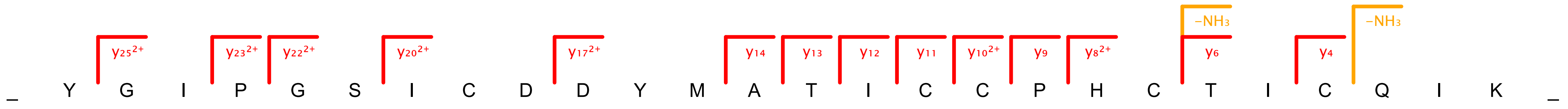
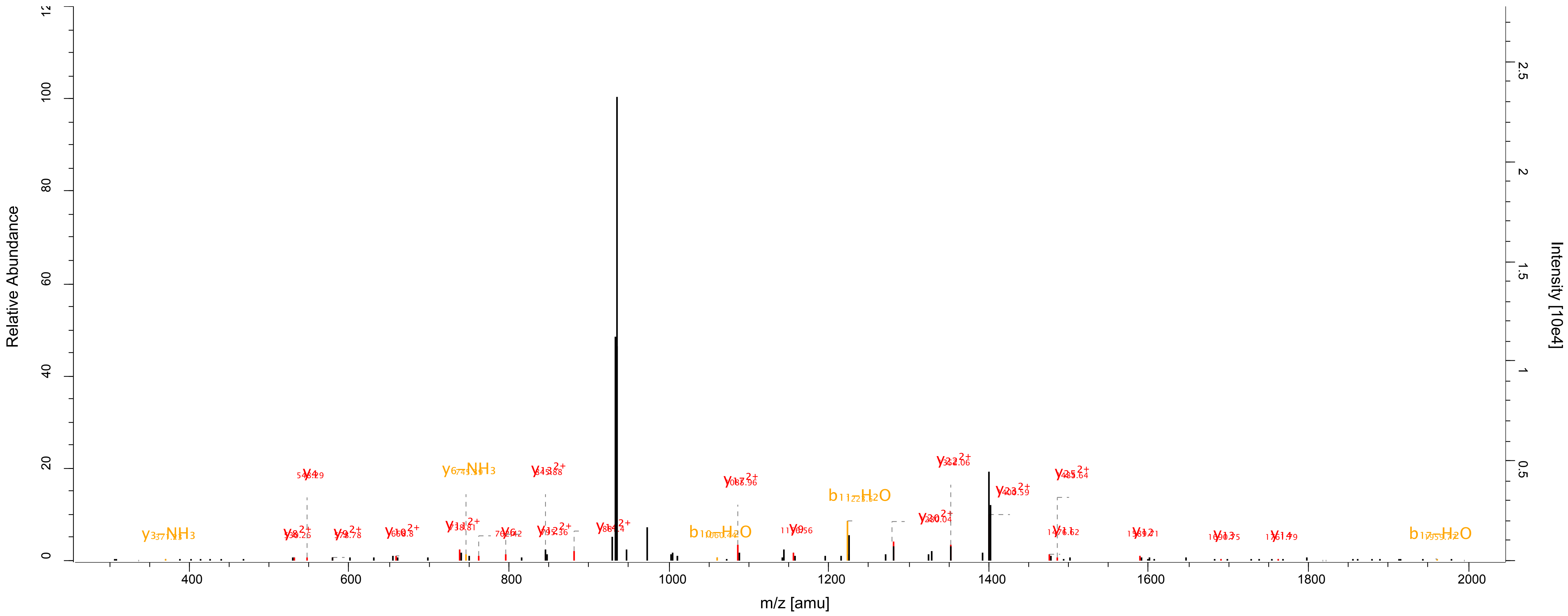
Scan number	15622	Raw file	20080621_Orbi3_SZ_Matrigel_Exp2_24h_InGel_01
Method	ITMS; CID	Genenames	PLAC8





precursor information

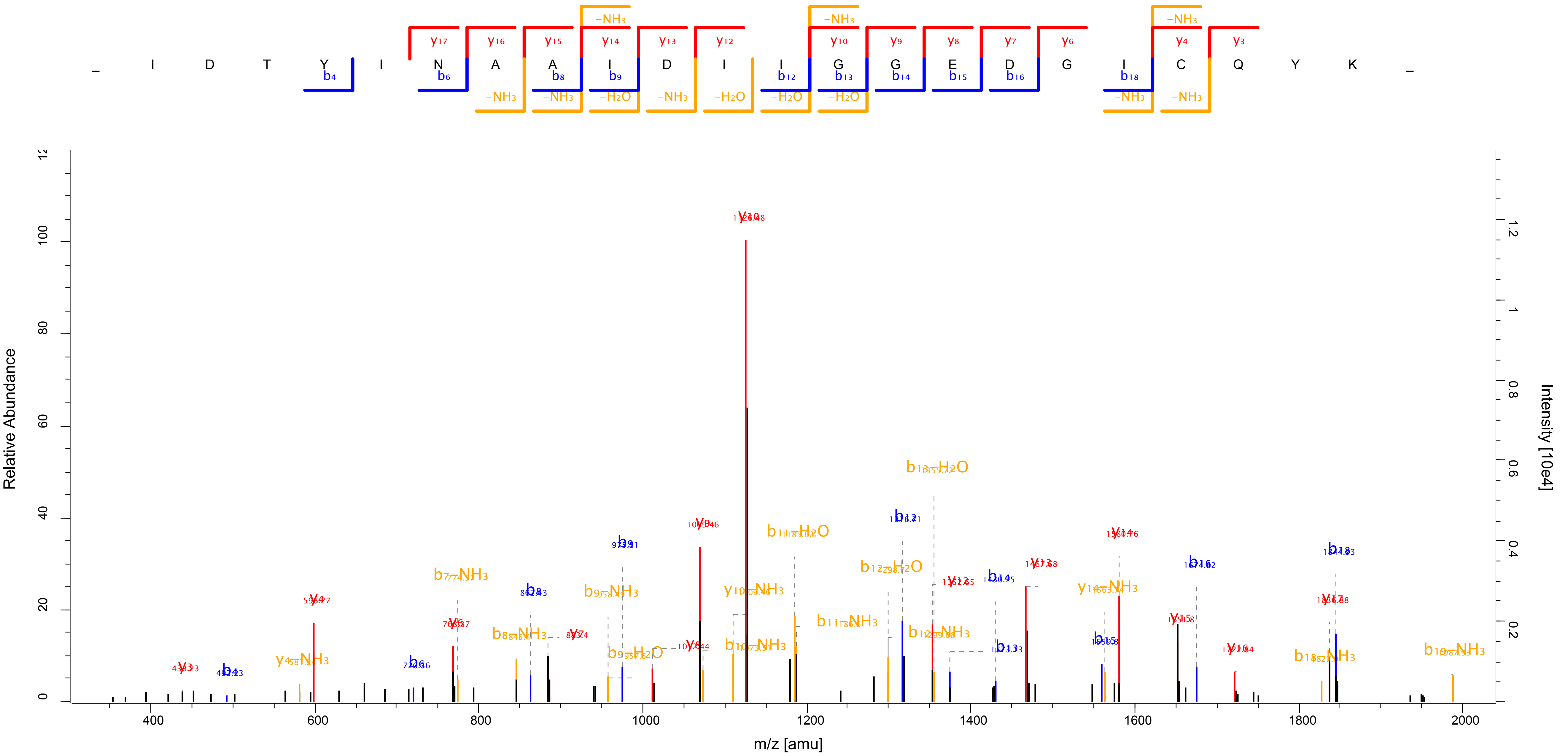
Mass:	3132.3283
m/z:	1045.11671
Charge:	3+
Retentiontime:	107.323394775391
Score:	79.2926
Mass Error [ppm]:	−0.7227
PEP:	0.00035125
Precursor Type:	ISO

general information

Annotation:	17 of 26
AminoAcids Coverage:	65 %
Intensity Coverage:	14 %
Peak Coverage:	24 %
Protein Localisation:	78 ... 103

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	164.070605005	1	Y	25				
	221.092068728	2	G	24	2970.274507959		1485.640892213	−0.1191637
	334.176132709	3	I	23	2913.253044235		2913.253044235	
	431.228896561	4	P	22	2800.168980255		1400.588128361	−0.0153745
	488.250360284	5	G	21	2703.116216403		1352.061746435	+0.4090788
	575.282388694	6	S	20	2646.094752679		2646.094752679	
	688.366452675	7	I	19	2559.062724269		1280.035000368	+0.2776217
	848.397100876	8	C	18	2445.978660289		2445.978660289	
	963.424043908	9	D	17	2285.948012088		2285.948012088	
	1078.45098694	10	D	16	2170.921069056		1085.964172761	+0.1815792
	1241.514315478	11	Y	15	2055.894126024		2055.894126024	
	1372.554800085	12	M	14	1892.830797485		1892.830797485	
	1443.591913872	13	A	13	1761.790312879	+0.2743844	881.398794673	−0.1039949
	1544.639592347	14	T	12	1690.753199091	+0.1092277	845.880237779	−0.1208384
	1657.723656327	15	I	11	1589.705520617	−0.025711	795.356398542	−0.3135519
	1817.754304528	16	C	10	1476.621456637	−0.0174527	738.814366552	+0.4034069
	1977.78495273	17	C	9	1316.590808436		658.799042451	+0.2460015
	2074.837716582	18	P	8	1156.560160234	−0.0325723	578.78371835	+0.0251195
	2211.896628444	19	H	7	1059.507396382		530.257336424	+0.457019
	2371.927276646	20	C	6	922.44848452		922.44848452	
	2472.97495512	21	T	5	762.417836318	+0.1734723	762.417836318	
	2586.0590191	22	I	4	661.370157844		661.370157844	
	2746.089667301	23	C	3	548.286093864	−0.0791847	548.286093864	
	2874.148244813	24	Q	2	388.255445662		388.255445662	
	2987.232308793	25	I	1	260.196868151		260.196868151	
		26	K	0	147.112804171		147.112804171	

Scan number	21114	Raw file	20080621_Orbi3_SZ_Matrigel_Exp2_24h_InGel_02
Method	ITMS; CID	Genenames	PLA2G12A



precursor information

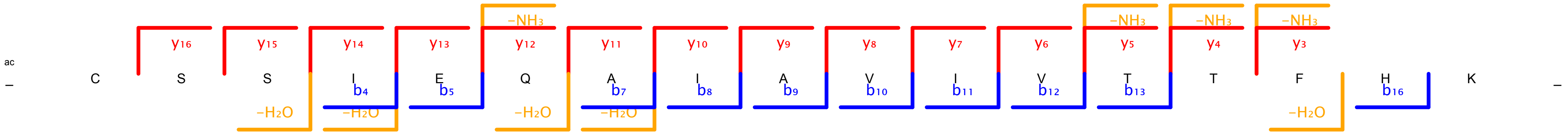
Mass:	2441.17903
m/z:	1221.59679
Charge:	2+
Retentiontime:	128.652679443359
Score:	168.7883
Mass Error [ppm]:	0.24165
PEP:	1.5334E-18
Precursor Type:	ISO

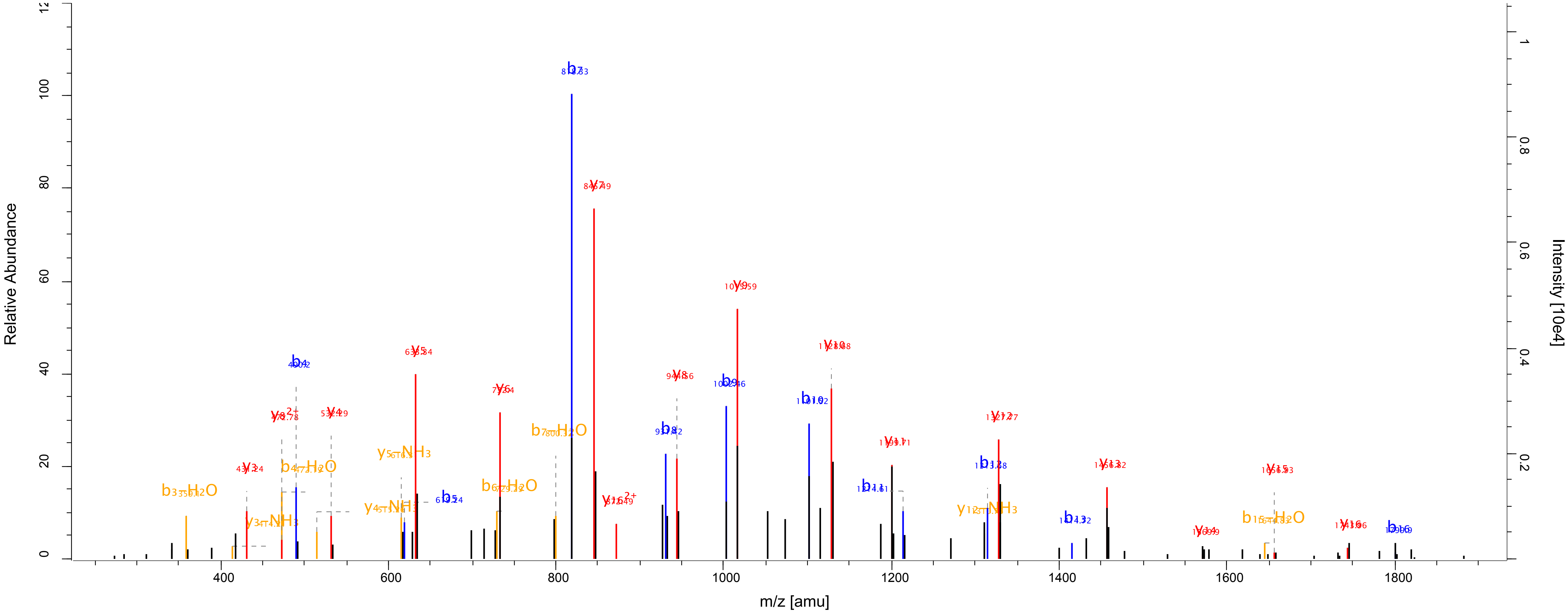
general information

Annotation:	17 of 22
AminoAcids Coverage:	77 %
Intensity Coverage:	59 %
Peak Coverage:	39 %
Protein Localisation:	45 ... 66

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	114.091340447	1	I	21		
	229.118283479	2	D	20	2329.101653722	
	330.165961953	3	T	19	2214.07471069	
+0.2042117	493.229290491	4	Y	18	2113.027032216	
	606.313354472	5	I	17	1949.963703678	
+0.147136	720.356281919	6	N	16	1836.879639697	+0.0186757
	791.393395707	7	A	15	1722.83671225	-0.1273617
-0.2156657	862.430509495	8	A	14	1651.799598462	-0.185951
-0.0072493	975.514573475	9	I	13	1580.762484674	+0.1260651
	1090.541516507	10	D	12	1467.678420694	-0.1096951
	1203.625580487	11	I	11	1352.651477662	+0.037121
-0.0946542	1316.709644468	12	I	10	1239.567413682	
+0.0600295	1373.731108191	13	G	9	1126.483349701	-0.0696534
-0.1214684	1430.752571915	14	G	8	1069.461885978	-0.0934778
+0.0177012	1559.795165011	15	E	7	1012.440422254	+0.0224684
-0.1728161	1674.822108043	16	D	6	883.397829158	+0.0596904
	1731.843571767	17	G	5	768.370886126	+0.0170533
-0.3180166	1844.927635747	18	I	4	711.349422402	
	2004.958283949	19	C	3	598.265358422	+0.0643535
	2133.01686146	20	Q	2	438.23471022	+0.155396
	2296.080189998	21	Y	1	310.176132709	
		22	K	0	147.112804171	

Scan number	19874	Raw file	20080621_Orbi3_SZ_Matrigel_Exp2_24h_InGel_03
Method	ITMS; CID	Genenames	S100A2





precursor information

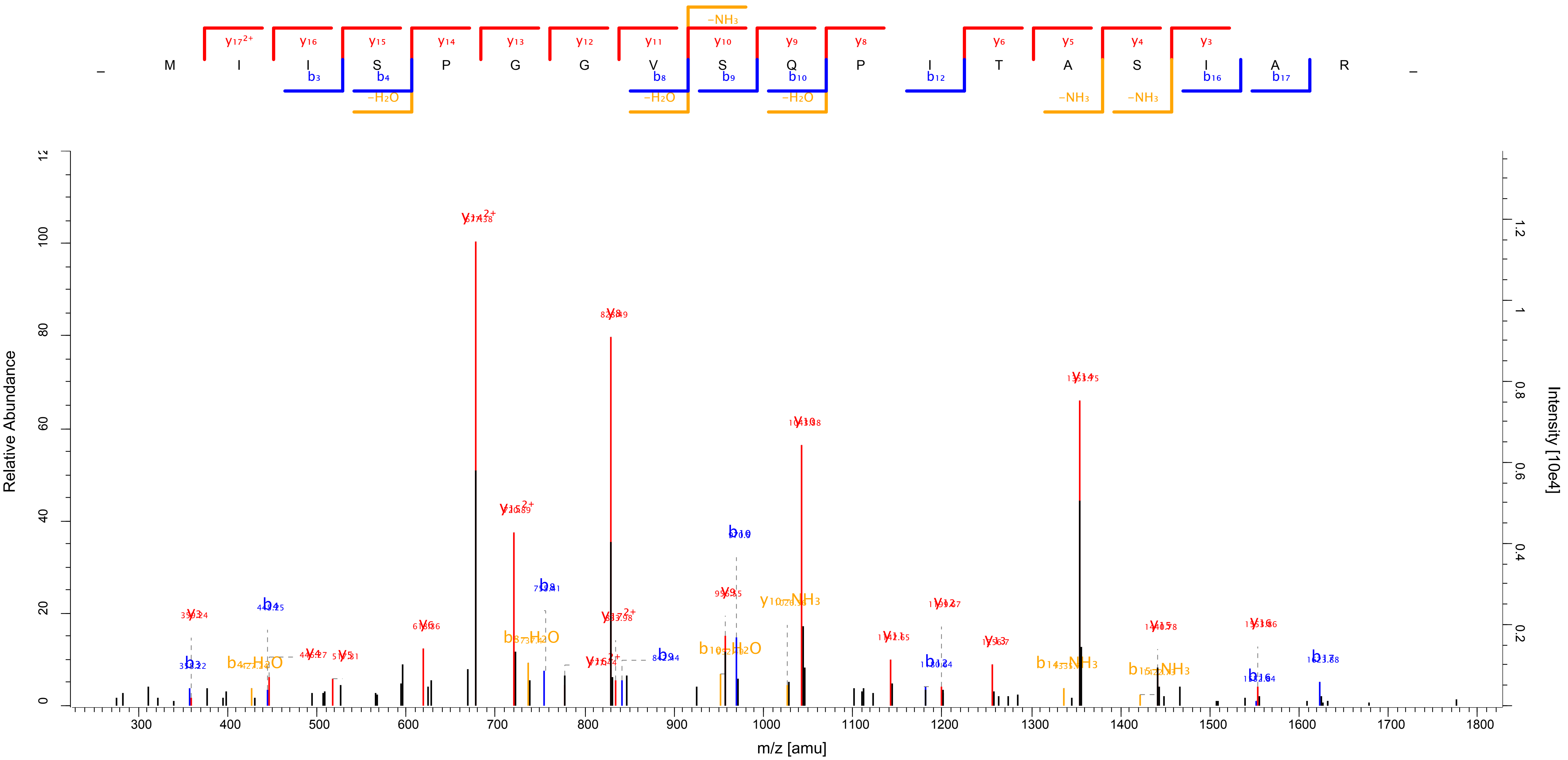
Mass:	1944.99755
m/z:	973.50605
Charge:	2+
Retentiontime:	133.935012817383
Score:	171.2645
Mass Error [ppm]:	-0.17817
PEP:	9.7868E-12
Precursor Type:	ISO

general information

Annotation:	15 of 17
AminoAcids Coverage:	88 %
Intensity Coverage:	62 %
Peak Coverage:	36 %
Protein Localisation:	2 ... 18

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	203.048489354	1	C	16				
	290.080517764	2	S	15	1743.963961674	−0.2192107	872.48561907	−0.020287
	377.112546174	3	S	14	1656.931933264	+0.0628177	1656.931933264	
−0.2229773	490.196610154	4	I	13	1569.899904854	−0.106814	1569.899904854	
+0.1047909	619.239203251	5	E	12	1456.815840874	−0.0972129	1456.815840874	
	747.297780762	6	Q	11	1327.773247778	+0.0130071	1327.773247778	
+0.0302788	818.33489455	7	A	10	1199.714670266	−0.151682	1199.714670266	
−0.1688365	931.41895853	8	I	9	1128.677556478	−0.0878348	1128.677556478	
−0.0546441	1002.456072318	9	A	8	1015.593492498	+0.0465832	1015.593492498	
−0.1106679	1101.524486234	10	V	7	944.55637871	+0.1233088	472.781827588	+0.2847007
−0.3736869	1214.608550215	11	I	6	845.487964794	+0.0872916	845.487964794	
−0.1911243	1313.676964131	12	V	5	732.403900814	+0.1250909	732.403900814	
−0.2250088	1414.724642605	13	T	4	633.335486897	−0.0035167	633.335486897	
	1515.772321079	14	T	3	532.287808423	+0.1343718	532.287808423	
	1662.840734995	15	F	2	431.240129949	−0.0012383	431.240129949	
+0.2132682	1799.899646858	16	H	1	284.171716033		284.171716033	
		17	K	0	147.112804171		147.112804171	

Scan number	14477	Raw file	20080621_Orbi3_SZ_Matrigel_Exp2_24h_InGel_07
Method	ITMS; CID	Genenames	CCDC137



precursor information

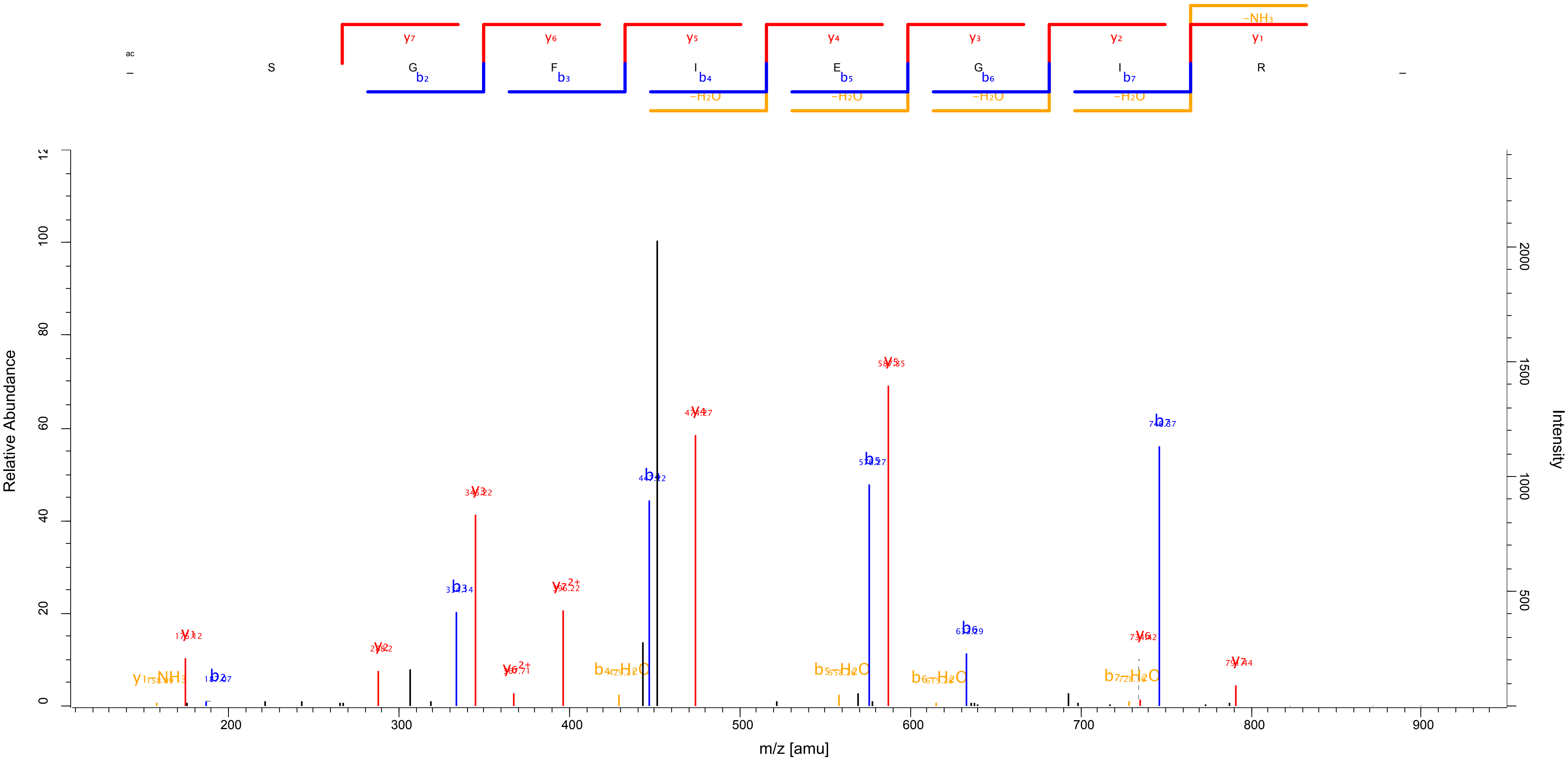
Mass:	1796.98165
m/z:	899.4981
Charge:	2+
Retentiontime:	100.07063293457
Score:	147.0666
Mass Error [ppm]:	−0.11629
PEP:	7.0997E−06
Precursor Type:	ISO

general information

Annotation:	16 of 18
AminoAcids Coverage:	89 %
Intensity Coverage:	57 %
Peak Coverage:	33 %
Protein Localisation:	230 ... 247

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	132.047761073	1	M	17				
	245.131825053	2	I	16	1666.948645961		833.977961214	−0.0859934
−0.0926285	358.215889034	3	I	15	1553.86458198	+0.137127	777.435929224	−0.143937
−0.0835498	445.247917444	4	S	14	1440.780518	+0.0447994	720.893897233	+0.3180779
	542.300681296	5	P	13	1353.74848959	−0.0272982	677.377883028	+0.0408181
	599.322145019	6	G	12	1256.695725738	+0.0713641	1256.695725738	
	656.343608743	7	G	11	1199.674262014	+0.2587214	1199.674262014	
−0.1538439	755.412022659	8	V	10	1142.652798291	−0.0428129	1142.652798291	
+0.0830485	842.444051069	9	S	9	1043.584384375	+0.0606352	1043.584384375	
−0.0266154	970.50262858	10	Q	8	956.552355965	+0.0467651	956.552355965	
	1067.555392432	11	P	7	828.493778453	+0.0405843	828.493778453	
+0.2905973	1180.639456413	12	I	6	731.441014601		731.441014601	
	1281.687134887	13	T	5	618.356950621	−0.0005663	618.356950621	
	1352.724248675	14	A	4	517.309272147	+0.0258719	517.309272147	
	1439.756277084	15	S	3	446.272158359	+0.0376561	446.272158359	
−0.1551604	1552.840341065	16	I	2	359.240129949	+0.0763068	359.240129949	
−0.164198	1623.877454853	17	A	1	246.156065969		246.156065969	
		18	R	0	175.118952181		175.118952181	

Scan number	12885	Raw file	20080623_Orbi5_SZ_Matrigel_12h_InGel_01
Method	ITMS; CID	Genenames	TMEM50A



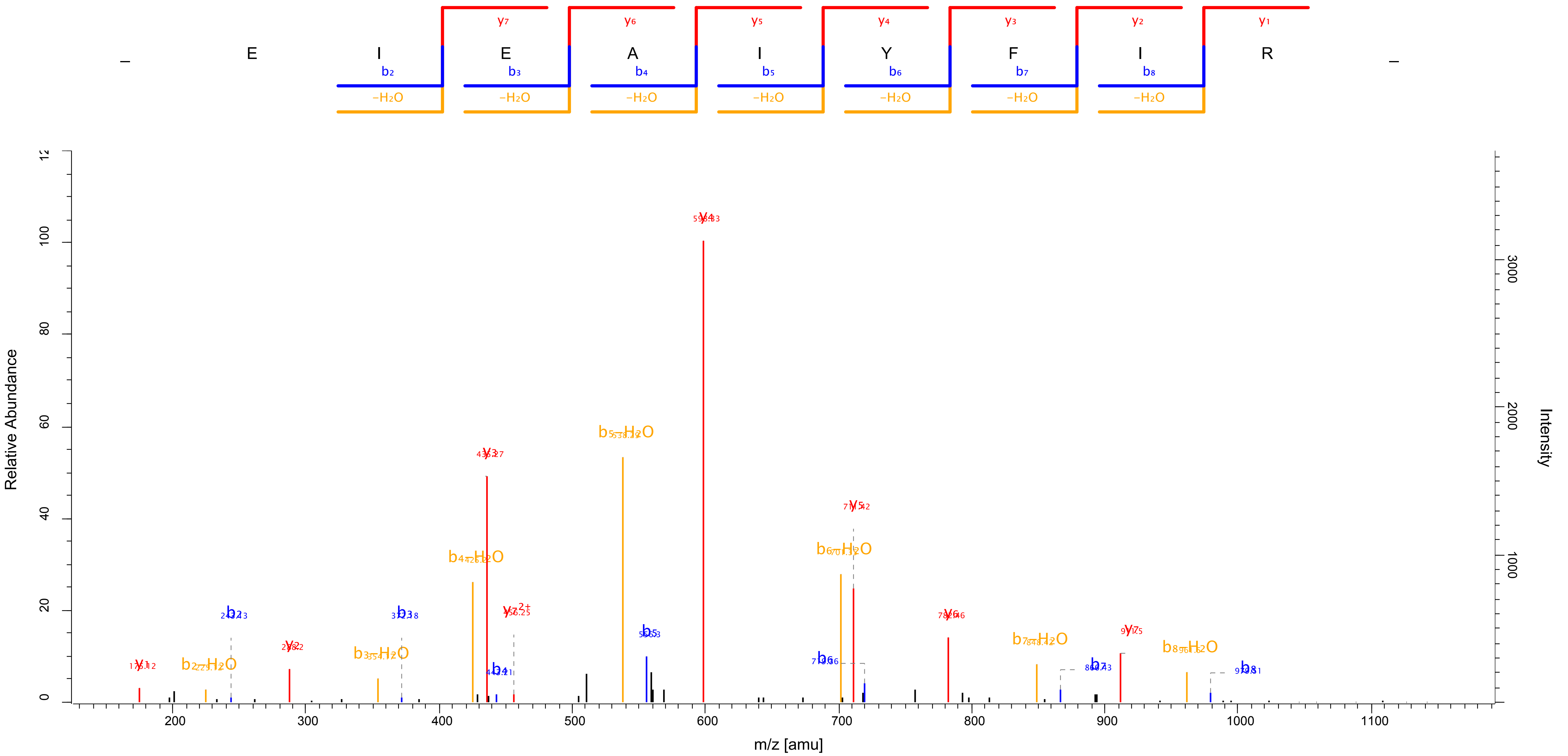
precursor
information

Mass:	919.47647
m/z:	460.74551
Charge:	2+
Retentiontime:	94.7955093383789
Score:	170.6648
Mass Error [ppm]:	0.15286
PEP:	0.00028085
Annotation:	7 of 8
AminoAcids Coverage:	88 %
Intensity Coverage:	75 %
Peak Coverage:	47 %
Protein Localisation:	2 ... 9

ge
ir

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.049869563	1	S	7				
−0.0613388	187.071333286	2	G	6	791.441014601	+0.0926158	396.224145534	+0.101355
+0.0427479	334.139747203	3	F	5	734.419550878	+0.1307421	367.713413672	+0.0479389
+0.0444078	447.223811183	4	I	4	587.351136962	+0.1275007	587.351136962	
−0.03148	576.266404279	5	E	3	474.267072981	+0.1287705	474.267072981	
−0.0207171	633.287868003	6	G	2	345.224479885	+0.0760877	345.224479885	
+0.0576945	746.371931983	7	I	1	288.203016161	+0.0082265	288.203016161	
		8	R	0	175.118952181	−0.1036018	175.118952181	

Scan number	13703	Raw file	20080623_Orbi5_SZ_Matrigel_12h_InGel_01
Method	ITMS; CID	Genenames	LYRM5

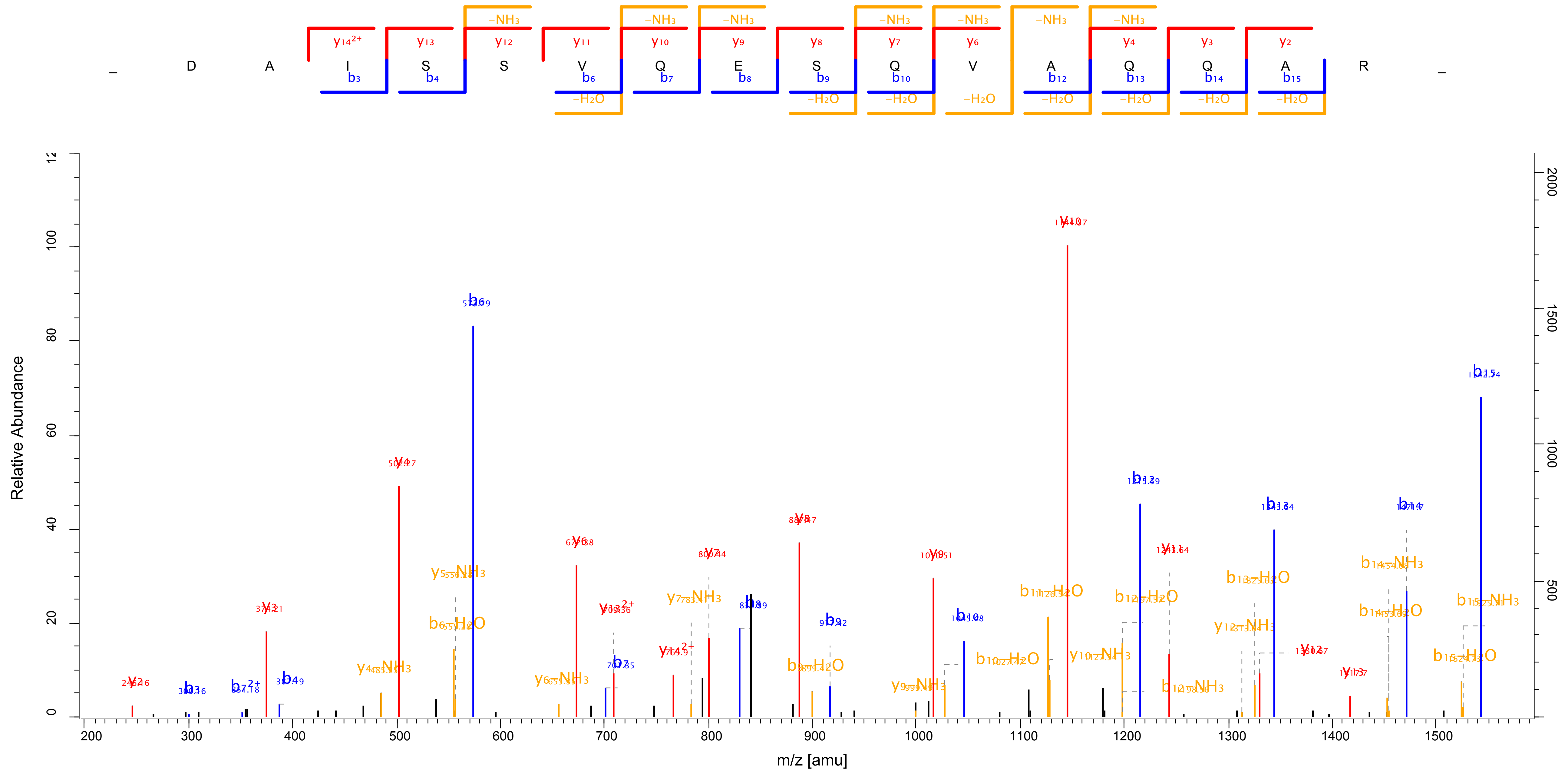


precursor
information

Mass:	1152.61789
m/z:	577.31622
Charge:	2+
Retentiontime:	100.285949707031
Score:	207.9511
Mass Error [ppm]:	−0.018614
PEP:	7.6627E−15
Annotation:	8 of 9
AminoAcids Coverage:	89 %
Intensity Coverage:	88 %
Peak Coverage:	38 %
Protein Localisation:	63 ... 71

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.049869563	1	E	8				
+0.0670247	243.133933543	2	I	7	1024.582593461		1024.582593461	
+0.1479973	372.176526639	3	E	6	911.49852948	+0.137701	456.252902973	+0.1722679
+0.059736	443.213640427	4	A	5	782.455936384	−0.024662	782.455936384	
−0.0118768	556.297704408	5	I	4	711.418822596	+0.0348517	711.418822596	
+0.0794578	719.361032946	6	Y	3	598.334758616	+0.0456125	598.334758616	
+0.0297817	866.429446862	7	F	2	435.271430078	+0.0913019	435.271430078	
+0.0645531	979.513510843	8	I	1	288.203016161	−0.0478648	288.203016161	
		9	R	0	175.118952181	−0.02743	175.118952181	

Scan number	6382	Raw file	20080623_Orbi5_SZ_Matrigel_12h_InGel_01
Method	ITMS; CID	Genenames	APOC3



precursor
information

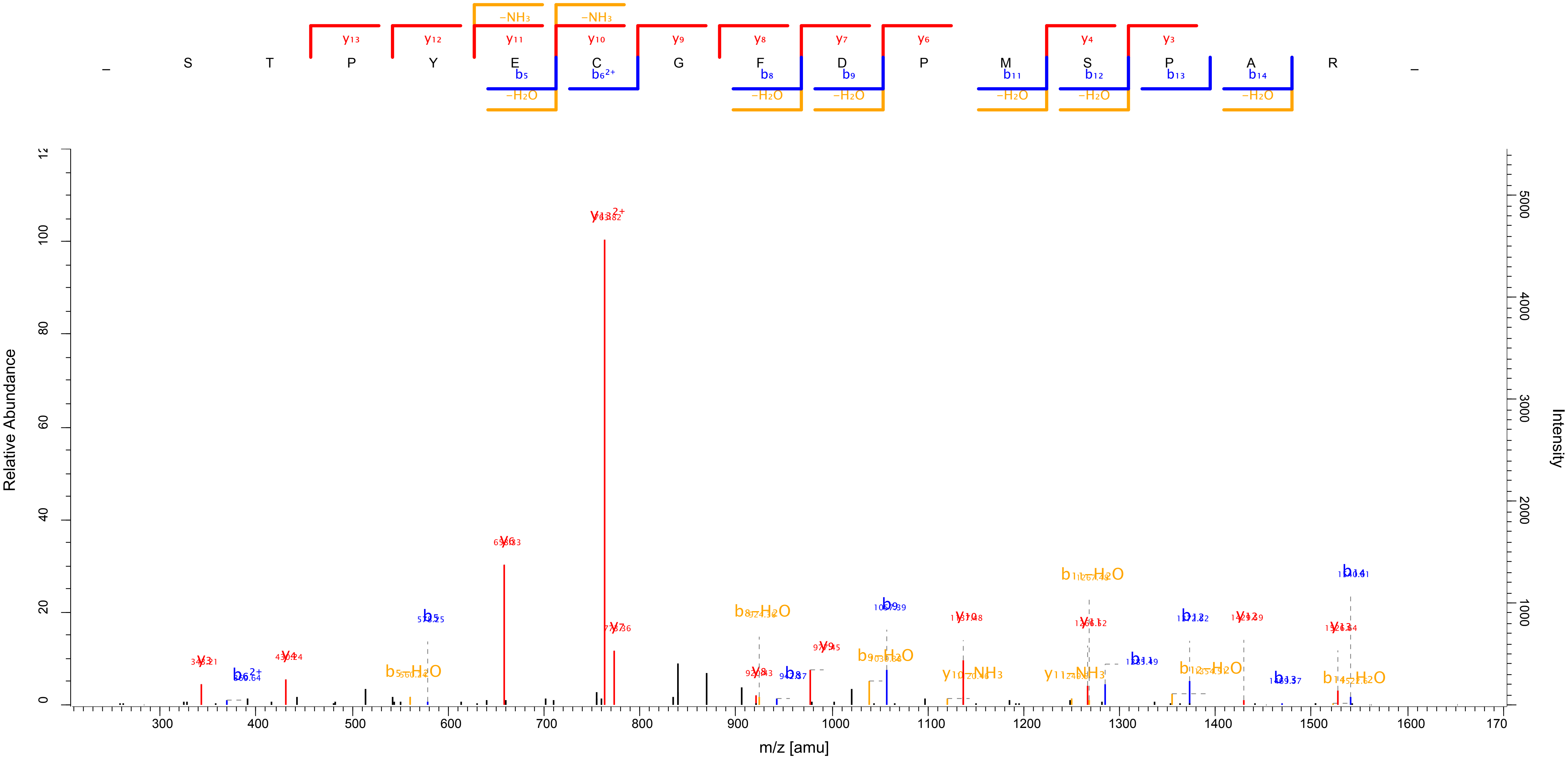
Mass:	1715.84375
m/z:	858.92915
Charge:	2+
Retentiontime:	55.0172843933105
Score:	332.2167
Mass Error [ppm]:	−0.052593
PEP:	6.04825E−149
Precursor Type:	ISO

general
information

Annotation:	13 of 16
AminoAcids Coverage:	81 %
Intensity Coverage:	87 %
Peak Coverage:	54 %
Protein Localisation:	45 ... 60

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342195		116.0342195	1	D	15				
	187.07133329		187.07133329	2	A	14	1601.8241737		1601.8241737	
	300.15539727	+0.0144636	300.15539727	3	I	13	1530.7870599		765.8971682	−0.0119753
	387.18742568	+0.0989818	387.18742568	4	S	12	1417.702996	+0.048591	709.35513621	+0.1144072
	474.21945409		474.21945409	5	S	11	1330.6709676	+0.1221233	1330.6709676	
	573.287868	+0.010777	573.287868	6	V	10	1243.6389391	+0.1167982	1243.6389391	
+0.1255682	351.17686099	−0.0662331	701.34644551	7	Q	9	1144.5705252	+0.0106515	1144.5705252	
	830.38903861	+0.0355219	830.38903861	8	E	8	1016.5119477	+0.0232696	1016.5119477	
	917.42106702	−0.0856178	917.42106702	9	S	7	887.46935462	+0.0249691	887.46935462	
	1045.4796445	−0.0123594	1045.4796445	10	Q	6	800.43732621	+0.1080229	800.43732621	
	1144.5480584		1144.5480584	11	V	5	672.3787487	+0.1255238	672.3787487	
	1215.5851722	−0.0478187	1215.5851722	12	A	4	573.31033478		573.31033478	
	1343.6437497	−0.0586667	1343.6437497	13	Q	3	502.27322099	+0.1736174	502.27322099	
	1471.7023273	−0.0121417	1471.7023273	14	Q	2	374.21464348	+0.0891895	374.21464348	
	1542.739441	−0.034485	1542.739441	15	A	1	246.15606597	+0.0365915	246.15606597	
				16	R	0	175.11895218		175.11895218	

Scan number	8767	Raw file	20080623_Orbi5_SZ_Matrigel_12h_InGel_01
Method	ITMS; CID	Genenames	MT-ND3;ND3



precursor information

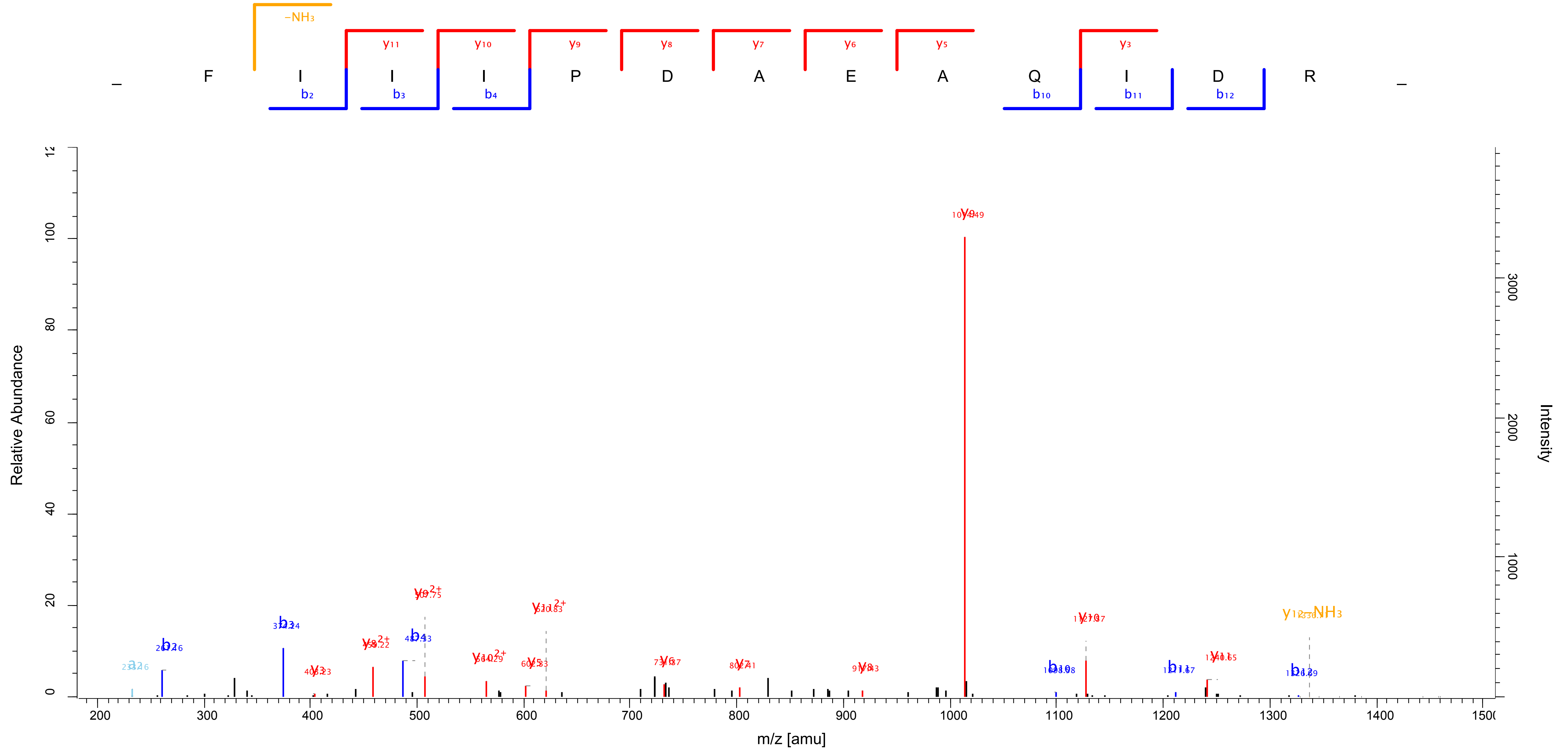
Mass:	1713.71268
m/z:	857.86362
Charge:	2+
Retentiontime:	68.8057250976563
Score:	198.4864
Mass Error [ppm]:	−0.006737
PEP:	8.1654E−21
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverage:	80 %
Intensity Coverage:	77 %
Peak Coverage:	33 %
Protein Localisation:	34 ... 48

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876		88.039304876	1	S	14				
	189.08698335		189.08698335	2	T	13	1627.6879395		1627.6879395	
	286.1397472		286.1397472	3	P	12	1526.640261	+0.1116921	763.82376876	+0.1053084
	449.20307574		449.20307574	4	Y	11	1429.5874972	+0.0752225	1429.5874972	
	578.24566884	+0.0588356	578.24566884	5	E	10	1266.5241687	+0.0074476	1266.5241687	
−0.3414427	369.64179675		738.27631704	6	C	9	1137.4815756	+0.1424479	1137.4815756	
	795.29778076		795.29778076	7	G	8	977.45092736	+0.0772098	977.45092736	
	942.36619468	+0.0271769	942.36619468	8	F	7	920.42946364	+0.0475871	920.42946364	
	1057.3931377	−0.0962627	1057.3931377	9	D	6	773.36104972	−0.0130883	773.36104972	
	1154.4459016		1154.4459016	10	P	5	658.33410669	+0.012512	658.33410669	
	1285.4863862	+0.0513336	1285.4863862	11	M	4	561.28134284		561.28134284	
	1372.5184146	−0.0438052	1372.5184146	12	S	3	430.24085823	+0.0565051	430.24085823	
	1469.5711784	+0.1337776	1469.5711784	13	P	2	343.20882982	+0.1577168	343.20882982	
	1540.6082922	−0.0016028	1540.6082922	14	A	1	246.15606597		246.15606597	
				15	R	0	175.11895218		175.11895218	

Scan number	13896	Raw file	20080623_Orbi5_SZ_Matrigel_12h_InGel_02
Method	ITMS; CID	Genenames	TMEM128



precursor information

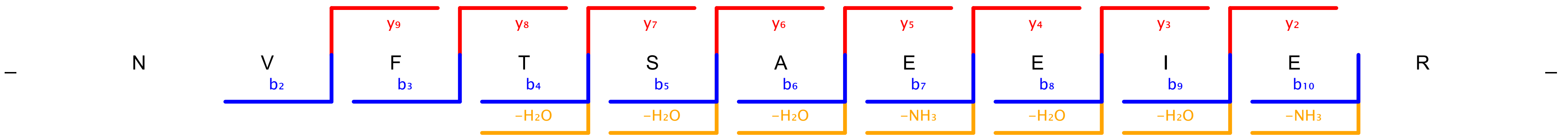
Mass:	1499.79818
m/z:	750.90636
Charge:	2+
Retentiontime:	97.5685729980469
Score:	132.3229
Mass Error [ppm]:	-0.14469
PEP:	1.9615E-05
Precursor Type:	MULTI

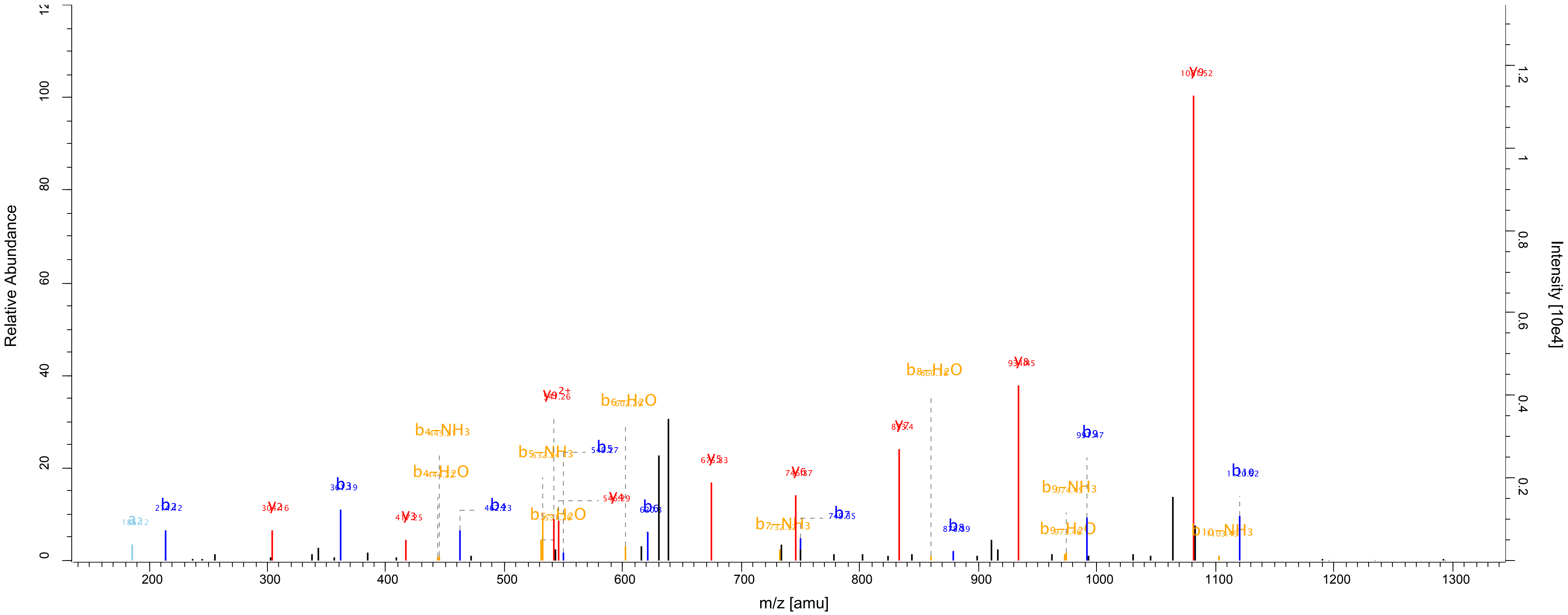
general information

Annotation:	11 of 13
AminoAcids Coverage:	85 %
Intensity Coverage:	72 %
Peak Coverage:	28 %
Protein Localisation:	14 ... 26

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08077576		148.07569038	1	F	12				
+0.0685129	233.16483974	+0.0331778	261.15975436	2	I	11	1353.7372562		1353.7372562	
	346.24890372	+0.039751	374.24381834	3	I	10	1240.6531922	+0.2097228	620.83023434	+0.0434839
	459.3329677	-0.0654312	487.32788232	4	I	9	1127.5691282	-0.0128538	564.28820235	+0.1206111
	556.38573155		584.38064618	5	P	8	1014.4850643	+0.0224431	507.74617036	+0.1129605
	671.41267459		699.40758921	6	D	7	917.43230041	+0.1582147	459.21978844	+0.1481925
	742.44978837		770.444703	7	A	6	802.40535738	+0.39225	802.40535738	
	871.49238147		899.48729609	8	E	5	731.36824359	+0.0868956	731.36824359	
	942.52949526		970.52440988	9	A	4	602.32565049	+0.0948207	602.32565049	
	1070.5880728	+0.1491903	1098.5829874	10	Q	3	531.2885367		531.2885367	
	1183.6721367	+0.0068988	1211.6670514	11	I	2	403.22995919	+0.1581634	403.22995919	
	1298.6990798	+0.1022702	1326.6939944	12	D	1	290.14589521		290.14589521	
				13	R	0	175.11895218		175.11895218	

Scan number	9398	Raw file	20080623_Orbi5_SZ_Matrigel_12h_InGel_02
Method	ITMS; CID	Genenames	FAM176A





precursor information

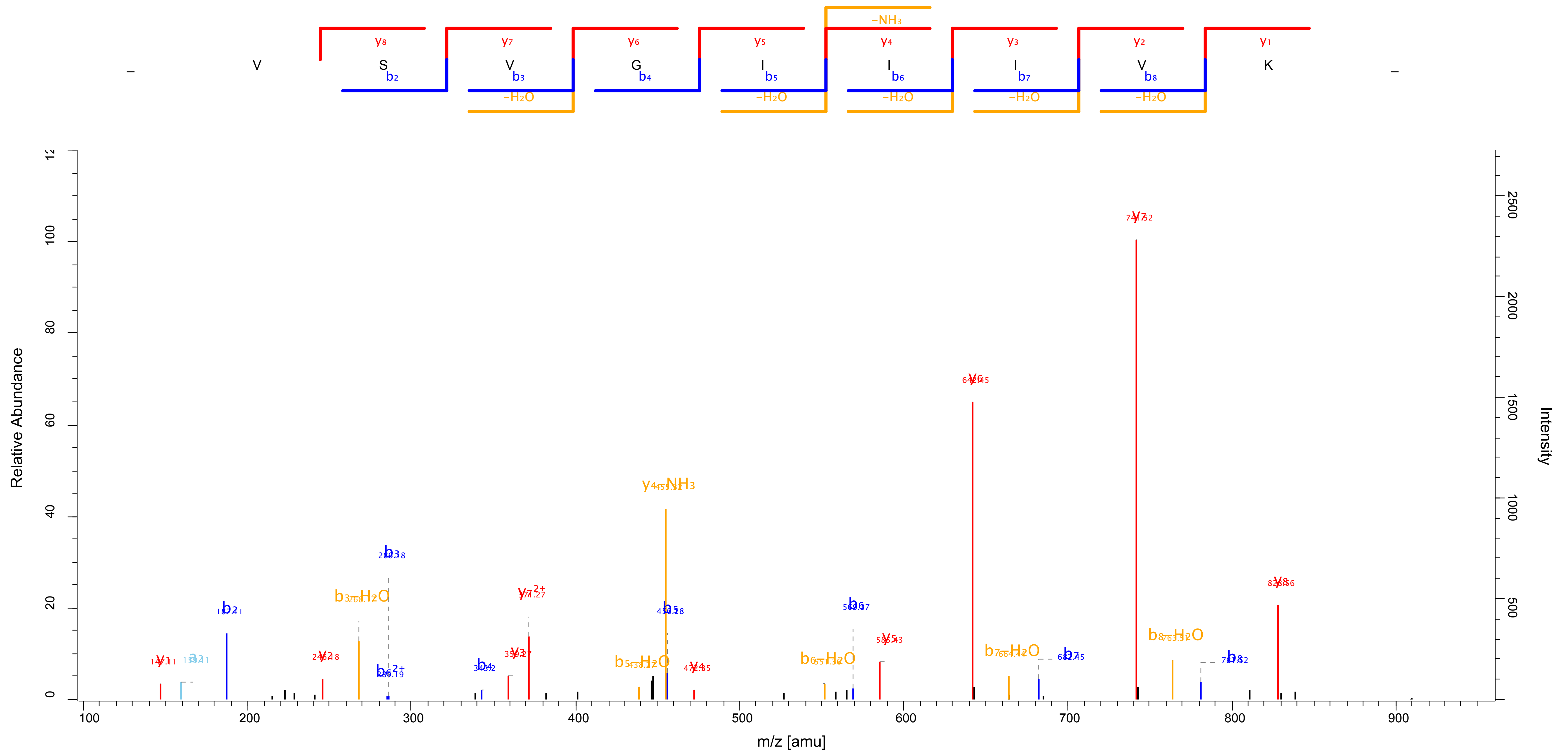
Mass:	1293.62147
m/z:	647.81801
Charge:	2+
Retentiontime:	69.9148559570313
Score:	217.1355
Mass Error [ppm]:	1.0611
PEP:	3.3596E-27
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverage:	82 %
Intensity Coverage:	73 %
Peak Coverage:	45 %
Protein Localisation:	110 ... 120

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	87.055289292		115.05020391	1	N	10				
+0.0409544	186.12370321	+0.058674	214.11861783	2	V	9	1180.584444		1180.584444	
	333.19211712	+0.0261641	361.18703175	3	F	8	1081.51603	-0.0270164	541.26165325	+0.0883223
	434.2397956	+0.1466374	462.23471022	4	T	7	934.44761612	+0.0106358	934.44761612	
	521.27182401	-0.0146024	549.26673863	5	S	6	833.39993765	+0.0506849	833.39993765	
	592.3089378	+0.037151	620.30385242	6	A	5	746.36790924	+0.160289	746.36790924	
	721.35153089	-0.0540261	749.34644551	7	E	4	675.33079545	+0.003372	675.33079545	
	850.39412399	+0.1318964	878.38903861	8	E	3	546.28820235	+0.1445979	546.28820235	
	963.47818797	-0.0201607	991.47310259	9	I	2	417.24560926	+0.0953331	417.24560926	
	1092.5207811	-0.0315648	1120.5156957	10	E	1	304.16154528	-0.0146947	304.16154528	
				11	R	0	175.11895218		175.11895218	

Scan number	10318	Raw file	20080623_Orbi5_SZ_Matrigel_12h_InGel_03
Method	ITMS; CID	Genenames	ZG16B



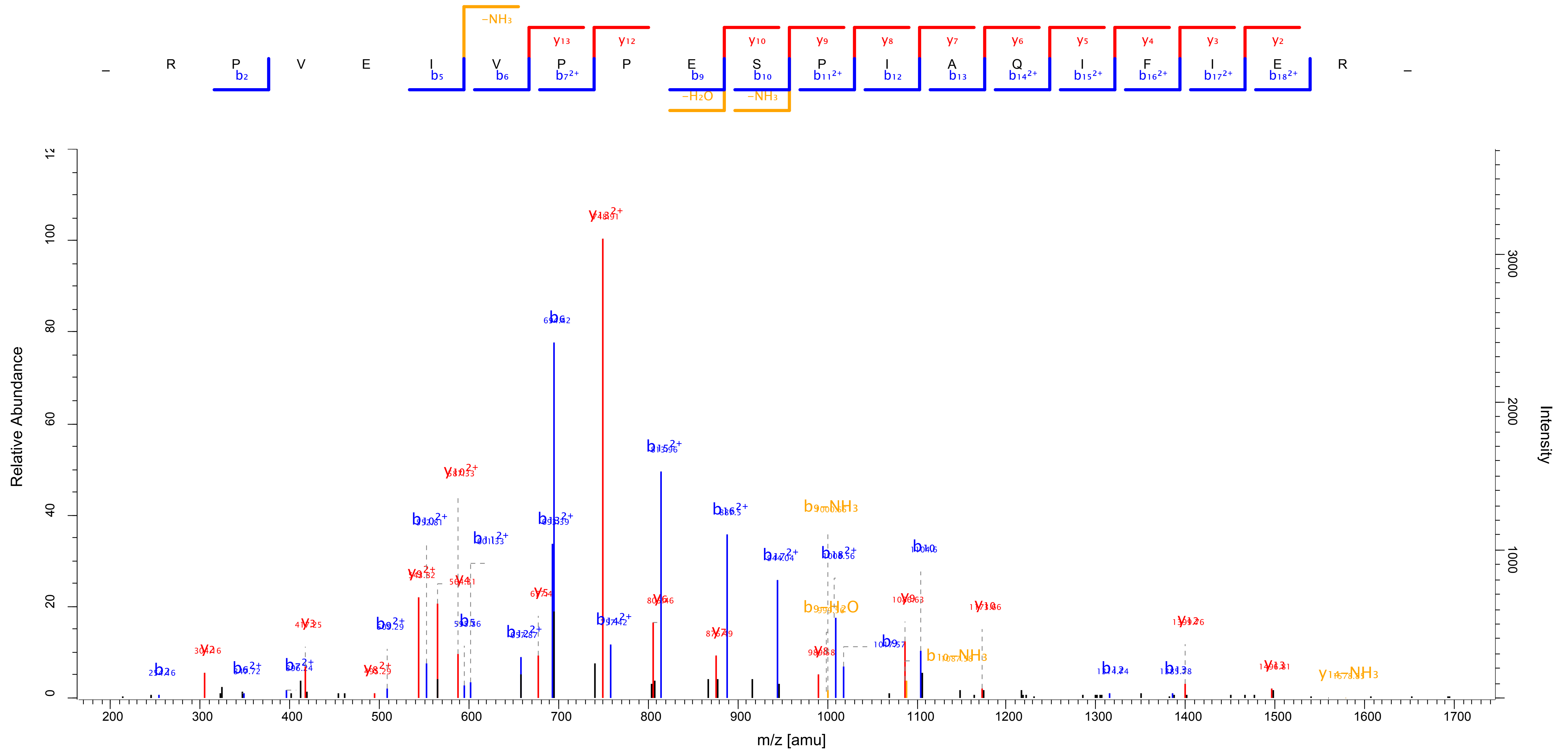
precursor information

Mass:	926.61682
m/z:	464.31569
Charge:	2+
Retentiontime:	77.4807815551758
Score:	204.3623
Mass Error [ppm]:	0.39416
PEP:	1.945E−06
Annotation:	8 of 9
AminoAcids Coverage:	89 %
Intensity Coverage:	90 %
Peak Coverage:	53 %
Protein Localisation:	79 ... 87

ge
ir

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.0807758		100.07569		100.07569	1	V	8				
+0.0074961	159.112804		187.107719	−0.0293954	187.107719	2	S	7	828.555316	+0.0002869	828.555316	
	258.181218		286.176133	+0.1105799	286.176133	3	V	6	741.523288	+0.0636874	371.265282	+0.0260387
	315.202682		343.197596	−0.0158948	343.197596	4	G	5	642.454874	−0.0425202	642.454874	
	428.286746		456.28166	−0.0669082	456.28166	5	I	4	585.43341	+0.0144659	585.43341	
	541.37081	+0.3315965	285.1865	+0.058531	569.365724	6	I	3	472.349346	+0.1215402	472.349346	
	654.454874		682.449788	−0.0287679	682.449788	7	I	2	359.265282	+0.101112	359.265282	
	753.523288		781.518202	+0.150682	781.518202	8	V	1	246.181218	+0.0085097	246.181218	
						9	K	0	147.112804	−0.0494955	147.112804	

Scan number	15914	Raw file	20080623_Orbi5_SZ_Matrigel_12h_InGel_05
Method	ITMS; CID	Genenames	ASB9



precursor information

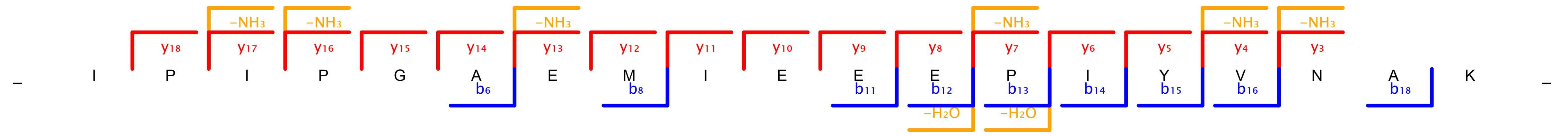
Mass:	2189.22114
m/z:	730.74766
Charge:	3+
Retentiontime:	112.613190246582
Score:	235.8828
Mass Error [ppm]:	0.138
PEP:	5.9499E-82
Precursor Type:	MULTI

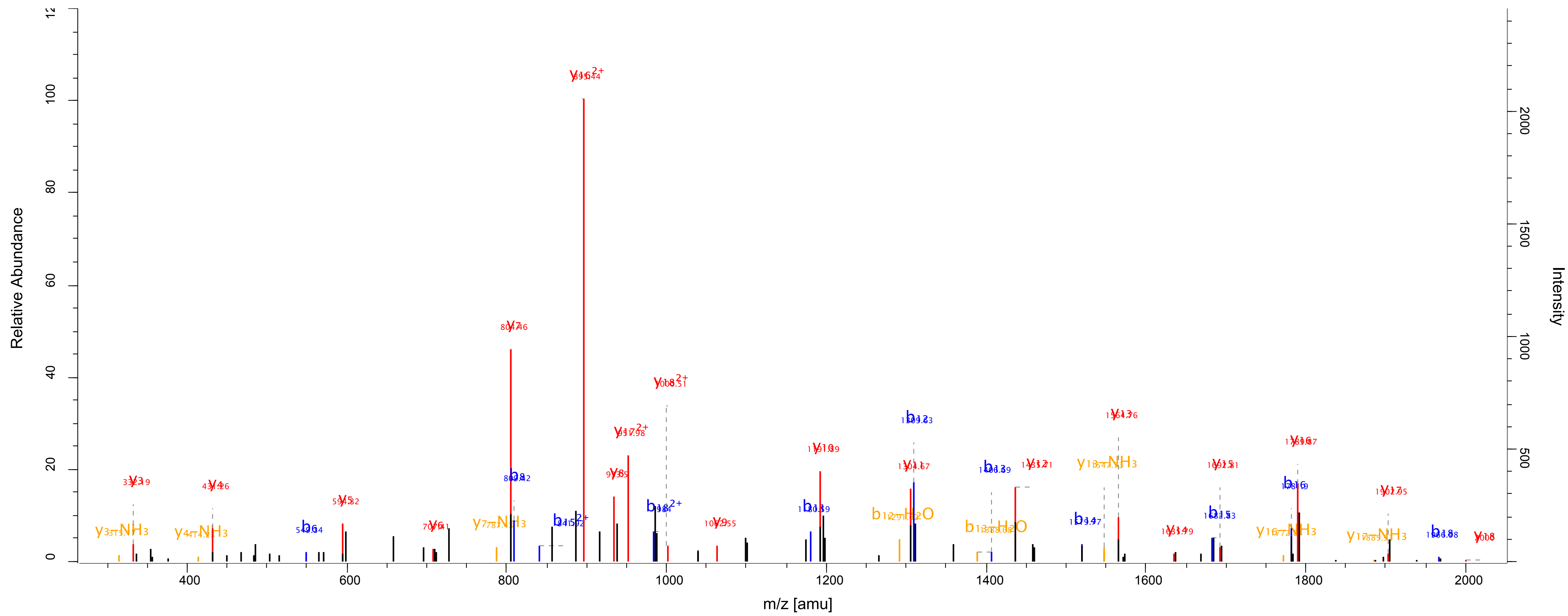
general information

Annotation:	15 of 19
AminoAcids Coverage:	79 %
Intensity Coverage:	84 %
Peak Coverage:	44 %
Protein Localisation:	234 ... 252

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	157.10838749		157.10838749	1	R	18				
	254.16115135	+0.0913206	254.16115135	2	P	17	2034.1270043		2034.1270043	
	353.22956526		353.22956526	3	V	16	1937.0742404		1937.0742404	
	482.27215836		482.27215836	4	E	15	1838.0058265		1838.0058265	
	595.35622234	+0.0058992	595.35622234	5	I	14	1708.9632334		1708.9632334	
+0.185716	347.71595636	+0.0511328	694.42463626	6	V	13	1595.8791694		1595.8791694	
+0.2110919	396.24233829		791.47740011	7	P	12	1496.8107555	+0.0004017	748.90901598	+0.2094533
	888.53016396		888.53016396	8	P	11	1399.7579916	+0.0149576	1399.7579916	
+0.0490335	509.29001676	+0.0430266	1017.5727571	9	E	10	1302.7052278		1302.7052278	
+0.115783	552.80603097	-0.001514	1104.6047855	10	S	9	1173.6626347	+0.0741817	587.33495558	+0.1499687
+0.0777434	601.33241289		1201.6575493	11	P	8	1086.6306063	+0.0186857	543.81894138	+0.2270181
+0.0305234	657.87444488	+0.2724248	1314.7416133	12	I	7	989.57784243	+0.0960467	495.29255945	+0.010236
+0.1909826	693.39300178	-0.0577798	1385.7787271	13	A	6	876.49377845	-0.0163004	876.49377845	
+0.2836421	757.42229053		1513.8373046	14	Q	5	805.45666467	+0.0869755	805.45666467	
+0.2410608	813.96432252		1626.9213686	15	I	4	677.39808715	+0.1449426	677.39808715	
+0.1803646	887.49852948		1773.9897825	16	F	3	564.31402317	+0.0208767	564.31402317	
+0.1952173	944.04056147		1887.0738465	17	I	2	417.24560926	+0.1091881	417.24560926	
+0.1468212	1008.561858		2016.1164396	18	E	1	304.16154528	+0.1209254	304.16154528	
				19	R	0	175.11895218		175.11895218	

Scan number	15368	Raw file	20080623_Orbi5_SZ_Matrigel_12h_InGel_09
Method	ITMS; CID	Genenames	NFYA





precursor information

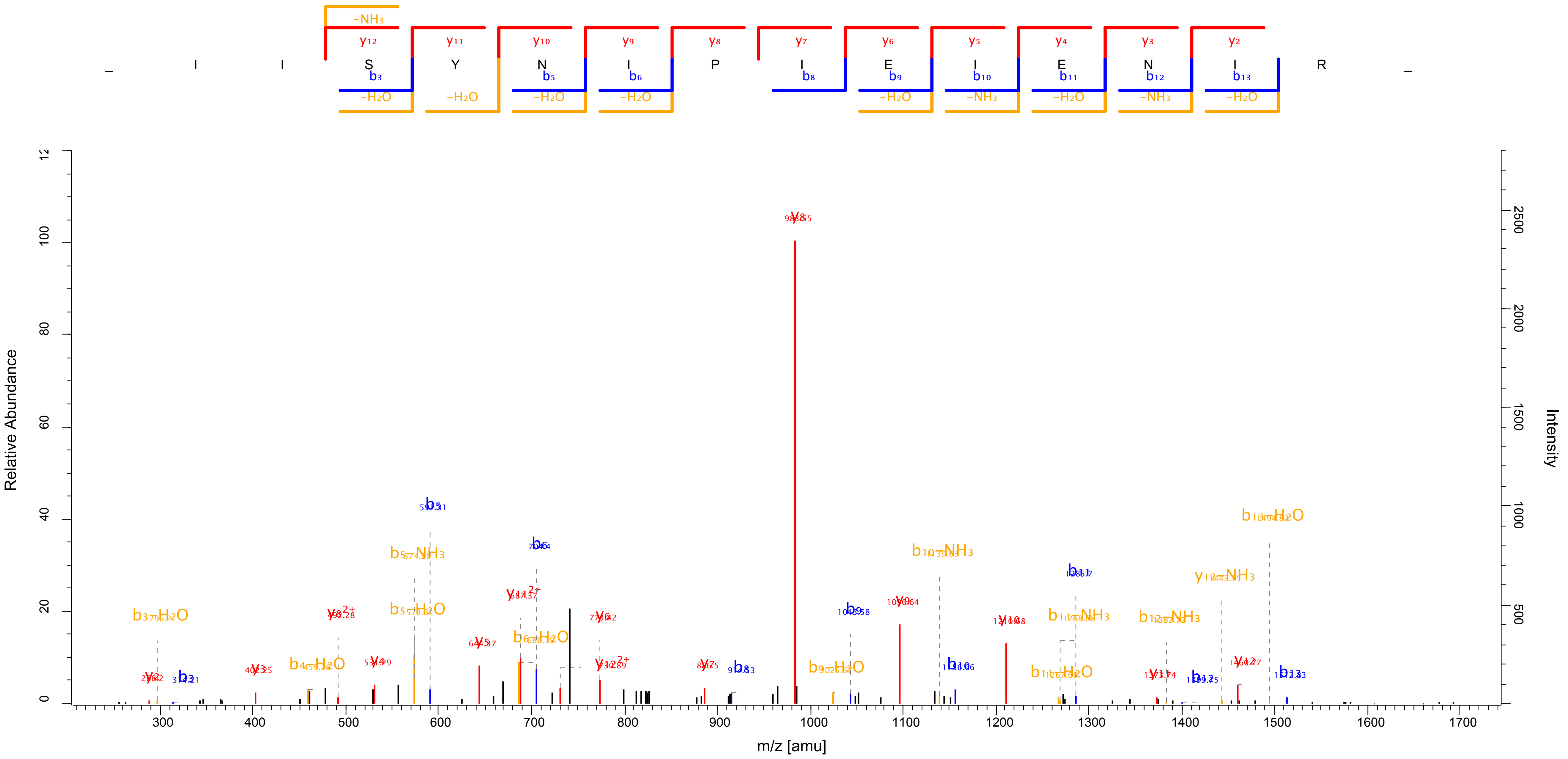
Mass:	2112.082
m/z:	1057.04828
Charge:	2+
Retentiontime:	104.035942077637
Score:	233.7795
Mass Error [ppm]:	0.33597
PEP:	1.6611E−81
Precursor Type:	MULTI

general information

Annotation:	17 of 19
AminoAcids Coverage:	89 %
Intensity Coverage:	61 %
Peak Coverage:	39 %
Protein Localisation:	252 ... 270

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045		114.09134045	1	I	18				
	211.1441043		211.1441043	2	P	17	2000.0045059	−0.0980117	1000.5058912	+0.3682543
	324.22816828		324.22816828	3	I	16	1902.951742	−0.1477869	951.97950924	+0.264021
	421.28093213		421.28093213	4	P	15	1789.867678	−0.029055	895.43747725	+0.2402571
	478.30239586		478.30239586	5	G	14	1692.8149142	−0.0254855	1692.8149142	
	549.33950964	−0.02408	549.33950964	6	A	13	1635.7934505	−0.0858089	1635.7934505	
	678.38210274		678.38210274	7	E	12	1564.7563367	+0.0147815	1564.7563367	
	809.42258735	−0.0003461	809.42258735	8	M	11	1435.7137436	+0.0759293	1435.7137436	
	922.50665133		922.50665133	9	I	10	1304.673259	−0.0343429	1304.673259	
	1051.5492444		1051.5492444	10	E	9	1191.589195	+0.032265	1191.589195	
	1180.5918375	−0.0445963	1180.5918375	11	E	8	1062.5466019	+0.172026	1062.5466019	
	1309.6344306	−0.0340888	1309.6344306	12	E	7	933.50400879	+0.0363965	933.50400879	
	1406.6871945	+0.2207645	1406.6871945	13	P	6	804.46141569	+0.0351663	804.46141569	
	1519.7712584	+0.0163392	1519.7712584	14	I	5	707.40865184	+0.0802398	707.40865184	
−0.3981046	841.92093173	+0.0006181	1682.834587	15	Y	4	594.32458786	+0.0582246	594.32458786	
	1781.9030009	−0.0178691	1781.9030009	16	V	3	431.26125932	+0.0143144	431.26125932	
	1895.9459283		1895.9459283	17	N	2	332.19284541	+0.085597	332.19284541	
+0.3531073	983.9951593	+0.1397606	1966.9830421	18	A	1	218.14991796		218.14991796	
				19	K	0	147.11280417		147.11280417	

Scan number	15797	Raw file	20080623_Orbi5_SZ_Matrigel_12h_InGel_10
Method	ITMS; CID	Genenames	CHKA



precursor information

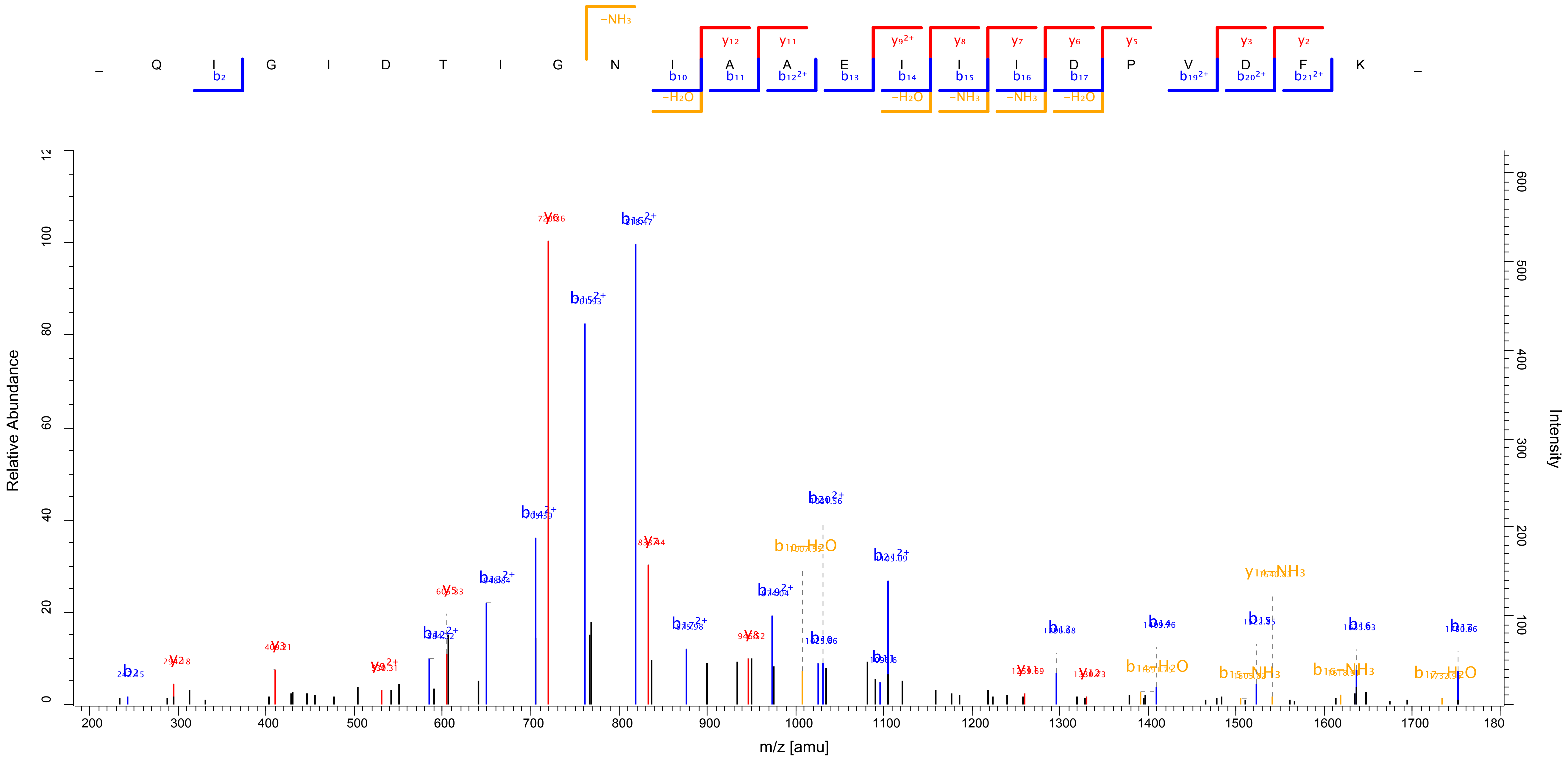
Mass:	1685.93632
m/z:	843.97544
Charge:	2+
Retentiontime:	107.907760620117
Score:	224.4317
Mass Error [ppm]:	0.65266
PEP:	2.5613E-37
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverage:	79 %
Intensity Coverage:	69 %
Peak Coverage:	40 %
Protein Localisation:	277 ... 290

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.091340447	1	I	13				
	227.175404427	2	I	12	1573.85843397		1573.85843397	
+0.0258435	314.207432837	3	S	11	1460.77436999	−0.0423143	730.890823228	+0.0898286
	477.270761376	4	Y	10	1373.74234158	−0.1335769	687.374809023	+0.0654376
+0.0238966	591.313688823	5	N	9	1210.679013041	−0.0181244	1210.679013041	
+0.0633068	704.397752803	6	I	8	1096.636085594	+0.0683822	1096.636085594	
	801.450516655	7	P	7	983.552021614	+0.0160936	492.27964904	+0.0248554
−0.0658306	914.534580636	8	I	6	886.499257762	−0.1816918	886.499257762	
−0.1238046	1043.577173732	9	E	5	773.415193781	−0.0036948	773.415193781	
−0.1487865	1156.661237712	10	I	4	644.372600685	+0.0813178	644.372600685	
−0.0400124	1285.703830808	11	E	3	531.288536705	+0.0774911	531.288536705	
+0.0492623	1399.746758256	12	N	2	402.245943609	+0.1607947	402.245943609	
−0.0523799	1512.830822236	13	I	1	288.203016161	−0.0042857	288.203016161	
		14	R	0	175.118952181		175.118952181	

Scan number	19352	Raw file	20080623_Orbi5_SZ_Matrigel_12h_InGel_18
Method	ITMS; CID	Genenames	ARID2



precursor information

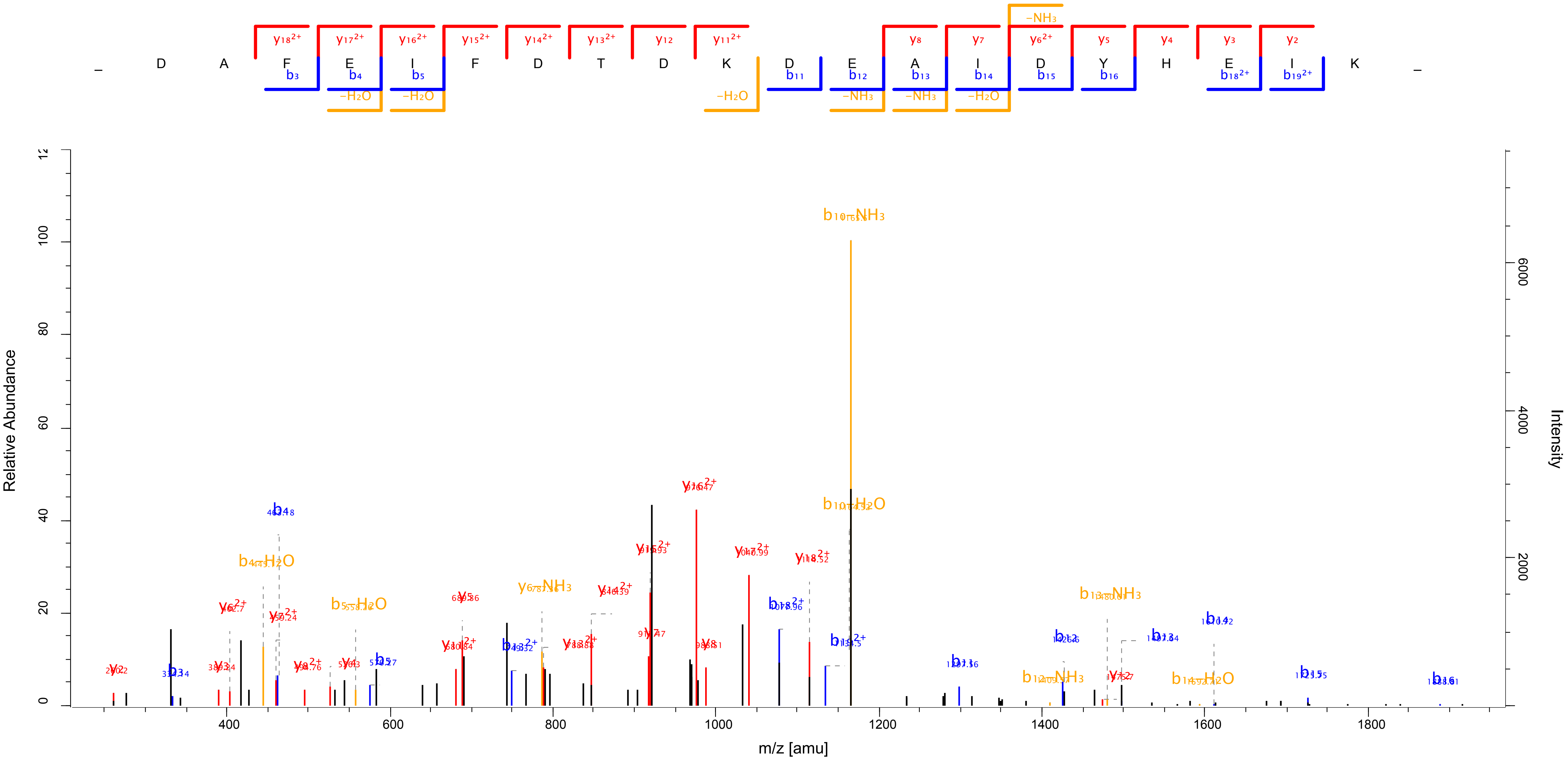
Mass:	2354.27211
m/z:	785.76465
Charge:	3+
Retentiontime:	125.405151367188
Score:	170.4952
Mass Error [ppm]:	−0.51537
PEP:	6.943E−33
Precursor Type:	MULTI

general information

Annotation:	14 of 22
AminoAcids Coverage:	64 %
Intensity Coverage:	71 %
Peak Coverage:	37 %
Protein Localisation:	329 ... 350

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.06585398		129.06585398	1	Q	21				
	242.14991796	+0.0659481	242.14991796	2	I	20	2227.2220269		2227.2220269	
	299.17138168		299.17138168	3	G	19	2114.1379629		2114.1379629	
	412.25544566		412.25544566	4	I	18	2057.1164992		2057.1164992	
	527.28238869		527.28238869	5	D	17	1944.0324352		1944.0324352	
	628.33006717		628.33006717	6	T	16	1829.0054921		1829.0054921	
	741.41413115		741.41413115	7	I	15	1727.9578137		1727.9578137	
	798.43559487		798.43559487	8	G	14	1614.8737497		1614.8737497	
	912.47852232		912.47852232	9	N	13	1557.852286		1557.852286	
	1025.5625863	−0.1331429	1025.5625863	10	I	12	1443.8093585		1443.8093585	
	1096.5997001	−0.0999442	1096.5997001	11	A	11	1330.7252945	+0.1300521	1330.7252945	
+0.0799934	584.32204517		1167.6368139	12	A	10	1259.6881807	+0.1909696	1259.6881807	
+0.0856134	648.84334172	+0.0675413	1296.679407	13	E	9	1188.651067		1188.651067	
+0.1248192	705.38537371	−0.1320012	1409.763471	14	I	8	1059.6084739		530.30787516	+0.1774764
+0.099877	761.9274057	−0.2128914	1522.8475349	15	I	7	946.52440988	+0.2244305	946.52440988	
+0.141097	818.46943769	+0.0447194	1635.9315989	16	I	6	833.4403459	−0.0086442	833.4403459	
+0.1304331	875.98290921	−0.033371	1750.9585419	17	D	5	720.35628192	+0.1147874	720.35628192	
	1848.0113058		1848.0113058	18	P	4	605.32933889	−0.3446587	605.32933889	
+0.0919389	974.04349809		1947.0797197	19	V	3	508.27657504		508.27657504	
+0.1601935	1031.5569696		2062.1066627	20	D	2	409.20816112	+0.1490777	409.20816112	
−0.0941063	1105.0911766		2209.1750767	21	F	1	294.18121809	+0.0472975	294.18121809	
				22	K	0	147.11280417		147.11280417	

Scan number	14132	Raw file	20080623_Orbi6_SZ_Exp2_Susp_InGel_02
Method	ITMS; CID	Genenames	CETN3



precursor information

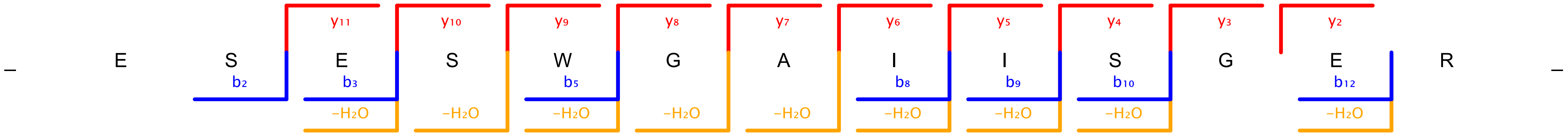
Mass:	2413.09714
m/z:	805.37299
Charge:	3+
Retentiontime:	93.7374877929688
Score:	185.1434
Mass Error [ppm]:	0.41094
PEP:	4.6274E−41
Precursor Type:	MULTI

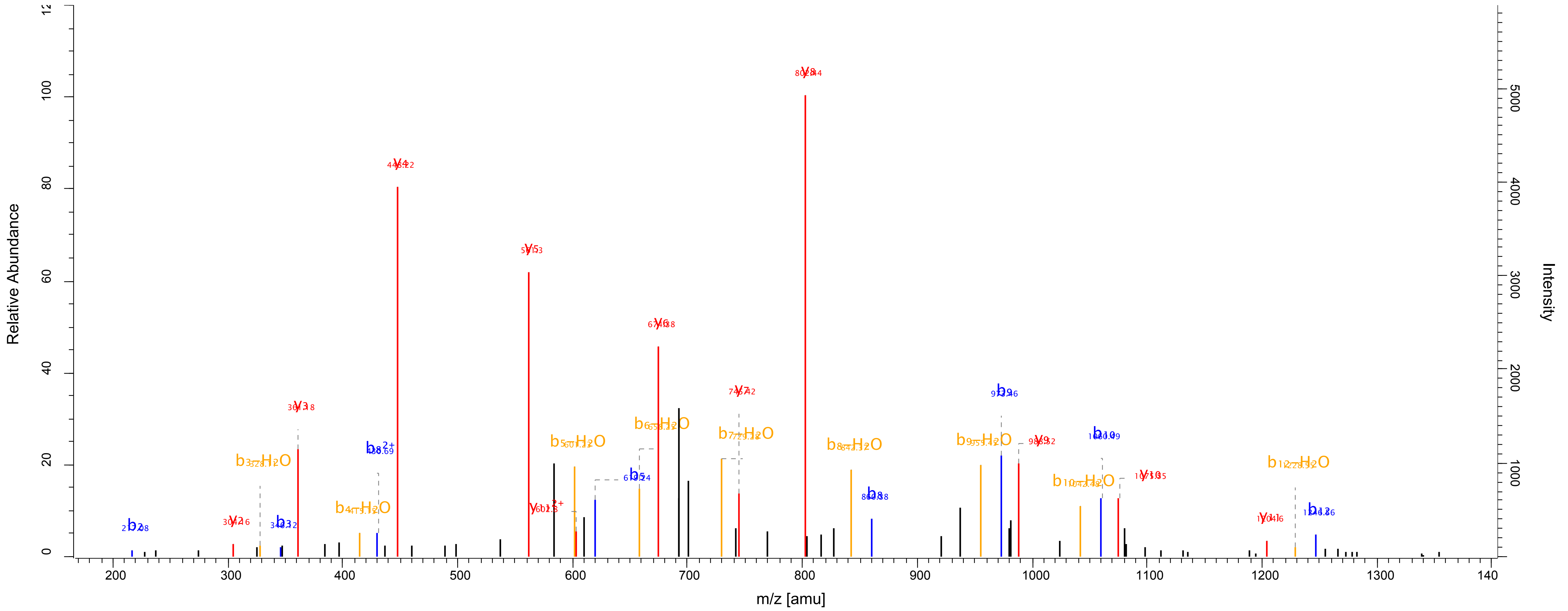
general information

Annotation:	17 of 20
AminoAcids Coverage:	85 %
Intensity Coverage:	55 %
Peak Coverage:	40 %
Protein Localisation:	32 ... 51

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342195		116.0342195	1	D	19				
	187.07133329		187.07133329	2	A	18	2299.0764848		2299.0764848	
	334.1397472	−0.0315319	334.1397472	3	F	17	2228.039371		1114.5233238	+0.0914223
	463.1823403	−0.228666	463.1823403	4	E	16	2080.9709571		1040.9891168	+0.3752631
	576.26640428	−0.1975566	576.26640428	5	I	15	1951.928364		976.46782025	+0.2004537
	723.3348182		723.3348182	6	F	14	1838.8443		919.92578826	−0.02082
	838.36176123		838.36176123	7	D	13	1691.7758861		846.3915813	+0.0544636
	939.4094397		939.4094397	8	T	12	1576.7489431		788.87810978	−0.3010224
	1054.4363827		1054.4363827	9	D	11	1475.7012646	−0.4621289	1475.7012646	
	1182.5313458		1182.5313458	10	K	10	1360.6743216		680.84079903	−0.11326
	1297.5582888	−0.0838015	1297.5582888	11	D	9	1232.5793586		1232.5793586	
	1426.6008819	−0.3014434	1426.6008819	12	E	8	1117.5524155		1117.5524155	
−0.0078778	749.32263607	−0.110774	1497.6379957	13	A	7	988.50982245	−0.134029	494.75854946	+0.297847
	1610.7220596	−0.0649552	1610.7220596	14	I	6	917.47270866	−0.167716	459.23999256	−0.0309472
	1725.7490027	−0.2679236	1725.7490027	15	D	5	804.38864468		402.69796057	−0.0226676
	1888.8123312	+0.0176248	1888.8123312	16	Y	4	689.36170165	+0.0273364	689.36170165	
	2025.8712431		2025.8712431	17	H	3	526.29837311	+0.099332	526.29837311	
−0.1130221	1077.9605563		2154.9138362	18	E	2	389.23946125	+0.120402	389.23946125	
−0.198145	1134.5025883		2267.9979002	19	I	1	260.19686815	−0.130584	260.19686815	
				20	K	0	147.11280417		147.11280417	

Scan number	12373	Raw file	20080623_Orbi6_SZ_Exp2_Susp_InGel_05
Method	ITMS; CID	Genenames	SLC39A13





precursor information

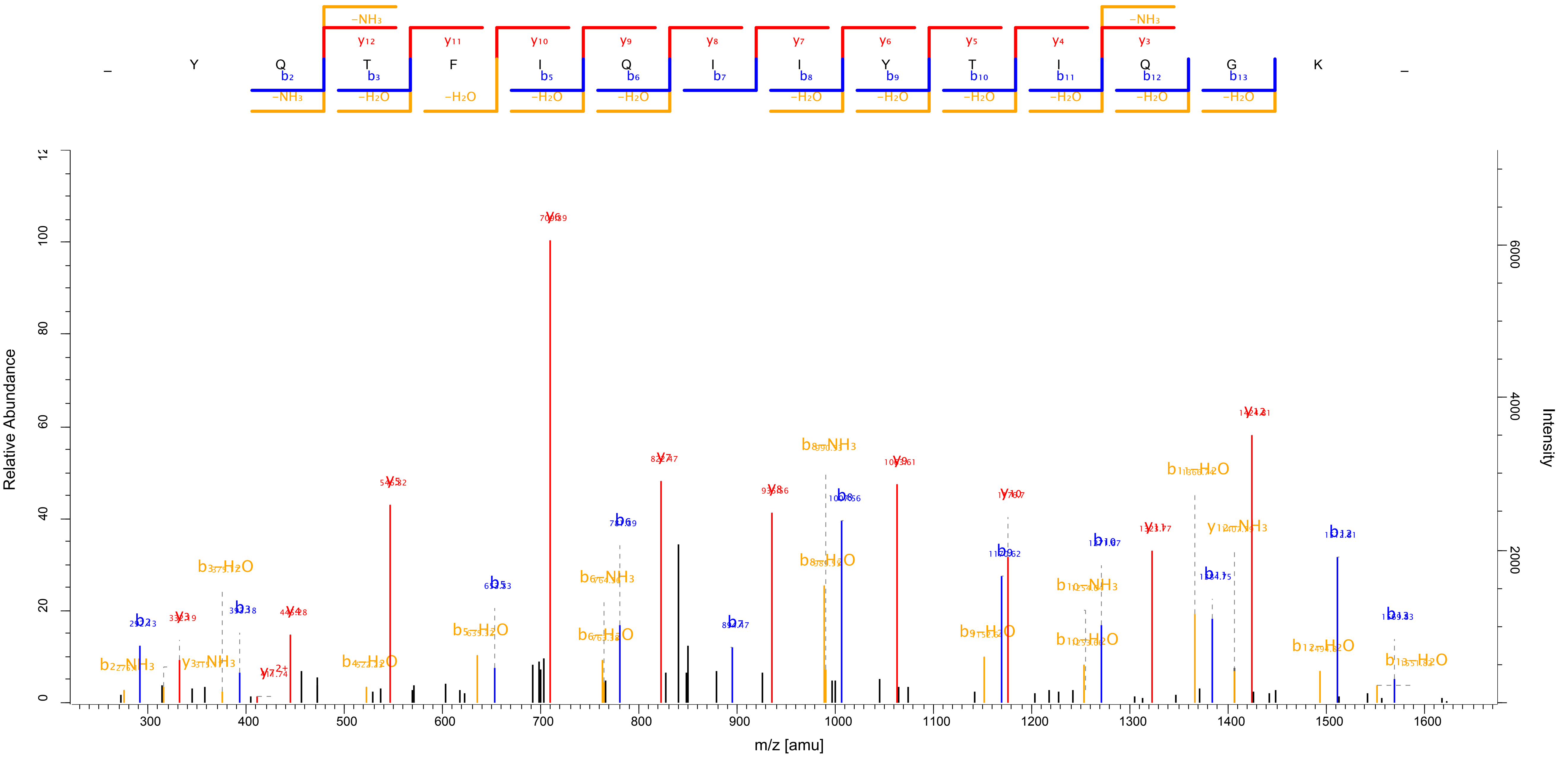
Mass:	1419.66315
m/z:	710.83885
Charge:	2+
Retentiontime:	83.1333847045898
Score:	188.0599
Mass Error [ppm]:	0.091694
PEP:	4.8798E-09
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverage:	85 %
Intensity Coverage:	73 %
Peak Coverage:	39 %
Protein Localisation:	52 ... 64

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.04986956		130.04986956	1	E	12				
	217.08189797	+0.0632589	217.08189797	2	S	11	1291.6277058		1291.6277058	
	346.12449107	+0.1775719	346.12449107	3	E	10	1204.5956773	−0.0790758	602.8014769	−0.0144896
	433.15651948		433.15651948	4	S	9	1075.5530842	−0.1337727	1075.5530842	
	619.23583243	−0.2332079	619.23583243	5	W	8	988.52105584	−0.1564928	988.52105584	
	676.25729616		676.25729616	6	G	7	802.44174288	−0.1238108	802.44174288	
	747.29440994		747.29440994	7	A	6	745.42027916	−0.0132967	745.42027916	
−0.416569	430.6928752	−0.1676585	860.37847392	8	I	5	674.38316537	−0.0380726	674.38316537	
	973.4625379	−0.2142469	973.4625379	9	I	4	561.29910139	−0.0094896	561.29910139	
	1060.4945663	−0.224913	1060.4945663	10	S	3	448.21503741	−0.047618	448.21503741	
	1117.51603		1117.51603	11	G	2	361.183009	+0.0308582	361.183009	
	1246.5586231	−0.4776905	1246.5586231	12	E	1	304.16154528	+0.4527736	304.16154528	
				13	R	0	175.11895218		175.11895218	

Scan number	18536	Raw file	20080623_Orbi6_SZ_Exp2_Susp_InGel_07
Method	ITMS; CID	Genenames	ZWINT



precursor
information

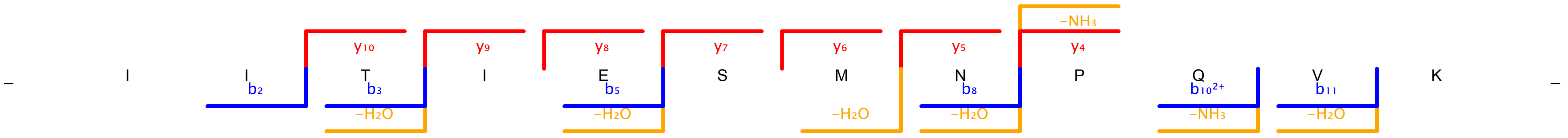
Mass:	1714.92969
m/z:	858.47212
Charge:	2+
Retentiontime:	118.941192626953
Score:	279.7686
Mass Error [ppm]:	0.16723
PEP:	1.3065E-127
Precursor Type:	MULTI

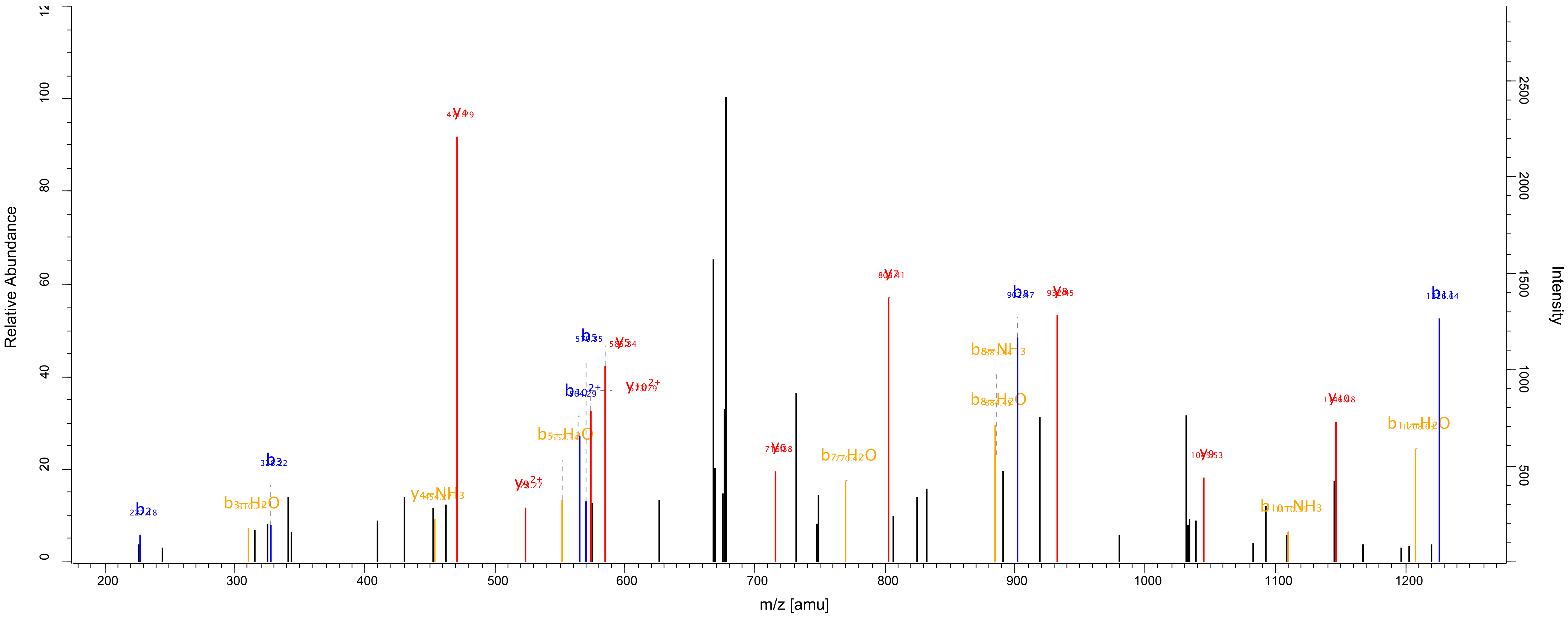
general
information

Annotation:	12 of 14
AminoAcids Coverage:	86 %
Intensity Coverage:	77 %
Peak Coverage:	44 %
Protein Localisation:	209 ... 222

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	164.070605005	1	Y	13				
−0.0502641	292.129182516	2	Q	12	1552.873355753		1552.873355753	
+0.0611761	393.17686099	3	T	11	1424.814778241	−0.2046708	1424.814778241	
	540.245274907	4	F	10	1323.767099767	−0.2368263	1323.767099767	
−0.329522	653.329338887	5	I	9	1176.698685851	−0.1560833	1176.698685851	
−0.1759413	781.387916398	6	Q	8	1063.614621871	−0.2275369	1063.614621871	
+0.0955855	894.471980379	7	I	7	935.556044359	−0.1046283	935.556044359	
−0.2063739	1007.556044359	8	I	6	822.471980379	−0.1082108	411.739628423	−0.3460737
−0.2189823	1170.619372898	9	Y	5	709.387916398	−0.1153944	709.387916398	
−0.3551617	1271.667051372	10	T	4	546.32458786	+0.0059785	546.32458786	
−0.2428146	1384.751115352	11	I	3	445.276909386	−0.0301442	445.276909386	
−0.3685308	1512.809692863	12	Q	2	332.192845406	+0.0948133	332.192845406	
−0.2940472	1569.831156587	13	G	1	204.134267894		204.134267894	
		14	K	0	147.112804171		147.112804171	

Scan number	10055	Raw file	20080623_Orbi6_SZ_Exp2_Susp_InGel_10
Method	ITMS; CID	Genenames	GPT2





precursor information

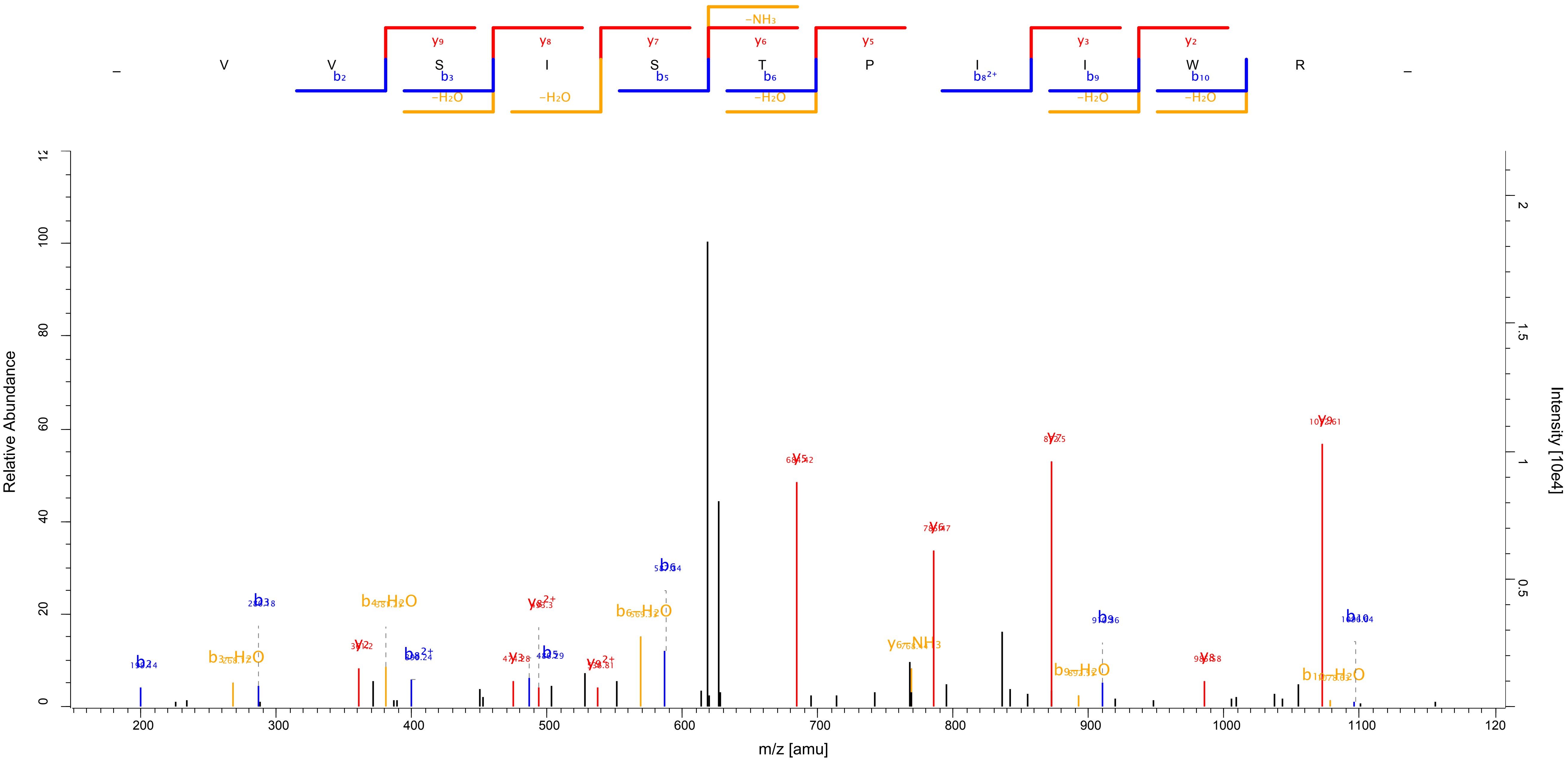
Mass:	1371.74299
m/z:	686.87877
Charge:	2+
Retentiontime:	71.7356491088867
Score:	136.0225
Mass Error [ppm]:	−0.1459
PEP:	0.0002594
Precursor Type:	ISO

general information

Annotation:	10 of 12
AminoAcids Coverage:	83 %
Intensity Coverage:	51 %
Peak Coverage:	38 %
Protein Localisation:	47 ... 58

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045		114.09134045	1	I	11				
	227.17540443	−0.1324052	227.17540443	2	I	10	1259.6663994		1259.6663994	
	328.2230829	+0.1058966	328.2230829	3	T	9	1146.5823355	−0.0945425	573.79480597	+0.029779
	441.30714688		441.30714688	4	I	8	1045.534657	−0.1489148	523.27096673	−0.0955517
	570.34973998	−0.0839319	570.34973998	5	E	7	932.45059301	−0.1307078	932.45059301	
	657.38176839		657.38176839	6	S	6	803.40799991	−0.1600141	803.40799991	
	788.42225299		788.42225299	7	M	5	716.3759715	−0.1700999	716.3759715	
	902.46518044	−0.2286082	902.46518044	8	N	4	585.3354869	−0.0160899	585.3354869	
	999.51794429		999.51794429	9	P	3	471.29255945	−0.1013363	471.29255945	
+0.4032913	564.29189914		1127.5765218	10	Q	2	374.2397956		374.2397956	
	1226.6449357	−0.2082902	1226.6449357	11	V	1	246.18121809		246.18121809	
				12	K	0	147.11280417		147.11280417	

Scan number	13124	Raw file	20080623_Orbi6_SZ_Exp2_Susp_InGel_10
Method	ITMS; CID	Genenames	TSPYL1



precursor information

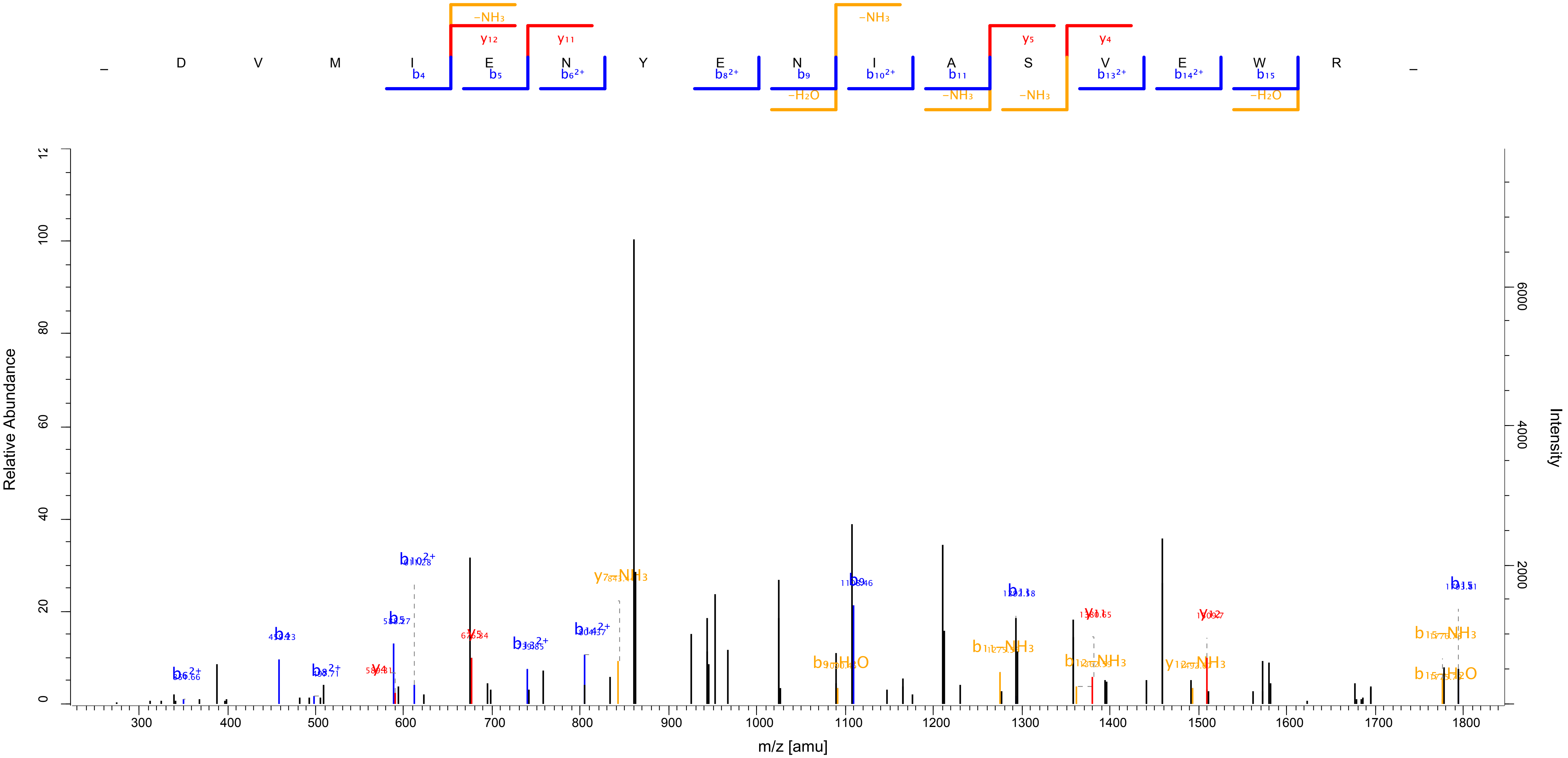
Mass:	1269.74421
m/z:	635.87938
Charge:	2+
Retentiontime:	88.3350677490234
Score:	152.5395
Mass Error [ppm]:	-0.23774
PEP:	1.577E-06
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverage:	82 %
Intensity Coverage:	54 %
Peak Coverage:	39 %
Protein Localisation:	348 ... 358

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.07569038		100.07569038	1	V	10				
	199.1441043	-0.073334	199.1441043	2	V	9	1171.6833701		1171.6833701	
	286.17613271	+0.0178065	286.17613271	3	S	8	1072.6149562	-0.1252101	536.81111634	+0.1004437
	399.26019669		399.26019669	4	I	7	985.58292781	+0.043537	493.29510214	-0.148984
	486.2922251	-0.0464976	486.2922251	5	S	6	872.49886383	+0.089332	872.49886383	
	587.33990357	-0.2177722	587.33990357	6	T	5	785.46683542	-0.1469502	785.46683542	
	684.39266743		684.39266743	7	P	4	684.41915695	-0.0120525	684.41915695	
-0.2139888	399.24200394		797.47673141	8	I	3	587.3663931		587.3663931	
	910.56079539	-0.2304731	910.56079539	9	I	2	474.28232911	+0.04427	474.28232911	
	1096.6401083	-0.2286093	1096.6401083	10	W	1	361.19826513	+0.128395	361.19826513	
				11	R	0	175.11895218		175.11895218	

Scan number	16262	Raw file	20080623_Orbi6_SZ_Exp2_Susp_InGel_15
Method	ITMS; CID	Genenames	ZNF778



precursor information

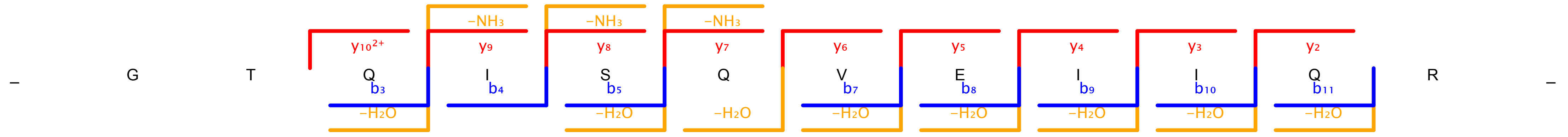
Mass:	1966.90972
m/z:	984.46214
Charge:	2+
Retentiontime:	102.448577880859
Score:	99.94125
Mass Error [ppm]:	0.12224
PEP:	0.00035152
Precursor Type:	MULTI

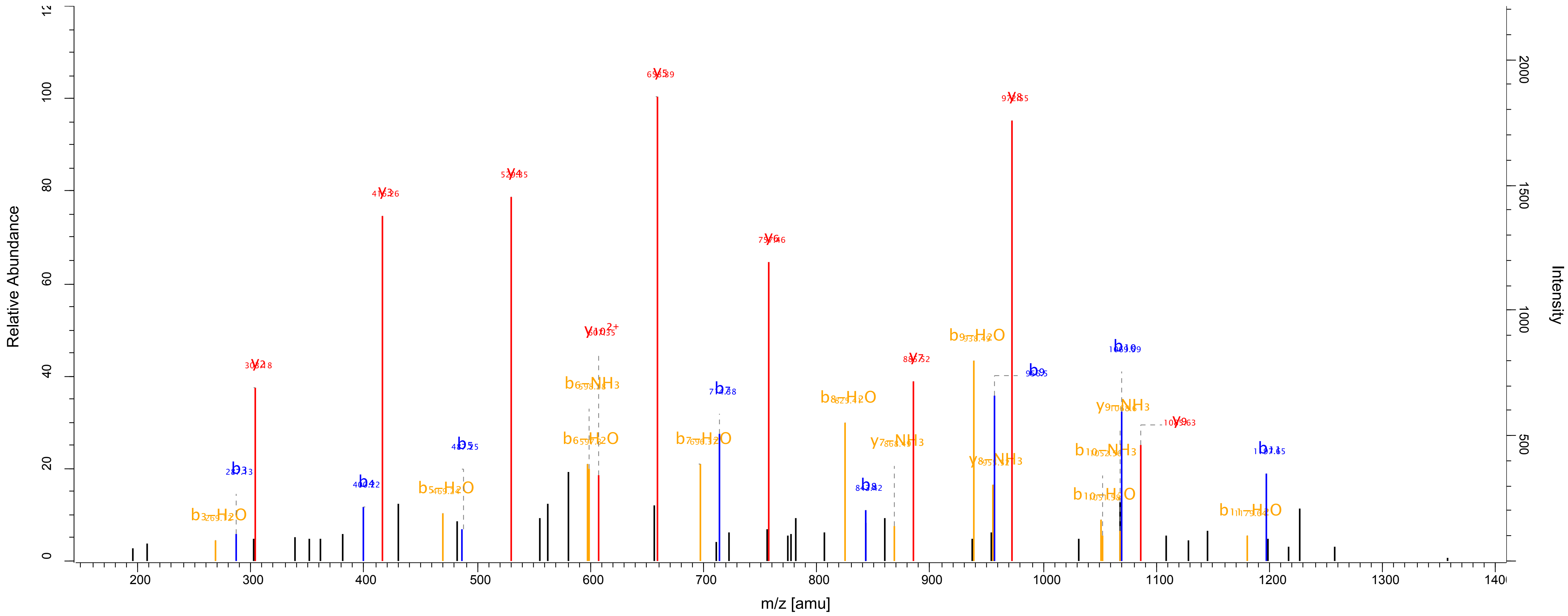
general information

Annotation:	11 of 16
AminoAcids Coverage:	69 %
Intensity Coverage:	17 %
Peak Coverage:	23 %
Protein Localisation:	69 ... 84

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	116.034219499		116.034219499	1	D	15		
	215.102633415		215.102633415	2	V	14	1852.889810453	
	346.143118021		346.143118021	3	M	13	1753.821396537	
	459.227182001	−0.0206696	459.227182001	4	I	12	1622.780911931	
	588.269775098	+0.0781253	588.269775098	5	E	11	1509.69684795	−0.3216038
−0.4032146	351.659989506		702.312702545	6	N	10	1380.654254854	−0.2699775
	865.376031083		865.376031083	7	Y	9	1266.611327407	
+0.4629225	497.712950323		994.418624179	8	E	8	1103.547998868	
	1108.461551626	−0.0855751	1108.461551626	9	N	7	974.505405772	
+0.1096624	611.276446037		1221.545615607	10	I	6	860.462478325	
	1292.582729395	−0.174038	1292.582729395	11	A	5	747.378414345	
	1379.614757805		1379.614757805	12	S	4	676.341300557	−0.1057049
+0.4085601	739.845224094		1478.683171721	13	V	3	589.309272147	+0.0457083
+0.0574296	804.366520642		1607.725764817	14	E	2	490.240858231	
	1793.80507777	−0.2892086	1793.80507777	15	W	1	361.198265134	
				16	R	0	175.118952181	

Scan number	10424	Raw file	20080627_Orbi4_SaZa_ADH_Matrigel_Exp2_BSA_InGel_01
Method	ITMS; CID	Genenames	ID3





precursor information

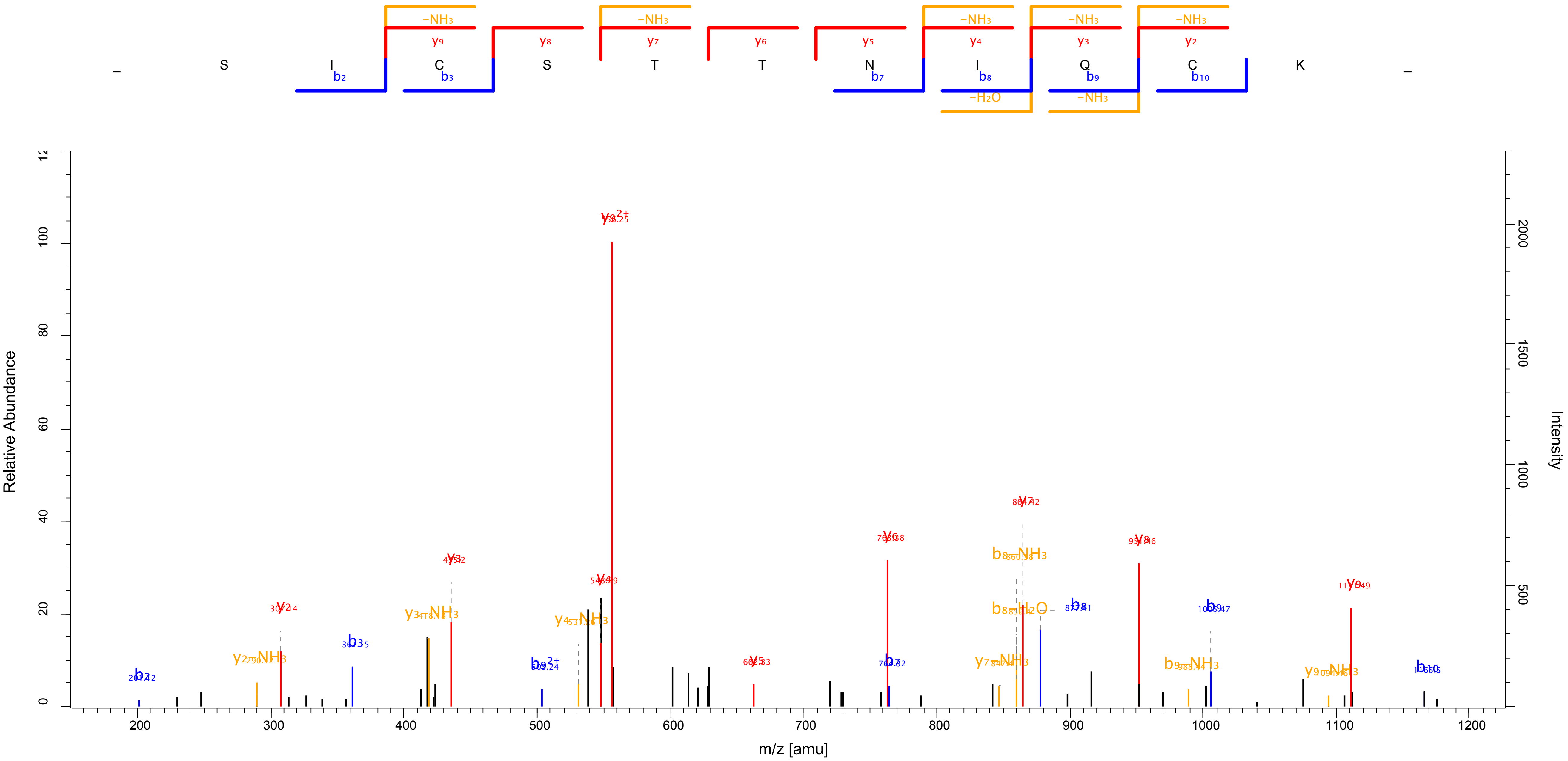
Mass:	1370.75118
m/z:	686.38286
Charge:	2+
Retentiontime:	80.9559020996094
Score:	192.682
Mass Error [ppm]:	-0.43866
PEP:	3.09635E-07
Precursor Type:	ISO

general information

Annotation:	9 of 12
AminoAcids Coverage:	75 %
Intensity Coverage:	79 %
Peak Coverage:	47 %
Protein Localisation:	61 ... 72

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019	1	G	11				
	159.076418664	2	T	10	1314.737590553		1314.737590553	
−0.0246446	287.134996176	3	Q	9	1213.689912079		607.348594273	+0.2079853
−0.1737721	400.219060156	4	I	8	1085.631334567	−0.0668814	1085.631334567	
−0.1573996	487.251088566	5	S	7	972.547270587	−0.0033863	972.547270587	
	615.309666077	6	Q	6	885.515242177	+0.1073164	885.515242177	
+0.0147423	714.378079994	7	V	5	757.456664666	+0.1655888	757.456664666	
+0.0992854	843.42067309	8	E	4	658.388250749	+0.1743103	658.388250749	
+0.2564324	956.50473707	9	I	3	529.345657653	+0.0979459	529.345657653	
+0.0933279	1069.588801051	10	I	2	416.261593673	+0.1626617	416.261593673	
−0.0267731	1197.647378562	11	Q	1	303.177529692	+0.10488	303.177529692	
		12	R	0	175.118952181		175.118952181	

Scan number	5111	Raw file	20080627_Orbi4_SaZa_ADH_Matrigel_Exp2_BSA_InGel_01
Method	ITMS; CID	Genenames	RNASE4



precursor information

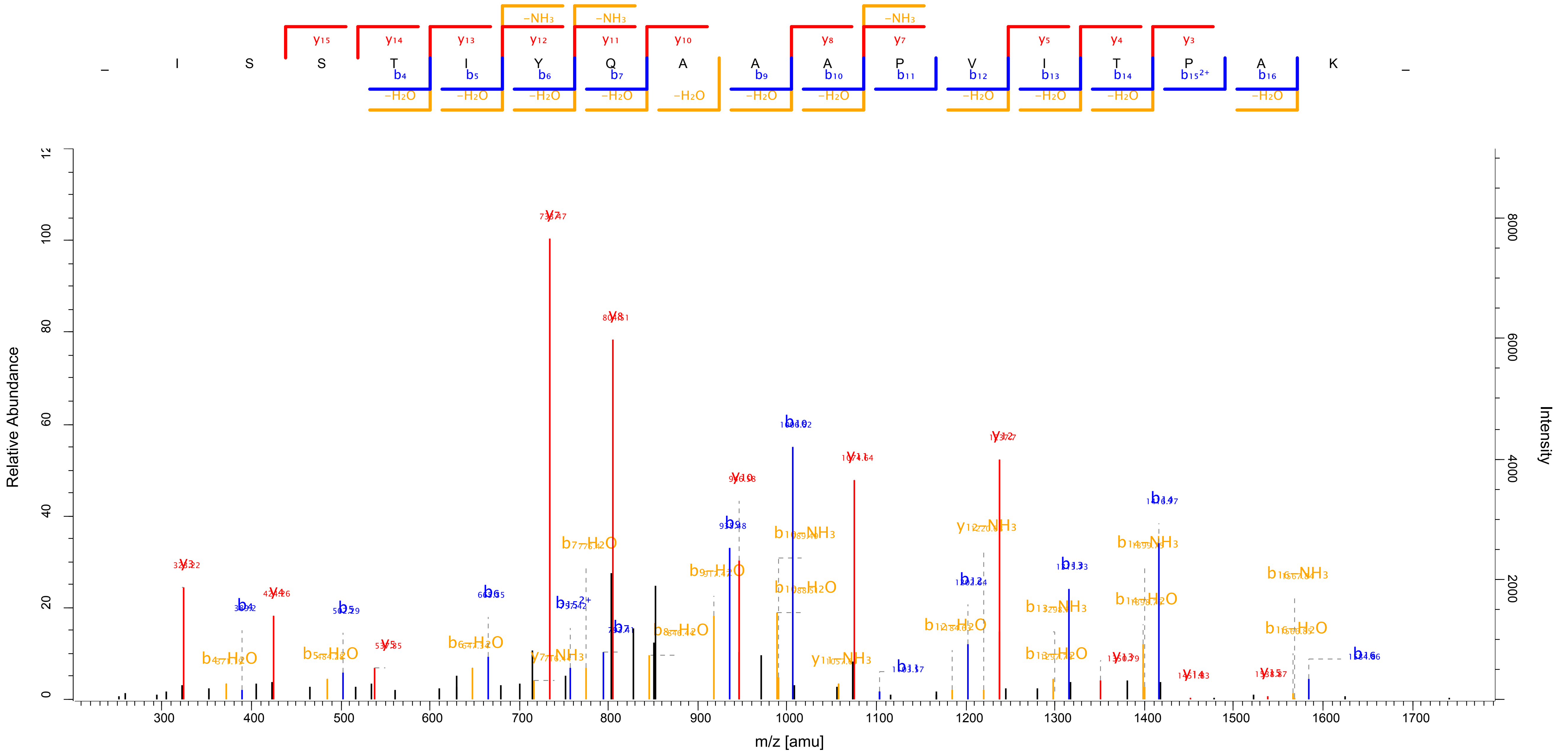
Mass:	1310.59609
m/z:	656.30532
Charge:	2+
Retentiontime:	51.9492416381836
Score:	164.3349
Mass Error [ppm]:	0.16954
PEP:	0.00010507
Precursor Type:	ISO

general information

Annotation:	9 of 11
AminoAcids Coverage:	82 %
Intensity Coverage:	65 %
Peak Coverage:	39 %
Protein Localisation:	83 ... 93

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876		88.039304876	1	S	10				
	201.12336886	−0.0556809	201.12336886	2	I	9	1224.5711189		1224.5711189	
	361.15401706	+0.0574087	361.15401706	3	C	8	1111.4870549	−0.011591	556.24716567	+0.0337792
	448.18604547		448.18604547	4	S	7	951.45640667	+0.0667867	951.45640667	
	549.23372394		549.23372394	5	T	6	864.42437826	+0.0885002	864.42437826	
	650.28140242		650.28140242	6	T	5	763.37669979	+0.0242402	763.37669979	
	764.32432986	+0.0526843	764.32432986	7	N	4	662.32902131	+0.0559274	662.32902131	
	877.40839384	+0.0002976	877.40839384	8	I	3	548.28609386	+0.1314476	548.28609386	
+0.1214576	503.23712391	+0.0053797	1005.4669714	9	Q	2	435.20202988	+0.0250209	435.20202988	
	1165.4976196	+0.0989381	1165.4976196	10	C	1	307.14345237	+0.0525925	307.14345237	
				11	K	0	147.11280417		147.11280417	

Scan number	11415	Raw file	20080705_Orbi6_SaZa_ADH_Exp_2_Matrigel_30h_InGel_01
Method	ITMS; CID	Genenames	KRTCAP2



precursor information

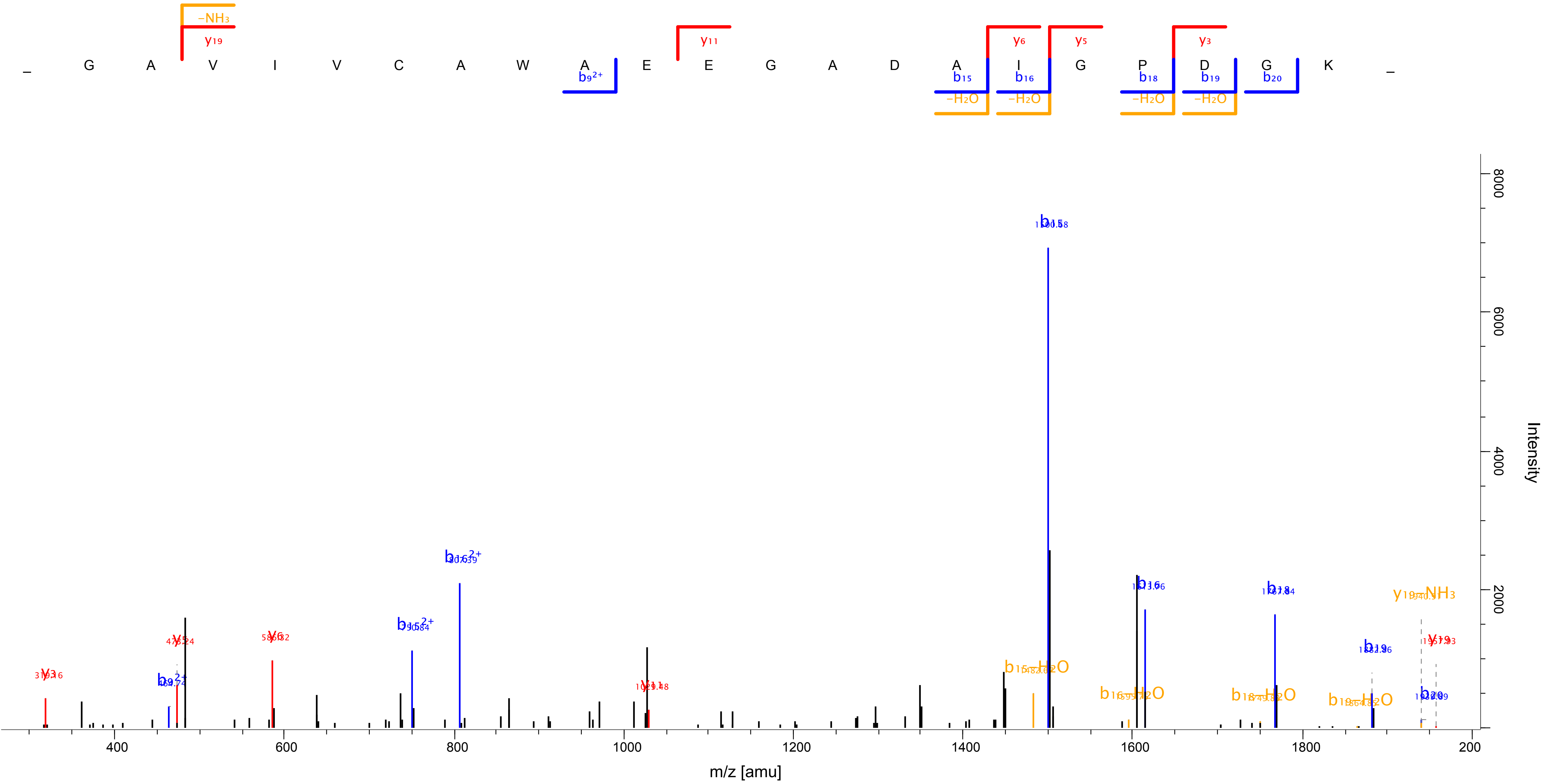
Mass:	1729.96154
m/z:	865.98805
Charge:	2+
Retentiontime:	82.4458465576172
Score:	258.4147
Mass Error [ppm]:	0.058472
PEP:	1.6418E−88
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverage:	82 %
Intensity Coverage:	76 %
Peak Coverage:	49 %
Protein Localisation:	137 ... 153

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	114.091340447		114.091340447	1	I	16		
	201.123368857		201.123368857	2	S	15	1625.898847534	
	288.155397267		288.155397267	3	S	14	1538.866819124	−0.0324685
	389.203075741	−0.0228084	389.203075741	4	T	13	1451.834790714	−0.1476569
	502.287139721	−0.0444639	502.287139721	5	I	12	1350.78711224	−0.0457792
	665.35046826	−0.0995527	665.35046826	6	Y	11	1237.703048259	−0.0279994
	793.409045771	−0.0667606	793.409045771	7	Q	10	1074.639719721	−0.0652568
	864.446159559		864.446159559	8	A	9	946.58114221	+0.0089457
	935.483273347	−0.2027558	935.483273347	9	A	8	875.544028422	
	1006.520387134	−0.1813368	1006.520387134	10	A	7	804.506914634	−0.0553765
	1103.573150986	+0.4604183	1103.573150986	11	P	6	733.469800846	−0.154127
	1202.641564903	−0.1869751	1202.641564903	12	V	5	636.417036994	
	1315.725628883	−0.2229433	1315.725628883	13	I	4	537.348623078	−0.0651148
	1416.773307357	−0.1860271	1416.773307357	14	T	3	424.264559098	+0.1258218
+0.039564	757.416673838		1513.826071209	15	P	2	323.216880624	+0.0206682
	1584.863184997	−0.1631118	1584.863184997	16	A	1	226.164116772	
				17	K	0	155.127002984	

Scan number 14809
Raw file 20080705_Orbi6_SaZa_ADH_Exp_2_Matrigel_30h_InGel_02
Method ITMS; CID
Genenames KHK



precursor information

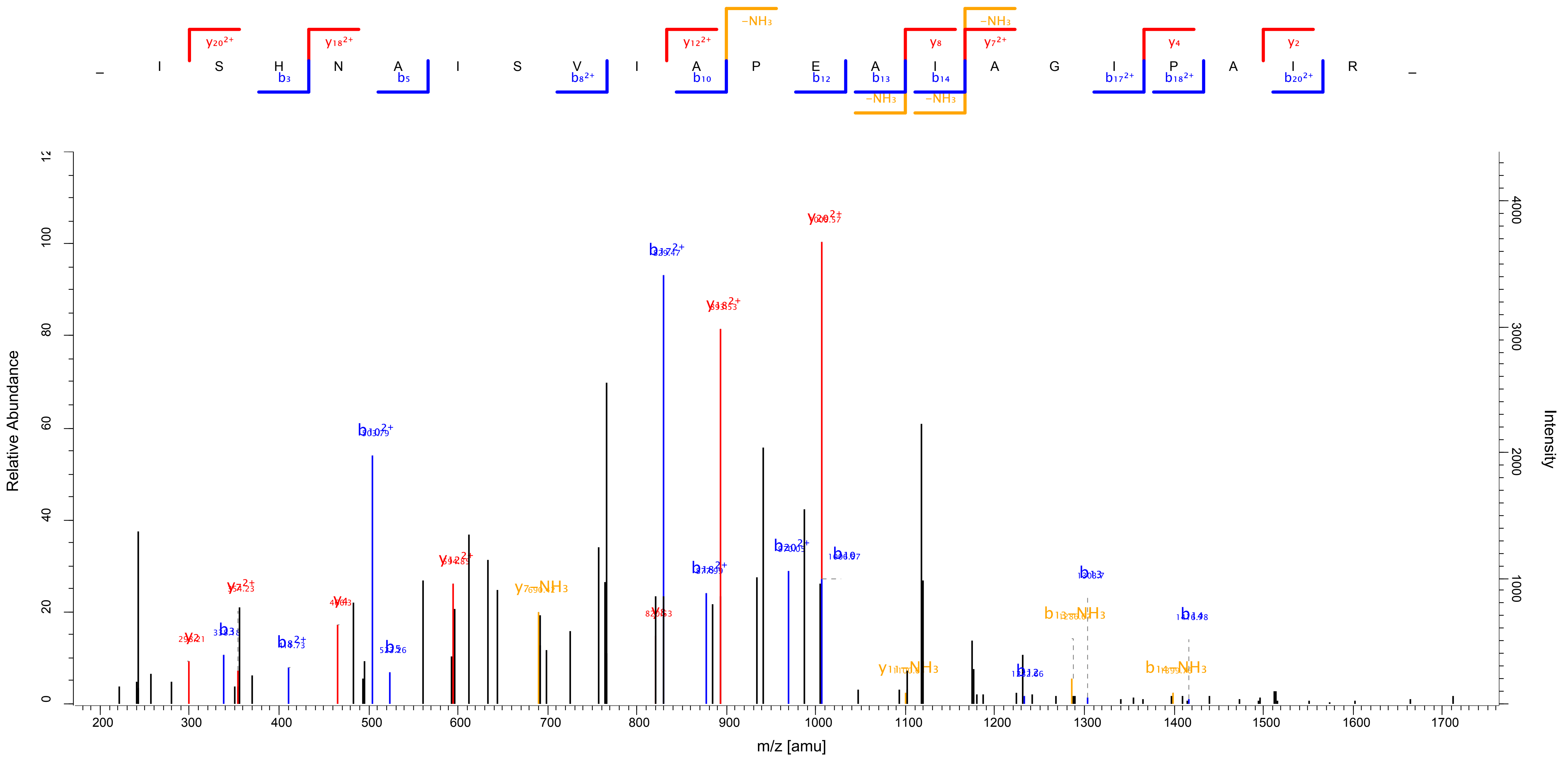
Mass:	2084.98436
m/z:	1043.49946
Charge:	2+
Retentiontime:	99.8215103149414
Score:	78.23442
Mass Error [ppm]:	0.31625
PEP:	0.00010578
Precursor Type:	MULTI

general information

Annotation:	9 of 21
AminoAcids Coverage:	43 %
Intensity Coverage:	43 %
Peak Coverage:	17 %
Protein Localisation:	218 ... 238

