Proteome wide reduction in AGE modification in STZ induced diabetic mice by hydralazine mediated transglycation

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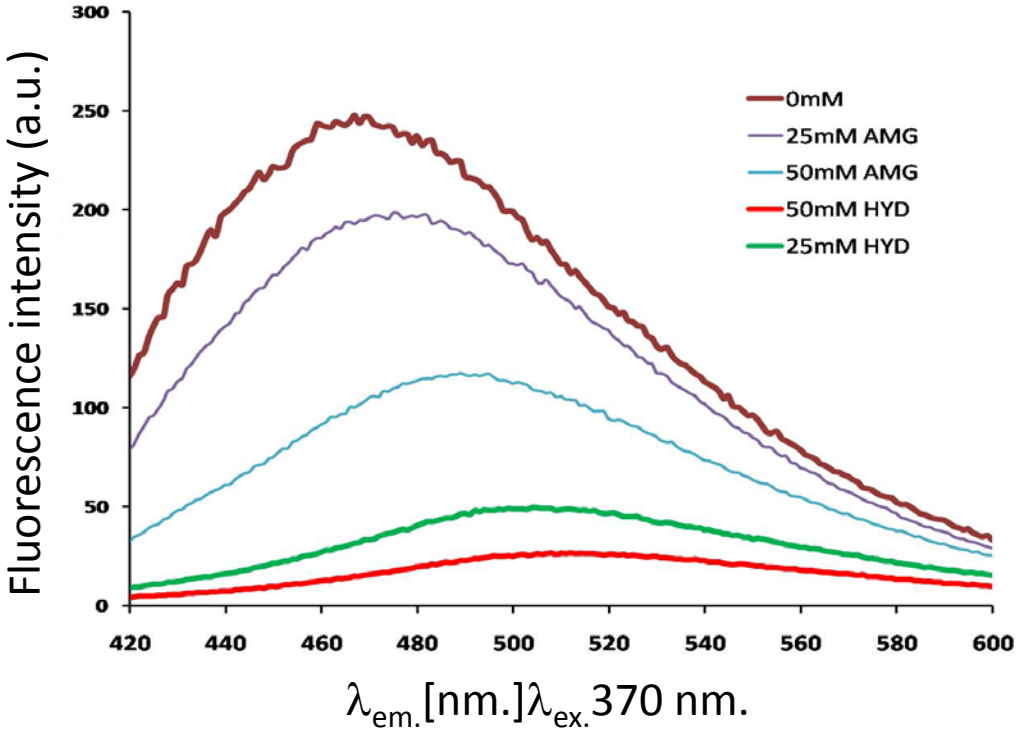
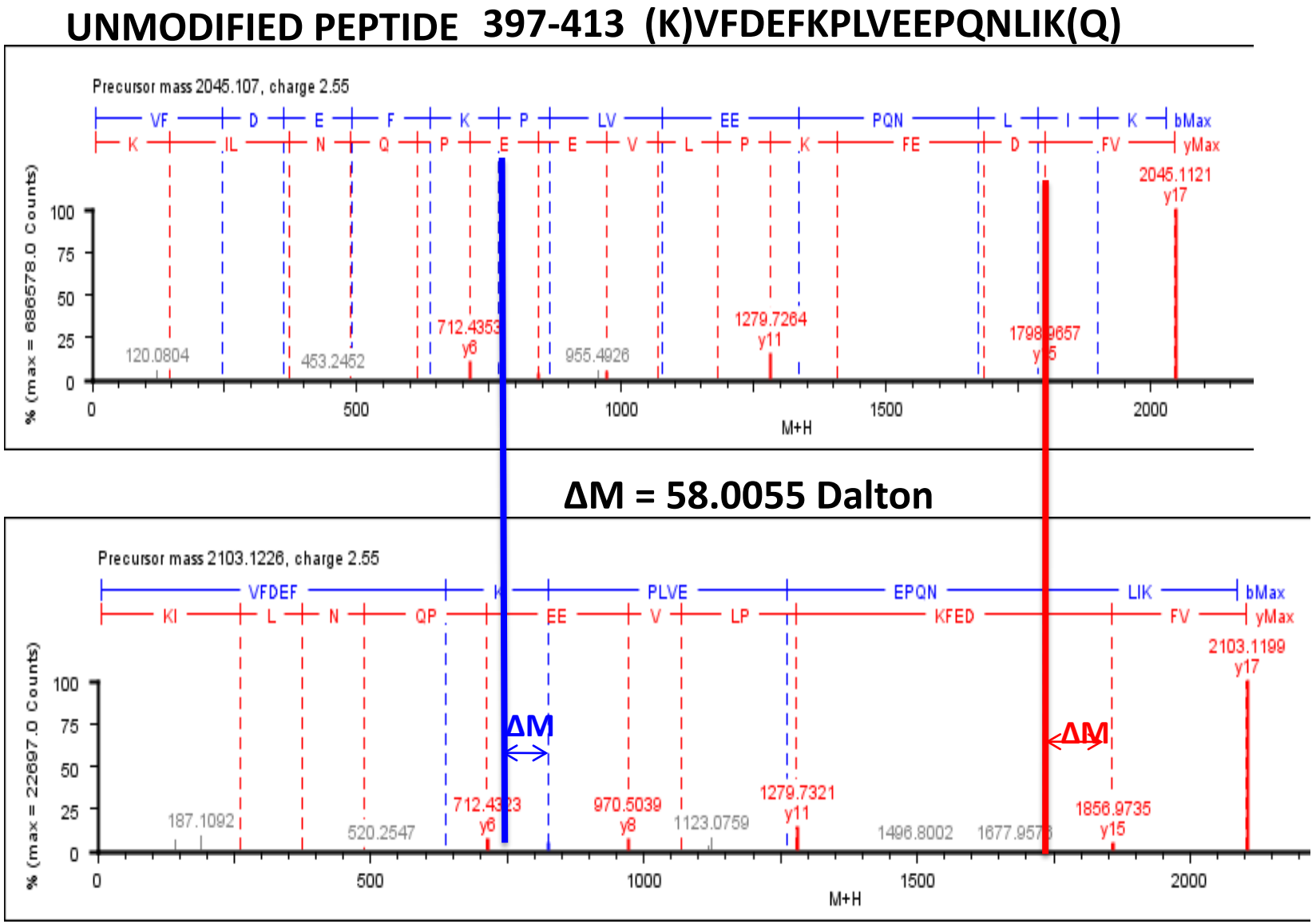
Supplementary Fig 1:
Fluorescence emission spectra of glycated AGE modified HSA at $\lambda_{ex.}$370 nm. The fluorescence emission profiles resulted from drug treated HSA shows decrease in AGE fluorescence. Hydralazine shows more potent inhibition than Aminoguanidine.



Supplementary Fig 2.

Representative Annotation of AGE modified peptide

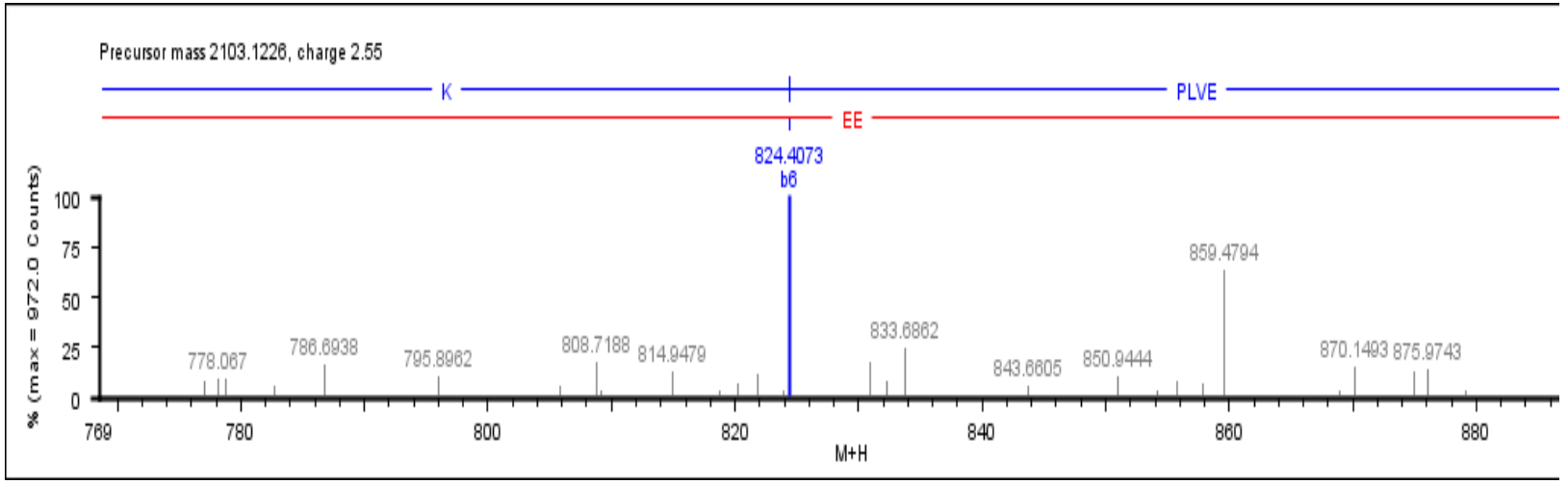
Fig 2a. Annotation of AGE modified peptide in comparison with unmodified peptide



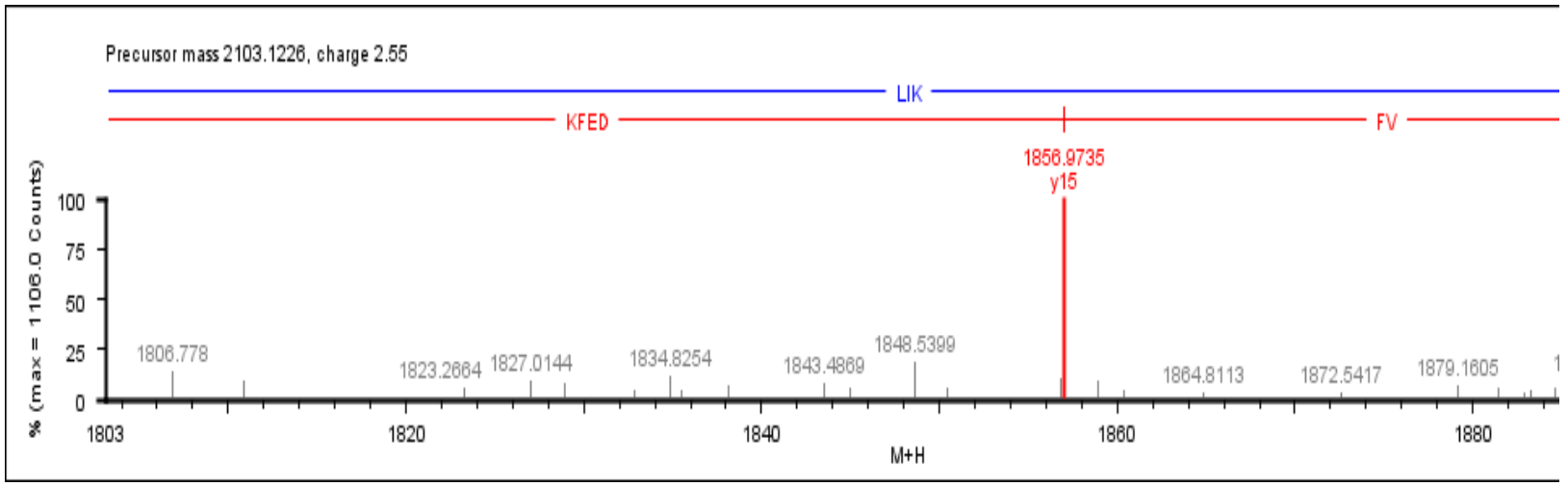
Supplementary Fig 2b.

Zoomed image of b and y ion showing increase in mass due to modification

Modified b ion VFDEFK + CML – H_2O = 784.3875 +58.0055 – 18.0105= 824.3780

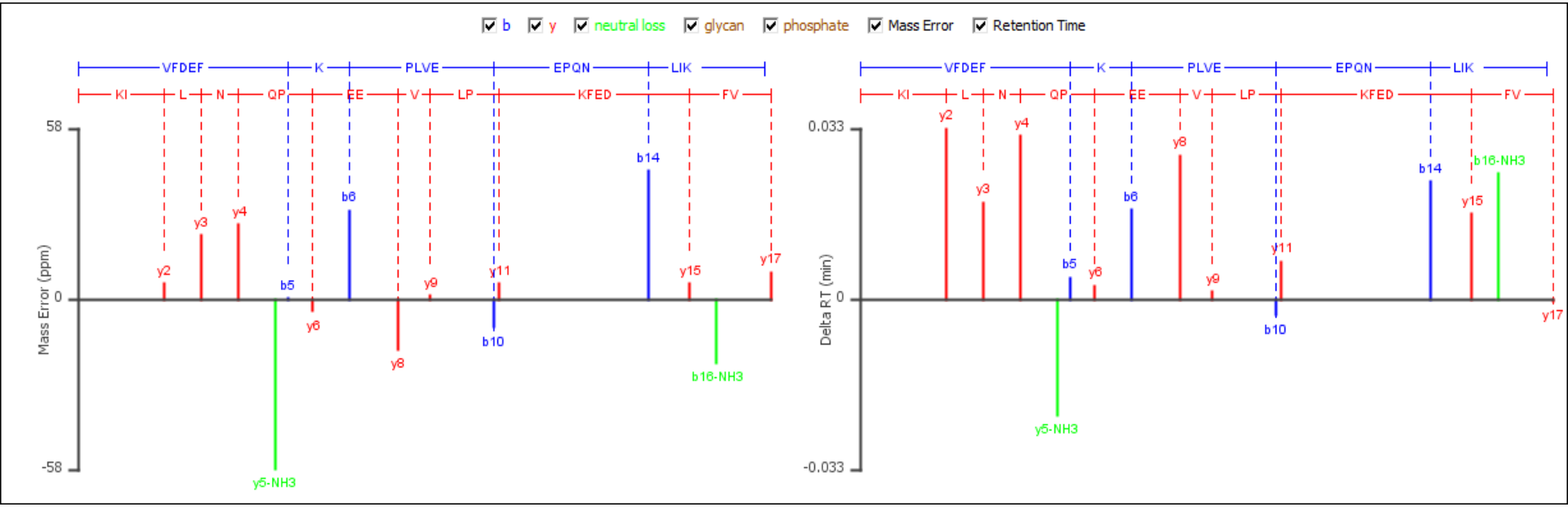


Modified Y ion DEFKPLVEEPQNLIK + CML = 1798.9584 + 58.0055 = 1856.9639

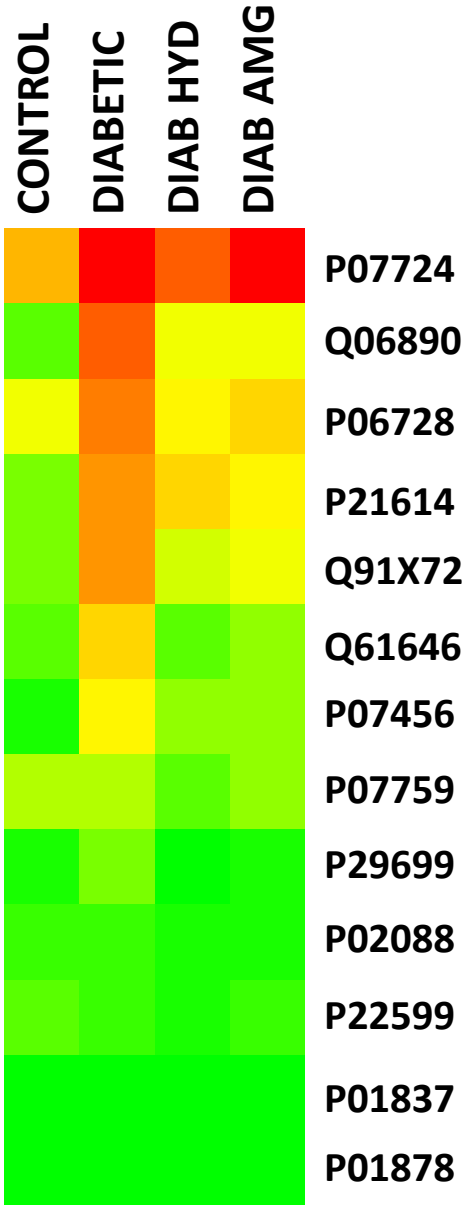


Supplementary Fig 2c.

Fragment mass error and fragment retention time error of the modified peptide



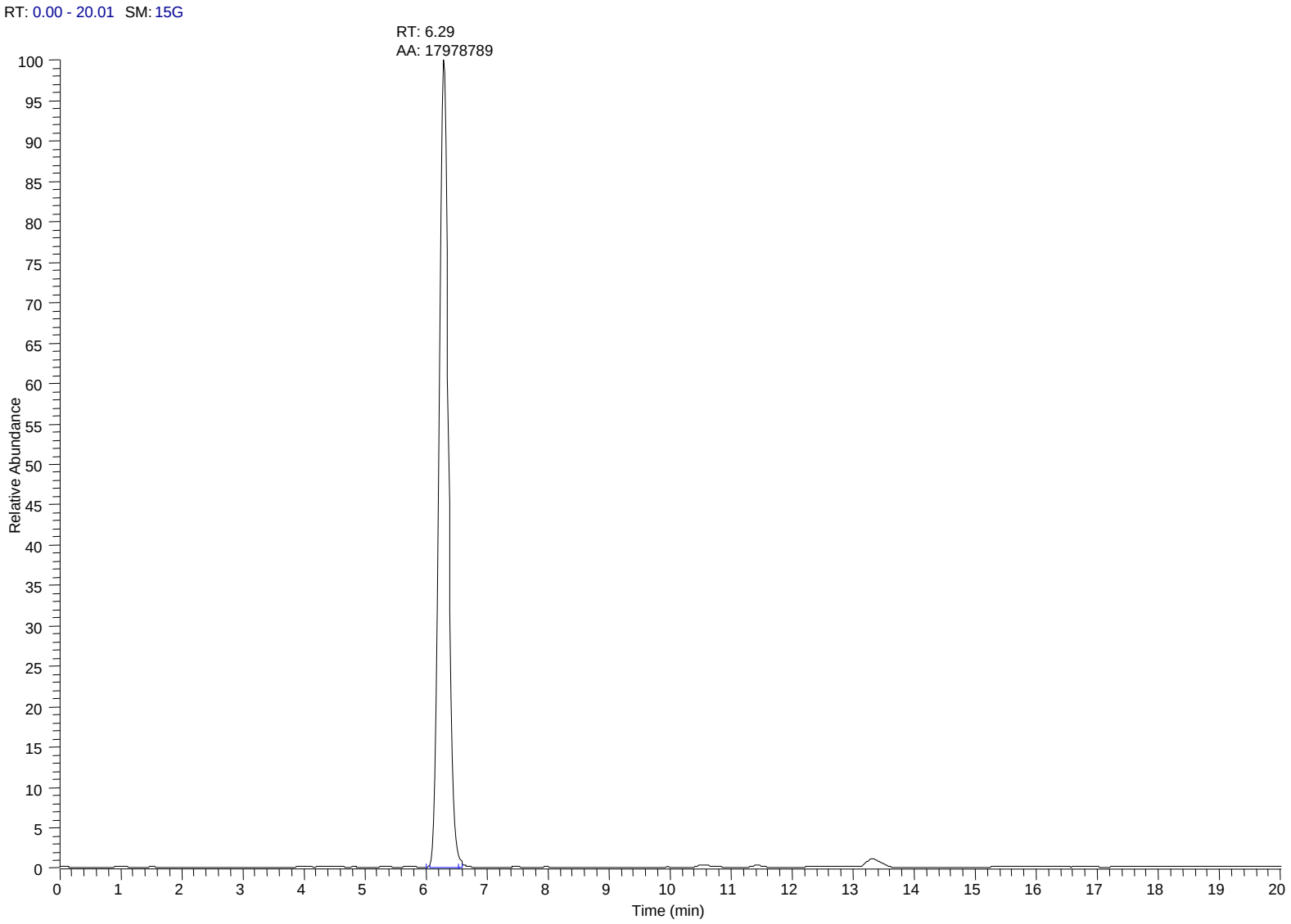
Supplementary Fig 3:
Heat map analysis of glycation modified peptides of some of the predominant plasma proteins



Uniprot ID	Protein Name
P07724	Serum albumin
Q06890	Clusterin
P06728	Apolipoprotein A IV
P21614	Vitamin D binding protein
Q91X72	Hemopexin
Q61646	Haptoglobin
Q07456	Protein AMBP
P07759	Serine protease inhibitor A3K
P29699	Alpha 2 HS glycoprotein
P02088	Hemoglobin subunit beta 1
P22599	Alpha 1 antitrypsin 1 2
P01837	Ig kappa chain C region
P01878	Ig alpha chain C region

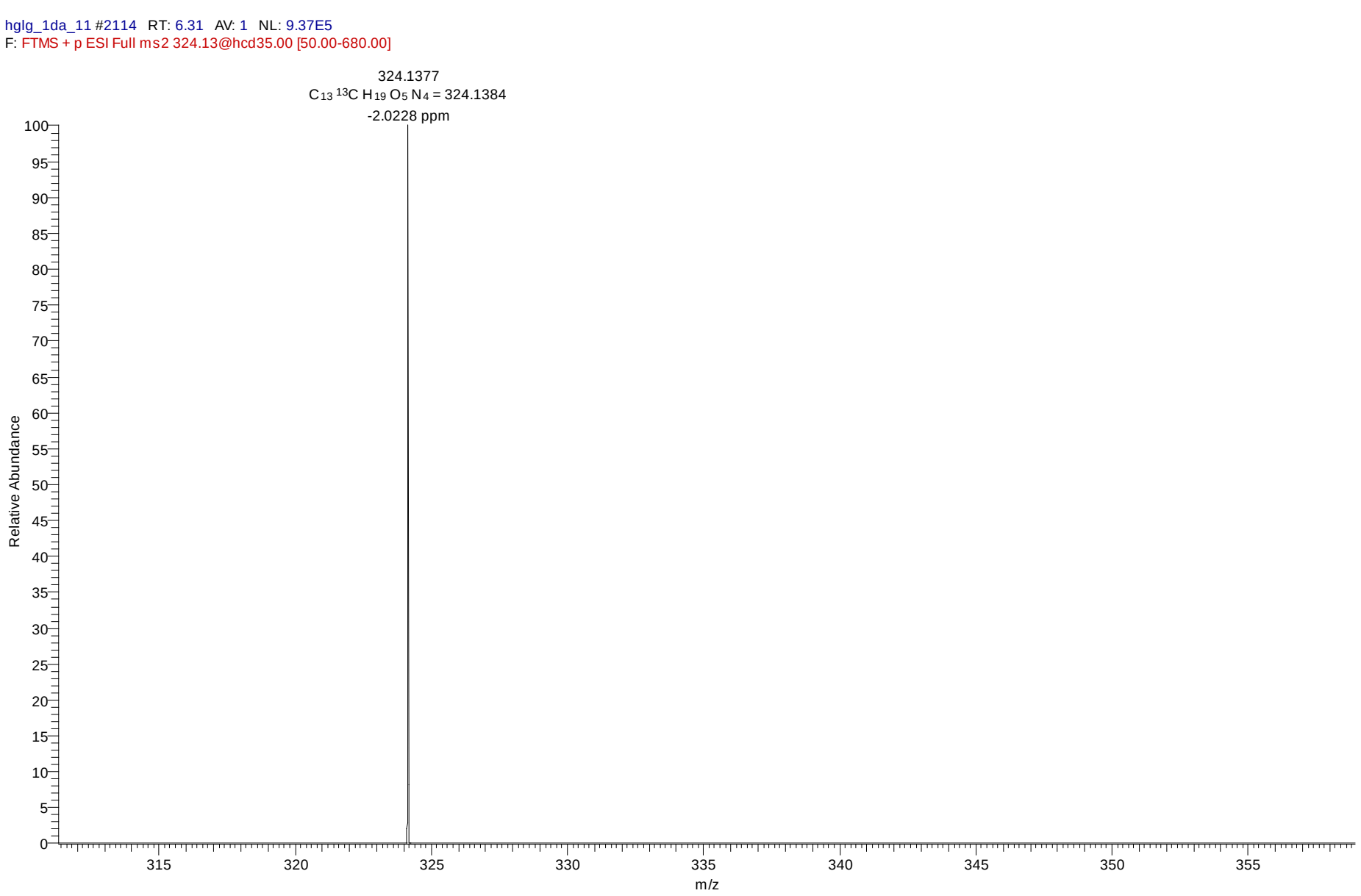
Supplementary Fig 4a:

