

SUPPORTING INFORMATION

Selected Protein Monitoring in Histological Sections by Targeted MALDI-FTICR in-source decay Imaging

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A *{MATRIX}* Mascot Search Results

Protein View

Match to: [gi|114199083](#) Score: 1002
myelin basic protein [Mus musculus]
Found in search of DATA.TXT

Nominal mass (M_r): 13806; Calculated pI value: 11.33
NCBI BLAST search of [gi|114199083](#) against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Mus musculus](#)

Variable modifications: Acetyl (Protein N-term)
No enzyme cleavage specificity
Sequence Coverage: 19%

Matched peptides shown in **Bold Red**

1 **MASQKRPSQR SKYLATASTM DHARHGFLPR** HRDTGILDSI GRFFSGDRGA
51 PKRGSGKVPW LKQSRSPPLS HARSRPGLCH MYKDSHRTT HYGSLPQKSQ
101 HGRTQDENPV VHFFKNIVTP RT

B *{MATRIX}* Mascot Search Results

Protein View

Match to: [gi|261278732](#) Score: 1581
Chain A, X-Ray Structure Of Monomeric Variant Of Hnp1
Found in search of DATA.TXT

Nominal mass (M_r): 3443; Calculated pI value: 8.68
NCBI BLAST search of [gi|261278732](#) against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Homo sapiens](#)
Links to retrieve other entries containing this sequence from NCBI Entrez:
[gi|261278733](#) from [Homo sapiens](#)

Variable modifications: Acetyl (Protein N-term)
No enzyme cleavage specificity
Sequence Coverage: 100%

Matched peptides shown in **Bold Red**

1 **ACYCRIPACI AGERRYGTCK YQRLWAFCC**

Figure S1. Mascot search results for protein identification of MBP (A) and HNP-1 (B) using MALDI-FTICR/MS. Sequence coverage of MBP and HNP-1 is indicated in red.

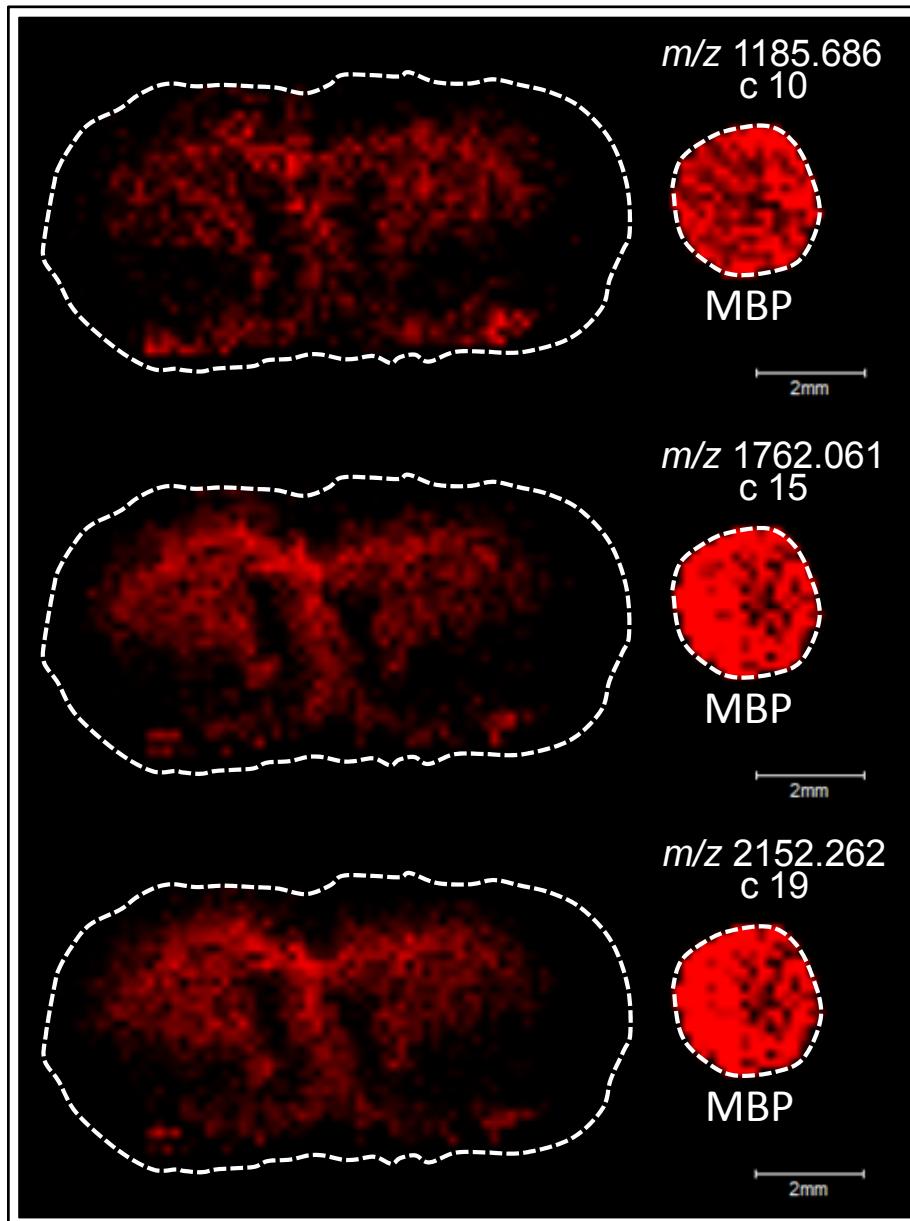


Figure S2. MALDI-FTICR ISD MSI on a mouse brain tissue section and a MBP pure solution. Ion images correspond to the signal detected for three ISD ions of the MBP (c_{10} , c_{15} and c_{19}).

