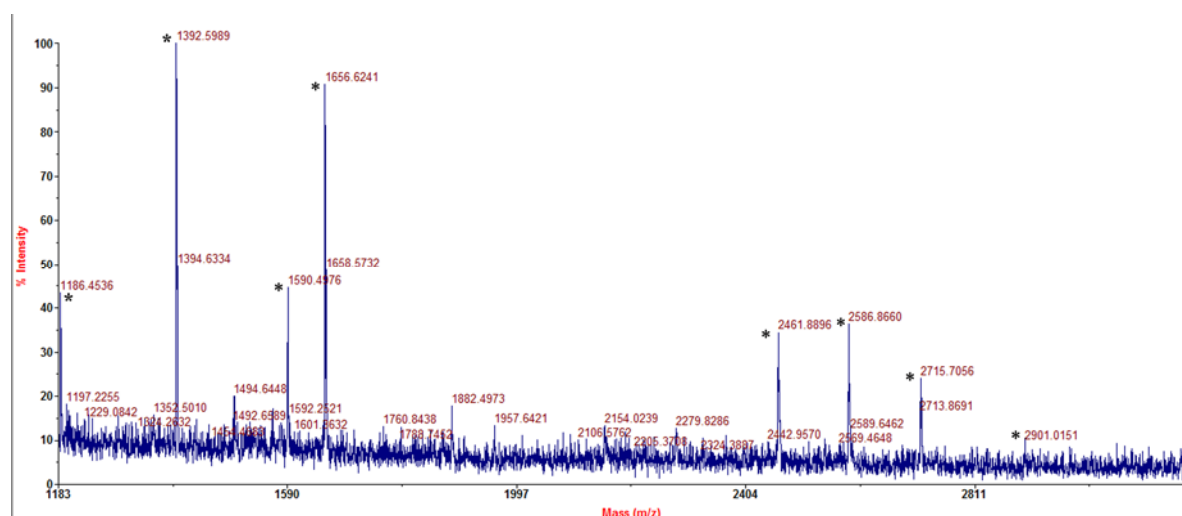


A. MALDI-TOF MS spectrum (spot 1)



B. Peptides detected by MALDI-TOF-MS

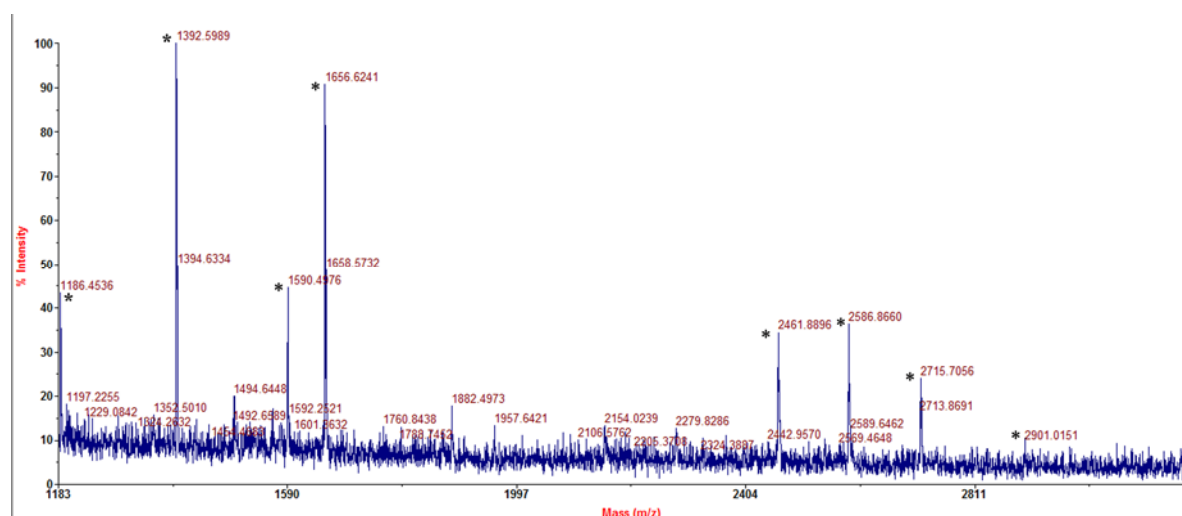
Peptide	Amino acid sequence	$[M+H]^+$	Matched
144 - 162	SAGWIPIGILLFCNLPEPR	2152.8170	+
237 - 251	ADRDQYELLCLDNTR	1881.5440	+
252 - 264	KPVDQYEDCYLAR	1656.5730	+
311 - 323	DLLFKDSAFGLLR	1494.6630	+
316 - 323	DSAFGLLR	878.3600	+
332 - 343	LYLGHSYVTAIR	1392.5980	+
362 - 370	WCALSHQER	1186.4070	+
478 - 491	TAGWNIPMGLLFSR	1562.5600	+
588 - 609	KPVTEFATCHLAQAPNHVVSR	2460.8360	+
630 - 642	GDKDCTGNFCLFR	1589.4930	+
647 - 655	DLLFRDDTK	1122.4230	+
660 - 682	LPEGTTYEYLGAEYLQAVGNIR	2585.9000	+
660 - 683	LPEGTTYEYLGAEYLQAVGNIRK	2713.9180	+

C. Matched peptides shown in **Bold Red**

1 MRFAVGALLA CAALGLCLAV PDKTVKWCAV SEHENTKCIS FRDHMKTVLP
 51 ADGPRILACVK KTSYQDCIKA ISGGEADAIT LDGGWVYDAG LTPNNLKPVA
 101 AEFYGSLEHP QTHYLAVAVV KKGTDQFQLNQ LQGKKSCHTG LGR**SAGWIIP**
 151 **IGLLFCNLPE** PRKPLEKAVA SFFSGSCVPC ADPVAFPQLC QLCPGCGCSP
 201 TQPFFGYVGA FKCLRDGGGD VAFVKHTTIF EVLPQK**ADRD QYELLCLDNT**
 251 **RKPVDQYEDC YLAR**IPSHAV VARNGDGKED LIWEILKVAQ EHFGKGKSKD
 301 FQLFGSPLGK **DLLFKDSAFG LLR**VPPRMDY R**LYLGHSYVT AIR**NQREGVC
 351 PEGSIDSAPV **KWCALSHQER** AKCDEWSVSS NGQIECESAE STEDCIDKIV
 401 NGEADAMSLD GGHAYIAGQC GLVPVMAENY DISSCTNPQS DVFPKGYAV
 451 AVVKASDSSI NWNNLKGKKS CHTGVDR**TAG WNIPMGLLFS** RINHCKFDEF
 501 FSQGCAPGYK KNSTLCDLCI GPAKCAPNNR EGYNGYTGAQ QCLVEKGDVA

551 FVKHQTVLEN TNGKNTAAWA KDLKQEDFQL LCPDGTK**KPV TEFATCHLAQ**
601 **APNHVVSRK** EKAARVSTVL TAQKDLFWK**G DKDCTGNFCL FRSSTKDLLF**
651 **RDDTKCLTKL PEGTTYEEYL GAEYLQAVGN IRKCSTSRLL** EACTFHKS

