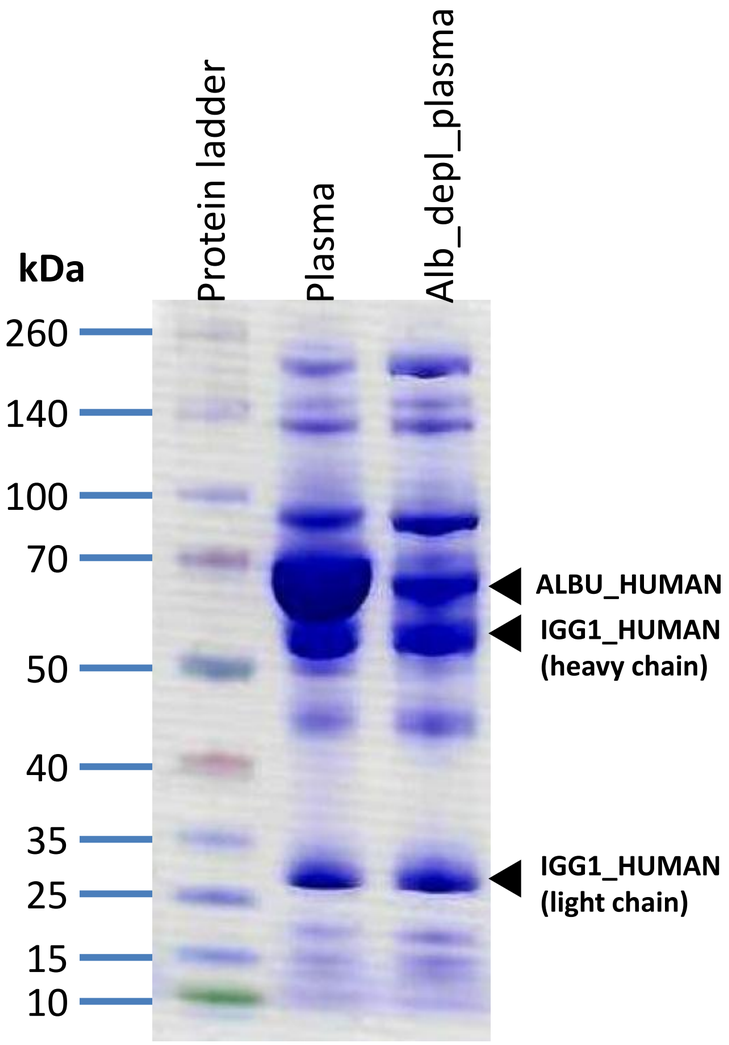
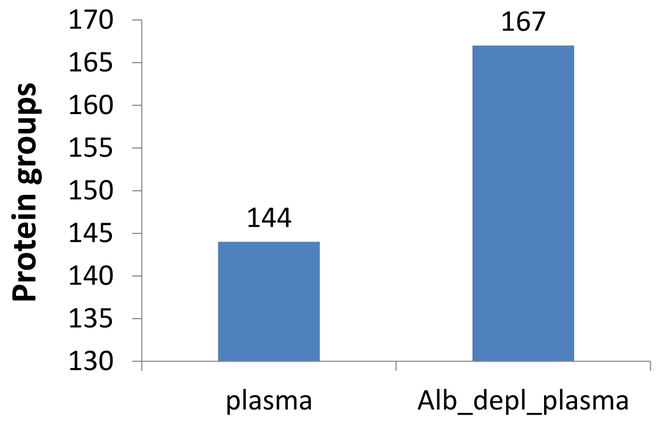
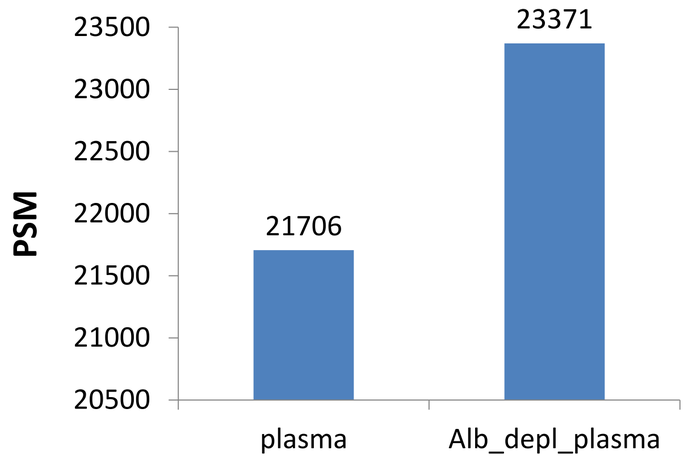
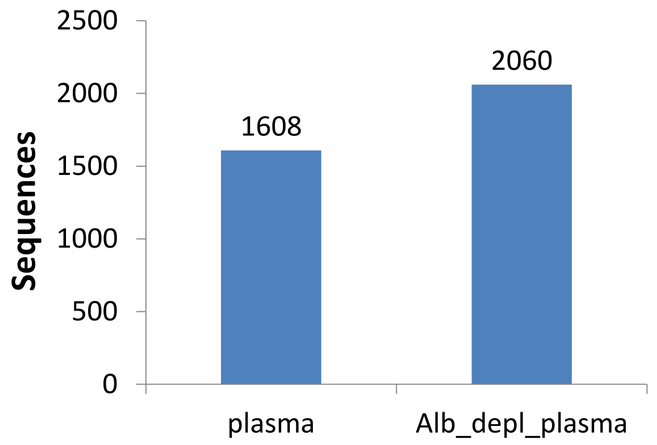
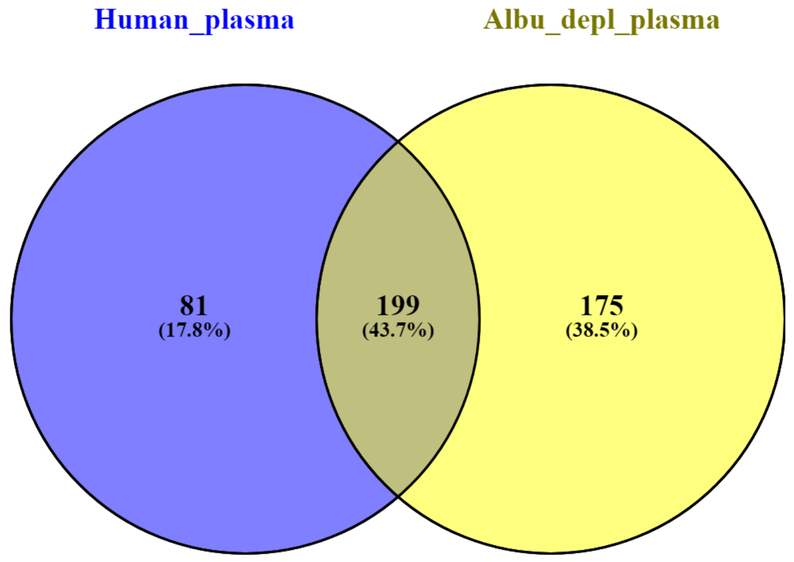
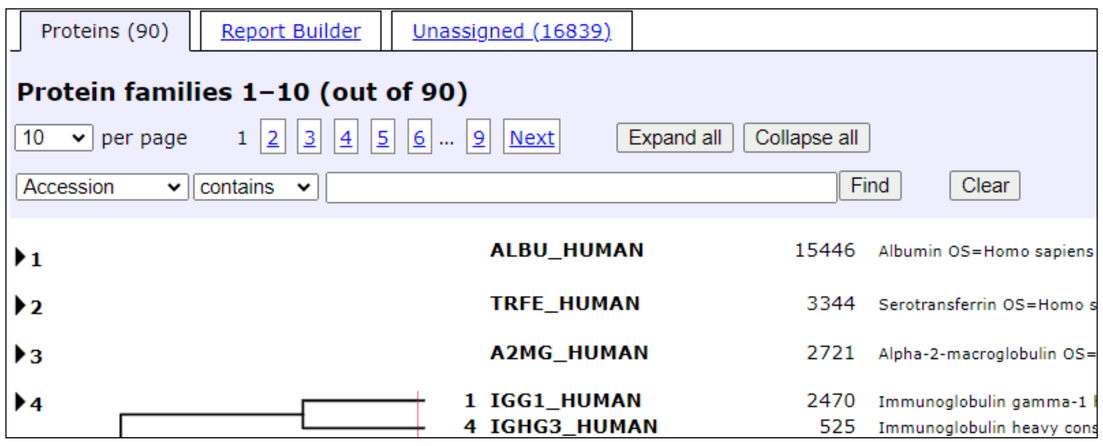












Albumin depletion

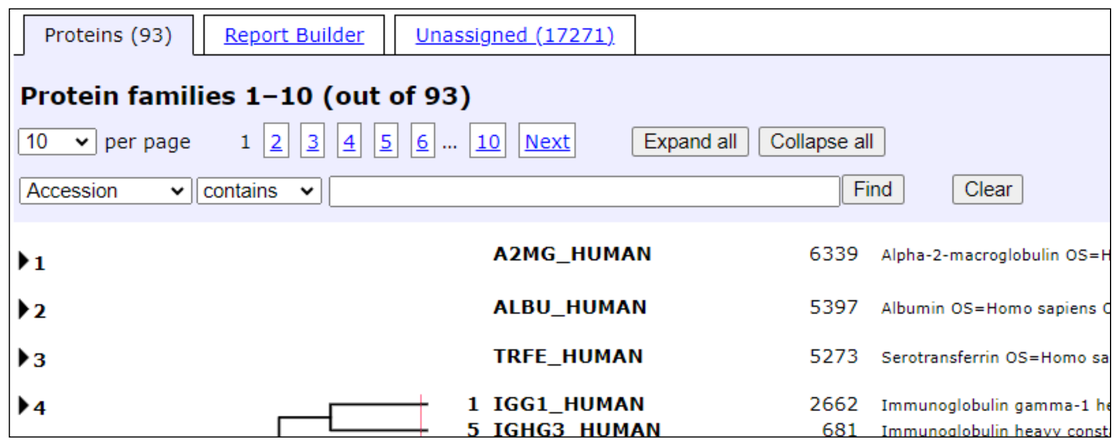
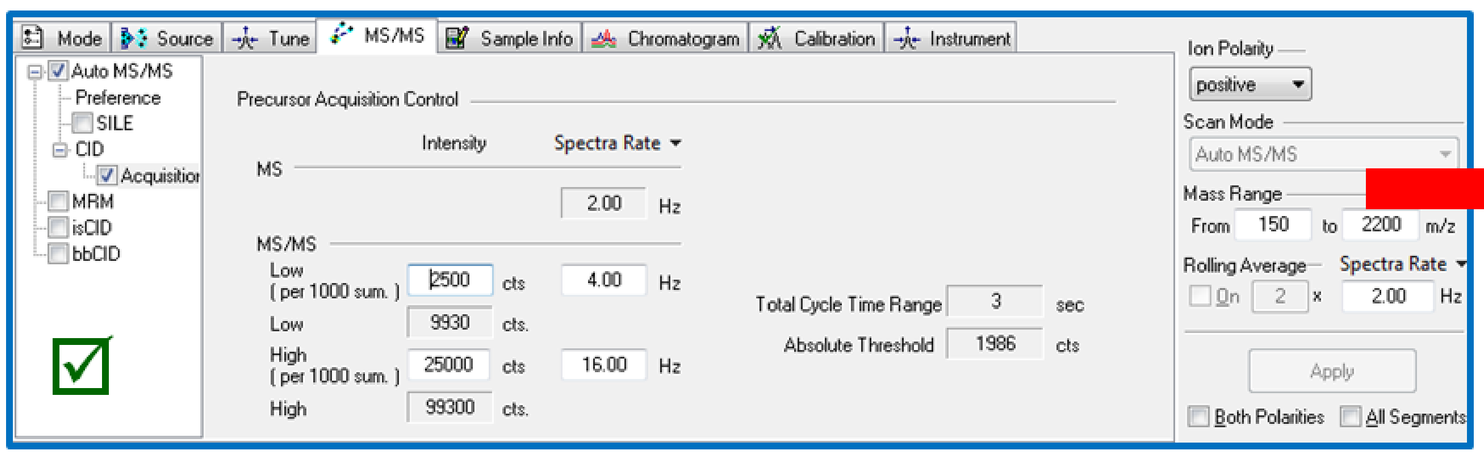


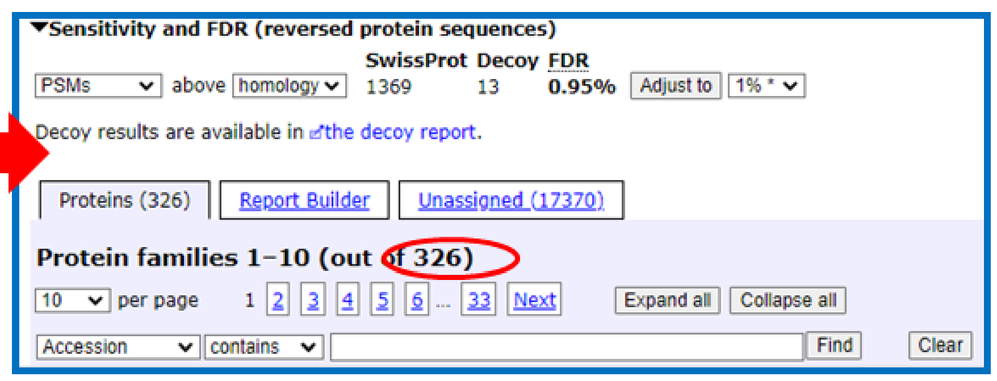
Figure S1. Albumin depletion from human plasma. The removal of the most abundant protein from plasma was performed using an Albumin depletion kit. Column charts display data generated from the PEAKS tool. A Venn diagram was created using the online Venny tool (https://bioinfogp.cnb.csic.es/tools/venny/index.html).

Method optimization on MS/MS panel

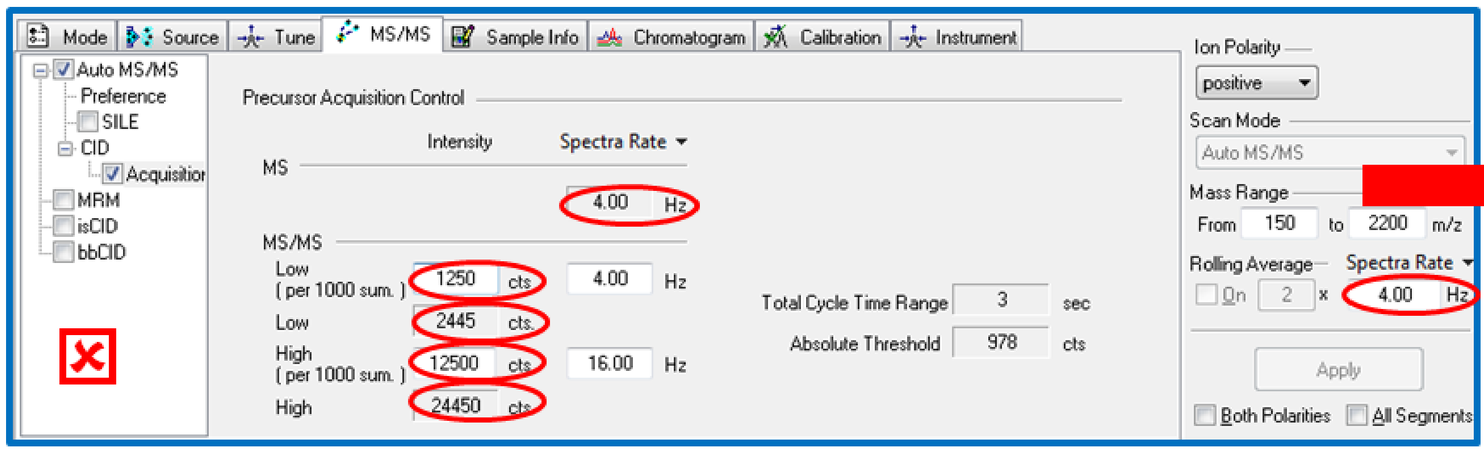
Mascot search results

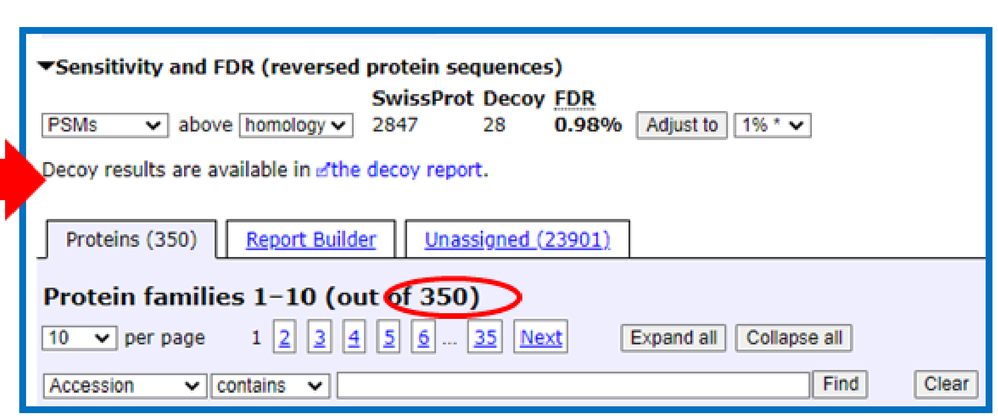
(a)



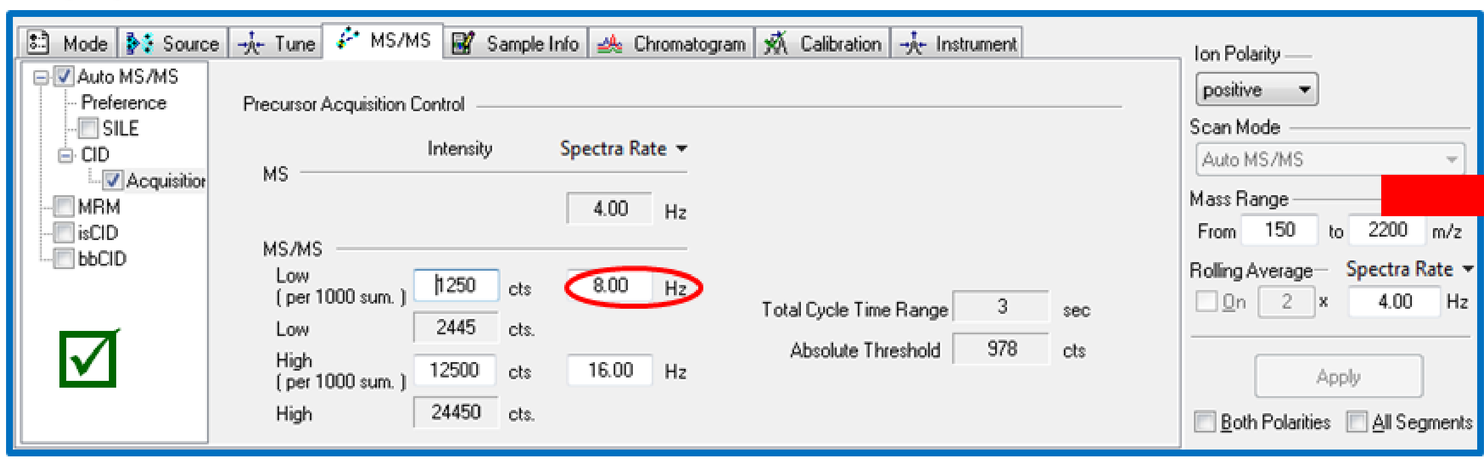


(b)





(c)



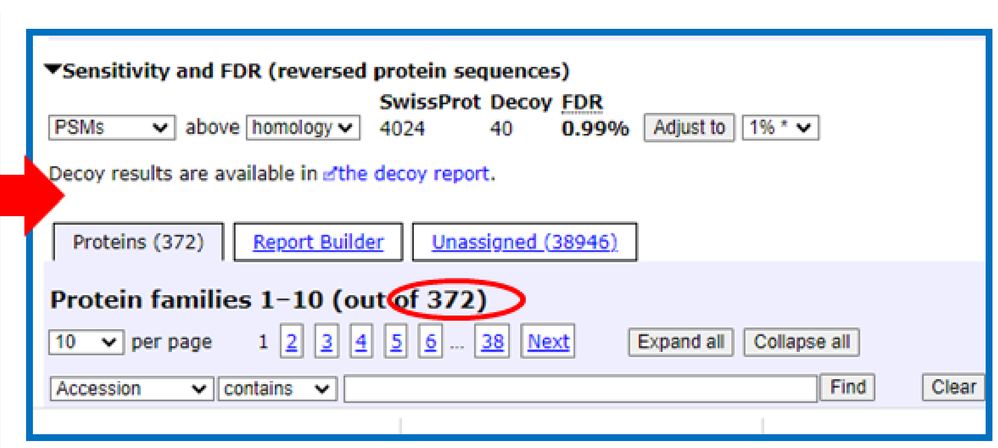


Figure S2. Optimization of MS/MS parameters of DDA mode for analysis of highly complex proteomics sample on example of HEK293T cell digest. Standard parameters are depicted on panel (a). Spectra rate was increased and thresholds were decreased correspondingly (marked in red ellipses on panel (b)). The highest number of protein group identifications was obtained in the case of the method with 4 Hz of MS and 8 Hz of MS/MS spectra rate (panel (c)). All Mascot search results were adjusted to FDR 1% (right panels). For further experiments method (a) as standard and method (c) as high frequency MS acquisition were used.