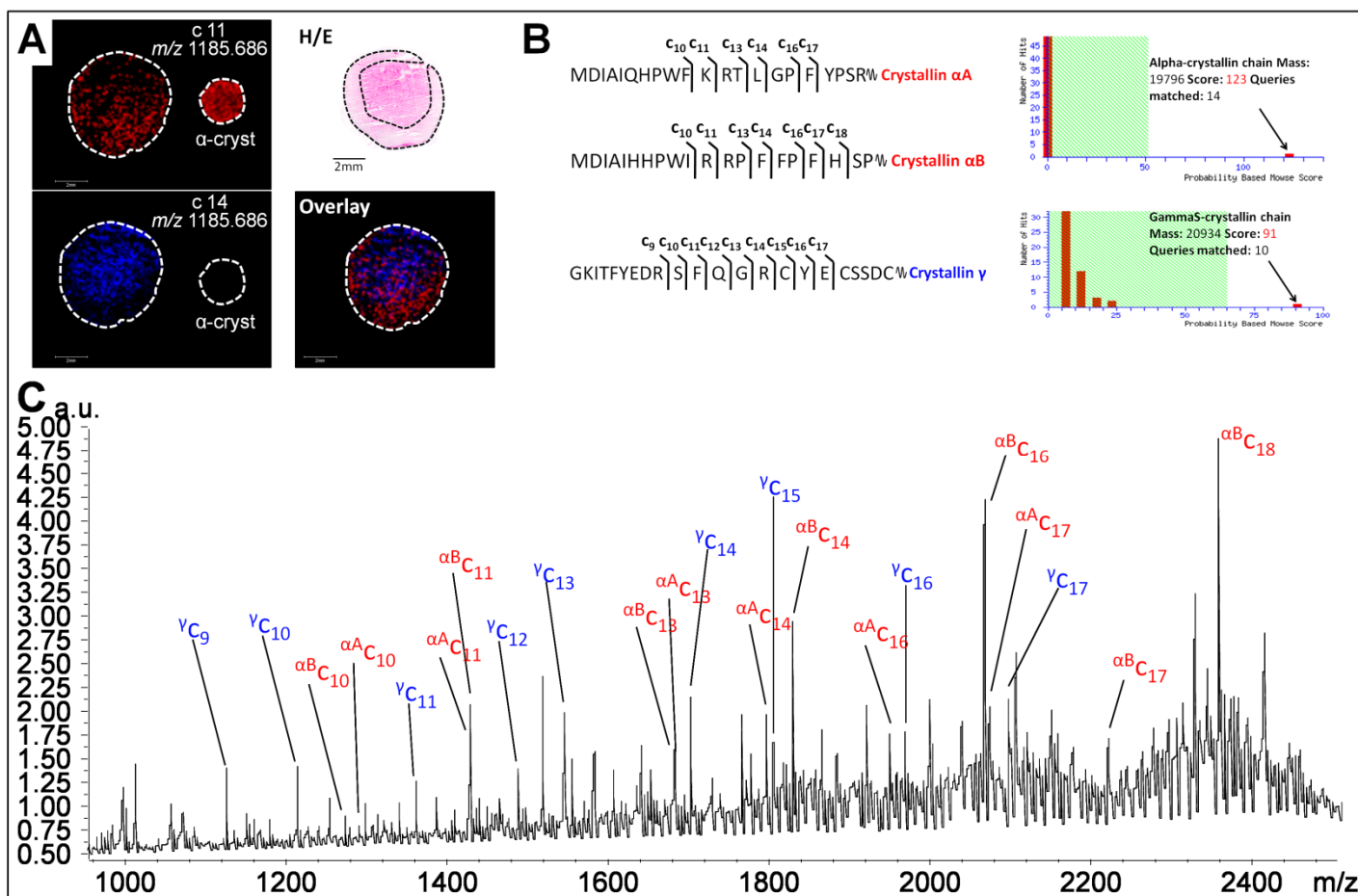


Figure S3. MALDI-FTICR ISD MSI of a porcine eye lens tissue section and a α A/B-crystallin spot.

A. Left panels show ion images of ISD fragments of α B-crystallin (c_{11}) and γ -crystallin (c_{14}). Right panel shows H/E staining of a serial eye lens section and an overlay of the two ion images of left panel. Dotted lines delineate eye lens central part and periphery.

B. Left part shows sequence coverage for α A/B-crystallin and γ -crystallin identification. Right part indicates Mascot search results for protein identification.

C. Average mass spectrum corresponding to the MALDI-FTICR ISD MSI analysis of the porcine eye lens. ISD fragments of α A/B-crystallin (in red) and γ -crystallin (in blue) are annotated on the average mass spectrum.

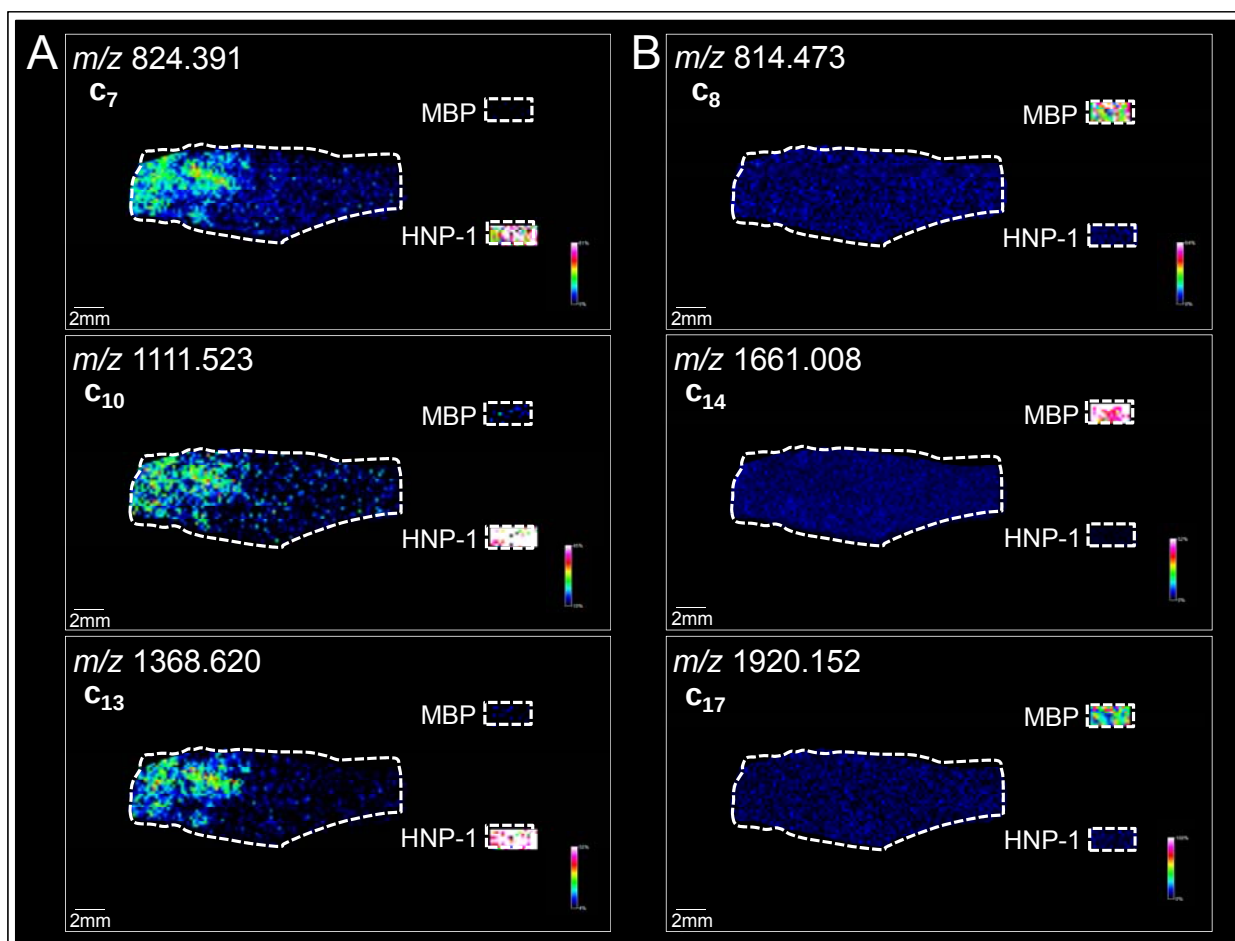


Figure S4. MALDI-FTICR ISD MSI on a liver with cancer liver metastasis tissue section and MBP and HNP-1 pure solutions.