A. MALDI-TOF MS spectrum (spot 2)



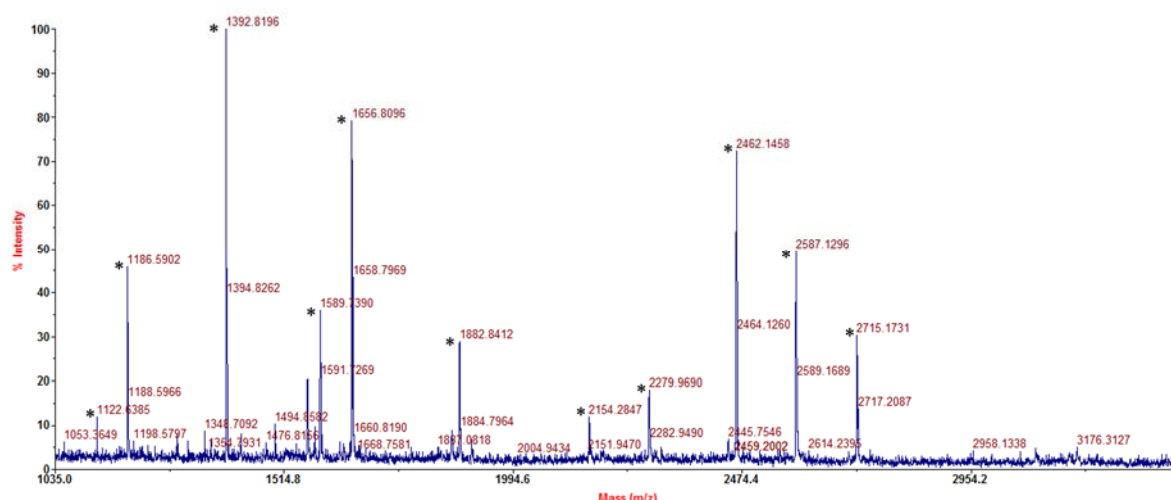
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
27 - 37	WCAVSEHENTK	1360.6230	+
123 - 135	GTDFQLNQLQGKK	1476.7770	+
144 - 162	SAGWIPIGILLFCNLPEPR	2153.1090	+
226 - 236	HTTIFEVL PQK	1312.7130	+
237 - 251	ADRDQYELLCLDNTR	1881.8200	+
240 - 251	DQYELLCLDNTR	1539.7160	+
252 - 264	KPVDQYEDCYLAR	1656.7540	+
265 - 273	IPSHAVVAR	949.5480	+
274 - 287	NGDGKEDLIWEILK	1629.8140	+
298 - 310	SKDFQLFGSPLGK	1423.7740	+
311 - 323	DLLFKDSAFGLLR	1494.8260	+
316 - 323	DSAFGLLR	878.4670	+
332 - 343	LYLGHSYVTAIR	1392.7660	+
362 - 370	WCALSHQER	1186.5410	+
455 - 466	ASDSSINWNNLK	1348.6510	+
478 - 491	TAGWNIPMGLLSR	1562.8140	+
572 - 587	DLKQEDFQLLCPDGTK	1906.8800	+
588 - 609	KPVTEFATCHLAQAPNHVVSR	2461.1780	+
630 - 642	GDKDCTGNFCLFR	1589.6840	+
633 - 642	DCTGNFCLFR	1289.5840	+
647 - 655	DLLFRDDTK	1122.5750	+
660 - 682	LPEGTTYEYLGAEYLQAVGNIR	2586.1700	+
660 - 683	LPEGTTYEYLGAEYLQAVGNIRK	2714.2800	+

C. Matched peptides shown in **Bold Red**

1 MRFAVGALLA CAALGLCLAV PDKTVK**WCAV SEHENTK**CIS FRDHMKTVLP
51 ADGPRLACVK KTSYQDCIKA ISGGEADAIT LDGGWVYDAG LTPNNLKPVA
101 AEFYGSLEHP QTHYLAVAVV KK**GTDFQLNQ LQGKKS**CHTG LGR**SAGWIIP**
151 **IGLLFCNLPE PRK**PLEKAVA SFFSGSCVPC ADPVAFPQLC QLCPGCGCSP
201 TQPFEGYVGA FKCLRDGGGD VAFVK**HTTIF EVLPQKADRD QYELLCLDNT**
251 **RKPVDQYEDC YLARIPSHAV VARNGDGKED LIWEILK**V AQ EHF GKGK**SKD**
301 **FQLFGSPLGK DLLFKDSA**FG LLRVPPRMDY RLYLGHSYVT **AIRN**QREGVC
351 PEGSIDSAPV K**WCALSHQER** AKCDEWSVSS NGQIECESAE STEDCIDKIV
401 NGEADAMSLD GGHAYIAGQC GLVPVMAENY DISSCTNPQS DVFPKGYAV
451 AVVK**ASDSSI NWN**NLK GKKS CHTGVDR**TAG WNIPMGLLFS R**INHCKFDEF
501 FSQGCAPGYK KNSTLCDLCI GPAKCAPNNR EGYNGYTGAF QCLVEKGDVA
551 FVKHQTVLEN TNGKNTAAWA **KDLKQEDFQL LCPDGTKKPV TEFATCHLAQ**
601 **APNHVVVSRK EKAARVSTVL TAQKDLFWK**G **DKDCTGNFCL FRSSTKDLLF**
651 **RDDTKCLTKL PEGTTYEEYL GAEYLQAVGN IRK**CSTSRLLEACTFHKS