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	58.02874019		58.02874019	1	G	20		
	129.065853978		129.065853978	2	A	19	2028.969517337	
	228.134267894		228.134267894	3	V	18	1957.932403549	−0.0902405
	341.218331875		341.218331875	4	I	17	1858.863989633	
	440.286745791		440.286745791	5	V	16	1745.779925652	
	600.317393992		600.317393992	6	C	15	1646.711511736	
	671.35450778		671.35450778	7	A	14	1486.680863535	
	857.433820734		857.433820734	8	W	13	1415.643749747	
−0.4633487	464.739105494		928.470934521	9	A	12	1229.564436794	
	1057.513527617		1057.513527617	10	E	11	1158.527323006	
	1186.556120714		1186.556120714	11	E	10	1029.48472991	−0.0129282
	1243.577584437		1243.577584437	12	G	9	900.442136813	
	1314.614698225		1314.614698225	13	A	8	843.42067309	
	1429.641641257		1429.641641257	14	D	7	772.383559302	
+0.000246	750.843015756	−0.1811965	1500.678755045	15	A	6	657.35661627	
+0.0722276	807.385047746	−0.1647966	1613.762819025	16	I	5	586.319502482	−0.0433794
	1670.784282749		1670.784282749	17	G	4	473.235438502	−0.1845962
	1767.837046601	−0.1991071	1767.837046601	18	P	3	416.213974778	
	1882.863989633	−0.2388676	1882.863989633	19	D	2	319.161210926	−0.0508288
	1939.885453356	−0.2613078	1939.885453356	20	G	1	204.134267894	
				21	K	0	147.112804171	

Scan number	18704	Raw file	20080705_Orbi6_SaZa_ADH_Exp_2_Matrigel_30h_InGel_02
Method	ITMS; CID	Genenames	CHADL



precursor information

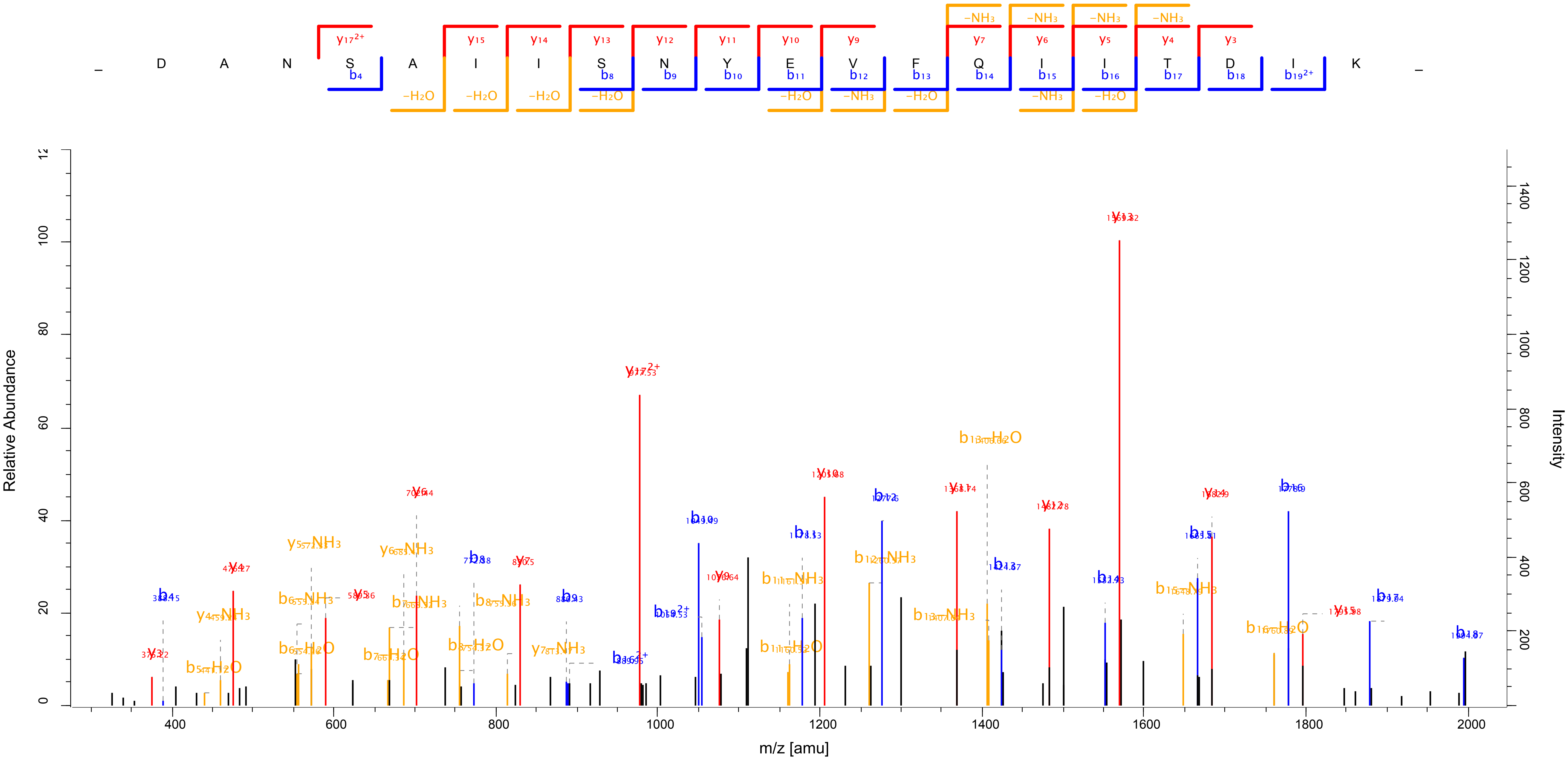
Mass:	2112.20576
m/z:	705.07586
Charge:	3+
Retentiontime:	122.002517700195
Score:	83.40437
Mass Error [ppm]:	0.1116
PEP:	6.6756E−05
Precursor Type:	MULTI

general information

Annotation:	14 of 21
AminoAcids Coverage:	67 %
Intensity Coverage:	38 %
Peak Coverage:	24 %
Protein Localisation:	189 ... 209

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045		114.09134045	1	I	20				
	201.12336886		201.12336886	2	S	19	2010.1370042		1005.5721403	+0.0319246
	338.18228072	−0.0016777	338.18228072	3	H	18	1923.1049758		1923.1049758	
	452.22520817		452.22520817	4	N	17	1786.0460639		893.52667019	+0.1447165
	523.26232195	−0.0700612	523.26232195	5	A	16	1672.0031365		1672.0031365	
	636.34638593		636.34638593	6	I	15	1600.9660227		1600.9660227	
	723.37841434		723.37841434	7	S	14	1487.8819587		1487.8819587	
−0.3780533	411.72705236		822.44682826	8	V	13	1400.8499303		1400.8499303	
	935.53089224		935.53089224	9	I	12	1301.7815164		1301.7815164	
−0.3321969	503.78764125	+0.0216546	1006.568006	10	A	11	1188.6974524		594.85236443	−0.4564294
	1103.6207699		1103.6207699	11	P	10	1117.6603386		1117.6603386	
	1232.663363	−0.180697	1232.663363	12	E	9	1020.6075748		1020.6075748	
	1303.7004768	+0.1680535	1303.7004768	13	A	8	891.56498166		891.56498166	
	1416.7845407	−0.2011667	1416.7845407	14	I	7	820.52786787	−0.3479973	820.52786787	
	1487.8216545		1487.8216545	15	A	6	707.44380389		354.22554018	+0.0214996
	1544.8431183		1544.8431183	16	G	5	636.4066901		636.4066901	
−0.1049857	829.46722935		1657.9271822	17	I	4	579.38522638		579.38522638	
−0.4680375	877.99361128		1754.9799461	18	P	3	466.3011624	−0.0932767	466.3011624	
	1826.0170599		1826.0170599	19	A	2	369.24839855		369.24839855	
+0.0886221	970.05420016		1939.1011239	20	I	1	298.21128476	+0.0745734	298.21128476	
				21	R	0	185.12722078		185.12722078	

Scan number	18935	Raw file	20080705_Orbi6_SaZa_ADH_Exp_2_Matrigel_30h_InGel_02
Method	ITMS; CID	Genenames	CRCP



precursor
information

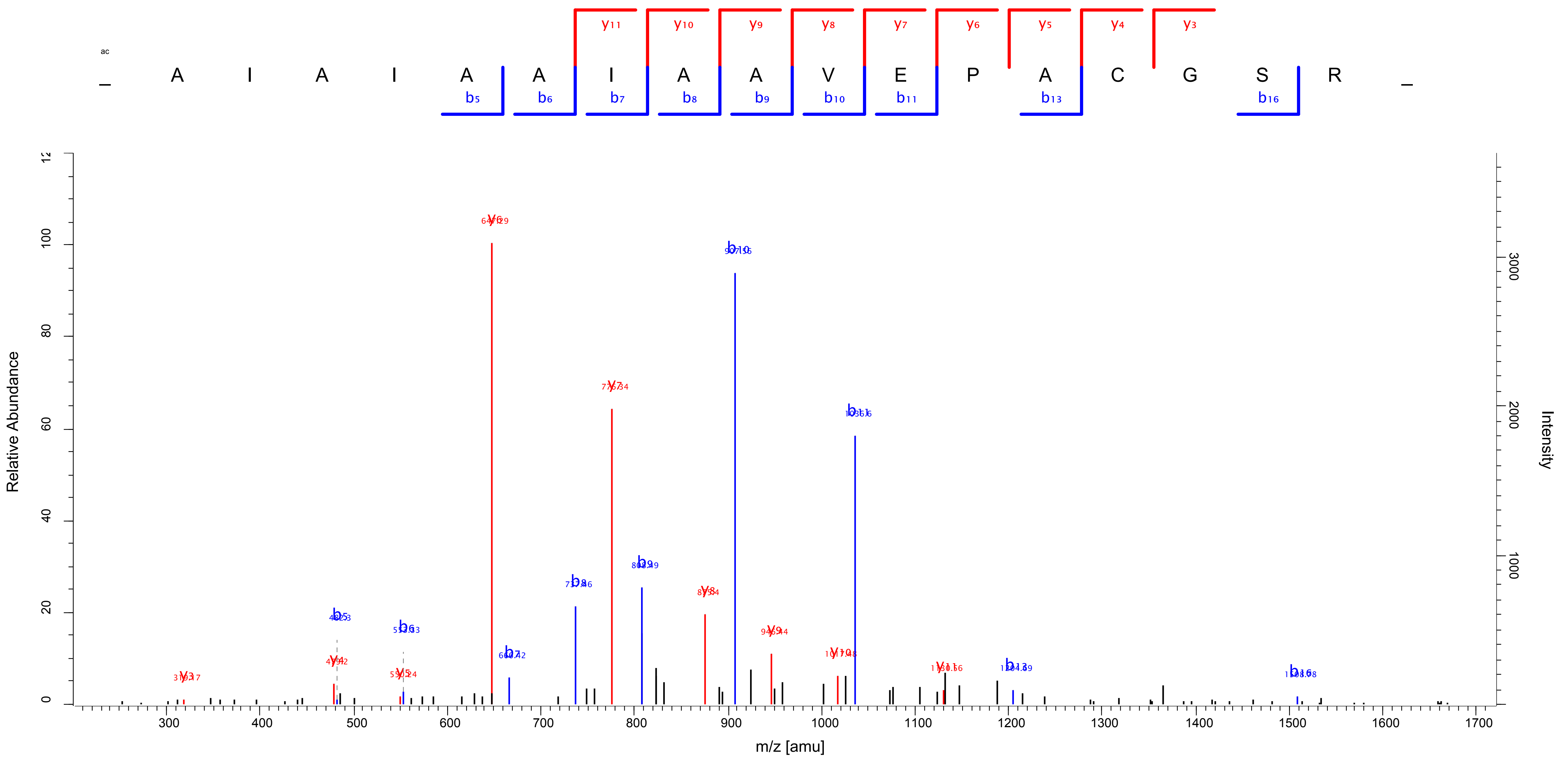
Mass:	2253.15138
m/z:	1127.58296
Charge:	2+
Retentiontime:	123.407089233398
Score:	267.3643
Mass Error [ppm]:	-0.66712
PEP:	4.0411E-131
Precursor Type:	MULTI

general
information

Annotation:	16 of 20
AminoAcids Coverage:	80 %
Intensity Coverage:	68 %
Peak Coverage:	45 %
Protein Localisation:	5 ... 24

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342195		116.0342195	1	D	19				
	187.07133329		187.07133329	2	A	18	2139.1332118		2139.1332118	
	301.11426073		301.11426073	3	N	17	2068.0960981		2068.0960981	
	388.14628914	+0.0250976	388.14628914	4	S	16	1954.0531706		977.53022354	-0.015453
	459.18340293		459.18340293	5	A	15	1867.0211422		1867.0211422	
	572.26746691		572.26746691	6	I	14	1795.9840284	-0.2741895	1795.9840284	
	685.35153089		685.35153089	7	I	13	1682.8999644	-0.0730601	1682.8999644	
	772.3835593	-0.2759543	772.3835593	8	S	12	1569.8159005	-0.2344796	1569.8159005	
	886.42648675	+0.1240504	886.42648675	9	N	11	1482.783872	-0.2459082	1482.783872	
	1049.4898153	-0.0626913	1049.4898153	10	Y	10	1368.7409446	-0.0572288	1368.7409446	
	1178.5324084	-0.3745715	1178.5324084	11	E	9	1205.6776161	-0.0943641	1205.6776161	
	1277.6008223	-0.2371748	1277.6008223	12	V	8	1076.635023	-0.2390269	1076.635023	
	1424.6692362	-0.1598368	1424.6692362	13	F	7	977.56660905		977.56660905	
	1552.7278137	-0.153717	1552.7278137	14	Q	6	830.49819513	-0.0655779	830.49819513	
	1665.8118777	-0.3472781	1665.8118777	15	I	5	702.43961762	+0.0301089	702.43961762	
-0.2100319	889.95160908	-0.1817083	1778.8959417	16	I	4	589.35555364	+0.0495977	589.35555364	
	1879.9436202	-0.3706221	1879.9436202	17	T	3	476.27148966	+0.1331124	476.27148966	
	1994.9705632	-0.2612126	1994.9705632	18	D	2	375.22381118	+0.0596361	375.22381118	
+0.0718314	1054.5309518		2108.0546272	19	I	1	260.19686815		260.19686815	
				20	K	0	147.11280417		147.11280417	

Scan number	19011	Raw file	20080705_Orbi6_SaZa_ADH_Exp_2_Matrigel_30h_InGel_04
Method	ITMS; CID	Genenames	NDFIP1



precursor information

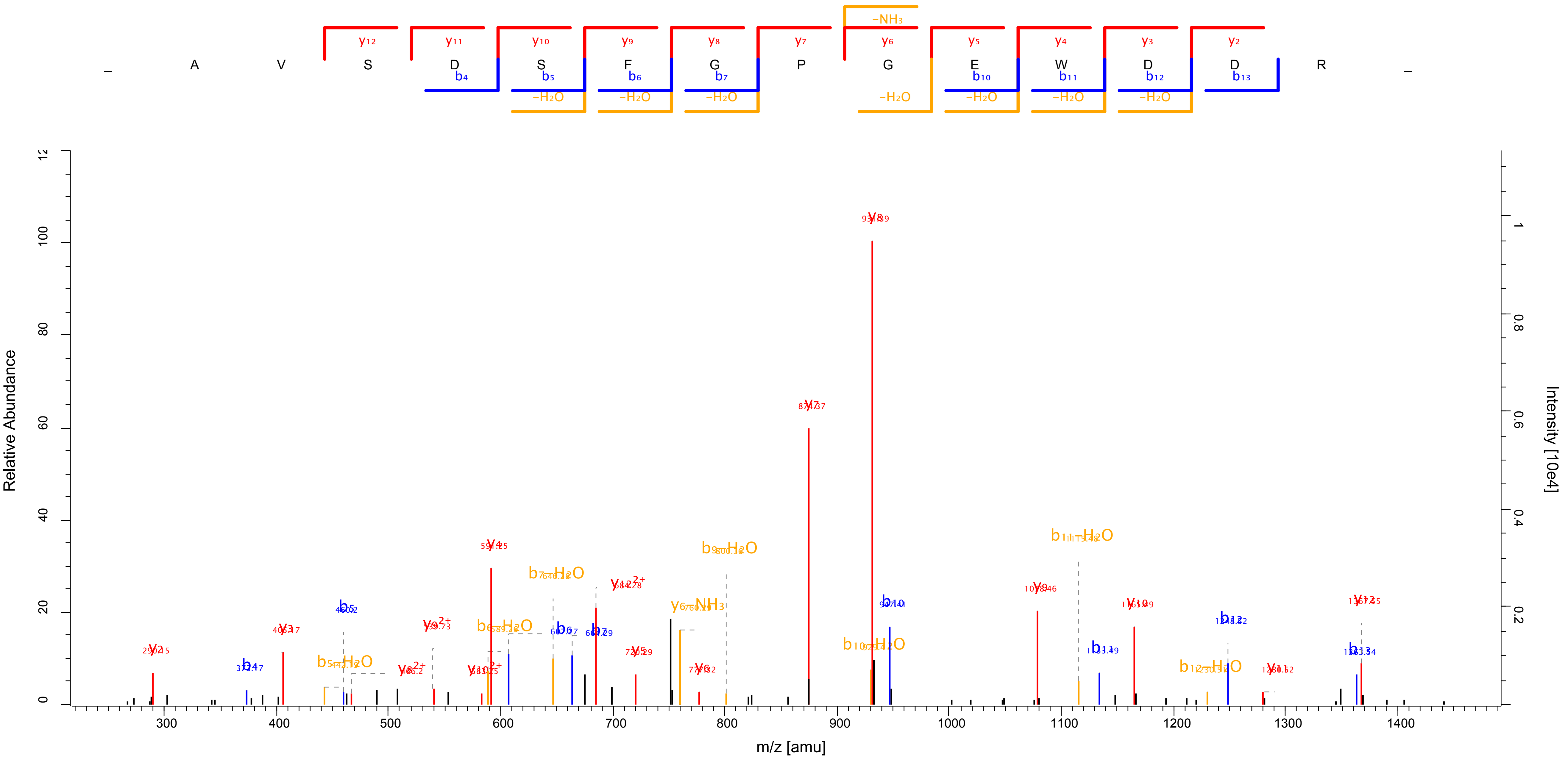
Mass:	1681.88211
m/z:	841.94833
Charge:	2+
Retentiontime:	123.491012573242
Score:	114.7424
Mass Error [ppm]:	−0.018553
PEP:	2.5519E−05
Precursor Type:	MULTI

general information

Annotation:	12 of 17
AminoAcids Coverage:	71 %
Intensity Coverage:	73 %
Peak Coverage:	22 %
Protein Localisation:	2 ... 18

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	114.054954941	1	A	16		
	227.139018921	2	I	15	1569.841738048	
	298.176132709	3	A	14	1456.757674068	
	411.260196689	4	I	13	1385.72056028	
+0.0424112	482.297310477	5	A	12	1272.6364963	
−0.0890629	553.334424265	6	A	11	1201.599382512	
−0.2717597	666.418488245	7	I	10	1130.562268724	+0.1796746
−0.3011221	737.455602033	8	A	9	1017.478204744	−0.0628605
−0.0714512	808.492715821	9	A	8	946.441090956	+0.090098
−0.351474	907.561129737	10	V	7	875.403977168	+0.0247948
−0.3297971	1036.603722833	11	E	6	776.335563252	−0.0513225
	1133.656486685	12	P	5	647.292970156	+0.0275254
−0.3256806	1204.693600473	13	A	4	550.240206304	+0.0619788
	1364.724248674	14	C	3	479.203092516	+0.0664387
	1421.745712398	15	G	2	319.172444314	+0.0358076
−0.1991275	1508.777740808	16	S	1	262.150980591	
		17	R	0	175.118952181	

Scan number	9433	Raw file	20080705_Orbi6_SaZa_ADH_Exp_2_Matrigel_30h_InGel_05
Method	ITMS; CID	Genenames	TMBIM1



precursor information

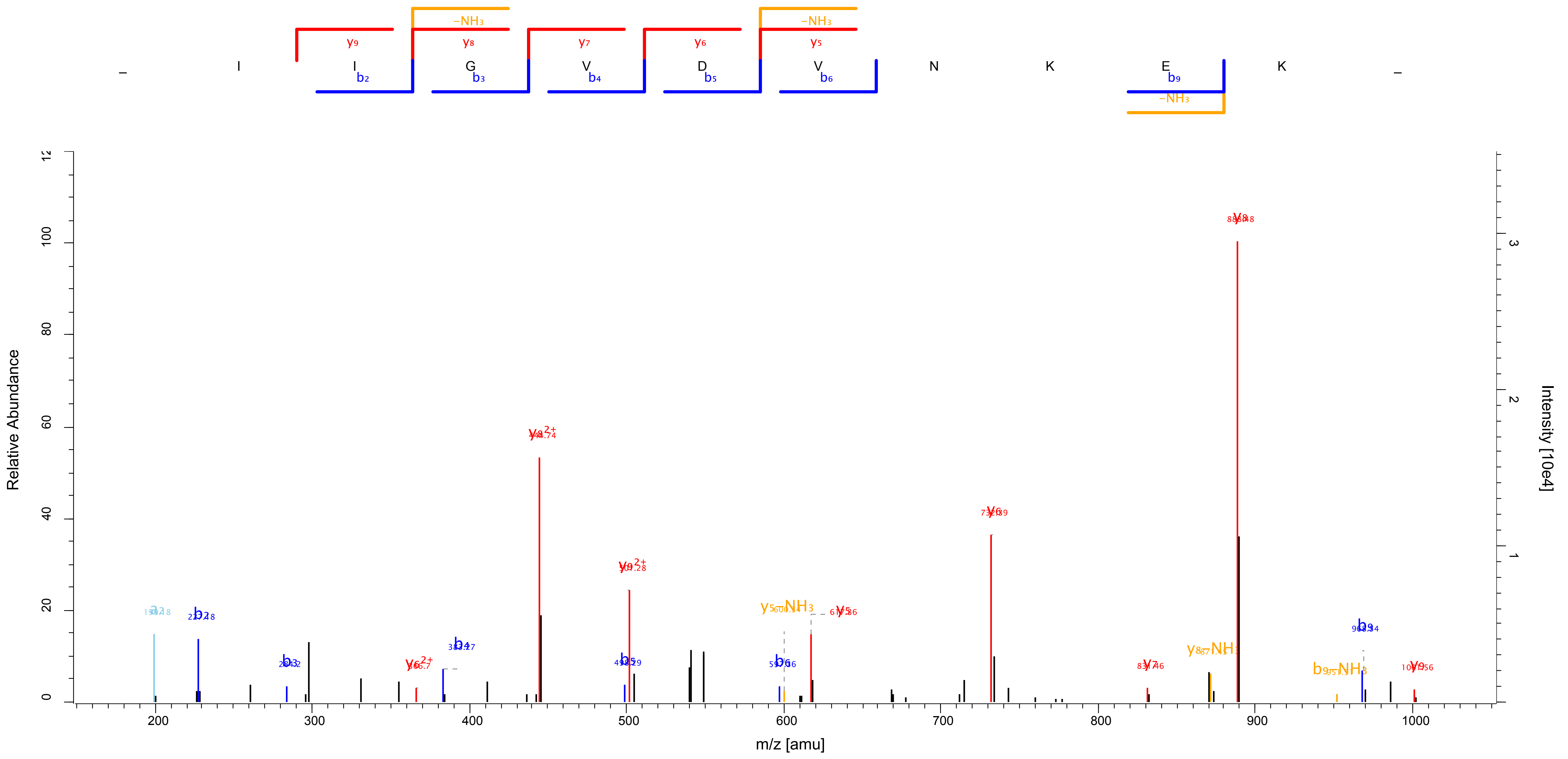
Mass:	1536.64803
m/z:	769.33129
Charge:	2+
Retentiontime:	69.8355255126953
Score:	200.9315
Mass Error [ppm]:	-0.048945
PEP:	8.0988E-17
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverage:	79 %
Intensity Coverage:	78 %
Peak Coverage:	42 %
Protein Localisation:	79 ... 92

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	13				
	171.112804171	2	V	12	1466.618263278		1466.618263278	
	258.14483258	3	S	11	1367.549849362	-0.1291951	684.278562914	+0.1554581
+0.0849383	373.171775612	4	D	10	1280.517820952	-0.2509752	1280.517820952	
-0.0165482	460.203804022	5	S	9	1165.49087792	-0.0982998	583.249077193	+0.1771313
+0.0399769	607.272217939	6	F	8	1078.45884951	-0.0546747	539.733062988	+0.0925596
+0.0310254	664.293681662	7	G	7	931.390435594	-0.0323423	466.19885603	+0.191891
	761.346445514	8	P	6	874.36897187	-0.0807028	874.36897187	
	818.367909238	9	G	5	777.316208018	+0.1118315	777.316208018	
-0.0531415	947.410502334	10	E	4	720.294744295	+0.0229437	720.294744295	
-0.0944295	1133.489815288	11	W	3	591.252151198	-0.0129544	591.252151198	
-0.0917095	1248.51675832	12	D	2	405.172838245	+0.0669078	405.172838245	
-0.0614015	1363.543701352	13	D	1	290.145895213	+0.0506075	290.145895213	
		14	R	0	175.118952181		175.118952181	

Scan number	4894	Raw file	20080705_Orbi6_SaZa_ADH_Exp_2_Matrigel_30h_InGel_06
Method	ITMS; CID	Genenames	ADH6



precursor information

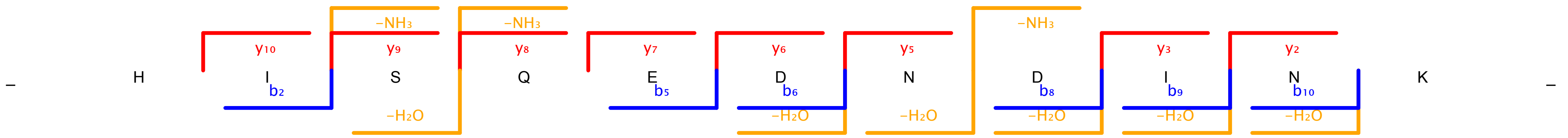
Mass:	1113.6394
m/z:	557.82698
Charge:	2+
Retentiontime:	46.5567512512207
Score:	141.1958
Mass Error [ppm]:	0.023465
PEP:	0.00020847
Precursor Type:	MULTI

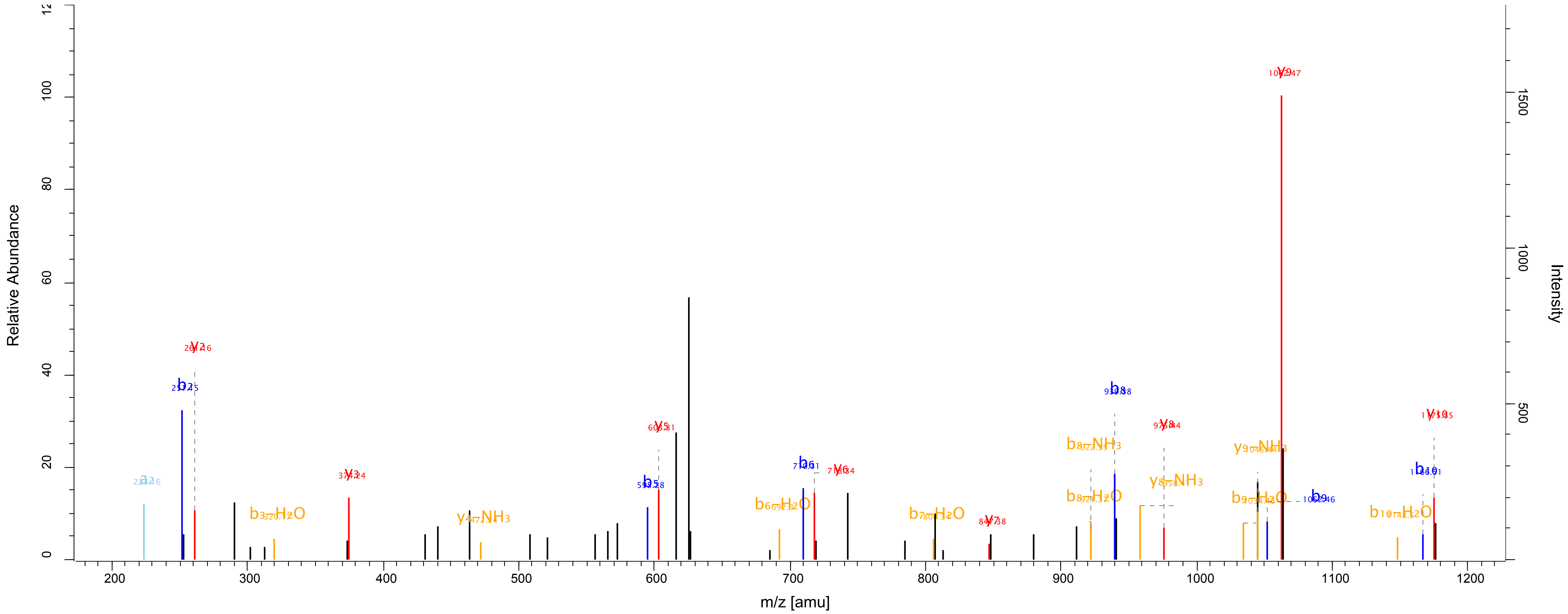
ge information

Annotation:	7 of 10
AminoAcids Coverage:	70 %
Intensity Coverage:	60 %
Peak Coverage:	32 %
Protein Localisation:	220 ... 229

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096425825		114.09134045	1	I	9				
−0.0237973	199.18048981	−0.0670365	227.17540443	2	I	8	1001.5625863	−0.0625253	501.28493138	+0.1444509
	256.20195353	+0.0783394	284.19686815	3	G	7	888.47852232	−0.0835638	444.74289939	+0.0243125
	355.27036745	−0.0039295	383.26528207	4	V	6	831.4570586	+0.1398042	831.4570586	
	470.29731048	+0.0387075	498.2922251	5	D	5	732.38864468	−0.0392184	366.69796057	−0.0431144
	569.36572439	−0.188764	597.36063902	6	V	4	617.36170165	+0.000542	617.36170165	
	683.40865184		711.40356646	7	N	3	518.29328773		518.29328773	
	811.50361486		839.49852948	8	K	2	404.25036028		404.25036028	
	940.54620795	−0.1778413	968.54112258	9	E	1	276.15539727		276.15539727	
				10	K	0	147.11280417		147.11280417	

Scan number	3043	Raw file	20080708_Orbi4_SaZa_ADH_Matrigel_Exp_2_30h_InGel_13
Method	ITMS; CID	Genenames	CCDC82





precursor information

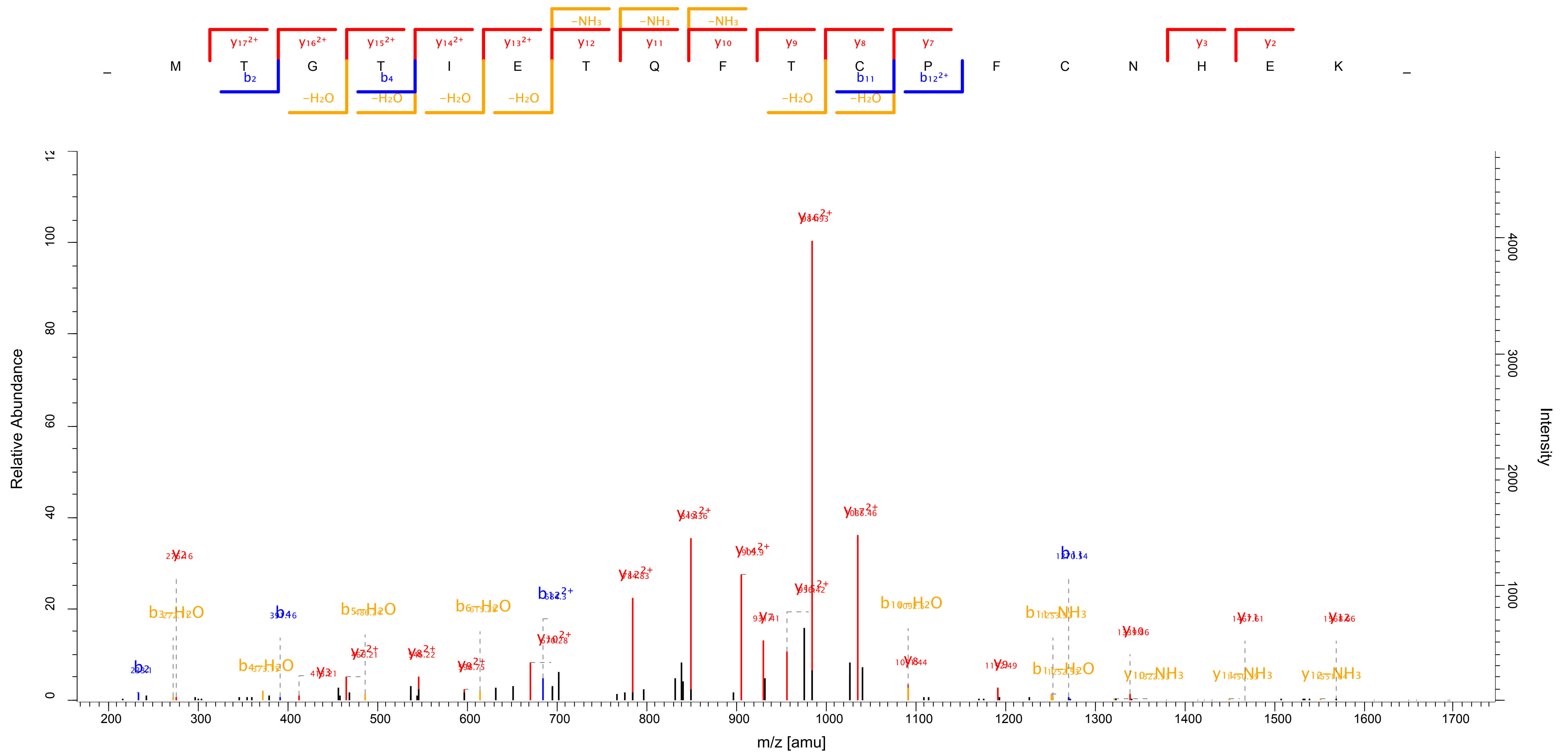
Mass:	1311.60572
m/z:	656.81014
Charge:	2+
Retentiontime:	40.5485649108887
Score:	141.095
Mass Error [ppm]:	0.16002
PEP:	0.0002298
Precursor Type:	ISO

general information

Annotation:	9 of 11
AminoAcids Coverage:	82 %
Intensity Coverage:	55 %
Peak Coverage:	46 %
Protein Localisation:	129 ... 139; 152 ... 162

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	110.071273707		138.066188329	1	H	10		
+0.0255858	223.155337687	+0.0234843	251.150252309	2	I	9	1175.553872107	+0.0337744
	310.187366097		338.182280719	3	S	8	1062.469808127	+0.0253091
	438.245943609		466.240858231	4	Q	7	975.437779717	+0.0263926
	567.288536705	+0.1502035	595.283451327	5	E	6	847.379202206	-0.0106109
	682.315479737	+0.0647887	710.310394359	6	D	5	718.336609109	+0.1483152
	796.358407184		824.353321806	7	N	4	603.309666077	+0.0920063
	911.385350216	+0.1500086	939.380264838	8	D	3	489.26673863	
	1024.469414196	+0.1410179	1052.464328818	9	I	2	374.239795598	+0.1153069
	1138.512341644	+0.2988961	1166.507256266	10	N	1	261.155731618	+0.0474544
				11	K	0	147.112804171	

Scan number	10432	Raw file	20080714_Orbi1_SaZa_SA_ADH_Matrigel_Exp_1_24h_InGel_01
Method	ITMS; CID	Genenames	ELOF1



precursor information

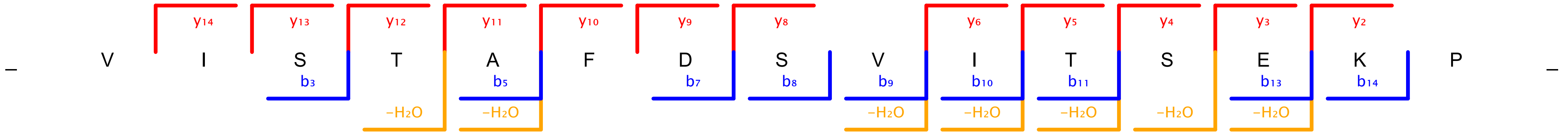
Mass:	2199.93819
m/z:	734.32001
Charge:	3+
Retentiontime:	81.0662841796875
Score:	192.1784
Mass Error [ppm]:	-0.25225
PEP:	1.293E-36
Precursor Type:	MULTI

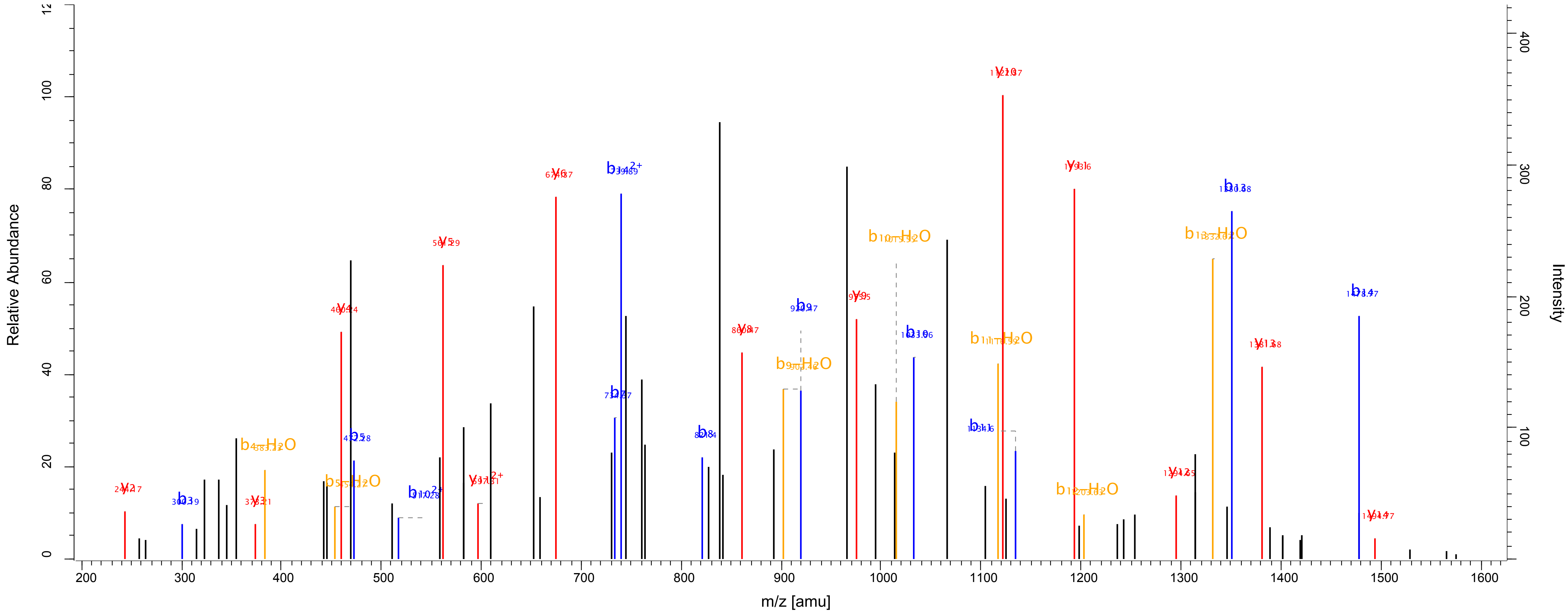
general information

Annotation:	14 of 18
AminoAcids Coverage:	78 %
Intensity Coverage:	71 %
Peak Coverage:	35 %
Protein Localisation:	16 ... 33

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	132.04776107		132.04776107	1	M	17				
	233.09543955	+0.097279	233.09543955	2	T	16	2069.9055369		1035.4564067	+0.1186666
	290.11690327		290.11690327	3	G	15	1968.8578584		984.93256743	+0.113331
	391.16458174	−0.0472722	391.16458174	4	T	14	1911.8363947		956.42183557	+0.0591215
	504.24864572		504.24864572	5	I	13	1810.7887162		905.89799633	+0.0952288
	633.29123882		633.29123882	6	E	12	1697.7046522		849.35596434	+0.0547412
	734.3389173		734.3389173	7	T	11	1568.6620591	−0.2466538	784.83466779	+0.0265993
	862.39749481		862.39749481	8	Q	10	1467.6143806	−0.3884285	1467.6143806	
	1009.4659087		1009.4659087	9	F	9	1339.5558031	−0.0755785	670.2815398	+0.0379792
	1110.5135872		1110.5135872	10	T	8	1192.4873892	−0.1204459	596.74733284	−0.1061585
	1270.5442354	−0.1009981	1270.5442354	11	C	7	1091.4397107	−0.1412488	546.22349361	−0.0946484
+0.4734359	684.30213786		1367.5969993	12	P	6	931.40906255	−0.1548511	466.20816951	+0.0082612
	1514.6654132		1514.6654132	13	F	5	834.35629869		834.35629869	
	1674.6960614		1674.6960614	14	C	4	687.28788478		687.28788478	
	1788.7389888		1788.7389888	15	N	3	527.25723658		527.25723658	
	1925.7979007		1925.7979007	16	H	2	413.21430913	+0.0113989	413.21430913	
	2054.8404938		2054.8404938	17	E	1	276.15539727	−0.0157183	276.15539727	
				18	K	0	147.11280417		147.11280417	

Scan number	11878	Raw file	20080714_Orbi1_SaZa_SA_ADH_Matrigel_Exp_1_24h_InGel_03
Method	ITMS; CID	Genenames	ITGB1BP1





precursor information

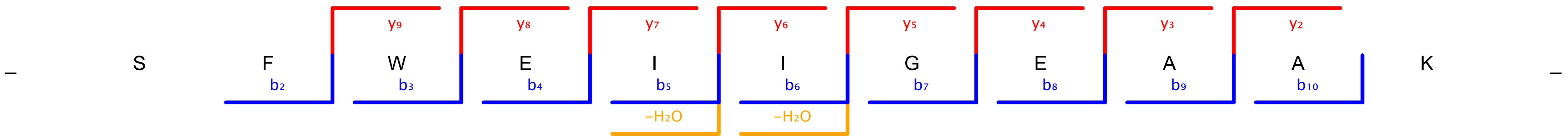
Mass:	0
m/z:	797.42259
Charge:	0+
Retentiontime:	94.7428588867188
Score:	202.6523
Mass Error [ppm]:	0.54887
PEP:	5.7954E−33
Precursor Type:	PEAK

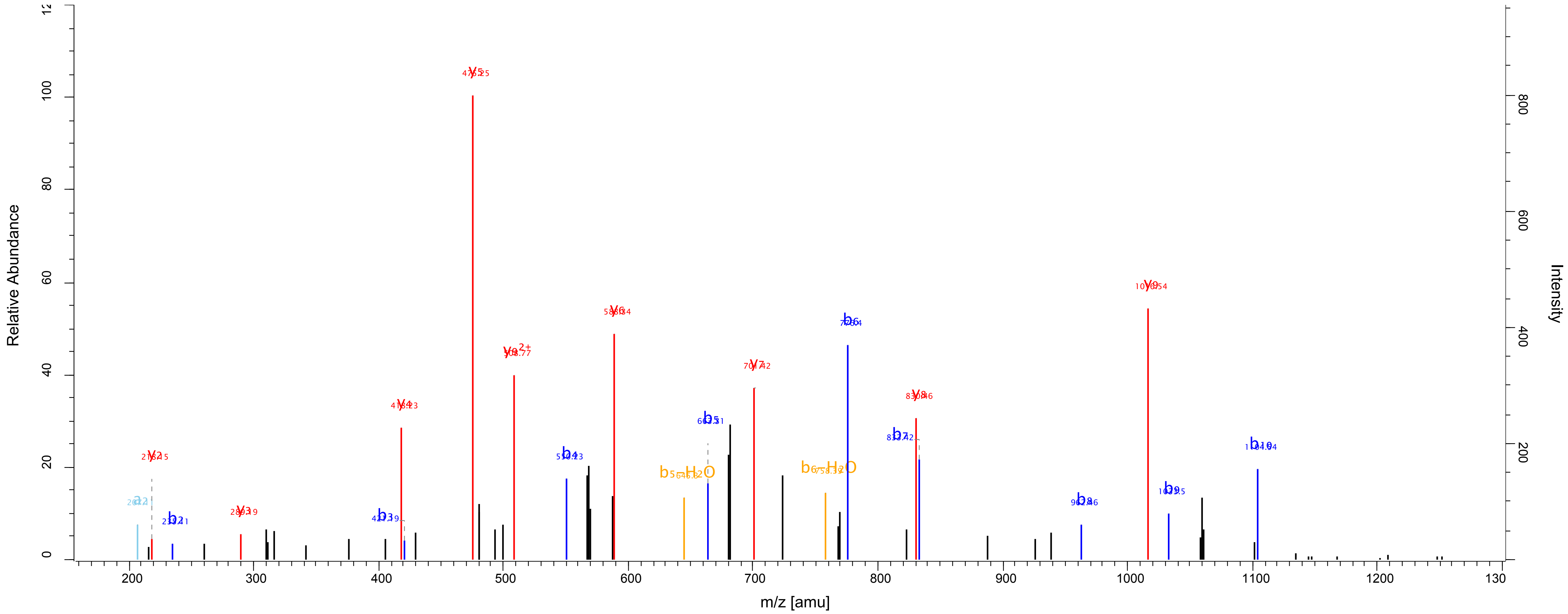
general information

Annotation:	13 of 15
AminoAcids Coverage:	87 %
Intensity Coverage:	53 %
Peak Coverage:	40 %
Protein Localisation:	186 ... 200

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.07569038		100.07569038	1	V	14				
	213.15975436		213.15975436	2	I	13	1494.7686159	−0.2334597	1494.7686159	
	300.19178277	−0.0311993	300.19178277	3	S	12	1381.6845519	−0.2371642	1381.6845519	
	401.23946125		401.23946125	4	T	11	1294.6525235	−0.1210294	1294.6525235	
	472.27657504	−0.0696659	472.27657504	5	A	10	1193.604845	−0.1063099	597.30606076	−0.2305603
	619.34498895		619.34498895	6	F	9	1122.5677313	−0.2492498	1122.5677313	
	734.37193198	−0.2165975	734.37193198	7	D	8	975.49931734	−0.2387583	975.49931734	
	821.40396039	−0.2751152	821.40396039	8	S	7	860.47237431	−0.2002796	860.47237431	
	920.47237431	−0.3967518	920.47237431	9	V	6	773.4403459		773.4403459	
−0.0356416	517.28185738	−0.2215994	1033.5564383	10	I	5	674.37193198	−0.1597127	674.37193198	
	1134.6041168	−0.3514312	1134.6041168	11	T	4	561.287868	−0.0894427	561.287868	
	1221.6361452		1221.6361452	12	S	3	460.24018953	−0.011857	460.24018953	
	1350.6787383	−0.2428252	1350.6787383	13	E	2	373.20816112	−0.0086372	373.20816112	
−0.2203839	739.89048888	−0.184712	1478.7737013	14	K	1	244.16556802	+0.0053304	244.16556802	
				15	P	0	116.070605		116.070605	

Scan number	14961	Raw file	20080714_Orbi1_SaZa_SA_ADH_Matrigel_Exp_1_24h_InGel_03
Method	ITMS; CID	Genenames	S100A14





precursor information

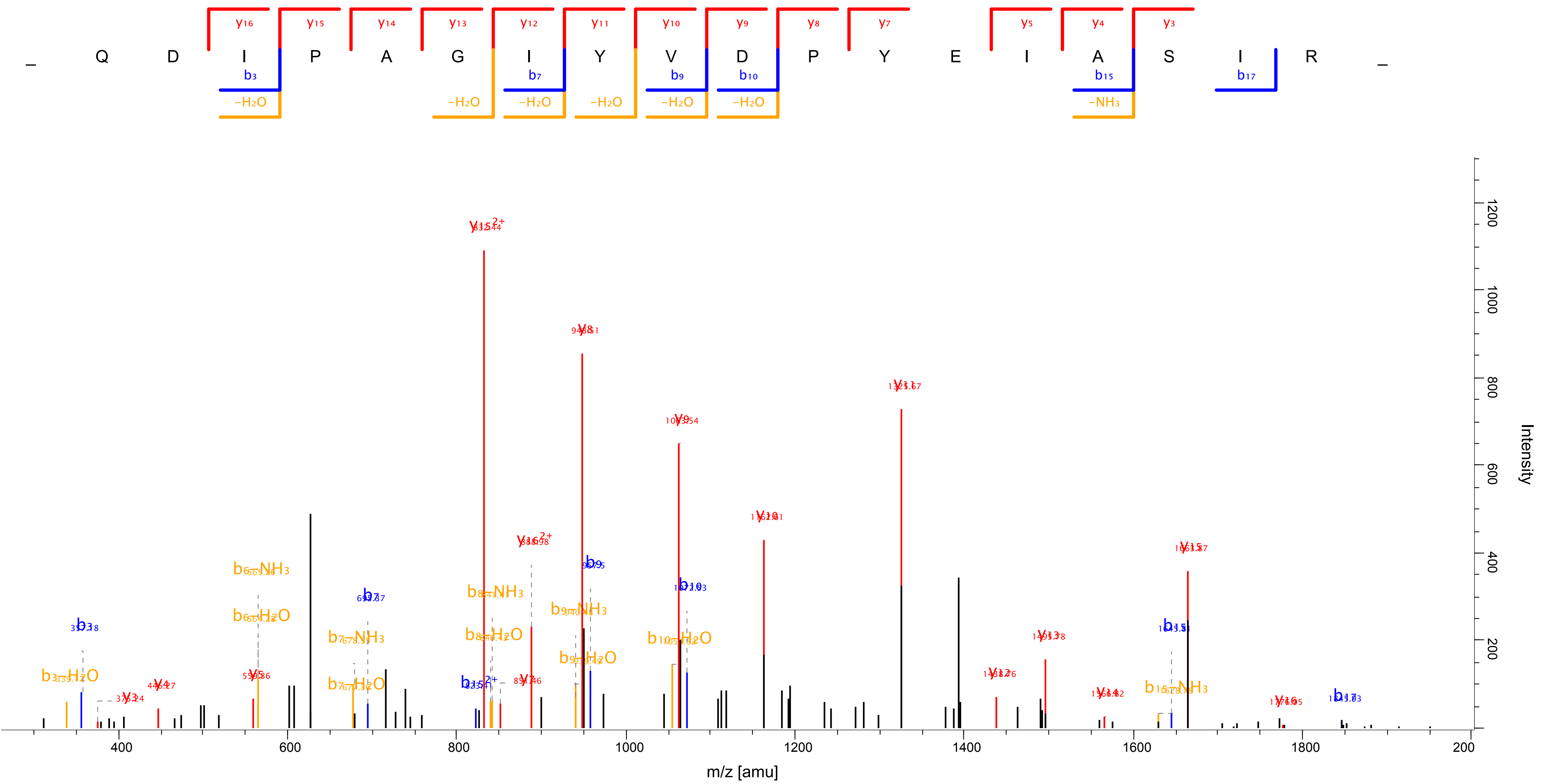
Mass:	0
m/z:	625.8245
Charge:	0+
Retentiontime:	114.124374389648
Score:	147.7437
Mass Error [ppm]:	0.1307
PEP:	0.00013747
Precursor Type:	PEAK

general information

Annotation:	9 of 11
AminoAcids Coverage:	82 %
Intensity Coverage:	64 %
Peak Coverage:	35 %
Protein Localisation:	83 ... 93

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	60.044390254		88.039304876	1	S	10				
+0.2296336	207.11280417	+0.0296713	235.10771879	2	F	9	1163.6095365		1163.6095365	
	393.19211712	−0.0592241	421.18703175	3	W	8	1016.5411226	−0.0982515	508.77419952	−0.0210867
	522.23471022	−0.0500594	550.22962484	4	E	7	830.46180962	−0.0275445	830.46180962	
	635.3187742	−0.0235887	663.31368882	5	I	6	701.41921653	−0.145718	701.41921653	
	748.40283818	−0.3223744	776.3977528	6	I	5	588.33515255	−0.1445398	588.33515255	
	805.4243019	−0.1676906	833.41921653	7	G	4	475.25108857	−0.1275534	475.25108857	
	934.466895	−0.2051568	962.46180962	8	E	3	418.22962484	−0.091014	418.22962484	
	1005.5040088	−0.2263404	1033.4989234	9	A	2	289.18703175	+0.0856428	289.18703175	
	1076.5411226	−0.3066671	1104.5360372	10	A	1	218.14991796	+0.0814358	218.14991796	
				11	K	0	147.11280417		147.11280417	

Scan number	15763	Raw file	20080714_Orbi1_SaZa_SA_ADH_Matrigel_Exp_1_24h_InGel_04
Method	ITMS; CID	Genenames	PIGX



precursor information

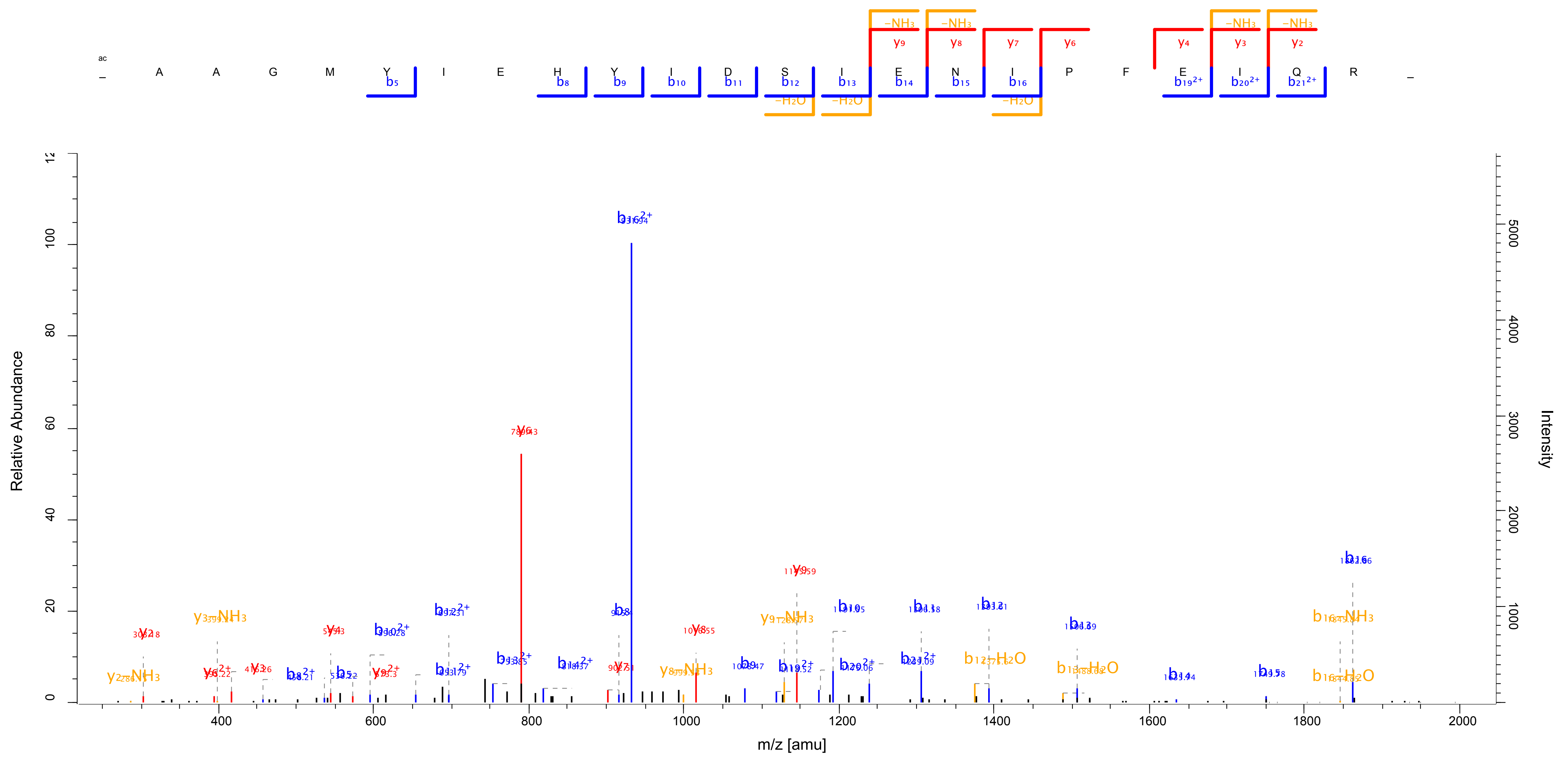
Mass:	2019.02751
m/z:	1010.52103
Charge:	2+
Retentiontime:	118.63374328613
Score:	149.0035
Mass Error [ppm]:	-1.8802
PEP:	5.5326E-06
Precursor Type:	ISO

general information

Annotation:	14 of 18
AminoAcids Coverage:	78 %
Intensity Coverage:	58 %
Peak Coverage:	34 %
Protein Localisation:	83 ... 100

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.06585398		129.06585398	1	Q	17				
	244.09279701		244.09279701	2	D	16	1891.9800057		1891.9800057	
	357.17686099	-0.1544916	357.17686099	3	I	15	1776.9530626	-0.0982042	888.98016955	-0.1035826
	454.22962484		454.22962484	4	P	14	1663.8689987	-0.1260787	832.43813756	-0.0212674
	525.26673863		525.26673863	5	A	13	1566.8162348	-0.1978266	1566.8162348	
	582.28820235		582.28820235	6	G	12	1495.779121	-0.1325146	1495.779121	
	695.37226633	+0.0098137	695.37226633	7	I	11	1438.7576573	-0.1757481	1438.7576573	
	858.43559487		858.43559487	8	Y	10	1325.6735933	-0.2033785	1325.6735933	
	957.50400879	-0.2569385	957.50400879	9	V	9	1162.6102648	-0.2247667	1162.6102648	
	1072.5309518	-0.1987985	1072.5309518	10	D	8	1063.5418509	-0.2158011	1063.5418509	
	1169.5837157		1169.5837157	11	P	7	948.51490783	-0.2354889	948.51490783	
	1332.6470442		1332.6470442	12	Y	6	851.46214397	+0.0849752	851.46214397	
	1461.6896373		1461.6896373	13	E	5	688.39881544		688.39881544	
	1574.7737013		1574.7737013	14	I	4	559.35622234	-0.0988981	559.35622234	
-0.192493	823.40904577	-0.0414059	1645.8108151	15	A	3	446.27215836	-0.0499904	446.27215836	
	1732.8428435		1732.8428435	16	S	2	375.23504457	+0.0604877	375.23504457	
	1845.9269075	-0.1245393	1845.9269075	17	I	1	288.20301616		288.20301616	
				18	R	0	175.11895218		175.11895218	

Scan number	17237	Raw file	20080714_Orbi1_SaZa_SA_ADH_Matrigel_Exp_1_24h_InGel_05
Method	ITMS; CID	Genenames	ING4



precursor information

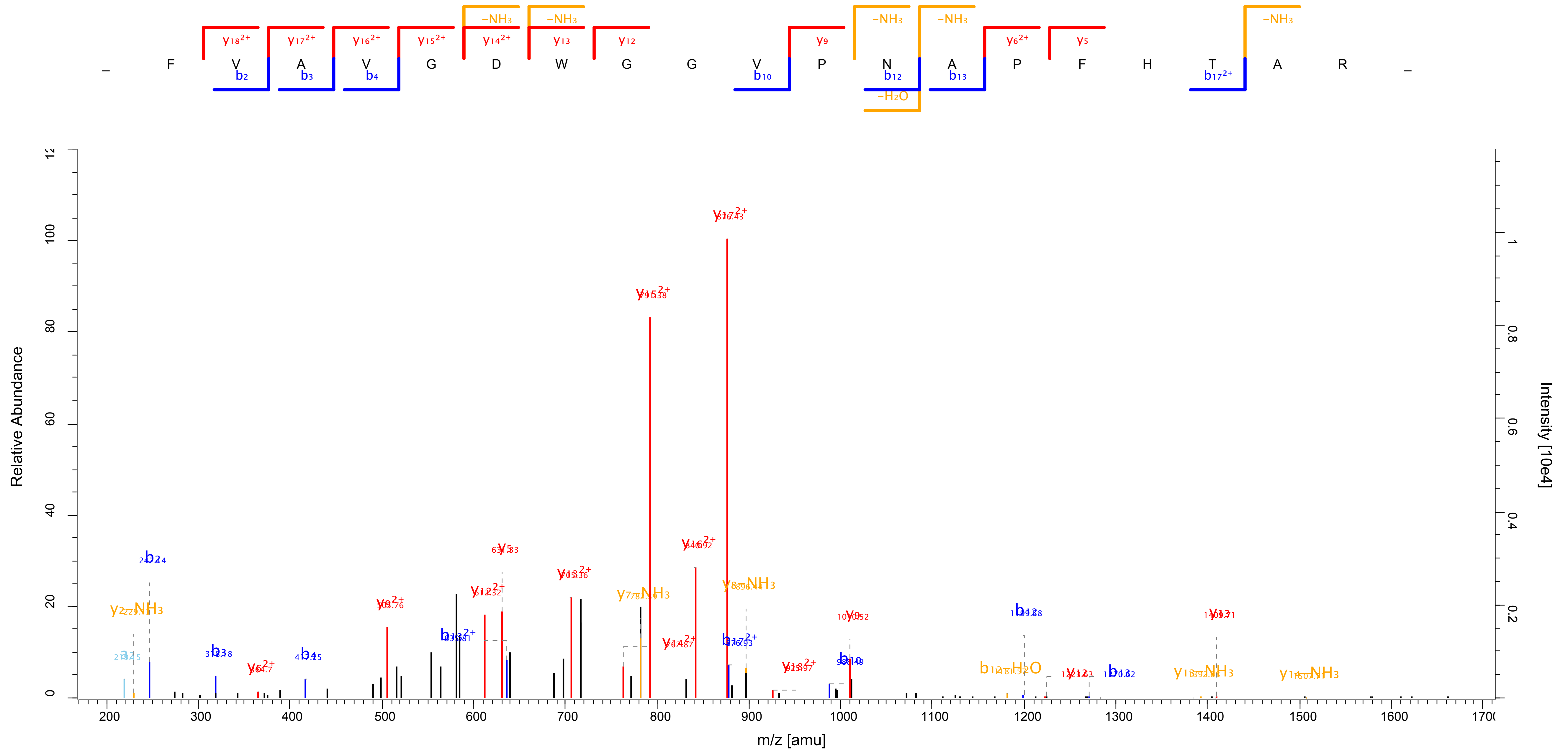
Mass:	2650.27555
m/z:	884.43246
Charge:	3+
Retentiontime:	131.094436645508
Score:	212.9538
Mass Error [ppm]:	0.68433
PEP:	2.2272E−52
Precursor Type:	ISO

general information

Annotation:	14 of 22
AminoAcids Coverage:	64 %
Intensity Coverage:	77 %
Peak Coverage:	35 %
Protein Localisation:	2 ... 23

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.05495494		114.05495494	1	A	21				
	185.09206873		185.09206873	2	A	20	2538.2333366		2538.2333366	
	242.11353245		242.11353245	3	G	19	2467.1962228		2467.1962228	
	373.15401706		373.15401706	4	M	18	2410.1747591		2410.1747591	
	536.2173456	−0.2442621	536.2173456	5	Y	17	2279.1342745		2279.1342745	
	649.30140958		649.30140958	6	I	16	2116.0709459		2116.0709459	
	778.34400267		778.34400267	7	E	15	2002.986882		2002.986882	
−0.0690481	458.2050955	−0.160727	915.40291454	8	H	14	1873.9442889		1873.9442889	
	1078.4662431	−0.2886308	1078.4662431	9	Y	13	1736.885377		1736.885377	
−0.3392776	596.27879176	−0.2647846	1191.5503071	10	I	12	1573.8220485		1573.8220485	
+0.4333837	653.79226328	−0.2208048	1306.5772501	11	D	11	1460.7379845		1460.7379845	
+0.1949574	697.30827748	−0.1158703	1393.6092785	12	S	10	1345.7110415		1345.7110415	
−0.198393	753.85030947	−0.3028395	1506.6933425	13	I	9	1258.679013		1258.679013	
−0.2527095	818.37160602	−0.1531719	1635.7359356	14	E	8	1145.5949491	−0.2333768	573.30111276	−0.0595356
	1749.778863	−0.1845027	1749.778863	15	N	7	1016.552356	−0.2015259	1016.552356	
−0.0455143	931.93510173	−0.1867795	1862.862927	16	I	6	902.50942852	−0.1450486	902.50942852	
	1959.9156909		1959.9156909	17	P	5	789.42536454	−0.17451	395.2163205	−0.0081906
	2106.9841048		2106.9841048	18	F	4	692.37260069		692.37260069	
−0.251118	1118.5169872		2236.0266979	19	E	3	545.30418677	−0.0601072	545.30418677	
−0.2511578	1175.0590192		2349.1107618	20	I	2	416.26159367	−0.0869111	416.26159367	
−0.0377708	1239.0883079		2477.1693394	21	Q	1	303.17752969	+0.0078341	303.17752969	
				22	R	0	175.11895218		175.11895218	

Scan number	11125	Raw file	20080714_Orbi1_SaZa_SA_ADH_Matrigel_Exp_1_24h_InGel_07
Method	ITMS; CID	Genenames	ACP5



precursor
information

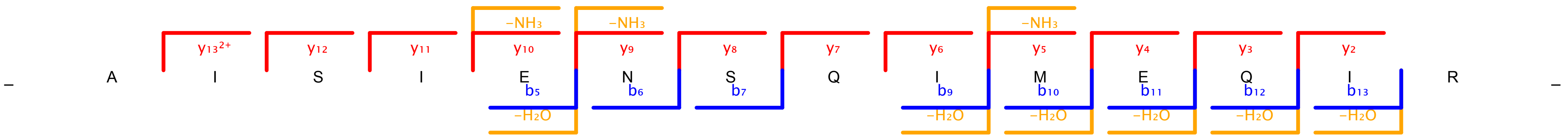
Mass:	1996.99183
m/z:	666.67122
Charge:	3+
Retentiontime:	92.4694213867188
Score:	137.4559
Mass Error [ppm]:	0.5277
PEP:	1.3314E-05
Precursor Type:	ISO

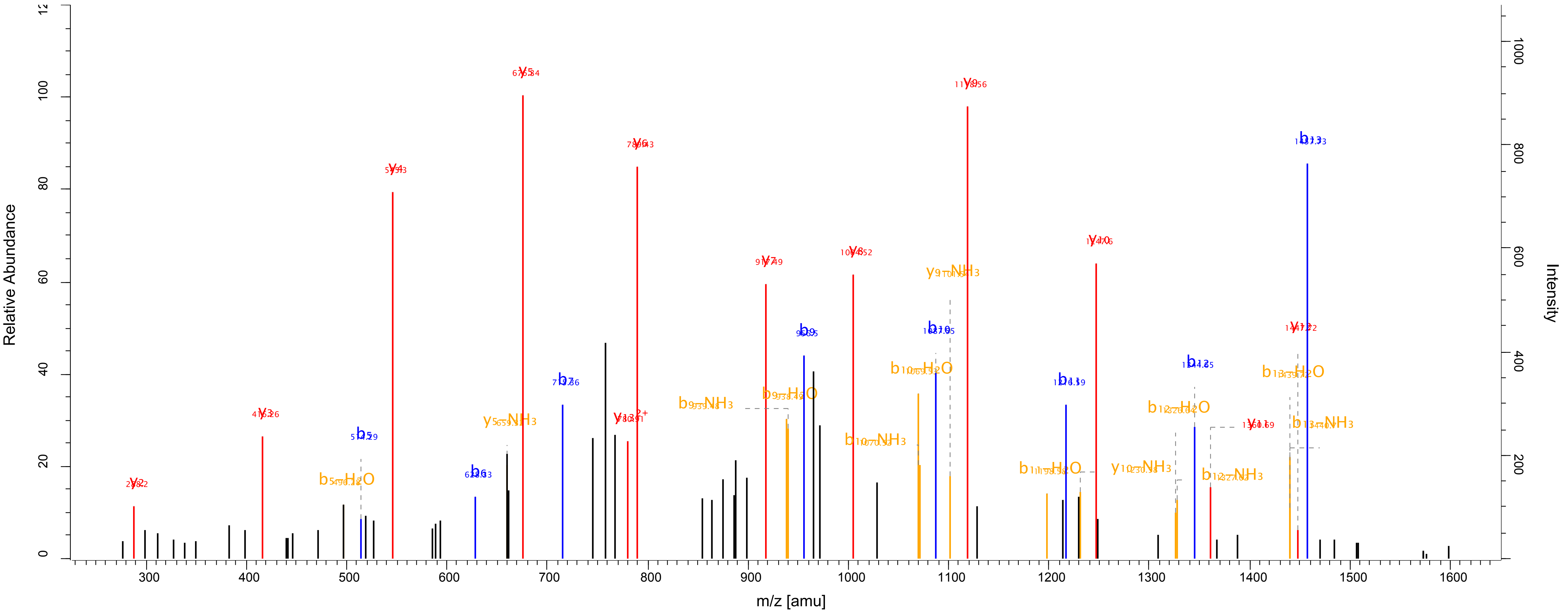
general
information

Annotation:	15 of 19
AminoAcids Coverage:	79 %
Intensity Coverage:	65 %
Peak Coverage:	34 %
Protein Localisation:	28 ... 46

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.080776		148.07569		148.07569	1	F	18				
+0.12025	219.14919		247.144104	+0.0279233	247.144104	2	V	17	1850.92964		925.968459	−0.2097311
	290.186303		318.181218	+0.0301467	318.181218	3	A	16	1751.86123		876.434252	+0.0283943
	389.254717		417.249632	−0.1304303	417.249632	4	V	15	1680.82411		840.915695	+0.0930938
	446.276181		474.271096		474.271096	5	G	14	1581.7557		791.381488	+0.1321225
	561.303124		589.298039		589.298039	6	D	13	1524.73424		762.870756	−0.2099899
	747.382437		775.377352		775.377352	7	W	12	1409.70729	+0.0109682	705.357285	+0.1164089
	804.403901		832.398815		832.398815	8	G	11	1223.62798	−0.4186299	612.317628	+0.0487655
	861.425365		889.420279		889.420279	9	G	10	1166.60652		1166.60652	
	960.493778		988.488693	−0.1254118	988.488693	10	V	9	1109.58505		1109.58505	
	1057.54654		1085.54146		1085.54146	11	P	8	1010.51664	−0.1178965	505.761958	+0.1226857
	1171.58947		1199.58438	−0.0410494	1199.58438	12	N	7	913.463875		913.463875	
	1242.62658	−0.4204664	635.814387	−0.3125382	1270.6215	13	A	6	799.420948		799.420948	
	1339.67935		1367.67426		1367.67426	14	P	5	728.383834		364.695555	+0.256227
	1486.74776		1514.74268		1514.74268	15	F	4	631.33107	+0.1645963	631.33107	
	1623.80667		1651.80159		1651.80159	16	H	3	484.262656		484.262656	
	1724.85435	+0.4329957	876.928271		1752.84927	17	T	2	347.203744		347.203744	
	1795.89147		1823.88638		1823.88638	18	A	1	246.156066		246.156066	
						19	R	0	175.118952		175.118952	

Scan number	11735	Raw file	20080721_Orbi1_SaZa_SA_ADH_Matrigel_Exp_1_Susp_InGel_01
Method	ITMS; CID	Genenames	LDOC1





precursor information

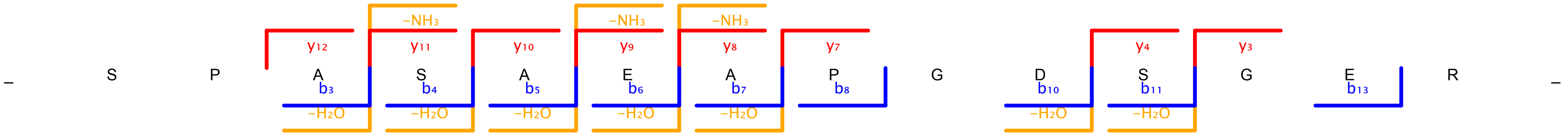
Mass:	1630.8355
m/z:	816.42503
Charge:	2+
Retentiontime:	92.1270904541016
Score:	230.0557
Mass Error [ppm]:	0.39755
PEP:	3.8408E−23
Precursor Type:	ISO

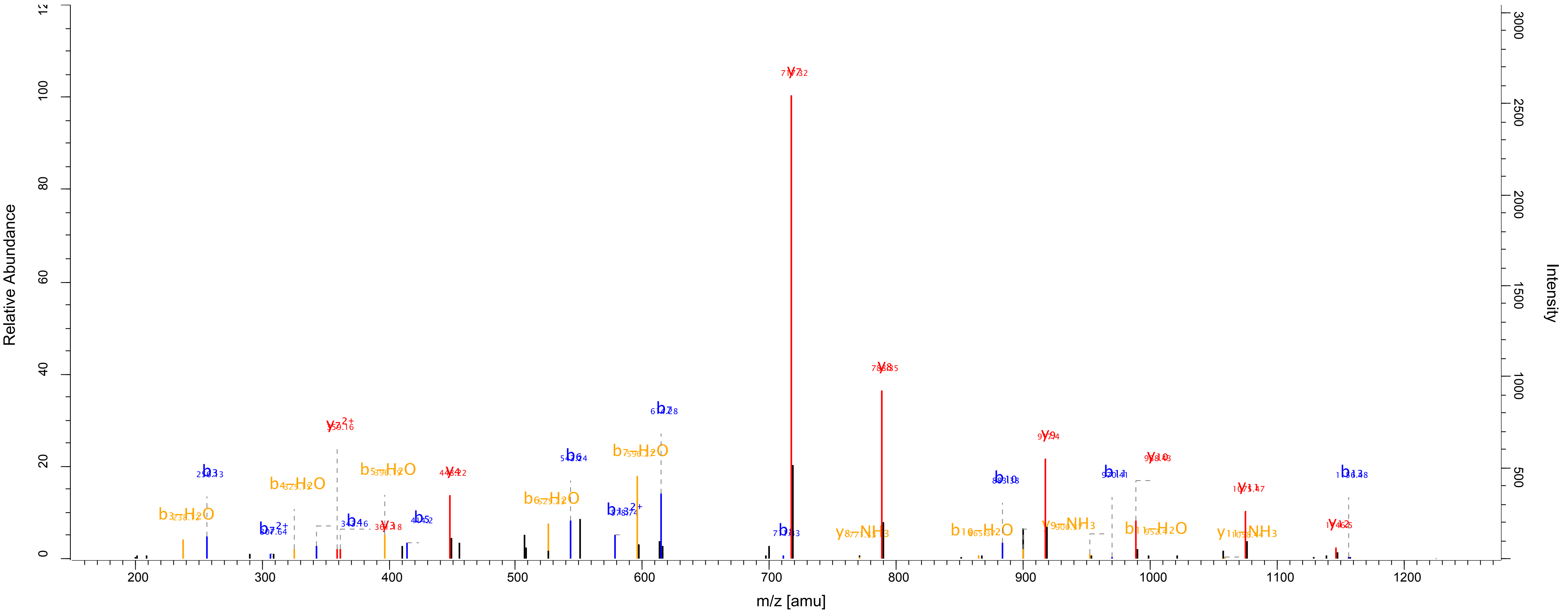
general information

Annotation:	12 of 14
AminoAcids Coverage:	86 %
Intensity Coverage:	69 %
Peak Coverage:	41 %
Protein Localisation:	18 ... 31

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	13				
	185.128454235	2	I	12	1560.805018191		780.906147329	−0.3304027
	272.160482645	3	S	11	1447.720954211	−0.0638497	1447.720954211	
	385.244546625	4	I	10	1360.688925801	+0.02604	1360.688925801	
+0.076874	514.287139721	5	E	9	1247.60486182	−0.0092808	1247.60486182	
+0.1906237	628.330067168	6	N	8	1118.562268724	+0.1141229	1118.562268724	
+0.2555192	715.362095578	7	S	7	1004.519341277	+6.9E−06	1004.519341277	
	843.42067309	8	Q	6	917.487312867	+0.0546183	917.487312867	
+0.0255364	956.50473707	9	I	5	789.428735356	+0.012793	789.428735356	
−0.0129951	1087.545221676	10	M	4	676.344671375	+0.145502	676.344671375	
−0.0145726	1216.587814773	11	E	3	545.304186769	+0.0466433	545.304186769	
−0.0304255	1344.646392284	12	Q	2	416.261593673	+0.1351959	416.261593673	
−0.2264279	1457.730456264	13	I	1	288.203016161	+0.0841237	288.203016161	
		14	R	0	175.11895218		175.11895218	

Scan number	2088	Raw file	20080721_Orbi1_SaZa_SA_ADH_Matrigel_Exp_1_Susp_InGel_05
Method	ITMS; CID	Genenames	ZNF511





precursor information

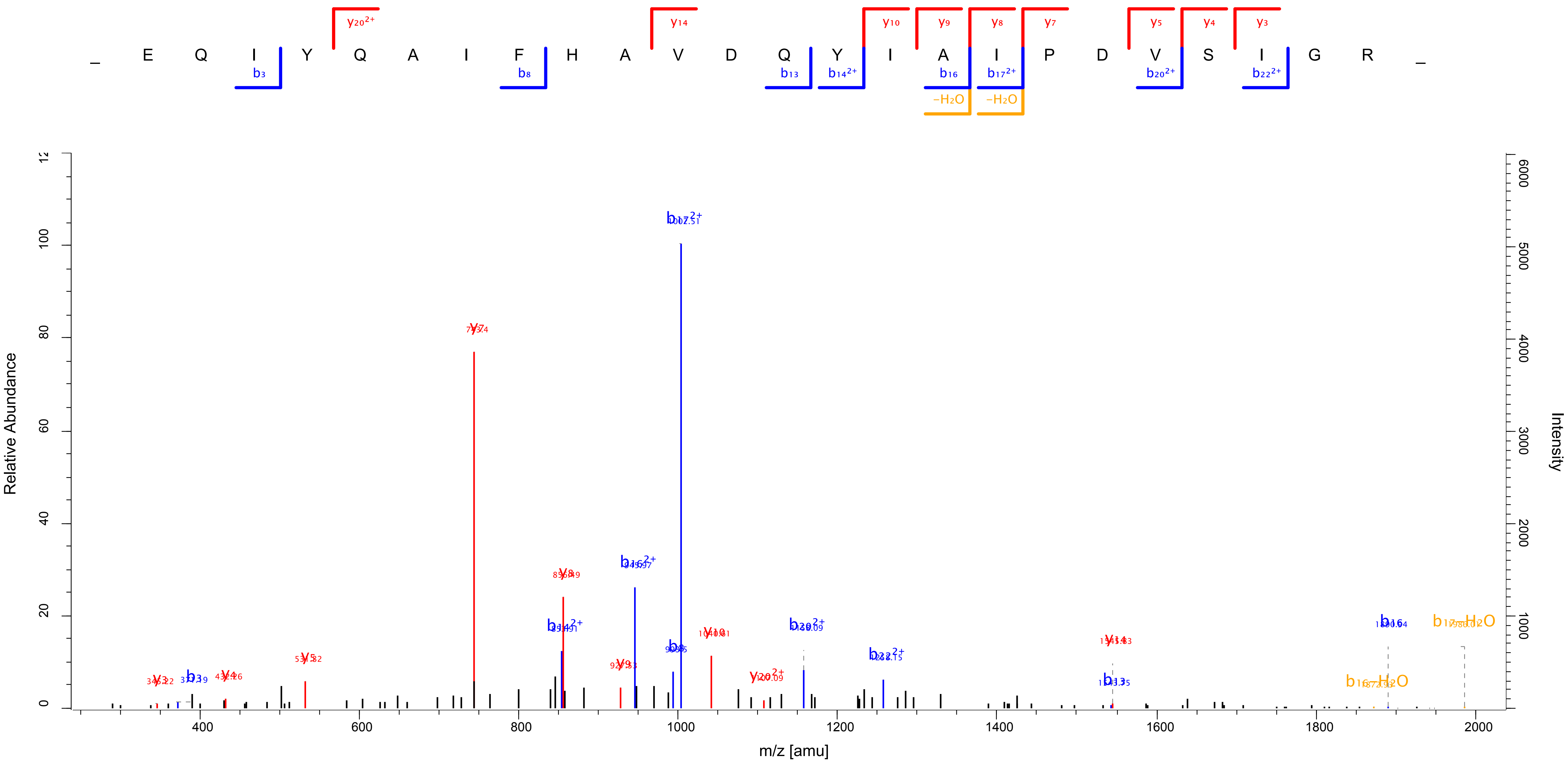
Mass:	1329.58028
m/z:	665.79742
Charge:	2+
Retentiontime:	38.6740036010742
Score:	206.363
Mass Error [ppm]:	0.44876
PEP:	4.9045E-17
Precursor Type:	ISO

general information

Annotation:	10 of 14
AminoAcids Coverage:	71 %
Intensity Coverage:	74 %
Peak Coverage:	46 %
Protein Localisation:	185 ... 198

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876		88.039304876	1	S	13				
	185.09206873		185.09206873	2	P	12	1243.5549347		1243.5549347	
	256.12918252	+0.1169418	256.12918252	3	A	11	1146.5021709	+0.0266377	1146.5021709	
	343.16121093	+0.0796338	343.16121093	4	S	10	1075.4650571	+0.0882876	1075.4650571	
	414.19832471	+0.0938506	414.19832471	5	A	9	988.43302869	-0.011703	988.43302869	
	543.24091781	+0.1011232	543.24091781	6	E	8	917.3959149	+0.0804035	917.3959149	
-0.363113	307.64265403	+0.0536334	614.2780316	7	A	7	788.35332181	+0.1223252	788.35332181	
	711.33079545	-0.0793306	711.33079545	8	P	6	717.31620802	+0.0647124	359.16174224	+0.050416
	768.35225917		768.35225917	9	G	5	620.26344417		620.26344417	
	883.37920221	+0.0478608	883.37920221	10	D	4	563.24198044		563.24198044	
	970.41123062	+0.3505492	970.41123062	11	S	3	448.21503741	+0.0610856	448.21503741	
	1027.4326943		1027.4326943	12	G	2	361.183009	+0.0405017	361.183009	
-0.3382058	578.74128195	+0.1891413	1156.4752874	13	E	1	304.16154528		304.16154528	
				14	R	0	175.11895218		175.11895218	

Scan number	18549	Raw file	20080721_Orbi1_SaZa_SA_ADH_Matrigel_Exp_1_Susp_InGel_07
Method	ITMS; CID	Genenames	MCOLN1



precursor information

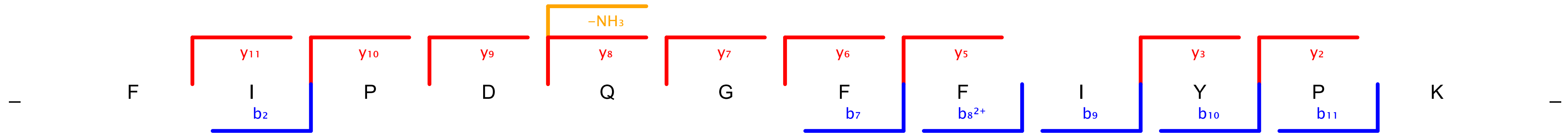
Mass:	2745.41409
m/z:	916.14531
Charge:	3+
Retentiontime:	130.188064575195
Score:	70.45306
Mass Error [ppm]:	0.53617
PEP:	0.00011201
Precursor Type:	MULTI

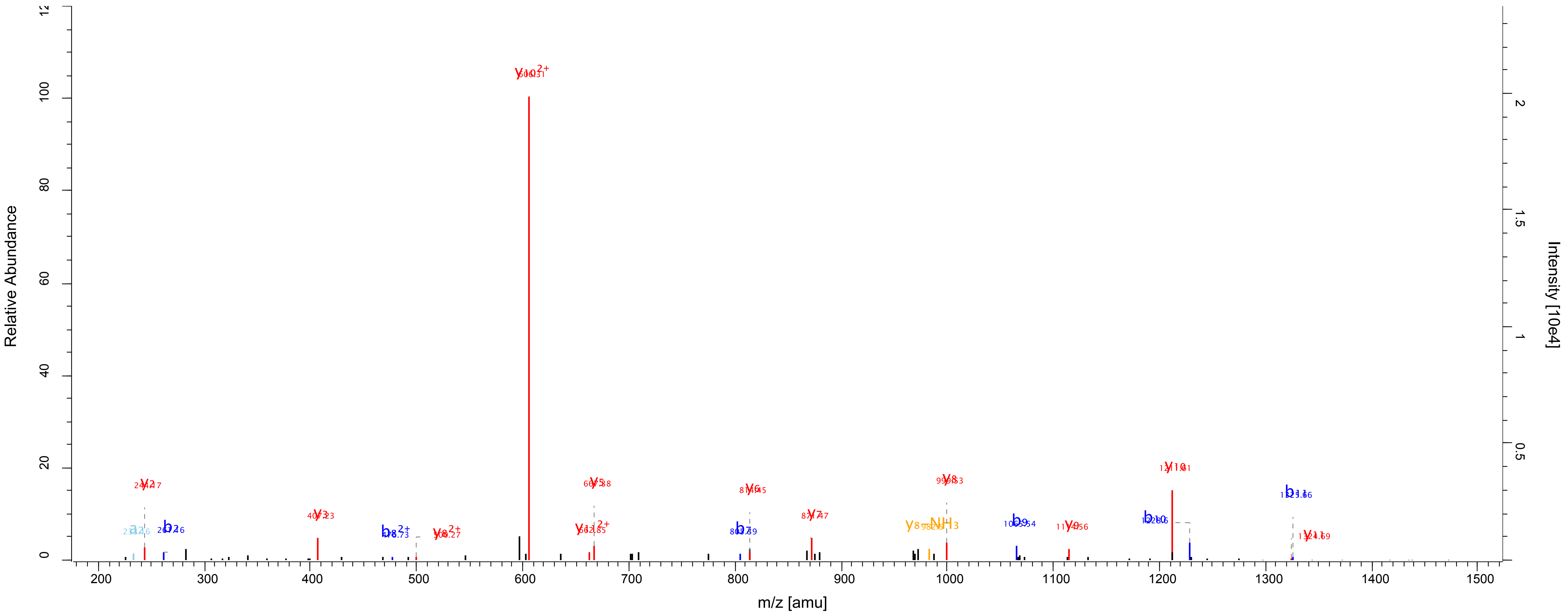
general information

Annotation:	13 of 24
AminoAcids Coverage:	54 %
Intensity Coverage:	66 %
Peak Coverage:	21 %
Protein Localisation:	123 ... 146

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.04986956		130.04986956	1	E	23				
	258.10844707		258.10844707	2	Q	22	2617.3772987		2617.3772987	
	371.19251105	+0.2585998	371.19251105	3	I	21	2489.3187212		2489.3187212	
	534.25583959		534.25583959	4	Y	20	2376.2346572		2376.2346572	
	662.3144171		662.3144171	5	Q	19	2213.1713287		1107.0893026	−0.1171346
	733.35153089		733.35153089	6	A	18	2085.1127512		2085.1127512	
	846.43559487		846.43559487	7	I	17	2014.0756374		2014.0756374	
	993.50400879	+0.342915	993.50400879	8	F	16	1900.9915734		1900.9915734	
	1130.5629207		1130.5629207	9	H	15	1753.9231595		1753.9231595	
	1201.6000344		1201.6000344	10	A	14	1616.8642476		1616.8642476	
	1300.6684484		1300.6684484	11	V	13	1545.8271338	−0.0342872	1545.8271338	
	1415.6953914		1415.6953914	12	D	12	1446.7587199		1446.7587199	
	1543.7539689	+0.1505721	1543.7539689	13	Q	11	1331.7317769		1331.7317769	
+0.073736	853.91228695		1706.8172974	14	Y	10	1203.6731994		1203.6731994	
	1819.9013614		1819.9013614	15	I	9	1040.6098708	+0.2584153	1040.6098708	
−0.018347	945.97287584	−0.1571031	1890.9384752	16	A	8	927.52580686	+0.1372791	927.52580686	
+0.1394501	1002.5149078		2004.0225392	17	I	7	856.48869308	−0.0491789	856.48869308	
	2101.075303		2101.075303	18	P	6	743.4046291	+0.0545384	743.4046291	
	2216.1022461		2216.1022461	19	D	5	646.35186524		646.35186524	
+0.1567593	1158.0889682		2315.17066	20	V	4	531.32492221	+0.1547531	531.32492221	
	2402.2026884		2402.2026884	21	S	3	432.25650829	+0.1740337	432.25650829	
−0.2306326	1258.1470144		2515.2867524	22	I	2	345.22447988	+0.0515821	345.22447988	
	2572.3082161		2572.3082161	23	G	1	232.1404159		232.1404159	
				24	R	0	175.11895218		175.11895218	

Scan number	13768	Raw file	20080721_Orbi1_SaZa_SA_ADH_Matrigel_Exp_1_Susp_InGel_08
Method	ITMS; CID	Genenames	GDF3





precursor information

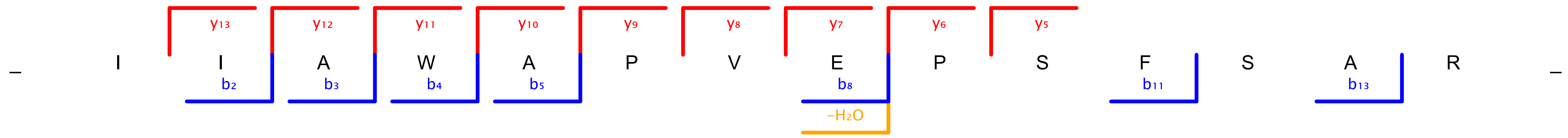
Mass:	1470.75558
m/z:	736.38507
Charge:	2+
Retentiontime:	107.72477722168
Score:	145.9146
Mass Error [ppm]:	0.57318
PEP:	6.30585E-05
Precursor Type:	ISO

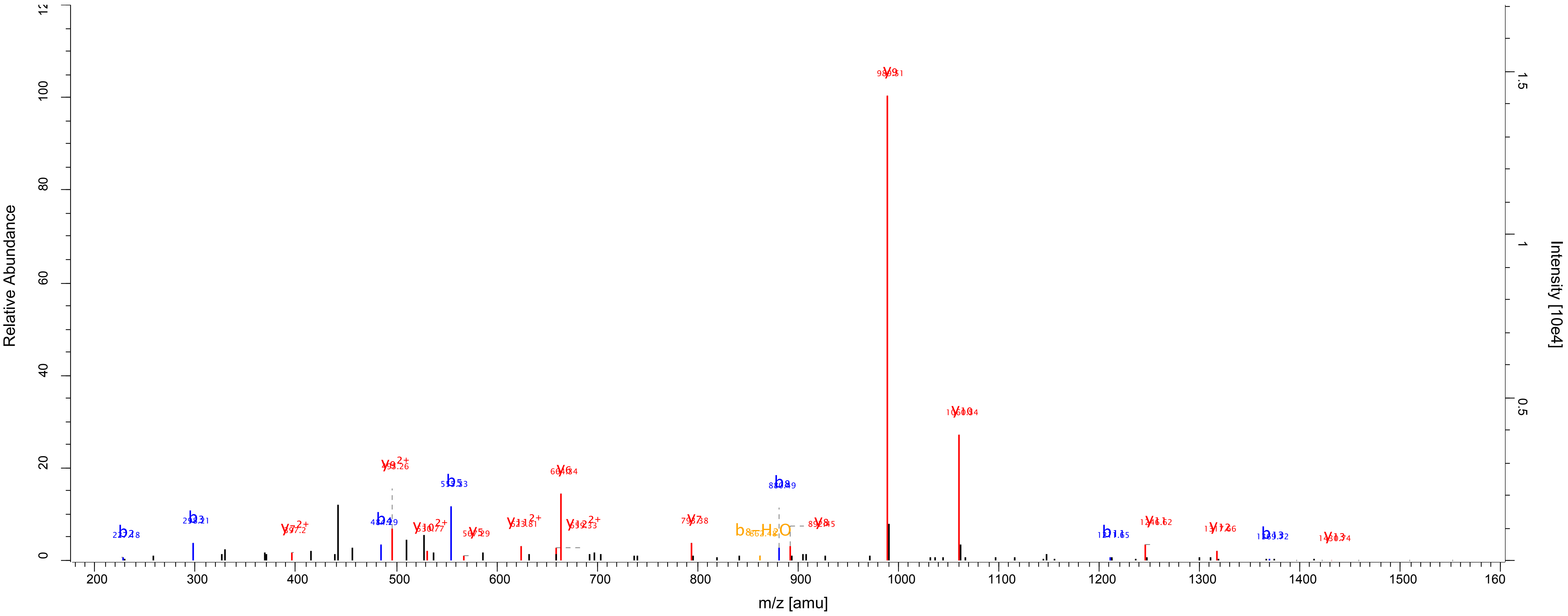
general information

Annotation:	10 of 12
AminoAcids Coverage:	83 %
Intensity Coverage:	77 %
Peak Coverage:	29 %
Protein Localisation:	85 ... 96

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.080776		148.07569		148.07569	1	F	11				
−0.001586	233.16484		261.159754	−0.0069834	261.159754	2	I	10	1324.6936	−0.1734589	662.850438	+0.0124155
	330.217604		358.212518		358.212518	3	P	9	1211.60954	+0.0534274	606.308406	+0.1314739
	445.244547		473.239461		473.239461	4	D	8	1114.55677	+0.1481834	1114.55677	
	573.303124		601.298039		601.298039	5	Q	7	999.52983	+0.0073408	500.268553	−0.0017684
	630.324588		658.319502		658.319502	6	G	6	871.471252	+0.0622562	871.471252	
	777.393002		805.387916	+0.199547	805.387916	7	F	5	814.449788	−0.0486043	814.449788	
	924.461416	+0.3941121	476.731803		952.45633	8	F	4	667.381374	+0.1340674	667.381374	
	1037.54548		1065.54039	−0.1351209	1065.54039	9	I	3	520.312961		520.312961	
	1200.60881		1228.60372	−0.0445187	1228.60372	10	Y	2	407.228897	+0.0363012	407.228897	
	1297.66157		1325.65649	+0.0533522	1325.65649	11	P	1	244.165568	+0.1530965	244.165568	
						12	K	0	147.112804		147.112804	

Scan number	13167	Raw file	20080721_Orbi1_SaZa_SA_ADH_Matrigel_Exp_1_Susp_InGel_10
Method	ITMS; CID	Genenames	PUS3





precursor information

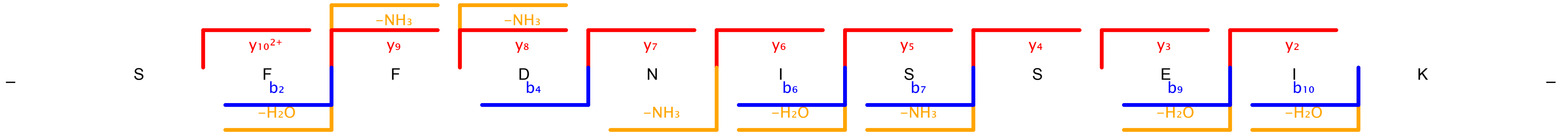
Mass:	1542.81963
m/z:	772.41709
Charge:	2+
Retentiontime:	97.9436950683594
Score:	128.6744
Mass Error [ppm]:	0.1111
PEP:	6.6846E-08
Precursor Type:	MULTI

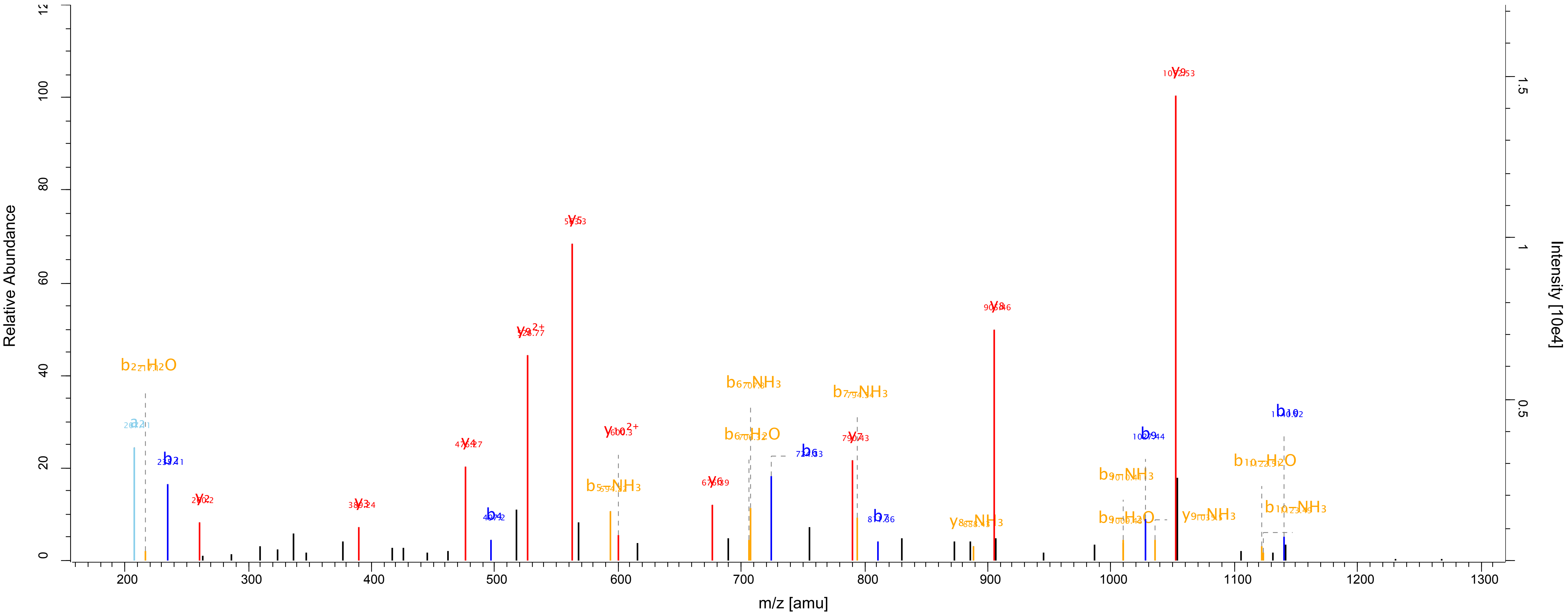
general information

Annotation:	11 of 14
AminoAcids Coverage:	79 %
Intensity Coverage:	71 %
Peak Coverage:	28 %
Protein Localisation:	174 ... 187

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.091340447	1	I	13				
+0.0786697	227.175404427	2	I	12	1430.742675931	+0.0828856	1430.742675931	
+0.0555787	298.212518215	3	A	11	1317.65861195	+0.0507386	659.332944208	−0.0140355
−0.1355812	484.291831169	4	W	10	1246.621498162	+0.0393905	623.814387315	−0.0009718
+0.0472147	555.328944956	5	A	9	1060.542185209	+0.0463158	530.774730838	+0.2137335
	652.381708808	6	P	8	989.505071421	+0.0590765	495.256173944	+0.075369
	751.450122725	7	V	7	892.452307569	+0.1482784	892.452307569	
−0.0279331	880.492715821	8	E	6	793.383893653	+0.2129081	397.19558506	−0.3757608
	977.545479673	9	P	5	664.341300557	+0.2139363	664.341300557	
	1064.577508083	10	S	4	567.288536705	+0.0851205	567.288536705	
−0.2349113	1211.645921999	11	F	3	480.256508295		480.256508295	
	1298.677950409	12	S	2	333.188094379		333.188094379	
−0.098487	1369.715064197	13	A	1	246.156065969		246.156065969	
		14	R	0	175.11895218		175.11895218	

Scan number	14054	Raw file	20080721_Orbi1_SaZa_SA_ADH_Matrigel_Exp_1_Susp_InGel_10
Method	ITMS; CID	Genenames	LSM14B





precursor information

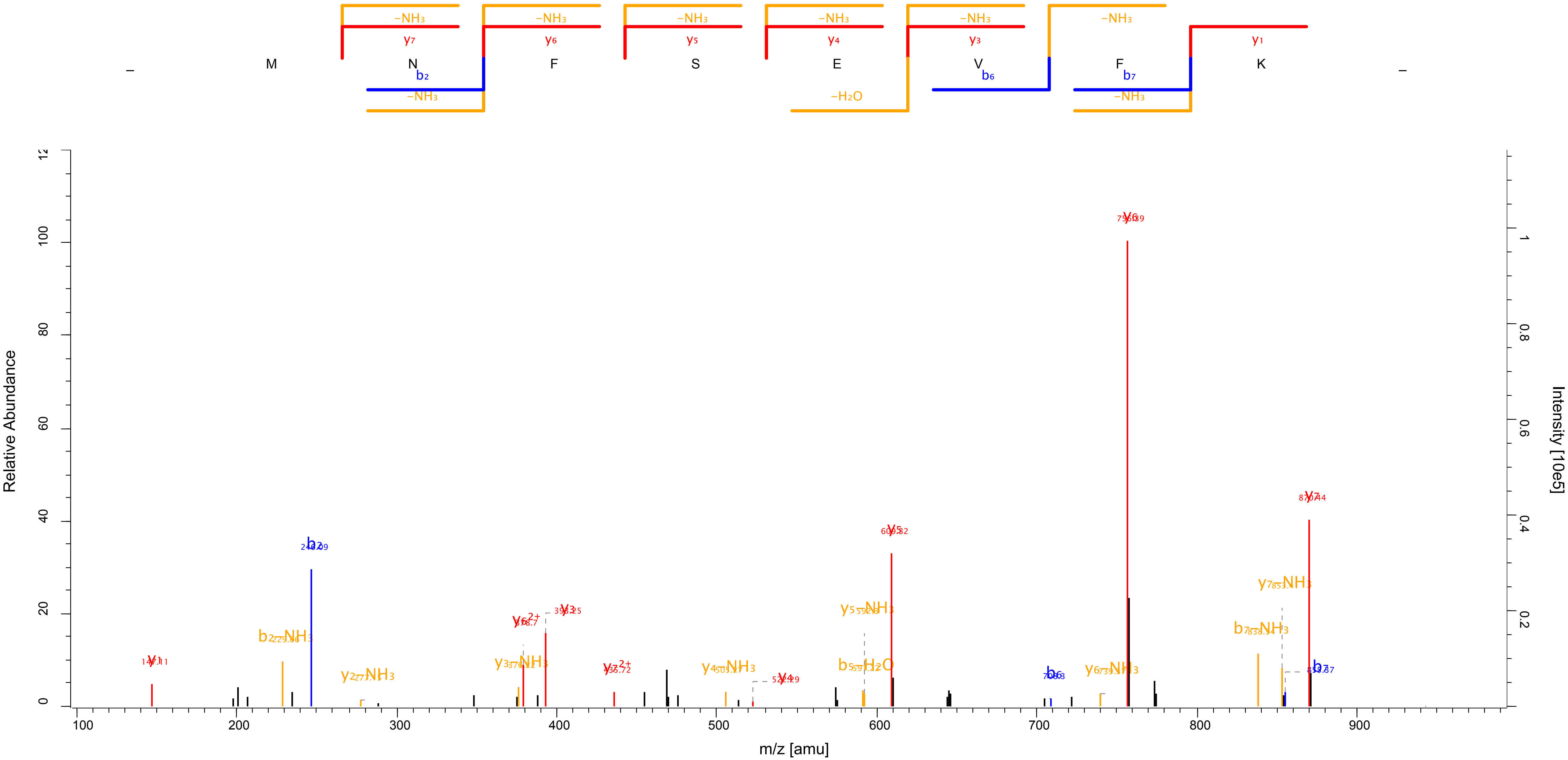
Mass:	1285.61902
m/z:	643.81679
Charge:	2+
Retentiontime:	103.104965209961
Score:	201.8443
Mass Error [ppm]:	-0.0074127
PEP:	9.3365E-17
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverage:	82 %
Intensity Coverage:	81 %
Peak Coverage:	50 %
Protein Localisation:	317 ... 327

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	60.044390254		88.039304876	1	S	10				
+0.0868113	207.11280417	-0.0092996	235.10771879	2	F	9	1199.5942804		600.30077841	+0.0433988
	354.18121809		382.17613271	3	F	8	1052.5258664	-0.0182981	526.76657145	+0.1390072
	469.20816112	-0.0028194	497.20307574	4	D	7	905.45745253	+0.078192	905.45745253	
	583.25108857		611.24600319	5	N	6	790.43050949	+0.1413289	790.43050949	
	696.33515255	+0.0883899	724.33006717	6	I	5	676.38758205	-0.0277798	676.38758205	
	783.36718096	+0.0860856	811.36209558	7	S	4	563.30351807	+0.099375	563.30351807	
	870.39920937		898.39412399	8	S	3	476.27148966	+0.0561471	476.27148966	
	999.44180246	+0.0386247	1027.4367171	9	E	2	389.23946125	+0.1147868	389.23946125	
	1112.5258664	-0.1658006	1140.5207811	10	I	1	260.19686815	+0.0278023	260.19686815	
				11	K	0	147.11280417		147.11280417	

Scan number	9339	Raw file	20080721_Orbi1_SaZa_SA_ADH_Matrigel_Exp_1_Susp_InGel_15
Method	ITMS; CID	Genenames	WRAP73;WDR8



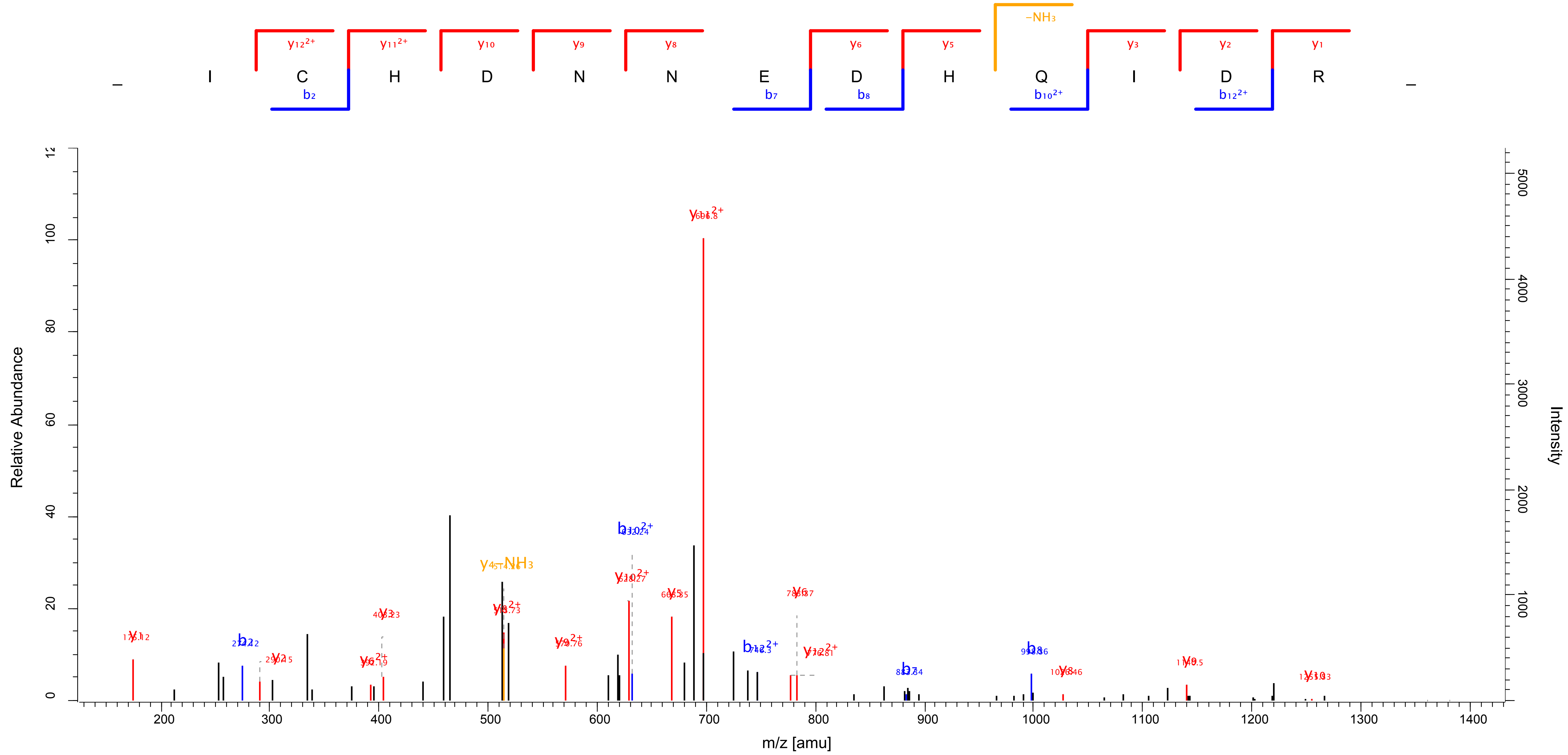
precursor information

Mass:	1000.46967
m/z:	501.24211
Charge:	2+
Retentiontime:	79.178825378418
Score:	164.5331
Mass Error [ppm]:	0.87106
PEP:	0.00039551
Annotation:	7 of 8
AminoAcids Coverage:	88 %
Intensity Coverage:	74 %
Peak Coverage:	43 %
Protein Localisation:	1 ... 8

ge
ir

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	132.047761073	1	M	7				
+0.099375	246.09068852	2	N	6	870.435594872	+0.0614144	435.72143567	+0.1679381
	393.159102436	3	F	5	756.392667425	+0.1012901	378.699971946	+0.0503943
	480.191130846	4	S	4	609.324253509	+0.058498	609.324253509	
	609.233723942	5	E	3	522.292225099	−0.0725596	522.292225099	
+0.1719832	708.302137859	6	V	2	393.249632003	+0.0563067	393.249632003	
+0.0976489	855.370551775	7	F	1	294.181218087		294.181218087	
		8	K	0	147.112804171	+0.0309794	147.112804171	

Scan number	2707	Raw file	20080804_Orbi1_SaZa_SA_ADH_Exp_1_BSA_InGel_05
Method	ITMS; CID	Genenames	RCHY1



precursor information

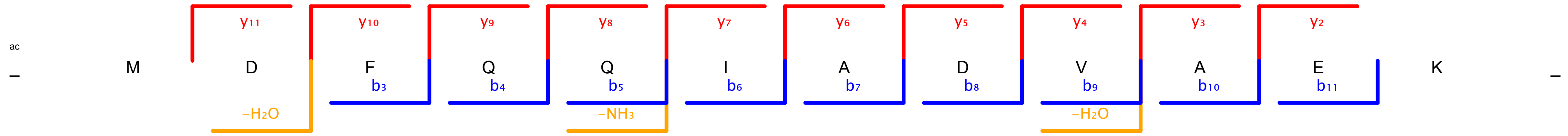
Mass:	1664.69611
m/z:	555.90598
Charge:	3+
Retentiontime:	38.4546775817871
Score:	105.2036
Mass Error [ppm]:	-0.013321
PEP:	0.00020273
Precursor Type:	MULTI

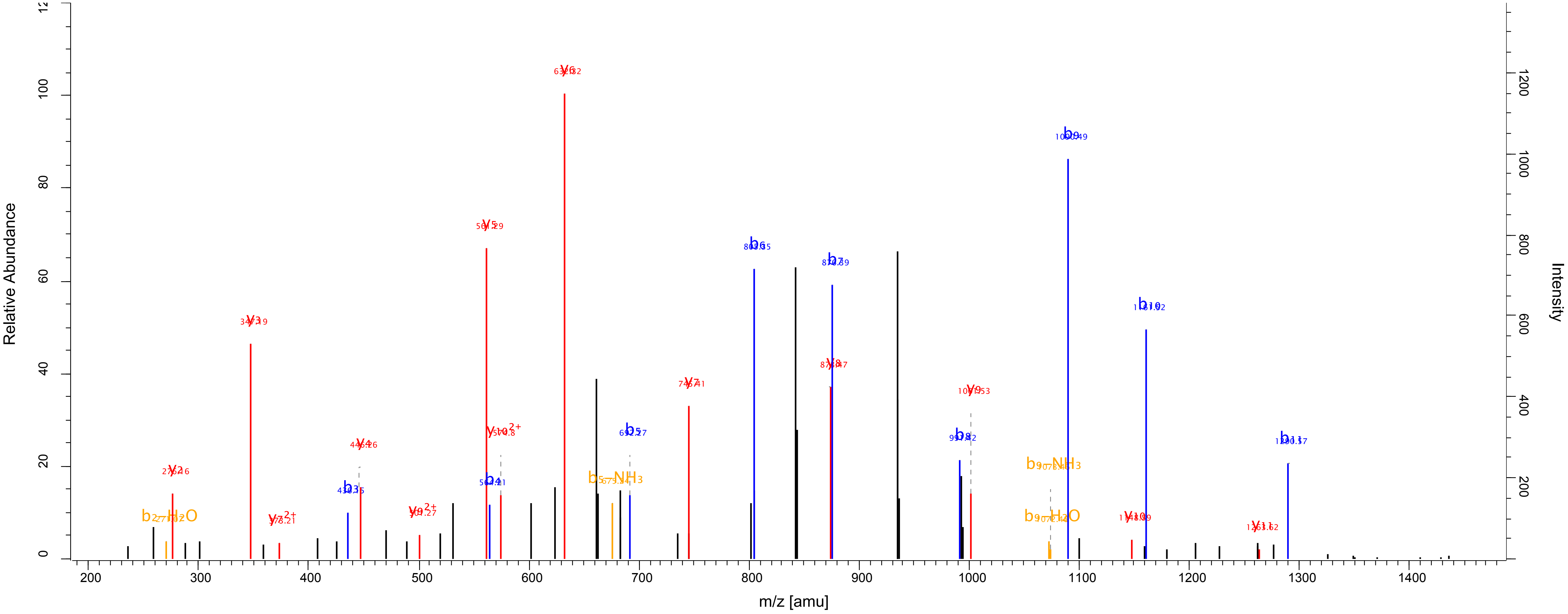
general information

Annotation:	12 of 13
AminoAcids Coverage:	92 %
Intensity Coverage:	46 %
Peak Coverage:	30 %
Protein Localisation:	42 ... 54

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045		114.09134045	1	I	12				
	274.12198865	+0.177755	274.12198865	2	C	11	1552.6193427		776.81330958	+0.3232871
	411.18090051		411.18090051	3	H	10	1392.5886945		696.79798548	+0.3011356
	526.20784354		526.20784354	4	D	9	1255.5297826	+0.0587184	628.26852954	+0.2304329
	640.25077099		640.25077099	5	N	8	1140.5028396	+0.1772141	570.75505803	+0.0847247
	754.29369844		754.29369844	6	N	7	1026.4599121	-0.0387696	513.7335943	-0.0207037
	883.33629153	-0.0276367	883.33629153	7	E	6	912.4169847		912.4169847	
	998.36323457	+0.1245584	998.36323457	8	D	5	783.3743916	+0.0529766	392.19083403	+0.1310043
	1135.4221464		1135.4221464	9	H	4	668.34744857	+0.0740602	668.34744857	
+0.2810852	632.2440002		1263.4807239	10	Q	3	531.2885367		531.2885367	
	1376.5647879		1376.5647879	11	I	2	403.22995919	+0.0337737	403.22995919	
+0.1995197	746.29950371		1491.591731	12	D	1	290.14589521	+0.0327547	290.14589521	
				13	R	0	175.11895218	+0.0491081	175.11895218	

Scan number	16648	Raw file	20080812_Orbi1_SaZa_SA_ADH_Matrigel_Exp_1_30h_InGel_01
Method	ITMS; CID	Genenames	C7orf41





precursor information

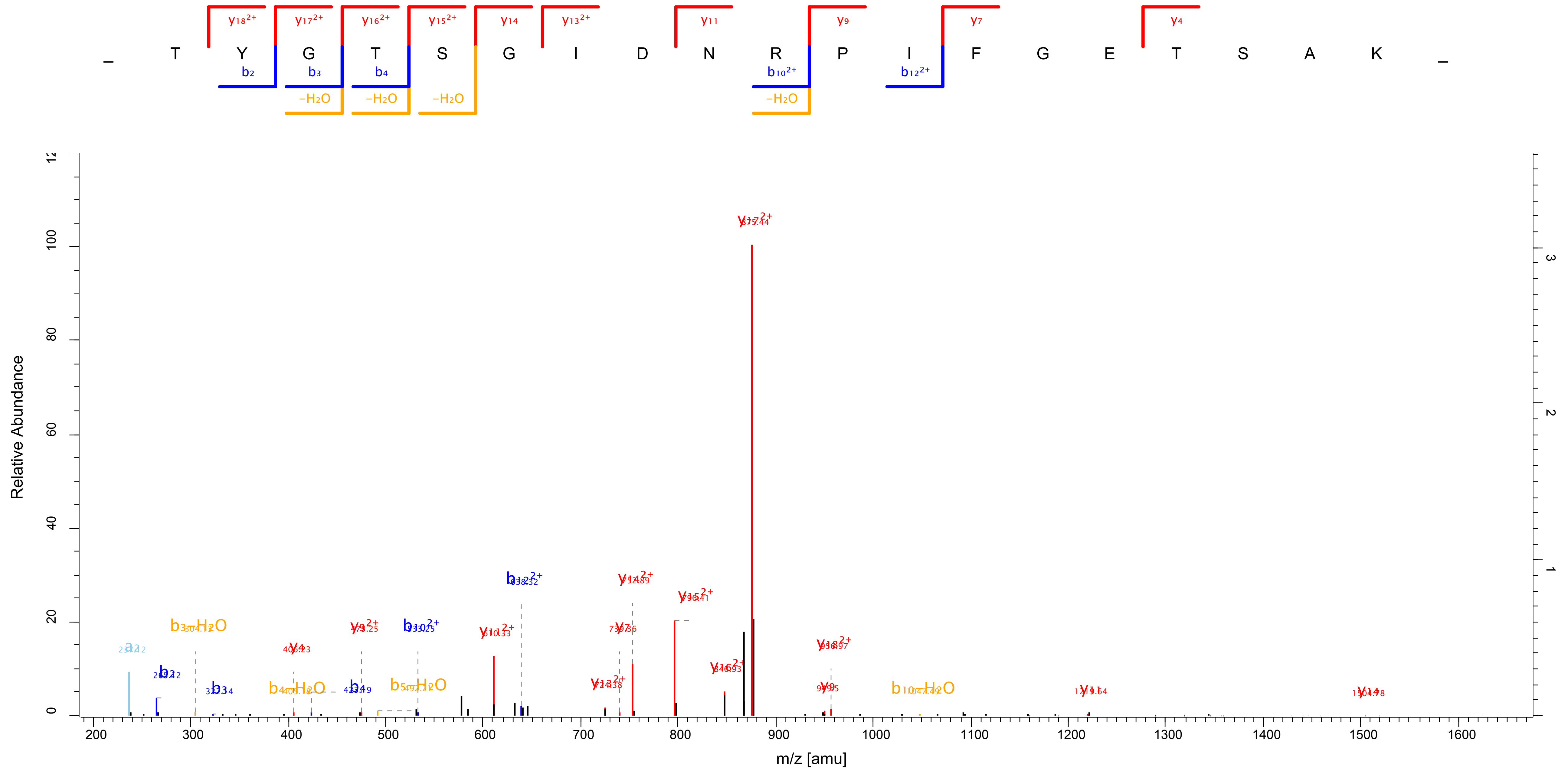
Mass:	1435.6661
m/z:	718.84033
Charge:	2+
Retentiontime:	118.112632751465
Score:	150.6929
Mass Error [ppm]:	0.53889
PEP:	2.6844E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverage:	83 %
Intensity Coverage:	61 %
Peak Coverage:	38 %
Protein Localisation:	1 ... 12

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	174.058325759	1	M	11				
	289.085268791	2	D	10	1263.621557742	−0.0296388	1263.621557742	
+0.0399818	436.153682707	3	F	9	1148.59461471	−0.0462749	574.800945588	+0.2971989
−0.0215254	564.212260219	4	Q	8	1001.526200794	+0.178328	501.26673863	+0.0414279
+0.0110226	692.27083773	5	Q	7	873.467623282	+0.1498694	873.467623282	
+0.1004816	805.35490171	6	I	6	745.409045771	+0.1702389	373.208161119	+0.1616509
−0.1262074	876.392015498	7	A	5	632.324981791	+0.1256408	632.324981791	
+0.0435048	991.41895853	8	D	4	561.287868003	+0.0441022	561.287868003	
−0.1151801	1090.487372446	9	V	3	446.260924971	+0.1531375	446.260924971	
−0.1270253	1161.524486234	10	A	2	347.192511055	+0.0490051	347.192511055	
−0.1646135	1290.56707933	11	E	1	276.155397267	+0.0841047	276.155397267	
		12	K	0	147.112804171		147.112804171	

Scan number	8383	Raw file	20080812_Orbi1_SaZa_SA_ADH_Matrigel_Exp_1_30h_InGel_01
Method	ITMS; CID	Genenames	C7orf23



precursor information

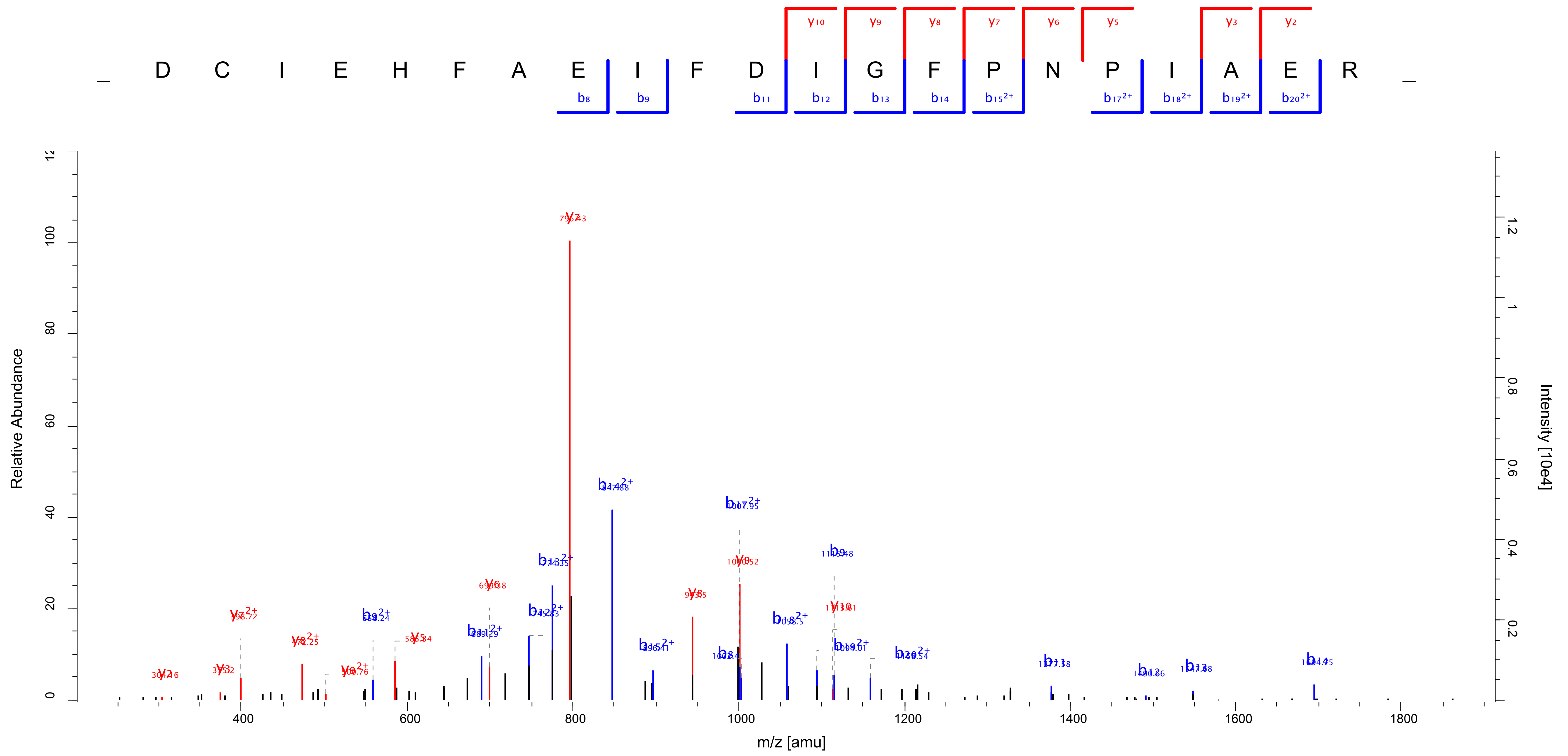
Mass:	2012.97907
m/z:	672.0003
Charge:	3+
Retentiontime:	69.7183685302734
Score:	107.7354
Mass Error [ppm]:	-0.6291
PEP:	2.1079E-07
Precursor Type:	MULTI

general information

Annotation:	12 of 19
AminoAcids Coverage:	63 %
Intensity Coverage:	69 %
Peak Coverage:	30 %
Protein Localisation:	8 ... 26

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.0600403		102.054955		102.054955	1	T	18				
+0.1033462	237.123369		265.118283	+0.0723903	265.118283	2	Y	17	1912.93993		956.973604	+0.4790936
	294.144833		322.139747	+0.2201161	322.139747	3	G	16	1749.8766		875.44194	+0.3200841
	395.192511		423.187426	+0.0987682	423.187426	4	T	15	1692.85514		846.931208	+0.1716363
	482.224539		510.219454		510.219454	5	S	14	1591.80746		796.407369	+0.2635297
	539.246003		567.240918		567.240918	6	G	13	1504.77543	+0.3103828	752.891355	+0.276187
	652.330067		680.324982		680.324982	7	I	12	1447.75397		724.380623	+0.14489
	767.35701		795.351925		795.351925	8	D	11	1334.6699		1334.6699	
	881.399938		909.394852		909.394852	9	N	10	1219.64296	+0.0745674	610.325119	+0.3010405
	1037.50105	+0.2571081	533.25162		1065.49596	10	R	9	1105.60003		1105.60003	
	1134.55381		1162.54873		1162.54873	11	P	8	949.498923	+0.1289452	475.2531	+0.1410651
	1247.63788	+0.412266	638.320034		1275.63279	12	I	7	852.44616		852.44616	
	1394.70629		1422.70121		1422.70121	13	F	6	739.362096	+0.105922	739.362096	
	1451.72775		1479.72267		1479.72267	14	G	5	592.293682		592.293682	
	1580.77035		1608.76526		1608.76526	15	E	4	535.272218		535.272218	
	1681.81803		1709.81294		1709.81294	16	T	3	406.229625	+0.0902604	406.229625	
	1768.85005		1796.84497		1796.84497	17	S	2	305.181946		305.181946	
	1839.88717		1867.88208		1867.88208	18	A	1	218.149918		218.149918	
						19	K	0	147.112804		147.112804	

Scan number	18932	Raw file	20080812_Orbi1_SaZa_SA_ADH_Matrigel_Exp_1_30h_InGel_03
Method	ITMS; CID	Genenames	RAMP2



precursor information

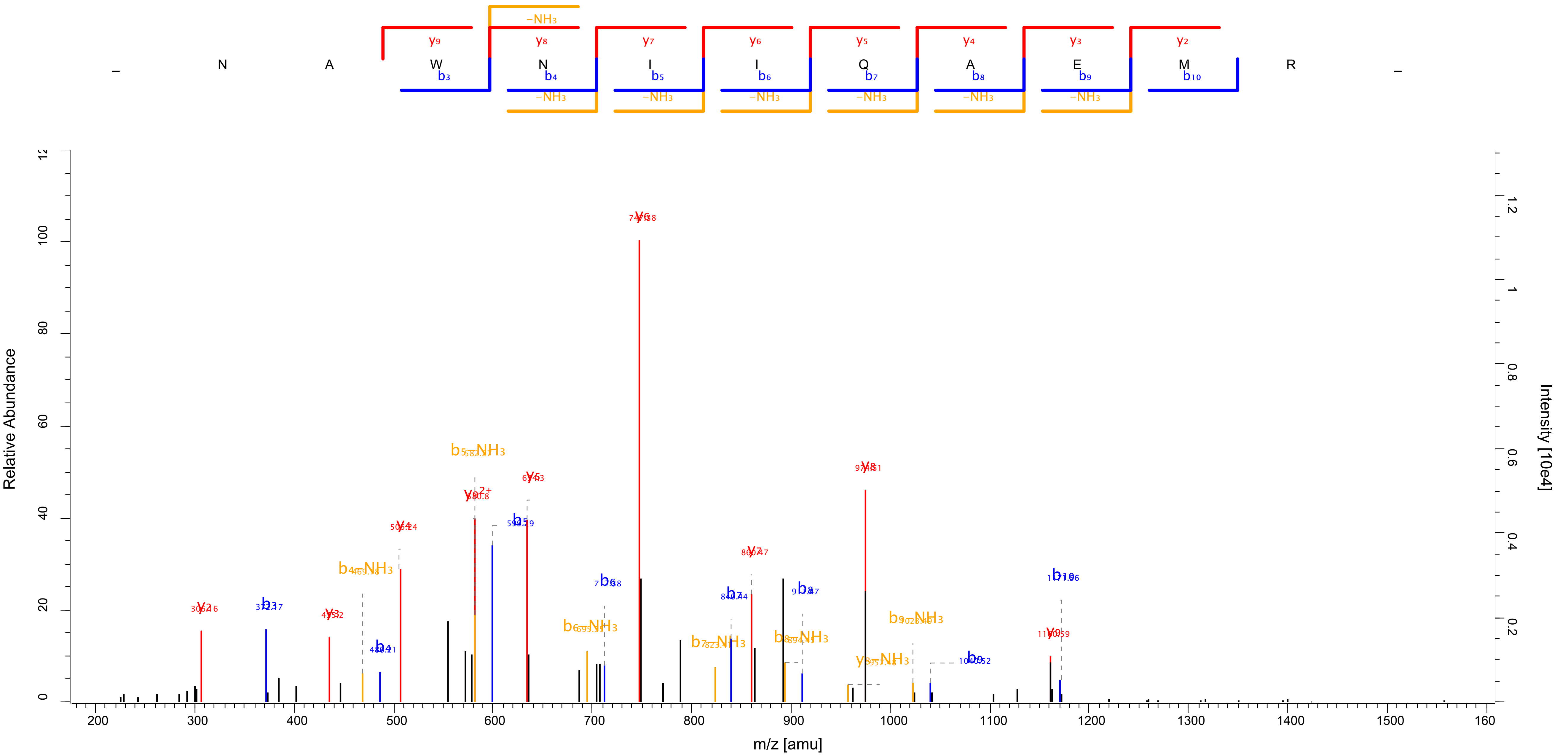
Mass:	2489.16793
m/z:	830.72992
Charge:	3+
Retentiontime:	128.451553344727
Score:	154.8232
Mass Error [ppm]:	-0.24812
PEP:	2.456E-12
Precursor Type:	ISO

general information

Annotation:	12 of 21
AminoAcids Coverage:	57 %
Intensity Coverage:	68 %
Peak Coverage:	30 %
Protein Localisation:	103 ... 123

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342195		116.0342195	1	D	20				
	276.0648677		276.0648677	2	C	19	2375.1488787		2375.1488787	
	389.14893168		389.14893168	3	I	18	2215.1182305		2215.1182305	
	518.19152478		518.19152478	4	E	17	2102.0341665		2102.0341665	
	655.25043664		655.25043664	5	H	16	1972.9915734		1972.9915734	
	802.31885056		802.31885056	6	F	15	1835.9326615		1835.9326615	
	873.35596434		873.35596434	7	A	14	1688.8642476		1688.8642476	
	1002.3985574	+0.1904929	1002.3985574	8	E	13	1617.8271338		1617.8271338	
+0.1626438	558.24494894	+0.1265094	1115.4826214	9	I	12	1488.7845407		1488.7845407	
	1262.5510353		1262.5510353	10	F	11	1375.7004768		1375.7004768	
+0.0346431	689.29262742	+0.1513917	1377.5779784	11	D	10	1228.6320628		1228.6320628	
+0.025448	745.83465941	+0.1333678	1490.6620423	12	I	9	1113.6051198	+0.1718577	1113.6051198	
+0.0249701	774.34539127	+0.0578269	1547.6835061	13	G	8	1000.5210558	+0.0797132	500.76416615	+0.2457826
+0.3311562	847.87959823	-0.0176671	1694.75192	14	F	7	943.49959211	+0.0829274	472.25343429	+0.1473225
+0.17422	896.40598015		1791.8046838	15	P	6	796.4311782	+0.0490464	398.71922733	+0.0232653
	1905.8476113		1905.8476113	16	N	5	699.37841434	+0.1766394	699.37841434	
-0.3473195	1001.9538258		2002.9003751	17	P	4	585.3354869	+0.211205	585.3354869	
+0.3151774	1058.4958578		2115.9844391	18	I	3	488.28272305		488.28272305	
-0.0206403	1094.0144147		2187.0215529	19	A	2	375.19865906	+0.1093854	375.19865906	
+0.4630681	1158.5357112		2316.064146	20	E	1	304.16154528	+0.0814967	304.16154528	
				21	R	0	175.11895218		175.11895218	

Scan number	14121	Raw file	20080812_Orbi1_SaZa_SA_ADH_Matrigel_Exp_1_30h_InGel_04
Method	ITMS; CID	Genenames	TSPAN9



precursor information

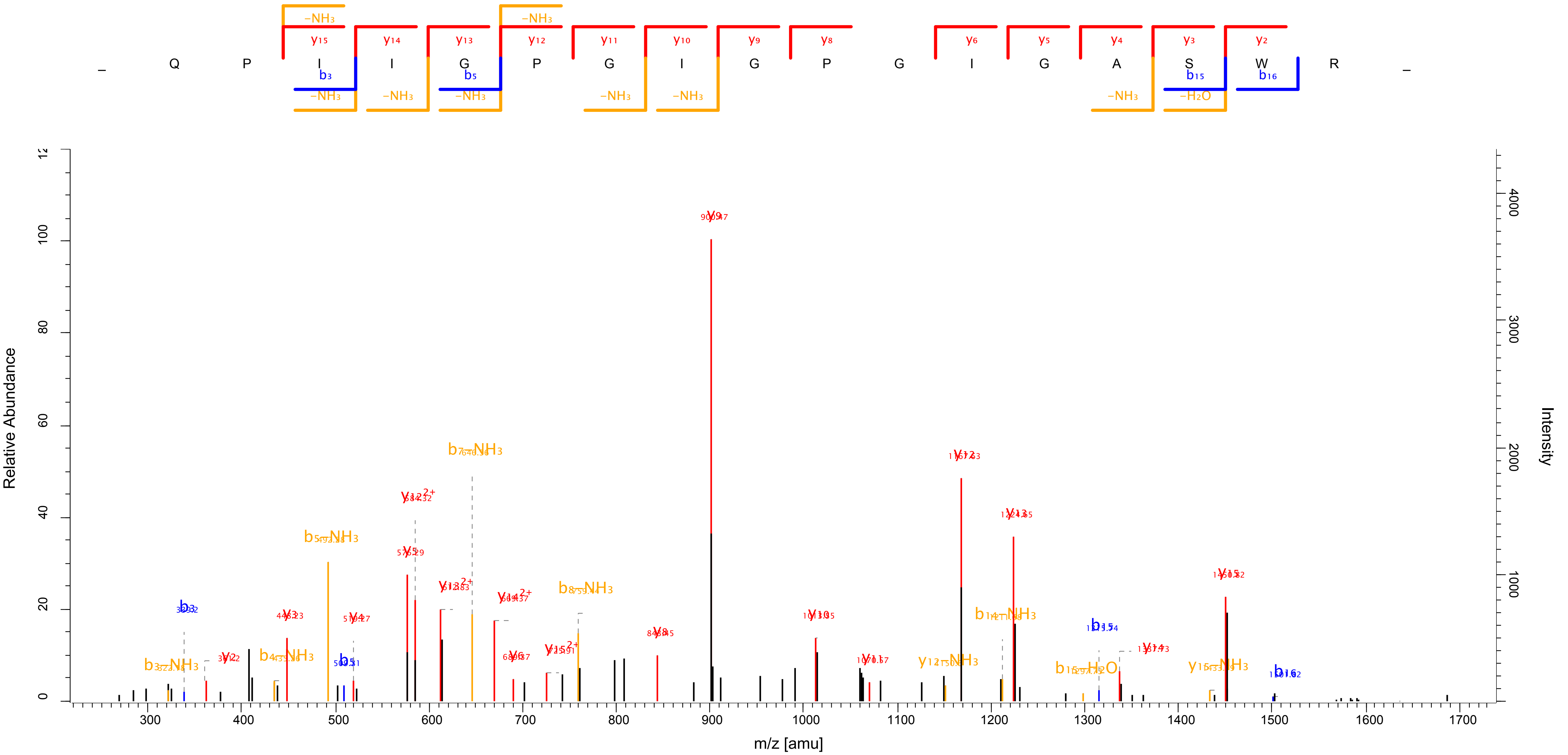
Mass:	2007.918
m/z:	670.31328
Charge:	3+
Retentiontime:	99.168815612793
Score:	177.5723
Mass Error [ppm]:	0.49576
PEP:	5.9363E−40
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverage:	73 %
Intensity Coverage:	66 %
Peak Coverage:	35 %
Protein Localisation:	136 ... 146

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.050203914	1	N	10				
	186.087317702	2	A	9	1231.625203332		1231.625203332	
+0.1285354	372.166630655	3	W	8	1160.588089544	−0.0070349	580.797683005	+0.3118751
+0.1740479	486.209558102	4	N	7	974.508776591	−0.0032224	974.508776591	
+0.0627622	599.293622083	5	I	6	860.465849143	−0.0215132	860.465849143	
+0.0556025	712.377686063	6	I	5	747.381785163	+0.050771	747.381785163	
−0.042831	840.436263574	7	Q	4	634.297721183	+0.0945518	634.297721183	
+0.2001456	911.473377362	8	A	3	506.239143671	+0.0612103	506.239143671	
−0.0250037	1040.515970458	9	E	2	435.202029883	+0.0057338	435.202029883	
−0.0673193	1171.556455065	10	M	1	306.159436787	+0.0568108	306.159436787	
		11	R	0	175.118952181		175.118952181	

Scan number	14326	Raw file	20080812_Orbi1_SaZa_SA_ADH_Matrigel_Exp_1_30h_InGel_05
Method	ITMS; CID	Genenames	DIRC2



precursor information

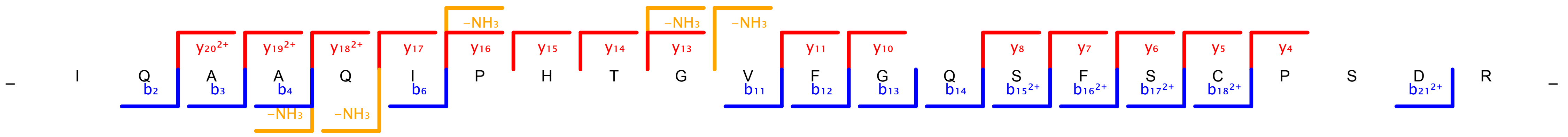
Mass:	1674.92007
m/z:	838.46731
Charge:	2+
Retentiontime:	101.204124450684
Score:	133.4825
Mass Error [ppm]:	−0.3003
PEP:	0.00023629
Precursor Type:	ISO

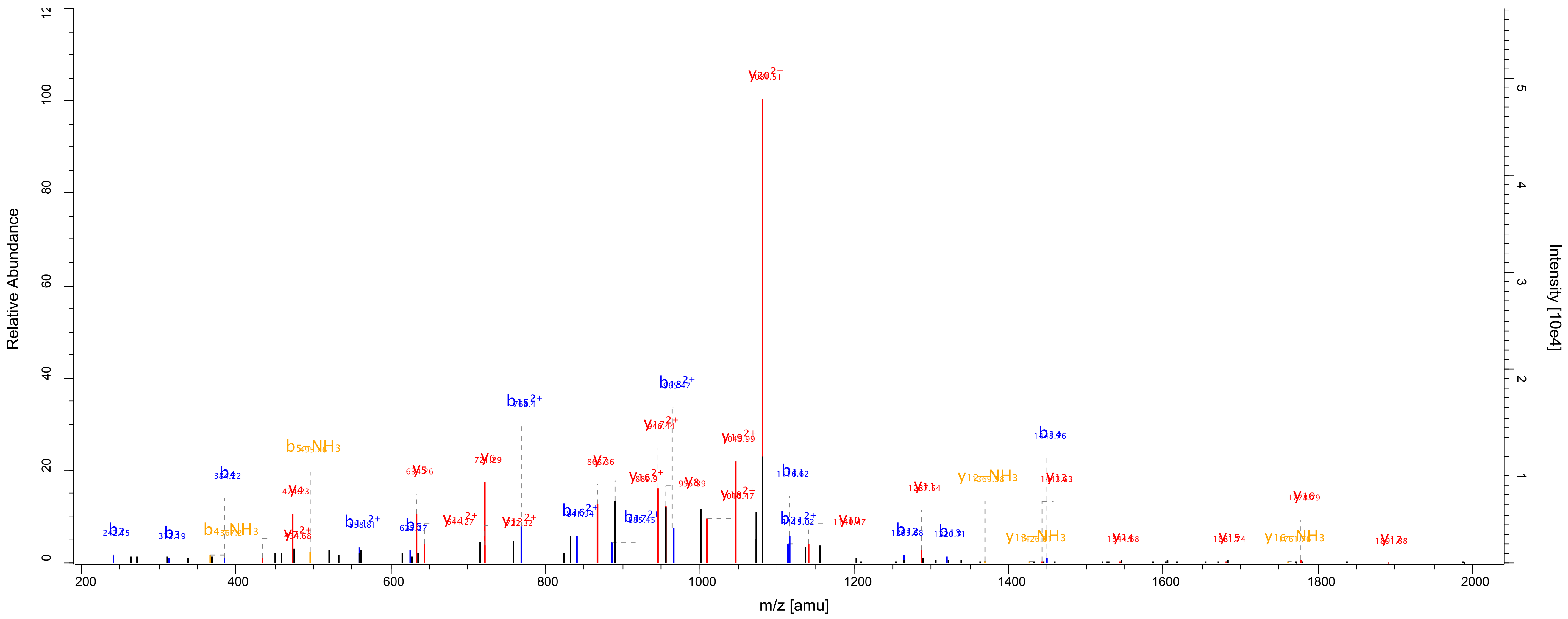
general information

Annotation:	13 of 17
AminoAcids Coverage:	76 %
Intensity Coverage:	58 %
Peak Coverage:	35 %
Protein Localisation:	12 ... 28

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.065853978	1	Q	16				
	226.11861783	2	P	15	1547.869273428		1547.869273428	
+0.046128	339.20268181	3	I	14	1450.816509576	+0.0090519	725.911893021	+0.2048062
	452.286745791	4	I	13	1337.732445595	−0.0533684	669.369861031	+0.2060057
−0.0980044	509.308209514	5	G	12	1224.648381615	−0.0094656	612.827829041	−0.0686738
	606.360973366	6	P	11	1167.626917891	+0.0349473	584.317097179	+0.0749316
	663.38243709	7	G	10	1070.574154039	−0.0814783	1070.574154039	
	776.46650107	8	I	9	1013.552690316	−0.0319994	1013.552690316	
	833.487964794	9	G	8	900.468626335	+0.0365006	900.468626335	
	930.540728646	10	P	7	843.447162612	+0.0879326	843.447162612	
	987.56219237	11	G	6	746.39439876		746.39439876	
	1100.64625635	12	I	5	689.372935036	−0.0166728	689.372935036	
	1157.667720074	13	G	4	576.288871056	+0.0794151	576.288871056	
	1228.704833861	14	A	3	519.267407332	+0.1575805	519.267407332	
−0.1162568	1315.736862271	15	S	2	448.230293544	+0.1359174	448.230293544	
+0.0694449	1501.816175225	16	W	1	361.198265134	+0.1221694	361.198265134	
		17	R	0	175.118952181		175.118952181	