Extracted ion chromatograms Hydralazine ^{13}C-Glucose conjugate



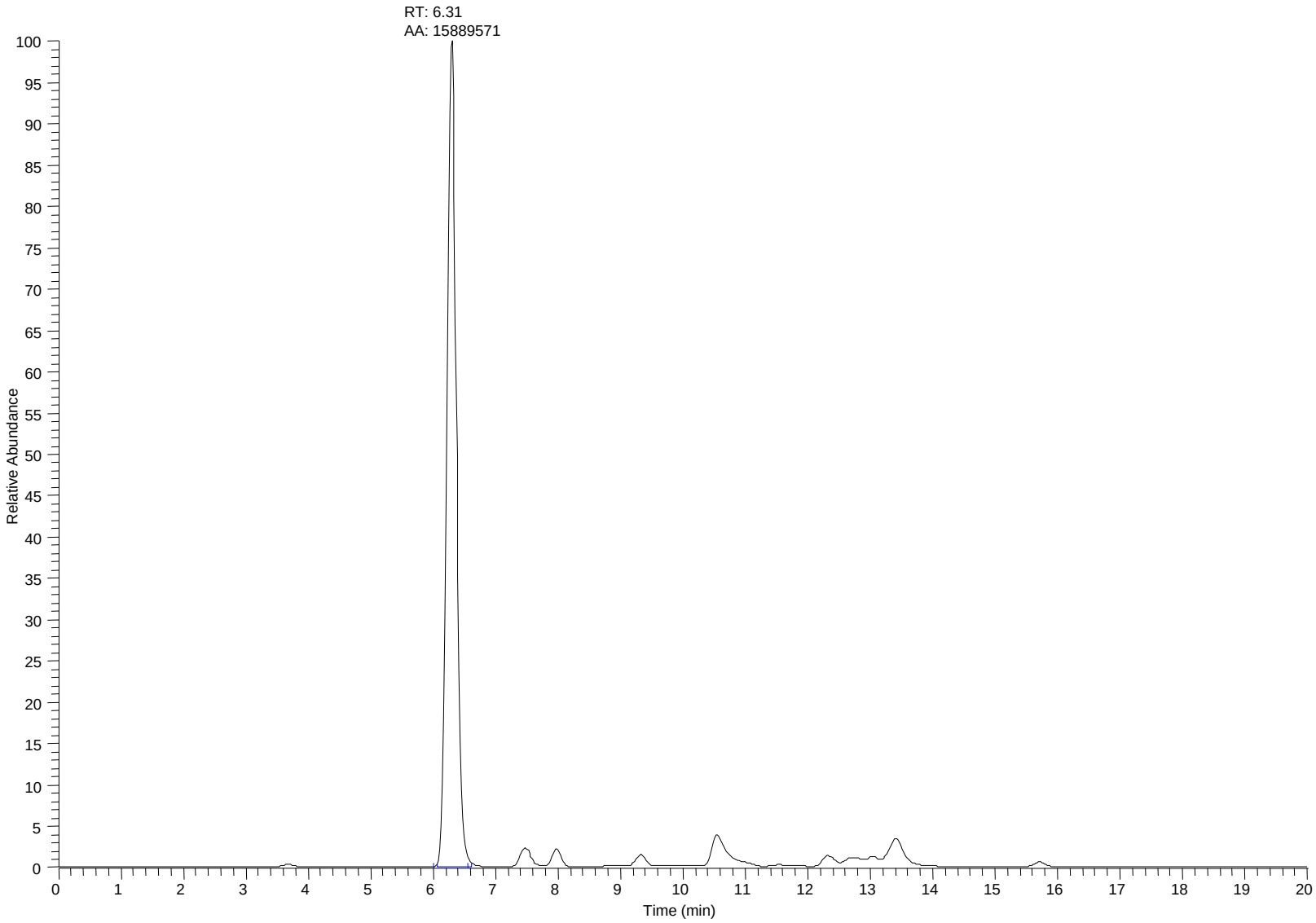
Supplementary Fig 4b:

Mass spectra of Hydralazine ^{13}C-Glucose conjugate



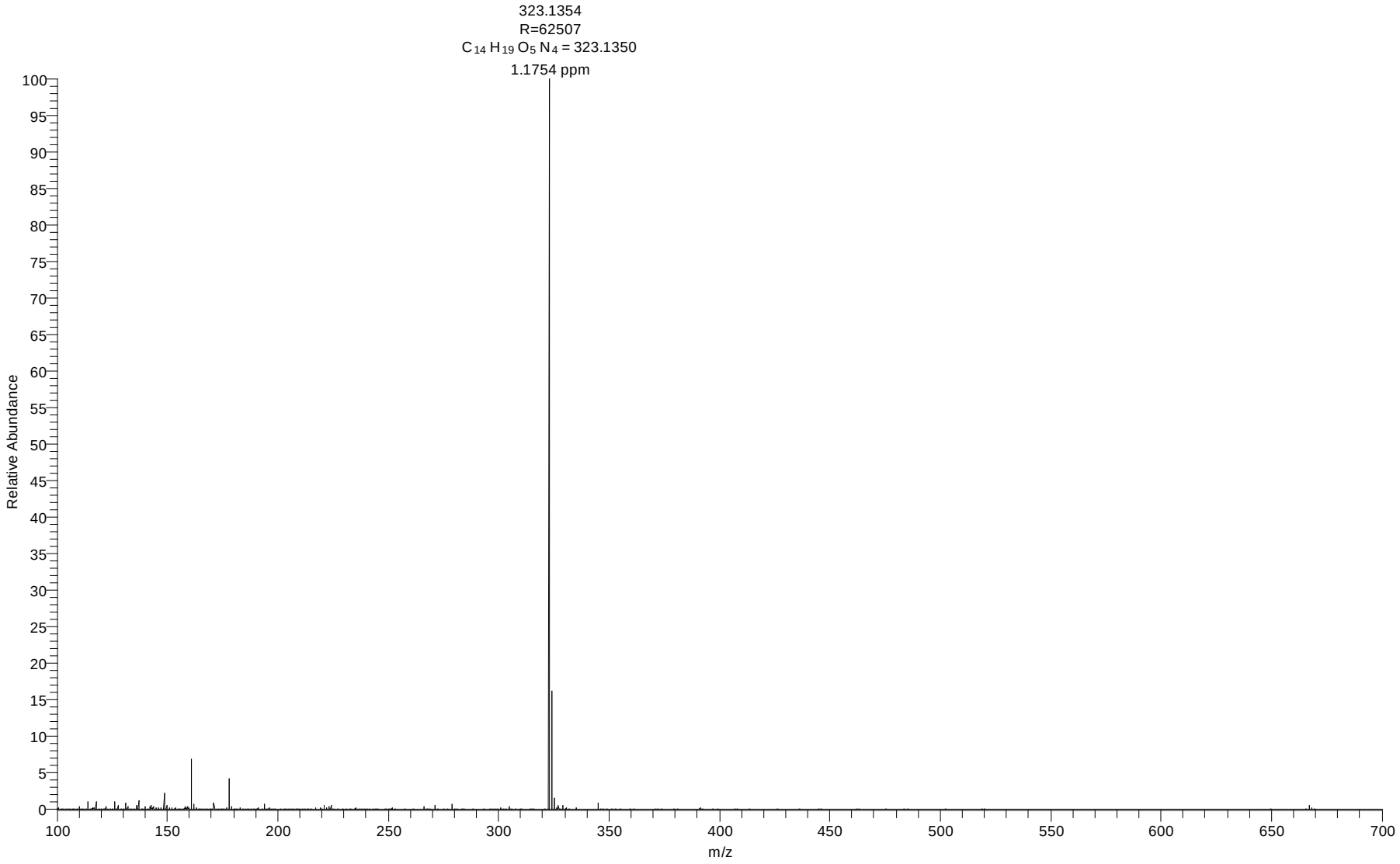
Supplementary Fig 4c:

Extracted ion chromatograms Hydralazine glucose conjugate

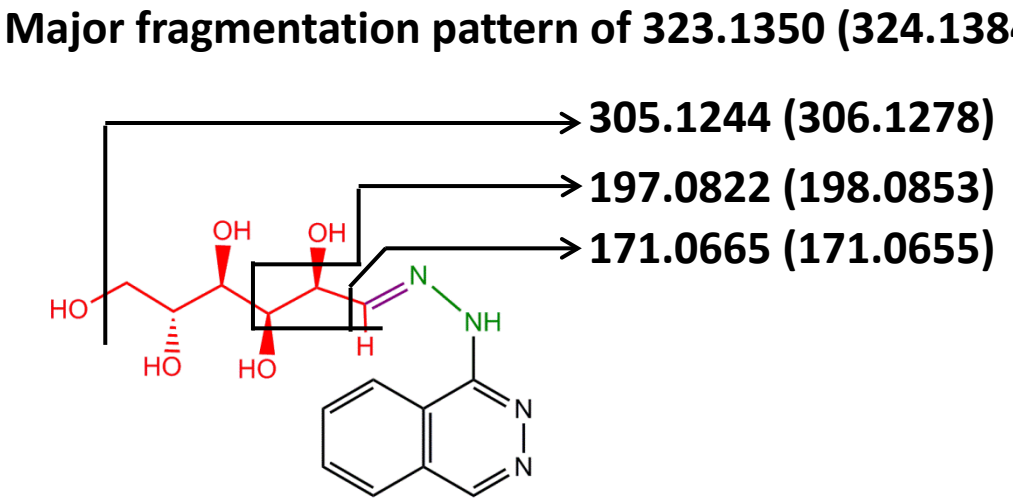


Supplementary Fig 4d:

Mass spectra of Hydralazine glucose conjugate

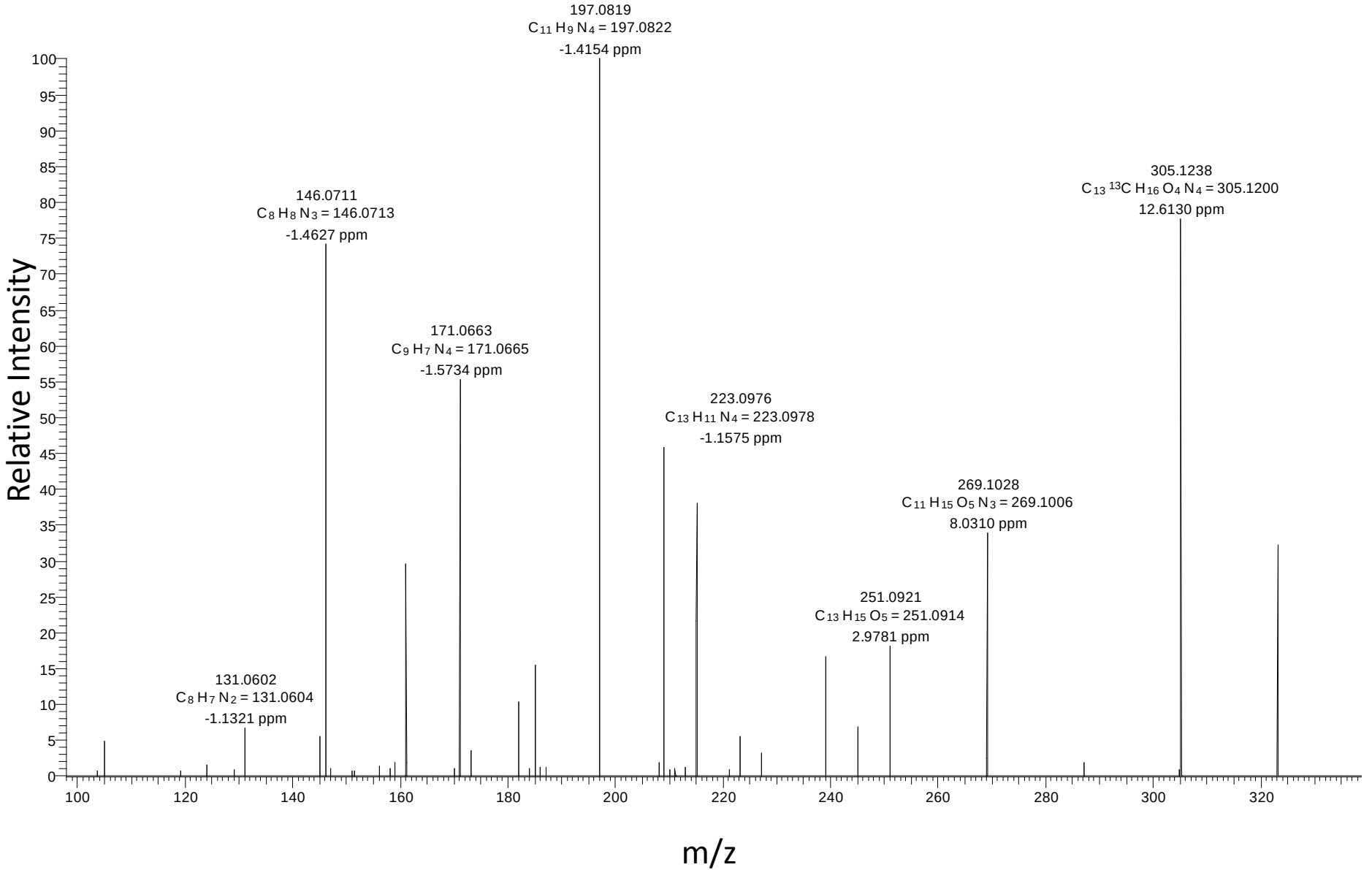


Supplementary Fig 5:
Fragmentation pattern for Hydralazine glucose conjugate (m/z 323.1350) along with Hydralazine ^{13}C glucose conjugate (m/z 324.1384)



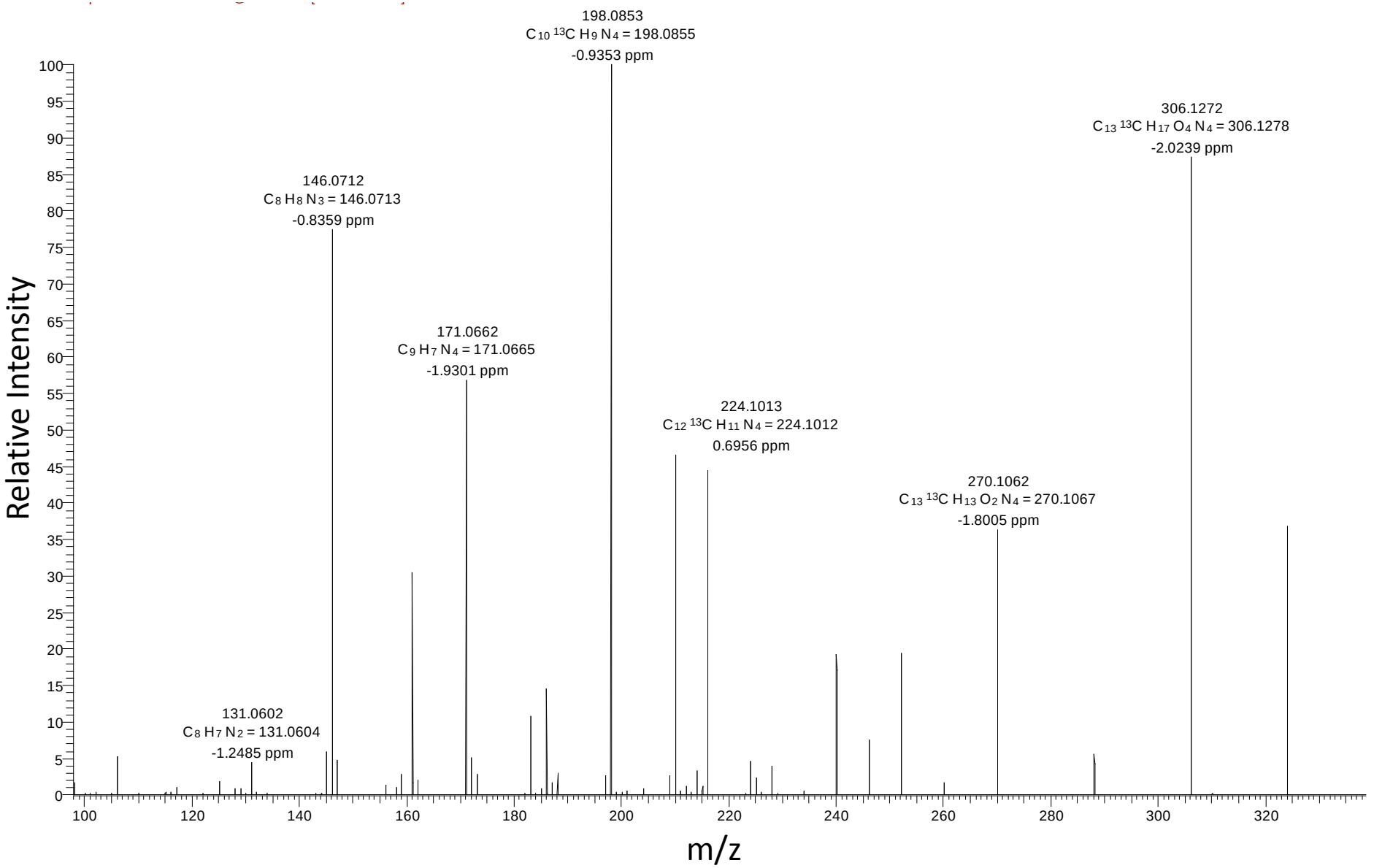
Supplementary Fig 6:

MS/MS Hydralazine glucose conjugate (m/z 323.1350)



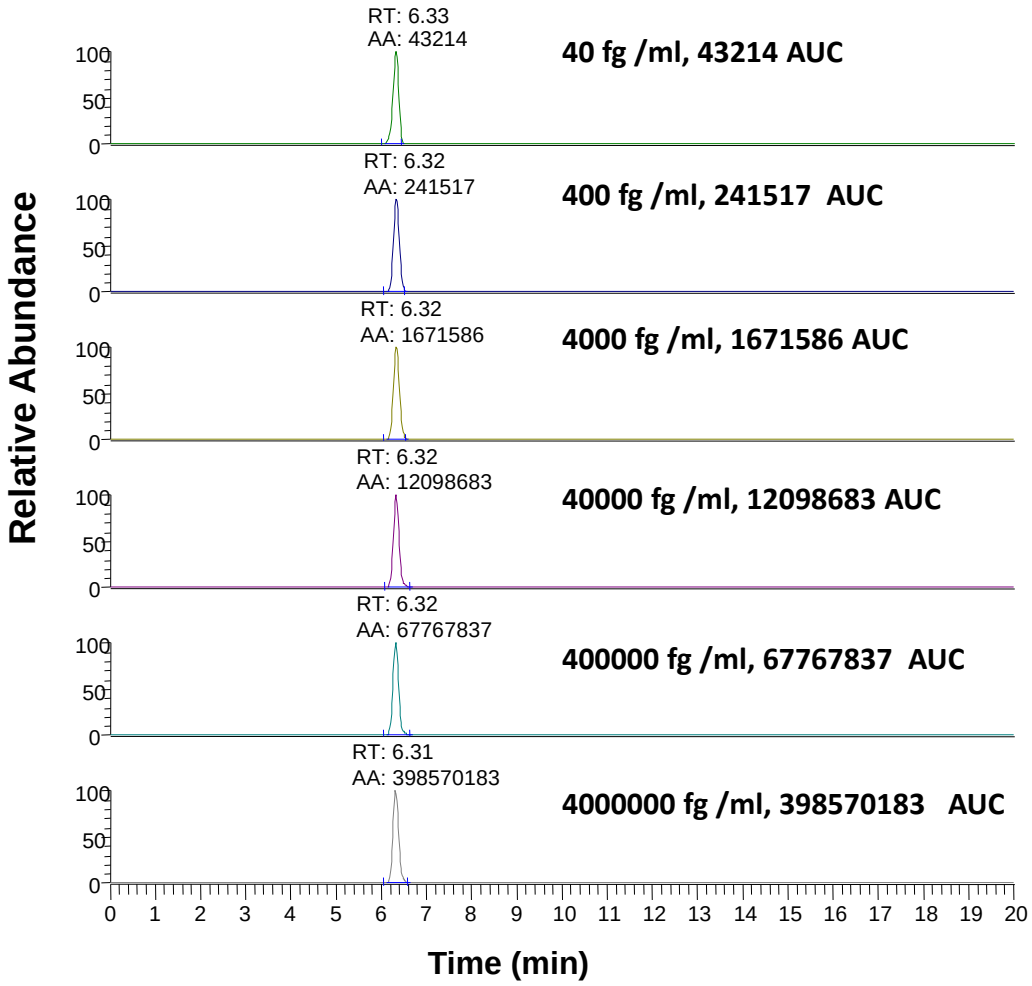
Supplementary Fig 7:

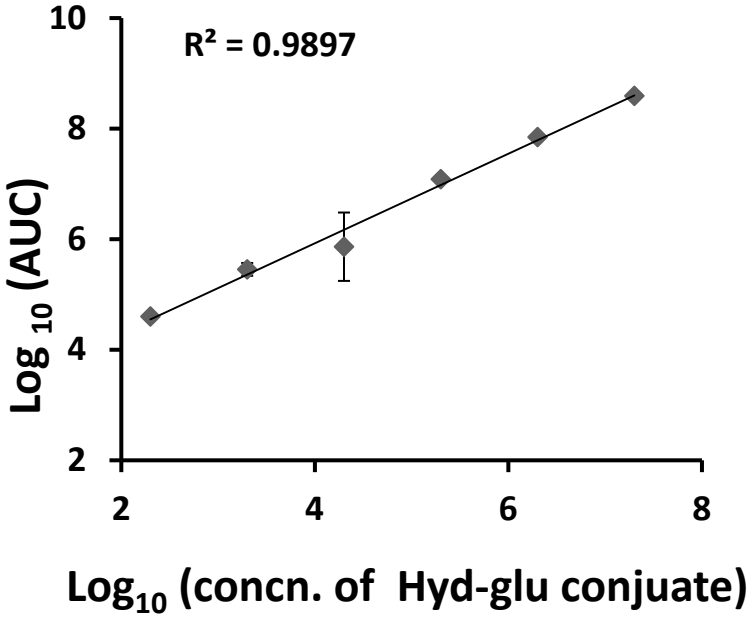
MS/MS of Hydralazine ^{13}C glucose conjugate (m/z 324.1384)