A. Ion images corresponding to the signal detected for three ISD ions of HNP-1 (c_7 , c_{10} and c_{13}).

B. Ion images corresponding to the signal detected for three ISD ions of the MBP (c_8 , c_{14} and c_{17}).

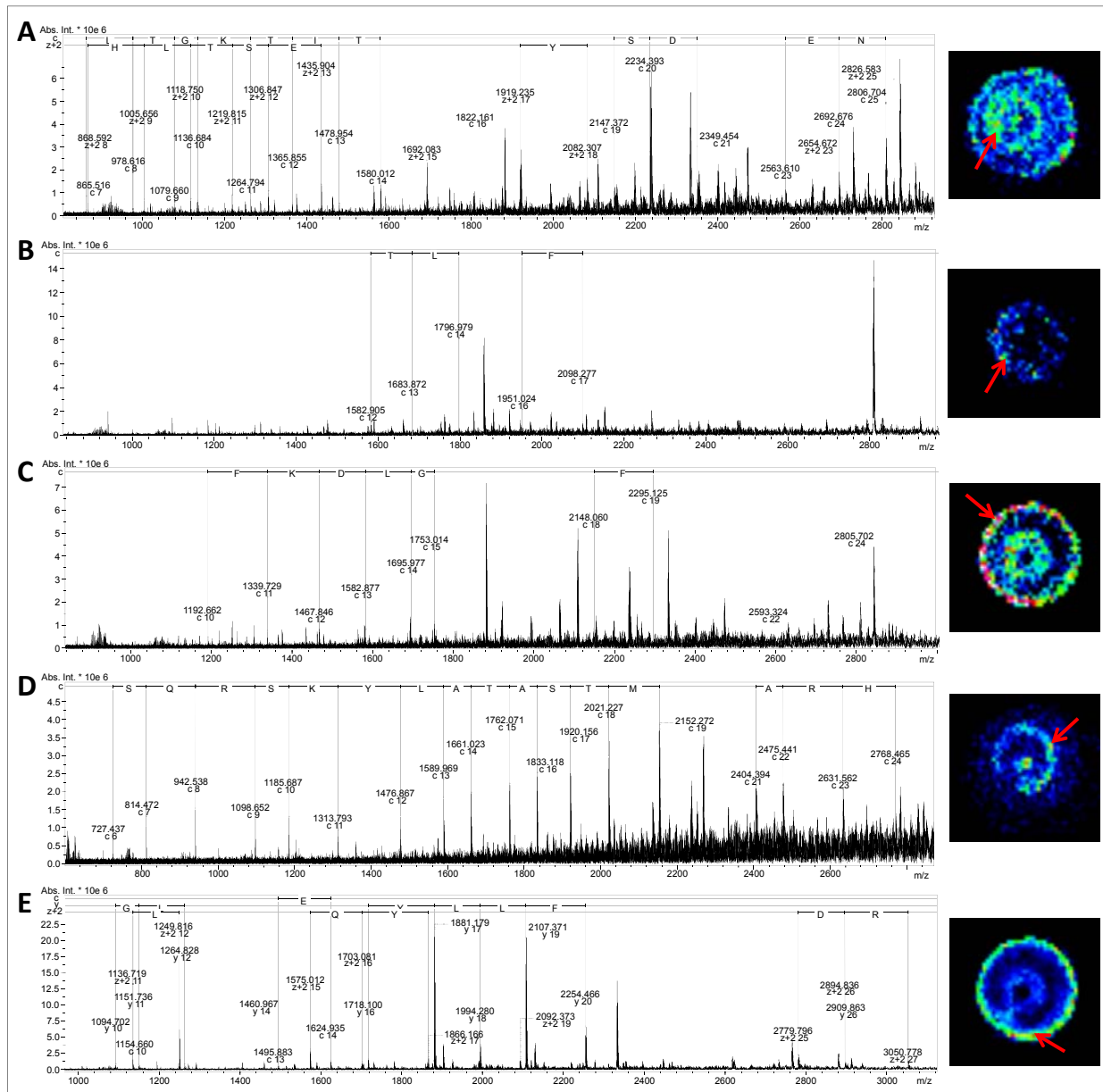


Figure S5. MALDI-FTICR ISD mass spectra of ubiquitin (A), α -crystallin (B), BSA (C), MBP (D) and β -casein (E) selected from the equimolar 5-proteins ion images. Red arrows indicate pixels with maximum intensity selected for each ISD mass spectrum of each protein.

A *(MATRIX)* Mascot Search Results

Protein View

Match to: UBC_PIG Score: 242
Polyubiquitin-C OS=Sus scrofa GN=UBC PE=2 SV=1
Found in search of DATA.TXT

Nominal mass (M_1): 59956; Calculated pI value: 7.10
NCBI BLAST search of [UBC_PIG](#) against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Sus scrofa](#)

Variable modifications: Acetyl (K), Phospho (ST)
No enzyme cleavage specificity
Sequence Coverage: 10%

Matched peptides shown in **Bold Red**

1 MQIFVKTITG KTITLVEVPS DTIENVKGI QKEGIPDPQ QRLIFAGKQL
51 EDGRTLSQYN IQKESTLHLV LRLRGQMIF VKITLTKITIT LEVPSDTIE
101 NVKAKIQDKE GIPPDQQLRI FAGKQLEDGR TLDYNIQKE STLHLVLRLR
151 GGMQIFVKTIT TKTITLVEVE PSDTIENVKA RIQKEGIPP DQQLIFAGK
201 QLEDGRTLSQ YNIQKSTLHL LRLRLRGQM IFVKITLTKIT ITLEVEPSDT
251 IENVKAKIQD KEGIPPDQQR LIFAGKQLED GRTLSQYNIQ KESTLHLVLRL
301 LRSGMQIFVK TLTGKTITIT LEVPSDTIENV KAKIQDKEGI PPDQQLIFAG
351 GKQLEDGRTL SDYNIQKEST LHLVLRLRGQ MQIFVKTITG KTITLVEVPS
401 DTIENVKAKI QKEGIPDPQ QRLIFAGKQL EDGRTLSQYN IQKESTLHLV
451 LRLRGQMIF VKITLTKITIT LEVPSDTIE NVKAKIQDKE GIPPDQQLRI
501 FAGKQLEDGR TLDYNIQKE STLHLVLRLR GGF