Scan number	10544	Raw file	20080812_Orbi1_SaZa_SA_ADH_Matrigel_Exp_1_30h_InGel_15
Method	ITMS; CID	Genenames	CD68





precursor information

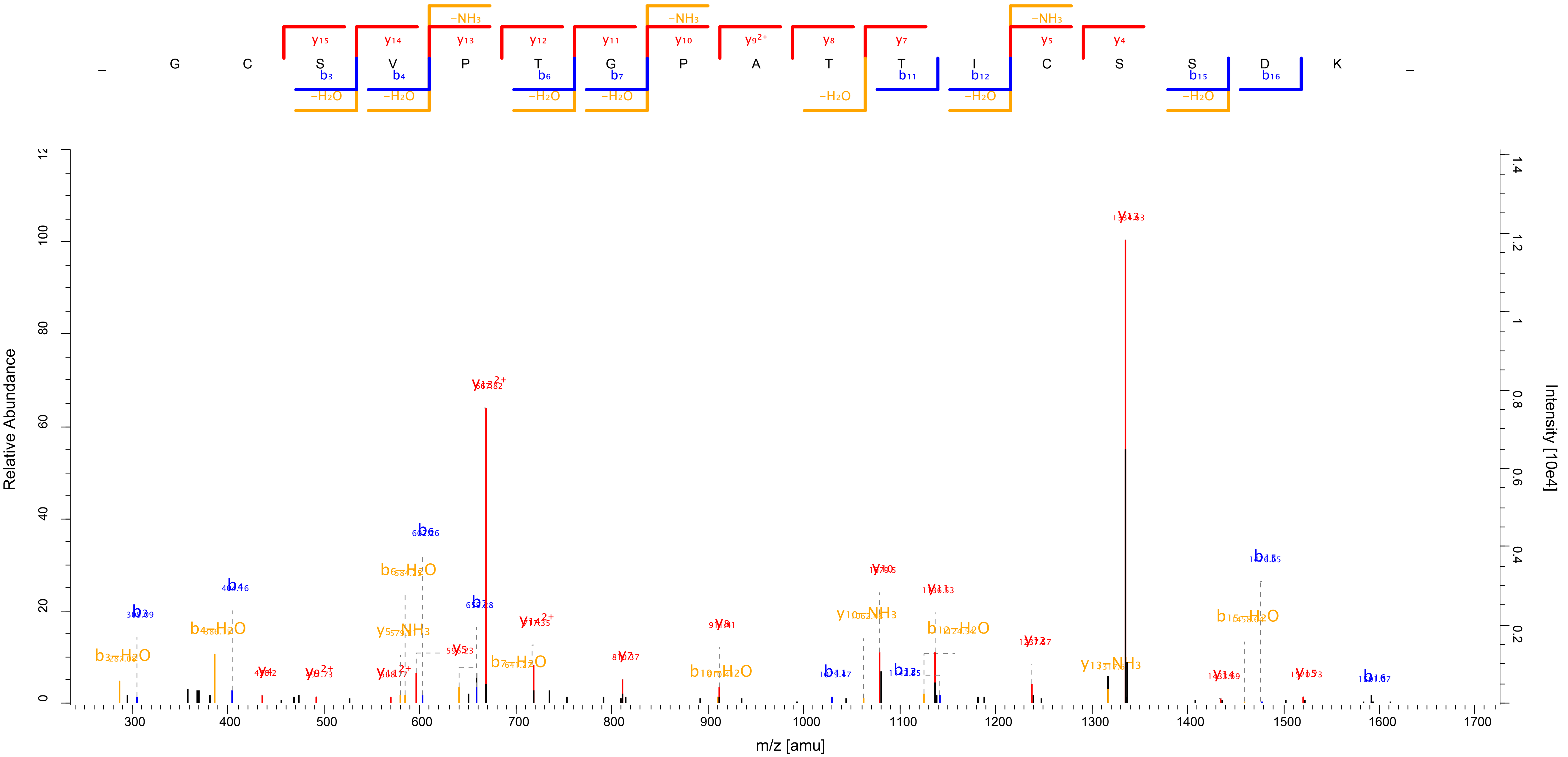
Mass:	2402.14378
m/z:	801.72187
Charge:	3+
Retentiontime:	79.8389892578125
Score:	194.9358
Mass Error [ppm]:	0.020242
PEP:	5.7974E−57
Precursor Type:	MULTI

general information

Annotation:	19 of 22
AminoAcids Coverage:	86 %
Intensity Coverage:	67 %
Peak Coverage:	38 %
Protein Localisation:	297 ... 318

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045		114.09134045	1	I	21				
	242.14991796	−0.2574009	242.14991796	2	Q	20	2290.06694		2290.06694	
	313.18703175	+0.0010786	313.18703175	3	A	19	2162.0083625		1081.5078195	+0.2900321
	384.22414553	−0.0456787	384.22414553	4	A	18	2090.9712487		1045.9892626	+0.2810011
	512.28272305		512.28272305	5	Q	17	2019.9341349		1010.4707057	+0.2534765
	625.36678703	+0.0220069	625.36678703	6	I	16	1891.8755574	+0.0776897	946.44141692	+0.3536881
	722.41955088		722.41955088	7	P	15	1778.7914934	−0.044301	889.89938493	+0.0133958
	859.47846274		859.47846274	8	H	14	1681.7387295	−0.0664883	1681.7387295	
	960.52614121		960.52614121	9	T	13	1544.6798177	+0.2221599	1544.6798177	
	1017.5476049		1017.5476049	10	G	12	1443.6321392	+0.116518	722.31970783	−0.0044002
+0.029722	558.81164766	−0.1296907	1116.6160189	11	V	11	1386.6106755		1386.6106755	
	1263.6844328	+0.1355135	1263.6844328	12	F	10	1287.5422616	+0.1207023	644.27476902	+0.1331289
	1320.7058965	+0.1194209	1320.7058965	13	G	9	1140.4738476	−0.1104443	1140.4738476	
	1448.764474	−0.1432582	1448.764474	14	Q	8	1083.4523839		1083.4523839	
+0.3191189	768.40188944		1535.7965024	15	S	7	955.39380641	+0.0269089	955.39380641	
−0.1242068	841.9360964		1682.8649163	16	F	6	868.361778	+0.0634539	434.68452723	−0.0171688
+0.1818616	885.4521106		1769.8969447	17	S	5	721.29336409	+0.1354079	721.29336409	
+0.1849701	965.4674347		1929.9275929	18	C	4	634.26133568	+0.0928513	634.26133568	
	2026.9803568		2026.9803568	19	P	3	474.23068747	+0.1203257	474.23068747	
	2114.0123852		2114.0123852	20	S	2	377.17792362		377.17792362	
+0.294935	1115.0233024		2229.0393282	21	D	1	290.14589521		290.14589521	
				22	R	0	175.11895218		175.11895218	

Scan number	8252	Raw file	20080910_Orbi4_SaZa_SA_ADH_Matrigel_Exp_1_12h_InGel_07
Method	ITMS; CID	Genenames	KRTAP3-3



precursor information

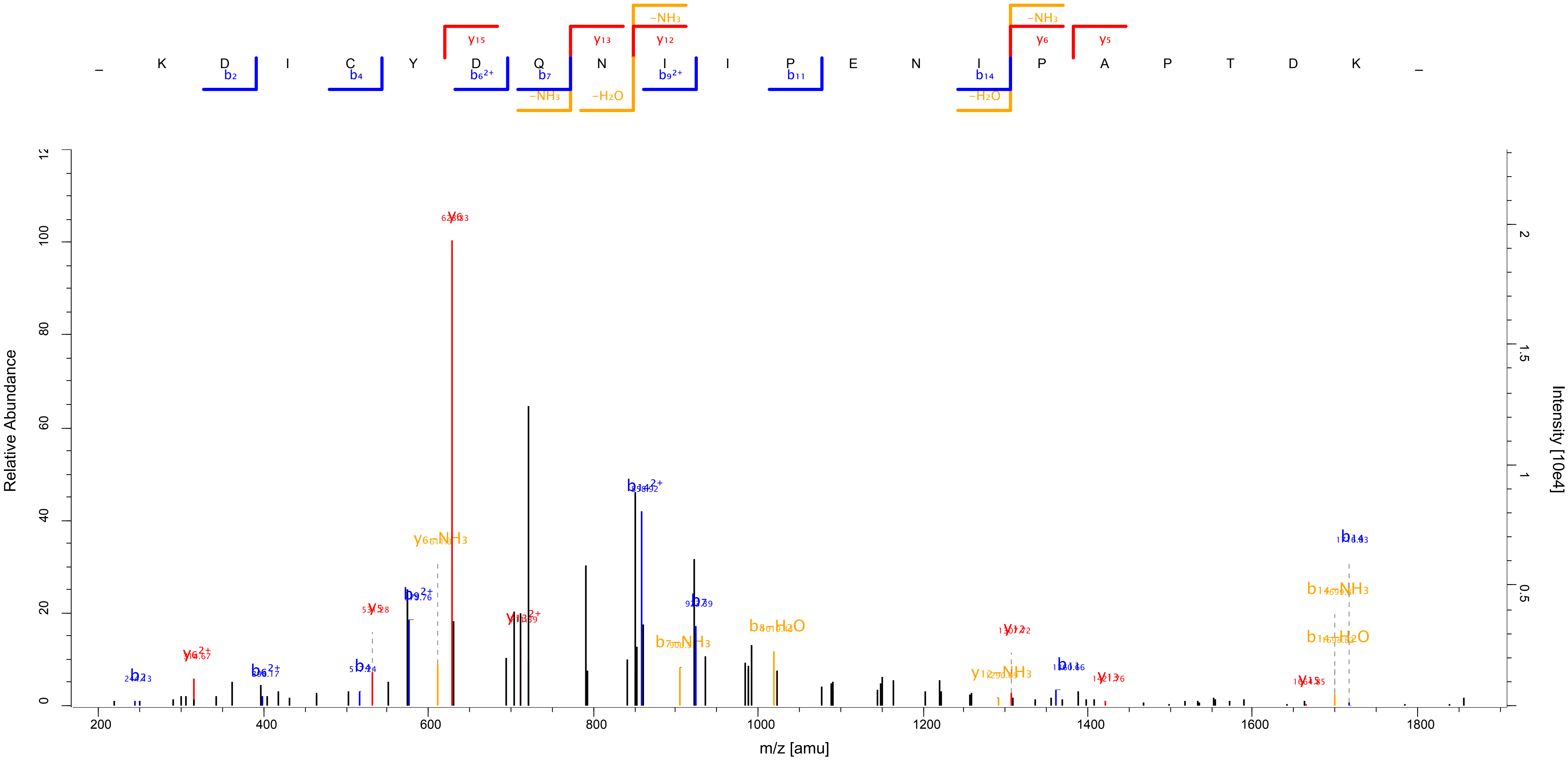
Mass:	1736.771
m/z:	869.39278
Charge:	2+
Retentiontime:	63.2597618103027
Score:	197.1886
Mass Error [ppm]:	0.037861
PEP:	2.8762E-25
Precursor Type:	ISO

general information

Annotation:	14 of 17
AminoAcids Coverage:	82 %
Intensity Coverage:	64 %
Peak Coverage:	41 %
Protein Localisation:	8 ... 24

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019	1	G	16				
	218.059388392	2	C	15	1680.756747369		1680.756747369	
+0.2565751	305.091416802	3	S	14	1520.726099168	−0.0058843	1520.726099168	
+0.0510457	404.159830718	4	V	13	1433.694070758	+0.3139859	717.350673612	+0.2525979
	501.21259457	5	P	12	1334.625656842	+0.0263207	667.816466654	+0.2862555
+0.3663749	602.260273044	6	T	11	1237.57289299	−0.0236987	1237.57289299	
+0.2278458	659.281736767	7	G	10	1136.525214516	+0.0430228	568.766245491	+0.0250753
	756.334500619	8	P	9	1079.503750792	−0.0198641	1079.503750792	
	827.371614407	9	A	8	982.45098694		491.729131703	+0.2531681
	928.419292881	10	T	7	911.413873152	+0.1001039	911.413873152	
+0.0955286	1029.466971355	11	T	6	810.366194678	+0.20955	810.366194678	
+0.0834861	1142.551035336	12	I	5	709.318516204		709.318516204	
	1302.581683537	13	C	4	596.234452224	+0.1021567	596.234452224	
	1389.613711947	14	S	3	436.203804022	+0.1025314	436.203804022	
+0.4705927	1476.645740357	15	S	2	349.171775612		349.171775612	
−0.4726101	1591.672683389	16	D	1	262.139747203		262.139747203	
		17	K	0	147.112804171		147.112804171	

Scan number	14342	Raw file	20080910_Orbi4_SaZa_SA_ADH_Matrigel_Exp_1_12h_InGel_08
Method	ITMS; CID	Genenames	CAPS2



precursor information

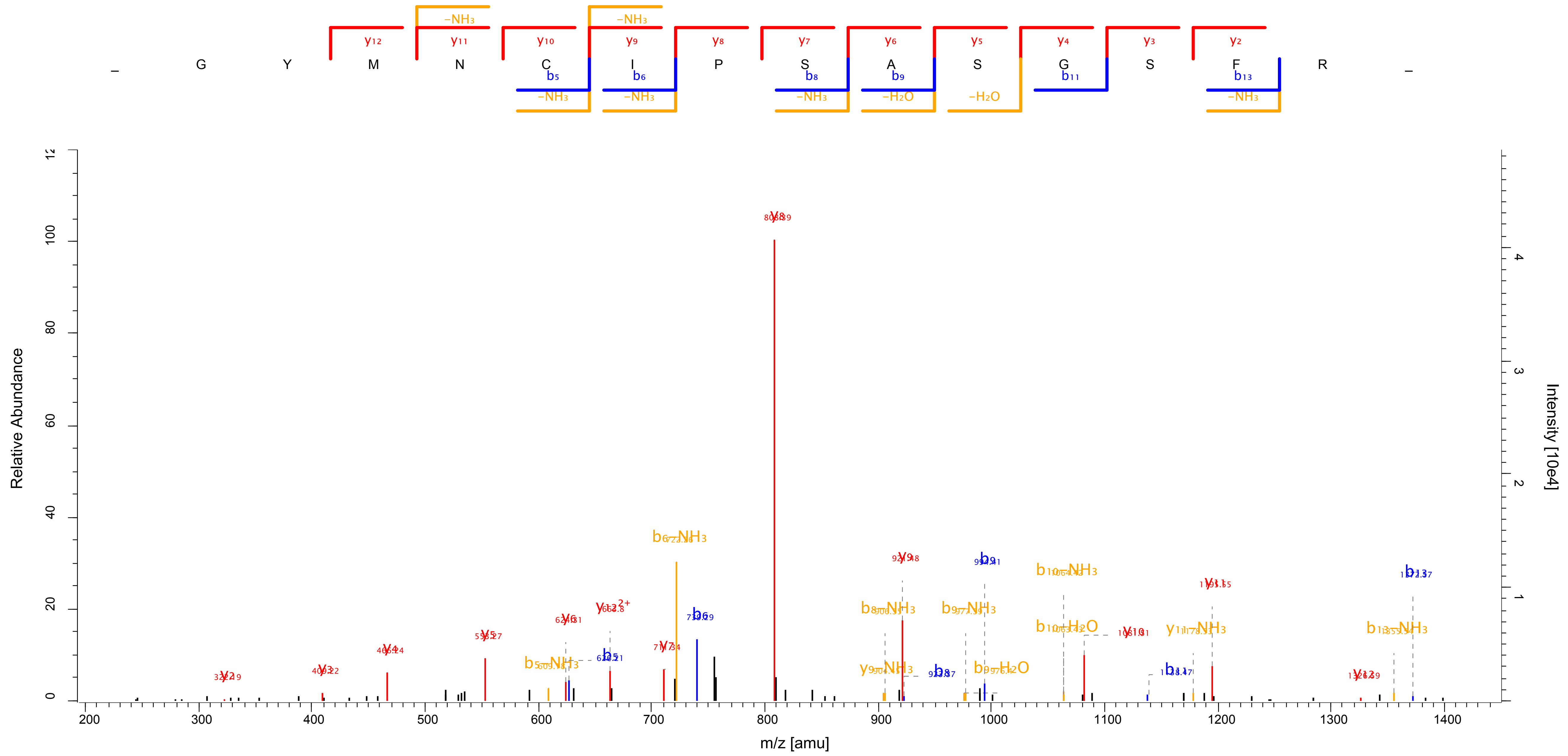
Mass:	2343.14571
m/z:	782.05585
Charge:	3+
Retentiontime:	99.0999908447266
Score:	85.56325
Mass Error [ppm]:	1.7268
PEP:	3.8986E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 20
AminoAcids Coverage:	50 %
Intensity Coverage:	32 %
Peak Coverage:	23 %
Protein Localisation:	7 ... 26

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.10223948		129.10223948	1	K	19				
	244.12918252	+0.0507796	244.12918252	2	D	18	2216.0539752		2216.0539752	
	357.2132465		357.2132465	3	I	17	2101.0270322		2101.0270322	
	517.2438947	-0.2640973	517.2438947	4	C	16	1987.9429682		1987.9429682	
	680.30722324		680.30722324	5	Y	15	1827.91232		1827.91232	
-0.1087707	398.17072137		795.33416627	6	D	14	1664.8489915	+0.040779	1664.8489915	
	923.39274378	+0.1833671	923.39274378	7	Q	13	1549.8220485		1549.8220485	
	1037.4356712		1037.4356712	8	N	12	1421.763471	+0.232989	711.38537371	-0.0065285
-0.1958178	575.76350584		1150.5197352	9	I	11	1307.7205435	-0.1017691	1307.7205435	
	1263.6037992		1263.6037992	10	I	10	1194.6364795		1194.6364795	
	1360.656563	+0.2085493	1360.656563	11	P	9	1081.5524155		1081.5524155	
	1489.6991561		1489.6991561	12	E	8	984.49965169		984.49965169	
	1603.7420836		1603.7420836	13	N	7	855.4570586		855.4570586	
-0.0570318	858.91671202	+0.0265136	1716.8261476	14	I	6	741.41413115		741.41413115	
	1813.8789114		1813.8789114	15	P	5	628.33006717	+0.2305407	314.66867182	+0.2102039
	1884.9160252		1884.9160252	16	A	4	531.27730332	+0.2638344	531.27730332	
	1981.9687891		1981.9687891	17	P	3	460.24018953		460.24018953	
	2083.0164675		2083.0164675	18	T	2	363.18742568		363.18742568	
	2198.0434106		2198.0434106	19	D	1	262.1397472		262.1397472	
				20	K	0	147.11280417		147.11280417	

Scan number	10563	Raw file	20080924_Orbi6_SaZa_SA_ADH_Matrigel_12h_Exp1_InGel_14
Method	ITMS; CID	Genenames	SELE



precursor information

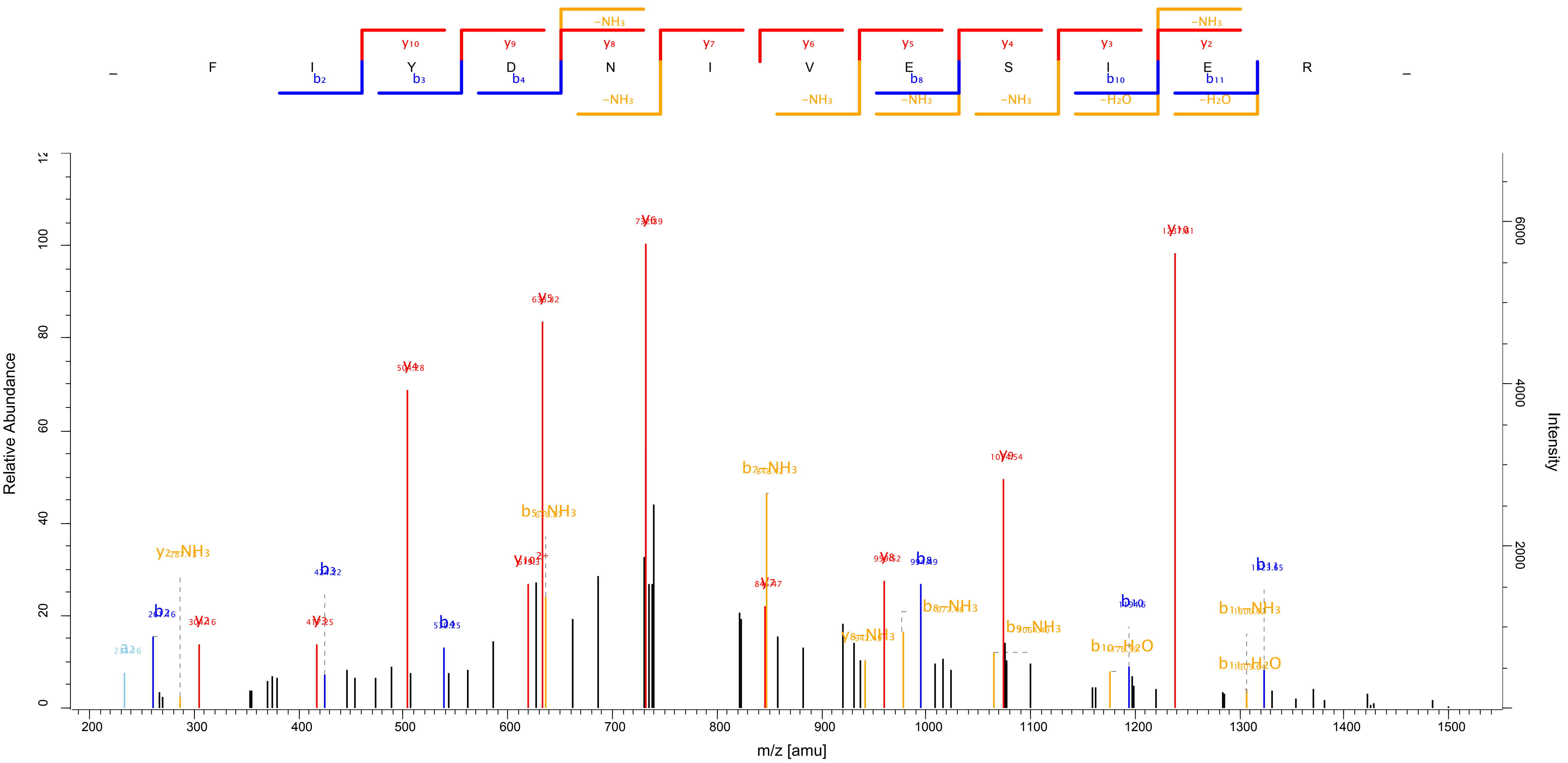
Mass:	1545.67174
m/z:	773.84315
Charge:	2+
Retentiontime:	70.8282318115234
Score:	175.7438
Mass Error [ppm]:	0.84658
PEP:	8.61515E-09
Precursor Type:	ISO

general information

Annotation:	11 of 14
AminoAcids Coverage:	79 %
Intensity Coverage:	75 %
Peak Coverage:	37 %
Protein Localisation:	376 ... 389

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019	1	G	13				
	221.092068728	2	Y	12	1489.656245464		1489.656245464	
	352.132553335	3	M	11	1326.592916926	+0.0729766	663.800096696	−0.0881826
	466.175480782	4	N	10	1195.552432319	−0.0220368	1195.552432319	
+0.1534291	626.206128983	5	C	9	1081.509504872	+0.0040449	1081.509504872	
−0.0320753	739.290192964	6	I	8	921.478856671	+0.0242561	921.478856671	
	836.342956816	7	P	7	808.39479269	+0.0089549	808.39479269	
+0.0807643	923.374985226	8	S	6	711.342028838	−0.1105225	711.342028838	
+0.0295514	994.412099013	9	A	5	624.310000428	+0.1045504	624.310000428	
	1081.444127423	10	S	4	553.272886641	+0.0276505	553.272886641	
−0.4281156	1138.465591147	11	G	3	466.240858231	+0.0414294	466.240858231	
	1225.497619557	12	S	2	409.219394507	+0.0744898	409.219394507	
+0.1715154	1372.566033473	13	F	1	322.187366097	+0.1117672	322.187366097	
		14	R	0	175.118952181		175.118952181	

Scan number	17097	Raw file	20080924_Orbi6_SaZa_SA_ADH_Matrigel_12h_Exp1_InGel_18
Method	ITMS; CID	Genenames	RAD54L2



precursor information

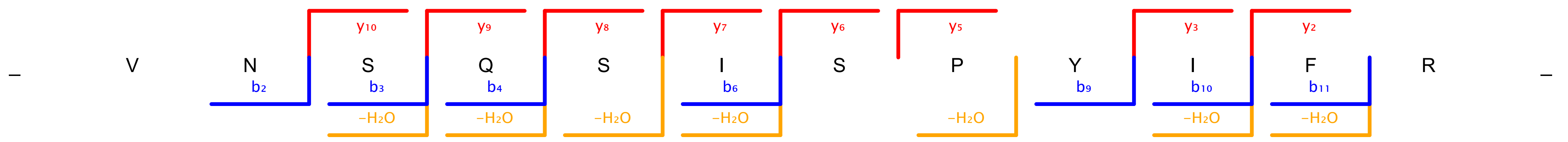
Mass:	1496.75132
m/z:	749.38294
Charge:	2+
Retentiontime:	105.782569885254
Score:	171.6158
Mass Error [ppm]:	0.13935
PEP:	1.5136E−06
Precursor Type:	ISO

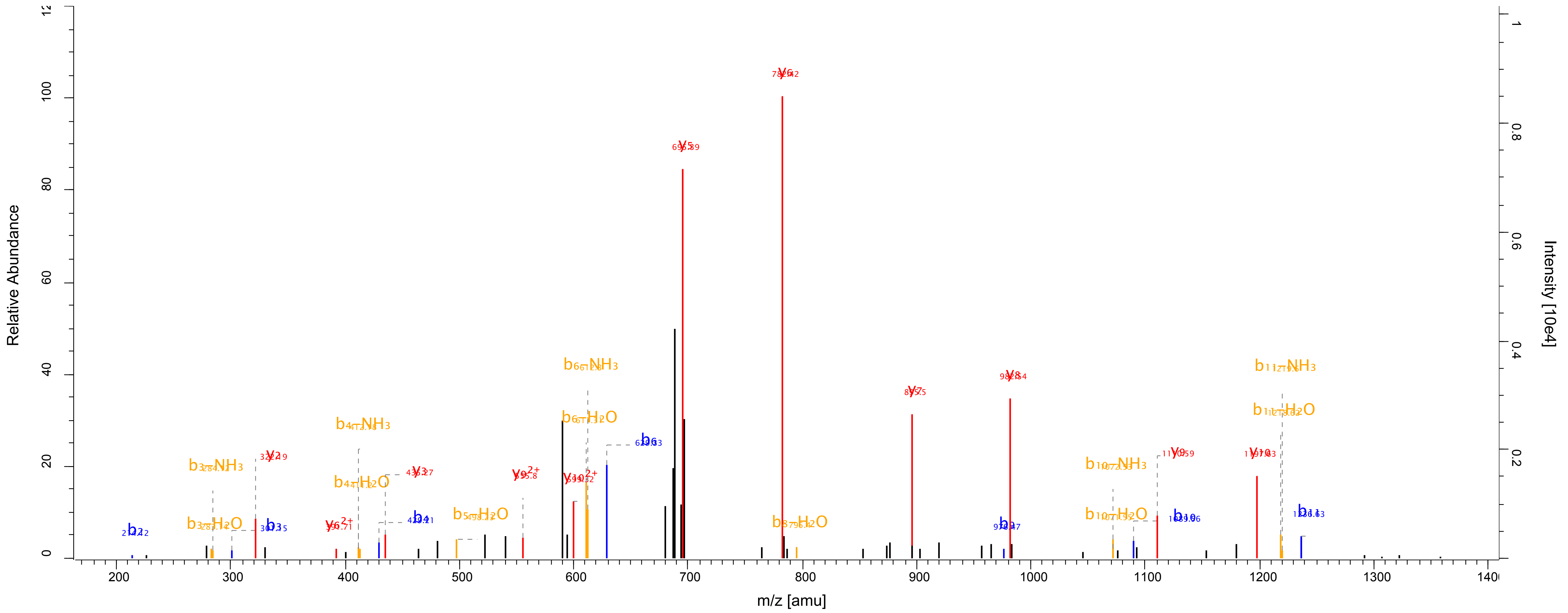
general information

Annotation:	10 of 12
AminoAcids Coverage:	83 %
Intensity Coverage:	55 %
Peak Coverage:	33 %
Protein Localisation:	281 ... 292

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08077576		148.07569038	1	F	11				
+0.1022959	233.16483974	−0.034205	261.15975436	2	I	10	1350.6899717		1350.6899717	
	396.22816828	+0.0766608	424.2230829	3	Y	9	1237.6059077	+0.0331304	619.30659207	+0.0544309
	511.25511131	−0.0553848	539.25002593	4	D	8	1074.5425791	−0.0416026	1074.5425791	
	625.29803876		653.29295338	5	N	7	959.51563611	−0.0354115	959.51563611	
	738.38210274		766.37701736	6	I	6	845.47270866	+0.0858241	845.47270866	
	837.45051666		865.44543128	7	V	5	732.38864468	+0.0528226	732.38864468	
	966.49310975	−0.1335932	994.48802437	8	E	4	633.32023076	+0.1136071	633.32023076	
	1053.5251382		1081.5200528	9	S	3	504.27763767	+0.0966299	504.27763767	
	1166.6092021	−0.2481597	1194.6041168	10	I	2	417.24560926	+0.0953331	417.24560926	
	1295.6517952	+0.0237003	1323.6467099	11	E	1	304.16154528	+0.105514	304.16154528	
				12	R	0	175.11895218		175.11895218	

Scan number	11888	Raw file	20080925_Orbi6_SaZa_SA_ADH_Laminin_24h_Exp1_InGel_01
Method	ITMS; CID	Genenames	SPP2





precursor
information

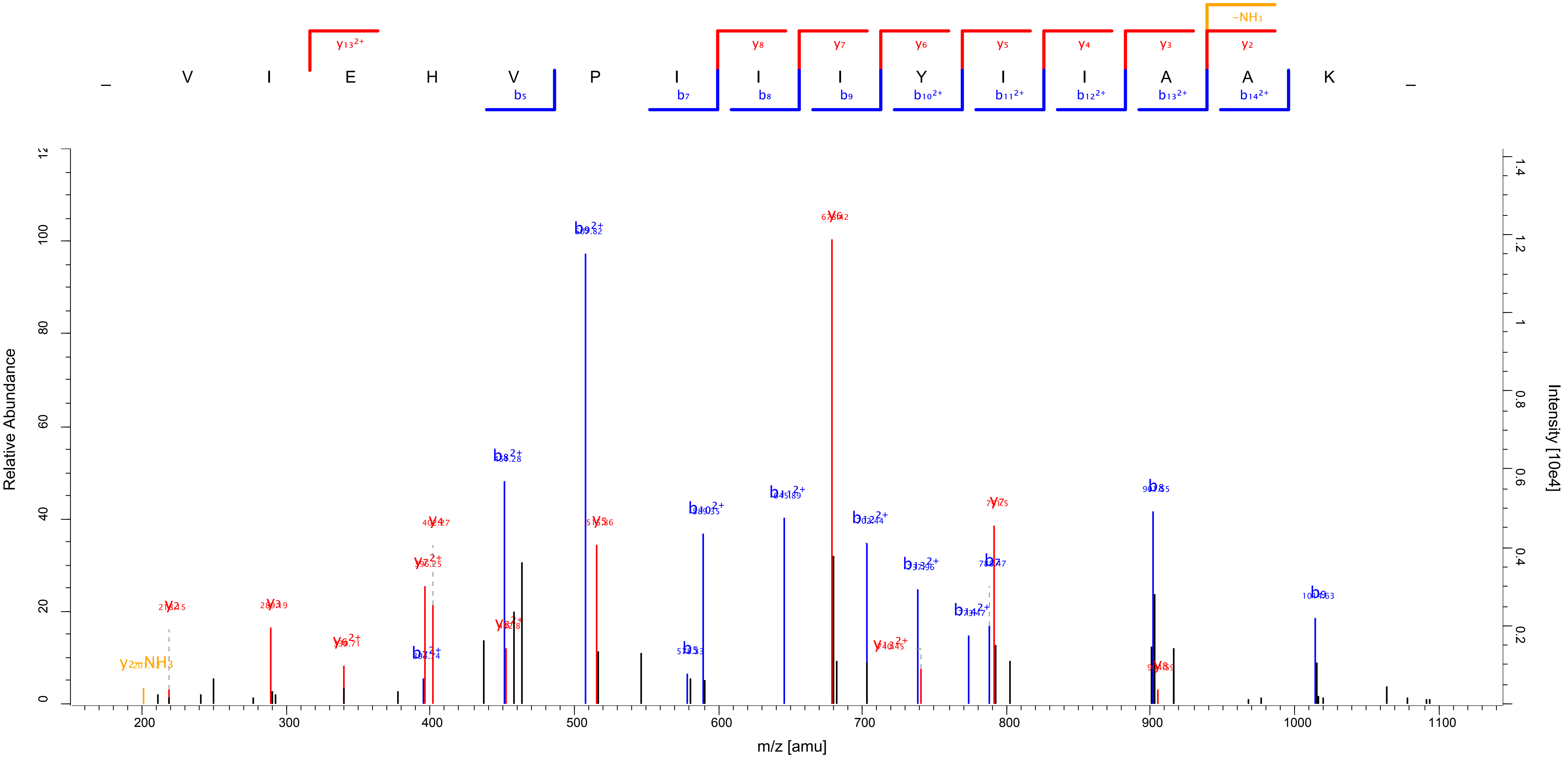
Mass:	1409.73047
m/z:	705.87251
Charge:	2+
Retentiontime:	80.8192520141602
Score:	193.2827
Mass Error [ppm]:	0.10834
PEP:	2.9376E-07
Precursor Type:	ISO

general
information

Annotation:	10 of 12
AminoAcids Coverage:	83 %
Intensity Coverage:	63 %
Peak Coverage:	45 %
Protein Localisation:	51 ... 62

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.075690383	1	V	11				
-0.1582754	214.11861783	2	N	10	1311.669176637		1311.669176637	
+0.004261	301.15064624	3	S	9	1197.626249189	+0.0287801	599.316762828	+0.0998631
-0.006465	429.209223751	4	Q	8	1110.59422078	-0.1047188	555.800748623	+0.1585409
	516.241252161	5	S	7	982.535643268	-0.0363757	982.535643268	
+0.0050672	629.325316142	6	I	6	895.503614858	+0.114122	895.503614858	
	716.357344552	7	S	5	782.419550878	+0.0318041	391.713413672	+0.4494892
	813.410108404	8	P	4	695.387522468	+0.0774434	695.387522468	
+0.1344122	976.473436942	9	Y	3	598.334758616		598.334758616	
-0.1140195	1089.557500922	10	I	2	435.271430078	-0.0707465	435.271430078	
+0.2161262	1236.625914838	11	F	1	322.187366097	+0.1120724	322.187366097	
		12	R	0	175.118952181		175.118952181	

Scan number	17789	Raw file	20080925_Orbi6_SaZa_SA_ADH_Laminin_24h_Exp1_InGel_01
Method	ITMS; CID	Genenames	FAM165B



precursor information

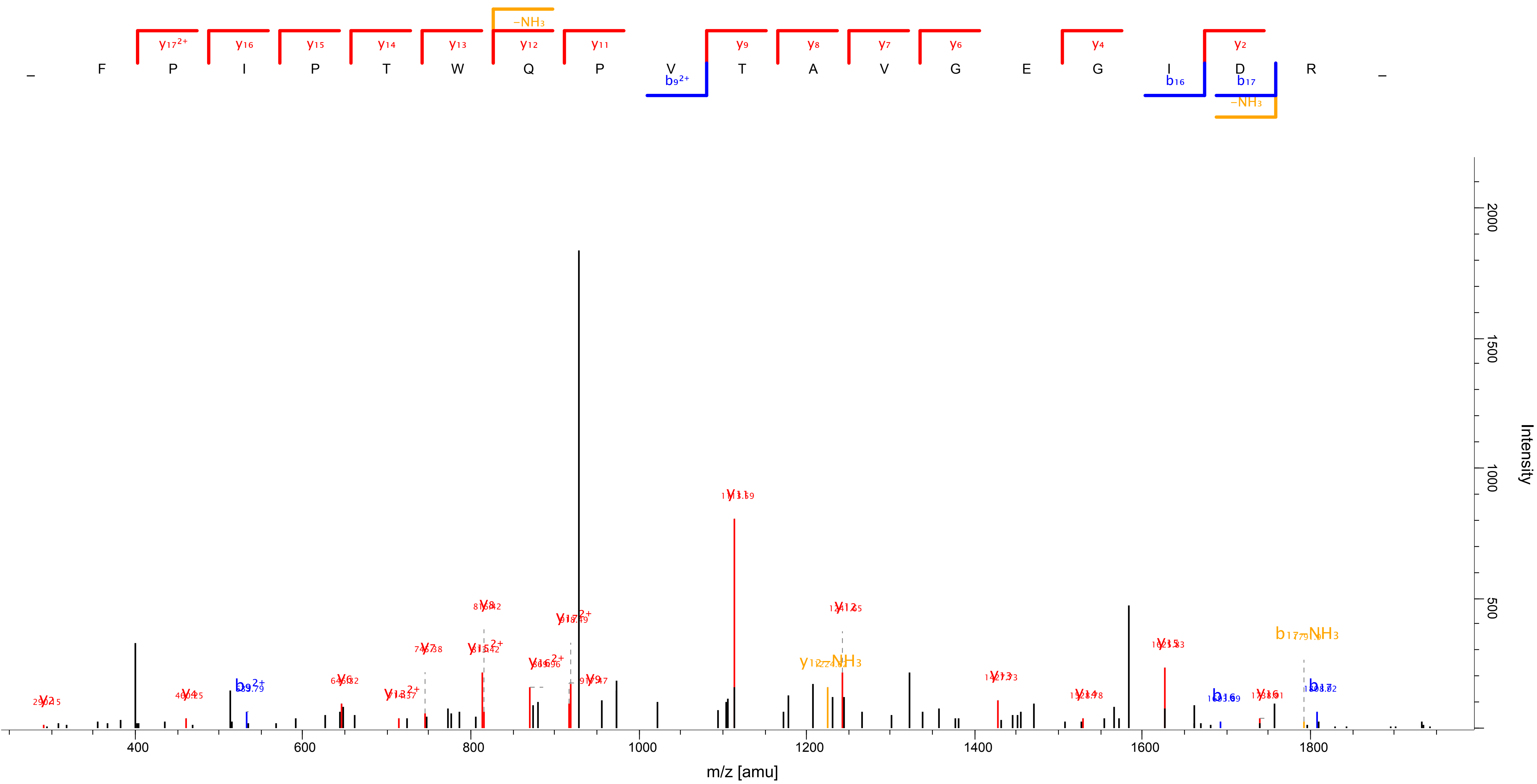
Mass:	1128.56613
m/z:	565.29034
Charge:	2+
Retentiontime:	114.001861572266
Score:	146.356
Mass Error [ppm]:	-0.038085
PEP:	8.4755E-34
Precursor Type:	ISO

general information

Annotation:	10 of 15
AminoAcids Coverage:	67 %
Intensity Coverage:	71 %
Peak Coverage:	41 %
Protein Localisation:	5 ... 19

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.07569038		100.07569038	1	V	14				
	213.15975436		213.15975436	2	I	13	1592.9774269		1592.9774269	
	342.20234746		342.20234746	3	E	12	1479.8933629		740.45031969	+0.252317
	479.26125932		479.26125932	4	H	11	1350.8507698		1350.8507698	
	578.32967324	+0.0718771	578.32967324	5	V	10	1213.791858		1213.791858	
	675.38243709		675.38243709	6	P	9	1114.723444		1114.723444	
-0.0382804	394.73688877	+0.0602934	788.46650107	7	I	8	1017.6706802		1017.6706802	
+0.3010353	451.27892076	+0.0729701	901.55056505	8	I	7	904.58661621	+0.0850147	452.79694634	+0.1605732
+0.1291815	507.82095275	-0.0731056	1014.634629	9	I	6	791.50255223	-0.0601084	396.25491435	+0.1999196
+0.1444533	589.35261702		1177.6979576	10	Y	5	678.41848825	+0.0439141	339.71288236	+0.0548789
+0.1588788	645.89464901		1290.7820215	11	I	4	515.35515971	+0.061039	515.35515971	
+0.1372936	702.436681		1403.8660855	12	I	3	402.27109573	-0.0416035	402.27109573	
+0.0501942	737.95523789		1474.9031993	13	A	2	289.18703175	+0.0657148	289.18703175	
+0.1192838	773.47379479		1545.9403131	14	A	1	218.14991796	+0.0686489	218.14991796	
				15	K	0	147.11280417		147.11280417	

Scan number	16573	Raw file	20080925_Orbi6_SaZa_SA_ADH_Laminin_24h_Exp1_InGel_04
Method	ITMS; CID	Genenames	FAM173A



precursor information

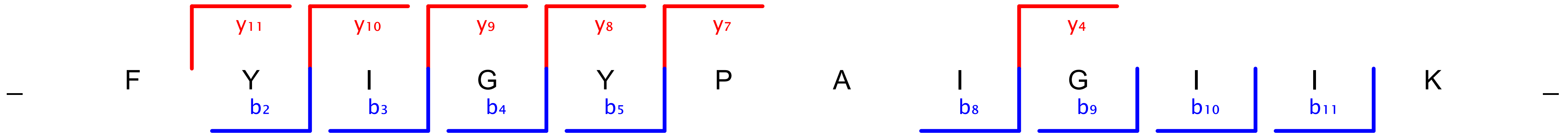
Mass:	1982.02589
m/z:	992.02022
Charge:	2+
Retentiontime:	106.256591796875
Score:	112.5004
Mass Error [ppm]:	−0.13523
PEP:	0.00016436
Precursor Type:	ISO

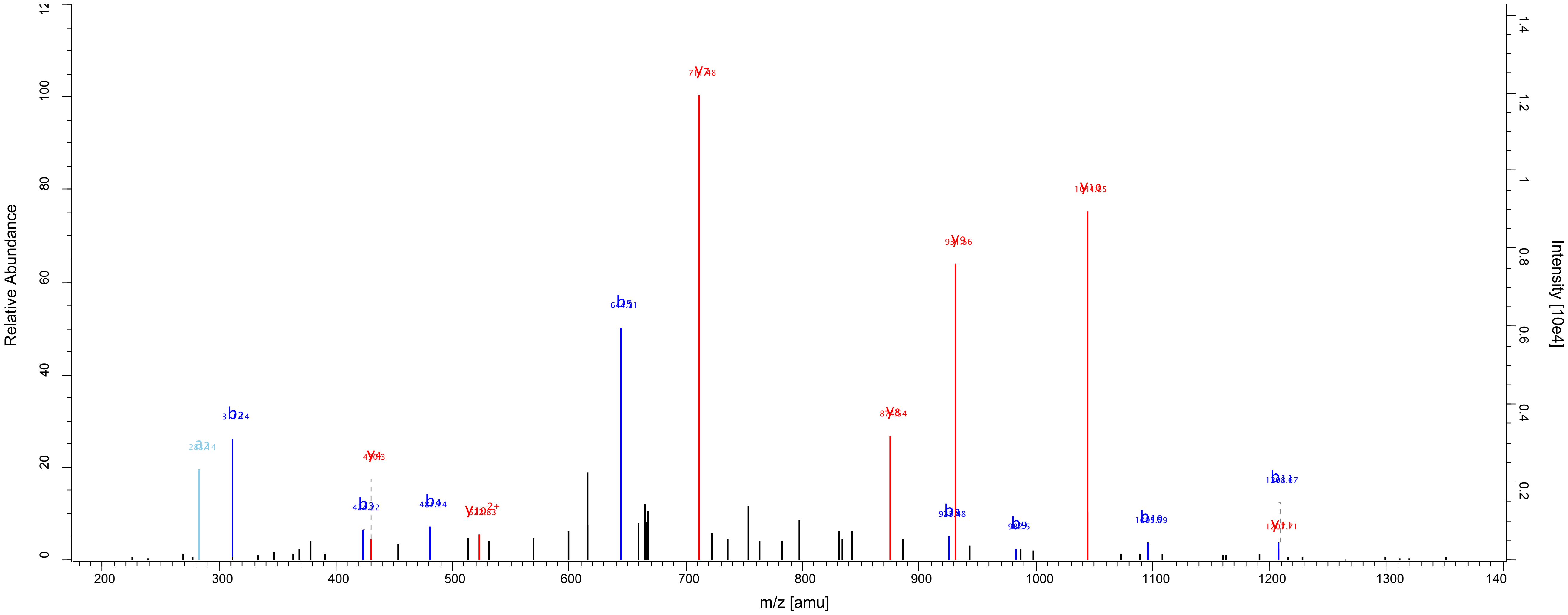
general information

Annotation:	15 of 18
AminoAcids Coverage:	83 %
Intensity Coverage:	28 %
Peak Coverage:	22 %
Protein Localisation:	176 ... 193

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.07569038		148.07569038	1	F	17				
	245.12845423		245.12845423	2	P	16	1835.9650243		918.48615039	+0.4899238
	358.21251822		358.21251822	3	I	15	1738.9122605	+0.0005813	869.95976846	−0.037161
	455.26528207		455.26528207	4	P	14	1625.8281965	−0.0637922	813.41773647	+0.0762821
	556.31296054		556.31296054	5	T	13	1528.7754326	−0.1689873	1528.7754326	
	742.39227349		742.39227349	6	W	12	1427.7277541	−0.1047073	714.36751531	+0.1346209
	870.45085101		870.45085101	7	Q	11	1241.6484412	+0.0743371	1241.6484412	
	967.50361486		967.50361486	8	P	10	1113.5898637	−0.0429887	1113.5898637	
−0.4026897	533.78965262		1066.5720288	9	V	9	1016.5370998		1016.5370998	
	1167.6197072		1167.6197072	10	T	8	917.46868591	+0.208194	917.46868591	
	1238.656821		1238.656821	11	A	7	816.42100744	+0.0280892	816.42100744	
	1337.725235		1337.725235	12	V	6	745.38389365	+0.1262992	745.38389365	
	1394.7466987		1394.7466987	13	G	5	646.31547974	+0.1295886	646.31547974	
	1523.7892918		1523.7892918	14	E	4	589.29401601		589.29401601	
	1580.8107555		1580.8107555	15	G	3	460.25142292	+0.2514152	460.25142292	
	1693.8948195	−0.2150099	1693.8948195	16	I	2	403.22995919		403.22995919	
	1808.9217625	−0.1228123	1808.9217625	17	D	1	290.14589521	+0.1645601	290.14589521	
				18	R	0	175.11895218		175.11895218	

Scan number	16781	Raw file	20080925_Orbi6_SaZa_SA_ADH_Laminin_24h_Exp1_InGel_06
Method	ITMS; CID	Genenames	TM2D1





precursor information

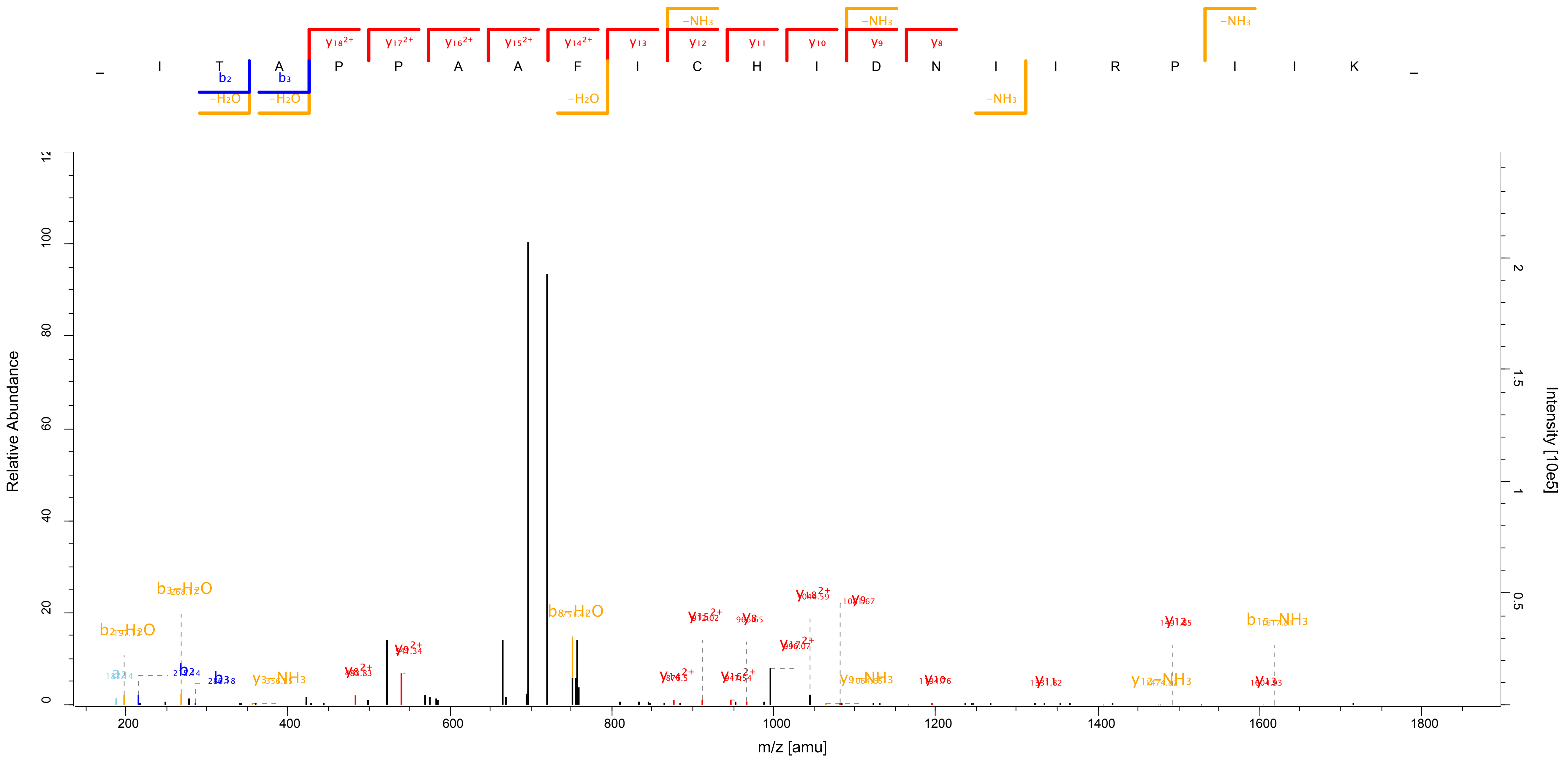
Mass:	1353.76976
m/z:	677.89216
Charge:	2+
Retentiontime:	107.536735534668
Score:	150.8537
Mass Error [ppm]:	0.07716
PEP:	1.4495E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverage:	75 %
Intensity Coverage:	66 %
Peak Coverage:	24 %
Protein Localisation:	139 ... 150

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.08077576		148.07569038	1	F	11				
+0.0134274	283.1441043	+0.043171	311.13901892	2	Y	10	1207.7085223	−0.1314959	1207.7085223	
	396.22816828	−0.1488031	424.2230829	3	I	9	1044.6451937	−0.0005404	522.82623509	+0.0848977
	453.249632	+0.0312712	481.24454663	4	G	8	931.56112974	+0.0043	931.56112974	
	616.31296054	−0.0689225	644.30787516	5	Y	7	874.53966601	−0.0803765	874.53966601	
	713.36572439		741.36063902	6	P	6	711.47633748	+0.0004081	711.47633748	
	784.40283818		812.3977528	7	A	5	614.42357362		614.42357362	
	897.48690216	−0.2151542	925.48181678	8	I	4	543.38645984		543.38645984	
	954.50836589	+0.0556184	982.50328051	9	G	3	430.30239586	+0.0787687	430.30239586	
	1067.5924299	−0.0820955	1095.5873445	10	I	2	373.28093213		373.28093213	
	1180.6764938	−0.2223118	1208.6714085	11	I	1	260.19686815		260.19686815	
				12	K	0	147.11280417		147.11280417	

Scan number	18118	Raw file	20080925_Orbi6_SaZa_SA_ADH_Laminin_24h_Exp1_InGel_06
Method	ITMS; CID	Genenames	NHEJ1



precursor information

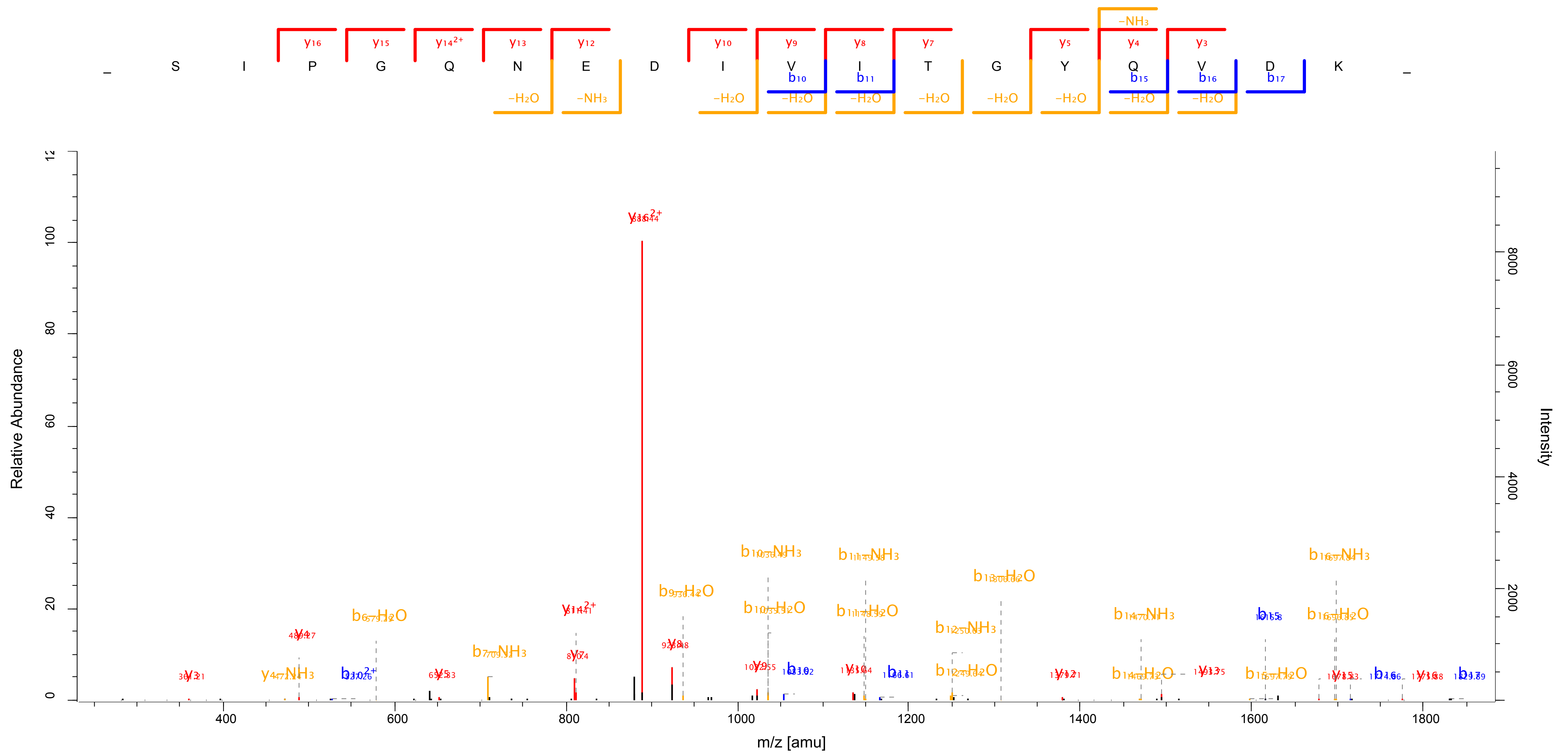
Mass:	2372.33945
m/z:	594.09214
Charge:	4+
Retentiontime:	115.267311096191
Score:	79.83656
Mass Error [ppm]:	−0.33546
PEP:	8.7684E−05
Precursor Type:	MULTI

general information

Annotation:	15 of 21
AminoAcids Coverage:	71 %
Intensity Coverage:	14 %
Peak Coverage:	27 %
Protein Localisation:	65 ... 85

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096425825		114.09134045	1	I	20				
−0.015961	187.1441043	−0.0891685	215.13901892	2	T	19	2260.2634549		2260.2634549	
	258.18121809	−0.3161168	286.17613271	3	A	18	2159.2157765		2159.2157765	
	355.23398194		383.22889656	4	P	17	2088.1786627		1044.5929696	+0.005175
	452.28674579		480.28166041	5	P	16	1991.1258988		996.06658764	−0.0368025
	523.32385958		551.3187742	6	A	15	1894.073135		947.54020572	+0.3182538
	594.36097337		622.35588799	7	A	14	1823.0360212		912.02164882	+0.0069156
	741.42938728		769.4243019	8	F	13	1751.9989074		876.50309193	+0.2595423
	854.51345126		882.50836589	9	I	12	1604.9304935	−0.0396243	1604.9304935	
	1014.5440995		1042.5390141	10	C	11	1491.8464295	+0.0317443	1491.8464295	
	1151.6030113		1179.5979259	11	H	10	1331.8157813	−0.0925147	1331.8157813	
	1264.6870753		1292.6819899	12	I	9	1194.7568694	−0.2037688	1194.7568694	
	1379.7140183		1407.708933	13	D	8	1081.6728055	+0.027634	541.34004096	−0.4534443
	1493.7569458		1521.7518604	14	N	7	966.64586242	−0.1672858	483.82656944	+0.1974784
	1606.8410098		1634.8359244	15	I	6	852.60293497		852.60293497	
	1719.9250737		1747.9199884	16	I	5	739.51887099		739.51887099	
	1876.0261848		1904.0210994	17	R	4	626.43480701		626.43480701	
	1973.0789486		2001.0738632	18	P	3	470.33369598		470.33369598	
	2086.1630126		2114.1579272	19	I	2	373.28093213		373.28093213	
	2199.2470766		2227.2419912	20	I	1	260.19686815		260.19686815	
				21	K	0	147.11280417		147.11280417	

Scan number	10038	Raw file	20081002_Orbi5_SaZa_SA_ADH_Laminin_24h_Exp_2_InGel_01
Method	ITMS; CID	Genenames	CSTA



precursor information

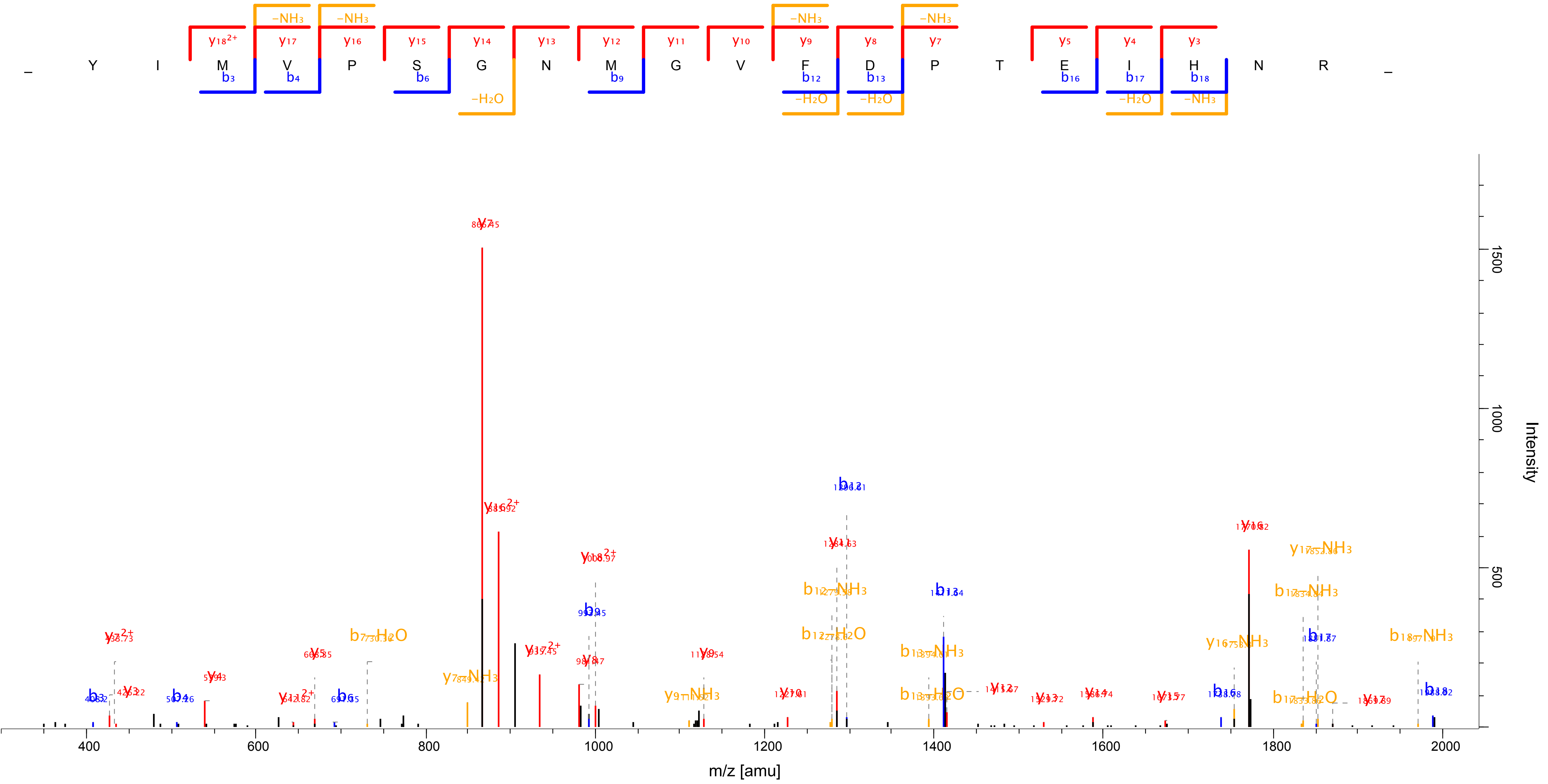
Mass:	1974.98888
m/z:	988.50171
Charge:	2+
Retentiontime:	77.3428268432617
Score:	162.2928
Mass Error [ppm]:	-0.48562
PEP:	9.7877E-09
Precursor Type:	ISO

general information

Annotation:	15 of 18
AminoAcids Coverage:	83 %
Intensity Coverage:	82 %
Peak Coverage:	38 %
Protein Localisation:	72 ... 89

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876		88.039304876	1	S	17				
	201.12336886		201.12336886	2	I	16	1888.9650839		1888.9650839	
	298.17613271		298.17613271	3	P	15	1775.8810199	+0.1099469	888.44414819	+0.2233323
	355.19759643		355.19759643	4	G	14	1678.8282561	-0.2224211	1678.8282561	
	483.25617394		483.25617394	5	Q	13	1621.8067923		811.4070344	-0.0422883
	597.29910139		597.29910139	6	N	12	1493.7482148	-0.0782929	1493.7482148	
	726.34169449		726.34169449	7	E	11	1379.7052874	-0.178676	1379.7052874	
	841.36863752		841.36863752	8	D	10	1250.6626943		1250.6626943	
	954.4527015		954.4527015	9	I	9	1135.6357512	-0.1375823	1135.6357512	
+0.0807748	527.26419594	-0.1226779	1053.5211154	10	V	8	1022.5516873	-0.113699	1022.5516873	
	1166.6051794	-0.1840368	1166.6051794	11	I	7	923.48327335	-0.1400116	923.48327335	
	1267.6528579		1267.6528579	12	T	6	810.39920937	-0.0048002	810.39920937	
	1324.6743216		1324.6743216	13	G	5	709.35153089		709.35153089	
	1487.7376501		1487.7376501	14	Y	4	652.33006717	+0.0931506	652.33006717	
	1615.7962276	-0.2348263	1615.7962276	15	Q	3	489.26673863	+0.0087435	489.26673863	
	1714.8646416	-0.0793632	1714.8646416	16	V	2	361.20816112	+0.0334465	361.20816112	
	1829.8915846	-0.176985	1829.8915846	17	D	1	262.1397472		262.1397472	
				18	K	0	147.11280417		147.11280417	

Scan number	11744	Raw file	20081002_Orbi5_SaZa_SA_ADH_Laminin_24h_Exp_2_InGel_01
Method	ITMS; CID	Genenames	CNIH4



precursor information

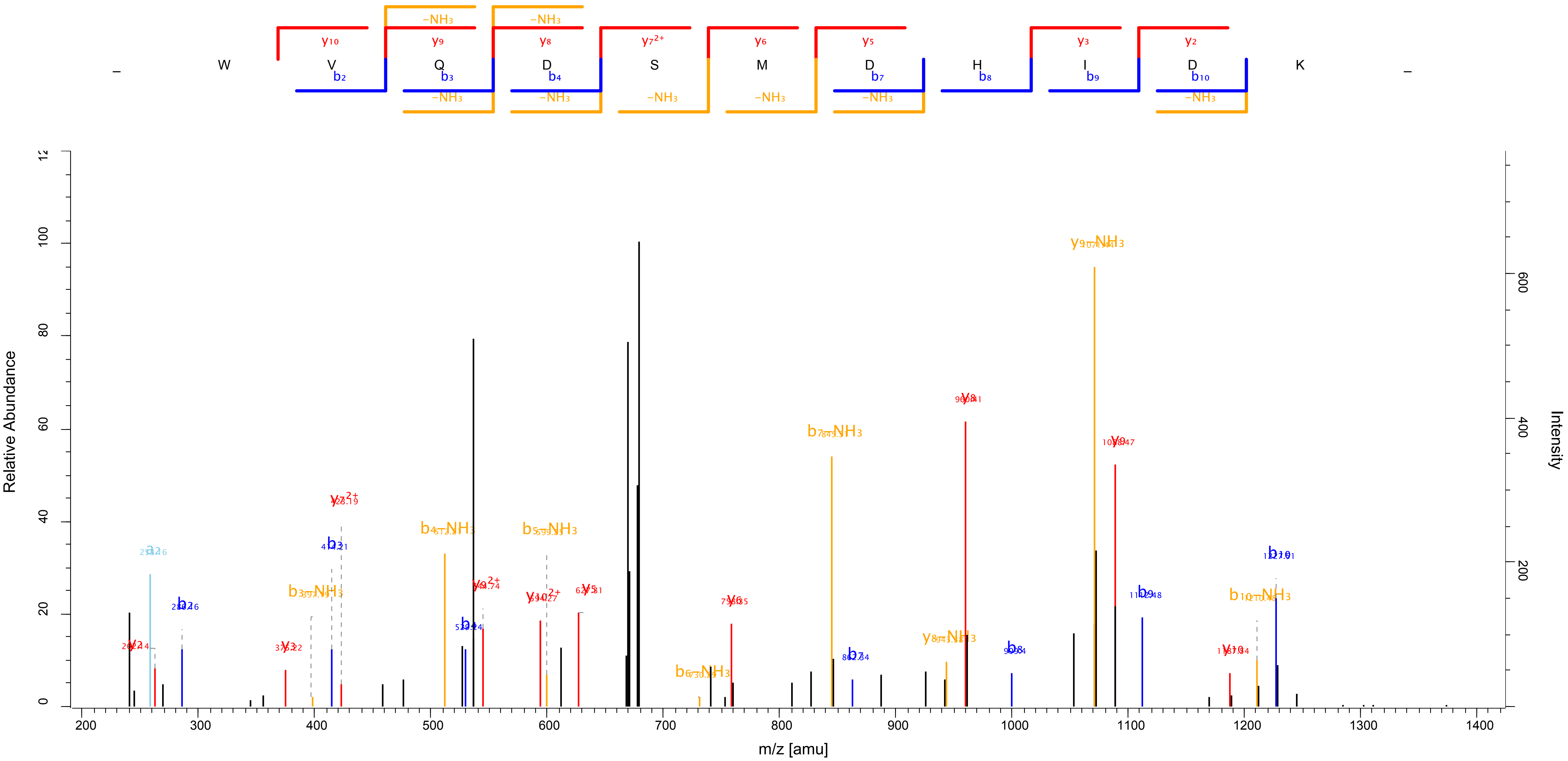
Mass:	2276.07182
m/z:	1139.04319
Charge:	2+
Retentiontime:	87.7266540527344
Score:	226.7388
Mass Error [ppm]:	0.0055299
PEP:	1.4206E-84
Precursor Type:	MULTI

general information

Annotation:	15 of 20
AminoAcids Coverage:	75 %
Intensity Coverage:	65 %
Peak Coverage:	39 %
Protein Localisation:	85 ... 104

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	164.070605005	1	Y	19				
	277.154668985	2	I	18	2114.015756023		2114.015756023	
+0.1421572	408.195153592	3	M	17	2000.931692043		1000.969484255	−0.1035175
−0.0703912	507.263567508	4	V	16	1869.891207436	−0.3284633	935.449241951	+0.0296399
	604.31633136	5	P	15	1770.82279352	−0.1549468	885.915034993	+0.2397502
+0.4949019	691.34835977	6	S	14	1673.770029668	−0.4016215	1673.770029668	
	748.369823493	7	G	13	1586.738001258	−0.1682991	1586.738001258	
	862.41275094	8	N	12	1529.716537535	−0.0569916	1529.716537535	
+0.1178094	993.453235547	9	M	11	1415.673610087	−0.1701921	1415.673610087	
	1050.47469927	10	G	10	1284.633125481	−0.0652544	642.820200974	+0.4456071
	1149.543113186	11	V	9	1227.611661758	−0.0640543	1227.611661758	
−0.4164587	1296.611527103	12	F	8	1128.543247842	+0.0127824	1128.543247842	
−0.2364926	1411.638470135	13	D	7	981.474833925	−0.0428271	981.474833925	
	1508.691233987	14	P	6	866.447890893	−0.1280667	433.72758368	+0.23372
	1609.738912461	15	T	5	769.395127041		769.395127041	
−0.3746452	1738.781505557	16	E	4	668.347448567	−0.0176146	668.347448567	
−0.1547541	1851.865569537	17	I	3	539.304855471	+0.0407256	539.304855471	
−0.1459169	1988.9244814	18	H	2	426.220791491	+0.0376314	426.220791491	
	2102.967408847	19	N	1	289.161879628		289.161879628	
		20	R	0	175.11895218		175.11895218	

Scan number 5427 Raw file 20081002_Orbi5_SaZa_SA_ADH_Laminin_24h_Exp_2_InGel_01
Method ITMS; CID Genenames CCL2



precursor information

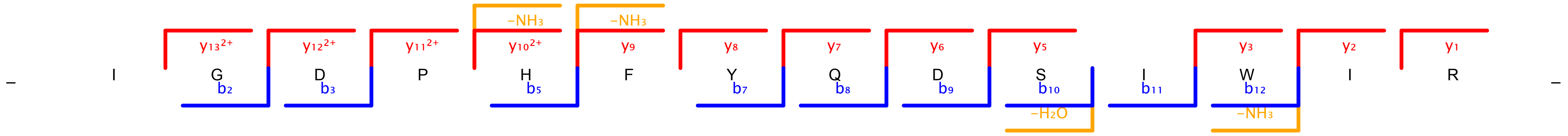
Mass:	1372.6085
m/z:	687.31153
Charge:	2+
Retentiontime:	50.3016929626465
Score:	164.6517
Mass Error [ppm]:	0.25703
PEP:	0.00010662
Precursor Type:	ISO

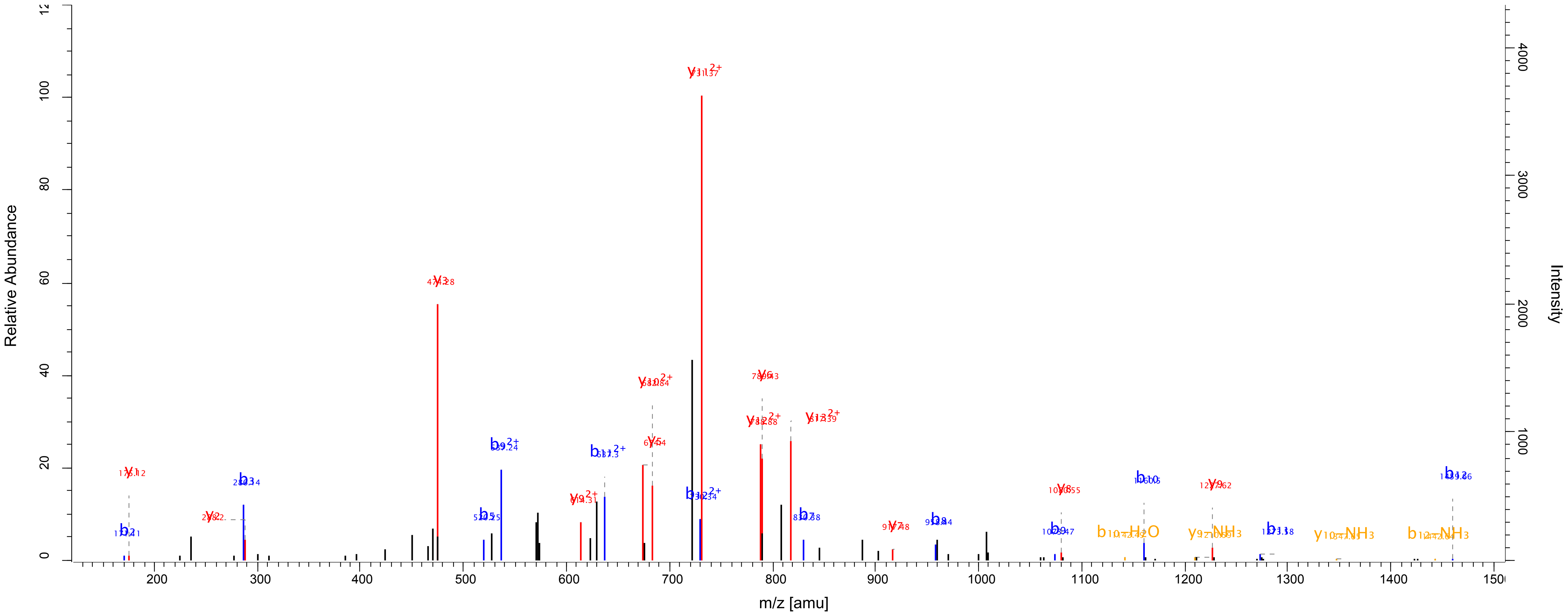
general information

Annotation:	9 of 11
AminoAcids Coverage:	82 %
Intensity Coverage:	47 %
Peak Coverage:	40 %
Protein Localisation:	82 ... 92

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	159.0916748		187.08658942	1	W	10				
−0.057214	258.16008871	+0.0804703	286.15500334	2	V	9	1187.5361136	+0.0002634	594.27169501	+0.1817352
	386.21866623	+0.0281184	414.21358085	3	Q	8	1088.4676996	−0.0704828	544.73748805	−0.0382083
	501.24560926	+0.0464024	529.24052388	4	D	7	960.40912213	−0.0519444	960.40912213	
	588.27763767		616.27255229	5	S	6	845.38217909		423.19472778	+0.0768787
	719.31812227		747.3130369	6	M	5	758.35015068	−0.0212933	758.35015068	
	834.34506531	+0.0836041	862.33997993	7	D	4	627.30966608	+0.0710102	627.30966608	
	971.40397717	−0.0271267	999.39889179	8	H	3	512.28272305		512.28272305	
	1084.4880411	−0.0500944	1112.4829558	9	I	2	375.22381118	+0.0192918	375.22381118	
	1199.5149842	−0.0938832	1227.5098988	10	D	1	262.1397472	+0.0434803	262.1397472	
				11	K	0	147.11280417		147.11280417	

Scan number	12181	Raw file	20081002_Orbi5_SaZa_SA_ADH_Laminin_24h_Exp_2_InGel_02
Method	ITMS; CID	Genenames	TMEM138





precursor
information

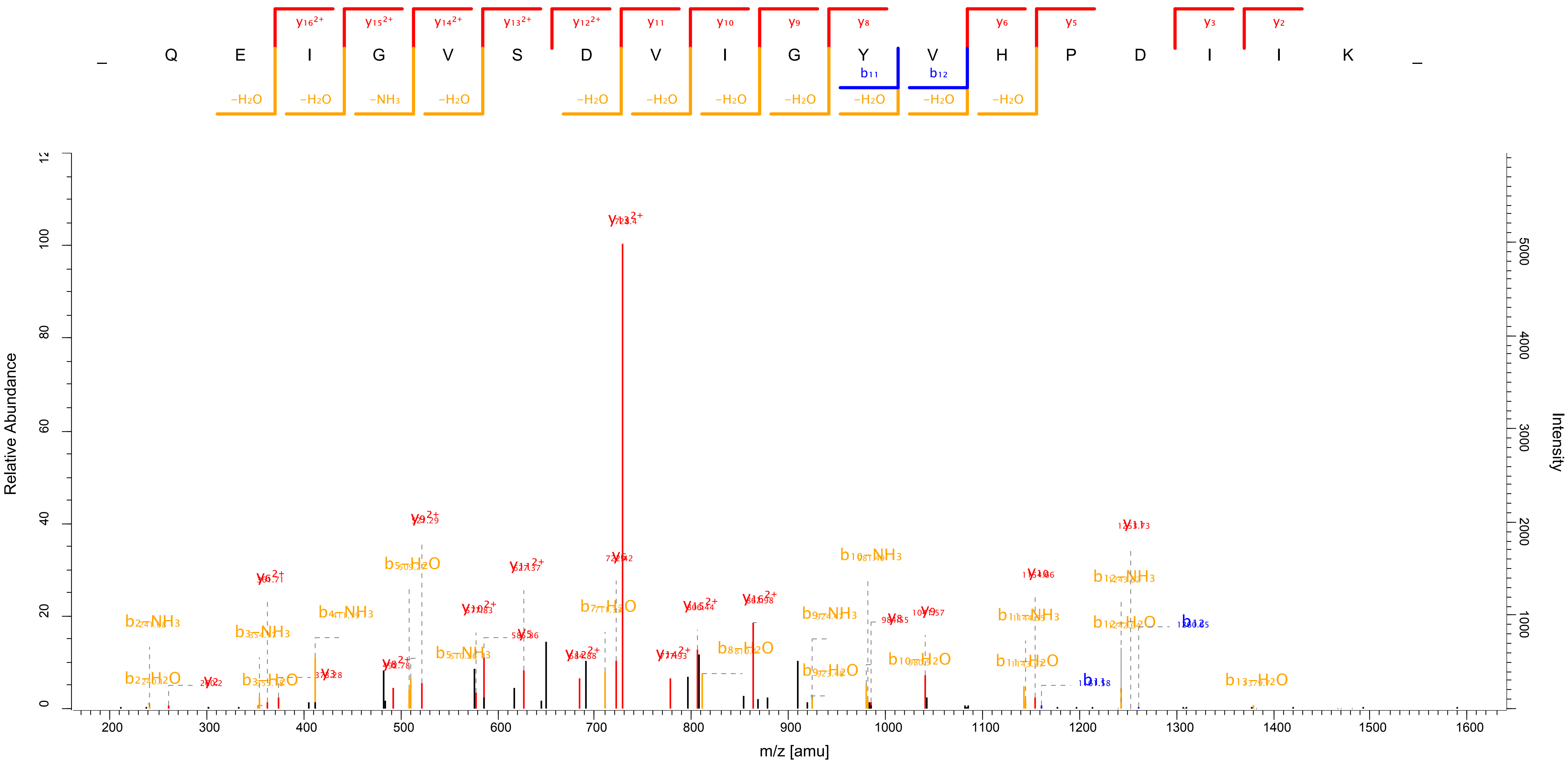
Mass:	1745.85383
m/z:	582.95855
Charge:	3+
Retentiontime:	86.6802673339844
Score:	194.2409
Mass Error [ppm]:	0.73168
PEP:	4.9841E-16
Precursor Type:	MULTI

general
information

Annotation:	13 of 14
AminoAcids Coverage:	93 %
Intensity Coverage:	67 %
Peak Coverage:	40 %
Protein Localisation:	141 ... 154

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045		114.09134045	1	I	13				
	171.11280417	+0.1652262	171.11280417	2	G	12	1633.775767		817.39152172	+0.0893743
	286.1397472	-0.0146251	286.1397472	3	D	11	1576.7543032		788.88078986	-0.0399085
	383.19251105		383.19251105	4	P	10	1461.7273602		731.36731834	+0.0991123
	520.25142292	-0.0212593	520.25142292	5	H	9	1364.6745964		682.84093642	+0.1647399
	667.31983683		667.31983683	6	F	8	1227.6156845	-0.2784042	614.31148048	+0.0969057
	830.38316537	-0.026598	830.38316537	7	Y	7	1080.5472706	-0.2189014	1080.5472706	
	958.44174288	-0.0605783	958.44174288	8	Q	6	917.48394205	-0.1648503	917.48394205	
+0.0919749	537.23798119	-0.0223969	1073.4686859	9	D	5	789.42536454	+0.0613908	789.42536454	
	1160.5007143	-0.0595522	1160.5007143	10	S	4	674.39842151	-0.0649864	674.39842151	
+0.2169121	637.29602739	-0.075501	1273.5847783	11	I	3	587.3663931		587.3663931	
+0.0750827	730.33568386	-0.066435	1459.6640913	12	W	2	474.28232911	-0.037395	474.28232911	
	1572.7481552		1572.7481552	13	I	1	288.20301616	+0.087206	288.20301616	
				14	R	0	175.11895218	-0.0117897	175.11895218	

Scan number	14537	Raw file	20081002_Orbi5_SaZa_SA_ADH_Laminin_24h_Exp_2_InGel_04
Method	ITMS; CID	Genenames	TMEM127



precursor information

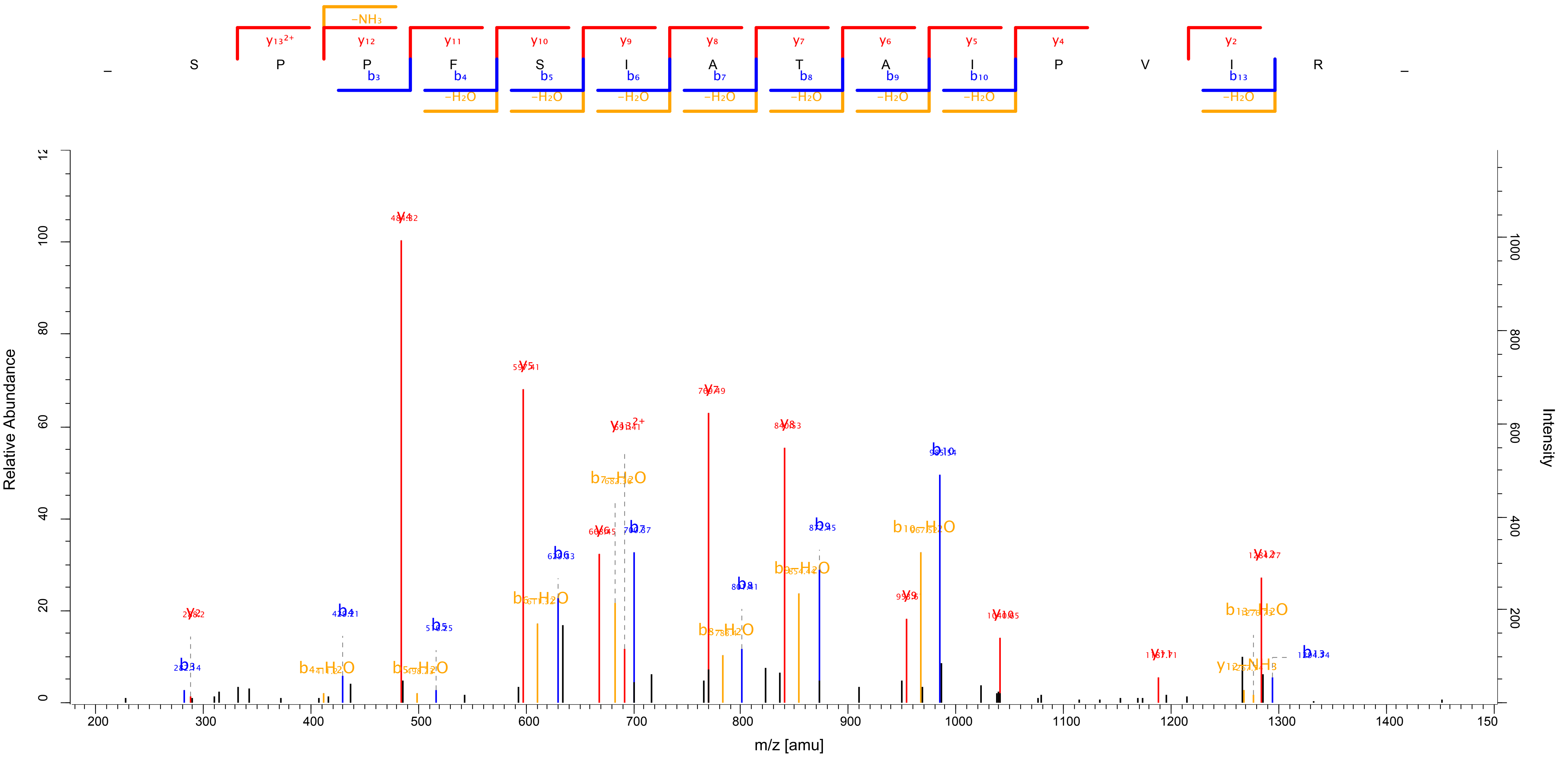
Mass:	1981.05155
m/z:	661.35779
Charge:	3+
Retentiontime:	100.602844238281
Score:	128.9506
Mass Error [ppm]:	-0.24869
PEP:	1.1643E-07
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverage:	83 %
Intensity Coverage:	72 %
Peak Coverage:	45 %
Protein Localisation:	64 ... 81

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.065853978	1	Q	17				
	258.108447074	2	E	16	1854.000741111		1854.000741111	
	371.192511055	3	I	15	1724.958148015		862.982712241	+0.1732326
	428.213974778	4	G	14	1611.874084034		806.44068025	-0.0643985
	527.282388694	5	V	13	1554.852620311		777.929948389	-0.0705124
	614.314417104	6	S	12	1455.784206394		728.39574143	+0.1760359
	729.341360136	7	D	11	1368.752177984		684.879727226	+0.1940643
	828.409774053	8	V	10	1253.725234953	-0.0567779	627.36625571	+0.1345377
	941.493838033	9	I	9	1154.656821036	-0.1465671	577.832048751	+0.1465279
	998.515301757	10	G	8	1041.572757056	-0.1020539	521.290016761	+0.0049661
+0.0534498	1161.578630295	11	Y	7	984.551293332	-0.1068964	492.779284899	+0.2100339
-0.1610823	1260.647044211	12	V	6	821.487964794		821.487964794	
	1397.705956073	13	H	5	722.419550878	-0.0619459	361.713413672	+0.2246356
	1494.758719925	14	P	4	585.360639015	-0.0401434	585.360639015	
	1609.785662957	15	D	3	488.307875163		488.307875163	
	1722.869726938	16	I	2	373.280932131	+0.0058721	373.280932131	
	1835.953790918	17	I	1	260.196868151	+0.0578316	260.196868151	
		18	K	0	147.112804171		147.112804171	

Scan number	14900	Raw file	20081002_Orbi5_SaZa_SA_ADH_Laminin_24h_Exp_2_InGel_05
Method	ITMS; CID	Genenames	UBXN2A



precursor information

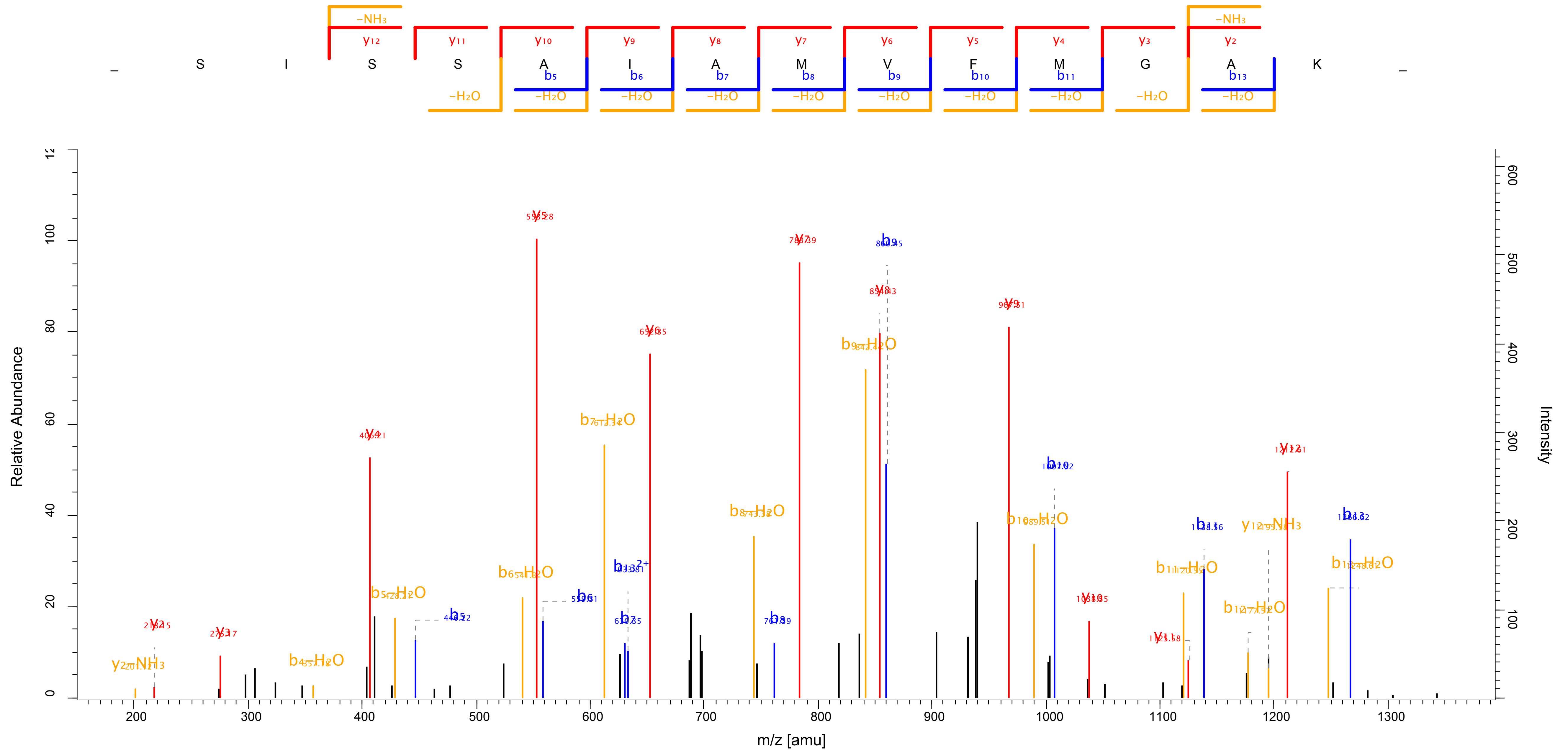
Mass:	1467.84757
m/z:	734.93106
Charge:	2+
Retentiontime:	102.77624511718 8
Score:	211.2633
Mass Error [ppm]:	1.7859
PEP:	9.2555E-18
Precursor Type:	ISO

general information

Annotation:	11 of 14
AminoAcids Coverage:	79 %
Intensity Coverage:	82 %
Peak Coverage:	41 %
Protein Localisation:	212 ... 225

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876	1	S	13				
	185.092068728	2	P	12	1381.82019797		691.413737218	-0.0583905
+0.0363198	282.14483258	3	P	11	1284.767434118	-0.2089624	1284.767434118	
+0.0452984	429.213246497	4	F	10	1187.714670266	-0.1073705	1187.714670266	
+0.0209604	516.245274907	5	S	9	1040.64625635	-0.0124673	1040.64625635	
-0.0616997	629.329338887	6	I	8	953.61422794	-0.0840155	953.61422794	
-0.236875	700.366452675	7	A	7	840.53016396	-0.0975468	840.53016396	
-0.1702957	801.414131149	8	T	6	769.493050172	-0.0990072	769.493050172	
-0.0846068	872.451244937	9	A	5	668.445371698	-0.0775738	668.445371698	
-0.2555848	985.535308917	10	I	4	597.40825791	-0.0429015	597.40825791	
	1082.588072769	11	P	3	484.32419393	-0.0242672	484.32419393	
	1181.656486685	12	V	2	387.271430078		387.271430078	
-0.3114735	1294.740550666	13	I	1	288.203016161	-0.2638072	288.203016161	
		14	R	0	175.118952181		175.118952181	

Scan number	15796	Raw file	20081002_Orbi5_SaZa_SA_ADH_Laminin_24h_Exp_2_InGel_08
Method	ITMS; CID	Genenames	HMSD



precursor information

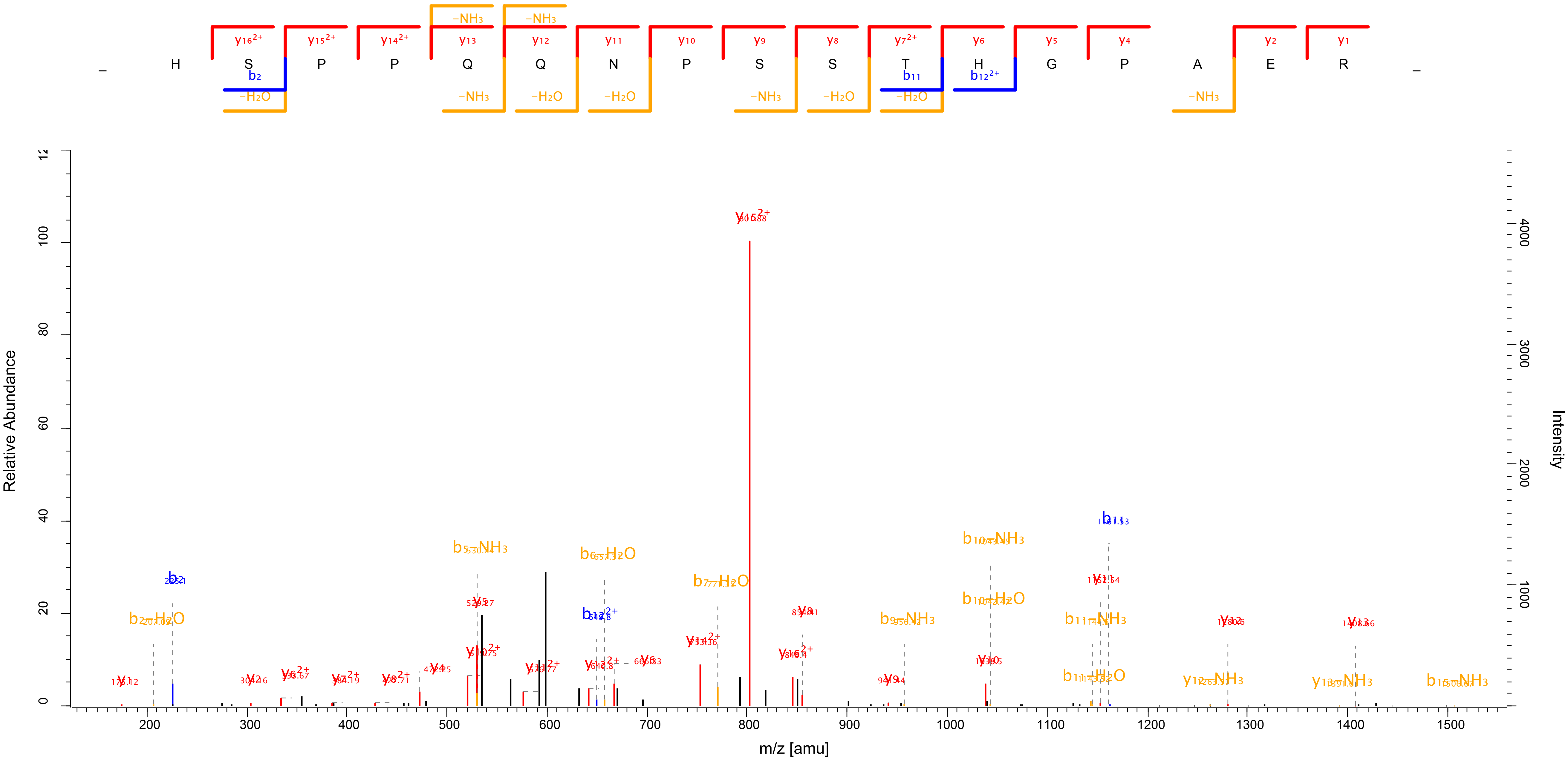
Mass:	1411.72068
m/z:	706.86762
Charge:	2+
Retentiontime:	111.24560546875
Score:	259.2298
Mass Error [ppm]:	0.23937
PEP:	2.39715E−75
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverage:	86 %
Intensity Coverage:	79 %
Peak Coverage:	48 %
Protein Localisation:	2 ... 15

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	88.039304876		88.039304876	1	S	13		
	201.123368857		201.123368857	2	I	12	1325.695591083	
	288.155397267		288.155397267	3	S	11	1212.611527103	−0.1901404
	375.187425677		375.187425677	4	S	10	1125.579498693	−0.0580143
	446.224539464	+0.0384	446.224539464	5	A	9	1038.547470283	−0.0134127
	559.308603445	−0.1715795	559.308603445	6	I	8	967.510356495	−0.026897
	630.345717233	+0.0086529	630.345717233	7	A	7	854.426292515	+0.069374
	761.386201839	+0.007658	761.386201839	8	M	6	783.389178727	−0.174396
	860.454615755	−0.0619156	860.454615755	9	V	5	652.348694121	+0.0130002
	1007.523029671	−0.1338085	1007.523029671	10	F	4	553.280280204	−0.0201484
	1138.563514278	−0.2092662	1138.563514278	11	M	3	406.211866288	+0.0738393
	1195.584978001		1195.584978001	12	G	2	275.171381682	+0.0564626
−0.1156485	633.814684128	−0.0951142	1266.622091789	13	A	1	218.149917958	−0.0002598
				14	K	0	147.112804171	

Scan number	1756	Raw file	20081002_Orbi5_SaZa_SA_ADH_Laminin_24h_Exp_2_InGel_08
Method	ITMS; CID	Genenames	SMPD2



precursor information

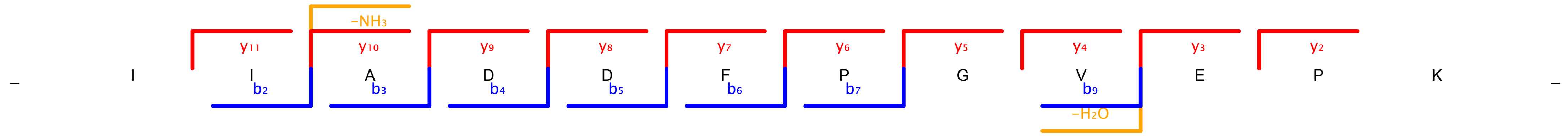
Mass:	1825.84632
m/z:	609.62272
Charge:	3+
Retentiontime:	28.7568588256836
Score:	173.0587
Mass Error [ppm]:	0.40934
PEP:	6.0817E−12
Precursor Type:	ISO

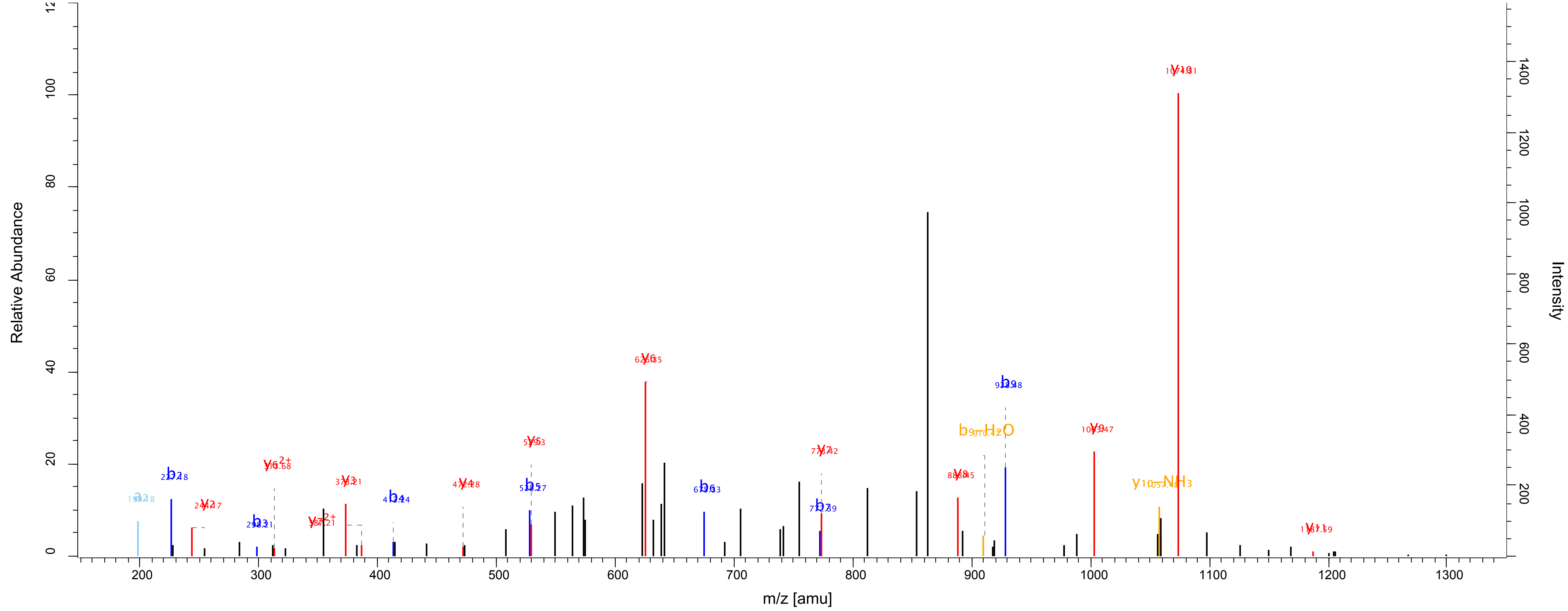
general information

Annotation:	16 of 17
AminoAcids Coverage:	94 %
Intensity Coverage:	64 %
Peak Coverage:	45 %
Protein Localisation:	283 ... 299

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.06618833		138.06618833	1	H	16				
	225.09821674	+0.1023295	225.09821674	2	S	15	1689.7939362		845.40060635	+0.1604288
	322.15098059		322.15098059	3	P	14	1602.7619078		801.88459214	+0.2147121
	419.20374444		419.20374444	4	P	13	1505.709144		753.35821022	+0.1965994
	547.26232195		547.26232195	5	Q	12	1408.6563801	−0.1877522	1408.6563801	
	675.32089947		675.32089947	6	Q	11	1280.5978026	+0.3715577	640.80253954	+0.1226924
	789.36382691		789.36382691	7	N	10	1152.5392251	−0.1356606	576.77325078	+0.1819494
	886.41659076		886.41659076	8	P	9	1038.4962976	−0.0994471	519.75178706	+0.2352125
	973.44861917		973.44861917	9	S	8	941.4435338	−0.2696446	941.4435338	
	1060.4806476		1060.4806476	10	S	7	854.41150539	−0.0545718	427.70939093	+0.0965783
	1161.5283261	+0.2143497	1161.5283261	11	T	6	767.37947698		384.19337672	+0.0923899
+0.0889122	649.79725719		1298.5872379	12	H	5	666.3317985	+0.0613289	333.66953748	+0.1133605
	1355.6087016		1355.6087016	13	G	4	529.27288664	+0.0294815	529.27288664	
	1452.6614655		1452.6614655	14	P	3	472.25142292	+0.0045585	472.25142292	
	1523.6985793		1523.6985793	15	A	2	375.19865906		375.19865906	
	1652.7411724		1652.7411724	16	E	1	304.16154528	−0.0004735	304.16154528	
				17	R	0	175.11895218	+0.1340996	175.11895218	

Scan number	8926	Raw file	20081002_Orbi5_SaZa_SA_ADH_Laminin_24h_Exp_2_InGel_10
Method	ITMS; CID	Genenames	MMP10





precursor information

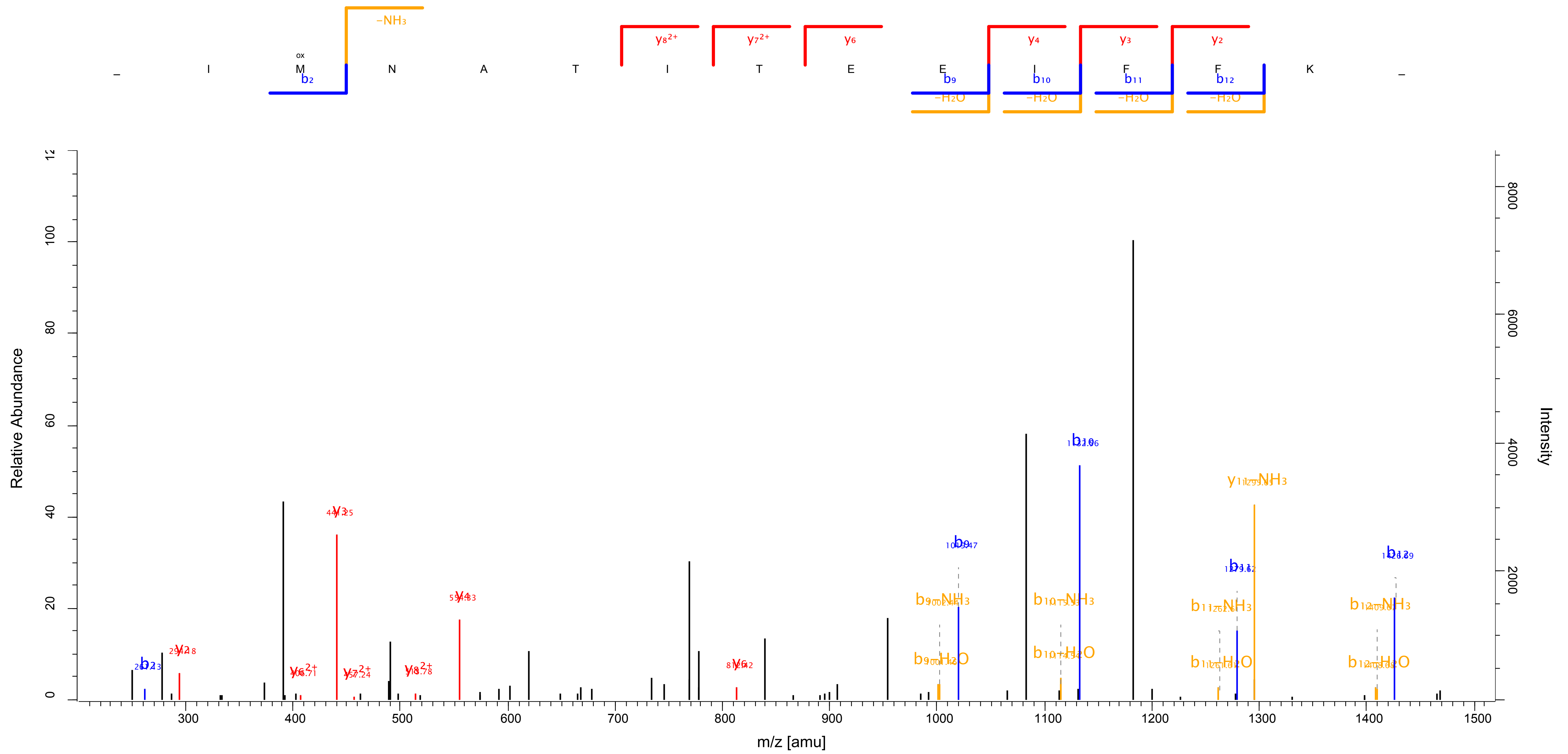
Mass:	1299.67119
m/z:	650.84287
Charge:	2+
Retentiontime:	69.2424011230469
Score:	136.5002
Mass Error [ppm]:	0.096884
PEP:	0.00024835
Precursor Type:	ISO

general information

Annotation:	10 of 12
AminoAcids Coverage:	83 %
Intensity Coverage:	47 %
Peak Coverage:	33 %
Protein Localisation:	424 ... 435

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096425825		114.09134045	1	I	11				
+0.0317294	199.18048981	+0.0141708	227.17540443	2	I	10	1187.5942804	−0.0734063	1187.5942804	
	270.21760359	+0.0258851	298.21251822	3	A	9	1074.5102164	−0.0723502	1074.5102164	
	385.24454663	+0.0666911	413.23946125	4	D	8	1003.4731026	−0.1171456	1003.4731026	
	500.27148966	+0.2179097	528.26640428	5	D	7	888.44615956	−0.0088427	888.44615956	
	647.33990357	−0.0336097	675.3348182	6	F	6	773.41921653	+0.0575291	387.2132465	+0.0426739
	744.39266743	+0.4563511	772.38758205	7	P	5	626.35080261	−0.1244843	313.67903954	−0.4511648
	801.41413115		829.40904577	8	G	4	529.29803876	+0.0004232	529.29803876	
	900.48254507	−0.1752746	928.47745969	9	V	3	472.27657504	+0.107092	472.27657504	
	1029.5251382		1057.5200528	10	E	2	373.20816112	+0.0412285	373.20816112	
	1126.577902		1154.5728166	11	P	1	244.16556802	+0.031545	244.16556802	
				12	K	0	147.11280417		147.11280417	

Scan number	13340	Raw file	20081010_Orbi7_SaZa_SA_ADH_Exp_3_Laminin_24h_InGel_08
Method	ITMS; CID	Genenames	NR2C1



precursor information

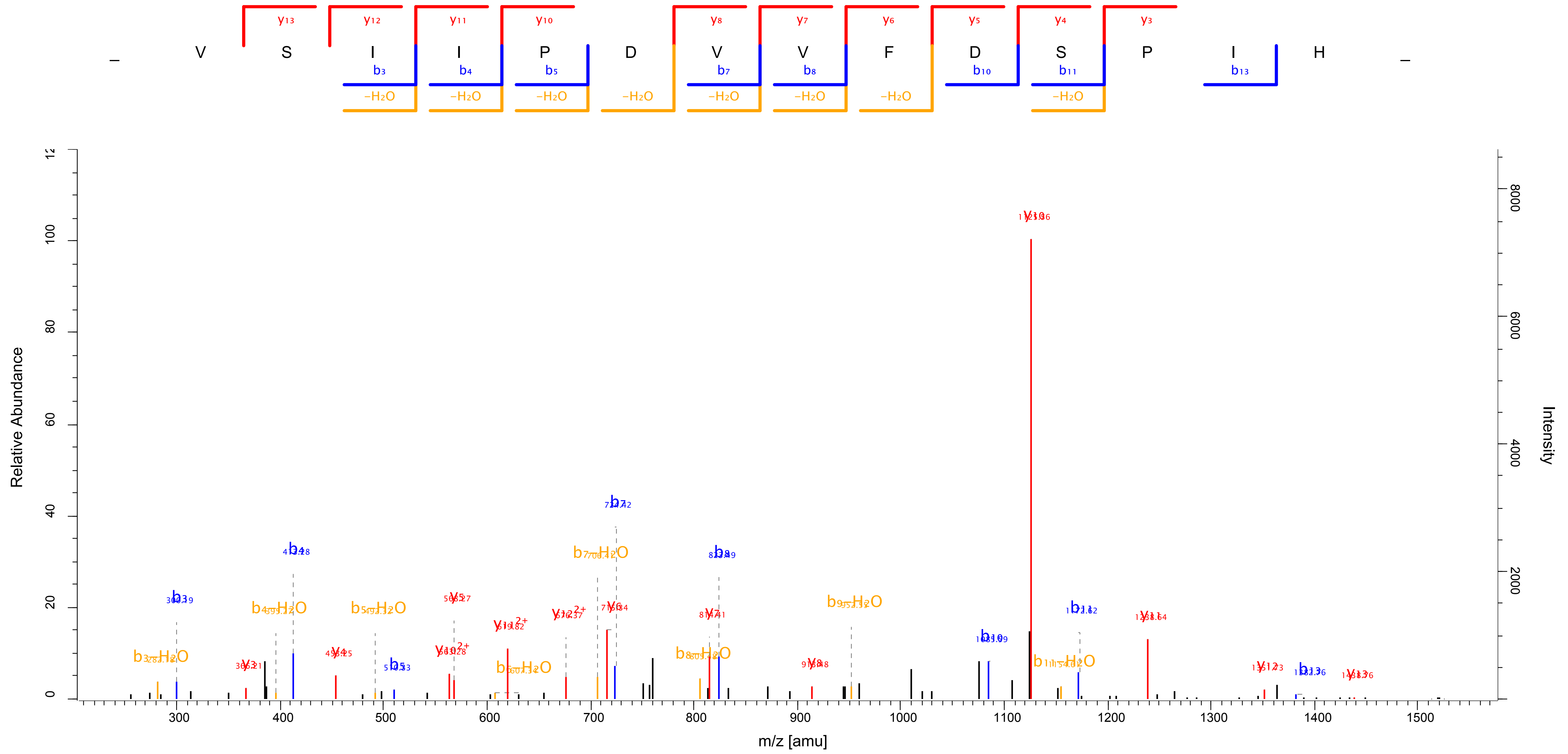
Mass:	1571.78976
m/z:	786.90216
Charge:	2+
Retentiontime:	96.416641235351 6
Score:	115.2865
Mass Error [ppm]:	−0.49026
PEP:	2.8778E−05
Precursor Type:	MULTI

general information

Annotation:	9 of 13
AminoAcids Coverage:	69 %
Intensity Coverage:	38 %
Peak Coverage:	29 %
Protein Localisation:	559 ... 571

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.091340447	1	I	12				
+0.0187681	261.126739675	2	M	11	1459.713743568		1459.713743568	
	375.169667122	3	N	10	1312.678344339		1312.678344339	
	446.20678091	4	A	9	1198.635416892		1198.635416892	
	547.254459384	5	T	8	1127.598303104		1127.598303104	
	660.338523365	6	I	7	1026.55062463		513.778950548	−0.2892045
	761.386201839	7	T	6	913.46656065		457.236918558	+0.1136674
	890.428794935	8	E	5	812.418882176	+0.2717306	406.713079321	−0.2210749
−0.2728407	1019.471388031	9	E	4	683.37628908		683.37628908	
−0.1354081	1132.555452012	10	I	3	554.333695983	+0.0095047	554.333695983	
−0.216029	1279.623865928	11	F	2	441.249632003	+0.0224627	441.249632003	
−0.3313179	1426.692279844	12	F	1	294.181218087	+0.1260634	294.181218087	
		13	K	0	147.112804171		147.112804171	

Scan number	16333	Raw file	20081010_Orbi7_SaZa_SA_ADH_Exp_3_Laminin_24h_InGel_10
Method	ITMS; CID	Genenames	SUFU



precursor information

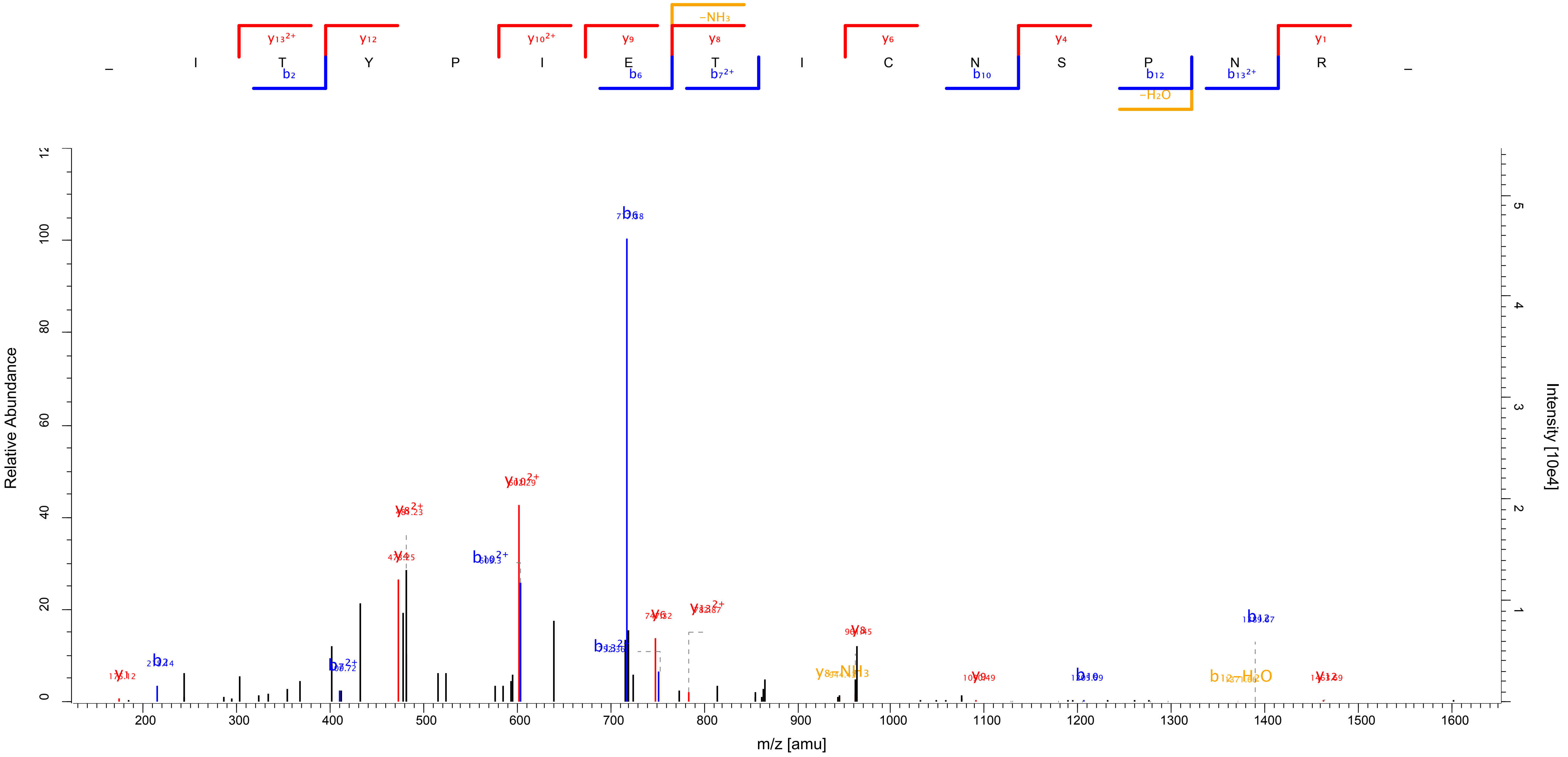
Mass:	1536.81822
m/z:	769.41639
Charge:	2+
Retentiontime:	111.107727050781
Score:	199.0759
Mass Error [ppm]:	−0.37218
PEP:	1.6507E−16
Precursor Type:	ISO

general information

Annotation:	12 of 14
AminoAcids Coverage:	86 %
Intensity Coverage:	69 %
Peak Coverage:	37 %
Protein Localisation:	471 ... 484

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.075690383	1	V	13				
	187.107718793	2	S	12	1438.757657293	+0.3064296	1438.757657293	
−0.2719525	300.191782773	3	I	11	1351.725628883	−0.3082705	676.366452675	+0.0054345
−0.1735518	413.275846754	4	I	10	1238.641564903	−0.0330444	619.824420685	−0.0217473
−0.1599094	510.328610606	5	P	9	1125.557500922	+0.0386905	563.282388694	+0.0696011
	625.355553638	6	D	8	1028.50473707		1028.50473707	
−0.1824514	724.423967554	7	V	7	913.477794038	−0.0757555	913.477794038	
−0.109569	823.49238147	8	V	6	814.409380122	−0.0035574	814.409380122	
	970.560795386	9	F	5	715.340966206	+0.0015021	715.340966206	
−0.2356876	1085.587738418	10	D	4	568.27255229	+0.082123	568.27255229	
−0.3043371	1172.619766828	11	S	3	453.245609258	+0.1080895	453.245609258	
	1269.67253068	12	P	2	366.213580848	−0.0330999	366.213580848	
−0.4200468	1382.75659466	13	I	1	269.160816996		269.160816996	
		14	H	0	156.076753015		156.076753015	

Scan number	15404	Raw file	20081015_Orbi6_SaZa_SA_ADH_Exp_1_Susp_InGel_16b
Method	ITMS; CID	Genenames	NOXIN



precursor information

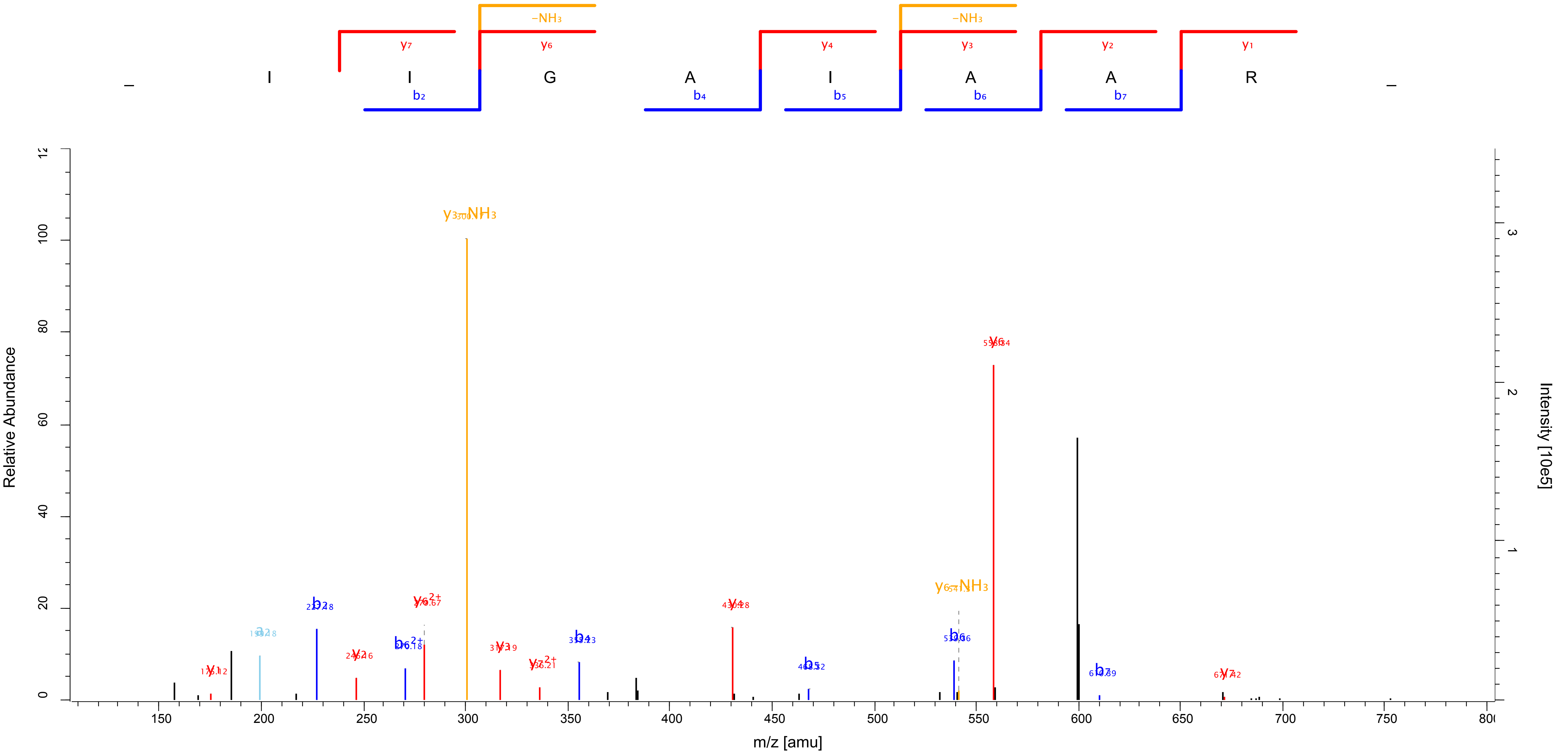
Mass:	1676.81777
m/z:	559.94653
Charge:	3+
Retentiontime:	99.543815612793
Score:	101.8882
Mass Error [ppm]:	-0.85362
PEP:	0.00032382
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverage:	79 %
Intensity Coverage:	51 %
Peak Coverage:	25 %
Protein Localisation:	631 ... 644

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045		114.09134045	1	I	13				
	215.13901892	+0.0180856	215.13901892	2	T	12	1564.7424179		782.8748472	+0.1405947
	378.20234746		378.20234746	3	Y	11	1463.6947395	-0.325843	1463.6947395	
	475.25511131		475.25511131	4	P	10	1300.6314109		1300.6314109	
	588.33917529		588.33917529	5	I	9	1203.5786471		602.29296177	+0.0735543
	717.38176839	+0.2600773	717.38176839	6	E	8	1090.4945831	+0.1882782	1090.4945831	
+0.4778053	409.71836166		818.42944686	7	T	7	961.45198999	-0.1243533	481.22963323	+0.1661798
	931.51351084		931.51351084	8	I	6	860.40431152		860.40431152	
	1091.544159		1091.544159	9	C	5	747.32024754	-0.0954551	747.32024754	
+0.1369616	603.29718148	+0.0442612	1205.5870865	10	N	4	587.28959934		587.28959934	
	1292.6191149		1292.6191149	11	S	3	473.24667189	+0.0285356	473.24667189	
	1389.6718788	-0.203495	1389.6718788	12	P	2	386.21464348		386.21464348	
-0.1875184	752.36104133		1503.7148062	13	N	1	289.16187963		289.16187963	
				14	R	0	175.11895218	-0.0156807	175.11895218	

Scan number	3764	Raw file	20081127_Orbi7_SaZa_SA_ADH_MatrigelGFR_Exp_2_InGel_16
Method	ITMS; CID	Genenames	TSPAN10



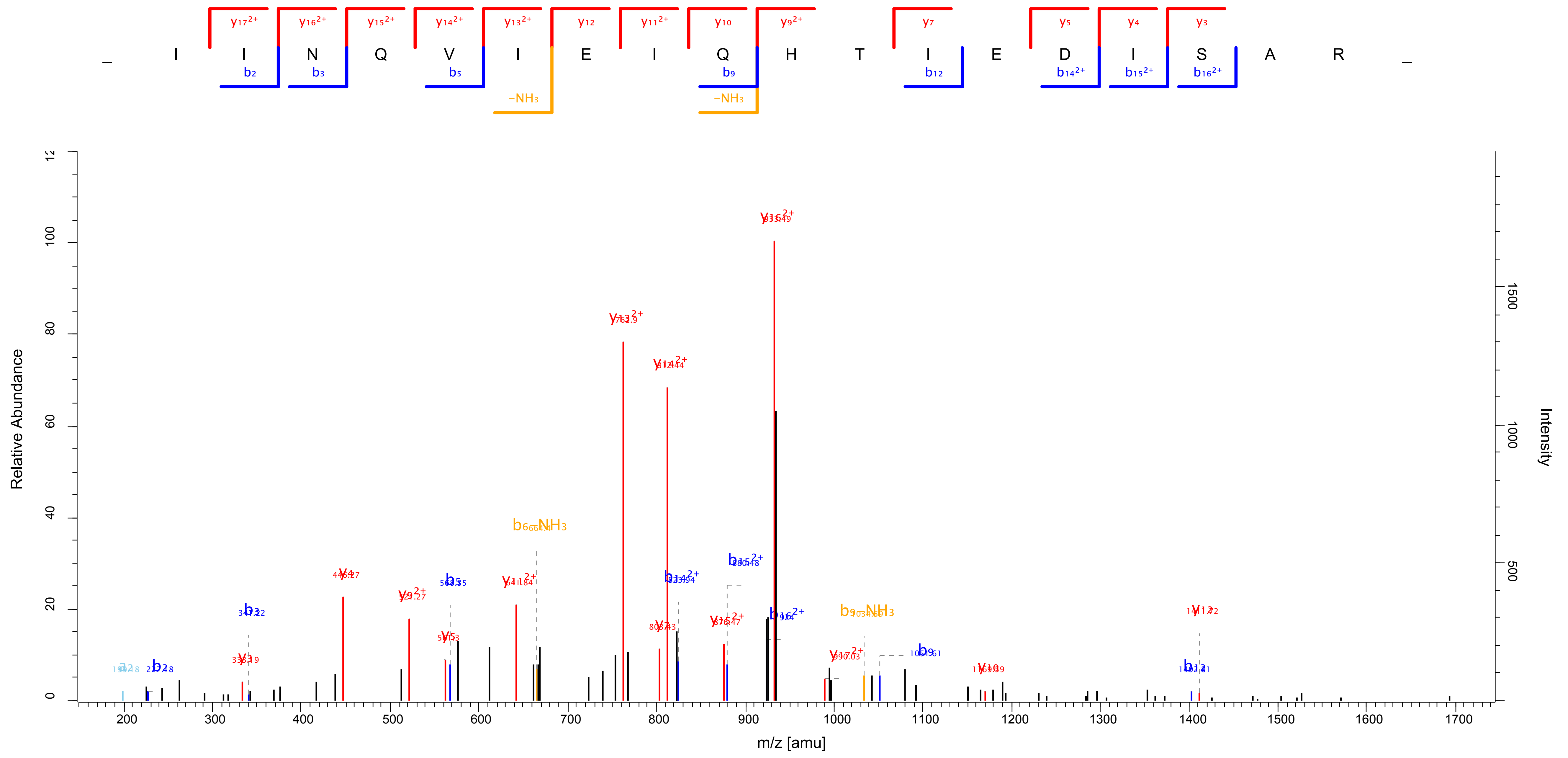
precursor
information

ge
ir

Mass:	783.4964
m/z:	392.75548
Charge:	2+
Retentiontime:	41.1161193847656
Score:	167.2529
Mass Error [ppm]:	-0.34975
PEP:	0.00028998
Annotation:	7 of 8
AminoAcids Coverage:	88 %
Intensity Coverage:	71 %
Peak Coverage:	45 %
Protein Localisation:	315 ... 322

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.0964258		114.09134		114.09134	1	I	7				
+0.056113	199.18049		227.175404	-0.0146989	227.175404	2	I	6	671.419885	-0.0151611	336.213581	-0.21294
	256.201954		284.196868		284.196868	3	G	5	558.335821	+0.0215396	279.671549	+0.0063686
	327.239067		355.233982	+0.0212366	355.233982	4	A	4	501.314358		501.314358	
	440.323131		468.318046	-0.1679605	468.318046	5	I	3	430.277244	+0.0571374	430.277244	
	511.360245	+0.4982863	270.181218	-0.0530357	539.35516	6	A	2	317.19318	+0.0589565	317.19318	
	582.397359		610.392273	-0.1643682	610.392273	7	A	1	246.156066	+0.0569467	246.156066	
						8	R	0	175.118952	+0.1007439	175.118952	

Scan number	15411	Raw file	20081206_Orbi7_SaZa_ADH_FN_Exp_1_InGel_01
Method	ITMS; CID	Genenames	SCOC



precursor information

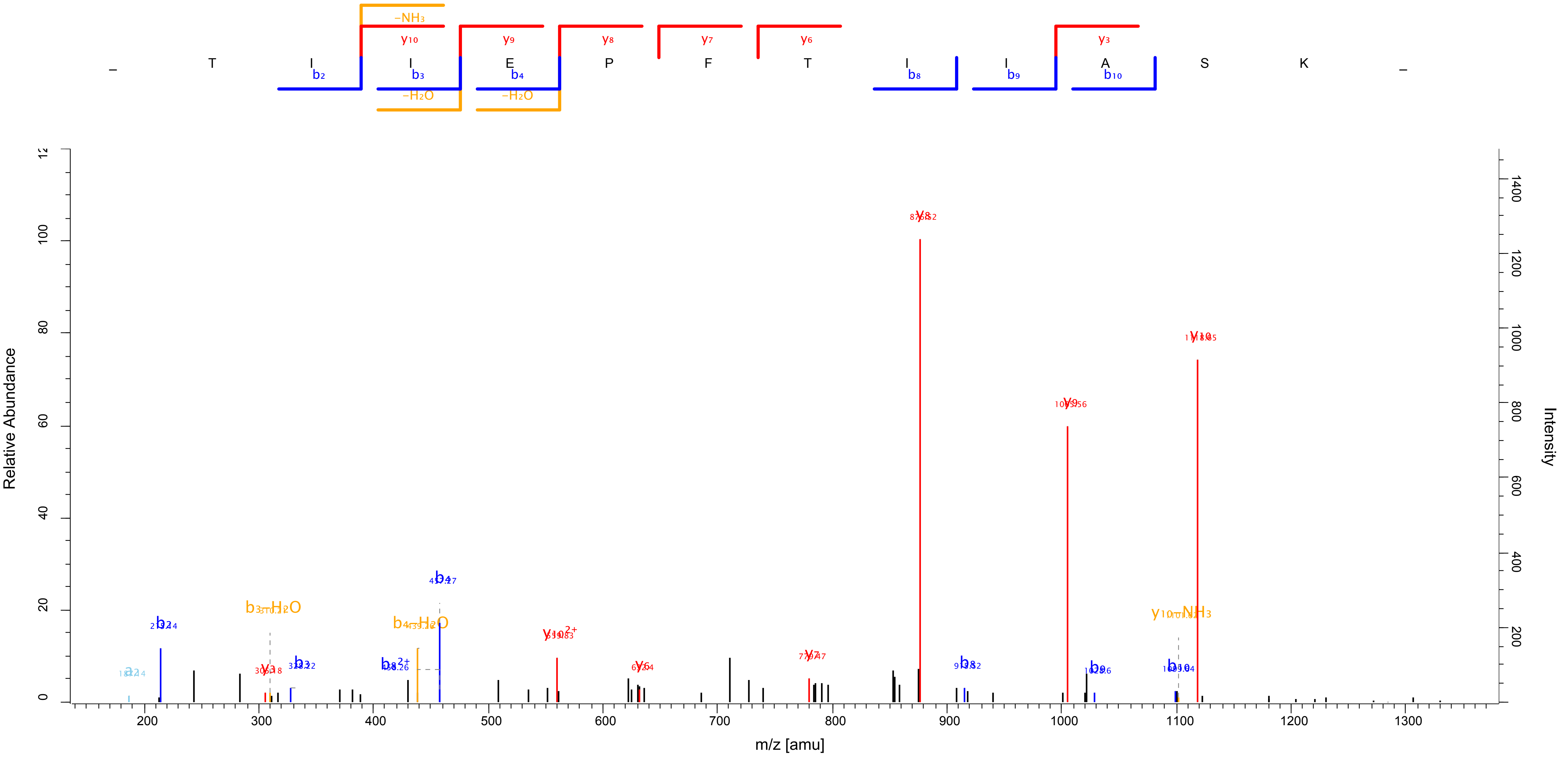
Mass:	2091.13183
m/z:	698.05122
Charge:	3+
Retentiontime:	118.56391143798
Score:	114.3098
Mass Error [ppm]:	−0.27938
PEP:	1.206E−06
Precursor Type:	MULTI

general information

Annotation:	13 of 18
AminoAcids Coverage:	72 %
Intensity Coverage:	57 %
Peak Coverage:	31 %
Protein Localisation:	100 ... 117

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.0964258		114.09134		114.09134	1	I	17				
+0.007468	199.18049		227.175404	−0.0378617	227.175404	2	I	16	1979.05563		990.031453	−0.0876057
	313.223417		341.218332	−0.1624237	341.218332	3	N	15	1865.97157		933.489421	+0.0345044
	441.281995		469.276909		469.276909	4	Q	14	1751.92864		876.467958	+0.1367177
	540.350409		568.345323	+0.1017592	568.345323	5	V	13	1623.87006		812.438669	+0.2640899
	653.434473		681.429387		681.429387	6	I	12	1524.80165		762.904462	+0.2340268
	782.477066		810.47198		810.47198	7	E	11	1411.71758	+0.3198922	1411.71758	
	895.56113		923.556044		923.556044	8	I	10	1282.67499		641.841133	+0.0559613
	1023.61971		1051.61462	−0.1263406	1051.61462	9	Q	9	1169.59093	−0.083358	1169.59093	
	1160.67862		1188.67353		1188.67353	10	H	8	1041.53235		521.269813	+0.0840082
	1261.7263		1289.72121		1289.72121	11	T	7	904.473437		904.473437	
	1374.81036		1402.80528	+0.0178439	1402.80528	12	I	6	803.425758	+0.0254744	803.425758	
	1503.85295		1531.84787		1531.84787	13	E	5	690.341694		690.341694	
	1618.8799	+0.3168291	823.941044		1646.87481	14	D	4	561.299101	+0.1166091	561.299101	
	1731.96396	−0.1408523	880.483076		1759.95888	15	I	3	446.272158	+0.0763524	446.272158	
	1818.99599	−0.1583313	923.999091		1846.9909	16	S	2	333.188094	+0.0583351	333.188094	
	1890.0331		1918.02802		1918.02802	17	A	1	246.156066		246.156066	
						18	R	0	175.118952		175.118952	

Scan number	14959	Raw file	20081206_Orbi7_SaZa_ADH_FN_Exp_1_InGel_03
Method	ITMS; CID	Genenames	NKIRAS1



precursor information

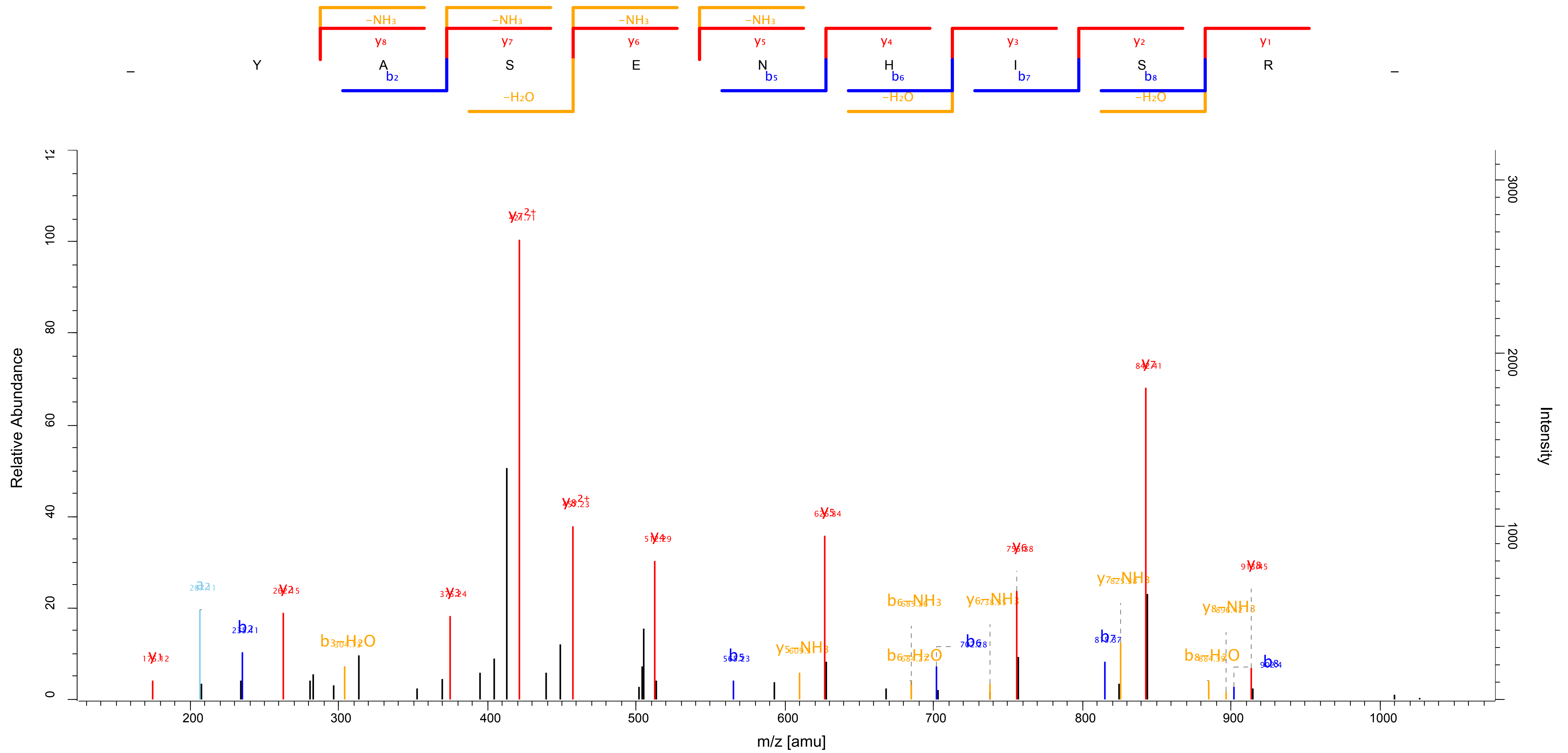
Mass:	1331.77006
m/z:	666.8923
Charge:	2+
Retentiontime:	110.403625488281
Score:	115.5738
Mass Error [ppm]:	0.0021197
PEP:	0.00019425
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverage:	75 %
Intensity Coverage:	68 %
Peak Coverage:	27 %
Protein Localisation:	156 ... 167

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.0600403		102.054955		102.054955	1	T	11				
−0.0466464	187.144104		215.139019	+0.0068551	215.139019	2	I	10	1231.72965		1231.72965	
	300.228168		328.223083	+0.1392828	328.223083	3	I	9	1118.64559	−0.0363347	559.826432	+0.099044
	429.270761		457.265676	+0.0028787	457.265676	4	E	8	1005.56152	−0.1470339	1005.56152	
	526.323525		554.31844		554.31844	5	P	7	876.518931	−0.0723363	876.518931	
	673.391939		701.386854		701.386854	6	F	6	779.466167	+0.0841262	779.466167	
	774.439618		802.434532		802.434532	7	T	5	632.397753	+0.1519908	632.397753	
	887.523682	−0.1144378	458.262936	−0.1448169	915.518596	8	I	4	531.350074		531.350074	
	1000.60775		1028.60266	−0.2564688	1028.60266	9	I	3	418.26601		418.26601	
	1071.64486		1099.63977	−0.1037632	1099.63977	10	A	2	305.181946	+0.0700678	305.181946	
	1158.67689		1186.6718		1186.6718	11	S	1	234.144833		234.144833	
						12	K	0	147.112804		147.112804	

Scan number	1630	Raw file	20081206_Orbi7_SaZa_ADH_FN_Exp_1_InGel_04
Method	ITMS; CID	Genenames	TM4SF1