Supplementary Fig 8:

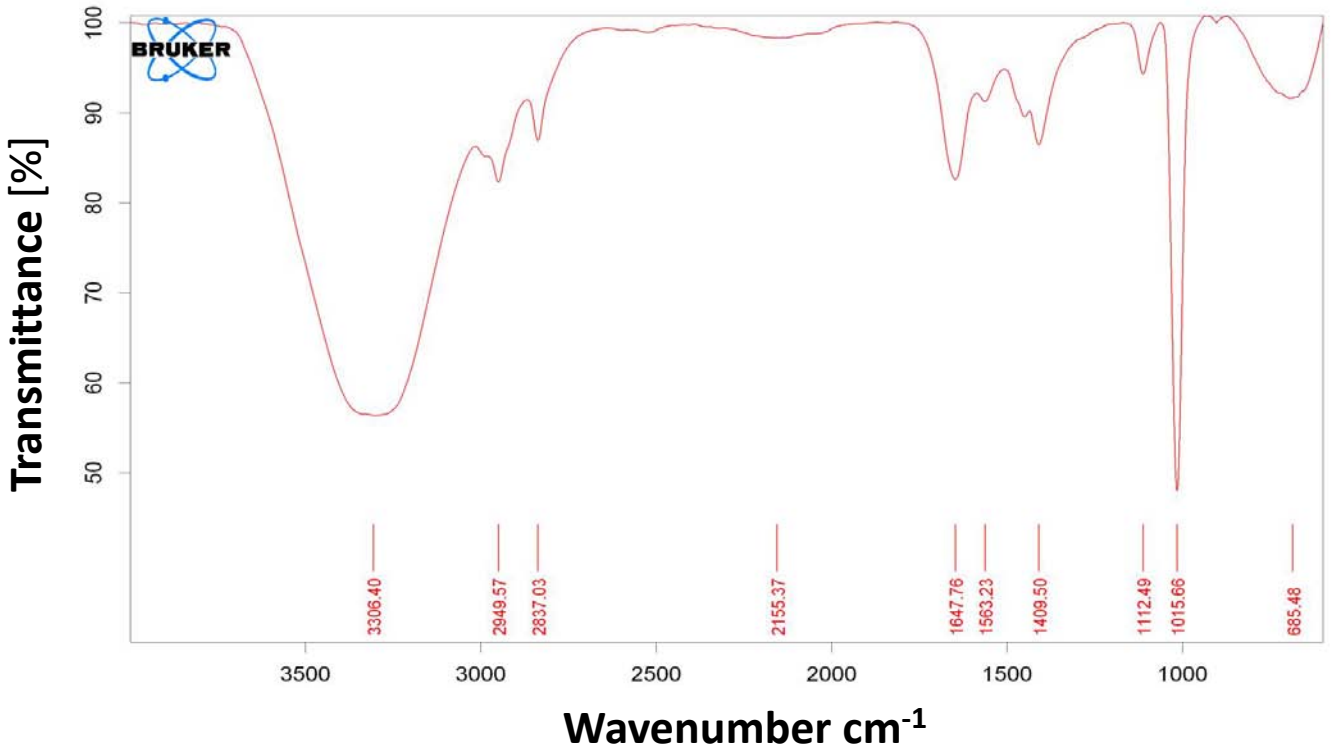
Standard curve of Hydralazine glucose conjugate generated by plotting $\log_{10}$(AUC) Vs $\log_{10}$ (concentration of hydralazine conjugate)





Supplementary Fig 9:

Fourier transform infrared (FT-IR) spectrum of Hydralazine glucose conjugate, on Bruker Optics ALPHA-E spectrometer with a universal Zn-Se ATR (attenuated total reflection) accessory in the 600-4000 cm^{-1} region. *IR* ν_{max} 3306 (broad, NH and OH) 1647 (C=N) and 1563 cm^{-1}(Ph).



Supplementary Information

Table 1a: Glucose sensitive amino acid residues (GSARs) in human serum albumin and their homologs in mouse serum albumin according to Reference No. 20.(Zhang et al.,. *Diabetes* **E-pub**(2013). doi: 10.2337/db13-0347

Sl.No.	Sequence	Amino acid location in Human Serum Albumin	Amino acid location in Mouse Serum Albumin
1	HFK	K44	K44
2	VAR	R168	R168
3	VKE	K210	K210
4	LTK	K264	K264
5	KAP	K438	K438
6	AAR	R452	R452

Table 1b: Extent of AGE modification of GSAR containing peptides. The values in the table represent the average cumulative intensity ratio (CIR) of AGE modified peptides containing Glucose Sensitive Amino acid Residues (GSARs) to their unmodified form (n=2)

Sample	K44	R168	K210	K264	K438	R452
HSA	0 ± 0	0± 0	0± 0	0± 0	0± 0	0± 0
GLY HSA	8.22± 1.42	8.13± 0.85	10.62± 0.93	136.45± 1.94	270.99± 3.49	31.44± 0.8
GLY HSA HYD	1.53± 0.23	3.08± 0.62	0.37± 0.26	22.59± 1.02	3.6± 0.17	3.08± 0.39
GLY HSA AMG	9.55± 0.55	4.44± 0.14	2.04± 0.13	63.71± 4.63	55.1± 1.89	77.14± 2.38

Table 1c: Extent of AGE modification of GSAR containing peptides in mouse The values in the table represent the average cumulative intensity ratio (CIR) of AGE modified peptides containing Glucose Sensitive Amino acid Residues (GSARs) to their unmodified form (n=2)

Sample	K44	R168	K210	K264	K438	R452
CONTROL	0 ± 0	2.63 ±0.33	0 ± 0	0.18 ±0.01	0 ± .0	0.44 ±.001
DIABETIC	9.33 ± 61	5.05 ±0.81	62.34 ±1.39	2.74 ±0.15	0 ±0.0	15.57 ±0.73
DIAB HYD	0 ± 0.0	6.43±.0.37	0 ± 0.0	5.96 ±0.47	0 ±0.0	0 ±0.0
DIAB AMG	1.55 ± 0.34	6.97 ±0.53	0 ± 0.0	0 ± 0.0	2.35 ±0.59	0.22 ±0.02

Supporting information for Table 1C: Sequence alignment of Mouse and Human serum albumin to identify glucose sensitive amino acid residues according to Zhang et al., (Ref. No. 20)

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ALBU_MOUSE   MKWVTFLLLLFVSGSAFSRGVFRREAHKSEIAHRYNDLGEQHFKGLVLIAFSQYLQKCSYDEHAKLVQEV 70
ALBU_HUMAN   MKWVTFISLLFLFSSAYSRGVFRRDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEV 70

ALBU_MOUSE   TDFAKTCVADESAANCDKSLHTLFGDKLCAIPNLRENYGELADCCTKQEPERNECFLQHKDDNPSLPPFE 140
ALBU_HUMAN   TEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLV 140

ALBU_MOUSE   RPEAEAMCTSFKENPTTFMGHYLHEVARRHPYFYAPELLY YAEQYNEILTQCCAEADKESCLTPKLDGVK 210
ALBU_HUMAN   RPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR 210

ALBU_MOUSE   EKALVSSVRQRMKCSSMQKFGERAFKAWAVARLSQTFPNADFAEITKLATDLTKVNKECCHGDLLECADD 280
ALBU_HUMAN   D EGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADD 280

ALBU_MOUSE   RAELAKYMCENQATISSKLQ TCCDKPLLKKAHCLSEVEHDTMPADLPAIAADFVEDQEVCKNYAEAKDVF 350
ALBU_HUMAN   RADLAKYICENQDSISSKLKCCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVF 350

ALBU_MOUSE   LGTFLYEYSR RHPDYSVSLLLRLAKKYEATLEKCCAEANPPACYGTVLAEFQPLVEEPKNLVKTNCDLYE 420
ALBU_HUMAN   LGMFLYEYAR RHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFE 420

ALBU_MOUSE   KLGEYGFQNAILVRYTQKAPQVSTPTLVEAARNLGRVGTKCCTLPEDQRLPCVEDYLSAILNRVCLLHEK 490
ALBU_HUMAN   QLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVV LNQLCVLHEK 490

ALBU_MOUSE   TPVSEHVTKCCSGSLVERRPCFSALTVDETYVPKEFKAETFTFHSDICTLPEKEKQIKKQTALAELVKHKPKATAEQLKT 570
ALBU_HUMAN   TPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKA 570

ALBU_MOUSE   VMDDFAQFLDTCCKAADKDTCFSTEGPNLVTRCKDALA- 608
ALBU_HUMAN   VMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 609
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Uniprot ID P07724-MOUSE SERUM ALBUMIN
Uniprot ID P02768-HUMAN SERUM ALBUMIN

Table 2: AGE modifications and their corresponding ΔM listed as below

Sl.no.	Modification name	Amino acid modification position	ΔM in Dalton(Da)
1	Amadori (Schiff base)	K or R	162.0211
2	Carboxy methyl lysine (CML)	K	58.0055
3	Carboxy ethyl lysine (CEL)	K	72.0211
4	Pyraline (PYR)	K	108.0211
5	1-alkyl-2-formyl-3,4-glycosyl-pyrrole (AFGP)	K or R	270.074
6	Imidazolone-B	R	142.02
7	Methyl glyoxal lysine dimer (MOLD)	K or R	49.0078
8	Crossline	K or R	252.11
9	Fructoselysine (FL-1H_2O)	K	144.04
10	Fructoselysine (FL-2H_2O)	K	126.03
11	Methylglyoxal derived imidazolium Crosslink (MODIC)	K or R	36.02
12	Glyoxalderived hydroimidazolone (GH1)	R	39.99
13	Carbamidomethyl C	C	57.0214
14	Oxidation M	M	15.9949

Table 3: List of AGE modified peptides for *in vitro* modified Human Serum Albumin.

LC-MS^{E} analysis depicting the number of AGE modified peptides in HSA, glycated HSA, glycated HSA in presence of hydralazine (50mM) and aminoguanidine (50mM). The values in the table represent the number of AGE modified peptides in at least two replications. Glycated HSA had more number of AGE modified peptides than unglycated HSA. In presence of Hydralazine and aminoguanidine the number of AGE modified peptides were decreased

Sample	No. of Modified Peptides
HSA	8
GLY HSA	31
GLYHSA HYD	14
GLYHSA AMG	24

(The details of the modified peptides is continued on the next page)

CONtrol								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
1938.945	2.55	7.6521	7.0157	566	581	(K)EQLKAVMDDFAAFVEK(C)	MOLD (4), MOLD (16)	b1°b2°b3b4*b5*b8*b10b10*b11b11°b12*b13b13°b14b14*b15*b15°y3y3°y5y9y11°y12y12°y16
4209.944	4.9	0.5513	7.3105	509	543	(R)RPCFSALEVDETYVPKEFNAETFTFHADICTLSEK(E)	Carbamidomethyl C (3), Carbamidomethyl C (30), CML (35)	b1b5°b8°b12b14b15y1y2y6y7y11y11°y19y23°y24°y31*y35
2086.138	3	0.9107	6.6488	439	456	(K)VPQVSTPTLVEVSRNLGK(V)	MODIC (14), FL-2H2O (18)	b3b3*b4*b9°b11°b13b18y2y4y5*y6°y7°y10°y18
3031.405	3.38	-6.4221		414	434	(K)QNCELFEQLGEYKFQNALLVR(Y)	Carbamidomethyl C (3), AFGP (13), AMADORI (21)	b4°b6°b10b20°y19°y21
4223.988	4.86	2.3411		397	426	(K)VFDEFKPLVEEPQNLIKQNCELFEQLGEYK(F)	AFGP (6), PYRALINE (17), Carbamidomethyl C (20), AMADORI (30)	b3°b4°b7b9b13°b24*b25b29*y3°y4y4°y8°y9y23°y28°y29
1778.915	3	1.5216	6.4525	170	183	(R)HPYFYAPELLFFAK(R)	MODIC (14)	b1b2b4b7b10°b12°y14
2908.37	4	-5.4955	6.4679	139	161	(R)LVRPEVDVMCTAFHDNEETFLKK(Y)	Carbamidomethyl C (10), CEL (22), CML (23)	b2b6b7b14°b17*b23*y8°y9y11*y11°y12°y15y15*y19°y23*
1812.814	3	0.8754	6.634	118	130	(K)QEPERNECFLQHK(D)	MOLD (5), Carbamidomethyl C (8), MOLD (13)	b1b1*b2b2°b3*b4*b6*b8b10b10*y1y5*y7y7°y8*y9*y11

GLY								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
1328.5718	2	3.2365	7.0894	589	598	(K)ETCFAEEGKK(L)	Carbamidomethyl C (3), CEL (9), CML (10)	b1°b3b4b5b9°y3y6y7°
2114.8926	2.71	-1.89	6.7653	570	584	(K)AVMDDFAAFVEKCCK(A)	AMADORI (12), Carbamidomethyl C (13), Carbamidomethyl C (14), AMADORI (15)	b11°b14b15y7°y8°y9°y13y13°
1186.6981	1.98	-5.1278	7.7327	549	558	(K)KQTALVELVK(H)	CML (1)	b3°b4b4°b6*y3y4y5y6y7y8y9y9*y9°y10
2617.2063	4	7.2165	6.3873	525	545	(K)EFNAETFTFHADICTLSEKER(Q)	Carbamidomethyl C (14), CEL (19)	b5°b6°b17b21y2°y3y4y20*
4535.0806	4.75	-3.3259	6.2918	509	545	(R)RPCFSALEVDETYVPKEFNAETFTFHADICTLSEKER(Q)	Carbamidomethyl C (3), Carbamidomethyl C (30), MOLD (35), MOLD (37)	b11°b15°b16b25y3°y11°y24*y25°
3102.4421	3	2.9673	6.7722	500	524	(K)CCTESLVNRRPCFSALEVDETYVPK(E)	Carbamidomethyl C (1), Carbamidomethyl C (2), Carbamidomethyl C (12), CEL (25)	b2b11b13b13*b16b16°b18*b23y15y16y24°
1982.958	3	-4.7964	6.6194	509	524	(R)RPCFSALEVDETYVPK(E)	MODIC (1), Carbamidomethyl C (3), MODIC (16)	b3b10b14b14°b15b15°y11y15
1524.7242	2.47	6.3755	7.8885	497	508	(R)VTKCCTESLVNR(R)	CML (3), Carbamidomethyl C (4), Carbamidomethyl C (5)	b2b2°b4b8b9y2*y3y4y5y5*y6y7y8y9y9*y10y10°y11y12
3492.6143	3.54	-2.97	7.1034	470	496	(R)MPCAEDYLSVVLNQLCVLHEKTPVSDR(V)	Carbamidomethyl C (3), Carbamidomethyl C (16), AFGP (21), MOLD (27)	b16b16*b17°b22b23b27°y3y3°y5°y8y14y14*y17y19y19*y20*y27
2576.1929	3.61	-10.3	6.1926	470	490	(R)MPCAEDYLSVVLNQLCVLHEK(T)	Carbamidomethyl C (3), Carbamidomethyl C (16), CML (21)	b9°b11b12b14*b17°b21*y9*y9°y14y16*
2836.4004	3.61	11.5126	6.3931	469	490	(K)RMPCAEDYLSVVLNQLCVLHEK(T)	AMADORI (1), Carbamidomethyl C (4), Carbamidomethyl C (17)	b10b11b11°b14°b16*b21*y2°y3y15y16
1697.9583	2.23	8.8665	7.2515	438	452	(K)KVPQVSTPTLVEVSR(N)	CML (1)	b5b7b7°b10°y6y7y9y13y15

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
4007.9998	3.62	5.9354	6.7278	397	426	(K)VFDEFKPLVEEPQNLIKQNCELFEQLGEYK(F)	CROSSLINE (6), MODIC (17), Carbamidomethyl C (20), MODIC (30)	b9b11b12b13b16*b23*y4y4°y9°y12*y13°y15y23°y30
2103.1145	2.64	6.4338	7.683	397	413	(K)VFDEFKPLVEEPQNLIK(Q)	CML (6)	b2b3b4b5b6b12y4y6y8y9y9°y10*y11y11°y15y16y17
2680.1497	3.44	10.5857	7.7348	376	396	(K)TYETTLEKCCAAADPHECYAK(V)	AMADORI (8), Carbamidomethyl C (9), Carbamidomethyl C (10), Carbamidomethyl C (18)	b1°b2°b3b3°b4°b6b8°b14b14°b17b21y3y4y5y5°y6y7y8y10y11°y12y13°y14y16°y17°y19y21
1404.7281	3	1.8095	7.1501	373	383	(R)LAKTYETTLEK(C)	PYRALINE (3)	b3b6b6°b7°b8b8°b10b10°b11y2y2°y7°y9
3620.6116	5	1.0166	6.5725	311	341	(K)SHCIAEVENDEMPADLPSLAADFVESKDVCK(N)	Carbamidomethyl C (3), FL-1H20 (27), Carbamidomethyl C (30)	b2b10b11*b14*b15*b18*b20°y2y9°y10°y13y13°y17°y18y26y28
1708.8525	4	1.6776	6.9291	299	310	(K)LKECCEKPLLEK(S)	AMADORI (2), Carbamidomethyl C (4), Carbamidomethyl C (5)	b7b8°b10°b11y4y6y9y12
2035.9572	2.87	5.6155	6.2978	282	298	(R)ADLAKYICENQDSISSK(L)	MODIC (5), Carbamidomethyl C (8), CML (17)	b6°b10b11°b12*b13*b14°b15*b16b16*y5°y11°y12*y12°y15y16°
1812.9558	2.58	4.4799	7.9739	250	264	(K)AEFAEVSKLVTDLTK(V)	AMADORI (8)	b3b5b6b9b12b15y3y3°y4y4°y5y5°y6y6°y7y12y13y13°y15
1005.539	1.98	-0.7938	7.6089	222	229	(R)LKCASLQK(F)	CML (2), Carbamidomethyl C (3)	b4y1y2y2*y3y4y5y6y6*y8
1128.557	2.04	3.3856	7.2926	206	214	(K)LDELRDEGK(A)	MGH1 (5)	b1b2b6b8°y2y3°y5y5°y6°y8y9
2058.869	3.56	-4.0921	6.5787	185	198	(R)YKAAFTECCQAADK(A)	FL-1H20 (2), Carbamidomethyl C (8), Carbamidomethyl C (9), CROSSLINE (14)	b5b6°b8b8°b11y2°y8y8*y8°y9y10y10°y11*y12°y13*y14
1217.6459	2.03	3.8532	7.9496	161	168	(K)KYLYEIAR(R)	AMADORI (1)	b3b8y1y3y4y4°y5y6y7y8
2926.3909	3.53	5.4049	6.6068	139	161	(R)LVRPEVDVMCTAFHDNEETFLKK(Y)	GH1 (3), Carbamidomethyl C (10), PYRALINE (23)	b10b12°b14°b16b20*y2y3y8°y9*y11°y14y14*y15
1876.8546	3	2.7636	6.2211	118	130	(K)QEPERNECFLQHK(D)	Carbamidomethyl C (8), AMADORI (13)	b3°b6b11*b11°y9y11*y12y12°
2708.1746	3.66	6.2592	6.4248	76	97	(K)TCVADESAENCDKSLHTLFGDK(L)	Carbamidomethyl C (2), Carbamidomethyl C (11), MOLD (13), AMADORI (22)	b2b9°b10°b14°b15b16*y11y12°y13

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
3516.703	4.34	-8.3814	6.6108	37	65	(K)DLGEENFKALVLIAFAQYLQQCPFEDHVK(L)	MODIC (8), Carbamidomethyl C (22), CML (29)	b13°b23°b25b26°b27b27°b29*y5y13y15*y21°y24y29*
1284.6173	2.06	5.154	7.9313	35	44	(R)FKDLGEENFK(A)	CML (2)	b3y2y3y3*y5y6y7y8y10
1720.745	2.38	8.0633	7.719	185	198	(R)YKAAFTECCQAADK(A)	CML (2), Carbamidomethyl C (8), Carbamidomethyl C (9)	b3b4b9°b10b12b13y1y2y3y4y5°y7y8y9y10y12y12*y14
2511.161	3.59	-1.9191	6.8772	342	360	(K)NYAEAKDVFLGMFLYEYAR(R)	MOLD (6), AMADORI (19)	b2b2*b3*b4b5b11b14*b15°b16b16°b19y7y8y13°

GLY HYD

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1290.756	2.05	3.7303	7.9389	549	558	(K)KQTALVELVK(H)	AMADORI (1)	b5°b7°y3y4y4°y5y5°y6y7y8y8°9y10
1812.96	2.56	6.7966	7.7066	250	264	(K)AEFAEVSKLVTDLTK(V)	AMADORI (8)	b3b5b6°b8b15y1y2y2°y3y4y5y6y6°y7y13y13°y15
1802.008	2.39	9.7419	6.8221	438	452	(K)KVPQVSTPTLVEVSR(N)	AMADORI (1)	b1b4b6b6*b6°b15y3°y7°y8y9°y12°y13*y13°y14y15
2008.942	2.82	-2.4446	6.7999	509	524	(R)RPCFSALEVDETYVPK(E)	MOLD (1), Carbamidomethyl C (3), MOLD (16)	b2b3b11b12°y1y6°y8y9y10y10°y11°y12y16
1284.614	2.09	2.8186	7.9139	35	44	(R)FKDLGEENFK(A)	CML (2)	b3b5°b6°y2y3y4y4°y5y6y6°y7y8y10
1217.645	2.05	3.4426	7.6848	161	168	(K)KYLYEIAR(R)	AMADORI (1)	b8°y3y4y4°y5y6y7y8
2707.315	3.95	-1.3918	7.0826	414	434	(K)QNCELFEQLGEYKFQNALLVR(Y)	Carbamidomethyl C (3), PYRALINE (13)	b2*b5b9b9*y6y7y7*y8y10*y11°y19y21
1303.751	1.92	3.4246	7.2522	598	609	(K)KLVAASQAALGL(-)	AMADORI (1)	b1b4b9b10b11°b12*y2y3y8y9°y10*y12
1672.831	3.22	1.5942	6.9659	299	310	(K)LKECCEKPLLEK(S)	Carbamidomethyl C (4), Carbamidomethyl C (5), FL-2H2O (12)	b2b3b8b9b12y2y3y9
2659.165	3.62	5.7728	6.8846	76	97	(K)TCVADESAENCDKSLHTLFGDK(L)	Carbamidomethyl C (2), Carbamidomethyl C (11), AMADORI (13)	b2b12b22y3y4y6y7y7°y22
1354.713	2.21	2.3192	7.4443	373	383	(R)LAKTYETTLEK(C)	CML (3)	b5b6b8b10b10°y4y5y7y8y9y11
2690.27	4	3.9698	6.9863	139	160	(R)LVRPEVDVMCTAFHDNEETFLK(K)	GH1 (3), Carbamidomethyl C (10)	b3b11b13°b20°b22*y1y2y3y4y5y5°y10*y11y11*y13°y14y14*y14°y15°y16
1323.583	2	-4.1442	6.6434	338	347	(K)DVCKNYAEAK(D)	Carbamidomethyl C (3), FL-2H2O (10)	b2°b4b5b7b8b8*y7y10
2086.134	3	-1.0067	6.6544	439	456	(K)VPQVSTPTLVEVSRNLGK(V)	MODIC (14), FL-2H2O (18)	b3*b4b6*b8b8*b9*b11°b12*b16°y5*y6y6*y8y13*y15

