

N-glycoproteomics of urinary exosomes.

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SUPPLEMENTS

All the supplementary data is given here except supplementary Table 3 and 4 which are given as separate files.

Page 2: Supplementary methods.

Page 3: Supplementary Figure 1.

Page 3: Supplementary Figure 2.

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Page 6: Supplementary Table 1.

Page 7-10: MALDI parameters

Page 11: Supplementary Table 2. Optimal viewing conditions for this table are 100% zoom.

Page 12 onwards: Annotated spectra of all the glycopeptides which can be differentiated based on the m/z value. M/z value and charge of the precursor ion can be found on the top left corner of each spectra. These m/z values can be found as the name of the sheet in supplementary Table 3 (supplied separately) which is annotation of the fragment ions from every spectra (Glycan assignment).

Supplemental methods

Negative transmission electron microscopy

50 µg of urinary exosomes (P 200,000 g) were fixed with glutaraldehyde (1% (v/v), Sigma Aldrich) in water and spotted onto a Formvar/Carbon 300 mesh grid (Agar Scientific, Stansted, UK). The grids were dried at RT and washed twice in 0.1 M PBS. Thereafter the grids were incubated with 1% (w/v) OsO₄ in 0.1 M PBS for 30 min at +4°C. After three washes with PBS and two with water (five minutes each), exosomes were stained with 5% (w/v) uranyl acetate in water for 10 min. After staining, vesicle populations were imaged by JEM-2100 transmission electron microscopy (Jeol Ltd, Tokyo, Japan).

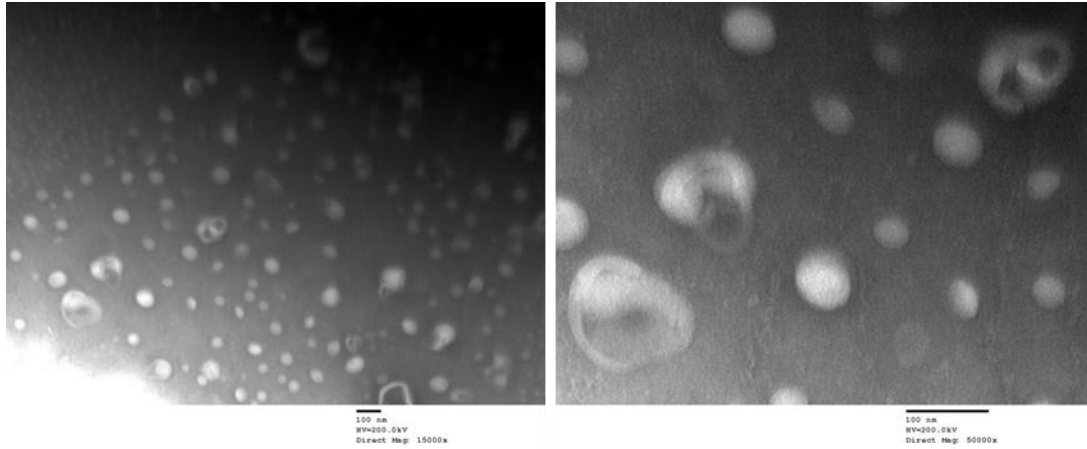
Protein quantification, SDS-PAGE and Western blotting

The protein concentrations in all urine fractions were measured by Coomassie Protein Assay (1). SDS-PAGE was carried out according to Laemmli (2). The gels were blotted to nitrocellulose membrane. The membranes were blocked overnight at RT with the Odyssey blocking buffer solution (LI-COR Biosciences, Lincoln, NE, USA). All incubation steps with antibodies were performed in a 1:1 (v/v) mixture of Odyssey blocking buffer and PBS with 0.1 % (v/v) Tween 20 (PBST). Antibodies were diluted in accordance with supplier's guidelines (anti-TSG101, Sigma, St. Louis, MO). Images were acquired by Odyssey Infrared Laser Scanner (LI-COR Biosciences, Lincoln, NE).

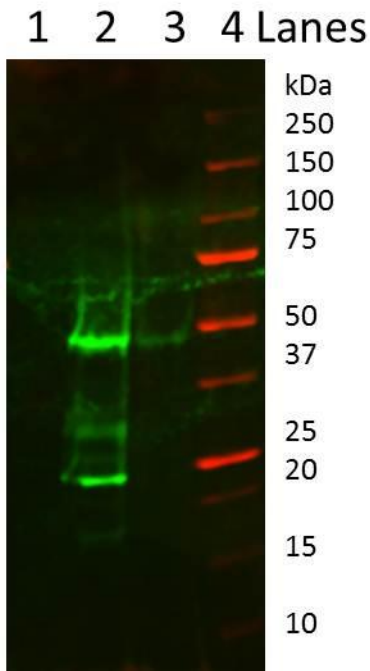
References:

1. Bradford, M. M. (1976) A rapid and sensitive method for the quantitation of microgram quantities of protein utilizing the principle of protein-dye binding. *Analytical biochemistry* 72, 248-254
2. Laemmli, U. K. (1970) Cleavage of structural proteins during the assembly of the head of bacteriophage T4. *Nature* 227, 680-685

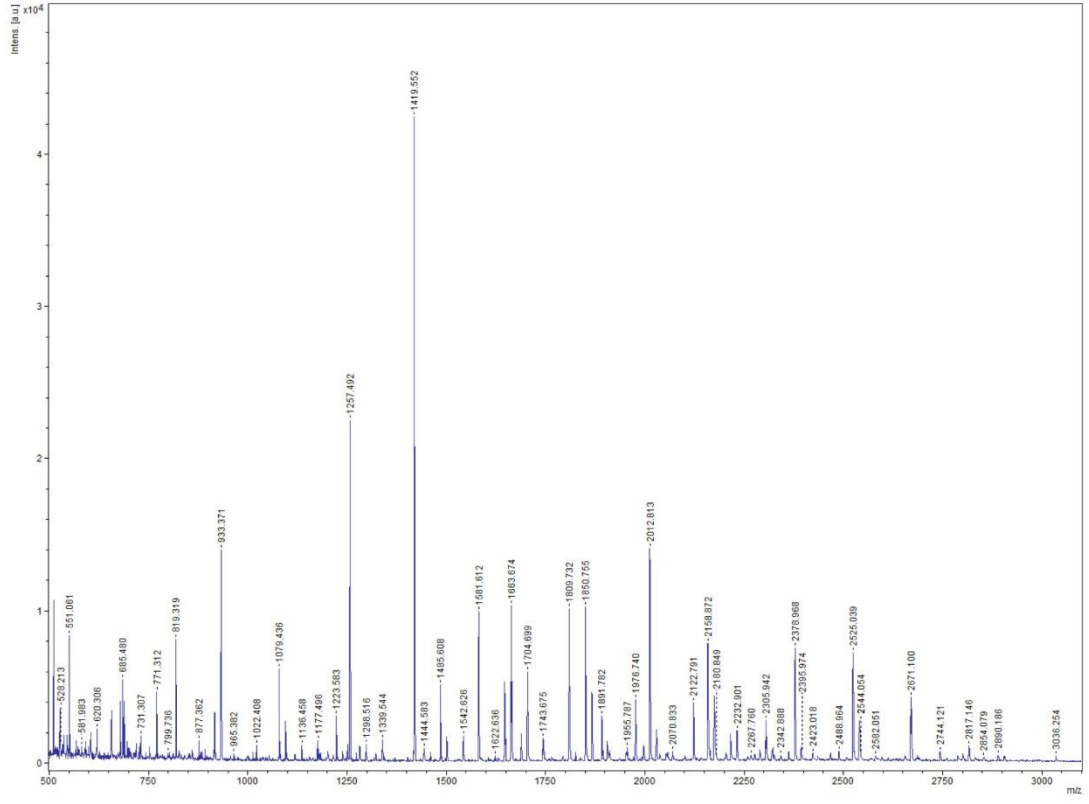
Supplemental Figures:



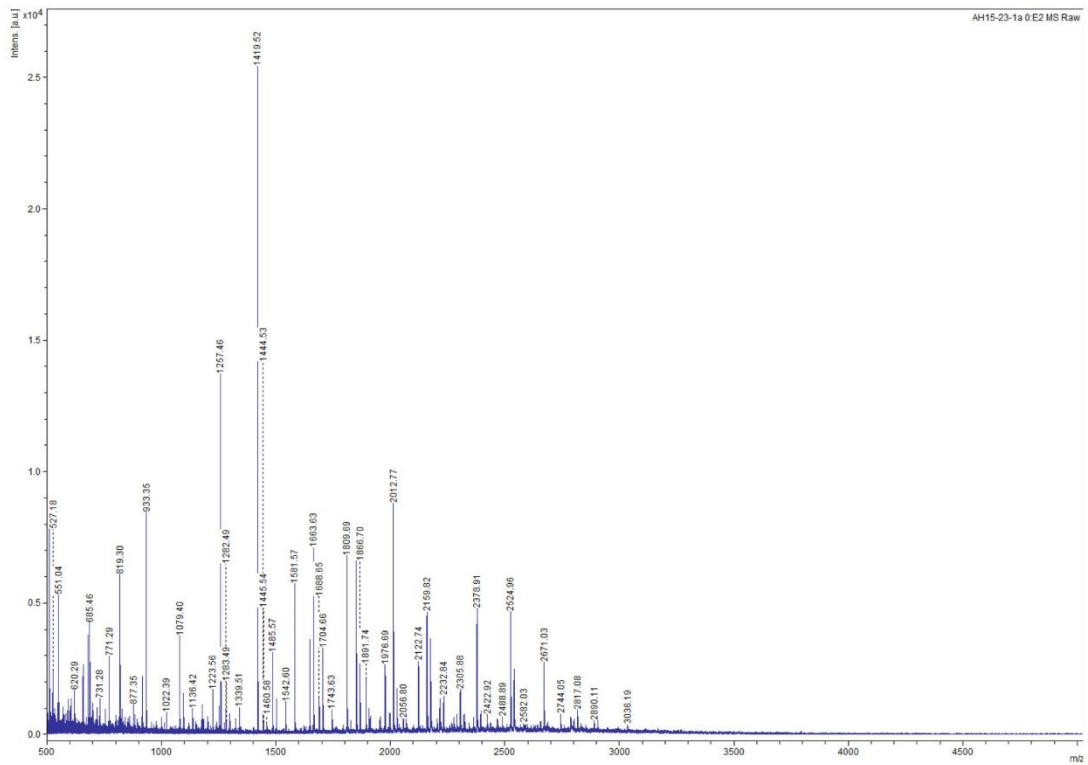
Supplemental Figure 1: Transmission electron microscopy pictures of exosomal fractions (P200,000g) at various magnifications. Panel on the left has direct magnification of 15,000 x and the panel on the right has 50,000 x. The bar shown below the picture is 100 nm in both the panels.



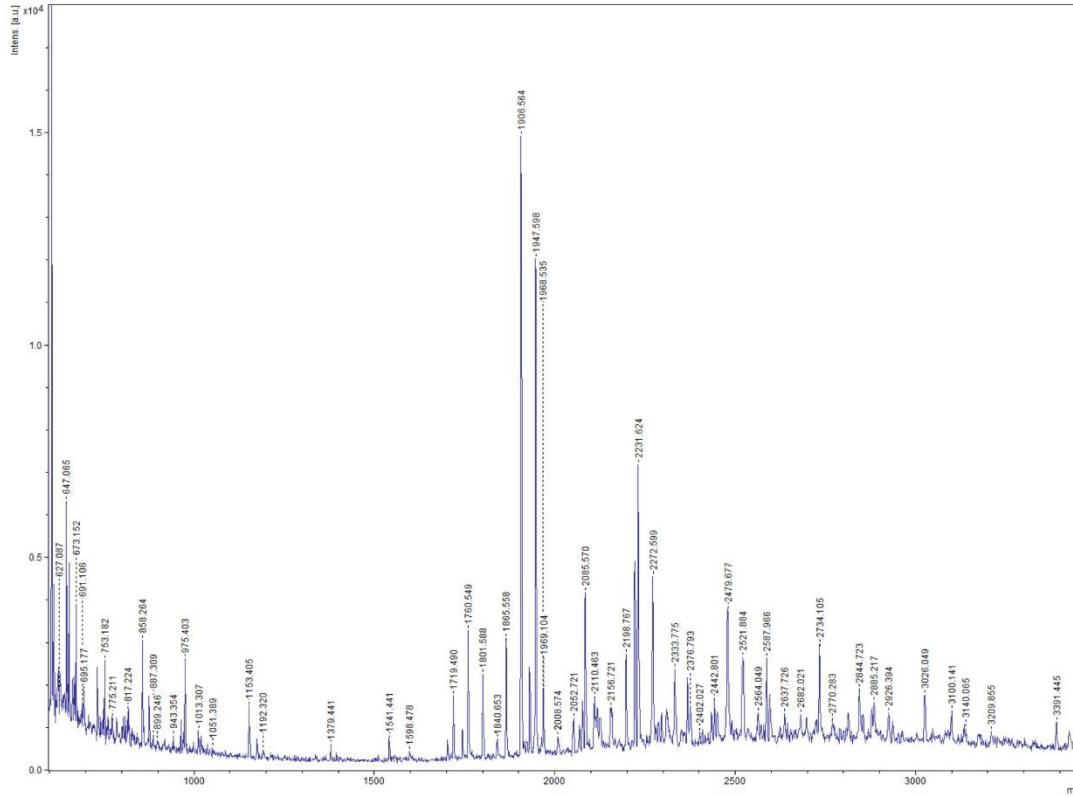
Supplementary Figure 2: Western blotting of urine fractions using anti-TSG101 antibody. Lanes 1: SN 200,000 g, 2: P 200,000 g, 3: P 18,000 g, 4: Molecular weight markers. Antibody dilutions were 1:1000 in Odyssey blocking buffer: PBS (1:1). The expected molecular weight of TSG101 is ~50 kDa.



Supplementary Figure 3 MALDI spectrum of neutral N-glycans. X-axis is the m/z value and Y-axis is the relative intensity.



Supplementary figure 4: MALDI spectrum of total (Neutral and acidic) N-glycans. X-axis is the m/z value and Y-axis is the relative intensity.



Supplementary figure 5: MALDI spectrum of acidic N-glycans. X-axis is the m/z value and Y-axis is the relative intensity.

Supplemental table 1:

Supplementary Table 1: Combur¹⁰ test values for volunteers A, B and C.

Parameters/Volunteers	A	B	C
Specific gravity	1.015	1.020	1.020
pH	6	5	6
Leukocytes	Negative	Negative	Negative
Nitrite	Negative	Negative	Negative
Protein	Negative	Negative	Negative
Glucose	Normal	Normal	Normal
Ketones	Negative	Negative	Negative
Urobilinogen	Negative	Negative	Negative
Bilirubin	Negative	Negative	Negative
Erythrocytes	Negative	Negative	Negative

(Neutral spectra) Below are all the parameters used for the analysis of neutral glycans.

File name: X:\MALDI\Annari\AH15-kirja\AH15-23\AH15-23-1-1\0_F2\1

Date: 2014-09-19 13:27:09

User name: Ultraflex3

Method: D:\Methods\flexControlMethods\RePo.par

Sample: AH15-23-1-1\0_F2\1

Delay: 40907 ns

HiTurbo: false

Realtime smooth: off

RepRate: 100 Hz

SampleRate: 0.5 ns

SpecSize: 176185 pts

Uhimass: 0 kV

ULinDet: 1.653 kV

URefDet: 1.737 kV

Analog Offset: 51.8 mV

Electronic Gain: 100 mV/fullscale

Laser Focus: 27

DPCal: 0

Matrix suppression: deflection

Matrix suppression

cut-off mass: 450

PIEDelay: 60 ns
Polarity: POS
UIS1: 18 kV
UIS2: 15.8 kV
ULens: 7.9 kV
URef1: 19 kV
URef2: 9.99 kV

Processing Calibration:

c0: 195.123
c1: 300576.138
c2: -0.117
CalDate: 2014-09-19T13:21:18.000+00:00
CalRef:
HPCUse: false
Mass error: 0.913
MClst: Sugar_neutral

(Acidic spectra) Below are all the parameters used for the analysis of acidic glycans.

File name: X:\MALDI\Annari\AH15-kirja\AH15-23\Happamat\Uusinta\AH15-23-1-2\0_I1\1
Date: 2014-10-03 14:44:23
Instrument: GLYD054
User name: Ultraflex3
Method: D:\Methods\flexControlMethods\Puolikkaat\ReNe12kV.par
Sample: AH15-23-1-2\0_I1\1

Delay: 55205 ns
HiTurbo: false
Realtime smooth: off
RepRate: 100 Hz
SampleRate: 0.5 ns
SpecSize: 153872 pts
Uhimass: 0 kV
ULinDet: 1.653 kV
URefDet: 1.819 kV

Analog Offset: 53 mV
Electronic Gain: 100 mV/fullscale
Laser Focus: 27
DPCal: 0
Matrix suppression: deflection

Matrix suppression

cut-off mass:	500
PIEDelay:	20 ns
Polarity:	NEG
UIS1:	12 kV
UIS2:	10.44 kV
ULens:	4.7 kV
URef1:	12.5 kV
URef2:	6.69 kV

Processing Calibration:

c0:	195.184
c1:	197635.438
c2:	-0.146
CalDate:	2014-10-03T14:42:08.000+00:00
CalRef:	
HPCUse:	false
Mass error:	2.911
MClst:	Sugar

Supplementary table 2: all the glycopeptides sequences, glycan composition and structure are given in this table along with other parameters. The false positive rate calculated was 2.56%.

mz	charge	SNA/SEC	protein	peptide_mass	start	end	N_site	N_site_DB	sequence	score_peptide	composition	structure_matching_to_Glycome_DB	GlycomeDB ID/ De novo composition	ppm	score_glycan	rank_all	score_all
1170,737	4	SEC	A1AG1_HUMAN	2894,449	58	81	72	72	SVEQIQATFFYFPTNKTEDTIFLR	17,09	H6N4		denovo	35,55027	9,94	1	27,03
927,0483	3	SEC	AMN1_HUMAN	758,4286	90	96	93		LNLNASK	18,52	H6N3F3		denovo	12,30069	4,75	1	23,27
982,7845	3	SEC	AMPN_HUMAN	1281,7081	231	241	234	234	AEFNITLHPK	36,83	H4N5	HNH(NH)(N)HNN	1033	-5,21986	30,72	1	67,55
950,6725	4	SEC	AMPN_HUMAN	1315,6997	126	136	128	128	KLNYLTSQGHK	21,27	H6N6F2		denovo	-13,7324	29,69	1	50,96
1139,474	4	SEC	AMPN_HUMAN	2876,3635	40	69	42		NANSSPVASTTTPASATNPPASATLDDQSK	17,69	S2H3N3		denovo	18,51293	18,55	1	36,24
1269,308	4	SNA	APOD_HUMAN	2722,402	83	108	98	98	ADGTVNQIEGATPVNLTPEAKLEVK	23,15	S2H5N4F1	SHNH(SHNH)HN(F)N	216	5,786618	59,99	1	83,14
1098,147	3	SEC	APOD_HUMAN	2253,112	83	104	98	98	ADGTVNQIEGATPVNLTPEAK	40,76	H3N2F1		denovo	20,61351	28,31	1	69,07
1097,932	4	SEC	APOD_HUMAN	1526,698	61	73	65	65	CIQANYSMLMENGK	33,3	S3H6N5	SHNH(SHN(SHN)H)HNN	1255	-0,57381	31,81	1	65,11
1244,821	3	SEC	APOD_HUMAN	1526,698	61	73	65	65	CIQANYSMLMENGK	22,45	S2H5N4	SHNH(SHNH)HNN	855	8,143074	30,49	1	52,94
933,8698	4	SEC	APOD_HUMAN	1526,698	61	73	65	65	CIQANYSMLMENGK	27,19	S2H5N4	SHNH(SHNH)HNN	855	5,429022	20,12	1	47,31
896,3768	3	SEC	ASAH1_HUMAN	1469,6885	255	267	259	259	TVLENSTSYEEAK	45,84	H5N2	H(H)H(H)HNN	234	1,007761	32,8	1	78,64
950,3925	3	SEC	ASAH1_HUMAN	1469,6885	255	267	259	259	TVLENSTSYEEAK	43	H6N2	HHH(H)H(H)HNN	235	2,949659	35,5	1	78,5
1004,411	3	SEC	ASAH1_HUMAN	1469,6885	255	267	259	259	TVLENSTSYEEAK	40,12	H7N2	HHH(H)H(H)HNN	240	1,795414	34,46	1	74,58
842,3589	3	SEC	ASAH1_HUMAN	1469,6885	255	267	259	259	TVLENSTSYEEAK	34,34	H4N2	HH(H)H(H)HNN	5746	1,428528	18,03	1	52,37
1007,75	3	SEC	ATRN_HUMAN	1317,6524	411	422	416	416	IDSTGNVTNELR	35,68	H8N2	HHH(H)H(H)HNN	242	1,690234	40,87	1	76,55
899,7146	3	SEC	ATRN_HUMAN	1317,6524	411	422	416	416	IDSTGNVTNELR	41,24	H8N2	HHH(H)H(H)HNN	235	2,226632	33,42	1	74,66
953,7311	3	SEC	ATRN_HUMAN	1317,6524	411	422	416	416	IDSTGNVTNELR	32,8	H7N2	HHH(H)H(H)HNN	240	3,253887	39,88	1	72,38
845,6984	3	SEC	ATRN_HUMAN	1317,6524	411	422	416	416	IDSTGNVTNELR	32,63	H5N2	HH(H)H(H)HNN	234	0,713414	32,56	1	65,17
1074,46	3	SEC	BGAL_HUMAN	1185,6717	458	468	464	464	NNVTILNITK	25,93	S1H7N3		denovo	4,997858	36,15	1	62,43
830,368	3	SEC	BGLR_HUMAN	1271,683	269	281	272	272	VVANGTGTGGQLK	26,56	H5N2	H(H)H(H)HNN	240	9,477726	22,21	1	48,77
1083,699	4	SEC	CFRU_HUMAN	2125,9916	396	415	397	397	ENLTAGSDSVAFFVGGQTR	28,97	S2H5N4	SHNH(SHNH)HNN	855	-0,67362	35,07	1	64,04
1025,18	4	SNA	CEFL_HUMAN	1891,8337	129	144	138	138	EHEGAYPPDNTDFQR	23,62	S2H5N4	SHNH(SHNH)HNN	855	-20,6842	31,21	1	54,83
957,1561	4	SEC	CLUS_HUMAN	1682,8264	372	385	374	374	LANLTQGEDQYYLR	34,53	S1H2N6F1	SNNH(NNH)HN(F)N	8842	5,009632	41,83	1	76,36
1019,677	4	SEC	CLUS_HUMAN	1682,8264	372	385	374	374	LANLTQGEDQYYLR	22,21	S2H4N5F1	SNNH(SHNH)HN(F)N	8844	0,975799	29,72	1	51,93
1103,789	3	SNA	COA4_HUMAN	1103,593	1326	1336	1328	1328	GLNVTLSSTR	18,54	S2H5N4	SHNH(SHNH)HNN	855	6,10322	52,06	1	70,6
1125,47	3	SEC	CUBN_HUMAN	1109,5578	1800	1810	1802	1802	EGNATGHLVGR	23,47	H5N5F3	FHNH(FHNH)HN(F)N	2023	1,187652	76	1	99,47
1076,783	3	SEC	CUBN_HUMAN	1109,5578	1800	1810	1802	1802	EGNATGHLVGR	25,93	H5N5F2	FHNH(HNH)HN(F)N	24655	2,572478	66,4	1	92,33
1121,468	3	SEC	CUBN_HUMAN	1186,5942	3457	3468	3457	3457	NGSNSNPLLGK	30,47	H5N6F1		denovo	3,242774	57,56	1	88,03
984,0692	3	SEC	CUBN_HUMAN	977,4719	2082	2090	2085	2085	AGFNASFHK	27,67	H5N5F1	HNH(F)H(NH)HNN	5782	1,697035	52,27	1	79,94
1053,11	3	SEC	CUBN_HUMAN	1184,6098	778	788	781	781	VCNGTSTSHK	18,45	H5N5F1	FHNH(FHNH)HN(F)N	1043	6,491883	59,02	1	77,47
897,0562	3	SEC	CUBN_HUMAN	1186,5942	3457	3468	3457	3457	NGSNSNPLLGK	35,37	H3N5	NH(NH)HN(NH)N	1032	1,044156	51,92	1	77,29
1278,194	3	SEC	CUBN_HUMAN	1348,6782	2526	2537	2531	2531	LCSSVNVSEIK	25,65	H6N6F2		denovo	7,356736	40,94	1	76,59
916,3778	3	SEC	CUBN_HUMAN	977,4719	2082	2090	2085	2085	AGFNASFHK	30,49	H5N4F1	HNH(H)H(NH)HNN	887	-0,06911	44,26	1	74,75
951,073	3	SEC	CUBN_HUMAN	1186,5942	3457	3468	3457	3457	NGSNSNPLLGK	35,5	H4N5	HNH(NH)HN(F)N	1033	1,826008	38,98	1	74,48
999,7589	3	SEC	CUBN_HUMAN	1186,5942	3457	3468	3457	3457	NGSNSNPLLGK	32,72	H4N5F1		denovo	1,803768	41,13	1	73,85
937,3969	3	SEC	CUBN_HUMAN	1186,5942	3457	3468	3457	3457	NGSNSNPLLGK	35,48	H5N4		denovo	2,457159	33,38	1	68,86
1107,791	3	SEC	CUBN_HUMAN	1186,5942	3457	3468	3457	3457	NGSNSNPLLGK	30,32	H6N5F1	HNH(NH)H(NH)HNN	32456	4,516469	37,7	1	68,02
844,3534	4	SEC	CUBN_HUMAN	1109,5578	1800	1810	1802	1802	EGNATGHLVGR	23,46	H5N5F3	FHNH(FHNH)HN(F)N	24641	2,362755	42,83	1	66,29
1107,802	3	SEC	CUBN_HUMAN	1348,6782	2526	2537	2531	2531	LCSSVNVSEIK	25,25	H5N5F1	HNH(H)H(NH)HNN	1043	4,335915	40,47	1	65,72
935,3835	3	SEC	CUBN_HUMAN	977,4719	2082	2090	2085	2085	AGFNASFHK	27,59	H5N5	HNH(H)H(NH)HNN	1035	1,500276	37,05	1	64,64
1229,506	3	SEC	CUBN_HUMAN	1348,6782	2526	2537	2531	2531	LCSSVNVSEIK	18,26	H6N6F1	HNH(H)H(NH)HN(F)N	17650	8,813837	46,18	1	64,44
1326,878	3	SEC	CUBN_HUMAN	1348,6782	2526	2537	2531	2531	LCSSVNVSEIK	18,41	H6N6F3		denovo	7,966065	44,75	1	63,16
1105,785	3	SEC	CUBN_HUMAN	977,4719	2082	2090	2085	2085	AGFNASFHK	19,79	H6N6F1	HNH(H)H(NH)HN(F)N	17650	-2,98129	40,82	1	60,61
1180,824	3	SEC	CUBN_HUMAN	1348,6782	2526	2537	2531	2531	LCSSVNVSEIK	20,38	H6N6	HNH(H)H(NH)HN(F)N	5374	6,41078	34,43	1	54,81
1218,502	3	SEC	CUBN_HUMAN	1186,5942	3457	3468	3457	3457	NGSNSNPLLGK	18,23	S1H5N6F1		denovo	1,261112	36,46	1	54,69
1053,773	3	SEC	CUBN_HUMAN	1186,5942	3457	3468	3457	3457	NGSNSNPLLGK	22,63	H5N5F1	HNH(F)H(NH)HNN	5782	5,507198	31,95	1	54,58
1067,45	3	SEC	CUBN_HUMAN	1186,5942	3457	3468	3457	3457	NGSNSNPLLGK	22,63	H4N6F1	NNH(H)H(NH)HN(F)N	1492	3,500554	31,81	1	54,44
958,8961	4	SEC	CUBN_HUMAN	1348,6782	2526	2537	2531	2531	LCSSVNVSEIK	27,81	H6N6F2		denovo	8,311641	26,3	1	54,11
995,4046	4	SEC	CUBN_HUMAN	1348,6782	2526	2537	2531	2531	LCSSVNVSEIK	25,36	H6N6F3		denovo	14,00938	23,74	1	49,1
918,1528	4	SEC	DPEP1_HUMAN	1550,8416	56	70	57	57	ANLTLTAGTHTNPK	16,94	H5N5F2	FHNH(HNH)HN(F)N	24655	9,87853	23,59	1	40,53
994,9092	4	SEC	FETUA_HUMAN	1770,864	145	159	156	156	VCQDCFLAPLNDTR	21,68	S2H5N4	SHNH(SHNH)HNN	855	7,206688	27,48	1	49,16
917,7096	3	SEC	FGFR3_HUMAN	877,4141	311	319	315	315	TAGANTTDK	17,04	S1H6N3		denovo	-15,4334	16,19	1	33,23
898,7083	3	SEC	FGFR3_HUMAN	877,4141	311	319	315	315	TAGANTTDK	17,02	S1H6N2F1		denovo	-22,2875	13,69	1	30,71
1139,238	4	SEC	GGTL1_HUMAN	1632,895	160	173	167	167	LHNQLLPVNTTVER	22,58	S1H6N6F3		denovo	7,368959	33,92	1	56,5
903,112	4	SEC	HEMO_HUMAN	1403,674	181	193	187	187	SWPAVNGCSSALR	17,6	S2H5N4	SHNH(SHNH)HNN	855	7,60703	19,98	1	37,58
1220,08	4	SNA	IghA1_HUMAN	2962,604	127	153	144	144	LSLRPALEDLLGSEANLCTLTGLR	40,46	S1H5N4	SHNH(SHNH)HNN	205	-2,03265	48,59	1	89,05
923,4094	3	SEC	IghA2_HUMAN	957,5495	200	208	205	205	TPLTANITK	36,77	H4N5F1	HNH(H)H(NH)HN(F)N	1041	3,324636	43,16	1	79,93
1006,767	3	SEC	IghA2_HUMAN	957,5495	200	208	205	205	TPLTANITK	30,58	S1H5N4F1	SHNH(HNH)HN(F)N	215	1,724994	45,2	1	75,78
977,4273	3	SEC	IghA2_HUMAN	957,5495	200	208	205	205	TPLTANITK	30,55	H5N5F1	HNH(H)H(NH)HN(F)N	1043	2,83397	44,49	1	75,04
1074,478	3	SNA	IghA2_HUMAN	957,5495	200	208	205	205	TPLTANITK	25,04	S1H5N5F1	SHNH(HNH)HN(F)N	4685	-15,01197	44,64	1	69,68
806,0957	4	SEC	IghA2_HUMAN	957,5495	200	208	205	205	TPLTANITK	27,86	S1H5N5F1	SHNH(HNH)HN(F)N	4685	3,12618	21,77	1	49,63
922,0402	3	SEC	IGHG2_HUMAN	1156,515	172	180	176	176	EEQFNSTR	27,55	H4N4F1	HNH(H)H(NH)HNN	1026	1,052015	49,42	1	76,97

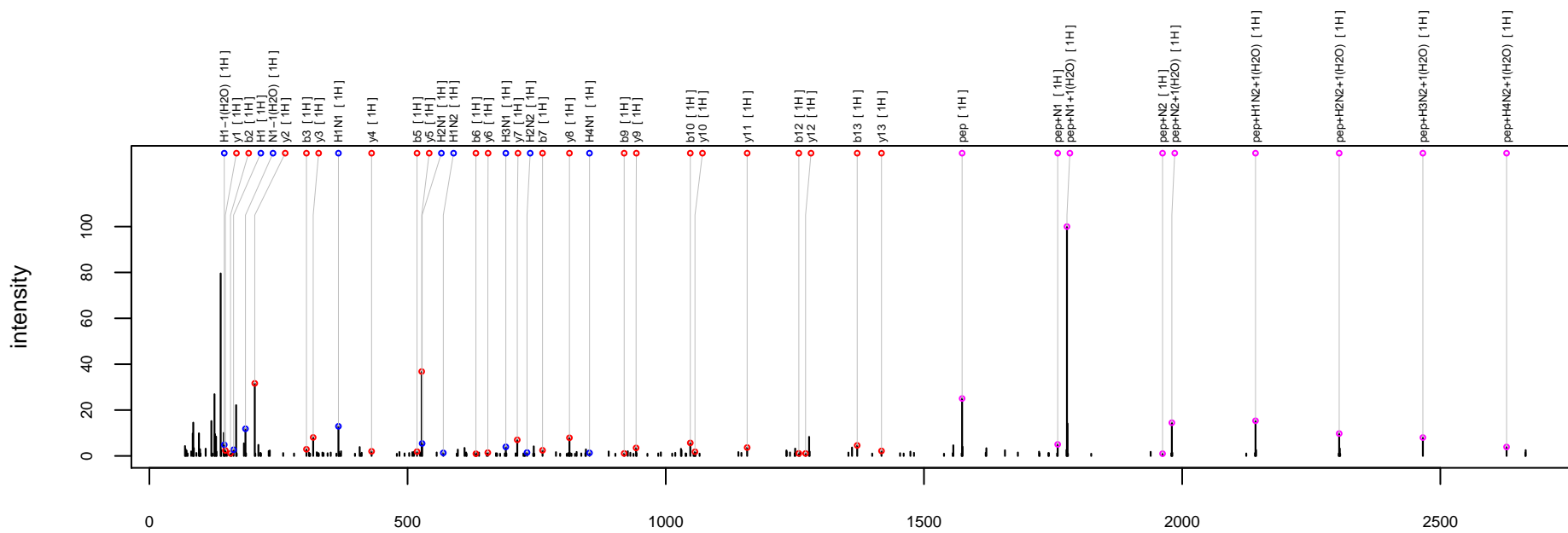
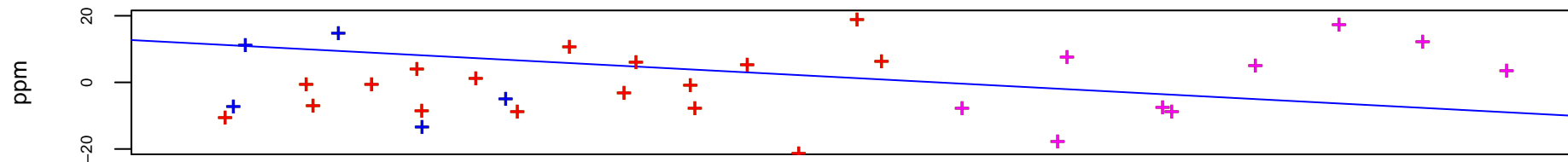
m/z 984.784 charge 3 scan 0-0

Score= 74.85 , Hits= 40 , Explained Intensity= 0.49

Peptide: LYAG_HUMAN[465,479]:GVFITNETGQPLIGK

Glycan: HH(H(H)H)HNN, H6N2

Charge: 3H



	2	3	4	5	6	7	8	9	10	11	12	13	14	15	
b	G	V	F	I	T	N	E	T	G	Q	P	L	I	G	K
	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1
															y

- peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
- glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
- intact peptide and glycan fragments, pep: intact peptide
- (): additions
- []: charge

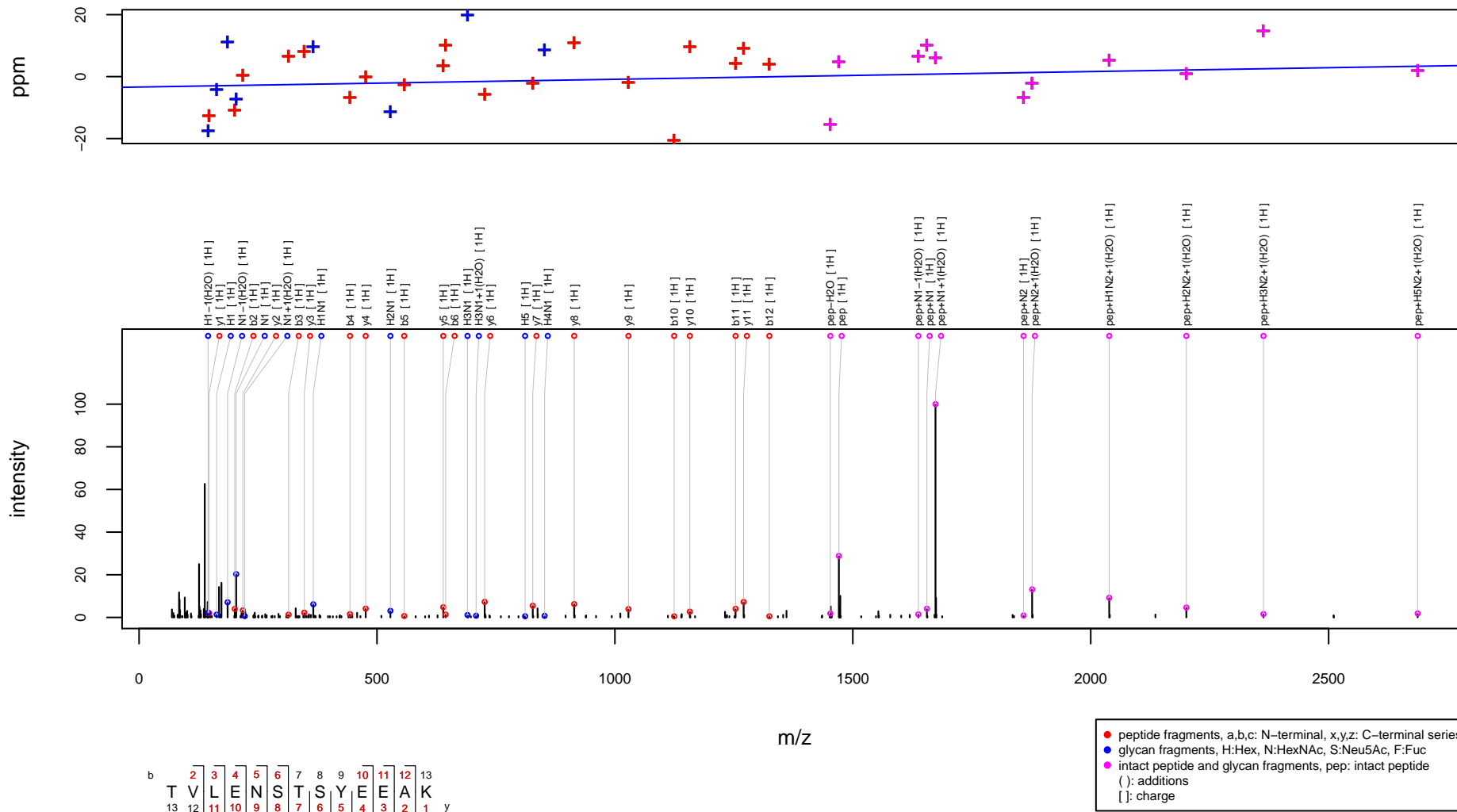
m/z 896.3768 charge 3 scan 0-0

Score= 78.64 , Hits= 41 , Explained Intensity= 0.49

Peptide: ASAH1_HUMAN[255,267]:TVLENSTSYEEAK

Glycan: H(H)H(H)HNN, H5N2

Charge: 3H



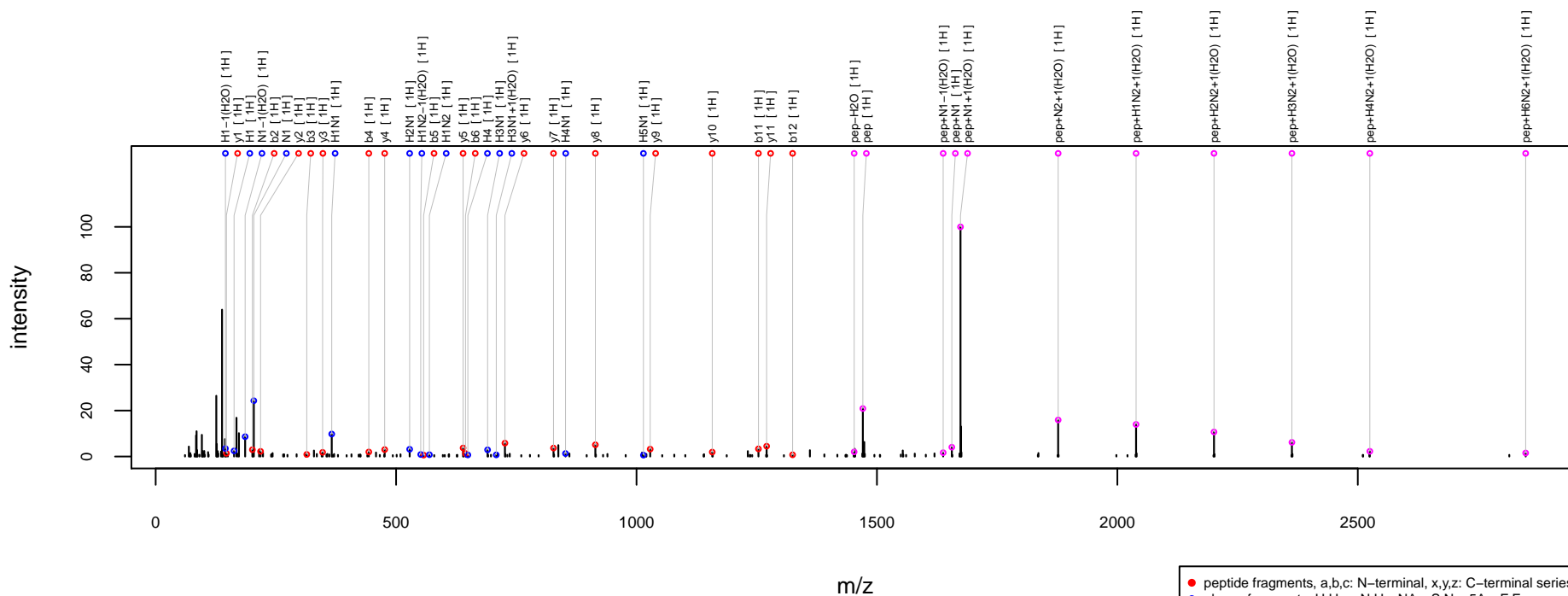
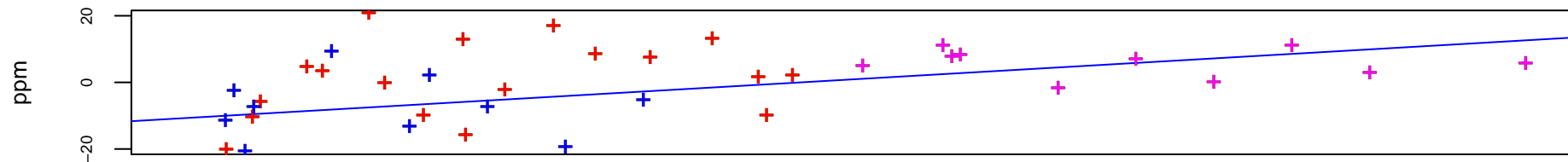
m/z 950.3925 charge 3 scan 0-0

Score= 78.5 , Hits= 42 , Explained Intensity= 0.5

Peptide: ASAH1_HUMAN[255,267]:TVLENSTSYEEAK

Glycan: HH(H(H)H)HNN, H6N2

Charge: 3H



b

2	3	4	5	6	7	8	9	10	11	12	13	
T	V	L	E	N	S	T	S	Y	E	E	A	K
13	12	11	10	9	8	7	6	5	4	3	2	1

y

- peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
- glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
- intact peptide and glycan fragments, pep: intact peptide
- (): additions
- []: charge

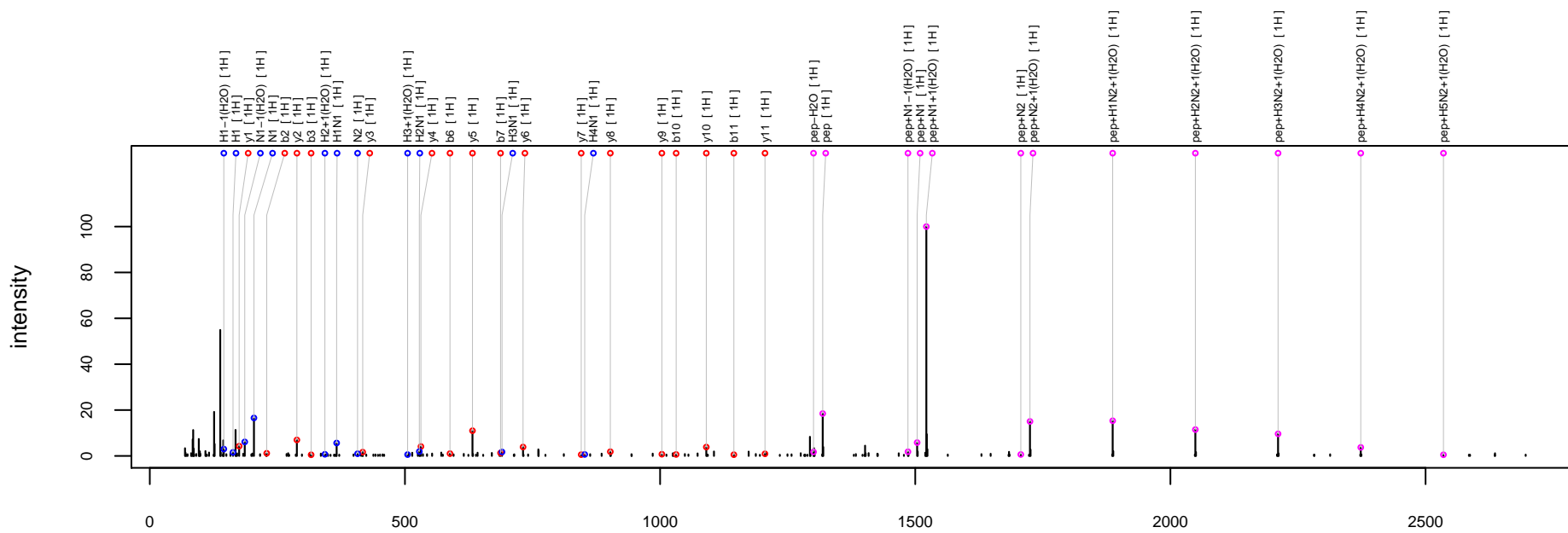
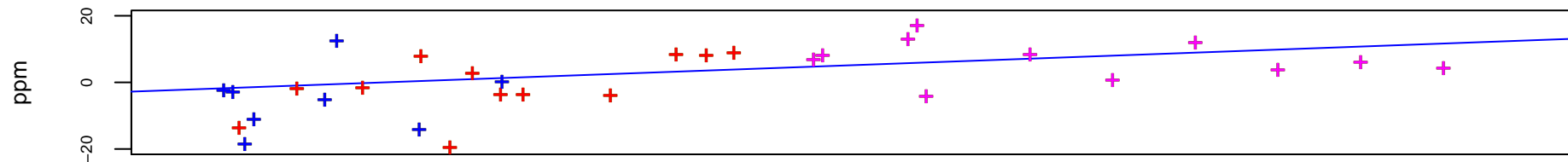
m/z 899.7146 charge 3 scan 0-0

Score= 74.66 , Hits= 40 , Explained Intensity= 0.53

Peptide: ATRN_HUMAN[411,422]:IDSTGNVTNELR

Glycan: HH(H(H)H)HNN, H6N2

Charge: 3H



	2	3	4	5	6	7	8	9	10	11	12	
b	I	D	S	T	G	N	V	T	N	E	L	R
	12	11	10	9	8	7	6	5	4	3	2	1

y

- peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
- glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
- intact peptide and glycan fragments, pep: intact peptide
- (): additions
- []: charge

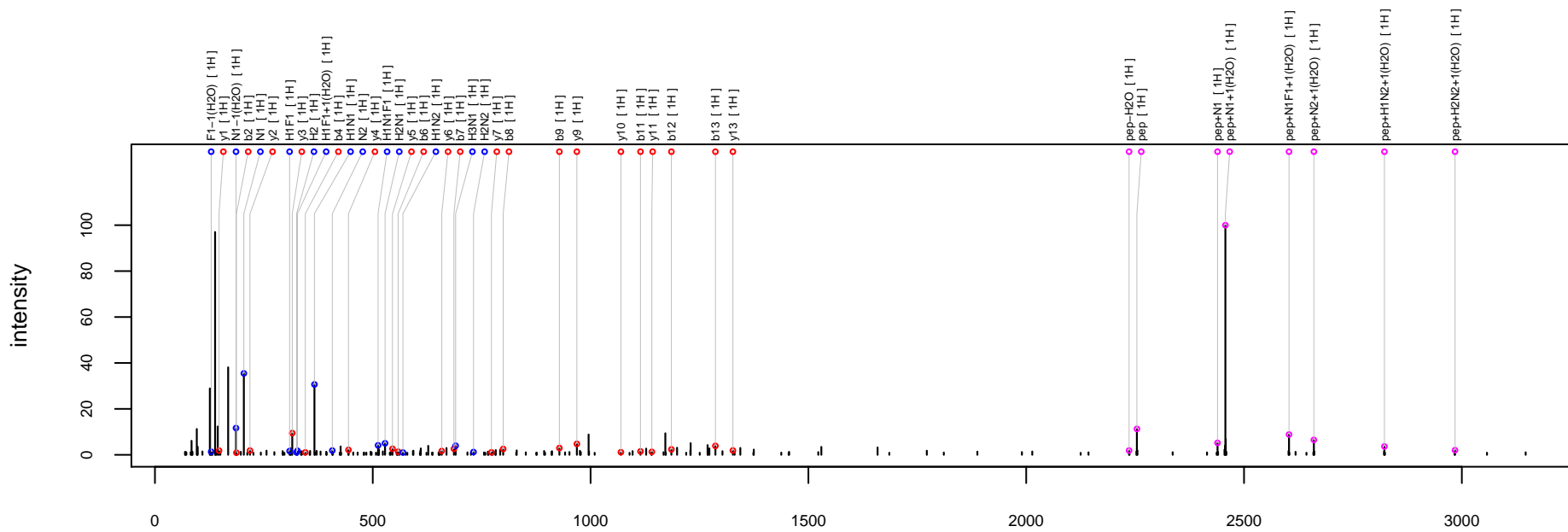
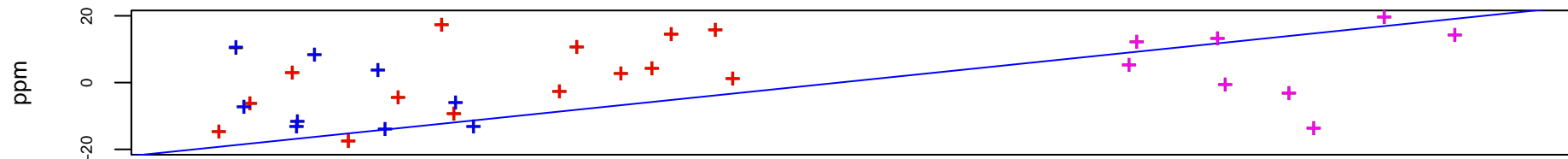
m/z 1098.147 charge 3 scan 0-0

Score= 69.07 , Hits= 41 , Explained Intensity= 0.43

Peptide: APOD_HUMAN[83,104]:ADGTVNQIEGATPVNLTEPAK

Glycan: H3N2F1

Charge: 3H



b 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22
 A D G T V N Q I E G E A T P V N L T E P A K
 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1 y

● peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
 ● glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
 ● intact peptide and glycan fragments, pep: intact peptide
 (): additions
 []: charge

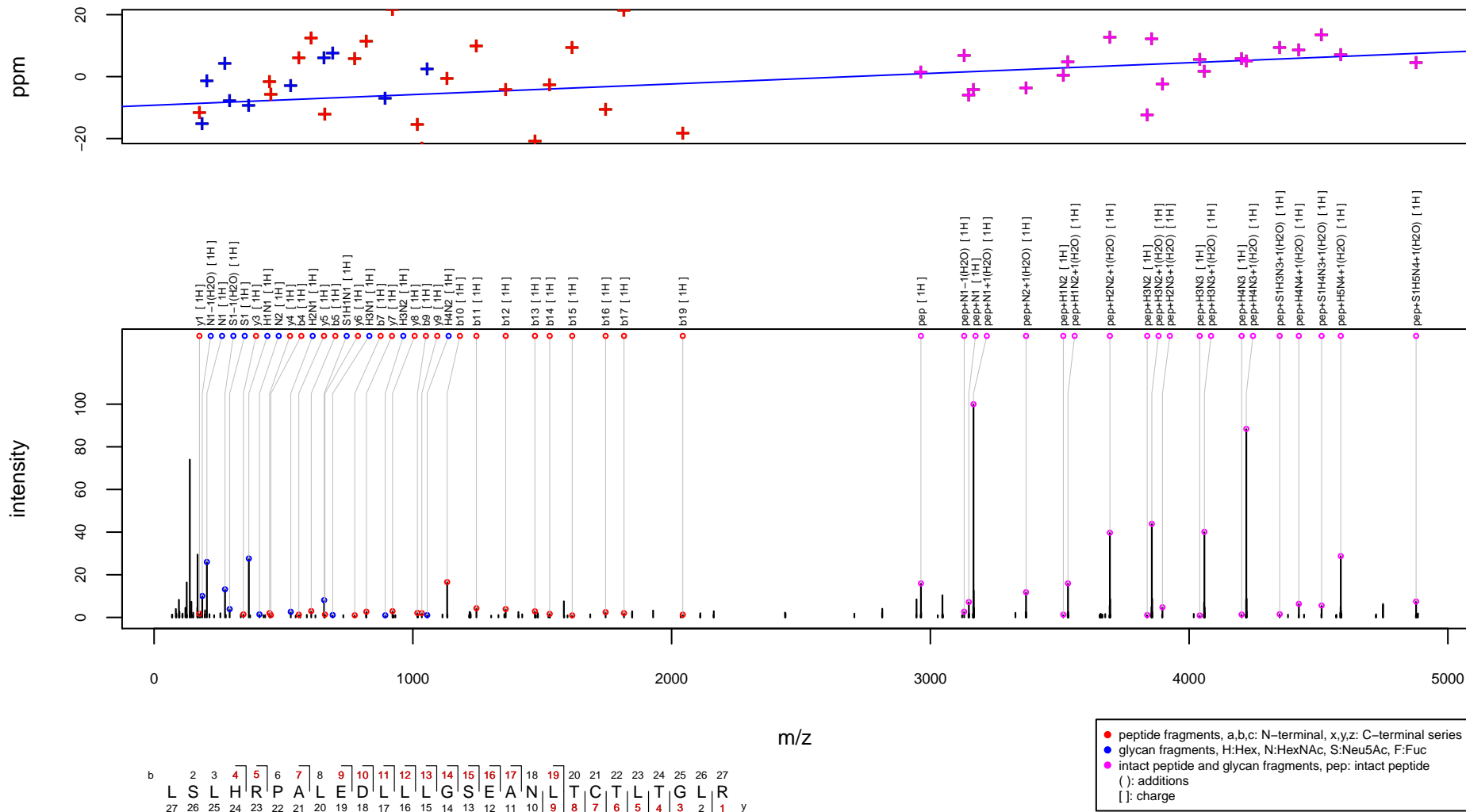
m/z 1220.08 charge 4 scan 0-0

Score= 89.05 , Hits= 52 , Explained Intensity= 0.59

Peptide: IGHA1_HUMAN[127,153]:LSLHRPALEDLLLGSEANLTCTLTGLR

Glycan: SHNH(HNH)HNN, S1H5N4

Charge: 4H



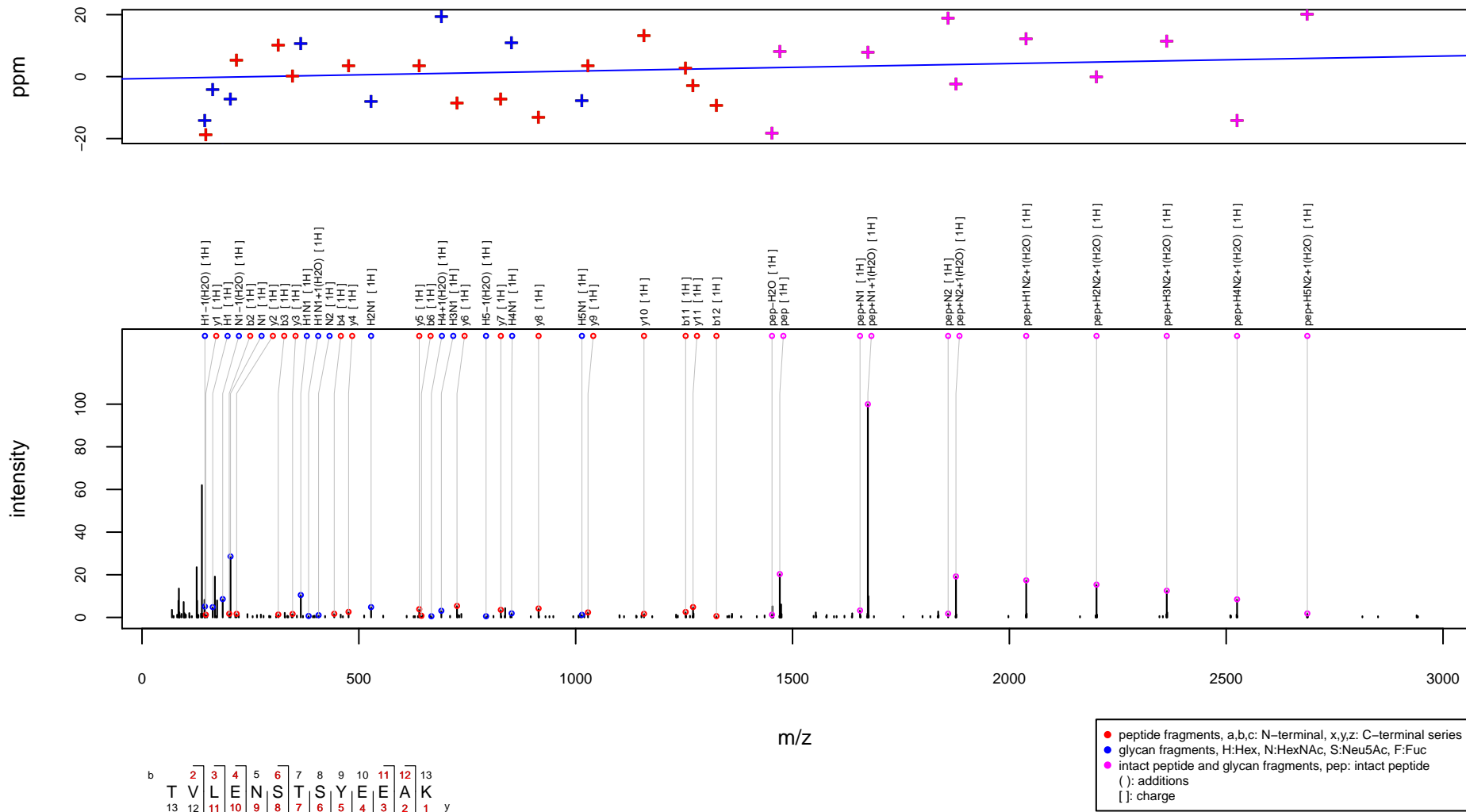
m/z 1004.4111 charge 3 scan 0-0

Score= 74.58 , Hits= 41 , Explained Intensity= 0.53

Peptide: ASAH1_HUMAN[255,267]:TVLENSTSYEEAK

Glycan: HHH(H(H)H)HNN, H7N2

Charge: 3H



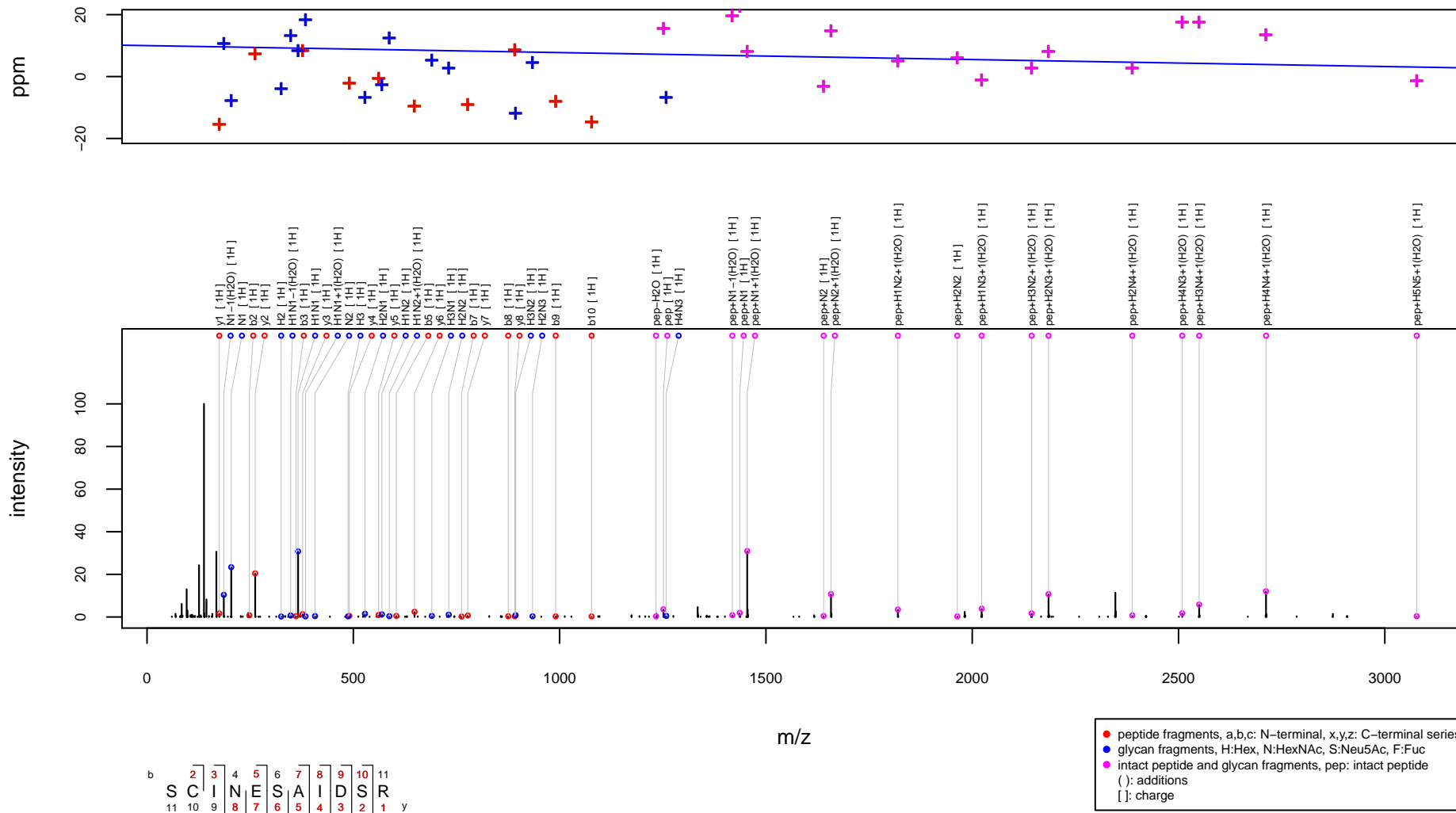
m/z 1026.4133 charge 3 scan 0-0

Score= 84.1 , Hits= 48 , Explained Intensity= 0.44

Peptide: NEP_HUMAN[142,152]:SCINESAIDSR

Glycan: HNH(HNH)(N)HNN, H5N5

Charge: 3H



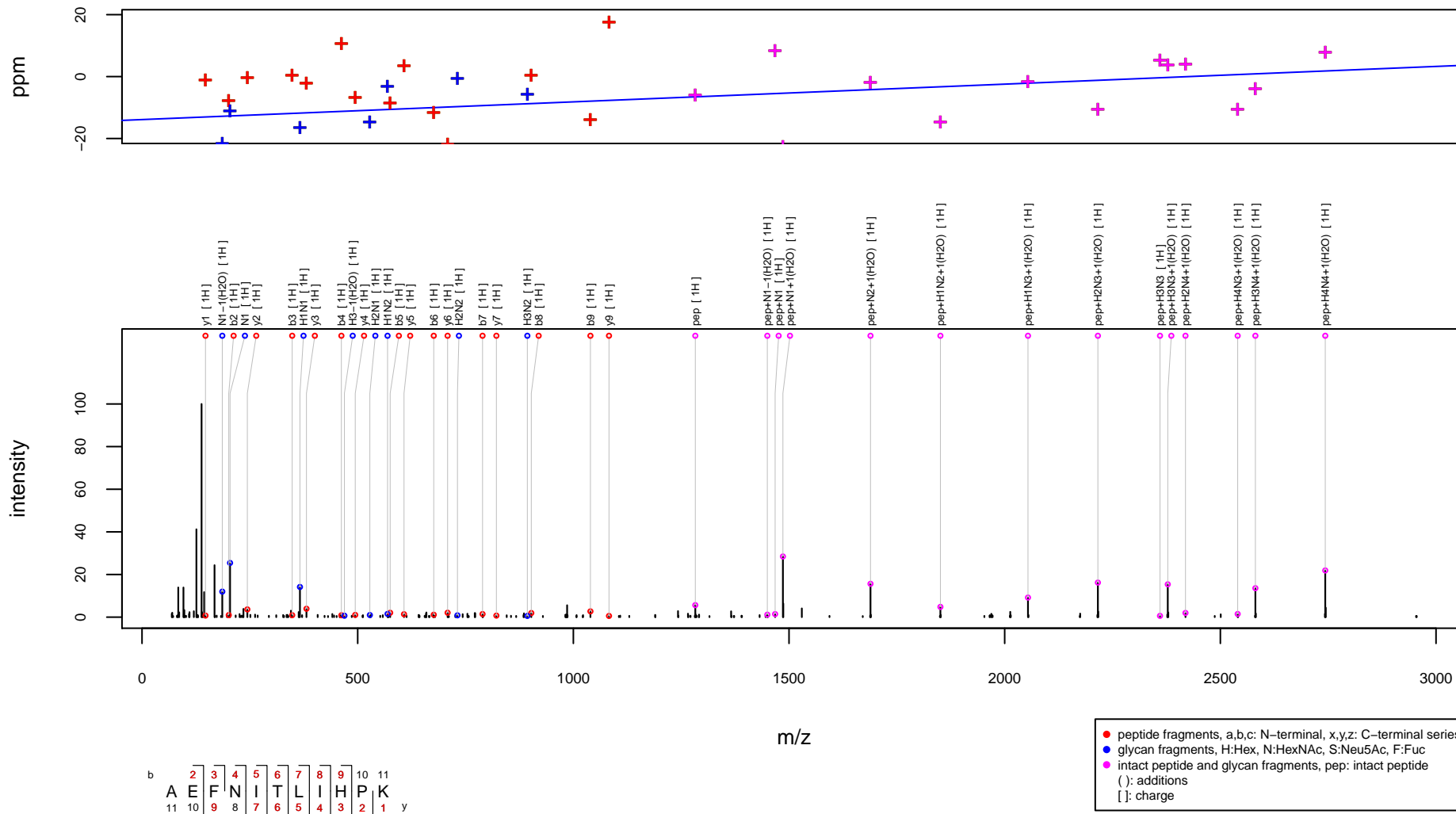
m/z 982.7845 charge 3 scan 0-0

Score= 67.55 , Hits= 38 , Explained Intensity= 0.38

Peptide: AMPN_HUMAN[231,241]:AEFNITLIHPK

Glycan: HNH(NH)(N)HNN, H4N5

Charge: 3H



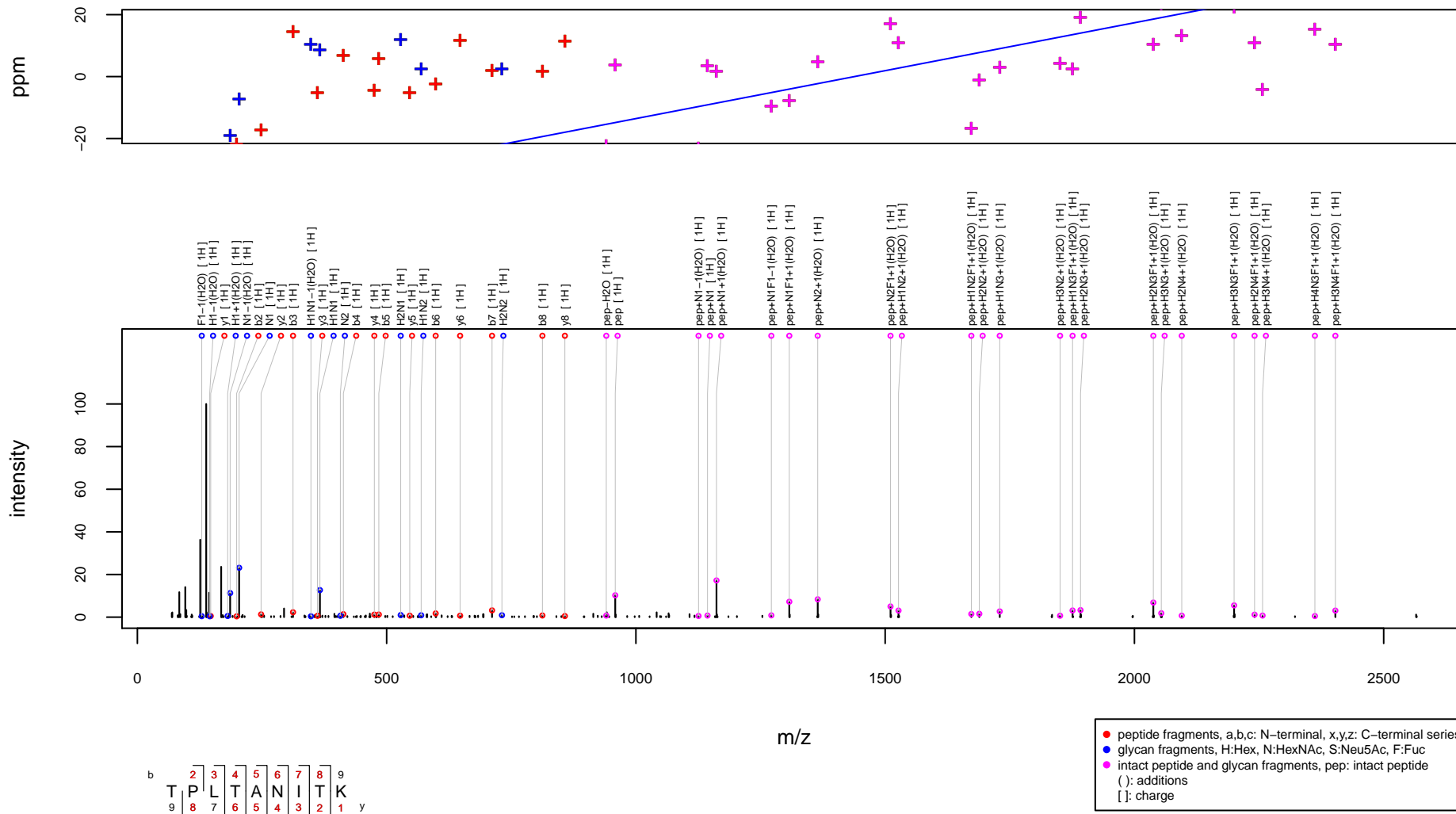
m/z 923.4094 charge 3 scan 0-0

Score= 79.93 , Hits= 49 , Explained Intensity= 0.36

Peptide: IGHA2_HUMAN[200,208]:TPLTANITK

Glycan: HNH(NH)(N)HN(F)N, H4N5F1

Charge: 3H



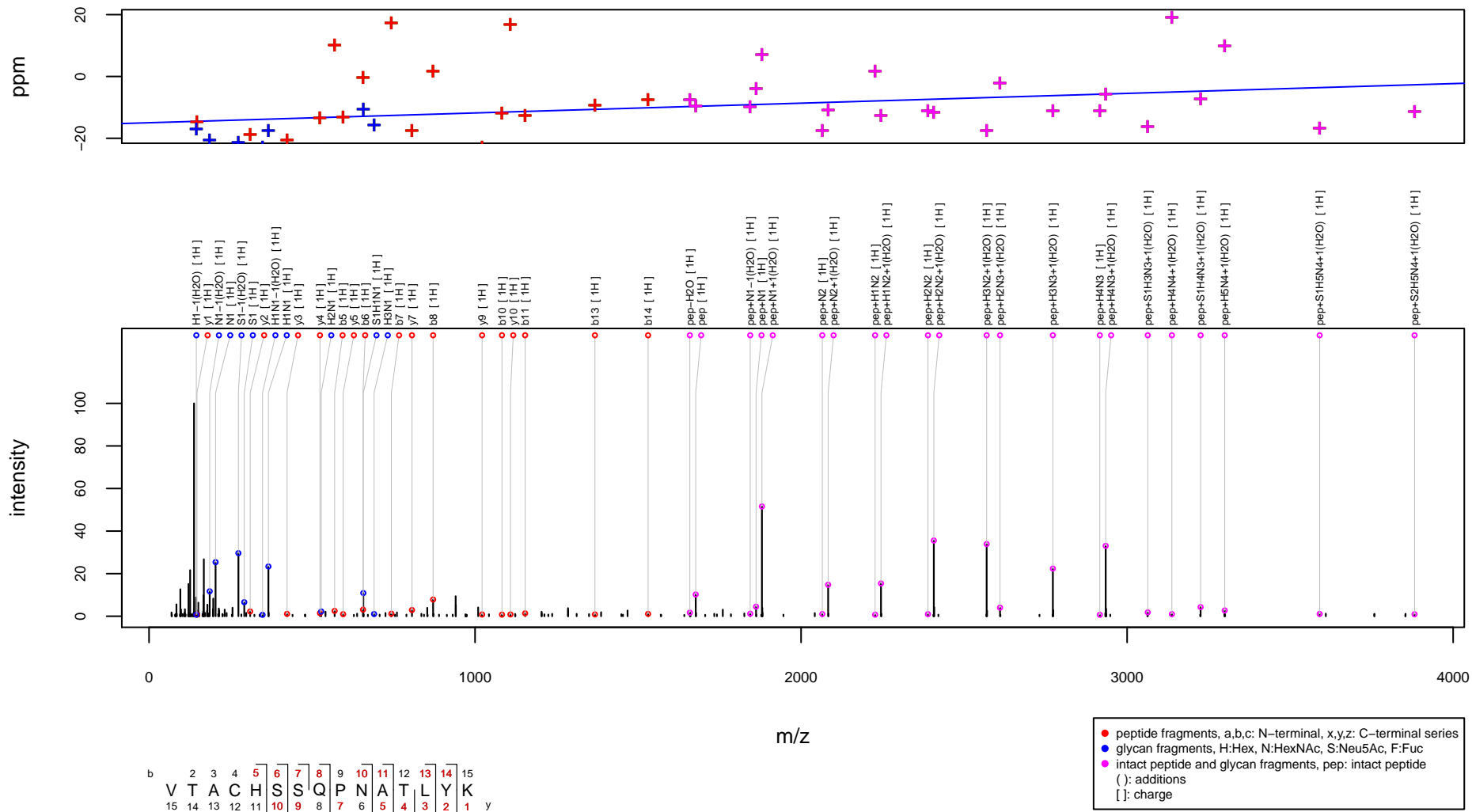
m/z 971.168 charge 4 scan 0-0

Score= 80.87 , Hits= 48 , Explained Intensity= 0.5

Peptide: THBG_HUMAN[27,41]:VTACHSSQP NATLYK

Glycan: SHNH(SHNH)HNN, S2H5N4

Charge: 4H



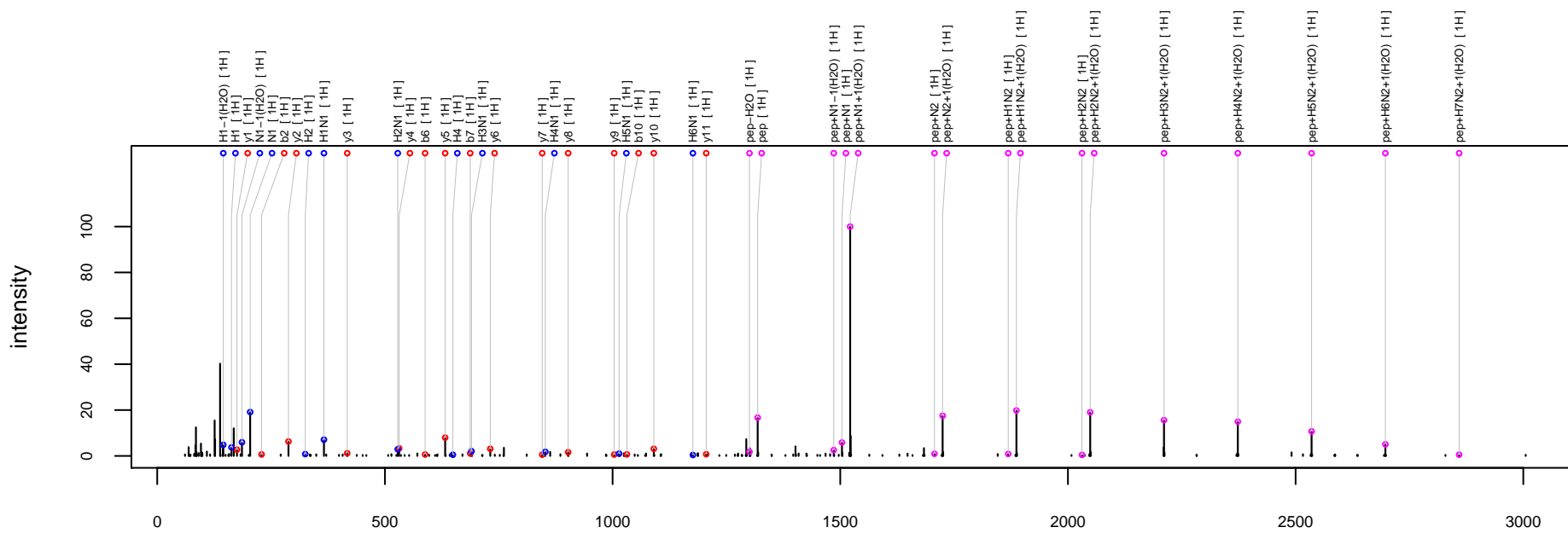
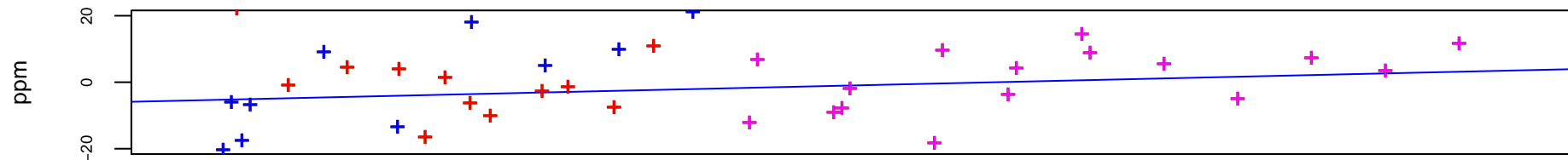
m/z 1007.7501 charge 3 scan 0-0