A. MALDI-TOF MS spectrum (spot 3)



B. Peptides detected by MALDI-TOF-MS

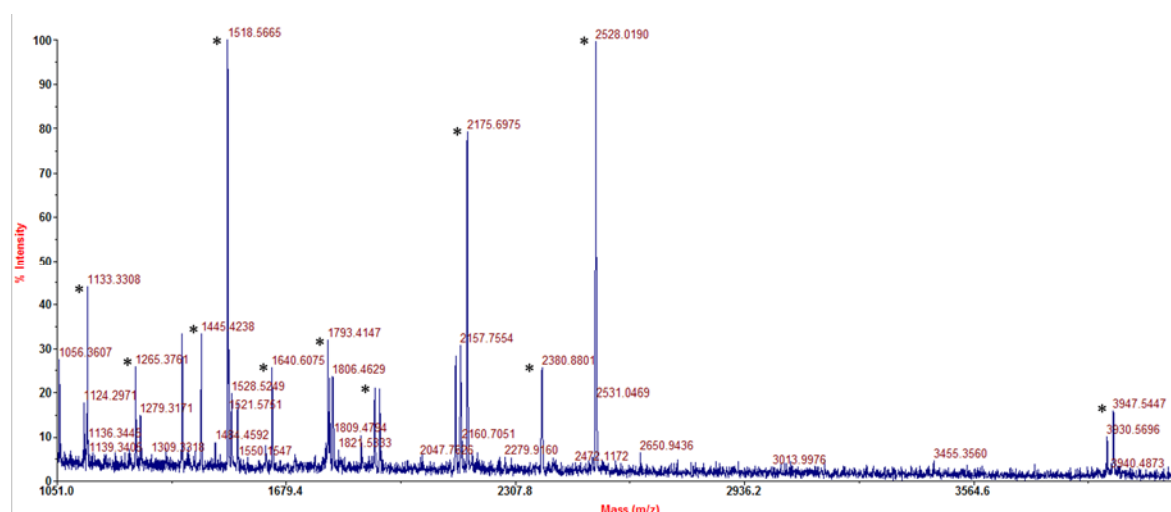
Peptide	Amino acid sequence	$[M+H]^+$	Matched
123 - 134	GTDFQLNQLQGK	1348.7100	+
144 - 162	SAGWIPIGILLFCNLPEPR	2153.1090	+
226 - 236	HTTIFEVLQK	1312.7510	+
237 - 251	ADRDQYELLCLDNTR	1881.8410	+
252 - 264	KPVDQYEDCYLAR	1656.8090	+
298 - 310	SKDFQLFGSPLGK	1423.7940	+
311 - 323	DLLFKDSAFGLLR	1494.8580	+
316 - 323	DSAFGLLR	878.4940	+
332 - 343	LYLGHSYVTAIR	1392.6440	+
332 - 343	LYLGHSYVTAIR	1392.8180	+
362 - 370	WCALSHQER	1186.5890	+
478 -491	TAGWNIPMGLLSR	1562.8720	+
478 - 491	TAGWNIPMGLLSR	1578.8130	+
572 - 587	DLKQEDFQLLCPDGTK	1906.8430	+
588 - 609	KPVTEFATCHLAQAPNHVVSR	2461.1530	+
630 - 642	GDKDCTGNFCLFR	1589.7300	+
633 -642	DCTGNFCLFR	1289.5940	+
647 - 655	DLLFRDDTK	1122.6310	+
660 - 682	LPEGTTYEEYLGAEYLQAVGNIR	2586.1390	+
660 - 683	LPEGTTYEEYLGAEYLQAVGNIRK	2714.1850	+

C. Matched peptides shown in **Bold Red**

1 MRFVAGALLA CAALGLCLAV PDKTVKWCAV SEHENTKCIS FRDHMKTVLP
51 ADGPRLACVK KTSYQDCIKA ISGGEADAIT LDGGWVYDAG LTPNNLKPVA
101 AEFYGSLEHP QTHYLAVAVV KK**GTDFQLNQ LQGK**KSCHTG LGR**SAGWIIP**
151 **IGLLFCNLPE PR**KPLEKAVA SFFSGSCVPC ADPVAFPQLC QLCPGCGCSP
201 TQPFFGYVGA FKCLRDGGGD VAFVK**HTTIF EVLPQKADRD QYELLCLDNT**

251 **RKPVDQYEDC YLARIPSHAV** VARNGDGKED LIWEILKVAQ EHFGKGK**SKD**
301 **FQLFGSPLGK DLLFKDSAFG LLR**VPPRMDY **RLYLGHSYVT AIR**NQREGVC
351 PEGSIDSAPV **KWCALSHQER** AKCDEWSVSS NGQIECESAE STEDCIDKIV
401 NGEADAMSLD GGHAYIAGQC GLVPVMAENY DISSCTNPQS DVFPKGYAY
451 AVVKASDSSI NWNNLKGKKS CHTGVDR**TAG WNIPMGLLFS** RINHCKFDEF
501 FSQGCAPGYK KNSTLCDLCI GPAKCAPNNR EGYNGYTGAF QCLVEKGDVA
551 FVKHQTVLEN TNGKNTAAWA **KDLKQEDFQL LCPDGTKKPV TEFATCHLAQ**
601 **APNHVVSRK** EKAARVSTVL TAQKDLFWK**G DKDCTGNFCL FRSSTKDLLF**
651 **RDDTKCLTKL PEGTTYEEYL** GAEYLQAVGN **IRK**CSTSRLLEACTFHKS

A. MALDI-TOF MS spectrum (spot 4)



B. Peptides detected by MALDI-TOF-MS

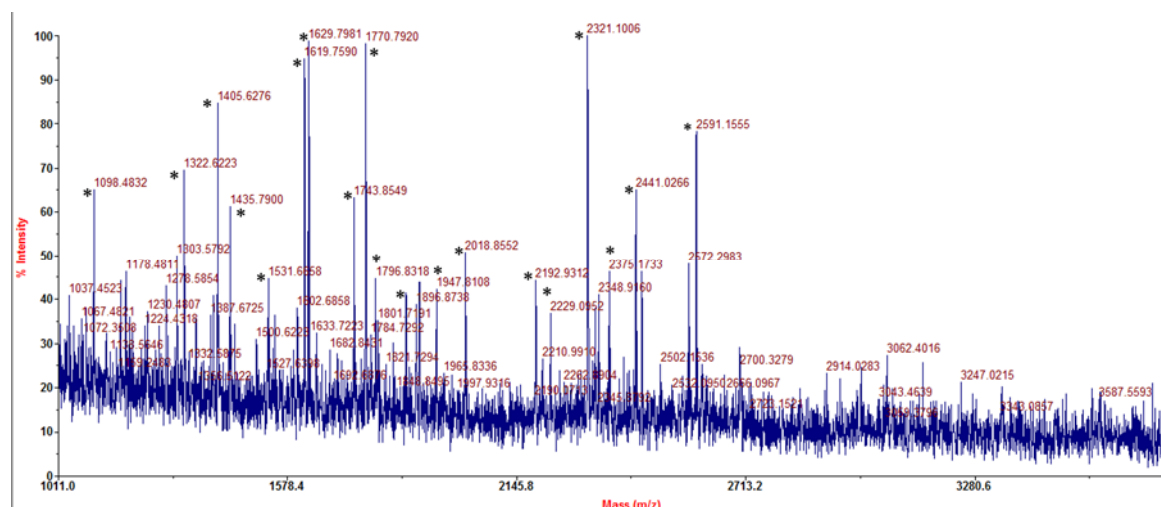
Peptide	Amino acid sequence	[M+H] ⁺	Matched
46 - 67	SNVASTAACSSASSLGLGLAYR	2142.7180	+
68 - 83	RLPASDGLDLSQAAAR	1640.5580	+
69 - 83	LPASDGLDLSQAAAR	1484.4670	+
92 - 104	TNEKEQLQGLNDR	1544.4500	+
112 - 120	VHQLETQNR	1124.3020	+
121 - 130	ALEAELAALR	1056.3500	+
139 - 145	VGELFQR	848.2310	+
62 - 177	AQALLERDGLAEVQR	1797.6320	+
216 - 228	KVESLLDELAFVR	1518.5740	+
229 - 266	QVHDEEVAELLATLQASSQAAA EVDVAVAKPDLTSALR	3945.5350	+
291 - 300	FANLNEQAAR	1133.3080	+
323 - 330	TIEIEGLR	930.2770	+
339 - 346	QILELEER	1029.3040	+
347 - 366	HSAEVAGYQDSIGQLESDLR	2174.6980	+
375 - 386	HLREYQDLLNVK	1527.5420	+
387 - 397	MALDIEIAAYR	1265.3820	+
387 - 398	MALDIEIAAYRK	1393.4450	+
399 - 430	LLEGEETRFSTGLSISGLNPLPNPSYLLPPR	3454.3450	+
407 - 430	FSTGLSISGLNPLPNPSYLLPPR	2527.0110	+
471 - 487	VGESFEETLEETVVSTK	1883.5440	+