GLY AMG								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
1802.0076	2.14	9.4644	7.1586	438	452	(K)KVPQVSTPTLVEVSR(N)	AMADORI (1)	b2b4b5b6b6°b8*b9°b10b11*b12°b14b15y2°y7°y8y8°y13y13°y14°
3656.9028	5.1	0.7689	6.363	45	75	(K)ALVLIAFAQYLQQCPFEDHVKLVNEVTEFAK(T)	Carbamidomethyl C (14), MODIC (31)	b16b17°b19°b31y4y6°y7y14*y21*y26*
3561.616	4.62	6.9297	6.5086	311	341	(K)SHCIAEVENDEMPADLPSLAADFVESKDVCK(N)	Carbamidomethyl C (3), MODIC (27), Carbamidomethyl C (30), MOLD (31)	b1°b3b11*b17b17*b18°y8°y17y22y26y27y29y29°y30*
1952.8549	2.68	5.5831	6.6262	570	584	(K)AVMDDFAAFVEKCCK(A)	AMADORI (12), Carbamidomethyl C (13), Carbamidomethyl C (14)	b4b10°b15b15°y3y7°y8y13y14°
1588.9276	3	4.2015	6.9423	550	562	(K)QTALVELVKHKPK(A)	MOLD (11), MOLD (13)	b1b3°b4°b7b8b9b13y3y5y13
1284.6147	1.94	3.13	7.6734	35	44	(R)FKDLGEENFK(A)	CML (2)	b3b7°y3y4y5°y6y7y8y10
1654.8131	4	-2.9207	6.7051	299	310	(K)LKECCEKPLLEK(S)	PYRALINE (2), Carbamidomethyl C (4), Carbamidomethyl C (5)	b4°b5b6b6°b7b9°b11°y1y12
1404.7207	3	-3.5296	6.6921	373	383	(R)LAKTYETTLEK(C)	PYRALINE (3)	b3b5°b6b7°b8°b9°b10b11y8°y9
1628.7646	2.4	1.7319	7.3438	497	508	(R)VTKCCTESLVNR(R)	AMADORI (3), Carbamidomethyl C (4), Carbamidomethyl C (5)	b1b2°b3°b4b8°b9°b11y2y2*y3y4y5y5°y6y7y8y12
2690.2556	4.54	-1.197	6.3179	139	160	(R)LVRPEVDVMCTAFHDNEETFLK(K)	GH1 (3), Carbamidomethyl C (10)	b6°b13b13°b17y2y10y12°y13°y14*y14°y15°
1776.936	3	5.3023	6.3805	250	264	(K)AEFAEVSKLVTDLTK(V)	FL-2H2O (15)	b11b12°y1y4°y9°y10y10°y11y11°
2176.1968	3.63	0.2297	6.6006	439	456	(K)VPQVSTPTLVEVSRNLGK(V)	CROSSLINE (18)	b2b3b5°b9b10*b12*b18y3y4y18

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1326.6494	2.36	-2.3964	7.0123	206	214	(K)LDELRDEGK(A)	CROSSLINE (5)	b2b3b7°b8b9b9°y1y2y3°y4y4°y9
3049.3882	3.65	0.5532	6.9852	525	545	(K)EFNAETFTFHADICTLSEKER(Q)	Carbamidomethyl C (14), CROSSLINE (19), CROSSLINE (21)	b4*b5b5°b8*b9*b13b14*y6y16
2110.9573	3	3.973	6.5508	118	130	(K)QEPERNECFLQHK(D)	CROSSLINE (5), Carbamidomethyl C (8), FL-1H20 (13)	b3°b4b4*b5*b6b7*b7°b12°y3*y6*y10*y11
1479.6534	2	-4.4396	6.9516	287	298	(K)YICENQDSISSK(L)	Carbamidomethyl C (3), MODIC (12)	b1b3b4°b5°b6b9y3y5°y9y9*
2662.2708	5	5.4333	6.6607	470	490	(R)MPCAEDYLSVVLNQLCVLHEK(T)	Carbamidomethyl C (3), Carbamidomethyl C (16), FL-1H20 (21)	b7°b9b10b12°b15b16°y7y7°y11*y20°
2833.3818	5	3.7171	6.2066	414	434	(K)QNCELFEQLGEYKFQNALLVR(Y)	Carbamidomethyl C (3), CEL (13), AMADORI (21)	b1b1*b5*b13*b15*y4y6*y9y10*y11°y12*
860.4809	2	-3.1705	7.2992	453	460	(R)NLGKVGSK(C)	CML (4)	b2*b3b5b5*b6b7b8*y2°y3y5y5°y6y7°
1720.7452	2	8.5283	6.7709	185	198	(R)YKAAFTECCQAADK(A)	CML (2), Carbamidomethyl C (8), Carbamidomethyl C (9)	b14*y3y3°y4y5°y7y10y12y14
2554.0867	3.61	0.106	7.0334	376	396	(K)TYETTLEKCCAAADPHECYAK(V)	MODIC (8), Carbamidomethyl C (9), Carbamidomethyl C (10), Carbamidomethyl C (18)	b3°b9°b13°b14°b15°y5y7°y11°y12y12°y14y14°y15y20°
2601.1987	5	-9.4645	6.6188	342	360	(K)NYAEAKDVFLGMFLYEYAR(R)	CROSSLINE (6), MOLD (19)	b3*b5b7°b12°b13b13°y4y4°y5y8y9y13°y17y19*
1815.895	4	-6.3826	6.2356	348	361	(K)DVFLGMFLYEYARR(H)	MODIC (13)	b1°b5°b12b14°y1y5y5°y6y9
3602.7493	5	-0.5482	6.2987	37	65	(K)DLGEENFKALVLIAFAQYLQQCPFEDHVK(L)	PYRALINE (8), Carbamidomethyl C (22), CEL (29)	b6*b11b11*b16°b24*y7°y12y15°

Table 4: List *of in vivo* AGE modified proteins and their corresponding modified peptides

UNIPROT ID	Protein Name	CON	DIAB	DIAB HYD	DIAB AMG
P07724	Serum albumin	14.0	28.0	17.0	**20.0**
Q06890	Clusterin	6	17	11	**11**
P06728	Apolipoprotein A IV	11.0	16.0	12.0	**13.0**
P21614	Vitamin D binding protein	7.0	15.0	13.0	**12.0**
Q91X72	Hemopexin	7.0	15.0	10.0	**11.0**
Q61646	Haptoglobin	6.0	13.0	6.0	**8.0**
Q07456	Protein AMBP	4.0	12.0	8.0	**8.0**
P07759	Serine protease inhibitor A3K	9.0	9.0	6.0	**8.0**
P29699	Alpha 2 HS glycoprotein	4.0	7.0	2.0	**4.0**
P02088	Hemoglobin subunit beta 1	5.0	5.0	4.0	**4.0**
P22599	Alpha 1 antitrypsin 1 2	6.0	5.0	4.0	**5.0**
P01837	Ig kappa chain C region	3.0	3.0	3.0	**3.0**
P01878	Ig alpha chain C region	3.0	3.0	3.0	**3.0**

P07724-Serum Albumin								
CON								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
1866.8033	2.8	-5.5142	6.2907	589	602	(K)DTCFSTEGPNLVTR(C)	Carbamidomethy C (3), AFGP (14)	b2b7*b8b23°y4y21y22°
1933.8646	2.7	-5.9354	6.6197	589	604	(K)DTCFSTEGPNLVTRCK(D)	Carbamidomethyl C(3), Carbamidomethyl C (15), MOLD (16)	b5b12°b17b17*b18y10°y13°y36
2107.9854	2.9	8.3564	6.4172	585	602	(K)AADKDTCFSTEGPNLVTR(C)	FL-2H2O (4),Carbamidomethyl C (7)	b2b3y9y11°y18°y19
2402.0195	2	-1.5576	6.6911	570	588	(K)TVMDDFAQFLDTCCKAADK(D)	Carbamidomethyl C(13), Carbamidomethyl C(14),PYRALINE (15), CML (19)	b1°b10°b14b16b18°b19y14°y19
2430.1296	3.8	-8.3642	6.7438	342	360	(K)NYAEAKDVFLGTFLYEYSR(R)	FL-1H20 (6)	b6°b7b8°b13*b14b16°b17y4y14y18
2552.2112	2	5.6837	6.4149	525	543	(K)EFKAETFTFHSDICTLPEK(E)	FL-1H20(3), Carbamidomethyl C (14), PYRALINE (19)	b3b5°b15°y10
2574.1475	3.4	-3.1544	6.6376	131	152	(K)DDNPSLPPFERPEAEAMCTSFK(E)	MODIC(11), Carbamidomethyl C (18)	b6b9*b11°b14b14°y9°y15°y17
2755.2102	4	1.0474	7.1541	66	88	(K)LVQEVTDFAKTCVADESAANCDK(S)	FL-2H2O(10), Carbamidomethyl C(12), Carbamidomethyl C (21), CML (23)	b2b3*b7b7°b8b10b11b12b14°y4y4°y5y19

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
818.4096	1	-7.8354	6.7092	563	569	(K)ATAEQLK (T)	CML (7)	b2°b7b13°y3y3°y6y9y9°y10y16°
1491.8286	2.1	1.1872	6.5491	361	372	(R)RHPDYSVSLLLR(L)	MODIC (12)	b3*b6°b8b10*y2y5y6°
1771.855	2.5	1.3049	6.5554	348	360	(K)DVFLGTFLYEYSR(R)	AMADORI (13)	b2°b3b4°b14°b15y13y16
2893.3357	2.4	-3.5905	6.6078	563	584	(K)ATAEQLKTVMDDFAQFLDTCCK(A)	CROSSLINE(7), Carbamidomethyl C(20), Carbamidomethyl C (21), MOLD (22)	b1b7*b8*b9*b9°b10b12b12°y5°y12
2950.3965	2.4	7.0709	6.6288	287	309	(K)YMCENQATISSKLQTCCDKPLLK(K)	Carbamidomethyl C (3), AMADORI (12), Carbamidomethyl C(16), Carbamidomethyl C (17)	b3b6*b15b17*b19*y19y22*
3668.5854	2.8	-6.4384	6.4546	123	152	(R)NECFLQHKDDNPSLPPFERPEAEAMCTSFK(E)	Carbamidomethyl C (3), Oxidation M (25), Carbamidomethyl C (26), CML (30)	b2b2°b3b4°b5b6

DIAB

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1096.5997	2	4.6862	7.4552	211	219	(K)EKALVSSVR(Q)	PYRALINE (2)	b2b4*b7b8b12*b15°b20*y10y12y14*

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1758.7522	2	-2.3694	6.5555	222	233	(R)MKCSSMQKFGER(A)	Carbamidomethyl C (3), AFGP (12)	b4°b5b10b10*b12*y2°y5°y6°y7y11
2146.0142	2.8	0.9611	6.257	453	469	(R)NLGRVGTKCCTLPEDQR(L)	IMIDAZOLONEB (4),Carbamidomethyl C(9), Carbamidomethyl C (10)	b1b1°b3b5b15b20b23°y6y9y14°y18°y19°y33
2186.0222	2	4.9307	6.6114	453	469	(R)NLGRVGTKCCTLPEDQR(L)	GH1(4), Carbamidomethyl C(9), Carbamidomethyl C(10), IMIDAZOLONEB (17)	b5*b18b20°b22b31y19*y26*y40
2204.9775	3.3	2.175	7.0059	220	233	(R)QRMKCSSMQKFGER(A)	AMADORI(2), Carbamidomethyl C (5), AFGP (10)	b1°y2y3y4y5y7y9
2549.1487	2.8	3.8023	7.0539	528	545	(K)AETFTFHSDICTLPEKEK(Q)	Carbamidomethyl C (11), AFGP (16), FL-2H2O (18)	b2°b3°b9b14b19°y13*y13°y17
2949.343	2.3	-9.0162	6.606	258	281	(K)LATDLTKVNKECCHGDLLECADDR(A)	CML (7),CML (10), Carbamidomethyl C(12), Carbamidomethyl C(13), Carbamidomethyl C (20)	b1b10°b13°b14*b15b16°y12°y14y15*y16y18°y23°
3664.7327	3	0.5629	7.0247	282	309	(R)AELAKYMCENQATISSKLQTCCDKPLLK(K)	Carbamidomethyl C (8), AFGP (17), Carbamidomethyl C(21), Carbamidomethyl C(22),MODIC (24), CML (28)	b1°b2°b3°y3y4y5y7y9

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
3668.587	2.8	-1.89	6.8473	58	88	(K)CSYDEHAKLVQEVTDFAKTCVADESAANCDK(S)	CarbamidomethylC (1), MOLD (8), CML(18), arbamidomethylC(20), CarbamidomethylC (29)	b1*b5b5*b7b7*b9°y4y8°y9y10
3926.693	3.4	-1.8023	6.8042	268	298	(K)ECCHGDLLECADDRAELAKYMCENQATISSK(L)	CarbamidomethylC(2), arbamidomethylC(3), arbamidomethyl C (10), CROSSLINE (14),Carbamidomethyl C (22)	b10*b11*y6°y8°y9°y11
4342.035	3	0.952	7.1198	491	524	(K)TPVSEHVTKCCSGSLVERRPCFSALTVDETYVPK(E)	FL-2H2O(9), CarbamidomethylC(10), CarbamidomethylC (11), AMADORI (18), CarbamidomethylC (21), FL-1H20 (34)	b1b18*b19°b28°y1y4y7°y9y9*y9°y17y23
4673.2266	3.6	0.31	7.0991	29	65	(K)SEIAHRYNDLGEQHFKGLVLIAFSQYLQKCSYDEHAK(L)	CML(16),CML(29), CarbamidomethylC (30), AMADORI (37)	b4b9°b13°b14°b16*b16°y9y10y12y14y14°y16
6056.5684	4	-2.3601	6.7145	106	152	(R)ENYGELADCCTKQEPERNECFLQHKDDNPSLPPFERPEAEAMCTSFK(E)	CarbamidomethylC(9), CarbamidomethylC (10), AMADORI (17), CarbamidomethylC (20), CML (25), AMADORI (36), CarbamidomethylC (43)	b6°b7b10°

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
6143.768	4.7	1.3392	6.6968	123	168	(R)NECFLQHKDDNPSLPPFERPEAEAMCTSFKENPTTFMGHYLHEVAR(R)	Carbamidomethyl C (3), CROSSLINE (8),CROSSLINE (19), Carbamidomethyl C (26), AMADORI (46)	b1°b3°b9°b22y6°y10°y12y16*y18*y19y22y24
1503.6387	2.4	-5.837	6.9805	287	298	(K)YMCENQATISSK(L)	Carbamidomethyl C (3), CEL (12)	b13b17b28°y13y16°
1584.7177	2	-3.7378	6.9824	220	229	(R)QRMKCSSMQK(F)	MOLD (2),CROSSLINE (4), Carbamidomethyl C (5)	b5°b6°b16b23°y22*
1749.862	2.4	-7.9845	7.0704	422	434	(K)LGEYGFQNAILVR(Y)	AFGP (13)	b5b9°b12°b16°y4°y6y6°y7°y9°y16
1771.8674	2	8.7118	6.7723	348	360	(K)DVFLGTFLYEYSR(R)	AMADORI (13)	b1b2b4°b7°b14b18b32*y7°y8y10y15*y20*y38°
2072.018	2	-6.611	6.8931	348	361	(K)DVFLGTFLYEYSRR(H)	CROSSLINE(13), MGH1 (14)	b1°b7°b10y2y6°y10y11°y15°
2107.9785	2.9	2.1264	6.9382	585	602	(K)AADKDTCFSTEGPNLVTR(C)	FL-2H2O(4), Carbamidomethyl C (7)	b3°b4°b7°b8°b10*b11*b13°b16y4y17
2306.0432	3	-1.7049	6.7467	585	602	(K)AADKDTCFSTEGPNLVTR(C)	AMADORI(4), Carbamidomethyl C(7),AMADORI (18)	b10°b20b25y20y20°y26*y27
2340.107	2.8	1.4396	6.9291	29	44	(K)SEIAHRYNDLGEQHFK(G)	CROSSLINE (6), FL-1H20 (16)	b2b5b5*b6b9°b10°b12b15*y4°y15*y17
2495.1912	2	-2.1297	6.5851	224	242	(K)CSSMQKFGERAFKAWAVAR(L)	Carbamidomethyl C (1), MOLD (6), AMADORI (10), MGH1 (19)	b2b4b7°b13°b14b14°b17°b21°b22b35b37b44*y4y5y8°y10y21*y32

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
2767.4863	3.7	2.6377	6.7972	362	383	(R)HPDYSVSLLLRLAKKYEATLEK(C)	FL-1H20(14), MOLD (15)	b2b2°b3*b5*b9*b13b15°b18*b19*b33*y5°y9°y10y10°y15y15°y17y17*y19y22y30°
2835.3513	3	-1.8363	6.6609	24	44	(R)REAHKSEIAHRYNDLGEQHFK(G)	AFGP (5)	b3b15*b16°b17*b19*b25°y11°y12y13*y17*y18*y22*y26
3347.56	3.5	2.765	6.7598	559	584	(K)HKPKATAEQLKTVMDDFAQFLDTCCK(A)	FL-1H20(2), MOLD (11), Carbamidomethyl C(24), Carbamidomethyl C (25), CEL (26)	b1*b5b6°b10b14*y8
3462.6255	6	-9.7345	6.8861	282	309	(R)AELAKYMCENQATISSKLQTCCDKPLLK(K)	FL-2H2O(5), Carbamidomethyl C(8), Carbamidomethyl C(21), Carbamidomethyl C(22),MODIC (24)	b1b3°y1y9°y13y19y22y34
3698.828	3.6	8.5244	7.0666	282	310	(R)AELAKYMCENQATISSKLQTCCDKPLLKK(A)	MODIC(5), Carbamidomethyl C(8), Carbamidomethyl C(21), Carbamidomethyl C(22),CEL(24), AMADORI (28)	b4b7b11°b12b14b16°b18b19b24b25°y17y17*y29

DIAB HYD

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1473.8105	3	-2.3127	0	361	372	(R)RHPDYSVSLLLR(L)	MODIC (1)	b6y9
1491.8207	2.1	-3.3577	6.3479	361	372	(R)RHPDYSVSLLLR(L)	MODIC (12)	b4°b10°b11°b12y9y11°y12
2144.1128	3	4.9031	6.1373	422	438	(K)LGEYGFQNAILVRYTQK(A)	FL-1H20 (17)	b1b4b6°b12°b13b14*b16*y4°y11y13°
2326.1355	2.1	-0.9392	6.8673	342	360	(K)NYAEAKDVFLGTFLYEYSR(R)	GH1 (19)	b1*b2b3*b4°b5b9*b13b15*b19y4y6y19
2375.3308	2.8	4.6632	6.6056	544	558	(K)EKQIKKQTALAELVK(H)	FL-1H20 (2), CROSSLINE (5), CROSSLINE (15)	b3*b4°b5°b6°b7b15y4y5°y13y14°y15
4673.24	3.7	-3.5962	6.9516	509	545	(R)RPCFSALTVDETYVPKEFKAETFTFHSDICTLPEKEK(Q)	Carbamidomethyl C (3), CROSSLINE (16), Carbamidomethyl C (30)	b12b13°y3y4°y5y5°y6y10°y11°y12y16y18°y37
1682.8588	2	2.7122	6.8713	559	569	(K)HKPKATAEQLK(T)	AFGP (2), AMADORI (11)	b5b8°b10y2y4y6y6*y8y10y10*
1965.9017	2	-0.4196	6.8898	220	233	(R)QRMKCSSMQKFGER(A)	Carbamidomethyl C (5), FL-1H20 (10), MOLD (14)	b6°b9b11°b13°b14y8y14
2051.9634	2	3.0029	6.6188	282	298	(R)AELAKYMCENQATISSK(L)	Carbamidomethyl C (8), PYRALINE (17)	b3°b9b13b13°b14b14°b15°y2°y3y5°y6°y8*y15°
2107.9785	3	8.7216	6.7388	585	602	(K)AADKDTCFSTEGPNLVTR(C)	FL-2H2O (4), Carbamidomethyl C (7)	b4°b12b13y1y14y15y17y18

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
2156.9148	2	1.3959	6.6526	106	122	(R)ENYGELADCCTKQEPER(N)	Carbamidomethyl C (9), Carbamidomethyl C (10), CML (12)	b1b1°b2*b4y1y3°y4y4°y5y8y12*y13y17
2324.1873	2.7	2.9061	6.9363	422	438	(K)LGEYGFQNAILVRYTQK(A)	AMADORI (13), AMADORI (17)	b1b5b6b6°b8b10°b11°b15b16y3y3*y6y16y17
2441.1675	3.2	2.4336	7.1488	224	242	(K)CSSMQKFGERAFKAWAVAR(L)	Carbamidomethyl C (1), AMADORI (10), MOLD (13)	b1b15b15*b17b18°y12y15°y16°y17y19y19*
2689.2488	3	0.596	6.7499	585	608	(K)AADKDTCFSTEGPNLVTRCKDALA(-)	Carbamidomethyl C (7), MOLD (18), Carbamidomethyl C (19)	b11b11°b15b16°b18b24y5°y7y8°
3251.6814	5	-7.6862	6.7073	1	24	(-)MKWVTFLLLLFVSGSAFSRGVFRR(E)	CROSSLINE (2), GH1 (23), IMIDAZOLONEB (24)	b16°b18b24°y7°y10°y11y11°y14y17y19y21y22y24
4299.9644	3.8	1.1793	7.0175	35	65	(R)YNDLGEQHFKGLVLIAFSQYLQKCSYDEHAK(L)	AFGP (10), AFGP (23), Carbamidomethyl C (24), CML (31)	b2*b3°b4*b5°b11b12*b13b17b20*b21y2y13*y14y19*y20°y25°y31

DIAB AMG

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1758.7463	2	-7.832	6.7035	222	233	(R)MKCSSMQKFGER(A)	Carbamidomethyl C (3), AFGP (8)	b4°b5b6b7*b9y1y2y2°y7y8°y9°
2326.136	2	-3.9519	6.8825	342	360	(K)NYAEAKDVFLGTFLYEYSR(R)	GH1 (19)	b1b1*b6°b9b10*b11*b16*y2°y3°y10y13y14y17°

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
2372.2427	2.4	9.0396	6.3036	237	257	(K)AWAVARLSQTFPNADFAEITK(L)	MODIC (6)	b11b12b15°b21*y3y4°y9*y11*y20°y21
2893.3555	2.2	-6.2956	6.6295	563	584	(K)ATAEQLKTVMDDFAQFLDTCCK(A)	CROSSLINE (7), Carbamidomethyl C (20), Carbamidomethyl C (21), MOLD (22)	b2°b6b12*b15°b18*b20*b22y5y7y9y13y14y14*
3497.653	3.7	-3.971	6.7539	410	434	(K)NLVKTNCDLYEKLGEYGFQNAILVR(Y)	AFGP (4), Carbamidomethyl C (7), AFGP (25)	b1b4b5b9b9*b11b15°b21y6y8*y12°
5944.5356	4	-1.0925	6.4776	106	152	(R)ENYGELADCCTKQEPERNECFLQHKDDNPSLPPFERPEAEAMCTSFK(E)	Carbamidomethyl C (9), Carbamidomethyl C (10), FL-2H2O (12), Carbamidomethyl C (20), MODIC (25), Carbamidomethyl C (43), PYRALINE (47)	b1b3b3°b5b9b12°b16b21*y10°y13y15°y23
1096.6007	2	9.3827	6.8003	211	219	(K)EKALVSSVR(Q)	PYRALINE (2)	b3°y3y4y5y7y9
1706.918	2	-2.0708	6.5592	211	223	(K)EKALVSSVRQRMK(C)	MOLD (9), FL-2H2O (13)	b3°b4°y5y6y8y13*
1928.0092	3	4.5611	6.4978	211	223	(K)EKALVSSVRQRMK(C)	CEL (2), AMADORI (9), AMADORI (13)	b1b11°y4y5y6y7y11*y13
1965.9097	2	4.2737	6.7605	220	233	(R)QRMKCSSMQKFGER(A)	FL-1H20 (4), Carbamidomethyl C (5), MOLD (10)	b3b8°b9b10b11b13*y5y7y11y14
2035.9542	2.6	7.4584	6.5716	585	602	(K)AADKDTCFSTEGPNLVTR(C)	Carbamidomethyl C (7), MGH1 (18)	b4b4°b5b6°b16*y2°y6y14