Score= 76.55 , Hits= 43 , Explained Intensity= 0.62

Peptide: ATRN_HUMAN[411,422]:IDSTGNVTNELR

Glycan: HHH(HH(H)H)HNN, H8N2

Charge: 3H



	2	3	4	5	6	7	8	9	10	11	12	
b	I	D	S	T	G	N	V	T	N	E	L	R
	12	11	10	9	8	7	6	5	4	3	2	1
												y

- peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
- glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
- intact peptide and glycan fragments, pep: intact peptide
- (): additions
- []: charge

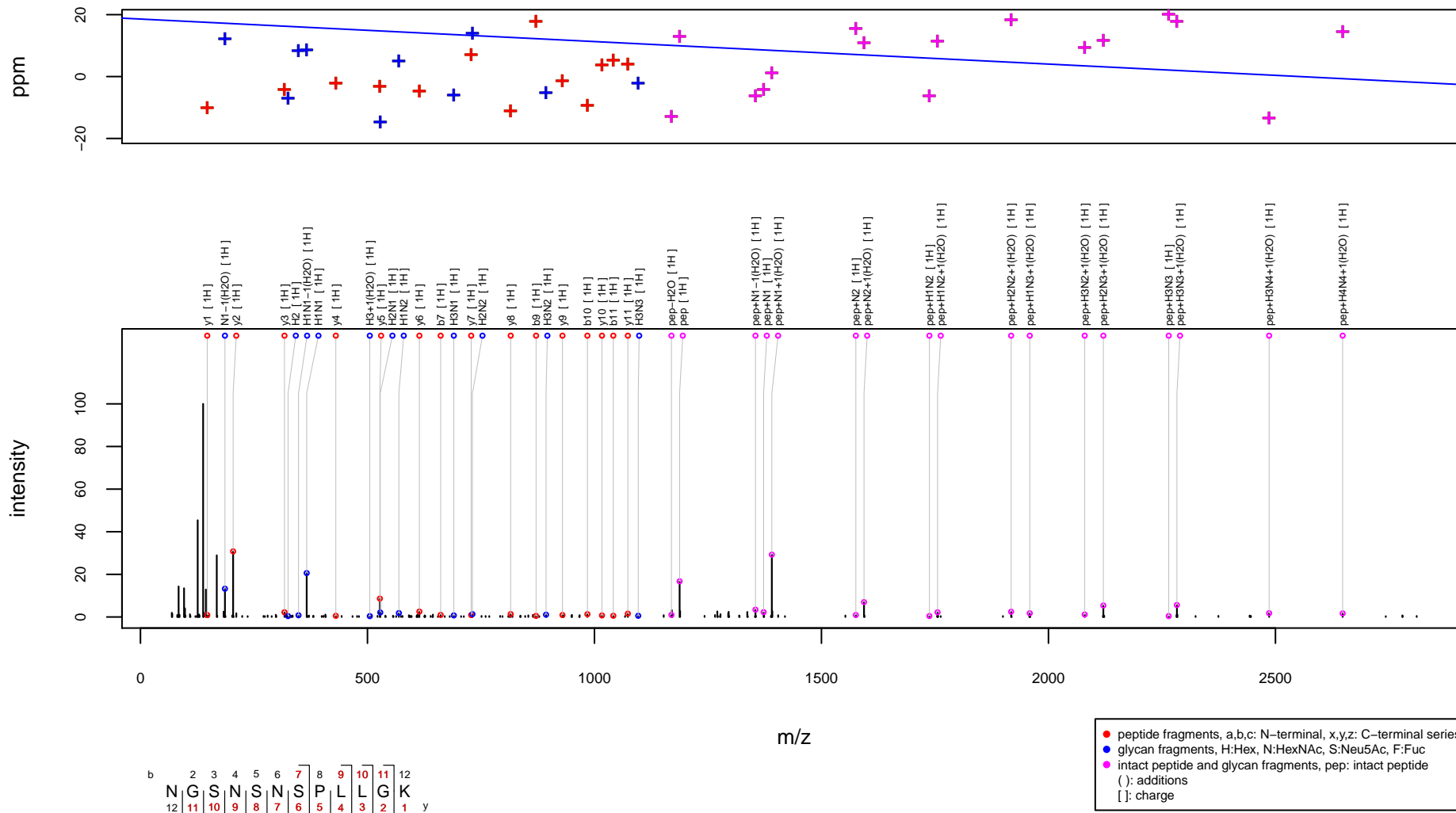
m/z 951.073 charge 3 scan 0-0

Score= 74.48 , Hits= 43 , Explained Intensity= 0.39

Peptide: CUBN_HUMAN[3457,3468]:NGSNSNSPLL GK

Glycan: HNH(NH)(N)HNN, H4N5

Charge: 3H



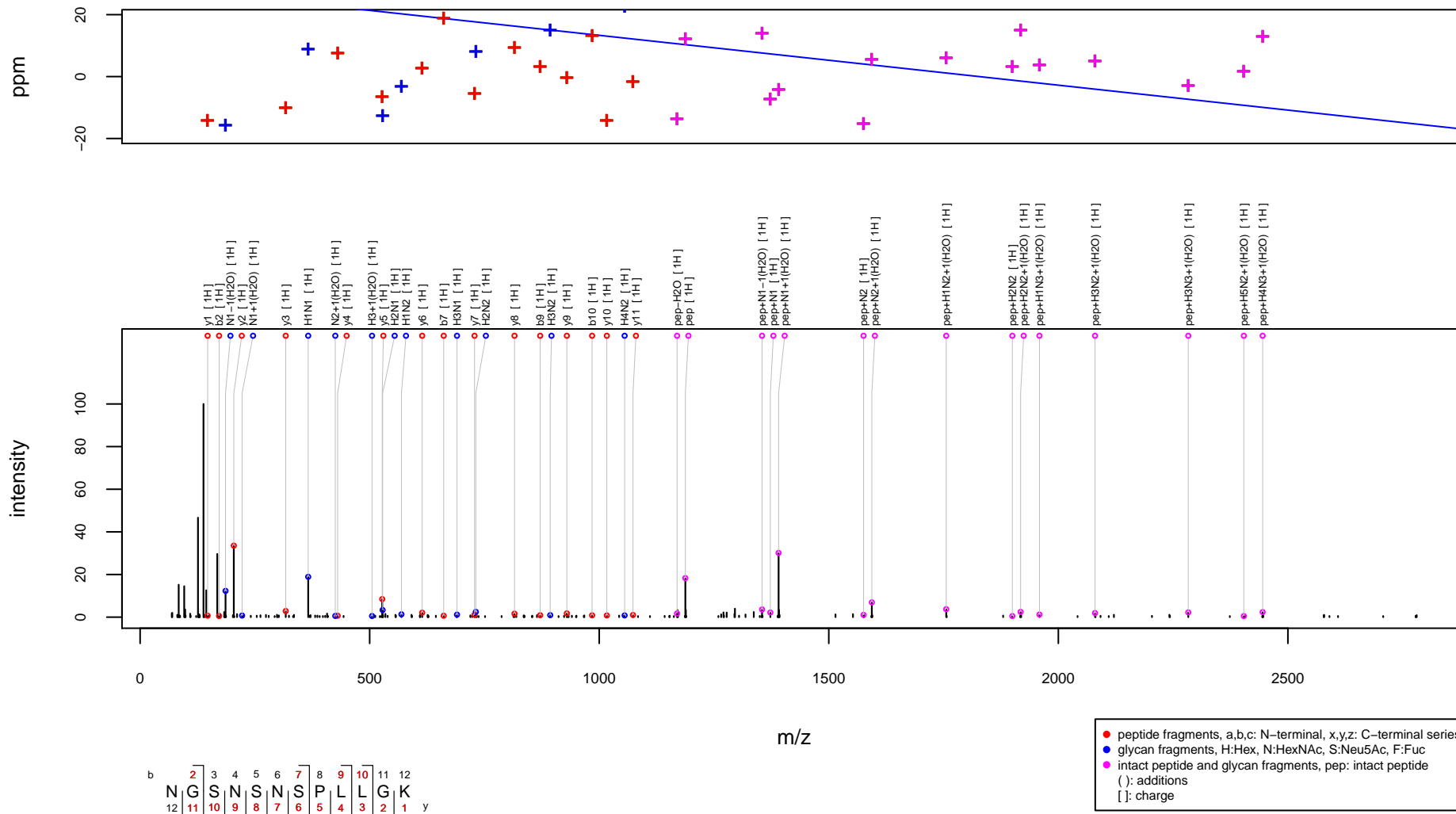
m/z 937.3969 charge 3 scan 0-0

Score= 68.86 , Hits= 41 , Explained Intensity= 0.36

Peptide: CUBN_HUMAN[3457,3468]:NGSNSNSPLL GK

Glycan: H5N4

Charge: 3H



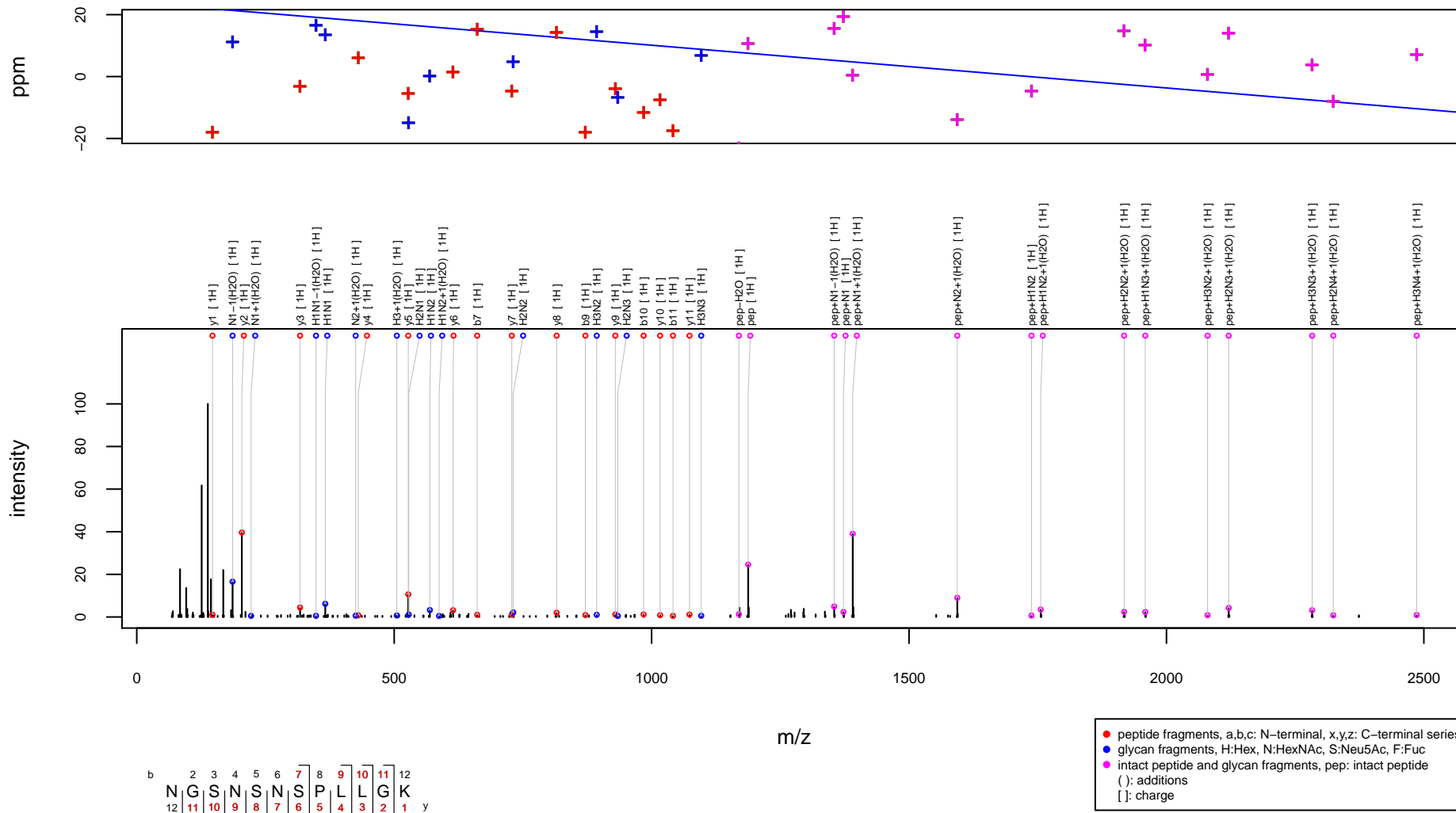
m/z 897.0562 charge 3 scan 0-0

Score= 77.29 , Hits= 43 , Explained Intensity= 0.38

Peptide: CUBN_HUMAN[3457,3468]:NGSNSNSPLL GK

Glycan: NH(NH)(N)HNN, H3N5

Charge: 3H



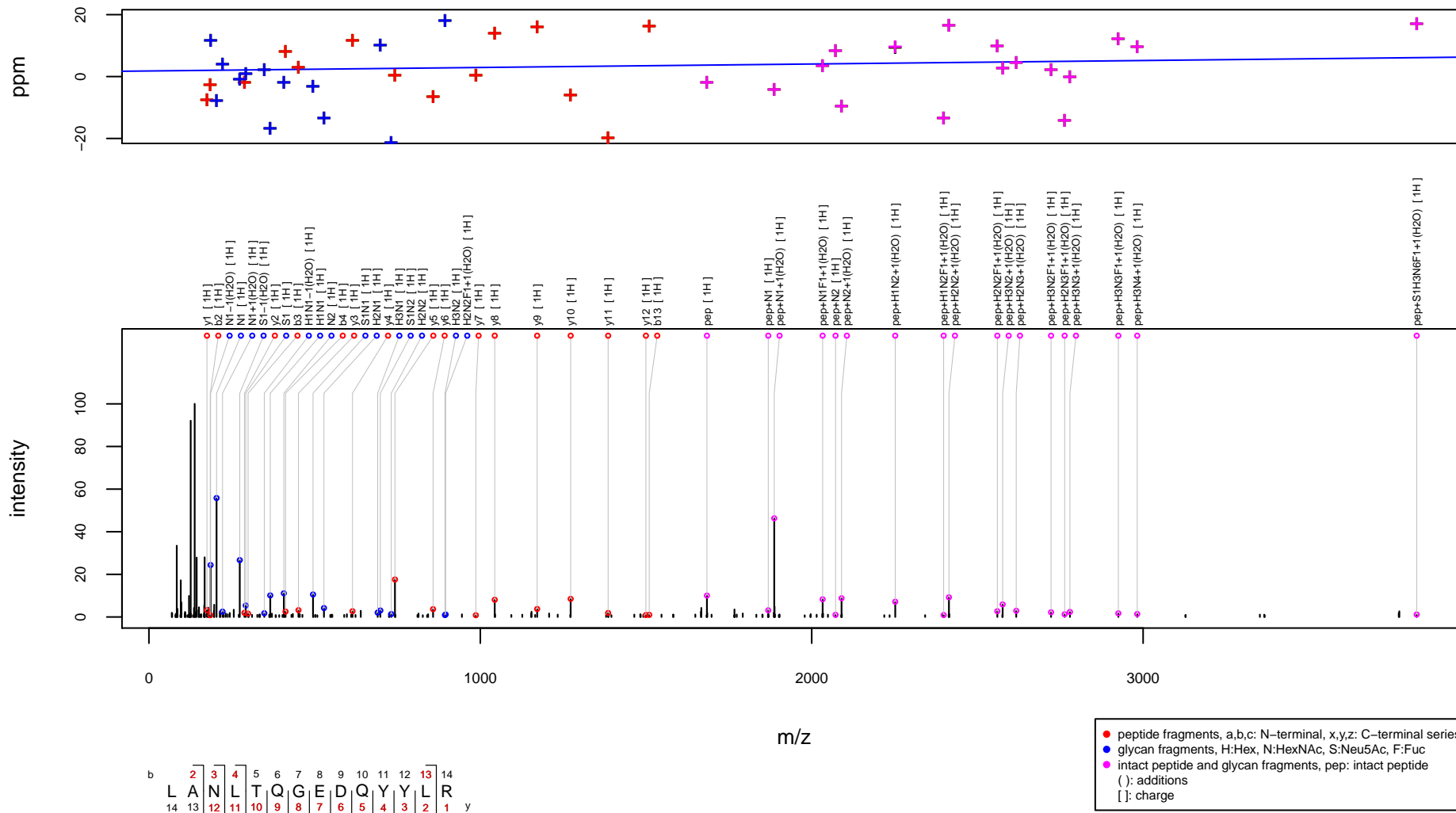
m/z 957.1561 charge 4 scan 0-0

Score= 76.36 , Hits= 49 , Explained Intensity= 0.42

Peptide: CLUS_HUMAN[372,385]:LANLTQGEDQYYLR

Glycan: SNNH(NNH)HN(F)N, S1H3N6F1

Charge: 4H



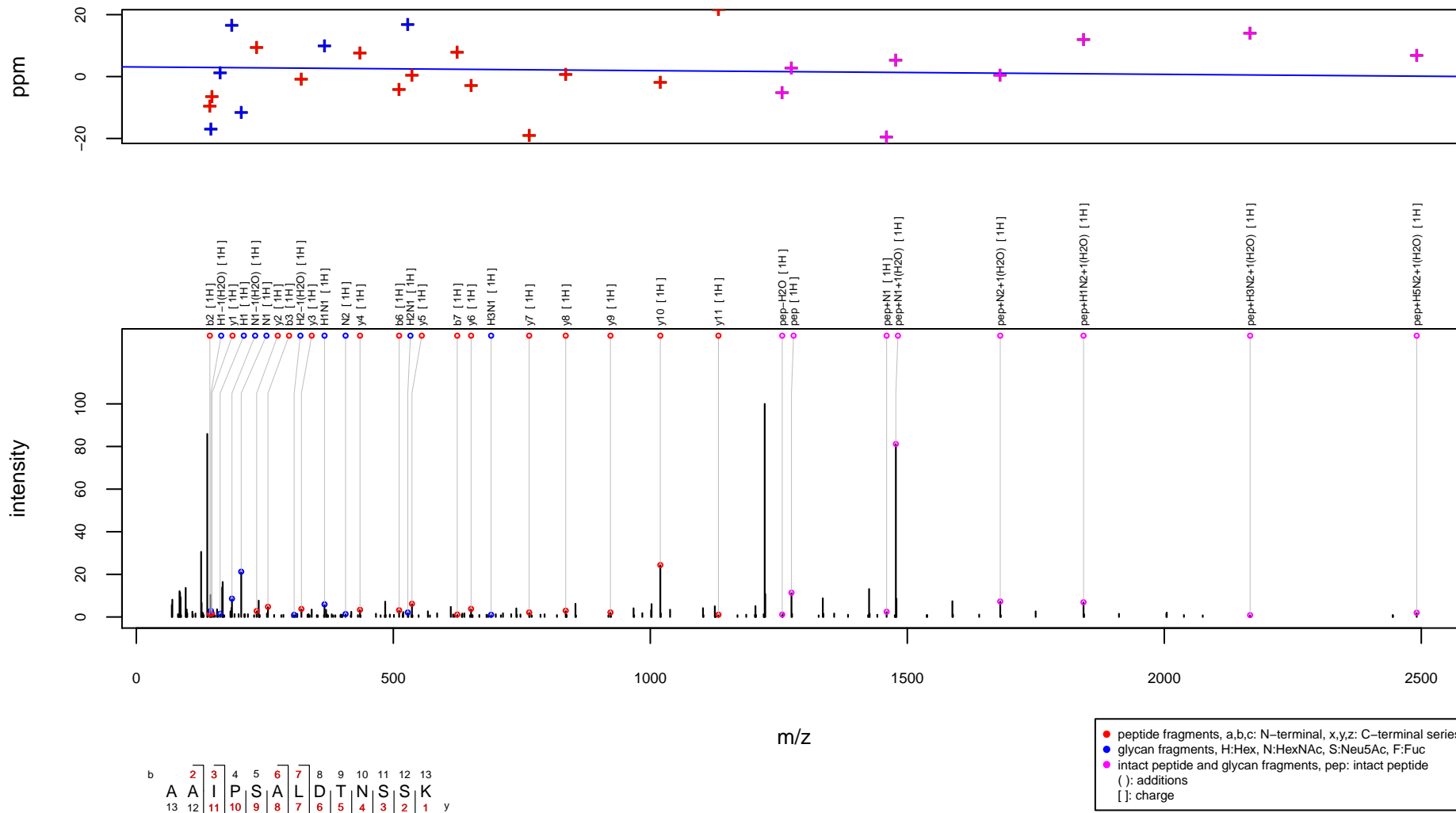
m/z 831.0299 charge 3 scan 0-0

Score= 56.74 , Hits= 32 , Explained Intensity= 0.29

Peptide: LG3BP_HUMAN[542,554]:AAIP³SALD³TNSSK

Glycan: H(H)H(H)HNN, H5N2

Charge: 3H



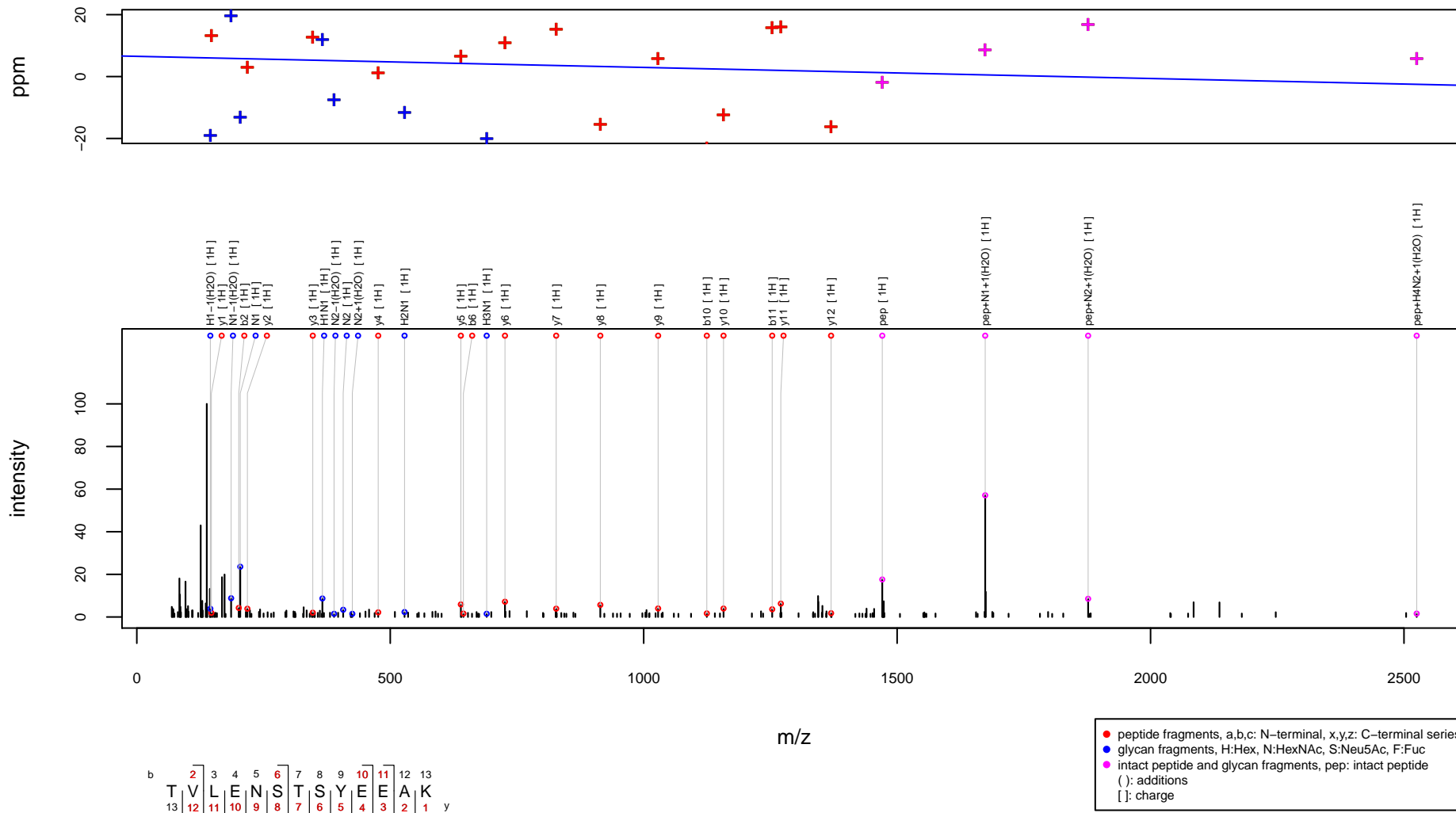
m/z 842.3589 charge 3 scan 0-0

Score= 52.37 , Hits= 29 , Explained Intensity= 0.25

Peptide: ASAH1_HUMAN[255,267]:TVLENSTSYEEAK

Glycan: HH(H)HNN, H4N2

Charge: 3H



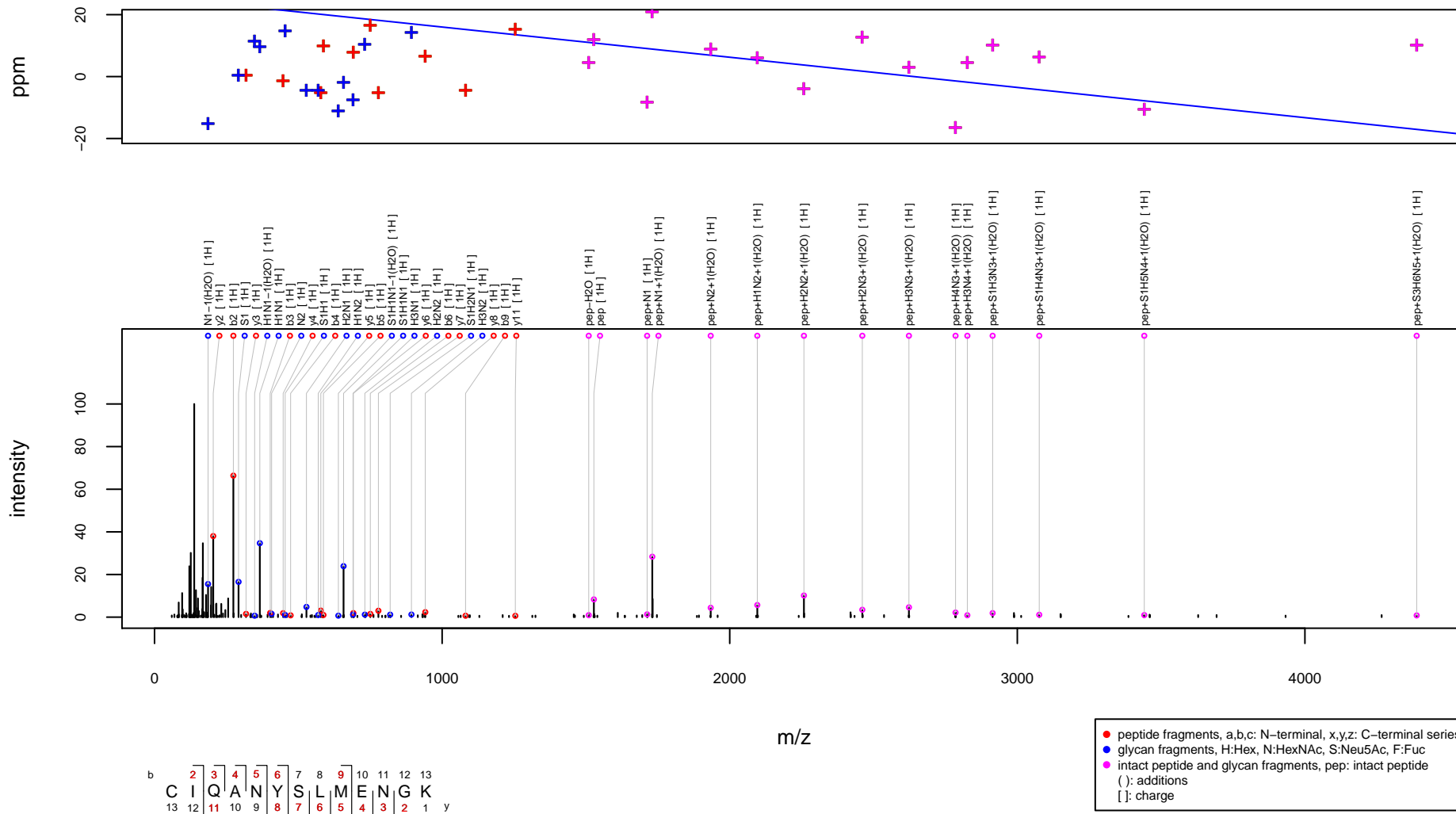
m/z 1097.9324 charge 4 scan 0-0

Score= 65.11 , Hits= 43 , Explained Intensity= 0.44

Peptide: APOD_HUMAN[61,73]:CIQANYSLMENGK

Glycan: SHNH(SHN(SHN)H)HNN, S3H6N5

Charge: 4H



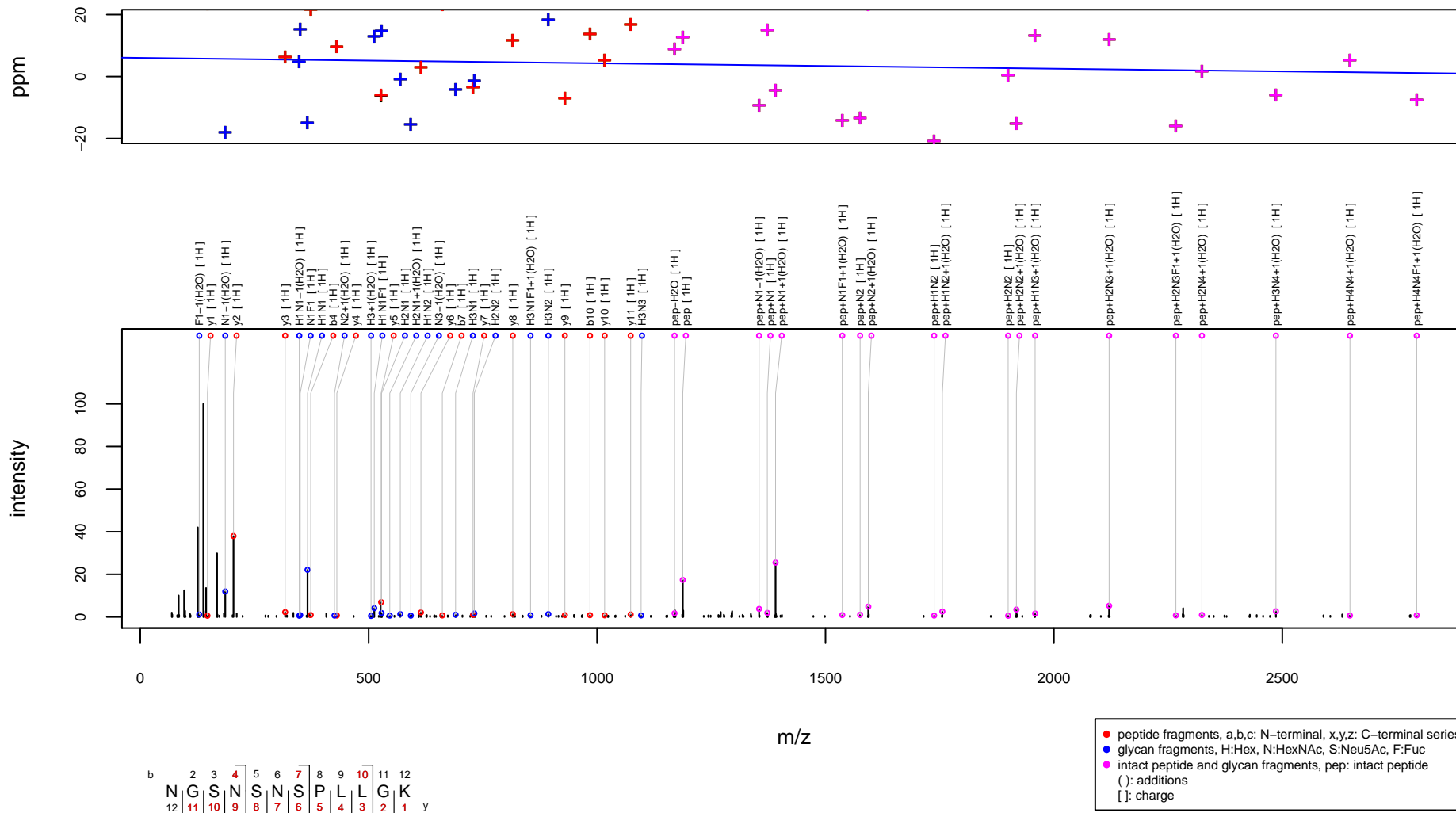
m/z 999.7589 charge 3 scan 0-0

Score= 73.85 , Hits= 50 , Explained Intensity= 0.39

Peptide: CUBN_HUMAN[3457,3468]:NGSNSNSPLL GK

Glycan: H4N5F1

Charge: 3H



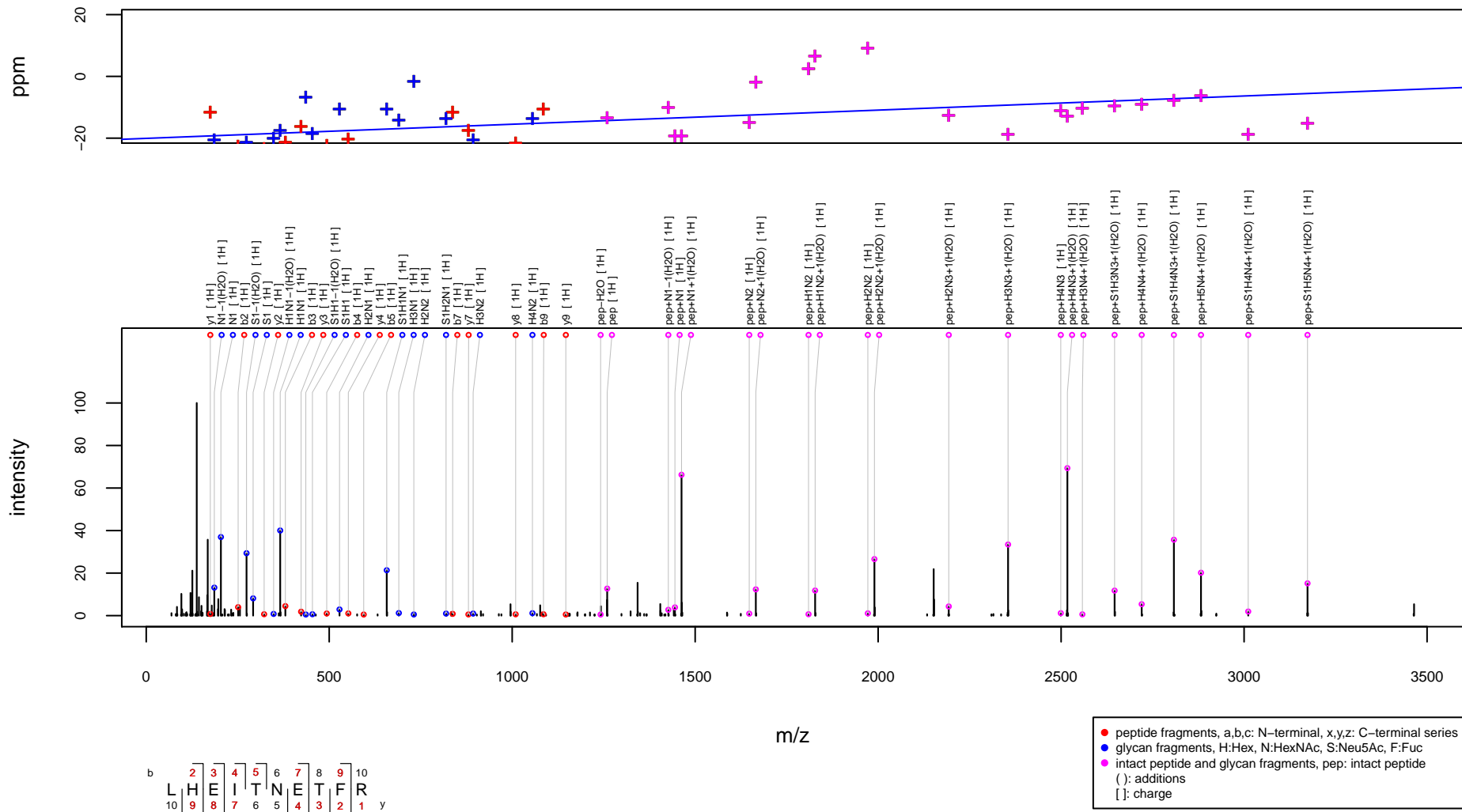
m/z 1155.495 charge 3 scan 0-0

Score= 85.96 , Hits= 50 , Explained Intensity= 0.55

Peptide: VASN_HUMAN[112,121]:LHEITNETFR

Glycan: SHNH(SHNH)HNN, S2H5N4

Charge: 3H



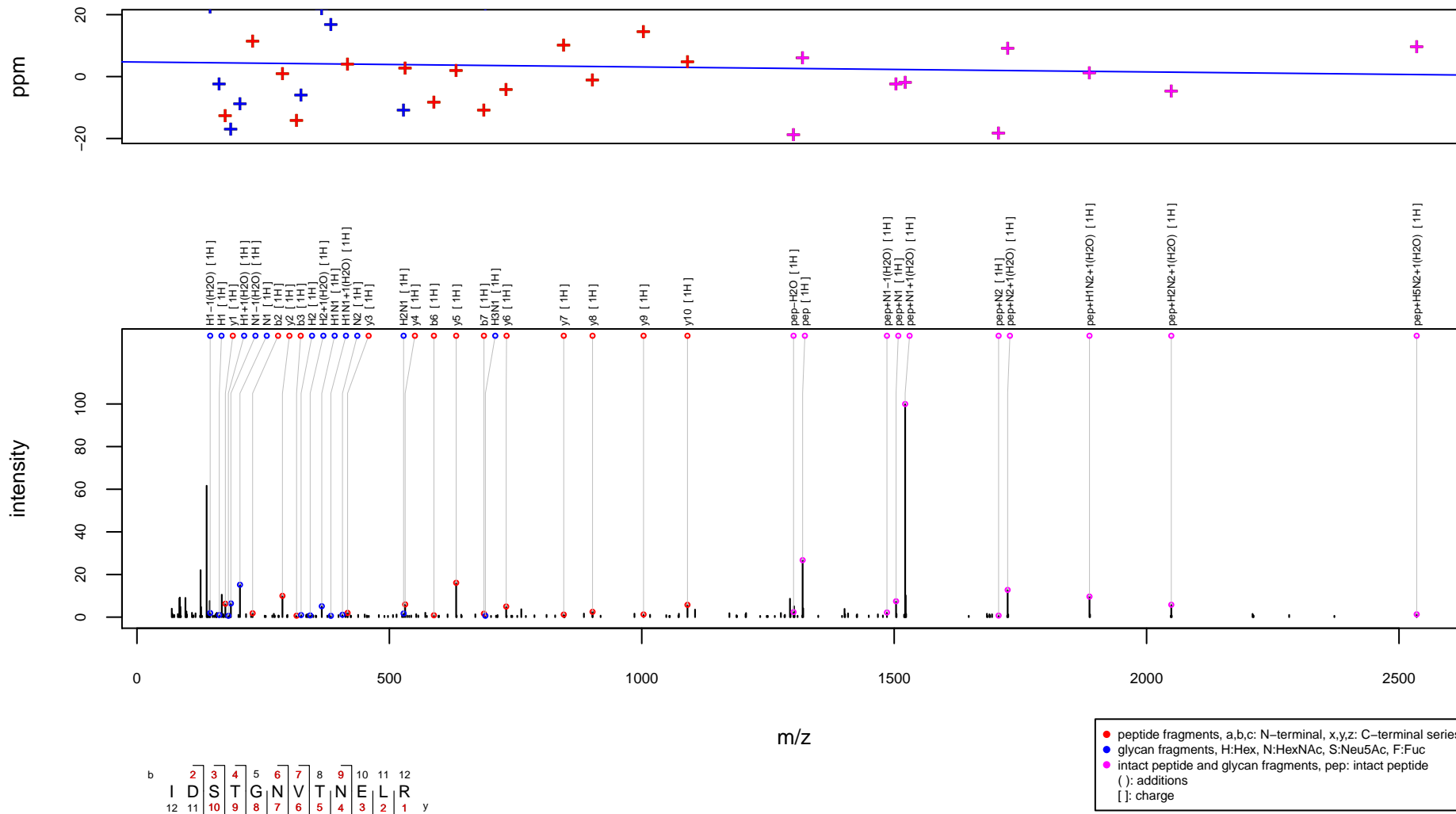
m/z 845.6984 charge 3 scan 0-0

Score= 65.17 , Hits= 36 , Explained Intensity= 0.5

Peptide: ATRN_HUMAN[411,422]:IDSTGNVTNELR

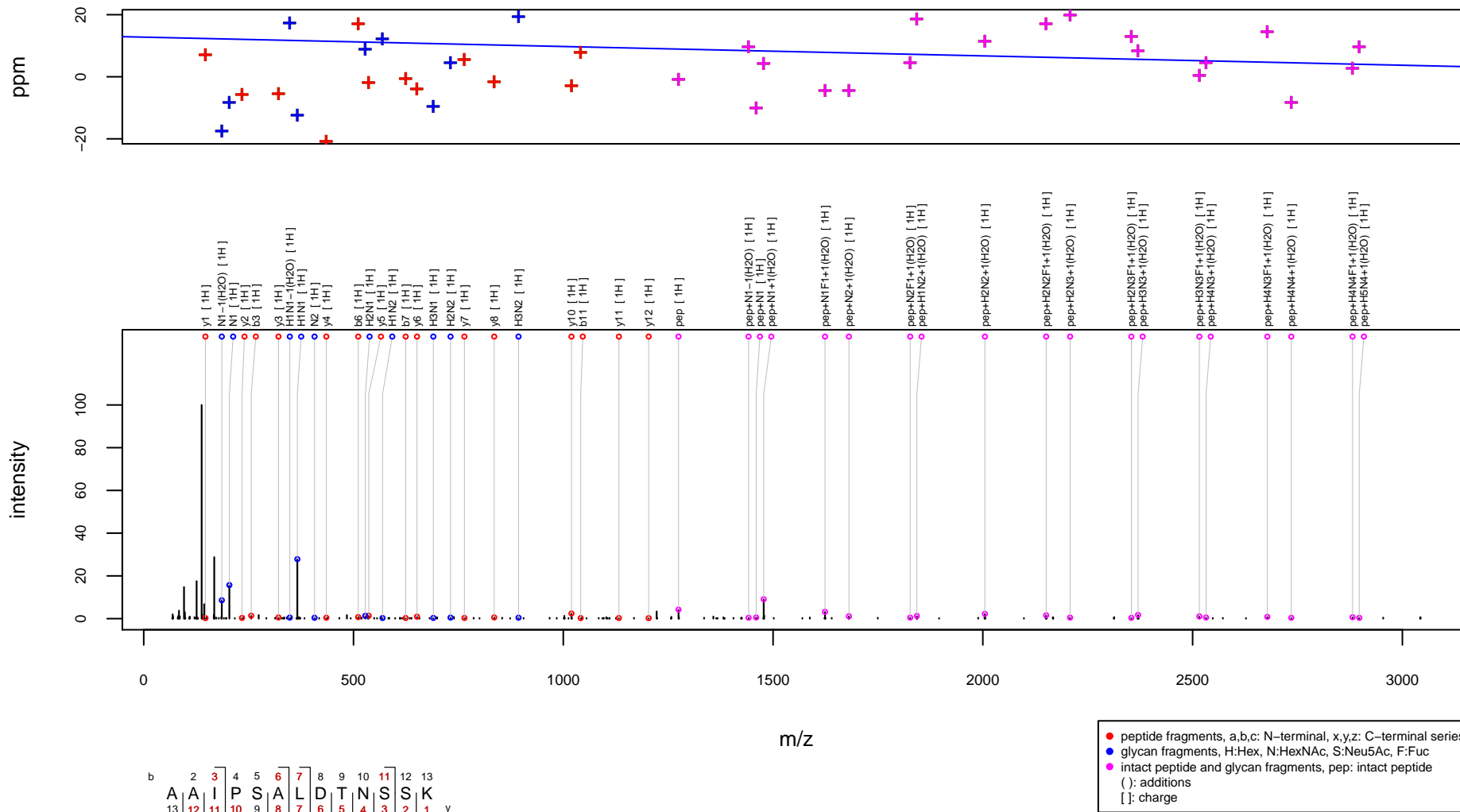
Glycan: H(H)H(H)HNN, H5N2

Charge: 3H



m/z 944.1437 charge 4 scan 0-0

Score= 62.05 , Hits= 44 , Explained Intensity= 0.29
 Peptide: LG3BP_HUMAN[542,554]:AAIPSAALDTNSSK
 Glycan: HN(HN)H(HN(HN)H)HN(F)N, H7N6F1
 Charge: 4H