C. Matched peptides shown in **Bold Red**

1 MSFGSEHYLC SASSYRKVFG DGSRLSARLS GPGASGSFRS QSLSR**SNVAS**
51 **TAACSSASSL GLGLAYRRLP ASDGLDLSQA AARTNEYKII RTNEKEQLQG**
101 **LNDRF**AVFIE **KVHQLETQNR ALEAELAALR** QRHAEPSR**VG ELFQRE**LREL
151 RAQLEEASSA R**AQALLERDG LAEEVQRL**RA RCEESRGRE GAERALKAQQ
201 RDVDGATLAR LDLEK**KVESL LDELAFVRQV HDEEVAELLA TLQASSQAAA**

251 **EVDVAVAKPD LTSALREIRA** QYESLAAKNL QSAEEWYKSK **FANLNEQAAR**
301 STEAIRASRE EIHEYRRQLQ ART**IEIEGLR** GANESLER**QI LELEERHSAE**
351 **VAGYQDSIGQ LESDLR**NTKS EMAR**HLREYQ DLLNVKMALD IEIAAYRKLL**
401 **EGEETRFSTS GLSISGLNPL PNPSYLLPPR** ILSSTTSKVS SAGLSLKKEE
451 EEEEEEEGA SKEVTKKTSK **VGESFEETLE ETVVSTK**KTE KSTIEEITTS
501 SSQKM

A. MALDI-TOF MS spectrum (spot 5)



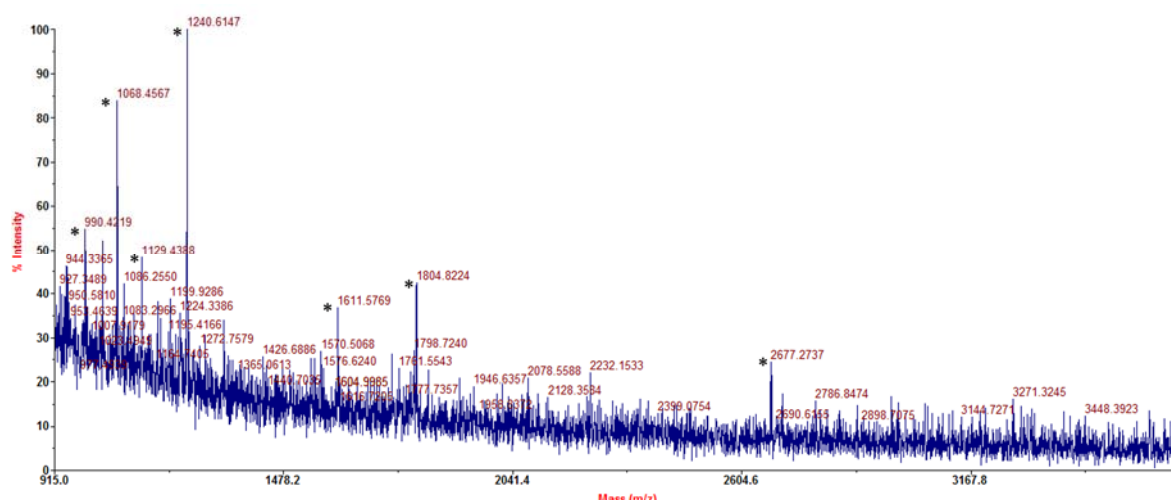
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
69 - 84	AEMMELNDRFASYIEK	1946.8140	+
110 - 119	LADVYQAE LR	1177.5040	+
135 - 150	LEVERDNLTQDLGTLR	1871.8600	+
188 - 200	VESLEEEIQFLRK	1619.7530	+
208 - 234	ELQEQLAQQQVHVEMDVAKPDLTAALR	3060.3720	+
367 - 388	LLEGEENRITIPVQTFNSNLQIR	2570.2440	+
375 - 388	ITIPVQTFNSNLQIR	1629.7980	+

C. Matched peptides shown in Bold Red

1 MERRRITSAR RSYASSETMV RGHGPTRHLG TIPRLSLSRM TPPLPARVDF
 51 SLAGALNAGF KETRASER**AE MMELNDRFAS YIEK**VRFLEQ QNKALAAELN
 101 QLRAKEPT**KL ADVYQAE**LR LRLRLDQLTT NSAR**LEVERD NLTQDLGTLR**
 151 QKLQDETNLRL LEAENNLAVY RQEAD EATLA RVDLERK**VES LEEEIQFLRK**
 201 IHEEEV**RELQ EQLAQQQVHV EMDVAKPDLT AAL**REIRTQY EAVATSNMQE
 251 TEEWYRSKFA DLTDVASRNA ELLRQAKHEA NDYRRQLQAL TCDLESLRGT
 301 NESLERQMRE QEERHARESA SYQEALARLE EEGQSLKEEM ARHLQEYQDL
 351 LNVKLALDIE IATYRK**LLEG EENRITIPVQ TFSNLQIRE**T SLDTKSVSEG
 401 HLKRNIVVKT VEMRDGEVIK ESKQEHKDVM

A. MALDI-TOF MS spectrum (spot 9)



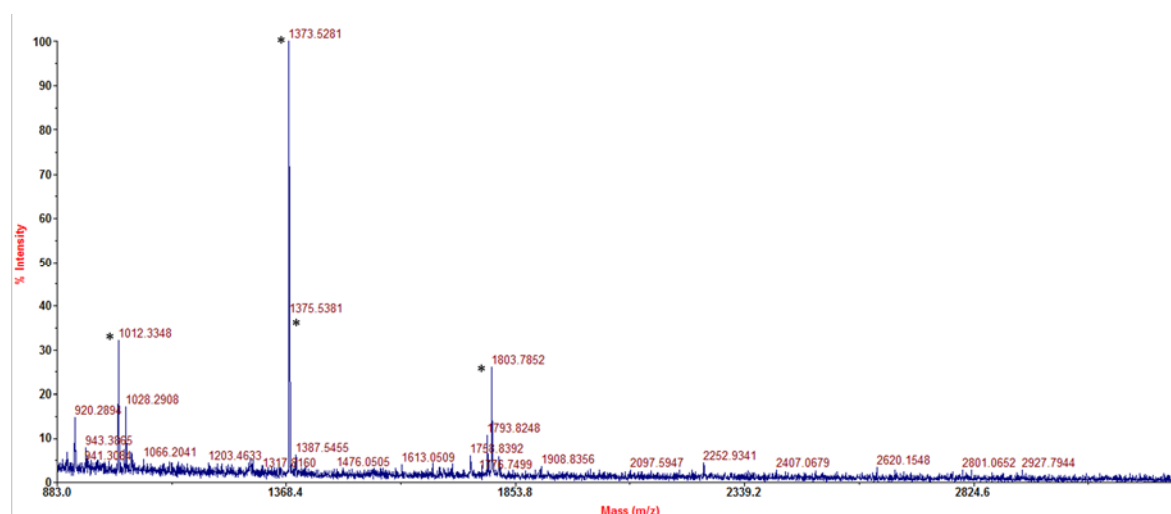
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
91 - 100	FLVVAHDDGR	1128.4240	+
202 - 217	LVARPEPATGFTLEFR	1803.8310	+
248 - 271	VGKDELFALEQSCAQVVLQAANER	2675.2530	+
380 - 389	LINRPIIVFR	1240.6170	+
390 - 398	GEHGFICR	1032.3320	+