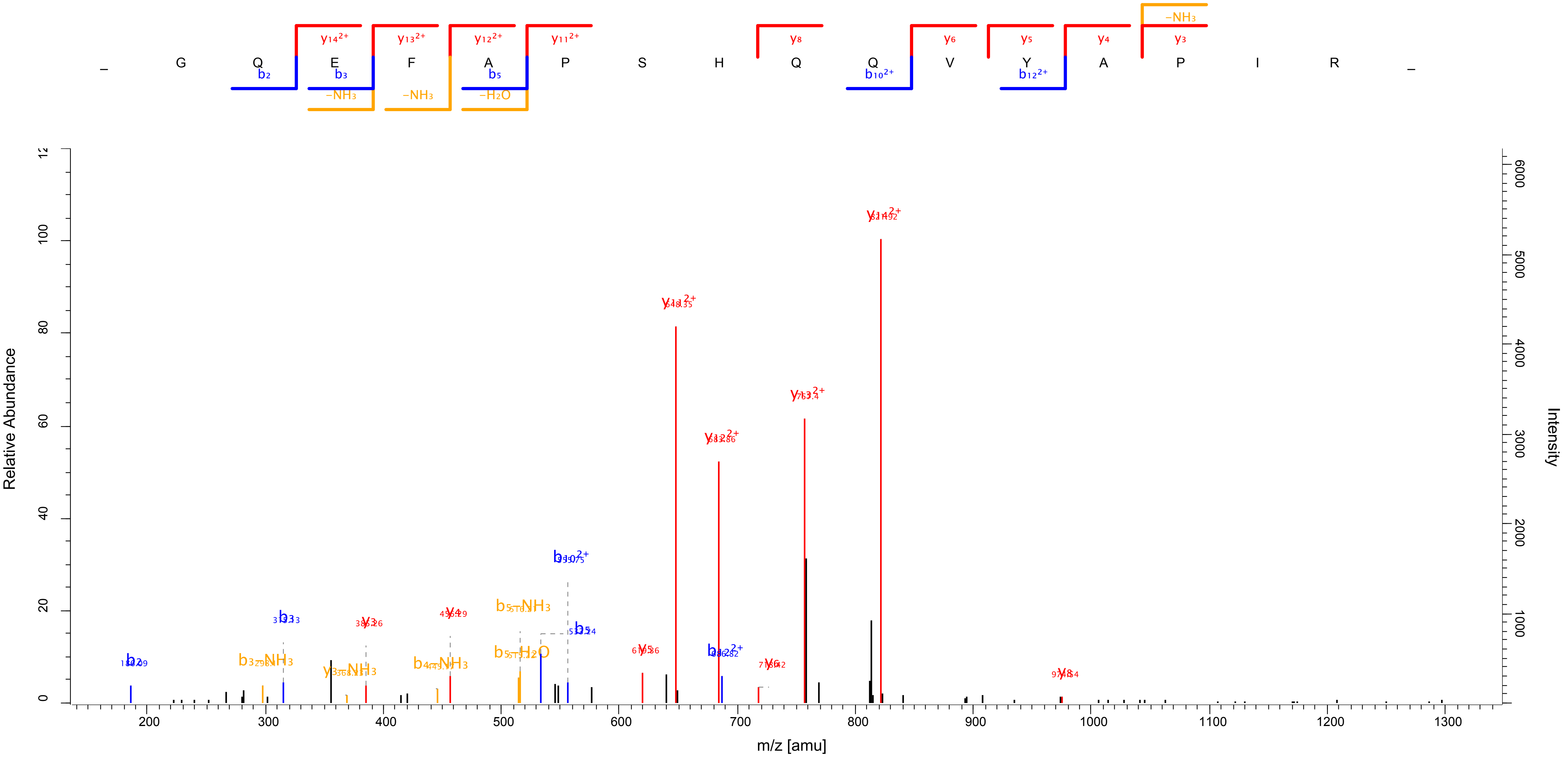
precursor
information

Mass:	1075.50464
m/z:	538.7596
Charge:	2+
Retentiontime:	32.6492691040039
Score:	206.7847
Mass Error [ppm]:	-0.03097
PEP:	7.9781E-15
Annotation:	8 of 9
AminoAcids Coverage:	89 %
Intensity Coverage:	68 %
Peak Coverage:	46 %
Protein Localisation:	37 ... 45

ge
ir

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.07569038		164.070605	1	Y	8				
-0.0415609	207.11280417	+0.0777365	235.10771879	2	A	7	913.44861917	+0.0599257	457.22794782	+0.2180361
	294.14483258		322.1397472	3	S	6	842.41150539	+0.0407041	421.70939093	+0.1505334
	423.18742568		451.1823403	4	E	5	755.37947698	+0.0416656	755.37947698	
	537.23035312	+0.0771004	565.22526775	5	N	4	626.33688388	+0.0158383	626.33688388	
	674.28926499	+0.0096436	702.28417961	6	H	3	512.29395643	-0.0249135	512.29395643	
	787.37332897	+0.0658995	815.36824359	7	I	2	375.23504457	+0.0808124	375.23504457	
	874.40535738	+0.014706	902.400272	8	S	1	262.15098059	+0.1143087	262.15098059	
				9	R	0	175.11895218	-0.0340523	175.11895218	

Scan number	7103	Raw file	20081206_Orbi7_SaZa_ADH_FN_Exp_1_InGel_06
Method	ITMS; CID	Genenames	TNFSF15



precursor information

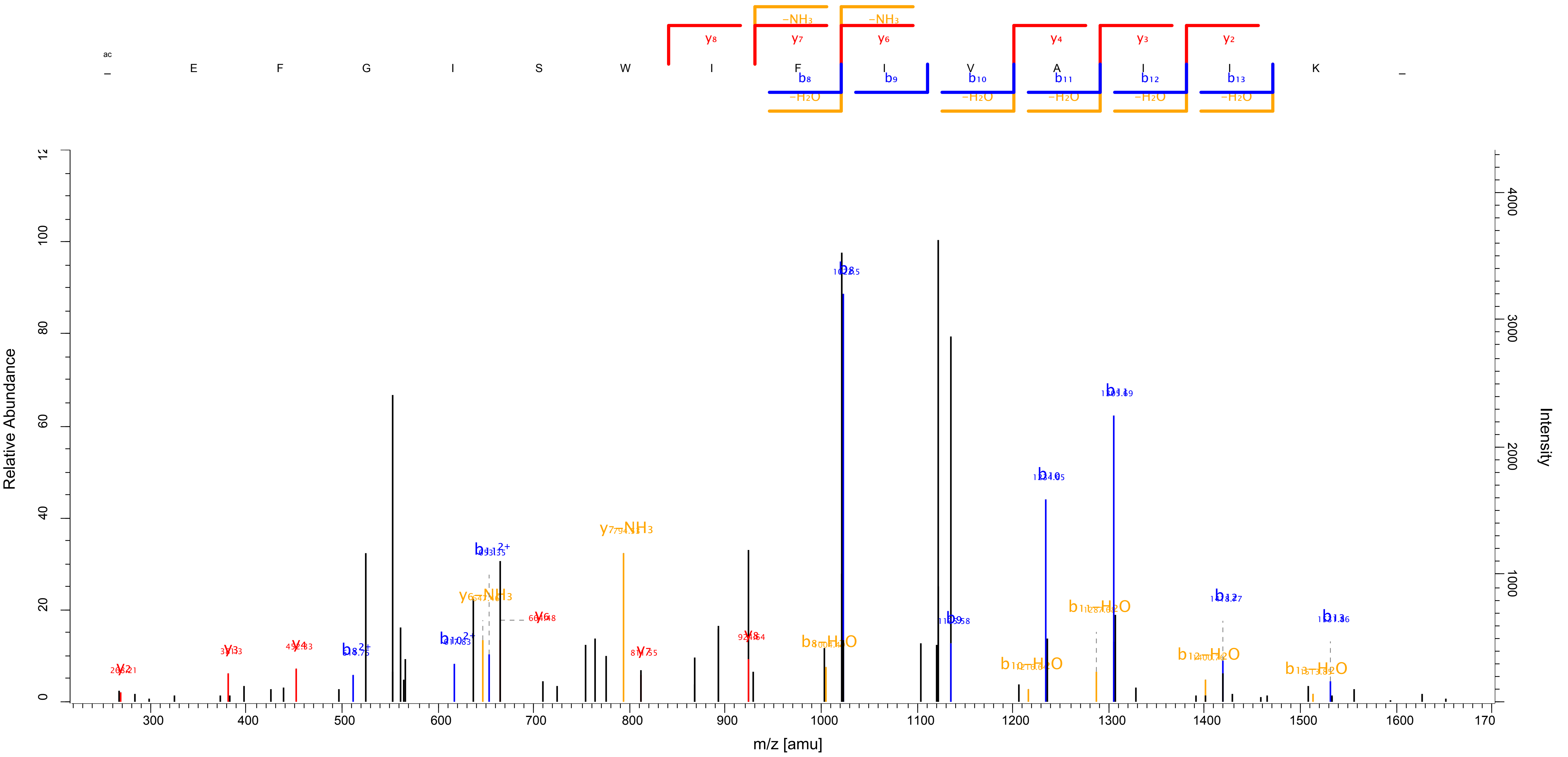
Mass:	1826.90459
m/z:	609.97547
Charge:	3+
Retentiontime:	62.0040664672852
Score:	98.94209
Mass Error [ppm]:	-0.97795
PEP:	0.00039882
Precursor Type:	MULTI

general information

Annotation:	11 of 16
AminoAcids Coverage:	69 %
Intensity Coverage:	75 %
Peak Coverage:	30 %
Protein Localisation:	74 ... 89

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019		58.02874019	1	G	15				
	186.0873177	+0.0228355	186.0873177	2	Q	14	1770.8921937		1770.8921937	
	315.1299108	-0.0843786	315.1299108	3	E	13	1642.8336162		821.92044633	+0.2754155
	462.19832471		462.19832471	4	F	12	1513.7910231		757.39914979	+0.0558063
	533.2354385	-0.0139419	533.2354385	5	A	11	1366.7226092		683.86494283	+0.2704942
	630.28820235		630.28820235	6	P	10	1295.6854954		648.34638593	+0.2452889
	717.32023076		717.32023076	7	S	9	1198.6327316		1198.6327316	
	854.37914263		854.37914263	8	H	8	1111.6007031		1111.6007031	
	982.43772014		982.43772014	9	Q	7	974.54179128	+0.0842463	974.54179128	
+0.0067579	555.75178706		1110.4962976	10	Q	6	846.48321377		846.48321377	
	1209.5647116		1209.5647116	11	V	5	718.42463626	+0.0981909	718.42463626	
-0.0434273	686.81765828		1372.6280401	12	Y	4	619.35622234	-0.0263273	619.35622234	
	1443.6651539		1443.6651539	13	A	3	456.2928938	+0.0846086	456.2928938	
	1540.7179177		1540.7179177	14	P	2	385.25578001	-0.045697	385.25578001	
	1653.8019817		1653.8019817	15	I	1	288.20301616		288.20301616	
				16	R	0	175.11895218		175.11895218	

Scan number	17478	Raw file	20081206_Orbi7_SaZa_ADH_FN_Exp_1_InGel_07
Method	ITMS; CID	Pepti...	128.08



precursor
information

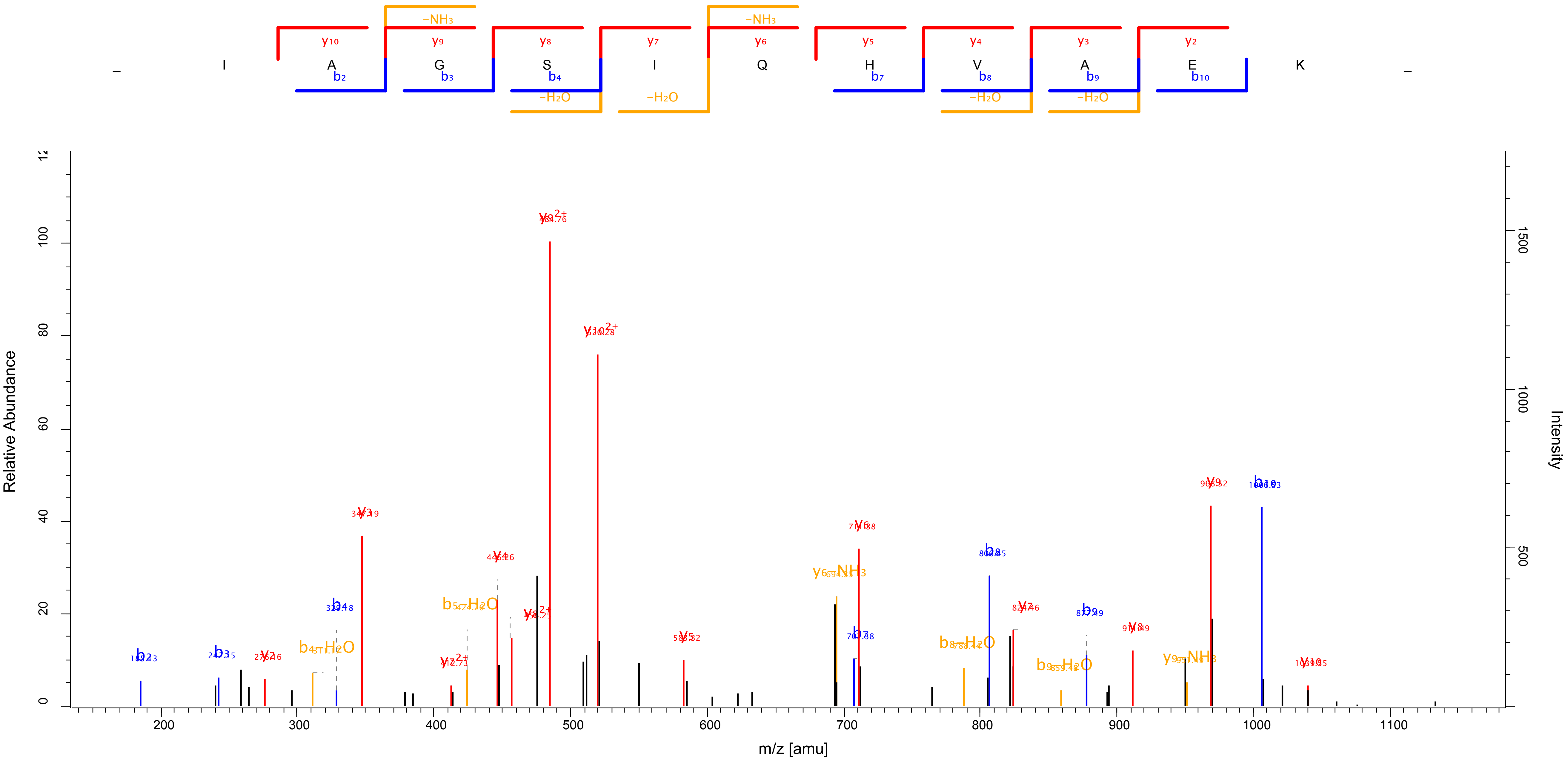
Mass:	1676.95247
m/z:	839.48351
Charge:	2+
Retentiontime:	126.270179748535
Score:	128.081
Mass Error [ppm]:	−1.0058
PEP:	1.2965E−07
Precursor Type:	MULTI

general
information

Annotation:	8 of 14
AminoAcids Coverage:	57 %
Intensity Coverage:	31 %
Peak Coverage:	28 %
Protein Localisation:	2 ... 15

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	172.060434249		172.060434249	1	E	13		
	319.128848165		319.128848165	2	F	12	1514.922483509	
	376.150311889		376.150311889	3	G	11	1367.854069593	
	489.234375869		489.234375869	4	I	10	1310.832605869	
	576.266404279		576.266404279	5	S	9	1197.748541889	
	762.345717233		762.345717233	6	W	8	1110.716513479	
	875.429781213		875.429781213	7	I	7	924.637200526	−0.1184017
+0.1527207	511.752735798	−0.1728167	1022.498195129	8	F	6	811.553136545	−0.1040399
	1135.58225911	+0.0501872	1135.58225911	9	I	5	664.484722629	+0.0857119
−0.1420241	617.828974746	−0.1820451	1234.650673026	10	V	4	551.400658649	
−0.0786718	653.34753164	−0.1388366	1305.687786814	11	A	3	452.332244732	−0.0273741
	1418.771850794	−0.3425295	1418.771850794	12	I	2	381.295130945	+0.1209457
	1531.855914774	−0.1789128	1531.855914774	13	I	1	268.211066964	+0.1894762
				14	K	0	155.127002984	

Scan number	3148	Raw file	20081206_Orbi7_SaZa_ADH_FN_Exp_1_InGel_07
Method	ITMS; CID	Genenames	CLEC1A



precursor information

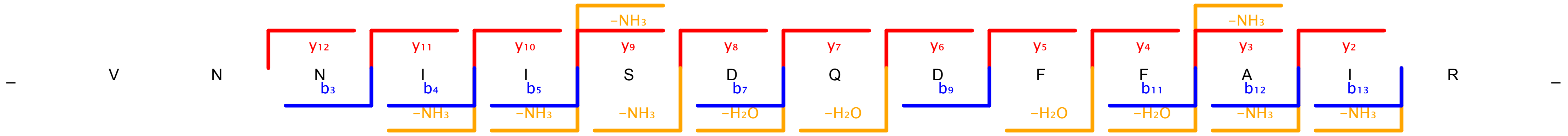
Mass:	1151.62937
m/z:	576.82196
Charge:	2+
Retentiontime:	41.218578338623
Score:	182.2843
Mass Error [ppm]:	–0.43753
PEP:	7.6931E–05
Precursor Type:	ISO

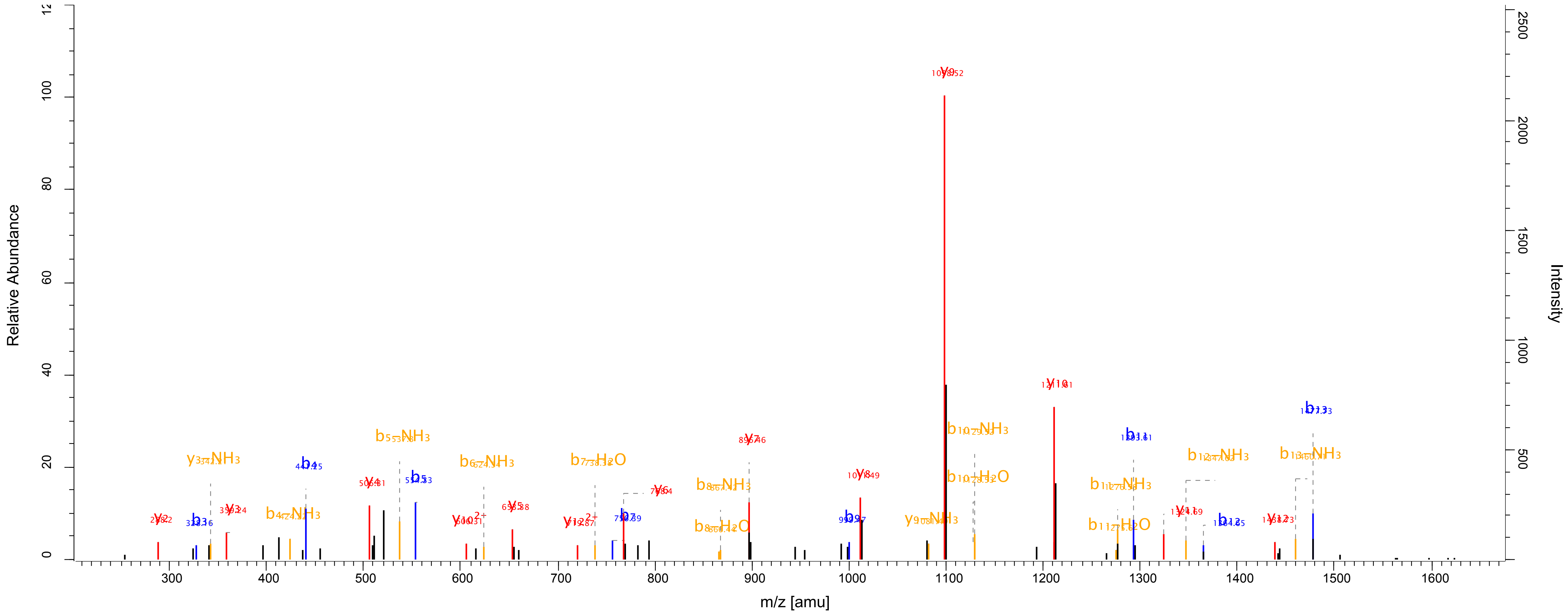
general information

Annotation:	9 of 11
AminoAcids Coverage:	82 %
Intensity Coverage:	69 %
Peak Coverage:	43 %
Protein Localisation:	110 ... 120

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.091340447	1	I	10				
−0.0830136	185.128454235	2	A	9	1039.553084246	−0.2571858	520.280180356	+0.0443436
+0.1464077	242.149917958	3	G	8	968.515970459	−0.0627844	484.761623463	+0.2154273
−0.2223516	329.181946368	4	S	7	911.494506735	−0.1062621	456.250891601	+0.2489863
	442.266010349	5	I	6	824.462478325	+0.133591	412.734877396	+0.0613262
	570.32458786	6	Q	5	711.378414345	−0.0908167	711.378414345	
−0.1119543	707.383499722	7	H	4	583.319836833	+0.0103634	583.319836833	
+0.0730497	806.451913639	8	V	3	446.260924971	−0.0267331	446.260924971	
+0.0541244	877.489027426	9	A	2	347.192511055	+0.0013976	347.192511055	
+0.01617	1006.531620523	10	E	1	276.155397267	+0.074278	276.155397267	
		11	K	0	147.112804171		147.112804171	

Scan number	14593	Raw file	20081206_Orbi7_SaZa_ADH_FN_Exp_1_InGel_08
Method	ITMS; CID	Genenames	LYSMD3





precursor information

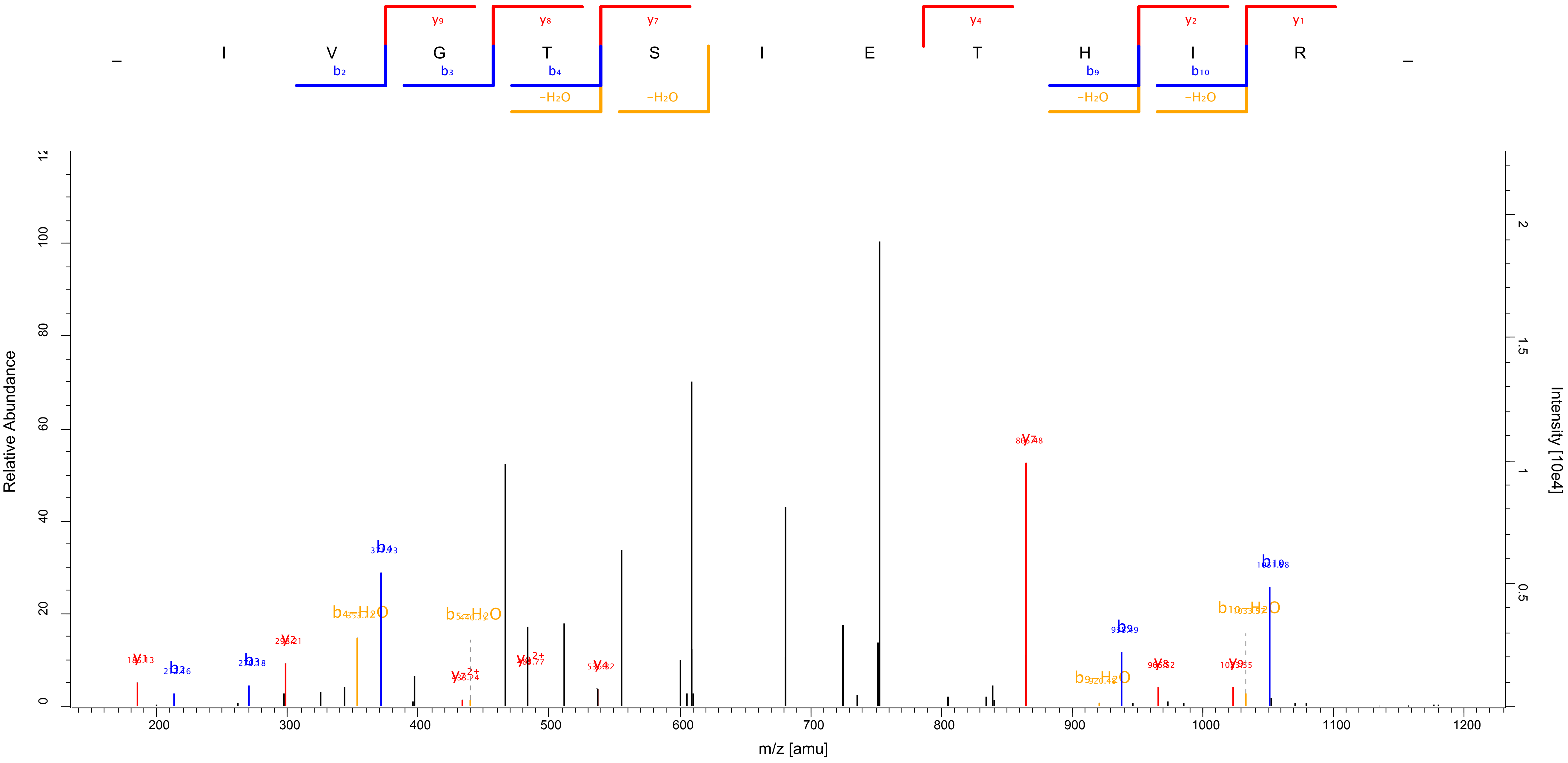
Mass:	1650.83602
m/z:	826.42528
Charge:	2+
Retentiontime:	106.197372436523
Score:	200.2063
Mass Error [ppm]:	−0.33499
PEP:	1.2282E−16
Precursor Type:	ISO

general information

Annotation:	11 of 14
AminoAcids Coverage:	79 %
Intensity Coverage:	66 %
Peak Coverage:	46 %
Protein Localisation:	92 ... 105

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.075690383	1	V	13				
	214.11861783	2	N	12	1552.775432622		1552.775432622	
+0.0699916	328.161545277	3	N	11	1438.732505175	+0.042153	719.869890821	+0.0272649
−0.0336952	441.245609258	4	I	10	1324.689577728	−0.084231	1324.689577728	
−0.1171488	554.329673238	5	I	9	1211.605513747	+0.0192421	606.306395107	+0.0172743
	641.361701648	6	S	8	1098.521449767	−0.0268209	1098.521449767	
−0.4741549	756.38864468	7	D	7	1011.489421357	−0.058208	1011.489421357	
	884.447222191	8	Q	6	896.462478325	+0.0827487	896.462478325	
+0.2243821	999.474165223	9	D	5	768.403900814	+0.0491632	768.403900814	
	1146.542579139	10	F	4	653.376957782	+0.0646926	653.376957782	
−0.0508124	1293.610993056	11	F	3	506.308543865	−0.029247	506.308543865	
−0.1213734	1364.648106843	12	A	2	359.240129949	+0.0642524	359.240129949	
−0.1487968	1477.732170824	13	I	1	288.203016161	+0.0079213	288.203016161	
		14	R	0	175.11895218 1		175.11895218 1	

Scan number	12869	Raw file	20081210_Orbi7_QC_SaZa_ADH_FN_Exp_1_13
Method	ITMS; CID	Pepti...	121.73



precursor information

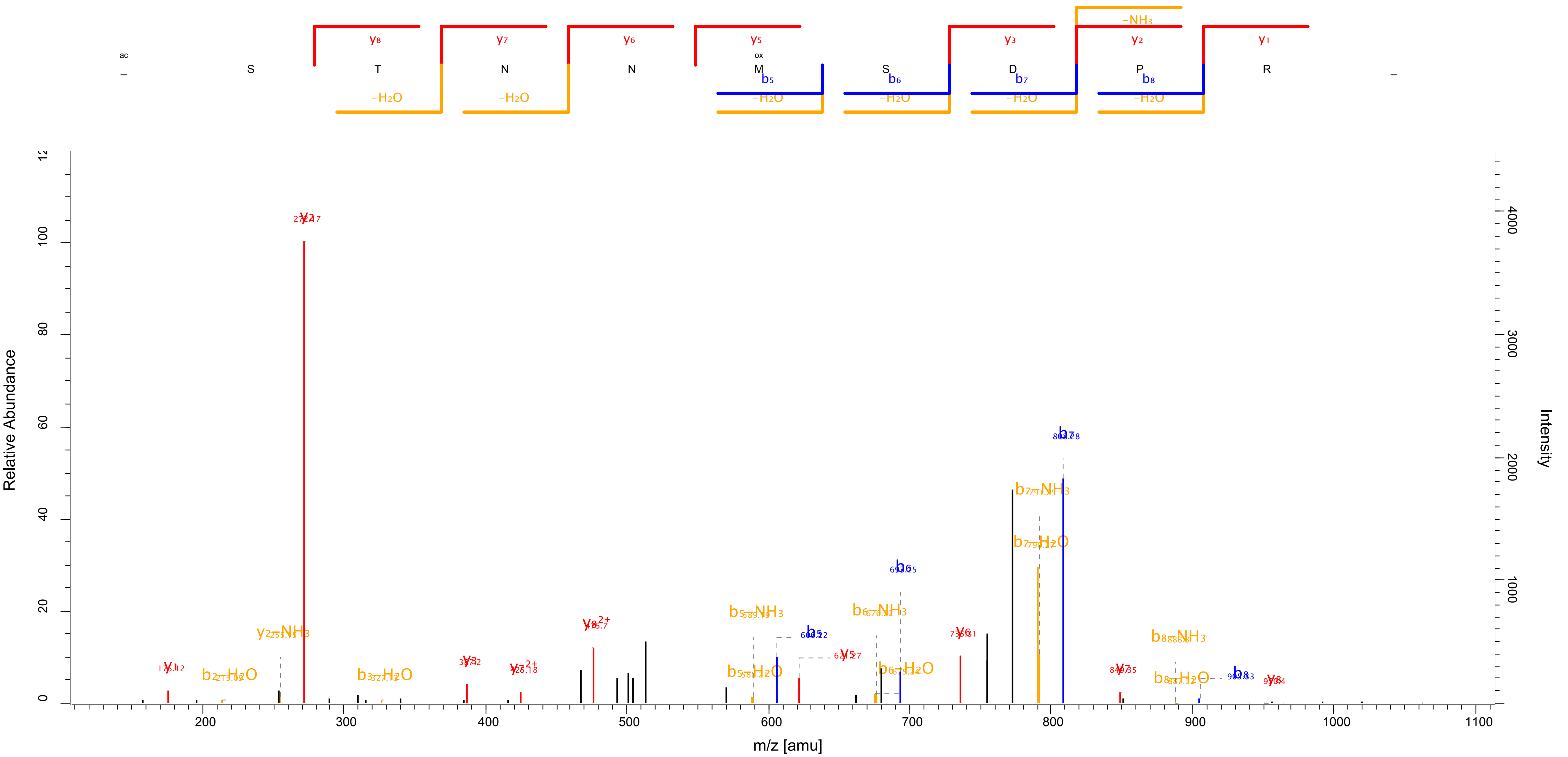
Mass:	1224.6825
m/z:	613.34853
Charge:	2+
Retentiontime:	85.820068359375
Score:	121.7328
Mass Error [ppm]:	−0.10966
PEP:	0.00021725
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverage:	73 %
Intensity Coverage:	28 %
Peak Coverage:	31 %
Protein Localisation:	516 ... 526

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.091340447	1	I	10				
−0.1280161	213.159754363	2	V	9	1122.614116698		1122.614116698	
+0.0381728	270.181218087	3	G	8	1023.545702782	+0.0048954	1023.545702782	
−0.0954127	371.228896561	4	T	7	966.524239058	+0.0131145	483.765757762	−0.2234604
	458.260924971	5	S	6	865.476560584	+0.0862446	433.241918525	+0.2757817
	571.344988951	6	I	5	778.444532174		778.444532174	
	700.387582047	7	E	4	665.360468194		665.360468194	
	801.435260522	8	T	3	536.317875097	+0.4821127	536.317875097	
−0.087251	938.494172384	9	H	2	435.270196623		435.270196623	
−0.3165176	1051.578236364	10	I	1	298.211284761	+0.1311225	298.211284761	
		11	R	0	185.127220781	+0.0109628	185.127220781	

Scan number	1723	Raw file	20081218_Orbi7_SaZa_SA_ADH_FN_Exp_2_InGel_01
Method	ITMS; CID	Genenames	WDR83OS

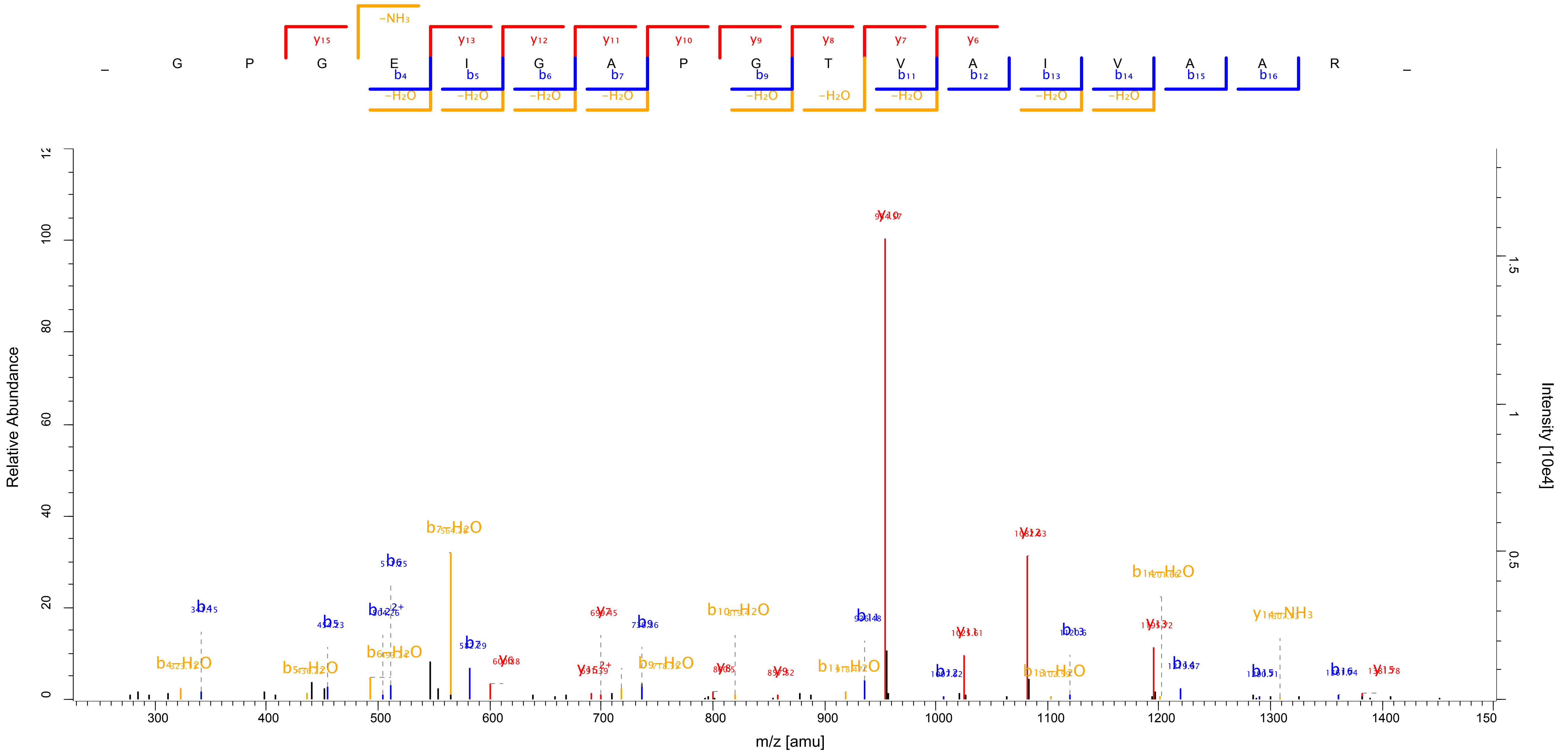


precursor information

Mass:	1078.43541
m/z:	540.22498
Charge:	2+
Retentiontime:	31.3200263977051
Score:	189.7022
Mass Error [ppm]:	0.44094
PEP:	2.5623E-07
Annotation:	8 of 9
AminoAcids Coverage:	89 %
Intensity Coverage:	66 %
Peak Coverage:	46 %
Protein Localisation:	2 ... 10

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.049869563	1	S	8				
	231.097548037	2	T	7	950.399620072	+0.1987686	475.703448269	+0.076459
	345.140475484	3	N	6	849.351941598	−0.1350837	425.179609032	−0.0207345
	459.183402931	4	N	5	735.30901415	−0.0209892	735.30901415	
−0.0081698	606.21880216	5	M	4	621.266086703	+0.1078147	621.266086703	
−0.1443853	693.25083057	6	S	3	474.230687475		474.230687475	
−0.2808254	808.277773602	7	D	2	387.198659065	+0.0952252	387.198659065	
−0.1947342	905.330537454	8	P	1	272.171716033	−0.0624631	272.171716033	
		9	R	0	175.118952181	+0.0663811	175.118952181	

Scan number	11330	Raw file	20081218_Orbi7_SaZa_SA_ADH_FN_Exp_2_InGel_15
Method	ITMS; CID	Genenames	COL13A1



precursor information

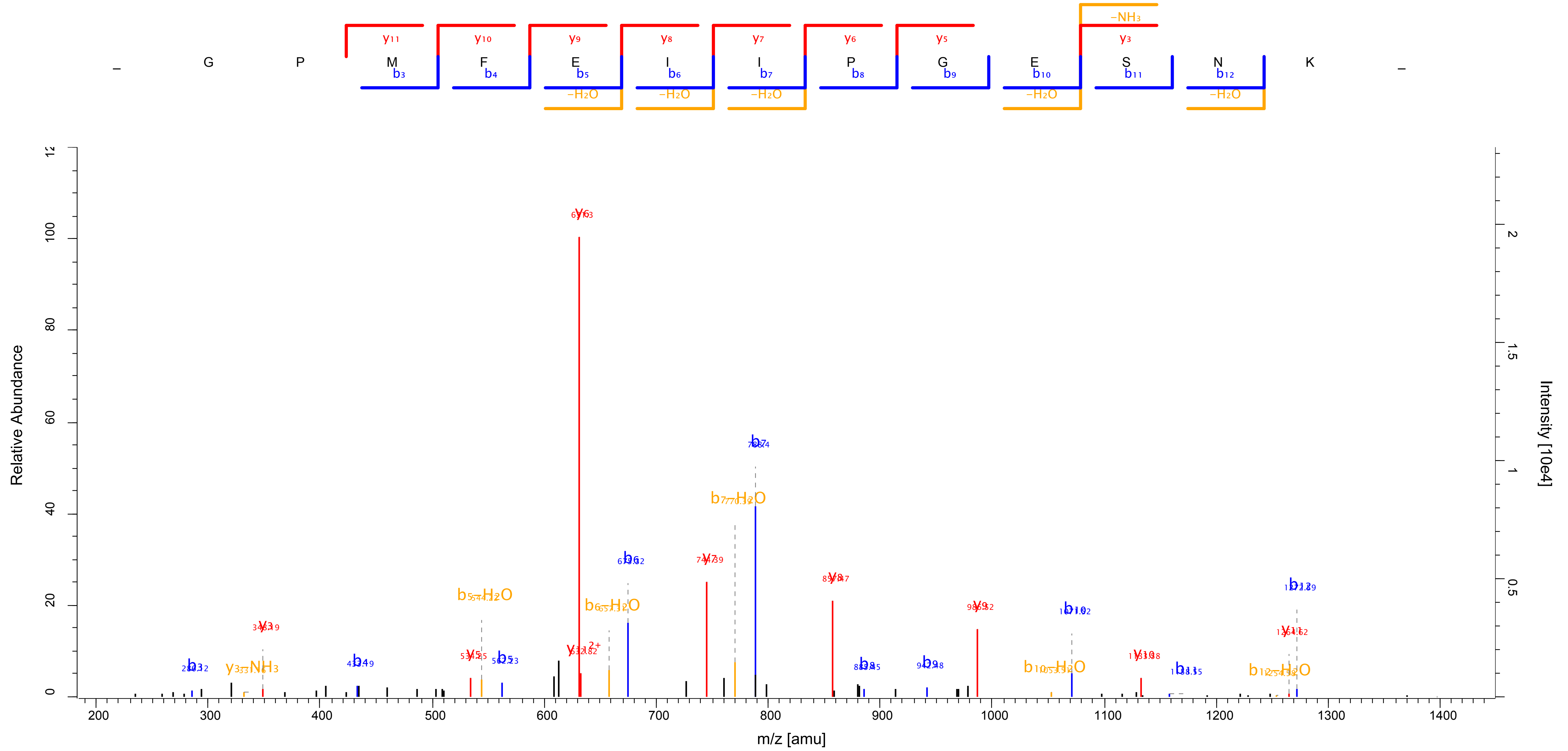
Mass:	1534.84693
m/z:	768.43074
Charge:	2+
Retentiontime:	77.555793762207
Score:	182.0156
Mass Error [ppm]:	0.12251
PEP:	1.3329E−26
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverage:	82 %
Intensity Coverage:	78 %
Peak Coverage:	45 %
Protein Localisation:	16 ... 32

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019		58.02874019	1	G	16				
	155.08150404		155.08150404	2	P	15	1478.8325536		1478.8325536	
	212.10296777		212.10296777	3	G	14	1381.7797897	−0.1384323	691.39353309	+0.1330172
	341.14556086	−0.0226971	341.14556086	4	E	13	1324.758326		1324.758326	
	454.22962484	−0.0585433	454.22962484	5	I	12	1195.7157329	−0.0455669	1195.7157329	
	511.25108857	−0.1708884	511.25108857	6	G	11	1082.6316689	−0.0551308	1082.6316689	
	582.28820235	−0.1094304	582.28820235	7	A	10	1025.6102052	+0.0147948	1025.6102052	
	679.34096621		679.34096621	8	P	9	954.57309141	−0.0334796	954.57309141	
	736.36242993	+0.3713958	736.36242993	9	G	8	857.52032755	+0.1377535	857.52032755	
	837.4101084		837.4101084	10	T	7	800.49886383	−0.0486075	800.49886383	
	936.47852232	−0.0004339	936.47852232	11	V	6	699.45118536	−0.2041761	699.45118536	
−0.2824524	504.26145629	−0.2375599	1007.5156361	12	A	5	600.38277144	+0.0793257	600.38277144	
	1120.5997001	+0.2036446	1120.5997001	13	I	4	529.34565765		529.34565765	
	1219.668114	−0.2081531	1219.668114	14	V	3	416.26159367		416.26159367	
	1290.7052278	−0.4023713	1290.7052278	15	A	2	317.19317976		317.19317976	
	1361.7423416	−0.2682205	1361.7423416	16	A	1	246.15606597		246.15606597	
				17	R	0	175.11895218		175.11895218	

Scan number	14123	Raw file	20081219_orbi2_WeStr_COLLAB_ADH_FN_Exp_2_InGel_18
Method	ITMS; CID	Genenames	SRGN



precursor information

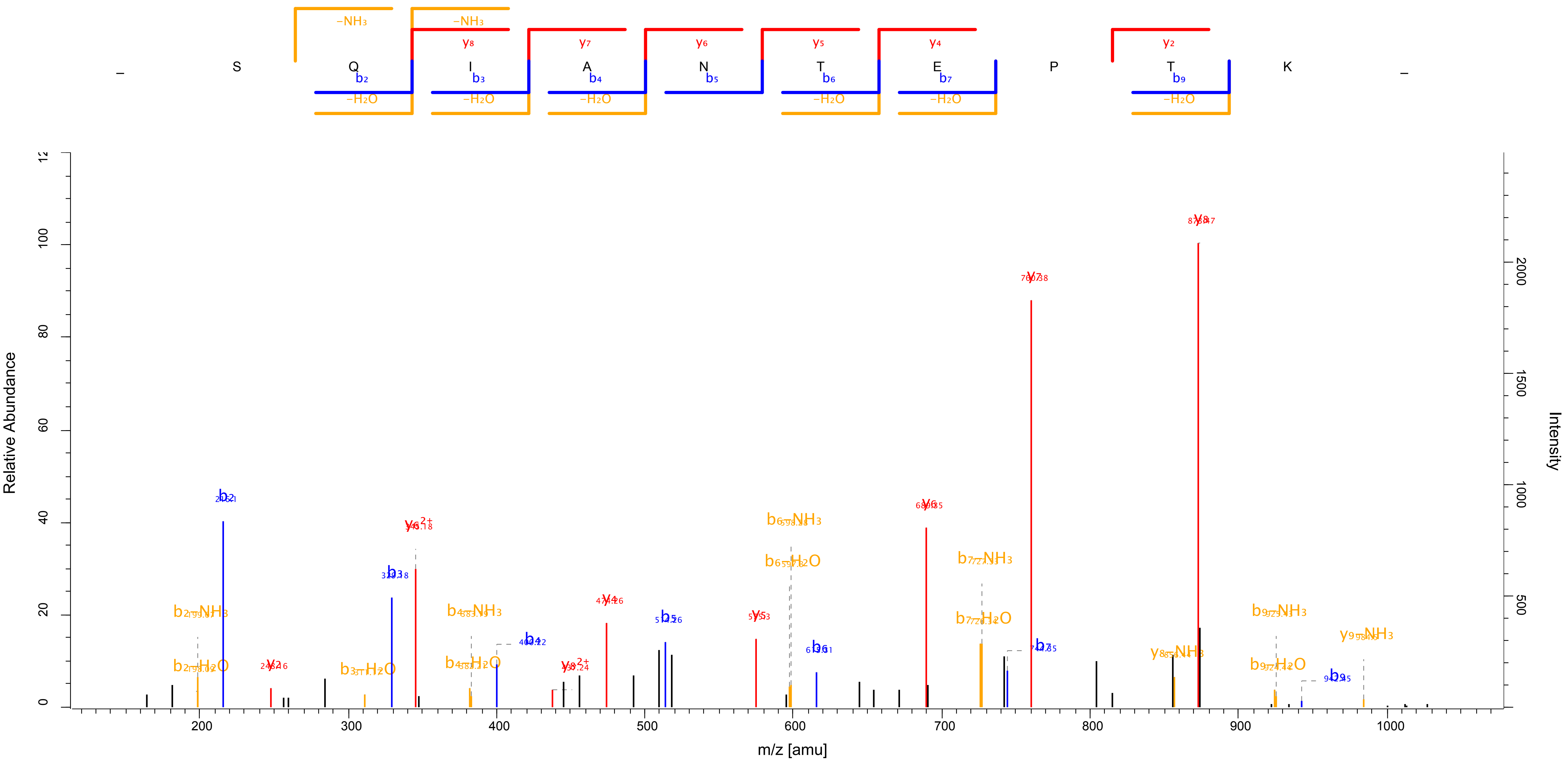
Mass:	1417.69115
m/z:	709.85285
Charge:	2+
Retentiontime:	97.0224609375
Score:	176.7758
Mass Error [ppm]:	−0.0015762
PEP:	6.8521E−08
Precursor Type:	ISO

general information

Annotation:	10 of 13
AminoAcids Coverage:	77 %
Intensity Coverage:	79 %
Peak Coverage:	38 %
Protein Localisation:	54 ... 66

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019	1	G	12				
	155.081504042	2	P	11	1361.676964131		1361.676964131	
+0.0294396	286.121988648	3	M	10	1264.624200279	−0.1611876	632.815738373	−0.3165929
+0.1575589	433.190402565	4	F	9	1133.583715673	−0.0959227	1133.583715673	
+0.1386474	562.232995661	5	E	8	986.515301757	−0.0292178	986.515301757	
−0.0574161	675.317059641	6	I	7	857.47270866	−0.0717077	857.47270866	
−0.0415655	788.401123622	7	I	6	744.38864468	+0.1039701	744.38864468	
−0.022552	885.453887474	8	P	5	631.3045807	+0.0240936	631.3045807	
+0.0204374	942.475351197	9	G	4	534.251816848	+0.004836	534.251816848	
−0.0804443	1071.517944293	10	E	3	477.230353124		477.230353124	
−0.1102754	1158.549972703	11	S	2	348.187760028	−0.0564124	348.187760028	
−0.113408	1272.59290015	12	N	1	261.155731618		261.155731618	
		13	K	0	147.112804171		147.112804171	

Scan number	3063	Raw file	20091015_Orbi6_MaHe_SA_ADH_exp3_Susp_Gel01_091017141217
Method	ITMS; CID	Genenames	HILPDA



precursor information

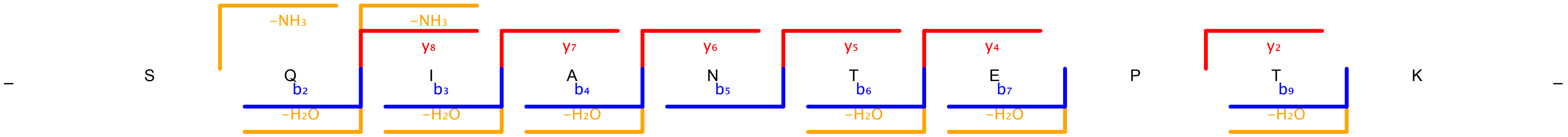
Mass:	1087.55121
m/z:	544.78288
Charge:	2+
Retentiontime:	29.8008804321289
Score:	225.6719
Mass Error [ppm]:	0.23858
PEP:	5.8482E-31
Precursor Type:	MULTI

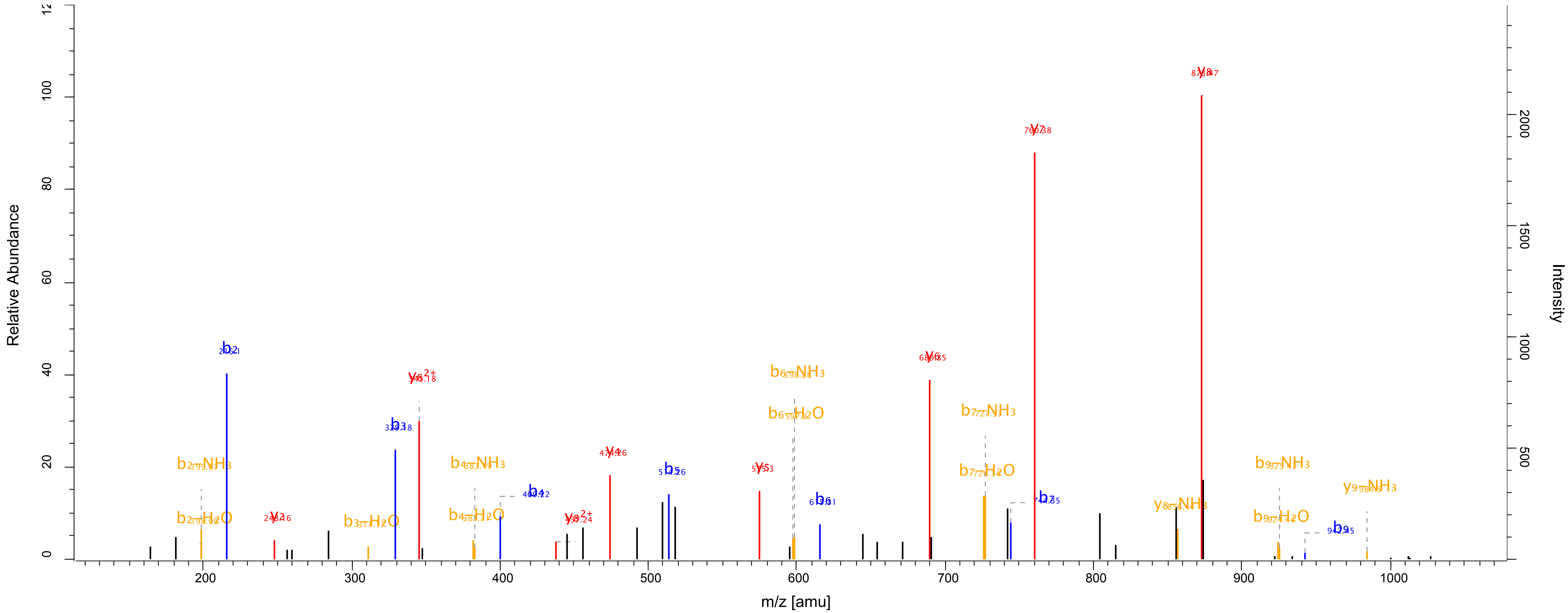
information

Annotation:	8 of 10
AminoAcids Coverage:	80 %
Intensity Coverage:	77 %
Peak Coverage:	51 %
Protein Localisation:	44 ... 53

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876	1	S	9				
+0.0620145	216.097882388	2	Q	8	1001.526200794		1001.526200794	
−0.0307623	329.181946368	3	I	7	873.467623282	−0.0880456	437.237449875	+0.0682142
−0.0504811	400.219060156	4	A	6	760.383559302	−0.0520163	760.383559302	
−0.2666263	514.261987603	5	N	5	689.346445514	−0.0066018	345.17686099	−0.0005304
+0.0401874	615.309666077	6	T	4	575.303518067	+0.0306494	575.303518067	
−0.0160775	744.352259174	7	E	3	474.255839593	+0.0686843	474.255839593	
	841.405023026	8	P	2	345.213246497		345.213246497	
+0.1052209	942.4527015	9	T	1	248.160482645	−0.0383818	248.160482645	
		10	K	0	147.112804171		147.112804171	

Scan number	3063	Raw file	20091015_Orbi6_MaHe_SA_ADH_exp3_Susp_Gel01_091017141217
Method	ITMS; CID	Genenames	HILPDA





precursor information

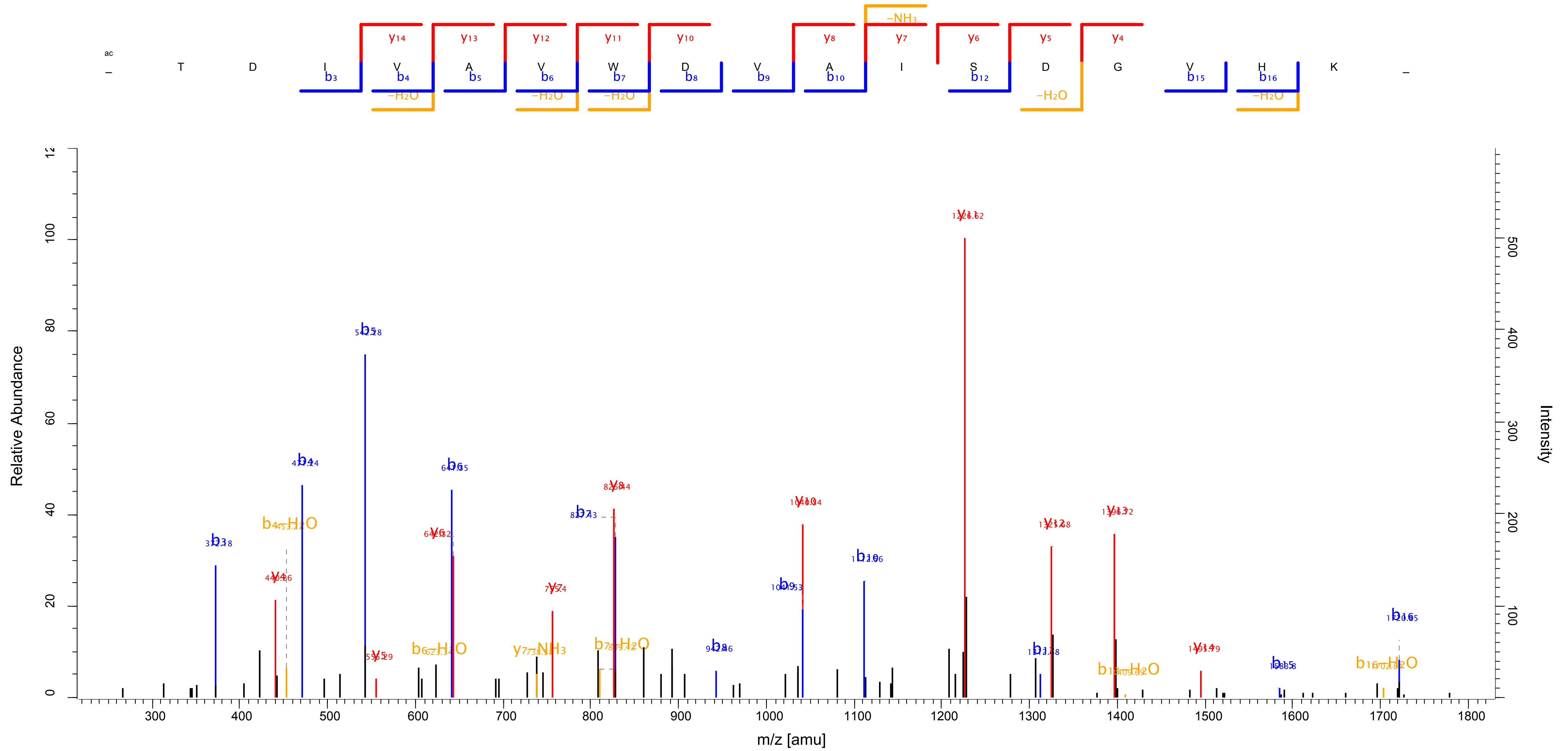
Mass:	1087.55121
m/z:	544.78288
Charge:	2+
Retentiontime:	29.8008804321289
Score:	225.6719
Mass Error [ppm]:	0.23858
PEP:	5.8482E−31
Precursor Type:	MULTI

ge information

Annotation:	8 of 10
AminoAcids Coverage:	80 %
Intensity Coverage:	77 %
Peak Coverage:	51 %
Protein Localisation:	44 ... 53

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876	1	S	9				
+0.0620145	216.097882388	2	Q	8	1001.526200794		1001.526200794	
−0.0307623	329.181946368	3	I	7	873.467623282	−0.0880456	437.237449875	+0.0682142
−0.0504811	400.219060156	4	A	6	760.383559302	−0.0520163	760.383559302	
−0.2666263	514.261987603	5	N	5	689.346445514	−0.0066018	345.17686099	−0.0005304
+0.0401874	615.309666077	6	T	4	575.303518067	+0.0306494	575.303518067	
−0.0160775	744.352259174	7	E	3	474.255839593	+0.0686843	474.255839593	
	841.405023026	8	P	2	345.213246497		345.213246497	
+0.1052209	942.4527015	9	T	1	248.160482645	−0.0383818	248.160482645	
		10	K	0	147.112804171		147.112804171	

Scan number	18233	Raw file	20091015_Orbi6_MaHe_SA_ADH_exp3_Susp_Gel03_091017190504
Method	ITMS; CID	Genenames	FAIM



precursor information

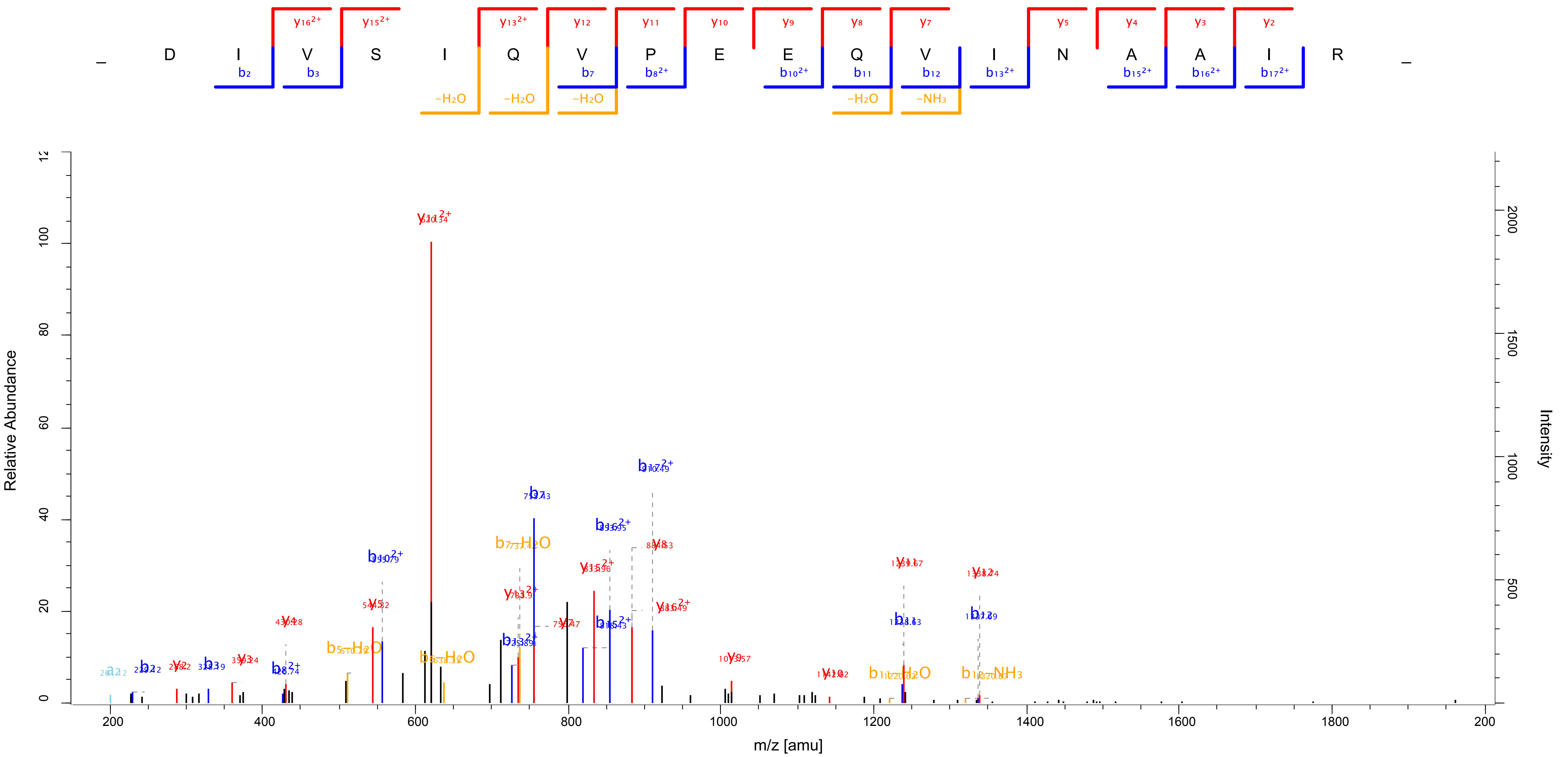
Mass:	0
m/z:	933.98336
Charge:	0+
Retentiontime:	118.851066589355
Score:	148.701
Mass Error [ppm]:	−0.086179
PEP:	2.3722E−09
Precursor Type:	PEAK

general information

Annotation:	14 of 17
AminoAcids Coverage:	82 %
Intensity Coverage:	67 %
Peak Coverage:	30 %
Protein Localisation:	2 ... 18

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	144.065519627	1	T	16		
	259.092462659	2	D	15	1723.901361417	
−0.1727119	372.176526639	3	I	14	1608.874418385	
−0.2986515	471.244940556	4	V	13	1495.790354405	+0.1846212
−0.2448839	542.282054343	5	A	12	1396.721940489	−0.1837325
−0.3054853	641.35046826	6	V	11	1325.684826701	−0.20448
+0.0131509	827.429781213	7	W	10	1226.616412785	−0.0937077
−0.1644269	942.456724245	8	D	9	1040.537099831	−0.0255032
−0.0263589	1041.525138161	9	V	8	925.510156799	
−0.4343223	1112.562251949	10	A	7	826.441742883	−0.0263986
	1225.64631593	11	I	6	755.404629095	−0.0380519
−0.4245602	1312.678344339	12	S	5	642.320565115	−0.0167931
	1427.705287371	13	D	4	555.288536705	−0.1852652
	1484.726751095	14	G	3	440.261593673	−0.0887421
+0.1085215	1583.795165011	15	V	2	383.240129949	
−0.2849851	1720.854076874	16	H	1	284.171716033	
		17	K	0	147.112804171	

Scan number	19450	Raw file	20091015_Orbi6_MaHe_SA_ADH_exp3_Susp_Gel05_091017235825
Method	ITMS; CID	Genenames	PPP1R35



precursor information

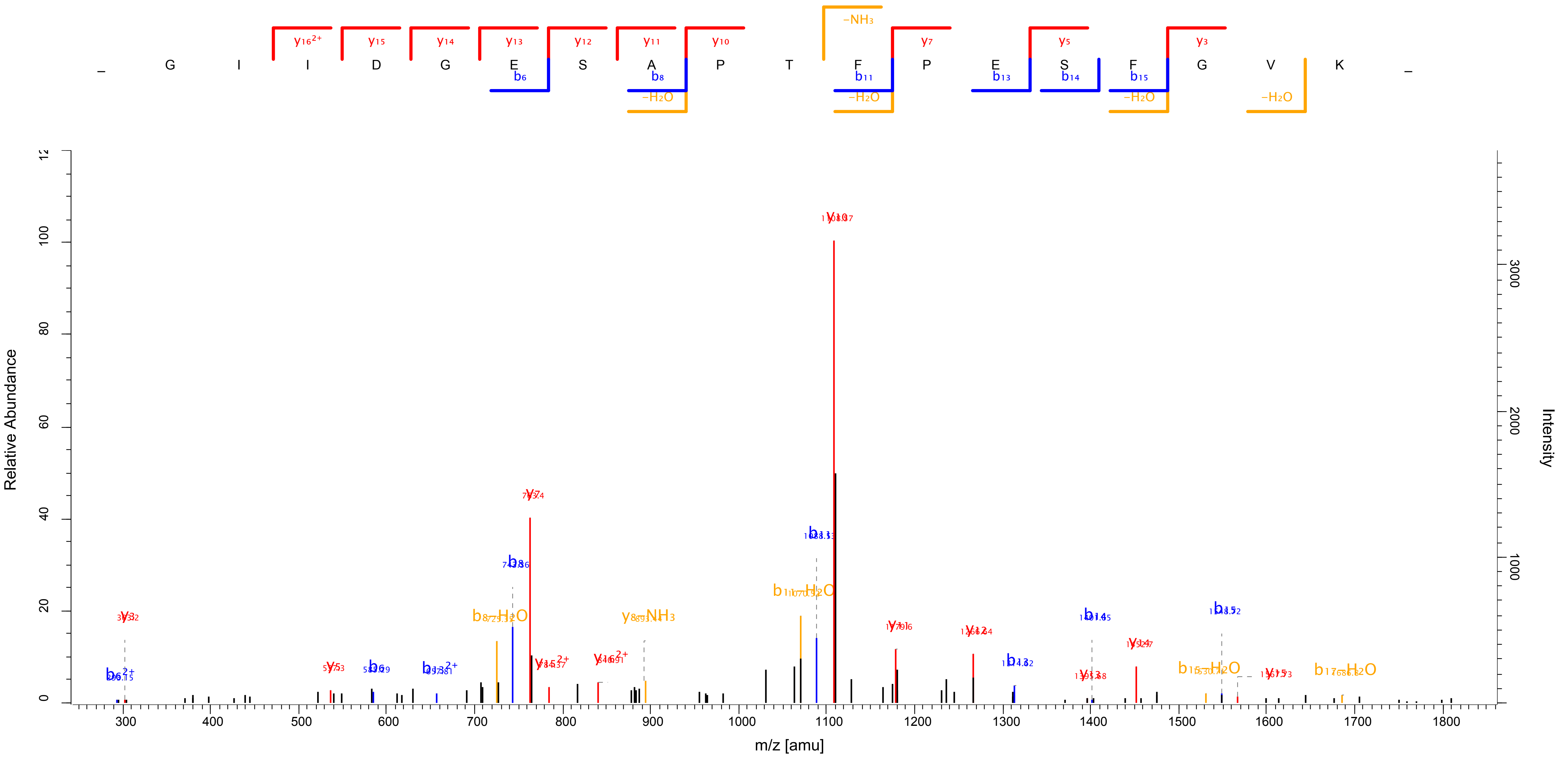
Mass:	1993.08561
m/z:	665.36915
Charge:	3+
Retentiontime:	112.845771789551
Score:	167.6136
Mass Error [ppm]:	0.60641
PEP:	1.5259E-12
Precursor Type:	ISO

general information

Annotation:	16 of 18
AminoAcids Coverage:	89 %
Intensity Coverage:	71 %
Peak Coverage:	38 %
Protein Localisation:	163 ... 180

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
	88.0393049		116.034219		116.034219	1	D	17				
+0.0104507	201.123369		229.118283	−0.0247624	229.118283	2	I	16	1879.06474		1879.06474	
	300.191783		328.186697	+0.0642792	328.186697	3	V	15	1765.98067		883.493975	−0.2927425
	387.223811		415.218726		415.218726	4	S	14	1666.91226		833.959768	−0.0508329
	500.307875		528.30279		528.30279	5	I	13	1579.88023		1579.88023	
	628.366453		656.361367		656.361367	6	Q	12	1466.79617		733.901722	−0.1013683
	727.434867		755.429781	−0.1175864	755.429781	7	V	11	1338.73759	+0.0883372	1338.73759	
	824.48763	+0.4085316	426.744911		852.482545	8	P	10	1239.66918	+0.0189337	620.338227	−0.0105288
	953.530224		981.525138		981.525138	9	E	9	1142.61641	+0.0110286	1142.61641	
	1082.57282	−0.0130898	555.787504		1110.56773	10	E	8	1013.57382	−0.1412025	1013.57382	
	1210.63139		1238.62631	−0.3044094	1238.62631	11	Q	7	884.531227	−0.4825816	884.531227	
	1309.69981		1337.69472	−0.1017051	1337.69472	12	V	6	756.472649	−0.1330495	756.472649	
	1422.78387	−0.2372698	725.893032		1450.77879	13	I	5	657.404235		657.404235	
	1536.8268		1564.82171		1564.82171	14	N	4	544.320171	+0.0016672	544.320171	
	1607.86391	+0.0860518	818.433052		1635.85883	15	A	3	430.277244	+0.0259789	430.277244	
	1678.90103	−0.0368752	853.951609		1706.89594	16	A	2	359.24013	−0.1302667	359.24013	
	1791.98509	+0.0979117	910.493641		1819.98001	17	I	1	288.203016	−0.0667857	288.203016	
						18	R	0	175.118952		175.118952	

Scan number	16101	Raw file	20091015_Orbi6_MaHe_SA_ADH_exp3_Susp_Gel06_091018022531
Method	ITMS; CID	Genenames	ADPRH



precursor information

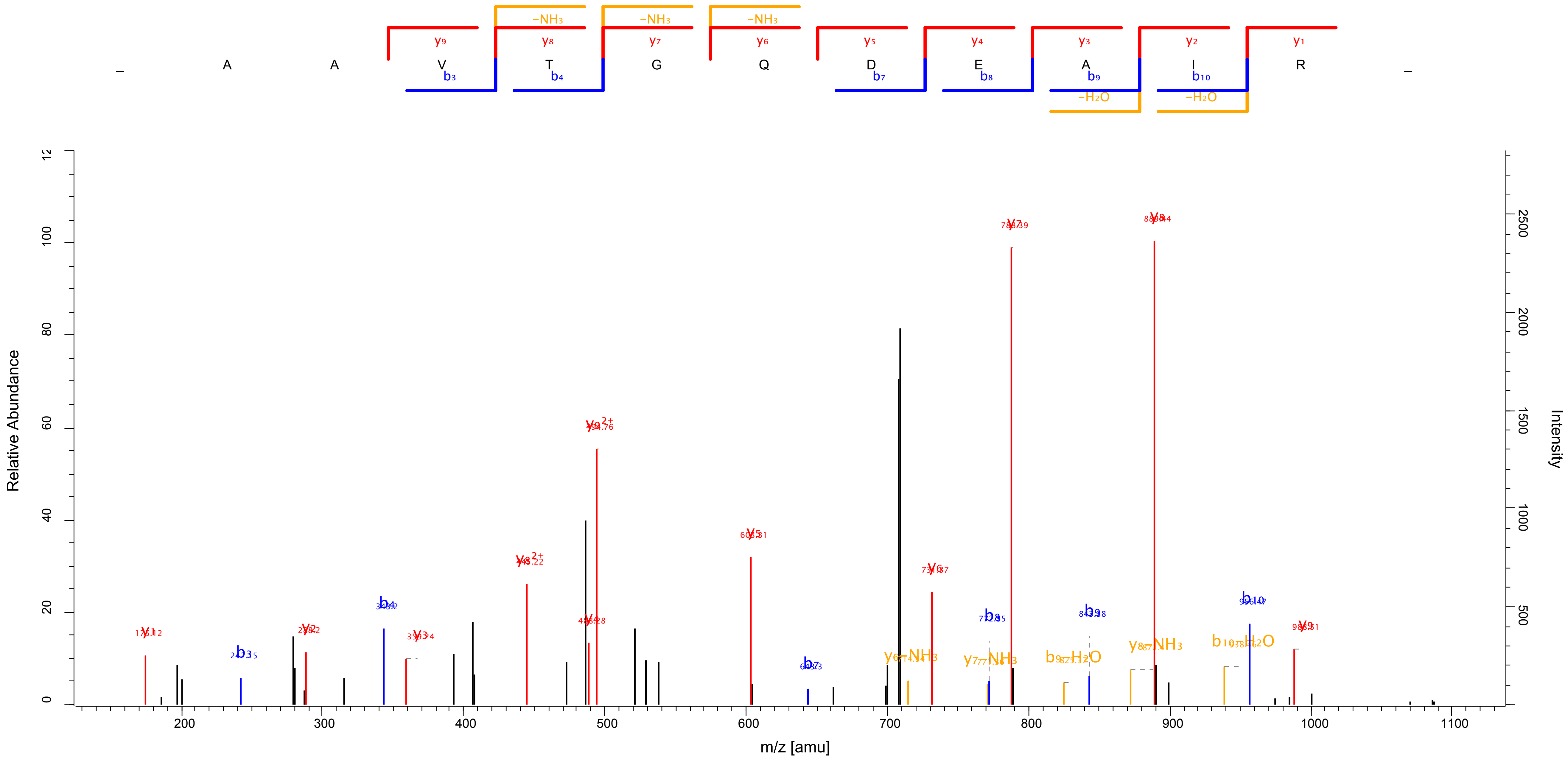
Mass:	1849.91009
m/z:	925.96232
Charge:	2+
Retentiontime:	94.7758483886719
Score:	112.964
Mass Error [ppm]:	0.15733
PEP:	2.8328E-06
Precursor Type:	MULTI

general information

Annotation:	14 of 18
AminoAcids Coverage:	78 %
Intensity Coverage:	55 %
Peak Coverage:	27 %
Protein Localisation:	235 ... 252

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019		58.02874019	1	G	17				
	171.11280417		171.11280417	2	I	16	1793.8956073		1793.8956073	
	284.19686815		284.19686815	3	I	15	1680.8115434		840.90940991	+0.328322
	399.22381118		399.22381118	4	D	14	1567.7274794	−0.1450819	784.36737792	+0.2267993
	456.24527491		456.24527491	5	G	13	1452.7005363	−0.2629143	1452.7005363	
+0.1156724	293.14757223	−0.0432391	585.287868	6	E	12	1395.6790726	−0.157222	1395.6790726	
	672.31989641		672.31989641	7	S	11	1266.6364795	−0.1009571	1266.6364795	
	743.3570102	−0.1169589	743.3570102	8	A	10	1179.6044511	−0.1990556	1179.6044511	
	840.40977405		840.40977405	9	P	9	1108.5673373	−0.0723422	1108.5673373	
	941.45745253		941.45745253	10	T	8	1011.5145735		1011.5145735	
	1088.5258664	−0.1082639	1088.5258664	11	F	7	910.466895		910.466895	
	1185.5786303		1185.5786303	12	P	6	763.39848108	−0.1196115	763.39848108	
−0.4772748	657.81424993	−0.347908	1314.6212234	13	E	5	666.34571723		666.34571723	
	1401.6532518	−0.4793016	1401.6532518	14	S	4	537.30312414	−0.0362174	537.30312414	
	1548.7216657	+0.0271136	1548.7216657	15	F	3	450.27109573		450.27109573	
	1605.7431294		1605.7431294	16	G	2	303.20268181	+0.1865089	303.20268181	
	1704.8115434		1704.8115434	17	V	1	246.18121809		246.18121809	
				18	K	0	147.11280417		147.11280417	

Scan number	3162	Raw file	20091015_Orbi6_MaHe_SA_ADH_exp3_Susp_Gel06_091018022531
Method	ITMS; CID	Genenames	ANKRD16



precursor information

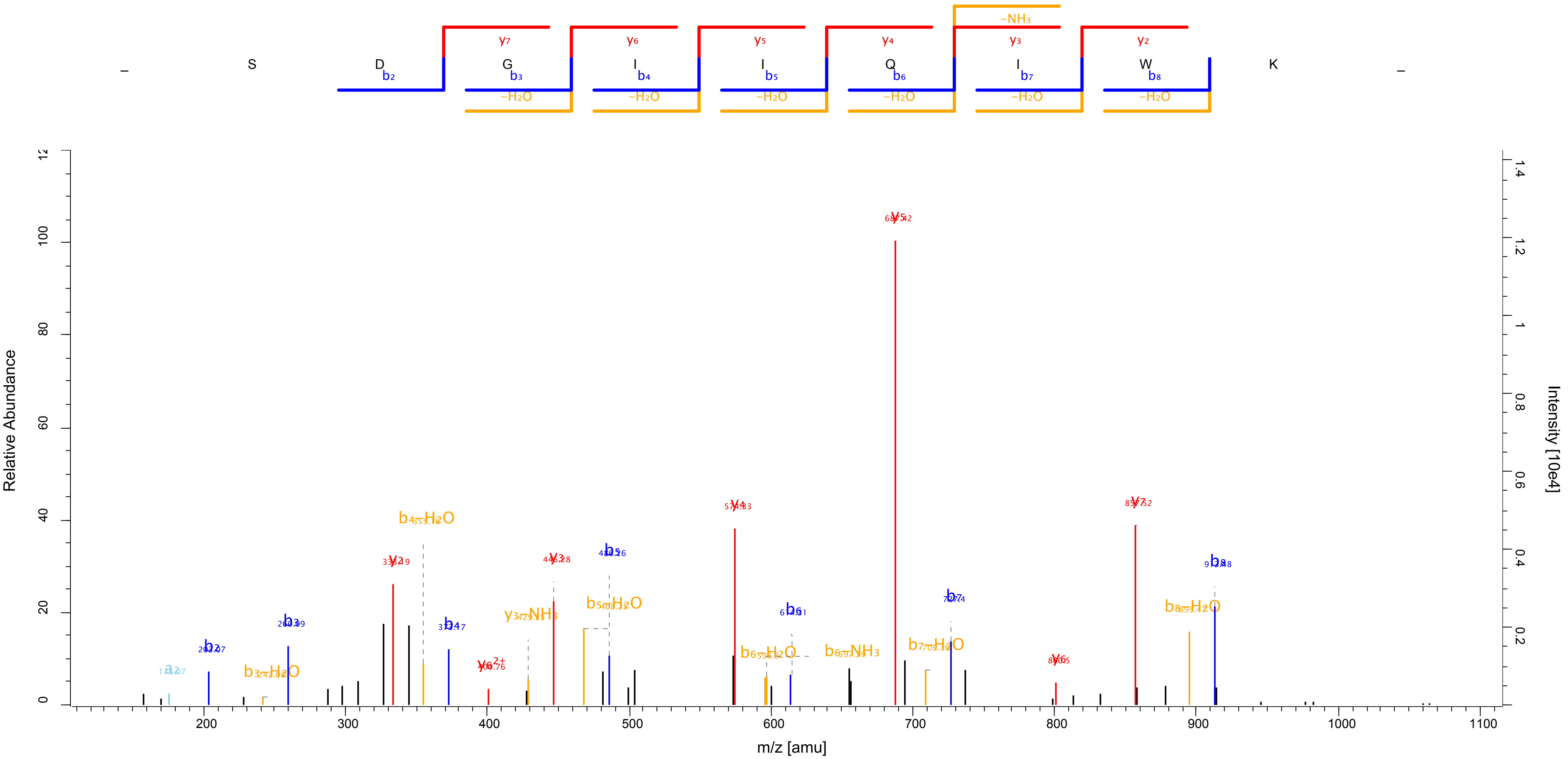
Mass:	1129.57286
m/z:	565.7937
Charge:	2+
Retentiontime:	25.484655380249
Score:	157.3782
Mass Error [ppm]:	0.093576
PEP:	7.1053E-05
Precursor Type:	ISO

general information

Annotation:	9 of 11
AminoAcids Coverage:	82 %
Intensity Coverage:	56 %
Peak Coverage:	42 %
Protein Localisation:	246 ... 256

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	10				
	143.081504042	2	A	9	1059.54291349		1059.54291349	
+0.0554043	242.149917958	3	V	8	988.505799703	−0.0749525	494.756538085	−0.0363232
+0.0617419	343.197596432	4	T	7	889.437385786	−0.0717242	445.222331127	+0.0058183
	400.219060156	5	G	6	788.389707312	−0.0218484	788.389707312	
	528.277637668	6	Q	5	731.368243589	+0.0061461	731.368243589	
+0.3595428	643.3045807	7	D	4	603.309666077	−0.0321392	603.309666077	
−0.0303403	772.347173796	8	E	3	488.282723045	+0.0980753	488.282723045	
+0.0223897	843.384287584	9	A	2	359.240129949	+0.0204291	359.240129949	
−0.1671431	956.468351564	10	I	1	288.203016161	+0.0748464	288.203016161	
		11	R	0	175.118952181	+0.0356346	175.118952181	

Scan number	13959	Raw file	20091015_Orbi6_MaHe_SA_ADH_exp3_Susp_Gel07_091018045243
Method	ITMS; CID	Genenames	PHLDA1

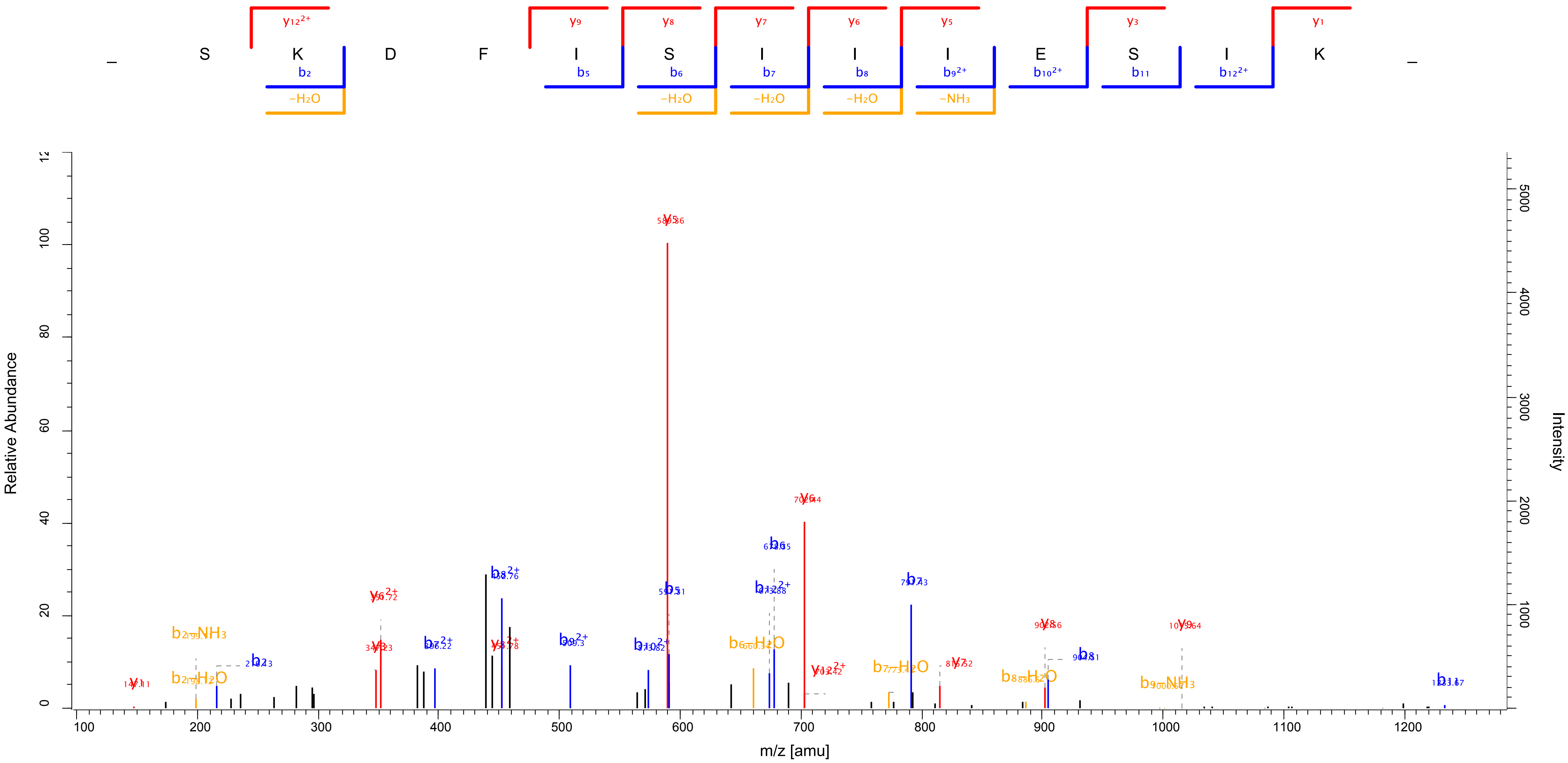


precursor information

Mass:	1058.57609
m/z:	530.29532
Charge:	2+
Retentiontime:	83.4236755371094
Score:	200.5383
Mass Error [ppm]:	0.044647
PEP:	3.7824E-06
Annotation:	7 of 9
AminoAcids Coverage:	78 %
Intensity Coverage:	73 %
Peak Coverage:	43 %
Protein Localisation:	160 ... 168

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	60.044390254		88.039304876	1	S	8				
+0.0288864	175.07133329	-0.0337772	203.06624791	2	D	7	972.55129333		972.55129333	
	232.09279701	-0.0250896	260.08771163	3	G	6	857.5243503	-0.1155979	857.5243503	
	345.17686099	-0.0438459	373.17177561	4	I	5	800.50288658	-0.0075863	400.75508152	-0.0217441
	458.26092497	-0.2706711	486.25583959	5	I	4	687.4188226	-0.1066278	687.4188226	
	586.31950248	-0.154566	614.3144171	6	Q	3	574.33475862	+0.0923044	574.33475862	
	699.40356646	-0.1055734	727.39848108	7	I	2	446.2761811	+0.0075103	446.2761811	
	885.48287942	-0.1469835	913.47779404	8	W	1	333.19211712	+0.0581881	333.19211712	
				9	K	0	147.11280417		147.11280417	

Scan number	19878	Raw file	20091015_Orbi6_MaHe_SA_ADH_exp3_Susp_Gel07_091018045243
Method	ITMS; CID	Genenames	TMEM39A



precursor information

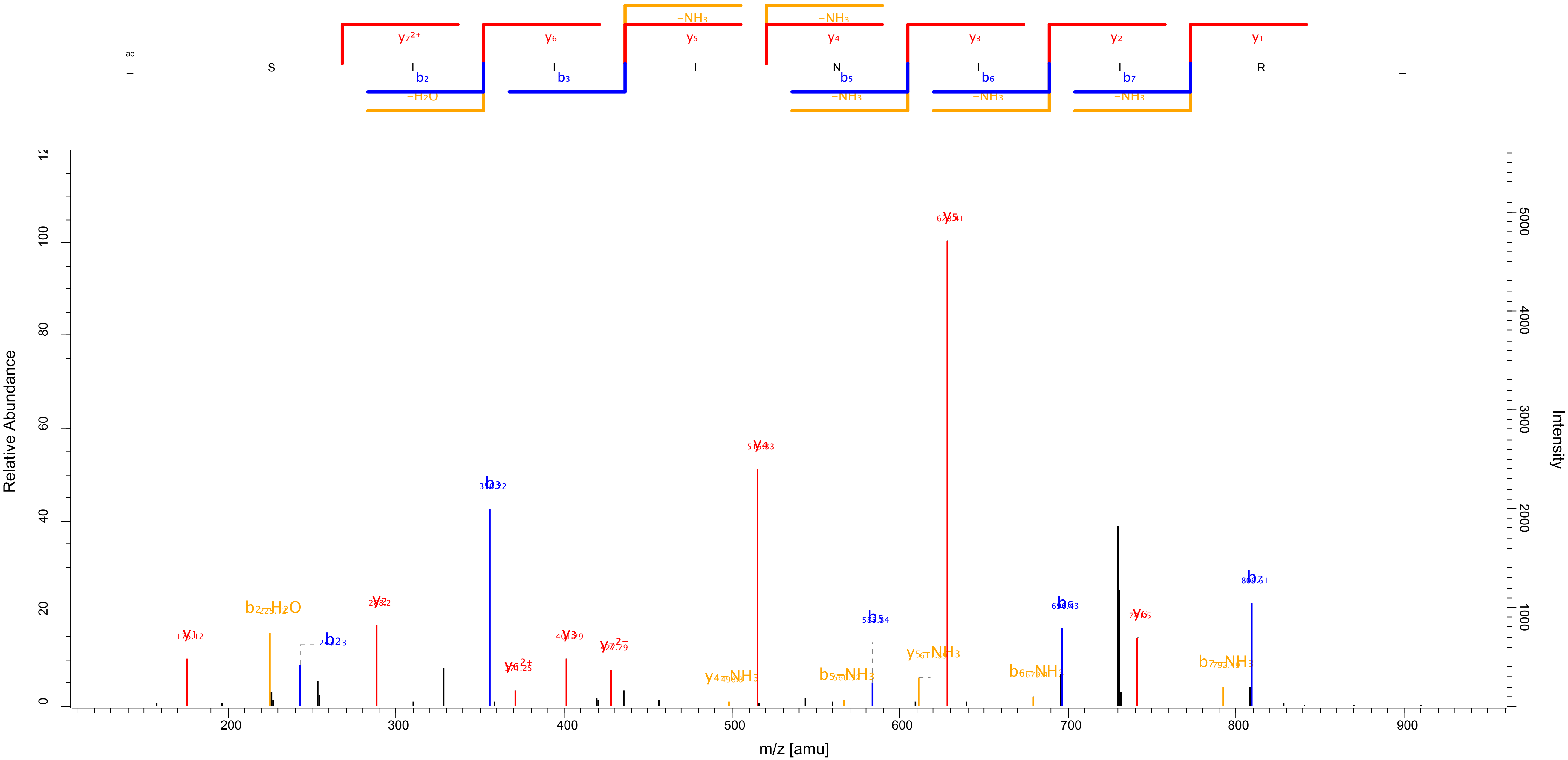
Mass:	1491.85448
m/z:	498.2921
Charge:	3+
Retentiontime:	118.756637573242
Score:	164.8112
Mass Error [ppm]:	−0.24453
PEP:	5.3349E−06
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverage:	77 %
Intensity Coverage:	71 %
Peak Coverage:	43 %
Protein Localisation:	237 ... 249

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876		88.039304876	1	S	12				
	216.13426789	+0.0194797	216.13426789	2	K	11	1405.830094		703.41868521	+0.0048377
	331.16121093		331.16121093	3	D	10	1277.7351309		1277.7351309	
	478.22962484		478.22962484	4	F	9	1162.7081879		1162.7081879	
	591.31368882	+0.021089	591.31368882	5	I	8	1015.639774	+0.1123622	1015.639774	
	678.34571723	−0.1214741	678.34571723	6	S	7	902.55571001	−0.1004488	451.78149324	+0.0834665
−0.0555955	396.21852884	−0.1357138	791.42978121	7	I	6	815.5236816	−0.0845336	815.5236816	
+0.0180647	452.76056083	−0.0552881	904.51384519	8	I	5	702.43961762	−0.0228085	351.72344704	+0.0593899
+0.1106762	509.30259282		1017.5979092	9	I	4	589.35555364	−0.0815058	589.35555364	
−0.017615	573.82388937		1146.6405023	10	E	3	476.27148966		476.27148966	
	1233.6725307	−0.1971889	1233.6725307	11	S	2	347.22889656	+0.0500341	347.22889656	
−0.0821309	673.88193556		1346.7565947	12	I	1	260.19686815		260.19686815	
				13	K	0	147.11280417	+0.0621073	147.11280417	

Scan number	20280	Raw file	20091015_Orbi6_MaHe_SA_ADH_exp3_Susp_Gel08_091018071949
Method	ITMS; CID	Genenames	FAM54A

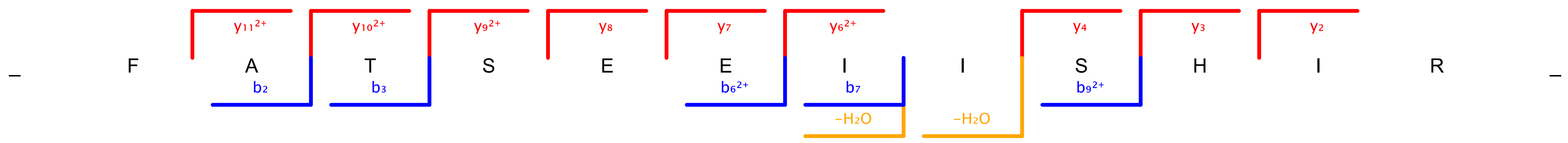


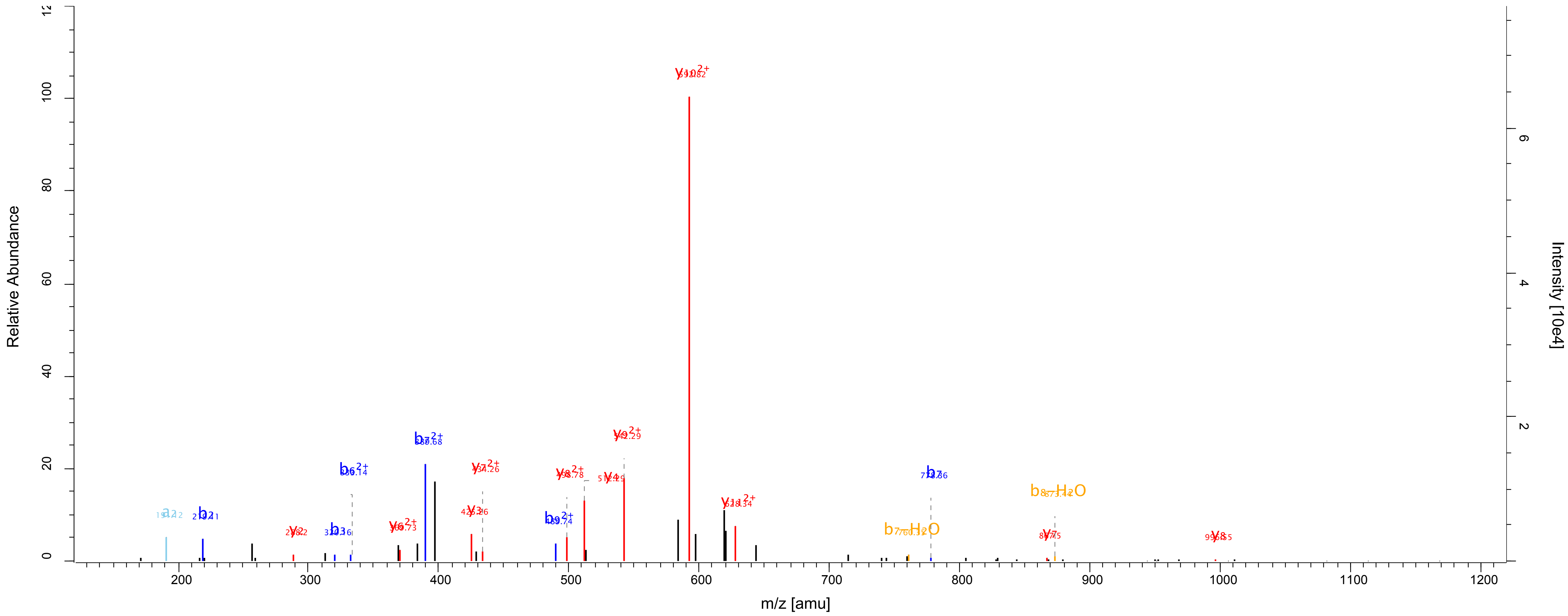
precursor information

Mass:	982.61731
m/z:	492.31593
Charge:	2+
Retentiontime:	119.180068969727
Score:	182.3865
Mass Error [ppm]:	−0.20946
PEP:	6.1928E-05
Annotation:	7 of 8
AminoAcids Coverage:	88 %
Intensity Coverage:	75 %
Peak Coverage:	41 %
Protein Localisation:	2 ... 9

b ion						y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.049869563	1	S	7				
−0.0814738	243.133933543	2	I	6	854.58219953		427.794737998	−0.0813591
−0.2437849	356.217997524	3	I	5	741.49813555	−0.1216707	371.252706008	−0.0262656
	469.302061504	4	I	4	628.414071569	−0.0318084	628.414071569	
−0.2899963	583.344988951	5	N	3	515.330007589	−0.0716458	515.330007589	
−0.0171877	696.429052932	6	I	2	401.287080142	−0.0130323	401.287080142	
−0.1185857	809.513116912	7	I	1	288.203016161	−0.0814036	288.203016161	
		8	R	0	175.118952181	+0.0487419	175.118952181	

Scan number	10756	Raw file	20091015_Orbi6_MaHe_SA_ADH_exp3_Susp_Gel10
Method	ITMS; CID	Genenames	ZNF503;ZNF703





precursor information

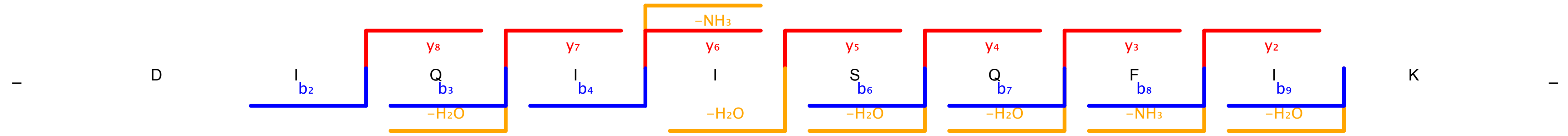
Mass:	1401.72604
m/z:	468.24929
Charge:	3+
Retentiontime:	64.6233596801758
Score:	137.9533
Mass Error [ppm]:	0.5757
PEP:	0.00021475
Precursor Type:	ISO

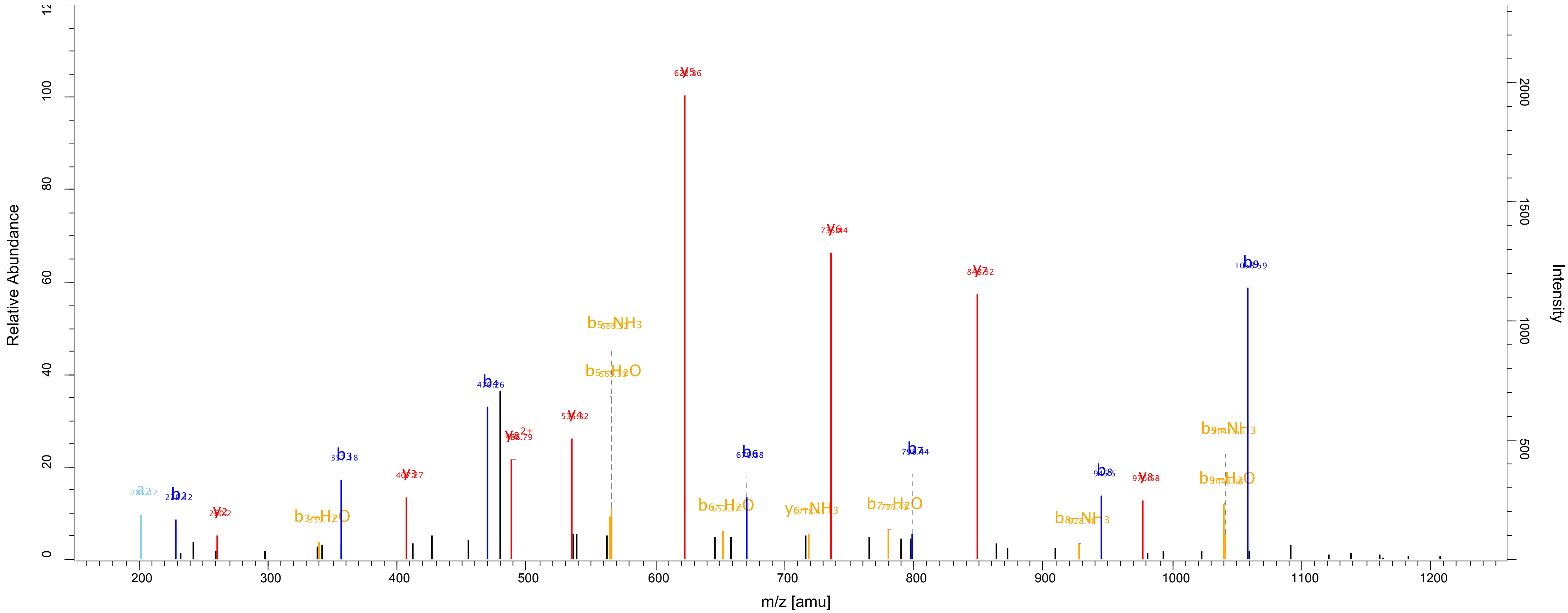
general information

Annotation:	10 of 12
AminoAcids Coverage:	83 %
Intensity Coverage:	71 %
Peak Coverage:	36 %
Protein Localisation:	529 ... 540

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.080776		148.07569		148.07569	1	F	11				
+0.018402	191.11789		219.112804	−0.1151082	219.112804	2	A	10	1255.66409		628.335684	+0.006052
	292.165568		320.160483	−0.0319731	320.160483	3	T	9	1184.62698		592.817127	+0.1513179
	379.197596		407.192511		407.192511	4	S	8	1083.5793		542.293288	+0.1138778
	508.24019		536.235104		536.235104	5	E	7	996.547271	−0.1505421	498.777274	−0.1055511
	637.282783	−0.1421512	333.142487		665.277697	6	E	6	867.504677	+0.0314553	434.255977	−0.1496843
	750.366847	−0.0921116	389.684519	+0.091791	778.361761	7	I	5	738.462084		369.73468	+0.2460325
	863.450911		891.445825		891.445825	8	I	4	625.37802		625.37802	
	950.482939	+0.1025582	489.742565		978.477854	9	S	3	512.293956	−0.0517079	512.293956	
	1087.54185		1115.53677		1115.53677	10	H	2	425.261928	+0.0590864	425.261928	
	1200.62591		1228.62083		1228.62083	11	I	1	288.203016	−0.0445079	288.203016	
						12	R	0	175.118952		175.118952	

Scan number	19805	Raw file	20091015_Orbi6_MaHe_SA_ADH_exp3_Susp_Gel11
Method	ITMS; CID	Genenames	GPR56





precursor information

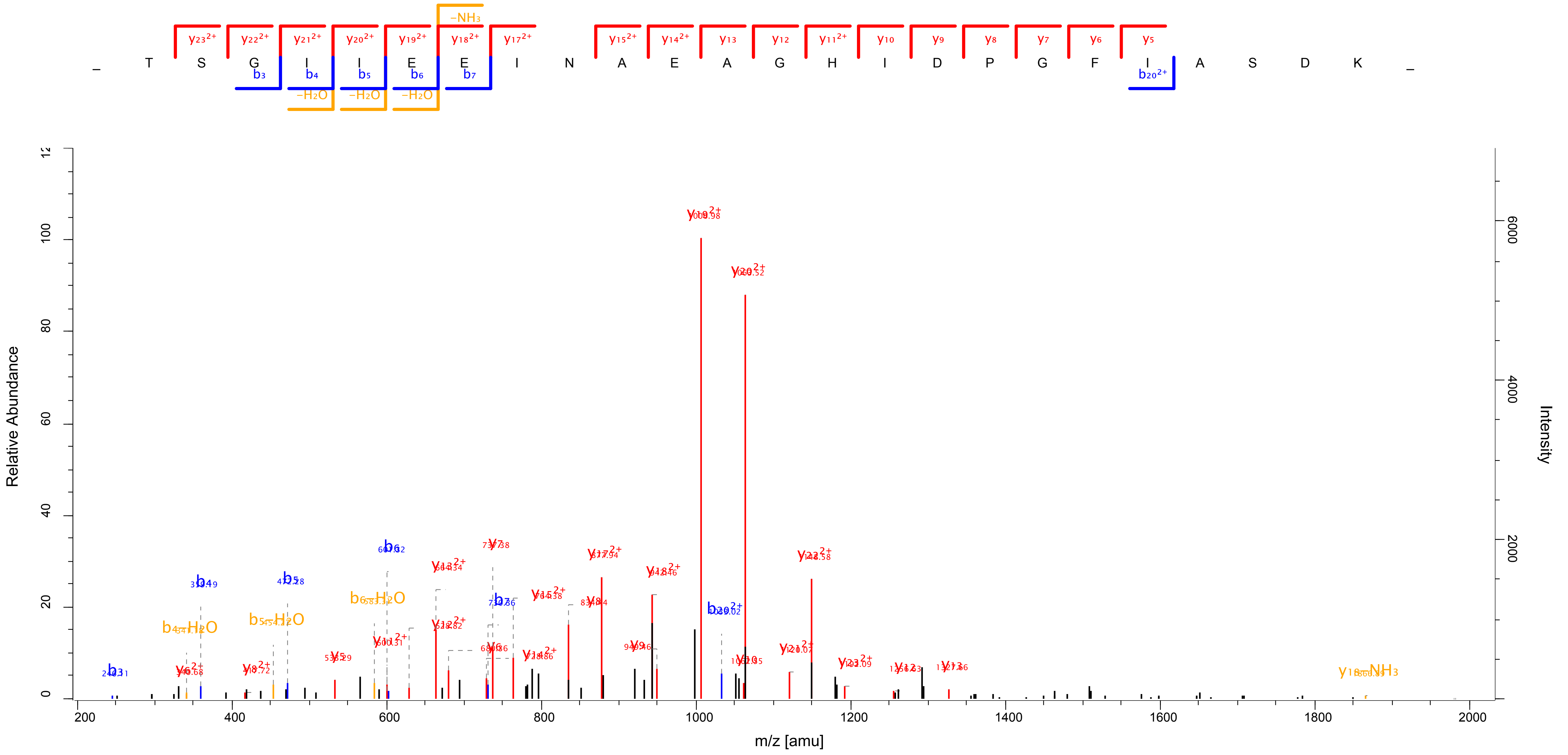
Mass:	1203.68718
m/z:	602.85087
Charge:	2+
Retentiontime:	112.248138427734
Score:	209.0951
Mass Error [ppm]:	0.71239
PEP:	2.1583E-16
Precursor Type:	MULTI

general information

Annotation:	8 of 10
AminoAcids Coverage:	80 %
Intensity Coverage:	80 %
Peak Coverage:	42 %
Protein Localisation:	182 ... 191

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876		116.0342195	1	D	9				
−0.0010849	201.12336886	−0.0028813	229.11828348	2	I	8	1089.6666574		1089.6666574	
	329.18194637	−0.0318415	357.17686099	3	Q	7	976.58259346	−0.047132	488.79493496	−0.0005624
	442.26601035	−0.0183713	470.26092497	4	I	6	848.52401595	−0.0867601	848.52401595	
	555.35007433		583.34498895	5	I	5	735.43995197	−0.0162459	735.43995197	
	642.38210274	−0.0498079	670.37701736	6	S	4	622.35588799	−0.0794598	622.35588799	
	770.44068025	+0.0396859	798.43559487	7	Q	3	535.32385958	−0.1795114	535.32385958	
	917.50909417	−0.0962329	945.50400879	8	F	2	407.26528207	+0.0669933	407.26528207	
	1030.5931581	−0.2056265	1058.5880728	9	I	1	260.19686815	+0.0849312	260.19686815	
				10	K	0	147.11280417		147.11280417	

Scan number	19147	Raw file	20091015_Orbi6_MaHe_SA_ADH_exp3_Susp_Gel12
Method	ITMS; CID	Genenames	C18orf25



precursor information

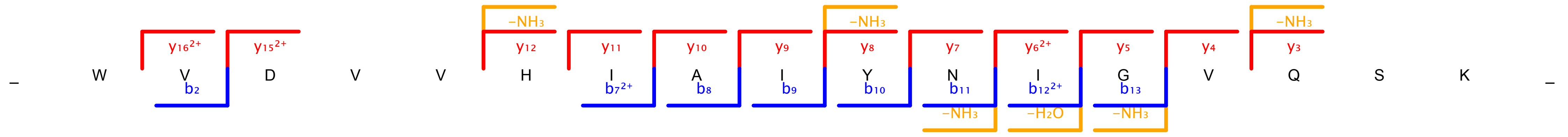
Mass:	2483.21843
m/z:	828.74675
Charge:	3+
Retentiontime:	108.934280395508
Score:	145.4257
Mass Error [ppm]:	0.17407
PEP:	2.3056E-17
Precursor Type:	ISO

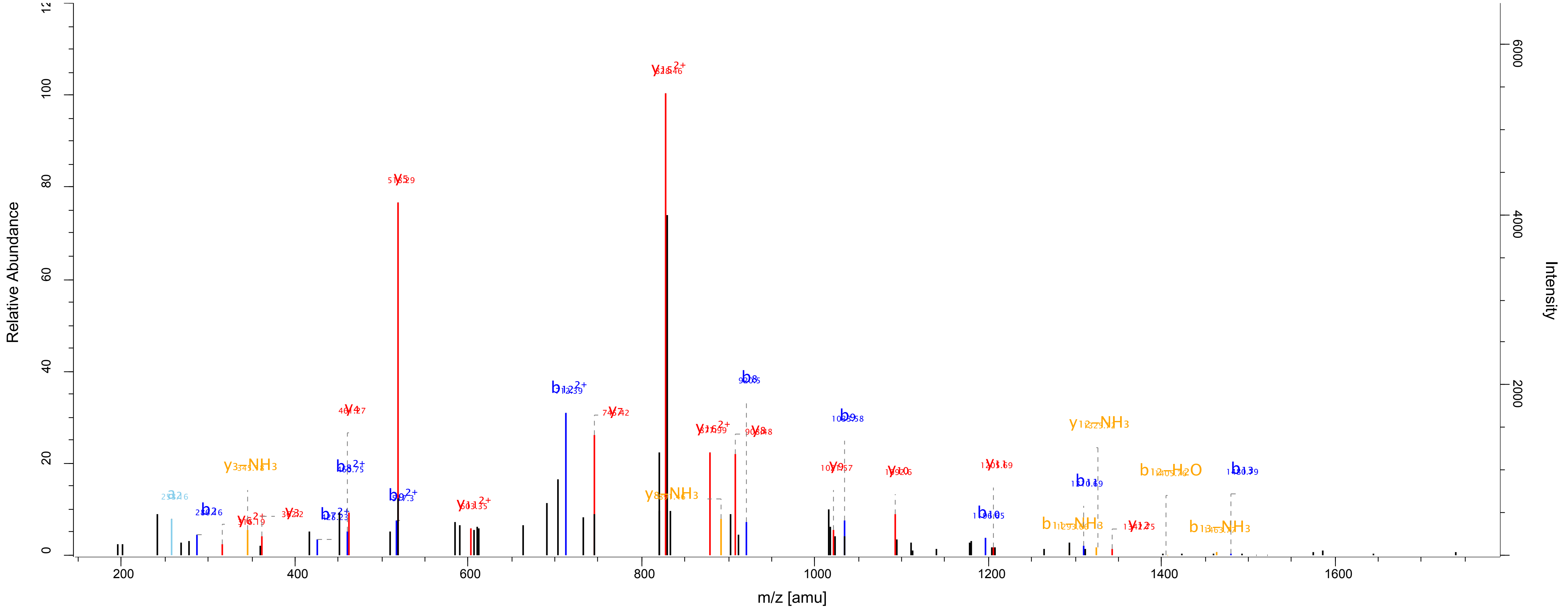
general information

Annotation:	18 of 24
AminoAcids Coverage:	75 %
Intensity Coverage:	68 %
Peak Coverage:	33 %
Protein Localisation:	288 ... 311

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05495494		102.05495494	1	T	23				
	189.08698335		189.08698335	2	S	22	2383.1775959		1192.0924362	+0.1818558
	246.10844707	+0.1410952	246.10844707	3	G	21	2296.1455674		1148.576422	+0.2241152
	359.19251105	-0.0786805	359.19251105	4	I	20	2239.1241037		1120.0656901	+0.3558187
	472.27657503	+0.0262204	472.27657503	5	I	19	2126.0400397		1063.5236581	+0.2466056
	601.31916813	+0.1365814	601.31916813	6	E	18	2012.9559758		1006.9816261	+0.2595848
	730.36176123	-0.1453306	730.36176123	7	E	17	1883.9133827		942.46032957	-0.0199609
	843.44582521		843.44582521	8	I	16	1754.8707896		877.93903302	+0.1598439
	957.48875265		957.48875265	9	N	15	1641.7867256		1641.7867256	
	1028.5258664		1028.5258664	10	A	14	1527.7437981		764.3755373	+0.1906858
	1157.5684595		1157.5684595	11	E	13	1456.7066844		728.85698041	+0.1820821
	1228.6055733		1228.6055733	12	A	12	1327.6640913	-0.0176069	664.33568386	+0.1930637
	1285.6270371		1285.6270371	13	G	11	1256.6269775	-0.3290038	628.81712697	+0.0586665
	1422.6859489		1422.6859489	14	H	10	1199.6055137		600.30639511	+0.4569106
	1535.7700129		1535.7700129	15	I	9	1062.5466019	-0.1910111	1062.5466019	
	1650.7969559		1650.7969559	16	D	8	949.4625379	+0.0032214	949.4625379	
	1747.8497198		1747.8497198	17	P	7	834.43559487	-0.012194	417.72143567	-0.0802614
	1804.8711835		1804.8711835	18	G	6	737.38283102	-0.0162539	737.38283102	
	1951.9395974		1951.9395974	19	F	5	680.3613673	-0.1448146	340.68432188	-0.3655353
-0.2019924	1033.0154689		2065.0236614	20	I	4	533.29295338	-0.2595061	533.29295338	
	2136.0607752		2136.0607752	21	A	3	420.2088894		420.2088894	
	2223.0928036		2223.0928036	22	S	2	349.17177561		349.17177561	
	2338.1197466		2338.1197466	23	D	1	262.1397472		262.1397472	
				24	K	0	147.11280417		147.11280417	

Scan number	20312	Raw file	20091015_Orbi6_MaHe_SA_ADH_exp3_Susp_Gel12
Method	ITMS; CID	Genenames	PHF19



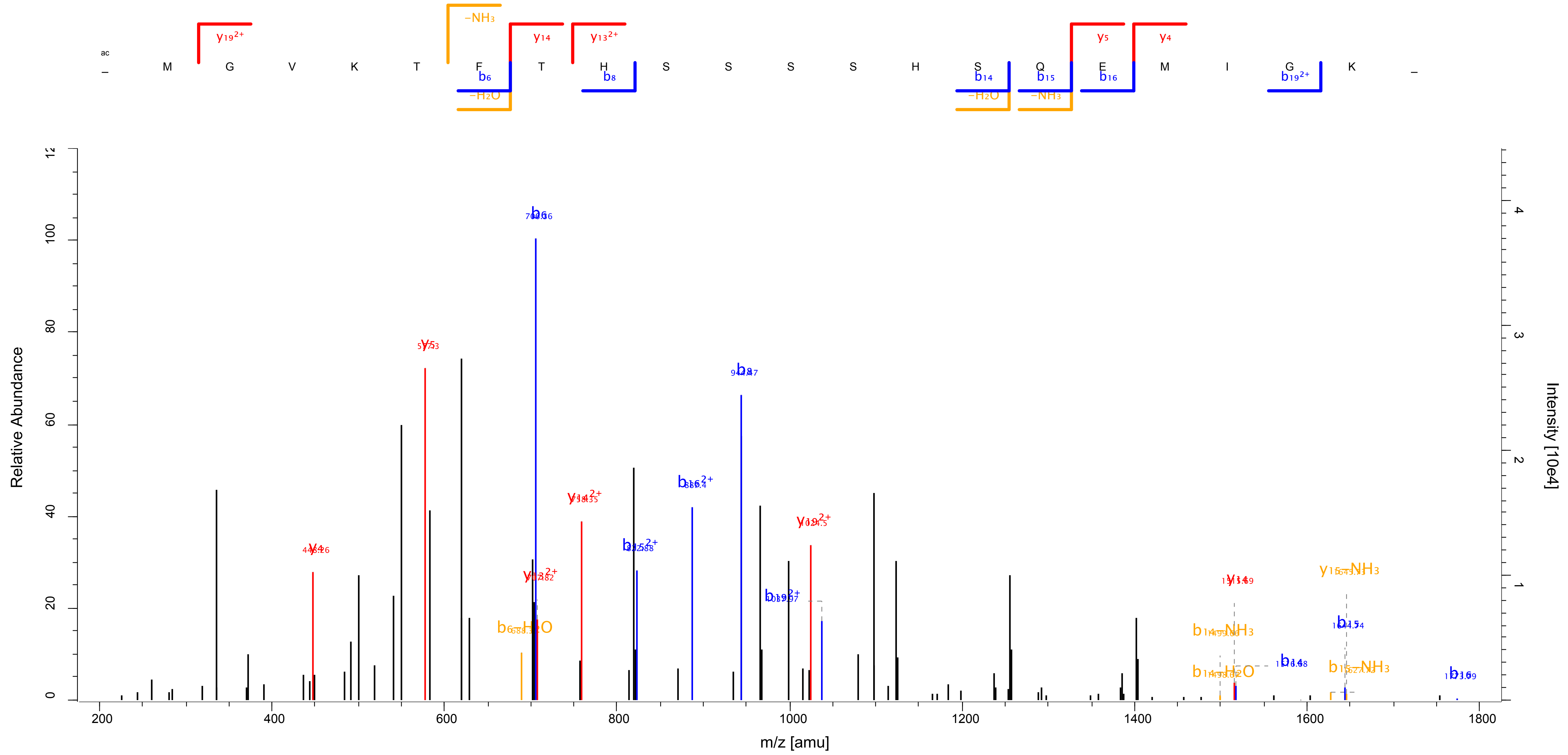


precursor information	
Mass:	1940.0519
m/z:	647.69124
Charge:	3+
Retentiontime:	115.727905273438
Score:	168.8851
Mass Error [ppm]:	−0.044324
PEP:	1.0819E−11
Precursor Type:	ISO

general information	
Annotation:	12 of 17
AminoAcids Coverage:	71 %
Intensity Coverage:	55 %
Peak Coverage:	37 %
Protein Localisation:	260 ... 276

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	159.091675		187.086589		187.086589	1	W	16				
+0.0731266	258.160089		286.155003	−0.0707748	286.155003	2	V	15	1754.97995		877.993611	+0.1973067
	373.187032		401.181946		401.181946	3	D	14	1655.91153		828.459404	−0.0408863
	472.255446		500.25036		500.25036	4	V	13	1540.88459		1540.88459	
	571.32386		599.318774		599.318774	5	V	12	1441.81618		1441.81618	
	708.382771		736.377686		736.377686	6	H	11	1342.74776	−0.0658765	1342.74776	
	821.466835	+0.0851889	425.234513		849.46175	7	I	10	1205.68885	+0.0786066	603.348063	−0.0176186
	892.503949	−0.1233704	460.75307	−0.1239249	920.498864	8	A	9	1092.60479	−0.0747562	1092.60479	
	1005.58801	+0.3320951	517.295102	−0.1649591	1033.58293	9	I	8	1021.56767	−0.3061971	1021.56767	
	1168.65134		1196.64626	−0.1014565	1196.64626	10	Y	7	908.483608	−0.0719866	908.483608	
	1282.69427		1310.68918	−0.3465324	1310.68918	11	N	6	745.420279	+0.0362028	745.420279	
	1395.77833	+0.1066251	712.390262		1423.77325	12	I	5	631.377352		316.192314	+0.0377274
	1452.7998		1480.79471	−0.1136812	1480.79471	13	G	4	518.293288	+0.0052352	518.293288	
	1551.86821		1579.86313		1579.86313	14	V	3	461.271824	+0.1156882	461.271824	
	1679.92679		1707.9217		1707.9217	15	Q	2	362.20341	−0.0509443	362.20341	
	1766.95882		1794.95373		1794.95373	16	S	1	234.144833		234.144833	
						17	K	0	147.112804		147.112804	

Scan number	20410	Raw file	20091015_Orbi6_MaHe_SA_ADH_exp3_Susp_Gel12
Method	ITMS; CID	Genenames	ZBTB44



precursor information

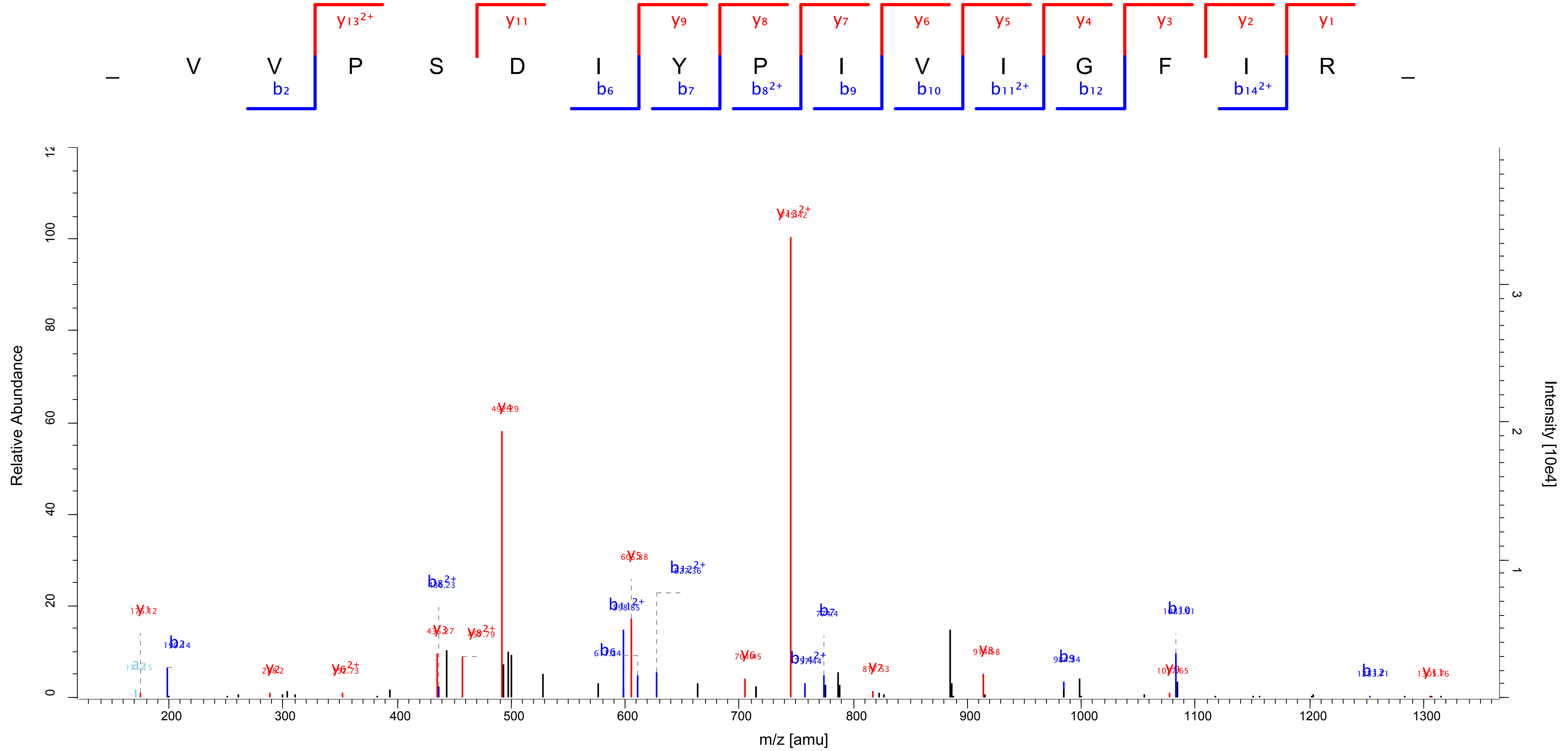
Mass:	2220.02981
m/z:	741.01721
Charge:	3+
Retentiontime:	116.258491516113
Score:	82.00659
Mass Error [ppm]:	−0.2375
PEP:	0.00025871
Precursor Type:	MULTI

general information

Annotation:	9 of 20
AminoAcids Coverage:	45 %
Intensity Coverage:	34 %
Peak Coverage:	21 %
Protein Localisation:	1 ... 20

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	174.05832576		174.05832576	1	M	19				
	231.07978948		231.07978948	2	G	18	2047.9865644		1024.4969204	−0.3217495
	330.1482034		330.1482034	3	V	17	1990.9651007		1990.9651007	
	458.24316642		458.24316642	4	K	16	1891.8966867		1891.8966867	
	559.29084489		559.29084489	5	T	15	1763.8017237		1763.8017237	
	706.35925881	−0.0584776	706.35925881	6	F	14	1662.7540453		1662.7540453	
	807.40693728		807.40693728	7	T	13	1515.6856313	−0.0779653	758.3464539	+0.0817077
	944.46584914	−0.1450484	944.46584914	8	H	12	1414.6379529		707.82261466	−0.4197216
	1031.4978776		1031.4978776	9	S	11	1277.579041		1277.579041	
	1118.529906		1118.529906	10	S	10	1190.5470126		1190.5470126	
	1205.5619344		1205.5619344	11	S	9	1103.5149842		1103.5149842	
	1292.5939628		1292.5939628	12	S	8	1016.4829558		1016.4829558	
	1429.6528746		1429.6528746	13	H	7	929.45092736		929.45092736	
	1516.6849031	+0.0185882	1516.6849031	14	S	6	792.3920155		792.3920155	
+0.1432982	822.87537852	−0.0900382	1644.7434806	15	Q	5	705.35998709		705.35998709	
+0.0603562	887.39667506	−0.2888813	1773.7860737	16	E	4	577.30140958	−0.0388974	577.30140958	
	1904.8265583		1904.8265583	17	M	3	448.25881648	−0.0639312	448.25881648	
	2017.9106222		2017.9106222	18	I	2	317.21833187		317.21833187	
−0.4655308	1037.9696812		2074.932086	19	G	1	204.13426789		204.13426789	
				20	K	0	147.11280417		147.11280417	

Scan number	20704	Raw file	20091015_Orbi6_MaHe_SA_ADH_exp3_Susp_Gel15
Method	ITMS; CID	Genenames	NOLC1



precursor information

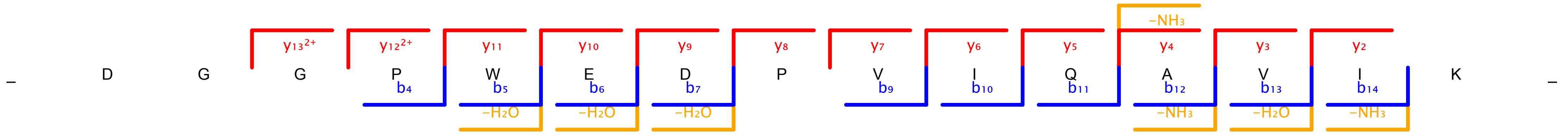
Mass:	1686.97083
m/z:	563.33089
Charge:	3+
Retentiontime:	119.667999267578
Score:	150.6929
Mass Error [ppm]:	-0.029526
PEP:	6.3664E-06
Precursor Type:	ISO

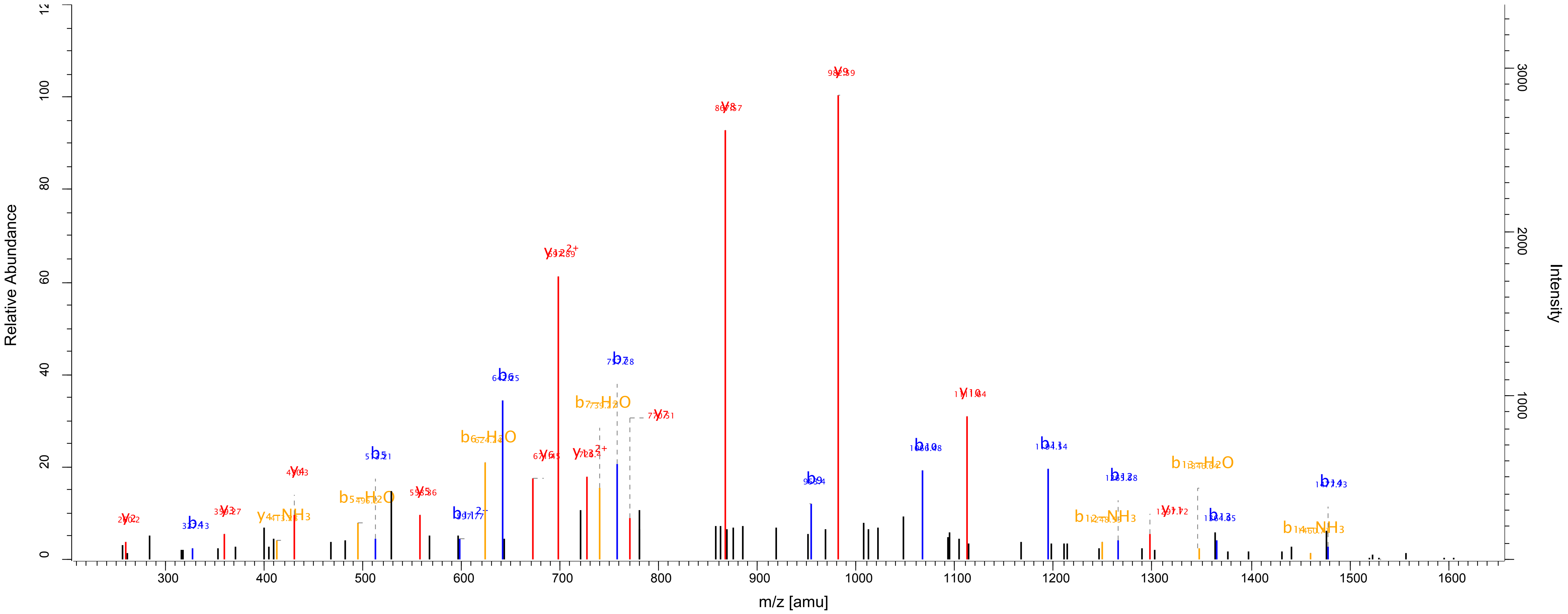
general information

Annotation:	13 of 15
AminoAcids Coverage:	87 %
Intensity Coverage:	72 %
Peak Coverage:	37 %
Protein Localisation:	9 ... 23

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.0807758		100.07569		100.07569	1	V	14				
−0.0835616	171.14919		199.144104	+0.0122373	199.144104	2	V	13	1588.90974		1588.90974	
	268.201954		296.196868		296.196868	3	P	12	1489.84133		745.424302	+0.1426537
	355.233982		383.228897		383.228897	4	S	11	1392.78856		1392.78856	
	470.260925		498.25584		498.25584	5	D	10	1305.75654	−0.2089277	1305.75654	
	583.344989		611.339904	−0.0877063	611.339904	6	I	9	1190.72959		1190.72959	
	746.408317		774.403232	−0.1755099	774.403232	7	Y	8	1077.64553	−0.0844929	1077.64553	
	843.461081	+0.0967329	436.231636		871.455996	8	P	7	914.5822	−0.1390843	457.794738	−0.0427238
	956.545145		984.54006	−0.3691615	984.54006	9	I	6	817.529436	+0.2472977	817.529436	
	1055.61356		1083.60847	−0.1631614	1083.60847	10	V	5	704.445372	+0.123476	352.726324	+0.0343571
	1168.69762	+0.04615	598.849907		1196.69254	11	I	4	605.376958	+0.0557204	605.376958	
	1225.71909	−0.0455755	627.360639	−0.1651734	1253.714	12	G	3	492.292894	+0.0367571	492.292894	
	1372.7875		1400.78242		1400.78242	13	F	2	435.27143	+0.0437555	435.27143	
	1485.87156	−0.1030767	757.436878		1513.86648	14	I	1	288.203016	+0.0817128	288.203016	
						15	R	0	175.118952	+0.0751244	175.118952	

Scan number	18835	Raw file	20091015_Orbi6_MaHe_SA_ADH_exp3_Susp_Gel16
Method	ITMS; CID	Pepti...	180.48





precursor information

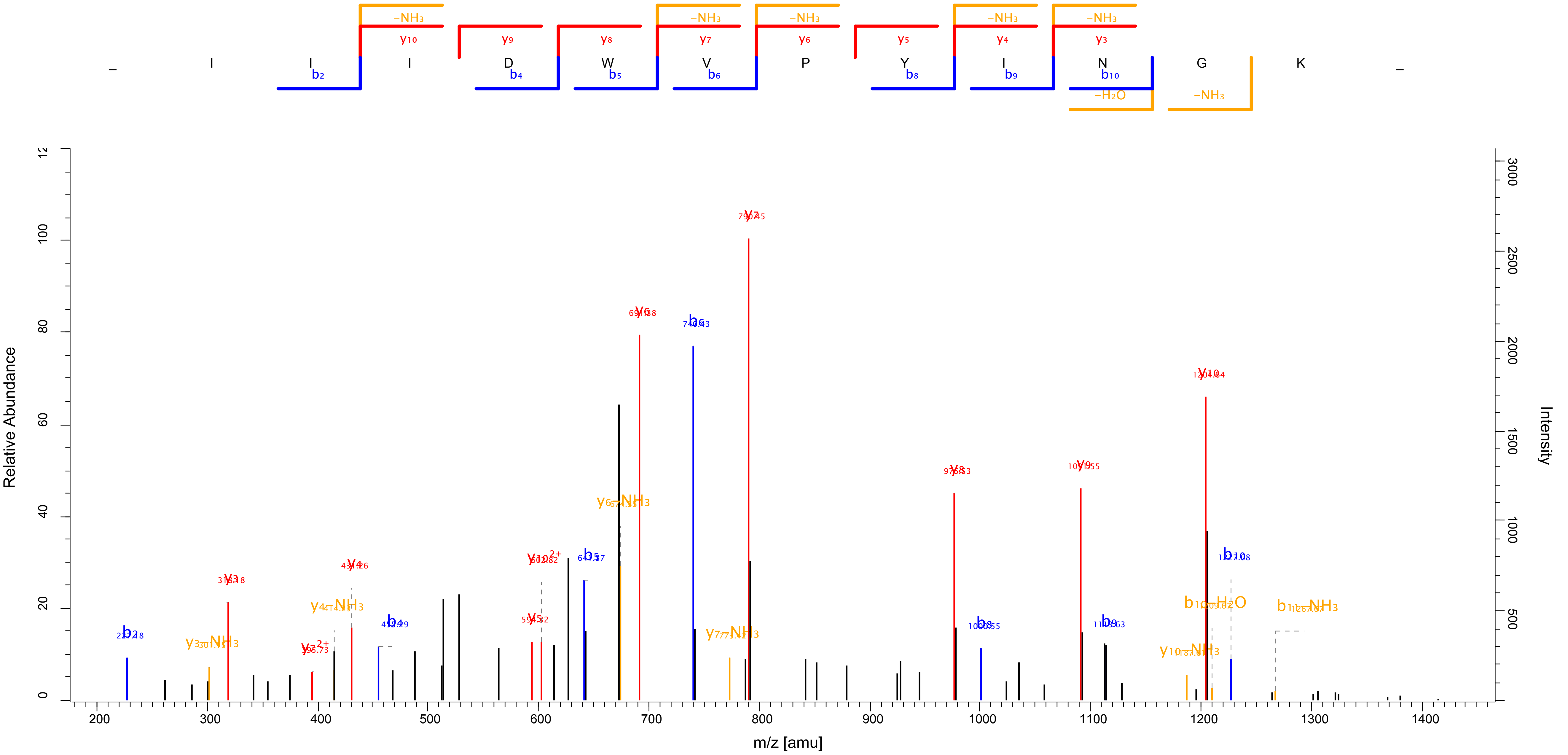
Mass:	1622.82991
m/z:	812.42223
Charge:	2+
Retentiontime:	109.847541809082
Score:	180.4791
Mass Error [ppm]:	-0.3149
PEP:	5.3471E-14
Precursor Type:	ISO

general information

Annotation:	12 of 15
AminoAcids Coverage:	80 %
Intensity Coverage:	69 %
Peak Coverage:	35 %
Protein Localisation:	161 ... 175

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342195		116.0342195	1	D	14				
	173.05568322		173.05568322	2	G	13	1508.8107555		1508.8107555	
	230.07714695		230.07714695	3	G	12	1451.7892918		726.39828412	-0.0310966
	327.1299108	+0.2276331	327.1299108	4	P	11	1394.767828		697.88755226	-0.0697422
	513.20922375	-0.0512037	513.20922375	5	W	10	1297.7150642	-0.0557624	1297.7150642	
	642.25181685	-0.0369731	642.25181685	6	E	9	1111.6357512	-0.1136565	1111.6357512	
	757.27875988	+0.0809813	757.27875988	7	D	8	982.59315815	-0.1082338	982.59315815	
	854.33152373		854.33152373	8	P	7	867.56621512	-0.1328045	867.56621512	
	953.39993765	+0.1349745	953.39993765	9	V	6	770.51345126	+0.0416024	770.51345126	
	1066.4840016	-0.1335378	1066.4840016	10	I	5	671.44503735	+0.0437932	671.44503735	
+0.2206166	597.7749278	-0.1314463	1194.5425791	11	Q	4	558.36097337	-0.035717	558.36097337	
	1265.5796929	-0.2648736	1265.5796929	12	A	3	430.30239586	+0.0152311	430.30239586	
	1364.6481068	+0.0862682	1364.6481068	13	V	2	359.26528207	-0.1548084	359.26528207	
	1477.7321708	+0.2369454	1477.7321708	14	I	1	260.19686815	-0.0476982	260.19686815	
				15	K	0	147.11280417		147.11280417	

Scan number	17916	Raw file	20091018_Orbi6_MaHe_SA_ADH_exp3_24h_Gel01
Method	ITMS; CID	Genenames	UQCR11

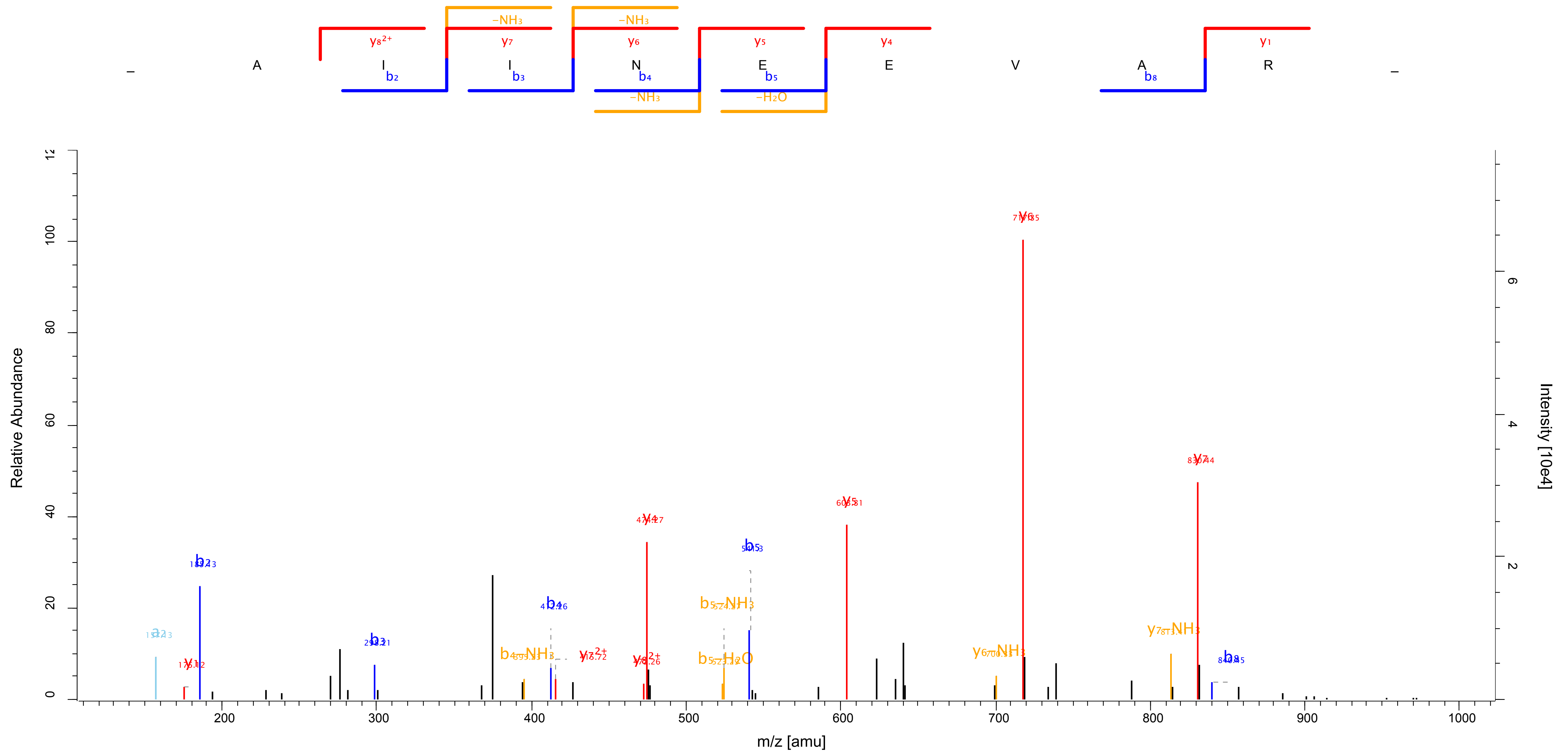


precursor information	
Mass:	1429.79744
m/z:	715.906
Charge:	2+
Retentiontime:	109.068099975586
Score:	167.1151
Mass Error [ppm]:	0.35304
PEP:	2.4419E-05
Precursor Type:	MULTI

general information	
Annotation:	10 of 12
AminoAcids Coverage:	83 %
Intensity Coverage:	57 %
Peak Coverage:	35 %
Protein Localisation:	40 ... 51

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.091340447	1	I	11				
-0.0872697	227.175404427	2	I	10	1317.720149575		1317.720149575	
	340.259468408	3	I	9	1204.636085594	-0.2139665	602.82168103	+0.1254625
+0.1940573	455.28641144	4	D	8	1091.552021614	-0.1333204	1091.552021614	
-0.1034563	641.365724393	5	W	7	976.525078582	-0.0621269	976.525078582	
-0.1696119	740.43413831	6	V	6	790.445765628	-0.1354019	395.726521047	-0.3372999
	837.486902162	7	P	5	691.377351712	+0.0218792	691.377351712	
-0.2221667	1000.5502307	8	Y	4	594.32458786	-0.2600737	594.32458786	
+0.069929	1113.63429468	9	I	3	431.261259322	-0.0998824	431.261259322	
-0.3223637	1227.677222127	10	N	2	318.177195341	+0.1023457	318.177195341	
	1284.698685851	11	G	1	204.134267894		204.134267894	
		12	K	0	147.112804171		147.112804171	

Scan number	7952	Raw file	20091018_Orbi6_MaHe_SA_ADH_exp3_24h_Gel01
Method	ITMS; CID	Genenames	LRAT

