1090.518	11	A	8	994.5018	-0.085098	994.5018	
	1147.539		1147.539	12	G	7	923.4647	+0.095082	923.4647	
	1303.641		1303.641	13	R	6	866.4433	-0.331391	866.4433	
	1466.704		1466.704	14	Y	5	710.3422		710.3422	
	1597.744		1597.744	15	M	4	547.2788		547.2788	
	1654.766		1654.766	16	G	3	416.2383		416.2383	
	1711.787		1711.787	17	G	2	359.2169		359.2169	
	1858.856		1858.856	18	F	1	302.1954		302.1954	
				19	K	0	155.127		155.127	

Source:	20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F05
Scannumber:	2651
Protein:	BSU13180; metC; metE
Peptide Score:	80.24
Method:	ITMS; CID; 3





precursor information

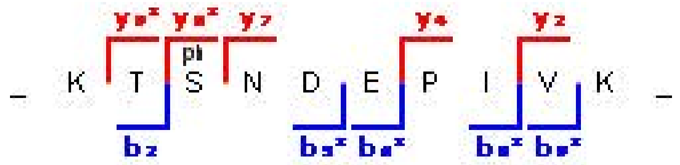
Mass:	1387.61341
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	80.24471
Mass Error [ppm]:	0.073627
PEP:	0.0056496
Precursor Type:	MULTI

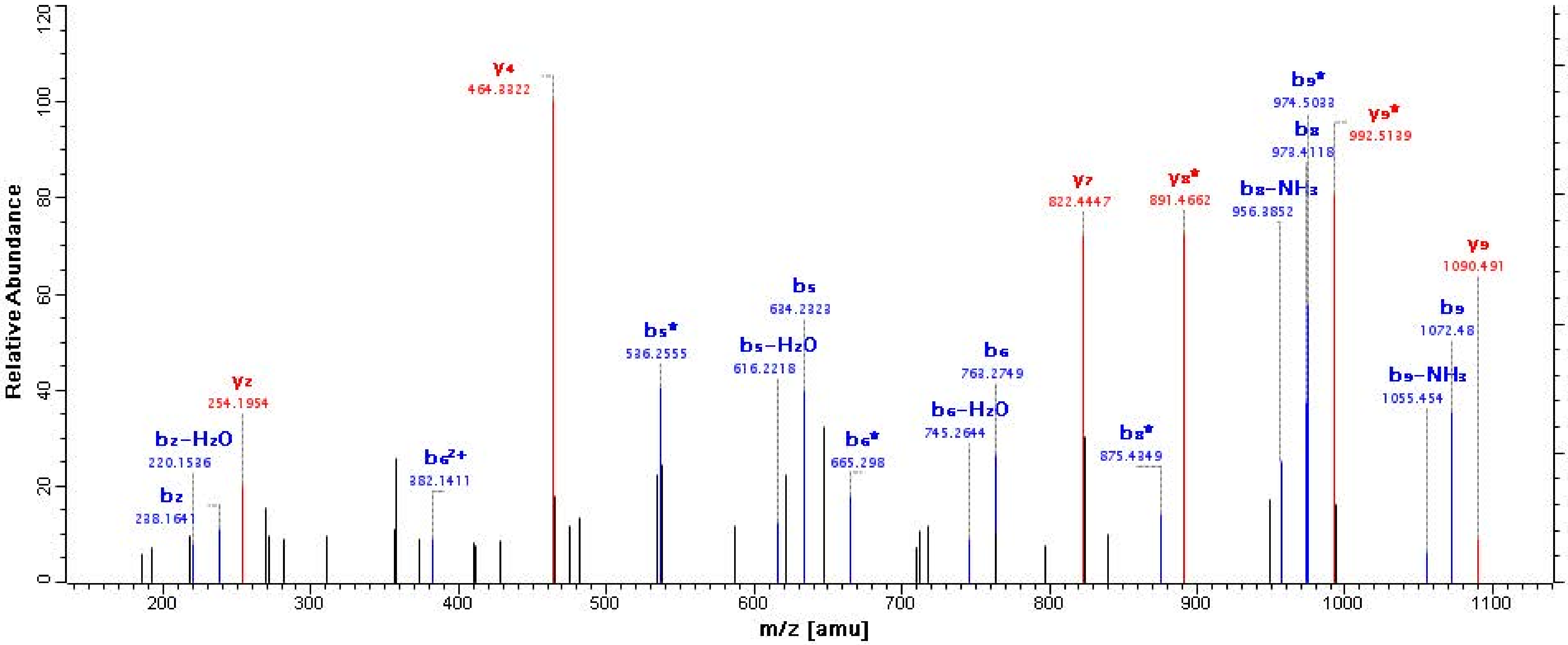
general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	37 %
Protein Localisation:	387 ... 398

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.06585398	1	Q	11				
	276.13426789	2	F	10	1276.5904054		1276.5904054	
	347.17138168	3	A	9	1129.5219915		565.26463396	+0.1157982
	448.21906016	4	T	8	1058.4848777	+0.1650247	529.74607707	-0.046248
	505.24052388	5	G	7	957.4371992	+0.294002	479.22223783	+0.272208
	576.27763767	6	A	6	900.41573548		900.41573548	
	690.32056511	7	N	5	829.37862169		829.37862169	
	857.31892393	8	S	4	715.33569424		715.33569424	
	986.36151703	9	E	3	548.33733542	+0.0840513	548.33733542	
	1114.4200945	10	Q	2	419.29474233		419.29474233	
	1250.5292564	11	K	1	291.23616481	+0.0780442	291.23616481	
		12	K	0	155.12700298		155.12700298	

Source:	20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F05
Scannumber:	3389
Protein:	BSU15470; pyrR
Peptide Score:	143.24
Method:	ITMS; CID; 3





precursor information

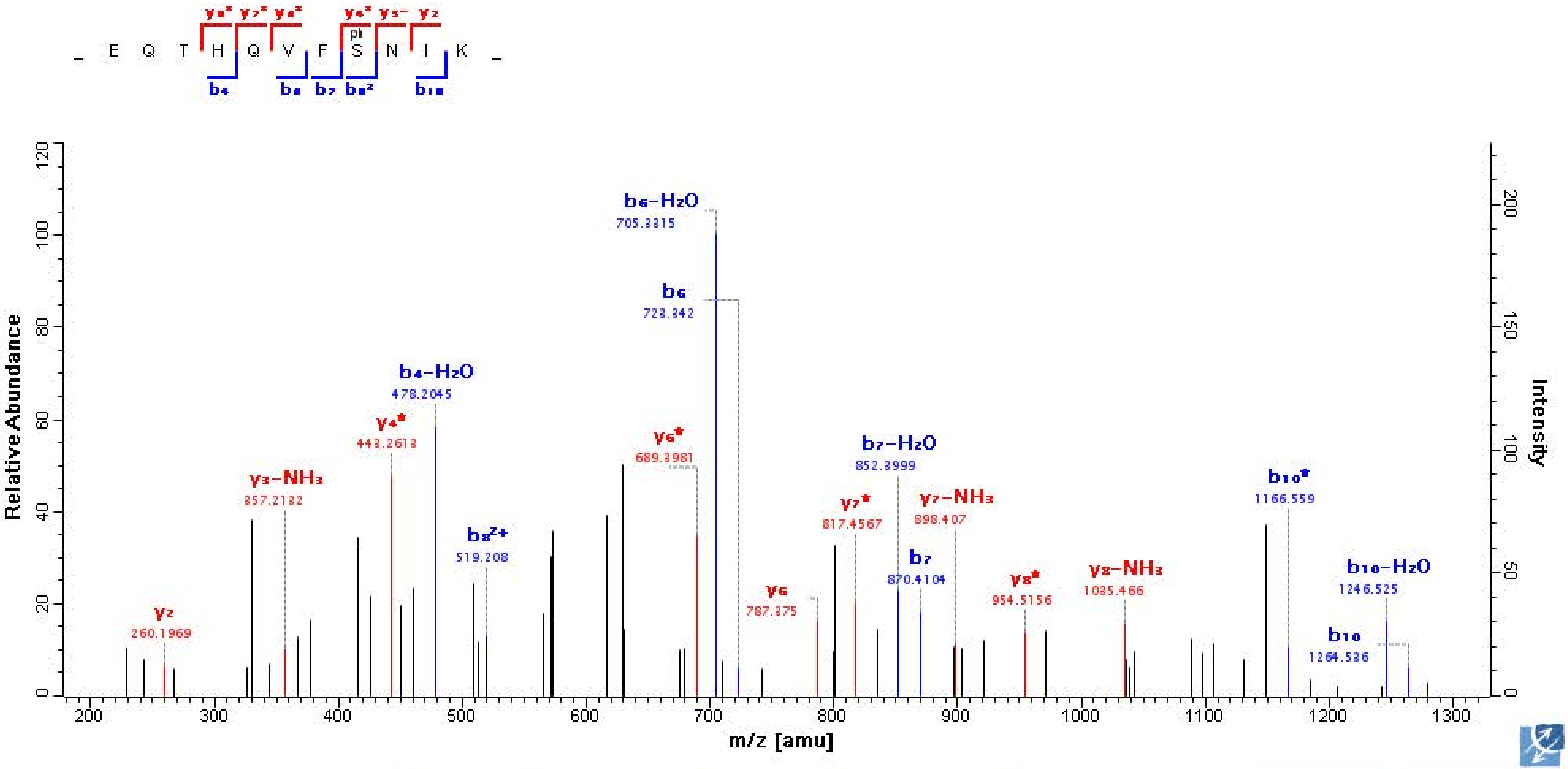
Mass:	1209.56424
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	143.2381
Mass Error [ppm]:	0.0027659
PEP:	9.54E-09
Precursor Type:	MULTI

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	61 %
Protein Localisation:	79 ... 88

b2+ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	137.1164383		137.1164383	1	K	9		
	238.16411677	+0.0524512	238.16411677	2	T	8	1090.4907456	-0.1543198
	405.16247559		405.16247559	3	S	7	989.44306713	
	519.20540304		519.20540304	4	N	6	822.44470831	-0.0601868
	634.23234607	+0.0893702	634.23234607	5	D	5	708.40178086	
-0.2192939	382.14110782	-0.0343996	763.27493917	6	E	4	593.37483783	
	860.32770302		860.32770302	7	P	3	464.33224473	-0.0083312
	973.411767	+0.2442999	973.411767	8	I	2	367.27948088	
	1072.4801809	-0.1042044	1072.4801809	9	V	1	254.1954169	+0.0397821
				10	K	0	155.12700298	

Source:	20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F05
Scannumber:	6130
Protein:	BSU00480; yabJ
Peptide Score:	78.69
Method:	ITMS; CID; 3



precursor information

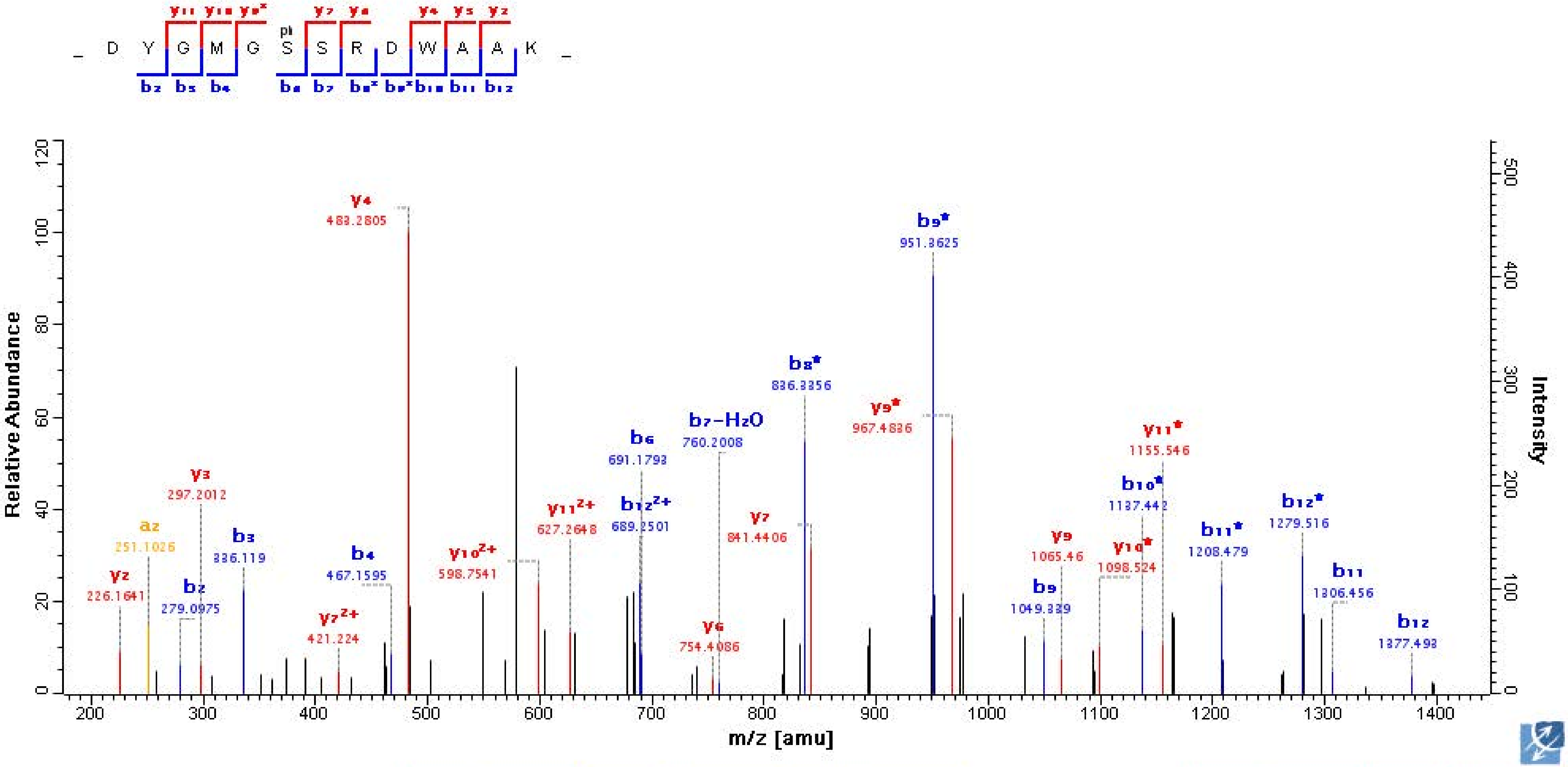
Mass:	1409.6346
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	78.69199
Mass Error [ppm]:	0.39263
PEP:	0.0092882
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	38 %
Protein Localisation:	48 ... 58

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	130.04986956		130.04986956	1	E	10		
	258.10844707		258.10844707	2	Q	9	1281.5987276	
	359.15612555		359.15612555	3	T	8	1153.5401501	
	496.21503741		496.21503741	4	H	7	1052.4924716	
	624.27361492		624.27361492	5	Q	6	915.43355976	
	723.34202884	-0.0235474	723.34202884	6	V	5	787.37498225	+0.0539118
	870.41044275	+0.2191959	870.41044275	7	F	4	688.30656833	
-0.2660835	519.20803902		1037.4088016	8	S	3	541.23815442	
	1151.451729		1151.451729	9	N	2	374.2397956	
	1264.535793	+0.2201884	1264.535793	10	I	1	260.19686815	-0.0827019
				11	K	0	147.11280417	

Source:	20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F05
Scannumber:	6653
Protein:	BSU18000; citB
Peptide Score:	151.99
Method:	ITMS; CID; 3



precursor information

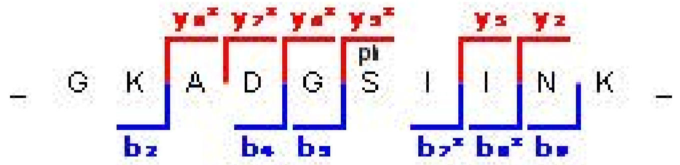
Mass:	1522.591
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	151.9937
Mass Error [ppm]:	-0.12559
PEP:	1.6281E-17
Precursor Type:	MULTI

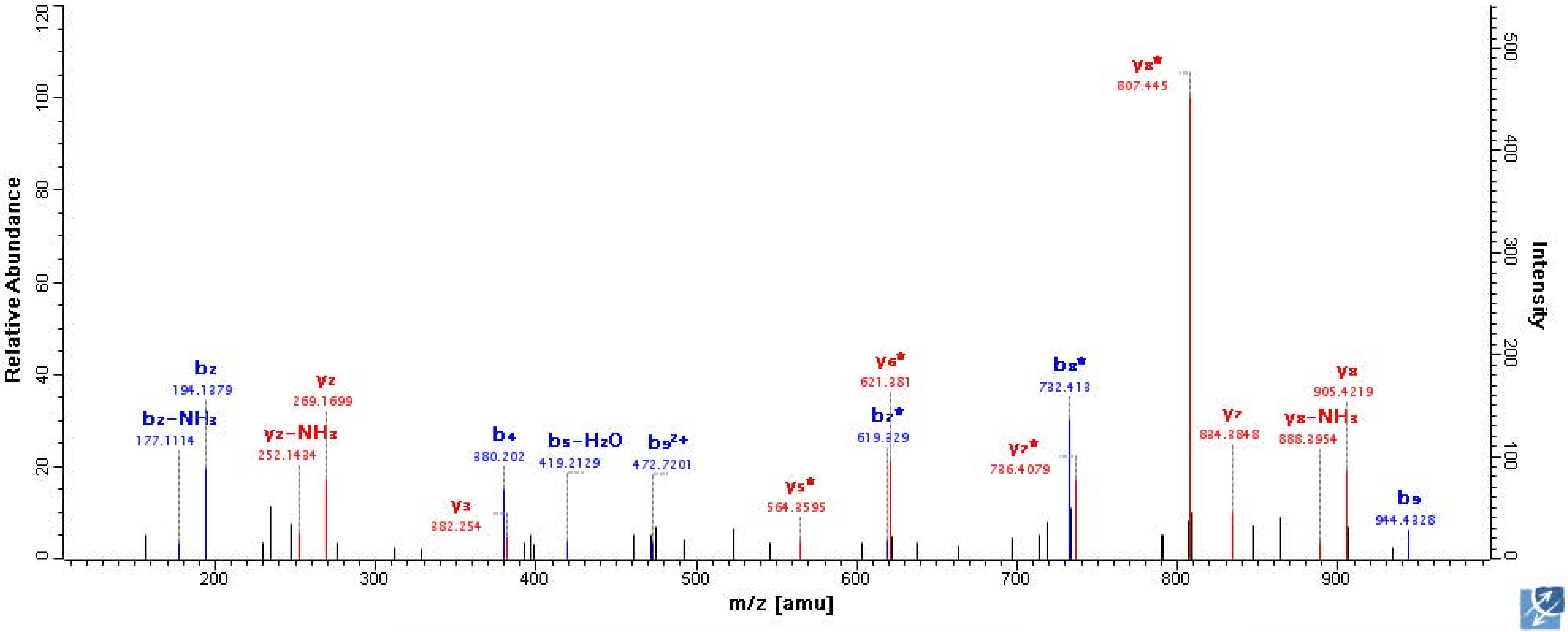
general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	53 %
Protein Localisation:	787 ... 799

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
	88.0393		116.034		116.034	1	D	12				
-0.0353	251.103		279.098	+0.05837	279.098	2	Y	11	1416.59		1416.59	
	308.124		336.119	+0.0409	336.119	3	G	10	1253.52		627.265	+0.0783
	439.165		467.159	-0.0069	467.159	4	M	9	1196.5		598.754	-0.1643
	496.186		524.181		524.181	5	G	8	1065.46	-0.0764	1065.46	
	663.184		691.179	-0.4551	691.179	6	S	7	1008.44		1008.44	
	750.216		778.211		778.211	7	S	6	841.441	-0.0834	421.224	-0.0153
	906.318		934.312		934.312	8	R	5	754.409	+0.07138	754.409	
	1021.34		1049.34	+0.11519	1049.34	9	D	4	598.307		598.307	
	1207.42		1235.42		1235.42	10	W	3	483.281	+0.01865	483.281	
	1278.46		1306.46	+0.11876	1306.46	11	A	2	297.201	+0.06952	297.201	
	1349.5	-0.3873	689.25	+0.11741	1377.49	12	A	1	226.164	+0.06583	226.164	
						13	K	0	155.127		155.127	

Source:	20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F07
Scannumber:	3586
Protein:	BSU25400; yqeY
Peptide Score:	108.47
Method:	ITMS; CID; 3





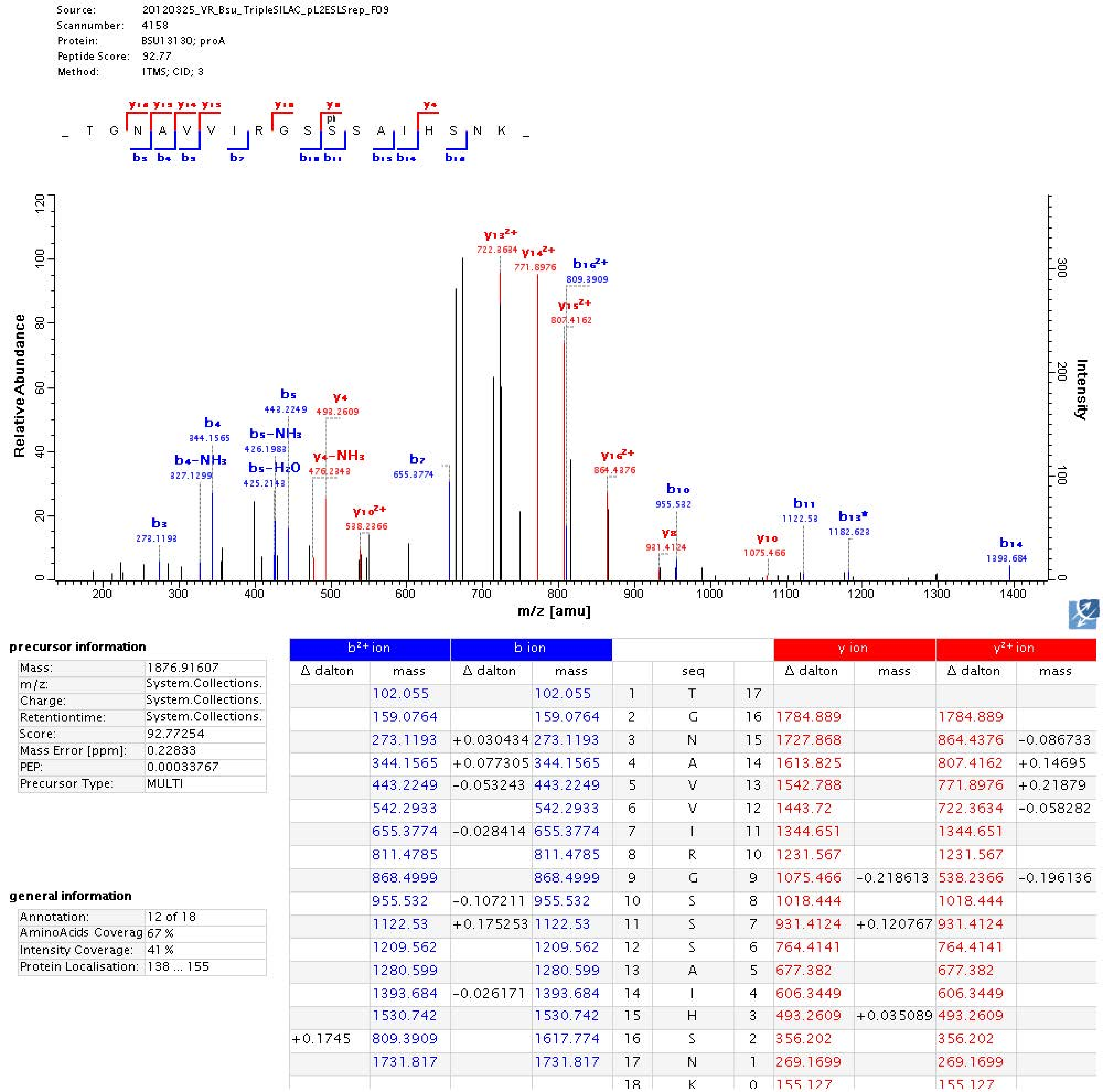
precursor information

Mass:	1081.51683
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	108.4698
Mass Error [ppm]:	-0.053096
PEP:	0.0020667
Precursor Type:	MULTI

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	62 %
Protein Localisation:	132 ... 141

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	58.02874019		58.02874019	1	G	9		
	194.13790202	-0.0417106	194.13790202	2	K	8	1041.5310996	
	265.17501581		265.17501581	3	A	7	905.42193775	+0.0820295
	380.20195884	+0.0319889	380.20195884	4	D	6	834.38482397	+0.0155667
	437.22342256		437.22342256	5	G	5	719.35788093	
	604.22178138		604.22178138	6	S	4	662.33641721	
	717.30584536		717.30584536	7	I	3	495.33805839	
	830.38990934		830.38990934	8	I	2	382.25399441	+0.0006443
+0.169958	472.72005663	-0.0466674	944.43283679	9	N	1	269.16993043	+0.0615454
				10	K	0	155.12700298	



Source: 20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F09
Scannumber: 4158
Protein: BSU13130; proA
Peptide Score: 92.77
Method: ITMS; CID; 3

precursor information

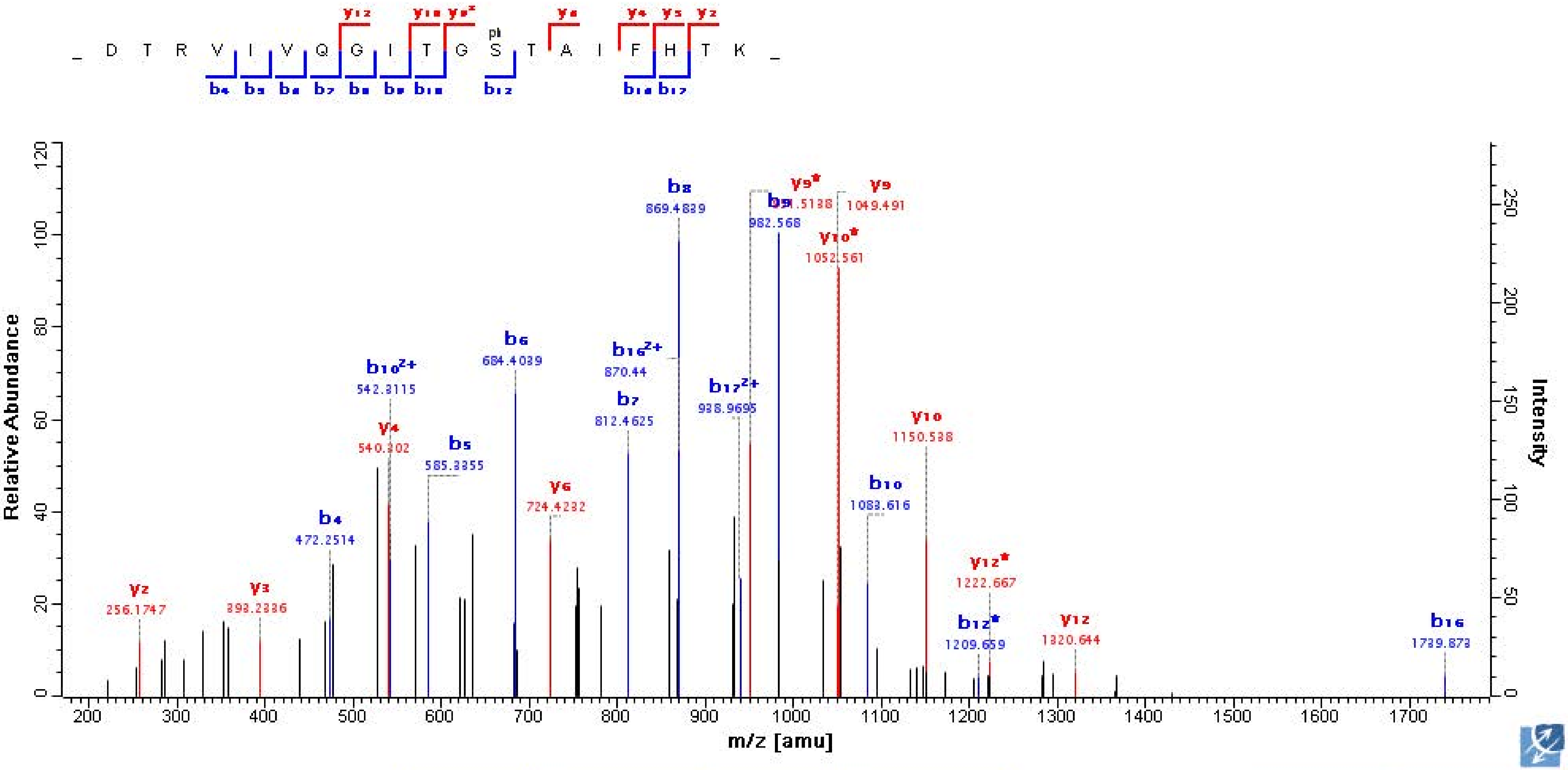
Mass:	1876.91607
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	92.77254
Mass Error [ppm]:	0.22833
PEP:	0.00033767
Precursor Type:	MULTI

general information

Annotation:	12 of 18
AminoAcids Coverag	67 %
Intensity Coverage:	41 %
Protein Localisation:	138 ... 155

b2+ ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055		102.055	1	T	17				
	159.0764		159.0764	2	G	16	1784.889		1784.889	
	273.1193	+0.030434	273.1193	3	N	15	1727.868		864.4376	-0.086733
	344.1565	+0.077305	344.1565	4	A	14	1613.825		807.4162	+0.14695
	443.2249	-0.053243	443.2249	5	V	13	1542.788		771.8976	+0.21879
	542.2933		542.2933	6	V	12	1443.72		722.3634	-0.058282
	655.3774	-0.028414	655.3774	7	I	11	1344.651		1344.651	
	811.4785		811.4785	8	R	10	1231.567		1231.567	
	868.4999		868.4999	9	G	9	1075.466	-0.218613	538.2366	-0.196136
	955.532	-0.107211	955.532	10	S	8	1018.444		1018.444	
	1122.53	+0.175253	1122.53	11	S	7	931.4124	+0.120767	931.4124	
	1209.562		1209.562	12	S	6	764.4141		764.4141	
	1280.599		1280.599	13	A	5	677.382		677.382	
	1393.684	-0.026171	1393.684	14	I	4	606.3449		606.3449	
	1530.742		1530.742	15	H	3	493.2609	+0.035089	493.2609	
+0.1745	809.3909		1617.774	16	S	2	356.202		356.202	
	1731.817		1731.817	17	N	1	269.1699		269.1699	
				18	K	0	155.127		155.127	

Source:	20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F09
Scannumber:	9050
Protein:	BSU16100; sucD
Peptide Score:	95.48
Method:	ITMS; CID; 3



precursor information

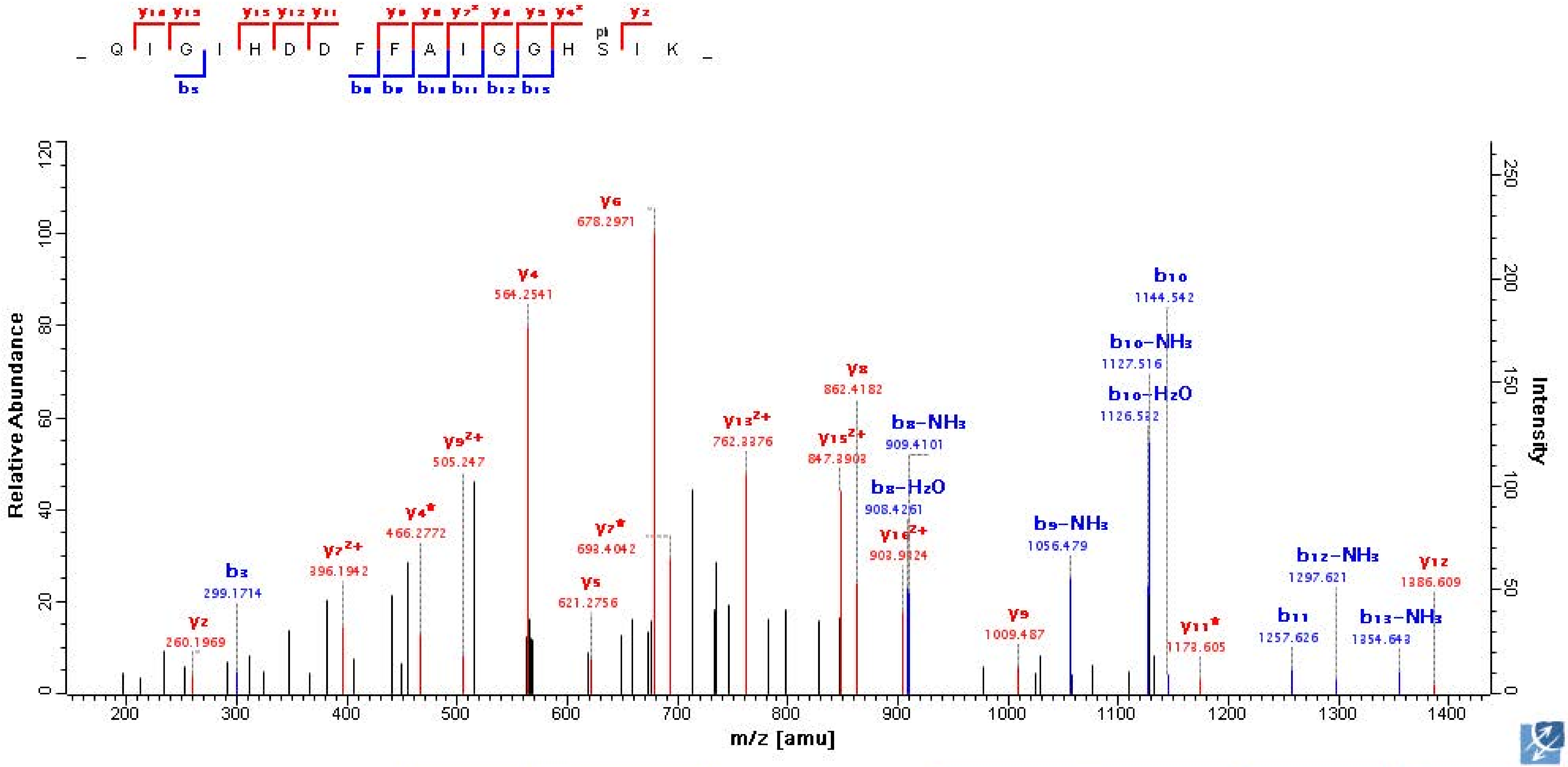
Mass:	2123.07775
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	95.48004
Mass Error [ppm]:	0.059881
PEP:	3.8836E-06
Precursor Type:	MULTI

general information

Annotation:	13 of 19
AminoAcids Coverag	68 %
Intensity Coverage:	52 %
Protein Localisation:	8 ... 26

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	116.0342195		116.0342195	1	D	18		
	217.08189797		217.08189797	2	T	17	2017.072151	
	373.183009		373.183009	3	R	16	1916.0244726	
	472.25142292	+0.2244682	472.25142292	4	V	15	1759.9233615	
	585.3354869	+0.0114369	585.3354869	5	I	14	1660.8549476	
	684.40390081	+0.1541436	684.40390081	6	V	13	1547.7708836	
	812.46247833	-0.0378567	812.46247833	7	Q	12	1448.7024697	
	869.48394205	+0.0155086	869.48394205	8	G	11	1320.6438922	-0.2369098
	982.56800603	+0.0522943	982.56800603	9	I	10	1263.6224285	
-0.0235777	542.31148048	+0.0887833	1083.6156845	10	T	9	1150.5383645	-0.0035745
	1140.6371482		1140.6371482	11	G	8	1049.490686	-0.1609741
	1307.635507		1307.635507	12	S	7	992.4692223	
	1408.6831855		1408.6831855	13	T	6	825.47086348	
	1479.7202993		1479.7202993	14	A	5	724.423185	-0.1030556
	1592.8043633		1592.8043633	15	I	4	653.38607122	
+0.0669922	870.44002684	-0.1556141	1739.8727772	16	F	3	540.30200724	+0.1699776
+0.3972165	938.96948277		1876.9316891	17	H	2	393.23359332	-0.0441402
	1977.9793675		1977.9793675	18	T	1	256.17468146	+0.1257641
				19	K	0	155.12700298	

Source:	20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F09
Scannumber:	9430
Protein:	BSU03510; srfA3; srfAC
Peptide Score:	77.42
Method:	ITMS; CID; 3



precursor information

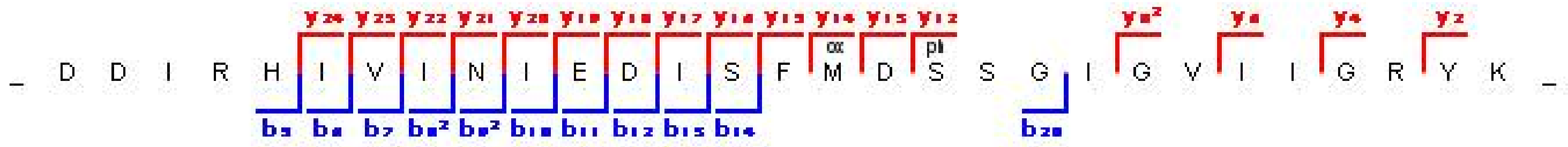
Mass:	1933.90939
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	77.42032
Mass Error [ppm]:	0.32502
PEP:	0.0050706
Precursor Type:	MULTI

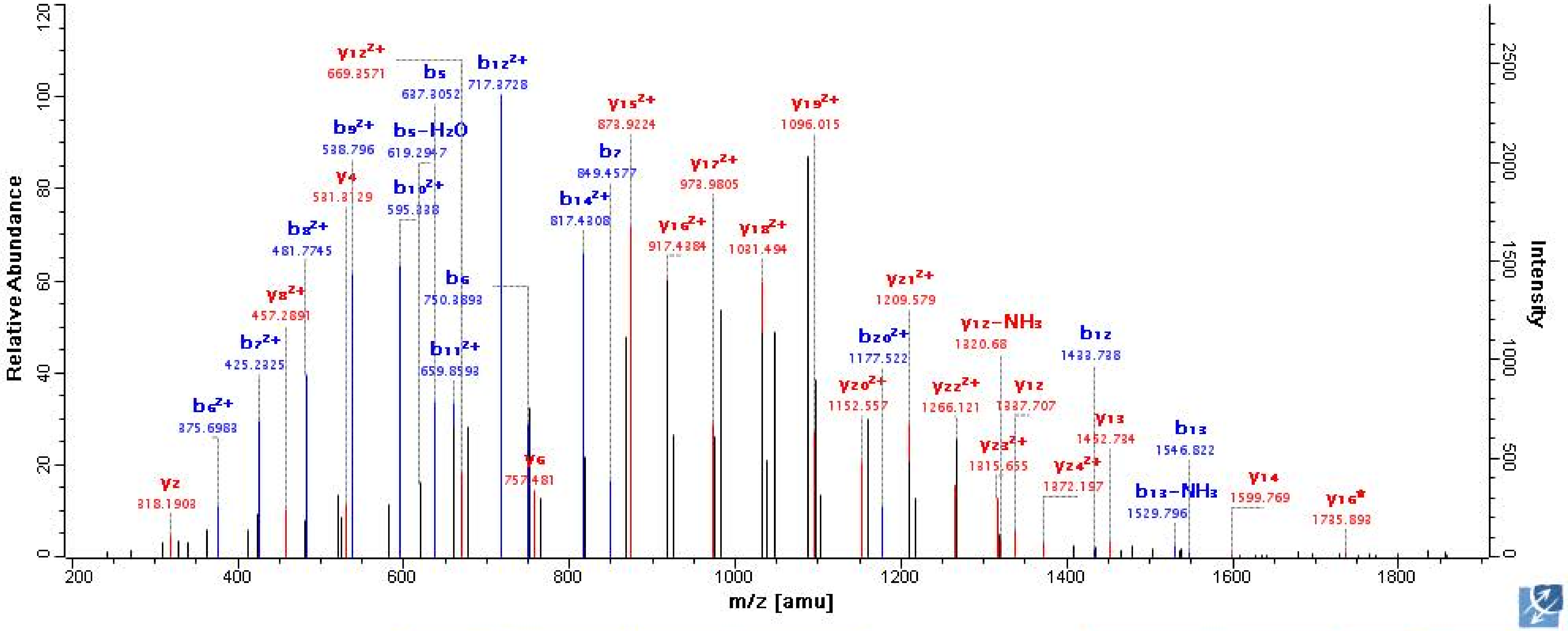
general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	51 %
Protein Localisation:	989 ... 1005

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.06585398	1	Q	16				
	242.14991796	2	I	15	1806.8574615		903.93236898	-0.0058553
+0.1134084	299.17138168	3	G	14	1693.7733975		847.39033699	+0.3473949
	412.25544566	4	I	13	1636.7519338		1636.7519338	
	549.31435752	5	H	12	1523.6678698		762.33757314	+0.0308961
	664.34130056	6	D	11	1386.6089579	+0.0609639	1386.6089579	
	779.36824359	7	D	10	1271.5820149		1271.5820149	
	926.43665751	8	F	9	1156.5550719		1156.5550719	
	1073.5050714	9	F	8	1009.486658	+0.0155393	505.24696721	+0.0948297
+0.1125999	1144.5421852	10	A	7	862.41824405	+0.1568902	862.41824405	
+0.0550252	1257.6262492	11	I	6	791.38113026		396.19420336	+0.1142073
	1314.6477129	12	G	5	678.29706628	-0.1518026	678.29706628	
	1371.6691766	13	G	4	621.27560256	-0.4712202	621.27560256	
	1508.7280885	14	H	3	564.25413883	-0.2619513	564.25413883	
	1675.7264473	15	S	2	427.19522697		427.19522697	
	1788.8105113	16	I	1	260.19686815	+0.0054634	260.19686815	
		17	K	0	147.11280417		147.11280417	

Source:	20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F16
Scannumber:	10208
Protein:	BSU23470; spoIIAA
Peptide Score:	156.29
Method:	ITMS; CID; 3





precursor information

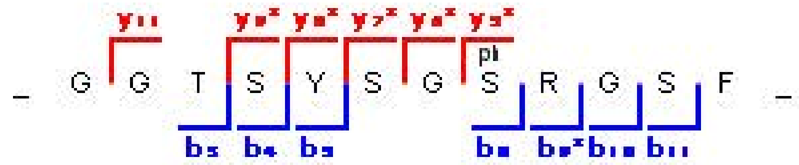
Mass:	3378.67644
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	156.2934
Mass Error [ppm]:	-0.29749
PEP:	4.2245E-45
Precursor Type:	ISO

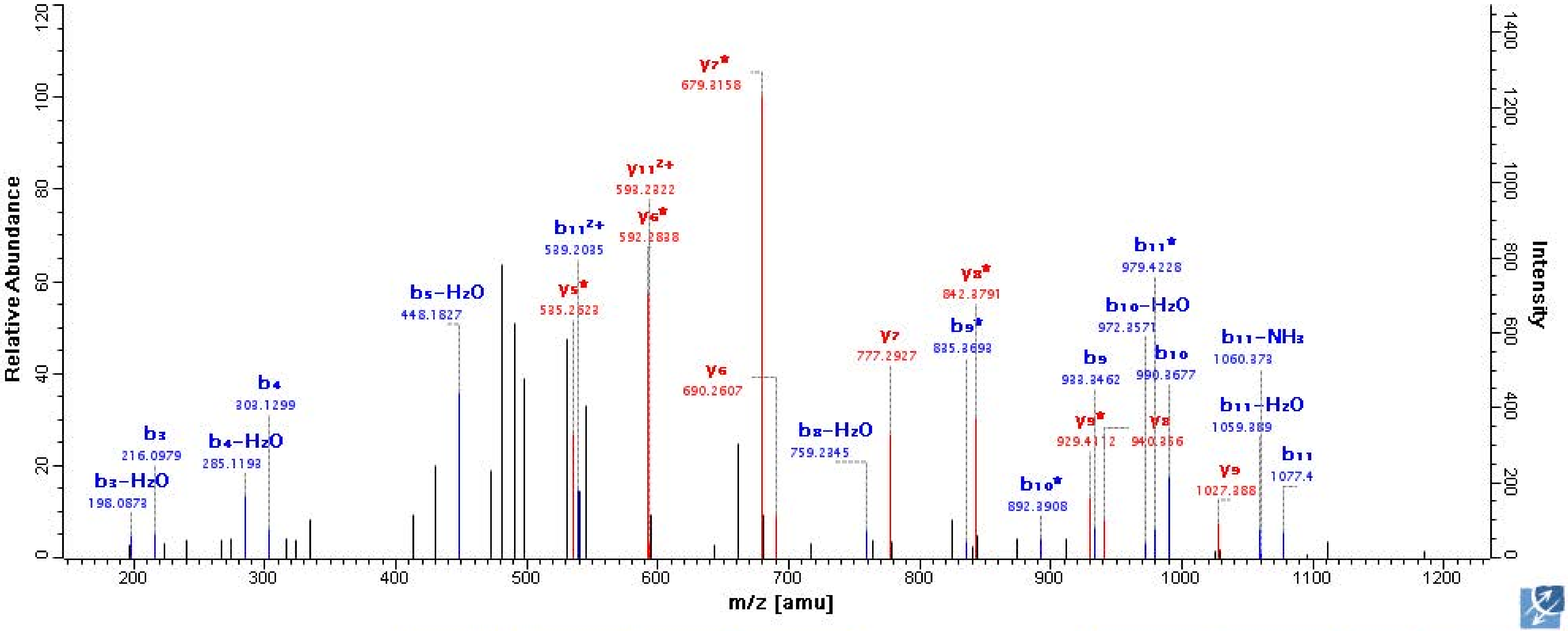
general information

Annotation:	21 of 29
AminoAcids Coverag	72 %
Intensity Coverage:	51 %
Protein Localisation:	41 ... 69

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342		116.0342	1	D	28				
	231.0612		231.0612	2	D	27	3264.658		3264.658	
	344.1452		344.1452	3	I	26	3149.631		3149.631	
	500.2463		500.2463	4	R	25	3036.547		3036.547	
	637.3052	+0.027575	637.3052	5	H	24	2880.446		2880.446	
+0.25599	375.6983	+0.032379	750.3893	6	I	23	2743.387		1372.197	+0.142589
+0.199749	425.2325	-0.178675	849.4577	7	V	22	2630.303		1315.655	+0.379323
+0.218203	481.7745		962.5418	8	I	21	2531.234		1266.121	-0.158491
+0.282372	538.796		1076.585	9	N	20	2418.15		1209.579	-0.048466
+0.190596	595.338		1189.669	10	I	19	2304.107		1152.557	-0.128565
+0.109241	659.8593		1318.711	11	E	18	2191.023		1096.015	-0.078476
+0.317205	717.3728	-0.247596	1433.738	12	D	17	2061.981		1031.494	+0.046336
	1546.822	+0.216436	1546.822	13	I	16	1946.954		973.9805	-0.12458
-0.177182	817.4308		1633.854	14	S	15	1833.87		917.4384	-0.017729
	1780.923		1780.923	15	F	14	1746.838		873.9224	+0.265681
	1927.958		1927.958	16	M	13	1599.769	+0.171993	1599.769	
	2042.985		2042.985	17	D	12	1452.734	-0.431402	1452.734	
	2209.984		2209.984	18	S	11	1337.707	+0.089804	669.3571	+0.479862
	2297.016		2297.016	19	S	10	1170.708		1170.708	
+0.269967	1177.522		2354.037	20	G	9	1083.676		1083.676	
	2467.121		2467.121	21	I	8	1026.655		1026.655	
	2524.143		2524.143	22	G	7	913.5709		457.2891	+0.128569
	2623.211		2623.211	23	V	6	856.5494		856.5494	
	2736.295		2736.295	24	I	5	757.481	-0.118791	757.481	
	2849.379		2849.379	25	I	4	644.397		644.397	
	2906.401		2906.401	26	G	3	531.3129	+0.146627	531.3129	
	3062.502		3062.502	27	R	2	474.2914		474.2914	
	3225.565		3225.565	28	Y	1	318.1903	+0.234656	318.1903	
				29	K	0	155.127		155.127	

Source:	20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F17
Scannumber:	5924
Protein:	BSU06200; ydjH
Peptide Score:	160.67
Method:	ITMS; CID; 3





precursor information

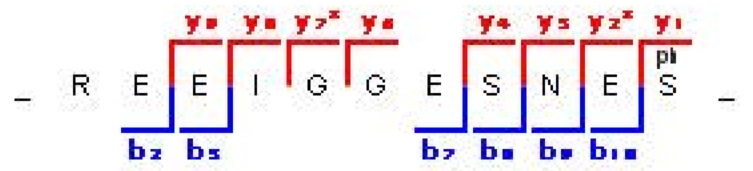
Mass:	1241.47132
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	160.6748
Mass Error [ppm]:	-0.064566
PEP:	5.8138E-23
Precursor Type:	ISO

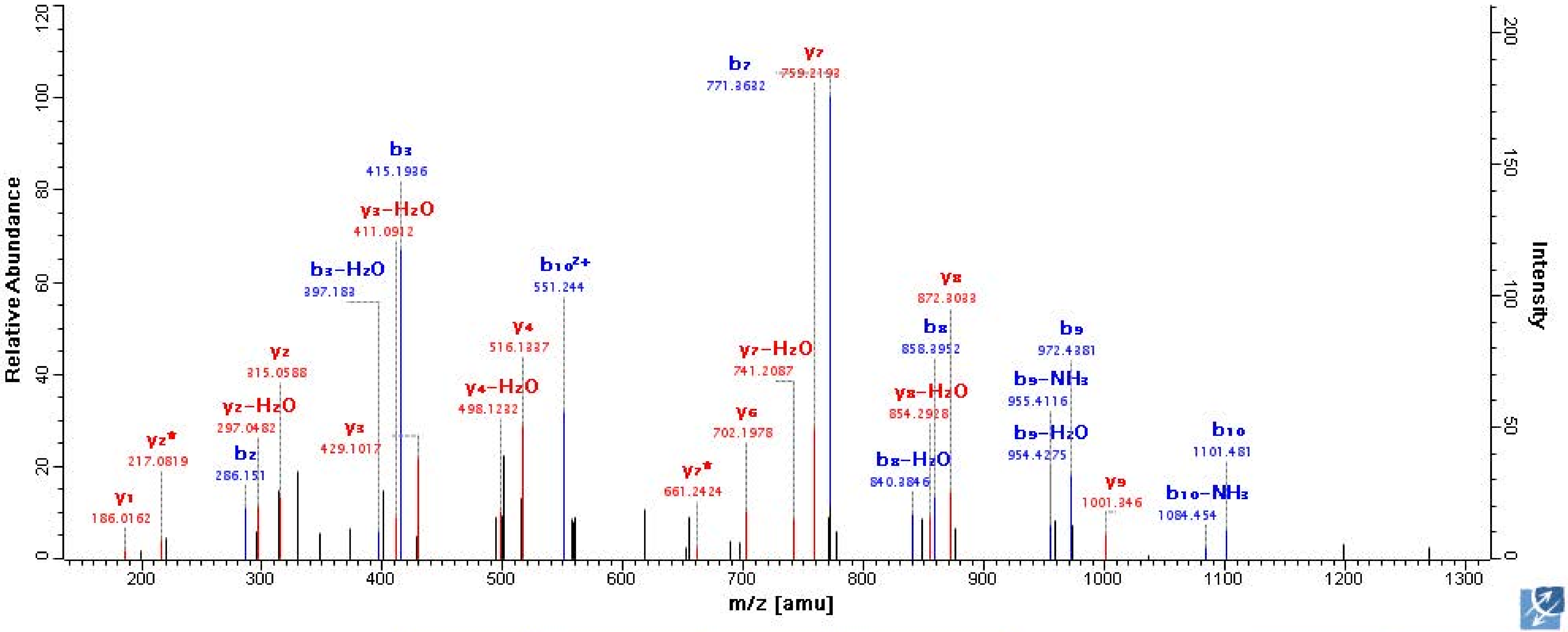
general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	50 %
Protein Localisation:	243 ... 254

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874		58.02874	1	G	11				
	115.0502		115.0502	2	G	10	1185.457		593.2322	+0.14172
	216.0979	+0.096454	216.0979	3	T	9	1128.436		1128.436	
	303.1299	+0.035586	303.1299	4	S	8	1027.388	+0.021968	1027.388	
	466.1932		466.1932	5	Y	7	940.356	+0.158428	940.356	
	553.2253		553.2253	6	S	6	777.2927	+0.168228	777.2927	
	610.2467		610.2467	7	G	5	690.2607	-0.103271	690.2607	
	777.2451		777.2451	8	S	4	633.2392		633.2392	
	933.3462	-0.00117	933.3462	9	R	3	466.2409		466.2409	
	990.3677	+0.047313	990.3677	10	G	2	310.1397		310.1397	
+0.094794	539.2035	-0.023107	1077.4	11	S	1	253.1183		253.1183	
				12	F	0	166.0863		166.0863	

Source: 20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F19
Scannumber: 2812
Protein: BSU01230; rplP
Peptide Score: 170.89
Method: ITMS; CID; 3





precursor information

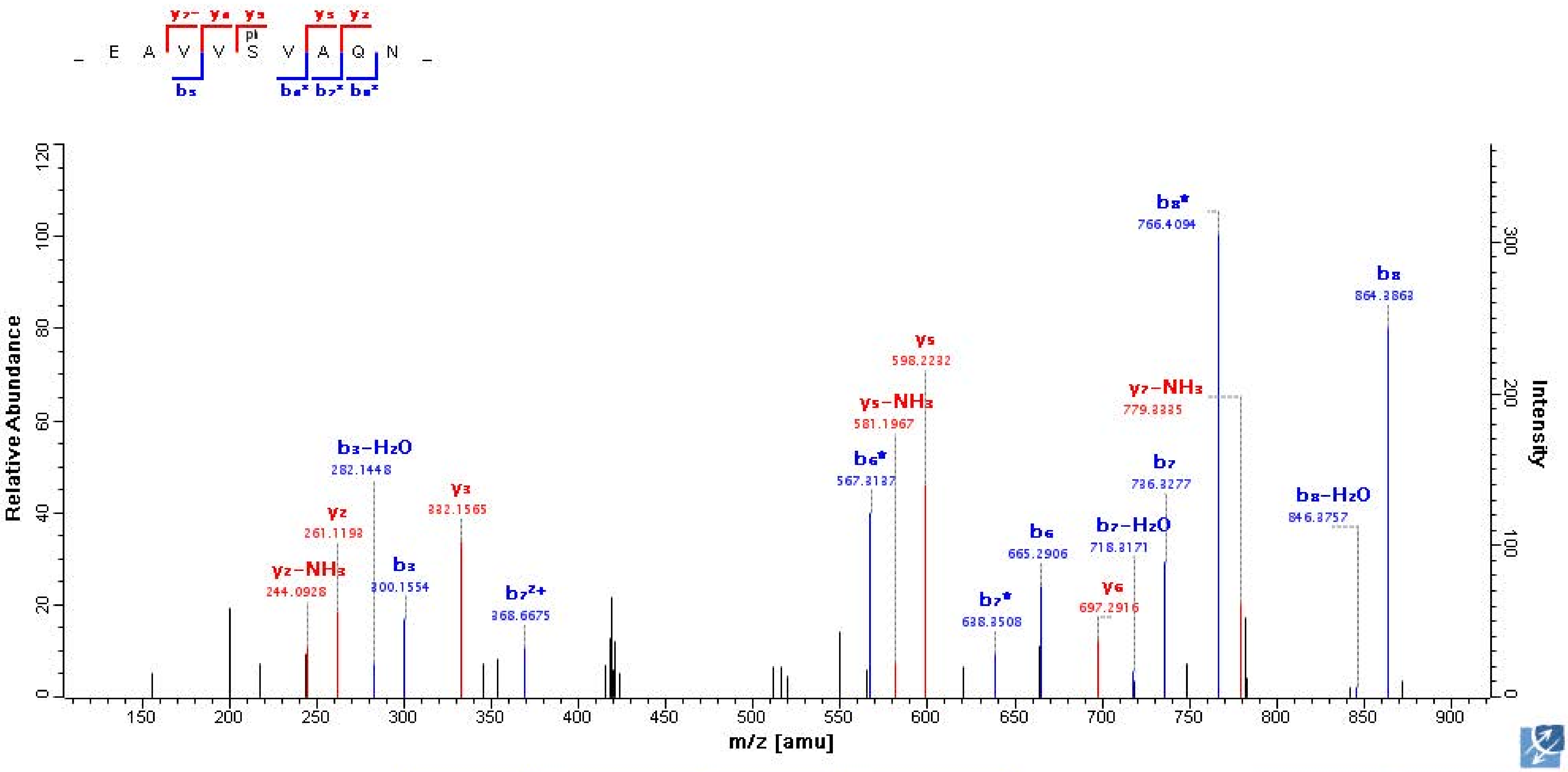
Mass:	1285.48226
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	170.8887
Mass Error [ppm]:	-0.071609
PEP:	3.0967E-33
Precursor Type:	ISO

general information

Annotation:	10 of 11
AminoAcids Coverag	91 %
Intensity Coverage:	65 %
Protein Localisation:	134 ... 144

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	157.10838749		157.10838749	1	R	10		
	286.15098059	+0.0351156	286.15098059	2	E	9	1130.3885196	
	415.19357369	+0.0071709	415.19357369	3	E	8	1001.3459265	-0.3282874
	528.27763767		528.27763767	4	I	7	872.30333345	-0.000538
	585.29910139		585.29910139	5	G	6	759.21926947	+0.0076592
	642.32056511		642.32056511	6	G	5	702.19780574	+0.0200287
	771.36315821	-0.039855	771.36315821	7	E	4	645.17634202	
	858.39518662	+0.0894936	858.39518662	8	S	3	516.13374892	-0.0720424
	972.43811407	-0.1162757	972.43811407	9	N	2	429.10172051	+0.1689704
+0.0481224	551.24399182	-0.0025578	1101.4807072	10	E	1	315.05879307	+0.1258993
				11	S	0	186.01619997	+0.1314746

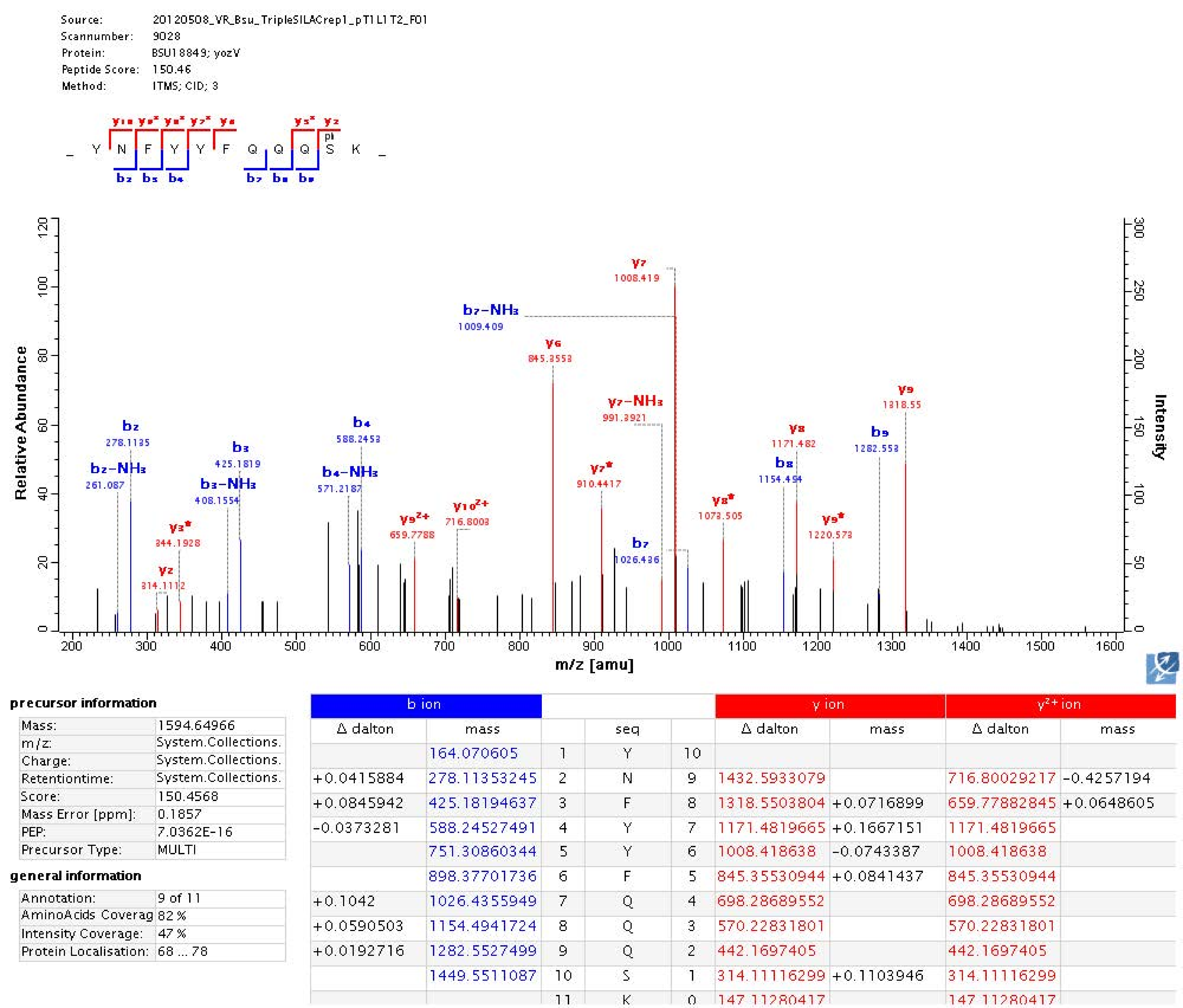
Source:	20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F21
Scannumber:	4471
Protein:	BSU28290; ilvC
Peptide Score:	118.71
Method:	ITMS; CID; 3



precursor information

Mass:	995.43253
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	118.7116
Mass Error [ppm]:	0.0391
PEP:	1.7967E-05
Precursor Type:	ISO
Annotation:	6 of 9
AminoAcids Coverag	67 %
Intensity Coverage:	69 %
Protein Localisation:	334 ... 342

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	130.04986956		130.04986956	1	E	8		
	201.08698335		201.08698335	2	A	7	867.39717425	
	300.15539727	-0.0854815	300.15539727	3	V	6	796.36006047	
	399.22381118		399.22381118	4	V	5	697.29164655	+0.0143227
	566.22217		566.22217	5	S	4	598.22323263	+0.0780979
	665.29058392	+0.0282027	665.29058392	6	V	3	431.22487382	
-0.2304143	368.66748709	-0.0485229	736.32769771	7	A	2	332.1564599	+0.0173682
	864.38627522	-0.1015462	864.38627522	8	Q	1	261.11934611	+0.0546956
				9	N	0	133.0607686	



Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F01
Scannumber: 9028
Protein: BSU18849; yozV
Peptide Score: 150.46
Method: ITMS; CID; 3

precursor information

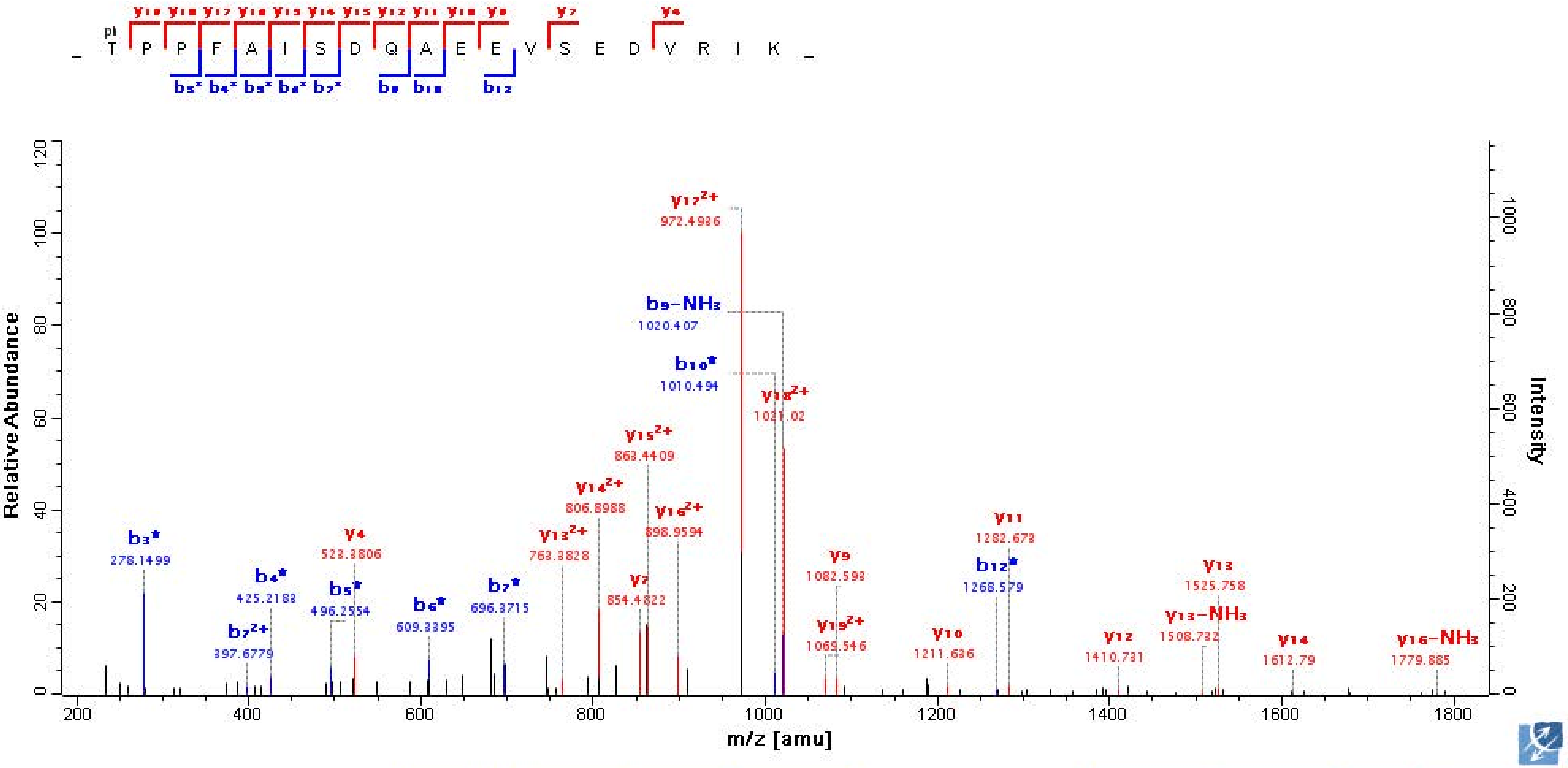
Mass:	1594.64966
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	150.4568
Mass Error [ppm]:	0.1857
PEP:	7.0362E-16
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	47 %
Protein Localisation:	68 ... 78

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	164.070605	1	Y	10				
+0.0415884	278.11353245	2	N	9	1432.5933079		716.80029217	-0.4257194
+0.0845942	425.18194637	3	F	8	1318.5503804	+0.0716899	659.77882845	+0.0648605
-0.0373281	588.24527491	4	Y	7	1171.4819665	+0.1667151	1171.4819665	
	751.30860344	5	Y	6	1008.418638	-0.0743387	1008.418638	
	898.37701736	6	F	5	845.35530944	+0.0841437	845.35530944	
+0.1042	1026.4355949	7	Q	4	698.28689552		698.28689552	
+0.0590503	1154.4941724	8	Q	3	570.22831801		570.22831801	
+0.0192716	1282.5527499	9	Q	2	442.1697405		442.1697405	
	1449.5511087	10	S	1	314.11116299	+0.1103946	314.11116299	
		11	K	0	147.11280417		147.11280417	

Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F01
Scannumber: 9723
Protein: aspS; BSU27550
Peptide Score: 89.56
Method: ITMS; CID; 3



precursor information

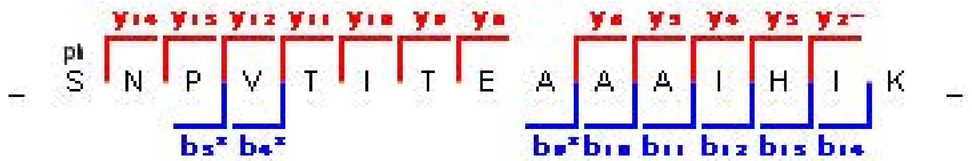
Mass:	2310.07717
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	89.55674
Mass Error [ppm]:	-0.38958
PEP:	2.9867E-06
Precursor Type:	MULTI

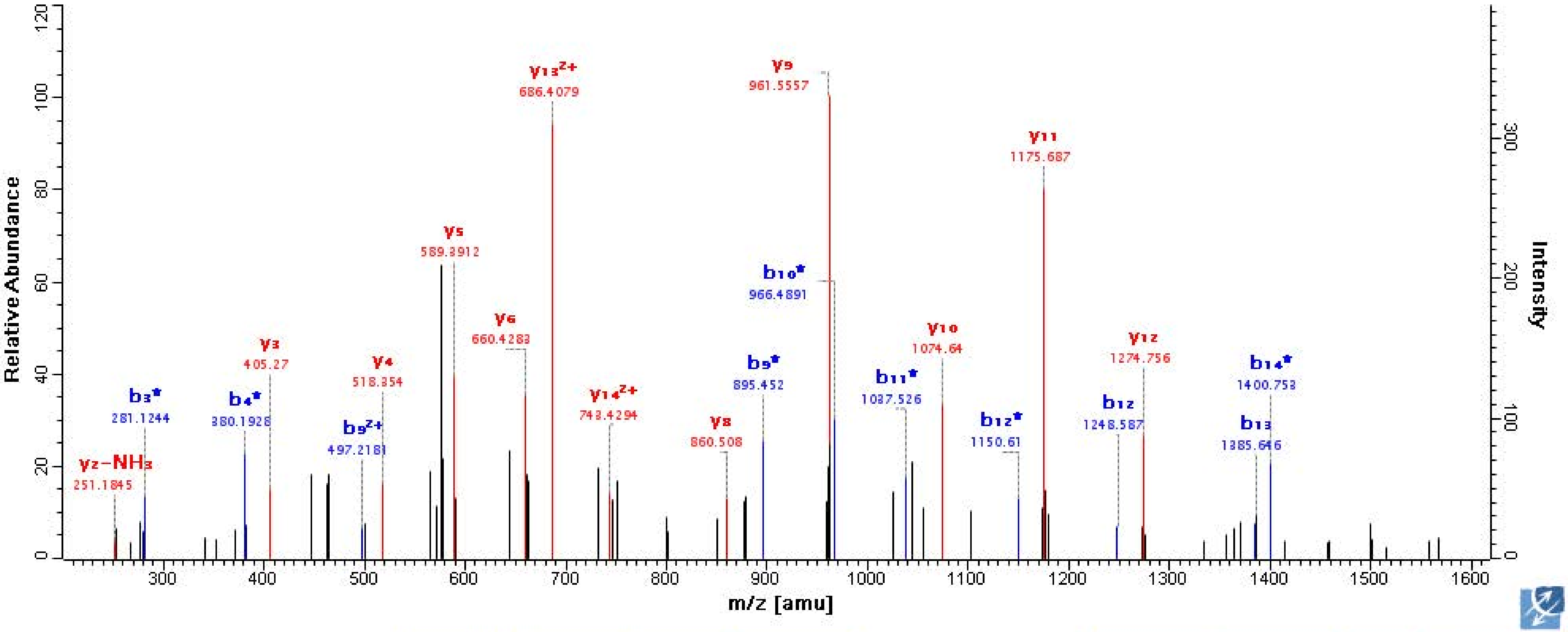
general information

Annotation:	15 of 20
AminoAcids Coverag	75 %
Intensity Coverage:	56 %
Protein Localisation:	110 ... 129

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	182.0213		182.0213	1	T	19				
	279.074		279.074	2	P	18	2138.086		1069.546	+0.08201
	376.1268		376.1268	3	P	17	2041.033		1021.02	+0.337823
	523.1952		523.1952	4	F	16	1943.98		972.4936	-0.021537
	594.2323		594.2323	5	A	15	1796.912		898.9594	+0.150121
	707.3164		707.3164	6	I	14	1725.874		863.4409	+0.087074
-0.195067	397.6779		794.3484	7	S	13	1612.79	+0.192125	806.8988	-0.038679
	909.3754		909.3754	8	D	12	1525.758	+0.423616	763.3828	+0.167032
	1037.434		1037.434	9	Q	11	1410.731	+0.259031	1410.731	
	1108.471		1108.471	10	A	10	1282.673	+0.089947	1282.673	
	1237.514		1237.514	11	E	9	1211.636	-0.174331	1211.636	
	1366.556		1366.556	12	E	8	1082.593	-0.002099	1082.593	
	1465.625		1465.625	13	V	7	953.5506		953.5506	
	1552.657		1552.657	14	S	6	854.4822	-0.04252	854.4822	
	1681.699		1681.699	15	E	5	767.4501		767.4501	
	1796.726		1796.726	16	D	4	638.4075		638.4075	
	1895.795		1895.795	17	V	3	523.3806	-0.038978	523.3806	
	2051.896		2051.896	18	R	2	424.3122		424.3122	
	2164.98		2164.98	19	I	1	268.2111		268.2111	
				20	K	0	155.127		155.127	

Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F03
Scannumber: 10209
Protein: BSU32160; yutM
Peptide Score: 113.59
Method: ITMS; CID; 3





precursor information

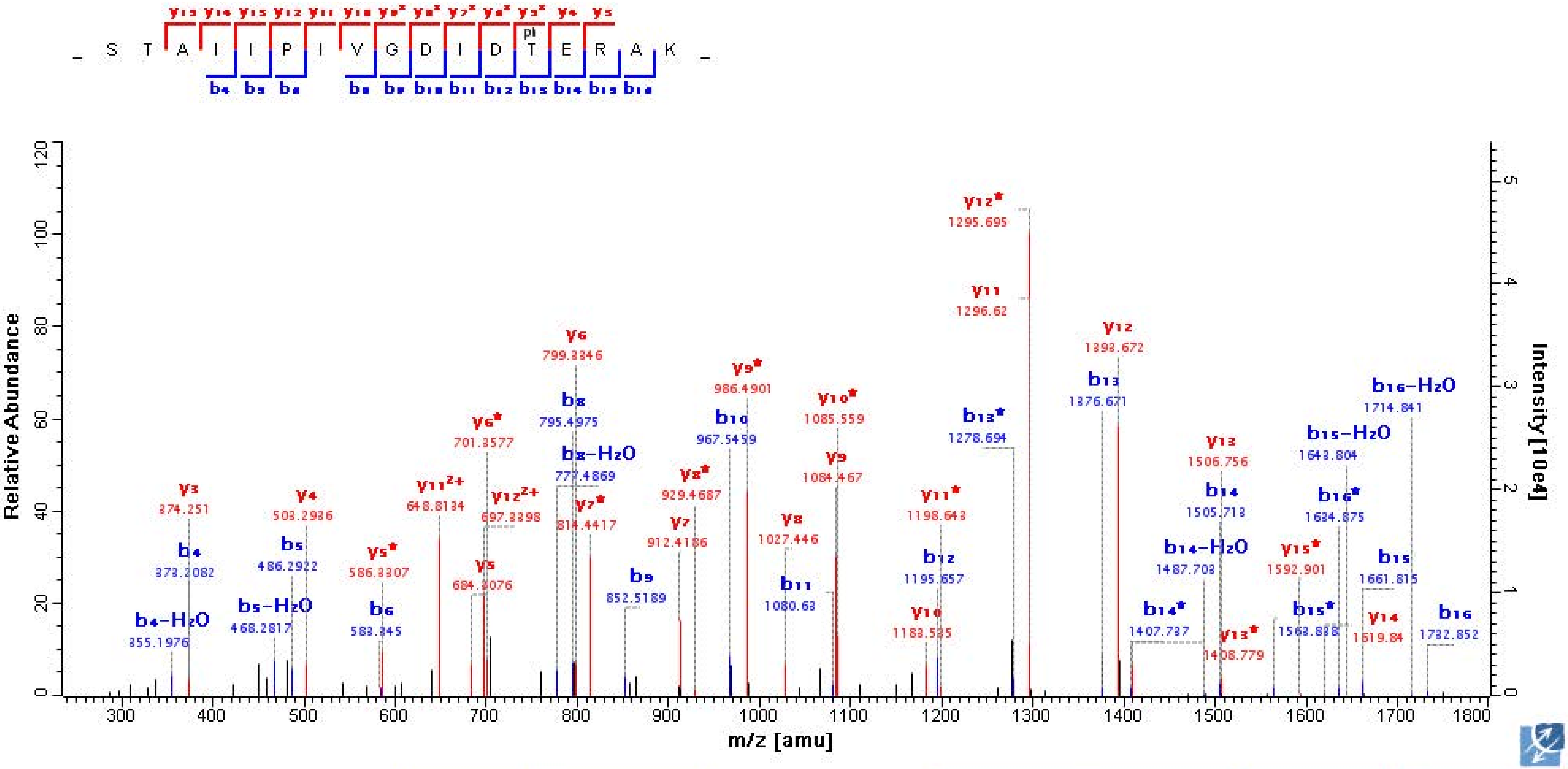
Mass:	1643.82886
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	113.5862
Mass Error [ppm]:	0.28586
PEP:	0.00034226
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	48 %
Protein Localisation:	2 ... 16

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.0056		168.0056	1	S	14				
	282.0486		282.0486	2	N	13	1485.852		743.4294	+0.001335
	379.1013		379.1013	3	P	12	1371.809		686.4079	+0.170016
	478.1697		478.1697	4	V	11	1274.756	+0.200853	1274.756	
	579.2174		579.2174	5	T	10	1175.687	-0.113424	1175.687	
	692.3015		692.3015	6	I	9	1074.64	+0.017385	1074.64	
	793.3492		793.3492	7	T	8	961.5557	+0.036324	961.5557	
	922.3918		922.3918	8	E	7	860.508	-0.000348	860.508	
+0.173529	497.2181		993.4289	9	A	6	731.4654		731.4654	
	1064.466		1064.466	10	A	5	660.4283	-0.001085	660.4283	
	1135.503		1135.503	11	A	4	589.3912	+0.0143	589.3912	
	1248.587	-0.268434	1248.587	12	I	3	518.354	+0.131431	518.354	
	1385.646	-0.23323	1385.646	13	H	2	405.27	+0.064067	405.27	
	1498.73		1498.73	14	I	1	268.2111		268.2111	
				15	K	0	155.127		155.127	

Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F03
Scannumber: 11086
Protein: BSU13200; rsbRB; ykoB
Peptide Score: 297.45
Method: ITMS; CID; 3



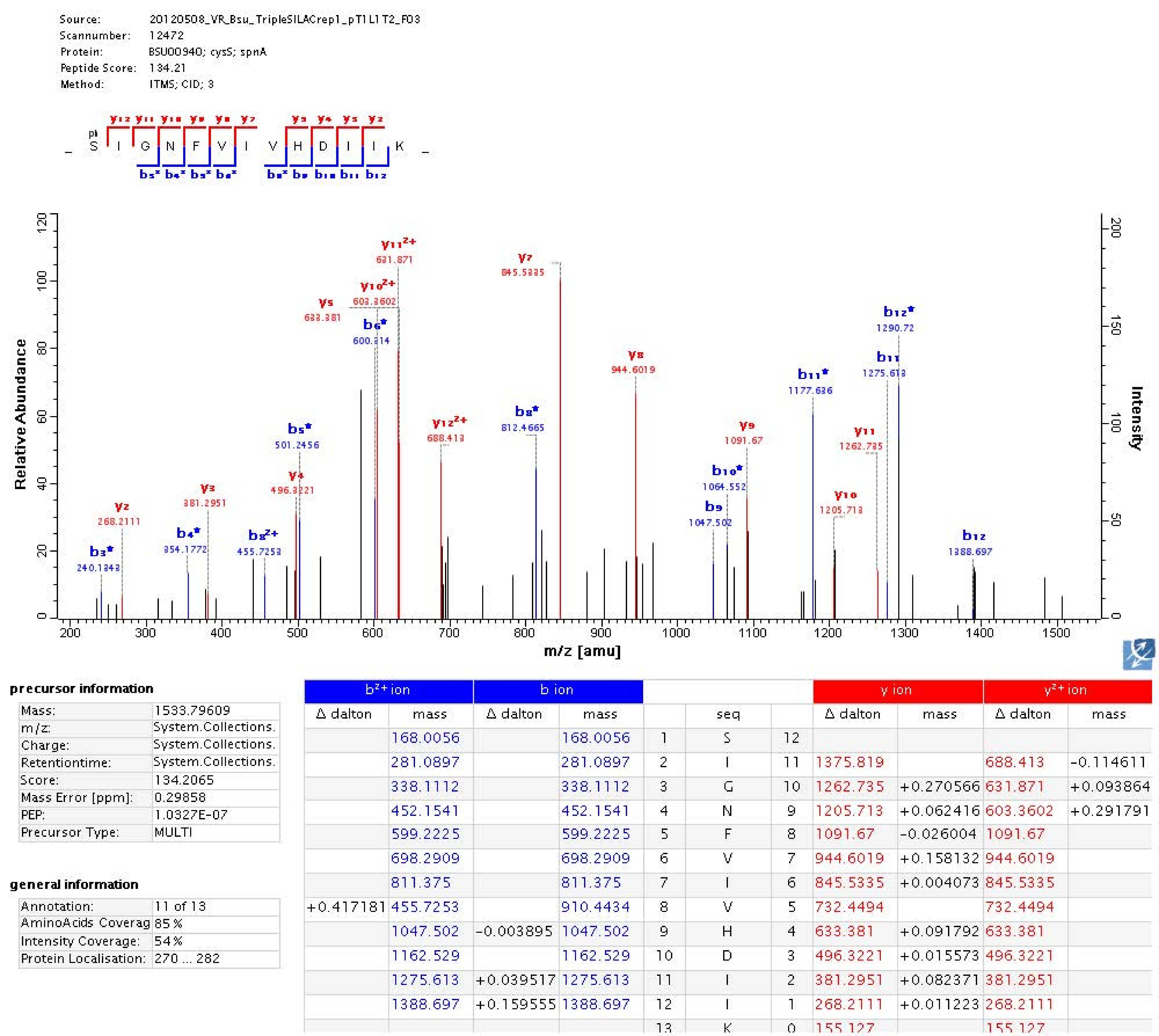
precursor information

Mass:	1877.94875
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	297.4548
Mass Error [ppm]:	-0.64494
PEP:	2.5647E-199
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	78 %
Protein Localisation:	174 ... 190

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876	1	S	16				
	189.08698335	2	T	15	1791.9252067		1791.9252067	
	260.12409714	3	A	14	1690.8775282		1690.8775282	
-0.0045784	373.20816112	4	I	13	1619.8404144	+0.1964508	1619.8404144	
+0.0087393	486.2922251	5	I	12	1506.7563505	+0.1048556	1506.7563505	
+0.1991395	583.34498895	6	P	11	1393.6722865	+0.0650182	697.33978147	-0.0226428
	696.42905293	7	I	10	1296.6195226	+0.2551112	648.81339955	-0.3156578
-0.0205381	795.49746685	8	V	9	1183.5354586	-0.0076266	1183.5354586	
+0.0280665	852.51893057	9	G	8	1084.4670447	+0.1005822	1084.4670447	
-0.0652217	967.5458736	10	D	7	1027.445581	+0.1484131	1027.445581	
-0.0054259	1080.6299376	11	I	6	912.41863798	+0.1270774	912.41863798	
-0.046407	1195.6568806	12	D	5	799.334574	-0.0659583	799.334574	
+0.2220548	1376.6708895	13	T	4	684.30763097	+0.0546127	684.30763097	
-0.0529601	1505.7134826	14	E	3	503.29362208	-0.0467959	503.29362208	
+0.0253722	1661.8145936	15	R	2	374.25102899	+0.0778895	374.25102899	
+0.1421891	1732.8517074	16	A	1	218.14991796		218.14991796	
		17	K	0	147.11280417		147.11280417	



Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F03
Scannumber: 12472
Protein: BSU00940; cysS; spnA
Peptide Score: 134.21
Method: ITMS; CID; 3

precursor information

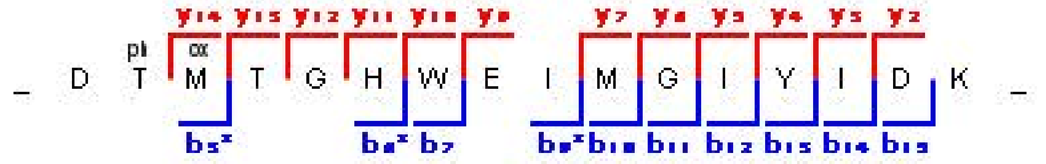
Mass:	1533.79609
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	134.2065
Mass Error [ppm]:	0.29858
PEP:	1.0327E-07
Precursor Type:	MULTI

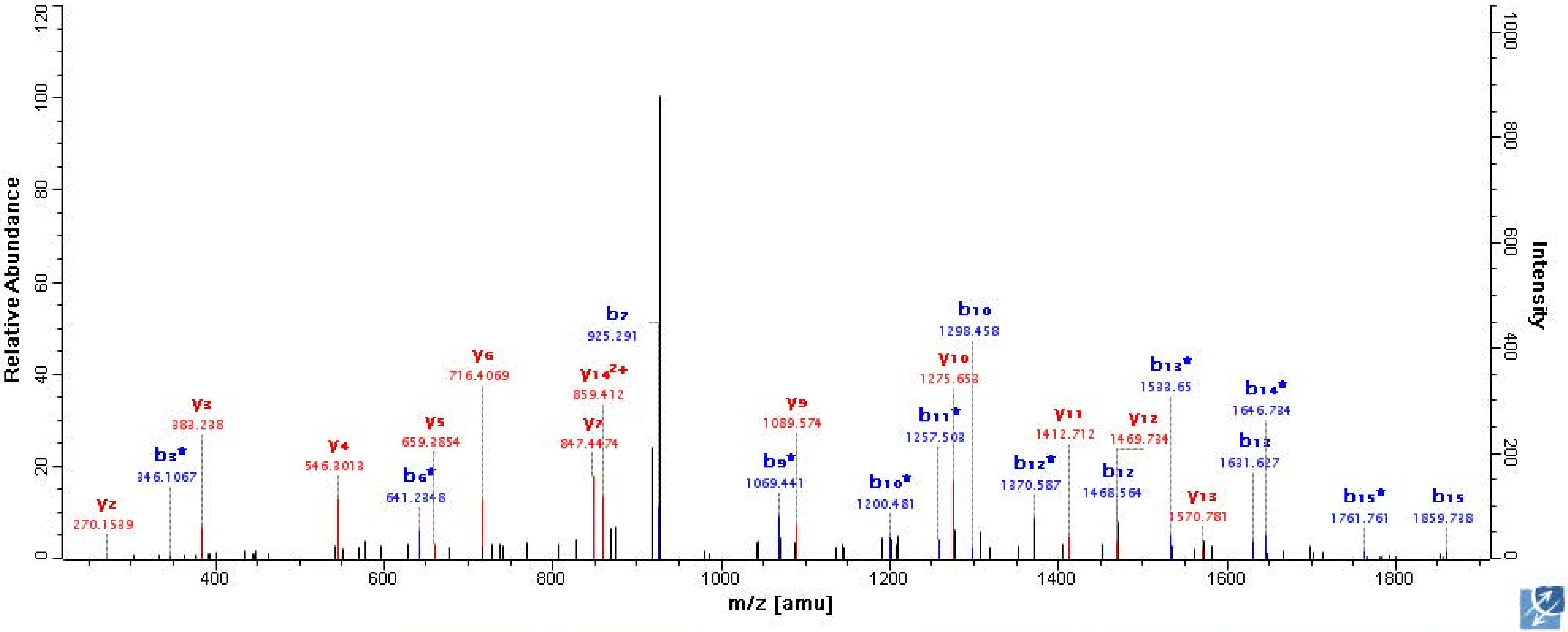
general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	54 %
Protein Localisation:	270 ... 282

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.0056		168.0056	1	S	12				
	281.0897		281.0897	2	I	11	1375.819		688.413	-0.114611
	338.1112		338.1112	3	G	10	1262.735	+0.270566	631.871	+0.093864
	452.1541		452.1541	4	N	9	1205.713	+0.062416	603.3602	+0.291791
	599.2225		599.2225	5	F	8	1091.67	-0.026004	1091.67	
	698.2909		698.2909	6	V	7	944.6019	+0.158132	944.6019	
	811.375		811.375	7	I	6	845.5335	+0.004073	845.5335	
+0.417181	455.7253		910.4434	8	V	5	732.4494		732.4494	
	1047.502	-0.003895	1047.502	9	H	4	633.381	+0.091792	633.381	
	1162.529		1162.529	10	D	3	496.3221	+0.015573	496.3221	
	1275.613	+0.039517	1275.613	11	I	2	381.2951	+0.082371	381.2951	
	1388.697	+0.159555	1388.697	12	I	1	268.2111	+0.011223	268.2111	
				13	K	0	155.127		155.127	

Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F03
Scannumber: 12499
Protein: BSU23500; drm; yqkN
Peptide Score: 146.16
Method: ITMS; CID; 3





precursor information

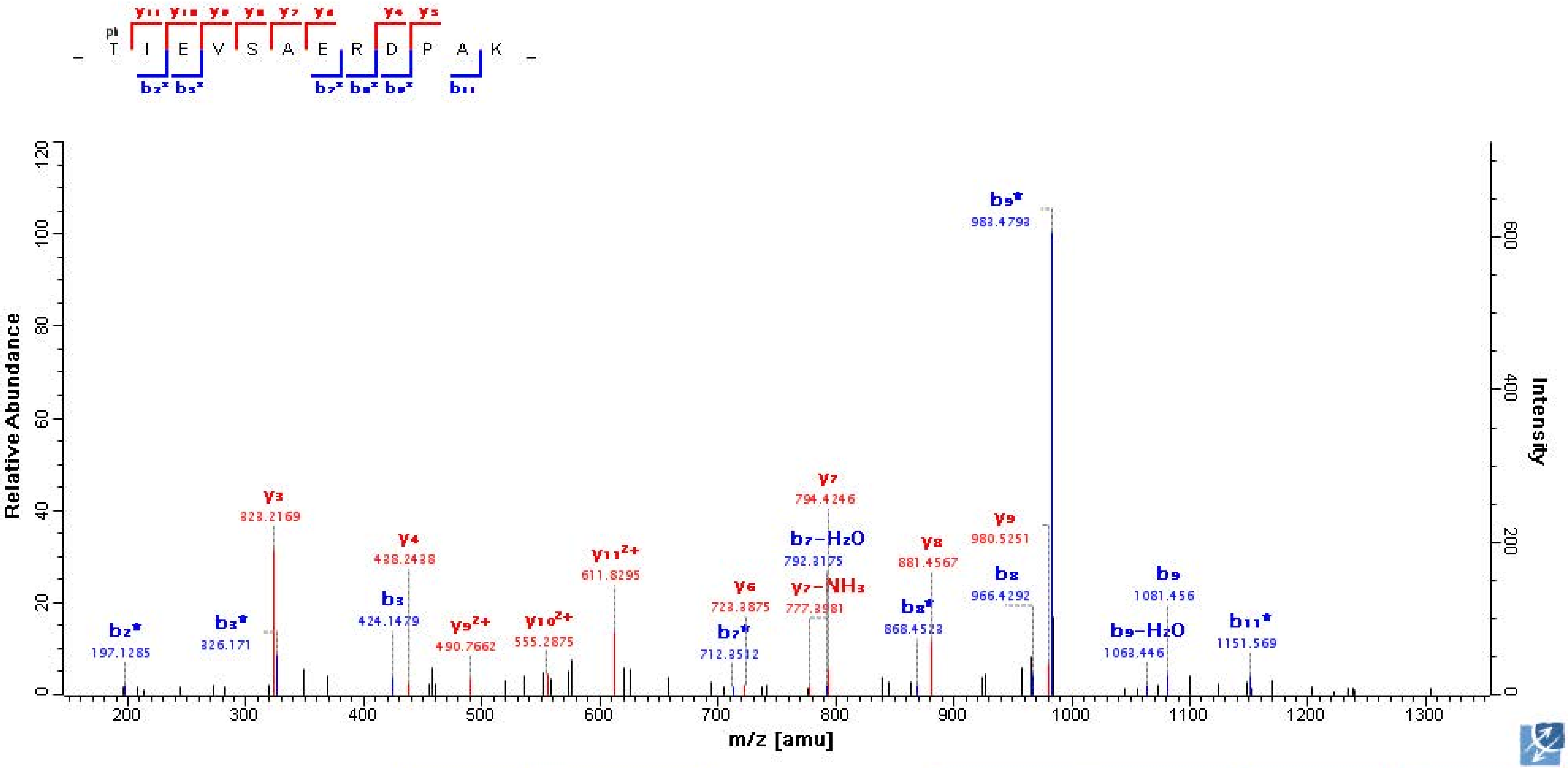
Mass:	2004.83672
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	146.1593
Mass Error [ppm]:	0.23539
PEP:	9.973E-12
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	34 %
Protein Localisation:	86 ... 101

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342195	1	D	15				
	297.04822838	2	T	14	1898.830783		1898.830783	
	444.08362761	3	M	13	1717.8167742		859.41202531	+0.4054796
	545.13130608	4	T	12	1570.7813749	+0.2416964	1570.7813749	
	602.15276981	5	G	11	1469.7336965	+0.0330272	1469.7336965	
	739.21168167	6	H	10	1412.7122327	+0.3612536	1412.7122327	
+0.4381314	925.29099462	7	W	9	1275.6533209	+0.0537104	1275.6533209	
	1054.3335877	8	E	8	1089.5740079	+0.0852938	1089.5740079	
	1167.4176517	9	I	7	960.53141483		960.53141483	
+0.1961606	1298.4581363	10	M	6	847.44735084	+0.1046511	847.44735084	
	1355.4796	11	G	5	716.40686624	+0.0214175	716.40686624	
+0.151546	1468.563664	12	I	4	659.38540251	+0.1702615	659.38540251	
-0.1980375	1631.6269925	13	Y	3	546.30133853	-0.0519489	546.30133853	
	1744.7110565	14	I	2	383.23801	+0.091061	383.23801	
+0.000892	1859.7379996	15	D	1	270.15394602	+0.1336211	270.15394602	
		16	K	0	155.12700298		155.12700298	

Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F03
Scannumber: 5136
Protein: BSU33940; gap; gapA
Peptide Score: 108.72
Method: ITMS; CID; 3



precursor information

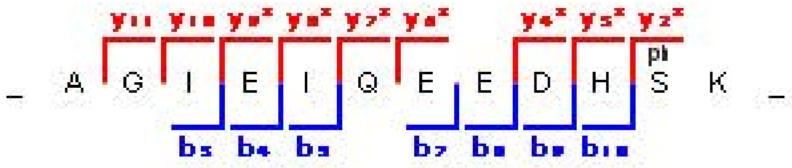
Mass:	1394.64457
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	108.7163
Mass Error [ppm]:	0.21196
PEP:	8.2235E-05
Precursor Type:	MULTI