C. Matched peptides shown in **Bold Red**

1 MTANGTAEAV QIQFGLISCG NKYLTAEEAFG FKVNASASSL KKKQIWTLEQ
 51 PPDEAGSAAV CLRSHLGPYL AADKDGNTVC EREVDPDGDCR **FLVVAHDDGR**
 101 WSLQSEAHRR YFGGTEDRLS CFAQSVSPAE KWSVHIAMHP QVNIYSVTRK
 151 RYAHLSARPA DEIAVDRDVP WGVDSLITLA FQDQRYSVQT SDHRFLRHDG
 201 **RLVARPEPAT GFTLEFR**SGK VAFRDCEGRY LAPSGPSGTL KAGKATK**VGK**
 251 **DELFALEQSC AQVVLQAANE R**NVSTRQGMD LSAHQDEETD QETFQLEIDR
 301 DTRKCAFRTH TGKYWTLTAT GGVQSTASTK NASCYFDIEW CERRITLRAS
 351 NGKFVTAKKN GQLAATVETA GDSEFLMK**L INRPIIVFRG EHGFICR**KV
 401 TGTLDANRSS YDVFQLEFND GAYNIKDSTG KYWTVGSDSS VTSSSDTPVD
 451 FFLEFCDYNK VALKVGGRYL KGDHAGVLKA CAETIDPATL WEY

A. MALDI-TOF MS spectrum (spot 12)



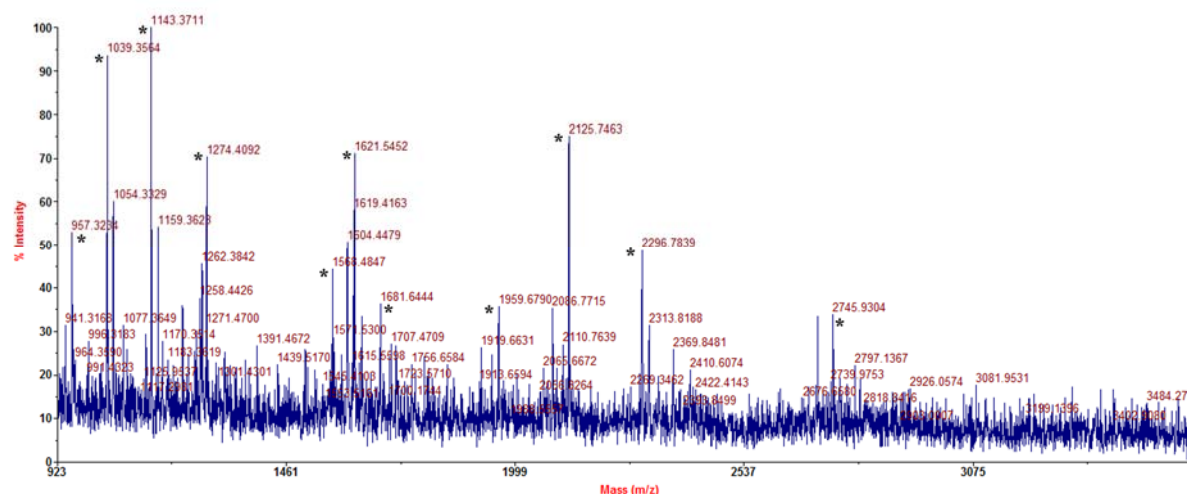
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
112 - 119	GSFPWQAK	920.3050	+
177 - 183	VVLHPER	849.3150	+
203 - 218	VMPICLPSKDYVAPGR	1802.8090	+
203 - 218	VMPICLPSKDYVAPGR	1818.7930	+
219 - 227	MGYVSGWGR	1012.3610	+
219 - 227	MGYVSGWGR	1028.3020	+
239 - 256	YVMLPVADQEKCELHYEK	2251.9250	+
321 - 332	SCAVAEYGVYVR	1373.5550	+

C. Matched peptides shown in **Bold Red**

1 MRALGAVVTLLWGQLFAVE LGNDATDIED DSCPKEPEIA NGYVEHLVRY
 51 RCRQFYKLQT EGDGIYTLNS EKQWVNPAAG DKLPKCEAVC GKPKHPVDQV
 101 QRIIGGSMDA K**GSFPWQAK**M ISRHGLTTGA TLISDQWLLT TAQNLFLNHS
 151 ENATAKDIAPI TLTYVVGKNQ LVEIEK**VVLH PER**SVVDIGL IKLKQKVLVT
 201 EK**VMPICLPS KDYVAPGRMG YVSGWGR**NVN FRFTERLK**YV MLPVADQEK**C
 251 **ELHYEK**STVP EKKGAVSPVG VQPILNKHTF CAGLTKYEED TCYGDAGSAF
 301 AVHDTEEDTW YAAGILSFDK **SCAVAEYGVY VR**ATDLKDWV QETMAKN

A. MALDI-TOF MS spectrum (spot 14)



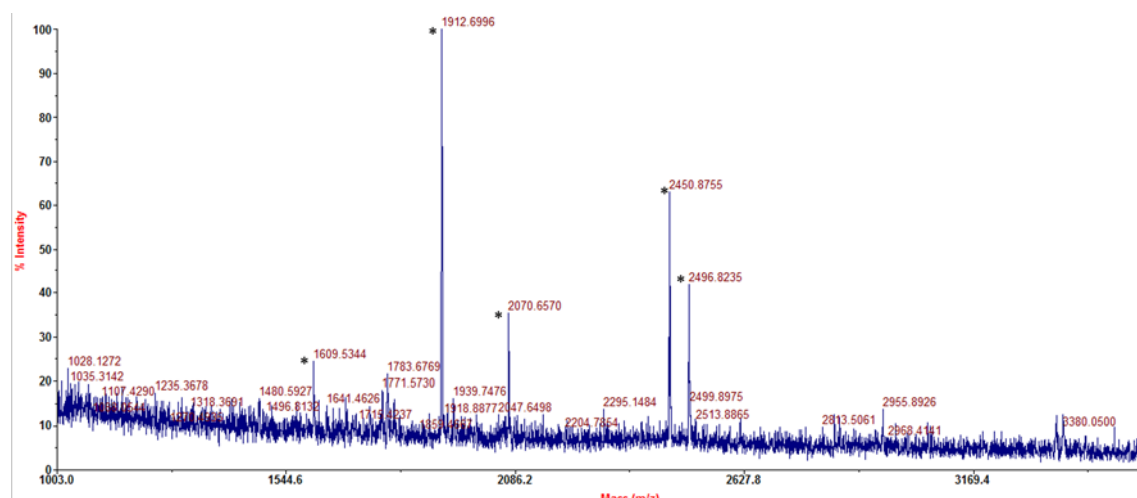
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
125 - 139	IPFNSHEGGCGAAMR	1603.4630	+
47 - 165	FPHPSQLDTLIQVSIESGR	2123.7660	+
166 - 191	MTHHHPTGYLGSLASALFTAYAVNGK	2744.9210	+
209 - 219	AYVTQSGYFVK	1262.3950	+
246 - 257	SAPVFPPKPGFVK	1273.4220	+
327 - 339	GVNPSNYEKLEYR	1568.4850	+