(a)

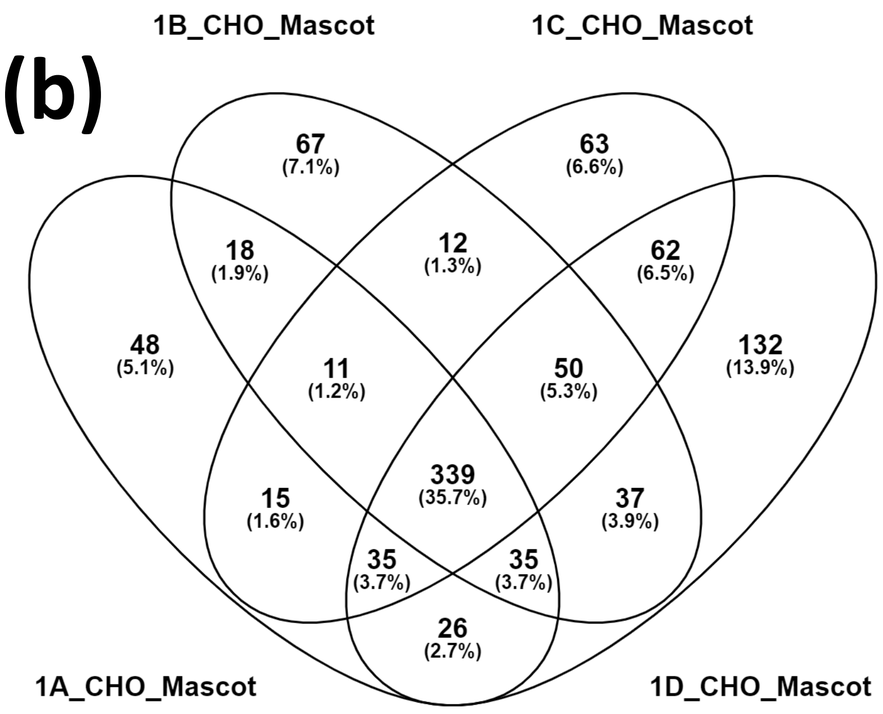
Mascot

	Family	Member	Database	Accession	Score	Mass	Num. of matches	Num. of significant matches	Num. of sequences	Num. of significant sequences	emPAI	Description
96	37	1	Cricetulus_griseus	G3GUP7_CRIGR	911	94171	18	18	2	2	0,06	Ubiquitin carboxyl-terminal hydrolase OS=Cricetulus griseus OX=10029 GN=Usp5 PE=3 SV=
97	38	1	Cricetulus_griseus	G3IGL0_CRIGR	869	36094	33	33	7	7	0,75	Putative heterogeneous nuclear ribonucleoprotein A1-like protein 3 OS=Cricetulus gr
98	38	2	Cricetulus_griseus	G3H1U2_CRIGR	785	27108	41	41	6	6	0,89	Heterogeneous nuclear ribonucleoprotein A3 OS=Cricetulus griseus OX=10029 GN=I7
99	38	3	Cricetulus_griseus	G3IJ98_CRIGR	546	20323	27	27	5	5	1,01	Heterogeneous nuclear ribonucleoprotein A3 OS=Cricetulus griseus OX=10029 GN=I7
100	38	4	Cricetulus_griseus	G3GS73_CRIGR	96	6610	9	9	2	2	1,22	Heterogeneous nuclear ribonucleoprotein A3-like 1 OS=Cricetulus griseus OX=10029
101	39	1	Cricetulus_griseus	G3GXB0_CRIGR	862	23466	22	22	3	3	0,44	Rho GDP dissociation inhibitor alpha OS=Cricetulus griseus OX=10029 GN=Arhgdia PE=3 S

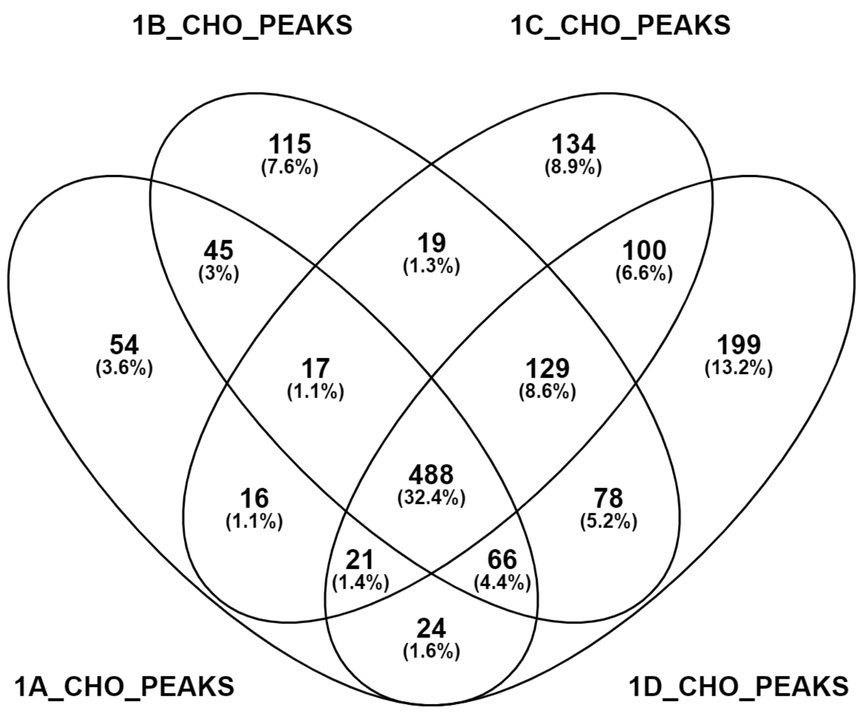
PEAKS

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W
1	Protein Group	Top	Accession	-10LgP	Coverage(%)	Coverage(%)	#Peptides	Area San	#Unique	#Spec Sample 4	PTM	Average Mass	Description										
232	134	true	G3I5H3_CRIGR	280,65384	24,7	24,7	5		5	31	Carbamidomethylation; (	36598,23	Elongation factor 1-delta OS=Cricetulus griseus OX=10029 GN=I79_018721 PE=3 SV=1										
233	135	true	G3H1U2_CRIGR	304,0588	23,37	23,37	6		2	54	Carbamidomethylation	26953,318	Heterogeneous nuclear ribonucleoprotein A3 OS=Cricetulus griseus OX=10029 GN=I79_004125 PE=4 SV=1										
234	135	false	G3HRU8_CRIGR	222,00642	30,48	30,48	3		1	39		12036,58	Heterogeneous nuclear ribonucleoprotein A3 OS=Cricetulus griseus OX=10029 GN=I79_013570 PE=4 SV=1										
235	135	false	G3GTK0_CRIGR	249,7039	17,81	17,81	4		1	37		16437,697	Heterogeneous nuclear ribonucleoprotein A3 OS=Cricetulus griseus OX=10029 GN=I79_000985 PE=4 SV=1										
236	137	true	G3GTB7_CRIGR	274,42212	14,59	14,59	6		4	23	Carbamidomethylation	62688,27	Heterogeneous nuclear ribonucleoprotein Q OS=Cricetulus griseus OX=10029 GN=Syncrip PE=4 SV=1										

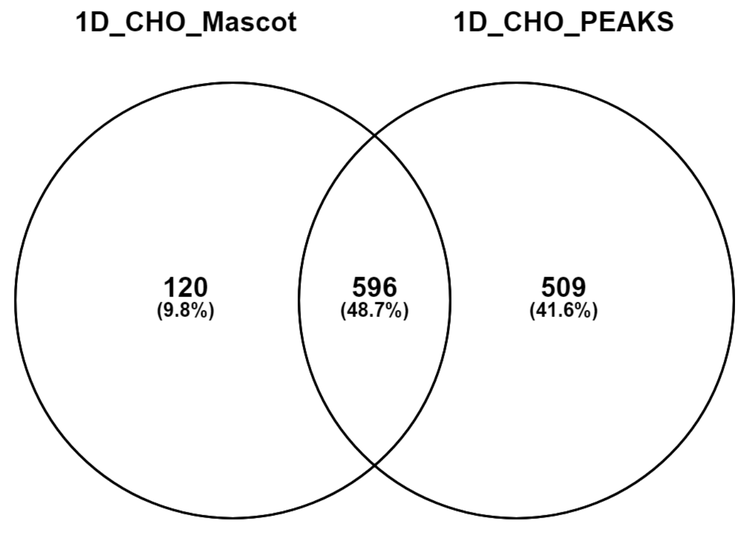
(b)



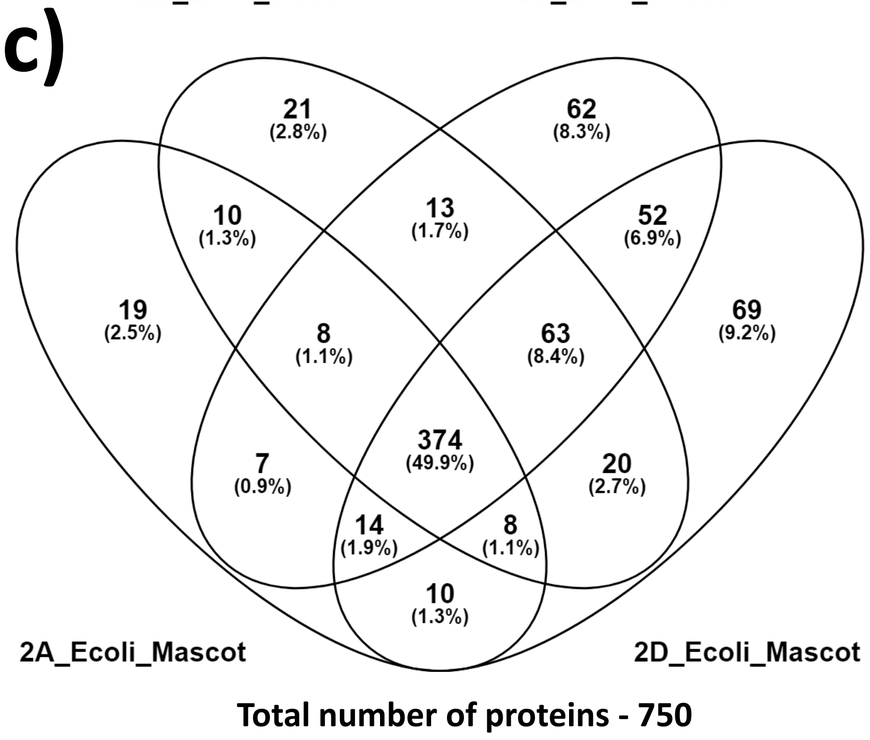
Total number of proteins - 950



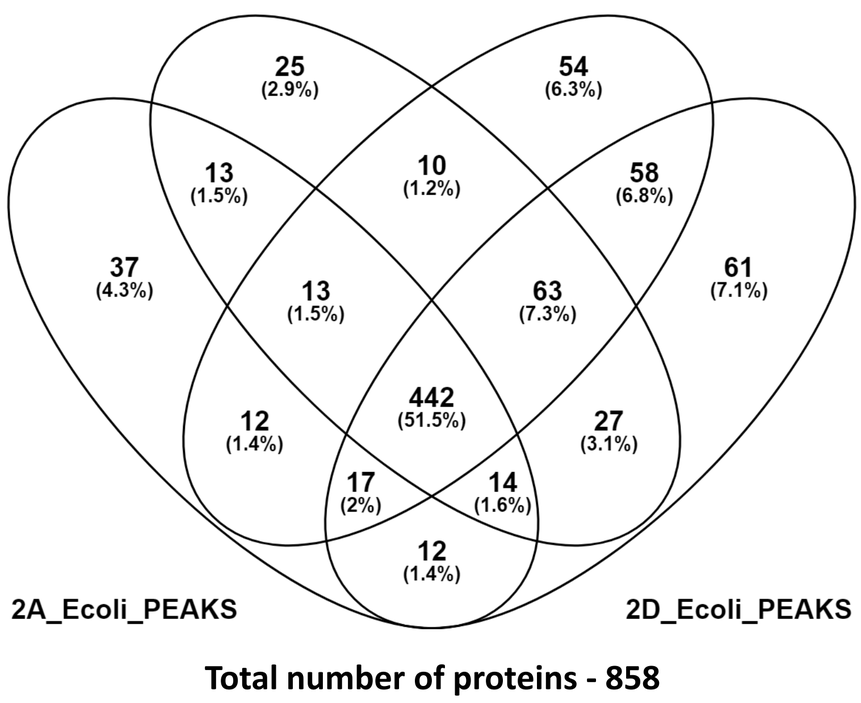
Total number of proteins - 1505



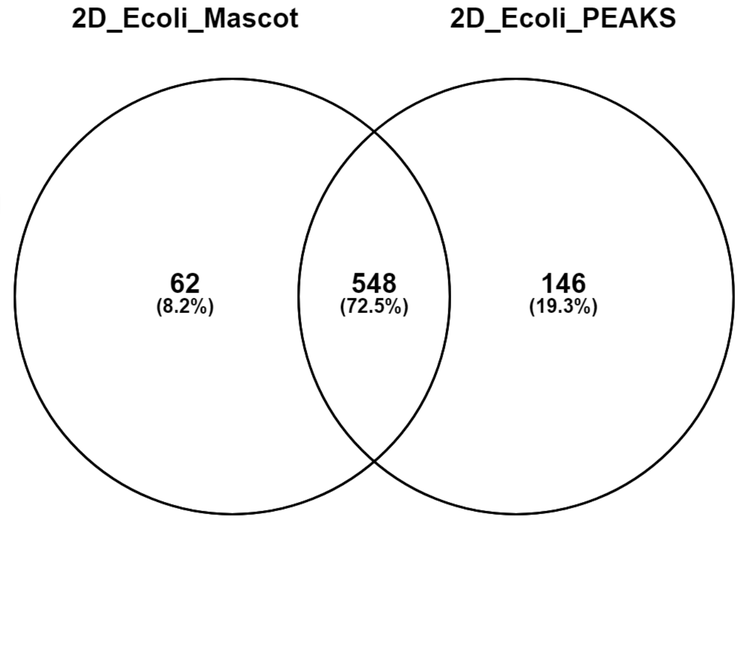
(c)



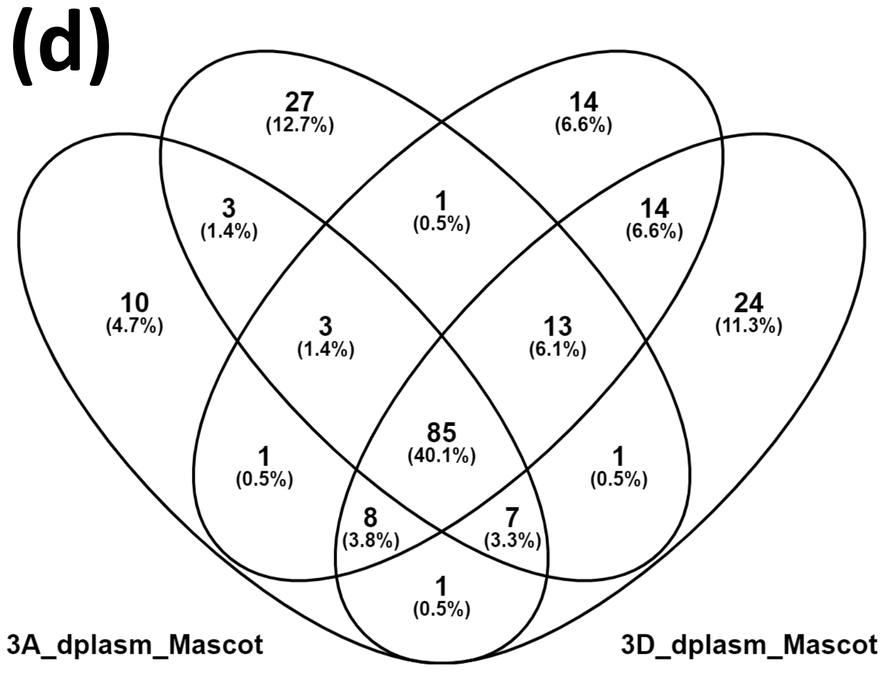
Total number of proteins - 750



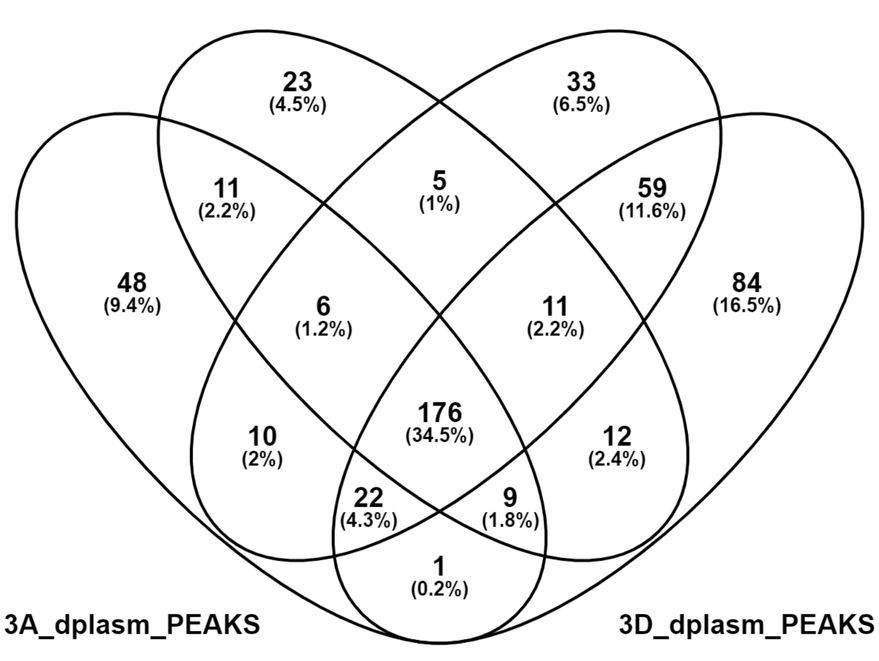
Total number of proteins - 858



(d)