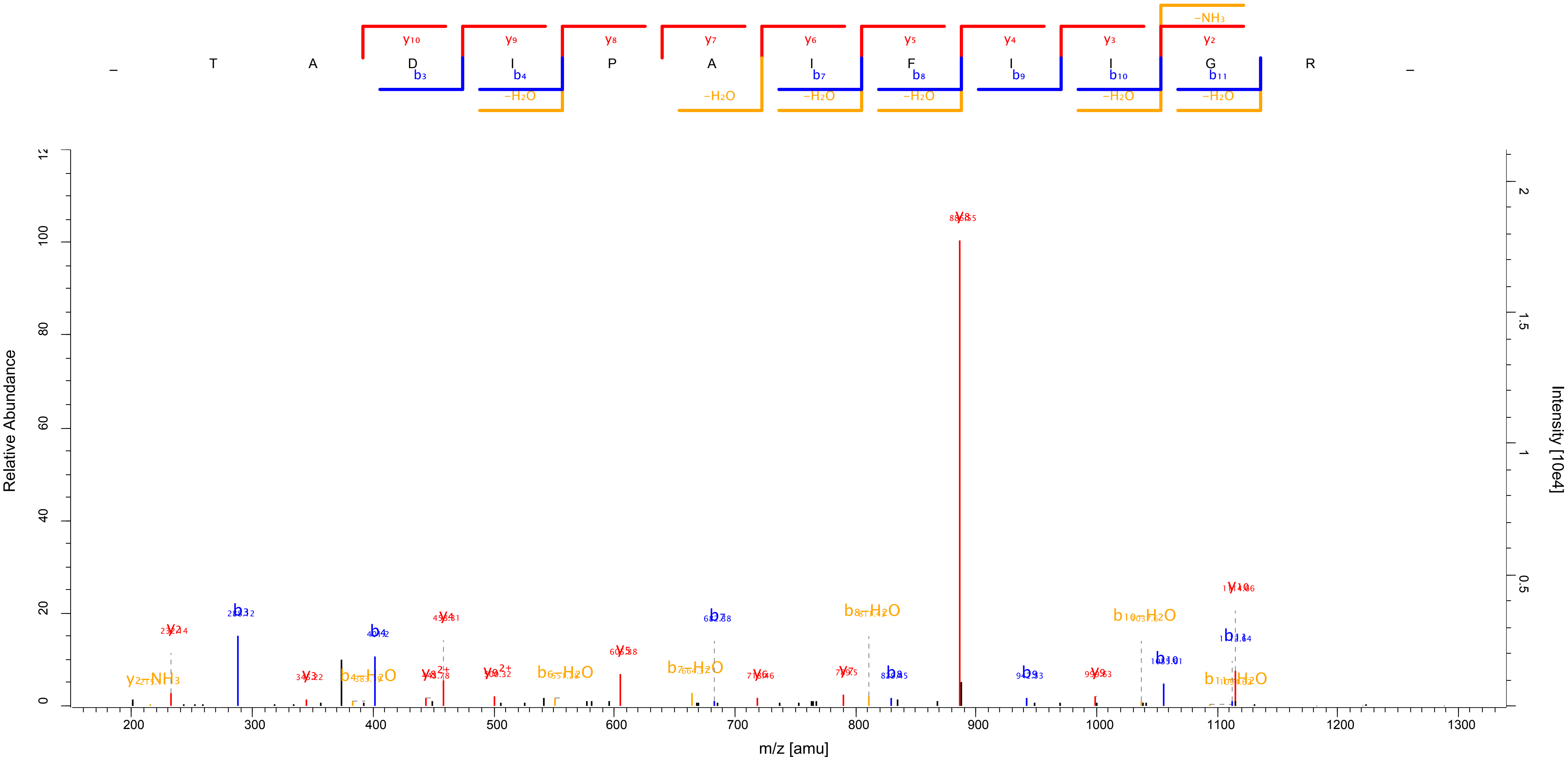


precursor information

Mass:	1013.55091
m/z:	507.78273
Charge:	2+
Retentiontime:	53.8176116943359
Score:	152.6302
Mass Error [ppm]:	0.34186
PEP:	0.00018742
Annotation:	7 of 9
AminoAcids Coverage:	78 %
Intensity Coverage:	68 %
Peak Coverage:	34 %
Protein Localisation:	135 ... 143

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	44.049475632		72.044390254	1	A	8				
+0.0642753	157.13353961	-0.0106259	185.12845423	2	I	7	943.52072149		472.26399898	+0.1063013
	270.21760359	-0.1077514	298.21251822	3	I	6	830.4366575	-0.036511	415.72196699	+0.0014522
	384.26053104	+0.008745	412.25544566	4	N	5	717.35259352	-0.0341731	717.35259352	
	513.30312414	-0.1264689	541.29803876	5	E	4	603.30966608	+0.0912128	603.30966608	
	642.34571723		670.34063185	6	E	3	474.26707298	+0.0345322	474.26707298	
	741.41413115		769.40904577	7	V	2	345.22447988		345.22447988	
	812.45124494	-0.33239	840.44615956	8	A	1	246.15606597		246.15606597	
				9	R	0	175.11895218	+0.1659904	175.11895218	

Scan number	18332	Raw file	20091018_Orbi6_MaHe_SA_ADH_exp3_24h_Gel03
Method	ITMS; CID	Genenames	PRADC1



precursor information

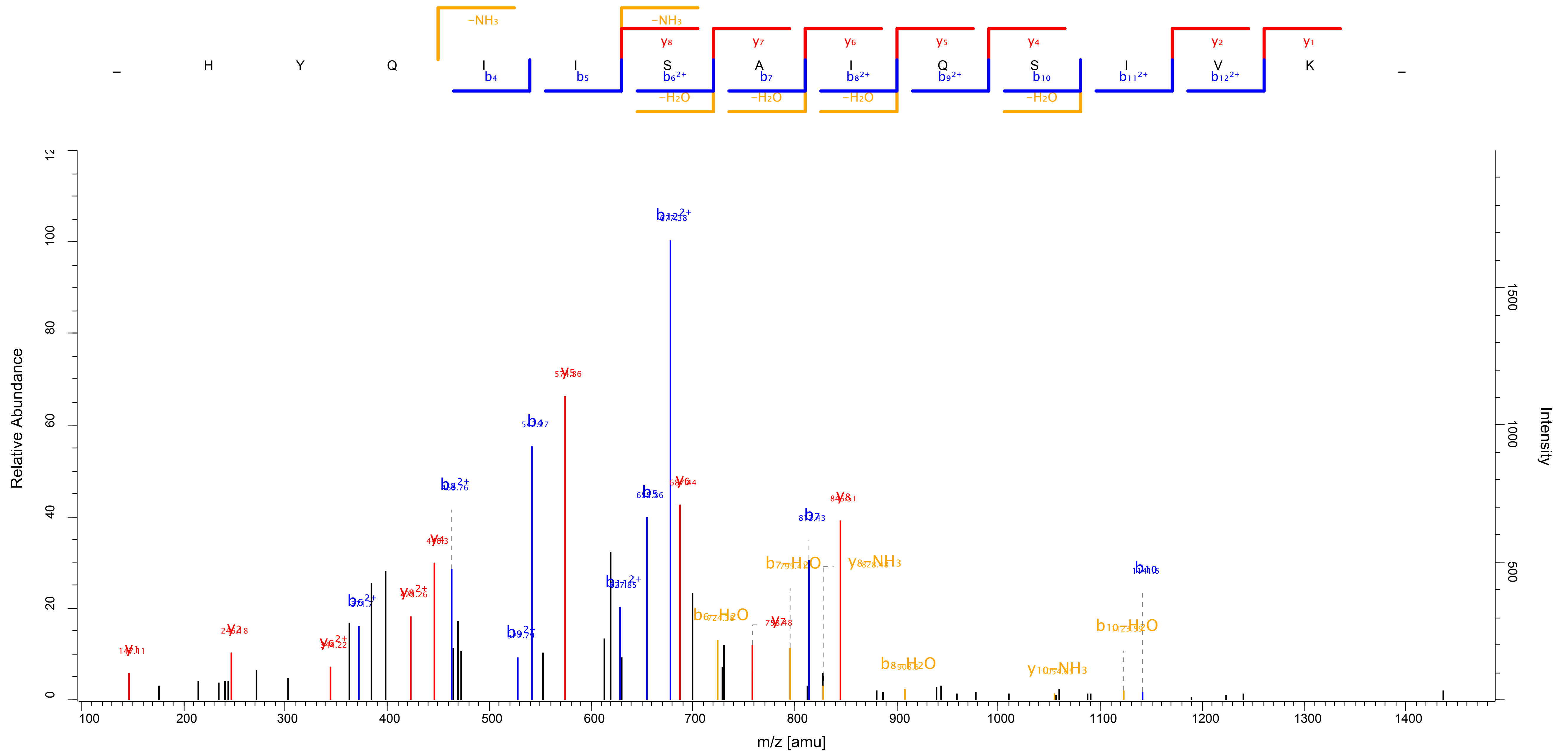
Mass:	1285.73983
m/z:	643.87719
Charge:	2+
Retentiontime:	107.88053894043
Score:	185.7693
Mass Error [ppm]:	0.32048
PEP:	2.0169E-08
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverage:	75 %
Intensity Coverage:	81 %
Peak Coverage:	39 %
Protein Localisation:	136 ... 147

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.054954941	1	T	11				
	173.092068728	2	A	10	1185.699020202		1185.699020202	
+0.0186225	288.11901176	3	D	9	1114.661906414	−0.0362961	1114.661906414	
−0.1505855	401.203075741	4	I	8	999.634963382	−0.132522	500.321119924	+0.0162824
	498.255839593	5	P	7	886.550899402	−0.0823935	443.779087934	+0.0187636
	569.292953381	6	A	6	789.49813555	−0.049344	789.49813555	
+0.0869719	682.377017361	7	I	5	718.461021762	+0.0395276	718.461021762	
−0.2184415	829.445431277	8	F	4	605.376957782	−0.0133714	605.376957782	
−0.0570831	942.529495258	9	I	3	458.308543865	+0.0632823	458.308543865	
−0.3452487	1055.613559238	10	I	2	345.224479885	+0.0737379	345.224479885	
−0.2998179	1112.635022962	11	G	1	232.140415905	−0.0096176	232.140415905	
		12	R	0	175.118952181		175.118952181	

Scan number	16511	Raw file	20091018_Orbi6_MaHe_SA_ADH_exp3_24h_Gel04
Method	ITMS; CID	Genenames	DGCR6;DGCR6L



precursor information

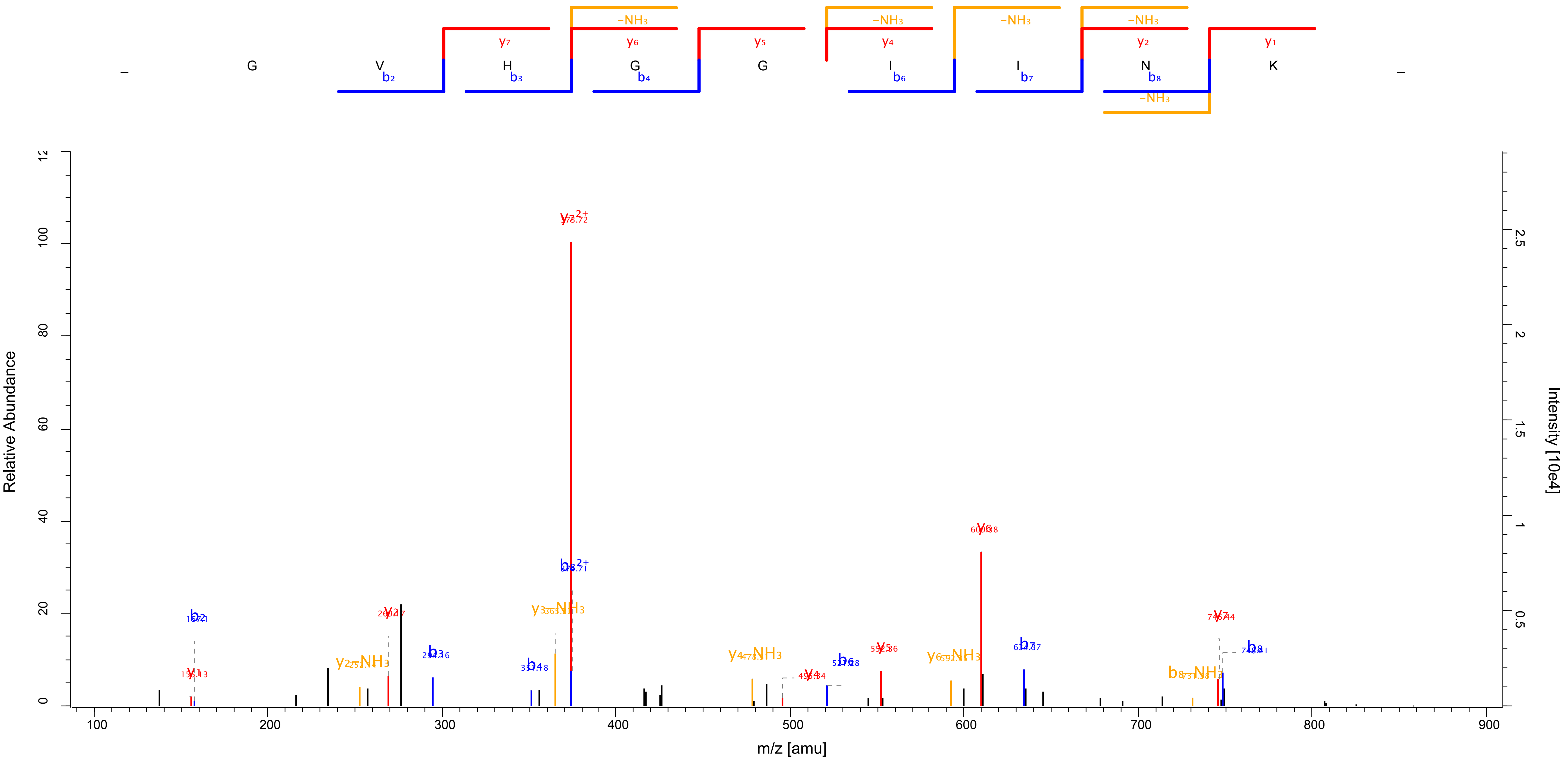
Mass:	1498.85075
m/z:	500.62419
Charge:	3+
Retentiontime:	93.8243103027344
Score:	142.0848
Mass Error [ppm]:	−0.0073928
PEP:	1.1462E−05
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverage:	77 %
Intensity Coverage:	66 %
Peak Coverage:	39 %
Protein Localisation:	21 ... 33

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.06618833		138.06618833	1	H	12				
	301.12951687		301.12951687	2	Y	11	1362.7991282		1362.7991282	
	429.18809438		429.18809438	3	Q	10	1199.7357996		1199.7357996	
	542.27215836	−0.1774928	542.27215836	4	I	9	1071.6772221		1071.6772221	
	655.35622234	+0.1410921	655.35622234	5	I	8	958.59315815		958.59315815	
−0.0466406	371.69776361		742.38825075	6	S	7	845.50909417	−0.040039	423.25818532	+0.0961543
	813.42536454	−0.1213484	813.42536454	7	A	6	758.47706576	+0.0518039	758.47706576	
−0.1758635	463.75835249		926.50942852	8	I	5	687.43995197	−0.0283919	344.22361422	+0.167377
+0.2424491	527.78764125		1054.568006	9	Q	4	574.35588799	−0.013969	574.35588799	
	1141.6000344	−0.1212747	1141.6000344	10	S	3	446.29731048	+0.0285867	446.29731048	
−0.035873	627.84568744		1254.6840984	11	I	2	359.26528207		359.26528207	
−0.0672723	677.3798944		1353.7525123	12	V	1	246.18121809	+0.0080367	246.18121809	
				13	K	0	147.11280417	−0.1236989	147.11280417	

Scan number	5541	Raw file	20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel01
Method	ITMS; CID	Genenames	PFN3

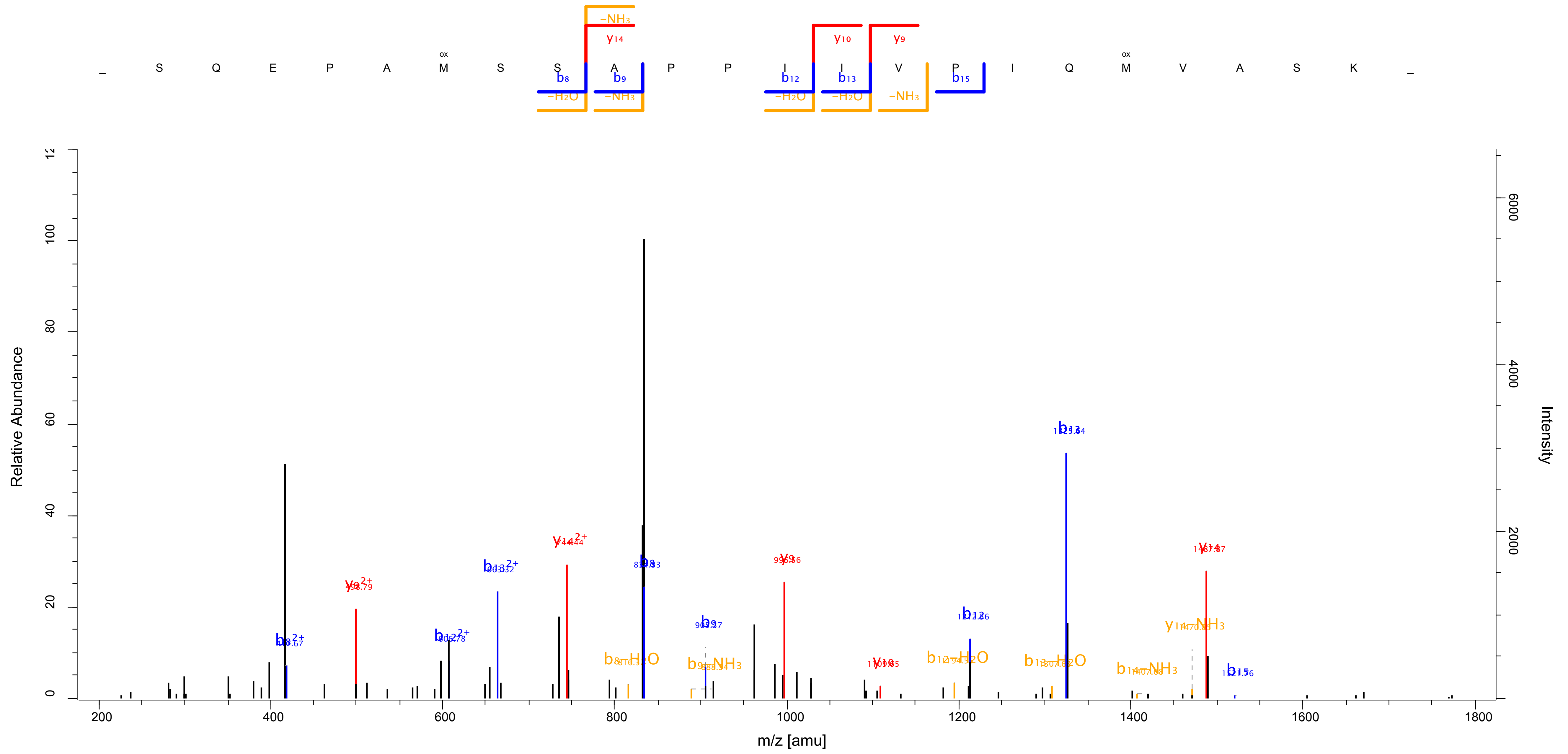


precursor information

Mass:	893.50867
m/z:	447.76161
Charge:	2+
Retentiontime:	46.1529006958008
Score:	161.1116
Mass Error [ppm]:	0.40655
PEP:	0.00018498
Annotation:	8 of 9
AminoAcids Coverage:	89 %
Intensity Coverage:	70 %
Peak Coverage:	40 %
Protein Localisation:	115 ... 123

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019		58.02874019	1	G	8				
	157.09715411	+0.1654649	157.09715411	2	V	7	845.50831162		845.50831162	
	294.15606597	-0.0549307	294.15606597	3	H	6	746.4398977	-0.1829397	373.72358708	-0.1126862
	351.17752969	+0.0652071	351.17752969	4	G	5	609.38098584	-0.0742231	609.38098584	
	408.19899342		408.19899342	5	G	4	552.35952212	-0.1734259	552.35952212	
	521.2830574	+0.0587395	521.2830574	6	I	3	495.33805839	+0.2683259	495.33805839	
	634.36712138	-0.0936839	634.36712138	7	I	2	382.25399441		382.25399441	
-0.4430376	374.70866265	+0.0631567	748.41004882	8	N	1	269.16993043	-0.0103235	269.16993043	
				9	K	0	155.12700298	+0.145458	155.12700298	

Scan number	20631	Raw file	20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel02
Method	ITMS; CID	Genenames	CNPPD1



precursor information

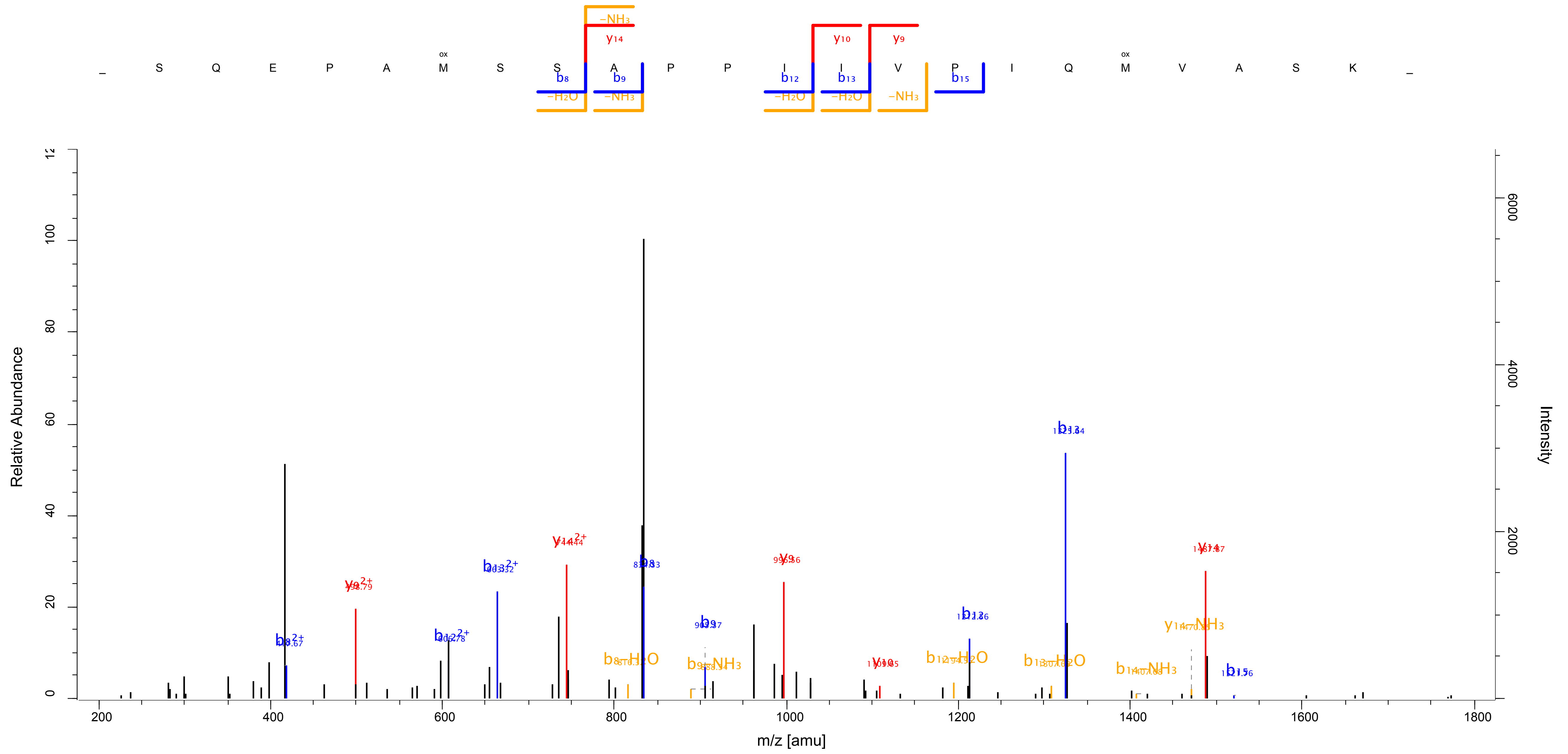
Mass:	2312.17321
m/z:	771.73168
Charge:	3+
Retentiontime:	122.701240539551
Score:	81.72297
Mass Error [ppm]:	-1.0309
PEP:	2.4188E-05
Precursor Type:	MULTI

general information

Annotation:	7 of 22
AminoAcids Coverage:	32 %
Intensity Coverage:	37 %
Peak Coverage:	23 %
Protein Localisation:	138 ... 159

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876		88.039304876	1	S	21				
	216.09788239		216.09788239	2	Q	20	2234.1650513		2234.1650513	
	345.14047548		345.14047548	3	E	19	2106.1064738		2106.1064738	
	442.19323934		442.19323934	4	P	18	1977.0638807		1977.0638807	
	513.23035312		513.23035312	5	A	17	1880.0111169		1880.0111169	
	660.26575235		660.26575235	6	M	16	1808.9740031		1808.9740031	
	747.29778076		747.29778076	7	S	15	1661.9386039		1661.9386039	
+0.0837155	417.66854282	+0.1028691	834.32980917	8	S	14	1574.9065754		1574.9065754	
	905.36692296	-0.0729776	905.36692296	9	A	13	1487.874547	+0.4307508	744.44091175	+0.2868104
	1002.4196868		1002.4196868	10	P	12	1416.8374333		1416.8374333	
	1099.4724507		1099.4724507	11	P	11	1319.7846694		1319.7846694	
-0.1277818	606.78189556	-0.0667686	1212.5565146	12	I	10	1222.7319055		1222.7319055	
+0.168321	663.32392755	-0.3621362	1325.6405786	13	I	9	1109.6478416	-0.0206443	1109.6478416	
	1424.7089925		1424.7089925	14	V	8	996.56377759	-0.0908772	498.78552703	-0.1235397
	1521.7617564	-0.1769175	1521.7617564	15	P	7	897.49536367		897.49536367	
	1634.8458204		1634.8458204	16	I	6	800.44259982		800.44259982	
	1762.9043979		1762.9043979	17	Q	5	687.35853584		687.35853584	
	1909.9397971		1909.9397971	18	M	4	559.29995833		559.29995833	
	2009.008211		2009.008211	19	V	3	412.2645591		412.2645591	
	2080.0453248		2080.0453248	20	A	2	313.19614518		313.19614518	
	2167.0773532		2167.0773532	21	S	1	242.15903139		242.15903139	
				22	K	0	155.12700298		155.12700298	

Scan number	20631	Raw file	20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel02
Method	ITMS; CID	Genenames	CNPPD1



precursor information

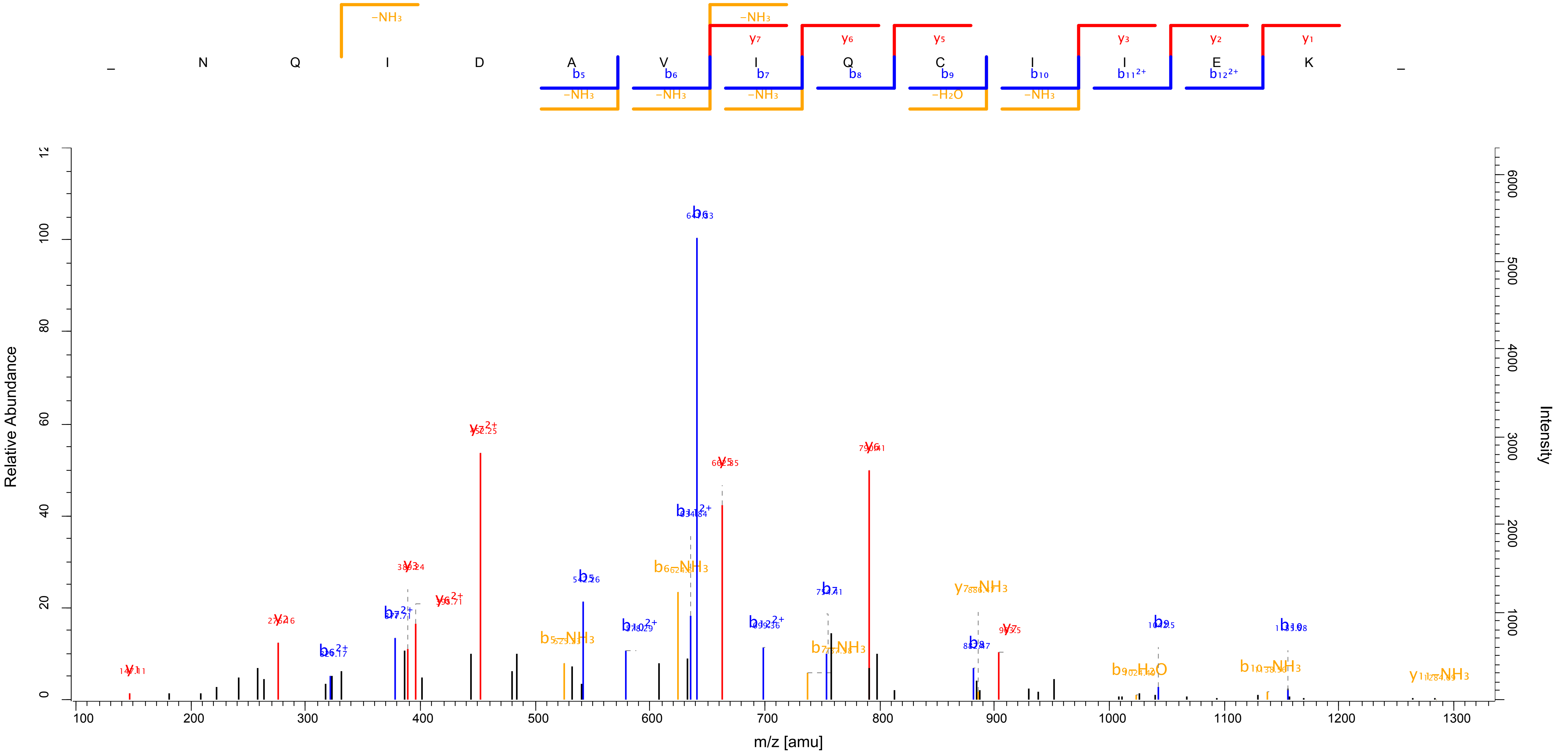
Mass:	2312.17321
m/z:	771.73168
Charge:	3+
Retentiontime:	122.70124053955l
Score:	81.72297
Mass Error [ppm]:	−1.0309
PEP:	2.4188E−05
Precursor Type:	MULTI

general information

Annotation:	7 of 22
AminoAcids Coverage:	32 %
Intensity Coverage:	37 %
Peak Coverage:	23 %
Protein Localisation:	138 ... 159

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876		88.039304876	1	S	21				
	216.09788239		216.09788239	2	Q	20	2234.1650513		2234.1650513	
	345.14047548		345.14047548	3	E	19	2106.1064738		2106.1064738	
	442.19323934		442.19323934	4	P	18	1977.0638807		1977.0638807	
	513.23035312		513.23035312	5	A	17	1880.0111169		1880.0111169	
	660.26575235		660.26575235	6	M	16	1808.9740031		1808.9740031	
	747.29778076		747.29778076	7	S	15	1661.9386039		1661.9386039	
+0.0837155	417.66854282	+0.1028691	834.32980917	8	S	14	1574.9065754		1574.9065754	
	905.36692296	−0.0729776	905.36692296	9	A	13	1487.874547	+0.4307508	744.44091175	+0.2868104
	1002.4196868		1002.4196868	10	P	12	1416.8374333		1416.8374333	
	1099.4724507		1099.4724507	11	P	11	1319.7846694		1319.7846694	
−0.1277818	606.78189556	−0.0667686	1212.5565146	12	I	10	1222.7319055		1222.7319055	
+0.168321	663.32392755	−0.3621362	1325.6405786	13	I	9	1109.6478416	−0.0206443	1109.6478416	
	1424.7089925		1424.7089925	14	V	8	996.56377759	−0.0908772	498.78552703	−0.1235397
	1521.7617564	−0.1769175	1521.7617564	15	P	7	897.49536367		897.49536367	
	1634.8458204		1634.8458204	16	I	6	800.44259982		800.44259982	
	1762.9043979		1762.9043979	17	Q	5	687.35853584		687.35853584	
	1909.9397971		1909.9397971	18	M	4	559.29995833		559.29995833	
	2009.008211		2009.008211	19	V	3	412.2645591		412.2645591	
	2080.0453248		2080.0453248	20	A	2	313.19614518		313.19614518	
	2167.0773532		2167.0773532	21	S	1	242.15903139		242.15903139	
				22	K	0	155.12700298		155.12700298	

Scan number	19744	Raw file	20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel05
Method	ITMS; CID	Genenames	LIN37



precursor information

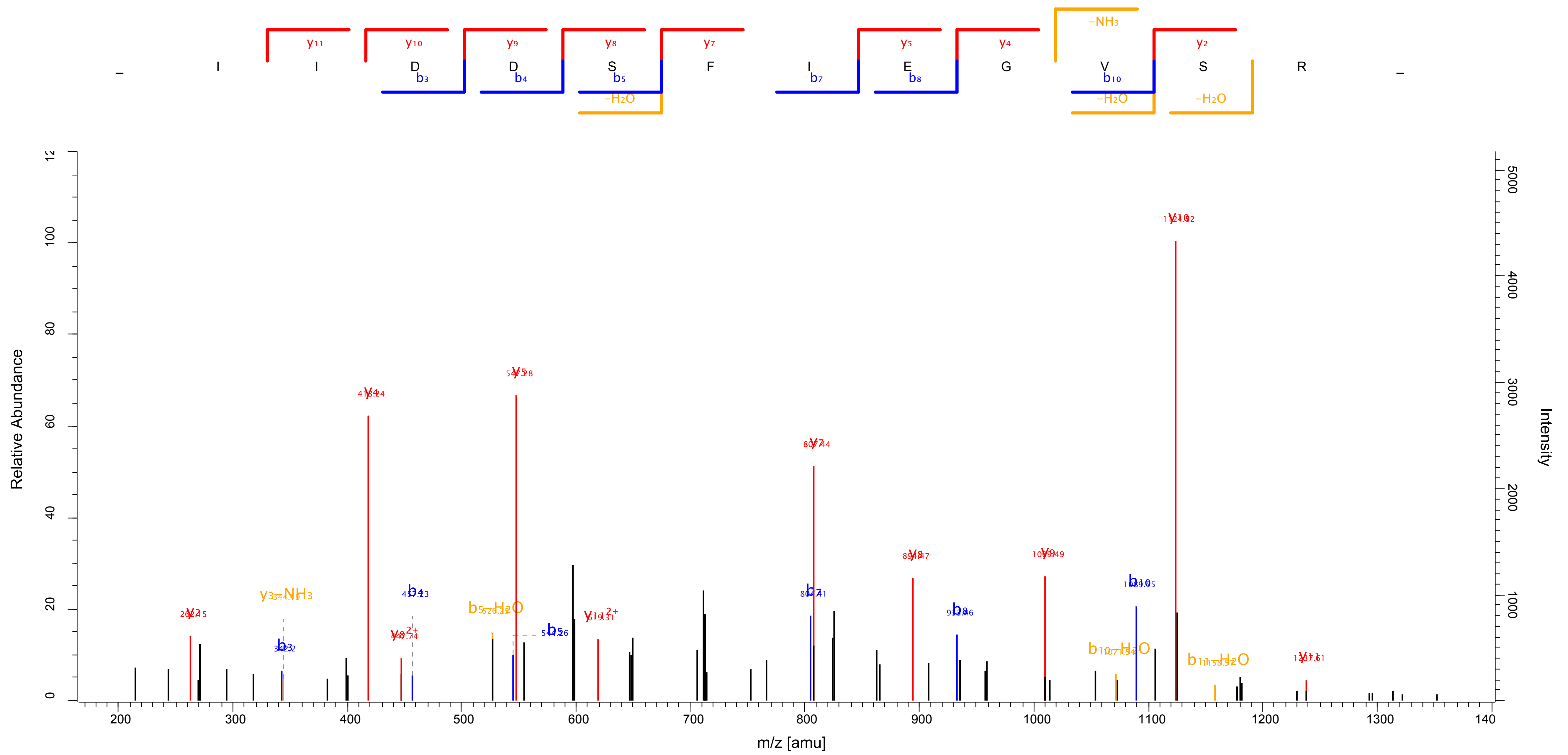
Mass:	1542.80769
m/z:	515.27651
Charge:	3+
Retentiontime:	115.092552185059
Score:	184.5518
Mass Error [ppm]:	0.074936
PEP:	1.6387E-10
Precursor Type:	ISO

general information

Annotation:	10 of 13
AminoAcids Coverage:	77 %
Intensity Coverage:	73 %
Peak Coverage:	40 %
Protein Localisation:	20 ... 32

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.05020391		115.05020391	1	N	12				
	243.10878143		243.10878143	2	Q	11	1429.7719271		1429.7719271	
	356.19284541		356.19284541	3	I	10	1301.7133496		1301.7133496	
	471.21978844		471.21978844	4	D	9	1188.6292857		1188.6292857	
	542.25690223	−0.0855765	542.25690223	5	A	8	1073.6023426		1073.6023426	
+0.0146729	321.1662963	−0.1799914	641.32531614	6	V	7	1002.5652288		1002.5652288	
−0.0773468	377.70832829	−0.0689871	754.40938012	7	I	6	903.49681492	+0.006542	452.25204569	+0.0735158
	882.46795763	−0.1635753	882.46795763	8	Q	5	790.41275094	−0.1271064	395.7100137	+0.0087363
	1042.4986058	−0.2291967	1042.4986058	9	C	4	662.35417343	−0.0759142	662.35417343	
−0.0652978	578.29497314	+0.1275353	1155.5826698	10	I	3	502.32352523		502.32352523	
−0.012054	634.83700513		1268.6667338	11	I	2	389.23946125	−0.0175985	389.23946125	
−0.0384775	699.35830168		1397.7093269	12	E	1	276.15539727	+0.0289289	276.15539727	
				13	K	0	147.11280417	+0.0345042	147.11280417	

Scan number	12622	Raw file	20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel06
Method	ITMS; CID	Genenames	ZDHHC6



precursor
information

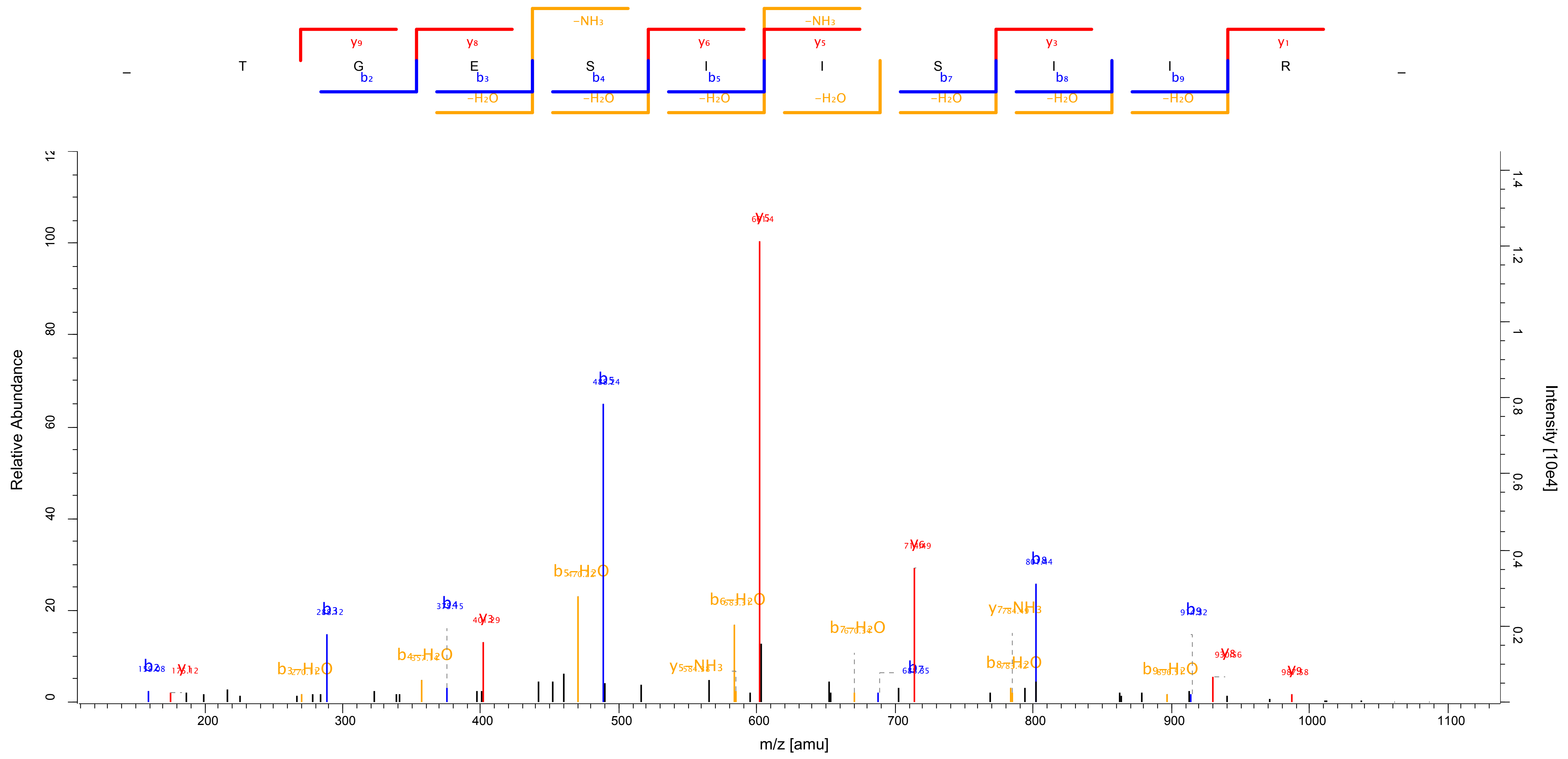
Mass:	1349.68306
m/z:	675.84881
Charge:	2+
Retentiontime:	75.3784103393555
Score:	116.5463
Mass Error [ppm]:	0.26912
PEP:	0.00018541
Precursor Type:	MULTI

general
information

Annotation:	10 of 12
AminoAcids Coverage:	83 %
Intensity Coverage:	53 %
Peak Coverage:	29 %
Protein Localisation:	372 ... 383

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.091340447	1	I	11				
	227.175404427	2	I	10	1237.605907678	−0.0263178	619.306592072	+0.1781491
+0.0083154	342.202347459	3	D	9	1124.521843697	−0.1372001	1124.521843697	
−0.1232724	457.229290491	4	D	8	1009.494900665	+0.0170622	1009.494900665	
+0.130954	544.261318901	5	S	7	894.467957633	−0.0218517	447.73761705	−0.0189891
	691.329732818	6	F	6	807.435929224	−0.0787515	807.435929224	
−0.0801176	804.413796798	7	I	5	660.367515307		660.367515307	
−0.2200007	933.456389894	8	E	4	547.283451327	−0.0357096	547.283451327	
	990.477853618	9	G	3	418.240858231	−0.1096326	418.240858231	
−0.290164	1089.546267534	10	V	2	361.219394507		361.219394507	
	1176.578295944	11	S	1	262.150980591	+0.0159506	262.150980591	
		12	R	0	175.118952181		175.118952181	

Scan number	15044	Raw file	20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel06
Method	ITMS; CID	Genenames	ALG3



precursor information

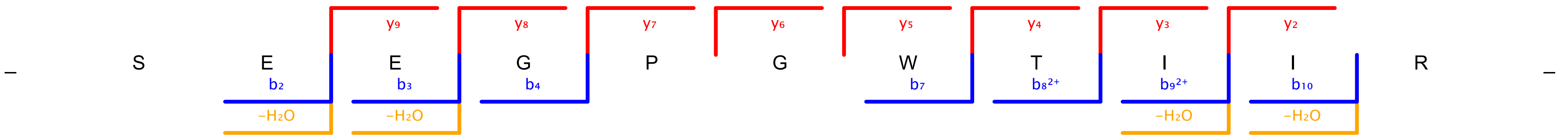
Mass:	1087.62415
m/z:	544.81935
Charge:	2+
Retentiontime:	88.4133911132813
Score:	157.6631
Mass Error [ppm]:	0.39008
PEP:	8.4966E-05
Precursor Type:	MULTI

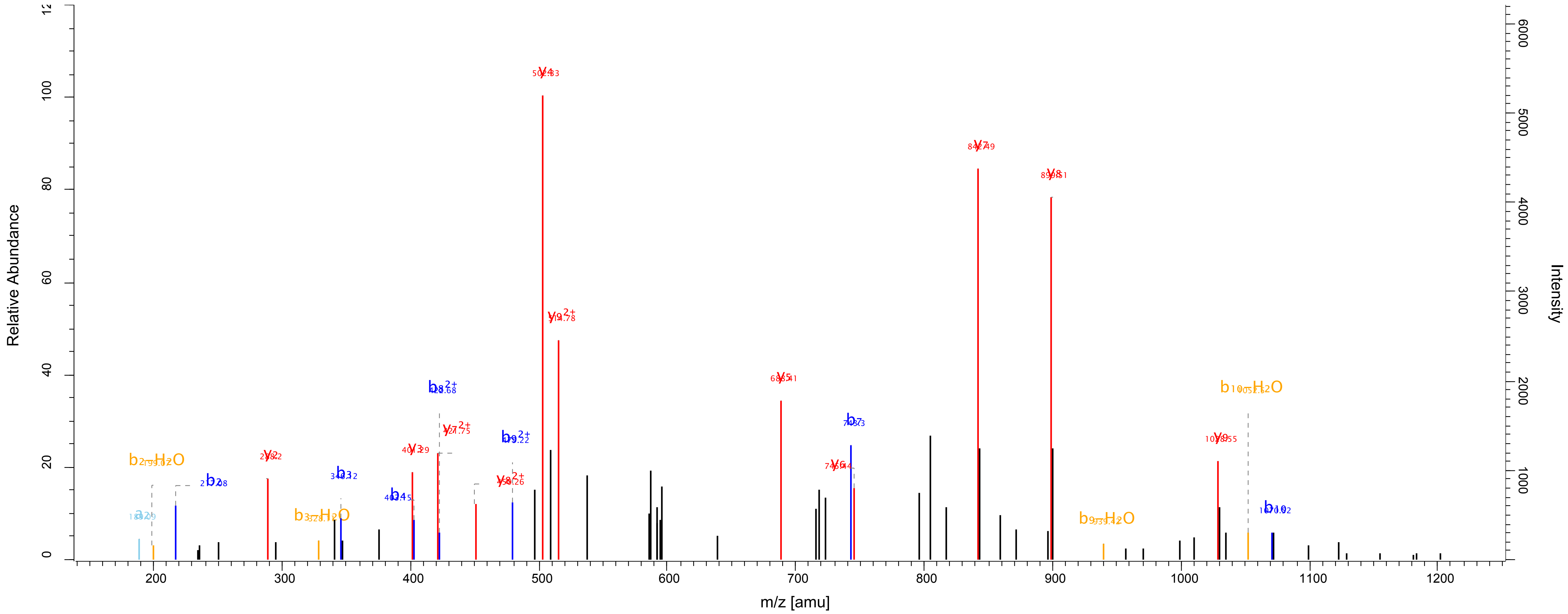
ge information

Annotation:	9 of 10
AminoAcids Coverage:	90 %
Intensity Coverage:	77 %
Peak Coverage:	37 %
Protein Localisation:	312 ... 321

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	102.054954941	1	T	9		
−0.0398433	159.076418664	2	G	8	987.583321742	−0.0683681
−0.0601739	288.11901176	3	E	7	930.561858019	−0.1165455
+0.1639623	375.15104017	4	S	6	801.519264922	
+0.0396761	488.235104151	5	I	5	714.487236513	−0.2185598
	601.319168131	6	I	4	601.403172532	−0.0219469
−0.2832644	688.351196541	7	S	3	488.319108552	
+0.0347712	801.435260522	8	I	2	401.287080142	+0.0746752
−0.2721932	914.519324502	9	I	1	288.203016161	
		10	R	0	175.118952181	+0.1389976

Scan number	10265	Raw file	20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel07
Method	ITMS; CID	Genenames	RRP15





precursor
information

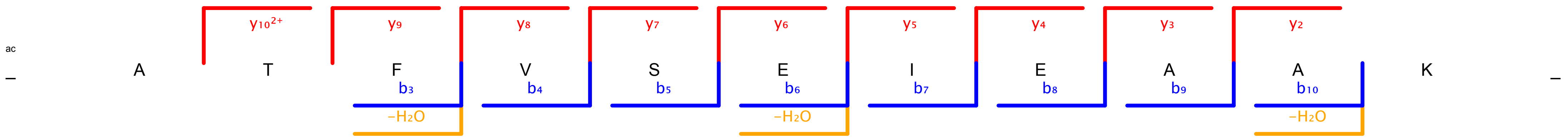
Mass:	1243.61955
m/z:	622.81705
Charge:	2+
Retentiontime:	64.4137878417969
Score:	153.9702
Mass Error [ppm]:	−0.12392
PEP:	7.4535E−05
Precursor Type:	ISO

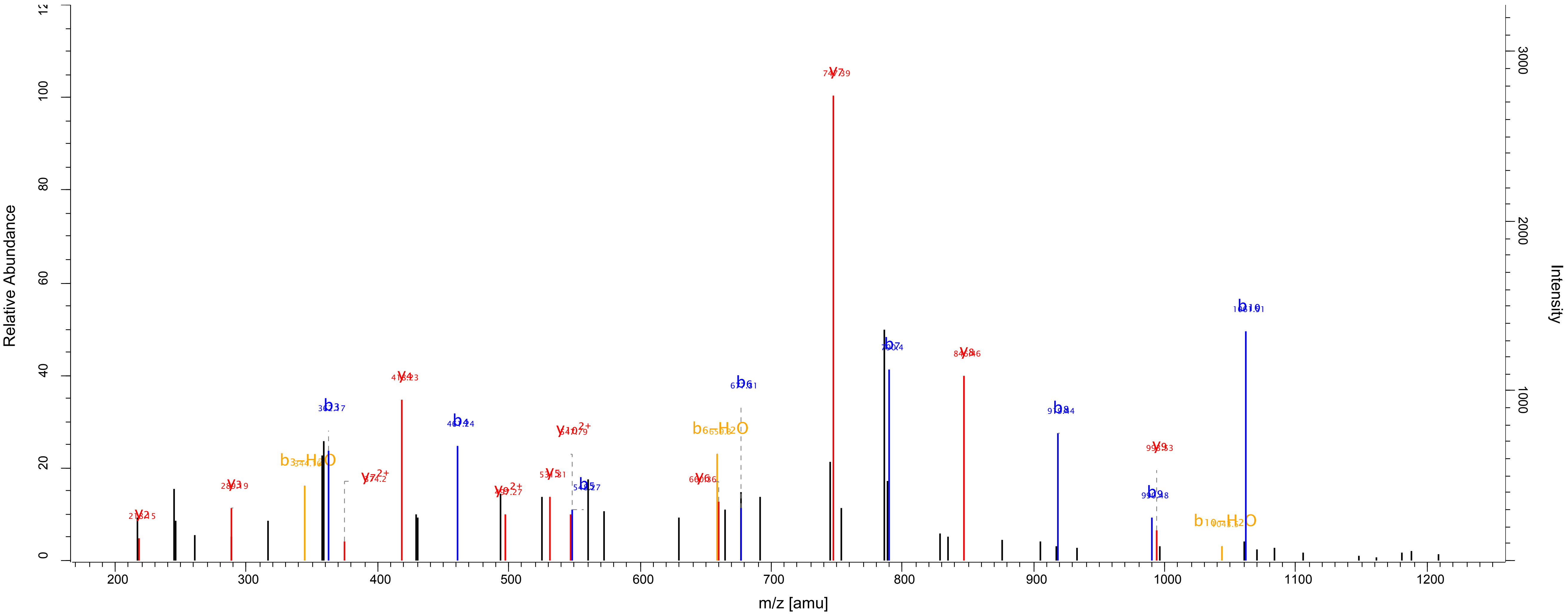
general
information

Annotation:	9 of 11
AminoAcids Coverage:	82 %
Intensity Coverage:	59 %
Peak Coverage:	35 %
Protein Localisation:	240 ... 250

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
	60.0443903		88.0393049		88.0393049	1	S	10				
+0.0249704	189.086983		217.081898	−0.0458872	217.081898	2	E	9	1157.59495		1157.59495	
	318.129576		346.124491	+0.0285241	346.124491	3	E	8	1028.55236	+0.0119751	514.779816	−0.0539251
	375.15104		403.145955	−0.0392653	403.145955	4	G	7	899.509763	−0.0746432	450.25852	+0.0749154
	472.203804		500.198719		500.198719	5	P	6	842.488299	−0.1253231	421.747788	+0.01918
	529.225268		557.220182		557.220182	6	G	5	745.435535	+0.0570184	745.435535	
	715.304581		743.299495	−0.0299641	743.299495	7	W	4	688.414072	−0.0196014	688.414072	
	816.352259	−0.2236118	422.677225		844.347174	8	T	3	502.334759	+0.0235788	502.334759	
	929.436323	−0.3216131	479.219257		957.431238	9	I	2	401.28708	+0.0251757	401.28708	
	1042.52039		1070.5153	−0.0715762	1070.5153	10	I	1	288.203016	+0.0084096	288.203016	
						11	R	0	175.118952		175.118952	

Scan number	16688	Raw file	20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel07
Method	ITMS; CID	Genenames	TADA1





precursor information

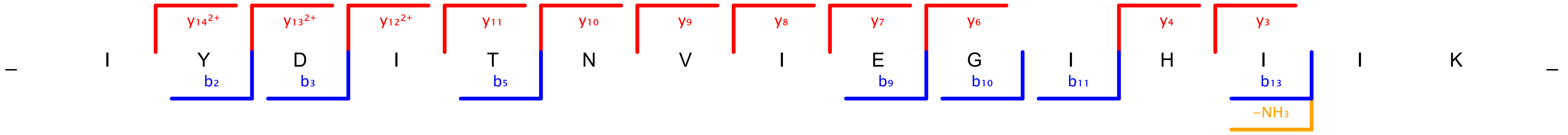
Mass:	1206.6135
m/z:	604.31402
Charge:	2+
Retentiontime:	100.548805236816
Score:	145.9875
Mass Error [ppm]:	0.22906
PEP:	0.000148
Precursor Type:	ISO

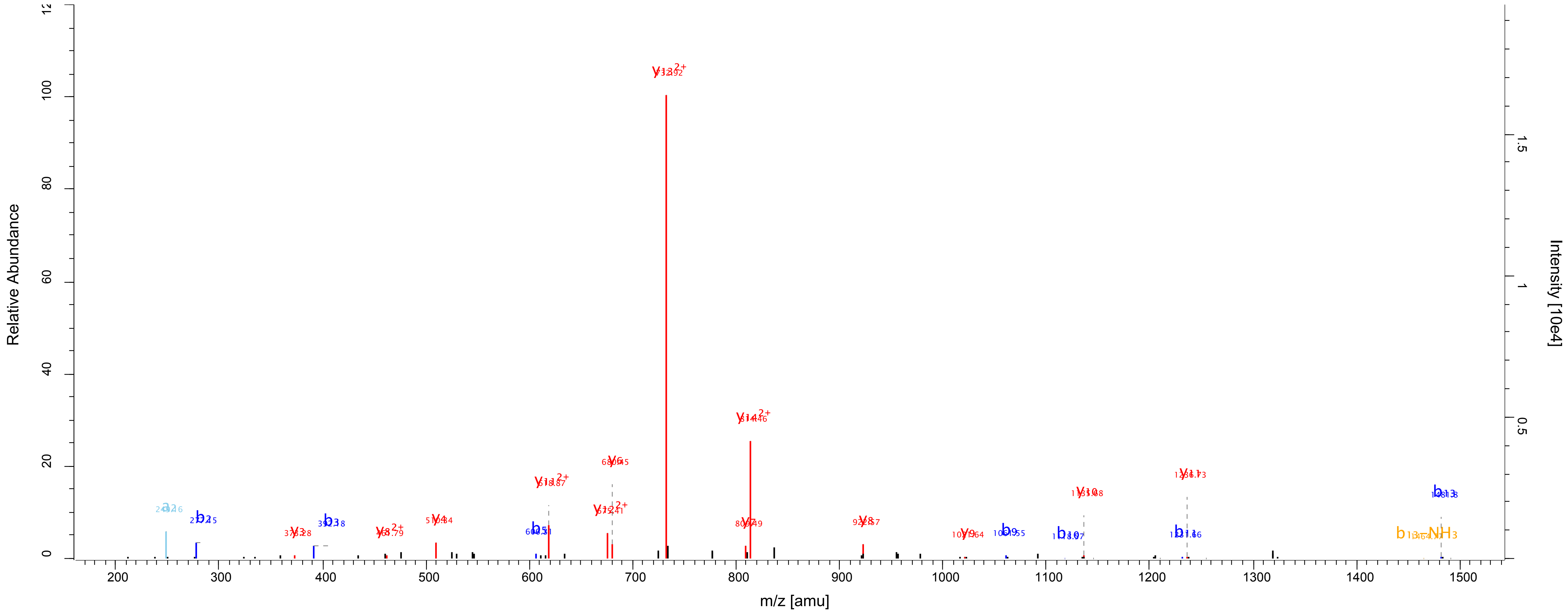
general information

Annotation:	9 of 11
AminoAcids Coverage:	82 %
Intensity Coverage:	57 %
Peak Coverage:	37 %
Protein Localisation:	2 ... 12

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.054954941	1	A	10				
	215.102633415	2	T	9	1094.572816635		547.790046551	-0.1389845
-0.130459	362.171047331	3	F	8	993.525138161	-0.115165	497.266207314	-0.0713831
-0.0142415	461.239461247	4	V	7	846.456724245	-0.1058331	846.456724245	
-0.002996	548.271489657	5	S	6	747.388310329	-0.0338792	374.197793398	+0.0509249
-0.0427204	677.314082753	6	E	5	660.356281919	-0.0177809	660.356281919	
-0.2071677	790.398146734	7	I	4	531.313688823	+0.0657057	531.313688823	
-0.3836109	919.44073983	8	E	3	418.229624842	+0.0411881	418.229624842	
-0.2983492	990.477853618	9	A	2	289.187031746	-0.019124	289.187031746	
-0.2266373	1061.514967406	10	A	1	218.149917958	+0.1171566	218.149917958	
		11	K	0	147.112804171		147.112804171	

Scan number	19077	Raw file	20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel07
Method	ITMS; CID	Genenames	E2F3;DKFZp686C18211





precursor
information

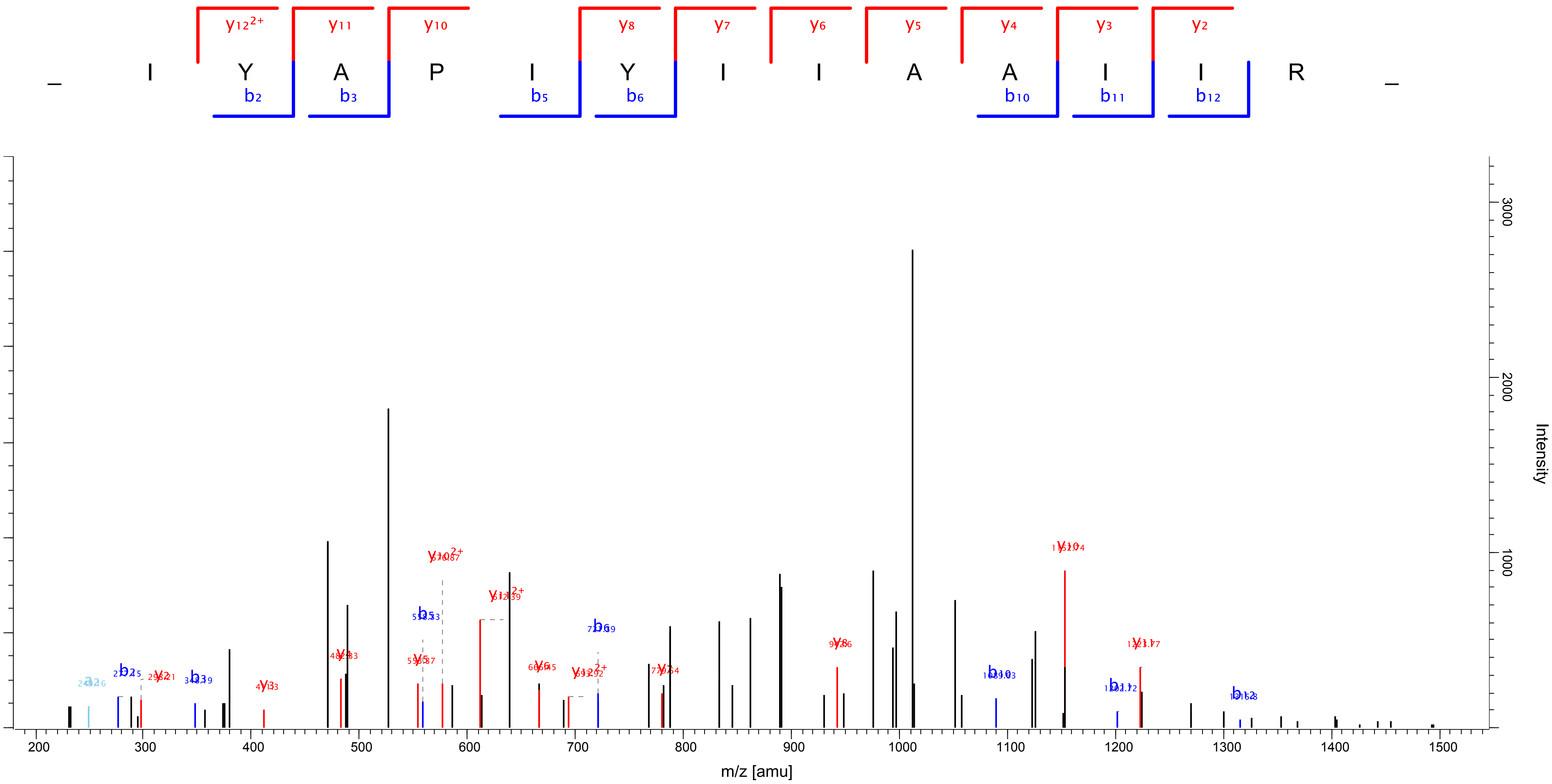
Mass:	1739.98262
m/z:	581.00148
Charge:	3+
Retentiontime:	114.385284423828
Score:	134.2065
Mass Error [ppm]:	0.25853
PEP:	0.00013181
Precursor Type:	ISO

general
information

Annotation:	12 of 15
AminoAcids Coverage:	80 %
Intensity Coverage:	82 %
Peak Coverage:	33 %
Protein Localisation:	218 ... 232

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096425825		114.09134045	1	I	14				
+0.0433859	249.15975436	−0.0189878	277.15466899	2	Y	13	1627.9053842		814.45633031	+0.125884
	364.1866974	−0.0679035	392.18161202	3	D	12	1464.8420556		732.92466605	+0.1126875
	477.27076138		505.265676	4	I	11	1349.8151126		675.41119453	+0.2069085
	578.31843985	−0.1069946	606.31335447	5	T	10	1236.7310486	−0.0516053	618.86916254	+0.1194239
	692.3613673		720.35628192	6	N	9	1135.6833701	+0.341166	1135.6833701	
	791.42978121		819.42469584	7	V	8	1021.6404427	+0.0893547	1021.6404427	
	904.51384519		932.50875982	8	I	7	922.57202877	+0.1062549	461.78965262	−0.4074505
	1033.5564383	+0.1174703	1061.5513529	9	E	6	809.48796479	−0.1006967	809.48796479	
	1090.577902	−0.2482317	1118.5728166	10	G	5	680.4453717	−0.0380841	680.4453717	
	1203.661966	−0.0807087	1231.6568806	11	I	4	623.42390797		623.42390797	
	1340.7208779		1368.7157925	12	H	3	510.33984399	−0.00647	510.33984399	
	1453.8049418	+0.3863008	1481.7998565	13	I	2	373.28093213	−0.1218745	373.28093213	
	1566.8890058		1594.8839204	14	I	1	260.19686815		260.19686815	
				15	K	0	147.11280417		147.11280417	

Scan number	20507	Raw file	20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel07
Method	ITMS; CID	Genenames	TMEM135



precursor information

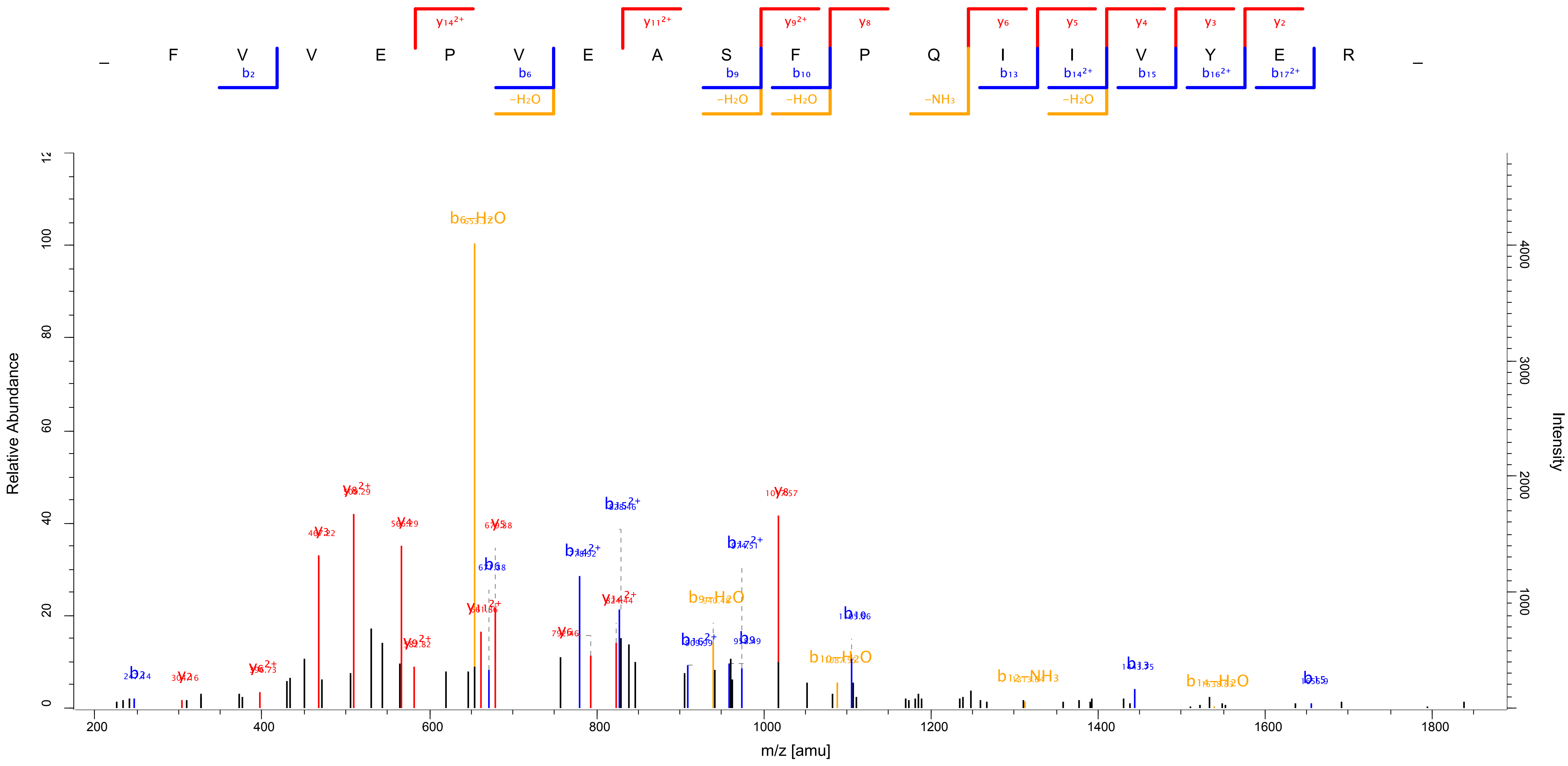
Mass:	1499.72048
m/z:	750.86752
Charge:	2+
Retentiontime:	122.459327697754
Score:	121.3605
Mass Error [ppm]:	-0.50079
PEP:	8.3486E-08
Precursor Type:	ISO

general information

Annotation:	11 of 13
AminoAcids Coverage:	85 %
Intensity Coverage:	18 %
Peak Coverage:	26 %
Protein Localisation:	41 ... 53

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096425825		114.09134045	1	I	12				
+0.016622	249.15975436	-0.1479551	277.15466899	2	Y	11	1386.838303		693.92278972	-0.0137931
	320.19686815	-0.0761212	348.19178277	3	A	10	1223.7749744	-0.1225086	612.39112545	-0.0945556
	417.249632		445.24454663	4	P	9	1152.7378606	-0.0156927	576.87256856	-0.0900368
	530.33369598	-0.0490696	558.32861061	5	I	8	1055.6850968		1055.6850968	
	693.39702452	+0.2837811	721.39193914	6	Y	7	942.60103282	-0.0191847	942.60103282	
	806.4810885		834.47600312	7	I	6	779.53770428	+0.0224154	779.53770428	
	919.56515248		947.5600671	8	I	5	666.4536403	-0.0417751	666.4536403	
	990.60226627		1018.5971809	9	A	4	553.36957632	+0.0540077	553.36957632	
	1061.6393801	-0.3326589	1089.6342947	10	A	3	482.33246253	+0.0783041	482.33246253	
	1174.723444	-0.2266594	1202.7183587	11	I	2	411.29534874	-0.0031124	411.29534874	
	1287.807508	+0.368842	1315.8024226	12	I	1	298.21128476	-0.0368463	298.21128476	
				13	R	0	185.12722078		185.12722078	

Scan number	18871	Raw file	20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel08
Method	ITMS; CID	Genenames	METTL22



precursor information

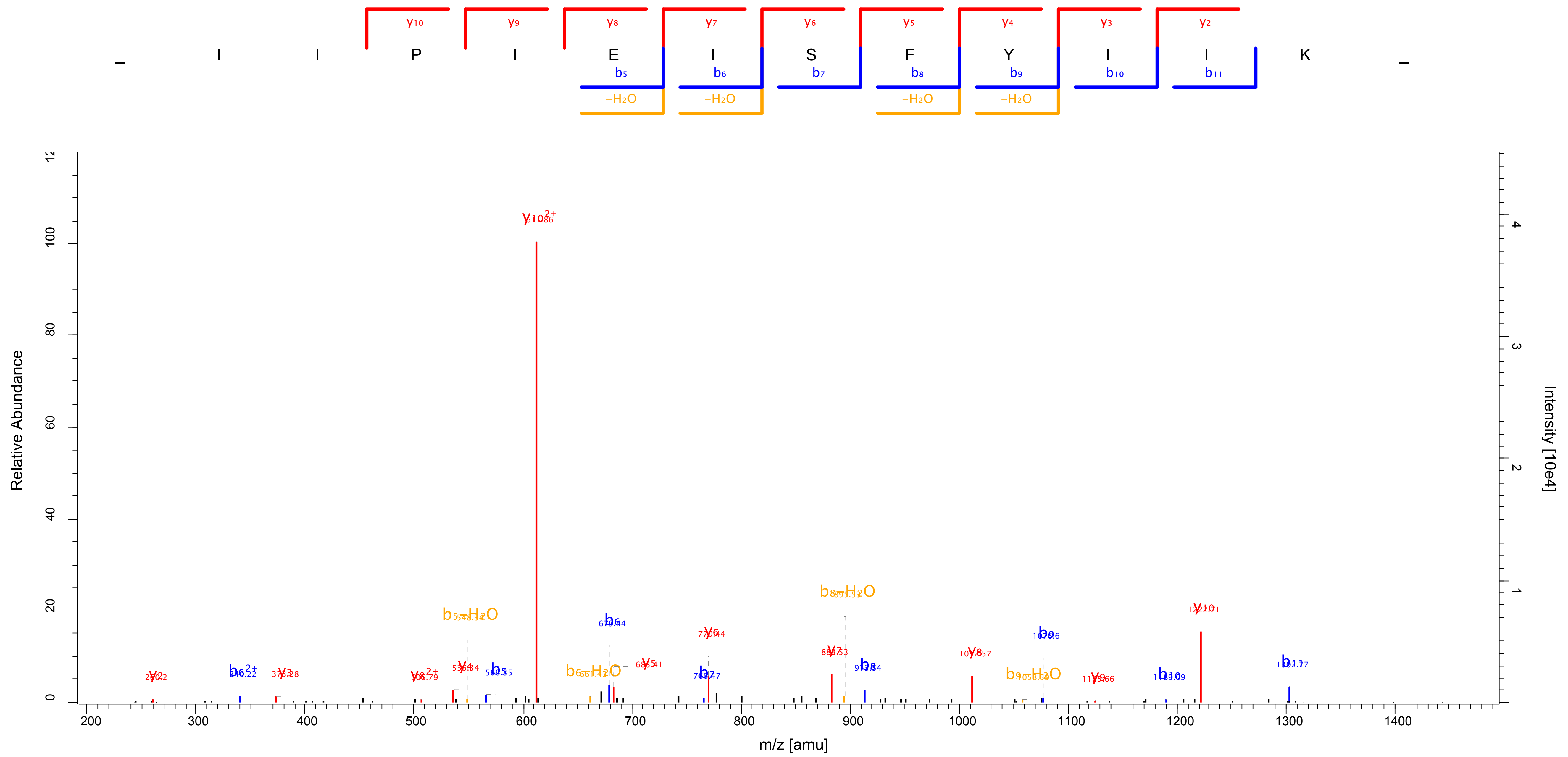
Mass:	2121.11554
m/z:	708.04579
Charge:	3+
Retentiontime:	112.175758361816
Score:	124.6202
Mass Error [ppm]:	0.42386
PEP:	1.3717E−07
Precursor Type:	MULTI

general information

Annotation:	13 of 18
AminoAcids Coverage:	72 %
Intensity Coverage:	62 %
Peak Coverage:	31 %
Protein Localisation:	372 ... 389

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.07569038		148.07569038	1	F	17				
	247.1441043	−0.1897586	247.1441043	2	V	16	1975.053505		1975.053505	
	346.21251822		346.21251822	3	V	15	1875.985091		1875.985091	
	475.25511131		475.25511131	4	E	14	1776.9166771		1776.9166771	
	572.30787516		572.30787516	5	P	13	1647.874084		824.44068025	+0.0185483
	671.37628908	−0.3071973	671.37628908	6	V	12	1550.8213202		1550.8213202	
	800.41888218		800.41888218	7	E	11	1451.7529063		1451.7529063	
	871.45599596		871.45599596	8	A	10	1322.7103132		661.85879482	+0.0164493
	958.48802437	+0.0016607	958.48802437	9	S	9	1251.6731994		1251.6731994	
	1105.5564383	−0.2037772	1105.5564383	10	F	8	1164.641171		582.82422372	−0.0076954
	1202.6092021		1202.6092021	11	P	7	1017.5727571	−0.0642121	509.29001676	+0.2328104
	1330.6677797		1330.6677797	12	Q	6	920.5199932		920.5199932	
	1443.7518436	+0.0518673	1443.7518436	13	I	5	792.46141569	+0.0691629	396.73434608	+0.0818771
+0.0425803	778.92159204		1556.8359076	14	I	4	679.37735171	+0.0136395	679.37735171	
−0.256092	828.455799	+0.164282	1655.9043215	15	V	3	566.29328773	+0.0806747	566.29328773	
−0.3434203	909.98746327		1818.9676501	16	Y	2	467.22487382	−0.0431111	467.22487382	
−0.0810865	974.50875982		1948.0102432	17	E	1	304.16154528	−0.134232	304.16154528	
				18	R	0	175.11895218		175.11895218	

Scan number	19957	Raw file	20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel08
Method	ITMS; CID	Genenames	FBXW2



precursor information

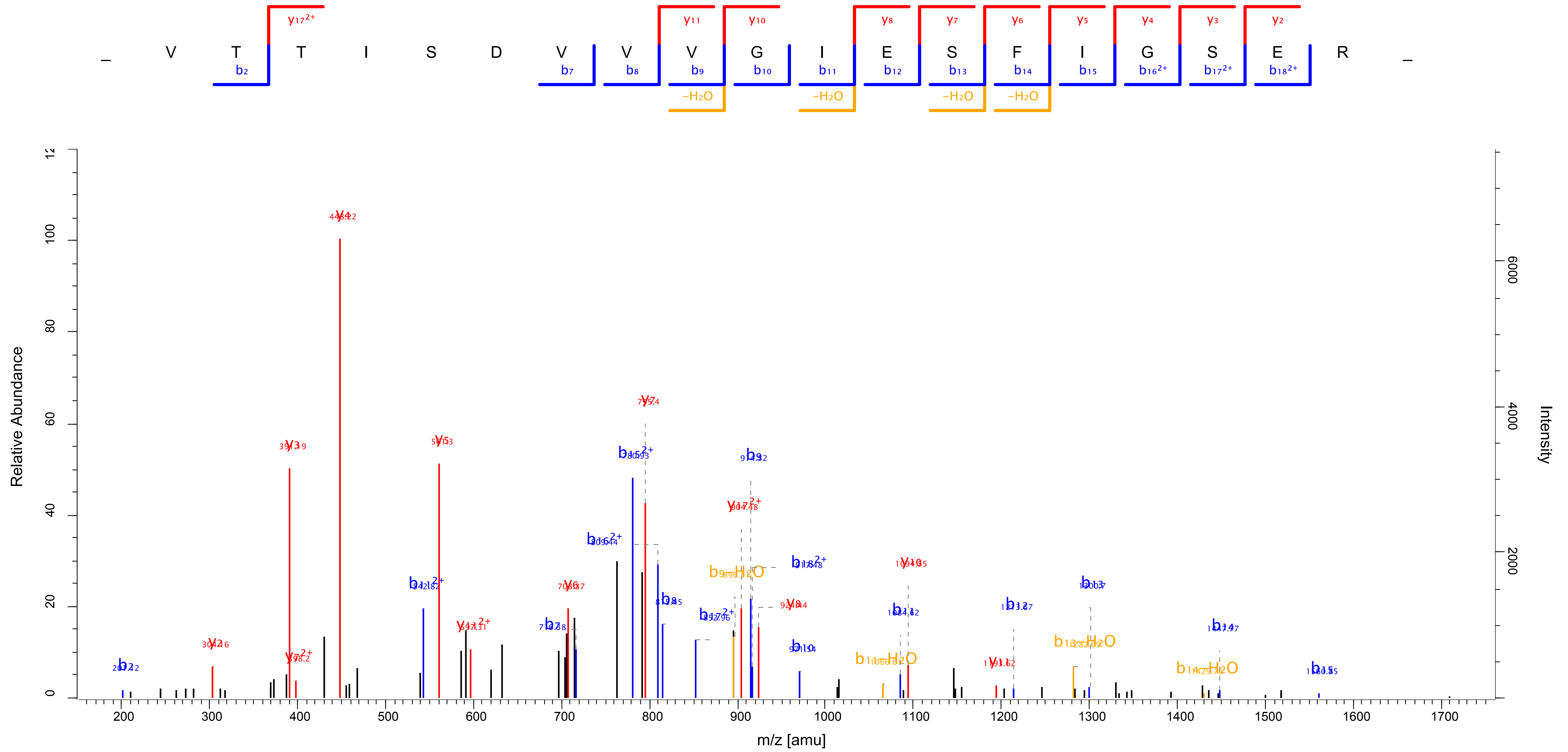
Mass:	1447.86943
m/z:	724.94199
Charge:	2+
Retentiontime:	118.374443054199
Score:	164.6517
Mass Error [ppm]:	0.27317
PEP:	1.5405E-05
Precursor Type:	ISO

general information

Annotation:	9 of 12
AminoAcids Coverage:	75 %
Intensity Coverage:	82 %
Peak Coverage:	31 %
Protein Localisation:	59 ... 70

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045		114.09134045	1	I	11				
	227.17540443		227.17540443	2	I	10	1335.7922519		1335.7922519	
	324.22816828		324.22816828	3	P	9	1222.7081879	-0.2744721	611.85773219	-0.0008596
	437.31223226		437.31223226	4	I	8	1125.6554241	+0.0198689	1125.6554241	
	566.35482536	+0.0361048	566.35482536	5	E	7	1012.5713601	-0.0906472	506.78931827	+0.3962896
-0.0661005	340.2230829	-0.0798805	679.43888934	6	I	6	883.52876698	+0.0159718	883.52876698	
	766.47091775	+0.0700368	766.47091775	7	S	5	770.444703	+0.0093986	770.444703	
	913.53933166	-0.2685797	913.53933166	8	F	4	683.41267459	+0.0532068	683.41267459	
	1076.6026602	-0.0264883	1076.6026602	9	Y	3	536.34426067	-0.1046366	536.34426067	
	1189.6867242	-0.1109185	1189.6867242	10	I	2	373.28093213	+0.1111577	373.28093213	
	1302.7707882	-0.0472774	1302.7707882	11	I	1	260.19686815	+0.1483772	260.19686815	
				12	K	0	147.11280417		147.11280417	

Scan number	20370	Raw file	20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel08
Method	ITMS; CID	Genenames	ELP4



precursor information

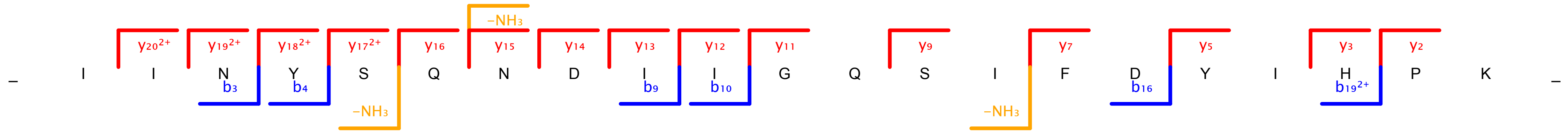
Mass:	2007.05357
m/z:	670.02513
Charge:	3+
Retentiontime:	120.760498046875
Score:	169.3689
Mass Error [ppm]:	0.5657
PEP:	6.7643E−22
Precursor Type:	MULTI

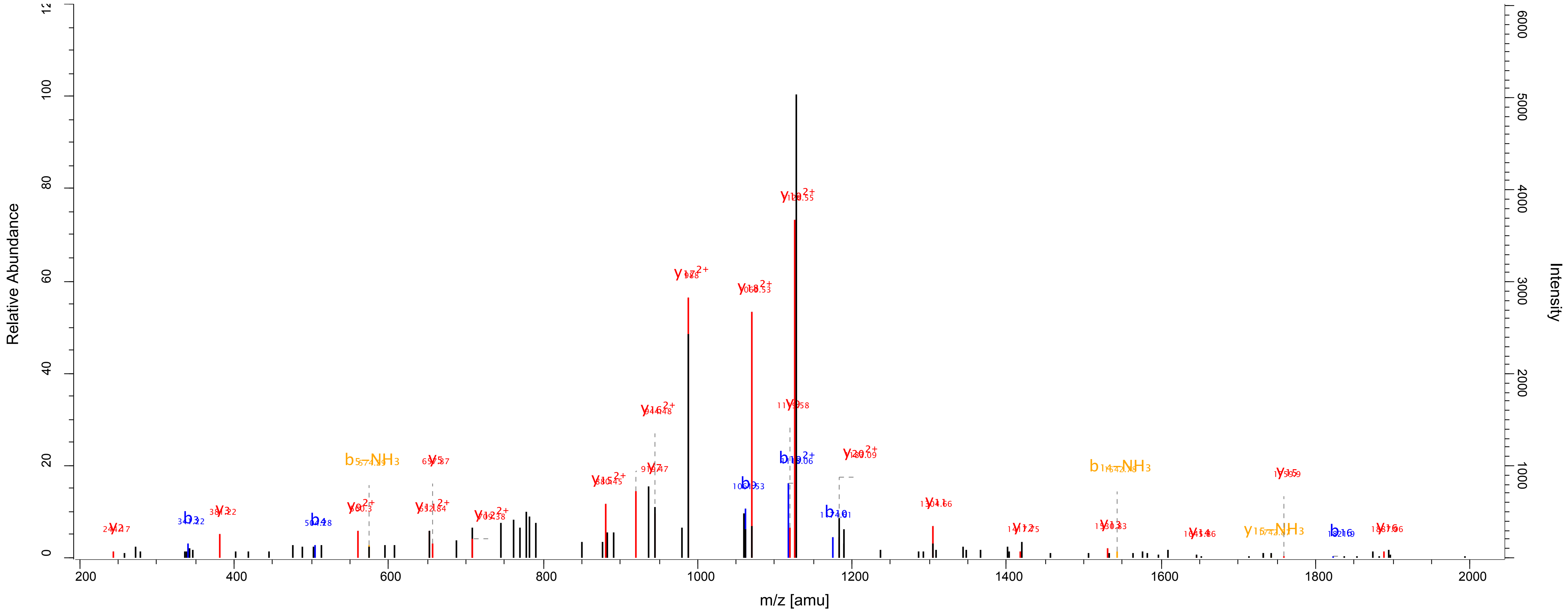
general information

Annotation:	14 of 19
AminoAcids Coverage:	74 %
Intensity Coverage:	66 %
Peak Coverage:	38 %
Protein Localisation:	317 ... 335

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.07569038		100.07569038	1	V	18				
	201.12336886	+0.0306228	201.12336886	2	T	17	1908.9912986		1908.9912986	
	302.17104733		302.17104733	3	T	16	1807.9436202		904.47544831	−0.2681119
	415.25511131		415.25511131	4	I	15	1706.8959417		1706.8959417	
	502.28713972		502.28713972	5	S	14	1593.8118777		1593.8118777	
	617.31408275		617.31408275	6	D	13	1506.7798493		1506.7798493	
	716.38249667	−0.0576676	716.38249667	7	V	12	1391.7529063		1391.7529063	
	815.45091059	−0.1388378	815.45091059	8	V	11	1292.6844923		1292.6844923	
	914.5193245	−0.0915291	914.5193245	9	V	10	1193.6160784	−0.1452532	597.31167745	+0.163115
	971.54078823	−0.1145797	971.54078823	10	G	9	1094.5476645	−0.1934165	1094.5476645	
+0.1803346	542.81606434	−0.3777819	1084.6248522	11	I	8	1037.5262008		1037.5262008	
	1213.6674453	−0.2723037	1213.6674453	12	E	7	924.44213681	+0.0449848	924.44213681	
	1300.6994737	−0.1883653	1300.6994737	13	S	6	795.39954372	+0.0275193	398.20341009	+0.2448321
	1447.7678876	−0.2318769	1447.7678876	14	F	5	708.36751531	−0.0246808	708.36751531	
−0.1974973	780.92961404	−0.39431	1560.8519516	15	I	4	561.29910139	−0.0433641	561.29910139	
−0.1615983	809.4403459		1617.8734153	16	G	3	448.21503741	+0.0439348	448.21503741	
−0.0228274	852.9563601		1704.9054437	17	S	2	391.19357369	+0.0688164	391.19357369	
+0.1196944	917.47765665		1833.9480368	18	E	1	304.16154528	−0.0696874	304.16154528	
				19	R	0	175.11895218		175.11895218	

Scan number	18717	Raw file	20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel13
Method	ITMS; CID	Genenames	ARNTL





precursor information

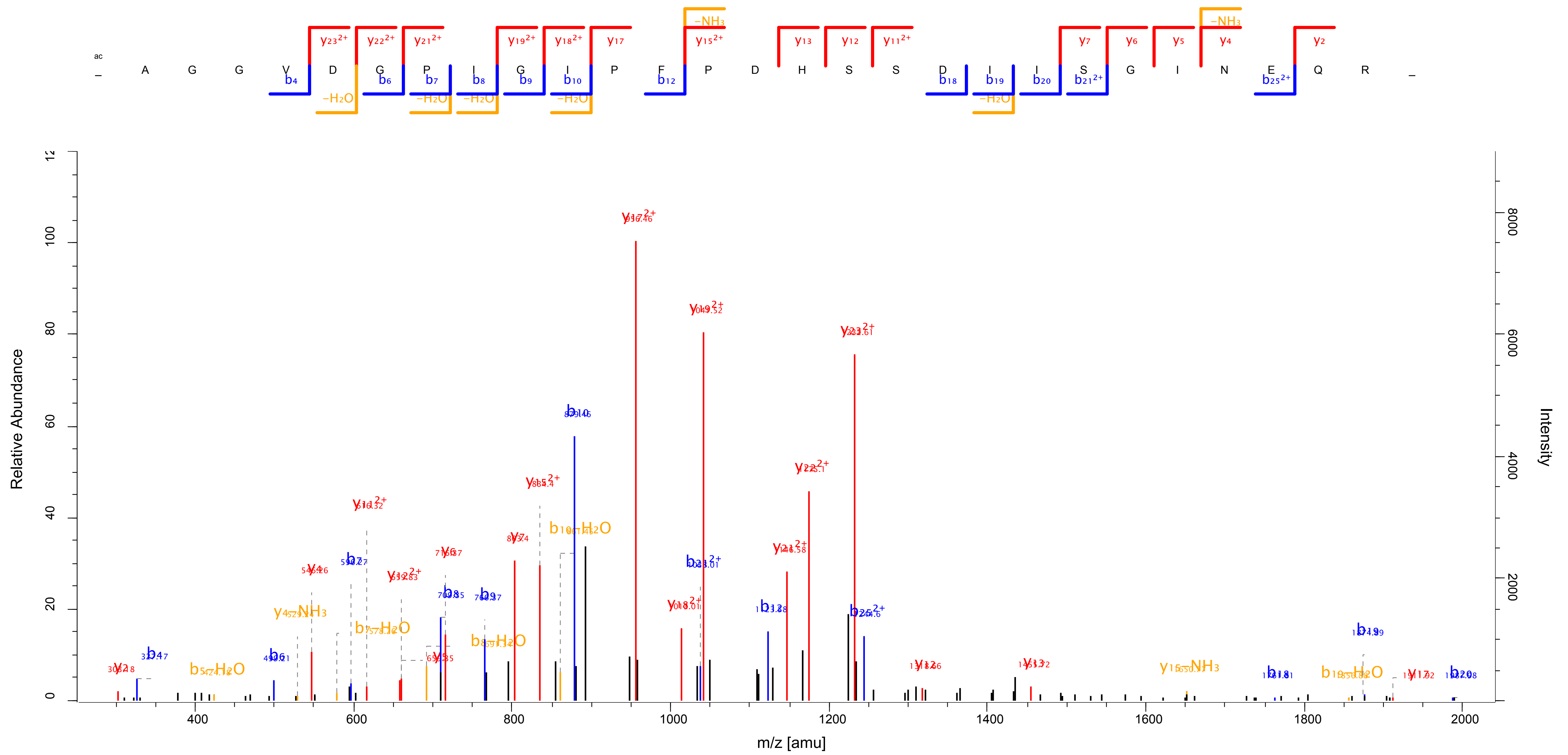
Mass:	2477.25931
m/z:	826.76038
Charge:	3+
Retentiontime:	109.367202758789
Score:	119.0757
Mass Error [ppm]:	0.094749
PEP:	3.9765E-07
Precursor Type:	ISO

general information

Annotation:	17 of 21
AminoAcids Coverage:	81 %
Intensity Coverage:	45 %
Peak Coverage:	28 %
Protein Localisation:	179 ... 199

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045		114.09134045	1	I	20				
	227.17540443		227.17540443	2	I	19	2365.1822873		1183.0947819	−0.0266667
	341.21833187	−0.0348602	341.21833187	3	N	18	2252.0982233		1126.5527499	−0.1215976
	504.28166041	−0.1900466	504.28166041	4	Y	17	2138.0552959		1069.5312862	+0.1715947
	591.31368882		591.31368882	5	S	16	1974.9919673		987.9996219	+0.0235715
	719.37226633		719.37226633	6	Q	15	1887.9599389	−0.2476587	944.4836077	−0.0393328
	833.41519378		833.41519378	7	N	14	1759.9013614	−0.2349796	880.45431894	+0.1648827
	948.44213681		948.44213681	8	D	13	1645.858434	−0.436681	1645.858434	
	1061.5262008	+0.0505814	1061.5262008	9	I	12	1530.8314909	+0.0896516	1530.8314909	
	1174.6102648	−0.2023058	1174.6102648	10	I	11	1417.747427	+0.1635838	709.37735171	−0.4877643
	1231.6317285		1231.6317285	11	G	10	1304.663363	−0.1133141	652.83531972	−0.1613085
	1359.690306		1359.690306	12	Q	9	1247.6418993		1247.6418993	
	1446.7223344		1446.7223344	13	S	8	1119.5833217	−0.2175991	560.2952991	+0.0025525
	1559.8063984		1559.8063984	14	I	7	1032.5512933		1032.5512933	
	1706.8748123		1706.8748123	15	F	6	919.46722935	−0.1574759	919.46722935	
	1821.9017553	−0.01052	1821.9017553	16	D	5	772.39881544		772.39881544	
	1984.9650839		1984.9650839	17	Y	4	657.3718724	+0.0039211	657.3718724	
	2098.0491479		2098.0491479	18	I	3	494.30854387		494.30854387	
+0.2868143	1118.0576681		2235.1080597	19	H	2	381.22447988	−0.0540392	381.22447988	
	2332.1608236		2332.1608236	20	P	1	244.16556802	+0.0218709	244.16556802	
				21	K	0	147.11280417		147.11280417	

Scan number 19432
Raw file 20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel13
Method ITMS; CID
Genenames ZBTB7A



precursor
information

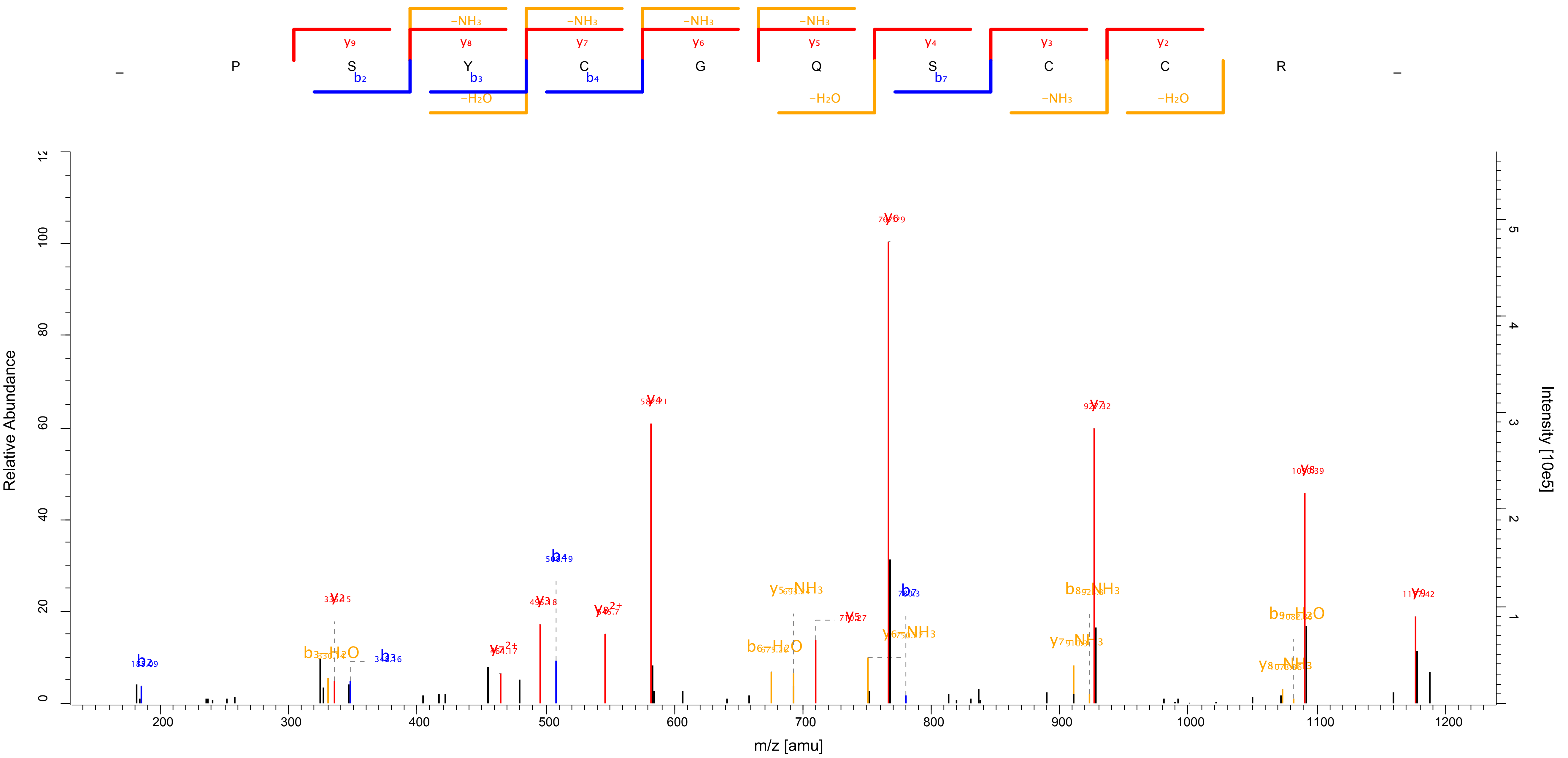
Mass:	2789.36162
m/z:	930.79448
Charge:	3+
Retentiontime:	113.483551025391
Score:	154.8418
Mass Error [ppm]:	-0.14787
PEP:	2.4358E-28
Precursor Type:	ISO

general
information

Annotation:	22 of 27
AminoAcids Coverage:	81 %
Intensity Coverage:	71 %
Peak Coverage:	35 %
Protein Localisation:	2 ... 28

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.05495494		114.05495494	1	A	26				
	171.07641866		171.07641866	2	G	25	2677.3216343		2677.3216343	
	228.09788239		228.09788239	3	G	24	2620.3001706		2620.3001706	
	327.1662963	-0.0167602	327.1662963	4	V	23	2563.2787069		2563.2787069	
	442.19323934		442.19323934	5	D	22	2464.210293		1232.6087847	+0.2127485
	499.21470306	-0.2193417	499.21470306	6	G	21	2349.1833499		1175.0953132	+0.2552727
	596.26746691	-0.0777086	596.26746691	7	P	20	2292.1618862		1146.5845813	+0.2028942
	709.35153089	-0.2129201	709.35153089	8	I	19	2195.1091224		2195.1091224	
	766.37299462	-0.0414516	766.37299462	9	G	18	2082.0250584		1041.5161674	+0.1897652
	879.4570586	-0.2608306	879.4570586	10	I	17	2025.0035947		1013.0054356	+0.1984219
	976.50982245		976.50982245	11	P	16	1911.9195307	+0.3678228	956.46340357	+0.1066038
	1123.5782364	-0.25475	1123.5782364	12	F	15	1814.8667668		1814.8667668	
	1220.6310002		1220.6310002	13	P	14	1667.7983529		834.40281469	+0.278948
	1335.6579432		1335.6579432	14	D	13	1570.7455891		1570.7455891	
	1472.7168551		1472.7168551	15	H	12	1455.718646	-0.2035093	1455.718646	
	1559.7488835		1559.7488835	16	S	11	1318.6597342	-0.0775808	659.83350531	-0.0947968
	1646.7809119		1646.7809119	17	S	10	1231.6277058		616.31749111	-0.1277328
	1761.807855	-0.0122007	1761.807855	18	D	9	1144.5956773		1144.5956773	
	1874.8919189	+0.1527588	1874.8919189	19	I	8	1029.5687343		1029.5687343	
	1987.9759829	-0.2778628	1987.9759829	20	I	7	916.48467033		916.48467033	
+0.3197487	1038.0076439		2075.0080113	21	S	6	803.40060635	+0.0516031	803.40060635	
	2132.0294751		2132.0294751	22	G	5	716.36857794	+0.0429211	716.36857794	
	2245.113539		2245.113539	23	I	4	659.34711422	-0.353706	659.34711422	
	2359.1564665		2359.1564665	24	N	3	546.26305024	+0.0991934	546.26305024	
+0.1038632	1244.603168		2488.1990596	25	E	2	432.22012279		432.22012279	
	2616.2576371		2616.2576371	26	Q	1	303.17752969	-0.1451811	303.17752969	
				27	R	0	175.11895218		175.11895218	

Scan number	2185	Raw file	20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel14
Method	ITMS; CID	Genenames	KRTAP1-1;KRTAP1-3;KRTAP1-5;KRTAP1-4



precursor information

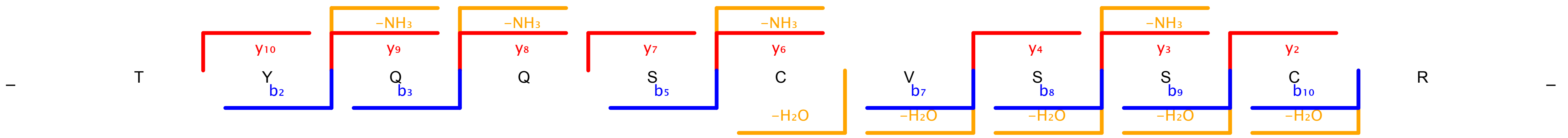
Mass:	1273.46157
m/z:	637.73806
Charge:	2+
Retentiontime:	20.0628414154053
Score:	155.4204
Mass Error [ppm]:	-1.7584
PEP:	0.0002907
Precursor Type:	ISO

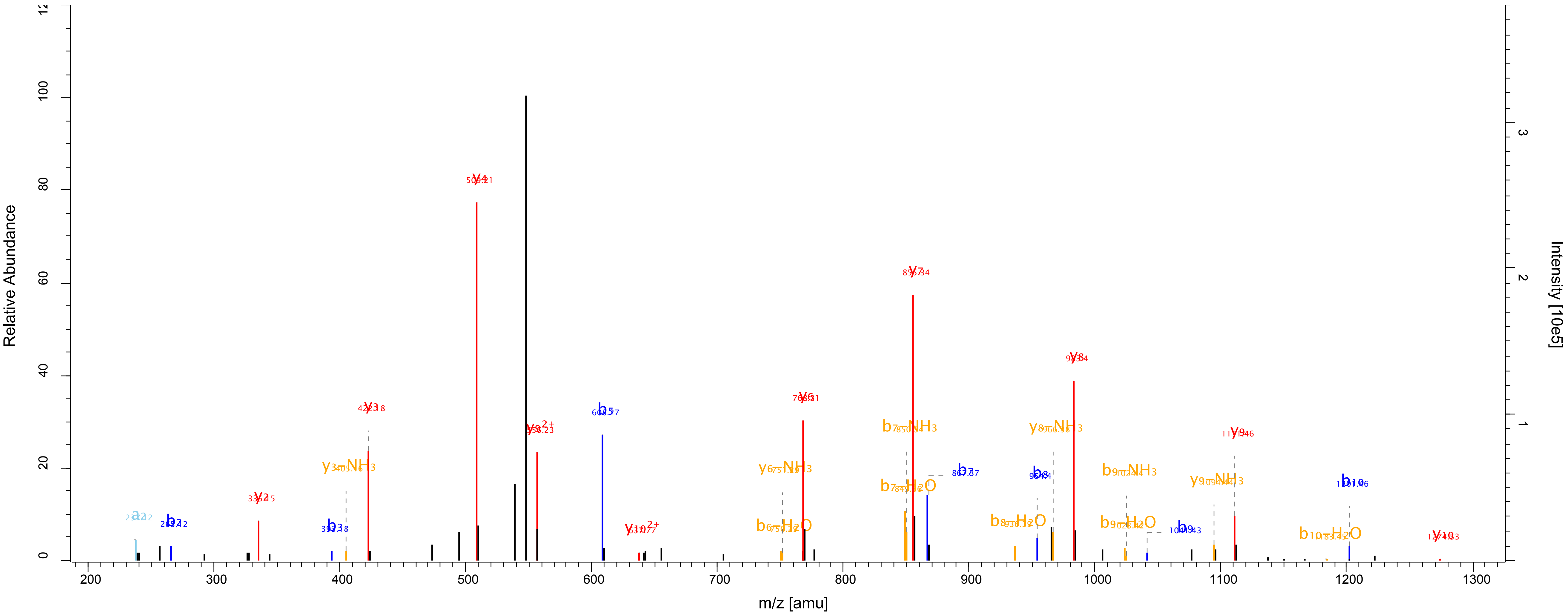
general information

Annotation:	8 of 10
AminoAcids Coverage:	80 %
Intensity Coverage:	70 %
Peak Coverage:	34 %
Protein Localisation:	156 ... 165

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	98.060040319	1	P	9				
+0.1286039	185.092068728	2	S	8	1177.418323378	−0.183216	1177.418323378	
−0.0275896	348.155397267	3	Y	7	1090.386294968	−0.0897862	545.696785718	+0.3048012
+0.0399677	508.186045468	4	C	6	927.32296643	−0.0978688	464.165121448	+0.2620636
	565.207509192	5	G	5	767.292318229	−0.047079	767.292318229	
	693.266086703	6	Q	4	710.270854505	−0.0030933	710.270854505	
−0.0957225	780.298115113	7	S	3	582.212276994	+0.0214877	582.212276994	
	940.328763315	8	C	2	495.180248584	+0.0004765	495.180248584	
	1100.359411516	9	C	1	335.149600382	+0.0334135	335.149600382	
		10	R	0	175.118952181		175.118952181	

Scan number	2420	Raw file	20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel14
Method	ITMS; CID	Genenames	KRTAP11-1





precursor information

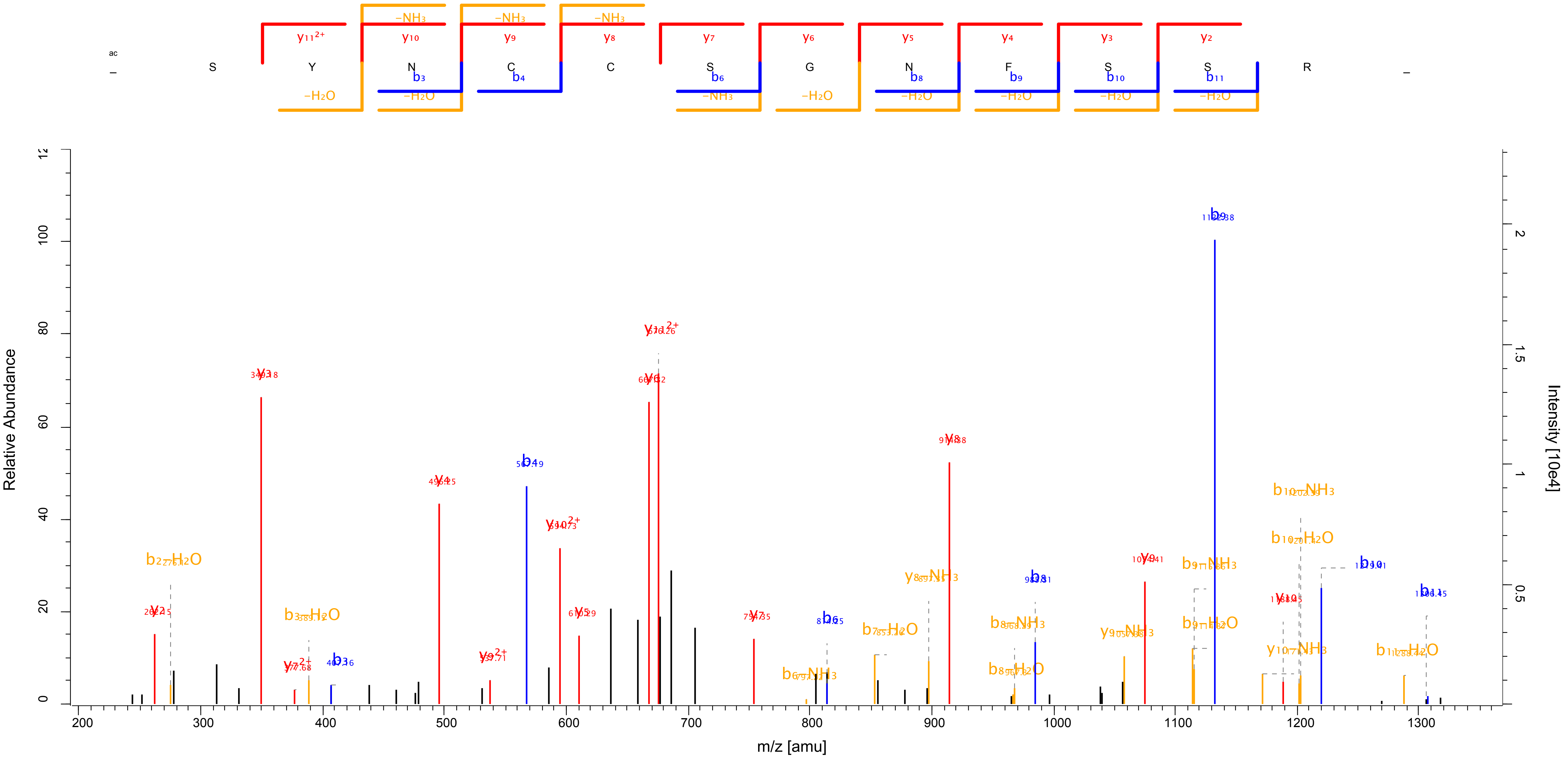
Mass:	1374.56497
m/z:	688.28976
Charge:	2+
Retentiontime:	21.2794799804688
Score:	208.5564
Mass Error [ppm]:	−0.47978
PEP:	4.9486E−06
Precursor Type:	ISO

general information

Annotation:	9 of 11
AminoAcids Coverage:	82 %
Intensity Coverage:	63 %
Peak Coverage:	45 %
Protein Localisation:	150 ... 160

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.060040319		102.05495494	1	T	10				
+0.113417	237.12336886	−0.0486118	265.11828348	2	Y	9	1274.5252313	+0.1421271	637.76625388	+0.0731626
	365.18194637	+0.1309393	393.17686099	3	Q	8	1111.4619028	−0.0479623	556.23458961	−0.0383616
	493.24052388		521.2354385	4	Q	7	983.40332524	−0.1931812	983.40332524	
	580.27255229	−0.0082506	608.26746691	5	S	6	855.34474773	−0.0113127	855.34474773	
	740.30320049		768.29811511	6	C	5	768.31271932	+0.0846806	768.31271932	
	839.37161441	−0.1414314	867.36652903	7	V	4	608.28207112		608.28207112	
	926.40364282	−0.1317728	954.39855744	8	S	3	509.2136572	−0.0503882	509.2136572	
	1013.4356712	−0.1554394	1041.4305858	9	S	2	422.18162879	+0.0955929	422.18162879	
	1173.4663194	−0.0846471	1201.4612341	10	C	1	335.14960038	+0.1316496	335.14960038	
				11	R	0	175.11895218		175.11895218	

Scan number	5866	Raw file	20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel14
Method	ITMS; CID	Genenames	KRTAP13-2;KRTAP13-1



precursor information

Mass:	1479.55007
m/z:	740.78231
Charge:	2+
Retentiontime:	39.1498641967773
Score:	248.0509
Mass Error [ppm]:	-0.43686
PEP:	1.6156E-27
Precursor Type:	ISO

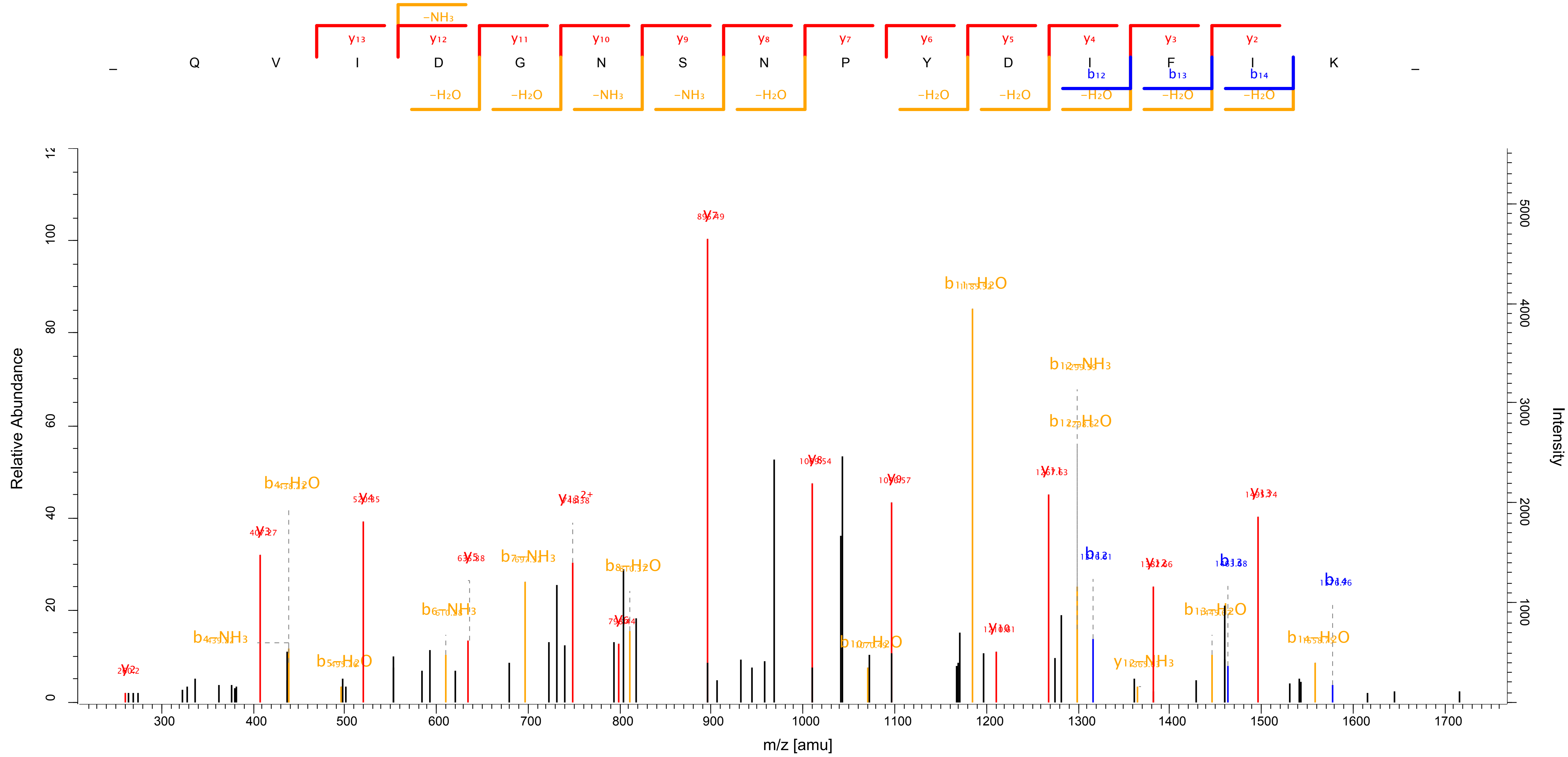
general information

Annotation:	10 of 12
AminoAcids Coverage:	83 %
Intensity Coverage:	78 %
Peak Coverage:	53 %
Protein Localisation:	2 ... 13

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.049869563	1	S	11				
	293.113198101	2	Y	10	1351.515394886		676.261335676	+0.029741
-0.0355811	407.156125548	3	N	9	1188.452066348	+0.0594083	594.729671407	+0.1657143
-0.0384583	567.18677375	4	C	8	1074.409138901	-0.0021565	537.708207684	+0.1177811
	727.217421951	5	C	7	914.378490699	+0.0801885	914.378490699	
+0.1593631	814.249450361	6	S	6	754.347842498	+0.102658	377.677559482	-0.4847494
	871.270914085	7	G	5	667.315814088	+0.2010927	667.315814088	
-0.1488635	985.313841532	8	N	4	610.294350364	+0.0273049	610.294350364	
-0.1469039	1132.382255448	9	F	3	496.251422917	-0.0650826	496.251422917	
-0.1878434	1219.414283858	10	S	2	349.183009001	+0.0592395	349.183009001	
+0.2883069	1306.446312268	11	S	1	262.150980591	+0.1037191	262.150980591	
		12	R	0	175.118952181		175.118952181	

Scan number 15593 Raw file 20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel15

Method ITMS; CID Genenames DDR2



precursor information

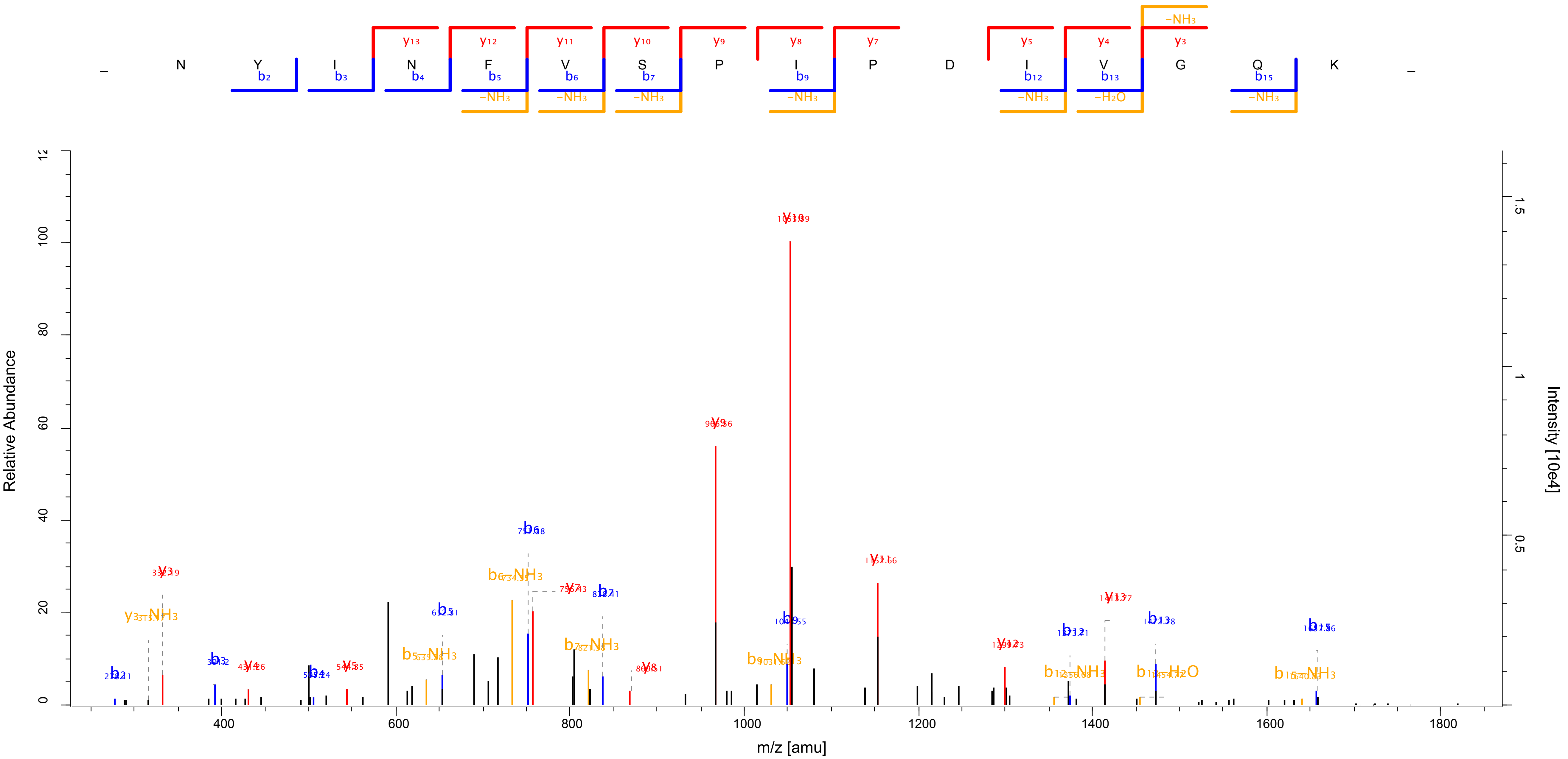
Mass:	1721.86232
m/z:	861.93844
Charge:	2+
Retentiontime:	90.8092498779297
Score:	106.5776
Mass Error [ppm]:	-0.075638
PEP:	0.0001055
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverage:	87 %
Intensity Coverage:	55 %
Peak Coverage:	35 %
Protein Localisation:	139 ... 153

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.065853978	1	Q	14				
	228.134267894	2	V	13	1594.811149426		1594.811149426	
	341.218331875	3	I	12	1495.74273551	−0.191588	748.375005988	−0.0914367
	456.245274907	4	D	11	1382.65867153	−0.0127975	1382.65867153	
	513.26673863	5	G	10	1267.631728498	−0.1389306	1267.631728498	
	627.309666077	6	N	9	1210.610264774	+0.0411024	1210.610264774	
	714.341694487	7	S	8	1096.567337327	−0.104935	1096.567337327	
	828.384621934	8	N	7	1009.535308917	−0.0672913	1009.535308917	
	925.437385786	9	P	6	895.49238147	+0.0361219	895.49238147	
	1088.500714325	10	Y	5	798.439617618	−0.101788	798.439617618	
	1203.527657357	11	D	4	635.37628908	−0.2465283	635.37628908	
+0.0716283	1316.611721337	12	I	3	520.349346048	−0.0981864	520.349346048	
−0.2403159	1463.680135253	13	F	2	407.265282067	−0.0309681	407.265282067	
+0.2337256	1576.764199234	14	I	1	260.196868151	+0.22873	260.196868151	
		15	K	0	147.112804171		147.112804171	

Scan number	17894	Raw file	20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel15
Method	ITMS; CID	Genenames	ZNF281



precursor information

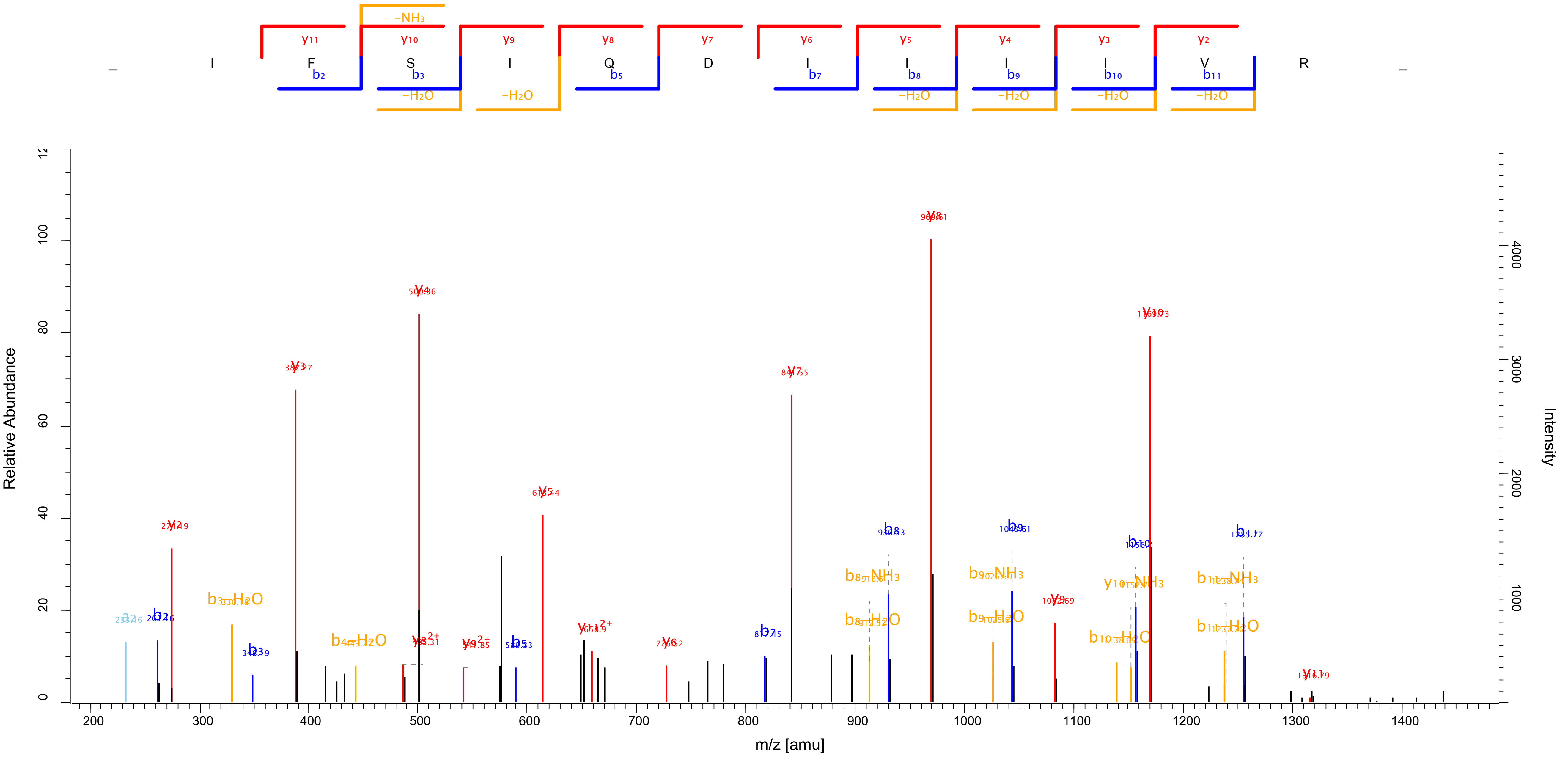
Mass:	1802.95456
m/z:	902.48456
Charge:	2+
Retentiontime:	103.74476235352
Score:	160.7796
Mass Error [ppm]:	−1.1787
PEP:	7.7251E−08
Precursor Type:	ISO

general information

Annotation:	13 of 16
AminoAcids Coverage:	81 %
Intensity Coverage:	57 %
Peak Coverage:	31 %
Protein Localisation:	478 ... 493

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	115.050203914	1	N	15		
−0.1672434	278.113532452	2	Y	14	1689.921034227	
+0.0933582	391.197596432	3	I	13	1526.857705688	
−0.1707607	505.24052388	4	N	12	1413.773641708	−0.1961271
−0.0201194	652.308937796	5	F	11	1299.730714261	−0.0577406
+0.0708294	751.377351712	6	V	10	1152.662300345	−0.1820757
−0.0280935	838.409380122	7	S	9	1053.593886429	−0.058486
	935.462143974	8	P	8	966.561858019	−0.0682057
−0.1756025	1048.546207954	9	I	7	869.509094167	−0.1718139
	1145.598971806	10	P	6	756.425030186	−0.0745053
	1260.625914838	11	D	5	659.372266334	
+0.4583561	1373.709978819	12	I	4	544.345323302	−0.2000596
−0.1889152	1472.778392735	13	V	3	431.261259322	−0.1186812
	1529.799856459	14	G	2	332.192845406	−0.0559436
−0.2162221	1657.85843397	15	Q	1	275.171381682	
		16	K	0	147.112804171	

Scan number	20767	Raw file	20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel16
Method	ITMS; CID	Genenames	NARG2



precursor
information

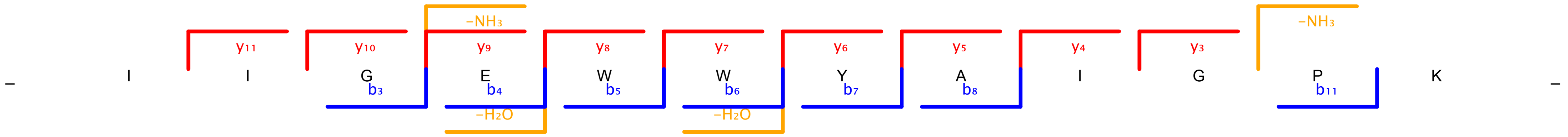
Mass:	1428.87073
m/z:	715.44264
Charge:	2+
Retentiontime:	122.493949890137
Score:	224.6584
Mass Error [ppm]:	0.20659
PEP:	3.1998E−14
Precursor Type:	ISO

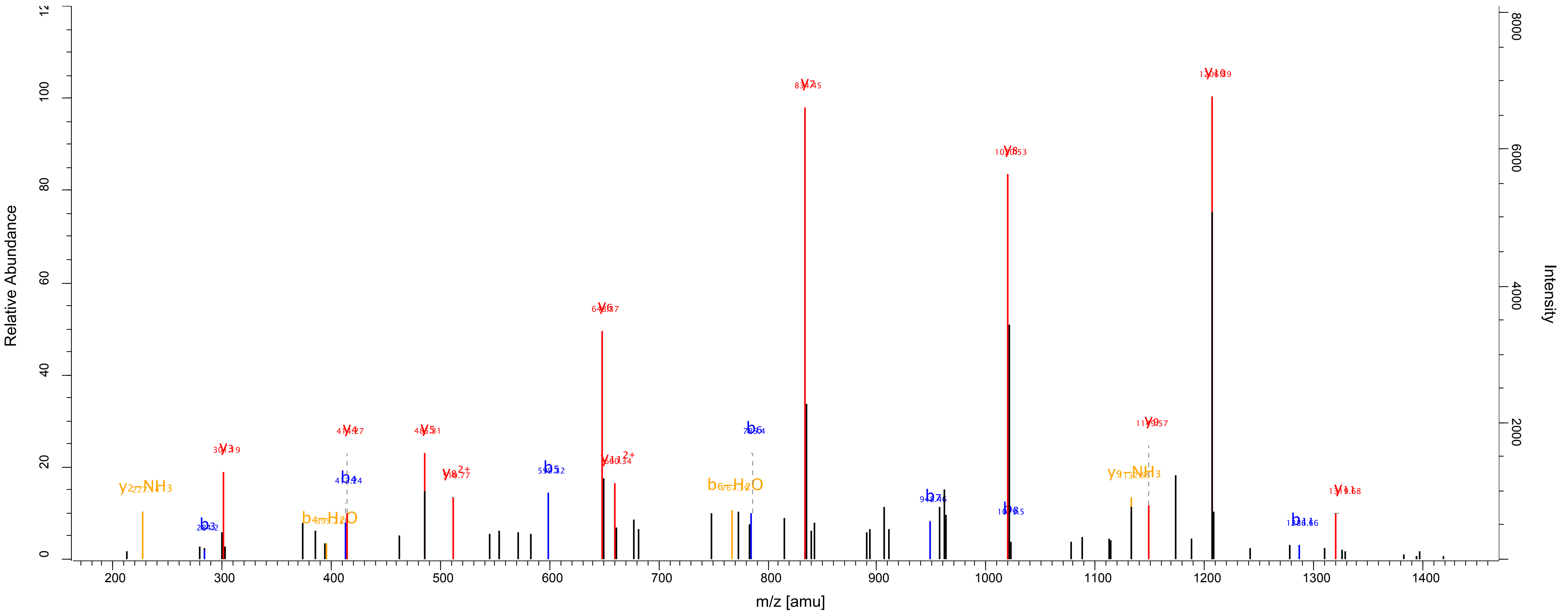
general
information

Annotation:	10 of 12
AminoAcids Coverage:	83 %
Intensity Coverage:	69 %
Peak Coverage:	45 %
Protein Localisation:	734 ... 745

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096425825		114.09134045	1	I	11				
+0.0601053	233.16483974	−0.110499	261.15975436	2	F	10	1316.7936489	−0.066476	658.90046267	+0.0220837
	320.19686815	−0.1472576	348.19178277	3	S	9	1169.725235	−0.0650787	1169.725235	
	433.28093213		461.27584675	4	I	8	1082.6932065	+0.062897	541.8502415	−0.2638768
	561.33950964	−0.1084111	589.33442426	5	Q	7	969.60914256	+0.0483892	485.30820951	+0.3616513
	676.36645267		704.3613673	6	D	6	841.55056505	−0.0702794	841.55056505	
	789.45051666	−0.0737882	817.44543128	7	I	5	726.52362202	+0.2112413	726.52362202	
	902.53458064	−0.2328644	930.52949526	8	I	4	613.43955804	−0.0229931	613.43955804	
	1015.6186446	−0.2528415	1043.6135592	9	I	3	500.35549406	−0.0657602	500.35549406	
	1128.7027086	−0.2280187	1156.6976232	10	I	2	387.27143008	−0.0570746	387.27143008	
	1227.7711225	−0.2820283	1255.7660371	11	V	1	274.1873661	+0.095837	274.1873661	
				12	R	0	175.11895218		175.11895218	

Scan number	17585	Raw file	20091019_Orbi6_MaHe_SA_ADH_exp3_12h_Gel18
Method	ITMS; CID	Genenames	CIC





precursor information

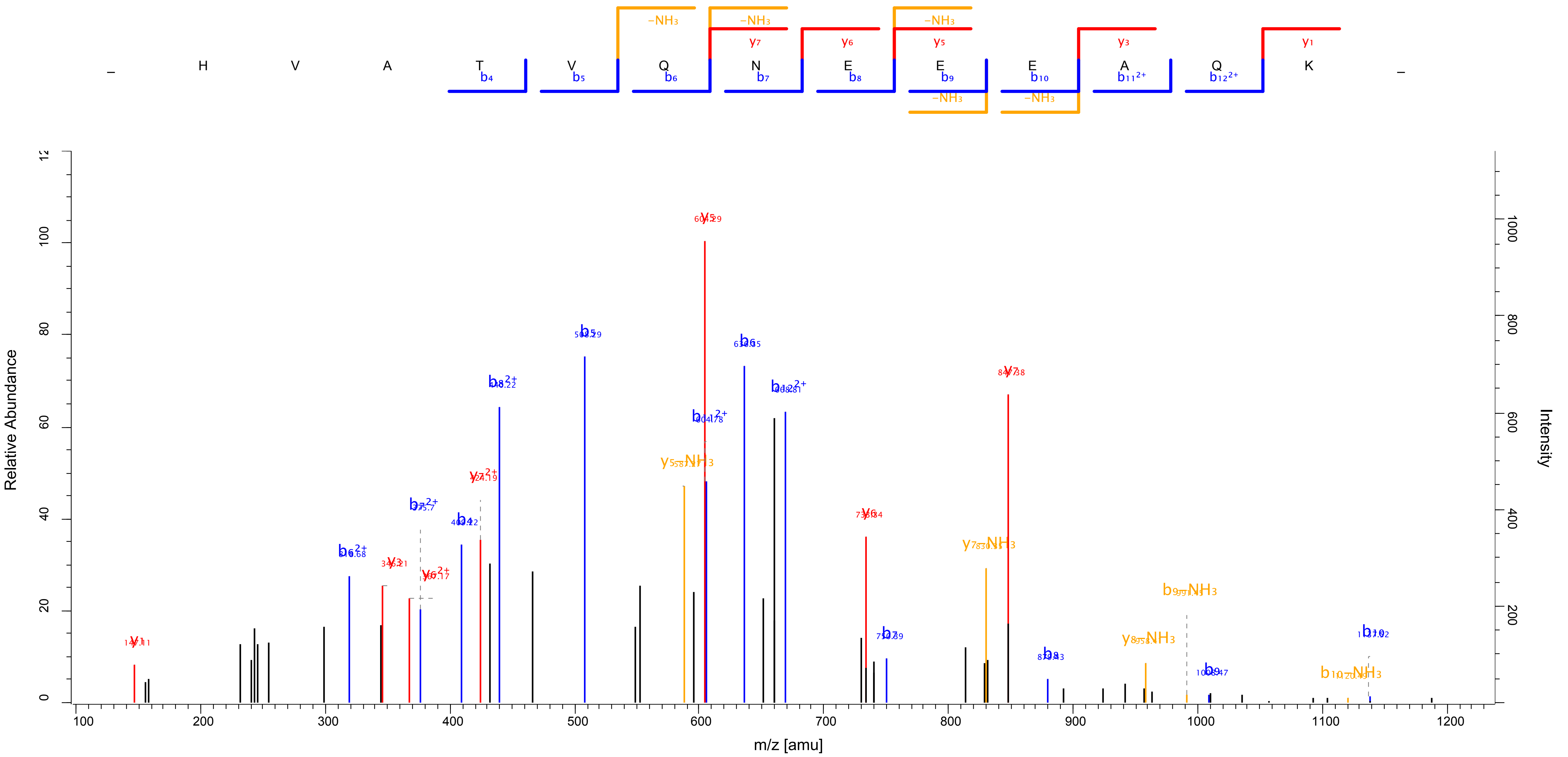
Mass:	1431.75704
m/z:	716.8858
Charge:	2+
Retentiontime:	102.822982788086
Score:	145.5543
Mass Error [ppm]:	1.3762
PEP:	6.3075E-05
Precursor Type:	ISO

general information

Annotation:	10 of 12
AminoAcids Coverage:	83 %
Intensity Coverage:	52 %
Peak Coverage:	29 %
Protein Localisation:	233 ... 244

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.091340447	1	I	11				
	227.175404427	2	I	10	1319.67828476	+0.2307729	660.342780613	−0.2070384
+0.0456245	284.196868151	3	G	9	1206.59422078	−0.1409737	1206.59422078	
+0.0450847	413.239461247	4	E	8	1149.572757056	−0.1232942	1149.572757056	
−0.0075559	599.318774201	5	W	7	1020.53016396	−0.1399662	510.768720213	+0.2303032
−0.0872961	785.398087154	6	W	6	834.450851006	−0.0486904	834.450851006	
+0.2266336	948.461415692	7	Y	5	648.371538053	−0.0262622	648.371538053	
−0.2326603	1019.49852948	8	A	4	485.308209514	−0.1377383	485.308209514	
	1132.582593461	9	I	3	414.271095727	−0.0103535	414.271095727	
	1189.604057184	10	G	2	301.187031746	+0.09373	301.187031746	
−0.3330906	1286.656821036	11	P	1	244.165568023		244.165568023	
		12	K	0	147.112804171		147.112804171	

Scan number	4445	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel01
Method	ITMS; CID	Genenames	C1orf21



precursor information

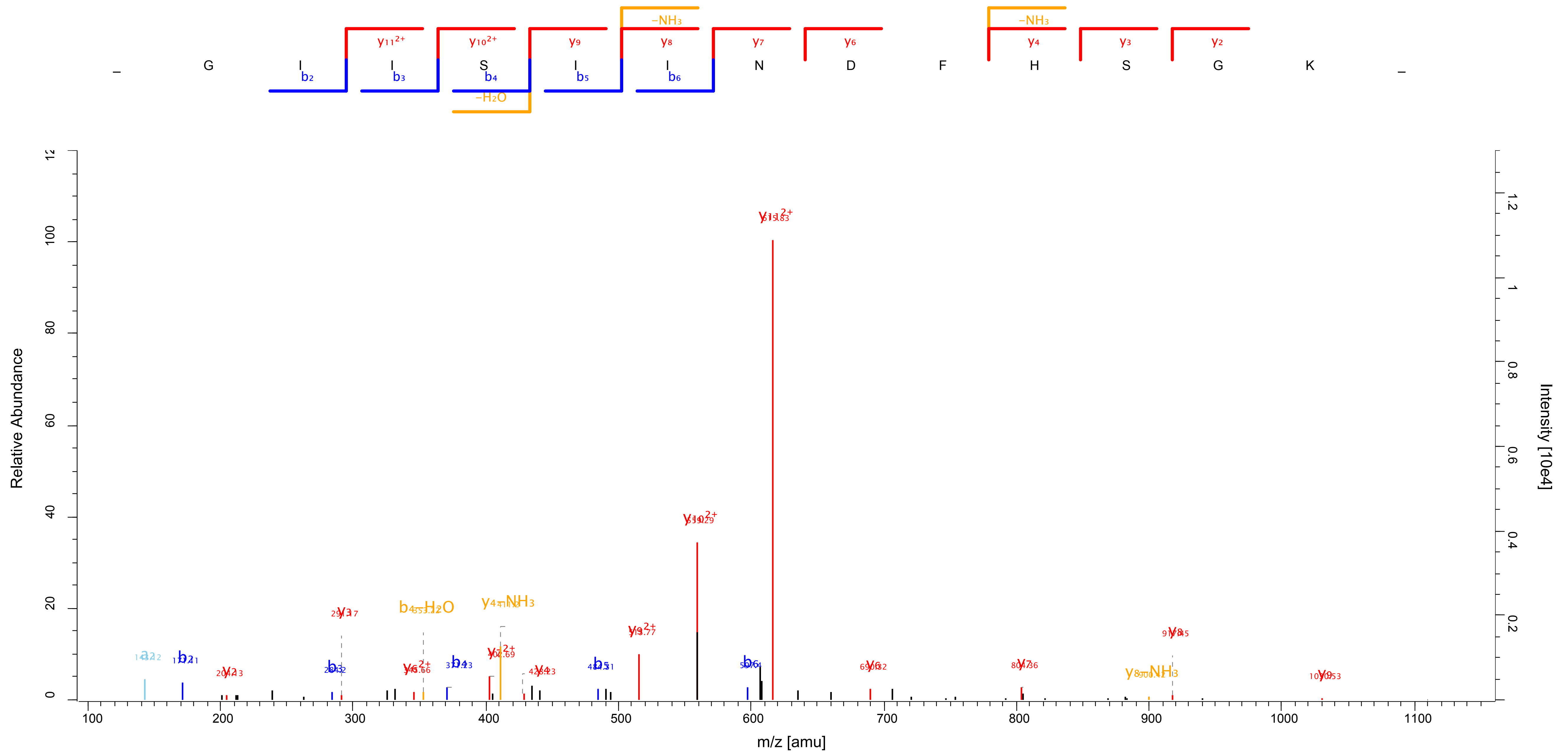
Mass:	1481.71083
m/z:	494.91089
Charge:	3+
Retentiontime:	37.2769241333008
Score:	142.0965
Mass Error [ppm]:	−0.13735
PEP:	5.3386E−05
Precursor Type:	ISO

general information

Annotation:	10 of 13
AminoAcids Coverage:	77 %
Intensity Coverage:	65 %
Peak Coverage:	39 %
Protein Localisation:	8 ... 20

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.06618833		138.06618833	1	H	12				
	237.13460225		237.13460225	2	V	11	1345.6593998		1345.6593998	
	308.17171603		308.17171603	3	A	10	1246.5909859		1246.5909859	
	409.21939451	−0.1096838	409.21939451	4	T	9	1175.5538721		1175.5538721	
	508.28780842	−0.0415011	508.28780842	5	V	8	1074.5061936		1074.5061936	
+0.1453124	318.6768312	+0.023365	636.34638593	6	Q	7	975.43777972		975.43777972	
+0.2976157	375.69829492	−0.1877753	750.38931338	7	N	6	847.37920221	−0.0401519	424.19323934	−0.0002767
−0.0948966	440.21959147	+0.0027249	879.43190648	8	E	5	733.33627476	−0.0534989	367.17177561	−0.1043012
	1008.4744996	−0.1103028	1008.4744996	9	E	4	604.29368166	−0.1100269	604.29368166	
	1137.5170927	+0.1846896	1137.5170927	10	E	3	475.25108857		475.25108857	
+0.383321	604.78074146		1208.5542065	11	A	2	346.20849547	+0.0199591	346.20849547	
+0.0830972	668.81003022		1336.612784	12	Q	1	275.17138168		275.17138168	
				13	K	0	147.11280417	+0.1090586	147.11280417	

Scan number	15146	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel03
Method	ITMS; CID	Genenames	CCDC28A



precursor information

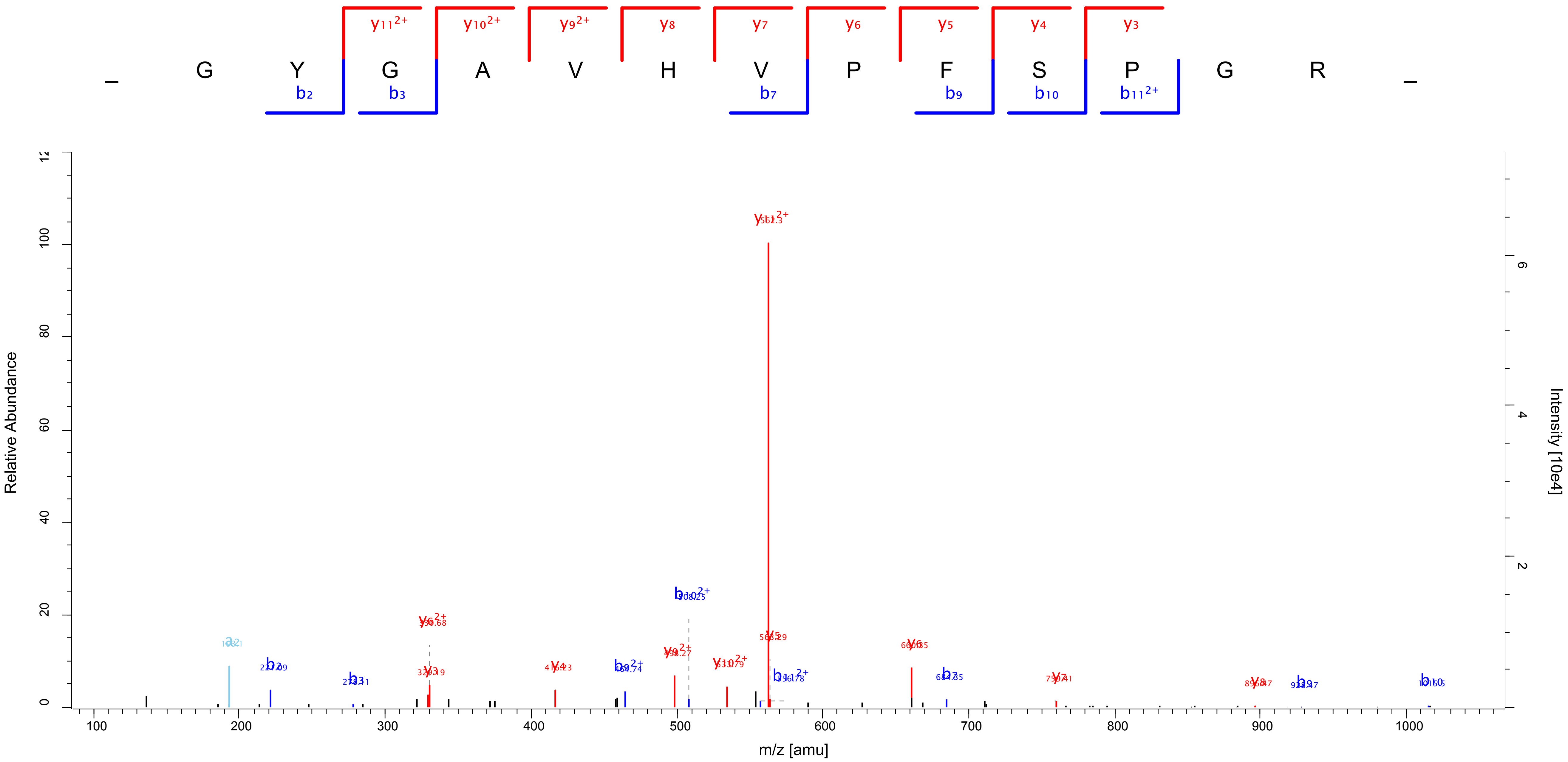
Mass:	1399.74579
m/z:	467.58921
Charge:	3+
Retentiontime:	91.6504745483398
Score:	130.006
Mass Error [ppm]:	−0.1251
PEP:	0.00027504
Precursor Type:	ISO

general information

Annotation:	10 of 13
AminoAcids Coverage:	77 %
Intensity Coverage:	76 %
Peak Coverage:	42 %
Protein Localisation:	181 ... 193