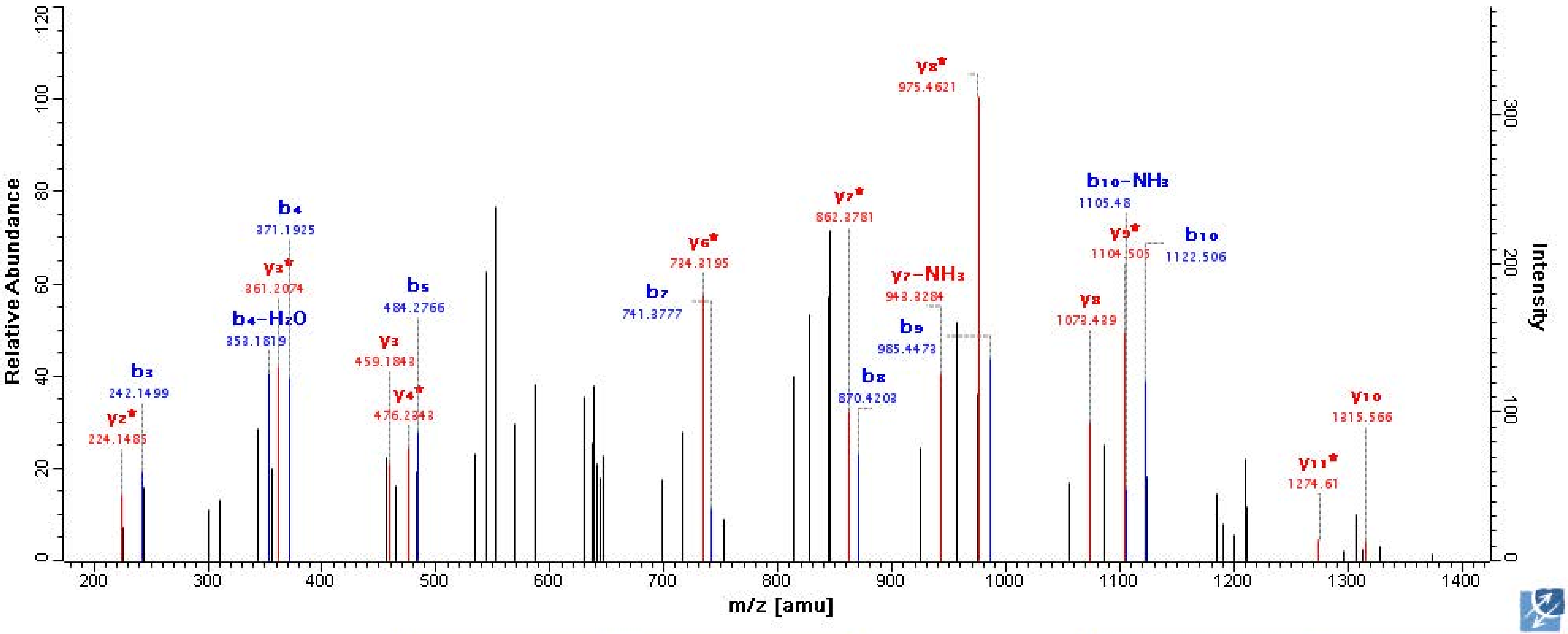
general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	57 %
Protein Localisation:	71 ... 82

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	182.02128535	1	T	11				
	295.10534933	2	I	10	1222.651741		611.82950872	+0.0139361
+0.1376411	424.14794243	3	E	9	1109.567677		555.28747673	+0.1902454
	523.21635634	4	V	8	980.52508389	-0.0648788	490.76618018	-0.2194273
	610.24838475	5	S	7	881.45666998	-0.0770923	881.45666998	
	681.28549854	6	A	6	794.42464157	-0.1139726	794.42464157	
	810.32809164	7	E	5	723.38752778	-0.2585605	723.38752778	
+0.0422939	966.42920266	8	R	4	594.34493468		594.34493468	
+0.0914617	1081.4561457	9	D	3	438.24382366	-0.0884892	438.24382366	
	1178.5089095	10	P	2	323.21688062	+0.0802996	323.21688062	
	1249.5460233	11	A	1	226.16411677		226.16411677	
		12	K	0	155.12700298		155.12700298	

Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F03
Scannumber:	5744
Protein:	aroA; BSU29750
Peptide Score:	101.39
Method:	ITMS; CID; 3





precursor information

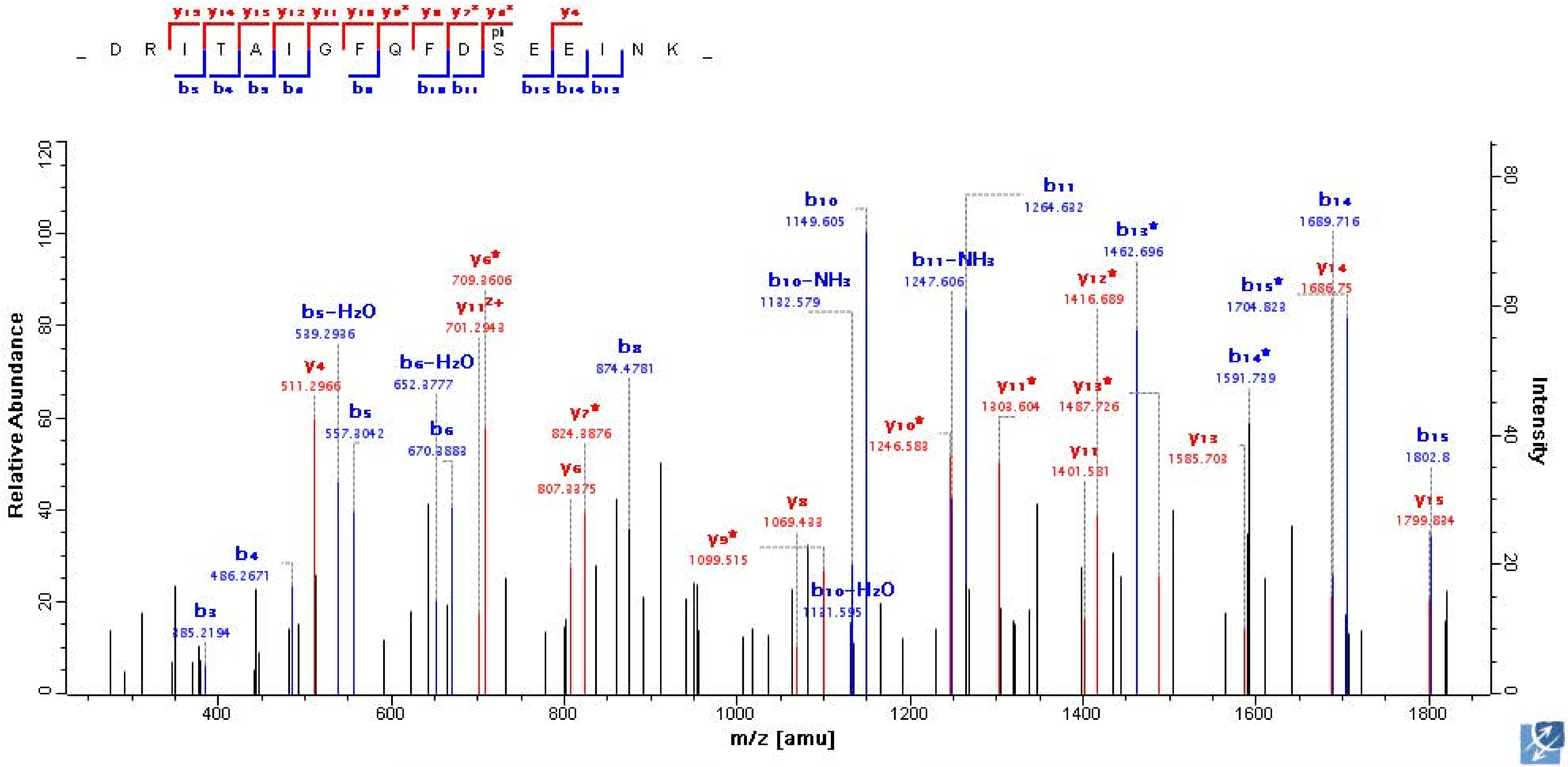
Mass:	1434.60338
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	101.3879
Mass Error [ppm]:	0.4013
PEP:	0.00031937
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	38 %
Protein Localisation:	81 ... 92

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	72.044390254	1	A	11		
	129.065853978	2	G	10	1372.587165181	
+0.0542599	242.149917958	3	I	9	1315.565701457	+0.3289519
-0.1054749	371.192511055	4	E	8	1202.481637477	
-0.0805911	484.276575035	5	I	7	1073.439044381	-0.1717104
	612.335152546	6	Q	6	960.3549804	
-0.0437613	741.377745643	7	E	5	832.296402889	
-0.066579	870.420338739	8	E	4	703.253809793	
-0.0375528	985.447281771	9	D	3	574.211216696	
+0.0805984	1122.506193633	10	H	2	459.184273664	+0.0396643
	1289.504552451	11	S	1	322.125361802	
		12	K	0	155.127002984	

Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F05
Scannumber:	11335
Protein:	BSU28280; leuA
Peptide Score:	154.39
Method:	ITMS; CID; 3



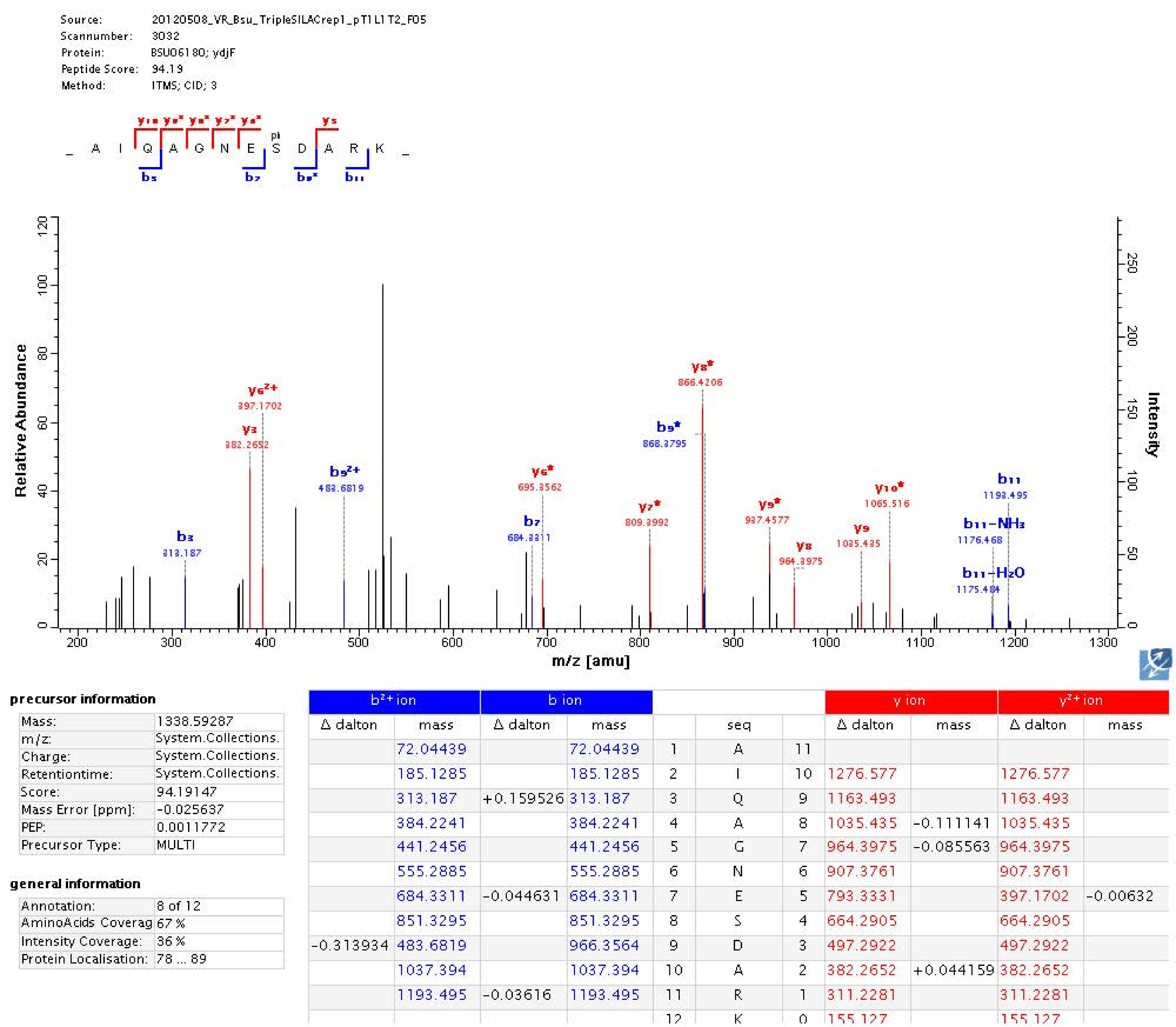
precursor information

Mass:	2061.94043
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	154.3935
Mass Error [ppm]:	-0.20546
PEP:	4.0345E-20
Precursor Type:	MULTI

general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	48 %
Protein Localisation:	338 ... 354

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342195	1	D	16				
	272.13533053	2	R	15	1955.9353828		1955.9353828	
+0.2114527	385.21939451	3	I	14	1799.8342717	-0.0961126	1799.8342717	
+0.0501878	486.26707298	4	T	13	1686.7502078	+0.3024045	1686.7502078	
+0.2407351	557.30418677	5	A	12	1585.7025293	+0.0748145	1585.7025293	
-0.00672	670.38825075	6	I	11	1514.6654155		1514.6654155	
	727.40971447	7	G	10	1401.5813515	+0.0712364	701.29431399	+0.2009863
+0.1419888	874.47812839	8	F	9	1344.5598878		1344.5598878	
	1002.5367059	9	Q	8	1197.4914739		1197.4914739	
+0.1263255	1149.6051198	10	F	7	1069.4328964	+0.2450821	1069.4328964	
+0.0957204	1264.6320628	11	D	6	922.36448245		922.36448245	
	1431.6304217	12	S	5	807.33753942	-0.0254056	807.33753942	
	1560.6730148	13	E	4	640.3391806		640.3391806	
+0.1155689	1689.7156079	14	E	3	511.29658751	+0.1740241	511.29658751	
+0.003917	1802.7996718	15	I	2	382.25399441		382.25399441	
	1916.8425993	16	N	1	269.16993043		269.16993043	
		17	K	0	155.12700298		155.12700298	



Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F05
Scannumber: 3032
Protein: BSU06180; ydjF
Peptide Score: 94.19
Method: ITMS; CID; 3

precursor information

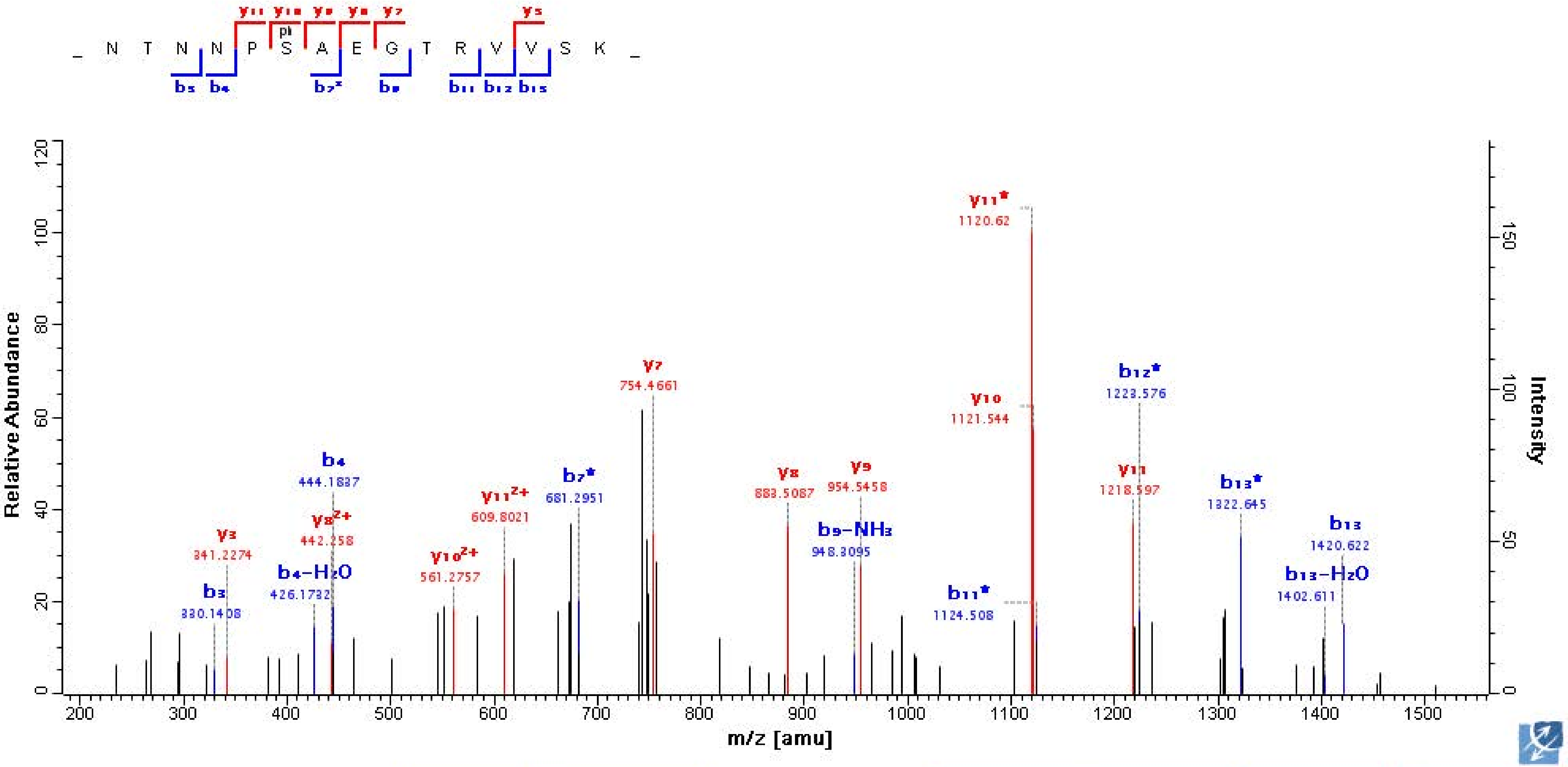
Mass:	1338.59287
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	94.19147
Mass Error [ppm]:	-0.025637
PEP:	0.0011772
Precursor Type:	MULTI

general information

Annotation:	8 of 12
AminoAcids Coverag	67 %
Intensity Coverage:	36 %
Protein Localisation:	78 ... 89

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439		72.04439	1	A	11				
	185.1285		185.1285	2	I	10	1276.577		1276.577	
	313.187	+0.159526	313.187	3	Q	9	1163.493		1163.493	
	384.2241		384.2241	4	A	8	1035.435	-0.111141	1035.435	
	441.2456		441.2456	5	G	7	964.3975	-0.085563	964.3975	
	555.2885		555.2885	6	N	6	907.3761		907.3761	
	684.3311	-0.044631	684.3311	7	E	5	793.3331		397.1702	-0.00632
	851.3295		851.3295	8	S	4	664.2905		664.2905	
-0.313934	483.6819		966.3564	9	D	3	497.2922		497.2922	
	1037.394		1037.394	10	A	2	382.2652	+0.044159	382.2652	
	1193.495	-0.03616	1193.495	11	R	1	311.2281		311.2281	
				12	K	0	155.127		155.127	

Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F05
Scannumber:	4381
Protein:	BSU03790; yclM
Peptide Score:	87.65
Method:	ITMS; CID; 3



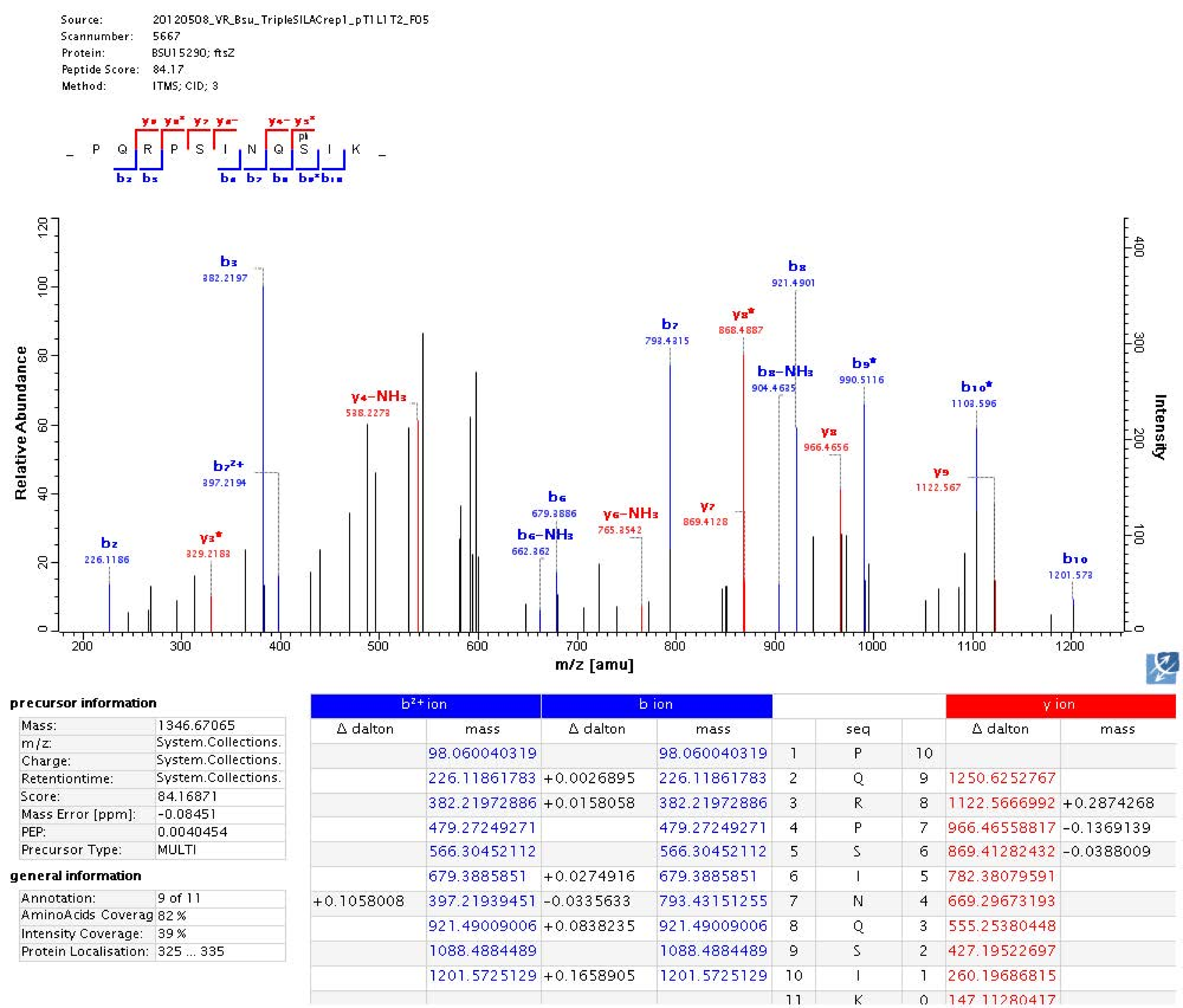
precursor information

Mass:	1652.75127
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	87.64727
Mass Error [ppm]:	-0.39541
PEP:	0.010602
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	41 %
Protein Localisation:	276 ... 290

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.05020391	1	N	14				
	216.09788239	2	T	13	1547.7304754		1547.7304754	
+0.1413862	330.14080984	3	N	12	1446.6827969		1446.6827969	
-0.1598115	444.18373728	4	N	11	1332.6398695		1332.6398695	
	541.23650113	5	P	10	1218.596942	+0.0209779	609.80210924	+0.1884303
	708.23485995	6	S	9	1121.5441782	+0.0234488	561.27572731	-0.4734202
	779.27197374	7	A	8	954.54581934	+0.1888608	954.54581934	
	908.31456684	8	E	7	883.50870555	+0.1773906	442.25799101	-0.0052444
	965.33603056	9	G	6	754.46611245	+0.0778939	754.46611245	
	1066.383709	10	T	5	697.44464873		697.44464873	
	1222.4848201	11	R	4	596.39697025		596.39697025	
	1321.553234	12	V	3	440.29585923		440.29585923	
+0.2041578	1420.6216479	13	V	2	341.22744531	+0.1170676	341.22744531	
	1507.6536763	14	S	1	242.15903139		242.15903139	
		15	K	0	155.12700298		155.12700298	



Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F05
Scannumber:	5667
Protein:	BSU15290; ftsZ
Peptide Score:	84.17
Method:	ITMS; CID; 3

precursor information

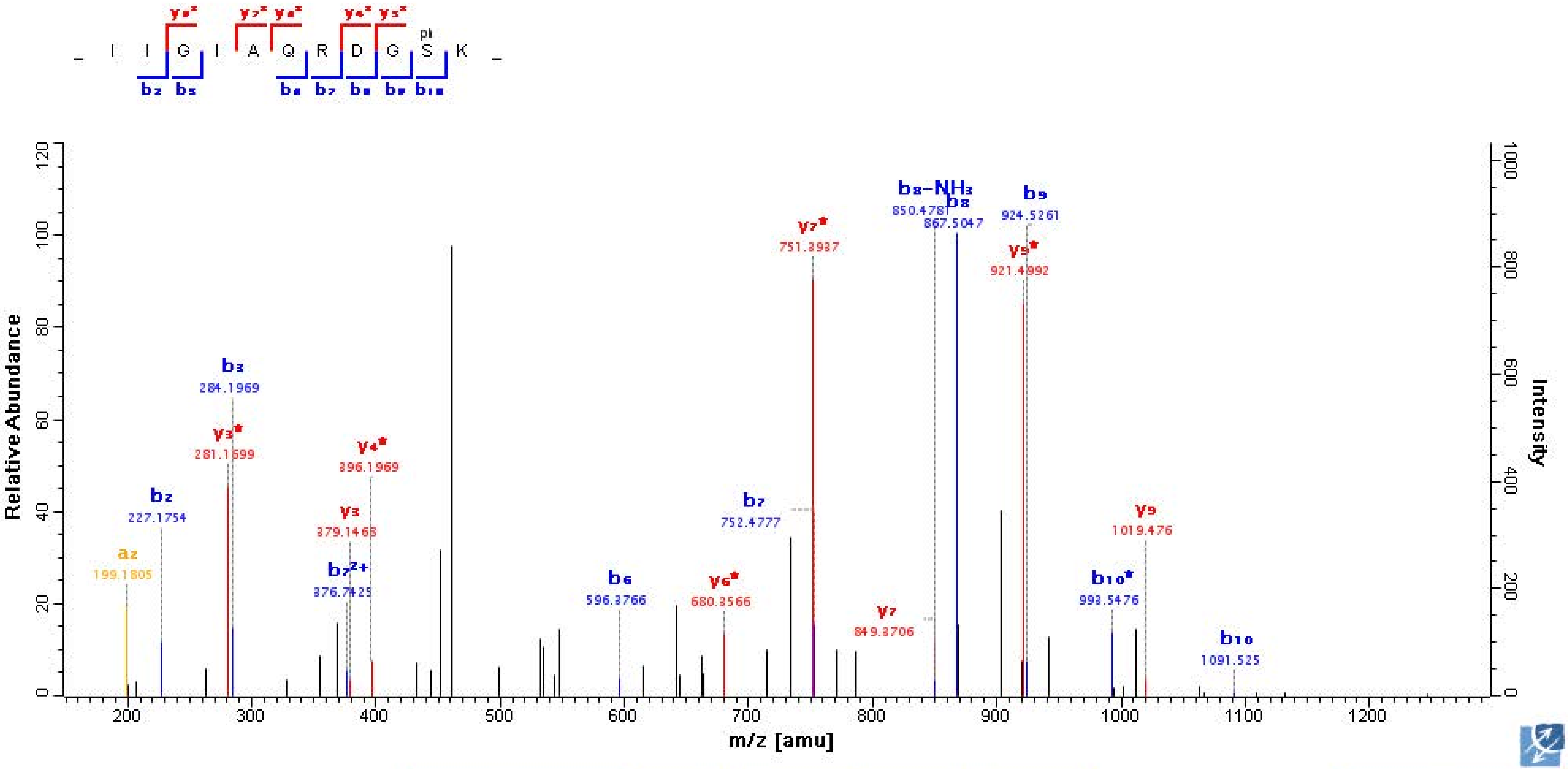
Mass:	1346.67065
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	84.16871
Mass Error [ppm]:	-0.08451
PEP:	0.0040454
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	39 %
Protein Localisation:	325 ... 335

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	98.060040319		98.060040319	1	P	10		
	226.11861783	+0.0026895	226.11861783	2	Q	9	1250.6252767	
	382.21972886	+0.0158058	382.21972886	3	R	8	1122.5666992	+0.2874268
	479.27249271		479.27249271	4	P	7	966.46558817	-0.1369139
	566.30452112		566.30452112	5	S	6	869.41282432	-0.0388009
	679.3885851	+0.0274916	679.3885851	6	I	5	782.38079591	
+0.1058008	397.21939451	-0.0335633	793.43151255	7	N	4	669.29673193	
	921.49009006	+0.0838235	921.49009006	8	Q	3	555.25380448	
	1088.4884489		1088.4884489	9	S	2	427.19522697	
	1201.5725129	+0.1658905	1201.5725129	10	I	1	260.19686815	
				11	K	0	147.11280417	

Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F05
Scannumber:	6218
Protein:	BSU32260; hom; tdm
Peptide Score:	117.09
Method:	ITMS; CID; 3



precursor information

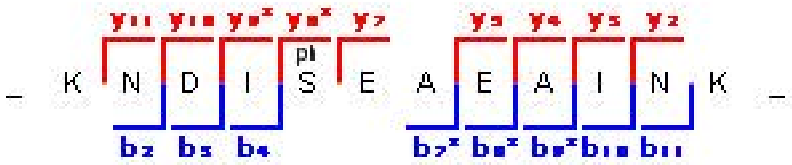
Mass:	1236.62298
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	117.0911
Mass Error [ppm]:	0.18369
PEP:	9.2207E-06
Precursor Type:	MULTI

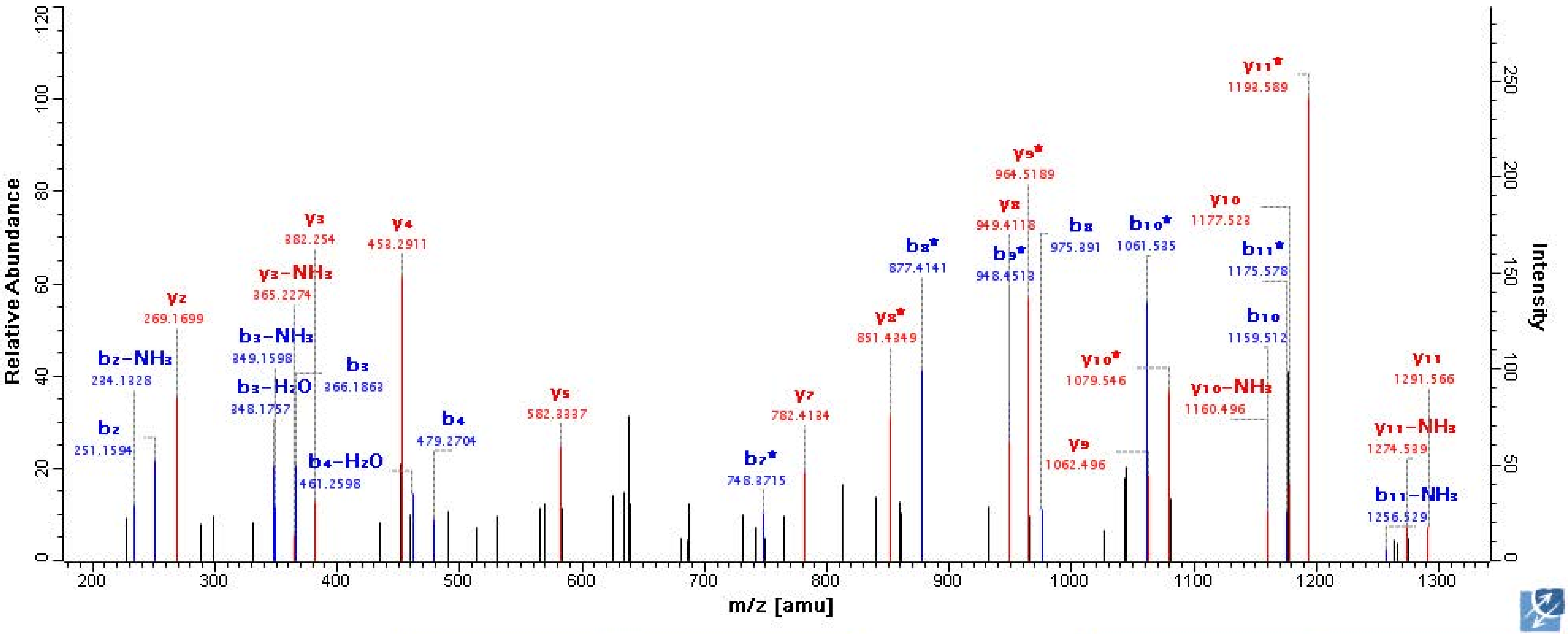
general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	51 %
Protein Localisation:	248 ... 258

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	86.09643		114.0913		114.0913	1	I	10		
+0.024832	199.1805		227.1754	-0.043858	227.1754	2	I	9	1132.56	
	256.202		284.1969	+0.036774	284.1969	3	G	8	1019.476	-0.175378
	369.286		397.2809		397.2809	4	I	7	962.4546	
	440.3231		468.318		468.318	5	A	6	849.3706	+0.069615
	568.3817		596.3766	-0.094458	596.3766	6	Q	5	778.3335	
	724.4828	-0.479383	376.7425	-0.031995	752.4777	7	R	4	650.2749	
	839.5098		867.5047	-0.004677	867.5047	8	D	3	494.1738	
	896.5312		924.5261	-0.108478	924.5261	9	G	2	379.1468	+0.050623
	1063.53		1091.525	+0.028234	1091.525	10	S	1	322.1254	
						11	K	0	155.127	

Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F05
Scannumber:	6522
Protein:	BSU08790; thiA; thiC
Peptide Score:	195.77
Method:	ITMS; CID; 3





precursor information

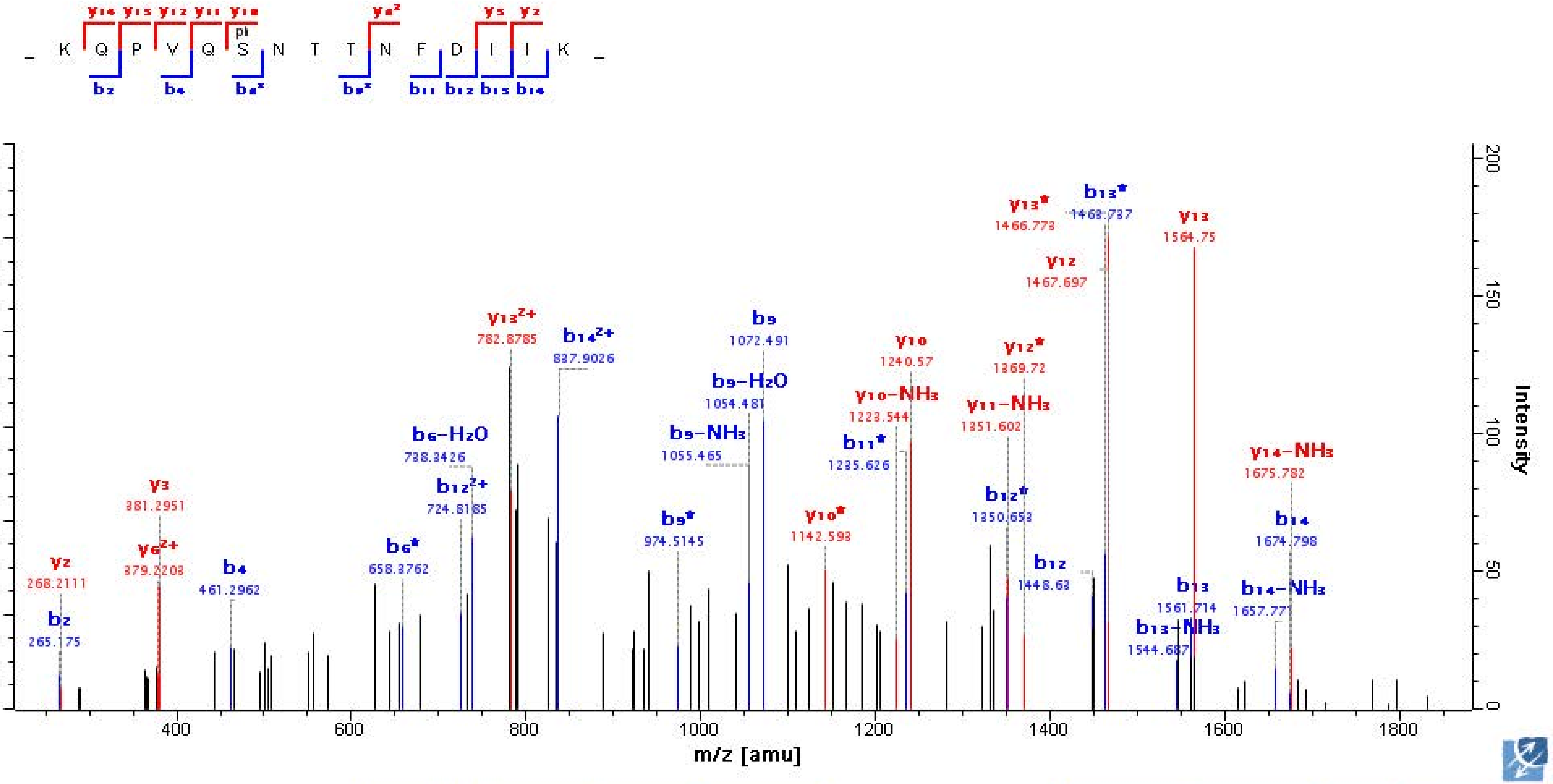
Mass:	1410.6391
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	195.7693
Mass Error [ppm]:	-0.063348
PEP:	5.4241E-45
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	63 %
Protein Localisation:	561 ... 572

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	137.116438298	1	K	11		
+0.1549043	251.159365745	2	N	10	1291.565701457	-0.2787142
+0.0862742	366.186308777	3	D	9	1177.52277401	+0.0704877
-0.0165275	479.270372757	4	I	8	1062.495830978	-0.0060849
	646.268731575	5	S	7	949.411766998	+0.06211
	775.311324672	6	E	6	782.413408179	+0.0947095
	846.348438459	7	A	5	653.370815083	
+0.1543786	975.391031556	8	E	4	582.333701295	+0.0395897
	1046.428145343	9	A	3	453.291108199	-0.108491
+0.1676002	1159.512209324	10	I	2	382.253994411	+0.0441013
	1273.555136771	11	N	1	269.169930431	-0.0011987
		12	K	0	155.127002984	

Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F05
Scannumber: 8665
Protein: P0CI74
Peptide Score: 149.3
Method: ITMS; CID; 3



precursor information

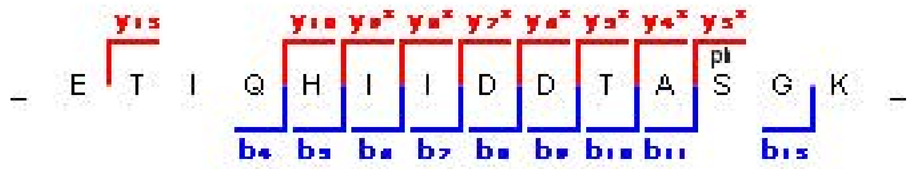
Mass:	1811.88232
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	149.2983
Mass Error [ppm]:	0.23989
PEP:	2.5907E-12
Precursor Type:	MULTI

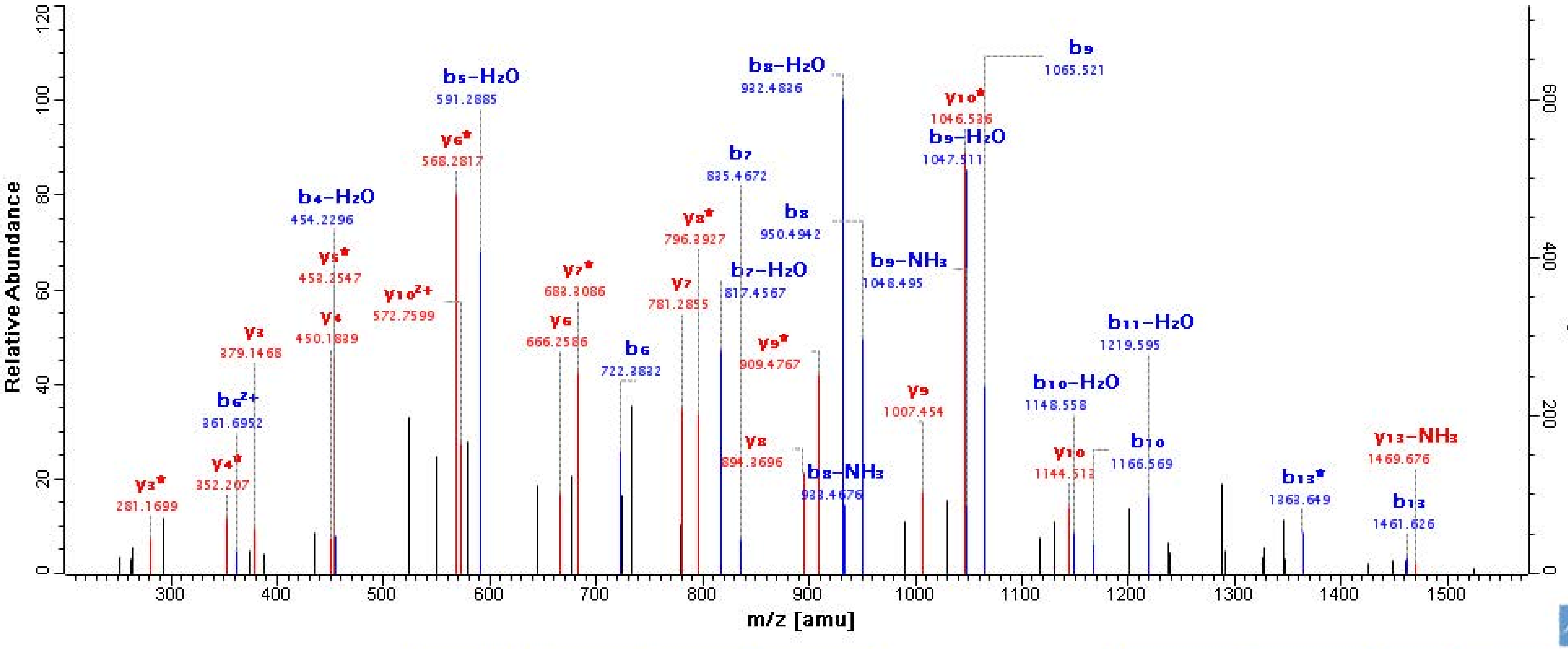
general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	45 %
Protein Localisation:	68 ... 82

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	137.1164		137.1164	1	K	14				
	265.175	+0.241397	265.175	2	Q	13	1692.808		1692.808	
	362.2278		362.2278	3	P	12	1564.75	+0.004214	782.8785	-0.294805
	461.2962	-0.076406	461.2962	4	V	11	1467.697	+0.153536	1467.697	
	589.3548		589.3548	5	Q	10	1368.629		1368.629	
	756.3531		756.3531	6	S	9	1240.57	-0.101919	1240.57	
	870.3961		870.3961	7	N	8	1073.572		1073.572	
	971.4437		971.4437	8	T	7	959.5288		959.5288	
	1072.491	+0.071208	1072.491	9	T	6	858.4811		858.4811	
	1186.534		1186.534	10	N	5	757.4334		379.2203	-0.178689
	1333.603		1333.603	11	F	4	643.3905		643.3905	
+0.038751	724.8185	-0.216124	1448.63	12	D	3	496.3221		496.3221	
	1561.714	+0.023054	1561.714	13	I	2	381.2951	+0.012975	381.2951	
-0.442163	837.9026	+0.311182	1674.798	14	I	1	268.2111	+0.044487	268.2111	
				15	K	0	155.127		155.127	

Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F05
Scannumber:	9421
Protein:	BSU32750; metN; yusC
Peptide Score:	171.26
Method:	ITMS; CID; 3





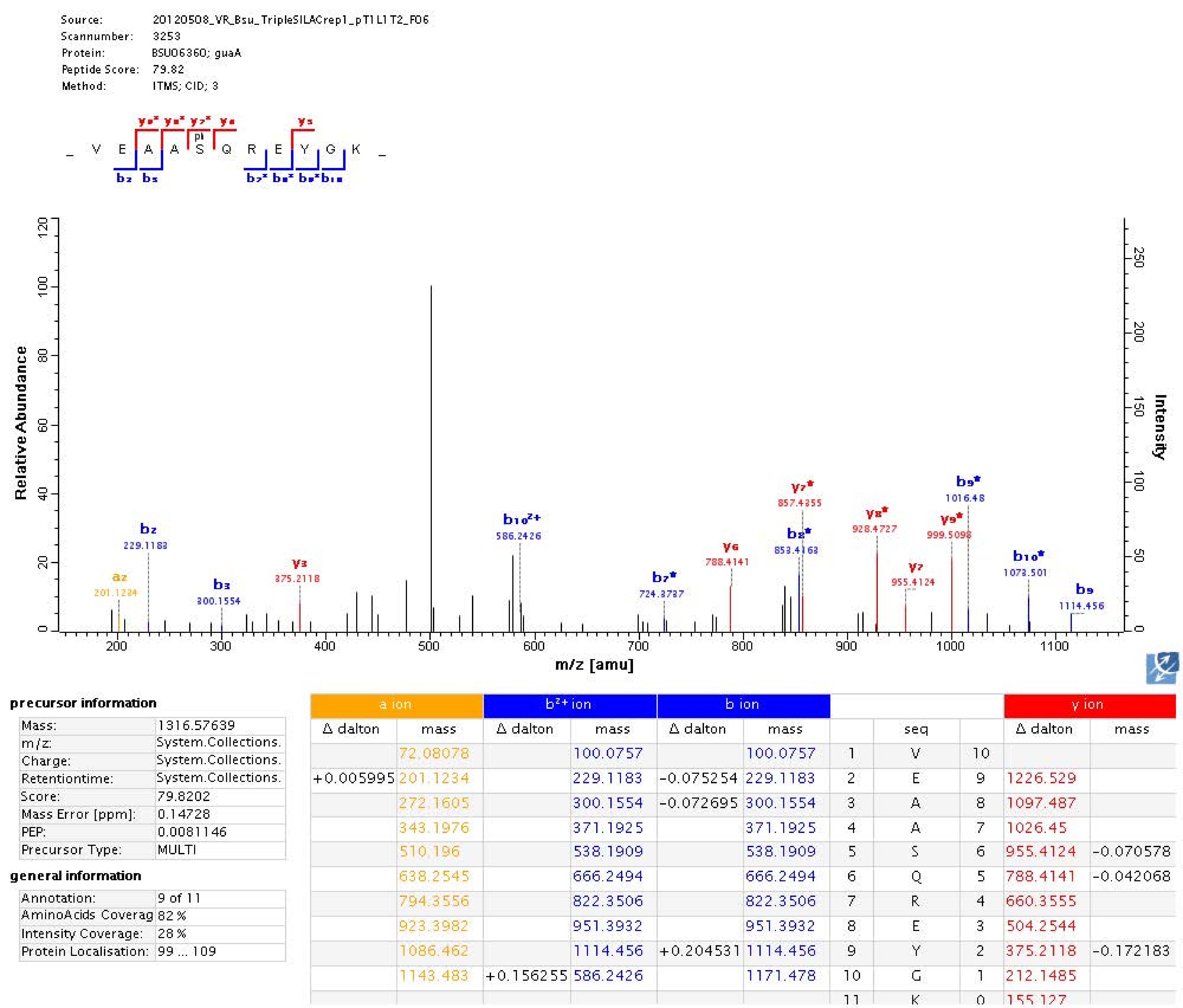
precursor information

Mass:	1606.72448
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	171.2553
Mass Error [ppm]:	0.30599
PEP:	6.7575E-25
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	69 %
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
	130.0499		130.0499	1	E	13				
	231.0975		231.0975	2	T	12	1486.703		1486.703	
	344.1816		344.1816	3	I	11	1385.655		1385.655	
	472.2402		472.2402	4	Q	10	1272.571		1272.571	
	609.2991		609.2991	5	H	9	1144.513	-0.185639	572.7599	+0.377602
-0.323761	361.6952	+0.012403	722.3832	6	I	8	1007.454	+0.085187	1007.454	
	835.4672	+0.146479	835.4672	7	I	7	894.3696	+0.120911	894.3696	
	950.4942	+0.053191	950.4942	8	D	6	781.2855	-0.051617	781.2855	
	1065.521	-0.012082	1065.521	9	D	5	666.2586	+0.140304	666.2586	
	1166.569	+0.063042	1166.569	10	T	4	551.2316		551.2316	
	1237.606		1237.606	11	A	3	450.1839	+0.212179	450.1839	
	1404.604		1404.604	12	S	2	379.1468	+0.011744	379.1468	
	1461.626	+0.320437	1461.626	13	G	1	212.1485		212.1485	
				14	K	0	155.127		155.127	



Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F06
Scannumber:	3253
Protein:	BSU06360; guaA
Peptide Score:	79.82
Method:	ITMS; CID; 3

precursor information

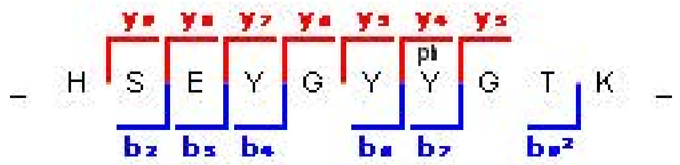
Mass:	1316.57639
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	79.8202
Mass Error [ppm]:	0.14728
PEP:	0.0081146
Precursor Type:	MULTI

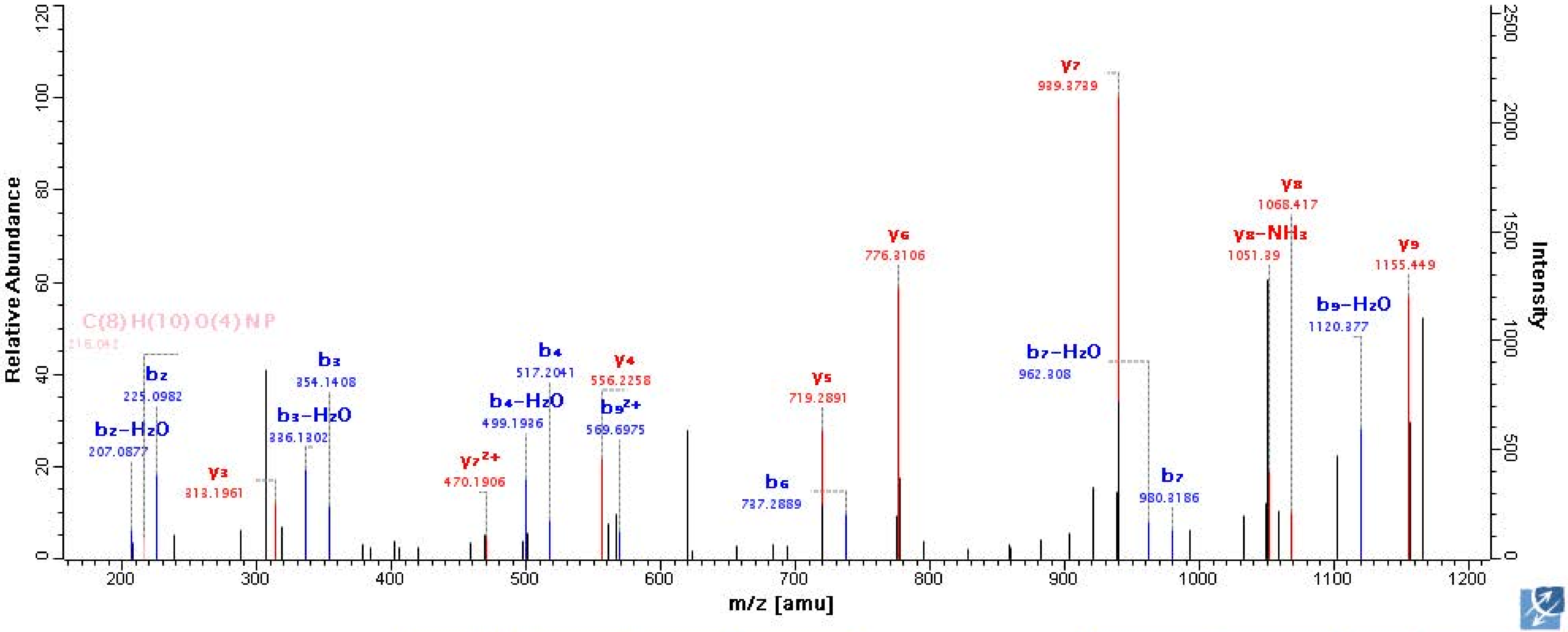
general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	28 %
Protein Localisation:	99 ... 109

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	72.08078		100.0757		100.0757	1	V	10		
+0.005995	201.1234		229.1183	-0.075254	229.1183	2	E	9	1226.529	
	272.1605		300.1554	-0.072695	300.1554	3	A	8	1097.487	
	343.1976		371.1925		371.1925	4	A	7	1026.45	
	510.196		538.1909		538.1909	5	S	6	955.4124	-0.070578
	638.2545		666.2494		666.2494	6	Q	5	788.4141	-0.042068
	794.3556		822.3506		822.3506	7	R	4	660.3555	
	923.3982		951.3932		951.3932	8	E	3	504.2544	
	1086.462		1114.456	+0.204531	1114.456	9	Y	2	375.2118	-0.172183
	1143.483	+0.156255	586.2426		1171.478	10	G	1	212.1485	
						11	K	0	155.127	

Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F07
Scannumber: 4519
Protein: BSU36250; ywqD
Peptide Score: 143.03
Method: ITMS; CID; 3





precursor information

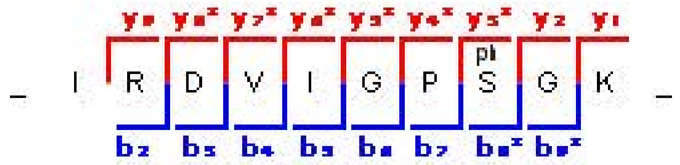
Mass:	1283.48596
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	143.0338
Mass Error [ppm]:	-0.013992
PEP:	1.1605E-08
Precursor Type:	MULTI

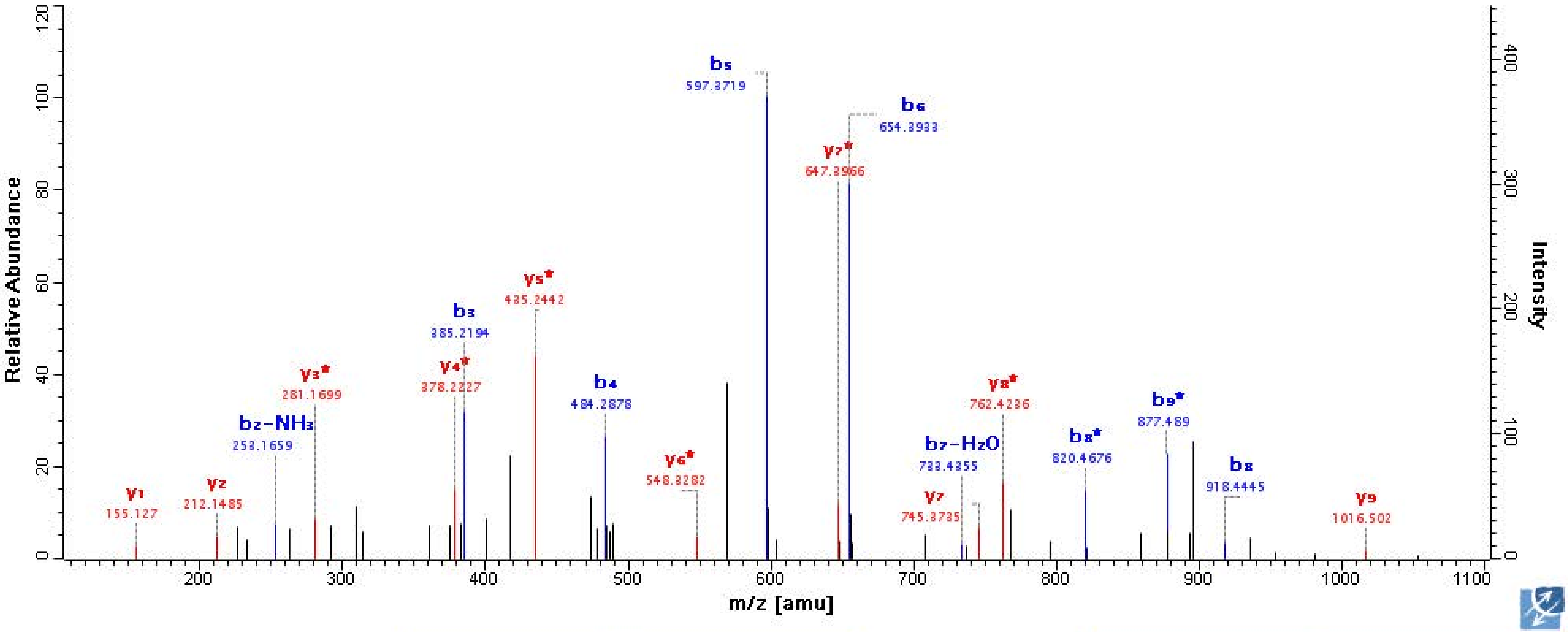
general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	48 %
Protein Localisation:	222 ... 231

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.0662		138.0662	1	H	9				
	225.0982	+0.059712	225.0982	2	S	8	1155.449	+0.057679	1155.449	
	354.1408	-0.021608	354.1408	3	E	7	1068.417	-0.077651	1068.417	
	517.2041	+0.135095	517.2041	4	Y	6	939.3739	+0.010169	470.1906	-0.025806
	574.2256		574.2256	5	G	5	776.3106	+0.146313	776.3106	
	737.2889	+0.014414	737.2889	6	Y	4	719.2891	+0.11669	719.2891	
	980.3186	-0.02263	980.3186	7	Y	3	556.2258	+0.118495	556.2258	
	1037.34		1037.34	8	G	2	313.1961	+0.027152	313.1961	
-0.136652	569.6975		1138.388	9	T	1	256.1747		256.1747	
				10	K	0	155.127		155.127	

Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F07
Scannumber:	5120
Protein:	BSU16690; comR; pnp; pnpA
Peptide Score:	110.66
Method:	ITMS; CID; 3





precursor information

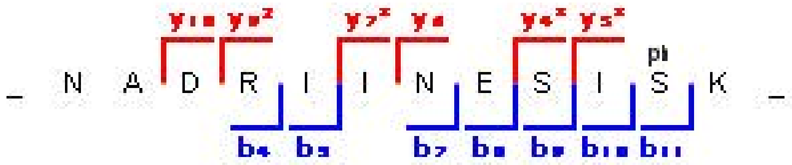
Mass:	1120.56456
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	110.6616
Mass Error [ppm]:	0.34429
PEP:	0.00078702
Precursor Type:	MULTI

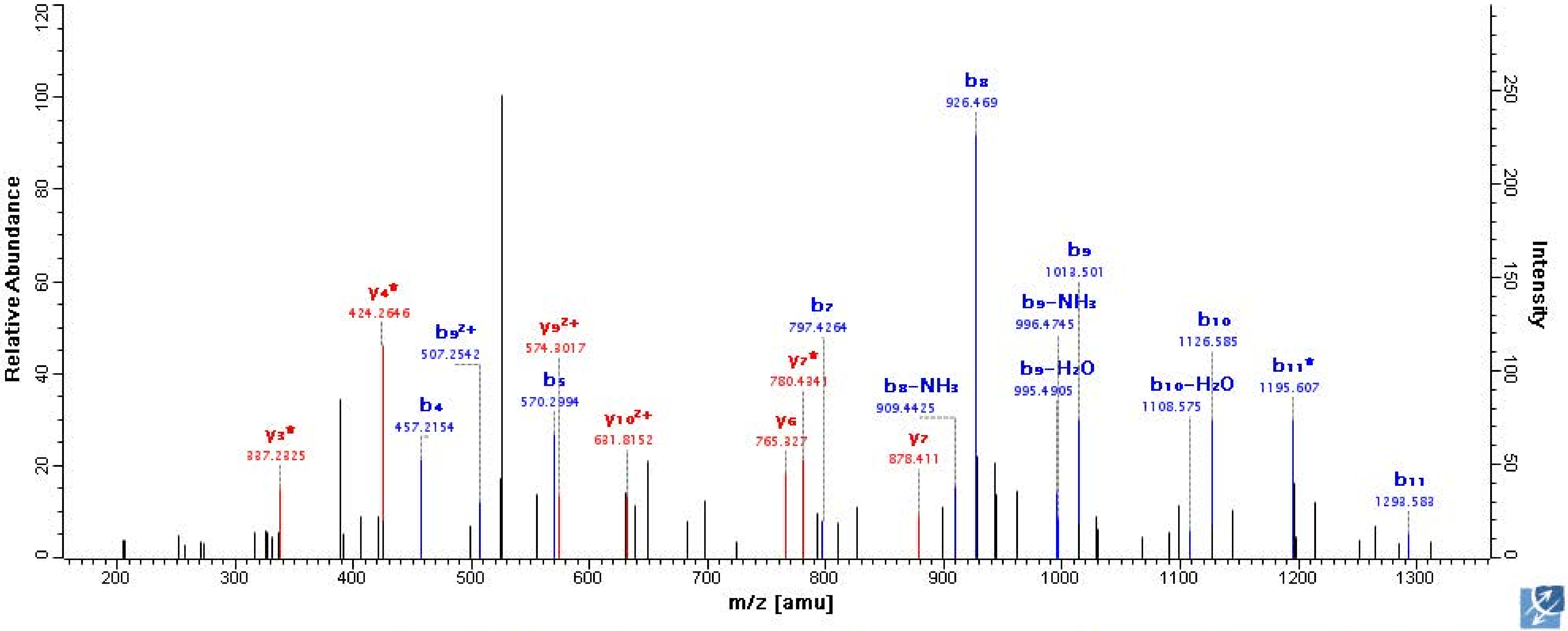
general information

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	59 %
Protein Localisation:	566 ... 575

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	114.091340447	1	I	9		
	270.192451475	2	R	8	1016.501585058	-0.1719952
+0.0629541	385.219394507	3	D	7	860.40047403	
-0.3315096	484.287808423	4	V	6	745.373530998	-0.0018269
-0.0303197	597.371872404	5	I	5	646.305117082	
+0.047826	654.393336127	6	G	4	533.221053101	
	751.446099979	7	P	3	476.199589378	
-0.1326302	918.444458798	8	S	2	379.146825526	
	975.465922521	9	G	1	212.148466707	-0.0124651
		10	K	0	155.127002984	+0.1198842

Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F07
Scannumber: 6182
Protein: BSU15420; divIVA; ylmJ
Peptide Score: 110.92
Method: ITMS; CID; 3





precursor information

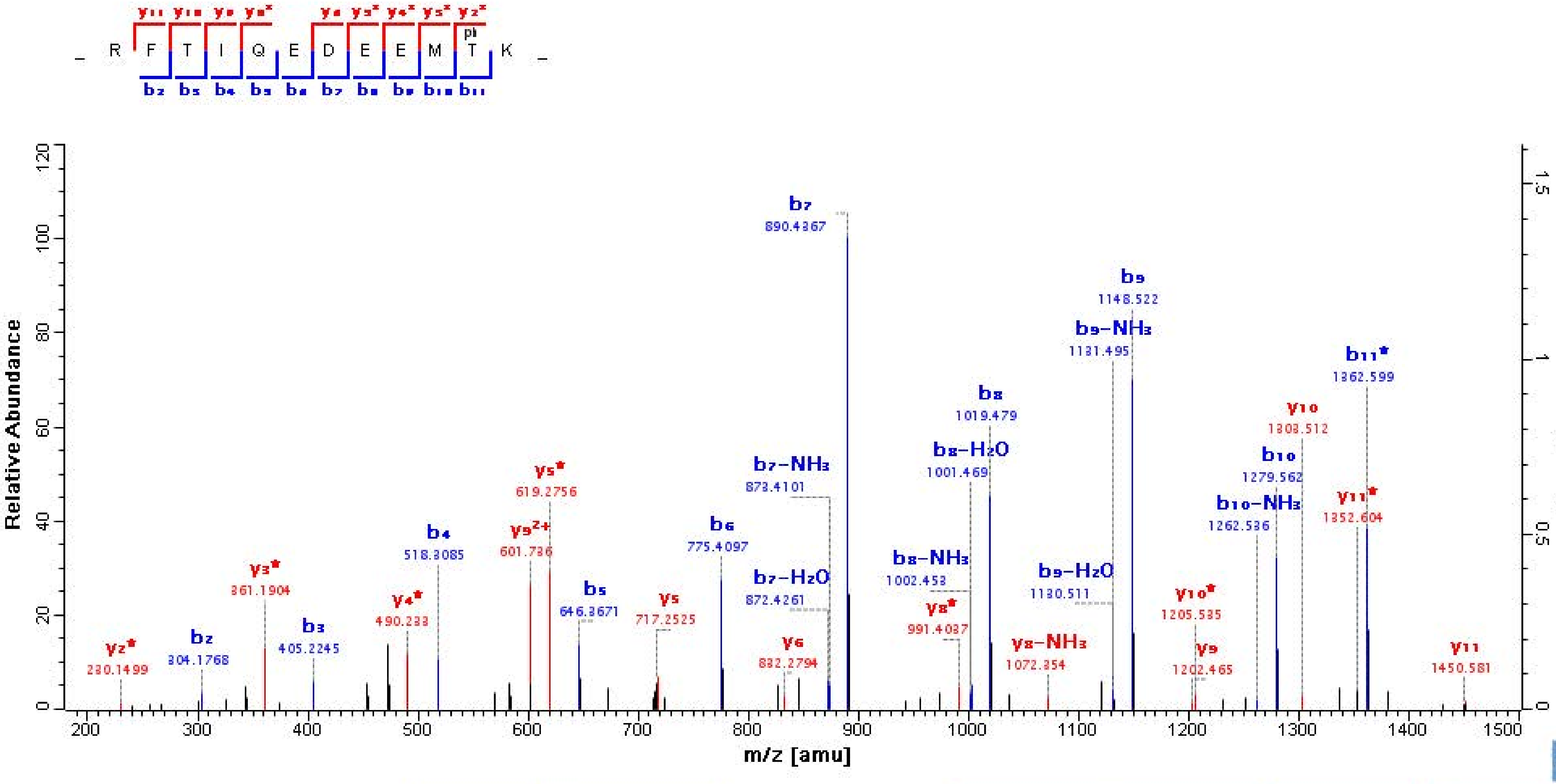
Mass:	1438.68238
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	110.9227
Mass Error [ppm]:	0.45153
PEP:	3.2744E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	44 %
Protein Localisation:	99 ... 110

b2+ ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502		115.0502	1	N	11				
	186.0873		186.0873	2	A	10	1333.66		1333.66	
	301.1143		301.1143	3	D	9	1262.623		631.8152	+0.256317
	457.2154	-0.17991	457.2154	4	R	8	1147.596		574.3017	+0.058912
	570.2994	+0.161075	570.2994	5	I	7	991.4951		991.4951	
	683.3835		683.3835	6	I	6	878.411	-0.218412	878.411	
	797.4264	-0.472204	797.4264	7	N	5	765.327	+0.109366	765.327	
	926.469	-0.017421	926.469	8	E	4	651.284		651.284	
+0.041126	507.2542	+0.15038	1013.501	9	S	3	522.2415		522.2415	
	1126.585	+0.018525	1126.585	10	I	2	435.2094		435.2094	
	1293.583	+0.029444	1293.583	11	S	1	322.1254		322.1254	
				12	K	0	155.127		155.127	

Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F07
Scannumber: 6444
Protein: BSU15770; prkC; yloP
Peptide Score: 196.5
Method: ITMS; CID; 3



precursor information

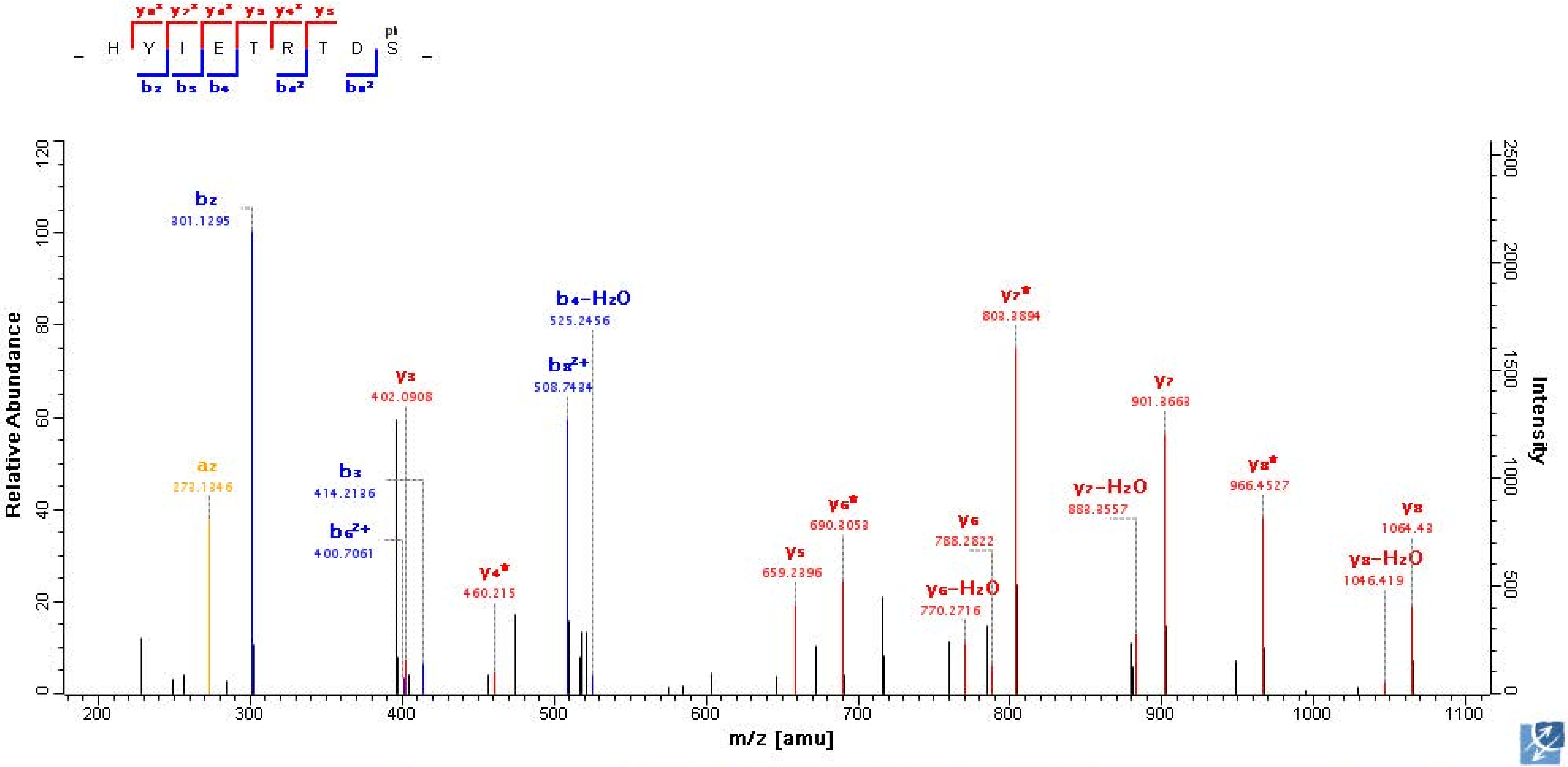
Mass:	0
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	196.4965
Mass Error [ppm]:	0.15906
PEP:	4.3146E-178
Precursor Type:	PEAK

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	68 %
Protein Localisation:	280 ... 291

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	157.10838749	1	R	11				
+0.0208304	304.17680141	2	F	10	1450.5807539	+0.2839922	1450.5807539	
-0.0186693	405.22447988	3	T	9	1303.5123399	+0.1296278	1303.5123399	
+0.1177257	518.30854387	4	I	8	1202.4646615	+0.1040641	601.73596897	-0.426948
+0.0948537	646.36712138	5	Q	7	1089.3805975		1089.3805975	
+0.0622704	775.40971447	6	E	6	961.32201998		961.32201998	
+0.0753664	890.43665751	7	D	5	832.27942688	-0.0933307	832.27942688	
+0.006162	1019.4792506	8	E	4	717.25248385	+0.200458	717.25248385	
+0.1190254	1148.5218437	9	E	3	588.20989076		588.20989076	
+0.1576424	1279.5623283	10	M	2	459.16729766		459.16729766	
	1460.5763372	11	T	1	328.12681305		328.12681305	
		12	K	0	147.11280417		147.11280417	

Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F09
Scannumber:	3720
Protein:	BSU02590; ycbP
Peptide Score:	108.43
Method:	ITMS; CID; 3

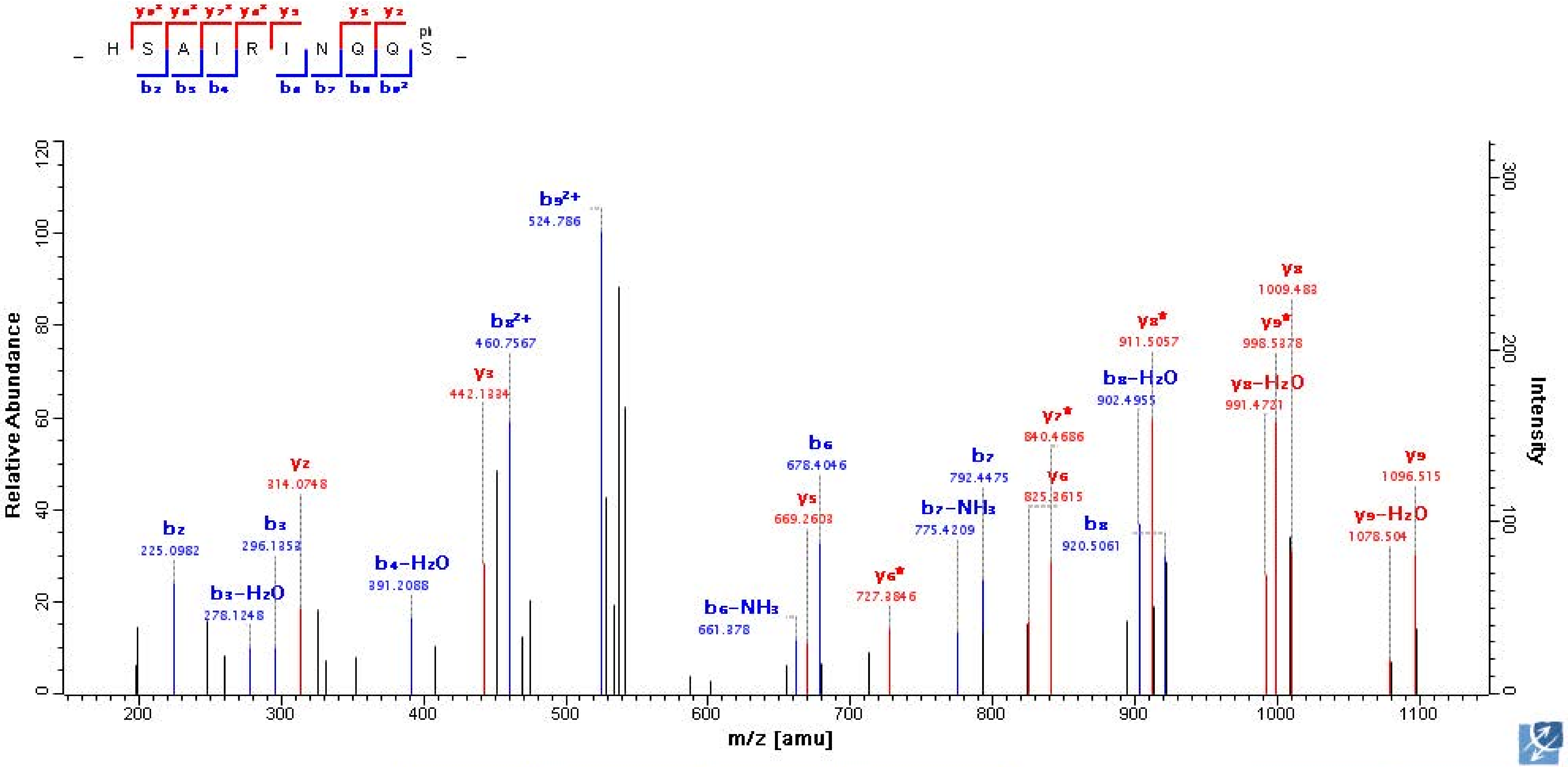


precursor information

Mass:	1200.48108
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	108.433
Mass Error [ppm]:	-0.12927
PEP:	0.0031622
g Precursor Type:	ISO
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	59 %
Protein Localisation:	120 ... 128

a ion		b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	110.0713		138.0662		138.0662	1	H	8		
+0.095134	273.1346		301.1295	-0.034668	301.1295	2	Y	7	1064.43	-0.01114
	386.2187		414.2136	+0.012371	414.2136	3	I	6	901.3663	+0.025822
	515.2613		543.2562		543.2562	4	E	5	788.2822	+0.131187
	616.3089		644.3039		644.3039	5	T	4	659.2396	-0.012255
	772.41	+0.19128	400.7061		800.405	6	R	3	558.1919	
	873.4577		901.4526		901.4526	7	T	2	402.0908	+0.095214
	988.4847	+0.008889	508.7434		1016.48	8	D	1	301.0431	
						9	S	0	186.0162	

Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F09
Scannumber:	4494
Protein:	BSU38020; ipa-52r; pdxK; ywdB
Peptide Score:	162.38
Method:	ITMS; CID; 3



precursor information

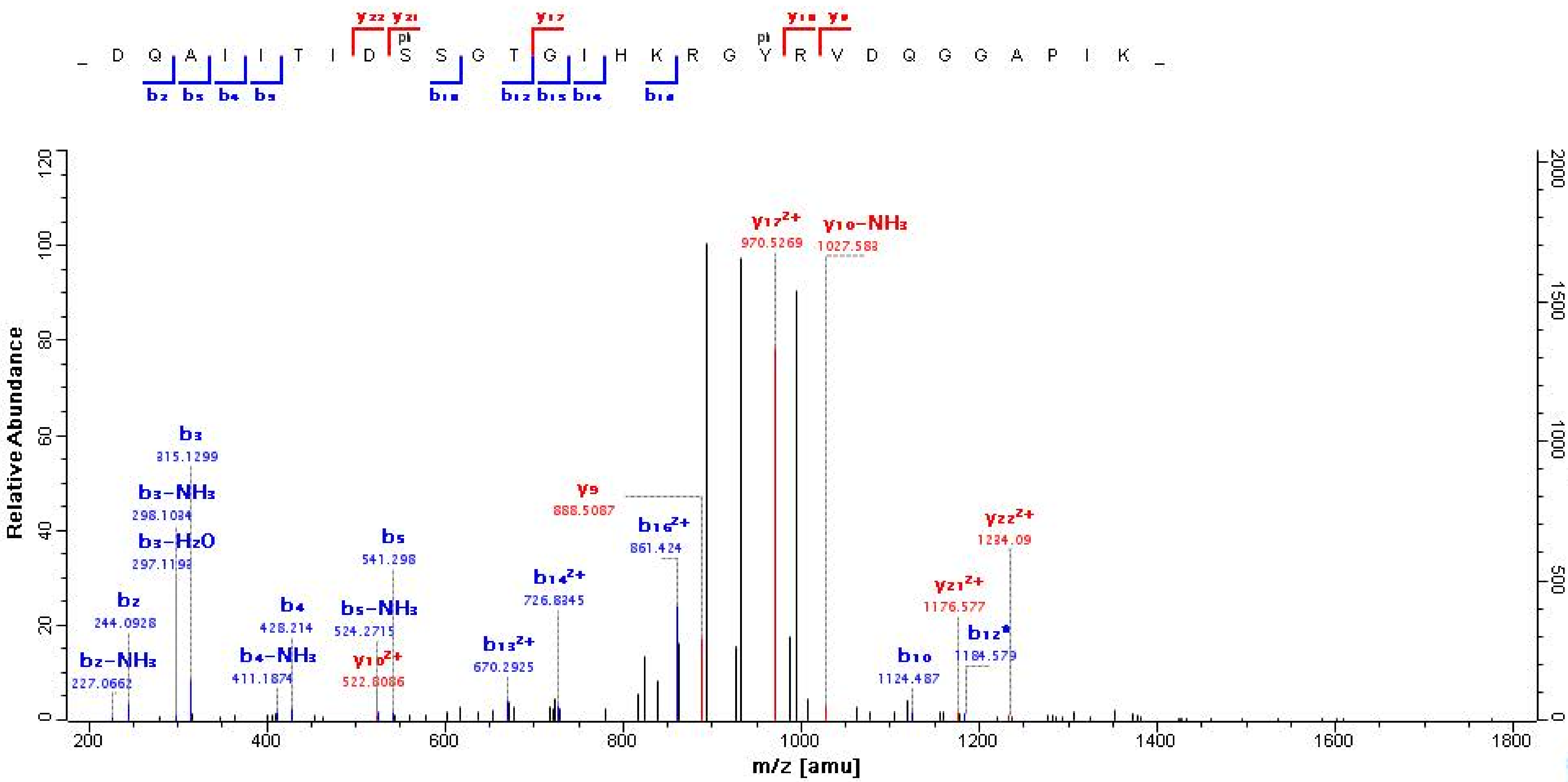
Mass:	1232.56624
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	162.3797
Mass Error [ppm]:	-0.04469
PEP:	7.1815E-26
Precursor Type:	ISO

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	56 %
Protein Localisation:	262 ... 271

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	138.06618833		138.06618833	1	H	9		
	225.09821674	+0.0562938	225.09821674	2	S	8	1096.5146636	-0.0426177
	296.13533053	+0.0359646	296.13533053	3	A	7	1009.4826352	+0.0154727
	409.21939451		409.21939451	4	I	6	938.44552143	
	565.32050554		565.32050554	5	R	5	825.36145745	+0.1500782
	678.40456952	-0.035673	678.40456952	6	I	4	669.26034642	+0.1407156
	792.44749696	+0.130506	792.44749696	7	N	3	556.17628244	
-0.2273176	460.75667547	-0.1344314	920.50607447	8	Q	2	442.13335499	+0.2393257
+0.0284279	524.78596423		1048.564652	9	Q	1	314.07477748	+0.1050321
				10	S	0	186.01619997	

Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F11
Scannumber: 8752
Protein: BSU22170; ypsC
Peptide Score: 64.68
Method: ITMS; CID; 3



precursor information

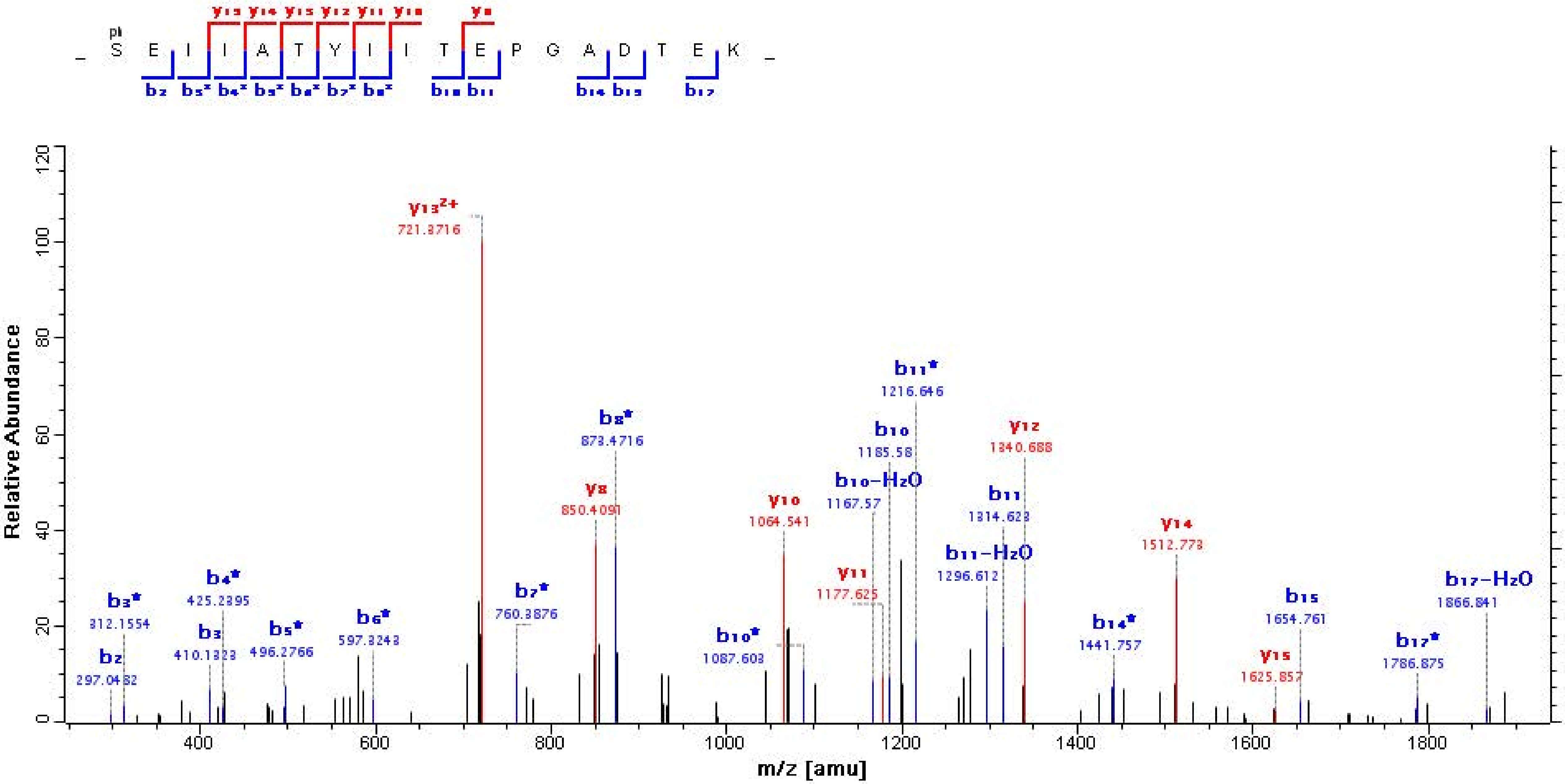
Mass:	3220.58821
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	64.67958
Mass Error [ppm]:	-0.019907
PEP:	0.0025987
Precursor Type:	ISO

general information

Annotation:	13 of 29
AminoAcids Coverag	45 %
Intensity Coverage:	25 %
Protein Localisation:	148 ... 176

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342		116.0342	1	D	28				
	244.0928	+0.055564	244.0928	2	Q	27	3106.569		3106.569	
	315.1299	+0.017153	315.1299	3	A	26	2978.51		2978.51	
	428.214	+0.141494	428.214	4	I	25	2907.473		2907.473	
	541.298	+0.008968	541.298	5	I	24	2794.389		2794.389	
	642.3457		642.3457	6	T	23	2681.305		2681.305	
	755.4298		755.4298	7	I	22	2580.257		2580.257	
	870.4567		870.4567	8	D	21	2467.173		1234.09	-0.221018
	1037.455		1037.455	9	S	20	2352.146		1176.577	+0.128757
	1124.487	-0.190603	1124.487	10	S	19	2185.148		2185.148	
	1181.509		1181.509	11	G	18	2098.116		2098.116	
	1282.556		1282.556	12	T	17	2041.094		2041.094	
+0.133895	670.2925		1339.578	13	G	16	1940.047		970.5269	-0.239325
+0.449162	726.8345		1452.662	14	I	15	1883.025		1883.025	
	1589.721		1589.721	15	H	14	1769.941		1769.941	
-0.286691	861.424		1721.841	16	K	13	1632.882		1632.882	
	1877.942		1877.942	17	R	12	1500.762		1500.762	
	1934.963		1934.963	18	G	11	1344.661		1344.661	
	2177.993		2177.993	19	Y	10	1287.639		1287.639	
	2334.094		2334.094	20	R	9	1044.61		522.8086	+0.440228
	2433.163		2433.163	21	V	8	888.5087	+0.216444	888.5087	
	2548.189		2548.189	22	D	7	789.4403		789.4403	
	2676.248		2676.248	23	Q	6	674.4134		674.4134	
	2733.27		2733.27	24	G	5	546.3548		546.3548	
	2790.291		2790.291	25	G	4	489.3333		489.3333	
	2861.328		2861.328	26	A	3	432.3119		432.3119	
	2958.381		2958.381	27	P	2	361.2747		361.2747	
	3071.465		3071.465	28	I	1	264.222		264.222	
				29	K	0	151.1379		151.1379	

Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F19
Scannumber:	13573
Protein:	BSU13590; mtnW; ykrW
Peptide Score:	103.88
Method:	ITMS; CID; 3



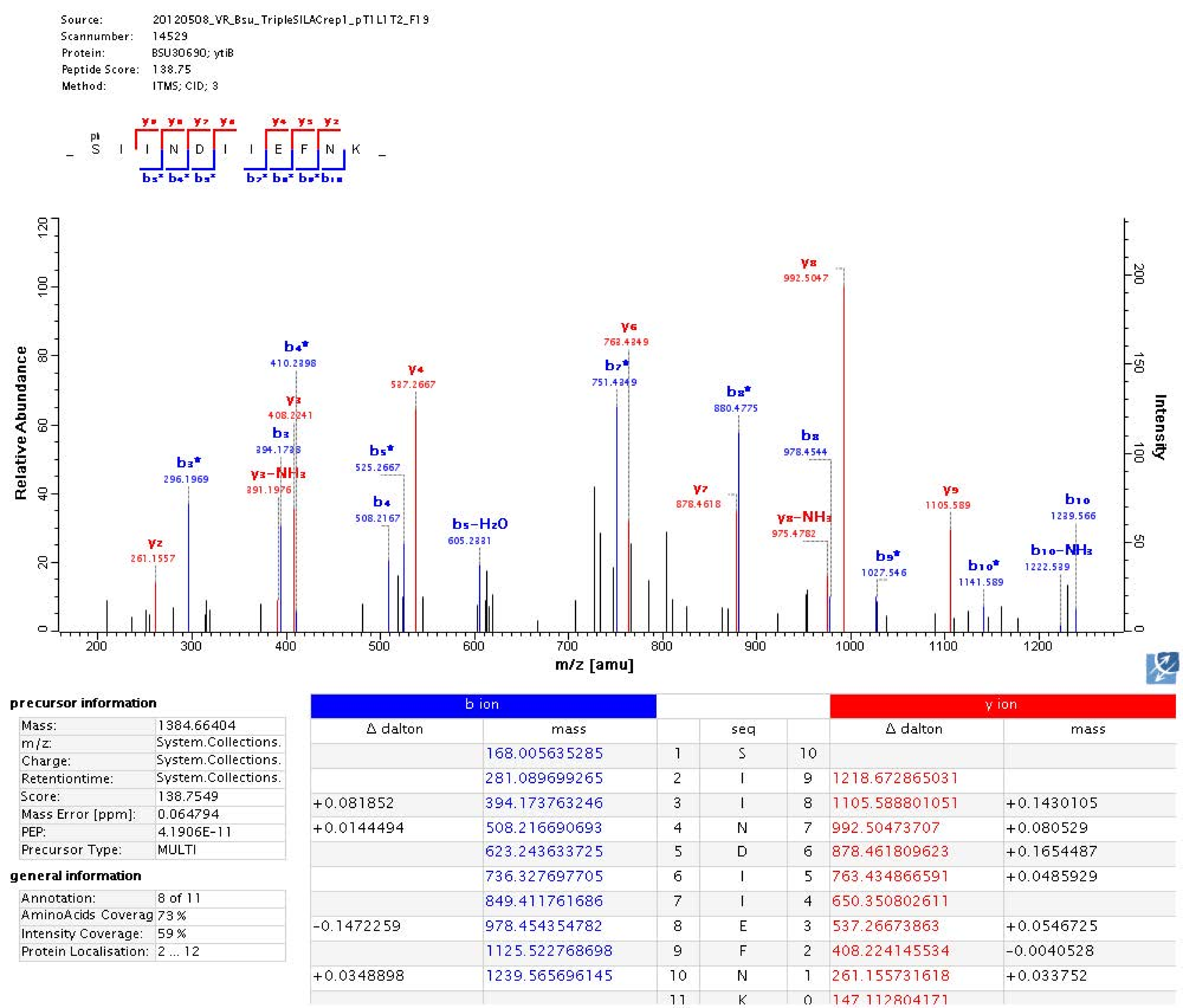
precursor information

Mass:	2029.9503
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	103.8806
Mass Error [ppm]:	0.30181
PEP:	3.1909E-05
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	43 %
Protein Localisation:	2 ... 19

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.00563528	1	S	17				
+0.0208939	297.04822838	2	E	16	1867.9837085		1867.9837085	
+0.1334852	410.13229236	3	I	15	1738.9411154		1738.9411154	
	523.21635634	4	I	14	1625.8570514	-0.0305133	1625.8570514	
	594.25347013	5	A	13	1512.7729875	+0.0105819	1512.7729875	
	695.3011486	6	T	12	1441.7358737		721.37157507	+0.1157296
	858.36447714	7	Y	11	1340.6881952	-0.0015497	1340.6881952	
	971.44854112	8	I	10	1177.6248667	+0.0874136	1177.6248667	
	1084.5326051	9	I	9	1064.5408027	+0.1731866	1064.5408027	
+0.0918356	1185.5802836	10	T	8	951.45673869		951.45673869	
-0.0454841	1314.6228767	11	E	7	850.40906022	+0.1091283	850.40906022	
	1411.6756405	12	P	6	721.36646712		721.36646712	
	1468.6971042	13	G	5	624.31370327		624.31370327	
	1539.734218	14	A	4	567.29223954		567.29223954	
+0.0639122	1654.7611611	15	D	3	496.25512576		496.25512576	
	1755.8088395	16	T	2	381.22818272		381.22818272	
	1884.8514326	17	E	1	280.18050425		280.18050425	
		18	K	0	151.13791115		151.13791115	



Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F19
Scannumber: 14529
Protein: BSU30690; ytiB
Peptide Score: 138.75
Method: ITMS; CID; 3

precursor information

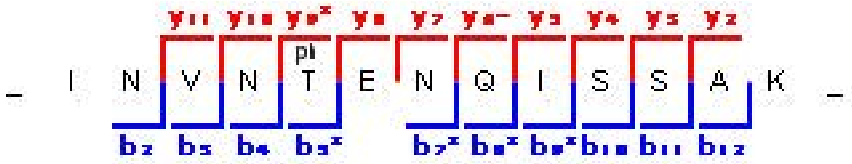
Mass:	1384.66404
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	138.7549
Mass Error [ppm]:	0.064794
PEP:	4.1906E-11
Precursor Type:	MULTI