Total number of proteins - 212



Total number of proteins - 510

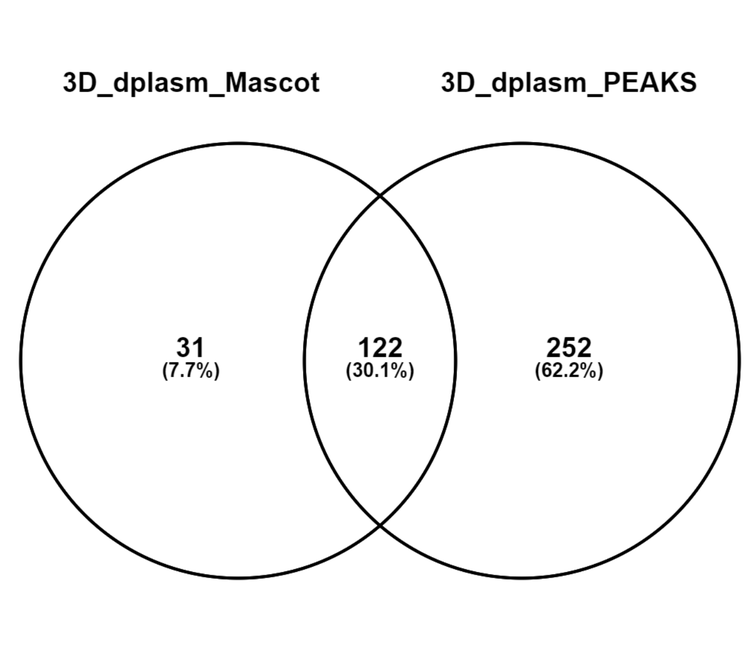
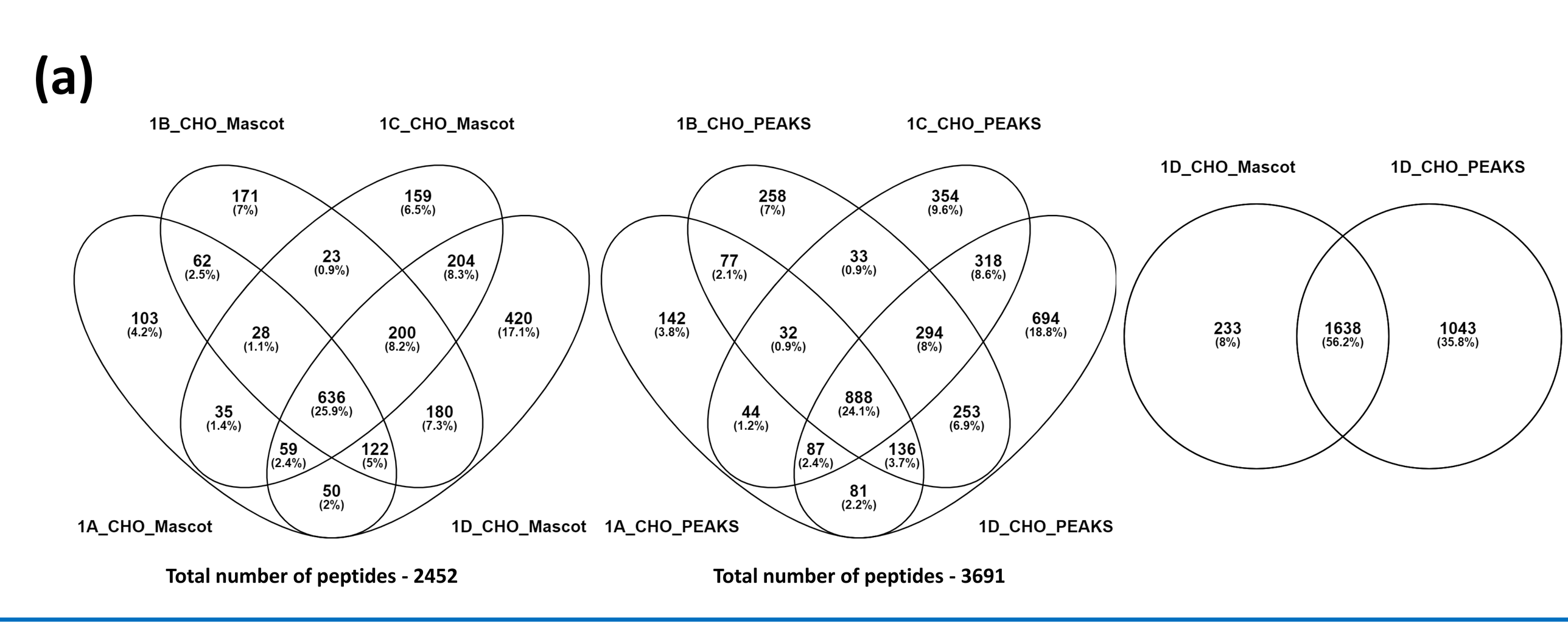
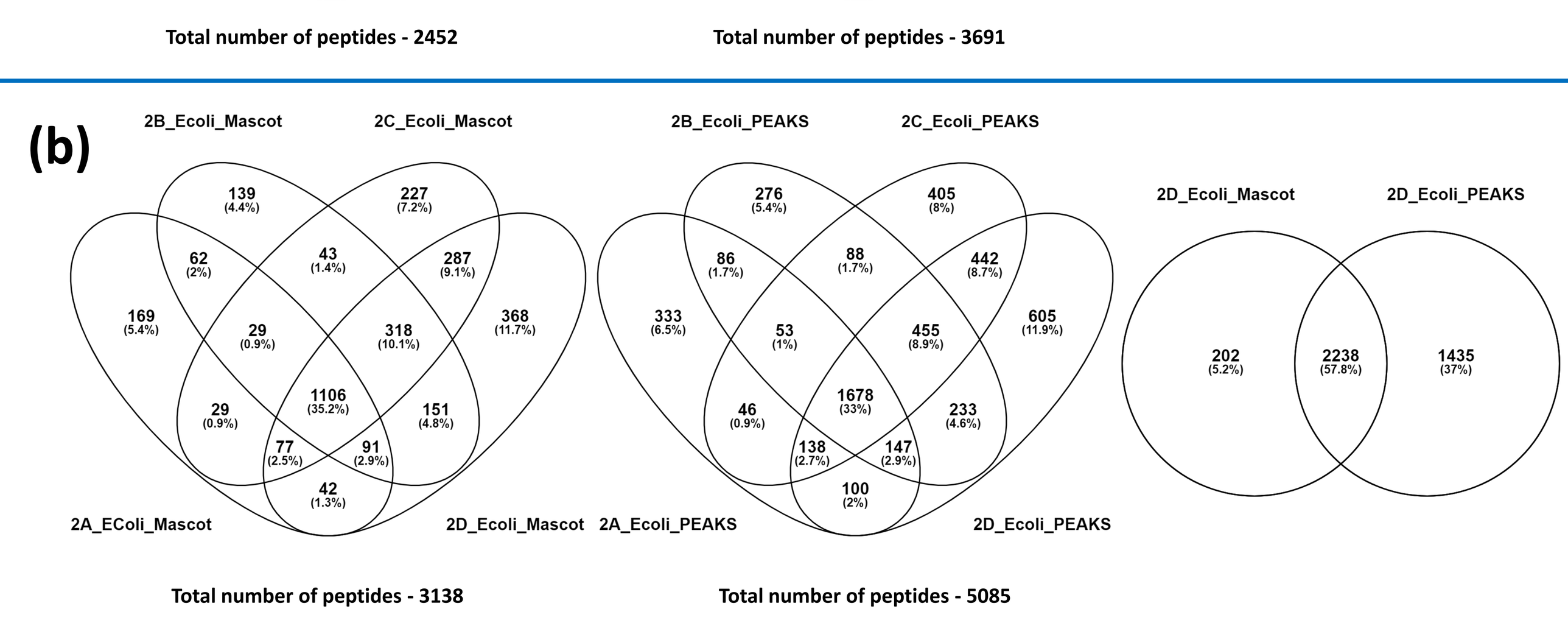


Figure S3. Protein groups and Venn diagrams. Protein grouping examples (in blue font) for Mascot and PEAKS (**a**). Venn diagrams showing the number of unique and commonly identified proteins from CHO (**b**) *E.coli* (**c**) and albumin depleted human plasma (**d**) identified by Mascot and PEAKS. The images were generated by Venny 2.1 from Oliveros, J.C. (2007-2015) "Venny. An interactive tool for comparing lists with Venn's diagrams" https://bioinfogp.cnb.csic.es/tools/venny/index.html. LC-MS/MS methods:

Method A: LC gradient 48 min, MS-2.00 Hz, MS/MS-4.00 Hz
Method B: LC gradient 48 min, MS-4.00 Hz, MS/MS-8.00 Hz
Method C: LC gradient 90 min, MS-2.00 Hz, MS/MS-4.00 Hz
Method D: LC gradient 90 min, MS-4.00 Hz, MS/MS-8.00 Hz.





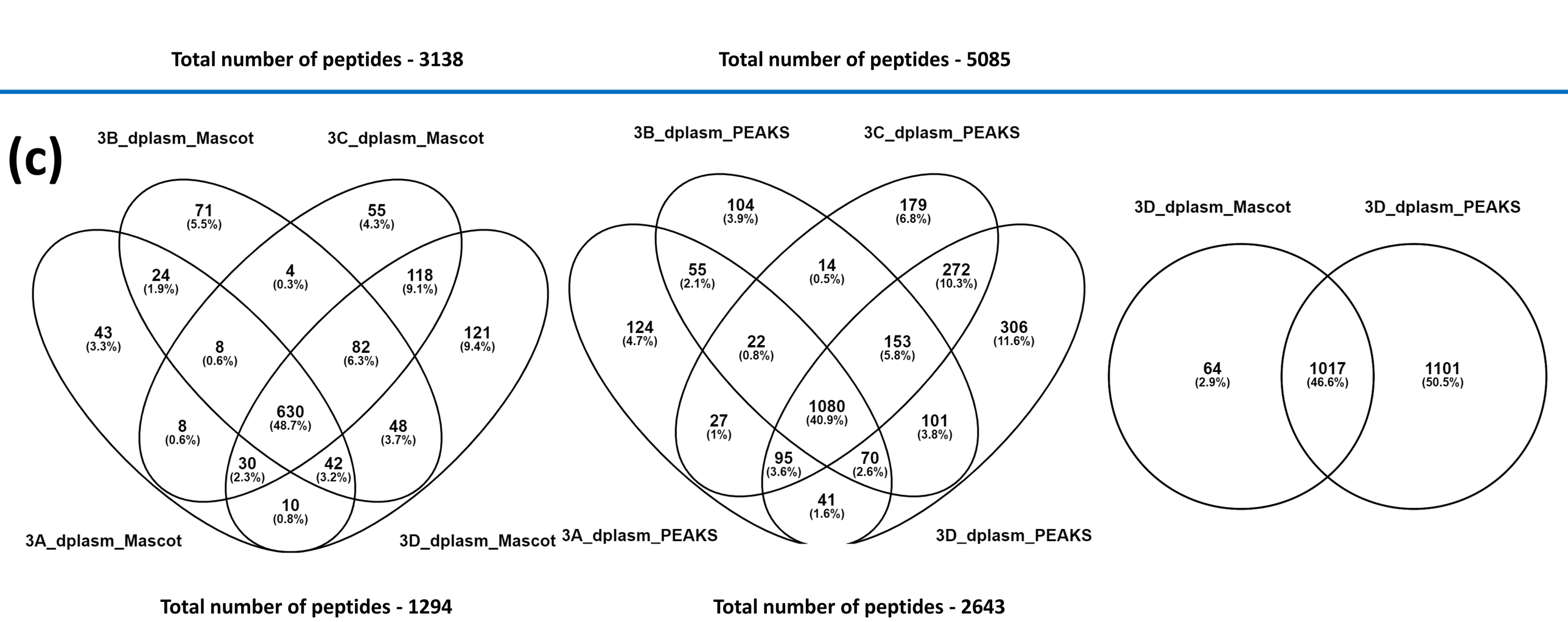


Figure S4. Peptide sequences and Venn diagrams. Venn diagrams showing the number of unique and commonly identified peptides from CHO (**a**) *E.coli* (**b**) and albumin depleted human plasma (**c**) identified by Mascot and PEAKS. The images were generated by Venny 2.1 from Oliveros, J.C. (2007-2015) “Venny. An interactive tool for comparing lists with Venn's diagrams” https://bioinfogp.cnb.csic.es/tools/venny/index.html.

LC-MS/MS methods:

Method A: LC gradient 48 min, MS-2.00 Hz, MS/MS-4.00 Hz

Method B: LC gradient 48 min, MS-4.00 Hz, MS/MS-8.00 Hz

Method C: LC gradient 90 min, MS-2.00 Hz, MS/MS-4.00 Hz

Method D: LC gradient 90 min, MS-4.00 Hz, MS/MS-8.00 Hz.

Mascot server

Protein View: G3I6I6_CRIGR

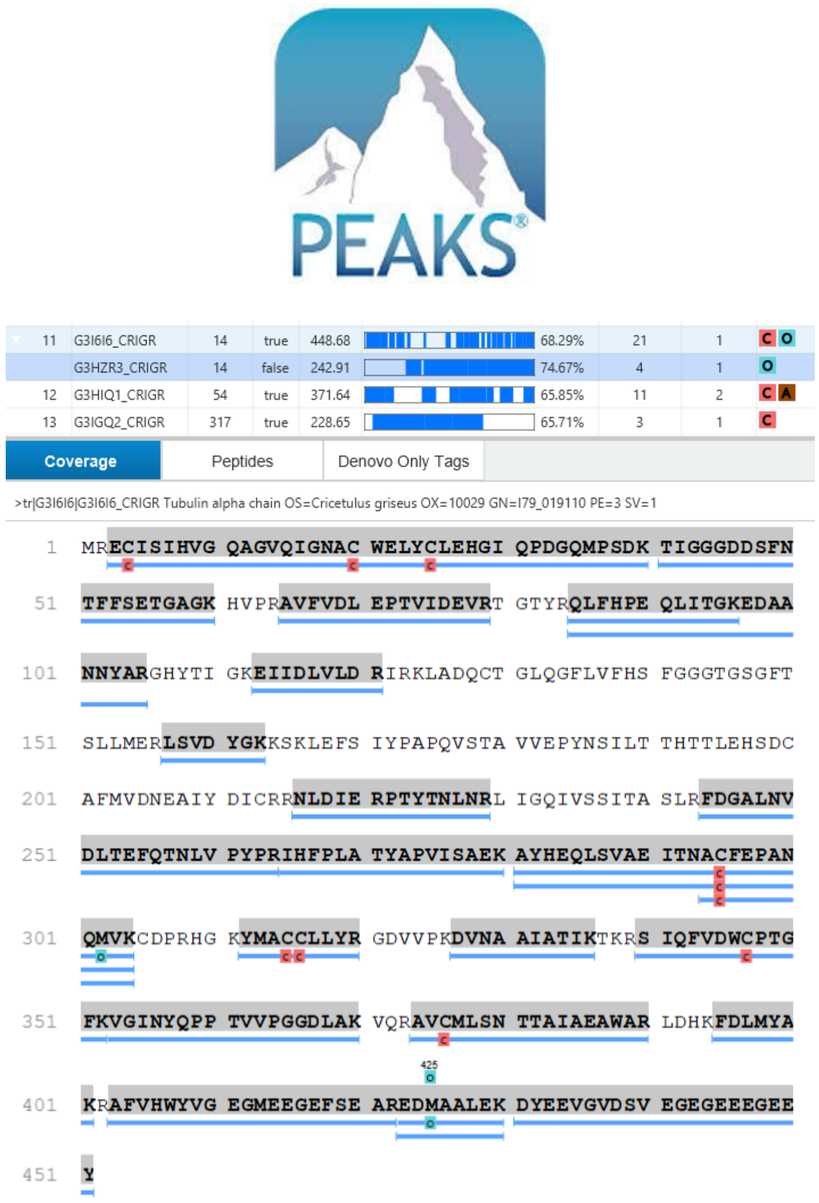
Tubulin alpha chain OS=Cricetulus griseus OX=10029 GN=I79_019110 PE=3 SV=1

Database:	Cricetulus_griseus
Score:	5502
Monoisotopic mass (M_r):	50774
Calculated pI:	4.94
Taxonomy:	Cricetulus griseus

Protein sequence coverage: 54%

Matched peptides shown in ***bold red***.

```
  1 MRECISIHVG QAGVQIGNAC WELYCLEHGI QPDGQMPSDK TIGGGDDSFN
 51 TFFSETGAGK HVPRAVFVDL EPTVIDEVRT GTYRQLFHPE QLITGKEDAA
101 NNYARGHYTI GKEIIDLVLD RIRKLADQCT GLQGFLVFHS FGGGTGSGFT
151 SLLMERLSVD YGKKSKLEFS IYPAPQVSTA VVEPYNSILT THTTLEHSDC
201 AFMVDNEAIY DICRRNLDIE RPTYTNLNRL IGQIVSSITA SLRFDGALNV
251 DLTEFQTNLV PYPRIHFPLA TYAPVISAEK AYHEQLSVAE ITNACFEPAN
301 QMVKCDPRHG KYMACCLLYR GDVVPKDVNA AIATIKTKRS IQFVDWCPTG
351 FKVGINYQPP TVVPGGDLAK VQRAVCMLSN TTAIAEAWAR LDHKFDLMYA
401 KRAFVHWYVG EGMEEGEFSE AREDMAALEK DYEEVGVDSV EGEGEEEGEE
451 Y
```



Protein View: G3IBF1_CRIGR

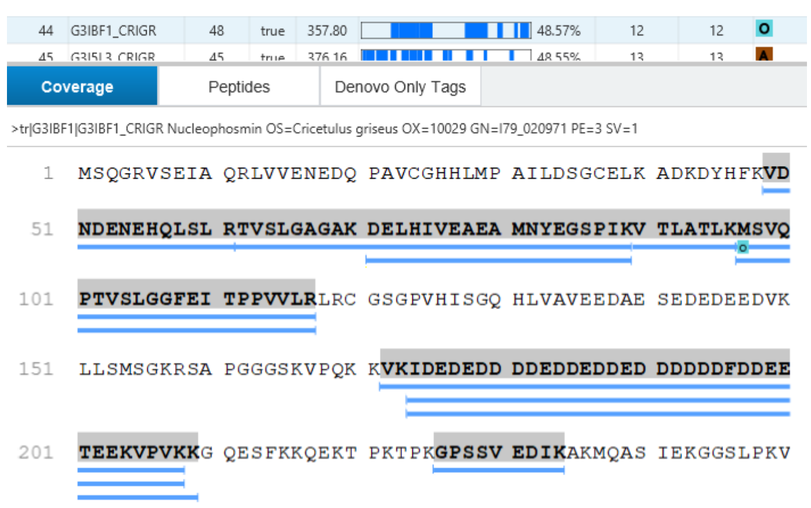
Nucleophosmin OS=Cricetulus griseus OX=10029 GN=I79_020971 PE=3 SV=1

Database:	Cricetulus_griseus
Score:	1320
Monoisotopic mass (M_r):	31261
Calculated pI:	4.52
Taxonomy:	Cricetulus griseus

Protein sequence coverage: 43%

Matched peptides shown in ***bold red***.

```
  1 MSQGRVSEIA QRLVVENEDQ PAVCGHHLMP AILDSGCELK ADKDYHFKVD
 51 NDENEHQLSL RTVSLGAGAK DELHIVEAEA MNYEGSPIKV TLATLKMSVQ
101 PTVSLGGFEI TPPVVLRLRC GSGPVHISGQ HLVAVEEDAE SEDEDEEDVK
151 LLSMSGKRSA PGGGSKVPQK KVKIDEDEDD DDEDDEDDED DDDDDFDDEE
201 TEEKVPVKKG QESFKKQEKT PKTPKGPSSV EDIKAKMQAS IEKGGSLPKV
251 EAKFINYVKN CFRMTDQEAI QDLWQWRKSL
```



Protein View: G3HJP6_CRIGR

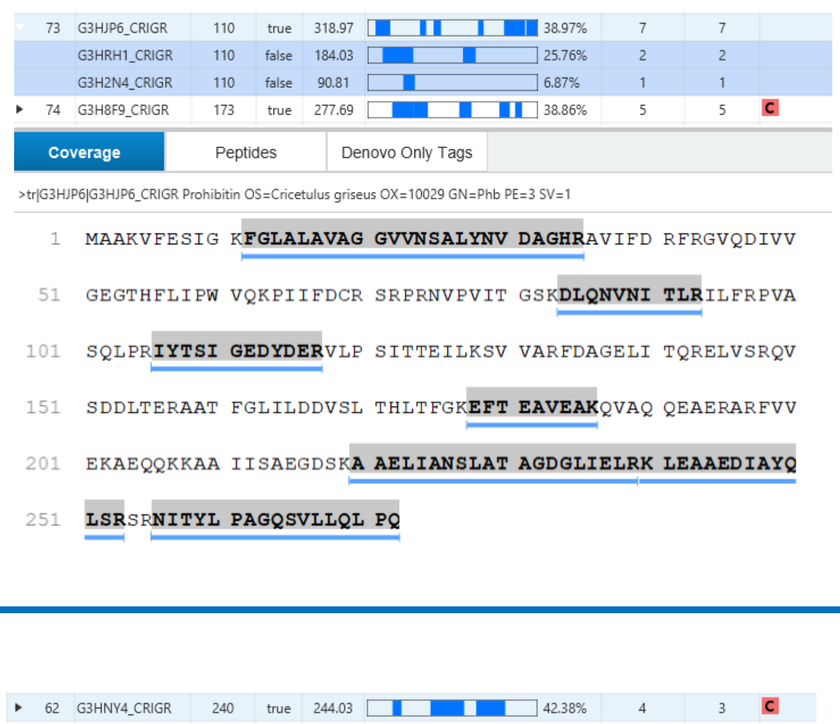
Prohibitin OS=Cricetulus griseus OX=10029 GN=Phb PE=3 SV=1

Database:	Cricetulus_griseus
Score:	351
Monoisotopic mass (M_r):	29859
Calculated pI:	5.57
Taxonomy:	Cricetulus griseus

Protein sequence coverage: 21%

Matched peptides shown in ***bold red***.

```
  1 MAAKVFESIG KFGLALAVAG GVVNSALYNV DAGHRAVIFD RFRGVQDIVV
 51 GEGTHFLIPW VQKPIIFDCR SRPRNVPVIT GSKDLQNVNI TLRILFRPVA
101 SQLPRIYTSI GEDYDERVLP SITTEILKSV VARFDAGELI TQRELVSRQV
151 SDDLTERAAT FGLILDDVSL THLTFGKEFT EAVEAKQVAQ QEAERARFVV
201 EKAEQQKKAA IISAEGDSKA AELIANSLAT AGDGLIELRK LEAAEDIAYQ
251 LSRSRNITYL PAGQSVLLQL PQ
```



Protein View: G3HNY4_CRIGR

Phosphoglycerate kinase OS=Cricetulus griseus OX=10029 GN=I79_012485 PE=3 SV=1

Database:	Cricetulus_griseus
Score:	201
Monoisotopic mass (M_r):	16451
Calculated pI:	9.01
Taxonomy:	Cricetulus griseus

Protein sequence coverage: 17%

Matched peptides shown in ***bold red***.

```
  1 MSLSNKLTLD KLDVKGKRVV MRVDFNVPMK NNQITNNQRI KAAVPSIKFC
 51 LDNGAKSVVL MSHLGRPDGV PMPDKYSLEP VAAELKSLLG KDVLFLKDCV
101 GPEVENACAN PAAGTVILLE NLRFHVEEEG KGKDASGNKV GPVVLILGLR
151 A
```

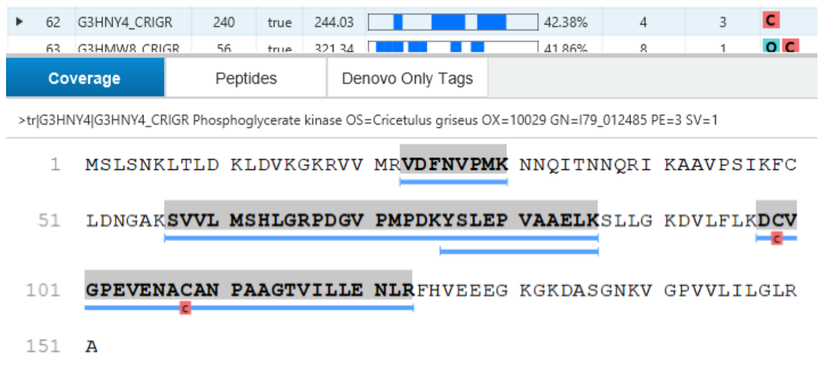


Figure S5. Protein sequence coverage results of Mascot (left) and PEAKS (right) of proteins from CHO cells.

