Supplementary Information for

Proteomic identification of an Upregulated Isoform of Annexin A3 in the Spinal Cords of Rats in a Neuropathic Pain Model

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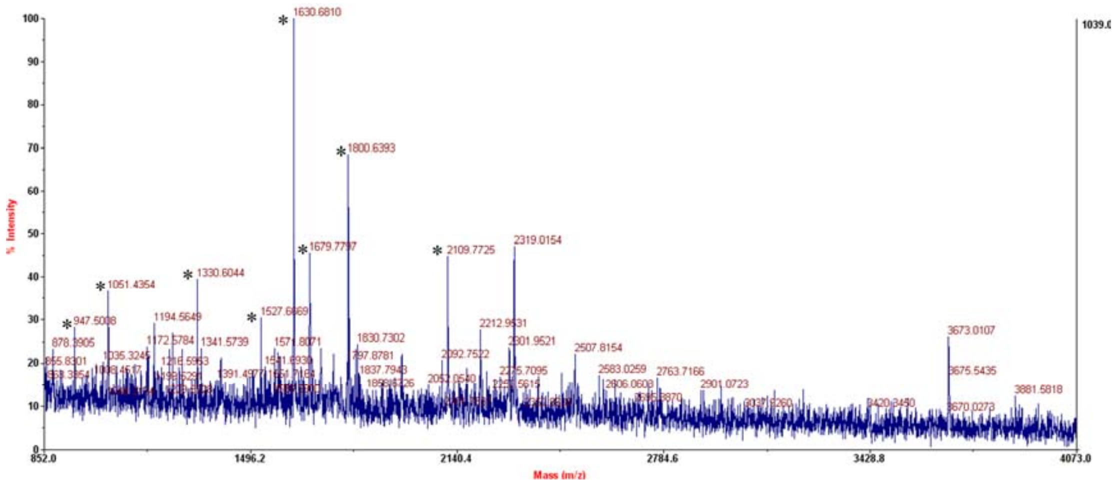
A. MALDI-TOF MS spectrum (spot 1)



B. Peptides detected by MALDI-TOF-MS

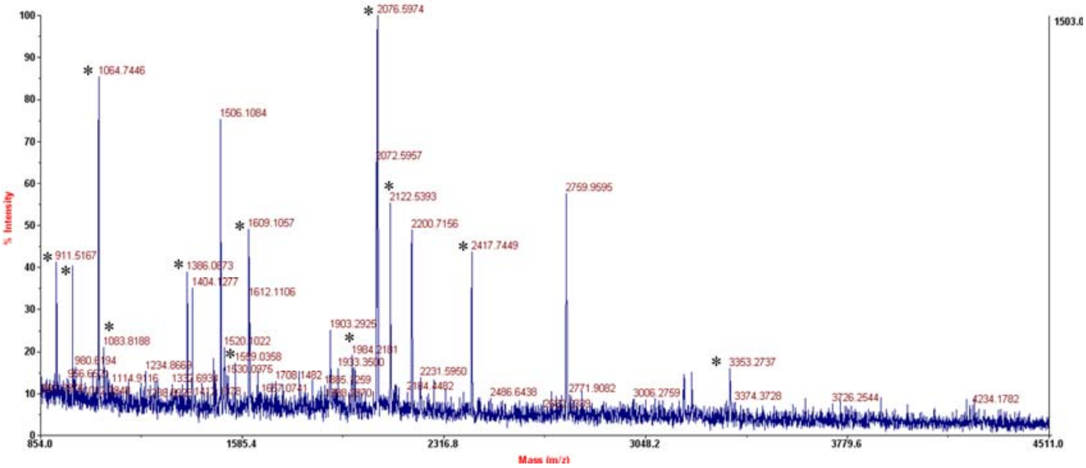
Peptide	Amino acid sequence	$[M+H]^+$	Matched
46-53	MDELQLFR	1051.4330	+
46 - 60	MDELQLFRGDTVLLK	1777.7970	+
66 - 83	EAVCIVLSDDTCSDEKIR	2109.7740	+
148 - 155	KGDIFLVR	947.4930	+
324 - 338	IVSQLLTLMDGLKQR	1714.8550	+
454 - 465	WALSQSNPSALR	1329.6130	+
600 - 614	VINQILTEMDGMSTK	1679.7840	+
754 - 766	KYEMFAQTLQQSR	1629.6840	+
755 - 766	YEMFAQTLQQSR	1501.6090	+

C. Matched peptides (Bold Red) in the TERA amino acid sequence

1 MASGADSKGD DLSTAILKQK NRPNRLIVDE AINEDNSVVS LSQPK**MDELQ**
51 **LFRGDTVLLK** GKKRR**EAVCI VLSDDTCSDE KIR**MNRVVRN NLRVRLGDVI
101 SIQPCPDVKY GKRIHVLPID DTVEGITGNL FEVYLKPYFL EAYRPIR**KGD**
151 **IFLVR**GGMRA VEFKVVETDP SPYCIVAPDT VIHCEGEPIK REDEEESLNE
201 VGYDDIGGCR KQLAQIKEMV ELPLRHPALF KAIGVKPPRG ILLYGPPGTG
251 KTLIARAVAN ETGAFFFLIN GPEIMSKLAG ESESNLRKAF EEAEKNAPAI
301 IFIDELDAIA PKREKTHGEV ERR**IVSQLLT LMDGLKQR**AH VIVMAATNRP
351 NSIDPALRRF GRFDREVDIG IPDATGRLEI LQIHTKNMKL ADDVDLEQVA
401 NETHGHVGAD LAALCSEAAL QAIRKKMDLI DLEDETIDAE VMNSLAVTMD
451 DFR**WALSQSN PSALR**ETVVE VPQVTWEDIG GLEDVKRELQ ELVQYPVEHP
501 DKFLKFGMTP SKGVLFYGPP GCGKTLLAKA IANECQANFI SIKGPELLTM
551 WFGESEANVR EIFDKARQAA PCVLFFDELD SIAKARGGNI GDGGGAADR**V**
601 **INQILTEMDG MSTK**KNVFII GATNRPDIID PAILRPGRLD QLIYIPLPDE
651 KSRVAILKAN LRKSPVAKDV DLEFLAKMTN GFSGADLTEI CQRACKLAIR
701 ESIESEIRRE RERQTNPSAM EVEEDDPVPE IRRDHFEEAM RFARRSVSDN

751 DIR**KYEMFAQ TLQQSR**GFGS FRFPSGNQGG AGPSQGSGGG TGGNVYTEDN
801 DDDLYG

A. MALDI-TOF MS spectrum (spot 2)



B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
63 - 68	FCYHER	911.5130	+
185 - 200	FASEIAGVDDLGTTGR	1609.1020	+
247 - 266	KTESIDVMDAVGSNIVVSTR	2121.4770	+
248 - 266	TESIDVMDAVGSNIVVSTR	1993.3830	+
292 - 299	FAYDGLKR	969.6620	+
409 - 417	FEAPLFNAR	1064.7480	+
429 - 450	VALIGSPVDLTYRYDHLGDSPK	2416.7160	+
451 - 464	ILQDIASGNHEFSK	1559.0540	+
465 - 483	VLNAAKKPMVVLGSSALQR	1982.3960	+
471 - 483	KPMVVLGSSALQR	1386.0600	+
519 - 538	IASQVAALDLGYKPGVEAIR	2071.5630	+
563 - 592	DCFIVYQGHHGDVGAPIADVILPGAAYTEK	3214.0580	+
646 - 655	LGEVSPNLVR	1083.8080	+
646 - 673	LGEVSPNLVRYDDVEEANYFQQASELAK	3185.0730	+
674 - 702	LVDQEFLADPLVPPQLTIKDFYMTDSISR	3352.2110	+

C. Matched peptides (Bold Red) in the NADH amino acid sequence

1 MLRIPVKRAL IGLSKSPKGY VRSTGTAASN LIEVFVDGQS VMVEPGTTVL
51 QACEKVGMQI PR**FCYHER**LS VAGNCRMCLV EIEKAPKVVA ACAMPVMKGW
101 NILTNSEKSK KAREGVMEFL LANHPLDCPI CDQGGECDLQ DQSMMFGSDR
151 SRFLEGKRAV EDKNIGPLVK TIMTRCIQCT RCIR**FASEIA GVDDLGTTGR**
201 GNDMQVGTYI EKMFMSELSG NIIDICPVGA LTSKPYAFTA RPWETR**KTES**
251 **IDVMDAVGSN IVVSTR**TGEV MRILPRMHED INEEWISDKT R**FAYDGLKR**Q
301 RLTEPMVRNE K**GLLTYTSWE DALSRVAGML QSFEGK**AVAA IAGGLVDAEA
351 LVALKDLLNK VDSDTLCTEE IFPNEGAGTD LRSNYLLNTT IAGVEEADVV
401 LLVGTNPR**FE APLFNAR**IRK SWLHNDLK**VA LIGSPVDLTY RYDHLGDSPK**

451 **ILQDIASGNH EFSKVLNAAK KPMVVLGSSA LQR**DDGAAIL AAVSSIAQKI

501 RVASGAAAEW KVMNILHR**IA SQVAALDLGY KPGVEAIR**KN PPKLLFLLGA

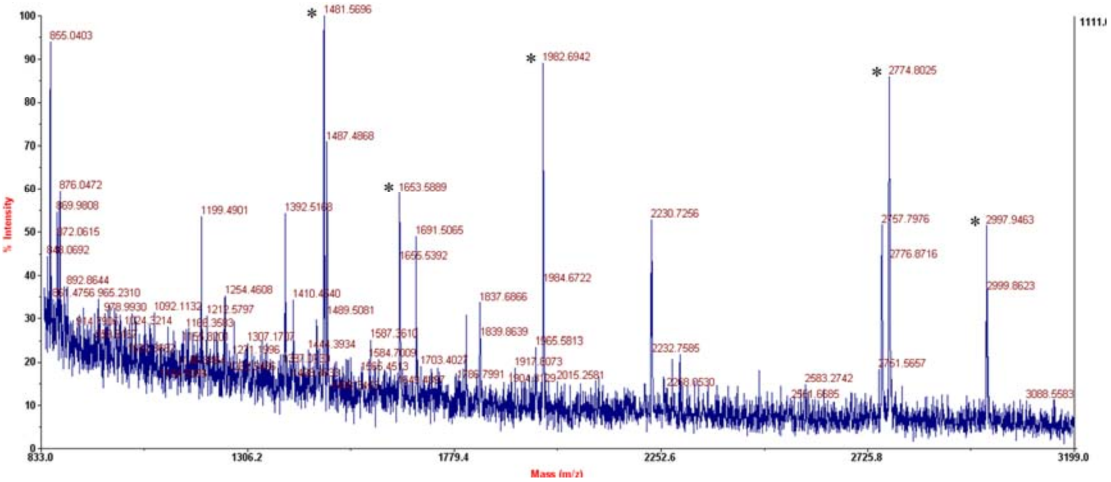
551 DGGCITRQDL PK**DCFIVYQG HHGDVGAPIA DVILPGAAYT EK**SATYVNTE

601 GRAQQTKVAV TPPGLAREDW KIIRALSEIA GITLPYDTLD QVRNR**LGEVS**

651 **PNLVRYDDVE EANYFQQASE LAKLVDQEFL ADPLVPPQLT IKDFYMTDSI**

701 **SR**ASQTMAKC VKAVTEGAQA VEEPSIC

A. MALDI-TOF MS spectrum (spot3)



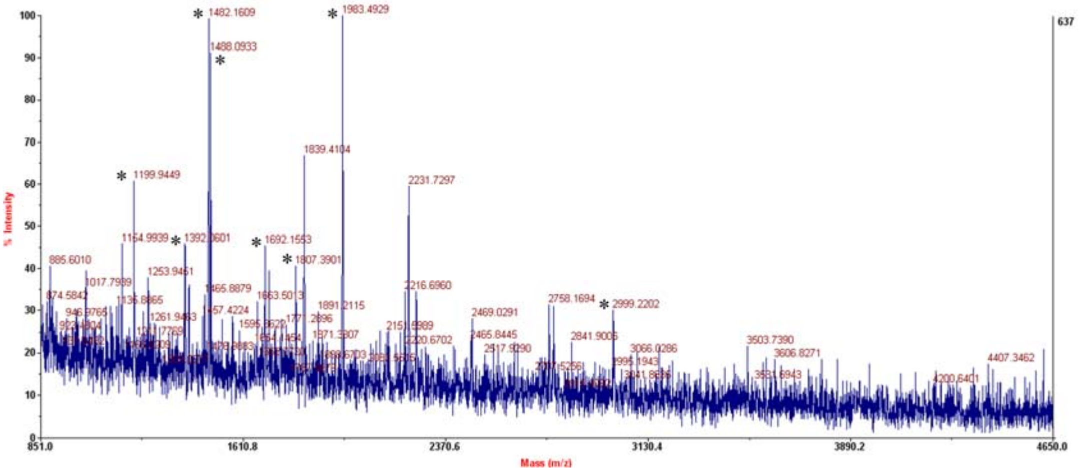
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
4 - 25	GPAVGIDLGTTYSCVGVFQHGK	2262.6820	+
57 - 72	NQVAMNPTNTVFDAKR	1805.5470	+
89 - 102	HWPFMVVNDAGRPK	1653.5380	+
138 - 155	TVTNAVVTVPAYFNDSQR	1981.6220	+
273 - 299	TLSSSTQASIEIDSLYEGIDFYTSITR	2996.9690	+
300 - 311	ARFEELNADLFR	1480.4660	+
424 - 447	QTQTFTTYSDNQPGVLIQVYEGER	2773.8670	+

C. Matched peptides (Bold Red) in the HSC70 amino acid sequence

1 MSK**GPAVGID LGTTYSCVGV FQHGK**VEIIA NDQGNRTTPS YVAFTDTERL
51 IGDAAK**NQVA MNPTNTVFDA KR**LIGRRFDD AVVQSDMK**HW PFMVVNDAGR**
101 **PK**VQVEYKGE TKSFYPEEVS SMVLTKMKEI AEAYLGK**TVT NAVVTVPAYF**
151 **NDSQR**QATKD AGTIAGLNVL RIINEPTAAA IAYGLDKKVG AERNVLIFDL
201 GGGTFDVSIL TIEDGIFEVK STAGDTHLGG EDFDNRMVNH FIAEFKRKHK
251 KDISENKRAV RRLRTACERA KR**TLSSSTQA SIEIDSLYEG IDFYTSITRA**
301 **RFEELNADLF R**GTLDPVEKA LRDAKLDKSQ IHDIVLVGGS TRIPKIQKLL
351 QDFFNGKELN KSINPDEAVA YGAAVQAAIL SGDKSENVQD LLLLDVTPLS
401 LGIETAGGVM TVLIKRNTTI PTK**QTQTFTT YSDNQPGVLI QVYEGER**AMT
451 KDNNLLGKFE LTGIPPAPRG VPQIEVTFDI DANGILNVSA VDKSTGKENK
501 ITITNDKGRL SKEDIERMVQ EAEKYKAEDE KQRDKVSSKN SLESYAFNMK
551 ATVEDEKLQG KINDEDKQKI LDKCNEIISW LDKNQTAEKE EFEHQQKELE
601 KVCNPIITKL YQSAGGMPGG MPGGFPGGGA PPSGGASSGP TIEEVD