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
2204.9785	3.3	7.3815	6.6078	220	233	(R)QRMKCSSMQKFGER(A)	AMADORI (2), CarbamidomethylC (5), AFGP (10)	b2*b6°b7b7°y4y10y11y11°y14
2340.1062	2.8	7.7565	6.6117	29	44	(K)SEIAHRYNDLGEQHFK(G)	CROSSLINE (6), FL-1H20 (16)	b5°b15°b16y5°y6y8y9*y10y12*y14°y16
2448.2021	2.4	0.9207	6.5614	342	360	(K)NYAEAKDVFLGTFLYEYSR(R)	AMADORI (19)	b2*b3*b6*b7°b9*b11°b12b12*b13y2y2°y4°y11y11°
2684.209	2.3	-5.635	6.9304	585	604	(K)AADKDTCFSTEGPNLVTRCK(D)	FL-1H20 (4), CarbamidomethylC (7), AMADORI (18), CarbamidomethylC (19), PYRALINE (20)	b3b4°b5b14b15b19y8*y10*y10°y16°y20
2949.341	2.4	1.2403	6.9858	265	286	(K)VNKECCHGDLLECADDRAELAK(Y)	FL-2H2O (3), CarbamidomethylC (5), CarbamidomethylC (6), CarbamidomethylC (13), AMADORI (17), CML (22)	b3b3*b4*b7b11b11°b12*b15b16*b17°b20°b22y11y12y12°y16°y22
3851.9102	3	3.6042	6.5988	45	75	(K)GLVLIAFSQYLQKCSYDEHAKLVQEVTDFAK(T)	FL-1H20 (13), CarbamidomethylC (14), MOLD (21), CML (31)	b3b19°b21*y6y8°y12y14°y18°
3926.676	3.4	0.2916	6.6473	268	298	(K)ECCHGDLLECADDRAELAKYMCENQATISSK(L)	CarbamidomethylC (2), CarbamidomethylC (3), CarbamidomethylC (10), CROSSLINE (19), CarbamidomethylC (22)	b16°y2y6°y9*y11y20y31

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
4445.003	3	8.8284	6.6688	118	152	(K)QEPERNECFLQHKDDNPSLPPFERPEAEAMCTSFK(E)	MODIC (5), CarbamidomethylC (8), MOLD (24), CarbamidomethylC (31), FL-2H2O (35)	b11b13*b14*b18°b19b20°b23b24b35*y2y3°y11y12°y20y20°y34°y35
4732.0825	3	4.0024	6.7172	570	604	(K)TVMDDFAQFLDTCCKAADKDTCFSTEGPNLVTRCK(D)	CarbamidomethylC (13), CarbamidomethylC (14), FL-2H2O (15), CROSSLINE (19), CarbamidomethylC (22), CarbamidomethylC (34), CROSSLINE (35)	b22y5y7°y13*y15*y16y24*y35

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Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1749.8616	2	9.593	4.9579	429	442	(K)FMDTVAEKALQEYR(R)	MOLD (8)	b2b3°b4b5b7°b11b11*b14°y2y3°y7y13*
2004.0444	2.04	4.5385	5.3612	336	350	(R)LTEQYKELLQSFQSK(M)	AMADORI (6)	b1b2°b5*b6b9b9*b11b11*b14°b15*y5*y6*y10y10*y11°y13°y14y15*
4641.221	3	-8.9264	4.5787	342	380	(K)ELLQSFQSKMLNTSSLLEQLNDQFNWVSQLANLTQGEDK(Y)	CEL (9), CEL (39)	b5*b5°b13°b18b19°b24*b25b29°b35°y2y4y7*
1488.6884	2	0.4433	5.0579	425	436	(K)DNPKFMDTVAEK(A)	MODIC (4), CML (12)	b3°b5*b6b7b7*b7°b8b8*b10°b11y3°y4°y8°y11*
1950.9803	2.92	1.036	5.4862	182	197	(R)ASGIIDTLFQDRFFAR(E)	GH1 (12), MGH1 (16)	b3°b4b10b14°b16b16*y2y3y10y16
4286.9995	3.37	3.442	5.4659	130	166	(R)SGSGLVGQQLEEFLNQSSPFYFWMNGDRIDSLLESDR(Q)	Oxidation M (24), MOLD (37)	b9b16b22b24°y11y13y14°y21*y27*y33*

DIAB

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1843.8785	2	2.7392	4.664	79	93	(K)KKEDALEDTRDSEMK(L)	MOLD (15)	b3°b6b11°b13b18b22y3y5y8y25°
2004.0127	2.04	7.0849	5.2008	44	56	(K)EIQNAVQGVKHIK(T)	AFGP (10), AFGP (13)	b9b15*b23*y1y3y4y8y9°y21*
2005.952	2	1.6904	5.0775	80	95	(K)KEDALEDTRDSEMKLK(A)	GH1 (9), CML (14)	b2°b3b5b5°b12*y1y10y13
2020.0076	4	-1.0728	5.6379	282	296	(R)TVCKEIRRNSTGCLK(M)	Carbamidomethyl C (3), FL-2H2O (4), MODIC (7), MODIC (8), Carbamidomethyl C (13)	b4°b6b7°b8b11°b15b16°y13

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
3071.399	2.69	-7.6583	5.3331	158	181	(R)IDSLLESDRQQSQVLDAMQDSFAR(A)	AFGP (9), MOLD (24)	b6*y3y5y5*
4343.9546	3	5.2083	5.0806	290	323	(R)NSTGCLKMKGQCEKCQEILSVDCSTNNPAQANLR(Q)	CarbamidomethylC (5), FL-2H2O (9), CarbamidomethylC (12), FL-1H20 (14), CarbamidomethylC (15), CarbamidomethylC (23), AMADORI (34)	b2°b3°b4°b5°b6b10°y7°y11°y13
1230.6302	2	5.1885	4.7573	289	298	(R)RNSTGCLKMK(G)	CarbamidomethylC (6), MODIC (8)	b2°b3°b6°b12b22°y3y5y14*y23°y25°
1446.7733	2	-4.3847	4.8878	57	67	(K)TLIEKTNAERK(S)	FL-1H20 (11)	b1b2b2°b3°b6b8b10y3y8°
1591.833	2	6.7419	4.8668	68	78	(K)SLLNSLEEAKK(K)	CROSSLINE (10), PYRALINE (11)	b3°b5b6°b11°b13b13°y9
1746.8374	2.73	-1.1664	5.3996	78	88	(K)KKKEDALEDTR(D)	AFGP (1), FL-1H20 (3)	b8b9°b10°y5y8y11
1749.8558	2.41	6.8692	5.4799	429	442	(K)FMDTVAEKALQEYR(R)	MOLD (8)	b2*b3*b4b7
1844.8724	3	7.8965	5.12	81	95	(K)EDALEDTRDSEMKLK(A)	MOLD (8), Oxidation M (12)	b2*b4*b7°b9°b13y2
1952.892	2	-0.6529	5.584	289	303	(R)RNSTGCLKMKGQCEK(C)	CarbamidomethylC (6), MOLD (8), MOLD (10), CarbamidomethylC (13), CML (15)	b2*b2°b4b6*b7b8b14°y9*y13*y13°y14°y15*
1956.0381	2.88	-0.9696	5.4333	67	79	(R)KSLLNSLEEAKKK(K)	FL-1H20 (1), AMADORI (12), AMADORI (13)	b6*b7y4*y6y7*y10*y10°y11y11°y15y15*
2031.9637	2.9	0.3977	5.3866	81	95	(K)EDALEDTRDSEMKLK(A)	CROSSLINE (8)	b1b2b4b6°b10y6°y8°y9y12°
2173.0334	2.07	9.2055	5.2892	79	93	(K)KKEDALEDTRDSEMK(L)	FL-2H2O (1), CROSSLINE (10)	
2366.1177	3	-1.7232	5.2695	425	442	(K)DNPKFMDTVAEKALQEYR(R)	FL-2H2O (4), MODIC (12), MOLD (18)	b4°b10°b12*b13°b18*b19°b20y4y4°y9y9*y9°y10*y13y14y22y24

DIAB HYD								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
1829.9729	2	-5.2503	5.2246	68	80	(K)SLLNSLEEAKKKK(E)	PYRALINE (10), CEL (11), AMADORI (12)	b3*b5b5*b13y3y3°y5°y8°
1854.8771	2	3.2269	4.7054	289	303	(R)RNSTGCLKMKGQCEK(C)	Carbamidomethyl C (6), CML (8), Carbamidomethyl C (13)	b7b13°b15y2°y3°y5°y9°y21*y21°y22
1862.9337	2	7.7515	5.2221	286	298	(K)EIRRNSTGCLKMK(G)	AMADORI (3), Carbamidomethyl C (9), PYRALINE (13)	b2b3b3°b8b12°y5y6°y9*y13
1881.888	3	3.0346	5.1764	289	303	(R)RNSTGCLKMKGQCEK(C)	Carbamidomethyl C (6), MODIC (8), MOLD (10), Carbamidomethyl C (13)	b2b3b3*b5b10°b12y3y5*y7°y11*y14*
2001.0573	2	5.9141	4.8829	62	77	(K)TNAERKSLLNSLEEAK(K)	MODIC (6), AMADORI (16)	b1b5°b10*b13*b15*b18°b36°y3*y3°y4y5y9°y10y13°y14°y17*y22*y23y25°y29y32°y36y36*
2004.0186	2.05	-4.7709	4.8765	336	350	(R)LTEQYKELLQSFQSK(M)	FL-2H2O (6), MODIC (15)	b1°b2°b3°b4b4°b6b6°b7°b9°y2y6y8y10y12°
2004.019	2.03	-6.1182	5.4377	336	350	(R)LTEQYKELLQSFQSK(M)	AMADORI (6)	b1b5°b10*b13*b15*b18°b36°y3*y3°y4y5y9°y10y13°y14°y17*y22*y23y25°y29y32°y36y36*
2020.0009	4	2.8876	5.5019	282	296	(R)TVCKEIRRNSTGCLK(M)	Carbamidomethyl C (3), FL-2H2O (4), Carbamidomethyl C (13), CEL (15)	b2b3b3*b5b10°b12y3y5*y7°y11*y14*
2196.087	2	-0.268	5.0335	80	95	(K)KEDALEDTRDSEMKLK(A)	CROSSLINE (1), MODIC (14)	b1b7b9°b14b16°b17°b19°b22*b24*b25b32°y2y12°y14y16y16°y17*y20y22*y23°y29y39°

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
2199.0874	3	9.5199	4.4945	62	77	(K)TNAERKSLLNSLEEAK(K)	AFGP (6), FL-2H2O (16)	b5b5°b6°b7°b8b9b10°b12y5y5*y6y6*y11°y14*y15y15*
3942.8345	3	6.6886	4.9911	304	335	(K)CQEILSVDCSTNNPAQANLRQELNDSLQVAER(L)	Carbamidomethyl C (1), Carbamidomethyl C (9), AFGP (20)	b6b6°b11b12*y4y10*y14*
4216.9736	4.69	-8.4916	5.0656	158	193	(R)IDSLLESDRQQSQVLDAMQDSFARASGIIDTLFQDR(F)	GH1 (9), MGH1 (24), MGH1 (36)	b14°b16b18°b20°b21b22y10°y12y15°y22

DIAB AMG

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1980.9254	2	5.2988	5.6041	289	303	(R)RNSTGCLKMKGQCEK(C)	GH1 (1), Carbamidomethyl C (6), CEL (10), Carbamidomethyl C (13), CEL (15)	b3*b4*b8b11b16y3°y6°y17*
1503.8325	2	5.7965	4.6342	67	78	(R)KSLLNSLEEAKK(K)	MODIC (1), PYRALINE (11)	b3°b4b5*b5°b12b13*b16b19°y1y2y3y5*y9°y10y13y14*y16°
1587.8127	2.35	5.583	4.5024	182	193	(R)ASGIIDTLFQDR(F)	CROSSLINE (12)	b10*b17y5°y6°y12*y17
1772.8964	2.68	0.1263	4.8731	286	298	(K)EIRRNSTGCLKMK(G)	MODIC (4), Carbamidomethyl C (9), FL-1H20 (13)	b6*b8°b15b18y4y10*
1790.9012	2	-8.2198	5.1708	286	298	(K)EIRRNSTGCLKMK(G)	Carbamidomethyl C (9), MODIC (11), AMADORI (13)	b1b14°y3y6y9*
1952.9645	3	2.5724	5.0535	286	298	(K)EIRRNSTGCLKMK(G)	AMADORI (3), Carbamidomethyl C (9), MODIC (11), AMADORI (13)	b1b6°b7b9°b11°b12y8y12
1986.0089	2	-7.2779	5.2383	336	350	(R)LTEQYKELLQSFQSK(M)	FL-1H20 (15)	b5b18b23°y3y5y5*y12y16°
2004.0193	2.04	-10.1901	5.0675	336	350	(R)LTEQYKELLQSFQSK(M)	AMADORI (15)	b7°b10*b11*y1y4°y5y7°y12
2005.9592	2	-5.8909	5.1115	80	95	(K)KEDALEDTRDSEMKLK(A)	MOLD (14), MOLD (16)	b4b8b10b10°b11°b16°y11y11°y12°y13

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
2019.9972	4	1.0064	5.5872	282	296	(R)TVCKEIRRNSTGCLK(M)	Carbamidomethyl C (3), FL-1H20 (4), MGH1 (8), Carbamidomethyl C (13)	b3°b7°b9°b12y1y6y9°y15°y16
2031.9608	2.91	3.4045	5.1365	80	95	(K)KEDALEDTRDSEMKLK(A)	Oxidation M (13), PYRALINE (14)	b10b15y6y9°y10y14y15

P06728-Apolipoprotein A IV

CON

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1479.7511	1.94	-2.1372	5.1467	248	259	(K)NAEELQTKVSAK(I)	AMADORI (8)	b2b3*b3°b4°b5°b6°b8b9b11b12y9y12
1853.928	2.73	6.6022	5.5618	280	294	(K)GNTEGLQKSLEDLNR(Q)	FL-1H20 (8), MODIC (15)	b4b5b6b10*b12b13y1y2*y3y4y5y9y9°y13*y15
3581.7637	3.66	-3.4277	4.8743	317	345	(K)ALVQQLEQFRQQLGPNSGEVESHLSFLEK(S)	AFGP (10)	b5*b6b7*b11°b12°b16b16°b21*b24b26°b27°y1y2°y14y14*y17*y25°y29
4397.198	4	2.7952	4.9487	131	163	(K)LQEHLKPYAVDLQDQINTQTQEMKLQLTPYIQR(M)	AFGP (6), FL-1H20 (24)	b3*b5°b6°b12°b20*b23y6*y25
4422.1973	5.36	9.5539	4.4017	120	154	(K)VTQTFGENMQKLQEHLKPYAVDLQDQINTQTQEMK(L)	CROSSLINE (17), MODIC (35)	b4b12*b23y4y4°y8y22°y24*
1397.7358	2.24	-2.226	4.9547	199	209	(K)GHLTPRANELK(A)	AMADORI (6)	b4°y5*y8y9*y11
1439.7673	1	-3.2707	5.1152	256	265	(K)VSAKIDQLQK(N)	CROSSLINE (4), CML (10)	b2°b4b4°b7b8b9°b10b10°y8y8°
1605.8367	2	2.1314	4.6307	248	259	(K)NAEELQTKVSAK(I)	CROSSLINE (8), MODIC (12)	b2b3b6b8*b8°b11°y2y11y12
1645.7948	2.9	8.7684	4.516	248	259	(K)NAEELQTKVSAK(I)	AFGP (8), CML (12)	b8°b10*b11*y8y9y11*y12
1667.8313	2	7.1157	4.7251	199	209	(K)GHLTPRANELK(A)	AMADORI (6), AFGP (11)	b5°b7b9*b11y2y3y3°y4y5°y10y10*
1682.7866	1	-1.3587	4.9606	349	360	(R)EKVNSFMSTLEK(K)	AFGP (12)	b1b2°b5*b5°b9°b11°b12°y2°y3y4y9°y10y10*y10°y11°y12*

DIAB

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1373.7065	2	0.6658	5.3637	317	326	(K)ALVQQLEQFR(Q)	IMIDAZOLONE B (10)	b2b4b5*b7*b8*b10b10*y3y3*y4y4°y5y6*y9

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1621.7726	2	-1.8446	4.636	188	198	(K)DKFNRNMEELK(G)	AMADORI (5), MODIC (11)	b5b5*b7b8b10*y6y7°y10°y11*
1713.8646	3	7.6039	4.5885	280	294	(K)GNTEGLQKSLEDLNR(Q)	GH1 (15)	b3b10b10°y5°
1771.8582	2.52	-8.0503	4.6081	280	294	(K)GNTEGLQKSLEDLNR(Q)	MOLD (8), MOLD (15)	b4°b10°b11y2y3y9°y10y15
1986.0013	2	1.3568	4.5349	190	204	(K)FNRNMEELKGHLTPR(A)	FL-1H2O (9)	b4b6*b9*b12*y4y13y14°
2009.0272	3	-7.3864	4.5854	278	294	(K)VKGNTEGLQKSLEDLNR(Q)	PYRALINE (10)	b6*b11b11°b13°b14*b16y1
2052.9404	2.75	-6.6214	4.8986	234	247	(K)LNHQMEGLAFQMKK(N)	AFGP (13), PYRALINE (14)	b2b8°b10b11b12*b12°b13°y2y4y6*y8y10°y14
2179.0088	2	2.0112	4.5781	105	119	(K)ELEDLRDRMMPHANK(V)	MGH1 (8), AFGP (15)	b8b11°b14y4y11°y13*
2311.21	2	-0.7334	5.1528	346	361	(K)SLREKVNSFMSTLEKK(G)	FL-2H2O (5), CROSSLINE (15), MODIC (16)	b4°b6b10b12°y10y10°y11y13y13*
2558.3687	3	9.0227	4.6025	199	220	(K)GHLTPRANELKATIDQNLEDLR(R)	MGH1 (6)	b4b8*b9°b11b13*y8*y10
2919.3987	2.57	-7.4902	5.1773	305	326	(R)RTVEPMGEMFNKALVQQLEQFR(Q)	FL-2H2O (12), IMIDAZOLONE B (22)	b4b8b11°b13b19°b21y4*y4°y8*y9y13*y14y18*y20y21*y22
3005.4468	2.87	-0.9473	4.9849	170	192	(K)ENVDNLHTSMMPLATNLKDKFNR(N)	Oxidation M (10), CROSSLINE (20), MOLD (23)	b4*b4°b7*b8°b13b14b16y3y8y9*y13*y14*y15y16°y19
3110.5337	4	8.223	4.6598	164	189	(R)MQTTIKENVDNLHTSMMPLATNLKDK(F)	Oxidation M (1), MOLD (24), CEL (26)	b6*b16*b19*b19°b20b25*y3°y5°y9*y13*y21*y24
3238.6074	3.03	-1.8178	5.0975	234	259	(K)LNHQMEGLAFQMKKNAEELQTKVSAK(I)	FL-1H2O (14), MOLD (22), CEL (26)	b3*b4b9*b10°b21b24b26y3y5y5°y7*y8y8°y9°y10*y13°y14*y17°y19y23°y26
3241.5918	3	-2.6792	4.7225	234	259	(K)LNHQMEGLAFQMKKNAEELQTKVSAK(I)	Oxidation M (5), FL-1H2O (14), PYRALINE (22)	b5*b11b12b15°b17b23b23*b23°y3°y23°
5129.5513	3.69	0.3977	5.2126	306	348	(R)TVEPMGEMFNKALVQQLEQFRQQLGPNSGEVESHLSFLEKSLR(E)	FL-2H2O (11), MODIC (21), MODIC (40)	b1b3b3°b6b10b11b13°b19y3y5°y22y22°y25°y33°y43

DIAB HYD								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
1621.7675	2	-3.3928	3.9969	188	198	(K)DKFNRNMEELK(G)	MODIC (2), AMADORI (11)	b4*b6*b9*y6*y7°y9°y11
1621.7717	2	10.2344	4.9717	188	198	(K)DKFNRNMEELK(G)	FL-2H2O (2), CEL (11)	b2°b3b3°b4°b7*b8y3y5y7*y7°y9*y10°y11
1895.9137	2.73	0.8797	5.1212	247	259	(K)KNAEELQTKVSAK(I)	AFGP (1), PYRALINE (9), CEL (13)	b3b4b8*b11°b12°y6y6°y10y12°
1939.9163	2	-8.3803	5.044	105	119	(K)ELEDLRDRMMPHANK(V)	MOLD (8), MODIC (15)	b1b9°b10b13°y2*y4y5y6*y8y14
1947.9683	2	-9.7291	4.8361	210	221	(K)ATIDQNLEDLRR(S)	CROSSLINE (11), CROSSLINE (12)	b4b4°b5°b6°b7b7°b11y7y9
1987.0182	2	3.3841	4.6029	205	220	(R)ANELKATIDQNLEDLR(R)	FL-1H20 (5)	b3°b5b6b9*b11°b14*y4
2391.18	2	-4.784	4.5707	188	204	(K)DKFNRNMEELKGHLTPR(A)	FL-1H20 (11), AMADORI (17)	b2°b3°b4b6*b10°b12y6y7y10y10°y12*y16*
2441.1682	3.26	4.7608	4.887	278	294	(K)VKGNTEGLQKSLEDLNR(Q)	AFGP (2), AFGP (17)	b5°b14°y7y8°y9y11°y16y17
2862.3809	2.62	5.6065	5.492	234	255	(K)LNHQMEGLAFQMKKNAEELQTK(V)	FL-1H20 (13), CEL (14), CML (22)	b2b5b6b6*b9b17*b20b22y5y8y9°y10°y11*y12y16y17y22
3110.5198	3.84	-10.439	4.8446	234	259	(K)LNHQMEGLAFQMKKNAEELQTKVSAK(I)	Oxidation M (5), MOLD (22), CEL (26)	b6°b10°b12b12*b16*b19b21*b21°y3y4y9*y15
3238.609	3.04	2.8496	5.0437	234	259	(K)LNHQMEGLAFQMKKNAEELQTKVSAK(I)	FL-1H20 (14), MOLD (22), CEL (26)	b3b4b5b7°b8b13b16b16°b24*b26y7*y9°y11y11*y12*y12°y14°y15*y16°
3698.84	4	9.0845	5.036	193	220	(R)NMEELKGHLTPRANELKATIDQNLEDLR(R)	FL-2H2O (6), AMADORI (17), AMADORI (28)	b1b5°b16*b22b23°y6y13y15y18*y22*