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	30.033825568		58.02874019	1	G	12				
−0.0309602	143.11788955	−0.1725423	171.11280417	2	I	11	1343.7317769		1343.7317769	
	256.20195353	−0.2801201	284.19686815	3	I	10	1230.6477129		615.82749469	+0.138997
	343.23398194	−0.1995387	371.22889656	4	S	9	1117.5636489		559.2854627	+0.0158679
	456.31804592	−0.1671781	484.31296054	5	I	8	1030.5316205	−0.1920209	515.76944849	+0.1219089
	569.4021099	+0.1544281	597.39702452	6	I	7	917.44755654	−0.0911723	917.44755654	
	683.44503735		711.43995197	7	N	6	804.36349256	−0.2143837	402.68538451	+0.1918433
	798.47198038		826.466895	8	D	5	690.32056511	−0.0834435	345.66392079	+0.1528212
	945.5403943		973.53530892	9	F	4	575.29362208		575.29362208	
	1082.5993062		1110.5942208	10	H	3	428.22520817	+0.1388971	428.22520817	
	1169.6313346		1197.6262492	11	S	2	291.1662963	+0.1573121	291.1662963	
	1226.6527983		1254.6477129	12	G	1	204.13426789	+0.1008243	204.13426789	
				13	K	0	147.11280417		147.11280417	

Scan number	7576	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel03
Method	ITMS; CID	Genenames	B9D1



precursor information

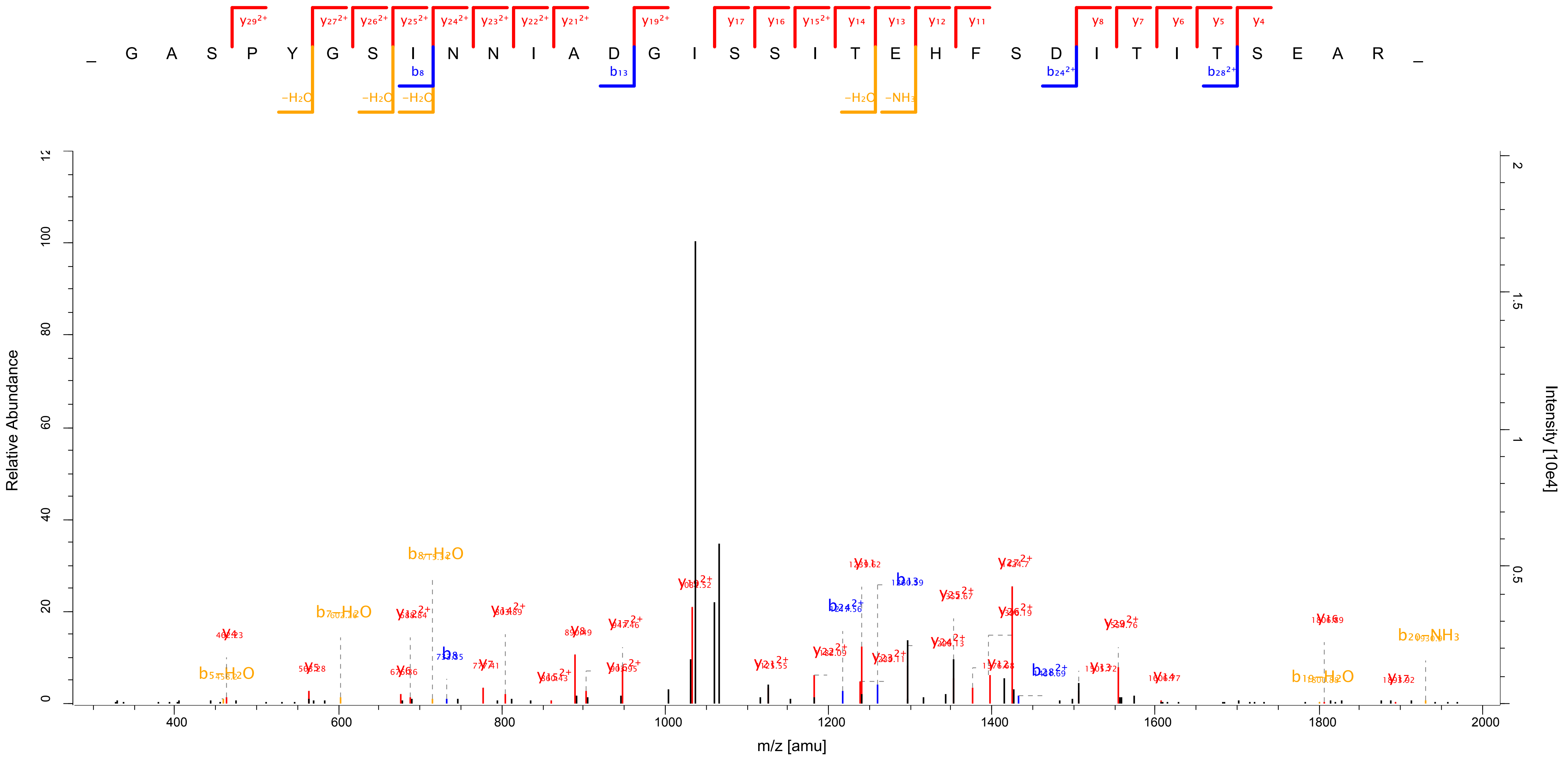
Mass:	1342.67912
m/z:	448.56698
Charge:	3+
Retentiontime:	50.9686241149902
Score:	121.8986
Mass Error [ppm]:	0.67287
PEP:	2.48615E−05
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverage:	77 %
Intensity Coverage:	84 %
Peak Coverage:	38 %
Protein Localisation:	102 ... 114

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	30.0338256		58.0287402		58.0287402	1	G	12				
+0.0838456	193.097154		221.092069	−0.0599337	221.092069	2	Y	11	1286.66403		1286.66403	
	250.118618		278.113532	+0.0552603	278.113532	3	G	10	1123.6007		562.30399	+0.1545673
	321.155732		349.150646		349.150646	4	A	9	1066.57924		533.793258	+0.0571449
	420.224146		448.21906		448.21906	5	V	8	995.542126		498.274701	+0.128192
	557.283057		585.277972		585.277972	6	H	7	896.473712	−0.1015804	896.473712	
	656.351471		684.346386	−0.0221672	684.346386	7	V	6	759.4148	+0.2871655	759.4148	
	753.404235		781.39915		781.39915	8	P	5	660.346386	+0.0002327	330.676831	+0.0132933
	900.472649	−0.4503717	464.73742	−0.0876809	928.467564	9	F	4	563.293622	+0.178729	563.293622	
	987.504677	+0.3563374	508.253434	−0.1585887	1015.49959	10	S	3	416.225208	−0.0051764	416.225208	
	1084.55744	+0.4090266	556.779816		1112.55236	11	P	2	329.19318	−0.0821568	329.19318	
	1141.57891		1169.57382		1169.57382	12	G	1	232.140416		232.140416	
						13	R	0	175.118952		175.118952	

Scan number	19729	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel04
Method	ITMS; CID	Genenames	ZCCHC24



precursor information

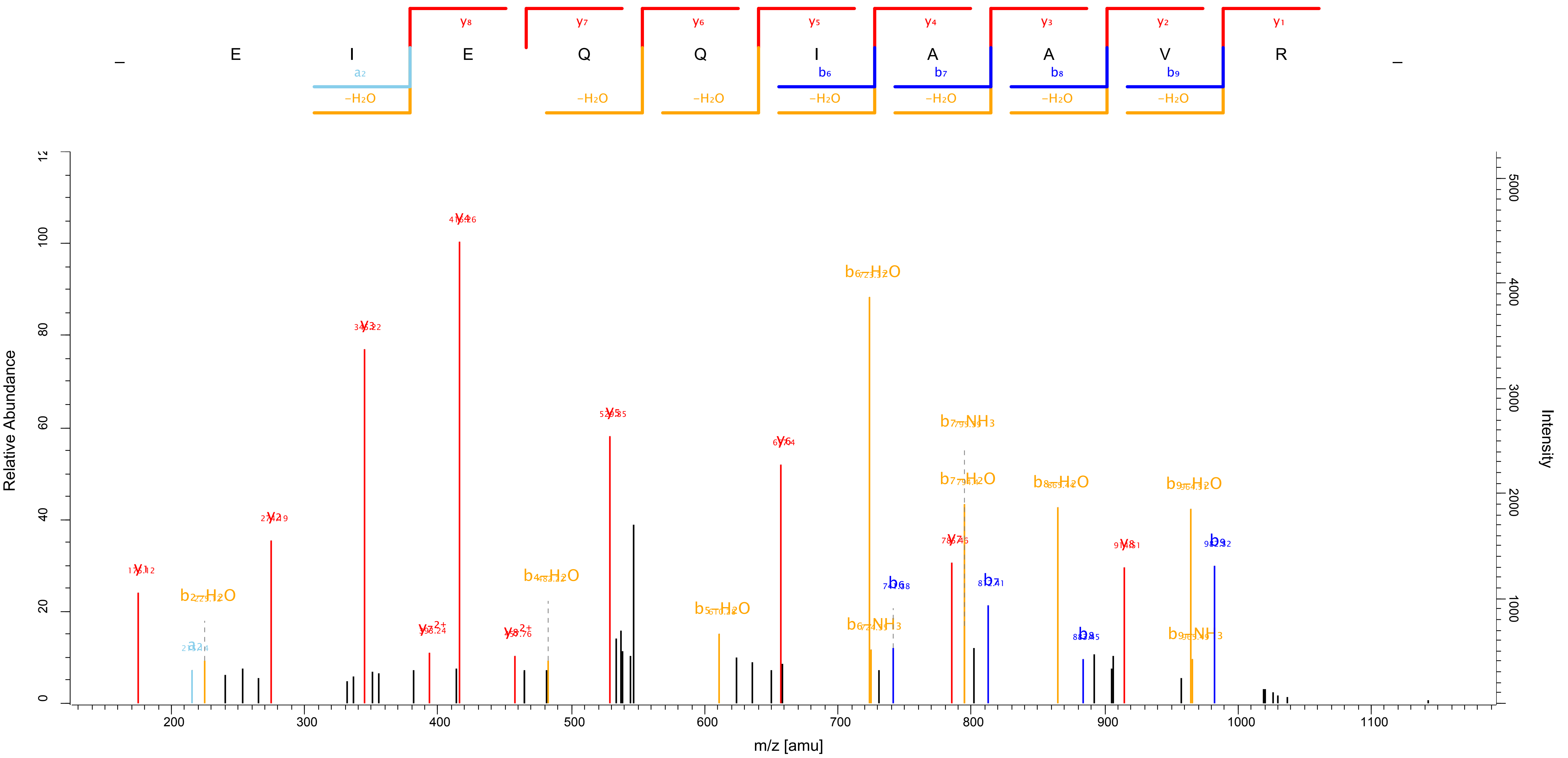
Mass:	3322.59468
m/z:	1108.53884
Charge:	3+
Retentiontime:	119.278984069824
Score:	100.0402
Mass Error [ppm]:	−0.20031
PEP:	4.2319E−20
Precursor Type:	MULTI

general information

Annotation:	24 of 32
AminoAcids Coverage:	75 %
Intensity Coverage:	38 %
Peak Coverage:	33 %
Protein Localisation:	91 ... 122

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019		58.02874019	1	G	31				
	129.06585398		129.06585398	2	A	30	3266.5811561		3266.5811561	
	216.09788239		216.09788239	3	S	29	3195.5440423		3195.5440423	
	313.15064624		313.15064624	4	P	28	3108.5120139		1554.7596452	+0.2730697
	476.21397478		476.21397478	5	Y	27	3011.45925		3011.45925	
	533.2354385		533.2354385	6	G	26	2848.3959215		1424.701599	+0.1846315
	620.26746691		620.26746691	7	S	25	2791.3744578		1396.1908671	+0.4879659
	733.35153089	−0.0587452	733.35153089	8	I	24	2704.3424294		1352.6748529	−0.0763422
	847.39445834		847.39445834	9	N	23	2591.2583654		1296.1328209	−0.0929039
	961.43738579		961.43738579	10	N	22	2477.2154379		1239.1113572	−0.0952439
	1074.5214498		1074.5214498	11	I	21	2363.1725105		1182.0898935	−0.0234872
	1145.5585636		1145.5585636	12	A	20	2250.0884465		1125.5478615	−0.0839943
	1260.5855066	−0.1722986	1260.5855066	13	D	19	2179.0513327		2179.0513327	
	1317.6069703		1317.6069703	14	G	18	2064.0243897		1032.5158331	+0.1736201
	1430.6910343		1430.6910343	15	I	17	2007.002926		2007.002926	
	1517.7230627		1517.7230627	16	S	16	1893.918862	+0.1774515	947.46306922	+0.2296798
	1604.7550911		1604.7550911	17	S	15	1806.8868336	+0.1408764	903.94705502	−0.0682708
	1717.8391551		1717.8391551	18	I	14	1719.8548052		860.43104081	−0.1245223
	1818.8868336		1818.8868336	19	T	13	1606.7707412	+0.123668	803.88900882	−0.062959
	1947.9294267		1947.9294267	20	E	12	1505.7230627	+0.094076	1505.7230627	
	2084.9883385		2084.9883385	21	H	11	1376.6804696	+0.1151847	688.84387304	−0.4537363
	2232.0567524		2232.0567524	22	F	10	1239.6215577	+0.0205321	1239.6215577	
	2319.0887808		2319.0887808	23	S	9	1092.5531438		1092.5531438	
−0.3346935	1217.5615002		2434.1157239	24	D	8	1005.5211154		1005.5211154	
	2547.1997879		2547.1997879	25	I	7	890.49417238	−0.1036695	890.49417238	
	2648.2474663		2648.2474663	26	T	6	777.4101084	+0.0181143	777.4101084	
	2761.3315303		2761.3315303	27	I	5	676.36242993	+0.0028655	676.36242993	
−0.0490776	1431.6932426		2862.3792088	28	T	4	563.27836595	−0.0586394	563.27836595	
	2949.4112372		2949.4112372	29	S	3	462.23068747	+0.0739695	462.23068747	
	3078.4538303		3078.4538303	30	E	2	375.19865906		375.19865906	
	3149.4909441		3149.4909441	31	A	1	246.15606597		246.15606597	
				32	R	0	175.11895218		175.11895218	

Scan number	6948	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel04
Method	ITMS; CID	Genenames	FAM109A



precursor information

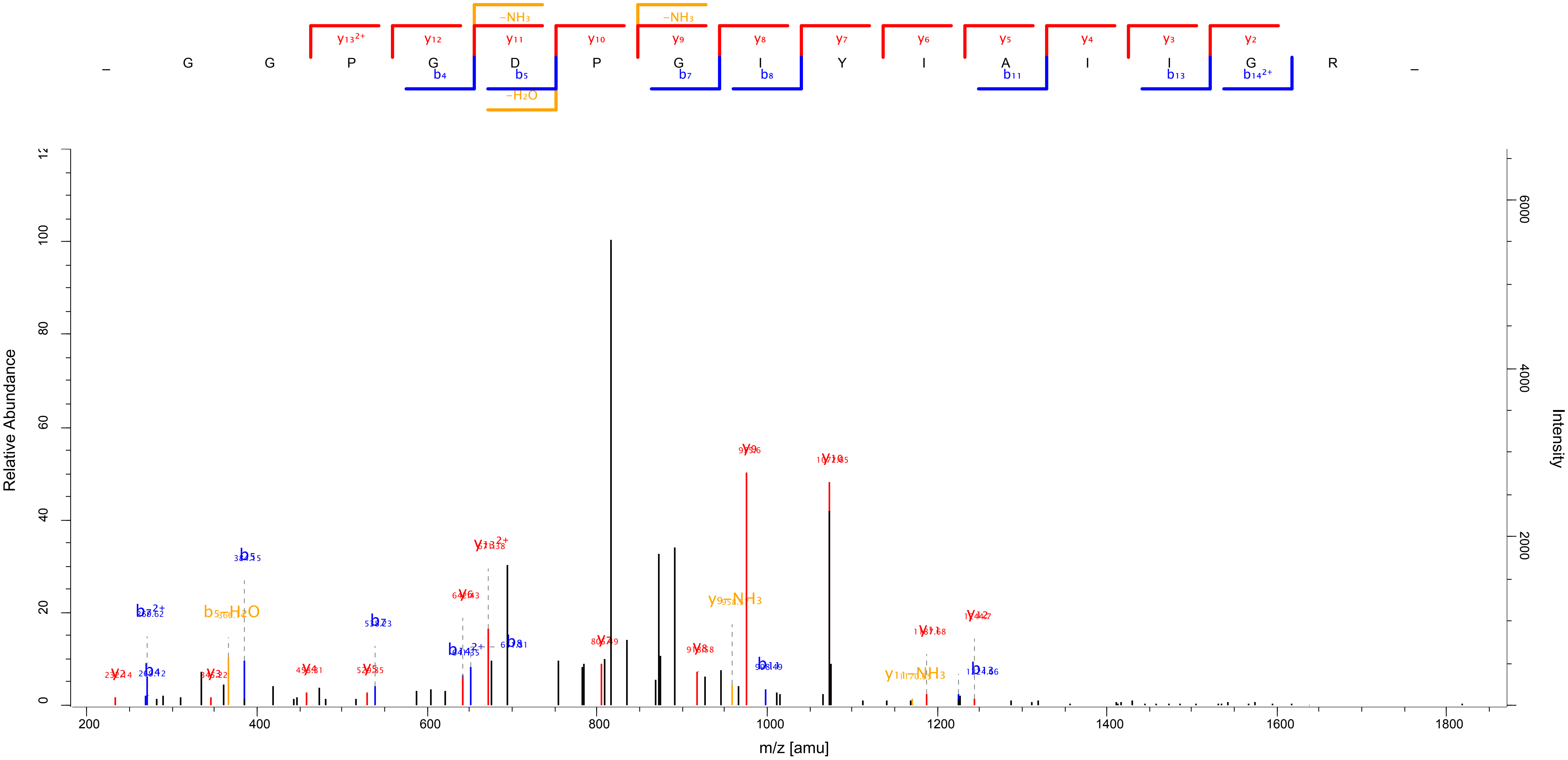
Mass:	1155.62461
m/z:	578.81958
Charge:	2+
Retentiontime:	47.8646965026855
Score:	179.8049
Mass Error [ppm]:	−0.14913
PEP:	6.0006E−07
Precursor Type:	MULTI

ge information

Annotation:	9 of 10
AminoAcids Coverage:	90 %
Intensity Coverage:	75 %
Peak Coverage:	43 %
Protein Localisation:	122 ... 131

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05495494		130.04986956	1	E	9				
+0.0326272	215.13901892		243.13393354	2	I	8	1027.5894698		1027.5894698	
	344.18161202		372.17652664	3	E	7	914.50540577	−0.0100444	457.75634112	+0.2287663
	472.24018953		500.23510415	4	Q	6	785.46281268	+0.0218065	393.23504457	−0.0131818
	600.29876704		628.29368166	5	Q	5	657.40423516	+0.0432136	657.40423516	
	713.38283102	−0.1260977	741.37774564	6	I	4	529.34565765	+0.0492398	529.34565765	
	784.41994481	−0.1511265	812.41485943	7	A	3	416.26159367	+0.0479156	416.26159367	
	855.4570586	−0.0151446	883.45197322	8	A	2	345.22447988	+0.0995558	345.22447988	
	954.52547251	−0.1925673	982.52038713	9	V	1	274.1873661	+0.154858	274.1873661	
				10	R	0	175.11895218	+0.0278679	175.11895218	

Scan number	17278	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel05
Method	ITMS; CID	Genenames	CYB5D2



precursor information

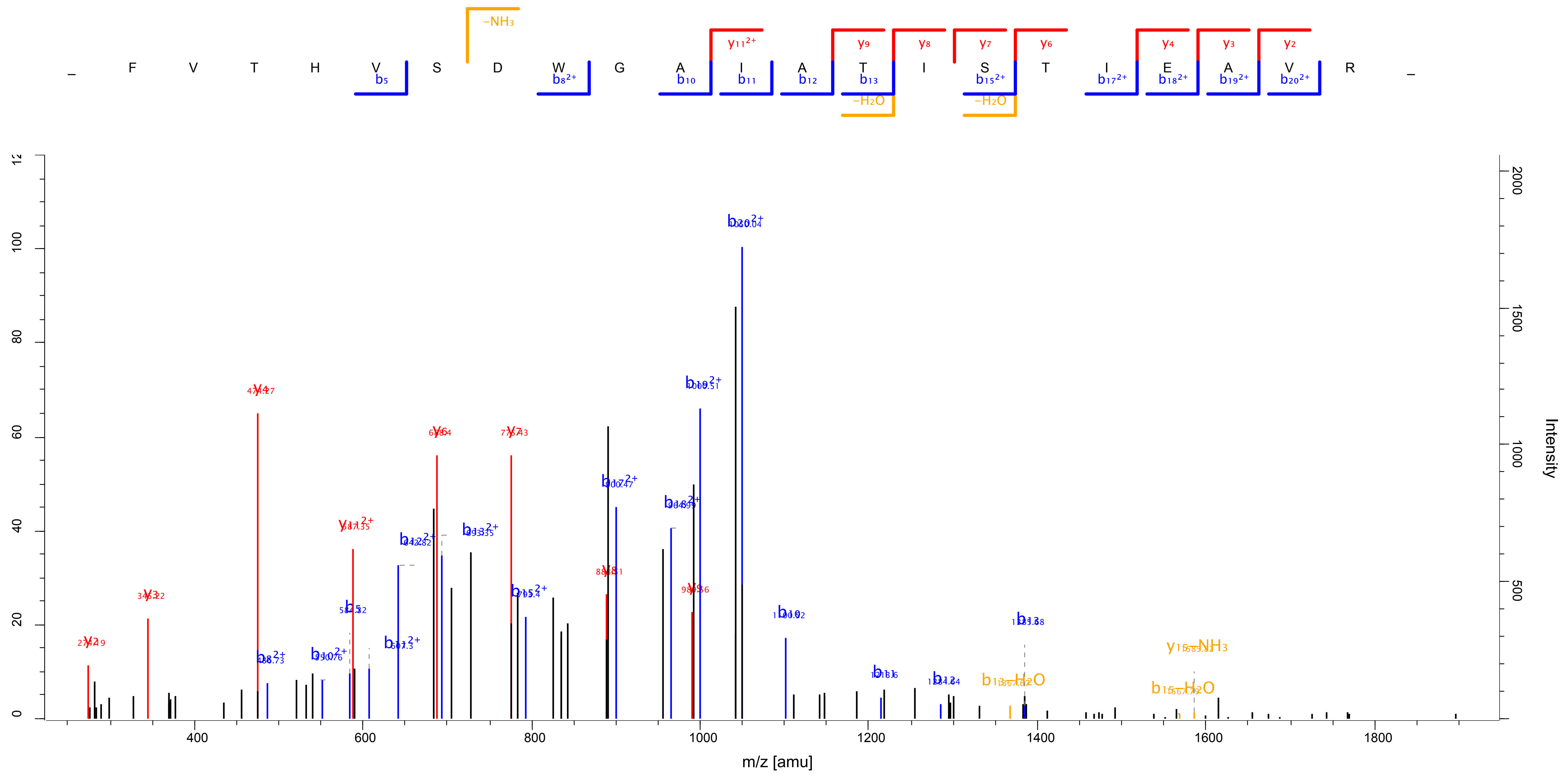
Mass:	2185.04509
m/z:	729.35564
Charge:	3+
Retentiontime:	102.46378326416
Score:	139.7806
Mass Error [ppm]:	0.96034
PEP:	7.4685E-30
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverage:	80 %
Intensity Coverage:	34 %
Peak Coverage:	27 %
Protein Localisation:	48 ... 62

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019		58.02874019	1	G	14				
	115.05020391		115.05020391	2	G	13	1398.7739761		1398.7739761	
	212.10296777		212.10296777	3	P	12	1341.7525123		671.3798944	+0.355152
	269.12443149	−0.014202	269.12443149	4	G	11	1244.6997485	+0.1592603	1244.6997485	
	384.15137452	+0.0534595	384.15137452	5	D	10	1187.6782848	+0.1508168	1187.6782848	
	481.20413837		481.20413837	6	P	9	1072.6513417	−0.0484365	1072.6513417	
+0.460465	269.61643928	+0.3606406	538.2256021	7	G	8	975.59857788	−0.487738	975.59857788	
	651.30966608	−0.3088726	651.30966608	8	I	7	918.57711415	−0.3005028	918.57711415	
	814.37299462		814.37299462	9	Y	6	805.49305017	−0.0780721	805.49305017	
	927.4570586		927.4570586	10	I	5	642.42972163	−0.1084936	642.42972163	
	998.49417238	+0.107207	998.49417238	11	A	4	529.34565765	+0.145065	529.34565765	
	1111.5782364		1111.5782364	12	I	3	458.30854387	+0.0780528	458.30854387	
	1224.6623003	−0.146065	1224.6623003	13	I	2	345.22447988	+0.1075514	345.22447988	
−0.3073733	641.34552027		1281.6837641	14	G	1	232.1404159	+0.0518143	232.1404159	
				15	R	0	175.11895218		175.11895218	

Scan number	18188	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel05
Method	ITMS; CID	Genenames	CREG1



precursor information

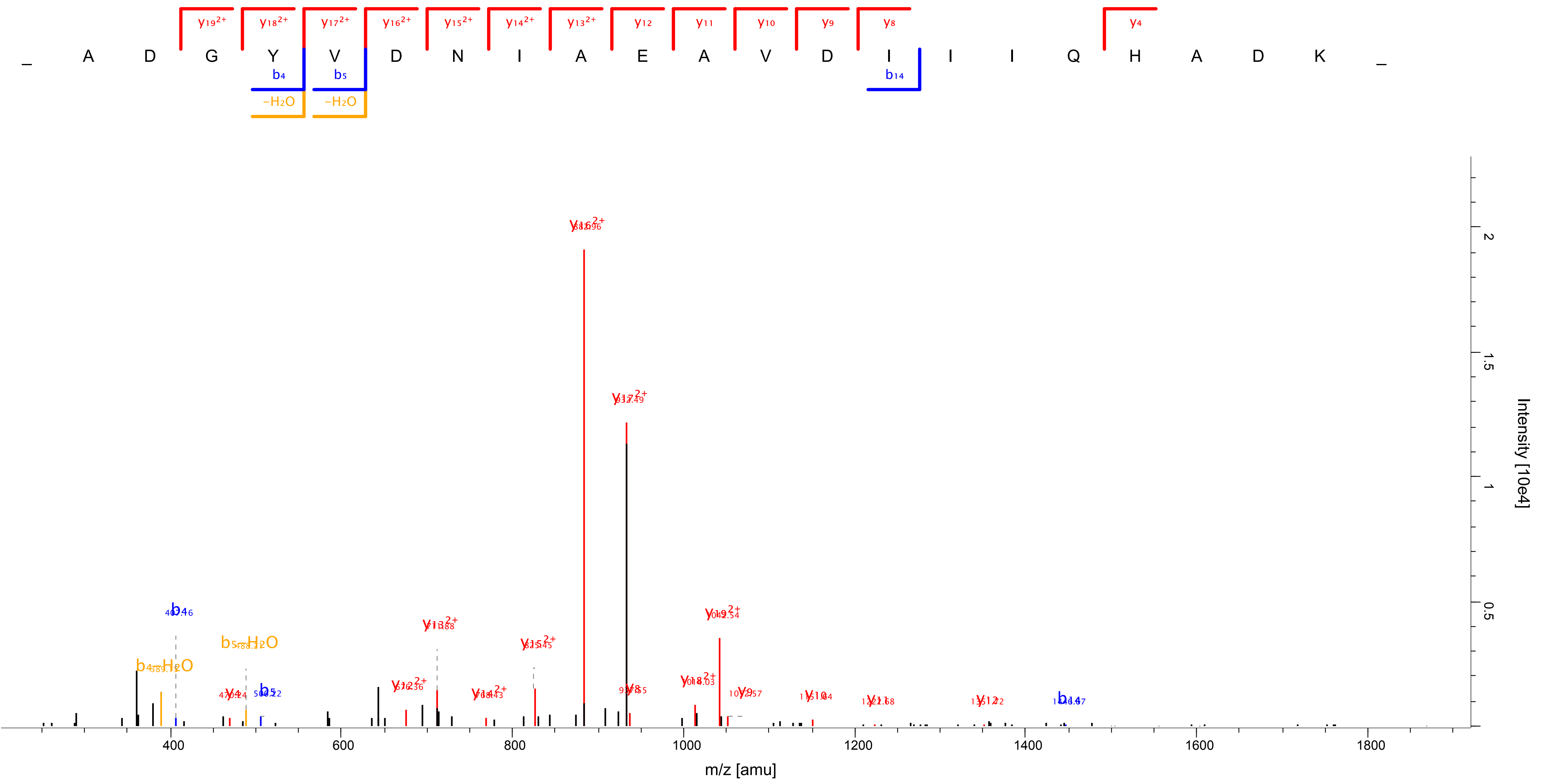
Mass:	2272.18593
m/z:	758.40258
Charge:	3+
Retentiontime:	107.925575256348
Score:	125.9752
Mass Error [ppm]:	0.32719
PEP:	7.4677E−15
Precursor Type:	MULTI

general information

Annotation:	15 of 21
AminoAcids Coverage:	71 %
Intensity Coverage:	49 %
Peak Coverage:	28 %
Protein Localisation:	61 ... 81

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.07569038		148.07569038	1	F	20				
	247.1441043		247.1441043	2	V	19	2126.1240441		2126.1240441	
	348.19178277		348.19178277	3	T	18	2027.0556302		2027.0556302	
	485.25069464		485.25069464	4	H	17	1926.0079518		1926.0079518	
	584.31910855	−0.1587692	584.31910855	5	V	16	1788.9490399		1788.9490399	
	671.35113696		671.35113696	6	S	15	1689.880626		1689.880626	
	786.37807999		786.37807999	7	D	14	1602.8485976		1602.8485976	
−0.4254499	486.73233471		972.45739295	8	W	13	1487.8216545		1487.8216545	
	1029.4788567		1029.4788567	9	G	12	1301.7423416		1301.7423416	
+0.1278419	550.76162346	+0.0555627	1100.5159705	10	A	11	1244.7208779		1244.7208779	
+0.1209661	607.30365545	−0.0326516	1213.6000344	11	I	10	1173.6837641		587.34552027	−0.0494387
−0.1491166	642.82221235	−0.1052879	1284.6371482	12	A	9	1060.5997001		1060.5997001	
−0.226972	693.34605158	+0.1277954	1385.6848267	13	T	8	989.5625863	−0.0633798	989.5625863	
	1498.7688907		1498.7688907	14	I	7	888.51490783	−0.0531769	888.51490783	
−0.144088	793.40409778		1585.8009191	15	S	6	775.43084385	+0.0491977	775.43084385	
	1686.8485976		1686.8485976	16	T	5	688.39881544	−0.017895	688.39881544	
+0.1716326	900.46996901		1799.9326615	17	I	4	587.35113696		587.35113696	
+0.2496402	964.99126555		1928.9752546	18	E	3	474.26707298	−0.0496047	474.26707298	
−0.1000934	1000.5098224		2000.0123684	19	A	2	345.22447988	−0.1020434	345.22447988	
−0.1650011	1050.0440294		2099.0807823	20	V	1	274.1873661	+0.0203365	274.1873661	
				21	R	0	175.11895218		175.11895218	

Scan number	20203	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel05
Method	ITMS; CID	Genenames	LHPP



precursor information

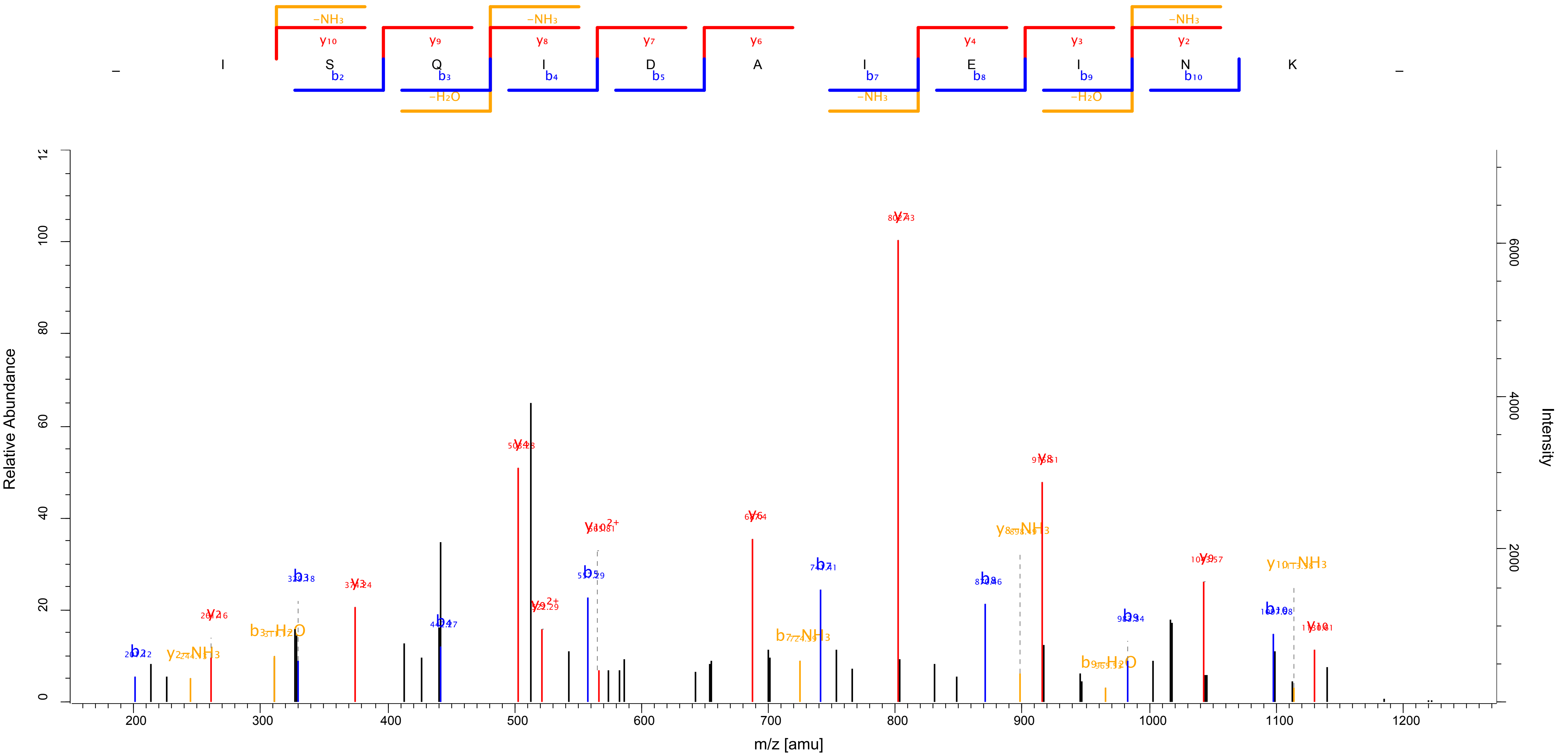
Mass:	2269.12157
m/z:	757.38113
Charge:	3+
Retentiontime:	119.84642791748
Score:	70.80228
Mass Error [ppm]:	−0.47342
PEP:	0.00032753
Precursor Type:	MULTI

general information

Annotation:	14 of 21
AminoAcids Coverage:	67 %
Intensity Coverage:	59 %
Peak Coverage:	22 %
Protein Localisation:	250 ... 270

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	20				
	187.071333286	2	D	19	2199.092803595		2199.092803595	
	244.09279701	3	G	18	2084.065860563		1042.536568515	+0.2045204
+0.0894799	407.156125548	4	Y	17	2027.04439684		1014.025836653	−0.0573308
−0.1623446	506.224539464	5	V	16	1863.981068301		932.494172384	−0.0227368
	621.251482496	6	D	15	1764.912654385		882.959965426	+0.2667802
	735.294409944	7	N	14	1649.885711353		825.44649391	+0.1654446
	848.378473924	8	I	13	1535.842783906		768.425030186	−0.0703549
	919.415587712	9	A	12	1422.758719925		711.882998196	−0.0245387
	1048.458180808	10	E	11	1351.721606138	−0.0778073	676.364441302	+0.1235348
	1119.495294596	11	A	10	1222.679013041	−0.1240814	1222.679013041	
	1218.563708512	12	V	9	1151.641899254	+0.1247023	1151.641899254	
	1333.590651544	13	D	8	1052.573485337	−0.2446279	1052.573485337	
+0.1982093	1446.674715524	14	I	7	937.546542305	−0.0326873	937.546542305	
	1559.758779505	15	I	6	824.462478325		824.462478325	
	1672.842843485	16	I	5	711.378414345		711.378414345	
	1800.901420997	17	Q	4	598.294350364		598.294350364	
	1937.960332859	18	H	3	470.235772853	−0.0114687	470.235772853	
	2008.997446647	19	A	2	333.17686099		333.17686099	
	2124.024389679	20	D	1	262.139747203		262.139747203	
		21	K	0	147.112804171		147.112804171	

Scan number	9888	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel05
Method	ITMS; CID	Genenames	PEX2



precursor information

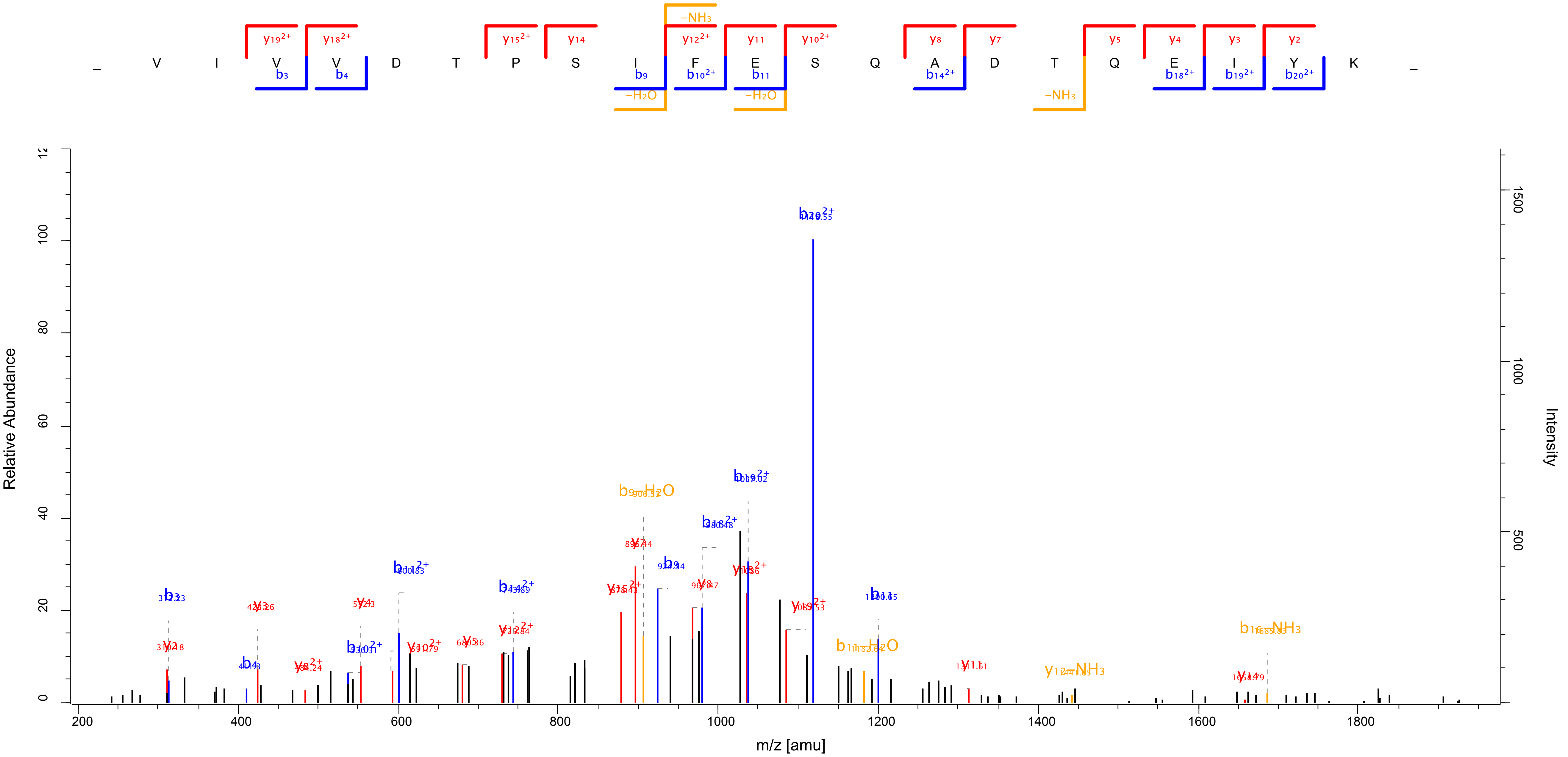
Mass:	1242.68141
m/z:	622.34798
Charge:	2+
Retentiontime:	61.9927978515625
Score:	151.7877
Mass Error [ppm]:	−0.44902
PEP:	1.6793E−06
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverage:	82 %
Intensity Coverage:	54 %
Peak Coverage:	39 %
Protein Localisation:	17 ... 27

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.091340447	1	I	10				
+0.0252365	201.123368857	2	S	9	1130.605179396	−0.0253454	565.806227931	+0.124253
+0.0511469	329.181946368	3	Q	8	1043.573150986	−0.1544498	522.290213726	−0.1351234
−0.0981026	442.266010349	4	I	7	915.514573475	−0.128404	915.514573475	
+0.0142366	557.292953381	5	D	6	802.430509495	−0.0298747	802.430509495	
	628.330067168	6	A	5	687.403566463	−0.0009175	687.403566463	
+0.0535813	741.414131149	7	I	4	616.366452675		616.366452675	
−0.0177594	870.456724245	8	E	3	503.282388694	+0.0354214	503.282388694	
−0.3423019	983.540788226	9	I	2	374.239795598	−0.0082282	374.239795598	
−0.1882079	1097.583715673	10	N	1	261.155731618	+0.0747676	261.155731618	
		11	K	0	147.112804171		147.112804171	

Scan number	16332	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel06
Method	ITMS; CID	Genenames	GIMAP5



precursor information

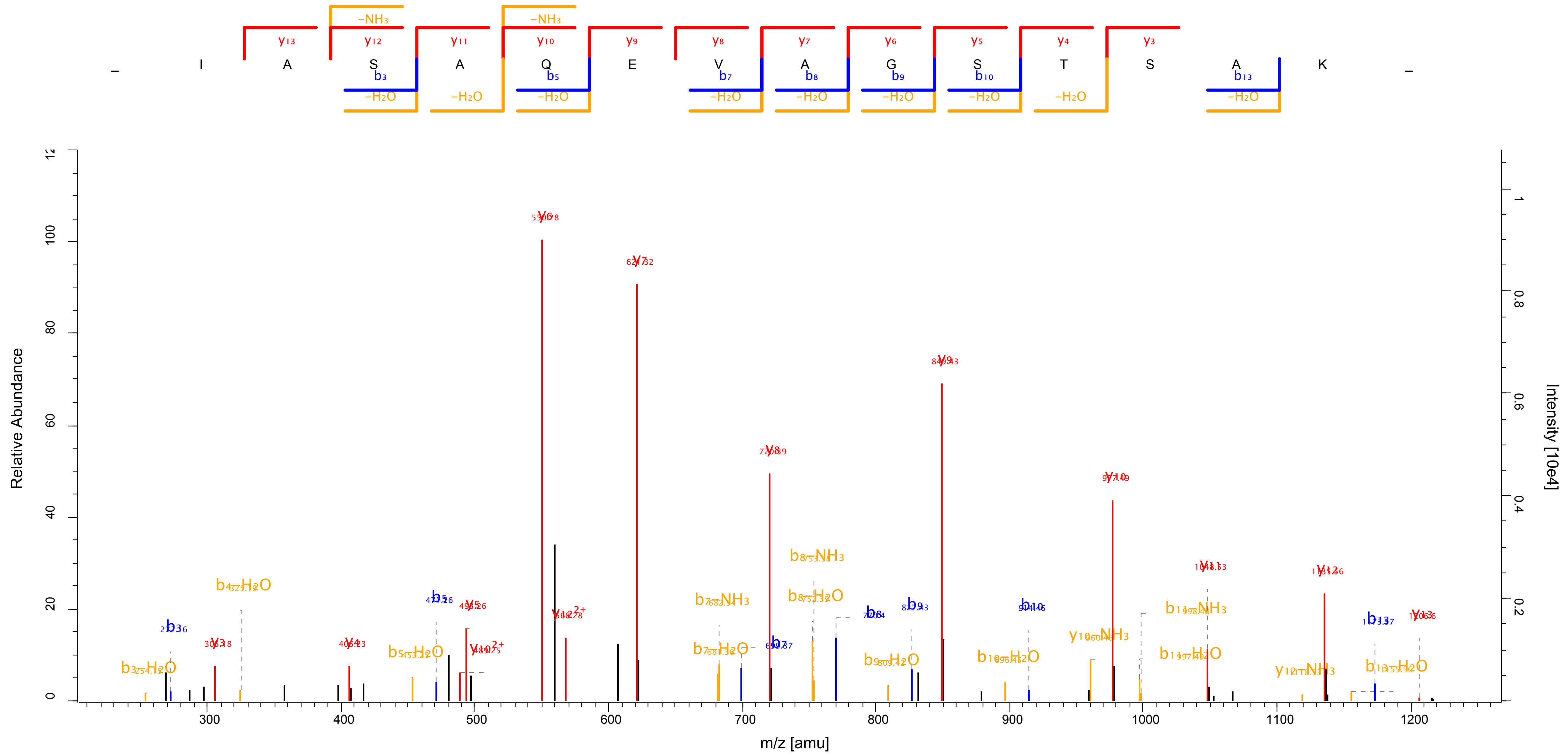
Mass:	2381.19924
m/z:	794.74036
Charge:	3+
Retentiontime:	96.1001434326172
Score:	130.0065
Mass Error [ppm]:	-0.41188
PEP:	2.66745E-10
Precursor Type:	ISO

general information

Annotation:	15 of 21
AminoAcids Coverage:	71 %
Intensity Coverage:	53 %
Peak Coverage:	28 %
Protein Localisation:	118 ... 138

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.07569038		100.07569038	1	V	20				
	213.15975436		213.15975436	2	I	19	2283.1390851		2283.1390851	
	312.22816828	-0.0363348	312.22816828	3	V	18	2170.0550211		1085.5311488	-0.2334193
	411.2965822	-0.0415773	411.2965822	4	V	17	2070.9866072		1035.9969418	+0.1143863
	526.32352523		526.32352523	5	D	16	1971.9181933		1971.9181933	
	627.3712037		627.3712037	6	T	15	1856.8912502		1856.8912502	
	724.42396755		724.42396755	7	P	14	1755.8435718		878.42542412	-0.1171355
	811.45599596		811.45599596	8	S	13	1658.7908079	-0.45072	1658.7908079	
	924.54005994	-0.0113124	924.54005994	9	I	12	1571.7587795		1571.7587795	
+0.0123153	536.30787516		1071.6084739	10	F	11	1458.6747155		729.840996	+0.2907789
+0.0419831	600.82917171	-0.0905201	1200.651067	11	E	10	1311.6063016	+0.4922091	1311.6063016	
	1287.6830954		1287.6830954	12	S	9	1182.5637085		591.78549249	+0.1523737
	1415.7416729		1415.7416729	13	Q	8	1095.5316801		1095.5316801	
-0.0920062	743.89303157		1486.7787867	14	A	7	967.47310259	-0.1799507	484.24018953	+0.238143
	1601.8057297		1601.8057297	15	D	6	896.4359888	-0.054458	896.4359888	
	1702.8534082		1702.8534082	16	T	5	781.40904577		781.40904577	
	1830.9119857		1830.9119857	17	Q	4	680.3613673	-0.0449	680.3613673	
-0.0818187	980.48092762		1959.9545788	18	E	3	552.30278979	-0.0075017	552.30278979	
+0.0825091	1037.0229596		2073.0386428	19	I	2	423.26019669	-0.0083046	423.26019669	
+0.0073878	1118.5546239		2236.1019713	20	Y	1	310.17613271	-0.0543676	310.17613271	
				21	K	0	147.11280417		147.11280417	

Scan number	3357	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel06
Method	ITMS; CID	Genenames	C1orf174



precursor
information

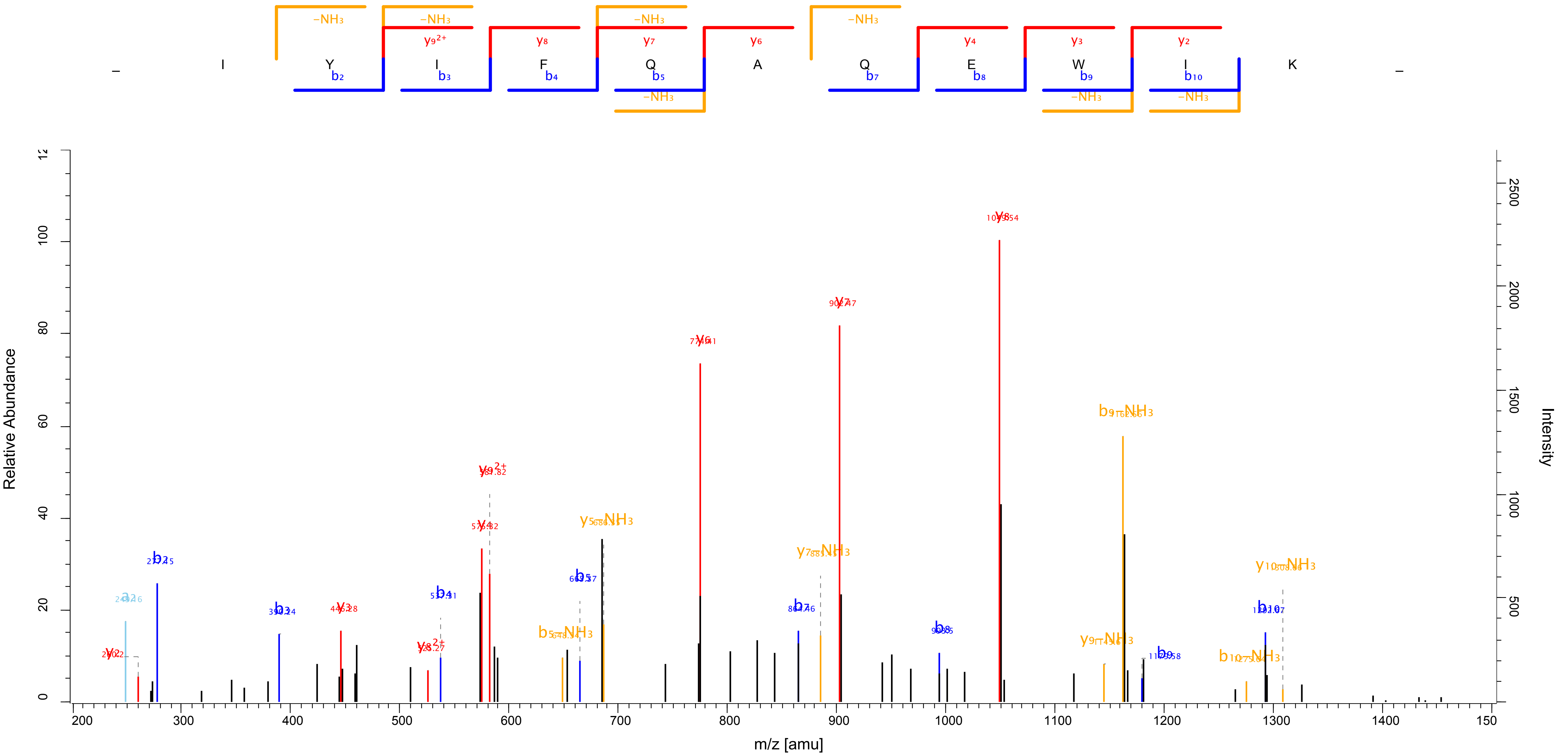
Mass:	1318.67305
m/z:	660.3438
Charge:	2+
Retentiontime:	27.7391567230225
Score:	199.7993
Mass Error [ppm]:	0.14839
PEP:	1.3803E-16
Precursor Type:	ISO

general
information

Annotation:	12 of 14
AminoAcids Coverage:	86 %
Intensity Coverage:	78 %
Peak Coverage:	58 %
Protein Localisation:	26 ... 39

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.091340447	1	I	13				
	185.128454235	2	A	12	1206.596071273	+0.1243877	1206.596071273	
−0.0183012	272.160482645	3	S	11	1135.558957485	−0.0825171	568.283116976	−0.0981805
	343.197596432	4	A	10	1048.526929075	−0.0802738	1048.526929075	
−0.1043795	471.256173944	5	Q	9	977.489815287	−0.0684286	489.248545877	+0.058522
	600.29876704	6	E	8	849.431237776	−0.0307251	849.431237776	
−0.0099422	699.367180956	7	V	7	720.38864468	−0.036716	720.38864468	
−0.0663431	770.404294744	8	A	6	621.320230764	−0.0044349	621.320230764	
−0.0531388	827.425758468	9	G	5	550.283116976	−0.0135857	550.283116976	
+0.0331799	914.457786878	10	S	4	493.261653252	−0.0019487	493.261653252	
	1015.505465352	11	T	3	406.229624842	+0.0448503	406.229624842	
	1102.537493762	12	S	2	305.181946368	+0.0314936	305.181946368	
−0.0914533	1173.574607549	13	A	1	218.149917958		218.149917958	
		14	K	0	147.112804171		147.112804171	

Scan number	16900	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel08
Method	ITMS; CID	Genenames	GPR180



precursor information

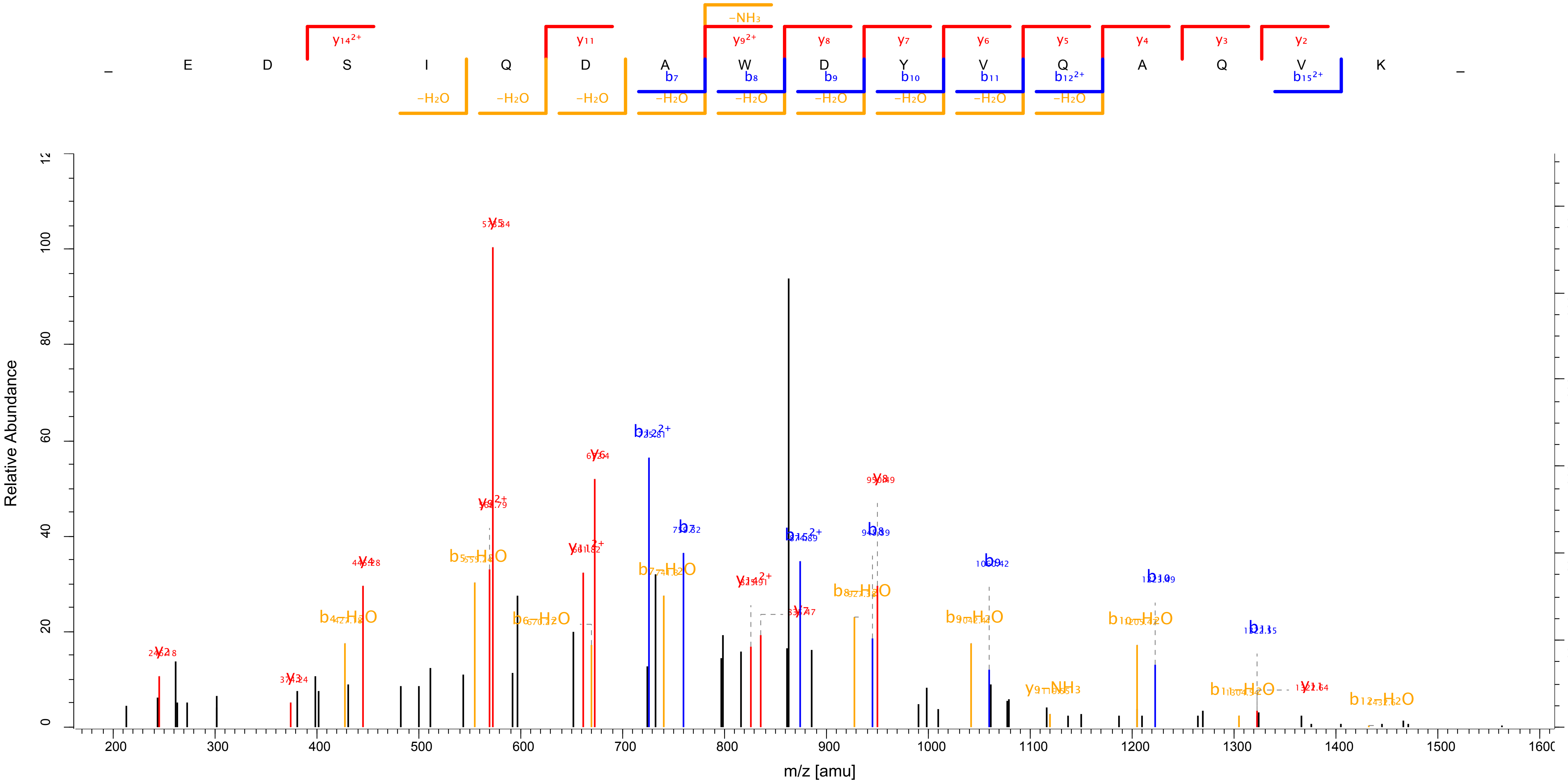
Mass:	1437.76501
m/z:	719.88978
Charge:	2+
Retentiontime:	100.897171020508
Score:	148.557
Mass Error [ppm]:	−0.4361
PEP:	2.1195E−06
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverage:	82 %
Intensity Coverage:	55 %
Peak Coverage:	34 %
Protein Localisation:	71 ... 81

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096425825		114.09134045	1	I	10				
+0.0638479	249.15975436	−0.0648863	277.15466899	2	Y	9	1325.6888494		1325.6888494	
	362.24381834	−0.4507691	390.23873297	3	I	8	1162.6255209		581.81639869	+0.1276931
	509.31223226	−0.2381161	537.30714688	4	F	7	1049.5414569	−0.1149433	525.2743667	+0.1150376
	637.37080977	−0.0037249	665.36572439	5	Q	6	902.47304301	−0.0897422	902.47304301	
	708.40792356		736.40283818	6	A	5	774.4144655	+0.0602049	774.4144655	
	836.46650107	−0.1267599	864.46141569	7	Q	4	703.37735171		703.37735171	
	965.50909417	−0.1078296	993.50400879	8	E	3	575.3187742	−0.0364866	575.3187742	
	1151.5884071	−0.2293178	1179.5833217	9	W	2	446.2761811	+0.053775	446.2761811	
	1264.6724711	−0.2095	1292.6673857	10	I	1	260.19686815	−0.0087578	260.19686815	
				11	K	0	147.11280417		147.11280417	

Scan number	18379	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel08
Method	ITMS; CID	Genenames	CD82



precursor information

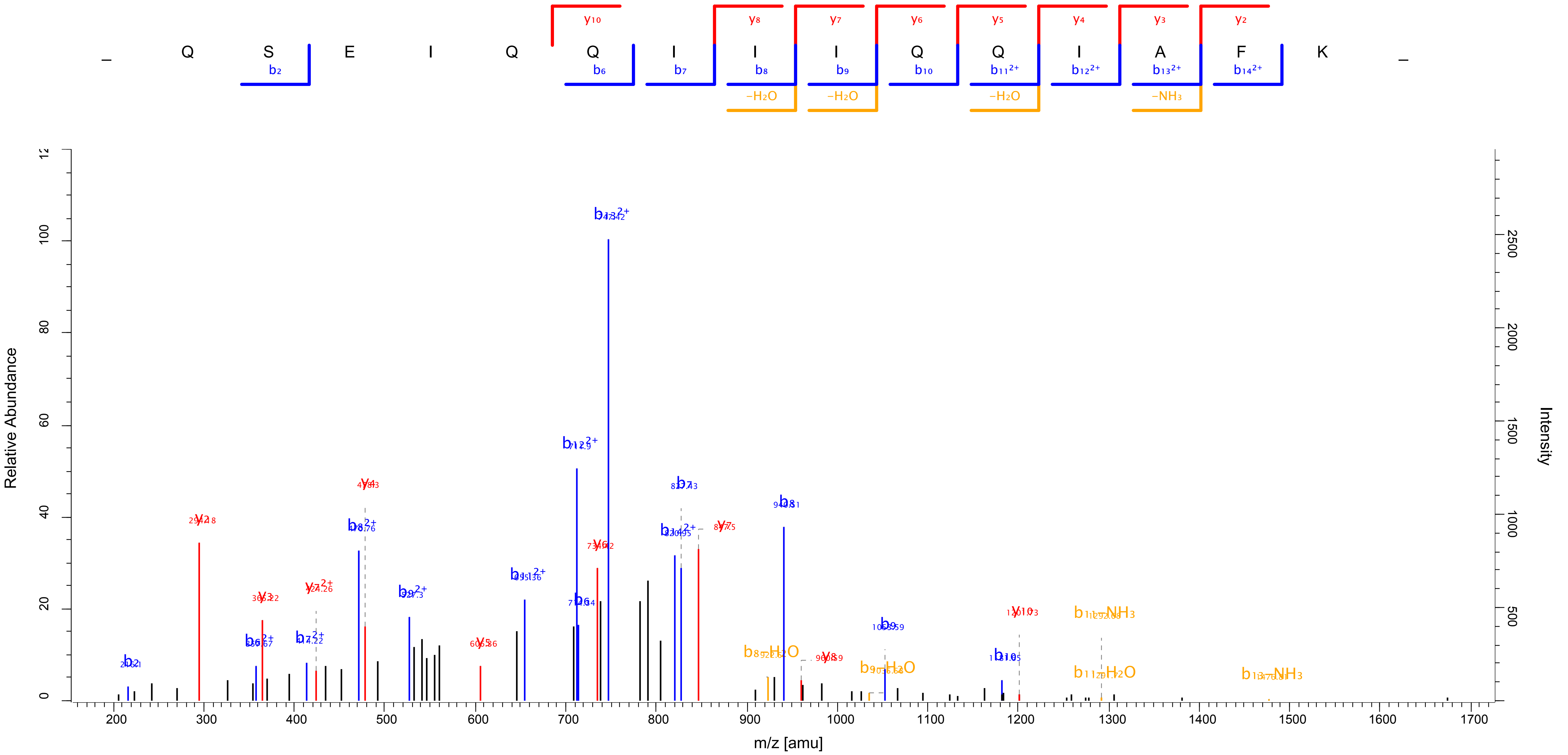
Mass:	1893.87306
m/z:	632.2983
Charge:	3+
Retentiontime:	109.696334838867
Score:	145.0983
Mass Error [ppm]:	-0.7477
PEP:	3.1038E-05
Precursor Type:	ISO

general information

Annotation:	13 of 16
AminoAcids Coverage:	81 %
Intensity Coverage:	58 %
Peak Coverage:	37 %
Protein Localisation:	133 ... 148

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.04986956		130.04986956	1	E	15				
	245.07681259		245.07681259	2	D	14	1765.8391551		1765.8391551	
	332.108841		332.108841	3	S	13	1650.8122121		825.90974426	−0.0716705
	445.19290499		445.19290499	4	I	12	1563.7801836		1563.7801836	
	573.2514825		573.2514825	5	Q	11	1450.6961197		1450.6961197	
	688.27842553		688.27842553	6	D	10	1322.6375422	+0.2623602	661.82240931	+0.1761869
	759.31553932	−0.1519651	759.31553932	7	A	9	1207.6105991		1207.6105991	
	945.39485227	−0.2318274	945.39485227	8	W	8	1136.5734853		568.7903809	+0.0970092
	1060.4217953	−0.3441586	1060.4217953	9	D	7	950.49417238	−0.1055615	950.49417238	
	1223.4851238	−0.0174725	1223.4851238	10	Y	6	835.46722935	−0.180242	835.46722935	
	1322.5535378	−0.3150124	1322.5535378	11	V	5	672.40390081	−0.07779	672.40390081	
+0.0141567	725.80969587		1450.6121153	12	Q	4	573.3354869	+0.0002675	573.3354869	
	1521.6492291		1521.6492291	13	A	3	445.27690939	+0.0045237	445.27690939	
	1649.7078066		1649.7078066	14	Q	2	374.2397956	+0.054699	374.2397956	
+0.0530757	874.89174847		1748.7762205	15	V	1	246.18121809	+0.0049697	246.18121809	
				16	K	0	147.11280417		147.11280417	

Scan number	18869	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel09
Method	ITMS; CID	Genenames	TFDP3



precursor information

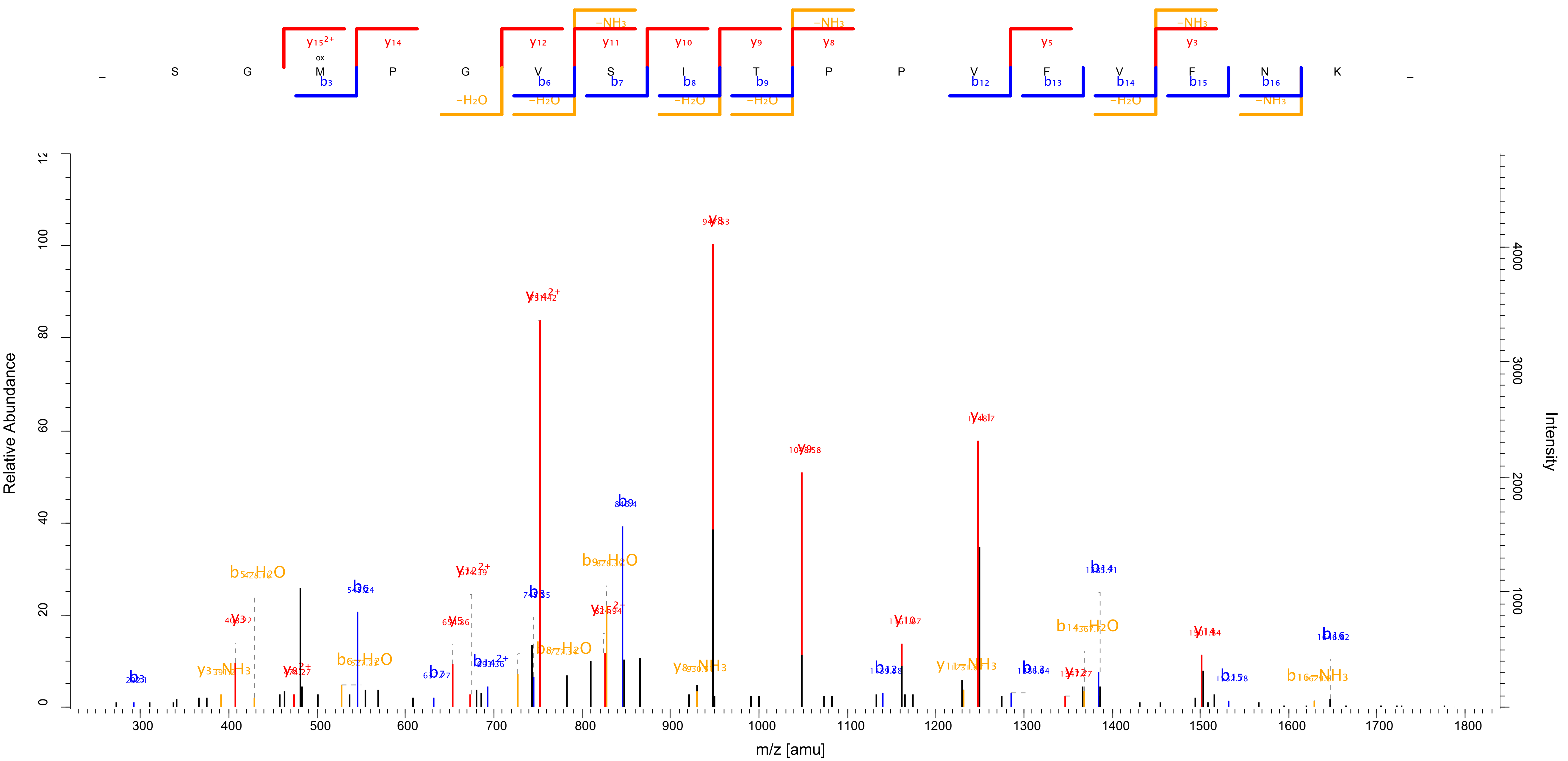
Mass:	1785.99907
m/z:	596.3403
Charge:	3+
Retentiontime:	108.980514526367
Score:	153.8087
Mass Error [ppm]:	0.10343
PEP:	2.5255E−06
Precursor Type:	ISO

general information

Annotation:	10 of 15
AminoAcids Coverage:	67 %
Intensity Coverage:	67 %
Peak Coverage:	39 %
Protein Localisation:	215 ... 229

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.06585398		129.06585398	1	Q	14				
	216.09788239	+0.0214871	216.09788239	2	S	13	1658.9475833		1658.9475833	
	345.14047548		345.14047548	3	E	12	1571.9155549		1571.9155549	
	458.22453946		458.22453946	4	I	11	1442.8729618		1442.8729618	
	586.28311698		586.28311698	5	Q	10	1329.7888978		1329.7888978	
−0.1481793	357.67448548	+0.0674242	714.34169449	6	Q	9	1201.7303203	+0.028957	1201.7303203	
−0.0578261	414.21651747	−0.1411515	827.42575847	7	I	8	1073.6717428		1073.6717428	
+0.0126908	470.75854946	−0.1075397	940.50982245	8	I	7	960.58767884	+0.0008832	960.58767884	
−0.1284013	527.30058145	−0.067031	1053.5938864	9	I	6	847.50361486	−0.0318741	424.25544566	+0.16057
	1181.6524639	−0.1470928	1181.6524639	10	Q	5	734.41955088	−0.136836	734.41955088	
+0.0356775	655.35915896		1309.7110415	11	Q	4	606.36097337	−0.0509758	606.36097337	
−0.0825874	711.90119095		1422.7951054	12	I	3	478.30239586	+0.0859098	478.30239586	
−0.0544524	747.41974784		1493.8322192	13	A	2	365.21833187	−0.0172821	365.21833187	
−0.1910764	820.9539548		1640.9006331	14	F	1	294.18121809	−0.0671434	294.18121809	
				15	K	0	147.11280417		147.11280417	

Scan number	15736	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel10_091024034333
Method	ITMS; CID	Genenames	TMCC3



precursor
information

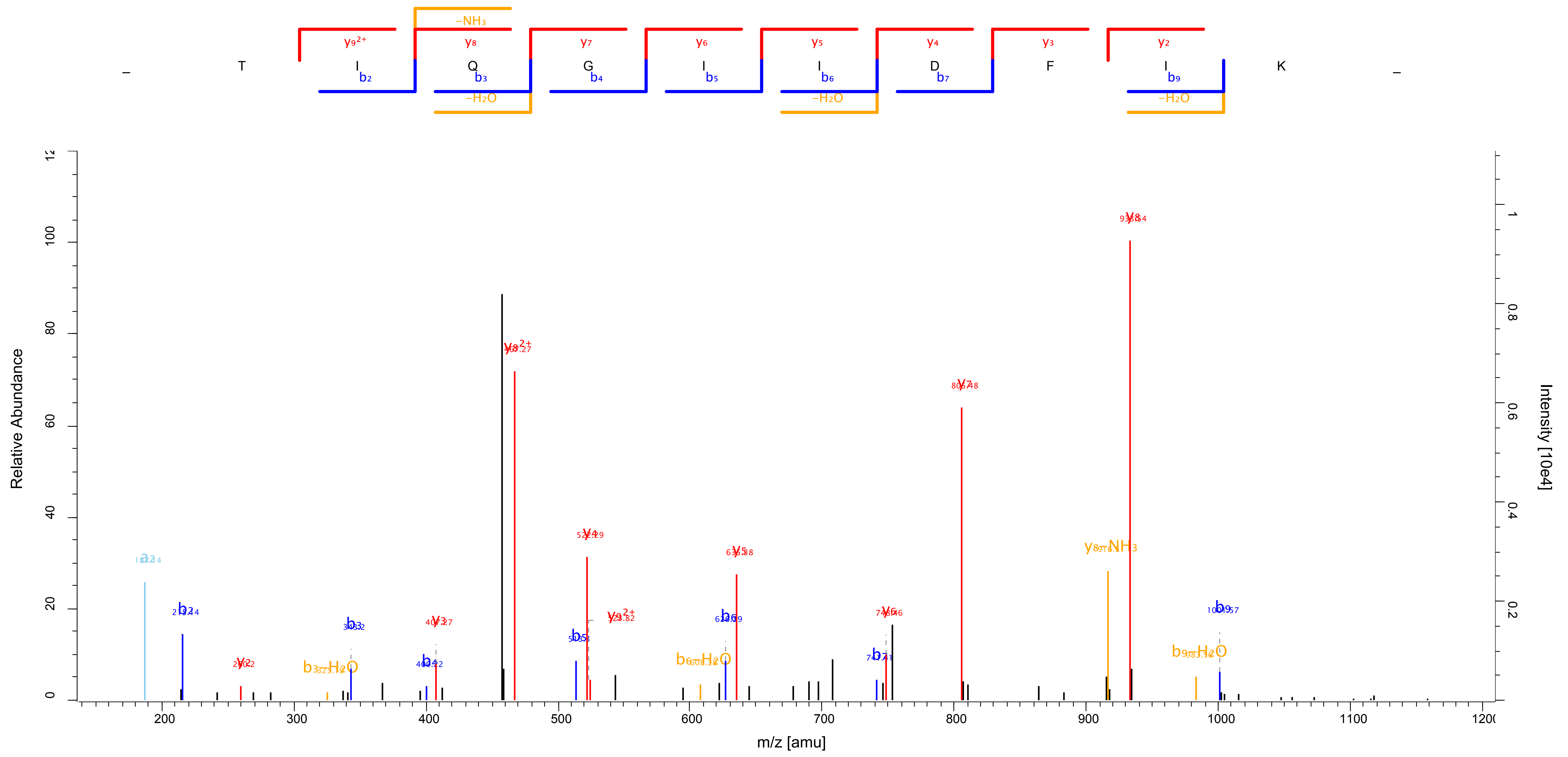
Mass:	1791.92256
m/z:	896.96856
Charge:	2+
Retentiontime:	93.0241546630859
Score:	183.9612
Mass Error [ppm]:	−0.21177
PEP:	7.5746E−18
Precursor Type:	ISO

general
information

Annotation:	13 of 17
AminoAcids Coverage:	76 %
Intensity Coverage:	64 %
Peak Coverage:	36 %
Protein Localisation:	186 ... 202

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876		88.039304876	1	S	16				
	145.0607686		145.0607686	2	G	15	1705.8981903		1705.8981903	
	292.09616783	+0.05465	292.09616783	3	M	14	1648.8767266		824.94200152	+0.3487089
	389.14893168		389.14893168	4	P	13	1501.8413273	−0.0081975	751.4243019	+0.1543724
	446.1703954		446.1703954	5	G	12	1404.7885635		1404.7885635	
	545.23880932	−0.0771272	545.23880932	6	V	11	1347.7670998	−0.3298439	674.38718812	−0.4005548
	632.27083773	+0.0634518	632.27083773	7	S	10	1248.6986859	−0.122514	1248.6986859	
	745.35490171	−0.0524725	745.35490171	8	I	9	1161.6666574	−0.1101389	1161.6666574	
	846.40258018	−0.0928268	846.40258018	9	T	8	1048.5825935	−0.0677009	1048.5825935	
	943.45534404		943.45534404	10	P	7	947.53491499	−0.1073637	474.27109573	−0.2620625
	1040.5081079		1040.5081079	11	P	6	850.48215113		850.48215113	
	1139.5765218	−0.050887	1139.5765218	12	V	5	753.42938728		753.42938728	
	1286.6449357	−0.0815812	1286.6449357	13	F	4	654.36097337	−0.0088005	654.36097337	
+0.0593036	693.36031305	−0.1885694	1385.7133496	14	V	3	507.29255945		507.29255945	
	1532.7817636	+0.1083732	1532.7817636	15	F	2	408.22414553	−0.0343262	408.22414553	
	1646.824691	−0.2071373	1646.824691	16	N	1	261.15573162		261.15573162	
				17	K	0	147.11280417		147.11280417	

Scan number	16204	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel10_091024034333
Method	ITMS; CID	Genenames	ATG12



precursor
information

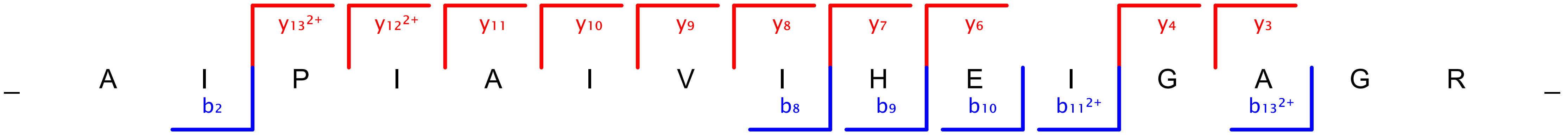
Mass:	1146.66485
m/z:	574.3397
Charge:	2+
Retentiontime:	95.6546020507813
Score:	169.374
Mass Error [ppm]:	−0.012892
PEP:	7.5465E−06
Precursor Type:	MULTI

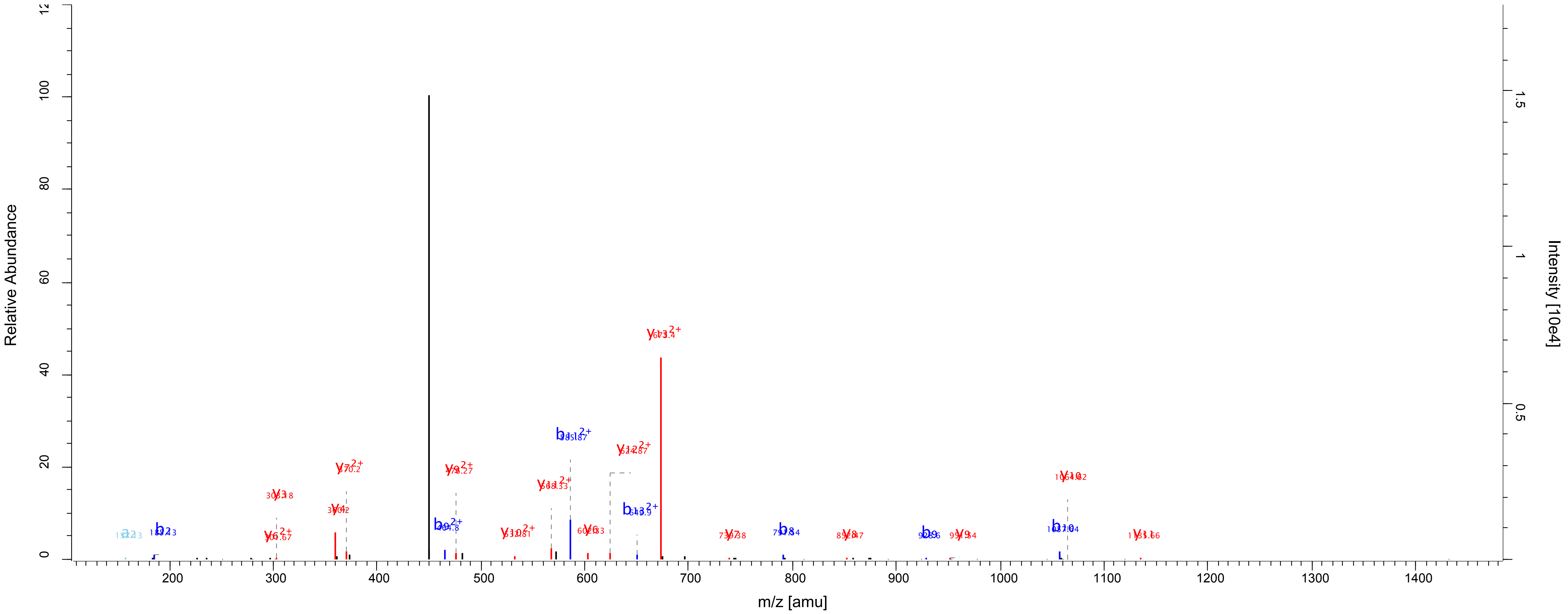
ge
information

Annotation:	8 of 10
AminoAcids Coverage:	80 %
Intensity Coverage:	68 %
Peak Coverage:	36 %
Protein Localisation:	80 ... 89

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.060040319		102.05495494	1	T	9				
−0.069855	187.1441043	+0.046177	215.13901892	2	I	8	1046.6244583		523.81586737	+0.0582171
	315.20268181	−0.1303357	343.19759643	3	Q	7	933.5403943	−0.0721326	467.27383538	−0.0402538
	372.22414553	−0.0083058	400.21906016	4	G	6	805.48181678	−0.0714164	805.48181678	
	485.30820951	+0.0933602	513.30312414	5	I	5	748.46035306	−0.1073257	748.46035306	
	598.39227349	+0.0219305	626.38718812	6	I	4	635.37628908	−0.0571362	635.37628908	
	713.41921653	−0.1644363	741.41413115	7	D	3	522.2922251	−0.1191294	522.2922251	
	860.48763044		888.48254507	8	F	2	407.26528207	−0.1079334	407.26528207	
	973.57169442	−0.1803175	1001.566609	9	I	1	260.19686815	+0.0702827	260.19686815	
				10	K	0	147.11280417		147.11280417	

Scan number	18608	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel10_091024034333
Method	ITMS; CID	Genenames	TYMP





precursor information

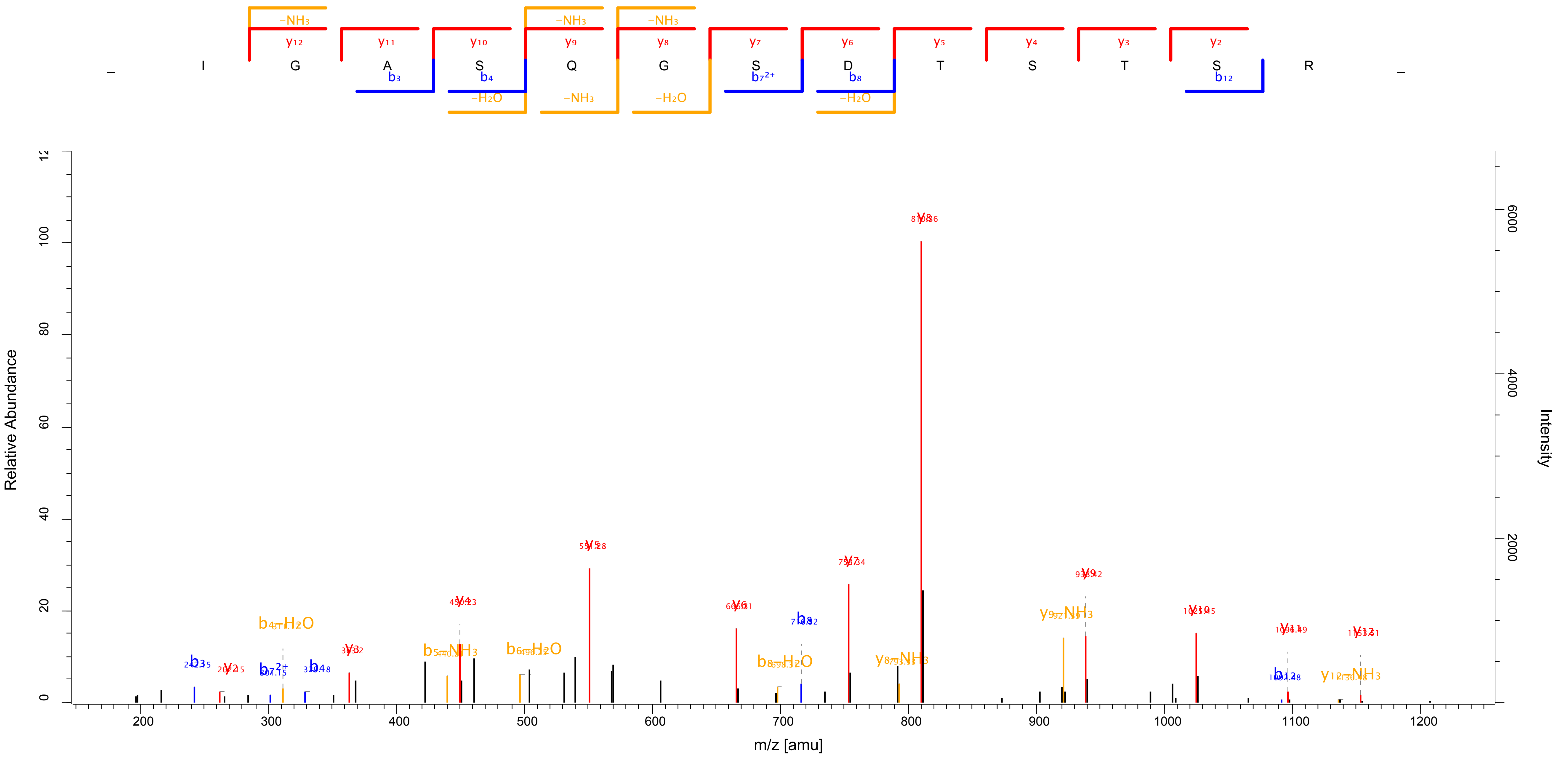
Mass:	1528.90889
m/z:	510.64357
Charge:	3+
Retentiontime:	109.710746765137
Score:	161.9885
Mass Error [ppm]:	-0.037678
PEP:	4.1253E-14
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverage:	80 %
Intensity Coverage:	40 %
Peak Coverage:	40 %
Protein Localisation:	394 ... 408

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
	44.0494756		72.0443903		72.0443903	1	A	14				
+0.0547691	157.13354		185.128454	+0.1216526	185.128454	2	I	13	1458.87911		1458.87911	
	254.186303		282.181218		282.181218	3	P	12	1345.79505		673.401161	+0.2130967
	367.270367		395.265282		395.265282	4	I	11	1248.74228		624.874779	+0.0029673
	438.307481		466.302396		466.302396	5	A	10	1135.65822	+0.2577976	568.332747	−0.1401813
	551.391545		579.38646		579.38646	6	I	9	1064.6211	+0.1202288	532.81419	−0.0160336
	650.459959		678.454874		678.454874	7	V	8	951.53704	−0.2905193	476.272158	+0.0522435
	763.544023		791.538938	−0.1631443	791.538938	8	I	7	852.468626	−0.214537	852.468626	
	900.602935	+0.0054814	464.802563	−0.0907085	928.59785	9	H	6	739.384562	+0.1839191	370.195919	+0.0706822
	1029.64553		1057.64044	−0.1525277	1057.64044	10	E	5	602.32565	−0.1141637	301.666463	+0.440287
	1142.72959	+0.0883931	585.865892		1170.72451	11	I	4	473.283057		473.283057	
	1199.75106		1227.74597		1227.74597	12	G	3	360.198993	−0.0803411	360.198993	
	1270.78817	−0.3384787	649.89518		1298.78308	13	A	2	303.17753	+0.0401827	303.17753	
	1327.80963		1355.80455		1355.80455	14	G	1	232.140416		232.140416	
						15	R	0	175.118952		175.118952	

Scan number	1512	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel12
Method	ITMS; CID	Genenames	SLCO2A1



precursor information

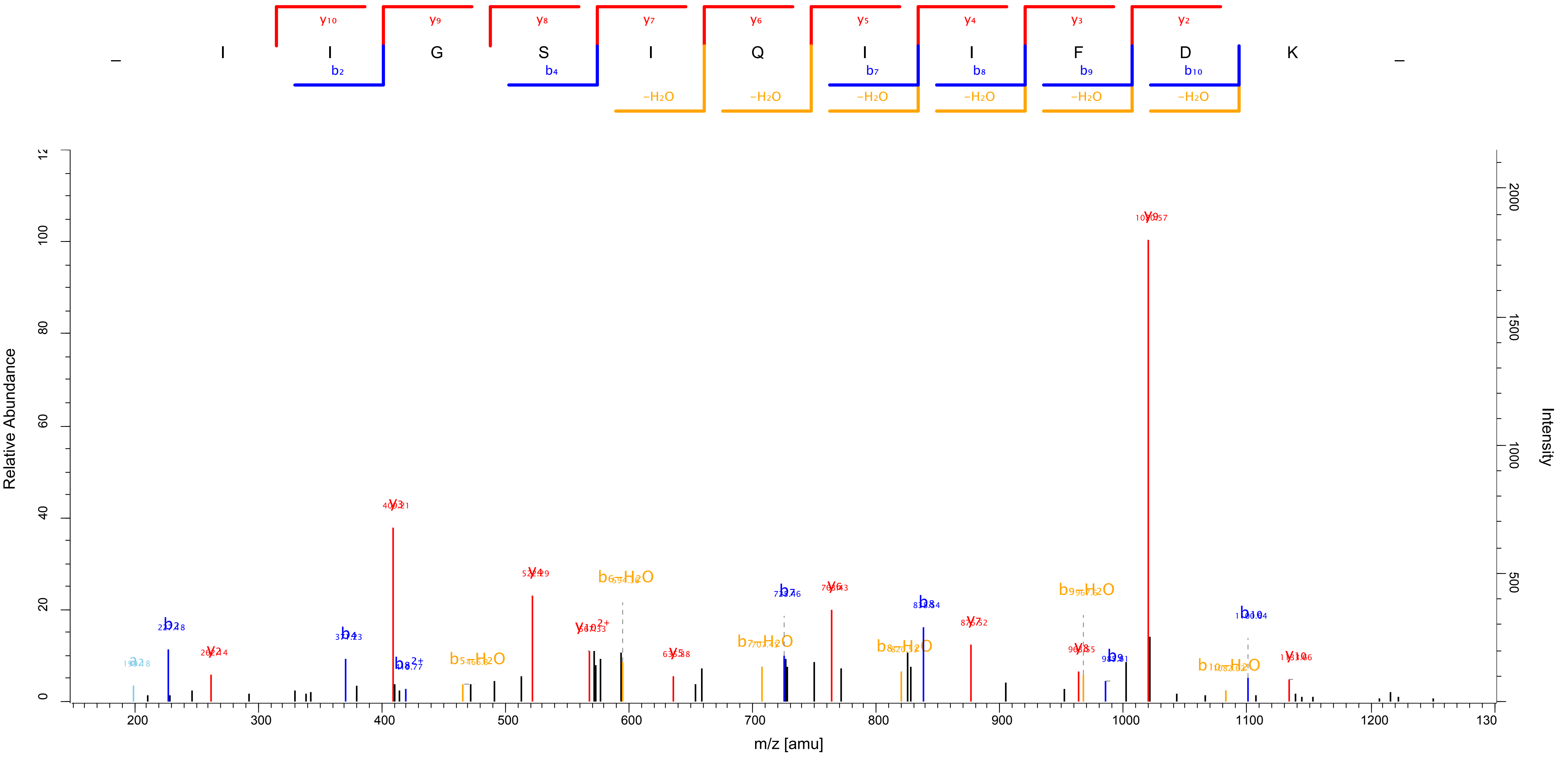
Mass:	1265.58455
m/z:	633.79955
Charge:	2+
Retentiontime:	19.3582286834717
Score:	128.8469
Mass Error [ppm]:	−0.17762
PEP:	0.0003097
Precursor Type:	ISO

general information

Annotation:	11 of 13
AminoAcids Coverage:	85 %
Intensity Coverage:	63 %
Peak Coverage:	39 %
Protein Localisation:	7 ... 19

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	114.091340447		114.091340447	1	I	12		
	171.112804171		171.112804171	2	G	11	1153.507984547	−0.1405529
	242.149917958	+0.0328976	242.149917958	3	A	10	1096.486520824	+0.0122585
	329.181946368	+0.2051386	329.181946368	4	S	9	1025.449407036	−0.1221365
	457.24052388		457.24052388	5	Q	8	938.417378626	+0.0155437
	514.261987603		514.261987603	6	G	7	810.358801114	−0.0518553
−0.0490227	301.15064624		601.294016013	7	S	6	753.337337391	−0.0263633
	716.320959045	+0.0425663	716.320959045	8	D	5	666.305308981	+0.0511974
	817.368637519		817.368637519	9	T	4	551.278365949	−0.0014494
	904.400665929		904.400665929	10	S	3	450.230687475	+0.1675059
	1005.448344403		1005.448344403	11	T	2	363.198659065	+0.0308942
	1092.480372813	−0.0680193	1092.480372813	12	S	1	262.150980591	−0.0183512
				13	R	0	175.118952181	

Scan number	17628	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel12
Method	ITMS; CID	Genenames	TRIM8



precursor information

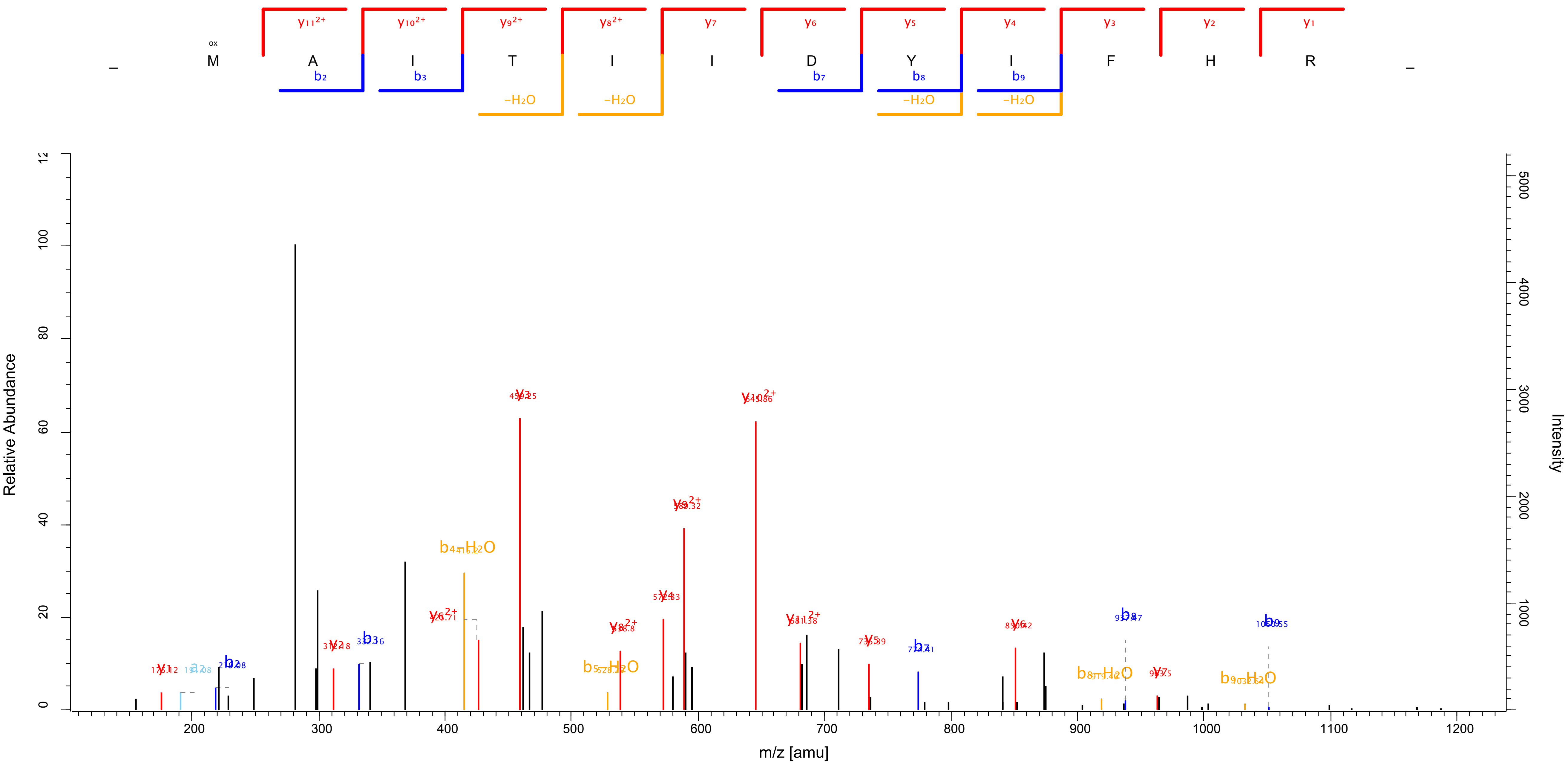
Mass:	1245.73368
m/z:	623.87412
Charge:	2+
Retentiontime:	102.610961914063
Score:	150.9421
Mass Error [ppm]:	0.32872
PEP:	9.2834E−05
Precursor Type:	ISO

general information

Annotation:	9 of 11
AminoAcids Coverage:	82 %
Intensity Coverage:	64 %
Peak Coverage:	38 %
Protein Localisation:	282 ... 292

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.0964258		114.09134		114.09134	1	I	10				
+0.0811069	199.18049		227.175404	−0.0292863	227.175404	2	I	9	1133.65649	+0.0294264	567.331882	+0.0254793
	256.201954		284.196868		284.196868	3	G	8	1020.57242	−0.1071517	1020.57242	
	343.233982		371.228897	+0.0328222	371.228897	4	S	7	963.550959	−0.0185493	963.550959	
	456.318046		484.312961		484.312961	5	I	6	876.518931	+0.0110377	876.518931	
	584.376623		612.371538		612.371538	6	Q	5	763.434867	+0.064462	763.434867	
	697.460687		725.455602	−0.3979238	725.455602	7	I	4	635.376289	−0.0344922	635.376289	
	810.544751	−0.3240083	419.773471	−0.1290825	838.539666	8	I	3	522.292225	+0.0695303	522.292225	
	957.613165		985.60808	−0.241869	985.60808	9	F	2	409.208161	+0.0751641	409.208161	
	1072.64011		1100.63502	−0.2423228	1100.63502	10	D	1	262.139747	+0.029076	262.139747	
						11	K	0	147.112804		147.112804	

Scan number	19715	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel12
Method	ITMS; CID	Genenames	BANP



precursor information

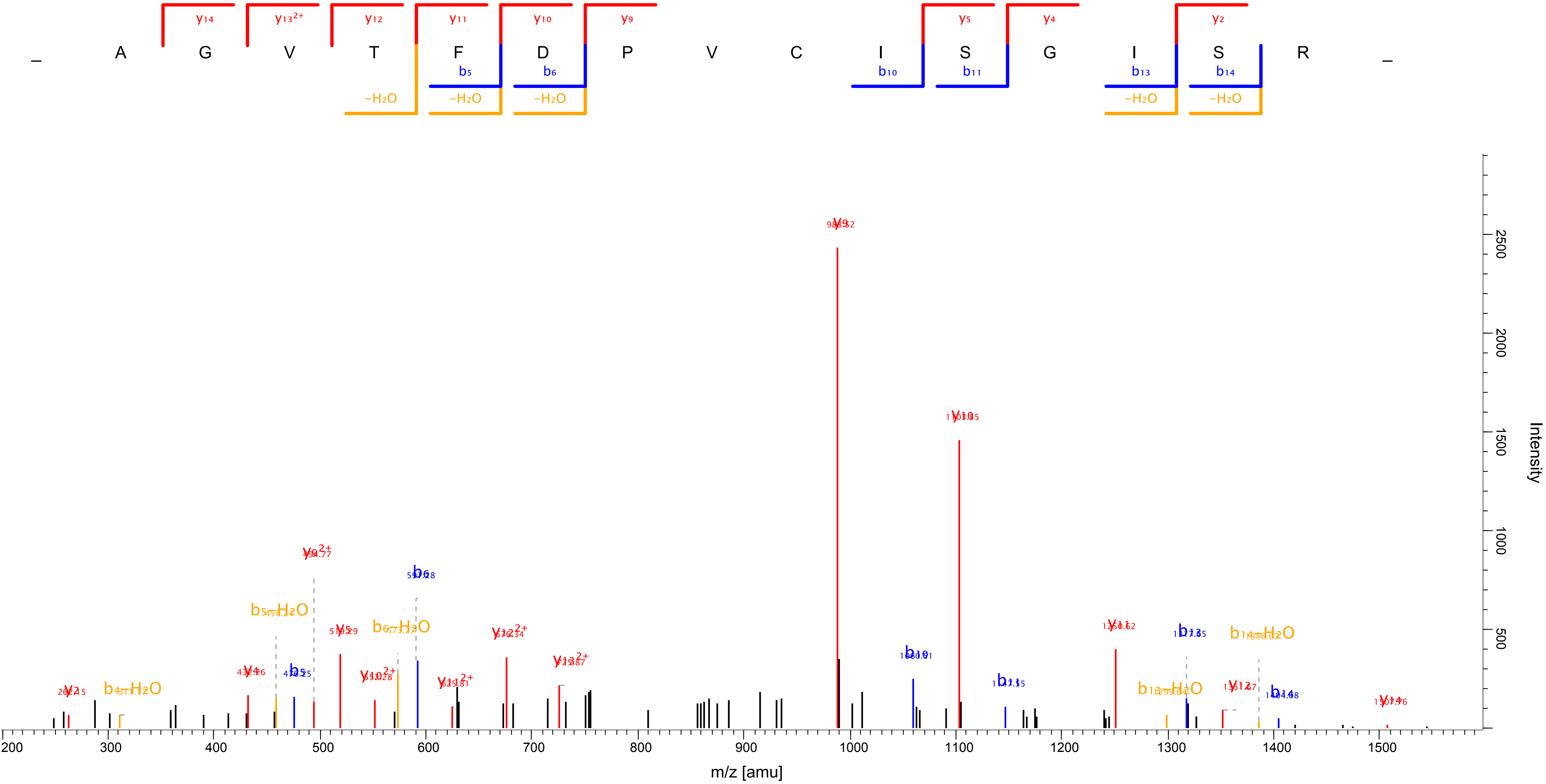
Mass:	1507.785
m/z:	503.60228
Charge:	3+
Retentiontime:	115.159126281738
Score:	142.8267
Mass Error [ppm]:	−0.47728
PEP:	3.3906E−05
Precursor Type:	MULTI

general information

Annotation:	11 of 12
AminoAcids Coverage:	92 %
Intensity Coverage:	48 %
Peak Coverage:	38 %
Protein Localisation:	251 ... 262

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.04776107		148.04267569	1	M	11				
+0.0593207	191.08487486	−0.0076764	219.07978948	2	A	10	1361.7575977		681.38243709	−0.1099151
	304.16893884	−0.1508225	332.16385346	3	I	9	1290.7204839		645.8638802	+0.1024284
	405.21661732		433.21153194	4	T	8	1177.6364199		589.32184821	−0.0074561
	518.3006813		546.29559592	5	I	7	1076.5887415		538.79800897	−0.0267687
	631.38474528		659.3796599	6	I	6	963.50467749	−0.0103538	963.50467749	
	746.41168831	−0.2727528	774.40660293	7	D	5	850.42061351	−0.1607869	425.71394499	+0.0227493
	909.47501685	+0.0237819	937.46993147	8	Y	4	735.39367048	+0.1030947	735.39367048	
	1022.5590808	+0.2571618	1050.5539954	9	I	3	572.33034194	+0.0806688	572.33034194	
	1169.6274947		1197.6224094	10	F	2	459.24627796	−0.1434948	459.24627796	
	1306.6864066		1334.6813212	11	H	1	312.17786404	−0.0502395	312.17786404	
				12	R	0	175.11895218	+0.12705	175.11895218	

Scan number	14529	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel13
Method	ITMS; CID	Genenames	ATHL1



precursor information

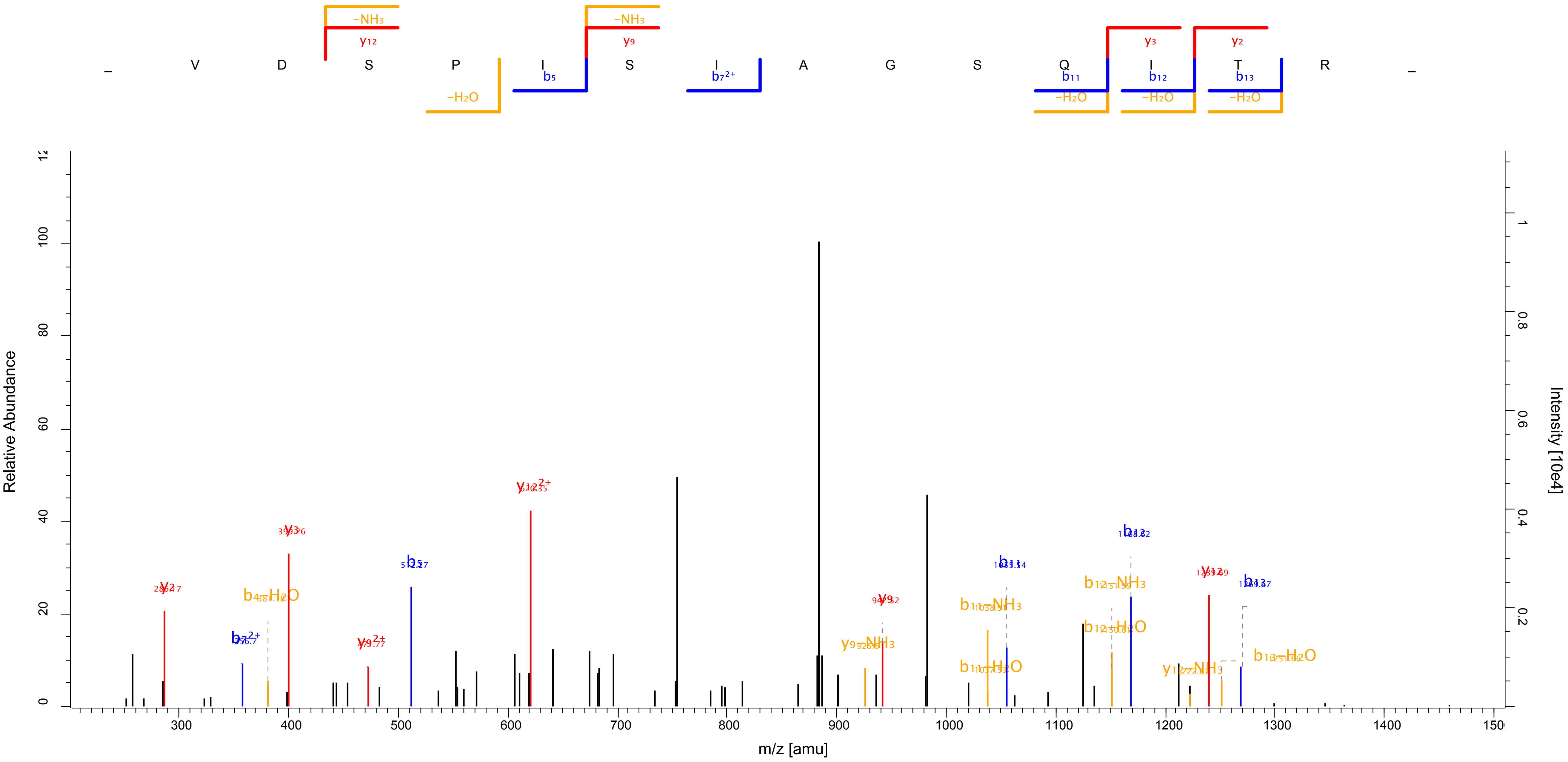
Mass:	1577.78735
m/z:	789.90095
Charge:	2+
Retentiontime:	83.555549621582
Score:	143.4244
Mass Error [ppm]:	0.10781
PEP:	2.6416E−05
Precursor Type:	ISO

general information

Annotation:	11 of 15
AminoAcids Coverage:	73 %
Intensity Coverage:	57 %
Peak Coverage:	31 %
Protein Localisation:	634 ... 648

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	14				
	129.065853978	2	G	13	1507.757339717	−0.1706698	1507.757339717	
	228.134267894	3	V	12	1450.735875993		725.87157623	+0.3621274
	329.181946368	4	T	11	1351.667462077	+0.1109803	676.337369272	+0.0345179
−0.1099794	476.250360284	5	F	10	1250.619783603	−0.0618002	625.813530035	−0.3767014
+0.0927528	591.277303316	6	D	9	1103.551369687	+0.0064916	552.279323077	+0.1299176
	688.330067168	7	P	8	988.524426655	−0.0378544	494.765851561	+0.0404229
	787.398481085	8	V	7	891.471662803		891.471662803	
	947.429129286	9	C	6	792.403248887		792.403248887	
+0.0162257	1060.513193266	10	I	5	632.372600685		632.372600685	
−0.1719307	1147.545221676	11	S	4	519.288536705	+0.1023324	519.288536705	
	1204.5666854	12	G	3	432.256508295	−0.0523457	432.256508295	
−0.0711595	1317.65074938	13	I	2	375.235044571		375.235044571	
+0.0873638	1404.68277779	14	S	1	262.150980591	+0.0876058	262.150980591	
		15	R	0	175.118952181		175.118952181	

Scan number	9938	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel15
Method	ITMS; CID	Genenames	C9orf63



precursor information

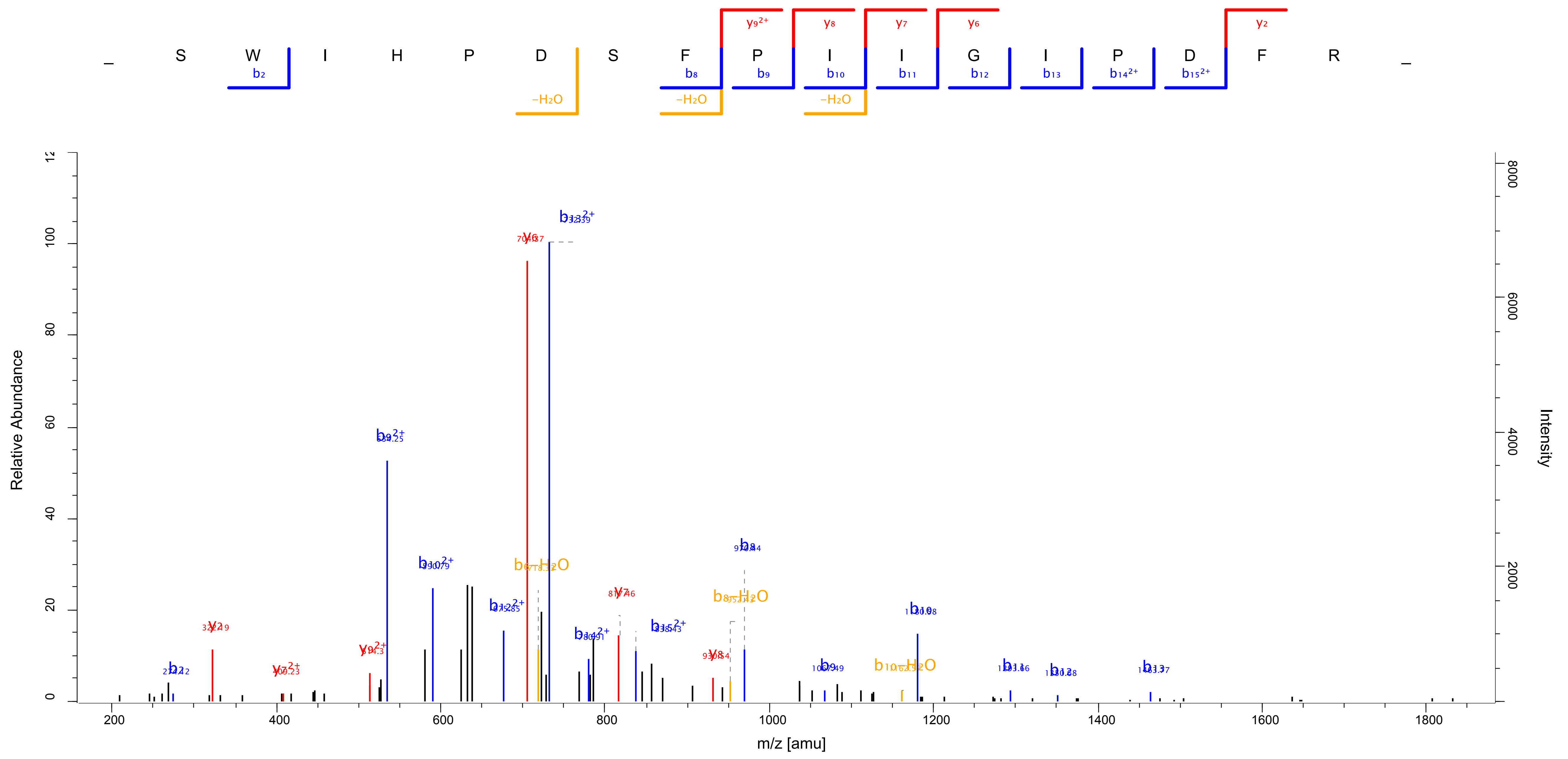
Mass:	1442.77287
m/z:	722.39371
Charge:	2+
Retentiontime:	59.8910865783691
Score:	105.649
Mass Error [ppm]:	−0.026598
PEP:	0.00014435
Precursor Type:	MULTI

general information

Annotation:	8 of 14
AminoAcids Coverage:	57 %
Intensity Coverage:	37 %
Peak Coverage:	27 %
Protein Localisation:	58 ... 71

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.07569038		100.07569038	1	V	13				
	215.10263341		215.10263341	2	D	12	1354.7200383		1354.7200383	
	302.13466182		302.13466182	3	S	11	1239.6930953	−0.0278121	620.35018588	+0.1376071
	399.18742568		399.18742568	4	P	10	1152.6610669		1152.6610669	
	512.27148966	−0.0212455	512.27148966	5	I	9	1055.608303		1055.608303	
	599.30351807		599.30351807	6	S	8	942.52423906	−0.0896687	471.76575776	+0.4493912
+0.4585156	356.69742926		712.38758205	7	I	7	855.49221065		855.49221065	
	783.42469584		783.42469584	8	A	6	742.40814667		742.40814667	
	840.44615956		840.44615956	9	G	5	671.37103288		671.37103288	
	927.47818797		927.47818797	10	S	4	614.34956916		614.34956916	
	1055.5367655	−0.0746073	1055.5367655	11	Q	3	527.31754075		527.31754075	
	1168.6208295	−0.1327924	1168.6208295	12	I	2	399.25896324	−0.0099398	399.25896324	
	1269.6685079	−0.2282003	1269.6685079	13	T	1	286.17489925	+0.1346711	286.17489925	
				14	R	0	185.12722078		185.12722078	

Scan number	20276	Raw file	20091021_Orbi6_MaHe_SA_ADH_exp3_30h_Gel16
Method	ITMS; CID	Genenames	ZNF316



precursor information

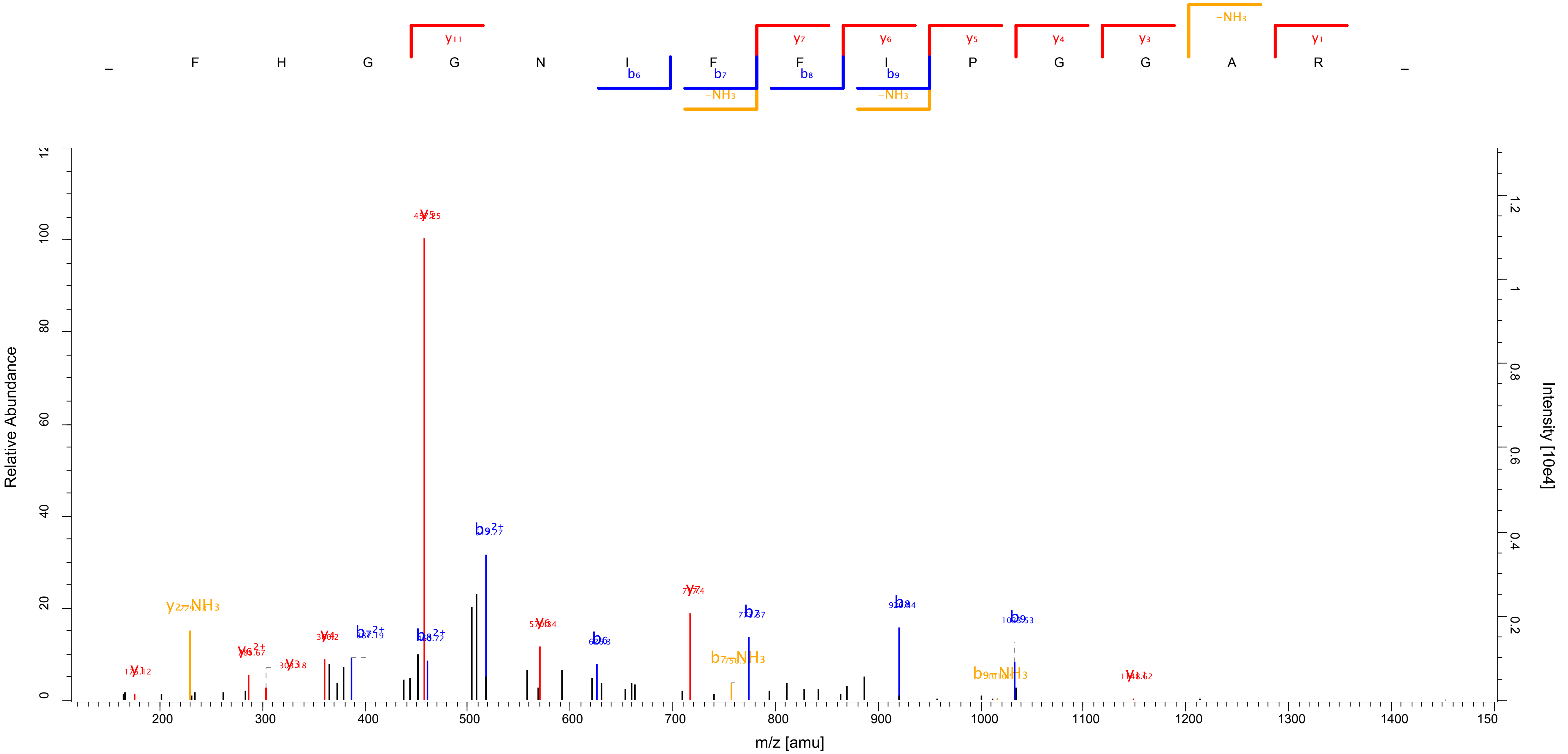
Mass:	1996.0213
m/z:	666.34771
Charge:	3+
Retentiontime:	115.604103088379
Score:	121.7603
Mass Error [ppm]:	0.31083
PEP:	1.3896E−05
Precursor Type:	MULTI

general information

Annotation:	11 of 17
AminoAcids Coverage:	65 %
Intensity Coverage:	65 %
Peak Coverage:	28 %
Protein Localisation:	606 ... 622

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876		88.039304876	1	S	16				
	274.11861783	−0.1318625	274.11861783	2	W	15	1909.9959305		1909.9959305	
	387.20268181		387.20268181	3	I	14	1723.9166176		1723.9166176	
	524.26159367		524.26159367	4	H	13	1610.8325536		1610.8325536	
	621.31435752		621.31435752	5	P	12	1473.7736417		1473.7736417	
	736.34130056		736.34130056	6	D	11	1376.7208779		1376.7208779	
	823.37332897		823.37332897	7	S	10	1261.6939348		1261.6939348	
	970.44174288	−0.0015573	970.44174288	8	F	9	1174.6619064		1174.6619064	
−0.0306157	534.2508916	−0.3785399	1067.4945067	9	P	8	1027.5934925		514.30038448	+0.0656433
−0.0147864	590.79292359	−0.0932192	1180.5785707	10	I	7	930.54072865	+0.2140931	930.54072865	
	1293.6626347	−0.083289	1293.6626347	11	I	6	817.45666467	−0.1513058	409.23197057	−0.2648075
−0.1268154	675.84568744	+0.0252522	1350.6840984	12	G	5	704.37260069	−0.003277	704.37260069	
−0.0227902	732.38771943	−0.2631575	1463.7681624	13	I	4	647.35113696		647.35113696	
−0.2511985	780.91410136		1560.8209263	14	P	3	534.26707298		534.26707298	
−0.2444674	838.42757288		1675.8478693	15	D	2	437.21430913		437.21430913	
	1822.9162832		1822.9162832	16	F	1	322.1873661	+0.0078243	322.1873661	
				17	R	0	175.11895218		175.11895218	

Scan number	12337	Raw file	20091023_Orbi6_MaHe_SA_ADH_exp3_GFR_Gel03
Method	ITMS; CID	Genenames	GFER



precursor information

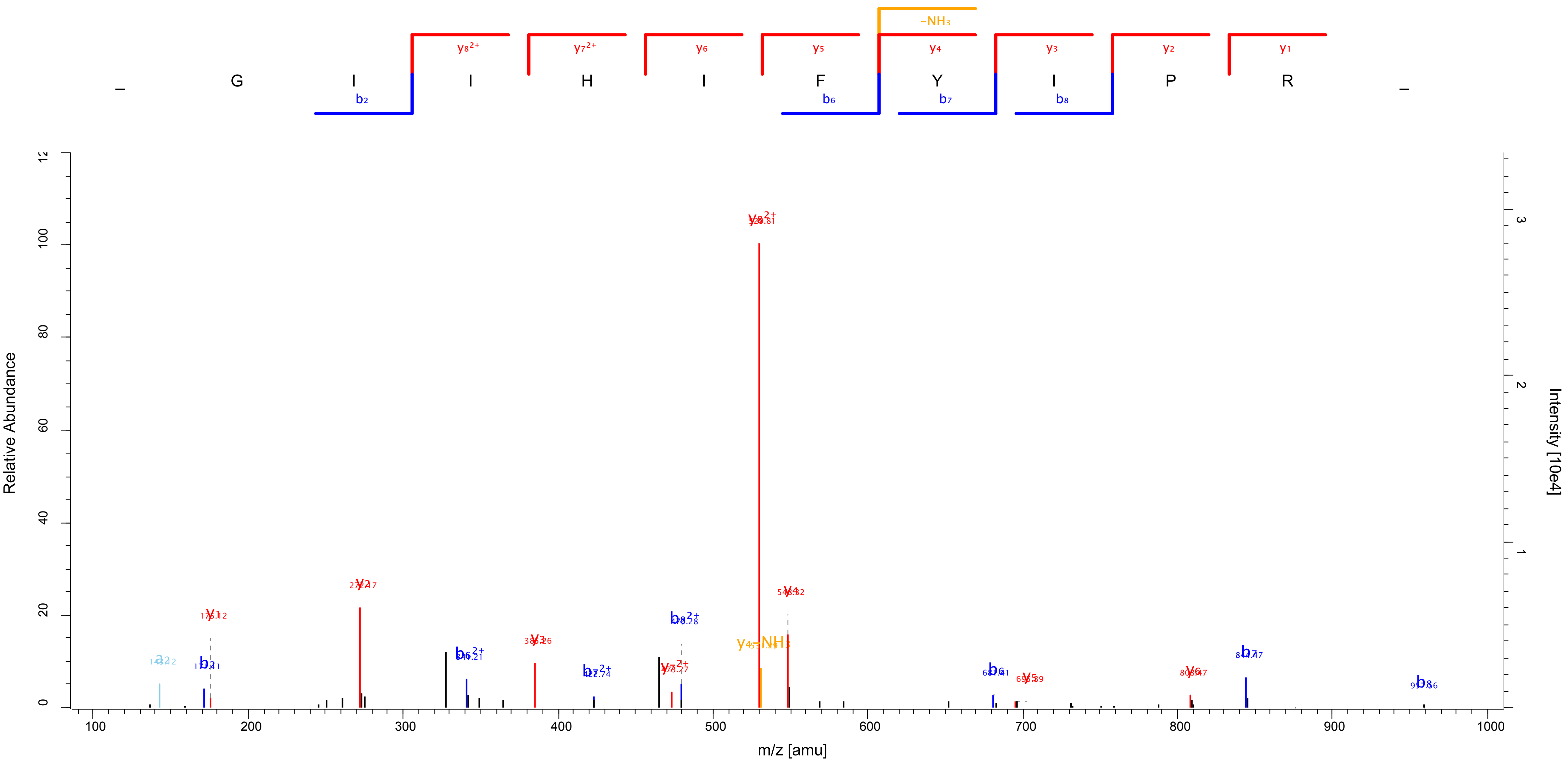
Mass:	1488.76258
m/z:	497.26147
Charge:	3+
Retentiontime:	75.4469833374023
Score:	105.1704
Mass Error [ppm]:	−0.021919
PEP:	0.00016127
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverage:	71 %
Intensity Coverage:	62 %
Peak Coverage:	31 %
Protein Localisation:	10 ... 23

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.07569038		148.07569038	1	F	13				
	285.13460225		285.13460225	2	H	12	1342.7014798		1342.7014798	
	342.15606597		342.15606597	3	G	11	1205.642568		1205.642568	
	399.17752969		399.17752969	4	G	10	1148.6211042	−0.1261091	1148.6211042	
	513.22045714		513.22045714	5	N	9	1091.5996405		1091.5996405	
	626.30452112	+0.1432328	626.30452112	6	I	8	977.55671306		977.55671306	
+0.0639531	387.19010575	+0.0537007	773.37293504	7	F	7	864.47264908		864.47264908	
+0.0396338	460.72431271	−0.1210975	920.44134895	8	F	6	717.40423516	−0.049804	717.40423516	
−0.0729243	517.2663447	+0.0259787	1033.5254129	9	I	5	570.33582125	−0.069708	285.67154886	+0.017416
	1130.5781768		1130.5781768	10	P	4	457.25175727	+0.0113653	457.25175727	
	1187.5996405		1187.5996405	11	G	3	360.19899342	+0.0991633	360.19899342	
	1244.6211042		1244.6211042	12	G	2	303.17752969	−0.0384916	303.17752969	
	1315.658218		1315.658218	13	A	1	246.15606597		246.15606597	
				14	R	0	175.11895218	+0.1438652	175.11895218	

Scan number	13337	Raw file	20091023_Orbi6_MaHe_SA_ADH_exp3_GFR_Gel03
Method	ITMS; CID	Genenames	LY96



precursor information

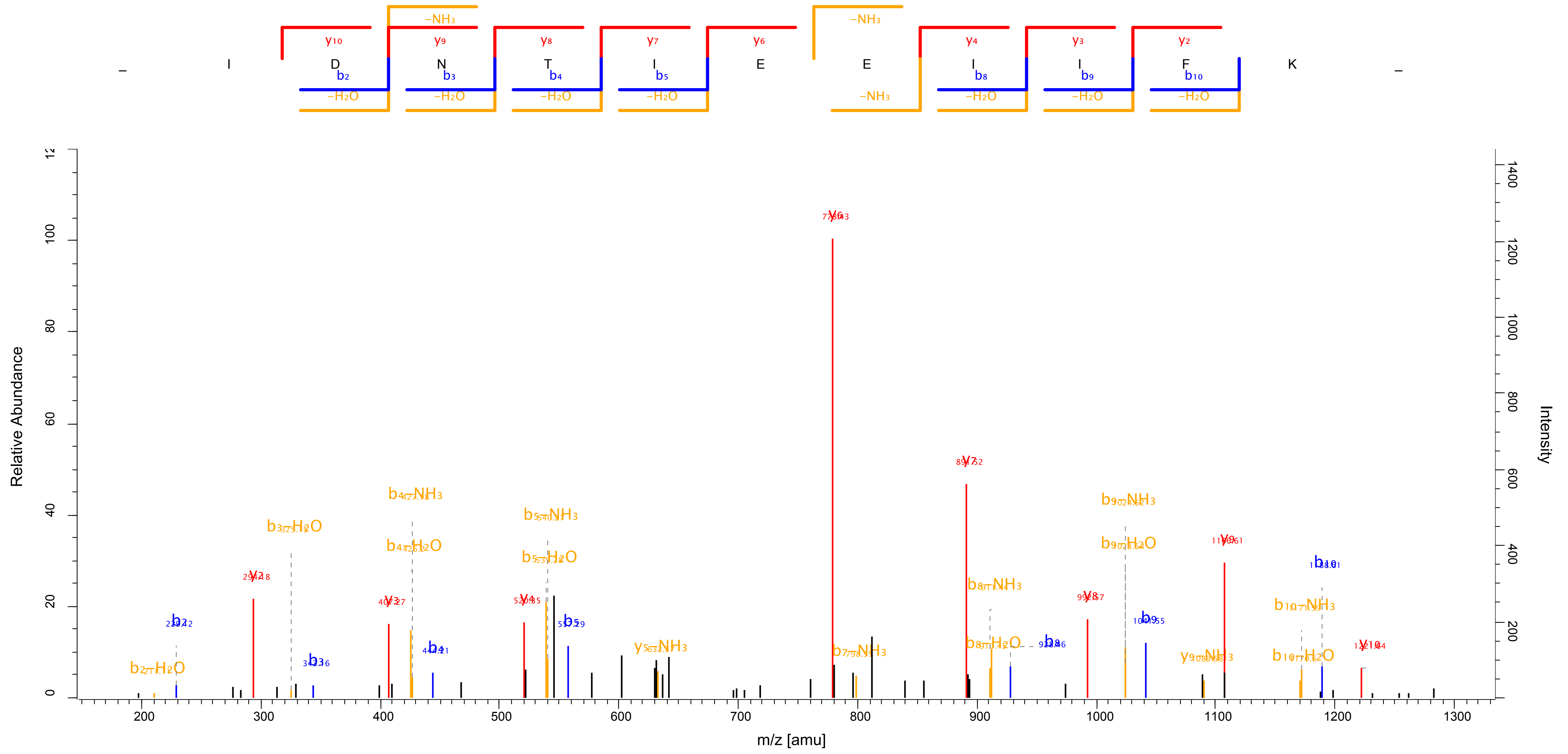
Mass:	1227.7127
m/z:	410.24484
Charge:	3+
Retentiontime:	80.7984237670898
Score:	173.2345
Mass Error [ppm]:	−0.09393
PEP:	1.7526E−06
Precursor Type:	MULTI

ge information

Annotation:	9 of 10
AminoAcids Coverage:	90 %
Intensity Coverage:	76 %
Peak Coverage:	35 %
Protein Localisation:	59 ... 68

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	30.0338256		58.0287402		58.0287402	1	G	9				
+0.0081786	143.11789		171.112804	−0.1224935	171.112804	2	I	8	1171.69863		1171.69863	
	256.201954		284.196868		284.196868	3	I	7	1058.61456		529.810919	+0.1738829
	393.260865		421.25578		421.25578	4	H	6	945.530498		473.268887	+0.0619537
	506.344929		534.339844		534.339844	5	I	5	808.471586	+0.0950029	808.471586	
	653.413343	−0.0358617	341.207767	−0.1047911	681.408258	6	F	4	695.387522	+0.0396626	695.387522	
	816.476672	−0.056265	422.739431	−0.0279829	844.471586	7	Y	3	548.319109	−0.0619064	548.319109	
	929.560736	−0.1347044	479.281463	−0.1630723	957.55565	8	I	2	385.25578	+0.0550415	385.25578	
	1026.6135		1054.60841		1054.60841	9	P	1	272.171716	+0.0359256	272.171716	
						10	R	0	175.118952	+0.0583244	175.118952	

Scan number	16912	Raw file	20091023_Orbi6_MaHe_SA_ADH_exp3_GFR_Gel04
Method	ITMS; CID	Genenames	PCGF5



precursor information

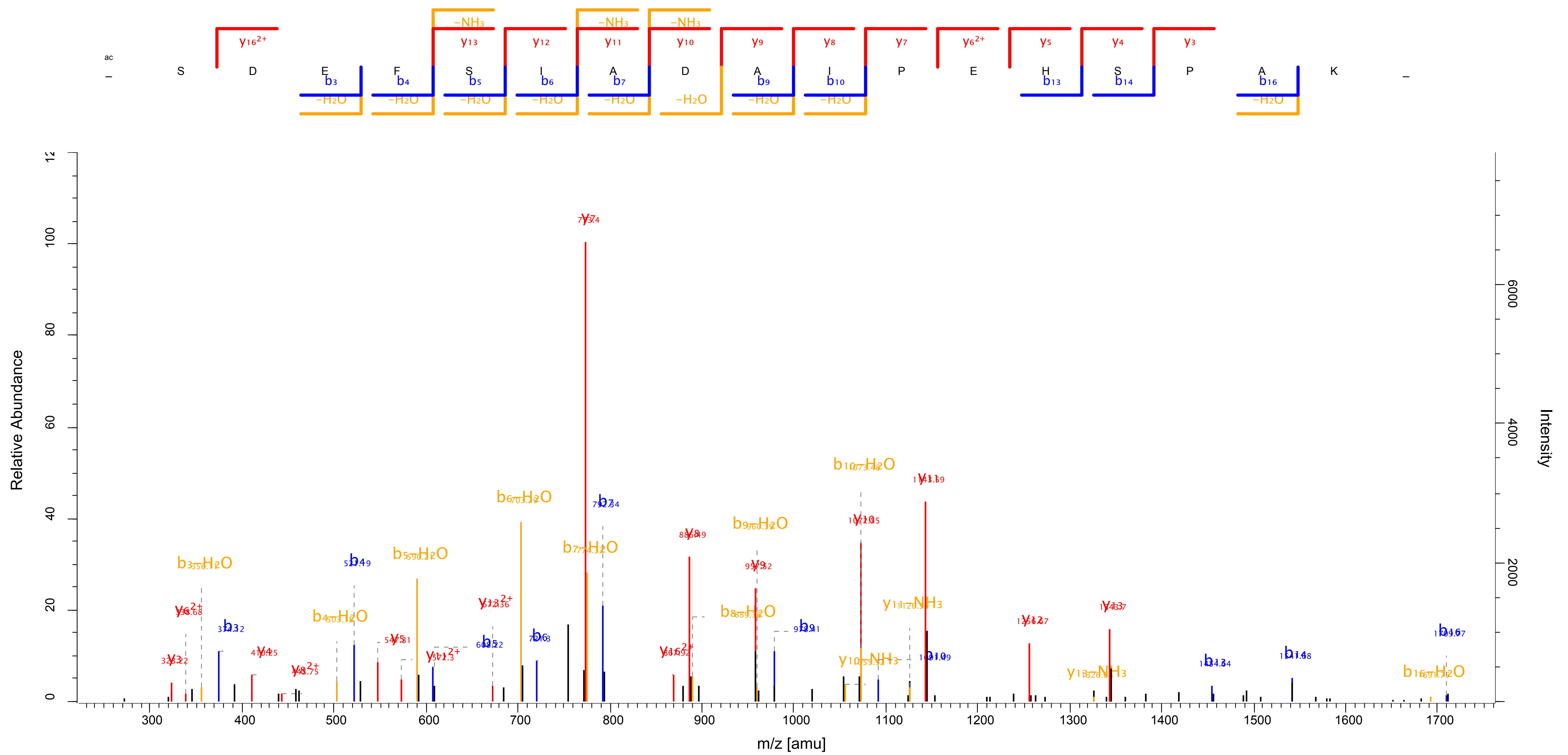
Mass:	1333.7134
m/z:	667.86398
Charge:	2+
Retentiontime:	100.291534423828
Score:	212.8151
Mass Error [ppm]:	0.35286
PEP:	6.6221E-27
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverage:	82 %
Intensity Coverage:	71 %
Peak Coverage:	45 %
Protein Localisation:	71 ... 81

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	114.091340447	1	I	10		
-0.0300572	229.118283479	2	D	9	1221.636145174	-0.0261598
+0.1991406	343.161210926	3	N	8	1106.609202142	+0.0198262
-0.0812649	444.2088894	4	T	7	992.566274694	-0.1168728
-0.0486297	557.292953381	5	I	6	891.51859622	-0.0853076
	686.335546477	6	E	5	778.43453224	-0.0995103
	815.378139573	7	E	4	649.391939144	
-0.277206	928.462203554	8	I	3	520.349346048	-0.1207694
-0.232913	1041.546267534	9	I	2	407.265282067	-0.0711292
-0.1958582	1188.61468145	10	F	1	294.181218087	-0.0946092
		11	K	0	147.112804171	

Scan number	13740	Raw file	20091023_Orbi6_MaHe_SA_ADH_exp3_GFR_Gel05
Method	ITMS; CID	Genenames	MAPK1IP1L



precursor information

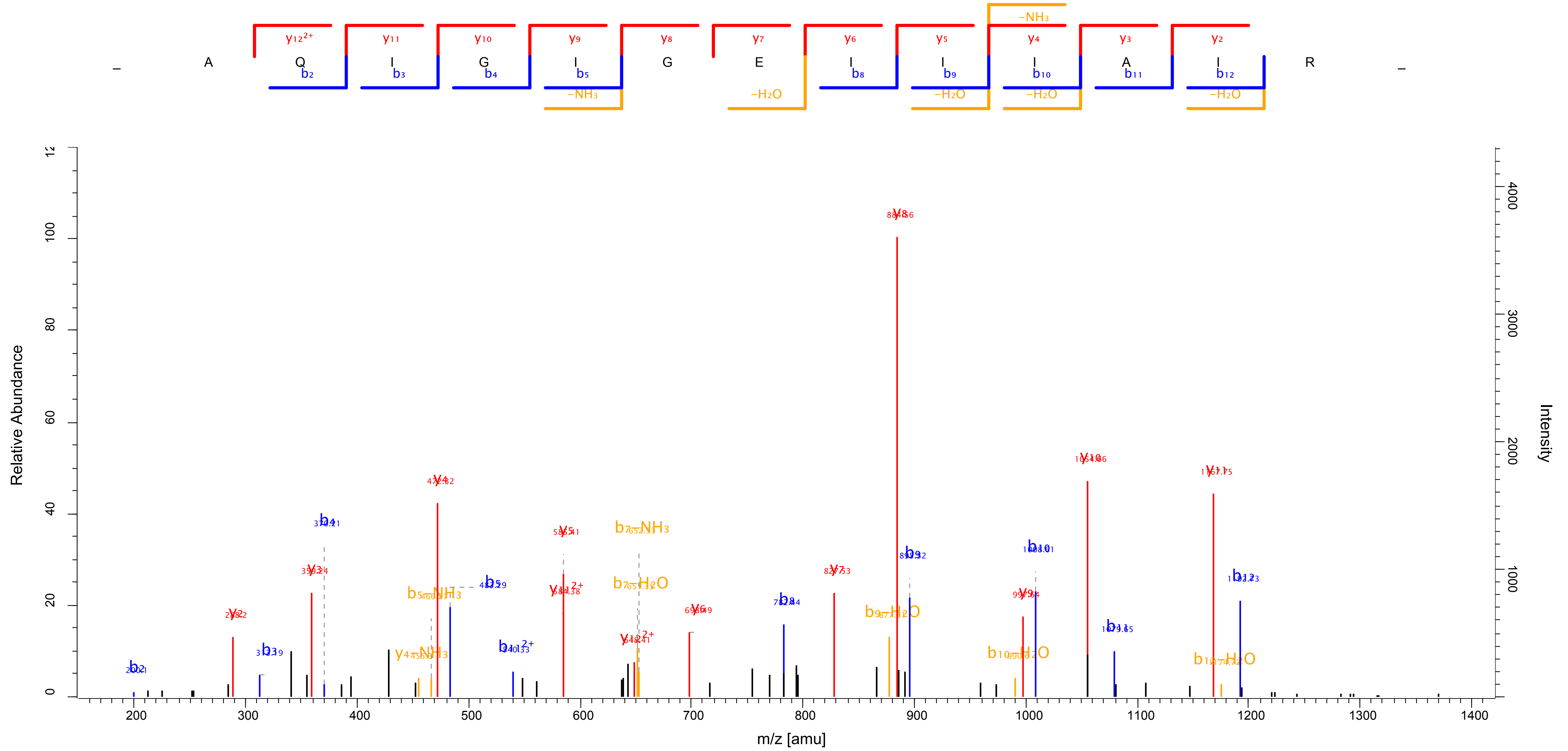
Mass:	1854.8642
m/z:	928.43938
Charge:	2+
Retentiontime:	82.1569442749023
Score:	237.4787
Mass Error [ppm]:	0.33639
PEP:	4.1322E-63
Precursor Type:	MULTI

general information

Annotation:	15 of 17
AminoAcids Coverage:	88 %
Intensity Coverage:	74 %
Peak Coverage:	41 %
Protein Localisation:	2 ... 18

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.049869563	1	S	16				
	245.076812595	2	D	15	1734.842454867		867.924865667	+0.4008179
−0.1744289	374.119405691	3	E	14	1619.815511835		1619.815511835	
−0.0741111	521.187819607	4	F	13	1490.772918739		1490.772918739	
−0.0778192	608.219848017	5	S	12	1343.704504822	−0.1261357	672.355890644	+0.0408989
−0.3549984	721.303911998	6	I	11	1256.672476413	+0.0337003	1256.672476413	
−0.2171855	792.341025785	7	A	10	1143.588412432	−0.1160003	572.297844449	+0.0112376
	907.367968817	8	D	9	1072.551298644	+0.0556349	1072.551298644	
−0.3453292	978.405082605	9	A	8	957.524355612	−0.0512721	957.524355612	
−0.2804064	1091.489146585	10	I	7	886.487241824	−0.0635968	443.747259146	−0.4266415
	1188.541910437	11	P	6	773.403177844	+0.0153402	773.403177844	
	1317.584503534	12	E	5	676.350413992		338.678845229	−0.3468445
−0.2513256	1454.643415396	13	H	4	547.307820896	+0.0441689	547.307820896	
−0.0926801	1541.675443806	14	S	3	410.248909033	+0.1217575	410.248909033	
	1638.728207658	15	P	2	323.216880624	+0.1274492	323.216880624	
+0.035826	1709.765321446	16	A	1	226.164116772		226.164116772	
		17	K	0	155.127002984		155.127002984	