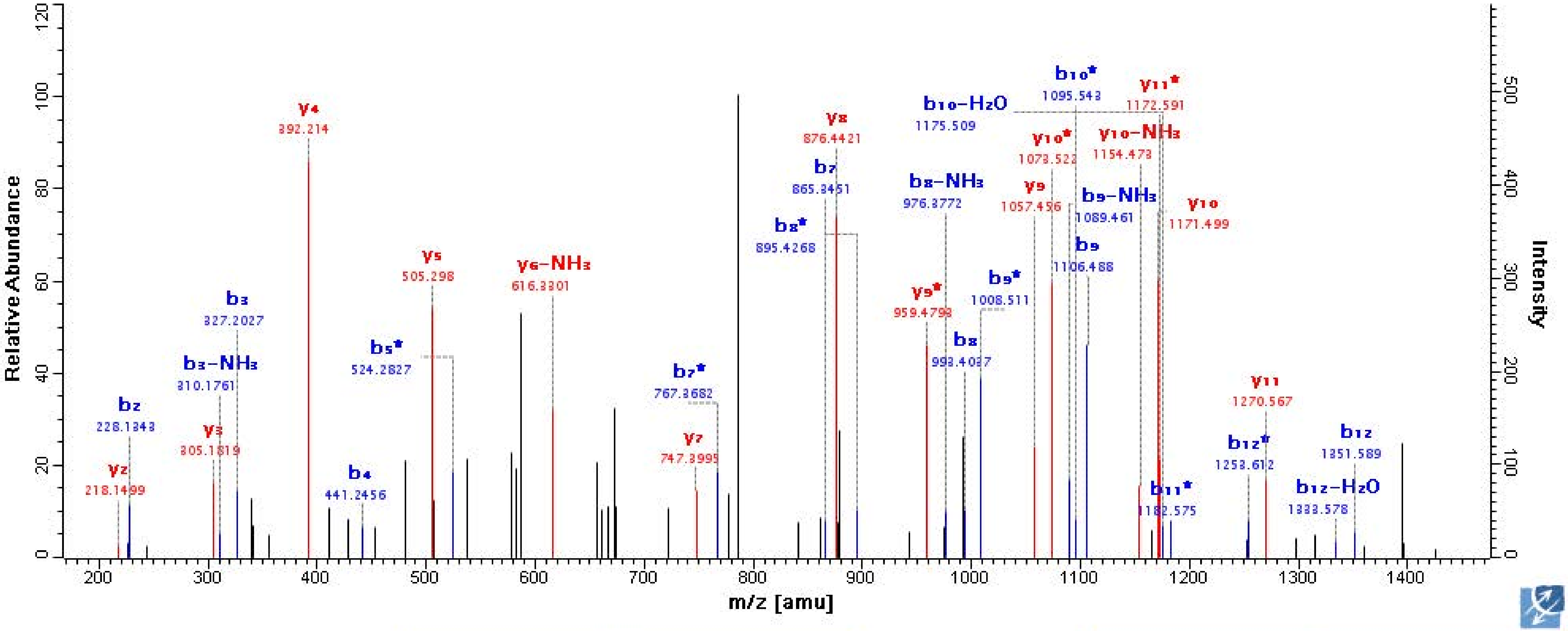
general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	59 %
Protein Localisation:	2 ... 12

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	168.005635285	1	S	10		
	281.089699265	2	I	9	1218.672865031	
+0.081852	394.173763246	3	I	8	1105.588801051	+0.1430105
+0.0144494	508.216690693	4	N	7	992.50473707	+0.080529
	623.243633725	5	D	6	878.461809623	+0.1654487
	736.327697705	6	I	5	763.434866591	+0.0485929
	849.411761686	7	I	4	650.350802611	
-0.1472259	978.454354782	8	E	3	537.26673863	+0.0546725
	1125.522768698	9	F	2	408.224145534	-0.0040528
+0.0348898	1239.565696145	10	N	1	261.155731618	+0.033752
		11	K	0	147.112804171	

Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F19
Scannumber:	6995
Protein:	BSU37120; fba; fba1; fbaA; tsr
Peptide Score:	213.18
Method:	ITMS; CID; 3





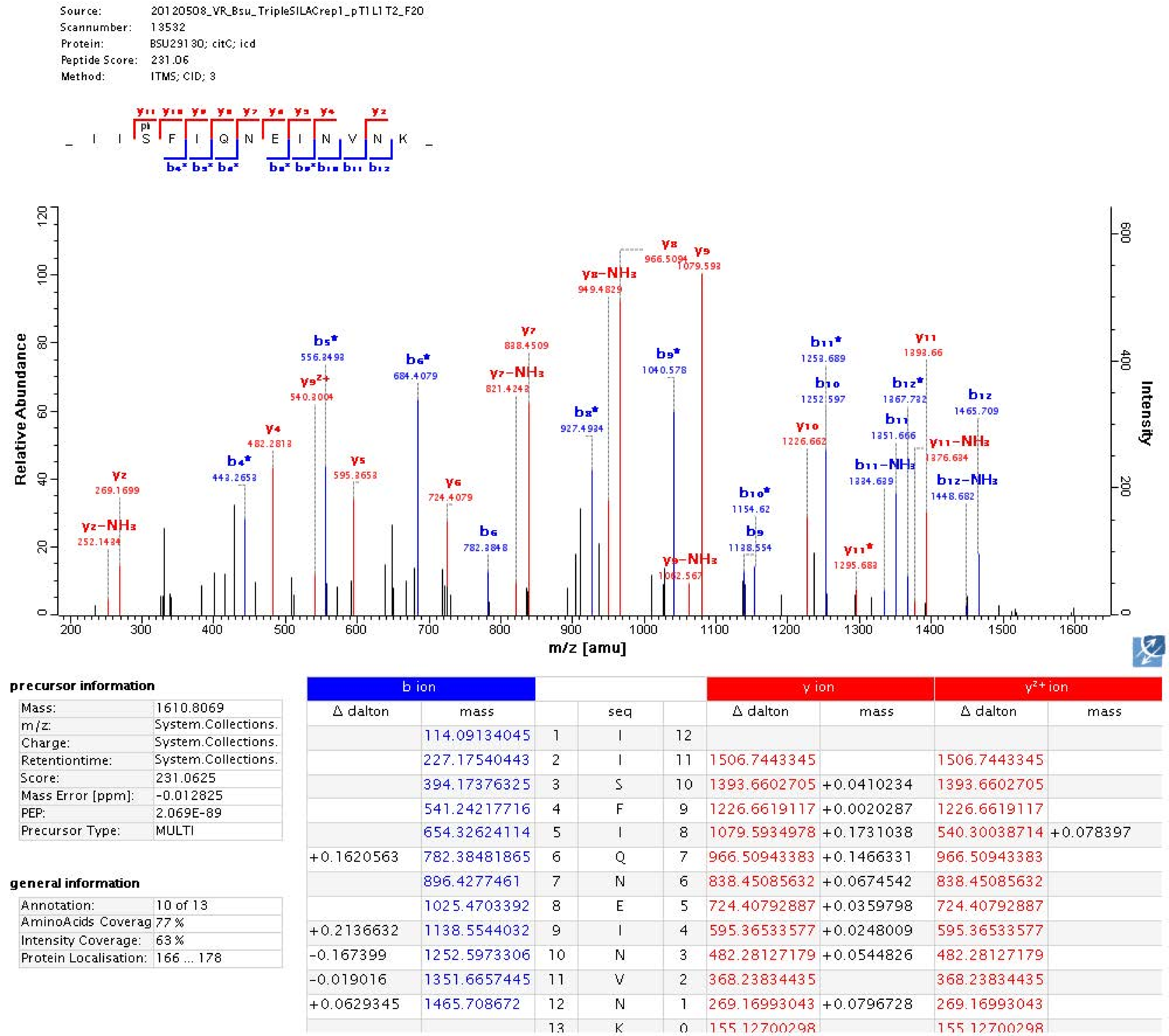
precursor information

Mass:	1496.6872
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	213.1823
Mass Error [ppm]:	-0.0039725
PEP:	1.4149E-59
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	55 %
Protein Localisation:	230 ... 242

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	114.091340447	1	I	12		
+0.0095309	228.134267894	2	N	11	1384.610414506	
-0.0211022	327.20268181	3	V	10	1270.567487059	+0.0520198
+0.1774864	441.245609258	4	N	9	1171.499073143	+0.1413077
	622.25961814	5	T	8	1057.456145696	+0.0630193
	751.302211236	6	E	7	876.442136813	+0.0452899
-0.033188	865.345138684	7	N	6	747.399543717	+0.0325242
-0.052703	993.403716195	8	Q	5	633.35661627	
-0.0244013	1106.487780175	9	I	4	505.298038759	+0.0308797
	1193.519808585	10	S	3	392.213974778	+0.1076805
	1280.551836995	11	S	2	305.181946368	+0.049682
-0.1842877	1351.588950783	12	A	1	218.149917958	+0.0090176
		13	K	0	147.112804171	



Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F20
Scannumber:	13532
Protein:	BSU29130; citC; icd
Peptide Score:	231.06
Method:	ITMS; CID; 3

precursor information

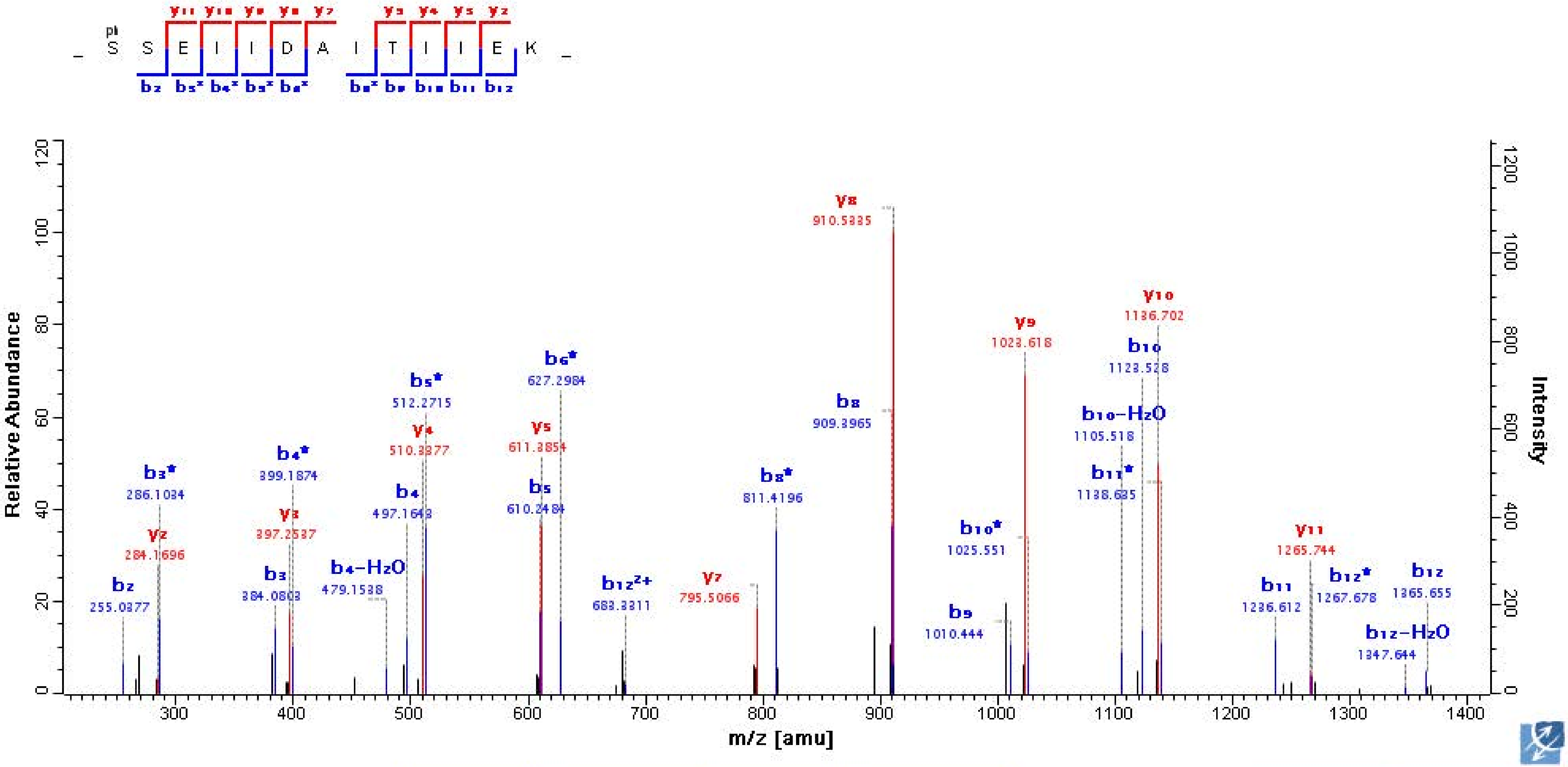
Mass:	1610.8069
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	231.0625
Mass Error [ppm]:	-0.012825
PEP:	2.069E-89
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	63 %
Protein Localisation:	166 ... 178

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045	1	I	12				
	227.17540443	2	I	11	1506.7443345		1506.7443345	
	394.17376325	3	S	10	1393.6602705	+0.0410234	1393.6602705	
	541.24217716	4	F	9	1226.6619117	+0.0020287	1226.6619117	
	654.32624114	5	I	8	1079.5934978	+0.1731038	540.30038714	+0.078397
+0.1620563	782.38481865	6	Q	7	966.50943383	+0.1466331	966.50943383	
	896.4277461	7	N	6	838.45085632	+0.0674542	838.45085632	
	1025.4703392	8	E	5	724.40792887	+0.0359798	724.40792887	
+0.2136632	1138.5544032	9	I	4	595.36533577	+0.0248009	595.36533577	
-0.167399	1252.5973306	10	N	3	482.28127179	+0.0544826	482.28127179	
-0.019016	1351.6657445	11	V	2	368.23834435		368.23834435	
+0.0629345	1465.708672	12	N	1	269.16993043	+0.0796728	269.16993043	
		13	K	0	155.12700298		155.12700298	

Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F20
Scannumber:	14211
Protein:	BSU16600; nusA
Peptide Score:	208.27
Method:	ITMS; CID; 3



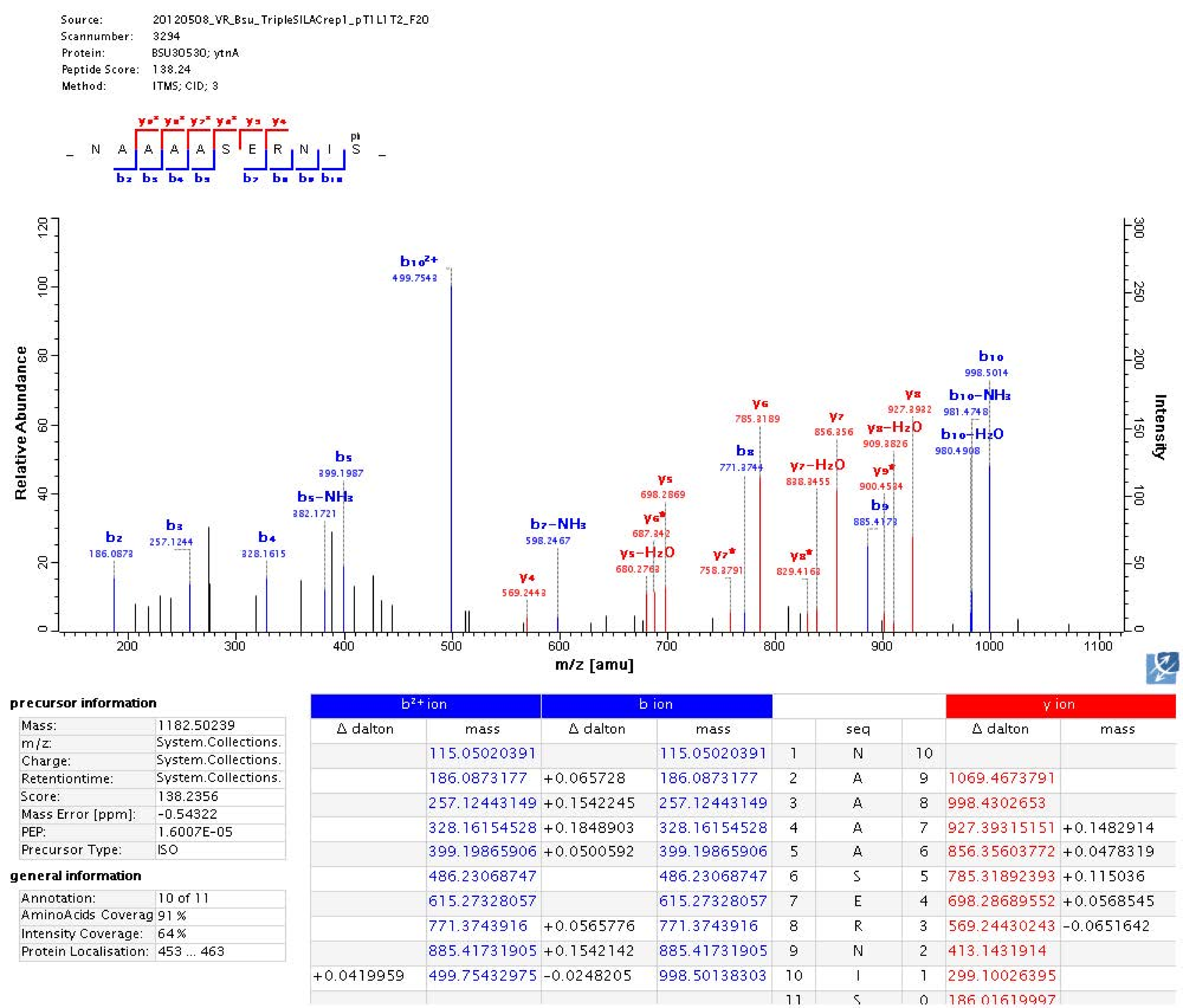
precursor information

Mass:	1510.75343
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	208.2719
Mass Error [ppm]:	0.18145
PEP:	3.4616E-59
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	76 %
Protein Localisation:	2 ... 14

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	168.00563528		168.00563528	1	S	12		
	255.03766369	-0.0031025	255.03766369	2	S	11	1352.7762728	
	384.08025679	-0.0845293	384.08025679	3	E	10	1265.7442444	-0.0258606
	497.16432077	-0.0783833	497.16432077	4	I	9	1136.7016513	+0.1085294
	610.24838475	+0.0270669	610.24838475	5	I	8	1023.6175873	+0.1839874
	725.27532778		725.27532778	6	D	7	910.53352332	+0.017319
	796.31244157		796.31244157	7	A	6	795.50658028	+0.066845
	909.39650555	+0.1789339	909.39650555	8	I	5	724.4694665	
	1010.444184	-0.0737617	1010.444184	9	T	4	611.38540251	+0.0452005
	1123.528248	+0.0957754	1123.528248	10	I	3	510.33772404	-0.0106977
	1236.612312	+0.0899585	1236.612312	11	I	2	397.25366006	+0.0435201
+0.0176031	683.33109077	-0.2766092	1365.6549051	12	E	1	284.16959608	-0.017588
				13	K	0	155.12700298	



Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F20
Scannumber: 3294
Protein: BSU30530; ytnA
Peptide Score: 138.24
Method: ITMS; CID; 3

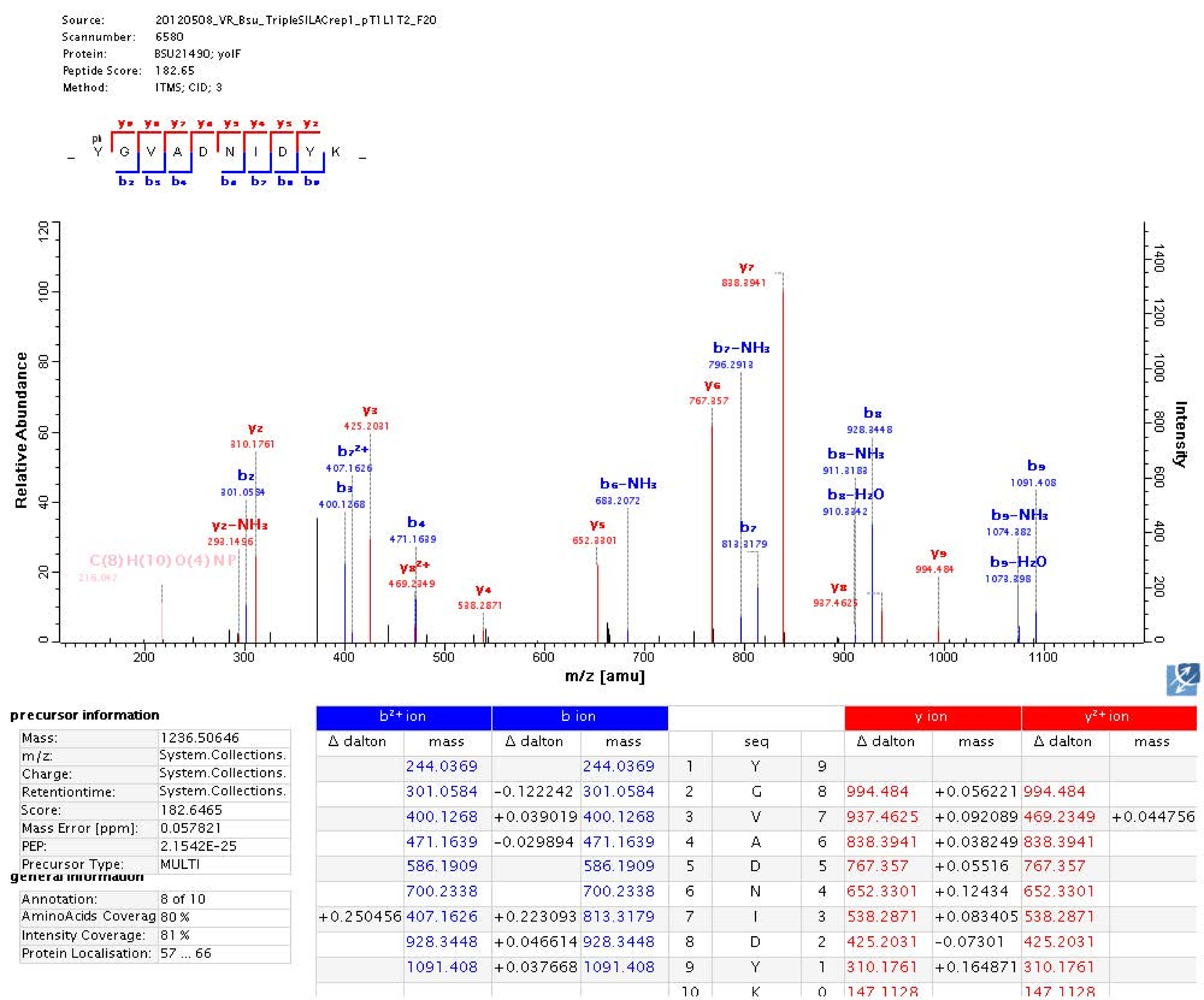
precursor information

Mass:	1182.50239
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	138.2356
Mass Error [ppm]:	-0.54322
PEP:	1.6007E-05
Precursor Type:	ISO

general information

Annotation:	10 of 11
AminoAcids Coverag	91 %
Intensity Coverage:	64 %
Protein Localisation:	453 ... 463

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	115.05020391		115.05020391	1	N	10		
	186.0873177	+0.065728	186.0873177	2	A	9	1069.4673791	
	257.12443149	+0.1542245	257.12443149	3	A	8	998.4302653	
	328.16154528	+0.1848903	328.16154528	4	A	7	927.39315151	+0.1482914
	399.19865906	+0.0500592	399.19865906	5	A	6	856.35603772	+0.0478319
	486.23068747		486.23068747	6	S	5	785.31892393	+0.115036
	615.27328057		615.27328057	7	E	4	698.28689552	+0.0568545
	771.3743916	+0.0565776	771.3743916	8	R	3	569.24430243	-0.0651642
	885.41731905	+0.1542142	885.41731905	9	N	2	413.1431914	
+0.0419959	499.75432975	-0.0248205	998.50138303	10	I	1	299.10026395	
				11	S	0	186.01619997	



Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F20
Scannumber: 6580
Protein: BSU21490; yolF
Peptide Score: 182.65
Method: ITMS; CID; 3

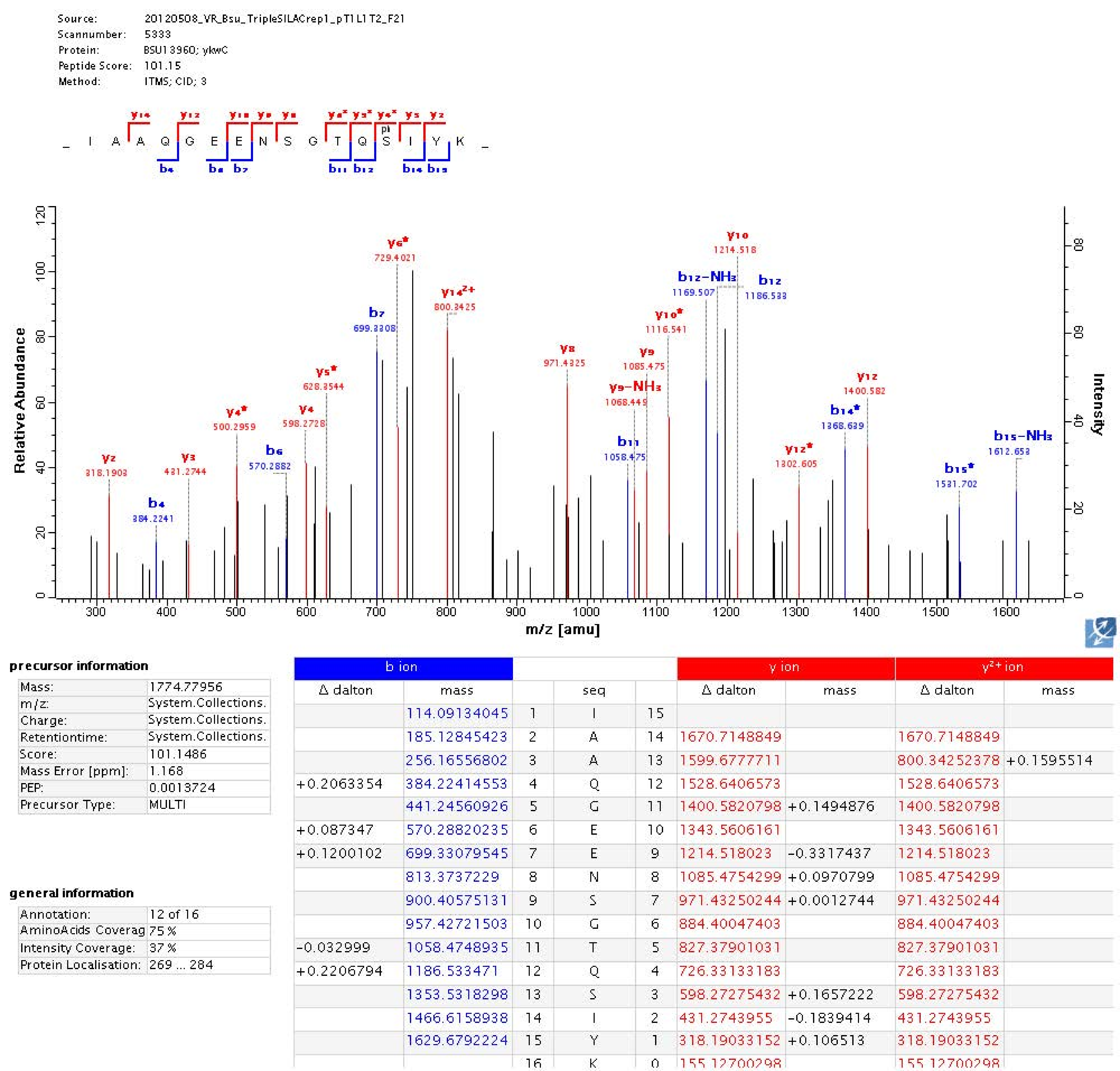
precursor information

Mass:	1236.50646
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	182.6465
Mass Error [ppm]:	0.057821
PEP:	2.1542E-25
Precursor Type:	MULTI

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	81 %
Protein Localisation:	57 ... 66

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	244.0369		244.0369	1	Y	9				
	301.0584	-0.122242	301.0584	2	G	8	994.484	+0.056221	994.484	
	400.1268	+0.039019	400.1268	3	V	7	937.4625	+0.092089	469.2349	+0.044756
	471.1639	-0.029894	471.1639	4	A	6	838.3941	+0.038249	838.3941	
	586.1909		586.1909	5	D	5	767.357	+0.05516	767.357	
	700.2338		700.2338	6	N	4	652.3301	+0.12434	652.3301	
+0.250456	407.1626	+0.223093	813.3179	7	I	3	538.2871	+0.083405	538.2871	
	928.3448	+0.046614	928.3448	8	D	2	425.2031	-0.07301	425.2031	
	1091.408	+0.037668	1091.408	9	Y	1	310.1761	+0.164871	310.1761	
				10	K	0	147.1128		147.1128	



Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F21
Scannumber: 5333
Protein: BSU13960; ykwC
Peptide Score: 101.15
Method: ITMS; CID; 3

precursor information

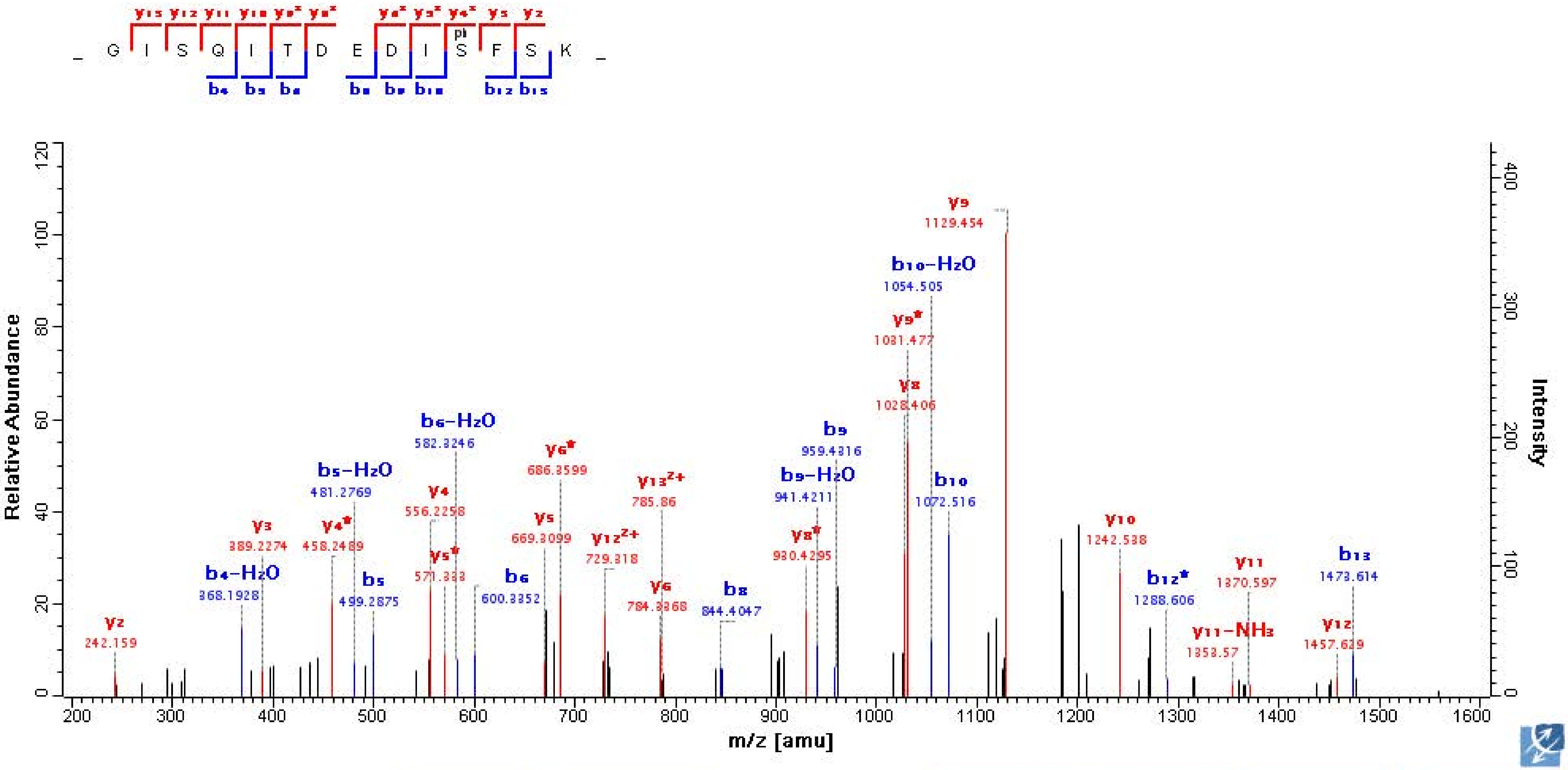
Mass:	1774.77956
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	101.1486
Mass Error [ppm]:	1.168
PEP:	0.0013724
Precursor Type:	MULTI

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	37 %
Protein Localisation:	269 ... 284

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045	1	I	15				
	185.12845423	2	A	14	1670.7148849		1670.7148849	
	256.16556802	3	A	13	1599.6777711		800.34252378	+0.1595514
+0.2063354	384.22414553	4	Q	12	1528.6406573		1528.6406573	
	441.24560926	5	G	11	1400.5820798	+0.1494876	1400.5820798	
+0.087347	570.28820235	6	E	10	1343.5606161		1343.5606161	
+0.1200102	699.33079545	7	E	9	1214.518023	-0.3317437	1214.518023	
	813.3737229	8	N	8	1085.4754299	+0.0970799	1085.4754299	
	900.40575131	9	S	7	971.43250244	+0.0012744	971.43250244	
	957.42721503	10	G	6	884.40047403		884.40047403	
-0.032999	1058.4748935	11	T	5	827.37901031		827.37901031	
+0.2206794	1186.533471	12	Q	4	726.33133183		726.33133183	
	1353.5318298	13	S	3	598.27275432	+0.1657222	598.27275432	
	1466.6158938	14	I	2	431.2743955	-0.1839414	431.2743955	
	1629.6792224	15	Y	1	318.19033152	+0.106513	318.19033152	
		16	K	0	155.12700298		155.12700298	

Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F21
Scannumber:	8720
Protein:	BSU32260; hom; tdm
Peptide Score:	155.57
Method:	ITMS; CID; 3



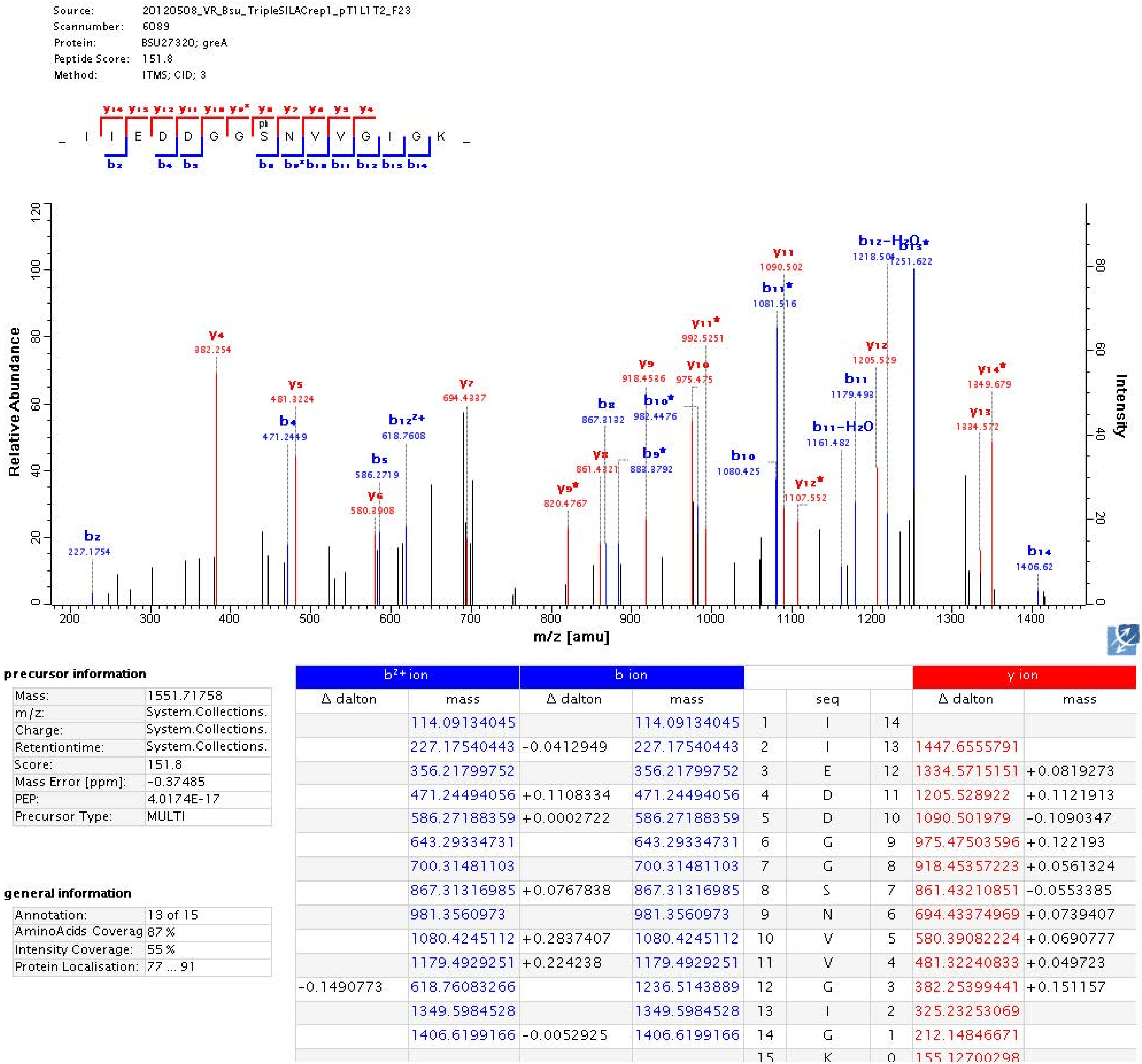
precursor information

Mass:	1618.7133
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	155.5715
Mass Error [ppm]:	0.34085
PEP:	5.5702E-17
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	51 %
Protein Localisation:	227 ... 240

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019	1	G	13				
	171.11280417	2	I	12	1570.7127596		785.86001805	-0.1592734
	258.14483258	3	S	11	1457.6286956	-0.1283294	729.31798606	+0.1174387
	386.20341009	4	Q	10	1370.5966672	+0.0763064	1370.5966672	
+0.0983292	499.28747407	5	I	9	1242.5380897	+0.1152306	1242.5380897	
-0.0223474	600.33515255	6	T	8	1129.4540257	-0.1056371	1129.4540257	
	715.36209558	7	D	7	1028.4063473	-0.0130367	1028.4063473	
-0.231654	844.40468867	8	E	6	913.37940424		913.37940424	
-0.4257723	959.43163171	9	D	5	784.33681114	+0.0787772	784.33681114	
+0.1422633	1072.5156957	10	I	4	669.30986811	+0.2880933	669.30986811	
	1239.5140545	11	S	3	556.22580413	+0.0132706	556.22580413	
	1386.5824684	12	F	2	389.22744531	+0.1298545	389.22744531	
+0.1001028	1473.6144968	13	S	1	242.15903139	+0.1690478	242.15903139	
		14	K	0	155.12700298		155.12700298	



Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F23
Scannumber:	6089
Protein:	BSU27320; greA
Peptide Score:	151.8
Method:	ITMS; CID; 3

precursor information

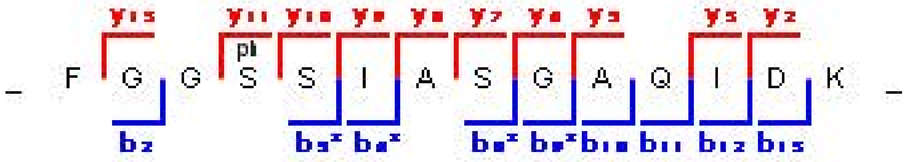
Mass:	1551.71758
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	151.8
Mass Error [ppm]:	-0.37485
PEP:	4.0174E-17
Precursor Type:	MULTI

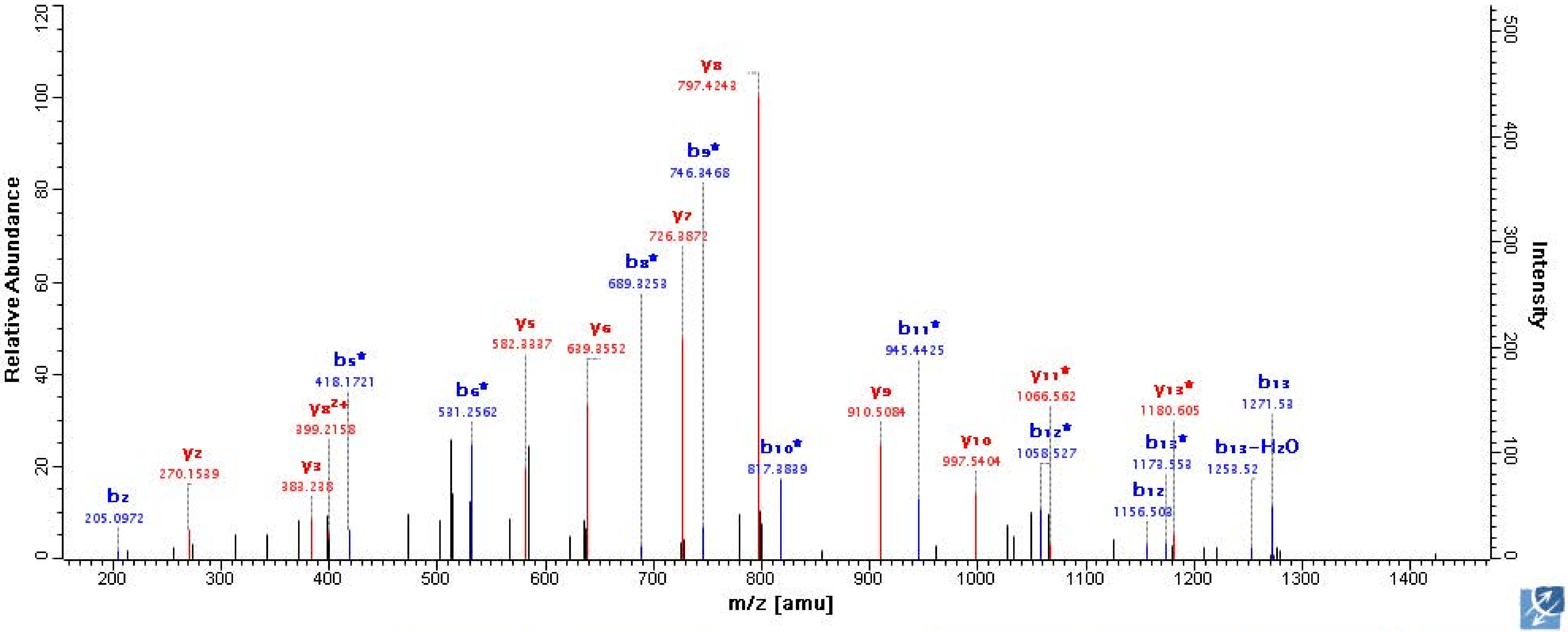
general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	55 %
Protein Localisation:	77 ... 91

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	114.09134045		114.09134045	1	I	14		
	227.17540443	-0.0412949	227.17540443	2	I	13	1447.6555791	
	356.21799752		356.21799752	3	E	12	1334.5715151	+0.0819273
	471.24494056	+0.1108334	471.24494056	4	D	11	1205.528922	+0.1121913
	586.27188359	+0.0002722	586.27188359	5	D	10	1090.501979	-0.1090347
	643.29334731		643.29334731	6	G	9	975.47503596	+0.122193
	700.31481103		700.31481103	7	G	8	918.45357223	+0.0561324
	867.31316985	+0.0767838	867.31316985	8	S	7	861.43210851	-0.0553385
	981.3560973		981.3560973	9	N	6	694.43374969	+0.0739407
	1080.4245112	+0.2837407	1080.4245112	10	V	5	580.39082224	+0.0690777
	1179.4929251	+0.224238	1179.4929251	11	V	4	481.32240833	+0.049723
-0.1490773	618.76083266		1236.5143889	12	G	3	382.25399441	+0.151157
	1349.5984528		1349.5984528	13	I	2	325.23253069	
	1406.6199166	-0.0052925	1406.6199166	14	G	1	212.14846671	
				15	K	0	155.12700298	

Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F23
Scannumber:	6207
Protein:	BSU03790; yclM
Peptide Score:	121.45
Method:	ITMS; CID; 3





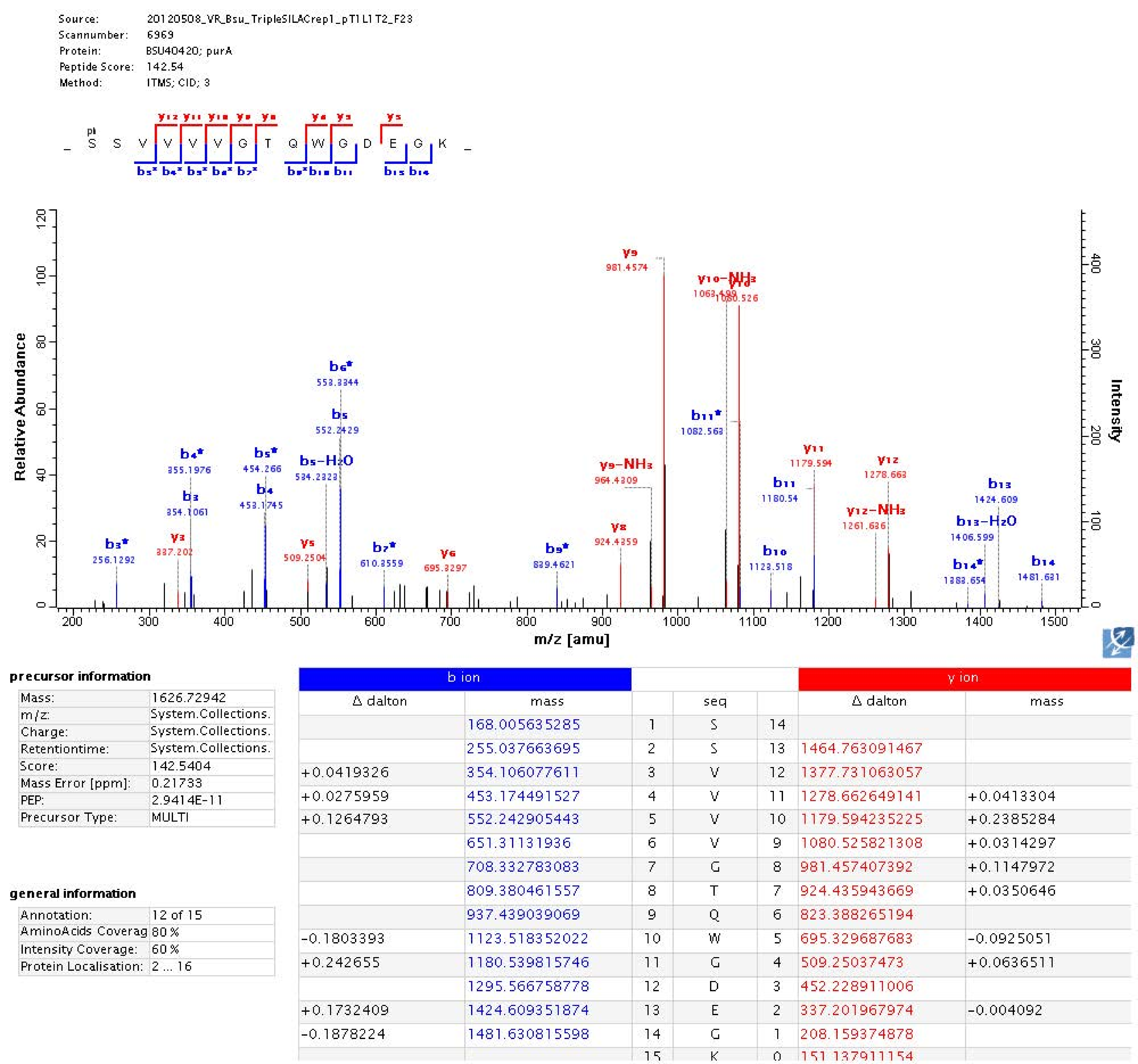
precursor information

Mass:	1416.62897
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	121.4488
Mass Error [ppm]:	0.2397
PEP:	0.00015885
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	58 %
Protein Localisation:	6 ... 19

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.07569038	1	F	13				
+0.0292497	205.09715411	2	G	12	1278.5816859		1278.5816859	
	262.11861783	3	G	11	1221.5602221		1221.5602221	
	429.11697665	4	S	10	1164.5387584		1164.5387584	
	516.14900506	5	S	9	997.54039961	+0.1090145	997.54039961	
	629.23306904	6	I	8	910.5083712	+0.0673124	910.5083712	
	700.27018283	7	A	7	797.42430722	+0.0454193	399.21579184	+0.38455
	787.30221124	8	S	6	726.38719343	-0.0488756	726.38719343	
	844.32367496	9	G	5	639.35516502	+0.1004014	639.35516502	
	915.36078875	10	A	4	582.3337013	-0.4253761	582.3337013	
	1043.4193663	11	Q	3	511.29658751		511.29658751	
+0.1924926	1156.5034302	12	I	2	383.23801	+0.0586819	383.23801	
+0.1914285	1271.5303733	13	D	1	270.15394602	+0.0410003	270.15394602	
		14	K	0	155.12700298		155.12700298	



Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F23
Scannumber:	6969
Protein:	BSU40420; purA
Peptide Score:	142.54
Method:	ITMS; CID; 3

precursor information

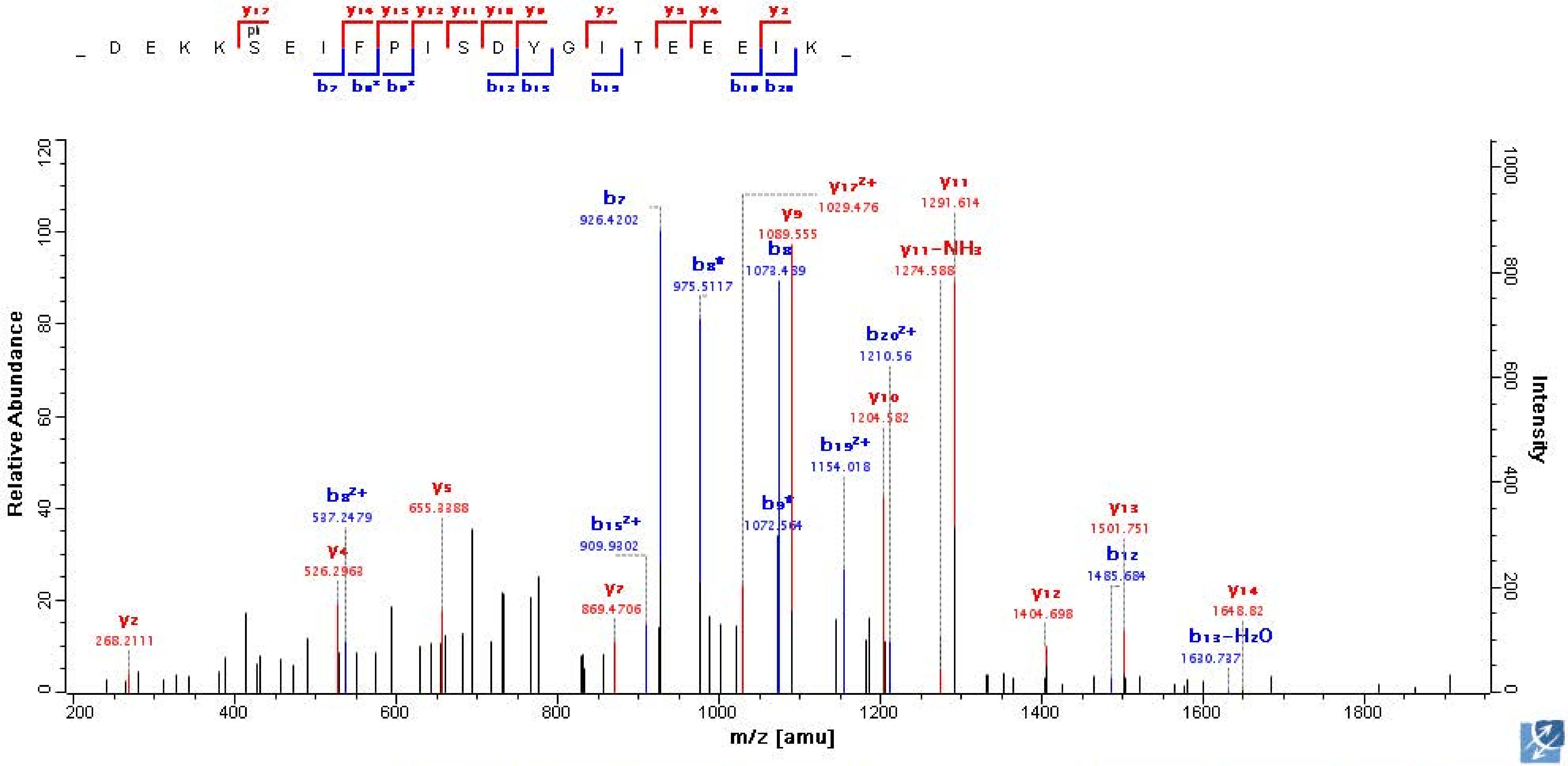
Mass:	1626.72942
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	142.5404
Mass Error [ppm]:	0.21733
PEP:	2.9414E-11
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	60 %
Protein Localisation:	2 ... 16

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	168.005635285	1	S	14		
	255.037663695	2	S	13	1464.763091467	
+0.0419326	354.106077611	3	V	12	1377.731063057	
+0.0275959	453.174491527	4	V	11	1278.662649141	+0.0413304
+0.1264793	552.242905443	5	V	10	1179.594235225	+0.2385284
	651.31131936	6	V	9	1080.525821308	+0.0314297
	708.332783083	7	G	8	981.457407392	+0.1147972
	809.380461557	8	T	7	924.435943669	+0.0350646
	937.439039069	9	Q	6	823.388265194	
-0.1803393	1123.518352022	10	W	5	695.329687683	-0.0925051
+0.242655	1180.539815746	11	G	4	509.25037473	+0.0636511
	1295.566758778	12	D	3	452.228911006	
+0.1732409	1424.609351874	13	E	2	337.201967974	-0.004092
-0.1878224	1481.630815598	14	G	1	208.159374878	
		15	K	0	151.137911154	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F07
Scannumber:	11562
Protein:	BSU19370; citK; odhA
Peptide Score:	95.21
Method:	ITMS; CID; 3



precursor information

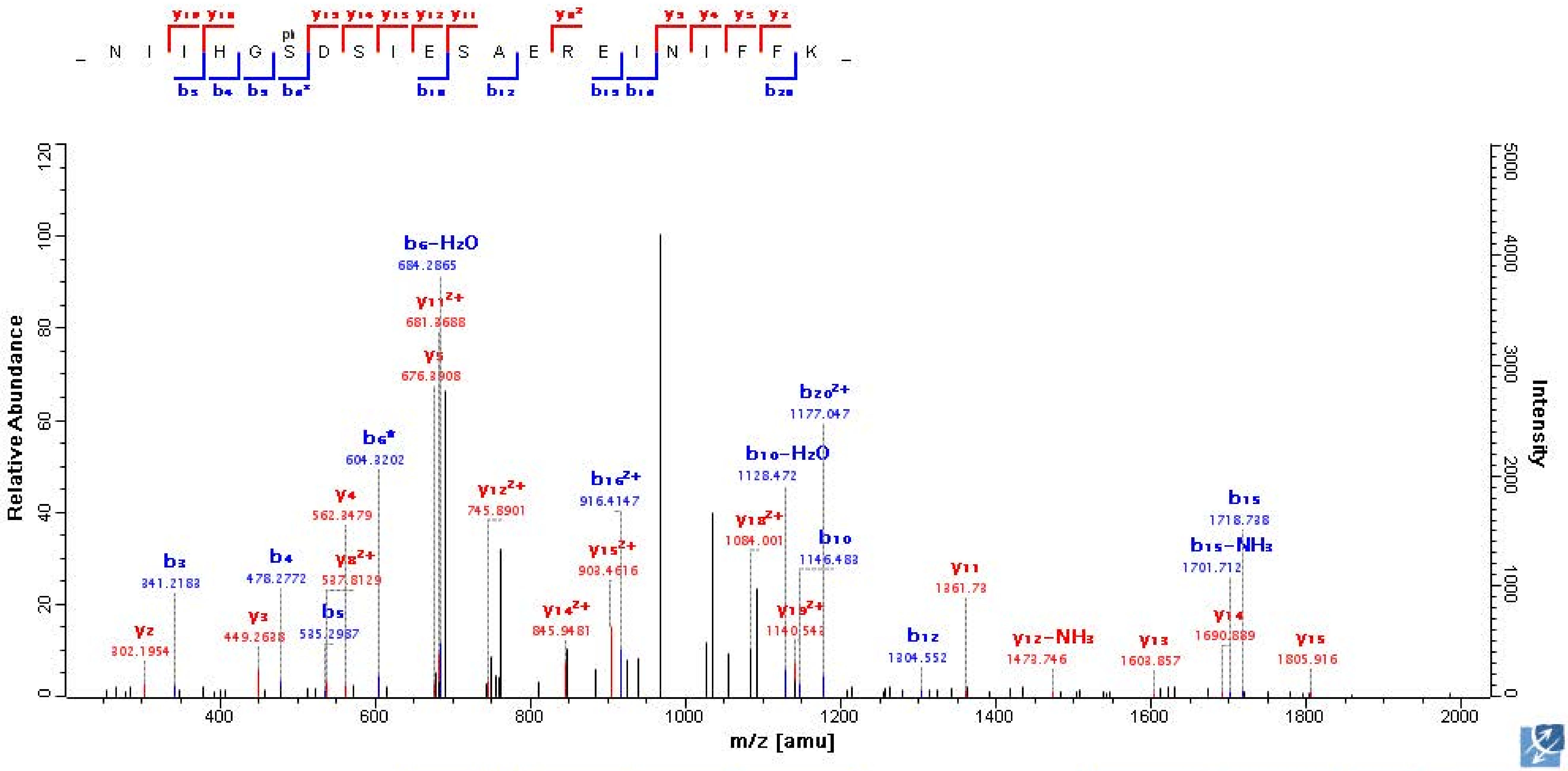
Mass:	2573.22695
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	95.20509
Mass Error [ppm]:	0.68433
PEP:	0.006057
Precursor Type:	ISO

general information

Annotation:	14 of 21
AminoAcids Coverag	67 %
Intensity Coverage:	51 %
Protein Localisation:	101 ... 121

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342		116.0342	1	D	20				
	245.0768		245.0768	2	E	19	2459.206		2459.206	
	381.186		381.186	3	K	18	2330.163		2330.163	
	517.2951		517.2951	4	K	17	2194.054		2194.054	
	684.2935		684.2935	5	S	16	2057.945		1029.476	-0.393424
	813.3361		813.3361	6	E	15	1890.946		1890.946	
	926.4202	+0.022292	926.4202	7	I	14	1761.904		1761.904	
-0.145626	537.2479	+0.111532	1073.489	8	F	13	1648.82	+0.291612	1648.82	
	1170.541		1170.541	9	P	12	1501.751	+0.134928	1501.751	
	1283.625		1283.625	10	I	11	1404.698	+0.09321	1404.698	
	1370.657		1370.657	11	S	10	1291.614	-0.018527	1291.614	
	1485.684	+0.250327	1485.684	12	D	9	1204.582	-0.056079	1204.582	
	1648.748		1648.748	13	Y	8	1089.555	+0.017983	1089.555	
	1705.769		1705.769	14	G	7	926.4921		926.4921	
-0.058179	909.9302		1818.853	15	I	6	869.4706	-0.103889	869.4706	
	1919.901		1919.901	16	T	5	756.3865		756.3865	
	2048.943		2048.943	17	E	4	655.3388	+0.074789	655.3388	
	2177.986		2177.986	18	E	3	526.2963	-0.133045	526.2963	
+0.39584	1154.018		2307.029	19	E	2	397.2537		397.2537	
+0.400439	1210.56		2420.113	20	I	1	268.2111	+0.075951	268.2111	
				21	K	0	155.127		155.127	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F07
Scannumber:	14106
Protein:	BSU22730; ndk
Peptide Score:	102.69
Method:	ITMS; CID; 3



precursor information

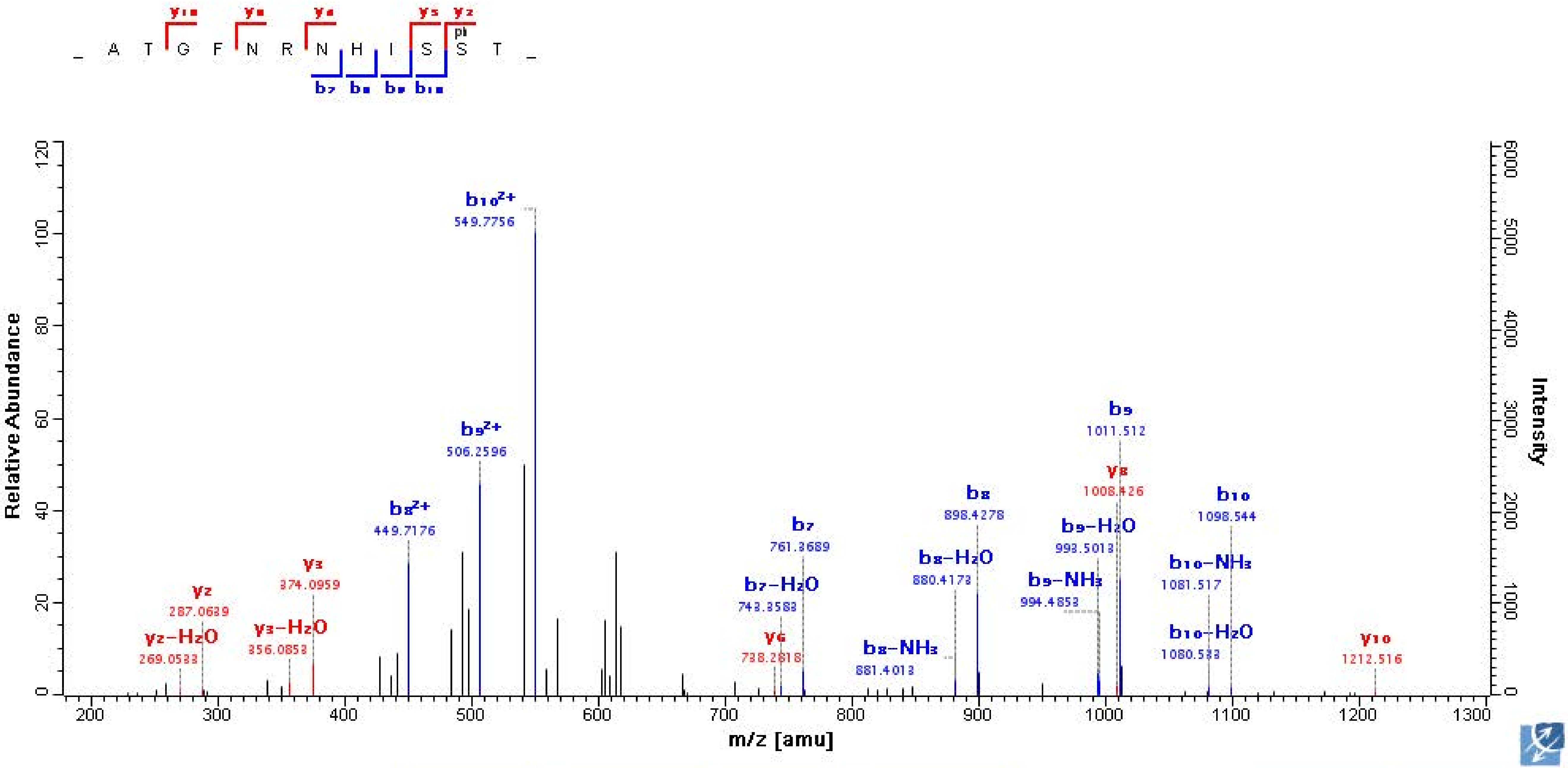
Mass:	2506.19961
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	102.6893
Mass Error [ppm]:	0.45608
PEP:	0.00065519
Precursor Type:	ISO

general information

Annotation:	17 of 21
AminoAcids Coverag	81 %
Intensity Coverage:	21 %
Protein Localisation:	113 ... 133

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502		115.0502	1	N	20				
	228.1343		228.1343	2	I	19	2393.163		2393.163	
	341.2183	+0.058951	341.2183	3	I	18	2280.079		1140.543	+0.140457
	478.2772	+0.031472	478.2772	4	H	17	2166.995		1084.001	+0.033197
	535.2987	+0.340514	535.2987	5	G	16	2029.936		2029.936	
	702.2971		702.2971	6	S	15	1972.914		1972.914	
	817.324		817.324	7	D	14	1805.916	+0.100892	903.4616	+0.417291
	904.356		904.356	8	S	13	1690.889	+0.169949	845.9481	+0.026954
	1017.44		1017.44	9	I	12	1603.857	+0.355175	1603.857	
	1146.483	-0.226957	1146.483	10	E	11	1490.773		745.8901	-0.037559
	1233.515		1233.515	11	S	10	1361.73	-0.089457	681.3688	+0.229771
	1304.552	-0.384479	1304.552	12	A	9	1274.698		1274.698	
	1433.594		1433.594	13	E	8	1203.661		1203.661	
	1589.696		1589.696	14	R	7	1074.619		537.8129	+0.272577
	1718.738	-0.103491	1718.738	15	E	6	918.5175		918.5175	
-0.403812	916.4147		1831.822	16	I	5	789.4749		789.4749	
	1945.865		1945.865	17	N	4	676.3908	+0.192979	676.3908	
	2058.949		2058.949	18	I	3	562.3479	+0.068304	562.3479	
	2206.018		2206.018	19	F	2	449.2638	+0.004358	449.2638	
-0.078629	1177.047		2353.086	20	F	1	302.1954	+0.011065	302.1954	
				21	K	0	155.127		155.127	

Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F07
Scannumber: 4070
Protein: bioYB; BSU32030; yuiG
Peptide Score: 132.25
Method: ITMS; CID; 3



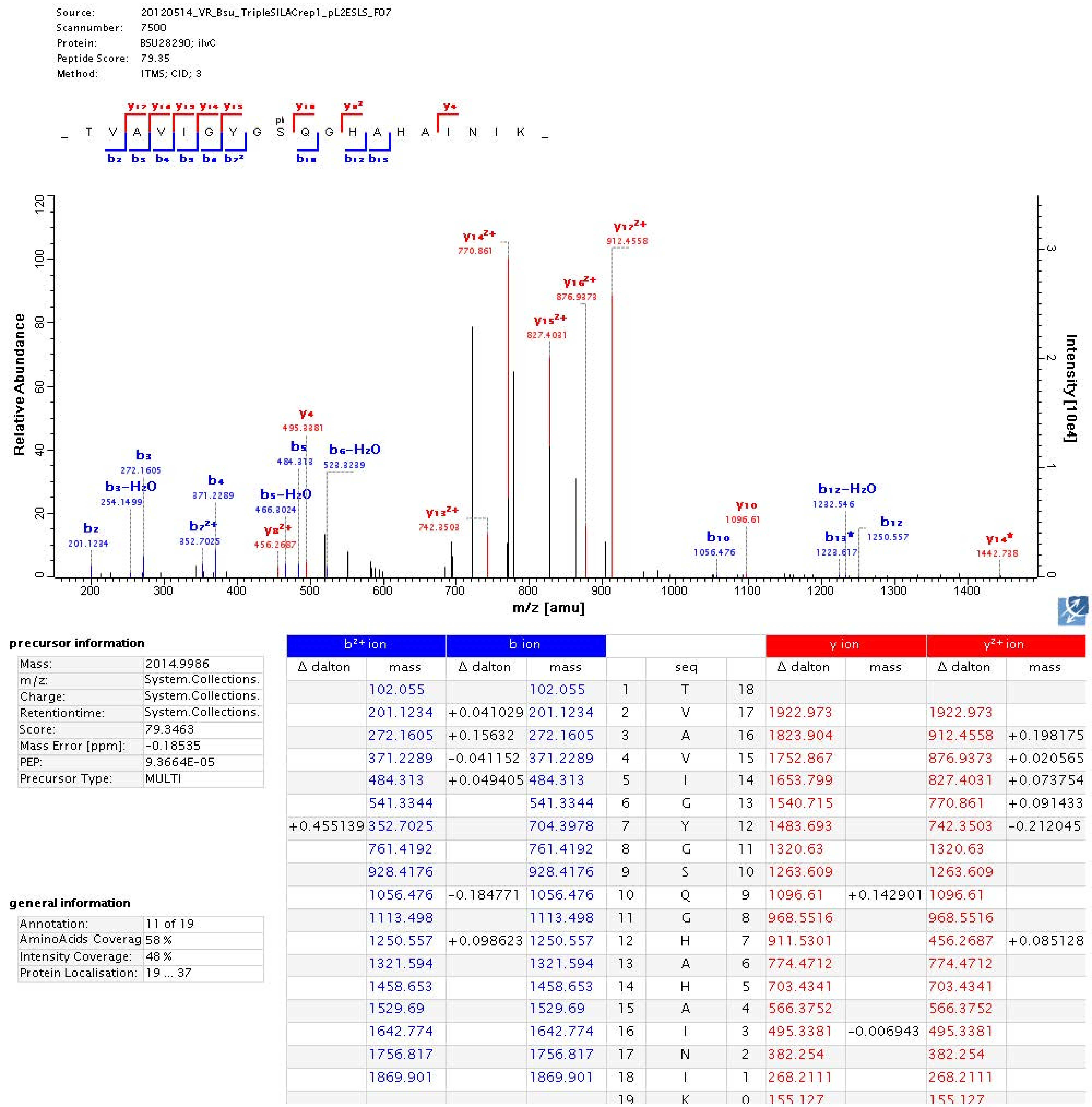
precursor information

Mass:	1383.59238
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	132.2496
Mass Error [ppm]:	-0.61988
PEP:	0.0059303
Precursor Type:	ISO

general information

Annotation:	7 of 12
AminoAcids Coverag	58 %
Intensity Coverage:	49 %
Protein Localisation:	189 ... 200

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	72.044390254		72.044390254	1	A	11		
	173.09206873		173.09206873	2	T	10	1313.5634047	
	230.11353245		230.11353245	3	G	9	1212.5157263	+0.3955286
	377.18194637		377.18194637	4	F	8	1155.4942625	
	491.22487382		491.22487382	5	N	7	1008.4258486	-0.0545107
	647.32598484		647.32598484	6	R	6	894.38292117	
	761.36891229	+0.1064905	761.36891229	7	N	5	738.28181015	-0.0210069
+0.1742344	449.71755031	+0.0508746	898.42782415	8	H	4	624.2388827	
+0.1550906	506.2595823	+0.0156998	1011.5118881	9	I	3	487.17997084	
+0.0704118	549.77559651	-0.1413287	1098.5439165	10	S	2	374.09590686	+0.1512245
	1265.5422754		1265.5422754	11	S	1	287.06387845	+0.0443979
				12	T	0	120.06551963	



Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F07
Scannumber: 7500
Protein: BSU28290; ilvC
Peptide Score: 79.35
Method: ITMS; CID; 3

precursor information

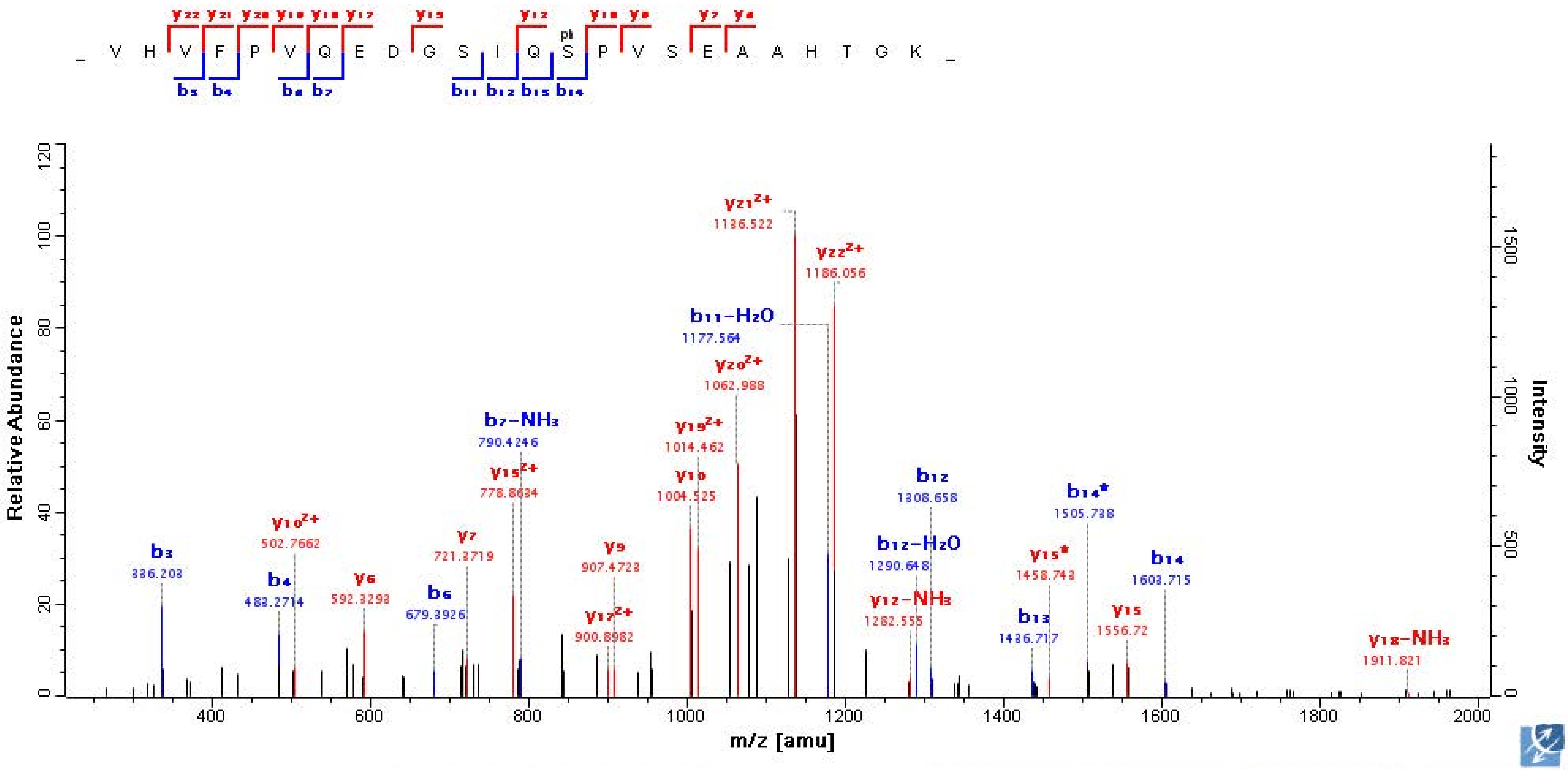
Mass:	2014.9986
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	79.3463
Mass Error [ppm]:	-0.18535
PEP:	9.3664E-05
Precursor Type:	MULTI

general information

Annotation:	11 of 19
AminoAcids Coverag	58 %
Intensity Coverage:	48 %
Protein Localisation:	19 ... 37

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055		102.055	1	T	18				
	201.1234	+0.041029	201.1234	2	V	17	1922.973		1922.973	
	272.1605	+0.15632	272.1605	3	A	16	1823.904		912.4558	+0.198175
	371.2289	-0.041152	371.2289	4	V	15	1752.867		876.9373	+0.020565
	484.313	+0.049405	484.313	5	I	14	1653.799		827.4031	+0.073754
	541.3344		541.3344	6	G	13	1540.715		770.861	+0.091433
+0.455139	352.7025		704.3978	7	Y	12	1483.693		742.3503	-0.212045
	761.4192		761.4192	8	G	11	1320.63		1320.63	
	928.4176		928.4176	9	S	10	1263.609		1263.609	
	1056.476	-0.184771	1056.476	10	Q	9	1096.61	+0.142901	1096.61	
	1113.498		1113.498	11	G	8	968.5516		968.5516	
	1250.557	+0.098623	1250.557	12	H	7	911.5301		456.2687	+0.085128
	1321.594		1321.594	13	A	6	774.4712		774.4712	
	1458.653		1458.653	14	H	5	703.4341		703.4341	
	1529.69		1529.69	15	A	4	566.3752		566.3752	
	1642.774		1642.774	16	I	3	495.3381	-0.006943	495.3381	
	1756.817		1756.817	17	N	2	382.254		382.254	
	1869.901		1869.901	18	I	1	268.2111		268.2111	
				19	K	0	155.127		155.127	

Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F07
Scannumber: 8478
Protein: BSU13010; ykgB
Peptide Score: 85.97
Method: ITMS; CID; 3



precursor information

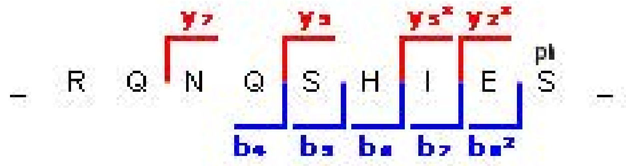
Mass:	2606.22626
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	85.97375
Mass Error [ppm]:	0.19689
PEP:	2.0642E-06
Precursor Type:	ISO

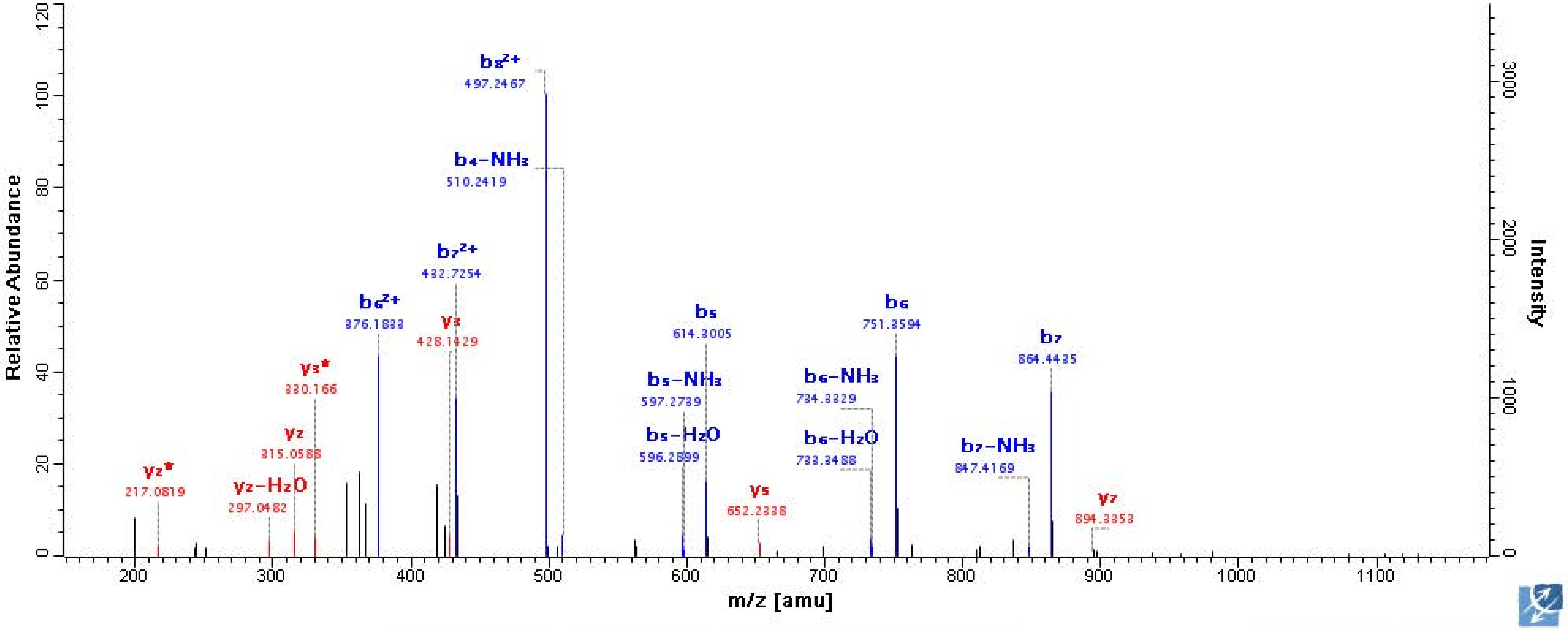
general information

Annotation:	15 of 24
AminoAcids Coverag	62 %
Intensity Coverage:	46 %
Protein Localisation:	114 ... 137

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.07569038	1	V	23				
	237.13460225	2	H	22	2508.1646074		2508.1646074	
+0.0818044	336.20301616	3	V	21	2371.1056956		1186.056486	+0.2070638
+0.1204767	483.27143008	4	F	20	2272.0372817		1136.5222791	+0.42401
	580.32419393	5	P	19	2124.9688677		1062.9880721	+0.3112443
-0.137664	679.39260785	6	V	18	2027.9161039		1014.4616902	+0.2958782
	807.45118536	7	Q	17	1928.84769		1928.84769	
	936.49377845	8	E	16	1800.7891125		900.89819447	-0.0129406
	1051.5207215	9	D	15	1671.7465194		1671.7465194	
	1108.5421852	10	G	14	1556.7195763	+0.2195106	778.8634264	+0.2704237
	1195.5742136	11	S	13	1499.6981126		1499.6981126	
-0.0086194	1308.6582776	12	I	12	1412.6660842		1412.6660842	
+0.0984525	1436.7168551	13	Q	11	1299.5820202		1299.5820202	
+0.3290976	1603.7152139	14	S	10	1171.5234427		1171.5234427	
	1700.7679778	15	P	9	1004.5250839	+0.1280533	502.76618018	-0.0330259
	1799.8363917	16	V	8	907.47232004	+0.1594549	907.47232004	
	1886.8684201	17	S	7	808.40390613		808.40390613	
	2015.9110132	18	E	6	721.37187772	-0.0483304	721.37187772	
	2086.948127	19	A	5	592.32928462	-0.0151367	592.32928462	
	2157.9852408	20	A	4	521.29217083		521.29217083	
	2295.0441526	21	H	3	450.25505704		450.25505704	
	2396.0918311	22	T	2	313.19614518		313.19614518	
	2453.1132948	23	G	1	212.14846671		212.14846671	
		24	K	0	155.12700298		155.12700298	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F09
Scannumber:	2089
Protein:	BSU31110; yubF
Peptide Score:	114.97
Method:	ITMS; CID; 3

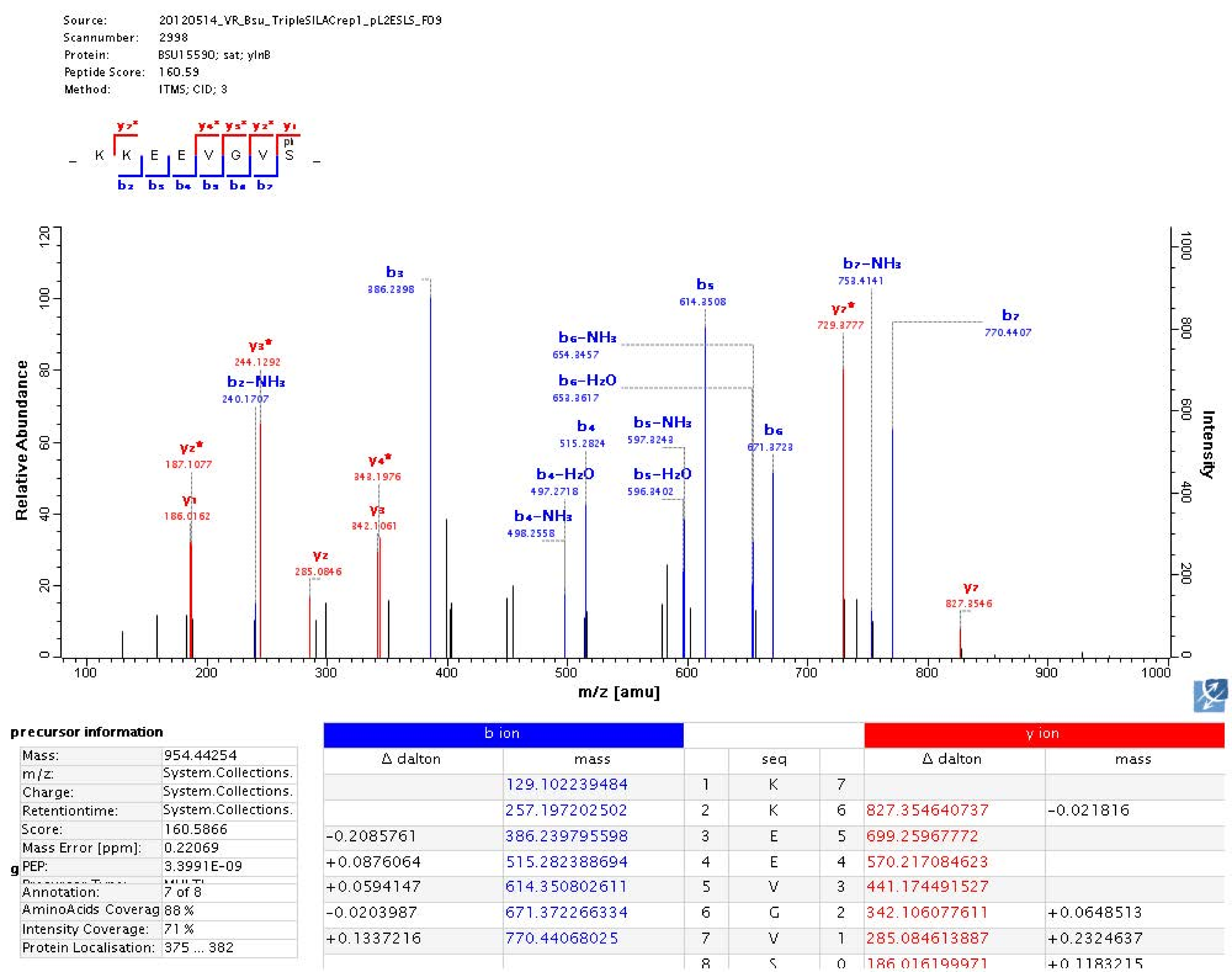




precursor information

Mass:	1177.4875
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	114.9683
Mass Error [ppm]:	-0.18127
PEP:	4.2569E-05
Precursor Type:	ISO
Annotation:	6 of 9
AminoAcids Coverag	67 %
Intensity Coverage:	68 %
Protein Localisation:	79 ... 87

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	157.10838749		157.10838749	1	R	8		
	285.16696501		285.16696501	2	Q	7	1022.3938798	
	399.20989245		399.20989245	3	N	6	894.33530228	+0.3656255
	527.26846996		527.26846996	4	Q	5	780.29237483	
	614.30049837	+0.0806662	614.30049837	5	S	4	652.23379732	+0.2206094
+0.0709901	376.18334335	+0.0099135	751.35941024	6	H	3	565.20176891	
+0.0467804	432.72537534	-0.0005421	864.44347422	7	I	2	428.14285705	-0.0231671
+0.2041948	497.24667189		993.48606731	8	E	1	315.05879307	+0.1804953
				9	S	0	186.01619997	

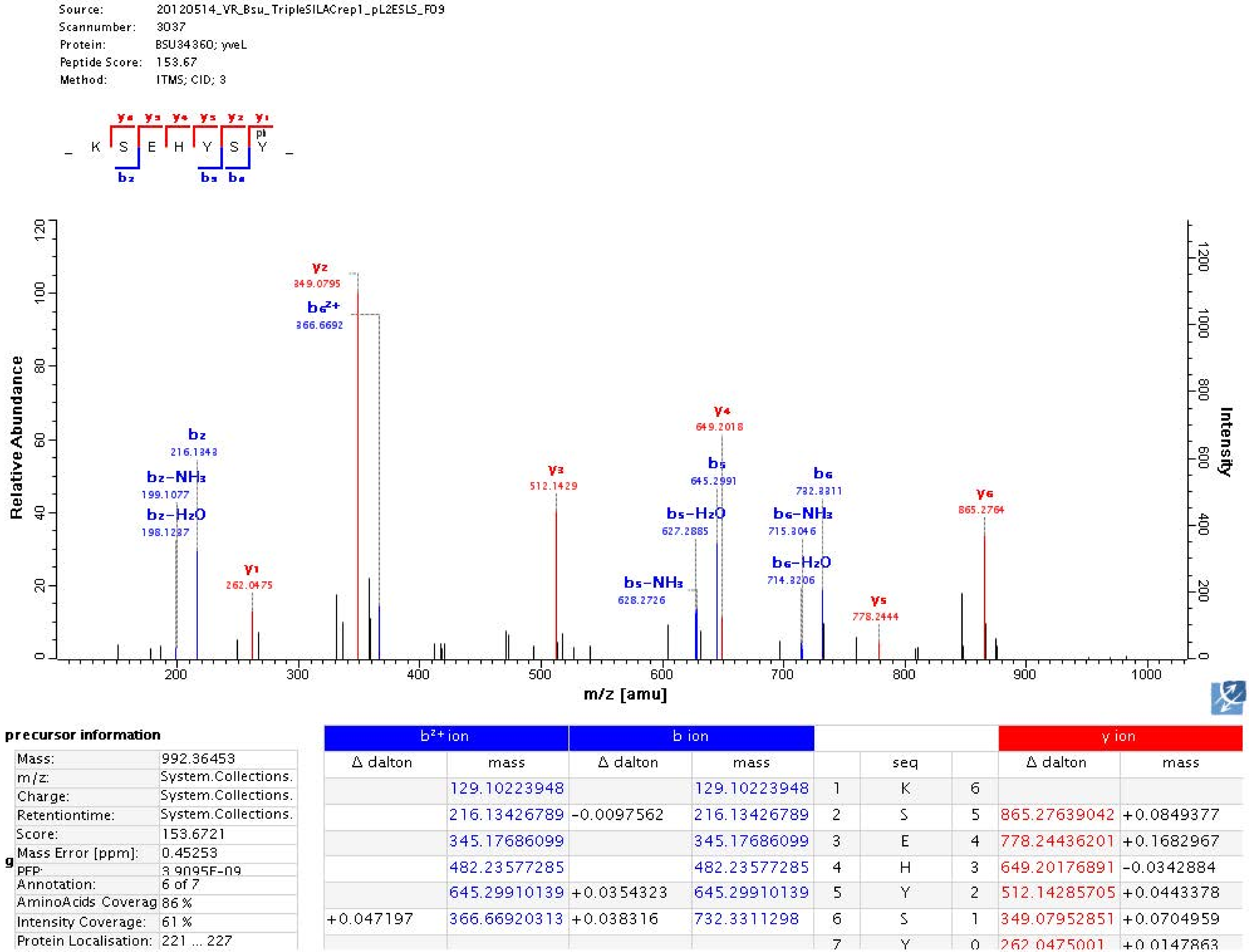


Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F09
Scannumber: 2998
Protein: BSU15590; sat; ylnB
Peptide Score: 160.59
Method: ITMS; CID; 3

precursor information

Mass:	954.44254
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	160.5866
Mass Error [ppm]:	0.22069
PEP:	3.3991E-09
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	71 %
Protein Localisation:	375 ... 382

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	129.102239484	1	K	7		
	257.197202502	2	K	6	827.354640737	-0.021816
-0.2085761	386.239795598	3	E	5	699.25967772	
+0.0876064	515.282388694	4	E	4	570.217084623	
+0.0594147	614.350802611	5	V	3	441.174491527	
-0.0203987	671.372266334	6	G	2	342.106077611	+0.0648513
+0.1337216	770.44068025	7	V	1	285.084613887	+0.2324637
		8	S	0	186.016199971	+0.1183215



Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F09
Scannumber: 3037
Protein: BSU34360; yveL
Peptide Score: 153.67
Method: ITMS; CID; 3

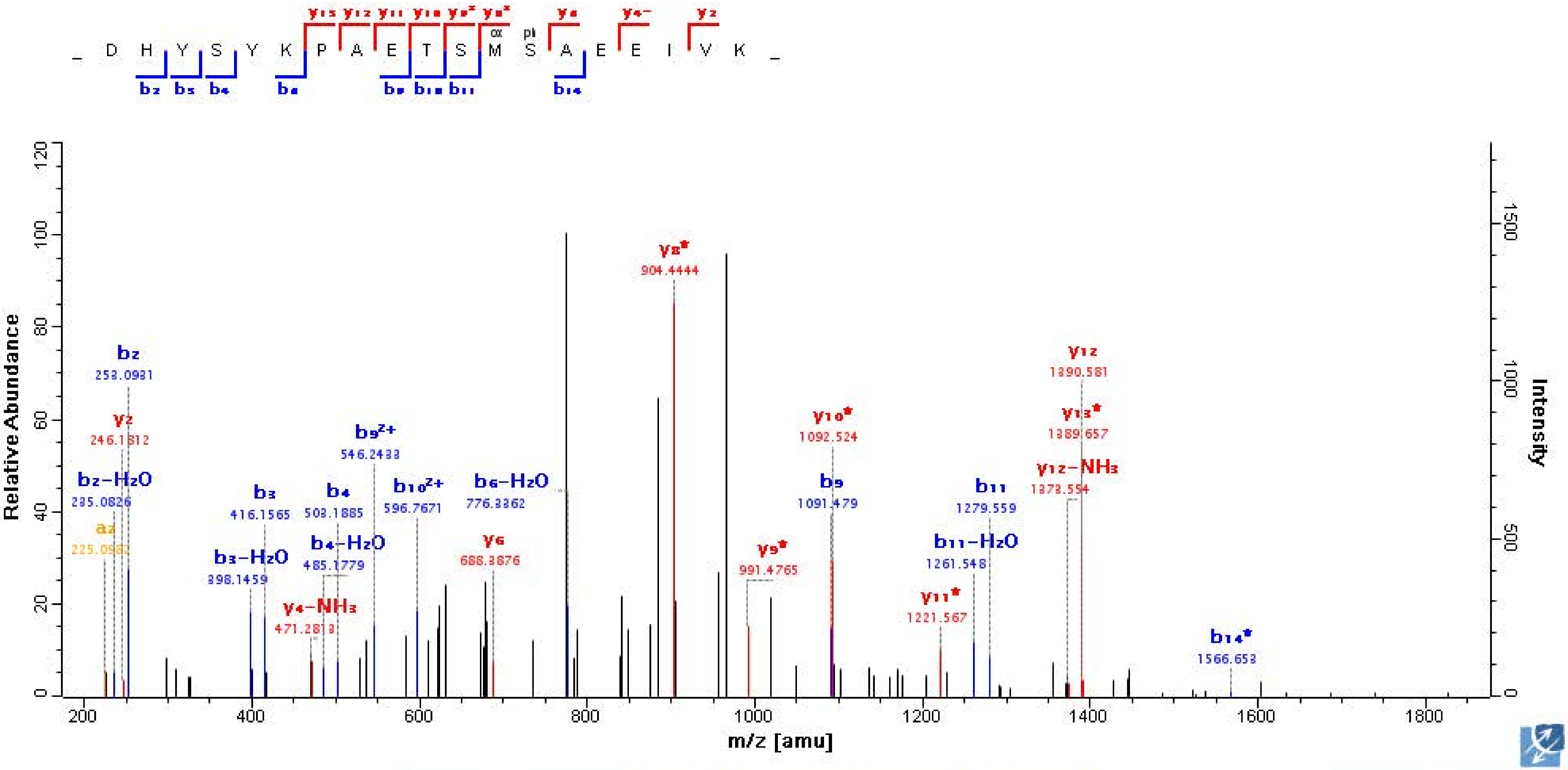
precursor information

g

Mass:	992.36453
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	153.6721
Mass Error [ppm]:	0.45253
PEP:	3.9095E-09
Annotation:	6 of 7
AminoAcids Coverag	86 %
Intensity Coverage:	61 %
Protein Localisation:	221 ... 227