DIAB AMG								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
1621.7704	2	-3.0372	5.4672	188	198	(K)DKFNRNMEELK(G)	MODIC (2), AMADORI (11)	b3b4*b8*b10b11y1y2y5°y8°y9y11
1926.932	2	-0.6753	4.2384	105	119	(K)ELEDLRDRMMPHANK(V)	CEL (15)	b3°b5°b11°b12b15*y3*y4*y6*
3385.832	3	6.8751	4.7848	248	277	(K)NAEELQTKVSAKIDQLQKNLAPLVEDVQSK(V)	MOLD (30)	b10°y5*y7y8y17
1271.7	2	0.5468	5.0587	199	209	(K)GHLTPRANELK(A)	MODIC (6)	b4y3y5*y7y9*
1439.7668	1	0.8267	5.5109	256	265	(K)VSAKIDQLQK(N)	CROSSLINE (4), CML (10)	b1b2b2°b4°b5b8b8°b9°b10b10°y8y8°
1600.7172	3	3.6776	5.368	247	255	(K)KNAEELQTK(V)	AFGP (1), AFGP (9)	b2b3b6y3°y5y6y7*y8*
1679.7719	2	-3.49	4.6359	351	361	(K)VNSFMSTLEKK(G)	AFGP (10), FL-2H2O (11)	b2b2*b3*b5°b7°b9b9*b10°y6°y10
1715.868	2.54	-1.0678	5.1384	247	259	(K)KNAEELQTKVSAK(I)	AFGP (9)	b2*b4b6b8°b9*b11y2y6°y7y13
1749.8584	2.41	-0.2799	5.0829	349	361	(R)EKVNSFMSTLEKK(G)	Oxidation M (7), FL-1H20 (12), MOLD (13)	b4b5*b11*b12b13y5°y7y8°y13y13*
1856.9261	2.68	1.3252	5.5324	100	112	(K)EEIKKELEDLRDR(M)	FL-2H2O (4), CML (5)	b7b11y8°y10y12
1985.9983	2	6.3737	5.0227	349	361	(R)EKVNSFMSTLEKK(G)	FL-1H20 (2), CROSSLINE (12), MOLD (13)	b3b3°b4°b7°b10°b11b13°y3y4°y12*y13y13*
2157.0642	2.53	-4.7088	5.1902	346	361	(K)SLREKVNSFMSTLEKK(G)	FL-1H20 (5), CML (15), CML (16)	b1b2b4°b6°b8b8°y3°y6y7°y8y16
2245.154	2.6	-0.7381	5.1604	248	265	(K)NAEELQTKVSAKIDQLQK(N)	CEL (8), CEL (12), CML (18)	b3b4°b5°b6b12*b13*b18y2y3y3*y4*y5y5*y6*

P21614- Vitamin D binding protein

CON

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
2382.0637	2.09	2.7977	5.6819	374	393	(R)ECCDTQDSVACFSTQSPLLK(R)	Carbamidomethyl C (2), Carbamidomethyl C (3), Carbamidomethyl C (11), MODIC (20)	b3b7b9b10b14°y2y5*y13y14
2950.3445	2.3	8.1226	5.2011	181	203	(K)NYLSMVGSCCTSANPTVCFVKER(L)	Carbamidomethyl C (9), Carbamidomethyl C (10), Carbamidomethyl C (18), AFGP (21)	b3°b11b13b13°b15b16b22y13°y15y15*y25*
1552.7366	2.22	4.6103	5.8524	26	37	(K)DKVCNELAMLGK(E)	FL-2H2O (2), Carbamidomethyl C (4), MOLD (12)	b1b1°b2b3b6b7*b9*b12b14b14*y9y13*y15
1825.7762	2	0.1304	6.0633	440	451	(K)DMVEKHSDFASK(C)	AFGP (5), AMADORI (12)	b2b3°b4°b9°b19*y20
2011.9784	3.11	-3.7392	5.5728	51	65	(R)KFSSSTFEQVNQLVK(E)	FL-2H2O (1), FL-1H20 (15)	b3°b12b12°b13b14b17*b20b21y8
2777.269	2	7.6547	5.6414	333	353	(K)DLCGQSTTQAMDQYTFELSRR(T)	Carbamidomethyl C (3), AFGP (20)	b16b17y3°y6y8y12y13°y14°y21°
2986.2969	2.41	-6.0404	5.8028	95	119	(K)SCESDAPFPVHPGTPECCTKEGLER(K)	Carbamidomethyl C (2), Carbamidomethyl C (17), Carbamidomethyl C (18), FL-2H2O (20)	b2b8b10*b11y4y11*y12*

DIAB

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1807.8413	2	-1.0707	5.0553	28	41	(K)VCNELAMLGKEDFR(S)	Carbamidomethyl C (2), FL-2H2O (10)	b1b3*b5*b5°b12*b14°y2y7y8
1945.9161	3	4.3807	5.5989	430	444	(K)TPNTSPAELKDMVEK(H)	Oxidation M (12), AFGP (15)	b1b3*b4b4°b6b7*b8*b10*b14*y5°y10y10°y14
2509.17	3	-1.0551	5.7319	22	41	(R)DYEKDKVCNELAMLGKEDFR(S)	Carbamidomethyl C (8), MOLD (16)	b4b10°b12b13y20

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
3068.3518	3	-0.6536	5.4731	395	419	(R)QLTSFIEKGQEMCADYSENTFTEYK(K)	MOLD (8), Carbamidomethyl C (13)	b2b2*b3°b5°b10*b11*b19°b23°y4y7°y8*y11y15y17y19*y20*
2204.9773	3.31	4.7429	5.8265	219	232	(R)VCSQYAAYGKEKSR(L)	Carbamidomethyl C (2), AFGP (10), FL-2H2O (12), AMADORI (14)	b1b2b4*b5*b6b12°b13°b14b14°y1y6y7y7°y11*y14
2281.0742	3	10.4103	6.0506	22	37	(R)DYEKDKVCNELAMLGK(E)	CROSSLINE (4), CML (6), Carbamidomethyl C (8), CML (16)	b1b2b4b11b12b16*y11y12y12*y12°y15y16
2429.1555	2.67	-2.4811	5.6904	26	41	(K)DKVCNELAMLGKEDFR(S)	CROSSLINE (2), Carbamidomethyl C (4), CROSSLINE (12)	b10°b15°b16°y3y5°y6y13°y16
2490.318	3	0.6971	5.8578	243	264	(K)VPTANLENVLPLAEDFTEILSR(C)	MOLD (22)	b5b6°b7°b8°b10*b11b13b17*b19°b22y9°y11y18°y19°y22
2546.1836	3.87	-1.2231	5.6618	430	451	(K)TPNTSPAELKDMVEKHSDFASK(C)	Oxidation M (12), MOLD (15), MOLD (22)	b1b5*b8b8°b9°b11*b12b12°b21°y9y17y22y22*
2612.2087	3	-9.0268	5.6365	20	37	(R)GRDYEKDKVCNELAMLGK(E)	CROSSLINE (6), CEL (8), Carbamidomethyl C (10), AMADORI (18)	b7°b8b11*b17y4y5y9y11y14
2742.2688	3	2.0657	5.7249	430	451	(K)TPNTSPAELKDMVEKHSDFASK(C)	FL-1H20 (10), PYRALINE (15), CML (22)	b7b9b10b10*b11*b12°b14b14°b16°y6y8°y9y17°
3238.6147	3.04	-2.2324	5.6913	28	51	(K)VCNELAMLGKEDFRSLSLILYSRK(F)	Carbamidomethyl C (2), FL-2H2O (10), AMADORI (23), PYRALINE (24)	b5*b18b19b24y1y4°y5y5°y8y15°y23°
3515.736	3.58	2.429	6.1177	26	50	(K)DKVCNELAMLGKEDFRSLSLILYSR(K)	FL-1H20 (2), Carbamidomethyl C (4), CROSSLINE (16), AMADORI (25)	b10*b11b12b13b15°b17b17*b18b19b20b23b25y2y13y17°
3941.8296	3	2.0413	5.8992	395	421	(R)QLTSFIEKGQEMCADYSENTFTEYKKK(L)	Carbamidomethyl C (13), CROSSLINE (25), CROSSLINE (26), AMADORI (27)	b6°b12b13b13°b15b23*b24b24*y20*

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
4299.97	4	-1.1586	6.0533	115	149	(K)EGLERKLCMAALSHQPQEFPTYVEPTNDEICEAFR(R)	MOLD (5), MODIC (6), Carbamidomethyl C (8), Carbamidomethyl C (31), MOLD (35)	b3°b9°b11b15*b22*b23*b25b25°y2y6y11°y14°y17y18°y20y20°y24y33°
DIAB HYD								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
1629.8041	3	4.6514	5.5562	26	37	(K)DKVCNELAMLGK(E)	CROSSLINE (2), Carbamidomethyl C (4)	b3b9*b10b10*b11*y3°y4y4°y9
4261.9814	4.39	-10.1713	6.845	509	543	(R)RPCFSALTVDETYVPKEFKAETFTFHSDICTLPEK(E)	Carbamidomethyl C (3), MOLD (16), Carbamidomethyl C (30), MOLD (35)	b2b9b10b12°b15b20y3y3°y5y6°y8y9°y11y12y19°y33°
1491.8207	2.13	-3.3577	6.3479	361	372	(R)RHPDYSVSLLLR(L)	MODIC (12)	b1b4b5*b9°b11°b12b14*y8y10y14
1717.833	3	6.6514	5.7472	28	41	(K)VCNELAMLGKEDFR(S)	Carbamidomethyl C (2), MODIC (10)	b7*b21b21°b22*b24°y6
1781.7675	2	1.6929	5.9737	219	230	(R)VCSQYAAYGKEK(S)	Carbamidomethyl C (2), AFGP (10), PYRALINE (12)	b5b6b9y5y9
1946.8894	2	-9.7811	5.7183	222	236	(R)MKCSSMQKFGERAFK(A)	Carbamidomethyl C (3), CEL (8), GH1 (12)	b3b3°b5°b6b7b9b13b14°b21°b31*b34b36*y2y2°y3°y11y14°y22
1947.9678	2	-1.019	5.579	430	444	(K)TPNTSPAELKDMVEK(H)	CROSSLINE (10), MODIC (15)	b4°b5b7b8b14*y4y6
1965.9017	2	-0.4196	6.8898	220	233	(R)QRMKCSSMQKFGER(A)	Carbamidomethyl C (5), FL-1H20 (10), MOLD (14)	b1°b3b4b4°b5b6b6*b6°y3y5°y10
2139.9175	2	7.3882	6.1625	265	281	(K)VNKECCHGDLLECADDR(A)	Carbamidomethyl C (5), Carbamidomethyl C (6), Carbamidomethyl C (13), MOLD (17)	b1°b2b7b12b12°b13°b15*b19*y8y9y10°y16°y19*y20
2294.0288	2	8.182	6.5935	570	588	(K)TVMDDFAQFLDTCCKAADK(D)	Carbamidomethyl C (13), Carbamidomethyl C (14), CML (19)	b18y10°y13y22°

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
2324.1873	2.7	2.9061	6.9363	422	438	(K)LGEYGFQNAILVRYTQK(A)	AMADORI (13), AMADORI (17)	b2°b3*b5*b7b7*b8b10b14°b15y3y4°y13°
2326.1348	2	-0.9414	6.5016	342	360	(K)NYAEAKDVFLGTFLYEYSR(R)	GH1 (19)	b2b9b10b11b16*b17*y1y17y19y31
2375.3308	2.78	4.6632	6.6056	544	558	(K)EKQIKKQTALAELVK(H)	FL-1H20 (2), CROSSLINE (5), CROSSLINE (15)	b1b1°b5b10b11*y4y10y10*y10°y11*y12

DIAB AMG

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1448.7513	2.25	2.3699	5.8655	428	439	(R)TKTPNTSPAELK(D)	AMADORI (12)	b1b1°b2b5*b11*b12°y4y6y10°y11°y14°
2333.1892	3	-1.6407	5.5674	426	444	(R)LRTKTPNTSPAELKDMVEK(H)	MOLD (2), FL-2H2O (4)	b13b14y8y10°y11°y14y18
2602.0913	2	-3.6888	5.2143	66	87	(K)EVVSLTEECCAEGADPTCYDTR(T)	Carbamidomethyl C (9), Carbamidomethyl C (10), Carbamidomethyl C (18), GH1 (22)	b3°b15b23b28y13°y16y20°y21y24
2841.351	3	-3.5389	5.7136	428	451	(R)TKTPNTSPAELKDMVEKHSDFASK(C)	PYRALINE (12), CEL (17)	b3b11b12*y9*y12
1129.5579	2	-6.0953	5.5915	430	439	(K)TPNTSPAELK(D)	CEL (10)	b13°y3y4°y7y9y10y13y14
1488.6841	2	-2.828	5.6487	219	230	(R)VCSQYAAYGKEK(S)	Carbamidomethyl C (2), MODIC (10), MOLD (12)	b10b12b16b21y2y10°y13°y18*y23
2159.057	2	-4.5517	5.7951	428	444	(R)TKTPNTSPAELKDMVEK(H)	PYRALINE (2), AMADORI (17)	b2b3°b10b14y3y8°y9y9°y10°y11°y12*y18*y20
2165.0027	2.86	-9.9986	5.8414	22	37	(R)DYEKDKVCNELAMLGK(E)	Carbamidomethyl C (8), CROSSLINE (16)	b1°b2b4°b6b11°b14b16b21b21°y3
2186.9526	4	4.1829	5.7206	219	232	(R)VCSQYAAYGKEKSR(L)	Carbamidomethyl C (2), AFGP (12), AFGP (14)	b2b3°b4b8*b12°y11*y12
2262.0024	3.34	-6.7993	5.9554	26	41	(K)DKVCNELAMLGKEDFR(S)	FL-2H2O (2), Carbamidomethyl C (4), MOLD (12), AMADORI (16)	b6b10°b21y15*y17y24y30°y41°y46*

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
2382.065	2.1	0.2931	5.5127	374	393	(R)ECCDTQDSVACFSTQSPLLK(R)	Carbamidomethyl C (2), Carbamidomethyl C (3), Carbamidomethyl C (11), MODIC (20)	b3b10b14y2y3°y6y11°y14°
2453.0298	2	-0.505	5.7388	403	420	(K)GQEMCADYSENTFTEYKK(K)	Carbamidomethyl C (5), FL-1H20 (17), PYRALINE (18)	b2b4*b6°b8°b10b16y5

Q91X72-Hemopexin

CON

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1458.6973	2	-1.3471	5.9172	180	192	(R)SWSTVGNCTAALR(W)	Carbamidomethyl C (8), MODIC (13)	b1°b3°b9b10°y4y6y7°y12°y13
1796.8245	2	-6.8706	5.7067	178	192	(K)ERSWSTVGNCTAALR(W)	MOLD (2), Carbamidomethyl C (10), GH1 (15)	b3b4b5b7°b10b11b12y7°
1898.9692	3	2.3501	5.5812	205	218	(K)FLRFNPVTGEVPPR(Y)	AFGP (14)	b7*b9°y4y5°y11°y13°y14
2165.004	2.83	1.1256	5.6103	270	287	(R)GATYAFTGSHYWRLDSSR(D)	MODIC (13), MGH1 (18)	b7b7°b11°b13°y3°y5y13°y17°y18
3664.698	3	-1.4283	5.9156	124	150	(K)ENGYPKLFQEEFPGIPYPPDAAVECHR(G)	CROSSLINE (6), Carbamidomethyl C (25), CROSSLINE (27)	b4°b11*b16b20b24°y15
3700.6406	3	2.5309	5.5009	124	150	(K)ENGYPKLFQEEFPGIPYPPDAAVECHR(G)	AFGP (6), Carbamidomethyl C (25), AFGP (27)	b3°b4b8°b9*b11*b13*b14b16y6°y11°
2742.2449	3	2.0443	5.6874	130	150	(K)LFQEEFPGIPYPPDAAVECHR(G)	Carbamidomethyl C (19), AFGP (21)	b4b4°b11°b13°b21°y5y8°y11y17y19

DIAB

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1773.9154	3	-5.1021	5.8736	331	345	(K)GGNNLVSGYPKRLEK(E)	IMIDAZOLONEB (12)	b3b5b9y2y4°y6°y8
3836.9255	4	1.8809	6.1527	92	122	(K)NPITSVDAAFRGPDSVFLIKEDKVWVYPPEK(K)	AFGP (20), MOLD (23)	b1b3*b4°b5°b6°b8°b26*y3y4°y6y7°y26
1420.7775	2.41	-1.5253	6.0123	440	451	(K)LNAAKSLPQPQK(V)	FL-2H2O (12)	b2b4b6*b7b7*y12
1883.9084	3	1.3181	6.0198	166	177	(R)KWFWDFATRTQK(E)	AFGP (1)	b1b2b5b7b8°b11*y4y8y12
1963.9401	3	3.0335	6.2766	167	179	(K)WFWDFATRTQKER(S)	MOLD (8), FL-1H20 (11)	b2b3b4b6b10b10*b10°b12°y4°y7y9*y11*
1991.878	2.73	-2.0969	6.3124	225	239	(R)DYFVSCPGRGHGRPR(N)	Carbamidomethyl C (6), MOLD (9), GH1 (13), IMIDAZOLONEB (15)	b2°b3b5°b11°b13b13°b14°b15y8y12°y13y15
2245.1658	2.49	-7.1693	6.1043	92	111	(K)NPITSVDAAFRGPDSVFLIK(E)	MOLD (11), MOLD (20)	b3b4°b6b16y8°y13y19°

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
2368.149	2.19	-3.0287	6.0532	72	89	(K)GEFVWRGHSGTRELISAR(W)	AFGP (6), GH1 (12)	b5b8b12b14y9y16y17°y18
2453.2014	2	-0.0656	6.1443	112	129	(K)EDKVWVYPPEKKENGYPK(L)	FL-2H2O (3), MOLD (11), CEL (18)	b1b2b2°b3b3°b5b6°b8°b10b15°b16°b17*y3y18
2742.257	3	-0.042	6.0231	130	150	(K)LFQEEFPGIPYPPDAAVECHR(G)	Carbamidomethyl C (19), AFGP (21)	b4*b5b8b8°b10b12°b13*b18°y10y12y12°y13°y15
3514.651	4	-0.5984	6.1403	346	376	(K)ELGSPPGISLETIDAAFSCPGSSRLYVSSGR(R)	Carbamidomethyl C (19), IMIDAZOLONEB (24), AMADORI (31)	b1°b5°b8°b10°b12b25°y3y5°y9°y14y18y23
3665.819	3.73	-0.5246	6.6848	343	376	(R)LEKELGSPPGISLETIDAAFSCPGSSRLYVSSGR(R)	Carbamidomethyl C (22), MODIC (27), MOLD (34)	b2°b3b4b5b7°b14°b21b23b24°b27b29b34b34°y5°y7y10y14y15°y17y18°y21y24°y26y31y34
3816.8882	3	-2.7438	6.0345	342	376	(K)RLEKELGSPPGISLETIDAAFSCPGSSRLYVSSGR(R)	Carbamidomethyl C (23), GH1 (28), GH1 (35)	b3°b5b6b6°y3°y4y4°y10y20y26y26°
4248.9077	3.11	1.8475	6.0468	255	287	(R)CSPDPGLTALLSDHRGATYAFTGSHYWRLDSSR(D)	Carbamidomethyl C (1), AFGP (15), IMIDAZOLONEB (28), IMIDAZOLONEB (33)	b2b2°b12°b15b16°b17°b25b26y2y2°y10y12y20y20°y33
4317.153	3	0.4851	6.1175	370	400	(R)LYVSSGRRLWWLDLKSGAQATWTEVSWPHEK(V)	CROSSLINE (7), CROSSLINE (8), FL-2H2O (31)	b6°b13°b15y3y3°y6y11y12°y15*y18y19*y21y30*

DIAB HYD

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1793.8738	2	-0.6466	6.3755	166	177	(R)KWFWDFATRTQK(E)	PYRALINE (1), CEL (12)	b2b9b10°b11y3y5*y7°y8*y10°y12*
2114.041	2	-4.5657	5.5993	175	192	(R)TQKERSWSTVGNCTAALR(W)	MOLD (5), Carbamidomethyl C (13)	b3*b3°b10b10*b17b17*y7y9y15*y17*
2133.0615	2	-1.4074	6.0576	166	179	(R)KWFWDFATRTQKER(S)	CEL (1), AMADORI (9)	b1b6b10b11y5*y10°

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
2159.0562	2.05	0.1099	6.4378	175	192	(R)TQKERSWSTVGNCTAALR(W)	GH1 (5), Carbamidomethyl C (13), MGH1 (18)	b2*b2°b5b6b7b10*b12°y9y14y15*y17°
2173.0378	2.06	10.4917	6.0456	270	287	(R)GATYAFTGSHYWRLDSSR(D)	MOLD (13), MOLD (18)	b4b4°b5°b6°b9°b13b18y2y5°y7°y10y15y18
2218.0515	2.91	1.6563	6.1346	166	179	(R)KWFWDFATRTQKER(S)	MOLD (9), AFGP (12)	b1b3b4b8°b9b9°b10°b11y5*y6*y11*y14
2919.4045	2.62	-0.2607	6.3955	175	196	(R)TQKERSWSTVGNCTAALRWLER(Y)	PYRALINE (3), AMADORI (5), Carbamidomethyl C (13)	b1b2°b4b7b8*b10b11b12°b19*y5y7y8y14*y22
3515.7307	3.6	-5.3796	6.3274	205	233	(K)FLRFNPVTGEVPPRYPLDARDYFVSCPGR(G)	MODIC (3), MGH1 (20), Carbamidomethyl C (26)	b2b8*b11°b17*b21b23y7°y8y11y12y18y24
3516.7021	3.83	2.274	6.0451	346	376	(K)ELGSPPGISLETIDAAFSCPGSSRLYVSSGR(R)	Carbamidomethyl C (19), CROSSLINE (24), MGH1 (31)	b6b8b13°b18b22°y2y4y7y9°y20y21
4366.956	3	-8.5979	6.0596	219	254	(R)YPLDARDYFVSCPGRGHGRPRNGTAHGNSTHPMHSR(C)	Carbamidomethyl C (12), AFGP (21), MODIC (36)	b1b3b11°b12b12°b19b20°b22*y5y7y11y13

DIAB AMG

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
2052.9453	2.74	0.3321	5.6163	225	239	(R)DYFVSCPGRGHGRPR(N)	Carbamidomethyl C (6), CROSSLINE (13), GH1 (15)	b1b2°b3b5b5°b11°b15y2y4y7
5636.4565	3.68	-3.5648	6.2454	33	77	(R)VAEVENGTKPDSDVPEHCLDTWSFDAATMDHNGTMLFFKGEFVWR(G)	FL-1H20 (9), Carbamidomethyl C (18), FL-1H20 (39), AMADORI (45)	b2b9°b14b19b19°b20b24*b26*y8°y9°y10y14
1230.6	2	-5.0293	5.239	92	102	(K)NPITSVDAAFR(G)	GH1 (11)	b3*b4*b5°b6°b7*y5y6y7°y11
1438.7922	2	1.5956	5.4117	440	451	(K)LNAAKSLPQPQK(V)	FL-1H20 (12)	b3b4y4y7*y9
1901.9095	3	1.408	5.6446	166	177	(R)KWFWDFATRTQK(E)	FL-1H20 (1), FL-1H20 (12)	b4b9b10y5*y6y8*y9°