Scan number	18511	Raw file	20091023_Orbi6_MaHe_SA_ADH_exp3_GFR_Gel05
Method	ITMS; CID	Genenames	TTC33



precursor information

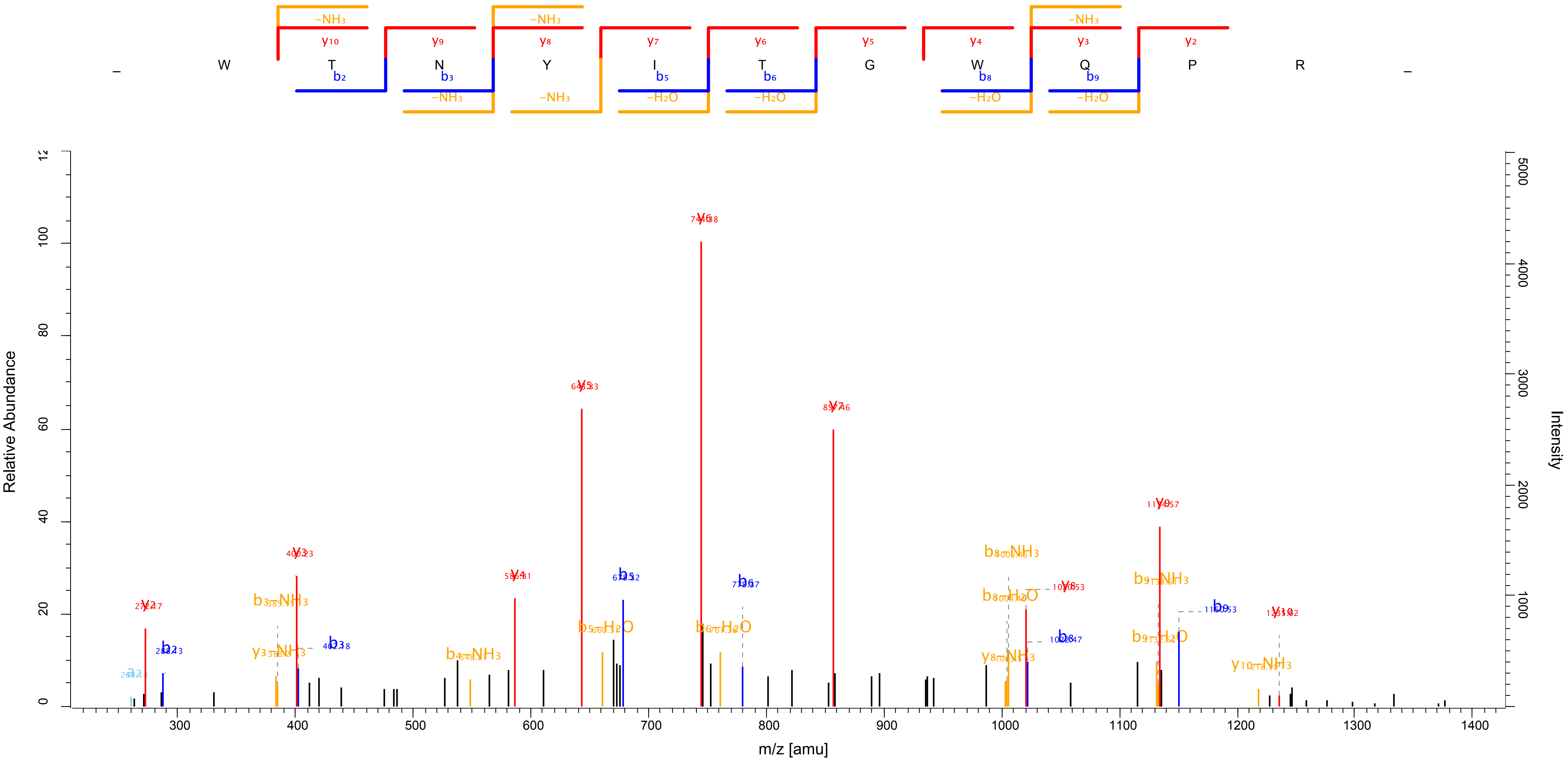
Mass:	1365.83453
m/z:	683.92454
Charge:	2+
Retentiontime:	109.013893127441
Score:	185.5934
Mass Error [ppm]:	0.10647
PEP:	7.5586E−09
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverage:	85 %
Intensity Coverage:	79 %
Peak Coverage:	41 %
Protein Localisation:	136 ... 148

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254		72.044390254	1	A	12				
	200.10296777	+0.1831803	200.10296777	2	Q	11	1295.8045479		648.40591219	−0.0259683
	313.18703175	−0.0767412	313.18703175	3	I	10	1167.7459704	−0.1215807	584.37662343	+0.1616456
	370.20849547	−0.093139	370.20849547	4	G	9	1054.6619064	−0.0677902	1054.6619064	
	483.29255945	−0.0228451	483.29255945	5	I	8	997.64044269	−0.0208748	997.64044269	
	540.31402317		540.31402317	6	G	7	884.55637871	−0.0365423	884.55637871	
	669.35661627		669.35661627	7	E	6	827.53491499	−0.041873	827.53491499	
	782.44068025	−0.0834415	782.44068025	8	I	5	698.49232189	+0.17583	698.49232189	
	895.52474423	−0.0895025	895.52474423	9	I	4	585.40825791	+0.0135561	585.40825791	
	1008.6088082	−0.1863839	1008.6088082	10	I	3	472.32419393	+0.0677128	472.32419393	
+0.0550536	540.32659923	−0.2200187	1079.645922	11	A	2	359.24012995	−0.0621514	359.24012995	
	1192.729986	−0.1610163	1192.729986	12	I	1	288.20301616	−0.0081309	288.20301616	
				13	R	0	175.11895218		175.11895218	

Scan number	13007	Raw file	20091023_Orbi6_MaHe_SA_ADH_exp3_GFR_Gel06
Method	ITMS; CID	Genenames	PLEKHA3



precursor information

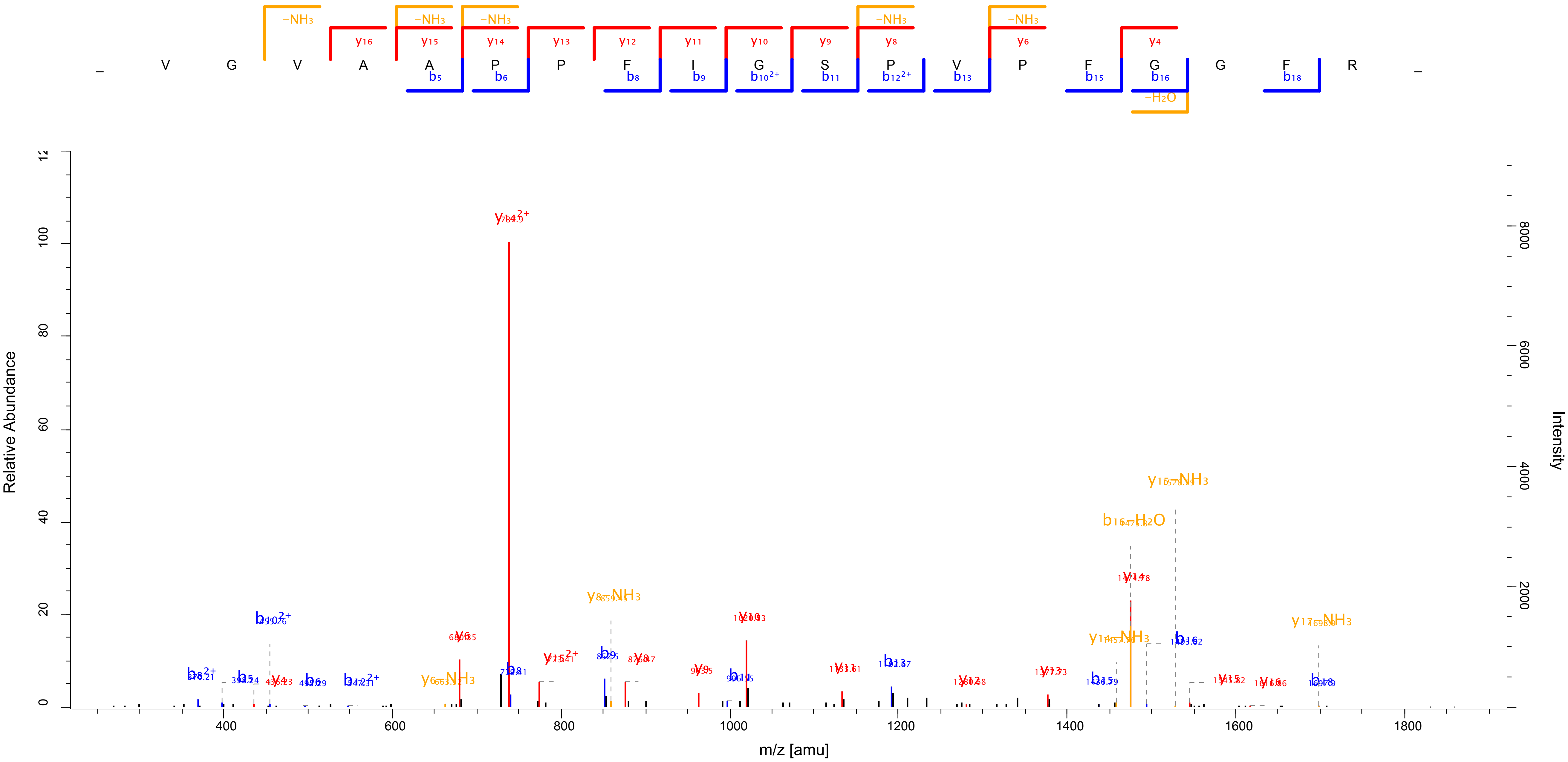
Mass:	1420.68864
m/z:	711.35159
Charge:	2+
Retentiontime:	78.967399597168
Score:	183.03
Mass Error [ppm]:	−0.1043
PEP:	7.7346E−11
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverage:	82 %
Intensity Coverage:	68 %
Peak Coverage:	39 %
Protein Localisation:	8 ... 18

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	159.091674798		187.08658942	1	W	10		
+0.1171165	260.139353272	−0.2153226	288.134267894	2	T	9	1235.616747136	−0.1660635
	374.182280719	−0.4365337	402.177195341	3	N	8	1134.569068662	−0.0912855
	537.245609258		565.24052388	4	Y	7	1020.526141214	−0.0349913
	650.329673238	+0.0087862	678.32458786	5	I	6	857.462812676	−0.0613234
	751.377351712	−0.0374885	779.372266334	6	T	5	744.378748696	−0.0219372
	808.398815436		836.393730058	7	G	4	643.331070222	+0.0429532
	994.478128389	−0.1217247	1022.473043011	8	W	3	586.309606498	+0.0415898
	1122.536705901	−0.0981488	1150.531620523	9	Q	2	400.230293544	+0.138664
	1219.589469753		1247.584384375	10	P	1	272.171716033	+0.010657
				11	R	0	175.118952181	

Scan number	17901	Raw file	20091023_Orbi6_MaHe_SA_ADH_exp3_GFR_Gel08
Method	ITMS; CID	Genenames	PYGO2



precursor information

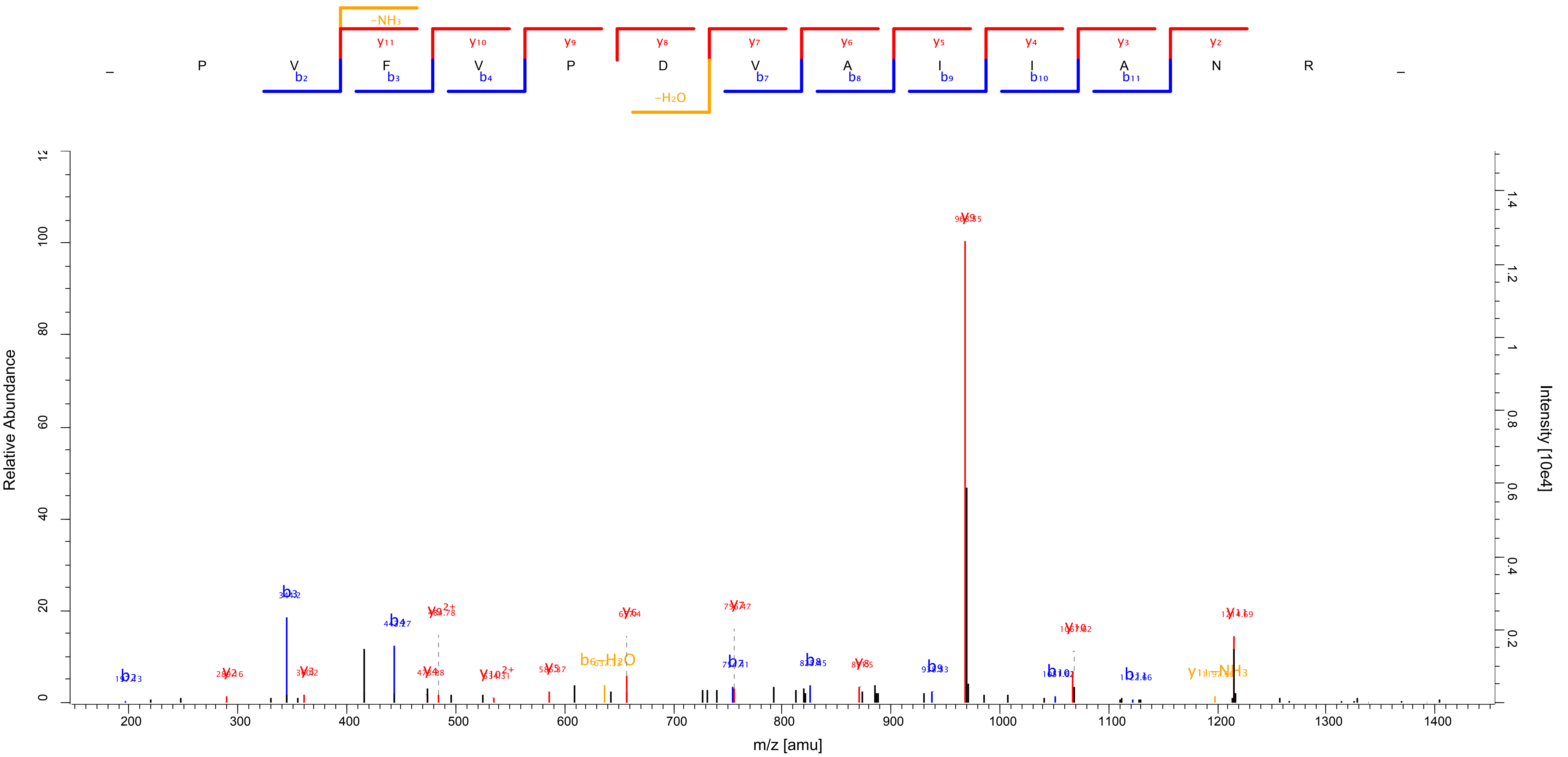
Mass:	1871.0093
m/z:	936.51193
Charge:	2+
Retentiontime:	107.696960449219
Score:	185.2698
Mass Error [ppm]:	−0.048073
PEP:	2.8148E−19
Precursor Type:	ISO

general information

Annotation:	15 of 19
AminoAcids Coverage:	79 %
Intensity Coverage:	78 %
Peak Coverage:	34 %
Protein Localisation:	87 ... 105

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.07569038		100.07569038	1	V	18				
	157.09715411		157.09715411	2	G	17	1772.948252		1772.948252	
	256.16556802		256.16556802	3	V	16	1715.9267883		1715.9267883	
	327.20268181		327.20268181	4	A	15	1616.8583744	+0.0650875	1616.8583744	
	398.2397956	−0.0665168	398.2397956	5	A	14	1545.8212606	−0.0842001	773.41426853	+0.2304458
	495.29255945	+0.0759708	495.29255945	6	P	13	1474.7841468	−0.0939613	737.89571164	+0.2169593
	592.3453233		592.3453233	7	P	12	1377.731383	−0.1527697	1377.731383	
−0.1139797	370.21050684	−0.1148481	739.41373722	8	F	11	1280.6786191	−0.04129	1280.6786191	
	852.4978012	−0.1725449	852.4978012	9	I	10	1133.6102052	−0.0379396	1133.6102052	
+0.0730941	455.26327069		909.51926492	10	G	9	1020.5261412	−0.0867491	1020.5261412	
	996.55129333	+0.03263	996.55129333	11	S	8	963.50467749	−0.0427634	963.50467749	
+0.173215	547.30566683		1093.6040572	12	P	7	876.47264908	−0.0469289	876.47264908	
	1192.6724711	−0.0701762	1192.6724711	13	V	6	779.41988523		779.41988523	
	1289.725235		1289.725235	14	P	5	680.35147131	−0.0074772	680.35147131	
	1436.7936489	−0.0071498	1436.7936489	15	F	4	583.29870746		583.29870746	
	1493.8151126	+0.3957028	1493.8151126	16	G	3	436.23029354	+0.0486371	436.23029354	
	1550.8365763		1550.8365763	17	G	2	379.20882982		379.20882982	
	1697.9049902	+0.0961084	1697.9049902	18	F	1	322.1873661		322.1873661	
				19	R	0	175.11895218		175.11895218	

Scan number	15291	Raw file	20091023_Orbi6_MaHe_SA_ADH_exp3_GFR_Gel12
Method	ITMS; CID	Genenames	AGO61



precursor
information

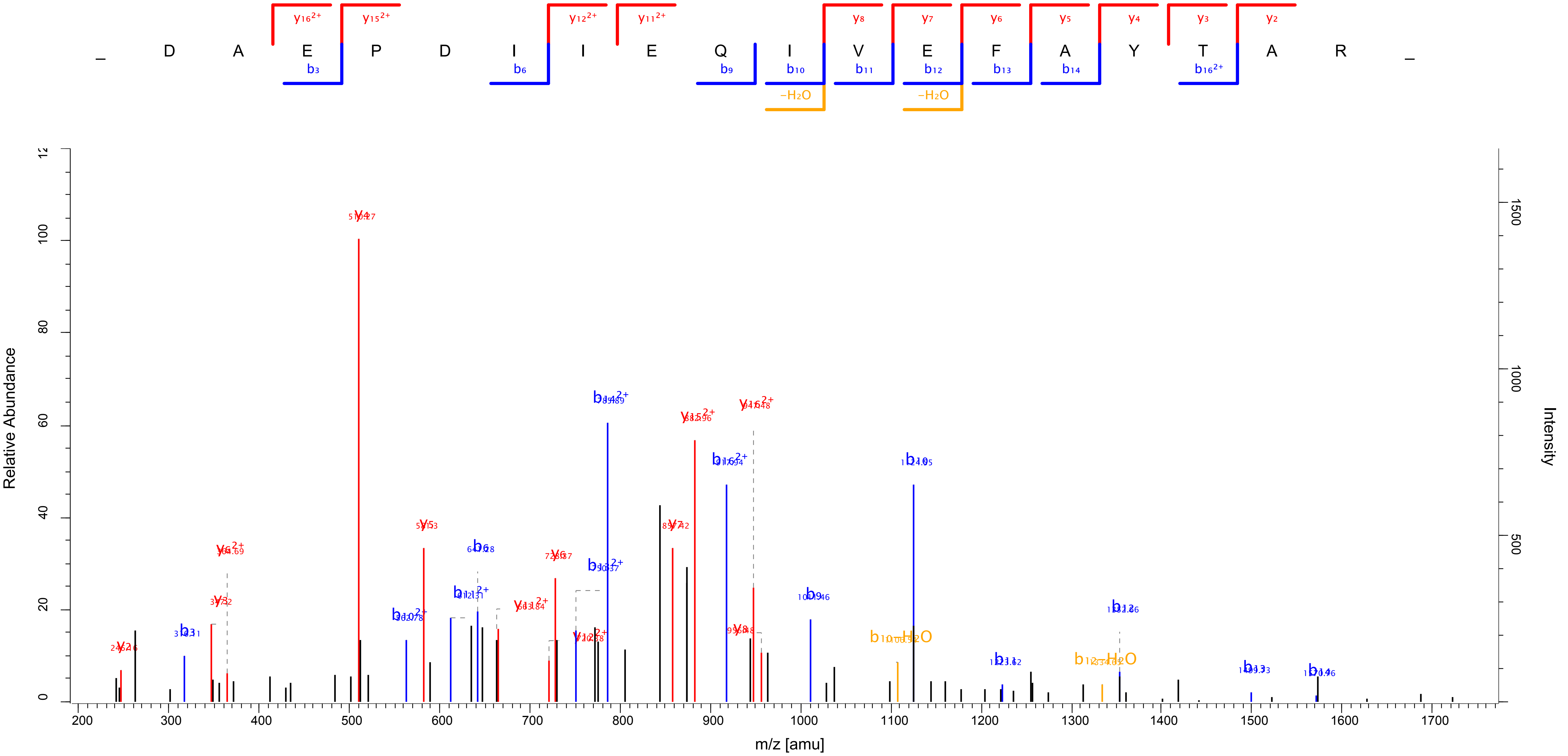
Mass:	1409.80328
m/z:	705.90892
Charge:	2+
Retentiontime:	92.1855316162109
Score:	130.5625
Mass Error [ppm]:	0.14156
PEP:	0.0002584
Precursor Type:	ISO

general
information

Annotation:	11 of 13
AminoAcids Coverage:	85 %
Intensity Coverage:	56 %
Peak Coverage:	31 %
Protein Localisation:	146 ... 158

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	98.060040319	1	P	12				
−0.0505123	197.128454235	2	V	11	1313.757597713		1313.757597713	
−0.071624	344.196868151	3	F	10	1214.689183797	−0.0284172	1214.689183797	
−0.0893177	443.265282067	4	V	9	1067.620769881	−0.0743832	534.314023174	+0.4724148
	540.318045919	5	P	8	968.552355965	−0.0789063	484.779816216	+0.0406794
	655.344988951	6	D	7	871.499592113	−0.3159984	871.499592113	
−0.0360835	754.413402867	7	V	6	756.472649081	−0.0687184	756.472649081	
+0.1514121	825.450516655	8	A	5	657.404235165	+0.2003181	657.404235165	
−0.267796	938.534580636	9	I	4	586.367121377	−0.000117	586.367121377	
−0.1796798	1051.618644616	10	I	3	473.283057396	+0.1561516	473.283057396	
−0.4525113	1122.655758404	11	A	2	360.198993416	+0.0558284	360.198993416	
	1236.698685851	12	N	1	289.161879628	+0.127366	289.161879628	
		13	R	0	175.118952181		175.118952181	

Scan number	20638	Raw file	20091023_Orbi6_MaHe_SA_ADH_exp3_GFR_Gel12
Method	ITMS; CID	Genenames	KLHL7



precursor information

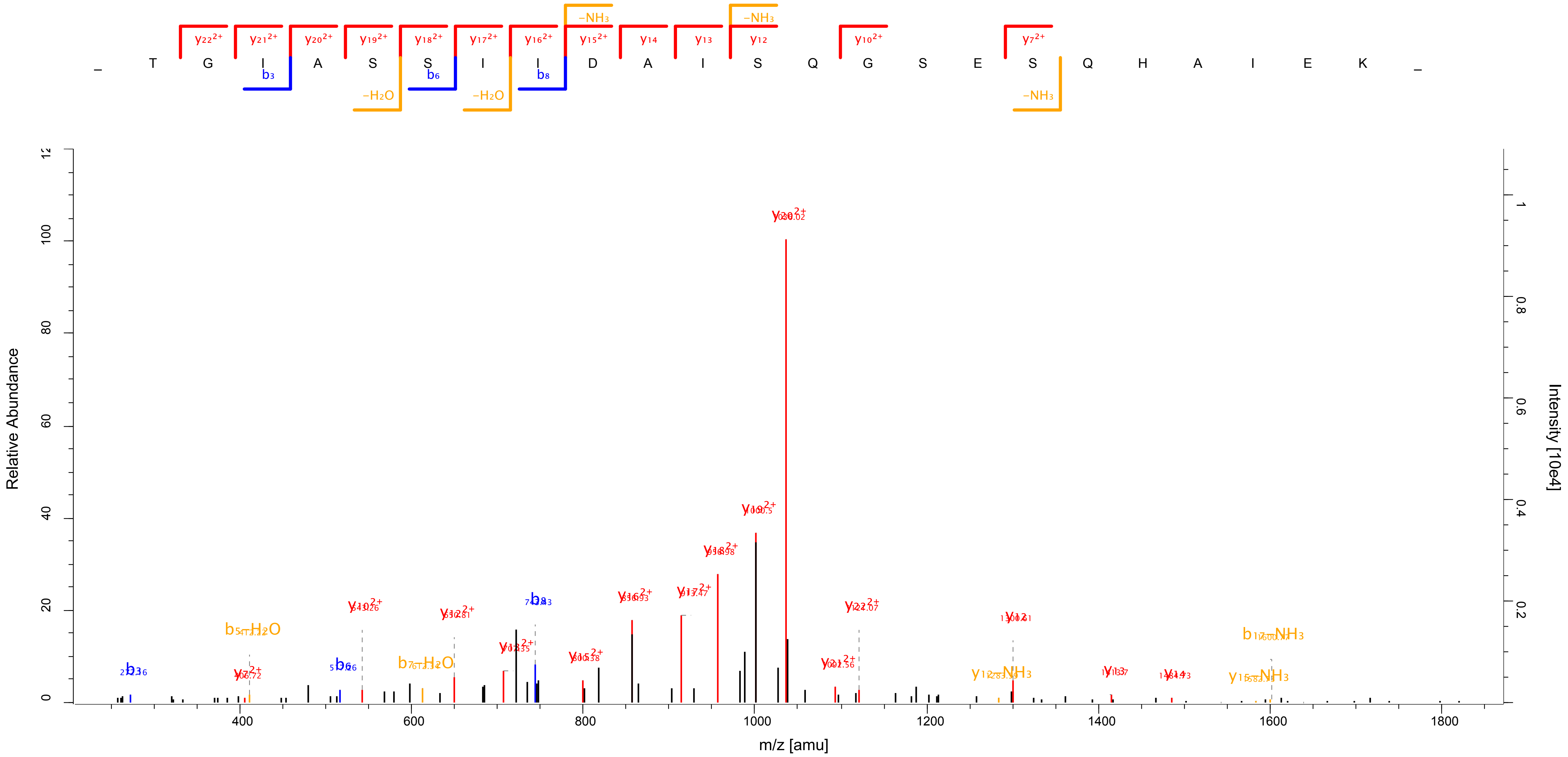
Mass:	2079.01563
m/z:	694.01248
Charge:	3+
Retentiontime:	123.178924560547
Score:	174.6167
Mass Error [ppm]:	-0.20467
PEP:	5.3672E-13
Precursor Type:	ISO

general information

Annotation:	15 of 18
AminoAcids Coverage:	83 %
Intensity Coverage:	60 %
Peak Coverage:	35 %
Protein Localisation:	89 ... 106

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342195		116.0342195	1	D	17				
	187.07133329		187.07133329	2	A	16	1964.996384		1964.996384	
	316.11392638	-0.1412091	316.11392638	3	E	15	1893.9592702		947.48327335	+0.006961
	413.16669023		413.16669023	4	P	14	1764.9166771		882.9619768	-0.0280779
	528.19363327		528.19363327	5	D	13	1667.8639133		1667.8639133	
	641.27769725	+0.0695928	641.27769725	6	I	12	1552.8369702		1552.8369702	
	754.36176123		754.36176123	7	I	11	1439.7529063		720.38009137	-0.283961
	883.40435432		883.40435432	8	E	10	1326.6688423		663.83805938	+0.4181662
	1011.4629318	-0.0923264	1011.4629318	9	Q	9	1197.6262492		1197.6262492	
+0.0385377	562.77713614	-0.2374255	1124.5469958	10	I	8	1069.5676717		1069.5676717	
-0.0864285	612.3113431	-0.2765425	1223.6154097	11	V	7	956.4836077	-0.286159	956.4836077	
	1352.6580028	-0.0571727	1352.6580028	12	E	6	857.41519378	-0.0140097	857.41519378	
+0.1836295	750.36684661	-0.1460945	1499.7264167	13	F	5	728.37260069	+0.0130805	364.68993858	+0.298831
-0.1040314	785.8854035	-0.2461965	1570.7635305	14	A	4	581.30418677	+0.040967	581.30418677	
	1733.8268591		1733.8268591	15	Y	3	510.26707298	-0.0074294	510.26707298	
+0.0685534	917.94090701		1834.8745375	16	T	2	347.20374444	+0.0060944	347.20374444	
	1905.9116513		1905.9116513	17	A	1	246.15606597	+0.0280008	246.15606597	
				18	R	0	175.11895218		175.11895218	

Scan number	16244	Raw file	20091023_Orbi6_MaHe_SA_ADH_exp3_GFR_Gel13
Method	ITMS; CID	Genenames	RAVER2



precursor information

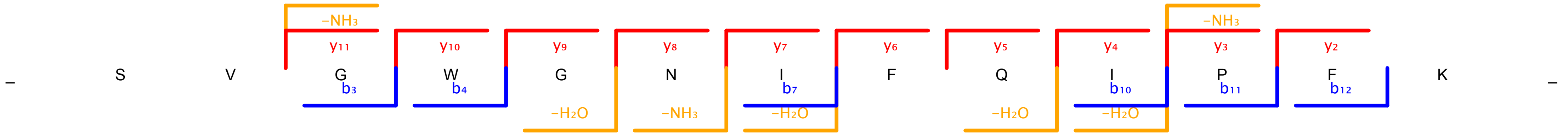
Mass:	2341.1756
m/z:	781.39914
Charge:	3+
Retentiontime:	96.9709167480469
Score:	98.79649
Mass Error [ppm]:	-0.2298
PEP:	3.8031E-06
Precursor Type:	MULTI

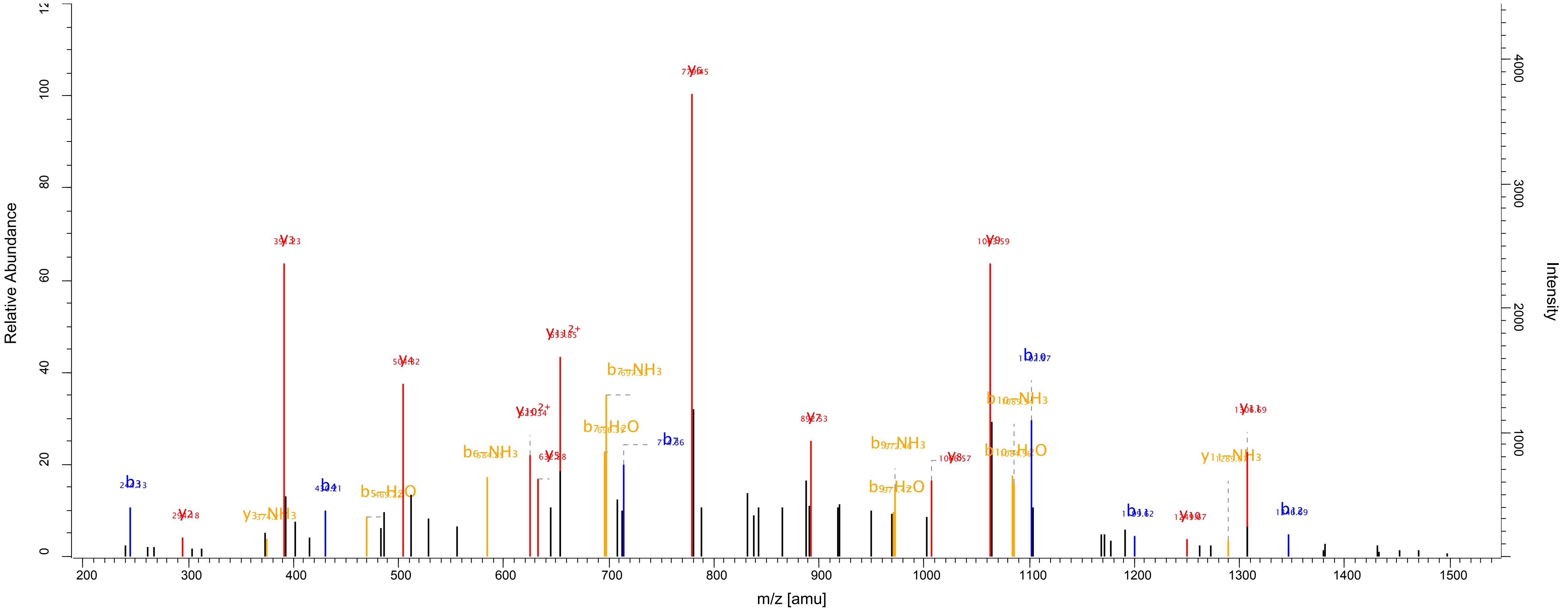
general information

Annotation:	13 of 23
AminoAcids Coverage:	57 %
Intensity Coverage:	55 %
Peak Coverage:	26 %
Protein Localisation:	608 ... 630

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.054954941	1	T	22				
	159.076418664	2	G	21	2241.135731042		1121.071503754	+0.2308644
+3.98E-05	272.160482645	3	I	20	2184.114267319		1092.560771893	-0.0120658
	343.197596432	4	A	19	2071.030203338		1036.018739902	+0.2219828
	430.229624842	5	S	18	1999.993089551		1000.500183009	-0.0919188
-0.0761674	517.261653252	6	S	17	1912.961061141		956.984168804	+0.2467272
	630.345717233	7	I	16	1825.929032731		913.468154599	+0.0920871
+0.1910684	743.429781213	8	I	15	1712.84496875		856.926122608	+0.0121098
	858.456724245	9	D	14	1599.76090477		800.384090618	-0.1203577
	929.493838033	10	A	13	1484.733961738	+0.2859357	1484.733961738	
	1042.577902013	11	I	12	1413.69684795	+0.3872585	707.352062208	-0.0239982
	1129.609930423	12	S	11	1300.61278397	+0.0650725	650.810030218	-0.0392172
	1257.668507935	13	Q	10	1213.58075556		1213.58075556	
	1314.689971658	14	G	9	1085.522178048		543.264727258	-0.0396296
	1401.722000068	15	S	8	1028.500714325		1028.500714325	
	1530.764593164	16	E	7	941.468685915		941.468685915	
	1617.796621574	17	S	6	812.426092819		406.716684643	-0.4351295
	1745.855199086	18	Q	5	725.394064409		725.394064409	
	1882.914110948	19	H	4	597.335486897		597.335486897	
	1953.951224736	20	A	3	460.276575035		460.276575035	
	2067.035288716	21	I	2	389.239461247		389.239461247	
	2196.077881812	22	E	1	276.155397267		276.155397267	
		23	K	0	147.112804171		147.112804171	

Scan number	19394	Raw file	20091023_Orbi6_MaHe_SA_ADH_exp3_GFR_Gel14
Method	ITMS; CID	Genenames	UNC93B1





precursor information

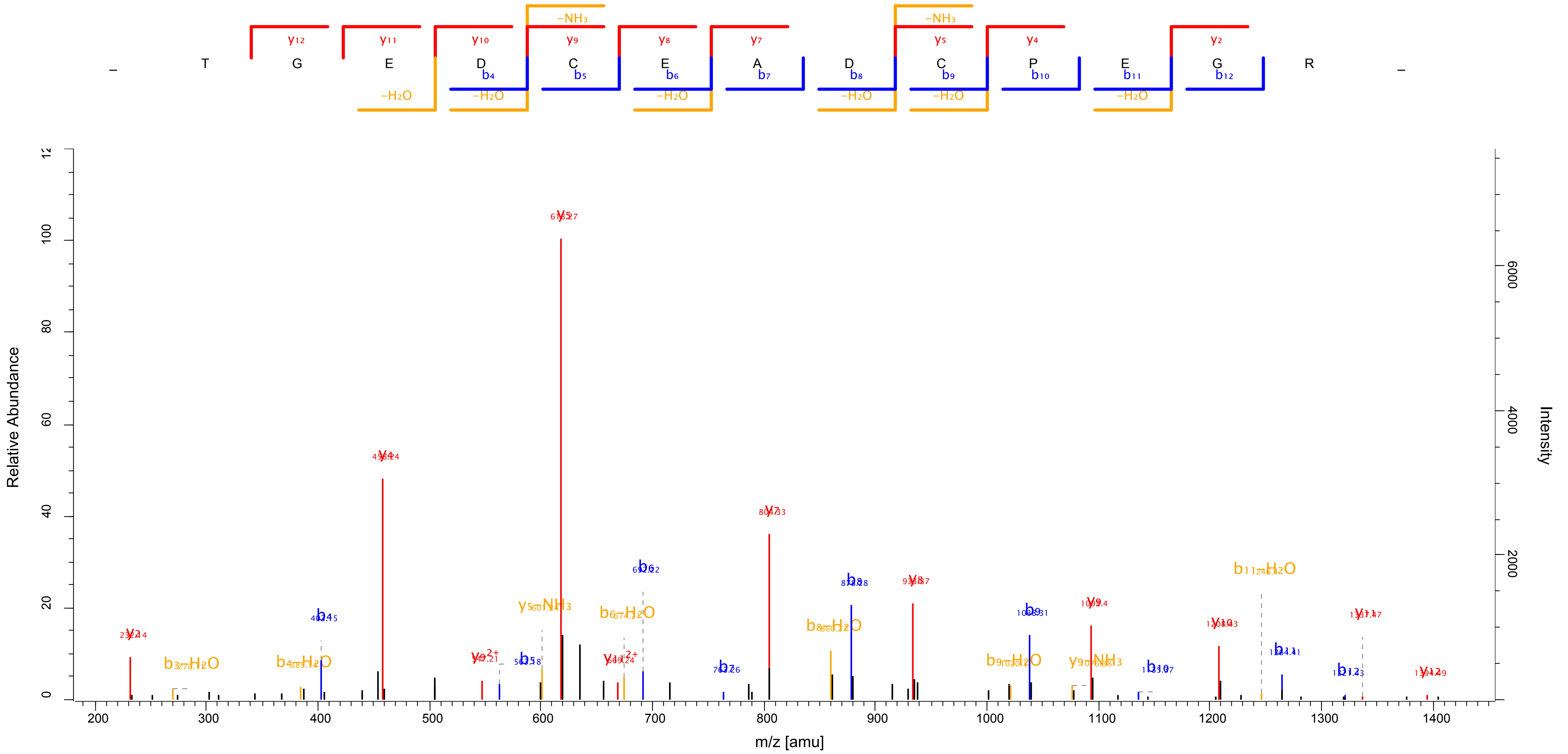
Mass:	1491.78781
m/z:	746.90118
Charge:	2+
Retentiontime:	115.394744873047
Score:	147.2444
Mass Error [ppm]:	0.25377
PEP:	1.87695E-05
Precursor Type:	ISO

general information

Annotation:	10 of 13
AminoAcids Coverage:	77 %
Intensity Coverage:	63 %
Peak Coverage:	37 %
Protein Localisation:	321 ... 333

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876	1	S	12				
	187.107718793	2	V	11	1405.762683091		1405.762683091	
+0.1556838	244.129182516	3	G	10	1306.694269175	+0.1183529	653.850772821	+0.0002404
-0.1317743	430.20849547	4	W	9	1249.672805452	+0.1025852	625.340040959	+0.2320416
	487.229959193	5	G	8	1063.593492498	-0.0634632	1063.593492498	
	601.272886641	6	N	7	1006.572028774	-0.2521435	1006.572028774	
-0.0564745	714.356950621	7	I	6	892.529101327	+0.0975466	892.529101327	
	861.425364537	8	F	5	779.445037347	-0.0871272	779.445037347	
	989.483942049	9	Q	4	632.376623431	-0.125952	632.376623431	
-0.0289435	1102.568006029	10	I	3	504.318045919	-0.0960611	504.318045919	
-0.0526546	1199.620769881	11	P	2	391.233981939	+0.0135156	391.233981939	
+0.2945809	1346.689183797	12	F	1	294.181218087	-0.0133104	294.181218087	
		13	K	0	147.112804171		147.112804171	

Scan number	2060	Raw file	20091023_Orbi6_MaHe_SA_ADH_exp3_GFR_Gel16
Method	ITMS; CID	Genenames	MEGF6



precursor information

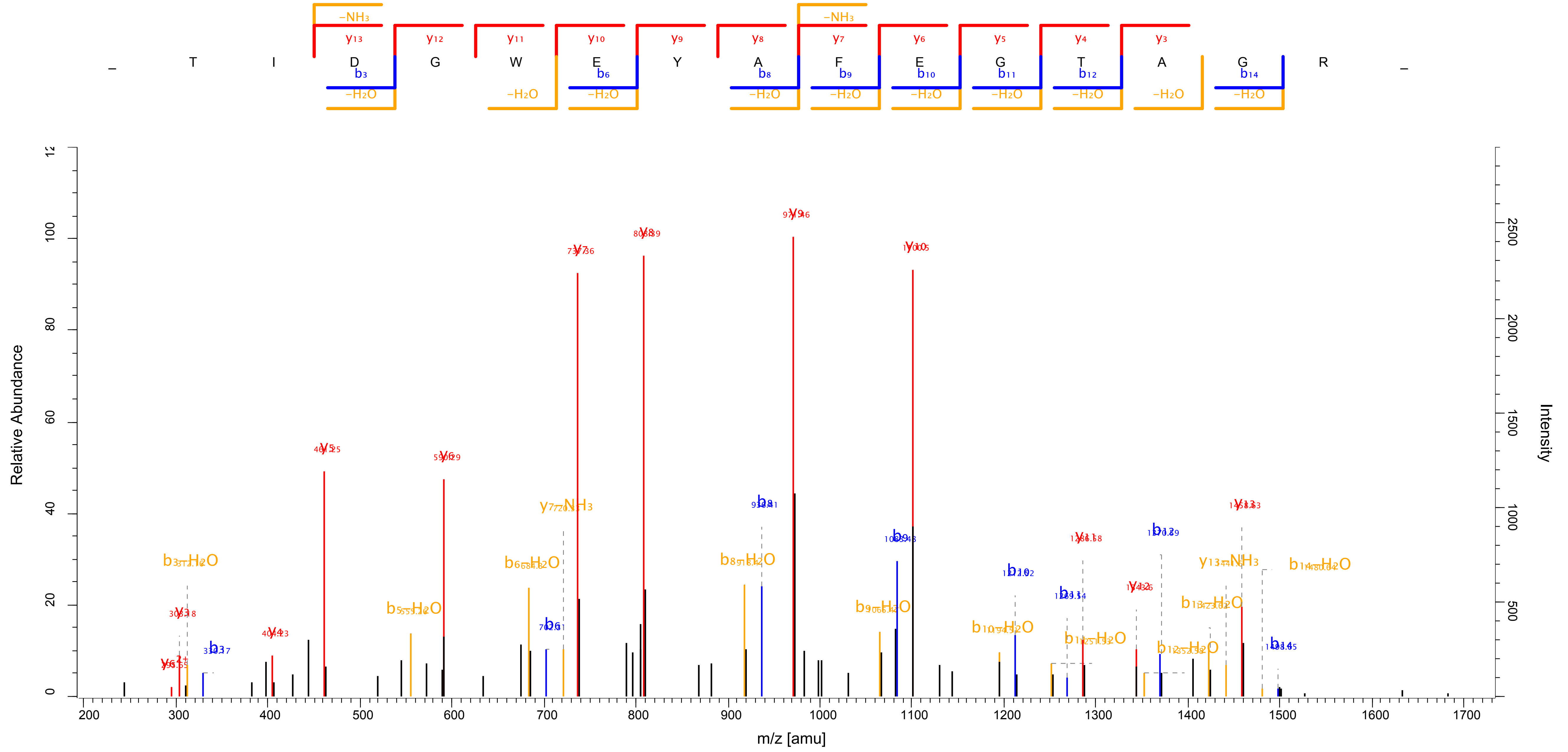
Mass:	1494.53398
m/z:	748.27427
Charge:	2+
Retentiontime:	20.9807167053223
Score:	198.8123
Mass Error [ppm]:	−0.76432
PEP:	2.0704E−11
Precursor Type:	ISO

general information

Annotation:	11 of 13
AminoAcids Coverage:	85 %
Intensity Coverage:	72 %
Peak Coverage:	39 %
Protein Localisation:	765 ... 777

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.054954941	1	T	12				
	159.076418664	2	G	11	1394.494719023	−0.0639329	1394.494719023	
	288.11901176	3	E	10	1337.4732553	−0.0623666	669.240265883	+0.4364309
+0.0491746	403.145954792	4	D	9	1208.430662204	+0.0803241	1208.430662204	
+0.1373618	563.176602994	5	C	8	1093.403719172	+0.0841959	547.205497819	+0.0128249
+0.091656	692.21919609	6	E	7	933.37307097	−0.0349972	933.37307097	
+0.2414318	763.256309878	7	A	6	804.330477874	+0.0782135	804.330477874	
−0.0505869	878.28325291	8	D	5	733.293364086		733.293364086	
−0.0204441	1038.313901111	9	C	4	618.266421054	+0.032346	618.266421054	
+0.0089454	1135.366664963	10	P	3	458.235772853	+0.0290587	458.235772853	
−0.0746633	1264.40925806	11	E	2	361.183009001		361.183009001	
−0.2069669	1321.430721783	12	G	1	232.140415905	+0.0954087	232.140415905	
		13	R	0	175.118952181		175.118952181	

Scan number	14134	Raw file	20091025_Orbi6_MaHe_SA_ADH_exp3_Matr_dil_Gel02
Method	ITMS; CID	Genenames	TM4SF18



precursor information

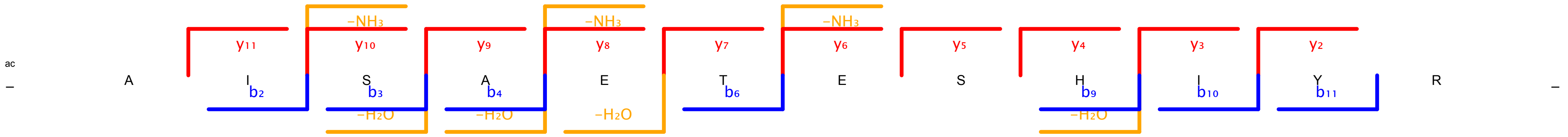
Mass:	1671.75322
m/z:	836.88388
Charge:	2+
Retentiontime:	88.1841583251953
Score:	199.7993
Mass Error [ppm]:	0.1892
PEP:	1.0125E−19
Precursor Type:	ISO

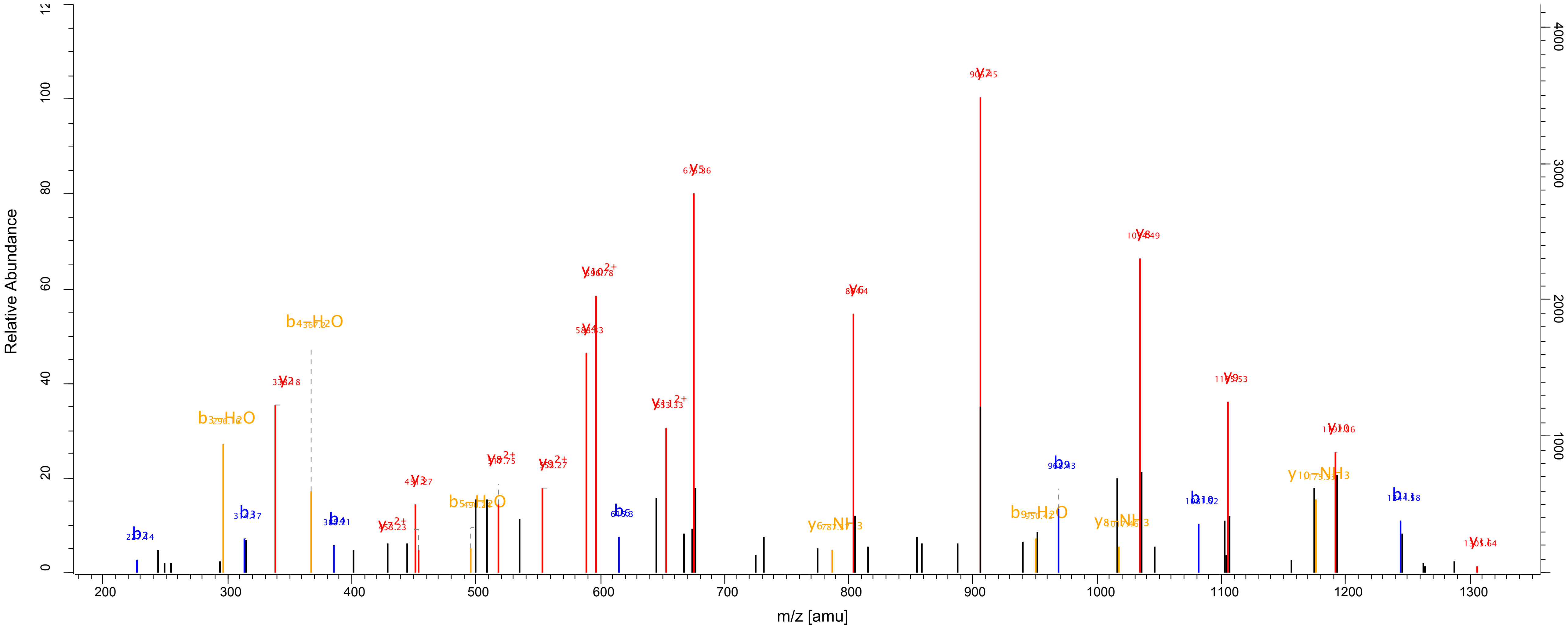
general information

Annotation:	12 of 15
AminoAcids Coverage:	80 %
Intensity Coverage:	64 %
Peak Coverage:	40 %
Protein Localisation:	123 ... 137

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.054954941	1	T	14				
	215.139018921	2	I	13	1571.712498014		1571.712498014	
−0.0712659	330.165961953	3	D	12	1458.628434034	−0.0645913	1458.628434034	
	387.187425677	4	G	11	1343.601491002	+0.0479231	1343.601491002	
	573.26673863	5	W	10	1286.580027278	−0.0575663	1286.580027278	
+0.002619	702.309331726	6	E	9	1100.500714325	−0.043561	1100.500714325	
	865.372660265	7	Y	8	971.458121229	−0.0801305	971.458121229	
−0.1426232	936.409774052	8	A	7	808.39479269	−0.0829641	808.39479269	
+0.0318218	1083.478187969	9	F	6	737.357678902	+0.0225091	737.357678902	
−0.044951	1212.520781065	10	E	5	590.289264986	+0.0411183	295.648270726	−0.4391643
−0.1075524	1269.542244788	11	G	4	461.24667189	+0.0373247	461.24667189	
−0.1342348	1370.589923263	12	T	3	404.225208166	−0.1325568	404.225208166	
	1441.62703705	13	A	2	303.177529692	+0.1311251	303.177529692	
−0.2954734	1498.648500774	14	G	1	232.140415905		232.140415905	
		15	R	0	175.118952181		175.118952181	

Scan number	7742	Raw file	20091025_Orbi6_MaHe_SA_ADH_exp3_Matr_dil_Gel02
Method	ITMS; CID	Genenames	CYB561D2





precursor information

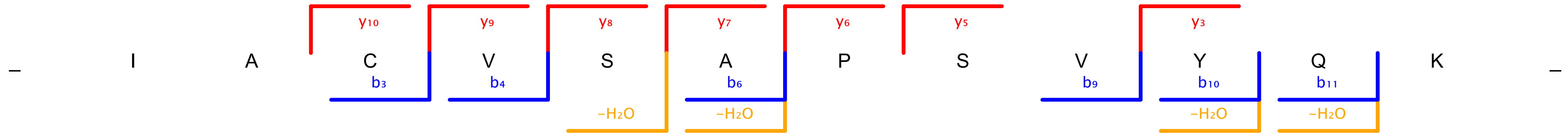
Mass:	1417.68389
m/z:	709.84922
Charge:	2+
Retentiontime:	52.3730049133301
Score:	208.3331
Mass Error [ppm]:	0.089937
PEP:	1.7044E-18
Precursor Type:	MULTI

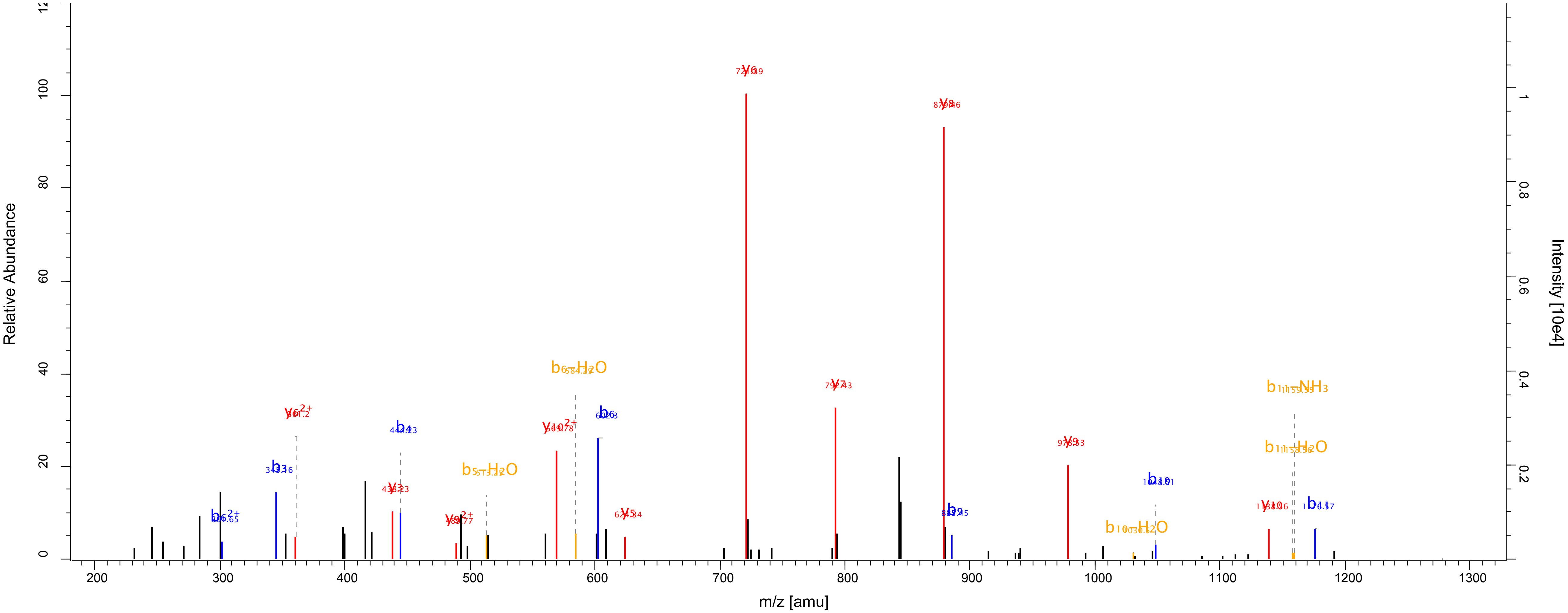
general information

Annotation:	10 of 12
AminoAcids Coverage:	83 %
Intensity Coverage:	67 %
Peak Coverage:	43 %
Protein Localisation:	2 ... 13

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.054954941	1	A	11				
+0.0319406	227.139018921	2	I	10	1305.643355817	+0.0141149	653.325316142	+0.2420056
−0.0852929	314.171047331	3	S	9	1192.559291836	−0.1073875	596.783284151	+0.2053633
−0.0420845	385.208161119	4	A	8	1105.527263426	−0.0023611	553.267269946	+0.4138214
	514.250754215	5	E	7	1034.490149639	−0.0303108	517.748713053	+0.0050711
−0.0050367	615.298432689	6	T	6	905.447556542	−0.0676737	453.227416504	+0.309876
	744.341025785	7	E	5	804.399878068	−0.0509401	804.399878068	
	831.373054195	8	S	4	675.357284972	+0.0285183	675.357284972	
−0.0645955	968.431966058	9	H	3	588.325256562	−0.1790163	588.325256562	
−0.2524802	1081.516030038	10	I	2	451.2663447	+0.052564	451.2663447	
−0.0872931	1244.579358576	11	Y	1	338.182280719	+0.0907906	338.182280719	
		12	R	0	175.118952181		175.118952181	

Scan number	5803	Raw file	20091025_Orbi6_MaHe_SA_ADH_exp3_Matr_dil_Gel03
Method	ITMS; CID	Genenames	N6AMT2





precursor information

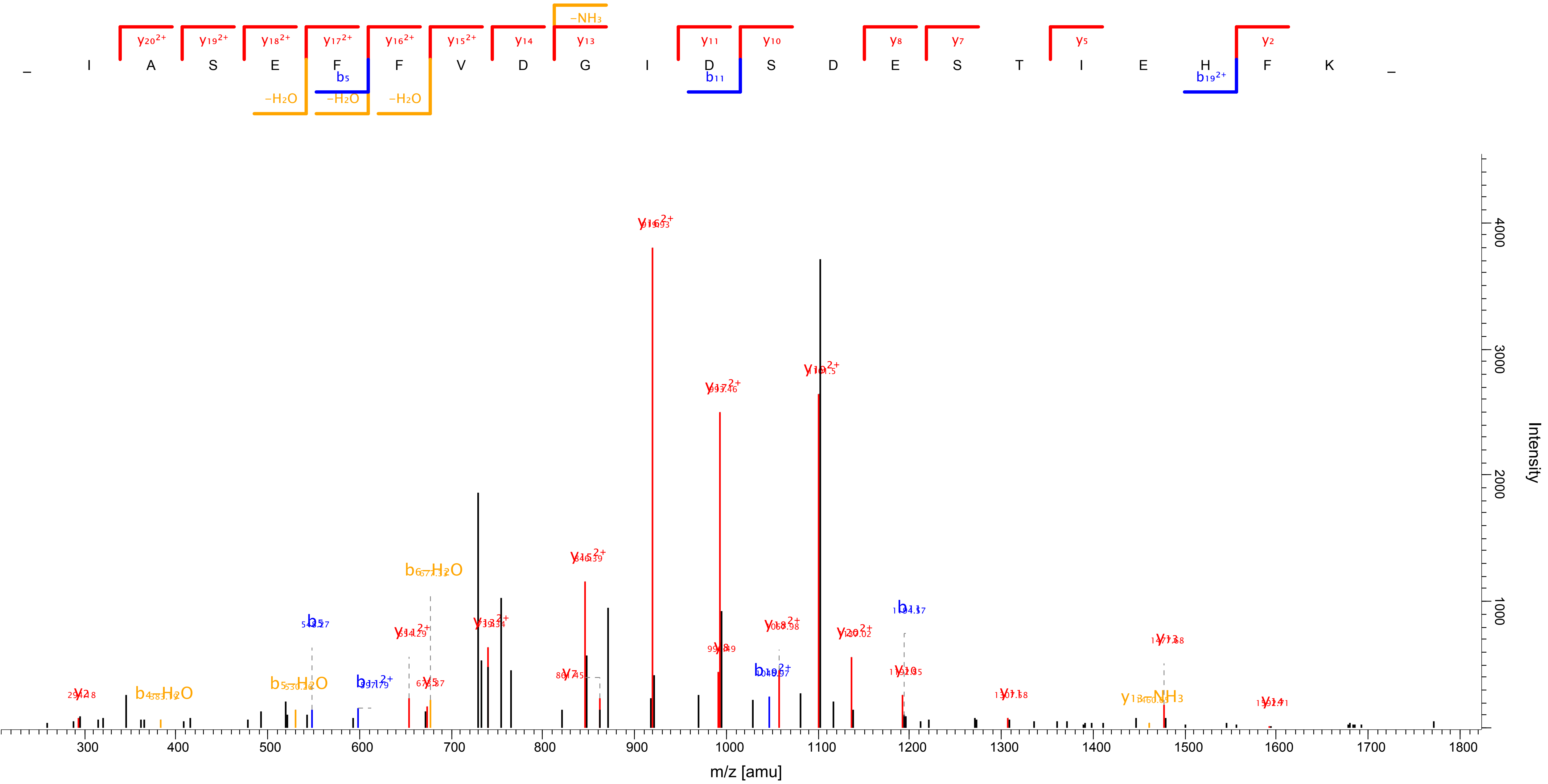
Mass:	1321.66972
m/z:	661.84213
Charge:	2+
Retentiontime:	42.4288330078125
Score:	150.1032
Mass Error [ppm]:	-0.23184
PEP:	1.7144E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverage:	75 %
Intensity Coverage:	65 %
Peak Coverage:	34 %
Protein Localisation:	77 ... 88

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045		114.09134045	1	I	11				
	185.12845423		185.12845423	2	A	10	1209.5932345		1209.5932345	
	345.15910244	-0.1312704	345.15910244	3	C	9	1138.5561207	-0.0148609	569.78169859	+0.0495392
	444.22751635	-0.0997087	444.22751635	4	V	8	978.52547251	-0.0569667	489.76637449	-0.357561
	531.25954476		531.25954476	5	S	7	879.4570586	-0.0486113	879.4570586	
+0.4268899	301.65196751	+0.0932951	602.29665855	6	A	6	792.42503019	+0.0813785	792.42503019	
	699.3494224		699.3494224	7	P	5	721.3879164	-0.0061415	361.19759643	-0.1374768
	786.38145081		786.38145081	8	S	4	624.33515255	+0.0341712	624.33515255	
	885.44986473	-0.11881	885.44986473	9	V	3	537.30312414		537.30312414	
	1048.5131933	-0.0423681	1048.5131933	10	Y	2	438.23471022	+0.0859685	438.23471022	
	1176.5717708	-0.195428	1176.5717708	11	Q	1	275.17138168		275.17138168	
				12	K	0	147.11280417		147.11280417	

Scan number	16207	Raw file	20091025_Orbi6_MaHe_SA_ADH_exp3_Matr_dil_Gel04
Method	ITMS; CID	Genenames	C15orf57



precursor information

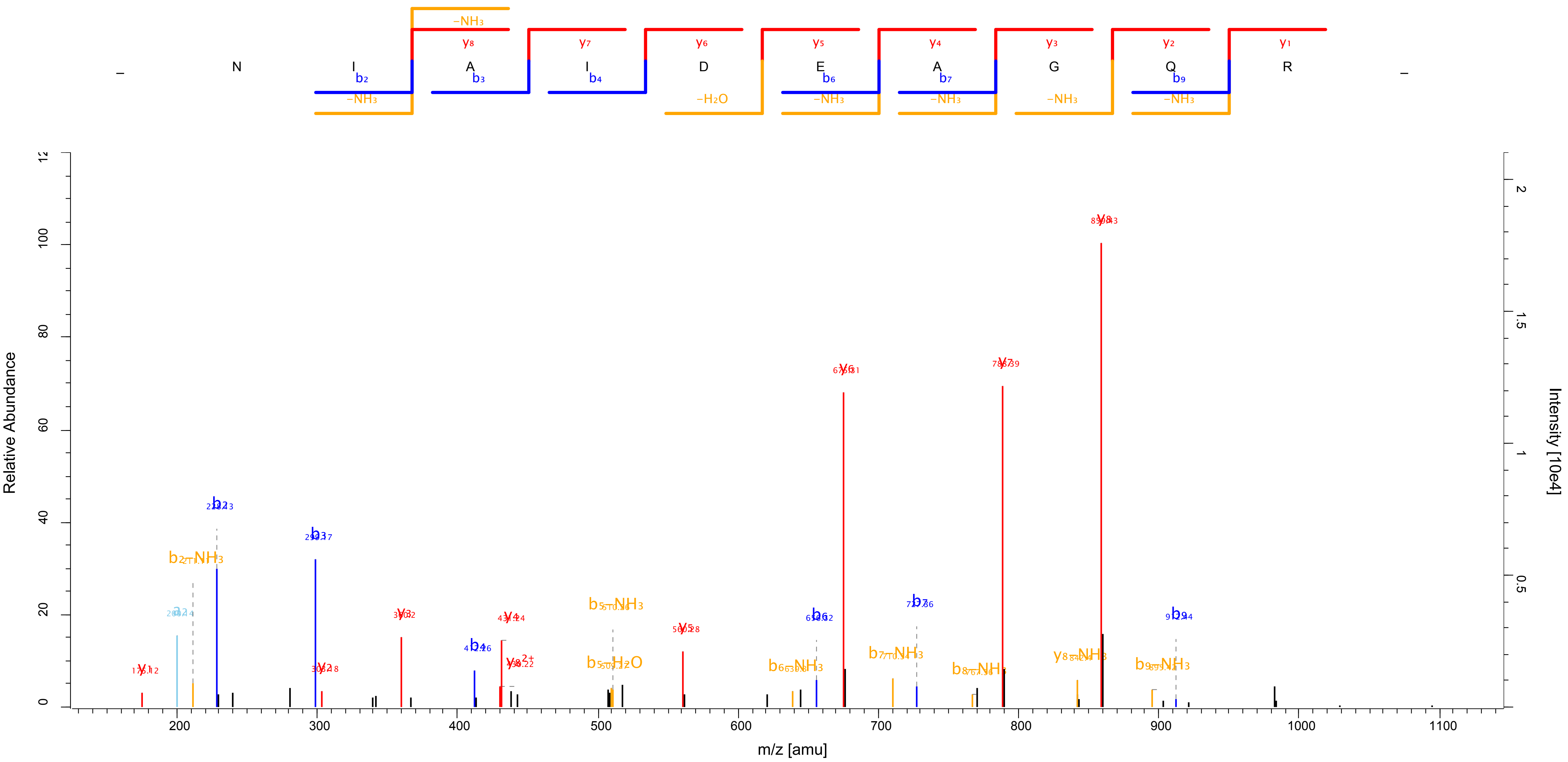
Mass:	2385.10097
m/z:	796.04093
Charge:	3+
Retentiontime:	101.526802062988
Score:	116.3475
Mass Error [ppm]:	−0.11245
PEP:	7.8002E−07
Precursor Type:	ISO

general information

Annotation:	15 of 21
AminoAcids Coverage:	71 %
Intensity Coverage:	48 %
Peak Coverage:	28 %
Protein Localisation:	129 ... 149

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045		114.09134045	1	I	20				
	185.12845423		185.12845423	2	A	19	2273.0244493		1137.0158629	+0.0505434
	272.16048264		272.16048264	3	S	18	2201.9873355		1101.497306	−0.0539466
	401.20307574		401.20307574	4	E	17	2114.9553071		1057.9812918	+0.1575022
	548.27148966	+0.2953438	548.27148966	5	F	16	1985.912714		993.45999522	+0.0072899
	695.33990357		695.33990357	6	F	15	1838.8443		919.92578826	+0.2333304
	794.40831749		794.40831749	7	V	14	1691.7758861		846.3915813	−0.0035808
	909.43526052		909.43526052	8	D	13	1592.7074722	+0.1049057	1592.7074722	
	966.45672425		966.45672425	9	G	12	1477.6805292	−0.121203	739.34390283	−0.1056826
	1079.5407882		1079.5407882	10	I	11	1420.6590655		1420.6590655	
+0.1854576	597.78750386	+0.1778742	1194.5677313	11	D	10	1307.5750015	−0.1610611	654.29113897	+0.0960681
	1281.5997597		1281.5997597	12	S	9	1192.5480584	−0.2482538	1192.5480584	
	1396.6267027		1396.6267027	13	D	8	1105.51603		1105.51603	
	1525.6692958		1525.6692958	14	E	7	990.48908701	−0.1169557	990.48908701	
	1612.7013242		1612.7013242	15	S	6	861.44649391	−0.1179417	861.44649391	
	1713.7490027		1713.7490027	16	T	5	774.4144655		774.4144655	
	1826.8330667		1826.8330667	17	I	4	673.36678703	+0.1747779	673.36678703	
	1955.8756598		1955.8756598	18	E	3	560.28272305		560.28272305	
+0.1974109	1046.970924		2092.9345716	19	H	2	431.24012995		431.24012995	
	2240.0029855		2240.0029855	20	F	1	294.18121809	+0.122737	294.18121809	
				21	K	0	147.11280417		147.11280417	

Scan number	4639	Raw file	20091025_Orbi6_MaHe_SA_ADH_exp3_Matr_dil_Gel04
Method	ITMS; CID	Genenames	CYBRD1



precursor information

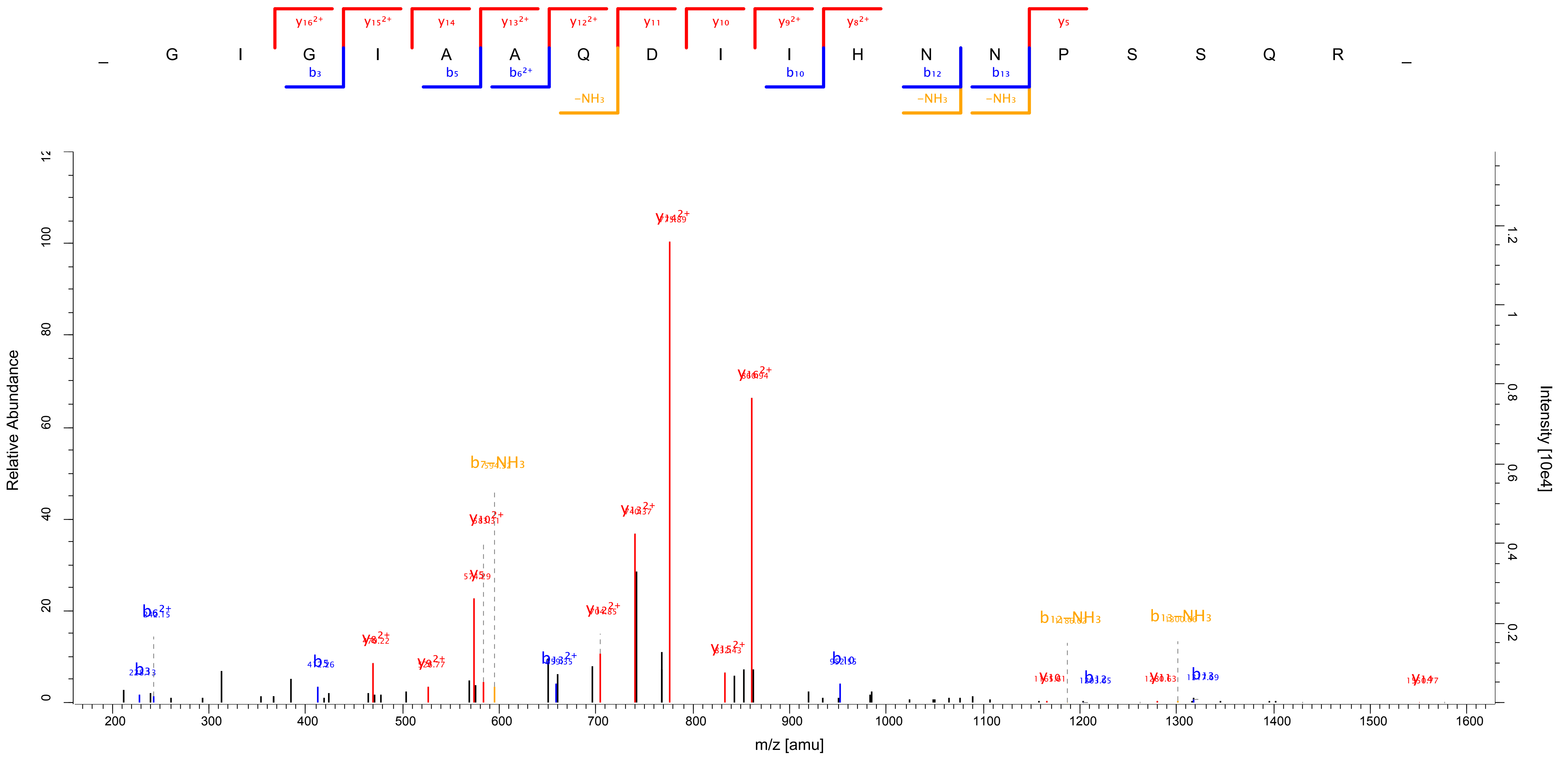
Mass:	1085.54633
m/z:	543.78044
Charge:	2+
Retentiontime:	36.8138580322266
Score:	187.6438
Mass Error [ppm]:	−0.19023
PEP:	3.1269E−08
Precursor Type:	MULTI

ge information

Annotation:	9 of 10
AminoAcids Coverage:	90 %
Intensity Coverage:	82 %
Peak Coverage:	47 %
Protein Localisation:	274 ... 283

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	87.055289292		115.05020391	1	N	9				
+0.0809684	200.13935327	+0.0056247	228.13426789	2	I	8	972.51088508		972.51088508	
	271.17646706	−0.0255687	299.17138168	3	A	7	859.4268211	−0.0058616	430.21704878	+0.1910323
	384.26053104	−0.082472	412.25544566	4	I	6	788.38970731	+0.0091574	788.38970731	
	499.28747407		527.28238869	5	D	5	675.30564333	+0.0307824	675.30564333	
	628.33006717	+0.014923	656.32498179	6	E	4	560.2787003	+0.0569931	560.2787003	
	699.36718096	−0.213597	727.36209558	7	A	3	431.2361072	+0.0781628	431.2361072	
	756.38864468		784.3835593	8	G	2	360.19899342	−0.0255315	360.19899342	
	884.44722219	+0.0156879	912.44213681	9	Q	1	303.17752969	+0.1316134	303.17752969	
				10	R	0	175.11895218	+0.1168114	175.11895218	

Scan number	9144	Raw file	20091025_Orbi6_MaHe_SA_ADH_exp3_Matr_dil_Gel04
Method	ITMS; CID	Genenames	NIPA1



precursor information

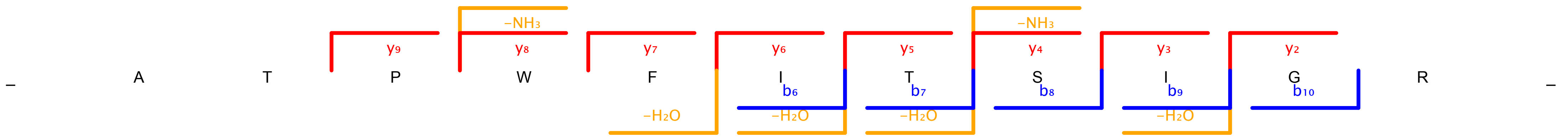
Mass:	1889.96972
m/z:	630.99718
Charge:	3+
Retentiontime:	61.4076194763184
Score:	110.438
Mass Error [ppm]:	-0.55536
PEP:	5.8862E-06
Precursor Type:	MULTI

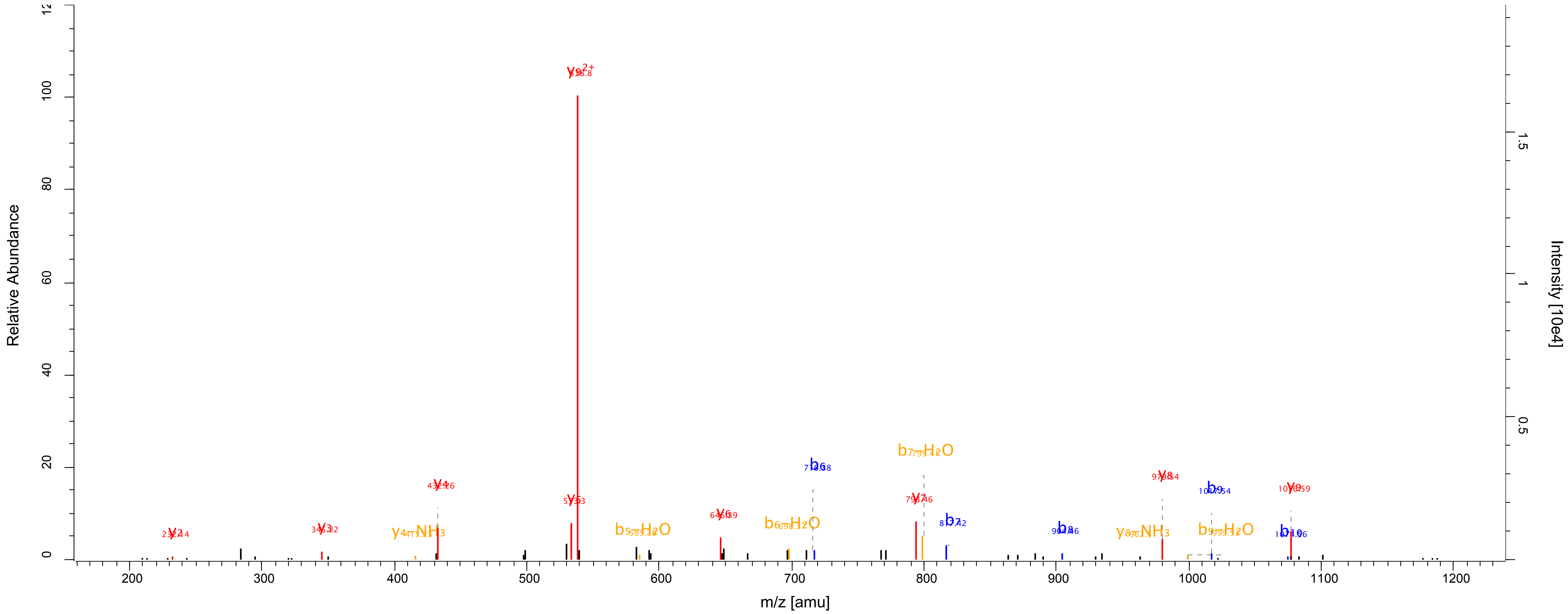
general information

Annotation:	12 of 18
AminoAcids Coverage:	67 %
Intensity Coverage:	65 %
Peak Coverage:	31 %
Protein Localisation:	208 ... 225

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019		58.02874019	1	G	17				
	171.11280417		171.11280417	2	I	16	1833.9565849		1833.9565849	
	228.13426789	+0.0498141	228.13426789	3	G	15	1720.8725209		860.93989869	+0.1736877
	341.21833187		341.21833187	4	I	14	1663.8510572		832.42916682	−0.0610638
	412.25544566	−0.0110609	412.25544566	5	A	13	1550.7669932	+0.0522207	775.88713483	+0.1829335
−0.0178074	242.14991796		483.29255945	6	A	12	1479.7298794		740.36857794	−0.0252552
	611.35113696		611.35113696	7	Q	11	1408.6927656		704.85002105	+0.0228427
	726.37807999		726.37807999	8	D	10	1280.6341881	−0.2700524	1280.6341881	
	839.46214397		839.46214397	9	I	9	1165.6072451	+0.0963682	583.30726077	+0.107351
	952.54620795	−0.0891767	952.54620795	10	I	8	1052.5231811		526.76522878	+0.2294001
	1089.6051198		1089.6051198	11	H	7	939.43911712		470.22319679	+0.0230801
	1203.6480473	+0.2348873	1203.6480473	12	N	6	802.38020526		802.38020526	
−0.0706832	659.34912559	+0.2935224	1317.6909747	13	N	5	688.33727781		688.33727781	
	1414.7437386		1414.7437386	14	P	4	574.29435036	+0.0232156	574.29435036	
	1501.775767		1501.775767	15	S	3	477.24158651		477.24158651	
	1588.8077954		1588.8077954	16	S	2	390.2095581		390.2095581	
	1716.8663729		1716.8663729	17	Q	1	303.17752969		303.17752969	
				18	R	0	175.11895218		175.11895218	

Scan number	15258	Raw file	20091025_Orbi6_MaHe_SA_ADH_exp3_Matr_dil_Gel05
Method	ITMS; CID	Genenames	TMEM44





precursor information

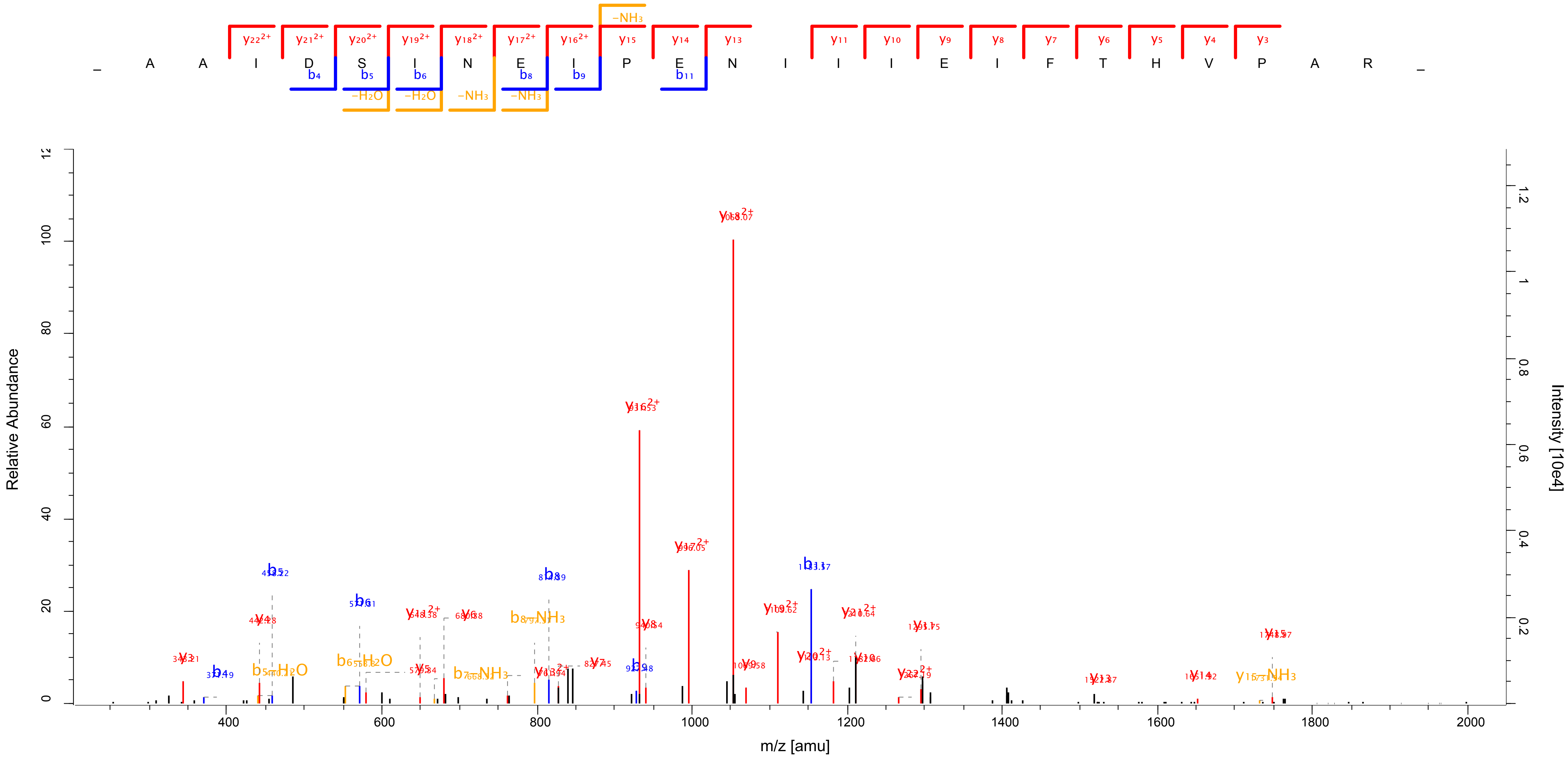
Mass:	1247.66654
m/z:	624.84055
Charge:	2+
Retentiontime:	93.5402374267578
Score:	159.4039
Mass Error [ppm]:	0.22532
PEP:	1.146E-06
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverage:	73 %
Intensity Coverage:	78 %
Peak Coverage:	34 %
Protein Localisation:	292 ... 302

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	10				
	173.092068728	2	T	9	1177.636419945		1177.636419945	
	270.14483258	3	P	8	1076.588741471	−0.0882532	538.798008969	−0.0032702
	456.224145534	4	W	7	979.535977619	−0.0394566	979.535977619	
	603.29255945	5	F	6	793.456664666	−0.1131588	793.456664666	
+0.1964357	716.376623431	6	I	5	646.388250749	−0.0182556	646.388250749	
−0.2460182	817.424301905	7	T	4	533.304186769	+0.0700198	533.304186769	
−0.1637888	904.456330315	8	S	3	432.256508295	+0.0871196	432.256508295	
−0.1410413	1017.540394295	9	I	2	345.224479885	−0.0746386	345.224479885	
−0.2310475	1074.561858019	10	G	1	232.140415905	−0.3349349	232.140415905	
		11	R	0	175.118952181		175.118952181	

Scan number	19994	Raw file	20091025_Orbi6_MaHe_SA_ADH_exp3_Matr_dil_Gel06
Method	ITMS; CID	Genenames	FBXO6



precursor information

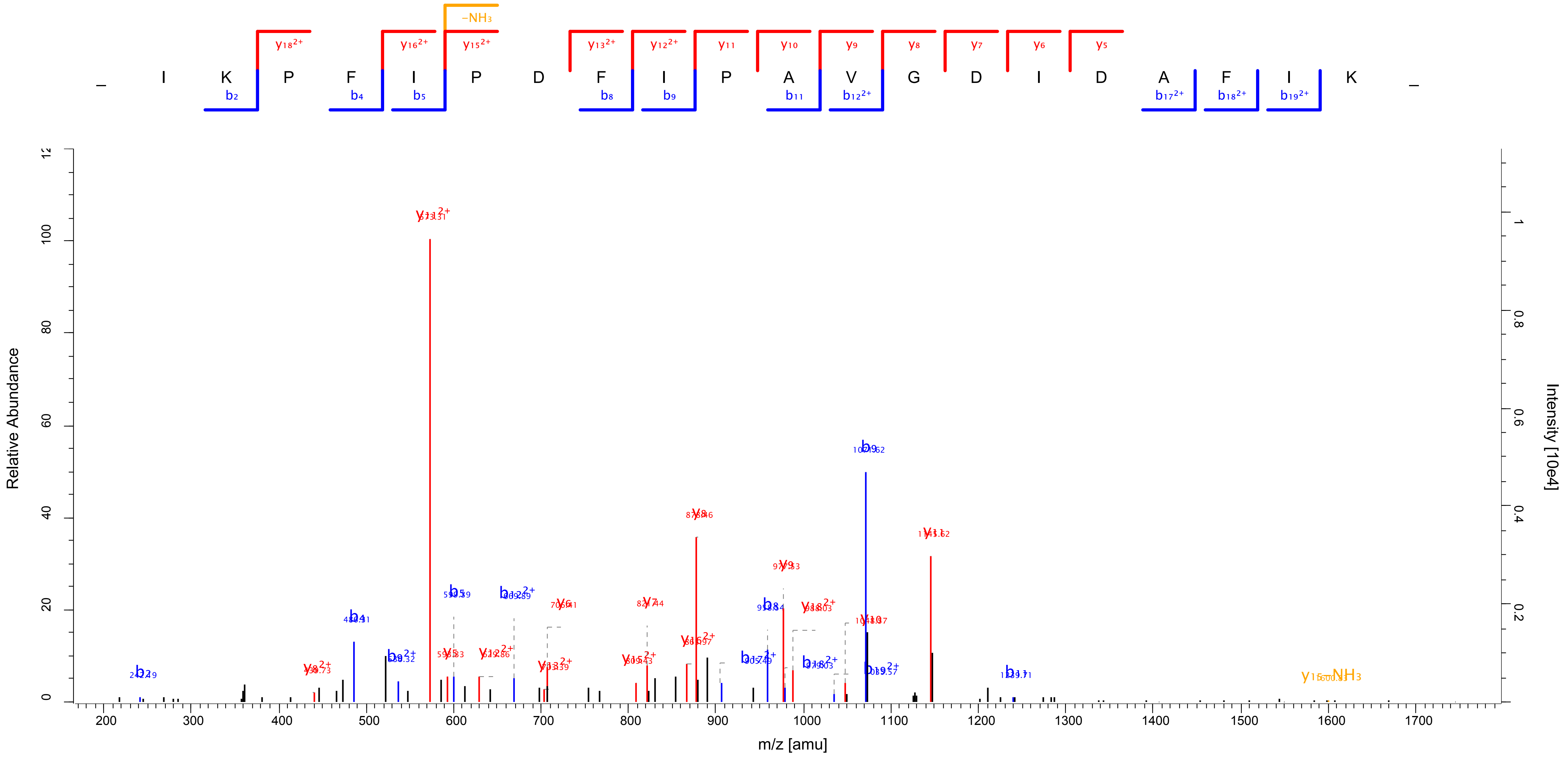
Mass:	2674.43524
m/z:	892.48569
Charge:	3+
Retentiontime:	121.375129699707
Score:	153.2496
Mass Error [ppm]:	0.83152
PEP:	5.7724E-18
Precursor Type:	ISO

general information

Annotation:	19 of 24
AminoAcids Coverage:	79 %
Intensity Coverage:	73 %
Peak Coverage:	32 %
Protein Localisation:	8 ... 31

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	23				
	143.081504042	2	A	22	2604.403179117		2604.403179117	
	256.165568023	3	I	21	2533.366065329		1267.186670898	+0.1562246
−0.0040955	371.192511055	4	D	20	2420.282001349		1210.644638908	−0.0952004
−0.1343905	458.224539464	5	S	19	2305.255058317		1153.131167392	−0.3303861
−0.0087377	571.308603445	6	I	18	2218.223029907		1109.615153187	+0.1275226
	685.351530892	7	N	17	2105.138965927		1053.073121197	+0.1906727
−0.0481157	814.394123988	8	E	16	1991.09603848		996.051657473	+0.1549465
−0.118874	927.478187969	9	I	15	1862.053445383		931.530360925	+0.167454
	1024.530951821	10	P	14	1748.969381403	−0.1206265	1748.969381403	
−0.0886816	1153.573544917	11	E	13	1651.916617551	−0.0017006	1651.916617551	
	1267.616472364	12	N	12	1522.874024455	−0.0554209	761.940650461	−0.1359019
	1380.700536344	13	I	11	1408.831097008		1408.831097008	
	1493.784600325	14	I	10	1295.747033027	+0.0592414	648.377154747	−0.1194033
	1606.868664305	15	I	9	1182.662969047	−0.0330862	1182.662969047	
	1735.911257402	16	E	8	1069.578905066	−0.1189441	1069.578905066	
	1848.995321382	17	I	7	940.53631197	−0.0734824	940.53631197	
	1996.063735298	18	F	6	827.45224799	+0.0836407	827.45224799	
	2097.111413772	19	T	5	680.383834074	−0.0271446	680.383834074	
	2234.170325635	20	H	4	579.336155599	−0.045201	579.336155599	
	2333.238739551	21	V	3	442.277243737	+0.0267724	442.277243737	
	2430.291503403	22	P	2	343.208829821	+0.1305256	343.208829821	
	2501.328617191	23	A	1	246.156065969		246.156065969	
		24	R	0	175.118952181		175.118952181	

Scan number	19571	Raw file	20091025_Orbi6_MaHe_SA_ADH_exp3_Matr_dil_Gel07
Method	ITMS; CID	Genenames	IFT46



precursor information

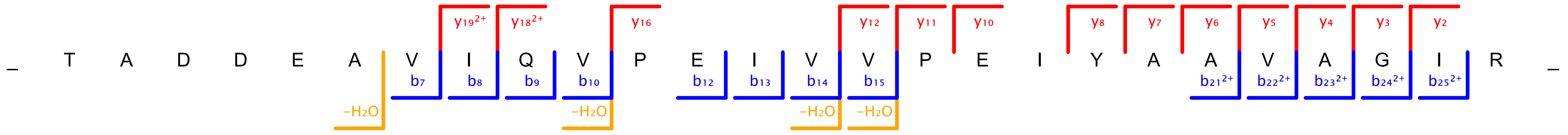
Mass:	2215.22872
m/z:	739.41685
Charge:	3+
Retentiontime:	118.838157653809
Score:	128.6401
Mass Error [ppm]:	−0.25145
PEP:	1.8274E−06
Precursor Type:	ISO

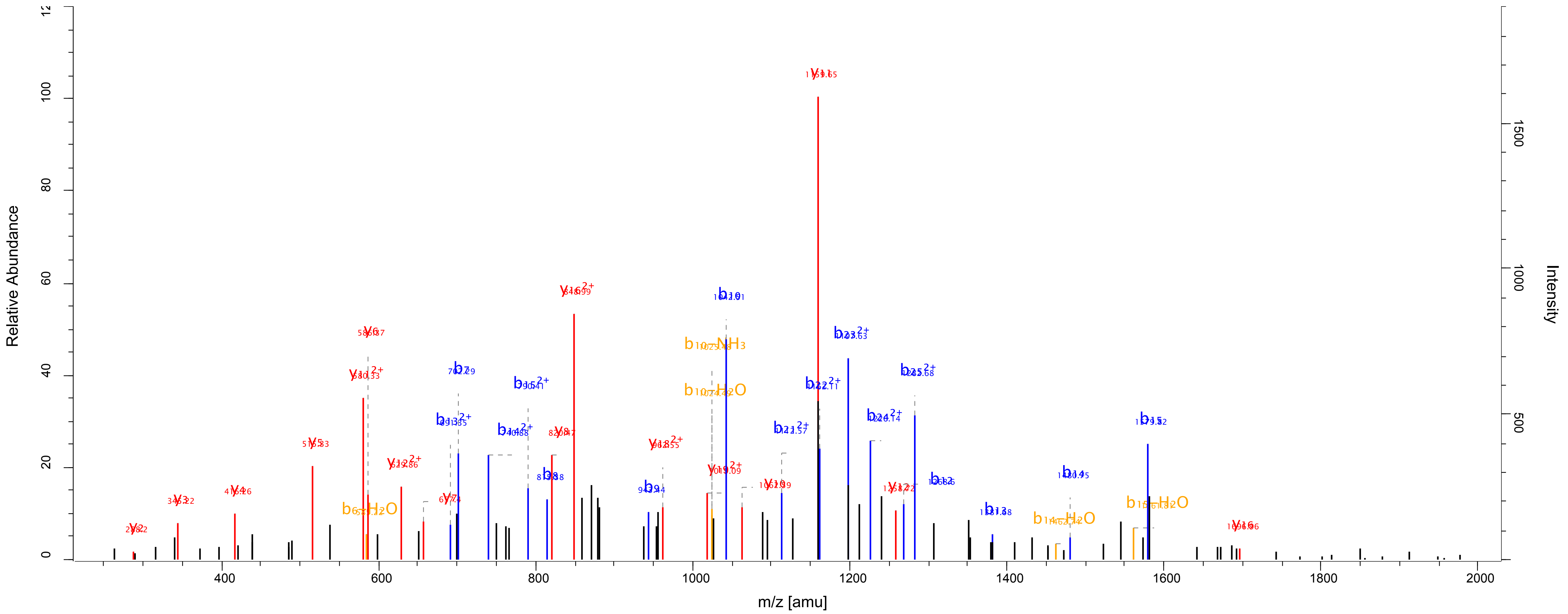
general information

Annotation:	17 of 20
AminoAcids Coverage:	85 %
Intensity Coverage:	72 %
Peak Coverage:	32 %
Protein Localisation:	150 ... 169

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045		114.09134045	1	I	19				
	242.18630346	−0.0340818	242.18630346	2	K	18	2103.1524907		2103.1524907	
	339.23906732		339.23906732	3	P	17	1975.0575277		988.03240209	+0.193367
	486.30748123	+0.0156389	486.30748123	4	F	16	1878.0047639		1878.0047639	
	599.39154521	−0.066472	599.39154521	5	I	15	1730.9363499		865.9718132	+0.3384285
	696.44430907		696.44430907	6	P	14	1617.852286		809.42978121	−0.2090781
	811.4712521		811.4712521	7	D	13	1520.7995221		1520.7995221	
	958.53966601	−0.1946953	958.53966601	8	F	12	1405.7725791		703.38992777	+0.0674087
−0.0846072	536.31550323	−0.1145747	1071.62373	9	I	11	1258.7041652		629.85572081	+0.0642011
	1168.6764938		1168.6764938	10	P	10	1145.6201012	−0.1313316	573.31368882	+0.1210646
	1239.7136076	−0.1439055	1239.7136076	11	A	9	1048.5673373	−0.1474155	1048.5673373	
−0.1088214	669.89464901		1338.7820215	12	V	8	977.53022354	−0.1157338	977.53022354	
	1395.8034853		1395.8034853	13	G	7	878.46180962	−0.1734795	439.73454304	+0.3652494
	1510.8304283		1510.8304283	14	D	6	821.4403459	+0.0031355	821.4403459	
	1623.9144923		1623.9144923	15	I	5	706.41340287	−0.0323604	706.41340287	
	1738.9414353		1738.9414353	16	D	4	593.32933889	−0.0651177	593.32933889	
+0.3496775	905.49291279		1809.9785491	17	A	3	478.30239586		478.30239586	
−0.3222858	979.02711974		1957.046963	18	F	2	407.26528207		407.26528207	
+0.2848522	1035.5691517		2070.131027	19	I	1	260.19686815		260.19686815	
				20	K	0	147.11280417		147.11280417	

Scan number	20014	Raw file	20091025_Orbi6_MaHe_SA_ADH_exp3_Matr_dil_Gel08
Method	ITMS; CID	Genenames	STYK1





precursor
information

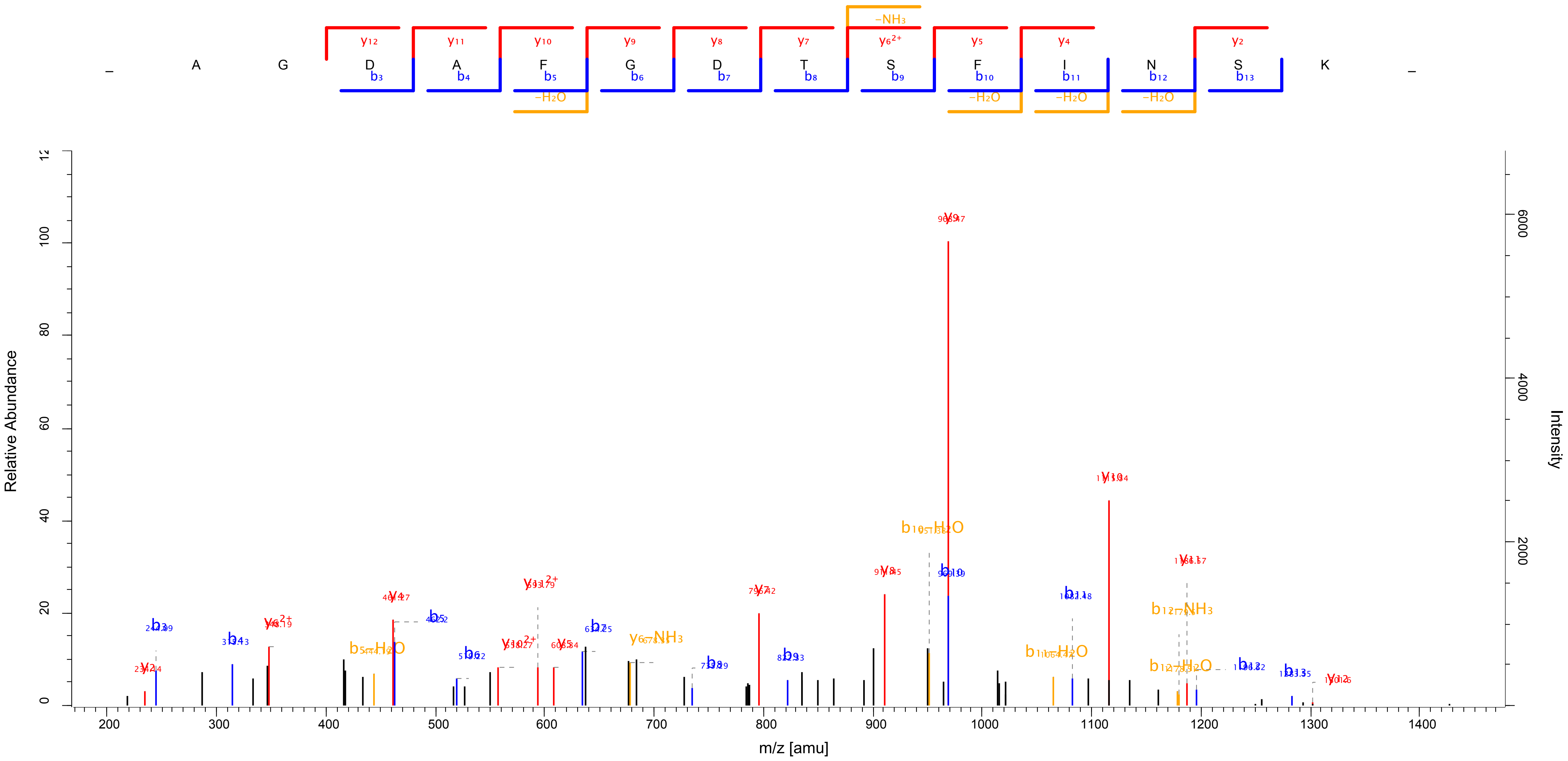
Mass:	2737.4536
m/z:	913.49181
Charge:	3+
Retentiontime:	122.323432922363
Score:	175.3285
Mass Error [ppm]:	−0.077657
PEP:	2.5387E−31
Precursor Type:	ISO

general
information

Annotation:	21 of 26
AminoAcids Coverage:	81 %
Intensity Coverage:	65 %
Peak Coverage:	37 %
Protein Localisation:	386 ... 411

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05495494		102.05495494	1	T	25				
	173.09206873		173.09206873	2	A	24	2637.4134095		2637.4134095	
	288.11901176		288.11901176	3	D	23	2566.3762957		2566.3762957	
	403.14595479		403.14595479	4	D	22	2451.3493526		2451.3493526	
	532.18854789		532.18854789	5	E	21	2336.3224096		2336.3224096	
	603.22566168		603.22566168	6	A	20	2207.2798165		2207.2798165	
	702.29407559	−0.2036825	702.29407559	7	V	19	2136.2427027		2136.2427027	
	815.37813957	−0.0213891	815.37813957	8	I	18	2037.1742888		1019.0907826	−0.1899648
	943.43671708	−0.1972762	943.43671708	9	Q	17	1924.0902248		962.54875064	−0.1434772
	1042.505131	−0.133549	1042.505131	10	V	16	1796.0316473		1796.0316473	
	1139.5578949		1139.5578949	11	P	15	1696.9632334	−0.0617441	848.98525493	+0.070226
	1268.6004879	−0.4416745	1268.6004879	12	E	14	1599.9104695		1599.9104695	
+0.0405604	691.3459142	−0.280133	1381.6845519	13	I	13	1470.8678764		1470.8678764	
−0.1754703	740.88012116	−0.1944942	1480.7529658	14	V	12	1357.7838125		1357.7838125	
−0.0815034	790.41432811	−0.2113944	1579.8213798	15	V	11	1258.7153985	+0.3092597	629.86133751	+0.0044462
	1676.8741436		1676.8741436	16	P	10	1159.6469846	−0.0752073	580.32713055	−0.006696
	1805.9167367		1805.9167367	17	E	9	1062.5942208	−0.3934151	1062.5942208	
	1919.0008007		1919.0008007	18	I	8	933.55162768		933.55162768	
	2082.0641292		2082.0641292	19	Y	7	820.4675637	+0.0598411	820.4675637	
	2153.101243		2153.101243	20	A	6	657.40423516	−0.0964959	657.40423516	
−0.2493303	1112.5728166		2224.1383568	21	A	5	586.36712138	−0.0216014	586.36712138	
+0.098787	1162.1070236		2323.2067707	22	V	4	515.33000759	−0.0888577	515.33000759	
−0.2627875	1197.6255805		2394.2438845	23	A	3	416.26159367	−0.0707978	416.26159367	
+0.0030919	1226.1363123		2451.2653482	24	G	2	345.22447989	−0.0237658	345.22447989	
−0.0804439	1282.6783443		2564.3494122	25	I	1	288.20301616	+0.1717397	288.20301616	
				26	R	0	175.11895218		175.11895218	

Scan number	10310	Raw file	20091025_Orbi6_MaHe_SA_ADH_exp3_Matr_dil_Gel09
Method	ITMS; CID	Genenames	CDC42EP4



precursor information

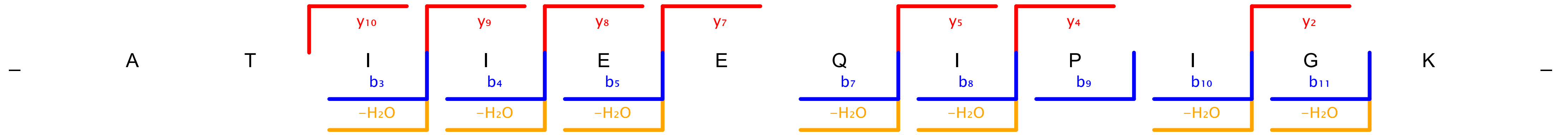
Mass:	1428.652
m/z:	715.33328
Charge:	2+
Retentiontime:	64.9989547729492
Score:	168.7589
Mass Error [ppm]:	-0.08588
PEP:	3.1073E-08
Precursor Type:	ISO

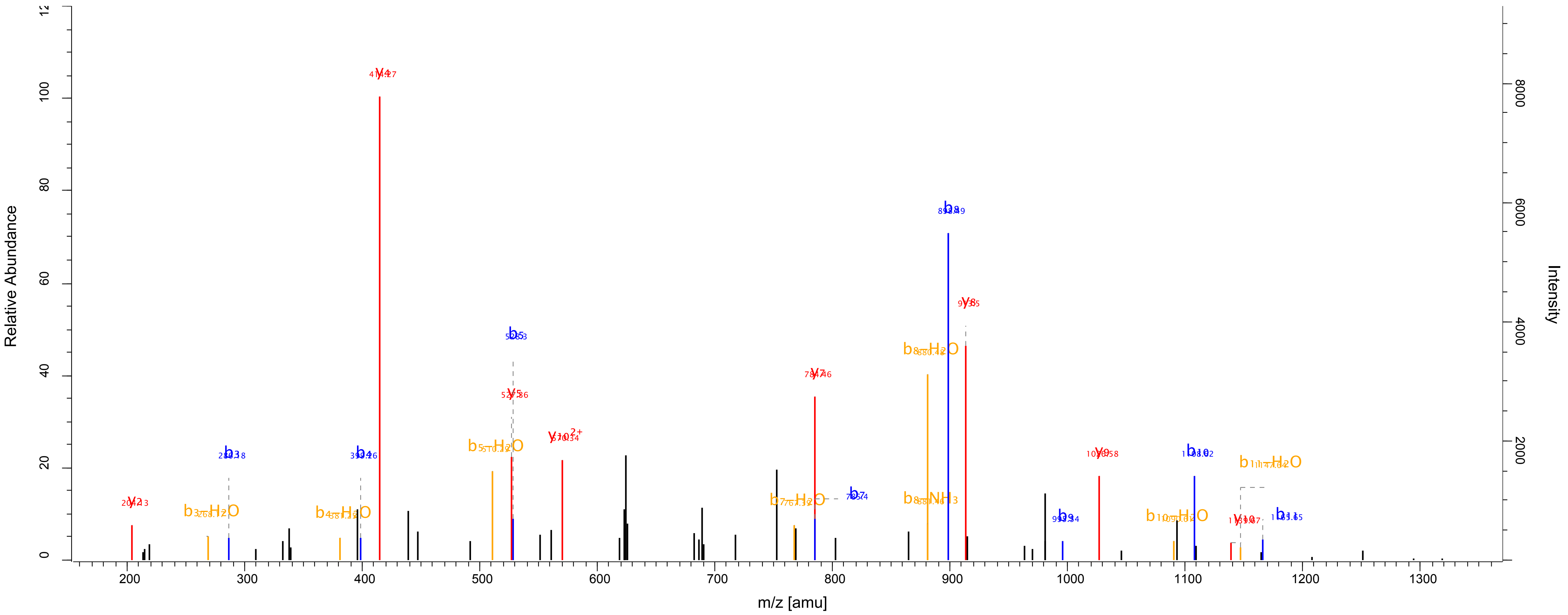
general information

Annotation:	11 of 14
AminoAcids Coverage:	79 %
Intensity Coverage:	64 %
Peak Coverage:	43 %
Protein Localisation:	43 ... 56

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	13				
	129.065853978	2	G	12	1358.622286024		1358.622286024	
+0.0770028	244.09279701	3	D	11	1301.6008223	+0.0288164	1301.6008223	
-0.0482458	315.129910798	4	A	10	1186.573879268	-0.1218529	593.790577867	+0.0830794
+0.0485015	462.198324714	5	F	9	1115.53676548	-0.1078104	558.272020973	-0.1431758
+0.1422111	519.219788438	6	G	8	968.468351564	-0.1465132	968.468351564	
-0.1560943	634.24673147	7	D	7	911.44688784	-0.1788214	911.44688784	
-0.1051399	735.294409944	8	T	6	796.419944808	-0.0464097	796.419944808	
+0.0669332	822.326438354	9	S	5	695.372266334		348.1897714	+0.0002921
+0.0195154	969.39485227	10	F	4	608.340237924	+0.0669886	608.340237924	
-0.1770364	1082.47891625	11	I	3	461.271824008	+0.0165061	461.271824008	
-0.3156669	1196.521843697	12	N	2	348.187760028		348.187760028	
+0.0083838	1283.553872107	13	S	1	234.14483258	+0.0399514	234.14483258	
		14	K	0	147.112804171		147.112804171	

Scan number	11894	Raw file	20091025_Orbi6_MaHe_SA_ADH_exp3_Matr_dil_Gel10
Method	ITMS; CID	Genenames	PDCD1LG2





precursor information

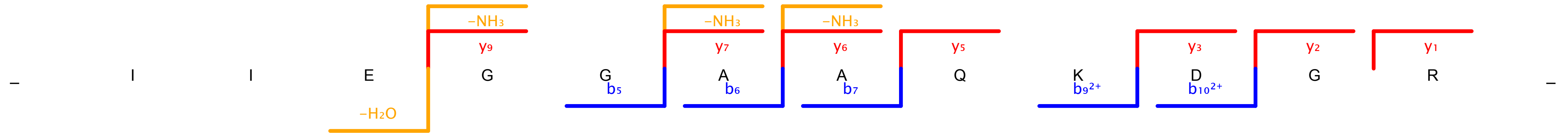
Mass:	1310.74495
m/z:	656.37975
Charge:	2+
Retentiontime:	73.7194290161133
Score:	167.1786
Mass Error [ppm]:	0.29203
PEP:	2.4245E-05
Precursor Type:	MULTI

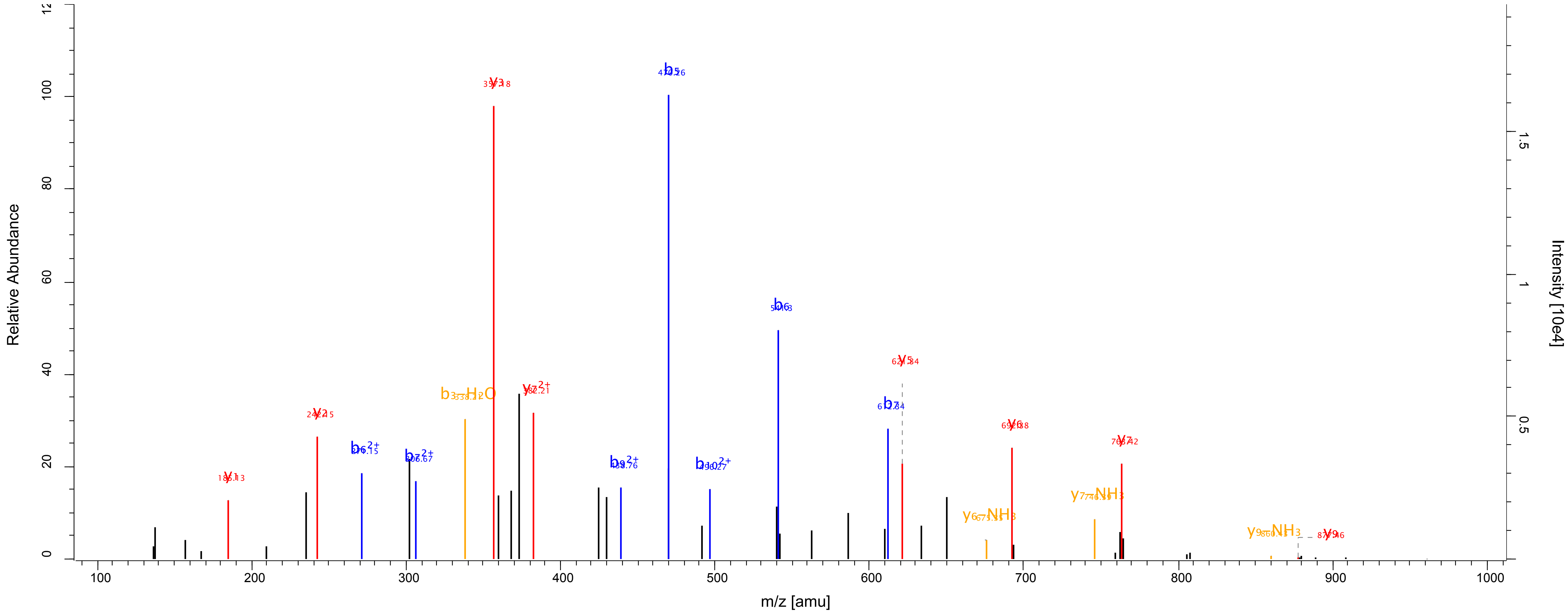
general information

Annotation:	9 of 12
AminoAcids Coverage:	75 %
Intensity Coverage:	67 %
Peak Coverage:	38 %
Protein Localisation:	73 ... 84

b ion						y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	11				
	173.092068728	2	T	10	1240.714729846		1240.714729846	
-0.2543493	286.176132709	3	I	9	1139.667051372	-0.1400738	570.337163919	+0.0070744
-0.0791054	399.260196689	4	I	8	1026.582987391	-0.1493936	1026.582987391	
-0.0683538	528.302789786	5	E	7	913.498923411	-0.0426856	913.498923411	
	657.345382882	6	E	6	784.456330315	-0.0233469	784.456330315	
-0.1163017	785.403960393	7	Q	5	655.413737218		655.413737218	
-0.1427485	898.488024374	8	I	4	527.355159707	-0.1414756	527.355159707	
-0.127153	995.540788226	9	P	3	414.271095727	-0.0536275	414.271095727	
-0.2089587	1108.624852206	10	I	2	317.218331875		317.218331875	
-0.1511987	1165.64631593	11	G	1	204.134267894	-0.0976468	204.134267894	
		12	K	0	147.112804171		147.112804171	

Scan number	3572	Raw file	20091027_Orbi6_MaHe_SA_ADH_exp3_FN_Gel01
Method	ITMS; CID	Genenames	DLG3





precursor information

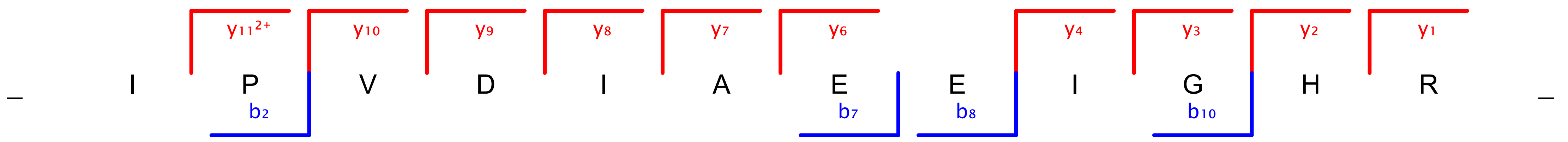
Mass:	1213.64088
m/z:	405.55424
Charge:	3+
Retentiontime:	35.7533111572266
Score:	135.8587
Mass Error [ppm]:	−0.49981
PEP:	9.3145E−05
Precursor Type:	MULTI

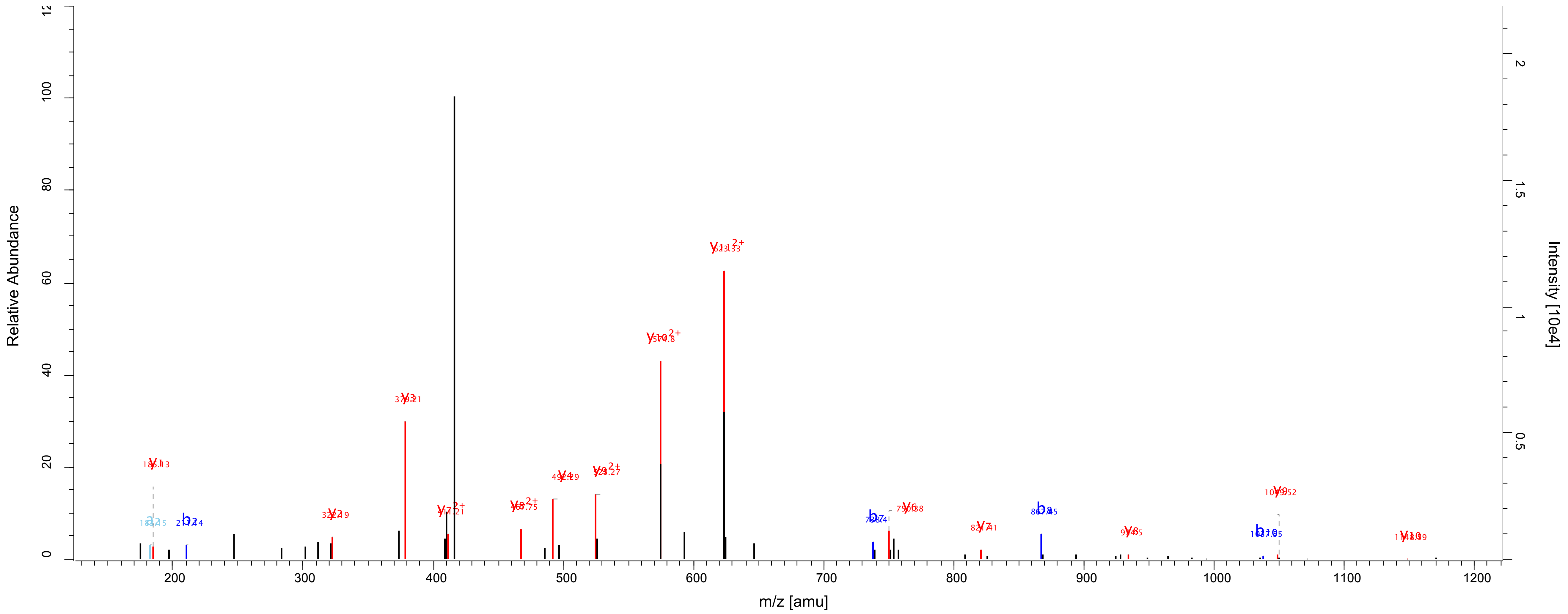
general information

Annotation:	10 of 12
AminoAcids Coverage:	83 %
Intensity Coverage:	67 %
Peak Coverage:	37 %
Protein Localisation:	278 ... 289

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045		114.09134045	1	I	11				
	227.17540443		227.17540443	2	I	10	1119.587179		1119.587179	
	356.21799752		356.21799752	3	E	9	1006.503115		1006.503115	
	413.23946125		413.23946125	4	G	8	877.4605219	+0.0067022	877.4605219	
	470.26092497	−0.049957	470.26092497	5	G	7	820.43905818		820.43905818	
−0.0222865	271.15265761	+0.0914876	541.29803876	6	A	6	763.41759445	−0.0290446	382.21243546	−0.0531642
+0.0536085	306.67121451	+0.0242835	612.33515255	7	A	5	692.38048067	+0.0230838	692.38048067	
	740.39373006		740.39373006	8	Q	4	621.34336688	−0.0234206	621.34336688	
+0.0697144	438.75508418		876.50289189	9	K	3	493.28478937		493.28478937	
+0.0874319	496.26855569		991.52983492	10	D	2	357.17562754	−0.0239857	357.17562754	
	1048.5512986		1048.5512986	11	G	1	242.1486845	−0.0003691	242.1486845	
				12	R	0	185.12722078	−0.0295035	185.12722078	

Scan number	10822	Raw file	20091027_Orbi6_MaHe_SA_ADH_exp3_FN_Gel02
Method	ITMS; CID	Genenames	CDKN2A





precursor information

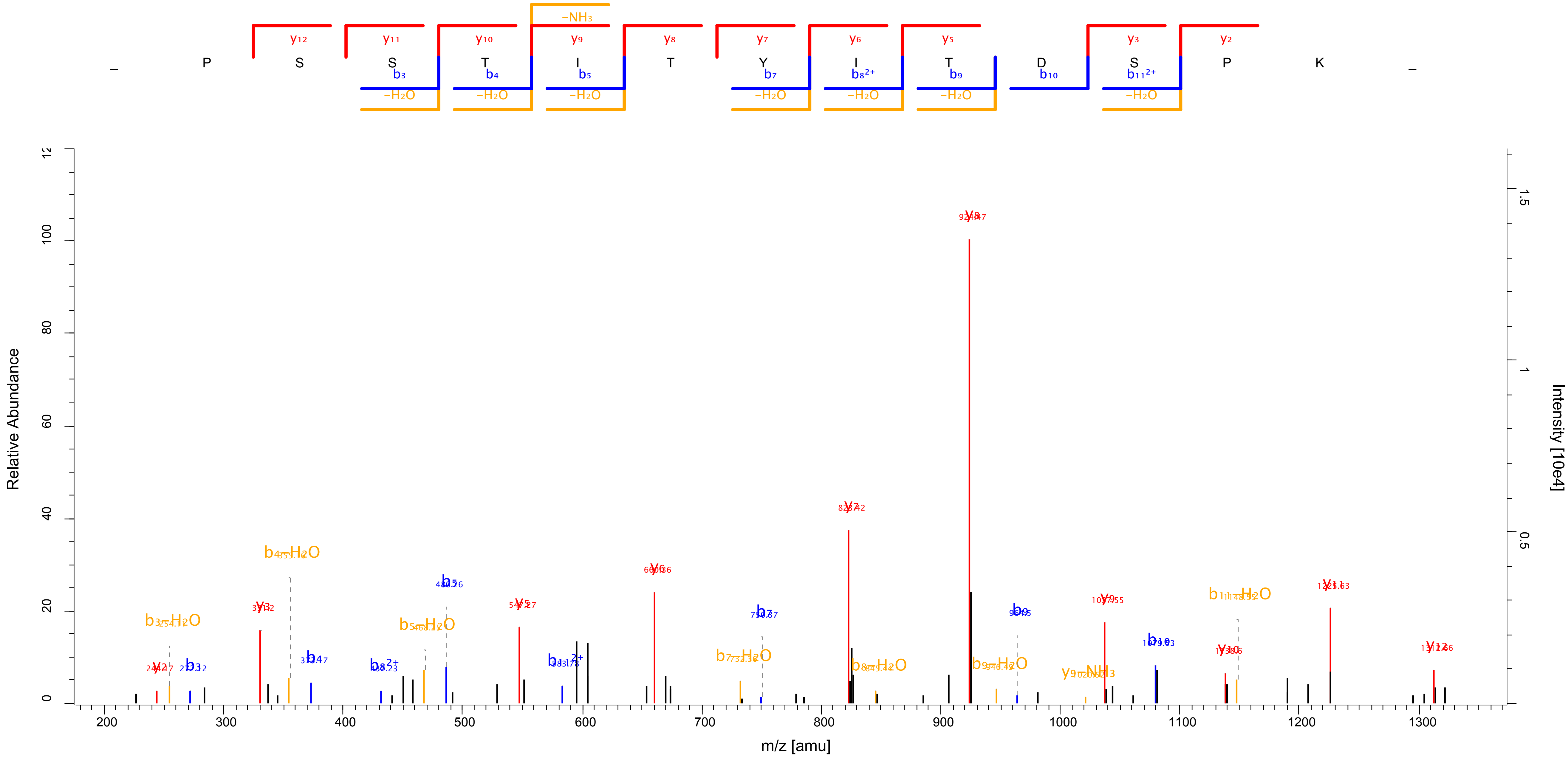
Mass:	1347.71361
m/z:	450.24515
Charge:	3+
Retentiontime:	68.193733215332
Score:	131.8187
Mass Error [ppm]:	-0.77272
PEP:	0.00010983
Precursor Type:	MULTI

general information

Annotation:	11 of 12
AminoAcids Coverage:	92 %
Intensity Coverage:	46 %
Peak Coverage:	34 %
Protein Localisation:	113 ... 124

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.096425825		114.09134045	1	I	11				
-0.1082961	183.14918968	-0.2537997	211.1441043	2	P	10	1245.6461451		623.32671079	-0.0396014
	282.21760359		310.21251822	3	V	9	1148.5933813	+0.0773951	574.80032886	-0.0986077
	397.24454663		425.23946125	4	D	8	1049.5249673	-0.2073404	525.2661219	-0.0105677
	510.32861061		538.32352523	5	I	7	934.49802431	+0.0588605	467.75265039	+0.0413865
	581.36572439		609.36063902	6	A	6	821.41396033	-0.0096635	411.2106184	+0.0885454
	710.40831749	-0.1462131	738.40323211	7	E	5	750.37684654	+0.0914152	750.37684654	
	839.45091059	-0.1988159	867.44582521	8	E	4	621.33425344		621.33425344	
	952.53497457		980.52988919	9	I	3	492.29166035	+0.0482139	492.29166035	
	1009.5564383	-0.2766947	1037.5513529	10	G	2	379.20759637	+0.0033106	379.20759637	
	1146.6153502		1174.6102648	11	H	1	322.18613264	+0.0140932	322.18613264	
				12	R	0	185.12722078	+0.0648569	185.12722078	

Scan number	7549	Raw file	20091027_Orbi6_MaHe_SA_ADH_exp3_FN_Gel02
Method	ITMS; CID	Genenames	TMEM69



precursor information

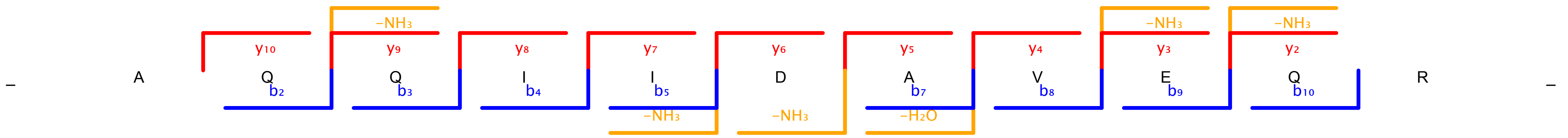
Mass:	1408.70902
m/z:	705.36179
Charge:	2+
Retentiontime:	50.5628318786621
Score:	151.9761
Mass Error [ppm]:	0.31511
PEP:	2.2625E-06
Precursor Type:	MULTI

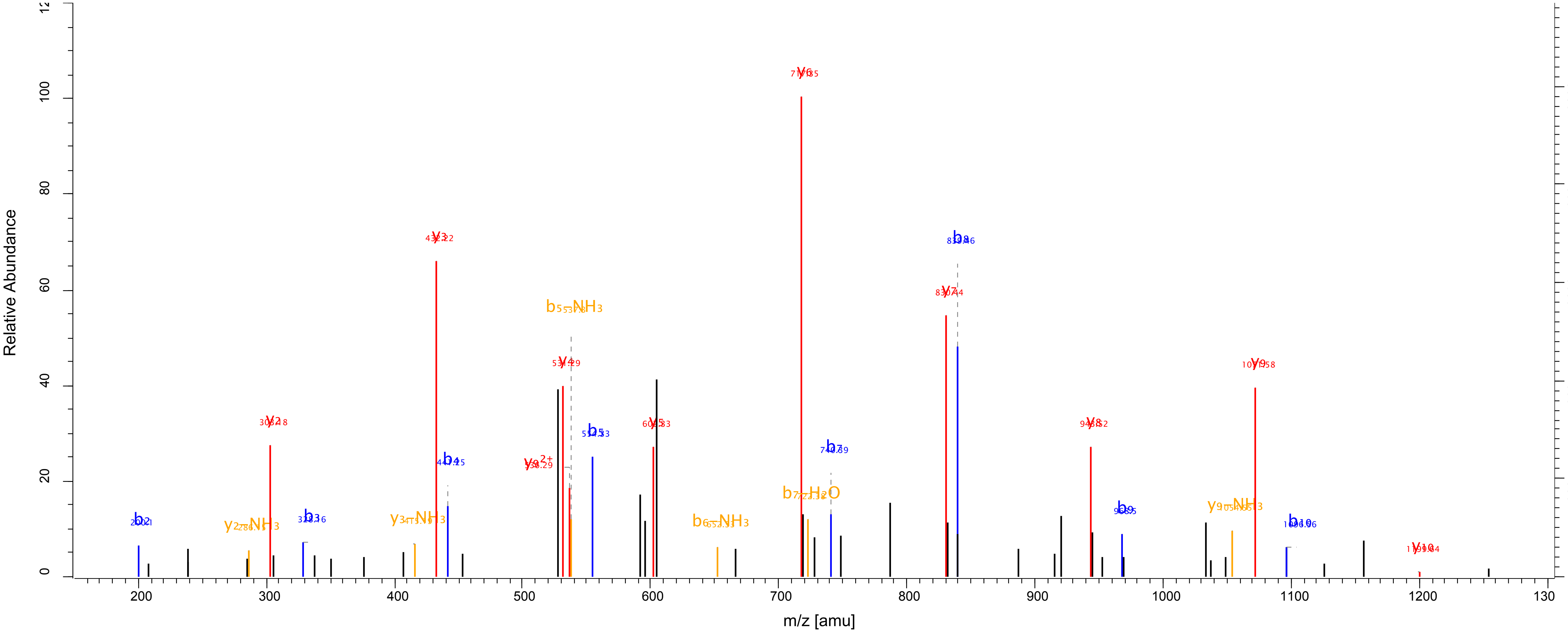
general information

Annotation:	11 of 13
AminoAcids Coverage:	85 %
Intensity Coverage:	61 %
Peak Coverage:	38 %
Protein Localisation:	83 ... 95

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	98.060040319		98.060040319	1	P	12		
	185.092068728		185.092068728	2	S	11	1312.663088206	−0.2125267
	272.124097138	−0.0174382	272.124097138	3	S	10	1225.631059796	−0.1195852
	373.171775612	+0.0074846	373.171775612	4	T	9	1138.599031386	+0.1836835
	486.255839593	+0.1053665	486.255839593	5	I	8	1037.551352912	−0.0598978
	587.303518067		587.303518067	6	T	7	924.467288931	−0.0487709
	750.366846605	−0.186915	750.366846605	7	Y	6	823.419610457	−0.0167784
−0.0486736	432.229093526		863.450910586	8	I	5	660.356281919	−0.0077712
	964.49858906	−0.0203176	964.49858906	9	T	4	547.272217939	−0.023988
	1079.525532092	−0.2069286	1079.525532092	10	D	3	446.224539464	
−0.4369595	583.782418484		1166.557560502	11	S	2	331.197596432	−0.0603284
	1263.610324354		1263.610324354	12	P	1	244.165568023	−0.0416972
				13	K	0	147.112804171	

Scan number	7825	Raw file	20091027_Orbi6_MaHe_SA_ADH_exp3_FN_Gel04
Method	ITMS; CID	Genenames	C1orf122





precursor information

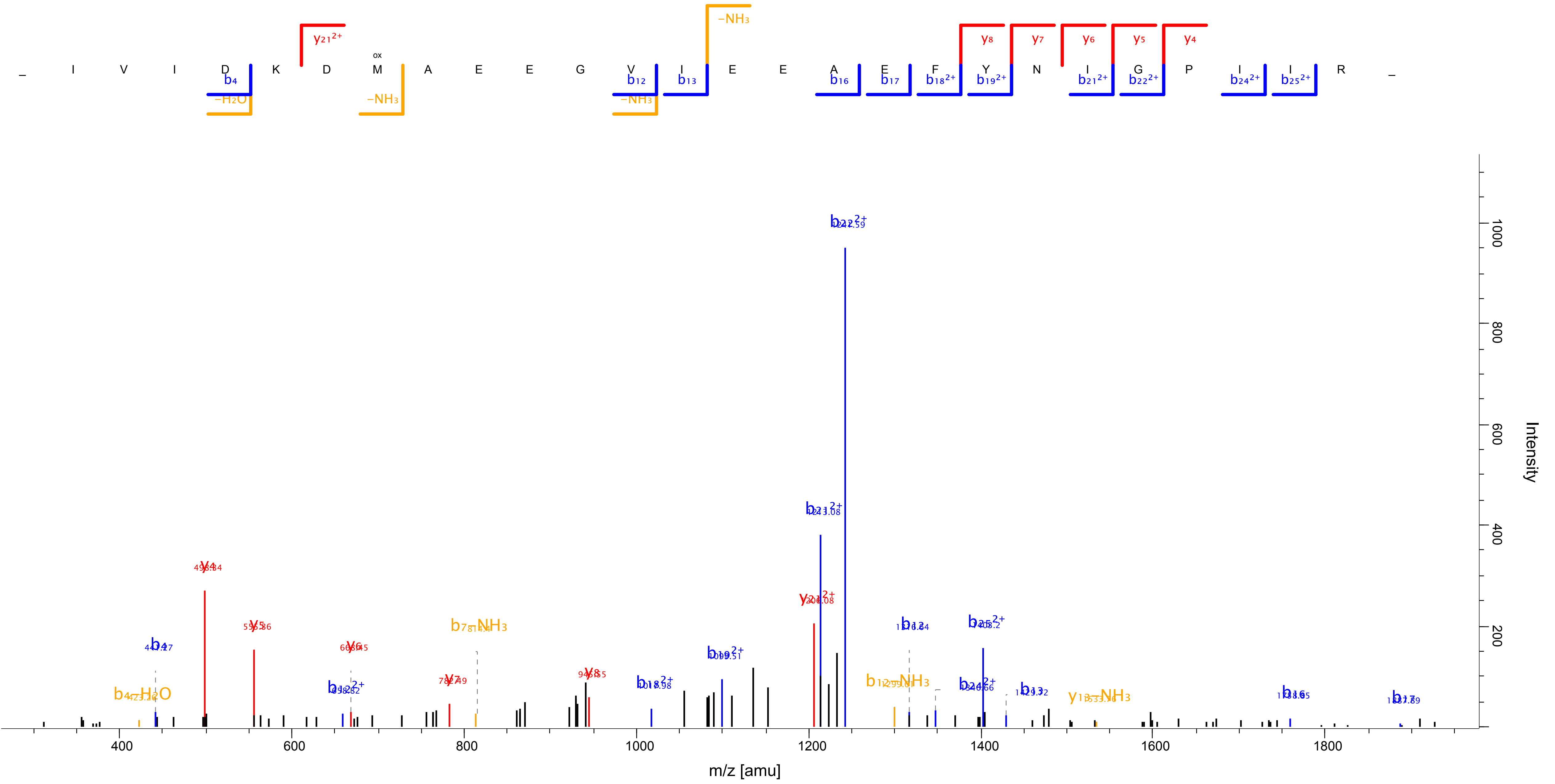
Mass:	1269.66823
m/z:	635.84139
Charge:	2+
Retentiontime:	53.6771659851074
Score:	170.5214
Mass Error [ppm]:	0.40896
PEP:	0.00010626
Precursor Type:	ISO

general information

Annotation:	9 of 11
AminoAcids Coverage:	82 %
Intensity Coverage:	66 %
Peak Coverage:	41 %
Protein Localisation:	40 ... 50

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	10				
+0.1299271	200.102967766	2	Q	9	1199.637876508	+0.1823139	1199.637876508	
-0.0230565	328.161545277	3	Q	8	1071.579298997	-0.0640402	536.293287732	+0.0461288
-0.0591469	441.245609258	4	I	7	943.520721485	-0.1645203	943.520721485	
+0.037087	554.329673238	5	I	6	830.436657505	-0.0080076	830.436657505	
	669.35661627	6	D	5	717.352593525	+0.0071477	717.352593525	
-0.1665572	740.393730058	7	A	4	602.325650493	+0.0997035	602.325650493	
-0.2216655	839.462143974	8	V	3	531.288536705	-0.0365225	531.288536705	
-0.2478401	968.50473707	9	E	2	432.220122789	+0.0743108	432.220122789	
-0.1328947	1096.563314582	10	Q	1	303.177529692	-0.0032743	303.177529692	
		11	R	0	175.118952181		175.118952181	

Scan number	18898	Raw file	20091027_Orbi6_MaHe_SA_ADH_exp3_FN_Gel05
Method	ITMS; CID	Genenames	KCTD17



precursor information

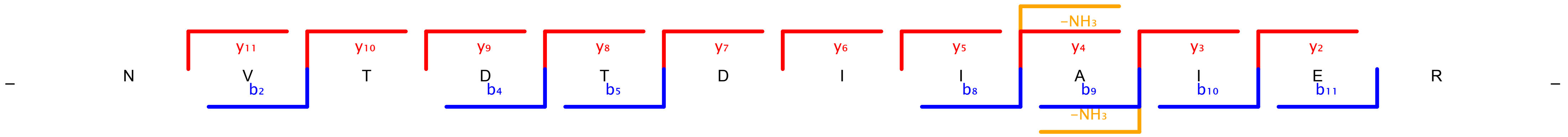
Mass:	2978.4942
m/z:	993.83867
Charge:	3+
Retentiontime:	113.787322998047
Score:	86.62476
Mass Error [ppm]:	−0.16602
PEP:	0.00017515
Precursor Type:	ISO

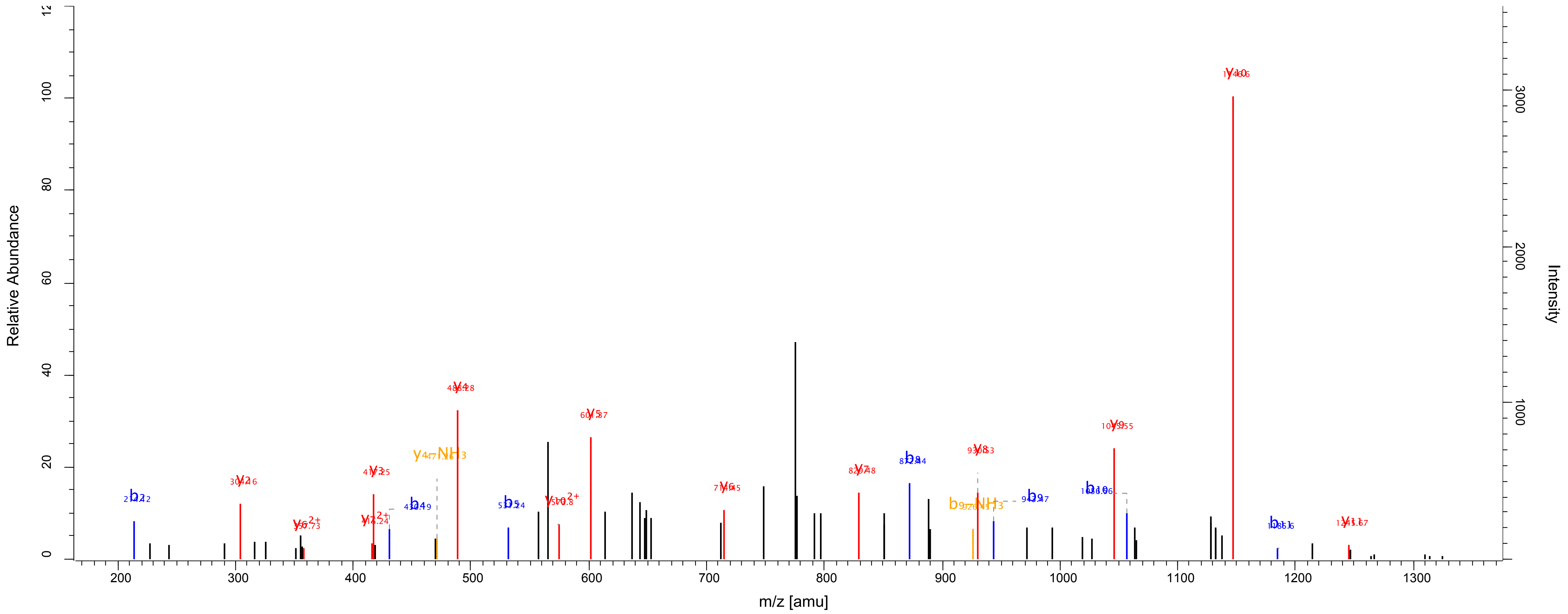
general information

Annotation:	16 of 26
AminoAcids Coverage:	62 %
Intensity Coverage:	54 %
Peak Coverage:	22 %
Protein Localisation:	97 ... 122

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045		114.09134045	1	I	25				
	213.15975436		213.15975436	2	V	24	2866.4179025		2866.4179025	
	326.24381834		326.24381834	3	I	23	2767.3494886		2767.3494886	
	441.27076138	+0.0036222	441.27076138	4	D	22	2654.2654246		2654.2654246	
	569.36572439		569.36572439	5	K	21	2539.2384816		2539.2384816	
	684.39266743		684.39266743	6	D	20	2411.1435185		1206.0753975	+0.3162041
	831.42806665		831.42806665	7	M	19	2296.1165755		2296.1165755	
	902.46518044		902.46518044	8	A	18	2149.0811763		2149.0811763	
	1031.5077735		1031.5077735	9	E	17	2078.0440625		2078.0440625	
	1160.5503666		1160.5503666	10	E	16	1949.0014694		1949.0014694	
	1217.5718304		1217.5718304	11	G	15	1819.9588763		1819.9588763	
−0.3191827	658.82376037	−0.2690285	1316.6402443	12	V	14	1762.9374126		1762.9374126	
	1429.7243083	−0.2705729	1429.7243083	13	I	13	1663.8689987		1663.8689987	
	1558.7669014		1558.7669014	14	E	12	1550.7849347		1550.7849347	
	1687.8094944		1687.8094944	15	E	11	1421.7423416		1421.7423416	
	1758.8466082	−0.3517352	1758.8466082	16	A	10	1292.6997485		1292.6997485	
	1887.8892013	−0.3468429	1887.8892013	17	E	9	1221.6626347		1221.6626347	
+0.1039799	1017.9824459		2034.9576152	18	F	8	1092.6200416		1092.6200416	
−0.2189441	1099.5141101		2198.0209438	19	Y	7	945.55162768	+0.0803303	945.55162768	
	2312.0638712		2312.0638712	20	N	6	782.48829914	−0.0407894	782.48829914	
−0.1089779	1213.0776058		2425.1479352	21	I	5	668.4453717	−0.0423566	668.4453717	
+0.0229904	1241.5883377		2482.1693989	22	G	4	555.36130772	+0.0805868	555.36130772	
	2579.2221628		2579.2221628	23	P	3	498.33984399	−0.0859072	498.33984399	
−0.0339489	1346.6567516		2692.3062268	24	I	2	401.28708014		401.28708014	
−0.0463178	1403.1987836		2805.3902907	25	I	1	288.20301616		288.20301616	
				26	R	0	175.11895218		175.11895218	