Mascot server

Protein View: MDH_ECOLI

Malate dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=mdh PE=1 SV=1

Database:	Escherichia_coli_(strain_K12)
Score:	10200
Monoisotopic mass (M_r):	32488
Calculated pI:	5.61
Taxonomv:	Escherichia coli K-12

Protein sequence coverage: 90%

Matched peptides shown in ***bold red***.

```
  1 MKVAVLGAAG GIGQALALLL KTQLPSGSEL SLYDIAPVTP GVAVDLSHIP
 51 TAVKIKGFSG EDATPALEGA DVVLISAGVA RKPGMDRSDL FNVNAGIVKN
101 LVQQVAKTCP KACIGIITNP VNTTVAIAAE VLKKAGVYDK NKLFGVTTLD
151 IIRSNTFVAE LKGKQPGEVE VPVIGGHSGV TILPLLSQVP GVSFTEQEVA
201 DLTKRIQNAG TEVVEAKAGG GSATLSMGQA AARFGLSLVR ALQGEQGVVE
251 CAYVEGDGQY ARFFSQPLLL GKNGVEERKS IGTLSAFEQN ALEGMLDTLK
301 KDIALGEEFV NK
```



Protein View: ATPB_ECOLI

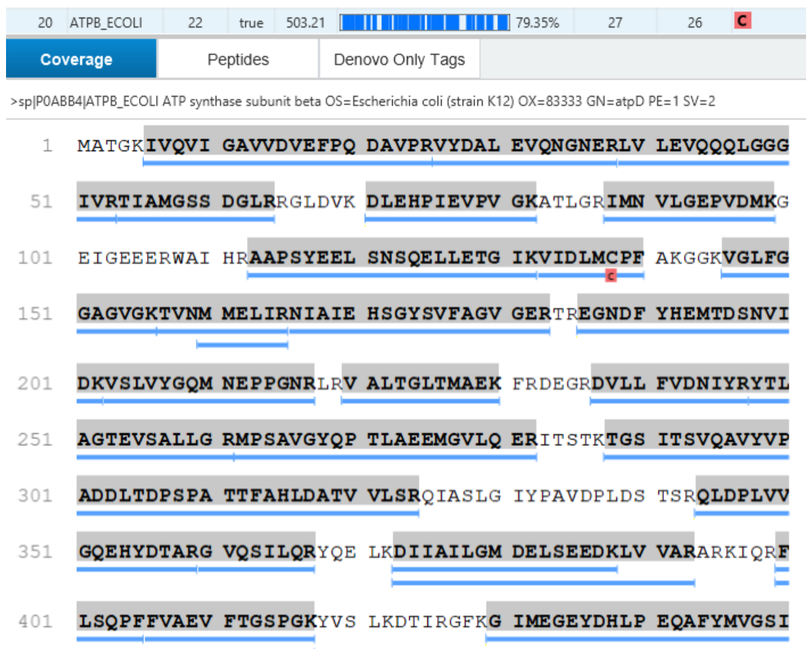
ATP synthase subunit beta OS=Escherichia coli (strain K12) OX=83333 GN=atpD PE=1 SV=2

Database:	Escherichia_coli_(strain_K12)
Score:	3173
Monoisotopic mass (M_r):	50351
Calculated pI:	4.90
Taxonomy:	Escherichia coli K-12

Protein sequence coverage: 73%

Matched peptides shown in ***bold red***.

```
  1 MATGKIVQVI GAVVDVEFPQ DAVPRVYDAL EVQNGNERLV LEVQQQLGGG
 51 IVRTIAMGSS DGLRRGLDVK DLEHPIEVPV GKATLGRIMN VLGEPVDMKG
101 EIGEEERWAI HRAAPSYEEL SNSQELLETG IKVIDLMCPF AKGGKVGLFG
151 GAGVGKTVNM MELIRNIAIE HSGYSVFAGV GERTREGNDF YHEMTDSNVI
201 DKVSLVYGQM NEPPGNRLRV ALTGLTMAEK FRDEGRDVLL FVDNIYRYTL
251 AGTEVSALLG RMPSAVGYQP TLAEEMGVLQ ERITSTKTGS ITSVQAVYVP
301 ADDLTDPSPA TTFAHLDATV VLSRQIASLG IYPAVDPLDS TSRQLDPLVV
351 GQEHYDTARG VQSILQRYQE LKDIIAILGM DELSEEDKLV VARARKIQRF
401 LSQPFFVAEV FTGSPGKYVS LKDTIRGFKG IMEGEYDHLP EQAFYMVGSI
451 EEAVEKAKKL
```



Protein View: SUCD_ECOLI

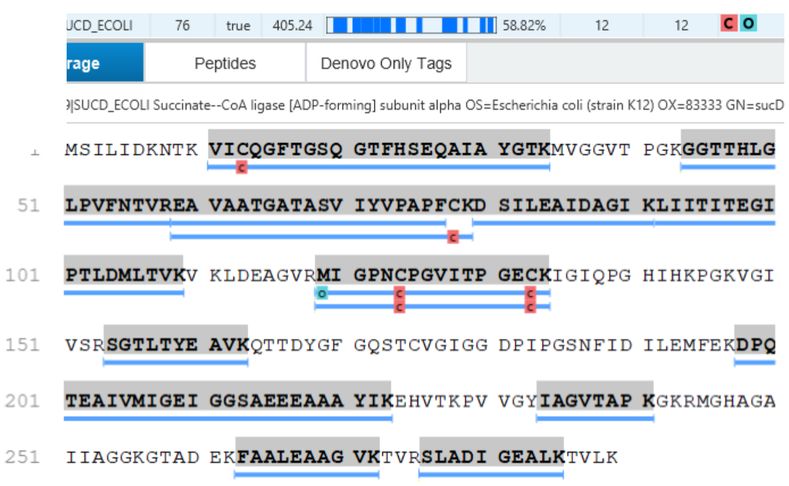
Succinate--CoA ligase [ADP-forming] subunit alpha OS=Escherichia coli (strain K12) OX=83333 GN=sucD PE=1 SV=2

Database:	Escherichia_coli_(strain_K12)
Score:	1334
Monoisotopic mass (M_r):	30044
Calculated pI:	6.32
Taxonomy:	Escherichia coli K-12

Protein sequence coverage: 40%

Matched peptides shown in ***bold red***.

```
  1 MSILIDKNTK VICQGFTGSQ GTFHSEQAIA YGTKMVGGVT PGKGGTTHLG
 51 LPVFNTVREA VAATGATASV IYVPAPFCKD SILEAIDAGI KLIITITEGI
101 PTLDMLTVKV KLDEAGVRMI GPNCPGVITP GECKIGIQPG HIHKPGKVGI
151 VSRSGTLTYE AVKQTTDYGF GQSTCVGIGG DPIPGSNFID ILEMFEKDPQ
201 TEAIVMIGEI GGSAEEEAAA YIKEHVTKPV VGYIAGVTAP KGKRMGHAGA
251 IIAGGKGTAD EKFAALEAAG VKTVRSLADI GEALKTVLK
```



Protein View: HNS_ECOLI

DNA-binding protein H-NS OS=Escherichia coli (strain K12) OX=83333 GN=hns PE=1 SV=2

Database:	Escherichia_coli_(strain_K12)
Score:	1984
Monoisotopic mass (M_r):	15587
Calculated pI:	5.43
Taxonomy:	Escherichia coli K-12

Protein sequence coverage: 59%

Matched peptides shown in ***bold red***.

```
  1 MSEALKILNN IRTLRAQARE CTLETLEEML EKLEVVVNER REEESAAAAE
 51 VEERTRKLQQ YREMLIADGI DPNELLNSLA AVKSGTKAKR AQRPAKYSYV
101 DENGETKTWT GQGRTPAVIK KAMDEQGKSL DDFLIKQ
```

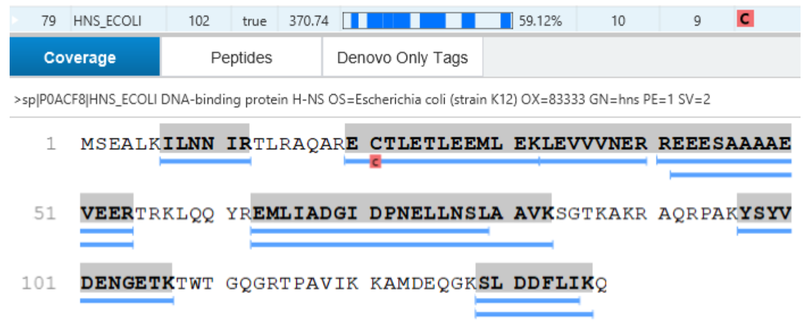


Figure S6. Protein sequence coverage results of Mascot (left) and PEAKS (right) of proteins from *E.coli* .

Mascot server

Protein View: IGKC_HUMAN

Immunoglobulin kappa constant OS=Homo sapiens OX=9606 GN=IGKC PE=1 SV=2

Database:	Homo_sapiens
Score:	37420
Monoisotopic mass (M_r):	11929
Calculated pI:	6.11
Taxonomy:	Homo sapiens

Protein sequence coverage: 82%

Matched peptides shown in ***bold red***.

```
  1 RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG
 51 NSQESVTEQD SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK
101 SFNRGEC
```

PEAKS

30 | IGKC_HUMAN | 29 | true | 477.97 | 88.79% | 25 | 25 | C

Coverage | Peptides | Denovo Only Tags

>sp|P01834|IGKC_HUMAN Immunoglobulin kappa constant OS=Homo sapiens OX=9606 GN=IGKC PE=1 SV=2

```
  1 RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG
 51 NSQESVTEQD SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK
101 SFNRGEC
```

Protein View: HV372_HUMAN

Immunoglobulin heavy variable 3-72 OS=Homo sapiens OX=9606 GN=IGHV3-72 PE=3 SV=1

Database:	Homo_sapiens
Score:	250
Monoisotopic mass (M_r):	13366
Calculated pI:	7.68
Taxonomy:	Homo sapiens

Protein sequence coverage: 15%

Matched peptides shown in ***bold red***.

```
  1 MEFGLSWVFL VVILQGVQCE VQLVESGGGL VQPGGSLRLS CAASGFTFSD
 51 HYMDWVRQAP GKGLEWVGRT RNKANSYTTE YAASVKGRFT ISRDDSKNSL
101 YLQMNSLKTE DTAVYYCAR
```

73 | HV372_HUMAN | 92 | true | 331.39 | 63.03% | 7 | 2 | C

Coverage | Peptides | Denovo Only Tags

>sp|A0A0B4J1Y9|HV372_HUMAN Immunoglobulin heavy variable 3-72 OS=Homo sapiens OX=9606 GN=IGHV3-72 PE=3 SV=1

```
  1 MEFGLSWVFL VVILQGVQCE VQLVESGGGL VQPGGSLRLS CAASGFTFSD
 51 HYMDWVRQAP GKGLEWVGRT RNKANSYTTE YAASVKGRFT ISRDDSKNSL
101 YLQMNSLKTE DTAVYYCAR
```

Protein View: LV39_HUMAN

Immunoglobulin lambda variable 3-9 OS=Homo sapiens OX=9606 GN=IGLV3-9 PE=3 SV=1

Database:	Homo_sapiens
Score:	784
Monoisotopic mass (M_r):	12438
Calculated pI:	6.81
Taxonomy:	Homo sapiens

Protein sequence coverage: 23%

Matched peptides shown in ***bold red***.

```
  1 MAWTALLLSL LAHFTGSVAS YELTQPLSVS VALGQTARIT CGGNNIGSKN
 51 VHWYQQKPGQ APVLVIYRDS NRPSGIPERF SGSNSGNTAT LTISRAQAGD
101 EADYYCQVWD SSTAH
```

79 | LV39_HUMAN | 84 | true | 322.88 | 57.39% | 7 | 3 | C

Coverage | Peptides | Denovo Only Tags

>sp|A0A075B6K5|LV39_HUMAN Immunoglobulin lambda variable 3-9 OS=Homo sapiens OX=9606 GN=IGLV3-9 PE=3 SV=1

```
  1 MAWTALLLSL LAHFTGSVAS YELTQPLSVS VALGQTARIT CGGNNIGSKN
 51 VHWYQQKPGQ APVLVIYRDS NRPSGIPERF SGSNSGNTAT LTISRAQAGD
101 EADYYCQVWD SSTAH
```

Protein View: APOA1_HUMAN

Apolipoprotein A-I OS=Homo sapiens OX=9606 GN=APOA1 PE=1 SV=1

Database:	Homo_sapiens
Score:	1557
Monoisotopic mass (M_r):	30759
Calculated pI:	5.56
Taxonomy:	Homo sapiens

Protein sequence coverage: 43%

Matched peptides shown in ***bold red***.

```
  1 MKAAVLTLAV LFLTGSQARH FWQQDEPPQS PWDRVKDLAT VYVDVLKDSG
 51 RDYVSQFEGS ALGKQLNLKL LDNWDSVTST FSKLREQLGP VTQEFWDNLE
101 KETEGLRQEM SKDLEEVKAK VQPYLDDFQK KWQEEMELYR QKVEPLRAEL
151 QEGARQKLHE LQEKLSPLGE EMRDRARAHV DALRTHLAPY SDELRQRLAA
201 RLEALKENGG ARLAEYHAKA TEHLSTLSEK AKPALEDLRQ GLLPVLESFK
251 VSFLSALEEY TKKLNTQ
```

37 | APOA1_HUMAN | 41 | true | 447.91 | 59.93% | 17 | 17

Coverage | Peptides | Denovo Only Tags

>sp|P02647|APOA1_HUMAN Apolipoprotein A-I OS=Homo sapiens OX=9606 GN=APOA1 PE=1 SV=1

```
  1 MKAAVLTLAV LFLTGSQARH FWQQDEPPQS PWDRVKDLAT VYVDVLKDSG
 51 RDYVSQFEGS ALGKQLNLKL LDNWDSVTST FSKLREQLGP VTQEFWDNLE
101 KETEGLRQEM SKDLEEVKAK VQPYLDDFQK KWQEEMELYR QKVEPLRAEL
151 QEGARQKLHE LQEKLSPLGE EMRDRARAHV DALRTHLAPY SDELRQRLAA
201 RLEALKENGG ARLAEYHAKA TEHLSTLSEK AKPALEDLRQ GLLPVLESFK
251 VSFLSALEEY TKKLNTQ
```

Protein View: SAMP_HUMAN

Serum amyloid P-component OS=Homo sapiens OX=9606 GN=APCS PE=1 SV=2

Database:	Homo_sapiens
Score:	257
Monoisotopic mass (M_r):	25485
Calculated pI:	6.10
Taxonomy:	Homo sapiens

Protein sequence coverage: 17%

Matched peptides shown in ***bold red***.

```
  1 MNKPLLWISV LTSLLEAFAH TDLSGKVFVF PRESVTDHVN LITPLEKPLQ
 51 NFTLCFRAYS DLSRAYSLFS YNTQGRDNEL LVYKERVGEY SLYIGRHKVT
101 SKVIEKFPAP VHICVSWESS SGIAEFWING TPLVKKGLRQ GYFVEAQPKI
151 VLGQEQDSYG GKFDRSQSFV GEIGDLYMWD SVLPPENILS AYQGTPLPAN
201 ILDWQALNYE IRGYVIIKPL VWV
```

89 | SAMP_HUMAN | 104 | true | 313.64 | 27.35% | 6 | 6

Coverage | Peptides | Denovo Only Tags

>sp|P02743|SAMP_HUMAN Serum amyloid P-component OS=Homo sapiens OX=9606 GN=APCS PE=1 SV=2

```
  1 MNKPLLWISV LTSLLEAFAH TDLSGKVFVF PRESVTDHVN LITPLEKPLQ
 51 NFTLCFRAYS DLSRAYSLFS YNTQGRDNEL LVYKERVGEY SLYIGRHKVT
101 SKVIEKFPAP VHICVSWESS SGIAEFWING TPLVKKGLRQ GYFVEAQPKI
151 VLGQEQDSYG GKFDRSQSFV GEIGDLYMWD SVLPPENILS AYQGTPLPAN
201 ILDWQALNYE IRGYVIIKPL VWV
```

Figure S7. Protein sequence coverage results of Mascot (left) and PEAKS (right) of proteins from albumin depleted human plasma.