C. Matched peptides shown in **Bold Red**

1 MGGGLIERYV AAMVLSAAGD TLGYFNGKWE FLRDGEKIHR QLAQMGDLEA
 51 IDVAQWRVSD DTIMHLATAE ALMEAGSSPD LPQLYSLLAK HYRDCMGMDD
 101 GRAPGGACMQ NAMQLDPDRA DGWR**IPFNSH EGGCGAAMRA** MCIGLR**FPH**
 151 **SQLDTLIQVS IESGRMTHHH PTGYLGSLAS ALFTAYAVNG K**SPRQWGKGL
 201 MEVLPEAK**AY VTQSGYFVKE** NLQHSYFEK EWKYLELRG ILDGK**SAPVF**
 251 **PKPFGVK**ERD QFYIEVSYSG WGGSSGHDAP MIAYDALLAA GDSWKELAHR
 301 AFFHGGSDS TATIAGCWWG VMHGFK**GVNP SNYEKLEYRQ** RLEEAGRALY
 351 SLGSKEDTIL GP

A. MALDI-TOF MS spectrum (spot 15)



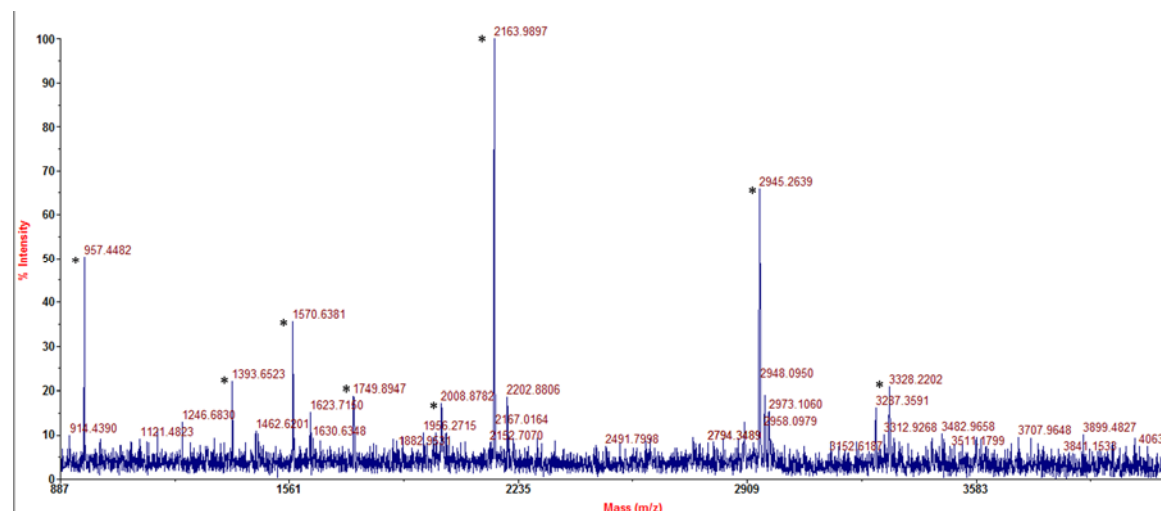
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
117 - 138	HVSSGSFPPSTNEHVKEDLNLR	2449.8590	+
174 - 190	HNIQFSSFDIFSDEEVR	2069.6540	+
174 - 194	HNIQFSSFDIFSDEEVRQGLK	2495.8360	+
268 - 292	QILEILNSTGVEYETFDILEDEEVR	2953.9430	+
268 - 296	QILEILNSTGVEYETFDILEDEEVRQGLK	3380.0590	+
297 - 310	TFSNWPTYPQLYVR	1771.6320	+

C. Matched peptides shown in **Red**

1 MAAGAAEAAE AAVAVVEVGS ARQFEELLRL KTKSLLVVHF WAPWAPQCVQ
 51 MNDVMAELAK EPHVSFVKL EAEAVPEVSE KYEISSVPTF LFFKNSQKVD
 101 RLDGAHAPEL TKKVQR**HVSS GSFPSTNEH VKEDLNLR**KL KLTHAAPCML
 151 FMKGTPQEPR CGFSKQMVEI LHK**HNIQFSS FDIFSDEEVR QGLK**TYSNWP
 201 TYPQLYVSGE LIGGLDIKE LEASEELDTI CPKAPKLEER LKVLTNKASV
 251 MLFMKGNKQE AKCGFSK**QIL EILNSTGVEY ETFDILEDEE VRQGLK**TFSN
 301 **WPTYPQLYVR** GDLVGGLDIV KELKDNGELL PILKGEN

A. MALDI-TOF MS spectrum (spot 17)



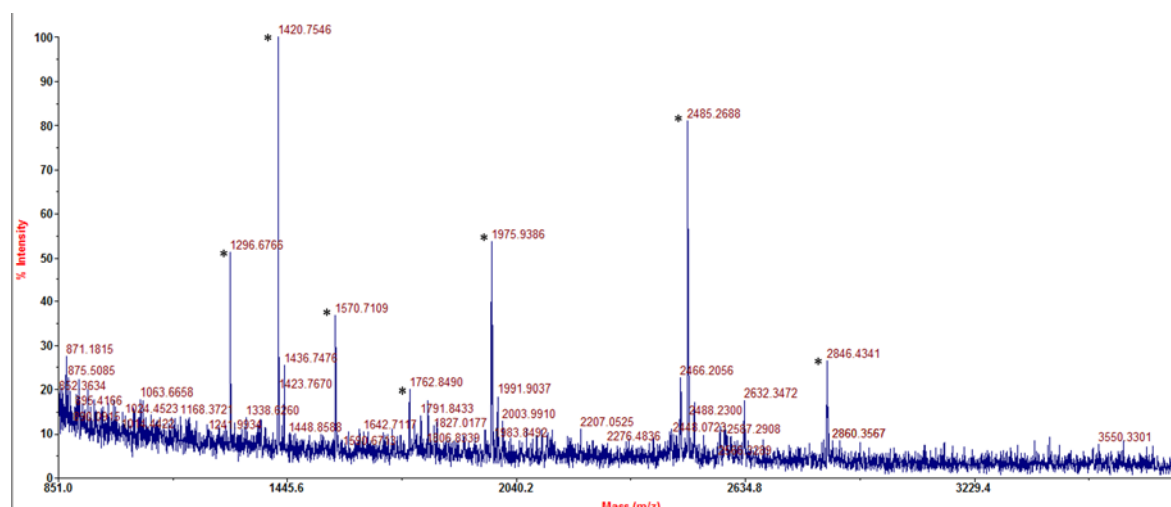
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	[M+H] ⁺	Matched
52 - 68	QVELALWDTAGQEDYDR	2008.8170	+
69 - 98	LRPLSYPD TDVILMCFSVDSPDSLENIPEK	3450.3750	+
105 - 119	HFCPNVPIILVANKK	1749.8950	+
165 - 176	EGVREVFETATR	1393.6500	+
183 - 194	YGSQNGCINCK	1460.6130	+