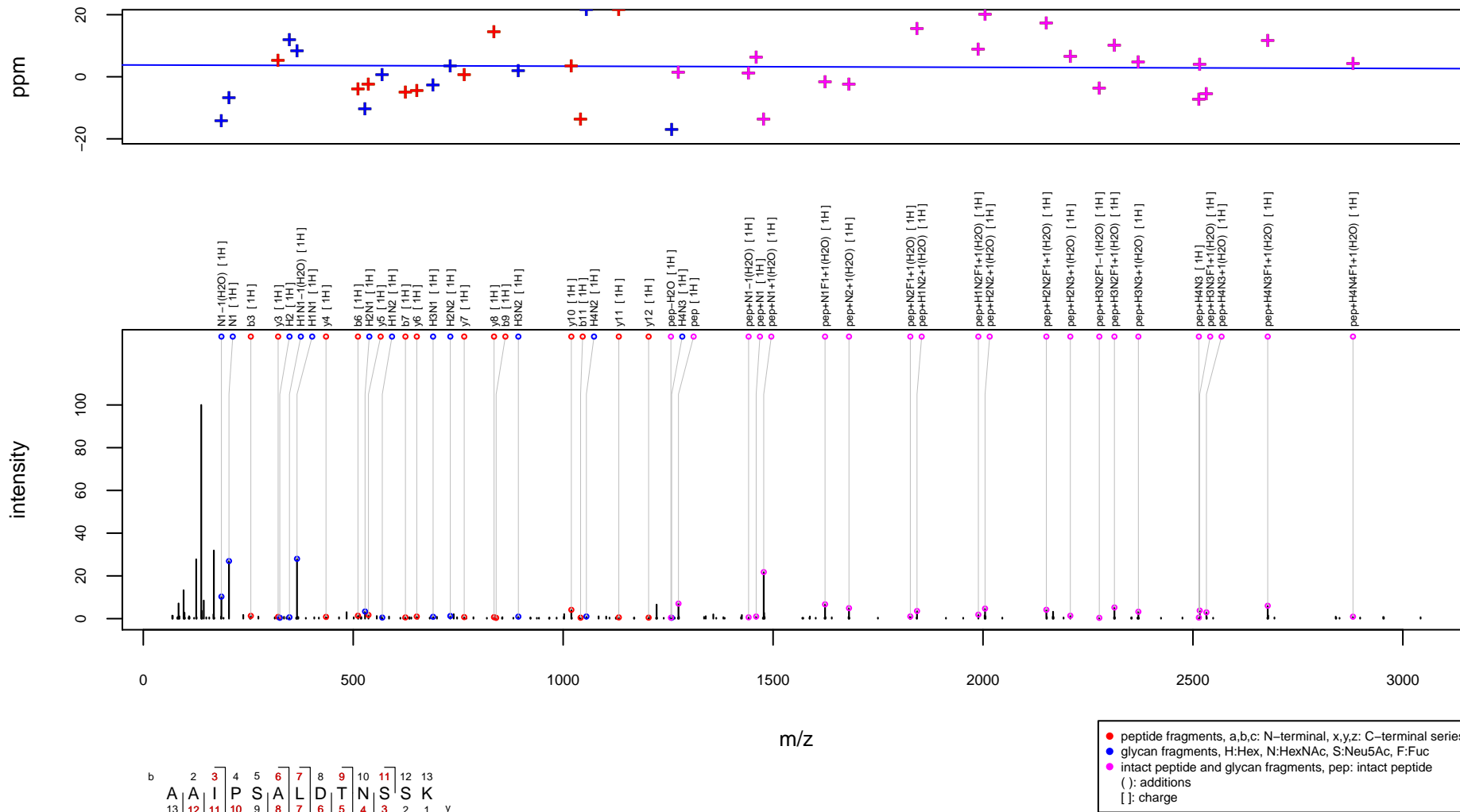
m/z 1015.101 charge 3 scan 0-0

Score= 74.82 , Hits= 47 , Explained Intensity= 0.38

Peptide: LG3BP_HUMAN[542,554]:AAIPSAALDTNSK

Glycan: HNH(HNH)HN(F)N, H5N4F1

Charge: 3H



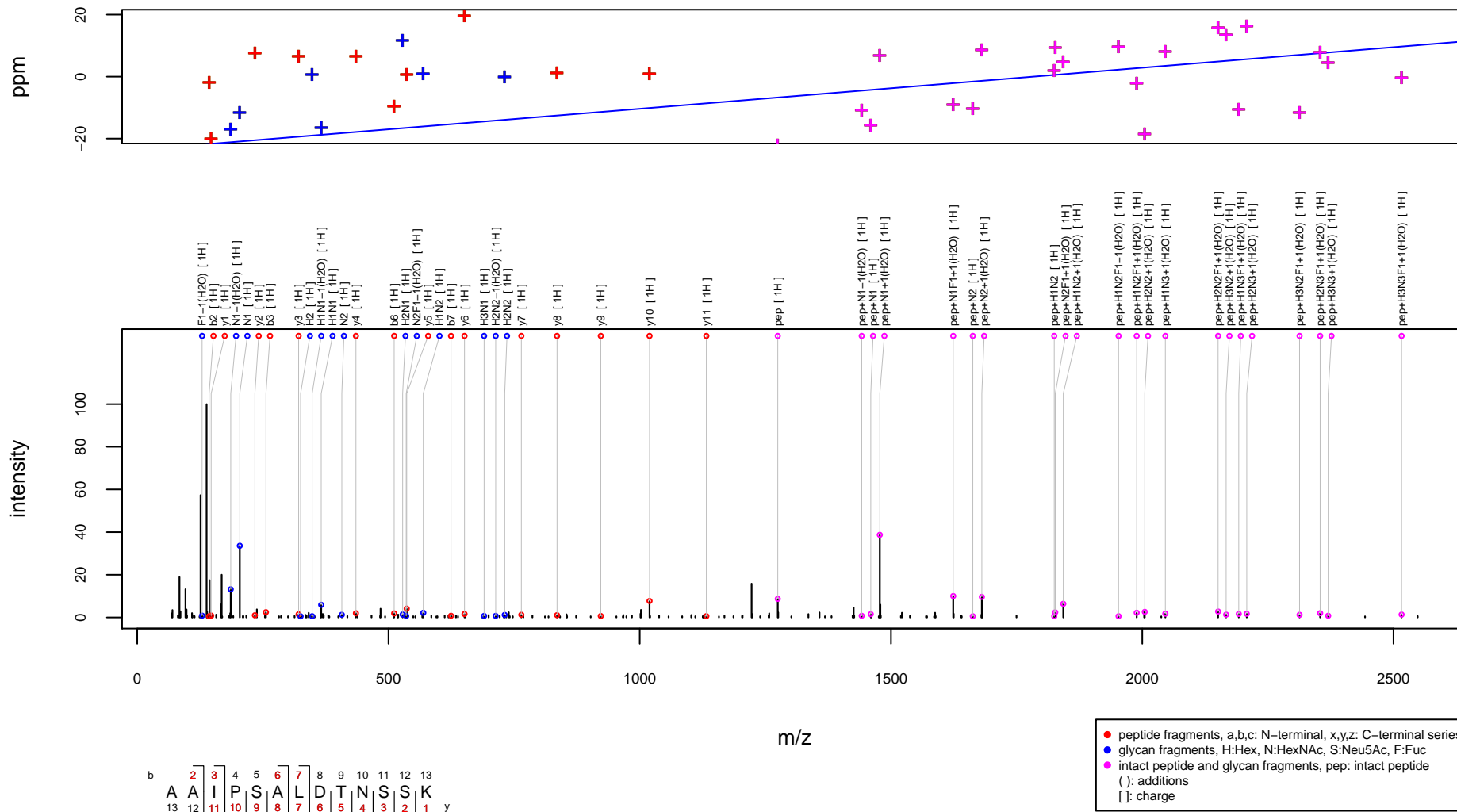
m/z 907.0682 charge 3 scan 0-0

Score= 81.76 , Hits= 50 , Explained Intensity= 0.34

Peptide: LG3BP_HUMAN[542,554]:AAIPSAALDITNSISK

Glycan: NH(N)(H)HN(F)N, H3N4F1

Charge: 3H



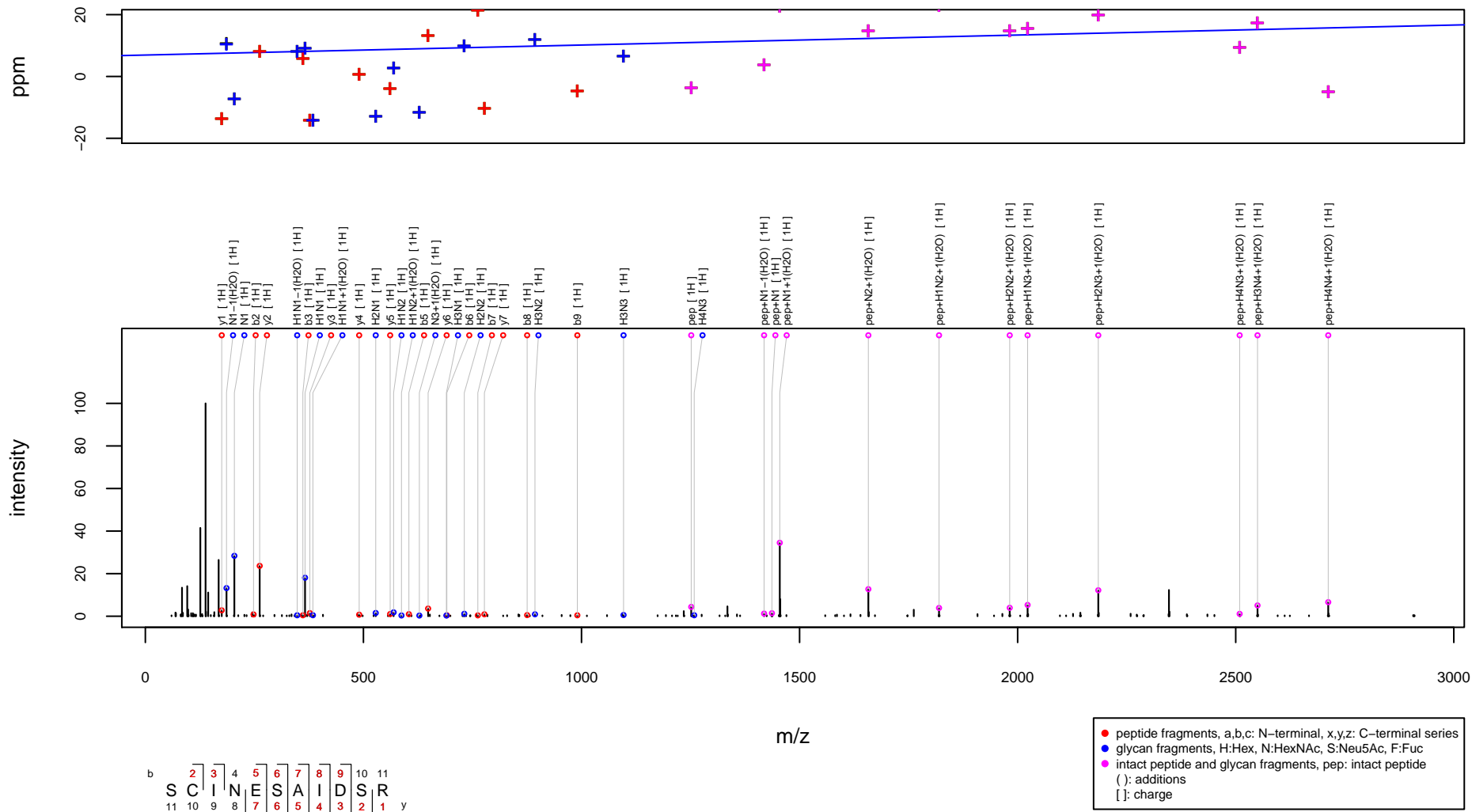
m/z 972.3946 charge 3 scan 0-0

Score= 67.03 , Hits= 40 , Explained Intensity= 0.4

Peptide: NEP_HUMAN[142,152]:SCINESAIDSR

Glycan: H4N5

Charge: 3H



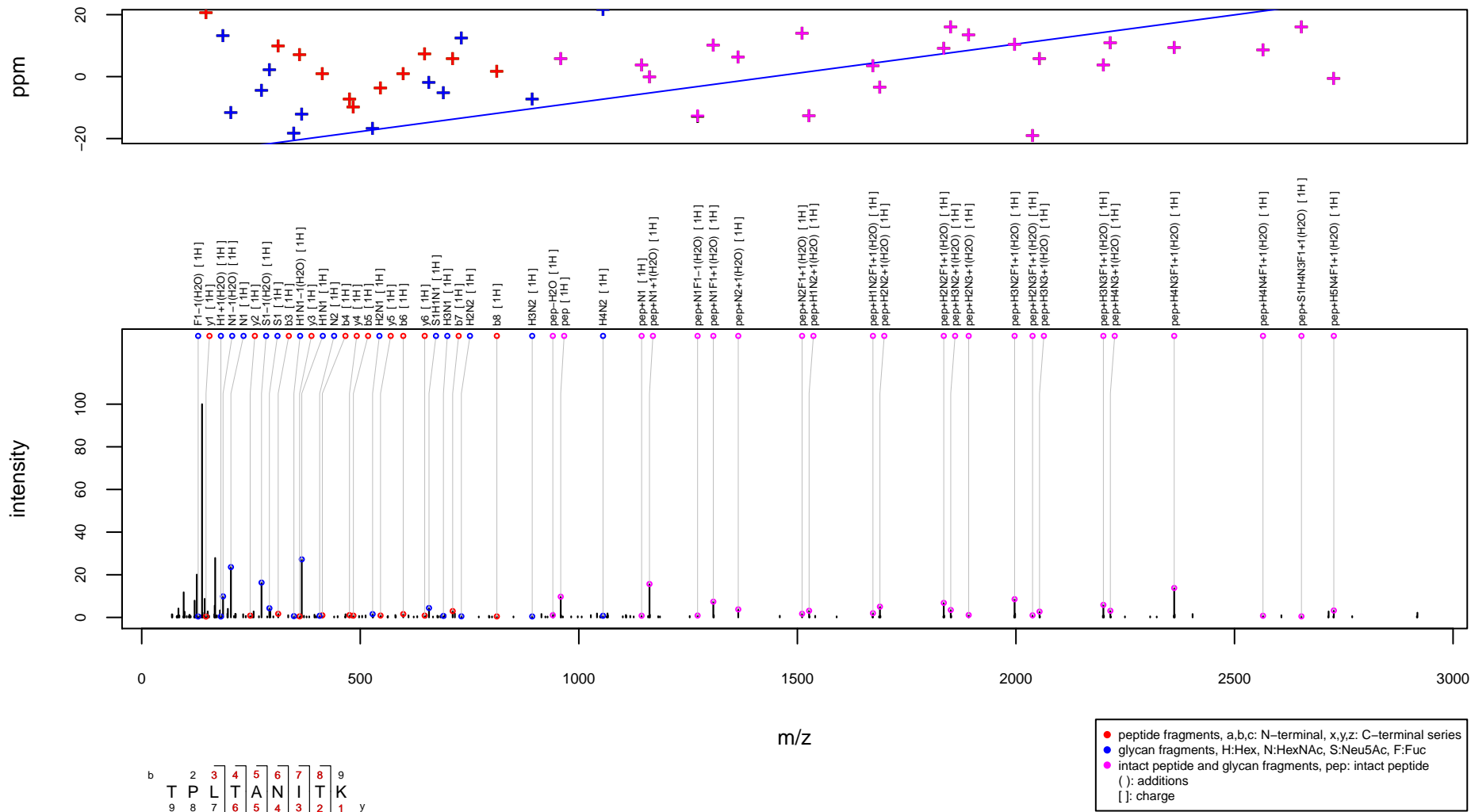
m/z 1006.767 charge 3 scan 0-0

Score= 75.78 , Hits= 50 , Explained Intensity= 0.41

Peptide: IGHA2_HUMAN[200,208]:TPLTANITK

Glycan: SHNH(HNH)HN(F)N, S1H5N4F1

Charge: 3H



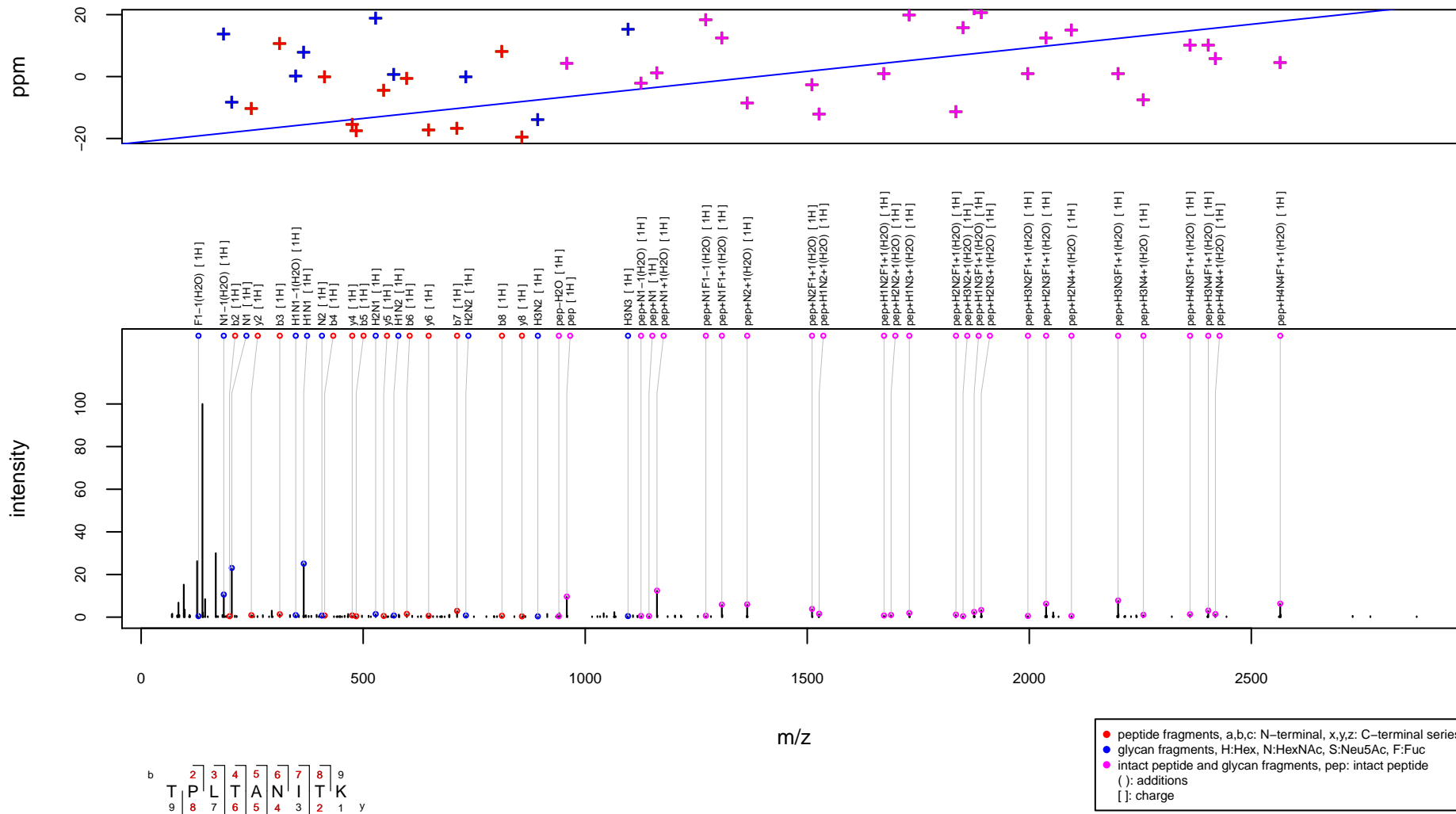
m/z 977.4273 charge 3 scan 0-0

Score= 75.04 , Hits= 49 , Explained Intensity= 0.37

Peptide: IGHA2_HUMAN[200,208]:TPLTANITK

Glycan: HNH(HNH)(N)HN(F)N, H5N5F1

Charge: 3H



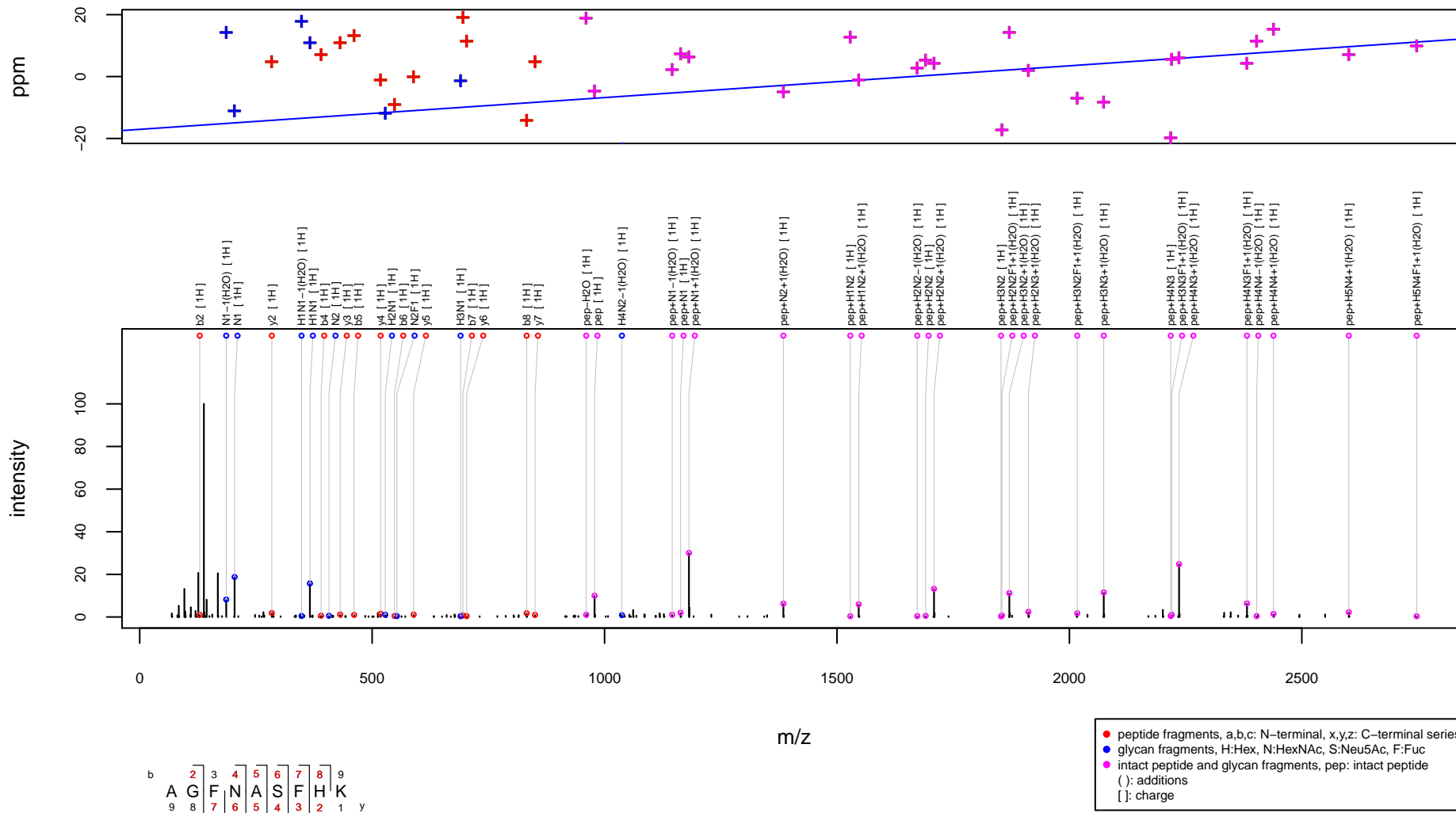
m/z 916.3778 charge 3 scan 0-0

Score= 74.75 , Hits= 46 , Explained Intensity= 0.42

Peptide: CUBN_HUMAN[2082,2090]:AGFNASFHK

Glycan: HNH(HNH)HN(F)N, H5N4F1

Charge: 3H



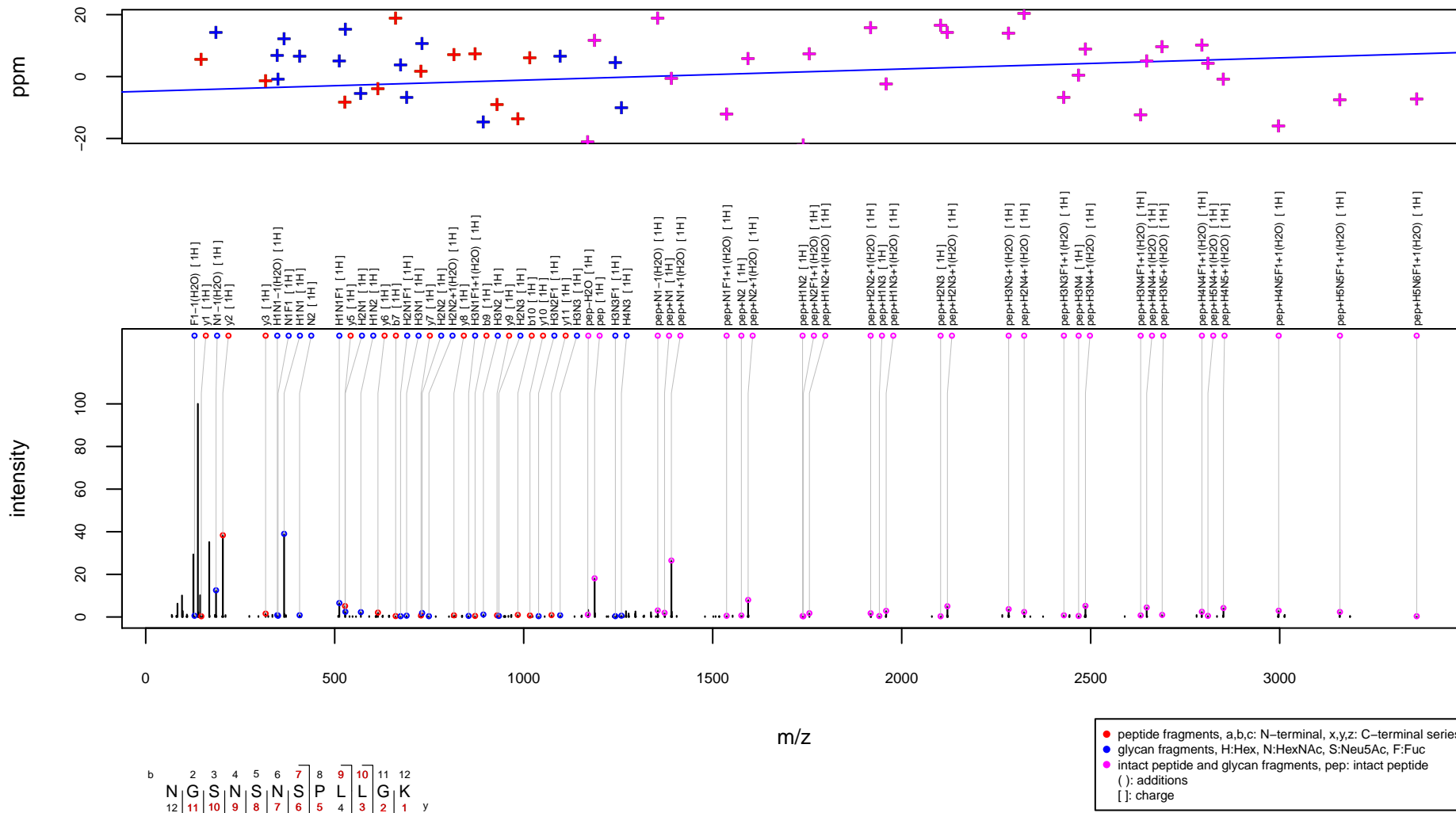
m/z 1121.4678 charge 3 scan 0-0

Score= 88.03 , Hits= 63 , Explained Intensity= 0.5

Peptide: CUBN_HUMAN[3457,3468]:NGSNSNSPLL GK

Glycan: H5N6F1

Charge: 3H



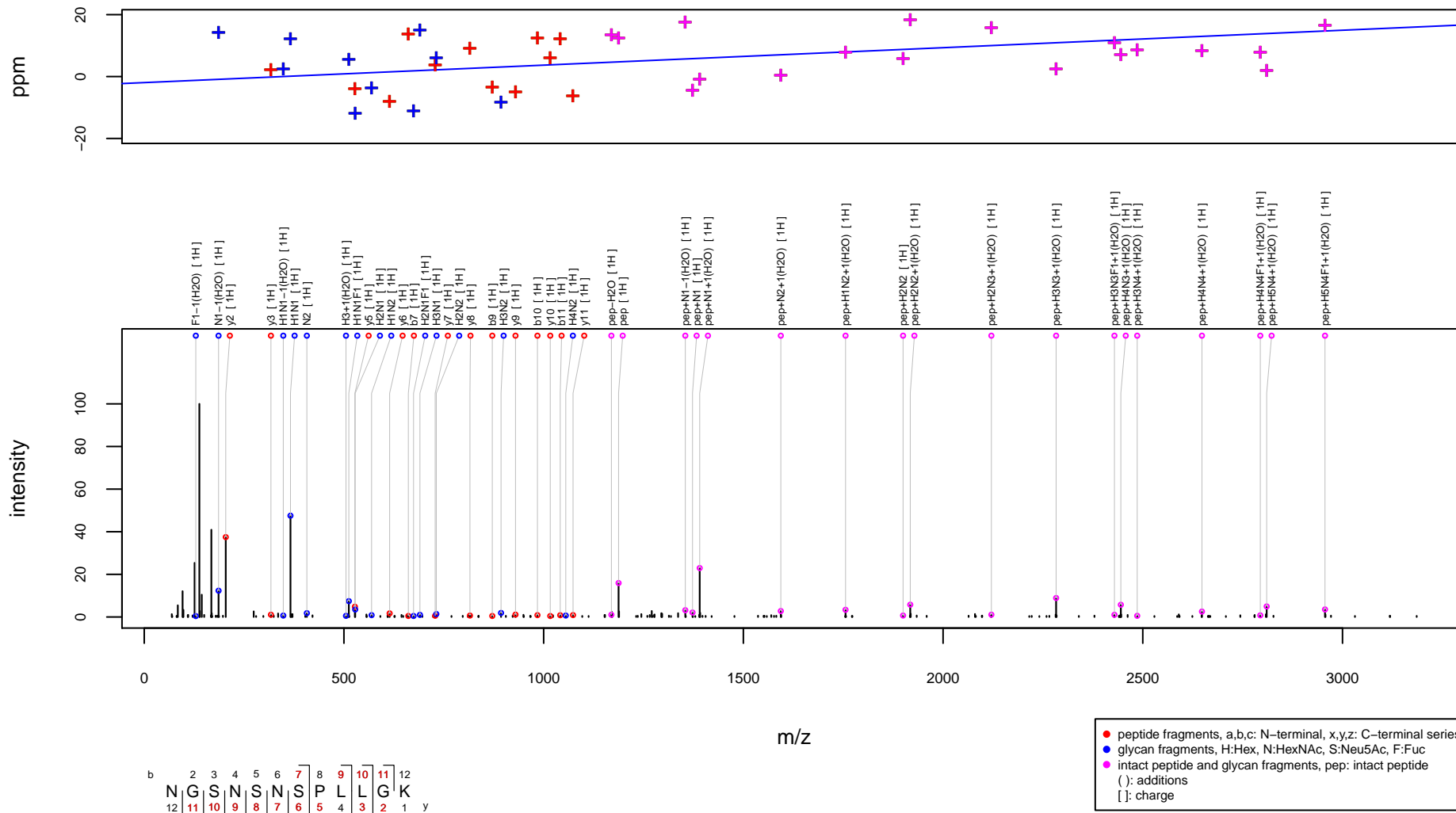
m/z 1107.7909 charge 3 scan 0-0

Score= 68.02 , Hits= 45 , Explained Intensity= 0.45

Peptide: CUBN_HUMAN[3457,3468]:NGSNSNSPLL GK

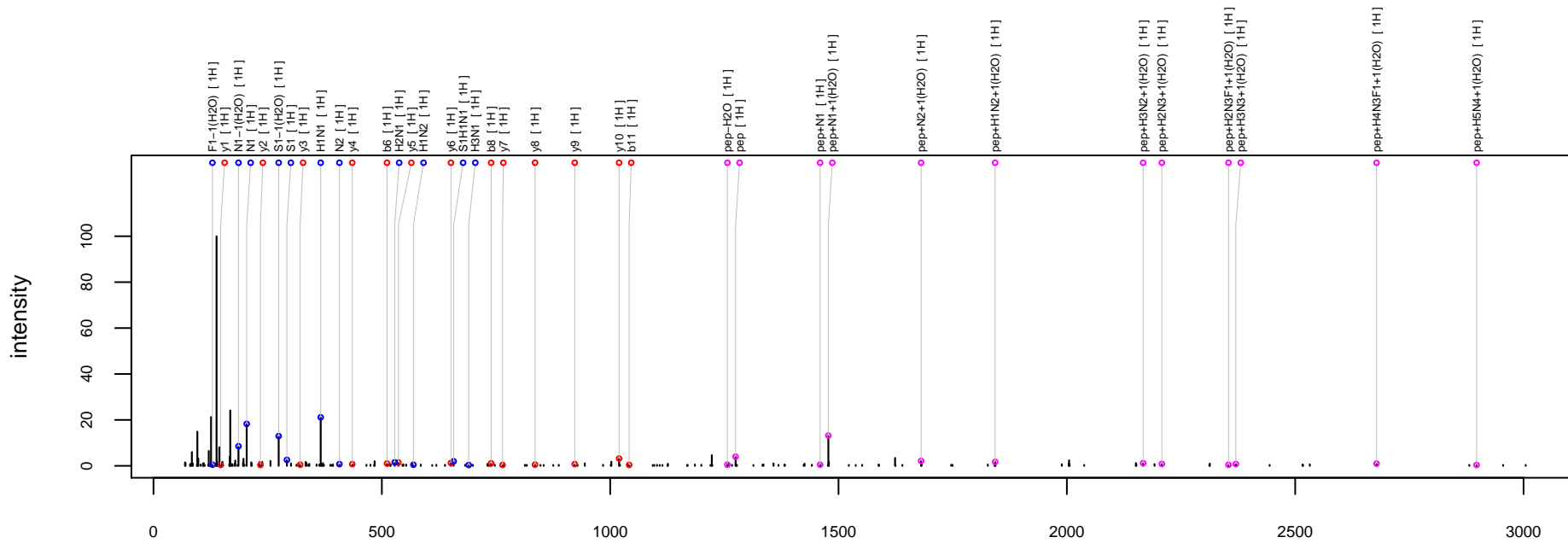
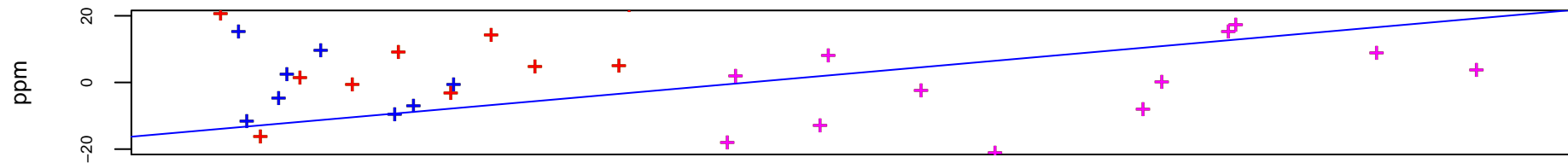
Glycan: HNHNH(F(H)NH)HNN, H6N5F1

Charge: 3H



m/z 925.6379 charge 4 scan 0-0

Score= 49.73 , Hits= 36 , Explained Intensity= 0.27
 Peptide: LG3BP_HUMAN[542,554]:AAIP¹SALD²TNS³SK
 Glycan: SHNHNH(F(H)NH)HNN, S1H6N5F1
 Charge: 4H



b 2 3 4 5 6 7 8 9 10 11 12 13
 A A I P S A L D T N S S K
 13 12 11 [10] [9] [8] [7] [6] [5] [4] [3] [2] [1] y

● peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
 ● glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
 ● intact peptide and glycan fragments, pep: intact peptide
 (): additions
 []: charge

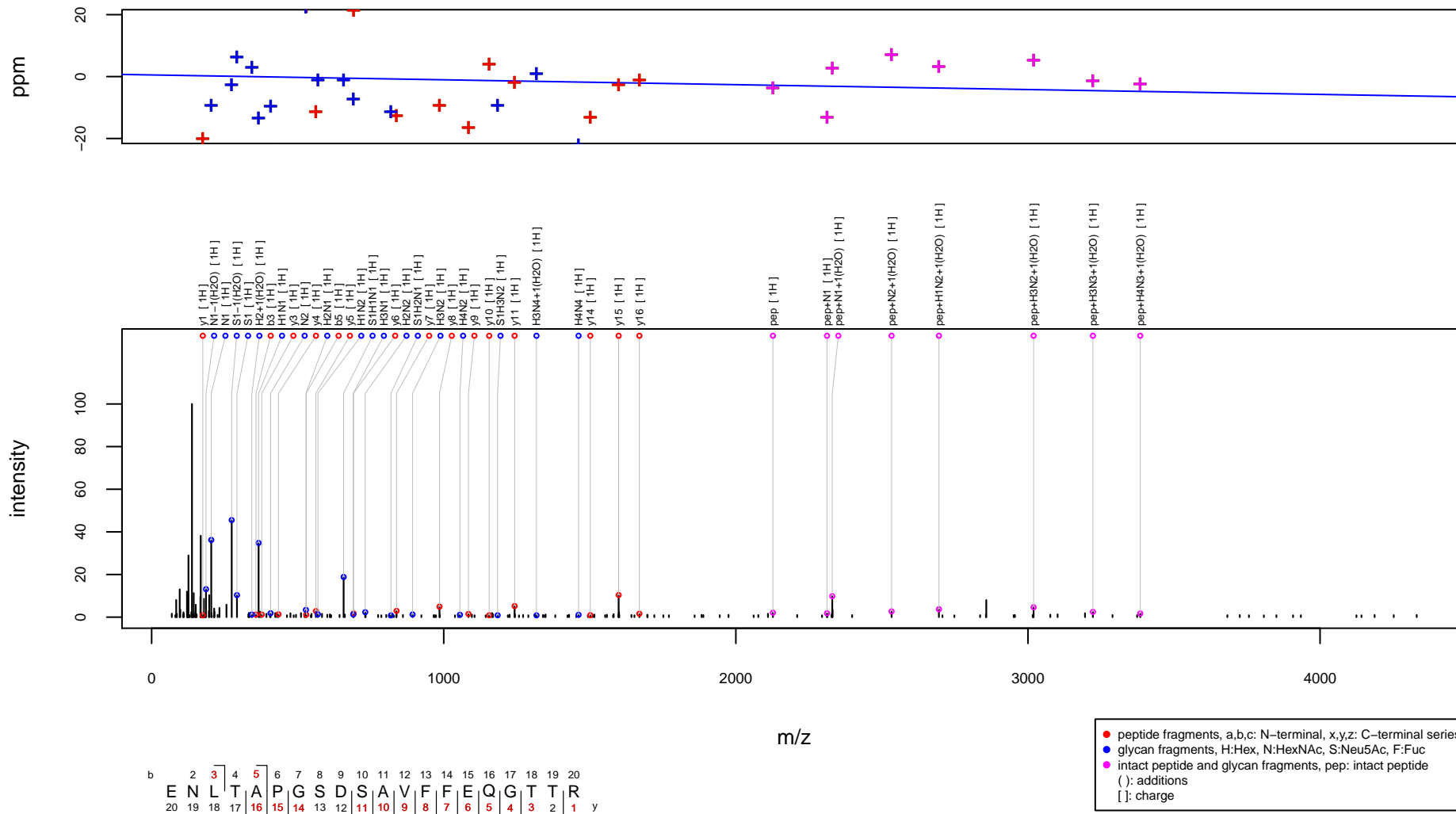
m/z 1083.699 charge 4 scan 0-0

Score= 64.04 , Hits= 41 , Explained Intensity= 0.37

Peptide: CERU_HUMAN[396,415]:ENLTAPGSDSAVFFEQGTTTR

Glycan: SHNH(SHNH)HNN, S2H5N4

Charge: 4H



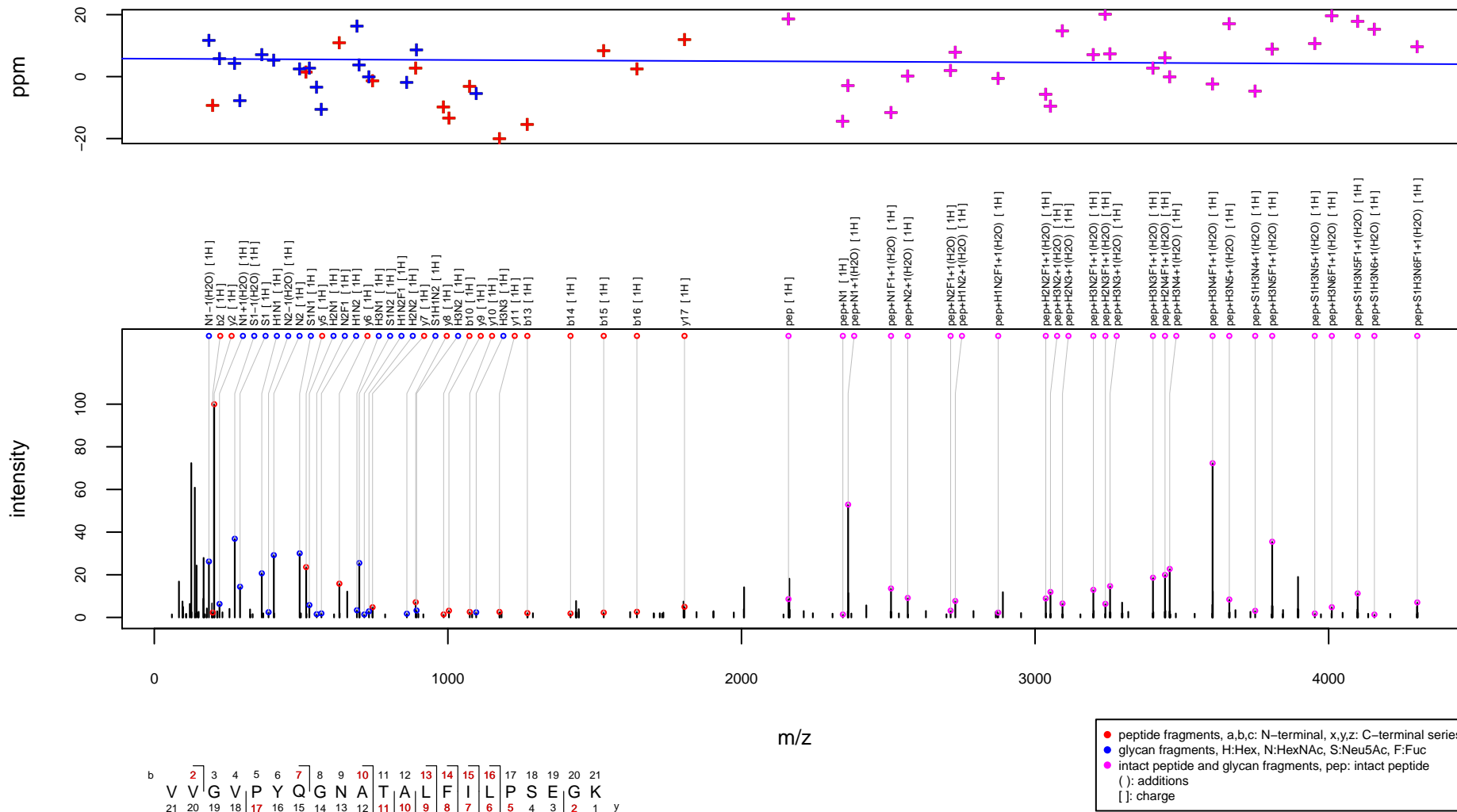
m/z 1434.658 charge 3 scan 0-0

Score= 92.99 , Hits= 59 , Explained Intensity= 0.6

Peptide: IPSP_HUMAN[254,274]:VVGVPYQGNATALFILPSEGK

Glycan: SNNH(NNH)HN(F)N, S1H3N6F1

Charge: 3H



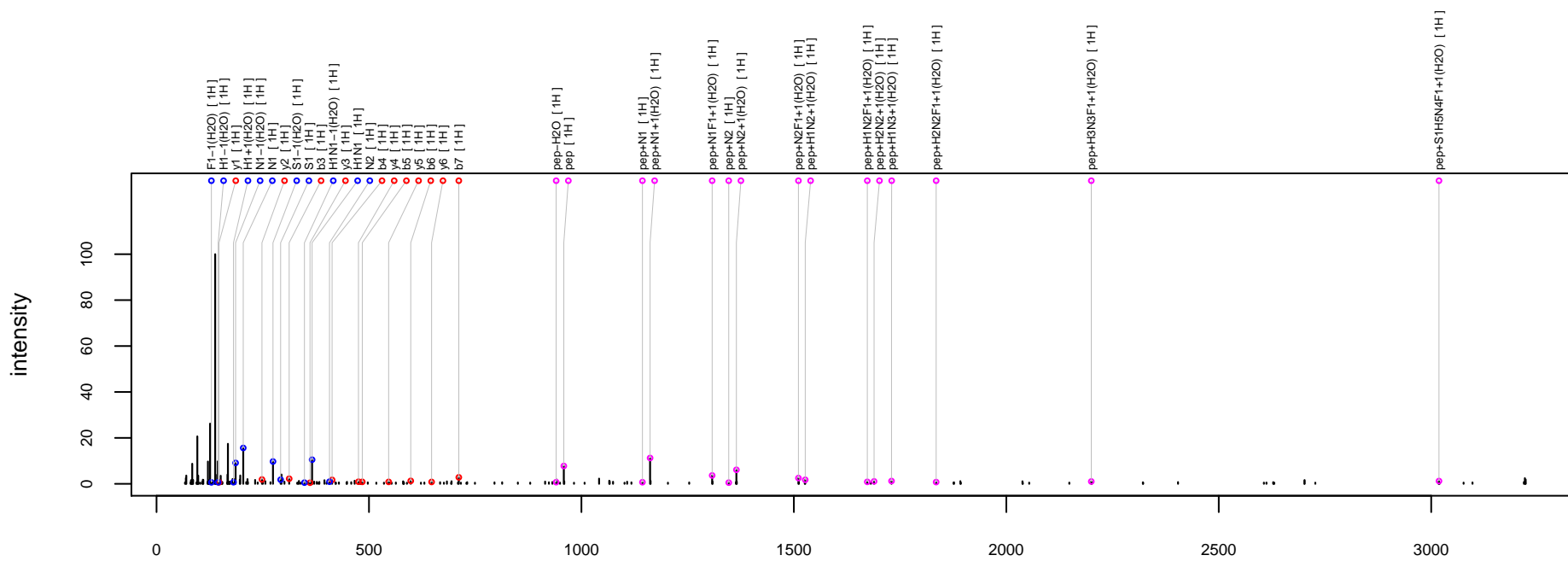
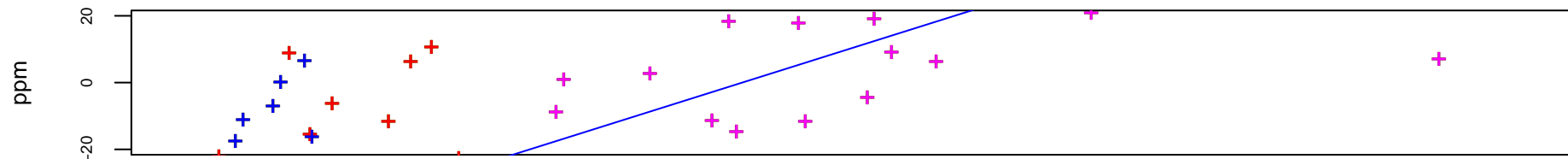
m/z 806.0957 charge 4 scan 0-0

Score= 49.63 , Hits= 36 , Explained Intensity= 0.24

Peptide: IGHA2_HUMAN[200,208]:TPLTANITK

Glycan: SHNH(HNH)(N)HN(F)N, S1H5N5F1

Charge: 4H



	2	3	4	5	6	7	8	9	
b	T	P	L	T	A	N	I	T	K
	9	8	7	6	5	4	3	2	1

- peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
- glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
- intact peptide and glycan fragments, pep: intact peptide
- (): additions
- []: charge

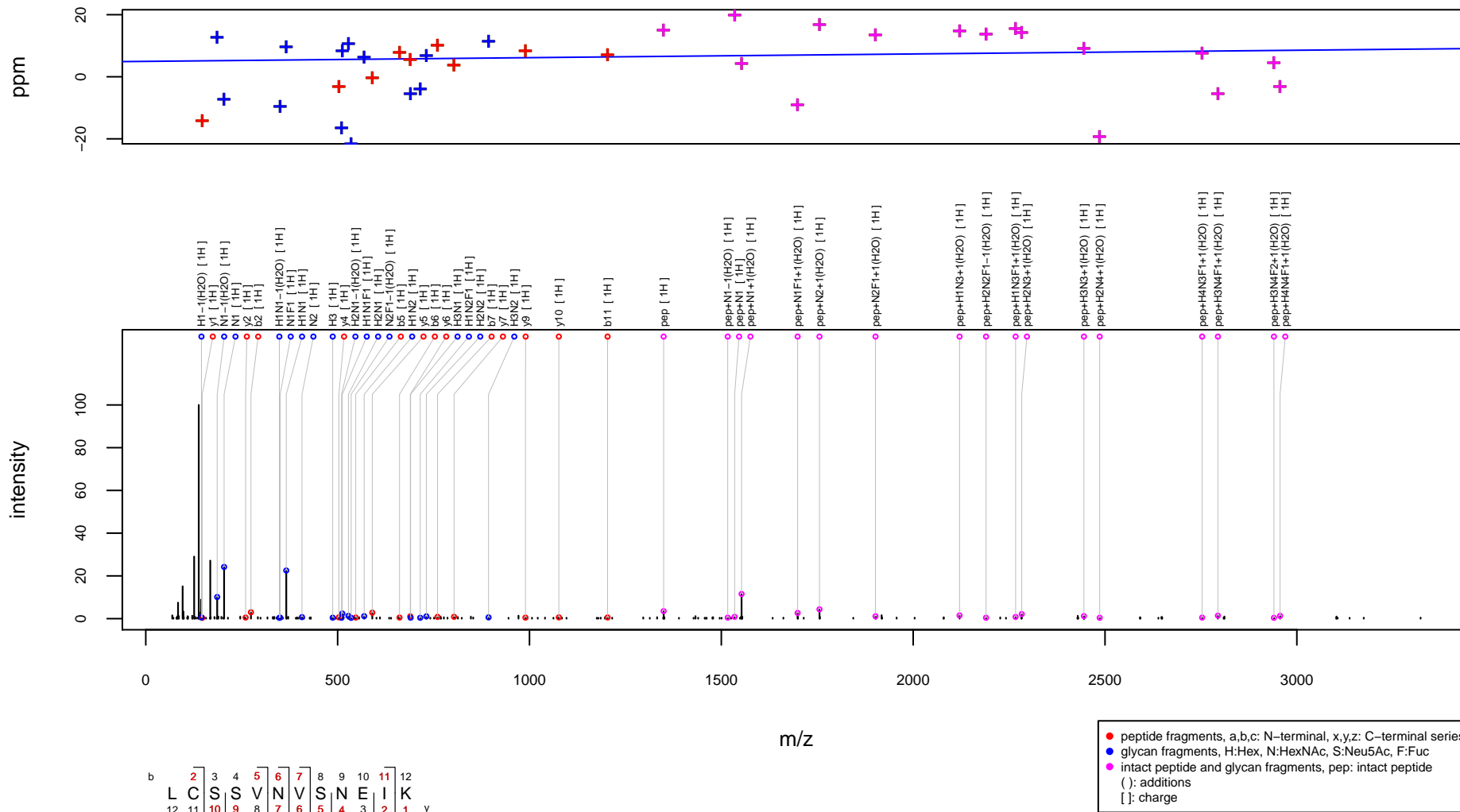
m/z 958.8961 charge 4 scan 0-0

Score= 54.11 , Hits= 47 , Explained Intensity= 0.3

Peptide: CUBN_HUMAN[2526,2537]:LCSSVNVSEIK

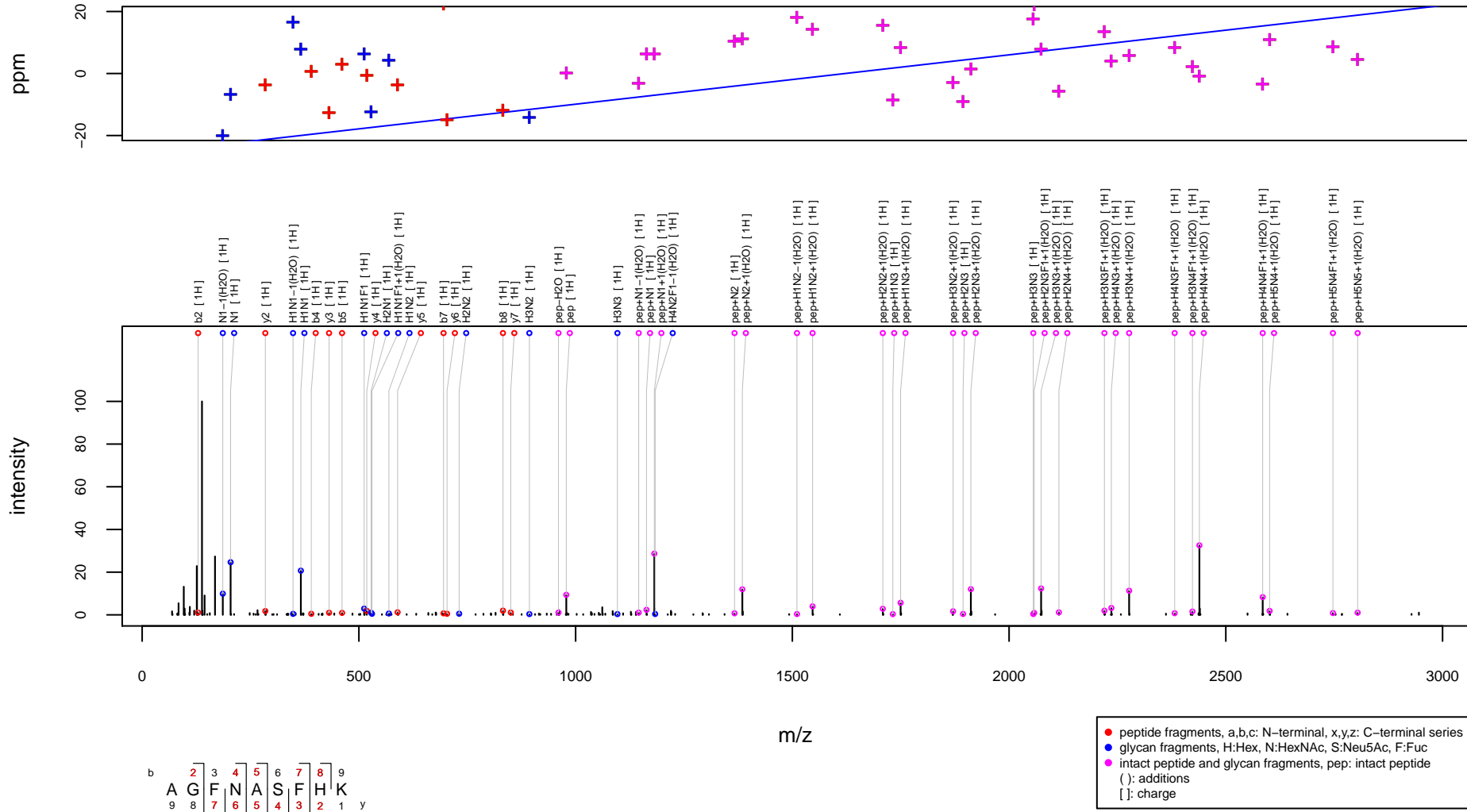
Glycan: H6N6F2

Charge: 4H



m/z 984.0692 charge 3 scan 0-0

Score= 79.94 , Hits= 52 , Explained Intensity= 0.47
 Peptide: CUBN_HUMAN[2082,2090]:AGFNASFHK
 Glycan: HNH(F(H)NH)(N)HNN, H5N5F1
 Charge: 3H



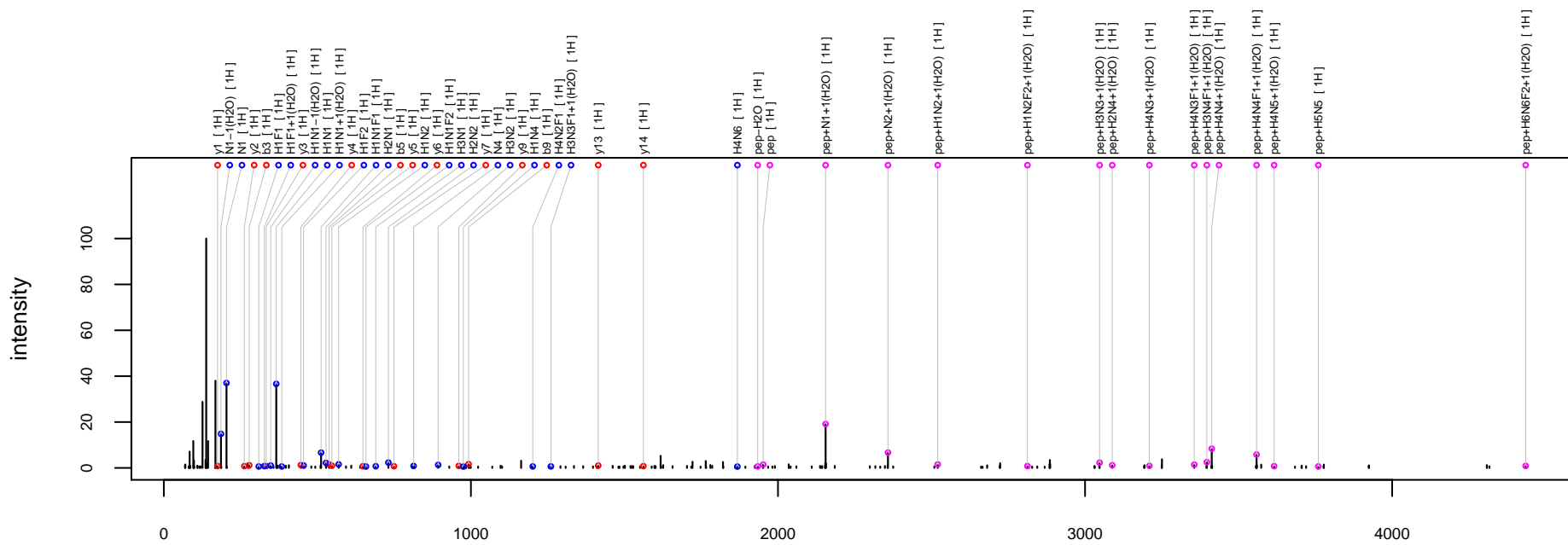
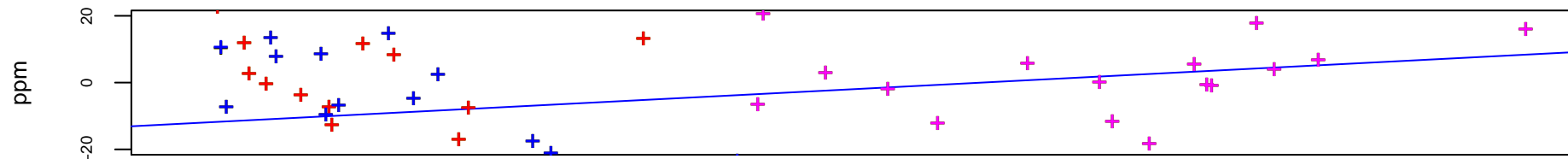
m/z 1109.4706 charge 4 scan 0-0

Score= 57.65 , Hits= 49 , Explained Intensity= 0.35

Peptide: MGA_HUMAN[817,834]:GGYIFPTQQPNTTTLASR

Glycan: H6N6F2

Charge: 4H



b 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18
 G G Y I F P T Q Q P N T T T L A S R
 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1 y

● peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
 ● glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
 ● intact peptide and glycan fragments, pep: intact peptide
 (): additions
 []: charge

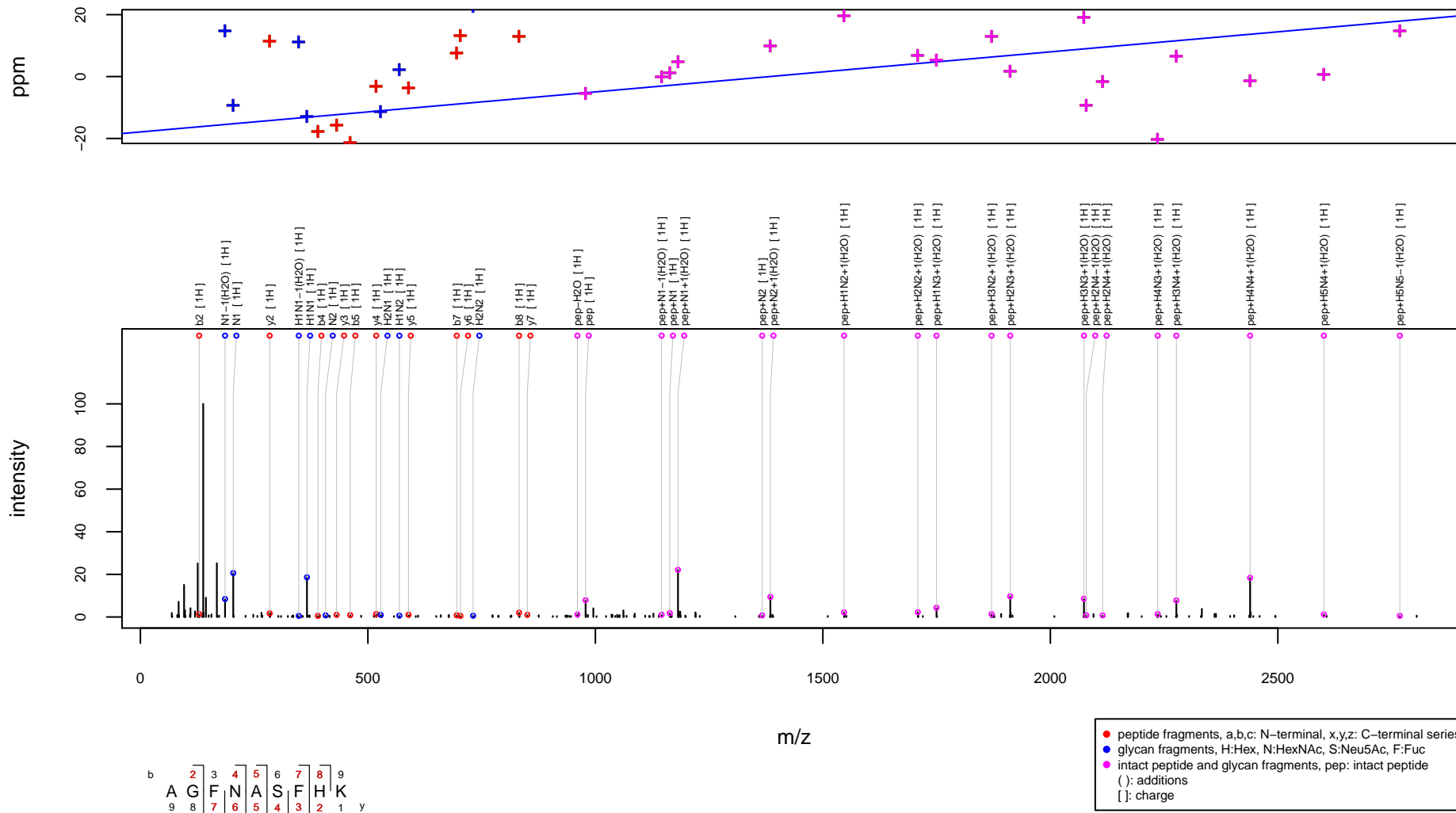
m/z 935.3835 charge 3 scan 0-0

Score= 64.64 , Hits= 39 , Explained Intensity= 0.35

Peptide: CUBN_HUMAN[2082,2090]:AGFNASFHK

Glycan: HNH(HNH)(N)HNN, H5N5

Charge: 3H



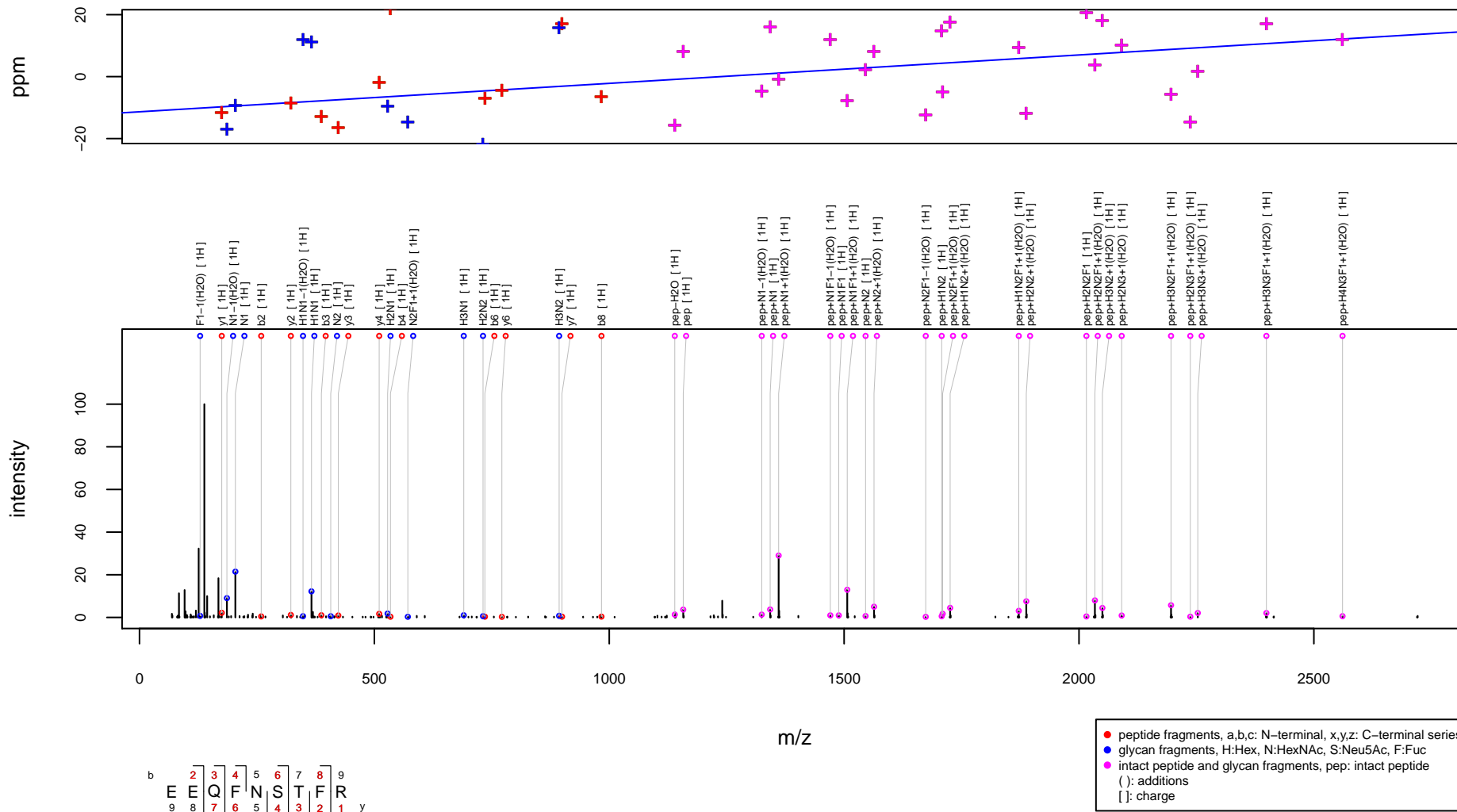
m/z 922.0402 charge 3 scan 0-0

Score= 76.97 , Hits= 47 , Explained Intensity= 0.37

Peptide: IGHG2_HUMAN[172,180]:EEQFNSTFR

Glycan: HNH(NH)HN(F)N, H4N4F1

Charge: 3H



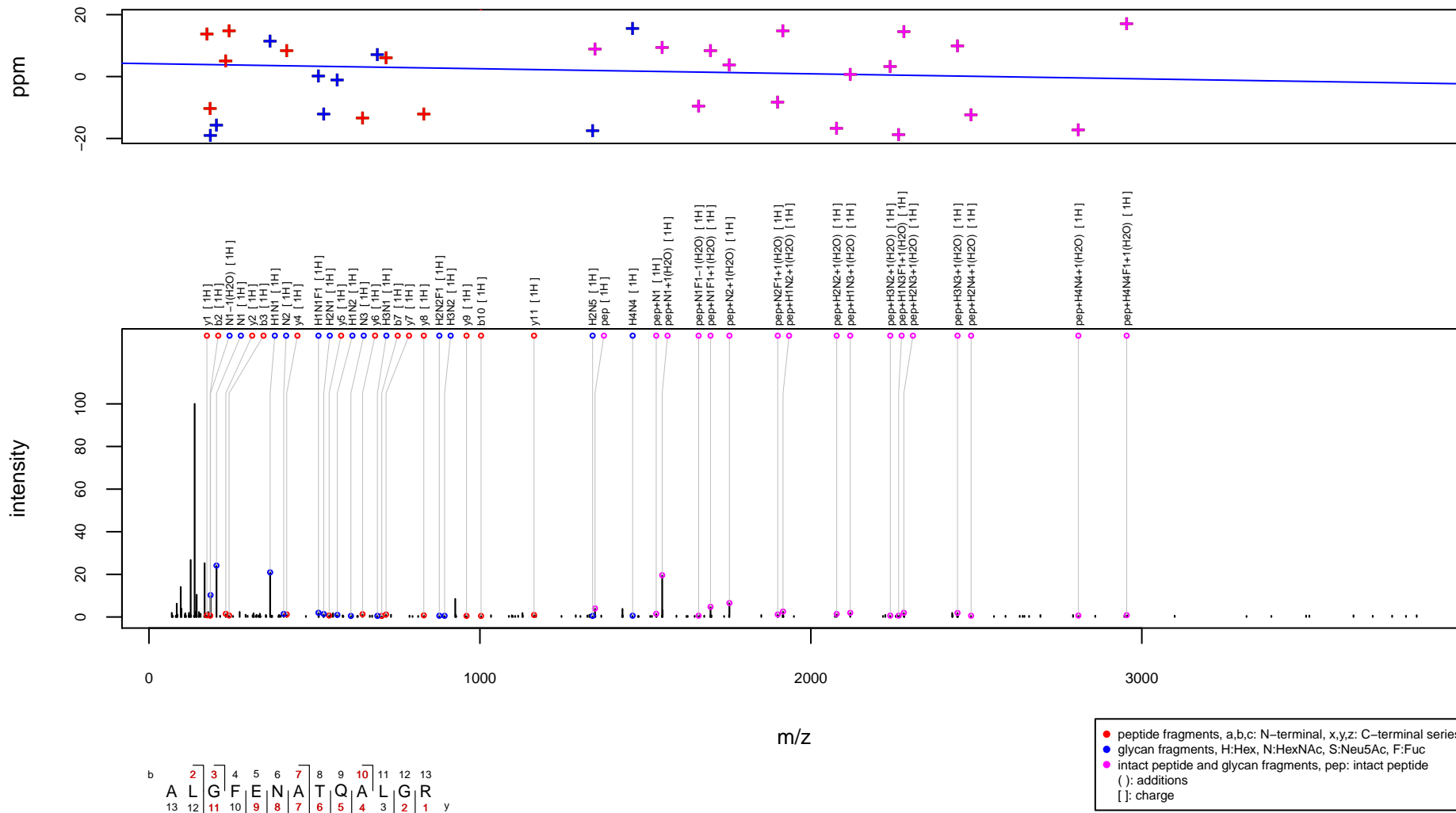
m/z 958.4092 charge 4 scan 0-0

Score= 50.24 , Hits= 43 , Explained Intensity= 0.3

Peptide: LG3BP_HUMAN[64,76]:ALGFENATQALGR

Glycan: H6N6F2

Charge: 4H



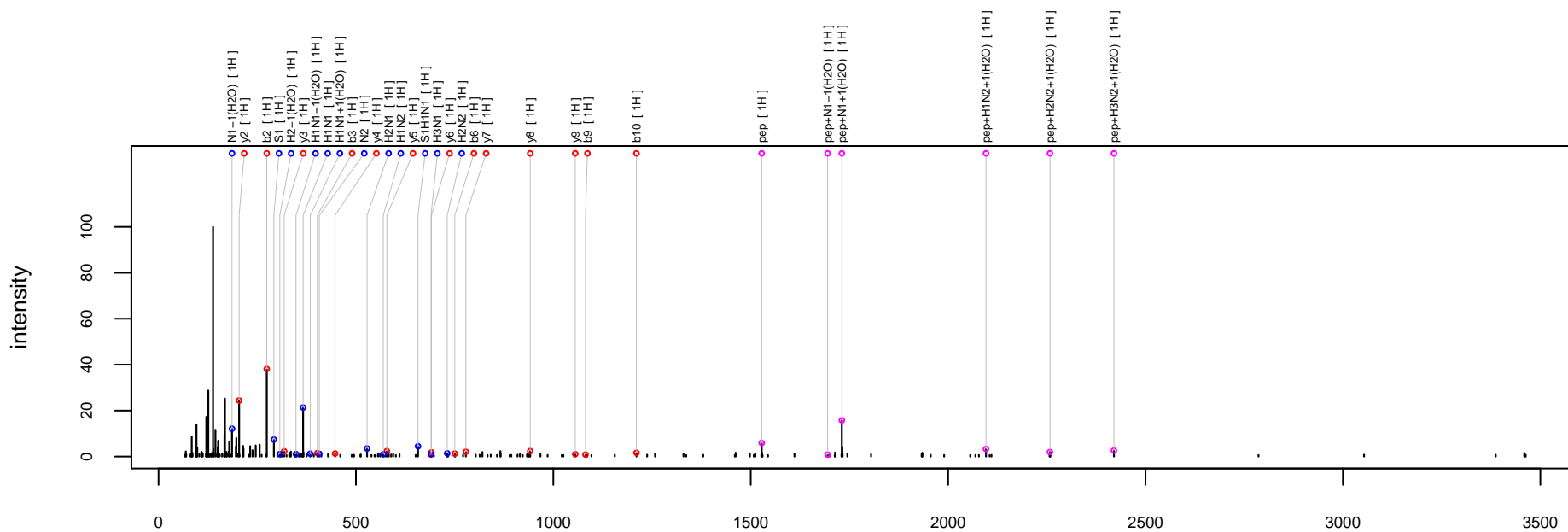
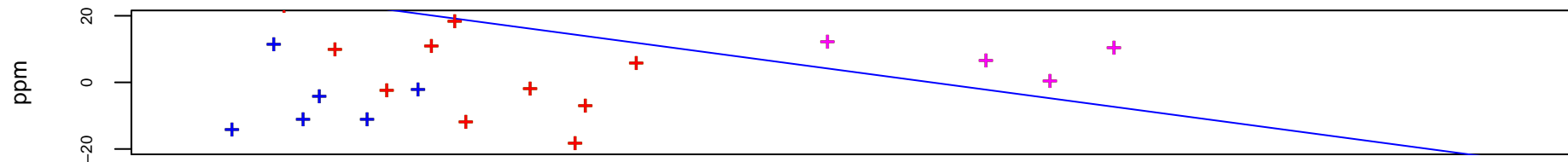
m/z 933.8698 charge 4 scan 0-0

Score= 47.31 , Hits= 31 , Explained Intensity= 0.3

Peptide: APOD_HUMAN[61,73]:CIQANYSLMENGK

Glycan: SHNH(SHNH)HNN, S2H5N4

Charge: 4H



b

	2	3	4	5	6	7	8	9	10	11	12	13
C	I	Q	A	N	Y	S	L	M	E	N	G	K
13	12	11	10	9	8	7	6	5	4	3	2	1

y

- peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
- glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
- intact peptide and glycan fragments, pep: intact peptide
- (): additions
- []: charge