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
2115.004	2	4.5684	5.6933	270	287	(R)GATYAFTGSHYWRLDSSR(D)	GH1 (18)	b5b14b15°b17°y3°y6y10°y12y15
2313.0754	2.76	-1.5007	5.9116	234	254	(R)GHGRPRNGTAHGNSTHPMHSR(C)	MOLD (4)	b11b14b17y3y3°y4y12*y15y15*y18y21
2367.1306	2.24	0.257	5.7742	234	254	(R)GHGRPRNGTAHGNSTHPMHSR(C)	MOLD (4), MGH1 (21)	b13b16°b18°y7y10y10°y11y13*y16°y17y18*y21
2422.0967	3	1.6634	5.5661	234	254	(R)GHGRPRNGTAHGNSTHPMHSR(C)	IMIDAZOLONEB (6), Oxidation M (18)	b5b12b14°b15*b18°b19*b20b20*y6y11y13°y14°y17
2430.126	3	-6.0668	5.6313	178	196	(K)ERSWSTVGNCTAALRWLER(Y)	MOLD (2), Carbamidomethyl C (10), MOLD (15), GH1 (19)	b3b4b4°b8b8°b15y10y15
2823.3943	3	0.273	5.6193	92	114	(K)NPITSVDAAFRGPDSVFLIKEDK(V)	IMIDAZOLONEB (11), AMADORI (23)	b2b5°b8b8°b19*y2°y3°y7y8°y11y20

Q61646- Haptoglobin

CON

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1806.9122	2	7.1349	5.4205	212	227	(K)DYIAPGRVGYVSGWGR(N)	MGH1 (7)	b1b3b3°b4b7y4
2013.931	2.77	-4.3228	5.6702	250	263	(K)CVVHYENSTVPEKK(N)	Carbamidomethyl C (1), AMADORI (13), AMADORI (14)	b1b4b10b12°b13b13°y3°y7y14*
1825.9347	2.48	7.7932	5.4905	237	249	(R)LKYVMLPVADQDK(C)	AFGP (2), MODIC (13)	b2b11*b13°y4*y8°y9y10*y13
1828.8971	2.57	-4.1312	6.2156	212	227	(K)DYIAPGRVGYVSGWGR(N)	MODIC (7), GH1 (16)	b2b4°b7°b8b12°b15b16y4y5y5°y7y7°y11y16
2289.1904	3.27	-7.4907	6.0372	124	143	(R)HGLTTGATLISDQWLLTTAK(N)	AMADORI (20)	b3b5b6b17°b18b20y2y5y9y12
2441.1797	3.52	-3.448	5.8495	83	102	(K)LPECEAVCGKPKHPVDQVQR(I)	Carbamidomethyl C (4), Carbamidomethyl C (8), MODIC (10), CML (12)	b2b11b13°b17b18b18°b19°b20y2*y13°y18y20

DIAB

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1864.9344	3	-1.8575	5.8652	103	119	(R)IIGGSMDAKGSFPWQAK(M)	CEL (17)	b6°b7b8b14b15*y7*y10*y12y13y16
3458.6965	3.62	-4.5373	6.1463	54	82	(R)QFYRLRAEGDGVYTLNDEKQWVNTVAGEK(L)	MODIC (4), MODIC (19)	b8*b10b15b21b23y19*y20°y23°
1032.5217	2	3.6702	6.0733	95	102	(K)HPVDQVQR(I)	MGH1 (8)	b4b4°b5°b7*y3y7°
1446.7777	3	-3.4768	6.0639	157	168	(K)DITPTLTLYVGK(N)	FL-2H2O (12)	b4b8b9°y4y6°y10
1489.7546	2	-1.0419	6.5221	228	238	(R)NANFRFTDRLK(Y)	MGH1 (5), MGH1 (9)	b2*b3b5b6b9b10y4°y8y10
2495.1868	2.11	-9.2112	6.1419	83	102	(K)LPECEAVCGKPKHPVDQVQR(I)	Carbamidomethyl C (4), Carbamidomethyl C (8), PYRALINE (12), GH1 (20)	b4°b11b13b13°b15°b17°y3y4y6°y7y8°y9y9°y10°y15*y16y18°y20
2548.2588	3	-7.9189	5.9392	103	123	(R)IIGGSMDAKGSFPWQAKMISR(H)	Oxidation M (18), CROSSLINE (21)	b2b5°b9b12°b16*y7*y8y9°y16*y21

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
3026.484	3	1.7647	5.9603	58	82	(R)LRAEGDGVYTLNDEKQWVNTVAGEK(L)	AMADORI (2), CEL (25)	b15b21b23°y2°y5°y8*y19y24*y25
3516.717	3.74	3.9829	6.0012	54	82	(R)QFYRLRAEGDGVYTLNDEKQWVNTVAGEK(L)	CEL (19), CML (29)	b1*b9y3y4°y11y25*y29
3625.7605	4.05	-2.7785	6.2734	73	102	(K)QWVNTVAGEKLPECEAVCGKPKHPVDQVQR(I)	MODIC (10), Carbamidomethyl C (14), Carbamidomethyl C (18), CEL (20), CML (22)	b1b2b3*b6b6*b7b7°b8*b10°b11*b14°b16b21*b30y2y8*y14y20y24y24°y25°y28
3840.9812	3	0.3823	6.111	124	156	(R)HGLTTGATLISDQWLLTTAKNLFLNHSETASAK(D)	CROSSLINE (20), MOLD (33)	b14*b18*b19°b20*b29y3°y4y17*y18y20*y23y24*
4329.175	3	-0.6635	5.9476	250	286	(K)CVVHYENSTVPEKKNLTSPVGVQPILNEHTFCAGLTK(Y)	Carbamidomethyl C (1), FL-2H2O (14), Carbamidomethyl C (32), MODIC (37)	b4b6b13°b15°b16b20y19y32
4527.16	3.61	-5.3742	6.5239	250	286	(K)CVVHYENSTVPEKKNLTSPVGVQPILNEHTFCAGLTK(Y)	Carbamidomethyl C (1), FL-1H20 (13), PYRALINE (14), Carbamidomethyl C (32), PYRALINE (37)	b2b4b22b24*b27*b28b32°y12°y14y35
DIAB HYD								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
1828.8925	2.59	-1.0559	6.0332	212	227	(K)DYIAPGRVGYVSGWGR(N)	MODIC (7), GH1 (16)	b4°b5°b6b6°b7°b8b8°b13b13°b14°y4y5°y8°y16
2283.0835	3	1.1203	6.0198	95	111	(K)HPVDQVQRIIGGSMDAK(G)	AMADORI (8), AFGP (17)	b3b4b6°b10*b14*y8°y12°y16°y17
3026.486	3	4.1097	6.0791	58	82	(R)LRAEGDGVYTLNDEKQWVNTVAGEK(L)	AMADORI (2), MODIC (15), MODIC (25)	b8b9b9°b11°b21y7°y9*y10°y13y24y25

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
3121.5083	3.74	3.7257	5.9796	212	236	(K)DYIAPGRVGYVSGWGRNANFRFTDR(L)	MODIC (7), MOLD (16), AMADORI (25)	b5b6b22*b24y2y5°y9y11y12y18y25
3977.8962	3.44	-0.0892	6.485	233	262	(R)FTDRLKYVMLPVADQDKCVVHYENSTVPEK(K)	FL-2H2O (6), FL-2H2O (17), Carbamidomethyl C (18), FL-1H20 (30)	b10°b11°b18b20b21°b26y3y4y5°y7y10y16y20*y20°y21y24°
5007.6577	3.57	8.1531	5.9795	124	168	(R)HGLTTGATLISDQWLLTTAKNLFLNHSETASAKDITPTLTLYVGK(N)	MODIC (20), CEL (33), CML (45)	b5b6°b7b9°b11b12°b15*b16*b20°b21*b22b24b26*b33*b41y3y12y44*
DIAB AMG								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
3837.9033	4	-8.7464	5.9896	112	143	(K)GSFPWQAKMISRHGLTTGATLISDQWLLTTAK(N)	Oxidation M (9), AMADORI (12), FL-1H20 (32)	b1b3°b10°b11*b12b13°b15*b22y4y6y11y20°
1492.7566	2	6.9907	5.8071	112	123	(K)GSFPWQAKMISR(H)	MODIC (8), MOLD (12)	b8b9b9°b11y3y4°y7*y10*y11*
1607.7301	2	-2.4776	6.5136	83	94	(K)LPECEAVCGKPK(H)	Carbamidomethyl C (4), Carbamidomethyl C (8), CML (10), AMADORI (12)	b2b3b4°b5b8b10°b12°y1y7y9y11y11°
1623.7863	2	-5.5259	5.9197	228	238	(R)NANFRFTDRLK(Y)	MOLD (5), MOLD (9), FL-1H20 (11)	b3b5*b8°b10*y1y3y6y9°y11
1671.7926	2	-1.6455	6.2381	219	232	(R)VGYVSGWGRNANFR(F)	MOLD (9), GH1 (14)	b3b5b7b11b13*y11°y12y14
2375.3127	2.74	-7.3085	6.3309	193	211	(K)LKQRVLVTERVMPICLPSK(D)	Carbamidomethyl C (15), PYRALINE (19)	b1b2b3b17b18°y3y3°y5°y6y7°y8y9y12°y13y18y19
2950.4055	3	-8.6666	6.0392	212	236	(K)DYIAPGRVGYVSGWGRNANFRFTDR(L)	MODIC (16), GH1 (25)	b3°b4°b8b10°b20b25b25°y3y6°y7°y8y9°y12°y17*y20y22*
2972.4336	4	-0.1245	6.0263	212	236	(K)DYIAPGRVGYVSGWGRNANFRFTDR(L)	MOLD (7), MOLD (21)	b2°b11b18°b22*y2°y4y4°y8y9°y11y11*

Q07456- Protein AMBP

CON

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
2236.1543	3.61	-2.8907	4.6763	149	165	(K)LYGREPQLRDSLLQEFK(D)	FL-1H20 (17)	b8b8*b9b9*b10b11y5y9y9*y13*y17
2475.078	3.5	2.8871	4.3309	331	348	(K)ECKEYCGVPGDGYEELIR(S)	Carbamidomethyl C (2), CROSSLINE (3), Carbamidomethyl C (6), MOLD (18)	b1b1°b2b2°b10y4°y5y10y11°y18
2971.4226	4	5.7215	4.3897	19	42	(R)ADPASTLPDIQVQENFSESRIYGK(W)	AMADORI (20), FL-1H20 (24)	b3°b4b5b10b13b21b24*y7y8°y12*
4248.303	2	-5.0516	4.9271	149	184	(K)LYGREPQLRDSLLQEFKDVALNVGISENSIIFMPDR(G)	MODIC (4), MOLD (36)	b3b10b18b23°y2y3y5°y10*y18y24*y26°

DIAB

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1498.7476	2.55	-3.1686	4.613	100	110	(K)TDIDGKFLYHK(S)	AMADORI (6)	b2b4°b5b7°b10y11
1974.8545	2.05	8.8433	4.4404	321	333	(K)GNGNKFYSEKECK(E)	AFGP (10), Carbamidomethyl C (12), FL-1H20 (13)	b6*b8°b9°b12y7y9°y11y13
2332.2405	2.83	0.2423	5.1035	204	225	(R)RAVLPQESEGSGTEPLITGTLK(K)	MOLD (1)	b8b14°b21°y3y3°y11y12y15°y16y18*y22
3121.5203	3.7	4.7387	5.4084	60	86	(K)DKMSVSTLVLQEGATETEISMTSTRWR(R)	Oxidation M (3), MOLD (25)	b1b1°b3b4°b5b11b12b13*b15°b22b22°y19*y23y27
1600.8225	2	-3.3173	5.0268	100	112	(K)TDIDGKFLYHKSK(W)	MOLD (13)	b2°b3b5b6b7°b8°b11°b13y3y6y7
3497.6582	3.43	-4.4341	5.2361	297	325	(R)AFIKLWAFDAAQGKCIQFHYGGCKGNGNK(F)	FL-2H2O (4), Carbamidomethyl C (15), Carbamidomethyl C (23), MODIC (24), MOLD (29)	b2b12b15*b23y2y5y8y8*y10y10*y13*y14y19y22
3625.7627	4.06	0.3764	5.5227	58	86	(R)IKDKMSVSTLVLQEGATETEISMTSTRWR(R)	AFGP (2), CML (4)	b10b10°b11b16b18b20°b29y5y8°y15y19*y20°y23y24y27*

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
2079.9507	4	1.1846	5.4478	43	57	(K)WYNLAVGSTCPWLSR(I)	Carbamidomethyl C (10), AFGP (15)	b2b3b9b10b15b15°y1y5y5°y9y12y13*y13°
2173.029	2.06	2.2655	5.1374	185	201	(R)GECVPGDREVEPTSIAR(A)	Carbamidomethyl C (3), CROSSLINE (8), MOLD (17)	b3b5°b6°b9°b10b12°b15°b16y3y4y9y13y17
3083.4973	2.94	-2.8266	5.4082	62	87	(K)MSVSTLVLQEGATETEISMTSTRWRR(G)	Oxidation M (1), MOLD (25), MOLD (26)	b6°b7b9b11b11*b12*b14b15°b24*y1y4y5°y7y13y14°y19°y22y22*y25y25°y26
3783.8054	3	-0.7643	5.4608	60	87	(K)DKMSVSTLVLQEGATETEISMTSTRWRR(G)	AFGP (25), CROSSLINE (27), MOLD (28)	b2°b3b4°b5b9°b12*b15°b20°b25*y4y10°y13°y14y17°y22y23
4161.1646	5.2	3.3548	5.1665	6	42	(R)TLFLLLTACLASRADPASTLPDIQVQENFSESRIYGK(W)	Carbamidomethyl C (9), MODIC (33)	b5°b21b28y3y8y17*y37

DIAB HYD

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1973.8544	2.02	-3.4292	4.7196	311	325	(K)CIQFHYGGCKGNGNK(F)	Carbamidomethyl C (1), Carbamidomethyl C (9), CEL (10), AMADORI (15)	b3b10b10*b12y5y12*y15
1991.8833	2.75	-0.4223	5.2098	311	325	(K)CIQFHYGGCKGNGNK(F)	Carbamidomethyl C (1), Carbamidomethyl C (9), CROSSLINE (10)	b5b9b13*b14y10y13*y15*
1994.947	2.81	4.0537	4.8915	85	99	(R)WRRGVCEEITGAYQK(T)	IMIDAZOLONEB (2), Carbamidomethyl C (6)	b1b3b13b15°y2y3y7°y8°y12*y14°y15y15*
2312.2007	2	-1.2216	5.1489	149	165	(K)LYGREPQLRDSLLQEFK(D)	AMADORI (4), CML (17)	b5°b10y9*y11*y12*y16
2495.1912	2	8.7909	4.8431	87	105	(R)RGVCEEITGAYQKTDIDGK(F)	MOLD (1), Carbamidomethyl C (4), AFGP (13), MODIC (19)	b3b8°b12b14b14°y4y5y7y9*y10*y12y13*

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
2707.4277	3	1.2934	4.9146	136	157	(K)KSSHHHGLTITAKLYGREPQLR(D)	MODIC (1), IMIDAZOLONEB (22)	b2°b7°b11°b12b18°b19y4y5*y8*y10y16*y18*
3315.6228	6	-2.8987	4.9746	58	84	(R)IKDKMSVSTLVLQEGATETEISMTSTR(W)	CROSSLINE (2), PYRALINE (4)	b3b6°b7b13*b14°b20*y3y7y9y11y14°y16°y23
3497.6592	4	-1.5085	4.8376	297	325	(R)AFIKLWAFDAAQGKCIQFHYGGCKGNGNK(F)	MOLD (4), AMADORI (14), Carbamidomethyl C (15), Carbamidomethyl C (23)	b3b10°b13*y3y5*y9y10*y19
DIAB AMG								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
1971.9456	2	1.2895	5.4381	43	57	(K)WYNLAVGSTCPWLSR(I)	Carbamidomethyl C (10), AMADORI (15)	b2b3*b5*b6b10*b11b11*b13°b14*y2°y4°y5°y6y8°y14°
1991.8806	2.71	-1.7778	6.0432	311	325	(K)CIQFHYGGCKGNGNK(F)	Carbamidomethyl C (1), Carbamidomethyl C (9), CROSSLINE (15)	b5b10*b12y1y3y7y10*y11y12y15
2332.2383	2.94	4.903	4.8779	204	225	(R)RAVLPQESEGSGTEPLITGTLK(K)	MOLD (22)	b9*b13°b14*b15*b19b20b20*y3y4y13y14y18*y20°y21*y22
2443.0771	2.66	-2.5247	5.2209	311	330	(K)CIQFHYGGCKGNGNKFYSEK(E)	Carbamidomethyl C (1), Carbamidomethyl C (9), MOLD (20)	b4b12b13b15*y3y3°y14*y18
2852.449	2	1.686	5.0887	88	110	(R)GVCEEITGAYQKTDIDGKFLYHK(S)	Carbamidomethyl C (3), MODIC (12), MODIC (18), PYRALINE (23)	b3b5°b14b16y3y4y6y14°
1745.8915	3	1.0447	5.3057	297	310	(R)AFIKLWAFDAAQGK(C)	PYRALINE (4), CEL (14)	b2b10°b14y3*y4y5*y6°y11*y13y14
1853.9392	2.26	-2.3687	5.3124	297	310	(R)AFIKLWAFDAAQGK(C)	FL-1H20 (4), FL-1H20 (14)	b3b9b12°y8*y9y9°y12y14
1901.9175	2.95	-1.374	5.5877	85	99	(R)WRRGVCEEITGAYQK(T)	MOLD (2), Carbamidomethyl C (6)	b8b9b14y1y2*y6y8°y11y12y12*y15

P07759- Serine protease inhibitor A3K								
CON								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
1895.926	2.61	-0.5711	6.0825	177	192	(K)NLINDYVSNQTQGMIK(E)	CML (16)	b1b5*b13y6°y10°
1981.958	2.7	-3.0088	6.9217	177	192	(K)NLINDYVSNQTQGMIK(E)	FL-1H20 (16)	b6°b8°b11b13b14b14°b16b16*y2y8*y12°y13y13*y15*y16y16*
3517.6963	4	-1.5928	6.81	323	350	(R)LEEDVLPEMGIKEVFTEQADLSGITETK(K)	FL-1H20 (12), CROSSLINE (28)	b1b2°b3°b6°b8b11b17b19b19°b21y5°y6y9°y10°y12y16y17°y19*y20*y23*y26°
1950.982	2.93	5.4111	6.4133	283	297	(R)MQQVEASLQPETLRK(W)	MOLD (14), FL-1H20 (15)	b3*b7b10y6y6°y10y14y15y15*
2011.9781	2.86	-1.4282	6.4749	335	351	(K)EVFTEQADLSGITETKK(L)	CML (16), CML (17)	b4b11y2y4°y12*y17
2267.0618	2	-3.7617	6.5506	158	176	(R)ALYQTEAFTADFQQPTEAK(N)	PYRALINE (19)	b2b8b8*b10b11°b13°y3y3°y5y10*y14°
3440.6316	4	0.0281	6.8758	323	350	(R)LEEDVLPEMGIKEVFTEQADLSGITETK(K)	AFGP (12), MOLD (28)	b2°b3b9°b10b12°b15°b17°b21*b22°y2y3°y4°y10y20y26*
3625.7583	3	-4.6821	6.6753	323	350	(R)LEEDVLPEMGIKEVFTEQADLSGITETK(K)	CROSSLINE (12), CROSSLINE (28)	b3b4b16b20*b25y2°y3y14
3665.8174	3.7	5.5685	6.7883	125	155	(S)LSQPEDQDQINIGNAMFIEKDLQILAEFHEK(T)	Oxidation M (16), MODIC (31)	b3b4b4°b5°b14*b15*b17*b18b21°b23*b23°b31y5y19°y21y21°y31
DIAB								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
1950.9797	2.9	-2.0119	6.7753	283	297	(R)MQQVEASLQPETLRK(W)	MOLD (14), FL-1H20 (15)	b3*b7b9b10b14°b15y7°y8y15
2767.4988	3.73	6.3682	6.8016	300	322	(R)KTLFPSQIEELNLPKFSIASNYR(L)	MODIC (15), MODIC (23)	b1b12°b21y1y2y3y4y4°y5*y10*y12y19y19°y20°y23y23*

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
2834.3025	2.39	-4.0885	6.9314	216	235	(K)WKISFDPQDTFESEFYLDEK(R)	CROSSLINE (2), CML (20)	b6°b9b11*b15b16*b16°y2y2°y6y9y12y13°y14y15°
2848.3176	2.47	-2.2621	6.8133	216	235	(K)WKISFDPQDTFESEFYLDEK(R)	CROSSLINE (2), CEL (20)	b3b8°b12y3y4y7°y8y8°y10°y12°y15y18y20y20*
2950.4111	3	-2.2788	7.1274	214	236	(K)GKWKISFDPQDTFESEFYLDEKR(S)	MODIC (2), MOLD (4)	b10°b11b18°b20°y9°y10y12y15*y20y20°y21y23
2972.402	3	-1.1642	6.9452	214	236	(K)GKWKISFDPQDTFESEFYLDEKR(S)	MOLD (2), CML (22)	b4b5b18*b19b20*b22*b23°y4y7y12y17y22y23
3390.6047	3	0.1261	6.9069	218	244	(K)ISFDPQDTFESEFYLDEKRSVKVPMMK(M)	Oxidation M (25), PYRALINE (27)	b3b8*b12b13°b14°b15°b21b22°b23*y2y3y15y20y27
3699.817	3.56	-2.2612	6.9487	323	351	(R)LEEDVLPEMGIKEVFTEQADLSGITETKK(L)	CROSSLINE (12), MODIC (28), AMADORI (29)	b5°b7b8°b10°b11b19°b20b25°b29y1y13*y19y20*y22y22*y29
4176.9937	4.68	-8.2777	6.6393	125	157	(S)LSQPEDQDQINIGNAMFIEKDLQILAEFHEKTR(A)	FL-1H20 (20), AMADORI (31)	b1b9b11*b12°b14b15*b15°b22*b24y7y8y13*y15y18y22*y33
DIAB HYD								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
1895.918	2.66	0.6476	6.941	177	192	(K)NLINDYVSNQTQGMIK(E)	CML (16)	b1b4*b5°b7*b8b13°b14*y2y3y8°y9y12y13y16
2116.0217	2.03	-9.4493	6.8472	335	351	(K)EVFTEQADLSGITETKK(L)	CML (16), AMADORI (17)	b4b6b7b7°b8b8°b12°b13°b14b14*b15b17y4°y5°y6y11°y17
2767.4922	3.71	4.0195	6.9118	300	322	(R)KTLFPSQIEELNLPKFSIASNYR(L)	MODIC (15), MODIC (23)	b6°b17b17*b19*b21b23y1y3y5y5*y7y7*y9*y10y15*y15°y19y23
2834.3232	2.43	-0.7045	6.6185	216	235	(K)WKISFDPQDTFESEFYLDEK(R)	CROSSLINE (2), CML (20)	b7b8b12*b19y2y3°y5y6°y7°y10y20

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
2950.4045	2.54	1.9658	7.02	214	236	(K)GKWKISFDPQDTFESEFYLDEKR(S)	MODIC (2), MOLD (4)	b3b7°b9°b12°b15b15°b16°b20b22b23y4°y7y13°y20y23
3701.8184	4.56	4.893	6.9425	125	155	(S)LSQPEDQDQINIGNAMFIEKDLQILAEFHEK(T)	Oxidation M (16), CEL (31)	b3b6b11*b12*b15y4y26°