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	129.10223948		129.10223948	1	K	6		
	216.13426789	-0.0097562	216.13426789	2	S	5	865.27639042	+0.0849377
	345.17686099		345.17686099	3	E	4	778.24436201	+0.1682967
	482.23577285		482.23577285	4	H	3	649.20176891	-0.0342884
	645.29910139	+0.0354323	645.29910139	5	Y	2	512.14285705	+0.0443378
+0.047197	366.66920313	+0.038316	732.3311298	6	S	1	349.07952851	+0.0704959
				7	Y	0	262.0475001	+0.0147863

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F09
Scannumber:	8418
Protein:	BSU12410; yjoA
Peptide Score:	85.51
Method:	ITMS; CID; 3



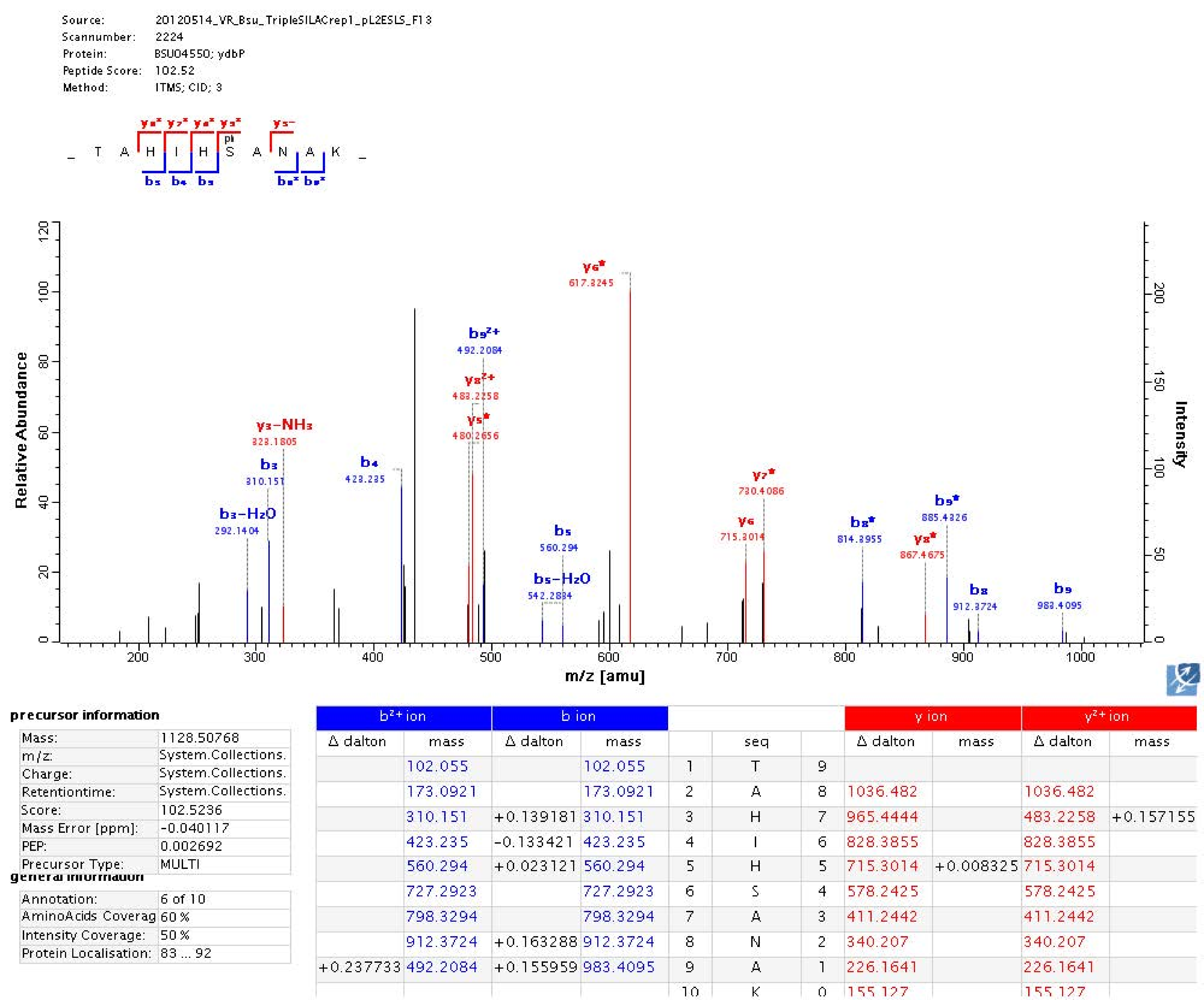
precursor information

Mass:	2279.96542
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	85.50999
Mass Error [ppm]:	-0.14137
PEP:	0.00010125
Precursor Type:	MULTI

general information

Annotation:	13 of 19
AminoAcids Coverag	68 %
Intensity Coverage:	32 %
Protein Localisation:	28 ... 46

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	88.0393		116.0342		116.0342	1	D	18		
+0.17255	225.0982		253.0931	+0.117531	253.0931	2	H	17	2165.946	
	388.1615		416.1565	+0.256016	416.1565	3	Y	16	2028.887	
	475.1936		503.1885	-0.129284	503.1885	4	S	15	1865.824	
	638.2569		666.2518		666.2518	5	Y	14	1778.792	
	766.3519		794.3468		794.3468	6	K	13	1615.728	
	863.4046		891.3995		891.3995	7	P	12	1487.634	
	934.4417		962.4367		962.4367	8	A	11	1390.581	+0.324886
	1063.484	+0.124839	546.2433	+0.084104	1091.479	9	E	10	1319.544	
	1164.532	+0.453539	596.7671		1192.527	10	T	9	1190.501	
	1251.564		1279.559	+0.211428	1279.559	11	S	8	1089.453	
	1398.599		1426.594		1426.594	12	M	7	1002.421	
	1565.598		1593.593		1593.593	13	S	6	855.3859	
	1636.635		1664.63		1664.63	14	A	5	688.3876	+0.11547
	1765.678		1793.672		1793.672	15	E	4	617.3505	
	1894.72		1922.715		1922.715	16	E	3	488.3079	
	2007.804		2035.799		2035.799	17	I	2	359.2653	
	2106.873		2134.867		2134.867	18	V	1	246.1812	+0.187358
						19	K	0	147.1128	



Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F13
Scannumber: 2224
Protein: BSU04550; ydbP
Peptide Score: 102.52
Method: ITMS; CID; 3

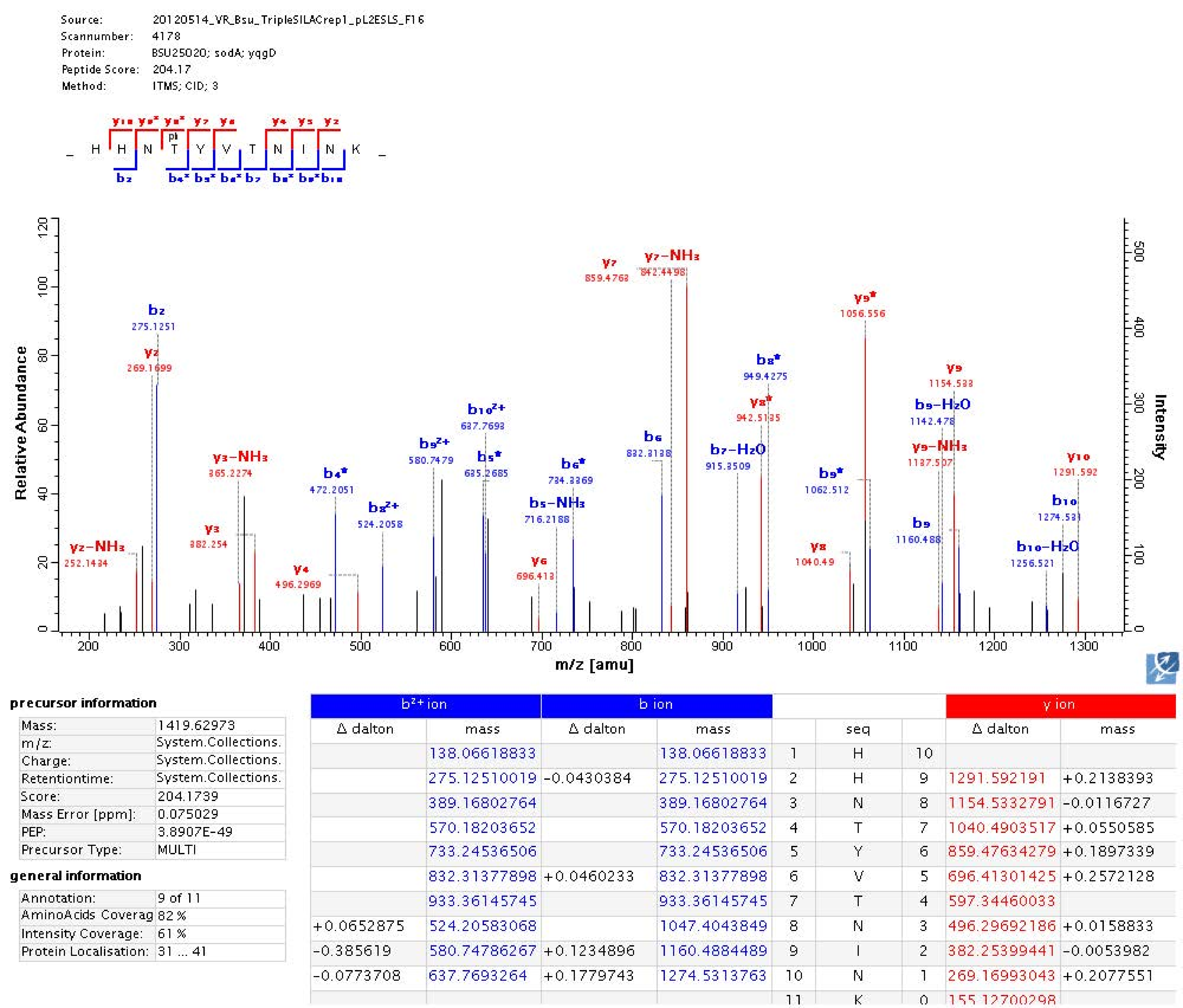
precursor information

Mass:	1128.50768
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	102.5236
Mass Error [ppm]:	-0.040117
PEP:	0.002692
Precursor Type:	MULTI

general information

Annotation:	6 of 10
AminoAcids Coverag	60 %
Intensity Coverage:	50 %
Protein Localisation:	83 ... 92

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055		102.055	1	T	9				
	173.0921		173.0921	2	A	8	1036.482		1036.482	
	310.151	+0.139181	310.151	3	H	7	965.4444		483.2258	+0.157155
	423.235	-0.133421	423.235	4	I	6	828.3855		828.3855	
	560.294	+0.023121	560.294	5	H	5	715.3014	+0.008325	715.3014	
	727.2923		727.2923	6	S	4	578.2425		578.2425	
	798.3294		798.3294	7	A	3	411.2442		411.2442	
	912.3724	+0.163288	912.3724	8	N	2	340.207		340.207	
+0.237733	492.2084	+0.155959	983.4095	9	A	1	226.1641		226.1641	
				10	K	0	155.127		155.127	



Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F16
Scannumber:	4178
Protein:	BSU25020; sodA; yqgD
Peptide Score:	204.17
Method:	ITMS; CID; 3

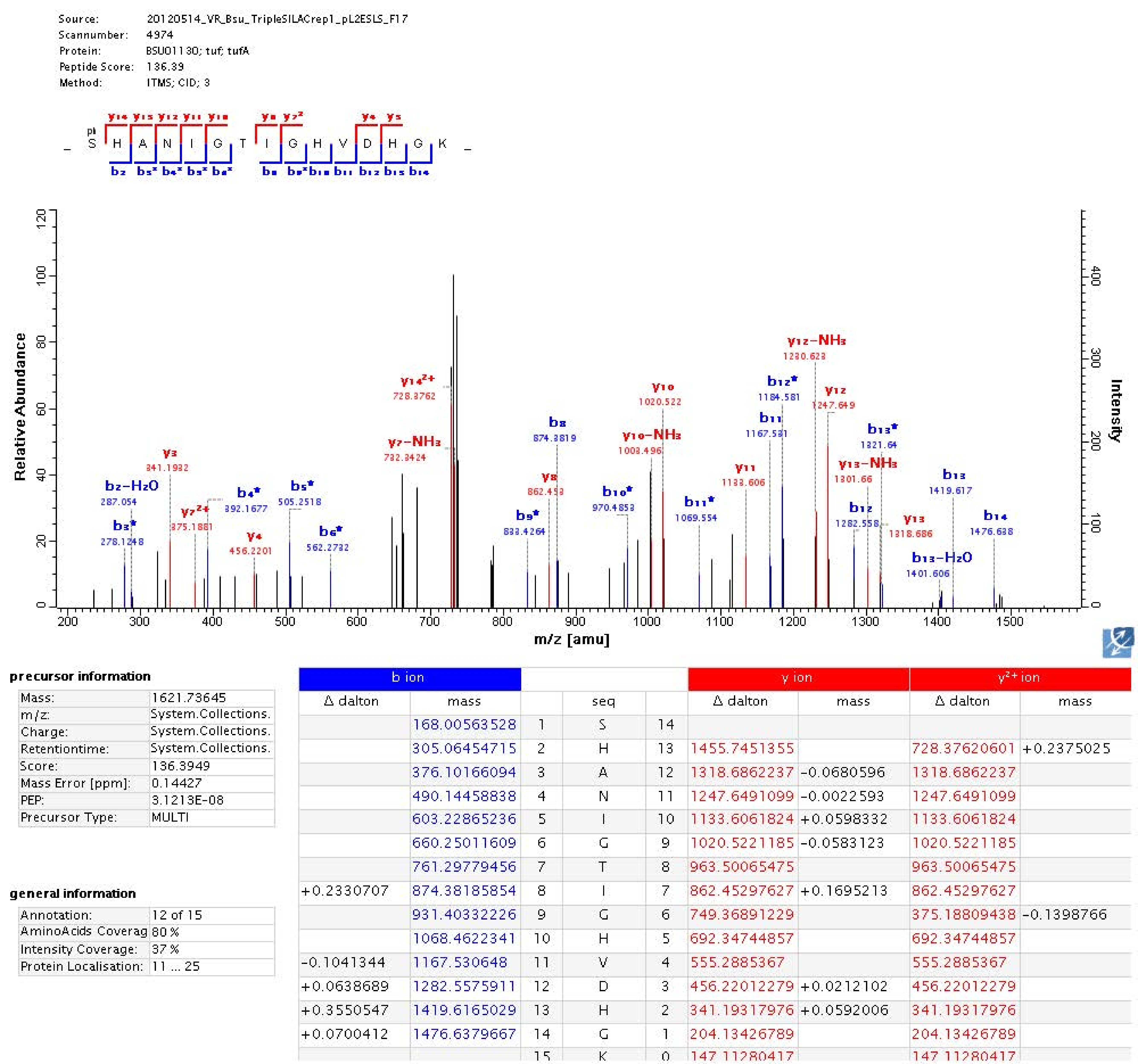
precursor information

Mass:	1419.62973
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	204.1739
Mass Error [ppm]:	0.075029
PEP:	3.8907E-49
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	61 %
Protein Localisation:	31 ... 41

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	138.06618833		138.06618833	1	H	10		
	275.12510019	-0.0430384	275.12510019	2	H	9	1291.592191	+0.2138393
	389.16802764		389.16802764	3	N	8	1154.5332791	-0.0116727
	570.18203652		570.18203652	4	T	7	1040.4903517	+0.0550585
	733.24536506		733.24536506	5	Y	6	859.47634279	+0.1897339
	832.31377898	+0.0460233	832.31377898	6	V	5	696.41301425	+0.2572128
	933.36145745		933.36145745	7	T	4	597.34460033	
+0.0652875	524.20583068		1047.4043849	8	N	3	496.29692186	+0.0158833
-0.385619	580.74786267	+0.1234896	1160.4884489	9	I	2	382.25399441	-0.0053982
-0.0773708	637.7693264	+0.1779743	1274.5313763	10	N	1	269.16993043	+0.2077551
				11	K	0	155.12700298	



Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F17
Scannumber: 4974
Protein: BSU01130; tuf; tufA
Peptide Score: 136.39
Method: ITMS; CID; 3

precursor information

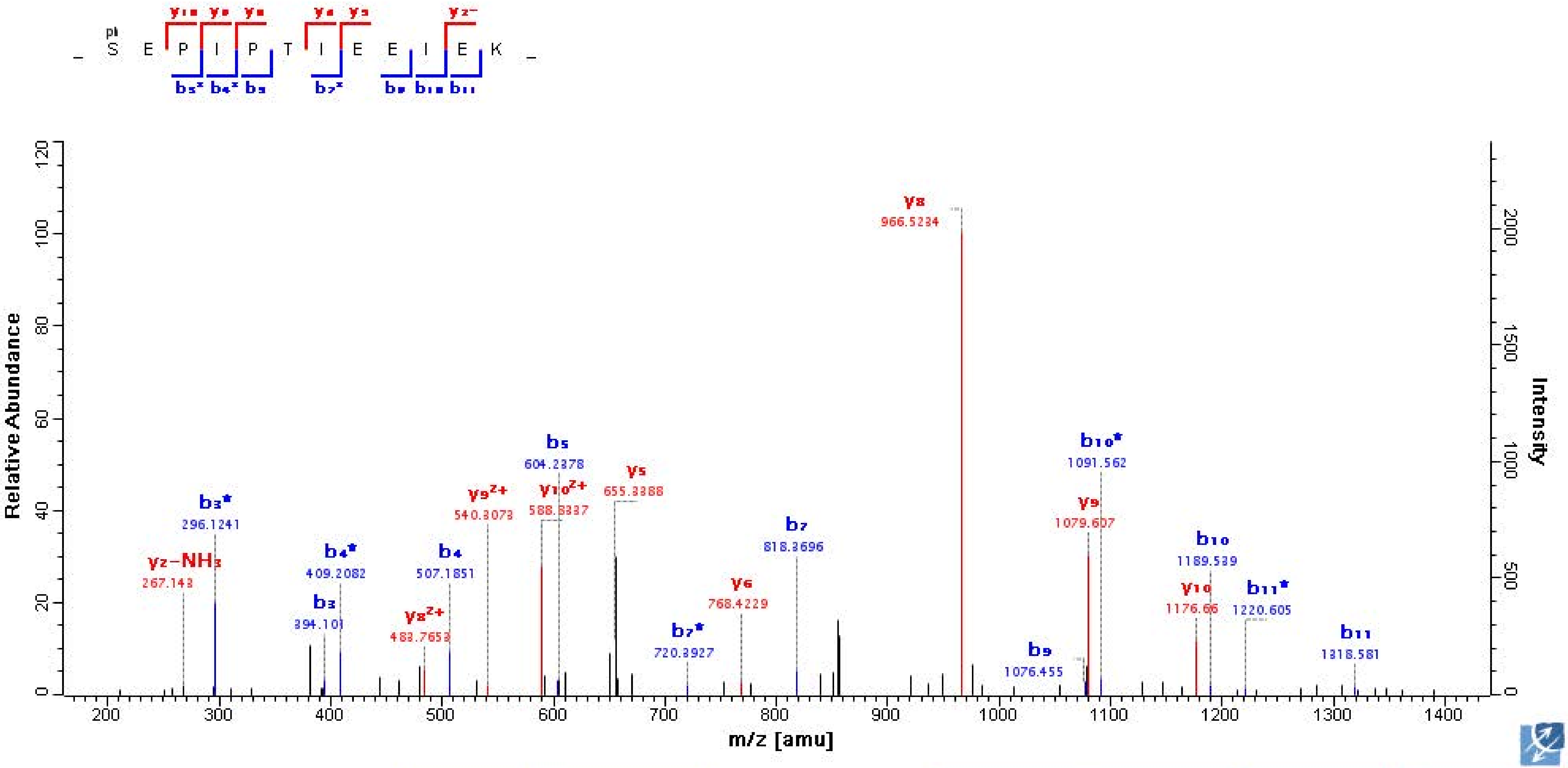
Mass:	1621.73645
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	136.3949
Mass Error [ppm]:	0.14427
PEP:	3.1213E-08
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	37 %
Protein Localisation:	11 ... 25

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.00563528	1	S	14				
	305.06454715	2	H	13	1455.7451355		728.37620601	+0.2375025
	376.10166094	3	A	12	1318.6862237	-0.0680596	1318.6862237	
	490.14458838	4	N	11	1247.6491099	-0.0022593	1247.6491099	
	603.22865236	5	I	10	1133.6061824	+0.0598332	1133.6061824	
	660.25011609	6	G	9	1020.5221185	-0.0583123	1020.5221185	
	761.29779456	7	T	8	963.50065475		963.50065475	
+0.2330707	874.38185854	8	I	7	862.45297627	+0.1695213	862.45297627	
	931.40332226	9	G	6	749.36891229		375.18809438	-0.1398766
	1068.4622341	10	H	5	692.34744857		692.34744857	
-0.1041344	1167.530648	11	V	4	555.2885367		555.2885367	
+0.0638689	1282.5575911	12	D	3	456.22012279	+0.0212102	456.22012279	
+0.3550547	1419.6165029	13	H	2	341.19317976	+0.0592006	341.19317976	
+0.0700412	1476.6379667	14	G	1	204.13426789		204.13426789	
		15	K	0	147.11280417		147.11280417	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F19
Scannumber:	11196
Protein:	BSU20420; yorD
Peptide Score:	123.95
Method:	ITMS; CID; 3



precursor information

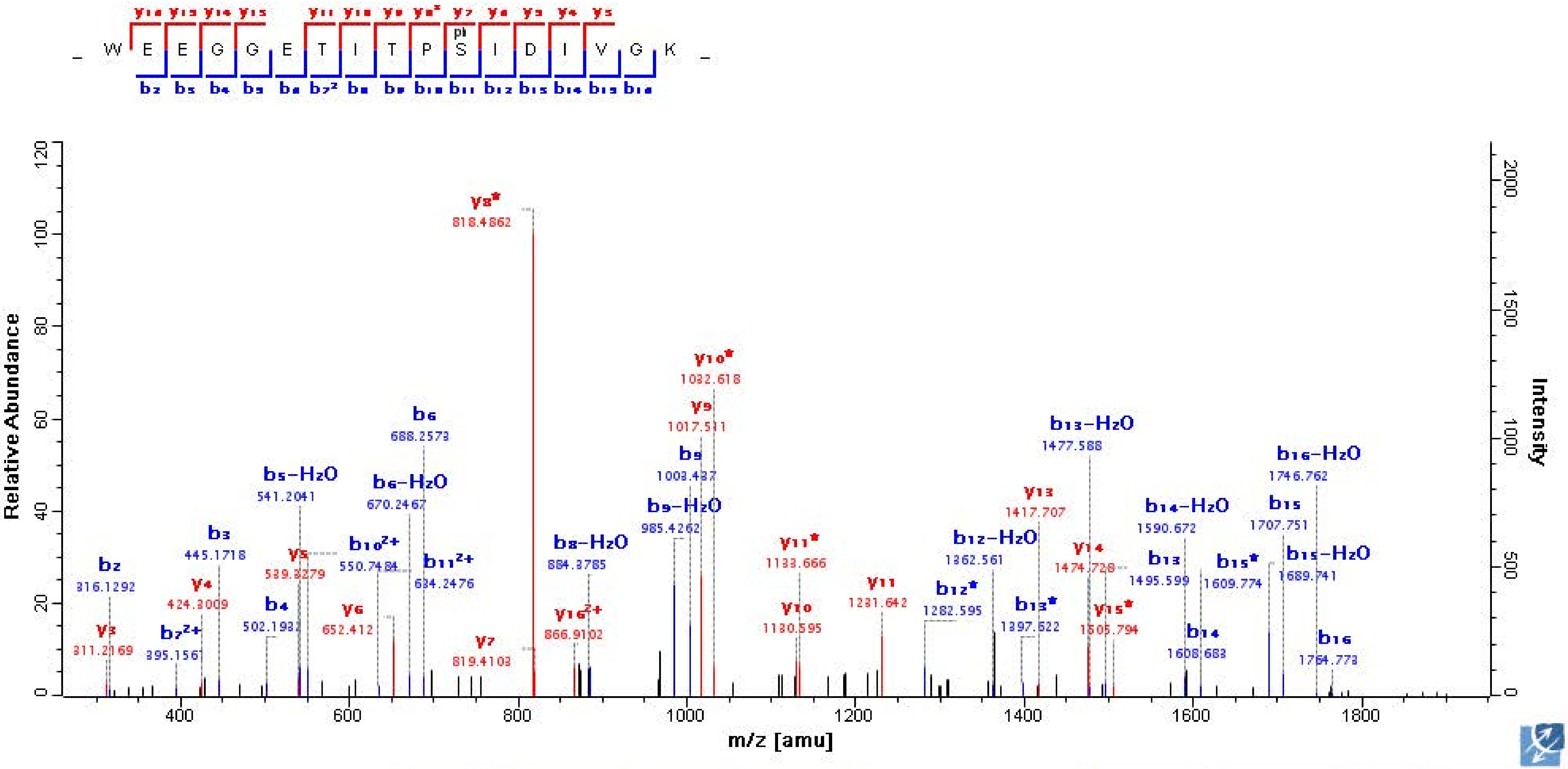
Mass:	1463.67947
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	123.9483
Mass Error [ppm]:	-0.12948
PEP:	6.6552E-08
Precursor Type:	MULTI

general information

Annotation:	8 of 12
AminoAcids Coverag	67 %
Intensity Coverage:	57 %
Protein Localisation:	54 ... 65

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.00563528	1	S	11				
	297.04822838	2	E	10	1305.7027735		1305.7027735	
+0.300436	394.10099223	3	P	9	1176.6601804	+0.0588137	588.83372843	-0.0894047
+0.0466332	507.18505621	4	I	8	1079.6074165	+0.1604057	540.3073465	+0.181362
-0.2934231	604.23782007	5	P	7	966.52335256	-0.1221685	483.76531451	+0.1350151
	705.28549854	6	T	6	869.47058871		869.47058871	
-0.0064644	818.36956252	7	I	5	768.42291023	+0.1256127	768.42291023	
	947.41215562	8	E	4	655.33884625	+0.1956996	655.33884625	
+0.3899779	1076.4547487	9	E	3	526.29625316		526.29625316	
-0.0266057	1189.5388127	10	I	2	397.25366006		397.25366006	
-0.0903169	1318.5814058	11	E	1	284.16959608		284.16959608	
		12	K	0	155.12700298		155.12700298	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F19
Scannumber:	12102
Protein:	ahpC; BSU40090
Peptide Score:	207.79
Method:	ITMS; CID; 3



precursor information

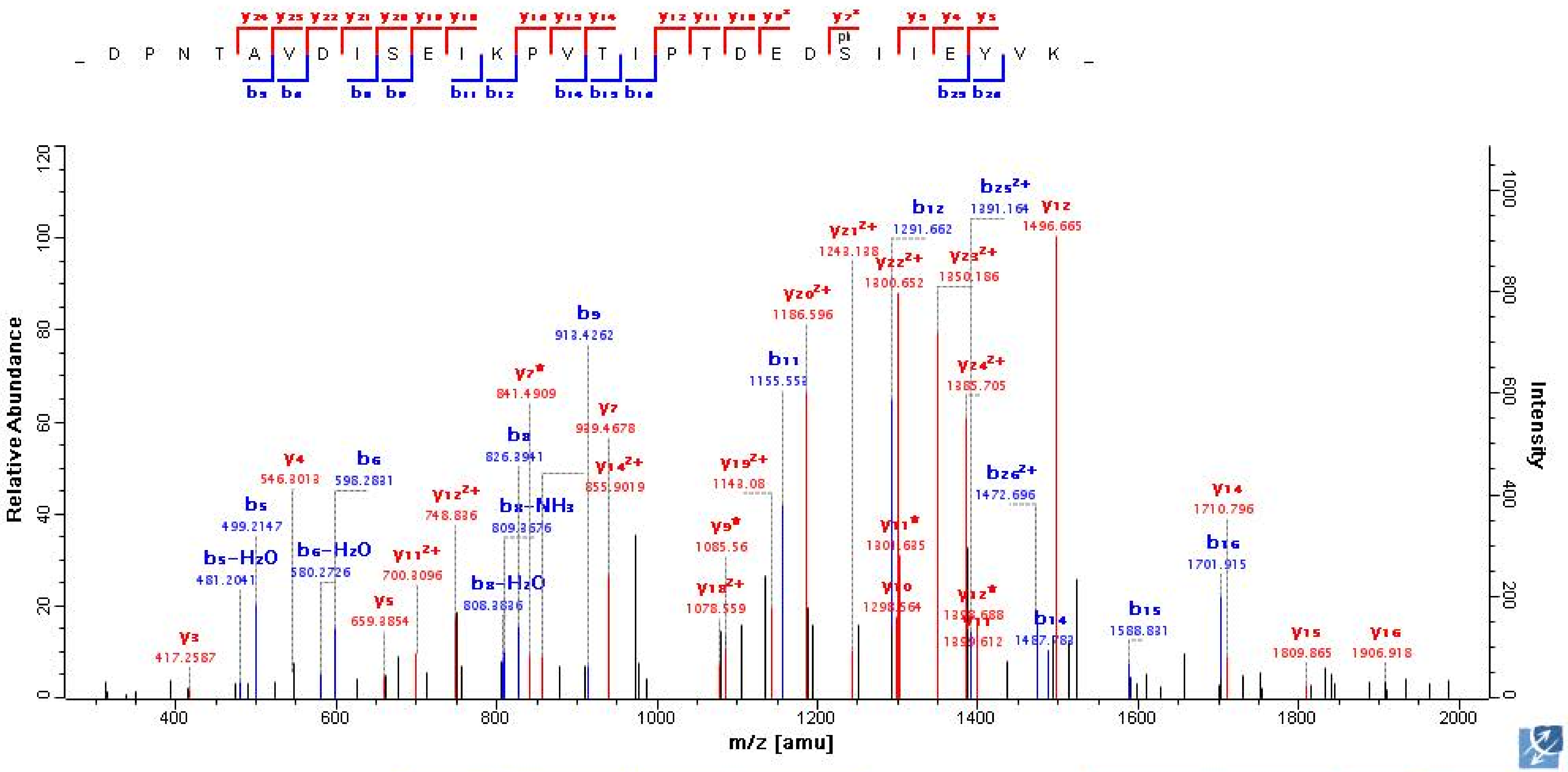
Mass:	1917.88584
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	207.7904
Mass Error [ppm]:	0.31165
PEP:	3.4131E-107
Precursor Type:	ISO

general information

Annotation:	15 of 17
AminoAcids Coverag	88 %
Intensity Coverage:	63 %
Protein Localisation:	170 ... 186

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	187.0866		187.0866	1	W	16				
	316.1292	-0.101289	316.1292	2	E	15	1732.813		866.9102	-0.395835
	445.1718	+0.071999	445.1718	3	E	14	1603.771		1603.771	
	502.1932	-0.287478	502.1932	4	G	13	1474.728	+0.0005	1474.728	
	559.2147		559.2147	5	G	12	1417.707	+0.105093	1417.707	
	688.2573	+0.232023	688.2573	6	E	11	1360.685		1360.685	
+0.107485	395.1561		789.305	7	T	10	1231.642	-0.011758	1231.642	
	902.389		902.389	8	I	9	1130.595	+0.065095	1130.595	
	1003.437	+0.028371	1003.437	9	T	8	1017.511	+0.223561	1017.511	
+0.478184	550.7484		1100.489	10	P	7	916.4631		916.4631	
+0.286805	634.2476		1267.488	11	S	6	819.4103	-0.024141	819.4103	
	1380.572		1380.572	12	I	5	652.412	-0.038111	652.412	
	1495.599	+0.146637	1495.599	13	D	4	539.3279	+0.088555	539.3279	
	1608.683	-0.076343	1608.683	14	I	3	424.3009	-0.079631	424.3009	
	1707.751	+0.042254	1707.751	15	V	2	311.2169	-0.010826	311.2169	
	1764.773	-0.135948	1764.773	16	G	1	212.1485		212.1485	
				17	K	0	155.127		155.127	

Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F19
Scannumber: 14285
Protein: BSU32250; thrC
Peptide Score: 140.42
Method: ITMS; CID; 3



precursor information

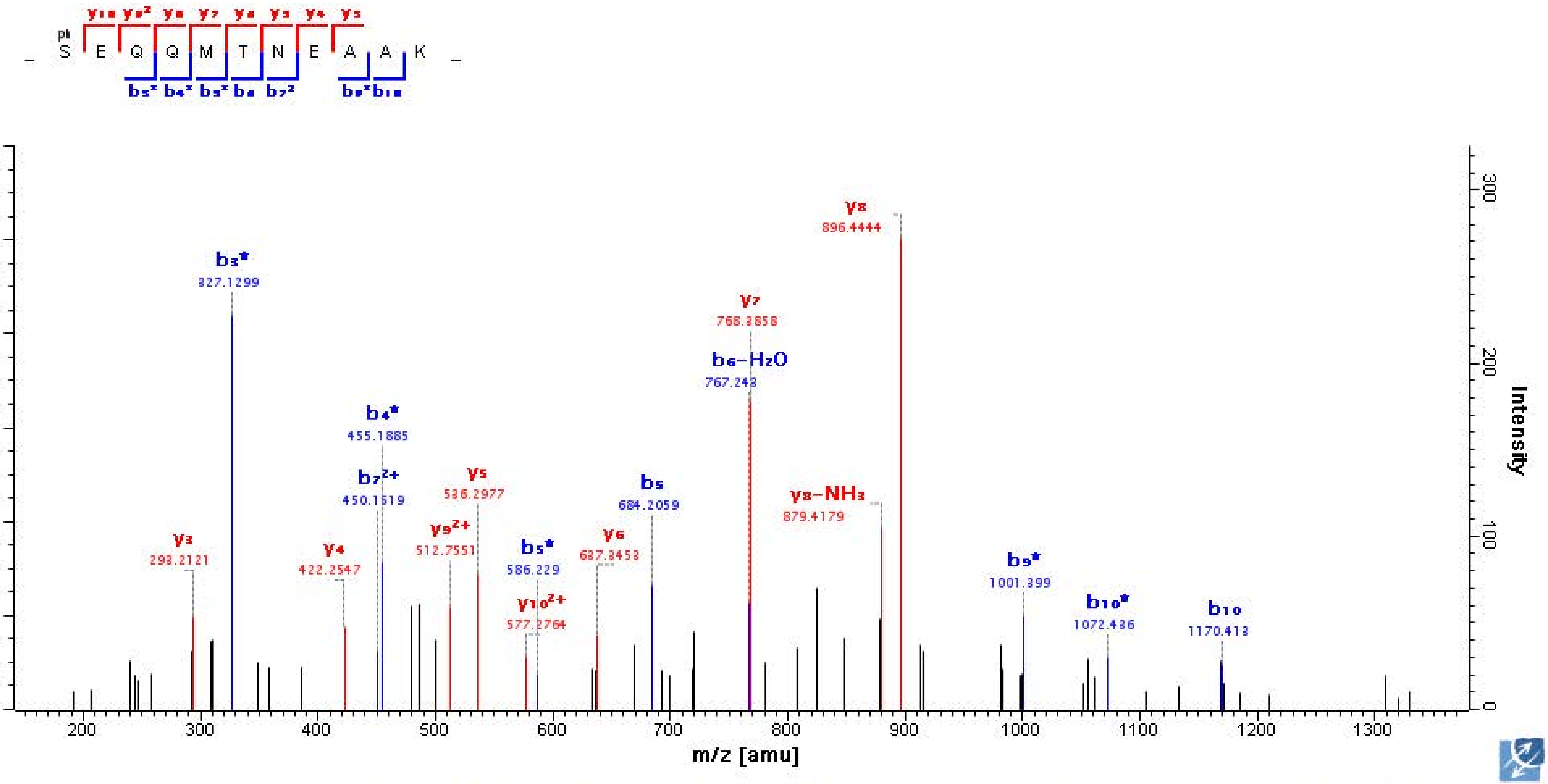
Mass:	3180.5366
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	140.4163
Mass Error [ppm]:	-0.027215
PEP:	4.2353E-25
Precursor Type:	MULTI

general information

Annotation:	20 of 28
AminoAcids Coverag	71 %
Intensity Coverage:	64 %
Protein Localisation:	320 ... 347

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342		116.0342	1	D	27				
	213.087		213.087	2	P	26	3082.545		3082.545	
	327.1299		327.1299	3	N	25	2985.493		2985.493	
	428.1776		428.1776	4	T	24	2871.45		2871.45	
	499.2147	+0.073749	499.2147	5	A	23	2770.402		1385.705	+0.097705
	598.2831	+0.139124	598.2831	6	V	22	2699.365		1350.186	+0.229055
	713.3101		713.3101	7	D	21	2600.297		1300.652	+0.389117
	826.3941	+0.073649	826.3941	8	I	20	2485.27		1243.138	+0.03418
	913.4262	+0.210078	913.4262	9	S	19	2372.186		1186.596	+0.086344
	1042.469		1042.469	10	E	18	2285.153		1143.08	+0.199892
	1155.553	+0.005662	1155.553	11	I	17	2156.111		1078.559	-0.163455
	1291.662	+0.013322	1291.662	12	K	16	2043.027		2043.027	
	1388.715		1388.715	13	P	15	1906.918	+0.117733	1906.918	
	1487.783	+0.193413	1487.783	14	V	14	1809.865	+0.269985	1809.865	
	1588.831	+0.175398	1588.831	15	T	13	1710.796	+0.096455	855.9019	+0.475803
	1701.915	+0.218165	1701.915	16	I	12	1609.749		1609.749	
	1798.968		1798.968	17	P	11	1496.665	+0.055346	748.836	+0.012987
	1900.015		1900.015	18	T	10	1399.612	+0.131425	700.3096	-0.308104
	2015.042		2015.042	19	D	9	1298.564	+0.191067	1298.564	
	2144.085		2144.085	20	E	8	1183.537		1183.537	
	2259.112		2259.112	21	D	7	1054.495		1054.495	
	2426.11		2426.11	22	S	6	939.4678	+0.024484	939.4678	
	2539.194		2539.194	23	I	5	772.4695		772.4695	
	2652.278		2652.278	24	I	4	659.3854	+0.166722	659.3854	
+0.191018	1391.164		2781.321	25	E	3	546.3013	+0.164238	546.3013	
+0.290945	1472.696		2944.384	26	Y	2	417.2587	+0.215132	417.2587	
	3043.453		3043.453	27	V	1	254.1954		254.1954	
				28	K	0	155.127		155.127	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F19
Scannumber:	4333
Protein:	BSU37670; ipa-87r; ywfI
Peptide Score:	121.08
Method:	ITMS; CID; 3



precursor information

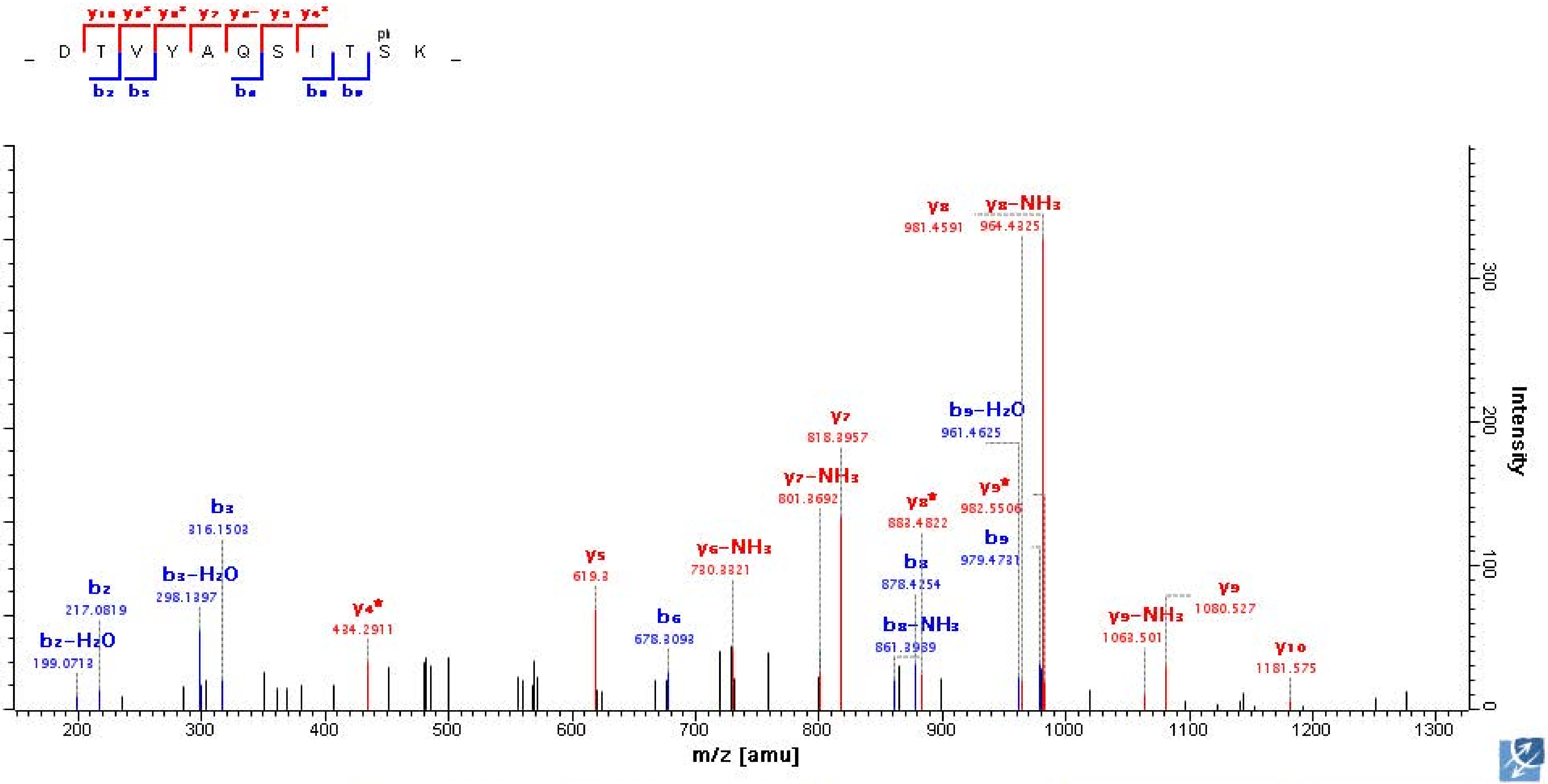
Mass:	1315.51144
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	121.076
Mass Error [ppm]:	-0.083049
PEP:	3.5208E-06
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	53 %
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
	168.0056		168.0056	1	S	10				
	297.0482		297.0482	2	E	9	1153.546		577.2764	-0.092647
	425.1068		425.1068	3	Q	8	1024.503		512.7551	+0.02771
	553.1654		553.1654	4	Q	7	896.4444	+0.084897	896.4444	
	684.2059	+0.146488	684.2059	5	M	6	768.3858	+0.086834	768.3858	
	785.2535		785.2535	6	T	5	637.3453	+0.227538	637.3453	
+0.190532	450.1519		899.2965	7	N	4	536.2977	+0.033701	536.2977	
	1028.339		1028.339	8	E	3	422.2547	+0.106901	422.2547	
	1099.376		1099.376	9	A	2	293.2121	+0.075764	293.2121	
	1170.413	+0.106725	1170.413	10	A	1	222.175		222.175	
				11	K	0	151.1379		151.1379	

Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F19
Scannumber: 7148
Protein: BSU13180; metC; metE
Peptide Score: 109.72
Method: ITMS; CID; 3



precursor information

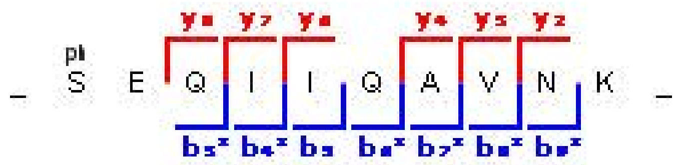
Mass:	1291.56974
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	109.7213
Mass Error [ppm]:	0.021581
PEP:	4.5736E-05
Precursor Type:	MULTI

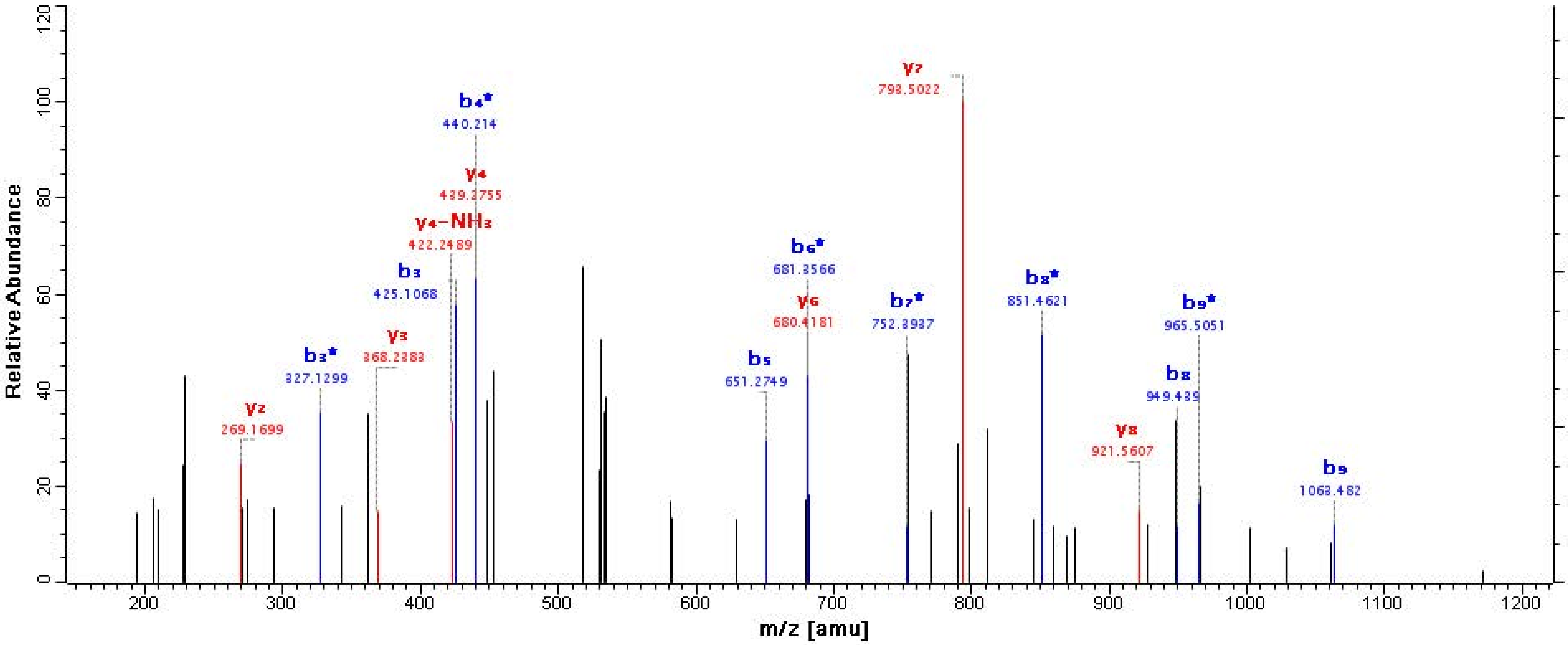
general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	53 %
Protein Localisation:	540 ... 550

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	116.034219499	1	D	10		
+0.1420095	217.081897973	2	T	9	1181.575153065	-0.1761052
+0.1353021	316.150311889	3	V	8	1080.527474591	+0.240958
	479.213640427	4	Y	7	981.459060674	+0.0065765
	550.250754215	5	A	6	818.395732136	+0.1153763
+0.1882879	678.309331726	6	Q	5	747.358618348	
	765.341360136	7	S	4	619.300040837	+0.0957722
+0.0631013	878.425424117	8	I	3	532.268012427	
-0.098774	979.473102591	9	T	2	419.183948447	
	1146.471461409	10	S	1	318.136269973	
		11	K	0	151.137911154	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F19
Scannumber:	7753
Protein:	BSU30650; dps; ytkB
Peptide Score:	87.67
Method:	ITMS; CID; 3





precursor information

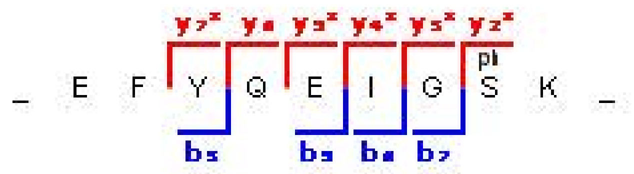
Mass:	1208.57958
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	87.66729
Mass Error [ppm]:	-0.52741
PEP:	0.0081312
Precursor Type:	MULTI

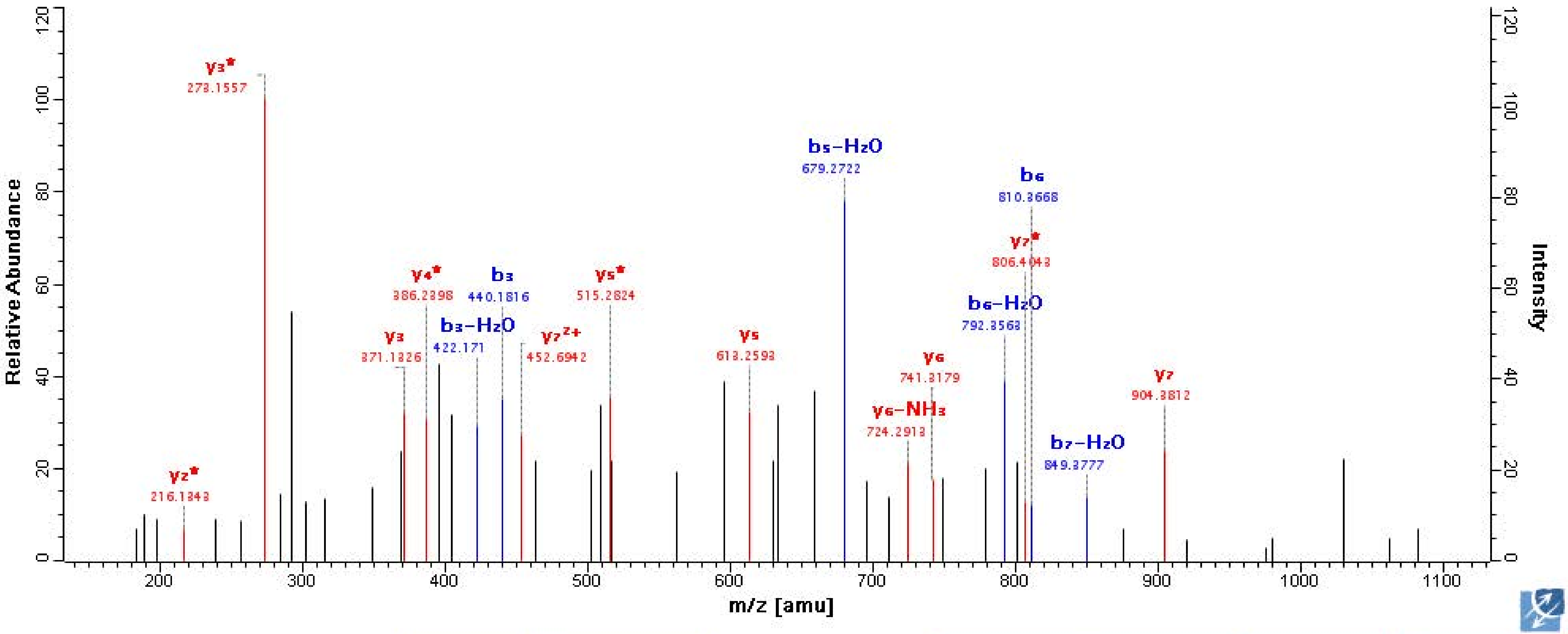
general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	40 %
Protein Localisation:	2 ... 11

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	168.005635285	1	S	9		
	297.048228381	2	E	8	1050.603334215	
+0.1818904	425.106805892	3	Q	7	921.560741119	+0.312794
	538.190869873	4	I	6	793.502163607	+0.1033662
+0.0509939	651.274933853	5	I	5	680.418099627	+0.0284946
	779.333511365	6	Q	4	567.334035646	
	850.370625152	7	A	3	439.275458135	+0.0433895
+0.0490591	949.439039069	8	V	2	368.238344347	+0.2047099
-0.1169763	1063.481966516	9	N	1	269.169930431	+0.1797095
		10	K	0	155.127002984	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F19
Scannumber:	7858
Protein:	BSU04400; gsiB
Peptide Score:	89.08
Method:	ITMS; CID; 3



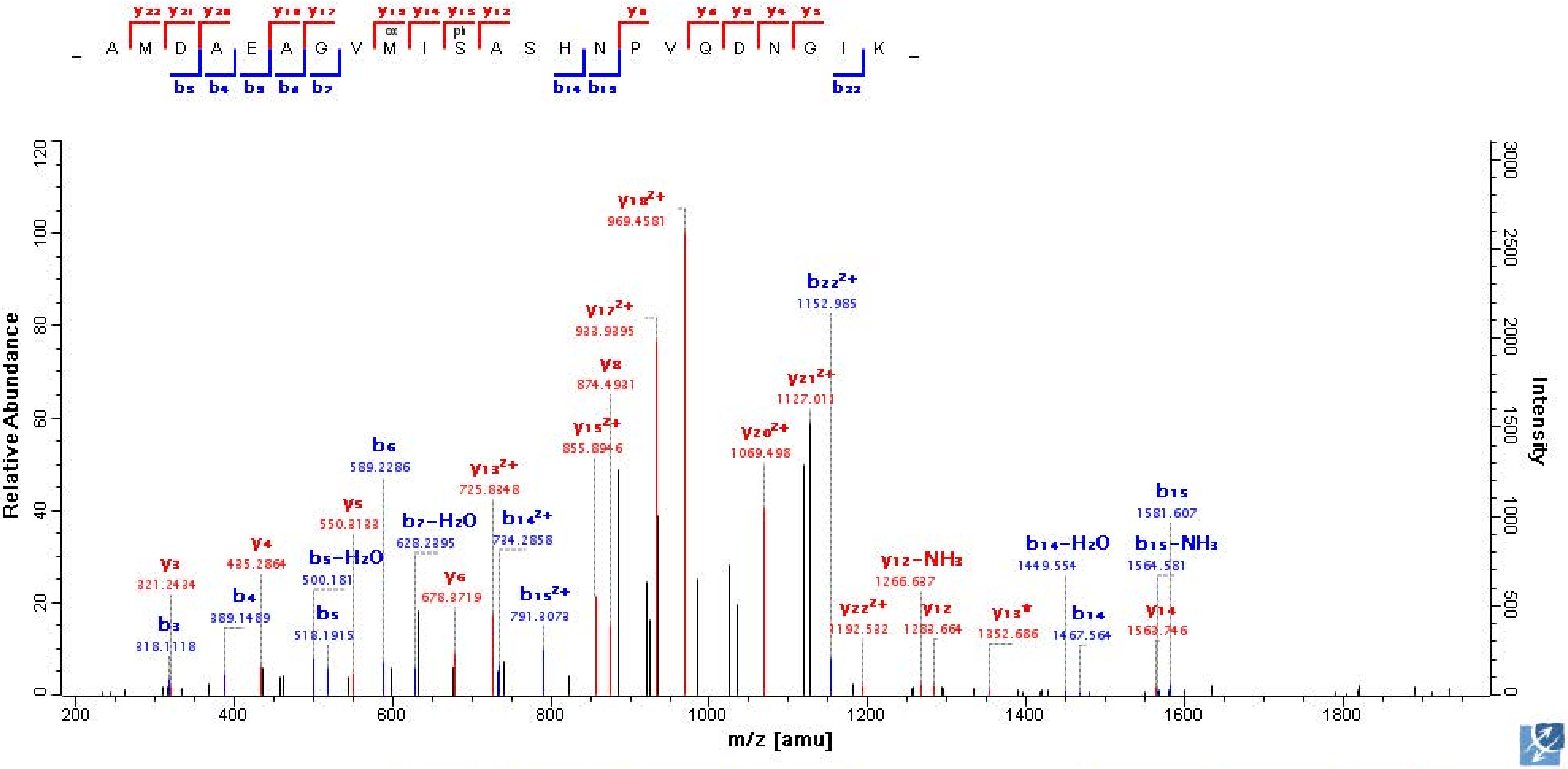


precursor information

Mass:	1179.4856
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	89.07951
Mass Error [ppm]:	0.57952
PEP:	0.010754
Precursor Type:	MULTI
Annotation:	6 of 9
AminoAcids Coverag	67 %
Intensity Coverage:	46 %
Protein Localisation:	107 ... 115

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.04986956	1	E	8				
	277.11828348	2	F	7	1051.4496038		1051.4496038	
+0.1474285	440.18161202	3	Y	6	904.38118984	+0.1888785	452.69423315	+0.2702444
	568.24018953	4	Q	5	741.3178613	+0.2836402	741.3178613	
	697.28278262	5	E	4	613.25928379	+0.3308041	613.25928379	
-0.0454965	810.36684661	6	I	3	484.21669069		484.21669069	
	867.38831033	7	G	2	371.13262671	-0.0837376	371.13262671	
	1034.3866691	8	S	1	314.11116299		314.11116299	
		9	K	0	147.11280417		147.11280417	

Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F19
Scannumber: 9799
Protein: BSU01770; glmM; ybbT
Peptide Score: 147.17
Method: ITMS; CID; 3



precursor information

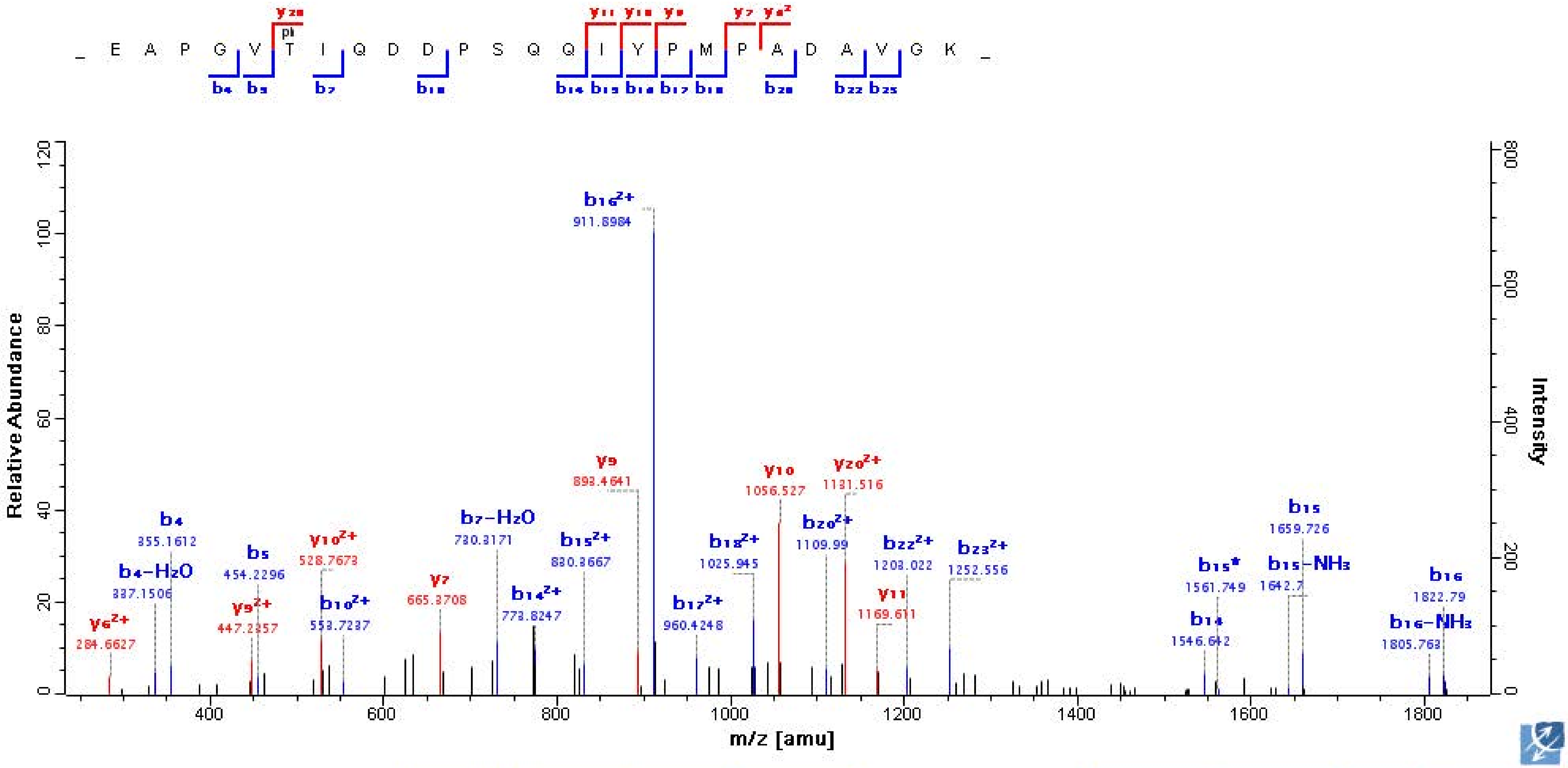
Mass:	2450.06073
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	147.1689
Mass Error [ppm]:	0.0014625
PEP:	9.3059E-28
Precursor Type:	MULTI

general information

Annotation:	19 of 23
AminoAcids Coverag	83 %
Intensity Coverage:	48 %
Protein Localisation:	88 ... 110

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439		72.04439	1	A	22				
	203.0849		203.0849	2	M	21	2384.056		1192.532	+0.099224
	318.1118	-0.091524	318.1118	3	D	20	2253.016		1127.011	-0.076334
	389.1489	-0.127142	389.1489	4	A	19	2137.989		1069.498	+0.328861
	518.1915	+0.100101	518.1915	5	E	18	2066.951		2066.951	
	589.2286	+0.023559	589.2286	6	A	17	1937.909		969.4581	+0.318848
	646.2501		646.2501	7	G	16	1866.872		933.9395	-0.035397
	745.3185		745.3185	8	V	15	1809.85		1809.85	
	892.3539		892.3539	9	M	14	1710.782		855.8946	+0.194966
	1005.438		1005.438	10	I	13	1563.746	+0.107779	1563.746	
	1172.436		1172.436	11	S	12	1450.662		725.8348	+0.184813
	1243.473		1243.473	12	A	11	1283.664	+0.223039	1283.664	
	1330.505		1330.505	13	S	10	1212.627		1212.627	
-0.382575	734.2858	-0.032044	1467.564	14	H	9	1125.595		1125.595	
-0.034044	791.3073	+0.260112	1581.607	15	N	8	988.536		988.536	
	1678.66		1678.66	16	P	7	874.4931	+0.087075	874.4931	
	1777.728		1777.728	17	V	6	777.4403		777.4403	
	1905.787		1905.787	18	Q	5	678.3719	+0.148621	678.3719	
	2020.814		2020.814	19	D	4	550.3133	-0.215836	550.3133	
	2134.857		2134.857	20	N	3	435.2864	+0.088267	435.2864	
	2191.878		2191.878	21	G	2	321.2434	-0.2276	321.2434	
+0.000599	1152.985		2304.962	22	I	1	264.222		264.222	
				23	K	0	151.1379		151.1379	

Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F20
Scannumber: 11003
Protein: asd; BSU16750
Peptide Score: 128.14
Method: ITMS; CID; 3



precursor information

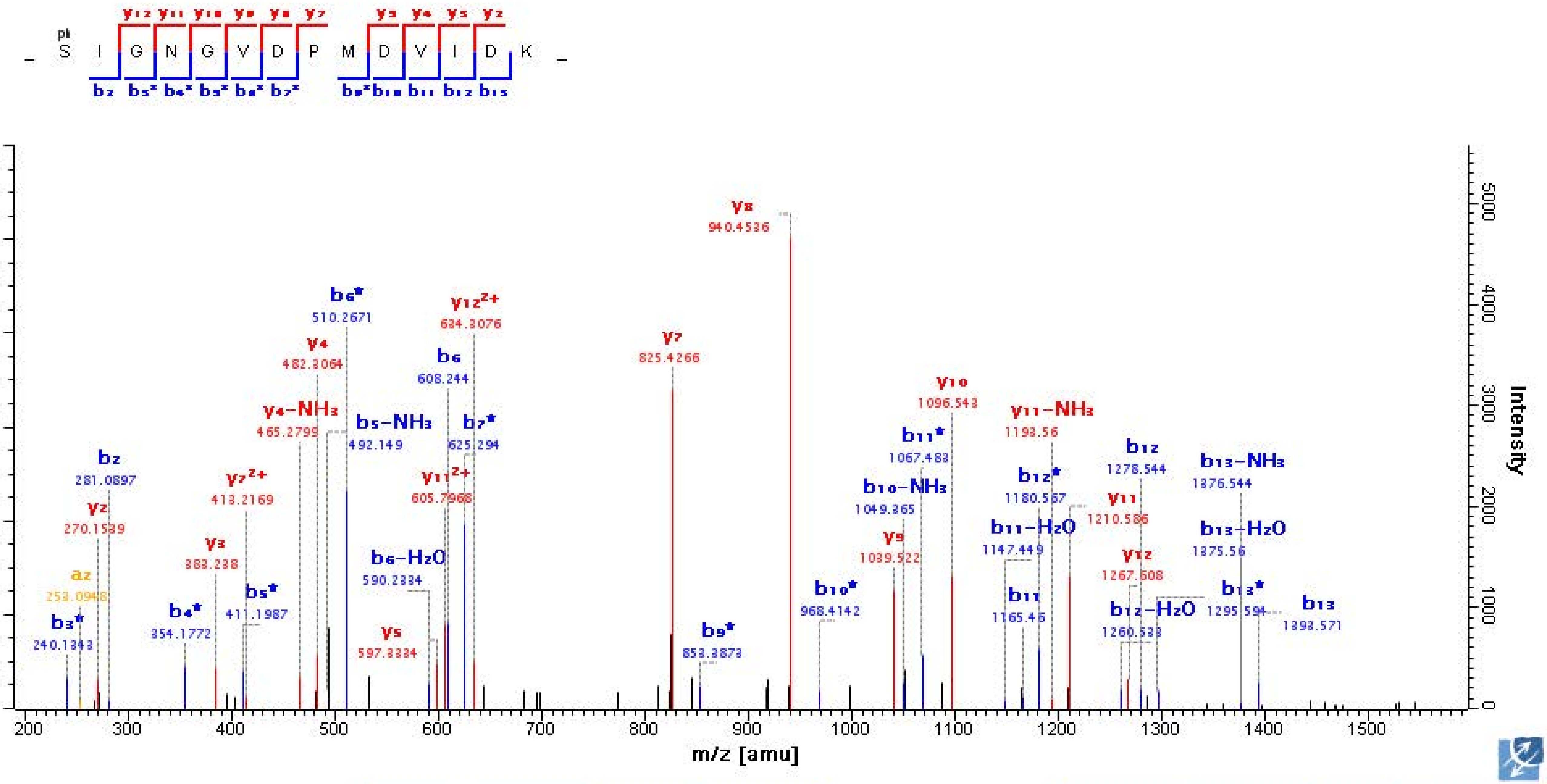
Mass:	2706.22512
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	128.1398
Mass Error [ppm]:	0.11445
PEP:	4.863E-18
Precursor Type:	MULTI

general information

Annotation:	15 of 25
AminoAcids Coverag	60 %
Intensity Coverage:	58 %
Protein Localisation:	274 ... 298

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499		130.0499	1	E	24				
	201.087		201.087	2	A	23	2586.204		2586.204	
	298.1397		298.1397	3	P	22	2515.167		2515.167	
	355.1612	+0.09355	355.1612	4	G	21	2418.114		2418.114	
	454.2296	+0.167531	454.2296	5	V	20	2361.092		2361.092	
	635.2436		635.2436	6	T	19	2262.024		1131.516	+0.266496
	748.3277		748.3277	7	I	18	2081.01		2081.01	
	876.3863		876.3863	8	Q	17	1967.926		1967.926	
	991.4132		991.4132	9	D	16	1839.867		1839.867	
+0.042028	553.7237		1106.44	10	D	15	1724.84		1724.84	
	1203.493		1203.493	11	P	14	1609.813		1609.813	
	1290.525		1290.525	12	S	13	1512.761		1512.761	
	1418.584		1418.584	13	Q	12	1425.729		1425.729	
-0.056199	773.8247	-0.006	1546.642	14	Q	11	1297.67		1297.67	
+0.314977	830.3667	-0.098487	1659.726	15	I	10	1169.611	-0.352057	1169.611	
+0.165149	911.8984	+0.055958	1822.79	16	Y	9	1056.527	-0.175952	528.7673	+0.039795
+0.003208	960.4248		1919.842	17	P	8	893.4641	-0.012281	447.2357	-0.009169
+0.454523	1025.945		2050.883	18	M	7	796.4113		796.4113	
	2147.936		2147.936	19	P	6	665.3708	+0.089268	665.3708	
-0.217491	1109.99		2218.973	20	A	5	568.3181		284.6627	-0.395208
	2334		2334	21	D	4	497.2809		497.2809	
-0.11158	1203.022		2405.037	22	A	3	382.254		382.254	
+0.156948	1252.556		2504.105	23	V	2	311.2169		311.2169	
	2561.127		2561.127	24	G	1	212.1485		212.1485	
				25	K	0	155.127		155.127	

Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F20
Scannumber: 11184
Protein: BSU28090; valS
Peptide Score: 237.48
Method: ITMS; CID; 3



precursor information

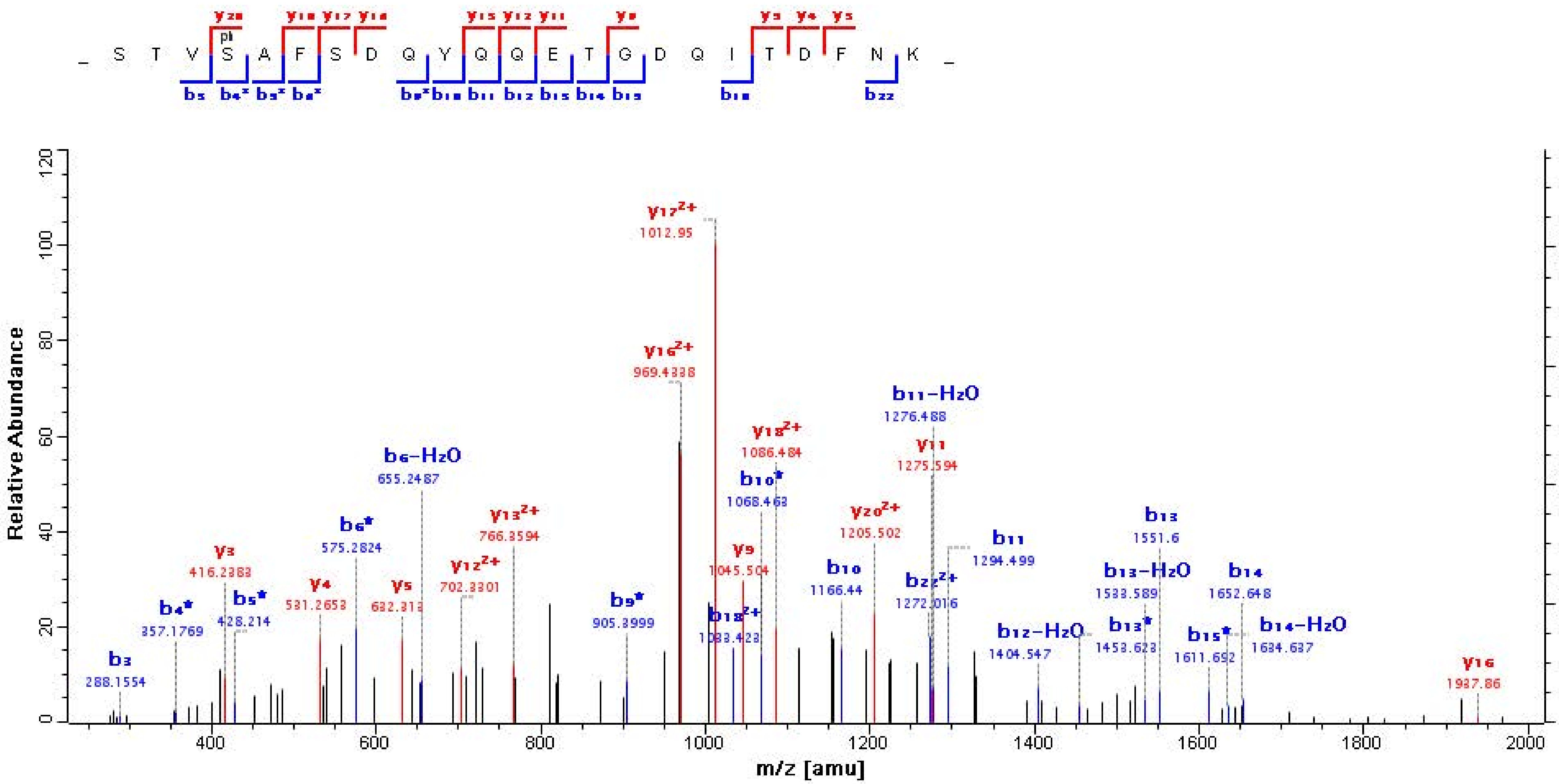
Mass:	1538.66802
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	237.4787
Mass Error [ppm]:	-0.48988
PEP:	1.1222E-89
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	77 %
Protein Localisation:	529 ... 542

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	140.0107		168.0056	1	S	13				
+0.130466	253.0948	+0.092674	281.0897	2	I	12	1380.692		1380.692	
	310.1162		338.1112	3	G	11	1267.608	-0.141641	634.3076	-0.175472
	424.1592		452.1541	4	N	10	1210.586	+0.118959	605.7968	+0.118646
	481.1806		509.1756	5	G	9	1096.543	+0.158224	1096.543	
	580.2491	+0.078969	608.244	6	V	8	1039.522	+0.128174	1039.522	
	695.276		723.2709	7	D	7	940.4536	+0.086786	940.4536	
	792.3288		820.3237	8	P	6	825.4266	+0.214925	413.2169	+0.118808
	923.3692		951.3642	9	M	5	728.3739		728.3739	
	1038.396		1066.391	10	D	4	597.3334	+0.071662	597.3334	
	1137.465	+0.088335	1165.46	11	V	3	482.3064	-0.034268	482.3064	
	1250.549	+0.135253	1278.544	12	I	2	383.238	+0.133999	383.238	
	1365.576	+0.208407	1393.571	13	D	1	270.1539	+0.086105	270.1539	
				14	K	0	155.127		155.127	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F20
Scannumber:	11390
Protein:	BSU03130; nadE; outB
Peptide Score:	108.5
Method:	ITMS; CID; 3



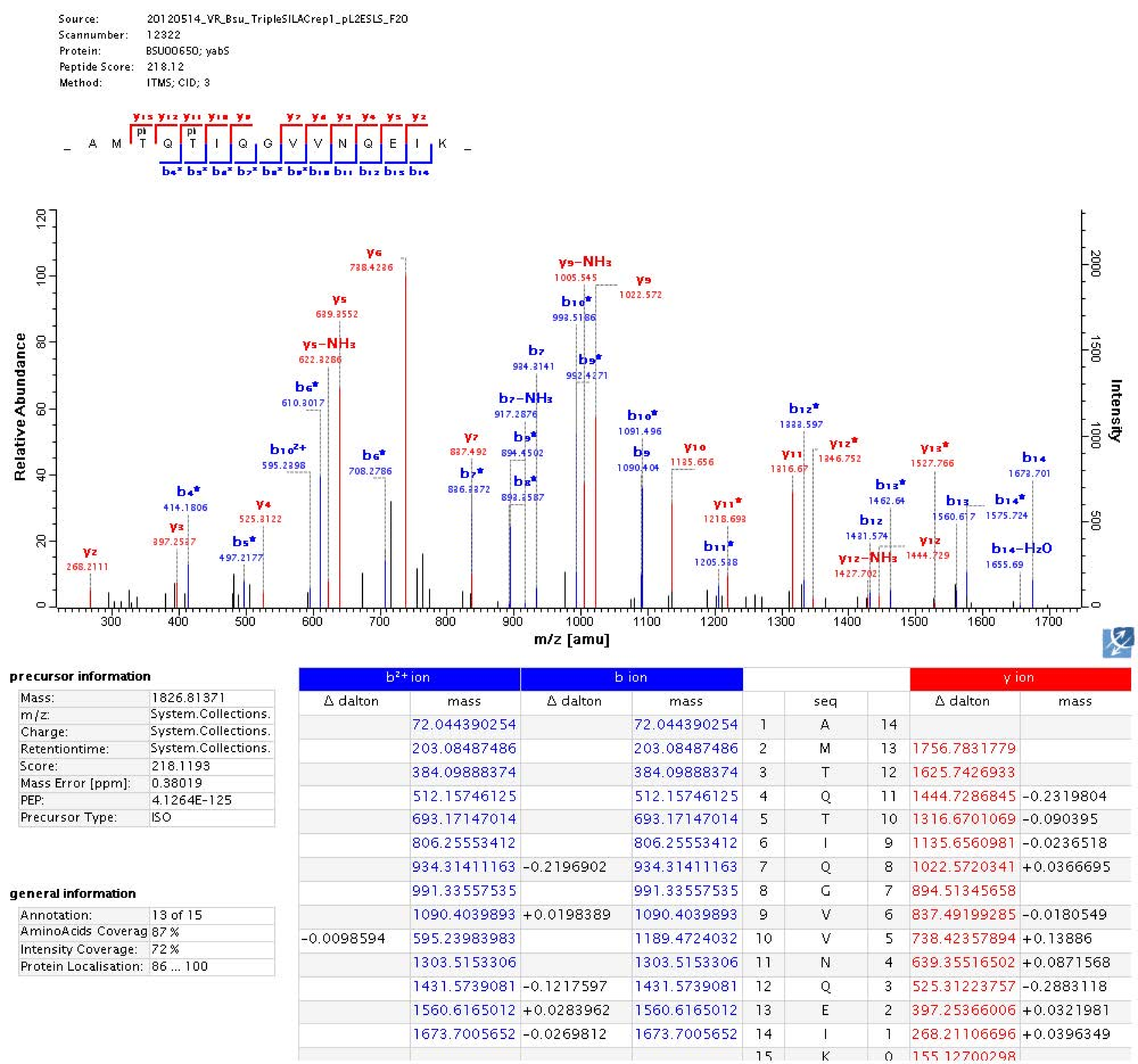
precursor information

Mass:	2696.13935
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	108.495
Mass Error [ppm]:	0.85509
PEP:	4.1463E-07
Precursor Type:	ISO

general information

Annotation:	18 of 23
AminoAcids Coverag	78 %
Intensity Coverage:	42 %
Protein Localisation:	110 ... 132

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393		88.0393	1	S	22				
	189.087		189.087	2	T	21	2610.112		2610.112	
	288.1554	-0.035311	288.1554	3	V	20	2509.065		2509.065	
	455.1538		455.1538	4	S	19	2409.996		1205.502	+0.447234
	526.1909		526.1909	5	A	18	2242.998		2242.998	
	673.2593		673.2593	6	F	17	2171.961		1086.484	+0.151982
	760.2913		760.2913	7	S	16	2024.892		1012.95	-0.085112
	875.3183		875.3183	8	D	15	1937.86	+0.337342	969.4338	+0.139947
	1003.377		1003.377	9	Q	14	1822.833		1822.833	
	1166.44	+0.02041	1166.44	10	Y	13	1694.775		1694.775	
	1294.499	+0.222331	1294.499	11	Q	12	1531.711		766.3594	-0.030013
	1422.557		1422.557	12	Q	11	1403.653		702.3301	+0.195504
	1551.6	+0.324773	1551.6	13	E	10	1275.594	+0.320143	1275.594	
	1652.648	+0.368403	1652.648	14	T	9	1146.552		1146.552	
	1709.669		1709.669	15	G	8	1045.504	+0.09059	1045.504	
	1824.696		1824.696	16	D	7	988.4826		988.4826	
	1952.755		1952.755	17	Q	6	873.4556		873.4556	
+0.234026	1033.423		2065.839	18	I	5	745.397		745.397	
	2166.886		2166.886	19	T	4	632.313	+0.037437	632.313	
	2281.913		2281.913	20	D	3	531.2653	+0.246737	531.2653	
	2428.982		2428.982	21	F	2	416.2383	+0.002073	416.2383	
+0.137138	1272.016		2543.025	22	N	1	269.1699		269.1699	
				23	K	0	155.127		155.127	



Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F20
Scannumber:	12322
Protein:	BSU00650; yabS
Peptide Score:	218.12
Method:	ITMS; CID; 3

precursor information

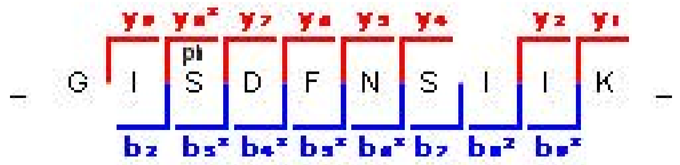
Mass:	1826.81371
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	218.1193
Mass Error [ppm]:	0.38019
PEP:	4.1264E-125
Precursor Type:	ISO

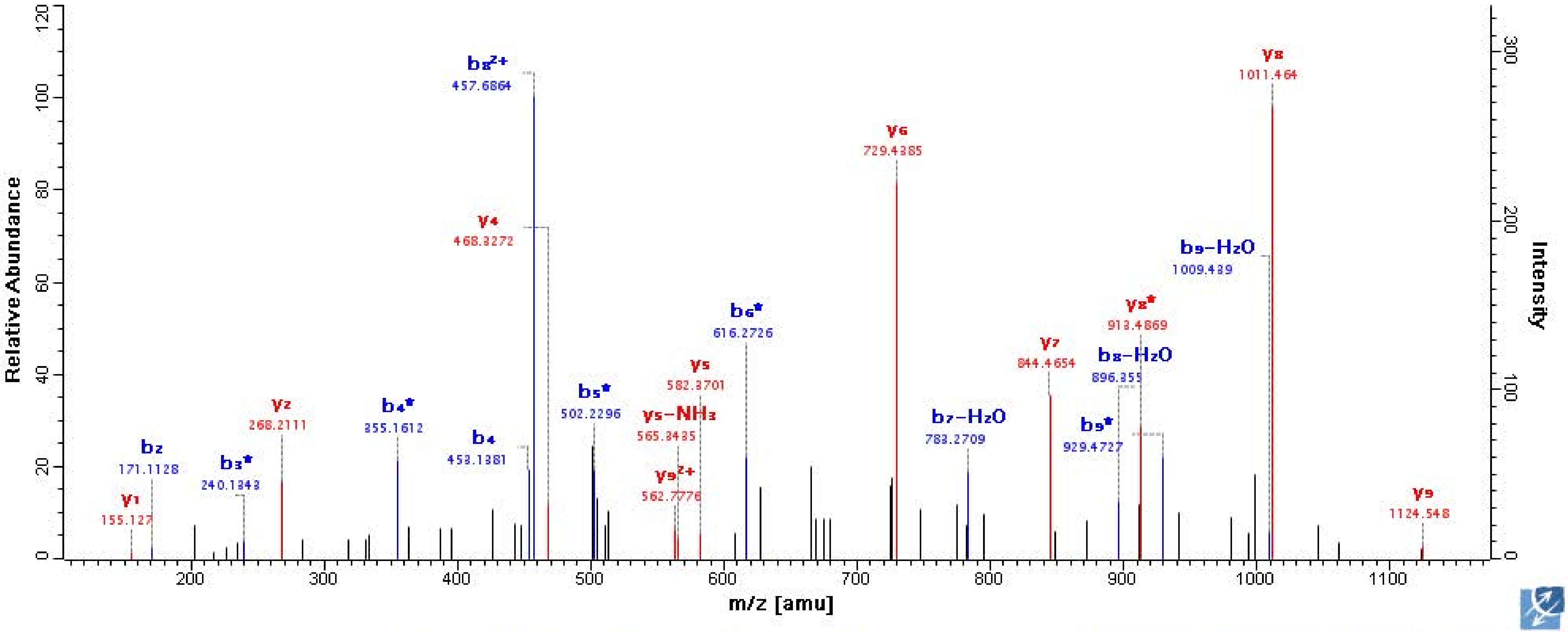
general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	72 %
Protein Localisation:	86 ... 100

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	72.044390254		72.044390254	1	A	14		
	203.08487486		203.08487486	2	M	13	1756.7831779	
	384.09888374		384.09888374	3	T	12	1625.7426933	
	512.15746125		512.15746125	4	Q	11	1444.7286845	-0.2319804
	693.17147014		693.17147014	5	T	10	1316.6701069	-0.090395
	806.25553412		806.25553412	6	I	9	1135.6560981	-0.0236518
	934.31411163	-0.2196902	934.31411163	7	Q	8	1022.5720341	+0.0366695
	991.33557535		991.33557535	8	G	7	894.51345658	
	1090.4039893	+0.0198389	1090.4039893	9	V	6	837.49199285	-0.0180549
-0.0098594	595.23983983		1189.4724032	10	V	5	738.42357894	+0.13886
	1303.5153306		1303.5153306	11	N	4	639.35516502	+0.0871568
	1431.5739081	-0.1217597	1431.5739081	12	Q	3	525.31223757	-0.2883118
	1560.6165012	+0.0283962	1560.6165012	13	E	2	397.25366006	+0.0321981
	1673.7005652	-0.0269812	1673.7005652	14	I	1	268.21106696	+0.0396349
				15	K	0	155.12700298	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F20
Scannumber:	12384
Protein:	BSU11720; fabI; yjbW
Peptide Score:	135.86
Method:	ITMS; CID; 3





precursor information

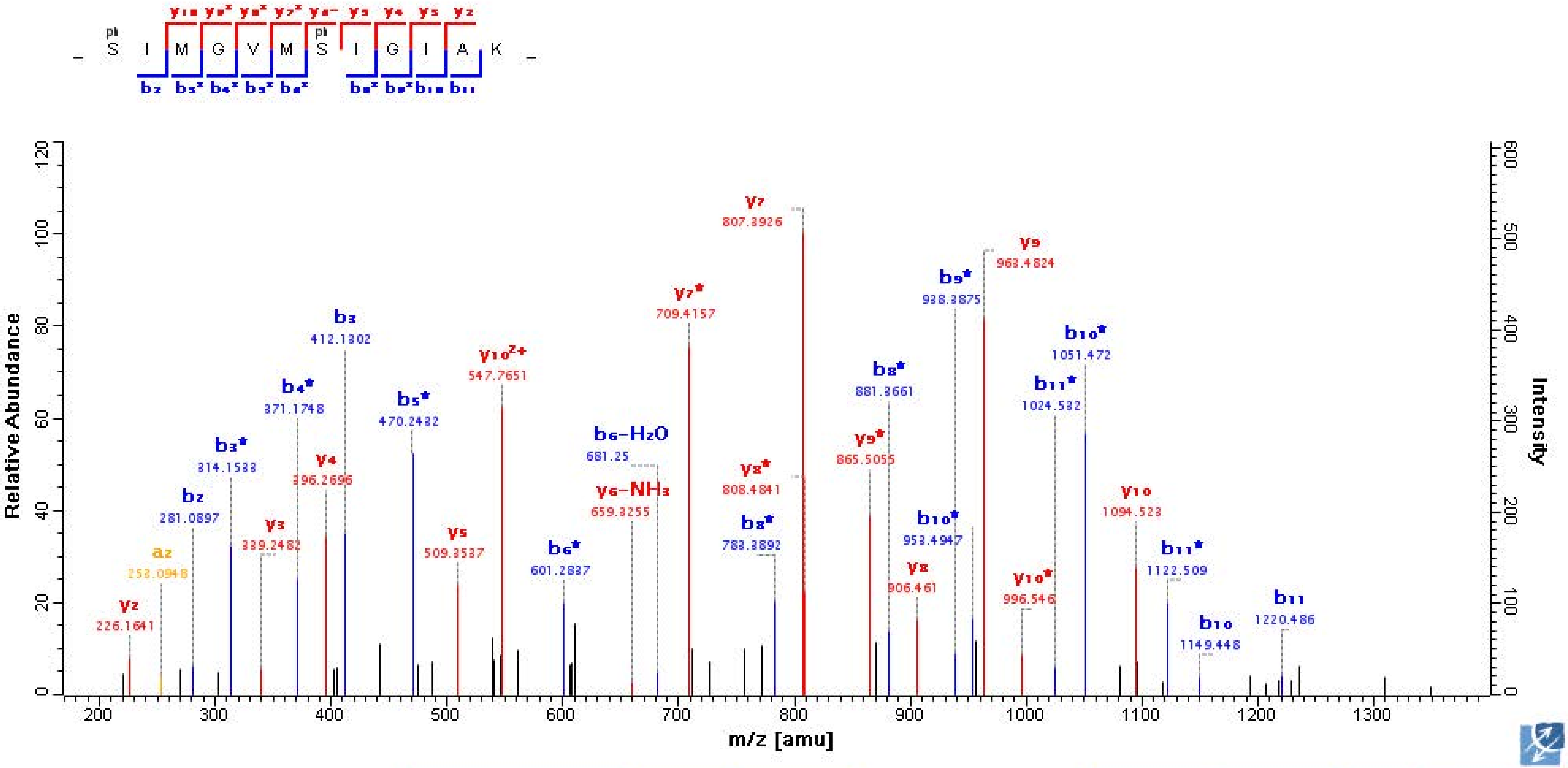
Mass:	1180.56214
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	135.8587
Mass Error [ppm]:	0.07697
PEP:	1.7348E-05
Precursor Type:	ISO

general information

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	60 %
Protein Localisation:	201 ... 210

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874		58.02874	1	G	9				
	171.1128	+0.047123	171.1128	2	I	8	1124.548	+0.102036	562.7776	+0.396318
	338.1112		338.1112	3	S	7	1011.464	+0.031803	1011.464	
	453.1381	+0.099748	453.1381	4	D	6	844.4654	+0.170237	844.4654	
	600.2065		600.2065	5	F	5	729.4385	+0.138526	729.4385	
	714.2494		714.2494	6	N	4	582.3701	-0.118378	582.3701	
	801.2815		801.2815	7	S	3	468.3272	-0.035655	468.3272	
-0.322517	457.6864		914.3655	8	I	2	381.2951		381.2951	
	1027.45		1027.45	9	I	1	268.2111	-0.031318	268.2111	
				10	K	0	155.127	+0.049999	155.127	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F20
Scannumber:	13118
Protein:	BSU13900; ptsH
Peptide Score:	214.88
Method:	ITMS; CID; 3



precursor information

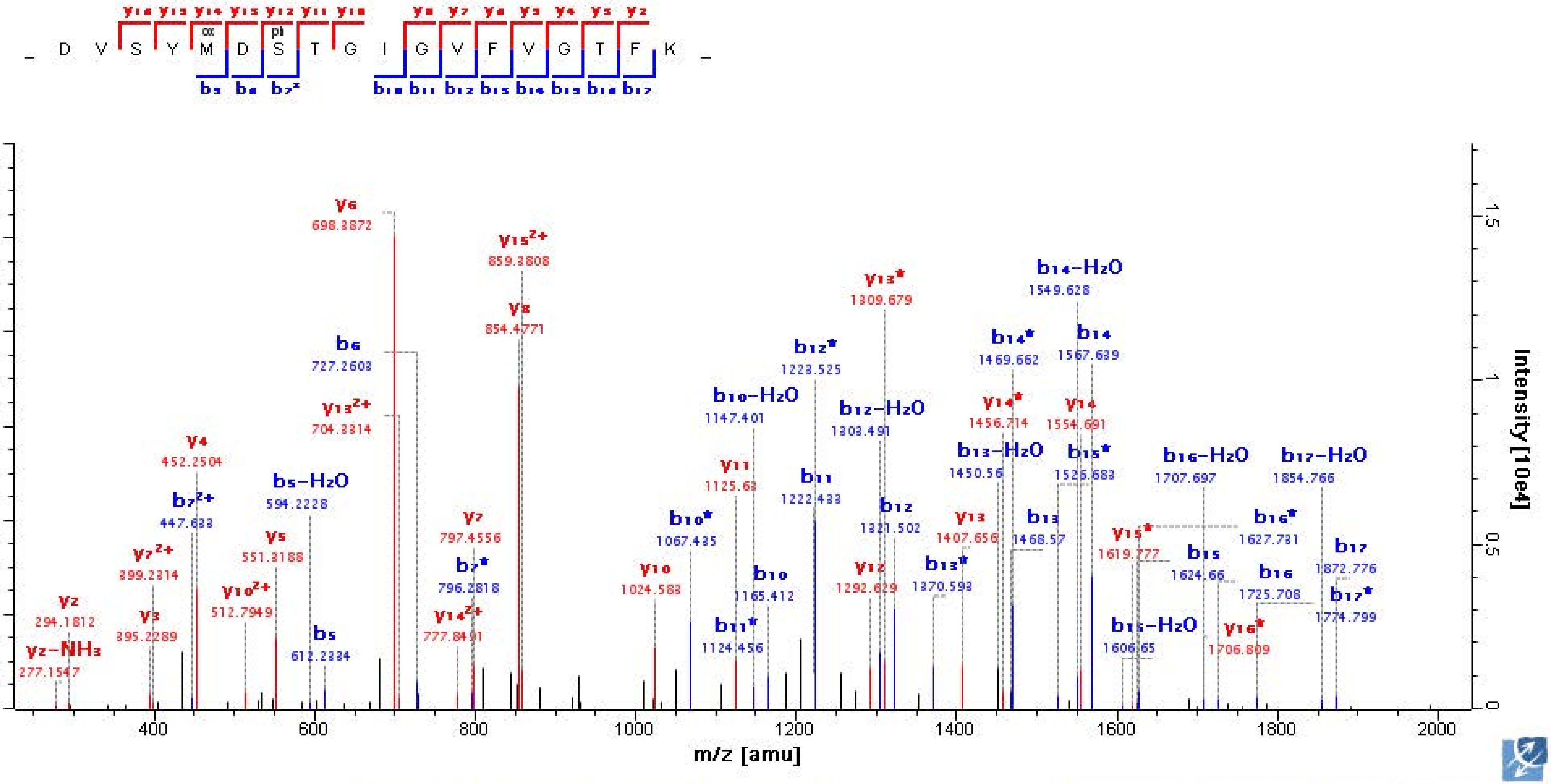
Mass:	1373.59834
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	214.8793
Mass Error [ppm]:	0.20363
PEP:	3.6979E-125
Precursor Type:	ISO

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	77 %
Protein Localisation:	46 ... 57

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	140.0107		168.0056	1	S	11				
+0.125415	253.0948	+0.022422	281.0897	2	I	10	1207.607		1207.607	
	384.1353	+0.068547	412.1302	3	M	9	1094.523	+0.205113	547.7651	+0.095073
	441.1567		469.1516	4	G	8	963.4824	+0.182915	963.4824	
	540.2251		568.2201	5	V	7	906.461	+0.07181	906.461	
	671.2656		699.2605	6	M	6	807.3926	-0.03983	807.3926	
	838.264		866.2589	7	S	5	676.3521		676.3521	
	951.3481		979.343	8	I	4	509.3537	-0.026987	509.3537	
	1008.37		1036.364	9	G	3	396.2696	+0.073556	396.2696	
	1121.454	+0.057851	1149.448	10	I	2	339.2482	-0.088391	339.2482	
	1192.491	-0.168472	1220.486	11	A	1	226.1641	-0.004571	226.1641	
				12	K	0	155.127		155.127	

Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F20
Scannumber: 14143
Protein: BSU04710; rsbV
Peptide Score: 342.42
Method: ITMS; CID; 3



precursor information

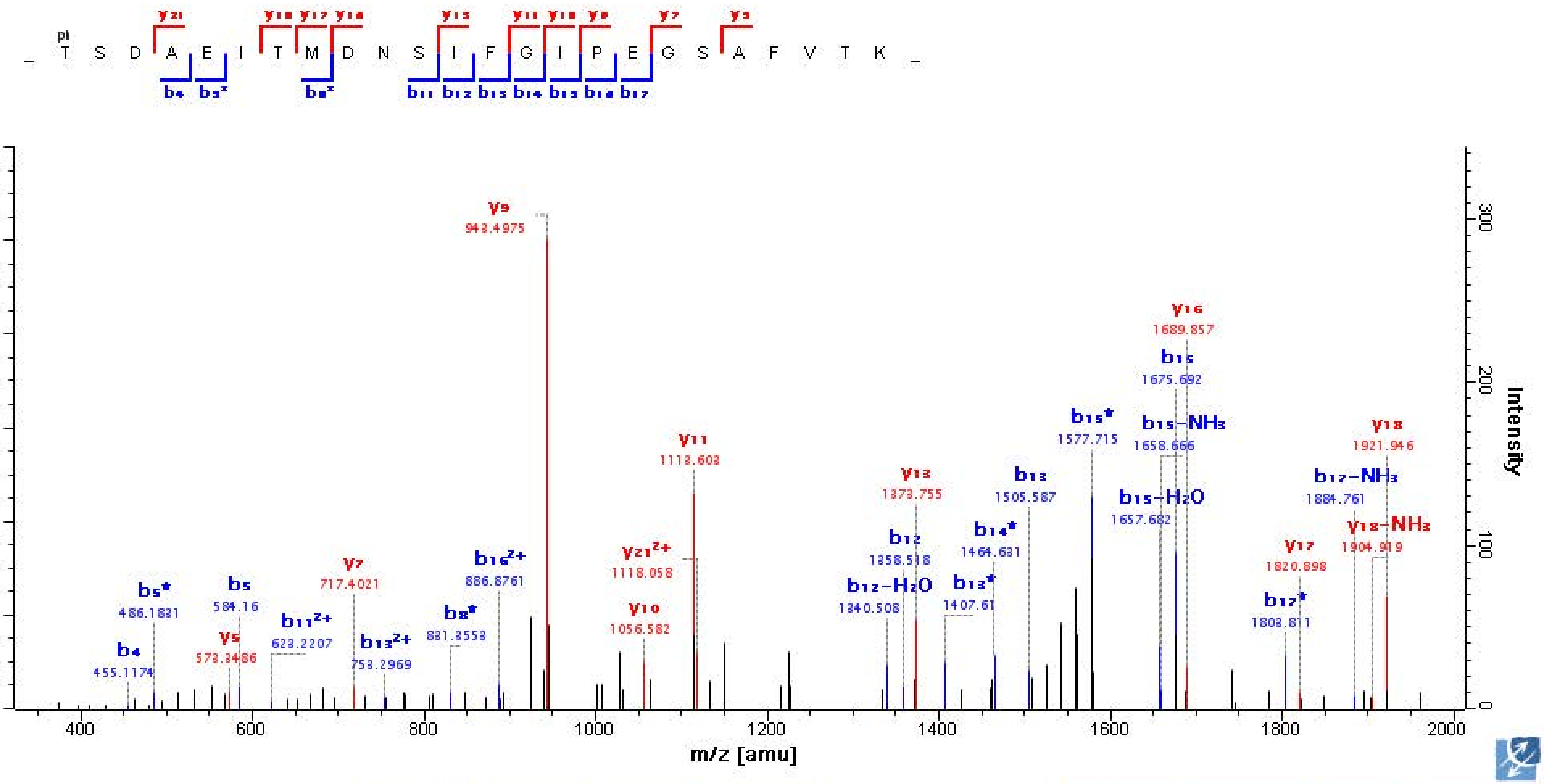
Mass:	2017.87423
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	342.4177
Mass Error [ppm]:	-0.088221
PEP:	6.0554E-285
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	76 %
Protein Localisation:	50 ... 67

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342		116.0342	1	D	17				
	215.1026		215.1026	2	V	16	1903.855		1903.855	
	302.1347		302.1347	3	S	15	1804.786		1804.786	
	465.198		465.198	4	Y	14	1717.754		859.3808	+0.118967
	612.2334	+0.003427	612.2334	5	M	13	1554.691	+0.207464	777.8491	+0.295895
	727.2603	-0.053179	727.2603	6	D	12	1407.656	-0.068049	704.3314	-0.066349
-0.34386	447.633		894.2587	7	S	11	1292.629	+0.013581	1292.629	
	995.3064		995.3064	8	T	10	1125.63	+0.062965	1125.63	
	1052.328		1052.328	9	G	9	1024.583	+0.079516	512.7949	+0.476305
	1165.412	+0.099577	1165.412	10	I	8	967.5611		967.5611	
	1222.433	+0.449451	1222.433	11	G	7	854.4771	+0.08165	854.4771	
	1321.502	+0.1524	1321.502	12	V	6	797.4556	+0.065638	399.2314	+0.195258
	1468.57	-0.098632	1468.57	13	F	5	698.3872	-0.02647	698.3872	
	1567.639	-0.021049	1567.639	14	V	4	551.3188	+0.116895	551.3188	
	1624.66	-0.096712	1624.66	15	G	3	452.2504	+0.000403	452.2504	
	1725.708	-0.012189	1725.708	16	T	2	395.2289	+0.026413	395.2289	
	1872.776	+0.183924	1872.776	17	F	1	294.1812	+0.188685	294.1812	
				18	K	0	147.1128		147.1128	

Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F20
Scannumber: 14162
Protein: BSU07260; ltaS1; yfnI
Peptide Score: 94.84
Method: ITMS; CID; 3



precursor information

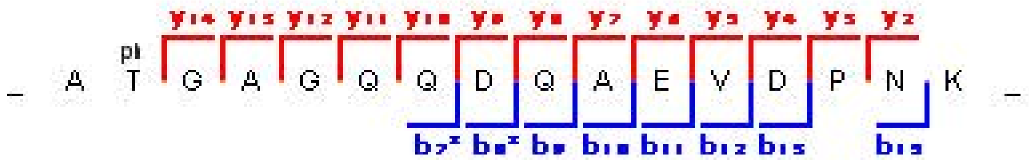
Mass:	2617.17538
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	94.83795
Mass Error [ppm]:	0.13942
PEP:	1.5648E-07
Precursor Type:	ISO

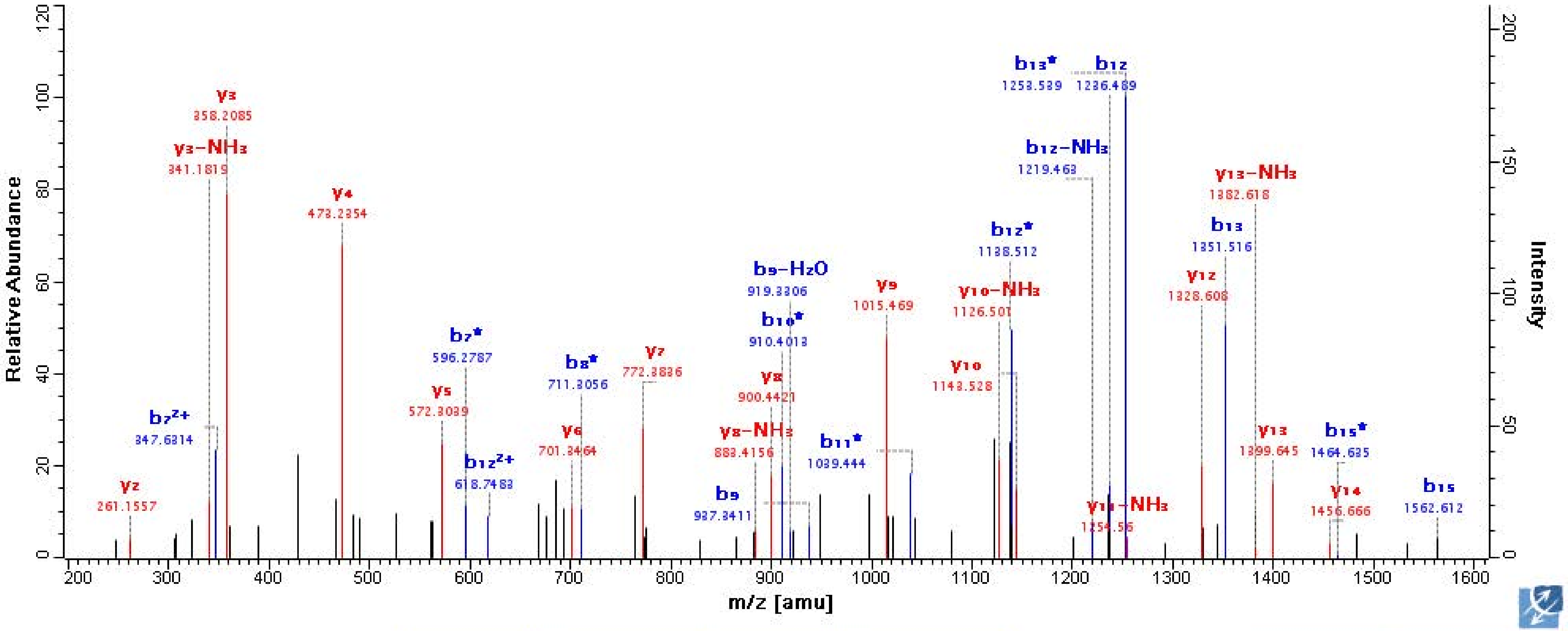
general information

Annotation:	14 of 24
AminoAcids Coverag	58 %
Intensity Coverage:	50 %
Protein Localisation:	297 ... 320

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	182.0213		182.0213	1	T	23				
	269.0533		269.0533	2	S	22	2437.168		2437.168	
	384.0803		384.0803	3	D	21	2350.136		2350.136	
	455.1174	+0.290344	455.1174	4	A	20	2235.109		1118.058	+0.221736
	584.16	+0.08552	584.16	5	E	19	2164.072		2164.072	
	697.244		697.244	6	I	18	2035.03		2035.03	
	798.2917		798.2917	7	T	17	1921.946	-0.09239	1921.946	
	929.3322		929.3322	8	M	16	1820.898	+0.297207	1820.898	
	1044.359		1044.359	9	D	15	1689.857	+0.041793	1689.857	
	1158.402		1158.402	10	N	14	1574.83		1574.83	
+0.093526	623.2207		1245.434	11	S	13	1460.788		1460.788	
	1358.518	-0.113613	1358.518	12	I	12	1373.755	+0.096085	1373.755	
+0.093093	753.2969	+0.111064	1505.587	13	F	11	1260.671		1260.671	
	1562.608		1562.608	14	G	10	1113.603	+0.044705	1113.603	
	1675.692	-0.021563	1675.692	15	I	9	1056.582	+0.042243	1056.582	
-0.353851	886.8761		1772.745	16	P	8	943.4975	+0.113001	943.4975	
	1901.787		1901.787	17	E	7	846.4447		846.4447	
	1958.809		1958.809	18	G	6	717.4021	+0.272995	717.4021	
	2045.841		2045.841	19	S	5	660.3807		660.3807	
	2116.878		2116.878	20	A	4	573.3486	-0.131948	573.3486	
	2263.946		2263.946	21	F	3	502.3115		502.3115	
	2363.015		2363.015	22	V	2	355.2431		355.2431	
	2464.063		2464.063	23	T	1	256.1747		256.1747	
				24	K	0	155.127		155.127	

Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F20
Scannumber: 5407
Protein: aceC; BSU14600; pdhC
Peptide Score: 183.23
Method: ITMS; CID; 3





precursor information

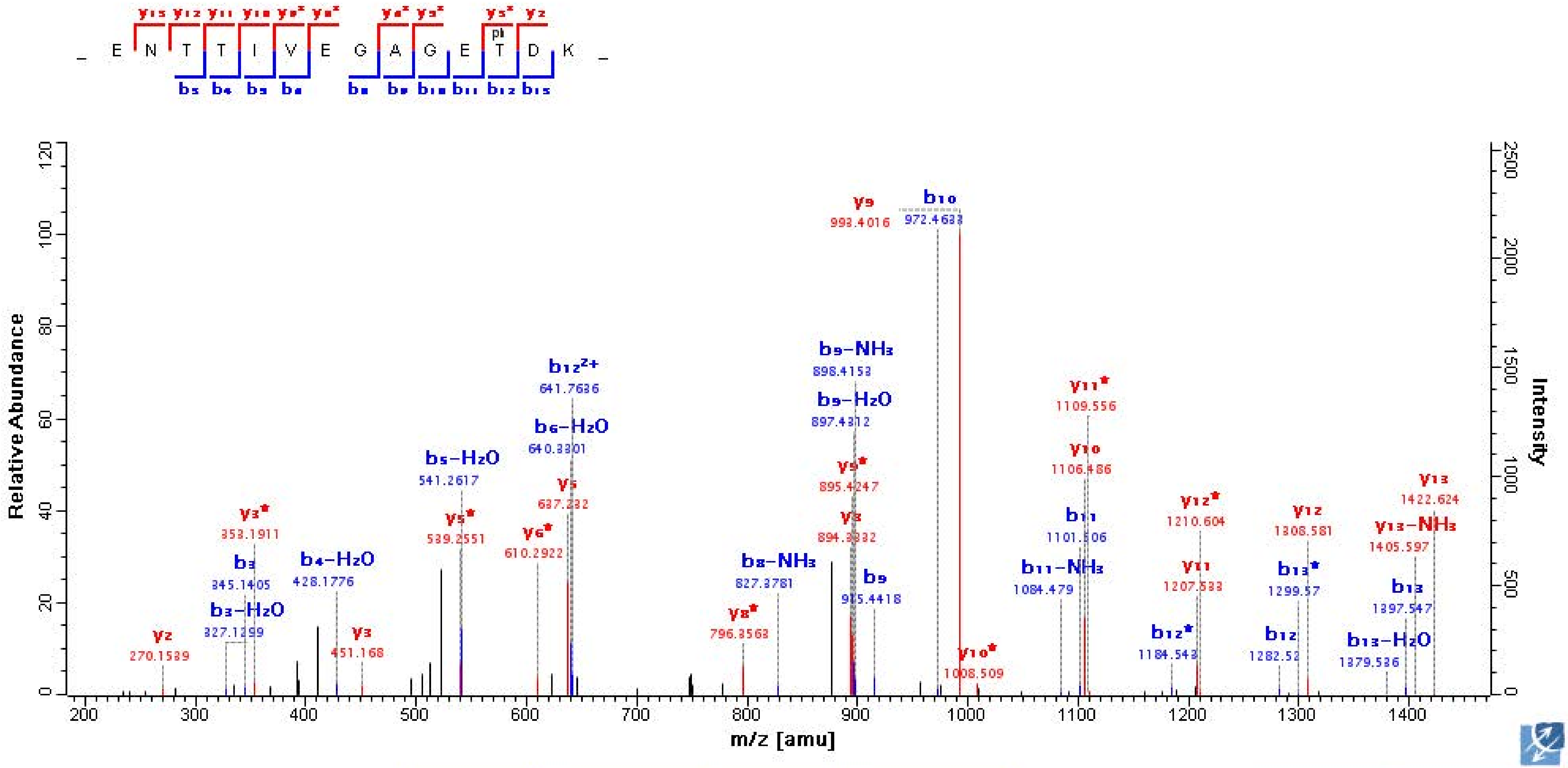
Mass:	1707.71006
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	183.2319
Mass Error [ppm]:	-0.037009
PEP:	4.018E-35
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	64 %
Protein Localisation:	123 ... 138

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	72.044390254		72.044390254	1	A	15		
	253.05839914		253.05839914	2	T	14	1637.680285	
	310.07986286		310.07986286	3	G	13	1456.6662761	-0.0680095
	381.11697665		381.11697665	4	A	12	1399.6448124	+0.0906613
	438.13844037		438.13844037	5	G	11	1328.6076986	+0.1569498
	566.19701788		566.19701788	6	Q	10	1271.5862349	
-0.4186063	347.63143593		694.25559539	7	Q	9	1143.5276574	+0.0595008
	809.28253843		809.28253843	8	D	8	1015.4690798	+0.0748044
	937.34111594	-0.0991726	937.34111594	9	Q	7	900.44213681	+0.0011615
	1008.3782297		1008.3782297	10	A	6	772.3835593	+0.1675271
	1137.4208228		1137.4208228	11	E	5	701.34644551	+0.1316429
-0.4076194	618.7482566	+0.1550504	1236.4892367	12	V	4	572.30385242	+0.1294362
	1351.5161798	+0.1609443	1351.5161798	13	D	3	473.2354385	+0.0729721
	1448.5689436		1448.5689436	14	P	2	358.20849547	+0.1318366
	1562.6118711	+0.0614688	1562.6118711	15	N	1	261.15573162	+0.0490718
				16	K	0	147.11280417	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F20
Scannumber:	6402
Protein:	BSU06030; groEL; groL; mopA
Peptide Score:	188.12
Method:	ITMS; CID; 3



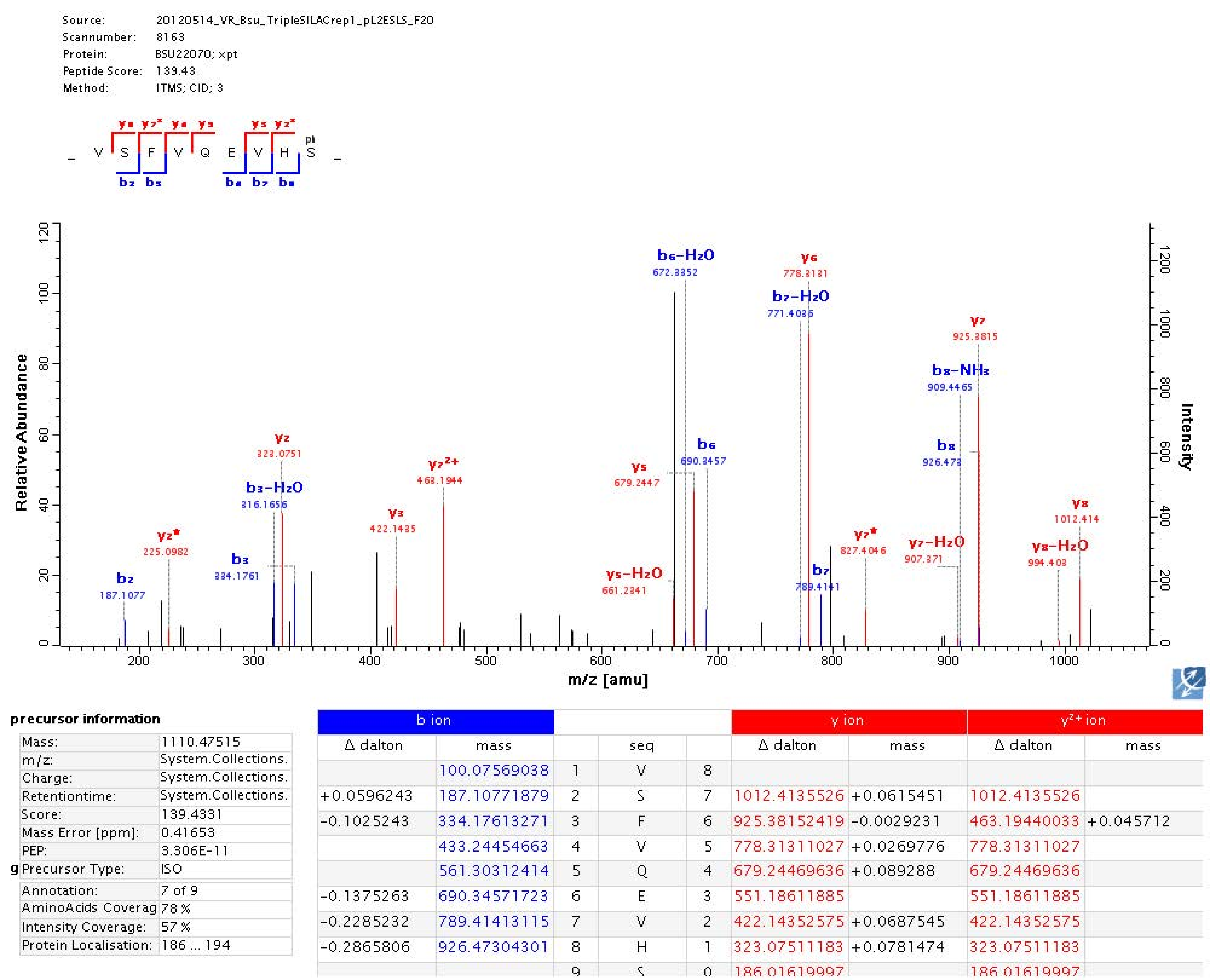
precursor information

Mass:	1542.6451
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	188.1244
Mass Error [ppm]:	0.026956
PEP:	7.3928E-35
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	66 %
Protein Localisation:	326 ... 339

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	130.04986956		130.04986956	1	E	13		
	244.09279701		244.09279701	2	N	12	1422.6239446	+0.3483454
	345.14047548	+0.0594147	345.14047548	3	T	11	1308.5810172	-0.032067
	446.18815396		446.18815396	4	T	10	1207.5333387	+0.0196398
	559.27221794		559.27221794	5	I	9	1106.4856602	+0.0751308
	658.34063185		658.34063185	6	V	8	993.40159624	+0.0210722
	787.38322495		787.38322495	7	E	7	894.33318233	+0.0404139
	844.40468867		844.40468867	8	G	6	765.29058923	
	915.44180246	-0.0374446	915.44180246	9	A	5	708.26912551	
	972.46326619	-0.0718477	972.46326619	10	G	4	637.23201172	-0.0233936
	1101.5058593	-0.0324706	1101.5058593	11	E	3	580.21054799	
-0.327232	641.76357232	-0.0214551	1282.5198682	12	T	2	451.1679549	+0.0552507
	1397.5468112	-0.0349704	1397.5468112	13	D	1	270.15394602	+0.089218
				14	K	0	155.12700298	



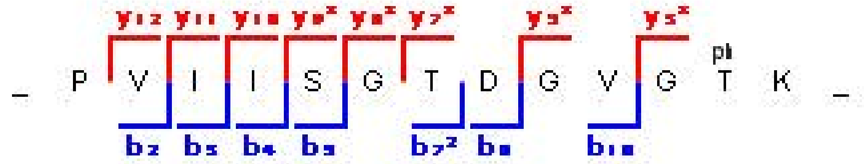
Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F20
Scannumber: 8163
Protein: BSU22070; xpt
Peptide Score: 139.43
Method: ITMS; CID; 3

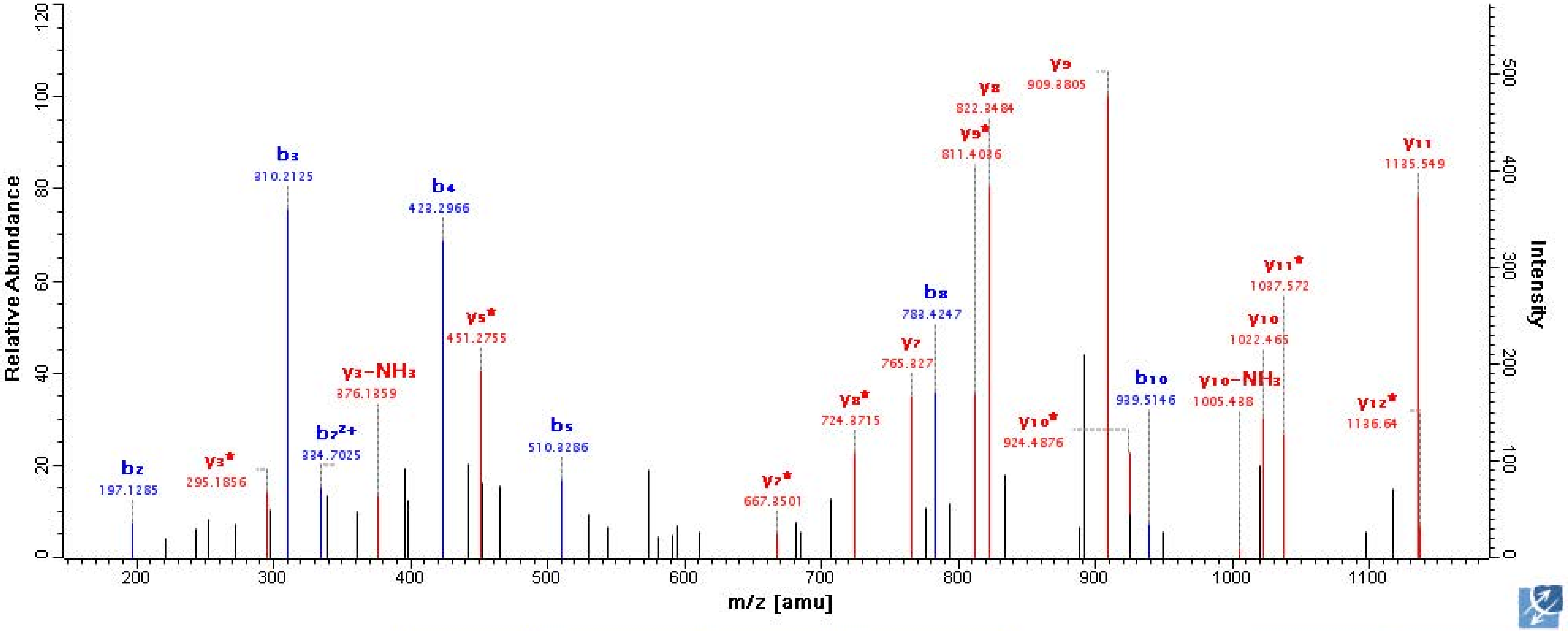
precursor information

Mass:	1110.47515
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	139.4331
Mass Error [ppm]:	0.41653
PEP:	3.306E-11
Precursor Type:	ISO
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	57 %
Protein Localisation:	186 ... 194

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.07569038	1	V	8				
+0.0596243	187.10771879	2	S	7	1012.4135526	+0.0615451	1012.4135526	
-0.1025243	334.17613271	3	F	6	925.38152419	-0.0029231	463.19440033	+0.045712
	433.24454663	4	V	5	778.31311027	+0.0269776	778.31311027	
	561.30312414	5	Q	4	679.24469636	+0.089288	679.24469636	
-0.1375263	690.34571723	6	E	3	551.18611885		551.18611885	
-0.2285232	789.41413115	7	V	2	422.14352575	+0.0687545	422.14352575	
-0.2865806	926.47304301	8	H	1	323.07511183	+0.0781474	323.07511183	
		9	S	0	186.01619997		186.01619997	

Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F20
Scannumber: 8279
Protein: ath; BSU06500; purM
Peptide Score: 132.59
Method: ITMS; CID; 3





precursor information

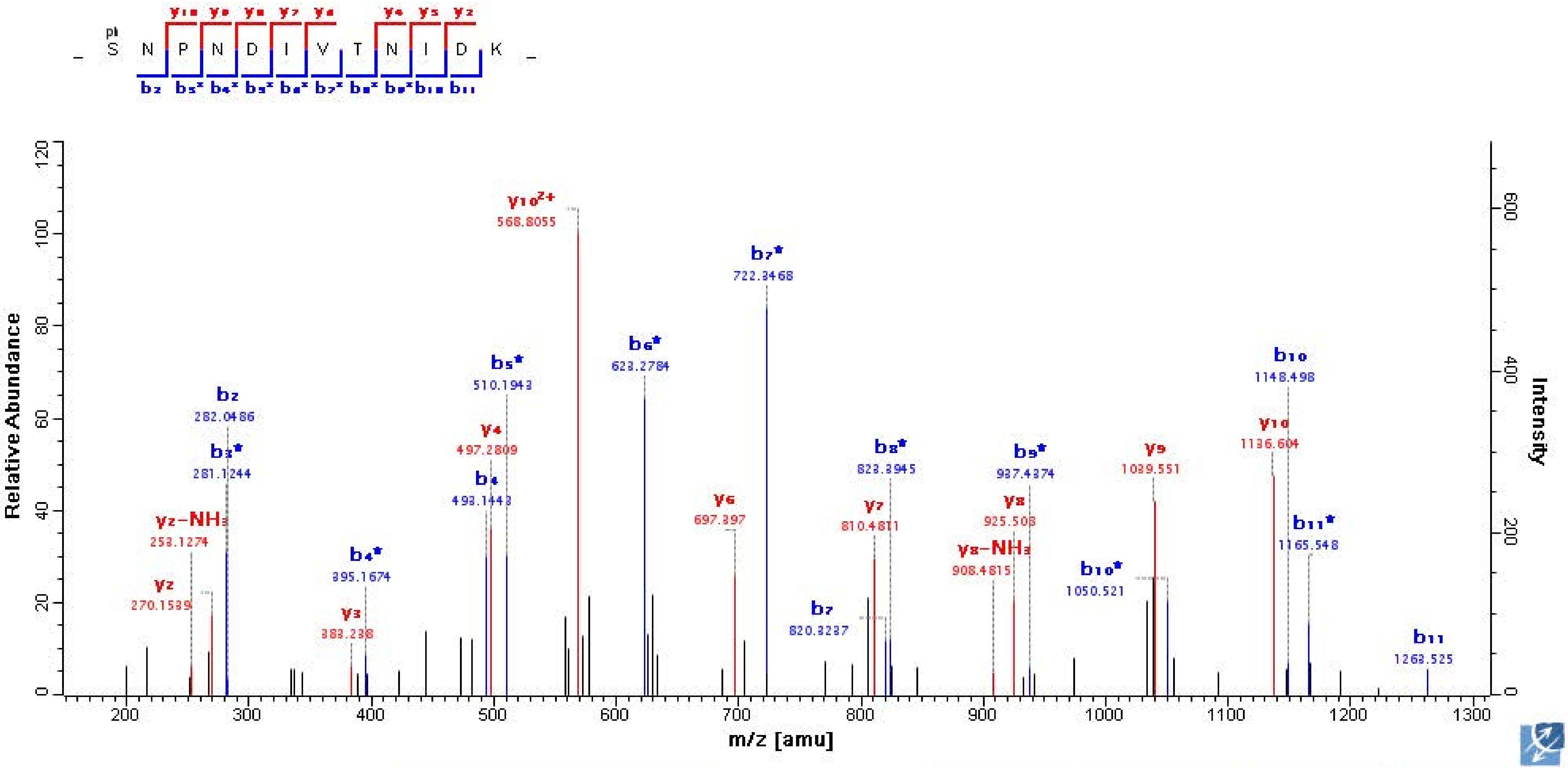
Mass:	1322.64844
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	132.5867
Mass Error [ppm]:	0.10885
PEP:	1.6815E-07
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	66 %
Protein Localisation:	55 ... 67

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	98.060040319		98.060040319	1	P	12		
	197.12845423	+0.127222	197.12845423	2	V	11	1234.6170087	
	310.21251822	+0.0262513	310.21251822	3	I	10	1135.5485948	+0.0237929
	423.2965822	+0.0101195	423.2965822	4	I	9	1022.4645308	-0.0164718
	510.32861061	+0.10303	510.32861061	5	S	8	909.38046687	+0.0609394
	567.35007433		567.35007433	6	G	7	822.34843846	+0.0871084
-0.2511902	334.70251463		668.3977528	7	T	6	765.32697474	+0.1419584
	783.42469584	+0.0674306	783.42469584	8	D	5	664.27929626	
	840.44615956		840.44615956	9	G	4	549.25235323	
	939.51457348	+0.0784441	939.51457348	10	V	3	492.23088951	
	996.5360372		996.5360372	11	G	2	393.16247559	
	1177.5500461		1177.5500461	12	T	1	336.14101187	
				13	K	0	155.12700298	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F20
Scannumber:	8399
Protein:	BSU14670; suhB; yktC
Peptide Score:	160.69
Method:	ITMS; CID; 3



precursor information

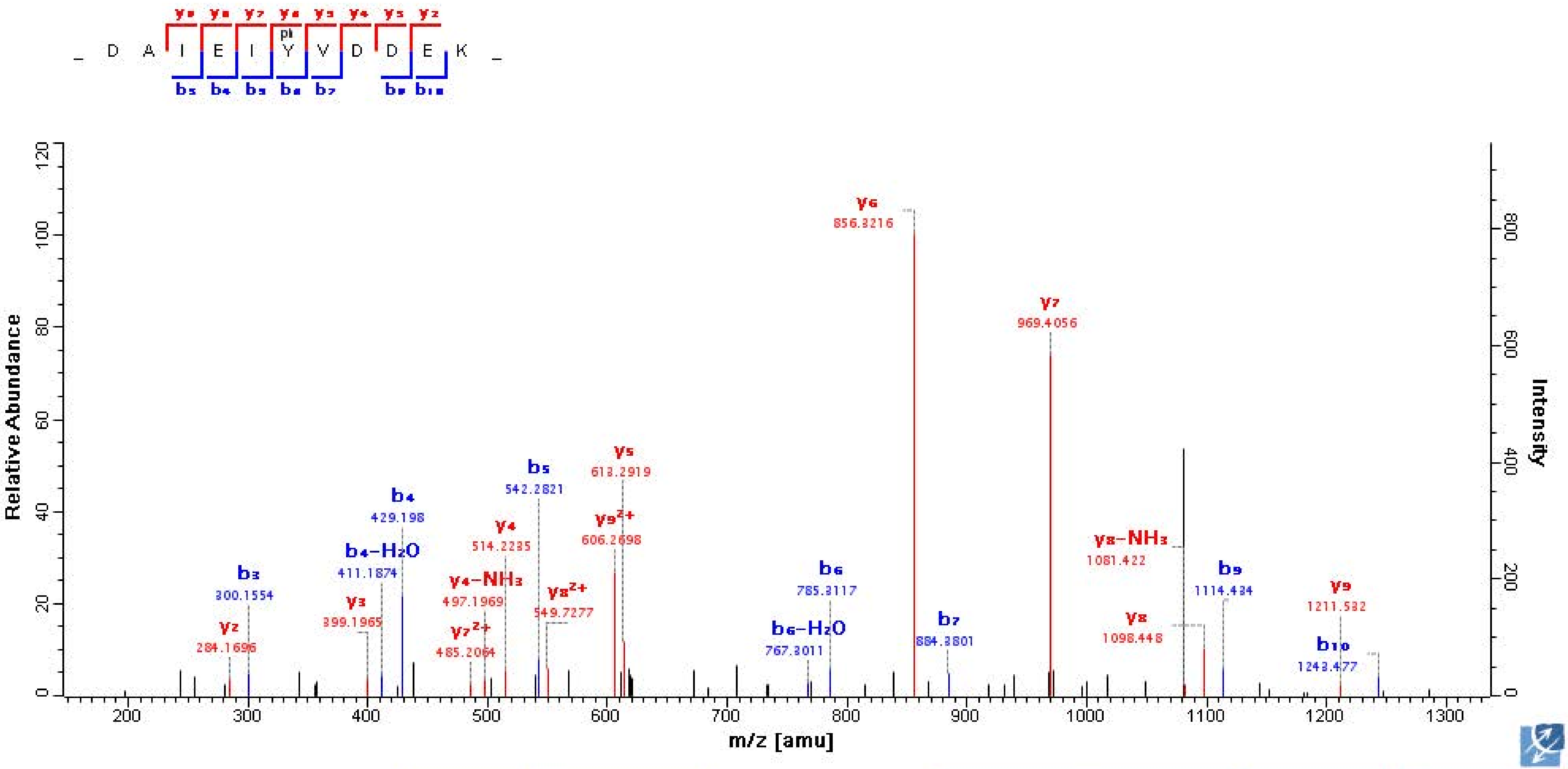
Mass:	1408.62377
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	160.6851
Mass Error [ppm]:	0.16473
PEP:	4.5388E-19
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	64 %
Protein Localisation:	36 ... 47

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.00563528	1	S	11				
-0.1091401	282.04856273	2	N	10	1250.6466556		1250.6466556	
	379.10132658	3	P	9	1136.6037281	+0.2480785	568.80550231	+0.042337
+0.0628993	493.14425403	4	N	8	1039.5509643	+0.289856	1039.5509643	
	608.17119706	5	D	7	925.50803685	-0.0973923	925.50803685	
	721.25526104	6	I	6	810.48109381	-0.1156763	810.48109381	
+0.0275824	820.32367496	7	V	5	697.39702983	+0.2169838	697.39702983	
	921.37135343	8	T	4	598.32861592		598.32861592	
	1035.4142809	9	N	3	497.28093744	+0.1544263	497.28093744	
+0.1928172	1148.4983449	10	I	2	383.23801	+0.0711331	383.23801	
+0.0546682	1263.5252879	11	D	1	270.15394602	+0.0132598	270.15394602	
		12	K	0	155.12700298		155.12700298	

Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F20
Scannumber: 8982
Protein: abrB; BSU00370; cpsX
Peptide Score: 162.36
Method: ITMS; CID; 3



precursor information

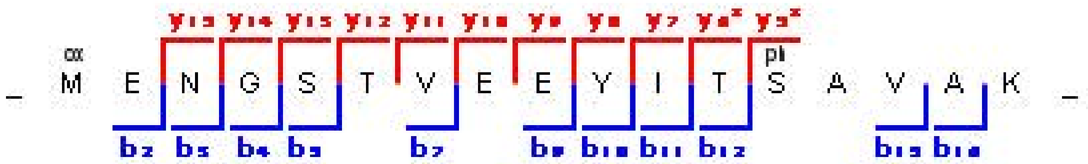
Mass:	1388.57536
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	162.3578
Mass Error [ppm]:	0.36146
PEP:	5.5744E-17
Precursor Type:	MULTI

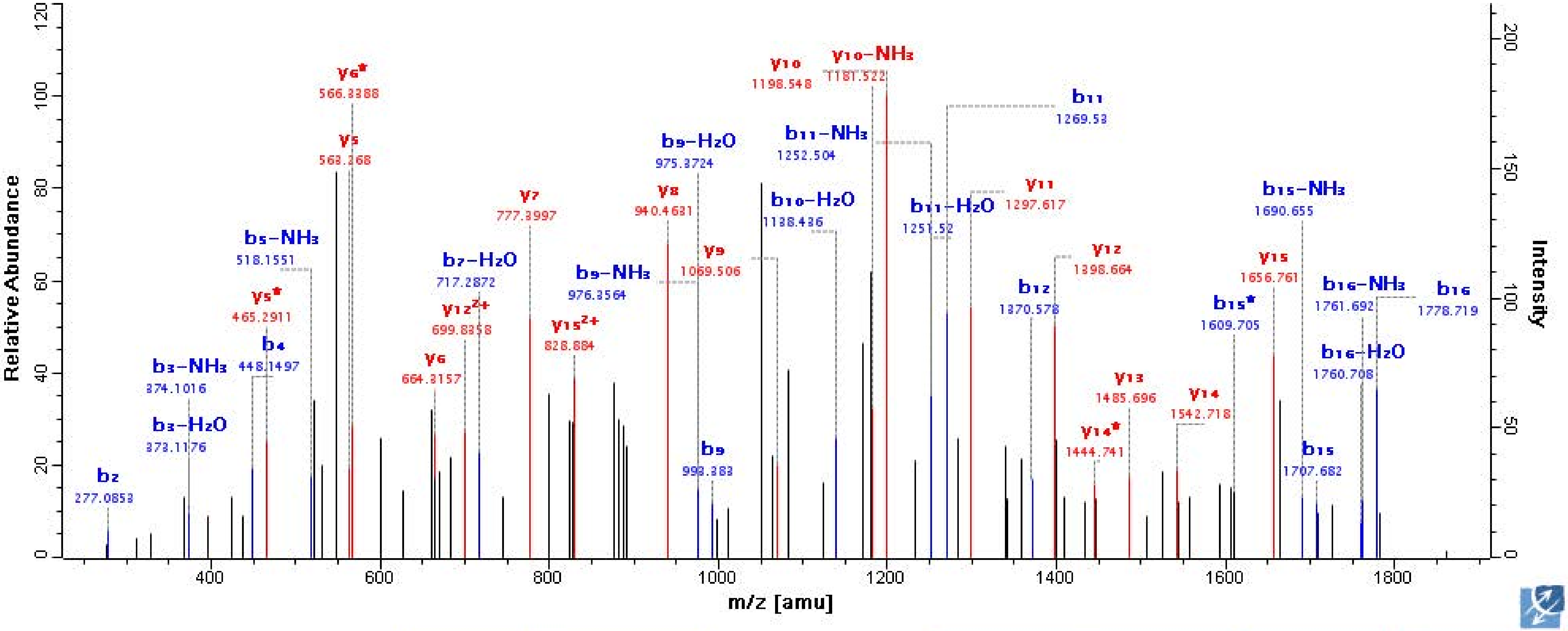
general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	61 %
Protein Localisation:	34 ... 44

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342195	1	D	10				
	187.07133329	2	A	9	1282.5693899		1282.5693899	
+0.0476972	300.15539727	3	I	8	1211.5322761	-0.0288581	606.26977627	-0.0397958
+0.0072709	429.19799036	4	E	7	1098.4482121	-0.1547551	549.72774428	+0.1612328
+0.0403334	542.28205434	5	I	6	969.40561899	+0.0600182	485.20644773	+0.2360572
+0.1148614	785.31171329	6	Y	5	856.32155501	-0.0070408	856.32155501	
+0.0902707	884.38012721	7	V	4	613.29189606	+0.0195663	613.29189606	
	999.40707024	8	D	3	514.22348214	-0.0935993	514.22348214	
-0.1956099	1114.4340133	9	D	2	399.19653911	+0.1487368	399.19653911	
-0.0184765	1243.4766064	10	E	1	284.16959608	+0.2104698	284.16959608	
		11	K	0	155.12700298		155.12700298	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F21
Scannumber:	10081
Protein:	BSU16500; tsf
Peptide Score:	168.64
Method:	ITMS; CID; 3





precursor information

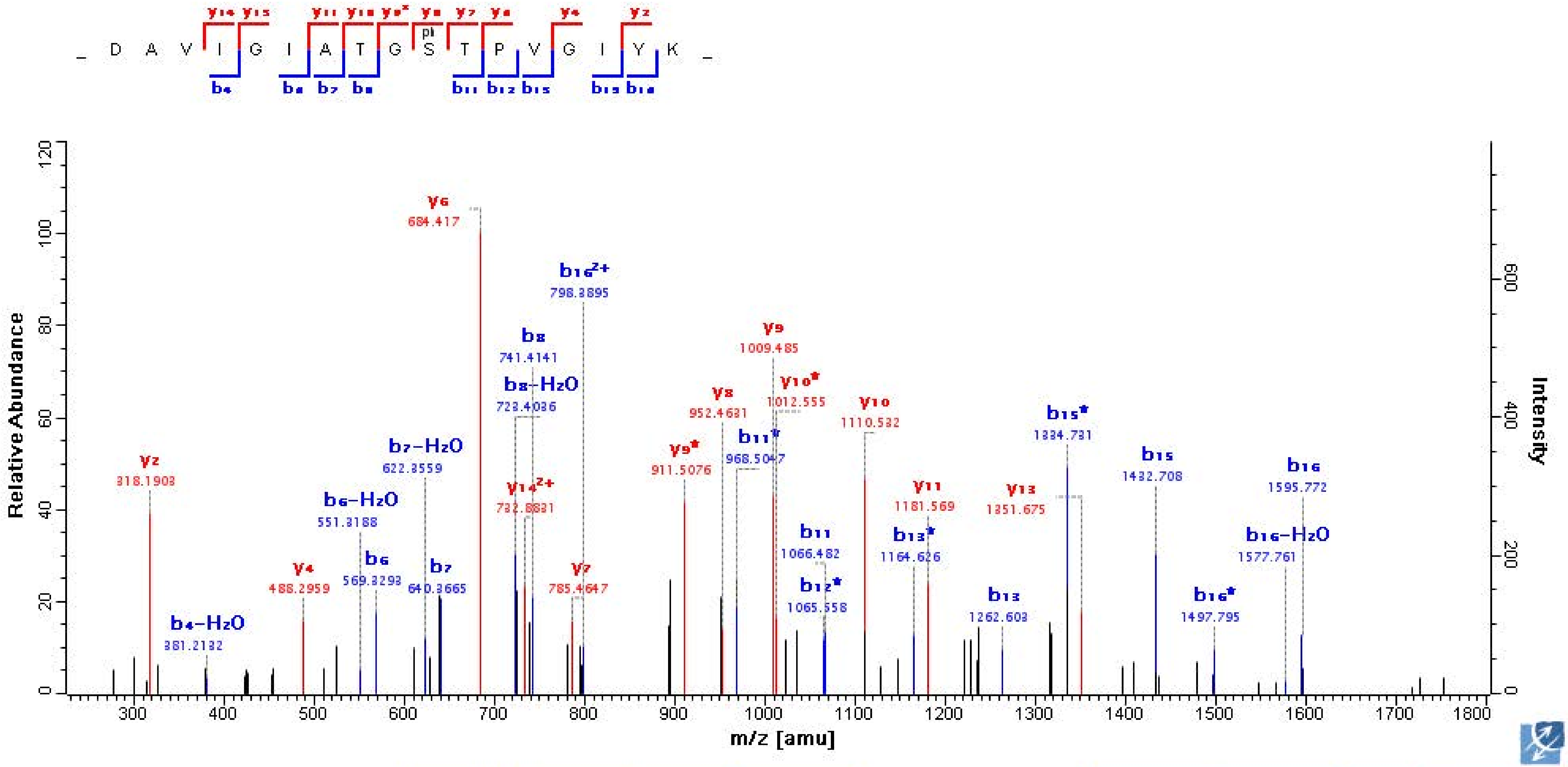
Mass:	1923.81798
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	168.6398
Mass Error [ppm]:	0.35881
PEP:	2.2298E-27
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	46 %
Protein Localisation:	115 ... 131

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.04267569	1	M	16				
-0.1148708	277.08526879	2	E	15	1785.8033655		1785.8033655	
	391.12819624	3	N	14	1656.7607725	+0.0069277	828.88402446	+0.2099086
+0.35034	448.14965996	4	G	13	1542.717845	+0.1124773	1542.717845	
	535.18168837	5	S	12	1485.6963813	+0.156524	1485.6963813	
	636.22936685	6	T	11	1398.6643529	+0.0928493	699.83581467	-0.4306023
	735.29778076	7	V	10	1297.6166744	+0.0476322	1297.6166744	
	864.34037386	8	E	9	1198.5482605	+0.0861389	1198.5482605	
+0.1826458	993.38296695	9	E	8	1069.5056674	+0.0729459	1069.5056674	
	1156.4462955	10	Y	7	940.46307429	+0.1384882	940.46307429	
+0.0143183	1269.5303595	11	I	6	777.39974575	-0.0429953	777.39974575	
+0.2282365	1370.5780379	12	T	5	664.31568177	-0.1653522	664.31568177	
	1537.5763968	13	S	4	563.26800329	-0.0009135	563.26800329	
	1608.6135106	14	A	3	396.26964448		396.26964448	
+0.0683197	1707.6819245	15	V	2	325.23253069		325.23253069	
+0.0561082	1778.7190383	16	A	1	226.16411677		226.16411677	
		17	K	0	155.12700298		155.12700298	

Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F21
Scannumber: 10646
Protein: BSU02360; gamA; ybfT
Peptide Score: 153.72
Method: ITMS; CID; 3



precursor information

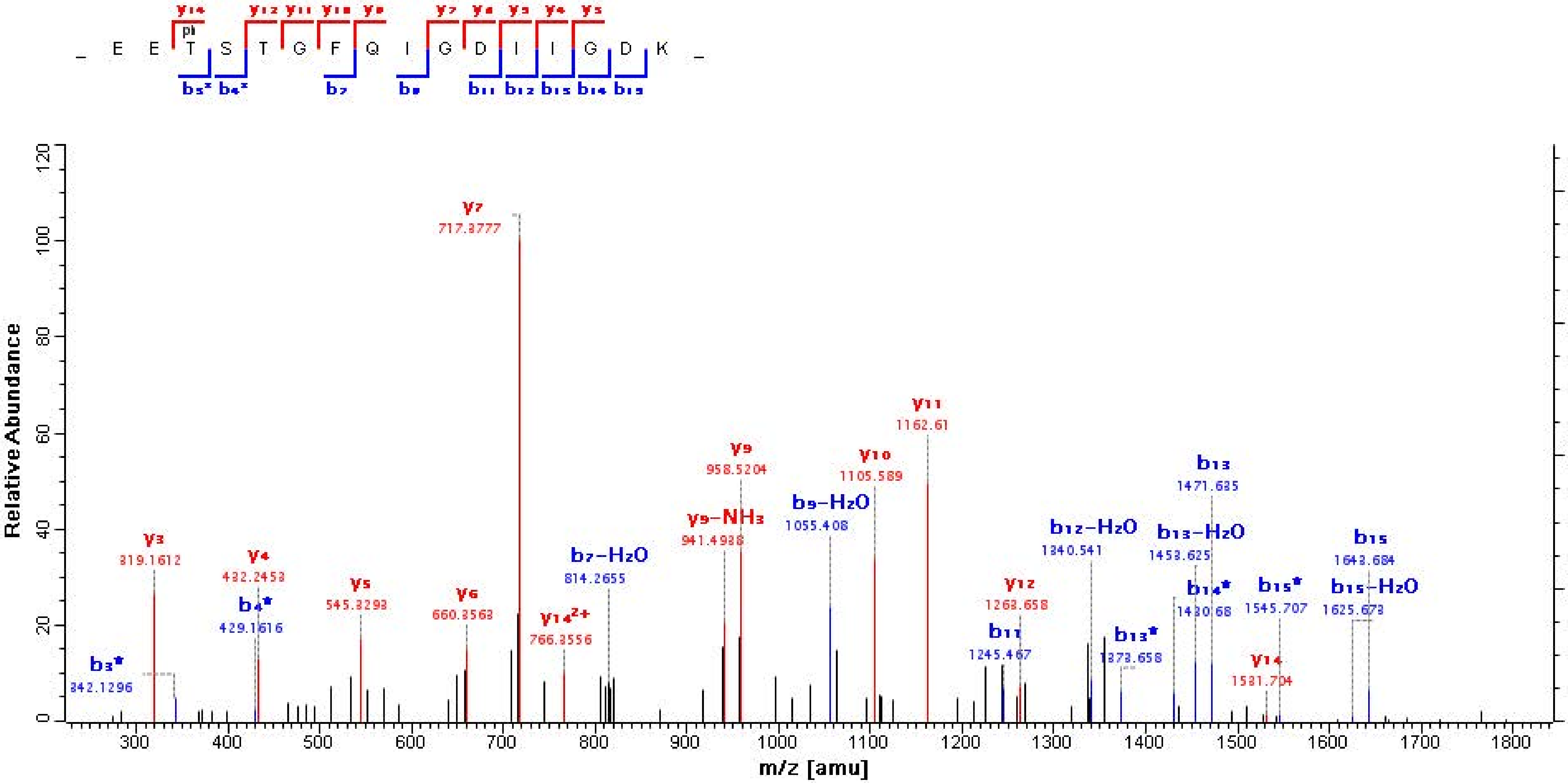
Mass:	1748.88404
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	153.725
Mass Error [ppm]:	-0.044937
PEP:	2.8942E-19
Precursor Type:	ISO

general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	59 %
Protein Localisation:	29 ... 45

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342		116.0342	1	D	16				
	187.0713		187.0713	2	A	15	1634.864		1634.864	
	286.1397		286.1397	3	V	14	1563.827		1563.827	
	399.2238		399.2238	4	I	13	1464.759		732.8831	+0.362323
	456.2453		456.2453	5	G	12	1351.675	+0.074288	1351.675	
	569.3293	+0.014777	569.3293	6	I	11	1294.653		1294.653	
	640.3665	+0.03876	640.3665	7	A	10	1181.569	+0.003179	1181.569	
	741.4141	+0.116447	741.4141	8	T	9	1110.532	-0.071645	1110.532	
	798.4356		798.4356	9	G	8	1009.485	-0.045024	1009.485	
	965.434		965.434	10	S	7	952.4631	+0.115539	952.4631	
	1066.482	+0.132259	1066.482	11	T	6	785.4647	+0.003363	785.4647	
	1163.534		1163.534	12	P	5	684.417	+0.013078	684.417	
	1262.603	-0.002468	1262.603	13	V	4	587.3643		587.3643	
	1319.624		1319.624	14	G	3	488.2959	+0.114053	488.2959	
	1432.708	+0.022986	1432.708	15	I	2	431.2744		431.2744	
-0.038092	798.3895	-0.087706	1595.772	16	Y	1	318.1903	+0.058082	318.1903	
				17	K	0	155.127		155.127	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F21
Scannumber:	11534
Protein:	BSU22880; jofD; ypfD
Peptide Score:	112.34
Method:	ITMS; CID; 3



precursor information

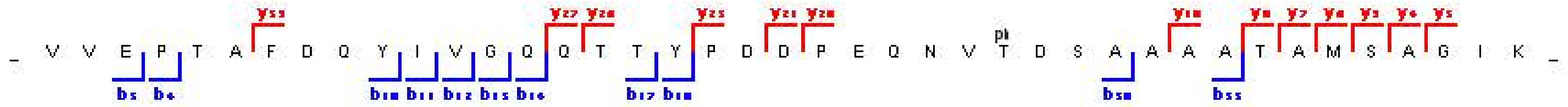
Mass:	1788.78053
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	112.338
Mass Error [ppm]:	-0.75925
PEP:	7.4948E-05
Precursor Type:	MULTI

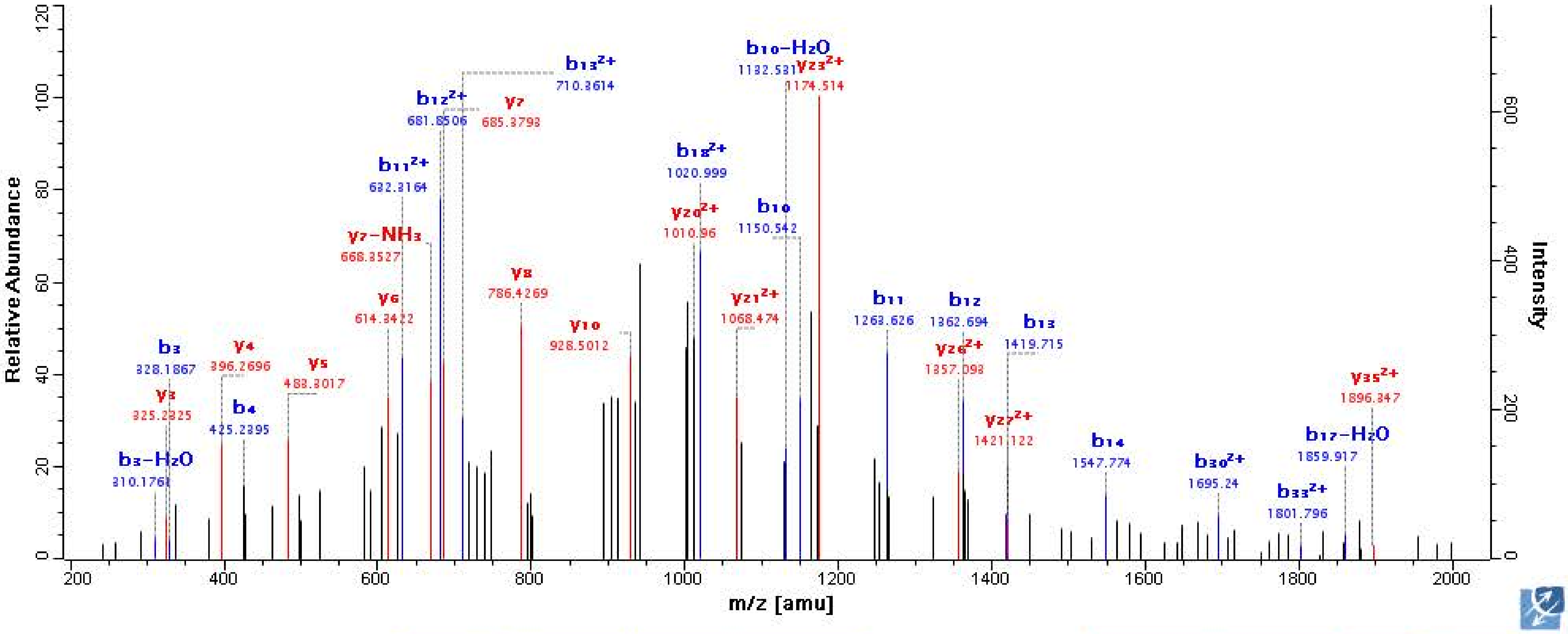
general information

Annotation:	14 of 16
AminoAcids Coverag	88 %
Intensity Coverage:	53 %
Protein Localisation:	362 ... 377

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.04986956	1	E	15				
	259.09246266	2	E	14	1660.7465736		1660.7465736	
	440.10647154	3	T	13	1531.7039805	+0.0775136	766.3556285	+0.1297231
	527.13849995	4	S	12	1350.6899717		1350.6899717	
	628.18617843	5	T	11	1263.6579432	+0.128922	1263.6579432	
	685.20764215	6	G	10	1162.6102648	+0.0198622	1162.6102648	
	832.27605607	7	F	9	1105.5888011	-0.0263011	1105.5888011	
	960.33463358	8	Q	8	958.52038713	-0.1124892	958.52038713	
	1073.4186976	9	I	7	830.46180962		830.46180962	
	1130.4401613	10	G	6	717.37774564	+0.022645	717.37774564	
-0.0546287	1245.4671043	11	D	5	660.35628192	+0.0204271	660.35628192	
	1358.5511683	12	I	4	545.32933889	+0.1049262	545.32933889	
+0.0226046	1471.6352323	13	I	3	432.24527491	-0.02152	432.24527491	
	1528.656696	14	G	2	319.16121093	+0.0941296	319.16121093	
+0.1325231	1643.683639	15	D	1	262.1397472		262.1397472	
		16	K	0	147.11280417		147.11280417	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F21
Scannumber:	12693
Protein:	BSU05740; phoAIII; phoB
Peptide Score:	81.73
Method:	ITMS; CID; 3





precursor information

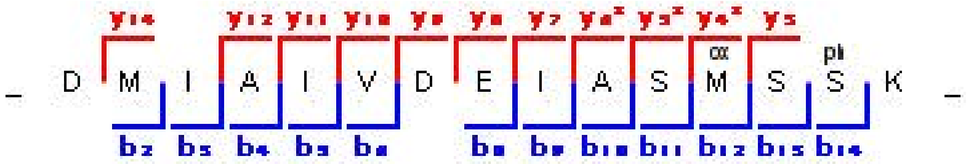
Mass:	4386.99592
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	81.73186
Mass Error [ppm]:	-0.25861
PEP:	2.2497E-22
Precursor Type:	ISO

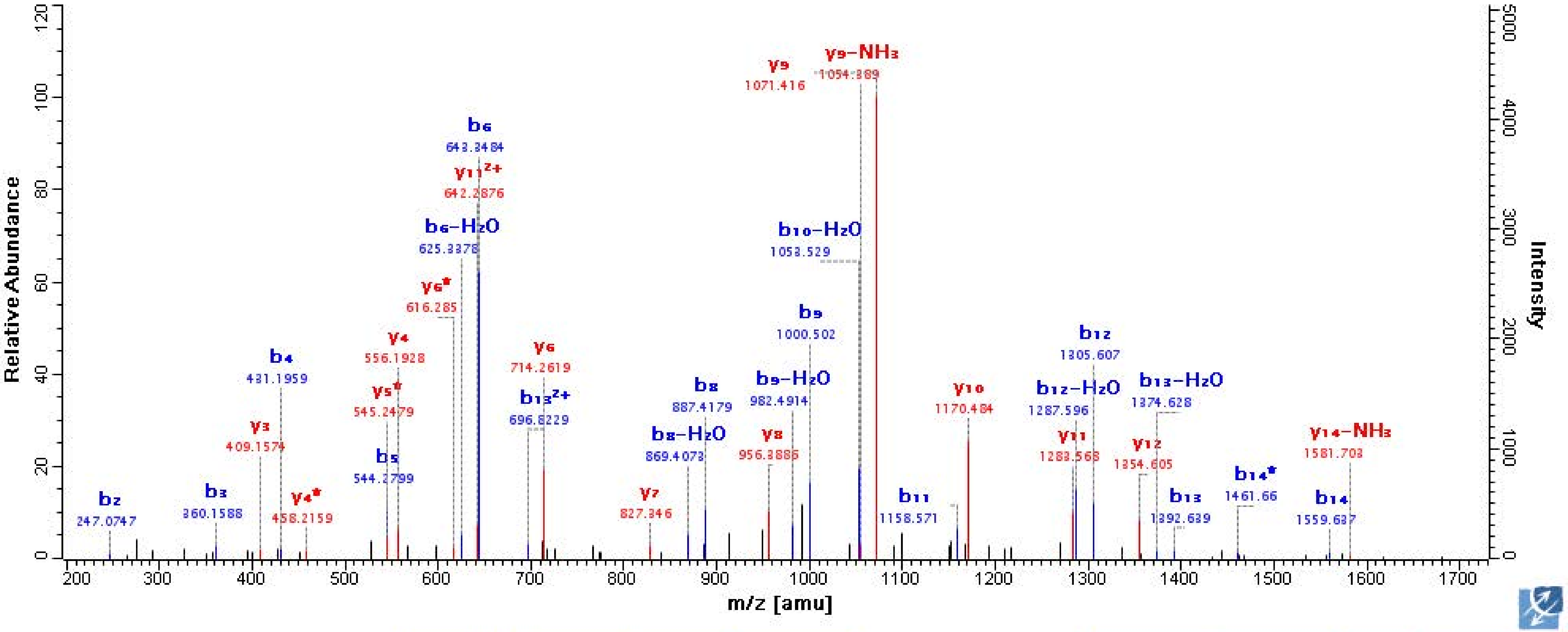
general information

Annotation:	24 of 41
AminoAcids Coverag	59 %
Intensity Coverage:	45 %
Protein Localisation:	73 ... 113

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757		100.0757	1	V	40				
	199.1441		199.1441	2	V	39	4288.936		4288.936	
	328.1867	-0.008231	328.1867	3	E	38	4189.868		4189.868	
	425.2395	+0.010722	425.2395	4	P	37	4060.825		4060.825	
	526.2871		526.2871	5	T	36	3963.772		3963.772	
	597.3243		597.3243	6	A	35	3862.724		3862.724	
	744.3927		744.3927	7	F	34	3791.687		1896.347	+0.207127
	859.4196		859.4196	8	D	33	3644.619		3644.619	
	987.4782		987.4782	9	Q	32	3529.592		3529.592	
	1150.542	+0.034411	1150.542	10	Y	31	3401.533		3401.533	
+0.276101	632.3164	+0.098541	1263.626	11	I	30	3238.47		3238.47	
+0.167492	681.8506	+0.043676	1362.694	12	V	29	3125.386		3125.386	
+0.286948	710.3614	-0.306645	1419.715	13	G	28	3026.318		3026.318	
	1547.774	+0.409924	1547.774	14	Q	27	2969.296		2969.296	
	1675.833		1675.833	15	Q	26	2841.238		1421.122	+0.398571
	1776.88		1776.88	16	T	25	2713.179		1357.093	-0.479489
	1877.928		1877.928	17	T	24	2612.131		2612.131	
-0.02535	1020.999		2040.991	18	Y	23	2511.084		2511.084	
	2138.044		2138.044	19	P	22	2348.02		1174.514	+0.139038
	2253.071		2253.071	20	D	21	2250.968		2250.968	
	2368.098		2368.098	21	D	20	2135.941		1068.474	-0.20563
	2465.151		2465.151	22	P	19	2020.914		1010.96	+0.403118
	2594.193		2594.193	23	E	18	1923.861		1923.861	
	2722.252		2722.252	24	Q	17	1794.818		1794.818	
	2836.295		2836.295	25	N	16	1666.76		1666.76	
	2935.363		2935.363	26	V	15	1552.717		1552.717	
	3116.377		3116.377	27	T	14	1453.648		1453.648	
	3231.404		3231.404	28	D	13	1272.634		1272.634	
	3318.436		3318.436	29	S	12	1157.607		1157.607	
+0.260557	1695.24		3389.473	30	A	11	1070.575		1070.575	
	3460.51		3460.51	31	A	10	999.5383		999.5383	
	3531.548		3531.548	32	A	9	928.5012	+0.084089	928.5012	
+0.063529	1801.796		3602.585	33	A	8	857.4641		857.4641	
	3703.632		3703.632	34	T	7	786.4269	-0.039193	786.4269	
	3774.669		3774.669	35	A	6	685.3793	-0.008422	685.3793	
	3905.71		3905.71	36	M	5	614.3422	+0.128912	614.3422	
	3992.742		3992.742	37	S	4	483.3017	+0.150903	483.3017	
	4063.779		4063.779	38	A	3	396.2696	+0.061227	396.2696	
	4120.801		4120.801	39	G	2	325.2325	+0.057081	325.2325	
	4233.885		4233.885	40	I	1	268.2111		268.2111	
				41	K	0	155.127		155.127	

Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F21
Scannumber: 13813
Protein: ahpF; BSU40100; ndh
Peptide Score: 228.19
Method: ITMS; CID; 3





precursor information

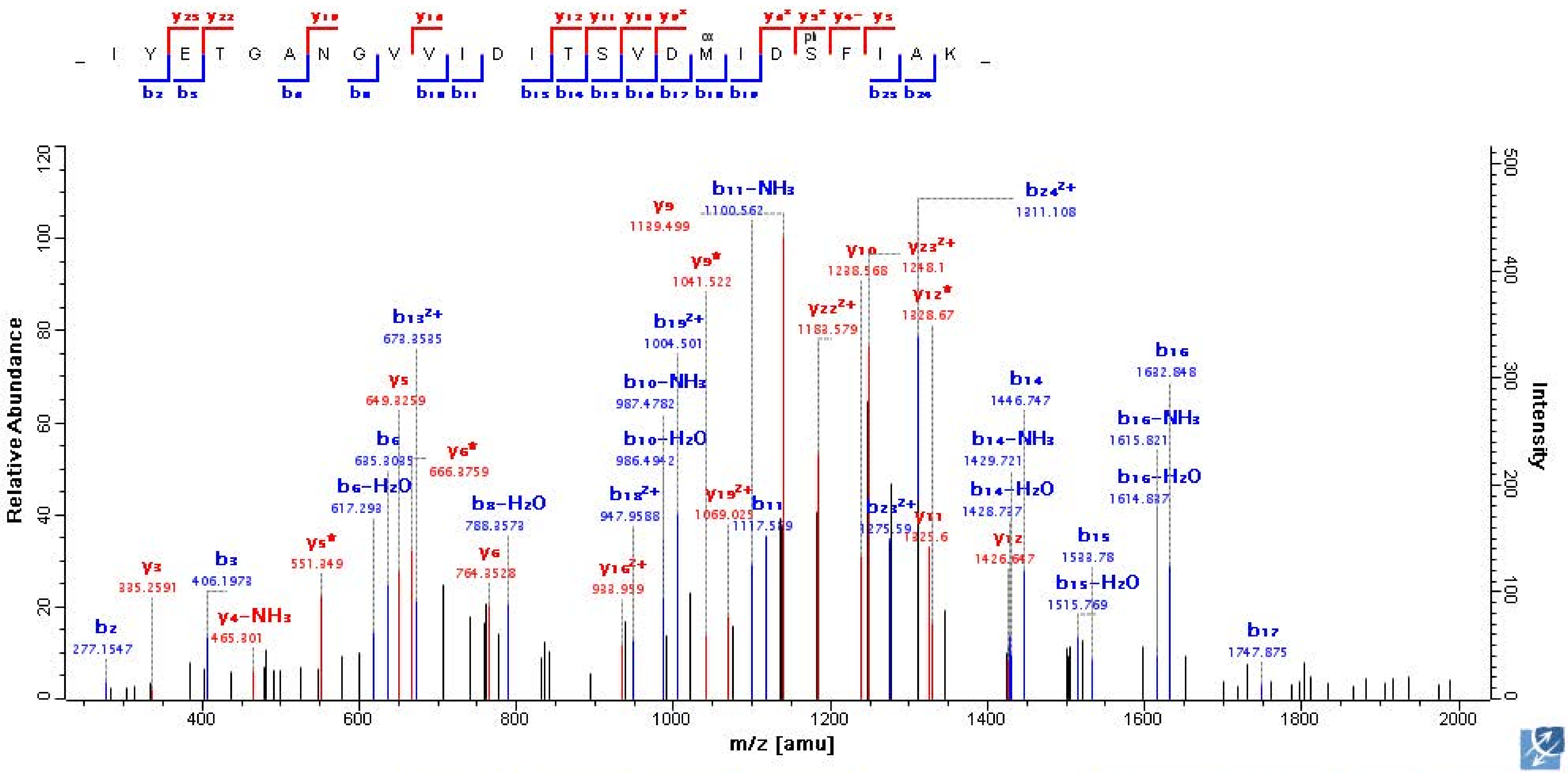
Mass:	1704.73524
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	228.1851
Mass Error [ppm]:	0.060042
PEP:	1.4988E-73
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	76 %
Protein Localisation:	36 ... 50

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342		116.0342	1	D	14				
	247.0747	+0.128604	247.0747	2	M	13	1598.73		1598.73	
	360.1588	-0.024979	360.1588	3	I	12	1467.689		1467.689	
	431.1959	-0.052693	431.1959	4	A	11	1354.605	+0.007059	1354.605	
	544.2799	+0.045433	544.2799	5	I	10	1283.568	+0.173568	642.2876	+0.271134
	643.3484	-0.023592	643.3484	6	V	9	1170.484	-0.064512	1170.484	
	758.3753		758.3753	7	D	8	1071.416	-0.051274	1071.416	
	887.4179	-0.086414	887.4179	8	E	7	956.3886	+0.205344	956.3886	
	1000.502	+0.161431	1000.502	9	I	6	827.346	+0.203565	827.346	
	1071.539		1071.539	10	A	5	714.2619	+0.047028	714.2619	
	1158.571	-0.064266	1158.571	11	S	4	643.2248		643.2248	
	1305.607	+0.00385	1305.607	12	M	3	556.1928	+0.043356	556.1928	
-0.221219	696.8229	+0.168721	1392.639	13	S	2	409.1574	+0.120869	409.1574	
	1559.637	+0.018629	1559.637	14	S	1	322.1254		322.1254	
				15	K	0	155.127		155.127	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F21
Scannumber:	13929
Protein:	BSU04680; rsbS; ycxS
Peptide Score:	149.07
Method:	ITMS; CID; 3



precursor information

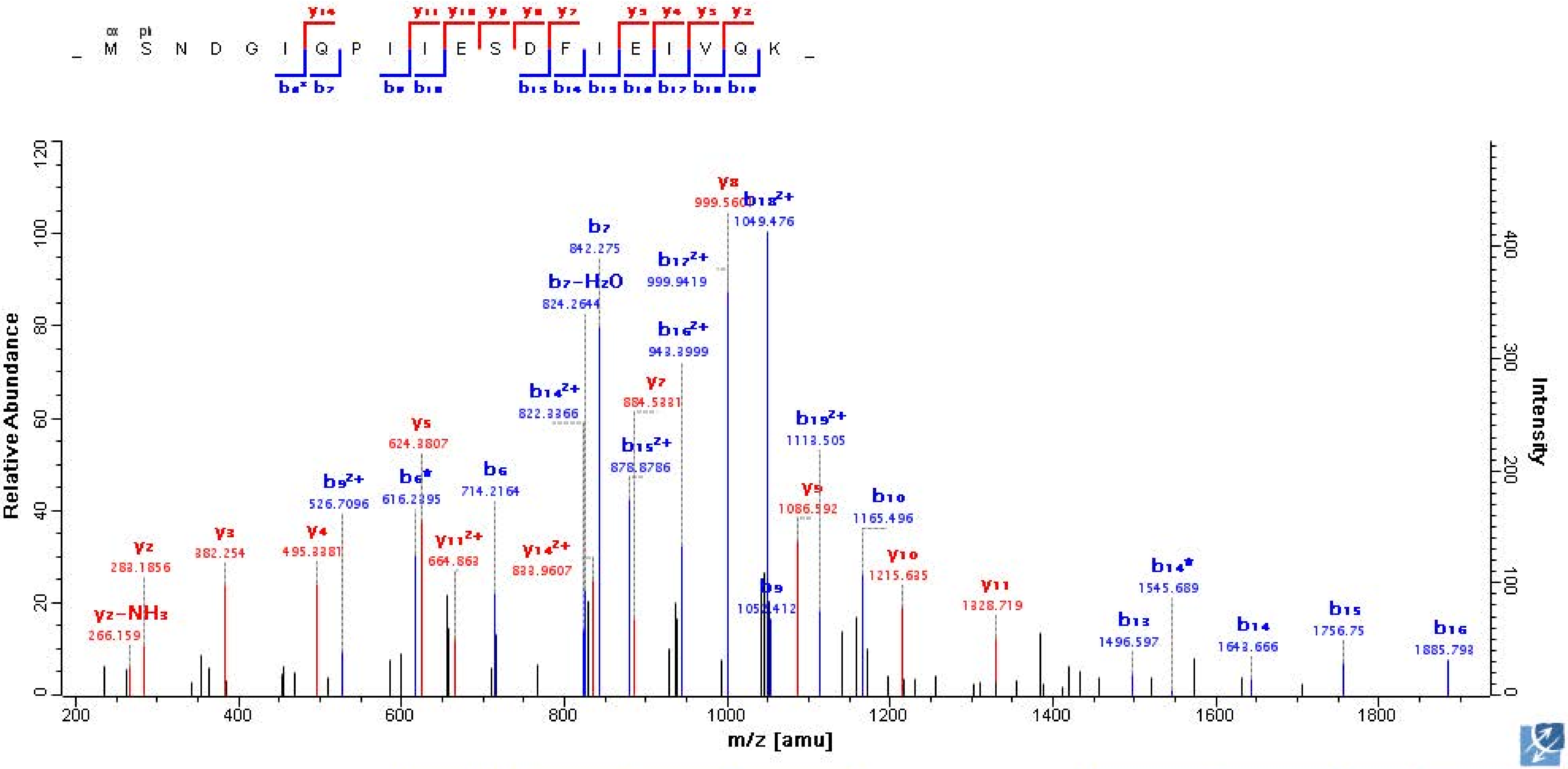
Mass:	2766.30844
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	149.0744
Mass Error [ppm]:	0.34677
PEP:	1.6655E-26
Precursor Type:	MULTI

general information

Annotation:	20 of 25
AminoAcids Coverag	80 %
Intensity Coverage:	56 %
Protein Localisation:	39 ... 63

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913		114.0913	1	I	24				
	277.1547	-0.181341	277.1547	2	Y	23	2658.256		2658.256	
	406.1973	-0.035092	406.1973	3	E	22	2495.192		1248.1	+0.180644
	507.2449		507.2449	4	T	21	2366.15		1183.579	+0.097692
	564.2664		564.2664	5	G	20	2265.102		2265.102	
	635.3035	+0.185801	635.3035	6	A	19	2208.081		2208.081	
	749.3464		749.3464	7	N	18	2137.044		1069.025	-0.106504
	806.3679		806.3679	8	G	17	2023.001		2023.001	
	905.4363		905.4363	9	V	16	1965.979		1965.979	
	1004.505		1004.505	10	V	15	1866.911		933.959	+0.252929
	1117.589	-0.001155	1117.589	11	I	14	1767.842		1767.842	
	1232.616		1232.616	12	D	13	1654.758		1654.758	
-0.005459	673.3535		1345.7	13	I	12	1539.731		1539.731	
	1446.747	+0.115673	1446.747	14	T	11	1426.647	+0.10987	1426.647	
	1533.78	+0.07632	1533.78	15	S	10	1325.6	+0.05269	1325.6	
	1632.848	-0.065336	1632.848	16	V	9	1238.568	+0.36133	1238.568	
	1747.875	+0.257086	1747.875	17	D	8	1139.499	+0.017146	1139.499	
-0.024997	947.9588		1894.91	18	M	7	1024.472		1024.472	
-0.110852	1004.501		2007.994	19	I	6	877.4369		877.4369	
	2123.021		2123.021	20	D	5	764.3528	+0.060342	764.3528	
	2290.02		2290.02	21	S	4	649.3259	+0.030034	649.3259	
	2437.088		2437.088	22	F	3	482.3275		482.3275	
+0.323756	1275.59		2550.172	23	I	2	335.2591	+0.352361	335.2591	
+0.288842	1311.108		2621.209	24	A	1	222.175		222.175	
				25	K	0	151.1379		151.1379	

Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F21
Scannumber: 13985
Protein: BSU23070; serA
Peptide Score: 147.56
Method: ITMS; CID; 3



precursor information

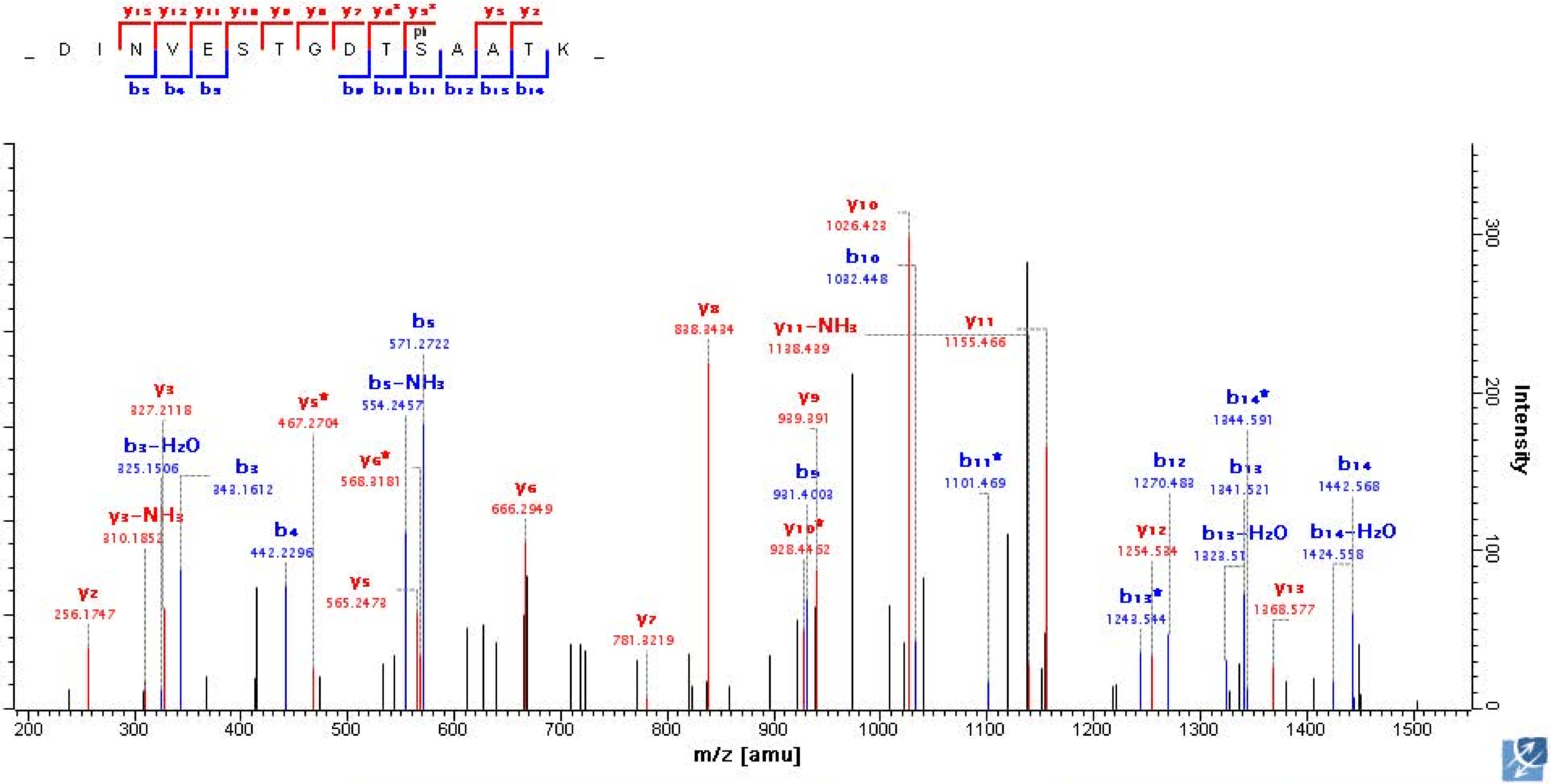
Mass:	2371.102
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	147.5625
Mass Error [ppm]:	0.06621
PEP:	3.1013E-19
Precursor Type:	MULTI

general information

Annotation:	14 of 20
AminoAcids Coverag	70 %
Intensity Coverage:	64 %
Protein Localisation:	10 ... 29

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.0427		148.0427	1	M	19				
	315.041		315.041	2	S	18	2233.088		2233.088	
	429.084		429.084	3	N	17	2066.09		2066.09	
	544.1109		544.1109	4	D	16	1952.047		1952.047	
	601.1324		601.1324	5	G	15	1837.02		1837.02	
	714.2164	+0.009947	714.2164	6	I	14	1779.998		1779.998	
	842.275	+0.131118	842.275	7	Q	13	1666.914		833.9607	-0.017971
	939.3278		939.3278	8	P	12	1538.856		1538.856	
+0.02024	526.7096	+0.019681	1052.412	9	I	11	1441.803		1441.803	
	1165.496	+0.054025	1165.496	10	I	10	1328.719	-0.037606	664.863	-0.286601
	1294.538		1294.538	11	E	9	1215.635	-0.048268	1215.635	
	1381.571		1381.571	12	S	8	1086.592	-0.044738	1086.592	
	1496.597	-0.061578	1496.597	13	D	7	999.5601	-0.050612	999.5601	
+0.141022	822.3366	+0.032606	1643.666	14	F	6	884.5331	+0.307142	884.5331	
+0.207754	878.8786	+0.173151	1756.75	15	I	5	737.4647		737.4647	
+0.111812	943.3999	-0.275204	1885.793	16	E	4	624.3807	+0.139368	624.3807	
+0.246843	999.9419		1998.877	17	I	3	495.3381	+0.110367	495.3381	
+0.10735	1049.476		2097.945	18	V	2	382.254	+0.086093	382.254	
-0.027041	1113.505		2226.004	19	Q	1	283.1856	+0.182889	283.1856	
				20	K	0	155.127		155.127	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F21
Scannumber:	5109
Protein:	BSU01320; rplR
Peptide Score:	159.69
Method:	ITMS; CID; 3



precursor information

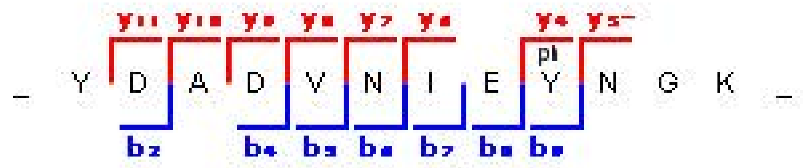
Mass:	1587.66654
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	159.6945
Mass Error [ppm]:	0.010843
PEP:	1.279E-17
Precursor Type:	MULTI

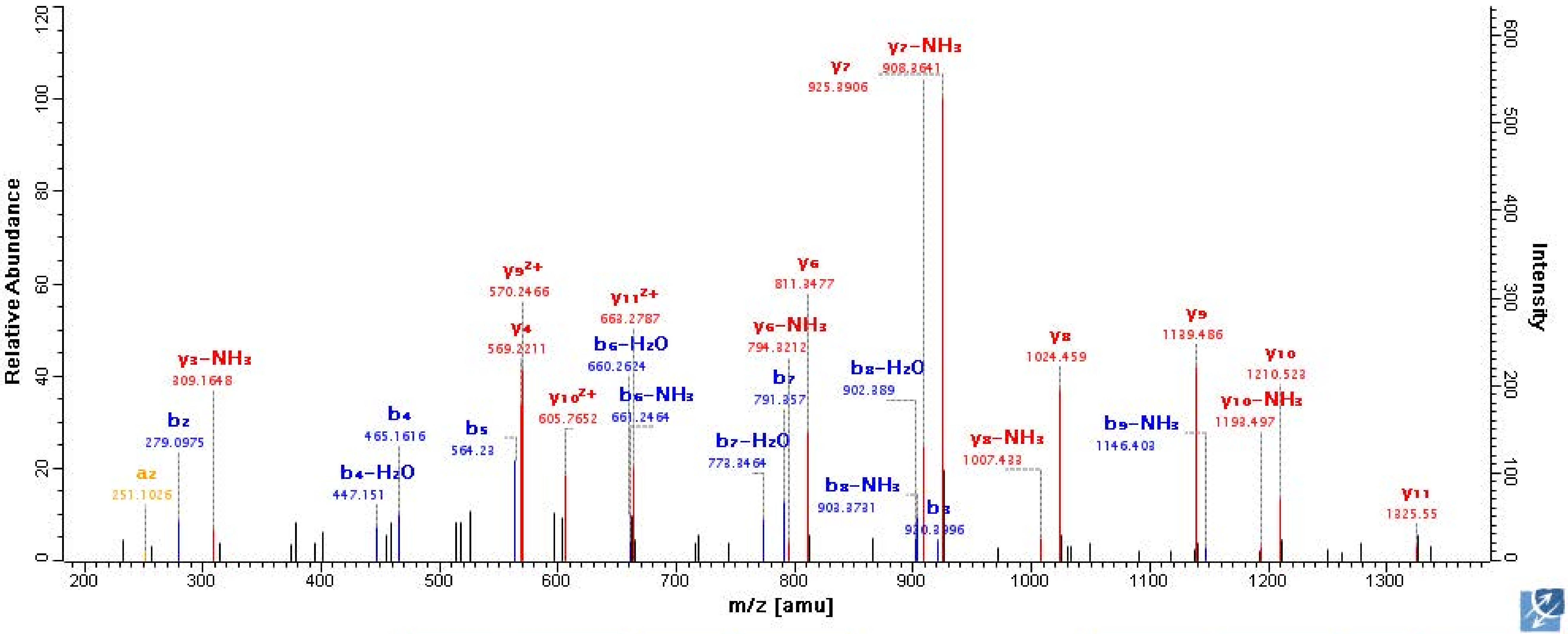
general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	52 %
Protein Localisation:	62 ... 76

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	116.034219499	1	D	14		
	229.118283479	2	I	13	1481.661058406	
-0.0513476	343.161210926	3	N	12	1368.576994425	+0.114656
+0.1448869	442.229624842	4	V	11	1254.534066978	-0.011606
-0.0315563	571.272217939	5	E	10	1155.465653062	+0.0782923
	658.304246349	6	S	9	1026.423059966	-0.0065561
	759.351924823	7	T	8	939.391031556	+0.2569177
	816.373388546	8	G	7	838.343353082	+0.0431826
-0.013857	931.400331578	9	D	6	781.321889358	-0.3679099
-0.055554	1032.448010052	10	T	5	666.294946326	+0.1416381
	1199.446368871	11	S	4	565.247267852	+0.0090798
-0.0690539	1270.483482658	12	A	3	398.248909033	
+0.21622	1341.520596446	13	A	2	327.211795246	+0.164517
+0.2585073	1442.56827492	14	T	1	256.174681458	+0.1295483
		15	K	0	155.127002984	

Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F21
Scannumber: 5972
Protein: BSU13900; ptsH
Peptide Score: 162.38
Method: ITMS; CID; 3





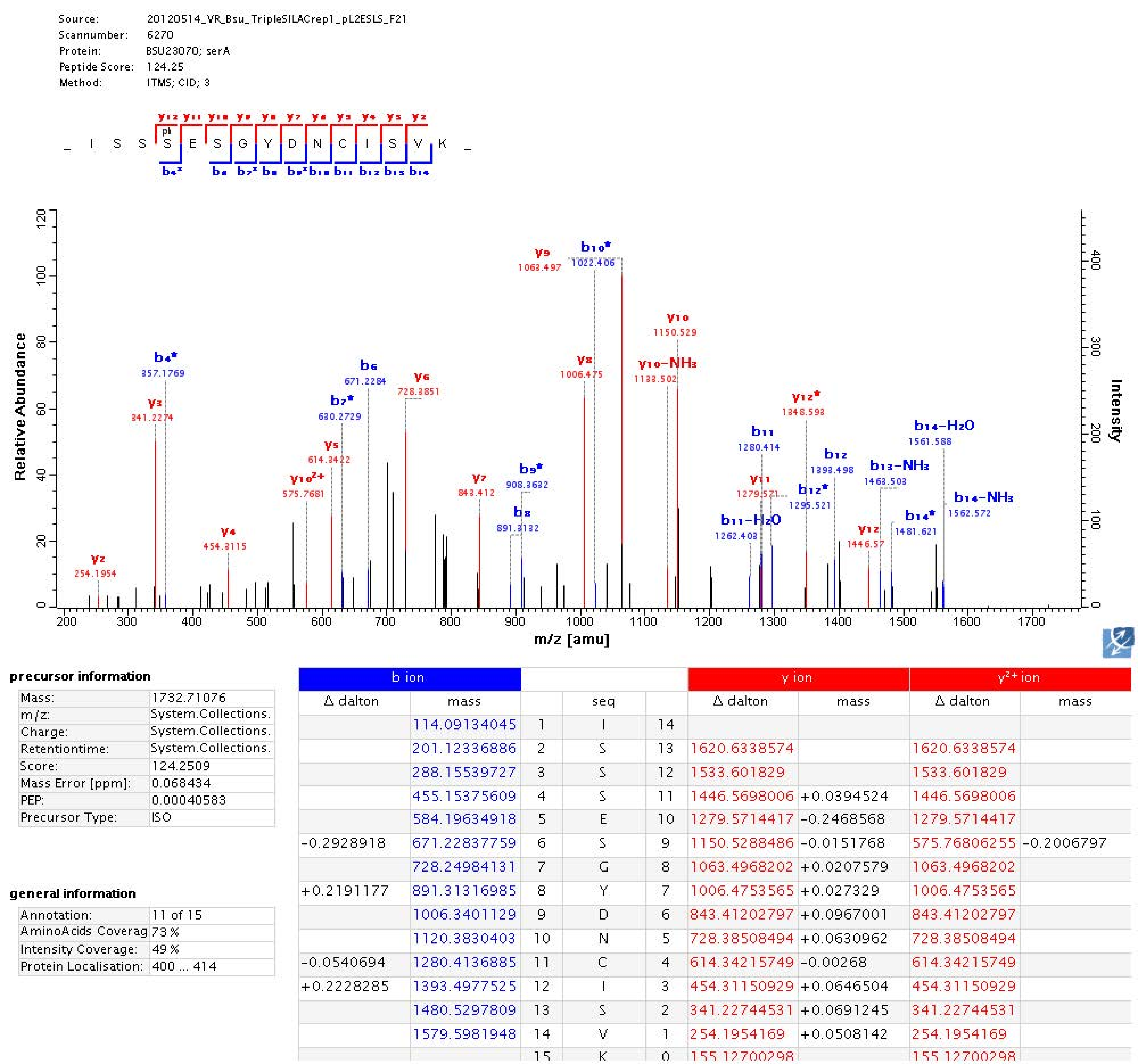
precursor information

Mass:	1487.60598
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	162.3797
Mass Error [ppm]:	-0.082306
PEP:	4.3103E-23
Precursor Type:	ISO

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	70 %
Protein Localisation:	29 ... 40

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.0757		164.0706	1	Y	11				
+0.014707	251.1026	+0.075212	279.0975	2	D	10	1325.55	-0.158572	663.2787	+0.058922
	322.1397		350.1347	3	A	9	1210.523	+0.066125	605.7652	-0.081843
	437.1667	+0.167253	465.1616	4	D	8	1139.486	+0.100797	570.2466	+0.118111
	536.2351	-0.407753	564.23	5	V	7	1024.459	+0.041193	1024.459	
	650.278		678.2729	6	N	6	925.3906	+0.014453	925.3906	
	763.3621	-0.120133	791.357	7	I	5	811.3477	+0.070564	811.3477	
	892.4047	-0.153937	920.3996	8	E	4	698.2636		698.2636	
	1135.434		1163.429	9	Y	3	569.2211	+0.073686	569.2211	
	1249.477		1277.472	10	N	2	326.1914		326.1914	
	1306.499		1334.494	11	G	1	212.1485		212.1485	
				12	K	0	155.127		155.127	



Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F21
Scannumber: 6270
Protein: BSU23070; serA
Peptide Score: 124.25
Method: ITMS; CID; 3

precursor information

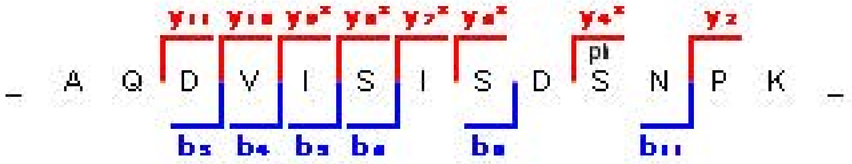
Mass:	1732.71076
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	124.2509
Mass Error [ppm]:	0.068434
PEP:	0.00040583
Precursor Type:	ISO

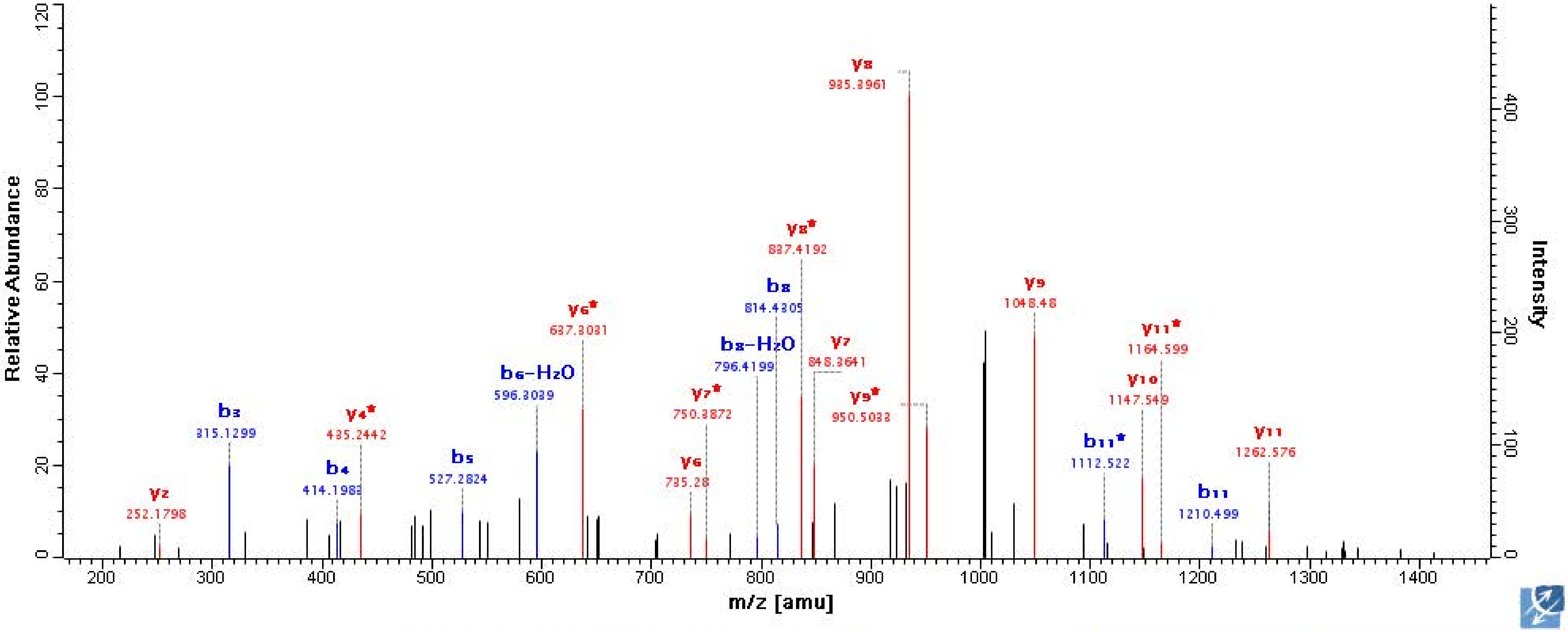
general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	49 %
Protein Localisation:	400 ... 414