B *(MATRIX)* Mascot Search Results

Protein View

Match to: CRYAA_BOVIN Score: 30
Alpha-crystallin A chain OS=Bos taurus GN=CRYAA PE=1 SV=1
Found in search of DATA.TXT

Nominal mass (M_1): 19778; Calculated pI value: 5.78
NCBI BLAST search of [CRYAA_BOVIN](#) against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Bos taurus](#)

Variable modifications: Acetyl (Protein N-term)
No enzyme cleavage specificity
Sequence Coverage: 13%

Matched peptides shown in **Bold Red**

1 MDIAIQHPWF KRTLGPFYPS RLPDQFFGEG LFEYDLLPFL SSTISPYRQ
51 SLFRITVLDG ISEVRSRDK FVIFLDVKHF SPEDLTVKQV EDFVEIHGM
101 NERQDDHGYI SREFHRRYRL PSNVDSQALS CSLSDAGMLT FSGPKIPSGV
151 DAGHSERAI VSREEKPSSA PSS

C *(MATRIX)* Mascot Search Results

Protein View

Match to: ALBU_BOVIN Score: 49
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4
Found in search of DATA.TXT

Nominal mass (M_1): 69248; Calculated pI value: 5.82
NCBI BLAST search of [ALBU_BOVIN](#) against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Bos taurus](#)

No enzyme cleavage specificity
Sequence Coverage: 3%

Matched peptides shown in **Bold Red**

1 MGVFTFISLL LFFSAYSARG VFRDTHKSE IAHREFDLGE EHFQGLVIA
51 FSQVLQCPD DEHVKLWNL TEFARTCVAD ESHAGCEKSL HTLFGDELCK
101 VASIRETYGD MADCEKQEP ERNECFLSHK DSDPDLCKLK PDPNLCDEF
151 KADEKFWGR YLYEIAARRHP YFYAPELLY ANKYNVGFQE CQQAEDKGC
201 LLPKIETMRE KVLASSARQR LRCAISIQKFG ERALKAWVA RLSQKFPKAE
251 FVEVTKLVD LTKVHKCCCH GDLEACADR ADLAKYICDN QDTISSKLKE
301 CCKPLLEKS HCTAEVKEDA IPENLPPLTA DFAEDKDVCK NYQEAADAFI
351 GSFLEYYSRR HPEYAVSVLL RLAKYEATL EECADKDDPH ACYSTVFDKL
401 KHLVDEPNQL IKQNCQDFEK LGEYGFQNAL IVRYTRKVPQ VSTPTLVEVS
451 RSLGKVGTRC CTRPESERMP CTEDYLSLIL NRLCVLHEKT PVSEKVIKCC
501 IESLVNRRFC FSALIPDETY VKAFDEKLF TFHADICILP DTEKQIKKQT
551 ALVELLHKFE KATEEQLRTV MENFVAFVDM CCAADDEKAC FAVEGPKLVV
601 STQTALA

D *(MATRIX)* Mascot Search Results

Protein View

Match to: gi|114199083 Score: 1002
myelin basic protein [Mus musculus]
Found in search of DATA.TXT

Nominal mass (M_1): 13806; Calculated pI value: 11.33
NCBI BLAST search of [gi|114199083](#) against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Mus musculus](#)

Variable modifications: Acetyl (Protein N-term)
No enzyme cleavage specificity
Sequence Coverage: 19%

Matched peptides shown in **Bold Red**

1 MASQKRPSSQ SKYLATASTM DHARHGFLPR HRDTGILDSI GRFFSGDRGA
51 PKRGSGKVPW LKQSRSPSPS HARSRPGLCH MYKDSHTRIT HYGSLPQKSQ
101 HGRTQDENPV VHFFKNIVIP RT

E *(MATRIX)* Mascot Search Results

Protein View

Match to: gi|225825 Score: 116
beta casein
Found in search of DATA.TXT

Nominal mass (M_1): 23608; Calculated pI value: 5.24
NCBI BLAST search of [gi|225825](#) against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Bos taurus](#)
Links to retrieve other entries containing this sequence from NCBI Entrez:
[gi|226030](#) from [Bos taurus](#)

No enzyme cleavage specificity
Sequence Coverage: 12%

Matched peptides shown in **Bold Red**

1 RELEELNVPG EIVESLSSE ESITRINKKI EKFQSEEQQQ TEDELQDKIH
51 PFAQTQSLVY PFGPIRNSL PQNIPPLTQT FVVVPPFLQP EVMGVSKVKE
101 AMARKHKEMP FPKYFVEFT ESQSLTLTDV ENLHLPLFL QSRMGPHQP
151 LPTVTFMFPQ SVLSLSQSKV LFVQKAVPY FGRMPIDAF LLIQEPVLGP
201 VRGPFPIIV

Figure S6. Mascot search results for protein identification of ubiquitin (A), α -crystallin (B), BSA (C), MBP (D) and β -casein (E) of the equimolar 5-proteins mixture using MALDI-FTICR/MS. Sequence coverage of protein termini is indicated in red.