A. MALDI-TOF MS spectrum (spot 4)



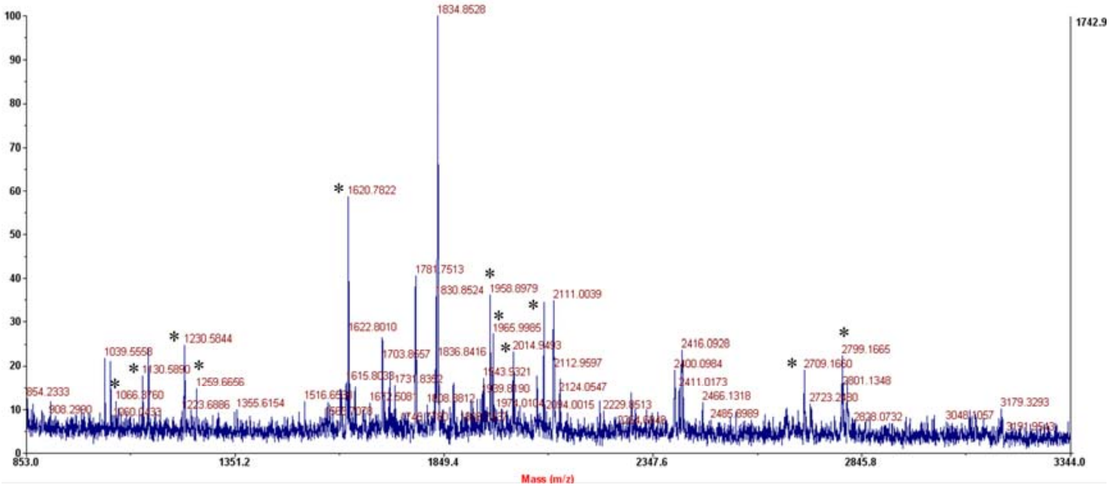
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
37 - 49	TTPSYVAFTDTER	1488.0990	+
57 - 72	NQVAMNPTNTVFDAKR	1806.3720	+
138 - 155	TVTNAVVTVPAYFNDSQR	1982.5020	+
160 - 171	DAGTIAGLNVLR	1199.9640	+
221 - 236	STAGDTHLGGEDFDNR	1692.1830	+
237 - 247	MVNHFIAEFKR	1392.0750	+
273 - 299	TLSSSTQASIEIDSLYEGIDFYTSITR	2998.1880	+
300 - 311	ARFEELNADLFR	1481.1550	+
326 - 342	LDKSQIHDIVLVGGSTR	1838.4920	+
362 - 384	SINPDEAVAYGAAVQAAILSGDK	2260.7990	+
424 - 447	QTQTFTTYSDNQPGVLIQVYEGER	2775.0770	+

C. Matched peptides (Bold Red) in the HSC70 amino acid sequence

1 MSKGPAVGID LGTTYSCVGV FQHGKVEIIA NDQGNR**TTPS YVAFTDTER**L
51 IGDAAK**NQVA MNPTNTVFDA KR**LIGRRFDD AVVQSDMKHW PFMVVNDAGR
101 PKVQVEYKGE TKSFYPEEVS SMVLTKMKEI AEAYLGK**TVT NAVVTVPAYF**
151 **NDSQR**QATK**D AGTIAGLNVL R**IINEPTAAA IAYGLDKKVG AERNVLIFDL
201 GGGTFDVSIL TIEDGIFEVK **STAGDTHLGG EDFDNRMVNH FIAEFKR**KHK
251 KDISENKRAV RRLRTACERA KR**TLSSSTQA SIEIDSLYEG IDFYTSITRA**
301 **RFEELNADLF R**GTLDPVEKA LRDAK**LDKSQ IHDIVLVGGS TR**IPKIQKLL
351 QDFFNGKELN K**SINPDEAVA YGAAVQAAIL SGDK**SENVQD LLLLDVTPLS
401 LGIETAGGVM TVLIKRNTTI PTK**QTQTFTT YSDNQPGVLI QVYEGER**AMT
451 KDNNLLGKFE LTGIPPAPRG VPQIEVTFDI DANGILNVSA VDKSTGKENK
501 ITITNDKGRL SKEDIERMVQ EAEKYKAEDE KQRDKVSSKN SLESYAFNMK
551 ATVEDEKLQG KINDEDKQKI LDKCNEIISW LDKNQTAEKE EFEHQQKELE
601 KVCNPIITKL YQSAGGMPGG MPGGFPGGGA PPSGGASSGP TIEEVD

A. MALDI-TOF MS spectrum (spot 5)



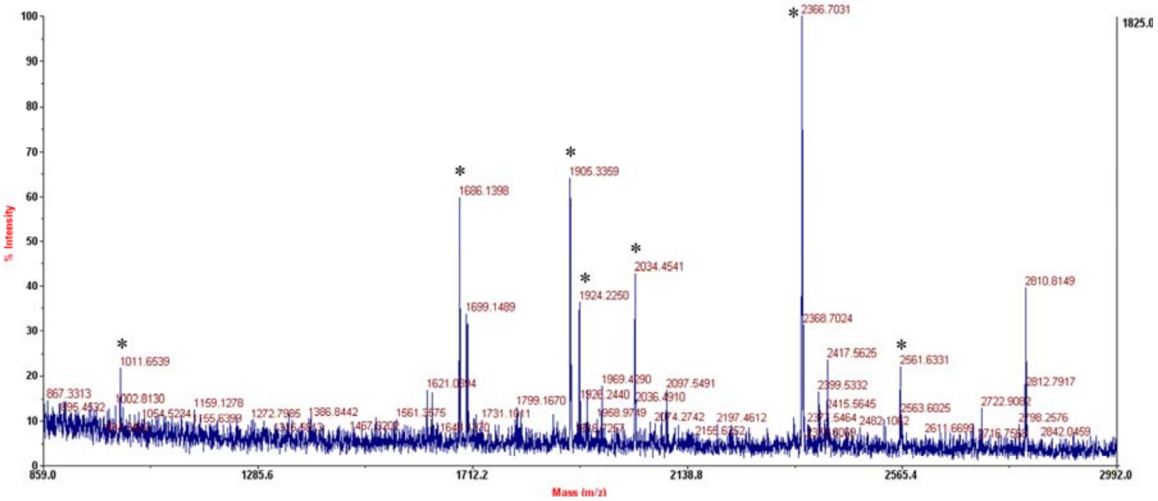
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
1 - 19	MREIVHIQAGQCGNQIGAK	2109.9740	+
47 - 62	INVYYNEAAGNKYVPR	1870.8500	+
78 - 103	SGPFGQIFRPDNFVFGQSGAGNNWAK	2798.1530	+
104 - 121	GHYTEGAELVDSVLDVVR	1958.9080	+
217 - 241	LTTPTYGDLNHLVSATMSGVTTCLR	2708.1630	+
242 - 251	FPGQLNADLR	1130.5870	+
242 - 252	FPGQLNADLRK	1258.6740	+
253 - 262	LAVNMVPFPR	1143.6220	+
263 - 276	LHFFMPGFAPLTSR	1620.8000	+
263 - 276	LHFFMPGFAPLTSR	1636.7920	+
310 - 318	YLTVAAIFR	1053.5920	+
363 - 380	MSATFIGNSTAIQELFKR	2013.9550	+
381 - 390	ISEQFTAMFR	1229.6140	+

C. Matched peptides (Bold Red) in the Tubulin amino acid sequence

1 **MREIVHIQAG QCGNQIGAK**F WEVISDEHGI DPTGSYHGDS DLQLER**INVY**
51 **YNEAAGNKYV PR**AILVDLEP GTMDSVR**SGP FGQIFRPDNF VFGQSGAGNN**
101 **WAKGHYTEGA ELVDSVLDVV RK**ESESCDCL QGFQLTHSLG GGTGSGMGTL
151 LISKIREEYP DRIMNTFSVM PSPKVSDTVV EPYNATLSVH QLVENTDETY
201 SIDNEALYDI CFRTLK**LTTP TYGDLNHLVS ATMSGVTTCL RFPGQLNADL**
251 **RKLAVNMVPF PRLHFFMPGF APLTSR**GSQQ YRALTVPELT QQMFDSKNMM
301 AACDPRHGR**Y LTVAAIFR**GR MSMKEVDEQM LNVQNKNSSY FVEWIPNNVK
351 TAVCDIPPRG LK**MSATFIGN STAIQELFKR ISEQFTAMFR** RKAFLHWYTG
401 EGMDEMEFTE AESNMNDLVS EYQQYQDATA DEQGEFEEEE GEDEA

A. MALDI-TOF MS spectrum (spot 6)



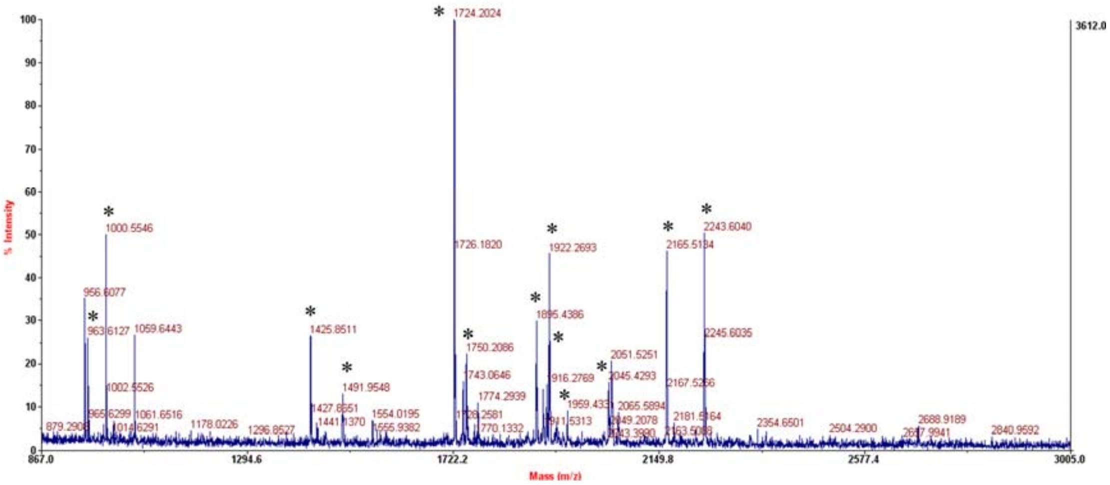
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
97 - 121	LVQDVANNTNEEAGDGTTTATVLAR	2560.6330	+
134 - 142	GANPVEIRR	1011.6500	+
206 - 221	TLNDELEIIEGMKFDR	1923.2330	+
206 - 221	TLNDELEIIEGMKFDR	1939.2330	+
250 - 268	KISSVQSIVPALEIANAHR	2033.4540	+
251 - 268	ISSVQSIVPALEIANAHR	1905.3260	+
269 - 290	KPLVIIAEDVDGEALSTLVLNR	2365.7010	+
345 - 359	VGEVIVTKDDAMLLK	1631.1390	+
430 - 446	AAVEEGIVLGGGCALLR	1685.1500	+

C. Matched peptides (Bold Red) in the HSP60 amino acid sequence

1 MLRLPTVLRQ MRPVSRALAP HLTRAYAKDV KFGADARALM LQGVDLLADA
51 VAVTMGPKGR TVIIEQSWGS PKVTKDGVTV AKSIDLKDKY KNIGAK**LVQD**
101 **VANNTNEEAG DGTTTATVLA R**SIAKEGFEK ISK**GANPVEI RR**GVMLAVDA
151 VIAELKKQSK PVTTPEEIAQ VATISANGDK DIGNIISDAM KKVGRKGVIT
201 VKDGK**TLNDE LEIIEGMKFD R**GYISPYFIN TSKGQKCEFQ DAYVLLSEK**K**
251 **ISSVQSIVPA LEIANAHRKP LVIIAEDVDG EALSTLVLNR** LKVGLQVVAV
301 KAPGFGDNRK NQLKDMAIAT GGAVFGEEGL NLNLEDVQAH DLGK**VGEVIV**
351 **TKDDAMLLK**G KGDKAHIEKR IQEITEQLDI TTSEYEKEKL NERLAKLSDG
401 VAVLKVGGTS DVEVNEKKDR VTDALNATR**A AVEEGIVLGG GCALLR**CIPA
451 LDSLKPANED QKIGIEIIKR ALKIPAMTIA KNAGVEGSLI VEKILQSSSE
501 VGYDAMLGDF VNMVEKGIID PTKVVRTALL DAAGVASLLT TAEAVVTEIP
551 KEEKDPGMGA MGGMGGGMGG GMF

A. MALDI-TOF MS spectrum (spot 7)



B. Peptides detected by MALDI-TOF-MS

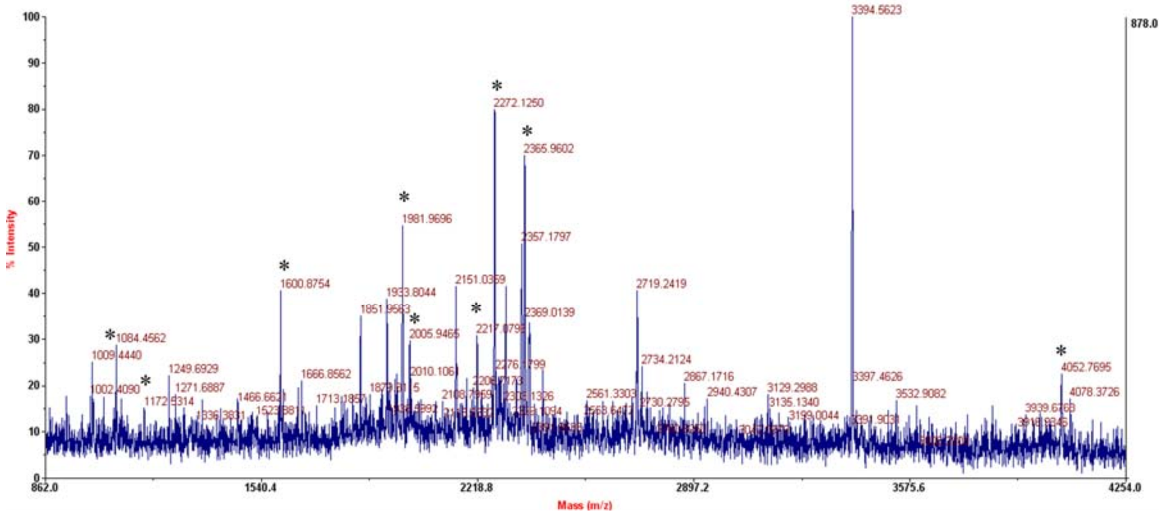
Peptide	Amino acid sequence	$[M+H]^+$	Matched
69-76	MVEGFFDR	1000.5540	+
108 - 123	IIKPCNHVLSLSFPIR	1894.4380	+
125 - 136	DDGSWEVIEGYR	1425.8600	+
137 - 143	AQHSQHR	863.4720	+
212 - 231	KGFIGPGIDVPAPDMSTGER	2044.4190	+
213 - 231	GFIGPGIDVPAPDMSTGER	1916.2980	+
303 - 318	TFVVQGFGNVGLHSMR	1749.2120	+
347 - 363	ELEDFKLQHGSILGFPK	1958.3770	+
400 - 420	IIAEGANGPTTPEADKIFLER	2242.5740	+
445 - 453	NLNHVSYGR	1059.6440	+
454 - 460	LTFKYER	956.6030	+
461 - 476	DSNYHLLMSVQESLER	1921.2680	+
481 - 496	HGGTIPVVPTAEFQDR	1724.1860	+
497 - 516	ISGASEKDIVHSGLAYTMER	2164.4730	+
504 - 516	DIVHSGLAYTMER	1491.9690	+
528 - 535	YNLGLDLR	963.6170	+

C. Matched peptides (Bold) in the GDH amino acid sequence

1 MYRRLGEVLL LSRAGPAALG SAAADSAALL GWARGQPSAV PQPGLTPVAR
51 RHYSEAATDR EDDPNFFK**MV** **EGFFDR**GASI VEDKLVEDLK TRENEEQKRN
101 RVRGILR**IIK** **PCNHVLSLSF** **PIRRDDGSWE** **VIEGYRAQHS** **QHR**TPCKGGI
151 RYSTDVSVDE VKALASLMTY KCAVVDVPFG GAKAGVKINP KNYTDNELEK
201 ITRRFTMELA K**KGFIGPGID** **VPAPDMSTGE** **REMSWIADTY** **ASTIGHYDIN**
251 **AHACVTGKPI** **SQGGIHGR**IS ATGRGVFHGI ENFINEASYM SILGMTPGLG
301 DK**TFVVQGFG** **NVGLHSMR**YL HRFGAKCVGV GESDGSIWNP DGIDPK**ELED**
351 **FKLQHGSILG** **FPK**AKVYEGS **ILEADCDILI** **PAASEK**QLTK SNAPRVKAK**I**

401 IAEGANGPTT PEADKIFLER NIMVIPDLYL NAGGVTVSYF EWLK**NLNHVS**
451 YGRLTFKYER DSNYHLLMSV QESLERKFGK **HGGTIPVVPT AEFQDRISGA**
501 SEKDIVHSGL AYTMERSARQ IMRTAMK**YNL GLDLRTAAYV NAIEKVFK**VY
551 NEAGVTFT