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045	1	I	14				
	201.12336886	2	S	13	1620.6338574		1620.6338574	
	288.15539727	3	S	12	1533.601829		1533.601829	
	455.15375609	4	S	11	1446.5698006	+0.0394524	1446.5698006	
	584.19634918	5	E	10	1279.5714417	-0.2468568	1279.5714417	
-0.2928918	671.22837759	6	S	9	1150.5288486	-0.0151768	575.76806255	-0.2006797
	728.24984131	7	G	8	1063.4968202	+0.0207579	1063.4968202	
+0.2191177	891.31316985	8	Y	7	1006.4753565	+0.027329	1006.4753565	
	1006.3401129	9	D	6	843.41202797	+0.0967001	843.41202797	
	1120.3830403	10	N	5	728.38508494	+0.0630962	728.38508494	
-0.0540694	1280.4136885	11	C	4	614.34215749	-0.00268	614.34215749	
+0.2228285	1393.4977525	12	I	3	454.31150929	+0.0646504	454.31150929	
	1480.5297809	13	S	2	341.22744531	+0.0691245	341.22744531	
	1579.5981948	14	V	1	254.1954169	+0.0508142	254.1954169	
		15	K	0	155.12700298		155.12700298	

Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F21
Scannumber: 6590
Protein: BSU13620; mtnD; ykrZ
Peptide Score: 109.83
Method: ITMS; CID; 3





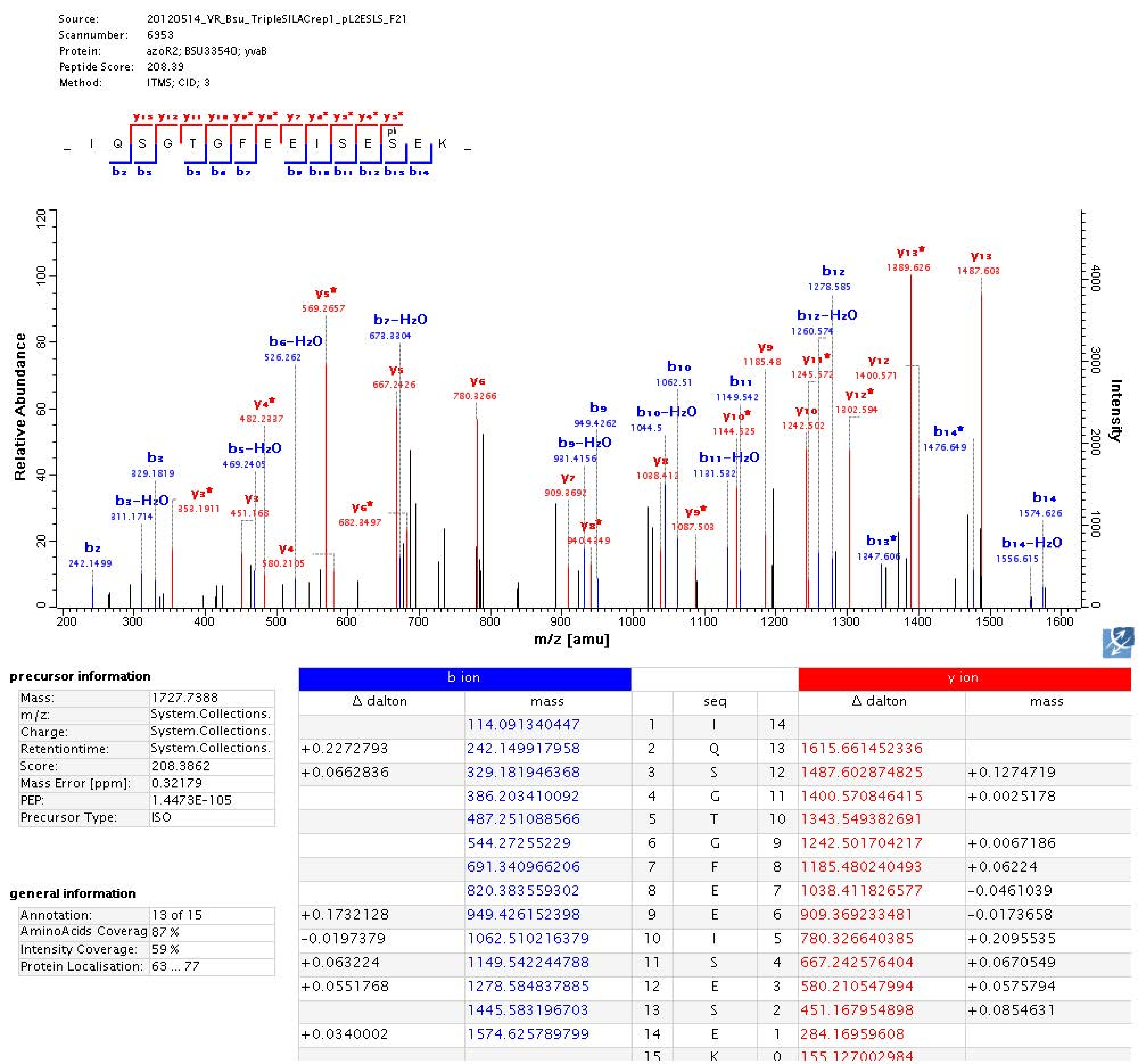
precursor information

Mass:	1452.6492
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	109.8349
Mass Error [ppm]:	-0.37622
PEP:	0.00032355
Precursor Type:	MULTI

general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	51 %
Protein Localisation:	76 ... 88

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	72.044390254	1	A	12		
	200.102967766	2	Q	11	1390.634115374	
-0.0227331	315.129910798	3	D	10	1262.575537862	+0.2903069
+0.1243071	414.198324714	4	V	9	1147.54859483	+0.1165663
+0.0910244	527.282388694	5	I	8	1048.480180914	-0.0749075
	614.314417104	6	S	7	935.396116933	-0.0228259
	727.398481085	7	I	6	848.364088524	-0.0045304
+0.105013	814.430509495	8	S	5	735.280024543	+0.1065111
	929.457452527	9	D	4	648.247996133	
	1096.455811345	10	S	3	533.221053101	
+0.1040444	1210.498738792	11	N	2	366.222694283	
	1307.551502644	12	P	1	252.179766836	-0.038974
		13	K	0	155.127002984	



Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F21
Scannumber: 6953
Protein: azoR2; BSU33540; yvaB
Peptide Score: 208.39
Method: ITMS; CID; 3

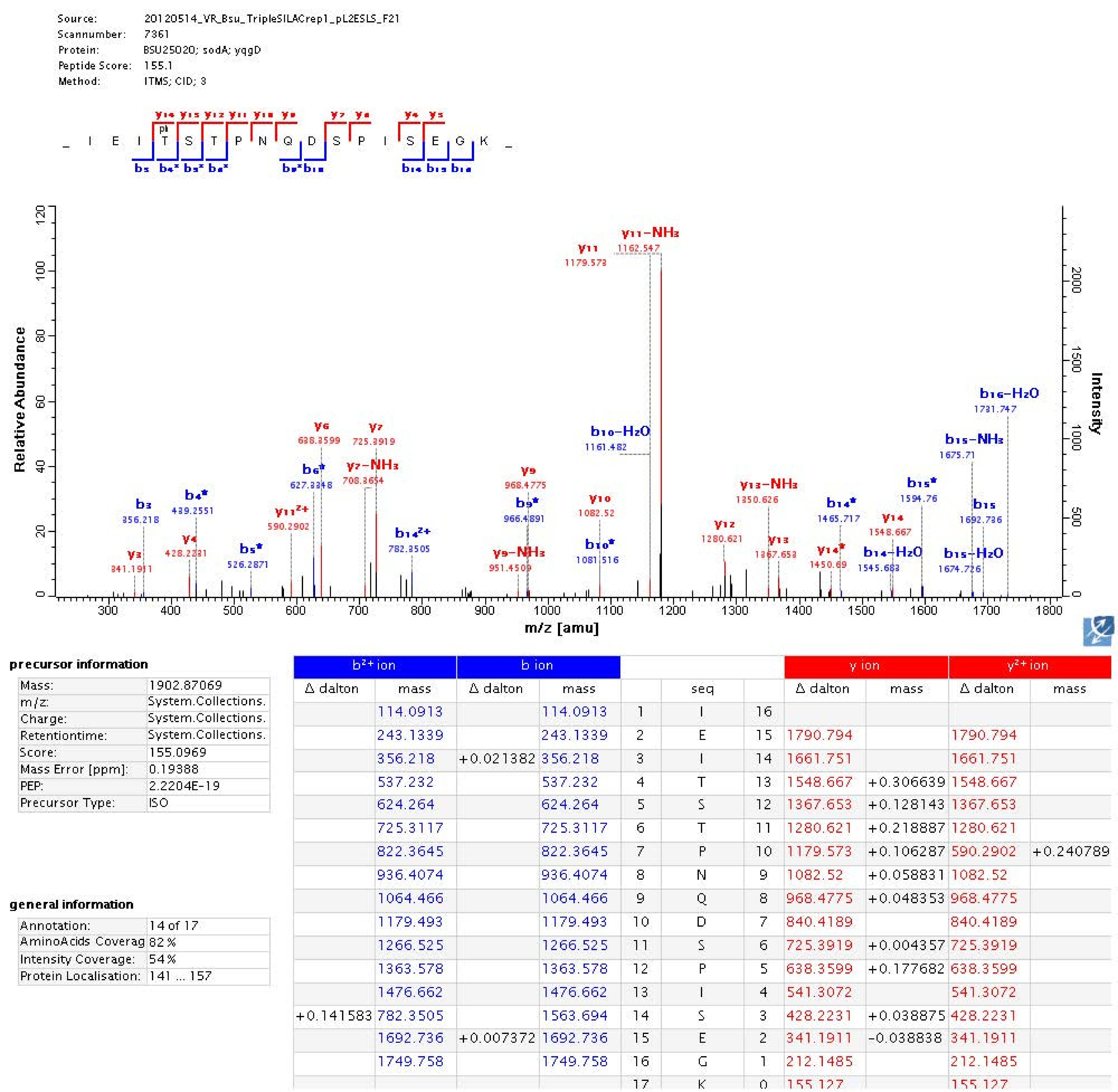
precursor information

Mass:	1727.7388
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	208.3862
Mass Error [ppm]:	0.32179
PEP:	1.4473E-105
Precursor Type:	ISO

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	59 %
Protein Localisation:	63 ... 77

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	114.091340447	1	I	14		
+0.2272793	242.149917958	2	Q	13	1615.661452336	
+0.0662836	329.181946368	3	S	12	1487.602874825	+0.1274719
	386.203410092	4	G	11	1400.570846415	+0.0025178
	487.251088566	5	T	10	1343.549382691	
	544.27255229	6	G	9	1242.501704217	+0.0067186
	691.340966206	7	F	8	1185.480240493	+0.06224
	820.383559302	8	E	7	1038.411826577	-0.0461039
+0.1732128	949.426152398	9	E	6	909.369233481	-0.0173658
-0.0197379	1062.510216379	10	I	5	780.326640385	+0.2095535
+0.063224	1149.542244788	11	S	4	667.242576404	+0.0670549
+0.0551768	1278.584837885	12	E	3	580.210547994	+0.0575794
	1445.583196703	13	S	2	451.167954898	+0.0854631
+0.0340002	1574.625789799	14	E	1	284.16959608	
		15	K	0	155.127002984	



Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F21
Scannumber: 7361
Protein: BSU25020; sodA; yqgD
Peptide Score: 155.1
Method: ITMS; CID; 3

precursor information

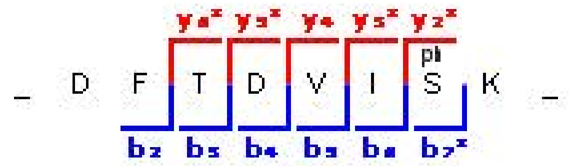
Mass:	1902.87069
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	155.0969
Mass Error [ppm]:	0.19388
PEP:	2.2204E-19
Precursor Type:	ISO

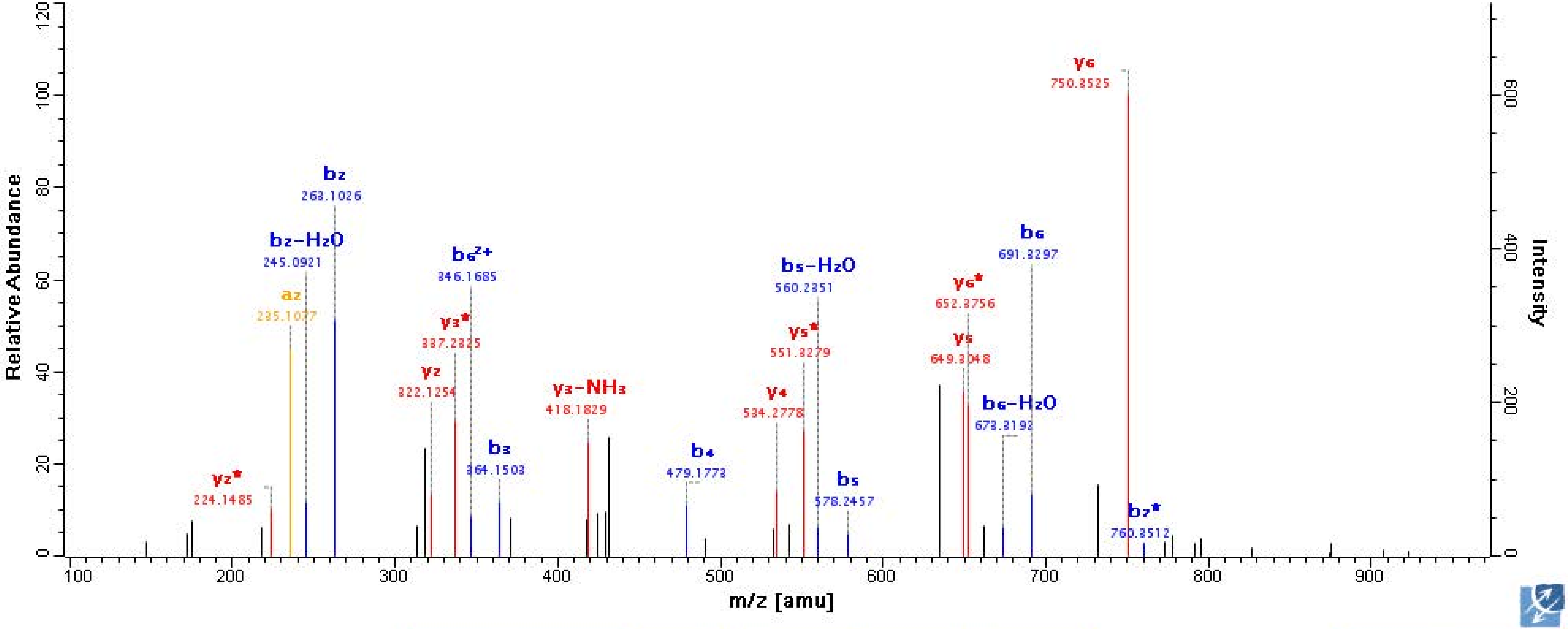
general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	54 %
Protein Localisation:	141 ... 157

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913		114.0913	1	I	16				
	243.1339		243.1339	2	E	15	1790.794		1790.794	
	356.218	+0.021382	356.218	3	I	14	1661.751		1661.751	
	537.232		537.232	4	T	13	1548.667	+0.306639	1548.667	
	624.264		624.264	5	S	12	1367.653	+0.128143	1367.653	
	725.3117		725.3117	6	T	11	1280.621	+0.218887	1280.621	
	822.3645		822.3645	7	P	10	1179.573	+0.106287	590.2902	+0.240789
	936.4074		936.4074	8	N	9	1082.52	+0.058831	1082.52	
	1064.466		1064.466	9	Q	8	968.4775	+0.048353	968.4775	
	1179.493		1179.493	10	D	7	840.4189		840.4189	
	1266.525		1266.525	11	S	6	725.3919	+0.004357	725.3919	
	1363.578		1363.578	12	P	5	638.3599	+0.177682	638.3599	
	1476.662		1476.662	13	I	4	541.3072		541.3072	
+0.141583	782.3505		1563.694	14	S	3	428.2231	+0.038875	428.2231	
	1692.736	+0.007372	1692.736	15	E	2	341.1911	-0.038838	341.1911	
	1749.758		1749.758	16	G	1	212.1485		212.1485	
				17	K	0	155.127		155.127	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F21
Scannumber:	7651
Protein:	BSU33240; oxdC; yvrK
Peptide Score:	143.28
Method:	ITMS; CID; 3





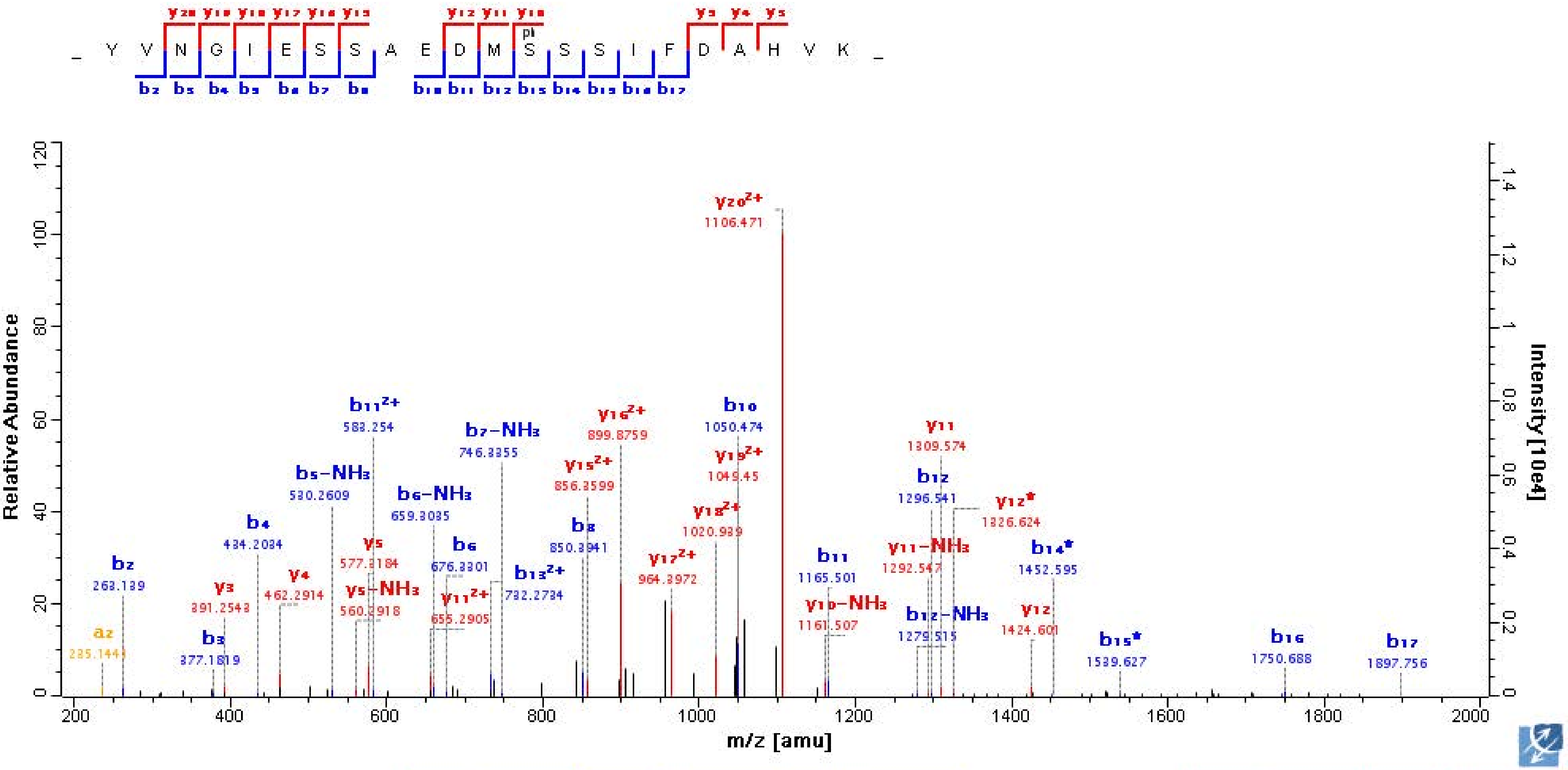
precursor information

Mass:	1011.44025
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	143.2845
Mass Error [ppm]:	-0.28966
PEP:	3.2125E-17
Annotation:	6 of 8
AminoAcids Coverag	75 %
Intensity Coverage:	69 %
Protein Localisation:	366 ... 373

g

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	88.0393		116.0342		116.0342	1	D	7		
+0.002877	235.1077		263.1026	+0.06854	263.1026	2	F	6	897.4209	
	336.1554		364.1503	+0.124133	364.1503	3	T	5	750.3525	+0.05092
	451.1823		479.1773	+0.026389	479.1773	4	D	4	649.3048	-0.052097
	550.2508		578.2457	+0.048093	578.2457	5	V	3	534.2778	+0.127983
	663.3348	+0.052595	346.1685	-0.070761	691.3297	6	I	2	435.2094	
	830.3332		858.3281		858.3281	7	S	1	322.1254	+0.104741
						8	K	0	155.127	

Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F01
Scannumber: 10769
Protein: BSU28440; citF; sdhA
Peptide Score: 148.52
Method: ITMS; CID; 3



precursor information

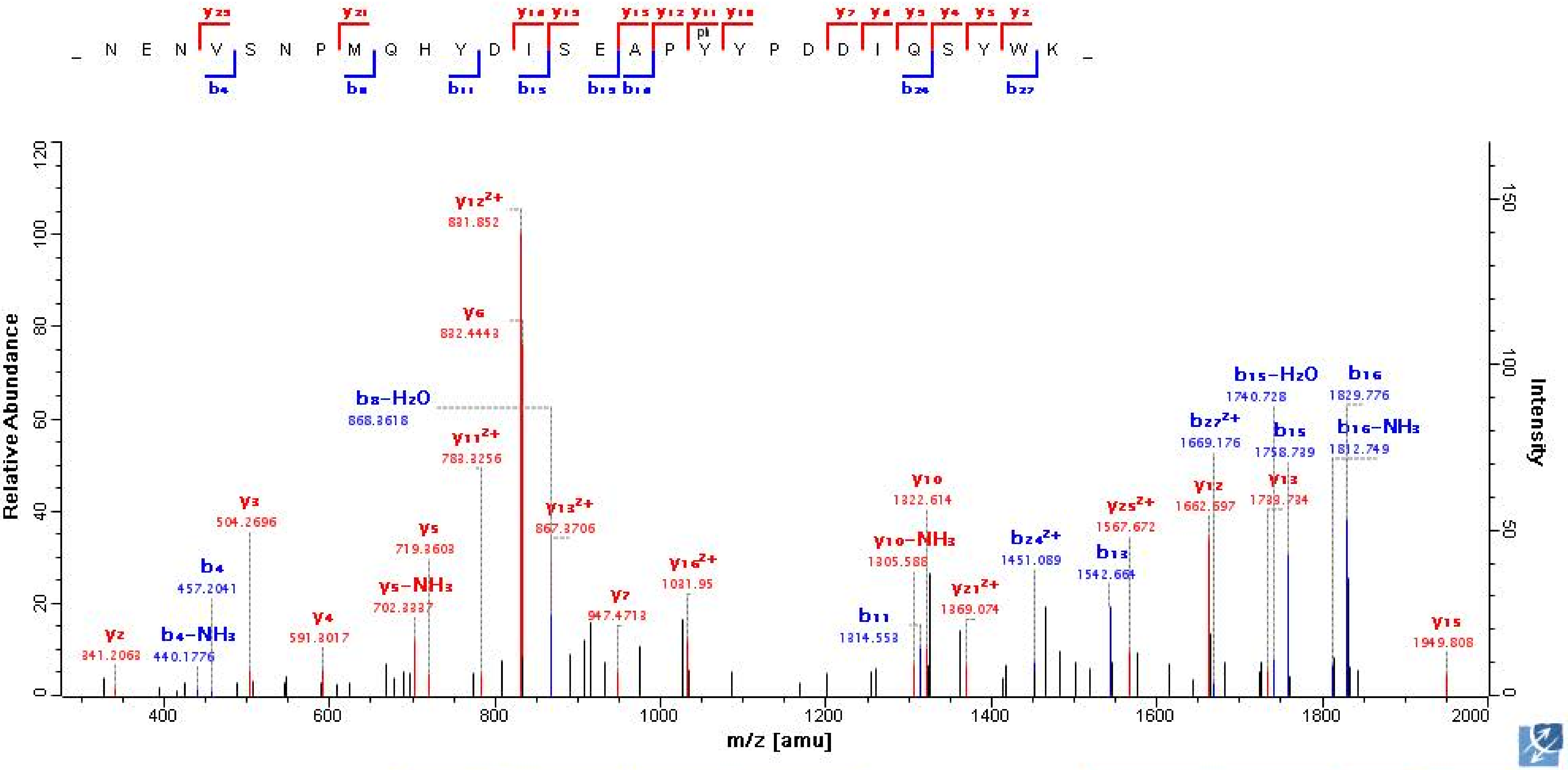
Mass:	2465.0453
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	148.5208
Mass Error [ppm]:	-0.19602
PEP:	3.1818E-25
Precursor Type:	MULTI

general information

Annotation:	18 of 22
AminoAcids Coverag	82 %
Intensity Coverage:	62 %
Protein Localisation:	409 ... 430

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
	136.076		164.071		164.071	1	Y	21				
+0.05122	235.144		263.139	+0.07116	263.139	2	V	20	2311		2311	
	349.187		377.182	+0.17047	377.182	3	N	19	2211.94		1106.47	+0.3872
	406.208		434.203	+0.04244	434.203	4	G	18	2097.89		1049.45	-0.1909
	519.293		547.287		547.287	5	I	17	2040.87		1020.94	+0.0077
	648.335		676.33	-0.0184	676.33	6	E	16	1927.79		964.397	+0.1656
	735.367		763.362		763.362	7	S	15	1798.74		899.876	+0.2151
	822.399		850.394	+0.47618	850.394	8	S	14	1711.71		856.36	+0.2598
	893.436		921.431		921.431	9	A	13	1624.68		1624.68	
	1022.48		1050.47	-0.3498	1050.47	10	E	12	1553.64		1553.64	
	1137.51	+0.00177	583.254	+0.11886	1165.5	11	D	11	1424.6	-0.0403	1424.6	
	1268.55		1296.54	+0.08801	1296.54	12	M	10	1309.57	+0.11496	655.291	-0.0851
	1435.54	+0.12871	732.273		1463.54	13	S	9	1178.53		1178.53	
	1522.58		1550.57		1550.57	14	S	8	1011.53		1011.53	
	1609.61		1637.6		1637.6	15	S	7	924.503		924.503	
	1722.69		1750.69	-0.0508	1750.69	16	I	6	837.471		837.471	
	1869.76		1897.76	+0.31794	1897.76	17	F	5	724.387		724.387	
	1984.79		2012.78		2012.78	18	D	4	577.318	+0.01261	577.318	
	2055.83		2083.82		2083.82	19	A	3	462.291	+0.15112	462.291	
	2192.88		2220.88		2220.88	20	H	2	391.254	+0.02918	391.254	
	2291.95		2319.95		2319.95	21	V	1	254.195		254.195	
						22	K	0	155.127		155.127	

Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F01
Scannumber: 11259
Protein: BSU39880; VE7D; yxaQ; yxbC
Peptide Score: 97.35
Method: ITMS; CID; 3



precursor information

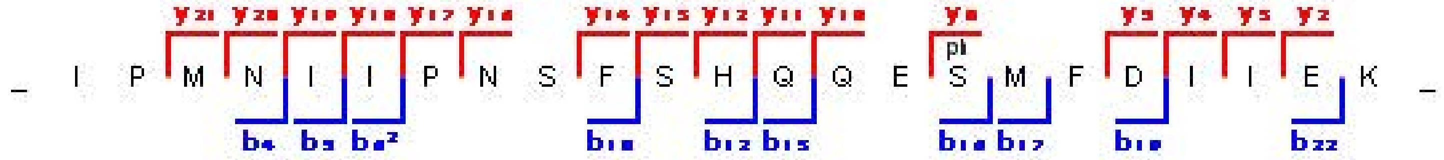
Mass:	3490.45836
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	97.35215
Mass Error [ppm]:	0.083491
PEP:	4.9517E-17
Precursor Type:	ISO

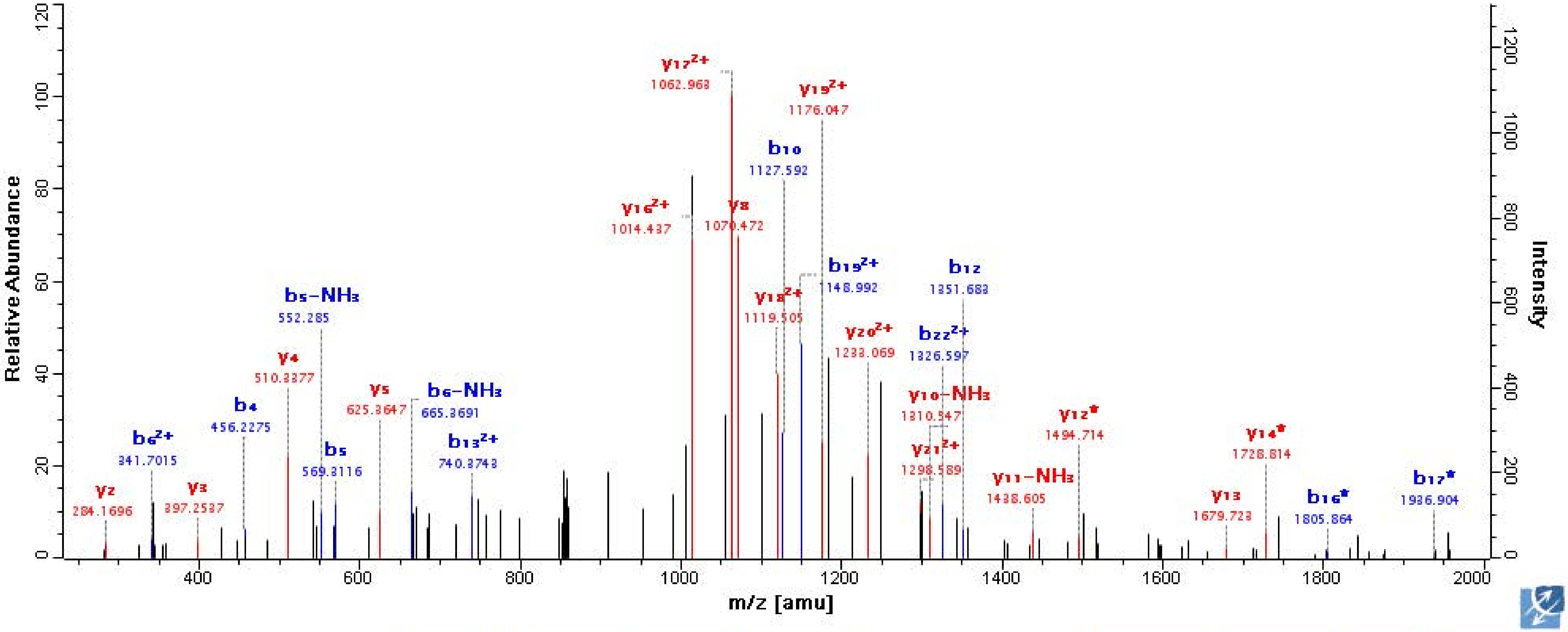
general information

Annotation:	17 of 28
AminoAcids Coverag	61 %
Intensity Coverage:	55 %
Protein Localisation:	167 ... 194

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502		115.0502	1	N	27				
	244.0928		244.0928	2	E	26	3377.422		3377.422	
	358.1357		358.1357	3	N	25	3248.38		3248.38	
	457.2041	+0.051233	457.2041	4	V	24	3134.337		1567.672	+0.198642
	544.2362		544.2362	5	S	23	3035.268		3035.268	
	658.2791		658.2791	6	N	22	2948.236		2948.236	
	755.3319		755.3319	7	P	21	2834.194		2834.194	
	886.3723		886.3723	8	M	20	2737.141		1369.074	+0.493608
	1014.431		1014.431	9	Q	19	2606.1		2606.1	
	1151.49		1151.49	10	H	18	2478.042		2478.042	
	1314.553	-0.107238	1314.553	11	Y	17	2340.983		2340.983	
	1429.58		1429.58	12	D	16	2177.919		2177.919	
	1542.664	+0.415178	1542.664	13	I	15	2062.893		1031.95	+0.193171
	1629.696		1629.696	14	S	14	1949.808	+0.334493	1949.808	
	1758.739	-0.316792	1758.739	15	E	13	1862.776		1862.776	
	1829.776	+0.079322	1829.776	16	A	12	1733.734	+0.221493	867.3706	+0.15496
	1926.829		1926.829	17	P	11	1662.697	+0.055848	831.852	+0.011896
	2169.858		2169.858	18	Y	10	1565.644		783.3256	-0.172416
	2332.922		2332.922	19	Y	9	1322.614	-0.310826	1322.614	
	2429.974		2429.974	20	P	8	1159.551		1159.551	
	2545.001		2545.001	21	D	7	1062.498		1062.498	
	2660.028		2660.028	22	D	6	947.4713	+0.083918	947.4713	
	2773.112		2773.112	23	I	5	832.4443	+0.095969	832.4443	
+0.064942	1451.089		2901.171	24	Q	4	719.3603	+0.133951	719.3603	
	2988.203		2988.203	25	S	3	591.3017	+0.29696	591.3017	
	3151.266		3151.266	26	Y	2	504.2696	+0.019906	504.2696	
+0.348823	1669.176		3337.346	27	W	1	341.2063	-0.033495	341.2063	
				28	K	0	155.127		155.127	

Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F01
Scannumber: 13090
Protein: BSU16810; ymfC
Peptide Score: 99.93
Method: ITMS; CID; 3





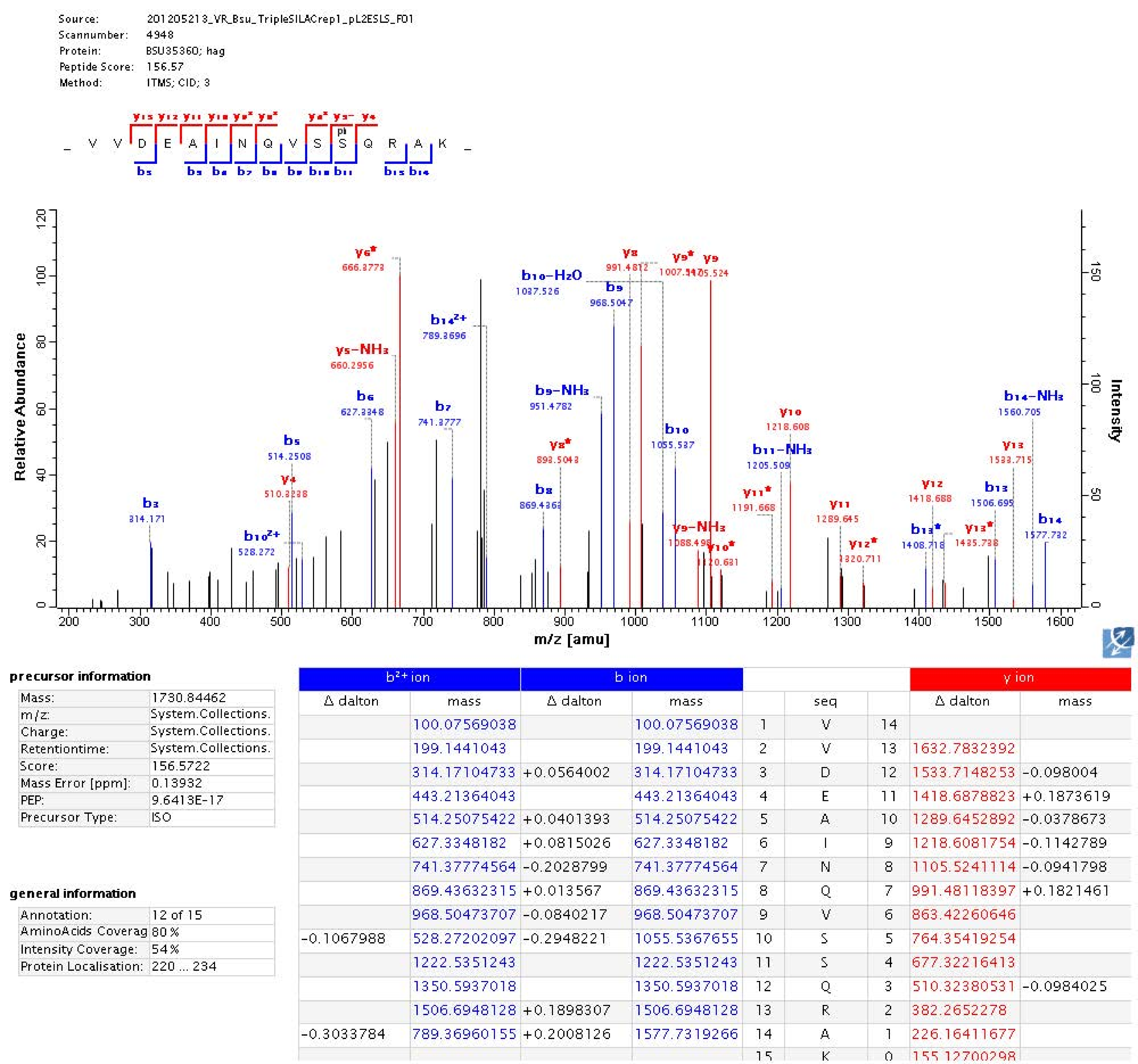
precursor information

Mass:	2805.30057
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	99.93027
Mass Error [ppm]:	0.25965
PEP:	3.9386E-07
Precursor Type:	ISO

general information

Annotation:	17 of 23
AminoAcids Coverag	74%
Intensity Coverage:	44%
Protein Localisation:	149 ... 171

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913		114.0913	1	I	22				
	211.1441		211.1441	2	P	21	2693.223		2693.223	
	342.1846		342.1846	3	M	20	2596.17		1298.589	-0.335974
	456.2275	+0.10836	456.2275	4	N	19	2465.13		1233.069	+0.375064
	569.3116	-0.013118	569.3116	5	I	18	2351.087		1176.047	+0.302778
-0.154097	341.7015		682.3956	6	I	17	2238.003		1119.505	+0.149742
	779.4484		779.4484	7	P	16	2124.919		1062.963	+0.100709
	893.4913		893.4913	8	N	15	2027.866		1014.437	+0.172807
	980.5234		980.5234	9	S	14	1913.823		1913.823	
	1127.592	-0.304424	1127.592	10	F	13	1826.791		1826.791	
	1214.624		1214.624	11	S	12	1679.723	+0.350385	1679.723	
	1351.683	+0.125753	1351.683	12	H	11	1592.691		1592.691	
+0.060895	740.3743		1479.741	13	Q	10	1455.632		1455.632	
	1607.8		1607.8	14	Q	9	1327.573		1327.573	
	1736.842		1736.842	15	E	8	1199.515		1199.515	
	1903.841		1903.841	16	S	7	1070.472	+0.444702	1070.472	
	2034.881		2034.881	17	M	6	903.4736		903.4736	
	2181.95		2181.95	18	F	5	772.4331		772.4331	
+0.235812	1148.992		2296.977	19	D	4	625.3647	+0.033404	625.3647	
	2410.061		2410.061	20	I	3	510.3377	-0.104326	510.3377	
	2523.145		2523.145	21	I	2	397.2537	+0.001284	397.2537	
+0.071735	1326.597		2652.187	22	E	1	284.1696	+0.04833	284.1696	
				23	K	0	155.127		155.127	



Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F01
Scannumber: 4948
Protein: BSU35360; hag
Peptide Score: 156.57
Method: ITMS; CID; 3

precursor information

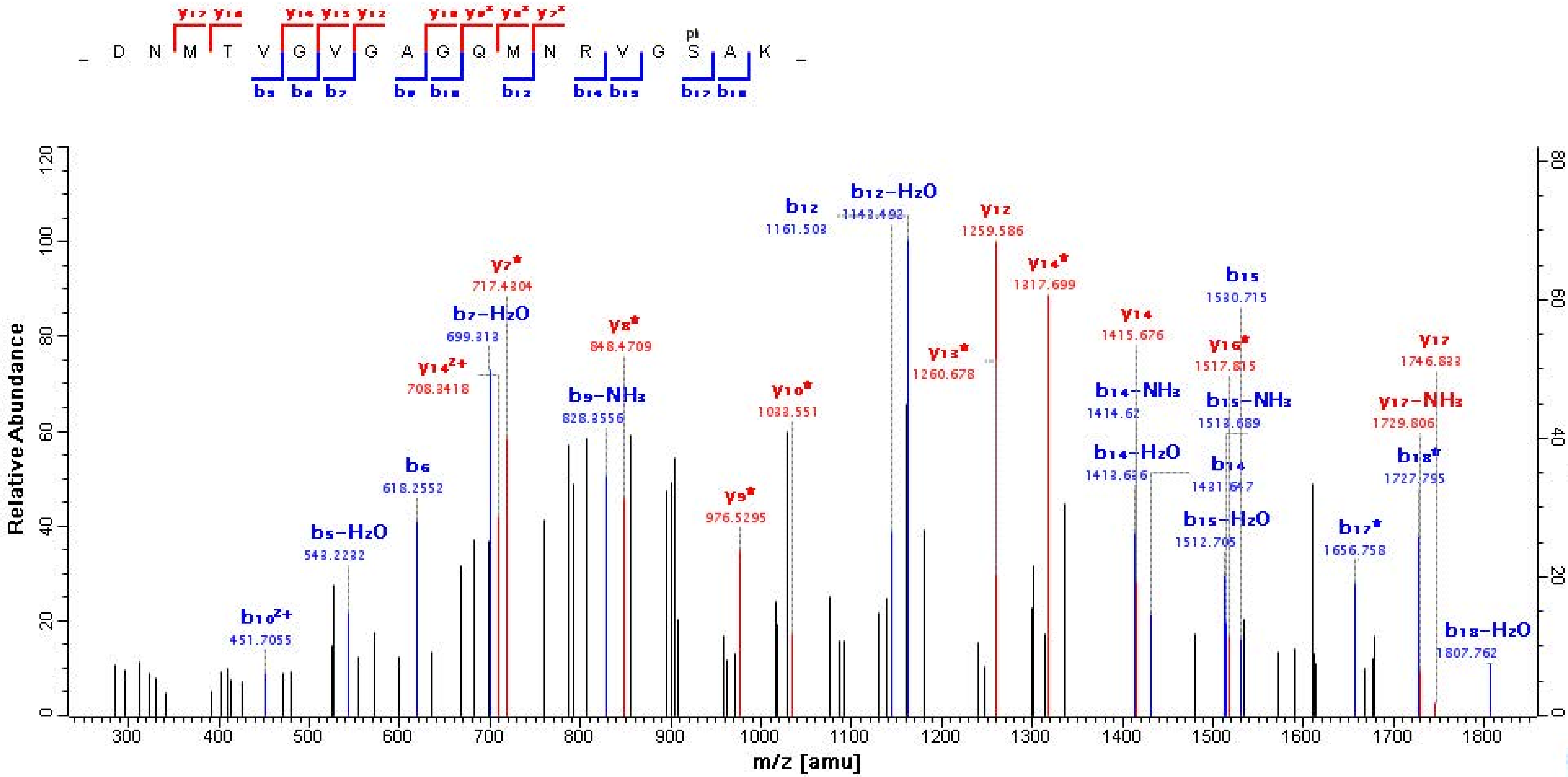
Mass:	1730.84462
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	156.5722
Mass Error [ppm]:	0.13932
PEP:	9.6413E-17
Precursor Type:	ISO

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	54 %
Protein Localisation:	220 ... 234

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	100.07569038		100.07569038	1	V	14		
	199.1441043		199.1441043	2	V	13	1632.7832392	
	314.17104733	+0.0564002	314.17104733	3	D	12	1533.7148253	-0.098004
	443.21364043		443.21364043	4	E	11	1418.6878823	+0.1873619
	514.25075422	+0.0401393	514.25075422	5	A	10	1289.6452892	-0.0378673
	627.3348182	+0.0815026	627.3348182	6	I	9	1218.6081754	-0.1142789
	741.37774564	-0.2028799	741.37774564	7	N	8	1105.5241114	-0.0941798
	869.43632315	+0.013567	869.43632315	8	Q	7	991.48118397	+0.1821461
	968.50473707	-0.0840217	968.50473707	9	V	6	863.42260646	
-0.1067988	528.27202097	-0.2948221	1055.5367655	10	S	5	764.35419254	
	1222.5351243		1222.5351243	11	S	4	677.32216413	
	1350.5937018		1350.5937018	12	Q	3	510.32380531	-0.0984025
	1506.6948128	+0.1898307	1506.6948128	13	R	2	382.2652278	
-0.3033784	789.36960155	+0.2008126	1577.7319266	14	A	1	226.16411677	
				15	K	0	155.12700298	

Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F01
Scannumber: 6106
Protein: BSU06520; purH; purHJ
Peptide Score: 114.99
Method: ITMS; CID; 3



precursor information

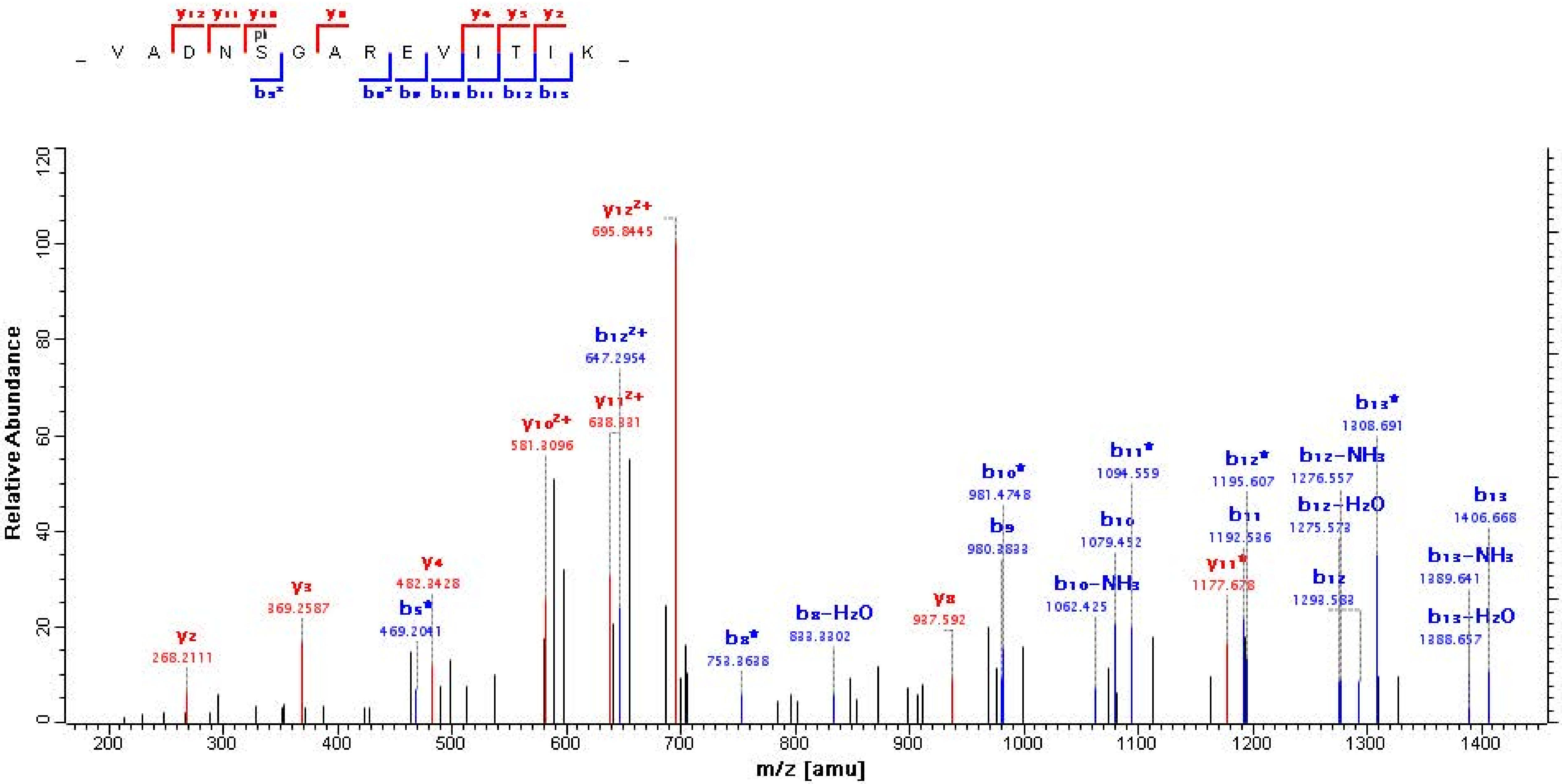
Mass:	1974.89561
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	114.9863
Mass Error [ppm]:	0.079259
PEP:	0.0035385
Precursor Type:	ISO

general information

Annotation:	15 of 19
AminoAcids Coverag	79 %
Intensity Coverage:	41 %
Protein Localisation:	423 ... 441

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342		116.0342	1	D	18				
	230.0771		230.0771	2	N	17	1860.876		1860.876	
	361.1176		361.1176	3	M	16	1746.833	-0.472384	1746.833	
	462.1653		462.1653	4	T	15	1615.792		1615.792	
	561.2337		561.2337	5	V	14	1514.745		1514.745	
	618.2552	-0.078247	618.2552	6	G	13	1415.676	+0.199574	708.3418	+0.097919
	717.3236		717.3236	7	V	12	1358.655		1358.655	
	774.3451		774.3451	8	G	11	1259.586	-0.156472	1259.586	
	845.3822		845.3822	9	A	10	1202.565		1202.565	
+0.167099	451.7055		902.4036	10	G	9	1131.528		1131.528	
	1030.462		1030.462	11	Q	8	1074.506		1074.506	
	1161.503	+0.030254	1161.503	12	M	7	946.4478		946.4478	
	1275.546		1275.546	13	N	6	815.4073		815.4073	
	1431.647	+0.148301	1431.647	14	R	5	701.3644		701.3644	
	1530.715	+0.342338	1530.715	15	V	4	545.2633		545.2633	
	1587.737		1587.737	16	G	3	446.1948		446.1948	
	1754.735		1754.735	17	S	2	389.1734		389.1734	
	1825.772		1825.772	18	A	1	222.175		222.175	
				19	K	0	151.1379		151.1379	

Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F01
Scannumber: 6170
Protein: BSU01260; rplN
Peptide Score: 128.95
Method: ITMS; CID; 3



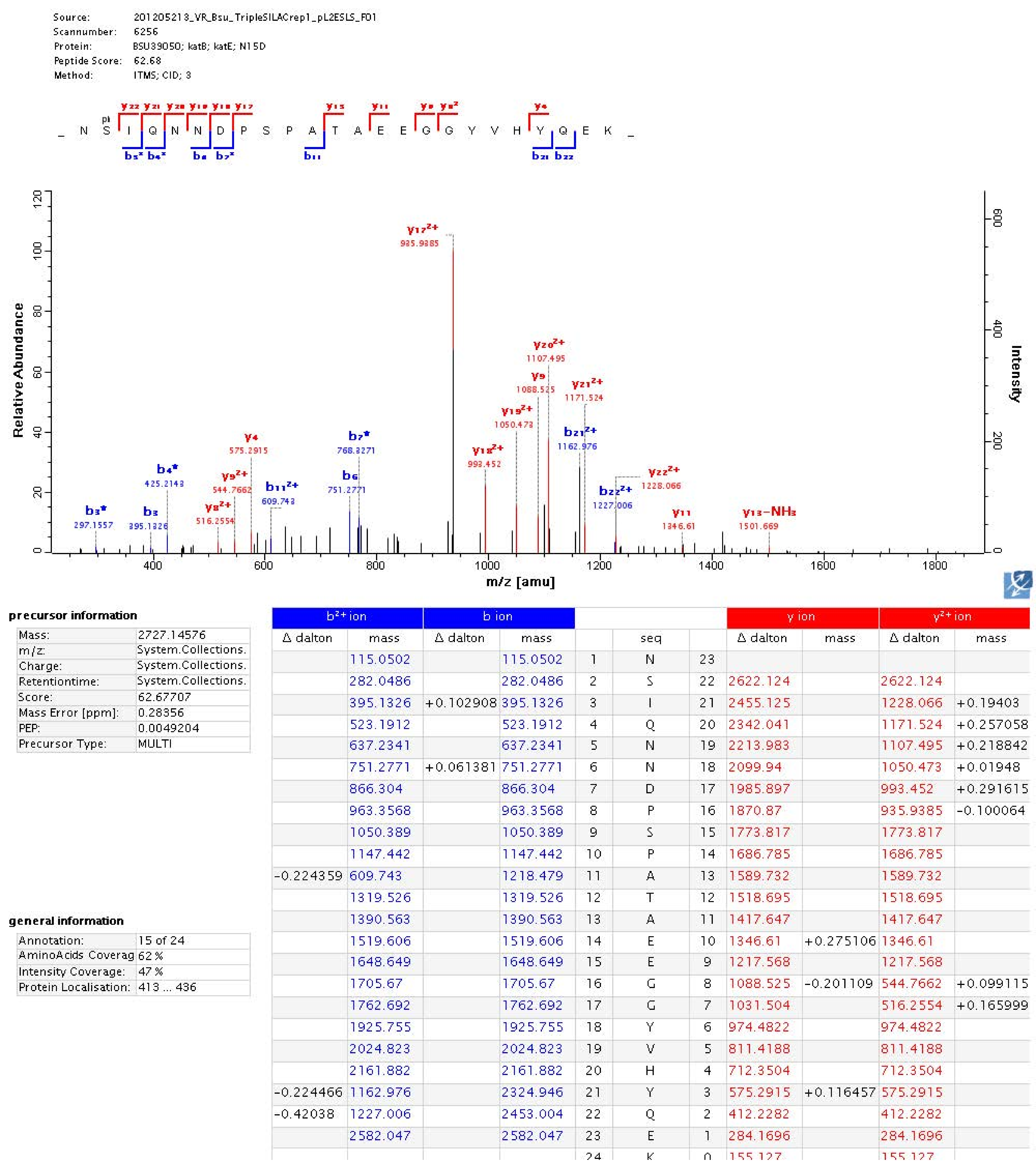
precursor information

Mass:	1551.76544
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	128.9506
Mass Error [ppm]:	-0.22463
PEP:	1.3836E-06
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	45 %
Protein Localisation:	10 ... 23

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757		100.0757	1	V	13				
	171.1128		171.1128	2	A	12	1461.719		1461.719	
	286.1397		286.1397	3	D	11	1390.682		695.8445	+0.405983
	400.1827		400.1827	4	N	10	1275.655		638.331	-0.031962
	567.181		567.181	5	S	9	1161.612		581.3096	+0.028137
	624.2025		624.2025	6	G	8	994.6135		994.6135	
	695.2396		695.2396	7	A	7	937.592	-0.044739	937.592	
	851.3407		851.3407	8	R	6	866.5549		866.5549	
	980.3833	-0.013869	980.3833	9	E	5	710.4538		710.4538	
	1079.452	+0.107963	1079.452	10	V	4	581.4112		581.4112	
	1192.536	+0.026951	1192.536	11	I	3	482.3428	+0.22317	482.3428	
-0.192774	647.2954	-0.342138	1293.583	12	T	2	369.2587	+0.044416	369.2587	
	1406.668	+0.159735	1406.668	13	I	1	268.2111	-0.049446	268.2111	
				14	K	0	155.127		155.127	



Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F01
Scannumber: 6256
Protein: BSU39050; katB; katE; N15D
Peptide Score: 62.68
Method: ITMS; CID; 3

precursor information

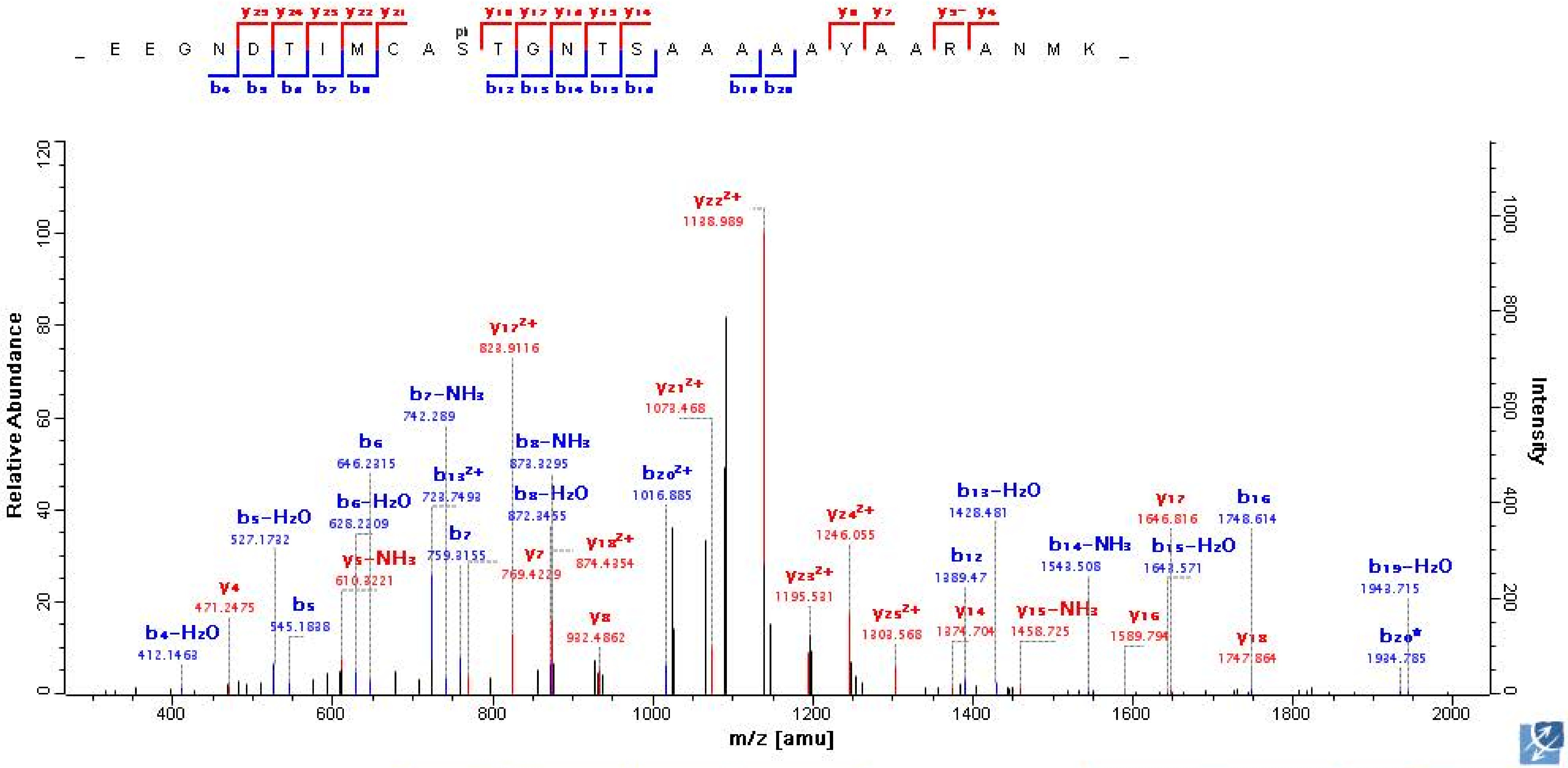
Mass:	2727.14576
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	62.67707
Mass Error [ppm]:	0.28356
PEP:	0.0049204
Precursor Type:	MULTI

general information

Annotation:	15 of 24
AminoAcids Coverag	62 %
Intensity Coverage:	47 %
Protein Localisation:	413 ... 436

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502		115.0502	1	N	23				
	282.0486		282.0486	2	S	22	2622.124		2622.124	
	395.1326	+0.102908	395.1326	3	I	21	2455.125		1228.066	+0.19403
	523.1912		523.1912	4	Q	20	2342.041		1171.524	+0.257058
	637.2341		637.2341	5	N	19	2213.983		1107.495	+0.218842
	751.2771	+0.061381	751.2771	6	N	18	2099.94		1050.473	+0.01948
	866.304		866.304	7	D	17	1985.897		993.452	+0.291615
	963.3568		963.3568	8	P	16	1870.87		935.9385	-0.100064
	1050.389		1050.389	9	S	15	1773.817		1773.817	
	1147.442		1147.442	10	P	14	1686.785		1686.785	
-0.224359	609.743		1218.479	11	A	13	1589.732		1589.732	
	1319.526		1319.526	12	T	12	1518.695		1518.695	
	1390.563		1390.563	13	A	11	1417.647		1417.647	
	1519.606		1519.606	14	E	10	1346.61	+0.275106	1346.61	
	1648.649		1648.649	15	E	9	1217.568		1217.568	
	1705.67		1705.67	16	G	8	1088.525	-0.201109	544.7662	+0.099115
	1762.692		1762.692	17	G	7	1031.504		516.2554	+0.165999
	1925.755		1925.755	18	Y	6	974.4822		974.4822	
	2024.823		2024.823	19	V	5	811.4188		811.4188	
	2161.882		2161.882	20	H	4	712.3504		712.3504	
-0.224466	1162.976		2324.946	21	Y	3	575.2915	+0.116457	575.2915	
-0.42038	1227.006		2453.004	22	Q	2	412.2282		412.2282	
	2582.047		2582.047	23	E	1	284.1696		284.1696	
				24	K	0	155.127		155.127	

Source: 20120521 3_VR_Bsu_TripleSILACrep1_pL2ESLS_F01
Scannumber: 8174
Protein: BSU32250; thrC
Peptide Score: 68.19
Method: ITMS; CID; 3



precursor information

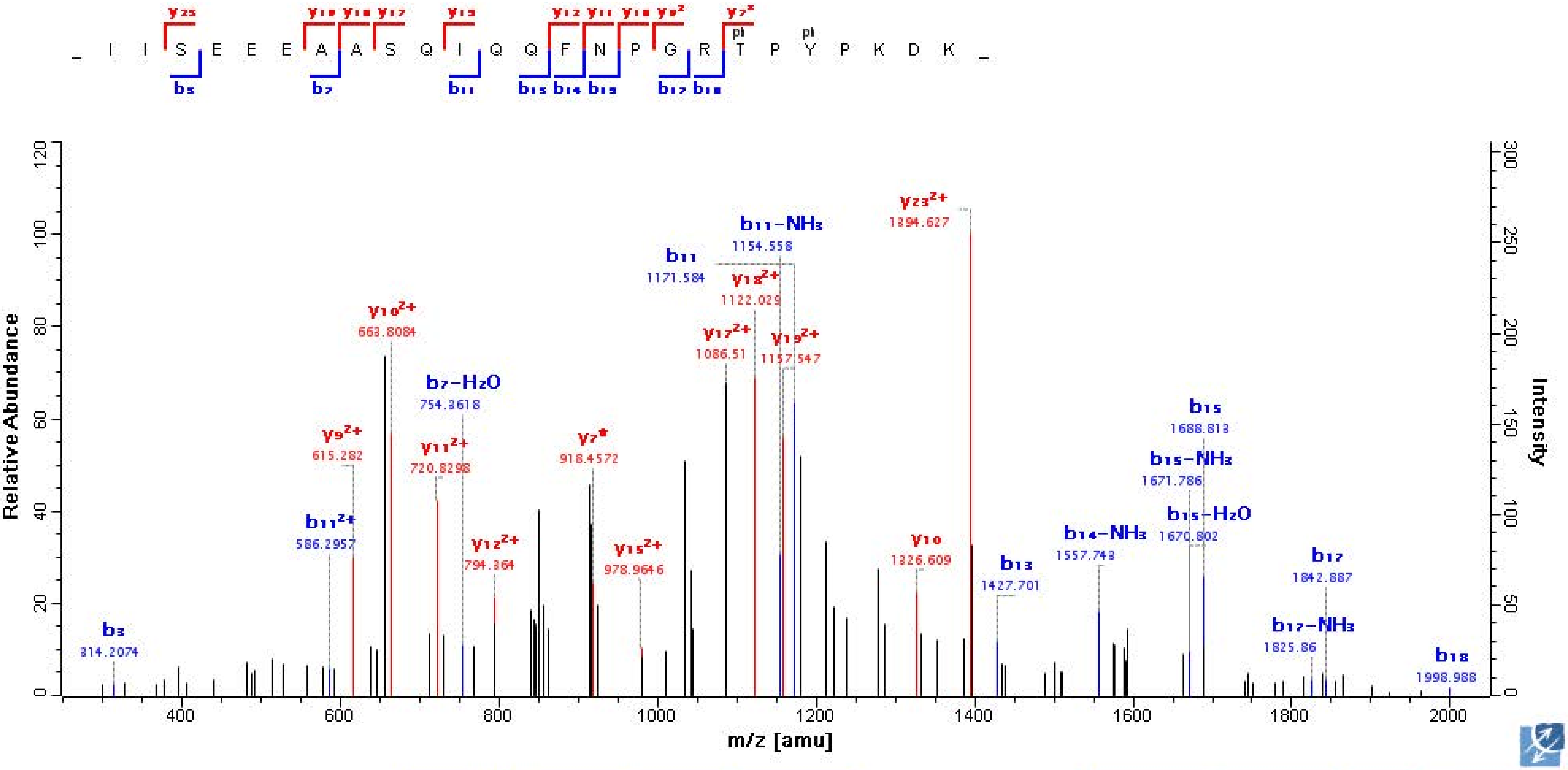
Mass:	3034.26931
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	68.19204
Mass Error [ppm]:	-0.60064
PEP:	7.9395E-06
Precursor Type:	ISO

general information

Annotation:	18 of 29
AminoAcids Coverag	62 %
Intensity Coverage:	40 %
Protein Localisation:	72 ... 100

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499		130.0499	1	E	28				
	259.0925		259.0925	2	E	27	2906.236		2906.236	
	316.1139		316.1139	3	G	26	2777.193		2777.193	
	430.1569		430.1569	4	N	25	2720.172		2720.172	
	545.1838	-0.08077	545.1838	5	D	24	2606.129		1303.568	+0.427307
	646.2315	-0.025299	646.2315	6	T	23	2491.102		1246.055	+0.030256
	759.3155	+0.258679	759.3155	7	I	22	2390.054		1195.531	-0.279523
	890.356		890.356	8	M	21	2276.97		1138.989	+0.199765
	1050.387		1050.387	9	C	20	2145.93		1073.468	+0.072912
	1121.424		1121.424	10	A	19	1985.899		1985.899	
	1288.422		1288.422	11	S	18	1914.862		1914.862	
	1389.47	+0.126002	1389.47	12	T	17	1747.864	+0.289413	874.4354	-0.069442
-0.44728	723.7493		1446.491	13	G	16	1646.816	+0.219904	823.9116	+0.461965
	1560.534		1560.534	14	N	15	1589.794	+0.268955	1589.794	
	1661.582		1661.582	15	T	14	1475.751		1475.751	
	1748.614	+0.26706	1748.614	16	S	13	1374.704	-0.282651	1374.704	
	1819.651		1819.651	17	A	12	1287.672		1287.672	
	1890.688		1890.688	18	A	11	1216.635		1216.635	
	1961.725		1961.725	19	A	10	1145.598		1145.598	
-0.37384	1016.885		2032.762	20	A	9	1074.56		1074.56	
	2103.799		2103.799	21	A	8	1003.523		1003.523	
	2266.863		2266.863	22	Y	7	932.4862	+0.188975	932.4862	
	2337.9		2337.9	23	A	6	769.4229	-0.238907	769.4229	
	2408.937		2408.937	24	A	5	698.3858		698.3858	
	2565.038		2565.038	25	R	4	627.3486		627.3486	
	2636.075		2636.075	26	A	3	471.2475	-0.031342	471.2475	
	2750.118		2750.118	27	N	2	400.2104		400.2104	
	2881.159		2881.159	28	M	1	286.1675		286.1675	
				29	K	0	155.127		155.127	

Source:	20120521 3_VR_Bsu_TripleSILACrep1_pL2ESLS_F01
Scannumber:	9725
Protein:	BSU03480; srfA; srfA1; srfAA
Peptide Score:	77.63
Method:	ITMS; CID; 3



precursor information

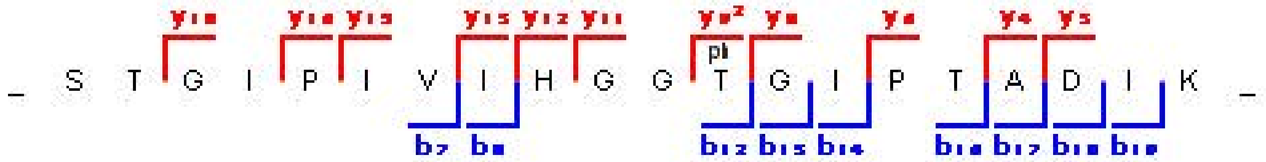
Mass:	3013.40639
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	77.63057
Mass Error [ppm]:	-0.37283
PEP:	0.00069147
Precursor Type:	ISO

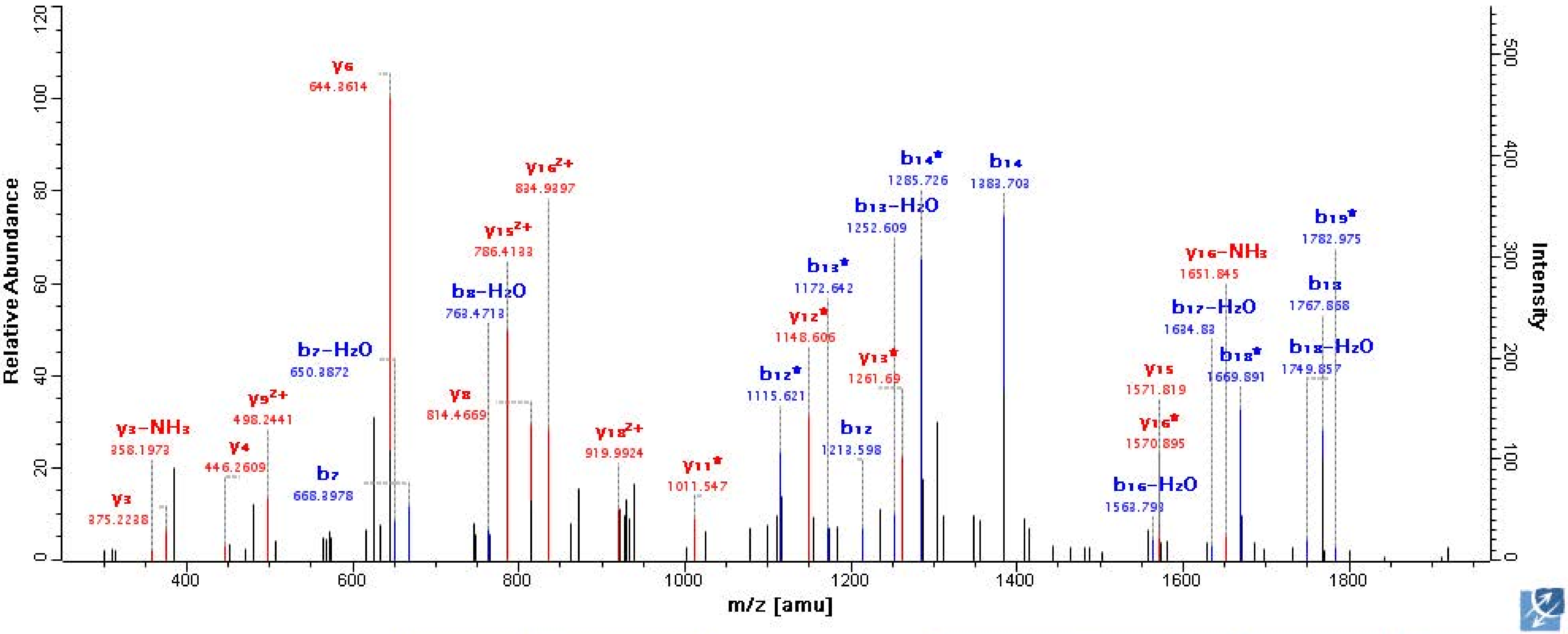
general information

Annotation:	13 of 25
AminoAcids Coverag	52 %
Intensity Coverage:	39 %
Protein Localisation:	1481 ... 1505

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913		114.0913	1	I	24				
	227.1754		227.1754	2	I	23	2901.331		2901.331	
	314.2074	+0.021357	314.2074	3	S	22	2788.247		1394.627	+0.305405
	443.25		443.25	4	E	21	2701.215		2701.215	
	572.2926		572.2926	5	E	20	2572.172		2572.172	
	701.3352		701.3352	6	E	19	2443.129		2443.129	
	772.3723		772.3723	7	A	18	2314.087		1157.547	+0.237848
	843.4094		843.4094	8	A	17	2243.05		1122.029	+0.335506
	930.4415		930.4415	9	S	16	2172.013		1086.51	-0.07477
	1058.5		1058.5	10	Q	15	2084.981		2084.981	
-0.148598	586.2957	+0.281857	1171.584	11	I	14	1956.922		978.9646	+0.309278
	1299.643		1299.643	12	Q	13	1843.838		1843.838	
	1427.701	+0.243438	1427.701	13	Q	12	1715.779		1715.779	
	1574.77		1574.77	14	F	11	1587.721		794.364	-0.131128
	1688.813	+0.109147	1688.813	15	N	10	1440.652		720.8298	+0.157046
	1785.865		1785.865	16	P	9	1326.609	-0.176475	663.8084	+0.307477
	1842.887	-0.342522	1842.887	17	G	8	1229.557		615.282	+0.046506
	1998.988	+0.38144	1998.988	18	R	7	1172.535		1172.535	
	2180.002		2180.002	19	T	6	1016.434		1016.434	
	2277.055		2277.055	20	P	5	835.4201		835.4201	
	2520.084		2520.084	21	Y	4	738.3673		738.3673	
	2617.137		2617.137	22	P	3	495.3377		495.3377	
	2749.257		2749.257	23	K	2	398.2849		398.2849	
	2864.284		2864.284	24	D	1	266.1649		266.1649	
				25	K	0	151.1379		151.1379	

Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F01
Scannumber:	9806
Protein:	BSU37120; fba; fba1; fbaA; tsr
Peptide Score:	105.5
Method:	ITMS; CID; 3





precursor information

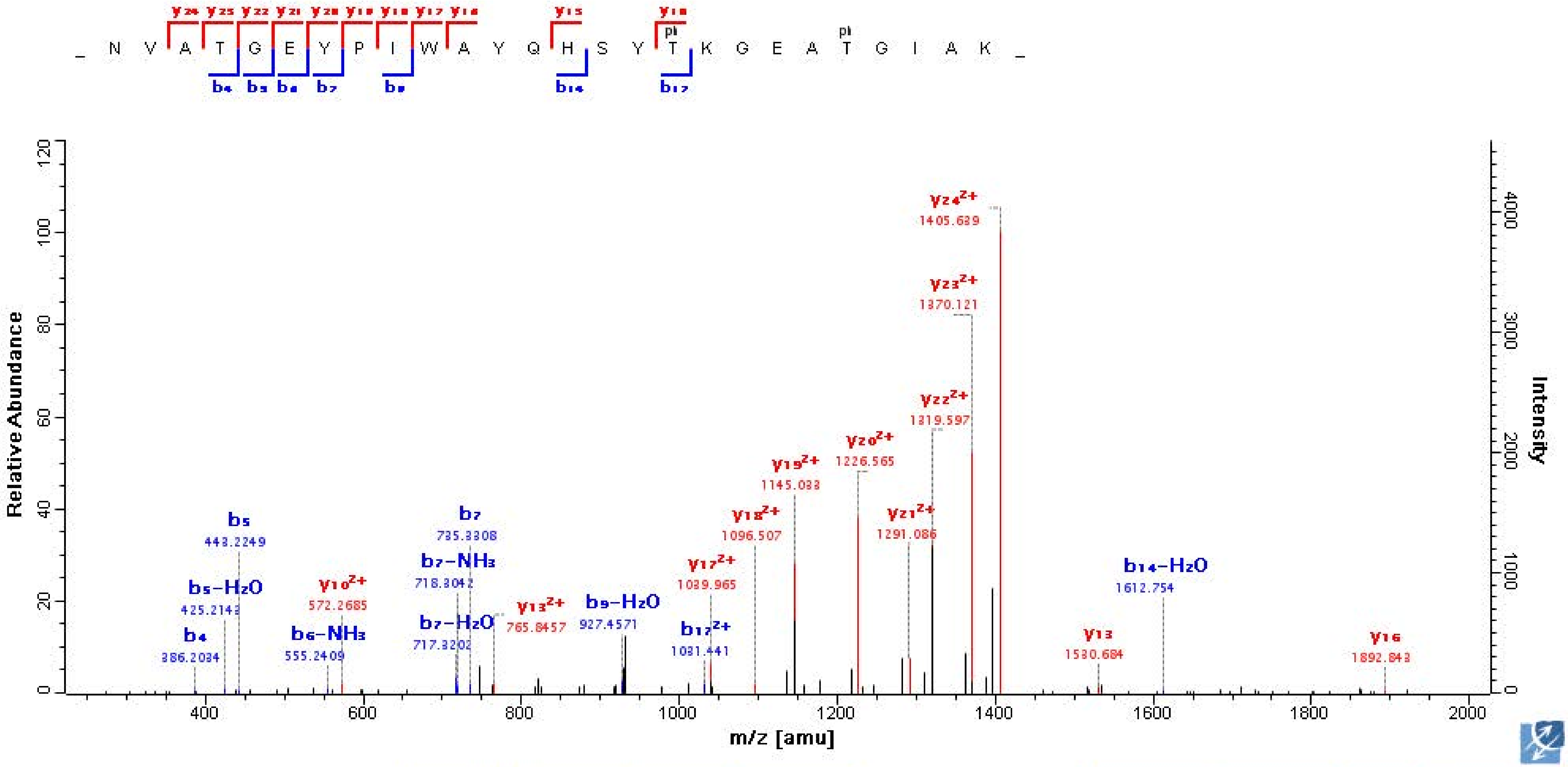
Mass:	2026.0498
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	105.5022
Mass Error [ppm]:	-0.10192
PEP:	1.064E-07
Precursor Type:	MULTI

general information

Annotation:	15 of 20
AminoAcids Coverag	75 %
Intensity Coverage:	53 %
Protein Localisation:	201 ... 220

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876	1	S	19				
	189.08698335	2	T	18	1940.0252551		1940.0252551	
	246.10844707	3	G	17	1838.9775766		919.99242655	-0.2499949
	359.19251105	4	I	16	1781.9561129		1781.9561129	
	456.24527491	5	P	15	1668.8720489		834.93966269	+0.3247416
	569.32933889	6	I	14	1571.8192851	+0.0778097	786.41328077	-0.3148921
+0.0521984	668.3977528	7	V	13	1458.7352211		1458.7352211	
	781.48181678	8	I	12	1359.6668072		1359.6668072	
	918.54072865	9	H	11	1246.5827432		1246.5827432	
	975.56219237	10	G	10	1109.5238313		1109.5238313	
	1032.5836561	11	G	9	1052.5023676		1052.5023676	
+0.0165928	1213.597665	12	T	8	995.48090388		498.24409018	+0.0803727
	1270.6191287	13	G	7	814.466895	+0.0321284	814.466895	
+0.0631647	1383.7031927	14	I	6	757.44543128		757.44543128	
	1480.7559565	15	P	5	644.3613673	-0.029336	644.3613673	
	1581.803635	16	T	4	547.30860344		547.30860344	
	1652.8407488	17	A	3	446.26092497	-0.1159665	446.26092497	
-0.2105873	1767.8676918	18	D	2	375.22381118	+0.163579	375.22381118	
	1880.9517558	19	I	1	260.19686815		260.19686815	
		20	K	0	147.11280417		147.11280417	

Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F01
Scannumber:	9854
Protein:	BSU24990; pstS; yqgG; yzmB
Peptide Score:	77.96
Method:	ITMS; CID; 3



precursor information

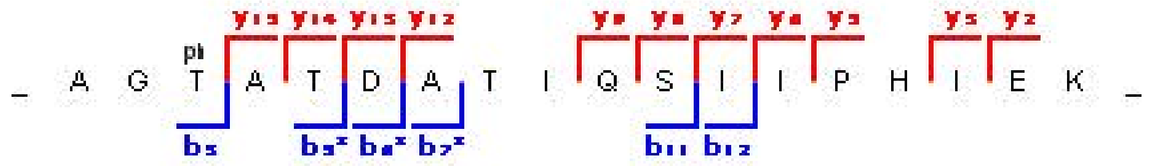
Mass:	3022.37408
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	77.95942
Mass Error [ppm]:	-0.46558
PEP:	0.00042399
Precursor Type:	ISO

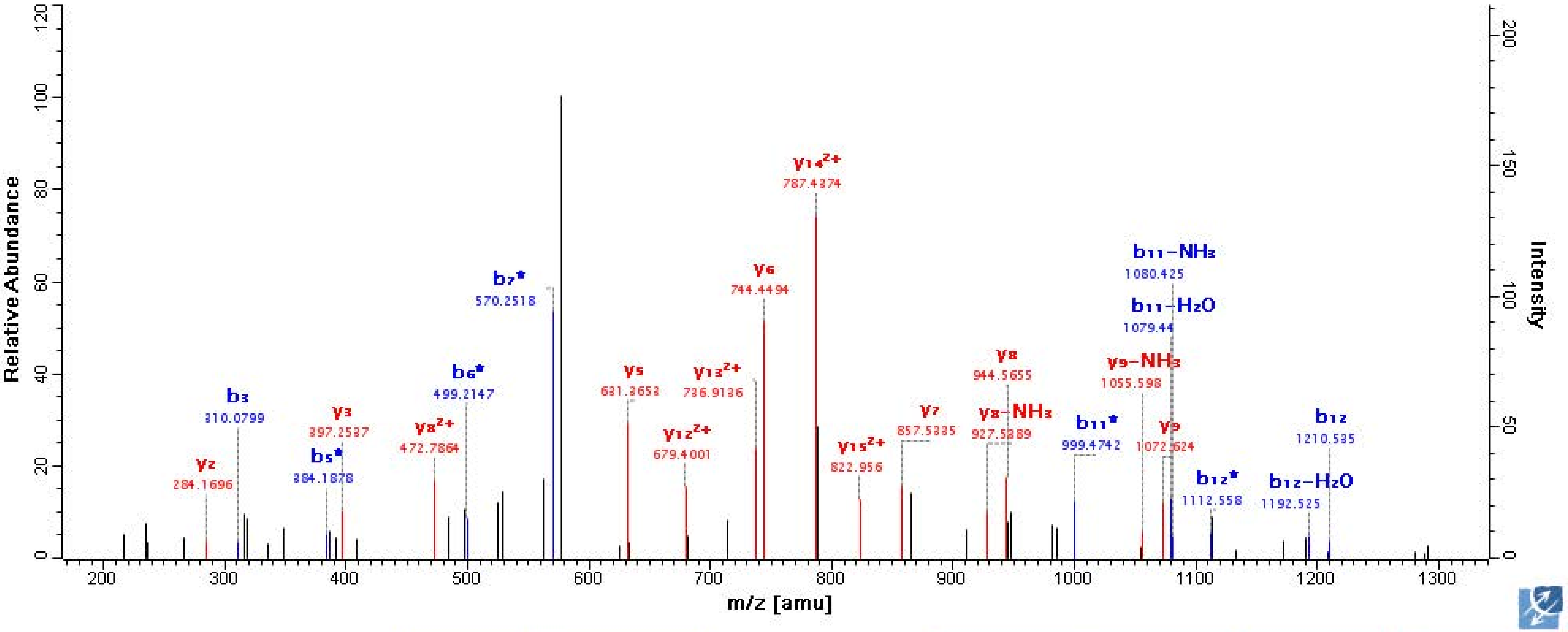
general information

Annotation:	11 of 26
AminoAcids Coverag	42 %
Intensity Coverage:	61 %
Protein Localisation:	237 ... 262

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502		115.0502	1	N	25				
	214.1186		214.1186	2	V	24	2909.34		2909.34	
	285.1557		285.1557	3	A	23	2810.271		1405.639	+0.33807
	386.2034	-0.039042	386.2034	4	T	22	2739.234		1370.121	+0.195616
	443.2249	-0.213826	443.2249	5	G	21	2638.187		1319.597	-0.010159
	572.2675		572.2675	6	E	20	2581.165		1291.086	+0.352135
	735.3308	-0.058212	735.3308	7	Y	19	2452.123		1226.565	+0.296283
	832.3836		832.3836	8	P	18	2289.059		1145.033	-0.022028
	945.4676		945.4676	9	I	17	2192.006		1096.507	-0.265177
	1131.547		1131.547	10	W	16	2078.922		1039.965	-0.054688
	1202.584		1202.584	11	A	15	1892.843	+0.122354	1892.843	
	1365.647		1365.647	12	Y	14	1821.806		1821.806	
	1493.706		1493.706	13	Q	13	1658.743		1658.743	
	1630.765		1630.765	14	H	12	1530.684	-0.152586	765.8457	-0.054174
	1717.797		1717.797	15	S	11	1393.625		1393.625	
	1880.86		1880.86	16	Y	10	1306.593		1306.593	
-0.46993	1031.441		2061.874	17	T	9	1143.53		572.2685	+0.028942
	2193.994		2193.994	18	K	8	962.5158		962.5158	
	2251.016		2251.016	19	G	7	830.3957		830.3957	
	2380.058		2380.058	20	E	6	773.3743		773.3743	
	2451.095		2451.095	21	A	5	644.3317		644.3317	
	2632.109		2632.109	22	T	4	573.2946		573.2946	
	2689.131		2689.131	23	G	3	392.2806		392.2806	
	2802.215		2802.215	24	I	2	335.2591		335.2591	
	2873.252		2873.252	25	A	1	222.175		222.175	
				26	K	0	151.1379		151.1379	

Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F02
Scannumber:	10079
Protein:	BSU23860; yqjI
Peptide Score:	83.89
Method:	ITMS; CID; 3





precursor information

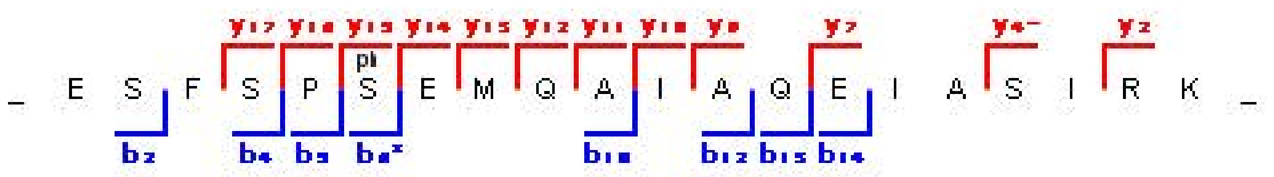
Mass:	1944.95515
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	83.89419
Mass Error [ppm]:	-0.31898
PEP:	0.00092185
Precursor Type:	MULTI

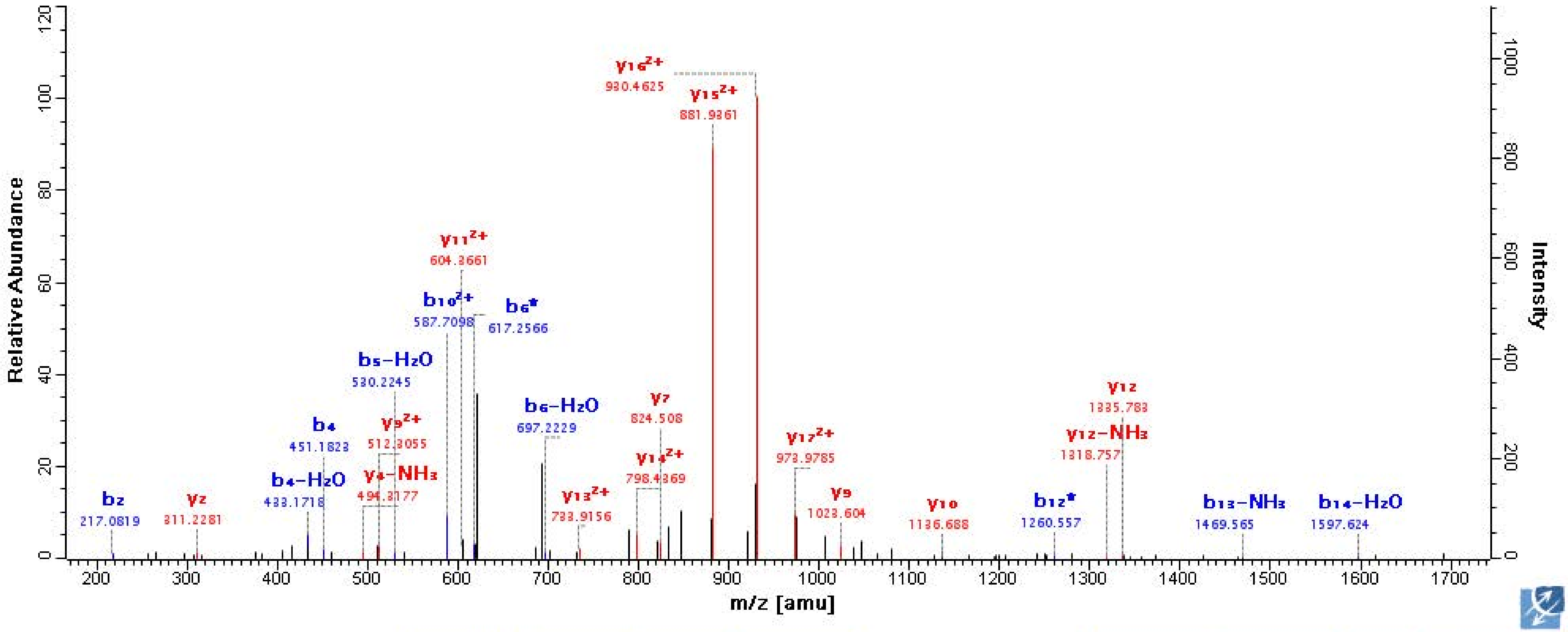
general information

Annotation:	12 of 18
AminoAcids Coverag	67 %
Intensity Coverage:	49 %
Protein Localisation:	76 ... 93

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	17				
	129.06585398	2	G	16	1882.9401338		1882.9401338	
-0.0213301	310.07986286	3	T	15	1825.9186701		1825.9186701	
	381.11697665	4	A	14	1644.9046612		822.95596883	+0.2310429
	482.16465512	5	T	13	1573.8675474		787.43741194	-0.1449925
	597.19159815	6	D	12	1472.8198689		736.9135727	+0.1183487
	668.22871194	7	A	11	1357.7929259		679.40010118	+0.2462611
	769.27639042	8	T	10	1286.7558121		1286.7558121	
	882.3604544	9	I	9	1185.7081336		1185.7081336	
	1010.4190319	10	Q	8	1072.6240697	+0.03157	1072.6240697	
	1097.4510603	11	S	7	944.56549215	-0.1573501	472.78638431	+0.1581347
-0.0436692	1210.5351243	12	I	6	857.53346374	-0.0636761	857.53346374	
	1323.6191883	13	I	5	744.44939976	+0.0024435	744.44939976	
	1420.6719521	14	P	4	631.36533577	+0.1314904	631.36533577	
	1557.730864	15	H	3	534.31257192		534.31257192	
	1670.814928	16	I	2	397.25366006	-0.2611674	397.25366006	
	1799.8575211	17	E	1	284.16959608	-0.1257728	284.16959608	
		18	K	0	155.12700298		155.12700298	

Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F02
Scannumber: 11365
Protein: BSU07870; yfkK
Peptide Score: 59.73
Method: ITMS; CID; 3





precursor information

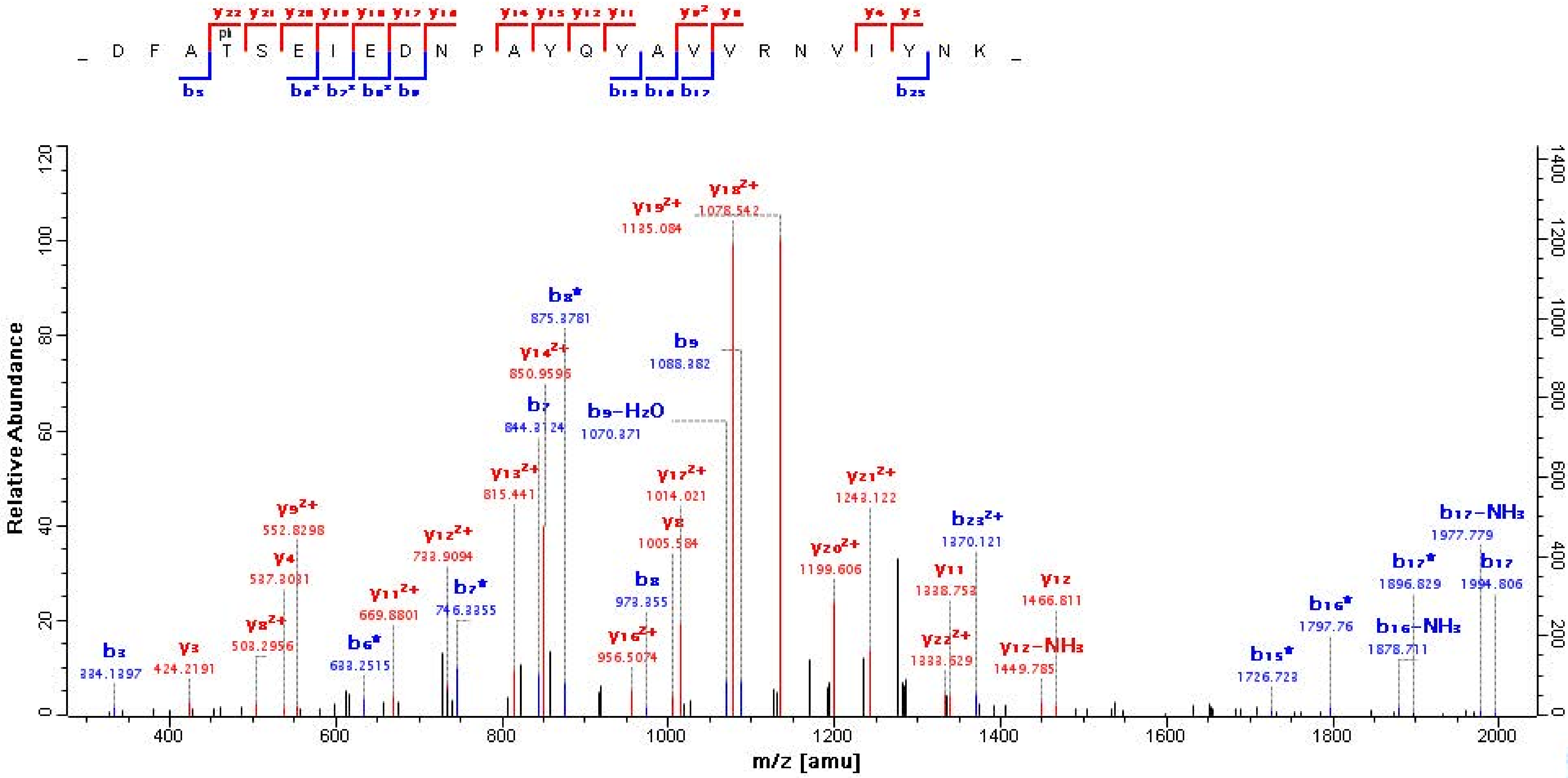
Mass:	2301.07116
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	59.72772
Mass Error [ppm]:	-0.021625
PEP:	0.0068311
Precursor Type:	MULTI

general information

Annotation:	14 of 20
AminoAcids Coverag	70 %
Intensity Coverage:	57 %
Protein Localisation:	52 ... 71