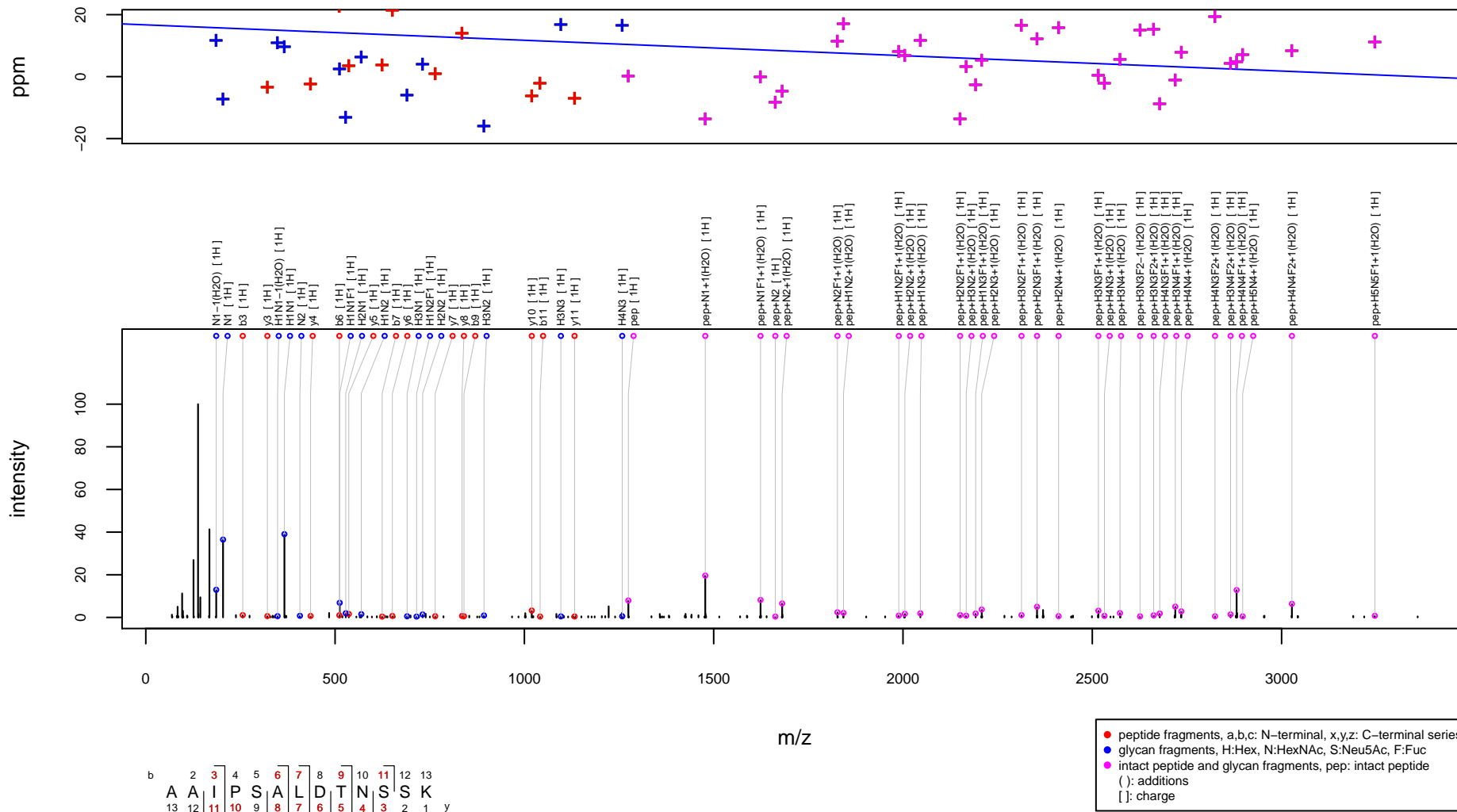
m/z 1131.4786 charge 3 scan 0-0

Score= 83.22 , Hits= 58 , Explained Intensity= 0.44

Peptide: LG3BP_HUMAN[542,554]:AAIPALSDTNSSK

Glycan: FHNH(HNH)(N)HN(F)N, H5N5F2

Charge: 3H



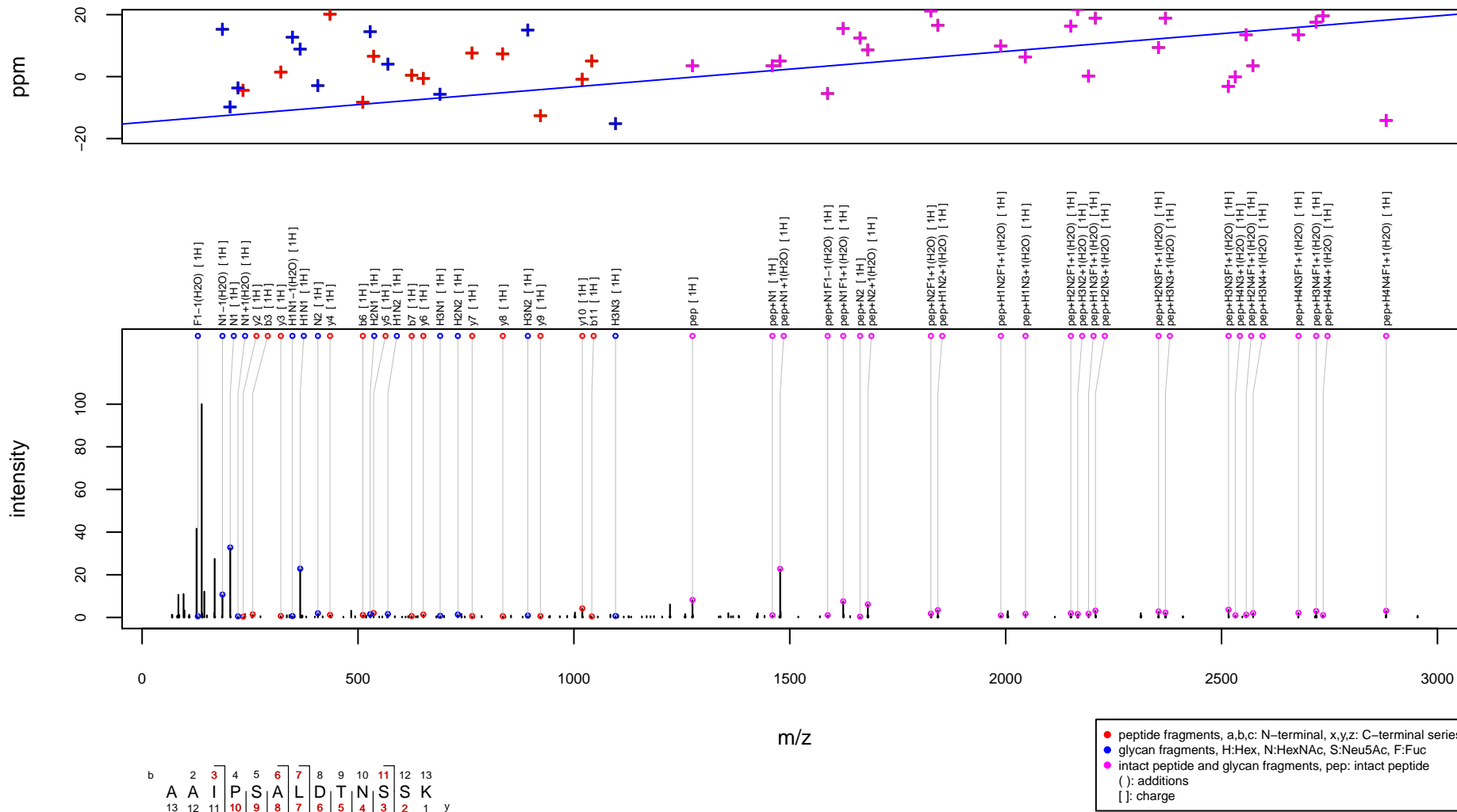
m/z 1028.7776 charge 3 scan 0-0

Score= 77.28 , Hits= 51 , Explained Intensity= 0.37

Peptide: LG3BP_HUMAN[542,554]:AAIP^SALD^TNSSK

Glycan: HNH(NH)(N)HN(F)N, H4N5F1

Charge: 3H



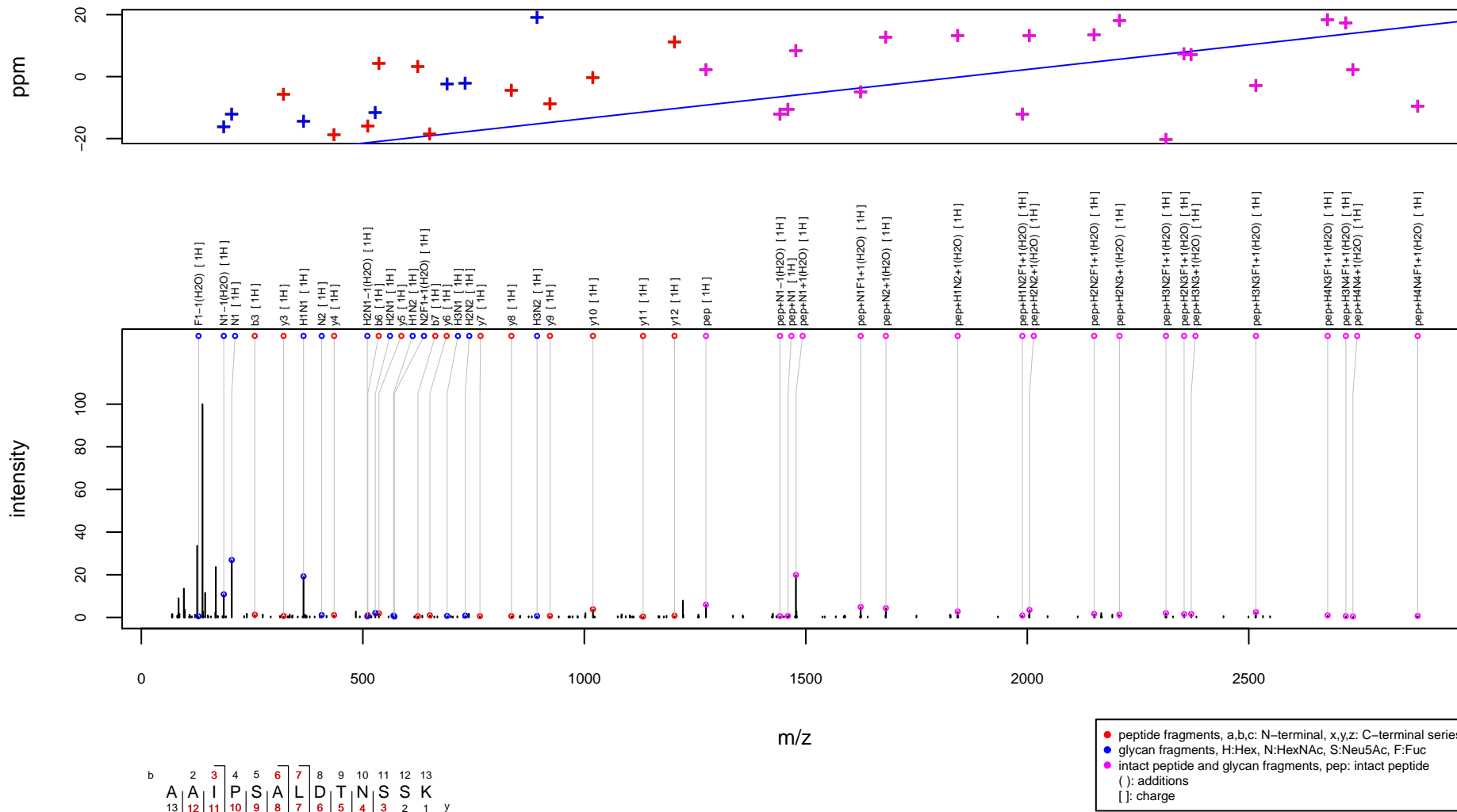
m/z 961.0837 charge 3 scan 0-0

Score= 68.96 , Hits= 44 , Explained Intensity= 0.31

Peptide: LG3BP_HUMAN[542,554]:AAIP^SALD^TNSSK

Glycan: HNH(NH)HN(F)N, H4N4F1

Charge: 3H



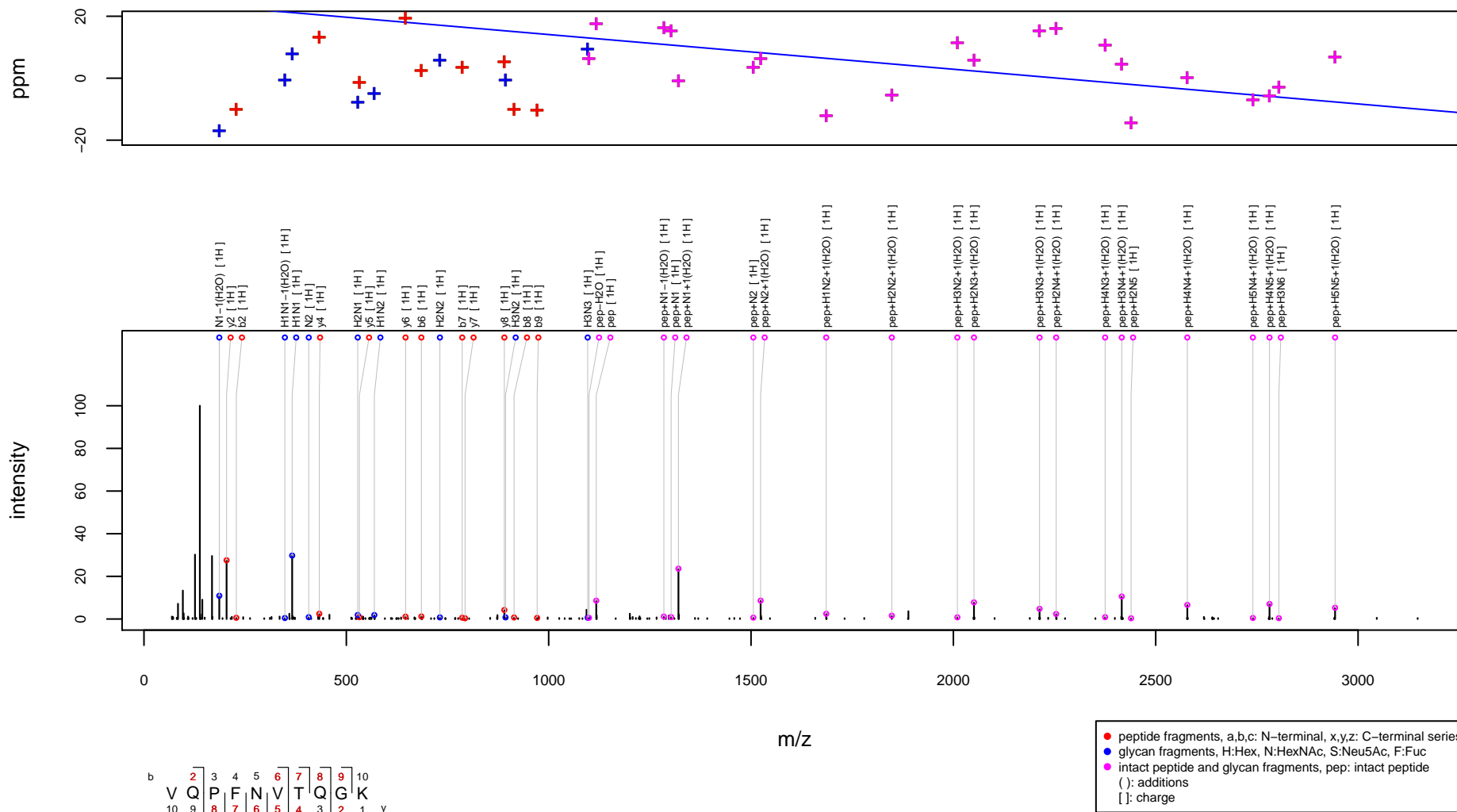
m/z 1049.4482 charge 3 scan 0-0

Score= 65.74 , Hits= 41 , Explained Intensity= 0.41

Peptide: LAMP2_HUMAN[352,361]:VQPFNVTQ GK

Glycan: HNH(NN(HN)H)HNN, H5N6

Charge: 3H



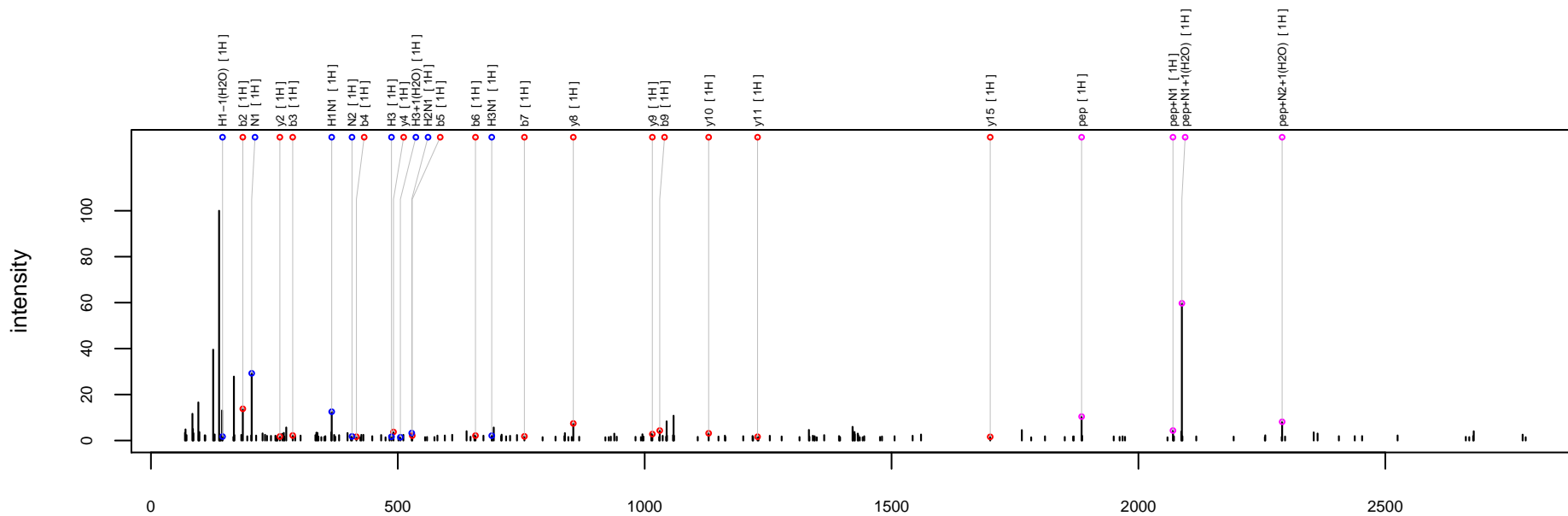
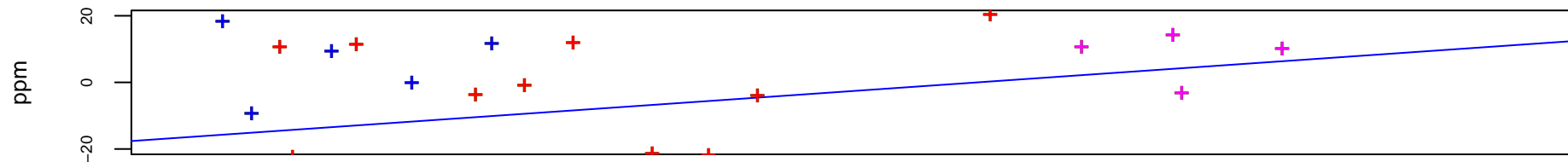
m/z 926.4069 charge 3 scan 0-0

Score= 44.28 , Hits= 26 , Explained Intensity= 0.25

Peptide: SYPL1_HUMAN[56,72]:GQTEIQVNCPPAVTENK

Glycan: H(H)HNN, H3N2

Charge: 3H



b

	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
G	Q	T	E	I	Q	V	N	C	P	P	A	V	T	E	N	K
17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	y

- peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
- glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
- intact peptide and glycan fragments, pep: intact peptide
- (): additions
- []: charge

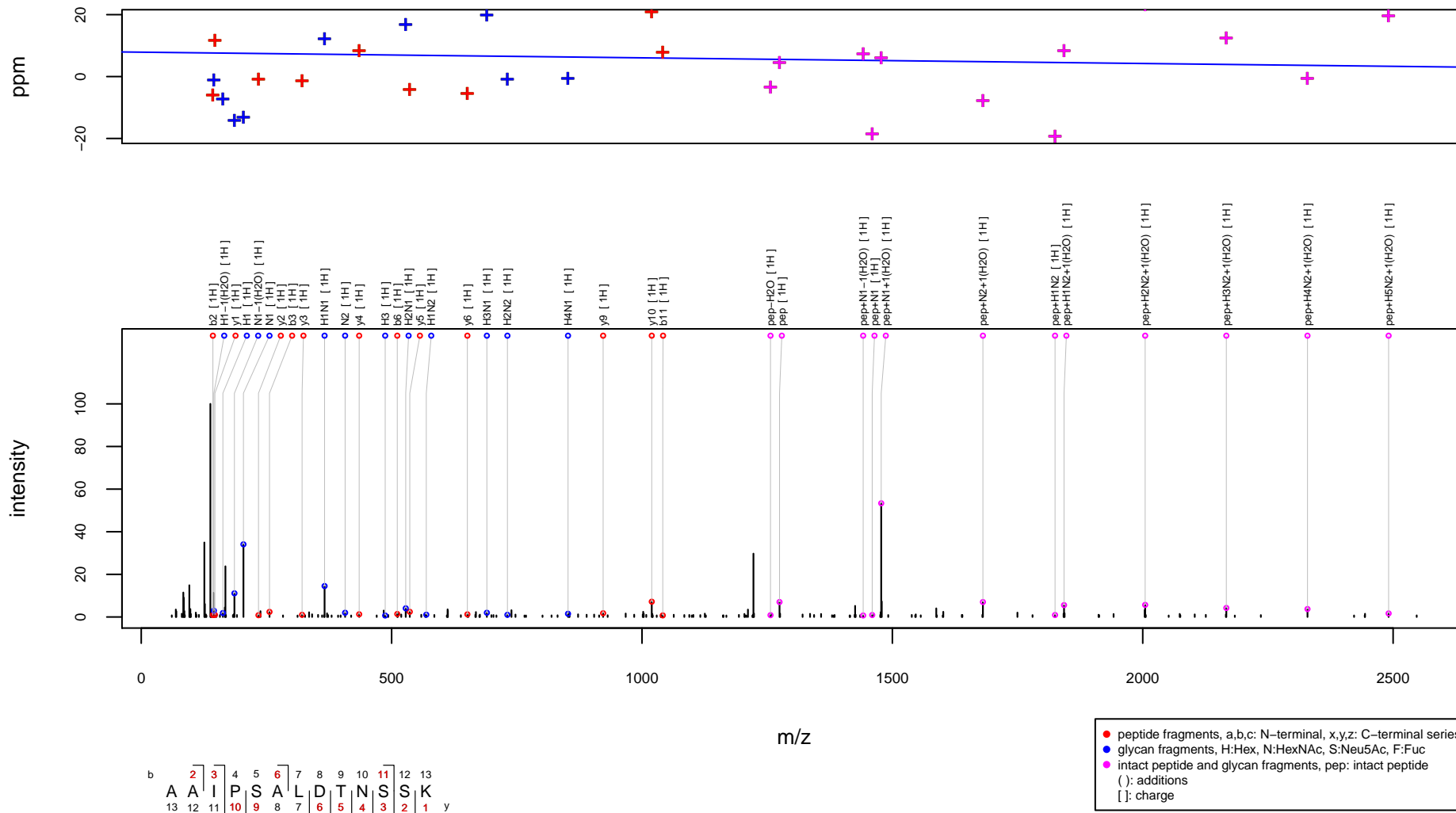
m/z 939.067 charge 3 scan 0-0

Score= 59.53 , Hits= 36 , Explained Intensity= 0.31

Peptide: LG3BP_HUMAN[542,554]:AAIPSAALDTNSSK

Glycan: HHH(H(H)H)HNN, H7N2

Charge: 3H



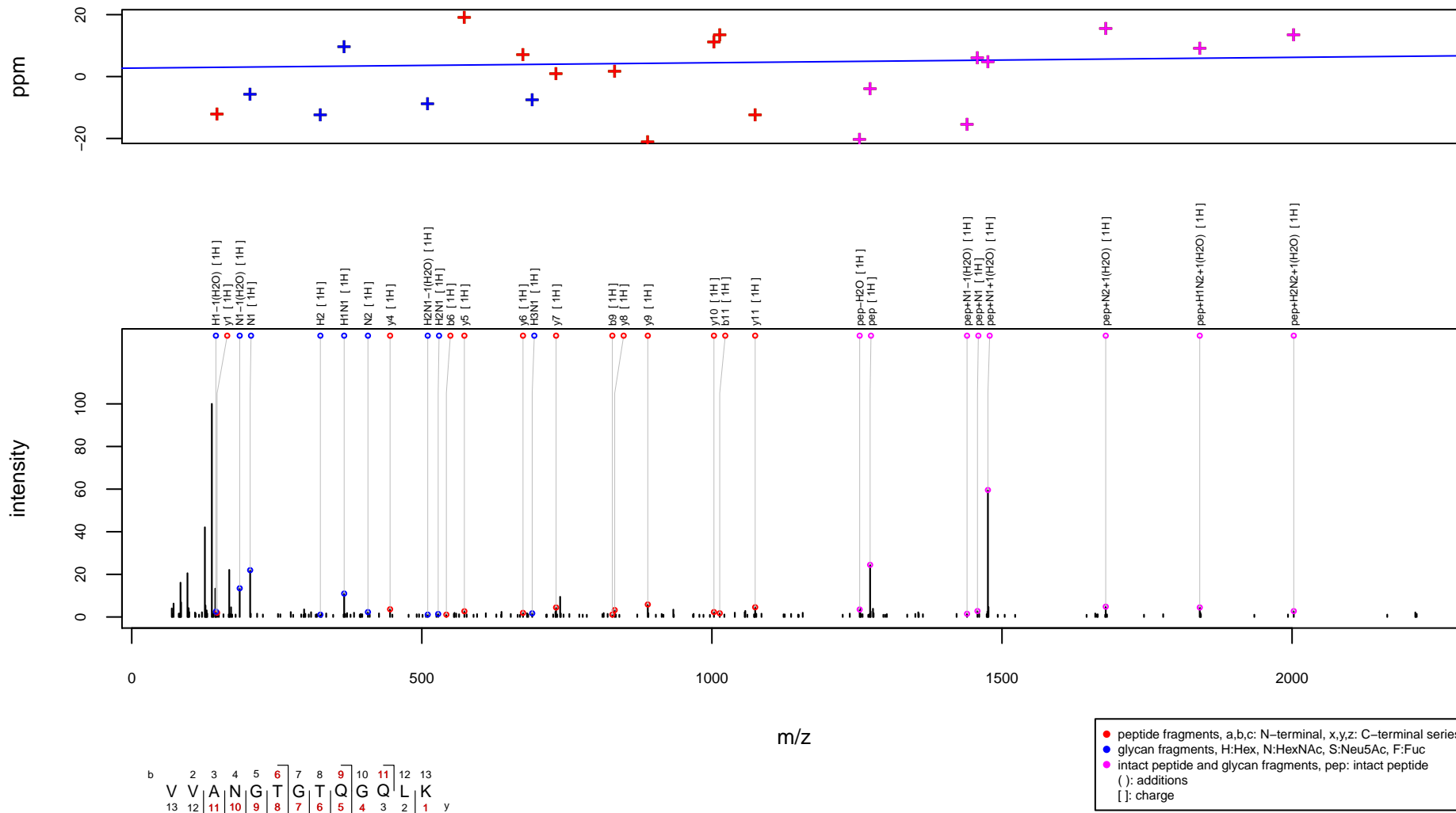
m/z 830.368 charge 3 scan 0-0

Score= 48.77 , Hits= 29 , Explained Intensity= 0.3

Peptide: BGLR_HUMAN[269,281]:VVANGTGTQGQLK

Glycan: H(H)H(H)HNN, H5N2

Charge: 3H



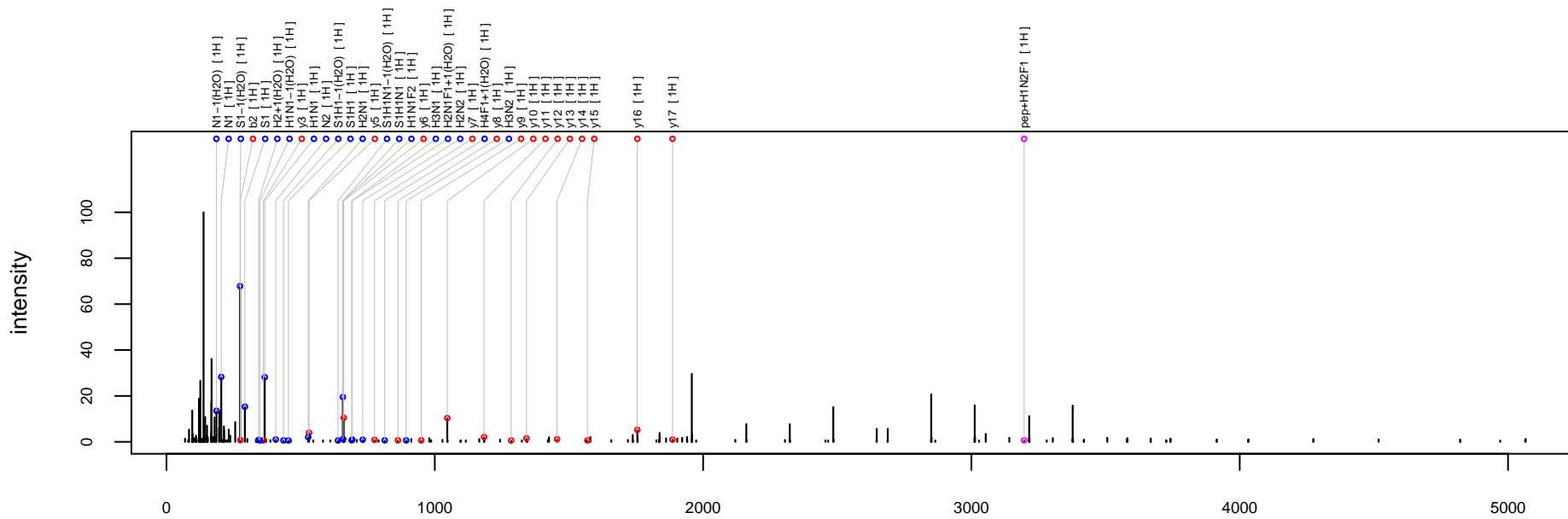
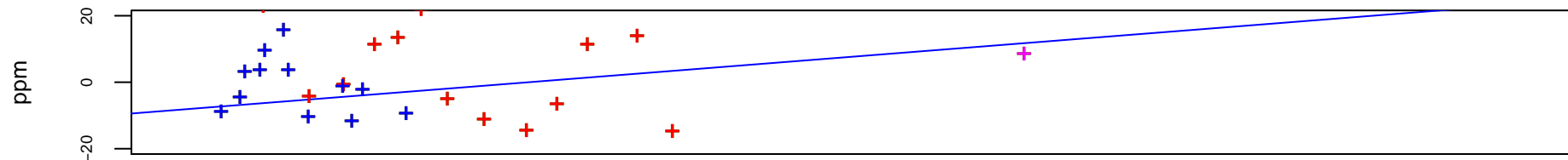
m/z 1055.2181 charge 5 scan 0-0

Score= 39.52 , Hits= 35 , Explained Intensity= 0.29

Peptide: UROM_HUMAN[223,245]:CNTAAPMWLNGTHPSSDEGIVSR

Glycan: S1H11N2F2

Charge: 5H



b 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23
 C N T A A P M W L N G T H P S S D E G I V S R
 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1 y

m/z

● peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
 ● glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
 ● intact peptide and glycan fragments, pep: intact peptide
 (): additions
 []: charge

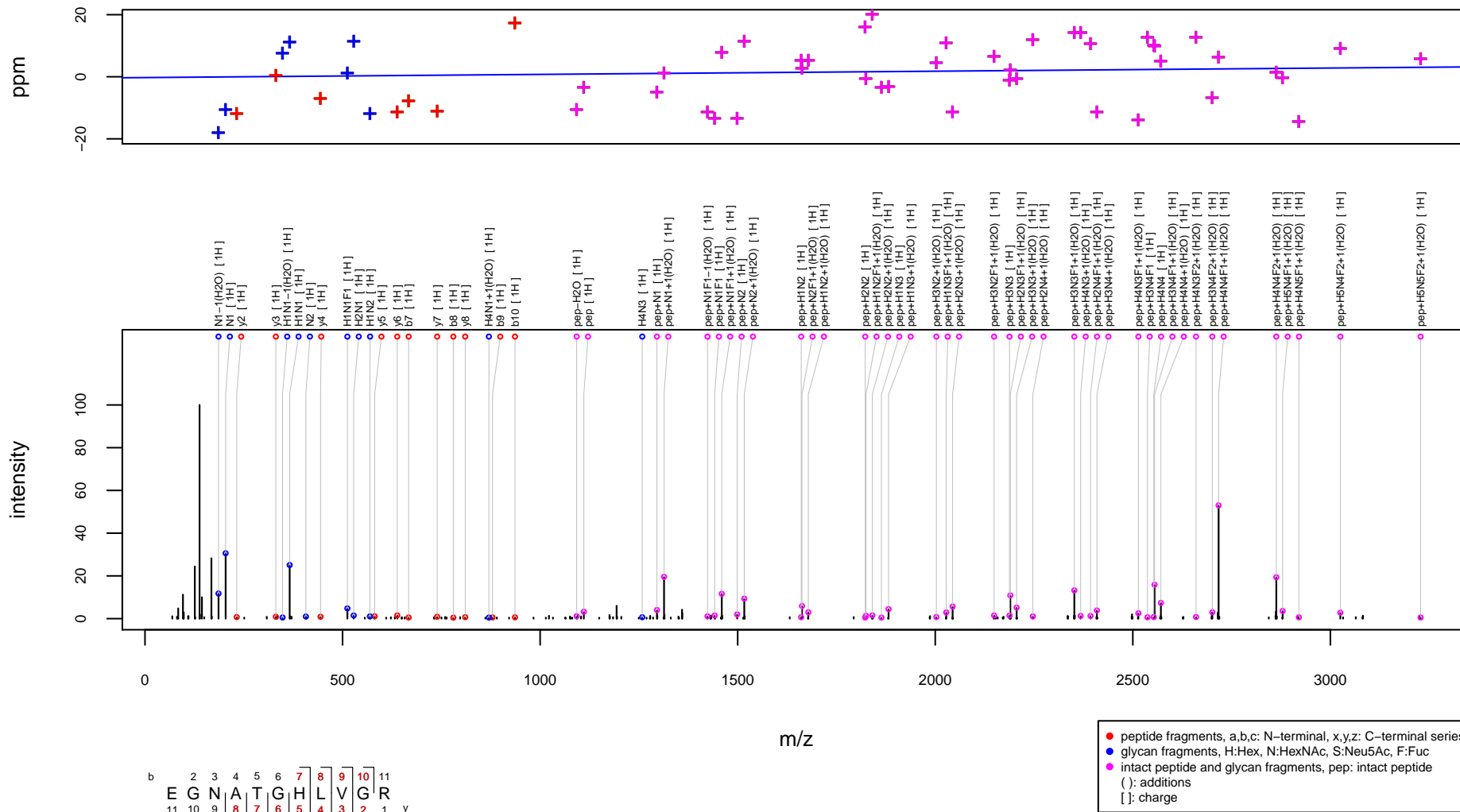
m/z 1076.7827 charge 3 scan 0-0

Score= 92.33 , Hits= 63 , Explained Intensity= 0.52

Peptide: CUBN_HUMAN[1800,1810]:EGNATGHLVGR

Glycan: FHNH(HNH)(N)HN(F)N, H5N5F2

Charge: 3H



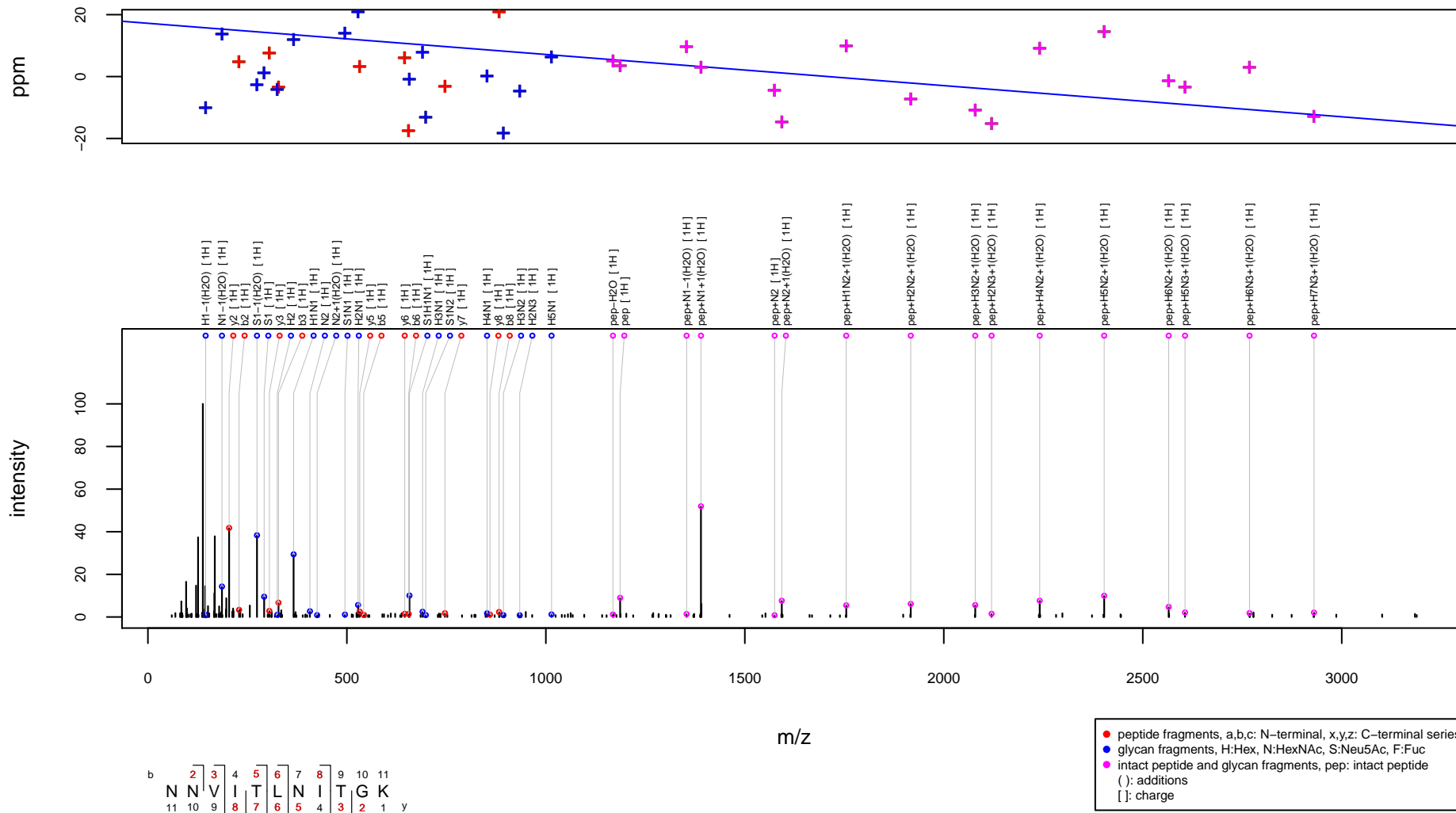
m/z 1074.4602 charge 3 scan 0-0

Score= 62.43 , Hits= 44 , Explained Intensity= 0.43

Peptide: BGAL_HUMAN[458,468]:NNVITLNITGK

Glycan: S1H7N3

Charge: 3H



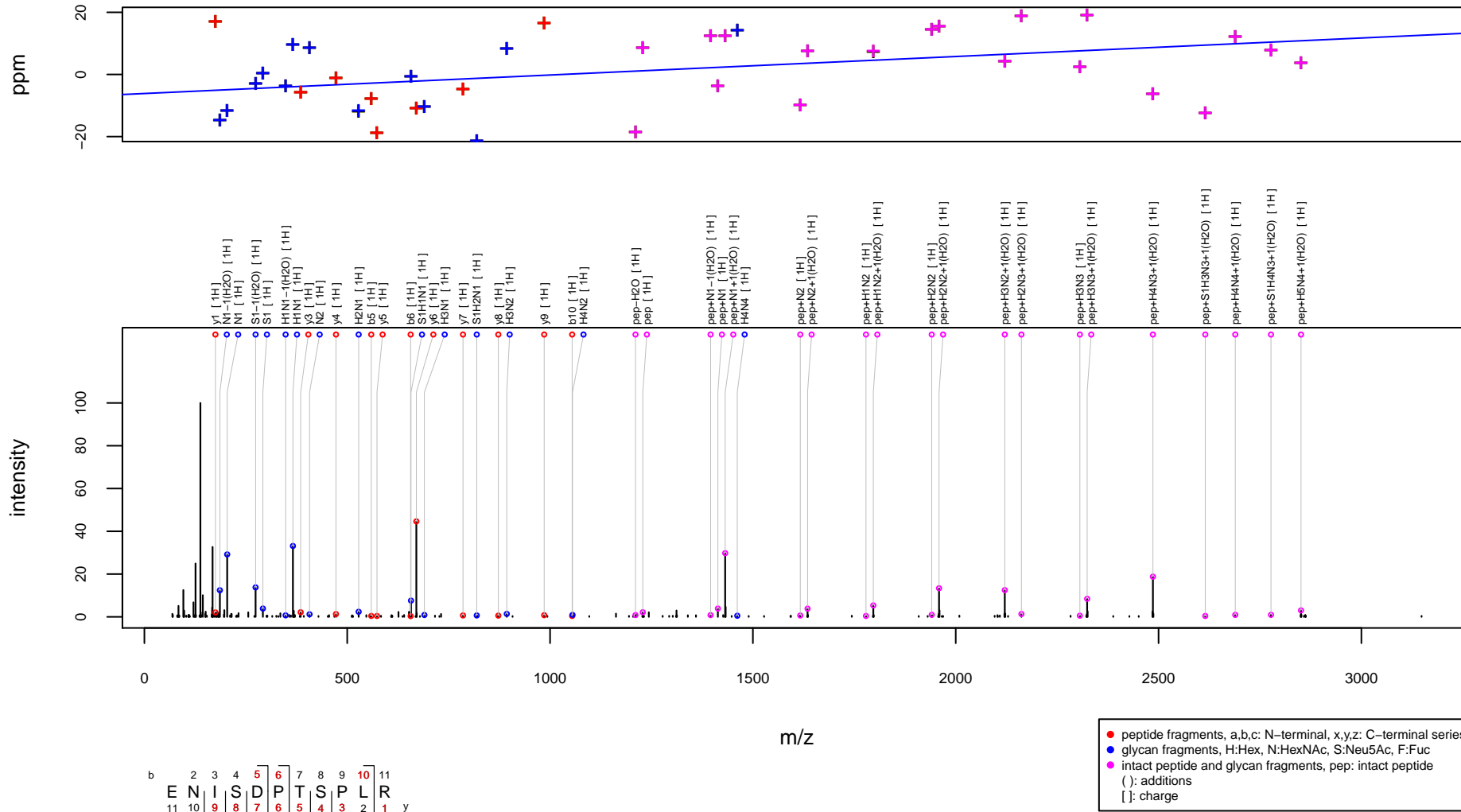
m/z 1048.1011 charge 3 scan 0-0

Score= 72.45 , Hits= 45 , Explained Intensity= 0.49

Peptide: IGJ_HUMAN[70,80]:ENISDPTSPLR

Glycan: SHNH(HNH)HNN, S1H5N4

Charge: 3H



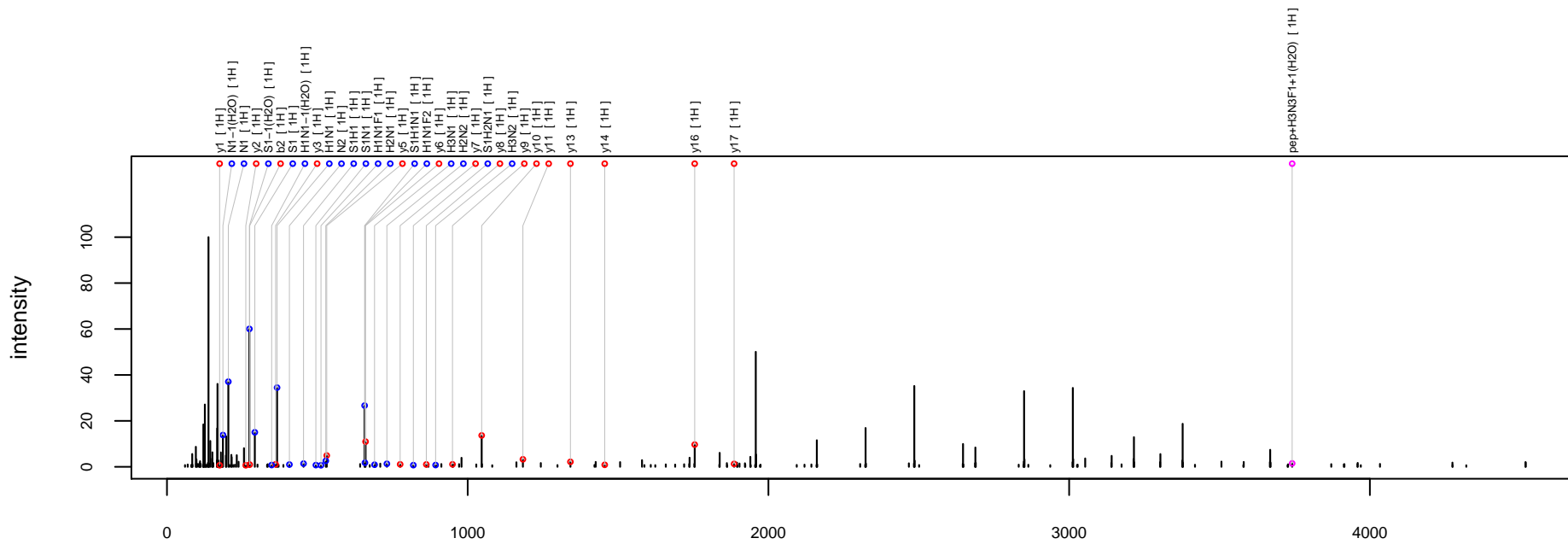
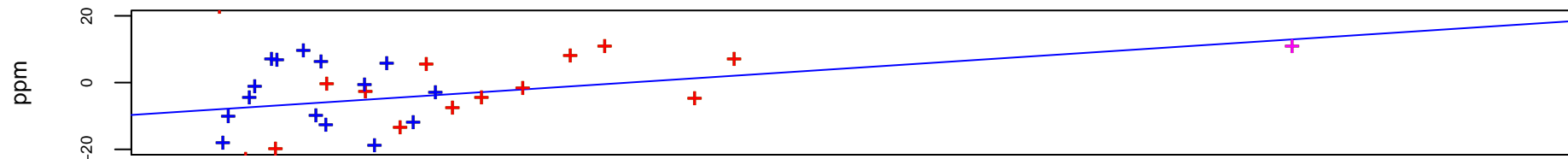
m/z 1154.7198 charge 4 scan 0-0

Score= 38.18 , Hits= 33 , Explained Intensity= 0.27

Peptide: UROM_HUMAN[223,245]:CNTAAPMWLNGLTHPSSDEGIVSR

Glycan: S2H3N3F3

Charge: 4H



b 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23
 C N T A A P M W L N G T H P S S D E G I V S R
 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1 y

● peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
 ● glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
 ● intact peptide and glycan fragments, pep: intact peptide
 (): additions
 []: charge

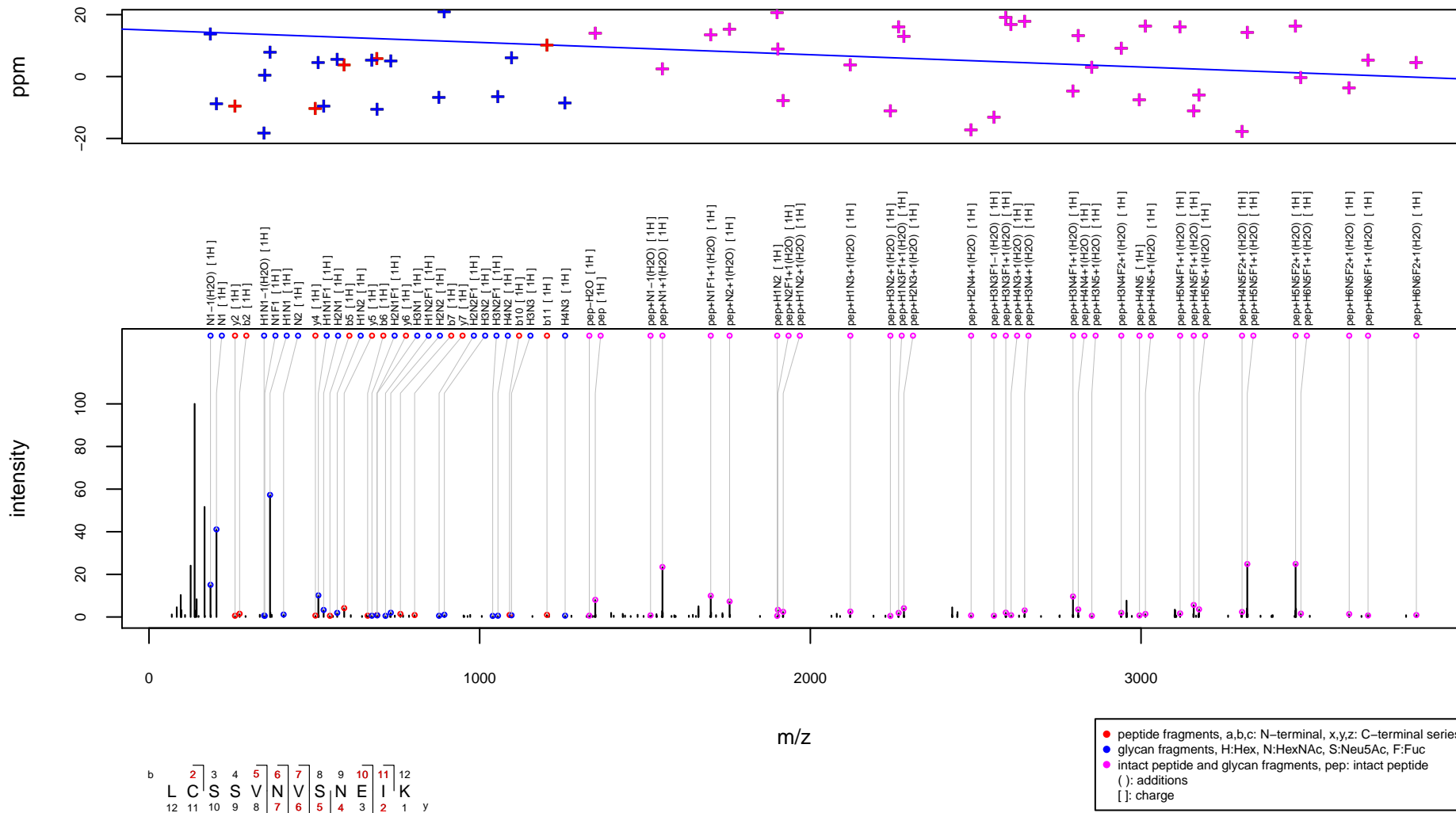
m/z 1278.1936 charge 3 scan 0-0

Score= 76.59 , Hits= 64 , Explained Intensity= 0.49

Peptide: CUBN_HUMAN[2526,2537]:LCSSVNVSEIK

Glycan: H6N6F2

Charge: 3H



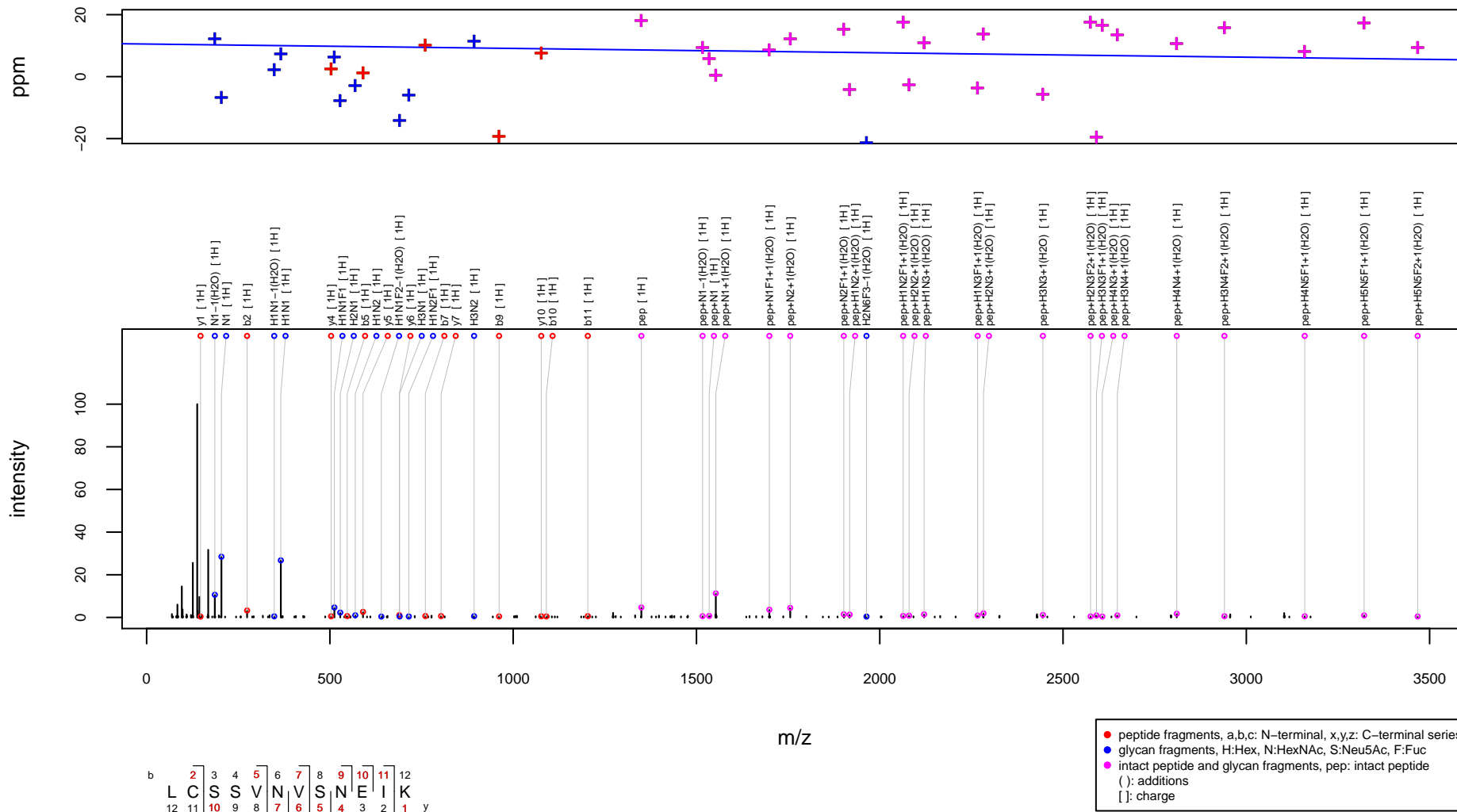
m/z 995.4046 charge 4 scan 0-0

Score= 49.1 , Hits= 47 , Explained Intensity= 0.33

Peptide: CUBN_HUMAN[2526,2537]:LCSSVNVSEIK

Glycan: H6N6F3

Charge: 4H



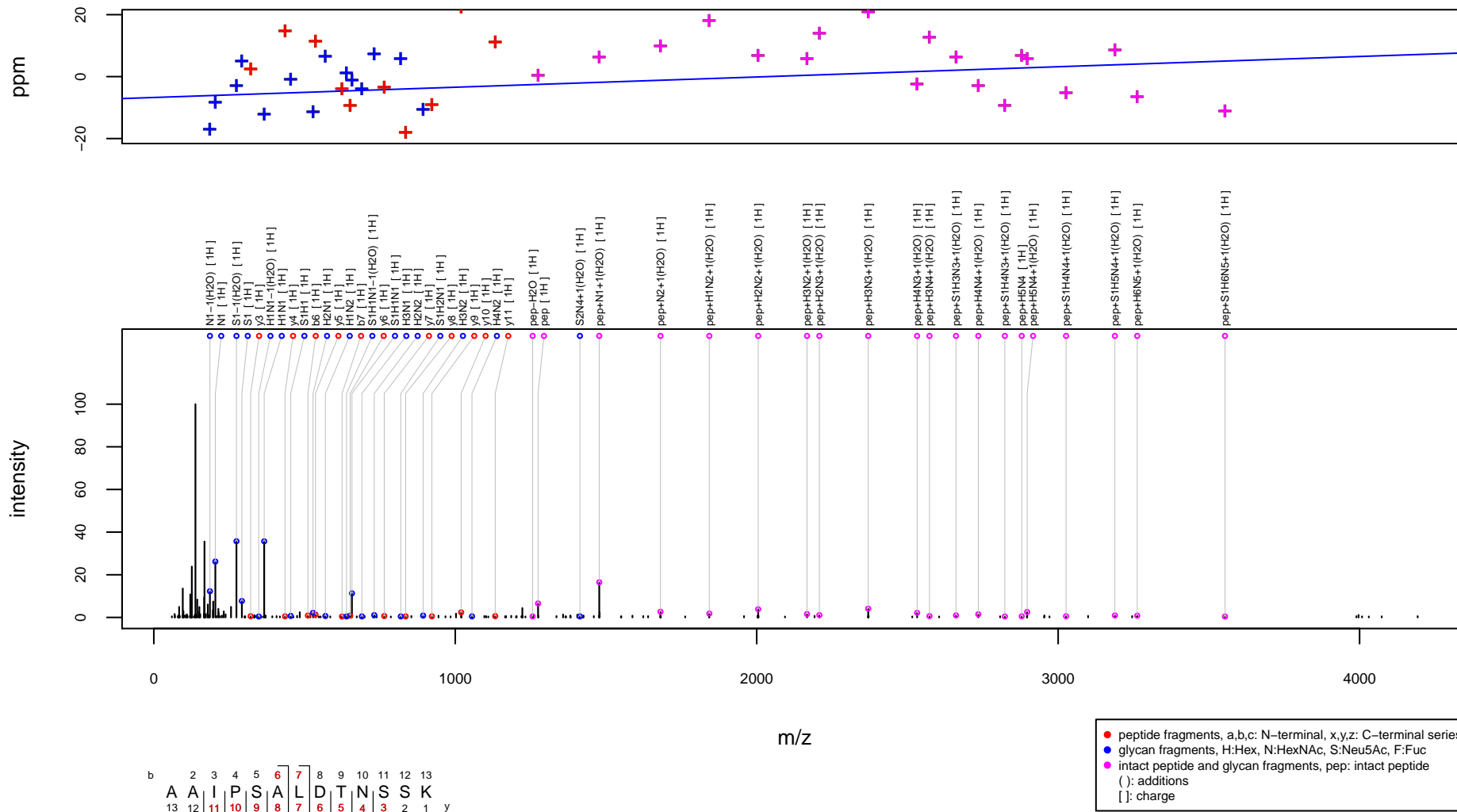
m/z 1053.1787 charge 4 scan 0-0

Score= 54.27 , Hits= 48 , Explained Intensity= 0.37

Peptide: LG3BP_HUMAN[542,554]:AAIPSAALDTNSSK

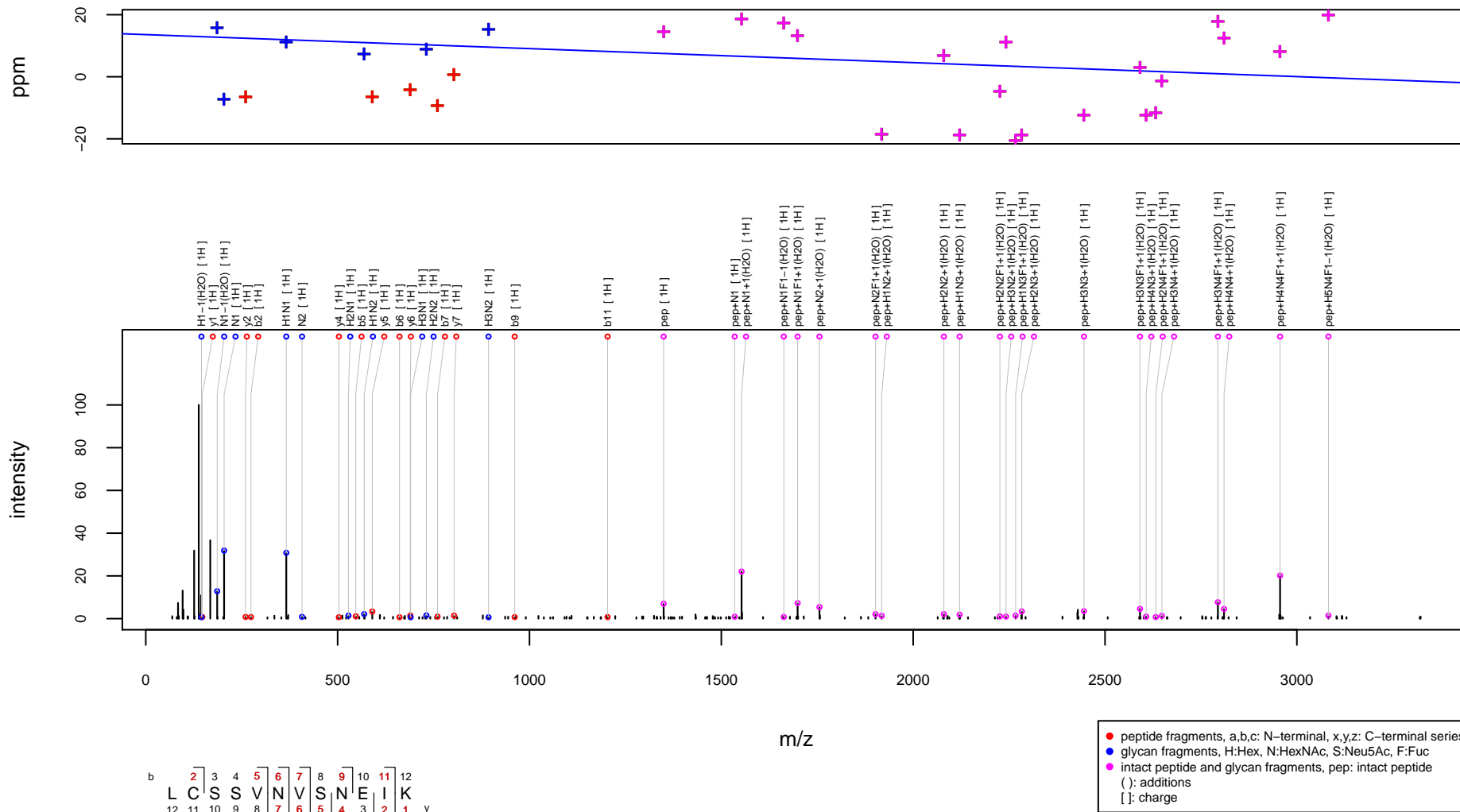
Glycan: S2H7N6

Charge: 4H



m/z 1107.8015 charge 3 scan 0-0

Score= 65.72 , Hits= 45 , Explained Intensity= 0.38
 Peptide: CUBN_HUMAN[2526,2537]:LCSSVNVSN EIK
 Glycan: HNH(HNH)(N)HN(F)N, H5N5F1
 Charge: 3H



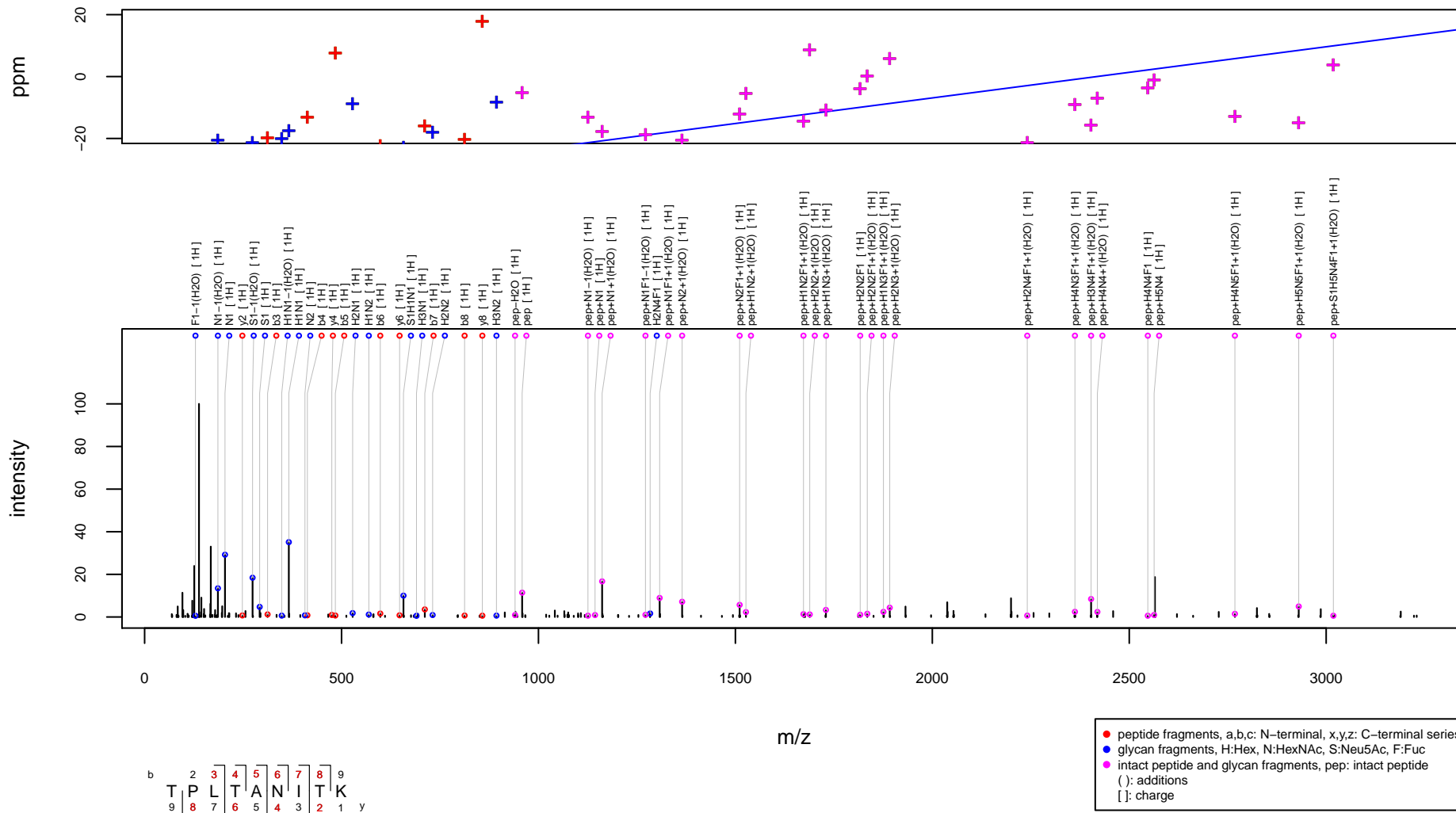
m/z 1074.478 charge 3 scan 0-0

Score= 69.68 , Hits= 51 , Explained Intensity= 0.37

Peptide: IGHA2_HUMAN[200,208]:TPLTANITK

Glycan: SHNH(HNH)(N)HN(F)N, S1H5N5F1

Charge: 3H



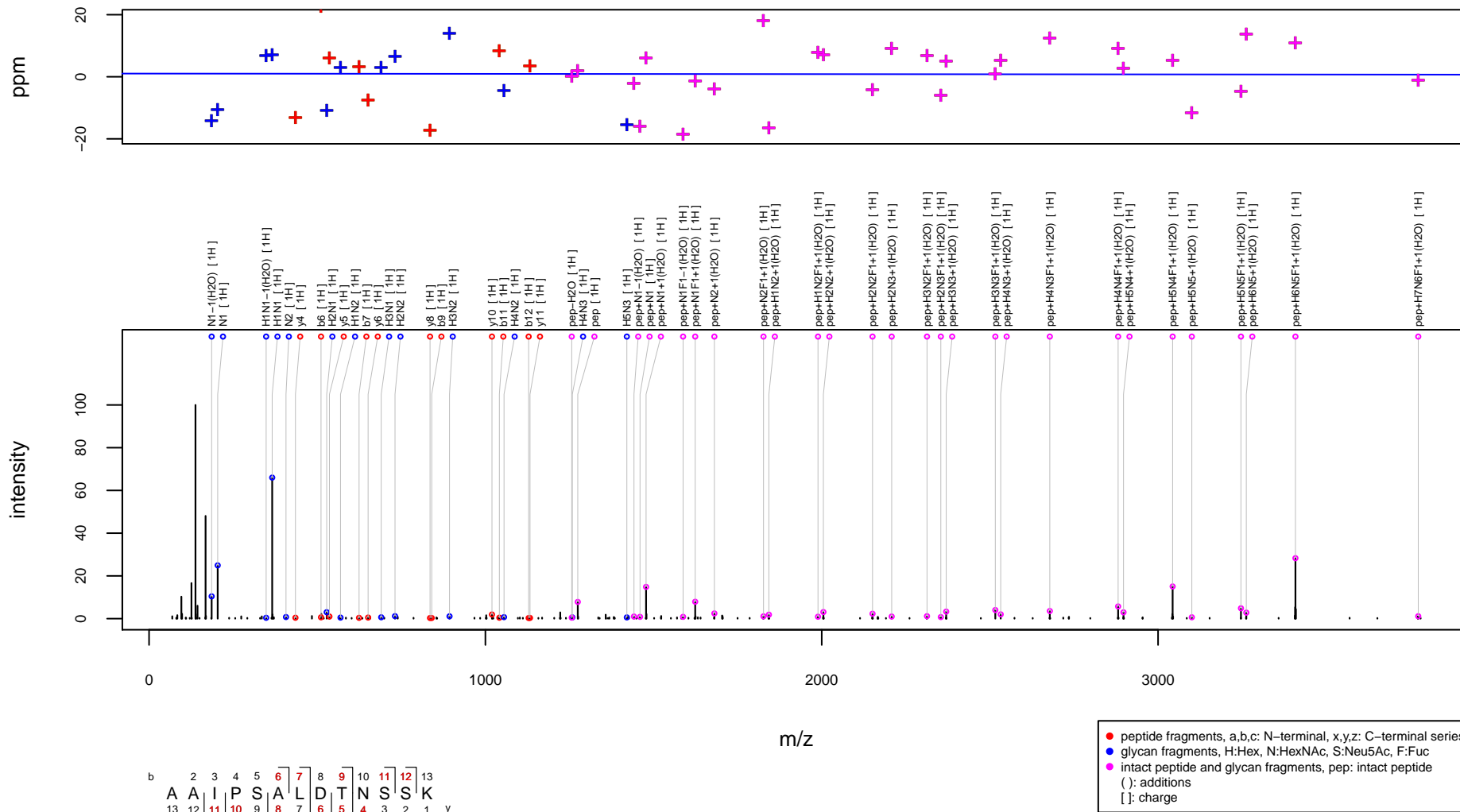
m/z 1258.5253 charge 3 scan 0-0

Score= 73.75 , Hits= 52 , Explained Intensity= 0.48

Peptide: LG3BP_HUMAN[542,554]:AAIPSAALDTNSK

Glycan: HN(HN)H(HN(HN)H)HN(F)N, H7N6F1

Charge: 3H



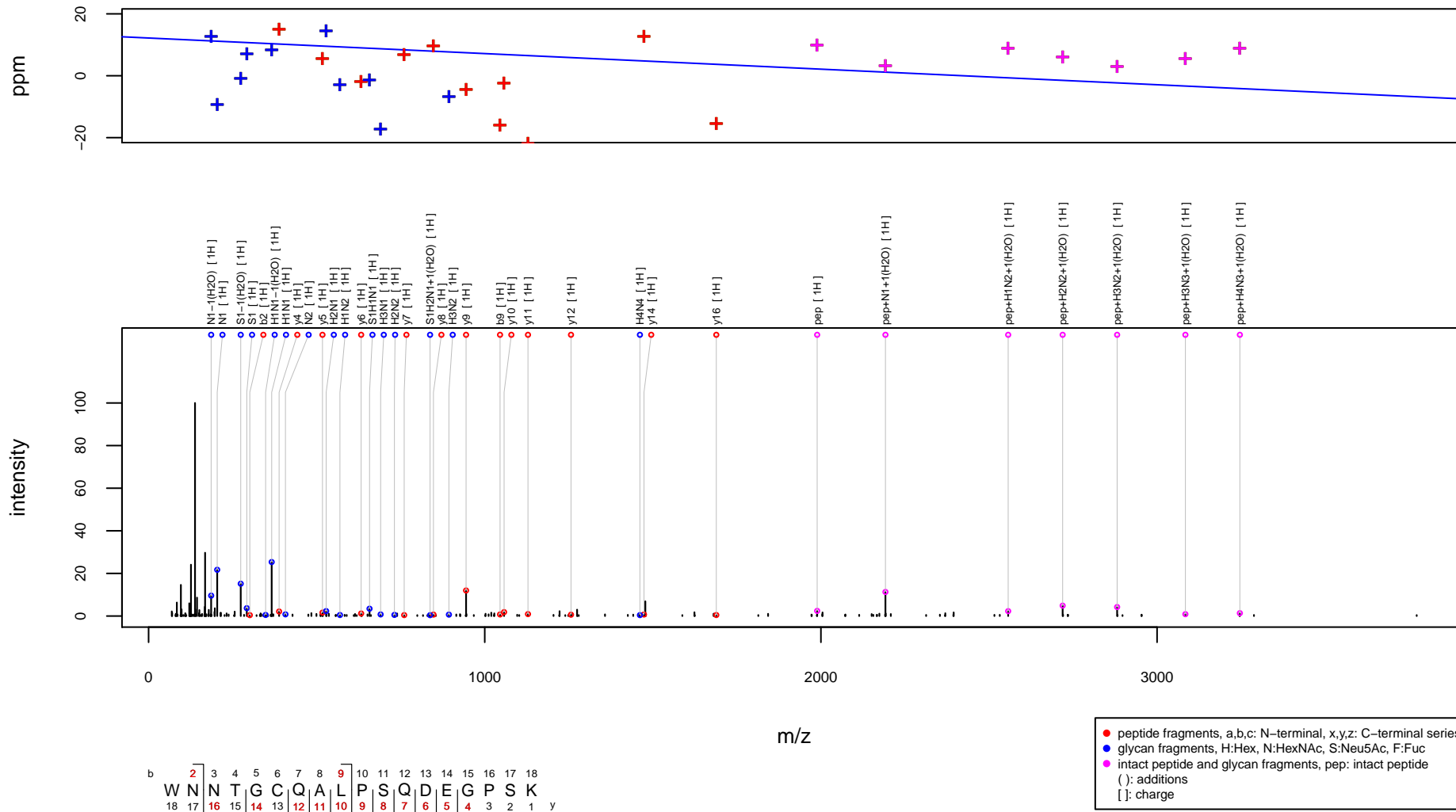
m/z 976.3981 charge 4 scan 0-0

Score= 52.32 , Hits= 35 , Explained Intensity= 0.31

Peptide: PIGR_HUMAN[498,515]:WNNTGQCALPSQDEGPSK

Glycan: SHNH(HNH)HNN, S1H5N4

Charge: 4H



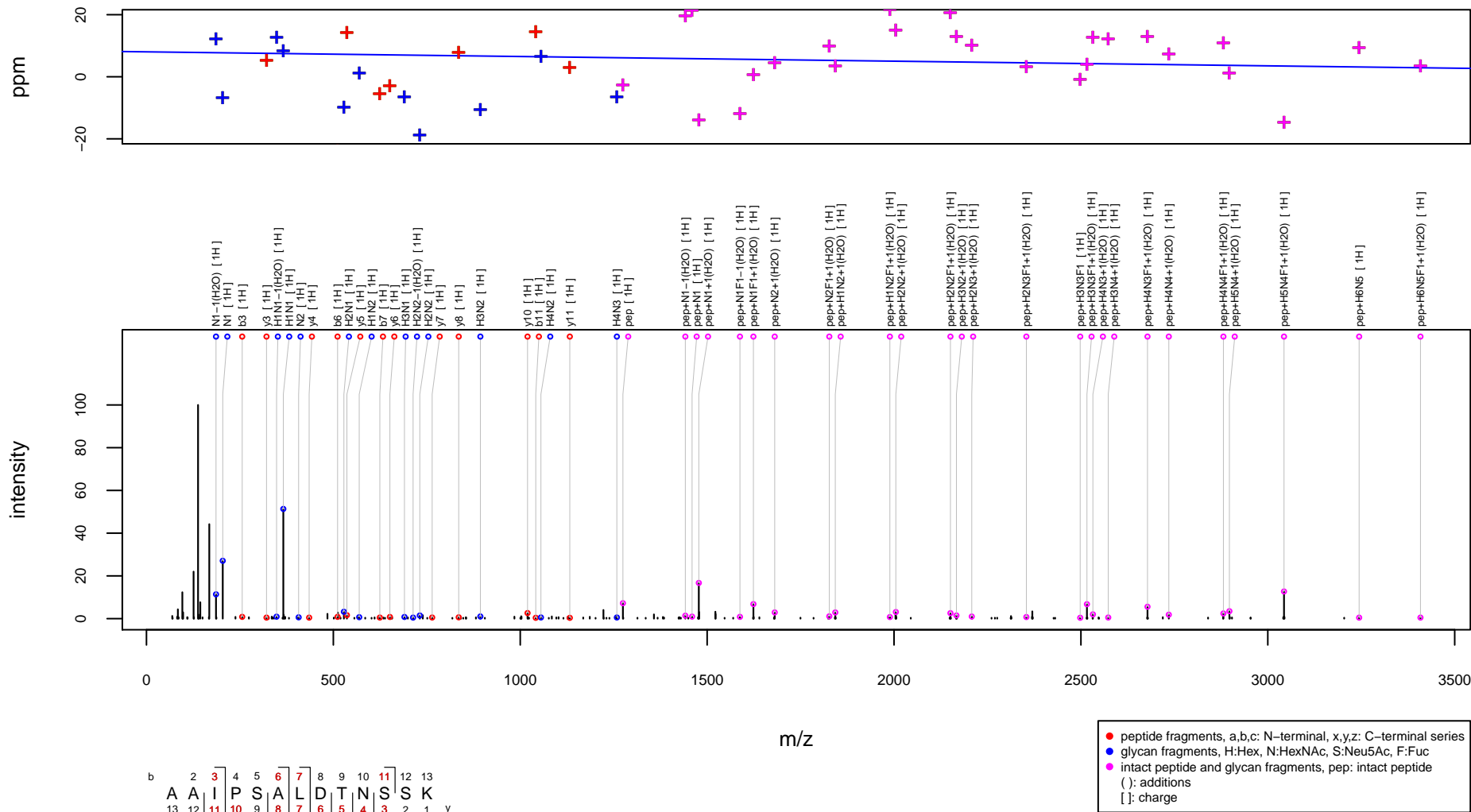
m/z 1136.8113 charge 3 scan 0-0

Score= 74.93 , Hits= 51 , Explained Intensity= 0.41

Peptide: LG3BP_HUMAN[542,554]:AAIP³SALD⁷TNS¹¹SK

Glycan: HNH(HN(HN)H)HN(F)N, H6N5F1

Charge: 3H



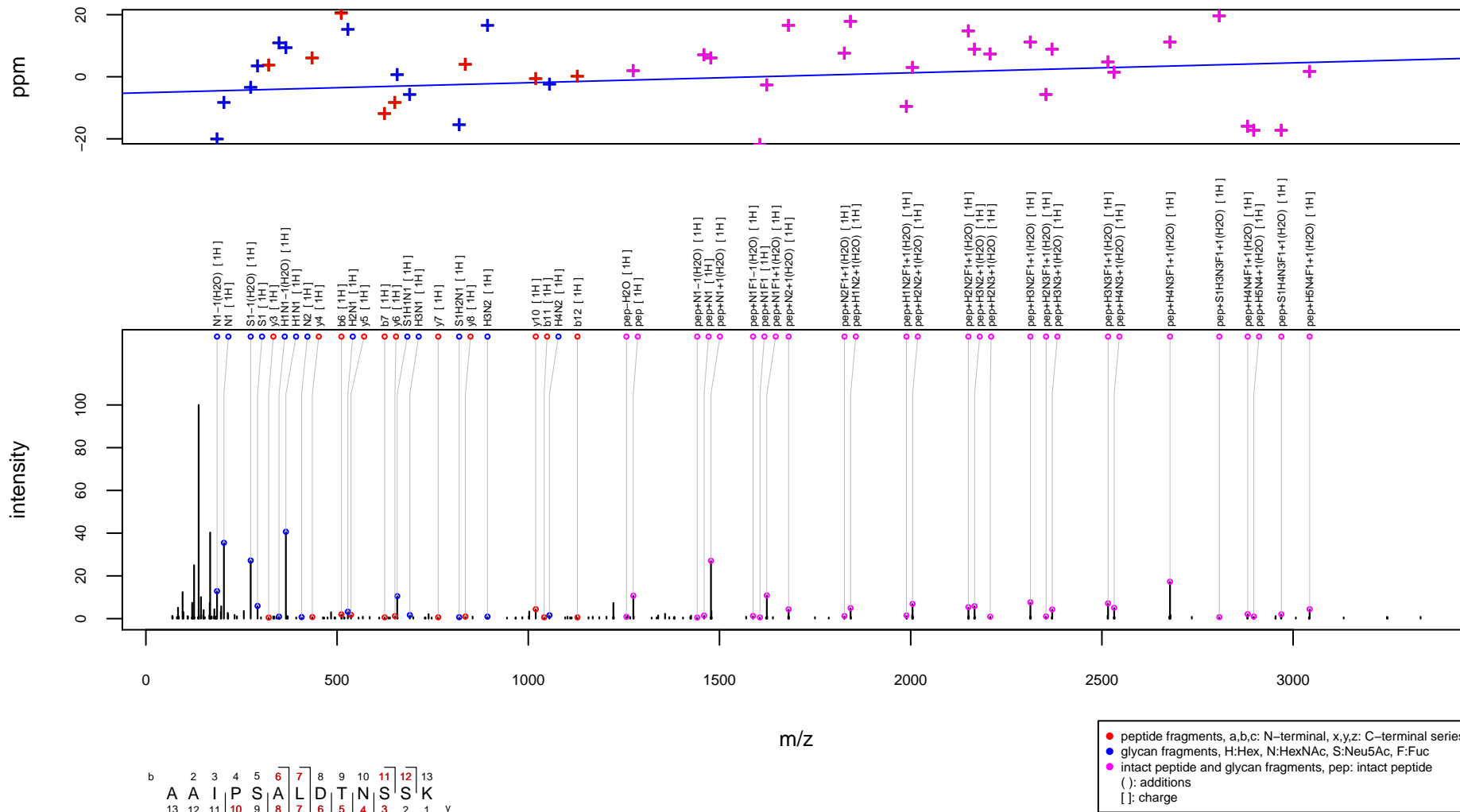
m/z 1112.1368 charge 3 scan 0-0

Score= 74.36 , Hits= 51 , Explained Intensity= 0.46

Peptide: LG3BP_HUMAN[542,554]:AAIP⁶SAL⁷DT⁸NS¹¹SK¹²

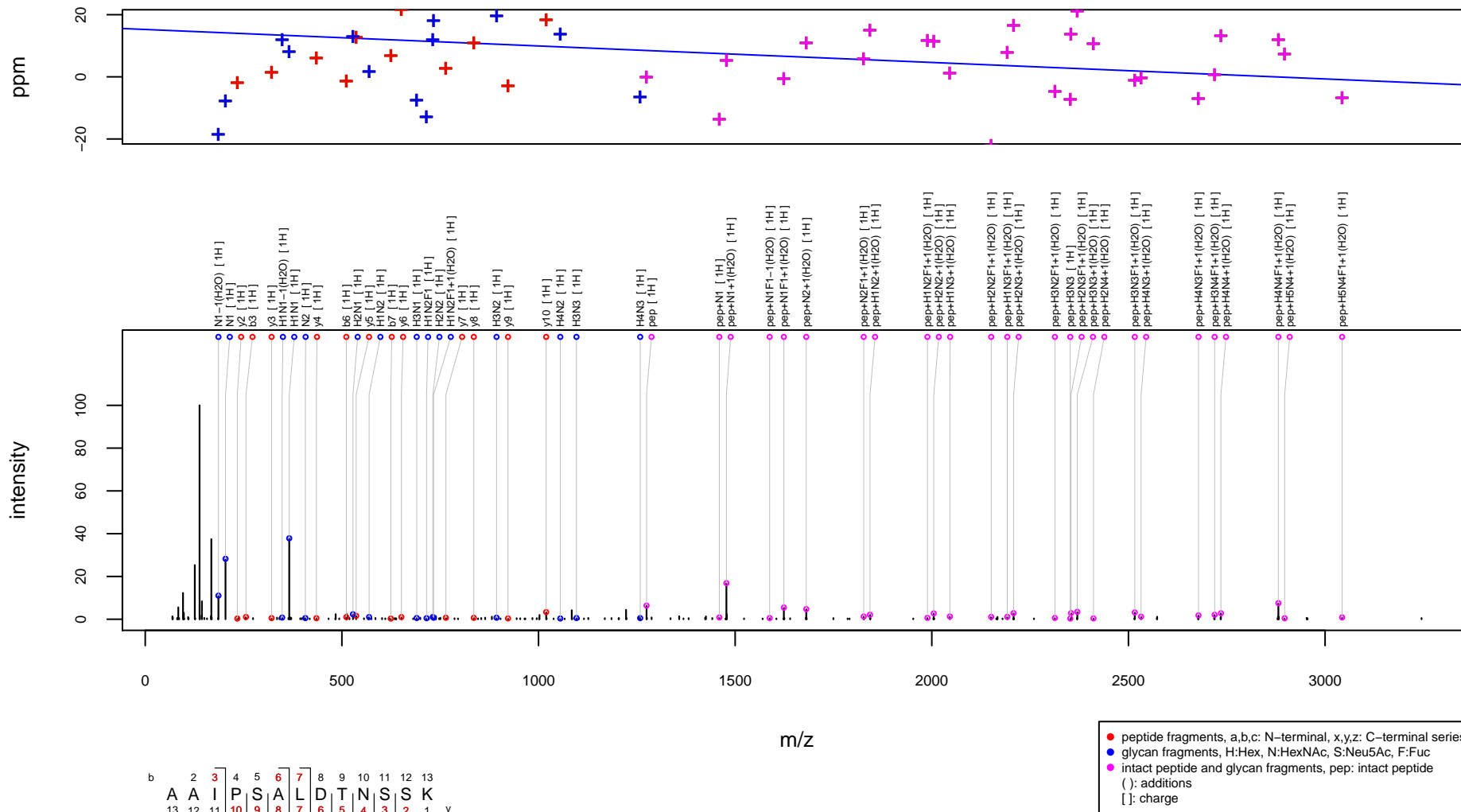
Glycan: SHNH(HNH)HN(F)N, S1H5N4F1

Charge: 3H



m/z 1082.7946 charge 3 scan 0-0

Score= 79.97 , Hits= 54 , Explained Intensity= 0.39
 Peptide: LG3BP_HUMAN[542,554]:AAIPSAALDTNISK
 Glycan: HNH(HNH)(N)HN(F)N, H5N5F1
 Charge: 3H