A. MALDI-TOF MS spectrum (spot 8)



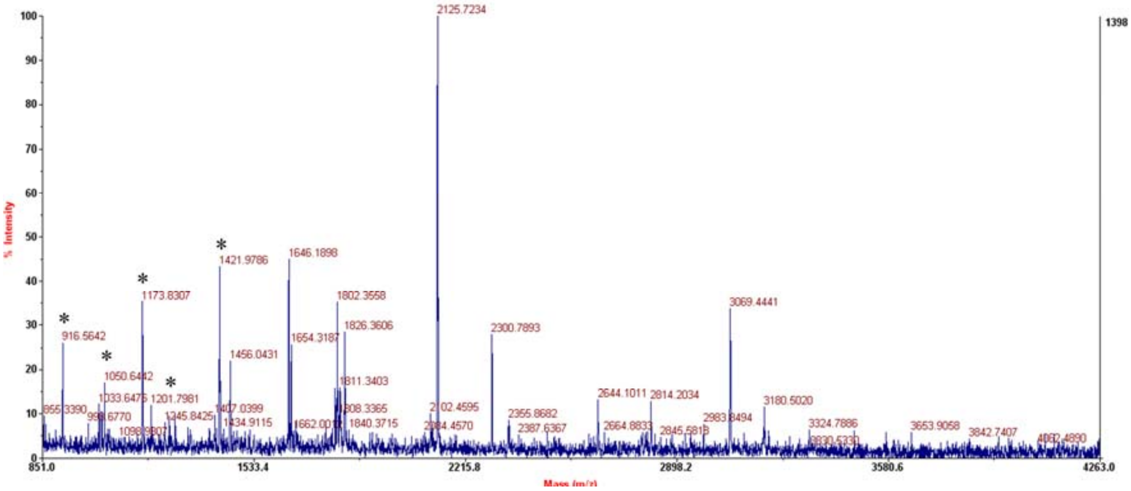
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
83 - 97	ASLQNLLSASQAQLR	1599.8770	+
106-142	AFTSQASATMHLPATIGDYTDFYSSLQHATNVGIMFR	4049.7500	+
143-162	GKENALLPNWLHLPVGYHGR	2271.2040	+
163-174	ASSVVVSGTPIR	1172.5610	+
175-194	RPMGQMRPDNSKPPVYGASK	2216.0580	+
195-211	RLDMELEMAFFVGPGNR	1981.9410	+
221-237	AQEHIFGMVLMNDWSAR	2004.9210	+
372-381	AIDVGQGQTR	1044.4740	+
382-402	TFLLDGDEVIITGHCQGDGYR	2366.0740	+

C. Matched peptides (Bold Red) in the Fumarylacetoacetase amino acid sequence

1 MSFIPVAEDS DFPIQNLPYG VFSTQSNPKP RIGVAIGDQI LDLSVIKHLF
51 TGPVLSKHQH VFDETTLNSF MGLGQAAWKE AR**ASLQNLLS ASQAQLR**DDK
101 ELRQR**AFTSQ ASATMHLPAT IGDYTDFYSS LQHATNVGIM FRGKENALLP**
151 **NWLHLPVGYH GRASSVVVSG TPIRRPMGQM RPDNSKPPVY GASKRLDMEL**
201 **EMAFFVGPGN R**FGEPIPISK **AQEHIFGMVL MNDWSAR**DIQ QWEYVPLGPF
251 LGKSFGTTIS PWVVPMDALM PFVVPNPKQD PKPLPYLCHS QPYTFDINLS
301 VALKGEGMSQ AATICRSNFK HMYWTILQQL THHSVNGCNL RPGDLLASGT
351 ISGSDPESFG SMLELSWKGT K**AIDVGQGQT RTFLLDGDEV IITGHCQGDG**
401 **YR**VGFGQCAG KVLPALSPA

A. MALDI-TOF MS spectrum (spot 9)



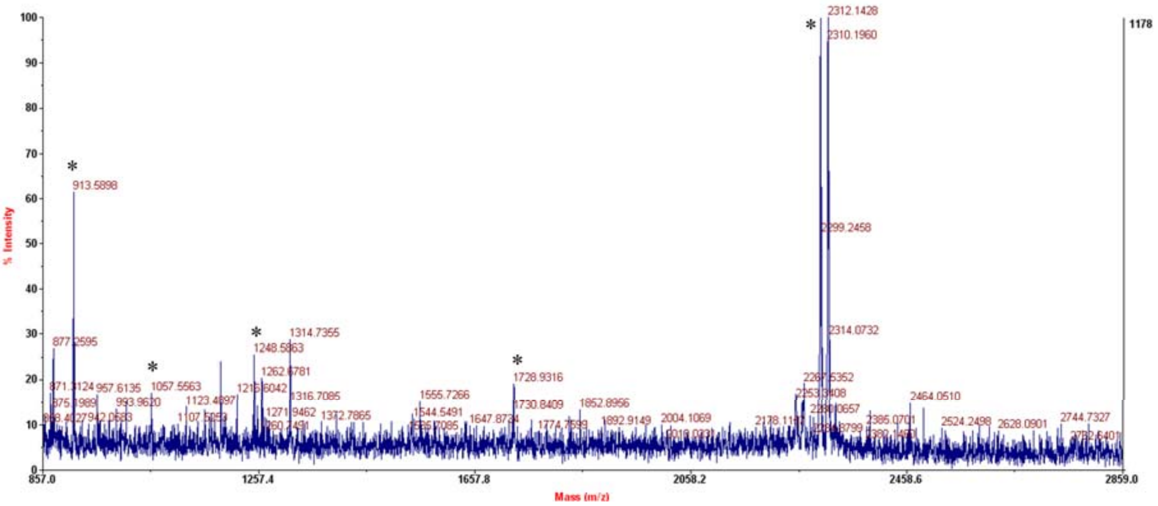
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
15-22	ELSDIALR	916.5810	+
61-69	QVLFSADDR	1050.6480	+
61-71	QVLFSADDRVK	1277.9280	+
102-111	GILVGIKVDK	1041.7720	+
305-315	ALQASALSAWR	1173.8340	+
319-331	DNAGAATEEFIKR	1421.9770	+
331-342	RAEMNGLAAQGK	1245.8630	+

C. Matched peptides (Bold Red) in the Fructose-bisphosphate aldolase C amino acid sequence

1 MPHSYPALSA EQKK**ELSDIA LR**IVAPGKGI LAADESVGSM AKRLSQIGVE
51 NTEENRRLYR **QVLFSADDRV K**KCIGGVIFF HETLYQKDDN GVPFVRTIQE
101 K**GILVGIKVD K**GVVPLAGTD GETTTQGLDG LLERCAQYKK DGADFAKWRC
151 VLKISDRTPS ALAILENANV LARYASICQQ NGIVPIVEPE ILPDGDHDLK
201 RCQFVTEKVL AAVYKALSDH HVYLEGTLLK PNMVTPGHAC PIKYSPEEIA
251 MATVTALRRT VPPAVPGVTF LSGGQSEEEA SLNLNAINRC SLPRPWALTF
301 SYGR**ALQASA LSAWR**GQR**DN AGAATEEFIK RAEMNGLAAQ GK**YEGSGDGG
351 AAAQSLYVAN HAY

A. MALDI-TOF MS spectrum (spot10)



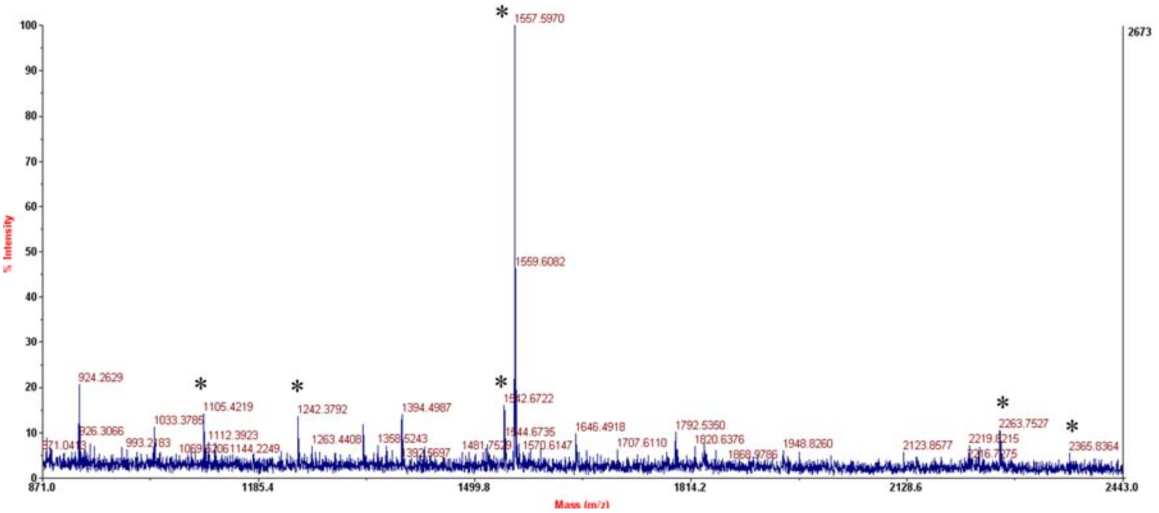
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
92-100	IVVVTAGVR	913.5910	+
92-107	IVVVTAGVRQQEGESR	1727.8920	+
159-170	VIGSGCNLDSAR	1248.5780	+
171-178	FRYLMAEK	1057.5650	+
280-299	GMYGIENEVFLSLPCILNAR	2296.1350	+
309-318	LKDDEVAQLR	1186.6320	+

C. Matched peptides (Bold Red) in the LDH amino acid sequence

1 MATLKEKLIA PVADDETAVP NNKITVVGVG QVGMACAISI LGKSLADELA
51 LVDVLEDKLK GEMMDLQHGS LFLQTPKIVA DKDYSVTANS K**IVVVTAGVR**
101 **QQEGESR**LNL VQRNVNVFKF IIPQIVKYSP DCTIIVVSNP VDILTYVTWK
151 LSGLPKHR**VI GSGCNLDSAR FRYLMAEK**LG IHPSSCHGWI LGEHGDSSVA
201 VWSGVNVAGV SLQELNPEMG TDNDSENWKE VHKMVVDSAY EVIKLKGYTN
251 WAIGLSVADL IESMLKNLSR IHPVSTMVK**G MYGIENEVFL SLPCILNAR**G
301 LTSVINQK**LK DDEVAQLR**KS ADTLWDIQKD LKDL

A. MALDI-TOF MS spectrum (spot 11)



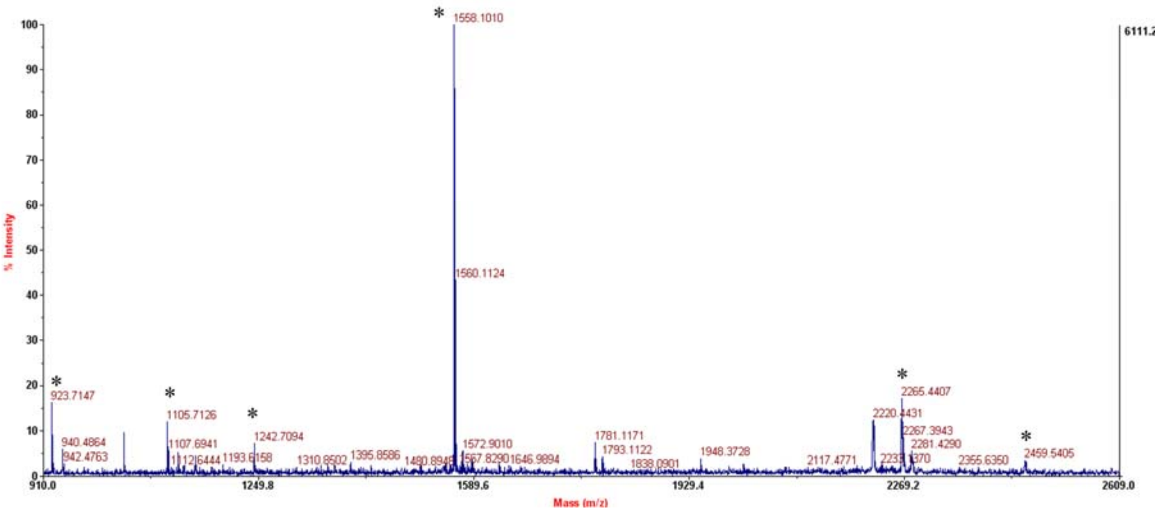
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
70-78	RQDLFIVSK	1105.4340	+
156-169	AIGVSNFNPLQIER	1557.5990	+
244-256	TTAQVLIRFPIQR	1542.6660	+
276-294	FRYLMAEK	2263.7400	+
280-299	VFDFELSNEDMATLLSYNR	2296.1350	+
307-316	HKDYPFHAEV	1242.3780	+

C. Matched peptides (Bold Red) in the AR amino acid sequence

1 MASHLELNNG TKMPTLGLGT WKSPPGQVTE AVKVAIDMGY RHIDCAQVYQ
51 NEKEVGVALQ EKLKEQVVK**R QDLFIVSK**LW CTFHDQSMVK GACQKTLSDL
101 QLDYLDLYLI HWPTGFKPGP DYFPLDASGN VIPSDTDFVD TWTAMEQLVD
151 EGLVK**AIGVS NFNPLQIER**I LNKPGLKYKP AVNQIECHPY LTQEKLIEYC
201 HCKGIVVTAY SPLGSPDRPW AKPEDPSLLE DPRIKEIAAK YNK**TTAQVLI**
251 **RFPIQR**NLVV IPKSVTPARI AENFK**VFDFE LSNEDMATLL SYNR**NWRVCA
301 LMSCAK**HKDY PFHAEV**

A. MALDI-TOF MS spectrum (spot 12)



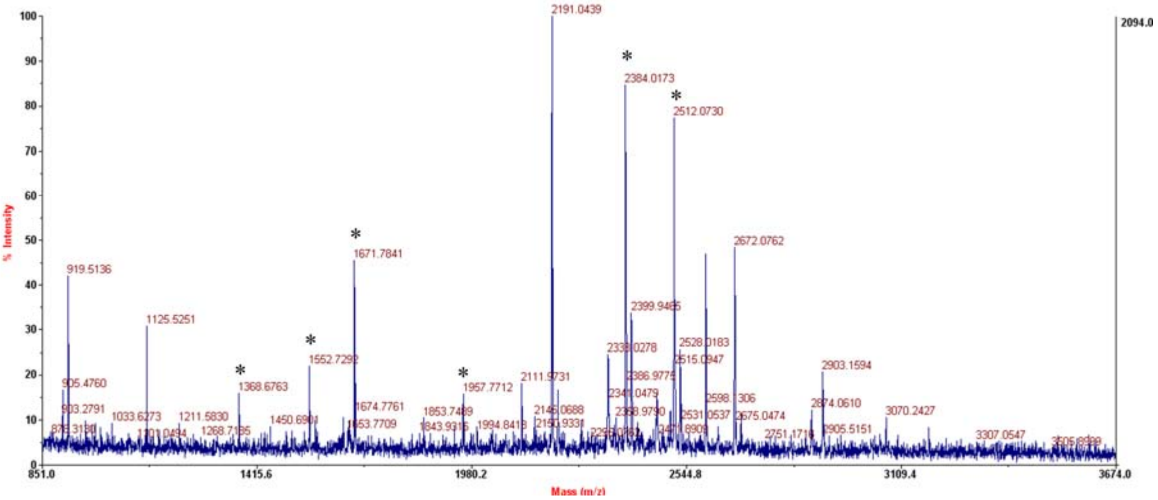
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
34-41	VAIDMGYR	924.4990	+
42-62	HIDCAQVYQNEKEVGVALQEK	2458.5160	+
70-78	RQDLFIVSK	1105.7080	+
156-169	AIGVSNFNPLQIER	1558.0120	+
196-203	LIEYCHCK	1122.5820	+
244-251	TTAQVLIR	901.5900	+
276-294	VFDFELSNEDMATLLSYNR	2264.3420	+
307-316	HKDYPFHAEV	1242.7110	+