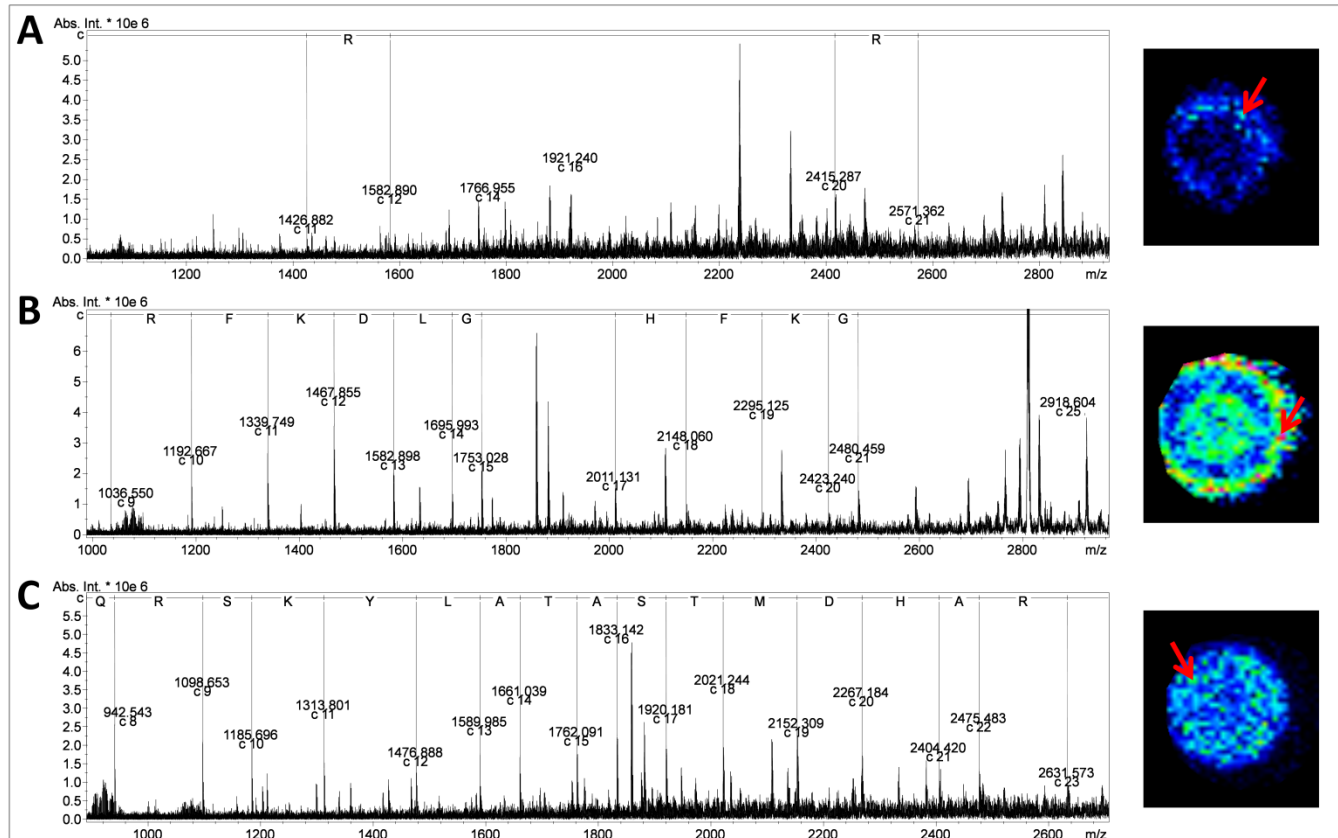


Figure S7. MALDI-FTICR ISD mass spectra of α -crystallin (A), BSA (B) and MBP (C) selected from the non-equimolar 5-proteins ion images.

Red arrows indicate pixels with maximum intensity selected for each ISD mass spectrum of each protein.

Figure S8. Mascot search results for protein identification of α -crystallin (A), BSA (B) and MBP (C) of the non equimolar 5-proteins mixture using MALDI-FTICR/MS. Sequence coverage of protein termini is indicated in red.

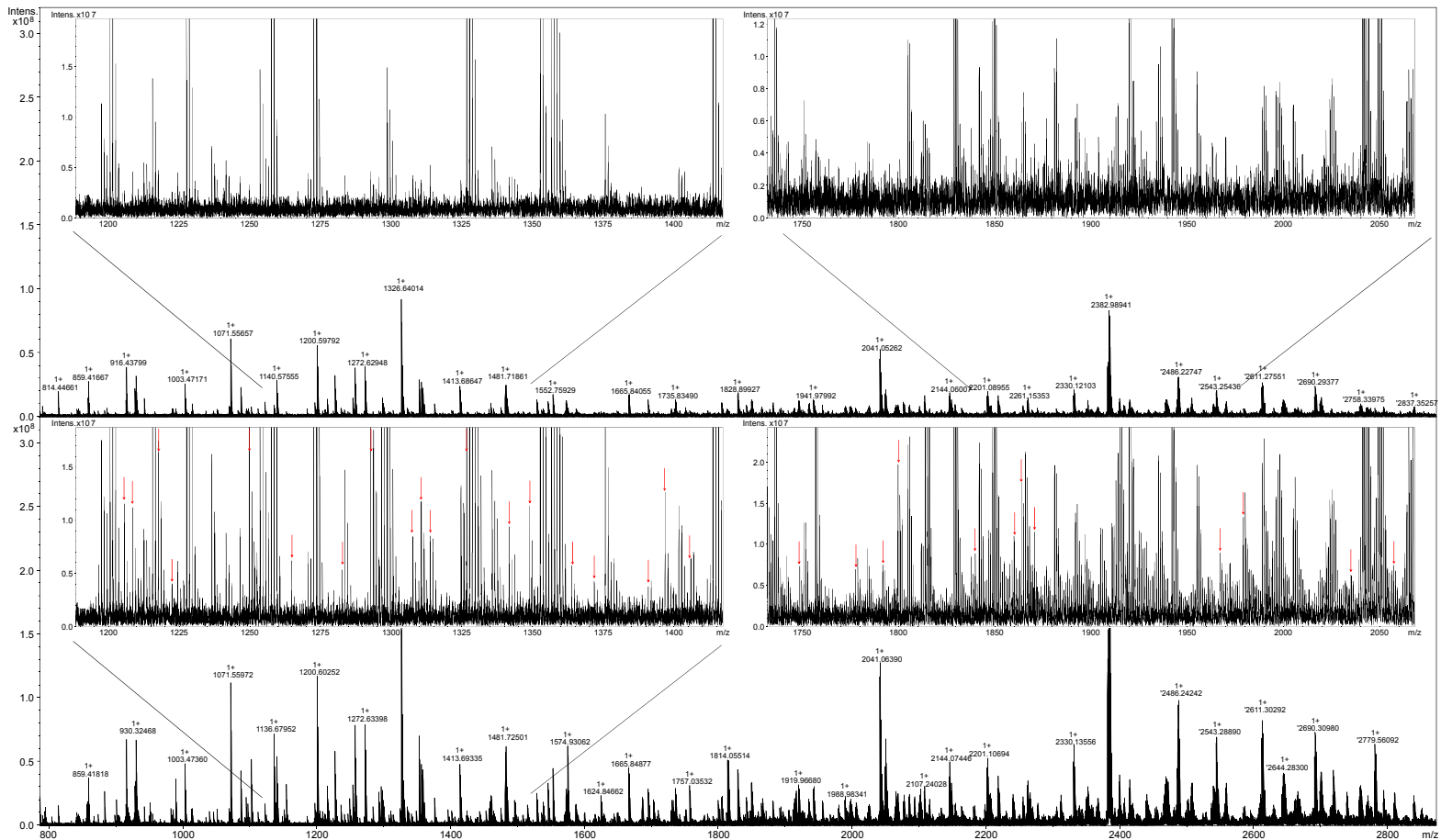


Figure S9. MALDI-FTICR ISD analyzes on an equimolar 10-protein mixture before and after HFIP extraction.

Upper and lower mass spectra correspond to MALDI-FTICR ISD analyzes on an equimolar 10-protein mixtures before and after HFIP extraction respectively. Red arrows on lower mass spectrum indicate peaks corresponding to supplementary ISD ions detected after HFIP extraction.