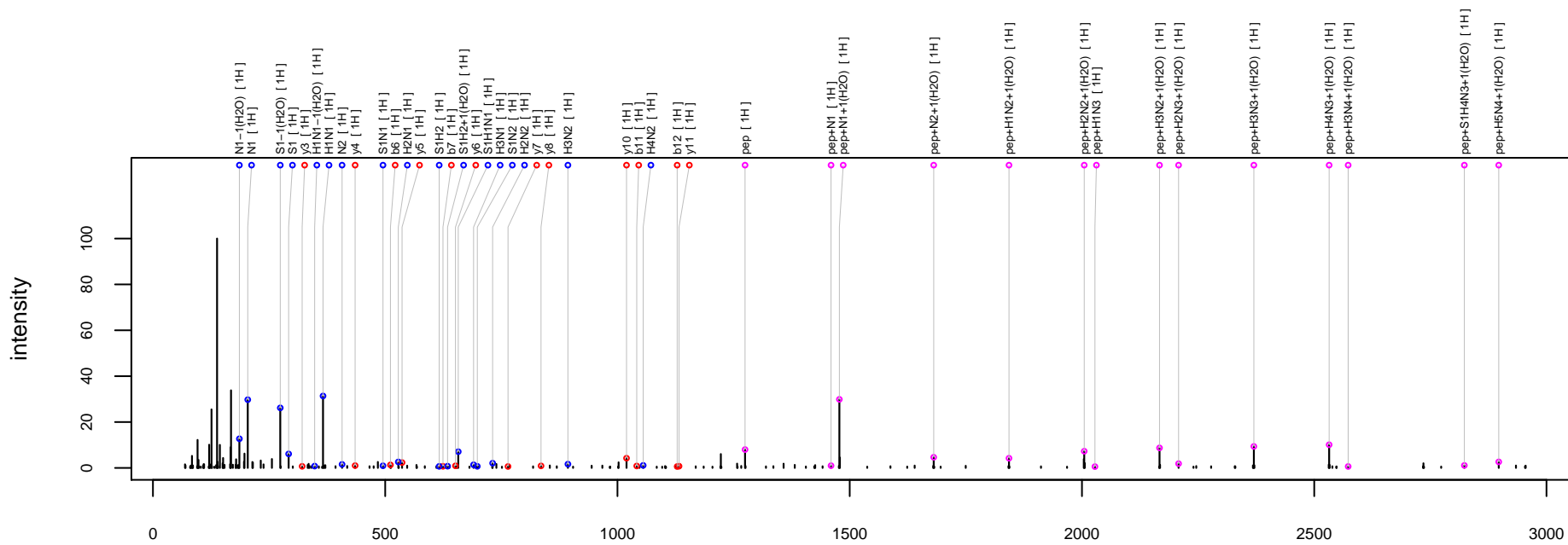
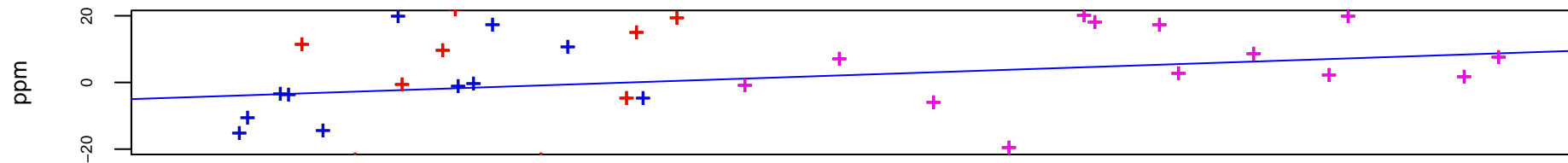
m/z 1063.446 charge 3 scan 0-0

Score= 60.24 , Hits= 43 , Explained Intensity= 0.39

Peptide: LG3BP_HUMAN[542,554]:AAIPSAALDTNSK

Glycan: S1H5N4

Charge: 3H



b 2 3 4 5 6 7 8 9 10 11 12 13
 A A I P S A L D T N S S K
 13 12 11 10 9 8 7 6 5 4 3 2 1 y

● peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
 ● glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
 ● intact peptide and glycan fragments, pep: intact peptide
 (): additions
 []: charge

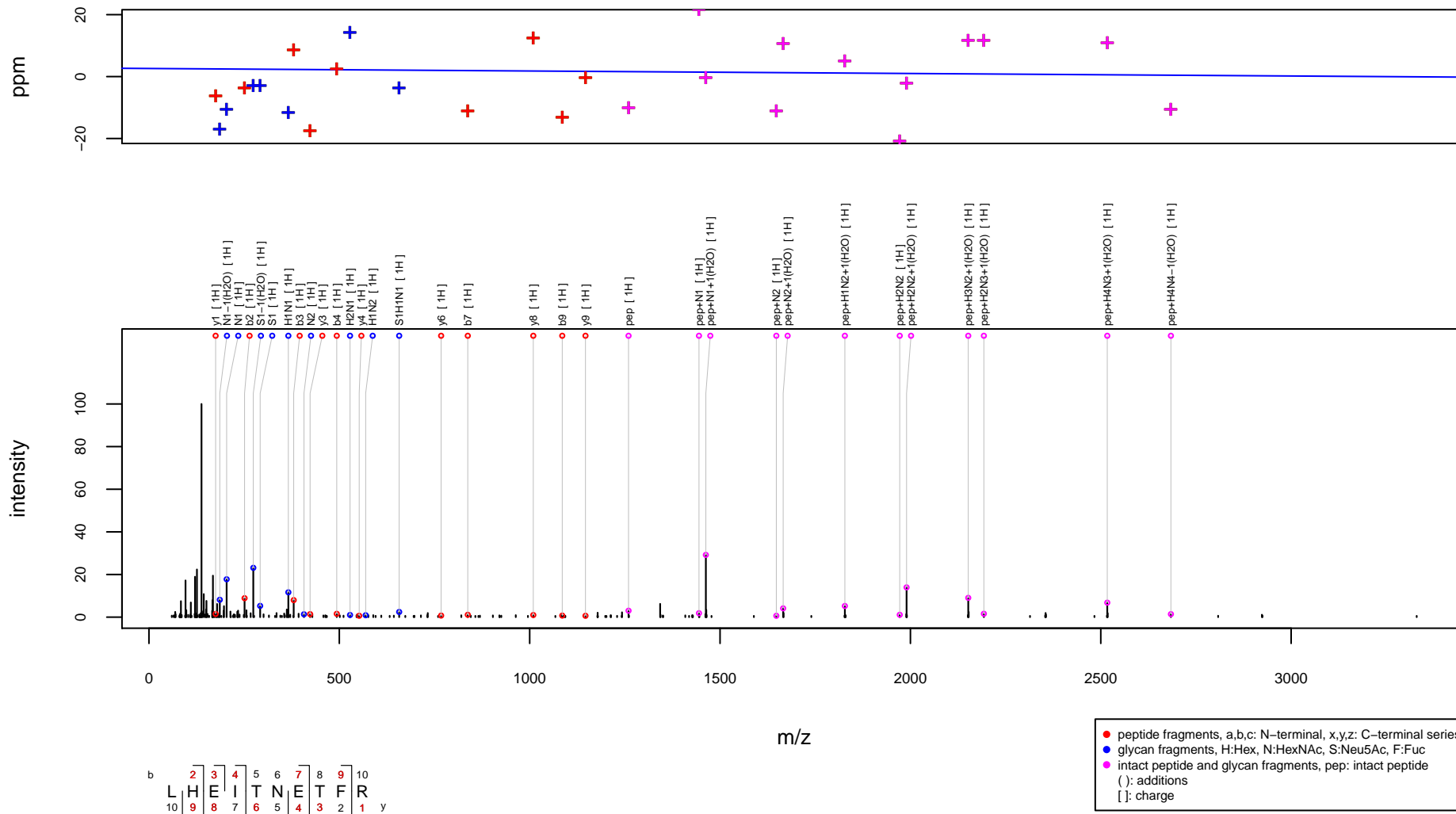
m/z 866.8555 charge 4 scan 0-0

Score= 49.11 , Hits= 32 , Explained Intensity= 0.31

Peptide: VASN_HUMAN[112,121]:LHEITNETFR

Glycan: SHNH(SHNH)HNN, S2H5N4

Charge: 4H



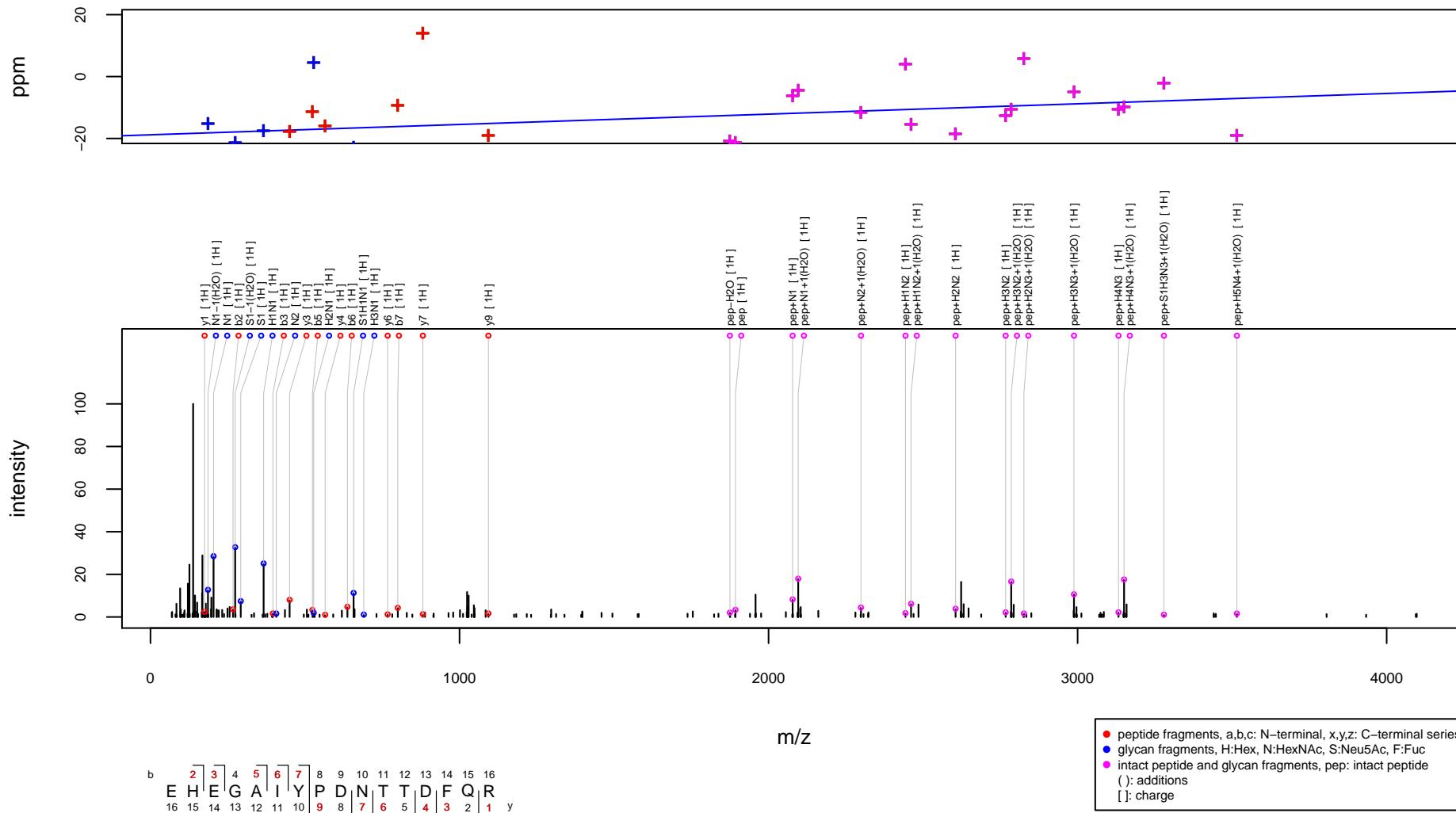
m/z 1025.18 charge 4 scan 0-0

Score= 54.83 , Hits= 36 , Explained Intensity= 0.32

Peptide: CERU_HUMAN[129,144]:EHEGAIYPDNTTDFQR

Glycan: SHNH(SHNH)HNN, S2H5N4

Charge: 4H



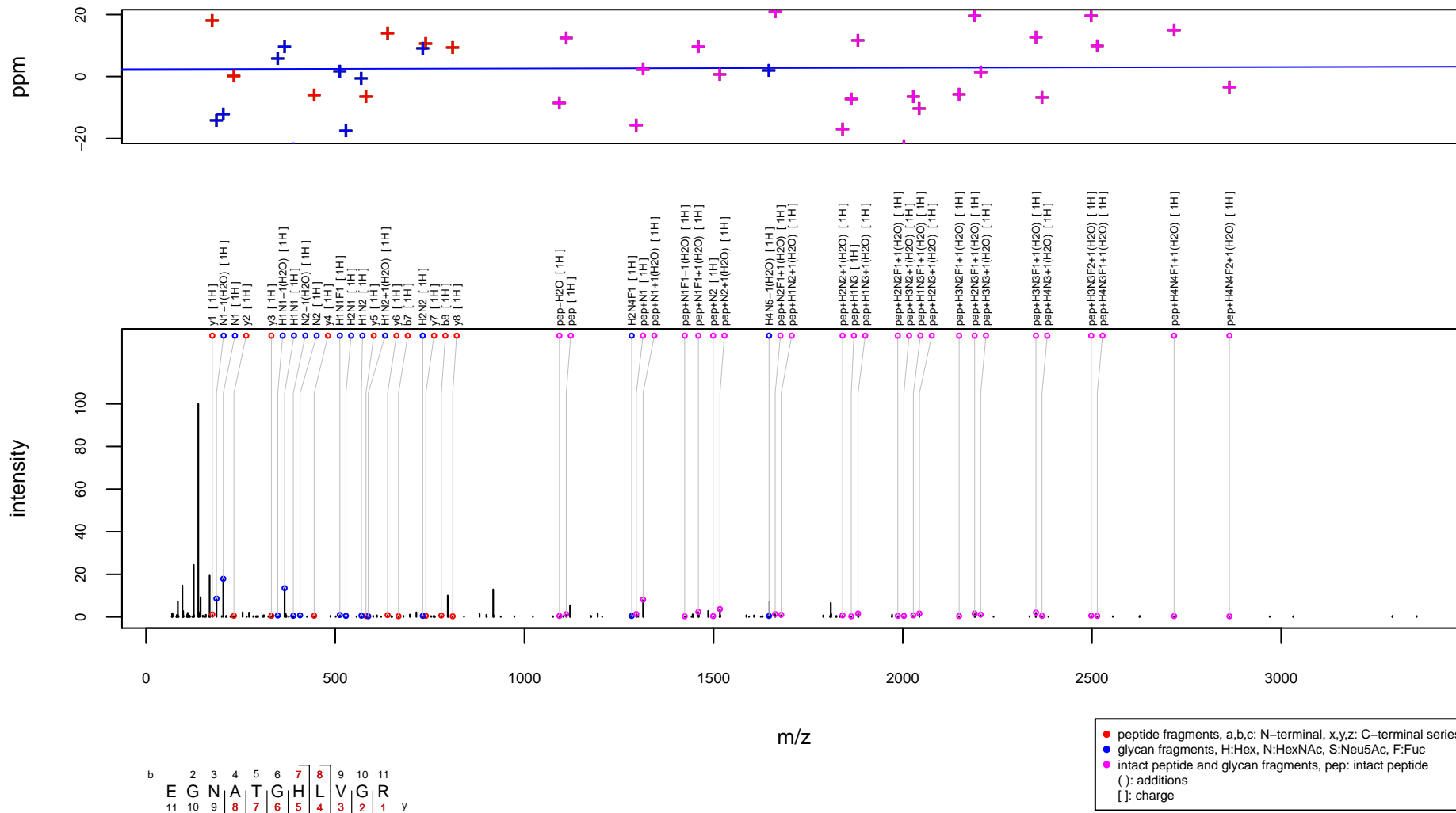
m/z 844.3534 charge 4 scan 0-0

Score= 66.29 , Hits= 49 , Explained Intensity= 0.22

Peptide: CUBN_HUMAN[1800,1810]:EGNATGHLVGR

Glycan: FHNH(FHNH)(N)HN(F)N, H5N5F3

Charge: 4H



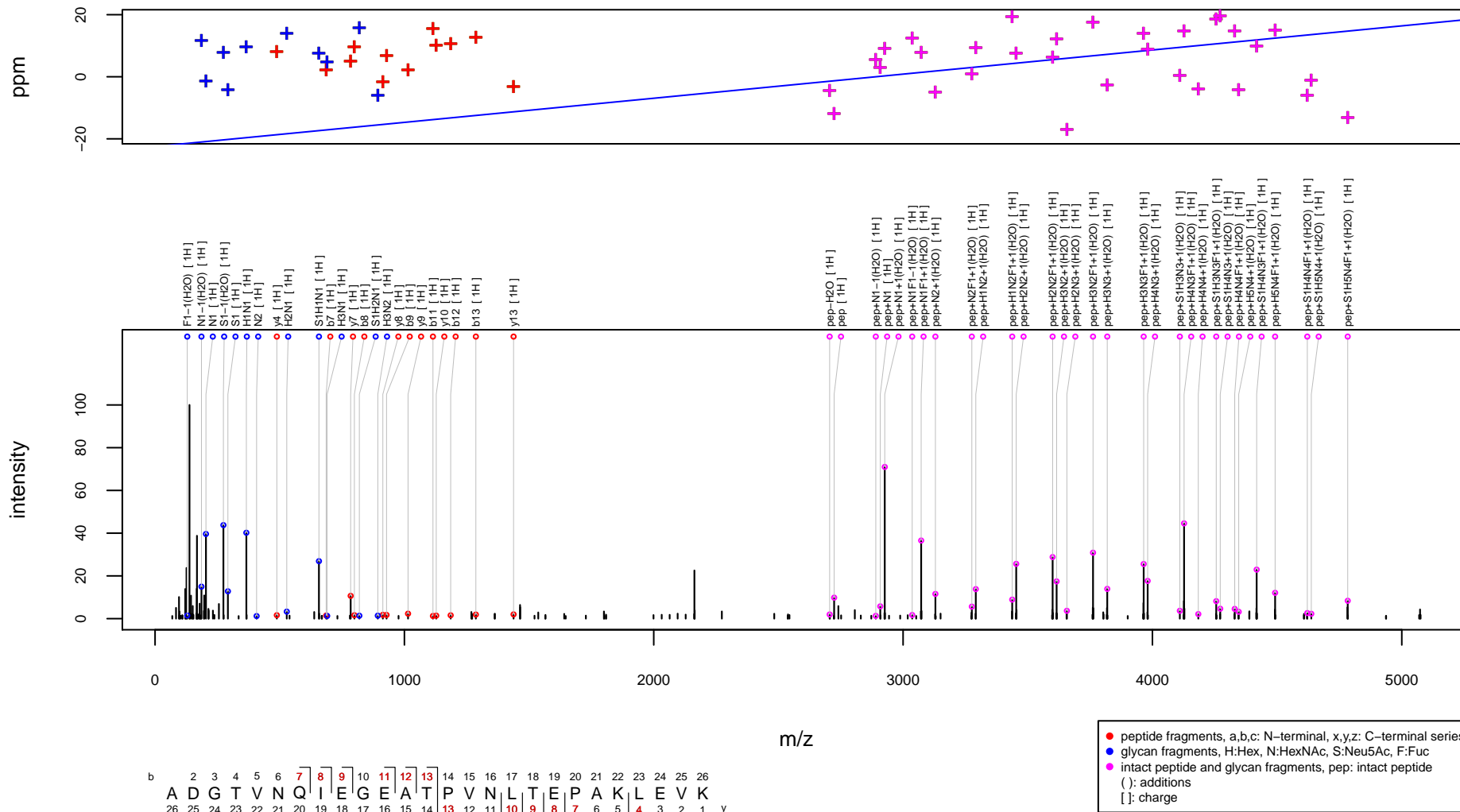
m/z 1269.308 charge 4 scan 0-0

Score= 83.14 , Hits= 55 , Explained Intensity= 0.55

Peptide: APOD_HUMAN[83,108]:ADGTVNQIEGEATPVNLTEPAKLEVK

Glycan: SHNH(SHNH)HN(F)N, S2H5N4F1

Charge: 4H



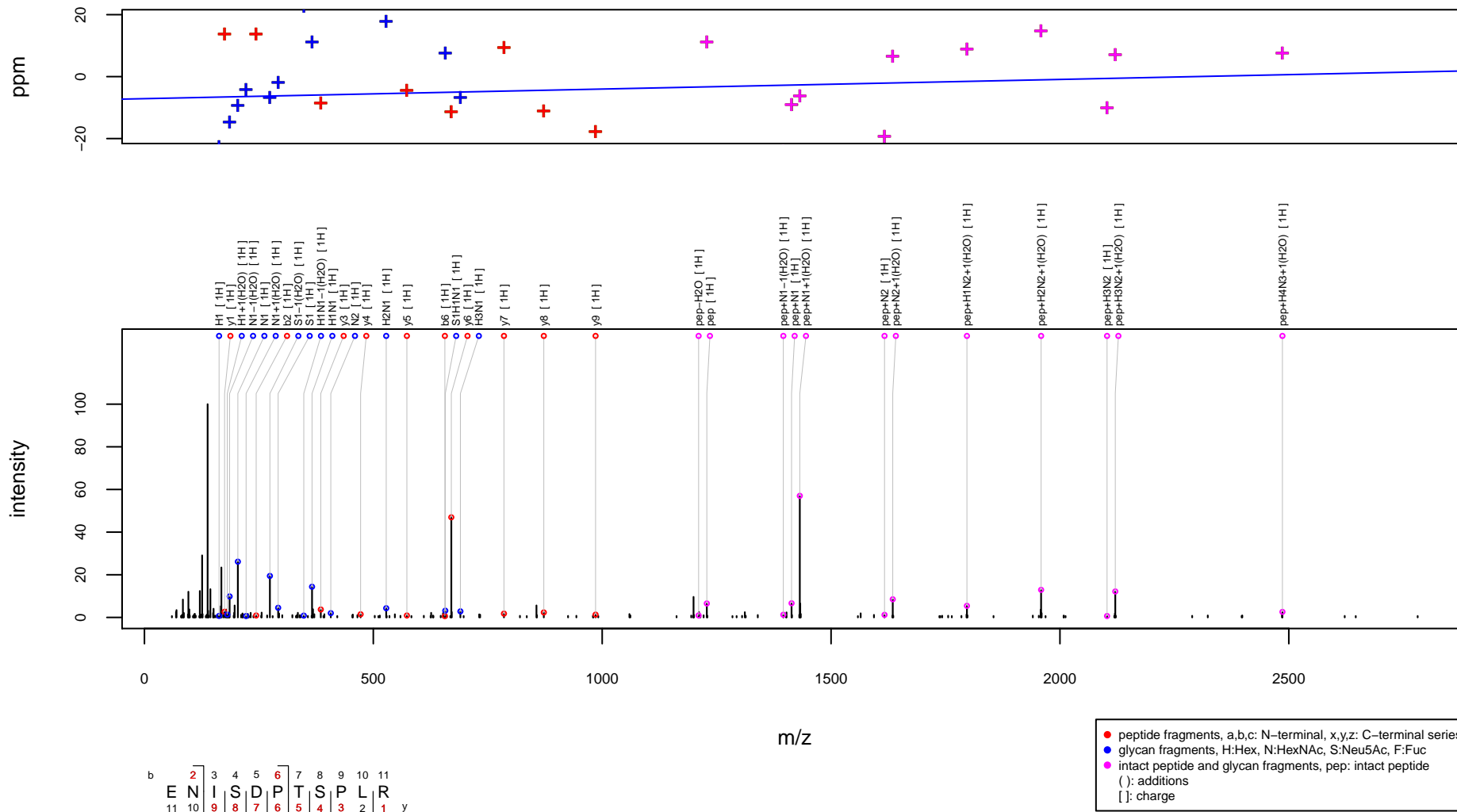
m/z 926.3891 charge 3 scan 0-0

Score= 57.09 , Hits= 35 , Explained Intensity= 0.43

Peptide: IGJ_HUMAN[70,80]:ENISDPTSPLR

Glycan: SHNH(H)HNN, S1H4N3

Charge: 3H



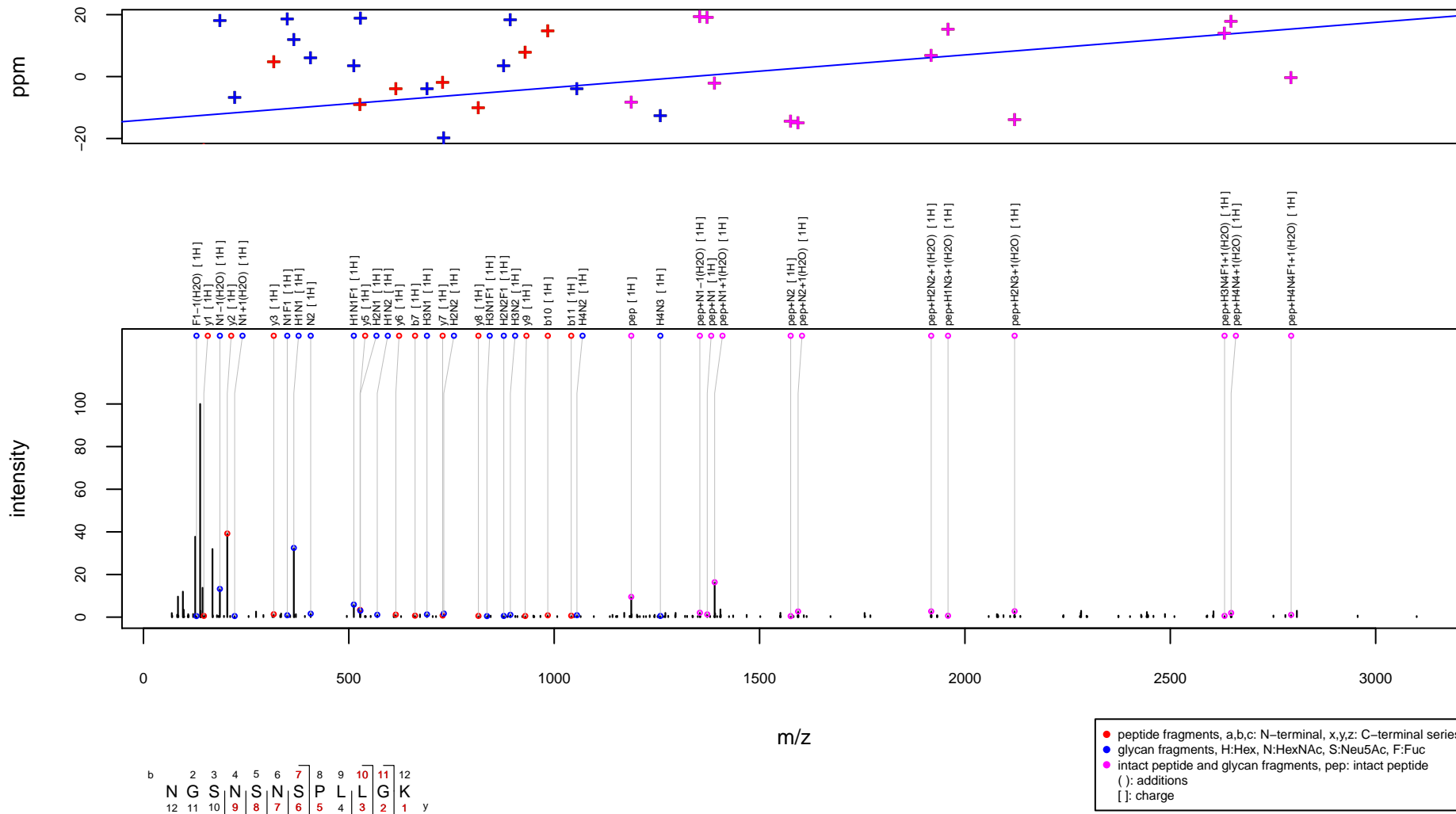
m/z 1053.7725 charge 3 scan 0-0

Score= 54.58 , Hits= 39 , Explained Intensity= 0.34

Peptide: CUBN_HUMAN[3457,3468]:NGSNSNSPLL GK

Glycan: HNH(F(H)NH)(N)HNN, H5N5F1

Charge: 3H



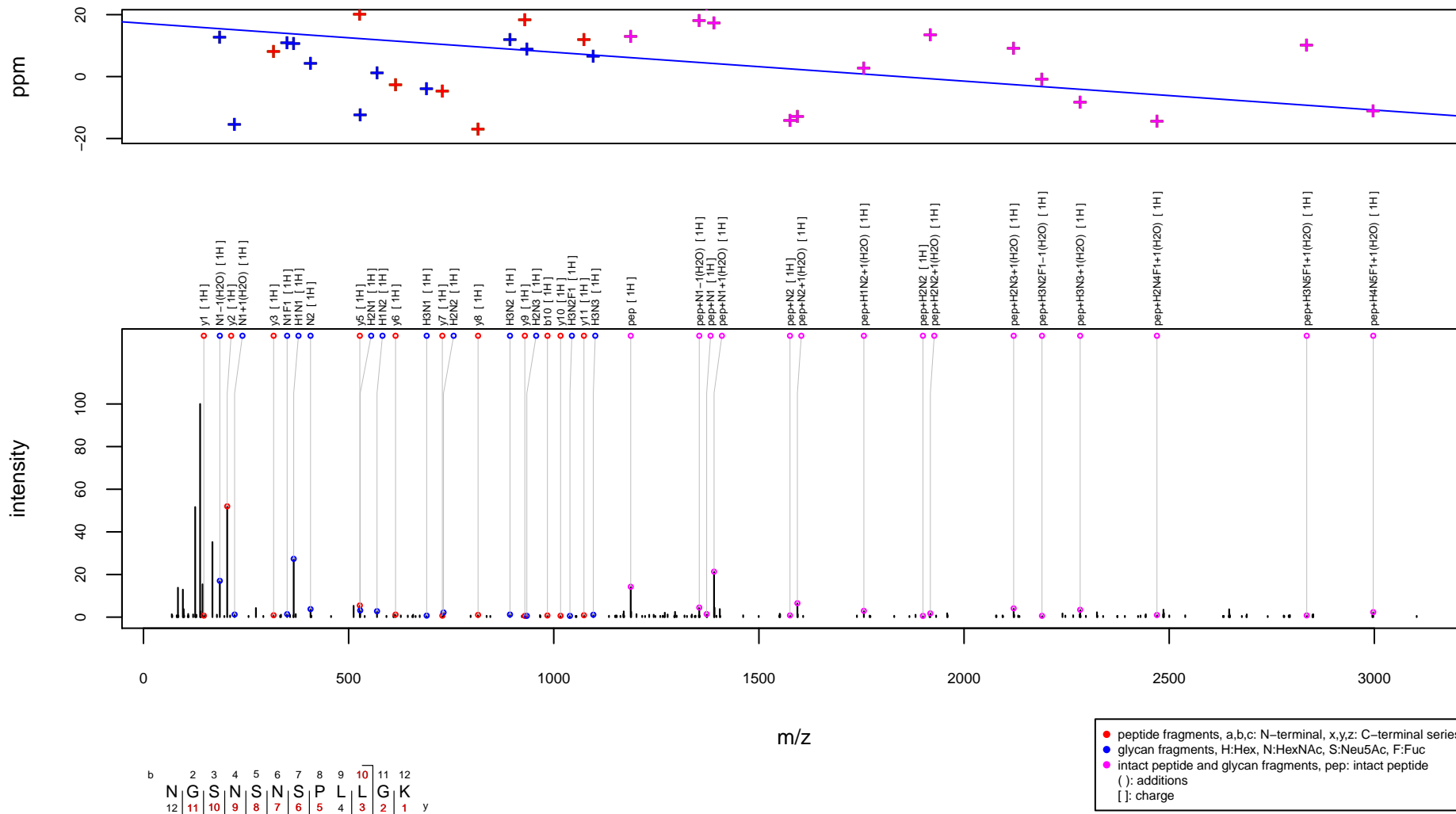
m/z 1067.4501 charge 3 scan 0-0

Score= 54.44 , Hits= 39 , Explained Intensity= 0.36

Peptide: CUBN_HUMAN[3457,3468]:NGSNSNSPLL GK

Glycan: NN(HN)H(NH)HN(F)N, H4N6F1

Charge: 3H



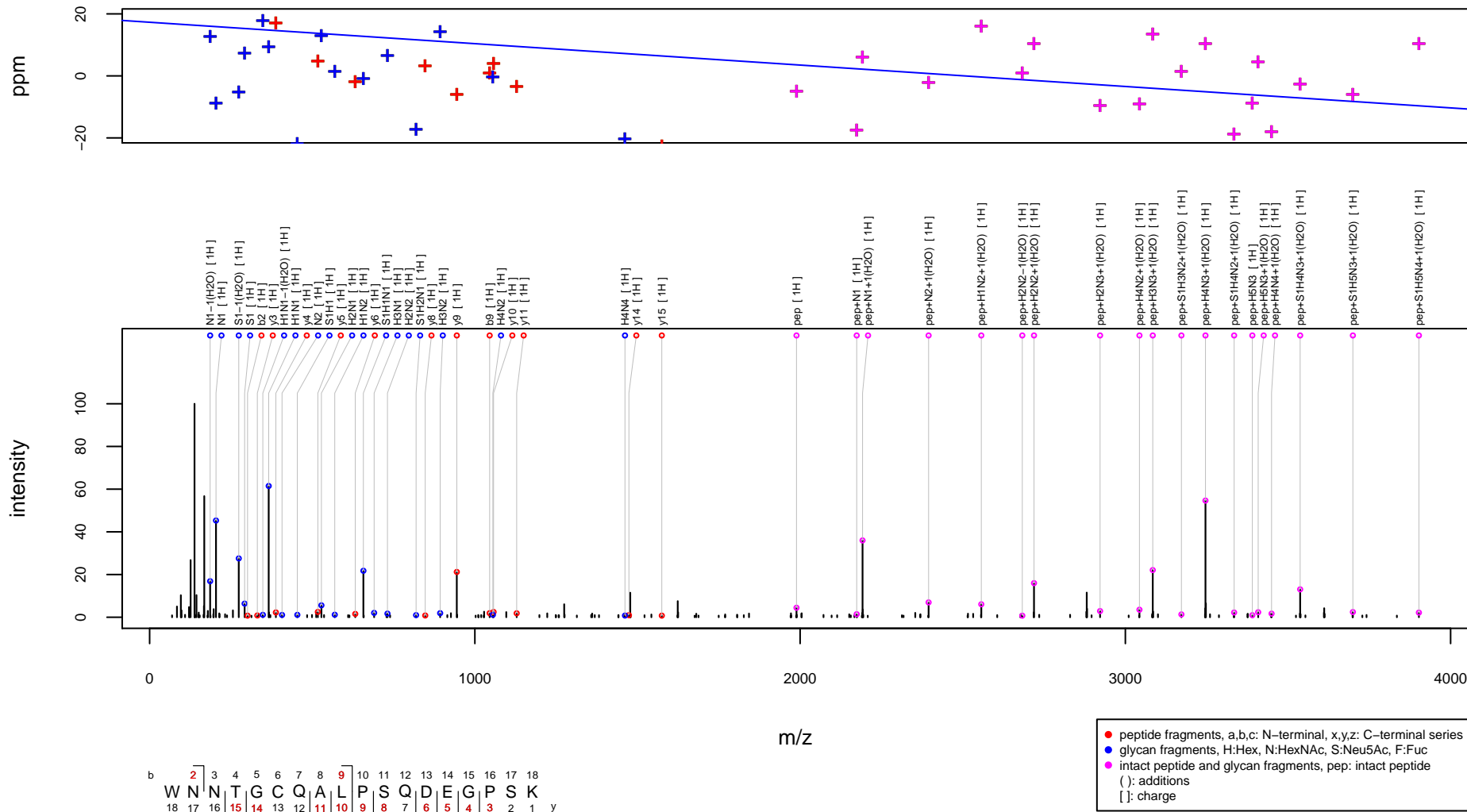
m/z 1301.5304 charge 3 scan 0-0

Score= 69.16 , Hits= 48 , Explained Intensity= 0.5

Peptide: PIGR_HUMAN[498,515]:WNN**T**GCQALPSQDEG**P**SK

Glycan: S1H5N4

Charge: 3H



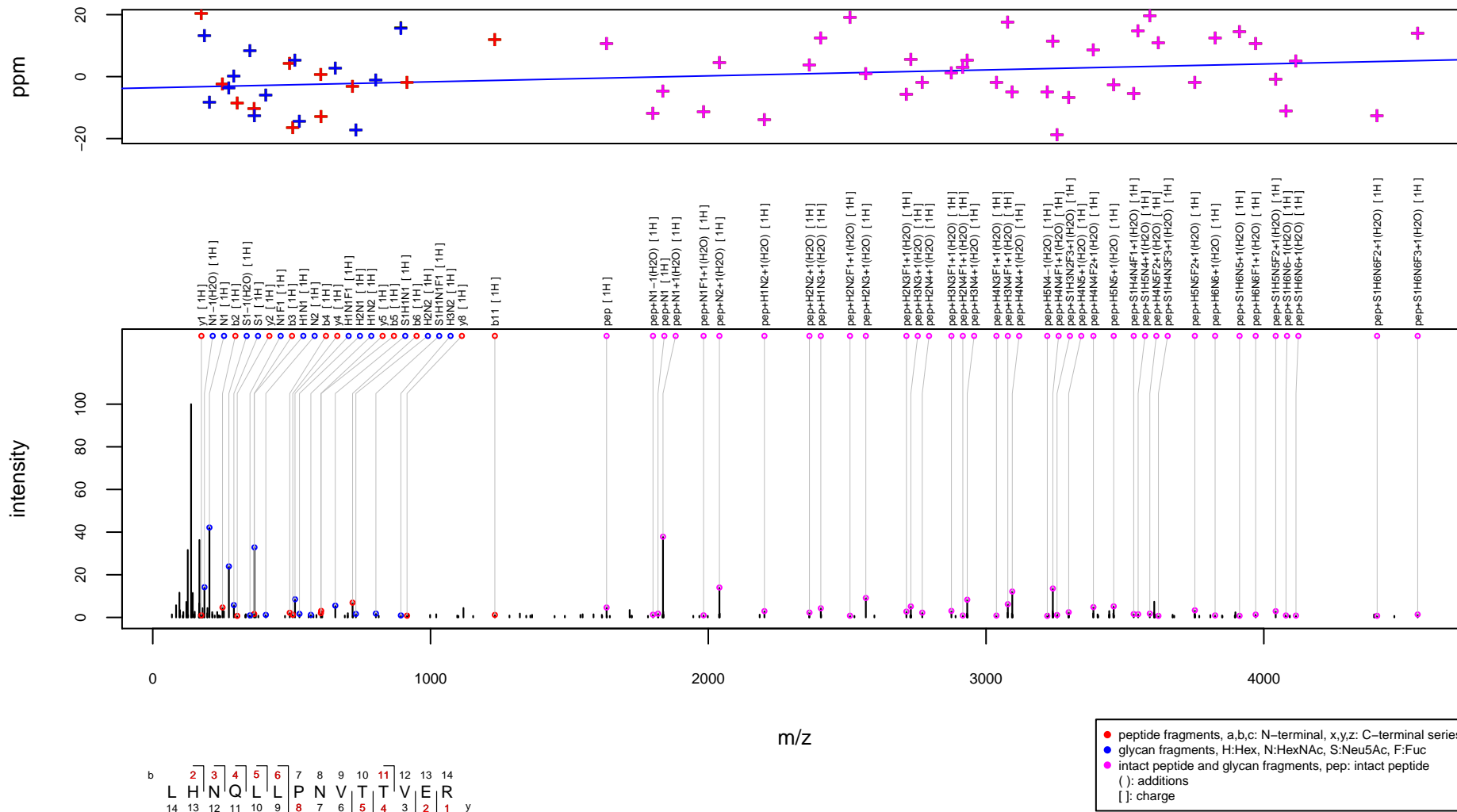
m/z 1139.2382 charge 4 scan 0-0

Score= 56.5 , Hits= 64 , Explained Intensity= 0.48

Peptide: GGTL1_HUMAN[160,173];LHNQLLPNVTTVER

Glycan: S1H6N6F3

Charge: 4H



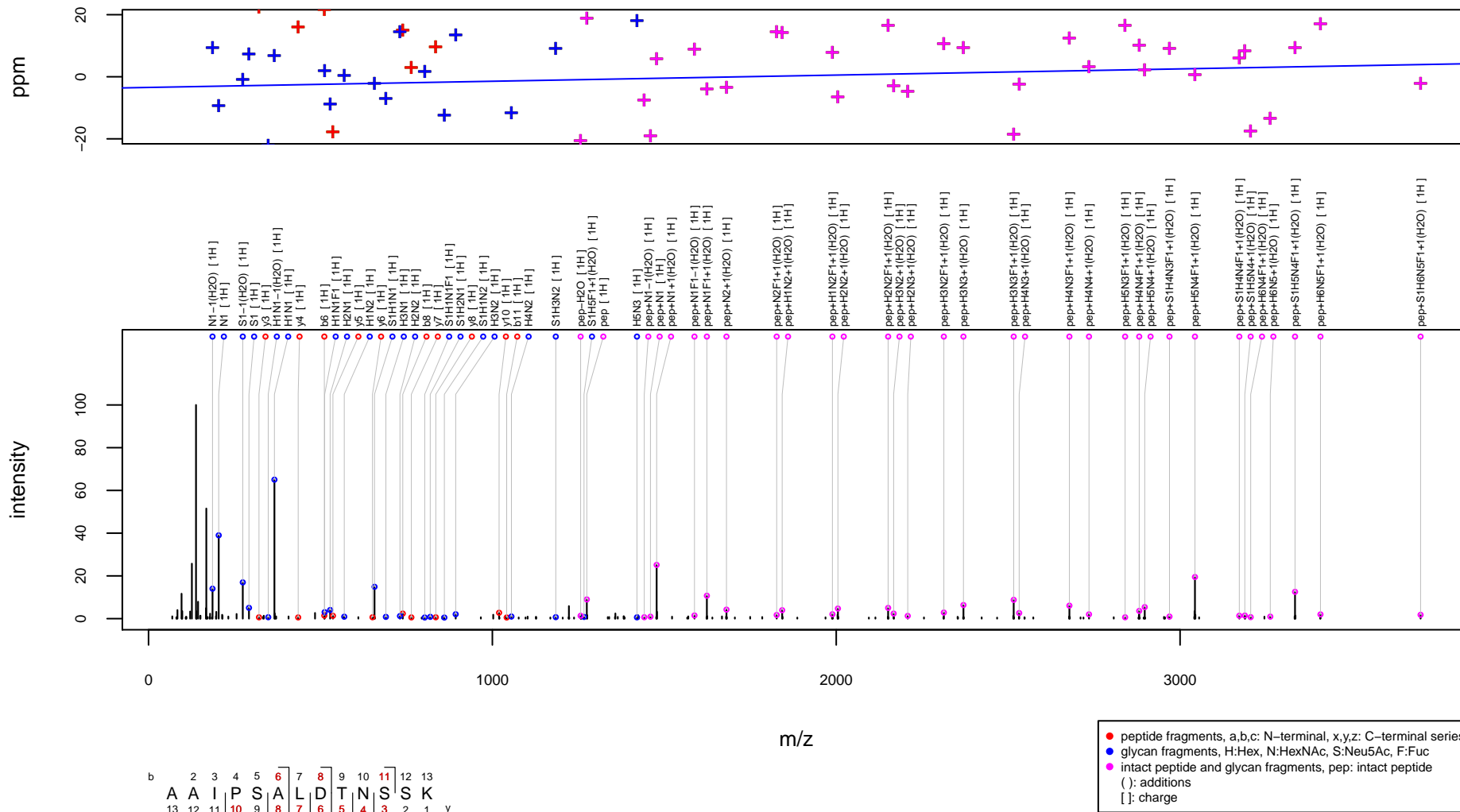
m/z 1233.8455 charge 3 scan 0-0

Score= 71.32 , Hits= 63 , Explained Intensity= 0.51

Peptide: LG3BP_HUMAN[542,554]:AAIPSAALDTNSK

Glycan: S1H6N5F1

Charge: 3H



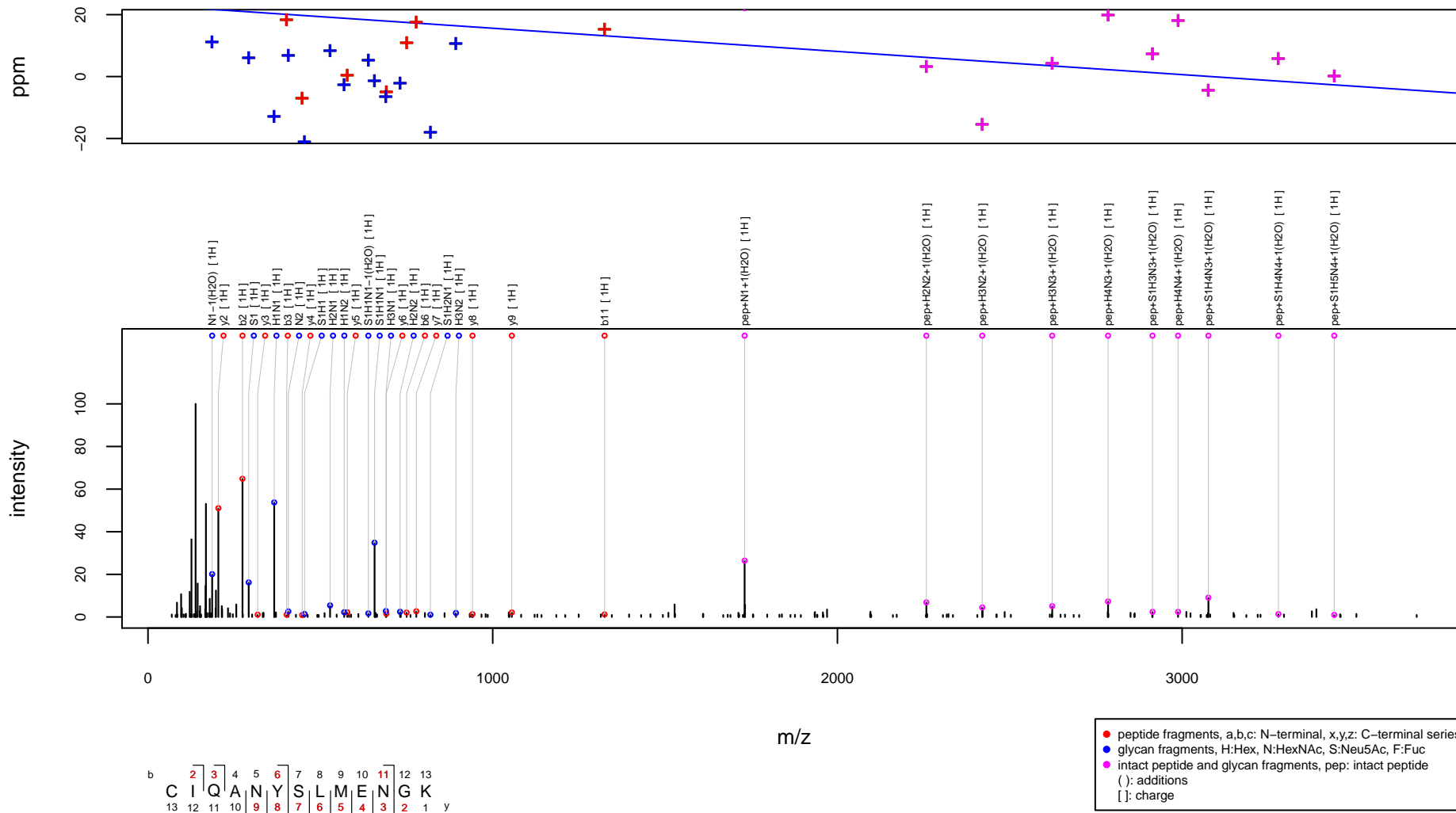
m/z 1244.8206 charge 3 scan 0-0

Score= 52.94 , Hits= 35 , Explained Intensity= 0.44

Peptide: APOD_HUMAN[61,73]:CIQANYSLMENGK

Glycan: SHNH(SHNH)HNN, S2H5N4

Charge: 3H



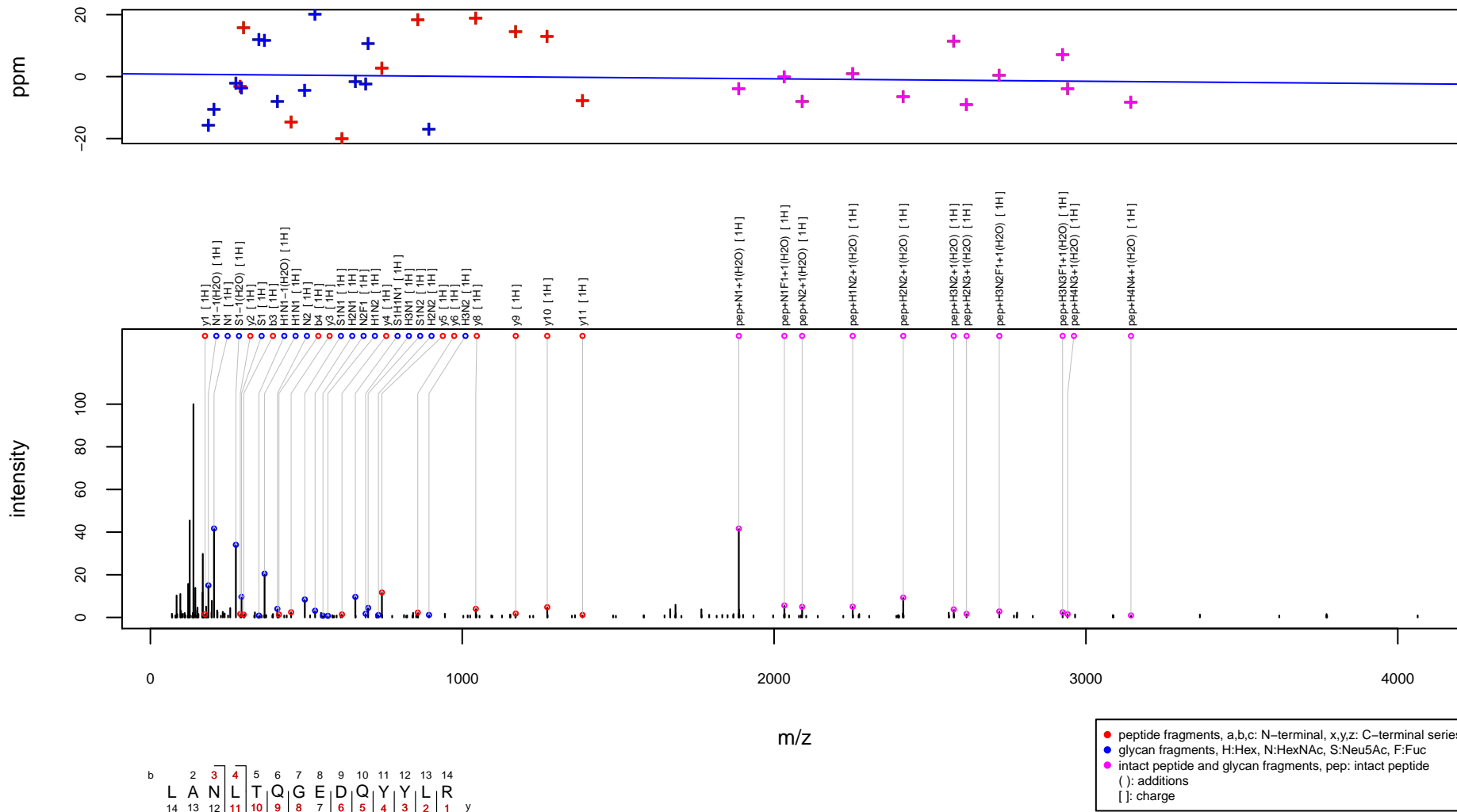
m/z 1019.6771 charge 4 scan 0-0

Score= 51.93 , Hits= 39 , Explained Intensity= 0.39

Peptide: CLUS_HUMAN[372,385]:LANLTQGEDQYYLR

Glycan: SNNH(SHNH)HN(F)N, S2H4N5F1

Charge: 4H



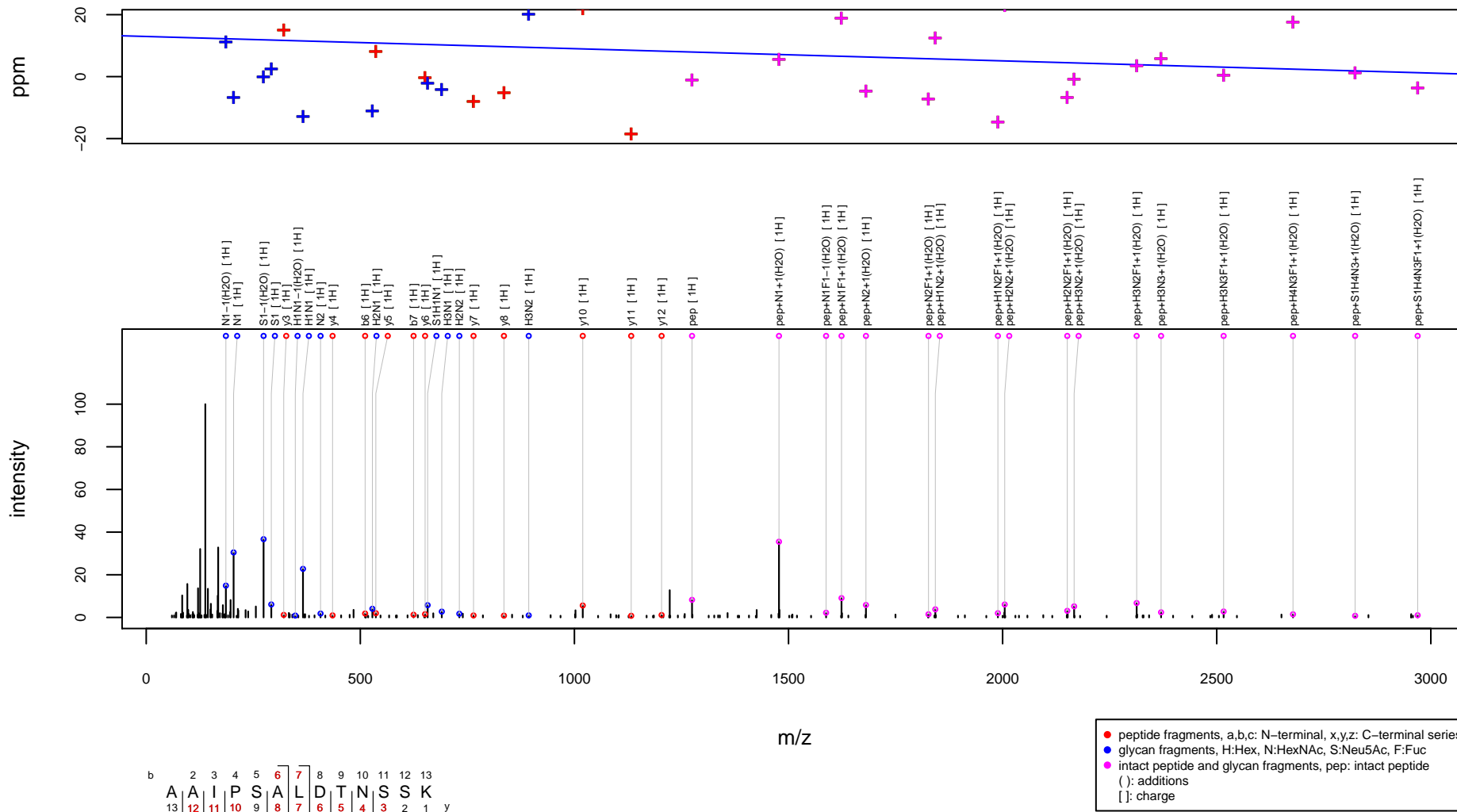
m/z 990.419 charge 3 scan 0-0

Score= 59.35 , Hits= 40 , Explained Intensity= 0.36

Peptide: LG3BP_HUMAN[542,554]:AAIPSA LDTNSSK

Glycan: SHNH(H)HN(F)N, S1H4N3F1

Charge: 3H



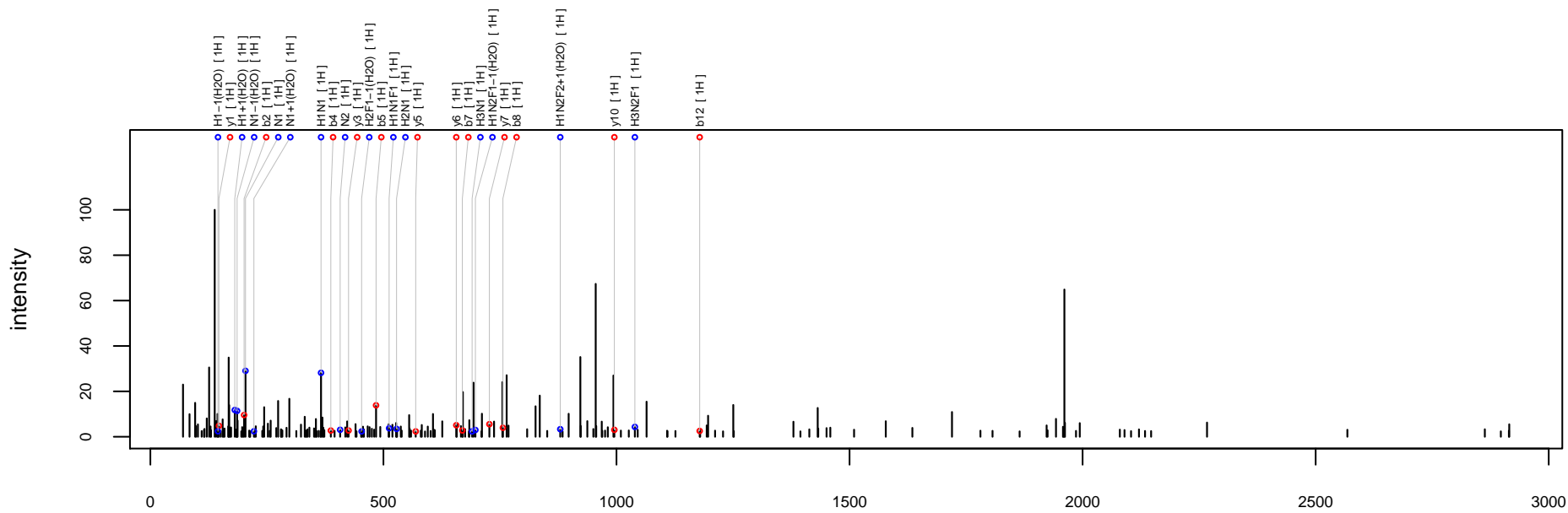
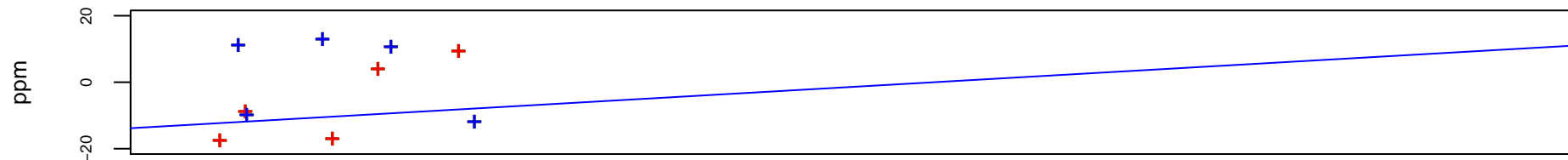
m/z 972.4312 charge 3 scan 0-0