C. Matched peptides (Bold Red) in the AR amino acid sequence

1 MASHLELNNG TKMPTLGLGT WKSPPGQVTE AVK**VAIDMGY RHIDCAQVYQ**
51 **NEKEVGVALQ EK**LKEQVVK**R QDLFIVSK**LW CTFHDQSMVK GACQKTLSDL
101 QLDYLDLYLI HWPTGFKPGP DYFPLDASGN VIPSDTDFVD TWTAMEQLVD
151 EGLVK**AIGVS NFNPLQIER**I LNKPGLKYKP AVNQIECHPY LTQEK**LIEYC**
201 **HCK**GIVVTAY SPLGSPDRPW AKPEDPSLLE DPRIKEIAAK YNK**TTAQVLI**
251 **R**FPIQRNLVV IPKSVTPARI AENFK**VFDFE LSNEDMATLL SYNR**NWRVCA
301 LMSCAK**HKDY PFHAEV**

A. MALDI-TOF MS spectrum (spot 13)



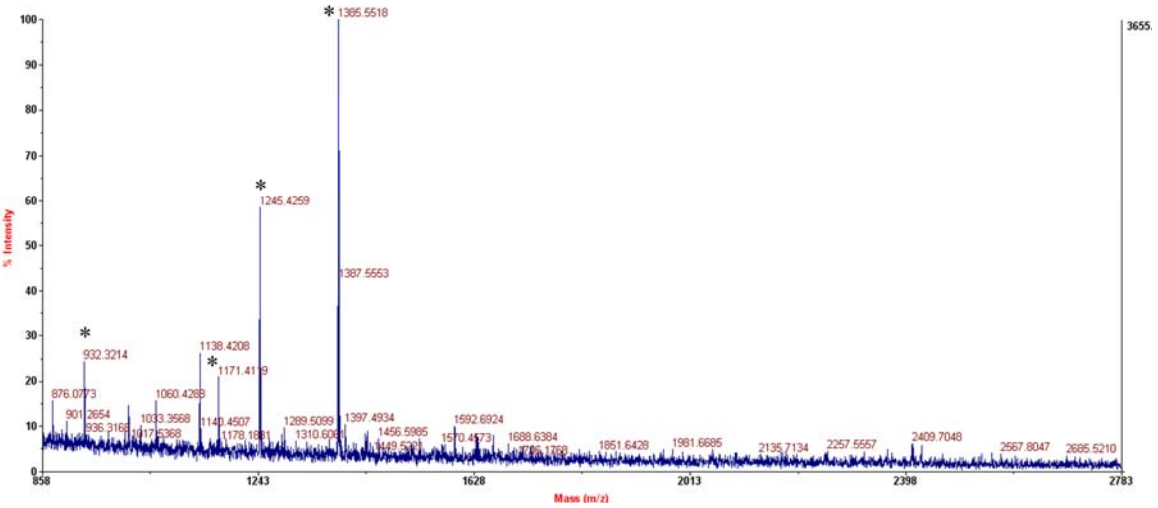
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	[M+H]$^+$	Matched
9-16	RVLVYGGR	924.4990	+
53 -70	MTDSFTEQADQVTAEVGK	1956.7540	+
136-151	AALDGTPGMIGYGMAK	1552.7290	+
152-164	GAVHQLCQSLAGK	1368.6720	+
165-188	NSGMPSGAAAIAVLPVTLDTPMNR	2382.9970	+
165-189	NSGMPSGAAAIAVLPVTLDTPMNRK	2511.0690	+
218-233	RPNSGSLIQVVTTDGK	1671.8010	+

C. Matched peptides (Bold Red) in the DHPR amino acid sequence

1 MAASGEAR**RV LVYGGR**GALG SRCVQAFRAR NWWVASIDVV ENEEASASVI
51 VK**MTDSFTEQ ADQVTAEVGK** LLGDQKVDAI LCVAGGWAGG NAKSKSLFKN
101 CDLMWKQSIW TSTISSHLAT KHLKEGGLLT LAGAK**AALDG TPGMIGYGMA**
151 **KGAVHQLCQS LAGKNSGMPS GAAAIAVLPV TLDTPMNRK**S MPEADFSSWT
201 PLEFLVETFH DWITGNK**RPN SGSLIQVVTT DGK**TELTPAY F

A. MALDI-TOF MS spectrum (spot 14)



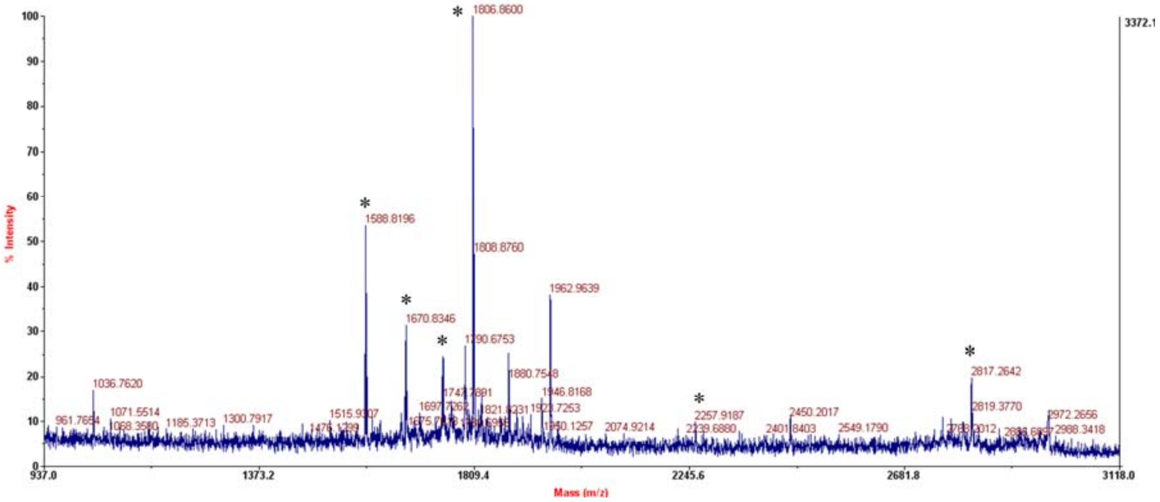
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
2-13	PGKPVLHYFDGR	1385.6230	+
130-138	NRYFPAFEK	1171.5620	+
142-152	SHGQDYLVGNR	1245.5900	+
142-155	SHGQDYLVGNRLSR	1601.6710	+
197-204	FLQPGSQR	932.4410	+

C. Matched peptides (Bold Red) in the GSTA3 amino acid sequence

1 M**PGKPVLHYF DGR**GRMEPIR WLLAAAGVEF EEQFLKTRDD LARLRNDGSL
51 MFQQVPMVEI DGMKLVQTRA ILNYIATKYN LYGKDMKERA LIDMYAEGVA
101 DLDEIVLHYP YIPPGEKEAS LAKIKDKAR**N RYFPAFEK**VL K**SHGQDYLVG**
151 **NRLSR**ADVYL VQVLYHVEEL DPSALANFPL LKALRTRVSN LPTVKK**FLQP**
201 **GSQR**KPLEDE KCVESAVKIF S

A. MALDI-TOF MS spectrum (spot 15)



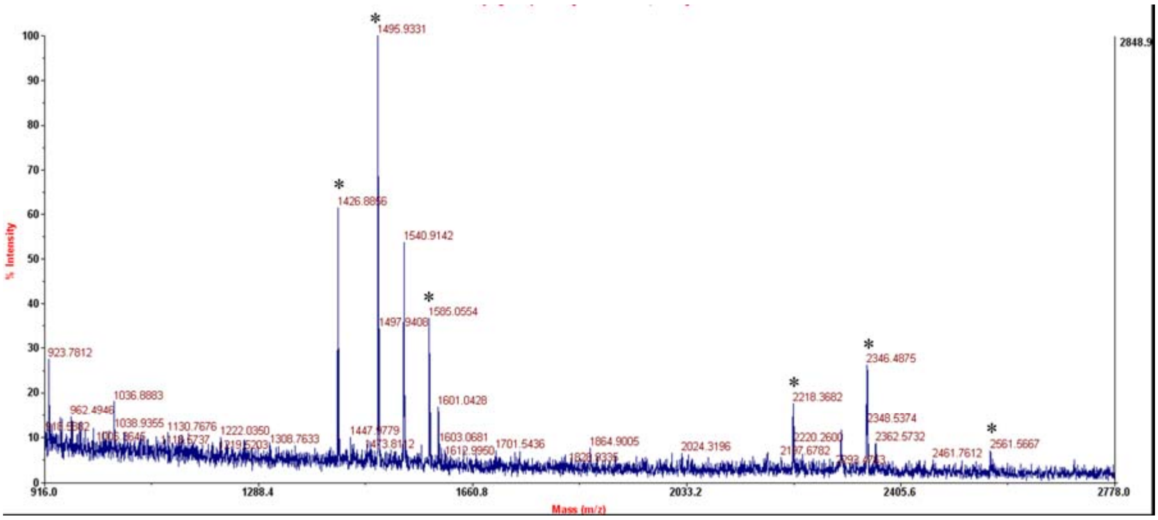
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
32-45	MLQLVEESKDAGIR	1588.8210	+
46-59	TLVMLDEQGEQLER	1660.8090	+
104-119	AWGNNQDGVVASQPAR	1669.7700	+
120-135	VVDEREQMAISGGFIR	1806.8720	+
137-161	VTNDARENEMDENLEQVSGIIGNLR	2816.2520	+
162-176	HMALDMGNEIDTQNR	1744.7850	
162-180	HMALDMGNEIDTQNRQIDR	2256.9290	

C. Matched peptides (Bold Red) in the SNP25 amino acid sequence

1 MAEDADMRNE LEEMQRRADQ LADESLESTR R**MLQLVEESK DAGIRTLVML**
51 **DEQGEQLER**I EEGMDQINKD MKEAEKNLTD LGKFCGLCVC PCNKLKSSDA
101 YKK**AWGNNQD GVVASQPARV VDEREQMAIS GGFIR**R**VTND ARENEMDENL**
151 **EQVSGIIGNL RHMALDMGNE IDTQNRQIDR** IMEKADSNKT RIDEANQRAT
201 KMLGSG

A. MALDI-TOF MS spectrum (spot 16)



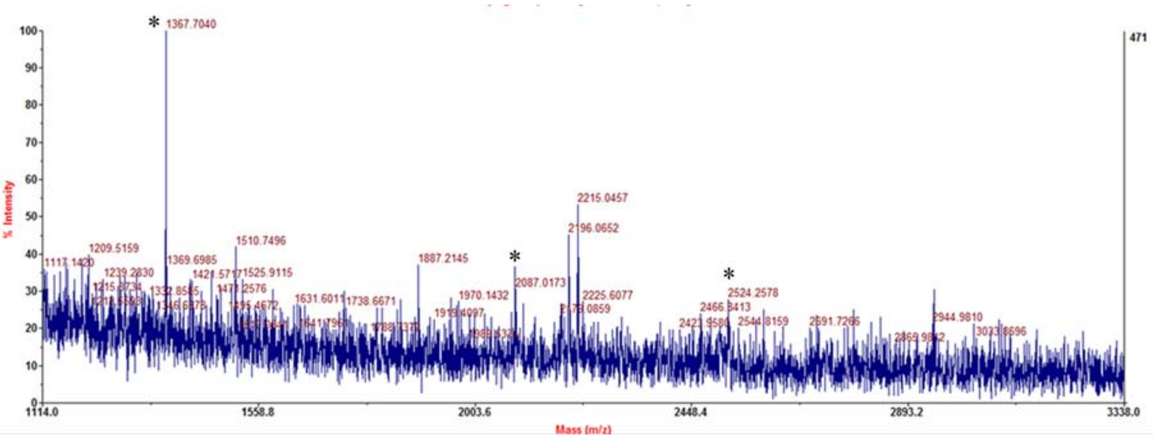
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
32-44	YGYTHLSTGDLLR	1495.9390	+
64 -77	GELVPLETVLDMLR	1585.0450	+
108-128	KIAQPTLLLYVDAGPETMTQR	2345.4940	+
109-128	IAQPTLLLYVDAGPETMTQR	2217.3710	+
156-167	ATEPVISFYDKR	1425.8930	+
172-194	KVNAEGSVDTVFSQVCTYLDSLK	2560.5700	+

C. Matched peptides (Bold) in the AK amino acid sequence

1 MEDKLKKAKI IFVVGGPGSG KGTQCEKIVQ K**YGYTHLSTG DLLR**AEVSSG
51 SSRGKMLSSI MEK**GELVPLE TVLDMLR**DAM LAKVDSSNGF LIDGYPREVK
101 QGEEFER**KIA QPTLLLYVDA GPETMTQR**LL KRGETSGRVD DNEETIKKRL
151 ETYYK**ATEPV ISFYDKR**GIV R**KVNAEGSVD TVFSQVCTYL DSLK**

A. MALDI-TOF MS spectrum (spot 17)



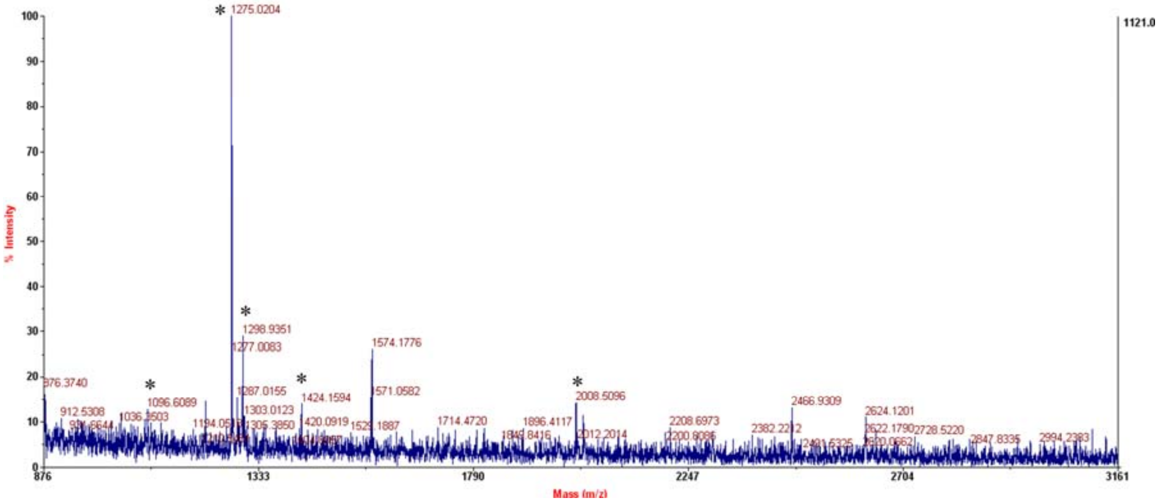
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
72-92	HGGPADEERHVGDLGNVAAGK	2085.9560	+
93-116	DGVANVSIEDRVISLSGEHSIIGR	2523.1270	+
104-116	VISLSGEHSIIGR	1367.7090	+

C. Matched peptides (Bold) in the SOD amino acid sequence

1 MAMKAVCVLK GDGPVQGVIH FEQKASGEPV VVSGQITGLT EGEHGFHVHQ
51 YGDNTQGCTT AGPHFNPHSK K**HGGPADEER HVGDLGNVAA GKDGVANVSI**
101 **EDRVISLSGE HSIIGR**TMVV HEKQDDLGKG GNEESTKTGN AGSRLACGVI
151 GIAQ

A. MALDI-TOF MS spectrum (spot 18)



B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
19-31	VNPDDVGGEALGR	1298.9430	+
32-41	LLVVYPWTQR	1275.0190	+
42-60	YFDSFGDLSSASAIMGNPK	2007.5030	+
68 -77	VINAFNDGLK	1090.8120	
134-147	VVAGVASALAHKYH	1423.1460	

C. Matched peptides (Bold Red) in the Hemoglobin subunit beta-1 amino acid sequence

1 MVHLTDAEKA AVNGLWGK**VN PDDVGGEALG RLLVVYPWTQ RYFDSFGDLS**
51 **SASAIMGNPK** VKAHGKK**VIN AFNDGLKHLD NLK**GTFAHLS ELHCDKLHVD
101 PENFRLLGNM IVIVLGHHLG KEFTPCAQAA FQK**VVAGVAS ALAHKYH**