Scan number	11135	Raw file	20091027_Orbi6_MaHe_SA_ADH_exp3_FN_Gel06
Method	ITMS; CID	Genenames	GPR89A;GPR89B;GPR89C





precursor information

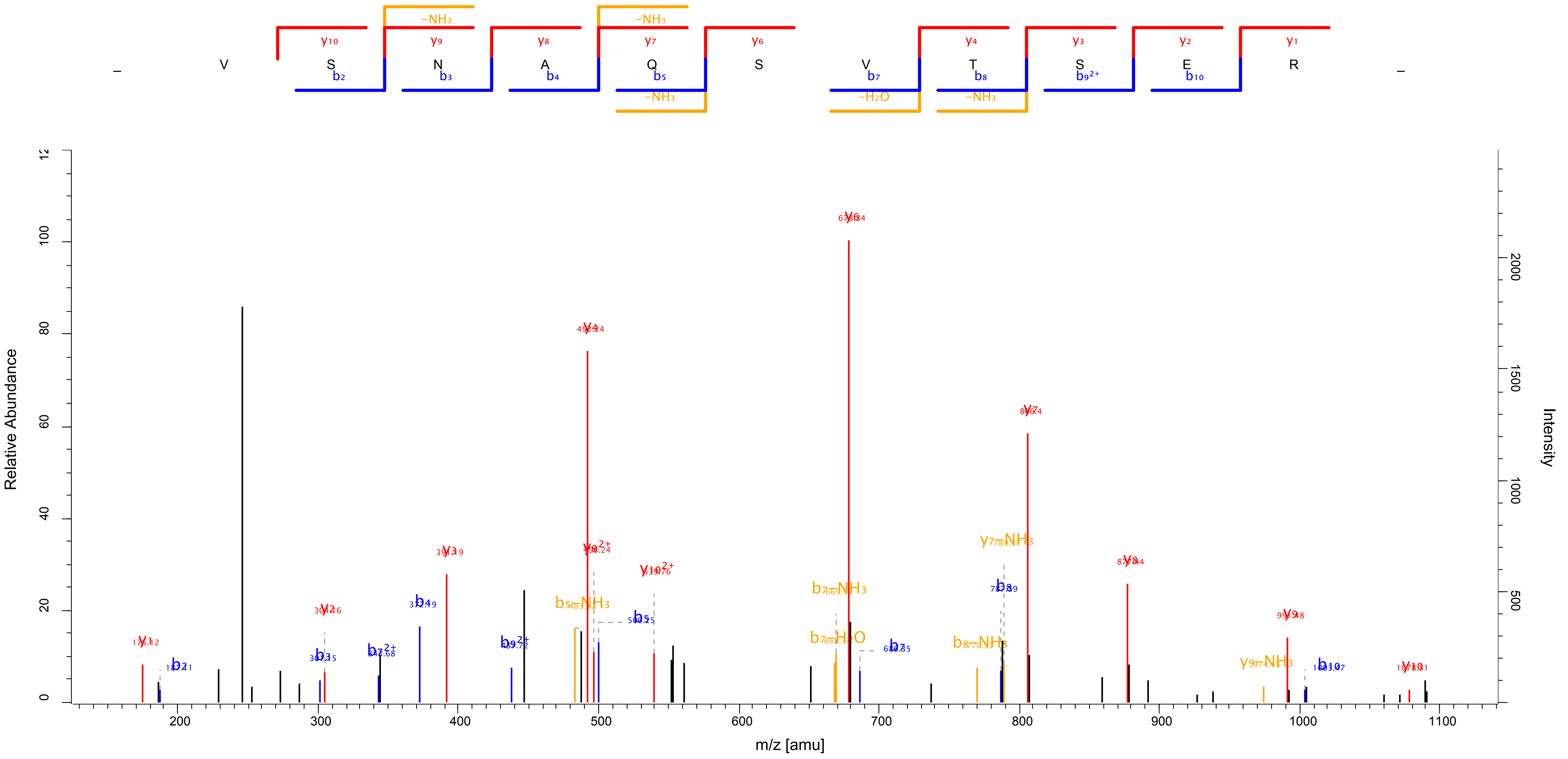
Mass:	1358.70419
m/z:	680.35937
Charge:	2+
Retentiontime:	71.0314102172852
Score:	124.8569
Mass Error [ppm]:	0.022873
PEP:	0.00011029
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverage:	83 %
Intensity Coverage:	48 %
Peak Coverage:	32 %
Protein Localisation:	180 ... 191

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.050203914	1	N	11				
-0.085903	214.11861783	2	V	10	1245.668507935	+0.0548807	1245.668507935	
	315.166296304	3	T	9	1146.600094018	-0.0881311	573.803685242	+0.2909803
-0.0188009	430.193239336	4	D	8	1045.552415544	+0.0259536	1045.552415544	
+0.1027712	531.24091781	5	T	7	930.525472512	+0.142069	930.525472512	
	646.267860842	6	D	6	829.477794038	-0.2129015	415.242535252	-0.0092589
	759.351924823	7	I	5	714.450851006	-0.0861659	357.729063736	+0.2903454
-0.0892481	872.435988803	8	I	4	601.366787026	+0.0489234	601.366787026	
-0.031025	943.473102591	9	A	3	488.282723045	-0.0282675	488.282723045	
-0.0708384	1056.557166571	10	I	2	417.245609258	+0.0014611	417.245609258	
-0.2458778	1185.599759667	11	E	1	304.161545277	+0.0825343	304.161545277	
		12	R	0	175.118952181		175.118952181	

Scan number	2051	Raw file	20091027_Orbi6_MaHe_SA_ADH_exp3_FN_Gel07
Method	ITMS; CID	Genenames	SLC16A7



precursor information

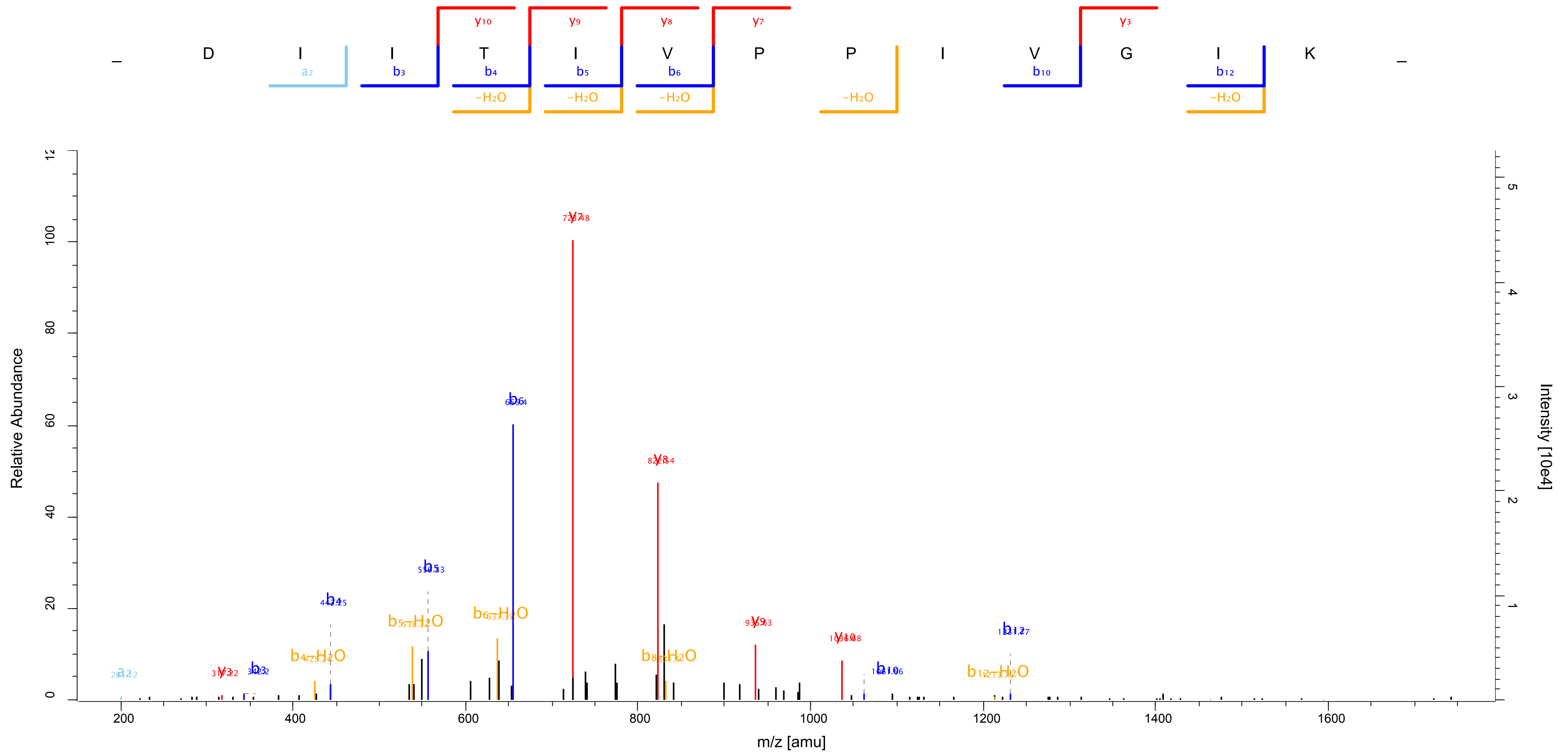
Mass:	1176.57367
m/z:	589.29411
Charge:	2+
Retentiontime:	21.8420314788818
Score:	177.4392
Mass Error [ppm]:	0.15947
PEP:	3.2764E-08
Precursor Type:	MULTI

general information

Annotation:	10 of 11
AminoAcids Coverage:	91 %
Intensity Coverage:	61 %
Peak Coverage:	46 %
Protein Localisation:	464 ... 474

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.07569038		100.07569038	1	V	10				
	187.10771879	+0.088555	187.10771879	2	S	9	1078.5123416	−0.070203	539.75980906	+0.0410943
	301.15064624	−0.0960808	301.15064624	3	N	8	991.48031323	+0.1044646	496.24379485	−0.0244955
	372.18776003	+0.0804284	372.18776003	4	A	7	877.43738579	+0.0574262	877.43738579	
	500.24633754	+0.0088504	500.24633754	5	Q	6	806.400272	+0.0551113	806.400272	
	587.27836595		587.27836595	6	S	5	678.34169449	−0.0626418	678.34169449	
−0.3586078	343.67702817	+0.027915	686.34677987	7	V	4	591.30966608		591.30966608	
	787.39445834	−0.1791873	787.39445834	8	T	3	492.24125216	−0.0614426	492.24125216	
+0.3515998	437.71688161		874.42648675	9	S	2	391.19357369	+0.0273125	391.19357369	
	1003.4690798	−0.2235354	1003.4690798	10	E	1	304.16154528	+0.0459132	304.16154528	
				11	R	0	175.11895218	+0.0031639	175.11895218	

Scan number	19774	Raw file	20091027_Orbi6_MaHe_SA_ADH_exp3_FN_Gel08
Method	ITMS; CID	Genenames	SLC41A3



precursor information

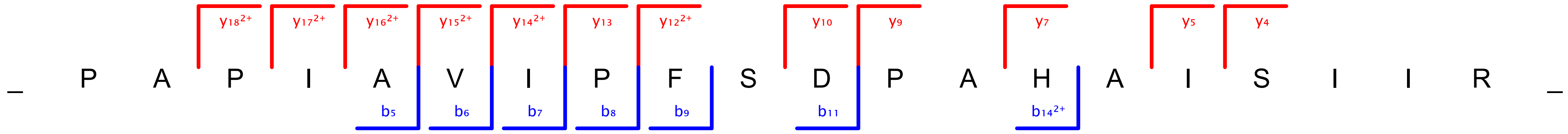
Mass:	2753.40892
m/z:	689.35951
Charge:	4+
Retentiontime:	118.871963500977
Score:	135.6624
Mass Error [ppm]:	0.14638
PEP:	1.1191E−21
Precursor Type:	MULTI

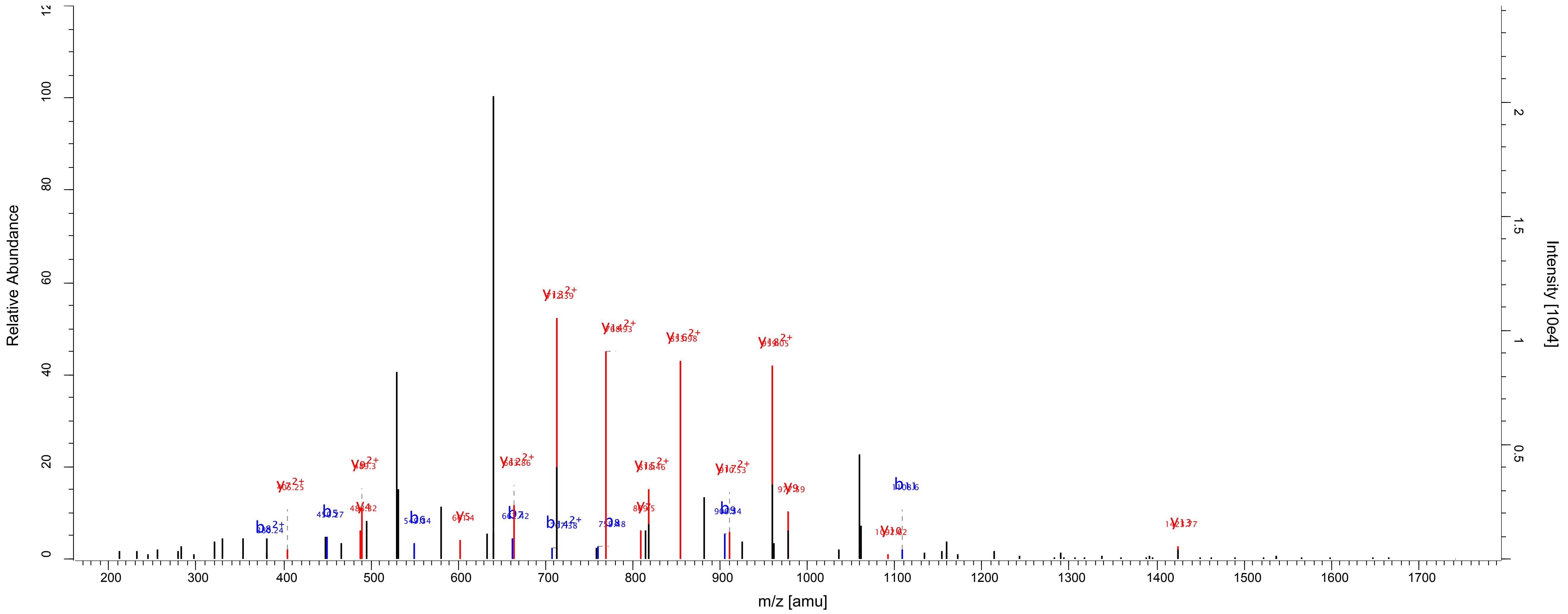
general information

Annotation:	10 of 13
AminoAcids Coverage:	77 %
Intensity Coverage:	67 %
Peak Coverage:	21 %
Protein Localisation:	101 ... 113

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	88.039304876		116.034219499	1	D	12		
+0.1874222	201.123368857		229.118283479	2	I	11	1262.844621807	
	314.207432837	−0.0402686	342.202347459	3	I	10	1149.760557826	
	415.255111311	−0.0343277	443.250025933	4	T	9	1036.676493846	−0.1209519
	528.339175292	−0.0851885	556.334089914	5	I	8	935.628815372	−0.1051948
	627.407589208	−0.1824721	655.40250383	6	V	7	822.544751391	−0.1052372
	724.46035306		752.455267682	7	P	6	723.476337475	−0.0644112
	821.513116912		849.508031534	8	P	5	626.423573623	
	934.597180892		962.592095515	9	I	4	529.370809771	
	1033.665594809	−0.3502067	1061.660509431	10	V	3	416.286745791	
	1090.687058532		1118.681973154	11	G	2	317.218331875	−0.0318084
	1203.771122513	−0.0153047	1231.766037135	12	I	1	260.196868151	
				13	K	0	147.112804171	

Scan number	19999	Raw file	20091027_Orbi6_MaHe_SA_ADH_exp3_FN_Gel12
Method	ITMS; CID	Genenames	KLHL21





precursor information

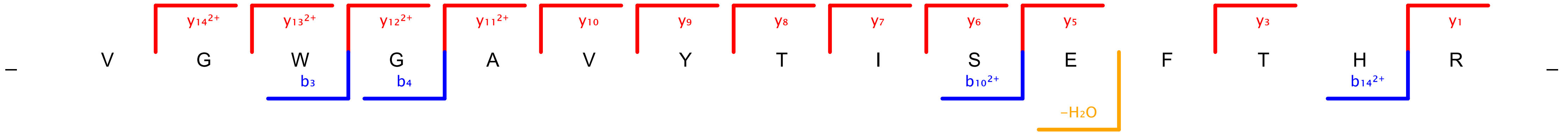
Mass:	2084.17844
m/z:	695.73342
Charge:	3+
Retentiontime:	117.368278503418
Score:	106.2999
Mass Error [ppm]:	0.09296
PEP:	2.642E−07
Precursor Type:	MULTI

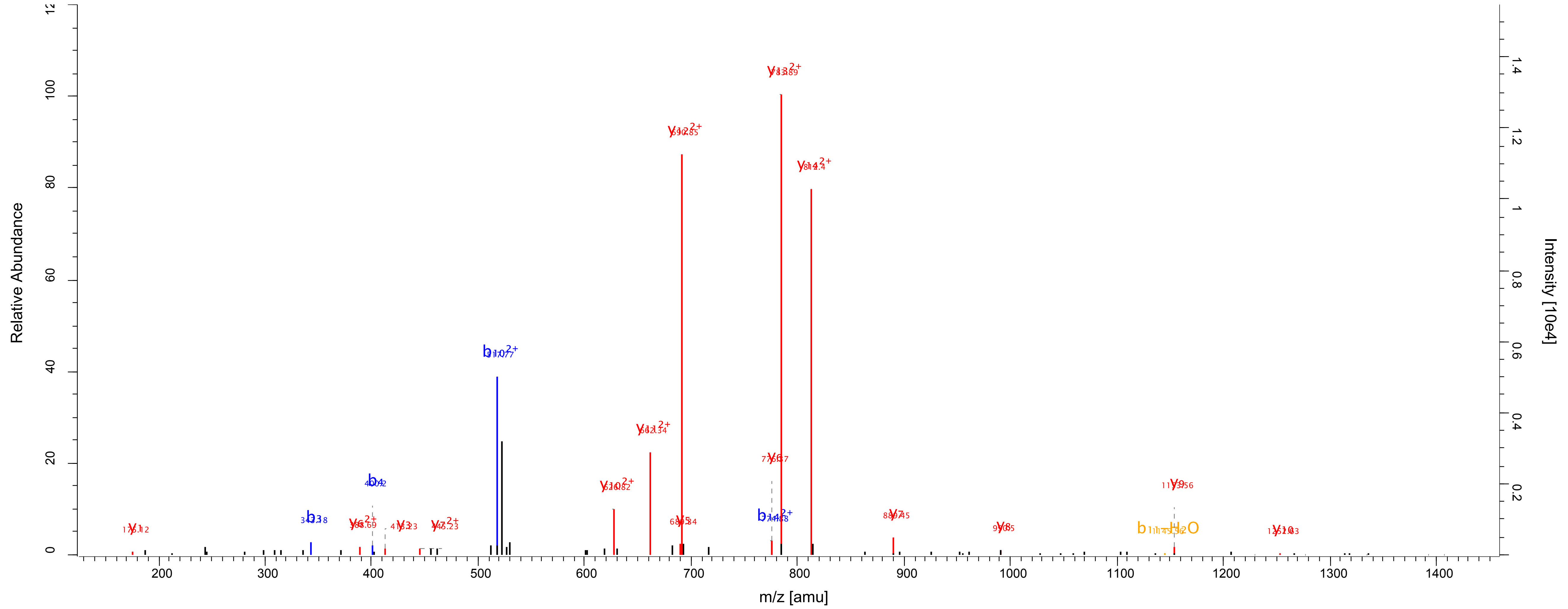
general information

Annotation:	12 of 20
AminoAcids Coverage:	60 %
Intensity Coverage:	44 %
Peak Coverage:	27 %
Protein Localisation:	4 ... 23

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	98.060040319		98.060040319	1	P	19				
	169.09715411		169.09715411	2	A	18	1988.1327583		1988.1327583	
	266.14991796		266.14991796	3	P	17	1917.0956445		959.05146051	−0.0763629
	379.23398194		379.23398194	4	I	16	1820.0428807		910.52507858	+0.0773994
	450.27109573	−0.059731	450.27109573	5	A	15	1706.9588167		853.98304659	+0.1023416
	549.33950964	−0.3539139	549.33950964	6	V	14	1635.9217029		818.4644897	−0.110852
	662.42357362	−0.1685077	662.42357362	7	I	13	1536.853289		768.93028274	+0.1103667
−0.1154642	380.24180697	+0.3170585	759.47633748	8	P	12	1423.769225	−0.0366811	712.38825075	+0.0586487
	906.54475139	−0.3975346	906.54475139	9	F	11	1326.7164612		663.86186882	−0.3113927
	993.5767798		993.5767798	10	S	10	1179.6480473		1179.6480473	
	1108.6037228	−0.0597775	1108.6037228	11	D	9	1092.6160189	+0.2042936	1092.6160189	
	1205.6564867		1205.6564867	12	P	8	977.58907582	+0.0232899	489.29817614	+0.1637379
	1276.6936005		1276.6936005	13	A	7	880.53631197		880.53631197	
+0.3745612	707.3798944		1413.7525123	14	H	6	809.49919818	−0.1580727	405.25323732	+0.0208716
	1484.7896261		1484.7896261	15	A	5	672.44028632		672.44028632	
	1597.8736901		1597.8736901	16	I	4	601.40317253	−0.0764513	601.40317253	
	1684.9057185		1684.9057185	17	S	3	488.31910855	+0.1694779	488.31910855	
	1797.9897825		1797.9897825	18	I	2	401.28708014		401.28708014	
	1911.0738465		1911.0738465	19	I	1	288.20301616		288.20301616	
				20	R	0	175.11895218		175.11895218	

Scan number	14817	Raw file	20091029_Orbi6_MaHe_SA_ADH_exp3_BSA_Gel04
Method	ITMS; CID	Genenames	WDYHV1;C8orf32





precursor information

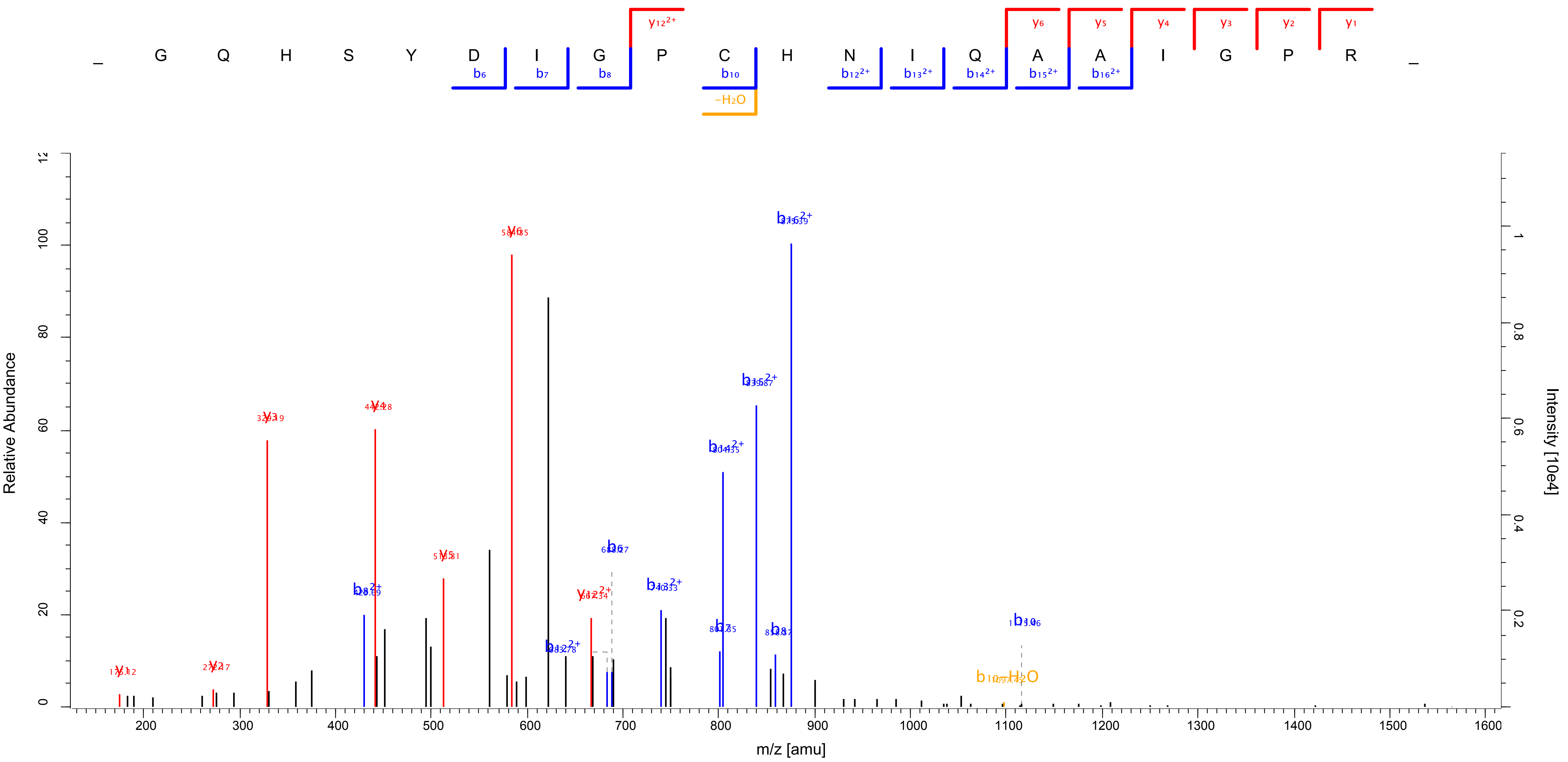
Mass:	1721.85257
m/z:	574.95813
Charge:	3+
Retentiontime:	89.9715957641602
Score:	117.7924
Mass Error [ppm]:	0.0077753
PEP:	1.2593E-05
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverage:	87 %
Intensity Coverage:	83 %
Peak Coverage:	27 %
Protein Localisation:	185 ... 199

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.07569038		100.07569038	1	V	14				
	157.09715411		157.09715411	2	G	13	1623.791417		812.39934675	+0.1734682
	343.17646706	−0.2112571	343.17646706	3	W	12	1566.7699533		783.88861489	+0.1757772
	400.19793078	−0.0209288	400.19793078	4	G	11	1380.6906404		690.84895841	+0.1099649
	471.23504457		471.23504457	5	A	10	1323.6691766		662.33822655	+0.114044
	570.30345849		570.30345849	6	V	9	1252.6320628	+0.1605397	626.81966966	+0.294283
	733.36678703		733.36678703	7	Y	8	1153.5636489	−0.0294692	1153.5636489	
	834.4144655		834.4144655	8	T	7	990.50032039	+0.1446381	990.50032039	
	947.49852948		947.49852948	9	I	6	889.45264192	−0.1620535	445.22995919	+0.2334807
−0.4071618	517.76891718		1034.5305579	10	S	5	776.36857794	+0.1436901	388.6879272	−0.0390625
	1163.573151		1163.573151	11	E	4	689.33654953	−0.0864275	689.33654953	
	1310.6415649		1310.6415649	12	F	3	560.29395643		560.29395643	
	1411.6892434		1411.6892434	13	T	2	413.22554252	+0.0957465	413.22554252	
+0.2684633	774.87771585		1548.7481552	14	H	1	312.17786404		312.17786404	
				15	R	0	175.11895218	+0.0062309	175.11895218	

Scan number	8176	Raw file	20091029_Orbi6_MaHe_SA_ADH_exp3_BSA_Gel04
Method	ITMS; CID	Genenames	ZDHHC24



precursor information

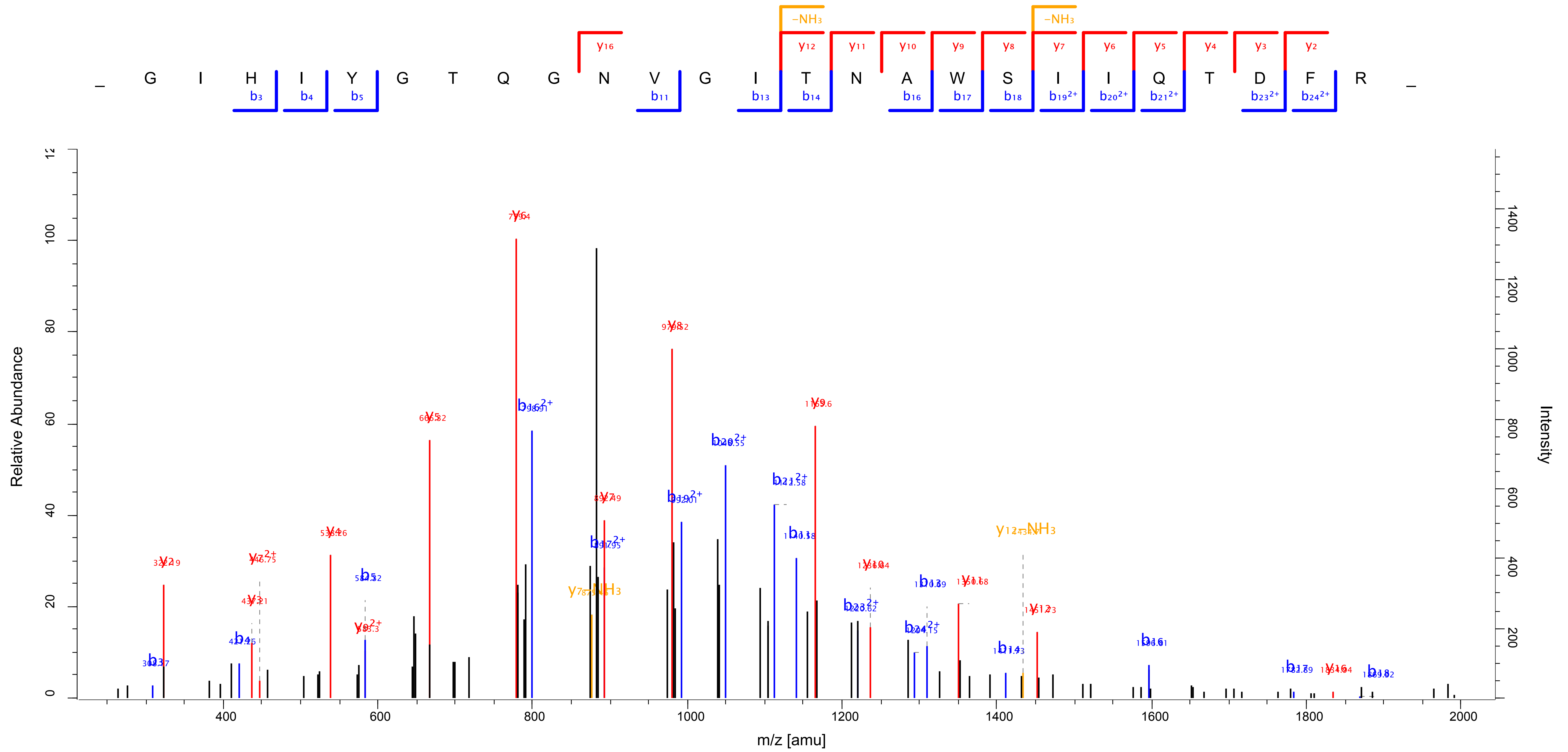
Mass:	2190.0384
m/z:	548.51688
Charge:	4+
Retentiontime:	54.1343421936035
Score:	81.31728
Mass Error [ppm]:	-0.21411
PEP:	0.00017026
Precursor Type:	MULTI

general information

Annotation:	14 of 20
AminoAcids Coverage:	70 %
Intensity Coverage:	63 %
Peak Coverage:	27 %
Protein Localisation:	233 ... 252

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019		58.02874019	1	G	19				
	186.0873177		186.0873177	2	Q	18	2134.0246812		2134.0246812	
	323.14622956		323.14622956	3	H	17	2005.9661037		2005.9661037	
	410.17825797		410.17825797	4	S	16	1868.9071919		1868.9071919	
	573.24158651		573.24158651	5	Y	15	1781.8751634		1781.8751634	
	688.26852954	-0.0145623	688.26852954	6	D	14	1618.8118349		1618.8118349	
	801.35259352	-0.0867244	801.35259352	7	I	13	1503.7848919		1503.7848919	
+0.1221383	429.69066686	+0.1162382	858.37405725	8	G	12	1390.7008279		1390.7008279	
	955.4268211		955.4268211	9	P	11	1333.6793642		667.34332032	+0.0395532
	1115.4574693	+0.0195815	1115.4574693	10	C	10	1236.6266003		1236.6266003	
	1252.5163812		1252.5163812	11	H	9	1076.5959521		1076.5959521	
+0.4456503	683.78329254		1366.5593086	12	N	8	939.53704025		939.53704025	
+0.161736	740.32532453		1479.6433726	13	I	7	825.4941128		825.4941128	
+0.1392222	804.35461328		1607.7019501	14	Q	6	712.41004882		712.41004882	
+0.1445911	839.87317018		1678.7390639	15	A	5	584.35147131	-0.2090763	584.35147131	
+0.1507534	875.39172707		1749.7761777	16	A	4	513.31435752	+0.0123637	513.31435752	
	1862.8602417		1862.8602417	17	I	3	442.27724374	-0.06417	442.27724374	
	1919.8817054		1919.8817054	18	G	2	329.19317976	-0.0340001	329.19317976	
	2016.9344692		2016.9344692	19	P	1	272.17171603	-0.2419065	272.17171603	
				20	R	0	175.11895218	+0.057119	175.11895218	

Scan number	19725	Raw file	20091029_Orbi6_MaHe_SA_ADH_exp3_BSA_Gel06
Method	ITMS; CID	Genenames	TSPAN4



precursor information

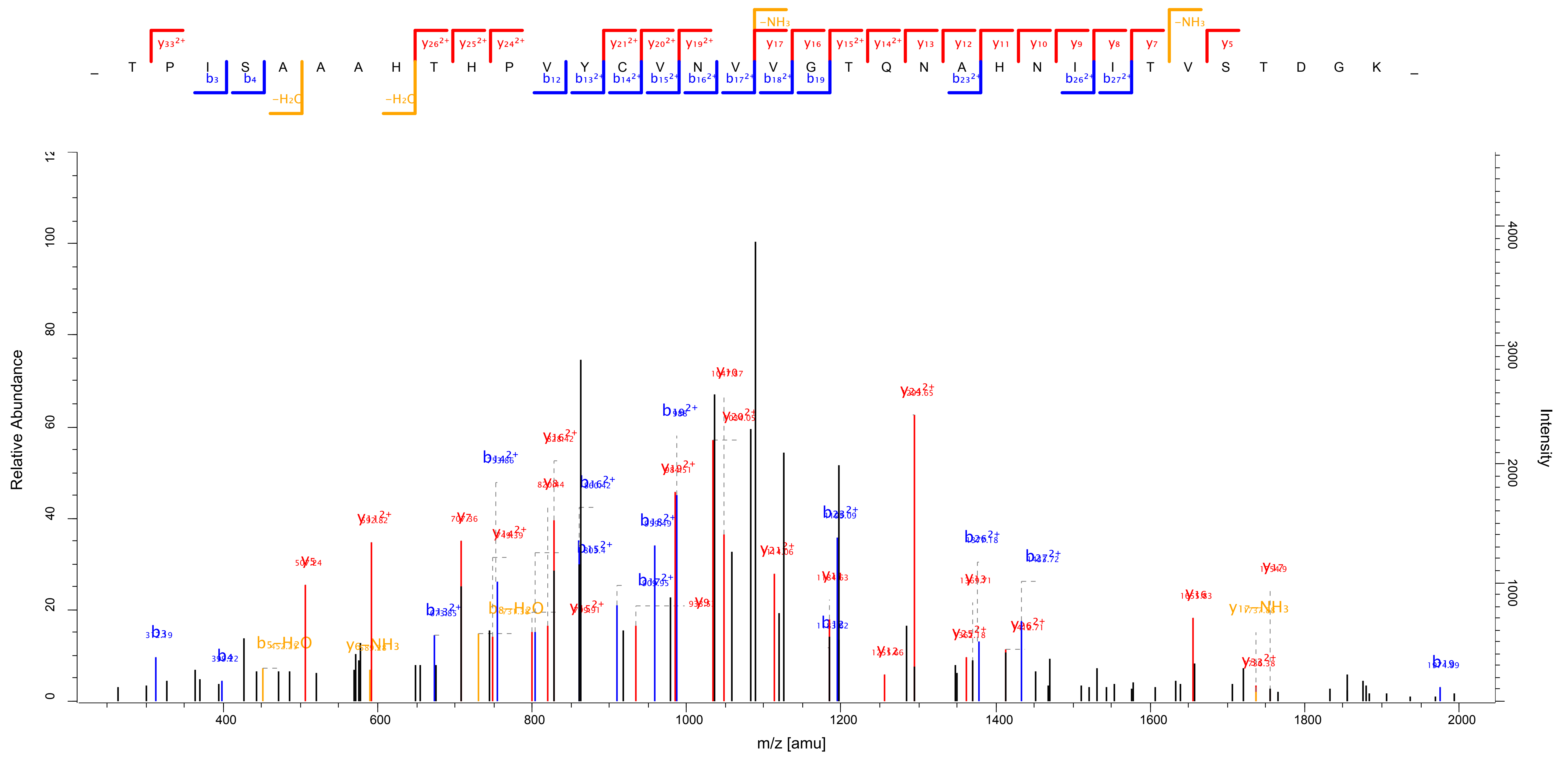
Mass:	2760.39707
m/z:	921.13963
Charge:	3+
Retentiontime:	113.739761352539
Score:	163.8484
Mass Error [ppm]:	−0.46859
PEP:	5.4548E−50
Precursor Type:	MULTI

general information

Annotation:	17 of 25
AminoAcids Coverage:	68 %
Intensity Coverage:	52 %
Peak Coverage:	32 %
Protein Localisation:	122 ... 146

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019		58.02874019	1	G	24				
	171.11280417		171.11280417	2	I	23	2704.384175		2704.384175	
	308.17171603	+0.0659549	308.17171603	3	H	22	2591.300111		2591.300111	
	421.25578001	−0.0629089	421.25578001	4	I	21	2454.2411992		2454.2411992	
	584.31910855	−0.1753708	584.31910855	5	Y	20	2341.1571352		2341.1571352	
	641.34057228		641.34057228	6	G	19	2178.0938066		2178.0938066	
	742.38825075		742.38825075	7	T	18	2121.0723429		2121.0723429	
	870.44682826		870.44682826	8	Q	17	2020.0246645		2020.0246645	
	927.46829198		927.46829198	9	G	16	1891.9660869		1891.9660869	
	1041.5112194		1041.5112194	10	N	15	1834.9446232	+0.4389217	1834.9446232	
	1140.5796333	+0.1034721	1140.5796333	11	V	14	1720.9016958		1720.9016958	
	1197.6010971		1197.6010971	12	G	13	1621.8332819		1621.8332819	
	1310.6851611	−0.0975146	1310.6851611	13	I	12	1564.8118181		1564.8118181	
	1411.7328395	+0.120554	1411.7328395	14	T	11	1451.7277541	−0.0750442	1451.7277541	
	1525.775767		1525.775767	15	N	10	1350.6800757	−0.0090552	1350.6800757	
+0.0929121	798.91007861	+0.3215187	1596.8128808	16	A	9	1236.6371482	−0.0978416	1236.6371482	
−0.0105871	891.94973509	+0.3823424	1782.8921937	17	W	8	1165.6000344	−0.1174905	583.30365545	+0.2112982
	1869.9242221	−0.4521762	1869.9242221	18	S	7	979.52072149	−0.1010438	979.52072149	
−0.087066	992.00778129		1983.0082861	19	I	6	892.48869308	+0.1170809	446.74798477	−0.460204
+0.1318273	1048.5498133		2096.0923501	20	I	5	779.4046291	−0.0382351	779.4046291	
−0.1092534	1112.579102		2224.1509276	21	Q	4	666.32056511	+0.0260535	666.32056511	
	2325.1986061		2325.1986061	22	T	3	538.2619876	+0.0591794	538.2619876	
−0.3250309	1220.6164128		2440.2255491	23	D	2	437.21430913	−0.0381006	437.21430913	
−0.1004488	1294.1506197		2587.293963	24	F	1	322.1873661	+0.0544552	322.1873661	
				25	R	0	175.11895218		175.11895218	

Scan number	12048	Raw file	20091029_Orbi6_MaHe_SA_ADH_exp3_BSA_Gel14
Method	ITMS; CID	Genenames	DYNC1I1



precursor information

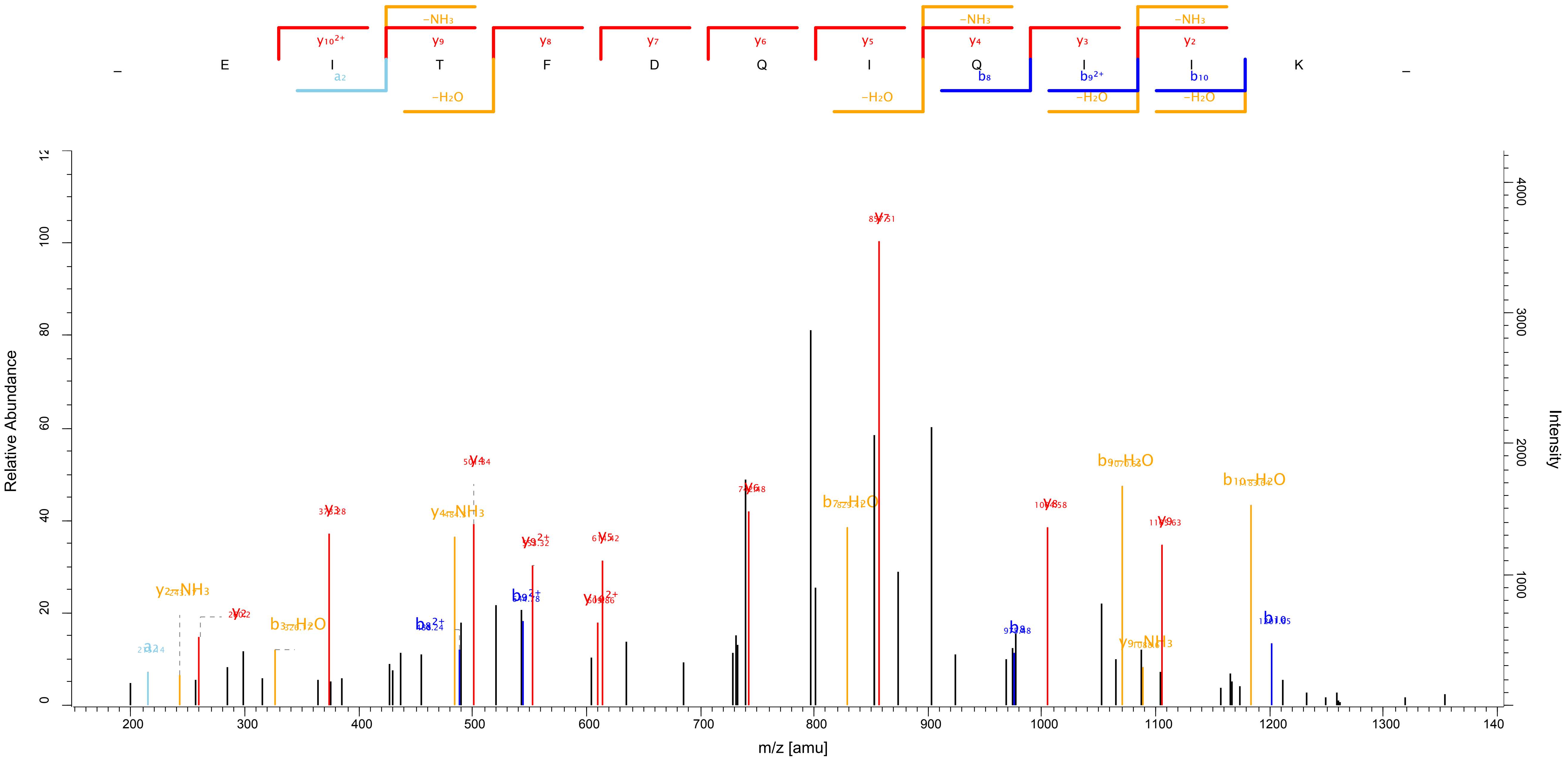
Mass:	3571.78337
m/z:	893.95312
Charge:	4+
Retentiontime:	71.8273696899414
Score:	140.0706
Mass Error [ppm]:	-0.22292
PEP:	9.3325E-58
Precursor Type:	MULTI

general information

Annotation:	27 of 34
AminoAcids Coverage:	79 %
Intensity Coverage:	47 %
Peak Coverage:	36 %
Protein Localisation:	381 ... 414

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05495494		102.05495494	1	T	33				
	199.10771879		199.10771879	2	P	32	3471.7437619		1736.3755192	+0.4255062
	312.19178277	-0.0243328	312.19178277	3	I	31	3374.6909981		3374.6909981	
	399.22381118	+0.0565843	399.22381118	4	S	30	3261.6069341		3261.6069341	
	470.26092497		470.26092497	5	A	29	3174.5749057		3174.5749057	
	541.29803876		541.29803876	6	A	28	3103.5377919		3103.5377919	
	612.33515255		612.33515255	7	A	27	3032.5006781		3032.5006781	
	749.39406441		749.39406441	8	H	26	2961.4635643		2961.4635643	
	850.44174288		850.44174288	9	T	25	2824.4046525		1412.7059645	-0.1636061
	987.50065475		987.50065475	10	H	24	2723.356974		1362.1821252	+0.4681433
	1084.5534186		1084.5534186	11	P	23	2586.2980621		1293.6526693	+0.3452555
	1183.6218325	+0.4352964	1183.6218325	12	V	22	2489.2452983		2489.2452983	
+0.1699556	673.84621876		1346.6851611	13	Y	21	2390.1768844		2390.1768844	
+0.2962941	753.86154286		1506.7158093	14	C	20	2227.1135558		1114.0604161	-0.0035314
-0.0949075	803.39574982		1605.7842232	15	V	19	2067.0829076		1034.045092	+0.2068611
-0.2232438	860.41721354		1719.8271506	16	N	18	1968.0144937		984.51088508	+0.2589513
-0.0186202	909.9514205		1818.8955645	17	V	17	1853.9715662		1853.9715662	
+0.1498706	959.48562746		1917.9639784	18	V	16	1754.9031523	-0.1378935	1754.9031523	
-0.0913911	987.99635932	-0.4007254	1974.9854422	19	G	15	1655.8347384	-0.2915255	828.42100744	-0.0887321
	2076.0331206		2076.0331206	20	T	14	1598.8132747		799.91027558	+0.0250272
	2204.0916982		2204.0916982	21	Q	13	1497.7655962		749.38643634	-0.2115706
	2318.1346256		2318.1346256	22	N	12	1369.7070187	-0.4869259	1369.7070187	
+0.2196962	1195.0895079		2389.1717394	23	A	11	1255.6640913	+0.2050494	1255.6640913	
	2526.2306513		2526.2306513	24	H	10	1184.6269775	+0.1298585	592.81712697	-0.2229497
	2640.2735787		2640.2735787	25	N	9	1047.5680656	-0.1195793	1047.5680656	
+0.3695424	1377.1824596		2753.3576427	26	I	8	933.52513816	-0.059562	933.52513816	
+0.1293903	1433.7244916		2866.4417067	27	I	7	820.44107418	+0.2990992	820.44107418	
	2967.4893851		2967.4893851	28	T	6	707.3570102	+0.0055997	707.3570102	
	3066.5577991		3066.5577991	29	V	5	606.30933173		606.30933173	
	3153.5898275		3153.5898275	30	S	4	507.24091781	+0.0819582	507.24091781	
	3254.6375059		3254.6375059	31	T	3	420.2088894		420.2088894	
	3369.664449		3369.664449	32	D	2	319.16121093		319.16121093	
	3426.6859127		3426.6859127	33	G	1	204.13426789		204.13426789	
				34	K	0	147.11280417		147.11280417	

Scan number	16401	Raw file	20091029_Orbi6_MaHe_SA_ADH_exp3_BSA_Gel14
Method	ITMS; CID	Genenames	GPCPD1



precursor information

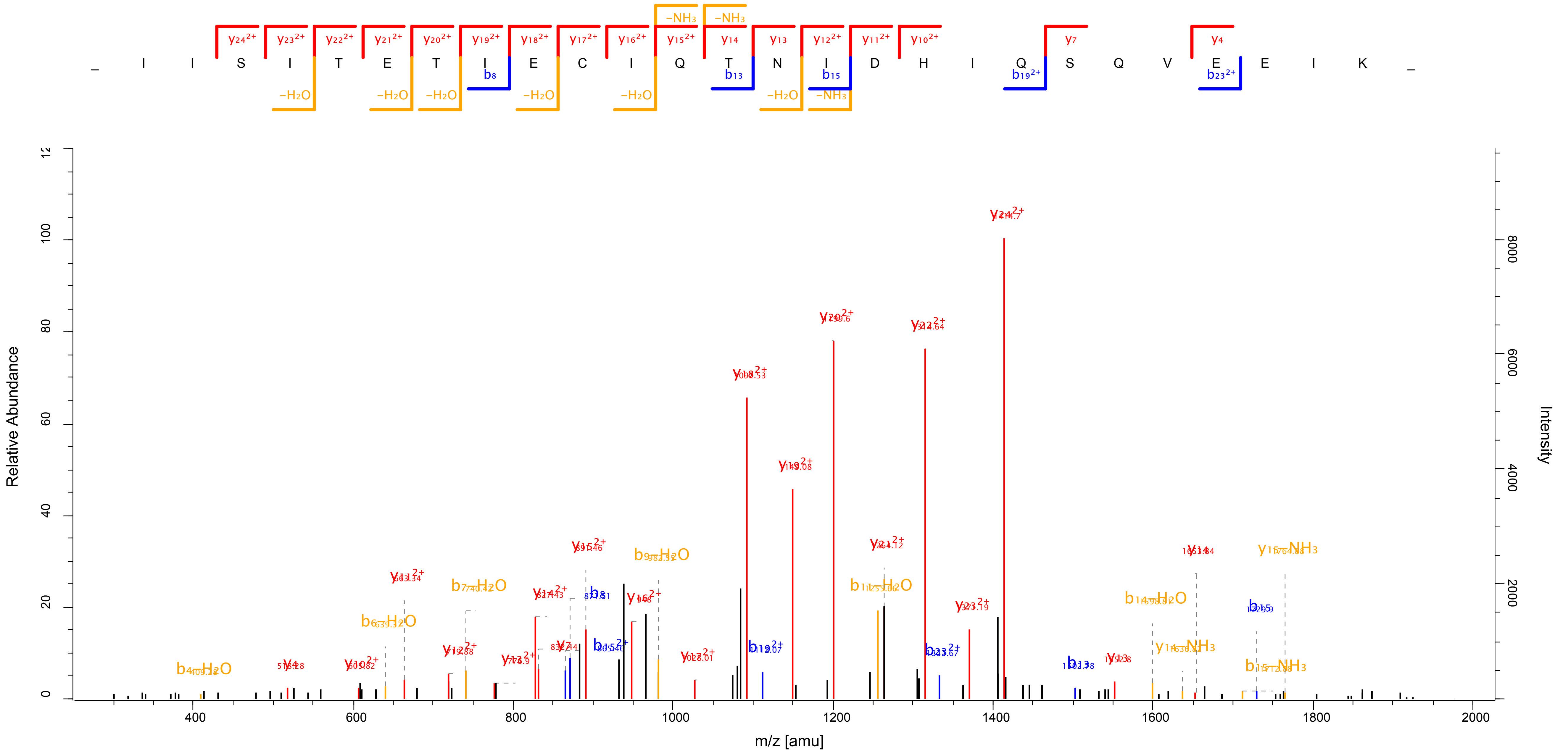
Mass:	1346.74349
m/z:	674.37902
Charge:	2+
Retentiontime:	94.5209579467773
Score:	141.9323
Mass Error [ppm]:	-0.79814
PEP:	0.00020576
Precursor Type:	ISO

general information

Annotation:	9 of 11
AminoAcids Coverage:	82 %
Intensity Coverage:	47 %
Peak Coverage:	31 %
Protein Localisation:	399 ... 409

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.054955		130.04987		130.04987	1	E	10				
-0.0031852	215.139019		243.133934		243.133934	2	I	9	1218.70925		609.858264	+0.0614753
	316.186697		344.181612		344.181612	3	T	8	1105.62519	-0.1268955	553.316232	-0.0509117
	463.255111		491.250026		491.250026	4	F	7	1004.57751	-0.171075	1004.57751	
	578.282054		606.276969		606.276969	5	D	6	857.509094	-0.1757812	857.509094	
	706.340632		734.335546		734.335546	6	Q	5	742.482151	-0.0485574	742.482151	
	819.424696		847.41961		847.41961	7	I	4	614.423574	-0.4882099	614.423574	
	947.483273	-0.3128616	488.242732	-0.1828388	975.478188	8	Q	3	501.33951	-0.0002152	501.33951	
	1060.56734	-0.4183091	544.784764		1088.56225	9	I	2	373.280932	+0.0598882	373.280932	
	1173.6514		1201.64632	-0.1807398	1201.64632	10	I	1	260.196868	-0.1438896	260.196868	
						11	K	0	147.112804		147.112804	

Scan number	21603	Raw file	20091029_Orbi6_MaHe_SA_ADH_exp3_BSA_Gel16
Method	ITMS; CID	Genenames	CDR2



precursor information

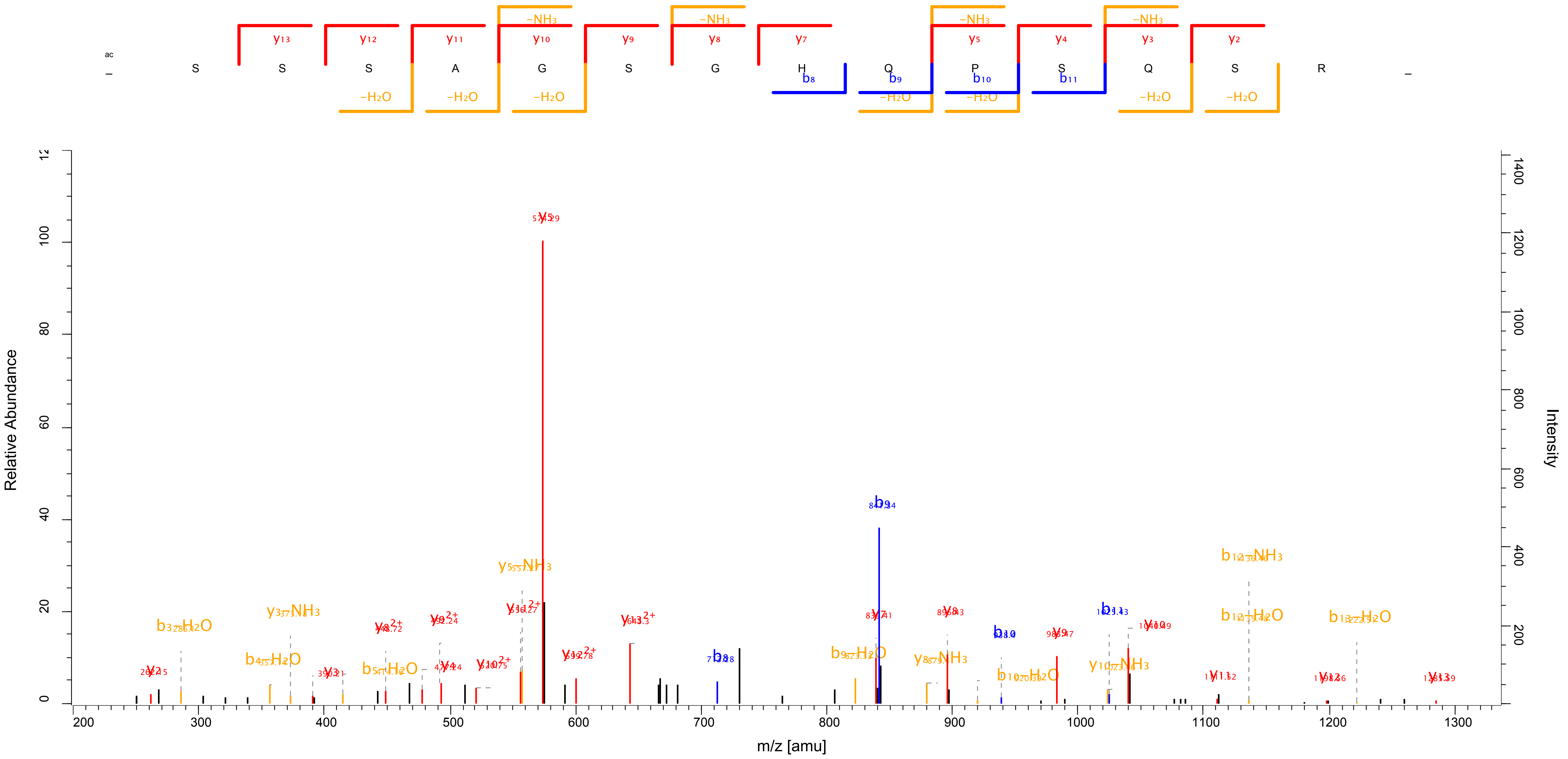
Mass:	3053.56107
m/z:	1018.86097
Charge:	3+
Retentiontime:	121.263198852539
Score:	129.4618
Mass Error [ppm]:	0.65244
PEP:	1.3916E-20
Precursor Type:	MULTI

general information

Annotation:	18 of 26
AminoAcids Coverage:	69 %
Intensity Coverage:	68 %
Peak Coverage:	35 %
Protein Localisation:	112 ... 137

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045		114.09134045	1	I	25				
	227.17540443		227.17540443	2	I	24	2941.4822937		2941.4822937	
	314.20743284		314.20743284	3	S	23	2828.3982297		1414.7027531	+0.1257381
	427.29149682		427.29149682	4	I	22	2741.3662013		1371.1867389	+0.2107221
	528.33917529		528.33917529	5	T	21	2628.2821373		1314.6447069	+0.1593703
	657.38176839		657.38176839	6	E	20	2527.2344588		1264.1208676	−0.1216001
	758.42944686		758.42944686	7	T	19	2398.1918657		1199.5995711	+0.2002336
	871.51351084	−0.369712	871.51351084	8	I	18	2297.1441872		1149.0757319	+0.1344732
	1000.5561039		1000.5561039	9	E	17	2184.0601233		1092.5336999	+0.1225501
	1160.5867521		1160.5867521	10	C	16	2055.0175302		1028.0124033	−0.1278818
	1273.6708161		1273.6708161	11	I	15	1894.986882		947.99707921	+0.1186434
	1401.7293936		1401.7293936	12	Q	14	1781.902818		891.45504722	+0.2565006
	1502.7770721	−0.2447235	1502.7770721	13	T	13	1653.8442405	−0.2620871	827.42575847	+0.1180648
	1616.8199996		1616.8199996	14	N	12	1552.796562	−0.1686323	776.90191923	−0.1477688
−0.0247618	865.45567	−0.0063585	1729.9040635	15	I	11	1438.7536345		719.88045551	−0.1858144
	1844.9310066		1844.9310066	16	D	10	1325.6695706		663.33842352	+0.0813763
	1981.9899184		1981.9899184	17	H	9	1210.6426275		605.824952	−0.0345467
	2095.0739824		2095.0739824	18	I	8	1073.5837157		1073.5837157	
+0.2679724	1112.0699182		2223.1325599	19	Q	7	960.49965169		960.49965169	
	2310.1645883		2310.1645883	20	S	6	832.44107418	+0.0330469	832.44107418	
	2438.2231658		2438.2231658	21	Q	5	745.40904577		745.40904577	
	2537.2915798		2537.2915798	22	V	4	617.35046826		617.35046826	
−0.4396456	1333.6707247		2666.3341729	23	E	3	518.28205434	+0.025807	518.28205434	
	2795.3767659		2795.3767659	24	E	2	389.23946125		389.23946125	
	2908.4608299		2908.4608299	25	I	1	260.19686815		260.19686815	
				26	K	0	147.11280417		147.11280417	

Scan number	1625	Raw file	20091031_Orbi6_MaHe_SA_ADH_exp3_Laminin_Re_Gel01
Method	ITMS; CID	Genenames	EIF4EBP2



precursor information

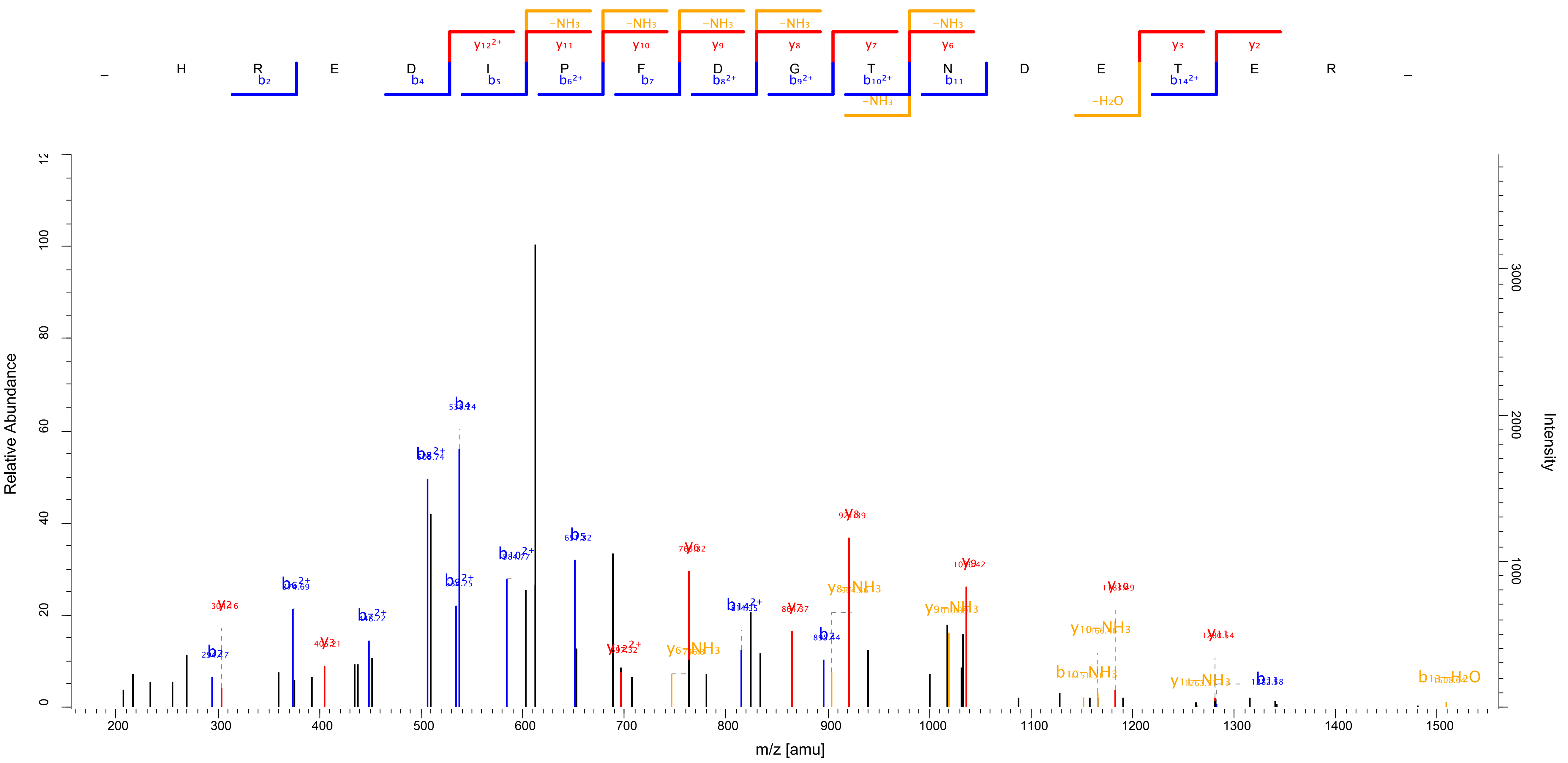
Mass:	1413.62311
m/z:	707.81883
Charge:	2+
Retentiontime:	24.6811904907227
Score:	188.9073
Mass Error [ppm]:	-0.12146
PEP:	1.3585E-12
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverage:	86 %
Intensity Coverage:	70 %
Peak Coverage:	49 %
Protein Localisation:	2 ... 15

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.049869563	1	S	13				
	217.081897973	2	S	12	1285.587966203	+0.1025856	643.297621335	+0.2474836
	304.113926383	3	S	11	1198.555937793	−0.1002493	599.78160713	+0.0360198
	375.15104017	4	A	10	1111.523909383	−0.1264484	556.265592925	−0.2081588
	432.172503894	5	G	9	1040.486795595	+0.0053919	520.747036031	−0.0844994
	519.204532304	6	S	8	983.465331872	+0.0070192	492.236304169	+0.3761836
	576.225996028	7	G	7	896.433303462	+0.0812839	448.720289964	−0.0279072
−0.0259357	713.28490789	8	H	6	839.411839738	+0.0101573	839.411839738	
−0.0157876	841.343485401	9	Q	5	702.352927876		702.352927876	
−0.0041594	938.396249253	10	P	4	574.294350364	+0.0004494	574.294350364	
+0.0123962	1025.428277663	11	S	3	477.241586512	+0.108206	477.241586512	
	1153.486855175	12	Q	2	390.209558102	+0.1650147	390.209558102	
	1240.518883584	13	S	1	262.150980591	−0.1322428	262.150980591	
		14	R	0	175.118952181		175.118952181	

Scan number	5075	Raw file	20091031_Orbi6_MaHe_SA_ADH_exp3_Laminin_Re_Gel06
Method	ITMS; CID	Genenames	RWDD2B



precursor information

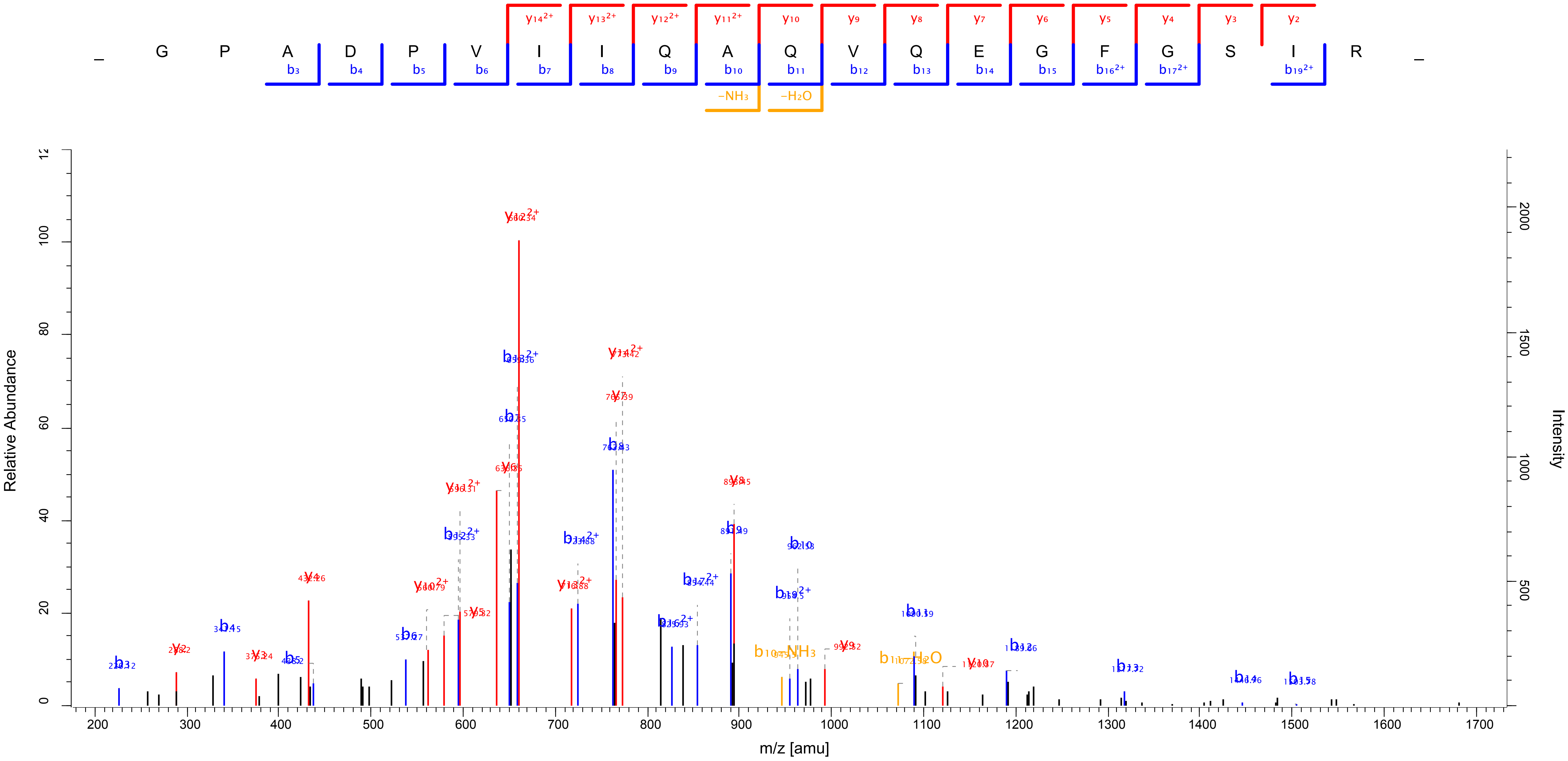
Mass:	1929.84404
m/z:	644.28862
Charge:	3+
Retentiontime:	39.5289649963379
Score:	148.4758
Mass Error [ppm]:	−0.65278
PEP:	1.5433E−08
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverage:	81 %
Intensity Coverage:	48 %
Peak Coverage:	41 %
Protein Localisation:	255 ... 270

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.06618833		138.06618833	1	H	15				
	294.16729936	+0.0429668	294.16729936	2	R	14	1793.7936615		1793.7936615	
	423.20989245		423.20989245	3	E	13	1637.6925504		1637.6925504	
	538.23683549	+0.0038872	538.23683549	4	D	12	1508.6499573		1508.6499573	
	651.32089947	−0.0636363	651.32089947	5	I	11	1393.6230143		697.31514539	−0.0201625
−0.0607091	374.69046989		748.37366332	6	P	10	1280.5389503	−0.1591896	1280.5389503	
+0.0625546	448.22467685	−0.10144	895.44207723	7	F	9	1183.4861865	+0.0803418	1183.4861865	
−0.0363661	505.73814837		1010.4690203	8	D	8	1036.4177726	−0.0645011	1036.4177726	
−0.1435946	534.24888023		1067.490484	9	G	7	921.39082952	−0.0775361	921.39082952	
+0.2701882	584.77271947		1168.5381625	10	T	6	864.3693658	+0.0653876	864.3693658	
	1282.5810899	+0.1274062	1282.5810899	11	N	5	763.32168733	+0.043486	763.32168733	
	1397.6080329		1397.6080329	12	D	4	649.27875988		649.27875988	
	1526.650626		1526.650626	13	E	3	534.25181685		534.25181685	
+0.219292	814.35279049		1627.6983045	14	T	2	405.20922375	+0.0268602	405.20922375	
	1756.7408976		1756.7408976	15	E	1	304.16154528	−0.1259618	304.16154528	
				16	R	0	175.11895218		175.11895218	

Scan number	15613	Raw file	20091031_Orbi6_MaHe_SA_ADH_exp3_Laminin_Re_Gel07
Method	ITMS; CID	Genenames	SAC3D1



precursor information

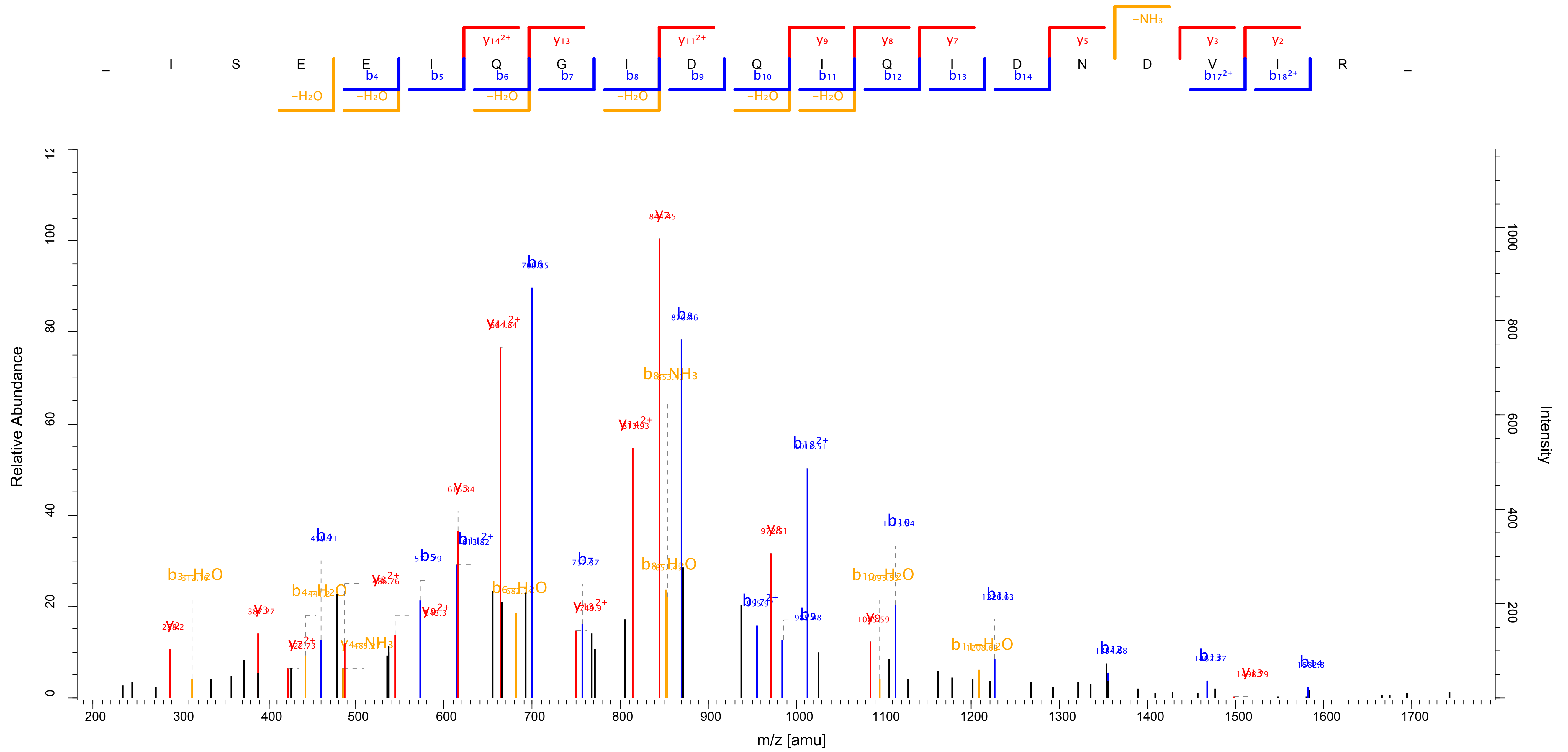
Mass:	2081.09035
m/z:	694.70406
Charge:	3+
Retentiontime:	97.7394104003906
Score:	184.2231
Mass Error [ppm]:	−0.096832
PEP:	3.9725E−21
Precursor Type:	ISO

general information

Annotation:	17 of 20
AminoAcids Coverage:	85 %
Intensity Coverage:	71 %
Peak Coverage:	44 %
Protein Localisation:	193 ... 212

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019		58.02874019	1	G	19				
	155.08150404		155.08150404	2	P	18	2025.0763657		2025.0763657	
	226.11861783	+0.1092569	226.11861783	3	A	17	1928.0236018		1928.0236018	
	341.14556086	+0.008736	341.14556086	4	D	16	1856.986488		1856.986488	
	438.19832471	−0.0057588	438.19832471	5	P	15	1741.959545		1741.959545	
	537.26673863	+0.0132907	537.26673863	6	V	14	1644.9067811		1644.9067811	
	650.35080261	+0.1890533	650.35080261	7	I	13	1545.8383672		773.42282185	+0.0920097
	763.43486659	−0.0338046	763.43486659	8	I	12	1432.7543032		716.88078986	+0.2472009
	891.4934441	−0.218969	891.4934441	9	Q	11	1319.6702393		660.33875787	+0.0767084
	962.53055789	+0.0631311	962.53055789	10	A	10	1191.6116618		596.30946911	−0.1487025
	1090.5891354	−0.4487545	1090.5891354	11	Q	9	1120.574548	−0.2763302	560.79091222	+0.3523983
−0.0855257	595.33241289	−0.0625786	1189.6575493	12	V	8	992.51597046	−0.1219885	992.51597046	
+0.0204395	659.36170165	+0.453795	1317.7161268	13	Q	7	893.44755654	−0.0684672	893.44755654	
−0.111819	723.8829982	−0.1836467	1446.7587199	14	E	6	765.38897903	+0.0562724	765.38897903	
	1503.7801836	+0.439665	1503.7801836	15	G	5	636.34638593	−0.0050773	636.34638593	
+0.2253833	825.92793702		1650.8485976	16	F	4	579.32492221	−0.0511795	579.32492221	
+0.0300201	854.43866888		1707.8700613	17	G	3	432.25650829	+0.0909038	432.25650829	
	1794.9020897		1794.9020897	18	S	2	375.23504457	+0.1824359	375.23504457	
−0.2648425	954.49671507		1907.9861537	19	I	1	288.20301616	−0.0158213	288.20301616	
				20	R	0	175.11895218		175.11895218	

Scan number	16061	Raw file	20091031_Orbi6_MaHe_SA_ADH_exp3_Laminin_Re_Gel07
Method	ITMS; CID	Genenames	USF1;usf1-bd



precursor information

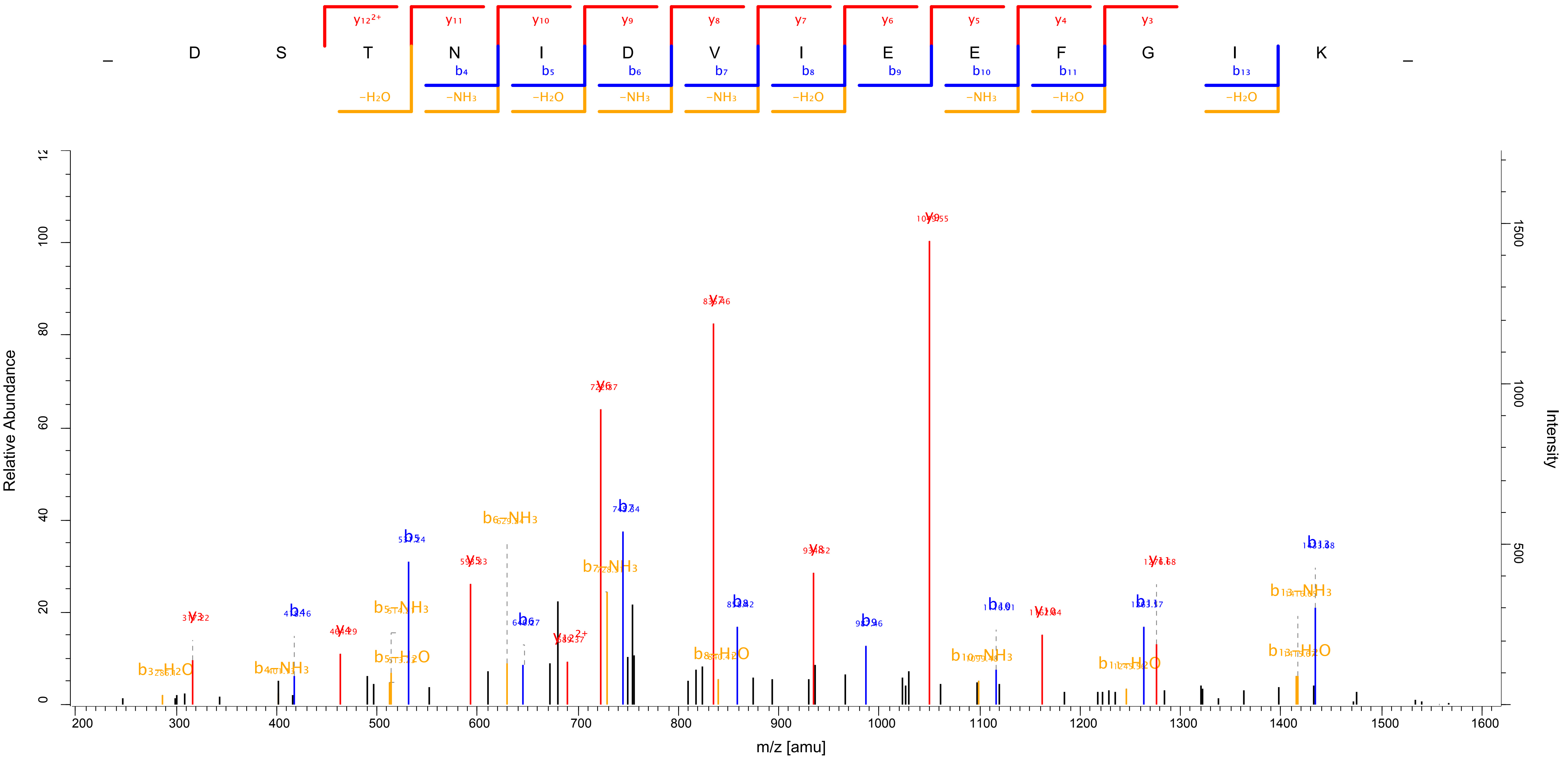
Mass:	2197.1228
m/z:	733.38154
Charge:	3+
Retentiontime:	100.48021697998
Score:	182.1539
Mass Error [ppm]:	0.074231
PEP:	1.3542E-29
Precursor Type:	MULTI

general information

Annotation:	16 of 19
AminoAcids Coverage:	84 %
Intensity Coverage:	70 %
Peak Coverage:	42 %
Protein Localisation:	261 ... 279

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045		114.09134045	1	I	18				
	201.12336886		201.12336886	2	S	17	2085.0458534		2085.0458534	
	330.16596195		330.16596195	3	E	16	1998.013825		1998.013825	
	459.20855505	+0.0584738	459.20855505	4	E	15	1868.9712319		1868.9712319	
	572.29261903	+0.0167071	572.29261903	5	I	14	1739.9286388		1739.9286388	
	700.35119654	-0.0601199	700.35119654	6	Q	13	1626.8445748		813.92592564	-0.1686625
	757.37266026	-0.1581217	757.37266026	7	G	12	1498.7859973	-0.212511	749.89663689	+0.4918519
	870.45672425	-0.1363507	870.45672425	8	I	11	1441.7645336		1441.7645336	
	985.48366728	-0.17074	985.48366728	9	D	10	1328.6804696		664.84387304	-0.1170054
	1113.5422448	-0.2863854	1113.5422448	10	Q	9	1213.6535266		1213.6535266	
-0.0428668	613.81679262	-0.2495998	1226.6263088	11	I	8	1085.5949491	-0.1200955	543.30111276	+0.1756328
	1354.6848863	-0.0019029	1354.6848863	12	Q	7	972.51088508	+0.0571691	486.75908077	-0.1045398
	1467.7689503	-0.1100147	1467.7689503	13	I	6	844.45230757	-0.0273808	422.72979202	-0.1079658
	1582.7958933	-0.0689646	1582.7958933	14	D	5	731.36824359		731.36824359	
	1696.8388207		1696.8388207	15	N	4	616.34130056	-0.0793377	616.34130056	
	1811.8657638		1811.8657638	16	D	3	502.29837311		502.29837311	
-0.1518184	955.97072708		1910.9341777	17	V	2	387.27143008	+0.1334161	387.27143008	
+0.0349094	1012.5127591		2024.0182417	18	I	1	288.20301616	+0.1185781	288.20301616	
				19	R	0	175.11895218		175.11895218	

Scan number	17974	Raw file	20091031_Orbi6_MaHe_SA_ADH_exp3_Laminin_Re_Gel07
Method	ITMS; CID	Genenames	DUSP6



precursor information

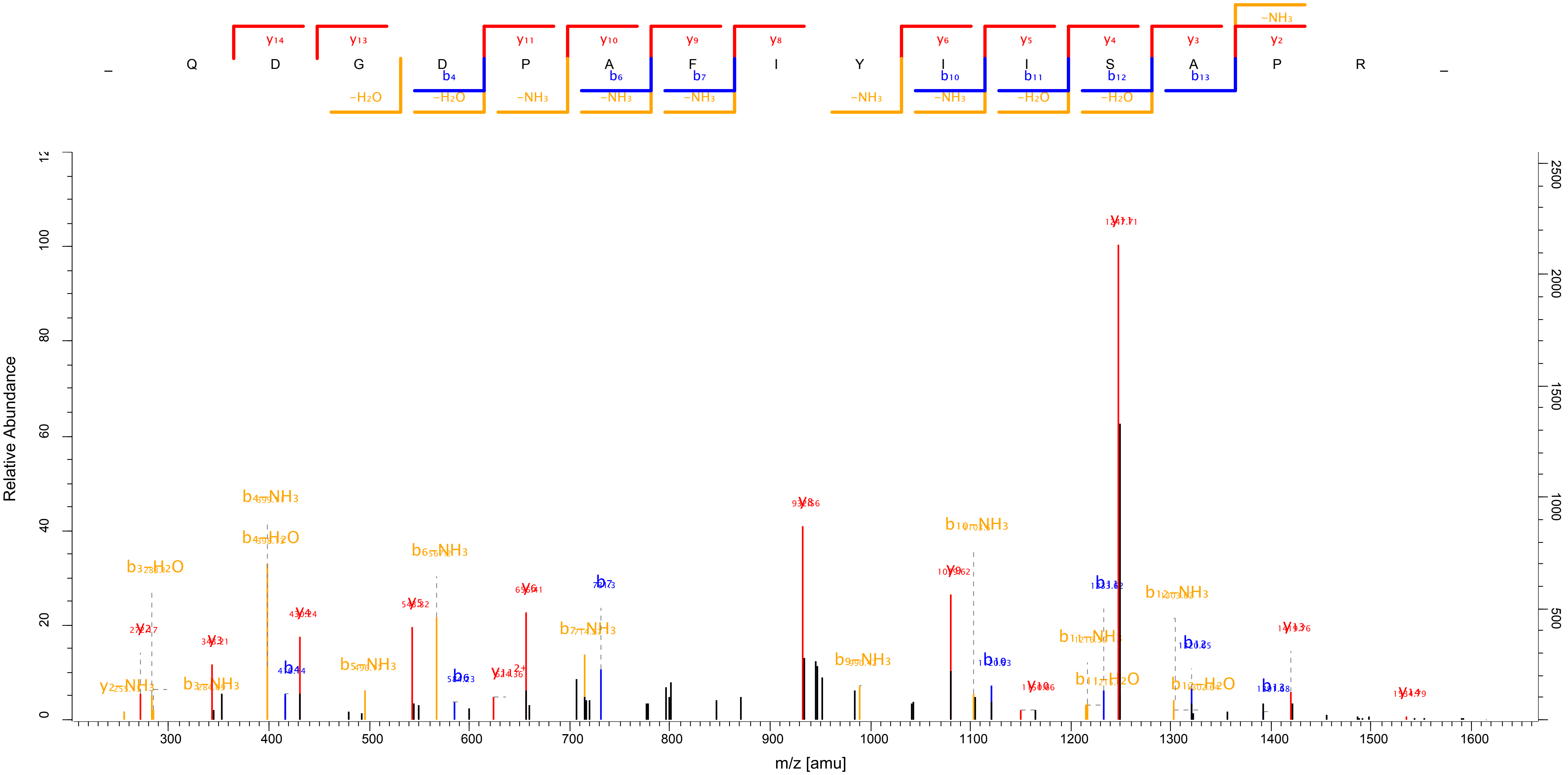
Mass:	1578.7785
m/z:	790.39653
Charge:	2+
Retentiontime:	112.47386932373
Score:	200.1268
Mass Error [ppm]:	0.49554
PEP:	1.25795E-16
Precursor Type:	ISO

general information

Annotation:	11 of 14
AminoAcids Coverage:	79 %
Intensity Coverage:	71 %
Peak Coverage:	38 %
Protein Localisation:	221 ... 234

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.034219499	1	D	13				
	203.066247908	2	S	12	1464.758051223		1464.758051223	
	304.113926383	3	T	11	1377.726022814		689.36664964	+0.0757332
−0.3395931	418.15685383	4	N	10	1276.678344339	+0.0187992	1276.678344339	
−0.0597044	531.24091781	5	I	9	1162.635416892	−0.2301435	1162.635416892	
−0.1545186	646.267860842	6	D	8	1049.551352912	−0.2327494	1049.551352912	
−0.0959183	745.336274758	7	V	7	934.52440988	−0.2047688	934.52440988	
+0.0192365	858.420338739	8	I	6	835.455995964	−0.0288109	835.455995964	
−0.2415573	987.462931835	9	E	5	722.371931983	−0.0342855	722.371931983	
−0.2984937	1116.505524931	10	E	4	593.329338887	+0.0005561	593.329338887	
−0.1640267	1263.573938847	11	F	3	464.286745791	−0.1444728	464.286745791	
	1320.595402571	12	G	2	317.218331875	−0.1306244	317.218331875	
−0.192406	1433.679466551	13	I	1	260.196868151		260.196868151	
		14	K	0	147.112804171		147.112804171	

Scan number	17308	Raw file	20091031_Orbi6_MaHe_SA_ADH_exp3_Laminin_Re_Gel08
Method	ITMS; CID	Genenames	SHARPIN



precursor information

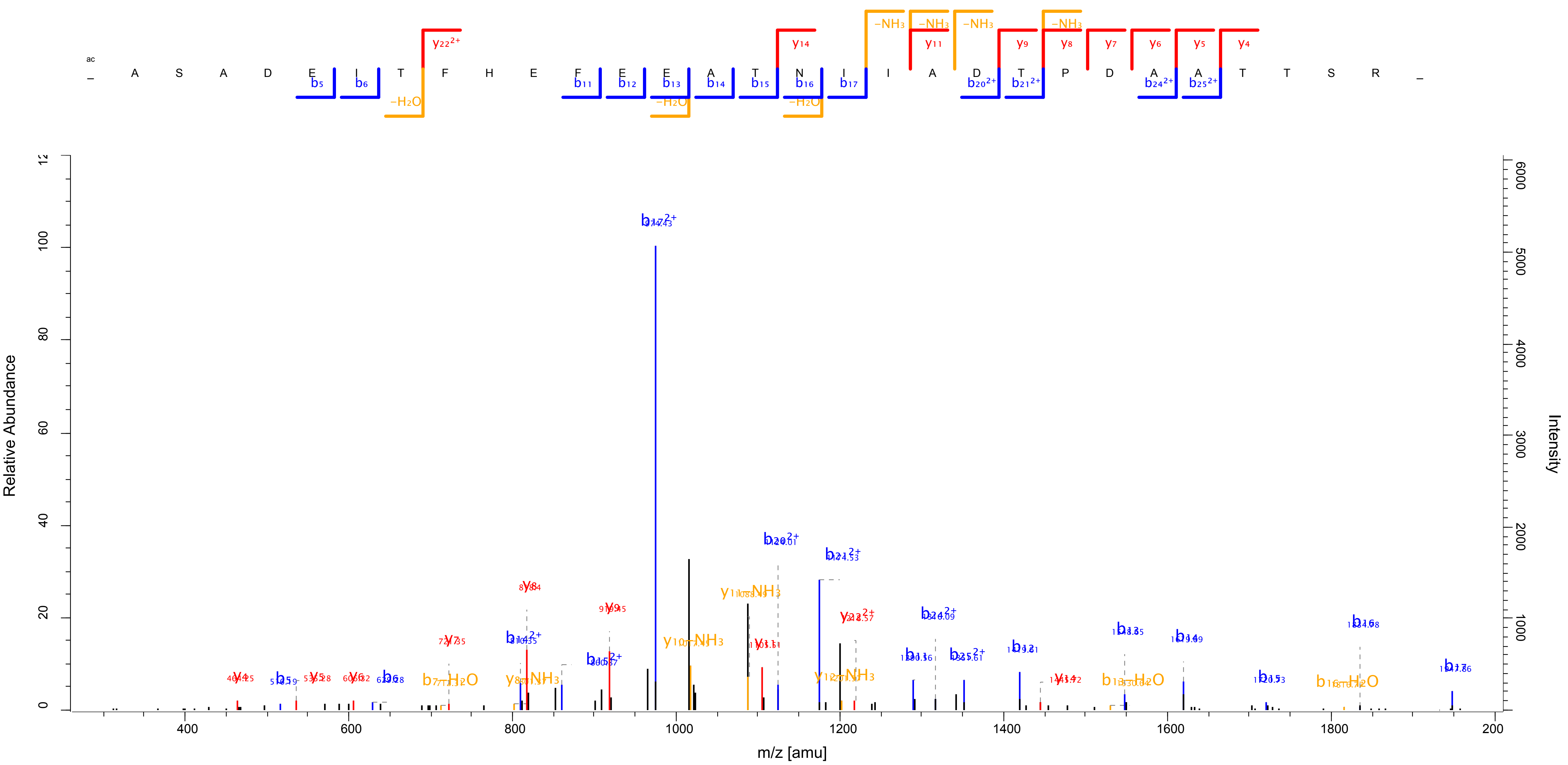
Mass:	1661.84083
m/z:	831.92769
Charge:	2+
Retentiontime:	108.626510620117
Score:	176.8723
Mass Error [ppm]:	-0.29842
PEP:	1.2011E-11
Precursor Type:	ISO

general information

Annotation:	13 of 15
AminoAcids Coverage:	87 %
Intensity Coverage:	61 %
Peak Coverage:	40 %
Protein Localisation:	290 ... 304

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.065853978	1	Q	14				
	244.09279701	2	D	13	1534.790020054	+0.2011909	1534.790020054	
	301.114260734	3	G	12	1419.763077022	-0.1399081	1419.763077022	
+0.1143504	416.141203766	4	D	11	1362.741613298		1362.741613298	
	513.193967618	5	P	10	1247.714670266	-0.1590062	624.360973366	+0.2072639
+0.106504	584.231081405	6	A	9	1150.661906414	+0.1059159	1150.661906414	
+0.0010418	731.299495322	7	F	8	1079.624792626	+0.013513	1079.624792626	
	844.383559302	8	I	7	932.55637871	-0.1127752	932.55637871	
	1007.44688784	9	Y	6	819.47231473		819.47231473	
-0.0703805	1120.530951821	10	I	5	656.408986192	-0.0429584	656.408986192	
-0.1999767	1233.615015801	11	I	4	543.324922211	+0.0541061	543.324922211	
-0.245555	1320.647044211	12	S	3	430.240858231	-0.0367567	430.240858231	
-0.2254178	1391.684157999	13	A	2	343.208829821	+0.0644856	343.208829821	
	1488.736921851	14	P	1	272.171716033	-0.0789426	272.171716033	
		15	R	0	175.118952181		175.118952181	

Scan number	19172	Raw file	20091031_Orbi6_MaHe_SA_ADH_exp3_Laminin_Re_Gel08
Method	ITMS; CID	Genenames	YIPF2



precursor information

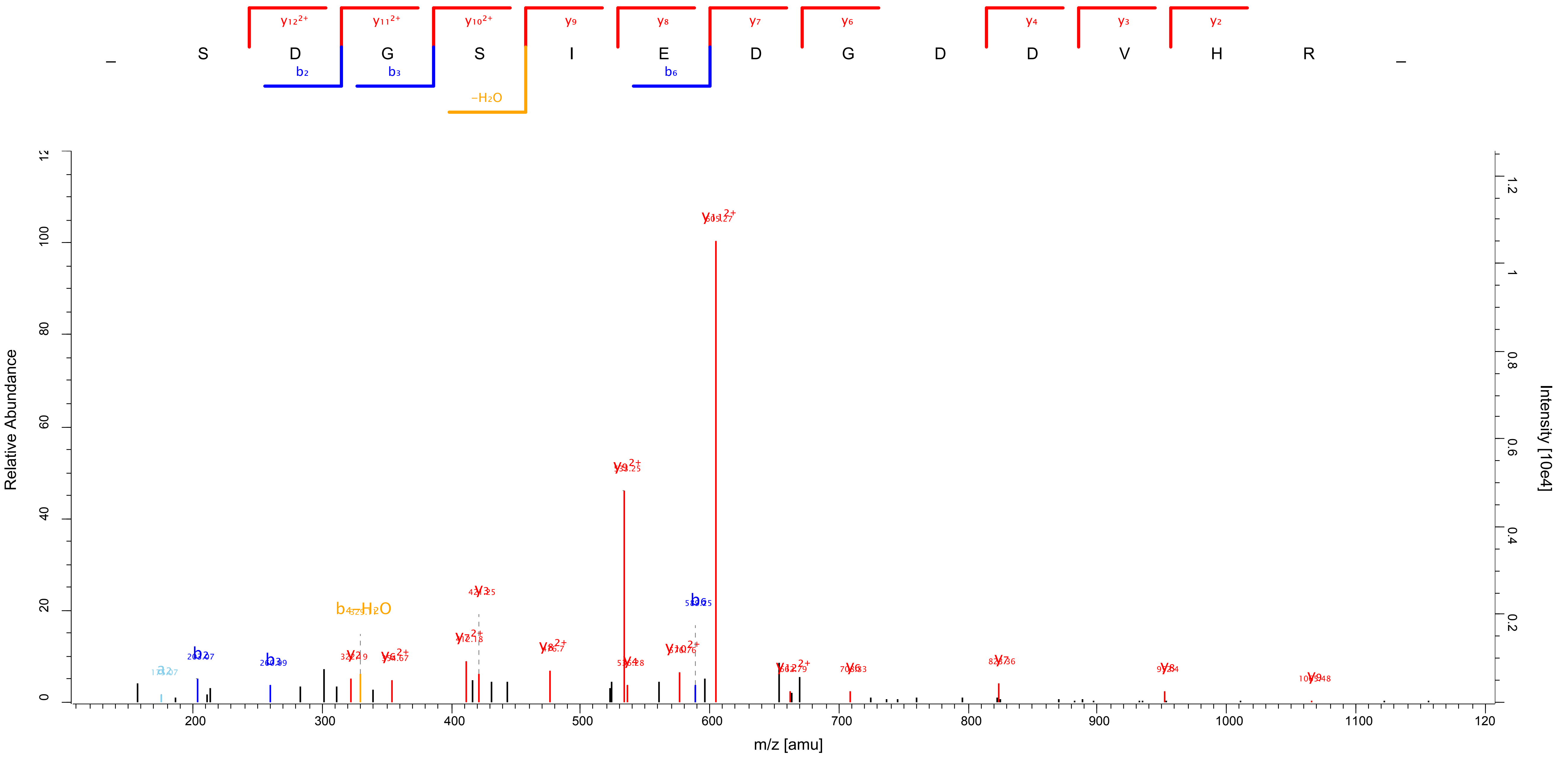
Mass:	3164.44265
m/z:	1055.82149
Charge:	3+
Retentiontime:	119.956748962402
Score:	134.8145
Mass Error [ppm]:	0.14267
PEP:	1.6049E-37
Precursor Type:	MULTI

general information

Annotation:	20 of 29
AminoAcids Coverage:	69 %
Intensity Coverage:	59 %
Peak Coverage:	32 %
Protein Localisation:	2 ... 30

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.05495494		114.05495494	1	A	28				
	201.08698335		201.08698335	2	S	27	3052.4017947		3052.4017947	
	272.12409714		272.12409714	3	A	26	2965.3697663		2965.3697663	
	387.15104017		387.15104017	4	D	25	2894.3326525		2894.3326525	
	516.19363327	−0.0987236	516.19363327	5	E	24	2779.3057095		2779.3057095	
	629.27769725	−0.0920893	629.27769725	6	I	23	2650.2631164		2650.2631164	
	730.32537572		730.32537572	7	T	22	2537.1790524		2537.1790524	
	877.39378964		877.39378964	8	F	21	2436.1313739		1218.5693252	−0.1754043
	1014.4527015		1014.4527015	9	H	20	2289.06296		2289.06296	
	1143.4952946		1143.4952946	10	E	19	2152.0040482		2152.0040482	
	1290.5637085	−0.2090943	1290.5637085	11	F	18	2022.9614551		2022.9614551	
	1419.6063016	−0.3237088	1419.6063016	12	E	17	1875.8930412		1875.8930412	
	1548.6488947	+0.0215155	1548.6488947	13	E	16	1746.8504481		1746.8504481	
−0.0530634	810.34664248	−0.093113	1619.6860085	14	A	15	1617.807855		1617.807855	
−0.1234114	860.87048172	−0.0698686	1720.733687	15	T	14	1546.7707412		1546.7707412	
	1834.7766144	−0.1102326	1834.7766144	16	N	13	1445.7230627	−0.1720373	1445.7230627	
+0.1124093	974.43397743	+0.0195706	1947.8606784	17	I	12	1331.6801353		1331.6801353	
	2060.9447424		2060.9447424	18	I	11	1218.5960713		1218.5960713	
	2131.9818562		2131.9818562	19	A	10	1105.5120073	−0.0835405	1105.5120073	
+0.3608587	1124.0080378		2247.0087992	20	D	9	1034.4748935		1034.4748935	
+0.1047196	1174.5318771		2348.0564777	21	T	8	919.44795047	−0.0935804	919.44795047	
	2445.1092415		2445.1092415	22	P	7	818.400272	−0.0450474	818.400272	
	2560.1361846		2560.1361846	23	D	6	721.34750815	+0.0941422	721.34750815	
−0.2334759	1316.0902874		2631.1732983	24	A	5	606.32056511	−0.000985	606.32056511	
−0.021564	1351.6088443		2702.2104121	25	A	4	535.28345133	−0.0272257	535.28345133	
	2803.2580906		2803.2580906	26	T	3	464.24633754	−0.310577	464.24633754	
	2904.3057691		2904.3057691	27	T	2	363.19865906		363.19865906	
	2991.3377975		2991.3377975	28	S	1	262.15098059		262.15098059	
				29	R	0	175.11895218		175.11895218	

Scan number	2494	Raw file	20091031_Orbi6_MaHe_SA_ADH_exp3_Laminin_Re_Gel08
Method	ITMS; CID	Genenames	SERINC1



precursor information

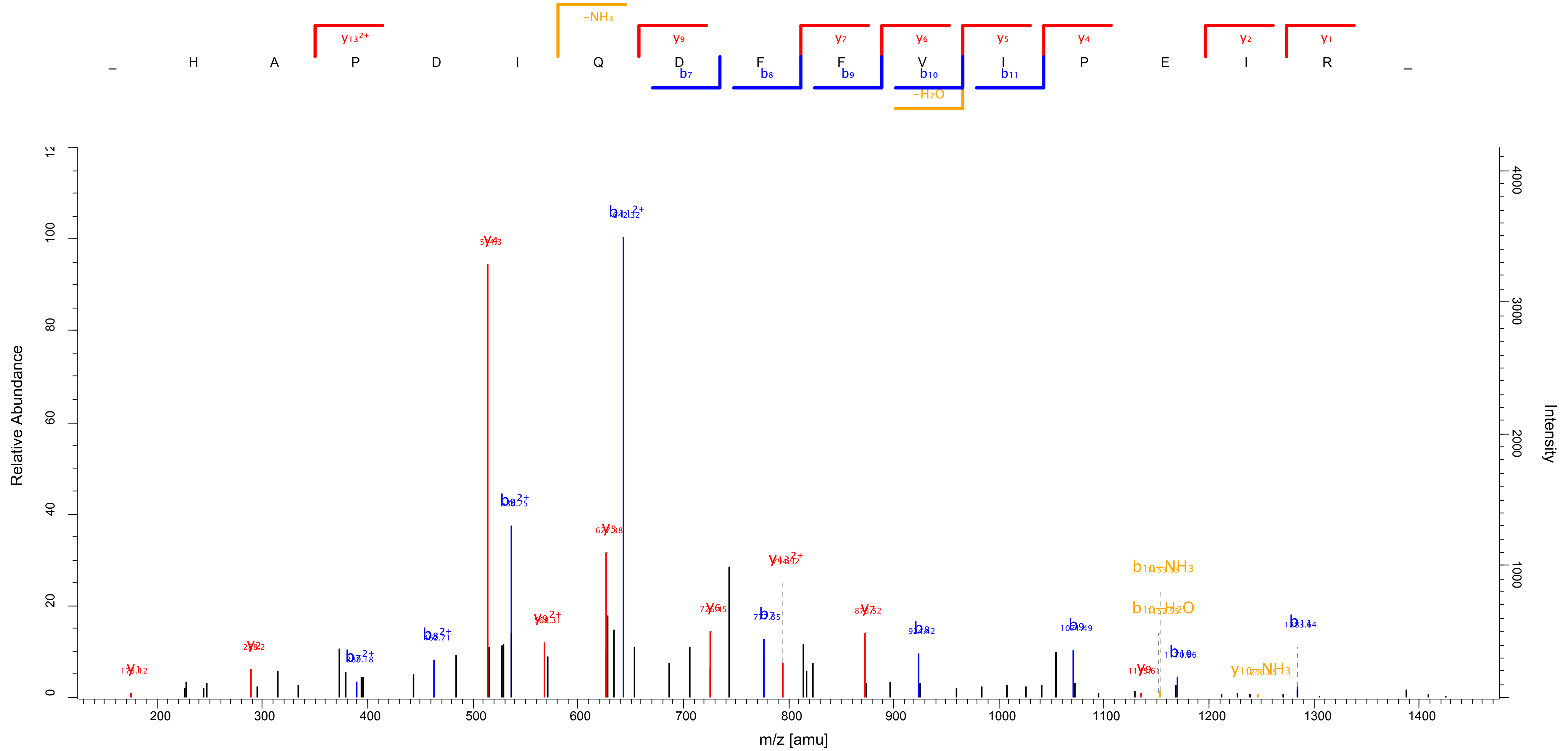
Mass:	1400.58007
m/z:	467.8673
Charge:	3+
Retentiontime:	26.6939506530762
Score:	112.1254
Mass Error [ppm]:	−0.24388
PEP:	8.77945E−05
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverage:	77 %
Intensity Coverage:	72 %
Peak Coverage:	35 %
Protein Localisation:	361 ... 373

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	60.044390254		88.039304876	1	S	12				
+0.1805588	175.07133329	+0.0542965	203.06624791	2	D	11	1324.5639316		662.78560404	−0.1129966
	232.09279701	−0.0248454	260.08771163	3	G	10	1209.5369886		605.27213253	+0.0619129
	319.12482542		347.11974004	4	S	9	1152.5155249		576.76140067	+0.099134
	432.2088894		460.20380402	5	I	8	1065.4834965	+0.0904782	533.24538646	+0.0771843
	561.2514825	+0.1223163	589.24639712	6	E	7	952.39943247	−0.0811341	476.70335447	+0.0251917
	676.27842553		704.27334015	7	D	6	823.35683938	+0.095126	412.18205792	−0.1364341
	733.29988925		761.29480387	8	G	5	708.32989635	−0.0083021	354.66858641	−0.357063
	848.32683228		876.32174691	9	D	4	651.30843262		651.30843262	
	963.35377532		991.34868994	10	D	3	536.28148959	+0.0498703	536.28148959	
	1062.4221892		1090.4171039	11	V	2	421.25454656	+0.122254	421.25454656	
	1199.4811011		1227.4760157	12	H	1	322.18613264	+0.021509	322.18613264	
				13	R	0	185.12722078		185.12722078	

Scan number	19813	Raw file	20091031_Orbi6_MaHe_SA_ADH_exp3_Laminin_Re_Gel09
Method	ITMS; CID	Genenames	SNX21



precursor information

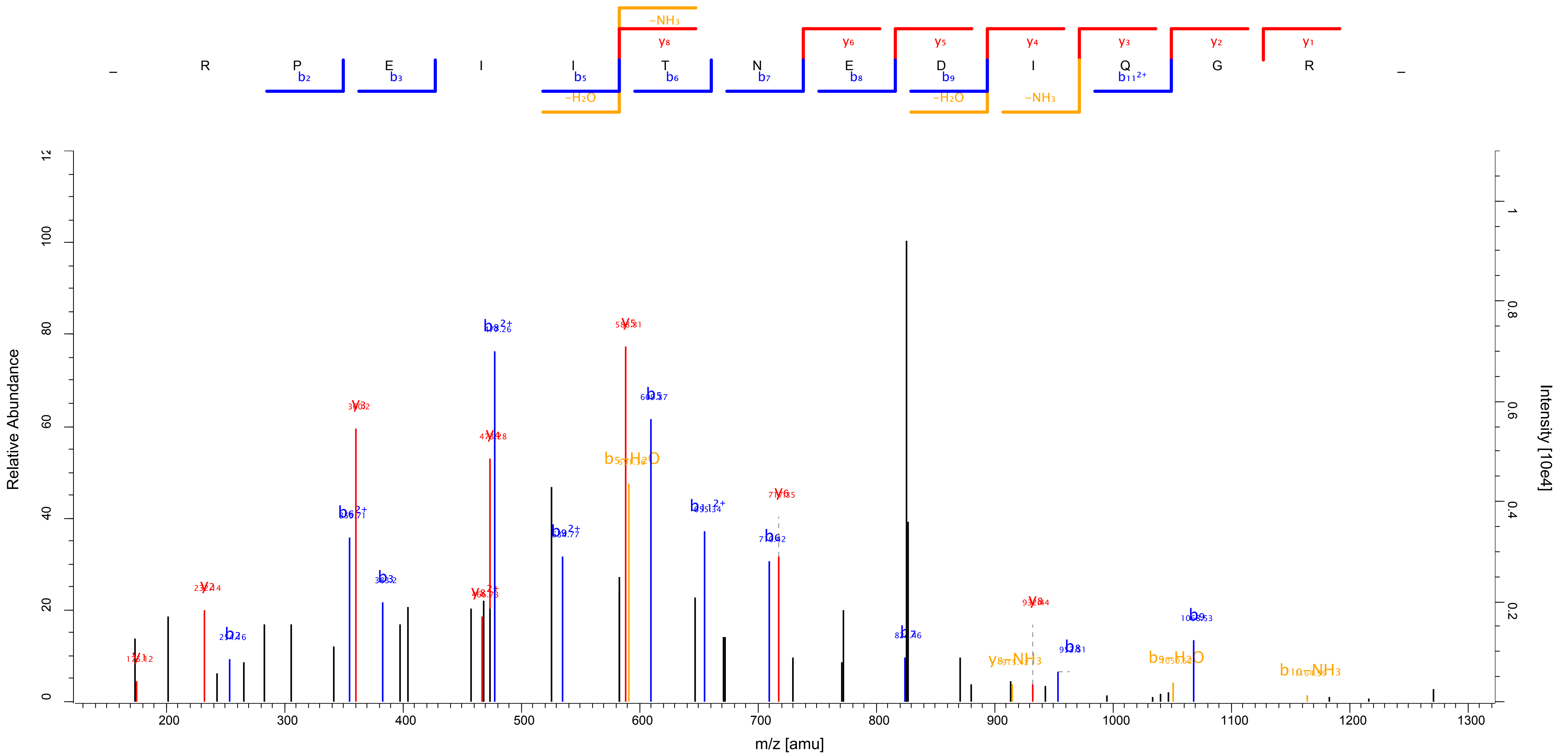
Mass:	1795.92596
m/z:	599.64926
Charge:	3+
Retentiontime:	113.709281921387
Score:	106.1299
Mass Error [ppm]:	0.13672
PEP:	0.00011032
Precursor Type:	MULTI

general information

Annotation:	10 of 15
AminoAcids Coverage:	67 %
Intensity Coverage:	56 %
Peak Coverage:	29 %
Protein Localisation:	231 ... 245

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.06618833		138.06618833	1	H	14				
	209.10330212		209.10330212	2	A	13	1659.874084		1659.874084	
	306.15606597		306.15606597	3	P	12	1588.8369702		794.92212336	+0.0508991
	421.183009		421.183009	4	D	11	1491.7842064		1491.7842064	
	534.26707298		534.26707298	5	I	10	1376.7572634		1376.7572634	
	662.32565049		662.32565049	6	Q	9	1263.6731994		1263.6731994	
+0.0429654	389.179935	−0.066888	777.35259352	7	D	8	1135.6146219	−0.1273172	568.31094917	−0.2131098
−0.0386048	462.71414195	+0.0235726	924.42100744	8	F	7	1020.5876788		1020.5876788	
−0.1051604	536.24834891	+0.0971265	1071.4894214	9	F	6	873.51926492	−0.0585716	873.51926492	
	1170.5578353	−0.0489241	1170.5578353	10	V	5	726.45085101	−0.0326992	726.45085101	
+0.0496187	642.32458786	−0.1199266	1283.6418993	11	I	4	627.38243709	−0.0604766	627.38243709	
	1380.6946631		1380.6946631	12	P	3	514.29837311	−0.065524	514.29837311	
	1509.7372562		1509.7372562	13	E	2	417.24560926		417.24560926	
	1622.8213202		1622.8213202	14	I	1	288.20301616	+0.0045034	288.20301616	
				15	R	0	175.11895218	+0.2141167	175.11895218	

Scan number	6513	Raw file	20091031_Orbi6_MaHe_SA_ADH_exp3_Laminin_Re_Gel13
Method	ITMS; CID	Genenames	PRMT7



precursor information

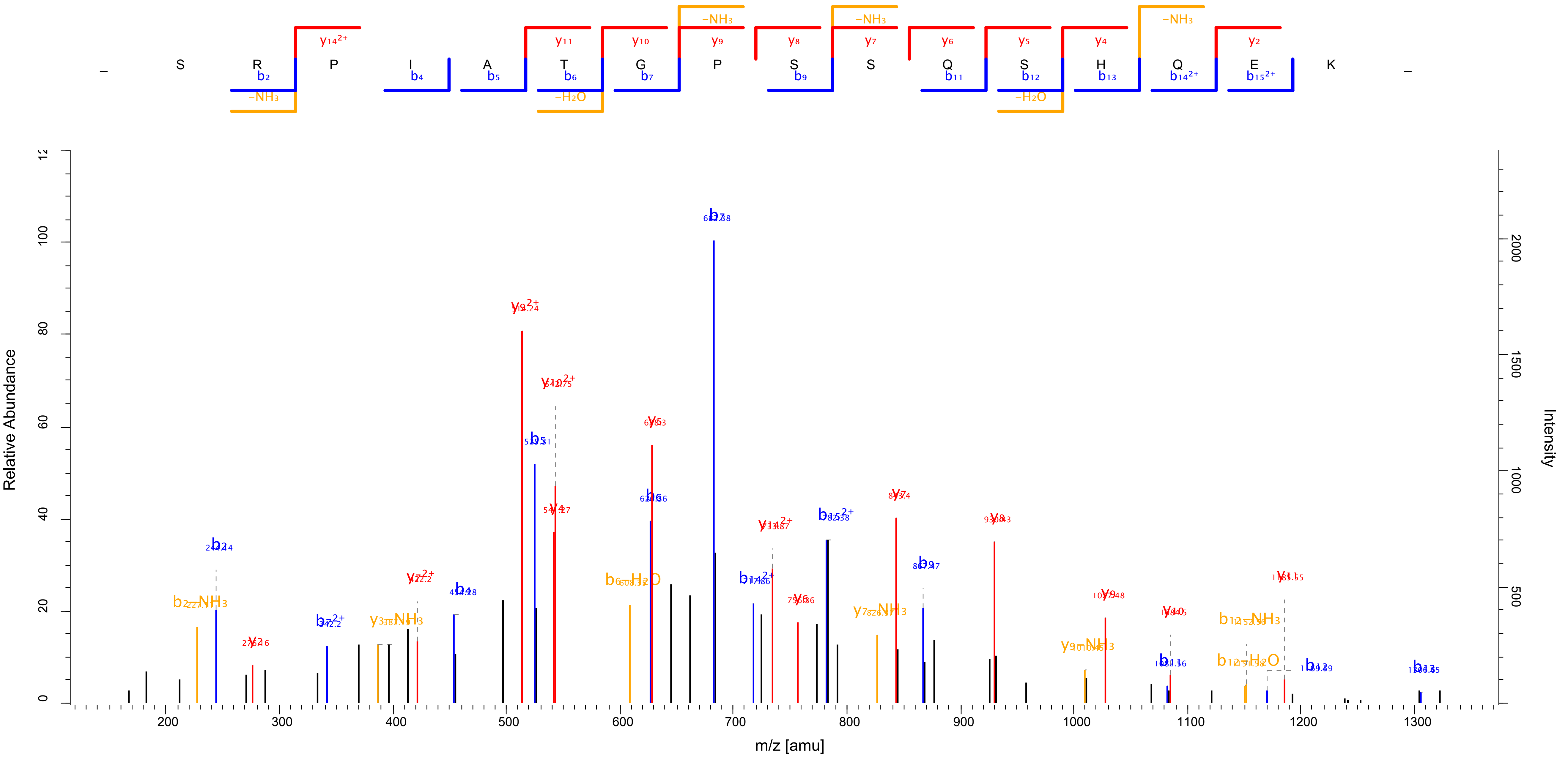
Mass:	1539.80073
m/z:	514.27418
Charge:	3+
Retentiontime:	44.5434112548828
Score:	144.4722
Mass Error [ppm]:	0.13421
PEP:	3.6732E-05
Precursor Type:	ISO

general information

Annotation:	11 of 13
AminoAcids Coverage:	85 %
Intensity Coverage:	54 %
Peak Coverage:	40 %
Protein Localisation:	458 ... 470

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	157.10838749		157.10838749	1	R	12				
	254.16115135	-0.0239138	254.16115135	2	P	11	1384.7066844		1384.7066844	
	383.20374444	+0.0681672	383.20374444	3	E	10	1287.6539205		1287.6539205	
	496.28780842		496.28780842	4	I	9	1158.6113274		1158.6113274	
	609.3718724	-0.150681	609.3718724	5	I	8	1045.5272634		1045.5272634	
+0.0230365	355.71341367	-0.072566	710.41955088	6	T	7	932.44319945	+0.4493787	466.72523796	+0.0165223
	824.46247833	-0.1594388	824.46247833	7	N	6	831.39552097		831.39552097	
-0.0460909	477.25617394	-0.2373102	953.50507142	8	E	5	717.35259352	+0.1595525	717.35259352	
+0.0462725	534.76964546	+0.0517258	1068.5320145	9	D	4	588.31000043	-0.0289946	588.31000043	
	1181.6160784		1181.6160784	10	I	3	473.2830574	-0.041053	473.2830574	
-0.0022211	655.34096621		1309.6746559	11	Q	2	360.19899342	-0.0174749	360.19899342	
	1366.6961197		1366.6961197	12	G	1	232.1404159	-0.0266464	232.1404159	
				13	R	0	175.11895218	+0.0008446	175.11895218	

Scan number	1333	Raw file	20091031_Orbi6_MaHe_SA_ADH_exp3_Laminin_Re_Gel14
Method	ITMS; CID	Genenames	UIMC1



precursor information

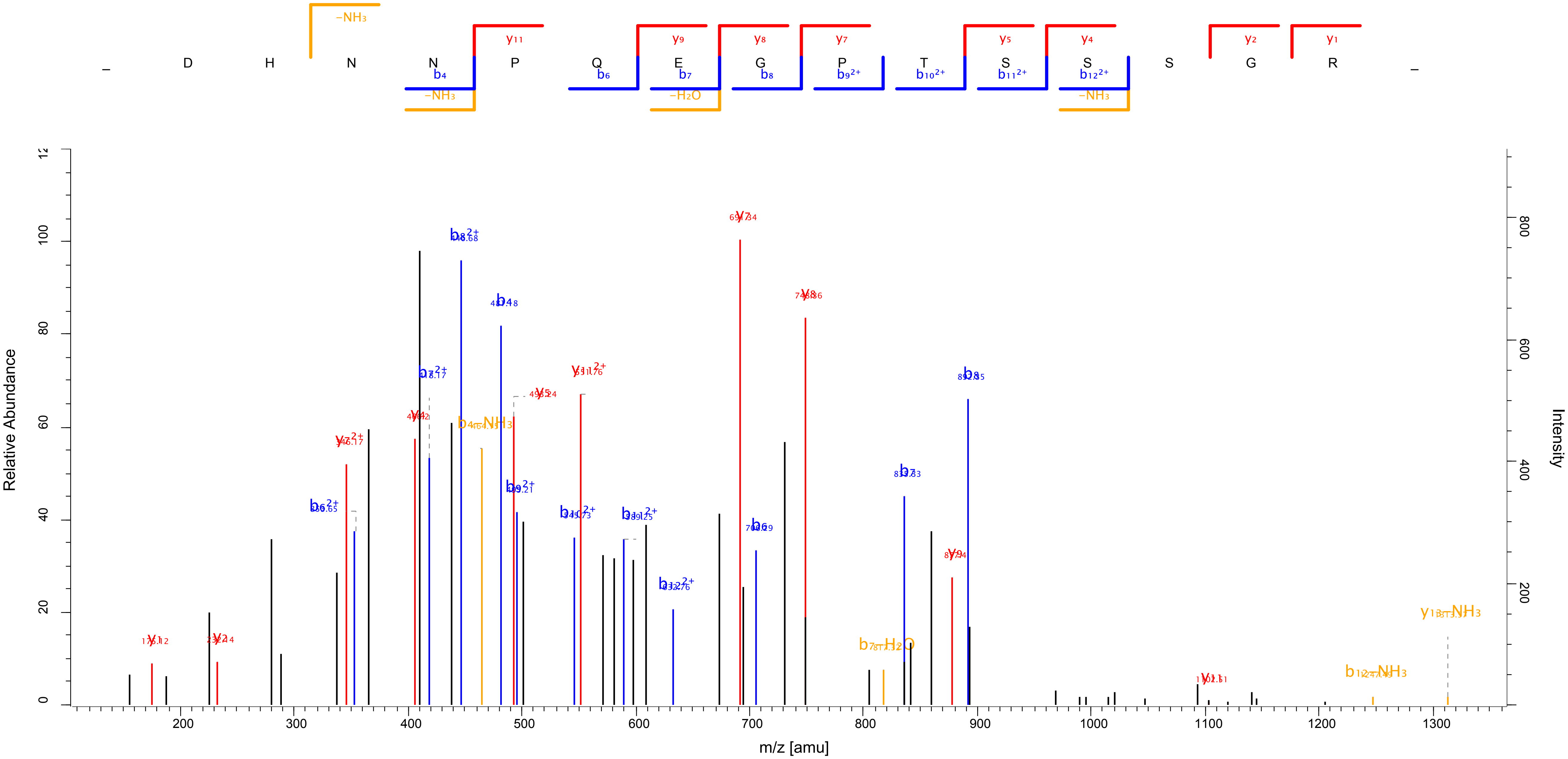
Mass:	1708.84936
m/z:	570.62373
Charge:	3+
Retentiontime:	18.8673553466797
Score:	190.8578
Mass Error [ppm]:	0.058061
PEP:	1.813E−24
Precursor Type:	MULTI

general information

Annotation:	14 of 16
AminoAcids Coverage:	88 %
Intensity Coverage:	67 %
Peak Coverage:	47 %
Protein Localisation:	131 ... 146

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876		88.039304876	1	S	15				
	244.1404159	−0.0112655	244.1404159	2	R	14	1622.8245081		1622.8245081	
	341.19317976		341.19317976	3	P	13	1466.7233971		733.86533676	+0.0176588
	454.27724374	−0.2038184	454.27724374	4	I	12	1369.6706332		1369.6706332	
	525.31435752	+0.000828	525.31435752	5	A	11	1256.5865692		1256.5865692	
	626.362036	−0.1118529	626.362036	6	T	10	1185.5494554	−0.0027025	1185.5494554	
+0.1487892	342.19538809	−0.0807653	683.38349972	7	G	9	1084.501777	+0.2526176	542.75452671	+0.0862326
	780.43626357		780.43626357	8	P	8	1027.4803132	+0.0467864	514.24379485	+0.1121622
	867.46829198	+0.0843814	867.46829198	9	S	7	930.42754938	−0.0332012	930.42754938	
	954.50032039		954.50032039	10	S	6	843.39552097	−0.043226	422.20139872	+0.0194875
	1082.5588979	+0.0756236	1082.5588979	11	Q	5	756.36349256	−0.1687904	756.36349256	
	1169.5909263	+0.0472573	1169.5909263	12	S	4	628.30491505	−0.0240923	628.30491505	
	1306.6498382	−0.2933929	1306.6498382	13	H	3	541.27288664	−0.1812118	541.27288664	
+0.0428497	717.85784608		1434.7084157	14	Q	2	404.21397478		404.21397478	
−0.01519	782.37914263		1563.7510088	15	E	1	276.15539727	+0.1051618	276.15539727	
				16	K	0	147.11280417		147.11280417	

Scan number	1360	Raw file	20091031_Orbi6_MaHe_SA_ADH_exp3_Laminin_Re_Gel14
Method	ITMS; CID	Genenames	RNASEL;DKFZp781D08126



precursor information

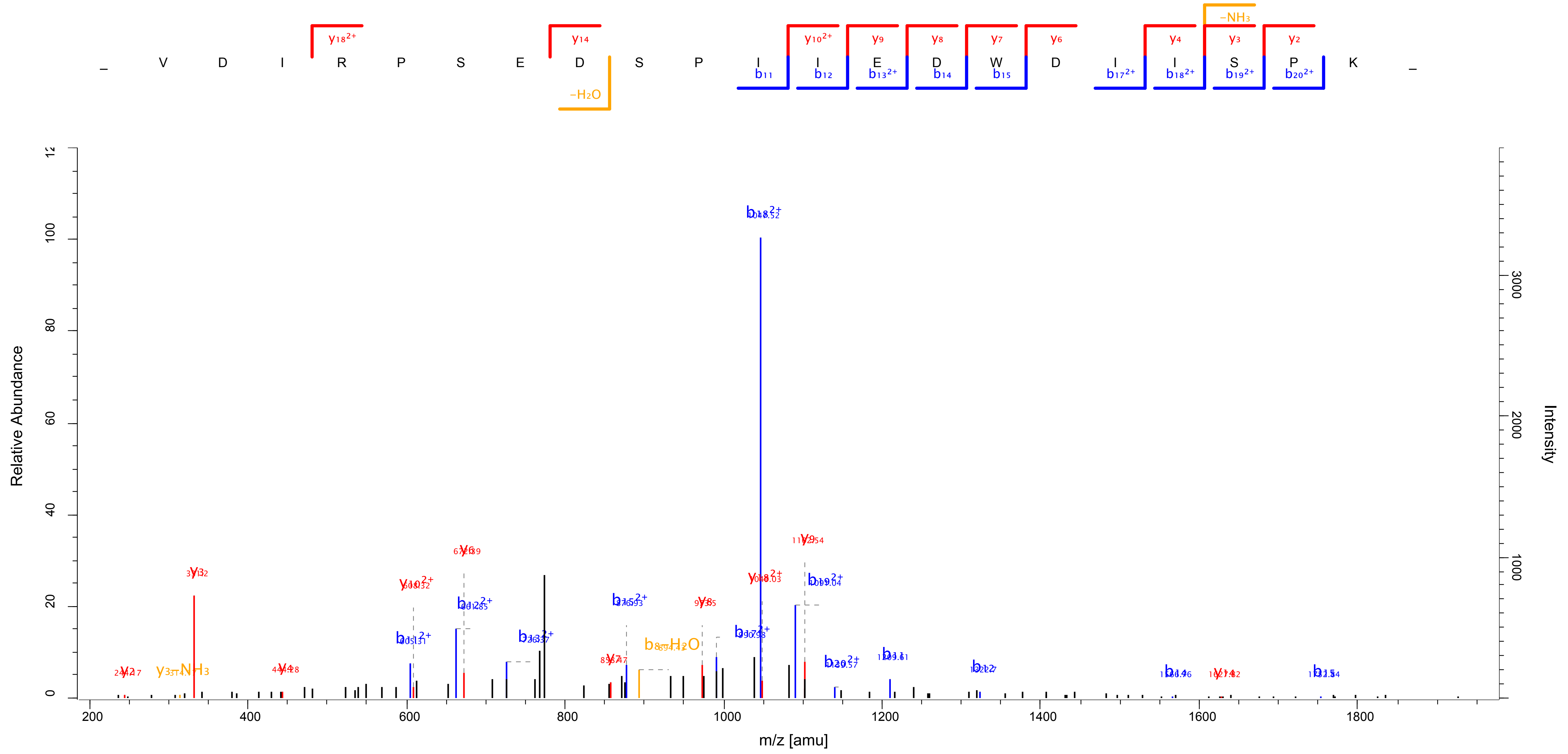
Mass:	1581.67719
m/z:	528.23301
Charge:	3+
Retentiontime:	19.0176258087158
Score:	129.3682
Mass Error [ppm]:	0.26467
PEP:	0.00020601
Precursor Type:	ISO

general information

Annotation:	12 of 15
AminoAcids Coverage:	80 %
Intensity Coverage:	59 %
Peak Coverage:	42 %
Protein Localisation:	5 ... 19

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342195		116.0342195	1	D	14				
	253.09313136		253.09313136	2	H	13	1467.6571084		1467.6571084	
	367.13605881		367.13605881	3	N	12	1330.5981965		1330.5981965	
	481.17898626	−0.107392	481.17898626	4	N	11	1216.5552691		1216.5552691	
	578.23175011		578.23175011	5	P	10	1102.5123416	−0.037244	551.75980906	+0.1345391
−0.0907576	353.64880204	−0.0521074	706.29032762	6	Q	9	1005.4595778		1005.4595778	
+0.1142642	418.17009859	−0.0426375	835.33292072	7	E	8	877.40100028	+0.0338142	877.40100028	
−0.0386796	446.68083045	−0.0211935	892.35438444	8	G	7	748.35840718	−0.0344936	748.35840718	
+0.4712544	495.20721238		989.40714829	9	P	6	691.33694346	+0.0233471	346.17210996	−0.0595001
−0.0334808	545.73105162		1090.4548268	10	T	5	594.28417961		594.28417961	
+0.068669	589.24706582		1177.4868552	11	S	4	493.23650113	+0.0748392	493.23650113	
−0.1096376	632.76308003		1264.5188836	12	S	3	406.20447272	−0.0147144	406.20447272	
	1351.550912		1351.550912	13	S	2	319.17244431		319.17244431	
	1408.5723757		1408.5723757	14	G	1	232.1404159	+0.0912735	232.1404159	
				15	R	0	175.11895218	+0.009771	175.11895218	

Scan number	18229	Raw file	20091031_Orbi6_MaHe_SA_ADH_exp3_Laminin_Re_Gel14
Method	ITMS; CID	Genenames	TBC1D25



precursor information

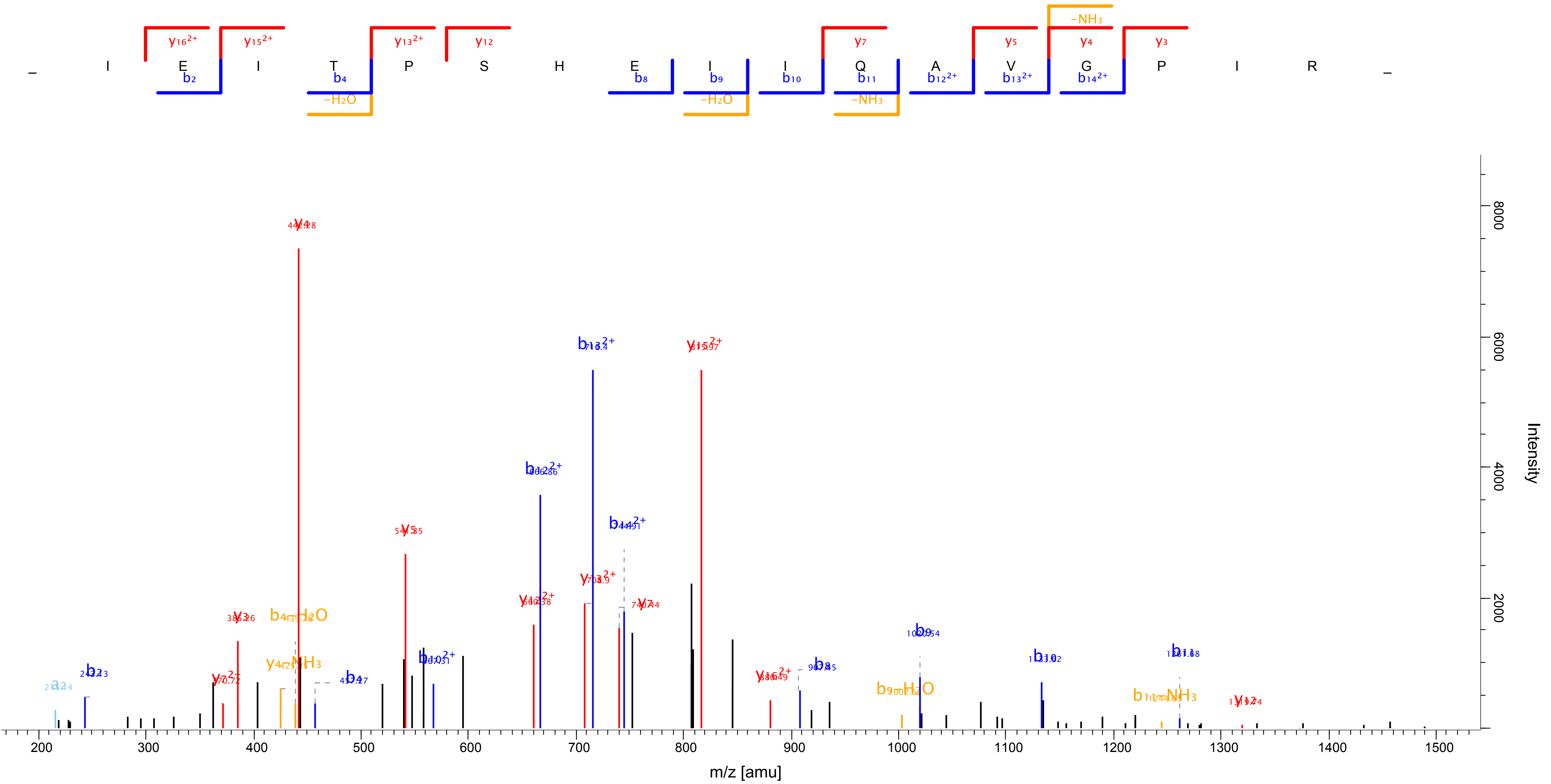
Mass:	2423.222
m/z:	808.74794
Charge:	3+
Retentiontime:	107.712173461914
Score:	105.8856
Mass Error [ppm]:	−0.0095253
PEP:	0.00036741
Precursor Type:	ISO

general information

Annotation:	12 of 21
AminoAcids Coverage:	57 %
Intensity Coverage:	57 %
Peak Coverage:	25 %
Protein Localisation:	122 ... 142

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.07569038		100.07569038	1	V	20				
	215.10263341		215.10263341	2	D	19	2325.1608832		2325.1608832	
	328.1866974		328.1866974	3	I	18	2210.1339401		2210.1339401	
	484.28780842		484.28780842	4	R	17	2097.0498761		1049.0285763	−0.0365109
	581.34057228		581.34057228	5	P	16	1940.9487651		1940.9487651	
	668.37260069		668.37260069	6	S	15	1843.8960013		1843.8960013	
	797.41519378		797.41519378	7	E	14	1756.8639729		1756.8639729	
	912.44213681		912.44213681	8	D	13	1627.8213798	−0.0451346	1627.8213798	
	999.47416522		999.47416522	9	S	12	1512.7944367		1512.7944367	
	1096.5269291		1096.5269291	10	P	11	1425.7624083		1425.7624083	
−0.1961587	605.30913476	+0.2476495	1209.6109931	11	I	10	1328.7096445		1328.7096445	
−0.0072336	661.85116675	+0.1433219	1322.695057	12	I	9	1215.6255805		608.31642848	+0.0227439
−0.1847802	726.3724633		1451.7376501	13	E	8	1102.5415165	+0.060046	1102.5415165	
	1566.7645932	−0.1421566	1566.7645932	14	D	7	973.49892341	−0.3194801	973.49892341	
−0.168084	876.92559129	+0.3896144	1752.8439061	15	W	6	858.47198038	−0.0367387	858.47198038	
	1867.8708491		1867.8708491	16	D	5	672.39266743	−0.1139199	672.39266743	
−0.2437901	990.9810948		1980.9549131	17	I	4	557.36572439		557.36572439	
+0.195257	1047.5231268		2094.0389771	18	I	3	444.28166041	−0.0892776	444.28166041	
+0.1070992	1091.039141		2181.0710055	19	S	2	331.19759643	+0.0049793	331.19759643	
+0.3431685	1139.5655229		2278.1237694	20	P	1	244.16556802	−0.0025126	244.16556802	
				21	K	0	147.11280417		147.11280417	

Scan number	13385	Raw file	20091031_Orbi6_MaHe_SA_ADH_exp3_Laminin_Re_Gel16
Method	ITMS; CID	Genenames	NFATC2



precursor information

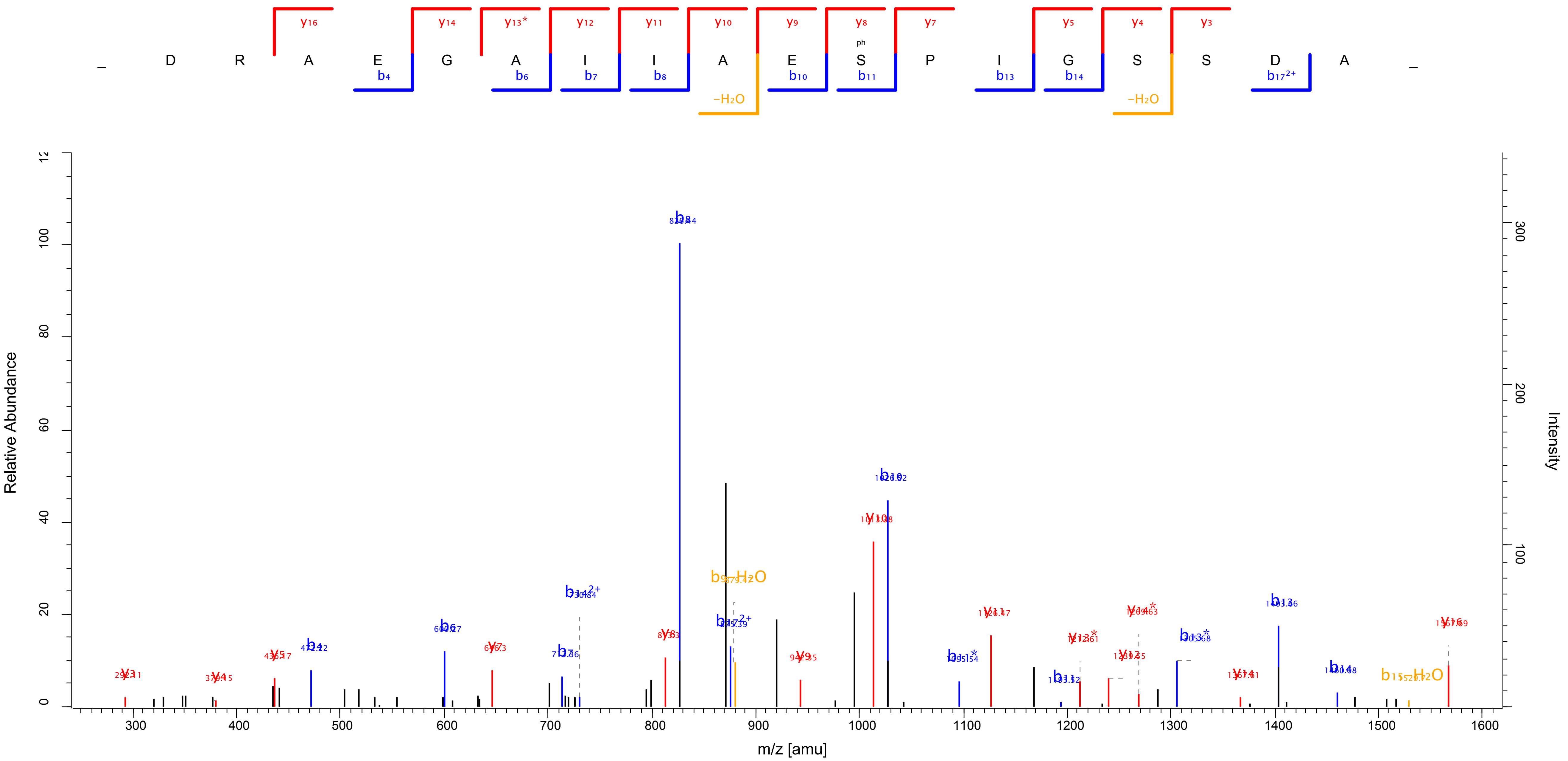
Mass:	1872.04736
m/z:	625.02306
Charge:	3+
Retentiontime:	79.169303894043
Score:	143.2488
Mass Error [ppm]:	0.24843
PEP:	5.1291E-07
Precursor Type:	MULTI

general information

Annotation:	13 of 17
AminoAcids Coverage:	76 %
Intensity Coverage:	66 %
Peak Coverage:	34 %
Protein Localisation:	113 ... 129

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.0964258		114.09134		114.09134	1	I	16				
+0.0811196	215.139019		243.133934	−0.0057597	243.133934	2	E	15	1759.97011		880.488693	+0.1768953
	328.223083		356.217998		356.217998	3	I	14	1630.92752		815.967397	+0.1332504
	429.270761		457.265676	−0.1418357	457.265676	4	T	13	1517.84345		1517.84345	
	526.323525		554.31844		554.31844	5	P	12	1416.79577		708.901525	−0.2385004
	613.355554		641.350468		641.350468	6	S	11	1319.74301	−0.0680835	660.375143	−0.4482025
	750.414465		778.40938		778.40938	7	H	10	1232.71098		1232.71098	
	879.457059		907.451973	+0.2850263	907.451973	8	E	9	1095.65207		1095.65207	
	992.541123		1020.53604	−0.0619161	1020.53604	9	I	8	966.609477		966.609477	
	1105.62519	−0.2580248	567.313689	−0.0461266	1133.6201	10	I	7	853.525413		853.525413	
	1233.68376		1261.67868	+0.0323809	1261.67868	11	Q	6	740.441349	−0.0468177	370.724313	+0.1685096
	1304.72088	−0.0624012	666.861534		1332.71579	12	A	5	612.382771		612.382771	
	1403.78929	+0.0128889	716.395741		1431.78421	13	V	4	541.345658	−0.0305331	541.345658	
	1460.81076	+0.1740321	744.906473		1488.80567	14	G	3	442.277244	−0.0428687	442.277244	
	1557.86352		1585.85843		1585.85843	15	P	2	385.25578	−0.0483215	385.25578	
	1670.94758		1698.9425		1698.9425	16	I	1	288.203016		288.203016	
						17	R	0	175.118952		175.118952	

Scan number	8769	Raw file	20090226_Orbi7_SaZa_SA_ADH_CLEC14A_IP_Dish_LabelFree_CLEC_InGel_05
Method	ITMS; CID	Genenames	CLEC14A



precursor information

Mass:	1837.80904
m/z:	919.91179
Charge:	2+
Retentiontime:	94.5901947021484
Score:	138.659
Mass Error [ppm]:	−0.25392
PEP:	0.043422
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverage:	83 %
Intensity Coverage:	63 %
Peak Coverage:	42 %
Protein Localisation:	473 ... 490

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	116.034219499		116.034219499	1	D	17		
	272.135330527		272.135330527	2	R	16	1723.789835435	
	343.172444314		343.172444314	3	A	15	1567.688724407	+0.1949426
	472.215037411	+0.0239152	472.215037411	4	E	14	1496.651610619	
	529.236501134		529.236501134	5	G	13	1367.609017523	−0.231454
	600.273614922	+0.0523128	600.273614922	6	A	12	1310.587553799	
	713.357678902	−0.0426765	713.357678902	7	I	11	1239.550440012	+0.1949213
	826.441742883	+0.0036917	826.441742883	8	I	10	1126.466376031	−0.3508975
	897.478856671		897.478856671	9	A	9	1013.382312051	−0.0757325
	1026.521449767	+0.1080668	1026.521449767	10	E	8	942.345198263	+0.0393232
	1193.519808585	−0.0090664	1193.519808585	11	S	7	813.302605167	+0.0476756
	1290.572572437		1290.572572437	12	P	6	646.304246348	−0.0884871
	1403.656636418	−0.0543415	1403.656636418	13	I	5	549.251482496	
−0.2365482	730.842688304	+0.1973881	1460.678100141	14	G	4	436.167418516	−0.013732
	1547.710128551		1547.710128551	15	S	3	379.145954793	+0.286876
	1634.742156961		1634.742156961	16	S	2	292.113926383	+0.1091571
−0.0529221	875.38818823		1749.769099993	17	D	1	205.081897973	
				18	A	0	90.054954941	