Score= 34.35 , Hits= 26 , Explained Intensity= 0.12

Peptide: Z518A_HUMAN[404,416]:AEEGPNASSGFMK

Glycan: H3N4F2

Charge: 3H



b

	2	3	4	5	6	7	8	9	10	11	12	13
A	E	E	G	P	N	A	S	S	G	F	M	K
13	12	11	10	9	8	7	6	5	4	3	2	1

 y

● peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
 ● glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
 ● intact peptide and glycan fragments, pep: intact peptide
 (): additions
 []: charge

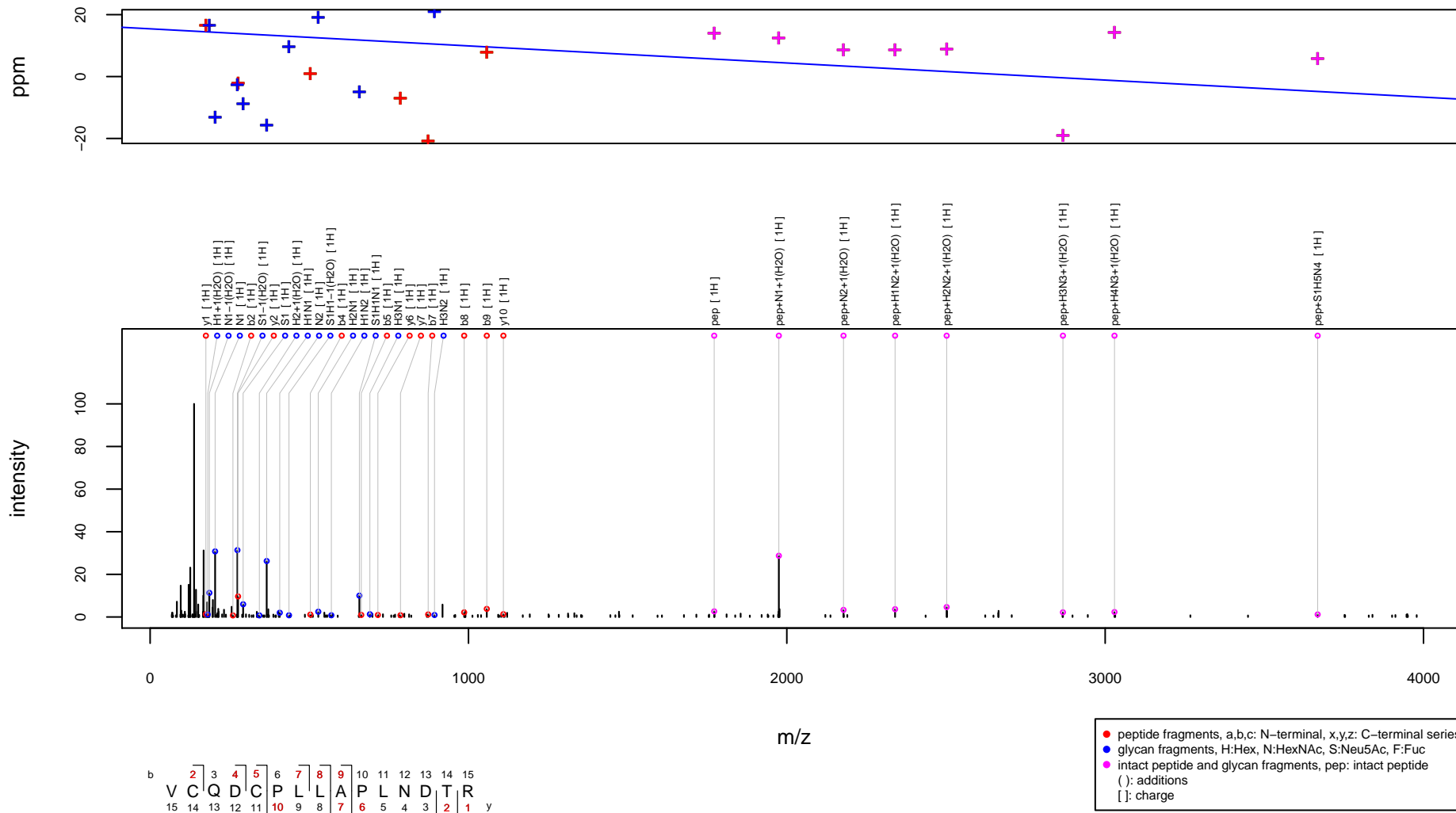
m/z 994.9092 charge 4 scan 0-0

Score= 49.16 , Hits= 33 , Explained Intensity= 0.32

Peptide: FETUA_HUMAN[145,159]:VCQDCPLLAPLNDTR

Glycan: SHNH(SHNH)HNN, S2H5N4

Charge: 4H



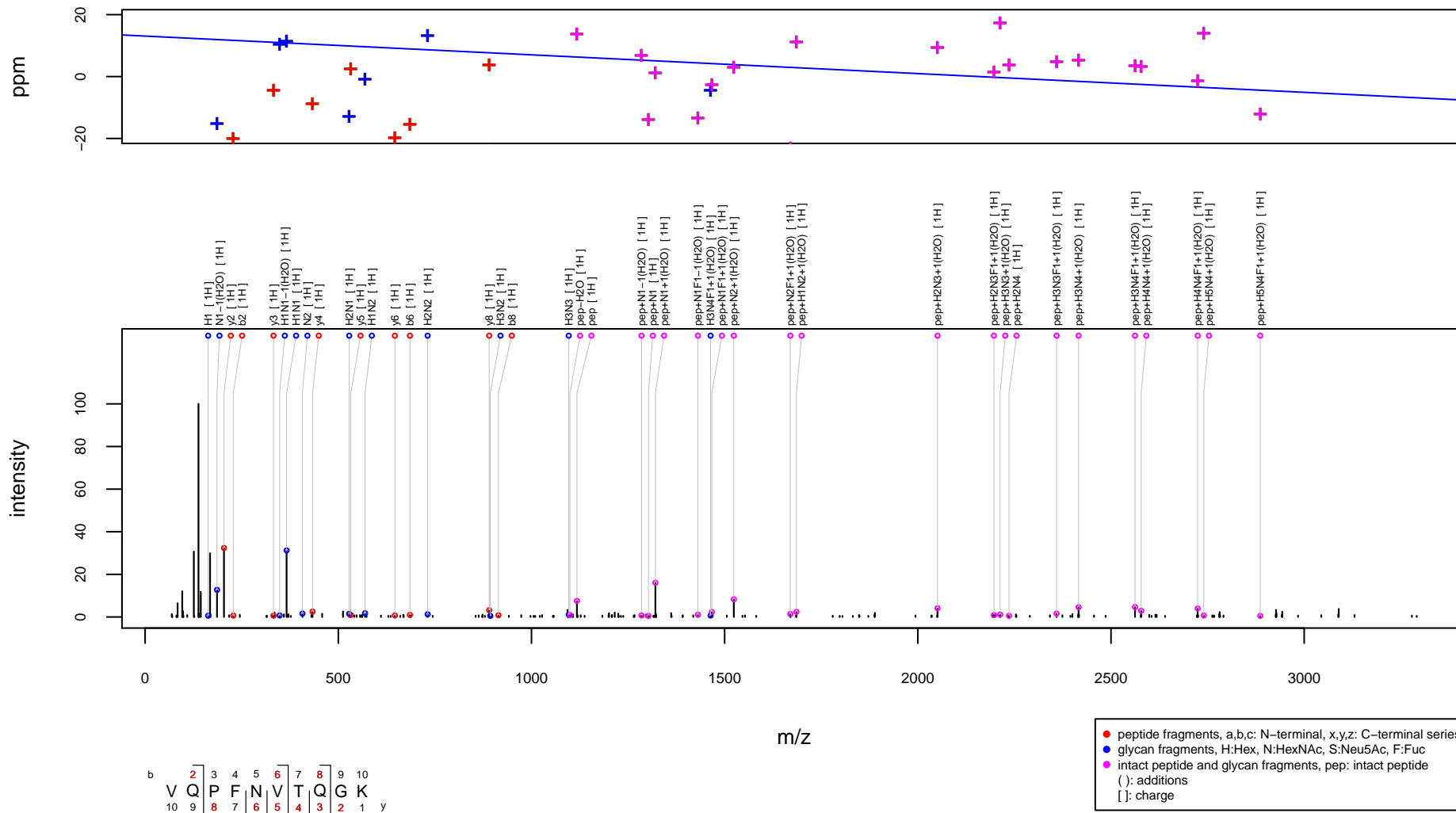
m/z 1098.136 charge 3 scan 0-0

Score= 56.91 , Hits= 41 , Explained Intensity= 0.36

Peptide: LAMP2_HUMAN[352,361]:VQPFNVTQ GK

Glycan: NNH(HN(HN)H)HN(F)N, H5N6F1

Charge: 3H



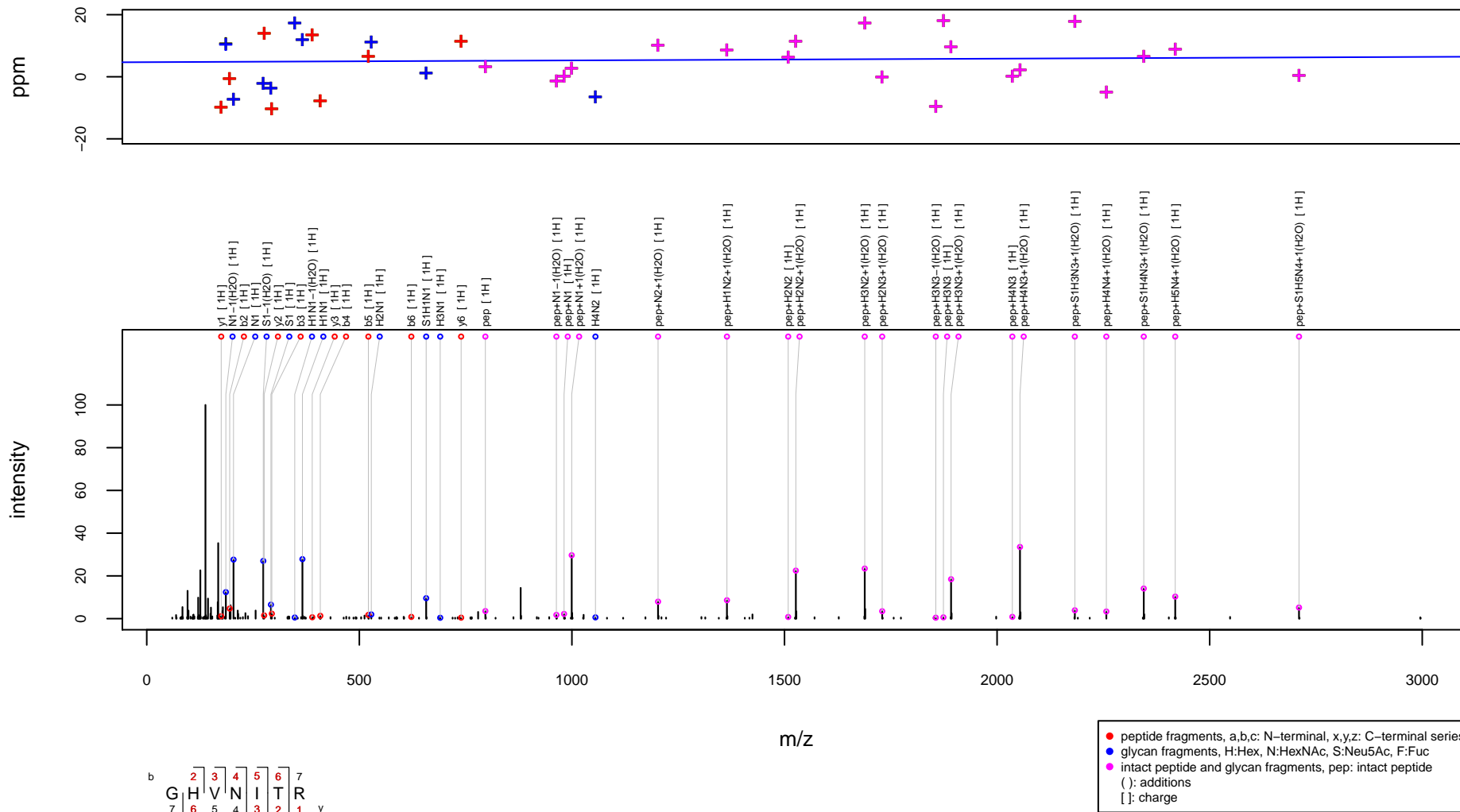
m/z 1001.0784 charge 3 scan 0-0

Score= 62.1 , Hits= 39 , Explained Intensity= 0.47

Peptide: THRB_HUMAN[118,124]:GHVNITR

Glycan: SHNH(SHNH)HNN, S2H5N4

Charge: 3H



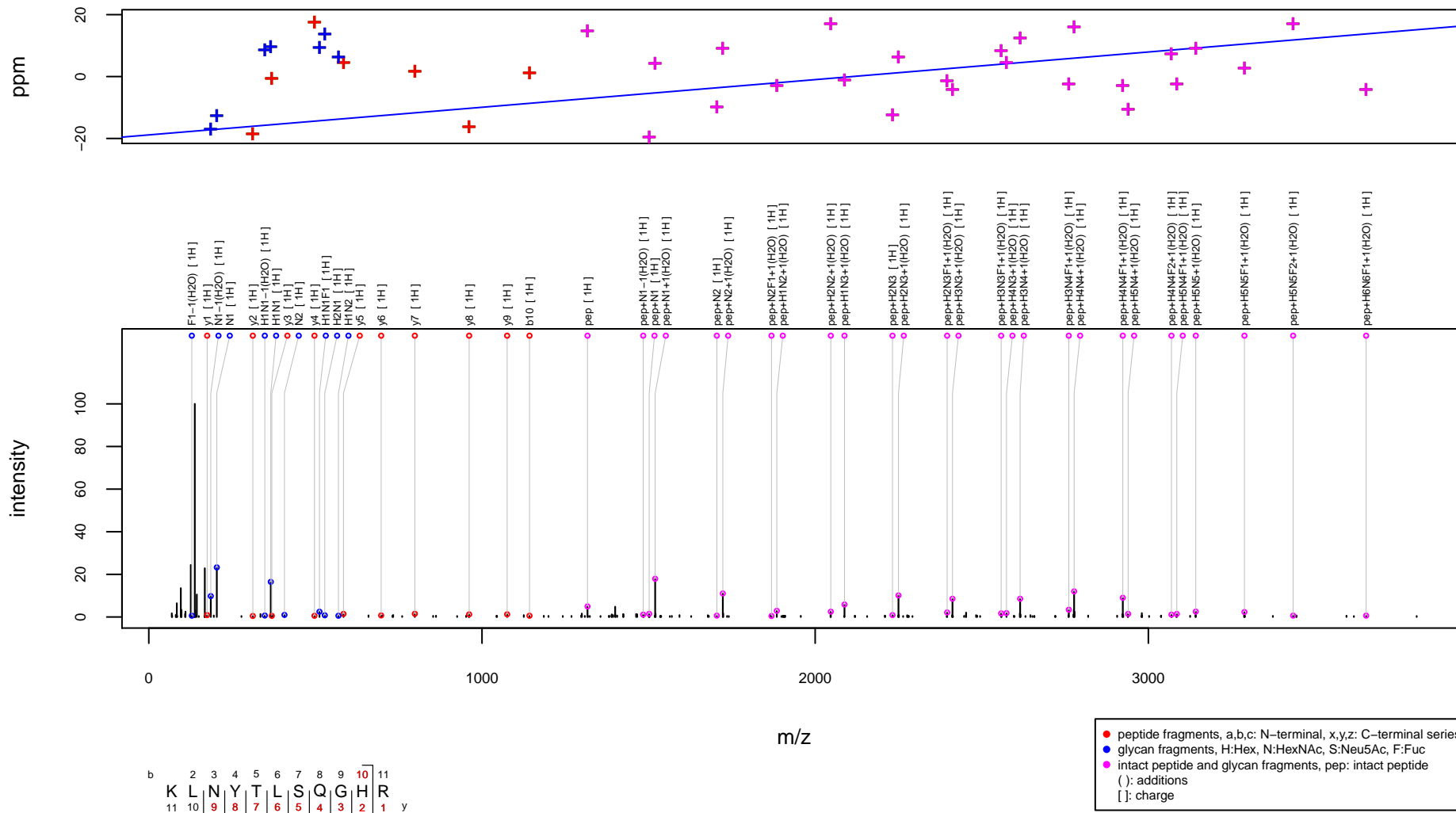
m/z 950.6725 charge 4 scan 0-0

Score= 50.96 , Hits= 46 , Explained Intensity= 0.39

Peptide: AMPN_HUMAN[126,136]:KLN^YTL^SQ^GH^R

Glycan: H6N6F2

Charge: 4H



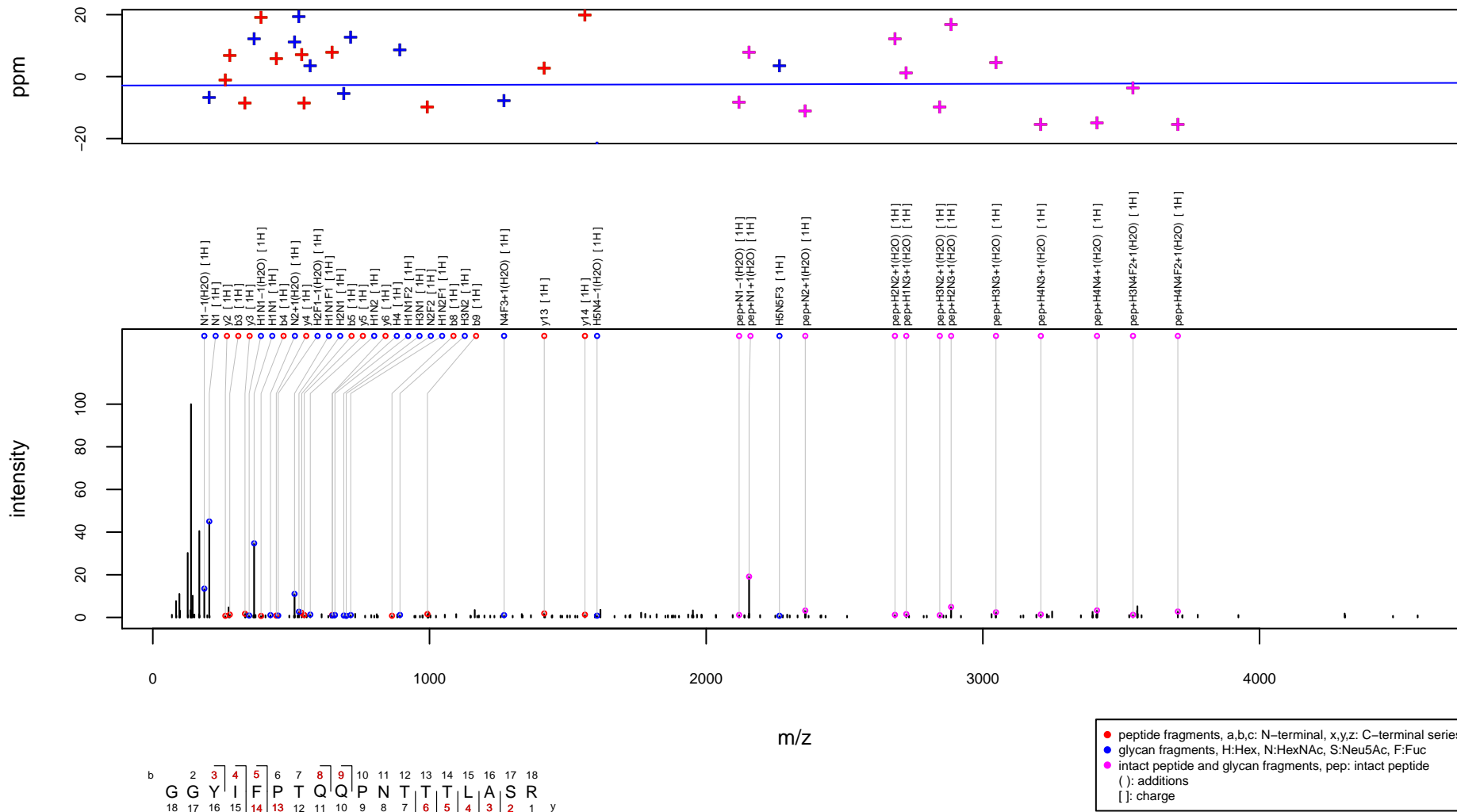
m/z 1145.9838 charge 4 scan 0-0

Score= 42.62 , Hits= 42 , Explained Intensity= 0.32

Peptide: MGA_HUMAN[817,834]:GGYIFPTQQPNTTTLASR

Glycan: H6N6F3

Charge: 4H



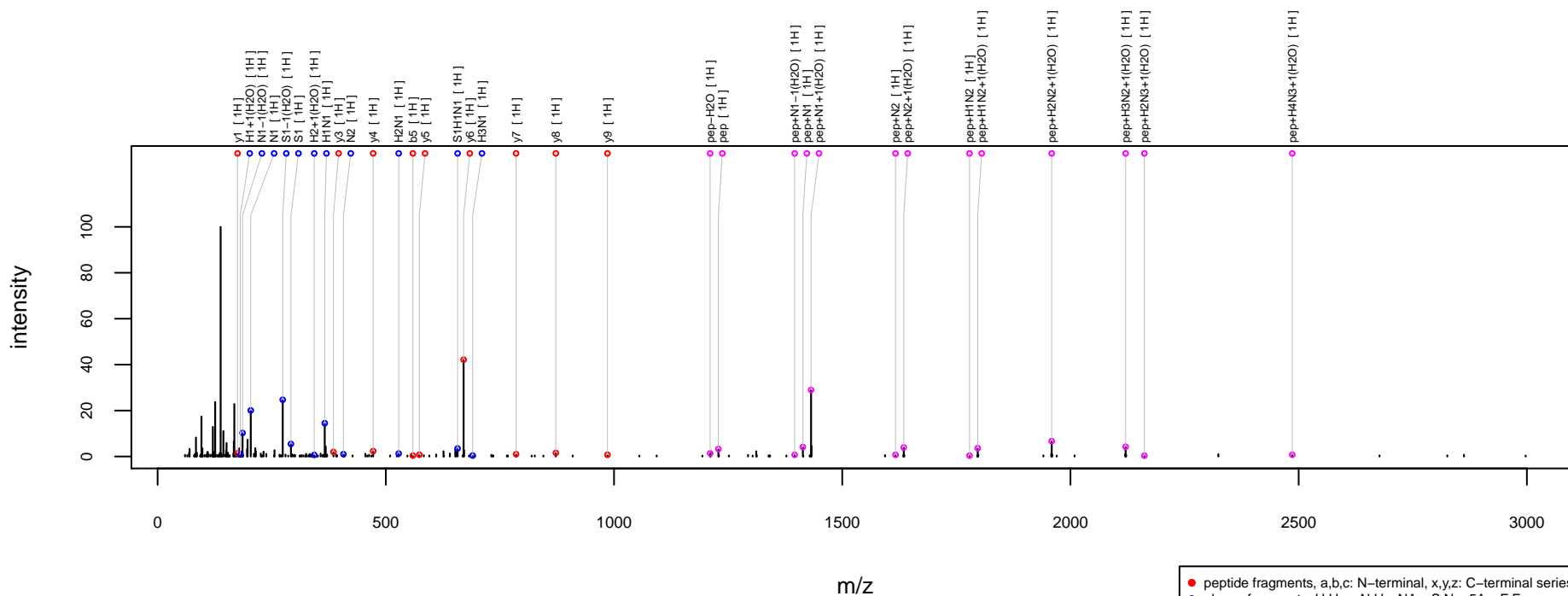
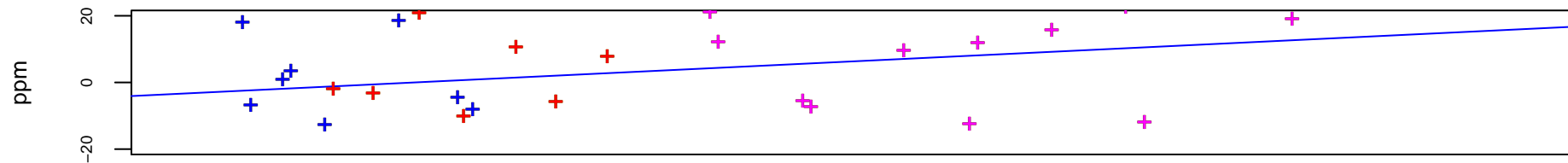
m/z 859.1006 charge 4 scan 0-0

Score= 48.32 , Hits= 33 , Explained Intensity= 0.37

Peptide: IGJ_HUMAN[70,80]:ENISDPTSPLR

Glycan: SHNH(SHNH)HNN, S2H5N4

Charge: 4H



b

	2	3	4	5	6	7	8	9	10	11
E	N	I	S	D	P	T	S	P	L	R
11	10	9	8	7	6	5	4	3	2	1

y

- peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
- glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
- intact peptide and glycan fragments, pep: intact peptide
- (): additions
- []: charge

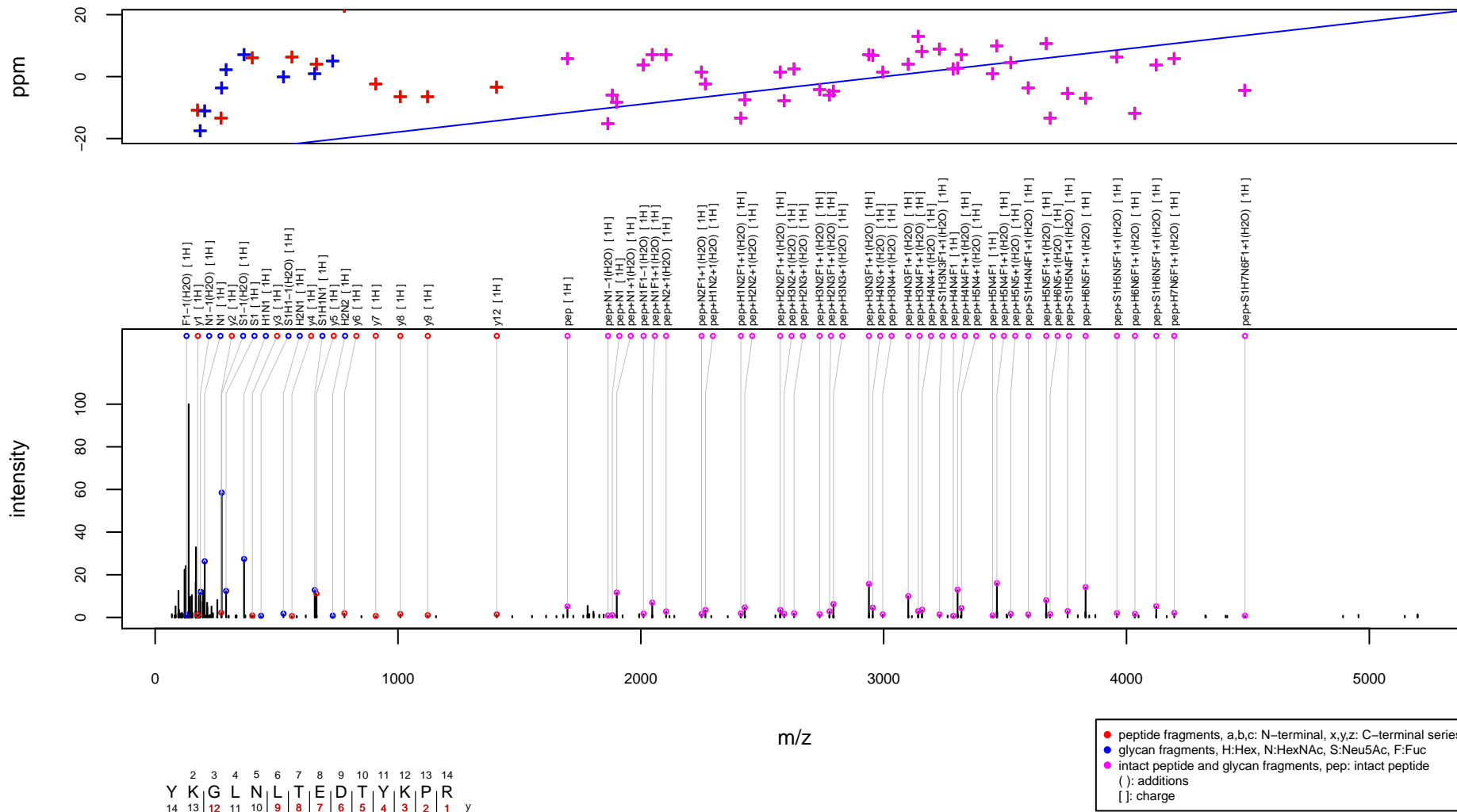
m/z 1073.0382 charge 5 scan 0-0

Score= 73.15 , Hits= 60 , Explained Intensity= 0.46

Peptide: LG3BP_HUMAN[394,407]:YKGLNLTEDTYKPR

Glycan: SHN(SHN)H(SHN(SHN)H)HN(F)N, S4H7N6F1

Charge: 5H



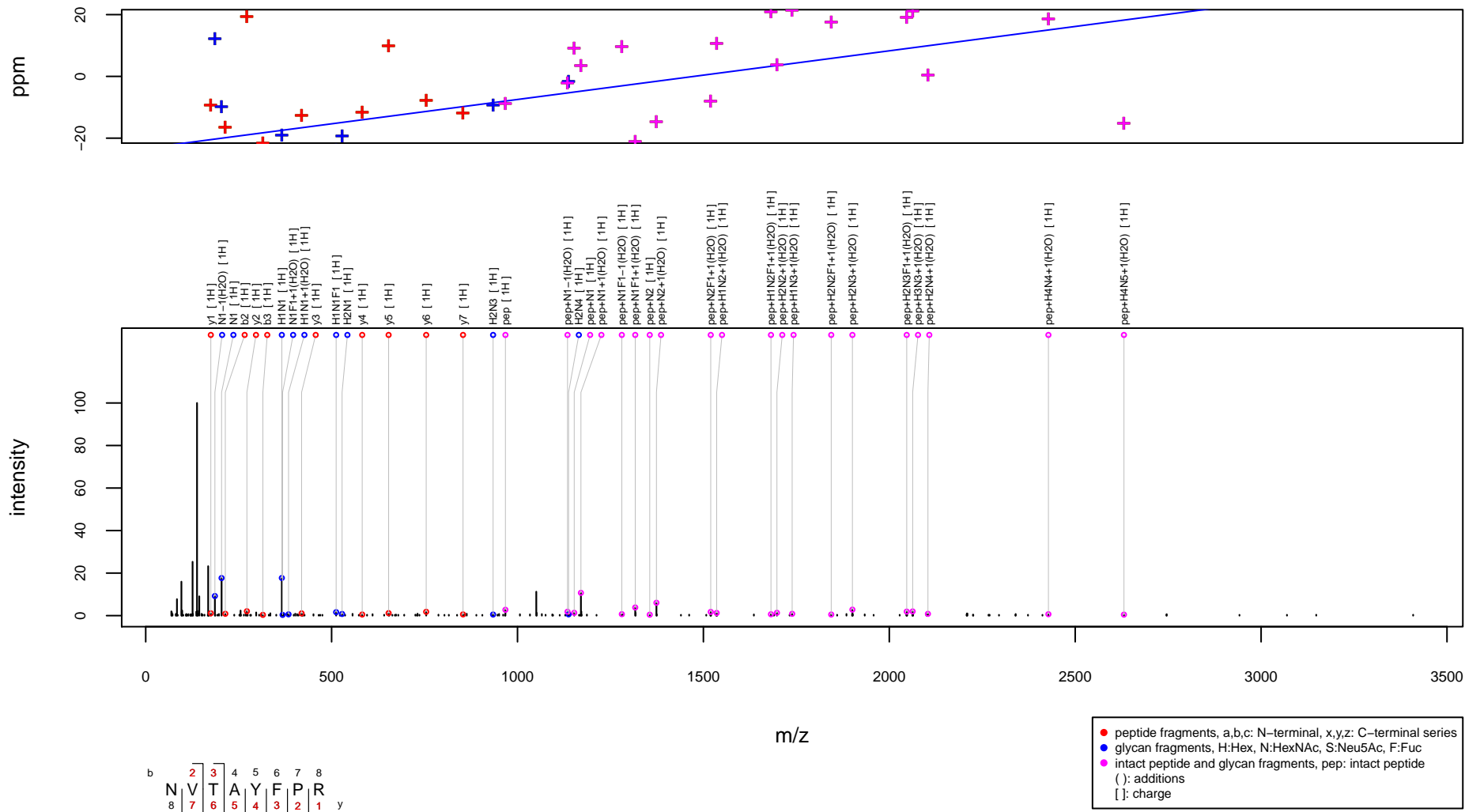
m/z 863.3547 charge 4 scan 0-0

Score= 41.32 , Hits= 38 , Explained Intensity= 0.27

Peptide: MGA_HUMAN[1672,1679]:NVTAYFPR

Glycan: H6N6F2

Charge: 4H



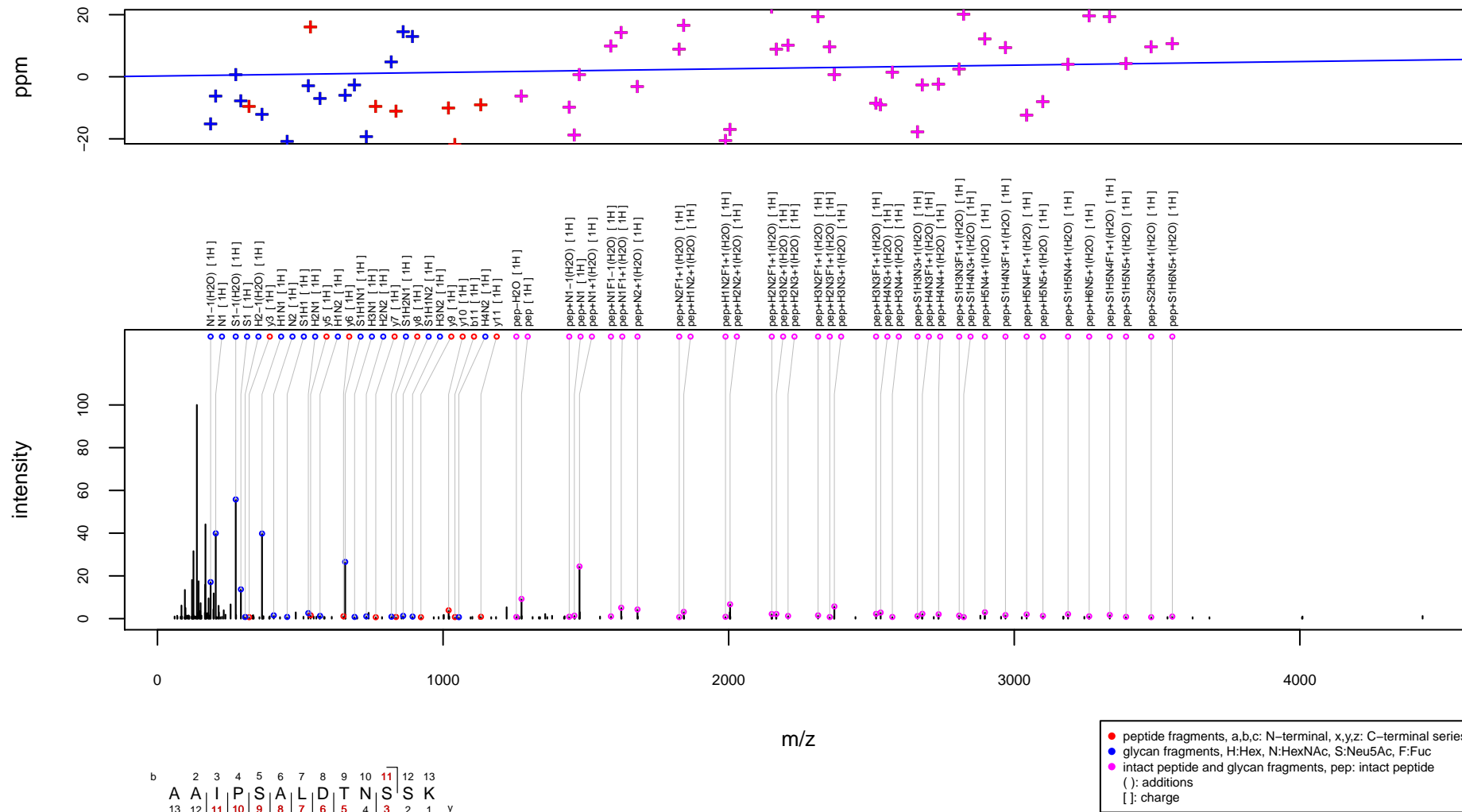
m/z 1121.954 charge 4 scan 0-0

Score= 75.48 , Hits= 62 , Explained Intensity= 0.43

Peptide: LG3BP_HUMAN[542,554]:AAIPALSDTNSSK

Glycan: SHNH(SHN(S(N)HN)H)HN(F)N, S3H6N6F1

Charge: 4H



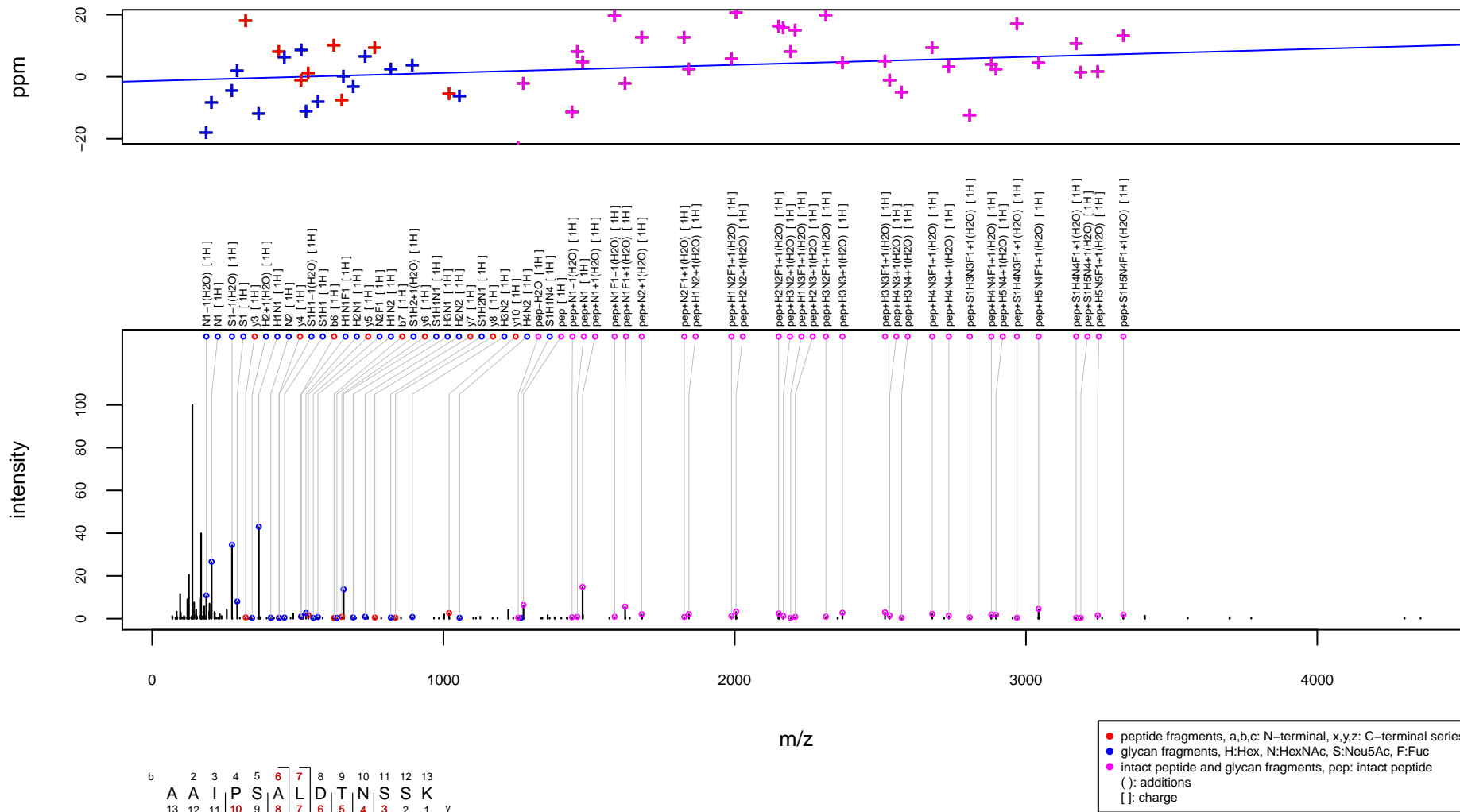
m/z 1089.6945 charge 4 scan 0-0

Score= 55.18 , Hits= 62 , Explained Intensity= 0.42

Peptide: LG3BP_HUMAN[542,554]:AAIPSAALDTNSK

Glycan: S2H7N6F1

Charge: 4H



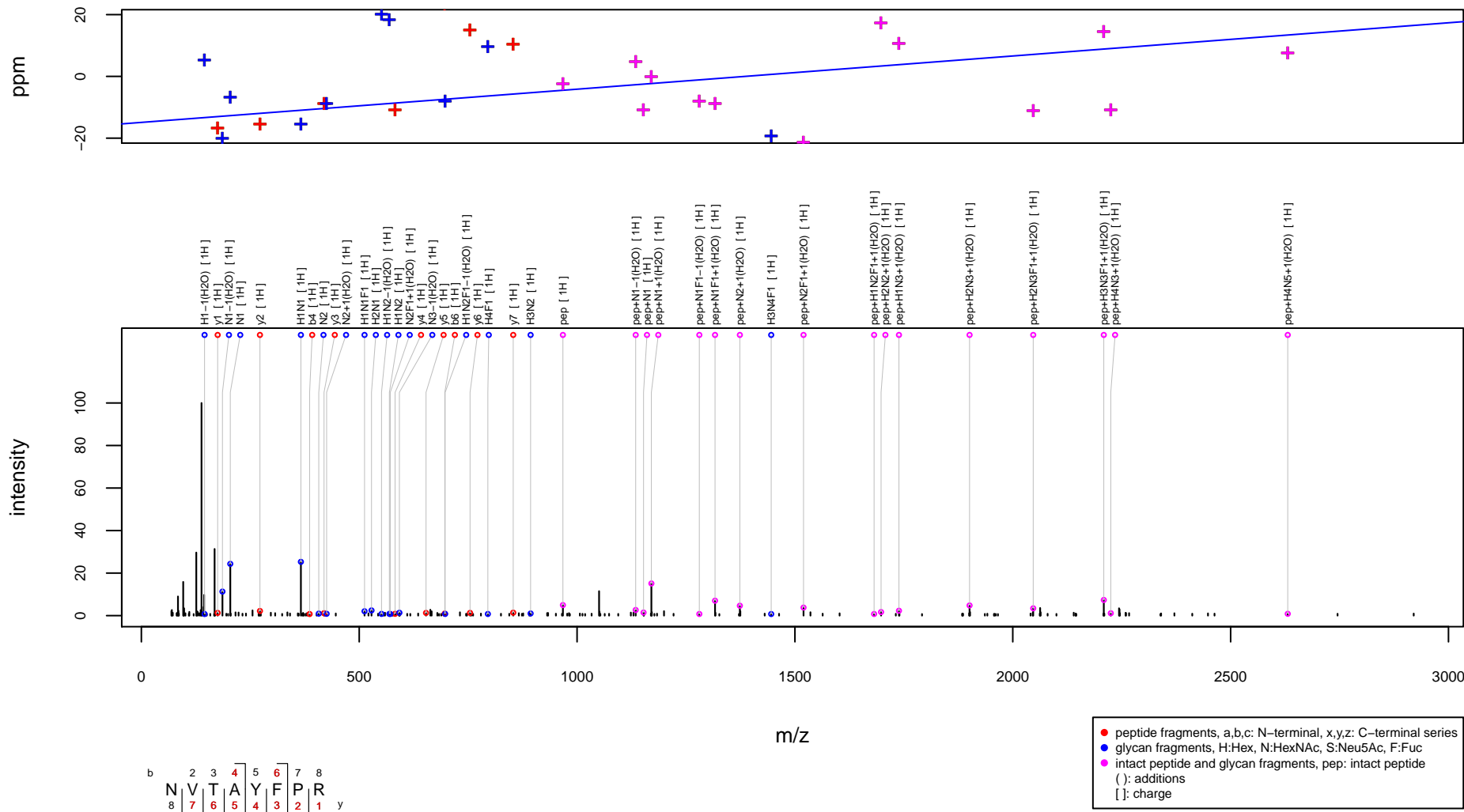
m/z 980.4078 charge 3 scan 0-0

Score= 53.67 , Hits= 41 , Explained Intensity= 0.29

Peptide: MGA_HUMAN[1672,1679]:NVTAYFPR

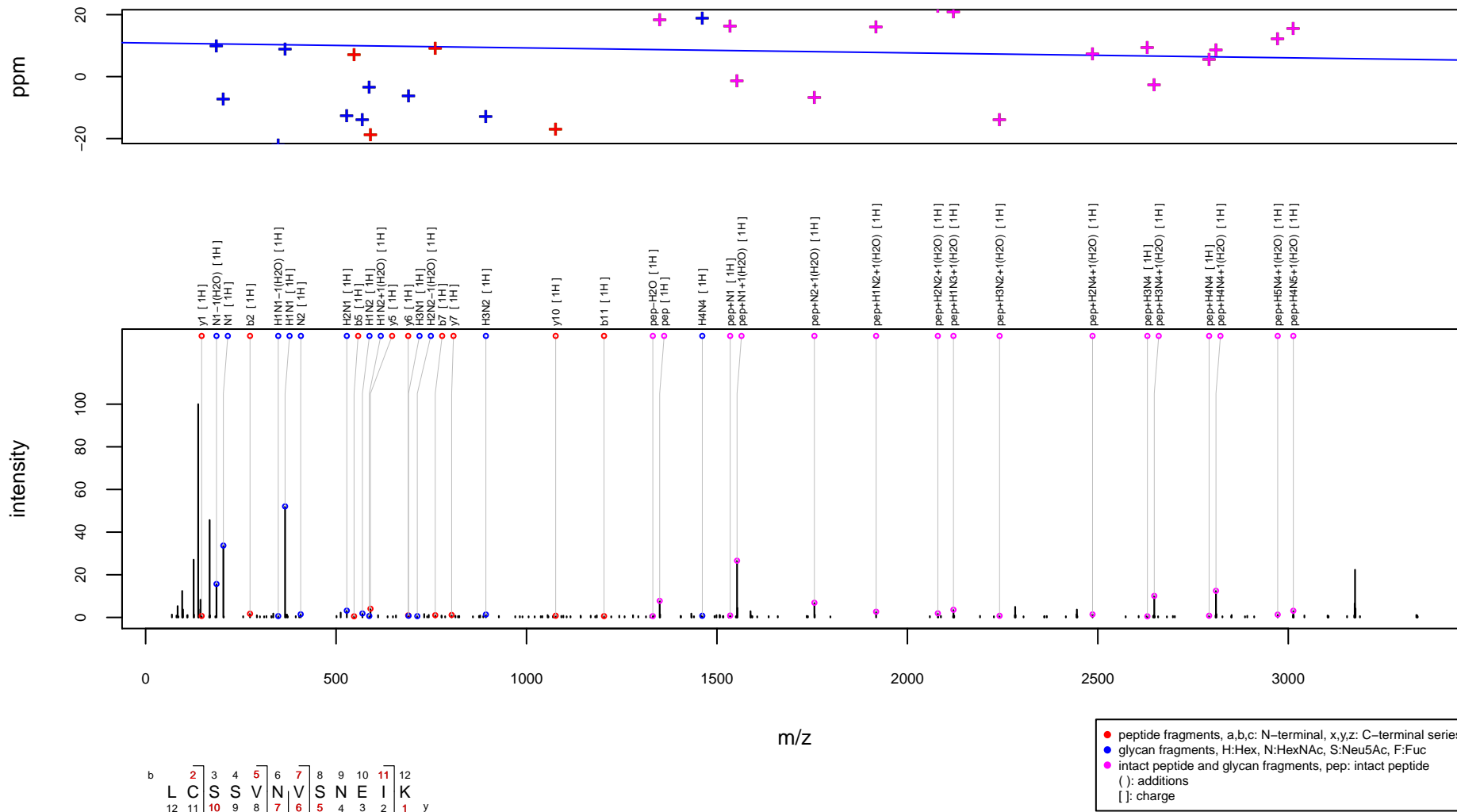
Glycan: H5N5F1

Charge: 3H



m/z 1180.8235 charge 3 scan 0-0

Score= 54.81 , Hits= 37 , Explained Intensity= 0.37
 Peptide: CUBN_HUMAN[2526,2537]:LCSSVNVSN EIK
 Glycan: HNH(HN(HN)H)(N)HNN, H6N6
 Charge: 3H



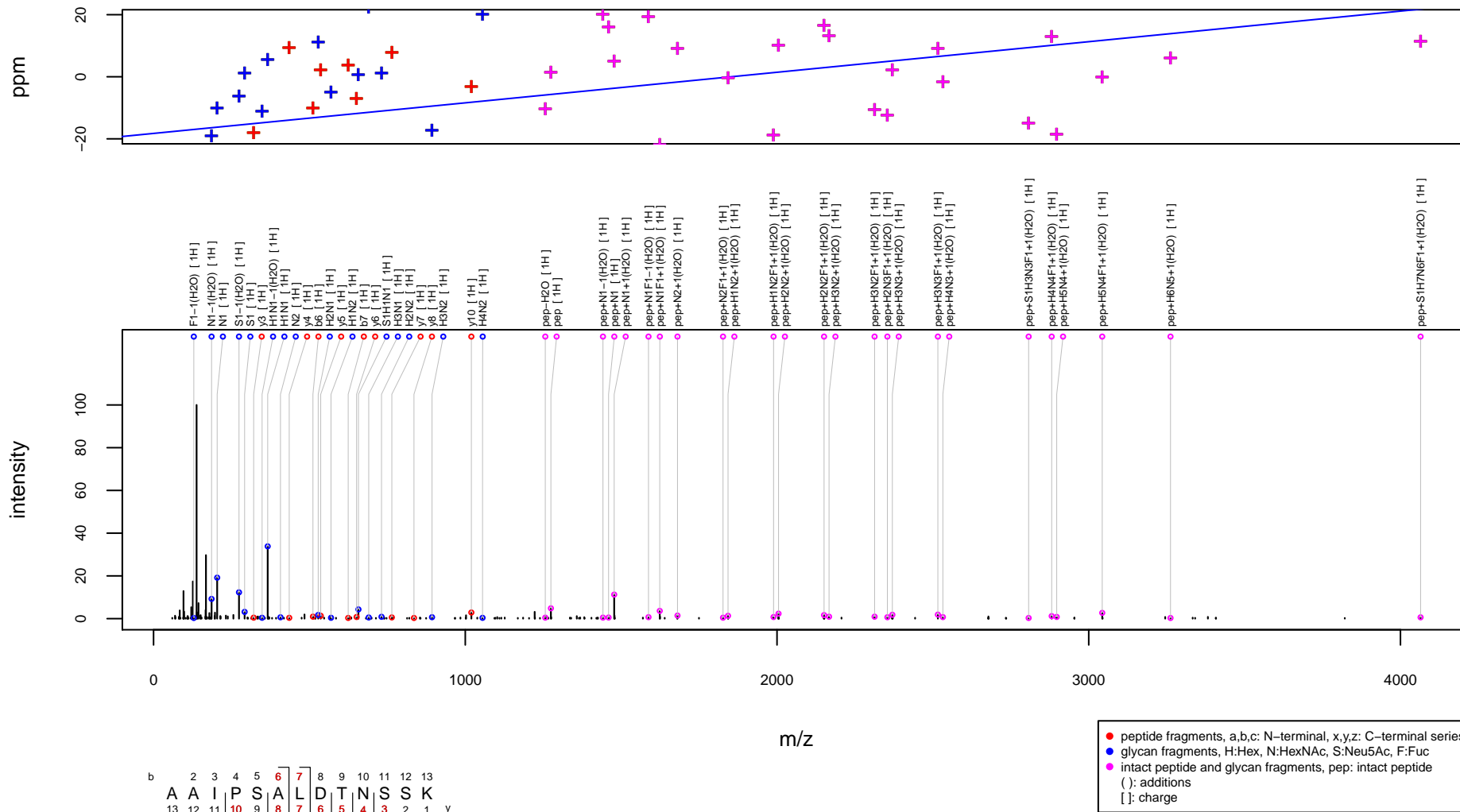
m/z 1016.92 charge 4 scan 0-0

Score= 59.23 , Hits= 49 , Explained Intensity= 0.34

Peptide: LG3BP_HUMAN[542,554]:AAIPSA LDTNSK

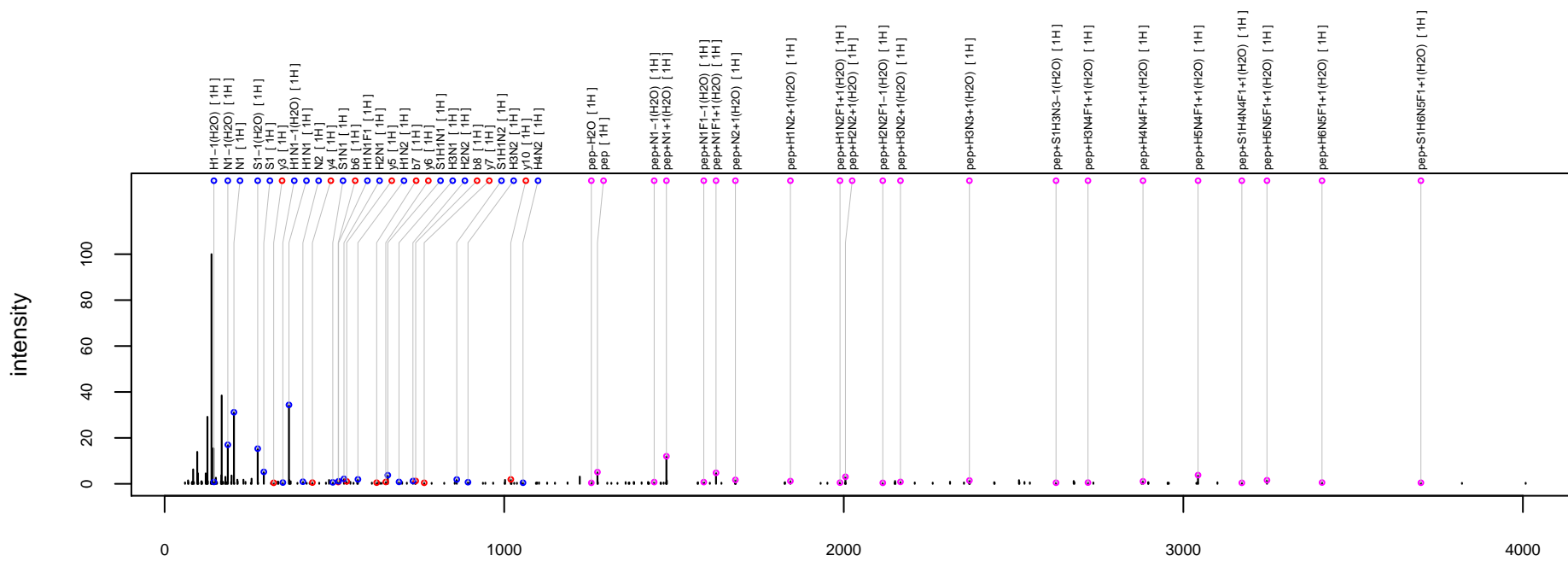
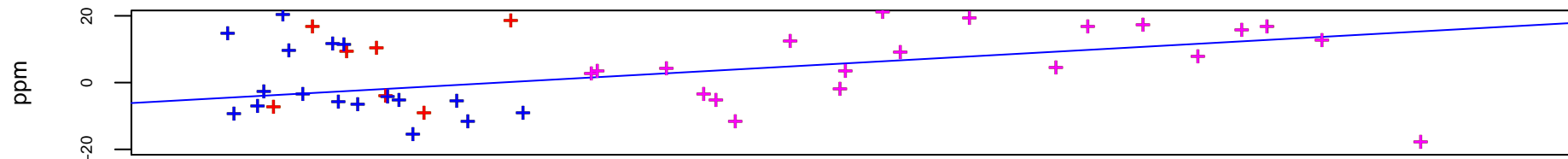
Glycan: SHN(HN)H(HN(HN)H)HN(F)N, S1H7N6F1

Charge: 4H



m/z 1067.6907 charge 4 scan 0-0

Score= 44.13 , Hits= 48 , Explained Intensity= 0.35
 Peptide: LG3BP_HUMAN[542,554]:AAIPSAALDTNPSK
 Glycan: S1H7N7F1
 Charge: 4H



b 2 3 4 5 6 7 8 9 10 11 12 13
 A A I P S A A L D T N P S K
 13 12 11 10 9 8 7 6 5 4 3 2 1 y

● peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
 ● glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
 ● intact peptide and glycan fragments, pep: intact peptide
 (): additions
 []: charge