C. Matched peptides shown in **Bold Red**

1 MAAIRKKLVV VGDGACGKTC LLIVFSKDEF PEVYVPTVFE NYVADIEVDG
 51 **KQVELALWDT AGQEDYDR**LR PLSYPD TDVI LMCFSVDSPD **SLENIPEK**WV
 101 PEVK**HFCPNV PIILVANKK**D LRSDEHVRTE LARMKQEPVR TDDGRAMAVR
 151 IQAYDYLECS AKTK**EGVREV FETATRAALQ** KRY**GSQNGCI NCCKVL**

A. MALDI-TOF MS spectrum (spot 20)



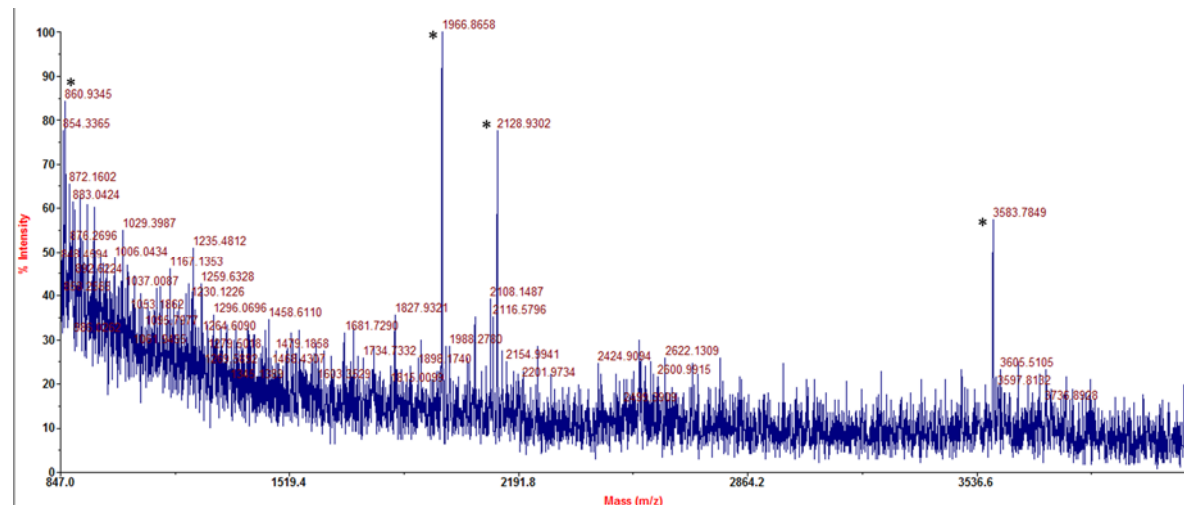
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
22 - 44	AAPAAAYDTS DTHLQILGKPVMER	2484.2640	+
22 - 44	AAPAAAYDTS DTHLQILGKPVMER	2500.2800	+
45 - 60	WETPYMHSLAAAAASR	1761.8570	+
64 - 77	VLEVGFGMAIAASR	1420.7600	+
64 - 77	VLEVGFGMAIAASR	1436.7510	+
78 - 98	VQQAPIKEHWIIECNDGVFQR	2567.3070	+
180 - 204	SKYTDITAMFEETQVPALLEAGFQR	2845.4300	+
182 - 204	YTDITAMFEETQVPALLEAGFQR	2630.3210	+
205 - 221	ENICTEVMALVPPADCR	1974.9330	+
205 - 221	ENICTEVMALVPPADCR	1990.9130	+
222 - 236	YYAFPQMITPLVTKH	1808.9350	+

C. Matched peptides shown in **Bold Red**

1 MSSSAASPLF APGEDCGPAW **RAAPAAAYDTS DTHLQILGKPVMERWETPYM**
 51 **HSLAAAAASR** GGR**VLEVGFG MAIAASRVQQ APIKEHWIIE CNDGVFQRLQ**
 101 NWALKQPHKV VPLKGLWEEE APTLPDGHFD GILYDTYPLS EETWHTHQFN
 151 FIKTHAFRLK KPGGILTYCN LTSWGELMK**S KYTDITAMFE ETQVPALLEA**
 201 **GFQRENICTE VMALVPPADC RYYAFPQMIT PLVTKH**

A. MALDI-TOF MS spectrum (spot 21)



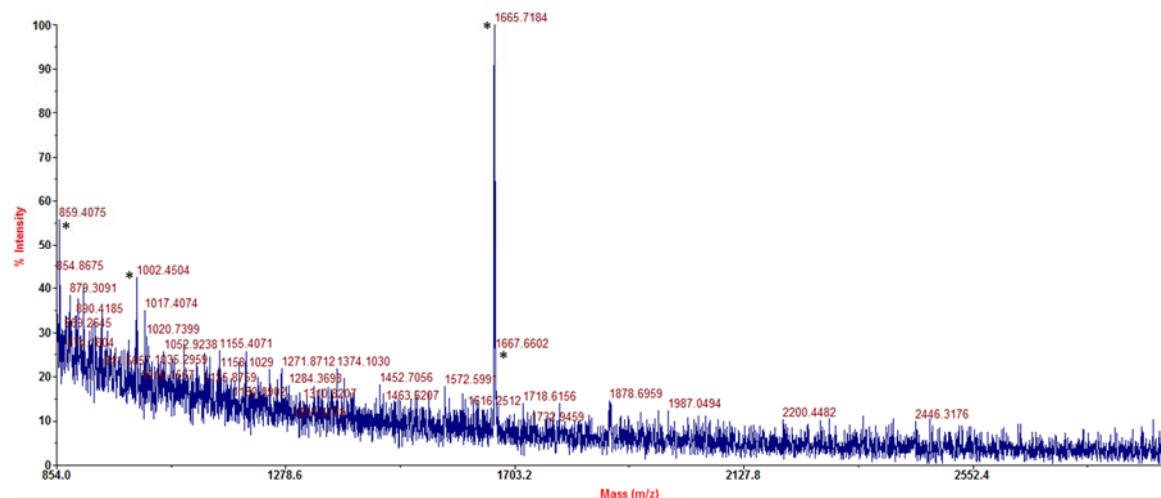
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
43 - 73	VPFALTSDSNMPEDYPDQFDDVMDFIQATIK	3581.7640	+
43 - 74	VPFALTSDSNMPEDYPDQFDDVMDFIQATIKR	3737.8640	+
115 - 137	NRGCVLTAIHLNVTDLGLGYETK	2544.3390	+

C. Matched peptides shown in **Bold Red**

1 MKLWDVVAVC LVLLHTASAF PLPAGKRLLE APAEDHSLGH RR**VPFALTSD**
51 **SNMPEDYPDQ FDDVMDFIQA TIKRLKRSPD** KQAAALPRRE RNRQAAAASP
101 ENSRGKGRRG QRGK**NRGCVL TAIHLNVTDL GLGYETKEEL** IFRYCSGSCE
151 AAETMYDKIL KNLSRSRRLT SDKVGQACCR PVAFDDDL SF LDDSLVYHIL
201 RKHSAKRGC I