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499		130.0499	1	E	19				
	217.0819	+0.184444	217.0819	2	S	18	2181.05		2181.05	
	364.1503		364.1503	3	F	17	2094.018		2094.018	
	451.1823	+0.034151	451.1823	4	S	16	1946.95		973.9785	-0.012156
	548.2351		548.2351	5	P	15	1859.918		930.4625	+0.251966
	715.2335		715.2335	6	S	14	1762.865		881.9361	-0.137973
	844.2761		844.2761	7	E	13	1595.867		798.4369	-0.094665
	975.3165		975.3165	8	M	12	1466.824		733.9156	+0.330684
	1103.375		1103.375	9	Q	11	1335.783	-0.28025	1335.783	
+0.240136	587.7098		1174.412	10	A	10	1207.725		604.3661	+0.193204
	1287.496		1287.496	11	I	9	1136.688	+0.151135	1136.688	
	1358.533		1358.533	12	A	8	1023.604	+0.237823	512.3055	-0.00463
	1486.592		1486.592	13	Q	7	952.5666		952.5666	
	1615.635		1615.635	14	E	6	824.508	-0.185651	824.508	
	1728.719		1728.719	15	I	5	695.4654		695.4654	
	1799.756		1799.756	16	A	4	582.3813		582.3813	
	1886.788		1886.788	17	S	3	511.3442		511.3442	
	1999.872		1999.872	18	I	2	424.3122		424.3122	
	2155.973		2155.973	19	R	1	311.2281	-0.134761	311.2281	
				20	K	0	155.127		155.127	

Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F02
Scannumber: 11578
Protein: BSU31350; pgi; yugL
Peptide Score: 159.46
Method: ITMS; CID; 3



precursor information

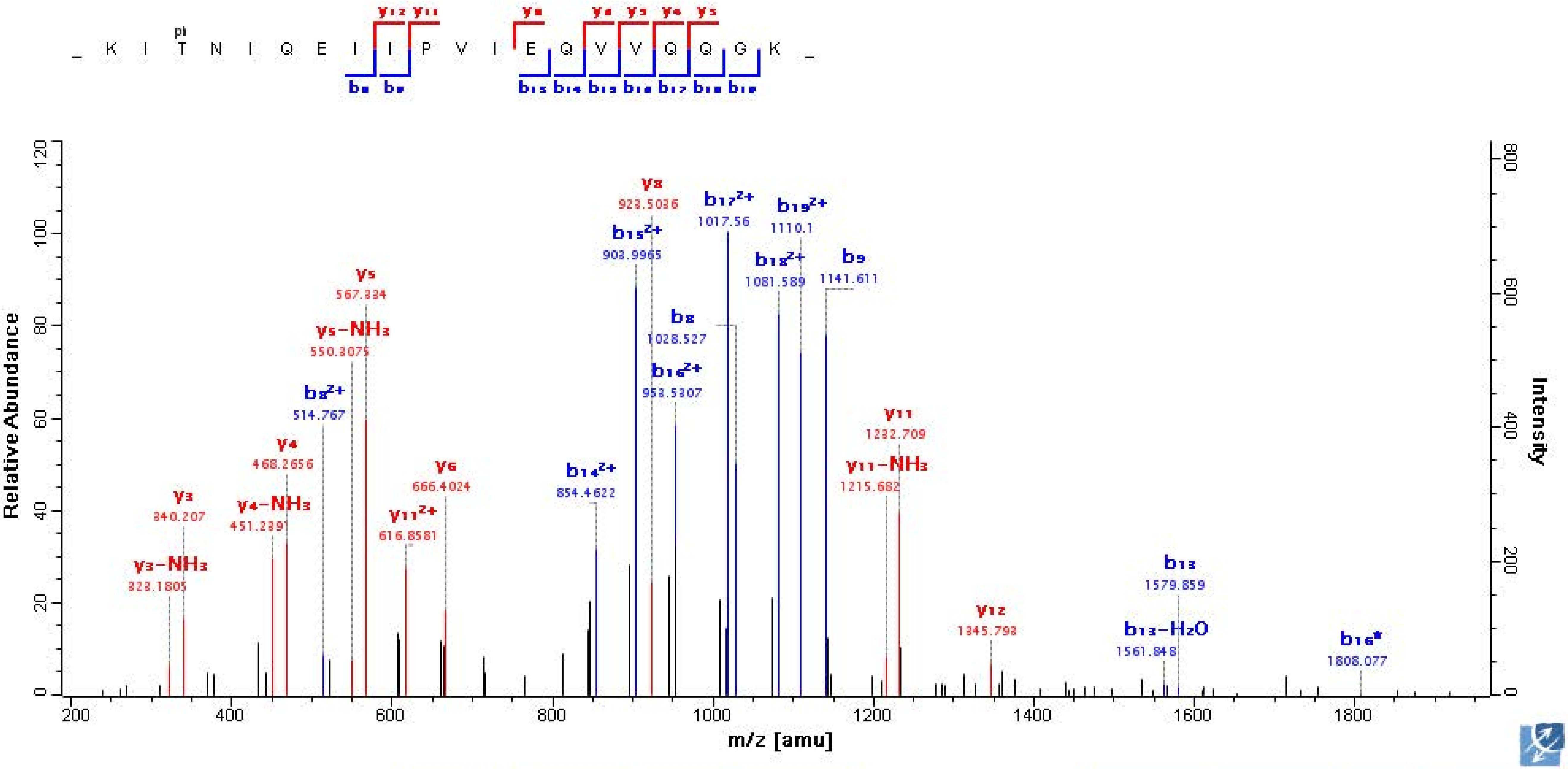
Mass:	2998.37533
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	159.4646
Mass Error [ppm]:	0.11698
PEP:	4.5718E-36
Precursor Type:	MULTI

general information

Annotation:	19 of 25
AminoAcids Coverag	76 %
Intensity Coverage:	61 %
Protein Localisation:	239 ... 263

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342		116.0342	1	D	24				
	263.1026		263.1026	2	F	23	2884.355		2884.355	
	334.1397	-0.035499	334.1397	3	A	22	2737.287		2737.287	
	515.1538		515.1538	4	T	21	2666.25		1333.629	-0.07653
	602.1858		602.1858	5	S	20	2485.236		1243.122	+0.295464
	731.2284		731.2284	6	E	19	2398.204		1199.606	+0.271561
	844.3124	+0.488584	844.3124	7	I	18	2269.161		1135.084	+0.293957
	973.355	+0.265205	973.355	8	E	17	2156.077		1078.542	+0.26592
	1088.382	+0.124614	1088.382	9	D	16	2027.035		1014.021	+0.309312
	1202.425		1202.425	10	N	15	1912.008		956.5074	+0.3898
	1299.478		1299.478	11	P	14	1797.965		1797.965	
	1370.515		1370.515	12	A	13	1700.912		850.9596	-0.059669
	1533.578		1533.578	13	Y	12	1629.875		815.441	+0.103297
	1661.637		1661.637	14	Q	11	1466.811	+0.280373	733.9094	-0.051684
	1824.7		1824.7	15	Y	10	1338.753	-0.367349	669.8801	-0.116023
	1895.737		1895.737	16	A	9	1175.69		1175.69	
	1994.806	-0.370609	1994.806	17	V	8	1104.652		552.8298	+0.046624
	2093.874		2093.874	18	V	7	1005.584	-0.040655	503.2956	+0.281881
	2249.975		2249.975	19	R	6	906.5156		906.5156	
	2364.018		2364.018	20	N	5	750.4145		750.4145	
	2463.086		2463.086	21	V	4	636.3715		636.3715	
	2576.17		2576.17	22	I	3	537.3031	+0.020545	537.3031	
-0.373348	1370.121		2739.234	23	Y	2	424.2191	-0.009099	424.2191	
	2853.277		2853.277	24	N	1	261.1557		261.1557	
				25	K	0	147.1128		147.1128	

Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F02
Scannumber: 12122
Protein: BSU06030; groEL; groL; mopA
Peptide Score: 136.48
Method: ITMS; CID; 3



precursor information

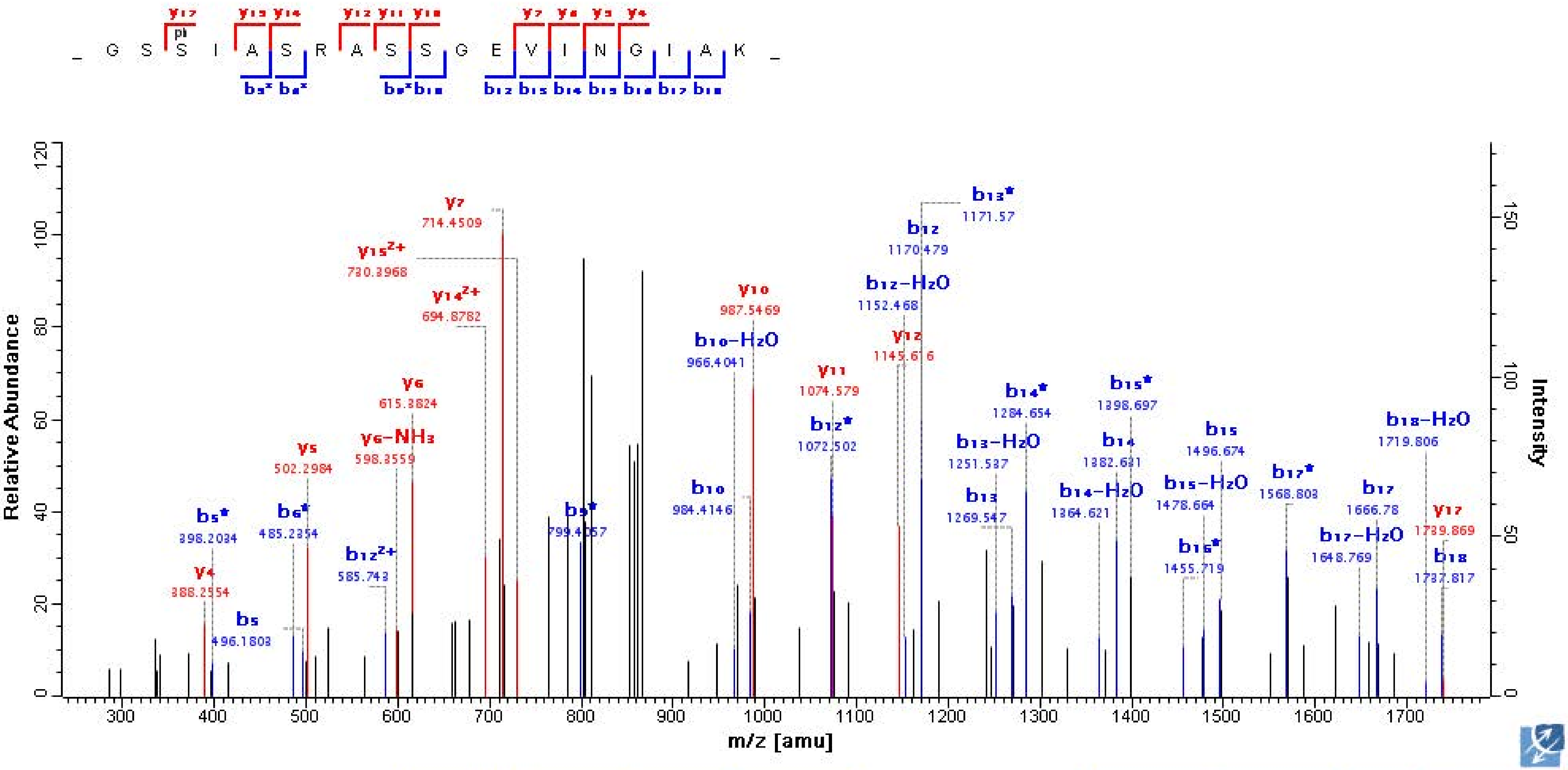
Mass:	2356.27502
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	136.4758
Mass Error [ppm]:	-0.71315
PEP:	6.4675E-16
Precursor Type:	MULTI

general information

Annotation:	10 of 20
AminoAcids Coverag	50 %
Intensity Coverage:	66 %
Protein Localisation:	224 ... 243

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	137.1164		137.1164	1	K	19				
	250.2005		250.2005	2	I	18	2237.203		2237.203	
	431.2145		431.2145	3	T	17	2124.119		2124.119	
	545.2574		545.2574	4	N	16	1943.105		1943.105	
	658.3415		658.3415	5	I	15	1829.062		1829.062	
	786.4001		786.4001	6	Q	14	1715.978		1715.978	
	915.4427		915.4427	7	E	13	1587.92		1587.92	
+0.063071	514.767	-0.05579	1028.527	8	I	12	1458.877		1458.877	
	1141.611	-0.068809	1141.611	9	I	11	1345.793	+0.070722	1345.793	
	1238.664		1238.664	10	P	10	1232.709	-0.090576	616.8581	+0.174646
	1337.732		1337.732	11	V	9	1135.656		1135.656	
	1450.816		1450.816	12	I	8	1036.588		1036.588	
	1579.859	-0.203607	1579.859	13	E	7	923.5036	-0.016254	923.5036	
+0.281529	854.4622		1707.917	14	Q	6	794.461		794.461	
+0.258675	903.9965		1806.986	15	V	5	666.4024	+0.026811	666.4024	
-0.082356	953.5307		1906.054	16	V	4	567.334	+0.059763	567.334	
+0.174855	1017.56		2034.113	17	Q	3	468.2656	-0.063473	468.2656	
+0.332883	1081.589		2162.171	18	Q	2	340.207	+0.04854	340.207	
+0.175789	1110.1		2219.193	19	G	1	212.1485		212.1485	
				20	K	0	155.127		155.127	

Source:	20120513_VR_Bsu_TripleSILACrep1_pL2ESLS_F02
Scannumber:	6236
Protein:	BSU17890; tkt; tktA
Peptide Score:	178.71
Method:	ITMS; CID; 3



precursor information

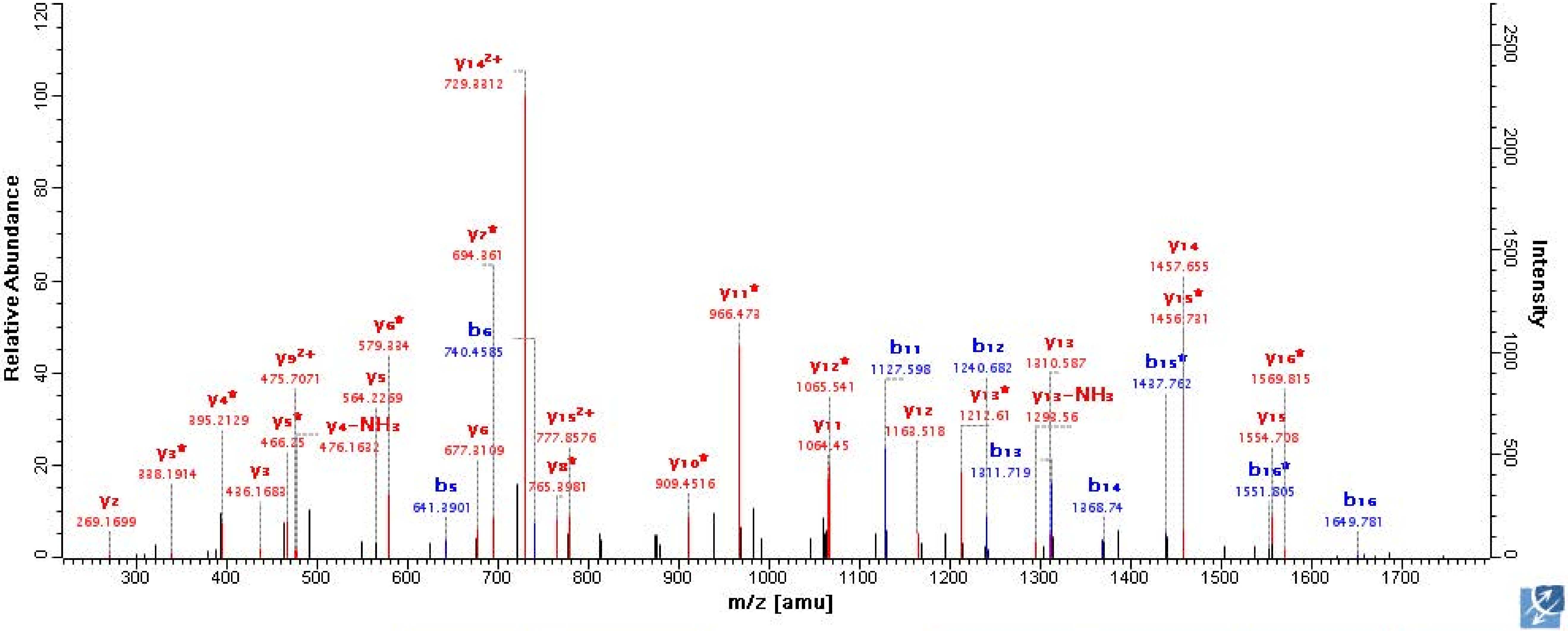
Mass:	1882.91433
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	178.7066
Mass Error [ppm]:	-0.33965
PEP:	3.4433E-41
Precursor Type:	MULTI

general information

Annotation:	14 of 19
AminoAcids Coverag	74 %
Intensity Coverage:	43 %
Protein Localisation:	351 ... 369

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874		58.02874	1	G	18				
	145.0608		145.0608	2	S	17	1826.901		1826.901	
	312.0591		312.0591	3	S	16	1739.869	-0.098613	1739.869	
	425.1432		425.1432	4	I	15	1572.87		1572.87	
	496.1803	-0.201362	496.1803	5	A	14	1459.786		730.3968	-0.112685
	583.2123		583.2123	6	S	13	1388.749		694.8782	-0.415296
	739.3134		739.3134	7	R	12	1301.717		1301.717	
	810.3506		810.3506	8	A	11	1145.616	+0.153331	1145.616	
	897.3826		897.3826	9	S	10	1074.579	-0.090073	1074.579	
	984.4146	+0.052182	984.4146	10	S	9	987.5469	+0.168945	987.5469	
	1041.436		1041.436	11	G	8	900.5149		900.5149	
+0.444648	585.743	-0.019932	1170.479	12	E	7	843.4934		843.4934	
	1269.547	-0.11984	1269.547	13	V	6	714.4509	-0.044967	714.4509	
	1382.631	-0.062058	1382.631	14	I	5	615.3824	-0.029654	615.3824	
	1496.674	-0.045659	1496.674	15	N	4	502.2984	-0.030368	502.2984	
	1553.696		1553.696	16	G	3	388.2554	+0.108263	388.2554	
	1666.78	+0.082822	1666.78	17	I	2	331.234		331.234	
	1737.817	-0.214912	1737.817	18	A	1	218.1499		218.1499	
				19	K	0	147.1128		147.1128	

Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F03
Scannumber: 10561
Protein: BSU17890; tkt; tktA
Peptide Score: 183.36
Method: ITMS; CID; 3



precursor information

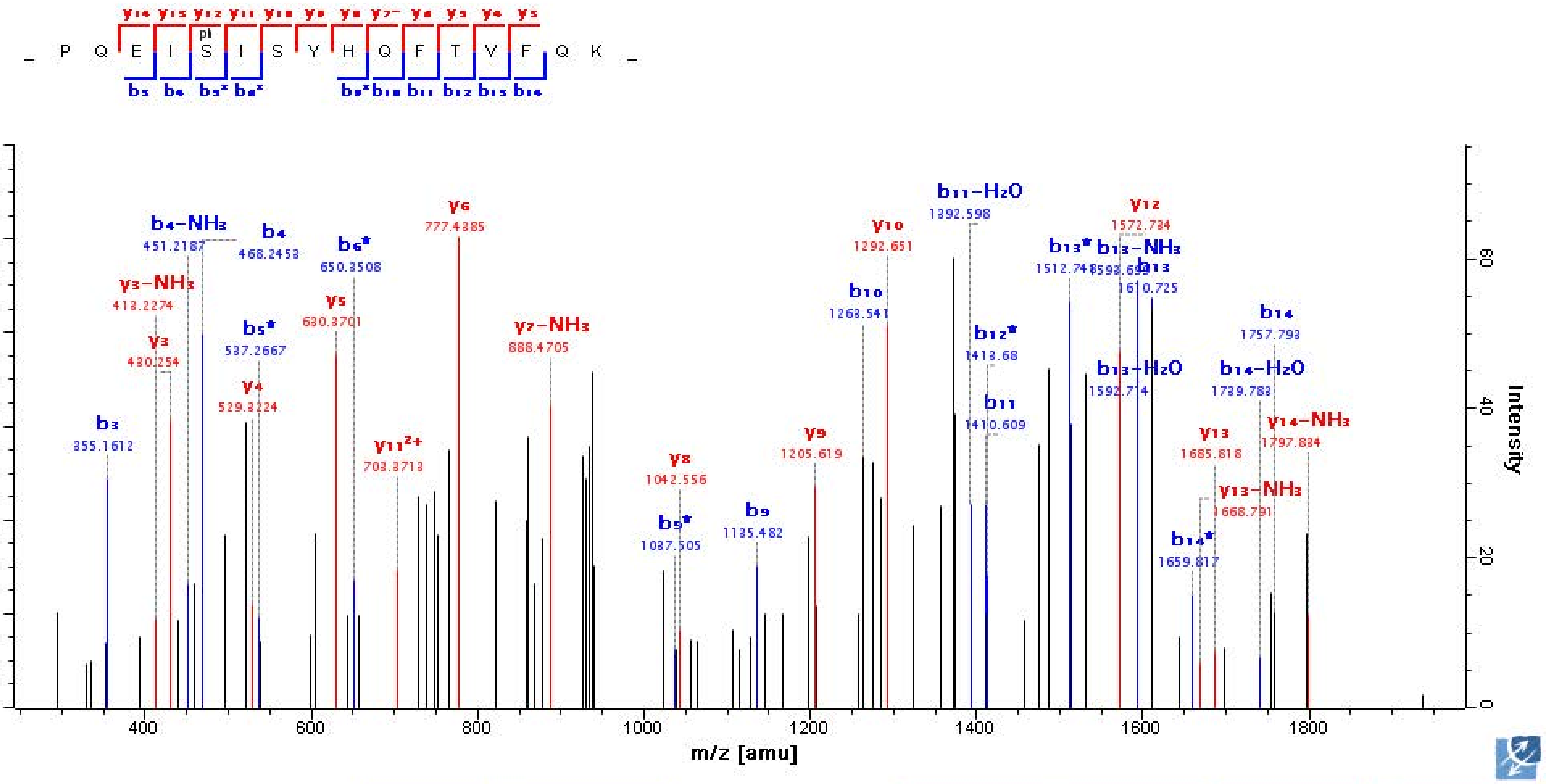
Mass:	1786.86531
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	183.3578
Mass Error [ppm]:	-0.10539
PEP:	2.1354E-37
Precursor Type:	MULTI

general information

Annotation:	15 of 17
AminoAcids Coverag	88 %
Intensity Coverage:	65 %
Protein Localisation:	370 ... 386

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	137.1164383	1	K	16				
	250.20050228	2	I	15	1667.792013		1667.792013	
	347.25326613	3	P	14	1554.707949	-0.0252098	777.85761274	+0.1378096
	494.32168005	4	F	13	1457.6551852	+0.2658353	729.33123082	-0.4368216
-0.001239	641.39009396	5	F	12	1310.5867713	-0.03245	1310.5867713	
+0.0106083	740.45850788	6	V	11	1163.5183573	+0.0915059	1163.5183573	
	797.4799716	7	G	10	1064.4499434	-0.1247481	1064.4499434	
	854.50143533	8	G	9	1007.4284797		1007.4284797	
	941.53346374	9	S	8	950.40701597		475.70714622	-0.4142385
	1012.5705775	10	A	7	863.37498756		863.37498756	
-0.0591905	1127.5975206	11	D	6	792.33787377		792.33787377	
-0.0479175	1240.6815845	12	I	5	677.31093074	-0.0079522	677.31093074	
-0.1140841	1311.7186983	13	A	4	564.22686676	+0.00879	564.22686676	
-0.0850107	1368.740162	14	G	3	493.18975297		493.18975297	
	1535.7385209	15	S	2	436.16828925	+0.1382293	436.16828925	
+0.0504609	1649.7814483	16	N	1	269.16993043	-0.0275049	269.16993043	
		17	K	0	155.12700298		155.12700298	

Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F03
Scannumber:	10944
Protein:	BSU03420; comJ; nin
Peptide Score:	158.17
Method:	ITMS; CID; 3



precursor information

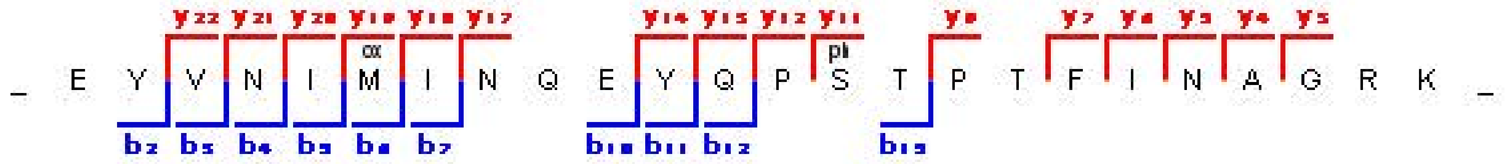
Mass:	2038.96491
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	158.1726
Mass Error [ppm]:	0.20329
PEP:	1.6451E-19
Precursor Type:	ISO

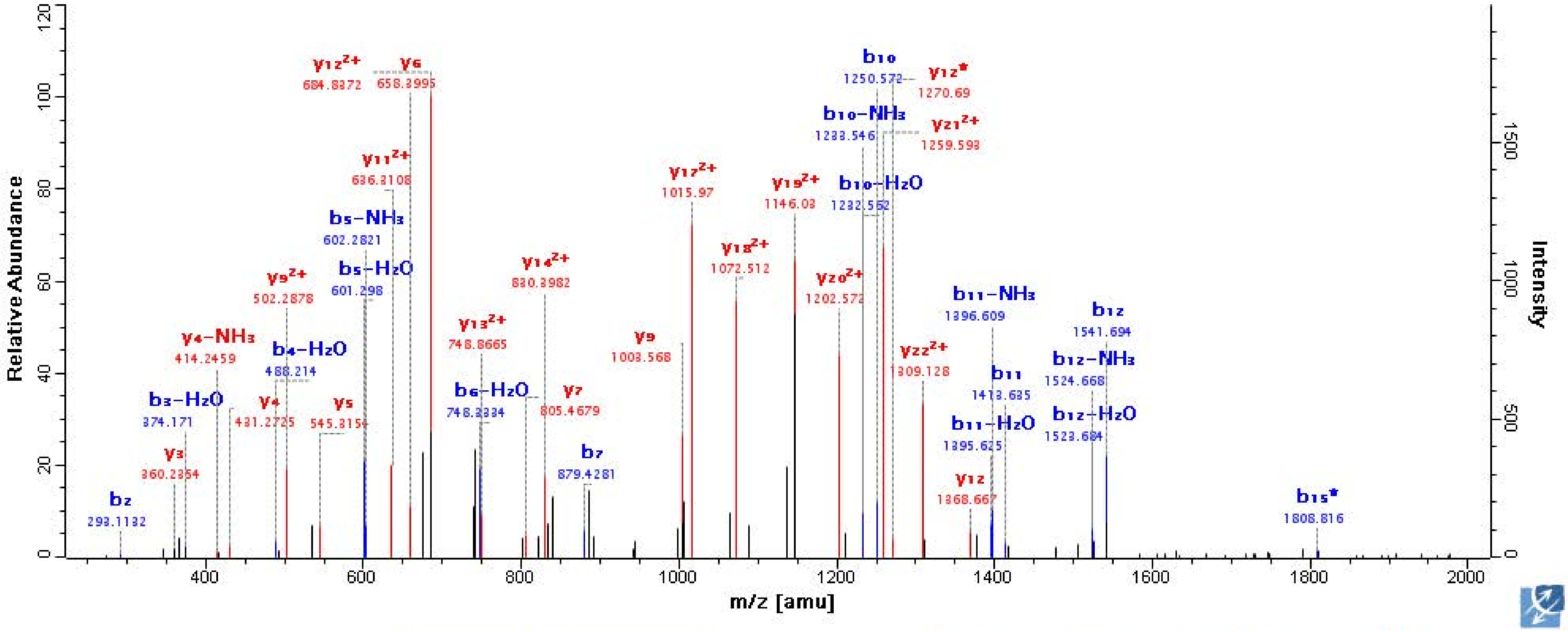
general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	40 %
Protein Localisation:	7 ... 22

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	98.060040319	1	P	15				
	226.11861783	2	Q	14	1942.9190044		1942.9190044	
-0.1854419	355.16121093	3	E	13	1814.8604269		1814.8604269	
-0.0313772	468.24527491	4	I	12	1685.8178338	+0.4591437	1685.8178338	
	635.24363372	5	S	11	1572.7337698	+0.076777	1572.7337698	
	748.32769771	6	I	10	1405.735411		703.37134374	+0.2925967
	835.35972612	7	S	9	1292.651347	-0.0075482	1292.651347	
	998.42305465	8	Y	8	1205.6193186	+0.0287527	1205.6193186	
+0.2035804	1135.4819665	9	H	7	1042.5559901	+0.1083165	1042.5559901	
+0.096663	1263.540544	10	Q	6	905.49707823		905.49707823	
+0.1022237	1410.6089579	11	F	5	777.43850072	-0.057031	777.43850072	
	1511.6566364	12	T	4	630.3700868	-0.0345155	630.3700868	
-0.2108902	1610.7250503	13	V	3	529.32240833	+0.1194862	529.32240833	
-0.0471264	1757.7934642	14	F	2	430.25399441	-0.0616116	430.25399441	
	1885.8520418	15	Q	1	283.1855805		283.1855805	
		16	K	0	155.12700298		155.12700298	

Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F03
Scannumber: 10985
Protein: BSU17380; nrdA; nrdE
Peptide Score: 132.62
Method: ITMS; CID; 3





precursor information

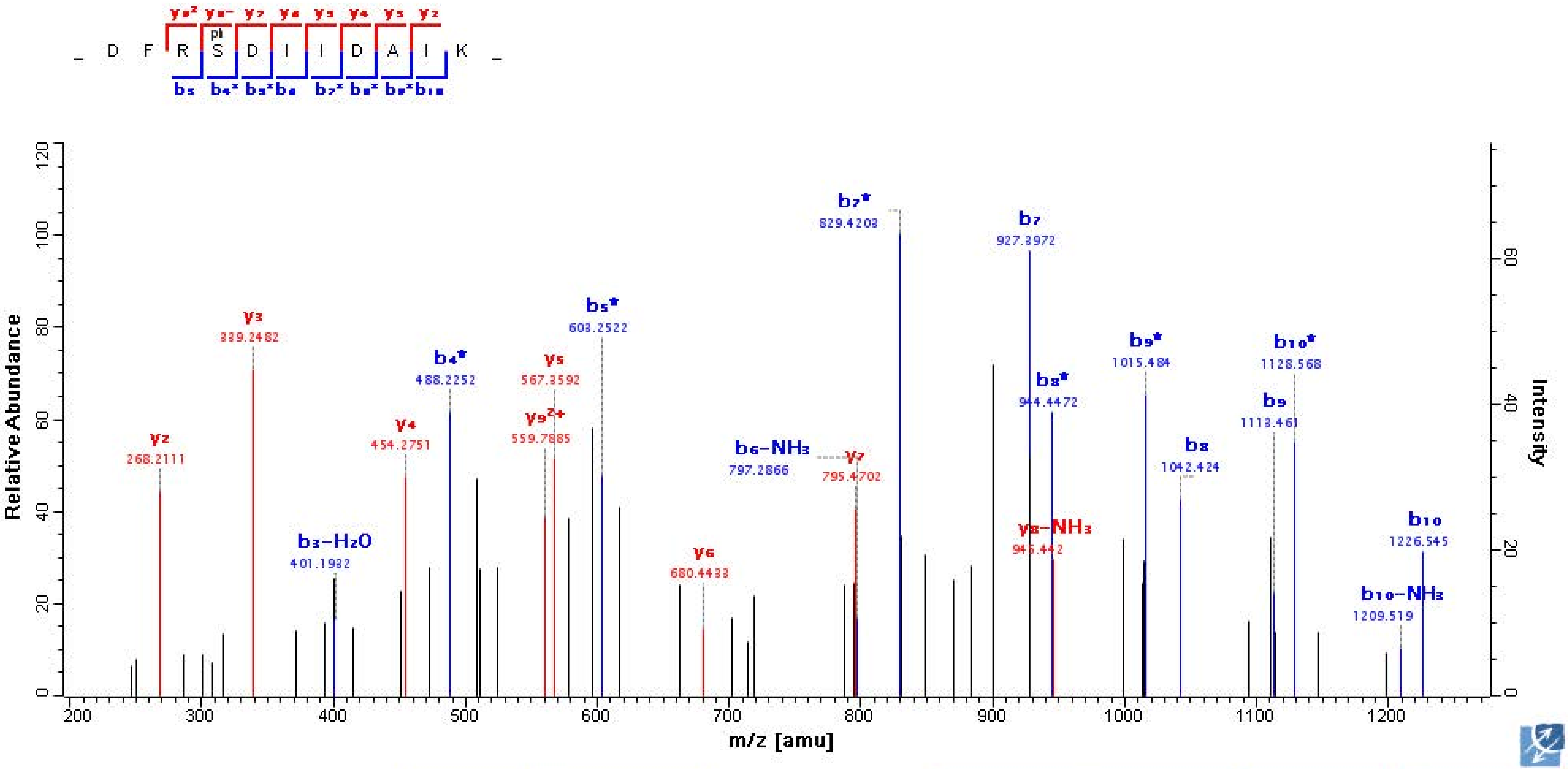
Mass:	2908.34911
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	132.6152
Mass Error [ppm]:	0.84332
PEP:	1.2212E-13
Precursor Type:	ISO

general information

Annotation:	19 of 24
AminoAcids Coverag	79 %
Intensity Coverage:	68 %
Protein Localisation:	139 ... 162

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.04986956	1	E	23				
-0.3434227	293.1131981	2	Y	22	2780.3113427		2780.3113427	
	392.18161202	3	V	21	2617.2480142		1309.1276453	+0.2037756
	506.22453946	4	N	20	2518.1796003		1259.5934384	+0.242255
	619.30860344	5	I	19	2404.1366728		1202.5719746	+0.1472636
	766.34400267	6	M	18	2291.0526088		1146.0299427	-0.1024524
-0.0212673	879.42806665	7	I	17	2144.0172096		1072.512243	+0.1984503
	993.4709941	8	N	16	2030.9331456		1015.970211	+0.1926918
	1121.5295716	9	Q	15	1916.8902182		1916.8902182	
+0.4402865	1250.5721647	10	E	14	1788.8316407		1788.8316407	
+0.0538378	1413.6354932	11	Y	13	1659.7890476		830.39816202	+0.2135323
-0.00181	1541.6940708	12	Q	12	1496.725719		748.86649775	+0.3371766
	1638.7468346	13	P	11	1368.6671415	+0.0110811	684.837209	+0.0244243
	1805.7451934	14	S	10	1271.6143777		636.31082707	-0.48081
	1906.7928719	15	T	9	1104.6160189		1104.6160189	
	2003.8456358	16	P	8	1003.5683404	-0.0510674	502.28780842	+0.0840177
	2104.8933142	17	T	7	906.51557653		906.51557653	
	2251.9617281	18	F	6	805.46789805	+0.1553319	805.46789805	
	2365.0457921	19	I	5	658.39948414	+0.0267244	658.39948414	
	2479.0887196	20	N	4	545.31542016	+0.0073948	545.31542016	
	2550.1258334	21	A	3	431.27249271	-0.0494092	431.27249271	
	2607.1472971	22	G	2	360.23537892	-0.0174224	360.23537892	
	2763.2484081	23	R	1	303.2139152		303.2139152	
		24	K	0	147.11280417		147.11280417	

Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F03
Scannumber: 13276
Protein: BSU15430; ileS
Peptide Score: 117.79
Method: ITMS; CID; 3



precursor information

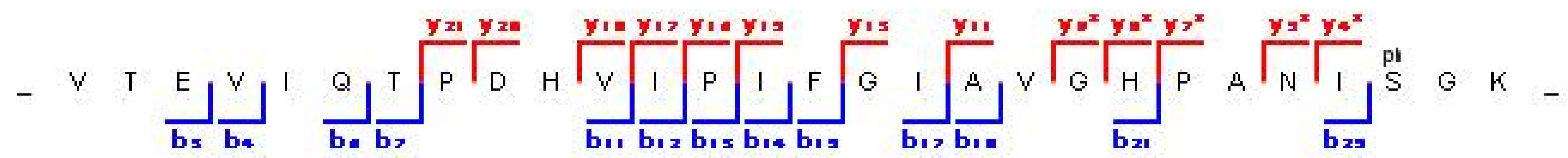
Mass:	1371.64382
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	117.7924
Mass Error [ppm]:	0.1969
PEP:	8.2176E-06
Precursor Type:	MULTI

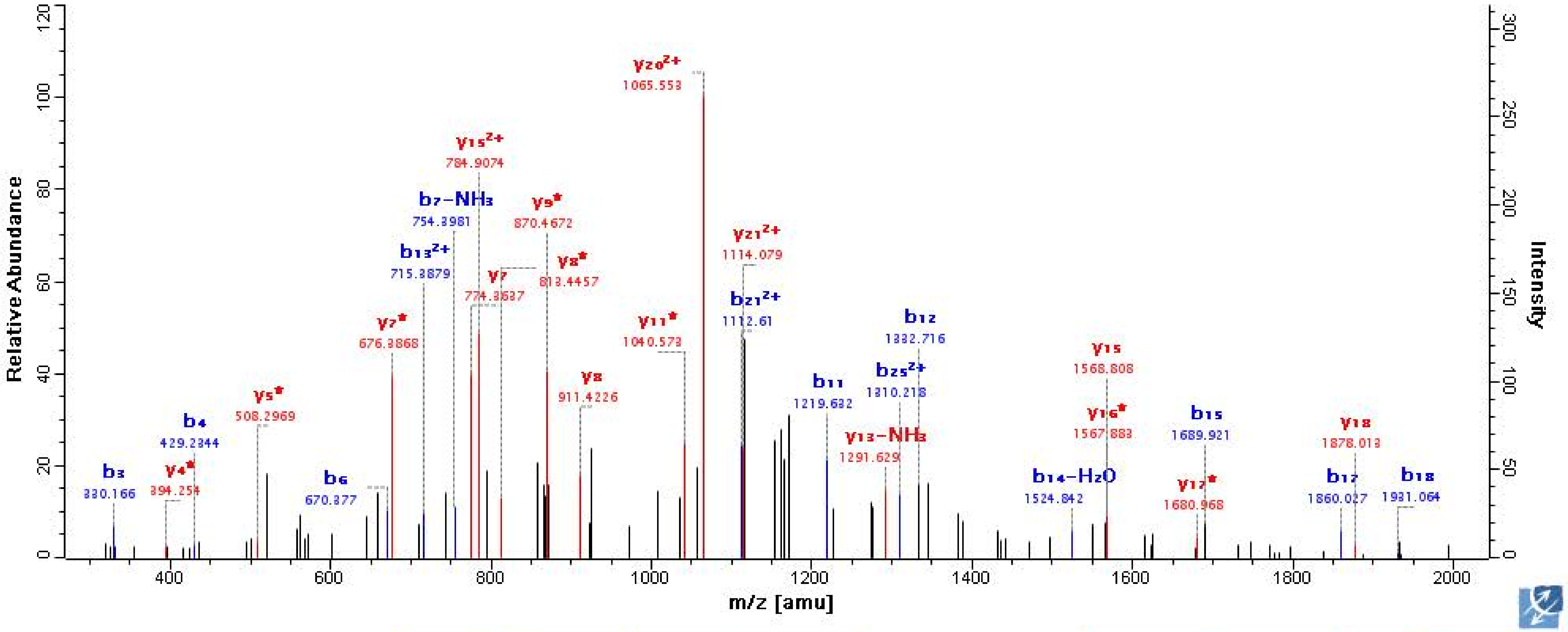
general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	50 %
Protein Localisation:	417 ... 427

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342195	1	D	10				
	263.10263341	2	F	9	1265.6380785		1265.6380785	
	419.20374444	3	R	8	1118.5696646		559.78847054	-0.0310853
	586.20210326	4	S	7	962.4685536		962.4685536	
	701.22904629	5	D	6	795.47019478	-0.0706586	795.47019478	
	814.31311027	6	I	5	680.44325174	+0.0072487	680.44325174	
+0.1020933	927.39717425	7	I	4	567.35918776	-0.0253255	567.35918776	
-0.0731651	1042.4241173	8	D	3	454.27512378	+0.1472395	454.27512378	
-0.344776	1113.4612311	9	A	2	339.24818075	+0.0094486	339.24818075	
+0.0358817	1226.5452951	10	I	1	268.21106696	+0.105736	268.21106696	
		11	K	0	155.12700298		155.12700298	

Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F03
Scannumber: 13633
Protein: BSU38110; ipa-43d; nfrA; nfrA1; ywcG
Peptide Score: 86.3
Method: ITMS; CID; 3





precursor information

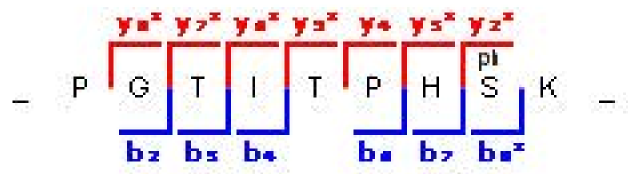
Mass:	2996.56127
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	86.30436
Mass Error [ppm]:	-0.11398
PEP:	1.8432E-11
Precursor Type:	ISO

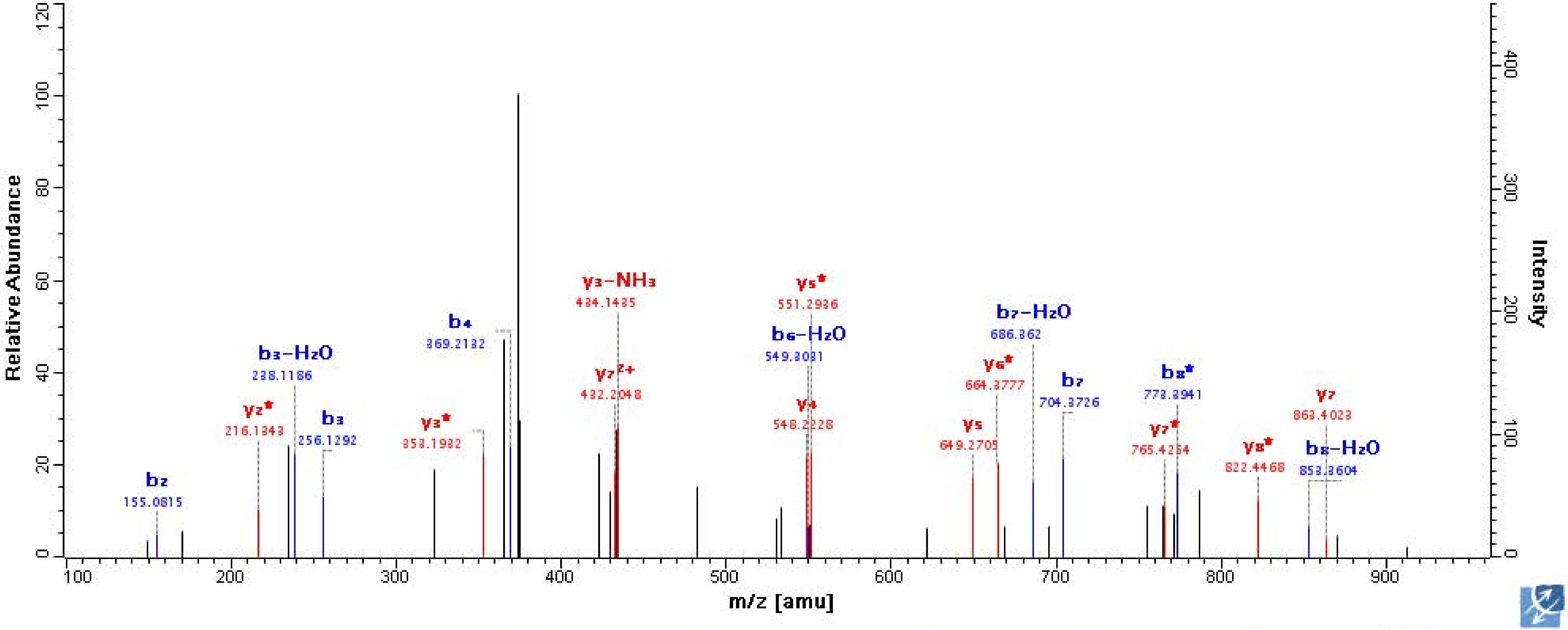
general information

Annotation:	19 of 28
AminoAcids Coverag	68 %
Intensity Coverage:	45 %
Protein Localisation:	145 ... 172

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757		100.0757	1	V	27				
	201.1234		201.1234	2	T	26	2898.5		2898.5	
	330.166	-0.046943	330.166	3	E	25	2797.453		2797.453	
	429.2344	+0.178588	429.2344	4	V	24	2668.41		2668.41	
	542.3184		542.3184	5	I	23	2569.342		2569.342	
	670.377	-0.06525	670.377	6	Q	22	2456.258		2456.258	
	771.4247		771.4247	7	T	21	2328.199		2328.199	
	868.4775		868.4775	8	P	20	2227.151		1114.079	+0.179175
	983.5044		983.5044	9	D	19	2130.099		1065.553	-0.19874
	1120.563		1120.563	10	H	18	2015.072		2015.072	
	1219.632	-0.152725	1219.632	11	V	17	1878.013	+0.140109	1878.013	
	1332.716	+0.036161	1332.716	12	I	16	1778.944		1778.944	
-0.029823	715.3879		1429.769	13	P	15	1665.86		1665.86	
	1542.853		1542.853	14	I	14	1568.808	+0.052626	784.9074	-0.026336
	1689.921	+0.035875	1689.921	15	F	13	1455.724		1455.724	
	1746.942		1746.942	16	G	12	1308.655		1308.655	
	1860.027	-0.05708	1860.027	17	I	11	1251.634		1251.634	
	1931.064	+0.351241	1931.064	18	A	10	1138.55		1138.55	
	2030.132		2030.132	19	V	9	1067.512		1067.512	
	2087.154		2087.154	20	G	8	968.4441		968.4441	
+0.173576	1112.61		2224.212	21	H	7	911.4226	+0.488404	911.4226	
	2321.265		2321.265	22	P	6	774.3637	+0.158766	774.3637	
	2392.302		2392.302	23	A	5	677.3109		677.3109	
	2506.345		2506.345	24	N	4	606.2738		606.2738	
+0.264361	1310.218		2619.429	25	I	3	492.2309		492.2309	
	2786.428		2786.428	26	S	2	379.1468		379.1468	
	2843.449		2843.449	27	G	1	212.1485		212.1485	
				28	K	0	155.127		155.127	

Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F03
Scannumber:	2470
Protein:	BSU01130; tuf; tufA
Peptide Score:	128.36
Method:	ITMS; CID; 3

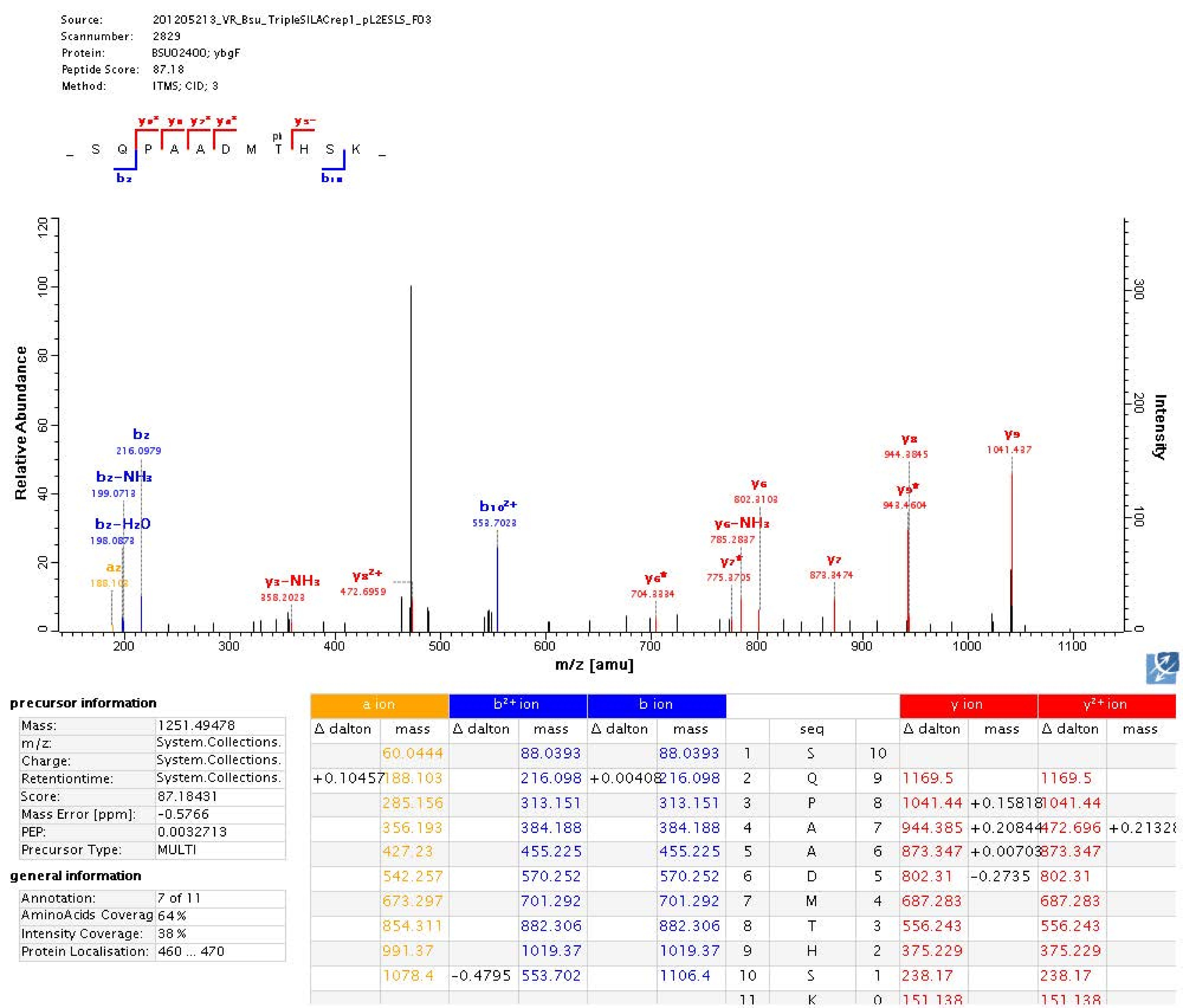




precursor information

Mass:	1016.46876
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	128.3611
Mass Error [ppm]:	-0.44033
PEP:	7.8389E-08
Precursor Type:	ISO
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	44 %
Protein Localisation:	298 ... 306

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	98.060040319	1	P	8				
+0.1636131	155.08150404	2	G	7	920.42372336		920.42372336	
-0.0377824	256.12918252	3	T	6	863.40225963	-0.0040663	432.20476805	-0.0477856
+0.001231	369.2132465	4	I	5	762.35458116		762.35458116	
	470.26092497	5	T	4	649.27051718	+0.071768	649.27051718	
	567.31368882	6	P	3	548.2228387	+0.0426642	548.2228387	
+0.0337103	704.37260069	7	H	2	451.17007485		451.17007485	
	871.3709595	8	S	1	314.11116299		314.11116299	
		9	K	0	147.11280417		147.11280417	



Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F03
Scannumber: 2829
Protein: BSU02400; ybgF
Peptide Score: 87.18
Method: ITMS; CID; 3

precursor information

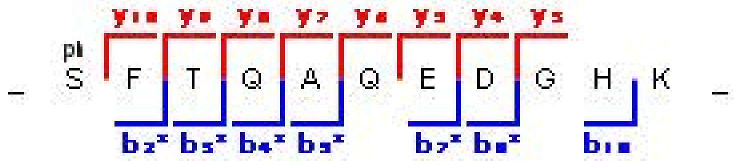
Mass:	1251.49478
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	87.18431
Mass Error [ppm]:	-0.5766
PEP:	0.0032713
Precursor Type:	MULTI

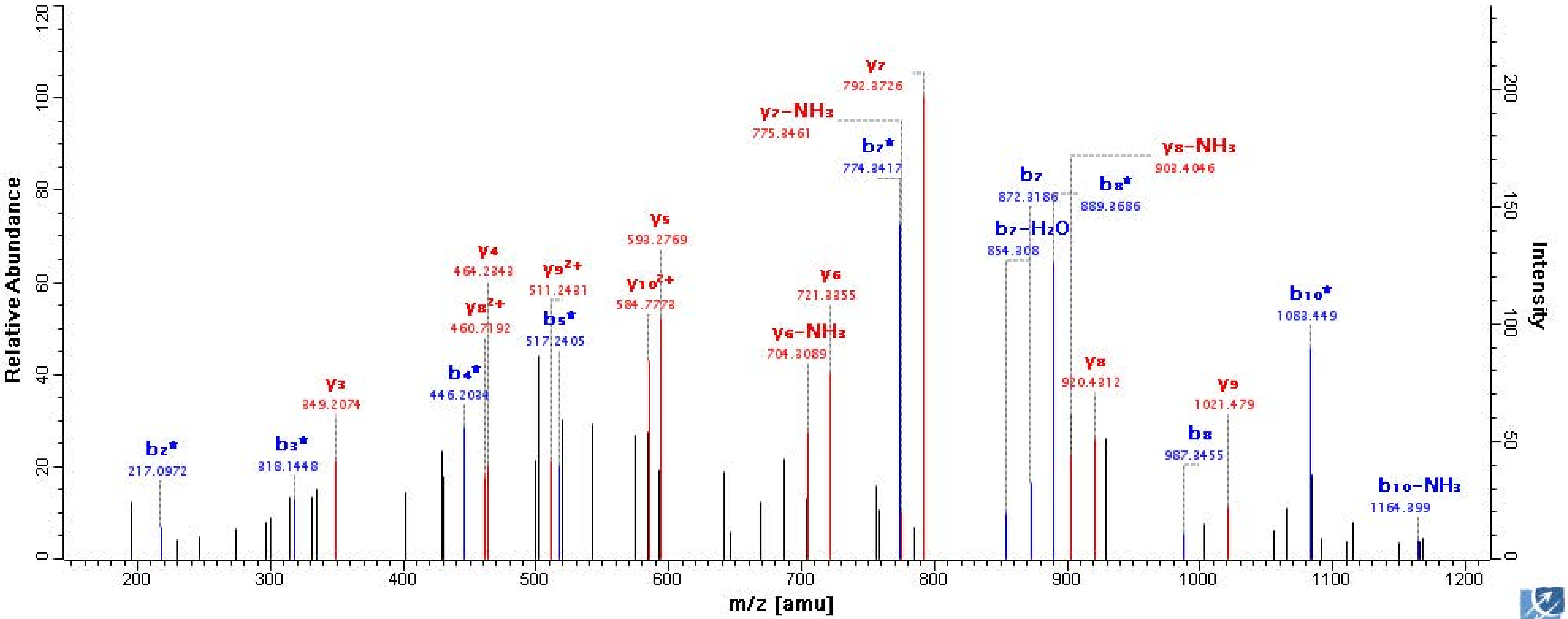
general information

Annotation:	7 of 11
AminoAcids Coverag	64 %
Intensity Coverage:	38 %
Protein Localisation:	460 ... 470

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
	60.0444		88.0393		88.0393	1	S	10				
+0.10457	188.103		216.098	+0.00408	216.098	2	Q	9	1169.5		1169.5	
	285.156		313.151		313.151	3	P	8	1041.44	+0.15818	1041.44	
	356.193		384.188		384.188	4	A	7	944.385	+0.20844	472.696	+0.2132
	427.23		455.225		455.225	5	A	6	873.347	+0.00703	873.347	
	542.257		570.252		570.252	6	D	5	802.31	-0.2735	802.31	
	673.297		701.292		701.292	7	M	4	687.283		687.283	
	854.311		882.306		882.306	8	T	3	556.243		556.243	
	991.37		1019.37		1019.37	9	H	2	375.229		375.229	
	1078.4	-0.4795	553.702		1106.4	10	S	1	238.17		238.17	
						11	K	0	151.138		151.138	

Source: 20120521 3_VR_Bsu_TripleSILACrep1_pL2ESLS_F03
Scannumber: 3402
Protein: BSU28290; ilvC
Peptide Score: 145.28
Method: ITMS; CID; 3





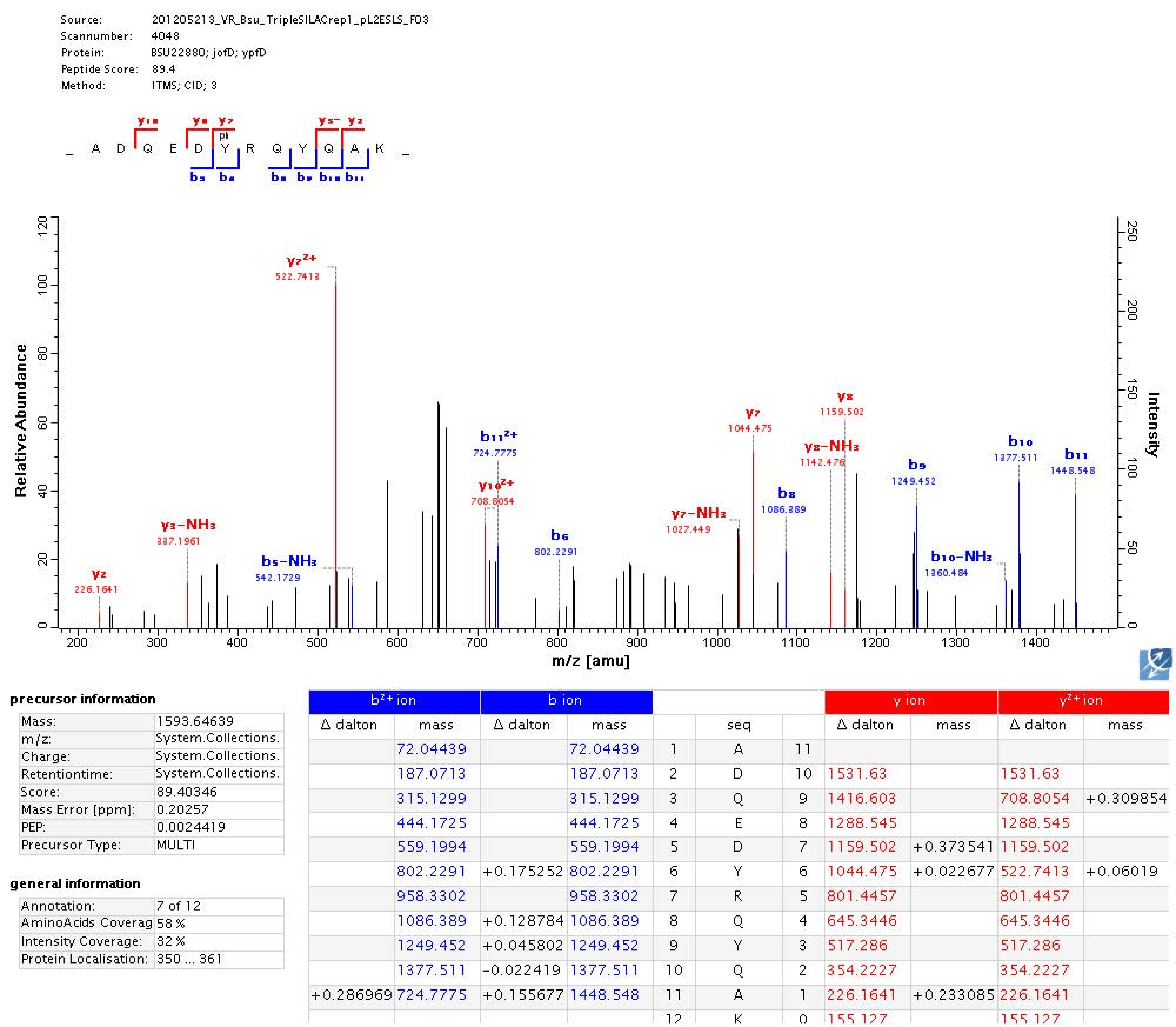
precursor information

Mass:	1326.52405
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	145.2753
Mass Error [ppm]:	-0.084509
PEP:	1.7785E-11
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	55 %
Protein Localisation:	52 ... 62

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.00563528	1	S	10				
	315.0740492	2	F	9	1168.5472759		584.77727618	+0.1612614
	416.12172768	3	T	8	1021.478862	-0.0364181	511.24306922	-0.0859037
	544.18030519	4	Q	7	920.43118351	+0.0724176	460.71922999	+0.105477
	615.21741897	5	A	6	792.372606	-0.0834825	792.372606	
	743.27599649	6	Q	5	721.33549221	+0.0180234	721.33549221	
+0.2642351	872.31858958	7	E	4	593.2769147	-0.0896588	593.2769147	
+0.1593502	987.34553261	8	D	3	464.2343216	+0.0100632	464.2343216	
	1044.3669963	9	G	2	349.20737857	+0.007221	349.20737857	
	1181.4259082	10	H	1	292.18591485		292.18591485	
		11	K	0	155.12700298		155.12700298	



Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F03
Scannumber: 4048
Protein: BSU22880; jofD; ypfD
Peptide Score: 89.4
Method: ITMS; CID; 3

precursor information

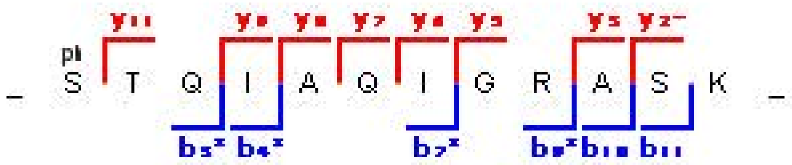
Mass:	1593.64639
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	89.40346
Mass Error [ppm]:	0.20257
PEP:	0.0024419
Precursor Type:	MULTI

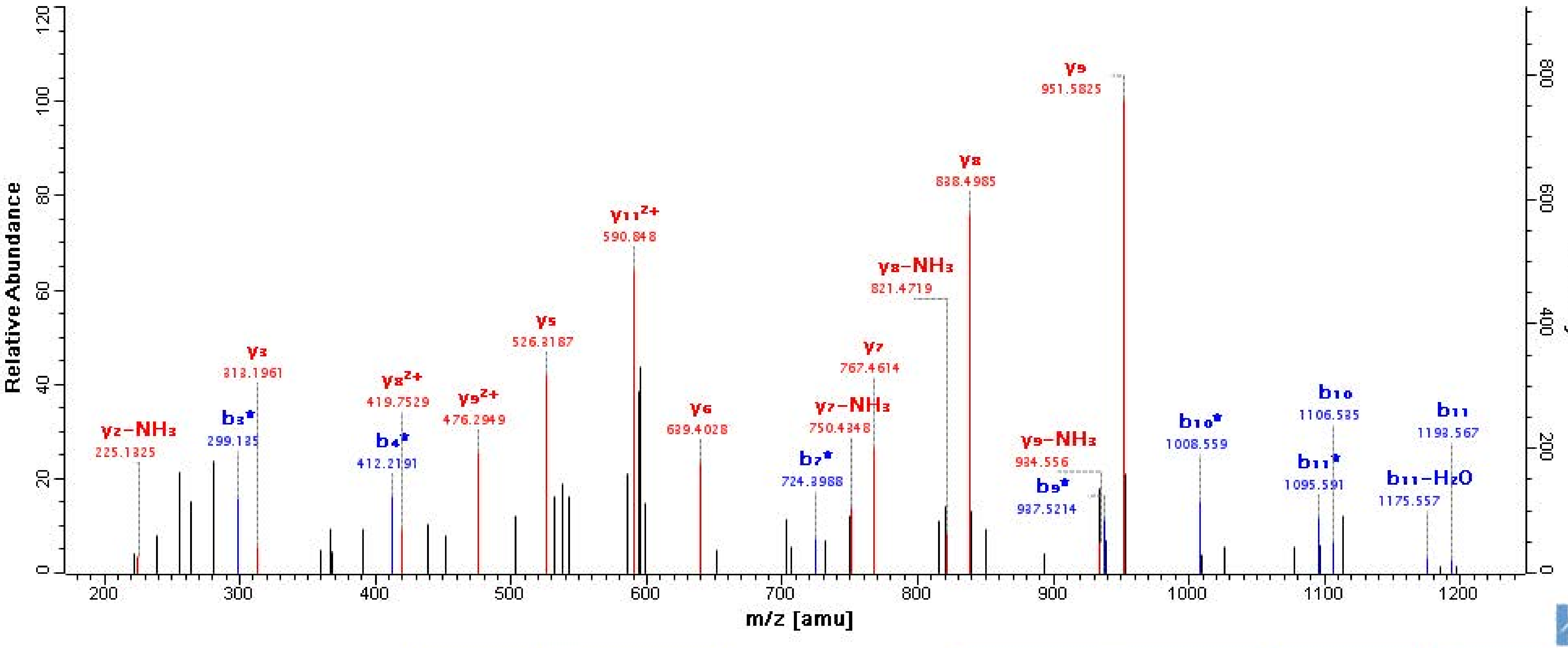
general information

Annotation:	7 of 12
AminoAcids Coverag	58 %
Intensity Coverage:	32 %
Protein Localisation:	350 ... 361

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439		72.04439	1	A	11				
	187.0713		187.0713	2	D	10	1531.63		1531.63	
	315.1299		315.1299	3	Q	9	1416.603		708.8054	+0.309854
	444.1725		444.1725	4	E	8	1288.545		1288.545	
	559.1994		559.1994	5	D	7	1159.502	+0.373541	1159.502	
	802.2291	+0.175252	802.2291	6	Y	6	1044.475	+0.022677	522.7413	+0.06019
	958.3302		958.3302	7	R	5	801.4457		801.4457	
	1086.389	+0.128784	1086.389	8	Q	4	645.3446		645.3446	
	1249.452	+0.045802	1249.452	9	Y	3	517.286		517.286	
	1377.511	-0.022419	1377.511	10	Q	2	354.2227		354.2227	
+0.286969	724.7775	+0.155677	1448.548	11	A	1	226.1641	+0.233085	226.1641	
				12	K	0	155.127		155.127	

Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F03
Scannumber:	5658
Protein:	BSU06030; groEL; groL; mopA
Peptide Score:	116.24
Method:	ITMS; CID; 3





precursor information

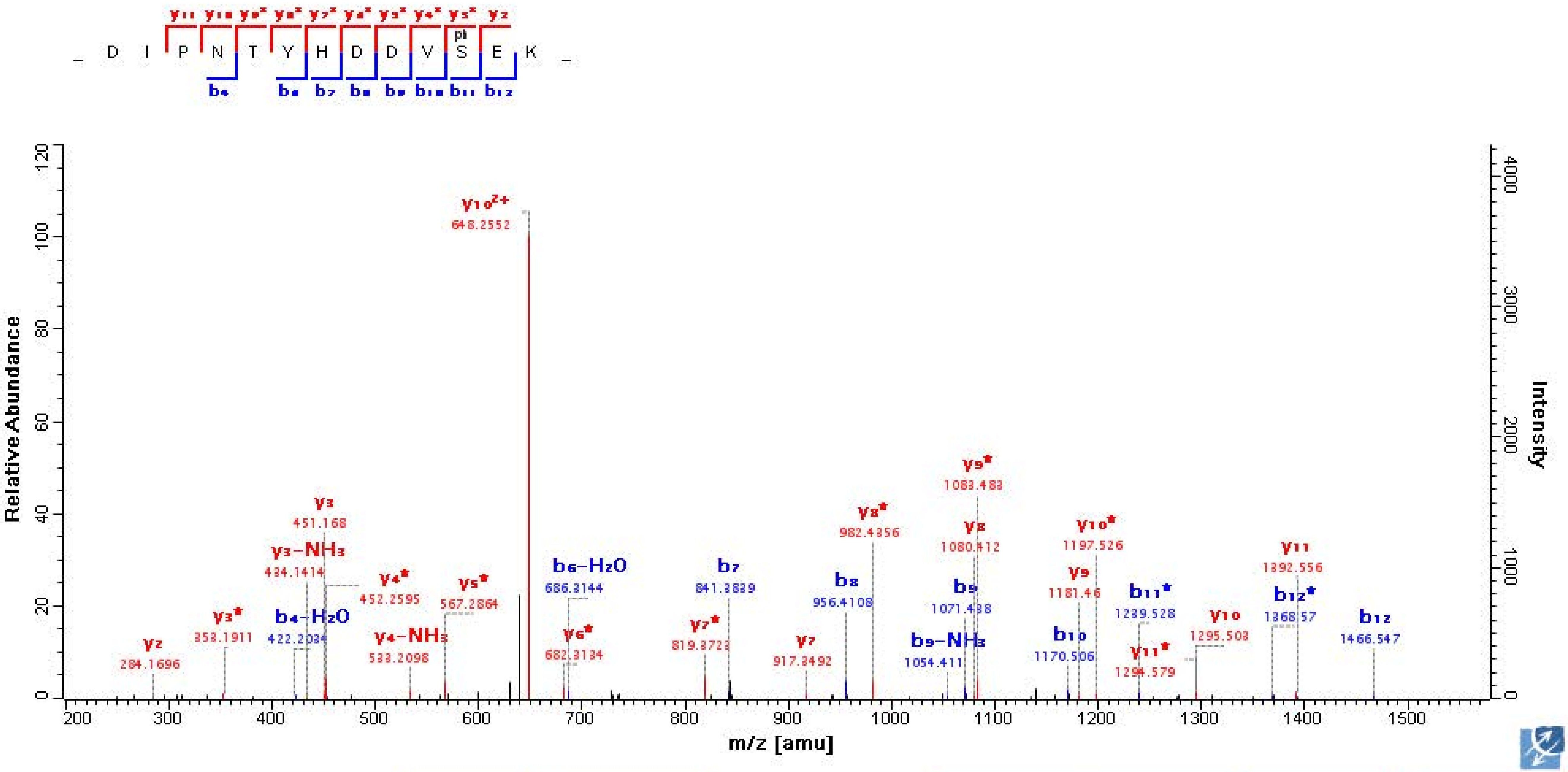
Mass:	1338.66497
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	116.2378
Mass Error [ppm]:	-0.52632
PEP:	1.892E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	51 %
Protein Localisation:	309 ... 320

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.00563528	1	S	11				
	269.05331376	2	T	10	1180.6887952		590.84803582	-0.0470104
	397.11189127	3	Q	9	1079.6411167		1079.6411167	
	510.19595525	4	I	8	951.58253919	-0.0722243	476.29490783	+0.0231464
	581.23306904	5	A	7	838.49847521	-0.0566417	419.75287584	+0.1074147
	709.29164655	6	Q	6	767.46136142	-0.0548673	767.46136142	
	822.37571053	7	I	5	639.40278391	+0.0251946	639.40278391	
	879.39717425	8	G	4	526.31871993	+0.1366634	526.31871993	
	1035.4982853	9	R	3	469.29725621		469.29725621	
-0.0693346	1106.5353991	10	A	2	313.19614518	-0.0163051	313.19614518	
-0.0591267	1193.5674275	11	S	1	242.15903139		242.15903139	
		12	K	0	155.12700298		155.12700298	

Source:	20120521 3_VR_Bsu_TripleSILACrep1_pL2ESLS_F03
Scannumber:	5780
Protein:	BSU16910; ymfM
Peptide Score:	151.99
Method:	ITMS; CID; 3



precursor information

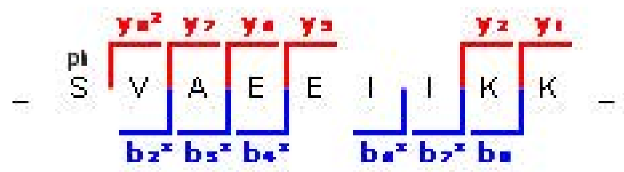
Mass:	1611.64559
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	151.9937
Mass Error [ppm]:	0.11904
PEP:	1.6281E-17
Precursor Type:	MULTI

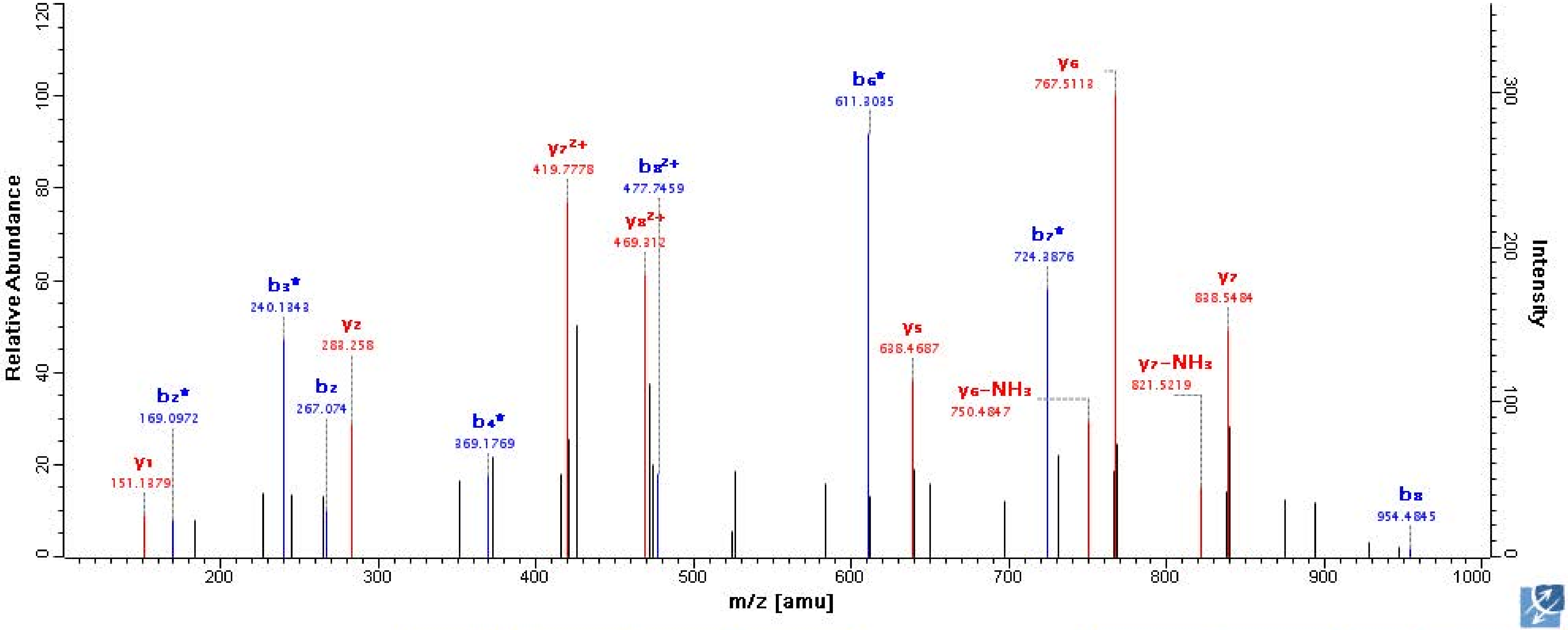
general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	72 %
Protein Localisation:	59 ... 71

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342195	1	D	12				
	229.11828348	2	I	11	1505.639929		1505.639929	
	326.17104733	3	P	10	1392.5558651	-0.1054256	1392.5558651	
	440.21397478	4	N	9	1295.5031012	+0.1354486	648.25518883	-0.3599252
	541.26165325	5	T	8	1181.4601738	-0.056121	1181.4601738	
	704.32498179	6	Y	7	1080.4124953	+0.1451219	1080.4124953	
-0.035566	841.38389365	7	H	6	917.34916674	+0.1198884	917.34916674	
+0.0194001	956.41083668	8	D	5	780.29025488		780.29025488	
-0.047643	1071.4377797	9	D	4	665.26331185		665.26331185	
+0.0187087	1170.5061936	10	V	3	550.23636881		550.23636881	
	1337.5045525	11	S	2	451.1679549	-0.362657	451.1679549	
-0.1048848	1466.5471455	12	E	1	284.16959608	+0.0643517	284.16959608	
		13	K	0	155.12700298		155.12700298	

Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F03
Scannumber:	5947
Protein:	BSU01120; fus; fusA
Peptide Score:	129.38
Method:	ITMS; CID; 3



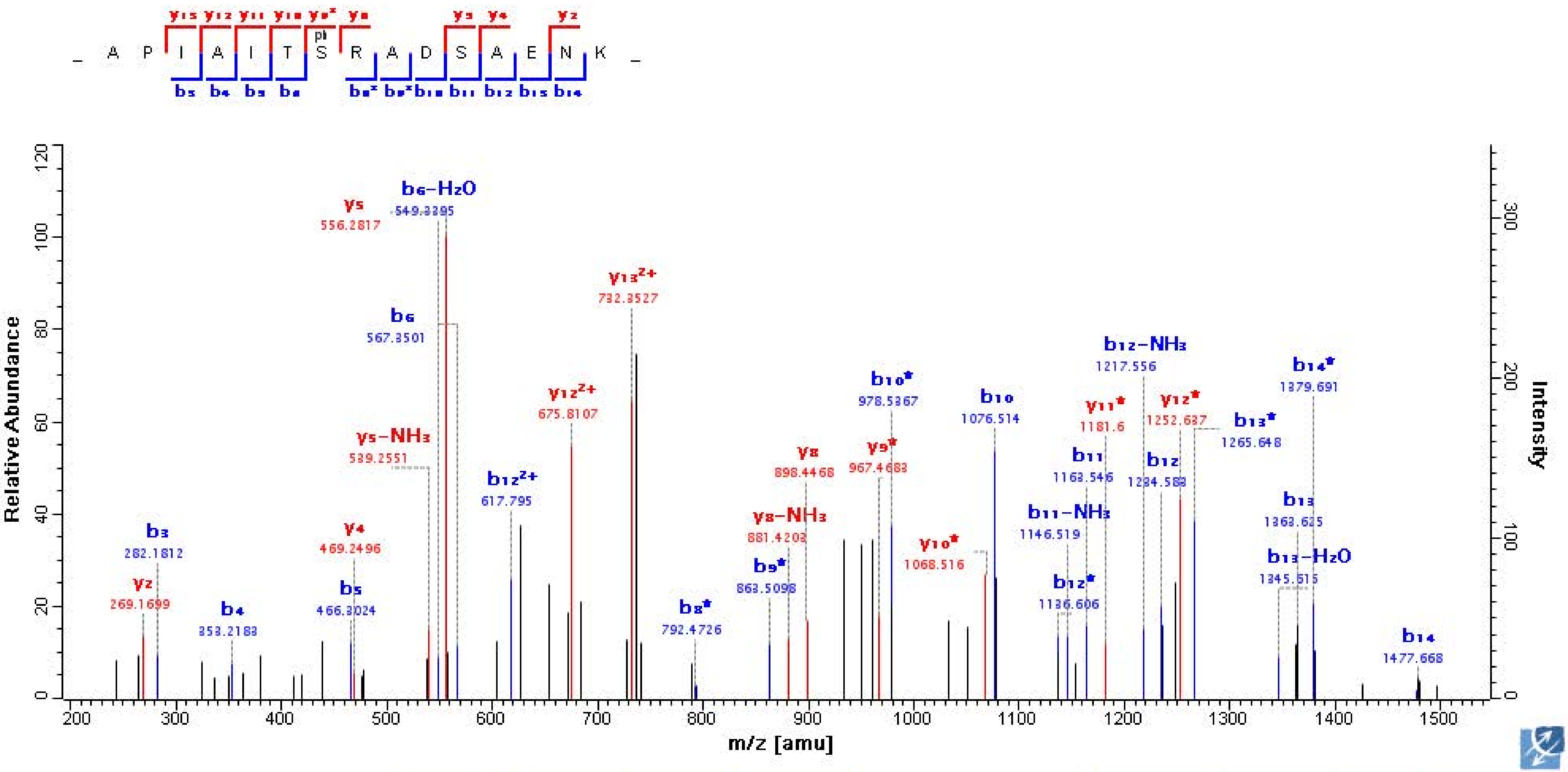


precursor information

Mass:	1095.55745
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	129.3825
Mass Error [ppm]:	-0.2171
PEP:	0.00019542
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	58 %
Protein Localisation:	680 ... 688

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.0056		168.0056	1	S	8				
	267.074	-0.089186	267.074	2	V	7	937.6168		469.312	-0.052467
	338.1112		338.1112	3	A	6	838.5484	+0.115165	419.7778	-0.059886
	467.1538		467.1538	4	E	5	767.5113	-0.000492	767.5113	
	596.1963		596.1963	5	E	4	638.4687	+0.034044	638.4687	
	709.2804		709.2804	6	I	3	509.4261		509.4261	
	822.3645		822.3645	7	I	2	396.342		396.342	
-0.269654	477.7459	+0.089427	954.4845	8	K	1	283.258	+0.020766	283.258	
				9	K	0	151.1379	+0.076505	151.1379	

Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F03
Scannumber:	5972
Protein:	BSU24090; yqiS
Peptide Score:	190.24
Method:	ITMS; CID; 3



precursor information

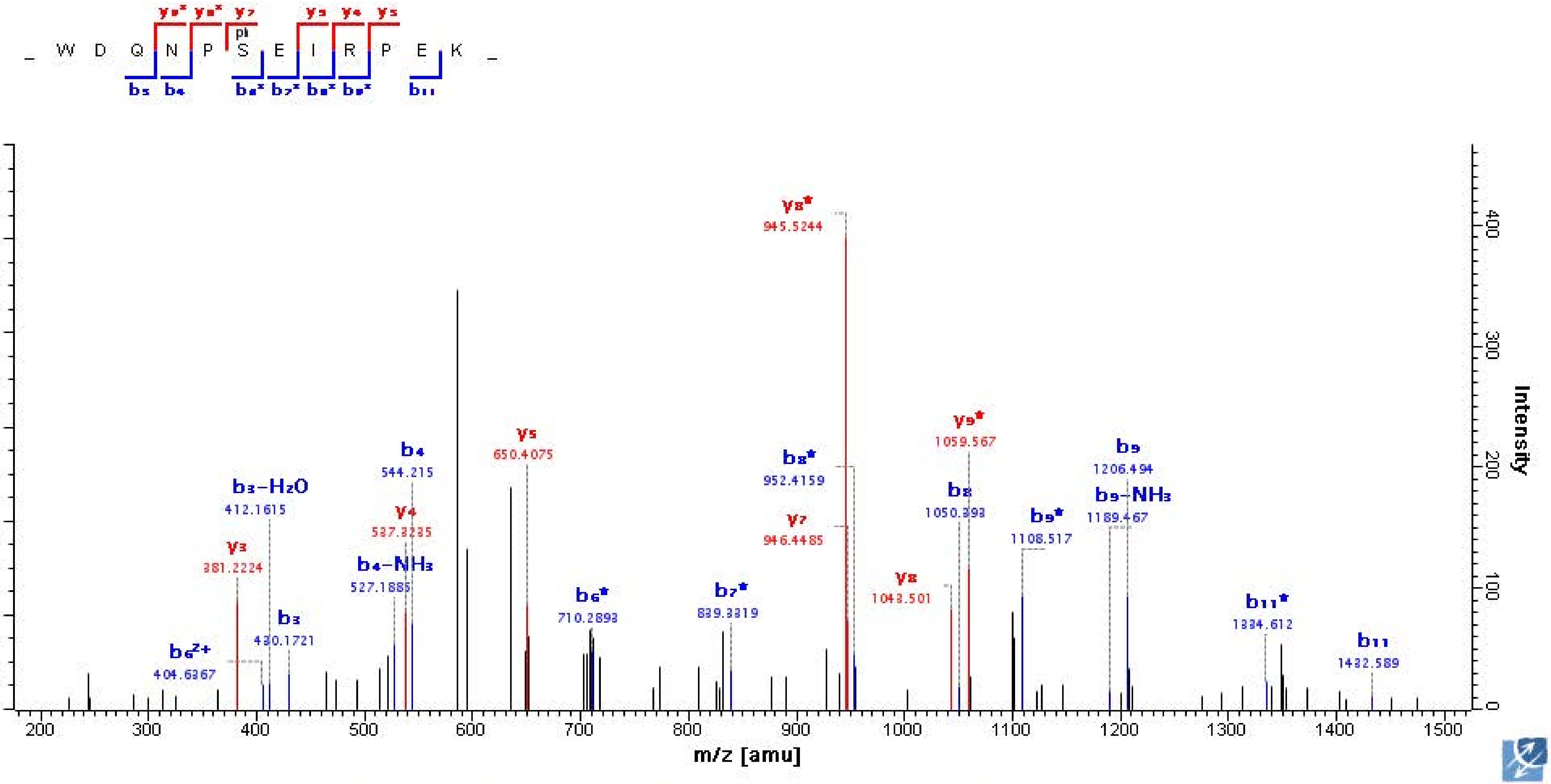
Mass:	1630.78067
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	190.2384
Mass Error [ppm]:	-0.026391
PEP:	3.327E-71
Precursor Type:	ISO

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	54 %
Protein Localisation:	269 ... 283

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439		72.04439	1	A	14				
	169.0972		169.0972	2	P	13	1560.751		1560.751	
	282.1812	-0.104863	282.1812	3	I	12	1463.698		732.3527	+0.318509
	353.2183	-0.069345	353.2183	4	A	11	1350.614		675.8107	+0.061957
	466.3024	+0.008395	466.3024	5	I	10	1279.577		1279.577	
	567.3501	+0.141503	567.3501	6	T	9	1166.493		1166.493	
	734.3484		734.3484	7	S	8	1065.445		1065.445	
	890.4495		890.4495	8	R	7	898.4468	+0.132817	898.4468	
	961.4867		961.4867	9	A	6	742.3457		742.3457	
	1076.514	-0.006399	1076.514	10	D	5	671.3086		671.3086	
	1163.546	+0.058985	1163.546	11	S	4	556.2817	-0.139759	556.2817	
+0.12302	617.795	-0.002787	1234.583	12	A	3	469.2496	+0.096554	469.2496	
	1363.625	+0.086089	1363.625	13	E	2	398.2125		398.2125	
	1477.668	-0.303396	1477.668	14	N	1	269.1699	+0.023032	269.1699	
				15	K	0	155.127		155.127	

Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F03
Scannumber: 6639
Protein: BSU28270; leuB; leuC
Peptide Score: 122.46
Method: ITMS; CID; 3



precursor information

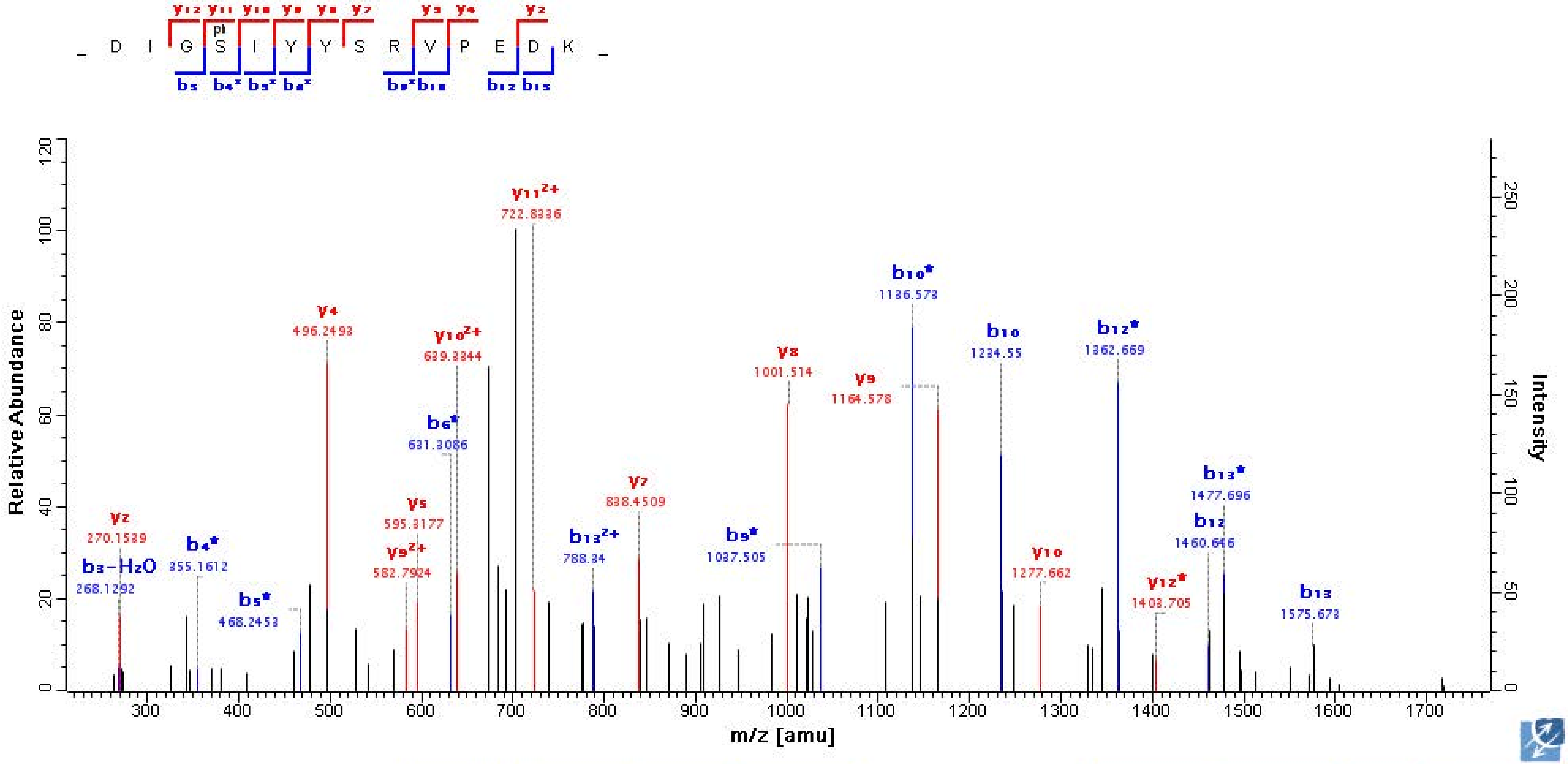
Mass:	1577.68747
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	122.4593
Mass Error [ppm]:	-0.043107
PEP:	2.7378E-06
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	39 %
Protein Localisation:	79 ... 90

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	187.08658942		187.08658942	1	W	11		
	302.11353245		302.11353245	2	D	10	1400.6296987	
	430.17210996	-0.0403961	430.17210996	3	Q	9	1285.6027557	
	544.21503741	+0.0155534	544.21503741	4	N	8	1157.5441782	
	641.26780126		641.26780126	5	P	7	1043.5012507	+0.0174261
+0.4937749	404.63671827		808.26616008	6	S	6	946.44848686	+0.1691279
	937.30875318		937.30875318	7	E	5	779.45012804	
	1050.3928172	+0.0994924	1050.3928172	8	I	4	650.40753494	-0.2741121
	1206.4939282	-0.1340649	1206.4939282	9	R	3	537.32347096	-0.0511931
	1303.546692		1303.546692	10	P	2	381.22235993	-0.0617764
	1432.5892851	-0.1896269	1432.5892851	11	E	1	284.16959608	
				12	K	0	155.12700298	

Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F03
Scannumber:	9012
Protein:	BSU26230; yqaP
Peptide Score:	128.76
Method:	ITMS; CID; 3



precursor information

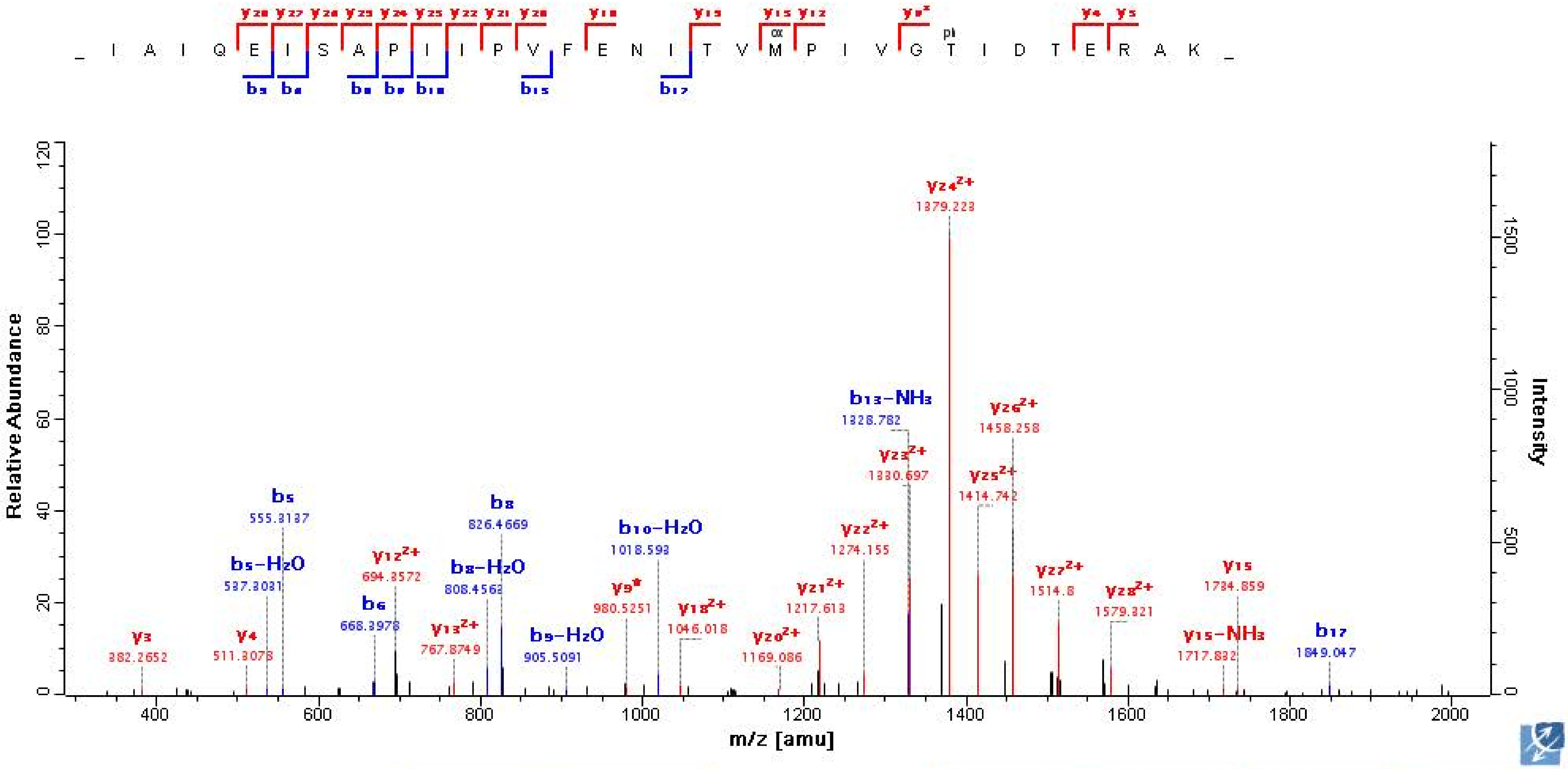
Mass:	1728.78429
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	128.7632
Mass Error [ppm]:	-0.48852
PEP:	0.0018507
Precursor Type:	ISO