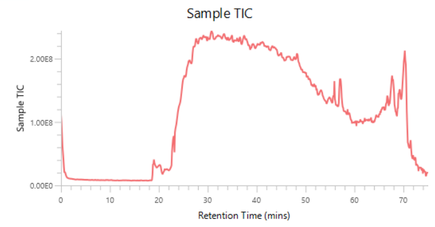
(a)

Data QC (PEAKS Studio 11, Chinese hamster ovary cells, CHO)

Method A

Data QC

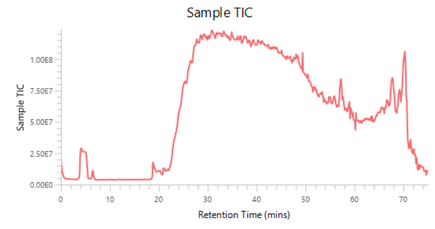
Sample Name	ALL Attributes	# MS1	# MS2	MS2/MS1 Rate	# Detected Feature	Full Width (min)	FWHM (sec)	BPC	TIC Correlation
Sample 1	Pass	1563	21529	13.77	103014	0.37	18.17	2.16E8	1.0000
Average	Pass	1563	21529	13.77	103014	0.37	18.17	2.16E8	1.0000



Method B

Data QC

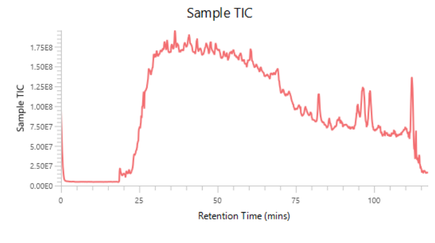
Sample Name	ALL Attributes	# MS1	# MS2	MS2/MS1 Rate	# Detected Feature	Full Width (min)	FWHM (sec)	BPC	TIC Correlation
Sample 2	Pass	1664	45804	27.53	97032	0.36	16.73	1.09E8	1.0000
Average	Pass	1664	45804	27.53	97032	0.36	16.73	1.09E8	1.0000



Method C

Data QC

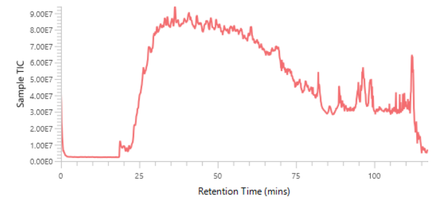
Sample Name	ALL Attributes	# MS1	# MS2	MS2/MS1 Rate	# Detected Feature	Full Width (min)	FWHM (sec)	BPC	TIC Correlation
Sample 3	Pass	2404	31914	13.28	94158	0.56	24.52	1.64E8	1.0000
Average	Pass	2404	31914	13.28	94158	0.56	24.52	1.64E8	1.0000



Method D

Data QC

Sample Name	ALL Attributes	# MS1	# MS2	MS2/MS1 Rate	# Detected Feature	Full Width (min)	FWHM (sec)	BPC	TIC Correlation
Sample 4	Pass	2541	70920	27.91	90875	0.51	22.25	7.93E7	1.0000
Average	Pass	2541	70920	27.91	90875	0.51	22.25	7.93E7	1.0000



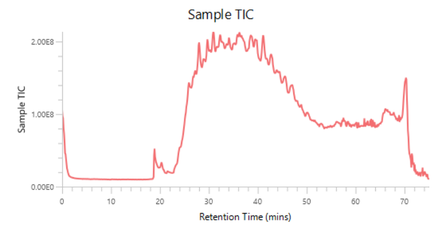
(b)

Data QC (PEAKS Studio 11, *Escherichia coli*, E.coli)

Method A

Data QC

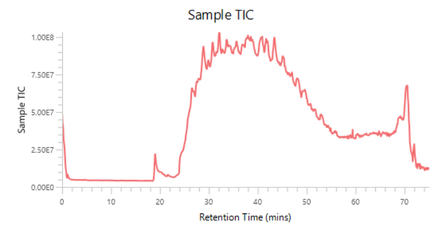
Sample Name	ALL Attributes	# MS1	# MS2	MS2/MS1 Rate	# Detected Feature	Full Width (min)	FWHM (sec)	BPC	TIC Correlation
Sample 1	Pass	1552	19689	12.69	100085	0.35	17.28	1.6E8	1.0000
Average	Pass	1552	19689	12.69	100085	0.35	17.28	1.6E8	1.0000



Method B

Data QC

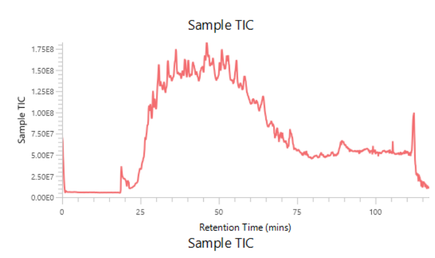
Sample Name	ALL Attributes	# MS1	# MS2	MS2/MS1 Rate	# Detected Feature	Full Width (min)	FWHM (sec)	BPC	TIC Correlation
Sample 2	Pass	1607	43617	27.14	92551	0.33	15.84	8.27E7	1.0000
Average	Pass	1607	43617	27.14	92551	0.33	15.84	8.27E7	1.0000



Method C

Data QC

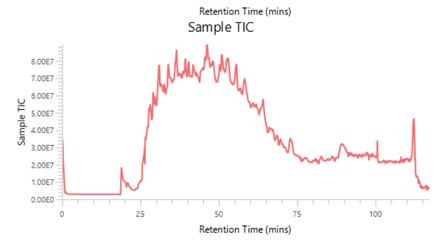
Sample Name	ALL Attributes	# MS1	# MS2	MS2/MS1 Rate	# Detected Feature	Full Width (min)	FWHM (sec)	BPC	TIC Correlation
Sample 3	Pass	2426	29809	12.29	87423	0.48	21.71	1.34E8	1.0000
Average	Pass	2426	29809	12.29	87423	0.48	21.71	1.34E8	1.0000



Method D

Data QC

Sample Name	ALL Attributes	# MS1	# MS2	MS2/MS1 Rate	# Detected Feature	Full Width (min)	FWHM (sec)	BPC	TIC Correlation
Sample 4	Pass	2528	66546	26.32	85709	0.44	19.96	6.55E7	1.0000
Average	Pass	2528	66546	26.32	85709	0.44	19.96	6.55E7	1.0000



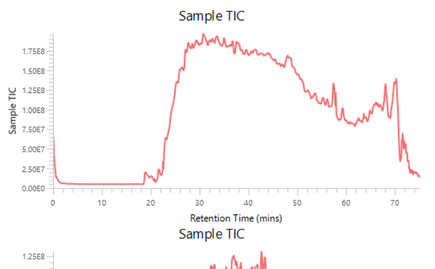
(c)

Data QC (PEAKS Studio 11, Albumin depleted plasma)

Method A

Data QC

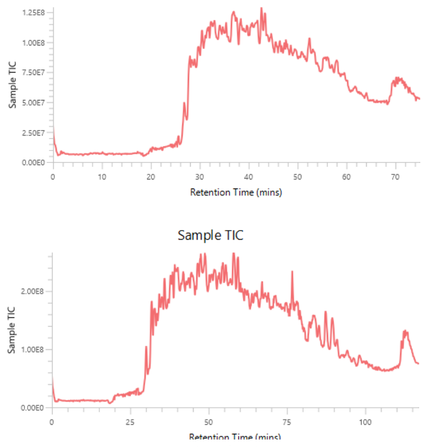
Sample Name	ALL Attributes	# MS1	# MS2	MS2/MS1 Rate	# Detected Feature	Full Width (min)	FWHM (sec)	BPC	TIC Correlation
Sample 1	Pass	1571	19843	12.63	120457	0.40	17.79	1.81E8	1.0000
Average	Pass	1571	19843	12.63	120457	0.40	17.79	1.81E8	1.0000



Method B

Data QC

Sample Name	ALL Attributes	# MS1	# MS2	MS2/MS1 Rate	# Detected Feature	Full Width (min)	FWHM (sec)	BPC	TIC Correlation
Sample 6	Pass	1727	43390	25.12	104035	0.29	13.79	9.56E7	1.0000
Average	Pass	1727	43390	25.12	104035	0.29	13.79	9.56E7	1.0000



Method C

Data QC

Sample Name	ALL Attributes	# MS1	# MS2	MS2/MS1 Rate	# Detected Feature	Full Width (min)	FWHM (sec)	BPC	TIC Correlation
Sample 7	Pass	2368	30894	13.05	108142	0.57	22.53	2E8	1.0000
Average	Pass	2368	30894	13.05	108142	0.57	22.53	2E8	1.0000

Method D

Data QC

Sample Name	ALL Attributes	# MS1	# MS2	MS2/MS1 Rate	# Detected Feature	Full Width (min)	FWHM (sec)	BPC	TIC Correlation
Sample 4	Pass	2705	67818	25.07	107647	0.53	23.36	8.16E7	1.0000
Average	Pass	2705	67818	25.07	107647	0.53	23.36	8.16E7	1.0000

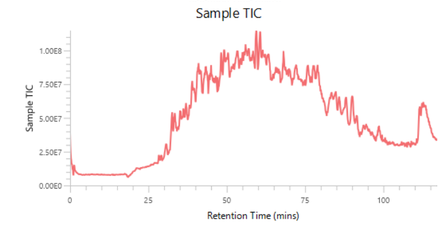


Figure S8. Data QC results from CHO (**a**) *E.coli* (**b**) and albumin depleted human plasma (**c**) computed by PEAKS.
LC-MS/MS methods:
Method A: LC gradient 48 min, MS-2.00 Hz, MS/MS-4.00 Hz
Method B: LC gradient 48 min, MS-4.00 Hz, MS/MS-8.00 Hz
Method C: LC gradient 90 min, MS-2.00 Hz, MS/MS-4.00 Hz
Method D: LC gradient 90 min, MS-4.00 Hz, MS/MS-8.00 Hz.

CHO

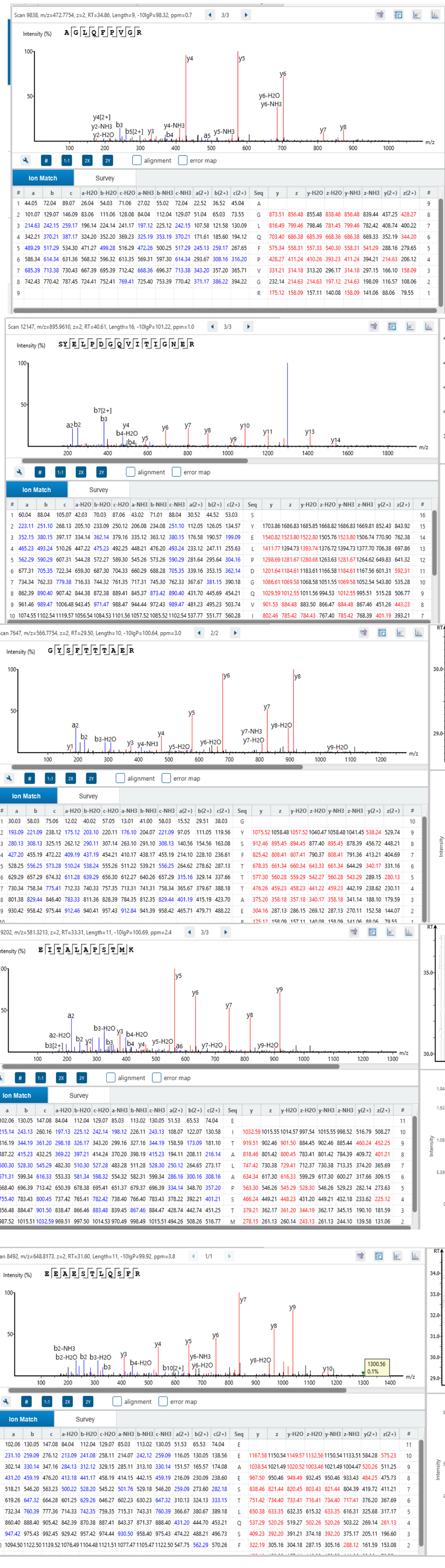
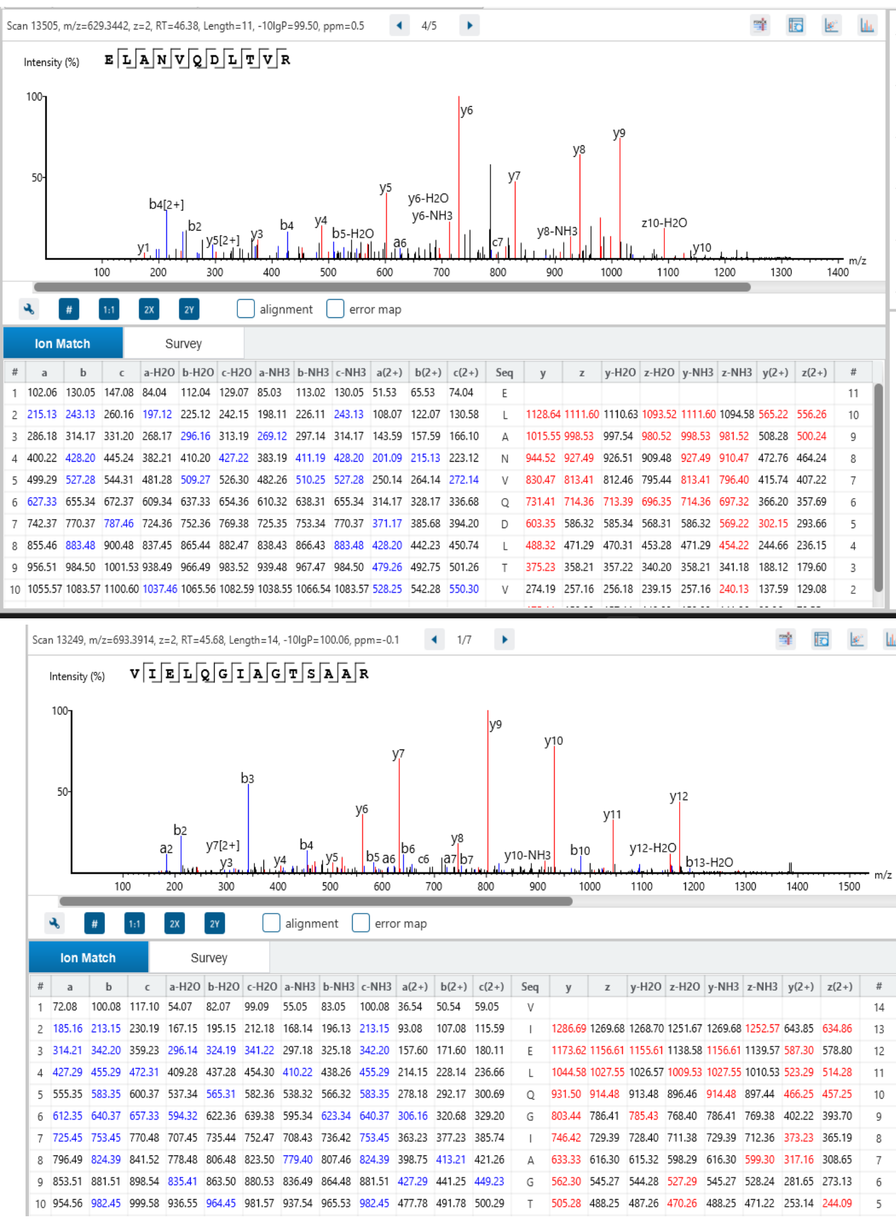
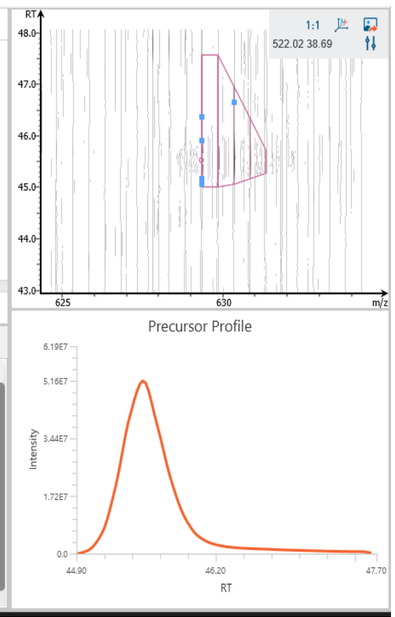


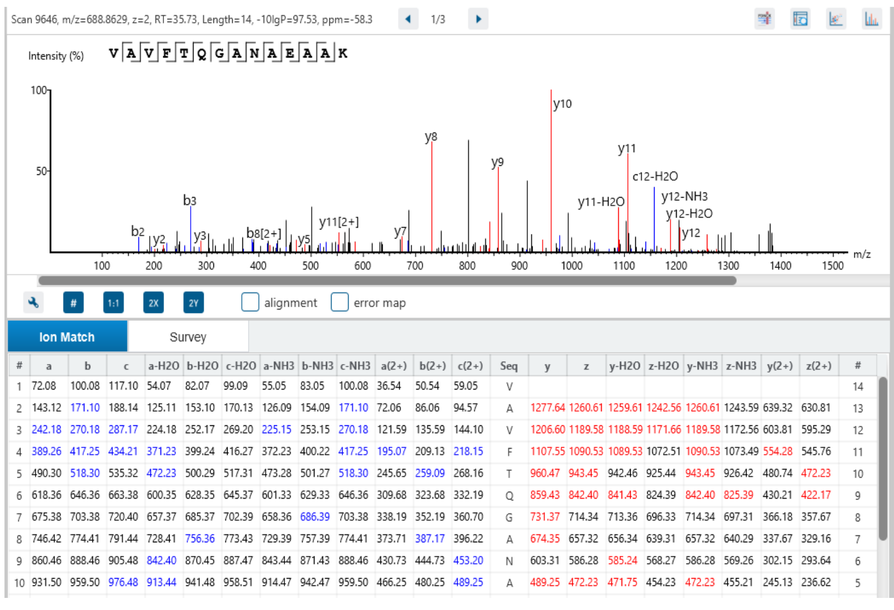
Figure S9. MS/MS spectra of peptides and precursor profiles from CHO sample (PEAKS Studio 11)

E.coli

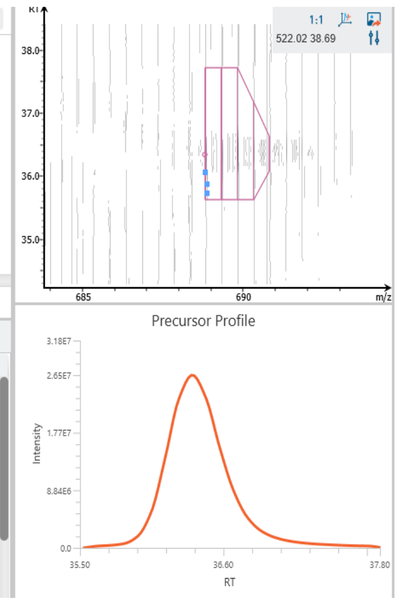


#	a	b	c	a-H2O	b-H2O	c-H2O	a-NH3	b-NH3	c-NH3	a(2+)	b(2+)	c(2+)	Seq	y	z	y-H2O	z-H2O	y-NH3	z-NH3	y(2+)	z(2+)	#
1	102.06	130.05	147.08	84.04	112.04	129.07	85.03	113.02	130.05	51.53	65.53	74.04	E									11
2	215.13	243.13	260.16	197.12	225.12	242.15	198.11	226.11	243.13	108.07	122.07	130.58	L	1128.64	1111.60	1110.63	1093.52	1111.60	1094.58	565.22	556.26	10
3	286.18	314.17	331.20	268.17	296.16	313.19	269.12	297.14	314.17	143.59	157.59	166.10	A	1015.55	998.53	997.54	980.52	998.53	981.52	508.28	500.24	9
4	400.22	428.20	445.24	382.21	410.20	427.22	383.19	411.19	428.20	201.09	215.13	223.12	N	944.52	927.49	926.51	909.48	927.49	910.47	472.76	464.24	8
5	499.29	527.28	544.31	481.28	509.27	526.30	482.26	510.25	527.28	250.14	264.14	272.14	V	830.47	813.41	812.46	795.44	813.41	796.40	415.74	407.22	7
6	627.33	655.34	672.37	609.34	637.33	654.36	610.32	638.31	655.34	314.17	328.17	336.68	Q	731.41	714.36	713.39	696.35	714.36	697.32	366.20	357.69	6
7	742.37	770.37	787.46	724.36	752.36	769.38	725.35	753.34	770.37	371.17	385.68	394.20	D	603.35	586.32	585.34	568.31	586.32	569.22	302.15	293.66	5
8	855.46	883.48	900.48	837.45	865.44	882.47	838.43	866.43	883.48	428.20	442.23	450.74	L	488.32	471.29	470.31	453.28	471.29	454.22	244.66	236.15	4
9	956.51	984.50	1001.53	938.49	966.49	983.52	939.48	967.47	984.50	479.26	492.75	501.26	T	375.23	358.21	357.22	340.20	358.21	341.18	188.12	179.60	3
10	1055.57	1083.57	1100.60	1037.46	1065.56	1082.59	1038.55	1066.54	1083.57	528.25	542.28	550.30	V	274.19	257.16	256.18	239.15	257.16	240.13	137.59	129.08	2