Supplementary Information for

Proteomic identification of an Upregulated Isoform of Annexin A3 in the Spinal Cords of Rats in a Neuropathic Pain Model

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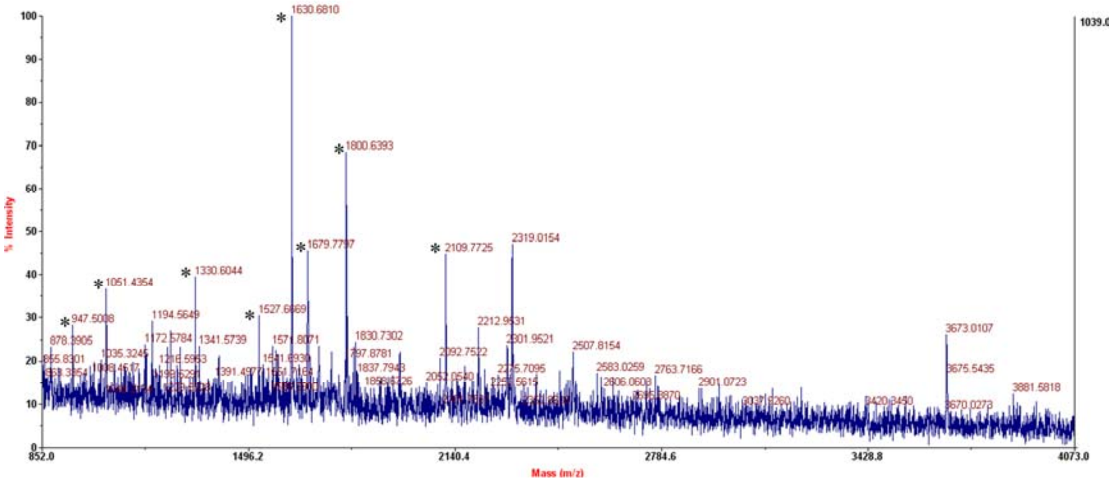
A. MALDI-TOF MS spectrum (spot 1)



B. Peptides detected by MALDI-TOF-MS

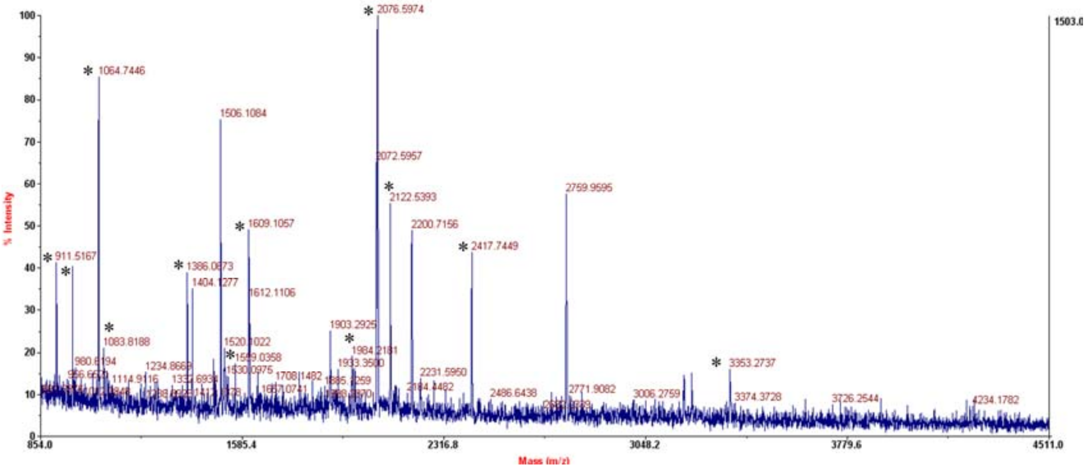
Peptide	Amino acid sequence	$[M+H]^+$	Matched
46-53	MDELQLFR	1051.4330	+
46 - 60	MDELQLFRGDTVLLK	1777.7970	+
66 - 83	EAVCIVLSDDTCSDEKIR	2109.7740	+
148 - 155	KGDIFLVR	947.4930	+
324 - 338	IVSQLLTLMDGLKQR	1714.8550	+
454 - 465	WALSQSNPSALR	1329.6130	+
600 - 614	VINQILTEMDGMSTK	1679.7840	+
754 - 766	KYEMFAQTLQQSR	1629.6840	+
755 - 766	YEMFAQTLQQSR	1501.6090	+

C. Matched peptides (Bold Red) in the TERA amino acid sequence

1 MASGADSKGD DLSTAILKQK NRPNRLIVDE AINEDNSVVS LSQPK**MDELQ**
51 **LFRGDTVLLK** GKKRR**EAVCI VLSDDTCSDE KIR**MNRVVRN NLRVRLGDVI
101 SIQPCPDVKY GKRIHVLPID DTVEGITGNL FEVYLKPYFL EAYRPIR**KGD**
151 **IFLVR**GGMRA VEFKVVETDP SPYCIVAPDT VIHCEGEPIK REDEEESLNE
201 VGYDDIGGCR KQLAQIKEMV ELPLRHPALF KAIGVKPPRG ILLYGPPGTG
251 KTLIARAVAN ETGAFFFLIN GPEIMSKLAG ESESNLRKAF EEAEKNAPAI
301 IFIDELDAIA PKREKTHGEV ERR**IVSQLLT LMDGLKQR**AH VIVMAATNRP
351 NSIDPALRRF GRFDREVDIG IPDATGRLEI LQIHTKNMKL ADDVDLEQVA
401 NETHGHVGAD LAALCSEAAL QAIRKKMDLI DLEDETIDAE VMNSLAVTMD
451 DFR**WALSQSN PSALR**ETVVE VPQVTWEDIG GLEDVKRELQ ELVQYPVEHP
501 DKFLKFGMTP SKGVLFYGPP GCGKTLLAKA IANECQANFI SIKGPELLTM
551 WFGESEANVR EIFDKARQAA PCVLFFDELD SIAKARGGNI GDGGGAADR**V**
601 **INQILTEMDG MSTK**KNVFII GATNRPDIID PAILRPGRLD QLIYIPLPDE
651 KSRVAILKAN LRKSPVAKDV DLEFLAKMTN GFSGADLTEI CQRACKLAIR
701 ESIESEIRRE RERQTNPSAM EVEEDDPVPE IRRDHFEEAM RFARRSVSDN

751 DIR**KYEMFAQ TLQQSR**GFGS FRFPSGNQGG AGPSQGSGGG TGGNVYTEDN
801 DDDLYG

A. MALDI-TOF MS spectrum (spot 2)



B. Peptides detected by MALDI-TOF-MS

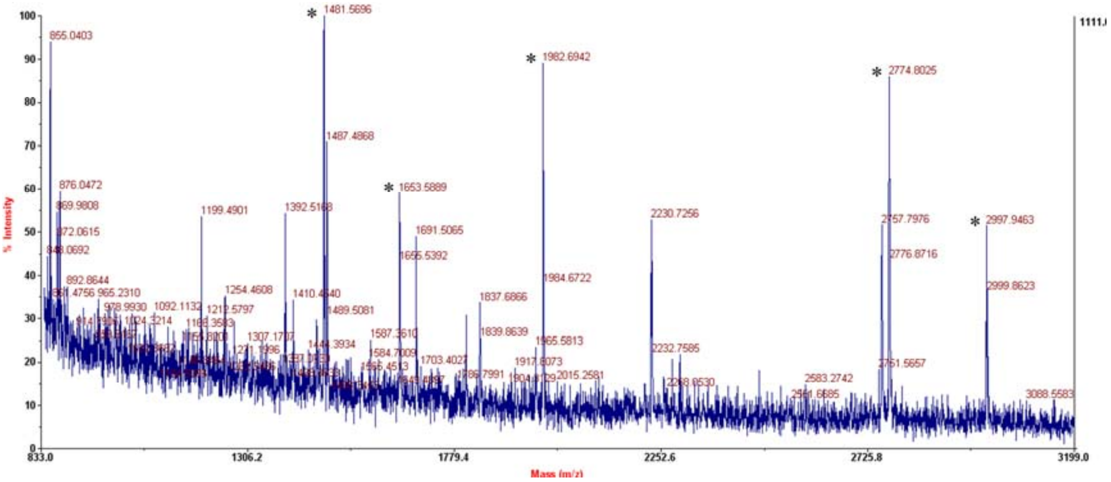
Peptide	Amino acid sequence	$[M+H]^+$	Matched
63 - 68	FCYHER	911.5130	+
185 - 200	FASEIAGVDDLGTTGR	1609.1020	+
247 - 266	KTESIDVMDAVGSNIVVSTR	2121.4770	+
248 - 266	TESIDVMDAVGSNIVVSTR	1993.3830	+
292 - 299	FAYDGLKR	969.6620	+
409 - 417	FEAPLFNAR	1064.7480	+
429 - 450	VALIGSPVDLTYRYDHLGDSPK	2416.7160	+
451 - 464	ILQDIASGNHEFSK	1559.0540	+
465 - 483	VLNAAKKPMVVLGSSALQR	1982.3960	+
471 - 483	KPMVVLGSSALQR	1386.0600	+
519 - 538	IASQVAALDLGYKPGVEAIR	2071.5630	+
563 - 592	DCFIVYQGHHGDVGAPIADVILPGAAYTEK	3214.0580	+
646 - 655	LGEVSPNLVR	1083.8080	+
646 - 673	LGEVSPNLVRYDDVEEANYFQQASELAK	3185.0730	+
674 - 702	LVDQEFLADPLVPPQLTIKDFYMTDSISR	3352.2110	+

C. Matched peptides (Bold Red) in the NADH amino acid sequence

1 MLRIPVKRAL IGLSKSPKGY VRSTGTAASN LIEVFVDGQS VMVEPGTTVL
51 QACEKVGMQI PR**FCYHER**LS VAGNCRMCLV EIEKAPKVVA ACAMPVMKGW
101 NILTNSEKSK KAREGVMEFL LANHPLDCPI CDQGGECDLQ DQSMMFGSDR
151 SRFLEGKRAV EDKNIGPLVK TIMTRCIQCT RCIR**FASEIA GVDDLGTTGR**
201 GNDMQVGTYI EKMFMSELSG NIIDICPVGA LTSKPYAFTA RPWETR**KTES**
251 **IDVMDAVGSN IVVSTR**TGEV MRILPRMHED INEEWISDKT R**FAYDGLKR**Q
301 RLTEPMVRNE K**GLLTYTSWE DALSRVAGML QSFEGK**AVAA IAGGLVDAEA
351 LVALKDLLNK VDSDTLCTEE IFPNEGAGTD LRSNYLLNTT IAGVEEADVV
401 LLVGTNPR**FE APLFNAR**IRK SWLHNDLK**VA LIGSPVDLTY RYDHLGDSPK**

451 **ILQDIASGNH EFSKVLNAAK KPMVVLGSSA LQR**DDGAAIL AAVSSIAQKI
501 RVASGAAAEW KVMNILHR**IA SQVAALDLGY KPGVEAIR**KN PPKLLFLLGA
551 DGGCITRQDL PK**DCFIVYQG HHGDVGAPIA DVILPGAAYT EK**SATYVNTE
601 GRAQQTKVAV TPPGLAREDW KIIRALSEIA GITLPYDTLD QVRNR**LGEVS**
651 **PNLVRYDDVE EANYFQQASE LAKLVDQEFL ADPLVPPQLT IKDFYMTDSI**
701 **SR**ASQTMAKC VKAVTEGAQA VEEPSIC

A. MALDI-TOF MS spectrum (spot3)



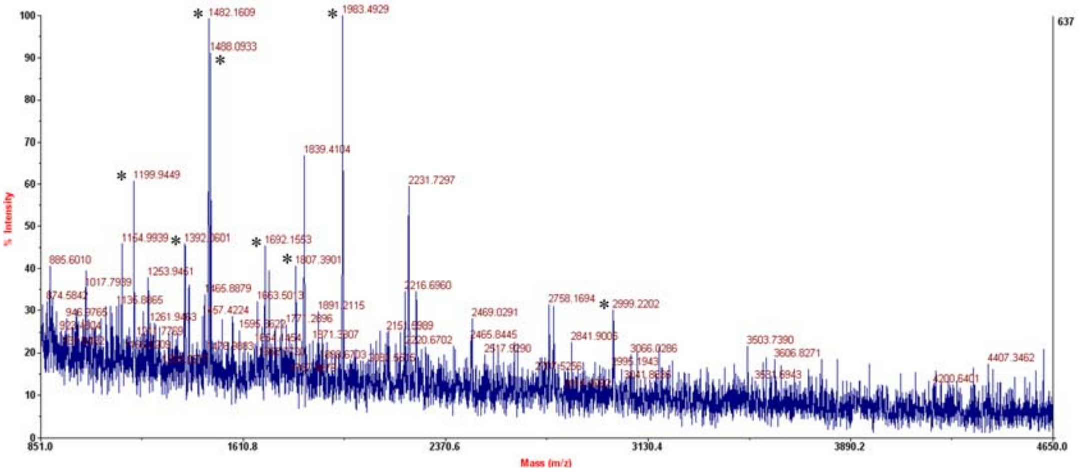
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
4 - 25	GPAVGIDLGTTYSCVGVFQHGK	2262.6820	+
57 - 72	NQVAMNPTNTVFDAKR	1805.5470	+
89 - 102	HWPFMVVNDAGRPK	1653.5380	+
138 - 155	TVTNAVVTVPAYFNDSQR	1981.6220	+
273 - 299	TLSSSTQASIEIDSLYEGIDFYTSITR	2996.9690	+
300 - 311	ARFEELNADLFR	1480.4660	+
424 - 447	QTQTFTTYSDNQPGVLIQVYEGER	2773.8670	+

C. Matched peptides (Bold Red) in the HSC70 amino acid sequence

1 MSK**GPAVGID LGTTYSCVGV FQHGK**VEIIA NDQGNRTTPS YVAFTDTERL
51 IGDAAK**NQVA MNPTNTVFDA KR**LIGRRFDD AVVQSDMK**HW PFMVVNDAGR**
101 **PK**VQVEYKGE TKSFYPEEVS SMVLTKMKEI AEAYLGK**TVT NAVVTVPAYF**
151 **NDSQR**QATKD AGTIAGLNVL RIINEPTAAA IAYGLDKKVG AERNVLIFDL
201 GGGTFDVSIL TIEDGIFEVK STAGDTHLGG EDFDNRMVNH FIAEFKRKHK
251 KDISENKRAV RRLRTACERA KR**TLSSSTQA SIEIDSLYEG IDFYTSITRA**
301 **RFEELNADLF R**GTLDPVEKA LRDAKLDKSQ IHDIVLVGGS TRIPKIQKLL
351 QDFFNGKELN KSINPDEAVA YGAAVQAAIL SGDKSENVQD LLLLDVTPLS
401 LGIETAGGVM TVLIKRNTTI PTK**QTQTFTT YSDNQPGVLI QVYEGER**AMT
451 KDNNLLGKFE LTGIPPAPRG VPQIEVTFDI DANGILNVSA VDKSTGKENK
501 ITITNDKGRL SKEDIERMVQ EAEKYKAEDE KQRDKVSSKN SLESYAFNMK
551 ATVEDEKLQG KINDEDKQKI LDKCNEIISW LDKNQTAEKE EFEHQQKELE
601 KVCNPIITKL YQSAGGMPGG MPGGFPGGGA PPSGGASSGP TIEEVD

A. MALDI-TOF MS spectrum (spot 4)



B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
37 - 49	TTPSYVAFTDTER	1488.0990	+
57 - 72	NQVAMNPTNTVFDAKR	1806.3720	+
138 - 155	TVTNAVVTVPAYFNDSQR	1982.5020	+
160 - 171	DAGTIAGLNVLR	1199.9640	+
221 - 236	STAGDTHLGGEDFDNR	1692.1830	+
237 - 247	MVNHFIAEFKR	1392.0750	+
273 - 299	TLSSSTQASIEIDSLYEGIDFYTSITR	2998.1880	+
300 - 311	ARFEELNADLFR	1481.1550	+
326 - 342	LDKSQIHDIVLVGGSTR	1838.4920	+
362 - 384	SINPDEAVAYGAAVQAAILSGDK	2260.7990	+
424 - 447	QTQTFTTYSDNQPGVLIQVYEGER	2775.0770	+