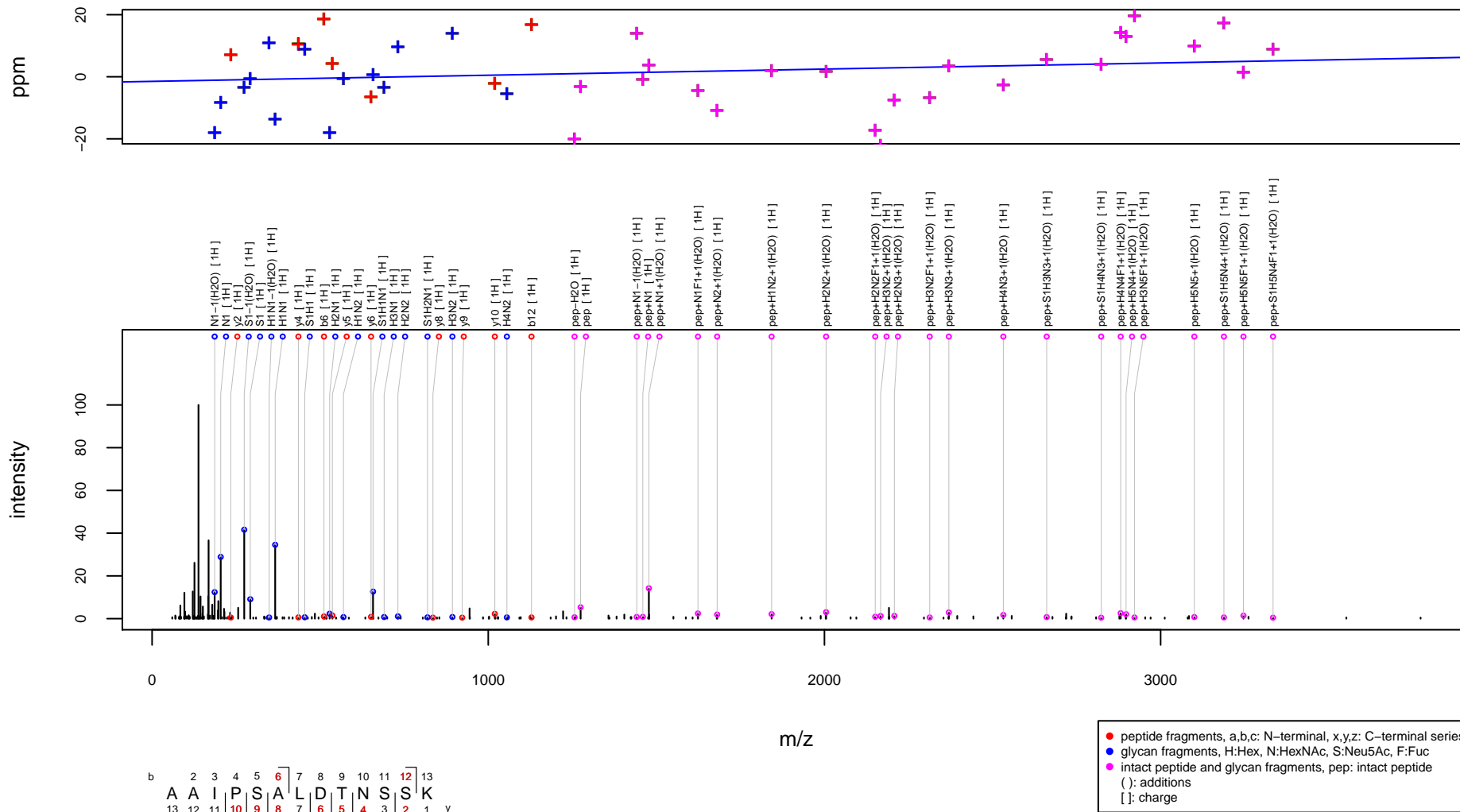
m/z 1049.1785 charge 4 scan 0-0

Score= 54.72 , Hits= 48 , Explained Intensity= 0.36

Peptide: LG3BP_HUMAN[542,554]:AAIP^SALDTN^SSK

Glycan: SHN(S(N)HN)H(HNH)HN(F)N, S2H6N6F1

Charge: 4H



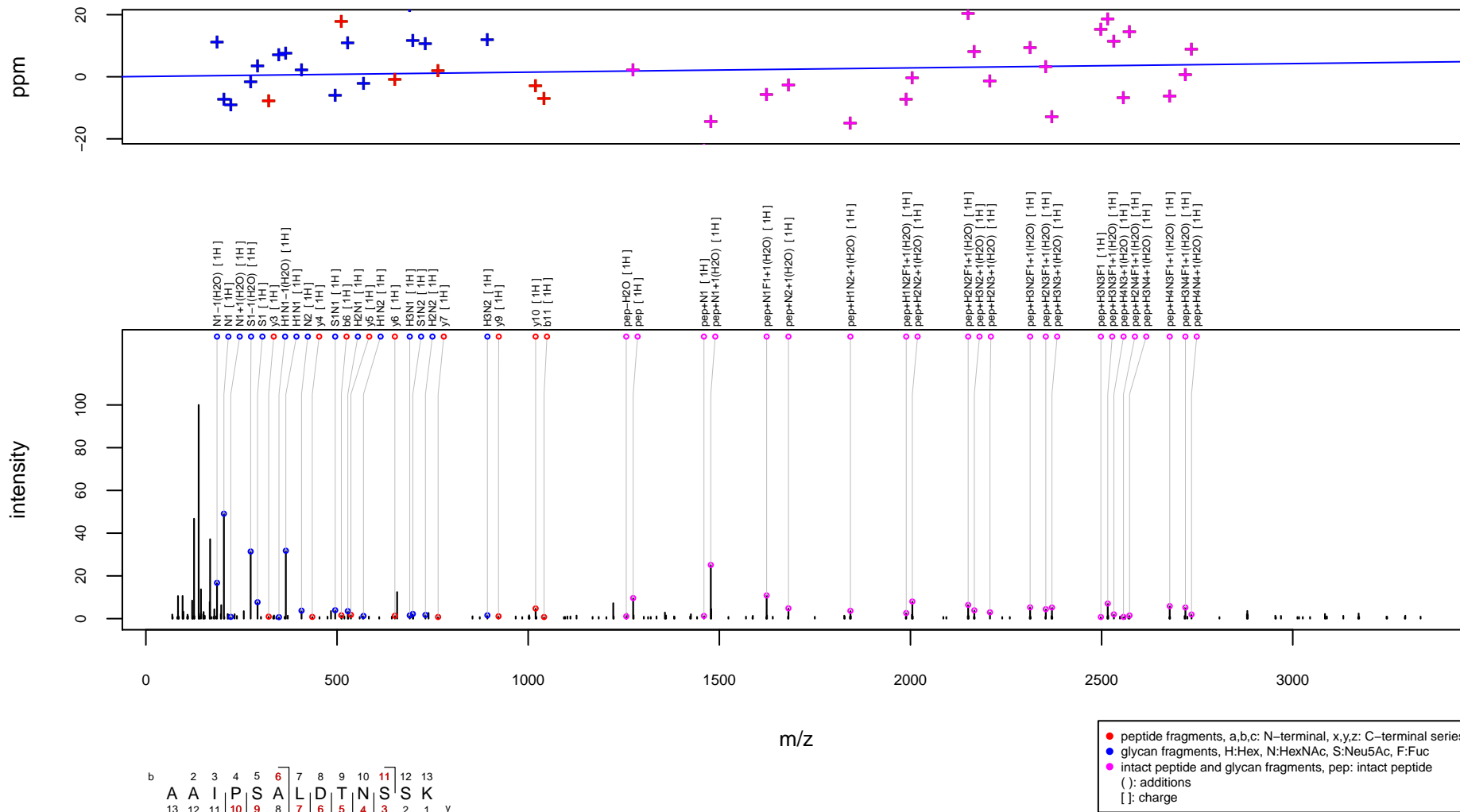
m/z 1125.8085 charge 3 scan 0-0

Score= 64.81 , Hits= 47 , Explained Intensity= 0.41

Peptide: LG3BP_HUMAN[542,554]:AAIP^SALD^TNSSK

Glycan: SNNH(HNH)HN(F)N, S1H4N5F1

Charge: 3H



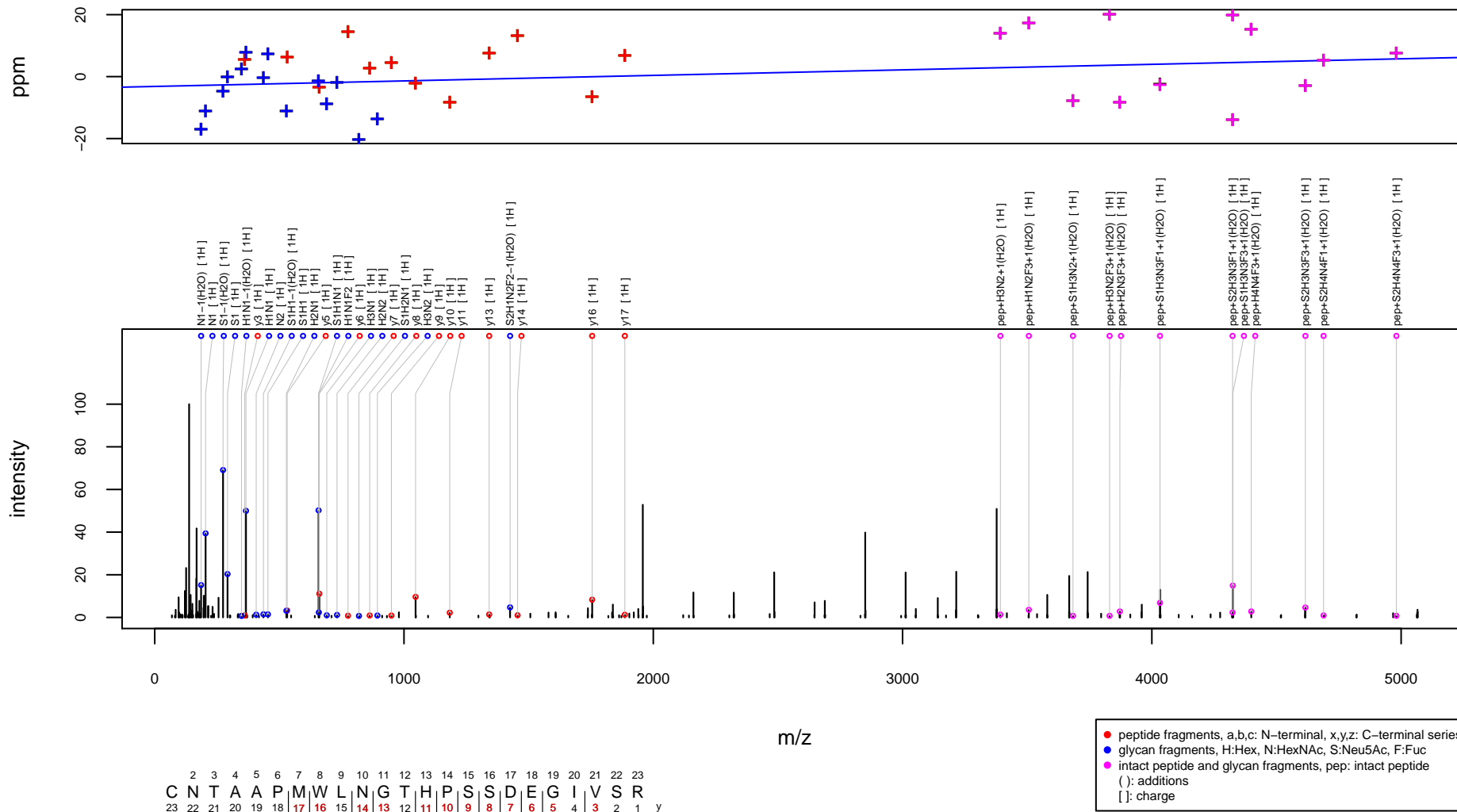
m/z 1318.776 charge 4 scan 0-0

Score= 36.02 , Hits= 41 , Explained Intensity= 0.31

Peptide: UROM_HUMAN[223,245]:CNTAAPMWLNGTHPSSDEGIVSR

Glycan: S3H4N4F3

Charge: 4H



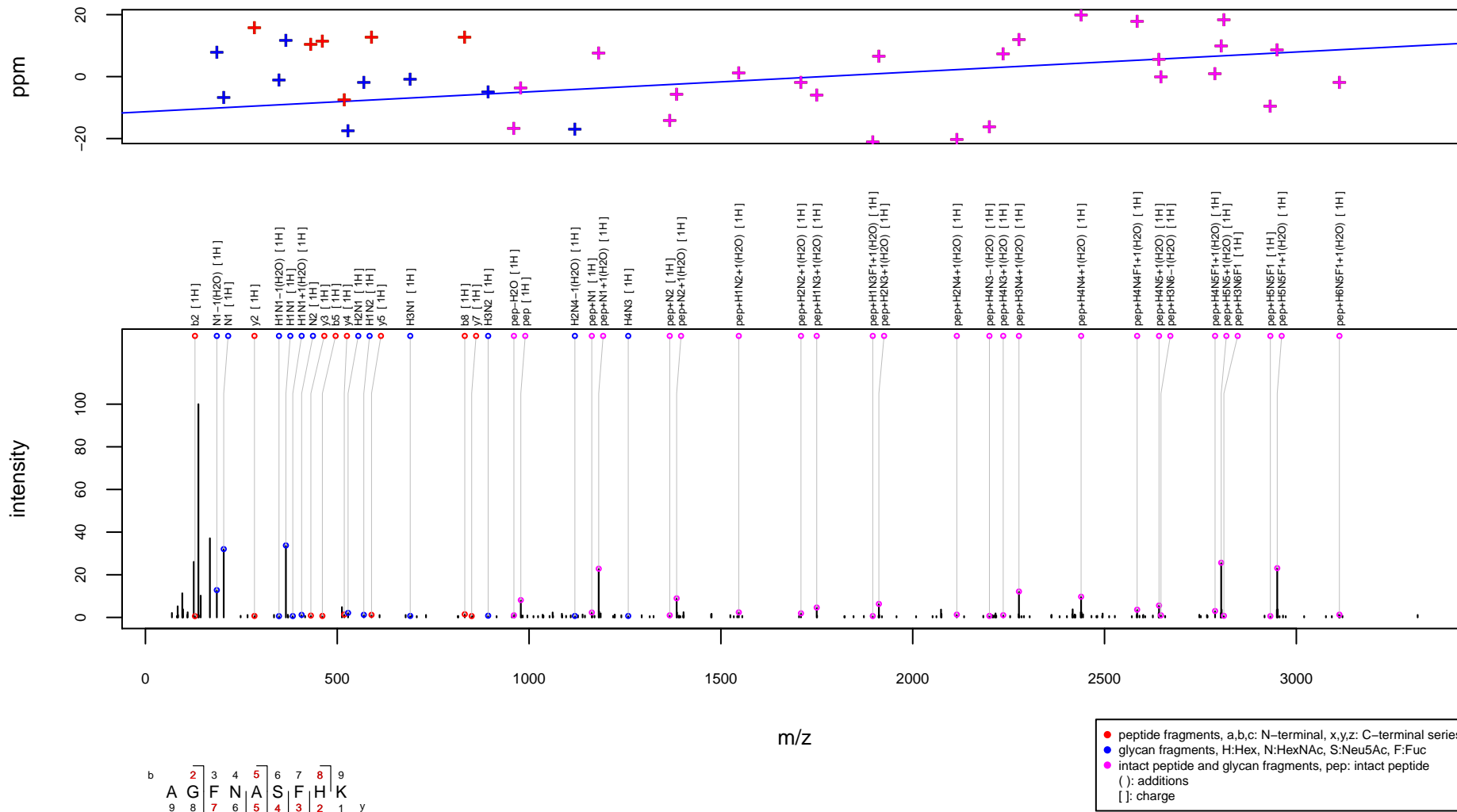
m/z 1105.7849 charge 3 scan 0-0

Score= 60.61 , Hits= 45 , Explained Intensity= 0.42

Peptide: CUBN_HUMAN[2082,2090]:AGFNASFHK

Glycan: HNH(HN(HN)H)(N)HN(F)N, H6N6F1

Charge: 3H



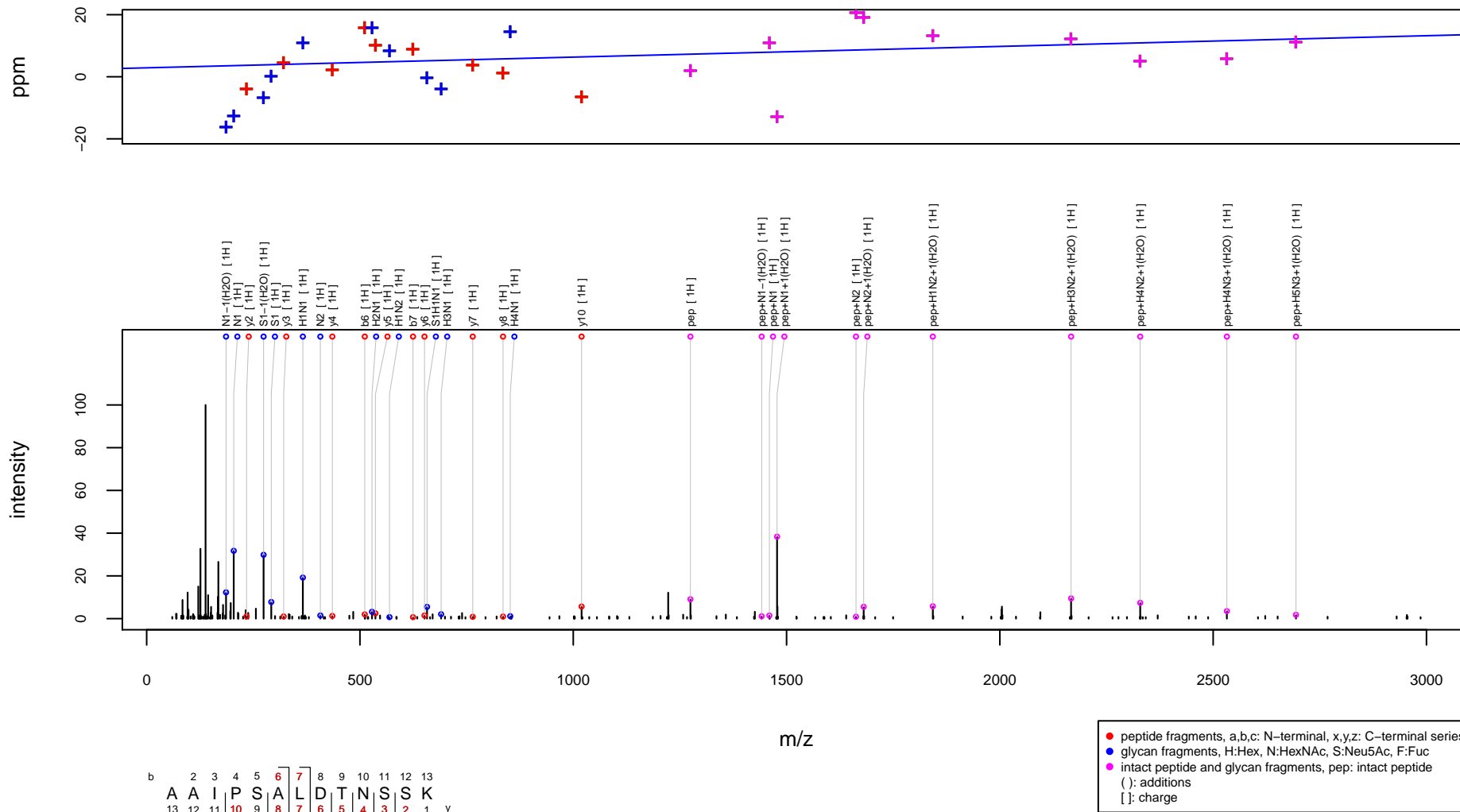
m/z 995.7552 charge 3 scan 0-0

Score= 47.74 , Hits= 32 , Explained Intensity= 0.33

Peptide: LG3BP_HUMAN[542,554]:AAIPSAALDTNSISK

Glycan: SHNH(HH)HNN, S1H5N3

Charge: 3H



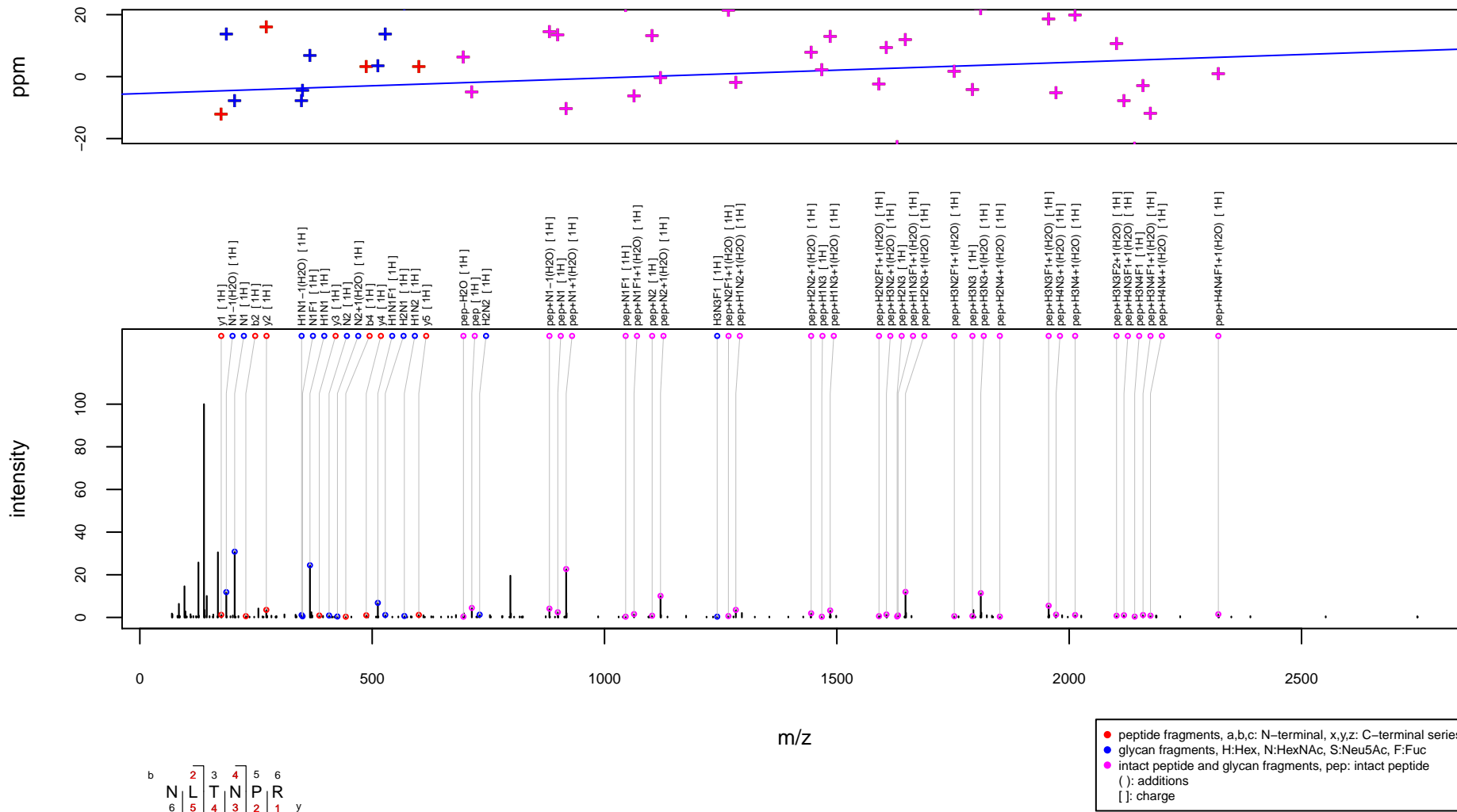
m/z 944.7243 charge 3 scan 0-0

Score= 70.63 , Hits= 51 , Explained Intensity= 0.38

Peptide: LRP2_HUMAN[1550,1555]:NLTNPR

Glycan: FHNH(HNH)(N)HN(F)N, H5N5F2

Charge: 3H



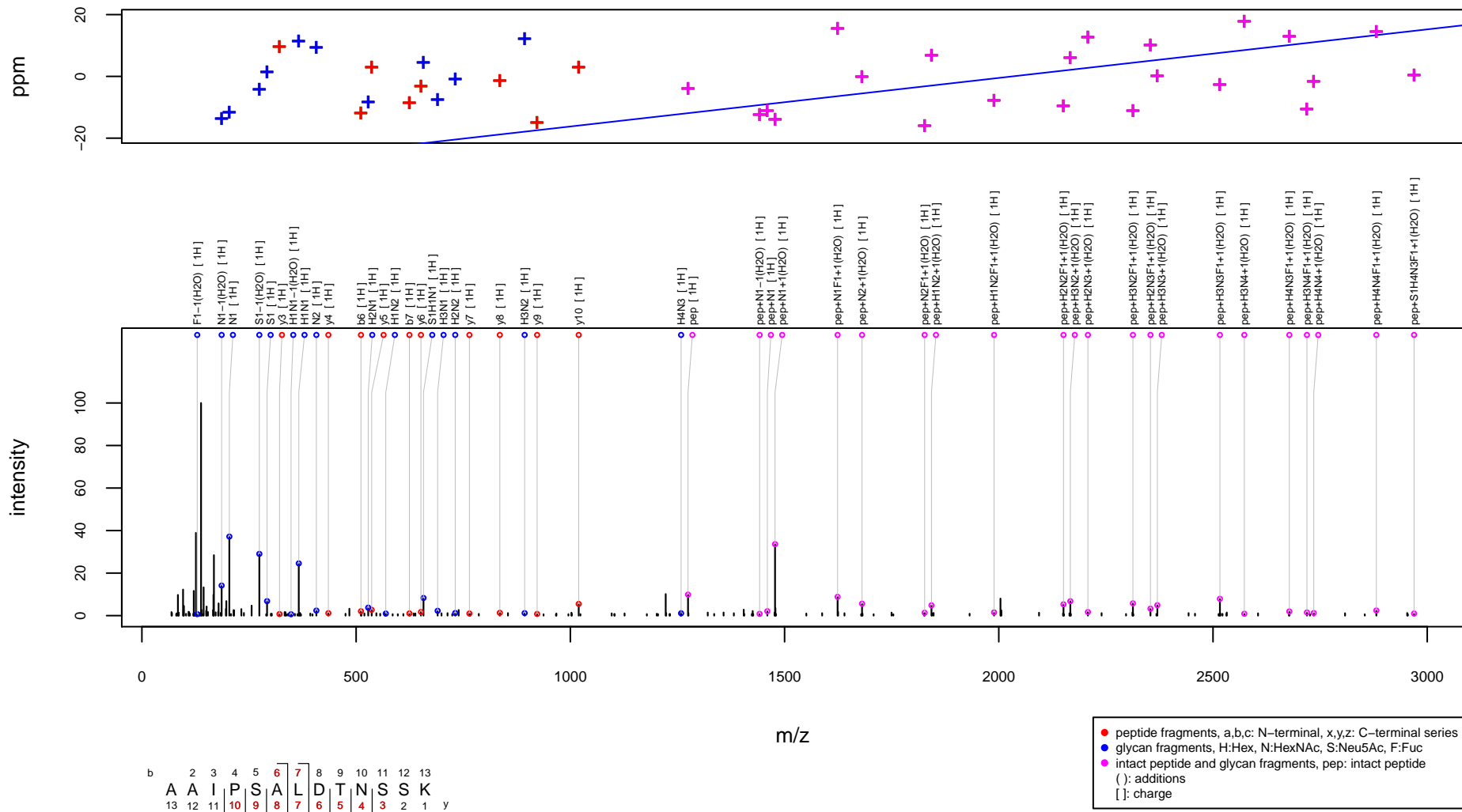
m/z 1058.1147 charge 3 scan 0-0

Score= 67.58 , Hits= 47 , Explained Intensity= 0.39

Peptide: LG3BP_HUMAN[542,554]:AAIPSAALDITNSK

Glycan: SHNH(NH)HN(F)N, S1H4N4F1

Charge: 3H



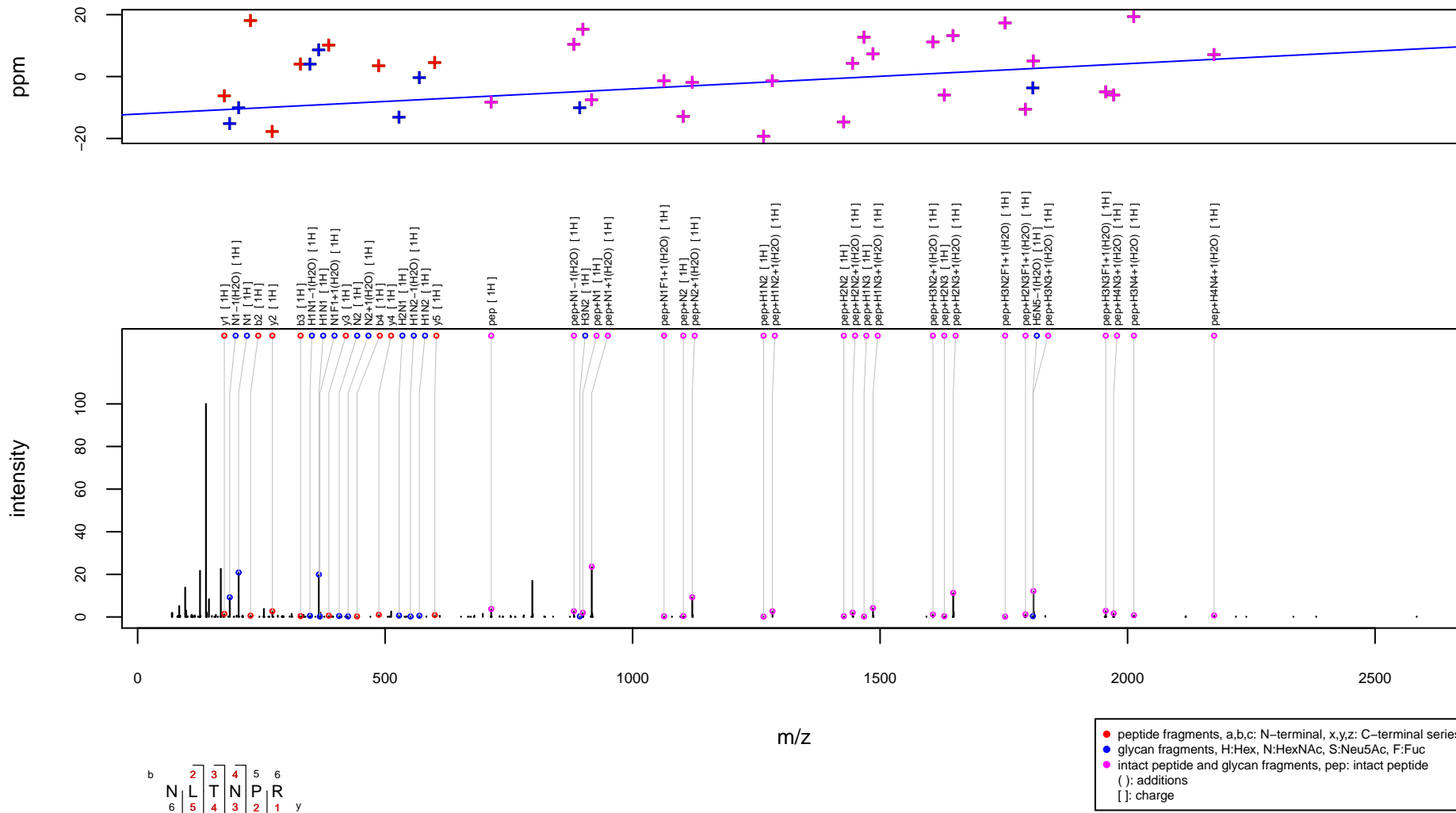
m/z 896.0397 charge 3 scan 0-0

Score= 61.8 , Hits= 43 , Explained Intensity= 0.36

Peptide: LRP2_HUMAN[1550,1555]:NLTNPR

Glycan: HNH(HNH)(N)HN(F)N, H5N5F1

Charge: 3H



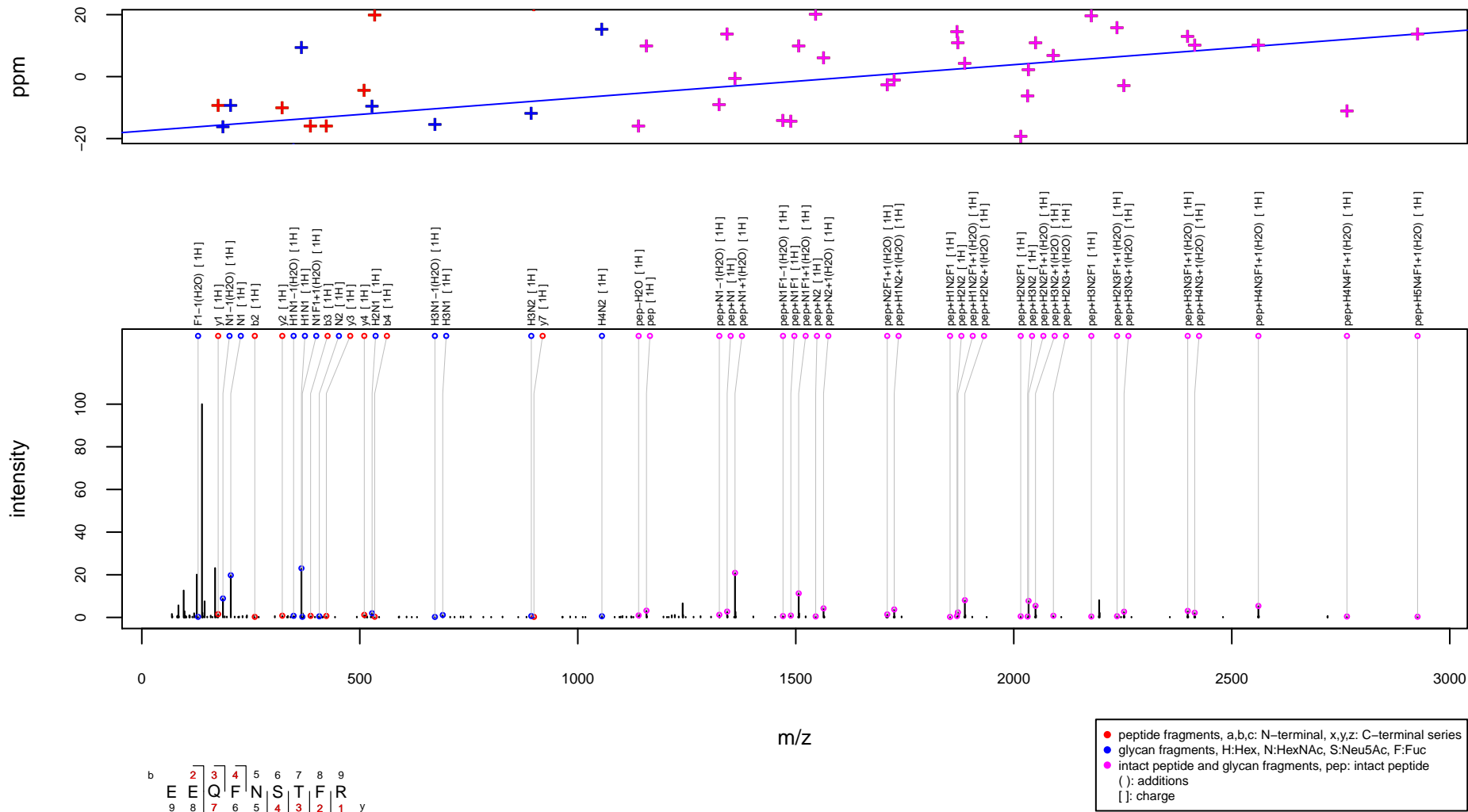
m/z 976.0581 charge 3 scan 0-0

Score= 76.41 , Hits= 49 , Explained Intensity= 0.38

Peptide: IGHG2_HUMAN[172,180]:EEQFNSTFR

Glycan: HNH(HNH)HN(F)N, H5N4F1

Charge: 3H



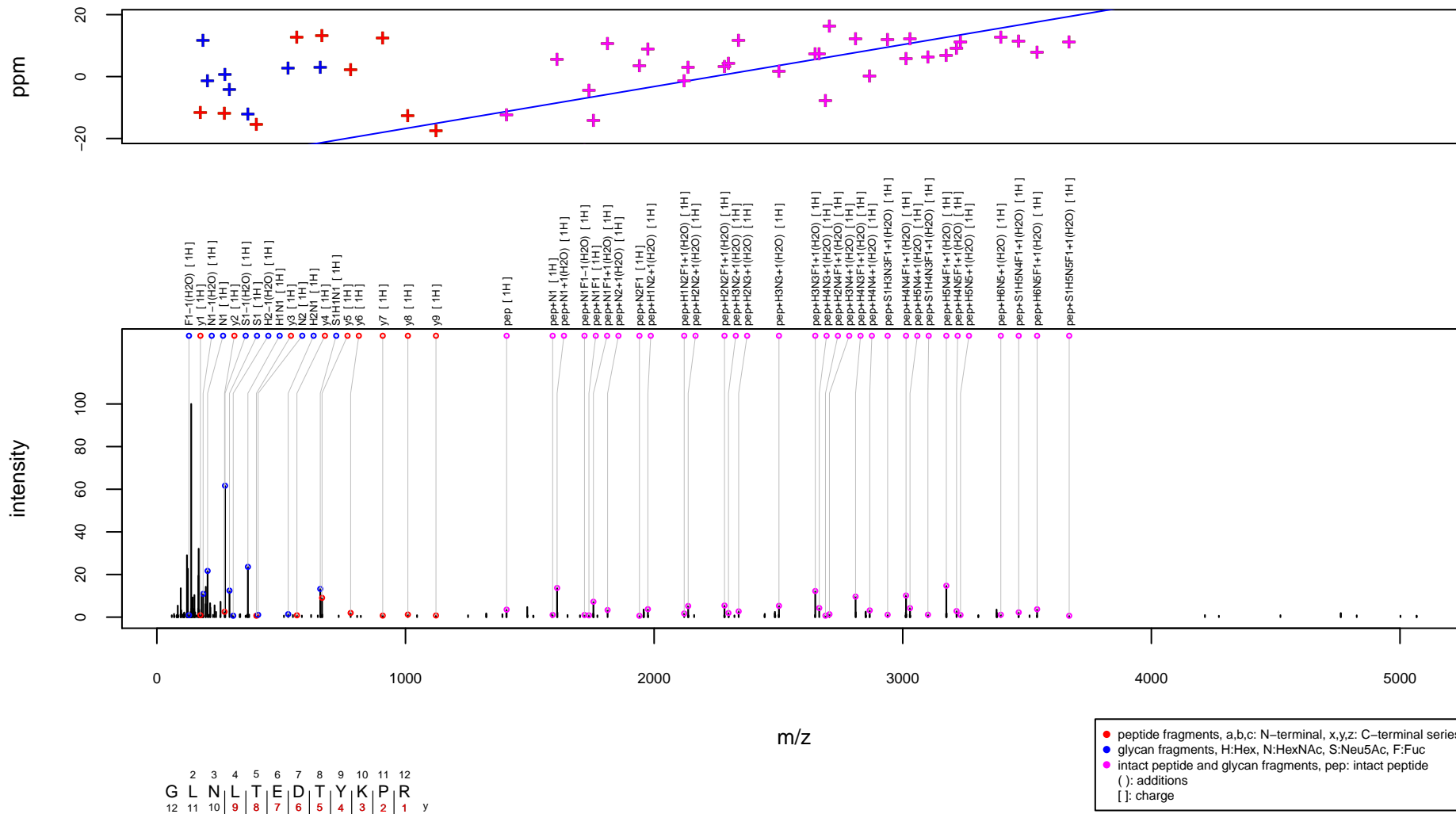
m/z 1014.809 charge 5 scan 0-0

Score= 59.86 , Hits= 51 , Explained Intensity= 0.39

Peptide: LG3BP_HUMAN[396,407]:GLNLTEDTYKPR

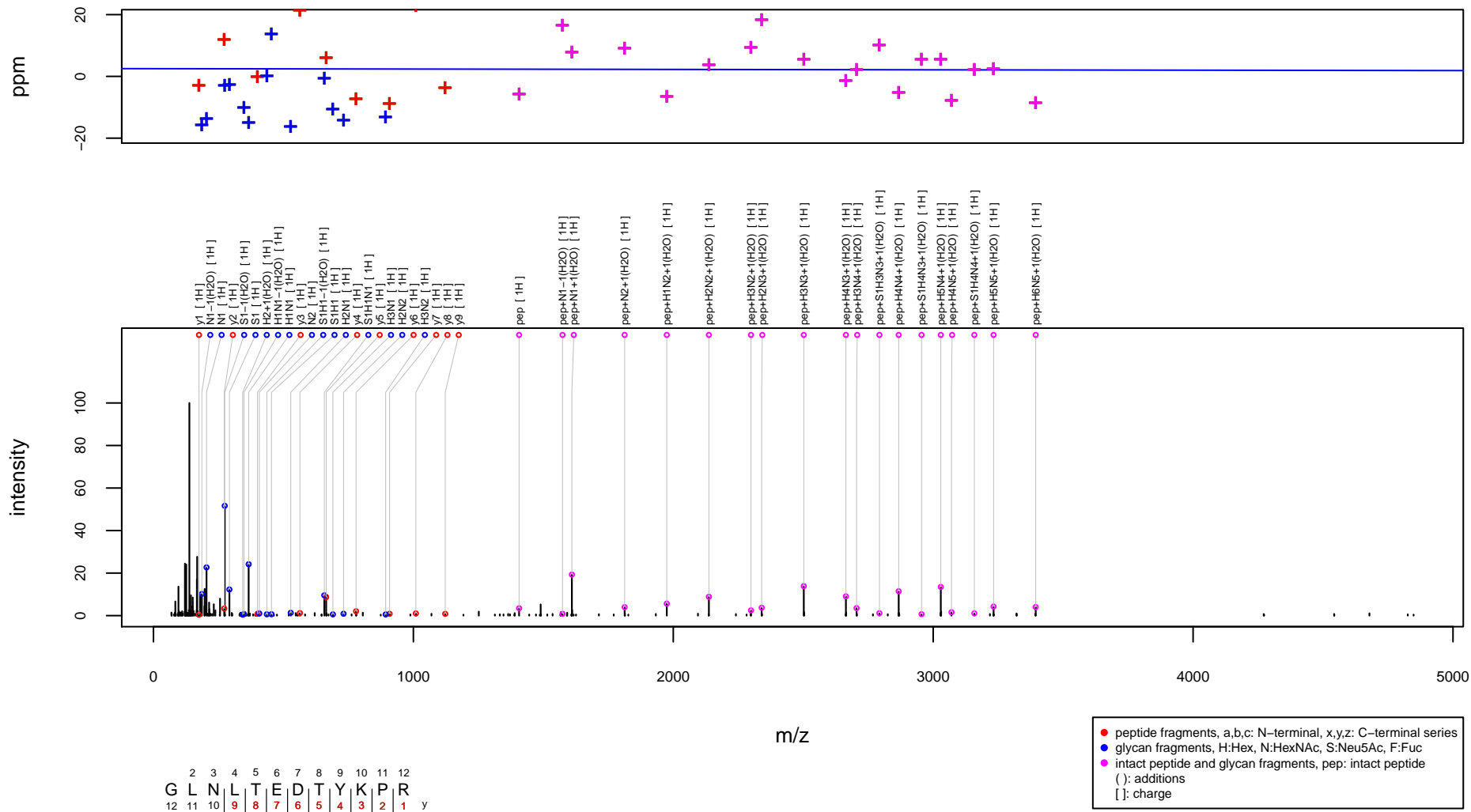
Glycan: SHN(SHN)H(SHN(SHN)H)HN(F)N, S4H7N6F1

Charge: 5H



m/z 985.5985 charge 5 scan 0-0

Score= 55.98 , Hits= 43 , Explained Intensity= 0.4
 Peptide: LG3BP_HUMAN[396,407]:GLNLTEDTYKPR
 Glycan: SHN(SHN)H(SHN(SHN)H)HNN, S4H7N6
 Charge: 5H



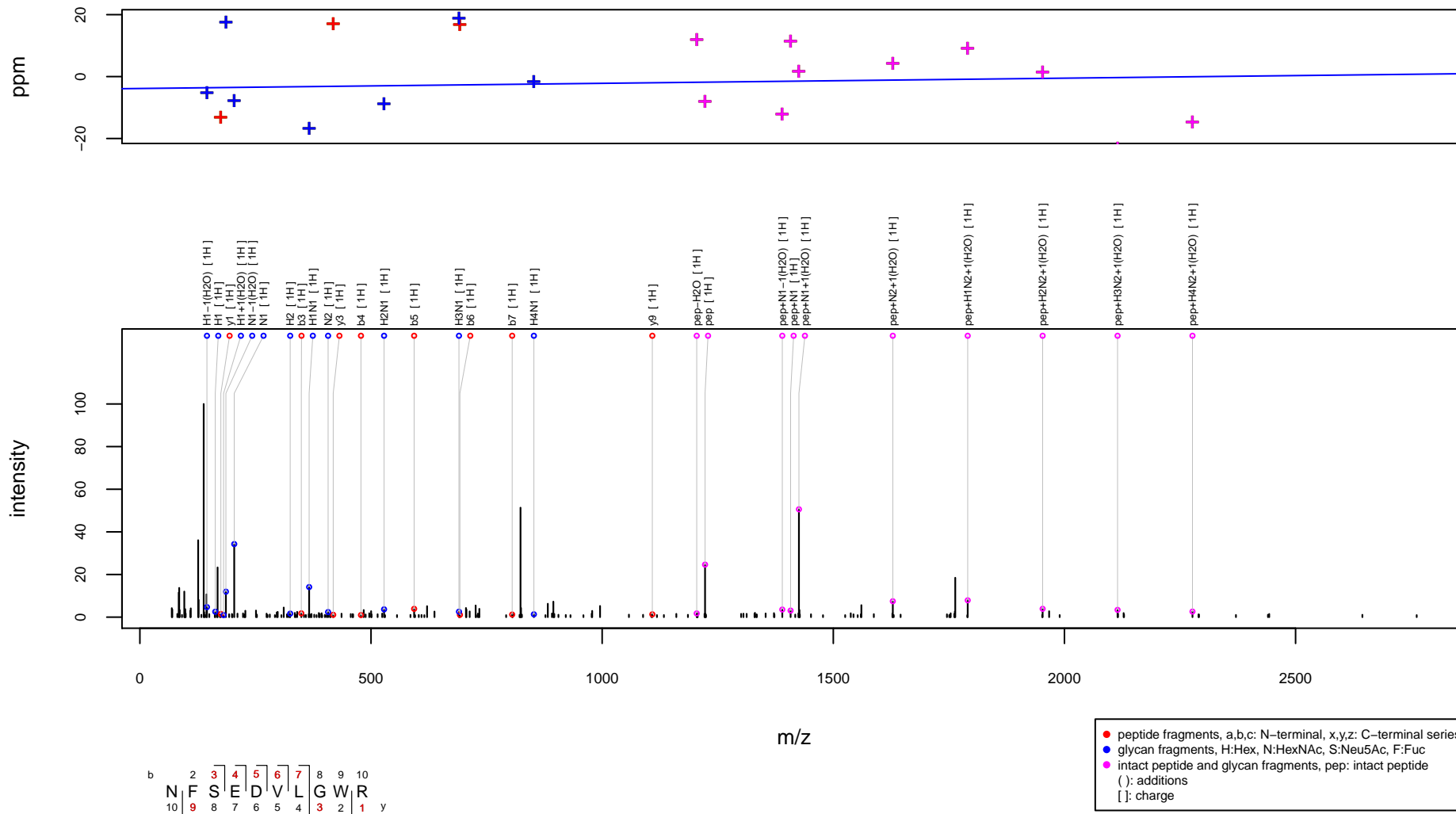
m/z 921.71 charge 3 scan 0-0

Score= 46.11 , Hits= 29 , Explained Intensity= 0.27

Peptide: RGS16_HUMAN[54,63]:NFSEDVLGWR

Glycan: HHH(H(H)H)HNN, H7N2

Charge: 3H



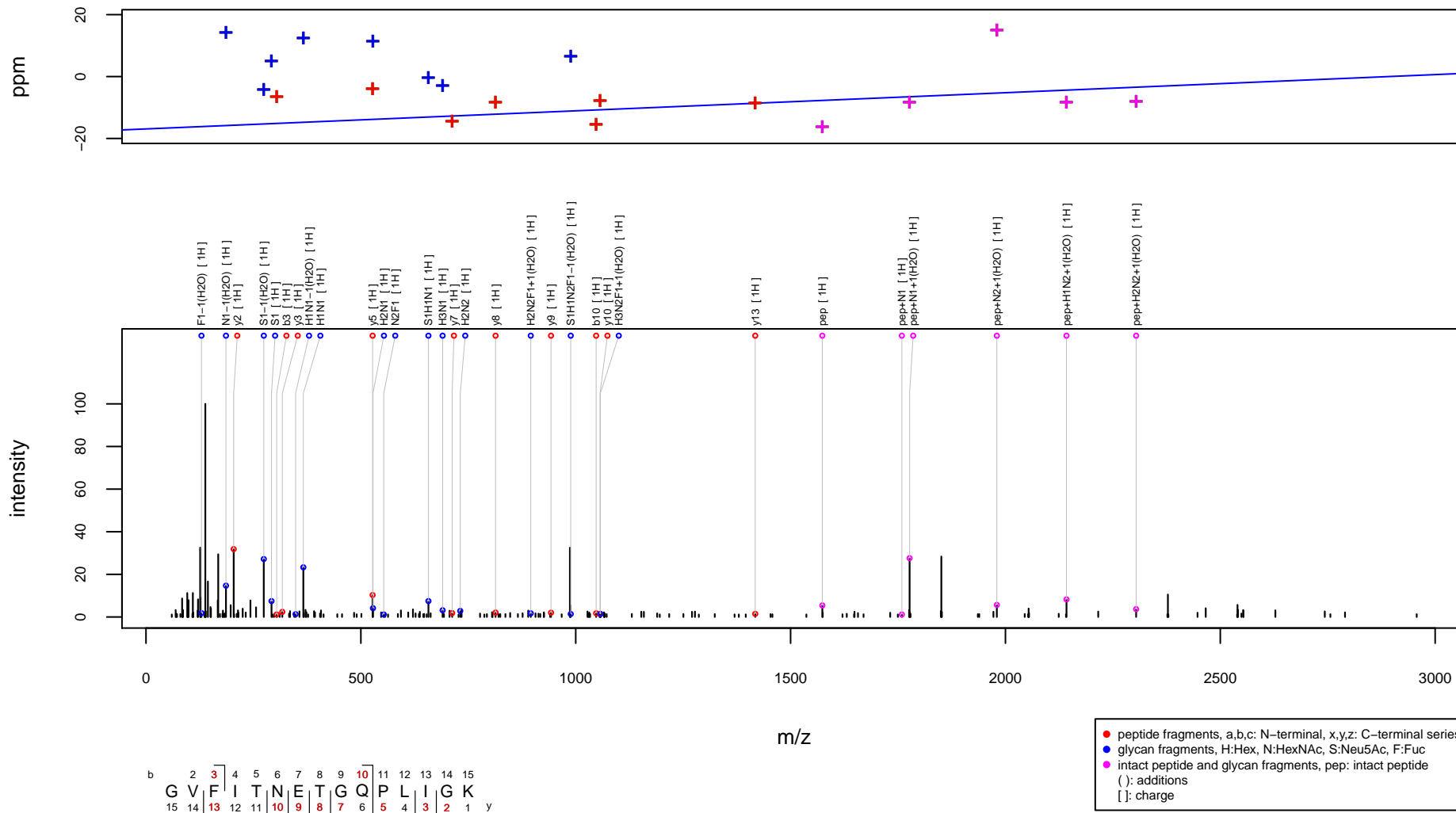
m/z 1065.4534 charge 3 scan 0-0

Score= 37.99 , Hits= 30 , Explained Intensity= 0.26

Peptide: LYAG_HUMAN[465,479]:GVFITNETGQPLIGK

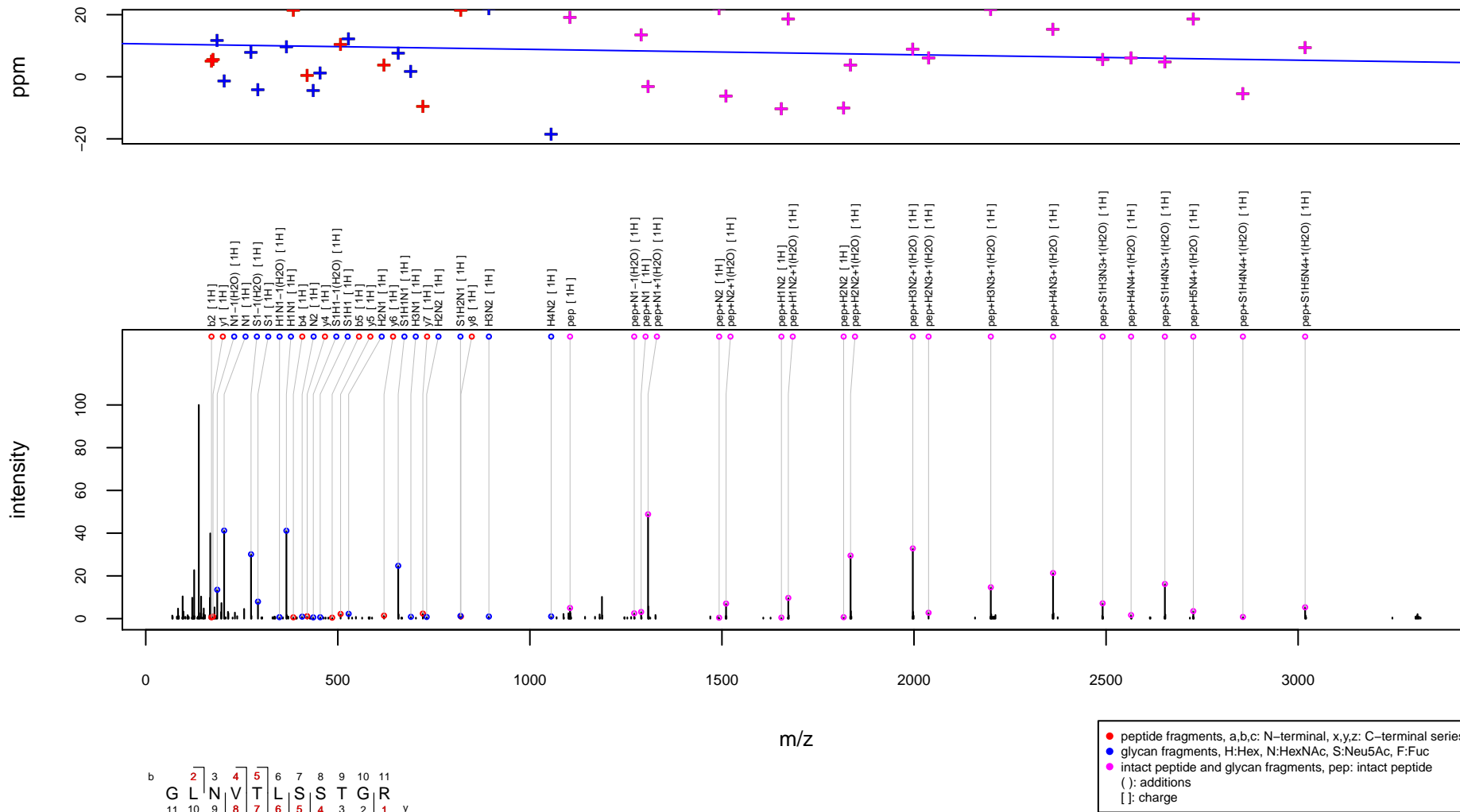
Glycan: S2H3N2F1

Charge: 3H



m/z 1103.789 charge 3 scan 0-0

Score= 70.6 , Hits= 45 , Explained Intensity= 0.51
 Peptide: CO4A_HUMAN[1326,1336]:GLNVTLSSSTGR
 Glycan: SHNH(SHNH)HNN, S2H5N4
 Charge: 3H



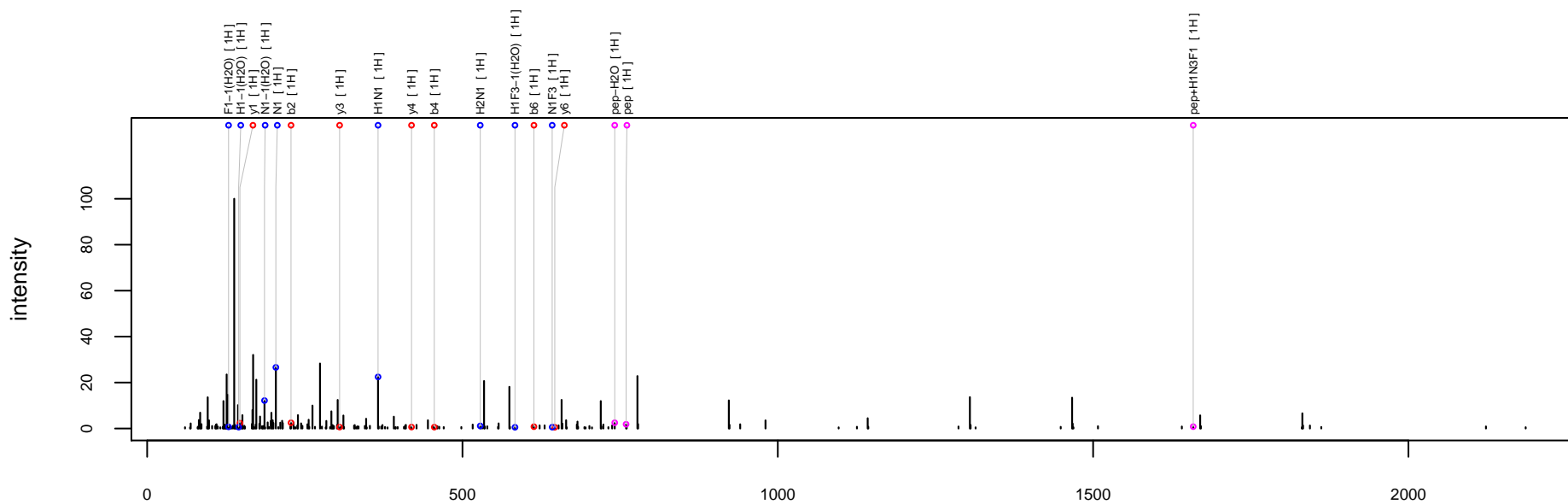
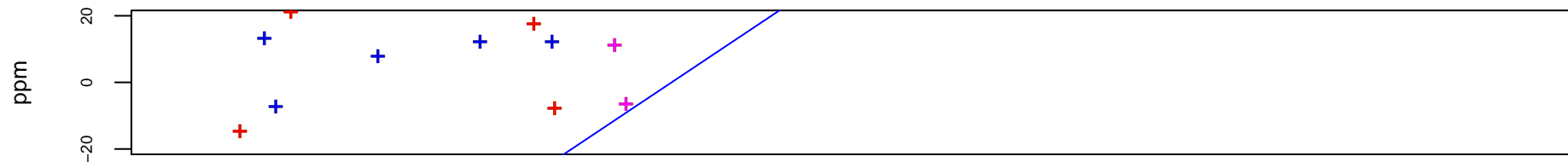
m/z 927.0483 charge 3 scan 0-0

Score= 23.27 , Hits= 18 , Explained Intensity= 0.11

Peptide: AMN1_HUMAN[90,96]:LNLNASK

Glycan: H6N3F3

Charge: 3H



b

	2	3	4	5	6	7
L	N	L	N	A	S	K
7	6	5	4	3	2	1

y

- peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
- glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
- intact peptide and glycan fragments, pep: intact peptide
- (): additions
- []: charge

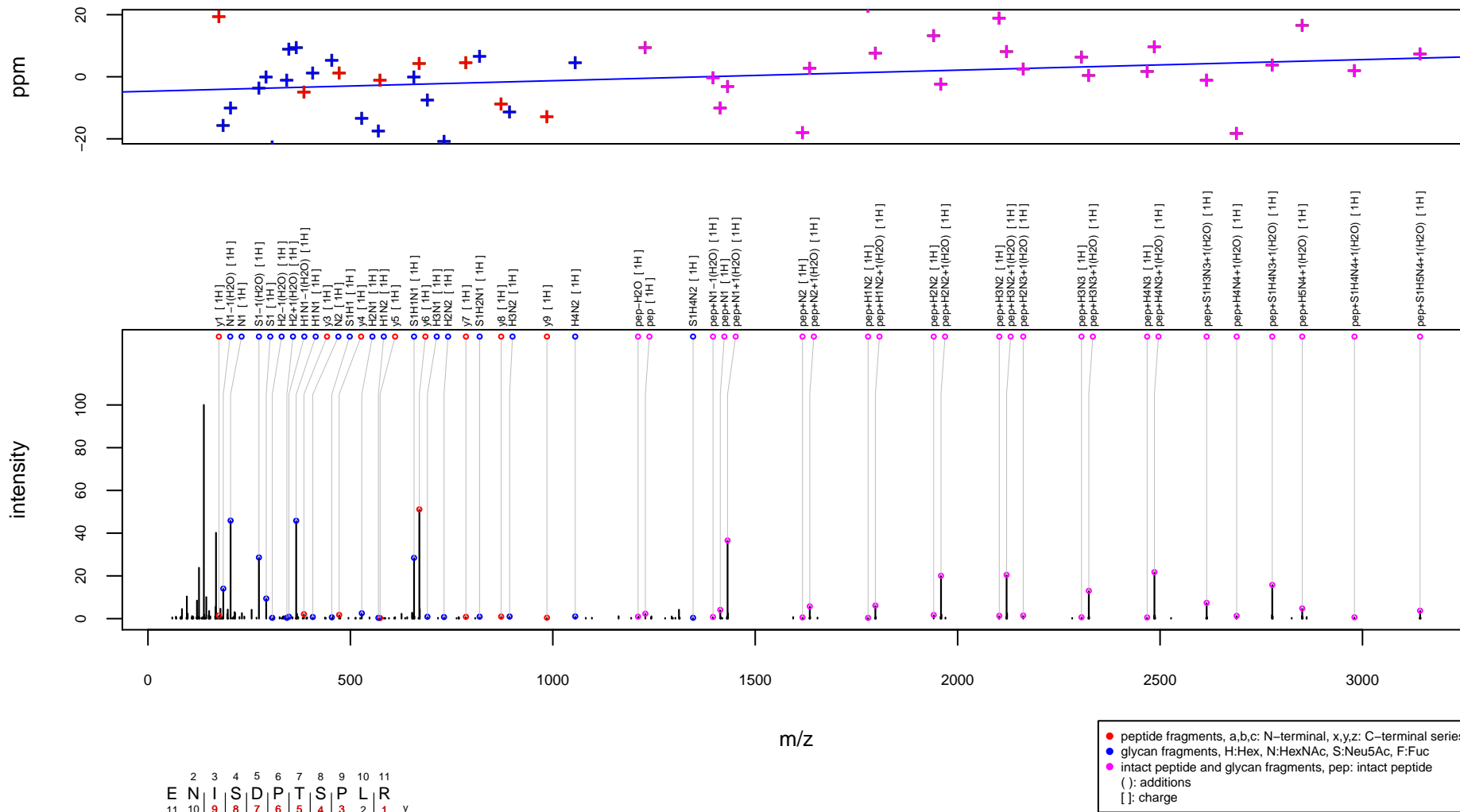
m/z 1145.1309 charge 3 scan 0-0

Score= 81.23 , Hits= 51 , Explained Intensity= 0.59

Peptide: IGJ_HUMAN[70,80]:ENISDPTSPLR

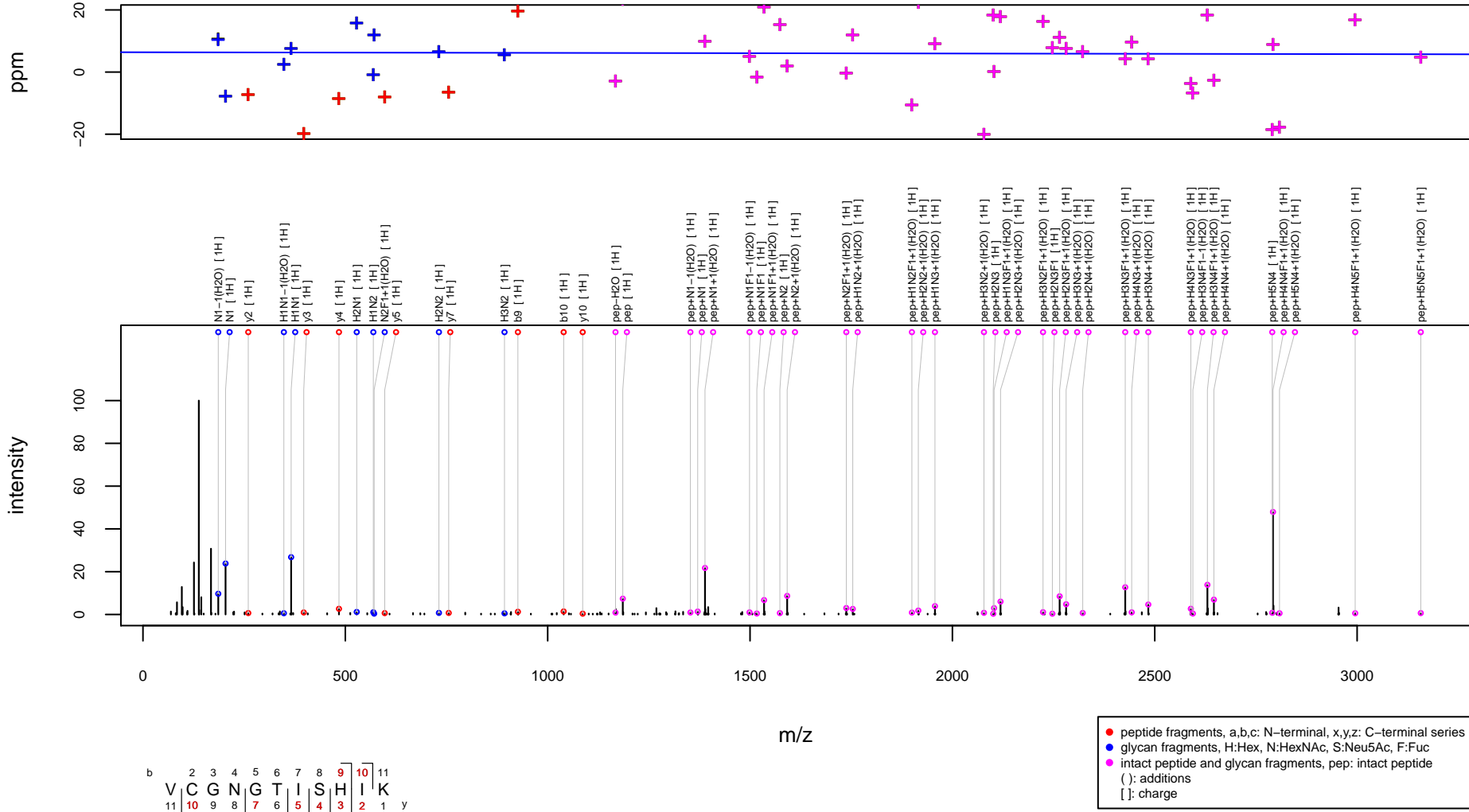
Glycan: SHNH(SHNH)HNN, S2H5N4

Charge: 3H



m/z 1053.11 charge 3 scan 0-0

Score= 77.47 , Hits= 53 , Explained Intensity= 0.48
 Peptide: CUBN_HUMAN[778,788]:VCGNGTISHIK
 Glycan: HNH(HNH)(N)HN(F)N, H5N5F1
 Charge: 3H



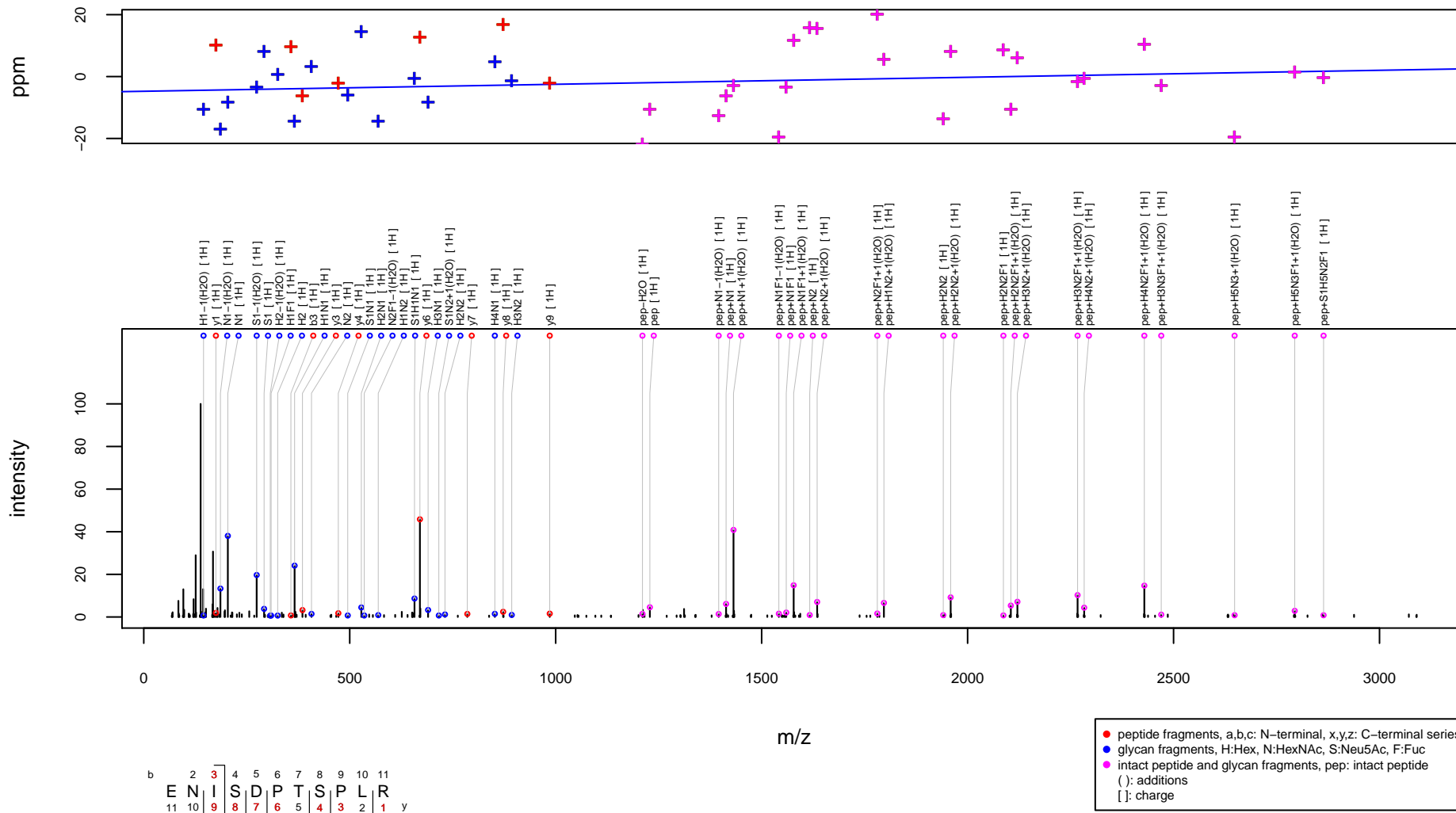
m/z 1029.0918 charge 3 scan 0-0

Score= 65.06 , Hits= 52 , Explained Intensity= 0.5

Peptide: IGJ_HUMAN[70,80]:ENISDPTSPLR

Glycan: S1H5N3F1

Charge: 3H



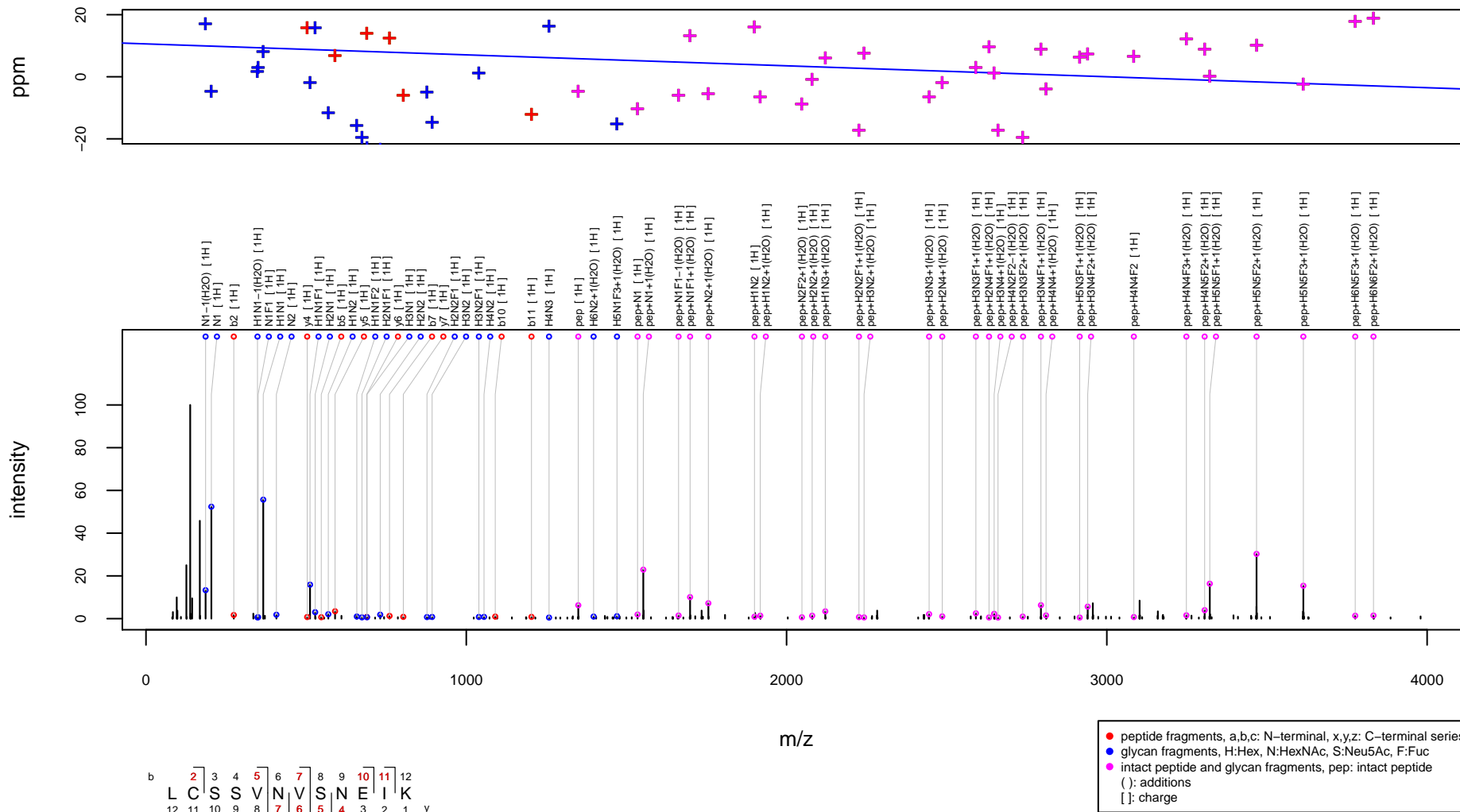
m/z 1326.8784 charge 3 scan 0-0

Score= 63.16 , Hits= 61 , Explained Intensity= 0.49

Peptide: CUBN_HUMAN[2526,2537]:LCSSVNVSEIK

Glycan: H6N6F3

Charge: 3H



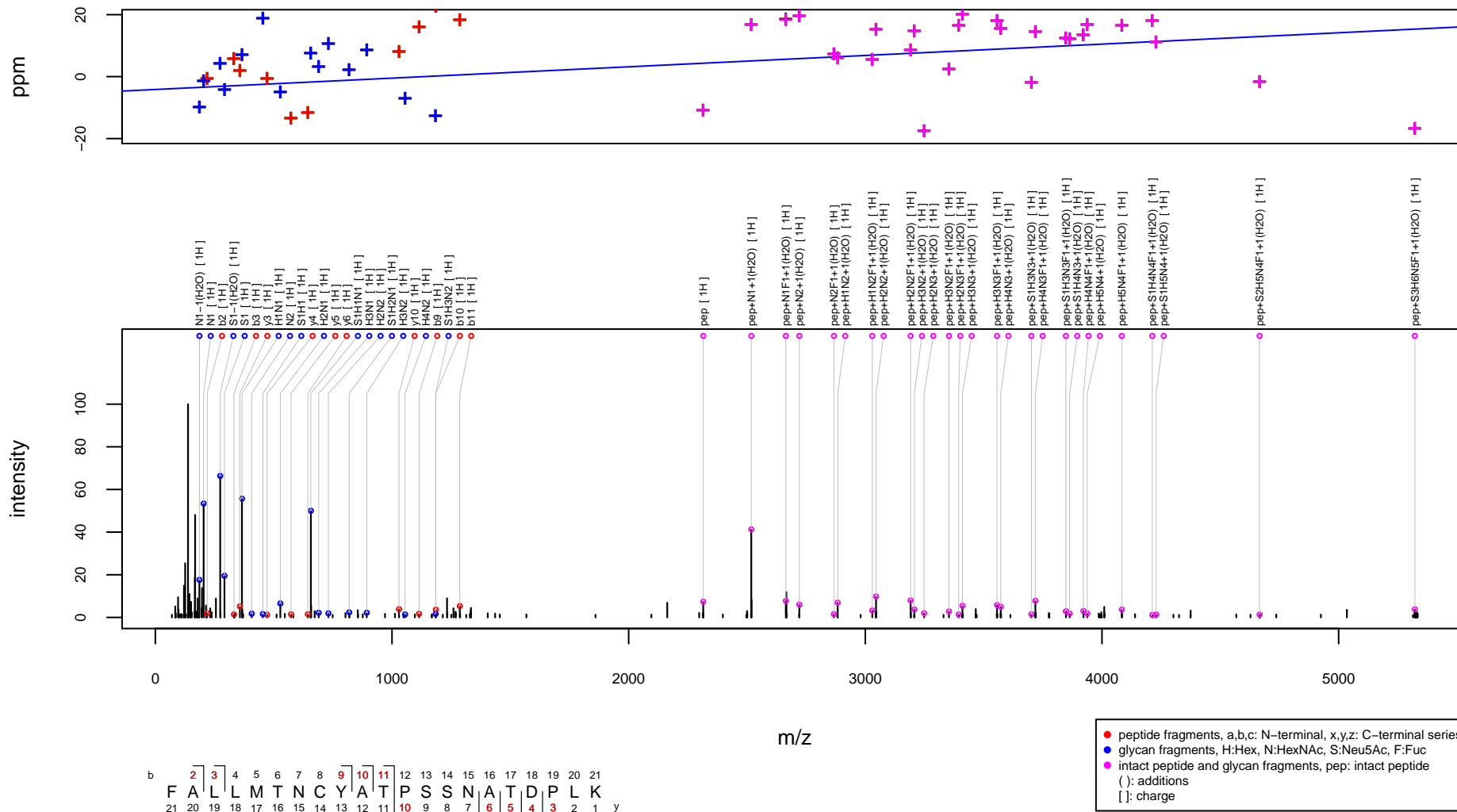
m/z 1331.293 charge 4 scan 0-0

Score= 66.81 , Hits= 52 , Explained Intensity= 0.46

Peptide: UROM_HUMAN[499,519]:FALLMTNCYATPSSNATDPLK

Glycan: SHNH(SHN(SHN)H)HN(F)N, S3H6N5F1

Charge: 4H



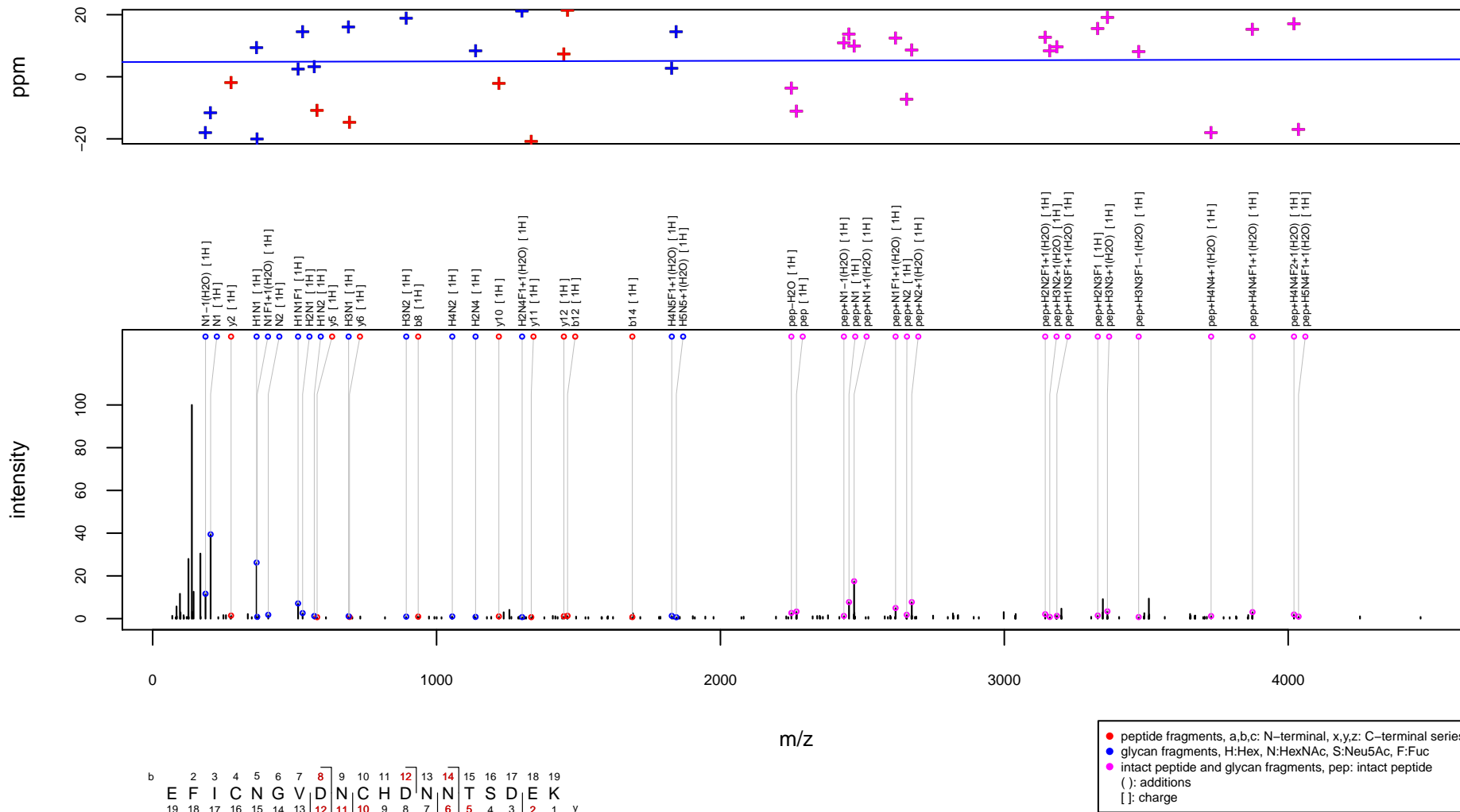
m/z 1133.6877 charge 4 scan 0-0

Score= 54.56 , Hits= 42 , Explained Intensity= 0.32

Peptide: LRP2_HUMAN[2797,2815]:EFICNGVDNCHDNNTSDEK

Glycan: FHNH(FHNH)(N)HN(F)N, H5N5F3

Charge: 4H



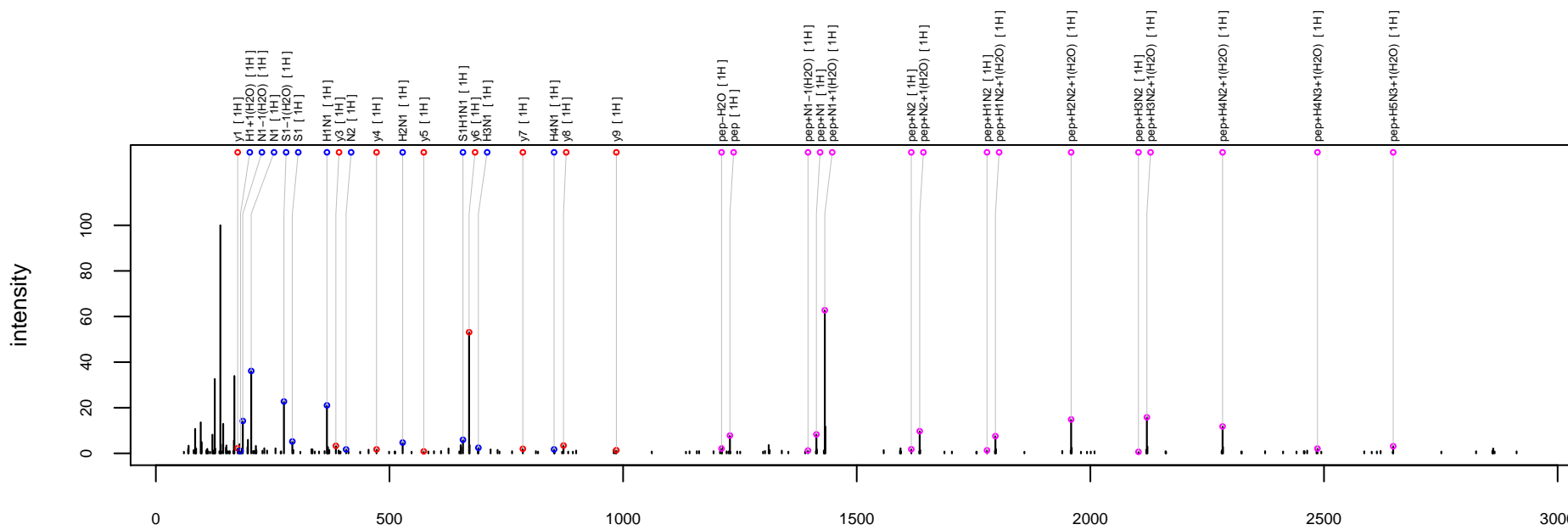
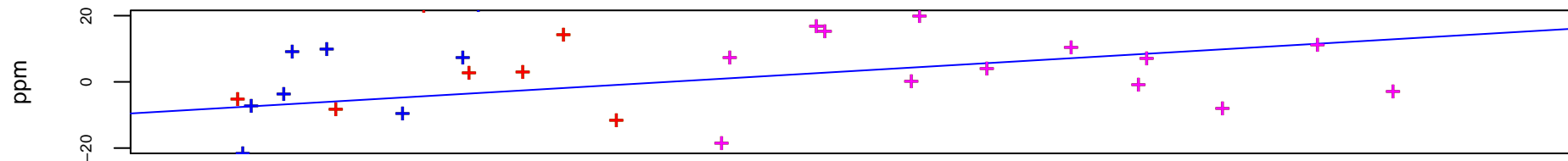
m/z 980.4081 charge 3 scan 0-0