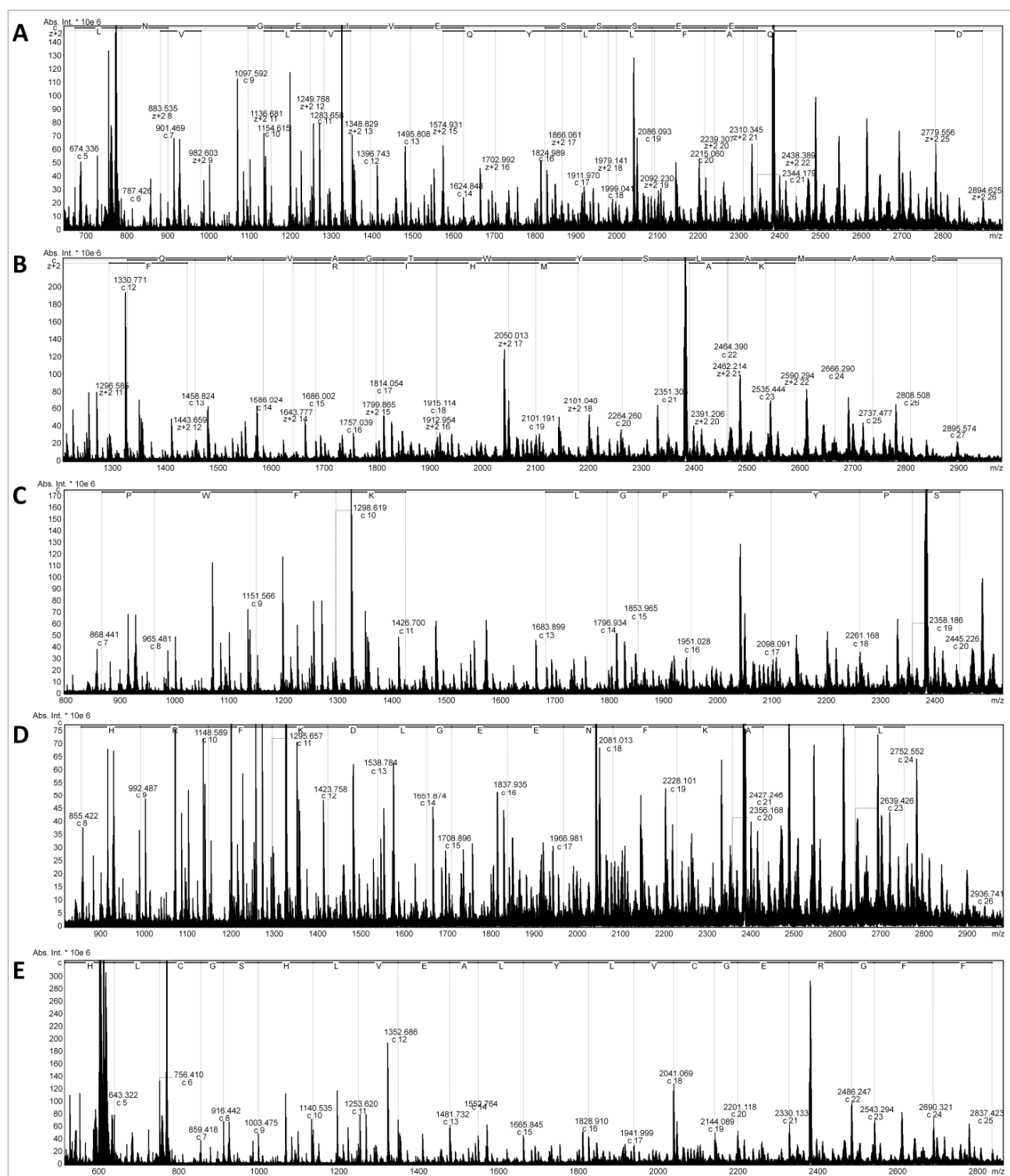


Figure S10. MALDI-FTICR ISD mass spectrum of an equimolar 10-protein mixture treated with HFIP. Same mass spectrum has been used for the assignment of the ISD ions peaks of β -casein (A), β -lactoglobulin (B), α -crystallin (C), HSA (D) and insulin (E).

A ^{MATRIX}_{SCIENCE} Mascot Search Results

Protein View

Match to: CASB_BUBBU Score: 909
Beta-casein OS=Bubalus bubalis GN=CSN2 PE=2 SV=1
Found in search of DATA.TXT

Nominal mass (M_r): 25090; Calculated pI value: 5.26
NCBI BLAST search of [CASB_BUBBU](#) against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Bubalus bubalis](#)

Variable modifications: Acetyl (Protein N-term)
No enzyme cleavage specificity
Sequence Coverage: 23%

Matched peptides shown in **Bold Red**

1 MKVLILACLIV ALALARELEE LNVPGEIVES LSSSEESITH INKKEKFQS
51 EEQQQMEDEL QDKIHFFAQT QSLVYFFPGP IPKSLPQNIPLTIQIPVVVP
101 PFLQPEIMGV SKYKEAMAPK HKEMPPFKYP VEPFIESQSL TLTDVENLHL
151 PLFLLQSMWH QPPQLPFTV MFPFQSVLSL SQSKVLPVFQ KAVPYQQRDM
201 PIQAFLLYQE FVLGPPVRGP PIIV

B ^{MATRIX}_{SCIENCE} Mascot Search Results

Protein View

Match to: LACB_BOVIN Score: 585
Beta-lactoglobulin OS=Bos taurus GN=LGB PE=1 SV=3
Found in search of DATA.TXT

Nominal mass (M_r): 19870; Calculated pI value: 4.93
NCBI BLAST search of [LACB_BOVIN](#) against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Bos taurus](#)

Variable modifications: Acetyl (Protein N-term)
No enzyme cleavage specificity
Sequence Coverage: 27%

Matched peptides shown in **Bold Red**

1 MKCLLLALAL TCGAQLIVT QTMKGLDIQK VAGTWYSLAM AASDISLLDA
51 QSAFLRVYVE ELKPTPEGDL EILLQKWENG ECAQKKIAE KIKIPAVFKI
101 DALNENKVLV LDTDYKKYLL FCMENSAEPE QSLACQCLVR TPEVDDEALE
151 KFDKALKALP MHIRLSFNPT QLEEQCHI

C ^{MATRIX}_{SCIENCE} Mascot Search Results

Protein View

Match to: CRYAA_BOVIN Score: 446
Alpha-crystallin A chain OS=Bos taurus GN=CRYAA PE=1 SV=1
Found in search of DATA.TXT

Nominal mass (M_r): 19778; Calculated pI value: 5.78
NCBI BLAST search of [CRYAA_BOVIN](#) against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Bos taurus](#)

Variable modifications: Acetyl (N-term),Acetyl (Protein N-term)
No enzyme cleavage specificity
Sequence Coverage: 11%