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	42 %
Protein Localisation:	60 ... 73

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342		116.0342	1	D	13				
	229.1183		229.1183	2	I	12	1614.765		1614.765	
	286.1397		286.1397	3	G	11	1501.681		1501.681	
	453.1381		453.1381	4	S	10	1444.66		722.8336	+0.017773
	566.2222		566.2222	5	I	9	1277.662	-0.044878	639.3344	-0.134903
	729.2855		729.2855	6	Y	8	1164.578	-0.062499	582.7924	-0.084814
	892.3488		892.3488	7	Y	7	1001.514	-0.066858	1001.514	
	979.3809		979.3809	8	S	6	838.4509	-0.349355	838.4509	
	1135.482		1135.482	9	R	5	751.4188		751.4188	
	1234.55	+0.08292	1234.55	10	V	4	595.3177	-0.116667	595.3177	
	1331.603		1331.603	11	P	3	496.2493	+0.032985	496.2493	
	1460.646	+0.183486	1460.646	12	E	2	399.1965		399.1965	
-0.22212	788.34	+0.461963	1575.673	13	D	1	270.1539	+0.023819	270.1539	
				14	K	0	155.127		155.127	

Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F04
Scannumber:	14214
Protein:	BSU04670; rsbR; rsbRA; ycxR
Peptide Score:	66.28
Method:	ITMS; CID; 3



precursor information

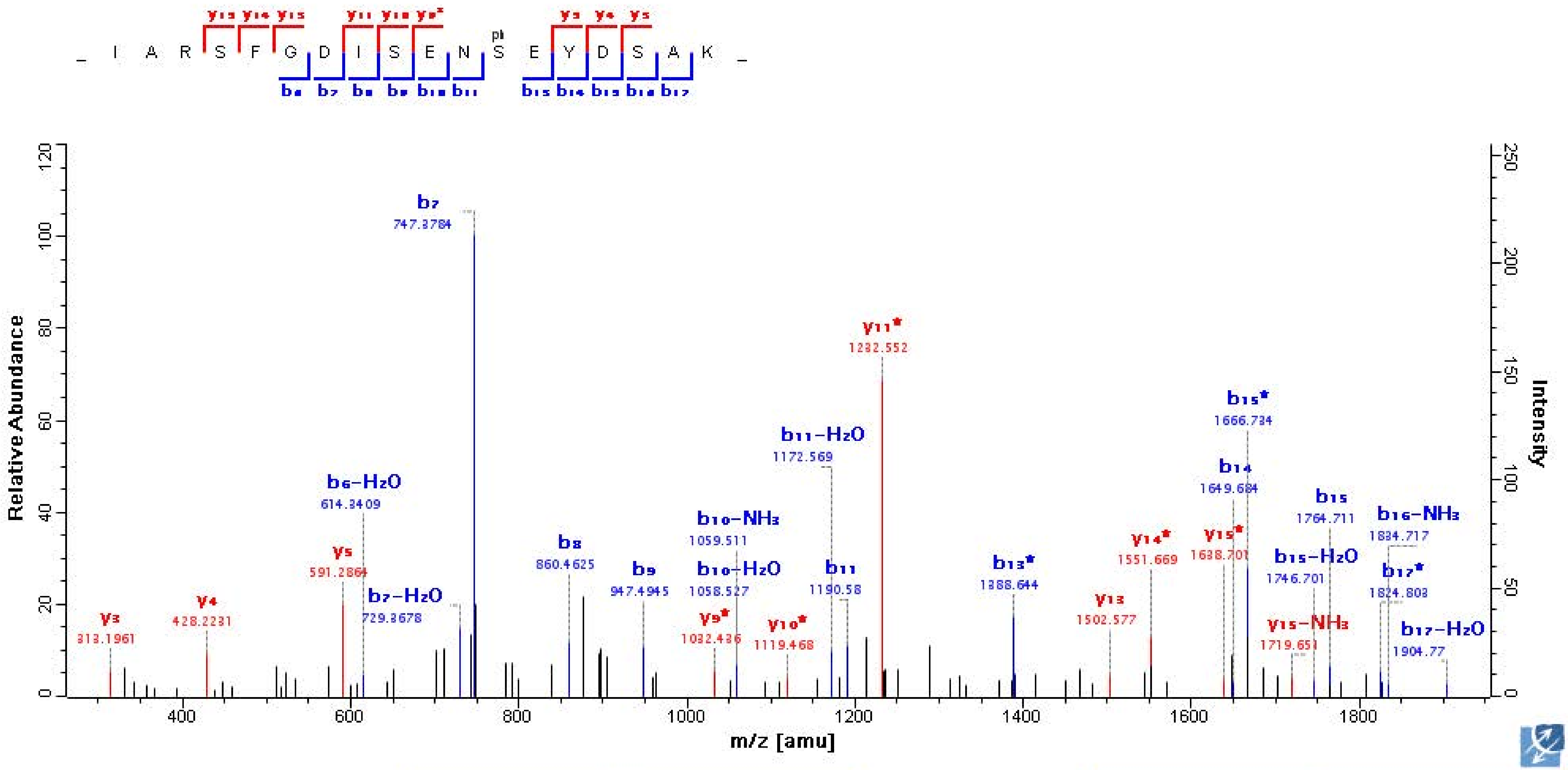
Mass:	3573.87849
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	66.2815
Mass Error [ppm]:	0.43682
PEP:	0.00023807
Precursor Type:	MULTI

general information

Annotation:	20 of 32
AminoAcids Coverag	62 %
Intensity Coverage:	47 %
Protein Localisation:	144 ... 175

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045	1	I	31				
	185.12845423	2	A	30	3469.8143349		3469.8143349	
	298.21251822	3	I	29	3398.7772211		3398.7772211	
	426.27109573	4	Q	28	3285.6931572		3285.6931572	
-0.0585008	555.31368882	5	E	27	3157.6345797		1579.3209281	-0.0762992
-0.1135731	668.3977528	6	I	26	3028.5919866		1514.7996315	-0.2089333
	755.42978121	7	S	25	2915.5079226		1458.2575995	+0.1487725
-0.0412969	826.466895	8	A	24	2828.4758942		1414.7415853	+0.2375407
	923.51965885	9	P	23	2757.4387804		1379.2230284	+0.1264589
	1036.6037228	10	I	22	2660.3860165		1330.6966465	-0.4998692
	1149.6877868	11	I	21	2547.3019525		1274.1546145	-0.3090335
	1246.7405507	12	P	20	2434.2178886		1217.6125825	+0.3138091
	1345.8089646	13	V	19	2337.1651247		1169.0862006	-0.3515814
	1492.8773785	14	F	18	2238.0967108		2238.0967108	
	1621.9199716	15	E	17	2091.0282969		1046.0177867	+0.3085073
	1735.962899	16	N	16	1961.9857038		1961.9857038	
+0.1280858	1849.046963	17	I	15	1847.9427763		1847.9427763	
	1950.0946415	18	T	14	1734.8587124	-0.1436245	1734.8587124	
	2049.1630554	19	V	13	1633.8110339		1633.8110339	
	2196.1984546	20	M	12	1534.74262		767.87494822	-0.2957246
	2293.2512185	21	P	11	1387.7072207		694.3572486	+0.1875512
	2406.3352825	22	I	10	1290.6544569		1290.6544569	
	2505.4036964	23	V	9	1177.5703929		1177.5703929	
	2562.4251601	24	G	8	1078.501979		1078.501979	
	2743.439169	25	T	7	1021.4805153		1021.4805153	
	2856.523233	26	I	6	840.46650638		840.46650638	
	2971.550176	27	D	5	727.3824424		727.3824424	
	3072.5978545	28	T	4	612.35549937		612.35549937	
	3201.6404476	29	E	3	511.3078209	+0.0892128	511.3078209	
	3357.7415586	30	R	2	382.2652278	-0.0749812	382.2652278	
	3428.7786724	31	A	1	226.16411677		226.16411677	
		32	K	0	155.12700298		155.12700298	

Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F04
Scannumber: 7050
Protein: BSU27320; greA
Peptide Score: 85.23
Method: ITMS; CID; 3



precursor information

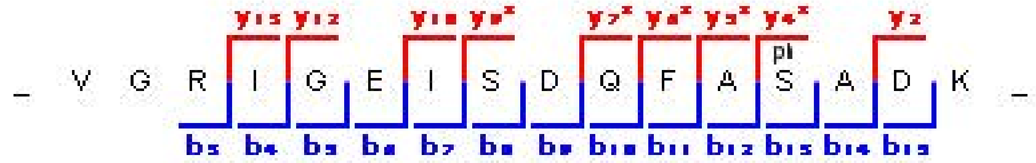
Mass:	2067.87908
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	85.23125
Mass Error [ppm]:	0.2078
PEP:	0.00083387
Precursor Type:	MULTI

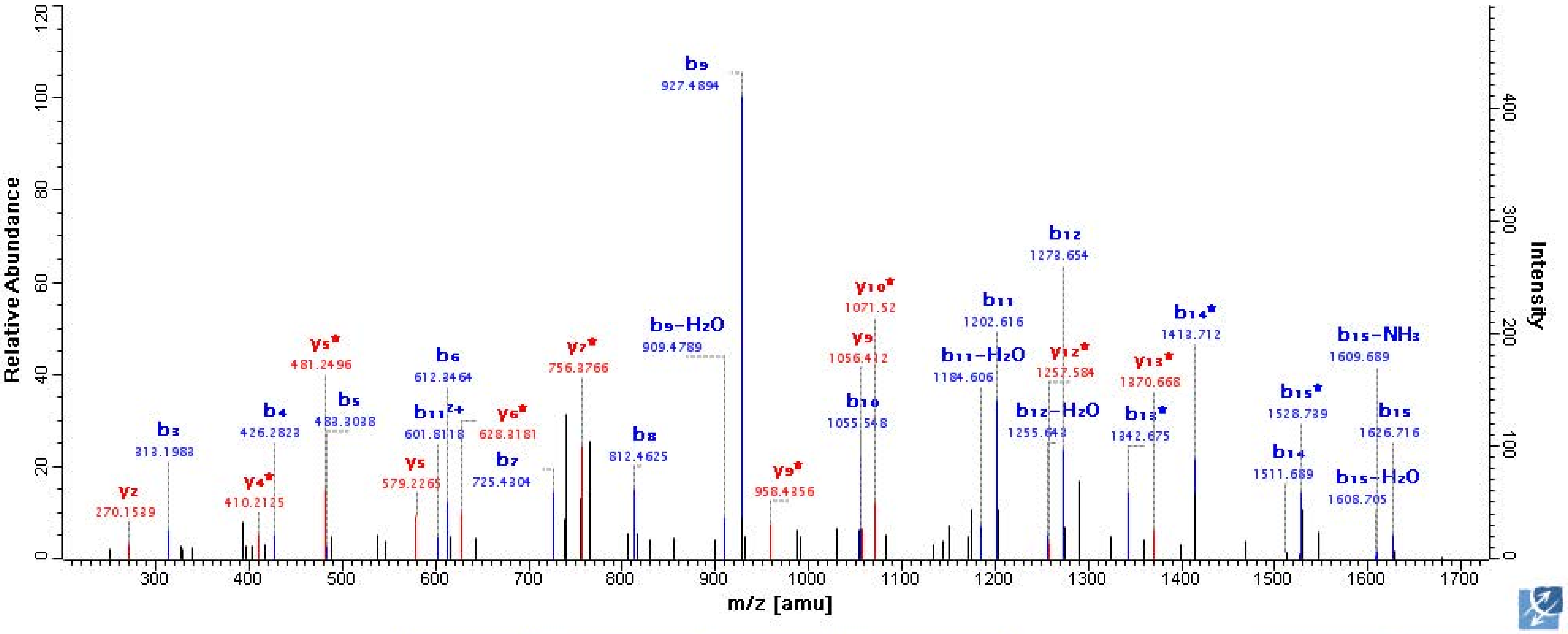
general information

Annotation:	13 of 18
AminoAcids Coverag	72 %
Intensity Coverage:	51 %
Protein Localisation:	38 ... 55

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	114.091340447	1	I	17		
	185.128454235	2	A	16	1963.816055498	
	341.229565263	3	R	15	1892.77894171	
	428.261593673	4	S	14	1736.677830682	
	575.330007589	5	F	13	1649.645802272	
	632.351471313	6	G	12	1502.577388356	+0.0355267
-0.0250208	747.378414345	7	D	11	1445.555924632	
+0.1608127	860.462478325	8	I	10	1330.5289816	
+0.1110841	947.494506735	9	S	9	1217.44491762	
	1076.537099831	10	E	8	1130.41288921	
-0.0794169	1190.580027278	11	N	7	1001.370296113	
	1357.578386097	12	S	6	887.327368666	
	1486.620979193	13	E	5	720.329009848	
-0.0107237	1649.684307731	14	Y	4	591.286416752	-0.0275056
+0.1418987	1764.711250763	15	D	3	428.223088213	-0.0825853
	1851.743279173	16	S	2	313.196145181	+0.1137303
	1922.780392961	17	A	1	226.164116772	
		18	K	0	155.127002984	

Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F04
Scannumber:	8025
Protein:	azoR2; BSU33540; yvaB
Peptide Score:	186.72
Method:	ITMS; CID; 3





precursor information

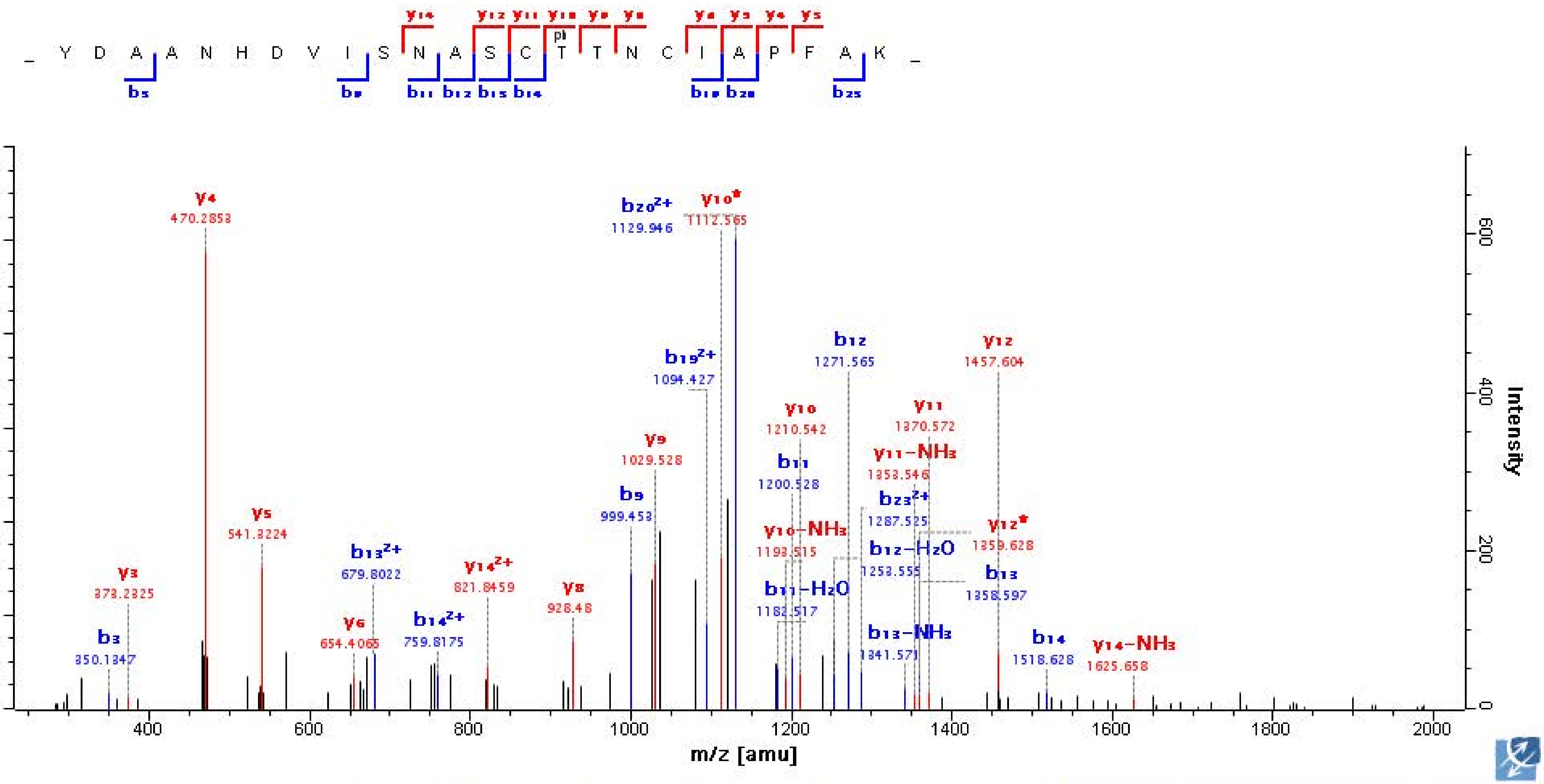
Mass:	1771.81379
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	186.7174
Mass Error [ppm]:	-0.22938
PEP:	1.9424E-35
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	58 %
Protein Localisation:	80 ... 95

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	100.07569038		100.07569038	1	V	15		
	157.09715411		157.09715411	2	G	14	1681.7672548	
	313.19826513	+0.1044998	313.19826513	3	R	13	1624.7457911	
	426.28232911	+0.1131787	426.28232911	4	I	12	1468.6446801	
	483.30379284	-0.1144007	483.30379284	5	G	11	1355.5606161	
	612.34638593	-0.263195	612.34638593	6	E	10	1298.5391524	
	725.43044992	+0.1051336	725.43044992	7	I	9	1169.4965593	
	812.46247832	+0.1755832	812.46247832	8	S	8	1056.4124953	+0.3035692
	927.48942136	+0.032063	927.48942136	9	D	7	969.38046687	
	1055.5479989	-0.1550545	1055.5479989	10	Q	6	854.35352384	
-0.3372963	601.81184463	-0.1728093	1202.6164128	11	F	5	726.29494633	
	1273.6535266	-0.0130236	1273.6535266	12	A	4	579.22653241	-0.2596135
	1440.6518854		1440.6518854	13	S	3	508.18941862	
	1511.6889992	+0.4222069	1511.6889992	14	A	2	341.1910598	
	1626.7159422	+0.1218263	1626.7159422	15	D	1	270.15394602	+0.127365
				16	K	0	155.12700298	

Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F04
Scannumber: 8766
Protein: BSU33940; gap; gapA
Peptide Score: 100.28
Method: ITMS; CID; 3



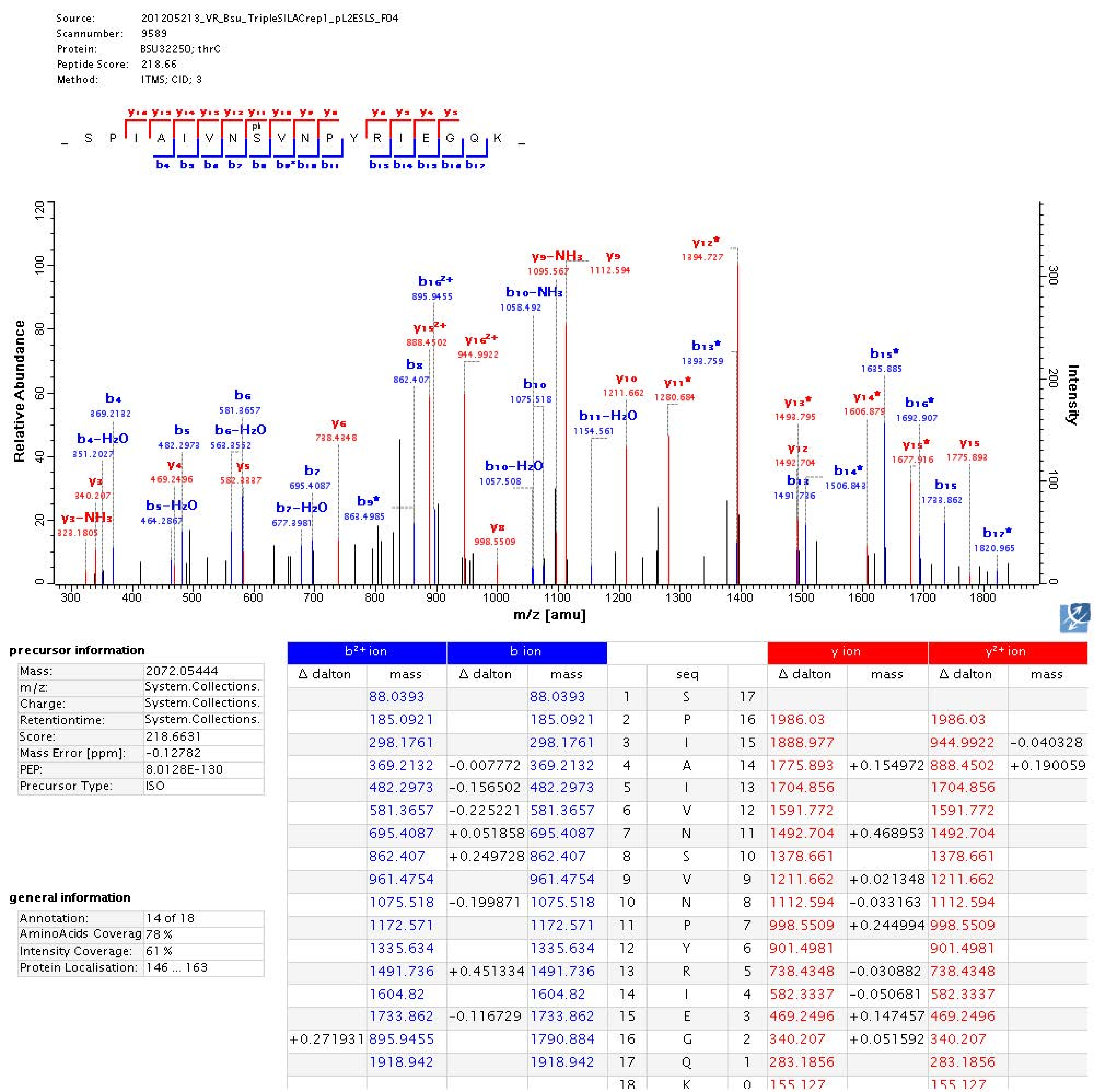
precursor information

Mass:	2727.15236
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	100.282
Mass Error [ppm]:	-0.95608
PEP:	1.9406E-07
Precursor Type:	ISO

general information

Annotation:	15 of 24
AminoAcids Coverag	62 %
Intensity Coverage:	54 %
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
	164.0706		164.0706	1	Y	23				
	279.0975		279.0975	2	D	22	2565.099		2565.099	
	350.1347	-0.046344	350.1347	3	A	21	2450.072		2450.072	
	421.1718		421.1718	4	A	20	2379.035		2379.035	
	535.2147		535.2147	5	N	19	2307.998		2307.998	
	672.2736		672.2736	6	H	18	2193.955		2193.955	
	787.3006		787.3006	7	D	17	2056.896		2056.896	
	886.369		886.369	8	V	16	1941.869		1941.869	
	999.453	-0.110323	999.453	9	I	15	1842.801		1842.801	
	1086.485		1086.485	10	S	14	1729.716		1729.716	
	1200.528	-0.026405	1200.528	11	N	13	1642.684		821.8459	+0.018149
	1271.565	+0.040485	1271.565	12	A	12	1528.642		1528.642	
+0.279094	679.8022	+0.075351	1358.597	13	S	11	1457.604	-0.083904	1457.604	
+0.085852	759.8175	-0.168676	1518.628	14	C	10	1370.572	+0.164067	1370.572	
	1699.642		1699.642	15	T	9	1210.542	-0.054675	1210.542	
	1800.689		1800.689	16	T	8	1029.528	-0.010026	1029.528	
	1914.732		1914.732	17	N	7	928.48	-0.095526	928.48	
	2074.763		2074.763	18	C	6	814.4371		814.4371	
+0.241508	1094.427		2187.847	19	I	5	654.4065	+0.082175	654.4065	
+0.290334	1129.946		2258.884	20	A	4	541.3224	-0.026266	541.3224	
	2355.937		2355.937	21	P	3	470.2853	+0.091048	470.2853	
	2503.005		2503.005	22	F	2	373.2325	-0.005053	373.2325	
-0.1466	1287.525		2574.043	23	A	1	226.1641		226.1641	
				24	K	0	155.127		155.127	



Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F04
Scannumber:	9589
Protein:	BSU32250; thrC
Peptide Score:	218.66
Method:	ITMS; CID; 3

precursor information

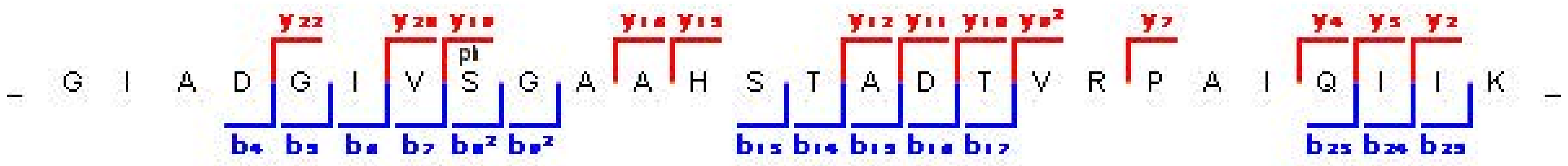
Mass:	2072.05444
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	218.6631
Mass Error [ppm]:	-0.12782
PEP:	8.0128E-130
Precursor Type:	ISO

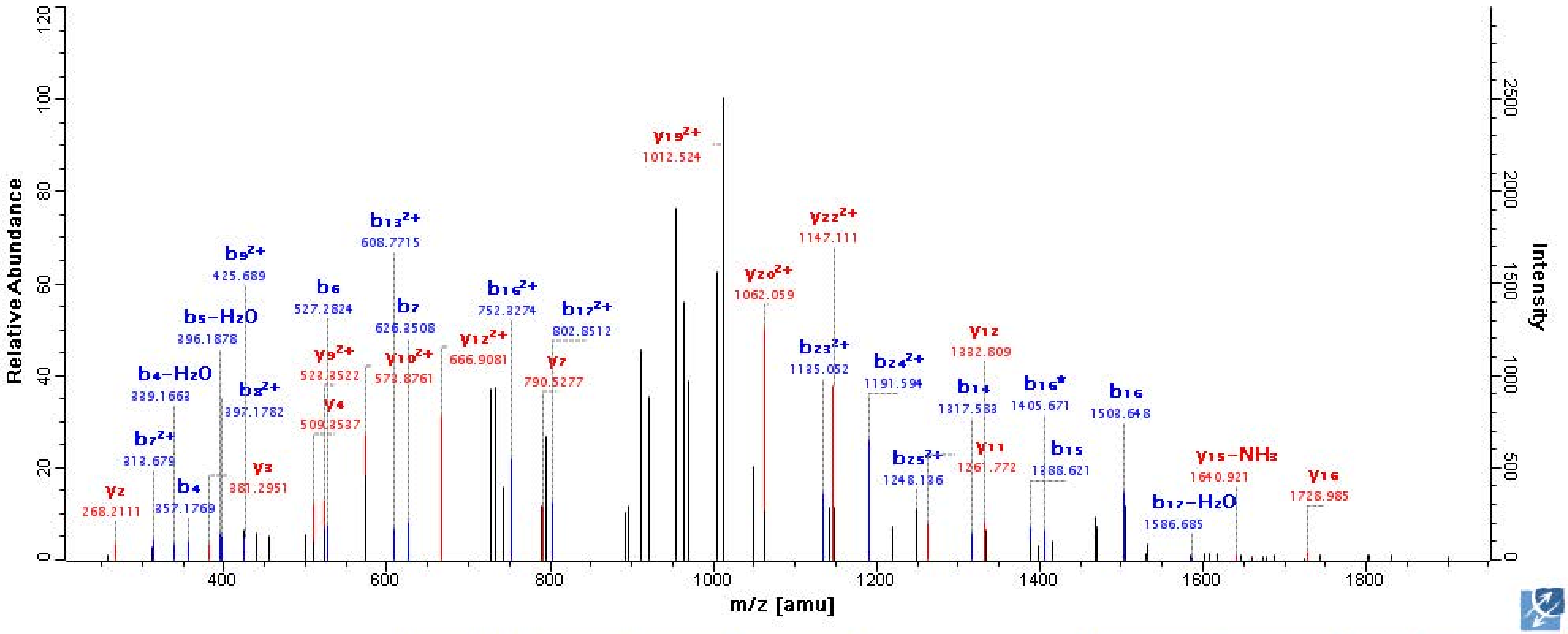
general information

Annotation:	14 of 18
AminoAcids Coverag	78 %
Intensity Coverage:	61 %
Protein Localisation:	146 ... 163

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393		88.0393	1	S	17				
	185.0921		185.0921	2	P	16	1986.03		1986.03	
	298.1761		298.1761	3	I	15	1888.977		944.9922	-0.040328
	369.2132	-0.007772	369.2132	4	A	14	1775.893	+0.154972	888.4502	+0.190059
	482.2973	-0.156502	482.2973	5	I	13	1704.856		1704.856	
	581.3657	-0.225221	581.3657	6	V	12	1591.772		1591.772	
	695.4087	+0.051858	695.4087	7	N	11	1492.704	+0.468953	1492.704	
	862.407	+0.249728	862.407	8	S	10	1378.661		1378.661	
	961.4754		961.4754	9	V	9	1211.662	+0.021348	1211.662	
	1075.518	-0.199871	1075.518	10	N	8	1112.594	-0.033163	1112.594	
	1172.571		1172.571	11	P	7	998.5509	+0.244994	998.5509	
	1335.634		1335.634	12	Y	6	901.4981		901.4981	
	1491.736	+0.451334	1491.736	13	R	5	738.4348	-0.030882	738.4348	
	1604.82		1604.82	14	I	4	582.3337	-0.050681	582.3337	
	1733.862	-0.116729	1733.862	15	E	3	469.2496	+0.147457	469.2496	
+0.271931	895.9455		1790.884	16	G	2	340.207	+0.051592	340.207	
	1918.942		1918.942	17	Q	1	283.1856		283.1856	
				18	K	0	155.127		155.127	

Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F05
Scannumber: 10921
Protein: BSU37660; ipa-88d; pta; ywfJ
Peptide Score: 119.62
Method: ITMS; CID; 3





precursor information

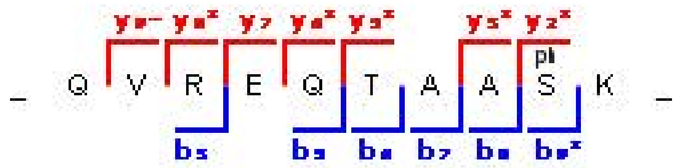
Mass:	2640.36321
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	119.6186
Mass Error [ppm]:	-0.15986
PEP:	1.0247E-11
Precursor Type:	MULTI

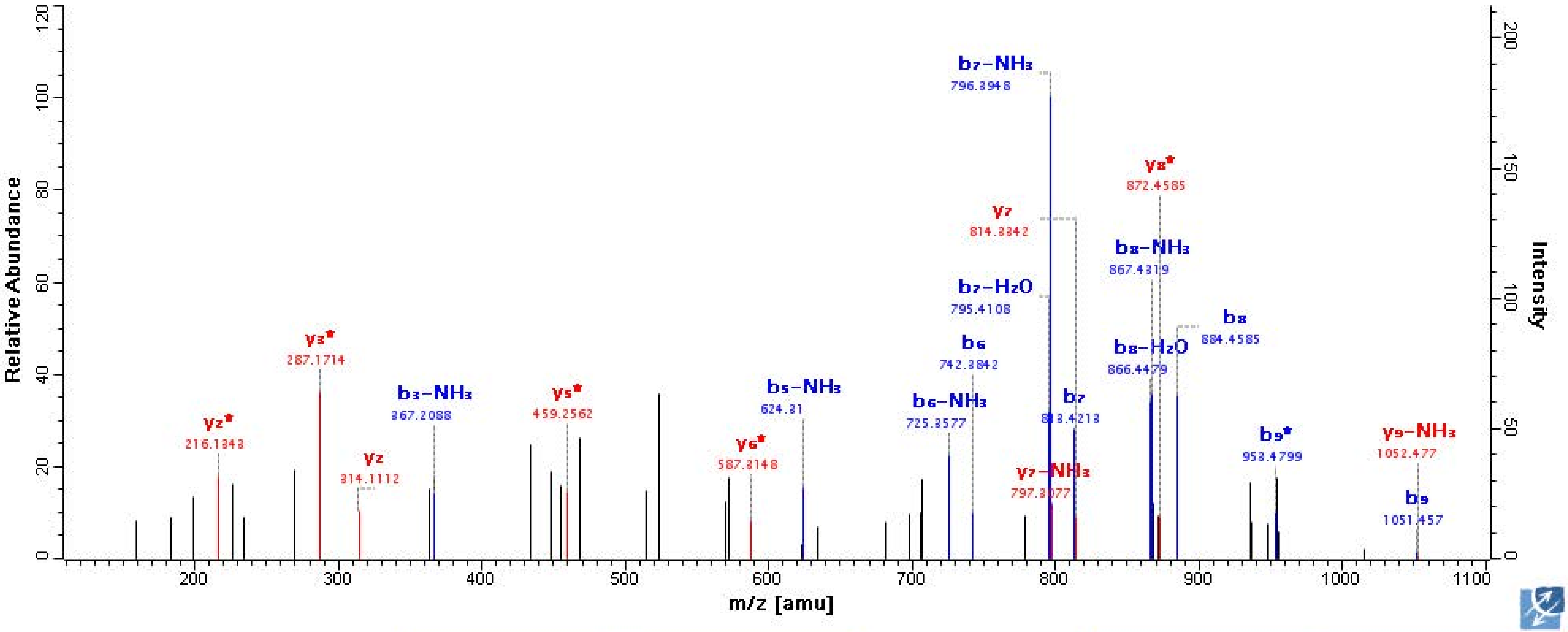
general information

Annotation:	18 of 26
AminoAcids Coverag	69 %
Intensity Coverage:	34 %
Protein Localisation:	116 ... 141

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874		58.02874	1	G	25				
	171.1128		171.1128	2	I	24	2592.364		2592.364	
	242.1499		242.1499	3	A	23	2479.28		2479.28	
	357.1769	-0.014477	357.1769	4	D	22	2408.242		2408.242	
	414.1983		414.1983	5	G	21	2293.216		1147.111	-0.128488
	527.2824	-0.040628	527.2824	6	I	20	2236.194		2236.194	
-0.275536	313.679	+0.084805	626.3508	7	V	19	2123.11		1062.059	+0.248494
+0.097843	397.1782		793.3492	8	S	18	2024.042		1012.524	+0.034166
-0.441636	425.689		850.3706	9	G	17	1857.043		1857.043	
	921.4077		921.4077	10	A	16	1800.022		1800.022	
	992.4449		992.4449	11	A	15	1728.985	-0.034325	1728.985	
	1129.504		1129.504	12	H	14	1657.948		1657.948	
-0.303822	608.7715		1216.536	13	S	13	1520.889		1520.889	
	1317.583	-0.146216	1317.583	14	T	12	1433.857		1433.857	
	1388.621	+0.008199	1388.621	15	A	11	1332.809	+0.087208	666.9081	-0.005811
-0.056589	752.3274	+0.146295	1503.648	16	D	10	1261.772	-0.148994	1261.772	
+0.428605	802.8512		1604.695	17	T	9	1146.745		573.8761	-0.090115
	1703.764		1703.764	18	V	8	1045.697		523.3522	+0.001351
	1859.865		1859.865	19	R	7	946.6288		946.6288	
	1956.917		1956.917	20	P	6	790.5277	+0.050902	790.5277	
	2027.955		2027.955	21	A	5	693.4749		693.4749	
	2141.039		2141.039	22	I	4	622.4378		622.4378	
+0.094221	1135.052		2269.097	23	Q	3	509.3537	-0.137156	509.3537	
+0.010685	1191.594		2382.181	24	I	2	381.2951	-0.039485	381.2951	
-0.10996	1248.136		2495.265	25	I	1	268.2111	+0.067253	268.2111	
				26	K	0	155.127		155.127	

Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F05
Scannumber:	1752
Protein:	BSU02920; yceF
Peptide Score:	104.43
Method:	ITMS; CID; 3





precursor information

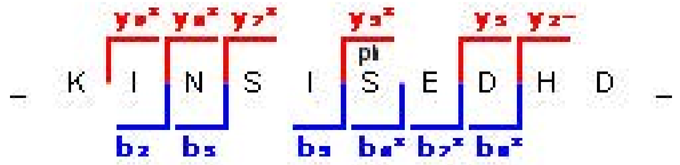
Mass:	1196.55519
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	104.434
Mass Error [ppm]:	0.10416
PEP:	0.0022241
Precursor Type:	MULTI

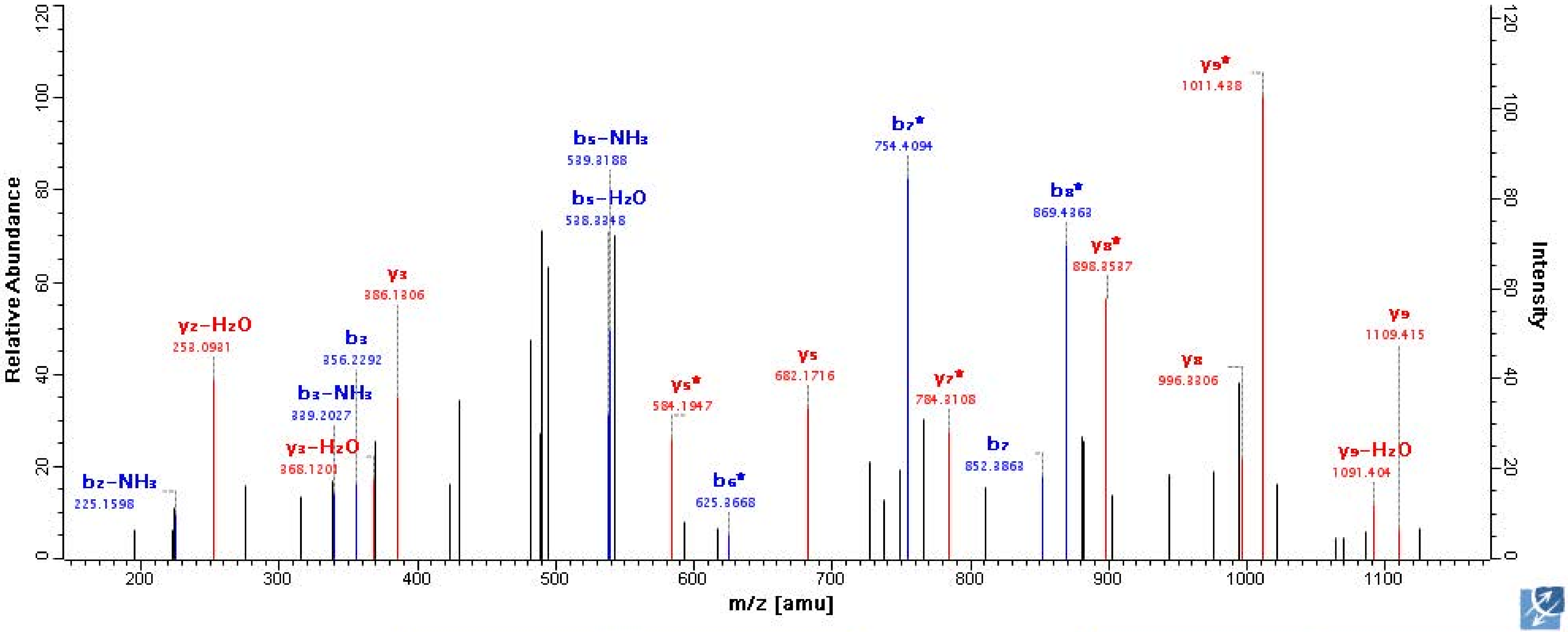
general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	51 %
Protein Localisation:	246 ... 255

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	129.065853978	1	Q	9		
	228.134267894	2	V	8	1069.50376459	
	384.235378922	3	R	7	970.435350674	
	513.277972018	4	E	6	814.334239646	+0.2722667
	641.33654953	5	Q	5	685.29164655	
+0.1495244	742.384228004	6	T	4	557.233069039	
+0.1169273	813.421341792	7	A	3	456.185390564	
+0.0591836	884.45845558	8	A	2	385.148276777	
+0.3084444	1051.456814398	9	S	1	314.111162989	+0.1680729
		10	K	0	147.112804171	

Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F05
Scannumber:	4620
Protein:	BSU23740; yqjU
Peptide Score:	90.83
Method:	ITMS; CID; 3





precursor information

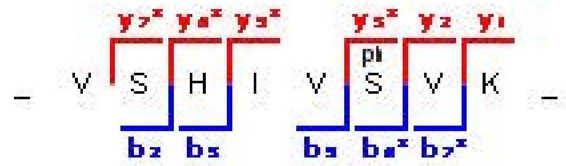
Mass:	1236.50206
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	90.82698
Mass Error [ppm]:	-0.24057
PEP:	0.0057064
Precursor Type:	MULTI

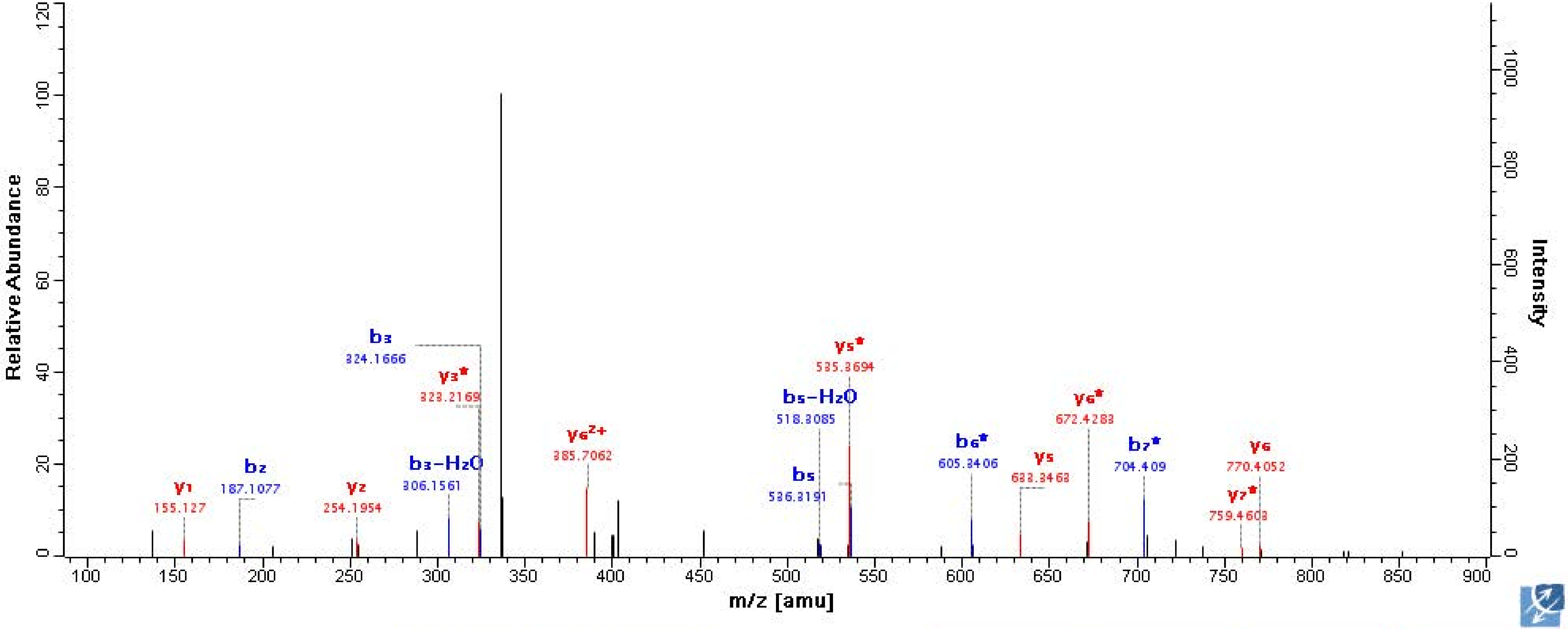
general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	47 %
Protein Localisation:	43 ... 52

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	129.102239484	1	K	9		
	242.186303465	2	I	8	1109.414674812	-0.1195088
+0.1084766	356.229230912	3	N	7	996.330610831	+0.0090498
	443.261259322	4	S	6	882.287683384	
	556.345323302	5	I	5	795.255654974	
	723.34368212	6	S	4	682.171590994	+0.00889
+0.0084391	852.386275217	7	E	3	515.173232175	
	967.413218249	8	D	2	386.130639079	-0.1172113
	1104.472130111	9	H	1	271.103696047	
		10	D	0	134.044784185	

Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F05
Scannumber:	5603
Protein:	BSU01340; rpmD
Peptide Score:	124.98
Method:	ITMS; CID; 3



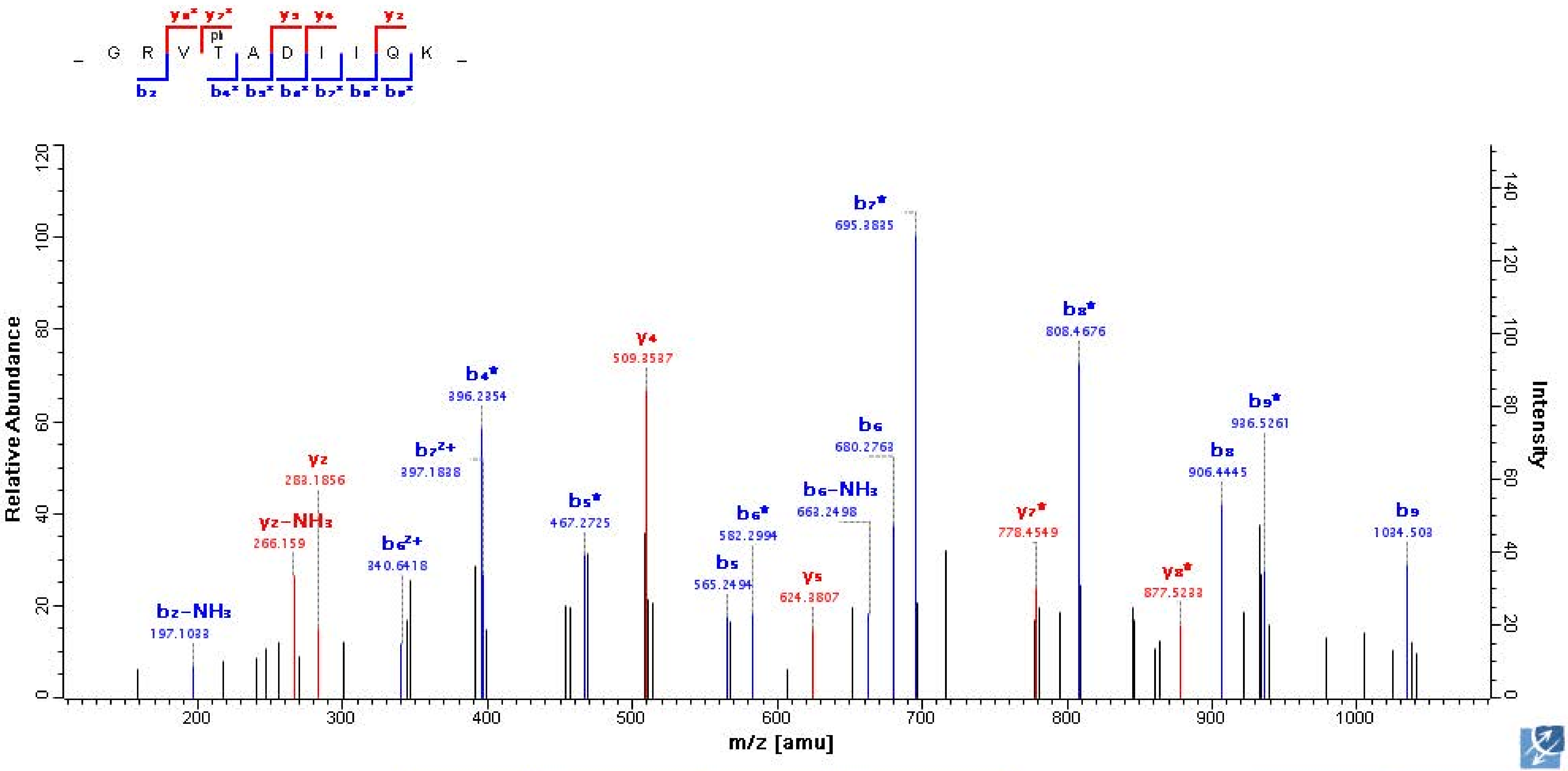


precursor information

Mass:	947.4841
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	124.9833
Mass Error [ppm]:	-0.029755
PEP:	0.0053818
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	38 %
Protein Localisation:	50 ... 57

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.07569038	1	V	7				
+0.0826499	187.10771879	2	S	6	857.43719389		857.43719389	
+0.0211745	324.16663066	3	H	5	770.40516548	-0.0764912	385.70622097	-0.2235855
	437.25069464	4	I	4	633.34625361	+0.1226185	633.34625361	
-0.0068527	536.31910855	5	V	3	520.26218963		520.26218963	
	703.31746737	6	S	2	421.19377572		421.19377572	
	802.38588129	7	V	1	254.1954169	+0.0843988	254.1954169	
		8	K	0	155.12700298	+0.1605642	155.12700298	

Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F05
Scannumber: 6351
Protein: BSU19370; citK; odhA
Peptide Score: 116.55
Method: ITMS; CID; 3



precursor information

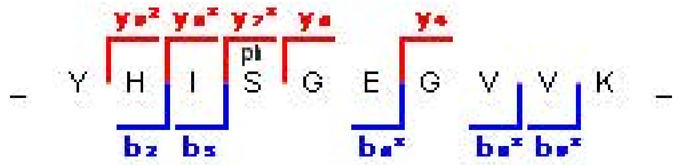
Mass:	1187.61562
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	116.5463
Mass Error [ppm]:	0.11227
PEP:	0.0011851
Precursor Type:	ISO

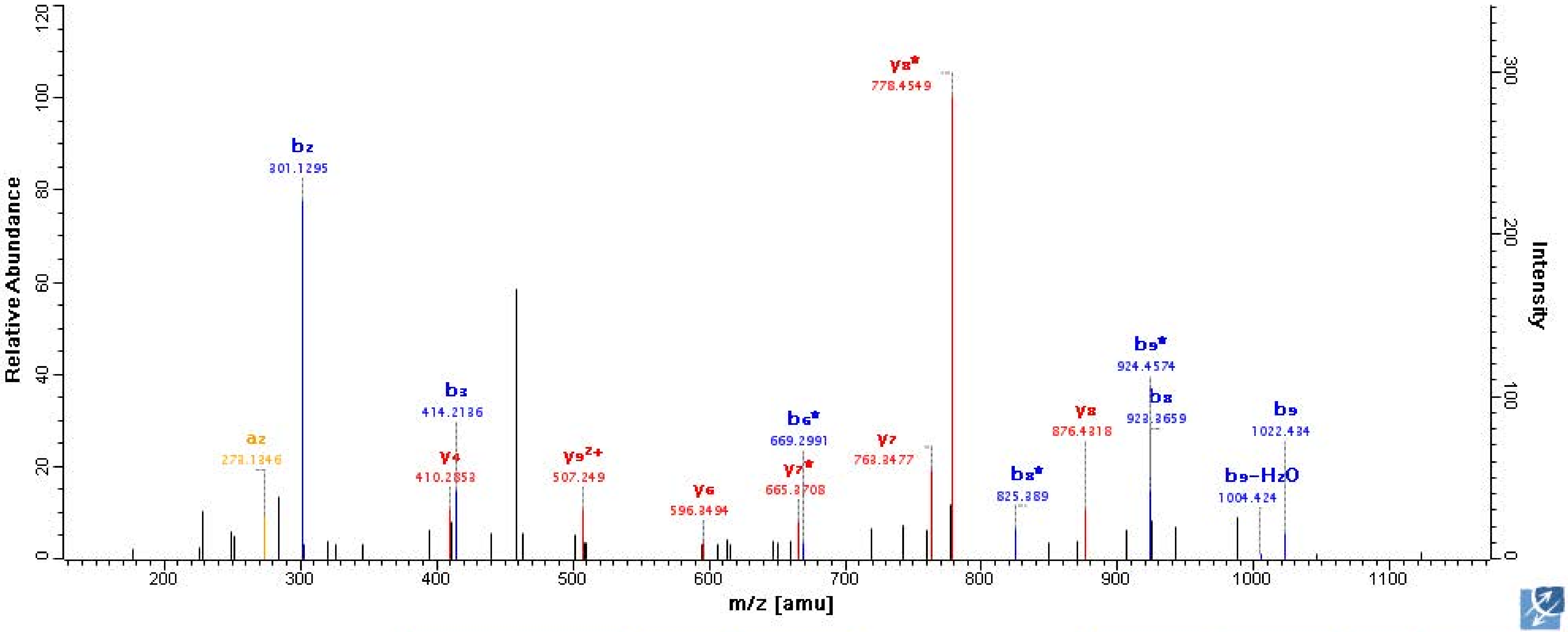
general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	48 %
Protein Localisation:	65 ... 74

b2+ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	58.02874019		58.02874019	1	G	9		
	214.12985122		214.12985122	2	R	8	1131.6012991	
	313.19826513		313.19826513	3	V	7	975.50018807	
	494.21227402		494.21227402	4	T	6	876.43177416	
	565.2493878	+0.2215595	565.2493878	5	A	5	695.41776528	
-0.3755683	340.64180365	+0.122778	680.27633084	6	D	4	624.38065149	+0.2135258
+0.0435814	397.18383564		793.36039482	7	I	3	509.35370846	+0.074209
	906.4444588	+0.0283806	906.4444588	8	I	2	396.26964448	
	1034.5030363	-0.0827482	1034.5030363	9	Q	1	283.1855805	+0.0900543
				10	K	0	155.12700298	

Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F05
Scannumber:	6621
Protein:	BSU33900; eno
Peptide Score:	105.98
Method:	ITMS; CID; 3





precursor information

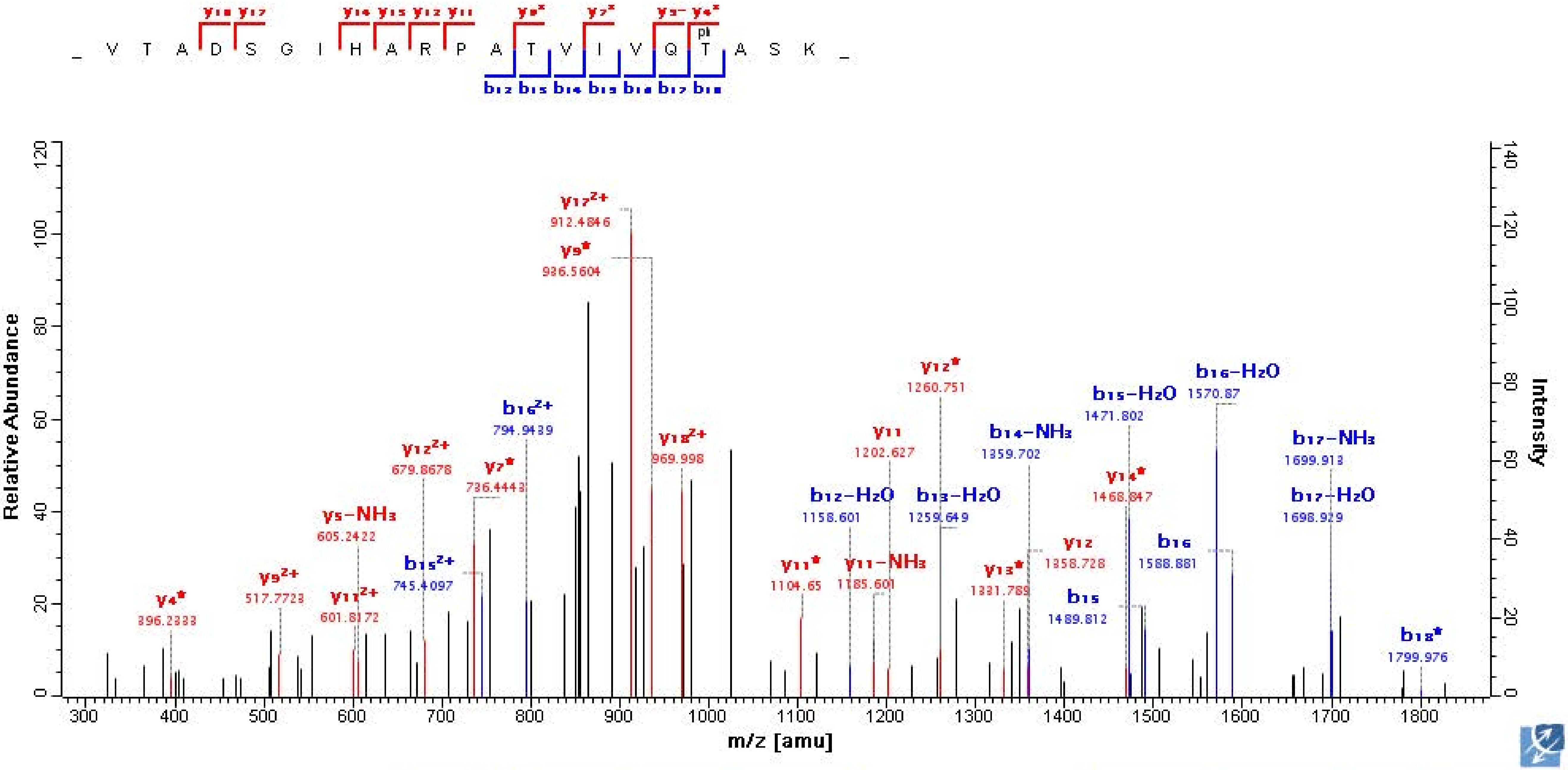
Mass:	1175.54677
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	105.975
Mass Error [ppm]:	0.026832
PEP:	0.0013694
Precursor Type:	ISO

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	56 %
Protein Localisation:	256 ... 265

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.0757		164.0706	1	Y	9				
+0.13853	273.1346	+0.005859	301.1295	2	H	8	1013.491		507.249	+0.042462
	386.2187	-0.01186	414.2136	3	I	7	876.4318	-0.084423	876.4318	
	553.217		581.2119	4	S	6	763.3477	-0.079583	763.3477	
	610.2385		638.2334	5	G	5	596.3494	-0.177659	596.3494	
	739.2811		767.276	6	E	4	539.3279		539.3279	
	796.3025		824.2975	7	G	3	410.2853	-0.15352	410.2853	
	895.371	+0.214936	923.3659	8	V	2	353.2638		353.2638	
	994.4394	-0.075645	1022.434	9	V	1	254.1954		254.1954	
				10	K	0	155.127		155.127	

Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F05
Scannumber:	7588
Protein:	BSU13900; ptsH
Peptide Score:	80.14
Method:	ITMS; CID; 3



precursor information

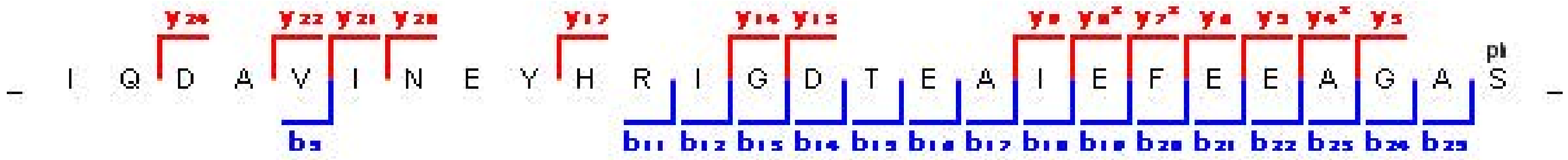
Mass:	2201.12036
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	80.14178
Mass Error [ppm]:	-0.083793
PEP:	8.4341E-05
Precursor Type:	MULTI

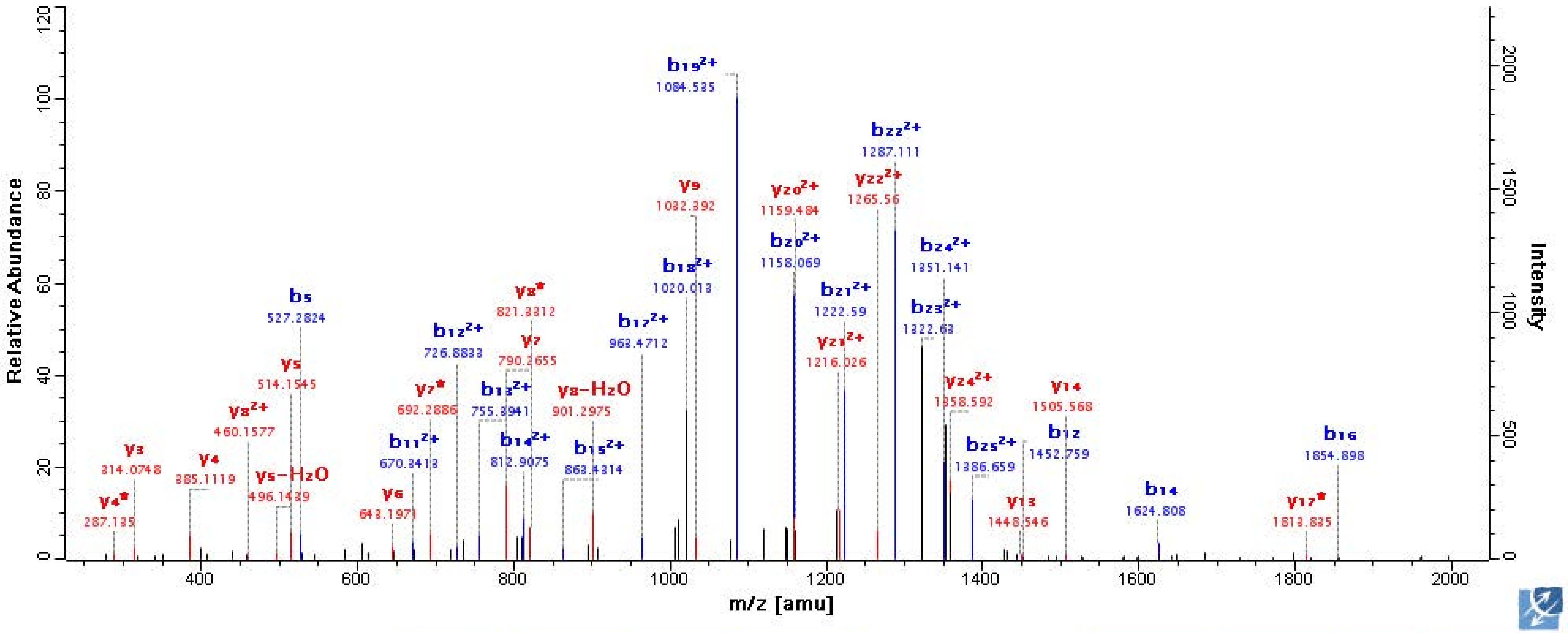
general information

Annotation:	13 of 21
AminoAcids Coverag	62 %
Intensity Coverage:	37 %
Protein Localisation:	8 ... 28

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757		100.0757	1	V	20				
	201.1234		201.1234	2	T	19	2111.074		2111.074	
	272.1605		272.1605	3	A	18	2010.026		2010.026	
	387.1874		387.1874	4	D	17	1938.989		969.998	+0.395143
	474.2195		474.2195	5	S	16	1823.962		912.4846	+0.055587
	531.2409		531.2409	6	G	15	1736.93		1736.93	
	644.325		644.325	7	I	14	1679.908		1679.908	
	781.3839		781.3839	8	H	13	1566.824		1566.824	
	852.421		852.421	9	A	12	1429.765		1429.765	
	1008.522		1008.522	10	R	11	1358.728	-0.203876	679.8678	+0.232802
	1105.575		1105.575	11	P	10	1202.627	-0.253766	601.8172	-0.456022
	1176.612		1176.612	12	A	9	1105.574		1105.574	
	1277.66		1277.66	13	T	8	1034.537		517.7723	-0.244457
	1376.728		1376.728	14	V	7	933.4896		933.4896	
+0.086074	745.4097	-0.008564	1489.812	15	I	6	834.4212		834.4212	
-0.168165	794.9439	+0.242969	1588.881	16	V	5	721.3371		721.3371	
	1716.939		1716.939	17	Q	4	622.2687		622.2687	
	1897.953		1897.953	18	T	3	494.2102		494.2102	
	1968.99		1968.99	19	A	2	313.1961		313.1961	
	2056.022		2056.022	20	S	1	242.159		242.159	
				21	K	0	155.127		155.127	

Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F06
Scannumber:	10819
Protein:	BSU00490; spoVG
Peptide Score:	156.92
Method:	ITMS; CID; 3





precursor information

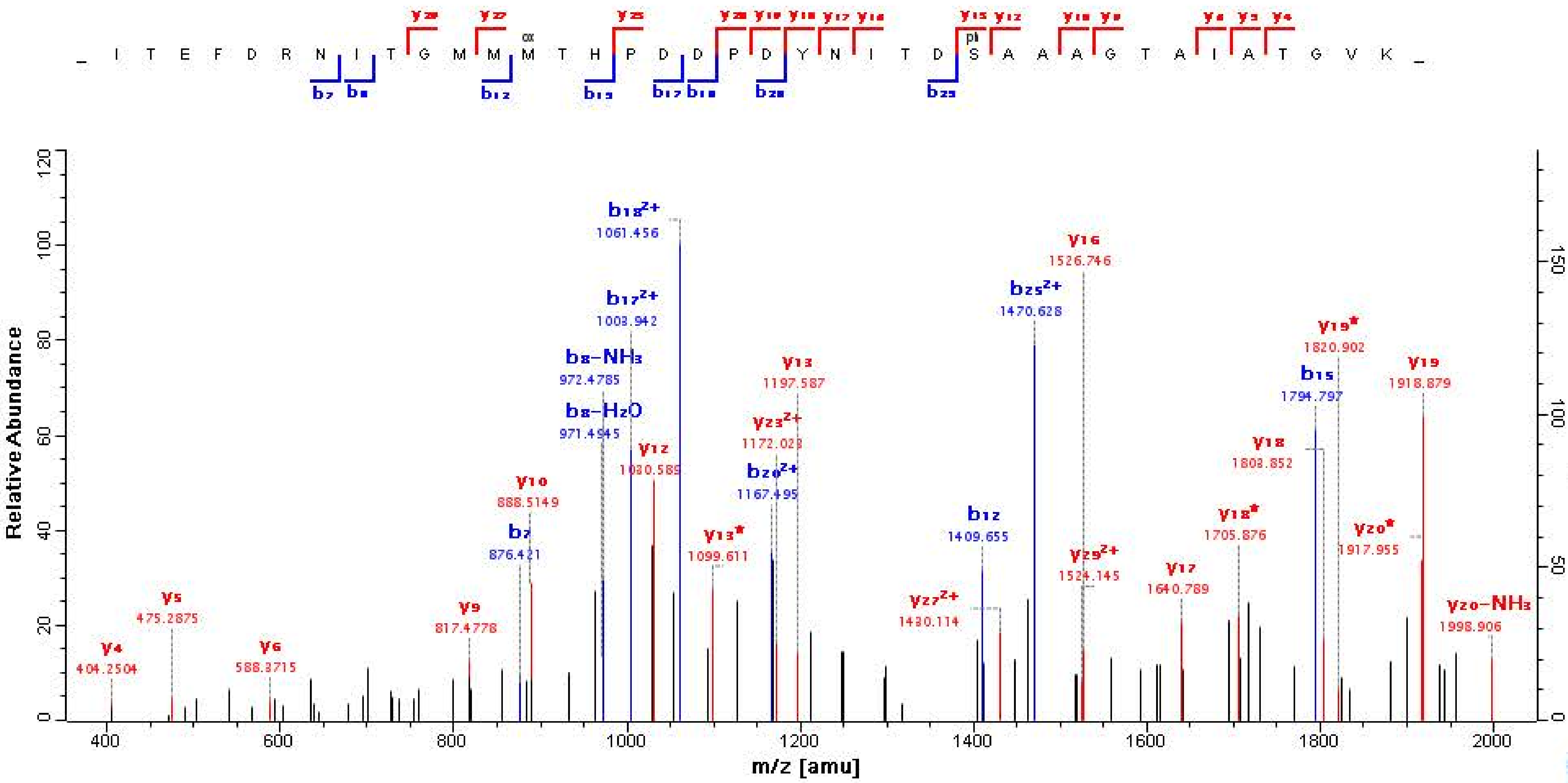
Mass:	2956.31426
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	156.9196
Mass Error [ppm]:	0.5019
PEP:	5.2043E-40
Precursor Type:	ISO

general information

Annotation:	20 of 26
AminoAcids Coverag	77 %
Intensity Coverage:	68 %
Protein Localisation:	72 ... 97

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913		114.0913	1	I	25				
	242.1499		242.1499	2	Q	24	2844.236		2844.236	
	357.1769		357.1769	3	D	23	2716.177		1358.592	-0.101865
	428.214		428.214	4	A	22	2601.15		2601.15	
	527.2824	-0.120646	527.2824	5	V	21	2530.113		1265.56	+0.429797
	640.3665		640.3665	6	I	20	2431.045		1216.026	+0.275039
	754.4094		754.4094	7	N	19	2317.961		1159.484	-0.2956
	883.452		883.452	8	E	18	2203.918		2203.918	
	1046.515		1046.515	9	Y	17	2074.875		2074.875	
	1183.574		1183.574	10	H	16	1911.812		1911.812	
+0.040535	670.3413		1339.675	11	R	15	1774.753		1774.753	
+0.11978	726.8833	-0.223378	1452.759	12	I	14	1618.652		1618.652	
+0.02659	755.3941		1509.781	13	G	13	1505.568	+0.258353	1505.568	
+0.237728	812.9075	+0.364812	1624.808	14	D	12	1448.546	+0.47574	1448.546	
-0.056497	863.4314		1725.855	15	T	11	1333.52		1333.52	
	1854.898	-0.232784	1854.898	16	E	10	1232.472		1232.472	
+0.284142	963.4712		1925.935	17	A	9	1103.429		1103.429	
-0.106522	1020.013		2039.019	18	I	8	1032.392	+0.081606	1032.392	
+0.30492	1084.535		2168.062	19	E	7	919.3081		460.1577	+0.278233
+0.199669	1158.069		2315.13	20	F	6	790.2655	-0.106922	790.2655	
+0.278714	1222.59		2444.173	21	E	5	643.1971	+0.028753	643.1971	
+0.313081	1287.111		2573.215	22	E	4	514.1545	+0.05389	514.1545	
-0.089509	1322.63		2644.253	23	A	3	385.1119	-0.023085	385.1119	
-0.018942	1351.141		2701.274	24	G	2	314.0748	-0.03895	314.0748	
+0.482765	1386.659		2772.311	25	A	1	257.0533		257.0533	
				26	S	0	186.0162		186.0162	

Source:	20120521 3_VR_Bsu_TripleSILACrep1_pL2ESLS_F06
Scannumber:	10836
Protein:	BSU09410; phoA; phoAIV
Peptide Score:	63.75
Method:	ITMS; CID; 3



precursor information

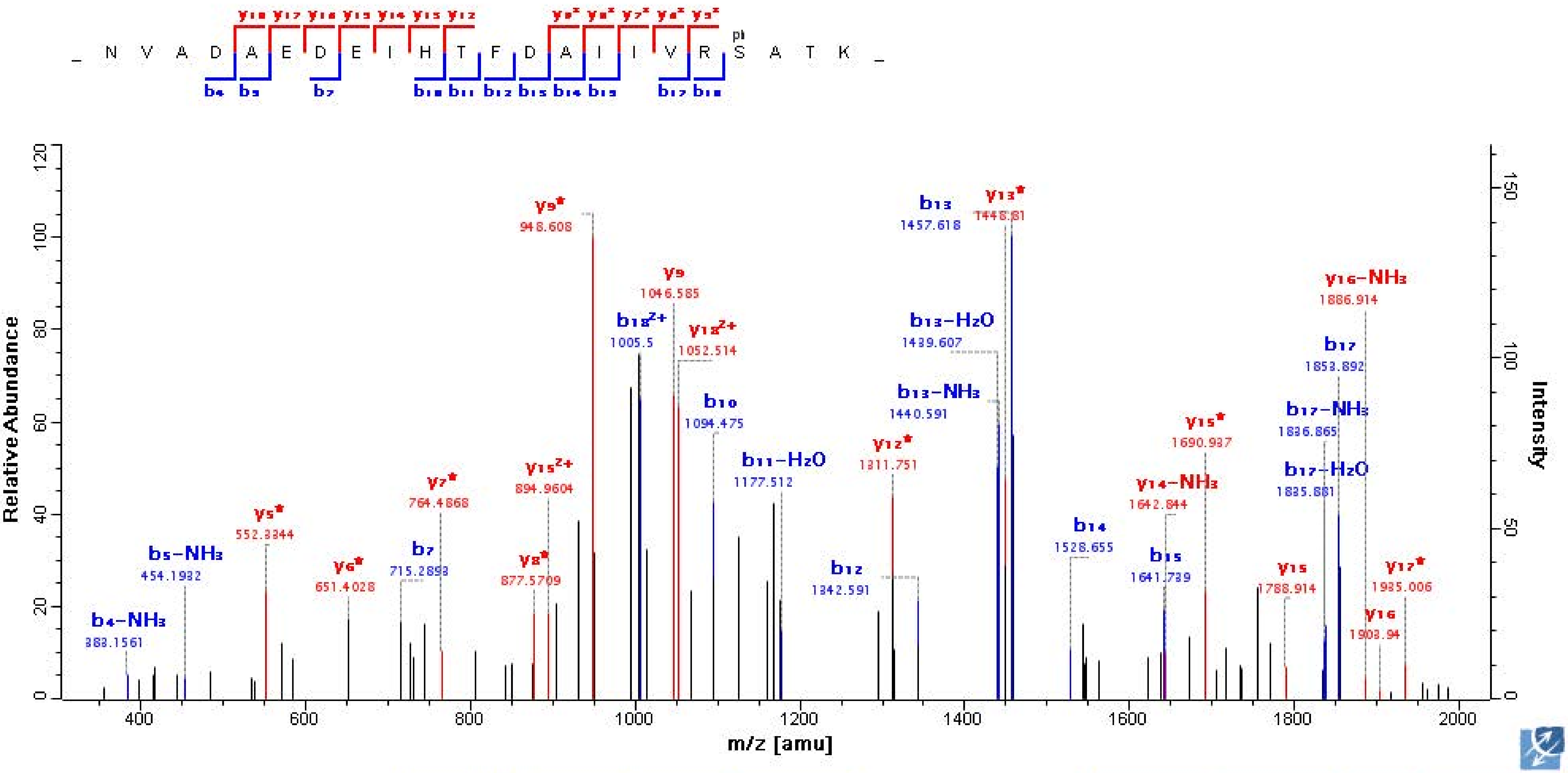
Mass:	4135.82044
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	63.75121
Mass Error [ppm]:	-0.2339
PEP:	4.3939E-08
Precursor Type:	ISO

general information

Annotation:	23 of 38
AminoAcids Coverag	61 %
Intensity Coverage:	53 %
Protein Localisation:	83 ... 120

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913		114.0913	1	I	37				
	215.139		215.139	2	T	36	4023.745		4023.745	
	344.1816		344.1816	3	E	35	3922.697		3922.697	
	491.25		491.25	4	F	34	3793.654		3793.654	
	606.277		606.277	5	D	33	3646.586		3646.586	
	762.3781		762.3781	6	R	32	3531.559		3531.559	
	876.421	-0.161364	876.421	7	N	31	3375.458		3375.458	
	989.5051		989.5051	8	I	30	3261.415		3261.415	
	1090.553		1090.553	9	T	29	3148.331		3148.331	
	1147.574		1147.574	10	G	28	3047.283		1524.145	+0.046038
	1278.615		1278.615	11	M	27	2990.262		2990.262	
	1409.655	-0.038362	1409.655	12	M	26	2859.221		1430.114	+0.288438
	1556.691		1556.691	13	M	25	2728.181		2728.181	
	1657.738		1657.738	14	T	24	2581.145		2581.145	
	1794.797	+0.227486	1794.797	15	H	23	2480.098		2480.098	
	1891.85		1891.85	16	P	22	2343.039		1172.023	+0.41471
+0.046936	1003.942		2006.877	17	D	21	2245.986		2245.986	
-0.041365	1061.456		2121.904	18	D	20	2130.959		2130.959	
	2218.957		2218.957	19	P	19	2015.932		2015.932	
+0.008992	1167.495		2333.984	20	D	18	1918.879	+0.137955	1918.879	
	2497.047		2497.047	21	Y	17	1803.852	+0.314312	1803.852	
	2611.09		2611.09	22	N	16	1640.789	-0.497969	1640.789	
	2724.174		2724.174	23	I	15	1526.746	+0.133825	1526.746	
	2825.222		2825.222	24	T	14	1413.662		1413.662	
+0.348811	1470.628		2940.248	25	D	13	1312.614		1312.614	
	3107.247		3107.247	26	S	12	1197.587	-0.01828	1197.587	
	3178.284		3178.284	27	A	11	1030.589	-0.238549	1030.589	
	3249.321		3249.321	28	A	10	959.552		959.552	
	3320.358		3320.358	29	A	9	888.5149	+0.207138	888.5149	
	3377.38		3377.38	30	G	8	817.4778	+0.046315	817.4778	
	3478.427		3478.427	31	T	7	760.4563		760.4563	
	3549.464		3549.464	32	A	6	659.4087		659.4087	
	3662.548		3662.548	33	I	5	588.3715	-0.063738	588.3715	
	3733.586		3733.586	34	A	4	475.2875	+0.006807	475.2875	
	3834.633		3834.633	35	T	3	404.2504	-0.066828	404.2504	
	3891.655		3891.655	36	G	2	303.2027		303.2027	
	3990.723		3990.723	37	V	1	246.1812		246.1812	
				38	K	0	147.1128		147.1128	

Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F06
Scannumber: 11813
Protein: BSU23070; serA
Peptide Score: 111.38
Method: ITMS; CID; 3



precursor information

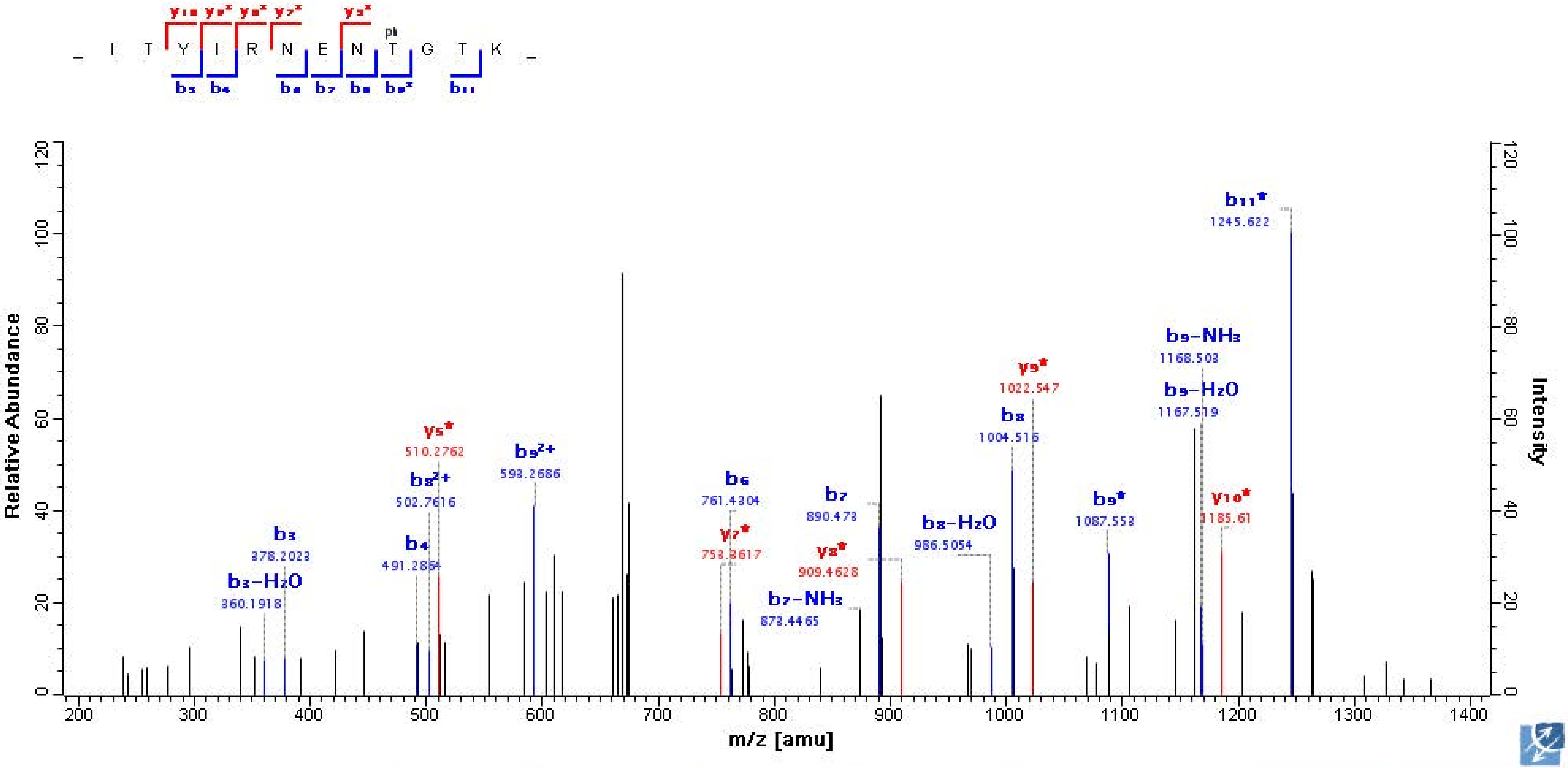
Mass:	2502.18899
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	111.3772
Mass Error [ppm]:	0.27791
PEP:	8.8654E-05
Precursor Type:	ISO

general information

Annotation:	15 of 22
AminoAcids Coverag	68 %
Intensity Coverage:	48 %
Protein Localisation:	30 ... 51

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502		115.0502	1	N	21				
	214.1186		214.1186	2	V	20	2389.153		2389.153	
	285.1557		285.1557	3	A	19	2290.084		2290.084	
	400.1827		400.1827	4	D	18	2219.047		2219.047	
	471.2198		471.2198	5	A	17	2104.02		1052.514	-0.2398
	600.2624		600.2624	6	E	16	2032.983		2032.983	
	715.2893	-0.064227	715.2893	7	D	15	1903.94	-0.055336	1903.94	
	844.3319		844.3319	8	E	14	1788.914	+0.326953	894.9604	-0.07063
	957.416		957.416	9	I	13	1659.871		1659.871	
	1094.475	-0.089395	1094.475	10	H	12	1546.787		1546.787	
	1195.523		1195.523	11	T	11	1409.728		1409.728	
	1342.591	+0.079424	1342.591	12	F	10	1308.68		1308.68	
	1457.618	-0.139535	1457.618	13	D	9	1161.612		1161.612	
	1528.655	-0.211927	1528.655	14	A	8	1046.585	-0.354452	1046.585	
	1641.739	-0.019624	1641.739	15	I	7	975.5478		975.5478	
	1754.823		1754.823	16	I	6	862.4637		862.4637	
	1853.892	+0.048601	1853.892	17	V	5	749.3797		749.3797	
+0.315322	1005.5		2009.993	18	R	4	650.3113		650.3113	
	2176.991		2176.991	19	S	3	494.2102		494.2102	
	2248.028		2248.028	20	A	2	327.2118		327.2118	
	2349.076		2349.076	21	T	1	256.1747		256.1747	
				22	K	0	155.127		155.127	

Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F06
Scannumber:	4546
Protein:	BSU36890; ipc-35d; upp
Peptide Score:	96.82
Method:	ITMS; CID; 3



precursor information

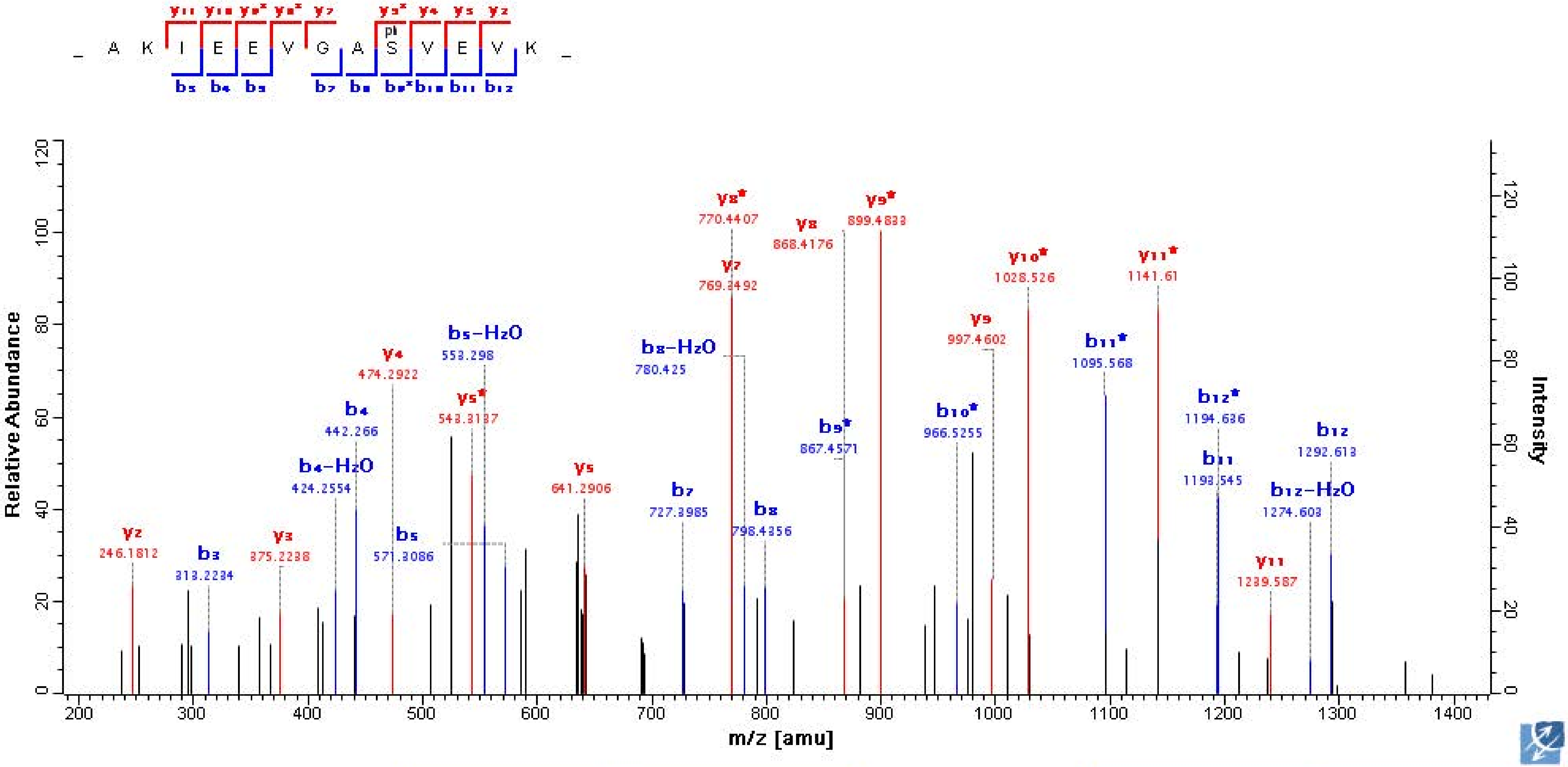
Mass:	1488.69685
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	96.81993
Mass Error [ppm]:	-0.35153
PEP:	0.00048291
Precursor Type:	MULTI

general information

Annotation:	8 of 12
AminoAcids Coverag	67 %
Intensity Coverage:	35 %
Protein Localisation:	16 ... 27

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	114.09134045		114.09134045	1	I	11		
	215.13901892		215.13901892	2	T	10	1384.6347841	
	378.20234746	-0.0438392	378.20234746	3	Y	9	1283.5871056	
	491.28641144	-0.2863504	491.28641144	4	I	8	1120.5237771	
	647.38752247		647.38752247	5	R	7	1007.4397131	
	761.43044992	+0.1309515	761.43044992	6	N	6	851.33860205	
	890.47304301	-0.0293785	890.47304301	7	E	5	737.29567461	
+0.1947364	502.76162346	+0.1264246	1004.5159705	8	N	4	608.25308151	
-0.2570312	593.2686279		1185.5299793	9	T	3	494.21015406	
	1242.5514431		1242.5514431	10	G	2	313.19614518	
	1343.5991215		1343.5991215	11	T	1	256.17468146	
				12	K	0	155.12700298	

Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F06
Scannumber:	6025
Protein:	BSU01050; rplL
Peptide Score:	176.87
Method:	ITMS; CID; 3



precursor information

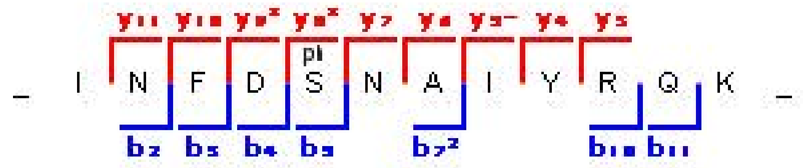
Mass:	1437.7117
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	176.8723
Mass Error [ppm]:	0.049125
PEP:	1.5005E-34
Precursor Type:	MULTI

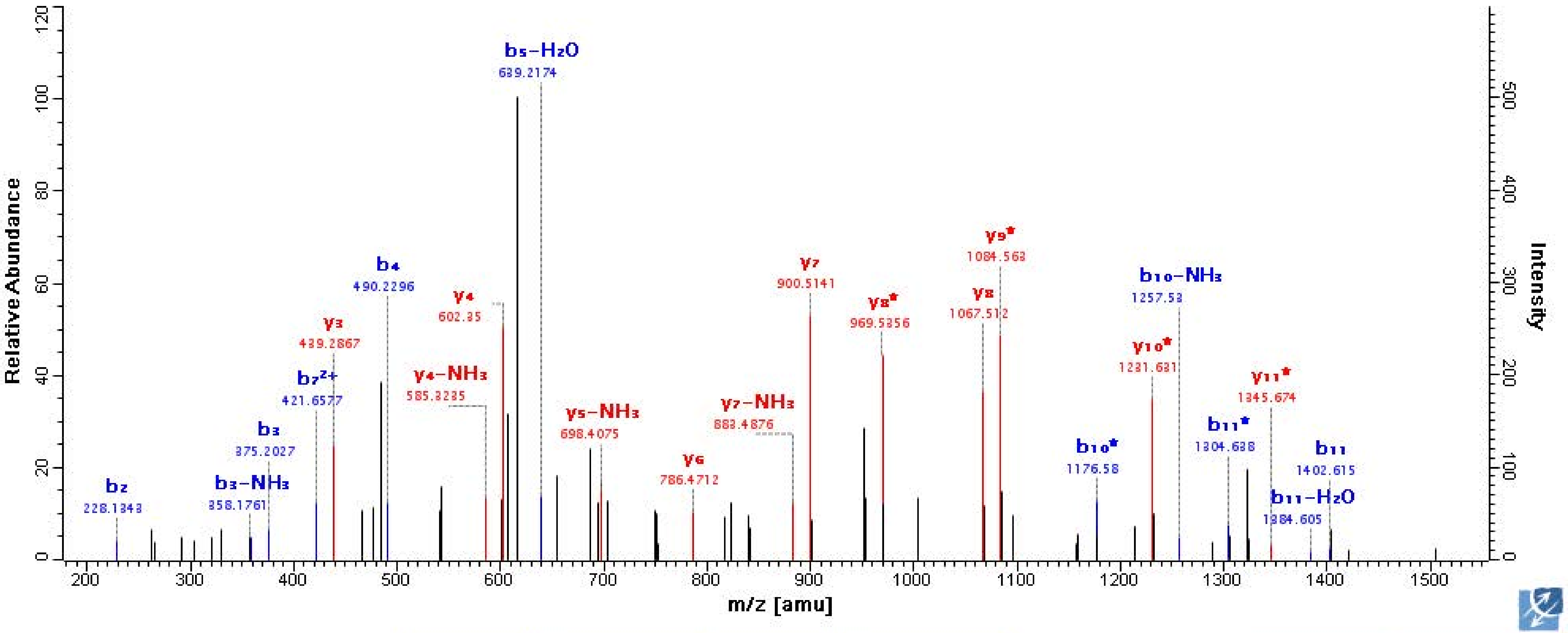
general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	56 %
Protein Localisation:	111 ... 123

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	72.044390254	1	A	12		
	200.139353272	2	K	11	1367.681788536	
+0.1880207	313.223417252	3	I	10	1239.586825518	-0.1066009
-0.0594063	442.266010349	4	E	9	1126.502761538	
-0.0656225	571.308603445	5	E	8	997.460168441	-0.2411133
	670.377017361	6	V	7	868.417575345	-0.0847506
+0.0751517	727.398481085	7	G	6	769.349161429	+0.0902307
+0.0394417	798.435594873	8	A	5	712.327697705	
	965.433953691	9	S	4	641.290583918	+0.2027633
	1064.502367607	10	V	3	474.292225099	+0.0225942
+0.0730813	1193.544960703	11	E	2	375.223811183	+0.154912
-0.1145953	1292.613374619	12	V	1	246.181218087	+0.0364638
		13	K	0	147.112804171	

Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F06
Scannumber:	7501
Protein:	BSU16090; sucC
Peptide Score:	126.1
Method:	ITMS; CID; 3





precursor information

Mass:	1547.71356
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	126.1012
Mass Error [ppm]:	0.12857
PEP:	5.539E-08
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	40 %
Protein Localisation:	216 ... 227

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	114.09134045		114.09134045	1	I	11		
	228.13426789	+0.0305118	228.13426789	2	N	10	1443.6507685	
	375.20268181	+0.0551917	375.20268181	3	F	9	1329.607841	
	490.22962484	+0.0851335	490.22962484	4	D	8	1182.5394271	
	657.22798366		657.22798366	5	S	7	1067.5124841	+0.034513
	771.27091111		771.27091111	6	N	6	900.51412528	+0.0527082
-0.3520477	421.65765068		842.3080249	7	A	5	786.47119783	+0.0397275
	955.39208888		955.39208888	8	I	4	715.43408404	
	1118.4554174		1118.4554174	9	Y	3	602.35002006	+0.0843671
	1274.5565284		1274.5565284	10	R	2	439.28669152	+0.0482694
	1402.615106	-0.1564878	1402.615106	11	Q	1	283.1855805	
				12	K	0	155.12700298	