C. Matched peptides (Bold Red) in the HSC70 amino acid sequence

1 MSKGPAVGID LGTTYSCVGV FQHGKVEIIA NDQGNR**TTPS YVAFTDTER**L

51 IGDAAK**NQVA MNPTNTVFDA KR**LIGRRFDD AVVQSDMKHW PFMVVNDAGR

101 PKVQVEYKGE TKSFYPEEVS SMVLTKMKEI AEAYLGK**TVT NAVVTVPAYF**

151 **NDSQR**QATK**D AGTIAGLNVL R**IINEPTAAA IAYGLDKKVG AERNVLIFDL

201 GGGTFDVSIL TIEDGIFEVK **STAGDTHLGG EDFDNRMVNH FIAEFKR**KHK

251 KDISENKRAV RRLRTACERA KR**TLSSSTQA SIEIDSLYEG IDFYTSITRA**

301 **RFEELNADLF R**GTLDPVEKA LRDAK**LDKSQ IHDIVLVGGS TR**IPKIQKLL

351 QDFFNGKELN K**SINPDEAVA YGAAVQAAIL SGDK**SENVQD LLLLDVTPLS

401 LGIETAGGVM TVLIKRNTTI PTK**QTQTFTT YSDNQPGVLI QVYEGER**AMT

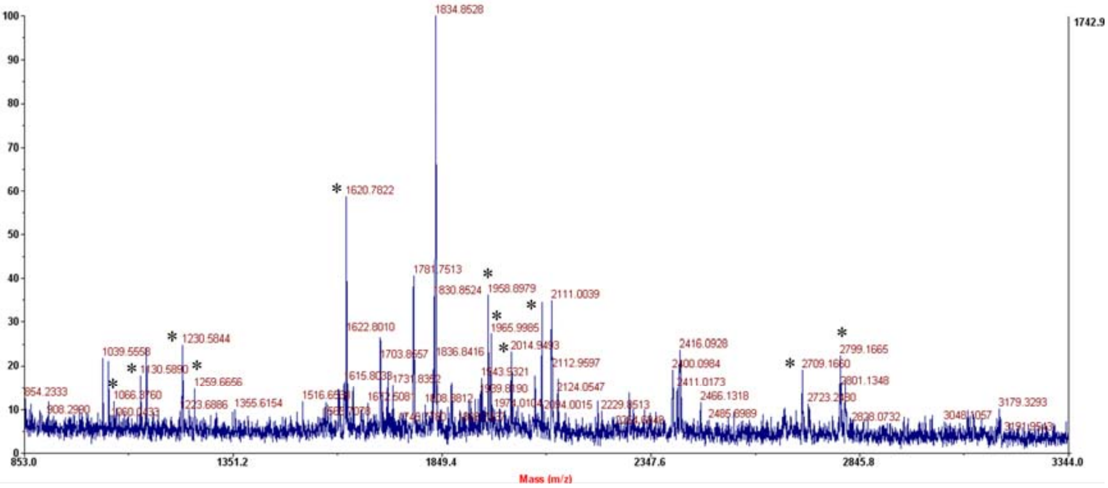
451 KDNNLLGKFE LTGIPPAPRG VPQIEVTFDI DANGILNVSA VDKSTGKENK

501 ITITNDKGRL SKEDIERMVQ EAEKYKAEDE KQRDKVSSKN SLESYAFNMK

551 ATVEDEKLQG KINDEDKQKI LDKCNEIISW LDKNQTAEKE EFEHQQKELE

601 KVCNPIITKL YQSAGGMPGG MPGGFPGGGA PPSGGASSGP TIEEVD

A. MALDI-TOF MS spectrum (spot 5)



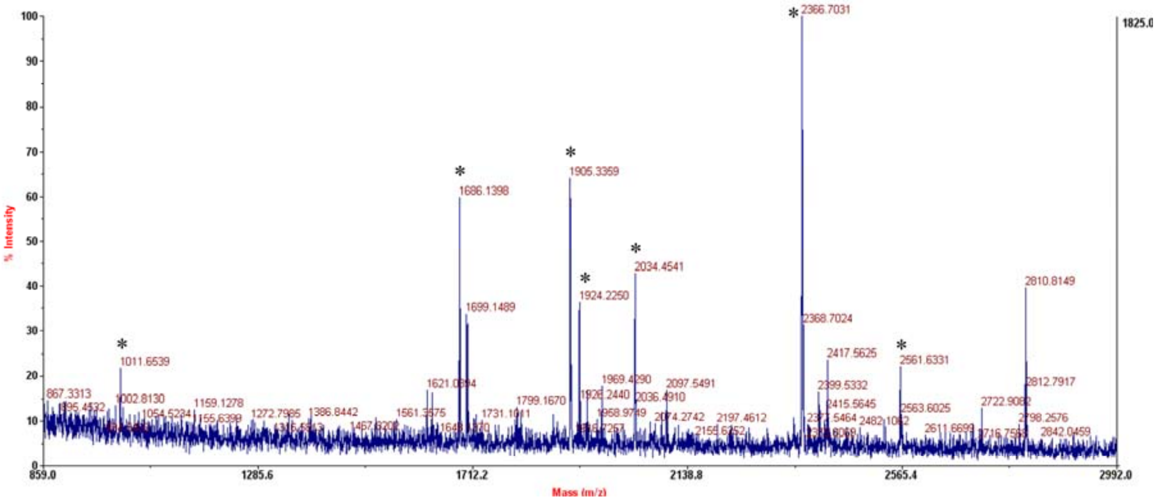
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
1 - 19	MREIVHIQAGQCGNQIGAK	2109.9740	+
47 - 62	INVYYNEAAGNKYVPR	1870.8500	+
78 - 103	SGPFGQIFRPDNFVFGQSGAGNNWAK	2798.1530	+
104 - 121	GHYTEGAELVDSVLDVVR	1958.9080	+
217 - 241	LTTPTYGDLNHLVSATMSGVTTCLR	2708.1630	+
242 - 251	FPGQLNADLR	1130.5870	+
242 - 252	FPGQLNADLRK	1258.6740	+
253 - 262	LAVNMVPFPR	1143.6220	+
263 - 276	LHFFMPGFAPLTSR	1620.8000	+
263 - 276	LHFFMPGFAPLTSR	1636.7920	+
310 - 318	YLTVAAIFR	1053.5920	+
363 - 380	MSATFIGNSTAIQELFKR	2013.9550	+
381 - 390	ISEQFTAMFR	1229.6140	+

C. Matched peptides (Bold Red) in the Tubulin amino acid sequence

1 **MREIVHIQAG QCGNQIGAK**F WEVISDEHGI DPTGSYHGDS DLQLER**INVY**
51 **YNEAAGNKYV PR**AILVDLEP GTMDSVR**SGP FGQIFRPDNF VFGQSGAGNN**
101 **WAKGHYTEGA ELVDSVLDVV RK**ESESCDCL QGFQLTHSLG GGTGSGMGTL
151 LISKIREEYP DRIMNTFSVM PSPKVSDTVV EPYNATLSVH QLVENTDETY
201 SIDNEALYDI CFRTLK**LTTP TYGDLNHLVS ATMSGVTTCL RFPGQLNADL**
251 **RKLAVNMVPF PRLHFFMPGF APLTSR**GSQQ YRALTVPELT QQMFDSKNMM
301 AACDPRHGR**Y LTVAAIFR**GR MSMKEVDEQM LNVQNKNSSY FVEWIPNNVK
351 TAVCDIPPRG LK**MSATFIGN STAIQELFKR ISEQFTAMFR** RKAFLHWYTG
401 EGMDEMEFTE AESNMNDLVS EYQQYQDATA DEQGEFEEEE GEDEA

A. MALDI-TOF MS spectrum (spot 6)



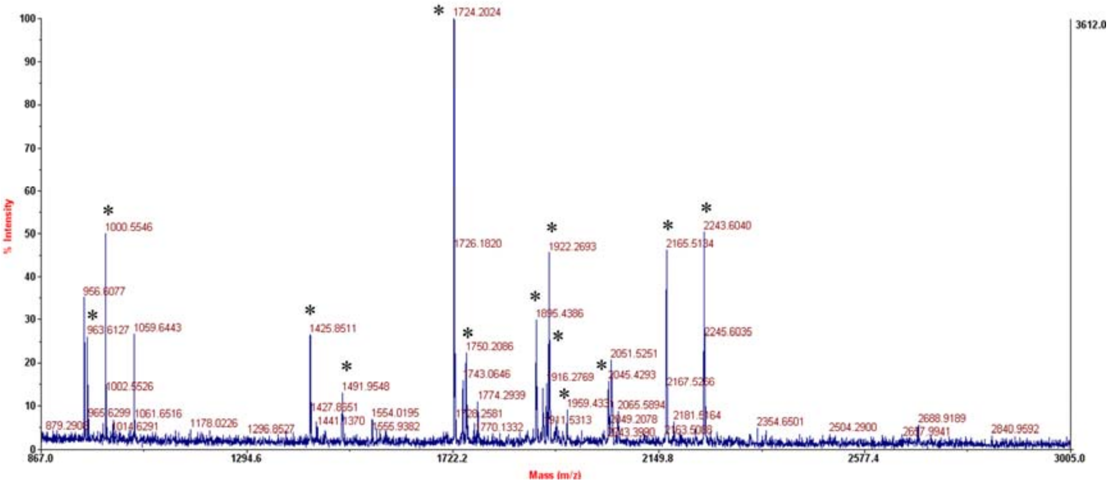
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
97 - 121	LVQDVANNTNEEAGDGTTTATVLAR	2560.6330	+
134 - 142	GANPVEIRR	1011.6500	+
206 - 221	TLNDELEIIEGMKFDR	1923.2330	+
206 - 221	TLNDELEIIEGMKFDR	1939.2330	+
250 - 268	KISSVQSIVPALEIANAHR	2033.4540	+
251 - 268	ISSVQSIVPALEIANAHR	1905.3260	+
269 - 290	KPLVIIAEDVDGEALSTLVLNR	2365.7010	+
345 - 359	VGEVIVTKDDAMLLK	1631.1390	+
430 - 446	AAVEEGIVLGGGCALLR	1685.1500	+

C. Matched peptides (Bold Red) in the HSP60 amino acid sequence

1 MLRLPTVLRQ MRPVSRALAP HLTRAYAKDV KFGADARALM LQGVDLLADA
51 VAVTMGPKGR TVIIEQSWGS PKVTKDGVTV AKSIDLKDKY KNIGAK**LVQD**
101 **VANNTNEEAG DGTTTATVLA R**SIAKEGFEK ISK**GANPVEI RR**GVMLAVDA
151 VIAELKKQSK PVTTPEEIAQ VATISANGDK DIGNIISDAM KKVGRKGVIT
201 VKDGK**TLNDE LEIIEGMKFD R**GYISPYFIN TSKGQKCEFQ DAYVLLSEK**K**
251 **ISSVQSIVPA LEIANAHRKP LVIIAEDVDG EALSTLVLNR** LKVGLQVVAV
301 KAPGFGDNRK NQLKDMAIAT GGAVFGEEGL NLNLEDVQAH DLGK**VGEVIV**
351 **TKDDAMLLK**G KGDKAHIEKR IQEITEQLDI TTSEYEKEKL NERLAKLSDG
401 VAVLKVGGTS DVEVNEKKDR VTDALNATR**A AVEEGIVLGG GCALLR**CIPA
451 LDSLKPANED QKIGIEIIKR ALKIPAMTIA KNAGVEGSLI VEKILQSSSE
501 VGYDAMLGDF VNMVEKGIID PTKVVRTALL DAAGVASLLT TAEAVVTEIP
551 KEEKDPGMGA MGGMGGGMGG GMF

A. MALDI-TOF MS spectrum (spot 7)



B. Peptides detected by MALDI-TOF-MS

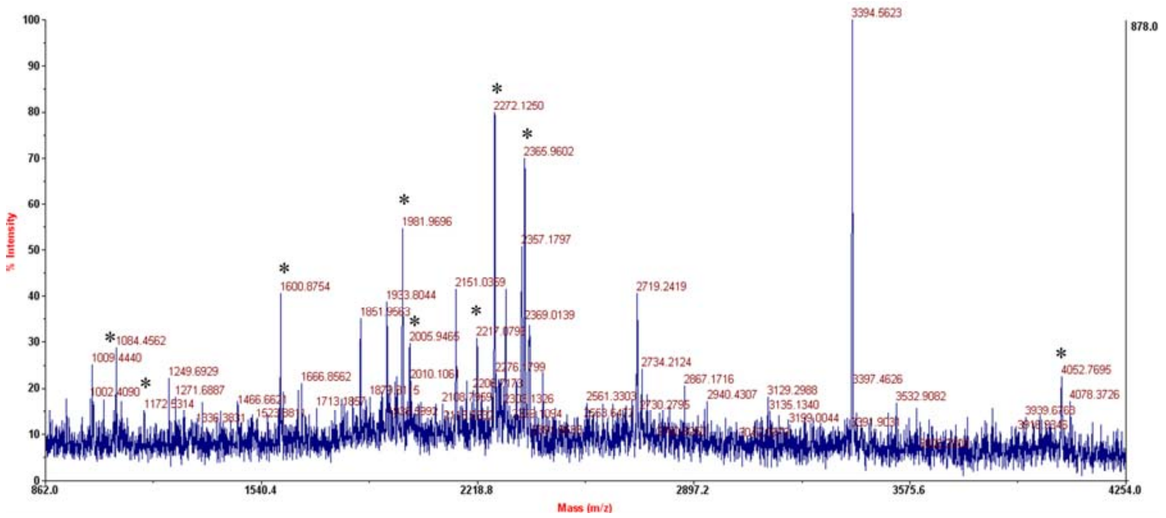
Peptide	Amino acid sequence	$[M+H]^+$	Matched
69-76	MVEGFFDR	1000.5540	+
108 - 123	IIKPCNHVLSLSFPIR	1894.4380	+
125 - 136	DDGSWEVIEGYR	1425.8600	+
137 - 143	AQHSQHR	863.4720	+
212 - 231	KGFIGPGIDVPAPDMSTGER	2044.4190	+
213 - 231	GFIGPGIDVPAPDMSTGER	1916.2980	+
303 - 318	TFVVQGFGNVGLHSMR	1749.2120	+
347 - 363	ELEDFKLQHGSILGFPK	1958.3770	+
400 - 420	IIAEGANGPTTPEADKIFLER	2242.5740	+
445 - 453	NLNHVSYGR	1059.6440	+
454 - 460	LTFKYER	956.6030	+
461 - 476	DSNYHLLMSVQESLER	1921.2680	+
481 - 496	HGGTIPVVPTAEFQDR	1724.1860	+
497 - 516	ISGASEKDIVHSGLAYTMER	2164.4730	+
504 - 516	DIVHSGLAYTMER	1491.9690	+
528 - 535	YNLGLDLR	963.6170	+

C. Matched peptides (Bold) in the GDH amino acid sequence

1 MYRRLGEVLL LSRAGPAALG SAAADSAALL GWARGQPSAV PQPGLTPVAR
51 RHYSEAATDR EDDPNFFK**MV** **EGFFDR**GASI VEDKLVEDLK TRENEEQKRN
101 RVRGILR**IIK** **PCNHVLSLSF** **PIRRDDGSWE** **VIEGYRAQHS** **QHR**TPCKGGI
151 RYSTDVSVDE VKALASLMTY KCAVVDVPFG GAKAGVKINP KNYTDNELEK
201 ITRRFTMELA K**KGFIGPGID** **VPAPDMSTGE** **REMSWIADTY** **ASTIGHYDIN**
251 **AHACVTGKPI** **SQGGIHGR**IS ATGRGVFHGI ENFINEASYM SILGMTPGLG
301 DK**TFVVQGFG** **NVGLHSMR**YL HRFGAKCVGV GESDGSIWNP DGIDPK**ELED**
351 **FKLQHGSILG** **FPK**AK**VYEGS** **ILEADCDILI** **PAASEK**QLTK SNAPRVKAK**I**