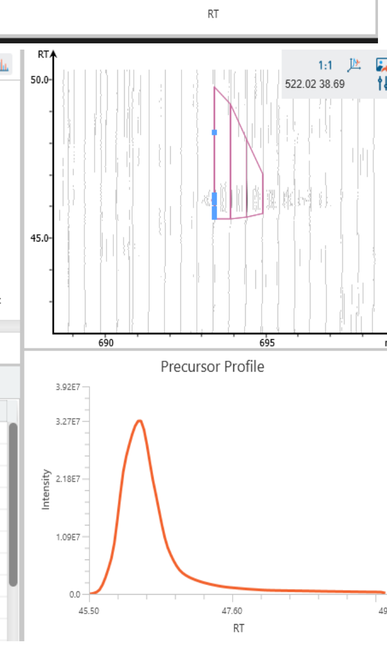


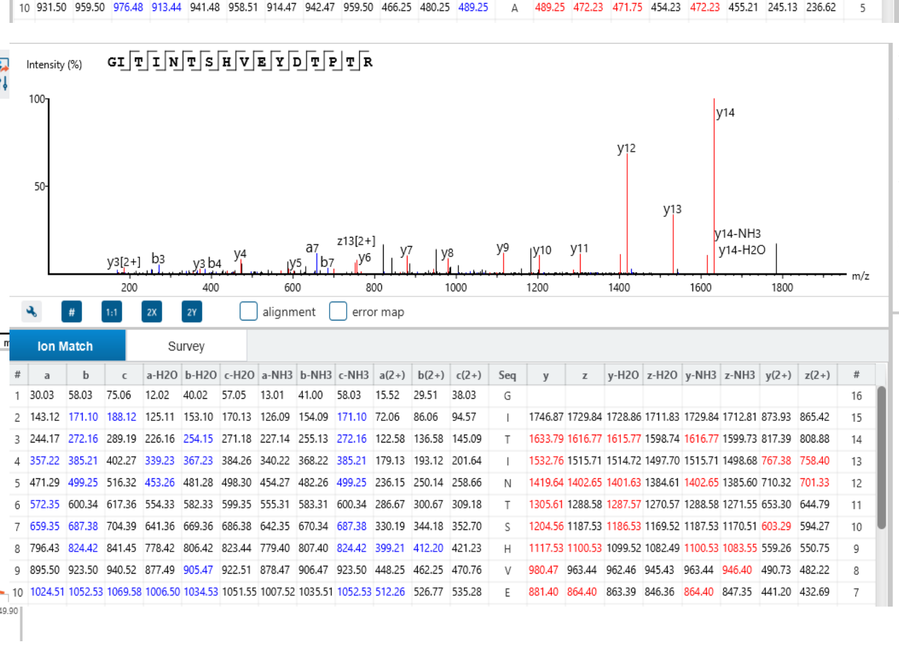


#	a	b	c	a-H2O	b-H2O	c-H2O	a-NH3	b-NH3	c-NH3	a(2+)	b(2+)	c(2+)	Seq	y	z	y-H2O	z-H2O	y-NH3	z-NH3	y(2+)	z(2+)	#
1	72.08	100.08	117.10	54.07	82.07	99.09	55.05	83.05	100.08	36.54	50.54	59.05	V									14
2	143.12	171.10	188.14	125.11	153.10	170.13	126.09	154.09	171.10	72.06	86.06	94.57	A	1277.64	1260.61	1259.61	1242.56	1260.61	1243.59	639.32	630.81	13
3	242.18	270.18	287.17	224.18	252.17	269.20	225.15	253.15	270.18	121.59	135.59	144.10	V	1206.60	1189.58	1188.59	1171.66	1189.58	1172.56	603.81	595.29	12
4	389.26	417.25	434.21	371.23	399.24	416.27	372.23	400.22	417.25	195.07	209.13	218.15	F	1107.55	1090.53	1089.53	1072.51	1090.53	1073.49	554.28	545.76	11
5	490.30	518.30	535.32	472.23	500.29	517.31	473.28	501.27	518.30	245.65	259.09	268.16	T	960.47	943.45	942.46	925.44	943.45	926.42	480.74	472.23	10
6	618.36	646.36	663.38	600.35	628.35	645.37	601.33	629.33	646.36	309.68	323.68	332.19	Q	859.43	842.40	841.43	824.39	842.40	825.39	430.21	422.17	9
7	675.38	703.38	720.40	657.37	685.37	702.39	658.36	686.39	703.38	338.19	352.19	360.70	G	731.37	714.34	713.36	696.33	714.34	697.31	366.18	357.67	8
8	746.42	774.41	791.44	728.41	756.36	773.43	729.39	757.39	774.41	373.71	387.17	396.22	A	674.35	657.32	656.34	639.31	657.32	640.29	337.67	329.16	7
9	860.46	888.46	905.48	842.40	870.45	887.47	843.44	871.43	888.46	430.73	444.73	453.20	N	603.31	586.28	585.24	568.27	586.28	569.26	302.15	293.64	6
10	931.50	959.50	976.48	913.44	941.48	958.51	914.47	942.47	959.50	466.25	480.25	489.25	A	489.25	472.23	471.75	454.23	472.23	455.21	245.13	236.62	5

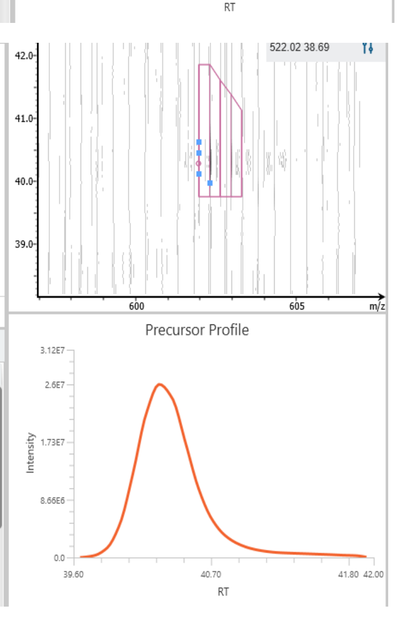


#	a	b	c	a-H2O	b-H2O	c-H2O	a-NH3	b-NH3	c-NH3	a(2+)	b(2+)	c(2+)	Seq	y	z	y-H2O	z-H2O	y-NH3	z-NH3	y(2+)	z(2+)	#
1	72.08	100.08	117.10	54.07	82.07	99.09	55.05	83.05	100.08	36.54	50.54	59.05	V									14
2	185.16	213.15	230.19	167.15	195.15	212.18	168.14	196.13	213.15	93.08	107.08	115.59	I	1286.69	1269.68	1268.70	1251.67	1269.68	1252.57	643.85	634.86	13
3	314.21	342.20	359.23	296.14	324.19	341.22	297.18	325.18	342.20	157.60	171.60	180.11	E	1173.62	1156.61	1155.61	1138.58	1156.61	1139.57	587.30	578.80	12
4	427.29	455.29	472.31	409.28	437.28	454.30	410.22	438.26	455.29	214.15	228.14	236.66	L	1044.58	1027.55	1026.57	1009.53	1027.55	1010.53	523.29	514.28	11
5	555.35	583.35	600.37	537.34	565.31	582.36	538.32	566.32	583.35	278.18	292.17	300.69	Q	931.50	914.48	913.48	896.46	914.48	897.44	466.25	457.25	10
6	612.35	640.37	657.33	594.32	622.36	639.38	595.34	623.34	640.37	306.16	320.68	329.20	G	803.44	786.41	785.43	768.40	786.41	769.38	402.22	393.70	9
7	725.45	753.45	770.48	707.45	735.44	752.47	708.43	736.42	753.45	363.23	377.23	385.74	I	746.42	729.39	728.40	711.38	729.39	712.36	373.23	365.19	8
8	796.49	824.39	841.52	778.48	806.48	823.50	779.40	807.46	824.39	398.75	413.21	421.26	A	633.33	616.30	615.32	598.29	616.30	599.30	317.16	308.65	7
9	853.51	881.51	898.54	835.41	863.50	880.53	836.49	864.48	881.51	427.29	441.25	449.23	G	562.30	545.27	544.28	527.29	545.27	528.24	281.65	273.13	6
10	954.56	982.45	999.58	936.55	964.45	981.57	937.54	965.53	982.45	477.78	491.78	500.29	T	505.28	488.25	487.26	470.26	488.25	471.22	253.14	244.09	5



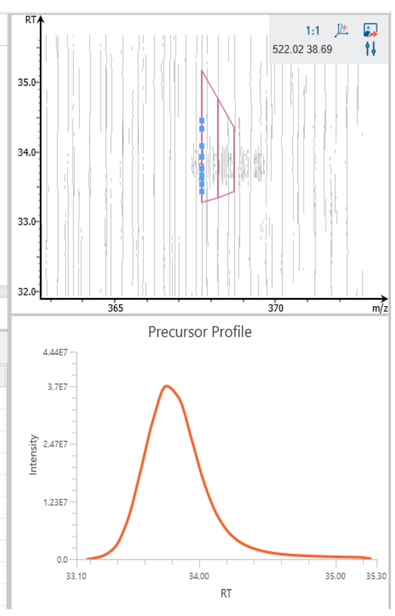


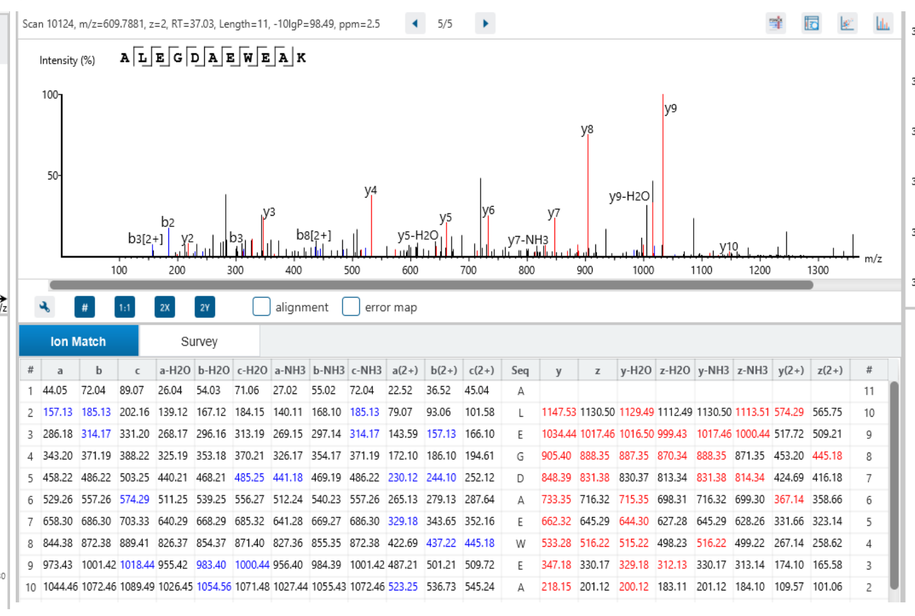
#	a	b	c	a-H2O	b-H2O	c-H2O	a-NH3	b-NH3	c-NH3	a(2+)	b(2+)	c(2+)	Seq	y	z	y-H2O	z-H2O	y-NH3	z-NH3	y(2+)	z(2+)	#
1	30.03	58.03	75.06	12.02	40.02	57.05	13.01	41.00	58.03	15.52	29.51	38.03	G									16
2	143.12	171.10	188.12	125.11	153.10	170.13	126.09	154.09	171.10	72.06	86.06	94.57	I	1746.87	1729.84	1728.86	1711.83	1729.84	1712.81	873.93	865.42	15
3	244.17	272.16	289.19	226.16	254.15	271.18	227.14	255.13	272.16	122.58	136.58	145.09	T	1633.79	1616.77	1615.77	1598.74	1616.77	1599.73	817.39	808.88	14
4	357.22	385.21	402.27	339.23	367.23	384.26	340.22	368.22	385.21	179.13	193.12	201.64	I	1532.76	1515.71	1514.72	1497.70	1515.71	1498.68	767.38	758.40	13
5	471.29	499.25	516.32	453.26	481.28	498.30	454.27	482.26	499.25	236.15	250.14	258.66	N	1419.64	1402.65	1401.63	1384.61	1402.65	1385.60	710.32	701.33	12
6	572.35	600.34	617.36	554.33	582.33	599.35	555.31	583.31	600.34	286.67	300.67	309.18	T	1305.61	1288.58	1287.57	1270.57	1288.58	1271.55	653.30	644.79	11
7	659.35	687.38	704.39	641.36	669.36	686.38	642.35	670.34	687.38	330.19	344.18	352.70	S	1204.56	1187.53	1186.53	1169.52	1187.53	1170.51	603.29	594.27	10
8	796.43	824.42	841.45	778.42	806.42	823.44	779.40	807.40	824.42	399.21	412.20	421.23	H	1117.53	1100.53	1099.52	1082.49	1100.53	1083.55	559.26	550.75	9
9	895.50	923.50	940.52	877.49	905.47	922.51	878.47	906.47	923.50	448.25	462.25	470.76	V	980.47	963.44	962.46	945.43	963.44	946.40	490.73	482.22	8
10	1024.51	1052.53	1069.58	1006.50	1034.53	1051.55	1007.52	1035.51	1052.53	512.26	526.77	535.28	E	881.40	864.40	863.39	846.36	864.40	847.35	441.20	432.69	7



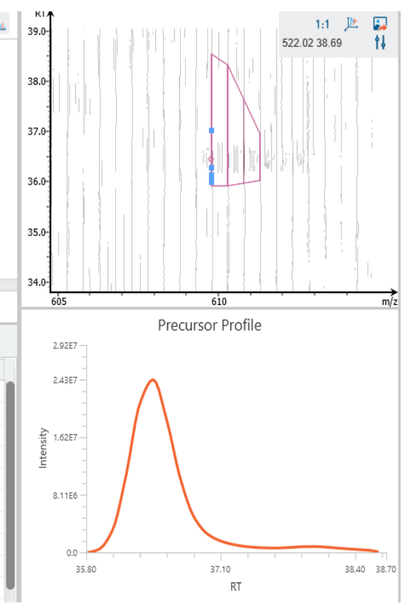


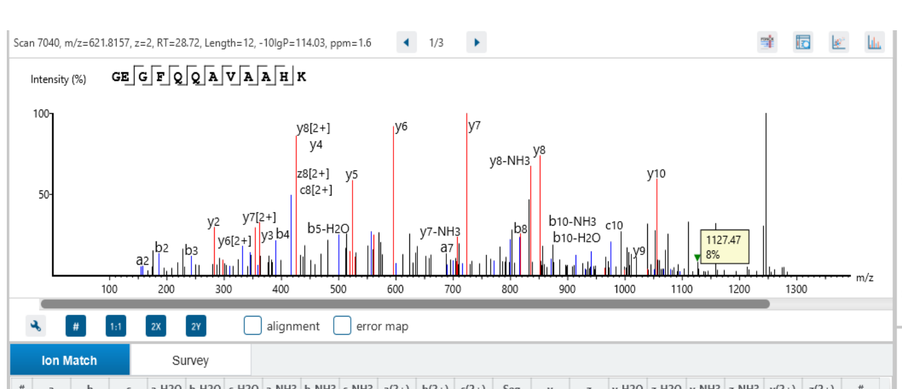
#	a	b	c	a-H2O	b-H2O	c-H2O	a-NH3	b-NH3	c-NH3	a(2+)	b(2+)	c(2+)	Seq	y	z	y-H2O	z-H2O	y-NH3	z-NH3	y(2+)	z(2+)	#
1	136.08	164.07	181.10	118.07	146.06	163.09	119.05	147.04	164.07	68.54	82.54	91.05	Y									6
2	233.14	261.20	278.15	215.12	243.11	260.19	216.11	244.15	261.20	117.06	131.06	139.58	P	571.35	554.32	553.34	536.31	554.32	537.29	286.17	277.66	5
3	332.20	360.19	377.22	314.19	342.18	359.21	315.17	343.17	360.19	166.60	180.60	189.11	V	474.29	457.28	456.29	439.25	457.28	440.24	237.65	229.11	4
4	447.22	475.22	492.25	429.19	457.28	474.29	430.20	458.19	475.22	224.11	238.11	246.62	D	375.22	358.20	357.21	340.19	358.20	341.17	188.11	179.60	3
5	560.31	588.31	605.33	542.29	570.29	587.32	543.28	571.35	588.31	280.65	294.65	303.17	L	260.19	243.17	242.19	225.16	243.17	226.14	130.60	122.08	2
6													K	147.04	130.09	129.10	112.08	130.09	113.06	74.06	65.54	1



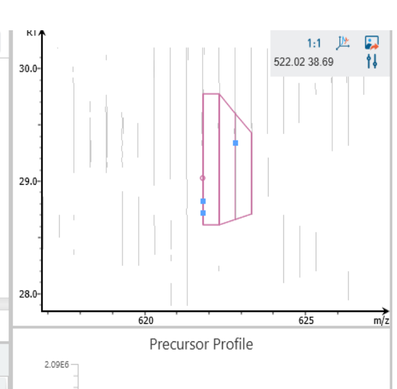


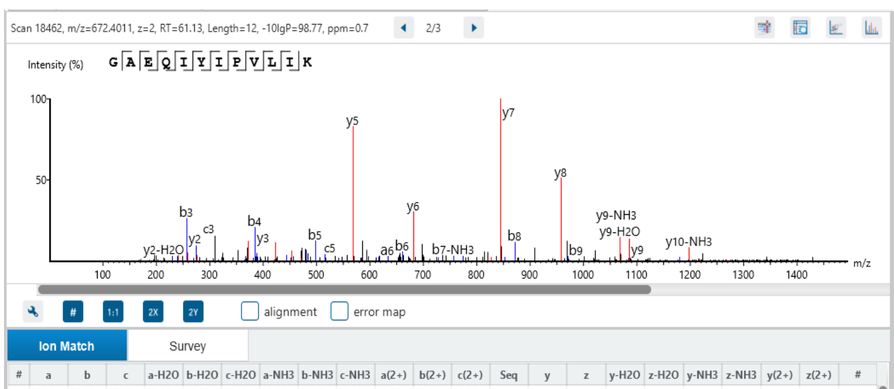
#	a	b	c	a-H2O	b-H2O	c-H2O	a-NH3	b-NH3	c-NH3	a(2+)	b(2+)	c(2+)	Seq	y	z	y-H2O	z-H2O	y-NH3	z-NH3	y(2+)	z(2+)	#
1	44.05	72.04	89.07	26.04	54.03	71.06	27.02	55.02	72.04	22.52	36.52	45.04	A									11
2	157.13	185.13	202.16	139.12	167.12	184.15	140.11	168.10	185.13	79.07	93.06	101.58	L	1147.53	1130.50	1129.49	1112.49	1130.50	1113.51	574.29	565.75	10
3	286.18	314.17	331.20	268.17	296.16	313.19	269.15	297.14	314.17	143.59	157.13	166.10	E	1034.44	1017.46	1016.50	999.43	1017.46	1000.44	517.72	509.21	9
4	343.20	371.19	388.22	325.19	353.18	370.21	326.17	354.17	371.19	172.10	186.10	194.61	G	905.40	888.35	887.35	870.34	888.35	871.35	453.20	445.18	8
5	458.22	486.22	503.25	440.21	468.21	485.25	441.18	469.19	486.22	230.12	244.10	252.12	D	848.39	831.38	830.37	813.34	831.38	814.34	424.69	416.18	7
6	529.26	557.26	574.29	511.25	539.25	556.27	512.24	540.23	557.26	265.13	279.13	287.64	A	733.35	716.32	715.35	698.31	716.32	699.30	367.14	358.66	6
7	658.30	686.30	703.33	640.29	668.29	685.32	641.28	669.27	686.30	329.18	343.65	352.16	E	662.32	645.29	644.30	627.28	645.29	628.26	331.66	323.14	5
8	844.38	872.38	889.41	826.37	854.37	871.40	827.36	855.35	872.38	422.69	437.22	445.18	W	533.28	516.22	515.22	498.23	516.22	499.22	267.14	258.62	4
9	973.43	1001.42	1018.44	955.42	983.40	1000.44	956.40	984.39	1001.42	487.21	501.21	509.72	E	347.18	330.17	329.18	312.13	330.17	313.14	174.10	165.58	3
10	1044.46	1072.46	1089.49	1026.45	1054.56	1071.48	1027.44	1055.43	1072.46	523.25	536.73	545.24	A	218.15	201.12	200.12	183.11	201.12	184.10	109.57	101.06	2



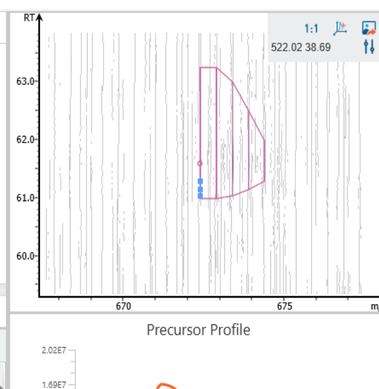


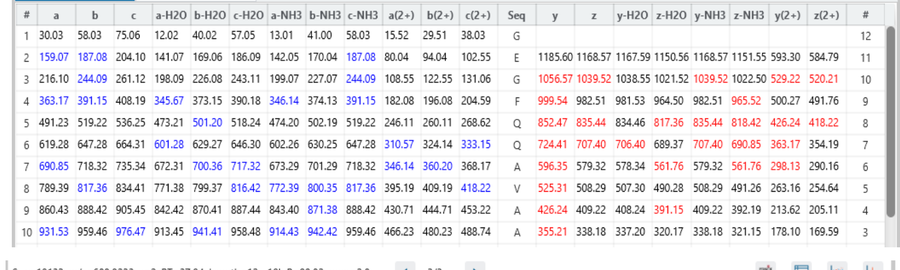
#	a	b	c	a-H2O	b-H2O	c-H2O	a-NH3	b-NH3	c-NH3	a(2+)	b(2+)	c(2+)	Seq	y	z	y-H2O	z-H2O	y-NH3	z-NH3	y(2+)	z(2+)	#
1	30.03	58.03	75.06	12.02	40.02	57.05	13.01	41.00	58.03	15.52	29.51	38.03	G									12
2	159.07	187.08	204.10	141.07	169.06	186.09	142.05	170.04	187.08	80.04	94.04	102.55	E	1185.60	1168.57	1167.59	1150.56	1168.57	1151.55	593.30	584.79	11
3	216.10	244.09	261.12	198.09	226.08	243.11	199.07	227.07	244.09	108.55	122.55	131.06	G	1056.57	1039.52	1038.55	1021.52	1039.52	1022.50	529.22	520.21	10
4	363.17	391.15	408.19	345.67	373.15	390.18	346.14	374.13	391.15	182.08	196.08	204.59	F	999.54	982.51	981.53	964.50	982.51	965.52	500.27	491.76	9
5	491.23	519.22	536.25	473.21	501.20	518.24	474.20	502.19	519.22	246.11	260.11	268.62	Q	852.47	835.44	834.46	817.36	835.44	818.42	426.24	418.22	8
6	619.28	647.28	664.31	601.28	629.27	646.30	602.26	630.25	647.28	310.57	324.14	333.15	Q	724.41	707.40	706.40	689.37	707.40	690.85	363.17	354.19	7
7	690.85	718.32	735.34	672.31	700.36	717.32	673.29	701.29	718.32	346.14	360.20	368.17	A	596.35	579.32	578.34	561.76	579.32	561.76	298.13	290.16	6
8	789.39	817.36	834.41	771.38	799.37	816.42	772.39	800.35	817.36	395.19	409.19	418.22	V	525.31	508.29	507.30	490.28	508.29	491.26	263.16	254.64	5
9	860.43	888.42	905.45	842.42	870.41	887.44	843.40	871.38	888.42	430.71	444.71	453.22	A	426.24	409.22	408.24	391.15	409.22	392.19	213.62	205.11	4
10	931.53	959.46	976.47	913.45	941.41	958.48	914.43	942.42	959.46	466.23	480.23	488.74	A	355.21	338.18	337.20	320.17	338.18	321.15	178.10	169.59	3