Score= 51.85 , Hits= 34 , Explained Intensity= 0.47

Peptide: IGJ_HUMAN[70,80]:ENISDPTSPLR

Glycan: SHNH(HH)HNN, S1H5N3

Charge: 3H



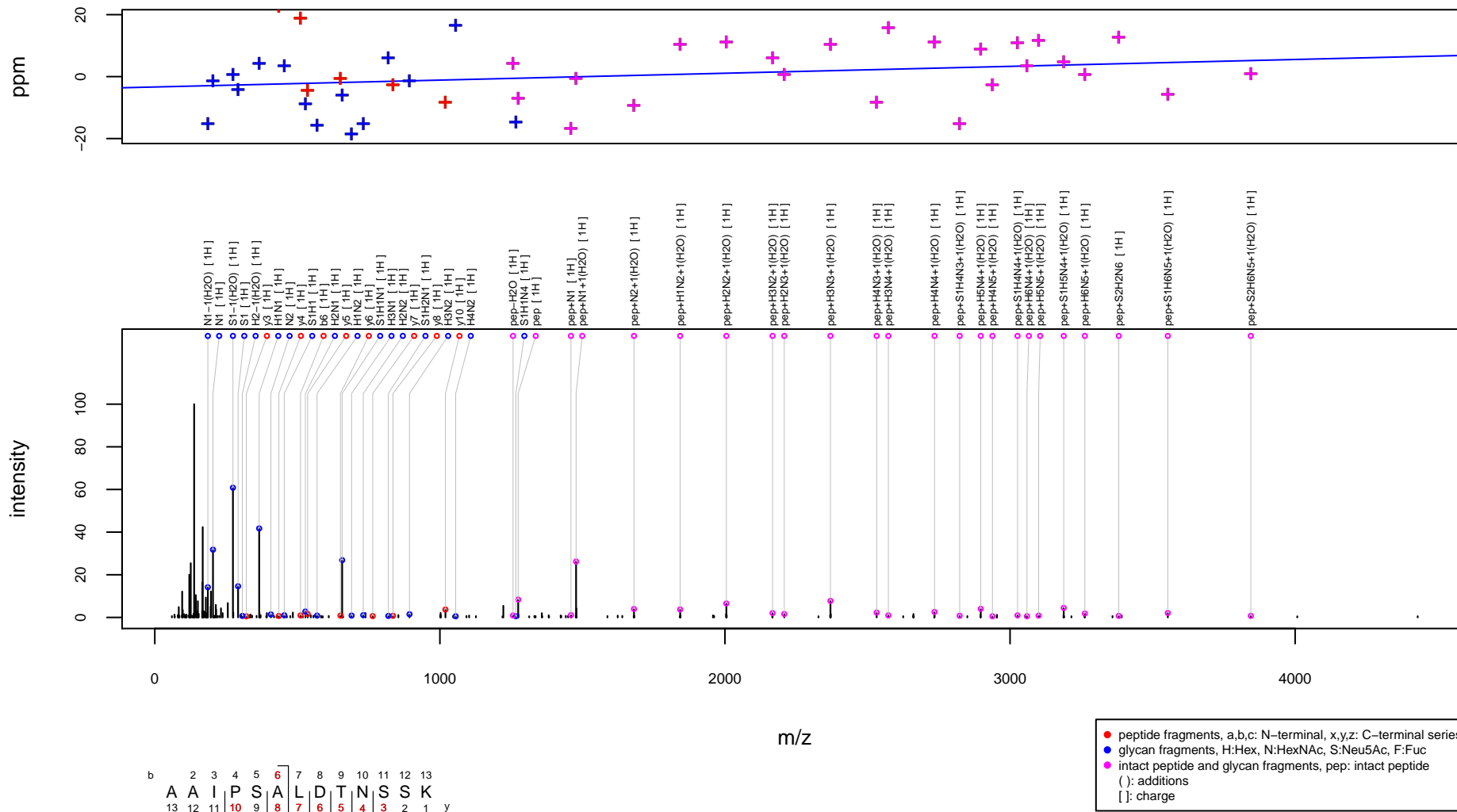
	2	3	4	5	6	7	8	9	10	11
E	N	I	S	D	P	T	S	P	L	R
11	10	9	8	7	6	5	4	3	2	1

y

- peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
- glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
- intact peptide and glycan fragments, pep: intact peptide
- (): additions
- []: charge

m/z 1125.954 charge 4 scan 0-0

Score= 48.17 , Hits= 49 , Explained Intensity= 0.42
 Peptide: LG3BP_HUMAN[542,554]:AAIPSAALDTNSK
 Glycan: S3H7N6
 Charge: 4H



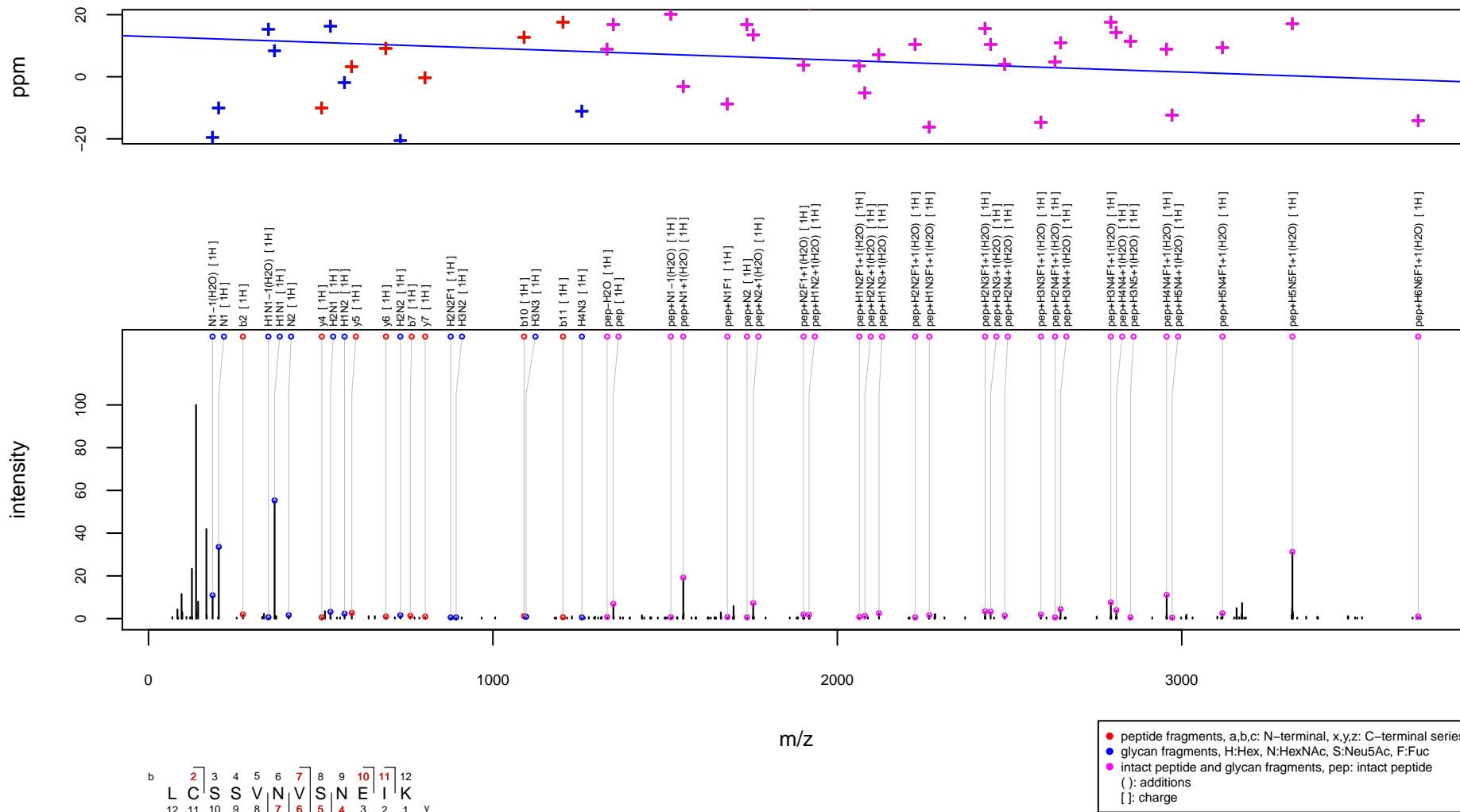
m/z 1229.5062 charge 3 scan 0-0

Score= 64.44 , Hits= 48 , Explained Intensity= 0.43

Peptide: CUBN_HUMAN[2526,2537]:LCSSVNVSNEIK

Glycan: HNH(HN(HN)H)(N)HN(F)N, H6N6F1

Charge: 3H



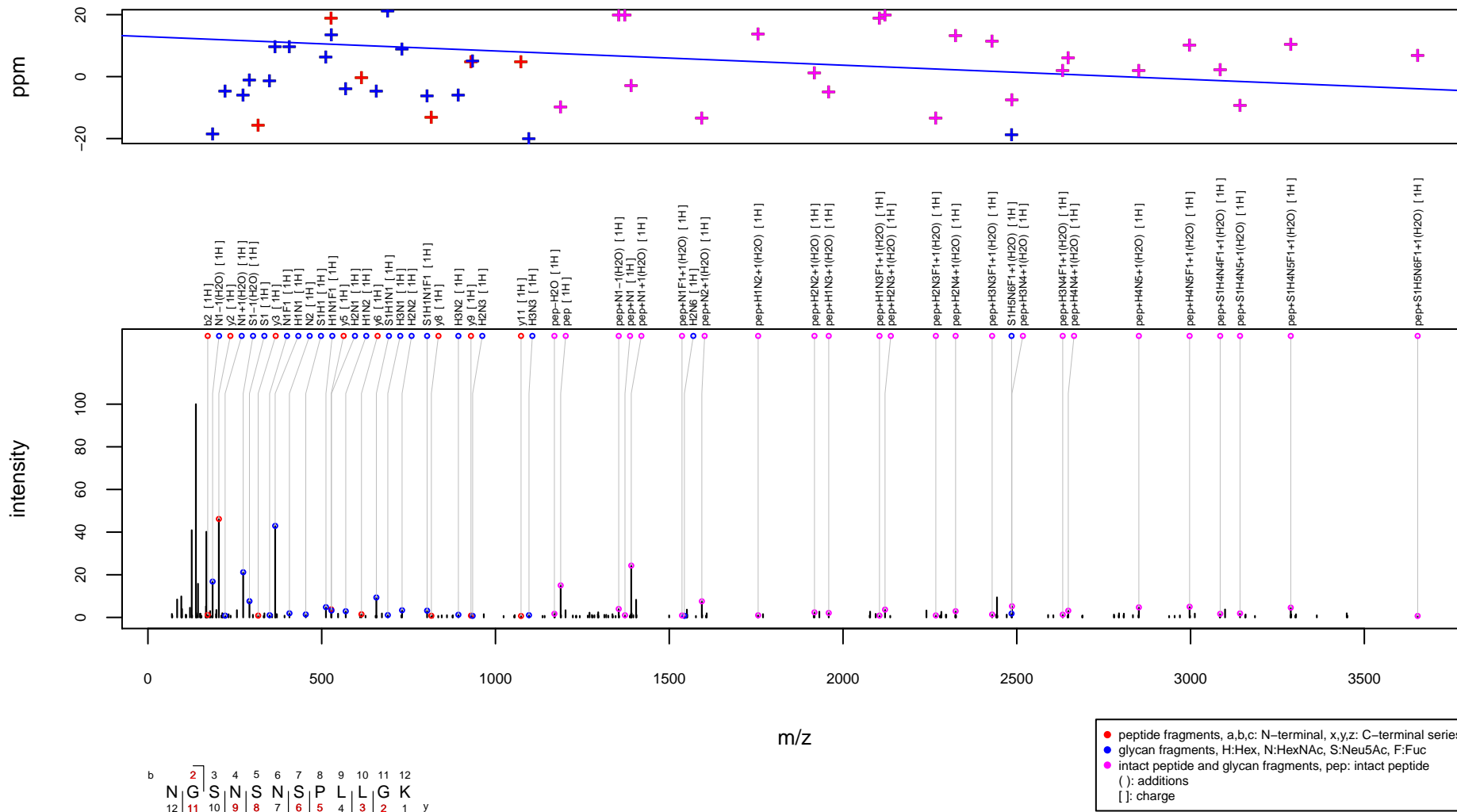
m/z 1218.5017 charge 3 scan 0-0

Score= 54.69 , Hits= 52 , Explained Intensity= 0.43

Peptide: CUBN_HUMAN[3457,3468]:NGSNSNSPLLGK

Glycan: S1H5N6F1

Charge: 3H



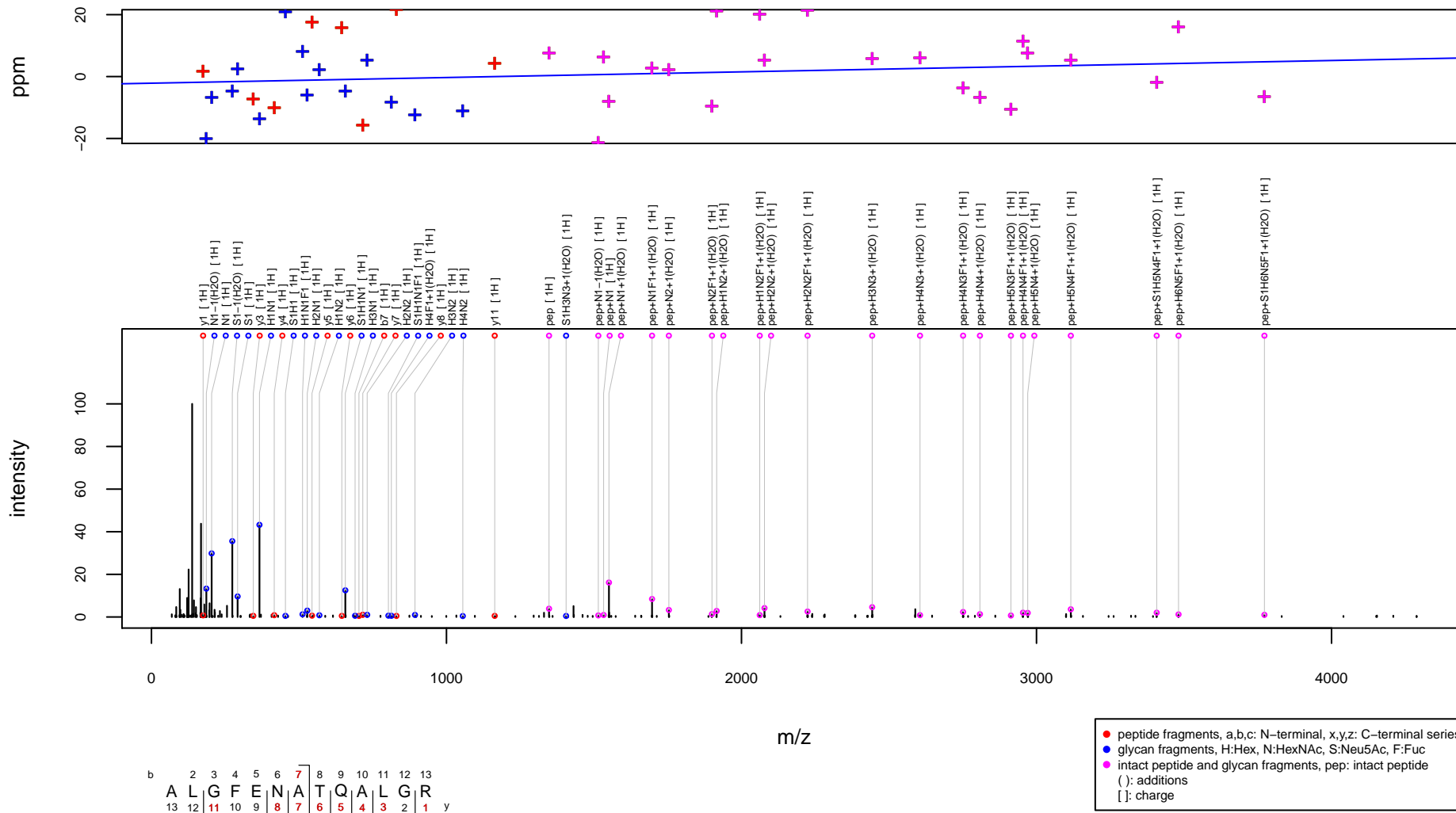
m/z 1107.9541 charge 4 scan 0-0

Score= 40.2 , Hits= 48 , Explained Intensity= 0.4

Peptide: LG3BP_HUMAN[64,76]:ALGFENATQALGR

Glycan: S2H7N6F1

Charge: 4H



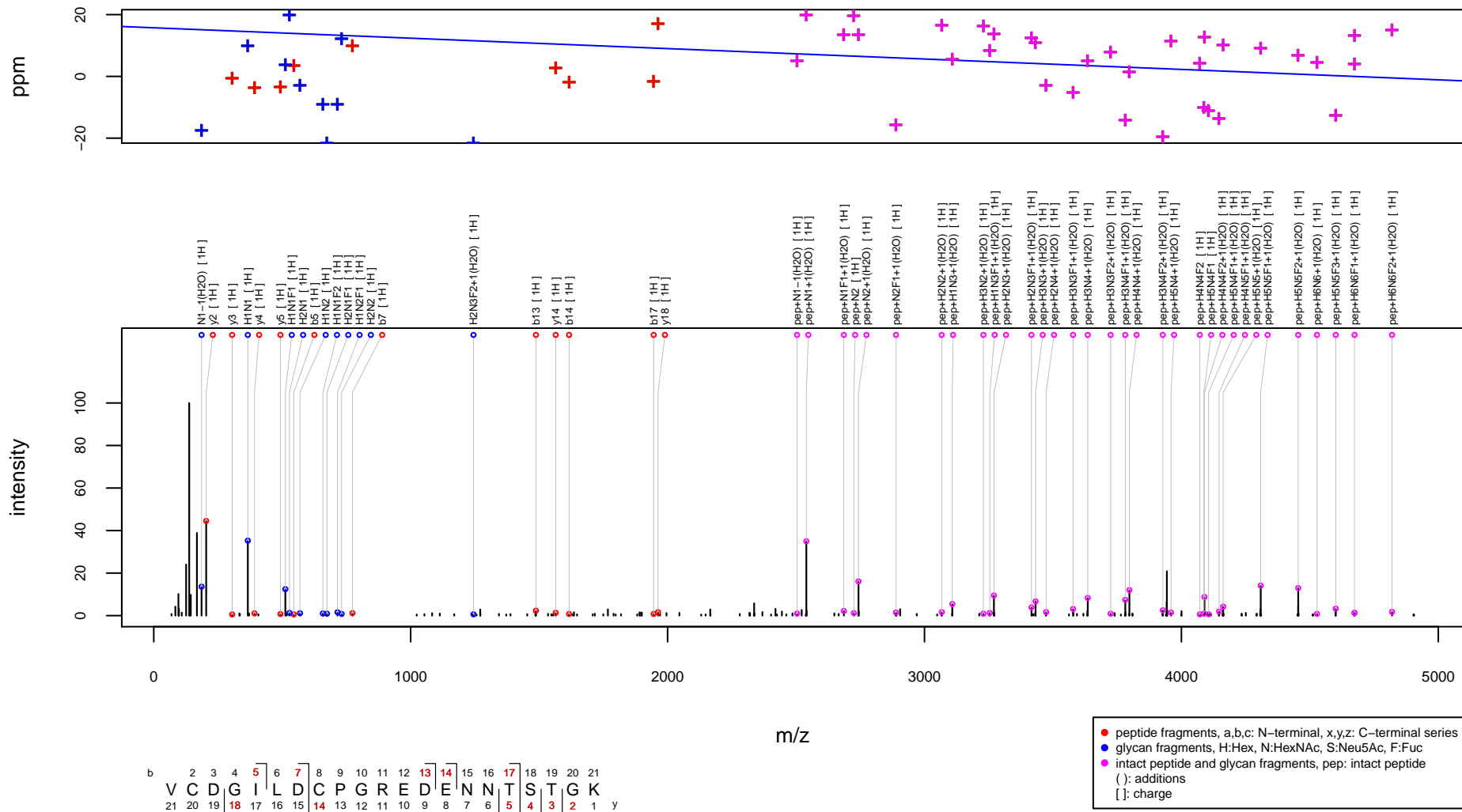
m/z 1242.2429 charge 4 scan 0-0

Score= 55.82 , Hits= 54 , Explained Intensity= 0.48

Peptide: LRP2_HUMAN[285,305]:VCDGILDCPGRDENNTSTGK

Glycan: H6N6F3

Charge: 4H



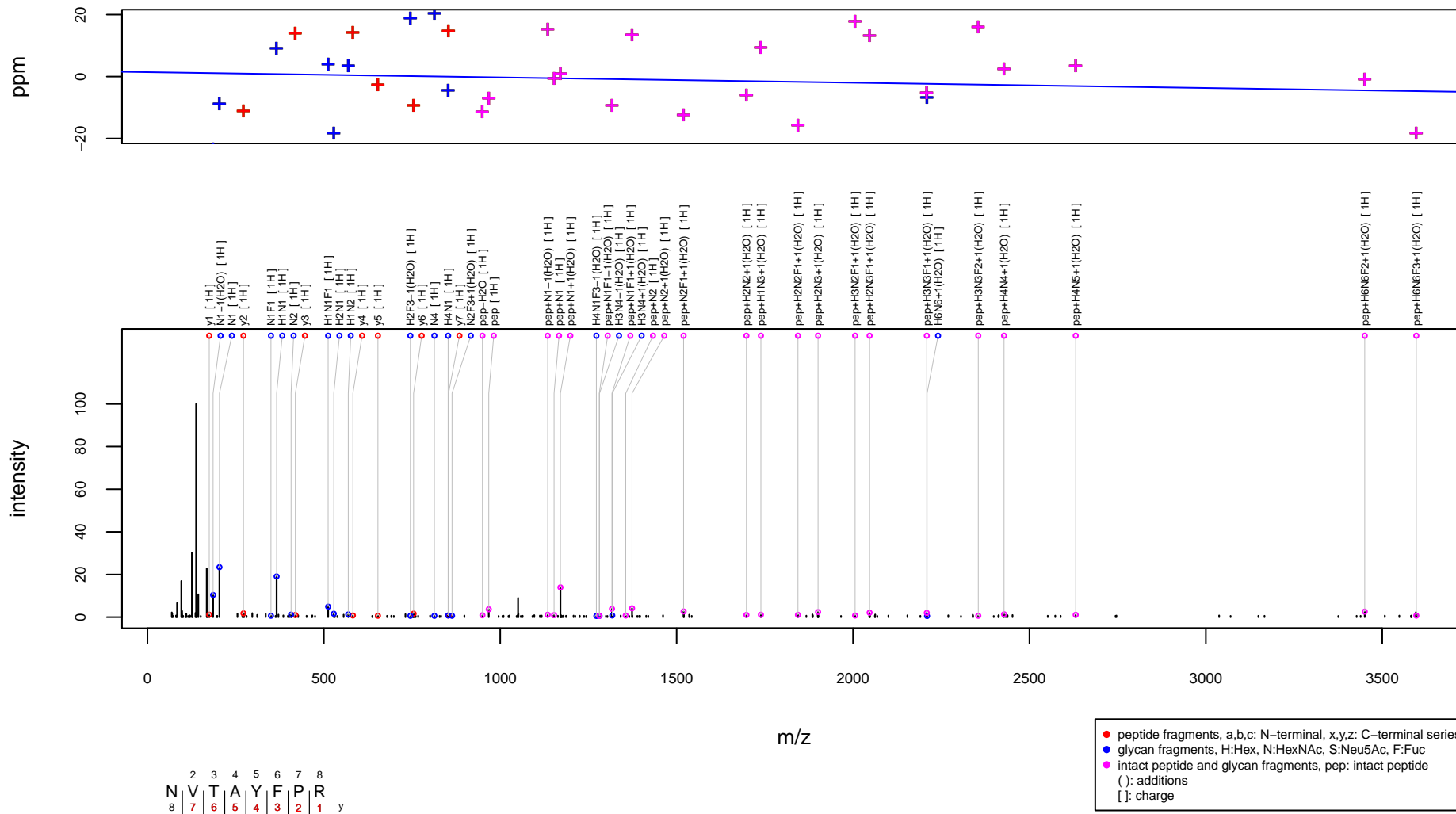
m/z 899.8685 charge 4 scan 0-0

Score= 43.9 , Hits= 45 , Explained Intensity= 0.29

Peptide: MGA_HUMAN[1672,1679]:NVTAYFPR

Glycan: H6N6F3

Charge: 4H



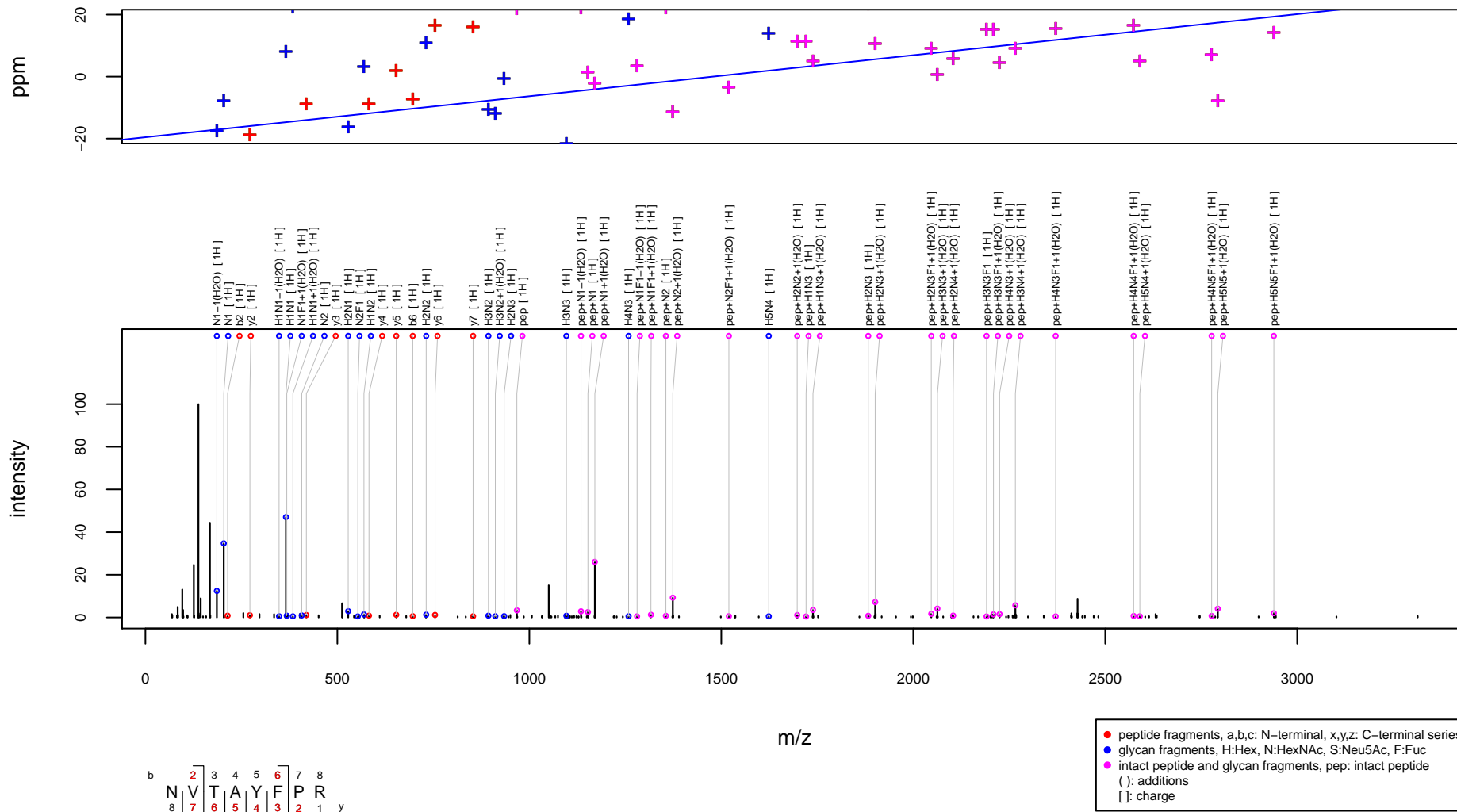
m/z 1102.1216 charge 3 scan 0-0

Score= 70.91 , Hits= 52 , Explained Intensity= 0.38

Peptide: MGA_HUMAN[1672,1679]:NVTA YFPR

Glycan: HNH(HN(HN)H)(N)HN(F)N, H6N6F1

Charge: 3H



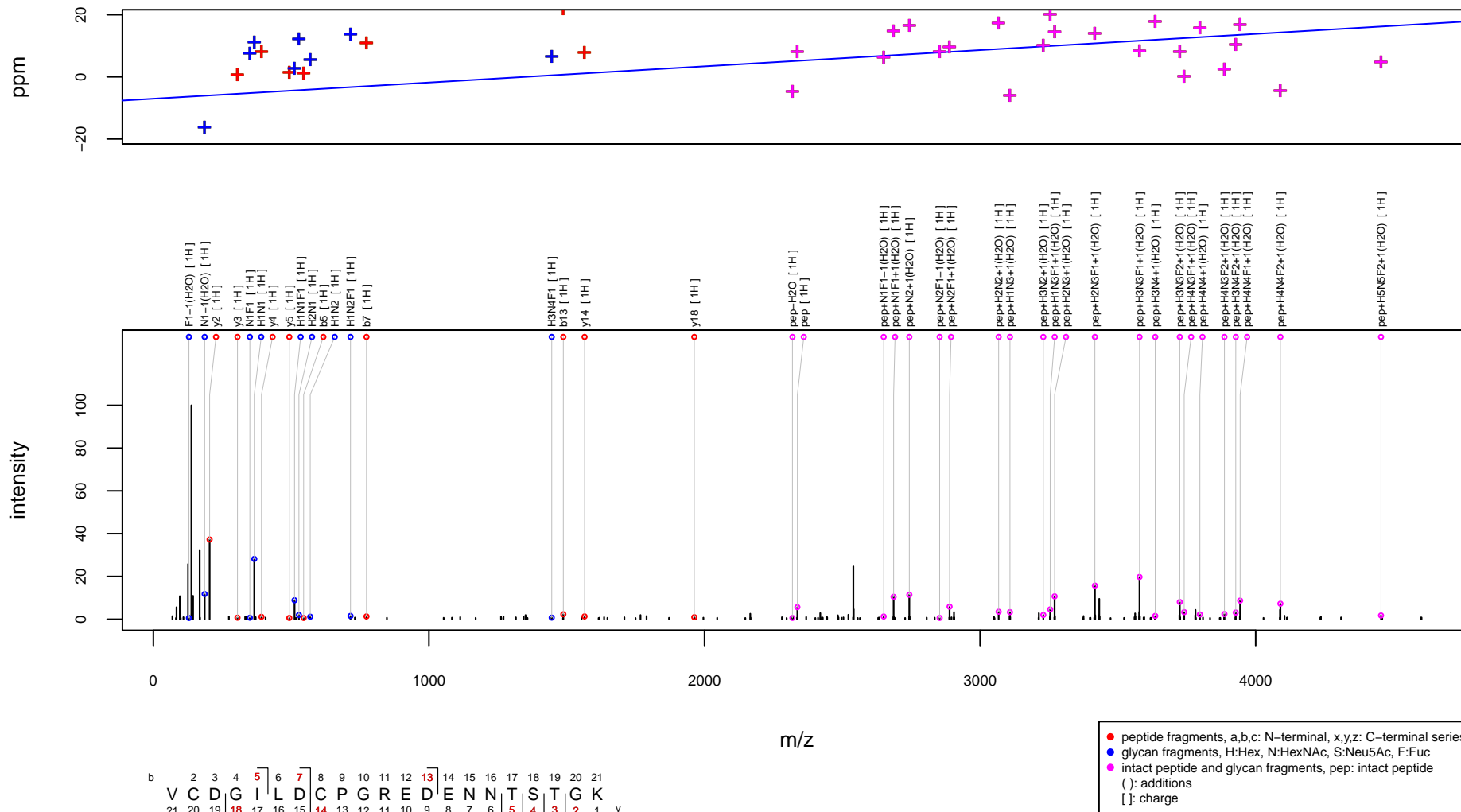
m/z 1150.963 charge 4 scan 0-0

Score= 53.07 , Hits= 41 , Explained Intensity= 0.41

Peptide: LRP2_HUMAN[285,305]:VCDGILDCP GRE DENNTSTGK

Glycan: FHNH(FHNH)(N)HN(F)N, H5N5F3

Charge: 4H



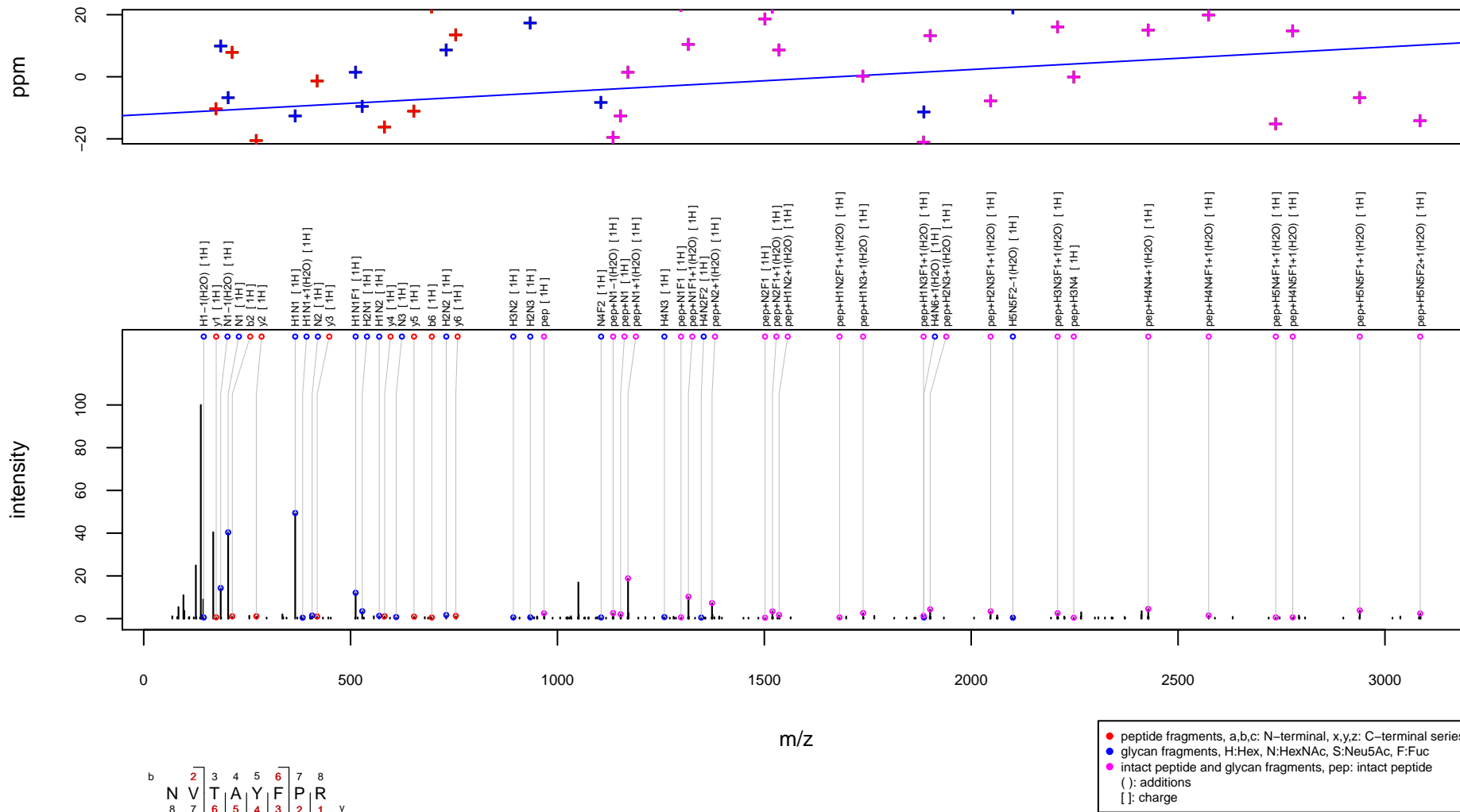
m/z 1150.8015 charge 3 scan 0-0

Score= 52.09 , Hits= 49 , Explained Intensity= 0.41

Peptide: MGA_HUMAN[1672,1679]:NVTAYFPR

Glycan: H6N6F2

Charge: 3H



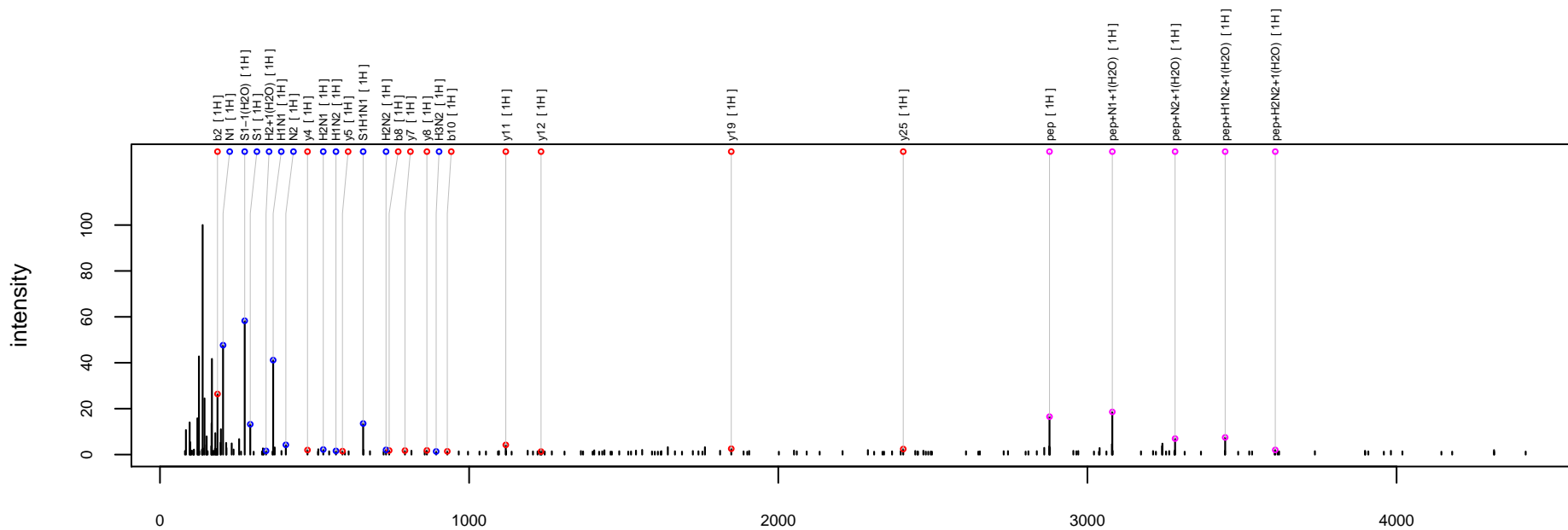
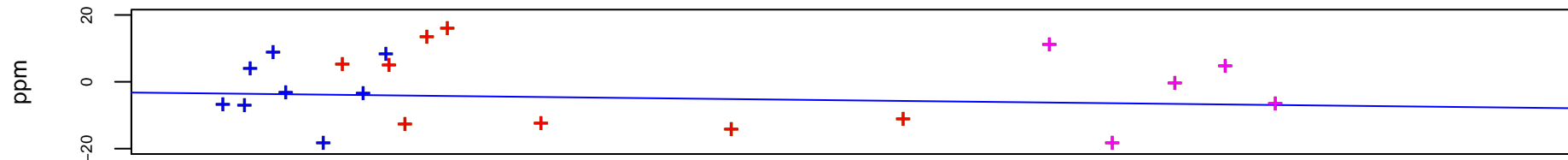
m/z 1139.4739 charge 4 scan 0-0

Score= 36.24 , Hits= 27 , Explained Intensity= 0.35

Peptide: AMPN_HUMAN[40,69]:NANSSPVASTTPSASATTNPASATTLQSK

Glycan: S2H3N3

Charge: 4H



b 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
 N A N S S P V A S T T P S A S A T T N P A S A T T L Q S K
 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1 y

● peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
 ● glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
 ● intact peptide and glycan fragments, pep: intact peptide
 (): additions
 []: charge

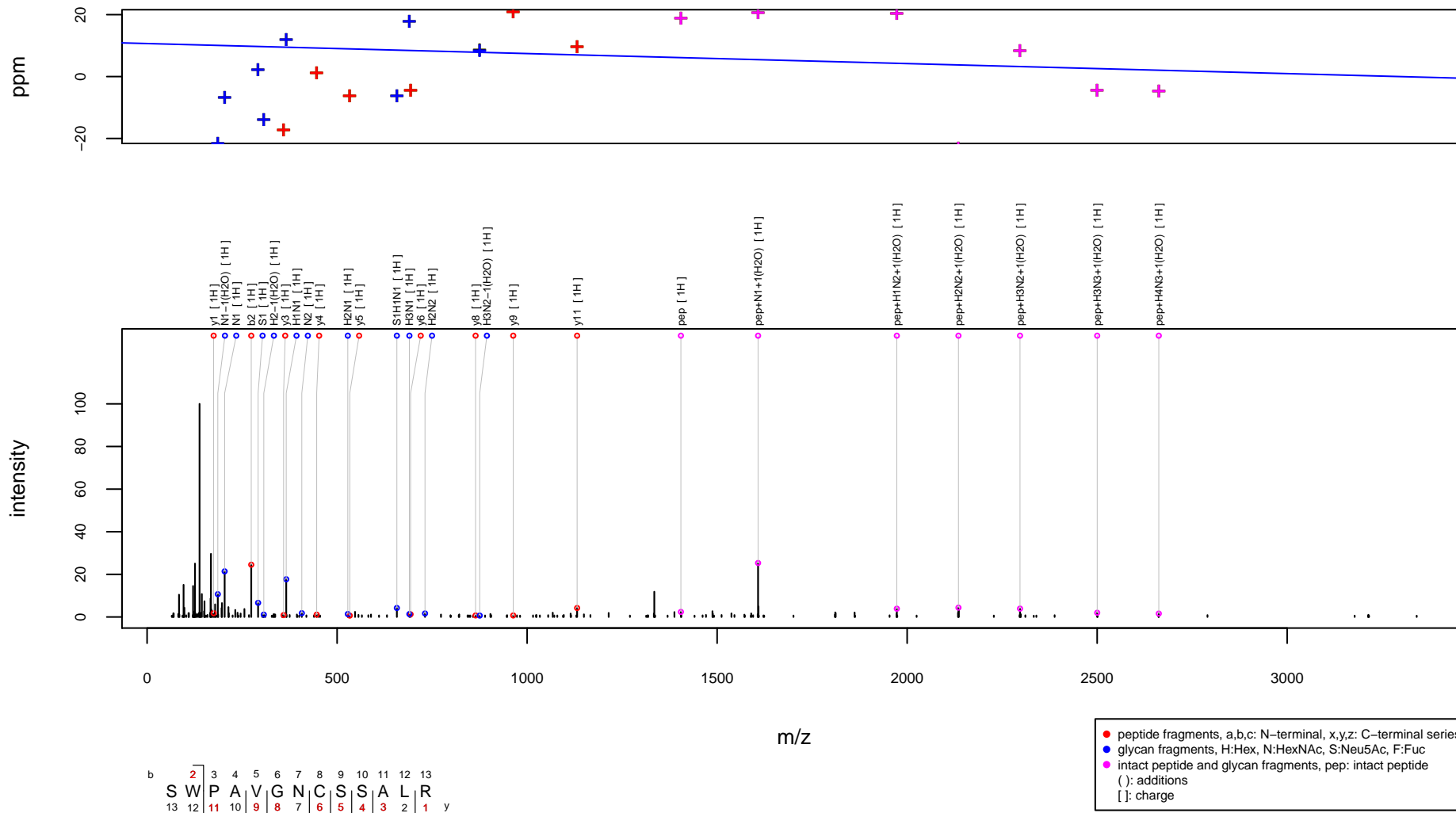
m/z 903.112 charge 4 scan 0-0

Score= 37.58 , Hits= 27 , Explained Intensity= 0.26

Peptide: HEMO_HUMAN[181,193]:SWPAVGCSSALR

Glycan: SHNH(SHNH)HNN, S2H5N4

Charge: 4H



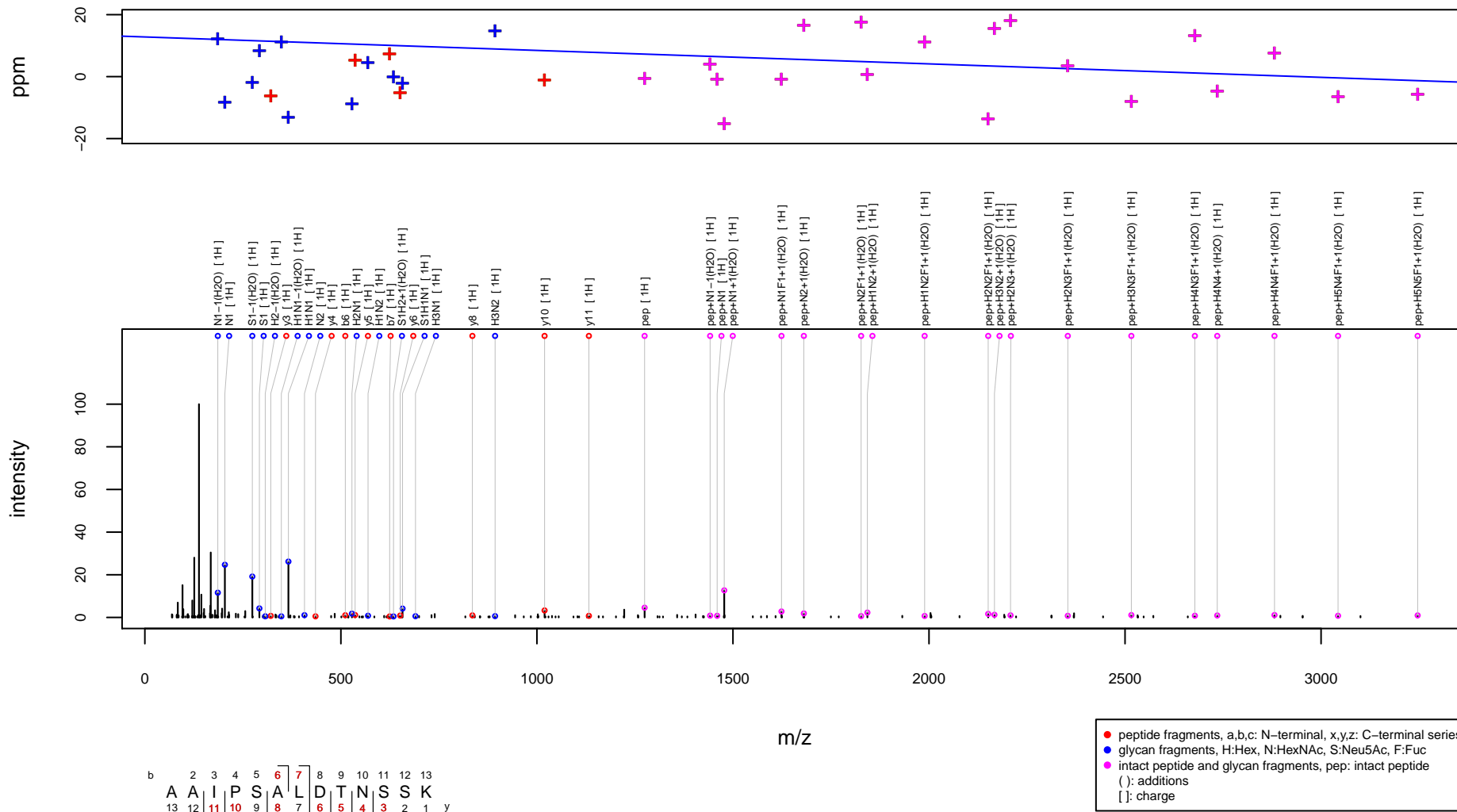
m/z 976.406 charge 4 scan 0-0

Score= 38.99 , Hits= 42 , Explained Intensity= 0.31

Peptide: LG3BP_HUMAN[542,554]:AAIPSAALDTNSK

Glycan: S1H6N6F1

Charge: 4H



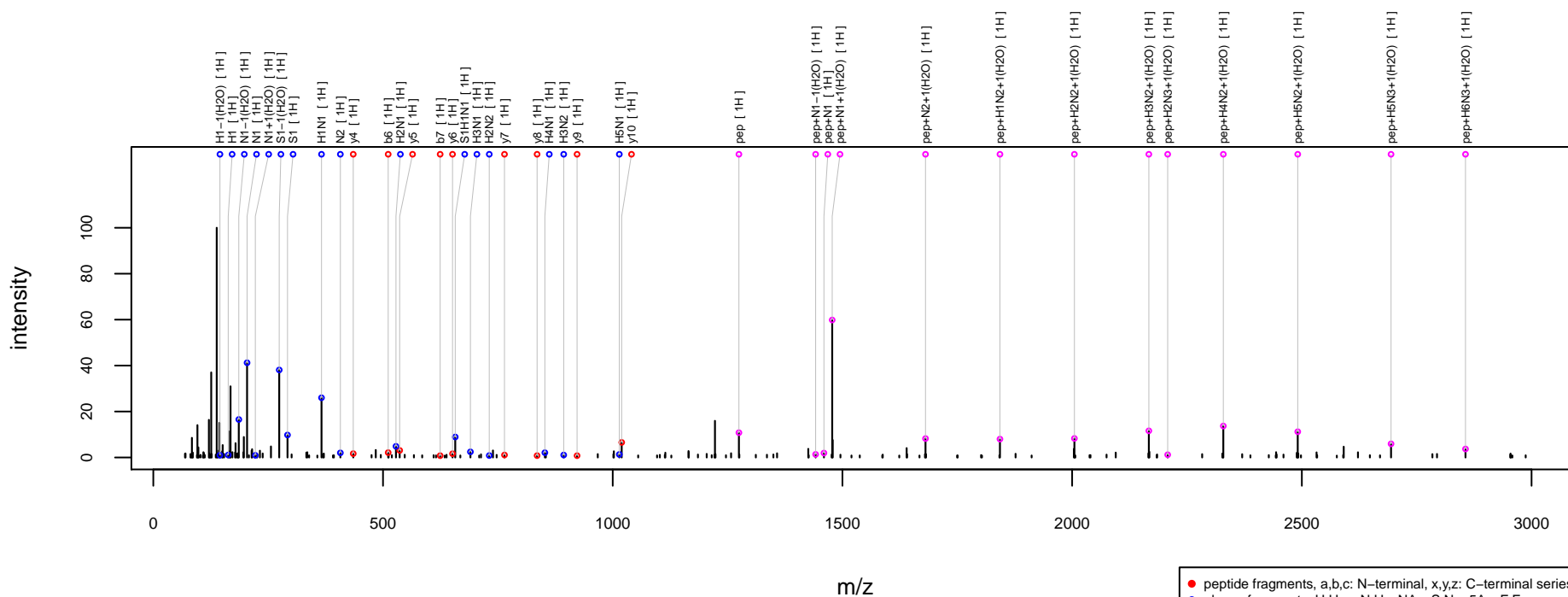
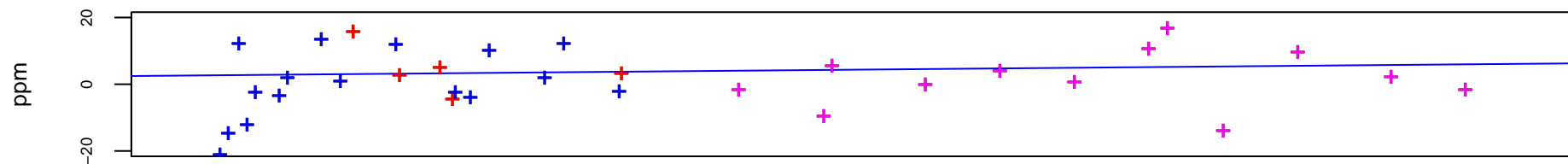
m/z 1049.7739 charge 3 scan 0-0

Score= 55.34 , Hits= 38 , Explained Intensity= 0.4

Peptide: LG3BP_HUMAN[542,554]:AAIPSA LDTNSSK

Glycan: SHNH(H(H)H)HNN, S1H6N3

Charge: 3H



b 2 3 4 5 6 7 8 9 10 11 12 13
 A A I P S A L D T N S S K
 13 12 11 10 9 8 7 6 5 4 3 2 1 y

● peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
 ● glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
 ● intact peptide and glycan fragments, pep: intact peptide
 (): additions
 []: charge

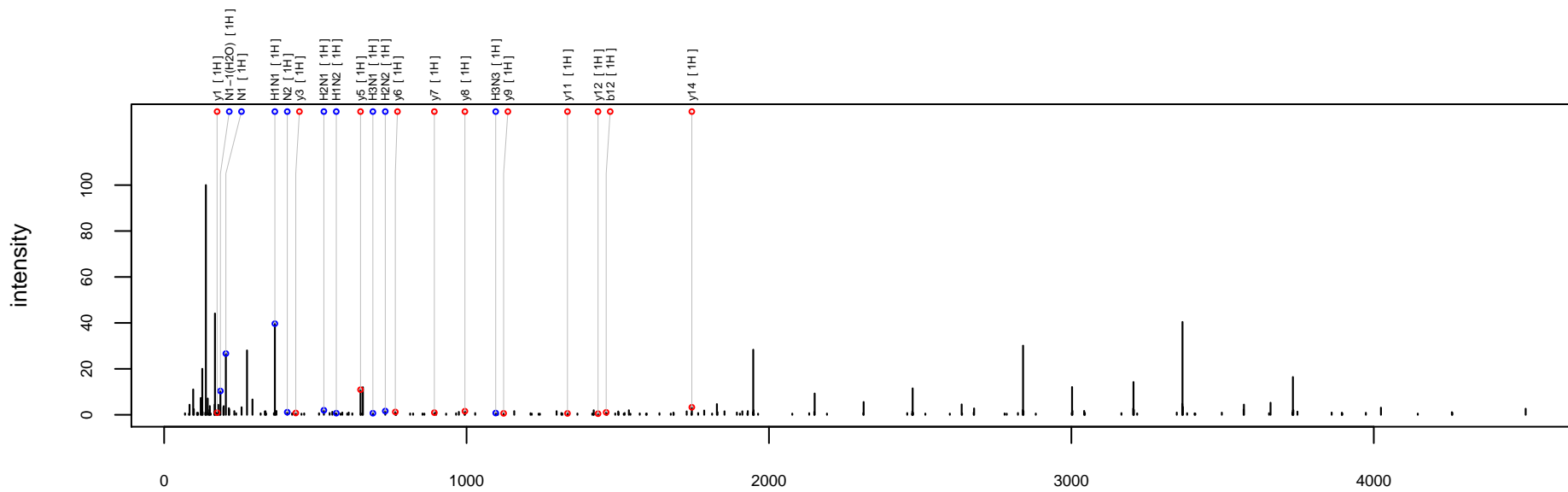
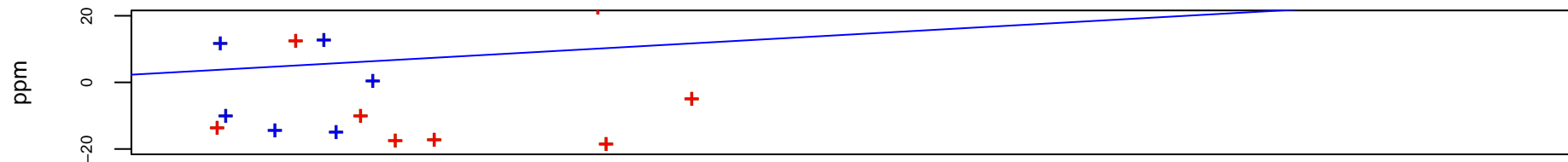
m/z 1170.7365 charge 4 scan 0-0

Score= 27.03 , Hits= 20 , Explained Intensity= 0.15

Peptide: A1AG1_HUMAN[58,81]:SVQEIQATFFYFTPKNKTEDTIFLR

Glycan: H6N4

Charge: 4H



b 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24
 S V Q E I Q A T F F Y F T P N K T E D T I F L R
 24 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1 y

● peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
 ● glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
 ● intact peptide and glycan fragments, pep: intact peptide
 (): additions
 []: charge

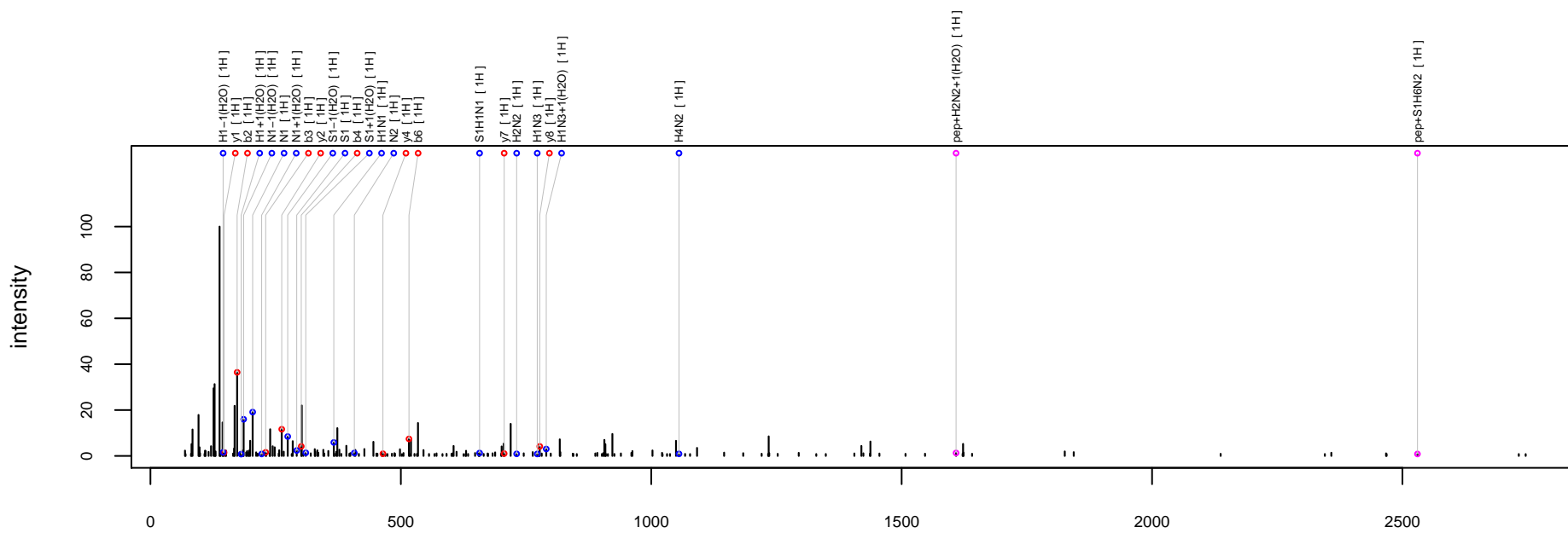
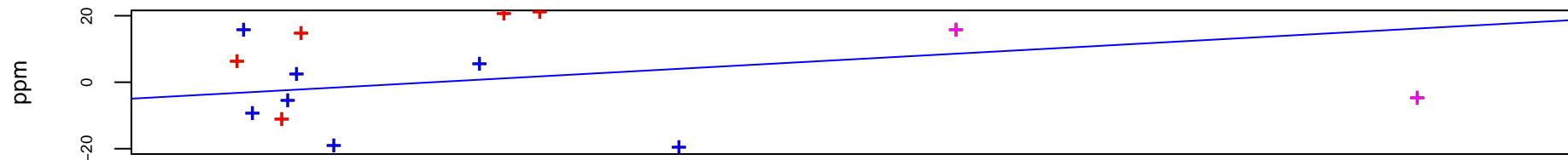
m/z 917.7096 charge 3 scan 0-0

Score= 33.23 , Hits= 26 , Explained Intensity= 0.19

Peptide: FGFR3_HUMAN[311,319]:TAGANTTDK

Glycan: S1H6N3

Charge: 3H



- peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
- glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
- intact peptide and glycan fragments, pep: intact peptide
- (): additions
- []: charge

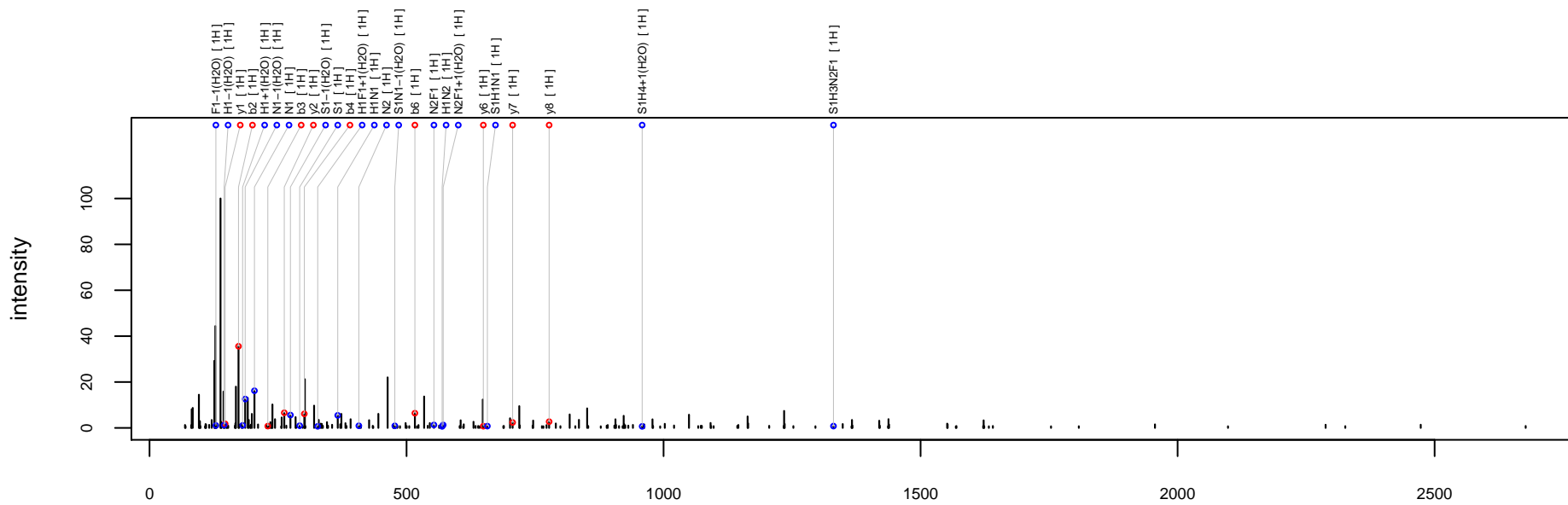
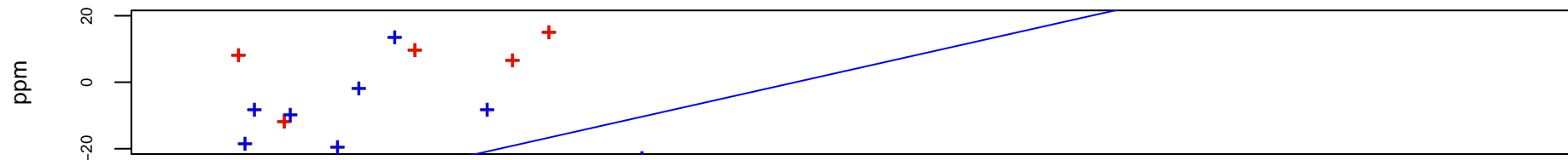
m/z 898.7083 charge 3 scan 0-0

Score= 30.71 , Hits= 26 , Explained Intensity= 0.16

Peptide: FGFR3_HUMAN[311,319]:TAGANTTDK

Glycan: S1H6N2F1

Charge: 3H



● peptide fragments, a,b,c: N-terminal, x,y,z: C-terminal series
 ● glycan fragments, H:Hex, N:HexNAc, S:Neu5Ac, F:Fuc
 ● intact peptide and glycan fragments, pep: intact peptide
 (): additions
 []: charge

m/z 918.1528 charge 4 scan 0-0

Score= 40.53 , Hits= 33 , Explained Intensity= 0.26

Peptide: DPEP1_HUMAN[56,70]:ANLTTLAGHTHNIPK

Glycan: FHNH(HNH)(N)HN(F)N, H5N5F2

Charge: 4H