401 IAEGANGPTT PEADKIFLER NIMVIPDLYL NAGGVTVSYF EWLK**NLNHVS**
451 YGRLTFKYER DSNYHLLMSV QESLERKFGK **HGGTIPVVPT AEFQDRISGA**
501 SEKDIVHSGL AYTMERSARQ IMRTAMK**YNL GLDLRTAAYV NAIEKVFK**VY
551 NEAGVTFT

A. MALDI-TOF MS spectrum (spot 8)



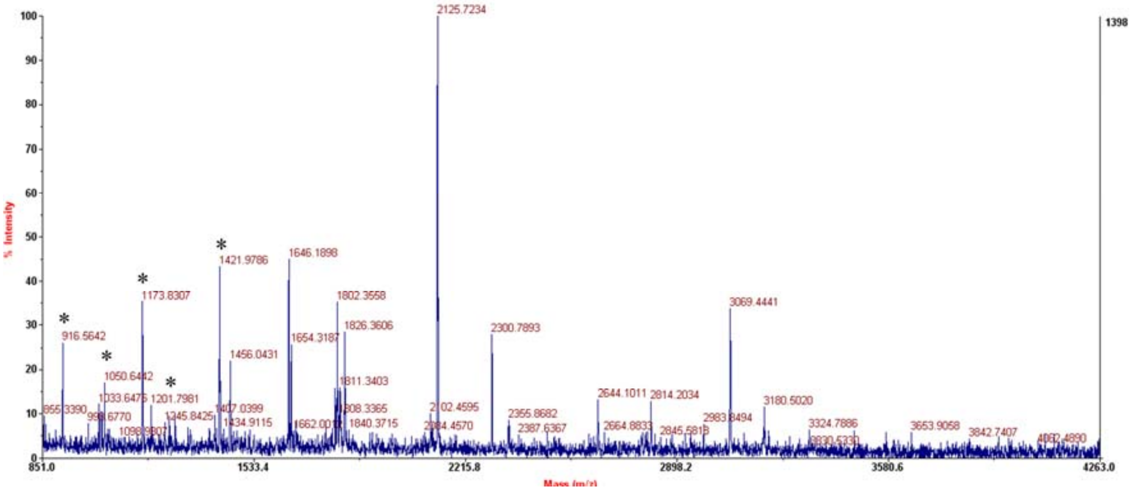
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
83 - 97	ASLQNLLSASQAQLR	1599.8770	+
106-142	AFTSQASATMHLPATIGDYTDFYSSLQHATNVGIMFR	4049.7500	+
143-162	GKENALLPNWLHLPVGYHGR	2271.2040	+
163-174	ASSVVVSGTPIR	1172.5610	+
175-194	RPMGQMRPDNSKPPVYGASK	2216.0580	+
195-211	RLDMELEMAFFVGPGNR	1981.9410	+
221-237	AQEHIFGMVLMNDWSAR	2004.9210	+
372-381	AIDVGQGQTR	1044.4740	+
382-402	TFLLDGDEVIITGHCQGDGYR	2366.0740	+

C. Matched peptides (Bold Red) in the Fumarylacetoacetase amino acid sequence

1 MSFIPVAEDS DFPIQNLPYG VFSTQSNPKP RIGVAIGDQI LDLSVIKHLF
51 TGPVLSKHQH VFDETTLNSF MGLGQAAWKE AR**ASLQNLLS ASQAQLR**DDK
101 ELRQR**AFTSQ ASATMHLPAT IGDYTDFYSS LQHATNVGIM FRGKENALLP**
151 **NWLHLPVGYH GRASSVVVSG TPIRRPMGQM RPDNSKPPVY GASKRLDMEL**
201 **EMAFFVGPGN R**FGEPIPISK **AQEHIFGMVL MNDWSAR**DIQ QWEYVPLGPF
251 LGKSFGTTIS PWVVPMDALM PFVVPNPKQD PKPLPYLCHS QPYTFDINLS
301 VALKGEGMSQ AATICRSNFK HMYWTILQQL THHSVNGCNL RPGDLLASGT
351 ISGSDPESFG SMLELSWKGT K**AIDVGQGQT RTFLLDGDEV IITGHCQGDG**
401 **YR**VGFGQCAG KVLPALSPA

A. MALDI-TOF MS spectrum (spot 9)



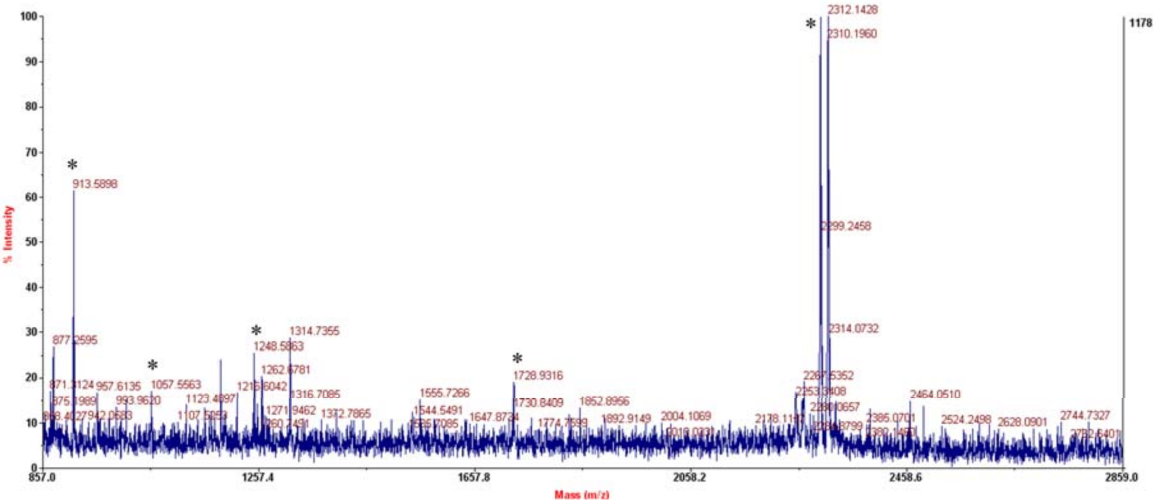
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
15-22	ELSDIALR	916.5810	+
61-69	QVLFSADDR	1050.6480	+
61-71	QVLFSADDRVK	1277.9280	+
102-111	GILVGIKVDK	1041.7720	+
305-315	ALQASALSAWR	1173.8340	+
319-331	DNAGAATEEFIKR	1421.9770	+
331-342	RAEMNGLAAQGK	1245.8630	+

C. Matched peptides (Bold Red) in the Fructose-bisphosphate aldolase C amino acid sequence

1 MPHSYPALSA EQKK**ELSDIA LR**IVAPGKGI LAADESVGSM AKRLSQIGVE
51 NTEENRRLYR **QVLFSADDRV K**KCIGGVIFF HETLYQKDDN GVPFVRTIQE
101 K**GILVGIKVD K**GVVPLAGTD GETTTQGLDG LLERCAQYKK DGADFAKWRC
151 VLKISDRTPS ALAILENANV LARYASICQQ NGIVPIVEPE ILPDGDHDLK
201 RCQFVTEKVL AAVYKALSDH HVYLEGTLLK PNMVTPGHAC PIKYSPEEIA
251 MATVTALRRT VPPAVPGVTF LSGGQSEEEA SLNLNAINRC SLPRPWALTF
301 SYGR**ALQASA LSAWR**GQR**DN AGAATEEFIK RAEMNGLAAQ GK**YEGSGDGG
351 AAAQSLYVAN HAY

A. MALDI-TOF MS spectrum (spot10)



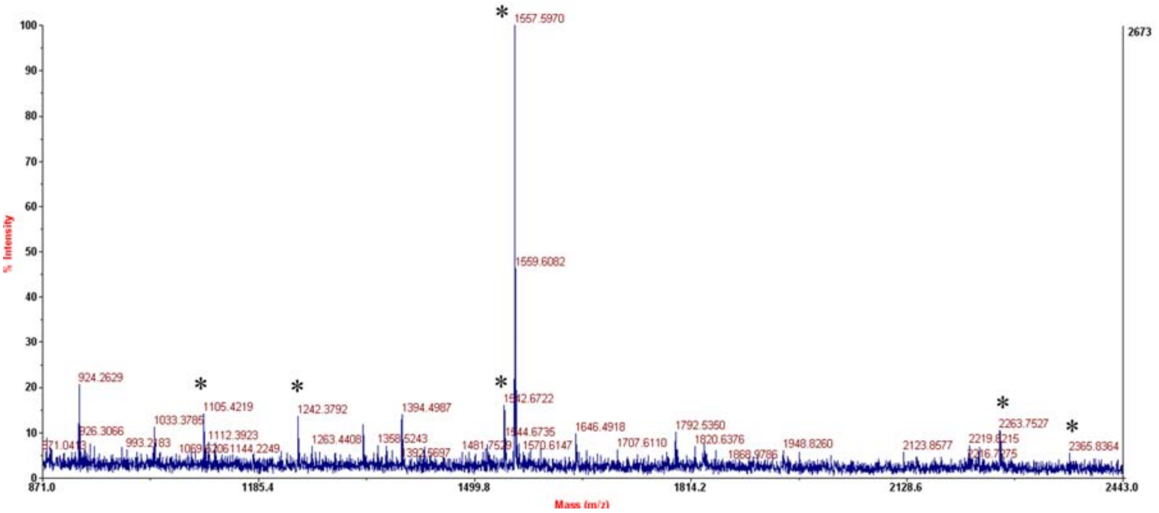
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
92-100	IVVVTAGVR	913.5910	+
92-107	IVVVTAGVRQQEGESR	1727.8920	+
159-170	VIGSGCNLDSAR	1248.5780	+
171-178	FRYLMAEK	1057.5650	+
280-299	GMYGIENEVFLSLPCILNAR	2296.1350	+
309-318	LKDDEVAQLR	1186.6320	+

C. Matched peptides (Bold Red) in the LDH amino acid sequence

1 MATLKEKLIA PVADDETAVP NNKITVVGVG QVGMACAISI LGKSLADELA
51 LVDVLEDKLK GEMMDLQHGS LFLQTPKIVA DKDYSVTANS K**IVVVTAGVR**
101 **QQEGESR**LNL VQRNVNVFKF IIPQIVKYSP DCTIIVVSNP VDILTYVTWK
151 LSGLPKHR**VI GSGCNLDSAR FRYLMAEK**LG IHPSSCHGWI LGEHGDSSVA
201 VWSGVNVAGV SLQELNPEMG TDNDSENWKE VHKMVVDSAY EVIKLKGYTN
251 WAIGLSVADL IESMLKNLSR IHPVSTMVK**G MYGIENEVFL SLPCILNAR**G
301 LTSVINQK**LK DDEVAQLR**KS ADTLWDIQKD LKDL

A. MALDI-TOF MS spectrum (spot 11)



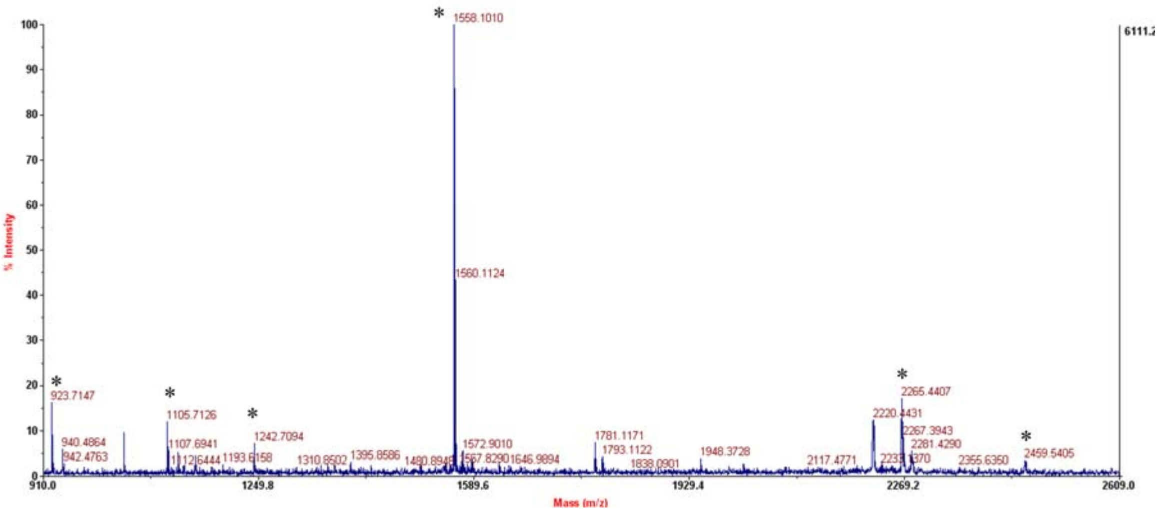
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
70-78	RQDLFIVSK	1105.4340	+
156-169	AIGVSNFNPLQIER	1557.5990	+
244-256	TTAQVLIRFPIQR	1542.6660	+
276-294	FRYLMAEK	2263.7400	+
280-299	VFDFELSNEDMATLLSYNR	2296.1350	+
307-316	HKDYPFHAEV	1242.3780	+

C. Matched peptides (Bold Red) in the AR amino acid sequence

1 MASHLELNNG TKMPTLGLGT WKSPPGQVTE AVKVAIDMGY RHIDCAQVYQ
51 NEKEVGVALQ EKLKEQVVK**R QDLFIVSK**LW CTFHDQSMVK GACQKTLSDL
101 QLDYLDLYLI HWPTGFKPGP DYFPLDASGN VIPSDTDFVD TWTAMEQLVD
151 EGLVK**AIGVS NFNPLQIER**I LNKPGLKYKP AVNQIECHPY LTQEKLIEYC
201 HCKGIVVTAY SPLGSPDRPW AKPEDPSLLE DPRIKEIAAK YNK**TTAQVLI**
251 **RFPIQR**NLVV IPKSVTPARI AENFK**VFDFE LSNEDMATLL SYNR**NWRVCA
301 LMSCAK**HKDY PFHAEV**

A. MALDI-TOF MS spectrum (spot 12)



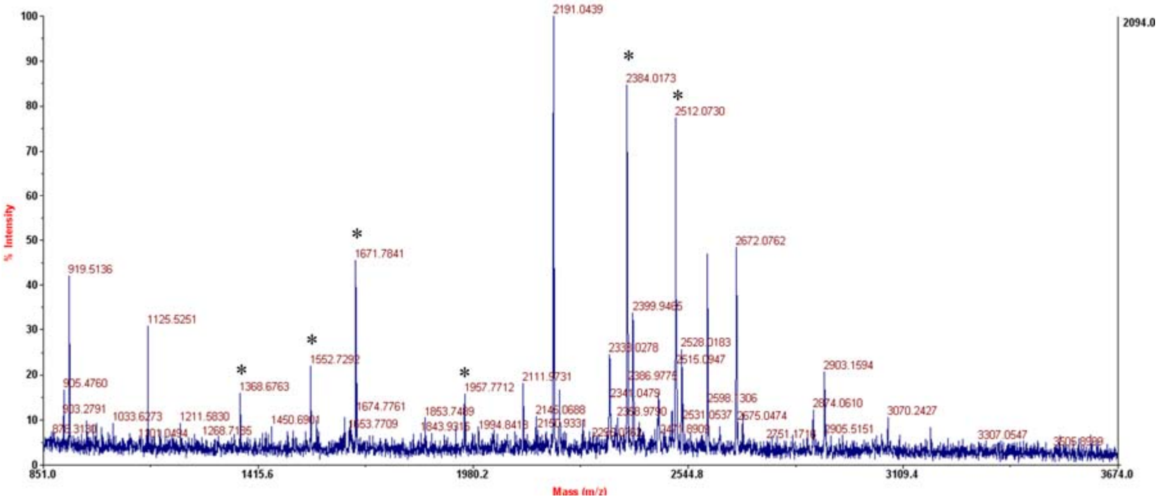
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
34-41	VAIDMGYR	924.4990	+
42-62	HIDCAQVYQNEKEVGVALQEK	2458.5160	+
70-78	RQDLFIVSK	1105.7080	+
156-169	AIGVSNFNPLQIER	1558.0120	+
196-203	LIEYCHCK	1122.5820	+
244-251	TTAQVLIR	901.5900	+
276-294	VFDFELSNEDMATLLSYNR	2264.3420	+
307-316	HKDYPFHAEV	1242.7110	+