A. MALDI-TOF MS spectrum (spot 22)



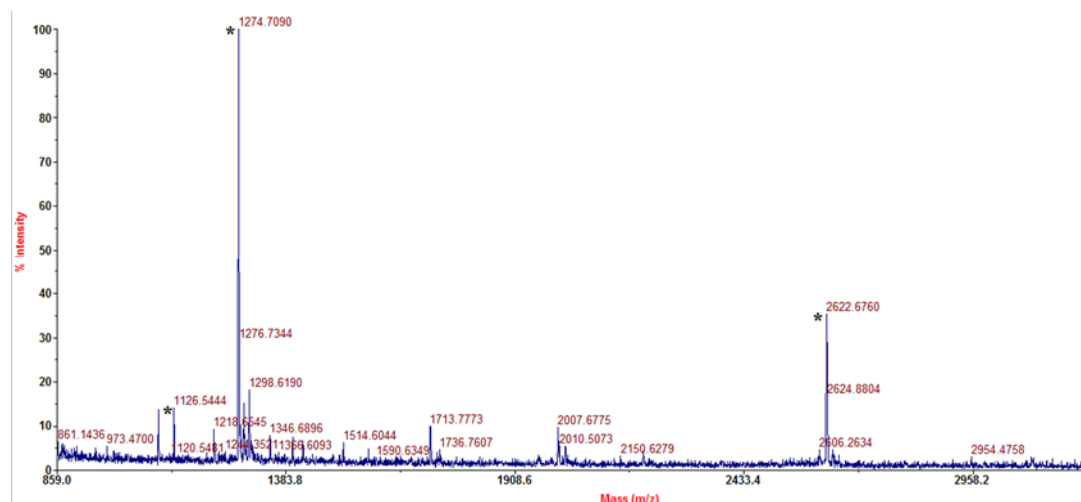
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
12 - 25	SISTIINVFHQYSR	1664.6990	+
45 - 52	DLPNFLKR	1002.4170	+
87 - 94	LIFACHEK	1017.3830	+
87 - 101	LIFACHEKLHENNPR	1877.7230	+
95 - 101	LHENNPR	879.2710	+

C. Matched peptides shown in **Bold Red**

1 MAAKTGSQLE R**SISTIINVF HQYSR**KYGHP DTLNKAEFKE MVNK**DLPNFL**
51 **KRE**KRNENLL RDIMEDLDTN QDNQLSFEEC MMLMGK**LIFA CHEKLHENNP**
101 **R**GHDSHSGKG CGK

A. MALDI-TOF MS spectrum (spot 23)



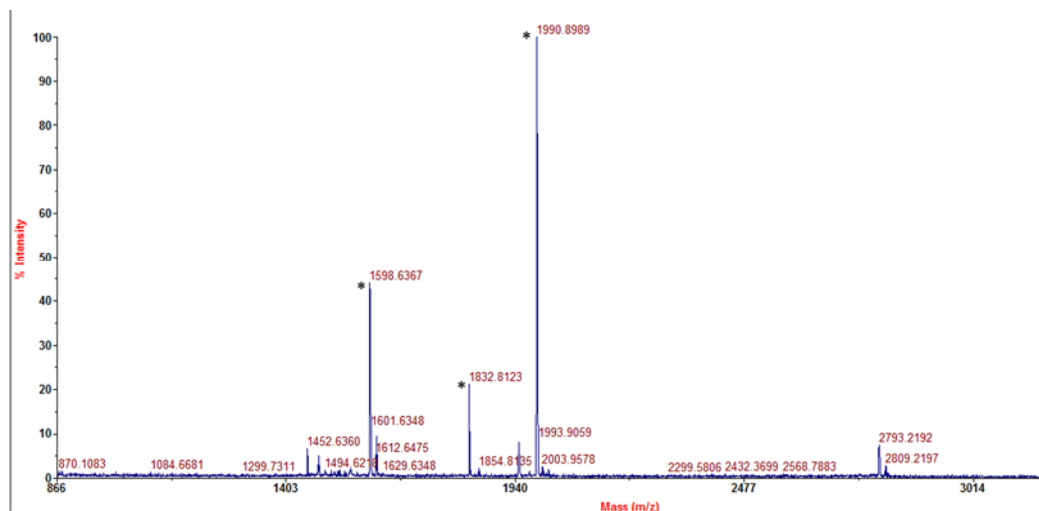
B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
19 - 31	VNPDDVGGEALGR	1298.6220	+
32 - 41	LLVVYPWTQR	1274.7280	+
42 - 60	YFDSFGDLSSASAIMGNPK	2006.6910	+
42 - 60	YFDSFGDLSSASAIMGNPK	2022.6260	+
67 - 77	KVINAFNDGLK	1218.6790	+
68 - 77	VINAFNDGLK	1090.6130	+
84 - 96	GTF AHLSELHCDK	1514.6160	+
84 - 105	GTF AHLSELHCDKLHVDPENFR	2621.8500	+
97 - 105	LHVDPENFR	1126.5620	+
106 - 121	LLGNMIVIVLGHHLGK	1713.9140	+
106 - 121	LLGNMIVIVLGHHLGK	1729.8850	+
106 - 133	LLGNMIVIVLGHHLGKEFTPCAQA AFQK	3092.3530	+
122 - 133	EFTPCAQA AFQK	1397.6320	+
134 - 147	VVAGVASALAHKYH	1422.7250	

C. Matched peptides shown in **Bold Red**

1 MVHLTDAEKA AVNGLWGK**VN PDDVGGEALG RLLVVYPWTQ RYFDSFGDLS**
 51 **SASAIMGNPK** VKAHGK**KVIN AFNDGLK**HLD NLK**GTF A**HL**S ELHCDKLHVD**
 101 **PENFRLLGNM IVIVLGHHLG KEFTPCAQA A** **FQKV**VAGVAS ALAHKYH

A. MALDI-TOF MS spectrum (spot 25)



B. Peptides detected by MALDI-TOF-MS

Peptide	Amino acid sequence	$[M+H]^+$	Matched
2 - 19	VNPTVFFDITADGEPLGR	1947.8990	+
20 - 31	VCFELFADKVPK	1452.6270	+
56 - 69	IIPGFMCQGGDFTR	1598.6380	+
77 - 91	SIYGEKFEDENFILK	1831.8070	+
92 - 118	HTGPGILSMANAGPNTNGSQFFICTAK	2807.2400	+
119 - 131	TEWLDGKHVVFGK	1515.6910	+
132 - 144	VKEGMSIVEAMER	1478.6100	+
132 - 144	VKEGMSIVEAMER	1494.6200	+
134 - 144	EGMSIVEAMER	1251.4420	+
155 - 164	KITISDCGQL	1134.4300	+

C. Matched peptides shown in **Bold Red**

1 M**VNPTVFFDI TADGEPLGRV C**FELFADKVP **K**TAENFRALS TGEKGFGYKG
 51 SSFHR**IIPGF MCQGGDFTR**H NGTGGK**SIYG EK**FEDENFIL **KHTGPGILSM**
 101 **ANAGPNTNGS QFFICTAKTE WLDGKHVVFG KVKEGMSIVE AMER**FGSRNG
 151 KTSK**KITISD CGQL**