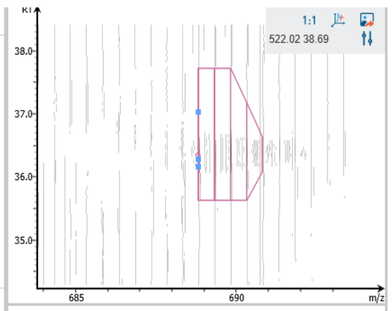


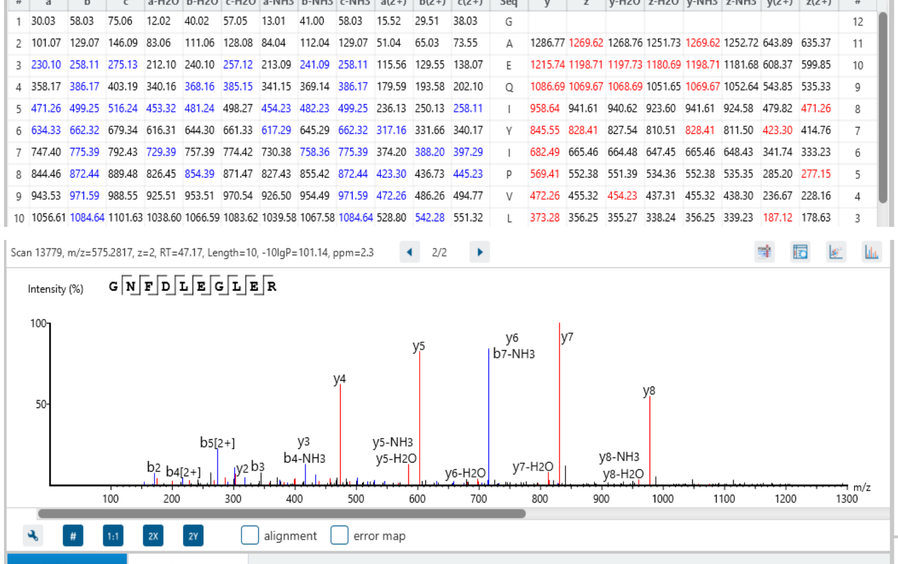
#	a	b	c	a-H2O	b-H2O	c-H2O	a-NH3	b-NH3	c-NH3	a(2+)	b(2+)	c(2+)	Seq	y	z	y-H2O	z-H2O	y-NH3	z-NH3	y(2+)	z(2+)	#
1	30.03	58.03	75.06	12.02	40.02	57.05	13.01	41.00	58.03	15.52	29.51	38.03	G									12
2	101.07	129.07	146.09	83.06	111.06	128.08	84.04	112.04	129.07	51.04	65.03	73.55	A	1286.77	1269.62	1268.76	1251.73	1269.62	1252.72	643.89	635.37	11
3	230.10	258.11	275.13	212.10	240.10	257.12	213.09	241.09	258.11	115.56	129.55	138.07	E	1215.74	1198.71	1197.73	1180.69	1198.71	1181.68	608.37	599.85	10
4	358.17	386.17	403.19	340.16	368.16	385.15	341.15	369.14	386.17	179.59	193.58	202.10	Q	1086.69	1069.67	1068.69	1051.65	1069.67	1052.64	543.85	535.33	9
5	471.26	499.25	516.24	453.32	481.24	498.27	454.23	482.23	499.25	236.13	250.13	258.11	I	958.64	941.61	940.62	923.60	941.61	924.58	479.82	471.26	8
6	634.33	662.32	679.34	616.31	644.30	661.33	617.29	645.29	662.32	317.16	331.66	340.17	Y	845.55	828.41	827.54	810.51	828.41	811.50	423.30	414.76	7
7	747.40	775.39	792.43	729.39	757.39	774.42	730.38	758.36	775.39	374.20	388.20	397.29	I	682.49	665.46	664.48	647.45	665.46	648.43	341.74	333.23	6
8	844.46	872.44	889.48	826.45	854.39	871.47	827.43	855.42	872.44	423.30	436.73	445.23	P	569.41	552.38	551.39	534.36	552.38	535.35	285.20	277.15	5
9	943.53	971.59	988.55	925.51	953.51	970.54	926.50	954.49	971.59	472.26	486.26	494.77	V	472.26	455.32	454.23	437.31	455.32	438.30	236.67	228.16	4
10	1056.61	1084.64	1101.63	1038.60	1066.59	1083.62	1039.58	1067.58	1084.64	528.80	542.28	551.32	L	373.28	356.25	355.27	338.24	356.25	339.23	187.12	178.63	3





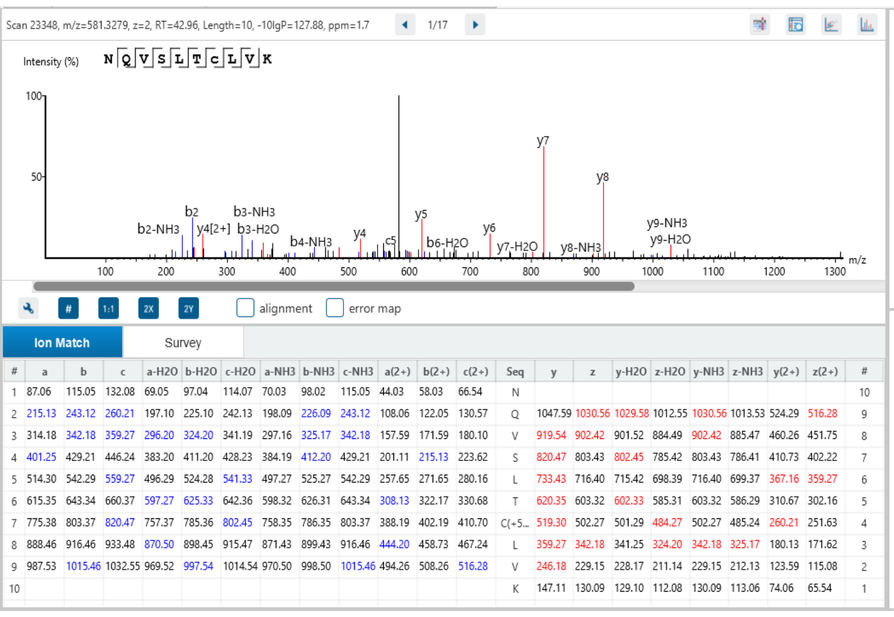
#	a	b	c	a-H2O	b-H2O	c-H2O	a-NH3	b-NH3	c-NH3	a(2+)	b(2+)	c(2+)	Seq	y	z	y-H2O	z-H2O	y-NH3	z-NH3	y(2+)	z(2+)	#
1	44.05	72.04	89.07	26.04	54.03	71.06	27.02	55.02	72.04	22.52	36.52	45.04	A									12
2	191.11	219.11	236.14	173.11	201.12	218.13	174.09	202.09	219.11	96.06	110.06	118.57	F	1305.56	1288.57	1287.59	1270.56	1288.57	1271.54	653.30	644.78	11
3	306.15	334.14	351.17	288.13	316.13	333.16	289.12	317.11	334.14	153.57	167.57	176.08	D	1158.53	1141.50	1140.52	1123.49	1141.50	1124.49	580.27	571.25	10
4	434.20	462.20	479.23	416.19	444.19	461.22	417.18	445.17	462.20	217.60	231.60	240.11	Q	1043.51	1026.48	1025.51	1008.46	1026.48	1009.46	522.25	514.26	9
5	547.29	575.29	592.31	529.28	557.30	574.30	530.27	558.26	575.29	274.14	288.14	296.65	I	915.44	898.41	897.43	880.43	898.41	881.39	458.22	449.71	8
6	662.31	690.31	707.34	644.30	672.30	689.33	645.29	673.28	690.31	331.66	345.65	354.17	D	802.36	785.33	784.35	767.32	785.33	768.33	401.68	393.24	7
7	776.36	804.35	821.38	758.35	786.34	803.36	759.33	787.34	804.35	388.68	402.68	411.19	N	687.33	670.30	669.32	652.29	670.30	653.30	344.17	335.65	6
8	847.39	875.39	892.42	829.38	857.39	874.41	830.37	858.38	875.39	424.20	438.19	446.26	A	573.29	556.26	555.28	538.25	556.26	539.23	287.14	278.63	5
9	944.45	972.47	989.47	926.44	954.43	971.47	927.42	955.42	972.47	472.20	486.72	495.23	P	502.25	485.22	484.25	467.21	485.22	468.20	251.63	243.11	4
10	1073.49	1101.49	1118.51	1055.48	1083.47	1100.50	1056.46	1084.46	1101.49	537.25	551.24	559.76	E	405.20	388.17	387.18	370.16	388.17	371.14	203.10	194.59	3

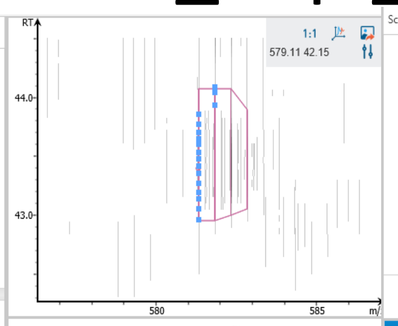


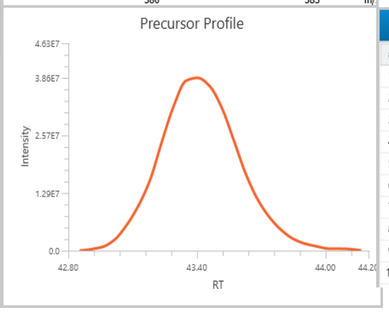


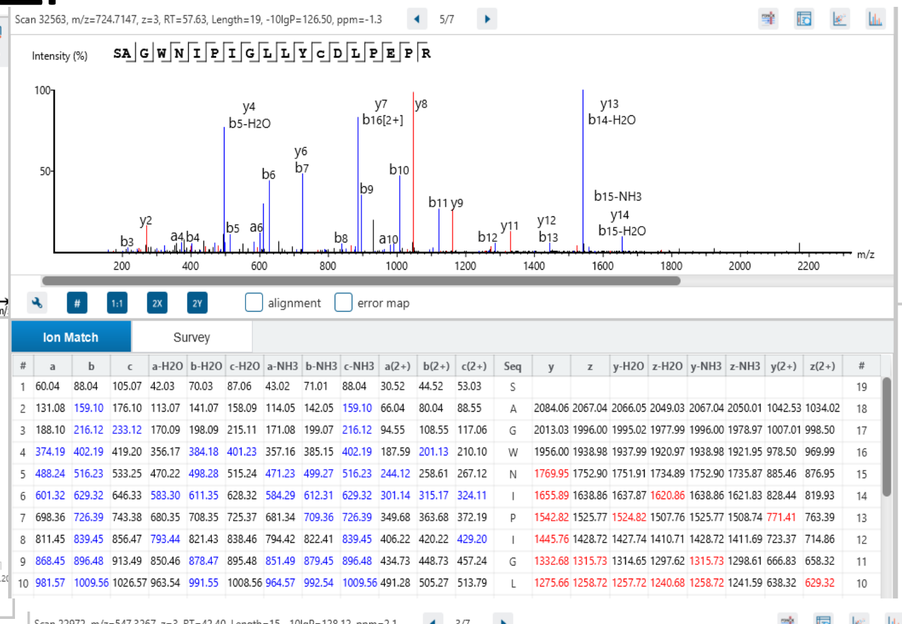
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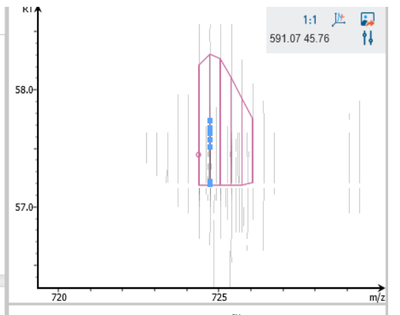
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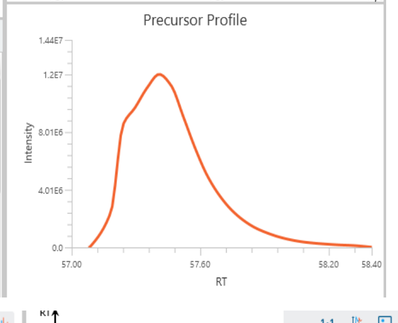






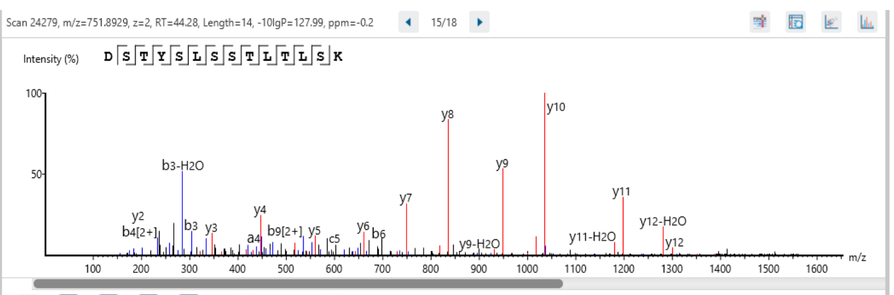


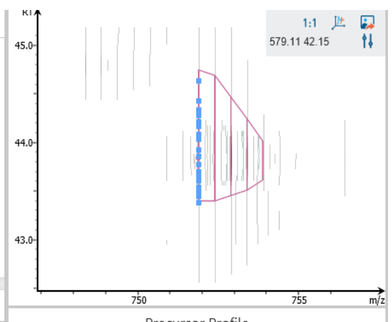


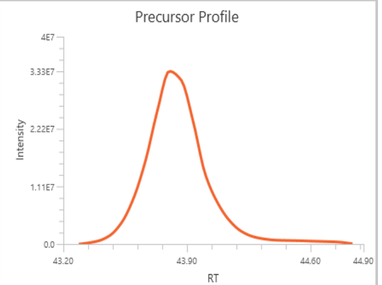


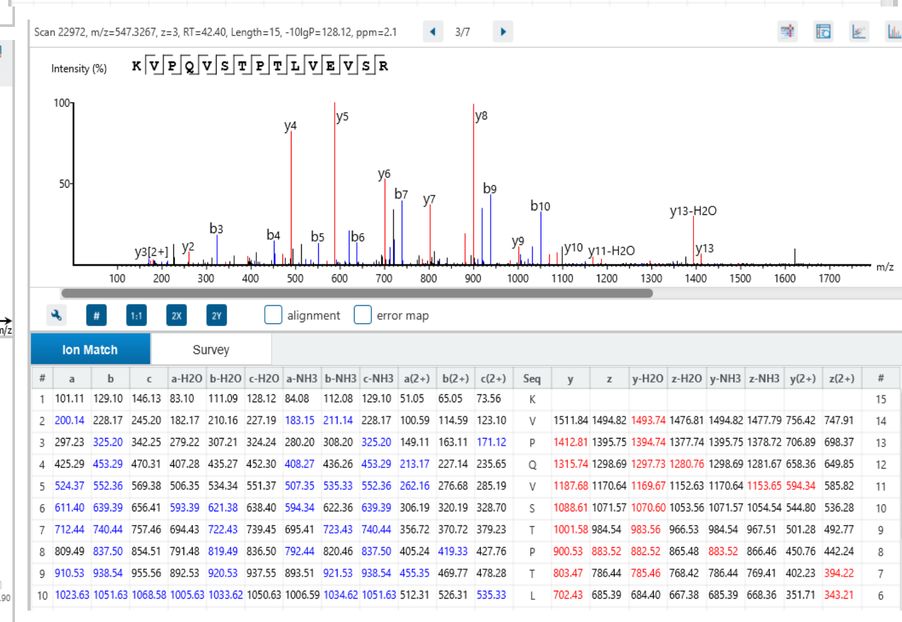
Ion Match | Survey

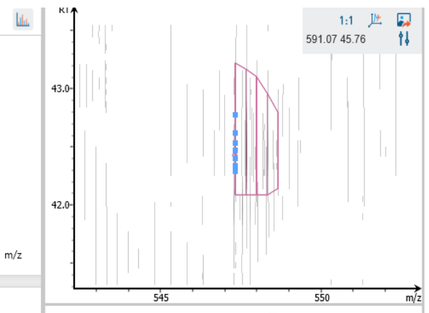
#	a	b	c	a-H2O	b-H2O	c-H2O	a-NH3	b-NH3	c-NH3	a(2+)	b(2+)	c(2+)	Seq	y	z	y-H2O	z-H2O	y-NH3	z-NH3	y(2+)	z(2+)	#
1	87.06	115.05	132.08	69.05	97.04	114.07	70.03	98.02	115.05	44.03	58.03	66.54	N									10
2	215.13	243.12	260.21	197.10	225.10	242.13	198.09	226.09	243.12	108.06	122.05	130.57	Q	1047.59	1030.56	1029.58	1012.55	1030.56	1013.53	524.29	516.28	9
3	314.18	342.18	359.27	296.20	324.20	341.19	297.16	325.17	342.18	157.59	171.59	180.10	V	919.54	902.42	901.52	884.49	902.42	885.47	460.26	451.75	8
4	401.25	429.21	446.24	383.20	411.20	428.23	384.19	412.20	429.21	201.11	215.13	223.62	S	820.47	803.43	802.45	785.42	803.43	786.41	410.73	402.22	7
5	514.30	542.29	559.27	496.29	524.28	541.33	497.27	525.27	542.29	257.65	271.65	280.16	L	733.43	716.40	715.42	698.39	716.40	699.37	367.16	359.27	6
6	615.35	643.34	660.37	597.27	625.33	642.36	598.32	626.31	643.34	308.13	322.17	330.68	T	620.35	603.32	602.33	585.31	603.32	586.29	310.67	302.16	5
7	775.38	803.37	820.47	757.37	785.36	802.45	758.35	786.35	803.37	388.19	402.19	410.70	C(+5...	519.30	502.27	501.29	484.27	502.27	485.24	260.21	251.63	4
8	888.46	916.46	933.48	870.50	898.45	915.47	871.43	899.43	916.46	444.20	458.73	467.24	L	359.27	342.18	341.25	324.20	342.18	325.17	180.13	171.62	3
9	987.53	1015.46	1032.55	969.52	997.54	1014.54	970.50	998.50	1015.46	494.26	508.26	516.28	V	246.18	229.15	228.17	211.14	229.15	212.13	123.59	115.08	2
10													K	147.11	130.09	129.10	112.08	130.09	113.06	74.06	65.54	1