Matched peptides shown in **Bold Red**

1 MDIAIQHPWF KRTLGPFPYS RLFDQFFGEG LFEYDLLPFL SSTISPYRQ
51 SLFRIVLDSG ISEVRSRDRK FVIFLDVKHF SPEDLIVKVQ EDFVEIHGKH
101 NERQDDHGYI SREFHRRYRL PSNVDQSALS CSLSADGMLT FSGPKIPSGV
151 DAGHSERAIP VSREEKPSSA PSS

D ^{MATRIX}_{SCIENCE} Mascot Search Results

Protein View

Match to: ALBU_HUMAN Score: 1497
Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2
Found in search of DATA.TXT

Nominal mass (M_r): 69321; Calculated pI value: 5.92
NCBI BLAST search of [ALBU_HUMAN](#) against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Homo sapiens](#)

Variable modifications: Acetyl (Protein N-term)
No enzyme cleavage specificity
Sequence Coverage: 4%

Matched peptides shown in **Bold Red**

1 MKWVTFISLL FLFSAYSRG VFRRDHAKSE VAHRFKDLGE ENFKALVLIA
51 FAQYLQQCPF EDHVKLNVET TEFARTCVAD ESAENCDSL HTLFGDKLCT
101 VATLRETYGE MADCCAKQEP ERNECFLOQHK DDNPNLPRLV RPEVDVMCTA
151 FHDNEETFLK KYLYEIAARR PYFYAPELLF FAKRYKAFT ECCQAADKAA
201 CLLPKLDELK DEKASSAKQ RLKCSLQKF GERAFKAWAV ARLSQRFPKA
251 EFAEVSKLVT DLTKVHTECC HGDLLCADD RADLAKYICE NQDSISSKLL
301 ECCEKPLLEK SHCIAEVEND EMPADLPSLA ADFVESKDVC KNYAEAKVDF
351 LGMFLYEPYAR RHPDYSVLL LRLAKTYETT LEKCCAAADP HECYAKVFDE
401 FKPLVEEPQN LIKQNCLEFE QLGEYKFQNA LLVRYTKKVP QVSTPTLVEV
451 SRNLGKVGSK CCKHPEAKRM PCAEDYLSVV LNQLCVLHEK TPVSDRVTKC
501 CTESLVNRRP CFSALEVDET YVPKEFNAET FTFHADICTL SEKERQIKKK
551 TALVELVKHK PKATKEQLKA VMDDFAAFVE KCKKADDKET CFAEEGKKLV
601 AASQAALGL

E ^{MATRIX}_{SCIENCE} Mascot Search Results

Protein View

Match to: INS_PIG Score: 4058
Insulin OS=Sus scrofa GN=INS PE=1 SV=2
Found in search of DATA.TXT

Nominal mass (M_r): 11664; Calculated pI value: 6.06
NCBI BLAST search of [INS_PIG](#) against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Sus scrofa](#)

Variable modifications: Acetyl (N-term),Acetyl (Protein N-term)
No enzyme cleavage specificity
Sequence Coverage: 23%

Matched peptides shown in **Bold Red**

1 MALWIRLLPL LALLALWAPA PAQA**FVNQHL** CGSHLVEALY LVCGERGFY
51 TPKARREAREN PQAGAVELGG GLGGLQALAL EGPPQKRGIV EQCCTSCSL
101 YQLENYCN

Figure S11. Mascot search results for protein identification of β -casein (A), β -lactoglobulin (B), α -crystallin (C), HSA (D) and insulin (E) using MALDI-FTICR/MS. Sequence coverage of protein termini is indicated in red.

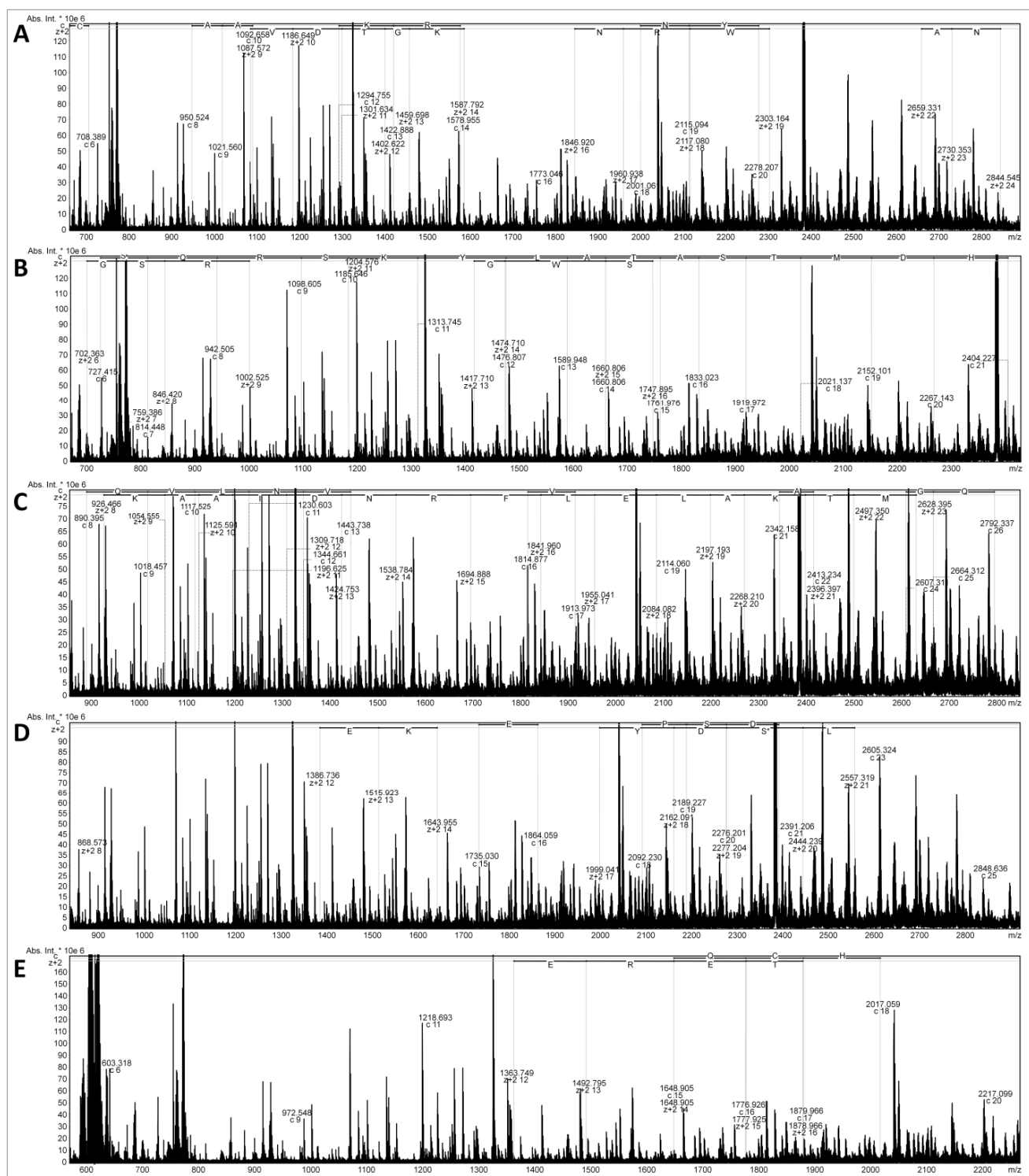


Figure S12. MALDI-FTICR ISD mass spectrum of an equimolar 10-protein mixture treated with HFIP. Same mass spectrum has been used for the assignment of the ISD ions peaks of lysozyme (A), MBP (B), myoglobin (C), ubiquitin (D) and cytochrome c (E).