C. Matched peptides (Bold Red) in the AR amino acid sequence

1 MASHLELNNG TKMPTLGLGT WKSPPGQVTE AVK**VAIDMGY RHIDCAQVYQ**
51 **NEKEVGVALQ EK**LKEQVVK**R QDLFIVSK**LW CTFHDQSMVK GACQKTLSDL
101 QLDYLDLYLI HWPTGFKPGP DYFPLDASGN VIPSDTDFVD TWTAMEQLVD
151 EGLVK**AIGVS NFNPLQIER**I LNKPGLKYKP AVNQIECHPY LTQEK**LIEYC**
201 **HCK**GIVVTAY SPLGSPDRPW AKPEDPSLLE DPRIKEIAAK YNK**TTAQVLI**
251 **R**FPIQRNLVV IPKSVTPARI AENFK**VFDFE LSNEDMATLL SYNR**NWRVCA
301 LMSCAK**HKDY PFHAEV**

A. MALDI-TOF MS spectrum (spot 13)



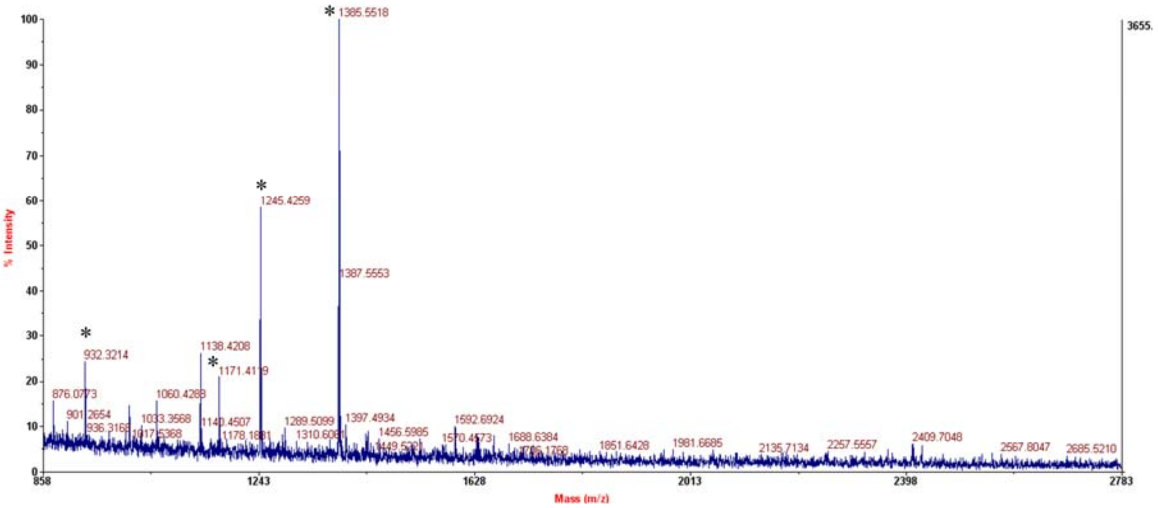
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
9-16	RVLVYGGR	924.4990	+
53 -70	MTDSFTEQADQVTAEVGK	1956.7540	+
136-151	AALDGTPGMIGYGMAK	1552.7290	+
152-164	GAVHQLCQSLAGK	1368.6720	+
165-188	NSGMPSGAAAIAVLPVTLDTPMNR	2382.9970	+
165-189	NSGMPSGAAAIAVLPVTLDTPMNRK	2511.0690	+
218-233	RPNSGSLIQVVTTDGK	1671.8010	+

C. Matched peptides (Bold Red) in the DHPR amino acid sequence

1 MAASGEAR**RV LVYGGR**GALG SRCVQAFRAR NWWVASIDVV ENEEASASVI
51 VK**MTDSFTEQ ADQVTAEVGK** LLGDQKVDAI LCVAGGWAGG NAKSKSLFKN
101 CDLMWKQSIW TSTISSHLAT KHLKEGGLLT LAGAK**AALDG TPGMIGYGMA**
151 **KGAVHQLCQS LAGKNSGMPS GAAAIAVLPV TLDTPMNRK**S MPEADFSSWT
201 PLEFLVETFH DWITGNK**RPN SGSLIQVVTT DGK**TELTPAY F

A. MALDI-TOF MS spectrum (spot 14)



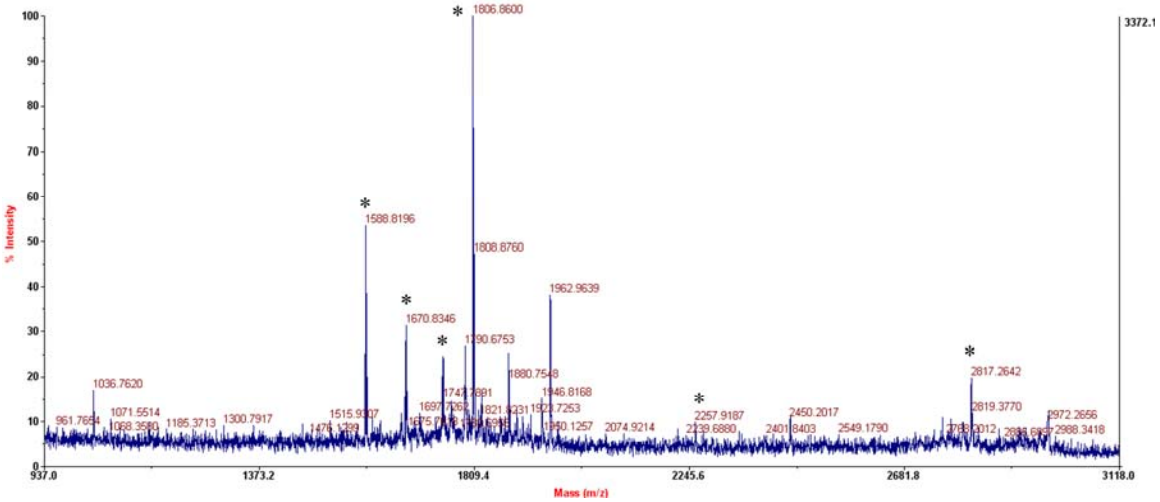
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
2-13	PGKPVLHYFDGR	1385.6230	+
130-138	NRYFPAFEK	1171.5620	+
142-152	SHGQDYLVGNR	1245.5900	+
142-155	SHGQDYLVGNRLSR	1601.6710	+
197-204	FLQPGSQR	932.4410	+

C. Matched peptides (Bold Red) in the GSTA3 amino acid sequence

1 M**PGKPVLHYF DGR**GRMEPIR WLLAAAGVEF EEQFLKTRDD LARLRNDGSL
51 MFQQVPMVEI DGMKLVQTRA ILNYIATKYN LYGKDMKERA LIDMYAEGVA
101 DLDEIVLHYP YIPPGEKEAS LAKIKDKAR**N RYFPAFEK**VL K**SHGQDYLVG**
151 **NRLSR**ADVYL VQVLYHVEEL DPSALANFPL LKALRTRVSN LPTVKK**FLQP**
201 **GSQR**KPLEDE KCVESAVKIF S

A. MALDI-TOF MS spectrum (spot 15)



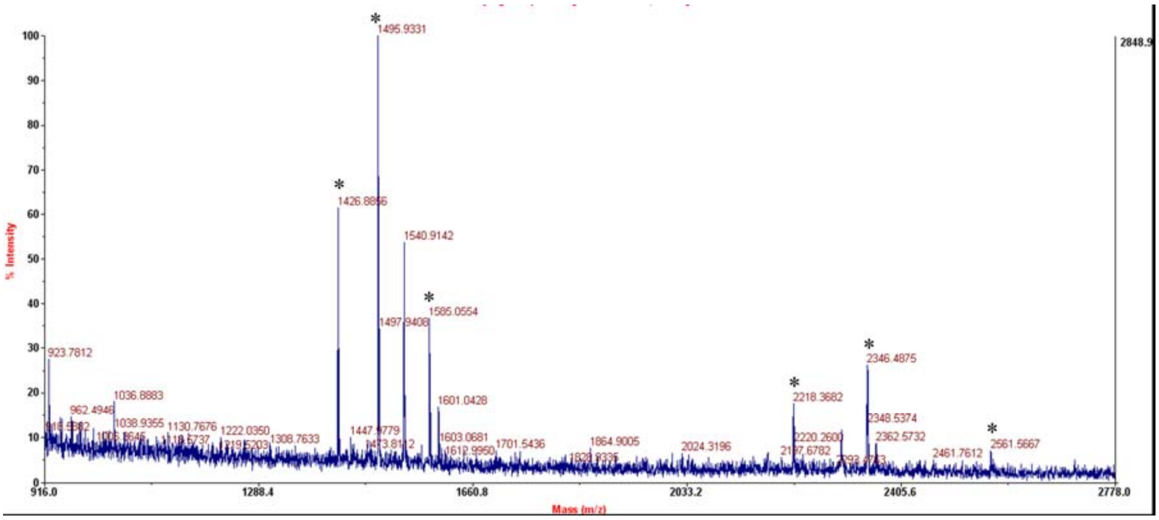
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
32-45	MLQLVEESKDAGIR	1588.8210	+
46-59	TLVMLDEQGEQLER	1660.8090	+
104-119	AWGNNQDGVVASQPAR	1669.7700	+
120-135	VVDEREQMAISGGFIR	1806.8720	+
137-161	VTNDARENEMDENLEQVSGIIGNLR	2816.2520	+
162-176	HMALDMGNEIDTQNR	1744.7850	
162-180	HMALDMGNEIDTQNRQIDR	2256.9290	

C. Matched peptides (Bold Red) in the SNP25 amino acid sequence

1 MAEDADMRNE LEEMQRRADQ LADESLESTR R**MLQLVEESK DAGIRTLVML**
51 **DEQGEQLER**I EEGMDQINKD MKEAEKNLTD LGKFCGLCVC PCNKLKSSDA
101 YKK**AWGNNQD GVVASQPARV VDEREQMAIS GGFIR**R**VTND ARENEMDENL**
151 **EQVSGIIGNL RHMALDMGNE IDTQNRQIDR** IMEKADSNKT RIDEANQRAT
201 KMLGSG

A. MALDI-TOF MS spectrum (spot 16)



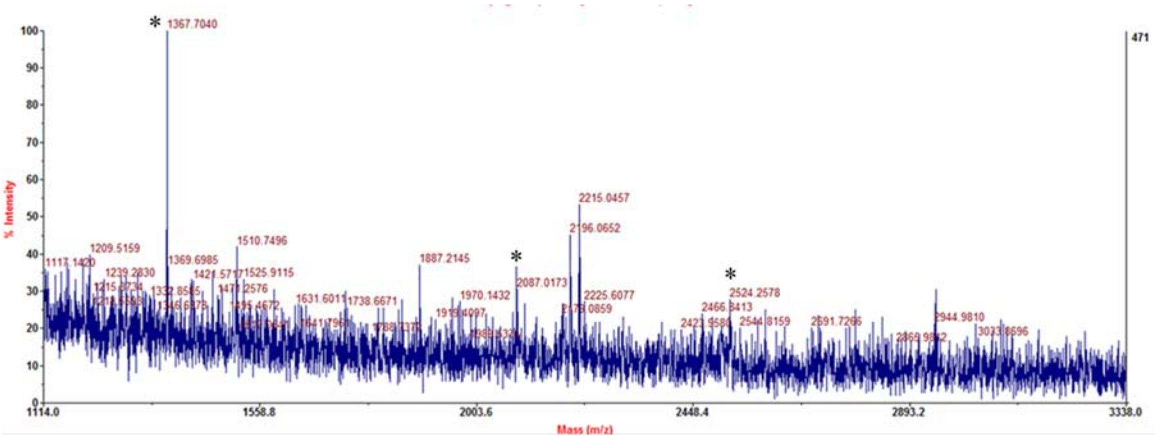
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
32-44	YGYTHLSTGDLLR	1495.9390	+
64 -77	GELVPLETVLDMLR	1585.0450	+
108-128	KIAQPTLLLYVDAGPETMTQR	2345.4940	+
109-128	IAQPTLLLYVDAGPETMTQR	2217.3710	+
156-167	ATEPVISFYDKR	1425.8930	+
172-194	KVNAEGSVDTVFSQVCTYLDSLK	2560.5700	+

C. Matched peptides (Bold) in the AK amino acid sequence

1 MEDKLKKAKI IFVVGGPGSG KGTQCEKIVQ K**YGYTHLSTG DLLR**AEVSSG
51 SSRGKMLSSI MEK**GELVPLE TVLDMLR**DAM LAKVDSSNGF LIDGYPREVK
101 QGEEFER**KIA QPTLLLYVDA GPETMTQR**LL KRGETSGRVD DNEETIKKRL
151 ETYYK**ATEPV ISFYDKR**GIV R**KVNAEGSVD TVFSQVCTYL DSLK**

A. MALDI-TOF MS spectrum (spot 17)



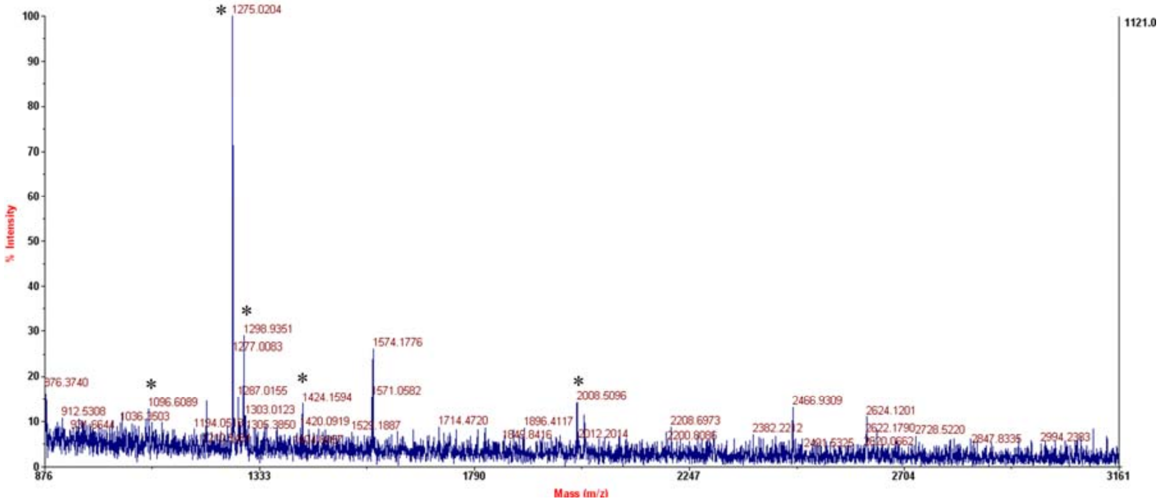
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
72-92	HGGPADEERHVGDLGNVAAGK	2085.9560	+
93-116	DGVANVSIEDRVISLSGEHSIIGR	2523.1270	+
104-116	VISLSGEHSIIGR	1367.7090	+

C. Matched peptides (Bold) in the SOD amino acid sequence

1 MAMKAVCVLK GDGPVQGVIH FEQKASGEPV VVSGQITGLT EGEHGFHVHQ
51 YGDNTQGCTT AGPHFNPHSK K**HGGPADEER HVGDLGNVAA GKDGVANVSI**
101 **EDRVISLSGE HSIIGR**TMVV HEKQDDLGKG GNEESTKTGN AGSRLACGVI
151 GIAQ

A. MALDI-TOF MS spectrum (spot 18)



B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
19-31	VNPDDVGGEALGR	1298.9430	+
32-41	LLVVYPWTQR	1275.0190	+
42-60	YFDSFGDLSSASAIMGNPK	2007.5030	+
68 -77	VINAFNDGLK	1090.8120	
134-147	VVAGVASALAHKYH	1423.1460	

C. Matched peptides (Bold Red) in the Hemoglobin subunit beta-1 amino acid sequence

1 MVHLTDAEKA AVNGLWGK**VN PDDVGGEALG RLLVVYPWTQ RYFDSFGDLS**
51 **SASAIMGNPK** VKAHGKK**VIN AFNDGLKHLD NLK**GTFAHLS ELHCDKLHVD
101 PENFRLLGNM IVIVLGHHLG KEFTPCAQAA FQK**VVAGVAS ALAHKYH**