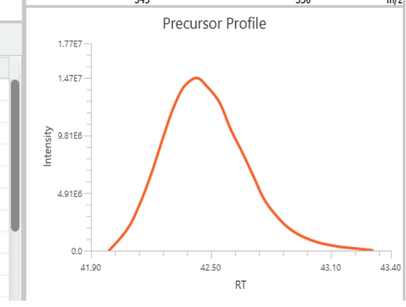






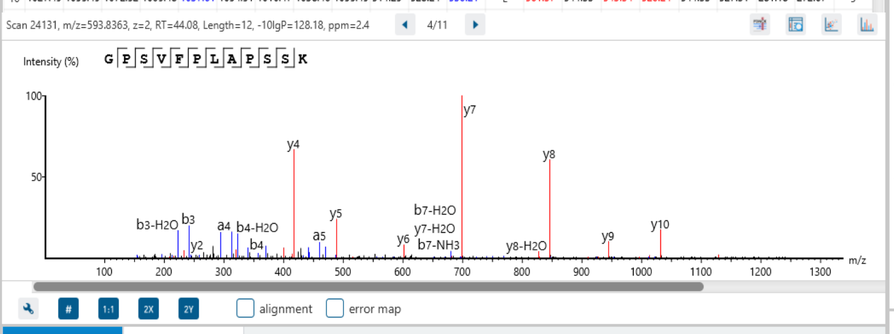


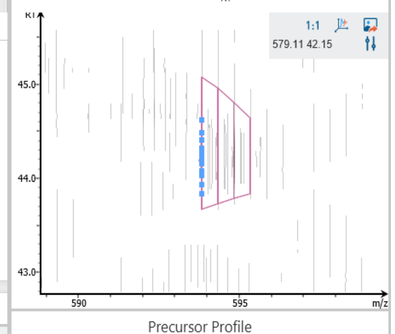


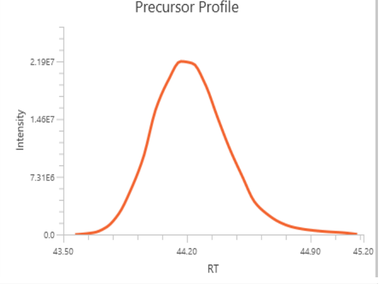


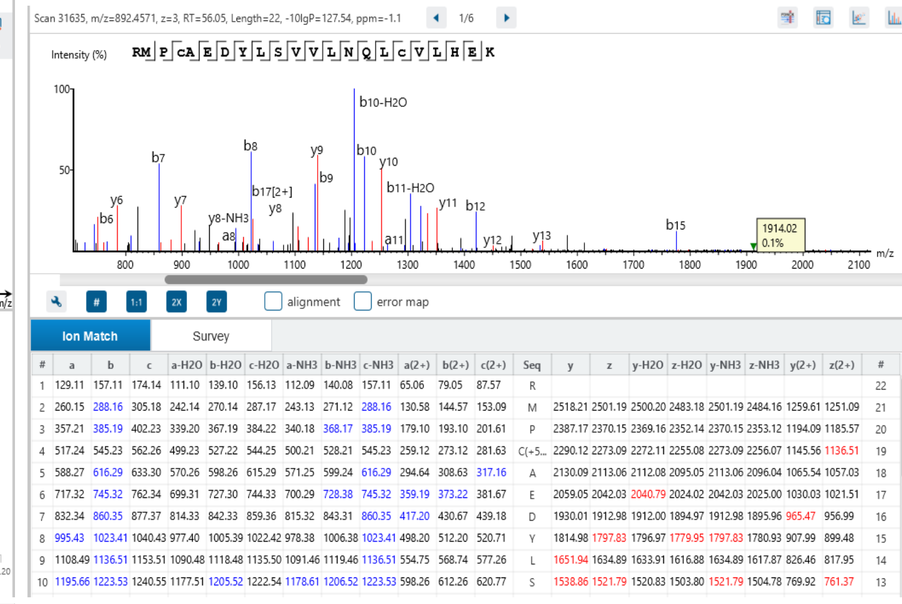
Ion Match | Survey

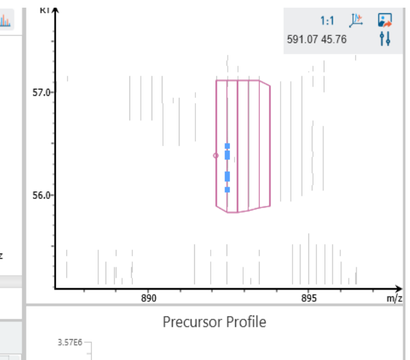
#	a	b	c	a-H2O	b-H2O	c-H2O	a-NH3	b-NH3	c-NH3	a(2+)	b(2+)	c(2+)	Seq	y	z	y-H2O	z-H2O	y-NH3	z-NH3	y(2+)	z(2+)	#
1	88.04	116.03	133.06	70.03	98.02	115.05	71.01	99.01	116.03	44.52	58.52	67.03	D									14
2	175.08	203.08	220.09	157.07	185.07	202.08	158.04	186.04	203.08	88.04	102.03	110.55	S	1387.75	1370.70	1369.72	1352.74	1370.70	1353.68	694.37	685.85	13
3	276.13	304.12	321.14	258.12	286.11	303.13	259.09	287.09	304.12	138.56	152.56	161.07	T	1300.72	1283.67	1282.71	1265.66	1283.67	1266.65	650.85	642.34	12
4	439.19	467.19	484.20	421.18	449.18	466.19	422.16	450.20	467.19	220.09	234.15	242.60	Y	1199.67	1182.62	1181.65	1164.61	1182.62	1165.60	600.33	591.81	11
5	526.24	554.22	571.32	508.20	536.21	553.31	509.19	537.18	554.22	263.61	277.60	286.11	S	1036.60	1019.56	1018.59	1001.58	1019.56	1002.53	518.20	510.28	10
6	639.32	667.31	684.32	621.30	649.29	666.31	622.27	650.27	667.31	320.15	334.15	342.66	L	949.57	932.53	931.56	914.52	932.53	915.50	475.28	467.19	9
7	726.33	754.34	771.35	708.32	736.34	753.34	709.30	737.30	754.34	363.67	377.66	386.18	S	836.49	819.45	818.48	801.43	819.45	802.42	418.24	410.22	8
8	813.36	841.36	858.38	795.35	823.35	840.37	796.34	824.33	841.36	407.18	421.18	429.28	S	749.45	732.41	731.44	714.40	732.41	715.39	375.22	367.19	7
9	914.41	942.41	959.43	896.43	924.42	941.42	897.38	925.38	942.41	458.23	472.25	480.22	T	662.42	645.38	644.40	627.37	645.38	628.35	331.70	323.18	6
10	1027.49	1055.49	1072.52	1009.48	1037.61	1054.51	1010.47	1038.46	1055.49	514.25	528.24	536.21	L	561.37	544.33	543.34	526.24	544.33	527.31	281.18	272.67	5

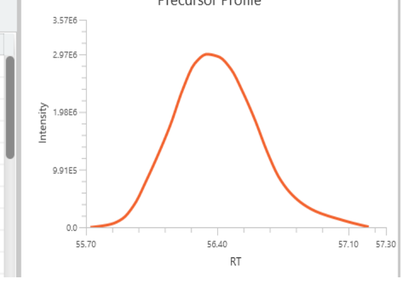






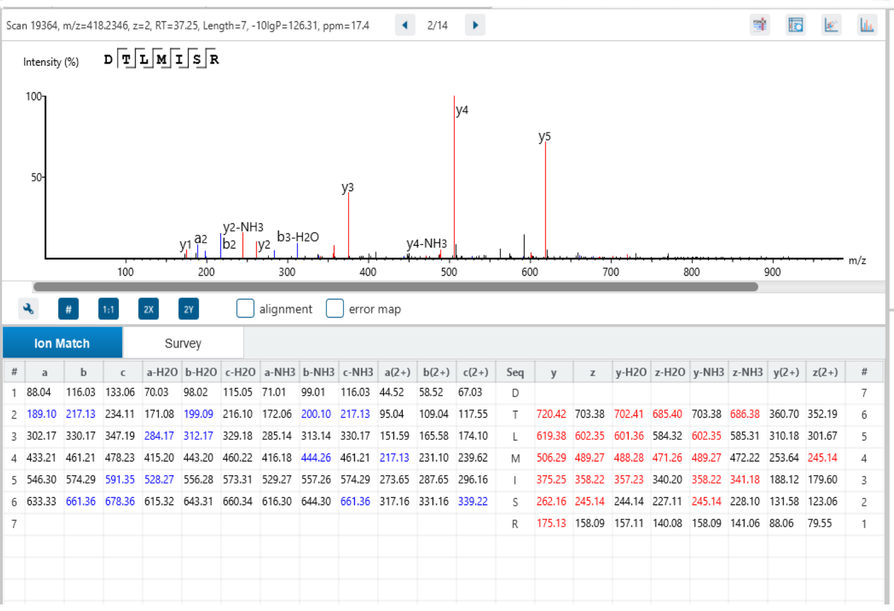


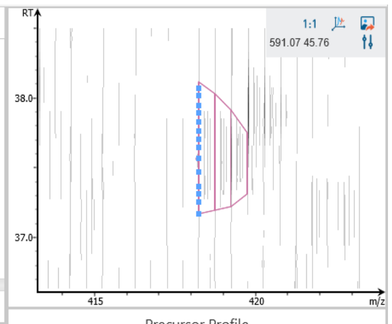


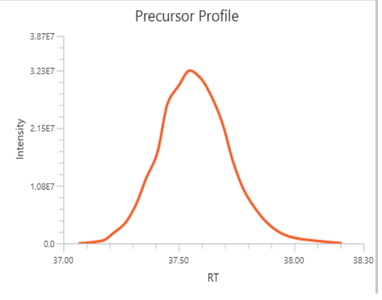


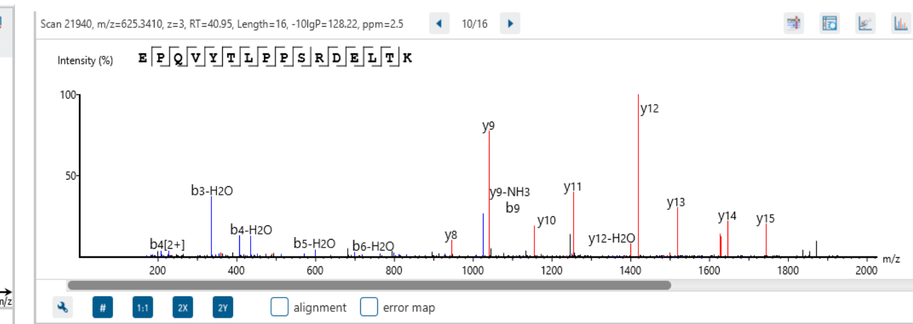
Ion Match | Survey

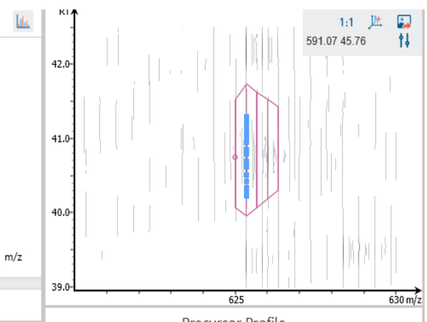
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1	30.03	58.03	75.06	12.02	40.02	57.05	13.01	41.00	58.03	15.52	29.51	38.03	G									12
2	127.09	155.09	172.11	109.08	137.07	154.10	110.06	138.06	155.09	64.04	78.04	86.55	P	1129.64	1112.60	1111.61	1094.59	1112.60	1095.57	565.31	557.32	11
3	214.13	242.12	259.15	196.11	224.11	241.13	197.10	225.09	242.12	107.56	121.56	130.07	S	1032.59	1015.55	1014.58	997.53	1015.55	998.52	517.30	508.27	10
4	313.20	341.19	358.22	295.19	323.18	340.20	296.16	324.16	341.19	157.11	171.09	179.60	V	945.55	928.51	927.54	910.52	928.51	911.49	473.27	464.76	9
5	460.27	488.26	505.28	442.26	470.25	487.27	443.24	471.26	488.26	230.63	245.14	253.14	F	846.49	829.48	828.48	811.43	829.48	812.42	423.74	415.24	8
6	557.32	585.32	602.36	539.30	567.30	584.83	540.28	568.28	585.32	279.15	293.15	301.67	P	699.42	682.40	681.41	664.37	682.40	665.35	350.20	341.19	7
7	670.40	698.40	715.41	652.37	680.39	697.40	653.37	681.41	698.40	335.70	349.69	358.22	L	602.36	585.32	584.83	567.30	585.32	568.30	301.68	293.16	6
8	741.44	769.44	786.45	723.43	751.43	768.44	724.40	752.40	769.44	371.18	385.21	393.73	A	489.28	472.24	471.26	454.23	472.24	455.21	245.14	236.62	5
9	838.48	866.48	883.50	820.47	848.49	865.49	821.46	849.45	866.48	419.74	433.27	442.26	P	418.24	401.25	400.23	383.19	401.25	384.18	209.14	201.10	4
10	925.46	953.52	970.54	907.50	935.50	952.53	908.49	936.48	953.52	463.26	477.25	485.77	S	321.19	304.15	303.17	286.14	304.15	287.12	161.09	152.57	3

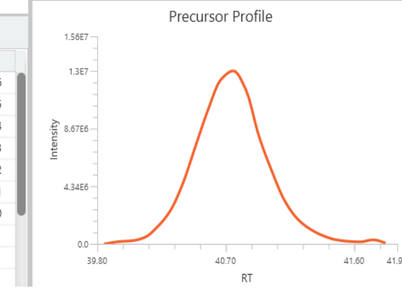






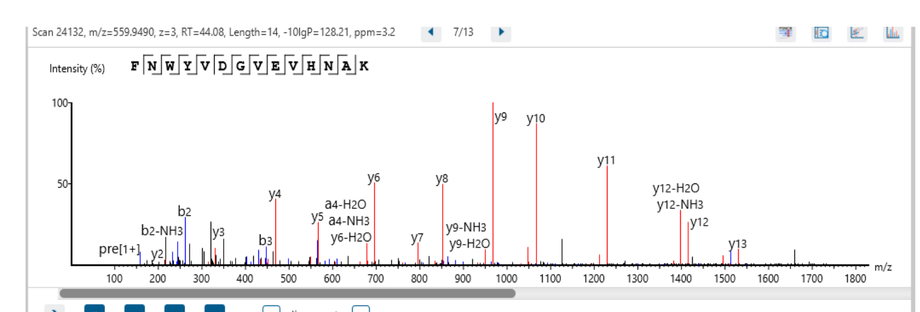


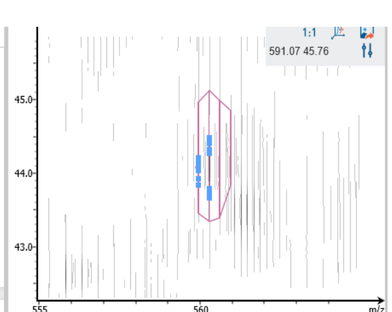


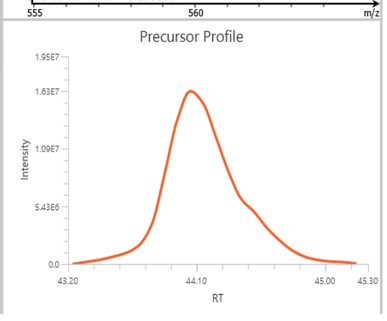


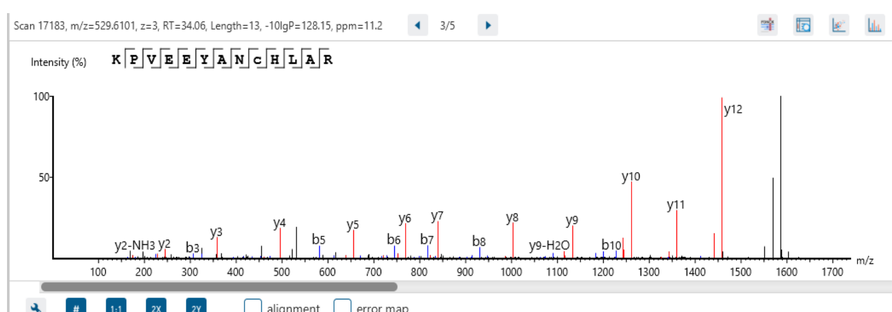
Ion Match | Survey

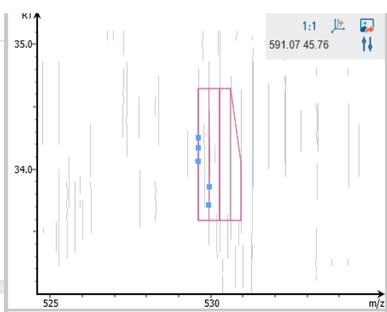
#	a	b	c	a-H2O	b-H2O	c-H2O	a-NH3	b-NH3	c-NH3	a(2+)	b(2+)	c(2+)	Seq	y	z	y-H2O	z-H2O	y-NH3	z-NH3	y(2+)	z(2+)	#
1	88.04	116.03	133.06	70.03	98.02	115.05	71.01	99.01	116.03	44.52	58.52	67.03	D									7
2	189.10	217.13	234.11	171.08	199.09	216.10	172.06	200.10	217.13	95.04	109.04	117.55	T	720.42	703.38	702.41	685.40	703.38	686.38	360.70	352.19	6
3	302.17	330.17	347.19	284.17	312.17	329.18	285.14	313.14	330.17	151.59	165.58	174.10	L	619.38	602.35	601.36	584.32	602.35	585.31	310.18	301.67	5
4	433.21	461.21	478.23	415.20	443.20	460.22	416.18	444.26	461.21	217.13	231.10	239.62	M	506.29	489.27	488.28	471.26	489.27	472.22	253.64	245.14	4
5	546.30	574.29	591.35	528.27	556.28	573.31	529.27	557.26	574.29	273.65	287.65	296.16	I	375.25	358.22	357.23	340.20	358.22	341.18	188.12	179.60	3
6	633.33	661.36	678.36	615.32	643.31	660.34	616.30	644.30	661.36	317.16	331.16	339.22	S	262.16	245.14	244.14	227.11	245.14	228.10	131.58	123.06	2
7													R	175.13	158.09	157.11	140.08	158.09	141.06	88.06	79.55	1

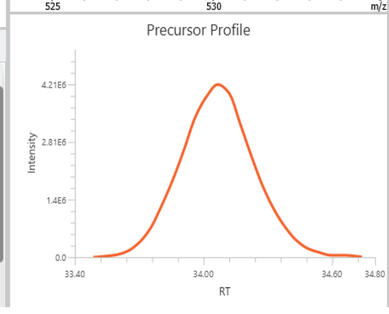












Ion Match | Survey

#	a	b	c	a-H2O	b-H2O	c-H2O	a-NH3	b-NH3	c-NH3	a(2+)	b(2+)	c(2+)	Seq	y	z	y-H2O	z-H2O	y-NH3	z-NH3	y(2+)	z(2+)	#
1	120.08	148.08	165.10	102.07	130.07	147.09	103.05	131.05	148.08	60.54	74.54	83.05	F									14
2	234.13	262.13	279.15	216.11	244.14	261.14	217.11	245.10	262.13	117.56	131.56	140.07	N	1530.75	1513.73	1512.41	1495.70	1513.73	1496.71	766.38	757.35	13
3	420.20	448.21	465.23	402.19	430.19	447.18	403.19	431.18	448.21	210.60	224.60	233.11	W	1416.70	1399.69	1398.68	1381.65	1399.69	1382.69	708.85	700.33	12
4	583.28	611.28	628.29	565.25	593.25	610.28	566.25	594.25	611.28	292.13	306.13	315.18	Y	1230.63	1213.61	1212.62	1195.60	1213.61	1196.56	615.81	606.82	11
5	682.34	710.33	727.36	664.32	692.32	709.35	665.31	693.30	710.33	341.67	355.67	364.18	V	1067.56	1050.55	1049.55	1032.53	1050.55	1033.49	534.27	525.76	10
6	797.36	825.36	842.38	779.35	807.35	824.37	780.34	808.35	825.36	399.18	413.17	421.69	D	968.49	951.47	950.47	933.46	951.47	934.43	484.74	476.23	9
7	854.47	882.39	899.44	836.45	864.39	881.40	837.36	865.37	882.39	427.69	441.69	450.20	G	853.47	836.45	835.45	818.42	836.45	819.40	427.23	419.18	8
8	953.45	981.48	998.47	935.44	963.44	980.48	936.43	964.43	981.48	477.23	491.22	500.25	V	796.44	779.40	778.42	761.39	779.40	762.38	398.72	390.20	7
9	1082.49	1110.50	1127.52	1064.48	1092.48	1109.51	1065.51	1093.49	1110.50	541.75	555.74	564.26	E	697.38	680.35	679.36	662.33	680.35	663.31	349.18	340.67	6
10	1181.56	1209.56	1226.59	1163.54	1191.55	1208.57	1164.54	1192.53	1209.56	591.28	605.28	613.79	V	568.33	551.28	550.31	533.28	551.28	534.27	284.66	276.15	5

Figure S11. MS/MS spectra of peptides and precursor profiles from albumin depleted pasma sample (PEAKS Studio 11)