A {MATRIX} {SCIENCE} Mascot Search Results

Protein View

Match to: LYSC_CHICK Score: 730
Lysozyme C OS=Gallus gallus GN=LYZ PE=1 SV=1
Found in search of DATA.TXT

Nominal mass (M_r): 16228; Calculated pI value: 9.37
NCBI BLAST search of [LYSC_CHICK](#) against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Gallus gallus](#)

No enzyme cleavage specificity
Sequence Coverage: 29%

Matched peptides shown in **Bold Red**

1 MRSLLILVLC FLPLAALGKV **FORCELAAM KRHGLDNYRG** YSLGNWVCAA
51 KFESNFTQA TNRTDGTSD YGILQINSRW WCNDGRTPGS RNLCHIPCAS
101 LLSSDITASV NCAKIVSDG NGMNAWVNR **NRCKGTDVQA WIRGCR**L

B {MATRIX} {SCIENCE} Mascot Search Results

Protein View

Match to: MBP_MOUSE Score: 1260
Myelin basic protein OS=Mus musculus GN=Mbp PE=1 SV=2
Found in search of DATA.TXT

Nominal mass (M_r): 27151; Calculated pI value: 9.58
NCBI BLAST search of [MBP_MOUSE](#) against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Mus musculus](#)

Variable modifications: Acetyl (N-term),Acetyl (Protein N-term)
No enzyme cleavage specificity
Sequence Coverage: 20%

Matched peptides shown in **Bold Red**

1 MGNHSGKREL SAEKASKDGE IHRGEAGKKR SVGKLSQTAS EDSDVFGEAD
51 AIQNNGTSAE DTAVTDKHT ADPKNNWGA HPADPGNRPH LIRLFSRDAP
101 GRENTFFKDR PSESDELQTI QEDPTAASGG LDVMA**SQRKP SQRSKYLATA**
151 **STMDHARHGF** LPRHRDTGIL DSIGRFFSGD RGAPKRGSGK DSHRTTHYHG
201 SLPQKSGHGR TQDENPVVHF FKNIV**TPRTP PPSQGRGGRD SRSGSPMARR**
251

C {MATRIX} {SCIENCE} Mascot Search Results

Protein View

Match to: MYG_EQUUBU Score: 864
Myoglobin OS=Equus burchellii GN=MB PE=1 SV=2
Found in search of DATA.TXT

Nominal mass (M_r): 17072; Calculated pI value: 7.21
NCBI BLAST search of [MYG_EQUUBU](#) against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Equus burchellii](#)

Variable modifications: Acetyl (Protein N-term)
No enzyme cleavage specificity
Sequence Coverage: 31%

Matched peptides shown in **Bold Red**

1 MGLSDGEWQQ VLVNWKGVKA **DIAGHGQEV**L IRLFTGMPET LEKFDKFKHL
51 KTEAEMKASE DLKKGHTVVL TALGGILKKK GHHEAELKPL AQSHATKHKI
101 PIKYLEFISD AIHVLHLSKH PGDFGADAQG **AMTKALELFR NDIAARYKEL**
151 **GFQG**

D {MATRIX} {SCIENCE} Mascot Search Results

Protein View

Match to: UBC_PIG Score: 375
Polyubiquitin-C OS=Sus scrofa GN=UBC PE=2 SV=1
Found in search of DATA.TXT

Nominal mass (M_r): 59956; Calculated pI value: 7.10
NCBI BLAST search of [UBC_PIG](#) against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Sus scrofa](#)

Variable modifications: Acetyl (K),Phospho (ST)
No enzyme cleavage specificity
Sequence Coverage: 9%

Matched peptides shown in **Bold Red**

1 **MQIFVKTLTG KTITLEVEPS** DTIENVKGI QEKEGIPPDQ QRLIFAGKQL
51 EDGRTLSDYN **IQKESTLHLV LRLRGMQIF** VKTLTGKTIIT LEVEPSDTIE
101 NVKAKIQDKE GIPPDQRLI **FAGKQLEDGR** TLDSDYNIQKE STLHLVLRRL
151 GGMQIFVKTL TGKITLEVE PSDTIENVKA KIQDKEGIPP DQQLIFAGK
201 QLEDGRTLSD YNIQKESTLH LVLRLRGMQ IFVKTLTGKT ITLEVEPSDT
251 IENVKAKIQD KEGIPPDQQR LIFAGKQLED GRITLSDYNIQ KESTLHLVLR
301 LRGGMQIFVK TLTGKTITLE VEPSTIENV KAKIQDKEGI PPDQQLIFA
351 GKQLEDGRTL SDYNIQKEST LHLVLRRLGG MQIFVKTLTG KTITLEVEPS
401 DTIENVKAKI QDKEGIPPDQ QRLIFAGKQL EDGRTLSDYN IQKESTLHLV
451 LRLRGMQIF VKTLTGKTIIT LEVEPSDTIE NVKAKIQDKE GIPPDQRLI
501 FAGKQLEDGR TLDSDYNIQKE STLHLVLRRL GGF

E {MATRIX} {SCIENCE} Mascot Search Results

Protein View

Match to: CYC_EQUAS Score: 172
Cytochrome c OS=Equus asinus GN=CYCS PE=1 SV=2
Found in search of DATA.TXT

Nominal mass (M_r): 11811; Calculated pI value: 9.59
NCBI BLAST search of [CYC_EQUAS](#) against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Equus asinus](#)

Variable modifications: Acetyl (Protein N-term)
No enzyme cleavage specificity
Sequence Coverage: 34%

Matched peptides shown in **Bold Red**

1 MGDVEKGKKI **FVQKCAQCHT** VEKGGKHKIG PNLHGLFGRK IGQAPGFSYT
51 DANKNGKITW KEETLMEYLE NPKKIYIPGK MIFAGIKKK**T EREDLIAYLK**
101 **KATNE**

Figure S13. Mascot search results for protein identification of lysozyme (A), MBP (B), myoglobin (C), ubiquitin (D) and cytochrome c (E) using MALDI-FTICR ISD. Sequence coverage of protein termini is indicated in red.