DIAB AMG

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1790.9062	2	-8.7526	6.3172	240	251	(K)VPMMKMKLLTTR(H)	AFGP (5), CEL (7)	b1b4b7b8b10y2y11°y12
2311.214	2	6.2634	6.6461	283	299	(R)MQQVEASLQPETLRKWR(K)	AMADORI (14), MOLD (15)	b3b5b6b6°b7*b9°b13°b15y13y17
2474.1067	2.84	1.3754	6.8713	218	236	(K)ISFDPQDTFESEFYLDEKR(S)	PYRALINE (18)	b3b3°b4°b7°b9*b10*b14b19*b19°y3°y7°y11°y15°y17y19y19*
2767.496	4	5.3564	6.2865	300	322	(R)KTLFPSQIEELNLPKFSIASNYR(L)	MODIC (1), MODIC (15)	b21°b22°y1y4°y7y12y22*y23
3517.6914	3.74	-2.9858	6.8843	323	350	(R)LEEDVLPEMGIKEVFTEQADLSGITETK(K)	FL-1H20 (12), CROSSLINE (28)	b1b12b19y4y11y14y17*y21*y28
3684.9517	3	-4.7211	6.6976	63	93	(K)LALKNPDTNIVFSPLSISAALALVSLGAKGK(T)	AFGP (4), AFGP (29), MODIC (31)	b1b7b9b10*b23b25b31*y7°y19y25
3994.9553	3	-1.3212	6.7688	252	282	(R)HFRDEELSCSVLELKYTGNASALLILPDQGR(M)	MOLD (3), Carbamidomethyl C (9), CROSSLINE (15), AMADORI (31)	b4°b5°b6b7°b11b23y5y13y22
5871.8115	4	-2.3792	6.6745	94	144	(K)TMEEILEGLKFNLTETPEADIHQGFGNLLQSLSQPEDQDQINIGNAMFIEK(D)	FL-2H2O (51)	b5b12°b23b26°y1y2°y3y17

P29699- Alpha 2 HS glycoprotein

CON

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
2755.2168	3.98	8.0193	6.6653	121	143	(K)QDGQFRV MHTQCHSTPD SAEDVR(K)	MGH1 (6), CarbamidomethylC (12)	b2°b3b9°b10°b12°b15°b17b19*b20*b22y6°y7y10°y12y21y22°y23
2879.2417	2.74	0.8262	6.754	121	143	(K)QDGQFRV MHTQCHSTPD SAEDVR(K)	Oxidation M (8), CarbamidomethylC (12), AMADORI (23)	b3b4b8°b9°b13b13*b16*b18y8y11°y23
2905.3577	2.44	8.181	6.254	226	248	(K)QHGFCKAN LMHNLGGEEV SVACK(L)	CarbamidomethylC (5), AFGP (6), CarbamidomethylC (22), MOLD (23)	b4b6b12*b13b14y3y5y11°y12y13°y23
2987.2957	2.5	-2.3754	6.056	121	143	(K)QDGQFRV MHTQCHSTPD SAEDVR(K)	Oxidation M (8), CarbamidomethylC (12), AFGP (23)	b5b5°b6°b8*b11°b19*y4°y10y13°y15y15*y20°

DIAB

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1472.7932	2	5.9331	6.4677	58	67	(K)QVLNQIDK VK(V)	FL-1H20 (8), FL-1H20 (10)	b3*b4*b5*b6y4y6*y7*y8y10
2453.1995	2	-0.1617	6.2651	212	231	(K)EVTDPAKC NLLAEKQHGF CK(A)	CarbamidomethylC (8), MODIC (14), CarbamidomethylC (19), CEL (20)	b2b2°b4b5b6b7°b8b8°b18y1y4y8y9y9°y10°y14°y17°y20
2490.321	2.85	7.6473	6.7999	323	345	(K)VGQPGAAG PVSPMCPGRIR HFKI(-)	CarbamidomethylC (14), CML (22)	b4b5b5*b7b7*b11b12*b12°b13b13*b22*b23y3y8y10y11y12y15y17°y18y21*y22*y23
2755.2178	4.03	8.346	6.2896	121	143	(K)QDGQFRV MHTQCHSTPD SAEDVR(K)	MGH1 (6), CarbamidomethylC (12)	b3b10b13b23y6°y9y9°y10°y11y14°y21°y22°y23
2995.305	2.86	-4.8365	6.4999	121	144	(K)QDGQFRV MHTQCHSTPD SAEDVRK(L)	CarbamidomethylC (12), GH1 (23), FL-2H2O (24)	b1b5*b7b10°b11°b12°b13b15*b17b17°b21*y6°y8y10°y12y17°y18y24
3045.3853	2.56	9.5291	6.1083	121	144	(K)QDGQFRV MHTQCHSTPD SAEDVRK(L)	MGH1 (6), CarbamidomethylC (12), AMADORI (23)	b2*b4b9b10b10°b11b12b13*b18b21y9y10y11°y15°y17y20*y22*y23

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
4459.1177	3	-0.7176	6.2817	212	248	(K)EVTDPAKCNLLAEKQHGFCKANLMHNLGGEEVSVACK(L)	Carbamidomethyl C (8), CROSSLINE (14), Carbamidomethyl C (19), MODIC (20), Oxidation M (24), Carbamidomethyl C (36)	b2b4°b5b6b6°b10b15*b17°b19b19°b25y3y4y12*y14*y16°y20

DIAB HYD

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1749.8577	2.47	-1.4596	6.718	212	225	(K)EVTDPAKCNLLAEK(Q)	FL-2H2O (7), Carbamidomethyl C (8), MODIC (14)	b1b1°b2b3b4°b5b5°b6b7b7°b12b14y4y6°y8*y11*y12°y14
2538.231	2	-1.2741	6.4537	212	231	(K)EVTDPAKCNLLAEKQHGFCK(A)	FL-1H20 (7), Carbamidomethyl C (8), MOLD (14), Carbamidomethyl C (19)	b1°b2b4°b5°b6b15y2y5y8*y13°y15

DIAB AMG

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1923.8691	2.32	0.9455	6.6226	219	231	(K)CNLLAEKQHGFCK(A)	Carbamidomethyl C (1), AFGP (7), Carbamidomethyl C (12), MOLD (13)	b4b6*b8b13y5y6y8y11
2603.2654	4	6.1238	6.5355	323	344	(K)VGQPGAAGPVSPMCPGRIRHFK(I)	Carbamidomethyl C (14), IMIDAZOLONEB (17), IMIDAZOLONEB (19)	b1b2b3*b4*b5b7b8b10b12b14b19b21°b22*y1y2y7y20°
2755.2205	4.04	9.2897	6.4277	121	143	(K)QDGQFRVMHTQCHSTPDSAEDVR(K)	MGH1 (6), Carbamidomethyl C (12)	b6*b8°b10b13°b22°y5y9y11y13y15°y19*y20*y23
2995.298	2.86	-2.5934	6.5714	121	144	(K)QDGQFRVMHTQCHSTPDSAEDVRK(L)	Carbamidomethyl C (12), GH1 (23), FL-2H2O (24)	b4b5b8°b10*b12°b13*b17b17*b21b22b22*y4°y6y6°y12°y15°y16y16°y20*y20°y21

P02088- Hemoglobin subunit beta 1

CON

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
2495.1938	2	-4.0917	6.1766	10	31	(K)AAVSCLWGKVNSDEVGGEALGR(L)	Carbamidomethyl C (5), CML (9), AMADORI (22)	b2b4°b13*b15*b16*b19y1y7y12y19*y20y22
2538.1848	3	-1.2864	6.2277	1	18	(-)MVHLTDAEKAAVSCLWGK(V)	AFGP (9), Carbamidomethyl C (14), CROSSLINE (18)	b4b6°b9b15y18
2052.9265	2.7	-1.5073	6.4317	42	60	(R)YFDSFGDLSSASAIMGNAK(V)	CEL (19)	b8b12°b15b15°b16°y5y9°y12°y14y14*y15y15*y16*y19
2218.0435	2.88	-3.8616	6.2151	1	18	(-)MVHLTDAEKAAVSCLWGK(V)	FL-1H20 (9), Carbamidomethyl C (14), CML (18)	b2b4b10b11°b12b14°b15°y2y11°y13°
2990.4812	2.87	3.6428	6.1329	19	41	(K)VNSDEVGGEALGRLLVVYPWTQR(Y)	AFGP (13), AMADORI (23)	b3*b4*b7b8b12*b12°b13y8y14*y22

DIAB

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1864.9406	3	-8.4006	6.0634	68	83	(K)VITAFNDGLNHLDSLK(G)	PYRALINE (16)	b1b3°b5°b10b11b13b15y3y8°y10
2088.917	3	-8.3107	5.4434	42	60	(R)YFDSFGDLSSASAIMGNAK(V)	PYRALINE (19)	b14y3*y9°y10°y12
2538.1992	2.78	-0.145	6.4333	1	18	(-)MVHLTDAEKAAVSCLWGK(V)	AFGP (9), Carbamidomethyl C (14), CROSSLINE (18)	b3b7b11°b13°b15b18y12y13y16y18
3836.921	4	2.0016	6.4988	10	41	(K)AAVSCLWGKVNSDEVGGEALGRLLVVYPWTQR(Y)	Carbamidomethyl C (5), AFGP (22), MODIC (32)	b2b3b13b28°b30°y2y5*y6y7y13y20y20*y21°
2368.138	2	1.2915	6.1782	42	62	(R)YFDSFGDLSSASAIMGNAKVK(A)	Oxidation M (15), FL-1H_2O (21)	b3°b6b15y5y7*y12°y13y17*

DIAB HYD								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
1456.71	2	9.8304	6.1303	122	133	(K)DFTPAAQAAFQK(V)	AMADORI (12)	b3°y5y9y9*y11y12
2495.193	2	-9.0608	5.7246	10	31	(K)AAVSCLWGKVNSDEVGGEALGR(L)	CarbamidomethylC (5), CML (9), AMADORI (22)	b6°b10b13*b17°b20°b21°y6y10°y11y12y19*y20°
3238.6106	3.06	-2.1088	6.2212	68	96	(K)VITAFNDGLNHLDSLKGTFASLSELHCDK(L)	MODIC (16), CarbamidomethylC (27)	b3b6*b7*b8*b9°b12*b13°b14b16°b21b25b25*b28*b29y1y2y5°y8°y10y15y18
3836.9043	4	-2.2988	5.9875	10	41	(K)AAVSCLWGKVNSDEVGGEALGRLLVVYPWTQR(Y)	CarbamidomethylC (5), AFGP (9), MODIC (22)	b4b8°b9b13b15b18y2y4*y6*y7y9*y32
DIAB AMG								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
3238.6084	3	2.108	6.2047	68	96	(K)VITAFNDGLNHLDSLKGTFASLSELHCDK(L)	MODIC (16), CarbamidomethylC (27)	b3b7b11°b12b20°b21b23b27b28y3°y4y5y5°y11y12°y25°
3497.6626	3.73	-1.4176	6.4987	1	31	(-)MVHLTDAEKAAVSCLWGKVNSDEVGGEALGR(L)	FL-2H2O (9), CarbamidomethylC (14), CEL (18)	b1b3b4b9b10b12°b15°b19b23°b26*y1y3y5°y14y15y18°y19y24°y26y27
3518.7097	4	-0.3229	6.0062	67	96	(K)KVITAFNDGLNHLDSLKGTFASLSELHCDK(L)	CEL (1), CML (17), CarbamidomethylC (28), CML (30)	b7°b10b14*y3°y14°y20y23y25
3816.894	3	0.9903	6.3761	10	41	(K)AAVSCLWGKVNSDEVGGEALGRLLVVYPWTQR(Y)	CarbamidomethylC (5), FL-1H_2O (9), IMIDAZOLONE B (32)	b4°b6°b10°b14°b16°y5y6y20y22*

P22599- Alpha 1 antitrypsin 1 2								
CON								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
2311.2192	2	1.0945	5.9531	193	211	(K)ELDQDTVFALANYILFKGK(W)	FL-2H_2O (19)	b4b4*b5°b7*b10b14b17°y2y12*
2502.1287	3.32	-5.9659	6.0722	154	173	(K)NHYQAEVFSVNFAESEEAKK(V)	FL-2H_2O (19), MOLD (20)	b10*b14°b18*y3y5y7°y8°y13y17y18°y20*
2606.2126	5	-5.0215	6.3382	214	235	(K)KPFDPENTEEAEFHVDKSTTVK(V)	CML (17)	b11*b14°b15*b15°b16y18y19y21
2704.2295	2.38	-4.3957	6.1147	214	235	(K)KPFDPENTEEAEFHVDKSTTVK(V)	MOLD (1), MOLD (17), CML (22)	b3b7b9b12b14b14°b16*y4°y5°y12y15
2975.382	3	4.1383	6.2972	214	235	(K)KPFDPENTEEAEFHVDKSTTVK(V)	FL-2H_2O (1), CROSSLINE (17), MOLD (22)	b5°b10*b11b12b12*b13b14b15y18
6050.8936	4	0.3054	6.2978	236	287	(K)VPMMMLSGMLDVHHCSILSSWVLLMDYAGNASAVFLLPEDGKMQHLEQTLNK(E)	Carbamidomethyl C (15), FL-1H_2 O (42), MOLD (52)	b14b18°b21y2*y21*y25*y33y41
DIAB								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
1578.804	2	-0.5997	6.172	174	186	(K)VINDFVEKGTQGK(I)	FL-1H_2O (8)	b2b4b4*b10b10°y3*y5y5*y6°y11y13
2325.0378	2	-5.0438	6.213	154	172	(K)NHYQAEVFSVNFAESEEAK(K)	FL-2H_2O (19)	b4*b5b9b14*b19y4y10y14°y15°y18°y19
2632.3225	2.89	-0.714	6.3011	174	192	(K)VINDFVEKGTQGKIVEAVK(E)	AFGP (8), FL-2H_2O (13), AMADORI (19)	b1b5b5*b8*b10b11b11*b16y3y4y7°y9°y16°y19
2890.288	2.43	-6.7791	6.5184	214	235	(K)KPFDPENTEEAEFHVDKSTTVK(V)	FL-2H_2O (1), PYRALINE (17), PYRALINE (22)	b3b4b6b10°b12*b14b14*b19y3y4y7y8y10°y12y13y14°
3440.622	4	1.8002	6.4781	148	173	(K)FLEEAKNHYQAEVFSVNFAESEEAKK(V)	CROSSLINE (6), CEL (25), CEL (26)	b3b3°b5b7*b8°b11*b14°b15*b16*b19°b21b23y4y4°y6°y8y11y21

DIAB HYD								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
1578.8008	2	0.3165	6.4383	174	186	(K)VINDFVEK GTQGK(I)	MODIC (8), PYRALINE (13)	b4b4*b6b7b9°b12 y3y4°y6°y8y8°y13
1692.8784	2	-3.6745	6.4979	173	186	(K)KVINDFVEK GTQGK(I)	CEL (9), CML (14)	b10b10*b11°b12* b13*y11°y12y14
2311.214	2	-2.4504	6.6045	193	211	(K)ELDQDTVF ALANYILFKGK(W)	FL-2H_2O (17)	b2b4b4*b7*b12°b 13°b14b18*y1y4y1 7y18°y19
2346.2864	3	-2.1925	6.0882	173	192	(K)KVINDFVEK GTQGKIVEAV K(E)	FL-1H_2O (20)	b4b6b7°b16*y1y7° y19*y20
DIAB AMG								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
2860.5068	2.63	1.7241	6.2977	329	354	(R)IFNNGADLS GITEENAPLKL SKAVHK(A)	MODIC (19), CML (22)	b1b2b5*b9*b11°b 13b16b20b20*b24 y1y13°y15°y16°y26
1335.6862	2	- 10.3113	6.1513	144	153	(K)LVEKFLEEA K(N)	CEL (4), CML (10)	b1b3b5y3y4y5°y10
2089.9539	2	-2.9736	6.1618	214	230	(K)KPFDPENTE EAEFHVDK(S)	CML (17)	b4°b8b12b14b16y 3y7y10y11*
2311.2136	2	-5.8378	6.327	193	211	(K)ELDQDTVF ALANYILFKGK(W)	FL-2H_2O (17)	b1°b2b4*b5°b7*b1 0*b13b13°b14b15 b17*b19*y1y5y8y 11y13
3497.6487	3.69	1.0035	6.2953	210	235	(K)GKWKKPFD PENTEEAEFHV DKSTTVK(V)	AFGP (2), FL-1H_2O(21), MODIC (26)	b3b13b15*b17b19 b19*b20*y5y13y1 8y19
3976.879	3.49	0.2916	6.4221	144	173	(K)LVEKFLEEA KNHYQAEVFS VNFAESEEAKK (V)	AFGP (10), FL-1H_20 (29), MOLD (30)	b5b11*b16°b19*b 20b20*b21b21°b2 2b23°b25*b28y9y 13y15y17y17*
4671.4307	6	-2.0848	6.2704	309	350	(R)LSISGDYNL KTLMSPLGITRI FNNGADLSGIT EENAPLKLSK(A)	MODIC (10), CEL (39), CEL (42)	b1b9°b11b21b22y 1y6y13y19*y26°y3 8*

P01837- Ig kappa chain C region

CON

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
3231.4841	3	6.4184	6.0658	48	75	(R)QNGVLNSWTDQDSKDSTYSMSSTLTLTK(D)	Oxidation M (20), PYRALINE (28)	b4b11b13°b18°b20°b21*b23b24y2°y5y6°y13°y16°y22y23°
3925.7556	3	0.0183	6.312	48	80	(R)QNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYER(H)	FL-2H_2O (14)	b15*b16b22b26°y3y13y19y21
4556.0806	4.29	5.8103	6.1997	48	80	(R)QNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYER(H)	CROSSLINE (14), CROSSLINE (28), CROSSLINE (33)	b8b11b11°b13*b13°b15b18b19b23y7°y9°y17y18°

DIAB

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1901.9045	2	1.781	6.2094	92	106	(K)TSTSPIVKSFNRNEC(-)	AMADORI (12), Carbamidomethyl C (15)	b2°b3°b5b11b14y4y5y9*
2309.945	2	-4.7213	6.1437	76	91	(K)DEYERHNSYTCEATHK(T)	AFGP (5), Carbamidomethyl C (11)	b10b11b12*b13b13*b14°y7
3390.6055	3	3.3542	6.2388	35	61	(K)DINVKWKIDGSERQNGVLNSWTDQDSK(D)	CML (7), IMIDAZOLONEB (13), CML (27)	b1°b4*b6*b12b12°b13b14°b17°b26*y3y4y6y10°y19*

DIAB HYD

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1775.8577	2	-4.233	5.9409	92	106	(K)TSTSPIVKSFNRNEC(-)	MODIC (8), Carbamidomethyl C (15)	b6y4°y7*y11y12*y15
1937.921	3	6.2737	6.0329	92	106	(K)TSTSPIVKSFNRNEC(-)	MODIC (8), AMADORI (12), Carbamidomethyl C (15)	b1b1°b2b2°b3°b4°b5b7b11b13b14°y9y10°y12*
3925.7693	3	3.4571	6.2843	48	80	(R)QNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYER(H)	CEL (28), MGH1 (33)	b1*b5b15b16b17*b21°b23°b27*y3y4°y9y9°y11°y20y24

DIAB AMG								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
1793.88	2	-1.1627	6.2433	35	47	(K)DINVKWKIDGSER(Q)	FL-2H_2O (5), PYRALINE (7)	b4°b5b8b9*b10b12°y4°y8y12*
2309.9436	2	-8.1865	6.3834	76	91	(K)DEYERHNSYTCEATHK(T)	AFGP (5), Carbamidomethyl C (11)	b3b8b13°b15y3y7y9y12°y13
4320.913	3	3.3414	6.5978	42	75	(K)IDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTK(D)	AFGP (6), Oxidation M (26), AFGP (34)	b2°b4b5°b8b8*b10b14°b17b17°b18b21b23b32*y11y17°y20y28*

P01878- Ig alpha chain C region

CON

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
2032.04	2.86	-0.8483	5.328	44	62	(K)SGKDITTVNFPPALASGGR(Y)	FL-1H_20 (3)	b1°b3°b11b18y11*y19
2445.21	3.4	2.8888	5.492	255	274	(R)WLHGNEELSPESYLVFEPLK(E)	CML (20)	b2b4b5*b8*b13b15*b16b20y10y12°y16*y20
4948.4	6	-8.3222	5.339	1	43	(-)ESARNPTIYPLTLPPALSSDPVIIGCLIHDYFPSGTMNVTWGK(S)	AMADORI (4), Carbamidomethyl C (26), CML (43)	b2°b9*b22°y6°y7y15y17y18*y19y21°

DIAB

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
1655.81	2.71	4.5773	6.281	145	159	(R)NPEGAVFTWEPSTGK(D)	MODIC (15)	b9b10°b13y8y15
2441.18	3.28	-1.3871	6.442	145	165	(R)NPEGAVFTWEPSTGKDAVQKK(A)	MODIC (15), CML (20), CML (21)	b15b16*b18b20b21°y3*y8*y12y12°y18y19°y21
5453.63	4	5.1441	6.449	275	322	(K)EPGEGATTYLVTSVLRVSAETWKQGDQYSCMVGHEALPMNFTQKTIDR(L)	Carbamidomethyl C (30), Oxidation M (31), MODIC (44)	b1°b3°b6b7b12°b14°b25°y3y4y8*y9*y10°y11*y11°y15°y21*y24*y26*

DIAB HYD								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
4233.9	4.76	4.5601	6.423	160	194	(K)DAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFK(C)	AFGP (5), CML (6), Carbamidomethyl C (12), Carbamidomethyl C (14), Carbamidomethyl C (24), CML (35)	b3b3°b7*b23*b24b32y3y3°y5y5°y6y9°y10y11y15y20*y20°y23y23*y26y34°y35y35*
5073.52	4	0.4844	5.804	255	297	(R)WLHGNEELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAETWK(Q)	AMADORI (36), MOLD (43)	b8°b10°b13b31*b42*y4°y7y10y17
5489.47	3.73	-3.0052	6.387	298	344	(K)QGDQYSCMVGHEALPMNFTQKTIDRLSGKPTNVSVSVIMSEGDGICY(-)	Carbamidomethyl C (7), MOLD (21), AMADORI (25), CML (29), Carbamidomethyl C (46)	b1*b4b6*b14b16b17*b21b24°b40*y5y12°y18y37*
DIAB AMG								
Precursor MH+ (Da)	**z**	**MH+ Error (ppm)**	**Score**	**Start**	**End**	**Sequence**	**Modifications**	**BY Matches**
2415.25	2	9.7324	6.334	145	165	(R)NPEGAVFTWEPSTGKDAVQKK(A)	FL-2H_2O (20)	b3°b9°b10*b11°b12°b21y6y6°y7y10°y16°y20*y21y21*
2441.18	3.56	-1.6329	6.137	145	165	(R)NPEGAVFTWEPSTGKDAVQKK(A)	MODIC (15), CML (20), CML (21)	b14y3*y4*y8°y19*y20y21

Precursor MH+ (Da)	z	MH+ Error (ppm)	Score	Start	End	Sequence	Modifications	BY Matches
5052.27	3.86	-1.3683	6.301	145	186	(R)NPEGAVFTWEPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAER(W)	AFGP (15), MOLD (20), AMADORI (21), Carbamidomethyl C (27), Carbamidomethyl C (29), Carbamidomethyl C (39)	b6*b14°b15b18b22*b25*y4°y27